>CDK02609.1 TPA: proteolysis tag peptide encoded by tmRNA Campy\_jejun\_81116, partial [Campylobacter jejuni subsp. jejuni 81116]

ANNVKFAPAYAKAA

>CDI30471.1 TPA: proteolysis tag peptide encoded by tmRNA Campy\_jejun\_81116, partial [Campylobacter jejuni subsp. jejuni 81116]

ANNVKFAPAYAKAA

>ABV53227.1 crossover junction endodeoxyribonuclease RuvC [Campylobacter jejuni subsp. jejuni 81116]

MKILGIDPGSRNCGYAIIEANKGKNILIEAGLIKIKPNTLQYQITELCEGLDLIFKNHSFDEVAIEDIFF

AYNPKTVLKLAQFRGALSLKILQIHGDFAEYTPLQVKKAVTGKAKATKEQVAFMVKRLLGLSKDIKPLDI

TDAIAVALTHAANLRVRV

>ABV53226.1 hypothetical protein C8J\_1629 [Campylobacter jejuni subsp. jejuni 81116]

MMRSLWSGVSGLQAHQVAMDVEGNNISNVNTTGFKYSRADFGTMFSQTVKIATAPTDGRGGSNPLQIGLG

VSVSSTTRIHSQGSVQTTDKNTDVAINGDGFFMVSDDGGLTNYLTRSGDFKLDAYGNFVNNAGFVVQGWN

INWDDQTIDSSRTPQNIFIDPGMHIPAAKSTEVAIKANLNSGLNIGTSSRNLYALDSVHGWNTKTQRAED

ENDTGTTQFYTTSKNSVEVTEKGVDAGALFNANGTGLNLRDGQGIWVSYADAKFTTDRANGANVFDPNLT

VAQQNNVIFWGNKDIAVTLDINLNGVRIQNDNIRSLDEAIAYINTFTAPTDTRDGTGVKAVKKADGSGIE

FVNNNADGTTDNMKNIDLTVNVGNSAGERNTINYNANTGVFSPQGGNLTTAQNDTDWIAGAAQAGQPQNV

KVVTAHKYIYSSNPVTIPPMINPDGGPAFQPNNGNRPTDPASANYWDAIQGSLKNTTERTFRTTEDLREL

LQRDARYGVDYNGSGIIDNATPTFDANDINQAVKVVVTENGNFAISNANETSTIPANAGAGAGAATTNPK

NMSFNITAYSNKQGTVSTNDAFTKIFKAFDGPLVIGNQIKESEQLKLSAFSAGLEIYDSLGSKHTLEVQF

VKQSTTQDGGNEWQMIIRVPEPAEINTTGEGPTNIIVGTARFNNDGSLANYTPKTINFSPNNGAAPNQQI

KLSFGTSGSNDGLVSSNSASTLTGQATDGYTSGNLKPDAIRVDDKGNILGEFTNGKTFAVAKIAMASVAN

NSGLEEIGGNLFKVTANSGNIVVGEAGTGGRGEMKTSALEMSNVDLSRSLTELIIIQRGYQANSKTISTS

DQMLQTLIQLKQ

>ABV53225.1 hypothetical protein C8J\_1628 [Campylobacter jejuni subsp. jejuni 81116]

MRYGEKEIKEFDVENMEIWPNDAKNDYIIKITLPEFMCCCPRSGYPDFATIYLEYMPDKFVVELKAIKLY

INTFMYRNVSHEASINEIYNTLKDKLKPKWIKVVGDFNPRGNVHTVIECCSDMVVPK

>ABV53224.1 hypothetical protein C8J\_1627 [Campylobacter jejuni subsp. jejuni 81116]

MNKKLLSIIASTTLFSNLALADENSGFFIGTDAAWMHAQVKSELKHKNTKRNFNGDISGNIPSFGLKLGY

RLNENHRIYAGYNYSDEFSDFIKTPKIQIEGDFTTHKFFTGYDFTPKLFEKTRAVLGVYGGYARTDLTLK

TSFLSLSQNFDGYFYGAKIGALYDLTPHNEIELGFKAEQIHYNSRNFYQNKVGSNFYDPKQTNYGVYLGY

NYKF

>ABV53223.1 hypothetical protein C8J\_1626 [Campylobacter jejuni subsp. jejuni 81116]

MLKELLEIKKEMEPVIHEANVKLNVLAREVIVRKKEYEIYGPMVDRVYLDNAIYVKVMSSGRDVKTDNVT

IKNGFYMVFVAPEKESTKDIKNKLKVAYEGLDNKFIATLIRSCQRFKEIINKTQATLAKASKMNVVVKTN

LGEASAALKFNITIEYTKENQKLTRENSKSAGSFRDTKTYINLVVEKNTESQICEKLLDDVEKYFIGGG

>ABV53222.1 2-isopropylmalate synthase [Campylobacter jejuni subsp. jejuni 81116]

MKDNKIIIFDTTLRDGEQALGSSLGINQKLQIALALENLGVDVIEAGFPVSSQGDFKAVQKIASKVKNST

ICALSRVLDKDIDMAYEALKVAKHFRIHTFIATSTLHMQDKLKKDFDEILSMAKRAIIRARSYTDDVEFS

CEDAGRTPIDNLCFMVENAIKAGAKTINIPDTVGYTLPSEFANIIKILFNKVPNIDKAIISVHCHNDLGM

ATGNSLSAILQGARQIECTINGLGERAGNCALEEVVMAIKTRKDYLKGFYTDIKCENIFKTSKLVSAITN

ESIPSHKAIVGSNAFSHSSGIHQDGVLKNRQTYEIISPSAIGIHENRMLMTARSGRAMIKTCLENLGYDE

NTYNLDDVYERFLRLADKKGQVYDYDLEALMFLSYENEEENKFILEKLSVISGNIPTACVCMRIKEELKT

EACTGNGPVEAVFNCIARITNLKPALKAYSINAKSSGVDAQGQVDVDLEFKGRKFHGKGISTDVIEASAQ

AFVSAYNAIYRSLKVEERKMA

>ABV53221.1 3-isopropylmalate dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MKTYKVAVLAGDGIGPLVMKEALKILTFIAQKYNFSFEFNEAKIGGASIDAHGVALSDETLKLCEQSDAI

LFGSVGGPKWDNLPIDQRPERASLLPLRKHFNLFANLRPCKIYESLTHTSPLKNEIIQKGVDILCVRELT

GGIYFGKQDLGKESAYDTEIYTKKEIERIAHIAFESARIRKKKVHLIDKANVLASSILWREVVANVAKDY

QDINLEYMYVDNAAMQIVKNPSIFDVMLCSNLFGDILSDELAAINGSLGLLSSASLNDKGFGLYEPAGGS

APDIAHLNIANPIAQILSAALMLKYSFKEEQAAQDIENAISLALAQGKMTKDLNAKSYLNTDEMGDCILE

ILKENDNG

>ABV53220.1 3-isopropylmalate dehydratase, large subunit [Campylobacter jejuni subsp. jejuni 81116]

MAKTLYEKVFDAHVVYEGKNELPILYIDRHLIHEVTSPQAFSGLKMAKRRMARADLTLATIDHDVSTKSI

DLNACSDMAKEQITTLMQNTKEFGVRLLGLGDKNQGIVHIVGPELGFTLPGVTLVCGDSHTATHGAFGAL

AFGIGTSEVEHVMATQTLKQAKLKTMKIECKGQFQKGVYAKDLILYLIAQYGTAKGTGYAIEFCGELIRK

LSMEARMTLCNMAIEFGAKVGMIAPDEITFEYIKGKEFAPKGEEFQKYCEYWKSLRSDEGAKYDESITLD

VSKIKPQISYGTNPSQVIGIDEKIPKISDFKNQSEQKSLLDALSYVNLEQDQVIEGVKIDIVFIGSCTNG

RLEDLKIAADILKGHKIHKNVKALIVPGSMQVRKEAENLGLDKIFIEAGCEWRYAGCSMCLGMNDDKANS

GQRVASTSNRNFVGRQGKGSITHLMSPASAAACAIEGVICDNRKYLGV

>ABV53219.1 3-isopropylmalate dehydratase small subunit [Campylobacter jejuni subsp. jejuni 81116]

MQKFIIHKGIACPLEYANIDTDQIIPKQFLLAVSKQGFGKHLFHDLRYLDDKESVLNMDFNLNKKEYQNS

SILVSFENFGSGSSREHAPWALVDYGIRAIIAPSFADIFKNNALGNGLLTIELAKDEVLEIVDELKKSQD

KNIEISLLEKRVFFKDKIFSFDLDDFHRICLLEGLDNIALTLKHEAQIKAYEKNSKSFLV

>ABV53218.1 putative acetyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MQNTIIQKAVNKDLNSILEITKDALNAMKTMNFHQWDENYPNEIVFQEDIQAQELYVFKENDEILGFICI

NEKFEPEFYKQVIFNKNYDDKAFYLHRLAVKQNAKGKGVAQKLLNFCENFALENHKASLRADTHSKNFPM

NSLFKKLDFNFCGNFDIPNYQDPFLAYEKILNQKAF

>ABV53217.1 hypothetical protein C8J\_1620 [Campylobacter jejuni subsp. jejuni 81116]

MKYKFIISLEGNDVASNLKWAMNSNSLVLAPKITCETWFMEGTLKPNYHFALIDNENLSAVIEYFKSRPK

DALEIINNAHQYIKKFLDKKKEFHIGILVLTKYFYYSRQLELNKKRDILELIK

>ABV53216.1 hypothetical protein C8J\_1619 [Campylobacter jejuni subsp. jejuni 81116]

MLNTTKLLENKLFQERYIKPNIDWYFSYLNGKRGMSRIYKTPYAILMKKFFLQKYFEKRIKKRIIDIPYL

ELVLTTKCTMRCQSCNNLMQYFSQNNQYTCTFEGIKKSLEILLSKVDSIARIRIIGGEPLLFKDLPKLID

YLNCQKKILTFSLVTNGTIDFKDELINKLKHSKKVRKITISNYKNSPNLKIPLKQEDIIKKLIKNKIPYS

LDSNKENSTWFDPEKIYKRGRNKEEIIKNYYYCKMPCVSLMTSEGENLKGKELASNGAIFVCPVSSSLSR

LKGLNEFEGDFLNLDDNIEKFFEFYIKDFYKACDYCRDFSKPYKRIPIAIQTNKTLKLEKED

>ABV53215.1 hypothetical protein C8J\_1618 [Campylobacter jejuni subsp. jejuni 81116]

MTMLDIFEIVFITAVVIIGFFGIIYFLNKER

>ABV53214.1 hypothetical protein C8J\_1617 [Campylobacter jejuni subsp. jejuni 81116]

MKELVNILDFLPEELGEKIKPMFRVKQIYQWIYQKYANNFSDMSSLPKYLRLELAQNFHFSPVKCVKNEQ

SKDGSIKYLFELVDGLRVESVLLPMKEEKIDAEGKRISHARYTICVSSQVGCKSGCSFCLTAKGGLKRNL

SAGEIVGQILWIKKQNNIPYERRVNIVYMGMGEPLDNLKNVSKAVKILAQNDGLAISPRRQTISTSGLAK

QIKELGQMNLGVLLAISLHAVNDGLRTELMPINKAYNIAAIMDAVREFPIDQRKRVMFEYLLIDGINDKL

EHAKELVKLLNGIKAKVNLILFNPHEGSLYKRPSLENAIKFQDLLSSKGVTCTIRESKGLDISAACGQLK

ERAKEQ

>ABV53213.1 hypothetical protein C8J\_1616 [Campylobacter jejuni subsp. jejuni 81116]

MIVCAGGNENFSFAKAIGIGLVESAFHLGQLCFKEKPSKLIFIGTCGLYDKGKILEIYKSSHAFNVEFSK

ISHAFYTPAKYEIYLEKENVSRETIKINSSNYICQNSKAAKEFSKLGFFAENMEAFSVLSVAKNLNIDAE

CILCATNFCNENAHEDFIKNHQKAKEKLEEYLKKYHYI

>ABV53212.1 dimethyladenosine transferase [Campylobacter jejuni subsp. jejuni 81116]

MVKAKKQYGQNFLIDKSVLAKIIQAIPKEMNNIIEIGPGLGDLTQELLKISQVKAYEIDNDLIPILKKKF

QKELECGKFNLIHQDASEAFNPSLDEKPYFLVANLPYYVASHIILKALEDKNCLGLIVMVQREMAEKFCA

KEGNSEFSSLGVLSAMICERKMLFDVDPQCFNPPPKVMSAVMSLIKTKDFDELCEIENFKNFLKDCFKAP

RKQLLGNLKTYKAKVLEVLSTLGLKENIRPHEICVDSYLKIYDKLKDEYGRKQRDK

>ABV53211.1 hypothetical protein C8J\_1614 [Campylobacter jejuni subsp. jejuni 81116]

MDENKEINKNEQNPNSNSKNNKRYKYKNRRKKLADSLQNENDTPKIDQNSNKEISENSENKTEKKKKKNR

NLPSKLTGNEDWQIALAECIEANRVSHENRLHPLKYNNSSEHKIRITPLGGLGEIGGNISVFETNKDAII

VDIGMSFPDGTMHGVDIIIPDFDYVRKIKDKIRGIVITHAHEDHIGAVPYFFKEFQFPIYATPLALGMIS

NKFEEHGLKAERKWFRPVEKRRVYEIGEFDIEWIHITHSIIDASALAIKTKAGTIIHTGDFKIDQTPIDG

YPTDLGRLAHYGEEGVLCLLSDSTNSYKEGYTKSESSVGPTFDQIFSRTKGRVIMSTFSSNIHRVYQAIT

YGLKYGRKVCVIGRSMERNLYTTMELGYIKLDRKIFIDADEVSKYKDNEVLIVTTGSQGETMSALYRMAT

DEHKFIKIKPTDQVIISAKAIPGNEASVSAVLDYLLKAGAKVAYQEFSEIHVSGHASIEEQKLMLTLTKP

KFFLPVHGEYNHITKHKETAMKCGIPERNIYLMSDGDQVELCQKYVKRIKTVKTGKVFVDNQINKQIADD

VVIDRQKLADSGIVVIIAQIDKTTKTLINKPRVFSYGLVADKHDHAFSKDMAEVLGQFFINVKDEVLNDP

RFLENQIRQVLRKHIFRKIKKYPTIVPTIFVM

>ABV53210.1 putative ribosomal pseudouridine synthase [Campylobacter jejuni subsp. jejuni 81116]

MRINKFISHNTRYSRREADELIKQGLVKINNKIALLSDEVKFDDKVFVKGKRVQKRTQFSVIIYHKQKGE

IVSKKDDRGRKTIYDTLPRQFSTWLSVGRLDYASEGLLLLTDSPVIADALMHSDLEREYYLKVKGTVSKQ

VIEAMQNGLEIKNEKKGAHAKTKITSMSFAPFIDFEIFGSSGGYTKLRVVINEGKNRELRRFFGHFDLEV

MDLKRVAFGALDLGMLKAGKHRYLENGEYEKLRDFLKFNEIRY

>ABV53209.1 30S ribosomal protein S10 [Campylobacter jejuni subsp. jejuni 81116]

MERIRLKLKAYDHRVLDRTVAAIVEAVKRTGADIRGPIPMPTKIKRYTVLKSPHINKDSREQFEIRIHAR

MLDIVAATPDTVDSLTKLDLAPEVSVEVRAMGK

>ABV53208.1 50S ribosomal protein L3 [Campylobacter jejuni subsp. jejuni 81116]

MEYIVEKIGMSRTITNPSIAVTLLRVVNAKVCEVEGGKALVAYPKGKASNKCVAGQQKKYNLSAEYNRFA

TLEVANTEAGDLDETPLNEAKILKVSFNTKGRGYSGVMKRHNFAGGPASHGSRFHRRHGSIGNREWPGRV

QPGMKMAGHYGNTKVTVKNEVVSYDAENKILVVKGAVPGYNGAMGKIRIAK

>ABV53207.1 ribosomal protein L4 [Campylobacter jejuni subsp. jejuni 81116]

MSKVVVLNDKLEKAGELDLPSKYAEVNPHNLYLYVKSYLASLRANTAHTKGRSDVSGGGKKPWRQKGRGG

ARAGSTRTNVWVGGAVAFGPTNERNYFQKVNKKQKRLALERALADKAAKGALFTADSLAIESGKTKDANA

VIKKLGVKDALIVKDLLDEKTLLAYRNLANCYVVDVSEVNAYLVSVFNAVIIEKSALESITKEG

>ABV53206.1 50S ribosomal protein L23 [Campylobacter jejuni subsp. jejuni 81116]

MADITDIKTILYTEKSLNLQEQGVVVIQTSPKMTKTGLKAVLKEYFGVTPKSINSLRMDGKVKRFRGRLG

QRNDYKKFYVKLPEGVSLENTEA

>ABV53205.1 50S ribosomal protein L2 [Campylobacter jejuni subsp. jejuni 81116]

MAIKTYKPYTPSRRYITGLSSEDITAKPSVRSLLVKLPAHAGRNSYGRITSRHKEAGAKKLYRIIDFKRR

KFGIEGKVEAIEYDPYRNCRIALIAYKDGEKRYILQPRGLSVGDIVAAAESGLDIKPGNAMKLKNIPVGT

IVHNVELKPGKGGQMIRSAGAYAQLMGKEEKYVILRLASGEMRQVLAECMASIGEVGNEEWANVTIGKAG

RNRHRGIRPQTRGSAMNPVDHPHGGGEGKKNSGRHPVTPWGKPTKGAKTRRKKASDKLIISRRKGK

>ABV53204.1 30S ribosomal protein S19 [Campylobacter jejuni subsp. jejuni 81116]

MARSLKKGPFVDDHVMKKVIAAKKANDNKPIKTWSRRSTITPDMIGLTFNVHNGKSFIPVYITENHIGYK

LGEFAPTRTFKGHKGSVQKKIGK

>ABV53203.1 hypothetical protein C8J\_1606 [Campylobacter jejuni subsp. jejuni 81116]

MSKALIKFIRLSPTKARLIAREVQGMNAELAMASLKFMPNKGAKYIANAISSAVANGGFEANEVIVKSCR

VDAAAVLKRFRPRARGSASRIRKPTSHILVEVAKAEVKAEEKKTVAKKAPAAKKTTTTKAPAKKTTSTKK

ATAKKES

>ABV53202.1 30S ribosomal protein S3 [Campylobacter jejuni subsp. jejuni 81116]

MGQKVNPIGLRLGINRNWESRWFPTKANLVENIGEDYKIRAFLKRKLYYAGISQILVERTAKKLRVTVVA

ARPGIIIGKKGSDVDNLRKELQDLIGKDVNINIKEERKAGASAQLAAESVATQLEKRIAFRRAMKKVIQG

AQKAGAKGIKVSVSGRLGGAEMARTEWYLEGRVPLHTLRAKIDYGFAEARTTYGNIGVKVWIFKGEVLHK

GMQPEKTEESAPAKKPRRTRRGK

>ABV53201.1 50S ribosomal protein L16 [Campylobacter jejuni subsp. jejuni 81116]

MLMPKRTKYRKMMKGRNRGYANRGTEFTFGEFALKATEAGRINSRQIEAARIALTRFVKRQGKTWIRVFP

DKPLTKKPLETRMGKGKGAVEEWVMNIKPGRIIYEMAGVSEEMAREALTLAMHKLPFKTKFVTRESQNEI

Y

>ABV53200.1 50S ribosomal protein L29 [Campylobacter jejuni subsp. jejuni 81116]

MKYTEIKDKTAAELATMLKEKKVLLFTLKQKLKTMQLTNPKEISQVKKDIARINTAINALR

>ABV53199.1 30S ribosomal protein S17 [Campylobacter jejuni subsp. jejuni 81116]

MAFKREIQGVVVKIAGEKTASVLVERKVVHPRYRKIVKRFKKYLIHDERNEVKVGDTVVAVECRPLSKRK

SFRLKSVLATGVE

>ABV53198.1 50S ribosomal protein L14 [Campylobacter jejuni subsp. jejuni 81116]

MIQSFTRLAVADNSGAKELMCIKVLGGSKRRYATVGDVIVASVKKALPNGKVKKGQVVKAVIVRTKKEIH

RDNGSLIRFDENAAVILDNKREPIGTRIFGPVGREVRYGGFMKIVSLAPEVL

>ABV53197.1 50S ribosomal protein L24 [Campylobacter jejuni subsp. jejuni 81116]

MAVKLKIKKGDSVKVITGDDKGKTGKVLAVYPKTLKVVVEGCKIAKKAIKPSEKNPNGGFINKEMPMDIS

NVAKVQE

>ABV53196.1 50S ribosomal protein L5 [Campylobacter jejuni subsp. jejuni 81116]

MMRLKEKYNQSIKPALVKEFDIKNPMLIPVIEKVVISVGAGELAKDQKVLQNVADTISLIAGQKAVITKA

KKSVAGFKVREGFPVGVMVTLRKENMYAFLDKLISIALPRVKDFRGLSRDGFDGRGNYNFGLDEQLMFPE

VEYDKILRTHGMNISIVTTAQNDKQAQKLLELIGVPFTKGK

>ABV53195.1 30S ribosomal protein S14 [Campylobacter jejuni subsp. jejuni 81116]

MAKKSMIAKAARKPKFKVRAYTRCQICGRPHSVYRDFGICRVCLRKMGNEGLIPGLKKASW

>ABV53194.1 30S ribosomal protein S8 [Campylobacter jejuni subsp. jejuni 81116]

MINDIISDSLTRIRNAGMRKLETTKLLHSKVVEALVGIFQAKGYIESFNVIEEDKKKFINVVLKYDEKGK

SVINELKRISKPGRRVYKGKDEIKRFKNGYGTIVVSTSHGVLANDEAYKAGVGGEILCTIW

>ABV53193.1 50S ribosomal protein L6 [Campylobacter jejuni subsp. jejuni 81116]

MSRIGKQPIAIPAGVEVKLEGNLLKFKKGNLAKELDTKANVNVEIKDNNILFSPKGEDRQSRAYWGTYRA

LAYNIVVGLTQGFSKTLEINGVGYKAALKGKVLELSLGFSHPINYDIPEGIEIVVDKNTIAVKGSDKQVV

GQVAAQIREFRPPEPYKGKGVKYSDERIIRKAGKTSKK

>ABV53192.1 ribosomal protein L18 [Campylobacter jejuni subsp. jejuni 81116]

MRANVLKRKLTLRIKRKKRIRAKISGCENFPRISVFKSNRTLYIQAIDDVKAVTLAAVDGRKLGVKANKE

GAKKIAAEFAKTLKAKKIEQAVFDRNGYVYHGVIAALAESLRENGIRL

>ABV53191.1 30S ribosomal protein S5 [Campylobacter jejuni subsp. jejuni 81116]

MEKYNREEFEEVIVDIGRVTKVVKGGRRFRFTALVIVGNRKGLVGVGYGKAKEVPDAIRKAVDDAFKNIV

EVKTKGSTIAHDVEVKYNASRILLKPASEGTGVIAGGSTRPIVELAGIKDILTKSLGSNNSANVVRATIK

ALTMLKG

>ABV53190.1 50S ribosomal protein L15 [Campylobacter jejuni subsp. jejuni 81116]

MNLTKAAGSTHKTKRIGRGQGSGMGKTATKGGKGQTARKGYNEKRGFEGGQQPLQRRLPKVGFTSKIQKP

YVINVEKITAVKELSEITFDSIKSVHKISKSVNKIKLIGASAKDLVSKIKDENISVTGSK

>ABV53189.1 preprotein translocase secY subunit [Campylobacter jejuni subsp. jejuni 81116]

MNRALTNKILITLAFLFAYRVLAYVPVPGVNADVIAEFFNNNQNNALGLFNVFSGGAAERFSIISLGIMP

YITASIIMELLAATFPNIGKMKKERDSMQKYMQIIRYATIVITLVQSIGVAIGLQSLHGRGGAGAIMVED

LNMFIALCAISMLAGTMLLMWLGEQITQRGIGNGISLIIFAGIVSGIPRAISGTVGQINSGEMNFLTAFA

IFALILITIGVIIYVELGERRIPISYSRKVVMQNQNKRIMNYIPIKLNLSGVIPPIFASAILMFPTTILQ

TSTNPYLQAINDFLNPNGYLFHVLTFLFVIFFAYFYASIVFNAKDIAENLKKQGGFIPGIRPGEGTSSYL

NEVASRLTLSGSIYLGLVATLPWVLVKFMGVPFHFGGTSVLIVVQVALDTMRKIEAQIYMSKYQTLSAVG

L

>ABV53188.1 hypothetical protein C8J\_1591 [Campylobacter jejuni subsp. jejuni 81116]

MKFIHLTDIHYGDKKEAIYSREPSAMMRLAIEDINKNHSDADFVFITGDLTHKGSLESYTLLKQDLTKLN

MPYYLILGNHDDRANALEIFNNLKQDENGFIQYEIQCNDNNVFLVLDTIKLKSHGGEYCQKRQIWLKNAL

ERNQNKNIFICLHHAPFKTGLRAMDFIGLDEKHSLELYKLFNSYKNIKHLFFGHYHSTLCGRWKDISFSS

LKGINHQVKFDLNSNEILLEFRNPEYAVVLLNNEVLNIHYNDFTFDKNLIFHEK

>ABV53187.1 hypothetical protein C8J\_1590 [Campylobacter jejuni subsp. jejuni 81116]

MIFFDFDGVLVDSLKLWEQACQFSAKKLGFKGIFPQKPYAKLNPVAHKEIGRILGFNPLEFEKIADEYFL

EHIHTLVFFDKTKELLKDLSLDFKLSILSASNENLVRILLEKEQILKYFTNLHCTSSIPKAQTLKKFKQN

HSIMIGDCISDIEAALEADVYSIGVLWGWQDKIMLEKANILVNNHAQLKNAIRSFYEIHPFN

>ABV53186.1 hypothetical protein C8J\_1589 [Campylobacter jejuni subsp. jejuni 81116]

MVNKNIPKDLTQNLINKKELGFNDNAFKATTLENKIYAIPFASSLPVVYYNMDLVKQAEWNKELPKTWDE

LFDLAQKINSLNGKSGVYFGETDTWLILALSLERGGKLINEKGKVDFNNKAWQETFKLLSDFHTLAKMPA

IKRSEAISSFYAGNLGILIQTSAALTQTEKSINFPLKLSKFPGVQSGGELPVGGSVVMLTNDKNKEAALK

YIHFVTGEANAYVPQYTGYMTSNLLANAKLKDFYNKNPNYTIAPSQIELMGNWPSFPGDNALKATNTLWN

YAEKLLMGTSTNYEEIAKQAQEEINALLP

>ABV53185.1 hypothetical protein C8J\_1588 [Campylobacter jejuni subsp. jejuni 81116]

MKKIFFTLALFGALNLAQAKTELVVSYAYPWFKDLHEKLKEDFEKQNPDIEIRFLAPAQNYEEQSARLLR

EKMINKFPDVSFNSYSYYLHW

>ABV53184.1 hypothetical protein C8J\_1587 [Campylobacter jejuni subsp. jejuni 81116]

MFRILRHLILGILSLFFIFPFVWMVITSFKPENEIFSNAFHFFPQNFTLIENYTKAFKENDLLHFLFNGF

FVCFAILLIQIIIAYPCAYALSKYKFKGQKFLLVIIVCSLLIPTQAICVPWYILMYYFGVLDSYLALILP

FSISVFGIFLIRQFINCIPNDIIYAARMDGLNEFSILCKIILPLTTPALISFGIFSIVAHWNDYFWPLIA

VSSPQYFTPTLGVISFKNNEAGTDYGTLMAASTIVVAPLIIGFLLAQKRFIQGIANTGIK

>ABV53183.1 hypothetical protein C8J\_1586 [Campylobacter jejuni subsp. jejuni 81116]

MKNSLATFCFISPAVLLMLLFLILPIIWVIILSFSDYQLGNGDFHFVGLINYKALLKDPVFFTSVKNTLI

YALIVLPLSVLGGLALALLIESKNSAKSFYRAVFFLPVMATLIAMSMVWEYILHPDIGIFNKILALFGVN

TINWLSNKDTVLYTLAGIGVWQQLGYNMILFTAGLMSIPTSVYEAAKLDGLNKTQILFKITLPLLLPILF

FVLIISSIKAFQVFDTVQVLTNGGPNHSSEVLLFTIYQEAFMFFRTNYASAISVIFLLFILILTLLKIKF

LDKKD

>ABV53182.1 hypothetical protein C8J\_1585 [Campylobacter jejuni subsp. jejuni 81116]

MLKINNLNKKFGNNEILKNINLEIKEGEFLTLVGESGSGKSTLLRIIAGLEEPSQGEILNLNNQDISKQN

PRDRNFAMVFQSYALYPHLSVRENLAMPIKARAKFIHKLPLASFYIKSYKEFKTHLEEKIEQVATKLKIT

HLLDKKPKQLSGGQCQRVALGRAIIREPNIFLMDEPLSNLDAKLRIHTRAELSAMHRELNKTFIYVTHDQ

SEAMTMSDRIAFLVDGELLQVASPDEMYNNPNHLKVAQFIGTPTINTLCVELKSYGFALINKNLSKHKSL

AIRAENCFIDPHSQIKAKIYNIENMGNEYLIYTKLLKNDNNFILSLNTQEGKKLQLDSVVGINFDYSKAF

IFDEEGKRMDIKLYNLSFAA

>ABV53181.1 major facilitator superfamily protein [Campylobacter jejuni subsp. jejuni 81116]

MNGKTYKFHPNDTKMDKKIIQITEKSGFKAAVFSMAAMTMLGSVVISSALPAINRHFEELLTQSGATLAS

SFTLAHLDILVRLVLTIPAIFVVILSPFAGILIDKFGKLKFILPAMVVWTISGVSGFFLNDIYAILTSRA

IFGMATAFIMTGASALLGDYYSRGGFNRRENALSLQGFFCAVGGAVFISIAGFVSSYSWRYPFLVYGLGI

LITLMAIIYLFEPRKFKFYNHTKIEAKTNYWQFFPIYFIGFFIMVVYYISPTQLPYYIEEHLGLDPKYIG

ISMSVSALCYGFFSLSYRYIIKFLSIKTIYVLTLFIVSCSFSLLFLVDSFFTVLIALALLGMGGGIMLVN

NTAYLFSICPENARARAYGILASCIFLGQFLSPIISQPIVRQMGLVDAFLIWSIVIFIVCIVFLFLKQKP

RIN

>ABV53180.1 DNA topoisomerase I [Campylobacter jejuni subsp. jejuni 81116]

MKKNLIIVESPAKAKTIGNFLGKDYEVIASKGHIRDLPKSSFGIKIEDDEFIPEYRITSDHSALVKELKS

KAKDAKEVYLATDEDREGEAIAYHIAKAIGKDENTLPRIVFHEITKNAIENALKNPRKLDMHSVNAQQTR

RLLDRIVGYKLSPLLGQKIQRGLSAGRVQSAALKIIVDREKEIRAFVPLEYFSIDMIFQKDLDAELVEFD

KAKIEKLTITNKDRAKLILEACKNEAYAISDIESKERKIAPPPPFMTSTLQQSASNRLGFNPKKTMMIAQ

KLYEGVNTHEGVMGVITYMRTDSLNLAKEAIENARKFIQTNFGKDYLPSKANVYTTKAKGAQEAHEAIRP

TNLSFTPEIAAKFLDKDELKLYTLIYNRFLACQMNPAISQTQNVFVKNDRALFKISGRKILFDGYYKVYG

DMDKDKILPNLKIGENLKIQNLEMNSHFTEPPSRYSEAGLVKKLESLGIGRPSTYAPTISILTSRDYVKI

DKKQLIPSDVAFNVTEVLEKNFSDIVDSKFTSNLENTLDEIAEDKADWQETLKEFYYPFMRKIEEGKTKI

ASQKTVTKLGESCPDCGGELAIRKGRFGEFVACLNFPKCKYSRNLKSESKNESENTAAKAKANGTGITCP

SCQKGEIVERFSKRGKFYGCSAYPKCNFISKYKPSEEKCEECGETLVIKELKKGTFLECLKCKIKKEMKD

>ABV53179.1 putative biotin synthase [Campylobacter jejuni subsp. jejuni 81116]

MQIMLCAISNIASGNCSEDCKYCTQSAHVKTDIQKYRRKELSQIVLEAKMAKKNEALGFCLVTAGLGLDD

EKLEYVCEAAKAVQKEVPNLLLIACNGMASVEQLKELKKAGIFSYNHNLETSKEFFPQICTTHTWESRFQ

TNLNAKEAGLMLCCGGIYGMGESEEDRLSFRKSLQELQPFSTPINFFIANENLKLQVPRLSADEALKIVR

DTKEALPQSVVMVAGGREVVLQERQYEIFQAGAGAIVIGDYLTTKGEEPSQDIIKLKEMGFTFASECH

>ABV53178.1 sodium/hydrogen exchanger family protein [Campylobacter jejuni subsp. jejuni 81116]

MHQSVIDPQGLIDLKILIVIALCLLFSPHIAKILRLPLSATEIILGAVIAYFGFIGKSENFALLANVGFY

YLMFIAGMEVNLRAFFNMDKEVAKKSFFYIFLLYALSSLIVWIFGLSLVFVIIIPVMSVGLLSLLFKDFG

KECYWLNIAMIVATLAEVISIVLLTIAGAFLREGTGIIDVAQSILYLNIFLGLCLLGFKMLGVLFWWYPQ

LKVVLMPWEDKNEKDIRFCMAIFILIIVAMVITKLEIVLGSFIAGSFIATFFDHKKDLEHKLSTFGHGFL

IPIFFIHIGSTFDLKMILDYKIVLQAFLLMFVMVGLRILCASVFLKRIGFKNMILFGLSHSMPLTLLIAT

ATLGYSGKVIDEKLYSALILTALFEAIIVMSMIKFLSNSKK

>ABV53177.1 citrate synthase [Campylobacter jejuni subsp. jejuni 81116]

MSNSVTITDNRNGKSYEFPIYDGTTGPSVVDMSSFYKQTGMFSYDEGLTSTATCKSKITYIDGENGILMH

RGYPIEWLAENKLYLDVVHLLLYKELPDATRLEAFRYEMKKRSFIHEGMHRLFDSFPDNAHPMAVLQGAV

SSLSAFYPDHLNMNVKEEYMEMAARIVAKIPTIVATAYRYKHGFPMAYPNLDRGFTENFLYMLRTYPYDH

VELKPIEVKALDTVFMLHADHEQNASTSTVRAVGSTHAHPYACIAAGIGALWGHAHGGANEGVIRMLEQI

GSVDRVDEFIKRAKDKNDPFRLMGFGHRVYKNFDPRAKVLKKLRDQLIDELGIDTNLIKVATRIEEIALS

DDYFVQRGLYPNVDFHSGLILKALGIPNEMFATLFVIGRTPGWIAQWIEQKEQESLKIVRPRQLYLGETS

KI

>ABV53176.1 CysQ [Campylobacter jejuni subsp. jejuni 81116]

MLNLDKFLEIAINASNQASKAILEERKNFKTWEKEDKSPLTSADLASNKILNDILGSTDIKILSEEKLLS

KEECEELKTFWLIDPLDGTSGFLKGSDEFCVMISLVHDNRPVLSLIQNPSKGDIFYAHAKTKVYKNDKPL

QIDQQEYEKNKYKALLSVNHLSKEDEDFAKEHQLEAINIGSGLKFCAILEARAGVYKRFEKLNIWDIVAG

DFLINQNGGFMGDFSKKYILYNPLNYKSSPFICVSSRNFLQDFL

>ABV53175.1 hypothetical protein C8J\_1578 [Campylobacter jejuni subsp. jejuni 81116]

MRYCFILFLSLVLSSNLLANNFSQKKVIKIEKSADSFEVIDLNQNVANPNLNQQKALFDSSTLIEKKSQI

TKDEDIDFAIVLTSRKNFGYFLDGFRVSDKEFSTLFAKNLIQSLKLNWVNSAANGIYQSPKTLSYFSPKD

AKLINVSPFLTQEKDKAKMYAKFTDYVVVVNLQDFYVNITNYFITTSKEGVANVNFKIISTSNGKILAAK

NAELNLTLKDQDAKQNYQDIVNQMPKMLASVIDNEIKKLKLTIN

>ABV53174.1 UDP-N-acetylenolpyruvoylglucosamine reductase [Campylobacter jejuni subsp. jejuni 81116]

MIIDFKKYSSVRIGNEFEVLVLDQICDFDGFLIGGANNLLISPKPKNIGILGDGFDFIQILDQNKDFIHL

RIGCKTKSSKMYRFAKENNLKGFEYLSKIPGTLGGLLKMNAGLKGECISQNLIKIATFQGEILRENINFD

YRFCPLNMPFFWAEFKLNFGFDILKDEALKNARSNQPSGASFGSIFKNPKNDFAGRLIEAVGLKGFSKGD

AMLSDKHANFLINKKNASFEDAFFLIELARKKVFEEFGINLENEVIII

>ABV53173.1 flagellar biosynthetic protein [Campylobacter jejuni subsp. jejuni 81116]

MDESTLVALGVQTFKITLLLSLPMLLAGLIAGLVISIFQATTQINEMTLSFVPKIILVVVILIFLMPWMT

TTMIDFTENILNQIPTFIK

>ABV53172.1 hypothetical protein C8J\_1575 [Campylobacter jejuni subsp. jejuni 81116]

MKKITIAHSPDADDIFMYMAIKFGWIGNDFAYENTALDIQTLNEFALKNEFDATAISFGLYPLIASEYAL

LRTAVSFGEGYGPKLIKKKDTHLKRNFKVALSGANTTNALIFRMKYPEARIIYKNFLDIENAVLSGEVDA

GVLIHESILEFDQSLCVEAELWDIWLEFAKENLPLPLGGMALRRSLPLSDAIKIERDLTYAVKIADANRK

ILAPMLMERKLIRVNEEKLDTYLNLYANKNSISMNQTQLLAVDTLFKLGYDYKFYDKIIHVNDYLIPSEY

EEARNS

>ABV53171.1 recA protein [Campylobacter jejuni subsp. jejuni 81116]

MDDNKRKSLDAALKSLDKTFGKGTILRLGDKEVEQIDSIGTGSVGLDLALGIGGVPKGRIIEIYGPESSG

KTTLTLHIIAECQKAGGVCAFIDAEHALDVKYAKNLGVNTDDLYVSQPDFGEQALEIVETIARSGAVDLI

VVDSVAALTPKAEIEGDMGDQHVGLQARLMSQALRKLTGIVHKMNTTVIFINQIRMKIGAMGYGTPETTT

GGNALKFYASVRLDVRKVATLKQNEEPIGNRVKVKVVKNKVAPPFRQAEFDVMFGEGLSREGELIDYGVK

LDIVDKSGAWFSYKDKKLGQGRENSKAFLKENPEIADEITKAIQNSMGIEGMISGSEDDEGEE

>ABV53170.1 phosphopyruvate hydratase [Campylobacter jejuni subsp. jejuni 81116]

MLVIEDVRAYEVLDSRGNPTVKAEVTLSDGSVGAAIVPSGASTGSKEALELRDNDERFGGKGVLKAVANV

NETIADEILGLDAFNQTQLDDTLRELDGTNNYSNLGANATLGVSMATARAAAAALGMPLYRYLGGANASI

LPVPMCNIINGGAHANNNVDFQEFMIMPFGFTSFKEALRSVCEIYAILKKELANSGHSTALGDEGGFAPN

LANNTEPIDLLMTCIKKAGYENRVKIALDVASTEFFKDGKYHMEGKAFSSEDLIERYVELCAKYPICSIE

DGLAENDFEGWIKLTEKLGNKIQLVGDDLFVTNEDILREGIIKKMANAVLIKPNQIGTITQTMRTVRLAQ

RNNYKCVMSHRSGESEDAFIADFAVALNTGQIKTGALARGERTAKYNRLLEIELESDEYLGEKL

>ABV53169.1 hypothetical protein C8J\_1572 [Campylobacter jejuni subsp. jejuni 81116]

MIFWAFLVVIGAIYFGNMFFGQYSLDTLLSLENTKEELNKKIILLKEQNAKAQKDYFELKGLYPNEN

>ABV53168.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKTRILAIFFIFTSLLYADENPFKTDQNITLVAPPEFQKEEVKFNSSARILKSITFNYINLDGSEDKIDL

DVNKSIDWHDTYTISRFKSPDPSKVLDVSVTIPEKNSSKQESNSTANVEIPLQVAKIYDFISYAVYKNKI

KLNTSDEMITDFSVGNPSKIVIDFRSNLISPTKNIRLSNSIFKRIDFGSHKGYYRLVIYLDGTYNYNIQK

DATGYMINLL

>ABV53167.1 putative ATP-dependent DNA ligase [Campylobacter jejuni subsp. jejuni 81116]

MRFIFLICCACLVFANEILLLSKFDKQDFNSKDFNAYLMSEKLDGVRGIWDGKYLKTRQNYKIKTPDFFT

KNFPPFAIDGELWIARNKFDEISALIRSGDSNLTLWKEVTYNIFDVPNACEEFQISTCTLKNRLAVLEEY

LQKYPSAYIKIIPQIPVENQNNLNQFYESIIKNQGEGIVIRKNLSPYEKGRSKNAMKLKPYDDAECELVG

FRKGKGKFENQVGALLCKMPNGQIIKIGSGLKDEDRKNPPKIGSIVTYKFNGLTKNSLPRFPVFLRIRDE

NP

>ABV53166.1 hypothetical protein C8J\_1569 [Campylobacter jejuni subsp. jejuni 81116]

MKKLGLALAALVALNVSAFAGVITIHDSNLVKVSGGDDTYAKIALDNAKEGMKNQFNTDNLEIYAIESIK

KDDPEHYNVIQRGSFKVMKQEIAKGKTVYYNEFLVVDRKTNWAAEWDIECDHLDRPIKLSNNVNCRSGIS

TRRYNFK

>ABV53165.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKTILTILFLLTLTQAKEIQVYESPTCGCCDLWADYMKAKGYEVSVHKTNDFLKIKEKMGIKDEYQSCH

TGVIEGYAIEGHVPESAIVWLLENKPKDVIGISAPGMPQGSPGMEQGYSEKYPVILMKKDGSYELYGYFI

GDKKL

>ABV53164.1 possible lipoprotein thioredoxin [Campylobacter jejuni subsp. jejuni 81116]

MGIFRIQAYFFALIIALFFVACDSGENFKALNSDKTYNFAYNGFEKSLKLNDKAQNFALVFFTKDCGVCK

EQIPILQNLAKNYDFNIFVVLGDANDANDAKAWADEKGLSNLAMFYEKRAAKYLSSAIGEIYGVPVLSFF

KEGKMDEKFIGLTPYSILEKEIKKVKS

>ABV53163.1 possible periplasmic thioredoxin [Campylobacter jejuni subsp. jejuni 81116]

MLNACSFENSKDTGKVGEKSAEISAKDTLGKAVKLADDNTSLKVLVFFQNGCPSCLKELPSLDEFIQNHP

NKISVYAINSIDNANVVKVLAEQFDFKNVKVLKDDLKITNDRYAVFATPTTIIIKDGMIKDRILGEKPWE

FFESKLISLL

>ABV53162.1 putative ABC transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKELIKINNLNKEFGKVKALNNINLSVYEGEWLAIMGPSGSGKSTLLNILSLMDTPSSGEYILDNENLE

QMDEEQKITLRREKIGLVFQQFHLIPYLNALENVMLSQYYHSSVDEEDTKMVLEKVGLSHRLTHLPSQLS

GGEQQRVCIARALINNPELLLADEPTGNLDEANEQIVLQTLQKLKNEGKTIVLITHNPDLAKFADRTLIL

QHGVLK

>ABV53161.1 ABC transporter, permease protein [Campylobacter jejuni subsp. jejuni 81116]

MVDKFFLNELFKSISFSYQRLFIIVLSVFIGALTCSAFLNIYFDIDTKLSKELKAYGANVMISPKQDENF

ISNAEYEKIKENLKARALTPFLYDFLNLGSTSGVVLGTDFRALKITKPFLEVKEGSFSLNDFDENSAFLG

VNLAKQLGLKTGNELQIYNPNNGKSIKLTIKGILSSNDEFDSIVLAPLSVVQNLSDRAGINYANAVVYGN

FDEVKAKTQAISNEFIDAKPISSVSLSEGLVLGKIKALMFLIILVVLIIVTTSVNTTLSSIIFSRKKEIA

LRLALGAKKSEIFKLFASECFIVSFFASLIGAFCGIFLANVFGYLIFNSSIDFRFIAVFIALIISLIFAF

LAAFFPIKRALKINVCENLKGE

>ABV53160.1 possible ABC transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MLAKMIFNSIFKNKIQKFLAFLTCFLATLLLSTMLNITLSIGDEVTKQLKSYGSNILVLPKGSSLSIEIG

NELYEPLKNKNYLEEKNLYMIKDIYWRNNITALAPFLEGKITIENSQQKALIYGTYFQKAIKIKDDDDFI

TGIKSLYPYLAVQGEWAKDDSNEIMLGEDFAKNNKLKLGDTIELTGENNQSKEAKIVGILLHANPKMSNK

IIAPLNLAQDLLNKQGLYSSAEVRAFTIPESALSEKVRRMGEEKLDQLEYDKWYCSAYVGSIASQISDGL

PGADAKALNAISDAQSLVVKKIQSLMGITCIICLIVASIAISSLMSSEIHRRKKEIGLLKVLGANTFQIY

LIFASENLIVALFAALFGFIFGTALSQIISLSIFGYFIDIAFIALPLSFIFAGLIALLGCLLPIKNITQL

SAAGVLYGR

>ABV53159.1 hypothetical protein C8J\_1562 [Campylobacter jejuni subsp. jejuni 81116]

MSIYFVHFLISVLPLSILMAFITPDKKYIFKSFLVVFLGFLFGYFAFFIAAQFLKTENLIFNFDFVFIGL

LLVSFIFYFWKKIEILNFILLGILSFCTALHYYFLSQDFPIFTSSLIDSEGISSLGFIALALLVCILIFF

FLKWQKNFNQKTSFMLFLLLILIESDKALANILLTLMRNSIIETHTFLVSFVGKSNYFGVFGIYVYLIFI

TFLAFLSLKIRKKNISKKQILDINYRKNEAKTSLINRYFSSVFISCVISFCIILYFFMVSSKPLTIDEPK

EILPNKNGKFIFDIALLRDNKLHRFAYISAEGKVIRFFLINKREDRDSPVAVFDACMICGDMGYIKKDGQ

LICISCNVRIFLPSVGKSGGCNPIPLKYEYDGKKITIDVKDVIAGSNYFSQIKEIEVQDPVSKTKIINTQ

APFSYSYKGITYYFSNQNNYEEFKKDPTKYVEENEAQFLIQRRNDVG

>ABV53158.1 periplasmic protein P19 [Campylobacter jejuni subsp. jejuni 81116]

MIKKVLSVVAAAAVISTNLFAGEVPIGDPKELNGMEIAAVYLQPIEMEPRGIDLAASLADIHLEADIHAL

KNNPNGFPEGFWMPYLTIAYELKNTDTGAIKRGTLMPMVADDGPHYGANIAMEKDKKGGFGVGNYELTFY

ISNPEKQGFGRHVDEETGVGKWFEPFKVDYKFKYTGTPK

>ABV53157.1 iron permease, FTR1 family [Campylobacter jejuni subsp. jejuni 81116]

MKIFKIIFLIISIFLSSSAFARVDDYINEANLIKDMLKQSIETYKKGDNLGAKKLSEDAYFQHFENMEGP

IGRNIGRKAITMERKFVNLRRMYKDEAPLTQINALIDSLYYDLDEVAPILQNGYRLKAEASDTNYDKAKA

EKSSLEANAKREADAEALIAQMMGVDKKDLAQSSLTTQASTPANNDTSKLTDDNASADLQAAAAMDARLQ

FILDNISTKFSQAANAFKEKNYQASKDFLNDALFSDYRNTKVEILVNKFTKAGNDQKIQQAIRTLIRQIN

DAKIDEKGLRDGLDNIEEQIFDVFLQIPNSELSSLQISGFNDETKGKDYAKVSNDIKLALDEILKNYDGF

SASIVDDLQGIYLDIFEASGMENKIGAVDSGLKLKIESLFSKGVALIKASADKKELEATFNDLEQLIASS

VDKIQDSTPYSLFIWALGIILREGLEALIIVVAIVSYLVQSGNKNRLNIAYSALFTGVILSFVTAFGVSW

LFKENAGQSRELIEGITMLIAVLLLFYVGFWLLSNAQNKKWTSFIKQGAIDAISNNSAKTLWITVFLAVY

REGAETVLFYQALLFDAKTSTDFSAVFGGLGLGILILIVLYFLLKAGAIRIPVKQFFYITSYIIFYMVFV

FTGKGIAELIEGKVIIPSLIPMNFEPILWLGIYPYYETLIPQFIVLIMLIIGILITKQISKKGVKS

>ABV53156.1 hypothetical protein C8J\_1559 [Campylobacter jejuni subsp. jejuni 81116]

MLLNTPCRGIVDTNFESKRINITSTLKFQEKKEKVEAKAEKEEANKDNSDSTNTDTNKKDKLLDISA

>ABV53155.1 hypothetical protein C8J\_1558 [Campylobacter jejuni subsp. jejuni 81116]

MVSDVSMGNANLMTAVNTSVLKKSMDTNEALMNELIEGMEGVSQASAPQVSSSSGLDIYA

>ABV53154.1 Na(+)/H(+) antiporter [Campylobacter jejuni subsp. jejuni 81116]

MVLSETFPGILLIFFTFLALLCKNSSLSVIYTDFFHANFTVGFDHFQISKSLDLWINDGLIAIFFLCIGL

ELKYEILRGQLKNIRAVSLPIFGALGGMITPALIFAAINYSHDFAMKGWAIPTATDIAFAVGILMLLGNK

IPTSLKLFLLSLAIFDDLGAIVIIALFYTDQLSALAIIICLFCIFALLLLNYYHITHLSLYVLVGVVLWI

AMLKSGVHATLAGVIISLFIPLDTKNKKPYLHEVLKDLNPWVVYFILPLFAFANAGIDIRDMHLGSVFSP

VSLGIILGLFLGKQLGVFTFCFIAIKLKLAKLPENIKYGKFYGICILTGIGFTMSLFIDGLAYKNSDIFE

HADKLAILIASFLSAIVGFIYLKIVK

>ABV53153.1 Na+/H+ antiporter NhaA [Campylobacter jejuni subsp. jejuni 81116]

MNNIVHKLKTLVLNEAFGGVLLIVCTLLALLVQNGSFSEHYREFLNLKVGFSVGEFELNKPFLLWINDGL

ISIFFFAIGLELKKEFLHGDFKNPKNIVLPFMAALGGILIPAMLFALVNIGDAYTLKGWAIPTATDTAFA

LAILMMCGKHIPSSLKIFLLSLAIFDDVGAILIIAIFYTTKLSIVAFVVAGIAILAMLVLNILGITRKSF

YFICSVILWISVLKSGVHATLAGIITAFFIPMQTKNGEAFLEEIYESLKFWLAFVILPLFAFANAGVNLS

NIDIGAIFSGVSVGIFLGLFVGKQVGVFLFSYLAIRFKFAALPQGSNLKQLYGVCILTGIGFTMSLFIDG

LAYEVSDIFNYADNLAILIASFCSGIWGFIYLKFFAARS

>ABV53152.1 lipoprotein NlpC [Campylobacter jejuni subsp. jejuni 81116]

MRHIFFIITIIFFISGCSFYQNLNYTRPIYNTNKETKLKTIAHEWKKTPYVLGGTSKKGADCSGFTQSAL

AQLNIRIPRTTKTQLGSGRKVSKSKLQTGDLVFFKTGRGPNGMHVGIYMSKGKFIHLSTKGGVKEVELNN

SYWKARYIGARRY

>ABV53151.1 glutamate racemase [Campylobacter jejuni subsp. jejuni 81116]

MKIGVFDSGVGGLSVLKSLYEARLFDEIIYYGDTARVPYGVKDKDTIIKFCLEALEFFEQFQIDMLIIAC

NTASAYALDALRAKAHFPVYGVIDAGVEATIKALHDKNKEILVIATKATIKSEEYQKRLLSQGYTNINAL

ATGLFVPMVEEGIFEGDFLQSAMEYYFKNITTPDALILACTHFPLLGRSLSKYFGDKTKLIHSGDAIVEF

LKERENIDLKNHKAKLHFYASSDVESLKNTAKIWLNL

>ABV53150.1 methionine aminopeptidase [Campylobacter jejuni subsp. jejuni 81116]

MIELKKPDEIEKLRIANQIVAKTLNFLENEIKIGMSLKQIDKMAEDYILSLGAKPSFKGLYGFPGAICTS

LNQVCIHGIPDDKIIKEGDILGLDVGSLIDGYYGDAARTIAIGEVSPTDKALISCAKDALYHAIDIIHDG

MRFKELSAALGEFIHTRGFVPLRGYCGHGIGRKPHGEPEILNYLEKGASAKSGPKIKNGMVFCIEPMICQ

KDGTPKHYNGKWDAGSIDGLNAAHYEHCVAVINGRAEILSMI

>ABV53149.1 hypothetical protein C8J\_1552 [Campylobacter jejuni subsp. jejuni 81116]

MKSDLEIFKKHLGEIQGVNEFKANQICSQINDANDFIGALQVLDMSLKKIEKSILERIDENSDDMQKRTL

DATASQLIQNCSFMGTALFGNIFNVYVGKKLFEFEIANPLLILQTSNYEGVLAYIQDKRDEIKIILSELA

TTITMGETMDNTGIYNSTMDFKNLFK

>ABV53148.1 lipoprotein, putative [Campylobacter jejuni subsp. jejuni 81116]

MLKQIFYIFTFIFILCGCSLKHETINKNENIILKDEGIDSNIFFKKTGKILKIRNANTPLYLNSRAIVYI

DNGFSNKYAHYFWGDLPSNLYSFLILSKFEQSNIFTTLLSSTSSLNADYALESRINSFEQILSNNENYAQ

ISISVNFINLENNQIIAHKIFNTKEKIEKKDIRSTYNAFQKALNKIGNEIIFWVNSNLS

>ABV53147.1 ABC transporter, periplasmic substrate-binding protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MENRANYFFVGLFVFGVFFASLGFILWLGGYSKEESFKYYEIHTQESVAGLGIKAPVRLLGVEVGSVEEI

SIYNQDELGVNIRIKVKNNTPIKEDTFATLQLQGITGLKFIQLQGGSKNSKDLVSIHGKLPVIPFKESFL

ATIDRQSEHIFSLVKTADDKSKELLSEKNLKNLEILLQNLAELSANLNANSKNLSLNLSNASLKIGKMAD

NISLSAQNFNSSLKNIKESTMILKNFIKKADEKLNTYDDIKASLMQNLELFKRVLIESNILIENLQNSPA

DLIFKETKPKLGPGEK

>ABV53146.1 ABC transporter, ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MVIKAQNIITKFGEKIVHDGVSFEIKKNEIFGILGGSGSGKSVLLKQMLMLEHFDGGEYEILGYKLKNID

EEDALALRKKWGVVFQFAALFSFFNVYENIAIPLKEYTHLDENSIQELVLMKLKMVGLNESVLKQFPSEL

SGGMQKRVAIARALALDSKLLFLDEPTSGLDPHSSREFDDLVLELKKSFDLNIILVTHDKESMKNLLDRF

IILENKKVGFCGTYEELRLQNERLFKKFME

>ABV53145.1 ABC transporter, permease protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MNANFKFQNNTLFIFGIWDKTSIYKLKIKDFLALIQSKEVIFDFKDLKAIDTAGVRFFLALENDLKDKNI

KITKEGLNSRFQTLFELCEKNYQRLSKTKKSHKNFSEYFIDLGKLSLELLKILIKFTNFTGAFFTSLFLC

LKNPKNFRFIAFLYHIENSAFKALPIVILTALLVGVVLAYQAAYQLAQFGANIFIVDLMGISATRELAPL

IAAIVIAGRSASSYTAQIGVMKITDEIAAMNTMGFRSFEFIIIPRVMALVVAMPLIVAISDAISIIGGMM

VAKLNLDISFAEFLRRFREAVDIKHIFIGLAKAPIFGFLIGLIACFRGFEVKNTTQSIGIYTTKSVVNAI

FWVIAFDALFSVVLTSAGI

>ABV53144.1 transketolase [Campylobacter jejuni subsp. jejuni 81116]

MDIQILQEQANTLRFLSADMVQKANSGHPGAPLGLADILSVLSYHLKHNPKNPTWLNRDRLVFSGGHASA

LLYSFLHLSGYDLNLEDLKNFRQLHSKTPGHPEISTLGVEIATGPLGQGVANAVGFAMAAKKAQNLLGSD

LIDHKIYCLCGDGDLQEGISYEACSLAGLHKLDNFILIYDSNNISIEGDVGLAFNENVKMRFEAQGFEVL

SINGHDYEEINKALEQAKKSTKPCLIIAKTTIAKGAGELEGSHKSHGAPLGEEVIKKAKEQAGFDPNISF

HIPQASKIRFESAVELGDLEEAKWKDKLEKSGKKELLERLLNPDFSKIAYPDFKGKDLATRDSNGEILNV

LAKNLEGFLGGSADLGPSNKTELHGMGDFIEGKNIHFGIREHAMAAINNAFARYGIFLPFSATFFIFSEY

LKPAARIAALMKIKHFFIFTHDSIGVGEDGPTHQPIEQLSTFRAMPNFLTFRPADGVENVKAWQIALNAD

IPSAFVLSRQKLKALNEPIFGDVKNGAYLLKESKDAKFTLLASGSEVWLCLESANELEKQGFACNVVSMP

CFELFEKQDKTYQERLLKGEVIGVEAAHSNELYKFCHKVYGIESFGESGKDKDVFEHFGFSVSKLINFIL

SK

>ABV53143.1 geranyltranstransferase [Campylobacter jejuni subsp. jejuni 81116]

MNLKELFIHHLEKNLPKVESFHPFFNEALALMLKAGGKHFRAQLLLSVVQSNKPELLNQALDVALALEFI

HTYSLIHDDLPAMDNADFRRGIPTLHKSYDETTAILVGDALNTEAFLVLSHAHLKDEIKIKLIKTLAFNA

GLNGMVIGQAIDCFFEDKRLSLNELEFLHTHKTARLIAAALKMGCEICELNNEESNQIYKLGLKLGLIFQ

INDDIIDVTTSQEQSGKPTNNDTHKNSFVNLLGLEQAIKTKENLLSECEQDLEKLNEKLAQMIQNLIIQY

L

>ABV53142.1 PDZ domain protein [Campylobacter jejuni subsp. jejuni 81116]

MKKILIICMLFTLSFGIERPKFEDFLAGYERNKASMLNYEGMPAFALSENLLAVLKQPNTKLNKYVKYDP

FLNLYLVRTDFSLIPTPMGDEEKLTRNDWVGIWDPNKPYIGHIKYLAQNIDEKDQLDFNSKIGLLGTPCC

EMMGIALNNSSFIGNRYLKHFMKYNDAYWGDIGVDFVVRENKIYVNNVRKNPQFLINDQVISVDGLPAND

LRKLNEKILFADRGSTLYFQVLRDNMDLNISTEVFAKDLSKFNLPDSKPKPKITNFTSNLGLTVNTSLVV

TKIDPKSKASNAGFMVGDKILRVNNIILNNFKELQNILSAGNDFSILIERKSTKLPLSNFNNELGGNANS

GGDGKFQFFIRLTK

>ABV53141.1 hypothetical protein C8J\_1544 [Campylobacter jejuni subsp. jejuni 81116]

MFENMDFSKMGELLNQVQEKAKNIELELANREFSAKSGAGLVKVSANGKGEIIDVSIDDSLLEDKESLQI

LLISAINDVLAMVAQNRSSMANDVLGGFGGMKL

>ABV53140.1 UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase [Campylobacter jejuni subsp. jejuni 81116]

MKLKLENSFITDNTLECEKECFFLQTTQNAKFHAQALEKGAKIIDVNECKKLLKIDEKIQIIGITGTNGK

TTTAAAIYSILLDLGYKCGLCGTRGAFINDEQIDEKSLTTSPILKTLEYLQIATQKKCDFFIMEVSSHAL

VQNRIEGLKFVAKIFTNITQDHLDFHGTFENYKEAKELFFTDESLKFINKDALAIKFNVRNAFTYGIENP

ALYQIKAYSLEEGISAIATNKNQTFHIDSPLLGLFNLYNLLVASACVNELVKPDLKDLEKAISGFGGVCG

RVEQVAKGVIVDFAHTPDGIEKVLDTLKNKKLIVVFGAGGDRDKTKRPLMGTIVEHFAKIAIITSDNPRS

EEPKTIMEEILSGFAKKEKVLMIEDRKEAIKKALELKENDDLVVILGKGDETTQEIKGIKYPFSDKVVVN

EILKNQG

>ABV53139.1 hypothetical protein C8J\_1542 [Campylobacter jejuni subsp. jejuni 81116]

MQNYKKLGIEHFYKKDFKTAKMYFSMAYEKRKNKRLLNFICLCDLALKSPKEASLLFDFYIEHYKISSID

KDLEEILSTIEFKKQENKQENEFEDGHALNYQDFLKSEEELGFQKSFENIINSTKLVIDNRDDFLDFLEK

LLDNGYKDMTLNYIENVMPHFWANDRFIKLQEKLIGFKSEIKT

>ABV53138.1 NifU-like protein [Campylobacter jejuni subsp. jejuni 81116]

MMPFSDEELINPVKASLEKSLPMLERDGGGLEFLGIKNGVVYVHLIGACKGCASSGTTLKYGLERQLKID

IHPEITIINLNGGADEFAKL

>ABV53137.1 DNA primase [Campylobacter jejuni subsp. jejuni 81116]

MITKESIENLSQRLNIVDIIENYIEVKKQGSSFVCICPFHADKNPSMHINPTKGFYHCFACKAGGDAFKF

VMDYEKLSFADAVEKVASLSNFTLSYTKEKQENKKELKSILPSLNAYFKDNLKHHKEVLTYLYQRALNDK

DIAKFELGFAGASEDSIRLLQNQKIPLEDAMSVGALKKDENNEFYASFIWRITFPIYDHKDLLVGFGGRT

LNPNVPAKYVNSPQNILFDKSRIFYAFNIAKENIAQKKEIIVCEGYMDAIAFHKAGFNNAVAVLGTALTE

HHLPLIRRYDAKVILCFDNDEAGLKAATRSAFLLSTNKIDGKVAILQGGKDPAELVAKNESTKLHDILDE

GIELGEFYIRRLISTHSIISALDKQKALETIQKFTFNLEPLVANSYTSLVSNLLKVDEKFIVLSQNSKKT

IQTPLISQNKYNFPKEKIHIAELELIAFLKQHPDICNDFKQISDSVCFKHKILLDKILEKKGYEDSDIRE

FESKNIRKNLNYSEFLLGICKVNLAFLNNVKIKNSTLALKKQLFTLIDKNLNLLIKNLNTEELNNFLKEY

LSFLKYEKNEEILQQSFRNLNGIFSNKNFTAYDLGFSAQDNDEPF

>ABV53136.1 hypothetical protein C8J\_1539 [Campylobacter jejuni subsp. jejuni 81116]

MDFFFVEYRDPLVGLIILTILVFVVAVANYIWKIFANKDEEQKLEKFIKKFEMDNAHKELLRNSSLSFGN

LSFLAEIFTKSGEFEKATQIYLIALEKCKDKQEREFIFLSLAKVYFKAGFLERAKEVLLQALKLRPRNIQ

ALKLLKIVYLKLRSYKENLELLECLFELNEDVQKEHDFIKALELCTFNITDEEKKKKLLEFKIEDNPMLG

RLVFEKYHMFLGQNFFDICDLLYRENEAFNLENQDFLEFFYALGKISKHDDTHQFVFKNSNFKMLKILKD

NSFNAGLEFSYRCSECKNVMPLFFYHCPVCYEFNTCKIIYEVKNNETH

>ABV53135.1 ribonuclease HI [Campylobacter jejuni subsp. jejuni 81116]

MKHIEIYTDGSCLNNPGFGGWAYILRYKEYQKEGFGAEANTTNNRMELMAIIESLKALKEPCEISLFTDS

NLMVQSINEWLEGWIKKDFKGKKNIDLWKEYIKVAKSHKIKAFWVKAHNGHLENERCDTLAREAALKIAR

ENDEKH

>ABV53134.1 ribonuclease III [Campylobacter jejuni subsp. jejuni 81116]

MKNIEKLEQSLTYEFKDKNLLIHALTHKSFKKSYNNERLEFLGDAVLDLVVGEYLFHKFAKDAEGDLSKL

RAALVNEKSFAKIANSLNLGDFIFMSVAEENNGGKEKPSILSDALEAIIGAIHLEAGFEFAKTIALRLIE

KNFPQIDAKILIKDYKTKLQEITQGKIGQTPQYETVRAFGPDHLKQFEIALMLDGKELARAIAGSKKEAQ

QMAAKIALEKLGAL

>ABV53133.1 chorismate synthase [Campylobacter jejuni subsp. jejuni 81116]

MNTFGTRLKFTSFGESHGVAVGCIIDGMPAGVKFDEEFLQNELDKRKGGSKFATPRKESDKAQVLSGVFE

GYTTGHPIAIVVFNENAHSKDYDNLKDLFRPAHADFTYFYKYGIRDHRGGGRSSARESVARVAGGAVAAM

LLREFDICVQSGVFGVGTFVSNLKEEEFDFEFAKKSEIFCLDPKLESDFKNEILNARNSKDSVGAAVFTK

VSGMLVGLGEVLYDKLDSKLAHALMGINAVKAVEIGEGINASKMRGSCHNDALKDGKFLSNHSGGILGGI

SNGENLILKTYFKPTPSIFAKQESIDKFGNNLEFELKGRHDPCVGVRGSVVASAMVRLVLADCLLLNASA

NLNNLKNAYGLK

>ABV53132.1 hypothetical protein C8J\_1535 [Campylobacter jejuni subsp. jejuni 81116]

MKALALFSGGLDSMLAMKLITAQGIEVKALNINIGFGSTSDKSEIMKKRAAMIGADFEMIDVRNSYLQEV

LFNPQYGYGKHFNPCIDCHAFMFKTALAMLKEENASFIITGEVLGQRPMSQRSDAMAKVKKLALDEEDLI

LRPMCAKNLPLTKPEREGWVDREKLEGISGRSRKRQLELAAKFGLEDFESPGGGCLLTLDNFAKKIRDFI

EFDKDMQVNDAQLLKYGRHLRLPNGAKMIIGRNELENTLLKGLKTPKYEVIELGDLIGAYSLVDEKISEK

DLELALKIALTYTKHEVGKSYELKFKNQAYTSIAFENKADINQFFIS

>ABV53131.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MLKIILVLSILSSFAFANSCANYEQELKKCNSLKNSHERKMCRLGLFAKCKKG

>ABV53130.1 hypothetical protein C8J\_1533 [Campylobacter jejuni subsp. jejuni 81116]

MKIDTSASLTHSLTNNVDKKELSVLKKEDQDKIPVQDLSSLNSDGVKIVFENKQGELIALNLSDENYSSL

QKNFGSYTNYVARNDGSIRLNGEANQFVSNWFESVKDNFGSLNSNLNNKQQSVKLNFNTSTLQQSMQNLG

FKTSDEKISDDANIEEKLNFFIDKDVNKDGKVDDSDVKEPSMREILSDIKEASGGGANAMKTIDPQKINK

KDDKENNIKEKEDEDLLQKAQEKGLSALSADEQAKLEASNPEEFEKLKQKSLQELSQNLSKDFQNKIENQ

EAQIVDKRV

>ABV53129.1 putative TonB transport protein [Campylobacter jejuni subsp. jejuni 81116]

MKTLFLNHKYQASYITFIVFIPLLFVIFHSNDFFKMEIKNEDSFSLAIKQFTQTNPTNETKPTESIIEPI

KPKPQPKVIKKTPEKIQKKIKKTPPHPIPNKTPIAPTQEVKTFTKTTDTNVKPKITQLTQGKDNHPVLKE

IQKAIQQAQFYPRQAKKMRMQGTVKVEFLWKENKTLADLKIIESSGYDLLDKSALESIRKASLNFPQYNG

DLRITLPIIYDFKTLRG

>ABV53128.1 biopolymer transport ExbD protein [Campylobacter jejuni subsp. jejuni 81116]

MLKLPKNEGLNIVPFIDIMLVLLAIVLSISTFIAHGKIQISLPSSENATNISNNEKKLLITIDEKNTFYL

NDKLADLNEVQNAIFSLDKKTIVELKSDKNAKFESFVKIIDFLKAKEHENFQILTEKNK

>ABV53127.1 putative ExbB/TolQ family transport protein [Campylobacter jejuni subsp. jejuni 81116]

MEFLKDYIDLIIFLILGIMAFIAFWCVVERMLFFRKINFKNYENQEQFDDAISENLTTIYIIYSNAPYIG

LLGTVIGIMVTFYEMGLAGNIDVKSIVVGLSLALKATALGLLVAIPALMAYNALLRKVSLLSNAYKANKN

A

>ABV53126.1 hypothetical protein C8J\_1529 [Campylobacter jejuni subsp. jejuni 81116]

MTIDLNHNFTSFVLLDEVDFNFSELKSILEDKFNIKIADENFTKEGVIFSYENMLITLNLIKNPIPNHEA

EYYANFNFMWKDALEQTKKHKAHLLIAVLSQDQSKLEQAKMFTKIAALCLDNKHALGFYTGAVVLEPSFY

IENAKMLDDNRLPVYNWIYVSVYPSENGVNAYTYGLRNFDKLELEVCDLNIEEKELFFCIYDIVLHILTY

DINLKDKDILKFEDGKEIKFIKSQGISVENESLKIIF

>ABV53125.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKAKLTLLALLGATVLLAKDMVVPASELPNNAKEFISKNFKTAQIGLVKKDIDSYDVILNDGTEIDFMIN

GDWKEVDGKYKALPHTILPSVMKKVSATQPNAQILEIDKEINGYKFKFNNNMKVYTDMQGNVLGQKLD

>ABV53124.1 serine transporter [Campylobacter jejuni subsp. jejuni 81116]

MNTPKWTSHDTRWVLSLFGTAIGAGVLLLPISAGLGGLIPLLVILVLAFPMTYLAHRNLCRFVLSSSNPK

DDITFVAESYFGKGGGFLITLLYFFAILPILLVYSANLTTTLLEFLINQFNFNADLTHAARWWVSFLIVG

VLVLISILGENVVTKAMSFLVFPFIIFLFIFSLLLIPQWNSSLFTNVDFSVISTSNFWVTLWLVIPVMVF

SFNHSPIISSLACYCKKEYGDYAEPRARKIISLAIILMVFVVMFFVFSCALTFTPEDFASAKDQNINILT

FIANKFPEVSLLAYVGPIVALVAISKSFLGHYLGSQEGLNGILYKASNGKIQGKFAQTLTAIITFAIAWL

VAYKNPSVIGIIEAIGGPVLAILLFLMPLYCIYRFDILARFRNKFLDLFILVMGIVAISAAIHDLL

>ABV53123.1 L-serine ammonia-lyase [Campylobacter jejuni subsp. jejuni 81116]

MSNLSIFKIGVGPSSSHTLGPMLAGNLFCKKVAKKLDEIDRVEVTLYGSLSLTGKGHLSDKAVIWGLNGL

EAKNLSAAIQDEVNKNAIENAQIDFCGEKKLCFNYEKDLIFSKDFLPLHENGMKIKAYDCKGGLVDEETY

YSVGGGFVLTAAQLEKKGKNSNQNKKKKLDIELNNAKEALELCDKRDWDLAELSYRYELQFHTKEEIRAY

CLEIWEVMQEVYYNGTHPNEDYLPGKLHLKRRAKGLKERVAMTADPMGIIDFISLYAIAIAEENASGAKV

VTAPTNGACAVIPAVMLYLKNHTIGFSDEKAIEFLLTAMLIGSFYKKNASISGAEAGCQAEIGSASSMAA

AAMATVLGANAFKACNAAEMAMEHHLGLTCDPVAGLVQIPCIERNAFGAIKAISAARMAMTRKSTPMVSL

DEVIETMYETGKDMNYKYKETSLGGLATNLKTVC

>ABV53122.1 hypothetical protein C8J\_1525 [Campylobacter jejuni subsp. jejuni 81116]

MAFMNFSGFFYARNDLRLFKIEKKNELKSFFYKDYTLSSYKDALNLNNEIFFYQSLKEGLFKENDEILVS

NLGKKIILFRNFTQNCDNFNEAKLKQILLLFFLLLASVFFASLAMINEFGAIDLVFLMICLLLLVMGVIN

LGLLFKQIRILKSFSKEEMKEFLSQRMKKYTKV

>ABV53121.1 diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase [Campylobacter jejuni subsp. jejuni 81116]

MSNFKIQGRQMKEFYMNLALNEAWKYQFLTYPNPAVGCVILDKNGKILAIKAHEKAGLAHAELNAIAHAF

KSLRPEISLPKEANALHEFICKNHQGVFKDSIAFVTLEPCSHQGKTPPCAKLFSELGFKKIFISVKDENK

IASGGAEFLKKQGIEIEFDILKEEGKKLLKPFLKWQKEQFKLFKLALSMNGSPFGKIVSNELSRTYAHKI

RAVIDLLVVGGETIRKDHPILDARLCKAKAPNLCILSRQNIDNFDKNIPLFKVPNRQIYTQIPSEAKFLM

YEGGENFLKTFKDEIDMFLIFQSSSLNDEKNVTIPLNFKPLYRNFLGSDTYGIYEL

>ABV53120.1 hypothetical protein C8J\_1523 [Campylobacter jejuni subsp. jejuni 81116]

MKNNTSVLLFLLYPKKLRKTMANIIKNKKYKWKI

>ABV53119.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MLAFFKGLGIGFLCLLLFVAGVVFNVEFLGKKDSNHDLYFSRNIEVSNTLKPDILYANINFWANENLSSK

ITLDNSEKAEIANTFNQILERSKKENFCSGGSFSLEPNFSYKDGIQTPKGQRFDAILECEFKENQLADFN

KLLNDINSIIAKNNFISVSTPAIQTKFSKDTLNNNKENLYKELLKTSYEYEKTYSLDLNKTCVLKNLQVN

TNVNIAPRMLNAKSDNIELSSPIISEKEQILSAKALFICK

>ABV53118.1 A/G-specific adenine glycosylase [Campylobacter jejuni subsp. jejuni 81116]

MQKKELEKLQENLLLWYEKNGRKTLPWRNLQSQNCDESLKHIDRAYGVYISEIMLQQTQVKSVLERFYFP

FLKKFPTLESLANANEDELLKAWQGLGYYTRARNLKKAALECVDKFGAKLPKEVEDLKKLSGIGVYTAGA

IACFGYDQKVSFVDGNIRRVLSRLFALENPSMKELEKGAKELLNVNHAFDHNQALLDVGALVCVSKNAKC

GICPLYDFCQGKFHTELYPRAKKILYESLNLNLFLFEFNKKFAIQKSQDKLYKGMYNFPFFKEGEYKLSK

DMSFVGEFKHGYTKYKLNIKVYHQILNNENKNYEFKTLKELESTALSVLSLNALKLIKL

>ABV53117.1 alpha-ketoglutarate permease [Campylobacter jejuni subsp. jejuni 81116]

MQELTRTKKIRSIIAASSGNLVEWFDFYIYAFTATYFAHTFSTSDNPVIQQINAFGVFAAGFFMRPIGSW

LFGSLADKVGRKKSMVISVVLMALGSFMIAALPSKDTVGDLAIILLLIARLIQGLSVGGEYGIAATYLSE

LATEGKRGFYSSFQYVTLIGGQLLAVASISIMFLFFSIDDMKDYAWRILFVIGGILALGSLFVRKMMNES

ATKLHQHEDRGTLKALCKSWKPFLMVLGVTSGGSLAFYTITTYTKTFMENTGMDKMLVNNLFLGALFILM

IIQPLFGYIGDKIGHKRSLIVFCILALVGIYPIFSLIANNAQNNPSLTFMLVVLLFVILSFYTSVAGIFK

AKLFPEHVRALGTGLGYAISNAVFGGSAPWVALQFKNAGIENGFFIYIAIFTIIMLIATLYLPKKSQLN

>ABV53116.1 hypothetical protein C8J\_1519 [Campylobacter jejuni subsp. jejuni 81116]

MFTLGNIMKFKKIYIELSDICGLKCDFCPSRKGIRGVMSEEKFQNLAHEISNKAELFTFHLLGDPLLLPN

LENYLKIAKSEAMKLEITTSGFYLNSKNQALLLGYENIHQINISLMSFLSQSKISLEQYFKPILELCKKH

LEQKSLSFINLRLWNLDANFKAPKSNLKIYEFLAKEFEVKIDTNLSKNRLQRHILLHQNKLFKWPNLKDE

PLYKKGKCHALKEQIGILSDGSLVPCCLDAKADINLGNVFENNFDKLFKSPRIKMMKKAFEEDKRIEKLC

QTCEFFKARLGD

>ABV53115.1 putative haemin transport system substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKILIIMSLFLITLNAKERLVVLDPASIETLFMLKAEDQIVGIATLQHSNIYPKDQTSKLTSVGTFSNP

SLEKIVALKPSLVILSSYSLNLEEGLKNFGIKSINLKAERLEDITKNITTLGQITKKEKEAEFLKQEFTQ

NLKKLSDKPLNKSAIYLYSSNPLMAFNDNSLIADILRLIGIKNLSPQSQISRPVISAEYILKQNPDILIL

GINAKNNLLDTNALLKNTKAVKTGSIYFNKDTHILLRLSPKIIDRIQEFKTKLENNNF

>ABV53114.1 hemin ABC transporter, ATP-binding protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MLKIQDLSFAYHQKDLLKNIHLELKNQAFIGILGPNGSGKSTLLKLILKNLSPNKGEISLFNTNIKDFSL

KEFAKICGFVPQKSELNTPLKVIDVLLMSKYANLKHAFSSYSKEDILEIKEFAKDLRLENFLERSILSLS

GGEFQRMLLARALLKKPKILFLDEPTSALDLNYAIELLSLCEKLVKEKNIAVVAILHDLNLASMFCDKIL

FLKEGEIKYFGTSKELFTQEILKEIYDLNCEIIYKNSKPYILALKEKK

>ABV53113.1 putative haemin transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MGMAETTMLNLNTHSKILVIIGLLVAYIIASFTALCLGDENLNPKELFSYIFSQDEILRQIIIDGRLPRI

IMAILIGMLLASSGAITQNVFSNPIADPYIIGIASAATFGAVLAYLLKLNDYYYGILGFVCSAFFALGVF

KISSKASIATLLIIGIAASSFLGAFTSFFTYLIGEDSFKIVAWLMGNIGNASWFRVGILILPLIFCLFYF

YAHKNELNILLSGDDEARNLGVNAQKLKINLLIVSSLAVSFAVAFSGLIGFVGLIIPHTIRLLLKNYDNA

LVIPLCTAFGGLFLLICDTLARTLLAPVQIPIGILTAFFGAPIFLYLALSARRFL

>ABV53112.1 haemin uptake system outer membrane receptor [Campylobacter jejuni subsp. jejuni 81116]

MHPNKKAFKLSLFALLLITNLNAQESNEAINLQKVVVSATGFEQDADSNLRNVISIEGKDLQNKGYVSLE

QALERISGISFVNFGLGRNIDMRGQGDKSNIAVKVMIDGRAINVLDNSHGVTPLDSINLDNVERIEIIPG

GGSVLYGSGTRGGVINIITKKQKSDAFAINLKSSAYDHGGLGGNLGINGAKQINENLAFSFDIQSFNLDG

YQEGYNEKGYFINTKTYIDINDNSDLTLGYDYFKSKNTSSGYLTKAQAQSDPTQKGNSDNITQINRPEIS

LDYHYYFDDIWEFNLEAFWQNQKIDYLKDEISMMGTTAYQNGSGFEDTLTGISLKNKLNYANNSYFIFGY

EFTNHDAKRKSLVYYSVPGVINYHRMTTLMDMTKQSHSIFALNSHNFNEFFTLSGGARYEFSTYDTDRSY

RNEMSMNIPRPPSDSTTLFDTNKNTNNFAFEITPNFKYSDTGNLYLKYERGFVSPAPAQFVNRNKTGNGI

PPYYSSNLKAEIFDTFELGIDDFWWDFYGFNLTLFYTLSKDEISYLGNPHSTSGSWWKYYNIDQTRRLGV

ELSLSQNFLDDDLIFRESLTYLDAKISKGVNDGMRIPYVSKIKATAGLEYAWNKNFSNFIDLTYFSRAKD

GGTIDENTGKMSKNSWIRDYFLTDIGMKYNYKKLQILAGIRNLFDKRYYTYQDSINDQYLVGNGRNYYVE

FKYAF

>ABV53111.1 hypothetical protein C8J\_1514 [Campylobacter jejuni subsp. jejuni 81116]

MNFESIISHMNDHHKSNLVDLCKKFGGIEQVQDVFLKSVDFNGLDLVYNDKENLRVEFPKKADENTIKDT

IISLCMSAKSEQNFSGVEKELNEFMLSFNSVALATLNANAEVVCSYAPFVSTQWGNYIYISEVSEHFNNI

KVNPNNIEIMFLEDESKAASVILRKRLRYRVNASFLERGERFDQIYDEFEKQTGGEGGIKTIRKMFDFHL

VKLEFKKGRFVKGFGQAYDIENGNVAHVGASGNPHKFPHKH

>ABV53110.1 peptide chain release factor RF-1 [Campylobacter jejuni subsp. jejuni 81116]

MLASKLDPFLKRFEELNSLLSSSDILNDISKMTTLSKEQKNLEPIVLKAKEYLKTLDNIEENKALLNDPE

LGELAKEELKTLEELKPKLEEEIKILLLPKDPNDERNIFLEIRAGTGGDEASLFVGDLVKAYARYAENRG

YKLEIVSSSEGSVGGFKEIIMLVKGTGAYSRLKYEGGTHRVQRVPQTESQGRVHTSAITVAVMPEVDDIE

IEINPNDLKVDVMRSSGHGGQSVNTTDSAVRITHIPTGIVVVNQDGKSQHKNKESAMKVLKARLYEMQES

ERLAKESEARKSQVGSGDRSERIRTYNFPQNRISDHRINLTLYRLDAIMQDGLFDEIIEPLITHHQAQAL

QEQNL

>ABV53109.1 ribosomal protein S20 [Campylobacter jejuni subsp. jejuni 81116]

MANHKSAEKRARQTIKKTERNRFYRTRLKNITKAVREAAANGDKNAANEALKVANKSIHAMVSRGFIKKQ

TASRRVSRLALLVNKIA

>ABV53108.1 phosphatidylglycerophosphatase A [Campylobacter jejuni subsp. jejuni 81116]

MQKLFLTFFYSGSIKKASGTFGTIAALIPAFFILKYLGINTLFLLSILIFVASIRVIDDYEKKTGIHDDK

HIVIDEVAGVFLACAIAASVENSIVNFILAFVLFRLFDITKPSIIGKIDKKVKGGLGVMLDDMLAGLFAG

LLSAVIYGFLLKFNLVFWDINLKDLF

>ABV53107.1 ATP-sulfurylase family protein [Campylobacter jejuni subsp. jejuni 81116]

MKSARKNKNITIDQNEFGILSLIKEGLLGTCTHLMNEKEVNEIIKSGKFKGESFPYPLSFAPKNAEEALN

DIKSGDRIDLILDEKVVGHIDFKSRFKNNKNFSDIFSPNTCSLEDMGTTCISGKIEIYNSQIKKIKENFQ

QIKNNLNAQKITAIVSSFDPLHRAHERMFRWTIDKADLVVIFLVESFDANGFEFELKEAYLKKFIQNYLP

PDRIFIFPLKNINIFHAHLNPGLESIIAKSLGCTKLVVGQNHTGLGMFYDDNQPKTILDDFSKDYGIEVI

VLPEFVFCDQCRMIVSTRSCPHGCHHHLHYNSQSLKDLLRAGIIPPAIFMRKEVSSVILTSLFPNRLKNM

QKIYNELFPTDGILEYKNDEEFYQKLLEIHQMSYMV

>ABV53106.1 DNA-binding response regulator, putative [Campylobacter jejuni subsp. jejuni 81116]

MKVLIIENEIYLAQSISIKLSDAGYSCEIINSFDEYNGEKYYDIVLLSTNTNNFLKAVGQFKHSIIILLI

SYISTDTVSNPLKLGASDYIQKPFMIEELIRKIKHYQDFRKLSILNKAYQSYIKSRLETIKIPEYNYKKL

KLPLILKSNKQSSADAFVFNYANECDITLSFIDLTSTNSVEKVMKLPTENNLLFLSNFQALKATEKEKLL

DFIQNKNVILHTNSNTDDLKINCINLNDNEKNIDSNEILTIDEYVKYVIINYQNIFPDTDLSKKLGISRK

SLWEKRKKYEISKKK

>ABV53105.1 2-C-methyl-D-erythritol 4- phosphate cytidylyltransferase / 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Campylobacter jejuni subsp. jejuni 81116]

MSEISLIMLAAGNSTRFNTKVKKQFLRLGNDPLWLYATKNLSSFYPFKKIVVTSSNITYMKKFTKNYEFI

EGGDTRAESLKKALELIDSEFVMVSDVARVLVSKNLFDRLIENLDKADCITPALKVADTTLFDNEALQRE

KIKLIQTPQISKTKLLKKALDQNLEFTDDSTAIAAMGGKIWFVEGEENARKLTFKEDLKKLDLPTPSFEI

FTGNGFDVHEFGENRPLLLAGVQIHPTMGLKAHSDGDVLAHSLTDAILGAAGLGDIGELYPDTDMKFKNA

NSMELLKQAYDKVREVGFELINIDICVMAQSPKLKDFKQAMQSNIAHTLDLDEFRINVKATTTEKLGFIG

RKEGMAVLSSVNLKYFDWTRL

>ABV53104.1 ATP/GTP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKEQILEKLKTVKYPGFEKDIVSFNFVKDIKIQDDGVFIDIEIVSANPEVANEIRKNATEALSSLALKNI

ELNIITPKIPEEKSNSRSGKNIAPQVKNFIMVSSGKGGVGKSTTTVNLAISMAKMGKRVGILDADIYGPN

IPRMLGETKTQPEVVGQRLKPILTHGVYMMSMGVLIEEGQGLMWRGAMIMKAIEQLLADVIWPELDVLFL

DMPPGTGDAQITSAQSIPITAGVCVSTPQTVSLDDSKRALDMFNKLHIPIAGVIENMSGFLCPDNGKEYD

IFGKGTAEDMAKAYKSEVLAQIPIEMIVREGGDEGKPVSFYHPESVSSKRYLTAAEKIWGFIEKINNEGG

ADNSAIQPVMNGKSACSH

>ABV53103.1 possible 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MINTKEDFLLLIKQIEQKSGYKKPKAFGIARLDRGQLNKNKILQASFALINYEQNFGSAAIMLEAFMQRG

VEIDFNASEFVQTLKLEDIDFALSCFKPFLEEEGHQNIDLLKIIKDKFKDDEFAFVCLFEDKEPLSVESV

YLKLYLLSTKKVPLRSINLNGAFGLLSNVAWSDDKPIELEYLRANEMRLKMSNQYPKIDFVDKFPRFLAH

IIPEDNTRILESSKVRMGASLAAGTTIMPGASYVNFNAGTTGACMVEGRISSSAIVGEGSDVGGGASILG

VLSGTSGNAISVGKACLLGANSVTGIPLGDNCIVDAGIAVLEGTKFLLKDAEELAKLNPYFNFDKEIYKG

LELKGLNGLHFRQDSISGAMIVALNKKAVKLNEALH

>ABV53102.1 phosphoribosyl-AMP cyclohydrolase/ phosphoribosyl-ATP pyrophosphohydrolase [Campylobacter jejuni subsp. jejuni 81116]

MQNFKELNEKIAWQKVDHLLPVIIQDAKTCEVLMLGFMNNEALEKSLESGKVVFFSRTKQRLWMKGEESG

NFLNIVDLSLDCDNDTLLILANPVGSTCHTGDISCFEKISKNADFVFLARLEKLINARKNADENTSYTAK

LFKSGTKRIAQKVGEEGVETALAATVKDKEELICEAADLMYHLSVLLADANLSFSDVISKLKERHKA

>ABV53101.1 cyclase hisF [Campylobacter jejuni subsp. jejuni 81116]

MLTKRIIACLDVKDGRVVKGTQFKNHKDMGDIIELARYYSQNGIDELVFYDIAASARKERISREWVSEVA

KNINIPFCVAGGIKSEEDAAELLANGADKISINSPALNDPSLITRLAKSFGVQCVVVGIDSFKDENGNLK

VFQYTGDEKTSKHSGKSTLEWVKEVQDLGAGEIVLNMMNQDGVKNGYDLEQLKAVYKICKVPLIASGGAG

KMEHFLEAFKLGIDGALAASVFHQKLIDIKELKIYLKNQGLSIRI

>ABV53100.1 phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Campylobacter jejuni subsp. jejuni 81116]

MTQIIPALDLIDGEVVRLVKGDYEQKKVYKYNPLEKFKEYEKAGAKELHLVDLTGAKDPSKRQLALIEKL

AKEVNVNLQVGGGIRSKEEVKALLDCGVKRVVIGSMAIKDATLCLEILKEFGSEAIVLALDTILKEDYVV

AVNAWQEASDKKLMEVLDFYSNKGLKHILCTDISKDGTMQGVNVRLYKLIHEIFPNICIQASGGVASLKD

LENLKGICSGVIVGKALLDGVFSVEEGIRCLQNA

>ABV53099.1 amidotransferase hisH [Campylobacter jejuni subsp. jejuni 81116]

MKIIIIDTACANLASLKFCLDRLGFNATISRDLKELESADKLFLPGVGTAKEAMKNLEQFNLIDFIKNTK

KPLLGICLGMQILGNFSEELNQETLKLIDFTTQKFKAKEGFTFPHMGWNQVHSSHALFKGLEGAYFYFVH

SYCVGLGEYTIADCEYSQKFSASVMKDNFYGVQFHPERSSEAGEILISNFIKDIG

>ABV53098.1 imidazoleglycerol-phosphate dehydratase/histidinol-phosphatase [Campylobacter jejuni subsp. jejuni 81116]

MSQKILFIDRDGTLIEEPKSDFQIDTLEKLRFEKDAIPTLLKLKNFGFKFIMVSNQDGLGTPSFPKENFE

IAHEKMLDILKSCGIEFQDIFICPHFENENCACRKPKTAMLEEYIKHELYDKEQSFVIGDRESDMILASN

LGVRGLRYGELSWKEIENEILSSFRSASYQRTTKETDIKVKVCLNGGKVSIKTGIDFFDHMLEQIAVHGG

IGLEISCKGDLEIDEHHSVEDVALALGACIKKALGDKIGIARYGFALPMDECLASCAMDFCNRPHLVYKA

KFKKSHLGALSTEMIEHFFYSLSYAMGVSLHLKVKGKNDHHKAEGLFKAFAKALKMAVKIESENLASSKG

VI

>ABV53097.1 histidinol dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MQILVYDNLDEKQKEEALKRPAISAKDEISKIVSSIVKEVQEKGDEALIEQALKFDKAEISNIKITQEEI

TQVSNRLDKDLQDAILVAYENIKKFHEAQIPHEIALETTKGVKCEVLTRPIEKVGLYIPGGLAPLFSTVL

MLAIPAKIAGCEKIVLASPAKINDAVLFCAKLCGVDEIYQMGGAGAIAALAYGTQSVLKVDKIFGPGNAF

VTEAKRQVSSDINGATIDMQAGPSEVLVIADDLANEKFVASDLLSQAEHGADSQVILVCLSQDFAKKASD

EVQSQLELLPRKELASKSIANSRIIIAKDLNQALEISNLYAPEHLIIQTQNPRELLKGVKHAGSVFLGAY

SPESMGDYASGTNHVLPTYGLTKTHSSLGLADFSKRMTVQELSKEGFLALGKSVEILAQNEHLDAHKNAV

TFRLESLK

>ABV53096.1 ATP phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MQENTRLRIAIQKSGRLSKESIELLSECGVKMHIHEQSLIAFSTNLPIDILRVRDDDIPGLIFDGVVDLG

IIGENVLEENELERQSLGENPSYKLLKKLDFGYCRLSLALPQENKFQNLKDFEGLRIATSYPQLLKRFMK

ENGINYKNCMLTGSVEVAPRANLADAICDLVSSGATLQANNLKEVKVIYESRACLIQKENALSKEKQALV

DKIMLRVAGVMQARESKYIMLHAPKEKLDKIQALLPGVERPTILPLAHDEKNVALHMVSKENLFWETMEA

LKEEGASSILVLPIEKMLK

>ABV53095.1 50S ribosomal protein L17 [Campylobacter jejuni subsp. jejuni 81116]

MRHKHGYRKLGRTSSHRAALLKNLTIALVNSGKIETTLPKAKELRGYVERLITRARLGDFNAHRAVFASL

QDKNATNKLVTEIAPKFKDRNGGYTRIIKTRIRRGDAAEMAFIEFVA

>ABV53094.1 DNA-directed RNA polymerase, alpha subunit [Campylobacter jejuni subsp. jejuni 81116]

MRNITTSAYTPTEFTIENISDTVAKISAWPFEIGYGITLAHPLRRLLYTSTIGYAPTAIHIDGVAHEFDS

MRGMLEDVALFIINLKKLRFKIKGESNKEIVEFSFKGSKEIYGKDLNNDQVEVVNKDAYLATINEDAELK

FTLIVEKGIGYVPSEEIKELINDPKFIALDAFFTPVREATYDIEKVLFEDNPDYEKVVLTVTTDGQITPN

EAFQNALEAMYKQLSVFDKITNVRSVIKNQATSNELENTKLLQNITDLNLSARSYNCLEKAGVVYIGELA

LMSVSELAGLKNLGKKSLDEIKNIMESIGFPVGTSKLSDNKEILKNKIAELKAQNEG

>ABV53093.1 30S ribosomal protein S4 [Campylobacter jejuni subsp. jejuni 81116]

MARYRGPVEKLERRFGVSLALKGERRLAGKSALDKRPYAPGQHGARKGKISEYGLQLREKQKAKFMYGVS

EKQFRRLFAEAARREGNTGVLLIQLLEQRLDNVVYRMGFATTRRFARQLVTHGHVLVNGKRVDIPSFRVE

AGAKIEIIEKSKNNPQITRAIELTAQTGIVAWVDVEKDKRFGIFTRKPEREEVVIPVEERFIVELYSK

>ABV53092.1 hypothetical protein C8J\_1495 [Campylobacter jejuni subsp. jejuni 81116]

MAKRKIVKKKVVKKNIAKGIVYISATFNNTMVTVTDEMGNAIAWSSAGGLGFKGSKKSTPYAAQQAVEDA

LNKAKEHGIKEVGIKVQGPGSGRETAVKSVGAMEGIKVTFLKDITPLAHNGCRPPKRRRV

>ABV53091.1 30S ribosomal protein S13 [Campylobacter jejuni subsp. jejuni 81116]

MARIAGVDLPKKKRIEYGLTYIYGIGLFTSRKILDKVGISYDKRVHELSEDEAAAIRKEIQENYMVEGDL

RKQVAMDIKALMDLGSFRGLRHRKGLPVRGQKTKTNARTRKGKRKTVGAKS

>ABV53090.1 hypothetical protein C8J\_1493 [Campylobacter jejuni subsp. jejuni 81116]

MKVRPSVKKMCDKCKVVRRKGVVRIICENPKHKQRQG

>ABV53089.1 translation initiation factor IF-1 [Campylobacter jejuni subsp. jejuni 81116]

MAKDDVIEIDGTVLEALPNANFKVELDNKHVILCHIAGKMRMHYIRIMPGDKVKVELTPYSLDKGRITFR

YK

>ABV53088.1 hypothetical protein C8J\_1491 [Campylobacter jejuni subsp. jejuni 81116]

MFNFITTLLKTNLYFLEEKTTSKSSNQTHIISLKQSDDEFLNLLFSFLVPQNDEDKNFIEKTRTKIKRNE

HNIALIKNPNFNALIDTGFLDTIDTLKEKLHTHKTDFKDITHIILTHAHPDHIGALMSEENLFPKAQILI

DKKEYDFWIKSDRQEIKNTLLKLKNIEFINHSKDLIFQNSGIKAIPAYGHTPGQNAIIIDDKIVFWGDLL

HLYDIQIPKPKIAIKFDIDQNEAIQTREKLLKEFKERKLKVIGTHVPFIEPKFLD

>ABV53087.1 putative transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MRKSKFGTKEIKILGLSSLGGTLEFYDFIIFVFFAEYIANVFFPKDMSEFWALLNTYGAFAAGYLARPLG

GIVMAHFGDKFGRKNMFMLSILLMVLPTFVLAFIPGYETLGFLAPVLLILIRIFQGIAIGGELPGAWVFV

REHCQEKQKAFFLSCLNSAMALGILLGSIVFLIINAFFSIEEIAAYAWRIAFFVGGIFGIISIYLRRFLQ

ETPVFKQMKKESSLSSFPLRDLFKEKDIVKNLFSSMMMTWVLTGCVIVLVLLMPKFMPSILNLSGVEGSY

LQILGILGIALGGAFMGYLVDKFGLFKICIFFSLTFVFFSFLYFYALYELKNLVLVCILYSIVCFLGGIN

VFAPILMSEVFRAKIRFSGISFSYNIAYAISGGITPQLVFWLNTLASKNENPFLYGMSIYMIFLALLAIC

AVFIVKDKIKF

>ABV53086.1 putative ABC transporter [Campylobacter jejuni subsp. jejuni 81116]

MPFIIELLKQNKLKLISFLLFSFITSAVGVLTLVFINDYLLKNAQNIPIFYFIVLLLIFFISSTIVELGL

SIFGQNFIFKMQRRVVKQILDTPLLRVAKVGKARILASLGSDVRNISFGLLRLPDFLQSSILILCTSVYL

CYLSPQIFVLCVVWIMVIFITNNFLMMKVYQYFRKARENDDALQNNYQNILDGHKELLINRDRAKLYYED

EFENNARLKKKNSTLGNLFNNLSNNWTNVTLLALVGVEFYLALKFEWASVADATTIALSILFLRTPLVSM

IGSFPTLLLAKIALDKIAKLELDDYIEGFKKTHYISEWKKISFRNTQFAYEENFHLNPVNIELKKGELVF

LIGKNGSGKSTFCMLLTGLFKPSKGGIYVDDTLIDDKKLDEYRSLISAVFSDFHLFTKTLNKENFASEEK

IAFWLEFLELKDKTSVKDNELTLTKLSTGQKKRLAMLIALLEERDILVLDEWAADQDPVFRRFFYKKLLP

LLKEQGKTIFAITHDDAYFDSADRIFLAQNGEISELKGENIKELAKNLVEKFD

>ABV53085.1 putative bacterial haemoglobin [Campylobacter jejuni subsp. jejuni 81116]

MTKEQIQIIKDCVPILQKNGEDLTNEFYKIMFNDYPEVKPMFNMEKQISGEQPKALAMAILMAAKNIENL

ENMRSFVDKVAITHVNLGVKEEHYPIVGACLLKAIKNLLNPDEATLKAWEVAYSKIAEFYIDIEKKLYDK

>ABV53084.1 hypothetical protein C8J\_1486 [Campylobacter jejuni subsp. jejuni 81116]

MQKLAIDIFINFLQNPPNHFLLEKLKKEEFWQNWFLKNNSKLQCTALKLLSSSNEDDKLIASDFTSLFLS

DVDYVKAPPFASFYLDENKEIYSDNSDKVKQIFAQNNFFSFFNEEPADSLINELLFISFLIKKQDDITLQ

KFLKEEFFTWFNMWSFDVINKAKTHFYKALTMLMQDFFNQLNTKF

>ABV53083.1 hypothetical protein C8J\_1485 [Campylobacter jejuni subsp. jejuni 81116]

MTSFNHILSEMPLVLFTILAQAVIGLSLVYAPAFINGYKNYANLKSFGLALGIAMMVAFIPSFFHLNDIT

HIFNVLNRMGVFYANNEWHIGWMNNEILFVSLVCALGFLLYLKTSNWVFYLTLICGILGLFFMSGAYGSM

QESVPTWDFKITLLYFFASAIFLGAIVYYCFFENSEHERKMSFFTGLIGIGLLSTAIVLQTLHVGQTWIM

GLVNPFELLGGTYDWFISLSFAFLGLGIVTWYLHNYLHEKFKSKFFAYFALLCAFLGVFTTRMLFYGLIS

TQIMLGHS

>ABV53082.1 hypothetical protein C8J\_1484 [Campylobacter jejuni subsp. jejuni 81116]

MKLEENSQFGFMLDQSKCVGCRTCSLSCKDYKNMPVGVNFRRVFETEGGNWTAKEDGSFEQSVFAYYTSI

SCNHCSNPSCLKACPTGATMKIKWGIVAIDDSMCIGCKACAMACPYGAPQFNHESGHMSKCDGCYERLKE

GKNPICVDSCPFRALKAGDITKLREEHGNLASITPLPDASITHPNLCIVPEKHSLPSGNKSAIFHLPQNY

QGVKNDII

>ABV53081.1 hypothetical protein C8J\_1483 [Campylobacter jejuni subsp. jejuni 81116]

MCECIVDVNVTRTPSNNYADYILPDATMLEQEDFIRPSAGYYSNKPYIIYCQKAIEPVGEAKPIYEMCLE

LAKRLSIEKEFSEGRTQKDWLKYLYEESMKKNPLLPSFEEMCEKGLVKFEPVKPVVALQSFIKDPINNPL

KTPSGKIEIYSTKLAQMQKTWKLKEGQQIVPIPVFESQREGILDPLKQKYPLQFFGYHYKGRTHSSFWEI

PQIREANPQEIWINTIDAEQRSIKTGDVVQVRNDLGIIQGIAKVTPKIIPGCAVTPQGAWAKYENGIDVG

TCVNSLASIVPTAISKGNGQHSILVEIAKV

>ABV53080.1 hypothetical protein C8J\_1482 [Campylobacter jejuni subsp. jejuni 81116]

MEQNRRDFLKWSSLFGGLTLSPISLSANLLKTPPLISKWAGCNVNCGTKCPVKVHTQDGIIKYVSTDNEG

DDSFDNRQARACIRGRSSRYKVYNANRLKKPLKRVGKRGEGKFMPISWEQAFDEISAKMQEIKEKYGNEA

FYINYATGTTGTIINRCTQGPWARLLSLYGGYLNYHNSYSTAQISNAMNFFYGGSPASDIYTLRSAKLAI

FFGANHVETRMGGGGVGYAYQKALEESGCKIIHIDPRYNDSMIGHCDEWIPIAPGTDAALIAALTYVMIK

EDLLDRTFLDKYTIGFSENTLPQDAAKNSSYESYVLGLNDGVEKTPNWASKITKIPARRIVQLAREIATI

KPCFIEQGWGVQRHSNGEQNARAIATLACITGNIGIEGTNTGCRTGSSKTYDIMGMPFKNPIKDSIPCFL

FTDAIYRGKEMTDISDGVRGTTQLNKISNLFSIQQEIVLQISTAPLKKCMIF

>ABV53079.1 peptide transport system substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MLRFLIFAMLLFVNLEAKIPKDTLIIAVENEIARINPAYSEDHDAVINLVFSGLTRFDENMSLKPDLAKS

WDVSKDGLVYDIFLRDDVLWHDGVKFSADDVKFSIEAFKNPKNNSSVYVNFEDIKSVEILNPSHVKITLF

KPYPAFLDALSIGMLPKHLLENENLNTSSFNQNPIGTGPYKFVKWKKGEYVEFKANEHFYLDKVKTPRLI

IKHIFDPSIASAQLKNGKIDAALIDVSLLNIFKNDENFGILREKSADYRALMFNFDNEFLKDLKVRQALN

YAVDKESIVKNLLHDYAFVANHPLERSWANSKNFKIYKYDPKKAEDLLVSAGFKKNKDGNFEKEGKILEF

EIWAMSNDPLRVSLAGILQSEFRKIGVVSKVVAKPAGSFDYSKVDSFLIGWGSPLDPDFHTFRVFESSQD

SALNDEGWNFGHYHDKKVDIALQKARNTLNLEERKKYYKDFIDALYENPPFIFLAYLDFALVYNKDLKGI

KARTLGHHGVGFTWNVYEWSK

>ABV53078.1 peptide ABC transporter, permease protein [Campylobacter jejuni subsp. jejuni 81116]

MLKRLVFSIVVAFFSTFLCFVLLYFSKGSIAYANGVNSQSKEFVQRIEQNLGLDKPLLEQYKIWLFKALK

GDLGVSFLSGESVLKLIKERIFNTFILGFSALMLLFLLSVFLALLGYSYKESFIDKIITFLAFNFFALPP

FVLALLFVLIFGIFWKILPVMGSSDIGFEDDFLNRLEHLILPVLVLVLSHLALFLRIARNFINESFSQIF

IQNLYARALREKDIYFLVLKYSLSPIVAYFGGSALSFMMGTYVVESVFAYEGLGSLLFKSIIFKDYPVVL

ALIFFSVLLAAFFTFLSDIVARILNPRLRRLDFV

>ABV53077.1 peptide ABC transporter, permease protein [Campylobacter jejuni subsp. jejuni 81116]

MFKFLIILAPLIFLFLCALFAPFLAPFDILSTHLENLHQAPNFTYILGTDFLGRDLFSRLLFALRNSLII

GVGGSLLSIIFALCYLFLARCFFYVFWMRILEFFLALPAFLLMMFFQSMITSDVFLMIFLIALIHWCFIA

RIIESELKRLENLDFYKANIVLGRTKFRAFFKDLIPALKTLIFTLFIFNIVHAIATEATLSFFGLGLGFE

IPTLGTLLSESSKAVFIGAWWMILFPLLSLLLLFLPLLWLGNFLQKIWGIRS

>ABV53076.1 peptide transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MLKDINLDIKTGKTLMILGQSGVGKSLLGKALVRLLDSNFTISFDELSFHNSCIFNFNKEELRNFRSKVA

LVLQDAELSLYPYLDIGNLCHLVLKTHTKLKQKERKDYAFSYFQKLGFENLDRLWHSYANELSLGMARRV

SLALALLNQPQILICDEITASLDKENASKIISILEELKNTTALVCITHDLNLVNSLADEILMLEKNSSNL

YSLNEFLRYYNA

>ABV53075.1 peptide ABC transporter, ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MLKVCNLSKFYELKKHWYLKKERHIIFDNINFSLNENDNLIILGKSGAGKSTLARILCFLEDPSEGEVWY

ENLNLHKLDKNKQRLLRKQIQYCFQDQKMALNPYKKIKNLIQDGLENFNLQKNDDLILEFFDFFSLKKQI

LKQKPYELSGGEATRVGLIRALVLNPKLLILDEITSALDIKTSKEILTFLYDYQQKNNISYIFITHQSDL

FYKFNHKKLKL

>ABV53074.1 NADH-quinone oxidoreductase, A subunit [Campylobacter jejuni subsp. jejuni 81116]

MSHIDASHPYFGIFLMLVLASVIFFGLVFLASKIGNNFAAKNRKKLGLGIYECGPIPVKQANKINSQFFI

IALIFILLDIEVVFLFPWALIFKDLGWFGLLEVFVFIVLLGVGFLYAYKKGAFAWQSIK

>ABV53073.1 NADH dehydrogenase I chain B [Campylobacter jejuni subsp. jejuni 81116]

MAEHQVNYASGLPVVLTSVDKLVQWGRSNSLWALSYGLACCAIEMMAAGGSRYDFDRFGTIFRASPRHSE

VMIIAGTLCKKHAEFTRRLYDQMPDPKWVISMGSCANTGGMFNTYSTVQGVDRIIPVDIYVPGCAPRPES

FQFALMILQKKIRKEKASRKIAPKRLV

>ABV53072.1 NADH dehydrogenase I chain C [Campylobacter jejuni subsp. jejuni 81116]

MRKYSDKKNAQTQNYYKDRFYHAPHAVKSDVNESVFKDDFEVLKTQVEILNSFVELDFWVIEIKKEDNVK

TLQMLKTLGYLSFTEASAIDFVADKNGFEVFYQLLNLEKKLRVRIKTFVGVKERLQSVAHVFKGANWSER

EIYDMFGIFIINHPNLKRILMPDDWFGHPLLKTYPLKGDEFARWYEIDKIFGKEYREVVGEEQRDSGFAD

DKDTLNFARLYHEVPKGSQKKEISFKQEYQEDEGVAFVKKVKRDEAKILEKRR

>ABV53071.1 NADH dehydrogenase I chain D [Campylobacter jejuni subsp. jejuni 81116]

MQIPSKLKPYYENIAFEQEDSKMIINLGPQHPSAHGNLRLILELDGEQVVKARPCIGYMHRGMEKMAENM

IYQEFIPTTDRMDYIAASANNYAYCAAVEKLCGLEIPRRAAVIRMILLELNRIASHLLWLATHALDIGAM

SVFLYCFREREYVLDLIEKYCGARLTHSSMRIGGVMLDLPENYLEEMLVFCDKFPNDLKDYEDLLDDNRI

WRLRTENVGVVTKEQALNWGCTGVMLRGSGIKYDIRKEEPYLLYNEVEFGVPYATQGDSYARYKVYMQEF

RESLKILRQCATLYKDTPPEILATHPEYVSASKEQILTQNYSLMQHFVLITQGLKPPKGEVYVPTESPKG

ELGFFIHSDGTGRPYRLKARTPSYWHCAFFEEMLVGTYLADVVAIMGNVNIVLGEIDR

>ABV53070.1 NADH dehydrogenase I chain E [Campylobacter jejuni subsp. jejuni 81116]

MRRVDLRKSKELFEDLAQIIKEAKQGEVLVVLFEIGDFSPVEKSFSFVKEQGCELLNSLKFNQVDWTIVI

KKERV

>ABV53069.1 NADH dehydrogenase I chain F [Campylobacter jejuni subsp. jejuni 81116]

MIYDNALCFLDMPSLKNKNLCEKIGVNSINISCLEDKNLKAKFYKCEIASLSFVLALLCKLSDEGHFCDL

DEGYLSAESCFGEEEAGEVLSFLKEAKYLIVDKNIHSYKDSENIKYFLNFLSIKYELKILDSDEEECDFK

KAKLNTLKELDNYDGLVLFRANLQDKNLHCSKQFLQIAKCKDQSEVEILAKDFSLKTKLCLDENLQGTIA

FLNYENNGFDFTPIRIKEAK

>ABV53068.1 NADH-quinone oxidoreductase, G subunit [Campylobacter jejuni subsp. jejuni 81116]

MTVKINGIDCAFEEGEYILNIARRNDIFIPAICYLSGCSPTLACRMCMVEADGKKVYSCNTKAKEGMIVE

SDLQNLWDERNEIMQAYCINHPLECGVCDKSGECELQNFTHKSRVNVQKHWIKDTHKPHKHWGMINYDPA

LCIVCERCITVCKDKIGESALKTVPRGGDSVDNSFKESMGKDAYAIWTKFQKSLIGPANGDTLDCSFCGE

CTSVCPTGALIGSKFQYTSNIWELKRIPASNPHSSDCELMYYDIKQSGISNQKEKIYRVSNDFAFASLNK

AARFAFDTQNEADKDEKAFKELVELFEKNEIKNIKFNSFITNEEALILQNLKKKFNLSLINEEALKFKEF

LQEFIANSGEFYSANTQDITKSDFLVVAGTLLRYDAPTLSYKINNALVINKGSGLYFHPMEDMGIAKYSK

NFISHIHKSGDEEQILYFLLQKFSQDEGIKTHLAEFFVSENKEIEESINEEVVEQVIEKDEEGNEIQKEV

KKVVPKKVKKIIEVQRSVFAKNLGIDEDKLEDLLLKKANFTLVVGNDFYFHKNAKKLAKLLALIQNTTPF

KVFLNPTHTNTLGVAMICDLDKNTQEGKTLGYNEKGDFSFSYEEHANLASASLNQQEGTFLNYDKRVVPT

NAALEFKGYFLNDLANALGFDEEYTINYTKRLPINKGFSPIDFDHLDNFYTNAGDCKRGYELNLECFKQV

AKKEFISPNFENLNPKEDEILLYSANPSYQFGRFSNRASAINEVIFLGVSENLAKEKNLKDKDLVKLKIK

DKELSLSVRVDKDIKNGAFLPYFDEKLDTLSFFDERFVVANLEKLGASHE

>ABV53067.1 NADH dehydrogenase I chain H [Campylobacter jejuni subsp. jejuni 81116]

MSDFAFFALEALIKCIIIIAIFASLAGLATYAERKVLAYFQRRIGPDMVGPFGLIQLVADMIKLFTKEDI

IPSNSQKFIFAIAPLISAICAFVSLAAIPMLPEFTLFGRVIQPIVADINVALLFVIGTSGLCFYAVFLGG

LASNNKWSILGAARGLVAIISYESVGALALIAIVMLVGSFSLVDINNYQSDGFFSWLIFKQPLAFVLFII

ALFIETNRTPLCLTENDAEIVAGYGTEYSGLRWGMFFIGEYASMIAGAILVTLLFLGGFNSFWIIPGWIM

MIVKSSFIFFWYFWARAAFPQLRPDQVMKMCYLILIPLAVLNLLITALAVLL

>ABV53066.1 NADH-quinone oxidoreductase, I subunit [Campylobacter jejuni subsp. jejuni 81116]

MKNYYLVDEKRKTPVSTWEKISQTFRRSVKLELFVGLFVMMRELLKRNNSATIKYPFEKVKLDNRYRAVH

RLMRFIESENERCIGCGLCEKICISNCIRMETSLDENGRKKVGNYSINLGRCIYCGFCAEVCPELAIVHG

TEYENAAEQRSYFGYKQDFLTPIDKLKNQVEFEGAGSLRKDADLLVVKTPNYYDVMIERALENQDTQEQG

ENK

>ABV53065.1 NADH dehydrogenase I chain J [Campylobacter jejuni subsp. jejuni 81116]

MIENLAFVFFSVVVLGFFGIAVLSKNMLYSLSALAGGMVFLSGFYFLLDAEFLGVIQIIVYSGAVLGLYS

FAIMFFDASKEFKEQLKAKKSFFTLVVLSAILLLAMLIGFKYQNISTDLPLNDPALFDFNKQLALAIFSK

YLLAFEFIAILLLIALVCAIVLTRKELTKEKQ

>ABV53064.1 NADH dehydrogenase I chain K [Campylobacter jejuni subsp. jejuni 81116]

MIEKYFFIAILMFVIGLVGILKRQNLIMLFISSEILLNSANLALVAASKMHNDLNGQVFALFIMGVAACE

VAVGVALCVLWYRRKGTLELKSLKEVEA

>ABV53063.1 NADH dehydrogenase I chain L [Campylobacter jejuni subsp. jejuni 81116]

MQNLALISLFSPFVAFLFASCFALSEKKQFVGIICSLLVALSAFCSLYLLFCNEAFNVSLFEWFAGVNFG

FDIDAISLTMMSVVGIVATCVHFYSIFYMAHDEGFNKFFAYLGLFVFSMLFLVMSDNFLGLFVGWEGVGL

CSWLLIGFWYKNDTYSFAANEAFIMNRIADLGMLLGIFWLYLQAGTLKYDEVFSMAQSLDHNALILIATC

LFIGAMGKSAQFPFHTWLADAMAGPTPVSALIHAATMVTAGVYLVIRASTLYDLVPEVSYIIALLGAFVA

IFAASMALVARDLKRIIAYSTLSQLGYMFVAAGLGAYGIALFHLATHAFFKSLLFLGAGNVMHAMNDKLD

IEKMGGLFKPLKFTAILMCIGSLALAGIYPFAGFFSKDLILGYSFISFHHGIFLVLLIAAFLTAFYSFRL

LMLVFFTPARHNEHPHEASKIALLAMSPLMVLAIVAGFFEHSFFEYLSTKLVFIDAQNQIVMICASVAAI

LGVILAIFAYKNSWFKESIEENKIHKLLSNDYFIPQFYHQFIVSKYESLCAILKHCDLYIFDRIVEKIAL

YSQIISQKMIMPNSLNLMLRFLVAAFVILLILVWMV

>ABV53062.1 NADH dehydrogenase I chain M [Campylobacter jejuni subsp. jejuni 81116]

MLNYLIFFPLISAFVVLLLNRGGIKVFSVVVSFMILALNLDIFADFLQGVSFDYNLSFKILKFFSFHVGV

DSIALILMLLSSLMIFLSFLFLKLEQKALVSCIFFLEFAIMGLFSAKDGLLFYVFWEFSLLPLLYIMGVY

GKDFRAGVKFFIYAFAGSILMLIALIYQAYLNYQLLNIFTFDLEIWKNNASAVNFTEQLLLFGAFFIAFA

IKAPLFPLHTWAPKVYVNSPVLVSVMLVVFKMAPFGFLLFCLPLFPDASVYFMPLIVALCIVSIVYNALI

AYRAENIKELIAYSSISHLGVMILGIFSLNALGISGAVFYMFAHGIVTGALFLMVELLYQRYHTYDISFY

HSLAKKAPLFSIFFMLILLASVSLPLTVSFVGEFLILLGIAKINLFYALLAGLVIILGAIYMFAVFRKIF

FMQKQSFIENFSLRLREIVALVCIIVMIFGLGLMPNILLKPIQKDVDNLIKTMNIRAVEQNTLDFLSKIG

EANVK

>ABV53061.1 NADH dehydrogenase I chain N [Campylobacter jejuni subsp. jejuni 81116]

MLNNFLNLELLNISLSYPFLFLITTAIVLLLCSGFWKFHRSFYIGISSLSLIVSAFLILNNANAQGLEAK

AFLATLNNDIVSFYAFLVILCFSFLYLLMQKEENQGEFYALFLFMIASLLLMVSSSNLVLIFIGLESSSL

ALYTLIAMRGSDNAISSAIKYFSVAAVGAGFFVMAVAFIYLKTGTLDLSANLALKNEFQKDPMLLGAGVM

IFVLCAIKLSLAPFHFWLKDVYYAAHTNLVAFISVVPKVAMLVVVIRLFDFLNNTGFEYIIIVLAIFSML

IGAFAALSQNNIKKMFAYSSVVHSSLVLVACIPLLKEQNFDGILLAIFGYWTLFAFANYAVFMILSNYEN

NSYESLNGLLVKKPLIVFCLSISVLSLAGIPPFGVFWGKFMILNTAILNGYWYLALFVALSSVIMLYAYL

KILIHALFMKNDRVYNIKFSFIQNFILACCVCVSTFAILLML

>ABV53060.1 paralyzed flagella protein PflA [Campylobacter jejuni subsp. jejuni 81116]

MRILFLILLSFLNAFAFELVLNTGRENNQAFAVLHASNDLEFTCQKFITEAKVHFECDIAGMVDNKLKDQ

SFSAFDLKFIQEAQKIKMIILPKIQARMFDTSQNIYIDKELSSSSSHKSKAFTFIFTPELVRVKDYDGLD

FNINFPHESLPYVGALDLNSDPVVIPQSADINTYLRIKKEYDKANYNQVVIDAQNAINRYRGSIFASEFI

LYKLRAQNKLYTQDPSMRDQQILEKMIDDAKNWTRTFTSDKNFSEVLHIMLRTYIALAQRADVEYTMSIL

DNEQPNNYFTQLSKLDYADYIYNLNEKEKAVNIYENTYFNTKNLDLAARAAMSLAKNLLSNEQVNKAIEY

INTILKANPEYFGKDIPRSLELAKLFNQKGQFDISASIYEDAFAKMSKLDPSYEETLKDLALVLSHTNRS

SDAKKYLDLYMDDYLDGKYLDEIKKASDEVFFALGDNNASFLHQRYTDLMKQYANKDENIANKALDEDVA

LYYKEGNFSAILAYKDLIESKKIPNATQFLEKAAINDLKNAIKADNCINAANIFMRFSAYDIGQKIENKK

QMLACLIRTSNVEQALDYIDKNYNEDSIFYGLQKASILFDNKQYPQVIKISKDIANSRILKSDDENFKAY

YLQFLSLLRLNDYNQAIKILQILESFPMNFSMVEAYDALLSYANDHNMQTTILTYAPKAIDYQNFKGINL

FSPNLEFIYLDALTKINKNEESLAVLTDLLKLKLSDEDRARALYIQALTYERMQNVQAEKESLKQCLEIK

SASNWQNLCKSKNQILNQ

>ABV53059.1 putative methyl-accepting chemotaxis signal transduction protein [Campylobacter jejuni subsp. jejuni 81116]

MNSIKIKLSLIANLIAIFALIVLGIVSFYFTKTSLHESALKNQTDLLKVTQSTVEDFRSTNQSFTRALEK

DITNLPYQSLITEENIINNVGPILKYYRHSINALNVYLGLNNGKVLLSQKSNDAKMPELRDDLDIKTKDW

YQEALKTNDIFVTPAYLDTNLKQYVITYSKAIYKDGKIIGVLGVDIPSEDLQNLVAKTPGNTFLFDQKNK

IFAATNKELLNPSIDHSPVLNAYKTHGDYNFFTYGLDGKERLGTCTKVFAYTACITESADIINKPIHKAA

FIQAIVVIIVVVFSVILLYFIVSKYLSPLAAIQTGLTSFFDFINHKTKNVSTIEVKSNDEFGQISNAINE

NILATKRGLEQDNQAVKESVETVSVVESGNLTARITANPRNPQLIELKNVLNKLLDVLQARVGSDMNAIH

KIFEEYKSLDFRNKLENASGSVELTTNALGDEIVKMLKQSSDFANALANESGKLQTAVQSLTTSSNSQAQ

SLEETAAALEEITSSMQNVSVKTSDVITQSEEIKNVTGIIGDIADQINLLALNAAIEAARAGEHGRGFAV

VADEVRKLAERTQKSLSEIEANTNLLVQSINDMAESIKEQTAGITQINESVAQIDQTTKDNVEIANESAI

ISSTVSDIANNILEDVKKKRF

>ABV53058.1 putative transcriptional regulator [Campylobacter jejuni subsp. jejuni 81116]

MAYTIKKVEKETKISAHTLRFWAKKGLFPFVQKDENSVKYFSKSDIEWAKWIEWLRISGMPIEQVKHYIK

LCSLGIKTAKERQEMLKQTKKKLQNQIKTLKESEKVLSKKIKIYEEMLANEVDGFNPESKDYQPCDKFCK

ES

>ABV53057.1 arsenical-resistance protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MLGFIDRFLTLWIFLAIFLGLILGIIFPNIALFWNLFEYKSVNVVLTLCLILMMYPPLAKVDYAKLSKVF

DSKKVILLSMILNWFIGPLLMFILAFIFLKDEPLYMQGVIIIGLARCIAMVVVWSDLAKGDREYTSALVA

MNSIFQILFFSTLAYIYLDFLPKLLGQSTLATSLDIDFSALSKNVLIYLGIPFLMGFITRTLLLKYKSKR

WYENTFLPKISPITLITLLATIIIMCSYKANEVFHLPLEALKIAFVLTLYFIFMFFLTWFISKKNHLSYP

KTCSLCFSASGNNFELAIIICIATFGLHSEQAFASIIGPLVEVPVLILLVKWALGKSLNSKKMNQAS

>ABV53056.1 arsenate reductase [Campylobacter jejuni subsp. jejuni 81116]

MKLAFICIHNSCRSQMAEALARHKAEKMGIDIEVFSAGSDTSKGVNSQAIRLMREIYQIDMKKHYSKLID

SLPQNLDIVVSMGCGVACPSLKSRYYFDFGLKDPSGSYDDEFRKIIQILDYKITALLQAIKTNSLKDFTC

>ABV53055.1 arsenical resistance operon repressor [Campylobacter jejuni subsp. jejuni 81116]

MQKFLTIISAINDESRVLILHHLLRYKELCVCDLQELLNMGQSRLSRHLKILKDAGFLYVKRKGTWAYYG

INNELLKLHSDLFENIKNLDIDNIVLEQNTCENDK

>ABV53054.1 hypothetical protein C8J\_1456 [Campylobacter jejuni subsp. jejuni 81116]

MQVFFSTFKEFLYLFVELSVLFIGINILVAFLNAKYSNFFEKHLKQDNFQTRLKAIFFGSLTPFCSCSSI

PLLNAFLKAKVPLSVCMAYLITSPLINPIIIVVFIVSFGIKISFIYIGFLYAIILFISFLLSKFDTSKFL

NNDFLENEFNEKSSCCSTKKCCSSKTHINLKQICIDSLKEYKKILPYALAGTFIGALIHGVFPSNFFEIY

LKDYGILGVFIAAFIGVLLYMNCTAMIPVALVLTQTGIPLGIMMSFLIAGSGCSLPELILLKRNFKTSFL

ILFALLIILIAILFGILMFFI

>ABV53053.1 transporter, putative [Campylobacter jejuni subsp. jejuni 81116]

MQALNQEKFNSLSDIKIILVLCLGVFGILSTELGMMGIIPIVSQNFSVSISDAGWSVSIFALVITFCAPI

VPLLCANFNPKKLMLICLAVFILSSLTSAFVSEFWQLLILRAIPAFFHPIYIALALSMVANLVEDKKEIP

KATAKIFAAVSAGMVLGVPMTSYFGGNFSFKMAMLFFVFLNTLSFIATLFFVPDFKKVNSVKISKQLLIL

RYPLLWISILCVICINAGIWGFYSYFSDFLHSVGKMNFTLISIVLAIYGFSNIIGNYIAGKTLVKNANFT

LILTPLIMIGFYILLFSFYSEIILIIFAFILGILAGVMNNGTHFMISYPFPKAANFSNGLFISVANIGLS

TGTAICGLVISLSDTRYIIVNTIVLLILGIIMIFVRSRIEKMKLRF

>ABV53052.1 hypothetical protein C8J\_1454 [Campylobacter jejuni subsp. jejuni 81116]

MQELEKAGIHGSFKGDSKFFSKNVKVSMMFKSNEWRNFSGALVEFEASARSAWHTHPQGQTLIVTEGEII

TKVPGQKAFIAKKGDVISCPIGVKHFHGATNTSSGAHIALTGEKEGKNVEWLELVSDEEYENALKEARE

>ABV53051.1 hypothetical protein C8J\_1453 [Campylobacter jejuni subsp. jejuni 81116]

MQLRQKAREIFEKFFGKVEEKLLFTSDKEFFTNHINFTFGESFVKANLDTQKYFLITLASTLAVGGKIEF

KALLQGAIKNDISPIVIKEVIYQATPYVGFARVCDFLSLCNKVFKKLNIALVLTPQGTTTQENRKIKGRE

IQNAIFSEANITKMIETTPEDKAFINDFLSANCFGDYYTRMGLDLKTRELLTLVYLISLGGLENQVKAHI

QGNLNMEQSRKDLLNIIAALIPYIGYPKALNALNLLDDIKK

>ABV53050.1 type I restriction-modification system, M subunit [Campylobacter jejuni subsp. jejuni 81116]

MQNKIDKITDILRRDDGISGAMHYTEQIGWILFLKFLDDYETNLKDLAFLDGKDYKSILEEKFSWSVWAA

PKKDGKLDVKNALSGSDLLEFVNKELFPYLKNFKNNDDFKSIEYKIGGIFEFIDNRIANGHTLREVINII

DEISFNKEDEVFALGEVYEKLLKDMGSDGGNSGEFYTPRPLIKTMVEVIDPKPKERIYDPSCGSCGFLVE

SFLHILYKDRTKGKKANLSVEELEFLKNDALFGKEKTPLSYAMGVMNMILHEISSPNIIKTNTLSKKITD

ITEKDKYEVILANPPFGGKEKEQIQENFPIKSNATELLFLQHILKSLKNNGRCAIIVPEGVLFQNSNAFV

SVKKDLLDDFNLECVLSLPSGVFLPYSAVKTNVLFFSKGKKCICEGDGVYYYELIPPYKLTKNKPLEYAH

FKEFLKCYKERKITANSWLVSKKELEERNYDLSAKNPNVKEEKILRTSEEILNSLEENLKTQQEYLNELK

SILK

>ABV53049.1 hypothetical protein C8J\_1451 [Campylobacter jejuni subsp. jejuni 81116]

MTNLPQGWEVKTLSEIGEIVTGSTPSKSNLDFYGKDYPFFKPSDFEQGYFLENAGDNLSKLGFGKARQLP

PKTILVVCIGSLGKVALTKVIGSCNQQINAIIPHKNIISEYIYYYCISSKFQSILFSKAPQTTLAILNKT

EFSKLEIIYPKDIKEQERIVGILDFAFSKIDENIKKAKENLANIDELMQSALQKAFNPLNDNTKENYQLP

QSWEWKSLGDTSNYGKTSQVKPSQLKGNDWILELEDIEKESGVLLQKVLFQDRQSKSNKIKFNKGDILFG

TLRPYLKKVIIADDNGACSSEIMPFSTGNSITNHFIYYYLFANFLHDRISSLTYGARMPRLGTKDGKSLQ

IPLPPLQEQEQIAEHLDFVFEKAKALKELYTKELKDYEELKQSLLDKAFKGEL

>ABV53048.1 RloB [Campylobacter jejuni subsp. jejuni 81116]

MGTDDLRKKRNTKTRDREAKRKKNEIILIVCEGEKTEKNYLNQLKDFFRLSNVSINIISSKKPNPSQIVE

FTKEKNKDYSYNKVYCVFDKDTHSDFDKARQECEKYKFEAITSNPCFEFWILLHFTYTTKSFSTNSPCNE

LIESDLKKHIKDYKKDYNFTSIIKQNLSTAIANAQKANKEAEKNNYTSSYTFMDKLALKFQELNSARINQ

>ABV53047.1 hypothetical protein C8J\_1449 [Campylobacter jejuni subsp. jejuni 81116]

MLIEFRVENFLSIQDEQILSMMASKDNTFFDSHTNGDKKLALLKSSVIYGANASGKSNIVKALQTMKTIV

ISSANTQRGDKLPITPFLLGDEDDKPTKFEIIFIQNDTKYQYGFILNSEKILEEWLLTFDENNTEQNWFE

RIYNKKEGRYNYSFGDQFLADEIYKQLWENSTRDNALFLSVAIQLNNEQLKPVFDFFNLKLQIANSNGWG

NGKSITINEYKKDKELVNSFFKIADLDIEGVEIKTSDIDENSLPSNLQNIPQELKEKIIQEVKNIQNLKN

VKILEDISFIHLSQKNQIKFLNFNDESDGTRKFFNIAGIWIDSLKKGNILIIDELNTHLHPLMTKFLVNL

FHNEDLNKSNAQLIFTTHDTSILNQDIFRRDQIWFCEKQNKATKLYPLSDFEESEERRDKTNLENDYLLG

RFGALPYFKEILSSWSDNGN

>ABV53046.1 hypothetical protein C8J\_1448 [Campylobacter jejuni subsp. jejuni 81116]

MQNLYSEDDTRVKFIDAKLYDSSWNEENIKRNYYFTDGRKLLGGKRAQRKFADYLLRYEGNNLAIIEAKK

FSKDPLDGLSQGIEYAKILNVPFVYSSNGEKIYEYDIRSHSGKYIDKFPSPKELFDRIYGNVKEWQYRLL

TQNVMYIPQKELRYYQKIAIDKVIEAIINNKNRILLTLATGTGKTTIAFNLCYRLLEARWNKENKDQKPK

ILFLCDRVSLRDQALGEFNPIESDCKAISAEEIKKNDGKIITNANVFFGIYQSLAANSKEQENTQEEQES

KFYLQYPKDFFDLIIIDECHRGGANEEGSWRAVLEYFSYATQLGLTATPKKEENIDTYEYFGESVYDYSL

KSGIEDGFLTPYKVKLIKTTLSDGYTYNPDDLIQGELEKGFYKQSEFERNIFLPNYNDFIAKKILELINP

MDKTIIFCANQAHANEVKRAIDKYKSVKRDDYCVRVTSDEGKIGLDYLKQFQDNDKSFPVILTSSKMLTT

GVDAKNVRNIVLLANIGSMVEFKQIIGRGTRVYEGKDFFTILDFVGATKLFYDPKWDGEKIKELKEQNKQ

EKITKEQIKQTKEESKEKKSVTIHLKGTKLKVLDITTSYVGAQGKPLSTKEFLEFLIGKLGEYYDDEAKL

REIWSDQKNRERFLKALANDGVDEDALKDLRKIFQKDCDIYDVLAHLSFNAEIKTRQERVLQVENGEFLK

RFQKEKAIKFIEFLLNRYQEYGIKDFDDGLKPLIELSSLGNVRELADEFGGLEILKQSFDDLQREIYAR

>ABV53045.1 putative NADP-dependent alcohol dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MQYKILENNRIASKGYAMLSKDAKFTPFEFSRHAIGDNDILIKILYAGICHSDIHTARSEWGEATYPCVP

GHEIAGEVIAVGKNVSKFKVGDYAGVGCMVNSCGECDACKRSQEQFCENGKTIFTYNSCDVFHGNENTYG

GYSNNIVVSEKFAICVPKNAPMHKVAPLLCAGITTYSPLKFSKIKEGSSVAIAGFGGLGMMAVKYAVKMG

AKVSVFARNENKKADALAMGVSSFYTSTDKNAVKERFDLIISTIPTPYNPAIYLDLLKFGGEMAIVGLPP

VEDKVNIGINELVHKAGKKVYGSLIGGIAETQEMLDFSLKHEIYPETELITPQEIDKAYENLTSGKAKFR

YVIDMTKE

>ABV53044.1 BLC-like protein [Campylobacter jejuni subsp. jejuni 81116]

MLELIGELSLQNYMGEWLEMARKPAFFQKSCLNSKAKYELKYKNGVPYVEIENFCSKENEISSIKGKAKI

VSNRQLAVRFNIFMNLFNKVNYEIIFIDSEYKVAIVGSPDKKYLWILARNIIDEKSIKELLDIAKQRGFS

VSDVIFDKY

>ABV53043.1 hypothetical protein C8J\_1445 [Campylobacter jejuni subsp. jejuni 81116]

MTKENSQCNFEECGFNYTLALINGKYKMSILYCLFRYEIVRYNELKRFLSSISFKTLTNTLRELENDGLI

IRKEYAQIPPKVEYSLSKRGQSLIPILQAMCKWGEKDKKEKNA

>ABV53042.1 MdaB-like protein [Campylobacter jejuni subsp. jejuni 81116]

MKNILLLNGAKEFGNSKGQLNLTLHNHALEILKTLGYEVDQTHIDQRYDPKEEIQKFIKADAVIYQMPAW

WMGEPWIVKKYIDEVFGLGAGVLFKNDGRTHENPSKNYGKGGLDHGKKYMFSLTWNAPLEAFNDKNEFFE

GKGVDMVYWHLHKAHEFIGMKALPTFMCNDVVKNPQVEKYLNEYELHLKKIF

>ABV53041.1 integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MTRTKYLYILLVLAMFLWGSSWPTSKILSAYADTSVITFWRFFFVLLGSLMVLGFLRIPLSLEKSILKWV

LIAGILNGLYTFVFFIAIKHGLAGKGGVLVTTMIPIFSYLIFMIAILFQKDKKSTHKIIKSEILGLFLGL

LSGFCLLNLGSLEDLFGKFNILFLTCSFIWALIAVFNHKAKGVHPLAINFYINLISVLMFSWVLFDVKSY

EIFHFEFKFWISMFVVAFLSTIIGTSIYYYGIHILGSVKANSFVLITPASALICSYFILDEVPNALTLLG

CALAIGAIYFINIYGKKA

>ABV53040.1 hypothetical protein C8J\_1442 [Campylobacter jejuni subsp. jejuni 81116]

MSIKIIEASINSSLQDFGRKKFAKFGIARSGAMDEDALRMANILLGNKQDEAGVELCLKGGKYEFLDGNY

FVLSGAEFEAKLNNQKIKTYKVYKANKGDILELGLAKIGFRGYLCVAGGFEIKSFLNSKSSDAKMGVGFF

EGRALQKDDILNTHNTFIPFNLEARECENPLFKSHKEPIIRVILGTNEDAFTQKGIDTFLNTSYKVGSKS

DRMAIYAESSKSIEHKNSADIISDPAVFGSIQVPKSGIPIILMAGRQSTGGYTKIGTVIENDLSLLAQAK

LGSSFKFQSISMQEALELYKQREMKFKAMDQKINLDFENLI

>ABV53039.1 hypothetical protein C8J\_1441 [Campylobacter jejuni subsp. jejuni 81116]

MFSVHFSGSKALLLRFEQEISPQINAYVLSTEQRIQKALKEGEIYGIDELVSAYASLLIYFNPCILSLNS

LLDFLEKIKKDIKLAEQNSSLCIEVPLCYDEEFGLDLEFVCKHNQISKEELISLHTKPYYLVFMLGFMAG

FPYLGGLDERLFTPRLSSPRAKIEAGSVGIADKQTGVYPISSPGGWQIIARTPLEFFDKEDEKNPTLLKA

GMFLKFKAISKDEFFDIQEQVAKKVYQREIYEYKNH

>ABV53038.1 hypothetical protein C8J\_1440 [Campylobacter jejuni subsp. jejuni 81116]

MFKVDLNSDLGESFGAYKMGMDEEILKFVSSVNVACGFHAGDPCVMDKTLNLAKQNGVCIGAHPSYPDLL

GFGRRNMQISFEEAKNYALYQLGALFGFAKAKGMKIQHFKAHGALYNMAAIDENLALALCEAVASFDENI

IFLGLSNSAMNEAAKKKGLRYANEVFADRAYNDDGTLVSRKLEGALIHDENLAIKRVIKMIKESKVTSIN

GKEIDLKADSICVHGDNIKALEFVKKIKENLEKEQIQICALENFI

>ABV53037.1 putative sulfate transport system substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIISLALALALSASAAELKMATTTSTDNTGLLDALKPLYEKESGNTLKWVAVGTGAALKMGEDCNADV

LFVHSPKAEKEFMKKGFGVDRTPVMYNDFIIIADKSLASKFKGKNLKESLELIKNEKLTFISRGDKSGTD

NKEKSLWKNLGGVPEKQSWYQQSGQGMLASIKIAEEKKGVILTDRGTYIKYEANEKGNPNLVIVNEGDDS

LKNFYSVIATNPKHCKNVNYTEASKFIKWVTSDKTLNFIADFKLLNKPLFVIDAKTRKD

>ABV53036.1 tungsten ABC transporter, permease protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MDYIFDGFKQALFLLFNADESVISAIKTTLLSSSISIVLALLIGFPLGFILGFFDFKFKRFIKLIIDTSL

SFPTVAVGLILYALISSRGPLGEFGLLFTIKALILGQFILALPIVIALFSNLIENMNKKHFLLIKSFHLS

PLKLVLTMIYELRFALISVVALAYGRIVAEVGVAMIVGGNIKYDTRTITTAISLETNKGEFASGIALALV

LILIAFCLNFITHKLKRT

>ABV53035.1 tungsten ABC transporter, ATP-binding protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MIEISNLFFNYQNKEVLKIKNLKLDTSKINILMGANGSGKSTFLRILKFLEGDFSKNISYFGNFKLNNKQ

KREIYLLFPEPILLNRSVRANFLFTLKTYGIKEDIEERIKESLMCLNLNESLLNKYPNELSSGQSQKIAF

AIALSVRAKYYLLDEPSAFLDKNTTLLFKKAILKMHENFNTGFLIASHDKHFLDSLAQKKLYLHSGEILE

FENTNVFELENQGVKFCNFIDFSNCKKYKDFKKPPSKIAIDPYKISFFNSKNIPKNNYEFILEKCYIIAL

RSRKSDVFIRVSCMDKILEFALEKQEFLKFDLKLYEELSLYFYEDAICFLN

>ABV53034.1 acetyl-coenzyme A synthetase [Campylobacter jejuni subsp. jejuni 81116]

MLNQNNQELFKPSKEFSRNARIKNLCEYYDLCDEAKEDFEGFWKRQALEKIEWFSPFSRVLNEDKAPFYK

WFEGGTLNVSYQCLDRHMKTRRNKAALIFEGEMGDYEVYTYRRLLHETCKAANLLKKFGVKKGDRVVIYM

PMIPETAIVMLACARIGAIHSVVFGGFSPEALRDRIIDAGAKLVVTADGAFRRGKPYMLKPAVDKALSEG

CESVEKVLIVIRNNEPIEYIKGRDYVYNELVKNESYKCEPEIMDSEDLLFLLYTSGSTGKPKGVMHASAG

YILWAQMTMEWVFDIKDYDNYWCSADVGWITGHTYVVYGPLACGATTIMHEGTPTYPNSGRWWRMIEEYQ

ISKFYTSPTAIRMLHADAPDEPRKYDLSTLEVLGTVGEPINPSAWKWFYDEIGGTKSPIVDTWWQTETGG

HMITPLPGATPLKPGCATLPLPGIFAEVIDEEGNKKDEGEDGLLCITKPWPSMIRGIWGNDERYIESYFS

QAKKDGKAVYFSGDGAFYDKNGYITITGRTDDVVNVAGHRIGTAEIESAIAKHPSVAESAVVSILDAIKG

ESLFAFVVLSPASSCDLGGAIETLKELNDILRVEIGPIAKIEKILYTPGLPKTRSGKIMRRILRTIARGE

EIKQDISTLEDSGVVETIVKLAKAEFE

>ABV53033.1 UTP--glucose-1-phosphate uridylyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MLQTCIFPAAGYGTRFLPATKTLPKEMLPILTKPLIHYGVDEALEAGMENMGFVTGRGKRALEDYFDISY

ELEHQISGTKKEYLLDEIRSLINRCTFTFTRQNQMKGLGDAVLKGKPLVGDEAFGVILADDLCVNEEGLN

VMAQMVKIYEKYRCTIIAVMEVPKEQVSNYGVIFGNFVEENLIMVNSMIEKPSPDEAPSNLAIIGRYILT

PDIFGILENTKAGKNGEIQLTDALLTQATNGMVLAYKFQGKRFDCGSVEGFVEATNYFYEKSKC

>ABV53032.1 glucose-6-phosphate isomerase [Campylobacter jejuni subsp. jejuni 81116]

MLNNTLFFKQSEIHTISSYANRINDEVKSGDIGYYHLIDTSLSLIDESLAFIKDKEHIKNIVLVGMGGSS

CGVKALRDMLFNEKSNQRELFILDNTSSHSFNKTLEKIKLEESLFLIISKTGSTIEVVSLFKLLIEHFKL

DMQELKKYFVFITDKDSKLHQEGENLGIKCFFIPANVGGRFSILSAVGIVPLCFCGYNAKALLEGAKACF

EDFFTHKKDEILQKAYHYCTHKNANINVLFSYSDAFKGFNEWYIQLIAESLGKKQGYKRIGLTPIALIGA

RDQHSFLQLIMDGPKNKTVTFLKIKDAQKAPIIPDIHFKFLDSLSNKVNLHELLNAQCDATMHALIAENL

SVDVIELEKLDAWHAGYLMYYYELFTSTCGVMLGINTYDQPGVEVGKLILKNILNS

>ABV53031.1 possible bacterioferritin [Campylobacter jejuni subsp. jejuni 81116]

MSVTKQLLQMQADAHHLWVKFHNYHWNVKGLQFFSIHEYTEKAYEEMAELFDSCAERVLQLGEKAITCQK

VLMENAKSPKVAKDCFTPLEVIELIKQDYEYLLAEFKKLNEEAEKESDTTTAAFAQENIAKYEKSLWMIG

ATLQGACKM

>ABV53030.1 hypothetical protein C8J\_1432 [Campylobacter jejuni subsp. jejuni 81116]

MKVLNFFYENHPKFEVSYERKNQISKPNIIIKGPRFCGKKTLIFNFLSQFKASEILFLDLYDTRFEKQSL

ERLADFLNENLQIKILCLYNLDFIPNLEKIKIPIILSTNIKDLNINGFEELELDYFDFEEFISVSKKNLP

INNLVGLFLQSGRSKFGEKNILLRQSFTLLELEILKYLALNLGQQISISKIFIELKKRLKTSKDSVYQAI

KKLENTYVIYTLKHDEKKLQKIYFKDFGLRNNLCISKDFSHLFENLVLSELFKFKEEFFYNKYFNFYSQI

SKIAYISSPTLDIDLIKLRAKKILPKALELGIFHVIFITLSSEDNFFEQGVKFEVISFDKFSLGF

>ABV53029.1 hypothetical protein C8J\_1431 [Campylobacter jejuni subsp. jejuni 81116]

MNEMFDQSFKKIEQERAFIEAFFKDAYKTGFRTSNQINLEKLITIKNKYRIENLYDFAEYKKRIQKIPKS

MGIAQALVESATGTSRFAREANNLFGEWTWGEKGLIPDLRHPDKKHKIKIFDSLQDSVDSYVLNLNRHFA

YEKFRDARAKFESEGKEITGLEAIKTLDSYSERKGYYINLITKIIKRYNLEKYDTNSNNT

>ABV53028.1 putative diaminopimelate epimerase [Campylobacter jejuni subsp. jejuni 81116]

MKFYKYCASGNDFVITNADRKEDRSALAKELCNRYEGIGADGFIVILPHEKYDFEWEFYNNDGSRAAMCG

NGSRAAAHFVHHINKINPNMSFLTGAGVIKAKVNQDKVEVSLGKIKSVQNTFEELGKTWQLCNTGVPHLV

HFCQNLDEFDTMLCQKMRQKYNANVNFVKILDENHLKVRTYERGVEDETLACGTGMGACFYLAFLNKKVQ

NKVKITPKSGEEVGFAYKNEELFFEGKVKYCFEANYNFS

>ABV53027.1 dephospho-CoA kinase [Campylobacter jejuni subsp. jejuni 81116]

MKNAFFVTASIACGKSTFIEIANSLGFKSISADKIAHEILDENALELEKIFSPFSLKNLLTKEKKIDRKI

LGEIVFNNKEAKKILENFTHPKIRAKILEQMQILDKENKAFFVEIPLFFESGAYENLGKVIVIYTPKELS

LKRIMQRDKLSLEAAKARLDSQIDIEEKLKKADFIIKNTNSYADFRQECVKVIQEISKGKM

>ABV53026.1 phosphoribosylformylglycinamidine cyclo-ligase [Campylobacter jejuni subsp. jejuni 81116]

MKISYEDAGVSIDNGNAFVEAIKPLVKETFNDNVVGGIGSFAGAFRMPSGFKKPVILGATDGVGTKLRLA

IDAKKYDTIGQDLVAMCVNDLICNFATPLFFLDYYATVKLEVEVAKAVVSGIAKGCKMANCALIGGETAE

MPGMYAKDDFDLAGFAVGMAEEDEIDRSKFVKNGDILLALPSSGLHSNGYSLARKVLFESLKLKFDDKIE

GKNLIDILLEPTRIYVRDFLTLKPYISALAHITGGGLVENLPRVLPSGMGATIRKHHLKTPEIFYTIGQA

VEESEMYRSFNMGVGLVMVVDPSNVSKVLENSDAFIIGEICINEGIVLE

>ABV53025.1 hypothetical protein C8J\_1427 [Campylobacter jejuni subsp. jejuni 81116]

MKNIVFHSDGFGDLLVCFKALYAIKQLYPEYKLFLLTNGLMESDFLEKIPFIDEVLIYKDDFLEKIQSKN

PVIFITTRRQGLYFKKLKFLNVQKCIVFPHLISIISKNLTTPLPFFRAKKHMSEIVLKLVRMINTRHFDK

NFNQIDFSKIKNLLPYDARLSDNFFKQIDTKYEKIIGINAFSNNSEYRGFNFFIKDWIGLARQLSLKYPK

FLFILLNFSTNSIQYNIDQNANLKVFCNNKNIASLVSISQKLDFLITVDTGNLHLCDILQIPTLAFTSSL

AAYRFGGGSYGGRFDKLIVKPAWQKEYRKIYEIFTKKAENNLENL

>ABV53024.1 hypothetical protein C8J\_1426 [Campylobacter jejuni subsp. jejuni 81116]

MPIFMICSTLLAVIVVAYYILKKYNPIFVFFLSGIILLIFAFYITGTPIPKAPSREHASFLNVLLDSYAF

ITATFKSQLSGVGLIIMSVAGFAAYMKHINASAKLAFLANKPLGKIKNKYLILSGTFVVGMALKIVISSY

AGLLLLLLACIYPVLISLKIRPITAVCVLSLIALDYGPKDGNSINMADMVGQSDNVVGLFLNYQIYSVIA

YVVVIAILIPFYFAWIDKRDKEKGVLNDEVEIPQIIDPRCPTFYILFPWLPVVFLFTAYFFTIKLDVVTA

NFVSISLVFLVEFARHRNARKLGEDMMVILKAMAEIFISVVSIIIAAGVFAEGIKALGGVNILANAVSNL

GTGNFAWFGILLSIAILSFLVYFATVIMGSGIAAFNAFGKLAPDIATKLGVAPITLVLPIEIASCLGRAA

SPIAGGIIALAGFAKVAPMDIIKRTTPLLLIAMLVNVLVAFYLAQTNPLPKEQNTTKIAVSLNNK

>ABV53023.1 hypothetical protein C8J\_1425 [Campylobacter jejuni subsp. jejuni 81116]

MARILAFDIGISSIGWAFSENDELKDCGVRIFTKAENPKTGESLALPRRLARSARKRLARRKARLNHLKH

LIANEFKLNYEDYQSFDESLAKAYKGSLISPYELRFRALNELLSKQDFARVILHIAKRRGYDDIKNNGDE

EKSEILKAIKQNEEKLVNYQSVGEYLYKEYFQKFKENSKEFINVRNKKESYERCITQSFLKDELKLIFQK

QREFGFSFSKKFEEEVLSVAFYKRALKDFSHLVGNCSFFTDEKRAPKNSPLAFMFVALTRIINILNNLKN

TEGILYTKDDLNALLNEVLKNGTLTYKQTKKLLGLSDDYEFKGEKGTYFIEFKKYKEFIKALGEHNLSQD

DLNEIAKDITLIKDEIKLKKALAKYDLNQNQIDSLSKLEFKDHLNISFKALKLITPLMLEGKKYDEACNE

LNLKVAINEDKKDFLPAFNETYYKDEVTNPVVLRAIKEYRKILNALLKKYGKVHKINIELAREVGKNHSQ

RAKIEKEQNENYKAKKDAEIECEKLGLKINSKNILKLRLFKEQKEFCAYSGEKIKLSDLQDEKMLEIDHI

YPYSRSFDDSYMNKVLVFTKQNQEKLNKTPFEAFGNDSTKWQKIEVLAKNLPEKKQKRILDKNYKDKEQK

DFKDRNLNDTRYIARLVLNYTKDYLDFLPLSDDENTKLNDTQKGSKVHVEAKSGMLTSALRHTWGFSAKD

RNNHLHHAIDAAIIAYANNSIVKAFSDFKKEQESNSVELYAKKISELDYKNKRKFFEPFSGFRQKVLDKI

DEIFVSKPERKKPSGALHEETFRKEEEFYQSYGGKEGVLKALELGKIRKVNGKIVKNGDMFRVDIFKHKK

TNKFYAVPIYTMDFALKVLPNKAVARSKKGEIKDWILMDENYEFCFSLYKDSLILIQTKDMQEPELVYFN

AFTSSTVSLIVSKHDNKFETLSKNQKILFKNANEKEVIAKSIGIQNLKVFEKYIVSALGEVTKAEFRQRE

DFKK

>ABV53022.1 CRISPR-associated protein Cas1 [Campylobacter jejuni subsp. jejuni 81116]

MSYDEAFKTLLISSNAKLNLELNHLVIKQDENIAKLFLKDINIIVLESLQVSLSSALFNAFARHKIILLT

CDETHSINGVFTPFLGHFQSAKIAKEQMNVSAQKKAILWQKIIKNKILNQAFVLKKHNKIGQSNELINLA

KKVSLNDSKNIEAVAAALYFKTLFGVSFSRDELCFENSALNYGYAIIRACIIRAVCISGLLPWLGIKHDN

IYNSFALCDDLIEVFRASVDDCVLKLKGESEFLSKDDKRALIGNLQSKINFDGQNYPLNRAINHYVANFK

NALLYEDELKIVKFDD

>ABV53021.1 CRISPR-associated protein Cas2 [Campylobacter jejuni subsp. jejuni 81116]

MIEDKFMRVLLMFDVPTKSKKEQKLASKFRNNLIKLGYFMLQFSVYMRICKGLSSAKSSIENVKKILPPY

GNVRALIITEKQFDKMELLLGGIVFNEKVNNETNLTLFDIDSHGEFKYKNSNNEEIQLNKKQEKYHQQNL

FEF

>ABV53020.1 putative molybdopterin biosynthesis protein [Campylobacter jejuni subsp. jejuni 81116]

MLMSYEESLKILHSHIKTYEKIEKIALTECLGRILAQDIKAPKNQPEFPTSAMDGYAIKFEDQDKPLKIL

GLTPAGTMPQFSVQNGTCVKTFTGSLMSEGSDTLVPVENVRVENDTLFIEKKVPQAFAVRAVGENYKKDE

ILLKKGTKLNYSEIALLAELGFFHISVFIKPIVGVLSSGSEIKDLGEALENPAQIRSSNHIAIANLAKNL

NCDTRVFPLLKDDEKATFSTLESALQSCDILITTGGVSMGDFDFLKKAVKEYEIIIDKADIKPGRHIKIA

KANEKFIIALPGFPYSAMVMFNLYAREILNSWLLQPKDYICKAFLQGSYKKKTPYLEFVACNVEFKNGRI

LANLEGKKEGSSAIINNLNNKAALMVVPKECEILENESLVDIIFMP

>ABV53019.1 molybdopterin converting factor, subunit 2 [Campylobacter jejuni subsp. jejuni 81116]

MKHFTLYQGSLDIPKIYSQWYEFAKDKNCGALLTFCGIVREEGGIEALSFDIYEPLLKKWFDEWQKRVDF

DDISLLFAHSIGDVAVHESSYFAGILSKQRKLGLKLLNEFVEDFKASAPIWKYDVINKERIYAKERSTKL

CGAGLLKG

>ABV53018.1 ThiS family protein [Campylobacter jejuni subsp. jejuni 81116]

MIKVEFLGPINKENLELEVKNLKELKEILQKDESLKEWLELCAVSLNDEIIFDENTKLKDGDKIALLPPV

CGG

>ABV53017.1 oxidoreductase, putative [Campylobacter jejuni subsp. jejuni 81116]

MNRRNFLKFNALTLASMGVAYANPMHDMHSMHKNHSINHDLDTSFINFAPKNLKLLDPKQFPQGEILKAL

PLLKNESKEKNIFRATLEIKENHIELIKGKKTLFYTYNGLVPAPKIEVFEGDKLEILVKNKLKEATTIHW

HGVPVPPDQDGSPHDPILAGKERIYHFEIPQDSAGTYWYHPHPHYTTSKQVFMGLAGAFVIKAKKDALSH

LKEKDLMISDLRLDENAQIPNNNLNDWLNGREGEFVLINGQFKPKIKLATNERIRIYNATAARYLNLRIQ

GAKFILVGTDGGLIEKAIYKEELFLSPASRVEVLIDAPKDGNFKLESAYYDRDKMMVKEEPNTLFLANIS

LKKENVELPKNLKIFKPSEEPKEFKEIIMSEDHMQMHGMMGKSESELKIALASMFLINGKSYDLKRIDLS

SKLGVVEDWIVINKSHMDHPFHIHGTQFELISSKLNGKVQKAEFRALRDTINVRPNEELRLRMKQDFKGL

RMYHCHILEHEDLGMMGNLEVKE

>ABV53016.1 carboxynorspermidine decarboxylase [Campylobacter jejuni subsp. jejuni 81116]

MFYEKIQTPAYILEEDKLRKNCELLASVGEKSGAKVLLALKGFAFSGAMKIVGEYLKGCTCSGLWEAKFA

KEYMDKEIHTYSPAFKEDEIGEIASLSHHIVFNSLAQFHKFQSKTQKNSLGLRCNVEFSLAPKELYNPCG

RYSRLGIRAKDFENVDLNAIEGLHFHALCEESADALEAVLKVFKEKFGKWIGQMKWVNFGGGHHITKKGY

DVEKLIALCKNFSDKYGVQVYLEPGEAVGWQTGNLVASVVDIIENEKQIAILDTSSEAHMPDTIIMPYTS

EVLNARILATRENEKISDLKENEFAYLLTGNTCLAGDVMGEYAFDKKLKIGDKIVFLDQIHYTIVKNTTF

NGIRLPNLMLLDHKNELQMIREFSYKDYSLRN

>ABV53015.1 hypothetical protein C8J\_1417 [Campylobacter jejuni subsp. jejuni 81116]

MEALMDLEKLRLARSLYYQCLGELFVFSFSEERLSKLQEYLKTMQECLFDENLKSNFDILLKHLDDENSI

QAFFKEYDLLFLSLKNSIPTTFSYIEEGFENSNPLLCVRQILVKSKIRRNEKFFKESEDSVGFCLLLMSE

FLRQNEDDLAKELFEKVINKSIDEFLGDVFMNKNANLYKEIASIAMAFMEFERLCFEVEKPAKINSKKVQ

NDLSRSEFLRREANKQRRTREKSQGIS

>ABV53014.1 possible periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKNRREFLKKSAFALGAAGVLGSTTLALAKDEERKDLVKGKSKKKEVLFQRSANWENYYIKAE

>ABV53013.1 hypothetical protein C8J\_1415 [Campylobacter jejuni subsp. jejuni 81116]

MSSVGENIKLTRRSFLKMAALSSLATPLLARSETLREASADELKEAYEGSKKVKTVCTACSVGCGIIAEV

QNGVWVRQEIAQDHPVSSGGHCCKGSDMIDMVRSHVRLKYPMKKENGEWKRISYEQALSEIGEKLAAYRK

ENPESVMFLGSAKMSNEQAYYVRKFAAFFGTNNVDHQARI

>ABV53012.1 hypothetical protein C8J\_1414 [Campylobacter jejuni subsp. jejuni 81116]

MTNHLGDIQRSKCIIIIGANPAVNHPVGFRHFLKAKEKGAKLIVVDPRFTKSAAKADIYARIRPGTDIAF

MYGMLKIIFDEGLEDTKYLDERVFGIDKIREEAAKWTAEEVENVTGISKELLVQITHEVAKNKPTTLIWA

MGLTQHTVGTSNTRLAPIVQMVLGNIGKFGGGVNILRGHDNVQGASDMACLSENLPGYYPLNEATWRYYA

KIWGVDYEWLLGNFVSKDWMHKTGLSLARWWAAALNGKDGNDAIDNAGTPLKALVVMGNGITSTAQQVKV

KEGLEALELLVLADPFVNEAGIIAERKDGIYLLPAATQFETSGSVTATNRSGQWRFKVVDPLYESMEDQE

ILFELAKKLGFYEDFTKTLRDEKGEIVWPENATREIAKAVRSIGLNGWSPERLKKHTLYWDKFDEVTLEG

KDEVAGEYYGLPWPCWSDKHPGSPVLYNTDIEVAKGGMGFRNNFGLEYEGESLLAKNAPLNSPIDTGYPQ

ITKDNIEKVLGITLSAQEKEKMGSTWSYDDSNIIATKCIEKGIVPYGNAKARAVVWTFKDKIPLHREPLH

SPRNDLVQKYPSFEDQKALYRVDTKFVSVQQAKDYSKEFPLNLVTARLVNLNGAGMENRASMYLTRLTPE

MFCEINPELAKEQDIKAGDMIWVHSPEGTKIHVRVKVNPGVAKDMIFLPFHFTGVMQGVDLTHNFPKGTK

PYASGESANTVTNYGYDIMCQIPETKGGLCRISKDGK

>ABV53011.1 putative formate dehydrogenase iron-sulfur subunit [Campylobacter jejuni subsp. jejuni 81116]

MSKVNFANLEKERLKFFCDNERCIDCNGCAVACDEAHELPIHIRRRRVITLNEGIQGKEVSTSISCMHCD

DAPCSIVCPVDCFYIRADGIVLHDKEICIGCGYCLYACPFGAPQFPKDSVFGNKGIMDKCTMCAGGPEAT

NSEKERELYGQNRIAEGKVPVCAAMCSTKALLVGESSKIEEIYHNRLMNRNYGIPNPSESLEWKIAYTGK

ERL

>ABV53010.1 formate dehydrogenase, cytochrome b subunit [Campylobacter jejuni subsp. jejuni 81116]

MRKVFVTLLLSVASLFAYGSERMGQDTQIWDFHRITNIPNYDTFGKLWTTLQGEYIATIALIAVIAVLSA

FALHYMVIGPKQFSHDGKKIYAFTLFERLFHFIAAISWVILVPTGFVMMFGATFGGGLFVRVCKNLHAFA

TVLFIISIIPMFLWWIKRMLPASYDIRWMMIVGGYLSKVKRPVPAGKFNFGQKSWYYIAVFGGFLMIITG

GFMYFLDFNSTAIQGLFGLTQIELLRISAIVHNFLGIVCAVFFGVHIYMAVFAIKGSIHSMISGYKEEEE

VYILHSYWYKELSNKKQIEPSFSYDPNVKI

>ABV53009.1 FdhD protein [Campylobacter jejuni subsp. jejuni 81116]

MDPLFTTQILKYKGDDSFTCDDTLVREIKLEIFINDERVGALMATPVDEQALAIGYLMSENIIAKVSDIE

SIETKDDGMSVHIKAKIDKENLAKLNAEGVVISGCGRAHTANIDPEAIEASKISSDVKFSKDEILKQMST

FYTQCELYEKTGCVHTAKLFVDEKTFFIGEDIAQHNTIDKALGKARLAGVDLSQCFLMVSGRLSSEMVAK

AVMHKIPVLVSRTAPTCLGVMIARKFDLTLCGFARENKINIYSGEFRIHG

>ABV53008.1 hypothetical protein C8J\_1410 [Campylobacter jejuni subsp. jejuni 81116]

MDKNQEKEIISYMRELLNSNEKLDCGTAFKIAKKFNVNIEKIGQLADENHMRIDNCELGQFGHLDFEKAK

IEVLKKIEPSLDEKRRIFCKDARDIAKEGCGLKSMRSALKAYKVDVKYCQLGCFKEKKGKQFIVRTKTWI

ENADGDLLFGRGKTELLELIGQTGSLLHASKLMGINYKKAWMHLQTLQKNSQEILVSTRQGRSKESGTKL

TPRALELMENYSILQKDIEEYANKRFKELFLKGKK

>ABV53007.1 methyl-accepting chemotaxis protein [Campylobacter jejuni subsp. jejuni 81116]

MFKSLNIGLKLIFSVATVVVIGLVILISLITKQVSQNITKNTEDILASITKEYATQTQGIFGEMIALNKS

ISGTLTEMFRSTSKEDLDIDNITNIITNTFDNSAYSNFTYLYLIDPPEYFKEESKFFNTQSGKFVMLYAD

EEKDNKGGIKAIQASDEIANLQVVQDILKKAKYGENKVYIGRPIKMNLEGQDFDAVNVAMPIFDRKNQVV

GVIGMTLDFSAIATYLLDPKSQKYNGELRILLNSDGLVAIHPNKNLVLKNLKDVNPNKGAQETYKAMSEG

KNGVFNYIAFDGDDSYAAINSFKVQDSSWTVLVTAPKYSVFEPLKKLQLIIIGASFIFIFVVLGVVYYCV

RKIVASRLPVILSSLESFFRFLNHEKIEPKAIEIRANDELGAMGRIINENIEKIQISLEQDQNAVDESVQ

TAREIEKGNLTARITKNPINPQLVELKNVLNRMLDVLQSKIGSNMNEINRVFDSYKALDFSTEVLDAKGE

VEITTNILGKEIKKMLVASSNFAKDLANQSEELKNSMQKLADGSNAQASSLEQSAAAVEEINSSMQNVSG

KTVEVASQADDIKNIVNVIKDIAEQTNLLALNAAIEAARAGEHGRGFAVVADEVRQLAERTGKSLSEIEA

NINILVQSVNEVAESVKEQTAGITQINDAIAQLETVTKENVEVANVTNNITNEVNQIAAAILEDVDKKRF

>ABV53006.1 hypothetical protein C8J\_1408 [Campylobacter jejuni subsp. jejuni 81116]

MKIDCRNLSCPQPIVETKNALEKLQENEILEIVLNSIISKNNVVKFLNSLNLNPIIDENAQEFCIKVQKK

NFNSSEVNIHDYNVLFLKTDKVGEGELGQNLLVGFLSTLKNLDHAPSKILCVNESVLINVDENHKAHLAM

KELENLGIEIISCGACLEFFNKSKELKIGNIGNAYEILNELFGKAKIITL

>ABV53005.1 putative selenide,water dikinase [Campylobacter jejuni subsp. jejuni 81116]

MQKTPALLSDIGNNEDASVYQISPDLALVQTLDFITPIVDSAYHFGAIAAANALSDVFAMGAEVINALNI

VGFDTCNHDINILKELLEGANDKVQECNALVVGGHTIESTELFFGLSVTGKVHPSKFIANNTAKVGDCII

LTKPLGTGILSTALKAQMLNQKHLDIMLKSMMELNYKASQIALKFHPSAMSDVTGFGLLGHLKEMLNKNI

SFEIFESELPFLDGVKEYFNMGLIPAGAYKNLEFIKELIPDLNEEKLLLCDPQTSGGLLISISEKESLEC

LKKLEDENIQAKIIAKVVNKQENDIIIS

>ABV53004.1 bifunctional PutA protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MIQKALALAEELQGQIEANISNSEKEFHAKMQKLLNNPKNKVMLIELLDRSFRCKDKNASFELIEYTLSK

YGIADFFSTFEKFLLFSFLNFGKFAPNLSVPFFVKHLREDTKAMVLDANASVLEPHIKKRKEQDKITLNV

NLIGEEVLGEAESKYRMQKYEEALKSSYITYISIKITTIFSQINIIDFDYSKEEVVKRLDYLYALALEEE

KKQGVSKFINLDMEEFRDLELTVAAFMESVAKFDIKAGIVLQAYIPDSYEYLKKLFSFSKERVLKGMKPI

KIRFVKGANMESEETIASQKGWELPTFYKKIDTDSNYNKMLDFILEGDNHKYINIGIASHNIFEIAYAYT

RISEAGALDSFTFEMLEGMSLQCSYELSKMHDLILYAPVCDEAHFNNAIAYLVRRLDENTSEDNFMRYFF

NLKVGDENWKAQKELFLKSLEGIKTLDNTTHRKQDRNKESNIISSYESKKFSNESDTDFILAQNRAWAKE

IKAKYENLKDYDVYPVIGELDFKAENLNVLEVKDKIEDRVIGKAYLAGEKEIKQALEVAKNSKFTQKSHD

EIYQILAKSAKLMRERRGDLIGLAALEVGKTFLEIDPEVSEAIDFIEFYPHSLEELKKQNPKVKFTPKGI

GVTIAPWNFPIGISVGTIAAPLAAGNVVIYKPSSLSTLTGYMLCKCFWDAGIPKDALIFLPSKGSDISKY

LLVDEAIKFSILTGGEDTAYAMLKANPTLLLSAETGGKNATIVSKFADRDSAIKNIIHSAFSNSGQKCSA

TSLLVLEEEVYNDEEFKKTLVDAASSMAVGNPFEFKNKLGTLADKPSSKVQKALDELQPYEEWALKPKFL

ENNPYLMTPGIKYGTKKGDFTHMNELFVPILSVMKAKDLKEAIDIVNSTGYGLTAGFESLDEREWEYFHT

HIEAGNIYINKPTTGAIVLRQPFGGVKKSAIGLGRKVGIYNYITQFLEIKQEDFDDHLIEDKFSKKLAQI

DLKEAQDFMNDLIKMSQSYAYHYKNEFSVSKDYVNIRGEDNLFSYTKIKNMVLRLCGNESLKDVLGVILG

ANIANIDLSISYDEQDISMIERIVQSIGAKVLFLKENKENFIKSIKEYERVRYLAKPDVNDEIYKEAAKL

AKIIIREKPLLNGRFELLNYFNEKALSISFHRYGNLGIRAIS

>ABV53003.1 sodium/proline symporter [Campylobacter jejuni subsp. jejuni 81116]

MEVVQINTPIAVMFVAYALLMLYIGFYFYKQNKNSEDYFLGGRTMGPVISALSAGASDMSGWLLMGLPGA

LYVSGFIDSYIAIGLTIGASLNWIFVAKRLRIYTSVIANSLTIPDYFETRFDDDKHILRIVCAVVILIFF

TFYVSSGLVSGAKLFESTFGIRYDYALTTGTIIIVAYTFLGGYKAVCWTDMIQGLLMMMALIIVPLVMLY

HLGGFGEAMNIVREIKPQALSMGEGVGVISIISALAWGLGYFGQPHILVRFMSIRSTKDIPMATFIGIAW

MAVCLLSACMIGILGIAYVHKFELSLQDPEKIFIVMSQLLFNPWIAGILLSAILAAIMSTASSQLLVSSS

TIAEDFYKKIFREDAPSHVVLNLGKLGVLLVAVIAFLISTDKNSSVLSIVSYAWAGFGASFGSVMLFSLF

WSRMTRVGAILGMITGAATVVLWKNFANSGLYEIVPGFLAASVVIIIASLFTNVRSGTKAAYEKMLKEL

>ABV53002.1 hypothetical protein C8J\_1404 [Campylobacter jejuni subsp. jejuni 81116]

MNSFKQKYLINFWDNSRSMIALGILSAVYFGIFGGVWAVTGEMTRWGGEFLELLGMNLDGYSYYQKQNLN

GTPLTRTDGIMLIGMFIGCLVAALLANKVKFRLPASNIRIFQAIVGGILSGYGARLAFGCNLANFFTGLP

YFSLHTWLFTVFMVLGIYLGVKICNTSFFKPKAKLERVNKENLPLNKQSLRTKLYFNLGILLFIAFLVWV

FYLVFTNGNISTQNKQSLLALALIFGFVFGFVISRGQICFTSCFRDLFLFGRDNAIKGALIGMIIASLIA

FAFILQGHTSKLIELSPAVAVGAFLFGFGIVFAGGCECGWAYRAFEGQSHFMIVGIANIIGTMILALSYD

FLPKAFKEGIKINLLTEFGNLNGFFINLILFILIFAFVVFYKKYFFKNQLKGSTVKITYSLNLQGEACPY

PAIATLDVLPKLQSGEILEVLCDCPQSINSIPQDAKNRGFKVLEIDQSGPTLRFLIQKP

>ABV53001.1 adenylosuccinate synthetase [Campylobacter jejuni subsp. jejuni 81116]

MSKADIIVGIQWGDEGKGKVVDKLCENYDFVCRSAGGHNAGHTIWVNGVRYALHLMPSGVLHPRCINIIG

NGVVVSPEVLIAEMAQFENLKGRLYISDRAHLNLKHHSLIDIAKEKLKGKNAIGTTGKGIGPSYADKINR

TGHRVGELLEPQRLCEALMKDFEANKTFFEMLEIEIPSAEELLADLKRFNEILTPYITDTTRMLWKALDE

DKRVLLEGAQGSMLDIDHGTYPYVTSSSTISAGALTGLGLNPKEAGNIIGIVKAYATRVGNGAFPTEDKG

EDGEKIAQIGKEIGVSTGRKRRCGWFDAVAVRYTARLNGLDALSLMKLDVLDGFEKIKICRAYEYKGMEI

DYIPSDLENVQPIYEEMDGWDKVFGIKDYDLLPENAKKYIARLEELAGVKVKYISTSPERDDTIIL

>ABV53000.1 hypothetical protein C8J\_1402 [Campylobacter jejuni subsp. jejuni 81116]

MKSKYNSVVKVRKQQLDKAESNLNQAKQRQLEHEKAYELSRQECESLGVLPKSGSIAELRSNLSMAQVGR

EALARAKEKVELSKKEMNHYQFLYQKAHLDYEKMKALETEEIKQKQKEFAKAEEKFLDEIAISRFFKGEK

DD

>ABV52999.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MIKKFILLVFISSVVFGAEQDCEQYFEARKAQIELQTREFDEARQSLEAYKASFEALQKERLENLEKKEA

EVNATLAKIEELKLENARLVEEQQKILNSINDKTQGRVKEIYSQMKDAAIADVLSQMDAEDASKIMLSLE

SRKISGVLSKMDPKKASELTLLLKNLDNNASN

>ABV52998.1 hypothetical protein C8J\_1400 [Campylobacter jejuni subsp. jejuni 81116]

MRIKLPHIPYIANKMMLDIANSSFVEIKDQLEKLKVCIIEVLEKDILNERKLDERVKELLEQQEDEMELM

QVDRKNMFWLVKKKLAPEFNVILDSEDRHNHLAHQILEELVENDYINFIVSENRVKNLIFSSIESYLKIY

EKLEDEVYEKISNYKTKPIPGSEEYDLIFEKLYQEELRKKGMF

>ABV52997.1 carbamoyl-phosphate synthase small chain [Campylobacter jejuni subsp. jejuni 81116]

MKAYIYLENDIFLSAKAFGKSGTFFGELVFNTSLTGYQEIISDPSYAGQFIVFSMPEIGIVGTNENDNES

KEIFASGVLMRELSSSFSNFRAKESLQDYLEKHGKIGIYELDTRYLVKMIRNNGNLRAVISTEISNKEDL

KIALEKSAKIDEVNFVKEVSTKKNYSHKQGVWNASFQKFNDAKRSEKKVAVIDYGVKTNILNELVEVGFE

VEVYPYNVKADELITLYKKGEIQGVFLSNGPGEPRILKQEIAEIKKLAEAKIPMLGICLGHQLLSNAFGY

ATYKMKFGQHGANHPVINLDTKTVEITAQNHNYNVPEELAQVAHITHRNLFGDNVEGVRYKDYPIISVQH

HPESSSGPHESKYIFKEFMNLM

>ABV52996.1 hypothetical protein C8J\_1398 [Campylobacter jejuni subsp. jejuni 81116]

MSIDFLAIISVAFLSSFGHCYSMCGGFNLLFINLNSKSNNLFLLTFIYHLFRIFAYIALGIIFGTFGNIL

AINAKVQSLSFFILGIFMMILGFALIFRGNMLSFIENNVFFDSFIKKIIKKSKNFKGLKSAIFLGFSNGF

VPCGLVYFFIANAMSKQNIFKGILVMMIFGISTLPAMLFFSKISQFFSDFLKNLFNYLSYGVIVCYGMNL

AYIGFKAFQ

>ABV52995.1 putative two-component sensor [Campylobacter jejuni subsp. jejuni 81116]

MKDFFKDQFFKALEKNTIFSRADVQGNLIFVSDKLCQISGYSKKELIGKKHSIFKHPDVEECYIEELLKK

LSYKKPYQVIFKNIDKLGKTFYLETLLIPILDKNNELIEIVAFSHDVSNSFKLNEELALNHAKLRELSIN

LENTVKNHQQEFIQLGKKFEKKMQIALEKNEKDIKIVYEEILKSSLEQMISDIAHQWRQPLNELGIAMFQ

MKQNLKDEKGFAEIYSQSKDMIKNMSETIDVFRTLFNKGVEQCVFIKETLNKALEIAFETIEKNHVNINI

VSKSDYEVLAYENGLIRVFLNLILNSIEAFKNKKRKIITITFSKFGKNYLKITIKDNAGGIDKENLDKIF

QPYFTTKHPSQGIGVGLYISRQIIESFQGKIKVKNGKDGACFEVFLKLKERVE

>ABV52994.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni 81116]

MSQECKELIILVVEDEIKTRESLINVLSERFSKVIGAQNGDEGLKKFKPDLVITDIAMPIMDGLDMTREI

KEISDDVPIVVLSAYSEKERLLRSIDIGIDKYLIKPVDIEELFKVLDCLVGEKIEANMLVKISEEYQFNK

TKRTLIHNGKEIVLTKKELAFISLLLKQPGVLVLHEDIKKNVWIGEHVSDTAVRTFIKRVRDKVGEDFIK

NVPSLGYKININK

>ABV52993.1 cb-type cytochrome c oxidase subunit I [Campylobacter jejuni subsp. jejuni 81116]

MHPGNVLNYDYTVARYFMFATILFGIVGMAIGTLIAFQMAYPNLNYLAGEYATFSRLRPLHTSGVIFGFM

LSGIWATWYYIGQRVLKVSMAESRFLMAVGKLHFWLYMLTMVLAVISLFMGVTTSKEYAELEWPLDILVV

LVWVLWGVSIFGLIGIRREKTLYISLWYYIATFLGIAMLYLFNNMEVPTYFVTGMGKWWHSVSMYAGTND

ALVQWWYGHNAVAFVFTVGIIAQIYYFLPKESGQPIFSYKLSLFAFWGLMFVYLWAGGHHLIYSTVPDWM

QTMGSVFSVVLILPSWGSAINILLTMKGEWSQLRESPLIKFMILASTFYMFSTLEGPILSIKSVNALAHF

TDWIPGHVHDGTLGWVGFMTMAALYHMTPRVFKRELYSKSLMEAQFWIQTTGIVLYFASMWIAGITQGMM

WRATDEYGNLLYSFIDTVVAIVPYYWIRAIGGLLYLIGFFMFTYNIYKTIACGRVLDKEPKSASPMAA

>ABV52992.1 cb-type cytochrome c oxidase subunit II [Campylobacter jejuni subsp. jejuni 81116]

MFSWLEKNPFFFAVAVFVVIAYAGIVEVLPNFAENARPIEGKKPYTVLQLAGRAVYIKDSCNACHSQLIR

PFKSETDRYGMYSVSGEFAYDRPFLWGSKRTGPDLARVGNYRTADWHENHMWDPTSVVPDSIMPSYKHMF

KNNADIETAYAEALTVKKVFNVPYDTENGTKLGSWEDAQAEVKAEAQAIVDQMKNQEVKDAFAKGEIKEI

VALIAYLNSLK

>ABV52991.1 cb-type cytochrome c oxidase subunit IV [Campylobacter jejuni subsp. jejuni 81116]

MEHLSIVFDVIKNLITFDLATVQKHEWEIFQGYGFFALVMFLSIVLYAYWYHLYRTEKKGERNYENYANL

ALKDDIDDSVLESKRSA

>ABV52990.1 cb-type cytochrome c oxidase subunit III [Campylobacter jejuni subsp. jejuni 81116]

MQWLNLEDNVNLLSLIGAILIILITLVIVGRMFKQMKEKKGESELSEHSWDGIGEYKNAVPTGWAVVFFL

TIVWAIWYFLWGYPLNSFSSIGQYNEEVATHNTKFEEKFKNLSPEDKIAMGQNIFLVQCSACHGITGDGI

NGKAQNLNIWGSEEGIINVIKHGSKGMNFPGGEMLGAADLGVAEEDIPAIAAYVAKDLSAIKKTANENLV

AKGKEAYATCAACHGEDGKGQDGMFPDLTKYGSAAFVVDVLHSGKAGFIGTMPSFPTLNDIQKEAVGEYV

ISLSRGE

>ABV52989.1 hypothetical protein C8J\_1391 [Campylobacter jejuni subsp. jejuni 81116]

MENNNRCVFSLSGVTGMLIATVLLLAILVVLTIWGLKAQQEVMQKPYSLKDVQSVKMFGSKEQDHRSIKE

AQ

>ABV52988.1 hypothetical protein C8J\_1390 [Campylobacter jejuni subsp. jejuni 81116]

MSKALEYLIVIGLVVAAAITAWSVLTVNHLHIG

>ABV52987.1 hypothetical protein C8J\_1389 [Campylobacter jejuni subsp. jejuni 81116]

MKKILQDGFFLAIFFFVLLPSRVFALDAVLFNENILSQKVSNEINLIGKELYQKSNIFIGVMVGDKTEIE

TLLNKQKELPQSYILLLLSKNSHKVDIVGSKGALALIDKEAVLSPYPGTGSILPILATNKGDIYNAAILN

GYADIVDRVAKSLGLQLEHSIGNANRDTINILRILIYGFICFALLYYAQRRIKRKKNVRN

>ABV52986.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MLETKKSFWPYGILLSLLAIIIACIVTIFIASHHPVYEDDFYFDSYQNVENNYNQIQKQQVNFDKFFKVN

FQNDKITFIGKRKIPSYEVDQNSYVANFKISALQNINSDDLKVQALLTRPFTKNFDQKLEGQVKNGILSI

ALPKLDKGRWELKLKFYANQETVGFFSYELNAQ

>ABV52985.1 hypothetical protein C8J\_1387 [Campylobacter jejuni subsp. jejuni 81116]

MKLRIFSSSRQIREYYNQKKQQNALLDSAIHIGEFLDKVCLSNFHKASSYESLLLMQEACLKSKDLEKKL

GISVEFFAFLKNNEYLFSFFKELSLEKKSIEDLKNNDYYATYNEHLEILDEVYKNYLALLEKNSFYDDLS

LPKNYTLNKDFLDEYEAIVYDLQGFLSKFEENLLSEISQIKEVVLSFKTSKFNLEYLLKLDFLKTFDLKI

NTYYEINLSKQEILKEEIFKTKNSKIKLKSFELRALQCAFVMDEISHFVRKGLKPENIVVITPDESFCEF

LRLFDKDNMLNFASGISIKESLFYQKFQALYESASSASFVYKNQEDYFEDTQMIFDYHNTLLHSLKLDFI

EFKKYFDEKCDFEYFEKLLALFLENEKQELVYLIRKELYFIKDLLKNQSLTLKELIHLFFMQISQLSLSD

VGGGKVTVMGLLESRGLCFDGVILVDFNEEFIPKRSVNELFLNNEVRKKAGLISYDRRENLQRFYYESLM

KNALEVSICFVENEEKSKSRFLDELDFDFFYETHIHQKAYLNALKLDYEGIKPNLTPIKAPILKHNPFEF

ALSFSRFNLLENQKRTYYYRYILNLAEPRVLSEESKAKNQGNFIHKMLEIYYKNYANNDFDIKVFANLLD

KEYQKYNISELDLEVFKLKFIQFAKNEKEHFSKGFYVAHTELELNNILKLGTDSIKLKGTIDRIDSSKEG

NLIIDYKSGKVPSNSYQLAFYQALYDENANVGFYDLNSMQILHQKAKSLDELRERLKDLVLMSKEEIEFE

NEQDEHCPYKLIYKKELK

>ABV52984.1 putative helicase [Campylobacter jejuni subsp. jejuni 81116]

MSQFEPFLALEASAGSGKTFALSVRFVALILKGARINEILALTFTKKAANEMQKRIIETFLNLEKENKTS

ECNELCKLLGKDKEELISLRDVKKEEFLRTELKISTFDAFFGKILRVFALNLGLSSDFTMSEERLDVREI

FLKLLKKDELKDLAYYINLVDEKENFFNELEKFYENAYFQNLPKIPNPSKAYINKAYSELRSYCLGLTHV

KNYKNLCDNFKSEVLDLSVFMQSSFMTKFESTKYLQDLESTNLHFSAKRMELINALNTYAIELENYKIAN

LMNLLNHYSEAKNIFHKDKNTLNFQDVSKKVYELITSEFKDMIYFRLDGFISHLLIDEFQDTSVIQYQIL

RPLIAELVSGEGVKKNRTFFYVGDKKQSIYRFRKGKKELFDLLKQEFSQIKSDSLNTNYRSKELLVDFVN

ETFKEKIKDYKEQFALESKKGGFVRIVESKEQKVKNQAQEIKEKTLETLFEQINFLRSKNISYDDICILC

WKNSDADMVLDFLREQKIPAFTQSNVLLENKASVRLVLEYAKYCIFGDEFYLVFLKELLGFEPRKITLDF

SKNAMENVLFLIKELKLDLNDIALIQFIEYAKTKENFLKLLFEPCTLKIVSEQNMGISIMSVHKSKGLEF

DHVILLDSLSKNNSNNEDIMLEYDINQGWQLHIKDKIRELTKEPIYTLFKENITRANYEDDINKLYVAFT

RAKESLIIVKRSEESVNGNYPSYFKGGFLNIYSQERGFLESKEQILSVKKESIQALQKFEKISPQEVQSE

EKLDSKELYFGNAFHFFMQNLKLPKGENFQMLTQRCKSKFRHFLDESDFEKLFKRIEILLKNTQFQNLIG

DGKLLKEQALSFNGEIKQLDLLALKDEEAFIIDYKTGLAMQDKHKEQVRTYKIAISEILKKDKVRAFIVY

CLENEIQILEI

>ABV52983.1 50S ribosomal protein L13 [Campylobacter jejuni subsp. jejuni 81116]

MTKITKPNEVKREWIVLDAEGKRFGRLLTEVATILRGKNKPCFTPNVDCGDYVIIINASKAVFTGANKAE

DKLYHRHSGYFGSVKSEKFGDLLEKNPAKLYKLAVRGMLPKTNLGRAMLKKLKIYAGSEHPHTAQIAKEG

K

>ABV52982.1 30S ribosomal protein S9 [Campylobacter jejuni subsp. jejuni 81116]

MATTYATGKRKTAIAKVWVKPGSGKISVNGVDLNTWLGGHEAIKLKVVQPLLVTKQETSMDIKATTLGGG

YSAQAEALRHGISRALAAMDADFRALLKPKGLLTRDSRTVERKKYGRRKARRSPQFSKR

>ABV52981.1 outer membrane fibronectin-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIFLCLGLASVLFGADNNVKFEITPTLNYNYFEGNLDMDNRYAPGIRLGYHFDDFWLDQLEFGLEHYS

DVKYTNTNKTTDITRTYLSAIKGIDVGEKFYFYGLAGGGYEDFSNAAYDNKSGGFGHYGAGVKFRLSDSL

ALRLETRDQINFNHANHNWVSTLGISFGFGGKKEKAVEEVADTRPAPQTKCPVEPREGALLDENGCEKTI

SLEGHFGFDKTTINPTFQEKIKEIAKVLDENERYDTILEGHTDNIGSRAYNQKLSERRAKSVANELEKYG

VEKSRIKTVGYGQDNPRSSNDTKEGRADNRRVDAKFILR

>ABV52980.1 putative hydrolase [Campylobacter jejuni subsp. jejuni 81116]

MNKTILFDLDGTLIDSTDAILNSFQGAFKALGLTSKNNEEIKNLIGYPLEQMFRMLYPDKVNLSKEFVLA

YREIYAQIYLEQTTLLPKAKEALELGSEIADLGIVTTKGGKFTPILLDYLGVKKFFKTLITLEDVTNPKP

SSEPIILALKRLNKTQENAYMIGDTILDIQAAISANITPLALACGYGNENELKAYSMVFLNAYEAVNYIA

RLN

>ABV52979.1 pyruvate ferredoxin/flavodoxin oxidoreductase [Campylobacter jejuni subsp. jejuni 81116]

MGKIMKTMDGNEAAAYAAYAFTEVAGIYPITPSSPMADYTDMWAAAGKKNLFGVPVKIVEMQSEAGAAGS

VHGSLQAGALTTTYTASQGLLLKIPNMYKIAGQLLPCVIHVAARSLAAQALSIFGDHQDIYAARQIGFAM

LCSHSVQETMDLAGVAHLAAIKGRVPFLHFFDGFRTSHEIQKVEVMDYAHFDRLLDREALLEFRNNALNP

ENPKTRGTAQNDDIYFQTREVSNRFYDALPDVVNEYMQEISKITGREYKPFTYYGHKEPERVIVAMGSVT

QALEEVVDYLNAKGEKVGILKVYLYRPFSLKYFFDVMPKSVKKIAVLDRTKEPGSLGEPLYLDVKSAFYG

RENAPVIVGGRYGLSSKDVDPAQMIAVFENLKLDNPKDGFTVGIVDDVTHTSLSTGEKISLGDESTIECL

FYGLGADGTVGANKNSIKIIGDKTDFYAQAYFAYDSKKSGGYTRSHLRFSKKPIRSTYLVSTPHFIACSV

AAYLEIYDVLAGIRKGGTFLLNSIWNAEETIRQLPDAVKKTLAEKEVNFYIINATKLARDIGLGNRTNTI

MQSAFFKLAKIIPYEDAQKYMKELAYKSYSKKGDAIVEMNYKAIDVGADGLVKVEVDPNWKNLELKEKEQ

TNAYKGTEFVEKIVKPMNAAKGDDLPVSAFLGYEDGSFEHGTTEYEKRGVGVMVPRWIEANCIQCNQCAS

VCPHAVIRPFLINDEEMANAPRGVKDHALEAKGTKGEKLSFKIQVSPLDCTGCELCVHECPTKEKSLVMV

PLQEEMDFGEQENADYLFKEITYKDDILNKETTKGAQFAQPLFEFHGACPGCGETPYITLITRLFGERMI

VANATGCSSIYGGSAPSTPYRKSVKNGHGPAWGNSLFEDNAEFGLGMKIATENTRHRIEHIMNESMQEVP

NALSALFKDWIANKDNGAMSVEIKDKMIPILEQNKNIKAVQDILELKQYLSKKSHWIFGGDGWAYDIGYG

GLDHVLASGENVNILVLDTEVYSNTGGQSSKSSRTGAVAQFAAAGKPIQKKDLGQIAMTYGYIFVAQVNS

TANYTHLIKAITAAEAYDGPSLVICYSPCIAHGIKGGLGYSGEQGELATKCGYWPLYTFDPRLEEQGKNP

LTLTGKEPDWDLYEQFLMNEVRYNSLKKANPEHAAELFERNKKDAQRRYRQLKRIAMADYSNEVES

>ABV52978.1 transformation system protein [Campylobacter jejuni subsp. jejuni 81116]

MFAQDNFEEYFKLIDKENRINFNTLQNPFVNPTFEKLRHIKITAIMLDKVKIYDRWYKKGDMIDDAIIHE

INTKEIKFQYDNLEIAIQINKNDKININ

>ABV52977.1 general secretory pathway protein D [Campylobacter jejuni subsp. jejuni 81116]

MIRLILINILFCHYLYALDCQKRLFDISINEKLSIQESLDELAKYCSFSIIVKDKIAKEKLETLQNSVNI

HQMSLDEIFNFFIKEHDLSYDFDGKILRISGINTKIFKISYITSIREGQSITKASVDAKPRQSEYSGSFD

DAEDNMIKSMEKFDFWQNIEKEIIVLLKNSHEDYEAKTPIINPNAGLIIVTGTNSQLKSVKNYLQKLENR

LKKQVIIDVSILAVSLNESHSSGINWQNFNIGLNSQVNNENSFIQFQNGQGFVKNLGLRANLNFDSIINF

LSQNGKTSVLSNPKLMALNNQQAIISVGDTINYQVKESSKGTENGTTVSESYNNYSIFVGILLNILPEIS

DDGKIMLRINPSLSDFKYPEDNKRQKEPRTIAPDTIQKKLSSVVQVENNQTLILGGLISHDKSNEKNSIN

FLSKIPILGSLFKGEVLNSKVTEIVFIITPSIVDSVNAPSLKDLGFKHYE

>ABV52976.1 putative ATP/GTP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MSKIIPFREEIFHQINQILESQKAFIFLWGKSGSGKSVLLQRLAKKYNVDFINENFKDQSFLKEKIEFLI

SQGQSLIILDEVGMYDYAMLESIRIYSDSISFVLSSHKKLNILKKEHFKSRLSACFELKNISLLELDDYI

KLKFGMNFSNKCLKFLQKISQGNLRYIDKTLKSFYEINSFFDKNKSQEYILKLSALENGLLR

>ABV52975.1 transformation system protein [Campylobacter jejuni subsp. jejuni 81116]

MQERIKELELRYKYFLLKKYLKYLLLVILISVIAFCFFVLMQKYNKQKNIYLQAIEHKKHLEQKILQAQI

LQEKNKISREKLYKELEEVKAVQENTHISKIEIDSKILNISDLKKSFYQNPSYEKALNLAKKYFDIKAYQ

KTIFWTLKANELDKQKQDSWLIFAQAKRALGEEKEAQSALDAYINYYGLMELDGK

>ABV52974.1 putative type II protein secretion system E protein [Campylobacter jejuni subsp. jejuni 81116]

MDKIFQAYIDNEISLDEICTKFNITSWDFFKKLANFCNLHFVDLDEDNDFIYEGIPFSLLLKFKFLLIKN

NDGFMIIRSKPCSLELLEQVKTFMICEKIDTAIADELKIAKILNQIRIQEEIKRLSIKLRLEWQENHKRD

DQSCISQIFDFLLHEILSFHASDIHIEARNDDALIRFRVDGILREFAIFEKDIYEALVFHVKFLACLNLA

ESRKTQDGSFELDFENERYDFRVSCLPLIYGESVVIRILKHDKEILDLHKLNLGDKNLEILKKILHRPNG

MILLTGPTGSGKSTTLYACLNELKSIEKKIISAEDPIEYKIPLVQQILLNSKVGVEFNSVLRAILRQDPD

IIMIGEIRDEESLDIALKASLTGHLLLSTLHTNDALSTIDRLLDMQAKSYLIASALSLVIAQRLVRKLCP

WCKQKSKKHYIEFEGEFFEPKGCERCHHSGFFGRELIAECLEINEDLACAIRENQDKTILMELAKKYGFQ

TMFEQGLKKAKEGLTSIDELLRVVR

>ABV52973.1 general secretory pathway protein F [Campylobacter jejuni subsp. jejuni 81116]

MKFYEVEFLKNNQNYTKTIKAENLNTAQAKALSKNWKIIDIKEIQKSNFQRLKDENFILFFKELALLCEV

GLSVQEAIRELYFMHSCKIMKKILDNLILAQNLNQAFENANFGLNRAELALIKTAEKTGKISEVFSQISK

LREKSLESQKQLKKAFRYPTLVFLSIIGAFLFLMLFVVPNFKDLFENLGASLPFITHVMLEIYNFLDDYG

IFCIFLFVIFIVMLILAYKNFHSFAFSCDFLFLKVPLISRLIIYNQNYYFFMVFSLLLKNGISISKAFDL

AIIGLENKFLIFQYKKLFSFIDSGLELSQAFKKIDIFDSLVFSMLSVAMKSGRLEVLSEEIAKYYQQKSE

NLMDRFLIFLEPMMTLFVALLVLFLALGIFLPMWELSSGVNFN

>ABV52972.1 hypothetical protein C8J\_1374 [Campylobacter jejuni subsp. jejuni 81116]

MGFEHLNTIYYFILFFVALFAGFIDSIVGGGGLITLPALIACGIPAHLSLATNKLQSVFGSFTATLTYFK

STTLPHLAWGVFFTTLGAAIGSYSVLFVKDEQLKLIILIFLTLTFLYTALRPNLGKHESEPKIKNIKIFH

LICGLTLGFYDGFLGPGTGSFWIFACVMLLGFNMRKASINTKILNFTSNIIALAIFLWQYELLWAVGLLM

GVGQVLGAYLGSKLVLKTNGKFIKTLFLIVVGATIIKVAWDYFS

>ABV52971.1 hypothetical protein C8J\_1373 [Campylobacter jejuni subsp. jejuni 81116]

MKNFIHLKAKLDFLANQKNTNHSLFETPDPLQIAKIHNDEFIALICALFAYGNAKNIVNFLKKLDFSLLN

LQEKQIKKELKNLKYRFQNEKDIQEIFITLSRLKNESSLYELFYQAYQERENTTDAILAFMQKIKTLNSY

SSYGYDFFFGKIWQNTPTSPLKRYNMYLRWMVRKDELDLGLFTKIHTKDLLIPLDTHAHKISLTLGLLKR

KIYDYKSVLELTQNLKKLDANDPIKYDFALYRLGQSKEIDKFKE

>ABV52970.1 flagellar hook-associated protein FlgK, putative [Campylobacter jejuni subsp. jejuni 81116]

MGIFGTLYTGVTGLKASEVQIATTGNNISNANATFYTRQRVVQTTNGYITTGGVQVGTGTAVESIVRLHD

EYSYYKLKGASTQLEYTKYMASTLQEIAQRFPDLQNTGILQDLENYNKAWNDFASNPNENATKIALVKAS

QTLTESVNNTFATLDKIQKKVNDDIKNTVDEINRIGEEIATINKQIYGQEALPTEHANELRDRRDELELT

LSKLVSAVASKNEINQDNRLDTTITDPGHQYNLSIEGFSIVDGINFHPLKLDYDDKNKSYSIYYETPDEK

VRDLTAKISGGQLGAQLDLRGRNYSKSEGKYEDGIIQGYMDSLDTFAKTMINETNNLYASSAKSSVTSDY

LSGLKGDIPLVNYDRTIQPGSFDIVIYDDKGDKKLTKTITIDVNTTMNDIMRQINANTDDNNDHNANNDV

DDHINASFSYDAKTGDGLFQINAKSGFKVAIEDKGTNFAGAFSIGGFFSGTDASNMKVKDSILNDPSTVR

ASLSGVDSGNDMANKIIQLQYEKVNFYNEDGTIDNLTMEEYYRKLTGKIASDGENNNVVNSSNETLYNSV

YSEYQSKSGVNTNEELAALIQYQSSYGAAAKIVSTVDQMLDTLLGLKS

>ABV52969.1 hypothetical protein C8J\_1371 [Campylobacter jejuni subsp. jejuni 81116]

MLKQRLDEVNAILAKLIALTEEDIENIKVAKHESVTPSVEEKNKLIAEFITAKKQLDVALVELNNSSTKG

LSELLDDEDKQKLDLLKKNLQNLHSKNKEYAKFVLIVKDFLDGLVNKMFNINDGTNNAYGDKKTNPESIF

KINV

>ABV52968.1 hypothetical protein C8J\_1370 [Campylobacter jejuni subsp. jejuni 81116]

MINPIQQSYVANTALNTNRIDKETKTNDTQKTENDKASKIAEQIKNGTYKIDTKATAAAIADSLI

>ABV52967.1 hypothetical protein C8J\_1369 [Campylobacter jejuni subsp. jejuni 81116]

MNSALLDRAAKARSLESSIKINDNDIVTKSKEDEALKEQTDAFEAFFLKQVLDVSLKSQNSLFGKDASDE

IYSSMYNDTMSKALSGGMGFSKLLYDFLKERG

>ABV52966.1 flagellar P-ring protein FlgI [Campylobacter jejuni subsp. jejuni 81116]

MRVLTIFLLFMTSIFAVQIKDVANTVGVRDNQLIGYGLVVGLNGSGDGTSSKFTLQSISNLLQGMNIKVD

PNDIKSKNTAAVMVTAKLPAFAKSGDKLDITVSSMGDAKSLQGGTLLLTALRGIDGEIYAIAQGSISTGG

LTPRPGGAGSHSTAATVMGGANVEREIPQNFSQNNDLTLSLKVADFKTANDIERVLNTVFGEEVAKAIDS

RTVKLKKPEDLSNVDFMARVLEQDIAYKPQSKVIIDERTGTVIAGVDVEVEPVLITHKDITIKIDPNNNA

VANQNEIDMKDGGFVDPSSNTLRINNAKSTVANIARMLNKLGATPNDIIAIMENLKRAGAINADLEII

>ABV52965.1 possible DNA methylase [Campylobacter jejuni subsp. jejuni 81116]

MNDEFISVKDFFNHNEKRKKFLQKQEIKPPKEKTKKTKETKLYTNIESGKYKGKKLLLPSLTTTRSTKSI

VKSCVFNVIREDLRSKIFIEAFGGSALIAAEALSNYALKAYAIELDIKAYKIALENAKNIDPNLEVIHAN

TFEILPKLIENSKNEIILYLDPPFDIREGFSDIYEKIYHFLENLDLKTLNLIIFEHHSTIKTPEKIQNFQ

KVKEKKFGSTSLSFYSS

>ABV52964.1 hypothetical protein C8J\_1366 [Campylobacter jejuni subsp. jejuni 81116]

MKISLECKDLIIEKTLELFLKDHLVMKKNCDFIISDEKIHTAKPLFIISKNSPFLSIPFSKEALFESLNE

FDNALKAAALQLALEQKRLLEEKIDAIALEFKKDYENKIDLAIKDLKNKLVKALNDE

>ABV52963.1 hypothetical protein C8J\_1365 [Campylobacter jejuni subsp. jejuni 81116]

MKKLELRIFRFDKTKDYEAYYKPYIYDNYENFASFYDLLLQVQDDDIYFDFDKDEDTYIVVNKQIIPLFT

PLEKIAKEFDFSLCIEPLSTKRAIKDLIIDKNDFLDKYKYLEKFGNEEDKKLYAKYDYLYYASEILDYLP

EYMGDGVFYLASKMIEKYPEKKIEILKTLADKEKGIFYHLESKNEILETTIKNLQNEILNLGLFDKNILH

FDLPKTNAFDNEIKELKEIKHNFQDFNIAFYGFNACDTLKSKLKAKFISYENSIKNNGFSLLNLNPTLSY

KIAADIVLDAYDSGADFMVVKEEKDFYLFDTCAKKLMQTSGREFEDFYILSRFEFLALIEGIQAPSLKNH

TLKVSLI

>ABV52962.1 thiamine-monophosphate kinase, putative [Campylobacter jejuni subsp. jejuni 81116]

MNKEDFIIKAFLNEKNGDDGAIIDDWCFSKDLFFENVHFKREWFSLEQIATKAMLVNISDAISMNAVPKY

ALLGLALPKNLSENEIKALQKGFLKTARKFNIKIIGGDTISNDKIDISLTIISKINDKAVFRKGLKKGHL

LAYTGKLGRSLKGLEILQNGGTLKPNHVFIKPKLRASFFYEVAPLISCAMDISDGLSKDLSRLLALNKCG

ISWFKKLDDYTLYSGEEYEILFAFDEKERQNIKTIAKKHGVKLNIFGKAVKGKYEFRGREHHF

>ABV52961.1 tRNA pseudouridine synthase D [Campylobacter jejuni subsp. jejuni 81116]

MNLEEENTIFKPLYSLKHSPINAYFSKNSDDFVVRERPLYEFSGKGEHLILHINKKDLTTNEALKILSET

SGVKIRDFGYAGLKDKQGSTFQYLSMPKKFESFLSNFSHPKLKILEIFTHENKLRIGHLKGNTFFIRLKK

VLPSDALKLEQALMNLDKQGFANYFGYQRFGKFGDNYKEGFEILRGKKMKNVKMKEFLISAFQSELFNRY

LSKRVELSHFANDFSEKELIQIYKISKEEAKELKKQEQFFKLLKGEVLGHYPFGKCFLCEDLSAELERFK

ARDISAMGLLIGAKAYETGEGLALNLENEIFKDALEFKAKMQGSRRFMWGYLEELKWRYDEEKAHFCIEF

FLQKGSYATVVLEEILHKNLFE

>ABV52960.1 hypothetical protein C8J\_1362 [Campylobacter jejuni subsp. jejuni 81116]

MKKILTSALALGAMTLIIGCGDGDLVELKNNGNDQAMFDLGNQEIMKKYPNYKLYDYTSVRAISDFKDPE

GKIKEMKRDLEIDKTPYSNYVFLLNPNDKKDYKVVSVYCDKDFKKRIYCSVNDAFRFYAR

>ABV52959.1 peptide chain release factor RF-2 [Campylobacter jejuni subsp. jejuni 81116]

MDNYEFSELLKTLKNKVGNIASIIKPENIQTRLKEIEELENSPSFWSDVKQAGIIGKEKTKITNLLKNYE

NAFNALNDASELFDLANSENDTETLEALFNDAPKLEDTITSLEISMLLSGENDGKNAIVSIHPGAGGTES

NDWASILYRMYLRFCEREGFKVETLDFQEGEEAGLKDVSFLVKGENAYGYLKAENGIHRLVRTSPFDSAG

RRHTSFSSVMVSPELDDDIEIEIEEKDIRIDYYRASGAGGQHVNKTESAVRITHFPTGIVVQCQNDRSQH

KNKATAFKMLKSRLYELELMKQQDSANAGEKSEIGWGHQIRSYVLFPYQQVKDNRSGEAFSQVDNILDGD

IKKMIEGVLIALKAE

>ABV52958.1 hypothetical protein C8J\_1360 [Campylobacter jejuni subsp. jejuni 81116]

MSKLYLMSLGCNKNLVDSEIMLGRLSAYELCDEPSKADVLIVNTCGFIDSAKKESINAILDLHEQRKKDS

LLVVTGCLMQRYREELMKELPEVDLFTGVGDYERIDEMILKKTNLFSNSTYLQSENSKRIITGSNSHAFI

KIAEGCNQKCSFCAIPSFKGKLKSREISSIIAELKDLVARGYKDFSFIAQDTSSYLFDKGEKDGLIRLID

EVEKIKGIRAARILYLYPTSASEALIKRIIASEIFINYFDMPLQHISDNMLKIMKRGANSTRLKEMLNLM

KSAPNSFLRTGFIVGHPGESEADFEELCEFVKDFGFDRISVFAYSKEEDTAAFDMEQVPFKVINKRLKII

EKIVDEVIEKSFEKEVGQKRLVVCTGKSSEGEFFIAAKDLRWDREIDGEILINESECGNLEMGQIYECEI

LQNLDKKLLAKALRKVDAN

>ABV52957.1 hypothetical protein C8J\_1359 [Campylobacter jejuni subsp. jejuni 81116]

MQIKDEILALLKRGKNLLAFSYGSDSSVLFYLLMQEKIDFDLVMINYKTRKNSDLEELKAKELALKFHKK

IFIKHAPKFQSNFEKKARDFRYDFFEKICLEQGYDHLILAHHLNDQFEWFLMQLSRGAGLAEILGMQECE

KRSNYTLLRPLLFISKDEISSFLKEKDIFYFHDESNENEKYFRNYIRKNFSNAFVSEFHQGLKRSFSYLD

EDRKKLYDFENIKEIQGLLICPKNESLIARAVKMKGLLLSTAQRKELLKGDCVLGGKIALAYKNEQAIVF

EYETCQKLPKNFKEECRIAKIPRLLRAYLYNHKIDISSLSF

>ABV52956.1 hypothetical protein C8J\_1358 [Campylobacter jejuni subsp. jejuni 81116]

MDILKLAIKDFLSLKFLKFALIPLIFSLILMLFLGVLGFSALLDYFNSLFSVGEDSFWAWFYALHFVQIL

ITIISFLFSGFIVVFASVFLALFITSFLTPFIAKEINQKYYHYDNTNEVSTLKTIFEIFKIFIKFIGILL

LCTLALFLPFINIFVYYLAFYYLFHKLLMIDVTSTILDKESFKNFHSDFSPLEFKFSTLCFYLLSSVPLL

GLFLQVFFVIFLTHLSYQRILKLKAKA

>ABV52955.1 putative dUTPase [Campylobacter jejuni subsp. jejuni 81116]

MTNIEILENMLKLQQKLNDETNGLNWENGYTKEGKLISWRRCIYMECAELIDSFTWKHWKNISSLTNWEN

VRIEIVDIWHFILSLLLEEYRDKNNKDFKAIATEVNAVSVFQDFCKEEEYPNEGDIYGILNDIELIIHKC

SGFGFNLGELLSTYFTLAIKCGLNLEILYKTYIGKNVLNIFRQNNGYKDGSYKKTWNGKEDNEVLAQILE

QELDFDTIYKKLEECYKKA

>ABV52954.1 putative ATP/GTP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MQIDASKNQSFSMDYTTKSGKHLALSMYDNQSVSYANNEEGKTLNLKRQYGFSFTFEGSKLTQNDLDEIK

NAMKEVEPMIKDFLANSKVGELKPKEIIESAMQMANVLPTPNDENHQNAIMNNFTNKLSDLLKQNQTDDK

DINASMLEDSKKLLDEVLEQMKKQLEKQQEKAKENQDKTDDSLNLYA

>ABV52953.1 hypothetical protein C8J\_1355 [Campylobacter jejuni subsp. jejuni 81116]

MDERILEFIKNEQLLSWAMIDEKGVYTASAFYAFDEKNLAFIIASHEDTKHIRLASENSSIALNIAKESK

IAFLKGVQAKAEFKMASKEQMKIYFSKFPFAKFDKSAKIYALELFWLKFTNNALGLSKKLEFYKK

>ABV52952.1 capsular polysaccharide ABC transporter, permease protein [Campylobacter jejuni subsp. jejuni 81116]

MLNVIYALFFRELKTRFGKNRYLGYIWVVGEPMSIVLLVTIIGTIVREYHHQVMPEGISIFMFLISGIMP

FFMFRSIVTQLMNGTQANLALFAYKPVKPIHVFIARTLLEFCIYFVIFIIILFFAGWFFRLDVFPVHLLG

VLFCIFLLICSAFALGICFAIIWHFVEPLRTLLAYFSIVFYWTSGIIFPTWLTPRPLLDIFYYNPLLHIF

ELLRFNFFENYPLQDEYSYFYAIFWILLVLFIGLFIYYYNRQALTAVKKE

>ABV52951.1 putative capsule polysaccharide export transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MIKLINLTKSYPLFSGGRHYVFKNFTFEFPENCSIGLMGYNGAGKSTLMRLLSGAELPDSGKIITNKKLS

WPLGLNGAFQGSLTARDNAKFVARVYGYKGKELQEKVKFVEDFAELGKFFDEPMKTYSSGMSARIAFGLS

MAFDFDYYLIDEAGAVGDPAFREKSVKLYRERLSKSKVIMVSHNVAEIKEWCDKIIYMKNGQITVYDDVD

EGIAVYQGKV

>ABV52950.1 putative capsule polysaccharide export transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MEENKTLLEKIKDLSIFDSFKIVWFIMIFVVIYYTLIAAPRYVSTMILDVRSTSGESAQTSGILSLLSST

STASEDLNYLKGYIESSDMLKILDEKIKLKNLYQEQHIDLPFKIWDSSSIESYLKYYQARVKVHTDETTK

LLKVEVEGFTPKSAHLIAQAIMQESEKFINEISHKAAREQMAFAENEVQKYKERYQKAQNDLIAFQNKYG

VFDPLKQAETKASLVAQIEANLAQKEAKLLTLQSYMNDAAPEVVALKAEIEAIKKQLLREKSKISANNSS

QKLNDLAAKFQDLTIEATFAQKAYEAALKAYESARIEALRKIKQLVIIQSPDIPESAKYPERIYDILTAF

IVLSLIFGIVKFIKMIIEEHKY

>ABV52949.1 putative capsule polysaccharide export system periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKILILLFSCILCFGAVDVSQIISAEDQGSATTSIDQNLSSNYDIANKENNLTKIHQILVFGAHLFNGN

FKNYNQRVYNPDYKIAVGDQISLKIWGAVEFSQVLVVDSQGNIFIPKVGAVNLLGVKNSALVSVIKARVN

KIYKSNVFVYADMNAYQNVSVFVTGNVNAPGLYQGLSSDSVIQYLDKAGGINLEYGSFRDIQILRNNSVI

KNIDLYDFLLKGQMDLFPFRSGDVILVGNVQNYAFVNGDVQRPFRFELSNDIKTLADLARVSGAKPIVTN

AIVKSYGEDHKLDVSAYNKMQFSKVLLRTGDEVEFHPEYVSENITISVNGEHNGLKTLVVGKGTTLEDIS

KLIKANPQSNMQALQVFRKSVARTQKELINAQLKELETLALTSGSVTAQGAAIRAQQAKTILEFIQRAKQ

VEPKGQIVIDNPKSYNSVILEDGDTINVPSKNNLIIVQGEVSLPGAFVYDKGKDLRYYINLAGGYGERAD

TSKVLVIRSNGKAEKYHSGIDMKRGDSVLVLPKVDSENLQIFSMLTQILYQIAIATNVVLNL

>ABV52948.1 arabinose-5-phosphate isomerase [Campylobacter jejuni subsp. jejuni 81116]

MNTLEIAKEVFEKEAQAILDLATNLDENFNQAVNLMLNTKGRCIVSGMGKSGHIGAKIAATLASTGTPSF

FIHPGEALHGDLGMLTSEDVLIAISNSGETEEILKIIPAIKKREIPLIVMCGKKNSTLVKQGDIFLNIAV

EKEACPLQLAPMSSTTATLVMGDALAAALMKVRNFKPDDFALFHPGGSLGRKLLTKVKDLMVSSNLPIVH

PDTEFNDLIDVMTSGKLGLCVVLENEKLIGIITDGDLRRALKASDKPRFDFRAKEIMSTNPKVVDADAMA

SEAEEIMLKHKIKEIVVSKENKVVGIIQLYAIGNV

>ABV52947.1 hypothetical protein C8J\_1349 [Campylobacter jejuni subsp. jejuni 81116]

MKYSVIVPVDLDLRPFDILKKVKSILKRSSNEVEIVFGHNDRGSIFDKYLKKICTKKNNVKLVSGKFYTK

LICQSLLRNRAVEQCSSEFIYLMDVDYLFDEALSDECINDIKNDKNPFIILPCLYLSRKGSREIFKFSRE

EMFEKYISFRKDLFISLASPSGGSIFMKKEDYFAVGGFDEDFVGRGGEDFEFMIKLALYKNVIKPTKDLM

INKFYKAPLLSEGFRKYLTFNGLPYFFEKKVAFHIYHGRNRLRGYFRQYDKNSNLLQEKIKLASNLEDTG

VSLIEFYEQLCKKYDVSIDKYAVLFDAYKPKLFSFERFMLFLRRL

>ABV52946.1 hypothetical protein C8J\_1348 [Campylobacter jejuni subsp. jejuni 81116]

MIKISILIPSFNSILYIKECLESVINQSLKEIEILCIDAYSDDGTLEVLQKYALKDKRIKIILSDKKSLG

YQINLGLEQVQGKYFTIVESDDYAHLLMCEKLWVLSQSYNCDMIKADIIGFYDKKRVKKFQNEAICYDKN

LYGKILYFDDKIEILKNSWNMNQSGIYKMDFIRKFNIRANETLGASYQDLGLWFLMVVFAKNIYFHNEGL

YFYRQDNPNASMQSKDKVYCVCDEYKFIENFLELHLGKNQYFKDVFLYRKFKSYWWNIRRIDTKFRLEFF

EYFAKDFEKELTDLNDKFFTYGELKEFRKIIKNPKKFYDFYRSPFFKIIKFLARIKNTFKRYLNYAR

>ABV52945.1 hypothetical protein C8J\_1347 [Campylobacter jejuni subsp. jejuni 81116]

MQDKKVGIVIPIYNVEKYLDECLQSVIDQTYTNLSIVLVNDGSNDNSLSIAKKYALQDERIIIIDKKNGG

LSSARNTGIDFFANQYTLQFEKEEQELLKFQIINENYLDICSIYRKNTMLDKNFEIPQIDYIIFLDSDDF

WKSNCIEECVKRINNVDIVWFGHDLLIEIPLKKKTKNQMQFFDYNQEQIITSLDWLKQVNSEYKPLFWFA

WQGMINFSFLMKIRLKFINGIIHEDNHFGILLFSMAKYIYVYPETLYVYRVRSGSIMTQNDRTKVASNSY

LYPLYLKANKNYELFKRYQAALSCVLSCVKVAEFIEENKAENLILIEIKKVFIPMLLDRAVVILFLEKDP

LNLSAYLNSLESYFKEFKLSGAESFKYELSYRLGYLFLNNYRSIKGLLTLIPKMKKEIQDYYLEKQNFKN

NIKYFPFIEFVSQLDENPSLKRIKNHYSYKVGKIFAWILKYFGVR

>ABV52944.1 hypothetical protein C8J\_1346 [Campylobacter jejuni subsp. jejuni 81116]

MLFLLIKNKEFYIIILDLIEKFRKGGVENMKNILITGGTGFLGSNLCKRLLGEGNKIICVDNNYTGRMEN

IKELLENENFTFIEHDICEPLKITQKLDQIYNFACPASPPAYQGKHAIKTTKTSVYGAINMLELAKEHNA

TILQASTSEVYGDPLIHPQNEEYRGNVNSIGIRACYDEGKRCAESLFFDYHRHEGVDIKIIRIFNTYGEN

MDPNDGRVVSNFICQALSGKDITIYGDGSQTRSFCYVDDLIDIIIKVMNSSKDFQGPINTGNPSEFTIKE

LAQKVIEKTGSKSKIIYKDLPLDDPTQRRPDISLAKAKFNWEPKINLDEGLEKTIKYFKEKITEFKG

>ABV52943.1 hypothetical protein C8J\_1345 [Campylobacter jejuni subsp. jejuni 81116]

MKIGIIGTGYVGLPTGVGLAELGNDVICIDREKSKIDALNDGILTIYEDNLEELFHKNVKEGRLKFTTSM

QEGIKDADLVIIAVGTPPHPVTKEADMKYIHAAATELADYLTGYTVIATKSTVPVGTGDDIESLISKKNP

NAEFDVLSLPEFLREGFAVYDFFNPDRIIVGTNSQRAKAVIEKLYEPFKGKSELLFVNRRSSETIKYASN

AFLAIKIHYINEMANFCEKAGADILEVARGMGLDTRIGNRFLNPGPGYGGSCFPKDTLAMAFMGKQNDID

LTLINAAIKGNEERKNHMSERILNSIKDIKNPKIAVLGLAFKDGTDDCRESPAVDIVFKLLEQKVQICAY

DPKAMDLAKQILGDRIDYANSMYEAIKDADAIAILTEWKEFSSLDLKKAYDLLNHKKIIDLRNLLDKNEA

IKLGFEYQGVGR

>ABV52942.1 hypothetical protein C8J\_1344 [Campylobacter jejuni subsp. jejuni 81116]

MKNILVVGGAGYIGSHTLKHLLDNNYNCIVMDNLIYGHKQAIDKRAKFIHADLLDTFSLTNVFKQEKIDA

VVHFAAFAYVGESVVNPAKYYQNNVVGTINLLNAMLENNVKDIVFSSTCATYGEPQYTPIDEKHPQNPIN

AYGRTKLMIEQVFADYEKAYGLRHISLRYFNAAGASKDGLIGESHEPETHLIPLVLKAIKGEIPAINIFG

NDYDTEDGTCIRDYIHVEDLALAHRLALENLHKFSGCINLGTGIGTSVKEIISAAEVVSGKKCPINYAPR

RAGDPARLYADNKKAKEILSWEAKYTDIKDIIKSAWVWENNRKY

>ABV52941.1 hypothetical protein C8J\_1343 [Campylobacter jejuni subsp. jejuni 81116]

MKKVKNLIVGCGLSGAILAERLASKGQEVLIIDKREHIGGNIYDYKDQESNITVHKYGPHVFHTSIKGVW

EYLSRFTKWHYFMYRVKAFIDGREVNIPFNLDTLHKVFPEYLAKELEQKLVSKFAFNSKIPILELKNAND

KDLEFLAEYIYKKVFLGYTVKQWGVKPEELDFSVSARVPVYISRDDRYFVDTYQAIPKDGYTKMIENIIN

HSLIEVQLNTDFKNIKKDIEYERLFYTGAIDEFFDYKFGKLPYRSLNIVFETFDKEYMQSCPQINYPENY

DFTRSVEYKYYLDEKSSKTILSYEFPCEYEEGKNERYYPIPNDENQKLYEKYLKESAKLNNVYFLGRLGD

YKYYDMDKTVERVLKFYKEKL

>ABV52940.1 hypothetical protein C8J\_1342 [Campylobacter jejuni subsp. jejuni 81116]

MRKNIHIFFTINDVYSGYLSACMISILDSLDRDYIPYFYIIDGGISEKNKNKLKFLNIGREFYVEFIAVN

QDLFKNLPNSSQSHISNETNYRFLVSTIKPNLDKCIFLDVDLVAVGDISKLWEICIDDYYMAAVSDQAPL

HSESWTLKLPLPYDYLYVNTGVTLINLKKWREDNIQELLFQNSAQYAEILQFPDQDTLNITLYKKIKYLS

HIYNAMPVQTYYNEKQKQEAFSNPQIIHWAGYKKPWKFPDAPYAEMFWHYARQTPFYEEILFKNITQNSL

NIIQNSIQGAVERVKAHLSYKLGKEILSVKENKLKVLILPFALILIYVKHKISNLIFKLILISNPNLKSL

PLNHYSDYQEALKIQNYLSYKLGNLLIKYPFTFVFRVASVYKEWKKNVKR

>ABV52939.1 hypothetical protein C8J\_1341 [Campylobacter jejuni subsp. jejuni 81116]

MLKDNKIVGVVIPVYNCEKYLIECLESVVNQSYYYLKIILINDGSTDRSLEILKKYAIRDDRIIVVDQIN

SGQGVARNVGMDLFKNKIKLQFYRNEQNLSVFNVNNQNNYNIKYIYIKQNQSSRQFNLSIDYIIFLDSDD

FWELNCIEECIKHMSNVDIVWFDYKLHYDLEYKYAVTLFDLYKFQKDMIISSEKWLKLSFKNEISEFWFT

WQGMINFKKLDDLNIYFKKGILYEDQVFGILLFGQVNSIYVLVKTLLNYRIRLNSSMNYDRETKQYSSYF

NGLSKTNINNIKKSFEYDINITNKYLQIARICNTYLTINKIIQNKNIFHLFKQVFLNKYLERSVQIFNFK

EDPLGIKHTLAGEIDKEIDNFFILPPQDKLSHIPIVFSCDANYFSYLTVVLQSIKEKSSENYNYDIYILH

NKLDKSLTQKLINYIQAENFSIKFVDISRILNLLKSQIQFYTALFFSEATYYRFFIPKIFKEFKKIIYLD

TDIIVKQDLNLLYSIDFDKPLAAAKCMIFSQVKQADHRITKLKMKQPENYFQAGVMVYNIQKCLKMDFTQ

KCLNKLQELKDPPLVDQDVLNAVFEGDIHYISLKWNCLWNVSYRIPNFKILYSKDFLKDYQEAERDPYII

HYCDYFKPWNSPHLPKADIWWHYARQTPFYEEILFKNITQNSLNIIQNSIQGAVERVKAHLSYKLGKEIL

SVKENKLKVLILPFALILIYVKHKISNLIFKLILISNPNLKSLPLNHYSDYQEALKIQNYLSYKLGNLLI

KYPFTFVFRVASVYKEWKKNR

>ABV52938.1 hypothetical protein C8J\_1340 [Campylobacter jejuni subsp. jejuni 81116]

MSREIQEFIEKLKDWKNNFSIQDYDYTKYNCEVADIAKWQKENNVNELINFWNEKIKEDYFELKHPLYNK

ILTRAVFSCNIHNFFNWVFFIDIKNKNPFLLGQVNSCINFILVKNSIIILDEGWSNLYIGAIDHARDFIC

GSCLDLKYKGIGFGFTLQNTRPAHFFNHILNGFINIDNTKPVYGKNIFFKPKFLLYTEQKDLVYFYPTTK

MNTNLVPMFNYVYQESIRDFITLIDKDIFKEKYDLTIWLGLPGERRNWVEQIEGVANILKHCNKYFKKIK

VYIDGMTGYDGQIQDFPENKMLFNKIVNTTRELFLQEYNKNIIFTFEELQKLVDISTENEEKIIVFKSLA

GYDYRTKICYCRDCNIAISDGGTTTFVPFIIFKKPGIIFCGHLNHINYANCILNDKRLQKVTGKDMFLQV

DRKTYFNFSFHLSYEHIYNLAAEVLEELSAVGKLKVKNLKMHRLDVPPVELIAKQYELEQKLNIKFSIEN

VALFSELEKKIDTLALNNTAIINNANNTTLLIQNKDQYIHNLEQNIQNLNHQILFKTAKARIQNHLSYKL

GQALIINSKSILGYIRMPYVLSYIKDKHRQEQKAYEEKIKDNPNLALPPLETYPDYNEALKEKECFTYKL

GEALIKADKEWYKAGYVKFYFKDVPRLKREFGKR

>ABV52937.1 hypothetical protein C8J\_1339 [Campylobacter jejuni subsp. jejuni 81116]

MKEIKIQNIIINEEKAPLVVPEIGINHNGSLELAKIMVDAAFSAGAKIIKHQTHIVEDEMSKAAKKVIPG

NAKISIYEIMQKCALDYKDELALKEYTEKLGLVYLSTPFSRAGANRLEDMGVSAFKIGSGECNNYPLIKH

IAAFKKPMIVSTGMNSIESIKPTVKILLDNEIPFVLMHTTNLYPTPHNLVRLNAMLELKKEFSCMVGLSD

HTTDNLACLGAVALGACVLERHFTDSMDRSGPDIVCSMDTKALKELIMQSEQMAIMRGNNESKKAAKQEQ

VTIDFAFASVVSIKDIKKGEVLSMDNIWVKRPGLGGISAAEFENILGKKALRDIENDTQLSYEDFA

>ABV52936.1 hypothetical protein C8J\_1338 [Campylobacter jejuni subsp. jejuni 81116]

MKKILFITGTRADYSKIKSLMYRVQNSSEFELCIFATGMHLSKNFGYTVKELYKNGFKNIYEFINYDKYY

QTDKALATTIDGFSRYVNELKPDLIVVHGDRIEPLAAAIVGALNNILVAHIEGGEISGTIDDSLRHAISK

LAHIHLVNDEFAKKRLMQLGEDEKSIFIIGSPDLELLNDNKISLNEAKKYYDINYENYALLMFHPVTTEI

TSIKNQADNLVKALIQSNKNYIVIYPNNDLGFELILQSYEELKNNPRFKLFPSLRFEYFITLLKNADFII

GNSSCILKEALYLKTAGILVGSRQNGRLGNENTLKVNANSDEILKAINTIHKKQDLFSAKLEILDSSKLF

FEYLQSGEFFKLSTQKVFKDIII

>ABV52935.1 hypothetical protein C8J\_1337 [Campylobacter jejuni subsp. jejuni 81116]

MKCYICGSESNIQREGKVRDSLKINILECKDCGLVFLDKQETDDEYYKASGMRKDFKNSVEVLTLNQNLS

LTDNERRIDFIKQNFSKDINLLDFGSGLGHFLILAKENHFLNICGVELEERVKSVYFDHNITLYENLDYI

QNDSLDVVTLFHCIAHIHDPIMLLKKLSEKLKKNGKIIIETPNANDALLDIYKNKGFSNFTYQKCMLYHF

NKYSLYQIARKSSLDIDFIKHIQRYPLSNTLYWLNNNLPAGQKYWGSIIDNKNLQNAYEATLASIGATDT

LFAQFSKI

>ABV52934.1 hypothetical protein C8J\_1336 [Campylobacter jejuni subsp. jejuni 81116]

MQFNIKNIDLILEKDIIKKYRRQIIKWIQTKEFEENYSHFLYPPLLNPNNVDYCQISPEVSWELNLPLPP

FYRFVYWGSHGCGNTAFGVFLAKYGGYNFYSTNENDGRKAYISLFKDMISKRHLLKKDKFGYLAIRNYVD

GNEHEKFHFLIHSSSAINLVRDPISCLKHYIGMKRYYNKSIRRFNLTFNPKDIFKELVGYSCGNEIKKTP

SLEAIESWIDFRYKCFHDGQLIQEMKNIKETIVIDMREIVGKNSFNTMQNIARYYKLKTKFYDDGTMQEK

VAEYEGILPLTLYVHPSDIKDFYYDNNLKSIDGIDIFITTHYWLPFNGFVPYETQSRFEGVVFPEKVEDI

TKYILNYQHDKIIICVRKGDFKKIKKSNKLYKAIQQYIIKLIPYIEKQKDIEEKKKIHERDILEFFNKNK

TLCAKFKNILDIHLSYIKLNRPDIVGSWNYYQEFEKIYKRLHT

>ABV52933.1 hypothetical protein C8J\_1335 [Campylobacter jejuni subsp. jejuni 81116]

MKAIMYHYVRYSDKDFPFFRYLSVENFCKQLDFFEKHYGFVQFNDFLEVCNKPFKTQIFEKIKNKILLTF

DDGFLDHFKFVMPELLKRNTFGLFFISTGVYQRKKALDVHRIHYLIGRYGGEVLVKLSNDLLDANMLENI

PYFKEKTYTKQNNDFYTNEFKKLFNYYIKYEFRESILDKIVKLCNENDEDIFKNLYMNKDQLKTMHKNGM

ILGSHSVNHRVFSKLNNEEQEKEIHDSFSFLEKTIGNLNAKIFCYPYGGFHTFTDFTQKILNNANCNFSF

NVESRDVILNDLINYPQALPRYDCNEFDFGKASCG

>ABV52932.1 hypothetical protein C8J\_1334 [Campylobacter jejuni subsp. jejuni 81116]

MKINGFNTKDTFEYENGFYLTMDNERMGKLIAHYVLYNKIINLPGAIVECGVFKGNSFFRWGHFRHLLEN

EKSRKLIGFDAFGEFPETSFDPDKQKRDSFVNVAGNGISIEDMEKVMSYKKFSHYELIKGDITKTIPEYC

DKHPEFKIAFLHIDVDIYEPTVTILENLFDKVVRGGG

>ABV52931.1 hypothetical protein C8J\_1333 [Campylobacter jejuni subsp. jejuni 81116]

MVIAVIPARSGSKGIKNKNLVLLNNQPLIYYTIKAALNSKCISKVLVSSDSEEILSYAKSQNVDILKRPI

ELAQDDTTSDKVLLHALEFYKDYEDVIFLQPTSPLRTNIHIDEAFKIYKNSDANALISVTECDNKILKAF

ICDNKGDLKGICDDEYPFMPRQKLPKTYMSNGAIYILSIKDFLNKPSFLQSKTKYFLMNKISSLDIDNLE

DLKQVENIQKMKGCVVWISGLAGAGKTTISSGLYKKLKEKYNNSVLLDGDELRKIFKHTGYTREERLESA

KKISSLCSFLAKNDIIVICATISLFEEIYLLNRNTIENYFEVFVDCPMEELILRDQKGLYSGALKGEIKD

VVGVDIKYAKPNAHYIIDNSSKTDLEKKINNLYNEVELFFNKER

>ABV52930.1 hypothetical protein C8J\_1332 [Campylobacter jejuni subsp. jejuni 81116]

MNSNIVYIAMSADLIHPGHINIMKLAREYANKIEGKVVLGLLTDSAIASYKRLPYMNYEQRKIIVESIGF

IDEVIPQNTLSYADNIIKLKPKFVIHGDDWKEGPQKRERSNVIALLKELGCGELIEPKYTQGISSTELNQ

NAKSLGITTNARLSLLRRLINAKKPLRILETHSAISALIAENTFVSKNGTNLRRLINAKKPLRILETHSA

ISALIAENTFVSKNGTKIEFDGFWSSSLTDSTSRGKPDIEAVELSSRLKYG

>ABV52929.1 hypothetical protein C8J\_1331 [Campylobacter jejuni subsp. jejuni 81116]

MIIEDKIGLKKNSLLGNDVIQNQDSIEDFCSKIQAGKKAQITNEFMIIARIESLILDKGMDDALQRAFAY

IQAGADGIMIHSRHKDGDEIIDFLKQFRLKDQDTPIVVVPTSFNEIKASDLATYGANIIIYANHMLRASF

VAMQNVAKEILENDRSKESESKCMKINEILNLIPGTV

>ABV52928.1 hypothetical protein C8J\_1330 [Campylobacter jejuni subsp. jejuni 81116]

MLNMEFFGEALKTIGCFQFSGVPCSYLSPMINYAINENSFIMSNNEGDAIAIATGISLANMEKKDNFGVV

LMQNSGLSNALSPLTSLNYTFEIPILGFVSLRGERDDQDRNTDEPQHELLGTITDRLLETCNIAYDFLSP

DYNQAIRQLQIAHKYLKQQKSYFFIVKNNTFEKCSLKNFNIPVKNIGREIIQQENSLAEFQPKRIEILEC

IANFSYKNNIALFATTGKTGRELYEIRDTENQLYMVGSMGCVSSLALGVSLQNSKKIIAIDGDSALLMRM

GALTTNAYYTKNNNKGNFCHILLDNESHDSTGGQFNLSPFINFPQIAHFCGYEKIFIINSLDDLIQALDF

FIARKEGGAVFIYVKILKGSKGKLGRPKITPKEVALRIAQFLNRKSDE

>ABV52927.1 hypothetical protein C8J\_1329 [Campylobacter jejuni subsp. jejuni 81116]

MSDFRYYNPVKINFNVSYEHIIDSLKTDSILLLTSKSFYKKGLTKILEDKLGDRLKGVIYDILPNPEINY

AELIKKDYRNYKEIIAFGGGSVLDMAKYFSVSGDVIRNGGNLDISNSCSFIPIFAIPTTAGTSSELTKWA

TLWDTPNNIKFSLSDENLYCKEAFYDPNLFLNIPRELTIYTALDALSHSIESIWNKNSNAISTNHAIKAI

ELILEYLPRLQNDLNSKELRLKIILASIYAGLAFSNTQTALAHAISYPITMKLGISHGLACSFTIPILLQ

CIDDVKINKLLSIYKEKIISLFHILNISTNLKSYGITKQFIEDIFDNLNSRAKNGMFDLELTKKRFLLCI

K

>ABV52926.1 hypothetical protein C8J\_1328 [Campylobacter jejuni subsp. jejuni 81116]

MQKERFFMFGFSLWKRHFIKPFFKAKDNEIIFLNSIKSLLRYKLKDDDKFFIWGKRIDYNTLKSTLIKKA

QDENLLHFTPKISLVEDGFIRSISLGSDLTRPFSLIVDDKGLYIDPNKPSKLEELLQNEIFDENILNRAK

NIIKILLENRFSKYNGLKHENLKINAKIGQKVILIPAQVEDDASMILGGFGLSTLDLLKEVRAKNQDAYI

IFKPHPDVLSGNRVGLKDETLILEFCDEIVKDCSIDSAIKIADEIHTITSTSGFDALLRAKKVFTYGMPF

YAGWGLTKDKYKCKRRTRKLSLEELVAGVLITYPRYINPKTKTLCEIEVCLDIMLNLQKDYFSKKHIKLA

IDFKTFMLRKIRRFYEFLAKK

>ABV52925.1 capsule polysaccharide export protein KpsS [Campylobacter jejuni subsp. jejuni 81116]

MRFSTKIKKEFSGKNVLLLQGPVGNFFHHLAMKMKKNQTKVFKLNFNGGDFFFYPSGTRCKCDEKDLENF

YRDFFQSKKIDAILMYNDCRIIHAKAIKVAKELEIEVWIFEEGYLRPYCITLEKDGVNANSSLPRDKNFY

LSQDIFTKESIKEILGGFKFMAFDAFLYWLFAFILAPFFNNKLHHRTLYPFEFLFWFRSLYRKYLYKITE

KKLNEKIYNLEKKYFLAILQVYSDTQIKYHYKKSIEHFIEQTILSFANHARAKSYLVFKHHPMDRGYKNY

SKLINDLSQKYHVEGRVLYVHDTHLPVLLRKALGCITINSTVGLSAILEGCPTKVCGNAFYDFEGLSYPK

KLQFFWREAHAYKPNPILVCNFKKYLLQTNQFNGNFYKNFFLDK

>ABV52924.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MDREVFYIAGYDPKSYRFYYDLFKKNLKDYSHAFNIEADLSKIEKKEQFPFFKISCEGVQTKYHFLTWND

IVKKNWSENYKDALADCYSFFRIYTITGLFIKFGKESIYQLITGYYPFFYVLFSLLFSLVLAFGSFAFLQ

NYMHFSLAIIIGCFLGFLLNHFLFKLGKKLAVFWIARICAFCATWQDKKTGTMQERIKLFANVIIDKLKR

NESKQDYELILVAHSVGTIVCIEVLECILRQNLDLSLLRKLKILTLGECIPLVSYQKKADEFRKKLEFVS

RFDLKWYDYTSIIDGACFPQVDFFRTSGVNAKFTPPFLSAKFHTLYEKHEYKKIKRDKNKAHFLYLYSIS

VKGDYDFFSFIIMPKFLEEKVKI

>ABV52923.1 putative cytochrome P450 [Campylobacter jejuni subsp. jejuni 81116]

MSECPFFPKPYKNKASTLLTFLLKRRSWLDGLYERSYKMQTGYVKMPNFDLYVINDTKEVKRMMVDEVRE

FPKSAFLHELLSPLLGESIFTTNGEVWKKQRELLRPSFEMTRINKVFNLMSEAVADMMDRFSKYPNHAVI

EVDEAMTFITADVIFRTIMSSKLDEEKGKKILNAFVTFQEQSVHTAMRRMFRFPKWLSYILGDRKRAKAG

DVIRQVLSDIIKPRYDMADNAEFEDILGSLLLVVDADTNKRFSFEEILDQVAMLFLAGHETTASSLTWTL

YLLSLYPKEQEKAYEEITQVLQGGAIEISHLRQFKYLTNIFKESLRLYPPVGFFAREAKKDTQVRDKLIK

KGSGVVIAPWLIHRHEEFWTNPHGFNPSRFEGEYKKDAYLPFGVGERICIGQGFAMQEAILILANILKTY

KLELEEDFVPDVVGRLTVRSANGMRIKFSKREL

>ABV52922.1 hypothetical protein C8J\_1324 [Campylobacter jejuni subsp. jejuni 81116]

MKRVRTKIRANFRRRVKRTLKGSLKEKLAGTILLCAIVPLAVLGYLFIVIIGTFFNTARARQGVRALDHF

VNASLFNGYAWESVSSHAWRERNRKKWARIVIKITDFFQKDHCKRANKREQPVVDFILSRNLDKQTIGK

>ABV52921.1 4'-phosphopantetheinyl transferase [Campylobacter jejuni subsp. jejuni 81116]

MRVGCDIIAISRIEKIHSRHGKNFLDKFLSPKEQILIKNPATLAGLWAAKEAASKALGVGICELCSFFDI

EISKDEKNAPKLKYSQKITKNFNITQTSLSISHDNGFAIAIVAIV

>ABV52920.1 possible flagellar protein [Campylobacter jejuni subsp. jejuni 81116]

MDEELENEETKKKKGGSLVIIIVILLFVLLLSIMGVIAWLISSSSSDESEVKEAPKEEAKADKPKVSAPT

QRGSDFANIGPMYPLDPFTLNLLSDSGSRYVKCTIELEQNSELLKPELDKKVPVIRDIIIRTLTAKTFEE

VSTQKGKERLKDELVGKINEILTDGFIKNVYFTDFVVS

>ABV52919.1 phosphomannomutase/phosphoglucomutase [Campylobacter jejuni subsp. jejuni 81116]

MLDVIFREYDIRGLYGKELNEKSVKAIGFCLGQTMLNKGCKNVSVGYDARYSANELFNYLVSGLNKAGIK

IYDIGLVPTPLGYFSLYEGLKFDANVMITGSHNPKDYNGFKITINKESFFGVELKEFSKEVYKHLDDEIE

ENLEVEKYDILSLYVKFMCEQFSFLKDFNYKFGVDCTNGAAGVVIKPLIKALNLKAHVMFAEPDGQFPNH

APDPTEEENLSAIREFLNQNQDYSLAFAFDGDADRMVALSKTHVFCGDELCYLFAKNIPNPRILGEVKCS

KNLFDEVAKFGTIFMGKTGHSNIKKMMKEKDIDLAAEVSGHIFFKHRYFGYDDGIYAFLRALELVYKGFD

LESMIKALPKLYTTPEIKIPVNEEEKFKLVEEFQKEIEKGALKGVKSLCEIDGARIDFGDGWALLRASNT

SPYLITRFEATSLERAKELESMVFTLFDDIKARLKN

>ABV52918.1 hypothetical protein C8J\_1320 [Campylobacter jejuni subsp. jejuni 81116]

MKKILVLLSLCAFAFGASECDRKIDRINKEISFSKAHNDTARTLSLELALKQVQNDCAKDPMFYDKKLEA

KKLKEQEVEKIEKELDALKEQKDYMSKAEYKAKKEALKEQKEKIKKEIKEYIDNL

>ABV52917.1 hypothetical protein C8J\_1319 [Campylobacter jejuni subsp. jejuni 81116]

MQERIDLIVKILDEKKAEDIKTIDMSEQEYFVKYVIIAATLGERHALSLIDELKTQLKAKGEEFLNIDSS

EEWSVIDLGDILIHLLTPEHRGIYNIEELLENLKKGRV

>ABV52916.1 nicotinate-nucleotide adenylyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKIALFGGSFDPPHNGHNSVVLEALEKLDIDKLIIMPTYINPFKQSFSADEKQRFLWVKKLWGHLPKVEI

CDFETKQKRPVPSIESVKYLYKLYNPSKFYLLIGADHLEKLHLWHDFEKLNSLVEFVIANRNDIEIPKNF

KDLKTDKKIASSFIRNTLNTNEVCEEIKDEVKKYYEKLQKN

>ABV52915.1 glyceraldehyde 3-phosphate dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MAVKVAINGFGRIGRCVARIILERNDIELVAINDTTDIELTKYLFKYDTVHGEFKGSVDSEGDDLVVNGK

KIKVFKSRNVKDLDFAKHGAQIVLECTGAHLTMAKCQEFIDMGVQKVIMSAPAKDDTPTYVLGVNSELYK

GESIISNASCTTNCLGPVCRVLQDNFGIEKGLMTTIHAYTNGQSIIDAKAKDKRRSRAAAQNIIPTSTGA

AKAMKLVMPELNGKLHGQSMRVPVIDVSSVDLTAQLSRKVSKDEINEAFRKAATTNLKGILMVDDDERVS

SDFITCSYGAIVASDLTQVIADDFIKVIAWYDNEWGYSSRLVDMAVYIANKA

>ABV52914.1 phosphoglycerate kinase [Campylobacter jejuni subsp. jejuni 81116]

MSDIISIKDIDLAKKKVFIRCDFNVPQDDFLNITDDRRIRSAIPTIRYCLDNGCSVILASHLGRPKEISS

KYSLEPVAKRLARLLDKEIIMAKDVIGEDAKTKAMNLKAGEILLLENLRFEKGETKNDENLAKELASMVQ

VYINDAFGVCHRAHSSVEAITKFFDEKHKGAGFLLQKEIDFASNLIKHPARPFVAVVGGSKVSGKLQALT

NLLPKVDKLIIGGGMAFTFLKALGYDIGNSLLEEELLEEANKILTKGKNLGVKIYLPVDVVAAPACSQDA

PMKFVPVQEIPNGWMGLDIGPASVRLFKEVISDAQTIWWNGPMGVFEIDKFSKGSIKMSHYISEGHATSV

VGGGDTADVVARAGDADEMTFISTGGGASLELIEGKELPGVKALRSKENE

>ABV52913.1 triosephosphate isomerase [Campylobacter jejuni subsp. jejuni 81116]

MIFAVNLKCNHTRASFKIYAEILNKTMGAKCDDIIVFPPSVAFLENENNFIQGAQNFYPCVNGAFTGELG

KEHLDEFGIKCVLIGHSERRALGDEEFIKAKFDFAKEHGYKIVFCIGENLDTKNSGKTLEFLKKQLEIID

LNYEKLIIAYEPIYSIGTGVSAQSTDIAKVLEFLASLTKAPLLYGGSVNENNIKEILSVKHCGGVLIGSA

ALKVENFIKLIKG

>ABV52912.1 putative enoyl-(acyl-carrier-protein) reductase [Campylobacter jejuni subsp. jejuni 81116]

MIMKGKKGLIVGVANNKSIAYGIAKACFDQGAELAFTFLNDALKKRVEPIAQEFNSNFVYELDVNNNEHL

DSIAEKIKKDLGEIDFVVHAVAFAPKEALENSFLETSKEAFDIAMQTSVYSLLSLTRALLPILKDKGSIL

TLSYLGGVKYVPHYNVMGVAKAALESSVRYLARDLGVKGIRVNAISAGPIKTLAASGIGDFRMILKYNEI

NSPLKRNVSIEDVGNSAMYLLSDLANGVTGEIHYVDAGYNIMGMGDVEKNEEGQTVLCWDNQKG

>ABV52911.1 hydrogenase small chain [Campylobacter jejuni subsp. jejuni 81116]

MAKLSNEELKNILEGRIKKLENSILKEDKVVNEESVKILAKHLSLGNEIPALAQRFFQIAPKTKLVWLHL

CECTGCSESLLRSELPSFDELIFDFFSLEYHETLMAANGTKAEELLEHVLEEDFILAVEGGVAAIDTFFL

TIGAQGESGYEILEKLAAKAKAIFAVGTCSSYGGIQAAYPNPSKTCGISEVLSQKVVNIPGCPPSDINII

ATLSFFALFGVLPELDEQNRPVWAYGKCLHDMCERKAKFESGIFAEHFDDEAAKNGACLFKVGCKGPYTY

NNCPKVKFNAKTSWPVAAGHGCIACSEKNFWDEFGNYEKPMANIFSYAKLCNEELKQEFFLEEQIKILEQ

IDFEFESNIKLILQNIAKNKLGALLVENYKKSFEKNYAFIEQNFDENPMPSKDFWKYLEISFILVKGAFL

KDKNDFLIAAKNYAFKHASPYDFKLNMNAEKPKLDVSKSFRMTLIYLCGGLDFEGVAYSILKAFEDNIAK

ISSLKAS

>ABV52910.1 ferrous iron transport protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIKIALVGQPNVGKSLLINALCKANMKVGNFSGVTIEKASAKTFYKNYEFEVIDLPGTYSLDGYSEEE

KITRHFLNQNDYDVIVNVLDATNLERNLILSAELLSLNKKMLLALNMCDEAKKEGIELDTSVLSQEFQSQ

VVEISAKTKENLELLLQKIIILFESKFIPRSQFYTPLCEKSPEKEDLLYFINELSKKIITHKKEERNLTK

KIDALLIHKFFGLPIFLFLMWLLFQLTFSLGQIPMDYIESGFNTLGEFVKNNISNTFIASALADGIIAGV

GAVILFLPNIMILFLGIALLETTGYMSRVAFLLDGILHKFGLHGKSFIPLITGFGCSVPAFMATRTLKNK

RDRLLTLFVINFMSCGARLPVYVLFIGAFFPSEKAGNYLFGIYILGAILGLCAAKFLRMTAFRGLDEPFV

MEMPKYRMPNWHLVWFMVYNKAKMYLKKAGTFILLASLLIWFASNFPKSEENLNDFNAQERAIEQSYLGQ

FGKGIEPIFKPLELDWKLSVSLISGLAAKEVMISTMGVLYSLGKDVDETNNDLKGIIAKNIPIPSAVAFI

LFVMIYNPCFAATIVFSKESGKLKYTLFLFLFTCTSAYIVAFIGLYIAKILLN

>ABV52909.1 hypothetical protein C8J\_1311 [Campylobacter jejuni subsp. jejuni 81116]

MTLNELKDGQKAIIVNLNAHKELKNRLLSFGFIKNKNLKKIHSSLKNATIMVELDTSCVILRSDEAKTIE

VNLI

>ABV52908.1 MmgE/PrpD family protein [Campylobacter jejuni subsp. jejuni 81116]

MFYSEILADFIFNLKYENIPNTVVQRAKELMLDSLGTAIAASKEECVLNAFKAFENLSTDKNTPIWVNDQ

KLVPIYAAMLDGIASHALDFDDTHTEAILHASAILTPLCLSYGFHVNKDAKKIIKAFIVGWEIAARVGIA

SKGTFHKRGFHTTAIAGIFGSVSASAILLDLNKEQIINALGLAGSFASGVNEFLSNGSNSKVLHIANAIK

NGIMVAHFAKNNMSGPLSIFEGRDNIFKCFGIEEECDKTELSKALGEIWQTMQVSIKPYPSCHFAHGLID

CAIALKNDGLKADEIKSIHCFVDEVPISFICDPLEAKYTPNSAYEAKFSMPFLMALGFFDGKITLDSYEN

LKREEVLEFAKKISYEKRKSQGFPKYFPGHLEASLQDGRIIQKDVFINKGNFDNPLSFEELKAKFLANAQ

IYLDNAKANKILDQIINLENLNHFSF

>ABV52907.1 adenylosuccinate lyase [Campylobacter jejuni subsp. jejuni 81116]

MTGISVFDHRLLADSWSTQEMRAIFCEQNRIQKWLDVEAALAKAQAKLKIIPKKAADEIAKKAHYKFMDM

DFIFAEFKKTKHPLVPTVRGLEKACDNNLGEYVHFGVTTQDIIDTGLVLQFKEAMTLVKSELKAIAKALA

KLAKTHKNTAMMGRTLALQALPITFGHKVAIWLSELERHFERILELEKRLYVGSIVGAVGTKASLSDECN

EVEKLTLENLGLDVPNISWQPARDRFIELGFVLGNINATFNKIAHEILILSHNEIDEVAEPFGKGQVGSS

TMPHKRNPAVSENAVTISNAFKANLAILSDIERHEHERDGQVWKMEWKLLPEMFLMLSVVLANMKFALSD

LEVKKDKMLKNLNTLNGFVLAERVMFALSDHYGKQHAHEIVYENAMLGIEKQKTFKEVLLADKRVSKVLK

EKEIDALLDATTYVGYAPKLVDEFLAKIKNSAILK

>ABV52906.1 cystathionine beta-lyase [Campylobacter jejuni subsp. jejuni 81116]

MNSKTKLIHCGRGDQGAEVRSVNPTLMRASTILFKDHATWQKYRELRKTDRVLSYGARGTTTNFELEKLI

CTLEGGYRAQLFPTGLAALAMVLLNYASKDAHFLITDAIYGPVRTICELFLDKMGVEIDFLKADASDVEE

KIKPNTKLILCESPGSILYEVIDLPKLCKIAHAHNIPVAIDNTYSSGYFLNPLELGVDISVIAATKYLSG

HSDVTMGIVVINEKEWKNFDKLPEALGFTTSPDDAYLVLRGMRTLDVRMKAHEKSADEIVEFLQSRKEIK

TIFYPKLKSHPNHEIFMRDHKGANGMITIEFTEGYSKDDAIKFVDKLEYFSIGASWGGYESLATVTTPPR

TATDWSARGPFVRFHIGLEDTKDLIADLTQAFDSIKK

>ABV52905.1 hypothetical protein C8J\_1307 [Campylobacter jejuni subsp. jejuni 81116]

MLGIVFSLFSVFLLVFMLYKKINAHMALLLSGLLLLSLAALFGLSPHIVAKGSLNLGFFDIFQVFNQTMS

STLAGLGLTLMTIAGFSAYMDHVGASYALFKVFEKPLKAVKSPYVLLIVAYFIVQFLVLFIPSHAGLALL

LMVTMYPILVRSGVSKLSALSVIAICQYIDHGPGSGNVIMASKVAEVDPAIYFVHYQLPTTLPIIIAVGI

AIYLCNKFFDKKDNFVFNAQEIEKELNENEGKEKELKKPPRIYAILPIIPLVLILGFSSVLDSILVLMGI

SSAEEVKAVASTAIKMNVPVAMVISTFVAIIFEMIRYKSIVETLNSIMIFFKGMGHLFVITISLIVCGQV

FASGLLSVGFVDTLIEFCKNAGFGVLAIIIAVSILLAVCAFLMGSGNAAFFSFAPLIPNIAKHFGVETIT

MIAPIQIMTGFGRCVSPIAPAILAISAIAKVSPFAVVKRTAIPMLVAAIVNVIMTYIYL

>ABV52904.1 hypothetical protein C8J\_1306 [Campylobacter jejuni subsp. jejuni 81116]

MSNYPKAIGPYSAYREANGLLFISGQLPINPASGEIESSDIKEQTKQSLKNIGAILEENGISYDKVIKTT

CFLADINDFVAFNEIYAEFFKAPYPARSAFAVKDLPKKAKVEIEIIAQKG

>ABV52903.1 hypothetical protein C8J\_1305 [Campylobacter jejuni subsp. jejuni 81116]

MDEGQKQQFIKLTYFLGEVLGEQYEIVFHVITEDGAYIAAIANNHISGRSLDSPLTAFASELMQNKKYLE

KDFLCDYKALVGKSKLIRGSTFFIKNHDKLVGILCINHDTSIMRDLICKMIDLEKIGDMGDILGNISFSQ

NDSSIETLSHSIEDILVQSVDSSYLNSNYQLSITQKEEIAEKLYEKGIFNIKGAVPIVAKFLKISEPSVY

RYLKKFKK

>ABV52902.1 hypothetical protein C8J\_1304 [Campylobacter jejuni subsp. jejuni 81116]

MTTLSLEEEKRFEELCKMAFNFARNNECENLKIMIEAGLNANLKTHKGDSLLMLAAYNNSYESAKMLLEK

GAKVDEKNDRGQTPLAGVCFKGYLPMCELLVKYGANIDENNGLGMTPYTFAIMFGRKDVAEFLLKKSKNN

FLKKTSLKILKFIKKF

>ABV52901.1 catalase [Campylobacter jejuni subsp. jejuni 81116]

MKKLTNDFGNIIADNQNSLSAGAKGPLLMQDYLLLEKLAHQNRERIPERTVHAKGSGAYGEIKITADLSA

YTKAKIFQKGEITPLFLRFSTVAGEAGAADAERDVRGFAIKFYTKEGNWDLVGNNTPTFFIRDAYKFPDF

IHTQKRDPRTHLRSNNAAWDFWSLCPESLHQVTILMSDRGIPASYRHMHGFGSHTYSFINDKNERFWVKF

HFKTQQGIKNLTNQEAAELIAKDRESHQRDLYNAIENKDFPKWKVQVQILAEKDIEKLGFNPFDLTKIWP

HSLVPLMDIGEMILNKNPQNYFNEVEQAAFSPSNIVPGIGFSPDKMLQARIFSYPDAQRYRIGTNYHLLP

VNRAKSEVNTYNVAGAMNFDSYKNDAAYYEPNSYDNSPKEDKSYLEPDLVLEGVAQRYAPLDNDFYTQPR

ALFNLMNDDQKTQLFHNIAASMEGVDEKIITRALEHFEKISPDYAKGIKKALEK

>ABV52900.1 hypothetical protein C8J\_1302 [Campylobacter jejuni subsp. jejuni 81116]

MSVLVIGADEITPIRAVLHDLGAKKIEHWDARNENRVNRKPIPCDTECIVMLTSFLNHNTMKKIKNEAKK

RKIPLVCAKRSVSCVYCEYCKIFNLNKEFSCYKG

>ABV52899.1 hypothetical protein C8J\_1301 [Campylobacter jejuni subsp. jejuni 81116]

MLFGFDDKREFIPQIYRYLNNQELMLTFLTQYNASVDSALKIPLLYAKNTKSLKMIFGNFLHNIMHVSFG

KIQNINIKLNTYAFYFQKRKSLIFNTKISKNIDLLRLLRIYLYGICFDAQILFSSYVYDKVSFQNNGKNI

DQDGDLIIIDKKFAILPLCKEINAHNLKIENEIHGLLNLIKENNFEKFYIVCPRNKNFTHFIEIKHFLCD

LNKTMLKLVPYKISNQIIRRK

>ABV52898.1 flavodoxin [Campylobacter jejuni subsp. jejuni 81116]

MSVAVIYGSAMGNTEGAANTIASKLGISDVFNISDIDAAKMNSYDKLICGTSTWGSGDLQDDWDGFDFSG

LSLGGKTVAVFGMGDSESYSDTFCGGMGKLAQNLKDAGANLVGEVSTDGYTFEASDAVVDGKFVGLALDN

DNQEDQTESRIDAWVEQIKPYFA

>ABV52897.1 lipoprotein, putative [Campylobacter jejuni subsp. jejuni 81116]

MSKITLILSFFIALFMSACTNATFIQSFIQTSNEGIFIRSQKQQSFKISFQNPSQLRTTLDRDLALKLKN

LGLKEVKENADYEILINLVDMKKHSYAQKITTSARFFYDFDPLESDGEWMVENYYTMQVNLQINSKNHNS

QKTSLLARTAYLGNKERCQLSLENKIINQIVSFFYF

>ABV52896.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKLSLILACSASLFAASNSEISDFYSKSIKAQFPNATVSVSNRQKVGNTGFESVIVSVELNGQKQENIL

FTKDSLITPDLIDLKTGISYAQEYEMKKFQEARENFTKNAKAVAQKETMVIALGDKNKPAIYVFSDPECP

YCREHLAQIDDELKNYQVNYILTPVHGKSAFEKSALIYKEAKKAKNDKEKIAILNKYYDANIKNYPKVSD

TELKEVFSLYEKYRSLGLSATPTIIK

>ABV52895.1 putative selenocysteine-specific elongation factor [Campylobacter jejuni subsp. jejuni 81116]

MKSVIIGTAGHIDHGKTSLIKALNGFEGDSLKEEQERQITINLSFSNLKLKDKNISFIDVPGHKDLVKTM

VSGAFGFSICLFVVDINEGLKEQSLEHLEILKILDIKNIILVLSKCDLCENIEQKSVEILEELKNLDYPI

LKVFHTSIKNNQGIEELKNYLYTIENKENNEELIFHYYIDRVFSLKGIGTVVTGSLNEGSITLNEKIICL

DTQKELIVKNIQNHDTNLEQIKACNRVALSLNCDYKELKKGYLLSKKGYFKAFKECDALVKAKNLQNSKM

IFCVGSRQIECKINILKKLENDEFFVHFSFDKNVFLSFDEAFILLQNNRVIGGGKVLNPLSEPLKKEQKN

KFLMFLKNKDFKAAFSFLKDAHKYGFGLLSSYQRFKLSHQKALKLAKELNQVFVDEKNLNVYHLQSLEEI

KNFIKFILEKNPYAMLSAHSLALRITWASENFCELGLKEMSNLLDFQNGIYFKKGIDFEKLQEKNNNQMY

EILKKQGIKPEAPYNLYDFLELDRKSGDNILKKLTQKGLVVRLSHNLFIEKQALEKLMQECLNLLKNQSL

DVQSMKEYFNLSRKYAIAYLEYLDKFPQVNKEAEKRFLTNI

>ABV52894.1 selenocysteine synthase [Campylobacter jejuni subsp. jejuni 81116]

MNKFRTFPQINTLIEDESLKSYPFYIKAFFCKKVVAKLKENFSQDEISKDKLLLEIKKEIKTFYRKDLQS

VINASGVVIHTNLGRSVIHEELYEACKDIICNYSNVEFDLENGKRGSRYALVLEKLKMLFECEDALVVNN

NAAAVFLVLNSLCYNKEIISSRGELVEIGGSFRVPEVIKAAGVKLCEVGTSNKTHLKDYEQAISENTALI

LKTHKSNFALMGFHSEVNIKDLHELAKEKGLLSYYDLGSGWCENLNEKLIKNEPKIKKLVQECDILSFSG

DKLFGSVQAGIILGKKELIEKLKQNQLLRMLRVDKLTLSFLNESLKAYLQKDYEKIITLKLLNDDLSFIE

KKALRVQKELKFQTQLKKSKSLVGGGSMPDKSLDTYILTFQGDALKLQTRFRKENIIGRIENDEFVLDFR

TIRENELQKLILIINQMENL

>ABV52893.1 iron-sulfur cluster-binding domain protein [Campylobacter jejuni subsp. jejuni 81116]

MQDFVYIKNDVLIPLPDAIEILDQANDKEVLVCNDKNQKAQIYAPEINFYLKNSQDEILEQSKNVLTLYK

ARASVYDLGLDLEQSKEVQNRLILADSDTQTVEFLKEHGFKVIALSSVEILAVFGSVGELCAVVKNQGEE

VEIDFDFLLFKAEDLSAVRKDFTRQSGCYNLLNFENLEVLLEFLQSKSPKYHYKTYISYNASVCQYHERR

SEHCAKCAEICPTVAILKDDEKKHLEFSQVDCLGCGGCISVCPSGSLDYAPMPRESFFTLCEFYKDKKIL

IIPKKMSLENLNLALPKDVLPFMIEGEKWLSSMHFLALLQNSGANLVFYTDFVSRGSNEAIVLLNTFFER

KFQKKAIFVAKDEKELQNVLKEQEFIQDLKYDFHNNTLTTRENFAKRMQEMIKNEDFGSIESGEWLRYGK

VEINPNTCTLCLSCVGACNVGALIADKQENALKFNASLCTTCGYCELSCAEKDTLKLFRSGMEFRASYFE

YQTMAKDELFACIECGKEFATKKAVEKIANLMKPKFGNDENKIKTLYCCADCKAKVMIKAMGFAGQN

>ABV52892.1 multidrug resistance efflux transporter, putative [Campylobacter jejuni subsp. jejuni 81116]

MLNNVLPLSFIVGTRFFGLFIVLPVLSLYALKLEGANEFLVGLLVGVYALTQMILQMPFGILSDKIGRKK

TMLIGLIIFIIGSLICSFAENIYTMLLGRMLQGAGAIGAVATAMISDFITEENRGKAMAVMGSFIGLSFA

ASMVISPLMSAKWGLSSLFDLSAALSLLCIILLYTVVPKENKITHENEKTPFFHLIKQKNLALMNLTNFM

QKMLMSIAFLSIPIILVKHLGFASDKLWIVYSASMVAGFIAMGFAGSLGEKRGLAKQILLLGIVFFILSY

LFFAFSNSIVFFIIAVVIFFIGFNLHEPIMQSCASKFCKVHEKGAALGLFNAFGYGGSFIGGIIGGIFLH

LDALNLLAIILVILALIWLVALFFLKNPADFKNLYLPLETPLSFSTFSENLGVVDIYKNSKNLVVKFDSK

LINKEELEGKIKI

>ABV52891.1 non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family [Campylobacter jejuni subsp. jejuni 81116]

MKIILATSNKHKVLELKEILKDFEIYAFDEVLMPFEIEENGKTFKENALIKARAVFNALDEKQKKDFIAL

SDDSGICVDVLEGNPGIYSARFSDKGDDKSNRDKLVNEMIKKGFNQSRAHYVAAIAMVGLMGEFSTHGTM

HGKVIDTEKGENGFGYDSLFIPKGFDKTLAQLSVDEKNNISHRFKALELAKIILKILNKG

>ABV52890.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MFAKLLKFFISRPKSTFFGTLFICLFLNFFAFKLSVDASAESLLLEDDADLKTFREISKHYKSDNFLLLA

FKPYDEKPFSNENLAKLKKLHEELEKAPLVERVFSIINAPLLQSSQNTDLKELLKNIPNIESQDINRTKA

QNEILNSPFYKNNIISKDGKVTGLIIYLKPDTVYNNLIEKRDLASDEKEKDQIRLAIKEHQDKQKVITKQ

SLDTIKSIVRNYEKNKDTLYLGGVSMIADDMIAYIKSDLVLYGVSLVFLLGLALYYFFRSWRFVFLPLFI

CFISLSAASGVFALLNFQITVISSNYVALVLIITLSVVVHLITHFIESTQNHPKAKVERIVLETLLAKAN

PSLYAIVTTMIGFFSLILSNIEPIIKLGIMMSIGIGLALIFSYLFLASILVLLKPKNYHKKEFKFNLLAF

CAKTALDPKKRRMIYGISVLAIILALIGILKLRVENSFVNYFKDGSEIKKGLLVIDKNLGGTLPLEVIIR

FPNNKNDQNTSDTLDSFESEFENLATQETYWFDSKKTRIAKKVHEFLENKEFVGSVLSLNSLLTLGENIN

DGKELDDFALAFLNENLPAKFKQDLLSPFVSIENNELRFSMRIVDSDPNLRRNEFLIDLKKQLNELVKND

GVEVQITGIMVLYNNMLQSLFSSQFDTLIFVILAIFILFIIVFRDLKFSVAAILVNVIPLSVVFALMGLL

GIPLDMMSITIAAIAIGIGVDDAIHYIYRFREEIKNKSLEEAIMISHLSIGSALYYTTISIVLGFSVMVS

SNFIPTIYFGILTVFVMILLLSGSLFLLPSFLITIYSKKTKFPNQYKEHILKQ

>ABV52889.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIFLILTLFFNAFALQLDEISSTMQKNIDASLKLLQDSKEDKKQAANGIFKLFDSIIDYKLMAKLSLS

KNYSKLTPKEQEKFTTAFETSLKKSFTDKLSLYKDQVLKVKNGELKNEKRYFLTTSTVVDGEEKNIIFKF

YNDNNNWLIYDVDVLGVSIVQTYRSQFGDILANQGFDALLQKLESIVIE

>ABV52888.1 putative periplasmic protein (vacJ-like protein) [Campylobacter jejuni subsp. jejuni 81116]

MRIKFISFILIFFTIFAFAKEQNLDDFEQEYQNYQVNDPLSGYNKAMTSFNVALYDYGLRPVLKGYNAIT

PEFIRLGARNFFDNLLAPLRFVGNVLQFKFEEAGEEFKRFTANTIMGFGGLMDVASKMGLKKHPADLGTV

LAHWGVGSGFHIVLPILGPSNLRDTLTLPATWYASFTAYIDPTWASIAISAYGFGNELSFRLDEIDEIYH

NTPNLYPFLRDAYEQRRNELSK

>ABV52887.1 putative nucleotide phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MIFYSYEEFKEDVKILAKEIKKDFNPDALLAIARGGMSLGHSLAVALKTRQLFALNSIHYDDTKKLDTIE

IFNIPDLSKHKKILLIDDIVDSGESLAEIKKVLLEKFPHIKLKIATIFYKKTALLEPDFKVKEATEWVDF

YWDINLD

>ABV52886.1 putative transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MDFFKLKENNTSFKTEVIAGLTTFLAMVYIIPVNSSIVGNTGMPIEALITATALITIVASAFNAFFANTP

VAMSVGMGLNAYFTFAVCLGQKIPWQSALGAVFISSIIFLLLSFTHFRLWVIRNIPKDLRLAICAGIGCF

IAFLGLSQMGVIMHNKDTLVSIGNFKSPHMLFGIFTLALIIFFWAIKLRGAFIFGVLASSIIAWIFHLDN

ASFPVQIFSLPNFSMENGLGAIFLQLDIKSALNITMIPIILTFFITQLFDSIGTITGVGERGKIFDDPKN

GEKKLSKTLMADATGSALGAMTGTSTVTAFVESTTGVESGGRTGLTALVVAICFAFTLFLLPLFKAIPAN

AIYPVLVMVGILMFMEVKNIDFKDSAIAVASFFTIIMMPFTYSITTGFAFGFLSYLLVRIFKREWDKINL

GIIVLSLLSLGNFLLMALQ

>ABV52885.1 hypothetical protein C8J\_1287 [Campylobacter jejuni subsp. jejuni 81116]

MKNLITKLENEERLNQEEANALWDLDLFTLGKYAHKKRTKLHGKKVYFNINRHINPTNICADTCKFCAFS

AHRKNPNPYLMTHEEIMKIVDETVKRETKEVHIVSAHNKDTTWQWYLEIFKMIKEKYPNLHVKAMTAAEI

DFLHRRFKMSYEEVIEKMLEYGVDSMPGGGAEIFDEEVRKKICHGKVSSENWLKIHKLWHEKGKQSNATM

LFGHIEERHHRIDHMLRLRDLQDQTGGFNAFIPLVWQRDNSFIQTDKIMDSEEILKTIAIARLVLDNIKN

IKAYWATMTLNLAMVAQEFGANDLDGTIEKESIQSAGGAKSAKGTSLKTFIDMIKTSNLIPVERDSLYNE

LKTY

>ABV52884.1 hypothetical protein C8J\_1286 [Campylobacter jejuni subsp. jejuni 81116]

MLTEKEFIEKAKIKDIFVKIIIKILKFKESRNFVK

>ABV52883.1 GlnD family protein [Campylobacter jejuni subsp. jejuni 81116]

MLNKELEIFKKNLSSYTQSCRKFFLKQGAFSLYHSKNMDNFIKKAYDIVLKDYFDDFSPPSDNIPFCVLA

SKAYANNSLCFNESISLIFVYKDIKAFHLKPMIKAFIEILNDAHLQIDSVILEFNGLYNASNELKTSIIQ

TRFICGSRILFKGIKTKFESILKENKNDFAKLLLENFKEFDIPFIKQEFNILKDFGGLNHLRSLESLLVL

FKTSPKNYALNFIDEKNLSELRLAGDFLLSLKSAMNLLSAKDEDEFLLINVHDLSELMYKKAKKHFGANE

LLVQKALQSMHTIGFYTHFLAKQIQDGLNHTLKQEYKFKTLVEVLEYLLKLEDKQVIFDLNLVFALRRLK

YSKKDIEKALILFEKIFYKRHSFCVLKLLLDSGILKDLCKPFWTVRFLSDEEGNYSFDEQVFLMLSEFEK

YEDELEILQKLKTDEKMILKLVILLSAIESENEISLAGIYRAYCSKFDLKNEILEWGLKIFKNNNALKDL

VEKEDIYNPIVVSSLVSKLENLENLELLYTLTWLKAKALNYNAFYFRVLDKLLENAKQGFEDENLLEESA

RRVKKELTLKRSKIFLEQDEILQDKIIHIKSNLFIIKNTFEDIVMISKLAKENDFKFWFSNETNLSLQIV

APLHFNIAIILSSLTNLNLIFMNFFELFDDKIYLRFEYDNIISDEQKLKLCELLNSNLSGFNLKKIKKPI

IKKDELKLDLNYSKMYAKLGLNTKDQQGLMAYLMNVFNELELVLCAAKIQTIRQRTRNIFIFQKNEKLEH

SEQKLVNLLISE

>ABV52882.1 glucosamine--fructose-6-phosphate aminotransferase (isomerizing) [Campylobacter jejuni subsp. jejuni 81116]

MCGIVGYIGNNEKKQIILNGLKELEYRGYDSAGMAVMQEGELSFFKAVGKLENLANKCTDFESQGYGFAI

GHTRWATHGKPTEINAHPHLGQYSCVIHNGIIENYKEIKDKLEKEGVSFLSQTDTEVIVQLFEFYARNLG

VFEAWQKTIKELRGAFATLLVTKKDPNHVYFAKNAAPLIIGKNANKEWYFSSGDAPLIGSCDEVMYLEDL

SLGYASKDELVVYENDVLKSLSFSKLSGDKAYAKKDGFRFFMEKEIYEQSRVMSEVLMGRIQGDEVVFDE

LNNEDLSQVDEITLCACGTSYHAAMASAYLFERIAKVKAKVEIASEFRYREAIIKKDSLFIVISQSGETA

DTLEALKIAKEQGAKTFAICNVDNSNIVRLAHLSLLTRAGIEKGVASTKAFATQVLTLWMLAIFMAQKRN

LNVSAEIKALLHTPNCVSVKQALHEKIHRLSKRYLDGHGFFFIGRDVFYPLALEGALKLKELSYLHAEGY

PAGEMKHGPIALADSKLYTIALMPKHMLYEKTKSNVEELIARDSTVLSISPLEFDLSDDFIKTNEQDHYM

CEFFEMMIITQLLAMEISIRLGNDVDMPRNLAKSVTVE

>ABV52881.1 fumarate hydratase [Campylobacter jejuni subsp. jejuni 81116]

MEYRVEHDTMGEVKVPNDKYWGAQTERSFENFKIGCEKMPKVLIYAFANLKKSLALVNNKLGKLDDAKKN

AIVQACDEIIAGKFDDNFPLAIWQTGSGTQSNMNMNEVIANRATEIMGGDFRKEKLVHPNDHVNMSQSSN

DTFPTAMSIVAVEQVEKKLIPALDELIATFEKKVKEFDGIIKIGRTHLQDATPLTLAQEFSGYLSMLLHS

KEQIIASLPTLRELAIGGTAVGTGLNAHPELSQKVSEELTQLIGTKFVSSPNKFHALTSHDAINFTHGAM

KGLAANLMKIANDIRWLASGPRCGLGELIIPENEPGSSIMPGKVNPTQCEAVTMVAVQVMGNDAAIGFAA

SQGNFELNVFKPVIIYNFLQSLDLLADSMHSFNIHCAVGIEPNRAKIDHNLHNSLMLVTALNPHIGYENA

AKVAKNAHKKGISLKESAMELGLVGEEDFNKFVDPTKMIGPKA

>ABV52880.1 acid membrane antigen A [Campylobacter jejuni subsp. jejuni 81116]

MQNGKFFLISFILVILFLLLYLFKGFLLVIIIASLMAVATSNINAKFLNLTKGHKFLASILTTTCMVLLF

FAPFVYAMIELAKALKNFDINLVTQTLDYVKNYQFTLPESFNFLEPKIKEFLASIDLNSISKQILSYASS

FTKSGAKFLIDMVLICVFYFFANLYGTELVIYLKSIIPIDKKELDDVLSEVGNVMAVVLYSMVIVAIFQG

ALFGLITMFYGYDGILMGVIFAVSSLIPAIGGALIYVPVSLYEFASNNLNSALVIFIYSVIVISFIADTL

IKPLIIKWINKKLVKTPTKINELLIFLAMIAGISTFGFWGIILGPAILTFFVSTLRMYVILKDKNLI

>ABV52879.1 holliday junction DNA helicase RuvB [Campylobacter jejuni subsp. jejuni 81116]

MDRIVEIEKYSFDETYETSLRPSNFDGYIGQESIKKNLNVFIAAAKKRNECLDHILFSGPAGLGKTTLAN

IISYEMGANIKTTAAPMIEKSGDLAAILTNLSEGDILFIDEIHRLSPAIEEVLYPAMEDYRLDIIIGSGP

AAQTIKIDLPKFTLIGATTRAGMLSNPLRDRFGMQFRLEFYKDSELALILQKAALKLNKTCEEKAALEIA

KRSRSTPRIALRLLKRVRDFADVNDEEIITEKRANEALNSLGVNELGFDAMDLRYLELLTAAKQKPIGLA

SIAAALSEDENTIEDVIEPYLLANGYIERTAKGRIASAKSYSALKLNYEKTLFEE

>ABV52878.1 hypothetical protein C8J\_1279 [Campylobacter jejuni subsp. jejuni 81116]

MGILTKLELDYEIDDIEKFLQFFRTMCDRFEPLIIKLGSDSVRYKEAIKELETLAHNTAWAARRLNLEEV

TDFCVFCEEMMAQANRFNGPASDEFTDWMLLMSDQFEKYCRSYENDDSVLAVFNPLIVNVPNIISK

>ABV52877.1 hypothetical protein C8J\_1278 [Campylobacter jejuni subsp. jejuni 81116]

MKKNASSKILLSLGVATLLYSGAFAAEITFNGDSDLDKYFDINEKDNVATFKNENYKNKQDVTFNISTSA

FDDAPEDTKINIDLGNNSLTLKNQMDYQGKTAALVKNFNVDAKDFKTTDIGLSYFNAGIINANFTMEGSG

KDFDLGNIDKNKASSLLIFNGSRENTNDTVNGSLTVNGDFSTTNSAIVSMKSDTFKVNGTATLKEAGLGF

LSQSYSNLDVNDFIALRAKDIKTDTLNEDTNAGALILKTASSYINENLLNGDDYAAYLDVTDDKKYGGAF

VDYKLSLKNCGGDKCLVINGGATAAAKNLTNQIAVDLEAITRIIDGLDNEQAKKALQEQKTELEKLQQEA

MQNGGKIDDEKYIDLVNKNSNLNLSANDKASILVLRSITEQLGSIGADLASREGVKLALQIKKDTDNTGK

SVSNFNSASSAVNTTMNISNDVSIGSRVAMLNNPFGTYASKMNGLKFAALDSDMRPSYVNEYTNSVWANA

FGGANIIDGDSGAMYGATVGVDKQANDNVLWGAYFTYANAKIKDNNLEQKSDNFQLGMYSTINIAPQWEL

NLKAYAQVSPTKQDNVQVDGAYNSDYTSKFLGLSANAGRVFDLSDNTLFIKPFAGVNYYFSYTPSHTENG

AIAKDIDSMKNNSVSVEVGAEFRKYMNENSYIFVTPKIEQFVINSGDDYTANLAVNNAFFTSVEANNKKK

TYGQIIVGGNVDFTNQLSMNLGFGAKQILAGKVDNKNETYLSGQVGLKYKF

>ABV52876.1 polyphosphate kinase [Campylobacter jejuni subsp. jejuni 81116]

MQTSPDMFINRELSWLRFNSRVLDQCSKNLPLLEKLKFIAIYCTNLDEFYMIRVAGLKQLFSAGVNASSS

DEMTPLQQLKAIRKYLHQEKELLERYFNEITSELEKENLFIKHYENLDENLKQKCDEYFFSNIFPVIVPI

AVDATHPFPHLNNLSFSLAVKICDKAHPELVKFGMIRIPRVLPRFYEVSANIYVPIESIVHQHAEEIFPG

YKLLASAAFRVTRNADMVIEEEEADDFMMILEQGLKLRRKGAFVRLQIQKDADEQIVEFLNTHMKIFHKD

VYEYSILLNLPSLWQIAGNKTFTHLLSPLYTPKTLPPFDENLSIFDAVEKEDILIIQPFESFDPVYKFIK

EASKDPEVISIRMTLYRVEKNSNIVQALIDAASDGKQVTVMVELKARFDEENNLHWAKALENAGAHVIYG

ITGFKVHAKVSQVIRKQGDKLKFYMHLSTGNYNASSAKIYTDVSYFTSKAEFARDTTSFFHILSGFSKNR

RLQTLSMSPNQIKEKVLEMIRIETSKKNEGVIVAKMNSLVDSDIIQALYEASMEGVQIDLIIRGICCLKP

DEEYSKNIRVRSIIGKYLEHARVFYFKHSEPNYFISSADWMPRNLERRLELMTPIYDERSKAKLAQFLRL

QLSDNVLAYELKNNGEYEKIPSSEKIIDSQQTLEEYVSKIYKTLKKDTDQSRATHLASKLFKEN

>ABV52875.1 putative periplasmic cytochrome c [Campylobacter jejuni subsp. jejuni 81116]

MKKTSNLFTIFLVLLFVFFAVGFYTFYNAKGTSYLSNASESCNNCHIMNEVYNEYMAGPHSQKVKGEPRA

TCVDCHLPHNFVAKWIAKAQSGLGHAYAFTFKLDELPTNLSATEKSRKMVQENCIRCHADFAQTAINATT

NPHADKSLNCASCHKDVGHKHGI

>ABV52874.1 cytochrome c552 [Campylobacter jejuni subsp. jejuni 81116]

MKKNILRLGIVVLVLLIAGVLWLNNDINQKKEDEANKNAIAANADFSLLSDDDPNFEKWGKVFPEQLKMY

LTVEKEEPKATEFGGNLAYSKLIRFPQLTILWAGYPFSLDFNEERGHFWVQIDQMKTARNNKDFLNAHGL

AAFKGQPAACMNCHSGWTPWLIKNVAKGDFTAFNSTNYWTMIKNIPAVDGIVENSPEHAGPHGGKRMGVT

CADCHNPNDMSLRLTRPAAINALVSRGYEKDPVQGVKATREEMRTLVCSQCHVEYYFKPTGEKVKVMGET

IVDDSSKKWWNGTQKNYDEYEFWRDGNKAKEIETDGIVLTFPWSEWKKGQPFRIEMLDDYYDKVRGVFGA

DFTHKLTGAQIIKIQHPESELYSGGVHAANGVSCVDCHMPYVREGAKKVTQHNITSPLRDINSACKSCHK

QSEDYLKAQVLDIQNSVAHDQRTAEYAIVSLIMDTKKLRDELGNMEKFQSDGKADTKKISEELKEVLELH

RKAQMRADFVNAENSTGFHNPREASRMLLQAVDMARMGQTKLVEIAAANGIKDFKTSNLGFEDIQKFNPG

ELYYKVDVNNHKAGERYYADEKDVNGNPPKELLEHDKELAPYNYQVIDKK

>ABV52873.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MINKNKLFRQVHIYLSLFFLPCALLFALTGIAYIFGINQDVGLKVEQYQLSKVIESGKEREALIEYLKTN

GLKVPSNTNIIKSKDKGITIGGAHYSANITQNSTNEYNITLKTRSLLGDMIMLHKDKGAWYFSVLSVGFG

ITLFMLYISGLMITLFANKKDRSKQFAVLGVGVVVTLLLAYLSL

>ABV52872.1 hypothetical protein C8J\_1273 [Campylobacter jejuni subsp. jejuni 81116]

MKIVPTPKFKNELRHIVNFIKLDSSFYAKEFLNDINSICKNLSFMPYKNRKSLSFDNENIRDLIFKGYII

PYLIDKSKNEIVILGIYKSNLWD

>ABV52871.1 MGC82361 protein [Campylobacter jejuni subsp. jejuni 81116]

MSLEFSKETQHFLTNYCKDNNLSEKEVLELALSYLEHKIRIDGYKKDIELYKQDKLKTLDFDETFNDIRK

DLE

>ABV52870.1 enterochelin transport system substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKSLVFAFFAFFLSLILTACNSNSNENNASSTTKTNTATMKVLPISMSDEGDSFLVKDSLGENKIPKNP

SKVVILDLGILDTFDALKLNDKVAGVPAKNLPKYLQQFKNKPSVGGVQQVDFEAINALKPDLIIISGRQS

KFYDKLKEIAPTLFVGLDNANFLSSFENNVLSVAKLYGLEKEALEKISDIKNEIEKAKSIVDEDKKALII

LTNSNKISAFGPQSRFGIIHDVLGINAVDENIKVGTHGKSINSEFILEKNPDYIFVIDRNIIVGNKERAQ

GILDNALVAKTKAAQNKKIIYLDPEYWYLASGNGLESLKTMILEIKNAVK

>ABV52869.1 enterochelin transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MIKLKNITKFYDNKAIISDLSLDFHKGKITSIIGANGAGKSTLLALASRLIKPSSGEIYIDGMKLKDYKE

QILAQKISILKQQNNINLRLKVEELVAFGRFPHSQGRLNANDKIKINEALEYMGLSNLRNEFLDTLSGGQ

KQRAFIAMIIAQDTEFIMFDEPLNNLDMKHSVQIMQLMKNLVKDFNKSIAVVLHDINFASIYSDEIIALK

DGKLLKQGSKDEIINQENLKQIYDMDIPVSQIDGKKICIYF

>ABV52868.1 enterochelin ABC transporter, permease protein [Campylobacter jejuni subsp. jejuni 81116]

MRKKMLILSFLTLGMIGIFILVGLNGFDEYALKSRFLQIAAIIIVAICIAVSTVIFQTLCNNKILTPAII

GLDSLYMLLQSALIFSFGAANLSVYKNDINFLITLVCMVVFSLGLYKILFSSDRSIYLIMLLGLVFGTLF

STLSSFFEVLIDPDEFMVIQGRMFASFDNIAFDILILAYIISFLSFIWIFRYMKFLDPLNLGKDLAINLG

INYQKISKQLMIIIAILTSISTALVGPITFLGLLVANITYELFKTAKHSILLSACILISILALLGGVFFV

SRVFDYNATISVVINFLGGIYFIYLVLKGNKL

>ABV52867.1 enterochelin transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MFFKHILSLKVLIALLLFFGMISLFIGVISINVKDILNLNSTQLEIITLTRIPRLIAILLTGMSLSICGL

IMQQLTQNKFVSPTTAGTMDCAKFGILISLIFFAGASFFTQAIIASVFALLGSFIFIQILRKIKLKDVIF

VPLIGLMFGGIISAITTFFAYALNYIQNIQGWLQGSMANVMQGNYELLYISLPLFILAYFLAHKITIVGM

GEDVALNLGISYNGILFLGLMIVSIITSLVIVSVGIIPFLGLIIPNLVALYLGDNLRKNLIYIALCGALF

LLVCDIISRLVIFPFEMPLSITTGVLGSLIFIFLLLKRKVYA

>ABV52866.1 phospholipase A [Campylobacter jejuni subsp. jejuni 81116]

MRKIALFLSLCVFIWASDLQQALEYEKQGDYKKAMEIYKKLALKNSSVLISQEQNNSSQATQTQNSITIK

KEEKQDFSRLALANYLGENESFNPLGISSYKMNYFLPLAYSFNSLGTNNNKSEAKFQLSVKKRLFENLLG

LDEKYYIAYTQTSWWQIYEHSSPFRETNYQPEFFIDFPLYLKDYEFFNNLRVGILHESNGKGDENLQSRS

WNRIYVSTAILYNKFLFVPRLWYRIPESKKDDDNPAILHYMGNFDVNLGYLGDDYFINLMLRNNLKFHDN

KGAIQVDLGYDIFNNGIYWYLQYFNGHGESLIDYNKHLQRLSTGFLISY

>ABV52865.1 putative molybdopterin-guanine dinucleotide biosynthesis protein [Campylobacter jejuni subsp. jejuni 81116]

MQLNELNCVILCGGKSSRMGQDKSKLILKNQNLTQFQVEKFSKIFKNVYVSAKEDKFENHFSLIKDSLEF

EVYSPMLALYSILSNFKNEFVFVLSVDSPKVGENELLKMLPFLEQNYKIIIAKTPLHKHPLCGFYHSSLA

QTCKNFLEKNEQKIGLLFSEIKTKFVEFEDEDAFLNLNFYEEYEKFKSELR

>ABV52864.1 possible fibronectin/fibrinogen-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKYTELLQLQTFFSQFKKIDFIKRINDNILELSFDRERFIFDLTRAMSAIYTAKFNAKNYNAPFDFMLKK

YFSNAFIKEVKVLEGNRILCFSVKANKAYKSYESKIYFEFTGKNTNVILTDEKDLIIEALRHIDKSYRVV

KPNVILEPLKPYKMDENFEEIKDFKDYFSCKFTSIYESKIKQIKNLKLAQVDKKIQNLQELFSSLDEENS

LLLKALEYRKRADVLFANLSVLKDYEREFKLDDFEGKELEFKLEFSPKQSANLYYKNAKKLEQKAKNLNI

QRQNLKEKLDFTLSLKELLLQAKSEIELEILLPKKNSKKNQDHKQEDLVANFYYNEFKICVGKNEKGNEF

LLKNAKKDDLWLHVRDIPSAHTLIVSNKQKISLDVIEFAARLCVSFSKLKKGSYWVDYTLKNFVKVQQKA

FVNYTNFKSINITKD

>ABV52863.1 putative coiled-coil protein [Campylobacter jejuni subsp. jejuni 81116]

MPVSPLGNVNYINQNMAYPATQASNELAKEGFAATLNMAEFNEKEKTLNKLEKVNETHEIKEEIKEKAEQ

EEKKKKHNQEAKTSDDEKNEEDESKDPNFKDAQSIHRLDISI

>ABV52862.1 phosphatidate cytidylyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MFNTTRIISALVMIGAIIIIALIDQFFINFIVFAVLLYLSFSEAKKLFALENISIIPLAIAFILGSLSHK

ALLFGILALLLVIGYLVYKKASLKSALIYIYPSLPILALWQVYLDQGMFALFWLIIIVAACDSGAYFIGK

LMGKTPFSPTSPNKTLEGVIGGLICASVIGTILGVFVYSFWLSLLCSFFVAIFAVIGDLLESYFKREAGV

KDSGDLIPGHGGVLDRIDAVIIAAFVMVALL

>ABV52861.1 putative 1-deoxy-D-xylulose 5-phosphate reductoisomerase [Campylobacter jejuni subsp. jejuni 81116]

MILFGSTGSIGVNALKLAALKNIPISALACGDNIALLNEQIARFKPKFVAIKDSKNKHLVKHDRVFIGQE

GLEQILTECQDKLLFNAIVGFAGLKSTLKAKELGKNIALANKESLVVAGSFLKGVKFLPVDSEHAALKFL

LEGKKNIAKLYITASGGAFYRYKIKDLNQVSVKDALKHPNWNMGAKITIDSATMANKLFEIIEAYHLYDF

KEIDALIEPRSLVHAMCEFKNGASTAYFSKADMKLAISDAIFEKQDTPILEAVDFSKMPALKFHPISTKK

YPIFKLKNTFLKEPNLGVIINAANEVGVYNFLENKSGFLDIAKCIFKALDHFGVPKISSIEEVFEYDFKT

REYLRS

>ABV52860.1 hypothetical protein C8J\_1261 [Campylobacter jejuni subsp. jejuni 81116]

MKFFLTILFFITSIFALELDFSVGENGKSLDDNNTVLIFGGIQGDEPGGFHAASLLLSDYNITKGKIIVA

PNLAFDSIIKRSRGNNGDLNRKFASISPKDPDYKTVQRIKELILLPEVSMVINLHDGWGFYKPTYIDAMQ

NPKRWGNSSVIDTSEINASKYPDLENIATQTVNSVNSSLADPKHAYHLKNTKTQELGDTEMLKALTYFVI

SNHKAAFANEASKNLPVNLRAYYHLLAIENYLKTAGIEFSRDFELTPKGVDKAINRELEVKLFNDRILLS

LKNPRKVINYVPFPVNKELNYNTSNELTAVIAEGNSFYIQYGNRFQTRLYPEYLEFSDAFNEVTFQVDGN

ETTVPFGTKVKVKENFLIPKIANVRVNIIGFDHGKDESGILVHKKNMQTQYSLDMAGKIYRVEFYELRGA

NLQQLLEANTNSKLIKNAKNLDLNTLKMARSKDKFLGSILVEFE

>ABV52859.1 putative glycoprotease [Campylobacter jejuni subsp. jejuni 81116]

MKNLILAIESSCDDSSIAIIDKNTLECKFHKKISQELDHSIYGGVVPELAARLHSEALPKILKQCKEHFK

NLCAIAVTNEPGLSVSLLSGISMAKTLASALNLPLIPINHLKGHIYSLFLEEKISLDMGILLVSGGHTMV

LYLKDDANLELLASTNDDSFGESFDKVAKMMNLGYPGGVIIENLAKNAKLKNISFNIPLKHSKELAYSFS

GLKNAVRLEILKHENLSDEIKAEIAYAFENTACDHIMDKLEKIFNLYKFKNFGVVGGASANLHLRSRLQN

LCQKYNANLKLAPLKFCSDNALMIARAAVDAYKKKEFVSIEEDILSPKNKNFSRI

>ABV52858.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MRKAFTILELVFVIVILGILAAIALPKMSSSKDEAEVSKSLNNLKTLINDISIYTLKNDHLSSIKTMSNV

IGVENVDLGNFNGTKEVNFGVGNDKECLKLVFINKADFILMGISSNEASKNAIINAANQSHEDLENIDFT

SSSSNKACVILSKNENFKNLASKTYLLIGGM

>ABV52857.1 hypothetical protein C8J\_1258 [Campylobacter jejuni subsp. jejuni 81116]

MIVSKTYEIDSCDDVELGIKRESKLEFKLWYDDEKTPEALVFVVQGVGADCNDIYLKFIVEYLLKNFNLA

FVGVNYHCIGNRPQTGSTFYLDDIDKLILKASCEAVDIKLPYDVDKIQDYKQMSEIFHFVNNQIVEGKQK

GNFMPNYFLNLHVSLQPAKNEYQNFGIMQAQDLLNVALYLKKNTPFDTMGGGIPVIMIGGSHGGYLAHLT

AKIAPWLVDGVIDNSSGAKFLWRVVGFGKEIDFMQYSEFATFDFFHHIKTHCSTKTFWTSNSSSPRFFSP

ARRKIRNLLEEDHLLEQSKCLKTCFISYHSLYDEYVSLKEKTMLYEELEKLGFDVTLHSITKESQVDGKF

IKNLNHGMGIPVKLLIKKELPLMLEKIKQNSKKDCKEKCISYPCEDLLYQFSEKDDKISLKIDKI

>ABV52856.1 hypothetical protein C8J\_1257 [Campylobacter jejuni subsp. jejuni 81116]

MTILEKNIQALLSGVNEPLGNKLLNFIQNKTCSRFNIDENLNIYDKTHNVFMYENLEEELNFFYQSILEK

TPRYPFICIYGIGNALLIKNLAKHYKHLFVFESEIELFILALSTIDLSEELCSGKIYLVDIQEKKINLQL

RILFDQNDVFLWLNLYEMFINNNFYKKYYYEEILNTDKIAYENINLVIRNLDPDSKISLSCYENFYKNIS

LMLKNIPLKRIINERKGLFDNCIVVCAGPSLQKQIPLLRQYQKKFVIFCVDGAYPLLVKNNIIPDYVLNL

DFEEYPLKFFEEVDAENKTLFILAASTHPSVVEYLYKKQIPLSIALNDNLPYQNLHIDEFGYLEFGTHVG

HACYALAIALKFKNIIIIGQDLSFDQRGNSHFDSFDLGSDIDATLDIPTLKRIAYGGIGEVLTHLAWDDY

RKKLEDLFARNLEVNFFNATEGGAKIEFTKELDFKSCCKQFANLNNKSNKYLPKTLTTNRGAKILNKILA

TFKREKQNTLICLEHAIRLNDVLKIILASDRKFPIDFLKNTYESIKKFEIFLEENSFLNDGVLKGVIFHK

GKLLSEVIVSKIEDEREYLLIYLTFYKQWLEIFICRFQLKCDIYNFLV

>ABV52855.1 hypothetical protein C8J\_1256 [Campylobacter jejuni subsp. jejuni 81116]

MGFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND

ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSG

NFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSV

GTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINA

VKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAI

GMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVG

SGKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVTTLKGAMAVM

DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKANILAQSGSYA

MAQANSSQQNVLRLLQ

>ABV52854.1 hypothetical protein C8J\_1255 [Campylobacter jejuni subsp. jejuni 81116]

MGFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATLGQAINNGND

AIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTTSFNGKQLLSG

NFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSV

GTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVVIGQINYKDGDNNGQLVSAINA

VKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAI

GMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVG

SGKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVTTLKGAMAVM

DIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFASESANFSKYNILAQSGSYA

MSQANAVQQNVLKLLQ

>ABV52853.1 hypothetical protein C8J\_1254 [Campylobacter jejuni subsp. jejuni 81116]

MQTNEIFKKNLEAMQGSTYEKLKYKLKNFQELRNFSFHIGKDPIDINIIDKKHLKKIYQNPIKELEENLK

LYQEQYTNYPFLFFYGLGNGILYKALLKNTLHKRIIIIEKELDIIFITLNLIDFSEDLFKGRIIITHTLD

YNNNIAELIFGLTEISLFLKTYQINLHSPFYRIYQEDIKKINNINLQTIKYLTLKKGTDPLDAMVGIEQA

IWNLPEMFKHYSYKELLDKRKNLSKNAIIVSTGPSLTKQLSLLKQYANKAIIFCADSSYPILAKHNIKPD

YVLSLERIPLTSEFFNNDFGEFDKDILFILPGLTHPNSIKYLKKFKKDYMLVARHLPFALSLDLKEYGYI

GGGMSVAHSAYELAILLKCENIILIGQDLAYSKEGKSHTDDYINLALHEKDFERNKGHFTTIAYGGEGEV

ESSEVWTLFRKIFENYAINNQKYIKTYNCTEGGARIKGTIEKPFAEICKEILTKDIKKPLKKLKKKTKKE

QFDKMLKSYRKIKTNIQLALNFQKECKKTLRKIQKITQKNKYINLENIVKDIDIIREKLSHKKYFFLHEI

LGPTLHHEESLIAPIYTQSVHNESQRQNKILSWIYANESLIETIIDLIESQNTRLKKAIIPLQDELEKRS

LI

>ABV52852.1 hypothetical protein C8J\_1253 [Campylobacter jejuni subsp. jejuni 81116]

MKFNLNQKELFNKNIEALDNIPLKESLKEIKSSKFKLILGKDILDINLQNTSDNTFLYENVIDELNTMLN

TYNDKYLLYPVLYFYGFGNGILFKALLQNKNHQHIVVFEKDIEIIWTMFHILDFSNELQKNNLIIINTNI

LSEFDLLNFYKKANSIFLQFSRIYFLELISNYYERYNEEILKLNDTILSTIKISIIQYGNDSIDNLMGIK

HFIYNLSKLLTHPHSEIFLKKRYKLSDTAIIVSTGPSLTKQLPLLKQYANKATIFCADSAYPILAKHNIK

PDYVCMLERDDIVSKCFDNDFKEFDKGILFILASVVHKEVIEFLERNNREYMLVPRAYDFFYYLNLAKYF

QPIDGMVSVAHMNYWLAKFLSHKNIIFIGQDLAYSKDQSSHAKDFIHEKLHEGHFQKDENLFTSIAYGGK

GEVESSYFWKLFREIFEKWISHDNNFINIYNCTEGGARIKGTIEKPFLWACENLLGKDLNKPFPKLNPLN

INKQNELMLKAYNKIYKSIYHCKDFNKKLLQEYNEIKELYLTLENLQIEESKELLNFIIQKIDTIKYQID

DAKNMQDLYEILGPLLVQFELNLARIYVLNPKTPEDSFNKSLIWIKEHLEWIEMIYGHIQAQENALFENI

IPLEQKLKERKMQKYLRRIKNANK

>ABV52851.1 hypothetical protein C8J\_1252 [Campylobacter jejuni subsp. jejuni 81116]

MNKDLFLKNTRALFEVDQILAYKLRSLEKIDFKILQNENGINFIKDDIALYKNPNQELLESLTLFKSEYE

KYPVLFFYGFGNGMFYKALCENKNHKHIIVFEDELEILALAFHLFDFSKELKNEKLILFYTPEVTTAQLT

TLFIYENIQKSVKIFNLYIHNNFYEKFYTQKIKNLNYKLMETIKYVVLNKGNDPYDSIIGIKHTLNNIPK

LLSHGIFQDFLKKRKRKVKNAIIVSTGPSLTKQLPLLKQYANKATIFCADSAYPILAKHNIKPDYVCMLE

RDDIVSKCFDNDFKEFDKGILFILASVVHKEVIEFLERNNREYMLVHRPLHFAVSLNLKEFGYIGVGASV

ANMAYELAASLRHENIIFIGQDLAYAKDGSSHPREHIYGNQGEKLRGEIYTLAYGGEKQVRTQLTWNLFR

QAFEKDIFWAKEKLKINTYNCTEGGARIEGAIEKPFQEVCETLLKENLKKPFDKPKILEKNKIKNKFLQT

QKLLIKNVKQSEEFIKKCQNELKKLDFELSKSQLNSQTLIKIKKNLLFFFNEFKRLKLFNELTQAIYYHN

ECEIMYYEVLNDLEQDKKIEDFLTNQKKWWLQSFEYLNTQNQIIKETLKKYKNDDI

>ABV52850.1 N-acetylneuraminic acid synthetase [Campylobacter jejuni subsp. jejuni 81116]

MQIGNFNTDKKVFIIAELSANHAGSLEMALQSIKAAKEAGADAIKIQTYTPDSMTLNSNKEDFIIKGGLW

DKRKLYELYESAKTPYEWHSQIFETAQNEGILCFSSPFAKEDLEFLKRFDPIAYKIASFEANDENFVRLI

AKEKKPTVVSTGIATEEELFKICEIFKEEKNPDLIFLKCTSAYPTAIEDMNLKGIVSLKEKFNVEVGLSD

HSFGFLAPVMAVALGARMIEKHFMLDKNIESEDSKFSLDFDEFKAMVDAVRQAESALGDGKLDLDEKALK

NRVFARSLYASKDIKKGEMFSEENVKSVRPSFGLHPKFYQELLEKKATKDIKFGDALKESDFR

>ABV52849.1 hypothetical protein C8J\_1250 [Campylobacter jejuni subsp. jejuni 81116]

MKFCKKCVMPDTKPDLHFDEEGICDACRSQEAKNQKINWQEREKEFFELVKKYKKHPVYDCVIGVSGGKD

STFQVVKMLELGLNPLCVCFEPSVPTKIGRKNLDNLNHLGVDLIHIKRDPKVYQKLAREAFIRTGDNEWQ

NHLGIFTSVPRIAVNFGVPLIIWGESPQIEYGGPASSKNKNILDREWLEEFGGLLGNRISDMIGVEGITQ

KDVYFYTYPINEELQRVGVTGLFLGYYFKWDYKKILEISKKYGFLTLDHPVETTYENFENLDCYSNHVHD

YLKYCKYGFGRATDNACLDIRLGYISREEGVRLVQKYDGKPPKKAIKKYLEFSGFSEEEFQKIVDSFTNK

KIFKRDENGKFIRDYDGSLVRKDECVLK

>ABV52848.1 imidazole glycerol phosphate synthase, glutamine amidotransferase subunit [Campylobacter jejuni subsp. jejuni 81116]

MIALIDYKTGNLNSVAKAFEKIGATNFIAKNPKDLQKADKLLLPGVGSFKEAMKNLKELGFIEALKEQVL

VQKKPILGICLGMQLFLERGYEGGVCEGLGFIEGEVVKFEEDLNLKIPHMGWNELEILKQEPLYQDIEDK

SDFYFVHSFYVRCKDEFVSAKAQYGHKFVASLQKDHIFATQFHPEKSQNLGLKLLENFVRL

>ABV52847.1 cyclase hisF [Campylobacter jejuni subsp. jejuni 81116]

MLKTRIIPCVLLKNSQLVKSIEFKNFRTIGHLTSTMRIYNARNVDELIILDIDASKSGEIDFESIEDLAK

ECFMPLTIGGGIKTLEDIQKILNLGADKISINSKALEDKDFISKAANRFGSQCIVCSIDVKRKGEQFCVY

DRGNLLEKSPLELALEYEKKGAGELLLTSVDFEGKAKGYDLELLKIFQNKLKIPLIVNGGLGKPSDGVKA

LNLGVDALAGAYIFHFSKYTPKDVKEELAKQGFAVRLL

>ABV52846.1 hypothetical protein C8J\_1247 [Campylobacter jejuni subsp. jejuni 81116]

MQDYRCNILLKNYINLNYIEKEKIRKYRNQPEVKKYLYQTHFISKLEHKNFIKKLKYNTKKSYFCVILDN

QIIGNINFYIRENEIDFGFYANPFSKILGIGRILEQIGIYYAFKIINVPILSLEVFSNNTQVINLHRKFG

FSIVQEFFIKKQKILKMSLKQSDCKALLS

>ABV52845.1 hypothetical protein C8J\_1246 [Campylobacter jejuni subsp. jejuni 81116]

MIKLKNFTELNPQEIELIFKWRNHPDISQFMKTKHIDFEEHLRFLKNLHQDSSKKYFLVFQDEQIIGVID

FVNITTKSCEFGLYAKPDLKGVGQILMNEIIKYAFENLKVNTLKAYVFKDNHKALKLYQQNHFTIYDEDK

NIFYIKLKNYNYKKQFAKRISKLDRGGGKYKY

>ABV52844.1 possible flagellar protein [Campylobacter jejuni subsp. jejuni 81116]

MKVLFRSDSSSQIGFGHIKRDLVLAKQYDDVSFACLPLKGSLIDEIPYPVYELSSESIYELINLIKEEKF

ELLIIDHYGISVDDEKLIKLETGVKILSFDDELKPHHCDILLNVNAYAKASDYEGLVPFKCEVRCGFSYA

LIREEFYQETKENREKKYDFFICMGGTDIKNLSLQIASELPKTKIISIATSSSNPNLKKLQKFAKLHSNI

RLFIDHENIAKLMNESNKLIISASSLVNEALLLKANFKAICVAKNQEKLANWLAQKGYEVEYKY

>ABV52843.1 acylneuraminate cytidylyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKNLCIIPARGGSKRIPRKNIIDFLGKPLIAYSIENALNSGIFDEVILSSDDEEIIEVALKYGAKAPFVR

DKNLSDDYASSTAVVQNAIEILQSQNQIYDNVCCLYATAPLLNKDILKQAYEKFIQNQSKFLFAATEFEY

PIQRAFYLNENNQVYMFDEKHYKSRSQDLTKAYHDAGAFYFGTSKAWLEEDFMFKPHSGVFVLPRNLVCD

IDTMQDLEFAKILYKANHESTF

>ABV52842.1 hypothetical protein C8J\_1243 [Campylobacter jejuni subsp. jejuni 81116]

MLINQTFEIDSCDDVELGIKRTSKLEYRISYDDEKDIKAIVFIVGGFGANANISFLDFDREYIAKKFDVV

AVHVFYHCFCHRRSNVEKYSAITMFTKEDVSNLSQALLDIGIKIDVDIQNAHQCYELLNQNITTLKSQGR

LVQNYQAKLSSTFIPPNGDYQNFGIMPAIDHINALKDLVKRFPKFADLPKIYGGGSYGGYLSLLIAKIAP

WYVDGVIDNSGTVLPLLECIIGRKLNKPEFIYNDPNTLIEMFIKTYWIREDENSSYFIANENYMIRSLLN

SSHLTIQANINKNIIFISYHSLKDEFNTAKDKQTLFLAYKELGYDATLYLIKDESEIDGRFIKDLKHGMR

ISNKALFRKELPLMLEKLQGRKSFMQENSISYPCRDQKFIFEDDKDKFTLIIT

>ABV52841.1 hypothetical protein C8J\_1242 [Campylobacter jejuni subsp. jejuni 81116]

MQNTVDLIKQFFINIDRADIDENMENLLSEDIIDSIDIMSLVAEIEKFYKKPLKAEFIKAENFESFKTIQ

DMINQAFK

>ABV52840.1 hypothetical protein C8J\_1241 [Campylobacter jejuni subsp. jejuni 81116]

MKKFENIYIIGTGKVAKECQKIASGFFKQEVIFVKNIENLDDFFKNLKNCLIISANNFYIFKKECIQNNA

IINYHNALLPFHKGCNAHIWSIWENDKKTGITWHMVEESIDTGAILTQKEIKLDDNFTALSLLNTQHNLA

MASFKEAVENLENKALKAQISKKGYHKKLALPNEGYLDLTWDKEKISRFLRAMDCGVLSGAPKARLKILG

EEKEILFYEINELDLILNLSDNTLLKITKE

>ABV52839.1 putative amino acid activating enzyme [Campylobacter jejuni subsp. jejuni 81116]

MTTHIYDFLEKSLIKFSEKTAFVEPFAKERKEITYKNFDLFSKKLASEILRNLGNDNPIQVPVLIILPKG

IDCLISFFGVALSGNFYTLLDEKSPKERVEKVIEVLKPKLFITSKNLNFNLNLPTLYTQDFEGFDINESL

LKNAKEKHIDTNLLYVFFTSGSTGIPKGVSIAHKSVIDYTFWVCETFKFDENEILANQAPFYFDNSILDI

FSSVKSGATLHLLPNHLFAFPNKILECLEKEKVSTIFWVPSVLIYFANTEALNNFSLNTLKKILFCGEIM

PNKQLNIWRKHLPNALFANLYGPTEITDVCSFYIINRTFKDEELLPIGKACKNTELLVFDENMNFISPKQ

IGVKGELFVRGTSLSLGYYNDKEKSKQAFIQNPLHDNYLDLLYKTGDIVSYNKFGELLCYGRADNQIKYM

GHRIELGEIESVINSHESVKNSACIFKEDIICFYESKDELDLKAFLKDKLPSYMIPKNFIKIDKFKLNQN

GKIDRKILNEKI

>ABV52838.1 hypothetical protein C8J\_1239 [Campylobacter jejuni subsp. jejuni 81116]

MKYFLEHNDKKYSDKDLIDAFYQLGIKRGDILCVHTELFNFGVPLLSRNEFLQTILNCFFEVIGKEGTLI

MPTFTYSFCKNEVYDKLNSKCTVGTLNEFFRKQQGVKRTNDPIFSFAIKGAKEELFLKNTTSCFGENSVY

DTLVKENGKIILLGTKIAGYTFTHFIEEKIKVPYRYFKEFKGKIILENKMPKEIVINYYVRDLEENSNLD

VYKQIEILKQNDNFKLQQFSNSCIVLINSKAYLEDTMQALNQNLKCLLMEP

>ABV52837.1 hypothetical protein C8J\_1238 [Campylobacter jejuni subsp. jejuni 81116]

MDKLDFRNQDFSQTGKAMYELACELFPIPRSITGQGFRASLEILNKTLGGGILKFHSIKSGTKVFDWIVP

DEWNAKEAYIITPEGEKICDFKKHNLHLLNYSEAIDQEIELEELQDHLYSIEEMPDAIPYVTSYYKRRWG

FCLTHNERKKLKKGKYKVYIDAKHDENGVLDYADFILPSTQNSKDEILISTYLCHPSMANNELSGPVVAI

FLAKWLLNLKERKYNYRFVIIPETIGSIVYLSKHLEHLKKHVKAGFVLSCIGDDHAYSLIHTPKENTLSD

KVALHTLKNKENFKAFSFLNRGSDERQYNAPLANLGIVGVCRTRYGDYDGYHNSKDDLNFISEKGLMGGL

QSMQEIILNLEINAIYENTIVCEPNLGKRGLYHTINKGVKQKPISADFLAYCDGQNDIIDIANILNMQAY

EFKELLEKIKFYGLVK

>ABV52836.1 putative aminotransferase (DegT family) [Campylobacter jejuni subsp. jejuni 81116]

MLTYSHQNIDQSDIDTLTKALKDEILTGGKKVNEFEEALCEYVGVKHACVLNSATSALHLAYTALGVKEK

IVLTTPLTFAATANAALMAGAKVEFIDIKNDGNIDEKKLEARLLKDSENIGAISVVDFAGNSVEMDEISN

LAKKYNIPLIDDASHALGALYKSEKVGKKADLSIFSFHPVKPITTFEGGAVVSDNEELIAKIKLLRSHGI

IKKRLWDSDMVELGYNYRLSDVACALGINQLKKLDHNLEKREKIASFYDKEFEKNPYFSTIKIKNYKKSS

RHLYPILLFPEFYCQKEELFESLLHAGIGVQVHYKPTYEFSFYKKLLGEIKLQNADNFYKAELSIPCHQE

MNLKDAKFVKDTLFSILEKVKKGYCG

>ABV52835.1 possible sugar nucleotide epimerase/dehydratase [Campylobacter jejuni subsp. jejuni 81116]

MFNGKNILITGGTGSFGKTYTKVLLENYKPNKIIIYSRDELKQFEMASVFNAPCMRYFIGDIRDNERLSA

AMRDVDFVIHAAAMKHVPIAEYNPMECIKTNIHGAQNVIDACFENGVKKCIALSTDKACNPINLYGATKL

ASDKLFVAANNIAGNKQTRFSVTRYGNVVGSRGSVVPFFKKLISEGAKELPITDTRMTRFWISLEDGVKF

VLSNFERMHGGEIFIPKIPSMKITDLAHALAPHLSHKIIGIRAGEKLHEIMISSDDSHLTYEFENYYAIS

PSIKFVDKDNDFSINALGEKGQKVKDGFSYSSDNNPLWASEKELLEIINHTEGF

>ABV52834.1 deoxycytidine triphosphate deaminase, putative [Campylobacter jejuni subsp. jejuni 81116]

MGLKADNWIRKMALERKMIEPFCEANIGKGVVSYGLSSYGYDIRVGREFKIFTNVNSTVVDPKNFVEENV

VDFEGDVCIVPANSFALARTIEYFKMPDDVLAICLGKSTYARCGIIVNVTPFEPGFEGHITIEISNTTPL

PAKIYANEGIAQVLFLQGDEKCDTTYKDKKGKYQAQTGITLPRILK

>ABV52833.1 acetyl-CoA carboxylase biotin carboxyl carrier protein [Campylobacter jejuni subsp. jejuni 81116]

MTKEEIKELVNLFAEANISKIKIKEQDGFEIELERDMCCDVPAPVCPPVPAPQPINVSVVNEAQPSQSAK

SNKPSINSPMVGTFYQAPSPGAAPFVKVGSTVKKGDTIAIIEAMKIMNEIEAEFDCRIAEILVADGQPVE

FGMPLFAVEKL

>ABV52832.1 acetyl-CoA carboxylase [Campylobacter jejuni subsp. jejuni 81116]

MEIKSILIANRGEIALRALRTIKEMGKKAICVYSEADKDALYLKYADASICIGKARSSESYLNIPAIITA

AEIAEADAIFPGYGFLSENQNFVEICAKHNIKFIGPSVEAMNLMSDKSKAKQVMQRAGVPVIPGSDGALA

GAEAAKKLAKEIGYPVILKAAAGGGGRGMRVVENEKDLEKAYWSAESEAMTAFGDGTMYMEKYIQNPRHI

EVQVIGDSFGNVIHVGERDCSMQRRHQKLIEESPAILLDEKTRTRLHETAIKAAKAIGYEGAGTFEFLVD

KNLDFYFIEMNTRLQVEHCVSEMVSGIDIIEQMIKVAEGYALPSQESIKLNGHSIECRITAEDSKTFLPS

PGKITKYIPPAGRNVRMESHCYQDYSVPPYYDSMIGKLVVWAEDRNKAIAKMKVALDELLISGIKTTKDF

HLSMMENPDFINNNYDTNYLARH

>ABV52831.1 hypothetical protein C8J\_1232 [Campylobacter jejuni subsp. jejuni 81116]

MKKILLSFAFFASLASANTINAIAVVVDKEPITTYDIDQTMKALKIDRNKALGVLINEKMEISQMKQLGI

VVNDLELDDAINKMLAQNKTTLNAFKANLKSKNQSYEQFRTNFKKDLEKRKLYEKIASMAKTDFSDDGAK

KFFEQNKDKFTFYTQINANIYLSNNPQTLENIKNTKKTILKPQNASLNTSNADPRLLGLLSQIPVGGFSP

VLNGKNGYELYEVKSKDGTQTPEYEQVKNEVLNAYVSEQRQNFIQDYFDKLRSKINIEYLR

>ABV52830.1 glutamyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MHEKLTTRFAPSPTGYLHIGGLRTALYNYLYARKNGGNFLLRIEDTDLKRNSKEATKAIIEAFKWCGLEH

DGEVTYQSERFDLYKEYVKKLLDEGKAYYCYMSKEELEELRAKQEAAKERPRYDGRYREFTGTPPQGIEP

VVRIKAPQSGEIVFEDGVKGEVRFKAEDIMDDFIIARSDGTPTYNFTVVIDDALMGVSDVIRGDDHLSNT

PKQIVLYEALGFKIPKFFHVAMIHGEDGKKLSKRHGATDVMEYKEMGILPQALLNFLVRLGWSHGDDEVF

SLEDLKKLFDPYHINKSASCYNAKKLEWLNAHYIKTLPFEEINRQLKDLGFDLSVYEKAGFLLDLLRERA

KTLHDIINGAKSIVNAPQNYDENAVQKFVNENNLELLQAFANTLKDQKTGKDFEDFTNDFLEKKEAKLKD

LAQPIRIALTGSAVSPSIFEVLEFLGVDECKKRIDNFLKVRGK

>ABV52829.1 malate oxidoreductase [Campylobacter jejuni subsp. jejuni 81116]

MNLKEEALKYHLGGKIDIVPSKPMATSYDLSLAYSPGVAEPCLEIAKDNELAYTYTNKANLVAIVSDGSA

VLGLGNIGAQASKPVMEGKACLFKKFANVNAYDIEINVHSIEEIVNFCKALAPTVGGINLEDIAAPKCFE

IEAALQDLGIPVMHDDQHGTAIISTAGLMNAMEISGKKFKDIKVVVSGAGAAGIASAKMYRNLGVENIIL

VDSKGVISKDRNDLTPQKLEFAVDSKEKTLKEVLKGADVFLGLSAPKILDDEMVLSMAKDPVIFALANPI

PEVMPEDVARLRKDAIVGTGRSDYPNQINNVLGFPFIFRGALDVRASKITENMKVAAAKALADLAKLPVS

DAVKKAYNLSTLEFGRDYVIPKPFDERVKAAVSTAVAAAAVKDGVAKVKNFDEKAYFESLK

>ABV52828.1 uracil phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKNIHCINHPLIEHKLGILRAKETKPFQFRMLIDEISSFLLFEASKDFSLKEIEISTPIQKTTVKKLDEK

IMICPILRAALGMLESVFKMIPDASVGFLGFVRNEETLKADFYFQKLPKDAKKRTAIVIDPMFATGGTAI

EACNFLKSQGVKKIKFISILAAPQGLKKFSQMHDDVEVFVACIDEGLNEKGYIIPGLGDAGDRVFNTL

>ABV52827.1 hypothetical protein C8J\_1228 [Campylobacter jejuni subsp. jejuni 81116]

MIFGKIDYINLLPLHIYLKKYPLPNGYKANMEYKKGVPSKLNKDLFYRRIDAAIISSIESARKKYKNLDL

GICANKRVLSVLVEKNTSNAKDPSSATSNALAKVLKQDGKVIIGDKALKLYLKDPSKYIDLCAKWHEKTG

LPFVFARFSCVQKKALYKQILKKFPKTKIKIPYYILQNYAKTRDLDIKDVRYYLDEVIYHKISTKEKTAL

KRFVKACKALNLA

>ABV52826.1 putative K+ uptake protein [Campylobacter jejuni subsp. jejuni 81116]

MKNLNYGIIGLGKFGSVVADELIAGGHTVIVADKDEEALKSIQNPPSYAYILDSTNISALKEAGFHDVEV

VIVSIGENVEKSILTLMALKDIGVKNIIAKATSNIHGQILSKLGATKVIYPEKESAKRLVKEFLTKDADY

EVFDLSANTIRAIKINIDEKLAGNSLKHVAQNMKVISYKKLNSDWEILPDLETTTVYSGDVVILLGTVKE

LREFEH

>ABV52825.1 putative K+ uptake protein [Campylobacter jejuni subsp. jejuni 81116]

MKQFGLDRRTFKILLAGYIIIALFGALLLHSSWAHTTPIDFLDAFFTSTSAVSMTGLVVKNTAVDFTLAG

QIIILALVQIGGLGYMGIGLFVYILIRKKVGFSARNLLKESLFYPSMDGLFKFFKKVLLFIFTIELIGAI

LLTMRFALEMNFKKALWFGIFHSISAFNNSGFTIFEHGLIAYKHDIAINLIITSLIIIGGLGYFVLVELY

FFQRKKLQNLSLHTKMVVVASIFLIFSSTLIIFAFEYSNPQTIGHFSFFDKILSSYFIAINYRTAGFSTL

DMGHLHDASLFFGSLFMVIGGAPGGTAGGMKVTTVMVLLLYAYWSIRDGRVRIFGHEIPRETISKAFIIA

VGSAVYIVIAVILLSLLESKFDFIALLFETSSAFATVGISVGNGGTLSLCALFSDPSKVIIIIMMLSGRI

GVFAFLLSVFKQDKAIHLKFPEGKVNL

>ABV52824.1 rod shape-determining protein RodA, putative [Campylobacter jejuni subsp. jejuni 81116]

MFRLDRRILTHFDYMQPILFLPIILISFFLIFEANPFLAEKQFVYACVGLFAFMVFFFFPIRKFIWIIPV

AYWINIFLLLSVDIFGVEKLGAKRWLEIPFTHFTIQPSEIFKPSFILMLAYLIYQNPPPKNGYKLKQFIK

LSFYIILPFLLIAKEPDLGSAMVLLLVGFGVLFIMGVHYKIWLSIVIAISVSSPIIYTHLLKPYQKQRIH

DFISEKPSYQVAQSMIAIGNGGLTGKSQDEATQTHFKFLPISTSDFIFAYMIERFGFIGGLTLIIFYILL

IFHLLSLNYKLKDDYFARVAINCVALFIFIYAAVNISMTIGFAPVVGIPLPFFSYGGSSFTIFMIFFGIL

QHLITFRYFWTDIKAK

>ABV52823.1 putative ribosomal pseudouridine synthase [Campylobacter jejuni subsp. jejuni 81116]

MQTFLVDENSRLDVFLAKKLNQSRNQVALLIEKDCVQVNDKIQDKNSFKLKNGDIISIASLKLCNEIKPQ

FEVDFDIDVLYEDEDLLVLNKPSNLVVHGASSVKNATLVDWLIEKKYTLSNLGGEIRAGLVHRLDKDTSG

AILIAKNNFTHQKLSEQLADKSMGRIYLALIDLPLKEDKIIVEKFLMRSPSNAIKKIAIDKENKFSKNAK

SAFINIVKTENLTLMAAKLFTGRTHQIRAHLASLNRHILGDSLYGYKGKYDCRIMLHAYFLYFIHPKTKE

QIFVKAPLMEDFKNIMFKQINLGENDEKISLGFLLEFFNSFA

>ABV52822.1 fibronectin type III domain protein [Campylobacter jejuni subsp. jejuni 81116]

MKRFRLGFYLSFLTLLLSACSVSQMNSLASSKEPAVNESLPKVESLKSLSDMSNIAFEWEPLYNENIKGF

YLYRSSDENPDFKLVGTIKDKFQTHYVDTKLEPGTKYRYMMKSFNEQGQISEDGKVIEVSTAPRLEAVPF

VQAVTNLPNRIKLIWRPHPDFRVDSYIIERTKGDDKEFKKIAEVKNRLNAEYIDSDLKPNENSSYRIIAV

SFNGIKSEPSQVVSSTSKALPPQVEHLSASTDGSNKIILTWDAPTYEDFSYYKVYSTSSSFLPFSVLAKT

DKNSYEDIVEGAGKSKYYKVTMVDKDGLESPMPKDGVEGKTLGNPLAPSIILAQSTSEGINLEWSDNDTR

AVEYEVRRYGGEQNAVFKGIKEKRLKDVKALPGVEYSYEVIAIDSAGLRSEPSSKVKAAQ

>ABV52821.1 tRNA (guanine-N7-)-methyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MPNFKSKKIKEINLPYSKDDVEFLWLAKNDNVSLIYTKVQEESFFLQIKKAQNGFVIKGDKHTKPSKIGY

LQKALKIFKEGFCEDIINEAFGLKNNALIEKTPFIVDNFDELLSKLQGKIYIEIGFGSGRHLLYQAKENP

NVLILGVEIYNPALTQVAKLAKVQNVNNILLIQSDARLLLSVLKSKSVEKIFLHFPVPWDKKPHRRVIGK

DFCKECARVLTQNGRFELRTDSFEYFNFTLEQFLTFPAPKFSLRKNENLEISSKYEDRWKKQEKNIYDLW

VWNFNQECKNYELNEFNLSSVEFSKEDLKKIEQNFKNITIKKDDFFLHFESIYKQDENLLLKVAFGAFNK

PEHCYLHLDKTIDFVFKEPFKIQENIKAINELKEILKVQFKI

>ABV52820.1 lipoprotein releasing system ATP-binding protein LolD [Campylobacter jejuni subsp. jejuni 81116]

MPNLIQANKLTLGYDELVIKEASFAFKDDDFVFITGKSGSGKSTLLKSFYGDLEPISGKLEVCGSLMNKI

GNLELLKLRQRIGIIFQDYKLVQEYSVEKNVMLPLMIKGYSKKVCHDQAAKLLKHVNLTFKADKLPNQLS

GGEQQRVAMARALAHNPKLLLCDEPTGNLDEYSSDIIWTLLKSARELLGTCVIVVTHRIPSNLRVDYRRF

NIENGKMNEIF

>ABV52819.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKFFKTHLSLILPLLFMMFAFEFILITNATLKHYEELVNKDYNIIVVSKTELDQNVVKTKVPFFAGLESL

DPKDLIDRLKNDVSEKNLKVLKDSLPKFYTLKLNSLPDQNELNSIKNQLLNIVGVSKVETFSKTHDKIYS

LLILMKFVFWLFLFIIILLAFVLFLKQMRIWLYEHTDRIEIMCLFGAPFWFRSFMLYKVVVVDCFIAFVI

LLAFFTQIFDLSIIQESLKAVDIIFPPINFILHLTLIFLATLFICLLCVNTVMFKVKR

>ABV52818.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MRKNILIFFCFFLFVDISLANAINEKTKSLEENKRIQEQLNKKLEDLASDILNGEKSLKDLSLQIESLNS

QTSKLEASAKAQNQELNTLTSQNEDLLKSKSNMEGKLISLMAKDFAYDLPIPQGYIESEESFMAFEILGS

LNKVLNEEIFKISKDYEGVSRLIDDKQAQINKINESLKDYNAQLAKLQSLKQKQISEINKQKTDRAIYAK

KLDDLQAQQEELRKTLNQLKIINDKEDANSNKNDTKIVKNNQKIRQLGSSYQGSSVKRYTGKKTIAPLDS

FTVKQKFGNYVDPVYNLKIFNENVVLRSNKSDAVVKNVLDGKIVFAKDTSMLARVVIVEHDNGIHTIYAH

LDKIAPNIKVGKNIKKGAVVGRIKNDLTFEVTQKNFHINPLELISLN

>ABV52817.1 uridylate kinase [Campylobacter jejuni subsp. jejuni 81116]

MQERKRVLVKFSGEALAGENGFGIENSILKFIASEIKELIKNQIEVGIVIGGGNIIRGVSAAKGGLIKRT

SGDHMGMLATVINAIAIQEALESSGLEVRVQSAIQMEAFCETYIMRRAQRHLEKGRVVVFAAGTGNPYFT

TDTTAILRAVEIDADMVIKATKVNGVYDKDPKQFDDAVFLNTLSYDEAMQDNIKVMDDTAIALAKDNKLP

IVVCNMFEEGNLLKIIQGDTSLCSIVKNN

>ABV52816.1 DNA-directed RNA polymerase subunit omega [Campylobacter jejuni subsp. jejuni 81116]

MDKRIEEVAAKALEKMGNDRYRLSLVVAKRAEQLANGATPLVDFDKNKNKLADIALYEIAENKITLEGLV

ETNR

>ABV52815.1 RelA/SpoT family protein [Campylobacter jejuni subsp. jejuni 81116]

MKPIDEELLLEQLIDNVKNCKDLEAAKALLFEICGHDAILEKAVDYCIFCHEGQFRKSGEPYAVHPILVA

TLVGFLSENKSNILAALLHDVIEDTNCTEEELREQFGSEVLKLVLGLTKIIEIREDNLISSKSKKSLTKS

ALTFRNMLLASIEDVGVLIVKLCDRLHNMLTLDILREDKQKRISEETLVVYAPIAHRLGISSIKNYLEDL

SFKYLMPDEYKLIDNYINSNNQEMQLGLNEFISKIELLFLSNGFRQGSFEIQKRIKHSYSIYLKMQRKGI

GIEEVLDLLGVRILVEKVSDCYLALGILHTHFNPLVSRFKDYIALPKQNGYQTIHTTLFDAKSIIEAQIR

TFDMHKIAEFGIAAHWKYKEDGSVVAPRLDWLTDISMQSINNLENAEDYNAIELYEYAKDSLYVEDVAVY

SPKGEIFTLPRGATVLDFAYEVHTKVGLHAKSAYVNRIKVPLLTELKNGDIVRVVTSNDKFYRCSWIDSV

KTGKAKASIREFCKQKIREINLASSINMLSFIFGVDKNRIETWIEKENLARRIRQVATDSAYLKDIVNGL

KKYAKKSYWFDKYEIKEQKIGNFTLYCNHKIANVDFDFCCHPKRGDAVLAFVKGGNAIVHHKLCDRADKM

IDNNQDMVFIKWDSNIPKSYKLIFSLENKKGVLAEFLAFLAKMQINLLTINLSSDLNSAVDYFEITMEIP

DNINPDSVKDRLKSRCKILDFTSLNDAYKEG

>ABV52814.1 tyrosyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MDIKKILAEVKRGCAELIDEERIENLIKNYYEKGENFFIKAGFDPTAPDLHLGHSVVLTKMAFLQKHGAI

VQFLIGDFTGQIGDPSGKSATRKKLDKEQVLINAKTYETQVFKVLDKEKTQIKFNSTWLNELGAAGIVEL

TSTFSVARMLERDDFTKRFKEQSPISICEFLYPLLQGYDSVALKSDIEMGGTDQKFNLLMGRQLQRVYNI

GKEQAVIMMPLLEGLDGVNKMSKSLNNYIGVTEKANDMYAKILSISDELMFRYYELLSQKSLEEIAQIKK

DIEQGNLHPKKAKENLALEITERFHSKEEANNAKSEFDRIHSQNALPSDMAEFEIQGKIWLAKALVECGL

ESSTSAARRSISANAVSVNSQKVSDEQMHLEQGEYILQIGKRKFAKLKVKE

>ABV52813.1 hypothetical protein C8J\_1214 [Campylobacter jejuni subsp. jejuni 81116]

MNLQPLQIGKHTIKYPIFQGGMGLGISWDRLASAVSLNGGLGIISSVGTGYYEERKYASKELNAKPYGSE

NFYSRKGLQALINNARKVCGDAPLGCNILCASNDYARIARDACEVGFNVIVSGAGLPTNLPEFTADFPDV

ALVPIISSAKALKIICKRWQSRYNRLPDAVVLEGPKSGGHQGFTYEQCLDPNYQLEKLIAPVVEEAKNWG

SFPVIAAGGIWDKKDIENAISLGASGVQMGTRFIGTFECDASEEFKSVLLASKEEDIELIKSPVGYPARG

VRTNLLNLVDKRIGPKINCISNCVAPCGRGKEATKVGYCIADRLFDAWSGKKETGLFFTGANGYRLDKLI

SVKELMEKLVNGE

>ABV52812.1 putative N-acetylmuramoyl-L-alanine amidase [Campylobacter jejuni subsp. jejuni 81116]

MAKIFVFLVFVFTTLFGAYENELANFDKNFIGSKSEVQVKFHHQLKSLYIQSVINEDEKTKIEILKRLII

SSNTLNLDDKSYANELKESGISEASINALRKAVIKDIKVQNISQDTEKSTFEPIKTVQKNEKKSSNEQIK

NTEKTNSKTSQAPKSSIVSKAKSDDKIYVLKSSKTNQGVEFELNADLDKDQLKSFALDEKGNYRFISDFE

GVLEGGKKEFKFDDYRLVISQFNPKTIRIVVYAKEKIPIDISFKEEKLIFSKETTSQKKTEQVSKISEKK

QDQKTEIKTKALETKKQDKKTNNEKENQEPLYVLDVDKISNAVVLNLSDDLDEKEIAVFDTKDQKFRYVV

SFKGVLEGNRKSFTFGQNVITVTQYNPKTVRVVLSAPKEFKLLKELDNKNLTLGFYAQTTNQNVNKKATQ

SSSKTLNTNYKSGKLVVIDAGHGGKDSGALSDKKGSLKEKDIVLSTALKLGNELKKRGYKVLYTRSSDKF

INLRDRTKYANDKRADLFISIHANAAPNATKAKSSEGVETFFLSPARSERSKKAAEKENQGDFEEINYFS

KQSILNFLNREKIVASNKLAIDVQKNILTQTRKKYKIVDGGVREAPFWVLVGAQMPAILIEIGYITHPNE

GKRIANKAFQDLLVKGIADGVESYFYNNR

>ABV52811.1 oxidoreductase, FAD-dependent [Campylobacter jejuni subsp. jejuni 81116]

MKKAKLIFKDNTPFSLDFDDFYFNSKDGLNESKFVYTHSFEWKNQENFIIAESGFGIGLNFFLTLKRFLQ

TTPSKRPKKLFYISIEAFYIEKEQLREIYQKLGFYEEFKELLEQFLKFYPKAKEGIYRFYFEDCFLDLVF

EDITILKELDFKADIWYLDGFSPNKNSQMFDENLIFEVARLSKKNTQICTFSSASFLQKNLKKYGFRVEK

TKGFRKREMIKAYLENELEFKDKEAYFSRTFSSLKNKKVAIIGAGISSAVLAYELSLRGFEIDVFEKHLE

LGKGASGNESGILSSLILKPKVNLGEFSELSFIEASRFYRQILDLEFKGVVEFAHNDLMQERFDTQRENV

LFKISKNQAFLEEGGVIFPKNLVKNLFEKSKACIYFNHEFQAYKFENECFTLKFKNDIVKSDYAVLIYAM

GADTKDFVFYDEMKLSKVRGQVTHLKPFLNTPFPLSSKAYICPVKDDLQVIGASYDRLDASLESKEEDDK

QNIENIAEFIDKNTKLEIIGSKVGFRSYSSDRFMIVGNAYDEVFYKEEYKALLWTKNKEQKLAKISCNLY

FNFAHGSRGFSTSVLAARYLCALINNEPLYLEKKYIHAIHPARFLIRKLKKGL

>ABV52810.1 hydrogenase small chain [Campylobacter jejuni subsp. jejuni 81116]

MIDYHQIESRLSALEKLPSLKDNDSITKALEKSGFSRRDFMKWAGAMTAFLALPASFTPMVAKAAELADR

LPVVWLHMAECTGCSESLLRSDTPTIDSLIFDYISLEYHETVMAAAGWQAEENLESAIQKHKNKYILMVE

GGIPMGDTEHFLTIGAHGKTGYELSKMASENALAIFAIGTCSSFGGIQAARPNPSNAQPLSKVTSKTVIN

VPGCPPSEKNIVGNVLHYLLFGELPALDVYNRPKWAYGLRIHDLCERRGHFDAGEFVHAFGDEGAKQGFC

LYKVGCKGPYTFNNCSRERFNQHTSWPIQAGHGCIGCSEPDFWDTMGPFEEPMASRKFDTVFGLGADSVS

DKIGIGVLTLTGVAIAAHAVISSMQKDKE

>ABV52809.1 hydrogenase large chain [Campylobacter jejuni subsp. jejuni 81116]

MSQKIIVDPITRIEGHLRVEVVVDDNNVVKEAYAGSTLWRGIETIVKGRDPRDAGFMTQRICGVCTFSHY

KAGIVAVENALGITPPLNALLTRTLMNAALFLHDHIVHFYQLHGLDWADVVSALSADVKKASDEAFKYTS

NPYATGADKLLEVQQRLKTFVDKGNLGPFANAYYGHPTYRLTPEQNLIVLSHYLECLRIQRIIAQCMAIF

GAKNPHPQSLTVGGVTCVMDLLDPARMGEYMVKFQEVQDFVNRAYYPDLVMAGKAYAHEASVLNDIGVNN

LYTFKEFQIGRDEWLFESGIIKNGDLSKVYEVEEDKITEEATHSWYADNEPLHPYDGKTNPNYTGLVDGE

SVDHHGNNVHSKVFDTKGKYSWIKAPRYEGNPMQVGPLANIVVNYAKGNPNVVPVVDEFLKETGLPLNAV

FSTLGRTAARCIEAKIVANNALKAFNNLVENLKVDQSTCAPYVIDNSKEYKGRYMGHVPRGTLSHWCRIK

NGVIENWQAVVPSTWNASPKDANGIGGSYEQCLIGLKIADVKQPLEIIRKIHSYDPCIACAVHVMDAKGN

NLSEYKVNVNL

>ABV52808.1 Ni/Fe-hydrogenase B-type cytochrome subunit [Campylobacter jejuni subsp. jejuni 81116]

MQNKEEKLQRKAEYEFSIGLRLTHWVRAIAIVILIGTGYYLSYVFQSPISNGEPVNFMQAKYRLVHQAVG

FVLIACIIFKVYLFFCDKVSAKERRSVWDIFNIKLWIEQVKFYIFLGKHPHLKGVYNPLQFVTYFFFYLV

MLGIILTGLILYTHTYHEGLGGLLYHILRPLEAAMGGLADVRTYHRILMWVIMIFVPVHIYMAIFNAVKG

KDGAMDAIISGYKYIKEEKH

>ABV52807.1 putative hydrogenase maturation protease [Campylobacter jejuni subsp. jejuni 81116]

MKFLVLGIGNIMFADEGLGVHLCKQLEKNYKFTHPEFTLDFIDGGTLALQLSYIIARYDRLIVLDCIEAQ

DASIGDIFFFPYDAMPNKISWSGSAHEIEMLQTLQYMELAGDLPKTHILACVPKRIEAMSFKLSDELIQG

AKIMEKTLLDFLTKEGFAYEKIADFSLQELADISYKNY

>ABV52806.1 recombination protein RecR [Campylobacter jejuni subsp. jejuni 81116]

MAKGLEKFNELVESFANLPTIGKKTAIRLAYHLCINNQIDGMKLAHNIENAIRFIKPCGQCGALSENELC

EICSDEERNKNILCIVESPKDILTLEESQSYNGLYFVLDELNEEKLEKLKQIILKLNISELIFALTHSIN

SDATIFFIEDKFKGLNLTFSKIAQGIPSGVNLENVDLISLNKAMNFRTKI

>ABV52805.1 sensor histidine kinase [Campylobacter jejuni subsp. jejuni 81116]

MTKNYSIYTKLIILFVVTFFLVCVLFIVLLKIEGNAYNEEESLKQENLIKNLLISYENTSGVEIGAYLGN

SGFNAIQNPHLVKAIRNNGQSLFKAGGELCTLSSLKYHSNLYFDVQCKDFDGLYEENTSDRVYNLLLIGF

FSFSLLVVFMYFSVLRSLEPLKKLRRQVAEVANGEQPDFLDYQEDEVGKIAFEFQKAFKKNQELIQSRQL

FLRTIMHELKTPIGKGRIISEMIKEDRQKERLIAIFLRMDSLINEFAKIENLFSKNYNLHFKPSRFSAIL

EEAKEHLMRDDFNKVVKVDIRYDALINVDMEIFSVILKNLIDNALKYSNNGTCELFCCKECFTIKNPGKP

LAEPIEHYLEAFTREKHNQVKGMGLGLYIVSEVCKLHNFDLIYFYDDGKHCFKIFFGDKEK

>ABV52804.1 two-component regulator [Campylobacter jejuni subsp. jejuni 81116]

MINVLMIEDDPDFAQLLSEYLAQFNIKITNFENPKSALNVGVQGYDCLILDLTLPGIDGLEVCREIRQKS

NIPIIISSARGDLSDKVVGLQIGADDYLPKPYDPKEMYARIMSLIRRTKRVEHANNENINSAFKIDERRH

EITYEDKVLTLTPAEFEILEYLIQQHGYSVSREQLVSRCKNLKDKDSKSLDVIIGRLRVKIGDSSKSPKH

IFSVRGIGYKLIG

>ABV52803.1 co-chaperone protein DnaJ [Campylobacter jejuni subsp. jejuni 81116]

MEISYYEILEITQSADKETIKKAYRKMALKYHPDRNQGDKEAEDKFKLVNEAYEVLSNDEKRAIYDRYGK

DALKGGGFGSSSSGFGGFEDLGDIFSSFFGEGFGSSSRRRKSSNDEKIPSDFIVNLKLSFKEAVFGCKKN

IDFTYKCSCKTCNGTGAKDGKLQTCPKCQGRGQVGVSQGFITFAQTCPDCQGSGEKASEKCSDCKGLGYN

ESKDSVELNIPEGIDTGMKLRVNAKGNILKNGTRGDMYVKIIAAEDDTFVRDDDDIYIEFPVFFTQAILG

QSIKVPTIRGEATLNLPKGAKDGQRFVLEKEGVKDVHSSRIGNQIVQISIKFPTSLNDEQKELLEKLSES

FGIKDGMHQEQKGLFEKIANWFKS

>ABV52802.1 major outer membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKLVKLSLVAALAAGAFSAANATPLEEAIKDVDVSGVLRYRYDTGNFDKNFVNNSNLNNSKQDHKYRAQV

NFSAAIADNFKAFVQFDYNAADGGYGANGIKNDQKGLFVRQLYLTYTNEDVATSVIAGKQQLNTIWTDNG

VDGLVGTGIKVVNNSIDGLTLAAFAVDSFMAAEQGSDLVGANGSAFKVDSIGNLYGAAAVGSYDLAGGQF

NPQLWLAYWDQVAFFYALDASYSTTIFDGINWTLEGAYLGNSLDSELDKTYANGNLFALKGSIEVNGWDA

SLGGLYYGDKEKASTVVIEDQGNIGSLLAGEEIFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFV

YGGTKTEAANHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNTNESADHSTVRLQALYKF

>ABV52801.1 possible phosphotyrosine protein phosphatase [Campylobacter jejuni subsp. jejuni 81116]

MKKILFICLGNICRSPMAEFIMKDLVKKANLEKEFFINSAGTSGEHDGEGMHYGTKNKLAQLNIEHKNFT

SKKLTQKLCDESDFLITMDNSNFKNVLKNFTNTQNKVLKITDFSPSLNYDEVPDPWYSGNFDETYKILSL

ACKNLLVFLSK

>ABV52800.1 putative efflux pump [Campylobacter jejuni subsp. jejuni 81116]

MENFNRTLLVCWFGVFTTSMGLSQIAPILPFYIKELGHVDTSEIAFYSGLAFGITPLFMAVFSPLWAFLG

AKYGYKNMLLRASFGMSVLTLWLSFAHSALEVVFVRGLTGIISGFTSAAVVFIAVIAPKEKVAYALGTLS

TASISGSLLGPLFGGFVAEFFSISAVFDVVAFLIACSFVTIYFFIHGRKIQKEAKKNTQKVKENKTLIIV

LFITTFVIQFGTFGVMPILSIYVEQIHQGGNLALWAGIVVAANGISNLFFAPKLGKIADKIGPSKIIFGA

LIFCGICFYLQAVASNVYTLIFVRLLIGVGLGGLLPCVNALLKKSVSAKNLSVIFGFNQTCQFLGNFCGA

FGGGLMASHFSVEFVFTFVCLIFIINAFIFLAFEKKYIFSNQGL

>ABV52799.1 hypothetical protein C8J\_1200 [Campylobacter jejuni subsp. jejuni 81116]

MEMILFVLVMILLVLLFVVLFRQYKSPKIEEKSTQSFSDIMQLKSIGELSVFQVFSKEIVTKKDSAFNGI

WKNLLGWSLSERQIALIFEFEITFLYDLRDKNFDILPLGDDAYKIIMPECRYKHSIIDMKFYDEKNAKFL

PFLLPDSINSTGISFSESDKNKLIKEAKDEVKDLSLNLIQNLESKIHKSAKDTLEAIAKGFGAKRVEFEF

KDNTQKLDVN

>ABV52798.1 hypothetical protein C8J\_1199 [Campylobacter jejuni subsp. jejuni 81116]

MPFVNIHITKENGEPTTEQKQELIARSNGFTC

>ABV52797.1 hypothetical protein C8J\_1198 [Campylobacter jejuni subsp. jejuni 81116]

MSKFLTHPFEPFFDKDSKILILGSFPSVKSRQDGFYYQHSRNRFWPILETLFDVKLENITEQQAFLRKKH

IALWDVLQSCKIKNSDDKTISYAKANDLSLILSQAKIQAIFTTGQSAYKFFVKFHPRLEAIALPSTSPAN

LNFSFEQLLQNYEIIKKFTK

>ABV52796.1 polyribonucleotide nucleotidyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MQYSIEINKNTEIFDIDKVAKQAAGAVLMRQGKSVVLATVAREEKQVEEDFLPLTVQYIEKAYAAGKIPG

GYVKRETKPSDAETLTARIIDRSLRPLFPKGYTYPTQIVVMVLSADPKVDLQVMSLNAASVALYLSDIPM

KAPVCGVRIGKIDGNFILNPNNEELQNSTLDLYVAGVKDELLMIEMRALPDQKENEIFIEAPYADVLTQT

TSQNMNELSEDEILEALNLAQKAILNGSNAYEEAFSKHKKNSQIELKNEIEHPEILAFIENNFQKQIKEA

INQMAKSERASELNKIAKEILNLEIAKDWSEESVLNTLAKVKRKLIREQILNEGKRADGRSLNEVRPISI

ETNILPNAHGSCLFTRGQTQALVVATLGGENDAQMIDLLTEKNPISERFMVNYNFPGFSVGEASPIKAPG

RRELGHGNLAKRALYPSVDENYPYVIRLVSEILESNGSSSMATVCGGSLALKAAGVPSLKLVAGVAMGLI

FEDNKHAVLTDIMGLEDHDGDMDFKVAGSKDGVTALQMDIKLGGIDQETLKQALYQAKEGRIHILNIMEE

AAKEIIVNEEVLPKLELFSVDPSKIVDIIGQAGKTIKEIIEKFGVSIDLDREKGEVKIAGSQNEQIKAAK

DYIINITSSQKGTKKGSKDKDISGFELGQEFQGIVKKIAPFGAFVELKNGVDGLLHSSKSKHLNLTENQS

LKVKISEIKNGKISVDLCE

>ABV52795.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MWRKFSLLLGTSIALNAAQVDIYALDAKKEGDILTANNDVIIFSDFYFITANKAIYNEKTGDVELFGDVN

ILRGQNERSHSDYAKINLNSNQADFSNFFFSNNNLEVWFQSKTSHLNDKVFESKISAVSSCNVEDPDWEI

RFSKGWLNRETNFVHLYNARLYVKNTPVFYLPYFGFSADTHRQSGLLIPKIVLKSSEGLYYEQPIYIATQ

ENWDLELDPQIRTNRGFGLYSTLRFLDSPYSTGELNFGAFRENSSYFHDENLKNQTHYGIELKYSRDDLI

KSLLSDNFQEGLWIDATYLNDVDYLNLGSRDYRDLNSLVTSKINYFLADENNFYGAYARYYIDTSKLSNN

TTLQEYPSFQYHRFLNNLFDERLRYSFDASFHNFYRPAGSYANELNLDLPISYHNAFFGDFLHFTFTERF

YASFVNYSNDPERNHEHYFRNTHDFNLYTDLSKAYENFFHTLNLGVNYILPGAKSGKITQNYLEEYDKEN

EHTSLYAVQYFYNNEGQKKLKHRISLDYLNKQNEFYELQNLLTYYFNENINLNSEVLYSYEQSRFTNVIS

QIEVNTNSKFNWMFSHAYQNDEYGKYSFIGTRANYIATPNYNLFGGIWFDTQRAHANMWELGYTYQRKCW

NYSLMYRERIDPQLTSGGITAKNQSGVYFIFNFYPLGGVKYDFSLAESENKI

>ABV52794.1 hypothetical protein C8J\_1195 [Campylobacter jejuni subsp. jejuni 81116]

MKENLQDRLERENLKIASFGKRVLAFLIDDMVISLIVFIIFYDRLIQAKDLFETTQIIGNFYLGFILLHF

SYQAIFTYLYGASLGKILCKIIILDENLLDKPNLIQSCIRSAIRQVSAMAFMLGFAWALSNDLRKAWEDY

LARTIVVDVA

>ABV52793.1 phosphoribosylamine--glycine ligase [Campylobacter jejuni subsp. jejuni 81116]

MKIMILGSGAREYSIALALRRVDKNLEFYFAPGNGATESLGTNLNLKDPVVLATYAKEKGFDLCIVGSES

FLAEGVVDIFKQQGLAIFGPSKAAAMLETSKSFMKSFLKKYRIKTAKFLNTNDIEKAKNFIYSLTPPIVV

KADGLCAGKGVIIAKTHEEAIEETAKMLSGESFGDAGKLVVIEEFLDGYELSIFAVCDGNDFVLLPAAQD

HKKLLDNDQGPNTGGMGAYAPSSLANESLLRKVQKDIILPTLAGMKKEGAEFCGVLFIGAMIVGNKPYVL

EFNVRFGDPECEVLMPLIEDPLELILAATQRRLRHAKIKIKKEFAVGVVCASENYPYKSSPKSEITVNNI

PENSHISYAGVSLEDGKLMADGGRVLVCVGTGKSIEEAQKNAYKLCDNVNFKGKQYRKDIAHQVLK

>ABV52792.1 hypothetical protein C8J\_1193 [Campylobacter jejuni subsp. jejuni 81116]

MPKQFVVFKVIQHIFINCDCVIYRVLWHRLSFEKSEKLQPLKIT

>ABV52791.1 hypothetical protein C8J\_1192 [Campylobacter jejuni subsp. jejuni 81116]

MHGKIAIYMDSTGRGTVTNSANTFFDFNRQIWNDKKSMPSVGMLVEFRTLSSEKKAEDGKPVQTSKTITG

IKPSKFQEFKEGDFITEHDFWKTDNDDELEDLQNSRRSAYITELYRTTDFDTIEKIPLSFTIPQAIQKYF

AHEILSVETLQANLQDEKEIPCILDYLILKRFLFKAYDTLIFMDNSIDQTQFSALKSIMMHLENSYKQMI

ADQKPNITKIFNETFLSLQCHYQALVATIDTRNNRLASLEAQMKTLQSEINLKSNAANADPEKLKARQER

LTKLQKEAEYYRTTLKRLDAIREDFYKKNYNIFENAFKLSREKLFKKIVTGLNLCATIMDVKIWHLSLKS

SGVKNSYFTMSNIENSFCSLSFAEHYLSRLNKSALNPFDQKLLVYIQKITKEQRKKFLVVTSDLDLLCKL

KIENFSQNPYYLVKYAPKKVNYQSLMRDNTFDIVYIDEKHVWENVADIILQGKHFDKSGKTKFKLI

>ABV52790.1 bifunctional GMP synthase/glutamine amidotransferase protein [Campylobacter jejuni subsp. jejuni 81116]

MKKADILVLDFGSQYTQLIARRLREQGVYAEILPFNVSLADIKAKEPKGIILSGGPASVYATDAYFCDKG

IFDLGLPILGICYGMQLMAHHYKATVAPAGHKEYGKANIEVKKDSALFKNLPKKQTVWMSHSDKVENLPQ

GFEVLATSENSPFCVFGNEDKKFFALQFHPEVQHSEFGKNILKNFAKYACNCESVWNMGSFAKTQAEKIR

EEVGSDKVLCAVSGGVDSSVVAALLASAIKEQVIVVFVDNGLLRSGEKEQVEFMFKNTLGIDLISIDASE

IFLSRLANVRDPEQKRKIIGNTFIEVFEEEAKKHKDVKYLAQGTLYTDIIESSVVGASKTIKSHHNVGGL

PEKMNLKLIEPLKEIFKDEVRALGLELGLSKEVVYRHPFPGPGLAIRIMGEVNRPSLELLRKADVILLEE

LKSTGWYDKTWQAFCVLLNIKSVGVMGDNRTYDNAVCIRVVDASDGMTATFSHLPYEVLENISRRIINEV

EGINRVVYDISSKPPATIEWE

>ABV52789.1 hypothetical protein C8J\_1190 [Campylobacter jejuni subsp. jejuni 81116]

MTKNASAVINELMDKPHYKPLKTLFFCKDFLSSFPLAKQRLIAKIYVKNHILNIITLHPAAYQELNHDDS

KIYIKFLIKAYGQKYPLSGFVDIKDIKIFSQKYTYAVNKNKNDEKLSKNSYLELSKGEFKNCFEDEKLFK

KFEDLRELIKKGSNLD

>ABV52788.1 excinuclease ABC subunit C [Campylobacter jejuni subsp. jejuni 81116]

MTKENLENELKTLPNSAGVYQYFNQEGKLLYVGKAKNLKNRVKSYFAFTPNLHANPRNSLRIQKMIEETV

HLEFITTNSEADALILENSFIKQLHPKYNILLRDDKTYPYIYVDFEEEFPRFEITRKLVKKSKIKYFGPF

FKGARELLDALYLYYPLKQKASCKSPCIFYQISRCLAPCDKRISREKYLEILDEAMHALLNPSILIKNLE

KQMLVLAQNENYEEAAKVRDQIVTIKDLEVKVEIDIAKLEDFEVFALAFENSMLSTLRFVVQNGKIISVN

SKITPIKNDIQWDKNEIYKQLILENFSMDIPLLANVIYVYEEFEDRMLLEEILSQRFDKKISIKIPKIGE

KRRICDLAFQNALLNIEKEQKNHDFTIQKELKSYFELENLPNDIEIFDNSHLQGVANVGAMVTYSANSWD

KSKYRKFHLKHKNDYDQMREVLMRRALDFDKIPPPDLWLIDGGKALLDLAKEIIVSSGANVDILAISKEK

IDAKAHRAKGGARDKIHSLKGEFSLSINDKKLQFLQKLRDEAHRFAISFHQNTKKKQDLNSSKLVNLGLS

SGVIQKLLAYYGNFESIYKADFKDLAMLVGKKVAQKIKEN

>ABV52787.1 hypothetical protein C8J\_1188 [Campylobacter jejuni subsp. jejuni 81116]

MILAGIIFIFNLILAYLSIDISKLDSVAEQLKIGMFSSIFVLSLTLFIFAFRQNRNINKIYQKIFYMQND

FLNFQKKIDVDSVLDLLKEKFETTGQNLTKTSHEKDRYLHLLEENLYQLGNISNAMRCLNEGYNKEINSL

ILNALNSQKDQIRLELNEALEHHKSIIGTSHGKVLQFEASVAIVNNDELENFLLANLLSYFGIESTCFKN

LSFDVNDFHLIFIKDKILNENVKKNYDFIVMGRHKNTHYEYFLTLPFEKKDLENILQNKLDKVCTLKFKT

PYQNNVLLFKQNDFDATLFFNIIEKQCDKNVCINSFSQLKQELSKETYRLILLDYELIKFDLEQMRNLLS

AYKKQHPQSHIIFFSKEKVGDFDCVSEVLSDVSRNDLITLLRKYLPKA

>ABV52786.1 radical SAM domain protein [Campylobacter jejuni subsp. jejuni 81116]

MKILFGPVSSRRFGRSLGIDLSPSKKQCNFDCVYCELDPKKAQEKQDEIISIDKIISEVKVVLEKNVEFD

FLTLTANGEPSLYPHLNELILSLRSIAKDKKLLILSNGTAVLDEDKFNALLKLDVVKFSLDSAVAKTFYR

IDRALKNIDLEKMIEKMADFRARFNGDLIMEILVVKDLNDNEEEFEALNQALKKIMPLRVDLSTIDRPPA

YAVKKVSEEKLLELSKLIDSTPVLLAKRHYEGEKLSFNEEELLKMLHLRSQSEIDIEVKFDEQSKTLLNQ

LIKEKKVKILDLAGVKFYKA

>ABV52785.1 uroporphyrinogen decarboxylase [Campylobacter jejuni subsp. jejuni 81116]

MIFIDACFKKPTPYTPIWMMRQAGRYLPEYMEVRKQAGDFLSLCKDYKKASEVSLQPIDILDVDAAIIFS

DILVVPLEMGMNLRFEKGEGPVFDNPISTLEDLEKLDDQNAHKKLNYVYDALKLTREKLSQNKALIGFCG

SPWTIATYMIEGSGSKNYAKCKKMLYQNPELLHKILNKLTQVLKLYLEEQIKAGANAIQIFDSWASALEY

DKFFEFSFNYMLEISNFIKSKYPNIPVILFPKGISGYLDRIDGNFDVFGVDWSTPLDLARDKLSHKYTLQ

GNMEPCRLYDKNAIKEGVEKILKTMQNKAHIFNLGHGILPDIPVENAKYFIKLVQESSAK

>ABV52784.1 hypothetical protein C8J\_1185 [Campylobacter jejuni subsp. jejuni 81116]

MVVDNTQKTSNAIFSTTTKVKEKNTSADEFQATLNEVKNKEEKEEEKTSSSKFTNEDIDLGAVREDFRSY

AWQKMREDQYKKNEETLLNKLFATIDAGNATNNTKA

>ABV52783.1 putative transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MQNYKKALFALALSAFCMGVTEFVMAGVLIDVEAYFSVDAKTAGYLTTLYAIGVVIGAPLITIPLSHFHR

HTQLLINLGIFALANFIIFFSQNFYLTAFARFIAGTQHGVFFVIATLAVSAIVPNDKKSSALAIMVTGLT

VALVTGVPLGTFIGHYFGFKFIFLLIFIITSLAFFGVWHMMPKNLHPSPTSLKNLIPAFSHQNLLKTYTI

TICSCGAQFVLYTYLQKLLVEISGFKVQDTAYILLLYGICAICGNLWGGKIVDKKGAIFSLRLILSIQVL

VFLSVFLTMHSKILIIFSVALIGFFAFSTIPALKMLSIAKAKRHTYKVIDSTVSVNEAAFNVGIALASFL

GGIVLAGLGIEFNALFSALFVSPALIFALLFAKDKLNYKKFQRKSLKKI

>ABV52782.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIIFLFGLSLASLEALSFDELIYKDEVKPSFDCSKVKDDGKSDDELMICNEIGVRNEFENKKLALADN

IYSSLYQNISKKADKKMKKDFKAISKKMLKERKICIKNMQNTKAGENPILPLLNASDCMQEAYIKALLEL

MQRAKKDTKTKEVLEQIFKNKVDKYENLLTQSLNTNKDLQDFIDSLAKEDLIDSRAKFKF

>ABV52781.1 4-hydroxythreonine-4-phosphate dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MKKLAISIGDINGIGLEILVRSHEELSKICTPFYFIHENLLNKASKLLNLKLFNAKIVAFKDDKDYEFNF

IKKENSLEIYSFCLPLGFKVDENFEIKAGEIDAKSGLYGFLSFKAASYFVYEKHAHALLTLPIHKKAWED

AGLKYKGHTDALRDFFKKNAIMMLGCKELFVGLFSEHIPLAKVSKKITFKNLSIFLKDFYKETHFKKIGL

LGFNPHAGDYGVIGGEEEKIMEKAIAFVNAFLHSKKDEKFFKKALKDENLQKELLLNFKGKGVYLPYPLV

ADTAFTKAGLKNCNRLVAMYHDLALAPLKALYFDKSINVSLNLPIIRVSVDHGTAFDKAYKNAKINTKSY

FEAAKFAINLSLKT

>ABV52780.1 putative pyridoxal phosphate biosynthetic protein [Campylobacter jejuni subsp. jejuni 81116]

MLLGVNIDHIAVLRQARMVNDPDLLEAAFIAAKHGDQITLHVREDRRHAQDFDLENIIKFCKSPINLECA

LNDEILNLALKLKPHRVTLVPEKREELTTEGGLCLNHTKLKQSIEKLQNANIEVSLFINPSLEDIEKSKN

LKAQFIELHTGHYANLHNALFSNISHTAFALKELGQDKKNLQAQFEKELQNLELCAKKGTELGLKVAAGH

GLNYKNVKPVVKIKEICELNIGQSIVARSVFTGLQNAILEMKELIKR

>ABV52779.1 possible phosphatase [Campylobacter jejuni subsp. jejuni 81116]

MLGIDLGSNTLRAVQMDEKLNKLKEYEFVIGAAKNLNQSGEISKEAIQRLKNALSILAKEQDLSKARAVA

TAAFRKASNTNEIFAHLKEEFGIDFKLIDAKSEAKISVLGMQSGLRRLKIWGEFAYCDLGGASCELSFRK

SFKSFDFGIISFYEKNCHSYYKSCISYKKLIKKYPKFIINIKDKKLKIHFLIANPYLKHLAFMAFDEVAM

IKKELRSLGVKTVVLNSGVPTTLSALKQNINYEKYEATRVNGKKLCHKDFLNYAIKLFHMEEKKAIKEVG

MMRKNYLSAGCLLFYALFDKHKLLVIDEGLREGVCLASMKNIKF

>ABV52778.1 hypothetical protein C8J\_1179 [Campylobacter jejuni subsp. jejuni 81116]

MKFSDFFHAWLHESYYKNAVSIGKNGDFFTAVSVGNLFSTLLAKHFLNLIDKKILQPPLELVEIGANEGY

LSRDFLAALLELRPEIFSQISFFVIEPHEKLKNLQKKTLEGVEFTHKNSLKECHFKNAFFFCNELFDSFT

CELIDHDKMAFVENFKLIFKNMDENLITKCKALNLTKGELSLELENFFKDLDQACERFIFAGFDYGTLNP

QNFSLRIYQKHEVFSPFEVSLKDFFGKSDLTYNVNFTHLQKLIKEYDFKPLAFKKQSLALMDFGFEDLLE

YTKNKNIKTYESFLSQAKILFFNFDEKFHFFEFQKN

>ABV52777.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKALWILLSLTLWLFGAQNLELIKGQALFLELDKKNFLSLKNNDKNIPTFAHPKNQEKILAIFSLPYKNP

PQNTKLIAFYKDKKEEIFIKTLEGNYKSEKLQVENKKIFPPKTVQERIAKELKEANAIYSSYTPKALFNG

AFNIPLNSFITSDFGKARTFNEKVASYHSGTDFRAATGTPIYAANSGIVKIAKDRYFAGNSVVIDHGFGI

YSQYYHLSKINVKVGQKIKKGELIGLSGASGRVSGPHLHFGILAGGKQVDPLDFVSKFNAIFQ

>ABV52776.1 glycyl-tRNA synthetase beta chain [Campylobacter jejuni subsp. jejuni 81116]

MSELLIEIGTEELPAIPLLKELANIEKKWKNVLEEYRLVNDFKFYYTPRRLVFFHENFAEKQEDSFAEFI

GAPKNVAYKDGVLTPAGQSFLQKAGISENELTFKEIKGKEVLYHQKAIKGLQSQEILGEMIEKFLKSLSF

GKSMRWGANSFEFIRAIRSIACILNDELVNFQSYGVKSAKKTFIHRSVSYDLQDFNNAKEYFELLEKNYI

ILDPNKRKEKILEQFKLIESQKNIQIGEDEELLAEVVAITEYPNALLGSFEEEFLEIPGEVIITSMRENQ

RYFAVFNDKGLSNHFIVVSNAVCKDYSKIIHGNERVLRARLSDAMFFYQNDLQNGLKPEKLAKMTYLEGL

GTMQDKSLREIKIAEILCQMLHNDKIENISTALKYAKADLATQMVYEFTDLQGIMGSYYAQKMGLDYEIC

LAIKEQYLPNSEQAPLPSTEFSSIVALANKLDTLIGLFSIGKIPSGTKDPYALRRAANGIIKIALNLNKE

FDIQILLEKLSSHYKSFDMQILKDFIFERLYTFYTVNASFVKAVLSSQNTDLIHINQSVNALIELSKKDN

FNENFATFKRLANIATKNPHKVDESLFVQEAESKLYKAFQEKTKANSLQEKLENLFALKPFIDEFFNQVM

INAEDEKLKNNRQALVYEIYAEFLKIADLKELSL

>ABV52775.1 putative hydrolase [Campylobacter jejuni subsp. jejuni 81116]

MINVFFDMDGTLIDSANAISCTVNEIRQDLNLAPLSREIIMQTINTPNIDWAKELYNIENFHHSSFKEGY

EKYFVKHYEQSVVLFEGVKELLEFLKSKNCFLAIATNAPQSSLSNILKKHQIIPYFDKILGVNLGIEPKP

HPMMLELLKSEAPYKTSVFIGDSQKDKECAKNANLPYFHAKWYQKDLKENEFSNASELKGFLEKYL

>ABV52774.1 hypothetical protein C8J\_1175 [Campylobacter jejuni subsp. jejuni 81116]

MTKNEEKALRVKYLRNLEKFFNGAISALKKEDFDKTKFEERMLKNAKFFEKNPAVNLNSTYAKNLEFFVN

ACLDFSKEKSELLNLANALDKQKKQGEKKEKHKNYLKDYE

>ABV52773.1 putative glutathione-regulated potassium-efflux system protein [Campylobacter jejuni subsp. jejuni 81116]

MDNFLEIFLITVAIAIVLNVIFKKFEIPTIIGYIAAGEIISEIYHLSGKGEITHIAEFGIVFLMFTIGLE

FSFKHLMAMKQEVFLNGSLQMLTCGFVFMLLAIGILGLGDKSATIVGFALALSSTAVVLKILNDNGDINE

QYGRKALGILLFQDIAVIPLLLLVDIFSSNNQNIEKLLFTSLISALILITLLFFIGKYLVDRIFRLIIHT

SSQEIFISTVLFMVIGASFLANYFGFSYSLGAFIAGALIAETKYKHKIEADLIPFRDLLLGLFFITVGMQ

IQLDVVAQNWFLIIVLTLLVMALKFGIVFGFLFLYTKKRVALKTAFAIAQIGEFALAIFSLLQAKNMLDI

KTSQILIVVSILTMIITPFILNNIRKITNVVEDIALNTNAVQNIDSNIKLKNHLVVFGYGRLGQEVVQKI

KNTGVPYLVLESDLNLVELGVSRGENVVFANAAQEETLKIANIEECAVAIITVTNEAKLEILCQVLANYP

KPIDTIIHVNGTLKKMLFSSIDENIRIIRSEKVIARNLVQEALECRIHKNT

>ABV52772.1 putative heat shock transcriptional regulator [Campylobacter jejuni subsp. jejuni 81116]

MEQHYDEPVYLISVVAKVLSIHPQTLRQYEREGLIEPSRTDGKIRLYSQRDIDRIKLILRLTRDMGINLA

GVDVILKLKNQLHEFENLIDELRLELSKQQDKEAASKAVVKHKNSFDLIFYEKK

>ABV52771.1 putative curved-DNA binding protein [Campylobacter jejuni subsp. jejuni 81116]

MNSLYETLGVSKNASADEIKKAYRRLARKYHPDINKEKGAEEKFKEINAAYEILSDEKKRAQYDQYGDSM

FGGQSFHDFSRNTGGVNLDDILKDLFGGGFGGRSRGGFNGFSSKGFSSGFGGFGGFEEENLDSNLELHIP

FEKAVKGGEHSFNFQGETIKFKIPHGIKEGEKLRIRSKGKQSRNGARGDLIIIVKIEESPIYTREDDDLY

QKVDISLKTALFGGKINIKTLKEGKEEATINITPNSKNNQKIRLKGYGVQNRKSDIYGDMYLILNVVLPN

LDTLDEKFIELLKEKLP

>ABV52770.1 protease DO [Campylobacter jejuni subsp. jejuni 81116]

MKKIFLSLSLASALFAASINFNESTATANRVNPAAGNAVLSYHDSIKDAKKSVVNISTSKTITRANRPSP

LDDFFNDPYFKQFFDFDFPQRKGKNDKEVVSSLGSGVIISKDGYIVTNNHVVDDADTITVNLPGSDIEYK

AKLIGKDPKTDLAVIKIEANNLSAITFTNSDDLMEGDVVFALGNPFGVGFSVTSGIISALNKDNIGLNQY

ENFIQTDASINPGNSGGALVDSRGYLVGINSAILSRGGGNNGIGFAIPSNMVKDIAKKLIEKGKIDRGFL

GVTILALQGDTKKAYKNQEGALITDVQKGSSADEAGLKRGDLVTKVNDKVIKSPIDLKNYIGTLEIGQKI

SLSYERDGENKQASFILKGEKENPKGVQSDLIDGLSLRNLDPRLKDRLQIPKDVNGVLVDSVKEKSKGKN

SGFQEGDIIIGVGQSEIKNLKDLEQALKQVNKKEFTKVWVYRNGFATLLVLK

>ABV52769.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni 81116]

MTNILMIEDDLELAEITAEYLEKFDMKVDIAHEPYIGLSKLALKEYQLIILDLSLPGLDGLEVCEEIRKK

YDTPIIVSSARHDITDKVNALELGADDYLPKPYNPKELQARIKSHLRRISNTKSAIAKSVKDLVYDQYKH

IITMKGQELTLTNAEFDILSYLIKKEGGVVSREELVYNCSSISEDSSNKSIDVIISRIRQKMGDDPKTPK

YIHSIRGIGYKLTQ

>ABV52768.1 putative two-component sensor [Campylobacter jejuni subsp. jejuni 81116]

MNKSSIFYTITFIFIFAGVSVILGFLWLIEYDQQNYTRELNTKYSLIANARLLNFAGVISEKEFEEQTKN

YNKMDEITEAKQIRKILFRGDVLARVEVNNGLIEIISYNRQVYLNIIYDGKVYLYKDQDYQTYRYFIIKA

IAVAVICILVLLYIYIFKKLKPLKRLKKQIDKFAQGKLNDIEDVSTGVDEISQVSEAFYQAIVQIRKLNQ

SRQFFLRNIMHELKTPITKGLLTLEMIEDNKYKERLNGVFTRLEILINEFAAIEQITSGAAFINRKKYNI

LDVLDEAKEIAMRDDSNIRIFMEESFFVNVDFKLFTTAIKNMIDNGIKHSEDGFVQIDIIDDYICFKNRG

PELNNTLEYYTQAFTQGSKQKSSFGLGLYIVNTILETHGMKLDYLYEDGVNLFYFRNLKSVIVKE

>ABV52767.1 hypothetical protein C8J\_1168 [Campylobacter jejuni subsp. jejuni 81116]

MKRNVKTYSFRMPLELKERLDNLSKNLSKPKSAIVKEAIEAYLNEVEDFSFAVNALEELKDGDYQKASKK

IDKIVKNLQEDSNDNELGDFDFAIEALEELKDGDYQKASKKIDKIVKNLKQTK

>ABV52766.1 non-heme iron protein, hemerythrin family [Campylobacter jejuni subsp. jejuni 81116]

MLPKWDNSYSVHNAKIDEQHKKLFELAAKVEVVSDRSVSKNEVKELLAEFFNYMKDHFNDEEKYMQLIGY

PNLEEHRKIHKEIIQTMINLIKDIKSTNDLKEKLYIVAKKWLLEHILYEDMKVEKWRSSSLSTDDGGDVS

FEAAEDEDNEHPQFYLYTCNCPGKIHDVPYSIHQKIELQGHKFTCKTCKQAIKFYKKHS

>ABV52765.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni 81116]

MAAKILLLEDDLSLSEIIEEFLNDEGYEVFLCDNAQEALDMAYERYFDLWILDVKVPLGDGFSLLKELRK

SGKQTPAIFMTSLNTTNDLKQGFDAGCDDYIKKPFELAELSIRVKALLKRAFSHKNEDFEDLGDGFRFEF

TTQILYHNNKALTLPSKEIKLLSLLLKNKNNFLSTERIFEELWDYDEEPSELSLRAYVKNLRKILGKEKI

INQRGRGYCYG

>ABV52764.1 sensor histidine kinase [Campylobacter jejuni subsp. jejuni 81116]

MAKKVIRQILLIYLTTTGIFLTIFFALWYQKLYEELVVLKGATLRENHRNIVISILNSRFTPIDISAKNI

AQSTALKFAIFDAKKIVFSNIDFDLRKAKIELKGRGICDNKVFFLAPMSADHYFLRHASNEEVNTNDGLQ

ILIQGEDVSKDLFWIRTKVFGFAIMAFCILGLISYILVKIALKPLEDKISTLNRFIKDSTHELNTPLSVI

LMSIEQLEHQNLGDNAKFTRIKLAAKSLSQVYSDLVFYNFPNTLETEKQKFDLRILLEERLEYFKVFFEQ

KKITLKLDLNQANIFAPKSQISKLIDNLISNAIKYNKKGGVISIILKANFLSIADTGCGISKSNLNHIFD

RYTRFNTDQGGFGIGLSLVKKVCDDNDIKIICESVENQGSVFKLNW

>ABV52763.1 co-chaperonin GroEL [Campylobacter jejuni subsp. jejuni 81116]

MAKEIIFSDEARNKLYEGVKKLNDAVKVTMGPRGRNVLIQKSFGAPSITKDGVSVAKEVELKDSLENMGA

SLVREVASKTADQAGDGTTTATVLAHAIFKEGLRNITAGANPIEVKRGMDKACEAIVAELKKLSREVKDK

KEIAQVATISANSDEKIGNLIADAMEKVGKDGVITVEEAKSINDELNVVEGMQFDRGYLSPYFITNAEKM

TVELSSPYILLFDKKIANLKDLLPVLEQIQKTGKPLLIIAEDIEGEALATLVVNKLRGVLNISAVKAPGF

GDRRKAMLEDIAILTGGEVISEELGRTLESATIQDLGQASSVIIDKDNTTIVNGAGEKANIDARVNQIKA

QIAETTSDYDREKLQERLAKLSGGVAVIKVGAATETEMKEKKDRVDDALSATKAAVEEGIVIGGGAALIK

AKAKIKLDLQGDEAIGAAIVERALRAPLRQIAENAGFDAGVVVNSVENAKDENTGFDAAKGEYVNMLESG

IIDPVKVERVALLNAVSVASMLLTTEATISEIKEDKPAMPDMSGMGGMGGMGGMM

>ABV52762.1 cpn10; 10 kDa chaperonin [Campylobacter jejuni subsp. jejuni 81116]

MNFQPLGKRVLVKRVEETKTTASGIIIPDNAKEKPLMGEVVAVSKEITDIANGDKIVFAKYGGTEIKLDN

NEYLVLNLDDILGILK

>ABV52761.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIFYGVIAFVVVLLIAIYTILFTSFGNNIVANIAQKKIKESAGLDVNITHFNLRFSSLELQANIANMA

DFNLKGALSPFKLGFDLDYLISLNQNYAKNLGLNLNQNLSFVGKIQGKASDFTLDGKGYLLGSNVLLNAR

MYNYSPIALNLDAQNLKIEEILHLLSYPSYAKGFLNAQAKISAQNLKPDGNIIIKLDTNYINYEAIKKDF

SLDLPLNSNPKAEILANVKEDKIYAVSKIYNDYLNLQTQKTLYDISKNALSTDFNLSIPSLVKLETLTKT

RLNGNLGVIGQTSVVNNALSSLNAQVIGLGGEVKASLKNNKIFADINEASLEKLLALAGYGALVSGNLNA

KLLNADLDFSNFDLEAKINNAKLNTNELKKIAKIELPNTIFSFDAKANAKNSNIAYNALLASNLLNIKKL

QGSYNLKNSELNTDLNAFIDDLSQFSAIAGQKLQGKADLAAKAHIIGTQIQNLNANANLADGVIKADSNG

KKLDLNIDKLDLSKLFVIAGMPNYASGIVNAKINLDNIDFNNLNGKANLEAKGILNATTLSKILNKNFPN

NTSYDLNTKINFKNNIAQFDSVLNSSLADLTKLQGSFDISKMLLNSDFNLKINDFSKLGFLLDRKLKGKA

EFNGKVGFDKSLNFVVNSPNLFEGRLQSTLKDNLLLADLNGVDLSSLAQGLDFMDVYQGKADVKANYNLL

SEEGEVNLDMKEGKLKPNLITNALKILTLKDITNDVYRTANAKALIKKENIKLDLNMQADRSYILVQSGA

LNSKSGALNLPFDIKLDRANFKGSITGTTENPKVNLNAGSVLNSIKNVVGGGVSDGAKSTGDKVDKAVNK

LLNKIF

>ABV52760.1 riboflavin synthase alpha chain [Campylobacter jejuni subsp. jejuni 81116]

MFNGLIREIAKVQSYQNNTLSLKAKYRPNLGDSIAINGACLSVTKLYEGGFEVELSRESRTHIAIENLKD

KVHIEPALRYGDRIDGHLMQGHIDFIGTLEKIQKDENGVDFYISLPKEAMKFMAEKGSIAVDGVSLTINE

ILKNGIRLTIIPITFKETLFKDYQVGRKINIESDLLARYIYAQLQGKNKGLSWEEVERISYLY

>ABV52759.1 hypothetical protein C8J\_1160 [Campylobacter jejuni subsp. jejuni 81116]

MGRSRKNFLSLLENDKVVIFCAFDKDYNVFRAKVYSENLFYHLGFKDIKKCVFMDQIHSHKVIIYEKNLK

NLSCDGLISKEKNIALCVLSADCLPLILYHESGIIAALHSGRKGSFENILKECVDQITMQNSHLDKNKFH

LFILPGICAKNYEIDGEILEFAKKEFKEFVQDDKLDLKALVKFQAQNLGIENIKDCGICSFDDESFFSYR

RDKTPKRFVSVVYLKD

>ABV52758.1 hypothetical protein C8J\_1159 [Campylobacter jejuni subsp. jejuni 81116]

MYERKDLRVLKIIQKAREFGDGDLLNEALVKQLIDADFCEINEKEKEELATLLNSLINAKDKALLSN

>ABV52757.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKLLLLFIFVVQSFAALSVEELTWDNGDTLLKFLQRNSIPMSLYYGLDREDQELASDIAYKIKYQVLKD

ENNNIEQVLIPISDDLQIHIYKDKDGQYTLAFTPVSYQKEDRILHLTIKSSAYQDVYEESGSSTLARAMV

RAFRGSINFRNIQKGDEVTLYYEQKRRMGKLWGDINIKMAMVEINKSAREVFSYNDIFYDRDGKELESFL

LTKPVNYTRISSPFTTARYHPILKRYRAHLGIDYAAPTGTPVKSAGKGVVTFIGTKGGYGNVIQIKHDSG

YMTLYAHLSRFAKIKNGQKVNQGQVIAYVGSTGMSTGPHLHFGVYLNNKAINPASVVKIAKSELSGKAKE

NFKHIIAGYEQVVKEALASNQPNPPKEEDFENYIEF

>ABV52756.1 hypothetical protein C8J\_1157 [Campylobacter jejuni subsp. jejuni 81116]

MFKTIVCFLALNLSLFAVGFDLKPIKSELVKVDDIYGYIKDSDDIKLYSSGVVVQHFSNSQSIIARASVI

DKKNGLAKLEFSVFSALKQDALPLPNVLPKVGDEVVLNFLYDRGLVIAPDEQTYNELVREFPQIYFTHID

IFGAQLIRTATLSPKRSDFRQFCDDNAVGILVVALENQAEVVDCQDFNKLYEVPISKPTSVQVPFYSRIG

GYKSNFFDFNSQEIGNYYRYYDALINLPKVQ

>ABV52755.1 putative glycolate oxidase subunit D [Campylobacter jejuni subsp. jejuni 81116]

MKKEFEQYFKRFLGEENAYFDEIHKRAYSYDATKKHYLPDGVLFPRNEEDIAQILKFCNENNIIVIPRGS

GSGFTGGALAVNGGVVLAFEKHMNKILEIDLENLVAVVQPGVINIHLQKEVAKYGLFYPPDPASMEYSSL

GGNVSENAGGMRAAKYGITKDYVMALRAVLSSGEIIRAGKRTIKDVAGYNLAGILIASEGSLAVLSELTL

KLIPLPKFKKTAFAIFPSVKSAMNAVYKSLASGVNPVSMEFLDNLSIRAVESKFNKGLPIEAGAILIADV

DGNVREAIDEDLRNLEHYFLEAGASEFKIAKDEQETADIWFARRNCSQSIAMYGTLKLNEDITVPRSKLP

ALLEGIDEISKKYGFKIPCFGHTGDGNVHTNVMVPDKNDKEQVKKGYEAVEEIFKLTVKLGGTLSGEHGI

GLSKAPFMNLAFSEAEMNLMRNIKKAFDPNNILNPFKMGL

>ABV52754.1 putative ribonuclease BN [Campylobacter jejuni subsp. jejuni 81116]

MKNFFTILLNLRDKEILNYAAALSFYTVLSLIPILFVCFSVFTQISSFKAYYEKAKQVIFAFLIPTQQDV

VATYIDTFLKNSVNLGIVGLIAMAFTSLAFFSGYDFVINRITKNEPKGLWQSISSYWTLLTLVPLGLGLS

FYISGFIQQTLDDYKIGFNFFEILPFVIIWGLFFISYSSSVHKGTLKSLALVSFGAGAIWYIGKNLFVYY

VVYNKTYASVYGSFSTILFFFIWIYISWIIYLFGLKLYYFLNYNHNEGNKIRKNTKKS

>ABV52753.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MSLWNSFFYSFKEFHYLFLSVVIIFIFNILLEYNNFLKFKNQKHYFINNALLTHQYTKYNKKNKKYWVLK

LQTENFTFYTTSFKDLNLSKNQLLSLRIITHNINFKDYLSKSFYVPSYDFEKLKEKEYNPIISYFLNQHT

NEKIKEFYGALFFALPISLELRNDVNYYGIAHLIAISGYHIGLLFSLIFFILAPIYSFFQKIYFPYRNLR

LDLSILIFTLLLAYACLIGFIPSFVRSLIMAFWVFYLLCKNIKIINFFTLFCSILLCISLYPRLLFSIGF

LFSILGVFYIFLYMHHFANKFNNLINIILLNIWTFFAMVLPVLYFFPLISYQQILGIILSGIFVIFYPLV

LFLHLINYGDLLNFILDEFFKFKIYGTNIYIPFWIFISYLIASLISVRFKYLAFLCIFANFIPFIMIVI

>ABV52752.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MQDMIDTLIKYGYIVLFFYSLGGGMVGILAAGVLSSQGKMDLSFCIALAFIANTIGSTLLFILGKYYKKD

IMPYFKKHRRKLALAMMKTKQHGIILLVTQKFIYGLKTFIPIAAGMAKYNFIKFFIINTLASLAWAIVLG

FAAYTFGYVIEAIFDKLSLYPYAAPLFLLFLAGIIWLYLSKFSKK

>ABV52751.1 hypothetical protein C8J\_1152 [Campylobacter jejuni subsp. jejuni 81116]

MIESLIALIAAIVGLGIGYLVAKKINDAKYEIFVEQAKAKAKAIEYEAELILKDAKNSILNAELEVKKKY

EEKTHKIQKDFNQKFDDLSKKEQKLQQEEEKLKEDKEYLCKSQKHIQDLQSDVDKLKNKYQEKLDDVLKI

LEHSTGLTQNEAKEIILKKVEENSREQIAHIVRKYEEEAKNEAKRKANFIIAQATSRFAGEFAAERLINV

INIKNDELKGRIIGKEGRNVKTLEMVLGVDIIIDDTPGAIIVSCFNLYRRAIATKVIELLVEDGRIQPAR

IEEIHEKVCKEFDSAILEEGETIVMDLGLNKIHPEIVKLIGKLKYRASYGQNALAHSLEVAHLAGIIAAE

CGGDENLARRAGILHDIGKALTHDFEGSHVDLGAELCKRYKEHPVVINAIYAHHGHEEATSIESAAVCAA

DTLSAARPGARREVLEAFLKRVSELEDIAKSKEGIKNAYAINAGREIRVIANAQLVNDDESVLLAKEIAA

EIQEKMQYPGEIKVNVIRELRAVEYAK

>ABV52750.1 hypothetical protein C8J\_1151 [Campylobacter jejuni subsp. jejuni 81116]

MEKTDFRALQKIRLFKHSKLNFKQDYKIFKECLKIIKLFKAKNILIFIPLHYEPNLIKFRHILNKNYKLF

VPFMQDKSLKIVKLRLPFIKKRFGVLEPIDSFFKAKIDLAIVPVIGVDKNLKRIGHGQGFYDRFFENLNY

KPHIIFVQSIDALSQNNLTQKHDISGKLYINPYKKYYKKERKNDRITYRTYSRYSRTRYRIFSCKKNQ

>ABV52749.1 lipoprotein, putative [Campylobacter jejuni subsp. jejuni 81116]

MKIKKILLLVAISCLFVACGNDKEKQQNDVNLSTEASINQSDDMNFKLNLIDGGSISVKKENAVLNFNDE

DKATLFVFFTTWCTPCIAEIPHLNKLQEKYNNDFNIVGVLLEDKSNDEIQKFIEQHKISYKVANGENNYL

LAKALGGVNGIPTMFLYNKHSKLINQYLGLIPEEMLEIDIQKAIL

>ABV52748.1 putative signal recognition particle protein [Campylobacter jejuni subsp. jejuni 81116]

MFNFFKKGLAKTLENIVGVKGENKKITKDLLEEILLEADVSYEIVEEIIYYLPPQNEVKKEDLKRVMGSY

FLYEKKETNQEKPFVELILGVNGAGKTTSIAKLAYLYKNQNQKVILGACDTFRAGAIEQLKLWAQKVDVD

IVLTAQGHDPSAVAFDTISKAKAKDFDRVIIDTAGRLQNQKNLAHELEKIVRISNKALEGAPHRKILVLD

GTQGNAGILQAKAFNELVKLDGVIITKLDGTAKGGALFSIARELELPIFYVGVGEQMTDLQEFNASAYLD

TLLDPIFE

>ABV52747.1 DNA repair protein [Campylobacter jejuni subsp. jejuni 81116]

MAKNKALFECQACGNQQSKWLGKCPDCGAWDSFVELKAEQIKVLKELAQVSMKTSEAVCIEDVELEHFTR

YSTDDNELDLVLGGGLVEGSLVLIGGSPGVGKSTLLLKIASNLAKQGKKVLYVSGEESKAQIKLRADRLE

ANTPNLFLLTELCLENILEELHKKDYSILIIDSIQTLYSNKITSVAGSITQVREITFELMRVSKAYNIST

FIIGHITKEGAIAGPRVLEHMVDVVLYFEGDATKEIRLLRGFKNRFGGTNEVGIFEMTAKGLISAKDLAN

RFFTRGKAISGSALGVVMEGSRALVLEVQALVCESSYPKRSATGYEKNRLDMLLALLERKLEIPLGHYDV

FVNISGGVKVSETAADLAVVAAIISSFKNRPLSKDSIFIGELSLNGEIREVFSLDTRLKEAKMQKFKNAI

VPSKPLEDIGLKCFVAKELSQVLEWM

>ABV52746.1 ATP synthase F0 sector A subunit [Campylobacter jejuni subsp. jejuni 81116]

MKDLFLFSSLLDASHTFSYFFHIGLVALIAVIVAMMATRSMQLVPRGMQNLGEAFLEGVLSMGRDTMGSE

KGARKYLPLVATLGIIVFFSNIIGIIPGFHAPTASLNLTLSLAIIVFVYYHFEGIRAQGFVKYFAHFMGP

IKLLAPLMFPIEIVSHLSRVVSLSFRLFGNIKGDDLFLMVILALVPYIAPLPAYVLLTFMAFLQAFIFMI

LTYVYLAGATVVEEGH

>ABV52745.1 5,10-methylenetetrahydrofolate reductase [Campylobacter jejuni subsp. jejuni 81116]

MCSFSFEVFPPRKDENIKNLHAILDDLGQLSPNFISVTFGAGGSINSQNTLEVASLIQEEYQIPSIVHLP

CIHSSKEKITQILQKCKEKNLNQILALRGDICENLEKSKDFSYASDLISFIKKQEYFEIYAACYPEKHNE

SKNFIEDIHHLKTKVNAGTDKLITQLFYDNEDFYTFKQNCALAGIDIPIYAGIMPITNKRQVLKISQLCG

AKIPPKFVKILEKYENNALALEDAGIAYACDQIVDLITSGVDGIHLYTMNKSKAAIKIYEAVKHLLKEEL

HA

>ABV52744.1 5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKNSIISYPRIGANRELKFAIEKYFKNQSSKEELLKSAKDLRIRHWQEIQKAGIDFIPSNDFSLYDNVLD

AAVLFNIVHTKYKNLNLDALDEYFAQSRGYQGENGDVTALAMKKWFNTNYHYLVPECDNADIIALTGDKI

FKEYLEAKELGIESKPVLIGIFTLFKLIAFKDEKTQKLAKEKLLNAYIELFDKLNELKVTWLELDEPYLV

YDLSKEDIALFEEFYQELLNHKKDLKILLQSYFGDLRDIYPKLLESKFDALGLDFIEGKQSLALIQKYGF

AKDKILFAGLINGKNIYANDYAKSLKLIKELQKYTQNIVLNTSCSLLHVPYSTEFESKLDSSYLKLFAFA

KEKLQELKDLKEILNSSEENPLFRANQELFKNIPERLDEKVKARLKALKKEDFTRTPSFKERALIQKEFL

KLPLLPTTTIGSFPQSADVRSNRLAFKQEKISAQNYTEFNQQKIKECIQIQEEIGLDVLVHGEFERNDMV

EYFGENLKGFLFTQNGWVQSYGTRCVKPPVIWGDVSRTKPITLAWSKFAQSLSQKIVKGMLTGPVTILNW

SFPREDISLKESTEQIALAIRDEVLDLENAGIKIIQIDEAALREKLPLRKSDWHSEYLDWAIPAFNLVHS

GVKAKTQIHTHMCYSEFSDILKEIDAMDADVISFEASRSNLSLLDTLKAIRFKTEVGPGVYDIHSPRVPS

VEELSLTIEKILNKLPKEQIWINPDCGLKTRAYEEVIASLKNLVTATQKIREQL

>ABV52743.1 lipoprotein, NlpA family [Campylobacter jejuni subsp. jejuni 81116]

MTLFTKAFCVATLFTSFAWANEELKVGSSITPHADILRFIKSALQKQGYDLKIYEFNDGVIPNVMVENGE

LDANYFQHEPYLKEFNQRQGTHLVKVASIHIEPMAVYSKKHKKFNPEEGQSISIPNNPTNESRALRIVAS

KGLIEVKDNELITPLDITKNPKKLKFVELKDAQLTRSLDDVDYSLINSNFAILAGLNPVKDGLYTESKYS

EYGNIIAVKEGNENLPKIKALVKALQSDEVKKFIEEKYQGALIPTF

>ABV52742.1 putative iron/ascorbate-dependent oxidoreductase [Campylobacter jejuni subsp. jejuni 81116]

MNLPILDLQAYEKDKSTFLKNLREIASKIGFFYLINTSIDKNLNEKLFKLGKEFFNLSRSSKELISMVHS

PQFRGYTSEGFEYTAGSKDYREQLDIGTERDALNWNLNSPLWQRLEGPNLWPSEIPELKKTFLTWHKQTK

KACLKLLKAFAQALDLPNNAFDKLYGENSYEHCKIIHYPKSSKNITQGVGSHKDGGLITFVFQEKQSGLE

AFIDGKWLSIPPLENSVVVNIGEFLELATNGYLKATIHRVNLSPKERFSIAYFLGVQLDKDIPIFKLNPE

LAKESKGMDTDPKIHF

>ABV52741.1 autoinducer-2 production protein LuxS [Campylobacter jejuni subsp. jejuni 81116]

MPLLDSFKVDHTKMPAPAVRLAKVMKTPKGDDISVFDLRFCIPNKDIMSEKGTHTLEHLFAGFMRDHLNS

NSVEIIDISPMGCRTGFYMSLIGTPDEKSVAKAWEEAMKDVLSVSDQSKIPELNIYQCGTCAMHSLDEAK

QIAQKVLNLGISIMNNKELKLENA

>ABV52740.1 aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, B subunit [Campylobacter jejuni subsp. jejuni 81116]

MFEVVIGLEVHTQLNTKTKIFCSCATSFGEAPNTNVCPTCLALPGALPVLNEEAVKKAIAFGKAVNATIN

KKSVFNRKNYFYPDLPKAYQISQFDIPIVEKGELFINVKGENKRIGITRAHLEEDAGKNIHENNFSKVDL

NRAGTPLLEIVSEPELRSSDEAVAYLKKLHSIIRFLDISDANMQEGSFRCDANVSIRPKGDTKLYTRVEI

KNLNSFRFIQKAIEYEVKRQSEAWEDGTYEQEVVQETRLFDTTNLVTRSMRGKEEAAEYRYFPDPDLLPV

LLKDEFLDIKIPELPDEKKARFIDELGIKESDAEVLISSLEMSRFFESLISQNLNSKLCVNWLNTELMGL

LKGELTIENSPVDAQKLGVLIKRIEDGTISAKAAKDVLAFVFENTSVEIDEAIEKLGLKQVSDDSAIEAV

IEQILNANADKVAEYKSGKDKLFGFFVGQTMKEGKGAFNPAKVNEILKTKLG

>ABV52739.1 glycerol-3-phosphate dehydrogenase NAD(P)-depenent [Campylobacter jejuni subsp. jejuni 81116]

MRIAVIGAGKWGSALHLALKENHNCFISSLHQRDLEDFVSIKEALECEYLVFALSSQGMRAWLKENFINK

GQKILIASKGIEDQSCQFLDEIFLDFVPKENFCVLSGPSFAAEVMQKLPTALMISGINQELCKKFASFFP

DFIKTYIDNDVRGAEICGAYKNVLAIASGISDGLKLGNNARAALISRGLIEMHRFGKFFGAKEETFLGLS

GAGDLFLTATSVLSRNYRVGLKLAQNQKLDSILVELNEVAEGVKTAYAIEKLAKMKGIYTPIVNEVVAIF

KGKSVQEATQSLLKQND

>ABV52738.1 dihydroorotase, putative [Campylobacter jejuni subsp. jejuni 81116]

MIIKNAKIYGDSLQDIEIKEGKITNIGSNLQGEEILDAKGMTLLPSFVDLCVSLKNDKFSLANLELLENE

CLKGGISSIVLRDCMDFDEESFALFLQNLAQRKMQIFSSVRVKDANGKLKNLATLLNKGACALELDSSLD

ANTLKVSSQYAFMKDSPIFVRCYDKDFDDNGVMNDCEMSFELGLIGMSKIAETSQIAKMKELAKFYKNKV

IFDLLSLKDSLVLLDEKDLKLVSIHHLIKDDSACEDFNTAAKLMPPLRSKEDVLALREALKEGKISFLTS

LHSAKSISLKDLAFDEAAFGIHSVCEFISLCYTFLIKEGFLNWQELCRFTSKNPSEFLGLNSGVIEVGKE

ANLVLFDENEEIFAPKSSLYSEDKLFGKIKMHIIKGKNILEK

>ABV52737.1 possible phosphate permease [Campylobacter jejuni subsp. jejuni 81116]

MQKDNLIAFVIFIISTIAFVIWGFGYISQHQLILFILASIFGIFMAFNIGGNDVANSFGTSVGAKTVTIK

QALIIAAVFELSGAIFAGAEVTKTIRSGIVIFPNSLDPMLFVIIMLAALLSSGVWIFIATKKGLPVSTTH

SIVGGIVGASIMMGLLKFDGIQTLSMVKWSEILRIAISWIASPLLGGIVAYIIYSYIDKKILKPSEKLND

DLKNIKKERKKFKEEYFLNLKTKSQEEQIKELSAIALDEEEQENNFYRNKMKEFKDQEKDIDIYSILKTH

MPIIACIAAAIISAMFLFKGLNNVSTLDILQNFWIIGIIGTISYVVTFAIVKIVKKTELNKTTDRIFSWF

QIFTASSFAFSHGANDIANAIGPFAAILDVLKNGTINATSPVPFAALAMFGVALVVGLWFLGKEVITTVG

SKLATIRPTTGFSAELGASIVILLATQFGIPVSSTHILIGAILGIGVYNKNANWIMMKPIGLAWIITLPA

AGIMAALVFLGFKLSLGI

>ABV52736.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MRGIFYIIALFSLLNADELTEALAKNNNQNSWEHFDYENTKEAPKIQEENVDFKSTFDSLLSKTLENNNG

IDKTDGNLDFQNENAQVKNLSSLYEGENNSLLFQKELFVAQDNYNYSWGLINRYEKDDFLFGVNGFIDKQ

KEQKDTKSFGTEFGYSKFIKAYSNYYIPNEAEKNLQLGMSFVIPTYTAFAFDISKDNDKTNYQVSYSPYS

VFSLNLLRRDYSARETVDDTVVQVGFSFNFNESFLKQFRKKDNTLEEVNRYDFLQRTH

>ABV52735.1 putative C4-dicarboxylate transport protein [Campylobacter jejuni subsp. jejuni 81116]

METLSQTLAERKPPLYKRIIKSLGFWVIIGIIAGIVLGYIDKELAIASKPGVDYFIGALKVLIGPIIFVT

LVLGIISLESLKKVGSIGAKAVIYFEVVSTLALAIGIFMANVMQPGHGMNLDPSQLDTKSVQKYISQTTE

VSASSEIMHILKDAMPTDIITPFTEGKTIQVLVIAIITALIISLMRIEDKQAIQRVFEVAQNFVFKILQI

IMYFSPIAAFSAMAVLIAQYGIGSLINLAYLLLVMLISCLVFIFGILGLICYFAKVNIFKFMRFISREVL

IVFATSSSESALAPLMRKLEKAGLSKATVGLVLPTGYSFNLDCTNIYLAMSLIFLAQAFNVNLSLAHEIS

ILIVLMIASKGAVGVTGSGFIVLGSTLAALGDMEISEANATLAQVLPVTAIGILLGVDKFMSEMRAVGNL

CGNSVAALIVAIWDKQIDWEKFRYAMDNPEKFHNAGMN

>ABV52734.1 putative signal-transduction sensor protein [Campylobacter jejuni subsp. jejuni 81116]

MKEIVLSENALITSKTDLKGNIIYANNDFLKYAGYKVDELLYKSHNIVRHEDMPRTVFKCLWDYIQKGDE

IFAFVKNKAKDGNFYWVFANVSASFDTNGNIINYYSVRRAPNRKSLSIIEEVYKILLEKEQKSGINAGVS

ALMDIVSSYKMTYNELIFNLQENN

>ABV52733.1 putative MCP-domain signal transduction protein [Campylobacter jejuni subsp. jejuni 81116]

MVKNGLLLTIFLSVIGVLGVIFIHIFVGAIIFVLIAVLMIYLLRQHKDEQIMIDKLLVLCRELKEGNFDN

RIIYVKTKSKKLAEIADNLNNTIDGLEAYLREINTSISCSQKGEFYRKALPEGLKGIFAHNIEFINKALA

NIEVTARSTFKNALSRTLMDLSLGNQNKDMSQISSSLNQDISMMKNVYDTVDAITHTATENGSEVDSLQS

AMGSLMDVVNSSKETVQTFVANSQNITSVVEVIRDIADQTNLLALNAAIEAARAGEHGRGFAVVADEVRK

LAERTQRSTSEISIAIQTMQQDFVNIQSGSEQVFNIVSESEERINKFSQAFKRLEENSSALGVNFGSFAK

RLILSVVKIDHILYKSNIYLNLNGAQNFNLESVDPISNLCQDERAQGVINELSSETELNLAKEFIKDNAK

KAIEESNQDYIDQKAYDAIVNDIKSLEQRSAEILAKLKI

>ABV52732.1 putative signal-transduction sensor protein [Campylobacter jejuni subsp. jejuni 81116]

MSREIFLQEDSLITSKTDLKGKIVYANDDFLKYAGYTMGEVLNKPHNIVRHEEMPKTVFKYLWDYMKEGK

EIFAYVKNKTKDNNYYWVFANVTPSIDINNNIIGYYSVRRMPNKSAISTIESLYSDLLRVEQQQGLNKGV

EMLKNFCKDADKTYNELIFSLQEAK

>ABV52731.1 glucose inhibited division protein A [Campylobacter jejuni subsp. jejuni 81116]

MFDVIVIGGGHAGVEASAAAARMGKKTLLLTTLIEQIGAASCNPAIGGLAKGHLVKELDAMGGLMGEITD

EAGIQFRILNESKGVAVQGSRAQIDMDKYRIIARNKLLKLPNLEISQEQASVLIVENDEVKGVKTNLENT

YFAKKVILTTGTFLNGLIHVGENKLQAGRVGELASVNLGNYLQTLGLKMGRLKTGTCPRVDAKSIDFSVL

EIQDGDVNPKAFSFRSKNFNPTQLPCYIARTNTTTHEIIKNNFYRAPLFTGQIEGVGPRYCPSIEDKINR

FSDKESHHLFIEPQTIDATEYYINGFSTSLPYEVQIQMLRSVKGFEDAKITRFGYAIEYDYIEPTELKHT

LELKKIKNLYCAGQINGTTGYEEAAAQGFMAGINASLSIDMKEPLILRRDEAYIGVLIDDLVVKGTKEPY

RMFTSRAEFRLLLREENAILRLGKYGYDLGLLSEQDFTYIQNIANNLQKGLEFLLSKEFTPNNQNNAFLE

SLGEDKISSIVNLQKIVARASFDIEKLKKLDPMFETMDNYSLREILNEAKYYHYISMQKAQVEKMKNLSE

LKIPENFDFKSVSGLSNEVVEKLNHHKPPTIFAASQISGITPAALDILQIYIKMQKKKA

>ABV52730.1 putative arsenical pump membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MLAFFIFLSTLVLLFWRPWNLPIWVFSSLGAFFVFIFQLVDFKDAYFVFSLVWDSSLTLVGLIILSFSLE

ALGFFDFIASKILHFSREKNQEKIYISTKKLMLFLLIFVFFLSAFFANDGAILIITPIIIALFSTLKDCK

NHAFILSSFLLSLSFLCDASSNALVISNLTNIITANYFKIEFLEFAKNMFLPNFFVLLSTIVMVFVLYVR

VLPKRLEFKLVKKEQISSKLFFLCIVFLFLFVISFFIGEIFDIKISFFALLWAGIFWLIVLKIQGKKSIK

ILFEAPYGVLLFSFGLYMVVFALHKIGVSEILVKSYTFLMQDKSGIFGVALISAFGSSVFNNLPMVLIGD

LALKEYFENFSFDSLMIYAHLLGVNIGPKLTPIGSLATLLWLGVLARKGINISFWQYCKFGFLITLPVLV

FSLFALIV

>ABV52729.1 putative ubiquinol-cytochrome C reductase iron-sulfur subunit [Campylobacter jejuni subsp. jejuni 81116]

MATSESRRSFMGFAFGSVAAVGGVFSLVAMKKTWDPLPSVKAAGFTTVDLSGMQDGELRTIEWRKKPIFI

LKKDASMPKDEKRDVVVDNAAYTVVIGLCTHLGCIPAYQPSEQLFKCACHGGEFDTSGKNVFGPPPKPLE

IPPFKIDGTKLVLGEEGPEYKKMIAEA

>ABV52728.1 putative ubiquinol-cytochrome C reductase cytochrome B subunit [Campylobacter jejuni subsp. jejuni 81116]

MAQIRKANGLVDWLDQRLAVHKLLDVLMVKYWIPKQINFLWAMGVILTTLFAVLFITGLLLVMYYKPDTA

LAFDSVNKTIMQEVDYGWLWRHMHGVAASVVFLIIYIHMLTGIYYGSYKKGREMIWVSGMLLFVVFSAEA

FSGYMLPWGQMSYWAAQVITNLFGGIPFIGPELVIWIRGDYAVSDPTLTRFFMLHVCLLPIVIIAIIAFH

FYSLRIPHVNNEISEELDFDLEAEKYMAGDTKGSKVIPFWPGFLSKDFMYISFFMIFFFYLVCFKFEFAM

DPINFDPANALKTPAHIYPEWYFLWSYEVLRGFFFDIAGIKAFDIGLAAFGIAQVIFFLLPWLDRSDVVK

PAHERPLFFIWFWILLIDLIVLTVYGKLPPTGVNAWVGFYASIVFLLLLIVVLPVITIMERKGAKQ

>ABV52727.1 ubiquinol--cytochrome c reductase, cytochrome c1 subunit [Campylobacter jejuni subsp. jejuni 81116]

MREIKIFLVVVVFTALVYWGVEPYAHSVMKPHVAPANFDFAVEDTTFAKGIVEAKELALKDAQASGDAKR

IESANKELEKAKEELSKVETLWADVAKIDFAKGDAKKGKEFFENNCFACHGVKEDGITANITDSSMGVIP

PDLSAAGAIFDEKFLAALIMHPALALKVDHKFGDAFIMTAYNKDTSGESEEATNANIANVIAYLKDVSVK

FEANEDATIKKDVEAKYAKMENSAQKVALMEKDIKFAKDKATFIEACGRCHDMKYDSFFTPSNQNDLKTY

LGSVPPDLSMMIRSRGEQYLHDFINNTQKLLPGTAMPRVGLTEAAQAKVVSYIDQVGDSKKEERKTTGIY

VMIFFVILSIFAIGWKRSVWSKLH

>ABV52726.1 cyclopropane-fatty-acyl-phospholipid synthase, putative [Campylobacter jejuni subsp. jejuni 81116]

MLEKQMIKFILSKWNYGNFRIVFWDQEEFHVGNQSAKFSLIFKEKIPFLKLFSDTSLVFAKHYMESKLEI

EGDYDEIAKVLYYFSNKRFLKNTEDILSKIAQKQESKNIKSHYDIGNDFYKLWLDDTMSYSCAYFKEPNN

TLYEAQINKIEHTLKKLDLKEGEKLLDIGCGWGWLSIMAAQKYGVKVVGITISEEQCKKAKERVKELGLE

DKIEIRLQNYQDLEFENYFDKVVSVGMFEHVGKENLGLYFMKVKQVLKPGGSMLLHSILAMFEGKTNAWI

DKYIFPGGYLPSLREVVSAMSEWDFHLLLAESLRMHYAKTLDLWDENFNKVLDKVREKYDEEFIRMWDLY

LRSCASAFRVGSVDLFQFLITKEINNNLSLTKDYIYK

>ABV52725.1 30S ribosomal protein S2 [Campylobacter jejuni subsp. jejuni 81116]

MVSMRDLLECGVHFGHQTRRWNPKMKKFIFGERKGIYVIDLQKTLRYFRYTYNIVRDAAAEGKTILFVGT

KKQAGGAIKEYAEKCGMPYVNHRWLGGMMTNFGTIRQSIRKLEVIEKMEEDGSIKLLTKKEALMLTRKKE

KLLAYLGGIRYMKTQPDMIFVIDTVKEKIAVQEANRLRIPVVAPLDTNCDPDLVTYPIPGNDDAIRSVQL

FCQEMAEAINEGKALREQDGEALANEEKEITDEEKKEVLDEAMSEEDFGEEQE

>ABV52724.1 elongation factor EF-Ts [Campylobacter jejuni subsp. jejuni 81116]

MAEITAAMVKELRESTGAGMMDCKNALSETNGDFDKAVQLLREKGLGKAAKKADRLAAEGLVSVKVSDDF

TSATVSEINSETDFVAKNDQFIALTKDTTAHIQSNSLQSVEELHSSIINGVKFEEYLKSQIATIGENLVV

RRFATLKAGANGVVNGYIHTNGRVGVVIAAACDSAEVASKSRDLLRQICMHIAAMRPSYLSYEDLDMTFV

ENEYKALVAELEKENEERRRLKDPNKPEHKIPQFASRKQLSDAILKEAEEKIKEELKAQGKPEKIWDNII

PGKMNSFIADNSQLDSKLTLMGQFYVMDDKKTVEQVIAEKEKEFGGKIKIVEFICFEVGEGLEKKTEDFA

AEVAAQL

>ABV52723.1 putative ABC transporter ATP binding protein [Campylobacter jejuni subsp. jejuni 81116]

MELLRAENLSHSFDYPLFEGLNLALNTKDCIAIQGSSGCGKSTLLHIFSSLLIPKKGEVFFKGSSLYQID

ENERLKIRRYDFGIIFQTHYLFKGFSALENIELASVLSGQNLDEKILKRLGIDTLLHQKIGKLSGGQQQR

VSIARVLCKKPKIIFADEATGNLDFDNAKNVIELLISYVKENDAALFFVTHDNKLASFCDKTYTINANGI

C

>ABV52722.1 flagellar biosynthetic protein FliR [Campylobacter jejuni subsp. jejuni 81116]

MEFVNYLGDKNVVTFMLLLARMSGLIVFFPFFSHNSIPMVIKSTIVLFLTMYLYPLARLESLHLDSFFVL

QLISEVIFGMIAGLMLQIIFAIIMMAGEQIAFTMGFTMASILDPSSGTSMPITSQILNLLALMFFLAFDG

HHLMLLFLSHSLGYISLGGFYPHENLMHYLNMGMFNIFIIGFTMSFPILGISLLADVIFGLLMKTMPQFN

LLVIGYPIKIALGFVVLIAILLVMMQYFKNLILELFTHMQTLFFS

>ABV52721.1 hypothetical protein C8J\_1122 [Campylobacter jejuni subsp. jejuni 81116]

MKILLLNENPVVSRLVSLSAKKMSYDFEELNAYSENLGNYDVIVVDSDTPAPLKILKEKCDRLIFLAPRN

QNVDIDAQILQKPFLPTDFLNLLNNKDTNKHTSIDLPILSNDENPYADISLDLDNLNLDDLPDENSLDIN

SEGMEDLSFDDDAQDDNANKALETQNLEDENLEQETTKEQTQEDIQTDLDLTLEDGGSQKEDLSQEHTAL

DTEPSLDELDDKNDEDLEIKEDDKNEEIEKQELLNDSKANTLEMQEELNESQDDNANKALETQNLEDENL

EQETTKEQTQEDIQTDLDLTLEDGGSQKEDLSQEHTALDTEPSLDELDDKNDEDLEDNKELQANISDFDD

LPVVEEQEKEMDFDDIPEDAEFLGQAKDNEESEENLEEFSPVVEEDVQDEMDDFISNLSTQDQIKEELAQ

LDELDYGIDSDNSSKVLEDFKDEPILDDTELGTNEEEVVVPNLNISDFDALKESDIQEALGEEIVEKNEE

PIVSNATKDDNSEEIVNELSQSIAGAITSSIKDDTLKAALKGMNMNININISFKED

>ABV52720.1 guanylate kinase [Campylobacter jejuni subsp. jejuni 81116]

MQGFILLISGPSGAGKSTLLKKLFDEFEDELYFSISSTTRKPREGEKNGIHYHFISHEEFQKGIDGDHFL

EWAKVHENFYGTSLKHTQDALDNGKIVVFDIDVQGFKIARQKMADKIVSVFITTKNKDELKKRLIKRNTD

TIIQLEKRLQNASDEMKELSDYDYLIINDELKQSYEALRAILIAHKFRTKGQNLGQIQNIWNEGE

>ABV52719.1 putative sec-independent protein translocase protein [Campylobacter jejuni subsp. jejuni 81116]

MGGWSSPSHWLIILLIVVLLFGAKKIPELAKGLGKGIKTFKDEMNNDDEVAKNTQKIEENKNTTNNTSAD

ASIDKTKKA

>ABV52718.1 arginyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MKSIIFNEIKKILECDFTLENPKDKNLAHFATPLAFSLAKELKKSPMLIASDLASKFQNHDCFESVEAVN

GYLNFRISKTFLNELANQALANPNDFSKGEKKQESFLLEYVSANPTGPLHIGHARGAVFGDTLTRLARHL

GYKFDTEYYVNDAGNQIYLLGLSILLSVKENILHENVEYPEQYYKGEYIADLAKEAFEKFGKEFFSEENI

PSLADWAKDKMLILIKQNLEQAKIKIDSYVSERSYYDALNATLESLKEHKGIYEQEGKIWLASSQKGDEK

DRVIIREDGRGTYLAADIVYHKDKMSRGYGKCINIWGADHHGYIPRMKAAMEFLGFDSNNLEIILAQMVS

LLKDGEPYKMSKRAGNFILMSDVIDEIGSDALRYIFLSKKCDTHLEFDISDLQKEDSSNPVYYINYAHAR

IHQVFAKAGKKIDDVMRADLQSLNQDGVNLLFEALNLKAILNDAFEARALQKIPDYLKNLAANFHKFYNE

NKVVGSINENDLLKLFSLVALSIKTAFSLMGIEAKNKMEH

>ABV52717.1 putative efflux protein [Campylobacter jejuni subsp. jejuni 81116]

MYIFIIVLSALLDIVANLLLKKSDGFKHKIWGLAAIVNAILAFFLLSFSLKYVPLSIAYSTWGAIGIIGT

CLGGWILYKEKLNKIGILGIIIVIIAVFLLNY

>ABV52716.1 putative efflux protein [Campylobacter jejuni subsp. jejuni 81116]

MNIAKKELFVAWFFLIAAIVFEVLGTSFLKMENQILGYIFMALFIAFSYFFMGKAIKKIQVGIAYAVWEL

LGIILILLVSFIVFKESLTLTQILGIVLSIVGIIMINIGEVKE

>ABV52715.1 hypothetical protein C8J\_1116 [Campylobacter jejuni subsp. jejuni 81116]

MGRAFEYRRASKEARWDKMSKLFPKLAKAIQVAAKEGGTDPDMNPKLRSAIATAKANNMPKDNIDAAIKR

ASGKDSADIKNIHYEGKAAHGALVIVECMSDNPTRTVANVKAIFSKNGGEVLQNGSLGFMFARKAVFHLE

KFAGDLEELELDLIDAGLEELEQNEEELVISGDYTAFGELSSAIEAKGLVLKKAGLEYIPNNPVSFSEEQ

LSDIEKLLDKLEDDDDVQAVYTNID

>ABV52714.1 peptidyl-prolyl cis-trans isomerase [Campylobacter jejuni subsp. jejuni 81116]

MIKTIDTSKVNEYKFALIETEKGTMKLKLFGDEAPQTVCNFATLANEGFYKDLNFHRVIPNFVIQGGCPH

GNGIGGPGYEIICECDDQEHKHERGTLSMAHAGRDTGGSQFFICHSPQAHLDGVHTVFGQIDPKDEESLE

VLDSIRQGDKILDIKICDKI

>ABV52713.1 hypothetical protein C8J\_1114 [Campylobacter jejuni subsp. jejuni 81116]

MKTKFSLILSACLLSSSLFAKNTDDEITKLQKQLAQIQAELAEIRKEREAQAKQNEAVKAELADLNDRAD

ETEFQAALSKVKFGLEFSTAVSNTNYKVGGQDYSANNKWMNELHLNMNADINDKTKFYGRLSMAKNWSQM

GWSGSPLDLDAGRNTRSSGPVLYVDRAYLDYYITPEWIATIGRQPGTDGPGSNLRNNALRQSTYPALAIN

ALGDAAVITYKPESLQDHKVAIRAAYGKTYQWDEESGKVRDWMSDQKDADANLYYAAVEGELPIEGMGDN

LIIFNVAHMTDFALPIPGSTTLLGDDDGVINLGNLTLANIHFENYKAFGTNFNYFVSLGYSNGANAHTLS

ANPTVQSQLEINEKDGYAVHVGGRYDFTKALKVGYEFFWGSRYWYTMSRPSINDPLNIRMTRGTAHDFYV

IYQLDRYQFLRLSYTNIQNIWGNRGLPFGGAKKDKARADNIMLMYNVKF

>ABV52712.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MRKILFASLLPIIALADCASLMAKYEAPEPESKTMKQVERWINKKVSDPADAAVLKECMIARAADNPNQV

SVAGK

>ABV52711.1 putative integral membrane protein (DedA-like protein) [Campylobacter jejuni subsp. jejuni 81116]

MQEIISFIVETASAWGYLGIIILMTLESCFIPFPSEVVMIPAGYLAHKGKLDITLCILSGTLGSVLGALI

NYYICFFWGKNFVLKWGKYFGINEVKFAKFEEFFNKHGEFSTFTCRLLPGIRQYISMPAGLVKMKLVNFI

LFTALGSAIWVAILVFLGYYIGQNEELIKTYLTQILIIIIVFVILASLIYIKIKKPFKKA

>ABV52710.1 L-lactate dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MAKIGIVGLGYVGASSAYSIVTQGICSELYLYDIKQDLALAHARDLEDMSAIHFSYTKIFHVPNLENLAS

CDIIILAFRKESLKELPSRLVELQNNILELKDIVLTLKNANFKGKYIVATNPNDTITYYTQVLSQLPKNH

VFGSGTNLDSSRLKKFLAKDLNINSKDIFACMIGEHGDSQFAALSNASVLGQNLLDFYKQKLGKDLDIQK

LEKAVISEGYFIYERKGRTEFGIGTSCANLAKAILEDRKSLHPVSVVFDDMAFSMPAIIGKDGIEKVFEL

KFNEKEKIKLENSKQQIKNAIQSVKDKI

>ABV52709.1 hypothetical protein C8J\_1110 [Campylobacter jejuni subsp. jejuni 81116]

MEKPDIQRLTNFLIVYTKTLLGAGTYTARVAKCVGRIAEVYGYEININFFFHHITLNVVDMDDNSIQRTY

VIPNHHAHVNFKLIFDLSALSWAIYDHKYDLEKAKVVFEQISQQKKHSYLLNLLFVSMANSAFCRLFGGD

FGAGNLVFFATFVGLLLRYILTKAKIDLRIQYILCSFISSWFVFFGLDMGYTNTSDVALGSSILYLIPGV

FFINSVIDILKDHILMGLSRIISVGILICCIALGIYMTLSISDFGILR

>ABV52708.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MIEFILRDMFFAAVAGFGFAYACNPPLKTLILSALLAAIAHGLRFTLVEYFHFQTLAIATFVASFCIGCL

GIALAKIIKTPAEIIAFPALIPMIPGIYAYKAILYLISFIRSDDLKAKSEFLVQFFDYFFTTVSVTLALA

IGVSVTLLIFFEQSFMMTRHAKKH

>ABV52707.1 hypothetical protein C8J\_1108 [Campylobacter jejuni subsp. jejuni 81116]

MLCPVCNVDLVMSDRSGVEIDYCPKCRGVWLDRGELDKIIERSVPNTANFNQASRQESRYNDSAYHQHND

YYKKKKKESWLGELFDF

>ABV52706.1 cation efflux family protein [Campylobacter jejuni subsp. jejuni 81116]

MYKFLSHEPLANKSCHHNHEEHSHEHHHSHADARSVDKKILKISLLMTFSMMLVQFIYSILSNSLALLSD

TLHMFSDVFALALSFLAIIAVEKWQDHQKTFGYFRLEVLVAFINALTIILSALFIIYEAIEKFINPKEID

AKTMIIVAILGFLVNGINALMMFKGANLENVNMKSAFLHMMSDLLGSLAVIIGGIVVYFSGIVYIDTILA

IVLSILLLRWAIILLKQSANVLLESSPVDIEKVRQVLLLNPSVDEVVDLHITQITNKMLVASMHLKVRVC

DLKEFEKLSQDLSHKLLHEFEIGHITIQPIRSENEI

>ABV52705.1 hypothetical protein C8J\_1106 [Campylobacter jejuni subsp. jejuni 81116]

MKFKVKNVNCMNCVNLIKNSLEDEFGNIEVDLEQKILSLNLEENQVSNFTKEFQDLGFEIIERL

>ABV52704.1 putative cation-transporting ATPase [Campylobacter jejuni subsp. jejuni 81116]

MEELRIKIGKMTCVNCSNAIERACKKIDGVKDASVSYVNSSGVFLLEDQEKRKDIIAKIKNLGFEILEDE

QSLNAYKVKKHLELRKNLLLSIVLSVIIMYFEMFVKSSFSQNIQMALSFFGIFYCGRDFFSHAFLGLKSK

NLDMNTLVALGTLSAFVYSFLVYLQIFKEEDLYFSGAMMIISFVLLGKYLESKAKFKAQDYQRILENIDT

KKTKILLEDESIKEISSSFVKSGDVLLVKEGESIVADGVVLLGSAELDMSFLNGEFLPVLKKEGDEVQAG

AVVLNGTLRIKANKKAMDSTLEQIKNLVFEAGNIKSPLANLADQISKYFVGGIIFFAFLVFVFWALKADL

NTAFLHACAVLLISCPCALGLATPIALVVASSNAAKNFILIKNPAALEKLALVKYAFFDKTGTLTKENLS

IFKHNLSKDDFDKLCQIESLSSHPIAKALHKDQIFDLKGEGRVIVGSGIKYKEDSDIYLAGSAKFLHENE

IDTKESDIFFDTFKEYVRVYFAKNKKCLGGVLLSNALKDGAKELVLNLKKQNLKTFILSGDHVKNVEKIA

KELQIDEFYAQLKSEEKLRIIQKFKKTLFVGDGINDAAALSAATVSMSFSKANELAKKTGDFILIKDDLS

AIFKCFKLAKKTRSIIKLNLFWAFIYNVLCIPIAAGFVPFITLSPHIAALAMCFSSITVVLNSLRLKRI

>ABV52703.1 hypothetical protein C8J\_1104 [Campylobacter jejuni subsp. jejuni 81116]

MQQKCFCISKMIRFSKIIILLTVASLAGIVVFGNVTDYNSNFQFVSHVMSMDTKPDYLGNAIVYRAITSP

VIHHIGYIAIILFETFITLTALKGAYDMFKARNLDAQSFHNAKIFGIISLTCCCILWFFAFQVVAAEWFG

MWMSKVWNGLPDATRLVTYMFLALIFISLKNDD

>ABV52702.1 DNA polymerase III, gamma/tau subunits [Campylobacter jejuni subsp. jejuni 81116]

MLQALAIKYRPKTFDELIGQKTVSVSLKYALNHNRLAHAYLFSGLRGSGKTSSARIFSRALVCEQGPSDT

PCGTCKHCLAALEGKHIDIIEMDAASNRGLEDIQALIEQTKYTPSMARFKIFIIDEVHMLTPQAANALLK

TLEEPPSYVKFILATTDPLKLPATVLSRTQHFRFKQIPQSEILNHLKEILLKENVKFEEEALKFIARSGN

GSLRDTLTLLDQAIIFCQNEISISKITDMLGFLDPQKIKAFYQAILTKDKEKVFAYLEELQDYEASSVID

EMLFYLKESFFAKSTEFSILIYERFFRILSKAKNMLCDDDGFTLCVMAFMMMEASHLKEIDAQIQEIKQE

NTTNITPRITPAPIIPNLEKKIEKNAYEILLDSIYDRDFDLAECFKQSTKFISFENNTLNISSNAQGQNR

DTLNKGFKLIQELFKAKFGENAKINVQKALTIDENKLQSLTQELPNNENKNIDIQSSINMLKEGAKKFDP

QEDLKEALKDCFGEPSIEN

>ABV52701.1 transcription termination factor [Campylobacter jejuni subsp. jejuni 81116]

MEKEKKQHQRTHVPVEGYKIEELKLLDLENLVKIANECEIENPREFRRQELIFEILKAQTKKGGFILFTG

ILEISSEGYGFLRGMDSNLSDSVNDAYVSNSQIRKFALRVGDIVTGQVREPKDQEKYYALLKIEAINYLP

LQEAKERPLFDNLTPIFPTEKIKLEYDAMKLTGRVLDLFTPIGKGQRGLIVAPPRTGKTELMKELATAIA

KNHPEMHLIVLLVDERPEEVTDMQRCVKGEVFSSTFDLPAYNHVRVAELVIEKAKRMVETGKDVIILLDS

ITRLARAYNTATPSSGKVLSGGVDANALHKPKRFFGAARNIENGGSLTIVATALIDTGSRMDDVIFEEFK

GTGNSEIVLDRNIADRRIYPAINIIKSGTRKEELLQGVANLQKIWAIRSAISQMDDVEALKFLYSKMLKT

KDNVELLSIMNE

>ABV52700.1 putative cation-transporting ATPase [Campylobacter jejuni subsp. jejuni 81116]

MKCEHCKLDYKQAQMIEYKGKFFCCKGCESVWEILHESGLDEFYEKLGNQTLSPVNFQNEMKNYDEFITK

TKEGFSEIYLMIHGIECAACVWLNEKILTKQEGILELDINHLSHKARIVFDEQSISLVQILRLIESIGYK

ASAYDASKASKKADLLKREFYSKLVVAIACVMNIMWIAVAKYAGLFSGMDKDTKDILNFAEFILCSPVLF

YTGSHFYKSAFKTLKMHSLNMDVLVISGASLAYVYSLWAMFFRVGEVYFDSVAMIICFVFIGKYLEMFSK

KRALDTIDGLNDFLQNEVLVFNGKEFAPKKVQKVCLGDRILLKTGDKILIDGICKSGEMSVDTSSLNGES

IPKLIQKEDEIFSACMVLDGSVEYEATKLYKDSKLSQIIQLLELASSKKAKLESLVNSLSAYFSRTVLLI

AFICFAFWFFYKEESFEISLVNAIAVLIIACPCALALATPVSNLVALGRALKKHILFKSSSVIEDLSKCD

CVVFDKTGILTKIELELKEVFLDKVLDLNELYNFVKLSKHPISQNIASYLKQKGAKDLNLNFKKHSSIQA

KGLSAELNEELLLGGSSKFLQEKSIATKEFDNTHFIFAKEGKILAFFEFDSVLREGAKELIAYLKKEKKE

LMILSGDHQKAVEKIARKLEIQNYQASCLPEDKMKAIENLSKNYKVLFVGDGVNDALALKYASVSMTLRE

GSDLAIESSDVLLLKNDLLSLKKAIKLSKNTFKIIKQNLAFSLFYNACTIPLAFLGMINPLFAAISMSFS

SIIVVLNALRIKE

>ABV52699.1 small hydrophobic protein [Campylobacter jejuni subsp. jejuni 81116]

MNSIIMMMIGVSILAFFIILATLLWGIKNKQFDDDYKFTTLNDDEDSLRDAIELERRKKEALNKKRLS

>ABV52698.1 putative periplasmic cytochrome c [Campylobacter jejuni subsp. jejuni 81116]

MKKLLVVSALACLGVSAFAADGATLFKKCAVCHGANADKVYLNKVPALKTLSSAERLQYMKEYSEGKRNA

YGQGAIMKLNLKGLTEEDFKAIEAHIETLK

>ABV52697.1 putative phosphatase [Campylobacter jejuni subsp. jejuni 81116]

MFIFFLKKLYYNVFMKTKALFLDRDGVINIDKKYVYKIEDFEFCDGIFELCRYFLARNYLLFVATNQSGI

ARRYYKESDFLKLCDYMLKEFAKQDVKIDKIYHCPHLEGCECRKPKAGMLLKAKDEFDLDMKNSIFIGDN

LSDMQAGLNANIGTLILVNEEKKEGDFFRQFKNLKEILSFFKEKDI

>ABV52696.1 ADP-L-glycero-D-manno-heptose-6-epimerase [Campylobacter jejuni subsp. jejuni 81116]

MKIAITGGAGFIGSQLALNLQEKHEILIIDKMRSSATFENGNLQSFGHFKNLLEFDGELFAGDINDEKVL

KKIKDFRPEIIFHQAAISDTTVFDQTKVLQTNLNTFKDFIELSIDLNAKLIYASSASVYGDAKSPQTVGK

DEKPKNPYAFSKLMMDKLAKKYYDKAHLVGLRYFNVYGKGEFYKNKTASMVLQFGHQILAGKNPCLFEGS

DQIYRDFTYIKDVISANLIALDSKCGVYNVGSGKARTFQDIVDILQKELKTDLPCEYIPNPYVKSYQFHT

EAKLDQTWDYRPKFTLEEGIKDYLGEIKRLFEKEVNA

>ABV52695.1 putative ADP-heptose synthase [Campylobacter jejuni subsp. jejuni 81116]

MLEFLSQQKPKILIIGDFMVDNYTWCDCSRISPEAPVLVAKTLKEDKRLGGAANVYANLKSLGADVFALG

VVGDDKSGKFLQENLKGEFLIQKGRKTPFKNRIMAHNQQVLRLDEEDISAILLENELIALFDEKIKDFKA

VVLSDYAKGVLTPKVCKAVIKKAKALNIPVLVDPKGSDFSKYSGATLLTPNKKEALEALKFENLEGENLE

KGIKKLKEDFALRYSIITLSEAGIALFDEGLKIAPAKALEVYDVTGAGDSVIAVLAFCLASGIEIFKACE

LANEAAAVVVSKIGSMSVSFDEIKSFNRVDFEKKIKSKEELLTLLKQNDKKIVFTNGCFDIVHFGHIKYL

EKAKRLGDVLIVGLNSDASVKRLKGESRPVNSEFQRACMLAAFYFVDFVVIFDEDTPLELISFLKPDILI

KGADYKDKLVVGADIVSKVELIDFEEGFSTSKIIEKIKDKK

>ABV52694.1 phosphoheptose isomerase [Campylobacter jejuni subsp. jejuni 81116]

MINLVEKEWQEHQKIAQESEILKGQIAKAGELLCECLKKGGKILICGNGGSAADAQHFAAELSGRYKKER

KALAGIALTTDTSALSAIGNDYGFEFVFSRQVEALGNENDVLIGISTSGKSPNVLEAFKKAKELNMLCLG

LSGKGGGMMNKLCDHNLVVPSDDTARIQEMHILIIHTLCQIIDEGF

>ABV52693.1 hypothetical protein C8J\_1094 [Campylobacter jejuni subsp. jejuni 81116]

MFASNKKFILFSLLCPLPLVIILFTLLYIRDPFWFFHPPYFRKETYMKDMRMQARGLILYKDFDSAIIGT

SMLENTSAKEANKKLGGNWINLSLGGSTFALRAVILDYLFKHKDIKNIIYSLDIRALNELETPKDKNFIS

LYNDKTIDLFKLYLSSRFINCAIFFSKKEKCIGKDNLDTLTNWFLENKNHFGGIEYWSKEWWHDKNFQNE

ILQAQNFQPNFDIDISHFKNYTKKYLLSFIKKYQKTQFYLIIPSYSRLNYRKLSYGEYYNKDSVLFSNYY

AILSWIIQETQKYPNVKIYGFDDLDYADNIKNYKDPAHYNTDMNSMQLNAIRDNTHILNTQNIVKYLNTM

ERKIKEFDLTPFVEYIKNQNF

>ABV52692.1 hypothetical protein C8J\_1093 [Campylobacter jejuni subsp. jejuni 81116]

MLFSSFTFIFAFLPLTLVGFYILKALQYYTSAKIFLILASLFFYAYFKIDYIFILTFSTLVNFFLANLIL

RKENNRAGYTLLYLGIIFNLCLLAIFKYTDFFLENFNLFSKLAHLDFNIPLPHILLPLGISFFTFQQIAF

LVDCYKKSNIEDLLENKKVDFIDYCLFISFFPQLIAGPIVHHKEMMPQFHSLLNKEKALIDWKLIAKGLF

IFSIGLFKKVYIADSFASWANAGFTVVQNGNFLNIFEAWATSLSYTFQLYFDFSGYCDMAIGLALFFGIA

LPVNFNSPYKALNIADFWRKWHITLGRFLKDYLYIPLGGNRFGKFINLRNLFIVAFLSGVWHGAGWGFVI

WGILHAIAMISHRIYSFWAKGKTFLNSKIYKIISWFITFNFINIAWIFFRSENLQGAINLLKSMFGVIWV

ELPLKFKAGLLFKKIGGNDTMVGFILVSFILCICFKNSINMLQDFKSSFKNSLIVMFLFYIALITLIATP

YTEFIYFNF

>ABV52691.1 ADP-heptose--LPS heptosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKIFIHLPTWLGDAVMASPALYAIKEHFKNTQFILYGSLVSTALFREFPNSKIIIENKQTRYKQALSLRK

ELGKIDLSFAFRSAFSSKIILHILKTKQRYFFDKNKHKEEHQVLKYLYFIENSLSIKAHFKDLKLPFKLK

FQNPLILKNGKKILGLNPGASFGSAKRWDASYFAKVALNFSQSHEILIFGAGKAEQELCNEIYQILKEQN

IKVKNLCNKTTIKTLCQNIAFCDLFITNDSGPMHISTVYKIKTVAIFGPTKFTQTSPWQNQNAKLVHLDL

ACMPCMQKTCPLKHHKCMKDLKPEKVIEEIKKLSTP

>ABV52690.1 lipooligosaccharide biosynthesis glycosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MPQLSIIIPLFNSCDFISRVLQSCINQTLKDIEILIIDDKSKDNSLNMVLEFAKKDPRIKIFQNEENLGT

FASRNLGVLHSSSDFIMFLDSDDFLTPDACEIAFKEMKKGFDLLCFDAFVHRVKTKQFYRFKQDEVFNQK

EFLDFLSKQRHFCWSVWAKCFRKDMILKIFEKVKIDERLSYGEDVLFCYIYFMFCEKIAVFKTCIYHYEF

NPNGRYENKNQEILNQNYQDKKKSNEIIKRLSREFLFDEFHQKLFEVLEREEKSLCMRANKI

>ABV52689.1 hypothetical protein C8J\_1090 [Campylobacter jejuni subsp. jejuni 81116]

MIDNEITIVTAFYDIGRKDIKNFERDNDKYLSYFEFLAGIKNKMIIYTQENIKEKILDTRKKHNLEDKTI

IITKELQEFDEQGYKKIIDTFRNYDQSINRKNPNNIECISPMYCYLMYLKPFFVCDAIQRGLTDENIMWL

DFGFNHGGNFFVDKDQFNFYLQKQNSIDENKINLFSIKNDDKQTLANIYFSMETFLMGGIIFAKSKNWLL

FKHHMQKCIKYFTSFGIIDDDQIMLLWCARNYRKNYNIIKVYFWFDSLYHFIPQNIAKKLKINTNQIKYY

KIIKEKLKEDFNNKNIKNIFINLIKYCYFKFINKNHKVL

>ABV52688.1 hypothetical protein C8J\_1089 [Campylobacter jejuni subsp. jejuni 81116]

MNNFVLYSLYFIYSAFFLNKHRRIIKGKILHQKEHENIANYLENAYIKKYFENKLDDIQIKKTRNINGKK

IIWQFWYQGIDNAPCIIKKCFKSVQKYKGNYEVVLLDKDNIKDYLIFPDFIYQKIDDKKFGEKTITIFSD

LLRVSLLNNYGGIWLDAGMFLSGEIQKEILDQDFFIFHRSTKKPQDYKNWINFNYNFFSWDEKFKVNIVN

GFILSNKNNEIMKIMQDILINYWKYENKLVYYFMFQILFDTLKKKYLNLNLYITNDTDIHLLQYHAKDKY

SDKLWNDIKNKTSIHSLKIFKKIRKHSMIDKILFKDTI

>ABV52687.1 hypothetical protein C8J\_1088 [Campylobacter jejuni subsp. jejuni 81116]

MKFFIINLKIAKDRKEYMQNLCLKHNLDYEIIQAVDGKELDSDFVKNISDFSLSEKYLGRTLSLGEIGCA

LSHKKCFERMFELNLNECLILEDDAYFDEKLNYILSLKDKFPKDLELFLLGHYRQVYLDDGFRIESPFSL

RYDYKIDDFYHAKRLVGGGNGTHGYYINKNGALKMYKYLEKIIFPYDHCTSNDNIINVYALYPVVITTDE

IFGAQTYVQDDNKRRYRKRSKISKYIKKIKNKIIFFIPSLKKLRKYE

>ABV52686.1 hypothetical protein C8J\_1087 [Campylobacter jejuni subsp. jejuni 81116]

MIYYPYYLKKYLAKIACLFIPNKNIRAIIREKLLNQYYANKT

>ABV52685.1 hypothetical protein C8J\_1086 [Campylobacter jejuni subsp. jejuni 81116]

MQIKLDNLNSYIPKDIVDNIEKYDNEHFYKINHIIKSKHKGFFDFDEKSKNPTSPLNPWAYIRVKNEALT

LKASLKSILPAIQRGIIGYNDCNDGSEEIILEFCKQYPSFIPVKYPYEVQIENPQSEENKLYSYYNYVAS

FIPQGEWLIKIDVDHIYDAKRLYKSFYIPKKDYDIVVYSKMDFLINDEDAFIVKYKNLNAIINNKSNDHW

LIKNNHLKWAESMHEDRYCIEYLDVKKLKIYQTEFLNYHFPYFKRSLDKNKIELIPIDDFSIKEYKDIIS

PDMVTKEKLLYLKKYIKENQ

>ABV52684.1 hypothetical protein C8J\_1085 [Campylobacter jejuni subsp. jejuni 81116]

MKKSKSIQIIKQQGIAEFIKYKKIKIYTKYEKKFNINIFTPYLLKFCKPLKDDYKFILFSYGVSGHWAFK

SFLKYCELDDFVLYQNNYSYYKEYKNFNKKNYYVEIASYQSIQPKYKHISKILNKNKPVVILTRDPISRL

KTMVNHGFYKIEELGKNELKNFYINEDIFENLDRIRYTDKNGYNANLKKPDLSSIYFIVNEELSFSYFSN

INLIKNKNILYVDTKSISKDNAFATIKTLAKELNFKEPNDNDEYKFKQKFWNELYYLLPYRLIVNNDILI

IVSDENKVFLDNDKHYNEIKDDLIDIKKELVNPKSKLFDKISINIENKNWIIVKDDKALINDLREYFEKF

MIILEKKANERLENMVKEEDVLNYLKEHQDLGKKLKNILDYELQHIKEHRPGIINSWEYYKKFLEIF

>ABV52683.1 hypothetical protein C8J\_1084 [Campylobacter jejuni subsp. jejuni 81116]

MFFLNLKQINDRFNTEFITKFKEILESGWYILGKQCEKFENNFAKYCGVKHCIGVANGLDALRLIIKAYD

FKENDEIIVPANTYIASILAITDNKCKPILIEPDINTYNINPDLIEEKITKKTKAIMVVHLYGQVCDMEK

IQLLANKYNLKIIEDCAQAHGAIYKDKRVGNLGDAAGFSFYPGKNLGALGDAGCICTNDDNFASKIRALA

NYGSHKKYENLYTGLNSRLDEIQAAFLDIKLKYLDEDNNKRKNIANFYLQNIKNENIILPSNKFDHVWHL

FVVKTKLRDELQHYLNNHDIQTIIHYPIPPHKQKCYKDLNHLKLPITENIHQEVLSLPISPTMKENDFKK

VADILNKWKV

>ABV52682.1 hypothetical protein C8J\_1083 [Campylobacter jejuni subsp. jejuni 81116]

MFLSNIMYYNYNDLLIWSKMEKNPLVSIIIPCYNAENFIENCINSIINQTYINYEIICVDDGSTDNTLKI

LKNLSINNSRLKAYSINHTGIPSVVKNYGLKLAKGEFLLILDSDDMITEYFLEKGIKYFQDNPVDIILYP

IKFMFSNNNYKIIGGIYNNSLNISDVNYLGATNKIISGRDAFRFNIYNKLIGFPFYKKTIDKIINFNEES

FNGDEYSFREHLLQAKKIAFIDTEFYVYNFNQESITKKIGVHHWDTWKTWFNLEKLAQKHNYEKKLIKKI

NKIRYSIYYELCIKFNKTEYLFSQNEKNIILNKILENKNHLSRINSIFDFLFYKCKDEKGKYIKFINKYT

FYYKKIKGNNVFFEFKTNK

>ABV52681.1 hypothetical protein C8J\_1082 [Campylobacter jejuni subsp. jejuni 81116]

MAKISILTPCFNHEKYVSYFLQSVLEQSFSDFELIIVDDCSNDNSTKEIQKFKDPRIKLIKHEFNKGINA

TLNTAFENSNGEYIVFCASDDILEKNALEIIYKTFKDNDIIAVYPNLICIDENNEILGNLYPLKQRNKVE

LLYYLFMRYNCLTSVGLSLKRDVFEKLYPLPNSMCNYQDMKMHIDILNIGEIKILETQLIRYRRTRSKTN

ISAHNSITTTRENLETEMLLDTYLKFDNIFLLEQIFHKEINKTNIKPYQETLPFFLGIMALESENIYKKY

WGYHKIMEFYKNDANAKILYEKYNFTFKDYLQLAKKCDTGDIFIKKYRKYKKISNFLIIVCFFLILCIII

ITIY

>ABV52680.1 hypothetical protein C8J\_1081 [Campylobacter jejuni subsp. jejuni 81116]

MIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNIEQ

IIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIIDQH

CFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSFEI

HNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>ABV52679.1 hypothetical protein C8J\_1080 [Campylobacter jejuni subsp. jejuni 81116]

MIHKMSDVQSSNIGKNTNIWQFCVVLPNAKIGDNCNICSHCFIENDVVIGDNVTIKCGVQIWDGITIEDN

VFIGPNVTFCNDKYPKSKQYPKEFLKTIIKKGASIGANATILPGVVIGENAVVGGGLSLQKILQPIQLII

AKLSNSLCKTKLYYHD

>ABV52678.1 hypothetical protein C8J\_1079 [Campylobacter jejuni subsp. jejuni 81116]

MIKNCKILNLRAIRDNRGSLIALENNKEVPFEIKRVYYIFDTDPNFPRGAHAHKNLEQVLIMMSGSCDII

LNDGKNYEKICLNRPDIGLYIGKNMWREMKNFSYGAKLLVLASDFYDEKEYIRNYDEFLRNINDT

>ABV52677.1 hypothetical protein C8J\_1078 [Campylobacter jejuni subsp. jejuni 81116]

MNYTILKFKTINSKNSILNVHQKDVNCPFEIKRIFYIYDFLDDSIRGDHANLNSEFIFIALNGSCEILID

DGKTKQKIILNNKTKGLYIDKMIWKQMYNFSKDCILLVLTNTYYDEKEYIYDYKYFCELKNNIVWRGGGM

L

>ABV52676.1 hypothetical protein C8J\_1077 [Campylobacter jejuni subsp. jejuni 81116]

MYILVTGGAGFIGSNFLLYFFEKNPNAKIINLDFLTYASDISNLNKLKNNPNYVFIQGDISDVSLVGEIF

SKYKINAVINFAAESHVDNSIKNPDIFIKTNIYGTWNLLNSAYKTWFLEPFLKKDEFKQSFFYQISTDEV

YGSLGENGKFTEDNAYAPNSPYSASKASADMLVRSYHHTYGLNAVISNCSNNYGPFQHDEKLIPTIIRNA

LNETPIPIYGDGKNIRDWLYVKDHCVAIESIYKYAFEKIKENNSFFDVFNIGTNEEWQNIDIANKICSYL

DNVLPKNTSYKEQITFVKDRAGHDRRYAIDSTKLQRVIGWKAQENFNSGLDKTIQWYIKKYKG

>ABV52675.1 hypothetical protein C8J\_1076 [Campylobacter jejuni subsp. jejuni 81116]

MKGIILAGGSGTRLYPSTLTLCKQLLPIYDKPMIYYPMSVLMLAKIKEVLIISTPKDIDRFKELFKDGSF

LGMQIQYKIQERPEGLAQGLILAQDFIQNDDIALILGDNIFYGQGFSDILENAKDDLKKGFASIFSYHVK

DPERFGVVEMDQNGNVLSLEEKPKNPKSNHVATGLYFYNNDAIDIAKNVKPSARGELEITDVNIEYLRLN

KLKSQHLGRGFAWIDTGTHDSLIEASSFVQTIELRQGYKIACLEEIAYNNNWIDNEILEKRALLLSKSNY

GQYLYKILSQGK

>ABV52674.1 hypothetical protein C8J\_1075 [Campylobacter jejuni subsp. jejuni 81116]

MNISIVILTFNSQKYLQEVLQSVNFANEIILIDSGSTDDSLIIAKTFKNVKIFHQDWLGFGKQKQFGVEK

ANNDWIFVLDSDEVFTEELKEEVLQIIKNPSFKAYKVARLNFFFGEAITKMGLYPDYNIRLFHKKYAKFN

EREVHESIICQEKIGKLKHHFLHYAYENIEQFIDKQNKYSSLNPKKNNLLKALINPYWTFFKLYFVKLGF

LEGKRGFIIAKLYAQYTFWKYIK

>ABV52673.1 lipid A biosynthesis lauroyl acyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKNSDRIYLSLYYILKFFVTFMPECILHFLALIVARITFYLNKKHRKIIDTNLQICFPQYTQKERDKLSL

KIYENFAQFGIDCLQNQNTTKEKILNKVNFINENFLIDALALKRPIIFTTAHYGNWEILSLAYAAKYGAI

SIVGKKLKSEIMYEILSQSRTQFDIELIDKKGGIRQMLSALKKERALGILTDQDCVENESVRLKFFNKEV

NYQMGASLIAQRSNALIIPVYAYKEDGKFCIEFFKAKDSQNANLEELTLYQAQSCEEMIKKRPWEYFFFH

RRFASYNQGIYS

>ABV52672.1 lipopolysaccharide heptosyltransferase I [Campylobacter jejuni subsp. jejuni 81116]

MKIAIVRLSALGDIIQSAVVLQFIKNFKKDIEIHWFVDEKFEGILKNHPLIDKLYALPLKDKKILKSLKI

LLKARKNNYNAVIDLQGLIKSAIVSRILSRNNFGFDKNSLKESFAHNFYNQKLELDYNENVFVRYLSLTS

FMLNTDFNVKNLAFKQDIFSVDENLKQLLNNKLKLDKNEKNILIHVGSSVENKIYPKTKLAILCKLLINE

FQQAKIWLAWGNVKEYEFAKEVLNLSGIDETHIELAPKFNLEELMAFTKMMDLIIGNDSGPTHLAFALNK

ASITIFGATPSYRNAFQTHINKIIDAGKKIQNTKHIDKSDFCITRIEEEDIFKLAKGLLNEK

>ABV52671.1 polysaccharide biosynthesis protein [Campylobacter jejuni subsp. jejuni 81116]

MAKNEGYICVFDCESVPDVELIRKTLGFEGSDLEVSLKALQWQKEQSGSEFLPLPYHKIISICAVLSDNF

GKFIKVNKIDGQNEKEMIANFFNFIENYEPKLVSFNGKNFDMPVLVLRALKYNLKAATYLDTQSDKWNNY

KTRFSELKHCDLLESLGSNGRGIKLDTLCSMVGLPGKYDVHGDEVMKLFCENELEKIHEYCESDVLNTYM

LFLKYELIKANVSEEDYIDFLSYMRDFLRAKKSDRSYTEVFAKACESEISKVQS

>ABV52670.1 UDP-glucose 4-epimerase [Campylobacter jejuni subsp. jejuni 81116]

MKILISGGAGYIGSHTLRQFLKTDHEICVLDNLSKGSKIAIEDLQKIRTFKFFEQDLSDFQGVKALFERE

KFDAIVHFAASIEVFESMQNPLKYYMNNTVNTTNLIETCLQTGVNKFIFSSTAATYGEPQTPVVSETSPL

APINPYGRSKLMSEEVLRDASMANPEFKHCILRYFNVAGACMDYTLGQRYPKATLLIKVAAECAAGKRNK

LFIFGDDYDTKDGTCIRDFIHVDDISSAHLSALDYLKENESNVFNVGYGHGFSVKEVIEAMKKVSGVDFK

VELAPRRAGDPSVLISDASKIRNLTSWQPKYDDLGLICKSAFDWEKQC

>ABV52669.1 ABC-type transport protein [Campylobacter jejuni subsp. jejuni 81116]

MLKKLFFILSKEDKNFLFFLLVFSVFVSFIETFAISLVMPFITLASDFSYFDRNKYLISLKEYLNIPVFE

IIVYFGVGLIVFYVFRALLNAYYFHLLARFSKGRYHAIAYKVFSKFLNINYEKFTQKNQSEILKSITGEV

YNLSTMISSFLLLMSEIFVVLLLYALMLLINYKITLFLSIFMVLNAFILVKILSPIIKKAGLRREEAMKN

FFEILNTNLNNFKFIKLKTKEDGVLSLFKAQSEAFSKANITNESVAAVPRIYLEGIGFCVLVFIVVFLVL

KNESDISGILSTISIFVLALYRLMPSANRIITSYHDLLYYHSSLNIIYQNLRQEEENLGEGKLSFNQELK

ICNLSFGYEGKKYLFKNLNLNIKKGEKIAFIGESGCGKSTLVDLIIGLLKPKEGQILIDKQELNASNAKN

YRQKIGYIPQNIYLFNDSIAKNITFGDAVDEEKLNKVIKQANLEHFIKNLPQGVQTKVGDGGSNLSGGQK

QRIAIARALYLEPEILVLDEATSALDTQSEAKIMDEIYKISKDKTMIIIAHRLSTITQCDKVYRLEHGKL

KEEK

>ABV52668.1 putative glycosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKISFIIATLNSGGAERVLVTLANALCKEHEVSIIKFHTGESFYKLENEVKVTSLEQFRFDTLYHKIASR

FKKFFALRKALKESKADVFISFLDTTNIACILANIGLKTPLIISEHSNEAYLKPKTWRFLRRVSYPFCDA

LSVLGSSDKVYYERFVKRVKLLLNPCHFSDEIPFDSSFEKENLVLFIGRLDHNKNPVMFLKAIAHLDKNL

QENYKFVIAGDGELRQELEYKVKSLGIKVDFLGRVENVKALYEKAKVLCLCSFVEGLPTVLIESLYFEVC

RISSSYYNGAKDLIKDNHDGLLVGCDDEIALAKKLELVLNDENFRKELVNNAKQRCKDFEISNIKEEWLK

LIVEVKNA

>ABV52667.1 general glycosylation pathway protein [Campylobacter jejuni subsp. jejuni 81116]

MPKLSVIVPTFNRQVLLEKAIKSIQNQDFKDLEIIVSDDNSSDDTKSVVQNLQKDDDRIKYFLNQNYKQG

PNGNKNNGLDQASGEFVTFLDDDDELLSGALSTLMQKANEGYAHVFGNCLIEKEGNLSKEFSGKGLEKDS

EISKKDFLMAKFSGEFFSVFKKSLLENKRFNEEFYGNEATLWVNLYKEKSFYIHKAFRIYRIFRQDSVTL

GASKNAHRVYLGYLELAKILENELRMSKDKDYKKTCASYYKMAAYYAKLAKNYKALYKCLFKSLSIKINA

PALILLILSIIPNNMIEKLSKIRVALCKN

>ABV52666.1 general glycosylation pathway protein [Campylobacter jejuni subsp. jejuni 81116]

MQKLGIFIYSLGSGGAERVVATLLPILSLKFEVHLILMNDKISYEIPECQIHFLECSKPSENPILKFLKL

PFLALKYKKLCRNLGIDTEFVFLNRPNYIALMARMFGNKTRLVINECTTPSVMYAKNNFNSLANKFLISL

LYPKADLILPNSKGNLEDLVQNFSINPKKCEILYNAIDLENIEQKALEDVALKDKFILSVGRLDKGKNHA

LLIRAYARLKTDLKLVILGEGVLKDELLALIKELNLEEKVLLLGFDNNPYKYMAKCEFFAFASVFEGFSN

VLIESLACSCAVVCTDHKSGARELFGDDEFGLLVEVDNENSMFQGLKTMLEDDKLRKAYKNKAKTRAKAF

DKVKIARDALKYLLG

>ABV52665.1 putative integral membrane protein (possible oligosaccharyl transferase) [Campylobacter jejuni subsp. jejuni 81116]

MLKKEYLKNPYLVLFAMIILAYVFSVFCRFYWVWWASEFNEYFFNNQLMIISNDGYAFAEGARDMIAGFH

QPNDLSYYGSSLSALTYWLYKITPFSFESIILYMSTFLSSLVVIPTILLANEYKRPLMGFVAALLASIAN

SYYNRTMSGYYDTDMLVIVLPMFILFFMVRMILKKDFFSLIALPLFIGIYLWWYPSSYTLNVALIGLFLI

YTLIFHRKEKIFYIAVILSSLTLSNIAWFYQSAIIVILFALFALEQKRLNFMIIGILGSATLIFLILSGG

VDPILYQLKFYIFRSDESANLTQGFMYFNVNQTIQEVENVDLSEFMRRISGSEIVFLFSLFGFVWLLRKH

KSMIMALPILVLGFLALKGGLRFTIYSVPVMALGFGFLLSEFKAIMVKKYSQLTSNVCIVFATILTLAPV

FIHIYNYKAPTVFSQNEASLLNQLKNIANREDYVVTWWDYGYPVRYYSDVKTLVDGGKHLGKDNFFPSFA

LSKDEQAAANMARLSVEYTEKSFYAPQNDILKTDILQAMMKDYNQSNVDLFLASLSKPDFKIDTPKTRDI

YLYMPARMSLIFSTVASFSFINLDTGVLDKPFTFSTAYPLDVKNGEIYLSNGVVLSDDFRSFKIGDNVVS

VNSIVEINSIKQGEYKITPIDDKAQFYIFYLKDSAIPYAQFILMDKTMFNSAYVQMFFLGNYDKNLFDLV

INSRDAKVFKLKI

>ABV52664.1 general glycosylation pathway protein [Campylobacter jejuni subsp. jejuni 81116]

MRIGFLSHAGASIYHFRMPIIKALKDRKDEVFVIVPQDEYTQKLRDLGLKVIVYEFSRASLNPFVVLKNF

FYLAKVLKNLNLDLIQSAAHKSNTFGILAAKWAKIPYRFALVEGLGSFYIDQGFKANLVRFVINNLYKLS

FKFAHQFIFVNESNAEFMRNLGLKENKICVIKSVGINLKKFFPIYIESEKKELFWRNLNIDKKPIVLMIA

RALWHKGVKEFYESATMLKDKANFVLVGGRDENPSCASLEFLNSGVVHYLGARSDIVELLQNCDIFVLPS

YKEGFPVSVLEAKACGKAIVVSDCEGCVEAISNAYDGLWAKTKNAKDLSEKISLLLEDEKLRLNLAKNAA

QDALQYDENNIAQRYLKLYDRVIKNV

>ABV52663.1 general glycosylation pathway protein [Campylobacter jejuni subsp. jejuni 81116]

MYEKVFKRIFDFILALVLLVLFSPVILITALLLKITQGSVIFTQNRPGLDEKIFKIYKFKTMSDERDEKG

ELLSDELRLKAFGKIVRSLSLDELLQLFNVLKGDMSFVGPRPLLVEYLSLYNEEQKLRHKVRPGITGWAQ

VNGRNAISWQKKFELDVYYVKNISFLLDLKIMFLTALKVLKRSGVSKEGHVTTEKFNGKN

>ABV52662.1 general glycosylation pathway protein [Campylobacter jejuni subsp. jejuni 81116]

MARTEKIYIYGASGHGLVCEDVAKNMGYKECIFLDDFKGMKFENTLPKYDFFIAIGNNEIRKKIYQKISE

NGFKIVNLIHKSALISPSASVEENAGILIMPYVVINAKAKIEKGVILNTSSVIEHECVIGEFSHVSVGAK

CAGNVKIGKNCFLGINSCVLPNLSLADDSILGGGATLVKSQNEKGVFVGVPAKRKI

>ABV52661.1 putative aminotransferase (DegT family) [Campylobacter jejuni subsp. jejuni 81116]

MRFFLSPPHMGGNELKYIEEVFKSNYIAPLGEFVNRFEQSVKDYSKSENALALNSATAALHLALRVAGVK

QDDIVLASSFTFIASVAPICYLKAKPVFIDCDETYNIDVDLLKLAIKECEKKPKALILTHLYGNAAKMDE

IVEICKENEIVLIEDAAEALGSFYKNKALGTFGEFGAYSYNGNKIITTSGGGMLIGKNKEKIEKARFYST

QARENCLHYEHLDYGYNYRLSNVLGAIGVAQMEVLEQRVLKKREIYEWYKEFLGEYFSFLDELENSRSNR

WLSTALIDFDKNELNACQKDINISQKNITLHPKISKLIEDLKNEQIETRPLWKAMHTQEVFKGTKAYLNG

NSELFFQKGICLPSGTAMSKDDVYEISKLILKSIKA

>ABV52660.1 putative sugar epimerase/dehydratase [Campylobacter jejuni subsp. jejuni 81116]

MIFYKSKRLAFFLTSDIVLILLSVYLAFSLRFSGDIPSIFYHGMMVSAIILLVLKLSFLFVFRIYKVAWR

FFSLNEARKIFIALLLAEFCFFLIFYFFSDFFNPFPRSAIVIDFVLSYMFIGTLRISKRMLVDFKPSKMK

EEETPCIVVGATSKALHLLKGAKEGSLGLFPVGVVDARKELIGTYCDKFVVEEKEKIKSYVEQGVKTAII

ALRLEQEELKKLFEELVAYGICDVKIFSFTRNEARDISIEDLLARKPKDLDDSAVAAFLKDKVVLVSGAG

GTIGSELCKQCIKFGAKHLIMVDHSEYNLYKINDDLNLYKEKITPILLSILDKQSLDEVLKTYKPELILH

AAAYKHVPLCEQNPHSAVINNILGTKILCDSAKENKVAKFVMISTDKAVRPTNIMGCTKRVCELYTLSMS

DENFEVACVRFGNVLGSSGSVIPKFKAQIANNEPLTLTHPDIVRYFMLVAEAVQLVLQAGAIAKGGELFV

LDMGKPVKIIDLAKKMLLLSNRNDLEIKITGLRKGEKLYEELLIDENDAKTQYESIFVAKNEKVDLDWLN

KEIENLQICEDISEALLKIVPEFKHNKEGI

>ABV52659.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MYIKDIQRFEDNRYRARAYMSYILTRNLPNKLPDIHLETIKTALDKIAHEVVVFDALYILDISGMQIENA

ISLNKAHEIGQGEDRSTRSYFYRAVKLKRCVLSDPYPSVLNNELCVTASIPIYDDKNNLLFVVCIDIKLE

DILKIIQAGKFEFVFTQFSRLVYFCFALVLFVITCFLFQKGFFSLFDNQAIGIEHMFESTIAITLALAIF

DLAKTLIEQEVLGRTKKEEGGIQKTMVRFLGSIIIALAIEALMLVFKLAIGDLSQMIYAIYLIGGVSLLL

LGLSVYLFTVKYKNNNI

>ABV52658.1 chemotaxis regulatory protein [Campylobacter jejuni subsp. jejuni 81116]

MKLLVVDDSSTMRRIIKNTLTRLGHDDVLEAEHGVEAWDLLTKNEDVKVLITDWNMPEMNGLELVKKVRA

EKKYEDMPIIMVTTEGGKAEVITALKAGVNNYIVKPFTPQVLKEKLEDVLGTGSGEGAAE

>ABV52657.1 ribosomal protein L11 methyltransferase, putative [Campylobacter jejuni subsp. jejuni 81116]

MQKKYYELFFIVEERYKNLFLDFAFDLGIEAIEEKDNGVYIRSHESLEELSWALEIFAQKLTTTFNLNHK

IISNLSLVEKENKDWIQEYKKGIKPILVDNVYIHTTWQEEKKNFINIKINPALAFGSGHHESTYSCVKFL

QKFSKSKLRALDLGCGSGILGIIMAKFGCNVEICDTDELAIDSSLENARLNGVDFHKAWCGSIDKANGLY

NLIVANIIADVILILEKDIKNHLEDNAILILSGILDKYSTRIKEKFQDLELIDEMQINEWCSFVYKNNKK

G

>ABV52656.1 cell division protein FtsH [Campylobacter jejuni subsp. jejuni 81116]

MNNNTPNNKGNPQGNNFFNKNPIFIFAIFAIVMIIIFKGFFDGNGSFGGALNGNEVNKNVPYSELKKLIE

SGQINQVSIGQTTIKAISSSHNTVYTAKKVNDPELVSLLDSKNIAYGAYSETNWFTDILFSWVLPVFIFF

GIWMFLASRMQKNMGSSILGIGSSKKLVNSEKPKVKFSDVAGVEEAKEEVKEIVDFLKYPERYIKLGAKI

PKGLLLVGPPGTGKTLLAKAVAGEADVPFFSVSGSSFIEMFVGVGASRVRDLFENAKKEAPAIVFIDEID

AIGKSRAASGMMGGNDEREQTLNQLLAEMDGFGTESSPVIVLAATNRPEVLDAALLRPGRFDRQVLVDKP

DFKGRCDILKVHMKDVKISPKVKVEDIARLTAGLAGADLANIINEAALLAGRDSKKYVEQNDLVEAVERA

IAGLEKKSRRINEKEKKIVTYHECGHALIAETTKGAKRVSKVSVIPRGLAALGYTLNTPEENKFLMQKHE

LIAEVDVLLGGRAAEEVFIGEISTGASNDLERATDIIKAMISMYGMSEIAGLMVLEKQRNTFLSGGQTIK

DYSEKMAESLDDYVKKTLDERYKDVKDTLNTYKGAIETMVAALYEEETIEGNKVREIIKEFEDQNSLPTR

LQELEEVKTEVKVEE

>ABV52655.1 phosphatidylserine decarboxylase-related protein [Campylobacter jejuni subsp. jejuni 81116]

MKDFIAKDGYLSLIILSLIFIFVWIFYSFSILLLALIVICIFLFRAPKRELVCSDEKAIFAPMDGRVTKI

ENIHHKDLGECVEITIKNALYDAGNFNTPFAMSIIDIRLRHGLFLCSELKSAKMMNERAFILAKVKENKT

IALRIYAGSFDRKLKLDNISHDLKAGDRMGFLINGSISLLLPKDTRIHIGLNDEIKAGSLLGYFA

>ABV52654.1 CDP-diacylglycerol--serine O-phosphatidyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MNNRPQLIYILPNLFTAASAFLGVISIIASIHGNYYTALIYIILSLICDGLDGRVARLTNSTSKFGVEFD

SLADLVAFGVAPAVLFYMAIGYDFGKLGSLITAFFVVFGAIRLARFNVTTGTYEPSVFIGLPIPTAAVVS

AIWTYAFISYDFLKPYGVVFLVLQAILGLLMVSNIRYPSFKKLDFNRSSVLKVLIILIIIFSFLYLYPLE

SLVILASLYVLYGIIRVLYTIIVSKFKIRNQE

>ABV52653.1 hypothetical protein C8J\_1054 [Campylobacter jejuni subsp. jejuni 81116]

MQKEFFQELQDILYEKNITIKFHSFQNFYEDFKSHKFIFNHEHQSIFKKNTSQQITLLHPTRIRRPKFVN

STHALAKIIHSVAHIEFNAINLALDASYRFKNLPLQFYYDWLEVADEEIKHFKLLNSALEELGYKYGDFP

VHDNLESALEATKDSLSFRMGIVHRGLEAKGLDANPFVVQKLQSSNHSIKNLLMEYLEIILNDEIKHVKK

GDTWWKFANQNKYDFIELCKTFKQFSLAGKKLNIQARIKAGFTQEECEVIEKFYS

>ABV52652.1 methionine-R-sulfoxide reductase [Campylobacter jejuni subsp. jejuni 81116]

MKELNEEEKKVILNKGTEAPFSGKYNDFYEKGIYQCKQCGASLYKSEDKFKSGCGWPSFDDEIKGAVKRI

PDKDGIRTEIVCANCNGHLGHVFEGEGFSAKNVRHCVNSISLEFVKTKD

>ABV52651.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MFSSMGSELYLMFFAAITLLAILNPFGNLTQFLAMSDGLPLMLRKKLFRTILYTAFTIVLVFLLSGPLFM

NYIFRVSLDDLRVSGGLVLIIMAIKNLLFSTKIATKDFSSYQDMDDKEILRQSLIPMAFPMLVGPGTLAS

VIVIAEDGGLDVALGGVMIAFIFMFILFHFAATIEKIVGKLILHVFSRIAQVFIAAMGFKMIIVGLKDIF

NL

>ABV52650.1 methyl-accepting chemotaxis protein [Campylobacter jejuni subsp. jejuni 81116]

MFGAKKNNTEIIEQLEKKCNGLGDILRSIGNTMAVIEFTTDGVILEANQNFLTTMKYSLSEIKGKHHSMF

CLPEVVNSSAYSDFWKDLRDGKARSGLFRRIAKGGIDVYLEANYLPISDNNGHVYKIIKFANDITQRHYE

MLDLRNTIAAANRSMAIIEFKPDGTIITANENFLRTMDFNIDEIKGKHHSMFCDSNYRHSKDYVQFWEDL

REGKFQSGKYIRYGRNNKKVYLEASYNPVKNDDGKIYKVIKFATDISEQVKKDQEKLRLISELAEKNDNL

TQDGDRVIENTVSNVQNIADMMSQSSNLVSSLNQQSDEIKSIIQTISDIADQTNLLALNAAIEAARAGEH

GRGFAVVADEVRNLAERTGHSVNEITTTINSIRNVTSQVVESIKSGLEDVNQSVELAKEARECMEKIRES

SAEVAKAMS

>ABV52649.1 putative leucyl/phenylalanyl-tRNA--protein transferase [Campylobacter jejuni subsp. jejuni 81116]

MESSNLYSKLLNAPKNAPVFLSQNLEADFIVKAYTFGLFPWTSKPVTWWCPDPRCILIPNQIHIQKNMKK

FINLYQIKLDYDFLKLITLCRDTRSQSWIDDEFITTYYKLFTQGYAHSLELYENNELIGGIYGLILGKVF

FGESMVSIKKNASKVAMIKLCDLLKPYDFIIDCQVYNQHLEFMGAHNISRKEFLNILKEKCNQESGFKNF

KDLIT

>ABV52648.1 ATP-dependent Clp protease, ATP-binding subunit ClpA [Campylobacter jejuni subsp. jejuni 81116]

MKYQENLQKYLDNAKNLSLINHHEFVTCEHVLFALLKLSIDFKDIFEEFSDGDLELLETELKNYISQNNQ

VIKQEIEPTISVVLDEILLSSKNKNNEIKIIDFLEKLIQDSRSYSSYLLKKHNINLTKIQELQNHENIQN

LSNHTSNLTLLAQNGKIDPLIGRKFELERMMQILSRRKKNNPILVGEAGVGKTAIVEGLALAIAEKKVPK

NLQNAKIFSLDMASILAGTKYRGDFEKRIKEILNELEKIPNAILFIDEIHTIVGAGSTGESHTDFSNLLK

PALSNGTLKCIGATTFMEYKNTFDKNKPLSRRFAKINVDEPSQEESLQILKGLKNKYEEFHHIKLNDEIL

QYAVIWGKKFFNDKFLPDCAIDLIDELGASFALNPKAKKNANLKDLENVLAKMTHHHKMFEFDQNKALMN

LKTNLKAKIFGQDEVIDSLVSSLKQSFAGFKNSNTPRGVFLFTGSSGVGKTEFCKALAEFLGLNLERFDM

SEYAEKHAISKLIGSPAGYIGFEEGGLLSNAIRKNPFSLVLFDEIEKAHPDLSNTFLQIFDNAELTDNSG

LKVDFKNTIIIMTSNLGLKESNELGFLSKNEEKSNRAIKDFFAPEFINRIDKILHFNDLNDAILVKIIEK

ELDEISKNLNNIKLSVDDKVKIYLAKKAYNKEFGVRLLKRIISEEIGEKISDEILFGKLKKGGIAKIKLG

KNGKLEFIF

>ABV52647.1 hypothetical protein C8J\_1048 [Campylobacter jejuni subsp. jejuni 81116]

MPKTQTLEQTKLSEPKMYKVILLNDDVTTMDFVIEILMNIFHQNLEKASQTMLEIHHNGSGICGIYTQEI

ALSKQKKVIDAAKLANFPLQAKVEEE

>ABV52646.1 possible periplasmic thioredoxin [Campylobacter jejuni subsp. jejuni 81116]

MKKILTLFLISLAFFLNACSKEEEIQNDFMFEEYHKGDKIVLNSVNGGSKTLIRTDKGFVVEGEEGKVLM

FDFFGTFCTPCKEEALDLSKLWKNNSSKFIIIGLTHFEDVSDETVKKFADDYGAYYFLSNGGSNDRIIAQ

ILKDIDYQNMEQLPFKVVLKNGIYQKISDYWNNNAPTNFYLGKIPTELMQEDLNKIYKGK

>ABV52645.1 small protein B-like protein [Campylobacter jejuni subsp. jejuni 81116]

MKIIARNKKALFDYSIIERFEAGIVLKGSEVVALRAGRANLKDSFVRIIKNEIFLLNSHISLLHTTHSFY

KHEERGARKLLMHRKQIDKLLGKVSIEGYTIVALDLYFNTKNKVKATLALAKGKNLHDKRETLKKKQADL

EARAAMKNYK

>ABV52644.1 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase [Campylobacter jejuni subsp. jejuni 81116]

MKAYAKANIFLKLTGFDSRKYHLLESRFILLKDLFDELELVDKESDSKKEFEIISNFKCENNIIQKAYLL

LSKRYNNELKELFSKKSLKLTKNIPVCAGLGGGSSDCASFLLLMNETLNLKLNLQELINLSIQLGSDIAF

FLSGFHSANVSGCGEIIEEFEDDIPNLKWTFPQISCQTKAVYDEFDRGIFDFQKNNNQAQIYKKLSTKEL

LQNFKNKELNDLFTPCATLYPKMKSYLQEDFFLSGSGSSVFKVDR

>ABV52643.1 carbon storage regulator-like protein [Campylobacter jejuni subsp. jejuni 81116]

MLILSRKENESIIIGEGIEIKVVQTGKGYAKIGIEAPKSLMILRKELVQQVKDENLHSVVQNDIKLDDLS

KKLIK

>ABV52642.1 tRNA pseudouridine synthase B [Campylobacter jejuni subsp. jejuni 81116]

MNKIFAAFKPRGLSSNAFLSTLKKKYKNKKAGYSGTLDPFAKGVLIVAFGQYTKLFRFLKKTPKTYKATL

WLGVYSLSLDDQNIKEIKNIKEFDLANLQQIIDQMQGIISYTPPQFSAKRINGTRAYELAKKGIEANLKP

CQMEVFDCKILSYNHPFLNIEITVSEGAYIRSYCELFARKLGINATLSSLERIKEGKFVYNNEKSLNVLK

YINLKPNFIKDLNKLENGAKIFVEELKFHDEGDYYIETEKYFSIINIKENTVKYLLNKVEKC

>ABV52641.1 ATP-dependent DNA helicase [Campylobacter jejuni subsp. jejuni 81116]

MNLFEDLNDSQKQAVSHIDGAMLILAGAGSGKTKTITTRLAYLIGEVGIPSHNTLTLTFTNKAASVMRHR

ALNFLQGNHNPLLCTFHKFGLLFLKLHFERLERKNSFIVIDTDDTKKIIKDLIHDKNKDNVYDIIKYISY

CKNEGKRVSNVFEDLNLLKEHNFEKYQNEYKFANYYRAYEEYLLKQNFVDFDDLLLLSNLILENDINFAK

EQSLLYNYITVDEYQDTNTLQYKILKNLCCMHENITVVGDDDQSIYSWRGAKIENILNFQNDFKNVKLVK

LEQNYRSVGTILQAANNLISHNEQRLGKTLICTKDTGENIKILKNENEKDEGLYIAQEVKKLLNSGVEAK

EIAVLFRVNALSRAIEEAFMKEKISYKLLSGMRFYERLEIKDLISYLRLILNPNDDLSFRRIINRPKRSI

GEKALKNLEEYAKKRQISLFDALCESDGGVGILTTKKAQNEANIFIQNIHTLKSYDNAKKVFDNIEELFK

IKDYFSEQDDGDERIRNLDEFYANLREKLKEDPEASLEDLLSEISLLSDQDNLDEECVCLMSIHASKGLE

FDYVFIIGFDEGFFPLNSEENLEEERRLAYVAITRAKKFLTISVANSRFYHGSRANINPSRFLEESKLIN

EKSKNQNIQKTSFCKGDLVKHKIFGIGRVVEVNKSGKEEKLNINFGGIMRVIMASFVEKAV

>ABV52640.1 hypothetical protein C8J\_1041 [Campylobacter jejuni subsp. jejuni 81116]

MLETILKNENFIHTMQKHCYEVISHLIEENIEFSIVANTNFIDFNPELPKELDVKQNPYALFALGGYTFE

SIQLNKDFIQFHAGFGNDDFDSFVKVDLGAITQIQIENNILFVNFSLYKREDSKNLQKSKNIFLNNPKNK

DIFKK

>ABV52639.1 peptidase (M3 family) [Campylobacter jejuni subsp. jejuni 81116]

MLEWDLSALFHDKEALQNFTQDQIQQSLNFKKNYENKLYALNANEFLQALKDYENLNQALGKIMTYAYLL

FAKNTQNGSFYAQYEEECKKIEENLLFFELEFCELAPEKSQEFTTFCKDYDFYLSNLLQNKRYNLSKNEE

RIMLYLSNTGANAFSRLFDESMSALKIPFEGKKLSEEEILSKMYDEDRKTRKKAAKKFSKVLQKNSRLLS

FIINMIKTERKNISLLRGYENAEISRHISNQISQKSVDSLIASAQKHFNLVSQFYKRKKQILGYDELKDY

DRYAPIGKEASFDFKTSKNIVLEAFQAFSPQFYDIAKNAFNQGWIDVYPQENKQGGAFSHSATSDAHPFV

LLNYTDKRRDLFTLAHELGHTIHQKLSYNVSYLNQNTPLTTAETASVFAEMLVFDFIKDKLKKEELLSLY

ANKIEDIFATFYRQINFTCFERRLHAQENELSTEEINKIWMEESQKMFQDSVKLTKNYASWWSYIPHFIH

SPFYCYAYAYAQLLVLALYGLYKSKKCENFKELYIKMLSLGGSVSPKELVGMFGFDIEDENFWEIGIKEI

QKLINEFMELQSC

>ABV52638.1 aspartate carbamoyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MRHLITTKDFNKVEIMELFKEASDFLDEKPRTFLKGKSITTIFFENSTRTLSSFESAARRLGARVLRLDV

SRSSSSKGETLYDTAANLDAMSPNAIVVRHANSGVPLILAKHIHCPVVNGGDGKHAHPTQALLDLFTIYN

HFQGDVEGKKICIVGDIKNSRVAASNIELLSRFNLDITLVAPPHFMPNTHLKKHYKLDENIIANSDIIMS

LRTQTERHNKTVYASLKDYANDFCIQKSLVKDKKLILLHPGPVNRNIDISDEMMSDERTLVLKQVKNGVA

IRMAVLKKLILENEG

>ABV52637.1 putative transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MFSKIIQSYAKGNLIVQICIGIVLGILIGISSKEISEIANLLGILFTSALKAIAPMLVFILILTSICTKD

FSQSGAKIKNIIILYIVGTFLASACAVLANFFFPVKLVLDGVQTATNSSPTHMSEIFKDLLFKIVDNPIN

ALSSGNYLGILTWAIAGGIALKHCSNEAKQVFIDINEGVLKIVKFIVKLAPFGIFGLVANSVAQTGAQGL

LSYVKLLILLVTTMLFVTFVINALIVFFYTRKNPFPLIFICLRHSAFFAFFTRSSAANIPVNMALCAKLG

IDKEFYGISIPLGATINMAGAAVTIAILSLTAANTVGIEISLLQAFLLSIIATFAACGASGVAGGSLLLI

PLACSLFNIDYDIAMKVVAIGFIIGVIQDSVETALNSSTDVLFTAICSKNELNYNIK

>ABV52636.1 S-adenosylmethionine synthetase [Campylobacter jejuni subsp. jejuni 81116]

MYLFTSEVVSAGHPDKCADIIADTIVDILLKNDKNSRVASEVFVAGNKVVIGGEVKSNHKLSKADYDNLV

KDVLKNIGYDGAGHFSKEQCLHPDEVDVMVFLNEQSPDINQGVDQEDGETGAGDQGIMFGFASCEAEEYM

PAAISYARMLCDRVYAYAKANPHELGVDIKTQVTIDYGTKANFENCEPQSIHTIVVSAPCVESMKIEDLR

SLVMKLILDSNLPKELFDPNKTRILINPTGKYVNHSSLHDSGLTGRKLIVDSFGGYSPIGGGAQSSKDYT

KVDRSGLYAGRWLAKNIVAAGLAKKCIVQLSYAIGVAKPTSVSVDCMGTNTSVNDDVLSDFVMQNFSLTP

NWIRDKFHLDKPSKETFLYADVAARGQVGQKDYPWEKLDALEQFKKLL

>ABV52635.1 apolipoprotein N-acyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKLKLNFLPYFSFIPKKLNTNSIIFKIIKVFFIAILLSNSIYLSFFENIFTQTISPFLAIWGLVLLLKSK

NSKQYFWIGFFVGILWFWWIGLSSIYFNLNYLVPIIPIIIGFIYGLLFRLCYLLKFDFLRLCGIFCISFI

HPLGFDWLNWGIFTVYGFFDPSYRGIICIFLIAYFIYEGYISRYYKIAIVLILFFSGFQYNEKQAQTLNL

NYKLINTNISQDQKFLQENLKSNSDILIQDILQAINEKKELVILPETAFAFDLKNTKYELILKELSYKIT

IITGAFHVEKEHTYNSTYIFKKGNVYILNKHFLVPFGEEIPFFKDLTKKYFLKNIEEFSKGPIQSKYKLD

NQIITNAICYEATKEQNYQNSQIIIALSNNAWFNNSSEYKLQQLLMKFYASKYGVSVYHATNGKENIVIL

PKKLLSKDWKNLSKEIFNDKK

>ABV52634.1 preprotein translocase YajC subunit [Campylobacter jejuni subsp. jejuni 81116]

MAENSILTSLLPLVVLFAIFYFLVIRPQQKQAKAHKQMLESLQKGDKIITNGGLICEVVKPEEDFIKVKL

NEDNVTAKISREFIAKKIDA

>ABV52633.1 protein-export membrane protein SecD [Campylobacter jejuni subsp. jejuni 81116]

MRNSKINYRLIIFIAVFIFGVAFSLPSFLQSERGAKINLGLDLQGGLYMLLGVDNEEAVKSKIKSIASSL

SYSFNKENILNDGLNTHDDILEFTLLDNADIAKVENLLKEIKGINIQSENMHYKISFTSEEVKNIENFAL

LQAVETIRNRLDQFGLAEPTVAKQGDDKILVELAGIKTKEDELRAKERITKAAHLQLMEVDDSKMGQAST

MSDAEAASYGLILVSDSRNPNLKYTLKSIPILDGSMLTDARVGISDKSNYPVINFTLNAEGSKKFADYTG

ANVGKRLAIVLDNKVYSAPSINERIGGGSGQISGAFTQEEARDVAVALRSGALLAPVKLLEQRSIGPSLG

ADSIKMSMIALIGASVFIVIFMMMYYGVVGIFANIAMLVNVLVVVAVMAMFGATLTLPGMAGLVLTVGMA

VDANVIINERIRELLRDGVNIRASIEQGYKNAMSAIIDSNITSLVTSVALYAYGTGAVKGFAVTLGIGIV

VSMITAILGTHGMFDYFMQRIEKSNNTRFWFGYRRR

>ABV52632.1 protein-export membrane protein SecF [Campylobacter jejuni subsp. jejuni 81116]

MQFFSEKKIYDFMRMRFAAISLSFILFFGSIYLLWDRGLQYGIDFSGGTLVQLKYENAAPITQIREILEK

QGTFQNLSVTEFGSNEEVTIRFLGSNDNVSNDIGEHISTLLKDTGKFEVRRADVVGPKVGDELRNKGLMA

IAVSLIAILIYIALRFEWRFALAAIISEIHDVVITLGAISLFKIDVNLDTLAAVLTVLGYSLNDTIIIFD

RIREGIKTSKKTELAPIINESVSATLSRTVLTSGLTLATVVILYFFGGEMIQGFSLALIVGIIAGTLSSI

FVASPTLLWFKFSVLEFRNKEIEKAKRKQDKERNRAMYEKGTV

>ABV52631.1 leucyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MAYEASLIEKKWQKIWDENEYFEPKDDLNLPKKYILSMFPYPSGRIHMGHVRNYTIGDALARYYRKIGFN

VLHPIGFDSFGMPAENAAIKHKIHPKSWTYENIAYMKKELFSLGFSFSKKRMLATSDPLYTKFEQEFFIK

MFEKGLIYTKEANVNWCEQDQTVLANEQVEDGKCWRCGHEVVQKKMPGYYVKITAYAEELLKDLEELKDK

WPNQVLTMQENWIGKSEGLEFSLNLDEESKQKTKESSLEVFTTRADTIYGVSYIALAPEHKIVQNLLSQN

LLNQDVLNKIKAIQNQSPRERQSSEKEGYFLGIYAIHPLSGEKIPLWVANFVLADYGSGAVMAVPAHDER

DFEFATKYNLAIKQVIQTQENLPYTQKSGKLIHSQEFDNLDCNEARLKIISQFEAKNIGKRVVNFKIRDW

GVSRQRYWGAPIPMIKCQSCGIVPQKLENLPITLPEDVQITGEGNPLDKHPTWKNCICPKCGKEAQKESD

TLDTFFESSWYFARFASDEKTWQEKALDEKSVKYWMSVDQYIGGIEHAILHLLYARFFQKALRDLGYLTQ

NEPFDRLLTQGMVLKDGAKMSKSKGNVVDPDEIIEKYGADTARLFILFAAPPAKELEWNDDAVEGAYRFI

CKLYDRAQNVKKGELVELKQENLNKEEKYARLKVYEALKKSFEVYHQSFAFNTLIAACMEALNALALCKN

EALEQEAFYIILNILEPIIPHVCFELSEELFKCKNFKKLELKEEIFVKDTLNLAVSINGKKRAEFEISSS

ASKEEILAFAKENTAKWLEGKSIVKEIYVEGKLVNLVIK

>ABV52630.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKKILIFCIGLFLGACGYVPTSKIANNIFDEKVYVNVELSQQDPKNSIYVADTLKEMVISKLGRKLALKH

EADDVINVKMNNLEFIPLAYDKNGYVISYKAKLNLDFNVVFKDGSSQAFSTSGSYNFEISPNSIISDSAR

YEAIRAASSEAFDEFISVIAIKGQKRDSKY

>ABV52629.1 hypothetical protein C8J\_1030 [Campylobacter jejuni subsp. jejuni 81116]

MIPNTNEIAKQTLIALKERKLKPTPENYTEIFEELSLKYGITSSNKAKLDKYKTLLLPIYQQELNSKTIR

SLEELISFLISVLNRQSGKQFSEFFDFLYTISKTLQISKDKKIRDLAKVTSIRISKTMDSESIYLLTKKW

KELERNYDENDLEEQARKYGISKYDDYDSVIKKLLVKLEERSYEHFSELLCLGLNPSLVEDLKIQGFIQN

LTQKPFVIGEENFKNELMEFINHRIMVDNMYVQKNLNFFNDNLKKIYELLVLLNKSNEKNMDFINTLKPD

ENGEVKLSFEDLKLKFKQLGEKITSLNNQIEFTQSLEEREAWSVLKELDKMDENFNKYKVNYSLALFSIV

NYRFIMEKYGMGSLNEIFVRFKKILKDSCSEFDELWMIDEKSYLIVSPGKSKDEITQLVNTNLKTIENFR

FIYKQDIITPKIHVAYLDKQSKPSINILDELIKQIAAVNEQHNES

>ABV52628.1 FolC bifunctional protein [Campylobacter jejuni subsp. jejuni 81116]

MKVENFLAQKSINYDKIDRFLMFRMYEKYKKYFKNIPIIQLIGTNGKGSTGRYLTQLLENLNYKIGHYTS

PHIFSFNERFYLDGKIANDEELEQAHIRLEEIFKQDLQKLSYFEYATFLAMILFQKCDFIVLEAGVGGEY

DATSVFERRMNIFTRIGFDHIQILGNSLEDIARTKLKVMAPVALISDEQEQNVLNLAKKIAFLKKANLQV

SSLNPFLKEKFEIYCKKFVLPCFLKHNLKLALKACEILTSQEKTLEALKKLQGLNLQGRCQEISPNFFVD

VGHNPMAAKAMLDKFQGEKINLIYNAYLDKDIFQILNTLKPIIDTIQIYKYKSAERKLADDEIYSIASKL

GIQCKEFVKLEENKKNLVFGSFMLVENFLKEWCGKK

>ABV52627.1 peptidase, M23/M37 family [Campylobacter jejuni subsp. jejuni 81116]

MVKNKFTITITDINGSRHFYLNQIIKKIVFYTIAFIVLFLVFSGFYIKYLDSKLSDISEKREELLKKSKE

LELSNSQMQKSIEEKTQQYAAIEDKIASFEEALGLEAENNLTISARLDNLQLTNEQQLGILGQIPNGWPI

ENKGITGNFGWREHPLLKRREFHPGIDLRAEIGTPIYAPASGVVEFSGYSDNGYGYNVILLHNFGFKTVF

AHMMRKEVVKAGQFVSKGQLIGYSGNTGLSTGPHLHYEVRFINKTLEPLYFLNLQRKNMNDFFNQERRVP

WQSLIKAVSAQHPALAQKQQ

>ABV52626.1 hypothetical protein C8J\_1027 [Campylobacter jejuni subsp. jejuni 81116]

MAIFNKGGISPTSSSSSETTVISSGARIEGKFYFASMLHVDGELSGIIHSESIVVIGKNGNLKGELQADK

IVVNGYFEGQLEANSLEILAGGVVNGDISTQKISIENGGRFNGTSKIKEDTIKLIENNNEE

>ABV52625.1 transcription-repair coupling factor [Campylobacter jejuni subsp. jejuni 81116]

MQASFYEYLQNPKICELLLCKDEKQADLLAQVSRFKGLKTFVLPDFRAQFGDDLRAFSKELFDLCKILNA

YHKEEEKKILISPLNTVLKKLPSKKHLQNYHIDKKQNFNLKCFEDEISRLGYEFVDIVQDKGEISIRADI

IDIFCINEENPIRILLFGEEIESIRYFDLQSQKSIPNELEHFEICPFLKYFDKENYEIFKDKLEDFQSDT

LIHDINSLGFWCIDDFFDYLELDFLACEKFDINEYEKDVSFVNAKILPQAKKFKELQSSYNKDFFEFHKN

KKITLLAKNEALFKALELEDTQNIYFVKSDLRLNLISPEELIISLNQKEKQKTRKKASLIIDELKNGDYI

VHEDYGVGKFLGLEMIVISGAKKEFVAIEYQNSDKLLLPVENLYLIDKYLGVSGSIPSLDKLGKTSFIKL

KEKLKTKLLAIASEIVIMAAKRSLVQAKKITVDLSRQADFITSAGFIYTSDQEKACHEILQDFQSGKVMD

RLLSGDVGFGKTEVAMNAIYPVVKSGFCAFLFAPTTLLSHQHYKTLKKRFDPFDIKVFKLDRFTSSAEKK

QVLQNLKENKACVVVGTHALLSVECENLALVIIDEEHKFGVKQKEKLKEITQNSHILSMSATPIPRSLNQ

ALSSIKSYSVLQTPPEDRMDVRTFVKENDDALLKEAIARELRRGGQIFYIHNHIASIEQCKKHLLELFST

LRILILHSKIDAKVQEEEMLKFENKEYDLLLSTSIVESGIDLPNANTIIVEKSDRFGMADLHQLRGRVGR

SDKQGYCYFLIEDKNAITKDALKRLVSLESNSFLGAGSVLAYHDLEIRGGGNLLGVDQSGHIEQIGYSLY

LKMLEDELNALSKNEVDQKENKLDLKLNVNAFLNSELISEDRLRLELYRRLSKCEQVHEVYEIEGEIEDR

FGKLDIYTKQFLSLIIIKILALNKFKSISNYEQNIQFTALNDEKELIKAKSKDDDDILEAILTHLRKA

>ABV52624.1 putative ATP/GTP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MDWNKTYAAIYRARKDYLKPIFEIDPITLKDLVGMESQKKALYENTLNFIQDKGANHALLWGSKGTGKSS

LIKAIFNEFKDQGLRLVELNKEDLFALVDIIDEIRLENFKFILFCDDFSFEKGDDSYKFLKPLLEGSIEK

APNNVIIYASSNRRHLLSESIADNLDTQIAHTELHLSDAAEERLSLSDRFGLWLSFYQGNLEEYLKMIDF

YFKDYSCDKELLHAKAKEFATLRASRSGRTAKQFYLAFKENFK

>ABV52623.1 possible nuclease [Campylobacter jejuni subsp. jejuni 81116]

MTGARIFTKLLNLDLNYHDFDWLENQGLSEFELLISVILTQNTNWKNVLKALENLKKENIVSLEQINTLS

NLELATLIKPSGFYNTKAKRLKGLVESIINTYENLENFKTNVSREWLLNIKGLGFESVDSILNYLCKREI

LVVDNYSLRLAFCLGYEFENYEELREFFQSGIESEQENLCKILGRKCELYELYQIFHALIVAFAKQSFKG

QKLSPKGEEWIKILKEDL

>ABV52622.1 phosphomethylpyrimidine kinase [Campylobacter jejuni subsp. jejuni 81116]

MKAKGSELIPVLTIAGSDCSGGAGIQADLKTFSAHNLFGMSVVLSVVAENTARVISVHDIPTQSVDEQIL

AVFEDIVPKATKIGMIGSCELMSCVAKNLSEFKPQNVVIDPVMFAKNGYALMPQENCDFFKQTIVKFADI

LTPNIPEAEFLCGFKIANEEQMIKAAKHLCSLGAKAVLLKGGHSEENANDVLYDGKEIYILKGERIETKN

THGTGCTLSSAIASNLAKGKDLFYAVSEAKEYVRNAIYYSLNLGKGCGPTNHFFKFLDEK

>ABV52621.1 thiamine-phosphate pyrophosphorylase [Campylobacter jejuni subsp. jejuni 81116]

MKNKLDLSLYLVASQGNKSEECFLNTLENAIKGGVSIIQLREKELNAREFYKLGLKVQKLCKAYKIPFLI

NDRVDIALALDADGVHLGQEDLEVKLARKLLGDEKIIGLSLKKLEQLEFIQGANYLGCGAIKATPTKESS

LLSLELLSQICDKSPIGVVAIGGVDKAVLDELKGINLSGVAVVRAIMDAKDAFLAAKELKRKIYENLPLK

>ABV52620.1 uroporphyrinogen-III synthetase [Campylobacter jejuni subsp. jejuni 81116]

MKIYLLNETPFKGVENLILNEIIFYDFSIDLSLYDALICTSKNALKALQNAKITLNFKLNLYAVGQSTAQ

YAKNLGFKKIKIPSKAYGKDLFLEFKEELKTQKCLYLRAKNIVSTLNLDLKNVGVDLDEVIVYENVFKKG

DKKLTHPAIFIFTSPLSVENFLKFYSLKEEDKVVVIGQSTAKKLLNFKNLYICENQSLLECVKLAKTLV

>ABV52619.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MSLTLNISSYTPKIIQDSYYYLQAQILSHNATQFSKYFLYQAKQENKECLDNIYFNYAKALIKIKYFYPI

AQCVNFKFSNFNPDANLNKDGVIIAHISIALNRDKNVNDEILLTKSIIIYPKENFWNLKN

>ABV52618.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MSKAFTLFELIISLILFTFITSLLSKSLMDFYHLNFTALHTNNLITQAHLNLLKIEKLIQNCINITFSQN

TLKCLLKDELISLKDNKLYLINSALILENNHTLYSPHSDFKTQLQNRKDLYNDNEHISYAYKINKIEKIS

ILENGISTNFTGSFIPLQAQLVIKLQNEELIYEIKPKFNEQLNQQGLISKNISSFNLQNNKLKICLKRQT

KYCLEKRILL

>ABV52617.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKAFILIESISAITIISLIFIGIFYHYTQLYKNYENLNIFERLYKLQEELYEKPIFKTIILQTSALKPI

VLQEQFINDGIFQFQKLYFQDQNYSVYFKE

>ABV52616.1 pyrroline-5-carboxylate reductase [Campylobacter jejuni subsp. jejuni 81116]

MLYILANGSMATALAYGLKDDYEICIVGRSIEKLQALAKEGFKTLLYKDFNIEGKDVILAFKPYALENIA

QMLKGQARILISVLANVDFEKLQTIKAQNYVRIIPNTAAKYKASTTPYILKNSHFENEILDILKTFGSAY

KLDNEIQMNAAMAISGCAPAFLALIAESIANAGVYEGLSKELSLNLTRSLFKSSSALLEHEHPAIIKENI

CSPGGVTIKGIKILEQKGIRGSFFEAINASSAK

>ABV52615.1 hypothetical protein C8J\_1016 [Campylobacter jejuni subsp. jejuni 81116]

MTLAVKCPILGFEETKNMEFSTIDEVFVRLKSLDGKDFSFVLINPYLIRPDYEFDIPTYYQELLSLTPES

NMKIFNIVAIAKSIEESTVNFLAPVVINLDNNTMVQVILDTVNYPDFFQADQIANYIKK

>ABV52614.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKKGIFLLVFLSIFFSACSTKNDEGLYNLSASEWYKQIIKDLQDKDLEKADDHYNGMASEHVADPLLETT

LIILAQAHMDEEEYKLAEFYLDEYNKKFGNSRNADYIRYLKIKAKFDAFAVPNRNQALMLESQKEIDTFL

KDYPYTEYEPLVQTMLTKFNLAVFYLNSTIENLYQRIGHDESAQIYKQRLQESEFYQQSIIKPELPWYRS

IFERF

>ABV52613.1 ATP-dependent protease La [Campylobacter jejuni subsp. jejuni 81116]

MQIEEIQNYPANLPVLVEDELFLYPFMITPIFINDLSNMKALDLAIKNDSMLFVAPSKLENGRNFDEIYN

CGVIGTIMRKVPLPDGRVKILFQGYAKGKIIEQISNKPLEAKIELIKEDFLEGTKKEALLEVLKEKVKNL

ANISHYFSPDLLRTIEEGFDASRICDLILNTVRIKKQVAYEFFVLTDLEQKLVKLIDLIAQEIEANKIQK

EIKNKVHSRIDKVNKEYFLKEQLRQIQKELGSDTQKEDEVREYQKRLELKKKFMHEDAYKEIKKQIEKFE

RIHQDNSEASMIQTYIETALDIPFEKISKKKLDIKEVSKQLNHDHYALNKPKERIEEYFAVRELLEKRKI

AEKDGAKVILCLYGPPGVGKTSLANSVSKALKRELIRIALGGLEDVNELRGHRRTYIGAMPGRITQGLIE

AKQINPVIVLDEIDKLNRSFRGDPSAVLLEILDPEQNSKFRDYYLNFNIDLSKVIFIATANDISNIPAPL

RDRMEFIELSSYTPSEKFHIMKKYLIPDELKKHGLKSNELSIDDETIELIISDYTRESGVRNLRRKVAEL

CRKSAKKLLLENIKKVIINTKNLNEFLDKKVFEIEKNNGENQVGQVNGLAWTSVGGDVLKVEAVKIKGKG

ELTLTGSLGDVMKESARIAFSMIKVLIDEGKIKIPKKIIIDPKVNVYDSYNIHIHVPDGATPKDGPSAGI

TISTAIASIFSDKKVKADVAMTGEIDLKGKVLPIGGLKEKLIAAYKADIKTALIPRKNYERDLKDIPSEV

RDNMEIIAVDTFSDVLEYTLI

>ABV52612.1 30S ribosomal protein S18 [Campylobacter jejuni subsp. jejuni 81116]

MAEKRKYSRKYCKYTEAKVEFIDYKDTAMLKHALSERFKIMPRRLTGTSKKYQEMVEVAIKRARHVALIP

YIVDRKEVINNPFEGL

>ABV52611.1 single-strand DNA binding protein [Campylobacter jejuni subsp. jejuni 81116]

MFNKVVLVGNLTRDIEMRYAQSGSAIGASAIAVTRRFTTNGEKREETCFIDISFYGRTAEVANQYLTKGS

KVLIEGRLRFEQWSDQNGQNRSKHSIQVENMEMLGNSNAPQQGGNFGNNSFSNNNYSGNYENQSYDPYMS

ENQNFNKAKTNPTPQRNQNPQHEEKLKEIDIDAYDSDDTNLPF

>ABV52610.1 ribosomal protein S6 [Campylobacter jejuni subsp. jejuni 81116]

MKHYEVLFILKPTLTEEEVNAKLEFVKEVLTKNGAEIETVVPMGTRKLAYKIKKYERGTYFVIYFKAPTN

LIAELERVLRITEEVIRFLIVKYENKKEIAAWEKLSHGIKQSKKEIKPLDAPEIQ

>ABV52609.1 hypothetical protein C8J\_1010 [Campylobacter jejuni subsp. jejuni 81116]

MNKKFSYPIPNFTDRRKSIIFWRYLRFQARKILYFPQVRLLEKTLNEEKNKHLKDFFSQRPYACYNAIRR

FCDKSFKANERVKTLIYDVDKGLTCFKFLPEEQMIFSFDEDFELFLGYNHNVYEEGFWAFSLKFKKYTIS

QCNFCFTLENNLLLSCIQGYKYKDFNILEINKILTKKCHGLRPVALLIECSKMLCEILKLQATLGVHEKN

QIRSQKGKEKGYFVDYQKIWLENGGELIKIDKHKYYKLHHSQKNLEEIPSQKRSMYKKRFAMLEEIKVNL

DKTLDIQD

>ABV52608.1 hypothetical protein C8J\_1009 [Campylobacter jejuni subsp. jejuni 81116]

MRSLLLLIVILILGIKFYSIEFLATVLVISFLIFFHELGHFLAARSLGVKVEVFSIGFGKSLIEREFKGT

NYRLSALPLGGYVKLKGQDDMRPGFENLDKDSYSILSPLKKIYILFAGPFFNLILAFFLYIIIGNLGLNK

LAPQIGNIAPNSAAQEIGLQKNDTILEINGVKIQSFDEISKHLSLEPLKILIDREGKNLEFTLTPKIGQG

YNDFGQIVEKPQLGVSPNGTSTLVKHQGLESFKYAIQESFQASTLIIKGIIKLISGEVEAKNLGGIITMT

EITSKAAQNSFTLLLFITALISINLGILNLLPIPMLDGGHILFNLYEMIFRRKVPQRAFEYLSYAGMAIL

LSLMLFATYNDISRIAGE

>ABV52607.1 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MNLPNILAIFRMVLAPLLFFLLIHKFENIHQSWINYFAALTFSLAALSDFFDGYIARTWKQTTKLGGILD

PLADKMLVLAAFLGLLLTGKANEWVIYIILVREFFITGFRVVMISENLNVNASFAGKLKTAFQMTAIGFL

IMEWIGGEILLYIALILTLYSGFEYIYTYIKAQKKGEK

>ABV52606.1 nitroreductase [Campylobacter jejuni subsp. jejuni 81116]

MKKELEIFSTRYSCRNFKNEKLKKEDLNSILEIARLSPSSLGLEPWKFIVVQDEKRKEELSKICNQQKHV

KDCAALIIIISRLDFLDYFEEKLRKRDMSETEMQKRLDTYMPFLKSLNQEQKISYAREQAHIALASILYS

ANALNIASCTIGGFDKEKLDSYLSLDIQKERSSLVVALGYCNDKKNPQKNRFSFDEVVKFI

>ABV52605.1 hypothetical protein C8J\_1006 [Campylobacter jejuni subsp. jejuni 81116]

MIGGFEKARVDNFLNLTYPFETAVILSLGYKAHEPKYSTQRLNFNEVVEFYKEK

>ABV52604.1 hypothetical protein C8J\_1005 [Campylobacter jejuni subsp. jejuni 81116]

MNFKELISKRRACKLFNDKKINEKDLHFILESGVLAPSSHGFEPWKFVVLEQKEHNLKLSTLCYNQQNVA

SASHNIIFLARKDLQSKDEFAQKQVRRFSGSSEENFQKILEIYTHKTNAMNDNELYHYAQLQCYLAMMQM

SLAAMSLGIDLV

>ABV52603.1 hypothetical protein C8J\_1004 [Campylobacter jejuni subsp. jejuni 81116]

MKEIKLKEDLEKIYPLIKQLRNNLSLKDFLDKIQLATQTQHYKLFAYENEGSYKAACGVMPFNVLYHNHC

LYICDFVVDEALRGKGIGQAFLKKNPNLGKRSRI

>ABV52602.1 hypothetical protein C8J\_1003 [Campylobacter jejuni subsp. jejuni 81116]

MKHLLYLIGDELTINEKFKNYIYRTYEEKFKEINEIRIQNKTDKDLPFLLENLLNQYDFITLFTSPLHYA

TVAKILATLNDDNLILKDDTLVPDKAEFSKNSFVCNFSNSKINVVKINPSEKLPNLLGHIKLNFAYFCIF

GMDDESAILLLQTLTKSYEISIKSTKLLDNLVLIKATCANFGKLDGFLNSVKNLFGQKVFLGKDPIHFIS

SKLLEKKLKISFAESCTGGLCASTLTKISGVSEIFEGSIVSYSNRIKHEWLGISKSVLENNGEYSERCVY

FMLKGIFKTANPDFALAISGVVGEKDEGKIKSGTIYIGAMFRDGTFIQETLYLDGDREFMQEQAVLATFC

LLLKLKPEIFEI

>ABV52601.1 isoleucyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MDYKETLLLPSTTFAMRANLAELEPQRFKKWFEQNYAYEKMKENRKNAKKSFTLHDGPPYANGHIHIGHA

LNKILKETIIKTHYFKGESVRFTPGWDCHGLPIEQQVEVKLGEKKKSLSKKEIREFCRQHASEFVDIQRE

EFKNLGIIADWDKPYLTMKFEFEAAIYRTLCEIAKKGLLCERSKPVFWSWAAKSALAEAEVEYQDKEDYS

IFVAFDLDVKACEKLGVSKASAVIWTTTPWTLVANQAIALNPNENYVITKEGLIFASALLKSMVEKGLTS

GEIQKELNAKEFEKLEAINPLNGRKSVLIMGEHVLMDGGSGLVHTAPGHGEDDYYACLKYGIEVLMPVDD

GGCYDETLRAKELLPSHLLEEFIGLHIFKANEKILELLGEKLLHSSKFIHSYPFCWRTHKPVIYRATKQW

FILMDEPKLQGKTLRECAKEQLLKTTFYPQSGVKRIGSMVENRPDWCISRQRDWGTPIAFFRDKNTKEVI

FDDELFDFVAAIFEKHGADAWWEFEIKDLIPTNSKYKAENLEKVYDILDVWFDSGSTFNAVLNSGLYDAG

EKRASMYLEGSDQHRGWFQSSLLVGTAINESAPYESILTHGFTTDEKGQKMSKSKGNVIAPEYVAKTYGV

EILRLWILLSDYSSDLKISDNILKQVGEQYRKIRNTIRFLLANTNDLKDLEVKEFSFIDKWILSRATKVF

KASKEAFFAYEFAKGFSLLLNFLSADLSGIYLDISKDRLYCDSENAQRRKSAQVAMALIAKELLNLLAPN

LSYSVDEALEHANVLIKGDAKDVFDLSLTQDFDYDFGIDDTFLMSAREKFFEQIDILKKDKIIKSTLELN

LNISFNKFPNEELADWFMVSQISNENEEILAEFEVENEKFKITKASLCKCPRCWKLQSKDEETPCLRCEE

VLKGIQC

>ABV52600.1 hypothetical protein C8J\_1001 [Campylobacter jejuni subsp. jejuni 81116]

MLENPIPNSIIITTIAVVLAFSALAVFLIKKTKENK

>ABV52599.1 aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, A subunit [Campylobacter jejuni subsp. jejuni 81116]

MITLKEALKYSKEELENLKKELNEKAKKEKKIGAYIEQFLDKDLSVSGEGVPVAIKDNISVKGWELTSAS

KILQGYIAPYDASVIVNLKANGFSPFGRCNMDEFAMGSSTASSYYGKTLNPLNFERVPGGSSGGSAAAVA

GGLALASLGSDTGGSVRQPAAFCGCVGFKPSYGRVSRYGLASYSSSLDQIGVLTQNVEDAAILYDAIAGY

DKMDSTSANIEFIKTAPNLNVNKKLKIAVIENYVNDADSEVKNALLKTIDMLKANGHEIVYKNLLDSKFD

IAAYYIIATAEASANLSRYDGVRYGKRSENIQNLKEMYVNTRSEGFGEEVKRRILLGTFVLSSGYYDAYY

IKAQKARAFIKAKYEEILQDCDLIFMPVTPTTAFKFDTQKSPMQTYLEDVYTISVNLAGLGGISVPVAKD

KEELNISAQLICKAYDEQTLLDGALSLEQMIKH

>ABV52598.1 inosine-5'-monophosphate dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MKIVKRALTFEDVLLRPGYSEVLPKEVKIHTKLTKNITLNMPLISAAMDTVTEHRAAIMMARLGGLGVIH

KNMDIASQVREVKRVKKSESGVIIDPIFVSPKASVAEALEIMAEYRISGVPVVDEDKKLIGILTNRDLRF

ESDFSNLVENVMTKMPLITAPKGCTLDDAEKIFSTNKVEKLPIVDEQGRLEGLITIKDLKKRKEYPDANK

DNFGRLRVGAAIGVGQMDRVNALVEAGVDVVVLDSAHGHSKGIIDTVKAIKAKYPNLDLIAGNIATAAAA

KALCEAGVDAVKVGIGPGSICTTRIVSGVGVPQISAIDECVEEANKFGVPVIADGGIKYSGDIAKALAVG

ASSVMIGSLLAGTDESPGELFTYQGRQYKSYRGMGSLGAMQKGSSDRYFQQGTAQDKLVPEGIEGRVPYV

GSIRSVVHQLLGGLRSSMGYVGAKDIEDFQKRAEFVEITTAGLKESHVHDVTITHEAPNYKVNHQ

>ABV52597.1 hypothetical protein C8J\_0998 [Campylobacter jejuni subsp. jejuni 81116]

MSFEENLKHANESLEKLNNQELALDESVKIYKEGLESIKKARLELEKAKLEVEQIDE

>ABV52596.1 hydrolase, carbon-nitrogen family [Campylobacter jejuni subsp. jejuni 81116]

MSKIAALQFPTLALSESRLDYYLKASKDNGANLVVLGEYVINSFFTELLHMPKNMIKEQSEAKKESLIKL

AKKYELEIIAPYVSVEAKSYKKLCLKVTPNGVKSYEQQILMPYEHWNEEKFFSNKTSSELKIFTFNYEKL

KCALLFGFEAHFDIFWQQIMTKKIDLVIVPSACTFESKQRWEELLKTRAFLNSTSILRVNRIGKTKDEWN

FYGDTLFINAFGEIESKLGSEEEMLIIEPKKSDEARKLWGFEKIIKEFKN

>ABV52595.1 UDP-N-acetylmuramate--alanine ligase [Campylobacter jejuni subsp. jejuni 81116]

MQNIHFIGIGGIGISALARFLKEKGFKISGSDLKESKITKELEKEGVKVSIPHHKDNILNKDLVIYSAAI

KEENPEFKHAKELGIKCLSRKEALPLILEDKRVFAVAGAHGKSTTSSILASLLDDASVIIGAILKEFGSN

MIYKESQNLVFEADESDSSFLNSNPYLAIVTNAEAEHLDHYGNEVSKLHHAYTQFLDVAKIRVINAEDEF

LKNYKNESIKLYPSKDIKNCTMCIENFKPFTSFELKDLGEFKVFGMGYHLALDASLAILAALNFLDIETI

RTRLKNYQGIKKRFDILHADENLVLIDDYGHHPTEIKATLSAAQEYAKLGGYKKITAIFEPHRYTRLAAN

LKEFAKAFEGVDELVILPVYAAGEEPIELDLKAVFPKALFVEDIKREGKFLVASKGQVFEEGLIIGFGAG

DISNKLRQKNE

>ABV52594.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MSRFFLYLLIILILALITFVLREKLGKKTKPFFGVLLVIFIVLAVFFEFENTQKSHLRTDIIVAFNQNKN

ILCKDINVSKAYFNYEFGTGSFISKDNNQSFNSLIIDIKDCRLNDE

>ABV52593.1 putative mismatch repair protein [Campylobacter jejuni subsp. jejuni 81116]

MNDTKEELISKLDLNSYLEEFKALFARDKEIFLQGDSNLHFKRIHELCEVEFPTMPELSNLDKALVHLSK

QGILHLDEIFEFVKIFRYFEKLKKIKLGTNLDSWLQKIEFASGALELCLNFDEKGELKESLDERLVNLNT

ALRLKNESIIAEFKKFCYTKALMPYLIDTQIHLINNLEALLVRGGFNHAIKAKIIGRSSGGGFYIVPLSV

ENLQNDIEKIKNQKEEIYYEYAKNFSAFLAKNLPFLKFINTAFDLFDHYSARVLFAKKRDFEFVLCDQST

DLVLKNFAHPALKNPKSVSLEFKKQVLIITGVNAGGKSMLLKSMLSAAFLAKHLLPMHIKASESKIGTFK

EFDAIIEDPQNVKNDISTFAGRMLHFSRLFSKKNLLLGIDEIELGTDFEEAACLYSVLISKLIANNLKII

ITTHHKRLAMLLAKNEQVELIAALYNEELSRPKYEFLKGTIGKSYAFETALRYQIPPNLVSEAKKLYGED

KENLEELVGKNINLELELKAKLENVEKKEQKVDEILLSLKDQKEKNEQEFRTSLRNLEFKFHKAIEEAKK

TIQLKDTKDKQRSLNKANELKKEIILPSMEQNEELRVGDFVKYEKIKGKIISISKNDAMVESDGIKLRVP

LKLLKKSGAMPKKVAKTSISISKPSNLSVTLDLHGLRSDEAISRLDKFISDALLAGFDEVLVYHGIGTGK

LAFAVREFLKTHKSVKGFNDAPINQGGFGAKVVRL

>ABV52592.1 hypothetical protein C8J\_0993 [Campylobacter jejuni subsp. jejuni 81116]

MITKDNLKQVLENLGFKNKNENYVKTINNYTLLIDYKNQSINYPKEIKIHDKTTSNFSHPENFVVFECVH

RLLEKGYKAEHLELEPKWNLGRDKKRW

>ABV52591.1 hypothetical protein C8J\_0992 [Campylobacter jejuni subsp. jejuni 81116]

MAGIKKGGKADILVKDNENNPYLIIECKTTDSKNSEFIKEWNRMQEDGGQLFSYFQQEKGVKYLCLYTSD

FSDKLEYKNYIIQAYDNEEYLKEKELQNSYKKSNNNIELFKTWKESYELQYFKQGIFEANVNAYKILEIT

PTFDNLKELKEEGKYHEFAKILRKHNISGKENAFDKLVNIFLCKIYDETFNKNNLKFGYFGVMADTYANM

QDRLMWLYKEAMKEFLGEKITFVSNEDIEKDFKQLKIKTLKEVMQNYIKELKFYSNNDFAFLEVHNKELF

LKNALVLKEIVELFANYKLTQNSTNQFLGNLFELFLQKGMKQDEGQFFTPIQICEFIMYSLPLQEMLSKS

SKALRVIDYACGAGHFLNTYANELKRYLTEDELKEHYKNIYGIEKEYRLSKVSKVSSAMYGQNEINILYA

DALASFELANTNNLEGEKAKPQIESNSFDLLIANPPYSVKGFLETLSDKSKNTYKLFNDDINIETNNSIE

CFFCERANQILNDNAKAAIILPSSILNKDSIYKNTREILFQNFDFIAIVELGNQTFGATGTNTIILFLRK

KETFKQENHLISQDYSLIKERIEAENLKDNENFYQNYLSAYCDFRKFDKELYSNFLNGNLDFNLAELEAF

KDYRNAFRQTSDYKKLKESKIYKESKDKQDLEDKAFLAYAQAIEKDKLLYFSLSLNQEVLIIKSPSDIKE

QKKFLGYEWSNRKGDEGLKELHEPYLSPLFERGNPQNETKLNTLIYKSFLNTLDVIPQELQTYATKARLV

DMIDFEKVEFNKAISLNPKTQREEIKSQYPLVKLKICGDFFMGGTPSRKNINYWNGDIKWLTISDYSNHQ

VIMDTKEKITREGFKNSNAKMIQKGAVVVSIYATIGRVGILGEDMTTNQAIVAIIPNEEFINKYLMYAID

YFKFQLYNEVITTSQQNINLGILQNMVIPKPPLEIQKQIVAECEKIEEQYNTLSLSIKEYQNLIKAMLQK

CGIIEDNQEYELNSILDKINNLCKINLDSEFLSSFNKTIKEYALSNPIFKLSIGKRVLNNELLENGQIPV

YSANVLEVFGFVNKEILQDYDNDSVLWGIDGDWMVGFIPKNKKFYPTDHCGVLRVDDTKINAKYISFILN

EAGKKQGFSRKLRASIDRIKALRVKLPSLEFQDQIADIIDKIEKKINEYKIELDRLEKEKEKILQKYLFS

>ABV52590.1 putative transferase [Campylobacter jejuni subsp. jejuni 81116]

MKNIMILSGAGLSAPSGLKTFRDNDGLWEEYDVMEVCSATGFRKNPKKVLDFYDARRAQLQNVKPNHAHE

KIAQLKEKWGKNLFVITQNVDDLLERAGCKDVIHLHGFLPELRCLKCEGIFNIGYEKFTDKQCPKCKSKD

LRHNIVMFEEQAPAYATLYSLLHQTSLFISIGTSGAVLPVGQYASMCEKSILNIYEKDVNLERYFDKIYI

EDIISAIDKITLDIENFMKDGNV

>ABV52589.1 hypothetical protein C8J\_0990 [Campylobacter jejuni subsp. jejuni 81116]

MFDSFLSGVFLGFGVSVPFGPVNILILTYALKAFKNSIAVGLGAFSIDMLYLFLLQFGLLNFLDNVIFMR

FLAIFGFCFLTYMAYLMLRKKKESLNLEHKEFKESLLKSYIKGIILNGSNPYVIGFWLSATGIVLSNQHT

YSTILGLVVAILFWIGALAFVVAKYSYLFSAKVIRIINIVSALIIEYFALSLLYKTFIG

>ABV52588.1 succinyl-diaminopimelate desuccinylase [Campylobacter jejuni subsp. jejuni 81116]

MNAKEFLIELLKFKSVTPNDDGALNFIAMELSDFEAFFIEKEGIKNLLLTKKFNDEGEHLAFGGHVDVVP

AGEGWKNDPFEPLEEEGFIYARGAQDMKSGVAAFIDAVKDVSFKGRRLSLILTSDEEGEAKYGTKAVLEW

MKEKNMLPDYAVVAEPTCVKKMGDSIKIGRRGSINGKLLIRGKQGHVAYPEKCINPVHDFAPVLKLLAGF

DLDPGSAEFSPSKIVITDIRGGMGVCNVTPNDLKLMFNVRNSPDTSLEDVKSYVEKICHGLNYELELKQS

SEAFLTNIDNKIVQKMNESVQKITHEVPELNTKGGTSDARYFAKYGVKVVEFGVCNDRIHAIDERVSIEE

FEKLCLVFKDLIENF

>ABV52587.1 hypothetical protein C8J\_0988 [Campylobacter jejuni subsp. jejuni 81116]

MIEEILKDSDYKLDLFSKKAIAELETKIIAKTNKNNQIIYYTNCLIRDKEIKLTPEEIVRQLYIDKLLNE

YNYPKDMIKIEFGVHFGREVKRADIVIMDKIQITVPYIIIEVKKPKLKDGKEQLKSYCNATGATMAVWCN

GKEISYYHRKDPNYFESIPNIPASNQTLPDLLKVKFTFDDLIKEDILKSQKRSLKNLVTEMEDEVLANAG

VDVFEECFKLIFIKLFDELEGVRDRTKSLEFRNYGGSDSELKQKIEKLFDKAKKKWEGVFNNDEKIKLSP

SHLSVCVSSLQNVKLFNSNLEVIDDAFEYLVNKSSKGEKGQYFTPRYVIDMCVKMLNPKKDESMIDTASG

SCGFPIHTCFYVWRSIYKERGIEASHLFTAQEKISECQDYVKEKVFGIDFDEKSVRVSKMLNLIAGDGHT

NVLYLNSIDFDRWDEWVKDDEDWQDVYFEGFKRLKNLRVTKNQNRDFNFDVLMANPPFAGDIKESRILAR

YELGKKENGKPQSKVGRDILFIERNLDMLKPGGRMAIVLPQGRFNNSSDKYIREFIAQKARILAVVGLHG

NVFKPHTGTKTSVLFLQKWDDKLCPKCEDYNIFFATMNEPSKDNSGEKIYYPLLDSHDHLVVKHDLFHPH

LEGDEPIKQKDESQEEFDKRIQEYRLNVEKYKDLQKDGIAEAFIEFAKAENLSFWKE

>ABV52586.1 RlfA [Campylobacter jejuni subsp. jejuni 81116]

MKEFKIFCDESNHLFYKDNPTLCSRVMVLGALKVPSSEIIKINKTIKYLKHKYKYNKEIKWTKLNLSQKG

FYDELLEFFFSSVYMWFKAVLIPNKTILQHDIYNQGDHDLFYYKMYYQALHNLIDIDTKIKIYLDYKDTK

SGDKIKGLEKVLFNKFKQSVNIKIFTIQSHESNIVQLVDLLIGAISYKARNDIEHVSEIKNYIINKIETL

ANIELDAGTPPWENKFNIFRIQLSKGEQ

>ABV52585.1 hypothetical protein C8J\_0986 [Campylobacter jejuni subsp. jejuni 81116]

MYHLLDFSTCKCENEKFDLAYKIFKQDFIEVPLYLAGCIYIDPQSHKKHKGKEKIFWHITTRENKQNKTR

EFDSQRACRINWIKQIIINHTHPEIKAFYYKEKRAIRFYLWLYNHNFIVILQKLGRSSSFLVTSFYIDKG

YNKNIYEKRYRNYINGNDIELKNCEWF

>ABV52584.1 hypothetical protein C8J\_0985 [Campylobacter jejuni subsp. jejuni 81116]

MNLNQTLQEKYPHLEVSVLKLSEVKKNIDFRIDDSFWTMKLIYNNKLNYKKIGECLLKSQYGISINMNEE

GDGIPIYRMNDIDNMLCNFEVKKYALIDKNELQTFRLNYGDVLFNRTNSYEFVGRTGIFYNNRENFVFAS

YLVRLVCNKEILLPEYLTVFLNTHIGKKEIRRRARPSINQANVNPEELKEIKIPIFPMEFQLEIQNLVKD

SHKALEESKELYKKAEETLYLELGLDPKNPLQSLLDSKTNNPTKSLNISIHTLKESFLKTGRLDSEYYQS

KYEDIEKMIRSYKDGFCNLKDLVNDISSGFAFSSDDYQDVGELVLIRINNIKNATLDLSNVIYLKNEAYN

LSPKDKIKKGDILISMSGSIGLSCVVRDDISAMVNQRILKISIKNFNSDVLVLLLNSFICKMQFERIGTT

GGVQTNLSSIDMQNILIPKIDSTTQEKIAKYIQESFNLRKKSKQLLDNAKIKVEEQIQGKI

>ABV52583.1 thiamine biosynthesis protein ThiS [Campylobacter jejuni subsp. jejuni 81116]

MIINGQKLELKELKFMDFIKEKGLKIELIALELNGEIIPKSEFENLILKENDKAEIVSFVGGG

>ABV52582.1 thiamine biosynthesis protein ThiF [Campylobacter jejuni subsp. jejuni 81116]

MRVKFNGKELDTDFKTSLEFFENISKNENDVWIINGFATKENIALNENDELFCIEKNTLPPKDALDAMMR

ARHTPKLHDKLKNGRVAVCGLGGLGSHIVINLARSGVGYLKLIDFDVIEPSNLNRQAYRVSDLGKFKTEA

LKEQISEINPYISVEICTLKIDEDNLESLFKDIDIVCEAFDSAIAKAMIAQNFHRFYKDGILICASGLAG

YGDSNSIQTRKIAKNFYVCGDLVNGAKVGNGLMAPRVNICAGHQSNLVLELLANKE

>ABV52581.1 thiamine biosynthesis protein ThiG [Campylobacter jejuni subsp. jejuni 81116]

MQENLKNDKLKIGKYEFDSRFILGSGKYSLELIKSAIEEAKTQIITLALRRANTGEIANILDYIPKNITL

LPNTSGARNADEALRIARLSRELGCGELIKIEVISDSRYLLPDNYETIKACELLAKEGFTPLPYMHADLY

AARAMRDAGAAAIMPLAAPIGSNKGLCAKEFIQILLNEIDLPIIVDAGIGSPSQACEAMQMGVSAVMVNT

AIAEAKDVALMAKAFSLAVNAGRAAFLAGLASVSKAKASSPLTGFLRD

>ABV52580.1 thiamine biosynthesis protein ThiH [Campylobacter jejuni subsp. jejuni 81116]

MQDYMQYLPHMQEIKSEILNKVLTQVQSYDESQFSAKDVKNALNQTHLSIEHLKALLSSAAEDFIEELAF

KSAKVKQKYFGNSISLFTPLYLSNYCNSKCVYCGFQKGNKIARAKLSEAEIHEEMQAIAKSGLEEILMLT

GEGREFASVEYIANACKIAREYFKVVGVEIYPMNEDEYKILHEKGCDYVTVFQETYNALKYSKIHLAGEK

RIFPYRFNAQERALKAGMRGVAFGALLGIDDFRKDALATALHAHFLQQAYPHAEISISVPRLRPIINNAK

IHPKDVSEKRLLQVLCAYRLFLPFAGITISSRERIGFRDEVIKLGATKMSAGVSVGIGEHKGEKKGDEQF

EISDDRSVDEILAMLKRSNLQAVMSDSIYVG

>ABV52579.1 possible transferase [Campylobacter jejuni subsp. jejuni 81116]

MWDKKIIAISDRKCVEIDFLKQIEKLAKAKVDAIVLREKDLSEFEYYDLAKEVLSICVKQKVTCFLHFFD

RECLKLGHRYFHAPLSLLRKEPKLIKYFHILGTSVHSKEELLEAMSYKVNYAFVGHIFESSCKVGLEPKG

IDFLKSLLEFSQIPLYAIGGINTQNIENFKDINIAGVCMREILMKEKDLKKYLLECRQNLR

>ABV52578.1 putative transcriptional regulatory protein [Campylobacter jejuni subsp. jejuni 81116]

MNKILSLPEDLKQLKGVNYKKIKSCTFAKYTQTDTSHSTFVNVGSHLLTFVRKGYKILHTASKDYKINSY

ETLFLKAGSYTLSNVGLSKGVYEAYLFFFDNAFLIELIYKYKDFFKLDQKFQNYEIFWVKNDKILQGILE

SFSPHFEENTQILDPIVSLKFEEIFLHLLLNKNIYFISFLSGILKEFRLDLSQLFEYCGREFLSVNEMSN

FAKLDLATFSKEFKKCFGQSPKKWLDEKRLQKAKILLKFSKKNINEIANECAFSSVAWFIERFKEKYEQT

PKQYQKTKNLYFLSKN

>ABV52577.1 hypothetical protein C8J\_0978 [Campylobacter jejuni subsp. jejuni 81116]

MKKYVLSLALLGSLLGASELKYQEFDGFKNPESIFVDKNYVYVSNVGEKLEPLAKDNDGFISKLDKNGKV

LEYKFLTHLNAPKGMMEIGKTLYVVDIDVLRGFDLKTKKEIFNLPIKGAIFLNDIEKLDDNTLLVSDTGT

GLILKVDLKTKQYDELLKLDLAKFGGPNGLYLDRKKHKLFIAGYHPDGVSGGVVMAYDLNTKELSIIKNE

KESYDGIVPYKDGLLVSSWGNNLNGYIYNLDNVKSVKLELPLMKGPADIFIEGNILWIPKMAEGKIFKVE

LNK

>ABV52576.1 putative transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MASFKKIFWINVIIVIIVAFNLRAPITAVGPIIDIIKDKYYLNSTVAGILTSLPLIAFGSISFIVGYFSP

IRAIVFGIFLIFLGEIIRSYFGVYGLFLGMLAMGCGIAIANVLLPSFIKEKFPKKMASIMGIYSLVLSIS

SIMGIALAIPLLSVFDLAGAMFFWAIFSFIALVVYYPQAKNGRFFRIKKKAHKKINLFTNLTTWKITLFM

GFQSFLAYSLFFWYVQIVVEKGFDKEFSTSMVLFAQLVAAPVSLFGPLLLGKLRQNLHTFYIAGLCSMYV

IAFGILFIFDSKISIIISAFIMGFPWGGVFGIALLFIAQKSSNAQIAARLSALAQGFGYLIAAQGQWIIG

FLHDKFENFSFAILMLVFVGILVNIFGYLSYKSQIIK

>ABV52575.1 UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Campylobacter jejuni subsp. jejuni 81116]

MTIALTGGGTGGHLAIVRCLLESAIKKNIECVYIGSQNGQDKAWFENEVRFKEKFFLSSKGVVNQSKFGK

ISSLLHTLKLSKDCREIFKKYHIQAVFSVGGYSAAPASFAALFSHLPLFIHEQNSKSGSLNMLLKPFATK

FFSAFEKEISPYPVADKFFDNARIRKELKNIIFLGGSQGAQFINELALNLAPKLQEQNIKIIHQCGKNDF

EKCKKHYQSLNIQADIFDFSLNLEEKMKNADLAISRAGASTLFELCANTLPTIFIPYPYAAKNHQYFNAK

FLQDQALCQIFMQNSINLDEFFKSILKLNLENISTRLQNITQKNGADMLIQKALFDNLTFIR

>ABV52574.1 probable cell division/peptidoglycan biosynthesis protein [Campylobacter jejuni subsp. jejuni 81116]

MVADKRLFYLSCILITIGIVFSYSLTAFTVLFLDYSEFHFFIRQLFFGISGILIMFFISRLDPDKALSKK

IILAILIISFIFIIILPFLPSVLATASGGAKRWIRLGPLSISPVEFFKIGLIYFLAWSYTRRIDDSKKAI

RHEALILLPYCILASIVIGYIYITQNDLGQSVISFFLILALAFFAGASKRLFAFGTLIIMMIGIMVIFSN

QRRIQRIASWWGNIQDAFLPMLPDWLANALRVSSNSEPYQISHSLNAIAHGGMFGEGLGLGTFKLGFLSE

VHTDFVLSGITEEIGLLGLGVICYIYLWMILRIFRIAGRCEAKQDFIFCSGIALLLLFSFFMNAFGIISL

TPLKGVAVPLLSYGGSSMWAICIGIGYVLMISKKVKL

>ABV52573.1 pyruvate carboxylase subunit A [Campylobacter jejuni subsp. jejuni 81116]

MNQIHKILIANRAEIAVRVIRACRDLHIKSVAVFTEPDRECLHVKIADEAYRIGTDAIRGYLDVARIVEI

AKACGADAIHPGYGFLSENYEFAKACEDAGIIFIGPKSEVIHKMGNKNIARKLMAKNGIPIVPGTEKLNS

YSMEEIKIFAEKIGYPVILKASGGGGGRGIRVVHKEQDLENAFESCKREALTYFNNDEVFMEKYVVNPRH

IEFQILGDNYGNIIHLCERDCSIQRRHQKVIEIAPCPGISDNLRKTMGVTAVAAAKAVGYTNAGTIEFLL

DDYNRFYFMEMNTRIQVEHPITEEITGIDLIVRQIRIAAGEILDLEQSDIKPRGFAIEARITAENVWKNF

IPSPGKIGEYYPALGPSVRVDSHIYKDYTVPPYYDSMLAKLIIKATSYDLAVNKLERALKEFVIDDIRTT

IPFLIAITKTREFRRGYLDTSFIETHMQELLEKTEDRHQENKEEVIAAIAATLKKIRESRE

>ABV52572.1 hypothetical protein C8J\_0973 [Campylobacter jejuni subsp. jejuni 81116]

MDFLDSLKSIKKEMQANTNTSKLAKKSSKSGASVKNLEKLAKDIREKNQETNIDKEMQEIFLKQEKLQDE

FSEFIKNTDIKKI

>ABV52571.1 possible transferase [Campylobacter jejuni subsp. jejuni 81116]

MLEIGFCTLEDQCPYLKDKRSRIEYKYIENCSKEINNELIKRGWRRFGRYFSRPICKDCDECLSLRILVN

EYNFSRSERRVINKNINTKVILRTPNLSNEHLFLYDKYHRFMEEKKNWKRYDLSFKQYYNLYVDGFMNFG

YELAFYIEDKLVCVDLIDILEDGISSIYCFYDPDFSYFSLGKFSLLNEIQIAKKMNLDYIYLGYFVKKCQ

SLSYKADYTPNEILKGTKELFENEVLWEK

>ABV52570.1 possible DnaJ-like protein [Campylobacter jejuni subsp. jejuni 81116]

MQIVQTLETINVNTDDISVFQYFKDLITKNFTKVIGRKNKIFSFFEENEIPQRRYFLKVLDQKYRKSTNE

GIENLQDAHFKTFRLIFEQNNMLKPMLFIKIDFVAGRILMKLSSNEKLFITYIRNYFQDHYIEYNEMTNI

LILEYKNENTLELFEAFADESEHLKYCVNFEVDREEYKKFRQNIHNKENMKWKFNALAKLFSNYFNTLEC

TPQNDLSEIRQKYLILVKLYHPDFHQGKSAIEKAYAREQFEKIQIAYDNLKALYKNNT

>ABV52569.1 putative integral membrane component of efflux system [Campylobacter jejuni subsp. jejuni 81116]

MFKLAINRPITVLMFFLALMIFGLISAFSMSVNLFPNVSIPLIKITSKVNGDLNFVESKVTKEIENALSE

IDGVKTITSAAYDNFSVSVVEFKLGKNLEVAANDVRDKIGTLSLPSKPEIEKISSDSGSAISLFLYSKDK

LQLMREINDKIKPFLQRVEGVGKIEAKGFLEPQIRIELKPNELRKYNLNALDVANIIKSQNFKQALGELN

NNQDNYIIKGYFEATNLEELSNLRIKTGVFLSDIANISSLYEDEKQSALYEGKEGVLLELGKITNYNTLE

MIKNVKNALPILEKQIPKDISINMLYDKSLNIHKHLSQVIFDMVLGIFLTLVIVFLFLRNLSATLIACIA

IPTSIISTFFIIDLLGYDLNRLTFIALTLSIGIFIDDAIVVIENIAKKLKTYPPLQAAFLGINEIGFSVL

SISIVLLCVFIPISYMNSISGLFFNALGISVASGIVISFLVSVFLIPSIGARFLNPKENKFYEKTEAFFE

KIEQKYENLLYKILQNKVKFILATLVFTGLSFALATRIGLDFLPMEDDSEIQVLLESKKDLSLEAMKEKS

LNLLEKIKNDSNVKYAFLLVGYDDAKDATKAKIYVKLKNLDERNLRQSAIVSLYRQKFQDESLKIKILEL

PKIEGAGIDDPVQFLILGDDLNTLKEAASQAKEILGTNARIVDISDNANATKDEVALHINKEKAKLLDVN

PQYIAGVLGYSFSQLSVGSMDRGNSKDDIILSFAPEFKKDIEALKRISIKNNQGINLELSSVVDFIYSKD

LKTINRYNKNRSVKITAGVNDLSLGAVQKLLLDNMDKILNNNPSLSYAFSGFINLLGETVQGFAMAVALA

FVLIYLVLAALYESFILPLIIMITMPLAFGGASIGLFITGHNFSLFVLIAIILLFGMVGKNAILLVDVAN

KKCHEGLDPDKALLIAGKSRLRAILMTTFAMIFAMLPLALSRGAGYEANSPMAIAIIFGLISSTLLTLLV

VPALFKFCFKLDSKLRKIYEREKLN

>ABV52568.1 hypothetical protein C8J\_0969 [Campylobacter jejuni subsp. jejuni 81116]

MKKILFLLLVFNCAFGEEIYASFNVEASKQSKLALESIGLVQKIPVEIGQKVSKGELLLTLDQESEKIAL

QNAQNSYQLALVEYENTKSKMQKIKAVENVIDKQSYEDMKAKFDAANLNLNKAKINIAYYKNIMTKKELR

APYDAIIANKFIQVGEGVGGVAQPLIEIFSYPQSKLILSFDEKYKDKVKLGDDFFYKIDQNGTELKGKIS

LIYPSIEVKTRKIYAEVQTTNLTPGLFGEGRIITKD

>ABV52567.1 putative outer membrane component of efflux system [Campylobacter jejuni subsp. jejuni 81116]

MFEKYLKSAIFLALYPLAMLASNLHEFIALSQNNESYLIKQMQSEQANLDKEQAFRNYLPSLSLNSAYVA

NNKDRFIIDPQESLFAKVSLNFLLFDGGAREANLRALESREKLSLLDKEQNKNYLALNAITLYFNTLSLE

KILLANQQKVSFLKSTFERLQKFYDAGLSPKDELESIKAKYHLSLLELSQNELKLANIQKEIKILSDTDF

KVQGNAFLENPQQEKSQNYEVMIAKEQINLAKESVNLAKAEYFPKFYIQDNFNFYKNNYNPKVPAPFANL

ADQFLEKYSQGNQFILGMEWKIFDFNARAKEVEKERLNVQIANANARFSERKNKEELNYLDKSLKVLQEQ

ILALNLSLNAANLAFESVDKKYQAGLVSYVEYLQALEVKFKAQSDLELAKNEFEITKANYYFNAGIDLNS

KVKE

>ABV52566.1 lepA GTP-binding-like protein [Campylobacter jejuni subsp. jejuni 81116]

MSVKNIRNFSIIAHIDHGKSTLADRIISECGAISDRQMSSQVMDTMDIEKERGITIKAQSVRLNYKFNNE

NFVLNLIDTPGHVDFSYEVSRSLASCEGALLVVDASQGVEAQTIANVYIALENNLEIIPVINKIDLPNAD

VEKVKHEIEHIIGIDCKDAICVSAKTGVGIKELIETIITKIPAPKTDDEAPTKALIYDSWFDNYLGALAL

VRIYEGSIAKNDEVLVMSTDKKHIVQDLFYPHPLSPIKTQSLQSGEVGVVVLGLKTVGDVQVGDTITLVK

NKAKEAIGGFEKAKAFVFAGLYPIETDKFEDLRDALDKLKLNDSSITYEPETSLALGFGFRVGFLGLLHM

EVIKERLEREFNLDLIATAPTVTYEIYQTDGELIKIQNPSELPPVNKIDHIKEPYVKATIITPSEFLGNL

ITLLNRKRGVQVKMDYITPERVLLEYDVPLNEIVMDFYDKLKSLTKGYASFDYEPIEFRVGDLVKLDIKV

AGENVDALSIIVPNEKAQSKGRELVSAMKEIVPRQLFEVAIQASIGNKIIARETVKSMGKNVTAKCYGGD

ITRKRKLLEKQKEGKKRMKAIGKVNLPQEAFLSVLKID

>ABV52565.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MFKKFLIFIVPILFLSACATKQDTFAQVNQISKNSQCSSCESPGGFEAKIKGLLYISDVGIQCCANKRTL

DTGIALKKVYLHRFYDLKEGQKVLNAKGKKLFVDVNFNAVFYTYLKQELEARGIVVLDNNDQNSPYVSKI

DLEFISYGATQDAIGLHSKLVGVLQVSDINKNKKFTIRTKQDVQGFDDLKETTFYTHLLIKQMANKAASL

ISEL

>ABV52564.1 hypothetical protein C8J\_0965 [Campylobacter jejuni subsp. jejuni 81116]

MLHSKHYFYGYFVYKMLAKLSFAKFKDFFDPRMTINVIALDDKVEDMLYSHSAILARYLKTKFVKPVFNV

LKAQNSVKYSGKSLEFRQKHKRNYKLLKTIHEPVILVDDIVTTGSSLLEAKKVLEENKISVLFALVLADA

KV

>ABV52563.1 DNA gyrase subunit A [Campylobacter jejuni subsp. jejuni 81116]

MENIFSKDSDIELVDIENSIKSSYLDYSMSVIIGRALPDARDGLKPVHRRILYAMQNDEAKSRTDFVKSA

RIVGAVIGRYHPHGDTAVYDALVRMAQDFSMRYPSITGQGNFGSIDGDSAAAMRYTEAKMSKLSHELLKD

IDKDTVDFVPNYDGSESEPDVLPSRVPNLLLNGSSGIAVGMATNIPPHSLNELIDGLLYLLDNKDASLEE

IMQFIKGPDFPTGGIIYGKKGIIEAYRTGRGRVKVRAKTHIEKKTNKDVIVIDELPYQTNKARLIEQIAE

LVKERQIEGISEVRDESNKEGIRVVIELKREAMSEIVLNNLFKSTTMESTFGVIMLAIHNKEPKIFSLLE

LLNLFLTHRKTVIIRRTIFELQKARARAHILEGLKIALDNIDEVIALIKNSSDNNTARDSLVAKFGLSEL

QANAILDMKLGRLTGLEREKIENELAELMKEIARLEEILKSETLLENLIRDELKEIRSKFDVPRITQIED

DYDDIDIEDLIPNENMVVTITHRGYIKRVPSKQYEKQKRGGKGKLAVTTYDDDFIESFFTANTHDTLMFV

TDRGQLYWLKVYKIPEGSRTAKGKAVVNLINLQAEEKIMAIIPTTDFDESKSLCFFTKNGIVKRTNLSEY

QNIRSVGVRAINLDENDELVTAIIVQRDEDEIFASGGEENLENQEIENLDDENLENEESVSTQGKMLFAV

TKKGMCIKFPLAKVREIGRVSRGVTAIKFKEKNDELVGAVVIENDEQEILSISAKGIGKRTNAGEYRLQS

RGGKGVICMKLTEKTKDLISVVIVDETMDLMALTSSGKMIRVDMQSIRKAGRNTSGVIVVNVENDEVVSI

AKCPKEENDEDELSDENFGLDLQ

>ABV52562.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKKIYFMLAIAGIFAGCVPSANSATKNSSANSTPPSQDVIVQKVDKDDVRDIIREEKMLAPDASETELSF

TAVGEGIAPMNTVSTAQALALAKRAAITDAYRQLASKLYGVKVNGKDTVKDAMLRSSTITAQVNGLIKNA

SIIDENFNQGLYRVNLELKIDADKWKELFAY

>ABV52561.1 hypothetical protein C8J\_0962 [Campylobacter jejuni subsp. jejuni 81116]

MTQSENVEEQWVCEISYSDQDIKVLPRTSLGLIDDNMPKTIKFNFLNSHKDELSDCFIGAKISVKDIVNT

DLLRAQSETYIKILPLRFTVEFGEQNAIIYYLKKK

>ABV52560.1 sigma-54 dependent DNA-binding response regulator [Campylobacter jejuni subsp. jejuni 81116]

MNLVIVEDDINMRKSLEIALAEYEEFNIKSYKSATEALKKIDENTDLIITDINMPGIDGIEFVKACENKY

DFIIMTGNATLSRAIEAVRLGVKDFLTKPFDVDTLVEAIKRAKIIREKTADKKSKKNEKKEENKDFFSTS

PNLEKTLNLSQKAAKTDASVMFFGESGVGKEVFSRYIHTHSKRSNKPFVAINMAAIPANLIESELFGFEK

GAFTDANATKIGLFEMANEGTLFLDEIGEMPYEIQAKLLRALQEKEITRLGSTKSIKIDVRIISATNANL

DEKIKNGEFRSDLYYRLNTVPINIPPLRERKEEILGIAQKVLEDTCKEYDFKEKQLSQEAKNALLEYDFP

GNIRELISVVQRACILSENDEISSEDLFLEARSIKKDVKNLEKELICEVLLSVDYDKDQASQILGMDIKI

LNEKIKKYQIKDR

>ABV52559.1 aspartate-semialdehyde dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MSKKQKIAIVGATGAVGEELLNVLDELDFPVESILPLASAKSVGSEVEFKGKAYKVKELTENVFKENPID

IAFFSAGGSVSEKYAKFAVESGAVVIDNTSHFRMEKDVPLVVPECNPEDIKDWKKTGIIANPNCSTIQMV

QVLKPLNDAFNLKRVDVSTYQAASGAGKEGMQELVEAMQSFFAFKLDEFEPQTFPYTLALNLIPQIDVFM

DNDYTKEELKMVNETQKILHKNLEVSATCVRVPVLRSHSEAITMHFEKEIDVKKAKEILEKAPSVVVIDD

PKNKKYPMPLMTSDTNETYVGRIRADVYDKKILHLWCVADQIRVGAATNAVRIAQKWLELKNK

>ABV52558.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MLEKIFESLLVRSRIVTILPVIFGLIGAFVLFFIASYDVLKVIFYTYNYFFDAGSNVDLHEDVVALIIGA

VDLYLMALVLFIFSFGVYELFISEIEEFKQTKQSKVLEVHSLDQLKDKLAKVIIMVLVVNFFQRVLQMKF

ATPVDMAFLAGSILALCVGLYFLHKGGH

>ABV52557.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIFLIGMILNHFVFAAPLDEVFKDIEVSGTVRYRYDIKKEKKYNKKTHRYQNKTQTEITIK

>ABV52556.1 putative cytochrome c [Campylobacter jejuni subsp. jejuni 81116]

MIIRWLFISSIFVVALFGINLKSFFTYTFDANKQYDMEKAKALYFQNKCNTCHGDNAEKSVIGSRILKDM

SPEDIKGALIGYTLDSSSSTTASQMAFYARNLSHEDIDNIIAYIKGGNFALDLQVKDLLEEEPAQKTKHN

IFLK

>ABV52555.1 branched-chain amino acid transport system substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKLTLTLSVLTMVNCLYAKDINIGVVLPLTGTVAAYGQDVFNGIELANKLQPKLSNGDVIKLITIDTKG

DKLETSNGVNRLIATDKVLGIIGEATTPNTIQAISIAEEKKIPLIAPVASGDKLLDKKKYASRVCFKDNF

QGDKFATYVSKDLGLKNAVIIIDQSNVYSLGLARAFENSFKNNGGKIIKKLVINSGDKDFRAVVSQLKSL

NPDFVYMPIYHPEAALIARQARQIGFDKLLAAGDGVNNQTFIDLGGSAVNGVIFTDSFDYNNPSTQLGKD

FVAAYEKVKGTKELPAFSAMGADAYFVMLNAMNACVDNLSSECINSKIHQTKDFQAVGGVISIDESGNAI

RSVVIKEIQNQKQNYKTIINP

>ABV52554.1 high affinity branched-chain amino acid ABC transporter, periplasmic amino acid-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKSLILASILSLSLSAAEVKIGVVLPLSGATAAYGQSALEGIKLANSMQSTLSNGDKVSLAIIDTKGDK

LESSSGANRLVSQDKVIGLIGEMVTANTLQVMRVAEDNKIPLIAPAATGDRLLDKKIYSSRVCFMDSFQG

SSLAKYVFSKLNYKSAVIVVDQSTDYSLGLAKAFEKQYKSNGGQILRILRVNSGDKDFRAIVAQVKSLNP

EFIFLPLYYSEASLFARQSKLAGLNIPMGSADGVADQTFISLAGDASEGYIFTDSFDANNPTTKLSKEFI

SVYEKAKGTKEVPNFSAMGADAYFVMLNAMNACVENLTSKCVNEKIHQTKNYQGVSGVISIDQTGNATRS

VVVKEIKNQKQNYKDIINP

>ABV52553.1 branched-chain amino acid transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MDSTLFLQQLVNGLSLGSMYALIAVGYTMVYGVLRLINFAHGDIMMVGAYAALFCMTNLNVPFLGALSLA

MIFAACVGIATDRIAYKPLRQAPRISLLITAIGISFFLQNLFNMLFTSTPRTFTPPSYFEESVNFGGVIT

TYGSLMVPALTFVILIAVLWILYKSKYGIAIRALAFDIQTVNLMGIDANRIIAIVFALGSALAAVGGVFW

AANYYSVEPTMGTLIGLKAFAAAVLGGIGSVVGAVLGGLIIGFTEVVVVAFFPDLSGFKDAFAFIFLVFI

LLFRPTGILGINFEKSRF

>ABV52552.1 branched-chain amino acid transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MVRIKVSHLIFLIASIVFIFVSPYIFGDYGLNIVNQIAIFIILAVSYNLINGVTGQFSLEPNGFVAIGAY

AAALVLLSADAKNDQFFLDGPSSFILAIHSNSFILALIVAGICSSLLALILAFAVFRVRGDYLAIVTLGF

GIIIKIAAINFPSITNGSRGLVDIPQFSTIYWTGGIAIVAVILILNIVYSKYGRAMKAIRDDEDAASAMG

INTFWIKTLAFSTSAFLEGVGGGLLACLLTTVSPTQFDFLLTFQLLIIIVLGGLGSTTGAIIGAILVIGG

SEWLRFLDELNIKIDSLNLDIQSTPGLRMVVFSIVLILVMLFARKGIMGYYELSDVIRGIKKRFKRSEK

>ABV52551.1 high affinity branched-chain amino acid ABC transporter, ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MILELKQISKSFGSVKAINETSFKINEGEIFALIGPNGAGKTTLFNIITGNYKPSSGSVEFLGERIDHLK

PHKIVHLGIARTFQNIRLFSSMNVLENVLIGFNKQMKYNIFEAFLHLGRFGKIEQVFKEKAYAILEELGI

AEFAYEKATSLSYGQQRKVEIARAMATQPRLLLLDEPAAGMNSSESDELAELIFKLRKDYKISVLLIEHD

MKFVNKLCDRVLVLDYGKTIFEGKLCDAVNHKEVIAAYLGDFDANS

>ABV52550.1 branched-chain amino acid transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MLIVKDLHVYYGLIEAVKGIDFKVETGHIVSLIGSNGAGKTSTLNALLNSVKRTGEVNFLGYDTKRHLTH

TLVQKGIALVPEGRRVFINLSVEENLKIGAFNNAENYEHLREQMYKLFPRLASKKHALAGTLSGGEAQML

AISRALMSEPKLLMLDEPSLGLAPKIVGEVFDIIVRLKEEGITILLVEQNAYSALKISDYAYVLENGRIV

MENEAKNLIGDDEIRKKYLGL

>ABV52549.1 hypothetical protein C8J\_0950 [Campylobacter jejuni subsp. jejuni 81116]

MKNIIKSIGDLRVSVVLFLLFALFCALATFIESAYGTPTAWAMVYDTFWFEYIQLLLGINLLCGMFRYKM

FGLKKLPLMIFHISFLFILVGSAMTRYAGFEGILPIREHTQNSLIESSKTSLRISAIKDGERYSAVNDRY

IGNLPFANSFKLKLNLGDDQAVLKYKDLILNAHYTYKENNNSNPLLVLMLSQKGSQGVDVKFEKGEVKNI

EGVNFAFMNDNVKAPFVKIDENLTLSSSENLHFLSMLDGQNLDLKIGEKANAKERRLYEINDISFVVKAA

SLHAQEALEGSNRPQDESFWLWFKSAWLEVGRTMLISTFGEPQNWKNSLLLHFKDFALSNENKNLELTGS

NALKLELSYKNESKEFYIFEYNKPIMIELAGQKFFISWALSYEQLPFDIYLRDFVLDRYPGSMSPASYAS

EITVKNNNENFDYRIFMNNVLDYDGYRFYQSSYDQDEKGTVLSVNKDPGKIPTYIGYFLLCLGMFMNFLN

PHSRFRTLARLINKDTLKHASVIIFILLLSFGSEKTFAQDLNLTLPVVNTNHAKALATLIVQKSADGRMV

PFDTLSREILEKIHQSDSYKGQNSNAVMLSMLVDVDKWQMEPFILMPQNQAVRDAIANILEIPSTKYISY

KDFFDENNRYKLQKYVENANRKNPNARGVFDKEIIKLDERANVVNLVFSGELFKFIPVQNNPNNVWLAPF

SAVTTLKGDEGHIVLALIQNYFSAVENAFKDGNWTRADEGLKFIKEYQEKIGYKVMPSKTKVEMEIFSNK

AEIFVKLAPVYLIAGFLLLILVFSKMVVPNLKISFIFKVVYVLNVLAFVIHTVGLGLRAYLSGHAPWSNG

YESMVYIAWALSLSGIFFSRKSPIALSLTSILSGVVLMVAHLSEMNPQITNLVPVLNSYWLSIHVSVITA

SYGFLGLCALLGIFTLFLMCFLKKDGKYNLNILRNITEATRINEMAMIFGLCLLTVGNFLGAIWANESWG

RYWSWDSKETWALVSILVYAAILHLRMIPKYCNQFVFALWSMFAYWVIIMTYFGVNYFLTGLHSYAAGEA

AQIPNYVYWGFALMVVLALFARRKRNFVGKL

>ABV52548.1 hypothetical protein C8J\_0949 [Campylobacter jejuni subsp. jejuni 81116]

MSHIFLVIFCAALALLLFLGMIAYLITSDGKKTIKKQKTSQKQHVAEKTKKFDTDLDKMIIAASDVKLTD

IELKELAKLYVQTHKLGSKTSKELDEATKKKLEFVSALAANINASAQTVSYLNKELKKISGSYKKEIDAY

EHMGLAKRKIKEDK

>ABV52547.1 hypothetical protein C8J\_0948 [Campylobacter jejuni subsp. jejuni 81116]

MLELHENLKKILQAKNLETFYSEIYGQKIFVYVGLNLETWLFNDEKIYKLQDEEFKLSSIEEFSNFIKSI

LEDFKVQNTHFQNLLEHKEGIILKGGFVKNFYKKSFVLRQKINKNLKQINLLSEAFNLLLSEQAQYKKHL

KILNLSISILSKNTKEHLVRVDTLYTLTSAIKNEKMNKSIYLLSILSSIFLPLNLIVGFFGMNTNNLFFK

DSPYGTLYIFSLICCILIVGFIFYHSKKTKEFDLDEGKKAKKQTK

>ABV52546.1 queuine tRNA-ribosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MEFKLKHKDGMARVCEITTAHSTFLTPVFMPVGTVGAVKSLDANDMKNELDAKIILANTYHMYLRPTSKV

VKDFGGLHGFTKFDRSFLTDSGGFQAFSLSKNSKHFNEGIEFKSHIDGSRHLFTPKSVLDTQYDFNSDIM

MILDDLVALPATKERVKISVDRTILWAKEAITYHKSMQNKGIGIGQNIFGIIQGGTDYKERKRCALSLNE

MPFDGLAIGGLSVGEENALMYETVQNLNPYLDENRPRYLMGVGTPEDLVENVERGVDMFDCVMPTRNARN

GTFFTSFGKFNIKKAEFINDHEAIDPACSCYTCCNFSRGYLNHLFKAKELTFFRLASLHNLHYYLELARK

MREAILNNSFTQFKRNFYHLRGK

>ABV52545.1 hypothetical protein C8J\_0946 [Campylobacter jejuni subsp. jejuni 81116]

MNNILIIIDGILAKHFLERLCFEKGLGYFFTVVCQNSEKNNLNISSEYIDLHYFDPTSTARLENIMSKDF

KQAFIYMQDEFETKKSYEALRSLNPNLEIEIMDFWGLSVNDTHANLADARMTLSRRFMDFLPDIALTAQY

IGLGVGEIMEVKIPAGSIFAYRHISSIQQKRWRIVLIYRNSKIYFVKPSFVLEPNDSILIVGDPVVLQSI

FHNIRGKAGQFPMPFGSNVFALIDMKNMNQNMQERVLDTTLKLTQKSNAKRFFIHVINPKLGVMYEKLKK

LSEDKEGVFFDYFNTDFKQISTWLQNNDVGLVVTDIKNFEKEKQAFFDLKIPIMKVGEASFDELKEAIIL

SADESELENNANVITDLSKQLDFGVILYYYNPNSQNTTDMEEYFRSLSKLYDKNIQIINKNDENPLLNLQ

YREDLLQFVSFQKELLNRDFGRNLSTNLNRHYYKMRQNYQLFIPVE

>ABV52544.1 3-dehydroquinate synthase [Campylobacter jejuni subsp. jejuni 81116]

MQVEVKLKENAYKVYIDELEELEFDSKVFILSNPKISGLHLKTLLSKIKAREIFIAAVKDGEEYKNLSTM

EEILNQMFNSKLDRKSVLISFGGGVISDMGGFAASIYQRGIDFINIPTTLLACVDAAVGGKTGVNNNFGK

NLIGTFYQPKAVYCESSFLKTLSSRELAAGMAEFIKMAAMFDDSILDFIEKIDEKSFLNATCENEIFTQI

IARSIELKSRVVEQDEKESGLRMLLNYGHTFAHVIENFTDYKLYLHGEAVAIGMVMANQLALNLGFLDKM

QSQKIKDILLKFGLPISYKINNVDEFYEAFFMDKKSSNKKINFVLAGPLGKGLIKGDISKEDIIATLREF

Q

>ABV52543.1 hypothetical protein C8J\_0944 [Campylobacter jejuni subsp. jejuni 81116]

MKKIIILTFFVVFAFGDVNRTIINNINEKINTLNTVISASIWNIRYENFIKYQDINDELIILNLNLKKTS

DIHQQEELKRKIANLEEQLSLLKEYKDLNFAQSLSAPDNIETLSKLTNPLAIIGAFSHIKKLKGEKEEYI

FKFNDFKNLVDKIREKNSELKELVGLKPSVENIEALKASDKKLEEFEQALNFASVSYSVYEKKIDEELSR

VSAEIKVQSLRAVNILVAIVIVIAIAFMLKFIAKKYIKDSERYYTATKIINFININIIFLILLFAYIENI

TYLVTILGFASAGLAIAMKDMFMSMLGWCVIIFGGSFRVGDRVKVFQNDTTYIGDIIDISFLRITLYEEL

TLETYNKNRRSGRIIFIPNNYVFTNLLANYTHHGMKTVLDGIDISVTFDSNLDKAQEIVENIVTRHAKGY

TELARKNIARLQHEYSIKNPKVEPRFFMFFEHWGMRISAWYMTNAYAALVLRSTISKEIIKEFNKHKDIK

IAYPSQNLYLGNLNQNHFEQHHENMHFHARNKD

>ABV52542.1 hypothetical protein C8J\_0943 [Campylobacter jejuni subsp. jejuni 81116]

MKEKVFFKTFGCRTNIYDTELLKSYVKDYEIINDENKAQIIVVNSCTVTNGADSGIKSYVNTMQKKGIKV

ILTGCGAVSKGKELLDKKQVFGVLGASNKDKINEFLGAKTSFYELGNLNFIDKDIVCEYENHTKAFVKIQ

EGCDFACSYCIIPSVRGKSRSVDEKALLKQVEILGANGYSEIVLTGTNIGSYGLKNGTSLGKLLQKMGQI

SGIKRIRLGSLEPAQIDESFLEILDETWLERHLHIALQHTSEKMLRIMRRRSHTDNDLKLFNTIASKGYA

LGTDFIVAHPGESEEVWQEALKKFKEFPLTHIHAFIFSPRNNTHSATMKDVINGTLAKERLNILKSIVEK

NNYEFRKKNQVPLEVLVENQKDGFFEGYDQFFNKIKIKSDKDIAKEWIFISQYEAQEKSNFANLKG

>ABV52541.1 putative membrane bound ATPase [Campylobacter jejuni subsp. jejuni 81116]

MKNKKIILASFMVLCMLLGILYFKNEPKYIDENLYQSLLSQNLIQKAVIDKDEIWLKAEGENYVIIKDGI

DIKTLLAKVPVEVKKDNTLWVFFILLVFIIALFISLGYFARKKELAKYPISNKNQNHTQAQNSNINLESS

HIKPVISNITFNDVAGVDEVKMELSELVDFLQNPKKYKEFGVKMPKGVLMVGPPGVGKTLIAKAVAGEAG

VPFFYQSGSSFVEIYVGMGAKRVRELFSKAKMMAPSIVFIDEIDAVGKARGEMSNVERDSTLNQLLTQMD

GFEDNSGVIVIAATNKIELMDPALLRSGRFDRRIFLSLPDFKDRLKILEIYMKDKNNNVNLNKIAKASVG

FSGAGLETLVNEAAINALRRNSALVEESDFYAVLNKVLLGKKKILSFNDEEKKIQATYQAAKALSAYYFD

IGFEKITLIEDRFKEYEHNIRSKSELINRIKVYLAGSRAMRLIYNESYTNSQDDFLKIKELLDYMLSFDM

LEEPNLNEQKKEMDEFLNSMKDKILKLSELLLEKEKIEHDDVKNIMQV

>ABV52540.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKIKFLSIITILSLSLNADIIISADNLPSVSKEFLQHNFKAPIGIVQKDKNSYEVYLSDGTELEFDIDGA

WKEIENKAFPFDLDFLPQNLANIIKNEFPNIKAREIERKINHYKIKLDNDVKILIDFNGTILHKEIDD

>ABV52539.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MLTIFLIFLNILCYFLISYDYYNILGLNILFFNGAYWQLLSSMFLHGNLTHLILNMIVLFQFGRILETYL

GALRFIFIYFIGGLLCSLLSVFYVYFDFKYFGENINVIGASGAICVLMGFYAVLDKNSTKGLIVAILLMS

FAPLLMGVNVAWYGHIFGFMCGYILAKIKEVK

>ABV52538.1 hypothetical protein C8J\_0939 [Campylobacter jejuni subsp. jejuni 81116]

MKKIYIIRHAKASKSGDIDDFERKLTKSGKEDLKKLFKNLALHEIHPDLVLSSPAVRTAKTAKKIAKFYN

FDKNKICFDERLYLCNVENLLKILQDIDDEFNEVFLVGHNPGLMELGELLSSLCLASFPTSSILCLEFDI

KEFKNLKKHSGKLVFFEHVRKLKEEKDLGF

>ABV52537.1 RNA polymerase sigma factor RpoD [Campylobacter jejuni subsp. jejuni 81116]

MNAKTQEAELEELFQENAKDYITYEKLVKYLTKQPSASTAKKVQALMKKHKVQLFSAAEIAQMKNIEDAK

RLQEEKQKLQDTSLENEFDLANENDLLEWSRSDSPVRMYLREMGQIALLNKDEEIEISKKIELGEDIIID

AFCSVPYLIDFILDYKEPLINRERRVKELFKSFDDEEKSDDKLDELDIDEDEENETELESDEENTKKNSK

KEDERTLKVIEKFKALEKAKKDWLKTSKDKESGDELLDKLSIAFKKNILKEKLMDLGPTSKLISEIVKSM

ETALKSDEEFDKELKRLEYRLPMFSDELKKRHADILKDITKLSKEEITERALETTMVSTYMEIKKLFQTK

EASEKSFDLEKSRLKEILEQIKRGKKISDEAKGRMAKSNLRLVVSIAKRYTNRGLPFLDLIQEGNIGLMK

AVDKFEYKRGYKFSTYATWWIRQAISRAIADQARTIRIPIHMIETINQINKIIREHLQKDGKEPDVSVIA

KEVGLSVDKVKQVIKITKEPISLEAPIGNEDDGKFGDFVEDRNSLSPMDHILKDDLKEQIDEVLDQLNDR

EKAVIRMRFGLMDDESDRTLEEIGKELNVTRERVRQIESSAIKKLKHPKVGRKLKNYIEGWK

>ABV52536.1 transcriptional regulator, LysR family [Campylobacter jejuni subsp. jejuni 81116]

MKIKDMEIFLDLLNTQSPTHTANNFSITQPNVSIVIKNLENKFDGILFERLGKKLLPTPKALELGKNWLK

IIQAYYQSLEKLNDESMLLGEIKIASTQSISEHFLAPILFDFKAEFKNIEIHSQTQNSKECLNLLKNGNI

EFAIIEAELDPALVEYENLEINFWQDDELIVATSDKKLNEKEFYIDELLEQKWILREAGSGLRDKFLNEI

GASSKKLNIFLELDRMAAIKELVLQKKAISIFSKKSIEKELKNSTLYEIKLKNIDLKRKFYTLKRKNYNF

NRALEKFEKIFKS

>ABV52535.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKTSFLAHSVAIVRSNFKGLLFTACIVIFAMYLSSVQSIKDTTHLAATAFAIIIGVLLSPWFFKYQHHFQ

AGVHFSAKKLLRLGIVLYGFNITLTELLSVGLKGFLLSAIVIFFVFMIALFVGMKIFKLDKETSMLVGAG

SAICGAAAVLALESSLKSDPFKGILAVGTVVIFGLVFMFLYPIAFSLNLFPFFDQNAMGVFMGATLHEVA

NVAGAAEMAKDMAGFEQGASNVAVIIKMMRVILLVPFLLIVTYFFAKNQHSSSGKTAKSITIPYFAFAFL

GMIVLNTYLASKESILGIATSDIISLGKTLCTLCIVFAMAALGLQIDFKKFLKSGSRVFGLAFVLGLVLI

FGGYFLTLAFKGILW

>ABV52534.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKILVSVLSSCLLASALSAVSFKEDSLKVSFEGYKTKDMIGTKGEFKNVEYKFSKNTKDLASYLKGAKA

TIKPSNAFMGEGNDIITNNITKVFFPALLGDTDIKVVFQDVIAGENKGVISAKITMDKKSTIVPLTYTIK

DNKFEAKGQLDLHTFKNGSKALKALSDVAAGHGGISWPLVDISFNADLAE

>ABV52533.1 methyltransferase GidB [Campylobacter jejuni subsp. jejuni 81116]

MIFKDYDFLQNYDLKNFEEKIKIYKELLSKFNRIHNLTHLKNIDENIFDSIKILDFYDFSKAKNIADIGS

GAGFPAVFLAFLLQNNFHLFEPNPKKAAFLRTLKIECELSNLHIYKEKVQEYQNIFKADIITSRALMDVK

PLLEICKNLKDENTVFILWKGSEIYQELENIKDYEIFENNLRKYCILK

>ABV52532.1 GTP cyclohydrolase II [Campylobacter jejuni subsp. jejuni 81116]

MKIKISEIANLPSKWGNFQIQSFKENDKEHLCIFKNTPKDTLNLRIHSECLTGDALGSLKCDCGEQLEFS

LKYIEKNGGMVIYLRQEGRGIGLFNKVNAYALQDKGFDTIKANHQLGFKADERTYEIVEFILKHYEISKV

NLLTNNPEKLESIKEKIITRIPILIEPNRFNVEYLNIKQTQMGHLK

>ABV52531.1 delta-aminolevulinic acid dehydratase [Campylobacter jejuni subsp. jejuni 81116]

MFKRFRRLRLNENLRAMVRENSLSVNDLIYPLFVVNGTGIKKEISSMPDVFQMGLDEILKECQNVVNLGI

KAIILFGVLENEKKDSCGSDALDDKGLVARSIREIKKNFPDLFIISDLCFCEYTDHGHCGIIDPKTKSVD

NDATLEISAKQALVHARAGVDMIAPSGMMDGIITTLRKALDKEGFENLPIMAYSTKFASSYYGPFRDVAE

SAPSYGDRKSYQMDFANGKEALEESLEDEAQGADILMVKPALAYLDVVKEISLHSNLPLCVYNVSGEYAM

LKAAKNAGVIDYEKVLYETMIAFKRAGAKLIITYHAKELAKMLKGEK

>ABV52530.1 ornithine carbamoyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKHFLTLRDFSKEEILSLVNHASELKKEPKKLLQDKTLAMIFEKNSTRTRMAFELAITELGGKALFLSSN

DLQLSRGEPVKDTARVIGTMVDFVMMRVNKHETLLEFARYSKAPVINALSEFYHPTQVLGDLLTIKEWNK

MQNGIAKVAFIGDSNNMCNSWLIVAAILGFEFSIAIPKNYKISPEIWEFAMKQALISGAKISLSHDKFEA

LKDKDVVITDTWVSMGEENEKERKIKEFEGFMIDEKAMSVANKDAILLHCLPAYRGYEVSEEIFEKHADV

IFEEARNRLYVVKALLCFLDNQRGRE

>ABV52529.1 hypothetical protein C8J\_0930 [Campylobacter jejuni subsp. jejuni 81116]

MKELEKYSTCLKRIDEFSQNLGIKKKDRTIFKMKQSENENEKCLVLENGSFDSPEPWFVIDENDEIHTLL

SLQSLKNILESLKQSQKENFELRLEKAIYQQIPVDFNDVWTVAMDEIKQKAQNGTMEVSIDLEKLISKIK

QEHPNLFVDMQAMIERVNQNERL

>ABV52528.1 oxygen-independent coproporphyrinogen III oxidase [Campylobacter jejuni subsp. jejuni 81116]

MRDYKAFVKYSKAGPRYTSYPTAVEFNTNFKYEEYIEILKKQDRSLSLYFHLPFCRSACYFCGCNVIYTA

KEESKERYLTYIFKELDILNTILDTKREVVQMHFGGGTPTFFSAKQLQNLILKIRSVFGNFSKDAEISCE

IDPRFLNEEQATVLTQNGFNRISFGVQDFDEKVQKEIHRIQPFELTQNALNLVRSKGIKSVNMDLIYGLP

YQNLQSFTQTLEKVMLLNPDRLAIFNYAHVPWLKKNMRKFDENTLPSPDVKLEILEFCEKFLSKNGYKMI

GMDHFAKENDELFKALENGTLHRNFQGYTTKGGADLVGVGLTSIGEGQRHYAQNFKDMSSYEAALDRGVL

PFERGVALSDDDELRKAVIMELMANFKLDIKSIEKEFCIDFQEYFKEDLKALEEYKDFINFDENFIKVNE

TGVLLIRNIAMCFDAYMKNISEDKKVFSKTV

>ABV52527.1 iron-sulfur cluster-binding domain protein [Campylobacter jejuni subsp. jejuni 81116]

MKFSQISDACVKCGKCIPVCTIHEENRDEITSPRGFLDLLAAYKEGSLELDKEAKKVFESCFLCTNCVEV

CPSKLRVDNAIEEVRYDIAKKFGIAWYKKLIFFFLRRRKILDLVAKLGYVFQSCAFKIQNENENTGMKAR

FSMPFVKKGRLLTSFNKKSFLNSNPKFINNDGEKTIGFFVGCLANYFYIDTANAVLKIAKELKINVDLMK

EQVCCGAPQFFTGDFKSVEVLAKKNIEYFEKKLEKLDAIIVPEATCSAMLKIDYEHFFIMQNDLDWAKRA

KCVSSKIYMASEYFYKFTSLEEILKTKNKFNYSITYHDPCHARKMQGVFKEPRELLKTNYHFVEMSNSNT

CCGFGGVSMQTDYYDRALSVGLKKAQMIDESKASVVSAECSACRMQISNALEQNSSKVVFVSPLELIAKA

L

>ABV52526.1 hypothetical protein C8J\_0927 [Campylobacter jejuni subsp. jejuni 81116]

MKIVFKGKSSEYEIQRSCFCVDAFVIKDKIEERDGVDFITSNVDLLEFSDDSFTFEEIVKHFNICDTEDM

IIVEDFDMKSNKDNQNQEDDIEHNILKSEKIIHENTKQTSMQFKNLKFFSRIFKNENFLSDFKESKQEVV

TIKKHEKLEIFKNLSQEDQEISFVKIEILNYDSNEDSLSFNLDIFPSGMSYKYGILKGSMHIILQGKTSS

TMLFPFLKSMIYKNKSENSSEKIFTLMINQKKHYKLIANLS

>ABV52525.1 hypothetical protein C8J\_0926 [Campylobacter jejuni subsp. jejuni 81116]

MEFLAFIFLIIIFLFVVFIIVTRYEKKIKLLNQNIQNMKEDIADLKETTQKNRSLIEKNRSNIENIIK

>ABV52524.1 hypothetical protein C8J\_0925 [Campylobacter jejuni subsp. jejuni 81116]

MEKSLLFHFRRIGVEFIIFSVYAVFSISWAATGSLMPLISNDLALNTQQATLITSMIVVAKIFGASFTAF

LVYKFGLKKGYFLGCILMSSGIFLSFVDSYSGILVIRFLTGLGSACALVCLVPIAQQWFEKKALHFVISF

NITSNLVGITLGLILAESISNYFGNWRDSLSFYAWINLILLILWLFVGKDENKKEEKKNNAKDLIYALKS

RVTWGMIIFYIGPILFLNSLFTFLPTFYAQYAGFSKELADFAKKEIPALANFAIIFGPYLGLFFKRKNIS

FKIMLLSGGACIFICGFCMLFLQNLVLIQIFAVLSGIFYSMWFPFFFNLPSELKNSNPNQTAYIMSAFWS

ITFVILSFNLWVVSWSVDKTHSFTLGFVYIFALIFISAILAQFVLPRRENFIQGEK

>ABV52523.1 hippurate hydrolase [Campylobacter jejuni subsp. jejuni 81116]

MNLIPEILDLQGEFEKIRHQIHENPELGFDELCTAKLVVQKLKEFGYEVYEEIGKTGVVGVLKKGNSDKK

IGLRADMDALPLQECTNLPYKSKKENVMHACGHDGHTTSLLLAAKYLASQNFNGTLNLYFQPAEEGLGGA

KAMIEDGLFEKFDSDYVFGWHNMPFGSDKKFYLKKGAMMASSDSYSIEVIGRGGHGSAPEKAKDPIYAAS

LLVVALQSIVSRNVDPQNSAVVSIGAFNAGHAFNIIPDIATIKMSVRALDNETRKLTEEKIYKICKGIAQ

ANDIEIKINKNVVAPVTMNNDEAVDFASEVAKELFGEKNCEFNHRPLMASEDFGFFCEMKKCAYAFLENE

NDIYLHNSSYVFNDKLLARAASYYAKLALKYLK

>ABV52522.1 hypothetical protein C8J\_0923 [Campylobacter jejuni subsp. jejuni 81116]

MKILFSPSESKNENCVKNPINENSFIFKELFPYRMEALKHYEEFIKNASLQNLQELFGIKNENEIDKFKH

DLKQAPTQEAILLYTGVSYEYLNFKALDKKSQAYILENTLIFSNLFGVVRANDTLPFYKFKQGAKIGNFA

IEKFYKEHFSKALDEYLENEEILDLRAGFYDKFYTPKKKFYTYKFVKNGKVISHFAKAYRGILLSISAKN

QVKNNKELLANLPSNLKLKEIQIKGLKEEIVLEILD

>ABV52521.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKKGIFLSIGIAVLFSACGNSIDEKTVKKYENQLNQTVKQEIASLSQDSGIKIEFSDFKCNADGDFIACL

SSNFKTLAKDNKDEYQELFQAKNIKIRSNEIYKGEANASISIKEYYNDLFKNQKSIQSNLVFENFKLGEK

VVSDINASLFQQDPKISSFINKLSSDSYTLSFDNSINKQENNYLDNLDIKFYNAKLNFNTNLNINLKEDL

LNYLDSKGIKFNTQTLAMDEQAINELLNMANYEQASDFSNTIQKYIILNNFKIDSTLKTEGVFSSYIATA

KENLQTLKAQSQNEEQALIFDKALAILNNITQNDDYKLNLDLKFKNIPVSDYSTQGIDSIEKLSINNQDA

TEALKIILPFIMFSMLMGGASF

>ABV52520.1 surface antigen, CjaA [Campylobacter jejuni subsp. jejuni 81116]

MKKILLSVLTAFVVVVLAACGGNSDSKTLNSLDKIKQNGVIRIGVFGDKPPFGYVDEKGNNQGYDIALAK

RIAKELFGDENKVQFVLVEAANRVEFLKSNKVDIILANFTQTPQRAEQVDFCLPYMKVALGVAVPKDSNI

TSVEDLKDKTLLLNKGTTADAYFTQNYPDIKTLKYDQNTETFAALMDKRGDALSHDNTLLFAWVKDHPDF

KMAIKELGNKDVIAPAVKKGDKELKEFIDNLIIKLGQEQFFHKAYDETLKAHFGDDVKADDVVIEGGKI

>ABV52519.1 transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MQKKYKNIIYASLGGILEFYDFVLFAFFLDIFAKVFFPQNDAFWMQINAYIAFGAAYLARPFGSIVMAHF

ADRYGRKNIFYISMLLMVLPSFALAFLPSYESIGIFATLILFTIRILQGLAVGTEVSGAWIYVSEFVKGR

QIPLALGFISATLTIGLLLGNIATLGIRSYFTPEEVQSYAWRIPFIIGGFFGILALFLRNKLSETPEFVK

VQNEKKILSFPLFEALKTHKMSMLVCFLMTMVLTSGVATLMILPKYFESLLAMSKTSALWVQNFAILAVI

FGALFQGFLASKWGSYRICSIFSIAFIIFGMLFSFYDEKFLFYFLLACFTQGIITFAPVFMTQIFKSELK

FSGLSFAYNISYAILGFLTPFVVNAFYKEYLGIYLAIVGSCSLFCVFLLKRVFARSKIKELSIVF

>ABV52518.1 aminoacyl-histidine dipeptidase [Campylobacter jejuni subsp. jejuni 81116]

MQNVIENFKQLCKIPHCSYETEQMKEFLSSYAKDKGFKVSVDKAGNIRAIKGKPKICLQSHYDMVCMGDA

PNLEVYEENGFLRAKNSSLGADNGIGIAIMMSAMAEFKNLECLFTNDEEVGLMGVNSLEHTLESKMLLNL

DHESDDEIMIGCAGGVDIEASLPFNTLRKKGKIYELYAQNFKGGHSGINIVRNEKSSIKEMAKFIQENKG

EIISFEGGERINSIPKHAKALVHFKNEVKSNNWIKCDFKEEGEFEICDQSNKLLSLINSFTHGVRAYDEN

LGIVQTSINLATLRMQDKQIKFALFARSNILDGLKQVEFETLEFFKAFDFKVRSFNFYPPWEGKPNALSD

MVFKALKKISPNAKVSAIHAGLECGIIEKKQELLCASIGPNIHNPHSTDEHCEIASVEKISKVVFEVLKD

NA

>ABV52517.1 thermonuclease family protein [Campylobacter jejuni subsp. jejuni 81116]

MRINYKKLFNLRKLLSDPKKLFSVLIFTLVVVFIQNYIAQNSSFEGKVVRIIDGDTIEVNHENKLTRIRF

FGIDAPELKQSFGKQSKEALSRILSGKQVEIIYKNKDTYGRIVAIVKLNNVDINRFLVSKGYAWADTYYS

NAYIKEQENAKKNHLGLWKEGNPIEPYKWRKHNKF

>ABV52516.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKKYTLMILLVLGISGCFVNERGISNRFYDDCKEYYDGSGTYHKVCPKNWVDIKMTP

>ABV52515.1 hypothetical protein C8J\_0916 [Campylobacter jejuni subsp. jejuni 81116]

MAKKDNFEEYAQLEEYASAEDISRVRAELLTCPELNTSLTGTIIEIDKNYAKSILITTSEMVADDQGLIF

DAFIFAAANYVAQASINKEFSVIIGSKCFFYAPLKLGDVLELEAHALFDETSKKRDVKVVGHVKEIKMFE

GTIQVVSTDEHIFKLKRPPLNTVKPTENQEQGAKINNPEAVAAALMASVGGK

>ABV52514.1 methyltransferase, putative [Campylobacter jejuni subsp. jejuni 81116]

MQENLLEKQFLNHPLYTKIQELKALNLACNFSLDDSVNLSTNSQAKDEILAITKELKPWRKGPFKIDDLF

IDTEWQSFIKFNILKPFMNEISQKCVADIGCNNGYYMFKMLEFNPAKLIGFDPSIKYRLQFELINALAKT

PIEYELLGVEDLPRYGLKFDVIFCLGVIYHRSDPIKMLKDLKAGLNKNGVVFLDTMYIEDEREIALVPNK

TYSKIPNIYFVPSISALKNWCERAGFKEFEVLATKKTDENEQRKTEWIDSFSLENFLDPKDKNLTIEGYE

APKRVYVRIGI

>ABV52513.1 hypothetical protein C8J\_0914 [Campylobacter jejuni subsp. jejuni 81116]

MIELIKNIKSTNDLKEKLYLAVKKWLLEHILYEDMKVEQYRRSSLASEDDKEVSFEEEGDEELENAVYLY

ICKCSGAIHDVPFGIHEKIKLQGKKFKCKKCREALEFYKVYSEGF

>ABV52512.1 hypothetical protein C8J\_0913 [Campylobacter jejuni subsp. jejuni 81116]

MLPKWDKTFSVHNAKIDEQHKKLFELAGKVEYLIDKPVYKDEIKNLLAEFFNYMKDHFYEEERYMELIKY

PDIETHKKFINILSNP

>ABV52511.1 hypothetical protein C8J\_0912 [Campylobacter jejuni subsp. jejuni 81116]

MDKLITWNEKYSIHDTMIDIQHQKLFELAGKVESAVYKFVKREELKEILTELFNYMKEHFDNEEQYMQEI

HYPYLNEHKIMHKNIIRDMSYLIQNIKTTNDLKEKLYTIMSEWLLEHILHHDVMIGKWIKAHNKNTKEEE

TKQEELTEDSQEKLEFIYSCPCKTTHALSYNEHLDILYHNKNLKCKNCQQTLFYFKNPI

>ABV52510.1 putative outer-membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKRIILLSSLAILSLYASDTKDNKKTIQMLEQSPYKEDANLKNYNNTLKVKDGVIIIDHSNTSDDNNSKT

INTKKNTQKDNNNTQKNQPNLSNDNTLKTKTPNSNTPSLKNTSKEESIHKVSFSFHITNKNINFKDLGLD

EQVLQEALNDYKKESISVQDLQDIANIISYYVQVSGYPAATAYIPQQELKDQIQINITLGVLGKYVVQNN

SSVRDYAIESKLPNHKGEIITTKLVEDAVYKVNEMYGIQTLASLKAGDNPGETDVVIETTPSDSFVSVLF

YGDNYGIKESGRYRGGASMSFNNIAHQGDSLNAYLQRSDEAQTNYGISYTTFLGNLKITPSYSKGNYALG

GIWREFDFIGTSENLGIDLKYPLWITTYNSFYLTSSYYHKKLSDSKFDILTFDKSSDTISFGIEGVYNGI

SNDSFSYSANVSYGNVKDEGMTIVGIGTSKVGGVEFGKFAKLNVNLNNAYFFNDTFTHLFSLNYQQVING

ATLDSSETISLRGPYGVRAYNNGDGEGDNAVVASFGLRMATPLKDFYITPFYDIGYSWYENDSYTNYMDA

YGLQLLYNKTGNFYVKLDLARALKKYKLDDDYSSKAYVSFGKYF

>ABV52509.1 hypothetical protein C8J\_0910 [Campylobacter jejuni subsp. jejuni 81116]

MKKLNKLSLSLVVGSLLFTQSYALPSGGKFTHGTSGSISVSGGTMNISGSKTNSVIQWGGGFNIANGETV

NFKGNGYNYLNIVYGSKSSHIDGTLEGGTNNIFLINPNGIVVGKDGSINANRVFLSASSIGDKEMKEFAK

DGKISAFEGNPLTTASPVIKSNAGNVINLGTITAGERVVMVGNQVSNMKYGSTDYGKFIFTNKKEQSNTV

YLDVYSNDIFVIRGPASNTIKKEDSVMLSIRPNKGSTGPGGDPTDTIGYKETSDLVAKDNISNEVLNSIF

NDLKFNSSVDISDLSKFYKDGKILTADELTSINQSMDFITALYGQTQDSNNATFANALKEVLGNSYGNLG

KANQAIIKTKEILSQIPKITEQQKNIQKAYDQAVDAYNEAVKKYNAALSGVTGSNASETITALKTVLDKA

YNDLKNAEANLESTTASNNSSLKSSNETLASVSIDGYKLTVNGEYLADYKTVNKPNDNNSGSNNGNDGTD

SGDINNGNNNGSNNNPNDTIGQQEPDIATALLMQTTDEDPNINEDDKQASIDEASTQESGNACIVSDNFK

AGNPCSR

>ABV52508.1 hypothetical protein C8J\_0909 [Campylobacter jejuni subsp. jejuni 81116]

MKSYDAPINISSEGVLALYTLKEQYPYLKNKEILILQSEQGFIDENSNTLNQEELQSFIEKMQKNKEDFK

LSSIDRLKKMNLQKLSYEVRISQDGKSIYAKIK

>ABV52507.1 hypothetical protein C8J\_0908 [Campylobacter jejuni subsp. jejuni 81116]

MREDEVLSFKARHGVNTADHSIKTVRVLPFLITAKTDHADASYNKLILEQGELSSVFYLKPKDTHIKNPS

NSKSNQRMNFLMSSTFTHYGNASYNQTILQKDAHISMGVENTYDLALNGAPYLIGAIATYGDSTNNSLNI

EAGSSVEFFTSLPKKDKNGNNTFDERITHLVGGLAYQGNVKNNKIFIKDANMIIHDPSKAYASSAAAHIS

AGYIDSGTDKNFQASKNLLDIDGFNLDMYMNHDKQPLAYNSVLFADFWGGKTEQGQALDNTINLKDIKNL

KKDKNNENIFAQALFNFYAGASNNGEANYNTLNIELKHPLEIANNFLGYNQHSFYGGFATKGANHNTINI

KNDLTTTDLSQSYKDALNIVAARTLEGSADYNKVYINNSMSTLPVYIYTAKKNILNNQDFYPSGANNNEV

VIKDFASFRNLTVLTEAKEASYNTINYNNVQSITDASNIDKGSKIIIRALDKANHNTIDIKNYSSNAADN

AYLIMAYNEAAYNKIIINDTLFGVASDKREGILSIIAGLSNNAHDNTLIINNLNLDEYKNNNSIFIAPSA

ITGLSEAKSYNNTLYIGGNLNIFKNTFIDILAGALVHYEDSNSASNAVAPSDISLSKNNRLI

>ABV52506.1 hypothetical protein C8J\_0907 [Campylobacter jejuni subsp. jejuni 81116]

MKMRVYYEDTDAGGVVYHSNYLKFCERARSEIFFNKKVDIFDASKGHFLLAKANCNFLKPAKLGDMIEIK

TKILEVKNASVEILQEIYKDEILLFKMELTLAFIKNEKPARMDMQLKKLFEELF

>ABV52505.1 hypothetical protein C8J\_0906 [Campylobacter jejuni subsp. jejuni 81116]

MKKIFLIFFLSCFLLNAKEQKLVDVKPVENFYPKLSVQECNTNCLFDLLESRLYLSFLSEFADQNDQFLS

NVYAKLLNSITDFEKNVQKITSVKLAIIIPEKTIKSYSNTIINSSIAYLLRQRAEIKVKVFLTGTEDSDK

IRAALDAAQAQGYQYAIAGFTLKGANELKNYSGNMKIFIPTIHKNNIQISNQNIIFGSIDYDAQIATLLS

KSNANIAIFSDGSALSSNLNSRILAQNNNARIYTIEGEKLDFSRLLRSQGGVNNASIFFNTPLIKTALAS

SQLRIYNIHPYVLLSTQINYNPTFLSLTQQGDRENFIIANSINNHDDNLVYLNEIFNQSIDYNWIAYATS

IGVDYFYTEFLNKKSESLFDEKIKNSQVDYKVRLMQGKQASFEELK

>ABV52504.1 DNA polymerase, bacteriophage-type [Campylobacter jejuni subsp. jejuni 81116]

MIRSLYYLKAMGFNFVDTHTNHFEQVQNFQELKQLVSSCTLCQFSKTRKFSLMEPKIKNVKLLILDVFGQ

KSENESGILLNSKKGEKLKHYIYQILGLCDEDFYFSYLFKCFCNGKFDDFSLQSCLPFFWNELKLIQPAF

LLCLGEYTFKSLGFKDYHILKGEIFAYKNFFIMPSYDLDFIEKNPSYEKNFIQDLKKIKGFL

>ABV52503.1 putative acetyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MSEFKIIDLRQEDLDILQEMIIEFAKYEDMLDFLQCTKEKLEHSLLKNKFARAFLLKENEKTIGYMIYFY

TFSSFWGSGGIYLEDIYIREDFRKKGYGKAVFKFLGEICKKENLKRLDWVCLNDNILGINFYESLNAKHL

KQWRNYRLSGENLEKLCDL

>ABV52502.1 hypothetical protein C8J\_0903 [Campylobacter jejuni subsp. jejuni 81116]

MKRTYQPHGTPRKRTHGFRVRMKTKNGRKVINARRAKGRKRLAV

>ABV52501.1 putative ribonuclease P protein component [Campylobacter jejuni subsp. jejuni 81116]

MKNFDKFSTNEEFSSVYKVGKKWHCEGVIIFYLNSYEKKIAVVASKKVGKAVVRNRSKRILRALFAKFER

YLQDGKYIFVAKNEITELSFSRLEKNLKWGLKKLECFK

>ABV52500.1 hypothetical protein C8J\_0901 [Campylobacter jejuni subsp. jejuni 81116]

MGIEKTRMFQMICLKILRFYQKFLSPLKPAACRYYPSCSEYALWQFQKKNFFLAFFSTFFRILRCNPFFK

GGFDYPRVSKNFYPMNLCFKPIFLAKKQLCFLYIPYKNKSFYLIKIIFKRTNQ

>ABV52499.1 60 kDa inner-membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MNNSNNIFQQKRILLAVVISFLFFVVYDYFFIPKQPLKIEQNITQQNQQNTSINNTPNIQNTTTNTPSAA

LVSQDSVISKVQSKHFEAQIDSFGRISAFYLKDKKYQNEKGEFINLVSKENSPYPLEMRFSDPSINSEAF

KIPYVANASNLFVDENGSQVLKLTQNLSGLKIEKDITFYPKGNYEIEVKLSKNANYFISPGYRPNIAVDS

YTVHGALVMDNKETIETYKDGDVEKDESANNVVMTSAFDRYYATFFYNFDKPLNVAISKDANKNPIVFAY

SDNEFKAGGYIGSKEHVILRSIDPRLEAVVEYGWFTFIAKPMFEFLNFLHQYIGNWGWAIVVMTLIVRII

LFPLTYKSMISMNKLKDLAPKMKDIRERYKGDPQKMNMHMMELYKKHGANPMSGCLPILLQIPIFFAIYR

VLLNAIELKAAPWAFWIHDLSVMDPYFILPILMGVTMFLQQLITPMTIQDPMQAKIMKFLPVIFTFFFIT

FPAGLTLYWFVNNLCSLVQQWVINKIFAKEHHKKQAEHEK

>ABV52498.1 hypothetical protein C8J\_0899 [Campylobacter jejuni subsp. jejuni 81116]

MKIEAIDLQSALTEASRSLECSVMDLEYEIIQHPRKGFFGFGRKKAIIEAKAKKRILKKNPKKEFASSKN

HKPETHEPKQENKIEIKNEKNKIQKEKYTVKSDEIFDSFHRESKGVRNTQDILDEIRIQLVKLLESSQFK

IELSELRMYNEDCVLIRLDGEDAALMIGKEAHRYKAISYLLHNWINLKYNLLVRLEIAQFLENQIQGMQL

YLQSVIEKIKIHGRGQTKPLDGVLIKIALEQLRAEFPDKYVGIKQNNDQRFVVINDFFKKDE

>ABV52497.1 tRNA modification GTPase TrmE [Campylobacter jejuni subsp. jejuni 81116]

MSDTIAAIATAHGVGSISIVRLSGERALEFALKLSHKTKLTPRHATFTKLFNQNNEIIDEAIMIYFKAPY

SFTGEDIVEFQTHGGFSVSEVLLEELVSLGARLALAGEFSKRACLNGKMTPLKALNIQDLILSKSALAAK

IIARNMQGNLGELLEKIRTDLVKTLAFVETSIDYADDDLPSDLLEQISTMCEENSKILKEIYTLSQSKKG

LIEGFKIAIVGKPNVGKSSLLNALLSYERAIVSDIAGTTRDTIEESFKLGTHLLRIIDTAGIRESKDAIE

QIGVALSKKSLEDADIILAVFDASRVQDKEDEKIFDLLANTDKKIFWILNKSDLENVFKNTQNKNFIKLS

AQKDITLLKEELQNYLNSFDSEGIMVSSLDLINACKISSEAIFRAKGLLEESSLELFAFELNLAINELAR

FTKDFQRDEILDEMFGNFCLGK

>ABV52496.1 phosphoribosylformylglycinamidine synthase [Campylobacter jejuni subsp. jejuni 81116]

MDKETIKAHKISDEEYAQILEILGREPNLLELGVISAMWSEHCSYKSSKKYLNGFPTKAPWVIQGPGENA

GVIDIGQGMAAVFKVESHNHPSFIEPFAGAATGVGGILRDVFTMGARVVAGLNSLKFGDIHDEKCGKHQK

YLVKGVVNGISHYGNCMGVPTIGGECAFDECFNGNILVNAFALGVCKSEDIFYAKAEGVGNPVIYVGSKT

GRDGLGGAVMASDSFNEESKSLRPTVQIGDPFSEKLLMEACLELFKTDYIVGIQDMGAAGLTSSSFEMAG

RSGSGMKLYLDKTPMRESGMTPYELMLSESQERMLICAKKGYEDKVIEIFKKWDLDAVVMGEVTNTGKME

LFWHDELVGLIPIEPLSEKAPILSRPTSEPKYLSEIKNYKFELKSSIQELFIQMLQNENINNKAFIYDQF

DSSVQTNTIKADGKLGASVIRIKENGASVAMAIECNSRLNYVNPKIGAALAVASAGRKVACTGAKPLAIS

DCLNYGNPQNPEVMWQFAQGCEGIKEACKELNTPVVSGNVSLYNETEGVSIYPSPTIVSVGVLEDANKTL

KASFEKENLSVYLLGESLGEFGGSMVMKIQDKKVSGSLKELDYKAELALWDLLYKANQNSLLECANSVGI

GGIAMTLAKMFAISSVGANLTSDFDDEKMIFDESASRAIIGLSKENEEAFLNLAKEFGVKAYKLGVSTSQ

KHFKLDSIELSKAELDKLYFESFKEQIQ

>ABV52495.1 putative DnaJ-like protein [Campylobacter jejuni subsp. jejuni 81116]

MTLVLIILVVLVFYWYYKTWGKQDFLNSATRGAKGFAKGFARGVMEERMDEFKRRMNYYVIALLAKIAKS

DGRVSENEAEMIKDLLDANAKDEKERAFLKASFNEHKENLSDAFYVAKDFLKEVPLPKNERFNVLRVLVF

MALIDADFNAKKREILEQIAKAFDIAKSELDAFIASLSNLKSTKKELSLDEAFAILELPNNADLNAVKKQ

YRNLAKKYHPDILNANNVSEEELKIGVEKFQKINEAYEKVKKYLER

>ABV52494.1 phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [Campylobacter jejuni subsp. jejuni 81116]

MRALLSVSDKEGIVEFGKELENLGFEILSTGGTFKLLKENGIKVIEVSDFTKSPELFEGRVKTLHPKIHG

GILHKRSDENHIKQAKENEILGIDLVCVNLYPFKKTTIMSDDFDEIIENIDIGGPAMIRSAAKNYKDVMV

LCDPLDYEKVIETLKKGQNDENFRLNLMIKAYEHTANYDAYIANYMNERFNGGFGASKFIVGQKVFDTKY

GENPHQKGALYEFDAFFRANFKALKSEASFNNLTDINAALNLASSFDKAPAIAIVKHGNPCGFAIKENLV

QSYIHALKCDSVSAYGGVVAINGTLDEALANKINEIYVEVIIAANVDEKALAVFEGKKRIKIFTQESPFL

IRSFDKYDFKHIDGGFVYQNSDEVGEDELKNAKLMSQREASKEELKDLEIAMKIAAFTKSNNVVYVKNGA

MVAIGMGMTSRIDAAKAAIAKAKEMGLDLQGCVLASEAFFPFRDSIDEASKVGVKAIVEPGGSIRDDEVV

KAADEYGMALYFTGVRHFLH

>ABV52493.1 hypothetical protein C8J\_0894 [Campylobacter jejuni subsp. jejuni 81116]

MFKTIGFKVSAAIFVVLLISFIVMQVILNLDFKNTANKMSRANLDTVSTSVFQTMRMAMNLGDPEKIKEA

IEDAKSIEGISDIKIYPSKDTIDLFEMKAPQISNDKRIIEQFSNPKIQALEENVNGVVHLRLIRPLIADE

SCVACHANANVGSVIGVMDISHSLEGVQKDISKTSQSYIIIFTIALIFTLCVVLLMLKVVVGKPVLELLN

HAKELAQGSGNLKARISVKGQDEIALACGYINQFIEKTHKAVSGASHNSKNVEKQSNLLNSNAISLSDIS

SQSHKQIDQSFKLGANVGNELGELASLSNKANSANEKSFLLLEQMLKSLFNVANKVSTVSQNENELAKKV

ENMVNQAGNIQKATQMMDEIADKTNLLSLNAGIEAARAGAFGRGFSVIAEDVRQLAQNSEEFLGNVAQIT

KELLQSINEVSAELKKNAQSVQALNDDTALLVDDANEVKLCNEDARALVTQCTEKIKISQENIQNLLSRM

QENVEVSEKNEEISKILLQVADELKIVCHNLESELNQFQI

>ABV52492.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKKTLQIALAAAFFAGCASTSVTSSTSKGNNELVQNQLFKIEKIIVNGKTFDPKNAEESPNISFENNKFY

GYSGCNRFFGSYQTKADTLQIEGDRVASTQMLCHPMDVMDFENSFLSNFKGTFKISNENGKLVLSNDEMK

IFFK

>ABV52491.1 peptidyl-arginine deiminase family protein [Campylobacter jejuni subsp. jejuni 81116]

MIKSIPEWSEQEYLMLSLPHEKSDWNPYLEEILQSYKEFVKAVSEFQKVLLIAPKQSDFENFKDIKNVEY

FKCDTNDTWIRDFGAIDIVENGRFKALDFTFNAWGNKFQSELDNAVNSKLFKEKFKEELKKVDFILEGGS

IDFNGEGVMLTSSHCLLNENRNSHLNKTQIDTKLKEIFGLKQIIWLENGFIKGDDTDHHIDTLARFIDKN

TIAHCICEDEEDEHYLPLQKMKEELKKTGFDLIELPIPKPLYYEGRRLGATYANFVFINNALIVPFYKDK

NDEIIAKRLSKALPNHKIIGVDARVFLRQNGSLHCSCQNRFKGLR

>ABV52490.1 putative transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MSLQKKATFVASLCAIVLALVKFIVGLTSGSVAVLSSAIDSLMDFAISAFNFLALKKSSQKANENYNFGF

SKIEALMGLLEGVFIVGVGIFIFYESILKIYYKEEIKDLNSSIYVMIFALIMTFFLVLFLNYVAKKTKSL

IIESDALHYKTDCLTNACTLGALVLIYFTNLHIIDAIFGIVISLYTAFSAFKIIKKALAFLMDEALPKKQ

VDKICTLISNNPEIISYHELKTRKTPSCNYLSVHLVFCPIISLLNAHKISDEIEEGVRKMFENEKWDIQI

HLDPYDDAEQERQRQ

>ABV52489.1 hydrolase, carbon-nitrogen family [Campylobacter jejuni subsp. jejuni 81116]

MKIALIQQKFHSNKEQTIKKTCEFIEEASKQGAELICLGELHQSEYFCQSENVDFFDYANDYEKDVKFWA

NIARKNQIVLITSLFEKRSAGLYHNTAVVFEKDGSIAGKYRKMHIPDDPCFYEKFYFTPGDLGFEPINTS

LGKLGVLICWDQWYPEAARIMALKGAEILIYPTAIGWFDKDKDEEKQRQLNAWLGVQKGHAIANGLYVVA

INRVGFEKDVSGVEEGIRFWGNSFVFGPQGEELCLLDSQNECVKIIEIDKKRSENVRRWWPFLRDRRIEY

FADLTKRFID

>ABV52488.1 lipoprotein, putative [Campylobacter jejuni subsp. jejuni 81116]

MKSCLYFTFIVLFLTACSTKNLTSLHHENLEQKNENQHYAKLEYEQNVSILPQFAYDINFDAKRYKKYFF

NPWHDSFKNYKGQNIFWSFPLYLNSKNTYYFFNKQIIPLSWFKNATNNANIQEFGKLNQKALIIQNTIIK

NLPTQRAILKNPFFENEGIPFDYASDGILNAGTPVLISHFSKDKRYAFVLGEAGFGFVESKNLEFFSNDR

AKIYENLNFITPLKEKFPIYSEDGKFFFESRIGAIYPYYKEDKNYFYGKIGSKKYKISKKDVSKFPLQFN

DKNLKNQLSQVLNLPYGWGGYNFERDCSLLTRDIFSAFGLYLPRNSAAQKNSFNHFDISTLSNSQKKDFL

NRFGKAYLSLLYLPGHIMLYVGQIADNNIAIHNIWGLRKDTTQRLLISSSVITSLEIGKNEILEDNLLLS

RLKEISFINLNEQEKEQIKSYLENIQNK

>ABV52487.1 hypothetical protein C8J\_0888 [Campylobacter jejuni subsp. jejuni 81116]

MLDKLEKILAYDNVFLSGGAGVGKSFLTNELIKSYRKQKKLAIALGSSALSAFNIGGVTLHSFFCLGYCD

DMMKLSALDRNQKQKEKLTKLKELLKTIELIIIDEISMVSASVFEMIGFRLKNSQFNGKILVVGDFFQLP

PVIKEKKETLFNHSYYAFSSFFWQDLNFKNIKLSQPKRTQNMEFYNYLSLIRQGFLDEKILSFFESLRID

YKELENLEDDYTLLCGINKKVNNINQEKLSKLETPLVCFKAQVKKEDKRIKDEELDSWVGSLNILEELNI

KIGARIIFCVNNWDKNYYNGEQGIIEDILYEEEKIYISIIKNNGMKILLEPYTFFMEELEQSGKDFVVNI

LASVTQFPIKLAYAITIHKSQGMSIEKLVCDIDHIFENGQLYVALSRATNPNTLKIYSTKKINFGFYFAN

ILKIDSNVIEFYKKHNFLDLEIQEQII

>ABV52486.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIFLSVFLALSLNAQNLEIDKIRTDLYSKSGANVLKKVEISLEFDGNNLKENENKLIDAVNTVISGFF

YEDIFTEIGKNNFKKTLEKFLDKKYKIKLDDIYIISLSGVEKFDLEEFKRFLESTEAKEKGMGSEVKKAL

ENLEVPKTQVPGVEKIPTPSVPNLEAKQVEQLFKDSDEENKNDNGEINIDNLNTPKMTPDIEEKIKRDLI

ANPPQIFKENNASKPYHLPQTGYDIKLDENSTQN

>ABV52485.1 outer-membrane lipoprotein carrier protein precursor [Campylobacter jejuni subsp. jejuni 81116]

MKKTFLIFFIFIGQLFALDLNFNTFSSDFIQIVKSKNSTLSYSGHFILSKDQAYWSYDTPSKKEIYINKN

QVTIVEHDLEQVIFSHLDNIPNLNEIFKKASLIDKDKLVAKYDNINYTIKLNQEQIQSISYKDEFENDVI

INLNNQIKNPKINSDVFKAKIPQNYDIVR

>ABV52484.1 translocase [Campylobacter jejuni subsp. jejuni 81116]

MFLNTLKAVFGTKNDREVKKYFKRVAQINALEGKYQNLSDDELKAEFAKFKEQILSGEKNENDILNDVFA

IVRETGKRTLNMRHFDVQLIGGMVLHDGKIAEMKTGEGKTLVATLPVVLNAMSGKGVHVVTVNDYLAKRD

AEQMSAIYNFLGFSVGVILSSQNSDIEHKQAYDCDITYGTNNEFGFDYLRDNMKFSKVEKVQREHNFVIV

DEVDSILIDEARTPLIISGPTNRTLDGYIKANEVAKQMQKGEAVLPPAKPEGDFVVDEKNRNILITEAGI

AKAEKLFGVENLYSLDNAILAHQLDQALKAHNLFEKDVHYVLRNNEVIIVDEFTGRLSEGRRFSEGLHQA

LEAKENVKIQEESQTLADITFQNYFRMYNKLAGMTGTAQTEATEFSQIYSLDVISIPTNIPIKRQDKDDL

IYKTQNEKFKAVIEEIKKANSKGQPVLVGTASIERSEVFHNMLVKEKIPHHVLNAKNHEQEALIIQDAGK

KGAVTIATNMAGRGVDIKIDDEIRALGGLYIIGTERHESRRIDNQLRGRAGRQGDPGISRFYLSLEDNLL

RIFGGDRIKNIMDRLGIEEGESIESRIVTRAVENAQKKVESLHFESRKHLLEYDDVANEQRKTIYRYRNE

LLDENYDIRAKISQNIAEYSANVMNDYILDESGSNVNFENLKAKILYECSTQISEKDFENLSVIEMQDKL

SQILENSYNEKMSRLGIKELRNIERILYLQVLDNAWREHLYQMDILKTGIGLRGYNQKDPLVEYKKESYN

LFLELVNRIKFDSIKLLFSVQFNQEEVQNLENKANEENEKLLQSSVEMGASEDNLGEAEFKKVPRNAPCP

CGSGKKFKECHGKSGPKQGILA

>ABV52483.1 permease, putative [Campylobacter jejuni subsp. jejuni 81116]

MNKSVLKYLLFKYLRFDKEQPFINLSMLLAFLGVCVGLCVLLVAMAIMNGFDKEFEKRFFVMNYPITILP

KFYAPVNDEFIDELRKTFPNLLFSPYISTQVVVKGDNRFEGGVLFGVNFNDEKKINEVVAKALRDENLSG

FDILVGSALIDEFGLHKNDKLSLIFSNLNPSGFSLVPQTKRFDVKARFTSGLAFYDKAYMYTDVDALKKV

LGMPKNPNYDGIHVYSDNAFKDVEKIKSYLKDDYAVVGWWEQNKNFFSALELEKRALFIVLMLIILVASL

NIVSSLLMIVMNRRSEIALLLALGASKNEVKKSFFALGMLIGGGGMIVGVVLAFFALWLLGNFDIVTLPA

DVYGTSKLPLDLSLMDFSLTIVGALIIIALSSFYPAKKATQINILDTLRNE

>ABV52482.1 putative glutamine transport system permease [Campylobacter jejuni subsp. jejuni 81116]

MSLFTQKNKNFKPLKPLSKSKIITNLILLILFLILFCYCSFSISAYHFDFSVIATYKEKFLQGFLNTLII

SFFSLLLSIILGGVFCAFSLSSIVFLRFLSTFYIELIRGTPLLVQVLLMYYIIANNLGLDNRYVAGVIIL

SCFSAAYLAEIFRAGILSISISQLESARALGLKEMQVFAYVIFPQALKNILAPLSGQFANLIKDSSLLSV

IAVNELTQSAQEINSYTFATLEAYVILAITYLILTLPISIFSRYLERKCQK

>ABV52481.1 hypothetical protein C8J\_0882 [Campylobacter jejuni subsp. jejuni 81116]

MLIIGHKLLKNLDFSFIESVEEVKDNKVYCIVYDEKLISYLSQNDFEFAILVQNKDEIFLANALGAKFLL

CNDKKLAKFASKVAEFYVFDSRVLMIVDKLENFKKFYKLKIDGIILKDNIDNFPKN

>ABV52480.1 2-acylglycerophosphoethanolamine acyltransferase / acyl-acyl carrier protein synthetase [Campylobacter jejuni subsp. jejuni 81116]

MQKKSFLKIYGLIPFLLIAFINAFVDLGHKIIIQNTIYKAYEGSEQLFLNAIVNALILLPFILMLSPSGF

LADKYPKNIVMKISAIFNVILTLIICICYYSGAFWMAFIFTFIMGAQAAIYSPSKYGFIKELVGKDFLAM

GNGVINAVSIMAILAGMALFSLSFESLYSSAYNQTDEILKEVAPLGIVLILFSCIEVFFAWRLPKLKQTN

KDLVFNKKDYIRGKLLINNLKLVFKNKTIWLCIIGFSFFWAISQLYLVSFPVFAKNELFIENTFYVQISL

AFSGIGVILGSLVAGKFSKNYIELGLIPLGALGMFLMAFLMPYFISLLSYSFLFFFFGFCGALFIIPLNT

LIQFHAKENELGQILAGNNFFQNIAMLGFLLLATLFAKFEINVVYLFYFITLVTFIGSFYILLKLPFSLV

RILLSIAFLQRYRLLVEGFENIPEKGGALLLGNHISFIDWAVVQMAIPRKIYFVMERSIYSKWYIKIFLD

KFGIIPVSSTGSKTSLELIAKHIKESNLVCLFPEGTLSRHGQLNEFKAGFELACEYLSEDDGKIIPFYIR

GLWGSAFSRSDEEFSARNRTLNKRKIAIAFGKAMPLHSKKDEVKAKVFELSFMAWKSQCEAMHTIARAWI

DTAKKNLNQIAIIDTLAGDISYRKMLTLSLILNFFIKRKSKELNINPQRGSYAPKEEAIGILLPASFASS

LTNLSVLIAEKIAVNLNFTAGEKALKAAIKNAQISQIYTSKIFLEKLANKGINLNFDTNIHLIYFEDIVE

DFKMQKTKIFSMMLAVSIIPSFILKSIFTPLKNNLAIAAILFSSGSEGSPKGVMLNNRNILSNIAQISDV

LCTRNNDVILSSLPPFHAFGLTVTTILPLLEGIKSITFSDPTDALGVAKAVAKNNVTIMCGTSTFLGIYA

RNKKLDALMFESLRIVVSGAEKLKNEVRTAFEMKFKKSIFEGYGATETTPVASVNLPNRFDADYWLIHRA

NKEGSVGMPLPGTAVHIVDPNNYENLKTNEDGLILIGGHQVMVGYLNDKEKTDEVIKEIDGIRWYNTGDK

GHLDEDGFLYIVDRYSRFAKIGGEMISLGAIEEEIAKFIDTEVVKFCATSLEDEKKGEQIALLIECNNEI

FERVCEAIKNSNIPTLFKPRYYFQIEKIPLLGSGKVDLKKVKELAKNLAL

>ABV52479.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MFVFIPLFTIFILLAGGYFAKRIGVLKQKQARTFLDFAIIFALPCLIFDKAYHLNFDFSLIIFIFIGLFS

CILAAFFAILIGKVFHFSKVTLVSMFLLSCFGNTIFVGMPIVAGIFNDPQFSAEVIFYDALATTLPISLF

GPFILSLGNGEKVSLLANVKKILSFPPFLALLFGFLCKLITLPEFIFSPIRLFGASATPVALFAIGLGLG

FMAIKTSYKPTIVVIFAKMILAPLFFVFCLKIFNLELKDSTIVAIIESAAPTMTLAGAMVMKAKLDSNLA

VSAVAFGVLFAFISMPILIWALL

>ABV52478.1 hypothetical protein C8J\_0879 [Campylobacter jejuni subsp. jejuni 81116]

MFGGLLGGGCCDKDNVFLGFVPCKEDKKKLAKLNDAGKCHEVGTYCSKKVSLGFTKICVEKRKVFVASIL

N

>ABV52477.1 hypothetical protein C8J\_0878 [Campylobacter jejuni subsp. jejuni 81116]

MFFAPSFLFGATEIANGNLIYTWGYGDVMNEIMQAVKGITTETSYIVNAALAISLLLFSIKKAMDGQTNP

VFEFGKMFVLFAVVWVMFLKAPNDNNHRFMIHDEVTSKDYVISQIPIGIGKSFALMTQFEKVILEAMEKH

FSTPQSTNFSNAGLGFSLQVMSTLPSVKLSAIDATLQKNIDFYFRNCVSVGILLNQQGRNLFQNSDNLMQ

DLFTNIGNGSQLTPLFTNNNNIEEQSVVPCSDAGPQIVEMIQKDTDEAMKIHAALLGMVDDMTNYEQKFL

GAAQIYNEQAVSARSYLQQSMIMLASQNAIINTAKSVGLNPASVAANTAYADQQFYASMHKHKDTWRKLI

CL

>ABV52476.1 hypothetical protein C8J\_0877 [Campylobacter jejuni subsp. jejuni 81116]

MPLAKAYLTAIIIGLSWLVALLSIVFGSYAHIKMFFTLCIWIVLWTPILCIINFINDFNLMNVAQVITGG

KAALSLGDNMLIFKEVANRSNFMNYLVMSTPVLAYAIAKASEQGFVTFASGLSQALTGASKAAGSFANQQ

ALSTQTSIATPRGDEVWSMNAGVASLQYARNIDGVVTKFNTQSVMGDNTKNSEISNANMTGTNVDGMMSG

AKLSAGTMTTVNSVSQANSDAWNKNFNDQYSHMSQSGRASAFK

>ABV52475.1 hypothetical protein C8J\_0876 [Campylobacter jejuni subsp. jejuni 81116]

MHLNEAKGFMEKGDEAFKKAFANNIGQEIQNRTDLTSEEKAEIALAASAHAGFSVLGNGAEIQSSASSKR

GIGNVETFSEAQKAAYNEIMERASLKTLSTTKGMDSSWSNTLSGGDSTAYSKMVGYTQSYTQTEQGIQSV

STNNIDNTLNVVARDLAAGDNKDFSNLNTAQQNEYFAKADNYVSDMVKNDPAQLAQYNSQYGAQSIVSPN

NTTMPHAAGMNFKTIDGSERSVLTQSNLNQDQVNQSSKRTSNTTTMPDSQEVKSGATHSQIAQDNKKGSN

AIRETSKNWNPIGKDTPSI

>ABV52474.1 hypothetical protein C8J\_0875 [Campylobacter jejuni subsp. jejuni 81116]

MLSTYLVVSFLIFIVLFFSILSFYMIFLKNRNTEKRETKIINKILFLLCFLLLISISILIGVYLGVLTTV

KSVVIAFIALVFILSLFFIAFSVNCAILDSILSLNKRL

>ABV52473.1 hypothetical protein C8J\_0874 [Campylobacter jejuni subsp. jejuni 81116]

MKDLDYYLNLPYEIIIKKLDEKDGGGYFARYKDFPYIMGDGENEIEALKDLKEAFKGALEVMLEKGDYIK

EPIDNEAKIRINITLPKSLVEAIDTISDNRSKFLADLANSAIKSYKIST

>ABV52472.1 ATP synthase F0 sector C subunit [Campylobacter jejuni subsp. jejuni 81116]

MKKVLFLLLACAAVAFAAETNAPVEQEAINVWIKAFSVLAAGLGLGVAALGGAIGMGNTAAATIAGTARN

PGLGPKLMTTMFIALAMIEAQVIYALVIALIALYANPFIVLQ

>ABV52471.1 putative transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MSSKFSKIGFILAVAGSAVGLGNAWKFPTLVGQSGGSAFILLYIILTLGVGFVIFLAELSIGKISEKDPV

NAYEKLAPSNKKAWSYVGFTMVGAILIVSFYTLVIGWIVKYVFLSITGNLPMDLEVSKAQFGFFTSEDFL

SQFICFTLVFLCVFYIVSKGVKNGIEKLNVWMMPSLFILLILMLVYAISKDGFMMAVKFLFVPDFSKINT

SNVLEALGLAFFSLSLGVGTIITYSASLPDKTNFITSTLNIIFINLLVGLLMGLVVFTFIFEFGYNPNQQ

GPGLVFISLATLFEKIGVIGCIFGAAFFISLIFAGITSAVSMIEPFAFYLINTFGMSRKKALILIGIVVY

ILGMLCILSSLKSTQFGFFGMSFFDLLDSISSKVIMPLGGILAAIFVGFVMKKEALKILFEPYMRGIFFE

LWYVFLRFISPLAVVIVMIAAFLK

>ABV52470.1 sodium transporter, putative [Campylobacter jejuni subsp. jejuni 81116]

MRTYFSKIGFVLAVAGGAVGLGNAWKFPTLSAENGGFVFVLLYLFFTLTIGFSIFLAEVAMGRLSKSDLA

NAYSNLAIKYGNRWRYGGVFMLGGIFVLSFYLVIMGWVLKYTVVSLYYLPKTLDEAASNFQNLITTNLTS

SVFFFILSFFLTLLIVSKGLIKGIEKLNVVIMPSLFLMLVFMLFYCMGFKQGFANAFSYLFYPDFSHFKF

SSIAEALGLAFFTLCLGIGCIVTYSSALDKKTNFIKSSVYIVLINLLISFIMGLIVFTFIFEFGADPHTQ

GAGIVFVSLMSLFNQLGALGYIFAFCFFLALFFAGITSAVSMIEPLTFYMINNYQISRVKALFLIGLFVF

VFGICCILSLNLNFFSMFSFFGKDFFTLLDKLTSNFLLPLGAIVCSIFVGFFMNKKQIYKIFSKFISRKI

FLIWLFFIRFISPIAIILVMCYQIFV

>ABV52469.1 oxaloacetate decarboxylase, alpha subunit, putative [Campylobacter jejuni subsp. jejuni 81116]

MAKKFIDVMDTSFRDGFQSVYGARVLMDDFFPAVEAAKEAGITHFEFGGGARFQSLYFYLNEDAFAMMDR

FRAIVGKDANLQTLARGVNTVTLDTGSSELIDLHAKLFAKHGTTTIRNFDALNDVNNLKFSGECIVKYGL

KHEITITLMDLPSNCKGAHDVPFYEKILKEILAAEIPFHSICFKDASGTSNPNKIYETIKMARKILPQDT

HIRLHTHETAGVSIACYLAALEAGVDGIDLAAAPVSGGTSQPDILTMMHALKDKDYDLGGFEEEKILKYE

EVLKDCLKEYFLPPEATMVNPLIPFSPMPGGALTANTQMMRDNNILDKFPQVIHAMREVVEKGGFGTSVT

PVSQFYFQQAFNNVMFGPWKKIAEGYGKMVLGYFGKTPVAPDANIIELASKQLNLEPTTELAINIADKDE

SKSIAYTKTLLEKEGIETSEENIFVAAACKEKGIAFLKGEAKVNVRKLASMPKPMSVDENKFTVAVNGNK

YHVEVSYGFDKDVNVKSVKKVEENKNIISSNSTSSVDAENEVLAGISGNVFKIYVNEGEEVKSGQAIMVL

EAMKMEIEVNAPKDGIISELCIKIGDTVNEGEVLAIYKN

>ABV52468.1 ATP; phosphoenolpyruvate carboxykinase [Campylobacter jejuni subsp. jejuni 81116]

MKKFDNLGLDNIKEIFHNLSYDELNAHEKANNEGLSTDNDTFCVDTGIFTGRSPKDKYFVKQDPSSKYIA

WGKINQPITKELFDKLLTKAKQELSGKKIYVQDAFCGASLQSRKAVRFVTEIAWQAHFVKNMFIRPSQEE

LENFKADFIVYNACKCINEDYKQDGLNSEVFVIFNVEENIAVIGGTWYGGEMKKGIFSMMNYWLPLENKL

SMHCSANVGEKDDVALFFGLSGTGKTTLSTDPKRRLIGDDEHGWDDEGVFNFEGGCYAKTINLDPEHEPE

IYGAIKRNALLENVVLRADKSVDYADASKTENTRVSYPIEHIENHEPSLKAGHPKNIIFLSADAFGILPP

VSKLSKEQAMYYFLSGYTAKVAGTERGITEPQATFSACFGEPFMPLHPTVYARLLGEKIEKHEVNVYLVN

TGWSGGSYGVGKRMSIKATRACINAILDGSIAKCEFENFEVFNLAIPKALEGVESTLLNPINTWLDKNAY

TETRDKLAHMFVQNFKRYEDVKEGIEFSKFGPKI

>ABV52467.1 argininosuccinate lyase [Campylobacter jejuni subsp. jejuni 81116]

MKNEMWSGRFSGASDELLKEFNASLNVDKTLFNEDIQGSIAHATMLESCGILKKEELDAIIKGLEQVKSE

IEQGKFVFDIKDEDIHMAIEKRLSEIIGSEIGGRLHTARSRNDQVATDFKLFVKKSHIELLKLLKELIQT

MLEHAKVHKKTIMPSFTHLQHAQPVSFSFYILAYAFMLMRDIKRLQNSLELADFSPLGSCACAGTSYATN

RELSAEILGFKDIMPNAMDGVSDRDFALDLLYDIAVIFTHTSRLCEEMILFSSSEFSFITISDSFSTGSS

IMPQKKNPDVCELIRGKTGRVYGNLISLLTIMKALPLAYNKDMQEDKEGLFDSVKTAKDSLIILNAMLKE

IQINKENMLNACKKGHLLATDLADYLVREKNIPFRKAHFIVGNVVAQAEAQGIDISEIKDLSKIDPVFDE

KAMELLNFEFSLNSKQSEGSSSIASVEKQIQILEGFIQNL

>ABV52466.1 GTP-binding protein YchF [Campylobacter jejuni subsp. jejuni 81116]

MSLSVGIVGLPNVGKSTTFNALTKAQNAQSANYPFCTIEPNKAMVEVPDLRLNELAKIVKPEKIMHSLIE

FVDIAGLVKGASKGEGLGNKFLSNIRETEVILHIVRCFDEENITHVEGGVDPLRDVEIINTELILADIEQ

LSKKIEKLTKEAKANQKGAKESLELANSLLDHLNKGLAASSYPEKESEIYQALIKELRLLSAKEVIYGAN

VNENGISEDNDYVKALKEYAKKNDHEVIKLCAKIEEELVGLSDEESHEFLSSLGVNESGLDQIIRTAFAK

LGLISYFTAGVVEVRSWTIKKGWKAPKAASVIHNDFEKGFIKAEVISYEDYIQYKGENGAKEAGKLRLEG

KDYIVLDGDVMHFRFNV

>ABV52465.1 aminopeptidase [Campylobacter jejuni subsp. jejuni 81116]

MKFELNDKKLDAIKADFELVFIQDKNLKIFNKEKDFFKLNNYKGEGALLDLNNKKLYLELKSLAYEDIRL

SLCTAYKTLEKLNIKSVKLPSIIGDCVVRSFASLVEGVLFGAYKFDKYKSEKKTRTLERFIISSEELNGK

KFNKDEAKIGLERGEILANATNFTKNIVNEIPEIYTPLKMAEDAQNLAKENKNITCKIYDEKFLAKEKMN

AFLAVNRASVHPPRLIHLSYKATNAKKRVVFVGKGLTYDSGGLSLKPADFMLTMKADKSGAAAAMGIIKA

VAELALDLEVHCILGATENMIGGNAYKPDDVLISREGVSIEVRNTDAEGRLVLADCLSFAQDLKPDLLID

MATLTGACVVGLGEFTSAIMGNNEELQNDFYLSSKKSGEYTTILHFNPHLRELIKSNIADVSNTASSRYG

GAITAGLFLDKFIRKEYKDKWLHLDIAGPAYTEKSWGYSSFGAGGAGVRMCVNYLIQILRKAK

>ABV52464.1 putative integral membrane protein (DedA family) [Campylobacter jejuni subsp. jejuni 81116]

MEEFLKNLLYQYKDLAYIIIFLWCILEGELALILAGIFAHQGHVNLGFVIFIAGLGGFVGDQIYFYIGRY

NKRYIQKKLKTQRRKFAVAHLLLQRFGWPIIFIQRYMYGFRTIIPMSIGITRYSAKKFAIINLFSAWVWA

SITILLAWYFGEQIWKMVTWAEEHWYYAAIIIIAFLSLLLFGFKQMEKAILKDKRKKS

>ABV52463.1 adenine phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MIKLTQEEQKYLLDSIRIIPDFPKKGIIFRDITTLLNNKEALNFLLKHLKERYKDYNLDFIAGTESRGFI

FASMICAKLNLPFVPIRKPGKLPFETFSCEYDLEYGSDKVELHKDAFKNIQNARVLLVDDLIATGGTAIA

SYELIQKAGAKCVEACFLMNLKDLNGANKLEKLTSVYSVLEI

>ABV52462.1 hypothetical protein C8J\_0863 [Campylobacter jejuni subsp. jejuni 81116]

MFTNWLVLTILICATIYLIVMLFYYKTLLNKEKTSKDFIKNNLDDTEIVIRKLQIQLQRSLGNIDILTEE

LNKIKADLTSLRTRNSQYRLENDKLRQRIKELEAKIEALL

>ABV52461.1 putative ribose 5-phosphate isomerase [Campylobacter jejuni subsp. jejuni 81116]

MLREKIYIASDHAGFELKEKICVFLKEKNIIFNDLGTNTCASCDYPDYAHLLAEKIDERSFGILICGSGI

GISIAANRHKNIRCALCHESLSAELARRHNDANVLALGGRLIGVELAIDIIEKFIQTPFEEGRHMQRIQK

IEVKI

>ABV52460.1 putative MCP protein-glutamate methylesterase [Campylobacter jejuni subsp. jejuni 81116]

MKLILIGSSTGGPNQLKFLLKDIDIKNTCVVIAQHMSASFIPSFVGQFNKEAFSEVCLLNDKEILSNKIY

ICPKNTILSGNLNIVAAWQDVASSFKPSVDLLFHSAVSLVKTNKILAIILTGMGDDGAKGLFELYKTGVR

CLCENEADSVVYGMPKRAKDMNPHLKPMSLKEIKKEIVNFIDQD

>ABV52459.1 putative MCP protein methyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MEKKITPSELELNEFIKIINEMSGIDLTDKKNILALKLNKFLEGTNTKNFSEFLGKLKSNRQLKQETLDF

VTIGETYFLRELAQLKEIIYYAKSLEKRVNILSAPCSSGEEVYSLALLAAQNFIKDMYILGIDINSSVIE

KAKLGKYQGRTLQRLSESEKRRFFLESEDKFYTINKNELCTCKFELCNVFEEKFSRLGKFDIIASRNMII

YFDHESKLKLMERFHRILNDKGRLYVGNADLIPETIYFKKIFSPRGVYYEKV

>ABV52458.1 putative polar amino acid transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MIELKNVNKYYGTHHVLKNINLSVKEGEKLVIIGPSGSGKSTTIRCMNGLEEVSSGEVVVNNLVLNHKNK

IEICRKYCAMVFQHFNLYPHMTVLQNLTLAPMKLQKKSKKEAEETAFKYLKVVGLVDKANVYPATLSGGQ

QQRVAIARSLCTKKPYILFDEPTSALDPETIQEVLDVMKEISHQSNTTMVVVTHEMGFAKEVADRIIFME

DGAIVEENIPSEFFSNPKTERARLFLGKILKN

>ABV52457.1 amino acid ABC transporter, periplasmic amino acid-binding protein PEB1 [Campylobacter jejuni subsp. jejuni 81116]

MVFRKSLLKLAVFALGACVAFSNANAAEGKLESIKSKGQLIVGVKNDVPHYALLDQATGEIKGFEVDVAK

LLAKSILGDDKKIKLVAVNAKTRGPLLDNGSVDAVIATFTITPERKRIYNFSEPYYQDAIGLLVLKEKNY

KSLADMKGANIGVAQAATTKKAIGEAAKKIGIDVKFSEFPDYPSIKAALDAKRVDAFSVDKSILLGYVDD

KSEILPDSFEPQSYGIVTKKDDPAFAKYVDDFVKEHKNEIDALAKKWGL

>ABV52456.1 putative polar amino acid transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MNESVGFVEHLRQILTSWGLYDENSISPFAVWKFLDALDNKDAFINGFIYTLEVSILALLIATIFGTIGG

VMATSRFKIIRAYTRIYVELFQNVPLVIQIFFLFYALPVLGIRLDIFTIGVLGVGAYHGAYVSEVVRSGI

LAVPRGQFEASASQGFTYIQQMRYIIVPQTIRIILPPMTNQMVNLIKNTSVLLIVGGAELMHSADSYAAD

YGNYAPAYIFAAVLYFIICYPLAYFAKAYENKLKKAHLTR

>ABV52455.1 putative polar amino acid transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MENVFNAQNIEFLMQGLFLTLKIALATCIISIVFGTFLAITKNYGDRLSKFLAACYIDIFRNTPLLLWML

AACFVLPVFFGQFPQAFWGTIGFSLYTSSVMAEIIRGGLNSIPKGQFEAAYSQGFGKFFTLFYIILPQTF

RKIIPALLSQIVTTVKDTAYLAGLGIAELTYNSKTILAKLTSFEEILAMIGVVAGIYFIICFSLSMLVRY

YAKKTAYIS

>ABV52454.1 ribose-phosphate pyrophosphokinase [Campylobacter jejuni subsp. jejuni 81116]

MRGYKIFSGSANVEFARQVSKYLSLPLSDAGVKRFSDGEISVQIDESVRGKDVFIIQSTCAPTNDNLMEL

LILTDALRRSSANSITAIIPYFGYARQDRKANPRVPITAKLVANLIQAAGIDRVATIDLHAGQIQGFFDI

PVDNLYGSIVFNDYIKAKHFKNAIIGSPDIGGVARARSVAKHLGLDIVIVDKRREKANESEVMNIIGDVK

DKEVILVDDIIDTAGTIVKAAEALKEKGAKSVMACCTHAVLSGKAYERIASGALDELVVTDTIPLKEQLP

NIKVLSVTPVFAEVIRRVYHNESVNSLFI

>ABV52453.1 carbon starvation protein A [Campylobacter jejuni subsp. jejuni 81116]

MTQLSTKILWLFVATLGAICFGYLALQNGESVSAIYLVVAAVCIYMIGYRFYGRFVAYKVLELDKNRATP

ALVENDGRDFVPTNKAVLFGHHFAAIAGAGPLVGPILAAQMGYLPSMLWILVGGVLAGAVHDFVVLFIST

RRKGRSLGEMIKDEMGKFTGGVAMVAIFGIMLIIIAILAMVVVKALAESPWGLFTIAMTIPIAIFMGIYM

RFIRPGRVGEASIIGFVLLILAIHYGSVIAADPYWAKIFTLEAPTLAIVMMAYGFIASVLPVWFLLAPRD

YLSTFLKIGVIVVMAVAIVLVAPDLQMPKANTQYFDGTGPVFAGGVFPFLFITIACGAISGFHALISSGT

TPKMLENETHALAVGYGSMLAESAVAIMALICACILHPGLYFAINSSSALIGTDVVNVAQTISSWGFSIT

PEEITTLTTNIGEHTILSRTGGAPTFAIGVALILHELFGGVDLMAFWYHFAILFEALFILTAVDAGTRAC

RFMVQDILGNVYKPLGDIHNYPAGLLATALSVAGWGYFLYQGAIDPKGGIYTLWPLFGVSNQMLAGMALL

LATTILVKMGKARYTWVTLVPAVFVLVATLYGGIQKIMPYEEGNKVANAVSHVAAVSIQVKKLKI

>ABV52452.1 hypothetical protein C8J\_0853 [Campylobacter jejuni subsp. jejuni 81116]

MIATLLVIISCIGICLGKIKIPLKETKYIKIDEFQKI

>ABV52451.1 hypothetical protein C8J\_0852 [Campylobacter jejuni subsp. jejuni 81116]

MMNFKKFKYYYEKAERFFHPLVGLSSYDKYLEHMKQKHPGKIPKTRGEFFKECLDKKYNSGGLNKC

>ABV52450.1 thioesterase family protein [Campylobacter jejuni subsp. jejuni 81116]

MRDMGEPKLKIVAMPSDTNPAGNIFGGWILSQIDLAGAIAARELSPERVVTISMDKVVFKEPVFIGDIIS

CYSKVVNVGNTSISVEVEVTAQRVDSQGCTSCINVTSALVTYVSVTRDGKKKPISEELKRIHGFLNA

>ABV52449.1 CiaB protein [Campylobacter jejuni subsp. jejuni 81116]

MNNFKEIAKLVRKYKERNNALYEFLDKEDVGEYFRSLISLSELKQDKTTMLAILRRLIDLKEENLVQEWK

KNNFKEDKIIELKHKFYEEVRKFYEKEHQNLINEIKEKKLLNNFYQSLIQGVHNIGLIMNIFEISWTKEI

IEKNNKILSTQFPNLDDAMEFLRKNHLYQKTPEGEICERSYGVLVRIGNLWKFVPYARFFENEILKLEFA

FENMIDQLKIFASSEEEKAYIEYFEKLKLAFCEKDEDRVIKAWQEAEFAWMKVKSPLQVGHPLEYYEDNY

THAVALEWDIRIEDENDFDVLKFGSEIKESFEHVYKNIGLEDCELEKEVLSNIEKTQLYICTPMIFYGAE

LKGLFSAQVVPNDEFVSSKAGKKIFAFINFVYENAKTKPFMKISSEVFDKEFLDFGRNILFYQEKIWKRV

YEVSTIGHEFGHIFFIANDTEKTMNQSGFFKNIEEYKATTGGLINFFYHEQDDLIMPVFHELIKRAIGLI

SWQRVDEVRPYYTEGLIHLSLLFESEVLIFENNNLKINFDLGHYEKFKELTLKNYHELAKHYALRLDAKE

FLSRFCEIKDNIFLPIMPKCKEFVKFYYDLYEKIGNEIDNSGEFERYKKK

>ABV52448.1 DNA-binding protein HU-like protein [Campylobacter jejuni subsp. jejuni 81116]

MTKADFISLVAQTAGLTKKDATTATDAVISTITDVLAKGDSISFIGFGTFSTQERAAREARVPSTGKTIK

VPATRVAKFKVGKNLKEAVAKASGKKKK

>ABV52447.1 cysteine synthase [Campylobacter jejuni subsp. jejuni 81116]

MKVHEKVSELIGNTPIIHLKKFGINVFVKCEFLNPSHSIKDRAAFEMIKDALDSKKINQDTTIVEATSGN

TGISLAMICADLGLKFIAVMPESMSLERRKMITLFGARLELTPVNLGMKGAVDKANEILLNTPNSFMVSQ

FENISNKNAHRKNTALEILRDLDNELDIFVAGFGTGGTISGVGEILKEKLEKVHIVGVEPLNSPLLSKGE

AGSHKIQGIGANFIPAILNKEIIDEVITVSNEDAINTAKELAKSGLMVGISSGANVFAASMLAKKFPDKR

ILTMLNDTAERYLSTDLFA

>ABV52446.1 SCO1/SenC family protein [Campylobacter jejuni subsp. jejuni 81116]

MKKNIILFIVIVAIILGVIFFIKNHQNSYDFILKSDLKEETTLKDFKGDKLIIYFGYTYCPDVCPATLSL

AGKALKQINNPKAHLLFISLDPNRDNNLSNTNEWLRYFYPKADALIAKDEKTLQKITKQYNVQYQKIDLN

DSFMGYSITHSNMLYLIDEKGHFYKEISDLNPQEILRELRIFLNSQ

>ABV52445.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MRKIIFILAFAFVIVILYIIFDFYIIKDSKKITKADFSTPLTCDLNVKDCTYSFNNKEVLISLNPKPLQS

LDVTNLKIVNLGNYNNLGIKIYGLNMYMGEIKPKIHRLNSTDYESKIVLAACVLDTMRFRVEFMDNNKPI

GFYFDFELKK

>ABV52444.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKILLLGALFAVNLWAVNDIEVKNAFVKQTPPHAQNSAIFLTIFNNTDKDIALISAKSDISEVSELHTH

IHKDGKMMMQKIPEIIIKAHSSTELKSGGYHIMLLKLKKPIIKDTKVNLDLKFNNHKIIELKNIDSKEF

>ABV52443.1 hypothetical protein C8J\_0844 [Campylobacter jejuni subsp. jejuni 81116]

MIRNFFIGMSFLGILFLAFYALYDKKKESVFSLNTCQPLTCDLNLQDCVFSFNKKNIEVSAYPKPIKIFN

KTTIKIKNFPHYSNLKIKIYSLNSYIGDIIPKFNIVNGDILINFIGRSITDDSRFRVEFLNNNAPTGFFF

DFDVTMQKNFQTGNTH

>ABV52442.1 hypothetical protein C8J\_0843 [Campylobacter jejuni subsp. jejuni 81116]

MLKRLALLITLSSLMLYASDLVKIYLNQGLDAVGVAIEKELTQKDFWLSEIGDKNISLGYYDDNVAIVLT

NKTDKILRVYSYEDGKIRKDFEQKEIITGLMGDKKIEGDLKTPVGFYELGRKFNPGDPYYGPFAFATTYP

NLLDKVQGKTGGGIWIHGYPLDGSRLDEFKTRGCIALFNNNLEKFAQVVQDKKVFVMTEEKEKIRAKKDQ

IASLLADLFTWKLAWTNSDTNTYLSFYDEQEFKRFDKMKFEQFASMKKSIFSRKEDKKIKFSDINISPYP

NLENETMYRISFYEDYYTKNYQFRGDKILYVKIDSKGKMKILAEQ

>ABV52441.1 alanine racemase [Campylobacter jejuni subsp. jejuni 81116]

MSLIKIDQKAYEYNLRHIAKKIGSFQRLICVFKDNAYGHGAKLLAPLAKNLGVSFVAVKSEEEAQEIEEF

FENILILSHRPHGNENSRFIYALNDISQVKKYKQDIKIHLKIDTGMHRNGICVENLEHAIDLIRSSDLKL

TGMFTHFASADEMDGSFFVQKENFQKAKKIVKKYFSNLLFHSHNSAALFRGKIPEDEYCRVGLVQFGYGD

SNLKRVLSLYAHRLSQRILQKGQSIGYGGIFTAAKDMEVATYDLGYADGLFRYNGKGELVLGNGKVMLGK

MSMDSFSCENSGEEICVFKDADIWADFFHTINYEILVKLNPNIQRVLV

>ABV52440.1 RNA methyltransferase, TrmH family [Campylobacter jejuni subsp. jejuni 81116]

MFNIVLVHPRIPQNTGSIGRMCFNAGFKLHIIKPTVFDISQKAVRRAGLDYWDKLEPIIWENLEEFLNEN

MIYKNRFFFATTKSQKAYFDAEFQKNDFLFFGSESYGLPMELMQLNWENAITIPMKSYGRSLNLATSVGI

ISYEALRQNFSNFVS

>ABV52439.1 putative amino-acid transport protein [Campylobacter jejuni subsp. jejuni 81116]

MNLDIMLDFANKASDIIANKIVPNTDIIMVVLLIVCGLYYSFLTRFVQFRMLSSVFKILTEKNEGHTKEH

ISPFQALMISTASRVGIGNIAGISLALATGGAGALFWMWVMAFFGGASAFAESTLAQVYKSKDDTGGFKG

GPAYYIKKALGSHFFGAFFAFILIITYAYGFNGLQSQTMTSSFKVYYDMFNPNAAVDFASSSWPMIIGIV

LTIFGVWMFFSHHTKIGKISSLIVPFMALAYVLLAVIAVLMNFDKIPSVVHMILQSAFDFKAIFGGFAGS

ALVIGIKRGLFSNEAGMGSAPNAAAAALTSHPAKQGVIQAFSVLIDVVVCTSSGFLVLFSMAYLGLGESK

IDGGMPLVQEAMREYYGSFGIHFITIAIVLFAITSLIGNYYYAQANVKYLTNSKFVMNLFRITAVAMIFI

GSQMNLKLAWNLADLTMAFMATTNIISLLLLGGIVNKVLKDFNTQQKSGIDPKFNASKLGIKNAECWD

>ABV52438.1 glutamine transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MIEVKNLQKKYGELEVLKNINTTISKGDVIAIIGPSGGGKSTFLRCINRLEPADSGEILINKQNILDKEI

DINKIRQKVSMVFQHFNLFANKNVMENLCLTPIKTGILSQEEAIKKAKILLAKVGLADKENIMPHKLSGG

QKQRIAIARSLMMNPDVILFDEPTSALDPEMIGEVLSIMKDVAKEGLTMLVVTHEMGFARNVANRIFFMD

KGKIAVDASPKEVFENPSNERLREFLNKVLNH

>ABV52437.1 putative polar amino acid transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MNQKNIRIFVFFVIIILWGYFSFPIEILKIQDPSGVVSYGYTENAKAYLKSYLITLLLTACAVIIGVIIG

FSLAILRFSKFKTLNFIIDEYIDIIRGTPVILQLMIFAFVIFTFIDNLYAAILALGLNSSAYIAEIVRSG

INSVDKGQMEAARAMGLDYKTSMKEIILPQATKNILPALANEFISLFKETSVVGFISVIDITMQSQSLQA

VLYNPKPIIFTGLVYYVSVKIFSYFAKKLELRMNKND

>ABV52436.1 hypothetical protein C8J\_0837 [Campylobacter jejuni subsp. jejuni 81116]

MEILDFILIVIFVFLMIVLVIGFNRQMMQKNKEREERFKKYKKGEQNE

>ABV52435.1 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis protein [Campylobacter jejuni subsp. jejuni 81116]

MSKKVLIPLAQGFEEAEFIGIADVLKRARELNPDLEVVIASLNSELLVKGANDISIKADCSIEDVDIENL

DAIALAGGFEGMMNLKNSNVILNIIKQLHSKNKIVAAICASPIVLNEAGVLEGEFACYPSCEVGLNGNRV

NKAVVVNKNVITSAGPATAILFGLELAKKLCGDEIYQKLYEGMLLPLTK

>ABV52434.1 HIT-family protein [Campylobacter jejuni subsp. jejuni 81116]

MQEKTIFELIVEGKLPCNKVLESDDFLAFHDIAPKAPIHILIIPKKHFKDFQEFDPELMAKMTSFIQELA

VLLGVDKSGYRLVTNCGKNSGQEVFHLHFHMLGGFELPKEKTKKENPQALF

>ABV52433.1 phenylalanyl-tRNA synthetase alpha chain [Campylobacter jejuni subsp. jejuni 81116]

MQNFIEQIQKCENLNDLEAIRISVLGKKGILTEGFTKLKELEDEAKKEFAAKLNAQKEIFNEAYLAKFKD

LENLALEERMKQDALNFNYFDESITTGALHPVMSTMDKIIEYFIALNFSIEKGPLIEDDFHNFEALNLPK

SHPARDMQDTFYFDDKRLLRTQTSPVQIRTMLAQKPPIRMIAPGAVFRRDFDITHTPMFHQVEGLVVEEG

QKVSFANLKSVLEDFLRYMFGDVKVRFRPSFFPFTEPSAEVDISCVFCKGKGCRVCKHTGWLEVLGCGIV

DPNVYNFVGYENVSGYAFGLGVERFAMLLHQIPDLRSLFEGDLRLLEQFR

>ABV52432.1 phenylalanyl-tRNA synthetase, beta subunit [Campylobacter jejuni subsp. jejuni 81116]

MIITKSWLNDWLELEEISSDKIAKTLNSIGIEVDRVGALKAPDKVVVGYVKEKIKHENSDKLSICQVDIG

SETLQIVCGAANVDAGQFVAVATKGAIMPNGMEIKEAKLRGVDSCGMLCSSLELGFEKINEGIMLLDESI

GKLELGRALNTYEIFNDELIEVELTPNRGDCLSIYGIARDLATALNLNLKEPKPFKESENVLGIGRILRL

AAEKELNGLYNYRAIELKEEIQTNLLLSLRLAQIEGLGKNSIENLLNYATHSTGVLFNAYDLSSFSEKDE

EFTINLSKQVHGETKVSCKDKLLSFSGIFQNNESRCKDDSKIIIIEANYTDPLVIADAKIYHKDQDEKML

YRSFRGSEPKLNLGMDFLLSIFEQIPNLVIYSSSQQILTDKELPIIPISIESIGDIIGQNVDKDEVLKIL

KKLGFELILSGEGLINVKAPLHRPDIKNLSDICEEVVRIIGIDNIASKGLEFIEKNRLNSAYKNYIEFLN

LRKRAVASGYFESLHYVLDNEEELKRLGFDSVKLKLINPITAELNTLRTTLLNHLLNAASLNAKNSKKII

KLFELGAVFNVNNQELNRIAFIHSGLKEEAKISNKAKPESVQFYDFLLDIKNIIGDFKLKSSKYNILSPY

EQADIYLSDIKVGFIGRLHLKIENERDLPKTYICELDLDLIRQDFKIAKPYSKFPAITRDLSVLIPKGFE

YNQIKNCIEELNLEILENFRLVDIYSDENLKEFYSITISFSFRDINKTLEDNQVNECMDKILNTLKNLGL

DLR

>ABV52431.1 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MQTPVNAILENIAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIIKNLGAKIEQKDSCVKIIPP

KEILSPNCILDCGNSGTAMRLMIGFLAGISGFFVLSGDKYLNNRPMRRISKPLTQIGARIYGRNEANLAP

LCIEGQNLKAFNYKSEISSAQVKTAMILSAFRANNVCAFSEISLSRNHSENMLKAMKAPIRVSNDGLSLE

ISPLKKPLKAQNIIIPNDPSSAFYFALAAIILPKSQIILKNILLNPTRIEAYKILQKMGAKLEMTITQND

FETIGEIRVESSKLNGIEVKDNIAWLIDEAPALAIAFALAKGKSSLINAKELRVKESDRIAVMVENLKLC

GVEARELDDGFEIEGGCELKSSKIKSYGDHRIAMSFAILGLLCGIEIDDSDCIKTSFPNFIEILSNLGAR

IDY

>ABV52430.1 lytB-like protein [Campylobacter jejuni subsp. jejuni 81116]

MIIELAKNYGFCFGVKRAIKKAEQIKDAATIGPLIHNNEEISRLQKNFNVKTLENIQALSNEKKAIIRTH

GITKQDLEELRKKDIEIFDATCPFVTKPQQICEQMSKEGYEVVIFGDENHPEVKGVKSYVSTKAYVVLDK

KELQNIKLPNKIAVVSQTTKKPEHFMEIVNFLILKTKEVRVFNTICDATFKNQDAIKELSLKSDVMVVVG

GKNSANTKQLFLIAKTNCEDSYLIETEEELKKEWFLDKKHCGISAGASTPDWIIQKVIAKIENFKIN

>ABV52429.1 30S ribosomal protein S1 [Campylobacter jejuni subsp. jejuni 81116]

MSEVNKKVQGGVDDYLEEEDFGQLLEAFDKSREEATTEGVIVEIKNDEVYVDIGKKSEGILALSEIQDDN

SKLLFNVGDSIKVAVMGSRGGRSLLSHKKALRKEKVIEFIKNYQENQDDIFTVKVVGKNKGGLIVVDEND

VEFFLPKSQYGFKETNNIIGKTFKVKIIKIDKDEQSIIVSRKKTLDDERRKRKELINNVAQQEDLIEGIV

KKITTYGMFVDVGGVDGLVHYSEISYKGPVNPGTLYKEGDKVPVKVIKYDKERKHLSLSIKAALPDPWSE

IKDTLDVGDTIKVIVSNIEPYGAFVDLGNDIEGFLHISEISWDKNIKNPKDYINKGQEIDVEVIEINPNE

RRLRVSLRNLLSRPFDEFMKSYKIADVVEGEITSVTSFGAFVKLGGIEGLLHNEDASWDRNDKCKDKFSQ

GDKIKVKIIKIDEENQKISLSTKELSSSPVQEYAKIHKVGDIVKGAIRDIKDFGVFVELSKNVDALIHKE

DISTSMLENLKIGDDIEAAIVFIDEKKNRIRLSVKNLVRMKEREVLNEINNDDKVTLGDIIKDQLA

>ABV52428.1 hypothetical protein C8J\_0829 [Campylobacter jejuni subsp. jejuni 81116]

MLAVVFTLLWQFKANVNFIPQFAKDTNTQPSIQTQNQDLSWQEELAKWPTRDFTPAAEKFTLYFDADTSE

LKEKNKYYQLIVGKYDIYSMFCLRQTLNSFNVKYFLLKSGDSPEIFLDTGNEKLIDDIIKELKKYKINTE

VKEIWL

>ABV52427.1 D-3-phosphoglycerate dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MKKKIIVCDAILDKGVDILRKAEDIELIEAAKVPKDELMQMLSDVEVAITRSSTDVDINFLNHAKKLKAL

VRAGVGVDNVDIPECSKRGVIVMNVPTANTIAAVELTMTHLLTSARSFVNAHNFLKIERKWEREKWYGIE

LMNKTLGVIGFGNIGSRVAIRAKAFGMKILAYDPYISASKITDLDMEQAKNLDEILEKSDFITIHTPKTK

ETNGMIGKQEIAKMKDGIRLINCARGGLYTEEALYEGLKSGKIAWLGIDVFDKEPATNHPLLDFENISVT

SHLGANTLESQDNIAREACEQALSAARGVAYPNALNLPIKTEDLPPFVAPYIELVSKMAFLAVQIDKNPI

KSIKLEAEGIIGEYANSMLTFAAVGALGGILGEKINYVNAEFVAKEKGVELSCETLPNSGYNNKLSVKII

TENSNISVSGTVFNENEQRIVGLNGFKTDFKPKGKMIIFKNKDIPGVIAKISSVLAAKNINIADFRLGRD

GFGYALAVVLIDEKVQKEVLDELKQLEACVFVQYVEI

>ABV52426.1 putative sensory transduction transcriptional regulator [Campylobacter jejuni subsp. jejuni 81116]

MSNMLKFKILIIEDDIDLNELLVLKLKSSGYEVISLVDFFGVEDLLDNEQIDLLIVDRNLPSGDSLEKIQ

DLREQGYKEAVIFLTAKALHQDLLEGFESGCDDYVCKPFDFNELLLRIKAILKRHKKEEEKLSFGDFILD

LANYEFFYKNQKLEISNLDYELLKCFFENPNTLLTRQFLSESVWKDDTTSDKTINIALTRLRNKFPKLKD

HIISVRGVGYKLC

>ABV52425.1 putative sensory trasnduction histidine kinase [Campylobacter jejuni subsp. jejuni 81116]

MLKTKNIFIVFFVVLALIFGFIFYTFTNSYLNFLLIKQYEQKIKSLDDVLKFSLLEHLNDANIKDFAKDT

RADFIILNNDMKISSVKNPDFFSNLKEGEILNFNSKKILTKSFIYKGYKYIIIVYPRFLDLELFWTKIAI

GFGVCLLFVFILMLLLGRRIEKNFNKILDFLDSIGDHKVVILEKGMFKEFNLLNEKLLKTKDKILKNTQK

NKKQSDKITLKNTQLASVISAISHELKNPLSVIDLSLEMLKDEKLEDKKLKKELLEKISRQSIKLNALTH

KLNFVFNLNSEALQMQEFDLFFLCEKITKNPGFERVVLQGKSTKVKADEFLIEQVIINLLSNALKYSQKE

VILTARDQKIIVQDFGKGIEEDKIKLITKKFYKIDVKSDNSFGLGLFLVKKILNIHKSYLEISSTLGYGS

SFSFKLSQG

>ABV52424.1 ABC transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MALIDLIEASKKFGDKIVLNEANFSANEGEKIAIIGKNGEGKSTFLKTLLGTLPLDSGRVIRQNGKSIAM

LSQSVDFNANLSVKEAIKQELAEIYNALEEYEILHKKLEEDPSNKDYLKKIDTLMTLIDSKDAWNIESKI

IRVLKEFSLLEYENRIISTLSGGEIRRVGLCILLLKNPDILLLDEPTNHLDVYMTSFLEELLKNSKMCVI

FISHDRYFIDAIAHKCVEVEQGKLSIFKGGYANYLEKKTQILQSLAKSHETLLKQLKSEEEWLRRGVKAR

LKRNEGRKERIFKMREEAKKNPGAIKRLKLEISRAALNFNGEKTINRKKMLFELKNISKNINNKNLFKDF

STRILQGERIAIVGRNGCGKSTLLKILLGQIKQDCGEIKRGELKIGYFDQARSLVNSDKSLLEIFCPNGG

DRVEVRGKNMHVYGYLKNFLFPKEFLDKSVALLSGGEKNRVALALLFTKEYDVLILDEPTNDLDIATINI

LEEYLLSFEGAILLVSHDRYFVDKIATKLYAFEGDGYINILHTLYTEYLENEKEIEELDNFALELQTQEQ

NNNQKEKSSKKLSYKENEILKNHPEKIDFLEQKIAKLNQDLSDPNVYQEIGINKLYQELEVMQKELEILE

NEYFLVLEKSENL

>ABV52423.1 putative flagellin [Campylobacter jejuni subsp. jejuni 81116]

MRITNKLNFTNSVNNSMGGQSALYQISQQLASGLKIQNSYEDASTYIDNTRLEYEIKTLEQVKESTSRAQ

EMTQNSMKALQDMVKLLEDFKVKVTQAASDSNSQTSREAIAKELERIKESIVQLANTSVNGQYLFAGSQV

ANKPFDSNGNYYGDKNNINVVTGAGTESPYNIPGWDLFFKADGDYKKQISTNVSFTDNRWDLNKDPDKTK

YLTGDSKWQQLIGQGYVKDNGLDPDKDFEYDDKLDFPPTTLYVQGTKPDGTSFKSAVLVKPEDTLEDVME

NIGALYGNTPNNKVVEVSMNDSGQIQITDLKQGNNKLDFHAVAFTPQADDRAELTGIIDAAKQEGISMDE

VTNRVMQAATAAPSNGDITKLNSPVTVTINNQQFTIDLKQTDFIKSKMTDTDGNATNGADYDNVYFEKNG

NTVYGNVSQVIKGSNAYATDSTKLSEVMAGDSLNGTTLNLKVNSKGGNSYDVTINLQTSTVSYPDPNNPG

QTISFPITHTDPATGNSGVVTGSNDITYGQINDIIGMFAADKIPTQSITATNGKVDANGYNNLQQLMKDS

QATVDVSMDYKGRISVTDKLSSGTNIEISLSDSQSGHFPQPPFSTTSSVTNGPNFSFSANNSLVIDEPNV

DIIKDLDSMIDAVLKGNMRADSESEDPRNTGMQGALERLDHLADHISKLNTTMGAYHNTIEDVNTRSTFL

SVNVQSIKSNVIDVDYGEAMMNLMQVQLAYQASLKASTTISQLSLLNYM

>ABV52422.1 putative cell division protein [Campylobacter jejuni subsp. jejuni 81116]

MLAPSMGEWVYKANLFLFGEFGYYYPFSLLILNYLYYKKNYKIENFKRRELFGFSLAFFSTLLLFSVFYR

GFGYILEIVYGFFSIILGHTGSGIFALLLLLFSLILLFPKFAKEILKIELDFTYLLKVEQAFKSLLMRVF

GGENEKEDIGKSEPMVPKLNILQDNIYENSQINEKEKTNNLEQIIKDSNINASKNSITTAKENFEKLKNQ

ILDETIEIDKQSLKESRSFVYEHSQQVRNFAQKASKMSISLDEDFNFISEEEVDMIPERFLKPKKLEDIK

QIDTNKNLDEPSYKRKNIEIPVSKQEVKPKIFTKELELRENLIKKEKLEQEYKAYQNEILENKVKQEIKK

LEEYDAINSSDIIEGNKYSFNSPKTIKTETEESNKINENKNPDKTDNIFEFAPIVEELNHPYIEPTPIKN

INEIVIEEKNTLDFIQNTETKIDDKKTNDQEIKLQKAVLAKEIAINQALLREIEQGEVEKPKDFTLPPLD

FLANPKEHRQEINESEIDKKIYNLLEKLRRFKIGGDVISTYVGPVVTTFEFRPSADVKVSRILNLQDDLT

MALMAKSIRIQAPIPGKDVVGIEVPNDEIQTIYLREILQSEVFKNAKSPLTIALGKDIVGNAFVTDLKKL

PHLLIAGTTGSGKSVGINSMLLSLLYRNSPKTLRLMMIDPKMLEFSIYNDIPHLLTPVITDPKKAVNALS

NMVAEMERRYRLMADAKTKNIENYNEKMKELGEEELPFIVVIIDELADLMMTAGKDVEFYIGRLAQMARA

SGIHLIVATQRPSVDVVTGLIKANLPSRISYKVGQKIDSKVILDAMGAESLLGRGDCLFTPPGTSSIVRL

HAPFASEFEIEKIVDFLKDQQSVEYDESFLKDQQSAGVTTNESFDGEVDELYEEAKRVILEDGKTSISYL

QRRLKIGYNRSANIIEQLTQNGVLSEPDAKGQREIL

>ABV52421.1 30S ribosomal protein S15 [Campylobacter jejuni subsp. jejuni 81116]

MALDSAKKAEIVAKFAKKPGDTGSTEVQVALLTARIAELTEHLKIYKKDFSSRLGLLKLVGQRKRLLSYL

KRKDYNSYSKLITELNLRDK

>ABV52420.1 hypothetical protein C8J\_0821 [Campylobacter jejuni subsp. jejuni 81116]

MLFTKASEYALLSLIYISQKETPQDVDSLALELDIPKSFLAKILQTLAKDGLLKSFKGAKGGFVLIKEPS

QYTIKEIVNSAEKKDISVFECSGGTCPNNKEENCTLMPMLVNLQNKVDEFLDSITLEDIMKNNGKK

>ABV52419.1 flagellar biosynthesis protein FlhA [Campylobacter jejuni subsp. jejuni 81116]

MAKNKIVDLVFPFLGPLIAPVLKAKSLTIVGFLVCILAIIIVPLPSPILDFFLALSIALSVLIILISIYI

PKPTDLTTFPTLILIITLFRLSLNIATTRMILSEGQNGPEAVSEIIAAFGEFVVGGNMVIGVIVFCILVL

INFMVVTKGSTRVSEVQARFTLDAMPGKQMAIDADLNAGLIDEQTARARRQEVIAEANFYGAMDGSSKFI

KGDAVAGIIITIINIIGGFLIGSFQHDMALSDAASTYTILTIGDGLVSQIPGLITSTATAIIITRASKDE

ENFAEGTLTQLLSEYRTLLIVGFVLFIFALVPGLPTLSLGFMALVFLSLGYLTKQVKEGKIDITTVKKSK

PSAAAASQSGAGGTTAAPAKKSEEEILKEEEHKINDILKVEILELELGYGLIKLAENELTERIRSMRRSI

AESLGFLMPKIRIRDNLRLKPNEYSFKLKGVSIASAEIYPDKYLAMDSGFITEEIEGIATKEPAFNSDAL

WIDANLKDEATLNGYIVIDPASVISTHMSELIKAHASELLTRQEVQNLLDKIKNDYPIIVEGALGVAPVS

LIQKILKDLLKHHIPIKDMLTILESVSDIAEVSKSFDMIIEHVRASLARMITNMYLDDKGNLDIFILDSA

SSAVLMENVQFRDGSYHLPLSVAQTGTLVDTLRAEVAAVANGRIKPFILCVEPQLRKFIADICYNFSINI

VVLSFAEIAENTNFNTEGIIRIEL

>ABV52418.1 hypothetical protein C8J\_0819 [Campylobacter jejuni subsp. jejuni 81116]

MKIYHLSHTDLDGYACQFIVNFYFKNVRFYNSNYGKEINENFNSIIGDIEKDENFGKAIILITDLNLNLN

QCEEFEKICKEKNIKIFLLDHHQSGEECAQKYSWYLLDSKRCATKIVYDFFSKICTPVLELSKFVDVVNA

VDIWLSEDENFELGKVFLGLIANAKEINRVMFKESQIDYMFFLLDKAWKFIGKENANILLDNATHFIKKD

YFARKNDDTLSNLISYFVVEKLSELKENFSIEYEGHKGILTSNIGNTSVIGNDFLVKNPDYDFFIDVSSR

KTLSFRANGKIDVSLMAKNLVGGGGHKNASGGLFATFKDGANYNYIKAQIIDLIKSKELKKENNESKQ

>ABV52417.1 hypothetical protein C8J\_0818 [Campylobacter jejuni subsp. jejuni 81116]

MNQNNNKTLKNELEDLQYELSIVLEAMLLYAGVKREKLENAIEAYIDNIDNVLENSNKEGVDEILEVVEF

LKNKYKDFFQ

>ABV52416.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKCILFFFSLYSLSFANIYEKLNDFAYEKKPNKDFKIQEVKLVQFSQENKDCLELLIEAGQVRILNSYN

SCQKLSKDESFQKFLNEDFLKLYKNNGYLINENLQNLKNTMQDIMIYYKLRYSFSKDVKDMSKNKNLDIL

NIDEKDGGTLLYKINNQACVGIELTRHDSRMAMKIYGIENLDKECKLFIQSPSFKDLSYTKKDFKWYYLE

>ABV52415.1 hypothetical protein C8J\_0816 [Campylobacter jejuni subsp. jejuni 81116]

MKNLSIQEKKDLDNCVFQNLGRQDTFTLSAIFKNFYLKIKAFIYSK

>ABV52414.1 hypothetical protein C8J\_0815 [Campylobacter jejuni subsp. jejuni 81116]

MNKFSIVLTLLLCGSCALALDPNLEKTKSATGIDLPTAKWNLPKALNEDGTIDETKMPKNSEYSKMVILG

NKILNETSKYVGPQAKDPKKRFAGNNLSCSSCHANGGSVQNQSGFVGIWARFPQYNARGDKVITLADRIN

GCFERSMNGKRMPSDTPEMKAMLTYMQWLSQGVPVGAKIEGQGLKKIDFISRAADPKKGKAIYMDKCAVC

HQENGLGLKNEDSAGAYYLYPPLWGDDSYNTGAGMYRLIKAASYIKENMPQGAPDLSLEDAYDVAAYMNS

QARPIKANRDKDFPDRKVKPLDMDVGPYDDSFSTTQHRYGPYTNMIKK

>ABV52413.1 thiol:disulfide interchange protein DsbA, putative [Campylobacter jejuni subsp. jejuni 81116]

MRKFFCKFVLTLVFCSSFALANNSFITLNPSLPNSENSVIEAFSYKCIHCYNHHKFGTLEKLREAFPNLH

FKLYPVSLMNGEFSKEMNELFAFAQYKDEQNGKDASYSDSLSHKLADVYFVSYFLNKQRNFSNLDEFYDI

GLKAMNVNKNEVLNFLNTPKAKEILSEFQRANDIAKTYGTPAFVVNGKYQINPSAINSMQDLEDLVKKLS

NMK

>ABV52412.1 arylsulfate sulfotransferase [Campylobacter jejuni subsp. jejuni 81116]

MRLSKTLCMALLAGSTLLAPNALMAMGGPSGAKIDWQIQGQIGAIKMNPYGLSPLTAIIMDNGYVLSDIK

VTIVPKPNGQTISYNVNSKMAKTYGGIPIFGLYPSYLNTVKVSYTKTANGKSQKVIDEIYKITTPGVSIE

PSGSTDQRGTPFENVKVLKMDPKFSDRLYLVNNAPGKQSGKGSQSVWNNPVGGAMEWDENSNVFIIDTKG

EIRWYFDNDKLMNWDNIYNRGIMMGFHQNKDGALTWGFGQRYVKYDILGREIFNRKLPAAYIDFSHAMDN

MQNGHYLLRVASANTLRPDGKHVRTVRDTIVEVDENGNVVDDWRLYEILDPYRSTIIKALDQGAVCLNID

ASKAGKTLSDEELAKMDESDKFGDIAGTGIGRNWAHVNSVDYDPSDDSIIISSRHQSAVVKIGRDKKIKW

ILGAHKGWNKEFQKYLLQPVDKNGKKIVCDDDYSKCPGYENDNGGFDFTWTQHTGWRIDSKSNKRYIYIS

VFDNGDARGAEQPAFASQKYSRAVIYKIDQQNKTVEQIWEYGKNRGNEWFSPVTSLTQYEPDKDSIMVYS

ATAGMAFDLSKGVSLGEPKPEIDEFNWGAKEPSVQIQFSGSGTGYQAMPFSVDQAFNLKK

>ABV52411.1 disulfide bond formation protein B [Campylobacter jejuni subsp. jejuni 81116]

MKDNCRKFSLSKWQDTRKPWLILIIVTIGLTCIAHFLFQEYLFMEPCEQCVYIRFDMLVMAIGGMIALIN

PTNNIIKIFSYSLAFYGIWLGLEHCLTLNHIHEVVHSENPFAGVDGCREIPIYPFNLPLHEWAPSWFLPT

GECGMDTPVVPENAYNHLNAFQKFFIGTPPDFENGLYSNGWYLIPSLKFMNMAICCLIAFLCCFIVLFAM

FIAYVLDKNKLNAKIFALVIVILVLVLKFIGEPKNPNQNIASLNHLNQVV

>ABV52410.1 thiol:disulfide interchange protein DsbA [Campylobacter jejuni subsp. jejuni 81116]

MKFPVKLARSIVVCAFLAGISASALSEGKEYIILKNPIANADNSLIEIFSYRCTHCYDHHKFNTMGKVKE

KLPNLTYKFYPVSSMGDYGRQANEIFAFAAFKDGVNKIDPTDKNSLTHKVAKAYFNAYFKKKQRWENGKN

PEAFYSVGLKAMNVSKADLENFLKTPEAAELLKSYEIANPISQNYGTPAFVVNGKYQIIPSAINSPEALI

EITKELSKQK

>ABV52409.1 site-specific recombinase, phage integrase family [Campylobacter jejuni subsp. jejuni 81116]

MKYPLDCEENFEKSFLFWLAKYVKFKLNSLSNKELKNPQALAEVNFALTKGVKNIDELDALAKKARNAGL

SGVNTYFNPLKKVFEYLNFYKLYSLKQIDEELIVEVLASITGALSDASKKNYRIAVINFFDFLDKQNEED

EKAHIFDINLKNWAGIAGSKGVKLPEFMSEEELKKFLDAIENADFRNNTVRNKLIIKIIIFTGIRVSEAI

NIKMGDISEENDLYIIRIRAKGNKYRVVMIKKELIYDLLKNVSINYMSKDALLFVNKKGTPLTQSYVSRI

VEQLLFRAGIRKQKNGAHMLRHTFATLLYKKQKDLVLVQEALGHASLNTSRIYTHFDNDKLKLAAQVAKE

LSDS

>ABV52408.1 para-aminobenzoate synthase glutamine amidotransferase, component I [Campylobacter jejuni subsp. jejuni 81116]

MTLENYAIFGKYFYHDLKHTLKAFNHKESKKCFKFIEKYKNDFYILMLADYELYRYFQDKNFTSKKAYLS

VFAFKKRKKFQKEDIDEEKFIPEFINFLDQDNYKENFIKVKEAISKGRVYQINLTQNFKFHSKMDSFELF

KLLLSRQDTEFKAFIKDETREILSFSPELFFKTKKRKIFTKPMKGTIKRDKDPIKDEENKTFLQNDTKNL

SENVMICDLLRNDLSKIITKKSLKTKLFEIQSHPTLHQMTSSVQGKLKKNISLYQIFKALFPCGSITGAP

KLESIKFIEELEQRDRGIYCGTIGLIHKNKNKFSVAIRTLEKQDEIYTYSTGSGLVWDSKFKDEFEELKL

KSAILNPCDFHLFETMYFKNSQILFLKEHLLRLINSALKFNFNTHKLFKDFYNILNQKSSYKEYQNFTLF

KLDEKIFHKKHSLFYNFPLPFKNPHKEGILKLILYKDGRYEFQQSALKQNSNDILLLSDDKINSKSDNLY

HKSSLRTFYNQHSYKWQQNLCYDIAFFNEKDELCEGSRTNLILEKNTQFYTPQIQSGMLNGVYRNFLINL

GLIKEKALFKQDLFEAENIYCINSVRGLKKVKLQ

>ABV52407.1 para-aminobenzoate synthase glutamine amidotransferase, component II [Campylobacter jejuni subsp. jejuni 81116]

MKKILFIDNYDSFSYTIIYYLKELGFECKVIKNDAFKKAKELEKFDFTHLIISPGPHSPKESKLSLKAIK

YFKKNKKILGICLGHQCIAEIFGGRVSKMQNPMHGKISKLYFKKDPIFKGIKKEIEICLYHSLHISSMPK

KCKILAHNSENIIMAIKHKKYPIYGLQFHPEAVLTQKGKKILKNFMKL

>ABV52406.1 probable integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MGVFLVLLGGIFWAISGVLAEYLFKNNYSVDWVCFYRLLSTGLILIFLSFKAQKILVFTNLKESLSICMF

GFFGLLLTQFGYFKAIYYTDAGTATMIQYCAPLIIMLYLCFKNKKFPKLIEIFALILIIFALFLLATKGD

IEAVVLNYWGIFWAVIGAFGVAFYSLSAREVILKYGLFWIMGWASLFASFVFLLILQFDKGLIHYAFNLK

AFFSMGGIVFIGTIGAFCLYLKGVEYIGALRASMIASIEPVAAALMSFLFLKTRYSLLDIFAFVLIILSV

ILNAKKTKAS

>ABV52405.1 hypothetical protein C8J\_0806 [Campylobacter jejuni subsp. jejuni 81116]

MQINNSLNSLSQYVKVNSNEENQNSKNQEQNALAQDPAVEVNISKEAKEKSNTSNQNNSQAPAQALNAQN

NTQQDSSSDSEDKLTELTQKLAEIQAKIVELTAKMSKANEDQIKSIESQIATLNAQASTIQAQIQELQSQ

QA

>ABV52404.1 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MTYLEIEGTNHLSGNVTISGAKNAALPLIVSSILAKNEVKINNVPNVADIKTLISLLENLGAKVNFQNNS

ALLNTNTLNQTIAKYDIVRKMRASILTLGPLLARFGHCEVSLPGGCAIGQRPIDLHLLALEKMGANIQIK

QGYVVASGNLKGNEILFDKITVTGSENIIMAAALAKGKTKLLNVAKEPEVVQLCEVLKDAGLEIKGIGTD

ELEIYGTDGELLEFKEFSVIPDRIEAGTYLCAGAITNSKITLDKVNATHLSAVLAKLHQMGFETLIAEDS

ITLLPAKEIKPVEIMTSEYPGFPTDMQAQFMALALKANGTSIIDERLFENRFMHVSELLRMGADIKLNGH

IATIVGGKELNAADVMATDLRASSALILAALAAKGTSKVHRIYHLDRGYENLEEKFKGLGAKITRLEE

>ABV52403.1 molybdopterin biosynthesis MoeA protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MKNIFETLKDLEDQISCLDESELISLEKAKDRILAKDLYARKNLPSFDNAALDGYAFNYTDINEALEIKG

TIFAGDKNFYTVAKNECYKIMTGAKMPKNADTILMLEDEYIEENKLIIKKAPKQYNAYRYKGEELKKGEI

LLQKGTKLNDKHIALLASQGLYKIEVIRKIRIGIFSSGNELKEPWQECDEESIYNTNALSLLTMLQNTSY

LGIIKDNFKSTKEALENTNFDLLITSGGASVGEADFMEKALDELGFTPLFKGLKARPARPTKLYRKGKNF

VLILPGNPMAAYLSCFIFAKKIIALLSGNLDNPLKFHATMGMDLKLKSGRNNLILGNLEKDIFTPFNENK

FGSGMILPLIKSEFLLISEENTSELKKGDEITLLKI

>ABV52402.1 signal peptidase I [Campylobacter jejuni subsp. jejuni 81116]

MEILKKLYKFSQSWTGTVVIVLLVIFFFIQAFVIPSGSMKNTLLVGDFLFVKKFSYGIPTPHIPWLEIPV

LPDFNKDGHLIKAQGPQRGDIVVFRNPRNEKEHFVKRCVGTGGDRIVYANKTLYVRMHEGDEFMKEHYPN

DLVTLGGQIYVKEPYKQKGIHYDPKKDIESDILRFLSIGDFAMSPTYIKELGNHIGFSGGNAYVFDVPEN

EYFMMGDNRDYSYDSRFWGSVPYRLIVGKPWFVYFSWDKDKNVRWERIGRFVDTLENDEQYIHDHDDEDK

LS

>ABV52401.1 methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase [Campylobacter jejuni subsp. jejuni 81116]

MTLLDGKALSAKIKEELKEKNQFLKSKGIESCLAVILVGDNPASQTYVKSKAKACEECGIKSLVYHLNEN

TTQNELLALINTLNHDDSVHGILVQLPLPDHICKDLILESIISSKDVDGFHPINVGYLNLGLESGFLPCT

PLGVMKLLKAYEIDLEGKDAVIIGASNIVGRPMATMLLNAGATVSVCHIKTKDLSLYTRQADLIIVAAGC

VNLLRSDMVKEGVIVVDVGINRLESGKIVGDVDFEEVSKKSSYITPVPGGVGPMTIAMLLENTVKSAKNR

LN

>ABV52400.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKIVLMFFLFSISLFGADFITLKEYSKMLYENPRGISCKECHGADGSEQILGYYMKNGIKTAYKVPSIQN

LSFENFKNSLNQSKDAKSIMPNYSLTNDEIVTLYNYIKQFSKEEK

>ABV52399.1 glutamate-1-semialdehyde aminotransferase [Campylobacter jejuni subsp. jejuni 81116]

MTNKKAFKEACKFIAGGVNSPVRAFANVQSEPKFISHGKGAYIFDIDGNSYIDYVQSWGPLLFGHCDKDI

QKACQKALHKGSSFGAPTLLETELAKLVLSDFPHLEKIRFVSSGTEATMSAIRLARGFTKKDKILKFEGC

YHGHSDSLLVSAGSGAATFNSPSSLGVLEDVAKHTLVAKYNDINSVKELFEKNKDIACVIIEPIAGNMGL

VPAKQDFLEELAKICKNNQTLLIFDEVMSGYRASYLGSYGINHIQADIITFGKVIGGGLPAAAFASRAEI

MDILSPLGGVYQAGTLSGNPLAMAAGIASLTKAKKKTKLYDKLGKLAKKLTQGMKKLADEKGLPLQACHV

GSMFGYFFTKDPVSNYQDALKSDLALFSKFHKNMLENGIYLAPSQFETGFICSKMDDKIIDTTLEAVRES

FKRI

>ABV52398.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MSNILKEEKNHLENSNSKRQKIIRKTLEAADGLSLGISMVVAVFIGVGIGYLLKKFTPYPWLFWLGVFWG

ISAAILNVYKAYKVQVKSYEEFKERDELIKEKIQKEKNK

>ABV52397.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MEHKKALFCIFAIIHLFFWIIFSSLNHFKLDTFLSYEIAFFSVLLIIFASYLNYKKVIIKKSKNYEKNFN

FISSLFIKKKQNLSKIIHFKVLKDDLKPNVKEKIHFFAMFFTLFKLMAYVILVAGFLFLHRQDKLDIFAY

ICGISSLLVCVFIFILYIKKYESKKNY

>ABV52396.1 major facilitator family protein [Campylobacter jejuni subsp. jejuni 81116]

MSPKKIIKSMTALFAGMAFLFAGNALIVSSIGVILKENGESSLAVGVVSSCFFVGALVGTISAHKIISRI

GHIRSFGLFGAIFGISAMLHTVSENLIFWAVLRFFIGICYYGLLMVIESWLNEKSKNAIRSRILGFYEIV

FYLAFGIGVLIIALNLSKHSVFILSATLILLSSLPLNLIKIKEPVLPASSPISIPKIFDIAPLAIVTSFI

AGMLINGFFSMASLFILLQGFDTKAVSYFIFCGVLGGFIAQTIIGTISDKLGRKFAIITCASIGFITMLI

FIFFKLHLYMQYFLGITLGIGIFCLYALALARANDVLVSKNKGVELGRGVLFCYSLGSLFGPLILGFLMQ

YFEIKGFIWFYIISLAFLILFAINKPNILNKKFKKKPGNMVIFDD

>ABV52395.1 hypothetical protein C8J\_0796 [Campylobacter jejuni subsp. jejuni 81116]

MINTQLASQIVNTQKNDLKVDNSASKDKTNLKDNPKEALAQALKQNLGLSKDASSEEILAKFVQNETGTK

LKELVNKLLDQINAQKNPDSPVLKQGKNLNLAPNFANELKTLSTELAKSDTFTQVLDRLNQILKPASEIK

NNNLAPLFKNSGVFLEAKLKDALNEELLPKSFHSLLSTIKGLSSEKLSVQIAQLANTNLSPKDTLKELKN

IINSSKNENKQILNQSSFKALLNLSSKLENFKNYISKNPSHAQEKITPIANKILKELNSIKNDFFKALNK

PENLMIKDPNILKQTATAFEKLENTLKNILGNQASKIQDKENILENLLSNKENMKEEKLNHNTKNQDEEK

HIKASKEETLTDDTKTDIKQDSKNEENSHAKETDIKEDENLDSDIKTHEEDTQDTKNDIQNNETENKPDN

DIKNSTPNQEKIKDGKQEKSKENIKENPKFYETKTENKTSINTNTNTSNPNTNNTQNLNNSQNIQSNNNQ

TMQNIFKNQEFIKQNIVKNLAFNVENLDLEQVQDLSKNLNNLSRRLNESLKELEPYTQNAKLNQAELKNL

EHKLNLSTKDLAQIKPKTEQDIAESLHHDVKSTLLQISNLAKNEGNEAVYNQANRLLAQIEINQLMSLAN

DSINTYLPFSWDDLNDSKIMFRRGKKDKFFAQIKLEFAKLGDLEILISLNNEKYIDINIMAENIEFRKTI

YENAHELKRNINKAGLLSANFFVGDIIRSKFDTRNMKNLDLEMGMDKKV

>ABV52394.1 putative flagellar biosynthesis protein [Campylobacter jejuni subsp. jejuni 81116]

MSKIKRSIKKAVALGYQKEKNSAPKVLASGKGESAAKIISLAKEHGVPIKEDEDLIEILSKLDLGDEIPP

NMYKAVAEVFAFIYQMANKTPKN

>ABV52393.1 phosphatidylserine decarboxylase [Campylobacter jejuni subsp. jejuni 81116]

MSFSKESSRLFGFVAGIKFPKMIQKVINENYVKYFNIDMSEFKSPCEYESLNALFTRTLHIPRKLEEGFI

SPSDGKILECGSTFLANEEHFAFSIKGHTYSIEELLKDSFEKDELKNGLDYVNIYLSPKDYHRYHSPCDM

QILSATYTSGALYSVNEKHLERISNLYVKNERVSLKCQNEKGIFWLVFVGAQNVGKMRFNFDTSIQTNAK

ISHNFTRKYENLNFKKGEELGNFELGSTIVLISQKGILNFNLKAGQGIKFGEKIAD

>ABV52392.1 Ser/Thr protein phosphatase family protein [Campylobacter jejuni subsp. jejuni 81116]

MIFGLANVYIYKRLIKKITLFKYFYKIFAFIFIVLFLAQAVFLIFRRDEYLSDTWYEILAMLYAPTYCLF

FMTLAWDFIKLILALMGKRDKKYNLILRLIFEFSLIVLSVFLIYISINNALKTPEVKSVDVEIPNLKQDL

KIAMLTDIHLGKNLHENFLDKLITKVNLQSPDMVVIVGDLIDTNPKDLKNYISKLNDFNSTYGTFYALGN

HEYYHGINEVLDLLRKHANMKILVNQNLDLGFINIAGLGDLAGLNKGLYAPDLARIKVDLNTSKASILLT

HQPKTALLYDLSDFDLVLSGHTHGGQIFPFMFLVKLQQGFVHGLYNLGEKTKLYVSSGAGFWGPSLRVFA

PSEIVILNLKGKK

>ABV52391.1 glutamyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MYRFAPSPTGDMHIGNLRAAIFNYICARQKNMDFILRIEDTDKARNIAGKEEEIKEILNLFGISWQHYYI

QSENLKFHRQMALKLISEKKAFACFCTEEELEAKKELAKKQGKAYRYDGTCEKLADIDVLECEKPFVIRL

KKPTHTMKFTDFIKGELSFEPENIDSFVIMRTDKTPTYNFACAVDDMLENVTCIIRGEDHVSNTPKQEHI

RASLGYNKAMTYAHLPIILNEEGVKMSKREAHSSVKWLLESGILPSAIANYLIMLGNKTPCEIFTLEEAI

KWFDISKVSKAPARFDLKKLLQINREHIKMIKDDELNKILDLNKDLAQLAKFYTQEASTIKELKEKMRAI

FNTKDFGEFETECKILKELLKDIELFENYEDFKNELLSKSDLKGKKFFMPLRIILTGNIHGPELGDLYPY

IKNFIHELARI

>ABV52390.1 YGGT family protein [Campylobacter jejuni subsp. jejuni 81116]

MVIDSFIISIFQVLQIVINIYTWIIIIAALLSWVNPDPYNPIVQILYKLSYPAYTLVRKIPTRIGNIDLA

PLIIVLALQFLGIFLGNILRSIL

>ABV52389.1 soluble lytic murein transglycosylase, putative [Campylobacter jejuni subsp. jejuni 81116]

MIKKILVFLFIFSSLNATQYSIEKLKKEENSLAKDYYIYRLLEKNKISKKDAQDLNSHIFRYIGKIKSEL

EKIIPLKPYINPKYAKCYTYTANTILDANLTCQSVRLNSLVFIASLNSKDRTTLAQTFKNQRPDLTNLLL

AFNTSDPMSYIVQKEDINGFFKLYNYSKKYDLDLNTSLVNKLPNHIGFKDFAQNIIIKKENPKFRHSMLE

INPENVSEDSAFYLGVNALTYDKTELAYDFFKKAAQSFKSQSNKDNAIFWMWLIKNNEEDLKTLSQSSSL

NIYSLYAKELTNTPFPKIESLNPSKKKNNFNMQDPFAWQKINKQIRDANASQLDVLAKEFDTQETLPIYA

YILERKNNFKKHYFIMPYYDNIKDYNKTRQALILAIARQESRFIPTAISVSYALGMMQFMPFLANHIGEK

ELKIPNFDQDFMFKPEIAYYFGNYHLNYLESRLKSPLFVAYAYNGGIGFTNRMLARNDMFKTGKFEPFLS

MELVPYQESRIYGKKVLANYIVYRHLLNDSIKISDIFENLIQNKANDLNKS

>ABV52388.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKIYSVILGAFLLGACSLKDQAIVDINLKSQTLMFTQKYKITQDKINAIITMSYLNPILDKTSKDDVLAL

SFTPNTLKIQNLEVFINNKKANIEKLDDEYLKYIIQNNYTDYFKVSLPNVKEETKLVTKICLDHLPCFEL

NFQKYPKSLYYRSEDVDTQYN

>ABV52387.1 molybdopterin-guanine dinucleotide biosynthesis protein MobB [Campylobacter jejuni subsp. jejuni 81116]

MKQLIMAFSGPSNSGKTTLITKIADNFLQQNLKVLIIKHDPADKAQFDFNGKDSFKFFQSGAEVMVLSPT

RTTFFSHENRDILKALKLAPNFDICLVEGLKTLDLPRISVFCKEIDESYFTFSNAIASYEKISHPYLTWL

DLNDIQAICRYILKNAKNLQGEL

>ABV52386.1 putative fructose-1,6-bisphosphatase [Campylobacter jejuni subsp. jejuni 81116]

MQEVISYIQKAVLEISNALKFPDTSYSQNQNFTGDTQLKFDVLSDGIITKTLSQCSSIKAIISEEKDEIL

TLNERANFIVAYDPLDGSSLMDVNFAIGSIFAIYEEKASAKNLRAALYSMYGARLELVICKDQPKLYRLN

ANNEFIFIKDLKMNEKGKINATGGTQKFWEEKHAKFIKSLFDEGYRLRYSGAMVSDINQILLKGGGIFSY

PATQDAPNGKLRAFFEVFPLAFIIEKAGGKTTNGKNHSLLELEFDKIHATTPCFFGSEYEISKLLKAYNE

>ABV52385.1 hypothetical protein C8J\_0786 [Campylobacter jejuni subsp. jejuni 81116]

MSDIRDEFEQDMDKKKEILLSCQNSKNLNSCYNCDEIFNCQTRKNYVDAVYNSMSKGKTEGGFDF

>ABV52384.1 methionyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MRYITTPIYYVNDVPHLGHAYTTIIADTLARFYRLQGHETRFLTGTDEHGQKIEEAAKLRNSTPQEYADK

ISFEFKKLWDEFEITYDIYARTTDTRHIEFVKAMFLKMWQKGDIYKDEYEGHYCISCESFFTQSQLINDC

SCPDCGKNTTILKEESYFFKLSKYQDKILQWYEEKDPILPKNKKNELINFVQSGLKDLSITRTSFDWGIK

LPQEINDDKHIIYVWLDALFIYISSLDFQSKGENAKFWPAHVHLVGKDILRFHAIYWPAFLMSVDLPLPK

FIGAHGWWTKEGEKMSKSKGNVVKPKEVVDAYGSEAFRYFLLREVPFGNDGDFSENMLINRINAELSNEF

GNLLNRIIGMSTKYSQGNILKEGVLKYYNTELNQAKEHLNLAVEFLENLQCNRYLEELFKALSVANLAIS

KYEPWNLIKENKHEQANALVALCANILAKTSLLLSPTLPKSCEKVALALNFEISSTNYAKMILDNELLDF

KANPCEALFPKVEKALLKQEIKEEPKKEESPKIKIDDFAKIEIKVAKVLDCQNIEGSEKLLKFQLELDDK

EIRQVLSGIAKHYKASDLIGKQVCIISNLKKAKIFGHESDGMILSAKSGDKLVLITPEQLVQNGSLVG

>ABV52383.1 hypothetical protein C8J\_0784 [Campylobacter jejuni subsp. jejuni 81116]

MQISNLGELLNATLIHEGSVLSVEGFAINLNELKAGFAFFNNDKKEITQAVKKGAYAIITENDITIEDKD

IFYFRVENLEQALVRFLRFFCEDKECEFLLFKSYELSLCKAFYFNILKGNIFADFEKLIKAKKGEIFCYC

EENYLNKLCAYSHSLKDANFTLLSRSSFFFTTLICENLYFKNLNLPFFYANSFAKIISFLKEKSQKIIFD

FNKIDDFKIYFIDDKFEITPFGSSSQAFIVSNNQNTFEFWKEKFKNIKDFKIASKNSLFCDFSYNQLSDL

RKLKNFKYCLILENYDIFEQEFENKENQTPSLF

>ABV52382.1 methylated-DNA--protein-cysteine methyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MFKVYYKMPLCYLSLHSDGKFLTRVDFCDNKRSEKNCSLLDLVKYELDLYFTHKLRKFSIPVLIQGTDFE

SKVYKALMKIPYGKIATYKDIAEKINHPKAFRAVGNANSKNQIPIFIPCHRVIASNGIGGYNGGLEIKRF

LLENEGVNLK

>ABV52381.1 aconitate hydratase 2 [Campylobacter jejuni subsp. jejuni 81116]

MSFMQEYNKLVEERAALGIPPLPLNANQTKELCKLLENENNEELANLLENRVNPGVDDAALVKCEFLNSI

LKGKISAPNIDKKRALRMLGTMLGGYNVKVLIDALKDENIAKDAAEVLKNIIFVHDNFHTIAELSKNNPH

AREVLQSWANADWFNKKEKLPQVIKCIVFKVAGETNTDDLSPAGDAFTRSDIPLHANAMLKVRQAGSLEK

IKELKKSGREVVYVGDVVGTGSSRKSAINSIQWHLGKEIEGVPNKHSGGIVMGSTIAPIFFNTAQDSGAL

PIICDVINLEMGDEFEIHPYEGKIIKNGSTIAEFTLSPNTLLDEVRAGGRIPLIIGRGLCAKAREFLGME

SENIFTKPEQPKSSSGGYTLAQKMLGRACGVEGVRPGMYIEPMTLTVGSQDTTGPMTRDEIKELASLGFN

ADFVMQSFCHTAAYPKVSDSNLHKTLPNFMTSRGGVSLKPGDGVIHSWLNRFVLPDTVGTGGDSHTRFPI

GISFPAGSGLVAFAAVTGSMPLNVPESVLVRFSGELQAGVTLRDLVNAIPYYAIKQGQLTVEKKNKKNIF

AGKILEIEGLPNLKVEQAFELSDASAERSAAACSVDLSIESVSEYIKSNISLIEAMIEAGYENKATLVRR

AEKMREWLKNPTLLRADKDAKYAYIIDINLNDIKEPILACPNDPDDVATLSEILADNKRPKNIDEVFVGS

CMTNIGHYRALGEILKDKGILKTRLWVVPPTKMDKAQLTNEGYYSIFGAAGARIEVPGCSLCMGNQARVN

DGAVVFSTSTRNFDNRMGMGAKVYLGSAELAAVCAILGKIPSKEEYLQIVSEKLSDEHKANIYRYLNFNE

IENFKLEN

>ABV52380.1 hypothetical protein C8J\_0781 [Campylobacter jejuni subsp. jejuni 81116]

MKLLFTSFCCFASLMASDAINCDNIKNNKTLLNESSNLDYLNIASSCKESLKNQDFTKKLYAISNEIRGS

NSSCNGVAYLPKLQQFDFLLLKIAIDPITYQKTLDTPENLEKKYDILKSYFRYWAYQSIGNFRLYKAFWQ

EYNNAIEPLEKYFESNFNFDKGSNIYYTSNALNEFLNWAVGETKIYKDISPLAKIMSNKNYSVSYIQDFI

FSNNPSQDDLTIALQAALLNQREKEILELLIRFGARIDEGYESAIFYALENYENTNFLIQNGANVNQANA

FGKTPLFYAIEFNRLDIIKLLLDNGANVNQKYINNNEKLALSANIGSNTPYFITFCALEHTSKNVLMHAA

AYGNVEILKLLISKGANLNAVDDLGFNALDFALAAGKKENADYLKSLGLKANENLFYGGSLE

>ABV52379.1 oxidoreductase, short chain dehydrogenase/reductase family [Campylobacter jejuni subsp. jejuni 81116]

MKTAFITGASSGFGRACVEAFIQKGYKVIALARRKERLEELKNSHKDKIYTLCIDVRNQKEIFEAIENLP

KEFQEIDVLFNNAGLALGVDEFDKLNLEDINTMVDTNIKGFLYVAKVVIPILRKQKNAYIFNLGSVAGRN

PYFGGNVYCGTKAFVGQFSLALRNDLRGSNIKVTNIAPGLCKTEFSEVRFKGDIQKADAVYENTQFISAN

DIAKVVMSIINLPSHINVNEIELMPVTQTWNGFYIERDE

>ABV52378.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MNKFLVLLFLPLVAFANSSEAAANANLFGAFTLIPPLVAIALAFITKDVILSLFAGVLSGTFLLSLSANI

FKAQHLAFVNFYNTAVESFSKIISYILGSTSDPVNAGIILQILCIGGLVALITKMGGAKAVALKFAKRAK

SAVSAQVNTWFLGLLIFFDDYANLLIVGPIMRPLADKFKISREKFAFIIDSTAAPVAGIAVISTWIGLEV

SLIKTAYEHIGISDISAFGIFVETIPYRFYNIFMLFFVVMTAIMGREFGSMYKAEVRARTTGQIAPLPKS

GTLDTAELEDQFLAPKEGIKIRAFDAIVPIFTLIILAILGFYFNGLSTLEGEELAKASANPLSFETFRAA

FGNADSSVVLFQAALFAAIVAIFIGVRRKIFNLKEAVETWIYGWKTMIFTIVLLLFAWSLSSIVKDLGTS

LFITSLLADKLPEFILPATIFAFASAISFAIGTSYGTMGILMPLAVPLAHEIAKINGMDANAMHHYMVIN

ISCVLTGAIFGNHCSPISDNVILSSMSAKCDHMEHVRTQIPYALFICGISLIAGYIPVSLGLSVWFVLPL

NFILIALLLRLIGKKVP

>ABV52377.1 tRNA (uracil-5-)-methyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MSLENFGNFLTLDEKHSFIKKYFKEFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYI

IEYLDFADEKICAFMPKLLEYLRQDNKLKEKLFGVEFLTTKQELSITLLYHKNIEDIKSNLENLSNILHI

NLIARSKGKKLIFKTENLRQTLNIQDRKIFYEFNNDCFIQPNTTINEKMITWVCEILNTQKRMDLLELYC

GYGNFTLALAPFFFKVLATEISKSNINFALKNCKLNNTTNIHFARLSSEELSLAIKKEREFFRLKDIRLD

DFNFSHVLVDPPRAGLDKSVIDLIKKYENIIYISCNPITLKENLKELSLTHRVEEFALFDQFVNTPHLEC

GVFLSKV

>ABV52376.1 hypothetical protein C8J\_0777 [Campylobacter jejuni subsp. jejuni 81116]

MEEFYPYTLTIHLLCAILFIGYLFVDVFVLGVVKKKNPNFDKSLFSATGVKIMPFVVLLLFLSGGALAGF

HFKPLNLLFAVKIILAFGILSLVVFSLFCHFILKKKNPLGAFIHPFVFVLCIAIVILAKLMNYFFIPC

>ABV52375.1 CoA-binding domain protein [Campylobacter jejuni subsp. jejuni 81116]

MNEKETISYIINASKNIAIFALSPDKTKASYRVAEFLQRKNYKIFPIYPKEEFILNEKVYRNLDQIEEKI

DTLILFRKGEVALEILPKLVEKNIKNLWLQLGISNETAKEECKKLDINFIQNRCIMLEYPYFKTKEK

>ABV52374.1 threonine dehydratase [Campylobacter jejuni subsp. jejuni 81116]

MLELNKIYKAKQQISGFVNKTPFIYSSFLSDICQSEIYLKNENLQITGAYKIRGAYNKIANLSAEQKQHG

VIAASAGNHAQGVAISAKKFGIKAVIVMPESTPLLKVSATKALGAEVILKGDNFDEAYVFATSYAKENNL

SFIHPFEDEFVMAGQGTLMLEMLDEISDLDMIIAPVGGGGLISGIASAAKQINPNIKIIGVGAKGAPAMY

ESFHAKKIKNAKSVRTIADGIAVRDANPINFNIILECVDDFIQVDDEEIANAVLFLLEKHKIIVEGAGAA

SVATLLHQKINTQNHKKIGVVLSGGNIDAQMLNIIIEKGLFKSYRKMQIHVTLVDKPGALLHLTDSLKIA

NANIVKIDYDRFSTKLDYGDAMISITLETKGKEHQEEIRKILTQKAFNFYESF

>ABV52373.1 putative tRNA pseudouridine synthase [Campylobacter jejuni subsp. jejuni 81116]

MKIKIIFSYDGSAFLGSATQPHKKGVQDALSGALSHLGIFSPLLMASRTDKGVHASYAVASVECGDYFTN

LEYLQKQLNKFSHPFIHIKKIEKVKDDFEVRFDVKSREYRYIFSHASYSPFMASYVHFYPKFDLGKANEL

LGFFVGKKDLKFFCKSGGDNKTTLREIFIARAYAYKDFSIFHFKANGFLRGQIRLSVASVLKVLEGKMSE

KELKEQIEAKKQYNHFLAPPNGLYLSRICY

>ABV52372.1 hypothetical protein C8J\_0773 [Campylobacter jejuni subsp. jejuni 81116]

MKLSLRYVLNQFLSTNLSIFFVLFAIVSMVFFIQLAKLTSSIEISFLDLLKLYGFMLPRILIFTLPISFF

ISLTLALFRLSKENESIVLFTLGFSPMILAKFFLKIASLISAFMLVVALVMIPIVFELQDNFVNYKSTQV

KFNYKTGEFGQKFLDWMIFIEKQDSDKYENIIMYRPKHKADDKEQLIIAKEAHVQRKDDSFAFSLNQGKM

YNFEQGQSIFSGEFDTLVVNTQFNTDNLQTKKFYEYWNDLNENPQRAREFVIYTTIALFPLASTLFALCF

GLVTYRYEKGYVYLGMFGVIAIYFGLLSSFSQPPILACLGIFSLSLFVSAYCFKKMILSRY

>ABV52371.1 peptidase, A24 family [Campylobacter jejuni subsp. jejuni 81116]

MGSFCTSLASRIIEKKPFFISRSFCFSCDTKLKYYEIIPIFSYIFLKAKCQTCKCHLPISLLINEILGII

LLILAYSLSQNFYDFLFLSLFLFNLFLLSLIDIKLKAVPQILLWSAFLFAFFYAFRESEILHFLIFKEFS

GGFLLNAFSFGGFVFLLKSLVFFLMNFRKKDEILENLGDADIIIMSCIGGILGFEYGFLVLLIASILTLP

FFIFFKIKAIKEQELAMIPFLNIAFVAVLFYKNLGLF

>ABV52370.1 putative undecaprenyl diphosphate synthase [Campylobacter jejuni subsp. jejuni 81116]

MNELKHLAVVMDGNRRWARAKGFLAKLGYSQGVKTMQKLMEVCMEENISNLSLFAFSTENWKRPKDEIDF

IFELLDRCLDEALEKFEKNNVRLRAIGDLSRLEDKVREKITLVEEKTKHCDALCVNLAISYGARDEIIRA

AKRVIEKKLELNEENLTQNLDLPLDVDLMLRVGNAKRLSNFLLWQCSYAEIYFSETLFPSLTKREFKRII

KEFRNRERTFGK

>ABV52369.1 hypothetical protein C8J\_0770 [Campylobacter jejuni subsp. jejuni 81116]

MSMINSTLPIQMKVLAKSGYGHYTLLLNHKKIQTKSMIELEIGAEYLAELYMQNGGVIQFKHLSKRPNFK

PFEEGLALIIAILEDKISYKKFIIQNLLDCKDIERYQILKEMLFASFENIYHIPFIFENKSCLFQMRKRA

KYLEIYLYFSVFGALKILIDSQGISVFTPFAKVQKFLNEHLDFNVSQENKIEPLFVFKRLFDFKG

>ABV52368.1 phosphopantothenoylcysteine synthase/decarboxylase [Campylobacter jejuni subsp. jejuni 81116]

MKTILLAISGSIAFYKSYELISLFKKEGFRVKVLLSNSLLKFASKMSFEALADEILCEENESWQNSNNHI

AFSKDVDLVLFAPASVNSINKLAFGIADNLFIQTLIAANKPLIIAPAANTNMFHHFSTQNSLKILKENKA

LIIEPICKVLACKDEGVGALAEVKDIFNITKRELLKEKFWCNKSVVITGGGTRERIDDVRCVSNFSSGKM

AKVIADAFYFLGARVKLLSSVEFDTPYELCKFESSKDLKELLDKNLSHDFLIMTAAVSDFIPQSVKGKIK

KNEHLQGLNLHLSLNEDLLKTCKFQGKKIGFKMEFDSQNALENAKKSLKDKQLDMVCLNIIDQKNYFGSD

QNELYFITLNNENKSTLQSKEKLAFELVKWCEKL

>ABV52367.1 UDP-N-acetylglucosamine pyrophosphorylase [Campylobacter jejuni subsp. jejuni 81116]

MKTSILILAAGLGTRMKSQKPKVLQELCQKSMILHILKKAFALSDDVSVVLSHQKERVEKEILEYFPKTQ

ILEQDLQNYPGTAGALRGFEPKNERVLILCGDMPLVEQTSLEALLSNNAKLNLAVFKARDPKSYGRVVIK

NDSVEKIVEFKDANTQEKEINTCNAGVYVIDSRLLKELLPLIDNNNAAKEYYLTDIVKLAKEKDVMIKAV

FVDEDEFMGINDKFELSIAENFMQEKIKKYWMQQGVIFHLPQSTFIGTDVEFMGECEVYENVRIEGKSKI

INSIIKSSSVIENSIVENSDVGPLAHLRPNCELKNTHIGNFVECKNAKLNTVKAGHLSYLGDCEIDSGTN

IGCGTITCNYDGVKKHKTIIGKNVFVGSDTQFIAPVKIEDEVIIAAGSTVSVNVEKGALFINRAEHKMIK

DYYYKKFQK

>ABV52366.1 flagellar biosynthesis protein [Campylobacter jejuni subsp. jejuni 81116]

MKKILLFLLLSMSLFAAEATIPTVNLSLSAPNTPNQLVTTLNIVIVLTILALAPSIVFVMTSFLRLIVVF

SFLRQAMGTQSMPPNTILVTLALILTFFIMEPVATKSYNEGIKPYLAEKIGYEEAFIKGAKPFKDFMLKN

TREKDLALFYRIRNLPNPKTIDDVPLTVLVPAFMISELKTAFEIGFLIYLPFLVIDMVVSSVLMAMGMMM

LPPTMISLPFKLLIFVLVDGWNLLVQRLVESFVT

>ABV52365.1 amino acid-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIILIFISFFALNLSAKDLVVGMELGYPPFEMSDKTGRASGISVDFLEAFAKKNGYKLVVKNIAWDGL

IPALKTAKIDLIMSSMTITDERKKVVDFSIPYAKANLAILTPLNSDITNIKDLDKKGKVLALKRGSTGHL

YAVKNLKNATINLFDKENAAILEVIQGKADGFFYDQLTIYRTWQKHQDTTRAILVPFQENPEFWGIAVQK

GNAELKKELDEFIAESKKDGLFDSLGEKYLKDVKDTFKKNNLEFFF

>ABV52364.1 hypothetical protein C8J\_0765 [Campylobacter jejuni subsp. jejuni 81116]

MSIFSINDNSNYNSILSQSKANKESKENSKISFANAFLKQNASKLNEIQSANSQTLARSEVLNSTNTTNT

SNNTNFSISSKTSSPNYDISSEFKNSIYTLKYKQADISNNTAYGYSVDKDGYMGSDFNKAAGLPEDFKIH

KSTLDEIKKAAENDPVASSTKEYLGVSEYYTNIDMAETIKQYYNLFSNALGQSFPNDKTSFSEADINSMP

SGYGVSGTQWMDFNDPSNRMNITGLKDFSNSLISNVYKTHEQAKEADDLWVDSGYMIDGLLPKTLGLSLE

EIKNVSKGEDWQFKPDMSFYPKNEDGTYTKEDLFMSFLKAQNGQPVESPKTTLNPKVEAYNRAMAKESFS

TTSVDIGDIMTGKVDFASLFKYLASKNGKLEGQLYMYENNISKESAMGNWALDAEIKQAIANGWKAKPST

INSYADSIMDRLNNLLGQTRV

>ABV52363.1 3-deoxy-manno-octulosonate cytidylyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MDAKMIIIPARLKSSRFHEKILCDIGGVPMFVATARRVSSVDEVCIALDDEKVLSIAKEYGLNAVLTSKD

HESGTDRINEACKKLALKDDEIIINVQADEPFIECENLLKFKEFASSCLDKKAFMASCYKKITQEEAMDP

NLVKVLCDKEGYALYFSRAKIPYERENYEESFKGHLGIYAYSVKALREFCSLSSSALERAEKLEQLRAIE

NGKKIKMLEISTTSMGIDTKEDYERALKIYLEK

>ABV52362.1 threonine synthase [Campylobacter jejuni subsp. jejuni 81116]

MKLVESRNVKNVSSFKEALINPNAPEGGLYSPLNLPIFEGEKYANLSYKDFALKLIESFGFGEEELFKKA

LKSYESFDDKNTPISLQKISEKTYINELWHGPTRAFKDMALQPFGVLLSEFSKDKNILIICATSGDTGPA

TLKSFENAKNVKVACMYPKGGTSGVQELQMRALDKDNLKVFAIDEDFDAAQRTLKELLFSKDFQNEIKAL

NYELCAANSVNFGRILFQIIYHYYASLKLFNEFLEEVQIIVPSGNFGNALGAFYAKKMGAKISKIKIASN

ANNILSEFFNQGVYDLREKSLKKTISPAMDILISSNIERLLFAKFKDKRTKELMNLLKNERYFKLEKEEL

QSLQEDFEADFCTDEECMQFIKQSKILIDPHTATCFKMLDPLKPSIITSTAEWTKFTPSMIKALYDRDSK

NEKEDLKFIAKEFNVQVKDEILTLFDLKNSDEKVFEARNIKKEILDWMQK

>ABV52361.1 tetraacyldisaccharide 4'-kinase [Campylobacter jejuni subsp. jejuni 81116]

MSEEKNYELWLDNYFFKPNFWQKCLAFILLPLSVFYAFFAILNTFFRKKIVFKKPVISVGNLSFGGNGKT

PLCKAIAREFDGVFIVLRGYKRKSKGLFVVKNQNEILCTLTQSGDEAMEYAFEENIKGVIVSEDRVKGIE

KAFELGAKIVVLDDAFSKFHIKKFDILLESKIKPYFNFTLPSGAYRLPKFYEKRADFIALEGRDFVRYSF

VKENPKAVLVTAIAKPFRLYEHFIKARACYFFKDHYEFKKEELENLLKKHNCDTLMLTFKDFVKVKDFGF

KCQIIELNIELKDSLREKIKTYIKEFEQ

>ABV52360.1 NAD+ synthetase [Campylobacter jejuni subsp. jejuni 81116]

MDWQKITEKMCDFIQEKVKNSQSQGVVLGLSGGIDSALVATLCKRALKENVFALLMPTQISNKANLEDAL

RLCADLNLEYKIIEIQSILDAFIKQSENTTLVSLGNFAARIRMSLLYDYSALKNSLVIGTSNKSELLLGY

GTIYGDLACAFNPIGSLYKSEIYTLAKYLNLHENFIKKAPSADLWENQSDEADLGFSYAKIDEGLKALET

NDEKLLRTLDPSLIAMLKNRMQKNTFKGKMPEILEI

>ABV52359.1 metallo-beta-lactamase family protein [Campylobacter jejuni subsp. jejuni 81116]

MQIIKQACGAYETNCYILFSEHGEIIIDPGFDALNFIKKHVKNPLAILNTHGHYDHVWDNEKVKQAYQIP

IYIHKNDAFMLEDPFNQGFMPSKADYLIDDENIISIGGLDFKFHFLPGHTPGCTMIEIVGKNIMFSGDFL

FYRSIGRWDFPYSDANLMKQSLEKVMTYKEDFKLLPGHGQETTLKEEQVHLPSWLRYF

>ABV52358.1 small hydrophobic protein [Campylobacter jejuni subsp. jejuni 81116]

MELDQILLYAFIFLNLFAFFGLFLGNKKKNQFNDKKFYKICPCKKMAENGSLSTICIYSAVGGFFYSVLS

IGFVGFGNWTLNFIFLLALLSVFLGWKLKLD

>ABV52357.1 7-alpha-hydroxysteroid dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MNTEFQGKTLVISGGTRGIGKAIVYEFAKVGVNIAFTYNSNAQIADEMVQDLEKNYKIKARAYEFNILEP

ETYKELFEKIDADFDRVDYFISNAIISGRAVVGGYTKFMKLKPKGINNIFTATVNAFVVGAQEAAKRMEK

VGGGSIISISSTGNLVYIENYSGHGTAKAAVEAMARYAATELGEKNIRVNVVSGGPIETDALRAFTNYEE

VKQATINLSPLNRMGQSEDLAGACLFLCSSKASWVTGHTFIVDGGTTFK

>ABV52356.1 dihydrodipicolinate synthase [Campylobacter jejuni subsp. jejuni 81116]

MDKNIIIGAMTALITPFKNGKVDEQSYARLIKRQIENGIDAVVPVGTTGESATLTHEEHRTCIEIAVETC

KGTKVKVLAGAGSNATHEAVGLAKFAKEHGADGILSVAPYYNKPTQQGLYEHYKAIAQSVDIPVLLYNVP

GRTGCEISTDTIIKLFRDCENIYGVKEASGNIDKCVDLLAHEPRMMLISGEDAINYPILSNGGKGVISVT

SNLLPDMISALTHFALDENYKEAKKINDELYNINKILFCESNPIPIKTAMYIAGLIESLEFRLPLCPPSK

ENFAKIEEVMKKYKIKGF

>ABV52355.1 putative zinc protease [Campylobacter jejuni subsp. jejuni 81116]

MIAYEKIQLKNKLEVYALPVNKNSDVISVDIFYKVGSRNEIMGKSGIAHMLEHLNFKSTKNLKAGEFDEI

VKGFGGVDNASTGFDYTHYYIKCAKKNLDKALELFAELMANLNLKDEEFQPERAVVLEERRWRTDNNPLG

YLYFRLFNHAFMYHPYHWTPIGFFKDIENWSIEDIKEFHSIYYQPKNAILLVSGDIESKEVFELSKKHFE

KIKNTRTIPKIHTKEPKQDGVKRIYLHKNSDTELLALAYKIPNFKHKDIPALNALSELLGSGKSSLMSEI

LIDKLNLINDYYAYVNDCIDENLFIFICNCNPNVNAEKVEKELLKIIDKLKMGKISQKDLQRVKNNVKSD

FIFSLNNASAVANIYGSYLARGDIDPLLNYEKDIQNLELKDLISCAKKYFIQENSTTVILRKDSNG

>ABV52354.1 dihydroorotate dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MAYEMIKPLLFKLNPEHAHALVEYSLRALSASFPGALSFLAHKYIVDDESLRQNLLGLDFNNPVGLAGGF

DKNATMIRPLSALGFGFLEVGTFTPKPQEGNEKPRLFRLVKQESIQNAMGFNNEGAEKIALRLAKTYPFV

LPLGVNIGKNKITPNDKALEDYFTLFRDFKDLCDYFIVNISSPNTKNLRELQNDDFLNTLLEEAKKITSK

PILIKIAPDMKIDDALNLCENAIKKGADGFILANTSVDYSLLDNNRTFGGISGRLITEKSGIFFKEVAKI

LFGKTLLIASGGIDSADIAYERIKNGANLVQVYTALIFKGPSLVKNINQNLIELLRKDGFLHISEAVGVN

LK

>ABV52353.1 lipid export ABC transport protein [Campylobacter jejuni subsp. jejuni 81116]

MHNEMNLKEVLIRFKPFYKRYWKQFAIAIFGMILASGGTAGSFYALEPILNYIFVEKNEALLYTVPFLLV

LMYFFKNLGTYLQSFYVSFIGTDMLRVLRARVLKNVLRLDMDFFKRYRSGELVSRCTNDINALQSIVSNI

IPDFFRELLTAIGLLAVVLYQSPTLAFFALVILPLAIFPLVWFAKKLKKYARNIQETNSDLLSYLGEIFS

NIELIKANDNEKKESDKFAKHNDTLCKLNLKSARIDALTSPLMDMMGSVGVAVVIIVGGREVINGSMSVG

SFISFVSALFAIYTPLKRLSSLYGKLQGAVAASERTFYLLDLEPQIKGGSKELKNIEKISFENVEFAYEN

PHKSVLKGVNFDFVKGQMLALVGTSGGGKSSIINLLMYFYEKQKGKILLNQEDISTFTIESLHAKIGLVT

QNIYLFNDSFAANIAYSEELEEEKVIQALKLANAYEFVKEMGGIWAEVKEHGKNLSGGQKQRIAIARALY

KNPDVLIFDEATSALDNESEKAIVKTIENLKQDRLILVVAHRLSTIENADKIVVLDKGKVLAIGKDEELL

QTCSLYQKFKSKEKTKPSFS

>ABV52352.1 cysteinyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MRLLDSVAKEKIKLDKKDISIYLCGPTVYDDAHLGHARSSVCFDLLRRVLLANGNRVKFARNYTDIDDKI

LKKMAQSGQTLEEITEFYIKSYEEDMRVLNVLDPDFKPRATHYITAMLDLIKKLAKDGFVYTLEDGIYFD

TSKDEKYLSLSNRNLEENISRLSNEVQKRNESDFVLWKFDENFYESEFGKGRPGWHTECVAMIDSIFENT

LDIHAGGIDLLFPHHENEAAQCRCGCKRKLANIWLHNGFVKIDGEKMSKSLNNSFFIKDALKEFMGEALR

FYLLSSHYRSHFNYSLSDLENAKKRLDKFYRLKKRLDLGEISDFDVLNDIEIKSEIAKQILEILNDDLNI

SKALALLDDFISSANLELDKESKNKILKQNIKEALSELAKIFGFGFMDTTLYFQWGVSKEEREEIEKLIL

ERTEAKKNKDFNTADAIRERLSSKKITLLDTPNGTIWEKINA

>ABV52351.1 integral membrane protein MviN [Campylobacter jejuni subsp. jejuni 81116]

MKSLVFKNFIINALGILFSRILGLARDVLIALFLGAGLYSDIFFVALKMPAFFRRIFAEGAFGQSFLPNF

VKAKKKGAFCVSVMMQFSLIVFLFCLLVSFFSSFFTKLFAFGFNADTIALAAPLVAINFWYLFFIFLVTF

LGAILNYRQKFFITSFSAALFNLSIVIAAFFVDKNAPQNTLYYFSYATVLSGVAQLILHLLVLKNNPVIR

AMALSIKFKKAKAKLQGFYGNFFHGVLGSSATQFSSLLDTTIASFLMSGSISYLYYANRVFQLPLALFAI

ALTQVSFPKILKHLKSGQENLALKFMQRALAFLSILLIASSIIGSAFALEISKLLFERGNFTHEDSVITA

YVLIAYLIGLLPFGLQKLFSLWLYAKFKQKTAAWIAVKSLIISALCSMAFIFLIKDESLKVIAVALSSSI

SAFYLLGANIKEFGFKKFFALISIKICLLVIVALIVFTILLILIKPYILSFFIGIFTSFKGVF

>ABV52350.1 hypothetical protein C8J\_0751 [Campylobacter jejuni subsp. jejuni 81116]

MALDEKIIAYTENPARELLSVASRTNLSLNELDFSLLAFSTQYRFGDLEWEKISEKELTLFDKDEIFLKN

DLQIKQEYKIEIFHGINQSKASQAVKLVANKNLTKIVAQIDFTNLDFHEKLALELLQNIYKKMLKLKFLI

GIRIFDFKKNLMSFCNQHKNTPLNKTIQITVAQGIDPIESQDESLILTYKEKTKNYTIDEKRSGIIVVDE

NEVVLKHAKFKQGKEGKDLNLHTLKVLAANENKVKFSCSSAFKQVEQDGYTEYIALKKGYVVQDGEKFDI

ANELDFNGVDFKNIGIIRAGLDKNVKINIKFLSEVKDAVNSGVGIECEELNVVGSVGSNTQLNATKMKIE

GTTHSKAKIQAKQAYIKTHRGFAEAEILNIDLLEGGTIKAKEVRIKKSLGGNIQADKIYIENLESNNSCV

FFENTTIERINGDNNKFHAKIKTLDKNYDEEFAILGEQISKLNHKINKIRQYILSSKNGILSVEKKITEL

KNQGQNVPVQYEKALKDFSLQNLELNKLQNEEKELLERKKSLQLELINLQKMLFEATFINKSGKWTDMNE

IKFSLLEPKEDIFYSSFVNESAKFIGIKKVIQNNQESIEIHKKLDYEEKDIAWLSASKE

>ABV52349.1 holliday junction DNA helicase RuvA [Campylobacter jejuni subsp. jejuni 81116]

MVVGIEGIITKKEPTFIIVKCASGLSYGIFISLFCSAKIQTQEKHEFFITQIIKEDSNKFYGFLDKDEQK

MFEMLLKVNGVGANTAMAVCSSLDVNSFYKALSLGDESVLKKVPGIGPKSAKRIIVELSDTKTKLENVSD

DKSEALAALLTLGFKQEKIISVLASAQATGTSELIKEALKKLG

>ABV52348.1 putative D-alanine--D-alanine ligase [Campylobacter jejuni subsp. jejuni 81116]

MKFAILFGGNSYEHEISIVSAVVLKKVINQNLEFVFCDEERRFYHIPSEKMNSKTFSTKAYKNEKELFIK

QGGFFSKGFLKENKLECECVINLIHGRDGEDGKIAALFEFYSIKFIGPRLEASVLSFNKELTKLYAKSVG

VKTLDYTMLRKNQNSKEKLSFPCIIKPARLGSSIGISIVKDEKDLEYAKDVGFEFDNDLVVEEFKNNIKE

YNLAGCMINDEFVFSIIEEPKKKEFLDFEQKYLSFSGHNELIEADLSEELKEKLKDSFKKIYNPLFKGAL

IRCDFFILDNEVYLNEINPNPGSLANYLFKDFNTTLNALADQISLEKMIKINYNFLHSINGQKGKL

>ABV52347.1 hypothetical protein C8J\_0748 [Campylobacter jejuni subsp. jejuni 81116]

MLSFKQDEIYTATEVVRNFSPIMEKLKKSESGKIVILKNNKFEAVMLSMKEFERLQNAMQLLENIYKNQK

A

>ABV52346.1 hypothetical protein C8J\_0747 [Campylobacter jejuni subsp. jejuni 81116]

MAQTQLSYKNKTYQISYEILGDLSLPQILILHGWGANKELMKQSFCPFLKDFCQIYMDLAGFGNSSVEEI

LNTQDYANITELFLKQKKLDVCFFMGHSFGGKVSTLLAKEKDTLILLSSAGILAKKSLKVRFKIRIFKIL

KLFGLGKFYRYFASKDGVNLSPMMYETFKKVVDEDFSEIFAKQKAKSLIFWGKSDEATPLYCGEKMHELL

KNSTFYPLEGDHFFFLKHSAFIAQKIKEI

>ABV52345.1 UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl- D-alanine ligase [Campylobacter jejuni subsp. jejuni 81116]

MLINALYFVNSLFFNFCIAFYLMSALQWYSYKFKRVFFHYHKPLWHLYFLFIPYFLFLAFPLYSLAYFAL

IHTPILYFWSKGIDKKLVFTSKVKWFFVFVFVYNAIFAILALRFSFLFNLFSLPFALFSLKIYEFFTNLY

YKKQAKAKLRANENLKIILITASFGKTSIKNFLYELLKDDFKSYKTPRSVNTLLGIVADINTNLSQDTQI

YIAEAGARLKGDIDEITRFLQPHISIVGEIGNAHLEYFKSVENIRSTKLEALNSKRLEKAFLHSSTQKEE

DKLISLYDDKLSLIHSSLEGLEFKIDIENKSYDFKSQILGDFNAQNLCVCILCAHYLGIKLEKIQKQVLN

INSVEHRLQVLSREPKFIIDDGFNGNFKGMSTSYELCKSYKGRKVLVSPGIVEVSEEENIKLAKIINECF

DLAIISAQINAEIFKKELKIKTIILKEKSQLVQTLAKETKNGDLILFSNDAPSFM

>ABV52344.1 hypothetical protein C8J\_0745 [Campylobacter jejuni subsp. jejuni 81116]

MSIFSINDNSNYNSILSQSKANKESKENSKISFANAFLKQNASKLNEIQSANSQTLARSEVLNSTNTTNT

SNNTNFSISSKTSSPNYDISSEFKNSIYTLKYKQADISNNTAYGYSVDKDGYMGSDFNKAAGLPEDFKIH

KSTLDEIKKAAENDPVASSTKEYLGVSEYYTNIDMAETIKQYYNLFSNALGQSFPNDKTSFSEADINSMP

SGYGVSGTQWMDFNDPSNRMNITGLKDFSNSLISNVYKTHEQAKEADDLWVDSGYMIDGLLPKTLGLSLE

EIKNVSKGEDWQFKPDMSFYPKNEDGTYTKEDLFMSFLKAQNGQPVESPKTTLNPKVEAYNTAMTKESFS

TTSVDLTDIMTGKVDFASLLKYELDRGRIAGELYMYEKGMSPKQALGNWALDAEIKQALANGWKASSESI

NSYVGSIMDRLNNLIGQTRA

>ABV52343.1 signal transduction histidine kinase [Campylobacter jejuni subsp. jejuni 81116]

MNESILKSLDSNEKETLQKGLESLIEQTYVIENEYKTLNENYNSLRAMVDEIIEVLPSALWILDKEKNII

LQNQEALKNPKLLSIISLDKIRDELEFEGRFYAVKIIAHNEKTIVSATDISDEKRNERLASMGSVAAHLA

HEIRNPIGSISLLASTLFARSELKNKHIVLEIQKAIARVERIVNSTLLFTKGVHINALNFNLLELKEECE

SAINSYNFTSQIDFEISFLDKQICADKALLGLVLQNLIYNAIDAIEESECEKPMIKILASYDNEKICIRV

YDNGCEIKDEKLVFEAFKTTKLKGNGLGLSLSKEIINAHKGELSFQSDPKNFYFTLPLV

>ABV52342.1 hypothetical protein C8J\_0743 [Campylobacter jejuni subsp. jejuni 81116]

MHKNLSLSKLFDFYSVFEGFEKLNILNFEDDVFTNIEQILLDDYLKTKSYFALDETSSYALTLLAKNNRK

RFSINRKIQHFKALSTLKYLLETGIIKLEYSKEAKKIKDKRQKIKKELRSYVVQDKIIFGNHFTRFFFYF

LKPNEKLILQNRYKEVLECIKEKFELYQSFCFEQLSRELLEKKFNINGVQSYWDKNVELDLYYQDENLCF

VGEVKFKNKKICKNILNLLKSKVKSLNLTPNYYIIISKNGFSKEFDKICEQNLLLLDLNDFKILLEE

>ABV52341.1 aminotransferase, putative [Campylobacter jejuni subsp. jejuni 81116]

MQISDLKKELILKKGILHFDFTASALALKCVEKEISKILPTYANTHSDSSLNSFKTQQIYEQARKDIKKS

LSLDENFALIACGTGSSSAIKKFQELIGIYIPPLVKERYFTQIDKNTLPLVIVGPYEHHSNELSFREGLC

ECIRIPLDKNGEIDFDFLEKTLQKNKKRKIIASFSLASNVTGILSDYKRISEMVRKFKGIVAFDASSFIP

YKNISCQYYDALFISSHKLIGGIGGSGLLAIKKDLCGNKPSFAAGGTVGYVSRTSQCYLCNEEALEEGGT

PGILQLIRASLAFKIKDSIGVKNIEKKEEILKDYFFEKLKTIPNLILYAKNLKTRLPIFAFNIKGISPFD

IAYELSKKYHIETRAGCACAGPYGHDLLGLKDNQKLKTKPGWLRISLHYTHEKENIDYFFNALNKTIVKL

SH

>ABV52340.1 formyltetrahydrofolate deformylase [Campylobacter jejuni subsp. jejuni 81116]

MISVLKICTKDQKGLIYRISDVIFKYHINIVKNDEFVGEGMFFFRALLEGEFDKEAFIGTLEAMLGQEAL

IELCEKRKKDIVVFATKESHCLGDLLIKHYSNELEANIKAVISNHNSLKDLVEKFEIPYHFISAENLDRK

EQENQILKCLEQYKFDYLVLAKYMRILSPDFVRHFEGKIINIHHSFLPAFIGANPYKQAFERGVKIIGAT

AHFVNNNLDEGPIITQAVLPVNHEFTWQDMQQAGRNIEKDVLSKALDLVFEDRIFIHNNKTIIF

>ABV52339.1 tRNA nucleotidyltransferase (CCA-adding enzyme) [Campylobacter jejuni subsp. jejuni 81116]

MQISKISLKNNSDLQFIAEFLKPYTKRAYLVGGSVRDLFLGLKICDYDIELYDIKLKDFEKIMQKLGAQG

FGKSFFVYKFKNYDLALARTENKISYGHKGFEVQICNDEKLGAKRRDFTINSMMINLFNDEFLDFYGGLK

DLGAGFLRHIDKQSFQEDSLRVLRAVVFASRFNFKITSESLKLMQSMDITDLSKDRINAELYKFFKSPRL

DVGYRYLQELGLEKQVFGFESVFKSLEFQNLLRQSREFVKSDALFLYLYLNFFNLEKDIFFKRTKLKKEY

LKYANQAFYLDDISDFELAKIAFEMPLKEWLGLWSKKRIEQAKRLGLYENKFESKILAKDFINAGFCGKI

LGLKLQEARENELKEYIKGLVK

>ABV52338.1 hypothetical protein C8J\_0739 [Campylobacter jejuni subsp. jejuni 81116]

MNLEDLAKKTISEVSSIMEEQRRQNEILKEQELNRKTEIKDELPPMEFVCEELDTPQDLEDKISMAKFEE

EQKIQNNIEISTQENKEFKKEEPFLQSEILNPSVITEVQTLNEDIFLKHLRERILVLFEGLNSIKKDDLE

NRLNLTINFLEFLLANIEDKLKK

>ABV52337.1 hypothetical protein C8J\_0738 [Campylobacter jejuni subsp. jejuni 81116]

MKNTVTEASIYEAQGLKDEALEIYKNILKEDPDNQNAIDAVRRLSGFRSKHKDLNTQMLDFFINMKSDEE

INEFKRWLIKI

>ABV52336.1 hypothetical protein C8J\_0737 [Campylobacter jejuni subsp. jejuni 81116]

MVFLIPLLIIIGVIFGIDYVYFKNQDLKAQVKKEQKELNSSLEKEKKEYIEKLFKTK

>ABV52335.1 NapD [Campylobacter jejuni subsp. jejuni 81116]

MNNLSSVLILVKEEYINDLKKAISEIPFCSVELCENEKIIVVIESENLEDELNSYKMLEKLPNIISINMV

FSYQDLNDDIQKAINSGAIETIEKNENAENIRYYGSVFNQFS

>ABV52334.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKFLFILSLFCVLSYAYELKLNANITALKLDKQNLYIGTDKGEILQYNIKDKSLKELLSLPKIKNYYGD

DFAKIYNIDVFKHTLLILSEGDFGAKNLSFYKENLQIKKLEENSIIKAFFINENTYLLISIGSEIELIDK

SLKNIKKFNFSHSSLNDAVLNEDKSRLVAGFESGEVELFDLKNWKMLKNYDKMHKDNIYQVDFKNNVILS

CGTDRRIGVVKNEEQNFLQKDFLIYTCALSPNGELAVYSDNEAGVSEVFSTSDFKPVKTFNNENLMSEFI

IFLNNKDFIISGFGDSIMFRSIDE

>ABV52333.1 periplasmic nitrate reductase small subunit (cytochrome C-type protein) [Campylobacter jejuni subsp. jejuni 81116]

MKKKLVLLGSAAVVFFAACAMNSGVSSEQIGLRKASLENENKVNLVEANFTTLQPGESTRFERSYENAPP

LIPHAIEDLLPITKDNNMCLSCHDKAIAADAGATPLPASHYYDFRHNKTTGDMISDSRFNCTQCHVPQSD

AKPLVGNSFKPEFKNEQLKSRSNLIDVINEGVK

>ABV52332.1 putative ferredoxin [Campylobacter jejuni subsp. jejuni 81116]

MKYLIARRIVQLGILALFSFKATDFILQGNLSSSRFFNTIPLSDPFAVLQIILASWSIDLMALIGALIIF

FIYGLLLGRVFCSWVCPVNLITDFAAFVRNKLTLNNKFLILPKNLRYFVLVLVLVLSFVFSLPVFESFSY

IGMIHRGIIFATSSWIFVAFILFCIDTFLSPRAICSHFCPLGAFYAFISRFALLKIKHDSDKCTKCYECI

RICPEKQVLWMVGKESTSVKSGECIRCARCIEVCNDDALNFNIFDLRNK

>ABV52331.1 ferredoxin-type protein NapG [Campylobacter jejuni subsp. jejuni 81116]

MKGRREFFVSAFKAACLCTGGGFLANLALKADDNYALRPPGAEDEARFLSKCIRCGLCVKACPYDTLKLA

SLLDSPKNGTPFFKAREIPCYLCKDIPCIRECPTDALDKKHLEQGIESLKMGIAIVDSASCVAHWGIQCD

ACYRACPLIDRALKLELKRNERTAKHAFLLPSVDHEVCVGCGLCELACITEKPAIRVLPREYVLGKAGSH

YVKGWDEKDEGRIKNADTSKHFDAKKATNYLNDGEL

>ABV52330.1 periplasmic nitrate reductase [Campylobacter jejuni subsp. jejuni 81116]

MNRRDFIKNTAIASAASVAGLSVPSSMLGAQEEDWKWDKAVCRFCGTGCGIMIARKDGKIVATKGDPAAP

VNRGLNCIKGYFNAKIMYGEDRLVMPLLRMNEKGEFDKKGKFQQVSWQRAFDEMEKQFKKAYNELGVTGI

GIFGSGQYTIQEGYAALKLAKAGFRTNNIDPNARHCMASAVVGFMQTFGVDEPSGCYDDIELTDTIITWG

ANMAEMHPILWSRVSDRKLSNLDKVKVVNLSTFSNRTSNIADIEIIFKPNTDLAIWNYIAREIVYNHPEA

MDMKFIKDHCVFATGYADIGYGMRNNPNHPKFKESEKDTVEKENVITLDDEEATSLSYLGVKAGDKFEMK

HQGVADKNWEISFEEFKKGLAPYTLEYTAKVAKGDDNESLEDFKKKLQELANLYIEKNRKVVSFWTMGFN

QHTRGSWVNEQAYMVHFLLGKQAKPGSGAFSLTGQPSACGTAREVGTFSHRLPADMVVANPKHREISEKI

WKVPAKTINPKPGSPYLNIMRDLEDGKIKFAWVQVNNPWQNTANANHWIAAAREMDNFIVVSDCYPGISA

KVADLILPSAMIYEKWGAYGNAERRTQHWKQQVLPVGAAMSDTWQILEFAKRFKLKEVWKEQKVDNKLTL

PSVLEEAKAMGYSEDDTLFDVLFANKEAKSFNPNDAIAKGFDNTDVKGDERKIQGSDGKEFAGYGFFVQK

YLWEEYRKFGLGHGHDLADFDTYHKVRGLRWPVVNGKETQWRFNTKFDYYAKKAAPNSDFAFYGDFNKML

TNGDLIAPKDEKEHSIKNKAKIFFRPFMKAPERPSKEYPFWLATGRVLEHWHSGTMTMRVPELYRAVPEA

LCYMSEKDGEKLGLNQGDLVWVESRRGKVKARVDMRGRNKPPVGLVYVPWFDENVYINKVTLDATCPLSK

QTDFKKCAVKIYKA

>ABV52329.1 thiol peroxidase [Campylobacter jejuni subsp. jejuni 81116]

MSTVNFKGNPVKLKGNSVEVGADAPKVNLKAKDLSVIEIGAAGKTQIILSVPSLDTPVCATEAREFNKKV

ASYNGAEVIVVSMDLPFAMGRFCSTEGIENLSVASDFVAKEFGEKYGVLINEGALEGLLARAVFVIKEGK

VAYKELVNEITEMPDIAKLDAFFGGSSCCGGCGCH

>ABV52328.1 major antigenic peptide PEB2 [Campylobacter jejuni subsp. jejuni 81116]

MKKILILSLVAASFLNAEILVYGPGGPAPVLKELALKFEEKTKEKVIVTAGPTPAWIDKAKENADLIFSG

NTSMMDDFAKKFPSLSLENLSVLNVRPSGIIVRPNNPKNIKNFEDILKDGVNVMVVDGAGQVGLYEDMAL

KSAKRENLVKLRKNIKIYAKNSKAAVDEWNNNPNIDALIIWSHWAKALGDDKALFIKDKNAVIYRAAEIA

PTKKGLENKKALEFVDFIKSKEAQKVWKKYTWKEVK

>ABV52327.1 putative ATP-dependent DNA helicase [Campylobacter jejuni subsp. jejuni 81116]

MPLSKLNNEQYLAATADFGRNLVIASAGTGKTSTIVARISYLLSKGVAPQKIMLLTFTNKASKEMIGRLG

KFFDKNITSKILAGTFHSTAYTLLRNADKNIALKQASELKTLLKSVYEKRTFRHLSDIKPYQSSYLYDLY

SLFQNKAHNQDFYTWFCQNYEDQSIYAEIYEDILKEYDNEKKRFNYVDFNDLLINLKELLKEEKYEFDEI

LVDEYQDTNTLQSSLIEAFHSKSLFCVGDYDQSIYAFNGADINIIGGFKDRFKDAKIFSLNKNYRSSRSI

LALANKVILNNERLYPKELIVTRNDEFKAPSLLTFEELFDQYQNIAKMILTSGVSLEEIAVIFRNNSSAD

GVEVALREQGIASVRKGSGSFFESLEVKAFSSMLALVVNPKDIMAFIHLVQYTKGVGGVLAKEIFDALLK

LGHGNLIKGFLDPDKNVNLQNHQKRNYQLGLFADLEELASETRFKFESEFDAHPILRLSKINDLCARNLE

KIYLFLKKAMEIKHSLTLVNLICENSFYREICEELATKRATNKAGQVDLLRKSENLEKIETKFNVLKELT

KNYSDIYKYYNFLTLGASEMSSGKGVNLLSVHASKGLEFDLVFVIDLAQGRFPNQKLMGMGGSLEEERRL

FYVAVTRAKNILYLSYAKYDKNKKTSFAPSRFLIEAGLCKGELTID

>ABV52326.1 hypothetical protein C8J\_0727 [Campylobacter jejuni subsp. jejuni 81116]

MNLKIFSIIVSILIAVIVILGGTYYYLFEYSKPKNYTLNTNTYTEQKSYTNNYDNSYSPSIQTNNSSSDI

NINNNTIQKQETNLLDENQSLNNDTFNTSISENNQSLNNDTNTSNNINTNENKQILDTDKEKLKQENKQA

KIEALKKEISKQQKILERERAVKKELQSNKSNKNKYLNTAREYLSIGKNSRLEPELSTENMKVYILDGKF

LSQYRINLLKDMLSVIQDNAKDYYLSIFVKMLPKGEMKLTIYNKEIIFSDMKKAYKYISLDRLSPYLNNP

KELNEHVAREEILERLKLQIKKDGKGSDFSKHIKSLKTGLNTAQYFFPFCEIIEISSIK

>ABV52325.1 valyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MYDKNLEKEYYQICEERGYFEIDGNKTIQEKDKNFCIMMPPPNVTGVLHIGHALTFTLQDIMTRYKRMDG

YKVLYQPGLDHAGIATQNVVEKQLLAQGIKKEELGREKFIEKVWEWKEQSGGKILDQMRTLGITPAWSRL

RFTMDEGLVNAVKKAFVELYDKRLIVRGNYMINWCTHDGALSDIEVEYKENKGKLYHIKYFLKDSDEFLV

VATTRPETFFGDTAVMVHPDDERYTKFVGKEVILPISKKAIKIIADEHVEKEFGTGVVKVTPAHDMNDYE

VGLRHNLDFISVFNEKGILNEHCLEFQGLERLEAREKIVAKLESLGFIEKIEEHNNQIGYCYRCNNIVEP

YISKQWFVKKEIAQESIEKVALGESKFYPNHWINSFNAWMKDLRDWCISRQLWWGHQIPVYYCECSHEWA

SQHTPKTCPKCQSQNFKQDEDVLDTWFSSGLWAMSTLGWGNENWGKDKIWSENDLEDFYPNSLLITGFDI

LFFWVARMMFQSTNALHQLPFKDIYLHALVKDEQGRKMSKSLGNVIDPNESIKEYSADILRFTLALLAIQ

GRDIKLSNDKLLQVRNFTNKIYNATNYLLLNESKFEDLENITLHSELAKYIYAKFQTCVKDVRENLDNYR

FNDAANTLYKFFWDDFCDWGIELSKAEKSSVKELGSIFKEALKLLNPFMPFISEYLYHKLSDTELKTSPS

IMISKYPKFKEQDKNIEKIFSLLIESIVGIRRAKSLIDLGNSKIEKAYIKFNDKKIKDEIKAYMNFIMML

AKCEQIEFSEEKLPKAICDVSENLEIFITLENVDLSGILTRLENQKNKLEKESFKLNSMLSNEKFIANAP

KEVVEQNKEALENLKIQLEKISVELQNLRG

>ABV52324.1 putative ABC transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MIKIKNLKKYYGKELVINDVSLEIKKGEIYAIVGHSGAGKSTLLRCINGLENYQEGSLKVFDQEIKDLSQ

KKSKELRVLRKDIGMIFQNFALMERKNVFENVAMPLRTHYTQCKFHAKLFNKEYMSEKEIAQKVNSLLEI

VGLDHKNKSYPRELSGGQKQRVAIARALALNPKILLSDEATSALDPNTTKNILELISKINAEFGITVVLV

THEMDVVKDIAQKALLLEHGQIIGSGAIDELFLRPNAKMKEFLGESDFLPEHGLNIKLYFPKEVAQNSVI

THMARTLNIDFNIVWGKIEKLNGKALGNLVININEKDKDKVLDYIEKSGVLWEVAS

>ABV52323.1 putative ABC transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MGGGIMNEENISIISAFFSRISQFFNEFSWQDIKEVSLSSITSFSENYENILKPALNETIYMSLMAVLFG

FLLAIIPGILLAIWDKNGIKENKIAYSILDFITNILRAFPFLILIVVLLPLSKIIVGTSIGTNAAIVPLA

IGIAPYLAKMLESAFKEIDKGIIEAAKSYGASNIQIIFKVIFSEALPAIISGITLTLIFTIGFSALAGTV

GGGGLGDVAIRYGYERFNKEVMIQTVVILLILVQLVQILGNLFYTWAKNSKTTYIIATLLILLGISIVIN

INNDENFFWQVIVFILFLGSLLYKGFEK

>ABV52322.1 putative ABC transport system substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKIKSLFIVSILTLSLNANALETITVAATPVPHAEILEQVKPDLEKQGYKLEIKEFTDYVLPNLAVDNGE

ADANFFQHTPYLEEFNKNKGTKLIKVAAIHIEPMAVYSKKYKSLDDIKEGVKIAIPNDPTNESRALDIIA

KKGLVKFKDKALKTPLDIIDNPKKIKFVELKPAQLPRALDDVDFAVINSNYALSANLNPAKDSVFIEDKE

SPYANILVVRVGHENDPKIKALTQALQSDKIKQFIIEKYNGSVLPAF

>ABV52321.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MNLFKIIILACILNLSSLFAQNITIGATPNPFGSLLELMKDDFKNKGYELKIVEFSDYILPNRALEEKEL

DANLYQHKPFLEEYNLKKGSNLIATTPVLIAPVGVYSKKIKNLENLKEGARVAIPNDATNESRALELLEK

AKLIELNKNTLKTPLDINKNPKKLKFIELKAAQLPRALDDVDIAIINSNFALGAGLNPSKDTIFREDKNS

PYVNYVVVRSEDKNSEKTKVIDEILRSDKFKAIINEHYKDILIPAF

>ABV52320.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MNIKKIFLSVLFTISLSFGADKTIIIGATPTPYAEILNFSKPLFQEKGWKLIVKEFNDYNIPNIALNEKD

LDANLYQHKPFLDDFNTHKGTNLSSLGAIVLVPMAIYSNSIKDIKDIPNGAKIAIPNDATNESRALDLLA

KANLIEFKSQSTLKTPIDISKNPKKLKFIELKAAQLPRALNDTDLAVITTNYALGAGLNPLKDGIFMEDK

DSLYAIVLATIKGEETSQKSLVIKEILTSDKIKNFIIEKYKGSVIPTF

>ABV52319.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKIIFLTFFIVINYIQAASLEEIKTALAKEFRNNFPKIIISQIDLKITSLPKDFDQYEFLRIANGRFNQA

QGFLRAEFKTPQNIQKNVFFRYFIQANLEVLKSERTIKRGDKLGAFDYKSVLIDFDKVPLNALTLDDVDN

LVAKSNINKNAILRANMFKTTALIRRNDPIIGVLSEANVDVLIELVALQSANMGERIRAKNKEGKVMQGI

VVGKNRMIIQ

>ABV52318.1 putative decarboxylase [Campylobacter jejuni subsp. jejuni 81116]

MKVLLGISGSSSVNLGLKLLKNLENQCELYCILTQGAKLSFKAENEVNLEEICQENFKYTHFLDDKNLSL

SVASGSFGIEKTIIAPCSISSLAKIHAGFADTLLMRAAAVALKERKKLILGVREMPFSTLNLEHMLKLSQ

MGVIIAPPIIASYSKANNLEQMENFIVGKWLDLLGIKHNLYEKWQNF

>ABV52317.1 pantetheine-phosphate adenylyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MTCLYPGTFDPITNGHLDVIKRALKIFDEVIVAIAKSEHKKPCYDLEKRKELALLATQNLKNVKIIAFDN

LLVDLAKELKVNTIIRGLRAVSDFEYELQIGYANHALWEDMETIYLMPSLKHAFISSSIVRSIVAHGGDV

SSLVPKEILPFLKDQSCM

>ABV52316.1 dTMP kinase [Campylobacter jejuni subsp. jejuni 81116]

MYVVFEGIDCVGKSTQISLLKEIYKDAIFTLEPGGTELGKHLREILLNKTHPISKRAELLLFLADRAQHF

EEILKTNQNKLIISDRSFISGMAYAKDFENDLLFALNSFALENFFPQKIIFLKGDANLIQERLSQKELDS

IEKRGIEYFLSVQDKLEKVLHFLKEKISIEILTLDAKESKEKLHQQIKEFLQ

>ABV52315.1 histidyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MINALKGMKDLLDKDAYYYEKVIKTCEEVAKNYGFTFINTPHLELCTLFKRSVGESSDIVGKEMYEFIDK

GENHVCMRPEGTAGVVRAYIEKKLDKNTSVKRWFYHGSMFRYERPQKGRLREFHQFGVESFGNASVYEDA

SIILMLVEIFSRLDIKFKLLINSLGCLKCMPKYRENLIHFLDSKEGFCEDCLRRKNLNPIRVLDCKNEHC

QSLLNDAPLLNQNLCSSCQKDFEILQSVLKENGVDFEVDSKLVRGLDYYSKTAFEFISDEIGAKAAIAGG

GRYDRLIEYLDGKSGFGVGFAMGIERIIAILEQKEEKVQREGIYLCAMDEIYIQKLLHIATNLRKEHKVL

LSYEARKLAKHLENADKNNAEIFLCMGENEAQNESLFYKNLVKKEEKMIKISDLKKVL

>ABV52314.1 biosynthetic arginine decarboxylase [Campylobacter jejuni subsp. jejuni 81116]

MDYGIDIWGNENFIIKNGKVCINHEKKPAIIDIVKELRDDGYKGPLLLRFPHLIQKQIENIYGNFNKARK

EFGYKGGFNAVYPLKVNQYPGFVKNLVKLGKDYNYGLEAGSKAELLLAMAYNNEGAPITVNGFKDRELIN

IGFIAAEMGHNITLTIEGLNELEAIIDIAKERFKPKPNIGLRVRLHSAGVGIWAKSGGINSKFGLTSTEL

IEAVNLLKENKLLEQFTMIHFHLGSQITEIHPLKKALNEAGNIYTELRKMGAKNLKAINLGGGLAVEYSQ

FKNEKSRNYTLREYANDVVFILKNIAEQKKDLEPDIFIESGRFVAANHAVLIAPVLELFSQEYAENKLIL

KKQNPKLIDELYDLYKSIKPSNALEYLHDSIDHLESILTLFDLGYVDLQDRSNAEILTHLITKKAILLLG

DKQNPADLLAIQDEVQERYLVNFSLFQSIPDFWGLEQNFPIMPLDRLDEEPTRSASIWDITCDSDGEISY

SKDKPLFLHDVDVEKENYFLGFFLVGAYQEVLGMKHNLFTHPTEAIISINEKGYEVEGIIEAQSILDALE

DLDYDIHAIMDILNERISNSKLVNDKQKKHILGELYLFLNDNGYLKSIGV

>ABV52313.1 serine acetyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MNFWGIIKEDFSQPKAQDPAFNSCIELFFNYPGVWAVVNYRFAHFFYIRNFKRIARMISGISQFLTGVDL

HPGAELGRRVFIDHANGVVIGQTAIIEDDVLIYQGVTLGGTSLEKGAKRHPTIKKGVIIGSGAKVLGNIT

IGENAKIGSNAVVVKDVGANLTAVGIPAYIIEERKNKNIRAIDANCDDKLEKLEKKILELENLILKQPES

QK

>ABV52312.1 aspartate aminotransferase [Campylobacter jejuni subsp. jejuni 81116]

MLTKRSQVLEESITLAITALANELKAKGEDIISFSAGEPDFDTPQIIKNAAISAIEKGCGKYTAVAGIPE

VLKAIQIKFKKDNNLDYETSEIITNVGAKHSLFECIECLVEKDDEVIIPSPYWVSYPEMVKFAGGKPVFV

EGLEENGFKITAEQLKKAITAKTKVLMLNSPSNPVGSIYSKEELTQIAKVLEGTQITVLSDEMYEKLRYD

GFDFVAFASVSEDALKRTVTINGLSKCGAMPGWRFGYMASKNKALISAVKRLQGQSTSNICSITQHAAIP

ALNGECDKDIEKMRQAFEKRRNLALDILKQIPNISVYKPEGAFYLFVNIQKIEKDSMNFCQKLLEQEKVA

VVPGVGFGMDGYFRLSYATSDELIKKGLERIANFIKNYK

>ABV52311.1 hypothetical protein C8J\_0712 [Campylobacter jejuni subsp. jejuni 81116]

MKIIQWNRAEFSPKEVKINVLIDNEKGKEIQILLAKDSVMKEHKAPFAIHVQVLSGKIWFEVEKEKFELN

VLDMISLEANVAHSLGGLENSIIRLSLNKSDSVQRVNAVLKKP

>ABV52310.1 hypothetical protein C8J\_0711 [Campylobacter jejuni subsp. jejuni 81116]

MNLSFKTFDISNVQRSKAKKVQGKKYEIFLNENEQSLITPKVSFKEILRYYYLYPKNAIPSFKLPFFKPD

LSGFSTPHITWLGHSSLFISFKEYKILIDPVFNTHASPISFINKAFKNTPVYNVNDFNEIFAVIITHSHF

DHLDAKSIKALKEKARFFITPLKVGNYLKSYGVSEKKIIELDWWSGVEFGDLKIIATPAQHSSSRGDGKN

KTLWASFVMEFLSVDKRVFFSADGGYFTHFKKIGEYFGSFDLACLESGQFNIAWPYSHSFPDQILKEAKD

LNAKAVMPIHWGRFLVGTHAWNEVIKFLYENLDLPLITPKMGEAYEIGAKFKQDFWWKEG

>ABV52309.1 chaperone protein DnaK [Campylobacter jejuni subsp. jejuni 81116]

MSKVIGIDLGTTNSCVAVYERGESKVIPNKEGKNTTPSVVAFTDKGEVLVGDSAKRQAVTNPEKTIYSIK

RIMGLMINEDAAKEAKNRLPYHITERNGACAIEIAGKIYTPQEISAKVLMKLKEDAEAFLGESVVDAVIT

VPAYFNDAQRKATKEAGTIAGLNVLRIINEPTSAALAYGLDKKDSEKIVVYDLGGGTFDVTVLETGDNVV

EVLATGGNAFLGGDDFDNKLIDFLANEFKDETGIDLKNDVMALQRLKEAAENAKKELSSANETEINLPFI

TADASGPKHLVKKLTRAKFEGMIDSLVAETITKINEVVSDAGLKKDEIKEIVMVGGSTRVPLVQEEVKKA

FNKDLNKSVNPDEVVAIGAAIQGAVIKGDVKDVLLLDVTPLSLGIETLGGVMTKIIEKGTTIPTKKEQVF

STAEDNQSAVTINVLQGEREFSRDNKSLGNFNLEGIPPAPRGMPQIEVTFDIDANGILTVSAKDKATGKA

QEIKITGSSGLSEEEINNMVKDAELHKEEDKKRKEAVDARNAADSLAHQVEKSLSELGEKVAAADKENIQ

KALDDLRETLKNQNASKEEIESKMKALSEVSHKLAENMYKKDEPNTANDKKKKDDDVIDAEVE

>ABV52308.1 heat shock protein grpE [Campylobacter jejuni subsp. jejuni 81116]

MSEQKQEFENENAENSEHLQDENLQNIEDVEQNRLQKDYDELKDKYMRANAEFENIKKRMEKEKLSAMAY

ANESFAKDLLDVLDALEAAINVECHDEISLKIKEGVQNTLDLFLKKLEKHGVALIKEEKEFDPNLHEAMF

HVDSQNHQSGEVVTVLQKGYKIADRVIRPTKVSVAK

>ABV52307.1 heat-inducible transcription repressor HrcA [Campylobacter jejuni subsp. jejuni 81116]

MKSRDKKDLILDSIIQTYLLDNVPIGSNELNLNLCIPASTIRVYLKRLSDEGLITQLHISSGRIPTILTM

QNYWQSFWKKEQDQDINIKSENFLKELSKEFEIYCLVYGGRSLVLKEVLDLNAKFIVLDFKEEELVLKYE

KEAWNFLQSLIGLDLFSIEKIALRVHFMDLVEKIASLRQNLICYRSNEERAYQIYQNDEFVKLLDCGVHR

YFKESLEFEPLFKEGFMGLKVDAQFLGEDVNIILAGSVYTDYKKILQYIKEAA

>ABV52306.1 hypothetical protein C8J\_0707 [Campylobacter jejuni subsp. jejuni 81116]

MDFIKFLNHFQPISKSSQQASVYKSFKLNLKPKILNEKDENSSSFQDQKTDVAQTMLQRLEDEKVFNQKV

SDKVKKAERGMTTIYFRDPITNNLVRSALSSTAINKMGIEFDKEDMTKRLDGSYILNGKAENFVAGWYAD

IAYTRAYVASDRNNDGYLEDYELEDTKSGFVAQETNLGLFVQSYTQLNGSVDTLFGFEKDFREMRPDDTK

DTDYAGRTIGLELDKMIRKDGDFDGELSFSETGMQAVKTKAPNSGWTESVGILTLTKFDQTNTMEIKDIL

DKLGKGVKYDDLSEDEKSLLKMQLSDKIFDEVEDKETGNKKLVFNLDKFKIFYEGFVDLFKQRSVKMLGL

KPEDATKLNYDNLGEIVNEMKQTYFDTNSTSYGKIADLIKIWA

>ABV52305.1 hypothetical protein C8J\_0706 [Campylobacter jejuni subsp. jejuni 81116]

MRKILVVLVLLQVFSHAEELNNNKIRELIESSPEANEPQNKNLKNTLKNQKSPVNFKEQNTTNITNSQTD

QNEAKVFVREYVLHIDNKDLTFKKLRISEKEIQDAIAEYRNQELSLQNLKDITNIIAYYCQVSGYPSATA

YIPPQDLSSNKVQINIAFGTLGKVIIKNNSGVRDYALESKLNKNLKGKVITTKNVENEIYKINEIYGIQT

NANLQSGDGYGESDVIIEVNKGDSATLTLYSNNYGTKETGRFRAGMSQSLNNIARQGDNLNFYLQDSDEN

QIDYGINYSTFIGNLKITPFATQGHYVLGGIYRNLGFYGDSMNVGVNFSYPVFLYTEYSLYLVSGFTHKK

IKDYYLDGLVSNEKASNSVNLGIEGTYKGLENNVLSYTLNFTYGNVENDGDSSGFNGVNLGNFGKMNLNL

SNEYQFQERLTHIFQLNYQKVIGGAVLDSSESVSLGGPYGVRAYLEGEGSADNVVSGTLGIRFQTPLEGL

YLTPFYDIGYSWYENKEYQSENHYFMDAMGMQILYTRSANFYVKMDAARAVHRFKHDGEHRARVYVSLGK

YF

>ABV52304.1 hypothetical protein C8J\_0705 [Campylobacter jejuni subsp. jejuni 81116]

MKKMSKHIVLSFAVSSLLFSQAYALPQGGKFTHGTSGTIHTSGNTVTITGKGQNHVIQWGGGFNIGQNES

VNFNGKNQNYLNIAYQKDASKIDGALNGGNNNIFLVNPMGVLIGKTGTITAGKFVASTTPLSDDNVKTFL

EKGASFSPAFDVSKQGNIINLGKINADNIVLIGNKVEIGVGAELAGQDGQTNAKTAHLIGNYVYVSVGKD

KENKNTIKIDKDGFKGTAIVEGFMQRDMTSFANDKYQFGDFGTILKSSCNGKESQNFYKAITIGGWENDK

NIQEWILFSNGWNKDELNGIFKDDLTTVRLVSDIDFGYKNAVDPVGASKYAFSGIFDGGNYTLKNILINA

QNTDKGWNTGIFGKVEGKDGNNKAKIYNLNVDGLKFSGKTNSGGAFVGQSSNADFSNIHLKNIGDLIFFD

PNSKNETSGFLYGGGFVGYAKSGSSFNRISLDNFSKIALQPEGKFSSAYIDIYLGGFAGYSEGSNFSNIL

LNNIGGVTILGSETGGNIFAGGFVGYAGDKSYFSQIDLKNIGSVQADGKTFVKHAGAGGFAGAINGTNSF

EKISLINFGDIIAKRGYVWVVNGNFKVGSGGFIGLLNPLDDKILYVDFKNILLNFDQKMQIYAKAGDGAS

SYFPDLNNWEYNFSGGFFGGLFTSKVGRANFNNIQLKFGQDVSIIAQKFRSNSNEKYQGLFYGYSVKNWN

DGIMKTDNVAIYYEKNYNTNQYNWYYQDIKDGFFGSAINDYAYKDGRSYEFYDYNVMKDMEINKQIIAIL

EKDGVVSKDYNNGYVSYYDGNAKITPEVPDFKDPVLSQNDFDPKLLQRILDDLMNGKYTYDFDTKTWTYT

DSKGVVGKDEASEITQSLNFLNAFKDTGVEQEFINLWKNSQDQNYKNYANLYEKWTQKKTAMDKIKTGEG

YFASFKEELQKYQEALAQLDKENKNYEKIKESGLVSDETLKVMYEKLLEQKEALEKQFADLSGNEGFHYK

LENEILNSQGFAINGSDVDGKAYIGNFNFKGKLASLPEKPNISIYEPDKQGGEDPANLLYCRLKFLKRL

>ABV52303.1 hypothetical protein C8J\_0704 [Campylobacter jejuni subsp. jejuni 81116]

MGVENIYTLPLNGVPYISGSVAFDGEAKDNKLILESNTKIDLHNSQYFSDEEGKDIYDKRITRLMGAFGI

NSNLQNNKVLIDSANIVLHGPDGEYTTRSTFEILGALADVNNLKKYNISKNSVIIKNLNLDLMVNSQNKI

TFYDAVLFGEIYGGRTLQGNAEKNSIEVYHFNSLDHLNKNIKTHASLNLYGGYSNDGEANGNKIVFRLKK

PLKISDNFYGKNYYNLYGGFATEGANFNVIDIQNDLTYEKVPQNYSDKFTVYAARTLSGKANNNILSIKD

SVISLPLYAFITSETTLDGIDYIADESNNNEVNFENIKSSKNLSLMINAKNVSNNKINYNLIQSLTEASS

LGKGSKIILKATQNANNNLIKLKDCSSAAVESSCIIKADKESAFNKIIINNTAFSTASDKRQGYVGLIAG

VSANSHDNIMELVNLNIDEYKNQDAIFLAPSGTSDISNFKSYNNTLYLGGELNFFKDVNIDLLSGSVFHE

VNKKGKIITQILPHQEDFSKNNRLIIDTQDVKSEVVNNFENFTFILPNKIKNPILTIEKLINLPANGSME

ILTKNKPTKGKYILIQSDVGIYDGDNRLLNQQELENLLEKMKNNKNKFNYNKIEKLAKSTLKNVNFSFEV

SDDAKIIYINIL

>ABV52302.1 hypothetical protein C8J\_0703 [Campylobacter jejuni subsp. jejuni 81116]

MIFKQKFLKKINGKNFYASKSKYPILNLTMIYNNPKSGNKNLCKLEILTPDTSKEEIITAFSTLGTVSSD

TQAVPSSFMPFIVTAYAQNTNATNNKLILENGELSSVYFCKPSIGDCGVPNNSQKGDRFKYLITAAFTDR

GGGFNNQTILQRKLLYQ

>ABV52301.1 hypothetical protein C8J\_0702 [Campylobacter jejuni subsp. jejuni 81116]

MKKYFNIFKIFTNKTNAKFGLGVCSVVLSSSVCFAAVQATSKDGKIFYISEHSFKDNQVYDFQAEIFKKN

>ABV52300.1 CjaC [Campylobacter jejuni subsp. jejuni 81116]

MKKILSIALVALVGLFLGACSDSKNKESNASVELKVGTAPNYKPFNYKENSKLTGFDTDLVEEIAKKNGI

KIVWVETNFDGLIPALKAGKIDMIASAMSATDERRQSVDFTKPYYMSKNLYLKLKNNDSLQTKNDLEGKK

IGVQLGTLQENTAKAIKNAQVQSNKDLNIAVLALKNNKIDAIVADQDTAKGFLAENPELVSFYQETDGGE

GFSFAFDKNKQKDIIEIFNKGIDEAKTDGFYDTLIKKYELE

>ABV52299.1 HAD-superfamily subfamily IB hydrolase [Campylobacter jejuni subsp. jejuni 81116]

MKLVLFDLDDTLIQGDSAKLWLKFCVEKGFLPQEYLEKIVFYQKQYQEKKLDMDEFMTFFLQSVKGKNED

RISSLVDEFIKIYIKPYEKAKELIIKYQDQRCIIISATAEFLVRKIASFLGVRESIAIKCERVGDKFSGK

AYGVYSFKEGKVLRLKEYLGKDYEKWMKDSYFFSDSINDLPLLESVSKAFVCNGDEKILKIAKERKYEIL

TF

>ABV52298.1 ABC transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MAYLKIKNFKKAYGDKIIFEDINFSAKKGEFITLLGPSGCGKSTLLRCIAGLSQINGGKISLNDKDLTKL

SPQKRNIGMVFQNYALFPNLNVFENIAFGLKIKKMDKKDIEKRVKKMLKLVELEEYAKTYPHKLSGGQMQ

RVALARSLVTKPDLLLLDEPLSALDAKIRKHLRVQIKEIQKELELTTIFVTHDQEEALELSDRIILMNKG

KIIQNSNANNLYLLPESHFVASFIGNYNILSPKELDNLGLKHDFKKDIALRPETIEISNEGLEAKIKEKS

LLGNIIRYRVRVQEIEFKVDTLNFSTHSTYEAGDKIALKFNLSLAKELK

>ABV52297.1 ABC transporter, permease protein [Campylobacter jejuni subsp. jejuni 81116]

MNENLSLKAKIYHYAVLFLVFLFLALPLMATFLYSISTSWGVSVLPDDLTLKWYQELFHDERFLLALWHS

LLVCVGSILLSVILVFPLVFVLNYYFLKLKAFVNILIIMPFAVPPIVSCVGLLQLYADNIGGTAWILIFT

YFTIALPFIYRALDNAISNVNLNELIASNAMLGGSLMGAIFKLVLPNLRNGILVAVFLSFSFLIGEFLYA

NILVGSAYETLQVYLYNIKNQSGHYSSALVIVYFVLIFITTFIASLIKE

>ABV52296.1 putative ABC transport system permease [Campylobacter jejuni subsp. jejuni 81116]

MKEKFLAFLSILPFFIVFTFFMIAPLIWIVFNAFYVEEDEIYSLANFIHIFESKFYLQSIINSLQISFIS

SIFGLLIGLLASYSLFVLAPSKICKFLFSLNTMISNFSGVPLAFAFIIVLGSNGVVNVFLKNLGIEPFVS

VYANFGVNIVYVYFQIPLAILLLLPAFKSLENSHLNACKMLGGGNFLYWLKIALPLLAPALFGVFVILFA

NAFGAYATIYALSSGNFNVAPVRIAALIAGDINLDPYMASALSIIITIIMLVVTFIANFLSKKYHFKVL

>ABV52295.1 hypothetical protein C8J\_0696 [Campylobacter jejuni subsp. jejuni 81116]

MSKVILVVLDGLNCKSASINMGYLNALCKENLGKFYSLECELPSMSRPLYECLLTGVKPVLSEIINNKLS

FSKQTSIFDLCKEQGLKAGGAAYHWVFELYNKKEFIPSLHRHIEDENLTLPYGHFYYEDDYLDSHLFADG

EHLRNKYNLDFTLMHSMNIDDAGHKFGSHSIEYANKTKKVDILISEYLPTWLEQGINVIITSDHGMTEGK

SHGGLSEDEILVPFFTFGSAFSYENAKIKQDEICGSICEILGLKHDKRYNDEILKAKK

>ABV52294.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKVILTSAMLCSVLFGVQEYEANLAGHIIIDSKSTVKPPKDAPDFFKTYGKFANITREEKIGTFKSKGN

RETDFYLPFKNQPIQGHSGIKYIPKKDVFWVISDNGLGKKYNSYDAMLYAHEFKFDFKNSKYELLKTVFF

KDSDKKYPYPITTETTKERYLSGVDFDTESIQVINDEFYIGDEFGPYLLHFDKNGNLKEVFDVYVEGKKL

ISPDNPSLKFSDKPDGENEKFNIKRSKGFEAMASSKDGSKLYLLLEGSIYNNNAYENEKGKEYLRIIEFD

VKNKKFTGKTYKYFLEDKSHSIGDFNMIDDKYGIIIERDQKEGTKDKVCKEGEDTKHCFNNVAQFKRNYK

VKLDDKTHEAQKISYIDLLNIKDRNKISKKPLVNDKFVFPFETIEGVDIVDDSHIVIENDNNFPYSSSRE

PNKTDDNEFILLEVKDFLKSK

>ABV52293.1 ABC transporter, periplasmic substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MSKKFFLSLGLVALLFSNSQAIDENLIKAAQAEGRVNSLAMPDTWANWKDTWADLKNLYGIEHSDTDMSS

AQEIAKFKAEKKNASGDIGDVGASFGEIAVKQGVAQPFKTSYWDQIPTWAKDKDGNWLLAYTGTIAFIVN

KDVVKDIPKTWQDLLKGNYKITVGDVSVAAQAVSAVLAANYALGGDEKDLSPALAFFNTLAKQGRLVNND

VSIANLEKGEVEVGLVWDFNGLGYRDKVGKDRYEVLIPADGSVISGYTTIINKYAKHPNAAKLAREFILS

DKGQINLAKGYARPIRIDHITLPDDIKAKLLPSEQYKNARAIKDQKAWEKSAKELPQLWQEKVIVDMK

>ABV52292.1 magnesium and cobalt transport protein [Campylobacter jejuni subsp. jejuni 81116]

MLYIYIKTQNALVQRINFNLDSQELPQNILWIDLLHPSVAEIAFISSEFNLEFPTKEEREEIELSAKYWE

DNATITINAHFLVRDLKSDEEDRNLIKLRTEIVTFATAKNILFTIRYNEFSTFEEIQARILASPKNFEDG

FDIIDKMFEVRVEKDADLLEWIDKEARRLRTSVLEKKDEYSYDEMLKDISSLQELNMRVRDSLFDKRRAM

TSLLKSDKIDKDIKQNLTIVLKDLNSLVEFSVSQLNILDNIQTILASQINIEQNKIIKIFTVATVAMMPP

TLIGTVYGMNFKFMPELELHYAYPIVLGVMVISIILPLVVFKKKGWL

>ABV52291.1 molybdopterin biosynthesis protein [Campylobacter jejuni subsp. jejuni 81116]

MDTINIGVLTLSDRASSGIYEDKATAEIERVLNSYIKNDIIYHKELIPDDYDLIIKKLLYLADEKKCDLI

VTSGGTGPALRDVTPEATEAVCDKMMPGFGELMRLESLKYVPTAILSRQSAGIRNKSFIINLPGNPKAIK

ECLEPVFPAIPYCIDLIEGAYIEANDEVIKVFRPKKKCQN

>ABV52290.1 hypothetical protein C8J\_0691 [Campylobacter jejuni subsp. jejuni 81116]

MFFKKKISQKQKEKPKIPINDVILDDRLCKFKNKVQKISKDEASASLLARQLSRLVRANKF

>ABV52289.1 putative integral membrane zinc-metalloprotease [Campylobacter jejuni subsp. jejuni 81116]

MTLIAILCLYTALLSWISYAQIRFLEREKDKQAQILSEKDYQNAADIAIENEKFKLFSNFYNLIINIAWI

GFGFLYLKELLISSNTRFENTLFLLSFLIITSILNLPLSIYKSFIKDKAHGFSNMTVKLFIKDTMKSLIL

TLIFGFLILYALLFCYDFFGTFWWIAAFIFAFCIIVIINLIYPTLIAPIFNKMKKLDDENLLKKISSLMK

QCGFSANGVYVIDASKRDKRLNAYFGGLFKSKRVVLFDTLLKALNERELLAVLGHELGHFVHKDIIKALF

NGAITMFLLFFVFANLPEFVYLESHLEGVNGGVFALLFILANIFSFLISPMLNALSRKNEFAADQHGAKV

TSKEDMKNALIALARENKAFIKTSKIYTFFYLSHPSISDRIKALS

>ABV52288.1 putative DNA methylase [Campylobacter jejuni subsp. jejuni 81116]

MTIKNALMEAKSSLKGYENEAVFILCEYLKKDKAWLFLNQDIQIDHEPYFELIKRFKSGEPFEYIFEKVD

FWGLEFKIKKGVLIPRYDSEILLFQILNLCKKNTFNGILEIGFGSGILSIVLAKELGLKITACDINPKAL

ELALENAKLHKVDHLIDFKLCNFKQIKENYDFIFSNPPYIKNSYPIDIWVQKEPKEALFGGEKGYEILEE

IIHFSLDKKVKFLACEFGYDQKEILEKILYQNNFIVDFFKDEQDYNRAFIAKFTNMRYDKK

>ABV52287.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKAVNLFLLASIIGVELILGIVVAPTIFFPQNLIGEGVLSHFQSGLMMTQIFIKMGYLLIFVSVVNFLYE

IYSLIKDEMKFQIKFSKFMLSLLILILSLIFVFYFTNTIIELQNLGENATKTQEFISIHNASEVVIKIIL

IMQVFLYFLSFKIAKK

>ABV52286.1 flagellin [Campylobacter jejuni subsp. jejuni 81116]

MMISDATMMQQNYYLNNAQKASDKALENIAAVRAISGVDSANLAIADSLRSQSSTIDQGVANAYDAIGVL

QIADASLTNISQSADRLNELSVKMNNAALNDSQKGMLRTEATRIQESINDSFNNATYNGKNVFQTMNFVV

GSGTETTNLNPLATGGLSIDNQDSITNFMDQLGSLRSEIGSGINAITSNINASVQNSINSKAAENNLLNN

DMAKNVNDFNANYLKENAAAFVAAQSNMQLQSKIANLLQ

>ABV52285.1 hypothetical protein C8J\_0686 [Campylobacter jejuni subsp. jejuni 81116]

MTLEQILEKTKNVRLVAASKYVDASTIEKLFDQGIVEFGENQVQALAQKKENLDEKKLDIKWHFIGTLQS

NKINLLIKQKPILWHSCNGIKIAKAMDKRLDYKLNTLLEINSANENSKSGLDPNQAVEEYLQIQEECSNL

NLCGVMSIGSHSQDKESIIKSFETTFKIYEILQKHGAKICSMGMSNDFEIAIKCGSNLVRLGSILFKNLK

>ABV52284.1 DNA polymerase III, alpha chain [Campylobacter jejuni subsp. jejuni 81116]

MSQFTHLHLHTEYSLLDGANKLKELALTLKEQGATSVAMTDHGNMFGAIDFYQTMKAQGLKPIIGMEAYL

HNHDELDDKSSRQRFHLCLYAKNEIGYQNLMYLSSQSYIKGLYYYPRINKKLLEDHSEGLICSSACLQGE

VNWHLNTYSERNVRFGAKGYEAAKEAALWYKKVFKDDFYFEIMRHGIGDQRMIDDDIIRLSKELNIKIIA

TNDTHYTFKERAAAHEVFMCIAMGKKLNDPDRMRHSVHEFYVKSPEQMSELFADIPEAIENTQEIAQKCN

LELNLGNPTPPNFKFTREYAKDHNITLPEETKEFSFDNDDIVFEELCKKGLEERLKFIDESKHEEYKQRL

EVEINIIKNMKFSGYMLIVHDFIKVAKDKGIPVGPGRGSAAGSLVSYCLRITDLDPIPYSLLFERFLNPE

RVSMPDIDVDFCQDRRAEVIDYVIDKYGADKVAQVITFGKLLAKGVIRDVARVCDMSIQDADELAKLVPE

ELKITLDAAYEKEPKIKEFIDRHPKGPEVWEYARALEGLNRNAGMHAAGVVISNESLWKKTPLFRQSKND

ERHLVTQYSKDHLEDVDLIKFDFLGLKTLTVINNAIKLIKKRYNKDIIWETIDVNDSKVYKTIQSGNTLG

IFQIESGGMQSLNARLKPERFEDIIAVLALYRPGPMESGMLDDFIDRKHGLKSIEYPFDSLEKVLEPTYG

VIVYQEQVMQIVQIIGGFSLGGADVVRRAMGKKDPEKMKKLKTDFADGAEKQGYDRAKAEDLWELIVKFA

GYGFNKSHSAAYALITFQTAYLKTYYPSEFMAALLTSEENNVDKIAVYIDEMKKMNIKLLPPSINKAIRE

FSALEQDGKDAIIYGLGAIKSVGIPAVENLLEARQDGEFKDINDFLGKIDPTKINRRTLESLIKAGAFDE

FGFTRKALFDNMENLSEASRKMAEVRKNAASSLFGEEELTSGVQVNFTPKNEEFEVMEKLGYEKEILGIY

VSGHPLDRFYEQINAIDYVKSLDFESLKNNGEILSIGKIEDFKSMMSKNNKRYGRIEILDYYSSFDATVF

ESNVEEIENIIKDENLKNNAYGFVLGFKAEGGEKPSFFLKAIKDLQSLEDGEIKAIKKFGAKKDFKNKEE

NHFTAEPKEFEKNIIELDLTRLNRELIYEIHEIARNAHNPNEKNNKKLVLKVISAGSCLLYHTDFIISDS

IVEEISNKYA

>ABV52283.1 hypothetical protein C8J\_0684 [Campylobacter jejuni subsp. jejuni 81116]

MKLYGIKNCNSVKKAMDALTQKGIVFDFMDIKKINQDILYTWLKQKSFEELINTAGLTSKKLGLNKEKVK

NLNEKELEKIVLENPSCIKRPIIEYEQNIYIGKEYEKML

>ABV52282.1 3-deoxy-7-phosphoheptulonate synthase [Campylobacter jejuni subsp. jejuni 81116]

MWTKNSWKNYPIKQQPIYPDQEEMNRVLARLEKLPPLVFAGEVRNLQKSLARVCKKEAFLLQGGDCAESF

ENFGAVNIRDMFKILLQMAIVLTFAGGCPVVKIGRIAGQFAKPRSSDFEELNGISLPSYRGDIINGFEFS

EQARIPDPHRMLEAYYQSATTLNLLRGFAKGGLADLHEVHRWNLGFLKKSELHKQYTDISEKISQALAFM

EACGINTSNTPSLREVSVYTSHEALLLPYEEALTRVDSLSGEIYDCSAHMLWIGERTRALDEAHVHFLRG

VKNPLGVKIGPSASADDIIALANVLNPNNEEGRLNIIIRMGADKIINNLPKIFSKLKSEGLNLVYSIDPM

HGNTVKAGNFKTREFDKIMQEVRSFFEIAISEGVYPGGVHLEMTGKDVTECTGGASNVTAQSLEDRYETQ

CDPRLNADQALELAFLIADLVKKARK

>ABV52281.1 transthyretin-like periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MFSIKKTLLILASVPMFLSATEYQLSTHVLDITSGQPAPKVKVELYKLEANQQWKKVSEEFTEENGRIGD

LLPYEKAENRAFGIYKLKFFTKDYYTSHKINTFYPFVEVSFELSKDQKHYHVPITLSPFGYSTYRGS

>ABV52280.1 50S ribosomal protein L19 [Campylobacter jejuni subsp. jejuni 81116]

MKNKYIEQFEAKQIEGKNVPDFRAGDTLKLAIRIKEGDKTRIQNFEGICIARRGNGVSETFIVRKMGANN

VGVERIFPIYSESLESITVLRRGRVRRARLFYLRDRRGKAARIKELKK

>ABV52279.1 tRNA (guanine-N1)-methyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKFSFVSLFPNLMEFYFQDSILARAKEKKLFKLNFYNPRDFSKNSYHKVDDYKIGGGAGLLMQAEPMYEV

LRSIQEKKENPYFIFLNPSGKTFNQKDAKRLSKKEHIVFVCGRYEGIDERVLEIFANEVFSIGDFILTGG

ELPALVMCDAILRNVNGVLGNMESLEEESFENNLLEAPAFSKPFIFEKKNKKFYTPSEFLKGNHARIASL

KTTLASCKTKFFRPDLFLEHERKK

>ABV52278.1 putative 16S rRNA processing protein [Campylobacter jejuni subsp. jejuni 81116]

MSEKDFVQVAKLGKTVGLKGYVKLHNLSDFSSQFKKDATFFIKNTKEMLKIKHYNASNSTVLFENYEDIE

KAKELINLILFQSIEKSRQTCKLKKDEFFYFDILECEVFEEDKRLGKVIDILETGASYLFEIQSDEKWVE

KKYPKIFFIPYLDKFVKNIDIEKRQIFCTQDAFLILENS

>ABV52277.1 hypothetical protein C8J\_0678 [Campylobacter jejuni subsp. jejuni 81116]

MVENFLREYAKLIADYPEQIDTQKIELSENFFEIVLFAHKVDTGKLIGKNGKMINAIKTVISAYKSKDAS

SYRVTVKALE

>ABV52276.1 30S ribosomal protein S16 [Campylobacter jejuni subsp. jejuni 81116]

MTVIRLTRMGRTKRPFYRIVVTDSRKRRDGGWIESIGYYNPMVEPEVIKVDAERLAYWKSVGAKLSDKVA

SITSK

>ABV52275.1 signal recognition particle protein [Campylobacter jejuni subsp. jejuni 81116]

MFELVSESFKSAINKLRFVDDEKALKNALETLKKALLKADVHHKVTKELLTLIEEDVKQNGIGQKQFLNA

IKVNLENILSVNGKNQGFVFASKPPTVVLMAGLQGGGKTTSTIKLANYLKLRNKKVLVAACDLQRLAAVE

QLRQLCEANEIELFFIENEKDPIRVAKEALKKAESSMVDVLLVDTAGRLAIDEALMNELKAVKDVLNPDE

IFYVADAMSGQDGVKTAASFNEALNISGVILSKFDADTKGGVALGIAKQIGIPLRFIGVGEKVADLEVFI

PDRIVSRIMGEGDLATLAEKTAAIIDEKEAKKLNQKIKKGEFNFNDFLNQMESIKKLGSMKSLIGMIPGL

GGMANAVKDIDLDNSKEIIRIKAMISSMTPKERENPDLLNNARKRRIAEGAGLSQVEVNRFLKQFSNAAK

LAKRFSGKKGMESLTQMMSQARRQF

>ABV52274.1 RNA pseudouridylate synthase family protein [Campylobacter jejuni subsp. jejuni 81116]

MQEKAYKLLALQEKISNREAKDLIDKGCVFSHGKKVVVARALMSDKARFNVIKTKNPQIIFEDDKIIAIN

KPYAYVSEDLEKKFNAKLLNRLDKETSGVILLCKDEDFRKLCIEEFKKHRVYKSYIAVLDGVLAEEVEVN

EPIFTIKAKGGALSKVSKDGLSALSIITPIMMQSKKTLAKIVIQTGRTHQIRVHAKFIKHGVVGDEKYAK

ISSDRMYLHSYEIKIFDYYFKAELDNSFAKVGFEIKNLDF

>ABV52273.1 3-deoxy-D-manno-octulosonic-acid transferase [Campylobacter jejuni subsp. jejuni 81116]

MIFFYYFLTWTAFLFCAVFILLLSFLKSKYKTSLKSRFFLYKNLHQEKADVHFHACSYGEVRSIKTLVLK

FDSRITTITQTGFEYAKEFCKKVNYLAFENFLPFWFKPCKVLVIFEAEYWLMLVFMAHIYKTKIILLNAR

ISDKSYHSYQRFSFFYKKIFSYIDEVFAQSELDKVRLESLGAKNVKIFKNIKANLEIKNNKIYAKPKEKL

IIFASTHKDEEELLLDHFKLEENEKLIIAPRHPERFKEVENLLLNKGLEFEKFSSLKDENKKFAKKILLL

DALGELVNFYAISDVVVLGGSFIEGIGGHNPIEVAYFDNVLISGKFIHNQKALFEEVENVYFCENLKDLN

DKIHYLNLKVKISKKENLDLIIQTIQKGIDARKSL

>ABV52272.1 hypothetical protein C8J\_0673 [Campylobacter jejuni subsp. jejuni 81116]

MNKYLEQLVLLSKIDQEIDSYEPKIDSINRTLKDAELKIGKINTDLEKIDEEIKDIENQKVQNNAHISEF

SAKIKELSKKSGAVKTEKEANALKIEEDIAKEQLDAANDEIVRLDKILENKETYKKELEEEKIKQEQNIN

EIRVSIKSEMEVLEKDRMSVYDKKTKLVGEMNQKVLSFYEKIRKWAKNTAVVPVKKQACYGCFMKIYDKT

YLSVVKGEEIVTCPHCGRILYKEQEEQN

>ABV52271.1 hypothetical protein C8J\_0672 [Campylobacter jejuni subsp. jejuni 81116]

MKLSEIYNFLDQLSPFDIQESWDNSGILLGDRDSEISTVYLSLDIDENIIKEASENSLIITHHPLIFKGL

KDLYDKTYPRAFIKEMICKNISLISMHTNYDLSHLNTYFTEEILGFKISFKDEFLIYVENSMSFEALCDW

VKKKLNLQILRVSDCGKKDIKRIAICTGSGGDLISKVDADCFLSGDFKYHQALEALSNQISLIDLGHFES

ERYFSQCLAKDLKNLPLQAIITVSKNPFQYF

>ABV52270.1 glycyl-tRNA synthetase alpha chain [Campylobacter jejuni subsp. jejuni 81116]

MTFSQMILNLQNYWQEQGCAIMQPYDMPAGAGTFHPATFLRSLGKKPWAAAYVAPSRRPTDGRYGENPNR

LGAYYQFQVLIKPSPDNIQELYLKSLENLGFDLKSHDIRFVEDNWESPSLGAWGLGWEVWLDGMEVTQFT

YFQQVGGIAVDLVSAEITYGLERIAMYLQNVDNVYDIVWSEFNGEKIKYADVHKQSEYEFSKYNFEVSDV

KILNEQFENSYKECKNILEQGLALPAYDYCMLAAHTFNLLDARGAISVAQRQDYMLKIRELSKNCAEIYK

KNLNETE

>ABV52269.1 hypothetical protein C8J\_0670 [Campylobacter jejuni subsp. jejuni 81116]

MQTYLELEEFCKLVHLNEDVVKGMMANGALNFKEEEGKIYIEAHQGTFSVVPSSAKSQTAMVNSMTLAGE

SFVEKTIGTILNLHEKVLDAKDETLEALKNENKFLKDALYSMQELYDEDRKTIETLNNELKHAREEIEFL

KRKYKLMWSKTAEIFGAKTEPDLEMNKNLEKPIENMEQ

>ABV52268.1 phosphoribosylaminoimidazole carboxylase catalytic subunit [Campylobacter jejuni subsp. jejuni 81116]

MNFVSILMGSKSDYETMKEAAKTLESFGVKYELIISSAHRSPKRTKEYIANAEEKGAKVFIAAAGMAAHL

AGAVAAYTTKPVLGVPMPGSNLASMDSLFSTVQMPSGIPVGTLAIGKAGAINAAYLAMQILAIYDVDLAQ

KLKEDRLEKEKKLVSDSKEVEVLL

>ABV52267.1 putative protease [Campylobacter jejuni subsp. jejuni 81116]

MIIPEIVAPAGNFTKLKIALAYGADAVYAGVNNFSLRSRTAREFNYESFEEAIKYTHERGKKIYVTLNGF

HLSSQIEGLKRHILKLREMKPDAFIVASVGAMRLVKELAPEISLHVSTQANILNYLDAQVYKDMGAKRVV

IARELGLKDAKALKENCDIELEAFVHGSMCFAYSGRCLISSVQSGRMSNRGSCANDCRFNYELYAKNPEN

GTLFRLEEDENGTHVFNSKDLNLCSYIEKIMQENCISAFKIEGRTKSEYYVALTTRTYKMAIQDALEGKF

ESSKYEKEIATLKNRGFTDGYLVSRPLEKTDTQNHNTSIEEGSHQVHAISEDGSFFKCKGKIVLNTPYEI

LAPLGDVIQTCDNELGKIYQKEDRYFIEFKKLIAKNNKEFSEIHSGNEHEIQLPNKISALSFLRKEI

>ABV52266.1 hypothetical protein C8J\_0667 [Campylobacter jejuni subsp. jejuni 81116]

MTQEELDALMNGDVDLDSETEAEVKTEESNTEEDALMLEDVKIADYKPNPSVVWPPPPPNQEHKVVHQLD

DVTKDSELKATEMMDKLESINNFFADSESLLKEINKAIEKNIDIFSKLNEKFPNVESFSEALELNNQAKK

SSKQIVGNLQSGQDEVMMAMDAMQYQDIHRQKIERVINVMRALSRYMSSLFEGKIDDKKRVSSAVHIEGD

STADVVSNDDIEALIASLGQK

>ABV52265.1 glutamine synthetase, type I [Campylobacter jejuni subsp. jejuni 81116]

MGKFVNNIDDFFKFCKQNEVLFVDFRFTDMIGTWHHITYNLHAINEETFQTGIPFDGSSIHGWQPIEKSD

MILKPDAQSAFLDPFTADPTIIVFCDVYDIYKGQMYEKCPRSIAKKAMEHLKNSGIADTAYFGPENEFFV

FDSVKIVDTTHCSKYEVDTEEGEWNDDREFTDSYNTGHRPRNKGGYFPVQPIDSLVDIRSEMVQTLEKVG

LKTFVHHHEVAQGQAEIGVNFGTLVEAADNVQIYKYVVKMVAHLNGKTATFMPKPLYGDNGNGMHVHMSL

WKDGVNLFYDKDGYSGLSQTAINYIGGILKNARSVAAFTNPSSNSYKRIVPGFEAPCILTYSCQNRSASC

RVPYGIGKNSARIEIRFPDSTANPYLAFVSLLMAGLDGIKNKTIPVGPMDENLFDLTLDEIREKGIEQLP

HTLRGSLEALIRHNSYLKPVMSDIFIDDYQHLKFETQVWPVEARPTAYEFKTCYSC

>ABV52264.1 flagellar basal-body rod protein [Campylobacter jejuni subsp. jejuni 81116]

MMRSLHTAATGMVAQQTQIDVTSNNIANVNTAGFKKSRAEFADLMYQVMKYAGTSTSATTLSPSGIEVGV

GVRPTAVTKVFTEGNLKSTSTDGLDMAIAGNGFFQIQLPDGTIGYTRNGQFTKDNEGNIVNSDGYRLLPE

MTIPEGATAINVATDGTVSVMLPGEQQETQIGQVELVQFINPAGLHSMGDNLYLETGASGAPVAGIAGQD

GLGTIRHGFIELSNVQLVEEMTDLITGQRAYEAGSKAITTSDDMLGIVNQLKR

>ABV52263.1 putative flagellar basal-body rod protein [Campylobacter jejuni subsp. jejuni 81116]

MQNGYYQATGGMVTQFNKLDVITNNLANINTSGYKRDDVVIADFKRIFKETQDELPIENHTRDASRFVNT

TIDGIPQVSQEYTDFSLGSLKATNNPLDLAMTREDAFYLVQTKDGEVRLTKDGNFQLDDEGYLVNKQGYK

VLSSDYFNNPQNAGIRIPNGAVQISVDKNGSIEVDGAQNARLFVAQVDDIRALQKDGDNVYKIDDLTRIR

DLENSNAIRQGFSQGSNVNPVTEMVGLIEANRMVEMYQKVMTAHMDDLNQEAINKLAAVK

>ABV52262.1 cell division protein ftsZ [Campylobacter jejuni subsp. jejuni 81116]

MSEFLVEEMQHNKGAKIKVIGCGGGGGNMINHMVKMGLNDLDLIAANTDAQAISISLAKTKIQLGEKKTK

GLGAGMLPEVGAESARESFEEIKASLSQSDIVFIASGFGGGTGTGATPVIAQAAKEIGALTVSVVTMPFA

FEGKQRKKLAESGLLELKKESDSILVIQNEKLLSIIDKKAGIKDAFRLVDDILARAVKGMVSILLDNGDI

NVDFADVRTIMSHRGLALMGVGSASGENAIEEALSNAIESPLLDGMDIKGAKGVILHFKTSSNCSLFEIS

AAANSIQEIVDENAKIIFGSTTDDSMEDRVEVTIIATGFEDKDTVAKKSTEEAQASKKNPYLSLKKVSGG

YDEEIMAQIETPTFLRRQMD

>ABV52261.1 cell division protein ftsA [Campylobacter jejuni subsp. jejuni 81116]

MNILGIDLGSTQTCAIIAQKDEDGLKIIGFSKSKTNGVKKGAITNIELASKSIEEAVRSAEMMSGVHYDK

VVVSISGAYTKSVDSIGVVNIPNHEIGIKEIHRAVSTAKHTANLPSGYEIIHVLPYNFKVNDLEHVDDPL

GMSGNRLEVSTHIVISQESHIKNLKKAVELADLRVDNIVLSGYASAIACLDDSEKELGAVLIDMGGAICD

MVVHTGNSIRYNDCLQIGSINITQDLSMALHTPLKEAEKIKLNYAALSQQPNTLIQIPSMGDERKVNEVS

LDIISNVIYARAEETLMILAKILSDNRYANAIGGGVVLTGGMTKLAGIDELAPATFDNRSVRLATARKDL

ITGFSEIFNDPENTCAIGLCLYGAGYFTPYELDSNEKLRYKGEIENFNRQIKQDIVLQKDAESEIKSDFF

DENLQENDTIAIQEQLDFKEPKEKKPSVFSNIWHKIMNQF

>ABV52260.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MLTWMQHHKKYLVVTIWVSTIAFVGAGFLGWGAYDFNLNRSSSVATVGNEKIGFSEFDTRYRQILSYYNQ

ISNGALTPENAEQLGIKNIALSSLVEDKLLLNFAKDLGIGVNENEILQKLANTREFQDPTGDFNKTIYYE

LLNANNLTPKDYETQLANEVITDKLNQIFNIPSKDEELKMLASSYFMQDALSIAKIDYDKKNIKINEEDL

KKLWNEHKEDYKTKKIYEISTYFLSVSNEKIDDKELEKFYNQDENKLKYKDFAGKVMDFQSAKNEVAKDY

ALIQLKNVANAKFLDLKNGKDNFQKDQNISESDVYYPIDLLNKAKNGDVLRPAPYNNGYIIVKLNKVDPI

RNKTFEEAREEVLPMYLSEQARKNLEEKAKNSLVNFKGDDIGFVSRDSSRESVKLSDKILNDSEFAYFLM

NVFNTDQNSSYVIINDNKAILYKINKQKLDMNSDKFEQYKTMLEQNLRNLKANELKQELVDELKKIYPIK

IYYKGN

>ABV52259.1 S-adenosyl-methyltransferase MraW [Campylobacter jejuni subsp. jejuni 81116]

MEIPHIPVLLNEVQEIFKNLKTGYFLDCTLGFGGHSEALLKNHPDLKFIACDQDQQALEFSKKRLKDFHN

RITFIQSNFSEVLEKISYKEELRGILADIGVSSFQLDNNERGFSVNSDFLDMRMNQNSKISAYEIINTYT

KEQLTSIFKDYGELHDAHFIAEKICLERSKNPIKSAKELYQIIGKGKQNHRKISKATLAFQAIRIEVNQE

LKVLKDFLGHLENLKPKNCILAIISFHSLEDRIVKNFFKKWSKNCICDEKIMRCECGNNHSLGQIITKKA

ISASKEELLKNSRSSCAKMRAFYFNNLDNK

>ABV52258.1 hypothetical protein C8J\_0659 [Campylobacter jejuni subsp. jejuni 81116]

MLEDDFIKERQNIRQKMLKFSRAINQGKPLDDDLRDEISSDDILRRRFKKKTPNKFLEELDEEYESKHTK

KSNIYLKEDLINVKLEEKQSLAKKFFSKMKERKKEENKKTKKIFSFGRKKINKIKNIQTKPKIQTKNDQN

PIQDKKEKKESIKSIEKIQKTEPKIQNSQTIEKRPDIKKQPDIKQSLENLQKKITPQENKQELPKPSNQA

QEKQQNDEDAQKAKNVLLEGFSNATKEDRNLNFNHLLFAALLVSFALFLFAPQIYIRNQIYYLSREIATL

RTEESVLNEENKDLKRRLENMRFQNQILDYLE

>ABV52257.1 hypothetical protein C8J\_0658 [Campylobacter jejuni subsp. jejuni 81116]

MKKFKEFSLRFLFKVSEQPVLVKDLLEANALFNDGMLVDPSKLNFNFKILNSYIYFGVFCAVVLLPLLLI

THYFLTKLDFHISIVSAVMVTACVFIGYDIFKVYTRKIISKKIIQKAWALHFPYFAYEKYSIMAGEIYKE

ALKEEIPKANLEQYVLDKIIHSK

>ABV52256.1 acetate kinase [Campylobacter jejuni subsp. jejuni 81116]

MKILVLNSGSSSIKFKFFDNKVVKASGLVEKIGEQNSKVILKNVLNNESFERELMINNHEEGLSIVNELF

KESGILADLNALDGCGHRIVHGGRNLSEHCLVDDYVLKEIDRVSIFAPLHNPAHLAGIKTMIKAAPSVAN

VAIFDTAFHRTMPDFAYMYALPYDFYDKHNIRRYGFHGTSHAFVSSRAASLLEKDKSELNVISAHLGNGA

SVCAIEKGKSVDTSMGFTPLEGLVMGTRCGDLDPAILPFISHLKGLTIEEIDTLMNKKSGVYGICGYNDF

RDIEREIEQGNDKARLALDMFCYRLVKYIGSYFAVLPKTDAIIFTGGIGENDSLVRQKVCERLAHLGIEL

DFELNKQRISGERMINHANSKVKVLVIPTDEELEIARITEELISN

>ABV52255.1 phosphate acetyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MANLYLMRSRSDELNTIISTNLLKNYSKIYKNIAIYCPVIYIHRVPVLQGWLEEFNINQTVKSAYGFTFR

EAMEEFSKDPHNFFNVILEEYEELKRKYDFVLVNSFCEFGILDGFDLSIKLAKNLNTPIAAIINDEDKLI

AQKYFDHALDGRNYVLINENFNFEEVQKLEEYDFITPHRFKYELIKQSVKNKKTVVLPESNDERILKAAE

ILLKSKVVDLILLGDEEKIKQDAARLSLDLSTIQIMNPLNSEYNQEFTSILYEARKSKGMSLEEAKMLVQ

DKTYFGTLLIHTGKADAMVSGASTTTAETIRPALQLIKTKEGISSVSGIFFMGLEDQVLAFADCAVNPSP

TAEQLATSAYVSAMTAKSFGLEPRIALLSYSSGDSGKGESVDLVKEALKIAKEKYPELNIDGPMQFDCAY

DPKTAAKKMPNSKIAGHANVYIFPDLNAANICYKAVQRTANALAIGPILQGLKKPVNDLSRGCLVDDIVD

TVILSAIQAQ

>ABV52254.1 putative flagellar L-ring protein precursor [Campylobacter jejuni subsp. jejuni 81116]

MKKVLFYVLPFAFFGCSATVDPQISMKPPAYVEELAPKQSNNVESAPGSLFGKGDNPLFSDKKAMNVNDL

VTVVIQESTTQSTQANKATSRTNTSNLGGGALTGSSGVVANALNKVNAYSNIGFQTNSSNNYTGTGSQSR

NESFNTTISTRVIKILSNGNYFIEGSRELLINGEKQIIQLSGVIRPYDIGQDNTIDSKYIADAKILYKTE

GEVDRSTRKPWGSKVIEAIWPF

>ABV52253.1 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Campylobacter jejuni subsp. jejuni 81116]

MEYKRFKTRQIKVGNVSIGGDAPISVQSMLFTKTRDIEGSLEQISRLYFAGANIVRLACLDMADARALKE

IKAKSPLPLIVDIHFNHNLAVYCAEFIDGVRINPGNIGSKENIKEVVKACKERGIPIRIGVNHGSIEKQF

SDKFGYGVDAMLESAMYNIKLLEDLDFFDIKISMKTSDAQKTIEAYERLRPLCDYPFHLGVTEAGTKFHS

TVKSSIALGNLLLKGIGDTMRVSMTGELEEEIRVARAILQDSGVQKSGVNIISCPTCGRIQSDLLSAIKI

VEEKTKHIKEPLNISVMGCVVNALGEAKGADVAIAFGKNQGLVIRHGEVVAKLKESELVDRFLAEVEDEV

KSRAVKE

>ABV52252.1 hypothetical protein C8J\_0653 [Campylobacter jejuni subsp. jejuni 81116]

MDFFKNGGVIWITGLAGSGKSYIAEALYKKLKEKYNNIIYLDGDELRDLLEHYGYDKQSRIDMSIKRSKF

AHFLSSQNMLVIVSAISMWNEIYEHNKKTLKNYFEIYIKCDFEELKKRDKKNLYSKNLKGEISNVVGMDI

DFDEPKSNLIIDNTYMTELDNKISYILTALKEKK

>ABV52251.1 invasion phenotype protein [Campylobacter jejuni subsp. jejuni 81116]

MQNLLLYIKNNLTPTLAQILLQALKNSNNEKFFTFVLKNIETICTWLNSSEFKNRYLSIKHPYPPLINPN

FIEIDASRHCAELAWDLNLPLPKHYKFIYISPHGVGAAAFLRYLNQCCDVTCFASWVLPPDAKERYCLNY

MCLNDNTITQYAINISEINLPYFDKYLSLLDFNSKIICGVRDPIGILKHNWGRDWSKVLRNYPSEFNLTY

DWRYYIDYLTHQNHKIKIDINELQQGVFIISYLLKYFNKDNVYYLDMEEIRQSKAFDTMNLLAINFNFTP

PHKDKLDLFKIKEFRGYIRYLFPITLYANSKDINNTFYLNTPKNNKNFNIDKTSSIPIILDRKHINHEKI

DIIQEIIKNDLCNDMGVYIDKNDFKQLEQNNLLFSTIKHYLYDFLYQIKITIDETESKMMKEKDVIDYFI

KNKSLVYTFFNIFENDLNHLKQKFPNIINSWTYYKEFEKCVKS

>ABV52250.1 hypothetical protein C8J\_0651 [Campylobacter jejuni subsp. jejuni 81116]

MMNYFETLQTFIENNRIDEGIIMEHFAHMLKDILERYDCYLNSDDFKKNNPLGLKKLIKLKNRCNTYIS

>ABV52249.1 hypothetical protein C8J\_0650 [Campylobacter jejuni subsp. jejuni 81116]

MKILKNKYFILWMIGFFAIVCLCLYFNLEVKIIASAISAYAVSISLVLNAYSIFEKTRADKFNLTMQLLS

KWDEKHFIEARDYTREQQNIKEKKEMKKY

>ABV52248.1 phage repressor protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MQMQEVIEKLKDILASEGKCNLKTKDIAKELGIHPDTFNSMKFRNSIPYPQILNFLNQRNISINYFFYGS

SPKDQLECENKYKILKLYKTNASLGGGGINDLIDSSDLIIDEKVLNFFGSKECEFITCYGESMEPIIKDG

SICVIDRNKTFKNKSICVINTRDGLFIKQVLKQDDGVILHSLNPLYEDIFYKNGDFLLIGVVIGELSRL

>ABV52247.1 hypothetical protein C8J\_0648 [Campylobacter jejuni subsp. jejuni 81116]

MDRVSADIRQGVNKRFINAICNHNNELVLEYLKNGMSVTKECMGKEPMFYAVTHNNFGAILLLLKYGAIL

DKEYLEESNKNFSKEALEFLASLL

>ABV52246.1 Domain of unknown function (DUF955) superfamily [Campylobacter jejuni subsp. jejuni 81116]

MTYKEIKDKTPYEILDLLEMKEPPFNPFEIAQKLGINVVKDLDLDKIDTEGQISVDEKGEPIIWINPLKN

ENRQRFTLAHELGHLANDILPSIENPIIDSYETLYRSNTYGGIETRANQFAARLLMPLRQIEDFIAECRK

TTPDLKAAEAILLIASKFEVSKQAVFHRLKNVGLIKQDYTYPF

>ABV52245.1 hypothetical protein C8J\_0646 [Campylobacter jejuni subsp. jejuni 81116]

MEEFERMVDLHINDKISILTDIDQEKSQIGGLE

>ABV52244.1 hypothetical protein C8J\_0645 [Campylobacter jejuni subsp. jejuni 81116]

MLSYNDCELIRELYKDFNIKELKVRYSLNNNVLKRKESKELLIMNF

>ABV52243.1 hypothetical protein C8J\_0644 [Campylobacter jejuni subsp. jejuni 81116]

MQRDANFYSIPKLNVSASTSGDNELIGLEGYETGEMLELSKAFFKTTPKNMKAIKVDGYSMVPMLLPDSW

VVFEETHKYQGDGLYILNFDNQLMVKLLQLDPISKVLDIISVNKDYKSYSLDLKDSQVELIIQGKVLRFI

I

>ABV52242.1 hypothetical protein C8J\_0643 [Campylobacter jejuni subsp. jejuni 81116]

MQKIDENFKKEKEQNKDLELNKFQITSREIFTIKTPENKDVEVELTCTAGLIQTSQINYEEIVRKEFLYK

CFPVTWNDFLKLNKYEKNWHIQLKIVMILDC

>ABV52241.1 hypothetical protein C8J\_0642 [Campylobacter jejuni subsp. jejuni 81116]

MKLYIILTFLKDDESIDIYYPPNFYEDTSIFNIVEHSFFNSREYYKNYKLLIVLI

>ABV52240.1 hypothetical protein C8J\_0641 [Campylobacter jejuni subsp. jejuni 81116]

MKQGDFTEVAKHYHNRPAYSPFLLEKLVACINDKNKNLKDLNIVEVGAGTGKLTKMLGEMFGCQISAVEP

NDNMREEGQKFTQNLSNISWHKGSGEETCMSNNQADWVIMASSFHWTDPKKSLPEFNRILTGGGYFTAIW

NPRHIVEGSVFDEIEKEIKHIVPELARVSSGTQNVKKWEEILVSTGDFTDCFFMECDYKEFWDKERYLGA

WHSVNDIQAQAGEKRWKEILEMIEAKISHMQSIEIPYKIRAWTARKA

>ABV52239.1 possible methyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MQKLVEQVWDYTKHAKFYSYRPNYAPKTIDMLISLVGKKDIKVADIGAGTGNLSIMLLERGCKVVSVEPN

DAMREIGIERTKGEKVDWVRATGLNSTLQNSEFDWVTFGSSFNVMDRNEALEEAHRLLKSEGYFSCMWNH

RDLNDPVQKIAEDTIVEFVPNYTRGTRREDQRPIIESRKDLFDNIVYIEEDFYFHQSIENYINAWKSVKN

PYWDLEADEGNELFNKISDKISQRLPKEFSIKYTTRCWSAKKI

>ABV52238.1 hypothetical protein C8J\_0639 [Campylobacter jejuni subsp. jejuni 81116]

MAELKFKTKAQNLKNLQTKLKKAKVLSLVLTSLEELISNEDKVLQDIQTLKANRLIIRSSSLSEDSMKNS

NAGAFLSLANIKADSKDELLKALYEVANSMPSKSDEILVQPMLENITLCGVGFSVDKDNFSPYFCLQYDE

NGSNSSITDGSSKSAKTYYHYRDYLEFKDIRLQKIIELIKELEVLYNCCFLDVEFAFAIQDDEEELFCLQ

VRPLVMHEKNNLFHSLPKEALYRFYKRFESLKESRSRVLGDKAIFGVMPDWNPAEIIGLRPKRLAFSLYK

EIITDNIWAYQRDNYGYRDLRSHPLIHSFLGIPYVDVRLSFNSFIPKKLDENIAQKLVNFYLDKLNKNHE

LHDKIEFNIVYSCYDFNSSKKLEELLNHGFNENEIKRLEFSLLELTNKIINPRSGLYLKDIQKAYKLKER

YDGIINSNFSLIDKIYWLIEECKRYGTLPFAGVARAAFVAMQLLNSLVEIDFITKEEKDDFLNSLNTVSK

NLSKQTNHLNFHNKDQFLKDFGHLRAGTYNILSPRYDEDFELYFDVDQKDSKVYLQDKAFVFSEEKTKAL

NALLREHGLEINACEFFDFLKQAIEGRELVKFEFTRLLSKAIVYIEELGKYYGIEKEDLAHLDIKSILNL

YSSLYSINPKEQFVEEINRNKKEYELTQAIKLPSLLCNADEIFSFYNHSIIPNFITQKSITAFTAKENDK

DLEGKIVLIYAADPGYDYLFTKNIAGLITCYGGANSHMAIRASELGMPAVIGVGEENFEKYLKAKKINIE

CESEQIFCL

>ABV52237.1 hypothetical protein C8J\_0638 [Campylobacter jejuni subsp. jejuni 81116]

MFIGITQRLIYNESYHEERECLALDWGKLFNKDLFKNFTPLPLSYEIDFSHYKHLIKAVILSGGNDLSFY

SPNVLSKKRDLYEKQVIEICLKEKIPLLGICRGAQMIAHYFNSHISPCENHIGKHEVFFSKEKFISNSFH

NFAIEKLGEDLVELCLAKDNTIEAFKHKYENIFGIMWHIERENGLNNIQILKEWFSLIKE

>ABV52236.1 putative sugar nucleotidyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MNAIILAAGFGSRLMPLTKDQPKCMVEYKNKKIIDYEIEALKSAGINEIAVVGGYLNDVLKNYLNKYDIE

HFFINSKYDKTNMVHTFFCAKDFILKCIEEKQDLIISYADIVYFQDCVQKLINAKEELAIVVDKSWRKLW

NKRFANPLEDAETLKMTNGYIIELGKKANAYDEIEAQYIGLFKFSYQFLSEVIAFYEMLDRDILYDNKNF

ENMYMTSFLQALIEKYNNAKAVEIDGNWCEIDFMSDLKINFI

>ABV52235.1 primosomal protein N' [Campylobacter jejuni subsp. jejuni 81116]

MQRSDIRYYELAICGLYLDNLTFHSFDEIKPLTQVLVDLKTKKNLKAIVLKECQKPDFKTVEIKEITKYF

LTPLQFELANFIVYYYASKLGFVLGFFETSPKYECQKMFFKDTPKLSNQQQNALSFLQKENNSLLFADTG

SGKTEIYISLIKECLEQGKQALLLMPEIALTPQMKKRLEVYFKDNFFLWHSKISKKKKQEYLERFCKGEV

LLVAGARSALFLPFRNLGLIVVDEEHDNSYKASNQPFINARDLALFLGQKNNIKVVLGSATPSLTSFYKQ

KSFRLKGTFFESKKHFLYDENELGITPMLLSELEKSLKHQKQAIVFLPTRANFRQIICKDCGETIKCPFC

SIAMSMHKKKNVLKCHYCNYTSLIEQNCPSCKGEMLEARKMGTAELLELLQNALPLAKIAKFDSDEITSV

KKLNTILKDFNENKIDILIGTSMLAKGHDYHSVDLSVILGLDEYLLRPSFRASEETLALAMQVAGRAGRK

GEARVLLQTKNRAFFERYIEDYDAFLKDELENRKDLYPPFKRLLRVLIEDKDQKNAQKLCEKLAYQFKNI

KQVELVGYGICGVEMLHEKYRFYLLLRSENYKALVAIENYILQFKNVSADIDPIDFI

>ABV52234.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MNKAFTLLELVFVILILGILSSLSLSFINTTKDEVKILKLKMDYEMLSSALALMRSQMRLKNLNFPEILD

NAQNNQAKEKLFYCLNDCDYSLLDTPIYSDFKSWIKIGKNHYRFALNAKEMVEFIYDSKEGLLKCIGSSR

CKDLI

>ABV52233.1 hypothetical protein C8J\_0634 [Campylobacter jejuni subsp. jejuni 81116]

MADNLKQVIVNVNAKDFIVKCSEEFANFLEDDIALISGGTKKIELKRFVDAFVKKSYENYILERELKKLI

KAINEELPTK

>ABV52232.1 hypothetical protein C8J\_0633 [Campylobacter jejuni subsp. jejuni 81116]

MFDEKIINTMTDKVNELIEKYNEVCEANEALRNELVSVKAQNEAKSNQIMRLEEELKSRNIESEDIYKKI

EAVLGR

>ABV52231.1 excinuclease ABC subunit B [Campylobacter jejuni subsp. jejuni 81116]

MLELTSKFKPSPDQQEAIKGIVKSIKKGNKYQTLLGVTGSGKTFTMANVIKELNIPTLIMSHNKSLCAQL

YSEFKGFFSKNHVEYFISYYDYYQPEAYIPRTDVFIEKDSSTNEDLERLRLSTTASLLSYEDVVCIASVS

ANYGLGNPNEYIGMVLIFELGMQISQKELLKKLVDMGYKRNDNFFDRADFRVQGDIIDIYPAYYEDEVVR

LEFFGDELDAMYHYNVLENKKGKDLKRFILYPTSQFSVGETRLKQAIKDIKAELNERLAYFEHENKLVEY

QRLKQRVEFDLEMLTSTGMCKGVENYARHLTGLKEGDTPYTLFDYFAIKDRKFLVIVDESHVSLPQFRGM

FAGDRSRKQTLVDYGFRLPSALDNRPLMFDEFIHKNCQFLFVSATPAPLELELSKENIFHQIMRPTGLLD

PLIELKDSDNQVEILFDEAKKVIQRNERVLVTVLTKKLAEELTRYYLELGIKVKYMHSDIDAIERNEIIR

GLRSGAFDMLIGINLLREGLDLPEVSLIAIMDADKEGFLRSTTSLIQTMGRAARNVNGKVLLFCKKITKS

MQEAMDTTNERRKLQMAYNKKYNITPTSVKRHIEESLKNEEDLGEIYRKGKKLEKMPASERAKLVKELRK

QMLEAAKALEFEKAAAIRDEINKLRDL

>ABV52230.1 truncated KdpD protein [Campylobacter jejuni subsp. jejuni 81116]

MQRQSPEQILKKLEVKAKEEEKNKLAKLKIFLGYAAGSGKTYAMLSEARTLRDNGVDVVLGYIEPHDRPE

TMALTQGFESIANLEIPYKNIVLKEFDLDATLKRKPALVLVDELAHTNAKGLRNEKRFQDIEELLKAGID

VYTTLNIQHLESLNDLVANISKIEVKERIPDRIFDEADQVELVDIEPNKLLKRMQDGKIYKEKQAKLALE

NFFRQERLIALREIALRRLASRVNLRASEQRLINDDLAYHTGEHILVCINASNAKVIRAAARLALAFHAK

LSALYIKNPNIKEEKALEENIELAKSFDAEIISVYDDDIARQIAEYSSLSNVSKIVLGKNKDKKKFKEEI

FEAVAKKAPNIDLYLVNENQISTPKIRSKKGFDFLGFLKITGVLLLATFIAFVFHKFNTQPSNIVMIFIL

AVFASSFISDNKIFAFYSSLVSVLIYNFFFLEPIFSLKVHDSGNIITFTTMFIVGFLTAVFTRRLKLQSK

ELTKRAYRTAILLENSEKLARVKSKQELWEQLGNQALKLLNLPIIIYPINKNNILSKPLLFFNDDKQMLK

NCFSADEIAIAQWVATNKERAGVCTNTLPNANAMYLPIEDGEKTKGVIGIVLKEKRPLQDFQYEILSALL

NEAGVRTRDIFLL

>ABV52229.1 potassium-transporting ATPase, C subunit, putative [Campylobacter jejuni subsp. jejuni 81116]

MLRTLLSFFVVMLILCTLIYPFALNTVAKFIFPYQSSGSLVDKEGRPTLDISKAVGSKLLGQDFNKPYFL

HSRASVSNYNTSDTNESSVSSGGFNYAMSNPALKERVQKDLQKFLDENPQITKEQIPLDLLSASGSGLDP

HISLQAALVQIPRISQSSKITKEELEKIIQENTESKFLGIFGEEKVNVLAVNIAIAKAMKKE

>ABV52228.1 potassium-transporting ATPase B chain [Campylobacter jejuni subsp. jejuni 81116]

MSKKQNKLITKEILNNAIKGAFLKFDPRFMVKNPVMFMVEVGLILTLILSIFPTLFNGNSDERIYNILIT

FILFITLLFANFAESIAEGRGKAQAATLRQSKKDSKARRIKSDGSEEMLNSSELKIGDIVLVKAGELIPN

DGEIIEGAASVDESAITGESAPVMREAGGDFSSVTGGTTVLTDFLKIKILVGAGESFLDKMINLVEGAAR

QKTPNEIALNTLLIVLSLSFLVVVVSLYPFMQFLGVSLPISWLVALLVCLIPTTIGGLLSAIGIAGMDRV

TRFNVIALSGKAVESCGDVDTMILDKTGTITFGNRLANEFYEVQGISKEEMIKACVLSSLKDETPEGKSI

VALAQKMGYELEGNDIKEFIEFSAQNRMSGVDLQDNTKIRKGAFDAIRAYISEMNGKIPSDLETKVMEIS

NLGGTPLVVCKNEKILGVIYLKDTVKPGLKERFDELRKMGIKTLMCTGDNPLTAATIAKEAGLDGFIAEC

KPEDKIEAIKKEQAQGKIVAMTGDGTNDAPALAQADVGIAMNSGTQAAKEAANMIDLDSNPTKILEVVEI

GKGLLITRGSLTTFSMANDIAKYFTILPAMFSVVLPQMQILNIMHLATPQSAILSALIFNAIIIPLLIPI

AMRGVKFKPMKSEHLLLRNLSIYGLGGMIAPFIGIKIIDIPTAWILRILGV

>ABV52227.1 hypothetical protein C8J\_0628 [Campylobacter jejuni subsp. jejuni 81116]

MLEILITLIIAFILALIFGNYLYKIASCKKTIFDFIFNPIDNLIYKICAIDRKNMTWQKYSLHLIAFNAL

VAIFSFVIFYLQDKLFLNPNLINSMKGDLNLNTVISFITNTNLQHYSGESALSLLSQNTGILLAMFVSSA

SGYSACMAFCRALCGMQMGNFYEDFTRIITRLMLPLSFILAVIFISEGVVQNYHANFSVLTLENKFQSIA

TGPVAALESIKHLGTNGGGFFGANSSMPFENPTSLTNFLQILSMMLIPSACVVAFGLMVYHRKERQGFAL

MGKEGGVIFGAMGIIFIISLLLIYFSEKMSNPNLDSLGLNANLGNLEGKEIRFGTDGSSLFSAVTTAFTT

GSVNNMHDSLNPLSISATLLNMMLNVAFGGEGVGLMNMIIYVLLTVFICALMIGRTPEFLGKKIESAQMK

LIALVILIHPLLILVLSALAVVFAKDSISNPSFHGLAQILYEFSSSAANNGSGLEGLKDDNLFWNLSTAF

AMFCGRYLVLIAQLAIAGSLLAKNTQENTANSLKTDNLTFMFVLVCIIYIFTALTFFPVLTLSSVAEYLS

LWH

>ABV52226.1 hypothetical protein C8J\_0627 [Campylobacter jejuni subsp. jejuni 81116]

MDVIFALLLLLAFGSLWFFIRFCEVQTRTRG

>ABV52225.1 anaerobic C4-dicarboxylate membrane transporter DcuB [Campylobacter jejuni subsp. jejuni 81116]

MDFLTSLSEGGQFAIQIIIVLICLFYGAKKGGIALGLLGGIGILMLVFAFHIKPGKPAIDVMLTILAVVV

ASATLQASGGLDVMLQIAERILRRNPKFLTILAPFVTCFLTILCGTGHVVYTIMPIIYDIAIKNGIRPER

PMAAASISSQMGIIASPVSVAVVSLTALLLNANHKLAGFDGYINLLQITIPSTLFGVLCIGIFSWFRGKD

LDKDEVFQEKLKDPEFKKYVYGDSKTLLGVKLPKSNWVAMWIFLGAIALVALLGVFDFLRPNWGQVVKNG

IPQVDALGNPKMDVLSMVSVIQMFMLLAGSLIIIFTKTDAKKIGSNEIFKSGMIALVAVFGISWMADTMF

AVHTPMMKAALGDIVKEHPWTYAVMLLLISKFVNSQAAAISAFVPLALGIGVEPGVIVAFAAACYGYYIL

PTYPSDLATIQFDRSGTTHIGKFVINHSFILPGLIGVITSCIAGYFIAMAAGYL

>ABV52224.1 RNA polymerase sigma-54 factor [Campylobacter jejuni subsp. jejuni 81116]

MLKQKITQAPKTKISQTLRSWLPILQANIEDLKENLDKFAEDNPFLNVQDSIQTHDKGKNYFDSFYKHNI

NSAFVDSKGLAKKSVYELLNEQILPPLFPTNKSQELAKKIIECLNEEGYFEYDEEFLKEYSLEEIERVRA

RFKFLDPVGVGAKDYKEAFLFALENMELDEDIDEFCRMLIMDFENIQNYTKEPLYKEALAVLKRFSTPPF

LEYFEDSRIIVPDIFVYKENGEIKVKINDDYYPEISIQTDGLEHDFLSHYIKEAKNLVDALAMRKATLYK

IGLMIVEYQYDFFMGKEIKPMTFKDLALDLERNASTISRAVANKYLSCERGLIPLRDFFAFALDEEGETS

NVGVKEFVANLVKNEDRNKPLSDSKILELIKEEFKVDIGRRTITKYRKHLNIASSTDRKKLYELEG

>ABV52223.1 ABC transporter, ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MSKLEIVNLEKIIKKTKIIHGISLEVNSGEVVGLLGPNGAGKTTTFYMICGLISPSSGKVLLDGLDVTKD

PLNKRARSGIGYLPQESSIFKDLSVEDNLLLAAQIFYKDKKILHDKVEQMLELLSIEPIRLRKGLSLSGG

ERRRCEIARSLMCEPKFLLLDEPFAGVDPIAVAEIQTLIKELKRLGIGVLITDHNVRETLAICDRAYVIR

SGSLLASGNADEIATNKDVKKYYLGAEFKLLD

>ABV52222.1 putative ATP/GTP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKEFILAKDEIKTMLQIMPKEGVVLLQGDLASGKTSLVQAWVKFLGLDARVDSPTFSTMQKYENHDICIY

HYDIYQEGLEGLLANGLFENFFEKGLHLVEWGGENLKKTLMKFGISTIQIKISIKDDKRKYEIYE

>ABV52221.1 S4 domain protein [Campylobacter jejuni subsp. jejuni 81116]

MIFFAKIAFMRVDKFLNVVNITKRRAISEDMCKSGVVGINGVIVKASKEVKVGDIITLHFTEYTQKYKVL

AIPSTKSIPKNAQNEYVVKL

>ABV52220.1 argininosuccinate synthase [Campylobacter jejuni subsp. jejuni 81116]

MKNEVKKVVLAYSGGLDTSIILKWLQDEYNCEVVTFTADIGQGEELEPARKKALSLGIKEENIFIKDLRD

EFVKDYVFPMFRANAIYEGEYLLGTSIARPLIAKTQAQIALQTGADAVSHGATGKGNDQVRFELGYLAFN

PDLKIIAPWREWDLNSREKLLAYAQKHGIDISKKKGKSPYSMDANLLHISYEGLVLEDPAHAPEEDMWRW

SKSPKDAPNESEIIELDFQKGDLVAINGEKLSPAGLLTKLNELGCKHGIGRLDIVENRYVGMKSRGCYET

PGGTILLKAHRALESITLDREAAHLKDELMPKYASLIYNGYWFSPERMMLQALIDESQIHANGRVKLELY

KGNVMIIGRESANDSLFNAAYCTFEEDEVYNQKDAAGFIKLNALRFIIAGKNGRKF

>ABV52219.1 50S ribosomal protein L9 [Campylobacter jejuni subsp. jejuni 81116]

MKVLLIKDVKALGKAGEIKEVKDGYGQNFLIAKGFAKAATNEVLRKYESDKKKEAENLRFEIANLEKLKE

ELSKITLEISKPVGANGSLFGGVTKDEIAHALKEQSHIEIDKKSLECDTFKSLGLHEVSVKLGHAIHAKF

NINIKAE

>ABV52218.1 putative heat shock protein [Campylobacter jejuni subsp. jejuni 81116]

MFHATTILAYKGKNKSVIGGDGQVSFGNTVLKGNAVKIRKLNNGKVLAGFAGSTADAFNLFDMFENLLQS

SKGDLLKAAIDFSKEWRKDKYLRKLEAMMLVLDRNHIFLLSGTGDVVEPEDGQIAAIGSGGNYALSAARA

LAKHASLDEEELVKSSLQIAGEICIYTNTNIKTYVIEDEK

>ABV52217.1 putative heat shock protein [Campylobacter jejuni subsp. jejuni 81116]

MNLTPKEIVKFLDDYVIGQKKAKKIIAIALRNRYRRMQLSPELQDDIVPKNILMIGSTGVGKTEIARRLA

KMMGFPFIKIEASKYTEVGFVGRDVESMVRDLANAALNLVKNEQREKNKDKIDEFIENKILEKLLPPLPK

GISDEKQEEYKNSLEKMRTKLRNGDLDESTIEIEISQNMFDTNPNLPPEMGAMQDIVKVIGVGSKKVKKE

MKIKDAKNALKNEAGEKILDQESIKSEALKRAENEGIIFIDEIDKIAVSSGNSNRQDPSKEGVQRDLLPI

VEGSNIQTKIGTLKTDHILFIAAGAFHLSKPSDLIPELQGRFPLRVELDSLDDKALYEILTRPKNSLLKQ

YSQLLKTENLELEFDDEAIKEIAKIASRANEEMQDIGARRLHTVIEKLLEDLSFEADEYAGKKFVVDKKM

VEEKLGDIIENKDLARYIL

>ABV52216.1 GTP-binding protein ERA-like protein [Campylobacter jejuni subsp. jejuni 81116]

MKSGFVSIIGRTNAGKSTLINSLLEEKIALVSHKQNATRRKIKAIVMHEKNQIIFIDTPGLHESGATLNQ

LLVQSAIKSMGDCDVILFVASVFDSTKDYENFLSLNPQVPHIIALNKVDLTDNATLLKKLSEYAKFSQHF

KAIIPYSSKKKSYKKGLLDEIVKYLDKHEYFYDPEFLSASSEKELYRDFILESIYENLSDELPYSSEVLI

HRTKDTPNLLILEANIITDTNSHKGMLIGKEGATLKRIGKDARFKISKLAQKKVLLKLFVTVKKNWQKDE

EFLKKLLNDEN

>ABV52215.1 putative transmembrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKINSLNKINFIKSTDLLYAQRTGISKEDELFNNLTADFKLSKPFDYQIAFFKHNEIYHCFLAPVYKLKK

SRFCFPEPLIFQALFDERFIEESDYCVLNLYDQTLYLYFYQEGKFINLKKIENFNPSNMDLFFKQNRFIE

LLKHYESKLLLYQDLDTIKHYFSSQIKCLNLNDILDKNSLLKLSSYSIKNLDQNCNFIKHNKIKISISFK

IILIFIFSFSLSMMILLFKDFIEYKQNKEIQNKNFIIQEEISKLKQDKQKLLTNIQDLNFTLSNKISSTQ

QQFHILSTITKEINLDKNKAIILNQIISWLNSNELKITNLEFKQTKIILSFIDENHFKKALENLNLTFKI

LDKNEETFNIILEVIHE

>ABV52214.1 hypothetical protein C8J\_0615 [Campylobacter jejuni subsp. jejuni 81116]

MNKIEVFLQNLNPREKFLFISFICLCALFLAFKIHDHFLENIFQKTLVEHNYLALNEAKIENSHLKEIGI

KLTKQIKTEEEKLKYYKEKLHLFSYDKDFFNKKINNLSKNLTINEIKFSQENKNFIHYNYVSLSLNGDFK

DLLNFIQNLENLPIALKIDKIKLYNTQGLKLKLDLMFKFVNL

>ABV52213.1 hypothetical protein C8J\_0614 [Campylobacter jejuni subsp. jejuni 81116]

MTKQEIQKLDTNFLGHPKPLFSLSMVELWERFAFYGIRSLLVLFMATTISKGGLGISTEYASAIYGIFAG

CLYLAALPGGWITDNYLGQKKALFLGSFIIALGHISIALSILSTPIFFLGLTFIVIGTGFFKTSASVTVG

MLYKQNDTRCDTGYTIFYIGINIGAFIAPLICGFVQAKWNYHLGFGIGGLGMLISLLILYFKATPELEEF

HKNCTLKQNWEQPFKKSKNLTLILSISLLSIIGFFLIFINLADINPIILSKKLLIVILLCLVIYFIYLFV

FKTLNKREKQQLTILIVLFFVATFFWSTFEQKPTAYNLFAQDFTNRNIFDWKIPTNWFQSFNPIFIIILA

PIASYIWIFLEKKNIYFSSIGKFTLGILFAGIGFMMMTFASQNLINNNGLPISMVWIIISIFFLTLGELC

VSPVGLSIMAKVAPDLIKNQIMGLWFVASALGNFVAGLIGGNVNIKNIDQLPNIFGQCMWMLFVVALLLF

IAKKPIYKILNEKNKQLSN

>ABV52212.1 di-/tripeptide transporter [Campylobacter jejuni subsp. jejuni 81116]

MSKNVKNLDTSFFGHPKPLLSLSLTELWERFSFYGIRPLLYLFMIASFEKSGMNLKPEEASAIMGIFASC

LYLAALPGGWLADNYLGQKRAILLGALTIAFGHLCIAFSYFNNKIIFVGMVFLVIGTGLFKTCASVMVGM

LYKKNDARRDSGFTLFYMCFNFGAFVAPLICGFLQKEYGWHFGFGAGGIGMLLAVIIFYLKTMPDLKEFD

EKVGIDSTWDRPSKKSKNAFYIIIVSGIVLLGAIFLILGGFIKLDAQVINKNIILTILACAGIYFLYLFA

FTSLKIEEKRNLIIFIVLFLAAALFWSVYEQQYTSFNFFAEKLTDKTILNYEIPTIWFQSLGGLFVILFA

PFSAFIWTICAKNNKEISSIIKFALGLLGAALAFLIMALASNHAISLNGDANTLRENLENSSQIILVSPW

WLVSSFLLMVLGELCLSPVGLSIMTKIAPNLIKSQVMGLWFVASALGNALAGFIGGKASEENIAYLPNLF

YQCMWILLGAVIILLILKKPINKILKN

>ABV52211.1 peptidase, M24 family [Campylobacter jejuni subsp. jejuni 81116]

MSIYKQRVLELRRLMKENNIDAYLILSADPHLSEYLPEYYKNRVFISGFKGSVGTVLITQEEGFLWVDGR

YWLQAQKELEGSGILLQKQDVKNTFTKWLEKNLSEDQILGIDFALLPLSLQKDLQINCKANLKHIDLISP

LWKDRPTLPQEKIYEHELEYCSYSRKEKLALVRQKMKNLNVTSHLISSLDDIAWLTNLRGNDVNYNPVFL

SHLLILEDKALLFVDQKKVNSELEKKLNLDGFWLKNYDEIIMELEKLANTNLLIEPSKMTALLINSLDKS

VKIIQEINPSTHLKAVKNTKEIAHIQDAMIEDGVALCKFFAWLEEAIENKELISELDIDAKASEFRAQSK

HYISDSFATIAGFNENAAYPHYKATKESFAYLKKDGLLLIDSGGQYKNGTTDITRVVPIGKANAEQIHDY

TLVLKAHIAISSAIFPKDIAMPLLDAITRAPLWKEQIDYIHGTGHGVGYFLNVHEGPQVLSYLSPVLEKT

KAKEGMLTSIEPGIYKVGKWGIRLENLVIHTKVENPKNKDFGEFLYFKPVTLCPFEISCIDTKMLDEKEK

EWLNNYHKEVFEKLSPKLGDYPKALVWLEKRTKAIF

>ABV52210.1 penicillin-binding protein 2 [Campylobacter jejuni subsp. jejuni 81116]

MRMRLVVGFILLFFIFLLSRVYYLSIKSNVYYEELAKQNAIKTEFLPPVRGQITDRNGTLLAINDLGFSI

SIKPYLSIKKSNKGILDKELSELTNLFPDLNASKLAEIYKRNDSYYNQDFIKVVDFIPYDEIIPHYSELN

LNKTIKIDPVVKRKYPFGKLASHIIGYVGKANLQDVQENEIAKLSNYTGKSGIERYYNDILQGEKGTRVY

KVNALNQEVEQLSYTPAMSNDIELTIDIELQSYLTSLFEGNAGAAIIMNVNDGSILAAGSFPEYDLNPFV

TGISFKDWDELSNSLDHPFTNKLINGYYPPGSVVKMGVGLSFLNSKNISPSTQYVCNGSIELGGRFFRCW

NRSGHGPVDLKHAIKYSCDVYFYNGSLQVGIDQISETLSRIGFGAKTGVDLPSEFVGTLPSKEWKMQRYR

QSWFQGDTLNTAIGQGNFLATPMQIARYTAQIAKGGEVIPHFLKSIENNNNTTIENQMDENKKEIFTLFE

KSQLPYIRDAMYAVANEQGGTSYRYLHNLDVKVAAKTGTAQVVGFSQTDKNRVDEKQFEYYTRSHAWLTS

YAPYSKPKYVVTVLLEHGGRNITSGATVAKIYQKMIELGYFK

>ABV52209.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MRRNLSAYKAKFNGAYVFLGFFFLIYQILGSTFVYAPLLYGIFFCYMFCLLEERERTFSKLDFRWYFSLF

FLFFTDITYNFFIFSSWLAFFIFYYLCADWIKTNLKIGKFIPVVFVLCAYGIILFLDMILSYIGDEKIKI

LGWAYIVSVFIECCLAYVFFKGKI

>ABV52208.1 GTP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MIISAKFITSLVKFDENLSSNFSEVAFLGRSNVGKSSLINSLCKQKNLAKSSATPGKTQLINFFEVTCKR

NEEKFNINFIDLPGFGYAKVSKNLKEIWNQNLDEFLKLRTSIKLFIHLIDSRHTHLEIDVNLNDYLKRFL

RPDQKILKVFTKCDKLNQSEKAKLKNEFKDSILVSNLNKFGLDSLEDIIIDQTLGLGK

>ABV52207.1 hypothetical protein C8J\_0608 [Campylobacter jejuni subsp. jejuni 81116]

MVARQIILLLVCVSVTWATQIEVKALNFYSDENKGESILSGNVEVIRGDDILNSEKLIIYTDKNRKPIRY

EAMQNARFKIVLKGKTYKGSGDKFIYNVIKDTYEINGHAYINELGSNQKLFGDKIIVDRKANIYRVESKD

QKPARFVFDLKDK

>ABV52206.1 hypothetical protein C8J\_0607 [Campylobacter jejuni subsp. jejuni 81116]

MAIKIFGILIALFTITFTILSLQDPYSLNLQTNALNFKNIEAKNLKAYESNTSTIKAYYKANSWVRYADR

DEFNDFITLNLDFNLSANRLEFFNKDMSKVLFEGNVTYIGANNVKIISQEVEYEPKNKVLYTNTDFKALI

NGSIINGNTLNYDVKNKILNIQGVNAWLQDK

>ABV52205.1 phosphatase, YrbI family [Campylobacter jejuni subsp. jejuni 81116]

MTELIFLDVDGCLTDGKIIYTSNGEFIKEFDVKDGAAIEAWLKLGKKIAIITGRNCPCVEKRAKDLKIEI

LYQGIKDKLACAKEILQKLNLDFSQCAAIGDYFNDKALLESVGLSFKPKDGHKDLNVDIVLSKKGGKAAV

AQMIEILVEKNHLEEEWNKLWL

>ABV52204.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MQIKTITLKLSAVSLGALFFSGCLGTSFFSSLDNAQVYYPSNDFKSSPSSSGTKGTMKPYTINGKTYYPT

VVAVGETADGIASWYGPGFHGKKTSNGETYNQNALTAAHKTLPMNTILKVTNLNNNRQVTVRVNDRGPFV

NNRIIDLSKGAASQIDMIASGTAPVRLEVIGFGSSNSGNNIVHSNVNYGNSGEIANNGQIYEGGNFMVQI

GAFKNPAGAQTIAARYKTYRTYSSTIRTSSVDGLNRVFLTGFRSEDEARDFAASGAFAGAFVVRE

>ABV52203.1 putative secreted transglycosylase [Campylobacter jejuni subsp. jejuni 81116]

MKKNLLCFLICFNFLFAQINTPEFYERQMNVLRNLDINPSFISDLIFVQTQQDIKSKHAQTLIDSMQNFS

KVTPMIRKILSQQEVPDEILYLAMVESGLKTHSVSNAKAVGVWQFMQPTARNLGLRIDAYVDERRDPVKS

TYAATNYLKELKEEFGKWYLALLAYNCGNGKLRQAIKQAGSDDLSVLLNPDKKYLSLETRNFIRKILTLA

FLANDRDFLLDKDASLMNYALSNEFAKVDVPSSASLKEIAKNLNMDLATFKKYNPQFKHNFTPPGKGYYM

YIPLNKVAFFDKNFKAEKLAKVDTTIPMTRTYTVKSGDSLYKIAKNYNISVDEIREFNKIAKNHLSINQK

LIIPIKENKNANKNNYTKVVSR

>ABV52202.1 hydrolase, TatD family [Campylobacter jejuni subsp. jejuni 81116]

MFLNLDFQDGLRIVDTHCHLDSEAFKDDLDETLNRAFKNGIEKIIIPGADIKDLPYAATIAHKYKNIFFA

VGVHPYEIDNYDEKILRQYLYDEKCVAVGECGLDYFRFKSDLAEEIQKEKENQKKIFIAQLELAIEFKKP

VIIHSREANHDTYEILHGYSKDLVGGVLHCFNASEHLLTLFEDGFYFGIGGVLTFKNAKKLVEILPKIPK

DRLLLETDAPYLTPEPYRGKRNEPLLTQFVANKMCEVLNLSRKELLEICFNNSEKLFFKGY

>ABV52201.1 response regulator/GGDEF domain protein [Campylobacter jejuni subsp. jejuni 81116]

MNKKILIIDDNKMLGKLLAKKIQMTLDYEVDIAFGFAEAKELMNNDYFLAFVDLCLPDAPNGEVVDYVIE

KKIPAIVLTASGDKATKEKFMDKDILDYIFKESETCIDEIISSIVKLNQYAKTKVILAMSKLPERNEIKK

ILTQRQFNVLAAAHGEEAMSYLNDNNDVKLIIADVNMPVISGFELLIQVRERFSDDELGVILLGDHNDSF

EANSFKNGVNEYLFKPLSKESFNCRLDHCLSYMDDKKFLSTYNVLDPVSGVKNYNALIDGIDDYFNEIAT

KDEEFAFAFLDIDNLQMINDEYGREVGDEVIKICANEIVNETKGRDLVGRYSAEKICILLKNISQERAIK

IFSRIRVNIKKAGVLVNLDEVFFTASIGVVFGKSGDKIDSLVDKASKILSQAKDNGKDRVEVCS

>ABV52200.1 putative DNA repair protein [Campylobacter jejuni subsp. jejuni 81116]

MINRIFMKENLGFKKAELEISKGLTVFTGLSGAGKSVLFKGILSAFSLSESEAKIVEIELDDKLDLESFG

IESEEENVFKLLKEKNTKYFINNQSIAKKSLQNLSKTFIKYLSAKENNEFGNEKFLNLLDALEMQENTNF

VSFLEDFKKDFNAYSQISNELNVILEEEKKVEELKELARVQIEKISSINPKIGEYEELLIFKKKLSKKDK

LEEAWSKAERIFELEKVVIEALNLSEVDPSFFSECLNELRVICENQKMEDLDFDVETLLDRIENLSYLIK

RYENIENALEVLKQKKHELEHYENLSFEKKELEKKFQELKQKLEEKAQILTQTRKKNLKKLEKCLNNYLK

DLYMKDASLTLKENEKISISGKDEIMLDINLAHLKNLSSGELNRLRLAFIATECKILNAGKGILFLDEID

ANLSGKEAMSIAKVLEELSKFYQIFAISHLPQLSSKAHNHFLVEKNGEESKVKKLDQEERIKELARMVSG

ELVSDEAIEFAKTLFKN

>ABV52199.1 ATP-NAD kinase, putative [Campylobacter jejuni subsp. jejuni 81116]

MQNKIDYKNIKKIGLVTRPNVSLDKEILKLQSILSIYKVELVLFKESSEILDLPKYGLDDLFKISDFVIS

LGGDGTLISLCRKACEYDKAVLGIHAGHLGFLTDFKVDEAENFFQAFFQGEFRIEKPYLLSVFLEDKQGK

ILEKLAFNDVVISKNNQASMAHIEVFRKEKKFNEYFGDGLIVATPAGSTAYNLSANGPIVYTLAQAFILT

PVCSHSLTQRPIVLPKGFEIEIMAKDCILCIDGQENYKMNDFKSIKVGLSDKNVALIHPKNRDYFQILKE

KLHWGN

>ABV52198.1 aspartyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MRSHYNTDLGISHVGQSVKLCGWVNSYRDHGGVIFIDLRDRSGIIQLVCDPNDSKEAHEIASNARNEFVL

IAEGTIRPRGEGLVNPKLKTGEIEVVVSKLTIENESAVPPFAIADESVNEELRLKYRFLDLRNPKLYENF

ALRSKACIAARNSLANMGFLEVETPILTKATPEGARDYLVPSRVHQGEFYALPQSPQLFKQLLMCSGFDR

YFQIAKCFRDEDLRADRQPEFTQIDVEMSFCEQKDVINVAETFLKDIFKACGKEIQTPFRQMQYKDAMEN

YGSDKPDLRFDLKFIDVIDIFAKSNNEIFANIAKDTKKNRIKAIRVPKGDTIFSKRQMQRFEEFVRKFGA

QGLAFIQVKEDGLKGPLCKFFSEEDLNELSKRCELEVGDVVFFGAGAKKTVLDYMGRFRIFLANELNLID

PNALEFLWVVDFPMFEQNDDGSYSAMHHPFTMPKNIDETDLEEISSIAYDVVLNGVELGGGSIRIHKNDI

QQKVFKLLNIDEEQQKEKFGFLLDALSFGAPPHGGIAIGLDRLIMLVTGANSIREVIAFPKTQRAQCLMT

DAPSPASNEAMRELGIKLRENIK

>ABV52197.1 adenylate kinase [Campylobacter jejuni subsp. jejuni 81116]

MKELFLIIGAPGSGKTTDASLIAQADATNITHYSTGDLLRAEVASGSELGKTIDSFISKGNLVPLDVVVN

TIVCALKAAPTKTIIIDGYPRSVEQMMEFDKVLSEQNEICLKGVIEVRVSEEVAKERVLGRNRGADDNEE

VFYNRMKVYTEPLNEILDFYQKKKLHFIIDGERTIEPIVADMKELIKKIQSI

>ABV52196.1 inorganic pyrophosphatase [Campylobacter jejuni subsp. jejuni 81116]

MDLSKIKIGDIPNKINAVIEIPYGSSIKYEIDKDSGAIMVDRVMASAMFYPANYGFIANTLADDGDPVDI

LVLNEYPIQAGAVIPCRLIGVLIMEDESGMDEKLLAVPNSKIDARYDNIKTYTDLPQATLNKIKNFFETY

KILEPNKWVKVQDFKDEKAAIEILEKAIKNYK

>ABV52195.1 putative peptide methionine sulfoxide reductase [Campylobacter jejuni subsp. jejuni 81116]

MKNIVLGGGCFWCVEAVFERLKGVIDTEVGYSGGNPNPSYESVCNGDGNIEVVKINYDEKQISLLEILTL

FFKIHDPTSIDKQGGDIGIQYRSIIFYENEEDKILAQNFIEEQQKIFSKKIVTKISRLQTYYKAENYHQH

YFINNPNQGYCQAVIAPKLQKIQSG

>ABV52194.1 NOL1/NOP2/sun family protein [Campylobacter jejuni subsp. jejuni 81116]

MLSRIEKLYTKDEMQNILSSFTQEKNVCVFANTLKISIEELEKEFLKQKLKFKKINAYCYLFDAKDKAIL

SSMKAFNEAHFYIQNYSSYLCALNLEVKAGQRVLDMCAAPGGKSINLANFMQNTGYLACNEMSRDRFFIL

QKNLKNYGVNAKVFMKDGKNIGNLCPLKFDKILLDAPCSTFAKIGFDLEKSYKEIKNIAKTQKKLLHSAL

KALKIGGELVYSTCTFTKEENEEVIENALKSEFKLELLDIDLENVEAKAGQSEEFAEISKCRRILPSLDY

DGFFIAKLRKLC

>ABV52193.1 putative Holliday junction resolvase [Campylobacter jejuni subsp. jejuni 81116]

MRALALDVGLKRIGVALCIDKKIALPLDAVLRKNRNQAANEIKNLLKIHEISLLIVGIPKGGSSEEEMTR

RIKHFVSLLEFDKEICFVDESGTSKEALGYGVANTRKKDGKLDSLSAFIMIKDYFAL

>ABV52192.1 DNA processing protein A [Campylobacter jejuni subsp. jejuni 81116]

MASEILPDEFLELFKDLKKPPKKLHYKGNLSLLKQDKIAIIGSRRMSVYTKNCVFSLASMLKNAHLCVVS

GGALGVDITASMAAMPNTIGIFANGLDQIYPRTNEKIIKQIYENALALSEYEDDYLPKNYDFLLRNRLVI

ALSKAVVVAQADIKSGSMQSAKLALELNKPLYVLPQRLGESTGTNLLLKENKAKLICDFKEFVSEFASID

INQDEFLEFCKKGVSVDEALKIYGQKVYEYELEGKISIEGLFIRVLA

>ABV52191.1 hypothetical protein C8J\_0592 [Campylobacter jejuni subsp. jejuni 81116]

MSKKKLVQIQRYLIIAILFLLCIALALGILVKYQNSQDVSSVKPDYFIDKQEDLISSNKDHYEIGIFQEN

EFDNNKFVSILEQKIQEIDDLNTSLNEQNLSSVEQNLSLEQNQSLEQNFIPKDTNLTQDQNLTFNEDIHL

NKISKKPKLAIIIDDMANASQVRGLKALNLKLNPSFFPPDKNHSETPKLALKFDFYMVHLPLAAINYNKP

ELDTLNPNDSKERIFKKIKQIKKDFKDLRYINNHTGSLFTSNEEAMRKLYEVLKNQNIFFVDSKTIGNSK

ANKIAKELNVPYIQRDVFLDNEDDVNYVKKQIQNAVKLAQKKGFVIAIGHPRKNTFKALEQSKDLLKSVD

LVYLSEIYGK

>ABV52190.1 ketol-acid reductoisomerase [Campylobacter jejuni subsp. jejuni 81116]

MAITVYYDKDCDLNLIKSKKVAIIGFGSQGHAHAMNLRDNGVNVTIGLREGSVSAVKAKNAGFEVMSVSE

ASKTADVVMILAPDEIQADIFNIEIKPNLSEGKAIAFAHGFNIHYGQIVAPKGIDVIMIAPKAPGHTVRN

EFTLGGGTPCLIAIHQDESKNAKNLALSYASAIGGGRTGIIETTFKAETETDLFGEQAVLCGGLSALIQA

GFETLVEAGYEPEMAYFECLHEMKLIVDLIYQGGIADMRYSISNTAEYGDYITGPKIITEETKKAMKGVL

KDIQNGVFAKDFILERRAGFARMHAERKNMNDSLIEKTGRNLRAMMPWISAKKLVDKDKN

>ABV52189.1 putative ribonuclease [Campylobacter jejuni subsp. jejuni 81116]

MKEFLNSLSYGISSHEVNNEFKQILRELLTNHIIKEHKNKYYLNNGFAFGVLDISSKGTGFLQCFDESFK

KDLLIENKNLKGANYKDIVAVKLLPLKKKRPSAKVILVLKRANETSLVITKRYGEAVLGMNIKTGLSTTL

KASQKSLKALPLGTILKIENENNNIIEVLGHIDDESVDEKISLALFNKNNEFSDACIKEALANGDSVDAS

MYENRMDLRALPFCTIDPIHAKDFDDAIYFDIQKREIYVAIADVSEYVYAYSAIDKEARNRGFSIYFPHI

AIPMLPRPLSENICSLKPHLDRLAYCFKIALDHENKVIKEELFEGIINSKRRFNYDEVDEILIQKPDLKE

LSWLYELFEITKNLRKMRLKNAFEFRTEELRMNLDENLSLKSTVFEKDTPSHNLIEDCMLLANKAAAKLI

DIGVFRNHLSADARKIDKLLNELRELGIDVNFKPNLPELIRDIQALADELNLRAEVDKLIIKAQKKAEYS

SVNAGHFGLGFDKYSHFTSPIRRYSDLILHRLLKAKQKNDEKLFNYLLLNIESTCENLSTLEREADKVAF

DFMDRKFARWAAKNIGKKFKALVVQNDGVCIAKLDDEIKGADIILYDTRVNLLESVEVQIMEADIVMAKI

YAKITQRLIKEENV

>ABV52188.1 putative DNA polymerase III, delta subunit [Campylobacter jejuni subsp. jejuni 81116]

MYRKELQILLSKDSIPNFFFLYGADNFQSELYAEFIKEKYKPDETLKLFFEEYNFTRASDFLSAGSLFSE

KKLLEIKTSKKIPTKDLKVLVDLCKNNADNFFLLELYDESSKQSDIEKIFSPHFVRFFKANGAKEGVELL

SIKAKQLGVEITQNALFTLFTSFDENLYLAASELNKFSGLRVDEKTIEQYCYSLNTGSFESFFEKILKKQ

DFKSELEKILDNFNEIALTNSLYNSFYRLFKIALYAKVNGKIDFKDLLGYTPPPQVGQNLSSQAFSLKIE

QYKEIFTLLLKSEYELKTNSKLVKKEFLISNLLKLARILKS

>ABV52187.1 hypothetical protein C8J\_0588 [Campylobacter jejuni subsp. jejuni 81116]

MDFENQLNAIVETIAERKTLVNTEEATKMTFIMPFLKTLGYDVFNPSIVVPEYTADIGTKKGEKVDYAIF

KDSKPFILIEAKNHTENLDNHNNQLVRYFNTNPSIKFAILTNGIEYRFFTDIEQQNLMDKIPFLVVNLEK

LKPRDIKDLKRFICTDLNLDEILSIAMEKKYYRSIQEIFKSEIENPSDEFTSFFAKQMTEKRMTSAVLEE

FKNYIKKSFKEIINDLAYEKITSIKNNLQNINDDENDEQIDESKDIVTTEEELQGFYIVKSILASVSANL

EDVSYKDTLSYFSILYQGKVTKWICRLYFNTSKKSISFPDGASYNIEKLEDIYQYKADIIKAFESRK

>ABV52186.1 hydrogenase nickel insertion protein HypA [Campylobacter jejuni subsp. jejuni 81116]

MHELSIVESLIELCEENALNNKAYNVQEIYVKIGRLSGIEVDLFKRCFETFKENSNICKNAKLFIELAPL

EILCLKCDQVSILEENVFKCPKCQSIEYKITQGEDLHLMRLVME

>ABV52185.1 hydrogenase isoenzymes formation protein [Campylobacter jejuni subsp. jejuni 81116]

MKNISLAHGGGGEEMNELLTKLFKIFDNEILNANNDAAILGNLALSTDSFVLSPIFLDEEVNIGKLCVCG

SINDVLMVGAKPKYLSLGLILEEGFELEKLERILKSIKEECEKCGVMLVCGDTKVVPKGKADEIYINTTA

LGEIISKKESKNIKAGLSILLSGDIGRHGASVLIKRNELEADVKSDCKALDKEVLELLEKDIKVVAMRDA

TRGGLSAVLNEWAKQSGNDLLIFEEKIIVQDEVLGLCELFGYEAYELANEGTFILCVEKEDELKALEILK

KYNVNASIIGEVLEEKKARVILQNAYGAKRFLESPKGELLPRIC

>ABV52184.1 hydrogenase isoenzymes formation protein [Campylobacter jejuni subsp. jejuni 81116]

MNFIDEFRDKESILALKKLIEQELKNPINIMEICGGHTHSIMKYALPSILPKEINFIHGPGCPVCVMPRV

RIDTAIKLASMKDTIFCTLGDLLRVPGSEISLLDLRAKGADVRALYSPLEVLEIAKQNLNKNIIFFAIGF

ETTTPMSALLLQKVIEEKINNVFFHINHITVPAPVEAIMNDENVKINAFLGPSHVSVITGYGIYEPLAAK

FKTPIAVSGFEPVDILESVLNIIKQSNEGTFKVYNQYKRAVSKEGNVKAQNLVKKYFRVCDFEFRGLGLI

KDGGLELKEEFSAYDASKKFDCTVQSKNESKACICGQILRGLAKPYDCKVFGKACTPRSPIGSCMVSGEG

ACAAYYKYSKVNV

>ABV52183.1 hydrogenase isoenzymes formation protein [Campylobacter jejuni subsp. jejuni 81116]

MCLSIPSEILEIDELNNALVQTLGVKRKVNLDLIDEPLKQGDYVLIHVGVAMEKIDKEAALESIKTYQEI

VEKMNSGEIKSDEGDLGLNEFHR

>ABV52182.1 hydrogenase isoenzymes formation protein [Campylobacter jejuni subsp. jejuni 81116]

MCKDCGCSINSSHTHGHHHDHHHENPSLKEGKTIEVISKILSKNDEEAKHNRAHFNEANTLCINLMSSPG

SGKTTLLESTIKALKNELKIAVIEGDLETNNDALRVKNAGALAYQITTGQSCHLDAFMVHEALHHLAIDD

VDLLFIENVGNLVCPASYDLGEHLNVVLLSVTEGSDKPQKYPVMFKKADIVLITKVDLAHHFDFDLKEAT

KLIKELNPRADIITLDAKNGTNMELWYKVLKLKKELF

>ABV52181.1 transcriptional regulatory protein hypF [Campylobacter jejuni subsp. jejuni 81116]

MCHLGYKIKISGLVQGVGFRPLVYELALKSKLFGEVRNDGFGVEIILACTQKECENFIENLKNHLPPLAR

IDQLIITQISISNYENFSITPSLENTKSTPMLSDFALCKECKKEFFDEKNPRFLYPFITCTHCGPRFSII

KSLPYDRFNTSMQELLMCEFCKSEYEDPKNRRFHAQPISCPKCKINVFLKNPKGEILAKDQEAFMQSAKF

LKEGKILAIKGIGGFHLMCDAFNEEALKTLRLRKNRPKKPFALMCKDLQSAKELAFIDEKEEALLGGVLA

PIVILKAKKAFSLIAPDVDKIGIMLAYTPLHLLLFEYFKGSLVATSANLSGESIIKDEFNLCKKLDKVFD

FYLDYDREIINASDDSIAQVVNGETMFLRTSRGLNPFYLERNFNKKGTFLALGAELKNEFVIFYENKLLI

SPYIGDLKSLDAHERFFKLLEFFKQNYDLKFDAILCDKHPHFSYAKEFEERIKISHHYAHFCAAYFEYEE

NFAKDEKALAFICDGTGYGEDGKIWGGEVFVGNLKEYERIAHFENFTLINSDIKNIQNLALSLIFHYDLE

DKAKDFLAKIPKIKLKNLKKIYSHSNLQTSSLGRIIDAFGSIVFNLEKSSYEAQVGLMCEAFYDKNLDFS

YKLFVEKGQVNFKNLILGALQDEKTKAITGMFNALANFIIDFSKDYDLKVLLSGGVFQNKTLLEILKAKN

FDFFIPLKYPCNDSSIALGQMVHFLNLEK

>ABV52180.1 hypothetical protein C8J\_0581 [Campylobacter jejuni subsp. jejuni 81116]

MTLDFDFIYNADNDIFEYLLRFYAKNYNYILSKEENTYHFSIDADEENLKTFCDSLNFMSHSVFLKKFDV

KAGHGFNPCMPEDKEFSRFSYITHLNSNAYQEKKLLNKNEWGVFCECEFSSNLSEFEKINEENFNTFLNL

AFDLLSQEKKIYLKDKNGIYEFSLFKNEFIGDFLLPCDIKAINSVFVCSNENLKFLASLEKPLMKLRLNA

MFRKNHNLDFNDFKIRLARDLFCFALGLKLFENEYKFLSVKKIEEYQKDFYISALDEQVVVLEGFEFINA

KARELIFSKEDKNMARISYLVSRYKEKAFILELSKDYEDILLVNKELNLLKLSLPKHSKELYEEIKKDEI

GARLLENFSKEFPLLDENFELQNNFYSLLGLVGRVLNLGKNLQESVSELLKIADESKMPRGVKIDYRLKE

DKSFDYTRTLRSAMSFMLAGVDSANIAYGAVESLAYFLRDTYDELREKKQSDLALISGSLFEHKSLLKNT

LKHLKNCQLSDVPLRV

>ABV52179.1 hypothetical protein C8J\_0580 [Campylobacter jejuni subsp. jejuni 81116]

MARQSSSLKSFIYKDECYFYSKKCIKTLRLRLNEKGEFVLSIPYFCTFKSVYEFLDKSSSWMNEAKIRFE

KKVLKDDELIFLAKKYKIIFDENAKKIYFDKDKIICQNKAKLDLFLRQNAKKIFTFYLKKWSKKTGLFYT

HLSIKNMKTRWGSCNHNKAYINLNLKLIQKSLRAIEYVILHEICHLKFPNHSKEFYTFIEHFMSDFRQRE

KEFLS

>ABV52178.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MAKKQLSLTRLSFPIFWDLLSKYLTVIINTAMVSHYSNFIVGAMGAGNQILDLFITIFSFLSVGCSVVIA

QAIGAKDHVLARKVIHQSLFLNALLGFVCGVLILWHGEYLLYLLKIPQELLKDSEIYLHMLAICLFFDAI

GIVLAAIVRVYNMAYWVMFIGFLMDIVVICGNYYVLHYTKSELFGIGLSNIFARIVAIVALFAILFYKLK

IHLKIKEMIKLEKEVLKKVLNIGGFSAGENLLWIVQYTIAFAFVASLGEASLSVQTIYFQISMLIMLIGQ

AISIANEIIVGKLVGARYENIAYKHAWRALYFSVIASALVAFLNYLCQDFTMQILGLKEELKNLMIPLFA

LSIFLEISRTFNIVMVNSLRASGDAKFPFFSGLVFMMGVSLPVGYVLCFHFNLGILGVWIGFCADEFLRG

MVNSYRWKSKKWQGKALV

>ABV52177.1 phosphate ABC transporter, ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MIAKTTNLNLFYGKKQALFDINMQIEQNKITALIGASGCGKSTFLRCFNRMNDKIAKIDGLVEIEGKDVK

NQDVVALRKNVGMVFQQPNVFVKSIYENISYAPKLHGMIKNKDEEEALVVDCLQKVGLFEEVKDKLKQNA

LALSGGQQQRLCIARALAIKPKLLLLDEPTSALDPISSGVIEELLKELSHNLSMIMVTHNMQQGKRVADY

TAFFHLGELIEFGESKEFFENPKQEKTKAYLSGAFG

>ABV52176.1 phosphate ABC transporter, permease protein PstA, putative [Campylobacter jejuni subsp. jejuni 81116]

MKKLFKKRQKASKSFKRLCKMGLYINLIFLCIFLGSVAYLGFPAFKQTYIFVEANRNSPAYDLLSRAEQR

KIRTGQITEKSWLLANSEVDQYMKQKYNRLSEKQRTLVDDLVQKGEIELKFNSNFFLNGDSKSPENSGIL

SSVVGTLLVMLVCMVVSVPIGVAAAIYLEEFAPQNILTHFIEVCINNLASIPSILFGLLGLGVFINLFGM

PRSSALVGGLTLAIMSLPIIIVSTKAALKSVDINMKNAAYALGMTKVQMVKGIMLPLAMPMILTGSILTL

AQAIGETAPLMIIGMIAFIPDVASSIFDPTSVLPAQIYSWSAMPERAFLERTAAGIIVLLGLLVVLNLSA

ILLRKYFQGKLK

>ABV52175.1 phosphate transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MLKEKIIKFALFLCAFVSVIVSFAIMLTILIEALKFFQKESVVTFLFSSQWAADAAFMNADGTSKQGVFG

ALSLFWGTFYISLIAMLTALPLGVMCAIYLGVFAGKKSKNYLKPILEIIAGIPTVVFGFFAAIVVAPFIV

WFFSLFGIQASFQSALGAGFIMGIMIVPIVASLSQDCIEAVSEKRINGAYALGMTKKEVVFAVILPEAIP

GIVAACLLGLSRALGETMIVVMAASLRPNLTMNFLEDMTTVTVKIVEALSGDQAFDSSLALSAFSLGLVL

FIITLIINMFSVYLINRFHKRKNL

>ABV52174.1 phosphate transport system substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKILSLSVASLALCGALNAADLKIAGSSTVYPFTSFVAEEYASIKNTKTPIVESLGTGGGFKVFCEGTT

DISNASRPMKLSEFETCKKAGVTDIVGIMIGYDGIVLAQNKTNAPLNITKKELFLALAKEIPQNGKLIPN

PYTNWNQINKNLPNRKISVYGPPSSSGTRDTIEELVMSDVSKKIPEYKGEYKTIRQDGAYIPSGENDNLI

VSKLTIDKDAFGIFGYSFLVSNSDKINAANIDGVTPSEESIADEKYELARSLFIYINAKKNPKEAFEFAK

IYMSDDLAKSGGELEKIGLVPLSDDKLKASQKHVEDRKILNDELVKAGKVF

>ABV52173.1 ferritin [Campylobacter jejuni subsp. jejuni 81116]

MLSKEVVKLLNEQINKEMYAANLYLSMSSWCYENSLDGAGAFLFAHASEESDHAKKLITYLNETDSHVEL

QEVKQPEQNFKSLLDVFEKTYEHEQFITKSINTLVEHMLTHKDYSTFNFLQWYVSEQHEEEALFRGIVDK

IKLIGEHGNGLYLADQYIKNIALSRKK

>ABV52172.1 putative transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MTYFSLEFSILMIAFFAIYWTFKNDYKIQNILILIFSYIIYILINPYFALVLFIYTFFIHYFALLIFVRR

KRYIFATCMAFIILNLCFFKYFPSIKGSVDEILNFFGLEFLNIDLVLPIGISFYTFTSITYLVEVYQKRR

LESFLNLATFLSFFPTLLSGPIMRSSFFFEQAYQKREFKHANLIIILLVFGIVKKVLIANYLGIYAKSIL

DFPQSYNFIQLLSAIYAYAIQIYCDFSGYVDLVCAFALMLGFTLPPNFNMPYLAKNLKDFWARWHISLST

FIRDYIYIPLGGNRKGMPRTIVNILIAFILSGMWHGNTLAFIVWGLLHGIGIVFIHLLALSKFSLQKIPA

LGRFLTFQFVCFTWIFFYYSKNLEDAIEYFKACYYNFFQIPSYNDIYMLVAFGVLFMVYPLFINFKEYCI

KILNLTPFLLKPFIIAFILLLVFAFMPDGIPDFIYSSF

>ABV52171.1 hypothetical protein C8J\_0572 [Campylobacter jejuni subsp. jejuni 81116]

MSVVRFFFILIIVLGLVVVVMNQSISSYIEQKYHFAFYPHNDLLKEANGFKIKLEQIRAILSNEPLPQTN

EETTNQESKSTDENLSKIDKVLNTLENDENTSHKETNLTLIQDANISFIDNTKLELQNGDEFLFIGDSLM

QGVAIALNRDLRNLNLKVTDLSKQNTGLSYKSYFDWSKATNEAFVKNSNIKYLVVLLGANDPWDIKKGGN

YHRFGSPSWIDIYTNRVDEIIKIAKKHKAKVFWFEIPPVKKEDLNKKIQVLNKIYSDEILKNKEIFINTK

LFFSVNDEYSAYIKDENNRSIKVRTDDGVHFTPSGAREMSKLLLEHIKLKEENASK

>ABV52170.1 hypothetical protein C8J\_0571 [Campylobacter jejuni subsp. jejuni 81116]

MLVNKFKIILLFFIIFTSSYAQNLNTNDTIDSILNQNKNHSALTSYVLKKDLKNLEKKLEKNQNIGIRIY

GDSHMAADFFPRVIRGYLIRSNSIGFAYPLQPKYQQNLNLVYSYKNFEILNSRNPANAGHNFPLGGIIAK

AKIKGAKINLDTTLDKKKFKIGFLFKAKQNTNAFSIKDAKNQSYELRTTQINKWSYKELELDLPLQISAL

QKDAELGGYFITNKDNNVFLDTIAINGAKSDLWLSWNQTVVKKELGLLHNDLIILAYGSNDALFKGFEKQ

KFKNNLKKWISILKTYNKNAVIMLISPPTVVQKQGKNYKLAPDFFTIRKALYEVAKEEKTLIFDMHQFMQ

DSGGKNKWIEQKLSLNDVHLTIKGYELMAKKLLEDLKNIIDY

>ABV52169.1 outer membrane efflux protein [Campylobacter jejuni subsp. jejuni 81116]

MRVIFSIFLAFFLSACGAKLSLPKEVDLTQEQMKDLNLTYDWYRSYDNAKLNEFLNFVLLNNSDINIARK

TLLSALARADLINYDLYPTLSGNLGFGGDKDLNSGKQSKNFNNSLNLSYELDIYGKLRDSASASEFSAKA

SAYDLENLKISMINTALNDVFELAYFNDVDKLLRAYLSNLEQMKELYSYKYKLGKIEELDLLNIEQSLLR

AKQNLLSNDQNRNLLIKNLQDLLAKQEGFAYIEYFKTLSLNDFKTLSPDFNIPLKALAYRADVRSKLNSL

KSAFKDYSSMQKSILPSISLGGALSGSDKKIDDSFKFEILSGNVKISLPFLDYGRVKQNIKISQFTYEQL

LISYEQALQSAMNEFALNYKDYQSNTLLLQNLQNINIKQELITKAYYEKYILGKSELKDYLDANNTLNST

QQEFLRARFNLLKTINSYYQITALSFNDENLEFPKY

>ABV52168.1 ABC-type transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MIFLKNICKNIGENAILKNVSLSIEKGEFVAIIGQSGSGKTSLLNIIGTLDTPSSGTYIFDEYEVTKLNN

DEKARLRREKIGFIFQRYNLLSLLSAKENVSLPAVYAGKKLQERSQNAKKLLNDLELAHKLDSKPNELSG

GQQQRVSIARALMNGGELILADEPTGALDSKSGIMVLEILQKLNAQGHTIVLVTHDPKIAAQAKRVIEIK

DGEILSDTKKEKAQEKLTLKTMSKEKKTLTLLKNQAFECFKIAYSSILAHKLRSVLTMLGIIIGIASVVC

VVALGLGSQAKVLESIARLGTNTIEIRPGRGFGDLRSGKTRLNFSDLETLRSLEYLEAVDAHSNTSGVAT

YTNISLSARAEGVGVNNFAIEGLRIDAGRILNNDDVKNSTNVAVLDFNAKKNLFPDEKSENILGRVVLFN

SQPFKIIGVLQKDTDKPIEDNVVRLYIPYTTLMNKLTGDRNLREIIVKVKDDVSSTLAENAIIRILEIKR

GQKDFFTFNSDTFKQAITANKRTTTILTACVAVIALIVGGIGVMNIMLVSVSERTREIGIRMAIGARRED

IMMQFLIEAVVICTIGAILGVILSIFVIFAFNTLSTDFPMILNAYSVLLGLLSSMFIGVVFGFFPARNAA

NLNPISALSKE

>ABV52167.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKKIVLIILIAILGSVGAYFIFFNNDEKISYLTQKIQKKDISQTIEAVGKVYAKDQVDVGAQVSGQIIK

LYVDVGTHVKQGDLIAQIDKDKQQNDLDITKAQLESAKANLESKKVALEIASKQYQREQKLYAAKASSLE

NLETQKNNYYTLKANVAELNAQVVQLEITLKNAQKDLGYTTITAPMDGVVINVAVDEGQTVNANQNTPTI

VRIANLDEMEVRMEIAEADVSKIKVGTELDFSLLNDPQKTYHAKIASIDPADTEVSDSSTSSSSSSSSSS

SSSSSNAIYYYAKFYVPNKDDFLRIGMSIQNEIVVASAKAVLAVPTYAIKSDPKGYYVEILENQKAVKKY

VKLGIKDSINTQILEGVNENEELIVSSSADGLAPKVKLRF

>ABV52166.1 putative amidohydrolase [Campylobacter jejuni subsp. jejuni 81116]

MQKLVENLALKYYDKVVDLRHQIHMHPELEFEEENTAHLVCKILDEFGIKYQKNIAKTGILATIEGKKKS

QKKPKCVLLRADMDALPVQEKTNLSYASKIDGKMHACGHDGHTAGLLGAALILNELKDEFCGTIKFMFQP

AEEGSGGAKPMIESGVLENPYVDAVFGCHLWGSLLENTAQIVSGEMMAGTDIFDLEFIGRGGHGAHPHTC

IDPIIMATQFVNNIQSVVSRRLAPYEAGVITVGQICAGTTYNVIPTNAYLKGTVRFLNDKTQDILKSSLE

EVAAATAKSNGGDYKLKYTKEFPPLINDEKAALIARKAFAKVLGEENIIVSSKPDMGAEDFAFLTRERMG

AYVFVGISKDLNHPALHHSSTFCWDDENLKVLMQGDVMMALEFLNL

>ABV52165.1 hypothetical protein C8J\_0566 [Campylobacter jejuni subsp. jejuni 81116]

MQENNSPKTQAVVKKNEIYVSVKRKKSTIEYEKDLKNLQIELLKFQNHVKAKGLKVLILIEGRDAAGKGG

AIKRLIEHLNPRGCRVVALEKPSDVEKTQWYFQRYIAHLPSAGEIVIFDRSWYNRAGVEPVMGFCTPQQH

KDFLREVPLFENMISNSDIIFFKFYFSVSKDEQKKRFEKRRSDPLKQYKLSPVDQKSQELWDKYTLAKYS

MLLASNTPTCPWTIISSDDKKKARLNLLRFILSKVEYPNKKTGDFSKIDAKLVRSGEEEIRKMEANLEKL

DSKKADEKIKDLD

>ABV52164.1 putative thiol:disulfide interchange protein [Campylobacter jejuni subsp. jejuni 81116]

MRIFGIILLSFCLCFASILSLNEAFNVKSNSYNNSISIDIELGKDIYLYSNKLKLYINEKDISSLINLPQ

SSTRGNENVYYQKLNLALPNLLLEHFAKNTTNLIKLEFQGCSEQGLCYNPQTWYFDLISKKDAFEISKPY

KTQKTDKKTKIESEESSIANFLATDNFFWILLSFFGYGLLLSLTPCILPMIPILSSLIVAKSNAKFSKKY

SFFLSFIYVFFMSLAYAIAGVIASFLGASIQGILQKPIILILFALIFIAFAFAMFGAFRFELPLRFQTFI

HKKSEKGKGVLGIAIMGFLSALIVGPCVAAPLAGALIYIANTGNALLGGSALFIMSFGMGIPLLFIGLGL

GFIKPGFWMEKVKIFFGFVMLAMAIWILSRIIEENYILIAYGILGVFFSVFMGIFEKSFTIISKIKKSIL

ILILAYSLSIFLGGLFGAKNFLNPLNFNTISASKSALSYDYINNFEQLKQEIQTNTKPIMLDFTASWCEN

CKLLDELTFSDERIIQKMQNYKLIKVDVSENNNEQIKTMKEFNVFGPPVLIFFENGKEKLKITGFISADD

LLKKLEP

>ABV52163.1 MOSC domain protein [Campylobacter jejuni subsp. jejuni 81116]

MKIQSLQIGKIKNYKNFQSAFIKDTYLEETQIDFLGILDDQIADKIHHGGYHKAIFANSCQNYPIWERFL

NKKLNFGSMGENLSIDGLCEQNVCIGDIHQISNAILQVSEPRKPCVKISKIHNNSNFTHEIFKTGLSGWY

YKVLQVGQIRKYENIKILEKNSTSLSVFELNQLFYSPHQALRQNPILLDKLEKLNSLISQNWHETIHKRL

KNTYDISYMDSL

>ABV52162.1 putative neurotransmitter:Na+ symporter protein [Campylobacter jejuni subsp. jejuni 81116]

MQRQTWSSTLTYILTVAGATIGFGATWRFPYLVGENGGGAYVLVFCIAMIIIGIPVILVENVIGRKAMTN

SVDAFKQKWQSIGYMGLLGSFGIMAYYMVLGGWVLVYIWELTLGNFSLANVVSKEFTHQFFNDKIAFNPL

GVGIFTTVFVIINYIILKRGIIDGIEKSVKFLMPLLFICLIIVVGRNLTLDGAMAGVKFYLEPDFSKILS

PKLLIDVLGQVFFALSLGFGVMITLSSHLNKNENMAKTAIYTGVLNTIIAVLAGFMIFPALFSAGLAPDS

GPSLVFETLPIAFSHIHFGTIVCILFFVLLLIAALTTSLPIYQVIISVLEEKFKYSKNLSINLTLGFIFI

LGNLPCILTYGPWRDIVIIKGKNIFDSFDFISGNILFVLTAFFCCIYVGWILGKQESLKELSNNNTLKSS

WFGIWFYYVKYIVPLIILIIFIYGILN

>ABV52161.1 hypothetical protein C8J\_0562 [Campylobacter jejuni subsp. jejuni 81116]

MNFIKTISPIQKINFNGFEFYIKRDDLLGEINGNKARKLAFYIHQRYPKNQSFISYGGSQSNALAALSIF

AKQRSYKLVFACEKISTFLKNNPCGNYALALENGVDFVENIHSLSLKQFAFSLCKKDDIFIEQGIANLEA

QYGYMELAQEIQMQSQSLKLDFDIFLPSGTGTSAAFLAKYSKFKVFTCACVGDIKYLKKQILTLDPSYDF

SNLEFLTSDKKYHFAKPYKEFYELYMDLKLKCNIEFDLLYDILGLSIALKQEWKKPLLYIHQGGILGNST

MLERYKFKKLV

>ABV52160.1 chemotaxis protein MotB, putative [Campylobacter jejuni subsp. jejuni 81116]

MKNESKEDSNFWIAYADLMAGLLFVFILLIGAIVVKYVLTQSDLKEIKDNLNKQEARLEESKEELRNKEA

IVFKLSSDLNNASSALNLANSQKAELEANITNYKQLSKDLNLTLDNKDKQILILLGQLEKKDEELKNLQE

DFQKAKEKVQNLGLIRENLSKELQSKLDNNITIDEKTGSISLPAEVLFDKDSYVLKNEAKASLRKILSEY

FDAILEDPKIFSNIENIIIEGHTDSDGSYIYNLDLSQKRAYEVMNFIYTFYKSDKLQKLLMASGRSFSDP

VFVNGVEDKDKSRRIEIKFSIKNDNALKDVEKFFEFH

>ABV52159.1 hypothetical protein C8J\_0560 [Campylobacter jejuni subsp. jejuni 81116]

MDIKSDEISELVLPEGKDARGSLVYFKIIFIPAFLYILILLGYFNVIDFKVELHTVIMTGVIFFTALIFA

RHSAEYAYSIFEQQKDEFKQALKRHIMRHFLAIGKDTKSNANFDDFAYTYIKGARNENFASIGSAIFPMM

GILGTFISIAFSMPNFSSSDTAALEQEIADLLSGVGTAFYVSIYGIFLALWWMFFEKYGKSKIDRLLNRQ

KNATSGFFWTKEELDQRYLTESLQHFEKIGAIFKQVSNDDFFAELDHAIDRKFGIFQDMLNVEEKAIRLS

SEHIKQTMGELSKAQRDQRDLGKLYSEMLNGIGLLNQNLKEINTRMSEQYNRLLDISSDKIHHLDKTLSA

FDEKVERFGKNFELYEKAMLESQEKVFEGFKASLFEGMHKFKEVYEEEKSIDAKIKMMDELKKEMKALDE

ETSQMMSKLSGDENQNKENETKQIEDFSESKTEENQDEIQAEISKQESNDELKNEDKENK

>ABV52158.1 fructose-bisphosphate aldolase [Campylobacter jejuni subsp. jejuni 81116]

MGVLDIVKAGVISGDELNKVYDYAKAEGFAIPAVNVVGTDSINAVLEAAKKVNSPVIIQFSNGGAKFYAG

KNCPNGEVLGAISGAKHVHLLAKAYGVPVILHTDHAARKLLPWIDGLIEANAQYKKTHGQALFSSHMLDL

SEESLEENLSTCEVYLQKFDALGVALEIELGCTGGEEDGVDNTGIDNSKLYTQPEDVALAYERLGKISDK

FSIAASFGNVHGVYKPGNVSLQPEILKNSQKFVKDKFALNSDKPINFVFHGGSGSELKDIKDAVSYGVIK

MNIDTDTQWAFWDGVREYELKNRAYLQGQIGNPEGDDKPNKKYYDPRVWLRSGEESMVKRLEIAFEDLNC

INKN

>ABV52157.1 cell binding factor2 (major antigen PEB4A) [Campylobacter jejuni subsp. jejuni 81116]

MKKFSLVAAALIAGVALNVNAATVATVNGKSISDTEVSEFFAPMLRGQDFKTLPDNQKKALIQQYIMQDL

ILQDAKKQNLEKDPLYTKELDRAKDAILVNVYQEKILNTIKIDAAKVKAFYDQNKDKYVKPARVQAKHIL

VATEKEAKDIINELKGSKGKELDAKFSELAKEKSIDPGSKNQGGELGWFDQSTMVKPFTDAAFALKNGTI

TTTPVKTNFGYHVILKENSQAKGQIKFDEVKQGIENGLKFEEFKKVINQKGQDLLNSAKVEYK

>ABV52156.1 endonuclease III [Campylobacter jejuni subsp. jejuni 81116]

MKRNLEIKELFLKHFDKPVTELKFSNLYELLVCVMLSAQCTDKRVNLITPDLFKAYPDIKSLANANLSSL

KTYIQTCSFFNNKAQNLIKMAKAVCENFDGEIPLEEEKLKSLAGVGQKTAHVVLIEWCGANFMAVDTHVF

RVSHRLGLSKAKTPEATEEDLTGIFKDNLNYLHQAMVLFGRYTCKAKKPLCKECFLNHLCKSKDKELK

>ABV52155.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKIFIFLLAISLNIFALESYKPSADFSSYFNNINCSQILDKFFYLNCYDYKLKGTKAVAYKVEASNLKDK

QIKKRPRFEDDTNIPKKYRTTWSDYKNSGYTRGHTAPNASFSFSKAAQNSVFLMSNITPQIAQINNKIWN

EIEQRERNLAFKFQSIEVLNLVLYDKEPLYIKNRIAIPSFYVKIIKTPKFKECYQVPNHEVNDENIKQYQ

INCDKF

>ABV52154.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MEINALTITTLYIIGISAEGMTGALAAGRHKMDLFGVIFIALVTAIGGGSIRDVLLGHYPLTWVKHPEYI

ILICFCALVATKIPRVVTKLETLFLTLDAIGLVVFSILGAQIAIDQNHGFIIAVAAAVITGVFGGILRDI

LCMRIPLVFQKEIYAGIAIIAGAIYYSLIIWLELNALVCTLLTLFIGVFARLLAIKYQWSLPIFSYNEEK

>ABV52153.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MRRLSILLTILIVINITACDSKTENYYKNHPSEAKEKAKECKESGTLSEDCINALKVGVKPTNEESKYSP

NTPKKSDNQILEALKQNDLKKEKTTKDINQSSENNESIIIPPITETPSEIYPSKTTENNQSSIFSDDVNI

TQEKLP

>ABV52152.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKITLFLSLIGIFFAACEQTKSVEYYQNHPEEAKKRSLECRHKAIISQDCVNAYRVGFPKDEWEDENISN

P

>ABV52151.1 hypothetical protein C8J\_0552 [Campylobacter jejuni subsp. jejuni 81116]

MKDELFKQSPKKQFEFDKSVASVFDDMINRSVPFYRENLELCGNLLAKILPINASICDLGCSSANFLIFL

ANLRKDFKLFGVDNSASMVEVAKSKAKAYGLDISFFETNLCEFDFFVCDVFVANYTMQFIRPPKRQELLD

KIYKNLNSKGILIMSEKILYEDAFLSKNIIELYADYKEKQGYSKFEIAAKREALENVLIPYSQKENLNML

EKAGFKKIESIFKWANFETFIAFKD

>ABV52150.1 putative riboflavin kinase /FMN adenylyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MNIFTTISKINITSLAIGCFDGMHLGHLKLVKCLDENGALLVINKFKGQFLCSNRQKEEISGKKVIEVDF

ESIKSLDGKDFLSFLKKEFVNLKFIVVGYDFSFGKNRAYNAKDIEFLSGIKTIIVDEFSIGGIGVHASLI

KDFLSKANLQKAKEFLGRDYSIKGKMIKGQGLGSKELFATINLDCKGYFLPQNGVYATLLKSQRKIYKSV

SFLGIRSSDENFAIESHILEELGEKFTQGEFFELEFISFLRENQKFQDLKKLKNQIAKDIEQAKELLRKN

DER

>ABV52149.1 hemolysin A [Campylobacter jejuni subsp. jejuni 81116]

MRFDFFVSKRLNISRNKALELIENEEVLLNGKSFKASFDVKNFLENLKKTQDLNPEDILLTDGLKLDLLS

EIYVSRAALKLKNFLEENDIEIKHKNCLDIGSSTGGFVQILLENQALKITALDVGNNQLHLSLRTNEKII

LHENTDLRAFKSEEKFELITCDVSFISLINLLYYIDNLALKEIILLFKPQFEVGKNIKRDKKGVLKDDKA

ILKARMDFEKECAKLGWLLKNTQKSSIKGKEGNVEYFYYYIKN

>ABV52148.1 hypothetical protein C8J\_0549 [Campylobacter jejuni subsp. jejuni 81116]

MSLLKNSSYILTLLSLFGFLLTWQRTVFSLFFLIPIFLTLFWEFFLFLKLRKNIIKEATLIKGSLFYRIS

MGDFYLYIFSFFLAIFGLISLFLNFLNLEKIDFVFIFIILPLLMIFLKKELHLQFVDNAYNDFRIVVIAS

FFTALFYAFYGLFFTYNEILNLELFSRKIIAYKSASFVYFDFLSEFLHFISNLKFFIFSYFGYLGFRVLN

FIFDFFNFFMFCSLLAFVFNFVLKIKIKIIVLFLCFIMVLGSYFLKEQRNNALKSEQEQILLWMNNFDFL

KDNNLSLIQKEKDLFEKDLKDLREIFKKNAFEIGIWWFSKEKEDLEKRINESLK

>ABV52147.1 DNA ligase [Campylobacter jejuni subsp. jejuni 81116]

MKKEEYLEKVALANLWMRAYYEKDEPLASDEEYDALIRELRAFEEQNKDEISKDSPTQKIAPTIQSEFKK

IAHLKRMWSMEDVFDESEFRAWAKRAKCEKNFFIEPKFDGASLNLLYENGKLVSGATRGDGEVGEDITLN

VFEIENIPKNIAYKERIEIRGEVVILKDDFEKINEKRALLNQSLFANPRNAASGSLRQLDTSITKERNLK

FYPWGLGENTLNFTKHSEVMQFIRELGFLKDDFVRLCVNLDEVLKAYDELLALREKKPMMMDGMVVRIDD

LALCEELGYTVKFPKFMAAFKFPALEKTTRLIGVNLQVGRSGVITPVAVLEPVNLDGVVVKSATLHNFDE

IARLDVKINDFVSVIRSGDVIPKITKVFKERREGLEMEISRPKLCPTCQSELLDEGTLIKCQNIDCEDRL

VNSIIHFVSKKCLNIDGLGENIVELLYKHKKITTLESIFHLKFNDFEGLEGFKEKKINNLLNAIEQAREC

ELFRFITALGIEHIGEVAAKKLSLSFGKEWHKQSFEAYANLEGFGEQMALSLCEFTRVNRTRIDEFYKLL

NLKIEKLEIKSDGVIFGKTFVITGTLSRSRDEFKALIEKLGGKVSGSVSKKTDYVLFGEEAGSKLIKAKE

LEIKCIDESAFNELVKE

>ABV52146.1 putative dihydropteroate synthase [Campylobacter jejuni subsp. jejuni 81116]

MKFFKINPNTDFNLLCSFINPHKMGQKIMSEKTKIHFIFIKDISTPAANILKQDALRVGAELITHKEVIT

AKITHSNVLLMASKEQIQKLIVKEKLQDFGLKNLALFLQKDFLKPKKAELMAVINVNEDSFNAKSRVSEE

DFEKRLNDFLALKPEYIDIGAVSSRPGSEYCGKEEEFKRLKKVLDLIYEKNYYEQAIFSLDSFDEYCLEY

ALNKGFKLINDITSLRNLNLAKLASKYEAKYCLMHMQNNPNNMQDNPFYEDLLDEMTLFFKEKLELLESF

GVKESILDVGIGFGKSAGHNMILIKHLEHFLQFNKPLLIGASRKSVINAYFQSEIKDRLAGTLYLHLKAF

ENGASIIRVHDLYEHKQLFALAQAMDNIGV

>ABV52145.1 DNA polymerase III, delta prime subunit-like protein [Campylobacter jejuni subsp. jejuni 81116]

MFISKIIISEDFLGIKEEMINNFGIKKLRFFMPQNEFLLDDARAVEKESYIAETEEKIIVLMADSYRIEA

QNFLLKLLEEPPKNIKFLIVIPSKNLLLPTIKSRLICEKRKVEKEVKKLDLDLKRMDLRMLFDFLQKNEN

LDKNELMDQIALLAKECVKYKDFNAEELEFFYESYELAKLNSKSGVLLATLLLNYYTKK

>ABV52144.1 hypothetical protein C8J\_0545 [Campylobacter jejuni subsp. jejuni 81116]

MSDFLSFTLENIRNGGAFMAWLESRRLEWAPLMAARLKYLLEGRTFVLMCDEQRSWYEEYFLKNINSKAA

RPMLPFVSLNSLCKKKVQSSEDIALLNDLLDISFPNGYVYFYIGSAFDNKSLIAKSRDDSLLWLFDEQLQ

DSFYLNSKDKDLDIKLISLYQLFDVSLDAILFSRVQLG

>ABV52143.1 aspartate kinase [Campylobacter jejuni subsp. jejuni 81116]

MLIVQKYGGTSVGTLERIEAVANRVIQSAQQGNQLVVVVSAMSGVTNTLIEQAEYFSKTPNGKDMDMLLS

SGERVTSALLSIALNEKGYPAISFSGRKAGIITDSVFTKARIHHIDTKAIKSELQNGKIVVIAGFQGVDE

EGNVTTLGRGGSDLSAVAVAGALNADLCEIYTDVDGVYTTDPRIEPKAKKLDKISYEEMLELASLGAKVL

QNRSVELAKKLNVNLVTRSSFNNNEGTMITKEDGMEQALVSGIALDKNQARVTLRNVEDKPGIAAEIFSV

LANENINVDMIIQNVGVDGATNLGFTVPQNELELAKNAMQKILSSKTTIESDSAVVKVSIVGVGMKSHSG

VASKAFKALADEGINIGMISTSEIKISMIVHEKYGELAVRALHECYGLDK

>ABV52142.1 probable (di)nucleoside polyphosphate hydrolase [Campylobacter jejuni subsp. jejuni 81116]

MENEKNYRPNVAAIVLSSSYPFECKIFIAKRSDMDNIWQFPQGGIDKGESVKNALFRELKEEIGTDEVEI

IAEYPEWLSYDFPSKIVKKMYPYDGQIQKYFLVRLKHGATININTKHPEFDDYQFVSVKQIFEMINHFKK

NIYVKVIKYFEEKGYI

>ABV52141.1 coproporphyrinogen III oxidase [Campylobacter jejuni subsp. jejuni 81116]

MHFYIHIPFCESKCNYCAFTSLKKNDYEKAYFKALKEDIVFQLKQFNIQSNQIKTLFIGGGTPSCVDAYN

YEDIFKILYPLLDKNVEISCEANPNSATLNWLKNMKNLGVNRISFGAQSFHPKKLHFLGRIHNQEMIIKA

LENANKVGFKNINLDLIYDTKLDNKKMLEFELLHLKQIKALITHLSAYNLTIESNTAFAKKEHFKKNAPN

LMKFFIKQLLELDFFQYEISNFSKTKSQICKHNLAYWQGKNYLACGLSAVGFYENKRFYTAKNLKNYIEN

PTFRSIEQLSSKDLNLEHLFLGLRSIVGIDETKLNQWQKDKINILLKEKKLFYKNKRYFNPNFLISDELA

LYLSS

>ABV52140.1 putative sec-independent protein translocase [Campylobacter jejuni subsp. jejuni 81116]

MSFGEIIVILVVAILVLGPDKLPEAIVQIAKILKAVKRNIDDAKSSIEKEIRINDLKEEAKKYKDEFSST

NENIRKKLSFEEFDDLKRDILDKTKVDLTFDSRDDNTKNNLSGQNLNTEEKPNLSKLETQDKTEK

>ABV52139.1 sec-independent protein translocase TatC [Campylobacter jejuni subsp. jejuni 81116]

MFEELRPHLIELRKRLFISVACIVVMFIVCFALRSYILDILKAPLIAVLPEVAKHVNVIEVQEALFTAMK

VSFFAAFIFSLPVIFWQFWKFVAPGLYDNEKRLVVPFVSFASIMFALGACFCYFVVVPLAFKFLINFGLN

EDFNPVITIGTYVDFFTKVVVAFGLAFEMPVIAFFFAKIGLIDDSFLKRHFRIAILVIFVFSAFMTPPDV

LSQFLMAGPLCGLYGLSILIVQKVNPAPKDKESDE

>ABV52138.1 S-adenosylmethionine:tRNA ribosyltransferase-isomerase [Campylobacter jejuni subsp. jejuni 81116]

MNKDLLLSSYDYTLANELIANYPTNPKEDARLLVFDRKNKEIFHTTFKNLQDFLPNCAIFFNDTKVIKAR

IYGNKVSGGKIELFLHQPFLNSHNPLFLAQIKGRVKKDEILYFKKDLKIRVVELLNDGLRKVQFFQNDKT

LDTSNLYNLLDKIGHIPLPPYIKREDEKSDLKDYQSIFAKNLGAVAAPTASLHFSETMLENLRKKHEIYH

LTLHVGAGTFKSVECENIQEHKMHSEFFNIPQQACEIIDSKQAILGVGTTVTRTIEYYARTKTKSGFCDL

FLHPQNPPIRQNHLLTNFHLPKSTLIMLVSAFIGREQCLKLYELAIKEKYRFYSYGDAMLIL

>ABV52137.1 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKLSEIAEFLSLEYKGEDIEISALNSLLKANFTELTYCDGEKNTKDIPHTGAAAILVSKEYENLVPKDTK

ALITQSPHLSFAFLSKLFAKPLISTAKEKVQNIAKSARIMPNVYIGDNVNIGENVIIMAGAYIGDNVSIG

DESIIHPNVVIYNDTKIGKKCHLLANCVIGSDGFGYAHNKNGEHYKIYHNGNVVLEDFVEVGACTTIDRA

VFDSTIIKAGTKVDNLVQIGHNCNIGQNCIIVAQTGISGSSELGRNVIMGGQSATSGHLKIGDFSTIAAR

GGVSKNLEGGRVYGGFPIMLQKDWLKLQAKIAIKFKEKSQD

>ABV52136.1 acetolactate synthase small subunit [Campylobacter jejuni subsp. jejuni 81116]

MRRVLSVIVLNEHGVLSRIVGLFSGRGYNIDSLTVAPLENKEFSRINIVTSGNERTFEQIVKQLHKLIPT

YKVIESEEFIDKEMALVKIPLNENLGGLDAVLKAYNGTIANSNENFLFLMVADDANRIDNFLKTIKKYNP

SDIVRSGSVLMEIK

>ABV52135.1 acetolactate synthase, large subunit, biosynthetic type [Campylobacter jejuni subsp. jejuni 81116]

MKELSGSAMICEALKEENVKIVFGYPGGAALNIYDEIYNQKYFKHILVRHEQAALHAADAYARMSGEVGV

AIVTSGPGFTNTITGLATAYSDSIPLVLISGQVANSLIGTDAFQEIDAVGISRPCVKHNYLVTCIEEFPR

ILKEAFYIARSGRPGPVHIDVPKDVSATLGLWEYPKEISMKTYKPVYKGNSKQIKKFAELLKEAKRPLFY

LGGGCISSNASEQIRELVKFTKIPAVETLMALGTLRSDDVFNLKMAGMHGSYAANMALSECDLLVSVGAR

FDDRITGKTSEFAKHATIVHVDIDPSSISKIINAHYPIVGDIKEVLKELLEELKKENFNTTFKEWHETLK

RYNELYPLSYEDSNEILKPQWVIEECAKMAPDARIITDVGQHQMWVAQFYPFNYPRQLATSGGQGTMGYS

LPAALGAKLAVGEEVVINFVGDGSVLMNIQELMTAYEYGIKTINIILNNAFLGMVRQWQSMFYKEHFSQT

DLSTQPDFIKIAQGFGCEGYEISNKEEFIQAFSQALKSDKTSLLNVKIDRFEDVLPMVPAGGAIYNMILP

KAKDRQ

>ABV52134.1 GatB/YqeY family protein [Campylobacter jejuni subsp. jejuni 81116]

MTLKEQILNDIKEAMKQKDDFKRDSLRTLNAAFKQIEVDERIELDNERIYKIIASEIKKRKDAIELYLKA

NREDLAQKEQNEISLFEIYLPKQLSDEELTLALKQLIEELGVSSLKEQGLVMKEAKIKLGASVDGKRLNL

ALKELLQ

>ABV52133.1 3,4-dihydroxy-2-butanone 4-phosphate synthase [Campylobacter jejuni subsp. jejuni 81116]

MKFVSVEQAIKDLQAGKMLVMVDAEDRENEGDLIFPAQFSTQEKVNFMIKEARGVVCVALDETLAKKFEL

PLMVPKNTSNHETAFTITVDAKDATTGVSAYERNMTIQIFADDNAKASDFVRPGHINPLIAKKGGVLERT

GHTEGTVDLCKLAGLKGACVICEIVKDNGDMARREDLEIFCQKHDLNMIAVSDLIEYRLKHESLIKLEEK

SQSVLAGFKAEKFIFSDHNQTQHIAFCFKDIKKCENVKFHISGSDFELLTSDKFSKLLEQIKFLSENGGV

IVFMQGEKSSTTQYKNYGIGAQILRYFGIEEIKLLSQSCDKDYIGLEGFGLNLKACNFN

>ABV52132.1 putative transcriptional regulator [Campylobacter jejuni subsp. jejuni 81116]

MKEYDKLSIRLVQILSKFNNGESLSAQELAQEFNVDTRTIQRDLNERLTFMPIKKENGRYVLESFALGKL

SFKDIQNFATLSGIAKLYPKLDQGFIVDLLSHRVNKVLMVKNEGFQKVDYELFKDLSVAILKHNVLIFFY

KEKERQIKPYKLVNYKGIWYLLGDENDKLKHFNLDKISKFRTKNENFIPNEKLEEQIQNDPNIWLGESKE

VILKLDKNAKEYFFRKEILSNYQIIDEDETSYTLSTQVSYEDEILHLVKQWIPYIKILAPIELKTRLENI

LKSYLNNLSK

>ABV52131.1 hypothetical protein C8J\_0532 [Campylobacter jejuni subsp. jejuni 81116]

MKDPSLYDLAYNVQGKSFILKDFFTQKPNLGSIKFLLRHENIQCHLGKSLTQFINYPFSKSLTLIQEIRN

EAVHAKAPSLNEVKKLRNEILGIEGVSLLKSILTHKEIS

>ABV52130.1 hypothetical protein C8J\_0531 [Campylobacter jejuni subsp. jejuni 81116]

MNHLLILYNPYYQEDVIKQHLSILQEKSQVAFGKIKSKLNDQEKQNFLEEIYQSTNEENFLQLFLSDYAN

LFVAKVVKISKNVDESLIPSYYKEKNLEVEDFFIISDLRELVREDFSLLRDKFLANFITPNDHTYAIYGN

NYTYPLPVRLKEECSYFLGDEKHYLSVYKSKEYLVMQENFIRFVFGKRIFYLLHPDSISNIIHAELELLQ

SENDLLNDFTSIVVKYS

>ABV52129.1 hypothetical protein C8J\_0530 [Campylobacter jejuni subsp. jejuni 81116]

MFSKIFSSLSLANAFKGFLFKRISSPMQSARIISMVLDIKNAFNDSKDQASSICKTLDLIVNFKKEHPQD

FNELFEILKDLIQEYEQNPNEIKQNLKEILK

>ABV52128.1 hypothetical protein C8J\_0529 [Campylobacter jejuni subsp. jejuni 81116]

MGLVGTRVNIKMKKINQNVFFPKFALIVKNQHDFEAPEILNPDNCYGYRRCTLCSIQVFDNFHNYYEIKK

DSKCRMHEKCNLCGHERLGQTRHNWKYDESGQKICLDCKETV

>ABV52127.1 hypothetical protein C8J\_0528 [Campylobacter jejuni subsp. jejuni 81116]

MNFLSSLKDKAVNASEAIKDKTIKTAEVVKDIGMEVKCGIGWHAGEYQNEKDKPKCFFSKICPDCEKST

>ABV52126.1 hypothetical protein C8J\_0527 [Campylobacter jejuni subsp. jejuni 81116]

MLELITQKDQDFLQNIENLDEEYIQKFINKKISEIAIAIETAAENADKAKDRTQKAKNLNTDSDWQTYIP

IFGRWLGETSEEKKEIKSNMILEVAELQNESMNQMTTILKEVVIFFTSSFCIATRMNQALSLIIAQGFVK

SDGKVIRLSKAAKEQFQQIQKFTLSFIEDHEKHKDTINNIQVELDKKNQIDDEQYKLIEKHYQEFIQYKN

YNDKIVQEQECKINELKDILNKRKNVFTNSISILALIVSVASIVLYFIGR

>ABV52125.1 hypothetical protein C8J\_0526 [Campylobacter jejuni subsp. jejuni 81116]

MNNYIHLEELDLKANYADLEKELENLSKKECLRIEIDKGLENSLKELEDLMEKLPEQQTQTLFEQCTKNA

MDAVTGHFGLASTILNAKDGGNVTTLHNFEKGIVATEEDLQKLTKYQQGYKRDSNYDKIKDNIRDNSPKI

VRSEYTGEEMERGAGKNKAQLDHVISLKEIDRDPNMHLFLDDAIRAEIANHPDNLKWLDASANASKGDRD

LMEWGKEIDPKTGKTNFEKYGIDEKKAEKIYNTAKSNLKKKVIKEKIVKYSNEVLSTGAKDSMKIFVYSA

FGVVLKDFIEAVVIELKTTFREFGKENIKEIFKRFARRMEKVWEKIKAKWKDIFKGSLEAGIQAFFSNLL

VFIINTIFTTLKKIVQIIRAGFTSLYQAVKIIINPPKNIPKDEIYFEASKIFVSGMISAISMLGSEMIHK

FLLSIPGFNVFLSLPIPFTDETIGDALSLCISAAGGAVLSTIAIFYMDKWRSNSKIGNLQIQIVTQKNLI

VQYKIAKTWFALNDAYHIVKNETLATIQQIKKDNQIREQSSQEVETAIEEFENCNITKKLYKKLNQTKEN

>ABV52124.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MGIILGILNLIAGFVAIVLMCSLYFIVFMVFVGMAILIFLSMQPYPYNIIFCAIYLITILALVLWRKT

>ABV52123.1 hypothetical protein C8J\_0524 [Campylobacter jejuni subsp. jejuni 81116]

MLKQIAFGGIALTATGYGIKKLYEKLSKPERKFDTHAIVPSCKDMINTEEYKLKREVEVEQKKNQIQEFL

CECMECYSGFSKYFNSKEFLEFEQNFTSKNNHKTEFLLSSYKDQMIKVIDYAKKFECLSAFLETQSEKND

LAVVKMISESMERKTQRFYLQTKFQTFPQYIFPSVWSSPMWNKQWE

>ABV52122.1 replicative DNA helicase [Campylobacter jejuni subsp. jejuni 81116]

MQQEYYDLDLERAILSSCIMSEEAYASIAGDISPKDFSLKAHQDIFKAVIACSNNKEPISVSFLRKHKKI

DEQILAEILATPSMIDLPAYVNELREKSVKRQLLSFAHLLPTRINEDRAVSEIADEIGKEIFSITNRVNS

RDIKDVDMVISELFEEFKKQKTLENKGIIGLDTGFEGLNKMTKGFKGGELIIIAARPGMGKTTLCLNFID

KILRQKKGVALFSLEMPATQIMQRMLSSKTSIPLQKILTADLNDDEWERLGDACNDYSQKKLYIYDSGYA

TIADVRAILRRLKSQDESIGLCVIDYIGLMMSNSNFNDRHLQVSEISRGLKLLARELDMPIIALSQLNRG

LEQRANKRPLMSDLRESGAIEQDADAILFVYRDEVYREQEEKERENKAKAEGKAYQRLFIPNPMQENAEI

IVGKNRNGPVGTIEVVFLKEKSCFVDKPIGYETTEFTG

>ABV52121.1 hypothetical protein C8J\_0522 [Campylobacter jejuni subsp. jejuni 81116]

MKKYLFSCVLASILTQSATAVEFQEGFSGNLSIGVGARDIKSNISTLANSDYLSSYNADNSDSSFIPFIG

VELYYGNLIDNDRIFIKNYNGRDISGIALGYERAYLERFSTSFSVISSLREKAYANPYATGNREETDVDR

YGFKISQLYESDFGKFTTSYLFSKNKYDKDTIAQSSLKREGYYHEFELNYNYSLLNLGLNYDYNDADGKA

QSYSRYGFSIGTNLAFANDYIFTPNLNLSKYEAVGTDPIFHKKQDGNIVKLNLKVVKNQFLGYNGLYGFA

NYGIEKRNSDIGFYDETYQIVLTGIGYKF

>ABV52120.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MSSIFSTLSPFRLFVKCAVPNVISMAFISFYYIVDGIFVGKYLGSDALAALALIIPFIMMSFALADMIAI

GSAVQISMYLGLGKKNLARKIFSSSMLIIFIISCFIGILEYFLGPVLIDCLNVSDEIKTMAKECMFVFAL

FAPFTMLSFALDNYLRICGKTAYSMVMNVIIALSNIVLDFIFIVELGWGLFSAALATCLGLVLGGIFGIF

PFLFQNLELKISSLYMNLKIFKNILYNGSSEFFGNISGSLYSIFANFVLLKISDTQAVAAFSIVLYIDSF

IIMLIIAMGDAMQPALSYNYAKKDFSRIKAIIKVVFFAGGFLSLFSIVLILIFGENLITLFTKENNQEFK

TFAYTALMLFAFNYFFAWFNVLSGSFLTAFNKASFSLVLSLAQNLFIPLFFLLFLSYFIGLNGVWLSPFF

AEFCVLILAWIFLKRIFKDLSL

>ABV52119.1 oxidoreductase [Campylobacter jejuni subsp. jejuni 81116]

MKKIDLIVVGAGPTGIGCAVEAKLKNKEVLILEKSNNICQTLMQFYKDGKRVDKAYKGCEGTNHGHVPFE

DGTKESTIETFQNALKEHNIEVEFGSEVESVKNENGVFLVSTAKGVYECKNIIVAIGRMGKPNKPDYKLP

MTLTKIINFNANSVLANEKILVVGGGNSAAEYAVDLANSNQVSLCYRKKEFTRLNDINLKDIHEAGNSGK

VELKLGIDINEVEDDNGKAKVNFTDGTSDIYDRIIYAIGGSTPLDFLQKCGINVDDKGVPLMDENKQSNV

KGIFVAGDIATKNGASIVTGLNDAVKILSVL

>ABV52118.1 gamma-glutamyl phosphate reductase [Campylobacter jejuni subsp. jejuni 81116]

MRNLLENIKKNSQKLLNLTPKDKEKIILKLAQILRENFKIILEANKKDMANFTKSGAMKDRLLLDEKRIL

ALCEGLEKIAHIEDPIGKISKGWKNYAGLNIQKISIPLGLICVIYEARPSLSAEIAALMIKSSNACVFKG

GSEAKFTNEAIFTLVNKVLKEFDLQDCFAMFTQRDEILQILAFDDLIDVIIPRGSSNMIQEIANNTKIPL

IRQDKGLCHAFVDQSANLDMALKIILNAKCQRVSVCNALETLLIHEKIAKNFISLLIPEFEKFKVKIHAH

ENALAYFNNSNLEVFKADENTFDTEWLDFALSVKLVKDCDEAIEHINKHSSLHSETIISNDASNIAKFQR

LINSSCIYANASTRFSDGGEFGFGGEVGISTSKLHARGPMGVEDICTYKYIISGEGQIRE

>ABV52117.1 hypothetical protein C8J\_0518 [Campylobacter jejuni subsp. jejuni 81116]

MLKQHFKEIAKLNSSEQVWQMPFFAALGVGIVLGLSVFFGKLNYGLIAMIGALSFLYVPNTPLYHRMAVV

MCCSFGIVSSFFLGILTHFLPAIFAFIPIGLVAMGSSILIRYYNIGAPGYFFFVFSCVLGAYSPFEAKDF

IFLVGLVFLGAMVANLMALLYSIVVIYGFKNALPSEIPPREYICFDAVFVDSLIMGSFVAFSIFIGTFLE

LERSYWIAISCTAIMQGVTLNSIWIKQIQRIIGTALGVCFAWWLLSKQFHDIELVLLMMSLFFIGQFLVN

RNYALAMIFFTPYATYLSKAANFMSENADTLILARLIDVVIGSILGLLGGFVIYKPYLRVHFERIAKYIF

RIKRKA

>ABV52116.1 hypothetical protein C8J\_0517 [Campylobacter jejuni subsp. jejuni 81116]

MKIDTHAHIFLKKLNTVANARYKPDYDASFKDYKANLDHYGFDKGVLVQPSFLGVDNEFLLQSIEKDENI

KAIVVVDEGIKFDELKKLKERKACGVRLNLIGKELPNFKTMVWTQFFENLSKLKMQIEIQRDLDNNLVDI

VKNLIPYGCNIVIDHLARANANLTNLEDLICLKNSRIFFKISGFYRAKIDYVNNEQAVKFAKKIYEILKE

YFPLSNFVFGSDWPHTNFEANVNFSSALAAFNEVVVSKKEQEQILGDNACALFDF

>ABV52115.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MVFLIISSIIVAIILGYITRHNVGIFAMIFAYIIGAFFMDLAPKKIIAFWPISIFFVIFAVSLFYNFATV

NGTLEKLAGHLMYRFANHPYLLPFVIFVVSAIIAALGAGFYTVLAFMAPLTFLLCDKIGLSKIAGAMAIN

YGALGGANFMTSQSGIIFRGLMENSGIEANEAFVNSSIIFAFTIILPIVVLSFFVFNAFKNNIKISVISK

PDSFDYKQKTTLILMFMMIVVVLIFPVLNIIFPHNETISYFNKKIDIAMIAMIFVAIALFLKLADEKQVV

ALIPWGTLIMICGVGMLISIAVEAGVIKLFSDLVENEINVIFIPLIMCAIAAFMSLFSSTLGVVTPALFP

IVPSIAASSGLSEALLFSCIVVGAQASAISPFSSGGSLILGSCPDKYKEKLFKDLLIKAVPIGFIAAILA

TIIMSFIL

>ABV52114.1 hypothetical protein C8J\_0515 [Campylobacter jejuni subsp. jejuni 81116]

MEKFIKQFSFIALENIFRELPNKITHSFNDINDIKPPKLMYPIFYGSYDWHSSVHSHWLLVKILKDFSHF

APKDEIIKALDSQFSKEKAEGELKYLQNPAHKGFERPYGWGWFLKLALEINLLAKENDKAKIWAKNLEGI

ADFFVKEFKEFLPKMDYPIRVGTHFNSSFALYFALEYARFKKDQELEYCIIQSAKKWFLNDKNMQALEPC

GDEFLSPVLMEAVLLSAVLPKNDFVKFFKVYLPNLEAKEPVTLFTPVSVSDRSDGKIAHLDGLNLSRAWC

FKILSNFCDENLKILLRNNAIEHFDKAIAHIEDDYLGSHWLGSFALLAMDVDIL

>ABV52113.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MISLDLLYYIVGILFLVFGILSFSNQAKDIKSRISGGVFWISYSFTFLLAGVLPHFVMGCIVILLALIAG

FNLLKPAKIEVSKEEKEYEIKHANIYKNKLFIPALMVPLITLIGTFLFPYLSFFENKNATLMALIIGIII

SSVVACFMFKASPKRAVKDAAHTMDHISWAALLPQILATLGVVFVSTGMGDQVSKLLSSYISLDNAFIAV

AVYCIAMALFTIVMGNAFAAFPVITAAIALPILIIQMHANPAIIGAIGMLSGFCGTLMTPMAANFNIVPA

ALLNLDDKNGVIKAQFMSGLVLLVANIFLMYFLAFRF

>ABV52112.1 hydrophobic protein [Campylobacter jejuni subsp. jejuni 81116]

MEWLLLASIPLIVLGFALKINPFLVVTSVGIYAGLVSGFDFIKVVSDIGKSFVDNRYVAIIWLILPLLAV

LERKGLREQAKNLISKIKVASTGRILMCYFVFRQVTAALGLLSLGGHAQMIRPLIAPMAEAAAKLKFKNL

THKDSQKIKAFSAGTDNVAVFFGEDIFIAVHSILFIKAFYESNGIIVEPLHLSVWAIPTGILALIIHCSR

LYLFDKRLEKTYKGLSDDKS

>ABV52111.1 elongation factor P [Campylobacter jejuni subsp. jejuni 81116]

MASYSMGDLKKGLKIEIDGIPFKIVEYQHVKPGKGPAFVRIKIKSFIDGKVLEKTFHAGDKCEAPNLEDK

TMQYLYDDGENCQFMDTQTYEQVAISDDDVGEAKKWMLDGMMVDVLFHNGKAIGVEVPQVVELKIIETAP

NFKGDTQGSNKKPATLETGAVVQIPFHVLEGEVIRVDTVRGEYIERANK

>ABV52110.1 hypothetical protein C8J\_0511 [Campylobacter jejuni subsp. jejuni 81116]

MKQWLSDFKLALIQEDVNKLENLLDELDMKAFIKNLTKESPSEDFLKENANDLFYQVQALLQEAVMLIEQ

KKKTKAVEIQKFQKALTYFKS

>ABV52109.1 flagellar protein [Campylobacter jejuni subsp. jejuni 81116]

MQNNLAYNAYSQNQAGIESPQKLIEMLYEGILRFCARAKVAIRNEDIEQRVYFVKRTTAIFIELINTLDY

EKGGEVAHYLSGLYTREIQLLSLANLENNEDRINEVINVTKGLLEAWREVHNNETVAQ

>ABV52108.1 flagellar hook-associated protein FliD [Campylobacter jejuni subsp. jejuni 81116]

MAFGSLSSLGFGSGVLTQDTIDKLKEAEQKARIDPYTKKIEENTTKQKDLTEIKTKLLSFQTAVSSLADA

TVFAKRKVVGSISDNPPASLTVNSGVALQSMNINVTQLAQKDVYQSKGLANDSGFVNANLTGTTDLTFFS

NGKEYTVTVDKNTTYRDLADKINEASGGEIVAKIVNTGEKGTPYRLTLTSKETGEDSAISFYAGKKDAQG

QYQSDPEAENIFSNLGWELDKTTQTIDPAKDKKGYGIKDASLHIQTAQNAEFTLDGIKMFRSSNTVTDLG

VGMTLTLNKTGEINFDVQQDFEGVTKAMQDLVDAYNDLVTNLNAATDYNSETGTKGTLQGISEVNSIRSS

ILADLFDSQVVDGTTEDANGNKVNTKVMLSMQDFGLSLNDAGTLSFDSSKFEQKVKEDPDSTESFFSNIT

KYEDINHTGEVIKQGSLNQYLDSSGTGNKGLDFKPGDFTIVFNNQTYDLSKNSDGTNFKLTGKTEEELLQ

NLANHINSKGIEGLKVKVESYDQNGVKGFKLNFSGDGSSDFSIKGNATILQELGLSDVNITSKPIEGKGI

FSKLKATLQEMTGKDGSITKYDESLTNDIKSLNTSKDSTQAMIDTRYDTMANQWLQYESILNKLNQQLNT

VTNMINAANNSNN

>ABV52107.1 possible flagellar protein [Campylobacter jejuni subsp. jejuni 81116]

MEISKANGQMDTALANISQRTSETQASLNIQTDRSQGQEGDDGQQRGVSEKLADITKKLNEQMDSLDTNV

RFGYSDKIGSMYISVTEKSTGREIRQIPSEEAMRLAEYFRDVIGMIFDKES

>ABV52106.1 3-octaprenyl-4-hydroxybenzoate carboxy-lyase, putative [Campylobacter jejuni subsp. jejuni 81116]

MKEFIQILKENDLLRVIEEPVDVDLEIAHLAYIEAKKGEKGKALLFKNPIDKKLNKQYKFPVLMNTFCNE

KALNLAFGRDYEEVAEEISKLTKLHIPTSFKAKMDFFMNLLSFKNIPPKRLKKNKALYDYEILNSLEELP

ILKTWEDDAGKFITMGQVYIQNLDKTQNNLGMYRLQMSDKNELLIHWQIHKDGANFYHEYKNVGFKKMPV

SIAIGGDPLYIWCSQAPLPKGIFELLLYGFIKKTPAKLTPCENGIFVPYDSDVVIEGYVDLEEFKIEGPF

GDHTGFYTPAELFPVMKVEKIYAKKDAIYQATVVGKPPLEDKIMGLGTERIFLPLLQTSVPDLIDYNMPE

NGVFHNLILAKIDAKYPAHAQQIMHAFWGVGQMSFVKHAIFVDKNAPSLKDYDALIPYMLDRFNTKKILI

SEGICDQLDHASPNSCFGGKAGLDACEEIQVEELEILEDEKLLELFKTKVELLNLKQFYKESKSPIVCIL

LDKKEKIEQSFDKLLEFKKHFRILVFLDAENKLENSYMLVWRVVNNIDAKRDIFIKEERLGVDASAKGEA

EGYLRAWPKQTDCTKSVIEDLILRNILENNPDLFNKFEIF

>ABV52105.1 porphobilinogen deaminase [Campylobacter jejuni subsp. jejuni 81116]

MKLIIATRKSQLALWQSEHVAQILKNTHQIEVLLEGFKTKGDVLLDSPLAKIGGKGLFTKELEESMLRKE

AHLAVHSLKDVPSFFPRGLVLAAVSKREQSNDAMLSQNYKDFLSLPKGAKIGTTSLRRKMQLLLLRPDLE

IISLRGNVNSRIEKLKNNDFDAIILAMAGIKRLNLDKQVNFVYEFSKDELIPAASQGALGIESINDEKIL

ELLKCLNDENALIETSIEREFIATLEGGCQVPIGINAELLGDEICVRAVLGLPDGSEILKDKRMIKKNDF

KGFGESLAKEFIAKGAKELLKKAESMI

>ABV52104.1 hypothetical protein C8J\_0505 [Campylobacter jejuni subsp. jejuni 81116]

MNYKLSLSPLFVLEIIASILFIVFFGFGNFLFFILLSMIFGVILLGIFWKNMLEFQMGGLKDMLTQFSFV

IAGFLLIFPGIITSVFGIFVFFFGIALKLMTKSKYQYTKQEYQNSNEEIIDVEIIEDRK

>ABV52103.1 prolyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MRFTKFYAPSLKEAPKDASLPSHIFLTRAGFIEQIGSGLYNFLPLGKRVLDKIKNIVKEEMDKAGAQEVN

LSFITPASLWQESGRYNVFGKELLRFKDRKENEFVLGPTHEEAMLSLVKNKITSYKQLPLHLYQIGLKFR

DEARPRFGLLRCREFLMKDGYSFHANEEDLGCEFELMYKTYSQILQRMGLDFRAVEADSGAIGGSGSKEF

MVLAKNGEDDILICENCDYAANVEAAKRAKKTCQDERPEANYASKFHTPNIKTIDSLAQFFKINAFYTIK

AVVKKAIYENESKLVVFFIRGSDDLQEIKAQNACSALELVDASEEELEKAGLVAGFIGFVGLKDIDFYID

FELENEKQMIMGANEKDYHLIGIDVVNLNKDRFKDLIEVKEGDCCAKCGAKLKQSKGIEVGHIFKLGQKY

SKAMNANFLDENGKSQPFYMGCYGIGVSRLLAVAIEASHDEKGCIWNKTLAPFVLEIIVSNLKDEKALEF

ANKLYEDLTNLGLEVLLDDRNERFGVKMNDFELMGFPYALVIGKGLENNEIELIQREGLVKELIKTDELM

EILKKKVL

>ABV52102.1 glutamyl-tRNA reductase [Campylobacter jejuni subsp. jejuni 81116]

MYYCISFTHKNTDIALREKLSFSNEAKKSEFLKIISTHENIEECLVISTCNRVEIVAFVKMACAEFIVKS

LALLCDVDKDILLEKADIFEDSGAIHHLFSVASSLDSLVVGETQIAGQLKDAFAFAVKNNFCGVHLSRAV

HSAFKCAAKVRNETQISKNPISVASVAVAKAKELADLAQKKAVVIGAGEMGELAAKHLIAAGAKVIILNR

DLQKAKDLCERLGVLSEYDSLENLKKYLNQYEFFFSATNAPNAIITNSLIEELPYKRYFFDIAVPRDIDI

NENENISVFAVDDLENVVQKNLALREQEARMAYGIIGRETSEFFRYLNDLALMPIIKAIRLQAKEYADKQ

LEIALKKGYLKKSDKEEARKLIHQVFKAFLHTPTVNLKHLQGKMQSDTVINAMRYVFDLQNNLEGLNQYK

CEFDMENNDEIY

>ABV52101.1 polyprenyl synthetase [Campylobacter jejuni subsp. jejuni 81116]

MQKIDELIKQFLEELGYEPILNMLSNVKSGKKLRSKLLLAIADESEIAFKICAAIELIHLASLLHDDIID

ESELRRGARSVNAEFGTKNALMLGDILYSKAFYELSKMDARFTSIISDAVVKLAIGELMDVDLGEKFNIN

KEAYLKMIYNKTAVLIEASARCGAILAGLYEKDFAEYGKNLGLAFQMIDDILDIKSDEKILGKPAMNDFK

EGKTTLPYIYLYENLQEQDRIYLQTLFKKDLNENEKEWLKTKFEEQKALEKAILEAKTYAKKASKAIEKY

DNNKLNDIIKAMIDREF

>ABV52100.1 hypothetical protein C8J\_0501 [Campylobacter jejuni subsp. jejuni 81116]

MFKISPYLICIFFIFSNVLASEPTFDYTYKFILKKDERASVQIKEIGYEDKVQNFDFYWTLFDNTNIIVH

SKFRKYPRQFVMSLRRNLDWVTQTLIPDYTNPHIDRARLILEFSGYNKGLATFTVYIEDKESRLMVEFLD

PRKKALQNPPQNNQVVPMINFNEPQVKPLTSKENNNSN

>ABV52099.1 hypothetical protein C8J\_0500 [Campylobacter jejuni subsp. jejuni 81116]

MDFFDEMFNKTPKEKFIEIIQNGNLGALEKVFEEFFADHIAMVELLEKQGLTEMDVKNFILENGDFIEER

QNDIYIELGAKILGHEG

>ABV52098.1 2-oxoglutarate ferredoxin oxidoreductase, gamma subunit [Campylobacter jejuni subsp. jejuni 81116]

MKYQLRFGGEGGQGVITAGEILAEAAIKEGRQAFKASTYTSQVRGGPTKVDIIIDDKEILFPYAVEGEVD

FMLSTADKGYKGFRGGVKEGGIIVVEPNLVHPESEDYKKWQIFEIPIITIAKDEVGNVATQSVVALAIAA

YMSKCIDLDVLKDTMLHMVPAKTRDANAKAFDLGIKYATQAKPHS

>ABV52097.1 2-oxoglutarate ferredoxin oxidoreductase, beta subunit [Campylobacter jejuni subsp. jejuni 81116]

MAFNYDEYLRVDKMPTQWCWGCGDGVVLKCIIRAIEKLGWNMDDVCLVSGIGCSGRMSSYVNCNTVHTTH

GRAIAYATGIKLANPSKHVIVVSGDGDTLAIGGNHTIHGCRRNIDLTHVVINNFIYGLTNSQTSPTTPKG

FYTVTAQFGNIDPNFDACELTKAAGASFVARGNVIEANKLENLIYKALAHKGYSFVDVFSNCHINLGRKN

KMGEAVAMLDWIKSRVVDKAKFESMDFEERKDKFPTGILHEDNSQPEYCHAYEEVRRAAKEKRMVDLGAL

K

>ABV52096.1 2-oxoglutarate ferredoxin oxidoreductase, alpha subunit [Campylobacter jejuni subsp. jejuni 81116]

MREVIATGNVLIAKAAIDCGCKFFGGYPITPSSEIAHELSHMLPANDGTFIQMEDEISGISVAIGAAMSG

VKSMTASSGPGISLKAEQIGLAFIAEIPLVIVNVMRGGPSTGLPTRVAQGDLFQAKAPTHGDFASIAIAP

ASLEEAYTETIRAFNLAEKYMTPVFLLMDETVGHMNGKAVLPDLKDIKIYNRKKFEGDKKDYKPYAAGEN

EPATLNPFFTGYRYHVTGLHHGDIGFPTEDGVIVKKNMERLIGKIKNNQEDICTYEEYMLDDAEFLIIAY

GSVSRSAKEAIQRLREQGIKVGLFRPITLYPVAEKKIAEVVSKFKKVMVSELNMGQYLEEIERVTSRRDF

ISLHRANGRPITPSEIIAKVKENI

>ABV52095.1 2-oxoglutarate:acceptor oxidoreductase, delta subunit [Campylobacter jejuni subsp. jejuni 81116]

MSMTAPKDTPVWVDEHRCKACNICVSYCPAGVLAMRDDVHAVLGQMIEVVHPESCIGCTECETHCPDFAI

MVAKRDEFKFAKLTAEAKDRAVAVKNNKYKKLA

>ABV52094.1 succinyl-CoA synthase, alpha subunit [Campylobacter jejuni subsp. jejuni 81116]

MSILVNKNTKVIVQGFTGKEATFHAEQCMAYGTNIVGGVTPHKGGQTHLGKPVFDTVADAVKATKADVSL

IFVPAFAVGDSVIEAADAGIKLAVVITEHTPVKDMMFAKQYANKKGMKIIGPNCPGIITSEECKLGIMPG

FIFKKGCVGLISKSGTLTYEAANQVVQGGYGISTAVGIGGDPIIGLAYKELLSEFQKDDETKAIVMIGEI

GGSLEVEAAKFIKENISKPVVAFIAGATAPKGKRMGHAGAIVGSADESAAAKKEALKSYGIHVVDSPALI

GEEIQKILG

>ABV52093.1 succinyl-CoA synthetase beta chain [Campylobacter jejuni subsp. jejuni 81116]

MNIHEYQAKAIFADNGIPTLKGKVAFSVDEAVSNAKELGGSVWAVKAQIHAGGRGLGGGVKIAKNLDEVK

DYASKILGMNLATHQTGPEGKLVQKLYIESGANIVKEYYLAILFNRMAEQITIIASSEGGMDIEKVAKES

PEKIAKVGIDPQIGFKMFHGLEVARVLGLDKDEGKKLISMIAKLYKLYMDKDMNMLEINPLIKTAEGDFY

ALDAKCSFDDSALYRHPEIAELRDITEENPAEREAAEFGLSYVKLDGDVACMVNGAGLAMATMDIINYSG

AKPANFLDVGGGASPETVAKAFEIILRDKNVKVIFINIFGGIVRCDRIANGILEATKNVEVNIPIVVRLD

GTNAAEAKTILDNSNLKNIKAATNLKNGAELVKSLVG

>ABV52092.1 malate dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MKITVIGAGNVGSSVAYALILREIANKIVLVDINEDLLYAKELELTQSIAALNLNIDLLCTKDYTHTKNS

DIVLFSAGFARKDGQSREELLQLNTSIMLDCAKKIKDFTEDPLFIILTNPVDFLLNTLYESGIFSSKKII

AMAGVLDNARFKYELAKKLNVKMSSVDTRLIGFHNDDMVLVKSYASVKNKNISEFLNEEEFDDLENEVKT

GGAKVIKHLKTSAYLAPASACIRMLESIRSGEFLPMSVILHGEFGVQNKALGVMARLGLEGVIEIMKMDL

SLQEKDKLEKSLIKYQYKGE

>ABV52091.1 isocitrate dehydrogenase, NADP-dependent [Campylobacter jejuni subsp. jejuni 81116]

MQITYTLTDESPALATYSFLPIVKAFLSRAHIGVKTSDISLSGRILATFSEYLKEEQRCEDALELLGELV

KRSDANLIKTPNISASIPQLKAAIKELQDKGYMLPNYPDEPKNDEELQIKTKYQKVLGSAVNPVLRQGNS

DRRSTKAVKDYAKNNPYRVVEFNPNSKTRVSYMKEGDFFSNEKAVLIDQDCVANIEFASVDGKKEILKEG

LKLEKNEILDATFMDVQKLQEFYAKEIKASKDDDVLFSLHLKATMMKISDPILFGYAVKVFFKELFIEFQ

DEFEKLGINPNNGLSELLSKIENSSKKDEILKKYNEILAKSADISMVNSDKGITNLHVPSDVIVDASMPA

MLKNGARLWDKEGKEKDTNAVIPDQTYATIYEAVIEDLHKNGTLNPSKLGSVSNVGLMAKKAQEYGSHDK

TFVAKEEGTFKIVSEGKVLLEHKVRKGDIYRANQAKFDAVLNWIDLGIERSELSGAEAIFWLDSKRASNK

IMITLVQNRLKEKGKNIAILTPKEACLRSLELIREGKDVISITGNVLRDYLTDLFPILELGTSAKMLSVV

PMLNGGAMFETGAGGSAPKQVEQLVEENHLRWDSLGEFLALQASLEFYANKCSNHKAKILAECLDEAIGE

WLENNKAPSRKVKEDDNRTSHFYLAMYFANYLARQASDMELQSFFKDIALELSSNEEKIRAEFNNAQGVK

VDLGGYYKFDDEKANKIMRPSATFNAILEKIGQR

>ABV52090.1 hypothetical protein C8J\_0491 [Campylobacter jejuni subsp. jejuni 81116]

MKKKILYIVVFFVVLILALFIVLKNGIVISSIQFDFLKLEQLYIKLDKKLIVRAKNITINETQNSEISSQ

THSSDNASTEILKITKNLKYLYAFVEEIDIQNLNIKDNHVRILFKDNEFFIDNDLLFLKLTLQRQNKELI

ADIKKLLLKDYDLNIDGNLSINTKSEFYYFQGRASGELLDFNASISYKDKNLAYKIEDLNIRNIMEIFKR

VNKRIELPQSLNLWVAYRAKGEFYHLDYLQGFIDFAKDNYYLDNISASGYVNNVKVRLDDKMNAIEIPKL

DLNLNKQKLDFVFNKAFYNGADLSSSKVYLYDLFDEKKAGIYLRIKSDNLKFDEKLAKALEDYHFSLPFY

QKSGKIKSDLELKIDFHDKGEISYSGILALENASISLADFNITKAFVKLNQNDLNIENASVKNSFLEADF

NAKFDLQKQQGNFNTQISRLYFDNGELLDLKNQNVEVKLDYSQNVNISIPQWNLILNFKDGLEANLNNPK

ILFSFSPLLKKFGFIDAKNVYYKTLNFEDFNASVNDAYFKNNLLINGQTPYENDSFDIVKNKGIMEIHTQ

SDTASAKISSDNKEIHLKNLSYIYKKDSNSSNSTFDISTNTQNISFGGANVALILPDSNKTLAFDRVEAD

LKGNALDLKGSRGNAKFDLYYSSNDLNLNVSNIDDNYLNEFLQKQAVQDGVFNLSIKGSGLEYFDGQIDF

KNTYVKDLRGINQLISFIDTVPSLLMFKSPTFNQKGLSLHDGKIIFNRKKDLLSVSAINLNGDSVDIYGL

GSANLRLNTVDFSLELKTLKSASEAISKVPILNYVILGKNQEISTNLKIDGSIDDPKFHTEILTDALKTP

FNLIKNIIQLPANLLN

>ABV52089.1 hypothetical protein C8J\_0490 [Campylobacter jejuni subsp. jejuni 81116]

MTIPFLSTINKANISTTKNTTIYKIFFFIRNFFLIFILGIFYYLTQPLKSNSVVFIPQGSISQIITYLKQ

NKYQMSSIDKYILFFLGHPQSGWINIGTKDLNRAEFLHKLTIAKAALQTITLIPGETSVIFLEQAAKQLE

LDKDMLLKEFQAQAPYDEGVFLPETYKIPKGITENLLIQMLLNHAEISNKKTSEKIFGDYNPKKWHQYII

IASVIQKEAANDNEMPIVASVIYNRLKKGMKLQMDGTLNYGIYSHVKVTPQRIRQDNSSYNTYKFTGLPK

EAVCNVSLAAIRAAIFPLKTDYLYFVRDKNTGVHIFSTNIDDHNKAINLQKGK

>ABV52088.1 flagellar basal-body rod protein FlgB [Campylobacter jejuni subsp. jejuni 81116]

MINPFKSKELVTGALAGRNLRNQLINANLANVDTPFYKARDIEFETALVNRANEIFKKNDNKELQLAVTE

EGHQKPWKFPDPSKSTIYLRDGHLARNDANTVDLDVETTEMSKNTVMITALDGVLRRQSNIFSSILDASS

KLS

>ABV52087.1 flagellar basal-body rod protein [Campylobacter jejuni subsp. jejuni 81116]

MAYLSDFDISGYGLSAQRFRMNVISSNIANANTTRTAEGGPYRRREVIFKATDFDKLLNEQINKDNNFLK

YENPLNDPSSPEEAKPAIQSVVVDKVVRDDKDFRMKYDPSHPDANAEGYVAYPNVNPVIEMADLIEATRA

YQANVSAFTSAKTIAQSAIDLLRG

>ABV52086.1 flagellar hook-basal body complex protein FliE [Campylobacter jejuni subsp. jejuni 81116]

MNNINDLRLNNNISNTNKSQNSTGIGDEFAKMLKNEIDDLNKAQESGEAAMTDIATGQVKDLHQAAIAIT

KAESSMKFMLEVRNKAISAYKEITRTQI

>ABV52085.1 putative penicillin-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MQEYKKNRVSKVAFAYCMALLFMIIFISSTFFLTSKRHIPNTEKDQYALALRGSIITKDNFTITSSKQIY

RAEIDLRSINKDKFDLFLKLFQIYSGISNDQVADIKKRMQNQKKRSYNFVLLQNLDSKQASYLKDLAKKL

YIQGFFKAFTNNSGRVETRGLNIIEHEEDRIYMSKDSFTPIIGYTKMILDPESGILKNIGVKGLEKYYDE

CLSPVQNEKIQGLKDIGGNIILNLNSLQQKKINGCDLYLNLSLKLQKSIEKAIDQRNEDLKANEIIVGVM

ESKTGRILALASSRRYDPQNRGKDLSVLNASAIEYGYEAGSVIKPFIFTTALRLGKIKMDEVINTYGGSY

KLGRFTIKDDHKMDKMTMEEVIRYSSNIGMIQIAKRLNNIEIVSGLKIFKFGEKSGIDLPYEQKGEIPNP

KRLRDIEKSVLSYGYGLKTTFIQLLAAYNVFNNDGFYITPRLAEKFYQNGRFTNLDDDVKKEKILSSEAA

KTMQNVLINVIEKGTGKKAITQGIIAGGKTGTARIAERQGYTSNRYNASFFGFANDLNHAYTIGVLVRHP

TKPYSYYAAQSALPMFKDVVDILINEEFLTPIQDNNQTSTNN

>ABV52084.1 Na/Pi-cotransporter, putative [Campylobacter jejuni subsp. jejuni 81116]

MQEERNSLKYFKFISWSIFILVLIFILIRYDELANLLAGVAILLIGMTNLGIGFKAFSGGLLEKILAKST

DTKIKSILFGTLSTLIMQSSTLVSIITISFLSAGLISLGAGIGIIFGANLGNTASSWLIVGLTNIKISML

AIPLLIIGVLFFFQKDSVLKGLGNIFIGIGFFFLGVDYIKSGFENFKHIIDLSRFDFAGFKGVFVFLGLG

ALLTGVIQSSTATMAIIVAALLAGQISLENSLAATLGTSVGGVVTAVLASLSTNIEGKKLAFANCIFNFG

IAFLIVLIFPYFIHFLNFLSIVLNIEDIALKVALFHTLFNLIGVVLFSFFTPQIVLFLNKIVKAPKDKNK

DKPLYLDSSLVKFSDTAIKALRKESEHLYNNTYAIVAHAIGFSRKDIQSDKSFKEILENKKWFSKNVDLD

YLYQTRIKVLFEAIIDFSTKAQVYINDETKNHKIFTFKMAAKNLAETTKNLKIIQANIKKYSSSSNEFLA

LEYNKIRSNLGELLRSIEELRVVEDREKLYLIIKNLQKGKEILKEIDTLTLGNVEHLISVRKITTAEGIS

ILNDTTFAAKIAEELIGAVEVIFSKDISN

>ABV52083.1 hypothetical protein C8J\_0484 [Campylobacter jejuni subsp. jejuni 81116]

MLGIYLLIAALSFLALYFAVKKLTLNIDEQTLLEPIKMDIYPKFCDLIDEKIREFKENVQNANLALKNSD

QKDEFLEKLGDLSRELTFIQTMNLSNKNDSIWQNELFSFLKELENLLLEYLEKGEEEAENLREFLMNEFE

KLKG

>ABV52082.1 hypothetical protein C8J\_0483 [Campylobacter jejuni subsp. jejuni 81116]

MIENIPASLWTKQDLNAYQIFDVRTPLEWEEGILPNAQCVALYDNQGLLNAKFLDEFQSKRDESKKLAFI

CRSGHRSMVAAEFIAERLGLESINLDGGMLALKGY

>ABV52081.1 heat shock protein HtpG [Campylobacter jejuni subsp. jejuni 81116]

MQFQTEVNQLLQLMIHSLYSNKEIFLRELISNASDALDKLNFLSVSDDKYKSLKFEPKIEIKIDKDKKTL

SISDNGIGMDKDDLINNLGTIAKSGTKSFLENLSGDAKKDSQLIGQFGVGFYSAFMVASKIEVLSKKALD

DKAYLWSSDANGYEINDANKEEQGTSITLYLKDDEFANTYKIESIIEKYSNHIQFPIFMEKEEFTPAKEG

EEEGKTELKISQINKANALWRMQKSSLKVEDYERFYEQNFHDSNKPLLYLHTKSEGKLEYNSLFFIPQNA

PFDLFRVDYQSGLKLYVKRVFISDDDKELLPTYLRFVRGIIDVEDLPLNVSREILQENQILKGVKEASVK

KILGELEKLKNNDKEKYLSFFKTFGKVLKEGLYGFGGEKDSLLKLMLYKSTKGENLRSLEEYKNDLQGEQ

KEIFYIAGNNESLLRTSPLLEEYKQKNIEVLLMDDEIDSLVTPMLEFEGLKFVAINQVEDKNELSDEEKN

TFAPLVAKFKELLKDQVEDVRLTSRLKDSPSCIVYDKNKPDFAMQQLLKQMGQEQNFKPILEINPKHAIF

TGLKNNESFSADIATLVLNMAKLSEGMGVDNPAEFNASLTKIINKAFS

>ABV52080.1 CrcB [Campylobacter jejuni subsp. jejuni 81116]

MLNTLLVVGFGGFIGAILRMFSINLVNKFFPYSISLGTLFVNVLGSFIIGLLFSYAQNKGLSPLLKSFIS

TGFLGAFTTFSTFSYQNLLLLQSGNYLHFALNIILNVFLCLFAAWLGFIIFK

>ABV52079.1 1-acyl-sn-glycerol-3-phosphate acyltransferase, putative [Campylobacter jejuni subsp. jejuni 81116]

MIYKKIKALYFWIFFVLSVALVVFCFCFTKSQNTLWKIRKIWAKFQRYTISYKQEIIGTFNPQAQMILMN

HQSALDIIALEELYPKNLCWIAKKELGEIPIFKVAMKKPKLLCIDRKNPRDLVRVLKEAKERISEDRVLA

IFPEGTRSKNEKMLKFQSGAKILSEKLNLKVQPILIVDSVKILDTKSFSASSGVLKIICMDLVDTNDDKW

LENTRKKMQELLDQERAKLC

>ABV52078.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKILLTLIFSVVVLFGRGEISVFGGQDENMQKELQKLPQEEQKIYQNIPPSDENNDFESNVDDPFVAKGS

LVLTNDEYPSRVYVGEVFPITIYARTTENTKFDFNISVEKTNLSFLNPDAKWEFINNEYKTTLWFEAKNS

NASLSKISIKLLRNNEAFQEADINLNPIKFENTLSNKDFSHLVASSLEIKKVKASYFDDANIIMMVELNA

TNTNLKSFFIEGIQKQGIENLKGDFNASSAFYYAILPLSKTNFEFSYFNKDSKKLENINLKLKISDDEIS

TQSDLNPVNKDLNIYKQYTLWFLAVLFGALFVWRKNYIILALAVVCFALSFLVDTNTQNAIIKAGSRAKI

LPTEPSTYFYTANADEKVEVLGKRQNYIKVLFSDGKIGWVNKDDLQKN

>ABV52077.1 phosphoribosylformylglycinamidine synthase subunit I [Campylobacter jejuni subsp. jejuni 81116]

MKVAIIRFPGTNCEFDTAYAFEKLGVKTQIVWHEEKEFDTDLVVLPGGFSYGDYLRCAAIAKLAPAMQGV

FNHAKKGGYILGICNGFQILLESGLLKGAMKHNNNLSFISKNQNLRVVSNDNAFLKNFKKDEIINLPIAH

GEGNYYADEATLKELQDKDLITLKYEPNPNGSVFDIAGICDENKKIFGLMPHPERACEKVLGNDIGLKML

KGFLF

>ABV52076.1 hypothetical protein C8J\_0477 [Campylobacter jejuni subsp. jejuni 81116]

MEVIVNISLKNGVLDPQGKAVEKALHSLNFNSVKEVKIAKQIKISLDEKDEKLAKEQVKKMCEELLVNSI

IEDYELVIEKE

>ABV52075.1 phosphoribosylaminoimidazole-succinocarboxamide synthase [Campylobacter jejuni subsp. jejuni 81116]

MTKKEMLYEGKGKKLFKTDDENLLISEFKDDLTAFNAEKRGNESGKGALNCKISTEIFHLLEKNGIKTHL

VETISDTEQVVKKCKIVPIEVIVRNVATGSLTKRLGIKDGTVLPFALVEFCLKDDALGDPFINDEHCLIL

NLVQNEAQISEIKNMARKINSILTPFFDNKNLRLIDFKIELGLTKDNELVLADEISPDSCRFWDKFSNEK

LDKDRFRQDLGNVKMAYEEVLKRILN

>ABV52074.1 putative secreted protease [Campylobacter jejuni subsp. jejuni 81116]

MMELILKTKRFFAGLAGFATTFILCLFLTSHLQAKVDQKEEQVQKRLEALDKLTKTLAIVEQYYVDDQNI

SDLVDKSLSGLLSNLDAHSSFLNEKDFNDMKIQTNGEFGGLGITVGMKDGALTVVSPIEGTPADKAGIKS

GDIILKINDEATLGINLNDAVDKMRGKPKTQITLTIFRKGATKPFDVTLTREIIKIESVYAKMIENENIL

YLRVTNFDKNVVDVASKELKKYPNVKGVILDLRNNPGGLLNQAIGLVNLFVDKGVIVSQKGRIASENQEY

KADPKNKISNASLVVLVNGGSASASEIVSGALQDLKRGVIVGENTFGKGSVQQIIPINKTEALRLTIARY

YLPSGRTIQAVGVKPDIEVFPGKVNTQEDGFSIKESDLKQHLESELEKIDKNKKEDKQENKDNKNLISQK

QINDDAQLKSAIDTIKILNIKQGQ

>ABV52073.1 hypothetical protein C8J\_0474 [Campylobacter jejuni subsp. jejuni 81116]

MCQEKHTHTHSQKHLKAVCNRLSRTIGHLSAIKRMVENDKDCSEILIQLAAVKAEVNNTAKVVLKEHLAH

CMVHAVEENDIQSIEELNKAIDMFMK

>ABV52072.1 ATP-dependent CLP protease ATP-binding subunit [Campylobacter jejuni subsp. jejuni 81116]

MANIQNFLTDNMLSNLESAASLAIHSKNNEVAPLHLLWALSVDSTSILNQILNKLNISKEALELEIKSRI

SKLATSSNVNRENIRFSNELINSLENAKGLMSANGDSYLSVDTWLISESQKSPTKEILAQFLDLREFQKE

LESLRAGRKIDSKTSDETLDSLNKFGIDLTLKASEGKLDPVIGREEEIERLMQILIRKTKNNPILLGEPG

VGKTAIVEALAQRIIKKDVPKSLQNKKVIALDMSALIAGAKYRGEFEDRLKAVVNEVIKSENIILFIDEI

HTIVGAGASEGSMDAANILKPALARGELHTIGATTLKEYRKYFEKDAALQRRFQPVNVGEPSVNEALAML

RGIKEKLEIHHNVTINDSALVAAAKLSKRYIADRFLPDKAIDLIDEAAAELKMQIESEPSSLRKVRKDIE

TLEVENEALKMENDEKNQKRLDEIAKELANLKEKQNALNSQFENEKSVFDGISAKKKEIDLLKNEASLAK

ARGEFQKAAELEYGKIPSLEKEVEILEDKWKKMSENGVLLKNQVDEDLVAGILSKWTGISVQKMLTSEKQ

KFLEVEKHLKESVIGQDKALSALARAIKRNKAGLNADNKPIGSFLFLGPTGVGKTQSAKALAKFLFDDEK

AMIRFDMSEFMEKHSVSRLLGAPPGYIGHEEGGELTEAVRRKPYSVLLFDEVEKAHKDVFNVLLGILDDG

RATDSKGVTVDFKNTIIILTSNIASSAIMNLSGKEQEDVVKNELKNFFKPEFLNRLDDIITFNPLGKDEA

YEIVKLLFKDLQMSLENKGIKASLSENAALLIAKDGFDPDFGARPLRRAIYDLIEDKLSDMILADELHEN

DSIIIDAKDDEIIIKKA

>ABV52071.1 penicillin-binding protein 1A [Campylobacter jejuni subsp. jejuni 81116]

MKILKYIFSFFTLLFIAGFIYVAYLFTSADTEGYTFKEYKPPLTTQIYDRNGKLVANIFEQHRFYAPYEE

LPPRLIEALVAIEDTSFFEHNGVNIDAIFRAAVKIIKSGGKTMEGASTLTQQFIKNTELTPERTITRKIR

EALLAYKMETILTKEQILERYLNFIFFGHGYYGVKTASLGYFHKNLNELSLKEIAMLVGMPKAPSSYDPT

KHLDLSISRANNVISRMYNLGWISKADYDTAIKEIPQVYDDTLTQNAAPYVVDEVIKQLSPNIKDLKTGG

YKIILNIDLDVQNMAQNALKFGYDEIVKRDKDANLSTLNGAMVVVNHQSGDVLALVGGVDYEKSNYNRAT

QSMRQPGSSFKPFVYQVAINLGYSPMSEIADISRIFEGGAGNNEDWKPKNEGGKFLGLITLKEALTRSRN

LATINLALDMGLDVLYSKLMEFGFKDIPPNLSIVLGSFGISPLEYSKFYTMFGNYGTIKDPQIIRQVQDK

TGKTIMEFNSNERKVSDEAQSFLVLDMMRNVVEKGTGRNARVKDIEIAGKTGTTNKSVDAWFCGLTPEIE

AIIWYGNDNNKPMRYTEGGARTAAPVFREFLTQYIEKFPDTTRKFSIPNGVYRGNYKGESAYYTTKSPLP

KANMKFNESEIIF

>ABV52070.1 MAF-like protein [Campylobacter jejuni subsp. jejuni 81116]

MLILASSSISRANLLKTAKIDFRQVSFDYDENLDKNISPFLYVQKIVLEKERQFLSTLGKDFQNQNLLFA

DSIVCIDEKILTKAKDKKEAYEMLALQNGKYASILSAFLLVKPEKRVFSLSKTTLYFKNFDENALRDYVE

NDLYKGKAGCIMCEGFHQNFITHQVGNLSTALGLDIQTLKAYL

>ABV52069.1 alanyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MDIRKAYLDFFASKGHEITPSSPLVPDDATLLFTNAGMVPFKSIFTGEIPRPNPPRKTSCQTCIRAGGKH

NDLDNVGYTARHHTFFEMLGNFSFGDYFKEQAIAYAWEFVTEFLKLPKDRLYVTVHENDDEAFNLWQKHI

QKERIYKFGDKDNFWQMGDTGPCGPCSEIFYDQGEEHFNSSEDYMGGDGDRFLEIWNLVFMQYERSADGV

LSPLPKPSIDTGMGLERVTAIKEGKFSNFDSSLFMPIINEISKLCNKTYIYESGASFRVIADHIRSSVFL

LAQGVSFDKEGRGYVLRRILRRALRHGYLLGFKQAFMYKLVDVVCDLMGGHYTYLNEKKDFIKEQIRLEE

ERFLSTIENGIEIFNEELKNTKEIFSGEVAFKLYDTYGFPLDLTADMLREKNLKVDEEKFELLMNEQKAR

AKASWKGSGDKTASGDFKNLLEKFGENHFVGYEKAECESKILALLDEDFKEVSTLKDAGWVMLKNTPFYA

TSGGQSADSGFMAKREVLDTQKFFNLNLSFVKAGEELKVGDIVHARIDTEKREQIARHHSATHLLHHALR

EILGSHVSQAGSLVESNKLRFDFTHHKALSKEELENIEKRVNEMIINSSEAILENMPLEEAKKSGAIALF

NEKYQGNVRVLTLGESKELCGGTHVKNTAQIGSFYIVKESGVSAGVRRIEAVVSKAALEFVKNQLEELSK

VKDELKNNDILSGIKKLKNEILSLKNELKNSSKTELDSKNIQGVEICVKRIDNGDIKAMIDDFKNKFAKA

VILLIQVKDEKITLAAGVKDVPLKAGALVKEAAQILGGNGGGRDDFATAGGKDLSKINEALKQSLETIEK

AL

>ABV52068.1 DegT/DnrJ/EryC1/StrS aminotransferase family [Campylobacter jejuni subsp. jejuni 81116]

MNFINLQAQYLAYKDEINAEIESVLSSSSFIGGAKLNEFEQNLAHFLGVKHAIGCSSGTSALYLALRALD

IGKDDEVIVPSFTFIATAEVVALVGAKPVFVDINLSNYNLDFEAVQKAITPKTKAVIAVSMFGQMSDLRA

LEEILKDKNITLIEDGAQSFGASFKGEKSCSIAKISCTSFFPSKPLGAYGDGGAIFCHDDEIAKKIRILL

NHGQTQRYKHEFIGINGRLDTLQAAILNVKLKYLEKELDKRQKLAQTYNANLKNCQIPQIDPNAFSAYAQ

YSVLVEDRASVLQKFEKANIPYAIHYPTPLHKQPCFSEFSNLELKNSEYASEHILSLPFSPFLSEEEQEQ

VICIFKD

>ABV52067.1 oxidoreductase, Gfo/Idh/MocA family [Campylobacter jejuni subsp. jejuni 81116]

MKIGIIGLGKMGQNHLNELSKNSHFKLNALFDLCKNPNLNIFDDIFYDDLDKFLNQNNDIIIIATPTNSH

LAIAKKVFKQCKCVLIEKPLALNLKEIDEISNLAKEYSVKVGVGFCERFNPAVLALKKELENEEIISINI

QRFSPYPQRISDVGILQDLAVHDLDLLCFLSKQEITKTNLLKKYTQDQTRESESIILCELEKCIASIHQS

WNSTQKLRKIHLITKNHFYEANLNDFSLLKDGNFIELTQQSPLFSEHEALLKLIDNQANHLASTSDAYKV

QEILERFA

>ABV52066.1 ferrochelatase [Campylobacter jejuni subsp. jejuni 81116]

MKLVLFLNMGGATNLQDCEVFLKNMFNDPYILGIKNRFLRKFVAWIITKARVKAMQENYKKMGGKSPLNE

LTQSLCNKLNLKQDEFKFDFVNLYVPPFATEILQKYTLNESDEIILFPLYPHHSCTTVTSSLEVLQNEIS

KQKIQAKVKTIDIFYKNELYNEMIVSHILAKKSKFDAKILIFSAHSLPQSIIDKGDLYEKHVNDHVEILK

EKLKDHFDEFILAYQSKLGPVKWLEPNTSDVLANLNDKALIYPISFCIDCSETIFELGMEYKHLAKCDYD

LISCPNDSDEFMEFILNSINSPLARKTSC

>ABV52065.1 putative outer-membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKRIILLSSLAILSLYASDTKDNKKTIQMLEQSPYKEDANLKNYNNTLKVKDGVIIIDHSNTSDDNNSKT

INTKKNTQKDNNNTQKNQPNLSNDNTLKTKTPNSNTPSLKNTSKEESIHKVSFSFHITNKNINFKDLGLD

EQVLQEALNDYKKESISVQDLQDIANIISYYVQVSGYPAATAYIPQQELKDQIQINITLGVLGKYVVQNN

SSVRDYAIESKLPNHKGEIITTKLVEDAVYKVNEMYGIQTLASLKAGDNPGETDVVIETTPSDSFVSVLF

YGDNYGIKESGRYRGGASMSFNNIAHQGDSLNAYLQRSDEAQTNYGISYTTFLGNLKITPSYSKGNYALG

GIWREFDFIGTSENLGIDLKYPLWITTYNSFYLTSSYYHKKLSDSKFDILTFDKSSDTISFGIEGVYNGI

SNDSFSYSANVSYGNVKDEGMTIVGIGTSKVGGVEFGKFAKLNVNLNNAYFFNDTFTHLFSLNYQQVING

ATLDSSETISLRGPYGVRAYNNGDGEGDNAVVASFGLRMATPLKDFYITPFYDIGYSWYENDSYTNYMDA

YGLQLLYNKTGNFYVKLDLARALKKYKLDDDYSSKAYVSFGKYF

>ABV52064.1 hypothetical protein C8J\_0465 [Campylobacter jejuni subsp. jejuni 81116]

MKKLNKLSLSLVVGSLLFTQSYALPSGGKFTHGTSGSISVSGGTMNISGSKTNSVIQWGGGFNIANGETV

NFKGNGYNYLNIVYGSKSSHIDGTLEGGTNNIFLINPNGIVVGKDGSINANRVFLSASSIGDKEMKEFAK

DGKISAFEGNPLTTASPVIKSNAGNVINLGTITAGERVVMVGNQVSNMKYGSTDYGKFIFTNKKEQSNTV

YLDVYSNDIFVIRGPASNTIKKEDSVMLSIRPNKGSTGPGGDPTDTIGYKETSDLVAKDNISNEVLNSIF

NDLKFNSSVDISDLSKFYKDGKILTADELTSINQSMDFITALYGQTQDSNNATFANALKEVLGNSYGNLG

KANQAIIKTKEILSQIPKITEQQKNIQKAYDQAVDAYNEAVKKYNAALSGVTGSNASETITALKTVLDKA

YNDLKNAEANLESTTASNNSSLKSSNETLASVSIDGYKLTVNGEYLADYKTVNKPNDNNSGSNNGNDGTD

SGDINNGNNNGSNNNPNDTIGQQEPDIATALLMQTTDEDPNINEDDKQASIDEASTQESGNACIVSDNFK

AGNPCSR

>ABV52063.1 hypothetical protein C8J\_0464 [Campylobacter jejuni subsp. jejuni 81116]

MKSYDAPINISSEGVLALYTLKEQYPYLKNKEILILQSEQGFIDENSNTLNQEELQSFIEKMQKNKEDFK

LSSIDRLKKMNLQKLSYEVRISQDGKSIYAKIK

>ABV52062.1 hypothetical protein C8J\_0463 [Campylobacter jejuni subsp. jejuni 81116]

MREDEVLSFKARHGVNTADHSIKTVRVLPFLITAKTDHADASYNKLILEQGELSSVFYLKPKDTHIKNPS

NSKSNQRMNFLMSSTFTHYGNASYNQTILQKDAHISMGVENTYDLALNGAPYLIGAIATYGDSTNNSLNI

EAGSSVEFFTSLPKKDKNGNNTFDERITHLVGGLAYQGNVKNNKIFIKDANMIIHDPSKAYASSAAAHIS

AGYIDSGTDKNFQASKNLLDIDGFNLDMYMNHDKQPLAYNSVLFADFWGGKTEQGQALDNTINLKDIKNL

KKDKNNENIFAQALFNFYAGASNNGEANYNTLNIELKHPLEIANNFLGYNQHSFYGGFATKGANHNTINI

KNDLTTTDLSQSYKDALNIVAARTLEGSADYNKVYINNSMSTLPVYIYTAKKNILNNQDFYPSGANNNEV

VIKDFASFRNLTVLTEAKEASYNTINYNNVQSITDASNIDKGSKIIIRALDKANHNTIDIKNYSSNAADN

AYLIMAYNEAAYNKIIINDTLFGVASDKREGILSIIAGLSNNAHDNTLIINNLNLDEYKNNNSIFIAPSA

ITGLSEAKSYNNTLYIGGNLNIFKNTFIDILAGALVHYEDSNSASNAVAPSDISLSKNNRLI

>ABV52061.1 putative ATP/GTP binding protein [Campylobacter jejuni subsp. jejuni 81116]

MLSEVEFAEFQKENFSLLIDARSPREFLHSHLIGALNFYALNDEEYQEIGTIYKKNQALAKARGASYICQ

NTAKHILKITQNFRIGEKVGIYCSRGGLRSKSIAVILSELGFRVVRLKGGFKAYRTFVTHYFENEINFDF

FTLCGNTGCGKTELLEQLPQAINLEKIANHLGSSFGDILGKQPTQKAFEAELFHNMQNLENFAFIESESR

KIGDIILPLKFYEKMQKAFKIYCFCSLENRVKRIQKIYQEKMTPLKFQQCVQKISPYISLNLRQDLLQSY

ERKEWQRLITMLLEYYDKTYKKPDKIDLELNTDDILKAKEEILRYFKLKNYILI

>ABV52060.1 Hit family protein [Campylobacter jejuni subsp. jejuni 81116]

MQYLYAPWRSEYFEKEKSICPFCDCANKIKSDEDLGVIFRAKHCFGVMNRYPYSVGHFMVIPYVHEEHIE

NLSDEIWQEMSHFVRLGVKILKEQIHANGVNIGMNLSKDAGAGIAPHCHYHLVPRWAGDTNFITTIGETR

VCGTNIEQVYQKLVLAFKNAQ

>ABV52059.1 indole-3-glycerol phosphate synthase [Campylobacter jejuni subsp. jejuni 81116]

MILDKIFEKTKEDLKERKLKLPYDMLGRSLASNPFFPKDVIKALKRVEKEVKIIAEVKKASPSKGVIRED

FDPLSIALNYEKNKAAAISVLTEPHFFKGSLEYLSLIRRYTQIPLLRKDFIFDEYQILEALVYGADFVLL

IAKMLSMKELKKLLEFARHLGLEALVEIHDKEDLSKAIFAGADIIGINHRNLEDFTMDMSLCEKLIPQIP

NSKIIIAESGLENKEFLEHLQNLGVDAFLIGEYFMREKDEGKALKALL

>ABV52058.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MYRYLLFVLAAFFLAACGSSKINVVYPDYTKYKSNDFDLRVMKAYNYEYYKQYKEARDEFLSLYQDYNNT

NFLENAFLLTLANNLDKQAELNNLAKPYLNQNDNLKRLSALYALNSNDINNAQKLMKELLTKKDSDPRNL

ELYGDILVKKNDLKNATKYYRSAYNQVQNEEILFKLIGIYAILNDTLNIKNVLEFSRKTNGCTLKTCVLL

AKIYFDEKNIEALKSIYKELYQLTKNKSFALALVELLNSQGKTEEALKISLQYDLDDDIKLALYQNLKRF

DDAKKMSLALYHKTKNKEYLLRAAVFEFEAANEAKKITPKVIDSVKEKFEQAIDKDSNALYLNYYGYLLI

DYDLDVKKGIELVKLALEKDPQNLYYLDSLAWGYYKLGDCRQAWEILKQTLDDKEFANSDESKAHIKAIK

ACVKP

>ABV52057.1 hypothetical protein C8J\_0458 [Campylobacter jejuni subsp. jejuni 81116]

MIFDKNFSYAFDENACEKCGGKCCTGESGNIFASKEELEALRKHLNLESKEFAEKYLRKVGFKMSFKEVE

FEDGFACIFFDTQKRNCSIYDFRPKQCRTFPFWEYFKTHQKELEKECIGICYLF

>ABV52056.1 hypothetical protein C8J\_0457 [Campylobacter jejuni subsp. jejuni 81116]

MSDLITLAQLSQGYRYNSDSLILADFILKQGIKGAVFDVGAGCGIIGILLKKNIANLSLSLIDIQKENIK

LIEKNLKSNQIQGDIFHDDFNQFQSIKKFDFIVCNPPFYRQGAYKSEDQHKAISKFQEFLPLHSFLTKAN

SMLKPNGTLYFCYEALALDEICFILKDIKIKITKLCFVHTHQNKKARLVLIQVKKGSKSPCEILPPFFVY

ENEILSKQMQEIHLRFRLKSYDI

>ABV52055.1 hypothetical protein C8J\_0456 [Campylobacter jejuni subsp. jejuni 81116]

MIKIAFFITFVISFLTAQSPVNFKEDNNITKEQNIFKEQPPKRIKIPTH

>ABV52054.1 elongation factor EF-G [Campylobacter jejuni subsp. jejuni 81116]

MSRSTPLKKVRNIGIAAHIDAGKTTTSERILFFTGMSHKIGEVHDGAATMDWMEQEKERGITITSAATTC

FWKDHQINLIDTPGHVDFTIEVERSMRVLDGAVAVFCSVGGVQPQSETVWRQANKYGVPRIVFVNKMDRI

GANFYNVEDQIRNRLKANPVPLQIPIGAEDNFKGVIDLVTMKALVWEDDTKPTDYVEKEIPAELKEKAEE

YRTKMIEAVSETSDELMEKYLGGEELSLEEIKTGIKAGCLSLSIVPMLCGTAFKNKGVQPLLDAVVAYLP

APDEVANIKGEYEDGTEVSVKSTDDGEFAGLAFKIMTDPFVGQLTFVRVYRGCLESGSYAYNSTKDKKER

IGRLLKMHSNKREEIKVLYAGEIGAVVGLKDTLTGDTLASEKDKVILERMDFPDPVISVAVEPKTKADQE

KMSIALNKLAQEDPSFRVSTDEESGQTIISGMGELHLEIIVDRMLREFKVEAEVGQPQVAYRETIRKTVE

QEYKYAKQSGGRGQYGHVFLRLEPLEPGSGYEFVNDIKGGVIPKEYIPAVDKGVQEALQNGVLAGYPVED

VKVTVYDGSYHEVDSSEMAFKLAASMGFKEGARKAGAVILEPMMKVEVETPEDYMGDVIGDLNKRRGQVN

SMDERGGNKIITAFCPLAEMFGYSTDLRSQTQGRATYSMEFDHYDEVPKNVADEIIKKRNG

>ABV52053.1 30S ribosomal protein S7 [Campylobacter jejuni subsp. jejuni 81116]

MRRRKAPVREVLPDPIYGNKVITKFINSLMYDGKKSTATTIMYGALEAIDKKGGEKKGIDIFNDAIENIK

PLLEVKSRRVGGATYQVPVEVRPARQQALAIRWIISFARKRSERTMIDKLAAELLDAANSKGASFKKKED

TYKMAEANKAFAHYRW

>ABV52052.1 30S ribosomal protein S12 [Campylobacter jejuni subsp. jejuni 81116]

MPTINQLVRKERKKVLEKSKSPALKNCPQRRGVCTRVYTTTPKKPNSALRKVAKVRLTSGFEVISYIGGE

GHNLQEHSIVLVRGGRVKDLPGVKYHIVRGALDTAGVAKRTVSRSKYGAKRPKAGTAK

>ABV52051.1 DNA-directed RNA polymerase, beta' subunit [Campylobacter jejuni subsp. jejuni 81116]

MSKFKVIEIKEDARPRDFEAFQLRLASPEKIKSWSYGEVKKPETINYRTLKPERDGLFCAKIFGPIRDYE

CLCGKYKKMRFKGVKCEKCGVEVANSKVRRSRMGHIELVTPVAHIWYVNSLPSRIGTLLGVKMKDLERVL

YYEAYIVENPGDAFYDNESTKKVEYCDVLNEEQYQNLMQRYENSGFKARMGGEVVRDLLANLDLVALLNQ

LKEEMAATNSEAKKKTIIKRLKVVENFLNSNLNANADSDEAVPNRPEWMMITNLPVLPPDLRPLVALDGG

KFAVSDVNDLYRRVINRNTRLKKLMELDAPEIIIRNEKRMLQEAVDALFDNGRRANAVKGANKRPLKSLS

EIIKGKQGRFRQNLLGKRVDFSGRSVIVVGPKLRMDQCGLPKKMALELFKPHLLAKLEEKGYATTVKQAK

KMIENKTNEVWECLEEVVKGHPVMLNRAPTLHKLSIQAFHPVLVEGKAIQLHPLVCAAFNADFDGDQMAV

HVPLSQEAIAECKVLMLSSMNILLPASGKSVTVPSQDMVLGIYYLSLEKAGAKGSHKICTGIDEVMMALE

SKCLDIHASIQTMVDGRKITTTAGRLIIKSILPDFVPENSWNKVLKKKDIAALVDYVYKQGGLEITASFL

DRLKNLGFEYATKAGISISIADIIVPNDKQKAIDEAKKQVREIQNSYNLGLITSGERYNKIIDIWKSTNN

VLSKEMMKLVEKDKEGFNSIYMMADSGARGSAAQISQLAAMRGLMTKPDGSIIETPIISNFREGLNVLEY

FISTHGARKGLADTALKTANAGYLTRKLIDVAQNVKITIEDCGTHEGVEINEITADSSIIETLEERILGR

VLAEDVIDPITNSVLFAEGTLMDEEKAKILGESGIKSVNIRTPITCKAKKGICAKCYGINLGEGKLVKPG

EAVGIISAQSIGEPGTQLTLRTFHSGGTASTDLQDRQVSAQKEGFIRFYNLKTYKNKEGKNIVANRRNAA

ILLVEPKIKTPFKGVINIENIHEDVIVSIKNKKQEVKYILRKYDLAKPNELAGVSGSIDGKLYLPYQSGM

QVEENESIVEVIKEGWNVPNRIPFASEILVEDGEPVVQNIKAGEKGTLKFYILKGDGLDRVKNVKKGDIV

KEKGFFVVIADENDREAKRHYIPRESKIEFNDSEKIDDANTIIASAPKKERKVIAEWDAYNNTIIAEIDG

VVSFEDIEAGYSADEQIDEATGKRSLVINEYLPSGVRPTLVIAGKGDKAVRYQLEPKTVIFVHDGDKIAQ

ADILAKTPKAAAKSKDITGGLPRVSELFEARKPKNAAVIAEIDGVVRFDKPLRSKERIIIQAEDGTSAEY

LIDKSKHIQVRDGEFIHAGEKLTDGVVSSHDVLKILGEKALHYYLISEIQQVYRGQGVVISDKHIEVIVS

QMLRQVKVVDSGHTKFIEGDLVSRRKFREENERIIRMGGEPAIAEPVLLGVTRAAIGSDSVISAASFQET

TKVLTEASIAGKFDYLEDLKENVILGRMIPVGTGLYGEQNLKLKEQE

>ABV52050.1 DNA-directed RNA polymerase, beta subunit [Campylobacter jejuni subsp. jejuni 81116]

MLDNKLGNRLRVDFSNISKQIEIPNLLQLQKKSFDYFLNLDNGESGIEKVFKSIFPIHDPQNRLSLEYVS

SEIGKPKYTIRECMERGLTYSVNLKMKIRLTLHEKDEKTGEKVGVKDIKEQEIYIREIPLMTDRVSFIIN

GVERVVVNQLHRSPGVIFKEEESSTVANKLVYTAQIIPDRGSWLYFEYDAKDVLYVRINKRRKVPVTMLF

RALGYKKQDIIKLFYPIQTIHVKKDKFLTEFNPNDFMDRIEYDIKDEKGKIVHQAGKRLTKKKAEQLIKD

GLKWIEYPVEILLNRYLANPIIDKESGEVLFDSLTLLDESKLAKIKEQKSFDIANDLANGVDAAIINSFA

QDGETLKLLKQSENIDDENDLAAIRIYKVMRPGEPVVKDAAKAFVNDLFFNPERYDLTKVGRMKMNHKLG

LEVPEYVTVLTNEDIIKTAKYLIKVKNGKGHIDDRDHLGNRRIRSIGELLANELHLGLAKMQKAIRDKFT

SLNADLDKVMPYDLINPKMITTTIIEFFTGGQLSQFMDQTNPLSEVTHKRRLSALGEGGLVKERAGFEVR

DVHATHYGRICPVETPEGQNIGLINTLSTYAKVNELGFVEAPYRKVVNGKVTNEVVYLTATQEEGLFIAP

ASTKVDAKGNIVEEFVEARQDGETILARREEVQLIDLCSGMVVGVAASLIPFLEHDDANRALMGSNMQRQ

AVPLLTASAPIVGTGMEQIIARDAWEAVKAKRGGVVEKVDNKSIFILGEDDKGPFIDHYTMEKNLRTNQN

TNYIQHPIVKKGDIVKAGQIIADGPSMDQGELAIGKNALIAFMPWNGYNYEDAIVVSERIIREDTFTSVH

IYEKEIEARELKDGIEEITKDIPNVKEEDVAHLDESGIAKIGTHIKPGMILVGKVSPKGEVKPTPEERLL

RAIFGEKAGHVVNKSLYATASLEGVVVDVKIFTKKGYEKDDRAIKSYDKEKMALEKEHHDRLLMMDREEM

LRVCALLSKAPLNSDQKIGDKNYKKGQTADISELEKINRFTLTTLIKAYSKEIQKEYDDLKNHFQNEKKK

LKAEHDEKLEILEKDDILPSGVIKLVKVYIATKRKLKVGDKMAGRHGNKGIVSTIVPEVDMPYLPNGKSV

DIALNPLGVPSRMNIGQILESHLGLIGLRLGDQIQEIFDRKQKDFLKELRAKMLEICSIPRLASEKEFIK

SLSDEELLNYARDWSKGVKFATPVFEGVNIEEFSKLFEMAKIDMDGKTELYDGRTGEKIAERVHVGCMYM

LKLHHLVDEKVHARSTGPYSLVTQQPVGGKALFGGQRFGEMEVWALEAYGAAHTLREMLTIKSDDVEGRF

SAYKALTKGENVPATGIPETFFVLTNELKSLALDVEIFDKDEDNE

>ABV52049.1 ribosomal protein L7/L12 [Campylobacter jejuni subsp. jejuni 81116]

MAISKEDVLEYISNLSVLELSELVKEFEEKFGVSAAPVMVAGGAAAGGAAAAAEEKTEFDIVLTDGGAKK

IEVIKIVRALTGLGLKEAKDAVEQTPSTLKEGVAKAEAEEAKKQLEEAGAKVELK

>ABV52048.1 50S ribosomal protein L10 [Campylobacter jejuni subsp. jejuni 81116]

MTRSEKVEIIAKLEEGFKASEAIVVCNYRGLSTKKLEELRNNARENNVKVQIVKNTLANIALNNSGKTGL

VLKDTNIYLWGEDQLSVSKVAAKFEENNDKFEIKTAYIEGEVADVAKVKALAKMPSRNELLAMLLQVWNA

PITNFTIGLNALKNKKESE

>ABV52047.1 50S ribosomal protein L1 [Campylobacter jejuni subsp. jejuni 81116]

MAKIAKRLKELSQKIDSNKEYALSDAIDTIKTLKSAKFDETVEIALKLNVDPRHADQMVRGSVVLPAGTG

KKVRVAVIAKDAKADEAKNAGADIVGSDDLVEEIQKGNMNFDVLIATPNLMGLVGKVGRILGPKGLMPNP

KTGTVTMDVAQAVNNAKSGQVNFRVDKQGNIHAGLGKVSFSKEQLWDNVSTFVKAINKHKPAAAKGRYIK

NAALSLTMSPSVKLETQELLDMK

>ABV52046.1 50S ribosomal protein L11 [Campylobacter jejuni subsp. jejuni 81116]

MAKKVVGEIKLQIAATKANPSPPVGPALGQQGVNIMEFCKAFNERTKDMAGFNIPVVITVYADKSFTFIT

KQPPATDLIKKAAGISKGTDNPLKNKVGKLTRAQVLEIVDKKIADLNTKDRDQAAKIIAGSARSMGVEIV

D

>ABV52045.1 putative transcription antitermination protein [Campylobacter jejuni subsp. jejuni 81116]

MSTHKWYAIQTYAGSEMAVKRAIENLVKDNGIEEQLKEIVVPTEDVIEFKNGKEKISERSLYSGYVFALL

DLNTELWHRIQSLPKVGRFIGESKKPTPLTEKDINLILEKVHNRAAPKPKISFEEGENVRITEGPFANFT

AIVEEYDMVRGLLKLNVSIFGRSTPVEILYSQVEKII

>ABV52044.1 preprotein translocase SecE subunit [Campylobacter jejuni subsp. jejuni 81116]

MEKLITYFKLSKAELRKVIFPLKEQVRNAYITVFVVVAVISLFLALVDWLMSSIVSAIV

>ABV52043.1 50S ribosomal protein L33 [Campylobacter jejuni subsp. jejuni 81116]

MRIKVGLKCEECGDINYSTYKNSKNTTEKLELKKYCPRLKKHTLHKEVKLKS

>ABV52042.1 elongation factor EF-Tu [Campylobacter jejuni subsp. jejuni 81116]

MAKEKFSRNKPHVNIGTIGHVDHGKTTLTAAISAVLSRRGLAELKDYDNIDNAPEEKERGITIATSHIEY

ETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHILLSRQVGVPYIVVFMNKADM

VDDAELLELVEMEIRELLSSYDFPGDDTPIISGSALKALEEAKAGQDGEWSAKIMDLMAAVDSYIPTPTR

DTEKDFLMPIEDVFSISGRGTVVTGRIEKGVVKVGDTIEIVGIKDTQTTTVTGVEMFRKEMDQGEAGDNV

GVLLRGTKKEEVIRGMVLAKPKSITPHTDFEAEVYILNKDEGGRHTPFFNNYRPQFYVRTTDVTGSIKLA

DGVEMVMPGENVRITVSLIAPVALEEGTRFAIREGGKTVGSGVVSKIIK

>ABV52041.1 polar amino acid transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MSILKIENLQKYYGSHHALKDINLEVKAKEVVVILGPSGCGKSTLLRCINGLEEIASGNIYIDNEKIDKD

FKEWPRMRQKVGMVFQSYELFEHLSVEENILLGPMKVQKRKKDEVLKEAKIWLEKVGLLHKIHAYPRELS

GGQKQRIAIVRSLCMNPELMLFDEVTAALDPEIVREVLEVMLNLAKEGMTMLIVTHEMGFAKAVADKIIF

MDEGKIIEENDPKSFFENPKSERAKKFLNLFDYHK

>ABV52040.1 polar amino acid transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MLELLNTDTLLRLWQGLFVTLEISFISIIITSIGGLFLGILMSFKNTYIYAFCRLGLEFVRVMPLLVWLF

VVYFGFPRWFGWDLSSVSAAIIVFSIWGCFEMMDLVRVSLQSIPKHQYESASSLGLNTVQSFVYIIIPQA

MRRLTPMSMNLLTRMIKSTTFAYLIGAVELVKVGQQIIEFHNRNDFAPFIIYGLIFFIFFILCYPITLYS

RKLEKKWS

>ABV52039.1 polar amino acid transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MDFDFILVQAPAFLTAAWLTIKLSFFGIIFSLIIGLFCILMSYFKIKILENICKLYIEFSRNTPLLIQLF

FLYYALPKFNIHLEQIPPLDLICLSVEETLRPSFACAIVGLSFLGGSYMAESLRAGFEAIRKQQFEAGLS

LGFSKFGNLRYVILPQALAISMPSISANIIFLIKETSVVSIIALPDLVNLMKSLNSLTYKTDELLFLLFM

GYLCIILPLSFILLKFEKRLLHA

>ABV52038.1 putative transcriptional regulator [Campylobacter jejuni subsp. jejuni 81116]

MKDYLELLSSVGKLKKIQKNSILFYEGEEAKKFFILLKGKIRIYKSTASDKEITLHYFNPPNFIAEMPAF

KKLNYPANAIFEEDGEILEIDFINFQNLCSENKEFNFLLISSLFDKIKILEKKLSQNALDLRTRLLKYLL

ENEKNLDTISQKQIAIDLNVRAQSLSRVLKELKISELIDTKKGRIEILNKDMIMKELW

>ABV52037.1 hypothetical protein C8J\_0438 [Campylobacter jejuni subsp. jejuni 81116]

MKFETINQESIAKLMEIFYEKVRKDKDLGPIFNNAIGTSDEEWKEHKAKIGNFWAGMLLGEGDYNGQPLK

KHLDLPPFPQEFFEVWLGLFEESLNMVYNEEMKAVILQRAQMIASHFQNMLYKYGGH

>ABV52036.1 ATP-dependent DNA helicase [Campylobacter jejuni subsp. jejuni 81116]

MKIKESDFEFFKKLKIRSAIDLALLLPKKIENLNPSKNPKENEICTQKITIKSVSSRKNQLFGLGFCEEW

QENISFVFFHPRAWHFGVCKVGKELIFNAKLSRFNHTWQFNNPKILTSFEGFSPKYQILGLKDTKIAAFI

HKYLNYENLKESGIEDKYIHFLLNLHAYDEKSFFMFENLQNFSKDLKYIEIYNFLKRLKAKQTHFKAHQI

NVFNIANWLKDLPFSLTKDQLNALKDIEKDLHSKEAKRRVIMGDVGCGKTLVLLGAALMVYPKQAILMAP

TSILAYQLYEEAKKFLPDFMNILFIKGGKKEKDLEQNIQKANLIIGTHALIHLESHNAVLVMIDEQHRFG

SAQREKIHSLNKQEFAPHFIQFSATPIPRTLSMIQSELLNFSFIKQMPFKKDITTYCIQNEGFSKLSEKI

KEEISKNHQIIIIYPLVSASDNIPYLSLEQAKEYWQSHYEKVFVTHGKDKQKDEILERFRDEGNILLSTT

VVEVGISLPRLSMIVIVGAERLGLATLHQLRGRVGRVGLKSTCYLYTKLKEIPSRLKEFASTLDGFKIAE

LDLKNRLSGDLLDGFMQHGNEFKFFDFSKDEEILEKVKKDLAKKLPN

>ABV52035.1 zinc protease-like protein [Campylobacter jejuni subsp. jejuni 81116]

MQYLESRGVKIPFIFEKNSDFPIVVLKLVFRNCARSYDEIAGLAKMFSRILNEGVDDKFFKDLEFRAINL

EASSGFESLEINLSCLKENFDFALKSLEKLLLKPRIEEKTLQKLKINALGELASKNSNFDYLAKNLLNAQ

IFKCKEFQSPNDGDEKSIETLSLKDLQNFYKNFIHLSDLVVILGGDLEEKQAKEDLLKLLSKLQIGKKNT

PKKYELSKNIKDEILVRPESEQAYIYFATPFFADFKDKDLYLAKIALFVLGQGGFGSRIMEEIRVKRGLA

YSAYAMLDMNMSFSRVFGYLQTKNESAKEAKKIVKELFEDFIKNGMTQNELDQAKNFLIGSTPLRYESLS

KRLSIAFNEFYQGLNLGYYKEELKLMEKVKLETINAYIKKHQELLNISFASIQNEN

>ABV52034.1 hypothetical protein C8J\_0435 [Campylobacter jejuni subsp. jejuni 81116]

MKRLDKKEALDLLHHASLTELGEMAYRRKLELHPEKITTFVVDRNINYTNVCCIDCSFCAFYRHHKEDDA

YILSFEEIDKKIEELEAIGGTQILFQGGVHPKLKIEWYEELVSWIKEHYPNITVHGFSAVEIAYIAKASK

ISITEVLQRLQAKGLFSIPGAGAEVLSDRVRDIIAPNKCDTATWLEVHRQAHKIGMKSTATMMFGTVEND

EEIIDHFEHLRKLQDETGGFRAFILWSFQSDNTALIQKHPEIMKQSSNKYLRLLALARLYLDNFKNLQSS

WVTQGSLIGQLALKFGANDLGSTMMEENVVSAAGASYRMNQDEMIRLIRSLGENPAKRNTAYEILERF

>ABV52033.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MNYIELLKNNKNIRILASVQFIVYFGAWFSQTGVFTLLVELNAPTWATATSAMLAFLPGVLLAPINGVIV

EKNKPKKLLLNMISIELISIFCLIFVTSLSMLWLLFILIFIRLCVASIYFQAEMSLLAKILTPQELKLAN

EMHSVIWAISYTAGMASAGIFIYFLGVKTAFLFDCMLILIGISFLVRLSIPDFHQKTQSRFFIMIKEGFF

YVLNNKIIFHLILLHAFIGLTAYETLVTLLAQHQYKEVLSAALVIGFLNAVRACSLAIGPMVLSKFINDK

NLFYMYLGQGFGIILWALTQFNFYISFLGLIGAGFFTSALWAYTYTMIQKNADKEYHGRVIAYTDMIYLS

FSAIISMLMGFLFEIDLSLELITGLLGMIFIFAAFYWKWFYKKYL

>ABV52032.1 transcription termination factor NusA [Campylobacter jejuni subsp. jejuni 81116]

MEKIADIIESIANEKNLNLENVREKVATALINTAKRIYGQEYEFFVDPKNLNLYQKITIVADNDERLQNK

SESFIALSKAKSEAPDVEIGDELTYECSLENLGRTAVNTLHKELEYHIQKLLEQTIFEKYKNKVGQMVFG

TVVRVDNEENTFIEIDELRAFLPRKNRIKGEKFKIGDVAKAVIRRVYTDKGIKIELSRTSPKFLECLLEA

EVPEIKDGYVNIIGCARIPGERAKIILQANGANIDPVGATVGVKGVRINAVSKELHNENIDCIEFTNESE

ILISRALAPAIVNSVKIEDKKAIVSLNSEQKSKAIGKNGINIRLASMLSGYEIELNELSSSQLNNAISNE

EAMKNLQDLFKI

>ABV52031.1 hypothetical protein C8J\_0432 [Campylobacter jejuni subsp. jejuni 81116]

MELKLARTLINEKPKNISLEKIEEAIEKEGQKFFYFDKDNTHKQLIALVNHFEKKGVSIYHRTVKYGLDD

NDFMYEVHIL

>ABV52030.1 tRNA-i(6)A37 thiotransferase enzyme MiaB [Campylobacter jejuni subsp. jejuni 81116]

MSAKKLFIQTLGCAMNVRDSEHMIAELTQKENYALTEDIKEADLILINTCSVREKPVHKLFSEVGGFEKV

KKEGAKIGVCGCTASHLGNEIFKRAPYVDFVLGARNISKITQAIKTPKFMGVDIDYDESEFAFADFRNSI

YKSYINISIGCDKHCTYCIVPHTRGDEISIPFNIIYKEAQKAVEKGAKEIFLLGQNVNNYGKRFRNEHKK

MDFSDLLEELSTIEGLERIRFTSPHPLHMDDKFLEVFANNPKVCKSMHMPLQSGSSEILKAMKRGYTKEW

YLNRALKLRELCPNVSISTDIIVAFPGESEKDFEETMDVLEKVRFEQIFSFKYSKRPLTKAATMPNQIDE

ETASRRLSTLQNRHSEILDEIVKKQENKTFKVLFEELRAGNSIAGRTDNNFLVQVEGSEELLGQFKEVKI

TNAKRMVLYGEIV

>ABV52029.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MQWLIFLSCKKHYKGEKVDRKASVILFWHGKLALMPFAFRHYRQKNKKAYVMISHHKDGEQIAKIIKLFG

LDTVRGSTSRGASSALRAAFKVLEQNDDIVITPDGPRGPYHSISDGSIILAQKKELKIRILNYEANRFWE

FKSWDKMILPKPFSKITYSLSEPLDILSLDKEKAKEFLMEQFDKINLADQFKE

>ABV52028.1 hypothetical protein C8J\_0429 [Campylobacter jejuni subsp. jejuni 81116]

MLFLLKKIFPQLFISIILEDKKNIVKASIYRGNKLISSNEKTFDKSENLLEYIKNLSKHFLFYHTALFLD

AKEQGLIPSTNIQDCEHFNIGKISLQHILFNNALVYTATEHVEYYSELFEEYRGLDFLYSPFALLYYNIQ

KEKQPDDQILLYGFKQGHLLAIIVAKGNTILYGDFKIFEQELGLELELPSEDNQEIENNNDDTEVTLDNF

NEALNNKFDLLDQENNLETLDNNDNFNLDELNQFSNDMELCRYIITSIEKFYNDDKYAGVFINGILLYSE

SDINISAIDFLESETFLEIKTKQINTLDLMIELMQKELK

>ABV52027.1 hypothetical protein C8J\_0428 [Campylobacter jejuni subsp. jejuni 81116]

MTYSFIQPRKKPIFTLFDKIWLGLFGFSILFILLVYFTYTIKIALINSSIDDEKQQVIVLQNQTKQNEML

YEILFDQSQIAKNFNTQNQIVKESLRNLFDIIVKTDNITLESVEQDEYSLKLIGVTPTREMFTLLLETPL

KSIFDQSYTTYYRLDNGWYRFVSISKQIPGVADER

>ABV52026.1 hypothetical protein C8J\_0427 [Campylobacter jejuni subsp. jejuni 81116]

MKDKSLEEIDLLKLIICALSFISVCTALILFLLLPTLKNYKQANLRENSQLAILKAAKSKFDFSEDKIST

LRSENNKSLEQFEQNFNIGNFDIFLQKYFQNVKIQETKPKKQEKYLKNRLAIKATMNNPRRLYDFIDALK

NYNNLIKLDYPLNLKAGEQGISIDLTLKVYSS

>ABV52025.1 thiamine biosynthesis protein ThiC [Campylobacter jejuni subsp. jejuni 81116]

MKTQMNYAKEGVFTKEMQIVAQKENLSKDFLLENIACGKIIIPANINHKSLDPNGIGFGLRTKVNVNLGV

SNDCVDYSEEMKKVELAHKFDIEAIMDLSNYGKTSRFRDELVNVSKAMIGTVPVYDAVGFLEKDLKQIGA

KDFLDVVYHHAKSGVDFMTIHAGINSRAAHIFKQSKRLTNIVSRGGSVLYAWMMMKDAENPFFEYYDDLL

DICLKYDVTLSLGDALRPGSTHDASDGAQISELIELSLLTQRAWDVGVQVMIEGPGHMAINEIEVNMQLE

KRLCKGAPFYVLGPLVTDIGAGYDHISGAIGGAVAAASGADMLCYVTPAEHLRLPNLEDVREGIVATKIA

AHAGDIAKLPKERARDDEMSKARQEIDWEKMFKLAIDGEKAKKMFNERRPDDLNSCSMCGKMCAMNTMNQ

ILKGEDVSLA

>ABV52024.1 exonuclease, possibly dna polymerase III epsilon subunit [Campylobacter jejuni subsp. jejuni 81116]

MSSQQIDQIISILNKQSKPYDWVMQEFAKVEELKNFDLDLETFELLGLGLTLNKDNIFTLKTRTTKIKDE

IFCIVDIESTGGVSKGEILEIGAVKIQNSKEIGRFQSFVKVKEIPENITELTGITYEMVENAPSLAKVLS

DFRLFLKDSIFVAHNVRFDYSFISKALNECGFGILLNRRICTIEFAQCCIESPKYKLEVLKEFLGVENTH

HRALDDALAAAEIFKYCLGKLPYHIKTTEELINFTKTARIKQK

>ABV52023.1 ribulose-phosphate 3-epimerase [Campylobacter jejuni subsp. jejuni 81116]

MYVAPSLLSANFLKLEEEVKAIEAAGADLLHIDVMDGHFVPNLTFGPCVIEKISTISKLPLDVHLMVKDV

SKFIDLFIPLKPKFISFHMESEVHPIRLCEYIRSQGIHPAIVLNPHTPIDSIKHMLEFVDMVLLMSVNPG

FGGQKFLPLVHEKIKELRQMIDKKNAKVFIEVDGGVNGLNASDLEESGADILVAGSYIFSSNDYKTAISS

LKLEF

>ABV52022.1 50S ribosomal protein L28 [Campylobacter jejuni subsp. jejuni 81116]

MARVCQITGKGPMVGNNVSHANNKTKRRFLPNLRTVRVTLEDGTTRKMRIAASTLRTLKKQNSK

>ABV52021.1 hypothetical protein C8J\_0422 [Campylobacter jejuni subsp. jejuni 81116]

MLHEYRELMSELKGKDAHFDKLFDRHNELDDMIKDAEEGRTSLSSMEISTLKKEKLHVKDELSQYLANYK

K

>ABV52020.1 putative MCP-type signal transduction protein [Campylobacter jejuni subsp. jejuni 81116]

MFGSKINHSDLQKLEEENKNLAHKIEKFQSENLELKNKITSLEQAALESKLKTDLLNVLLTGVLKNITIV

QGDMLENVNKAEVISSYSKTSLAEMDELNHIANSINASLGDITESANKTRDVAGTLHRSVDEITNVINLI

KDVSDQTNLLALNAAIEAARAGEHGRGFAVVADEVRKLAEKTQKATTEVEMNINLLKQNANEMYTQSEQV

EKISIDSNAHIMSFSEKFTHLVNEAHSTNSNAVGIASEAFVSLAKLDHIAFKLNGYKEIFSKSGKQLADH

TSCRLGKWLASTGKERFGQNKSFLKINEPHEKVHENMNNAITIANTEDISKDITQHSIINKCEVAENASL

DLFNVFKEMLDESDH

>ABV52019.1 hypothetical protein C8J\_0420 [Campylobacter jejuni subsp. jejuni 81116]

MAFKNLKELSFEKSNYIKPKRFAYESNGKFCTWDFIESKDSVSVLLYHKELESFIFVRQFRIPLWYHQMH

DKDYVKDDNMGYTIELCSGLVDKKLSLEEIAKEECIEELGYAPKNLEKIGDFYTGFGSGVSKQSFYFAEV

DEKDKISSGGGVDDEEIEAVYVKVQDFEKKCKNIIRTPLLDFAYMWFLKEKWEKY

>ABV52018.1 hypothetical protein C8J\_0419 [Campylobacter jejuni subsp. jejuni 81116]

MTQIKNMKFKKSLLCFLILSGALLKAEEKYQLNDVVVSASGFEQDLVDAPASISIITKEELEKKPIKDIG

EAIGDIPGVDVTMNKTGTYDFSIRGFGSSYTLVLIDGKRQSVANGFYDNGFSGSESGYLPPLSMIERIEV

IRGPASTLYGSDAVGGVINIITKKNPDKTEANIEFNTLLQQHSNHYGNAGGFNAYVATPLIEDTLSISAR

LKYYDKAASDLKWPTPVWNNSQQRPDNYQIASHSPGAFTSLGFGSRLNWTVDDKNNIYFDIERYINEISV

NSTSSRAIKSERQLFKDNIVLNHDGNYDFGSTNSYLQYGSTKDKELHSQIWVGEGKVVLPWNLGQYGNLV

NTFGARIDYEMLKNDQASAGSQIRGKNLDQTTVALYGENEYFITDDLIFTTGLRYIYSDLFDSEFTPRVY

LVYHLNDNIAFKGGVSKGYKTPAAKELTNGYYNYSNDNAYFGNPDLKPEESINYELGVDFRIFDFAHYSI

TGFITDFTNQISSEDLTGMQNGINCSNGTVCTRPINLGKTQTKGIEFAFNTKTYNGFSLNSSYTFMDNRY

KDGQKNWFGGDRIENLPRHIAMLKLNYERGKFSSYIKTRARLDTIAKAKGGGNGSLPWQKYKPFYIVDLG

INYKINKQSSLSFVVQNLFDKNFFDPQVTKWAGANPAGYANRYQDYTEGRSFWLSYKYDF

>ABV52017.1 acetyl-CoA carboxylase, carboxyl transferase, alpha subunit [Campylobacter jejuni subsp. jejuni 81116]

MASYLDFEKNIQQIDEDIINAQIKGDTEAVSILKKNLEKEISKTYKNLSDFQRLQLARHPDRPYALDYIE

LILNDAHEIHGDRAFRDDPAIVCFMGYLGEKKIIVIGEQKGRGTKDKIARNFGMPHPEGYRKALRVARLA

EKFQIPILFLIDTPGAYPGIGAEERGQSEAIARNLYELSDLKIPTIAIVIGEGGSGGALAIGVADRLAMM

KNSVFSVISPEGCAAILWNDPAKSEAATKAMKVTADDLKSQGLIDDVIDEPTNGAHRNKEAAAVAIADYV

KKSLNELENIDVRELSANRMQKILKLGAYQEA

>ABV52016.1 3-oxoacyl-[acyl-carrier-protein] synthase [Campylobacter jejuni subsp. jejuni 81116]

MKRVVVTGIGMINALGLDKESSFKAICNGESGVNKITLFDATDFPVQIAAEVKNFDPLEVVDGKEVKKID

RFIQLGIKAAREAMQDAGFSEELDKEEFGIVSAAGIGGLPNIEKNSIICSERGPRKISPFFIPSALVNML

GGLISIEHGLKGPNISCVTACAAGTHAIGEAYKSIALGNAKKMLVIGAEAAICPVGIGGFASMKALSTRN

EDPQHASRPFDKERDGFVMGEGAGALVFEEYEEAKKRGATIYAELIGFGESADAHHITSPTLDGPLRAMK

KALNMAGNPKVDYINAHGTSTPVNDKNETAAIKELFGNNIPLISSTKGQTGHCLGAAGAIEAVISVMALR

DGVVPPTINQLVKDDECDLDYVPNISRKVDLKVVMSNSFGFGGTNGCVVFKKVD

>ABV52015.1 acyl carrier protein [Campylobacter jejuni subsp. jejuni 81116]

MATFDDVKAVVVEQLSIDADAVKMESKIIEDLGADSLDVVELIMALEEKFEVEIPDSDAEKLIKIEDVVN

YIDNLKK

>ABV52014.1 putative transcriptional regulator [Campylobacter jejuni subsp. jejuni 81116]

MLFSNLIKENQKIWNAYLHHDFVKKLEDKSLKQENFLFYLKQDYIYLLNYAKCYARLALNSNTAKELRFA

MKFQNYIVEGEMELHRAILSLGINADELNIKDESLVNIAYSRYMLSVGENGDFLDMLVALSACAIGYAKI

GAEIINRLKNENLKDHPYKEWILTYGSENFQNEAKEFEDFVNSYTSSVSAQKFQKLSEIFHTATRLEVAF

WEHSLRMELNL

>ABV52013.1 putative succinate dehydrogenase subunit C [Campylobacter jejuni subsp. jejuni 81116]

MQKEYAFFPGCVLSQAAKESKISLEAIAPILGWKLNEIKGWSCCGASQAQCVDPIATLVANARNIALAEE

MKMPMLTTCSTCMLTLTKAKNTLDKGAKERINTFLAQGGMKYQGSTPITSLLWELYEDLDNLKSKVKKPL

SNLKVALFYGCHSLRPEDAFGKKESSTNPKSFESVVEVLGAKIVPFEKRLDCCGFHASYPAEKSVKKMSS

QIVNNASENQADCVVTPCPLCQMQLDIYQERFQDYTSSKARLPMIHLSQLVGLALGLSKEMVGLDYNIID

ASKIA

>ABV52012.1 succinate dehydrogenase, iron-sulfur protein subunit [Campylobacter jejuni subsp. jejuni 81116]

MKIIIDRFNGKEKYEQSYDIDDKDIQGKTLLSLLLFIKKTKDITLNFTASCQSAICGACAVRVNGHSYLA

CDTKMQDLLKEYDNPSSIRISPLGNFRVISDLIVDWEPSIENLRKIRPAMVAKNEFSAEKGCKQSQEEFD

RISKQWDCILCGSCASECNKLEADSSDYMQPFVFTHAWRAAADSRGKDPMLHVKPSVMNGLWLCVHCQEC

ADRCPKGISSVSDIANLRVMAIKKGLNEGLGPDHAEAFYKDLVEGSGRLNEIYLALRSEGVIGSMGKTDI

AFKLMRAGKMNPMHVFGEDEIEGHKDLVKMIKAAQEAAVKE

>ABV52011.1 succinate dehydrogenase flavoprotein subunit [Campylobacter jejuni subsp. jejuni 81116]

MGEFSRRDFIKTACISVGALAASSSGVYALDDSSKMDKDTNLPSCDVLVIGSGGAGLRAAAAVRKENPKL

SVVVATKMMPSRNATCMAEGGINGVTDFSNGDSYKLHAYDTIKGGAYLVDQDAALKFCELAGKAIFNMDF

IGTLFSRNEQGGVAQRLMGGASKKRCNYSADKTGHILMHSCLDDAISSGVKFLMDHELLDIGVMDGKCEG

VVLRDIQSGGIYPVLCKALVIATGGYTRIFYNRTSTPFIATGDGVAAALRAGLGFEDPEMIQFHPTGVAN

GGTLITEAARGEGGYLLNNRGERFMKNYHEKMELAPRDVVARAIETEIREGRGYGEGLGAYVLCDVRHLG

KEKILKDLPKIRHTAMLFENIDLVDTPVPIRPTAHYSMGGIEVAKFEDMSTKIAGIYVGGEASCISIHGA

NRLGGNSLADAVVTGHLAGIGATNYAKDASFGKGAKTHELAQKWQARFKEITNNGGNGQEMYELREELGS

QNWDNMGIFRTQEKLDLLAKNLEDIQARYEKIRIPNPNEVMNTAFTDYVELGNLILLSRCACLAARNRLE

SRGAHTREDYPKRDDKNFLKHSIVNLENDELKLSYKDVVVTEFSLDGRRVQ

>ABV52010.1 hypothetical protein C8J\_0411 [Campylobacter jejuni subsp. jejuni 81116]

MDLKEIAQFLDDNVPAFLATLGTCGNPRVRPIQSPLLVRDKIYFCTANTKGLFKHIKNYNGIEFCSCAKD

GTFLRLRANAVFEPNLEVKKMMFEKYPYLVNLYETPQNPKFEVFYLDHLSARMQFMNGEFKLFKA

>ABV52009.1 3-ketoacyl-(acyl-carrier-protein) reductase [Campylobacter jejuni subsp. jejuni 81116]

MKFSGKNVLITGASKGIGASIAKTLAGFGLKVWINYRSKPELADALKDEIIASGGVAAVIKFDASKEDEF

ENGVKTIVESDGELGYLVNNAGVTNDKLALRMKLEDFSSVVDTNLSSAFLGCREALKTMSKKRFGAVVNI

ASIVGEMGNAGQVNYSASKGGMIAMTKSFAKEGASRNLRFNCVTPGFIKSDMTEVLSDEIKQTYQDNIPL

KRFAEPEEVANCVAFLLSDYASYVTGDVLKINGGLYM

>ABV52008.1 phosphoglyceromutase [Campylobacter jejuni subsp. jejuni 81116]

MKQKCVLIITDGIGYNKNSKFNAFEAAKKPSYEKLFKEVPNSLLKTSGLAVGLPEGQMGNSEVGHMCIGS

GRIIYQNLVRINKAIENKELEKNENLQKLLAKCKRVHIIGLYSDGGVHSMDTHFKAMLEICAKNGNEVFA

HAITDGRDVSPKSGLNFIKDLKEFCENLGVHFATLCGRFYAMDRDKRWDRVKEYYECLLGKAYKVPNLLE

YLQKSYDENVTDEFIKAAQNENYKGMREEDGIIFINFRNDRMKQLVEVLNSKDFKEFEREKIFENLLTMS

VYDDKFKLPVLFEKEKIENTLAQVISKAGLSQLHTAETEKYAHVTFFFNGGKEELLENETRVLIPSPKVK

TYDEKPQMSAFEVCDAVKKGIEKGEDFIVVNFANGDMVGHTGDFNAAIKAVEAVDTCLGEIVECAKKHDY

AFIITSDHGNCEAMQDEKGNLLTNHTTFDVFVFVQAKGVSKIKDNMGLSNIAASVLKILDLEIPKEMNEA

LF

>ABV52007.1 phospho-N-acetylmuramoyl-pentapeptide-transferase [Campylobacter jejuni subsp. jejuni 81116]

MYYLSDLSHYAFFTYISVRAGFAFFIALCLSLFLMPKFITWAKAKNASQPIYEYAPETHKTKCHTPTMGG

LIFISSAVIASLFCIKFDNIFAISALLCLILFCLIGLIDDLGKVLKKDNHSGLSPRMKLLAQIIAGLICI

LPLYFSSELSTELFIPFYKHPLFDMEIFAIVFWILVLISSSNAVNLTDGLDGLATVPSIFSLSTLGIFLY

LSGNLNYSEYLLLPKIQGLGEVVIICAALIGALMGFLWYNCYPAQVFMGDSGSLALGGFIGFLAIISKNE

ILLLLIGFVFVLETVSVILQVGSFKIFNKRVFKMAPIHHHFEKVGWVENKIIVRFWMIALLSNLLALASI

KLR

>ABV52006.1 UDP-N-acetylmuramoylalanine--D-glutamate ligase [Campylobacter jejuni subsp. jejuni 81116]

MKISLFGYGKTTRAIAENLVDKFGPFDIYDDHFTETKKDTLGNLLLNPNDFDDNLSDIEIPSPGFPPKHK

LIQKAKNLQSEYDFFYDIMPKSVWISGTNGKTTTTQMATHLLSHIGAVIGGNVGTPLAELDPYAKLWILE

TSSFTLHYTHKAKPEIYALLPISPDHLSWHGSFDNYVQDKLSVLKRMNECDVVILPKIYANTPTKAHKIS

YKDEKDLAVKFGIDTEKISFKSPFLLDAIMALAIEKILLDTLSYELLNSFVMEKNKLEELKDSQNRLWVN

DTKATNESAVMAALNRYKDKKIHLIIGGDDKGVDLSNLFDFMKNFNIELYAIGISTEKMLDYAKKANLKA

YKCEVLSKAVNEISNHLRVNEVALLSPACASLDQFNSYVERGKVFKECVNKI

>ABV52005.1 hypothetical protein C8J\_0406 [Campylobacter jejuni subsp. jejuni 81116]

MIKAFSLLEFVFIILILGIVFNLGSLYLKKDNLLEGAIQILNDIQYTQSLAMMQEGIRVDELAIAKREWF

KSKWQIYFIKSAATGYDQTYTIFLDKNGDGNANLGKTEINIDREIAVDVINHNKLMNSGQSGVISKDDEK

TTQRFNITKRFGIEKVEFKGSCSGFTRLVFDEMGRVYSPLKNANYAYEKTLAKNNSDCIIRLLSKKHALC

IVIDTLSGYAYIPDFKTLKSQFVNIKNKNYECSKI

>ABV52004.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MEKIKNYKLIIILLSLDLLALLYGISTLSISADEADIYFGEQGKSLIFSHSLLYYISHFGTFIFGQNDFG

LRLPFLFFHFLSCLLLYLLALKYTKTKIDAFFSLLLFVLLPGTVASALLVNAASLVIFLTLAILCAYEYE

KKWLFYILLIIVLFVDKSFNILFLTFFFFGIYKRNAILFTLSLVLFGASISFYGFDTGGRPRGYFLDTLG

IFAACFSPLVFVYFFYTIYRLTFQKYKNLLWFLMSVTFVFCLLLSLRQKLFLDDFLPFCVICTPLLIKTL

MQSYRVRLPVFRLRYKIFIECSIIFLIFCYFLIVANQLLYYFINNPNRHFANNYHFAKELALELKKQDVL

ELATAPSLQKRLRFYGIKNSNKFYLKALKQADKHDMDKKIVKVKLGKYEKVYQILNYD

>ABV52003.1 hypothetical protein C8J\_0404 [Campylobacter jejuni subsp. jejuni 81116]

MQTIDQIFQTQIDIKKSIFLSFLCPFKDFKFLIETLKKEHPKAVHFVYAYRVLNDFNQIVEDKSDDGEPK

GTSGMPTLNVLRGYDLINAALITVRYFGGIKLGTGGLVRAYSDAANAVINNSSLLSFELKKNISIAIDLK

NLNRFEYFLKTYSFNFTKDFKDCKAILHIKLNEKEEQEFEIFYKNFAPFEIEKL

>ABV52002.1 hypothetical protein C8J\_0403 [Campylobacter jejuni subsp. jejuni 81116]

MQVNYRTISSYEYDAISGQYKQVDKQVEDYSSSGKSDFMDILNKADEKSSGDALNSSNSFQSNAQNSNSN

LSNYAQMSNVYAYRFRQNEGELSMRAQSASVHNDLVQQGANEQSKNNTLLNDLLNAI

>ABV52001.1 hypothetical protein C8J\_0402 [Campylobacter jejuni subsp. jejuni 81116]

MAKFRIQYSAGFGHYTQNHKGFGPTIYIEEVVEFDNGKDYFDYIDFYKTYSKSDDTYFHISFLEDRPLSD

KEITIRNEYRKMRDENCKKAKEEFIANNELDVEHLPTHHD

>ABV52000.1 ABC transporter ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MVEVKNLTMRFANQLLFENVNLKLVRGQRYGLIGANGAGKSTFLKILSGEIESSSGEIVFDEGLKIAVLG

QDQFAFENYTIKDAVMCANKRLYEALKEKEKLYMSEEFTDEINERLGELEIITAEEDPNYDCETRCEKIL

SSLKIKDFDALMSTLQSADKFKVLLAQVLFLGADVLFLDEPTNNLDLEAISWLENELLRHEGTLVVISHD

RHFLNKICTRILDVDFKQIRDFAGNYDDWYMASTLLAKQAELKRDKTLKEREELENFIRRFSANASKAKQ

ATSRAKALEKLELEEIKISSRRDPSIVFRTNREIGNEVLEFKGIGKAYDKQLFSNLELKIEKNDKIALIG

ANGVGKSTLAKIIAHAISPDTGSMHLGATIELGYFPQDTSNLICENLKLYEWLMSEKFKDLDEIRKCLGR

MLFSGSDQEKMAASLSGGEKHRLMLSRLMLERPNFLLLDEPDNHLDLESIIALGEALYNFKGVVLCISHD

RELVSAFANRIWHLENGKLTDFRGTYQEFLGENDG

>ABV51999.1 hypothetical protein C8J\_0400 [Campylobacter jejuni subsp. jejuni 81116]

MDYNVFLLNIQDKINQEDFFNLKLKFEQLQNKKEALSNLVFLRLQDPIKPLIMSMICGFLSLGWLAIDRF

MIKDYALGILRIILSLFPCVLFLILGISYENDSNLDISEIFFGLFGIFLLLGIIWWGVDLFLVYKKIKKQ

NYNKIIEFIFNYQKI

>ABV51998.1 lipoprotein, putative [Campylobacter jejuni subsp. jejuni 81116]

MKCFNAKFMFVGILAVFLSACSSGIPKCSDQDVQNVLTEIILEHNFGRFSEVDRKKLKFTYSGFMSDLTD

KESKTQYCKAQVKANGSIDSRPYKWDAWIEYFARYTDDGMVYVEITR

>ABV51997.1 hypothetical protein C8J\_0398 [Campylobacter jejuni subsp. jejuni 81116]

MDFNSVLFSIGDKLPKDATSTVMLKKKFDRLNEDKQKEVVAQLPMIKLKSPALVFWVGTFLFGAFGVGRF

MIGDWVLGLIRLGITIVAMICGVLMITYSALGIIYGLLWLVNWIWWIVDMFLVGKKLRKQNFEKIANIIQ

>ABV51996.1 hypothetical protein C8J\_0397 [Campylobacter jejuni subsp. jejuni 81116]

MTKKSKRDMAYELDIDVSTLYNWRKYKPNLYRIVMLGFKFDELLENSKKTHEELLHIEQTIQDEIAKFK

>ABV51995.1 hypothetical protein C8J\_0396 [Campylobacter jejuni subsp. jejuni 81116]

MFLLDFLISLSFIFEISALVLSFYFKNSRIFFLTLVLLGAKLPYFYTSFFQANLFVALFLPMIFTLFCLG

KHHALILSKKNIASITTLIFIGVLSIILPRNTTFNSAGLEFHFITLNFFKPVSELGFLFFLVGLILIFIK

IFKTKEYYLIIAFFAAYFQFLFQEGAGIRYFEFASLVFCFYLLNHAYKLAFFDILTKLPNEKSLTRFTKG

KNNYIIALLHFNELKDTKESYAKLILKQIAKILKRFRAKIFIVENDFILIFNDKNQALNHLAFLESTLKN

TEFNLENENFKPDFKLIWQESEENLDKNLQSLRARLLD

>ABV51994.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKVLLSSLVAVSLLSTGLFAKEYTLDKAHTDVGFKIKHLQISNVKGNFKDYSAVIDFDPASAEFKKLDA

TIKIASVNTENQTRDNHLQQDDFFKAKKYPDMTFTMKKYEKIDNEKGKMTGTLTIAGVSKDIVLDTEIGG

VVKGKDGKEKIGFSLNGKIKRSDFKFATSTSTITLSDDINLNIEVEANEK

>ABV51993.1 HIT family protein [Campylobacter jejuni subsp. jejuni 81116]

MIYENDLIYIEKEEAQVPWLKIFTKEIYKEFSDCPLELQKELFEKILLCEKAMIEFYKPEKINIASFANY

VPRVHFHVMARFKEDAFFPECMWGKQQREAIKLDLPKFEEFVKFLNSKIF

>ABV51992.1 hypothetical protein C8J\_0393 [Campylobacter jejuni subsp. jejuni 81116]

MQISSSYNSYDYYSSKPSFDKTNQSDSTQKDEKNLSENKDDKEKNGEQTQMVNGVELSQKEVAQVRELQS

IDRNVKAHEAAHQAAGGGLAGAASFTYTRGPDNQMYATAGEVPISMQKGNTPEETIANARQIAAAAMAPA

DPSPQDYKVAANATKMEFEARAEAMKLKAEEAKEKEEENKEKDDKNSENSLEKTDKDSKNNDKNSNFDKD

FKNFVARTYQQNSQNNDIKFNIAS

>ABV51991.1 hypothetical protein C8J\_0392 [Campylobacter jejuni subsp. jejuni 81116]

MLNILHANSSHRFHKCMPKEVHQIYDTLKLMEQQEDTKKVEAKKEEQSNSTNTDKADNKKDKFLDMSV

>ABV51990.1 hypothetical protein C8J\_0391 [Campylobacter jejuni subsp. jejuni 81116]

MITLSSFNRYFGNNPLQTLTKIRDESIENAKI

>ABV51989.1 oxidoreductase, putative [Campylobacter jejuni subsp. jejuni 81116]

MAEVLKKVDVVTVGAGWTGGIVAAELTKAGLNVLSLERGHMQSTENFNFIHDEWRYGINYGLMQDCSKDT

VTFRHDPSGLALPYRKMGSFLLGNNVGGAGVHWNGWTFRFMPYDFEIQTLSKQRYGNKLGNDYTLQDWGV

TYKDMEPYYDRFEKTCGVSGEPNPLAEKMGAFRSSPYPQEPLENTKMLKRFESAAKSSNLHTYRLPASNS

KGGYTNPDGQDLAPCQYCAYCERFGCEYGAKASPLNTVIPKAMSTGKYTIRTYSNVTQILKKDGKVTGVK

FVDTRTMKEYIQPADIVVLTSYMFNNAKLLMVSNIGEQYDPKTGKGTLGRNYCYQMNMGTTAFFDEQFNT

FMGSGALGTTSDDFNGDNFDHSKEKFLHGAMIYSVQLGTRPIQSAPLPAGAPTWGAEFKKALNYNFTRAI

TVGGQGASLPHKNNYLSLDPTYKDAFGMPLLRLTYNFTDQDRALHKFITDKTAEVAKRMQGVKSIKKGAY

LKDYSVVPYQSTHNTGGTTMGADRETSVVNTYLQHWDADNLFVVGAGNFQHNSGYNPTDTVGALAYRCAE

GILKYHKSGKSLA

>ABV51988.1 hypothetical protein C8J\_0389 [Campylobacter jejuni subsp. jejuni 81116]

MQDNIIDRRSFFKLGLLGGSVVAASTIGGGAVLKAAELTHSHQASQGKSNKVRGRMFFQTQTEFDTLSAA

CERIYPKDEQGEGAIGLGVPYFIDNQLASAYGYNDREYMQGPFMEGKAEQGYQTPMQRKDIFLEGVHALE

ENAQKRYKKSFSLLKGGDQDKILSDFEKGKIQTTGFKSSYFFTLLRDMTVAGVLADPIYGGNDNKNGWRM

MQYPGAQMSYVDKIASDEFFNIEPMSLADMES

>ABV51987.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MRIFLALFLFFNSLFALSELEEGLKLYEANKFDKAYEIFKNLCEKDISKACFSLAFMHESAKGVSKDLNQ

AYKFYDKACKLGLANACSNMALLLQNQGYKNEALLAFNKACTLGESLSCNNIALFYEKEKDGQMASSFYK

RSCDLKNARACYQLGSLYDKGELVKASVKSALAFYSKSCTLGFGEACYLLGRYNQLEKQDLTKAKRYFGM

ACDQKHQEACAAYKELNSKDIELY

>ABV51986.1 putative ATP/GTP binding protein [Campylobacter jejuni subsp. jejuni 81116]

MQINLLNDFIKAYENTYSVSFDDSFKGRIQELCKELNEPFMHASYALENELKELVFSLDKNVNIAIIGQF

SSGKSSLLNLILGCDCLPTGVVPVTFKPTFLRYAKEYFLRVEFEDGSDIITNIEKLAFYTDQRNEVKQAK

SLHIFAPIPLLEKITLVDTPGLNANENDTLTTLDELKNIHGAIWLSLIDNAGKKSEEDAIKANLELLGEN

SICVLNQKDKLSTEELDNVLNYAKSVFLKYFNELIAISCKEAKDEQSYEKSNFQSLLDFLTQLDTTALKE

KFVKRKILNLCEILEDENQLFVGIFDRLLNQFQNYEKHLLLAYENFLKEIEILNHQILEQLKSISERISS

EIFASVKEKDAYFYKESKGFLKKDLYTRYDYKAPYISSDDAFLAMFYNSDVMSKEFKKIKNELYKSFEEI

KMKLKDFINILEREILLFKAEFSNIQKDHIFQSDKNFSELRAFCNASDEYFLKDFKELLFKSILELDLFF

EKLNLKAFTNYENATKLSLAFFSRKINESRVLYELDSSEFVLFYPKKSEIYERVLNELNVYEFEALLINK

PILTKIAKNFLEQSQNLIQEKNKFLDLKKAELQKRRAQILNVRESIKED

>ABV51985.1 putative ATP/GTP binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKELFQKIWQNELQFLNFDAKFQDKNKLDTAECAIILSVNKDNYERYFLLKEFQELCKKIDLRVDIFSIQ

NAQICILNLFKSGFIPKQDLLKALKILEKISKNTEIFDFISQEKVQSIDQKALFQNDFKELNTINLELQK

LSFDENLKSRLQKTLEKFQNLEFNIAITGVMNAGKSSLLNALLKEDFLGVSNIPETANLTVLSYGKSEEA

KIYFWDKKEWQNILESSHFNADLKEFIDKLDKSVNIQDFIKDKPLIQNIALCELKNFSSAKNKISALIKK

IEIKSHLDFLKNNISIVDTPGLDDVVVQREIVTNEYLRESDFLIHLMNASQSLTQKDADFLVHCLLNSRL

SKFLIVLTKADLLSKKDLEEVIVYTKESLKSRLVDLDENLVEKIDFLCVSAKMASDFYKSLAPKESLQKS

GMQEFENYLFNELYAGEKSKIALRAYKKELHLELKNILSEYEMQNRLIKENKQGVSEENQKLLLELQKQN

TLLKEAQDEISNSVAKLKNIDSGIDNLVLLLVKKLKERLIDEFKYLKNNAQKLNLSRILNIVDITTKDGI

NDILREIKFENIKKIEELKTNLSLKYDFLKDDFDNGFEGFKDGISKNIDSIFQSEKFALLRLKIEKLSNL

KSDLYELETNLDTVIFDTFKEFKMSEILNSLNINGAFFEFLNDKLKHYEKNQKSKLESLEKVLQSLKNQD

ANILNSFEENLEKIEKLKQLEMGLLNAD

>ABV51984.1 fumarate reductase iron-sulfur protein [Campylobacter jejuni subsp. jejuni 81116]

MSRKLTIKAFKYNPLSKISKPHFVTYELEETPFMTVFVCLTLIREKMDADLSFDFVCRAGICGSCAMMIN

GVPKLACKTLTKDYPDGVIELMPMPAFRHIKDLSVNTGEWFEDMCKRVESWVHNEKETDISKLEERIEPE

VADETFELDRCIECGICVASCATKLMRPNFIAATGLLRTARYLQDPHDHRSVEDFYELVGDDDGVFGCMS

LLACEDNCPKELPLQSKIAYMRRQLVAQRNK

>ABV51983.1 fumarate reductase flavoprotein subunit [Campylobacter jejuni subsp. jejuni 81116]

MNIQYSDALVIGGGLAGLRAAIEVAKSGQSVTLLSICPVKRSHSAAVQGGMQASLANGAKGEGDNEDLHF

ADTVKGSDWGCDQEVARMFAQTAPKAVRELAAWGVPWTRVTKGPRTVVINAQKTVIEEKEEAHGLINARD

FGGTKKWRTCYIADATGHCMLYGVANEAIKHQVKIIDRMEAVRIIHDGKKCLGVIARDLTNGQLIAYIAR

GTMIATGGYGRIYKQTTNAVICEGTGAAIALETGLCRLSNMEAVQFHPTPIVPSGILLTEGCRGDGGILR

DVDGYRFMPDYEPEKKELASRDVVSRRMMEHIRKGKGVKSPYGDHLWLDISILGRAHVEKNLRDVQDICK

TFNGIDPADEGPKGWAPVLPMQHYSMGGIRTKPTGESQWLNGLFACGEAACWDMHGFNRLGGNSCAETVV

AGMIVGDYFADYCKNNGEVIDTNVVKDFLTKEYQYLKSLVDKEGKHNVFEIKNRMKEIMWDKVAIFRTGE

GLKEAVDELEKLYKDSQDVKVHCKELDCANPELEEAYRVPRMLKIALCVAYGALLRTESRGAHYREDYPK

RDDLNWMKRTNTFWVEGETLPRIEYEELDIMKMEIPPAFRGYGAKGNIIENPLSEKRQAEVDAIREKMEA

EGKGRYEIQNALMPYELQAKYKAPNQRIGVDYE

>ABV51982.1 fumarate reductase cytochrome B subunit [Campylobacter jejuni subsp. jejuni 81116]

MRELIEGYLGKSIEGKKSKMPAKLDFIQSASGLFLGLFMWVHMLFVSTILVSEDFFNSVVHFLELKFVYD

NPVMSYLTSFLAACVLVVFFVHALLAMRKFPINYRQYQILRTHSKKMNHSDTSLWWVQAFTGFIMFFLGS

AHLIFIVTNADKISGDMSGDRVVSHFMWLFYAVLLVCVELHGSIGLYRLCVKWGWFEGKNVKESRKKLKT

AKWIISIFFLVLGVLSLAAFIKIGYENYQNQTQTTAMIKNYNGANYEYTI

>ABV51981.1 prolipoprotein diacylglyceryl transferase [Campylobacter jejuni subsp. jejuni 81116]

MEFWQHIYSNFNVIAFSIFGLKVHWYGIMYVIALLLALLLAKFFVRKFQLDINEKHLDSYFIWVEIGVIL

GARLGYILIYDANTMYYITHPWQIFNPYINGEFVGIRGMSYHGAIIGFLIATLLFCKKYKTNPWIFLDLV

ALSVPLAYVFGRIGNFLNQELFGRITNVPWGIYVDGVLRHPSQLYEAFLEGIVVFIIVYLARFKQSFQGE

LILVYAGAYSLARFICEFYREPDFGIGFVLWGMSMGQILSFIMFITALLVYICIKFKKVNI

>ABV51980.1 lipoprotein, putative [Campylobacter jejuni subsp. jejuni 81116]

MKKYILLASSMLILAACGGTSSNFVNVSMPNFKPQVPTKVEPIDSGVSIALEPINIEQNNNYSDYFENSV

LKIRIEKEIDLLKRNLEEQIKTIAQLKGYKIVTTNPDYTLKSSISIYTEEKNAQKTSNFMSGDYVKSNLG

INFKGKIDFIDAHNPQNSTNLSSSTKLDSLVALNYPIKNDDGVNMFKTTISTVPTQLNKGLEQPAFEIDK

SFLAFYKNTLNTLYNNLPKATDIGKTIPNTNSGFNSFDGDATFEESLPQTNSNQNNTIENTPTQNIPTNP

SSTNQNNQSKNQDGVEIFE

>ABV51979.1 shikimate 5-dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MKFLAVIGDPISHSKSPRMHNNAINALGLDSIYTRYHLRNANCLREDFFKLGLSGANITLPFKEKALDIA

DVKDDFARNIGSANTLCLKEDKIYAYNTDALGFLEAIKDFDNIKKALILGAGGTALALAYALKQKGVEVY

IANRSKERFKDFLAYPTYLYKNLQDFDFDLVINSTSAGLKDENLPCDRELLDRILPKAKFAFEVIYGRET

PFYRLCKEYHLKIKDGLDMLLWQGVFAFELFFEIRDKREMIKNAMQQALILK

>ABV51978.1 hypothetical protein C8J\_0379 [Campylobacter jejuni subsp. jejuni 81116]

MENQKNEFDDIILEKSNKSEKVKKILLRVIALVILFLAIMIVMKLINGSGDENTQNQSVLPSEPIATQDN

NNDTSFESMPITDNTSAEDQFEALRKQFQDEQNTTQNTTTSSSNNNDTTNFAMPDQEVPAEPTATTSENT

TPQASTPKQEVTQTAKPKEEAKKQTAVKKEKESTKQIPKKEQNANDLFKNVDAKPVHPSGLASGIYVQIF

SVSNLDQKSKELASVKQKGYDYKLYKTTVGGKEITKVLIGPFEKADIAAELAKIRKDIAKDAFSFTLK

>ABV51977.1 hypothetical protein C8J\_0378 [Campylobacter jejuni subsp. jejuni 81116]

MISPMDMSLIKIIGDHYYIRRDKIVNKITHRGRLFFDKFERVDAPLNLNVMREHAAKKIVVAHDLITKDN

KVENIVFDYNGFNAERFYHRAQLILREEGFINFTAYKTKTPGHLHLYIHKGHTALNEGYSLASKLSMMFA

SKMPVEWKVFPSMDVPREFNILILPYEVYQKERGSSWSKHM

>ABV51976.1 serine hydroxymethyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MSLEMFDKEIFDLTNKELERQCEGLEMIASENFTLPEVMEVIGSILTNKYAEGYPGKRYYGGCEFVDEIE

TLAIERCKKLFNCKFANVQPNSGSQANQGVYAALINPGDKILGMDLSHGGHLTHGAKVSSSGKMYESCFY

GVELDGRIDYEKVREIAKKEKPKLIVCGASAYARVIDFAKFREIADEIGAYLFADIAHIAGLVVAGEHPS

PFPHAHVVSSTTHKTLRGPRGGIIMTNDEELAKKINSAIFPGIQGGPLMHVIAAKAVGFKFNLSDEWKVY

AKQVRTNAQVLANVLMDRKFKLVSDGTDNHLVLMSFLDREFSGKDADLALGNAGITANKNTVPGEIRSPF

ITSGLRLGTPALTARGFKEKEMEIVSNYIADILDDINNEKLQENIKQELKKLASNFIIYERAMF

>ABV51975.1 lysyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MFDNILEQQRIEKAKELKNLGINPYPHFLEKEMSLKTFKDKFSYILEQVEKRDESVNAVVAGRLKLLRIA

GKSIFANIEDEDTNLQIYFNKDSVGEELYAILKKNLEVGDIVLVKGFPFVTKTGEFSLHASEVKLATKAI

VPLPEKYHGLTDIEQRYRKRYVDMIMNAEVRKDFLVRSKVVSLIRHFFENKGFLEVETPMMHPIAGGANA

KPFVTFHNSLGVERFLRIAPELYLKRLVVGGFEAVFEINRCFRNEGMDLTHNPEFTTIEFYWAYHNYKDL

MDLTEELFALLLDKLNLGKTIEFDGKMIDFSKPFERITYKDALCKYGGLDRDLIEDKEKILTKLKVDGFE

ANEKLELGHLQAELFDNYVEEKLINPTFVIDFPISISPLSRRSDEDSQIAERFELFICGRELANGFNELN

DPLDQYERFLKQIEAKNAGDEEACEMDEDFVNALGYGMPPTAGQGIGIDRLVMLLTNKKSIRDVILFPAM

RPLKSELKEKE

>ABV51974.1 ferric uptake regulator [Campylobacter jejuni subsp. jejuni 81116]

MLIENVEYDVLLERFKKILRQGGLKYTKQREVLLKTLYHSDTHYTPESLYMEIKQAEPDLNVGIATVYRT

LNLLEEAEMVTSISFGSAGKKYELANKPHHDHMICKNCGKIIEFENPIIERQQALIAKEHGFKLTGHLMQ

LYGVCGDCNNQKAKVKI

>ABV51973.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MNFYWFDAFILGFTLLLGLKGIINGLIKEIFGLLGIIGGVFIASKYATQAAEFIQSTFYKIENQSLAGFA

GFLAILIIFWIVCLLAGNFLSKLIKLSGLGFLDRIGGFIFGGAKIFLIFAILVFCVARIDFLNDKLDNFA

KNSYTLNLLKETGSFIMNQPLTENSLDHASEKLQDIVSDLNNTQKGE

>ABV51972.1 putative Glu-tRNAGln amidotransferase subunit C [Campylobacter jejuni subsp. jejuni 81116]

MQIDEKLLSKLEKLSALQITKNRNETIVQLSEIVNFVEKLNELDLDSQEITVSTIKGGAPLRIDEIRNSN

VIDEVLDCAPKKQEHFFVVPKIIE

>ABV51971.1 hypothetical protein C8J\_0372 [Campylobacter jejuni subsp. jejuni 81116]

MGLKDNLKAVKNELNTEEQFIENFIKGERFIRKYKFYISAVVIILVAWFAGNFIISKINDYKTKEANEIY

ANLIQDPSNKNLLEQLKNKNTNLYAIFLLKENINDFNNTALQNELKQIYNNAQTNTLLKNIIALSLGDKS

IFLKNYDKLLEAYKLLEQNKIEEANVLLSQIKENSSLNQIAKNLKHYQGITQ

>ABV51970.1 lipoprotein, putative [Campylobacter jejuni subsp. jejuni 81116]

MKKIFLTLFCLIFLCACGTKRQYFEPEQTNGDLSHNGNLKSKIVDWNLVSAKLSNNTAILKNNISIDKFK

LPKNYILIAYQDGEYFTADDNGNLKIFDNSYNEIYNFQFDASVVGVASNGDDLALVLANNTIVLANRSLG

IKFSQTLTSAPAQDSRTANPIFLDNIIVYPTLDGKILILSRNNLQVIKDVVISAENFFNNVIHLSVIGDK

LIAATAKKIIVVSPARTLYLDADIKDVALSDDGIFILEKDGTIIKTDYNLRKIAEKKFEFAIFVKSNIYN

NYLYIFEKTGYLIKMNLNLDNTQVFKLSEAVDKISFMGNGKFYYGDKILDLL

>ABV51969.1 hypothetical protein C8J\_0370 [Campylobacter jejuni subsp. jejuni 81116]

MIKILEQTIKALKLNLKPYDLSMLTRKKSYICAKDQNNILFMYTGKTKFLMKDALFLENLAQQININNKY

FFSMASLCSKAKNHLEMKGFNIYVAL

>ABV51968.1 transcriptional activator, putative, Baf family [Campylobacter jejuni subsp. jejuni 81116]

MLLCDIGNSNANFLDDNKYFTLSIDQFLEFKNEQKIFYINVNEHLKEHLKNQKNFINLEPYFLFDTIYQG

LGIDRIAACYTIEDGVVVDAGSAITIDIISNSIHLGGFILPGIANYKKIYSHISPRLKSEFNTQVSLDAF

PQKTMDALSYGVFKGIYLLIKDAAQNKKLYFTGGDGQFLANYFDHAIYDKLLIFRGMKKIIKENPNLLY

>ABV51967.1 malate dehydrogenase (acceptor) [Campylobacter jejuni subsp. jejuni 81116]

MSQQEFDVLVIGAGISGAALFYELARYTNIKNIALIEKYNTAATLNSKGTSNSQTIHCGDIETNYTLEKA

RKVKRTADMIVKYGLMQNAQNNFMFSHQKIALAVGDIECDYMKKRYEEFKELYPYIKFFDKAKIKQIEPK

VVLGEDCNQDRPENICAMGVESGEVFTTVDFGKMSINLIEQAQKQNKNTFVAFNQEIVHIEKKDDIFILK

TSNHQEYHAKSVVVNAGAHSLYLAHKMNLGMDKSCWPVAGSFYLTKQKLLNGKVYMVQNPKLPFAALHGD

PDLLADMNTRFGPTALVIPKLERYHGLKSVPEFFEALKLDKTVLKVTFNMFKDATIRNYIFYNYLFELPF

IDKSLFVKDAKKIVPSLKTSDIYYAKGFGGVRPQVIDKTKGELMLGEASITETPGIIFNMTPSPGATSCL

GNAERDAKLICNYLGMEFNEDKFSSELL

>ABV51966.1 pyruvate kinase [Campylobacter jejuni subsp. jejuni 81116]

MLKKTKIVATVGPASEKEEILRQMIINGVNVFRLNFSHGTHEYHKKNLDTIRRVAKELHTRIGILQDISG

PKIRTGELKEPFELKKGDRLDFYRETILGEKIAQNHYKISINQKSILDMLKIDEYIYLYDGSIRAKVVSI

DNQKIETIIENDGFLNSNKGINFPNTKINIDVITQKDKNDLLWGIKNEVDFLAISFVQNAHDIDEVREIL

AQNNAKISIFAKIEKFDAVENIDEIIKSSDGIMVARGDLGIEVPYYKVPNIQKEIIQKANNASKPVITAT

QMLFSLAKSKTATRAEISDVANAVLDGTDAVMLSEESAVGIDPANAVDIMCQTIIETEKRYPYNKFNDFN

DLDNTDKIMRSSAHLATDLNADAIFSLTSSGKSAIKIARYRPNIEIIAVGHSEKTLNSLSIVWGVNPAIL

VNKSNELTELLKDSVRSSVEKGFMDEDKCYLLTAGFPTGVEGTSNLIRILNKEQIAYYLQ

>ABV51965.1 hypothetical protein C8J\_0366 [Campylobacter jejuni subsp. jejuni 81116]

MQVNTFSNIASMAQTQVSNKKADDAKENTKDKNVQSANSSKDVDKNTLEKLNALGGKGITQIYLVQFQQQ

TMNAVIGSSNAQTGLDSLLNGANLDTAKSILTNIDFASLGYSGKNPLDMNTDELQQLVSEDGFFGVENTA

NRIADFVIKGGGDDVEKLKKGLEGMKKGFEQAEKMWGGELPQISQDTIDAALKKVSDRIDELGGKTLDLQ

A

>ABV51964.1 putative transmembrane protein [Campylobacter jejuni subsp. jejuni 81116]

MAEQEDIILEKPEDGLNQPRLDESLEGFKGQEGQAPEDEEFASLPEELPQENSDSGFKFTRESAPEDVST

FEEVESQEPTPWYKDRKFMSLVGLSLGIICILVFTLFYLTFSEGKIKPDIIASKPLEQPVVMPDESYKYN

DMQRIDGMIQKANALYLKGEVEQALKVYEQVAVYNESLSNYNLGVSQMNENKFQEAFESFKKAIANGENQ

SVAAINAAVCALKLNDKEKFRYYIDLAQVYLPKEGKSKLYDYYLSLINYYKGYYPEALQMLQRTDVEPYS

DVAKYLSAKIYAKMDFDSKAIQQLNSQGNFESSLSLGLLYARIGEYAKAKVALSTAMKIERDFNQSLAAL

TLVDIKTGNYQDMLARLQNSYDNDKDRYKILDAYKIQVRLNKDLFNIAVAQNSFSKDLLKKQKDQFDLLF

YFAPYQVFDSKQAALYIKKANVTDFVDDSADAGVYLNTSKALSSTNVKIANIINYALNQKLRLANQEFQK

LIKDYPEHSILHYNLALTYAQMQNYELAYKHFSSSYHLNPKNYLAGAFAMFCAKLIDIDTTKLYNEILDN

IAADSNFKANMQKSMLFLVNNNYISMLPYLDETKKDTPLSLIFEAIVAKNNNLNNQVDVKIAKLRSELPE

DILANILYFNSLNSNLNIKEYAQNAQIHFKNLKLDYRSVFGGPSIAREFYVNLMHIAGLLNLERQKFKEL

INVSGAKDEGILQTLAYLDIFAQQYEEAYALYNSLIDDYGAKDTKTLFLAAVAAVGANNPNSAIALLQLS

KLTDKNNKESKAALGMLYQEVKNYEAAISQYKTLPNNFKSEFFTFDINNN

>ABV51963.1 seryl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MLDLKNLQNNFDEVAKKLKNKKVDENILKKLAELFASLKKEKTALEEFQAFQNKFSKELATAEDKESLKA

KLSENKSKINEQSVKVNALENELEEIAHAIPNIPDECVPVGEDEDENVELKKVLNPPSFDFTPKEHFELG

ESLNWLDFVRGVKISQSRFCVLKNEGALLSRALVNYMIDFNRSHGFEFVNVPFLVNGATMFGTGQLPKFK

EDMYKVDDEDLYLISTSEIPVTNLYSGEILASETLPIKMTCYSACFRKEAGSAGRDTRGIIRQHQFEKVE

LVSITKPEQSDSVFNEMLECASDLLSSLGLAHRHLMLCTGDLGFSAAKTVDLEVWLPGQNKYREISSVSN

CRDFQARRAKIRYKNEQGKNELVHTLNGSSLAVGRTLVAIMENYQDKEGKIHIPDALKKYF

>ABV51962.1 tryptophanyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MRVLTGLQPSGDLHIGNYFGAIKQMVDAQEKSQMFMFIANYHAMTSSQDGEKLKQNSLKAAAAFLSLGID

PQKSVFWLQSDVKEVMELYWILSQFTPMGLLERAHSYKDKVAKGLSASHGLFSYPVLMAADILLFDTQIV

PVGKDQIQHVEIARDIALKVNNEWGEIFTLPEAKVNEEVAVVVGTDGAKMSKSYQNTIDIFSSEKTLKKQ

ISSIVTDSTALEDPKDHENCNIFKIAKLFLDESGQKELQIRYEKGGEGYGHFKMYLNELVNAYFKEAREK

YNELLEKPSHLKEILDFGATKARKIAQEKMQKIYEKIGL

>ABV51961.1 shikimate kinase [Campylobacter jejuni subsp. jejuni 81116]

MKAKNIVFIGFMGSGKSTLARALAKDLDLVFLDSDFLIEQKFNQKISEIFAQKGEIFFREQEQKMADFFS

SCEKTCIATGGGFVNVSNLEKVGFCIYLKASFEYLKKRLDKDEISKRPLFYDEIKAKKLYNERLSKYELK

ANFILNIENKNIDELLSEIKKVIK

>ABV51960.1 putative GTP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MQSIILIGKPNVGKSSLFNRMARQRIAITSDISGTTRDTNKTQIHIHSKKAMLIDSGGLDESDELFKNVK

KNTLKVAKESDIILYLVDGKLAPDDEDRQFFYSLKKLGKPIALVVNKVDNKKDEERAWEFANFGVKEIFN

LSVTHNVGLDELYEWLEKFLHEEFLIPDEEENLEDFLEHYEEGKEFQFKEVDQNHIRVGIVGRVNVGKSS

LLNALVKQERSVVSSIAGTTIDPVNESVVHKDKVIEFVDTAGIRKRGKIQGLERFALNRTEKILSHSQIA

LLVLDAHEGFNELDERIAGLVAKHYLGVIIVLNKWDKSEMDFDKTVKELHLDRFKFLAYAPVISVSALSG

KRVHVLLDKILQIFENFTQKIQTSKLNTLIENATRSHPLPHDYGKLVKIYYAVQYDLAPPKIALIMNRPK

ALHFSYKRYLQNQIRKEFNFEGVPLVIASRKKGSKENDES

>ABV51959.1 integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MLKVIKHNLGIYFMILACLDFALMGACAKILSKEMSSIEIMFFRNIIGIFFIVYLLKRSKAHKEGGHFWL

LVFRGVVGTLSLYMFFYNVSNITLGGAFAFQKTAPIFITLIAFVVFKENIGIKGWIGILIAFGGVLLIAQ

PWAHNLNHSGFDLKNSVIGITSGFLAALALTSVRELRKSYTTEQIAFSFILLGTLMPLISMISAEFFEPQ

HLDSLHLDFILAPFVMPSLTAWLIIAIMGTLGTIYQIHVTKAYGIAKQAGVVAGVSYLDVVFSMIVGIIL

GDNLPSTMVFLGIIGIIFGGLILVKNKGKK

>ABV51958.1 2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase) [Campylobacter jejuni subsp. jejuni 81116]

MKKMILIAGPCVIESKDLIFKVAEQLKNFNENPNIEFYFKSSFDKANRTSINSFRGPGLEEGLKILQSVK

DEFGMKILTDIHESNQAAAVSEVADVLQIPAFLCRQTDLLVAAAKTKAKVNIKKGQFLNPSDIKYSVKKV

LQTRGIEDEGYEAAQKNGVFVAERGASFGYGNLVVDMRSLVIMREFAPVIFDATHSVQMPGAAGGSSGGK

SEFVEPLARAAAAVGIDGFFFETHINPCEALCDGPNMLNLTRLKNCVNTLLEIQNIIKENK

>ABV51957.1 riboflavin synthase beta chain [Campylobacter jejuni subsp. jejuni 81116]

MNIIEGKLNLDSNTKIAIINARFNHIITDRLVEGAKDAFLRHGGKEENLSLILVPGAFELPYALKKAIES

KKFDAICCVGAVIRGSTPHFDYVSAETTKGIANVSLNHNIPVSFGVLTTDTIEQAIERAGSKAGNKGFEA

MTTVIEMLNLSKEL

>ABV51956.1 transcription termination protein [Campylobacter jejuni subsp. jejuni 81116]

MATRHQVRQSVISLLYAFELNSQNNVFVDEILDEKKIRNEQKNFTLNLYHGILDNLNNIDETLNSFLNDN

QITALGHVERAILRLGAYELLFTDTPSAIVINEAIELAKELANDNSPKFINGVLDALIKAKK

>ABV51955.1 hypothetical protein C8J\_0356 [Campylobacter jejuni subsp. jejuni 81116]

MKLCVALDLSTKEECLQLAKELKNLDIWLKVGLRAYLRDGFKFIEELKKVDDFKIFLDLKIHDIPNTMAD

ACEEISKLGVDMINIHASAGKIAMQEVMTRLSKFSKRPLVLAVSALTSFDEENFFSIYRQKIEEAVINFS

KISYENGLDGMVCSVFESKIIKEHTQRNFLTLTPGIRPFGEKNDDQKRVANLTMARENLSDFIVVGRPIY

KDNNPRKICEKILQEI

>ABV51954.1 hypothetical protein C8J\_0355 [Campylobacter jejuni subsp. jejuni 81116]

MIITPENLYKKRRDFLKLGAGALISSSVLASKLSALNFTSDTNPNKLEISDEELATNYVNFYEFSTDKKK

AVSLAQNFNTQNWKIDISGEIEKPLTLSMEDILKFPLEERIYRFRCVETWSMVVPWVGFELRRLIEMAKP

TSEAKFVKFTTLLDKSQFPDQDALFPTIDYPYVEGLRMDEAMHPLTLLAVGMYKKALKPQNGAPIRLVVP

WKYGFKSIKSIVKIEFTKEQPKSTWESYAPSEYGFYANVNPNVSHPRWSQANERALGDFFTKPTLMFNGY

EKEVASLYKNMDLKVNF

>ABV51953.1 hypothetical protein C8J\_0354 [Campylobacter jejuni subsp. jejuni 81116]

MQTKYFKFLAYFSFIISLIYGFYHIIKAFDFVKEAYIYTGVFALIFLNLSLLFSLLKFKKTKNYPKILGI

FAAFWAILHFLNYFIFDRNAQILRLFDDISHRLLEASGFIAFLIIFLMLLSSFKIFKKLSKIRKLGYLCL

VLASYHYFLTPKIPMFWEWSALIIALFYFIVRYTKNIKKVKIQQSYFYQNLNLILFVCFL

>ABV51952.1 probable AAA family ATPase [Campylobacter jejuni subsp. jejuni 81116]

MEKLKNFLILKNIEDTQIYKELKCAKNEALILRELCRNYVVSISSINAFTLLSTIFGNDKYLYLDALEDL

KKLIERGFVNQNSSFFKSLENNKTQTLTLALLQSELSLSEYFLEFLEAKPRLNFEKQEAYADYLEYLKDE

FARIQLYERLSFIQKSAYNSEIKNQIKLYEKHIKERLKKSKFYNVLADIFKEYNLEHKEQIIFLALLKEE

YALSNESSISREMNSLLSLISENDLERHKNKKLLQENAPLLNLIEYDEYLNAFGDISKSFFIIDEILQRI

INFEPKQSKKIKIESVLKDQDIFELIEPSTDINDIIMPENTKELLENILKQQDKKVLERLHSWGIKSNKN

IEAKIIFYGPAGTGKTMSALAMAKSMKKSVLSFDCSKILSKWVGESEQNVRKIFDTYKNIVQTCKQSPIL

LLNEADQFLSTRVDGSSGSDKMHNQMQNIFLEQIERFSGVIIATTNFLESLDSAFSRRFDYKIEFQKPDF

KDRLKIWEKFLPKKALFEKDFDINILSNYELSGAQILMVVKNTALKVAVSKDGVFKMQDFIESIQKELNS

SFDKSKIVGF

>ABV51951.1 hypothetical protein C8J\_0352 [Campylobacter jejuni subsp. jejuni 81116]

MKFFLLVFCFVNLALAQVYKGELYFYHLQDKEIFAIVYDNAPMTPLFDRDKNQTSSSFLIIDDINGNLEI

PLVKTNDFWQDERKKYKINSSKMLTYDNKNFQGENLGTTTLELVETQDGIRIKRSLDFIGFNDDFKEFHP

VHKSVFSFEQIRQKPIFLQDGKISFEEWYYFYEDGMSRAILELNNFVYDINAHAFVKLNDLYNTKNQKFQ

NLLHEKLKNTCDECFEDLQNLQFNNNFLLNNGKLKICYLPFEGHFLDENICVEFNEDELKEFKK

>ABV51950.1 hypothetical protein C8J\_0351 [Campylobacter jejuni subsp. jejuni 81116]

MVLIASPMIKINDAAFLKKENNALNLEVYKLGQAFFELKIKDKICINAVCYDKKVFNQKFFKNVYYDDIL

NDILKANALWQGKNLEKTDCGFEQNLKAKNYEIFYQVCDNKVSFFDKISHTKIILTHIQN

>ABV51949.1 hypothetical protein C8J\_0350 [Campylobacter jejuni subsp. jejuni 81116]

MASEHSFDISAALDKQELKNAFEQAKKELDSRYDLKGIKCEIDLSEKESIFKLSSSSEGKLDVLKDIVIS

KLIKRGINPNAIKELSRESGAMFRLNLKANDAIDSENAKKINKAIKDSKLKVNSSIRGEEIRVAAKQIDD

LQAVMKLVKELDLELNISFKNLK

>ABV51948.1 putative D-2-hydroxyacid dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MKIVCLDAATLGDYDLSVFEKFGSLQIYTTTNKEQTIERLKDANVAMTNKVVIDKDVIDACKNLKLILET

ATGVNNIDIEYAKEKGIIVKNAAGYSTMSVVQHTFAFMFAFLNQVLYYDKWSKEGKWCESPIFTDYSRIL

NTLSGKKHGIIGLGAIGKEVAKISKAFGAEIYYYSTSGANKNVDFIHLELKDLLKTCDIISIHAPLNEKT

KNLLTFEELKLLKDNAILINVGRGGIINENDLAKIIDEKNIRVGLDVLEIEPMMKNHPLLSIKNKENLII

TPHVAWASKEALNALMDIVYNNLKEWIENGK

>ABV51947.1 hypothetical protein C8J\_0348 [Campylobacter jejuni subsp. jejuni 81116]

MQLLQVDKLQKDYLENIGFSWHTDEDGSDYISNKLVCVKESEANAYYEAVNELYDMFIAAAQEVIDNDRF

DELGIPFNLIDAIKMSWENEVHWHLYGRFDLAGGLDGKPIKLIEFNADTPTALFESAILQWALLKQNGMD

ESAQFNSIYESLMDNFKRLITLDESVEGFEEHYQGWKILFSSVAGSKEEEITTKLLSHIANEAGFQTNFS

FVDEVEFSEEGIFKEGENYEYWFKLIPWEDIAIEEGELAMLLTQIMRNQRAIILNPAYTLLFQSKGILKI

LWELYPNHPLLLETKDTPLEGKNYVKKPVFGREGANISIIKDGKTLHENVGPYGNNKAIYQEYVEFNSCE

NEYYQAGVFFAYEGCGLGFRKGGLVLDNYSKFVGHIIKD

>ABV51946.1 hypothetical protein C8J\_0347 [Campylobacter jejuni subsp. jejuni 81116]

MKKIKKIIQIGMIGGLAAVAGGALAGCGSNNDNADTLNQAANAQGAFVIIEETAPGQYKIKDQYPSDETR

VVLKDLNGTERILSKEEMDALIKEEAAKIDNGTSNLTKDNGQISSGGLSLGETLLASAAGAILGSWIGSK

LFNNQNFANQQRGAFSNQSAYQRSVNSFNKAGTTSSASSAKKSGFFGGGSKATSSSSSFGS

>ABV51945.1 30S ribosomal protein S21 [Campylobacter jejuni subsp. jejuni 81116]

MPGIKVHPNESFDEAYRKFKKQVDRNLVVTEVRARRFFEPMTEIRKKQKISARKKMLKRLYMLRRYESRL

>ABV51944.1 hypothetical protein C8J\_0345 [Campylobacter jejuni subsp. jejuni 81116]

MQGHITNYTKKRYFVYLIASIIIFALPFIRINENHFFLLSFDHSKLNLFFISFLTQEFYLMPFVLIFLFL

FIFFITTLGGRIWCAWSCPQTIFRVIYRDIIQTKFLKIRKNINNKQKEYEGQYFKKFLGVIIFYFISLVA

VSNLLWYFIPPEDFFNYIQNPGEHLLLLGILFCASLLFTLDITYLQEKFCVYICPYARIQSVMFDHDTMQ

VIYDEKRGGLIYDGHTKLHKKPPEGECIGCEACVSICPTHIDIRKGMQLECINCLECADACSKVQSKFNR

PSLINWTSAKAIETRSKVHYLRFRTIAYFIVLLIALLALIIMGSKKESMLLNINRSSELYNISNVKGELV

ISNAYTFLFQNTDSKPHEYYFTANLEGINDGIEIIRPNKPFKLKAGEQVKKIVVIRATKNLANNDKKDVI

FPLHIKAYAKDNEKISVFRKSIFVYPKSTLIKDKNELK

>ABV51943.1 transcriptional regulatory protein [Campylobacter jejuni subsp. jejuni 81116]

MNSNRTPSQKVLARQEKIKAVALELFLTKGYQETSLSDIIKLSGGSYSNIYDGFKSKEGLFFEILDDICK

KHFHLIYSKTQEIKNGTLKEILTSFGLAFIEIFNQPEAVAFGKIIYSQVYDKDRHLANWIENNQQNFSYN

ILMGFFKQQNNSYMKKNAEKLAVLFCTMLKEPYHHLNVLINAPLKNKKEQKEHVEFVVNVFLNGINSSKA

>ABV51942.1 RND efflux system, membrane fusion protein CmeA [Campylobacter jejuni subsp. jejuni 81116]

MKLFQKNTILALGVVLLLTACSKEEAPKIQMPPQPVTTMSAKSEDLPLSFTYPAKLVSDYDVIIKPQVSG

VIENKLFKAGDKVKKGQTLFIIEQDKFKASVDSAYGQALMAKATFENASKDFNRSKALFSKSAISQKEYD

SSLATFNNSKASLASARAQLANARIDLDHTEIKAPFDGTIGDALVNIGDYVSASTTELVRVTNLNPIYAD

FFISDTDKLNLVRNTQSGKWDLDSIHANLNLNGETVQGKLYFIDSVIDANSGTVKAKAIFDNNNSTLLPG

AFATITSEGFIQKNGFKVPQIAVKQNQNDVYVLLFKNGKVEKSSVHISYQNNEYAIIDKGLQNGDKIILD

NFKKIQVGSEVKEIGAQ

>ABV51941.1 RND efflux system, inner membrane transporter CmeB [Campylobacter jejuni subsp. jejuni 81116]

MFSKFFIERPVFASVVAIIISLAGAIGLTNLPIEQYPSLTPPTVKVSATYTGADAQTIASTVASPIEDAI

NGADNMIYMDSTSSSSGTMSLTVYFDIGTDPDQATIDVNNRISAATAKMPDAVKKLGVTVRKTSSTTLAA

ISMYSSDGSMNAVDVYNYITLNVLDELKRVPGVGDANAIGNRNYSLRIWLKPDLLNKFGITATDVISAVN

DQNAQYATGKIGEEPVTQKSPYVYSITMQGRLQNPSEFENIILRTNNDGSFLRLKDVADVEIGSQQYSSQ

GRLNGNDAVPIMINLQSGANALHTAELVQAKMQELSKNFPKGLTYKIPYDTTKFVIESIKEVVKTFVEAL

ILVIIVMYMFLKNFRATLIPMIAVPVSLLGTFAGLYVLGFSINLLTLFALILAIGIVVDDAIIVVENIDR

ILHENEQISVKDAAIQAMQEVSSPVISIVLVLCAVFVPVSFISGFVGEIQRQFALTLAISVTISGFVALT

LTPSLCALFLRRNEGEPFKFVKKFNDFFDWSTSVFSAGVAYILKRTIRFVLIFCIMLGAIFYLYKAVPNS

LVPEEDQGLMISIINLPSASALHRTISEVDHISQEVLKTNGVKDAMAMIGFDLFTSSLKENAAAMFIGLQ

DWKDRNVSADQIIAELNKKFAFDRNASSVFIGLPPIPGLSITGGFEMYVQNKSGKSYDEIQKDVNKLVAA

ANQRKELSRVRTTLDTTFPQYKLIIDRDKLKHYNLNMQDVFNTMNATIGTYYVNDFSMLGKNFQVNIRAK

GDFRNTQDALKNIFVRSNDGKMIPLDSFLTLQRSSGPDDVKRFNLFPAAQVQGQPAPGYTSGQAIEAIAQ

VAKETLGDDYSIAWSGSAYQEVSSKGTASYAFALGMIFVFLILAAQYERWLIPLAVVTAVPFAVFGSFLL

VYLRGFSNDIYFQTGLLLLIGLSAKNAILIVEFAMEERFKKGKGVFEAAVAAAKLRFRPIIMTSLAFTFG

VLPMIFATGAGSASRHSLGTGLIGGMIAASTLAIFFVPLFFYLLENFNEWLDKKRGKVHE

>ABV51940.1 RND efflux system, outer membrane lipoprotein CmeC [Campylobacter jejuni subsp. jejuni 81116]

MNKIISISAIASFTLLISACSLSPNLNIPEANYSIDNKLGALSWEKENNSSITKNWWKDFDDENLNKVVD

LALKNNNDLKLAFIHMEQAAAQLGIDFSSLLPKFDGSASGSRAKTAINAPSNRTGEVSYGNDFKMGLNLS

YEIDLWGKYRDTYRASKSSFKASEYDYEAARLSVISNTVQTYFNLVNAYENENALKEAYESAKEIYRIND

EKFQVGAVGEYELAQARANLESMALQYNEAKLNKENYLKALKILTSNDLNDILYKNQSYQVFNLKEFDIP

TGISSTILLQRPDIGSSLEKLTQQNYLVGVARTAFLPSLSLTGLLGFESGDLDTLVKGGSKTWNIGGNFT

LPIFHWGEIYQNVNLAKLNKDEAFVNYQNTLITAFGEIRYALVARKTIRLQYDNAQASEQSYKRIYEIAK

ERYDIGEMSLQDYLEARQNWLNAAVAFNNTKYSYANSIVDVIKAFGGGFEQSEDTSKNIKEESKNLDMSF

RE

>ABV51939.1 hypothetical protein C8J\_0340 [Campylobacter jejuni subsp. jejuni 81116]

MDKAKIVQNLNALFKQRAEFYSYFDENIAKINNTEVFDFKNAKNLNPEEVYKQFYHFDYAIRKLLPAIYK

AYEITDADLDKDF

>ABV51938.1 coproporphyrinogen III oxidase [Campylobacter jejuni subsp. jejuni 81116]

MNLFQNLALKYSHTMMEKSLQKGFNVELLKQPKEKIPKQDKSYMLYAHVPFCHTFCPYCSFHKYYYDENL

AKVYFQNLREEIKIMKDKGFDFSSMYVGGGTTLINEEELLKTLELCKKLFNIKEISCESDPNHIDPNKLS

MFKGIIDRLSCGIQSFDDETLKKVARYNKFGSSKELQEKISKALGILPIFSIDLIFNLPGQSEKQLLNDL

EIAKNLAPQQITTYPLMKSNLTKDNIAKSLGVSIKDNEFTYYQIIREFFKDYTQNNGWSFSLEKNKLNDE

YVSSHHEYLGVGSGAFSFLDGELLINAFNLNDYAKFIQEKQNANIAKACFDKKEIIKYIFLTEIFSGKIE

IDKFNKTLNCNLEKELFIELLGLKTSGAIIKDQNALIATEFGQYLFVVLMKDFYTGMDLVRAVFRDDKRL

KNKDYIDIMKENIDPLNSASMEFKAETN

>ABV51937.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MTEWINDYYFWIKWVHYLAFVSWMAGLFYLPRLFVYHAEHKDNKGFVEIVKIQERKLYFYIQTPAMIVTL

ITGSLMLHAHKEVLMVGAGFMHVKLTCVTLLIIFHIHNYYCLKALANDTSAKSGKYFRIYNEFPTIMFII

IALMMVIRPF

>ABV51936.1 lipoprotein signal peptidase [Campylobacter jejuni subsp. jejuni 81116]

MAKTFKFIFYFWGAFVLVFVLDQWVKSLTLAGLRWQSEYLDLTYALNTGVAFSMLSFLEHNLKYLHLALI

VVLFIYLFWQKTLLKTHSIAFGMMLGAGVSNLLDRFIHGGVVDMFFWHKWFNFAIFNVADVMINISVALI

LIQEIFKKRKKDDRMD

>ABV51935.1 putative phospho-sugar mutase [Campylobacter jejuni subsp. jejuni 81116]

MKLFGTDGVRGKAGEFLDSFLAMRLAMAAGIYFKDKSITNNILVGKDTRRSGYMIENAIVSGLTSIGYNV

IQIGPMPTPAIAFLTEDMRCDAGIMISASHNPYYDNGIKFFDAHGNKLSEDIEKKIEEIYFDDKLIQASK

VDMEKIGQAKRIDDVIGRYIVSIKNSFPKDLTLKSLRVVLDVAHGAAYKVAPTVFKELGAEVIVMSDKPN

GLNINENCGALHPANLAAEVKRLRADVGFAFDGDADRLVVVDEKGEVANGDSLLGVLALYLKEQGKLQSS

VVATIMSNGALKEFLNKHGIELDTCNVGDKYVLEKLKVNGGNFGGEQSGHIIFSDYAKTGDGLIAALQFS

ALMLSKKKSASSILGQVKPYPQLLTNLKIAEKKDLDKIKGLKELKKDLENKNINTLFRYSGTENLIRLLL

EAKDIKLLEKEMKNVVEFFKKALNG

>ABV51934.1 putative cytochrome C551 peroxidase [Campylobacter jejuni subsp. jejuni 81116]

MKVKSLLIASLVAFSSLNAASLIDEAKNSGLVALPKDQKGVDEILKQNGVKASEFTLEKVELGKKLYFEP

RLSKSGIISCNTCHNVGLGGTDGISTAIGHKWTANPHHLNSPTVYNAVLNNTQFWDGRAGTLADQAKGPI

QADPEMATPAKLAVEKISSLPEYVSEFKKIYGKSGVNFDNIADAIANFERTLITPSRFDKFLEGDEKALT

KEEQKGLKLFIDKGCVACHNGVNLGGNMQAFEVAGKYKFANLGDFKGDANGMVKTPTLRNVAETAPYFHN

GAIWNLKDAIKEMGSVQLGIKISDKEAKSIETFLKSLTGTKPAIVYPQLPISTEKTPKPEL

>ABV51933.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MENLIIYAFIYLLGSIPFGLILAKFFAKTDIKKEGSKSIGATNVLRVVKEKNPKLAKKLAIATIILDFAK

AAIPLLILKFLHYDQALLWSVAVLAIFGHCFSIYLLFEGGKGIATGAGAMIVLLPLEVLTAFIVWVVIGK

IFKISSLASLAALLAFVISSFIFNYDLEIHTHAPVFIIAFIIVYKHLPNIKRLIFKEECKVI

>ABV51932.1 FolB domain protein [Campylobacter jejuni subsp. jejuni 81116]

MQSHIKIKFHFKCIIGILDFERRKKQKIIIKLKAKANEFLNYAEVITKIKTWYKKEEFYTLEESLDFVSL

NLKKDFPNLTNLNIKIFKPHIIKNATVGVKLKKKY

>ABV51931.1 two-component regulator [Campylobacter jejuni subsp. jejuni 81116]

MRILVIEDEISLNKTIIDNLNEFGYQTDSSENFKDGEYFIGIRHYDLVLANWTLPDGDGAELVNTIKHKS

PRTSVMIMSSKTDKETEIKALKAGADDFVKKPLDFDILLARIEARLRLGGTNVIKIEDLVIDPDEEKITY

KGQDIELKGKPFEVLTHLARHSDQIVSKEQLLDAIWEEPELVTPNVIEVAINQIRQKMDKPLNISTIETV

RRRGYRFCFPKKS

>ABV51930.1 putative ferredoxin [Campylobacter jejuni subsp. jejuni 81116]

MSLLITKDCVCCDACREECPDEAIYENSPIYVIDPDLCSECVNDFSEPACIVACPYECIIPDPDNVETIE

ELKLKHRDREF

>ABV51929.1 phosphatase, Ppx/GppA family [Campylobacter jejuni subsp. jejuni 81116]

MAKKTAVVDLGSNSIRMVIFEKTSRYGFYTTCEYKRKVRLGENAYNNGKILQEEAMQRAEDALAFFKQCA

LKHKCKKIFIVGTSALRDAPNSKNFIKRIKDNLSLNIRCIDGKSESYLGGLAALNLLSPFKDGTTLDIGG

GSSELCLIKNNRIISCISLDIGTVRLKELFYDTGKMDSLEEFIKPILEQIPKEFCNQNLIAIGGSLRAIS

NSIMQKNSYPLKNLHDFRYMLDEEKGHILKIFNSNLDSLINFGIKKDRFDTIKEGIFIFLKIAEKIKAKQ

VITSGVGIREGVYLQDLLRPKITFPPNFNPSLKCLQDKFLQSKQKNKTPHFALQIFTTLKNLHKLNDNYK

HTLLNAAKLCHIGEYLNFYFANEHSAHFVLGGLNYGFSHKEKALIASIIKLNGKKVNPYNLEPYKQLLPN

IHTISWLNFILCLAKTLSTNEDKIDFAFANNTLYIYQENKILNLPKDELKKIAKPATIALAINQKI

>ABV51928.1 putative transmembrane protein [Campylobacter jejuni subsp. jejuni 81116]

MRLLVLFFLILPLYSVELISFNIYDRNDRVDLMLSFDNAYNGKISQKKEKNLTLLTFSDLTYSKDELKEL

NSQLVDKISISSKNNNTYIMLQNKQNINLELSSIIDKFGVRIRAIEQGKANIESVPTTTANNSQELMPKP

KSTSLEGYDYTNYILVMLILVILLIVLWWFKKTMVYKNNNVSRDFTMIFQRFLDKNNQLVVFDHANKRYT

MIIGNSNVLLESVEIPEEQIIKHTEKTEKNFDSFFEENKKRIQNLIEQRQKGKKS

>ABV51927.1 flagellar motor switch protein [Campylobacter jejuni subsp. jejuni 81116]

MSDDIEFNIHHGLLQSYEDILDITVDFVSELGTTNMSVAELLKLEVGSVIDLEKPAGESVELYINKRIFG

KGEVMVYEKNLAIRINEILDSKTVLQYFKKEI

>ABV51926.1 hypothetical protein C8J\_0327 [Campylobacter jejuni subsp. jejuni 81116]

MLKILEYSITHFCEHILRLRIEAAQDISGELYGASIPIMGKSEGECNFYLFFPKEFLKKIAEILINDEKF

KEDDWCDLTKECANQIIGYAKNLLNDAKGDDEYKLGIPEYLGKVDFSEIVLDEALTYKFENCYFRIGYCK

>ABV51925.1 tryptophan synthase alpha chain [Campylobacter jejuni subsp. jejuni 81116]

MVDFRKFYKENANVAYTVLGYPNLQTSEAFLQRLDQSPIDILELGVAYSDPIADGEIIADAAKIALDQGV

DIHSVFELLARIKTKKALVFMVYYNLIFSYGLEKFVKKAKSLGICALIVPELSFEESDDLIKECERYNIA

LITLVSVTTPKERVKKLVKHAKGFIYLLASIGITGTKSVEEAILQDKVKEIRSFTNLPIFVGFGIQNNQD

VKRMRKVADGVIVGTSIVKCFKQGNLDIIMKDIEEIFKK

>ABV51924.1 tryptophan synthase beta chain [Campylobacter jejuni subsp. jejuni 81116]

MKKAYYGDFGGQFLPESAMFALNELEGAFLKFSKDKLFKKELNELLKTYVGRPTPLYFARNLSKKYQHEI

YLKREDLNHTGAHKINNAIAQALLAKKMGKKKIIAETGAGQHGLATATAAALLGLECEIYMGATDVQRQA

LNVYKMELLGAKIHAVQSGLKTLKEATTAAIQAWVGDIKNIFYVVGSAVGPYPYPKMVMHFQSIIGKECK

MQLQKLNKKVDYIIAAVGGGSNAAGIFYDFIKDENVKLIGIEAGGLGIDTPYHAATLNKGKTGIIHGMKT

KVLQDDLGNILPVHSVSAGLDYPGIGPLHAFLFESKRAQYHAISDEECMQALKLLCKEEGIIAAIESSHA

LAFLEKLCPTLKKKSVIVVNLSGRGDKDMQMIRDYKKGVIYG

>ABV51923.1 N-(5'-phosphoribosyl)anthranilate isomerase [Campylobacter jejuni subsp. jejuni 81116]

MLKLKICGIKDEKNAKDLAFLNIDFFGFIFAKSPRRVSLEQARNLSAIFHEKDKKVVGVFVDENLEQILR

CIKEAKLDGIQIYRTITKEEFEILKVQNVFVWQVISVENSLDLKSEIFANLVLFDAKGILKGGNGISFDW

TLLGSYTKDFILAGGIGLDNVHKAVQTGAKILDLNSKLEDEKGLKDINKIKQILKELKK

>ABV51922.1 anthranilate synthase component II [Campylobacter jejuni subsp. jejuni 81116]

MILLIDNYDSFVFNVKSMLEQLSNDEILVRRNDEISLSEIKNLNPTHIILSPGPKHPSQSGICLEIFKAR

LNIPVLGICLGHQALALAFDSLVVKMQEPMHAKNSLIKQCRENELFSNLPLNFSVMRYHSLEVKQLSDEL

EILALDEKGVIMALGHKNLPYYGVQFHPESYFSEYGLQLFSNFLKQDIKKSQKQENPLSFYLQKMSENHF

LQSDDFEQICKIIMSKDYEILQVAALLILITEKSLNEKSLSAFVRQILRYSQTFSDESEMIDICGTGGDG

FKSINVSTTSAFILAALGVKVAKHGNRAISSSSGSTDVLEALSITTPNTLESVLKQLNNQGLSFLHAPFF

HPLVGELKEIRSRLGVRTVFNVLGPLLHPNLKLKYQLMGNYHAPVHRLLIEVLKNLGRKKALVVRGNDGM

DELSICDESKIYELCEGEILEYSICPEQFGFKRAFHSEIIGSSAYDNAKDLKDILSGRMQGAKFDLVVLN

AMFALYTANKASSPLVAKDMILEAIYSGKVIEYFKEYQAYAKA

>ABV51921.1 anthranilate synthase component I [Campylobacter jejuni subsp. jejuni 81116]

MFVKNVNFYYRQILEKFENSYFAEDLTKVIIGIDCDYLDANELSFSEFKAKYYEALSKNKICDFAGFFGV

FSANFVSLFEKIPLSSKKNYDFPLFLFANAKAYLIYEKNSKMFFKFGASKYFEYLKDDIEPIKTKQKNDF

EILNSLEDEKNDFLKMCEKAKEYLLSGDIFQVVLSKQLCIKHQVNAFDYYESLSTLNPSAYMFYFPSKYG

VVLGSSPEFLLKIKKREIYLAPIAGTRNLENNCDLLALEKDLLSDEKELSEHKMLVDLARNDASKFGTQT

RVENLFSIIKNKFVMHIVSEVYANMKEDASIFDVIEAVFPAGTLSGAPKIRALEIISELEDCDRGVYGGA

VGFLNFNEDITLAILIRCAFFTQDKAYLASGAGIVLQSESQKEYAEICAKRRALLVAFENLKKENQ

>ABV51920.1 hypothetical protein C8J\_0321 [Campylobacter jejuni subsp. jejuni 81116]

MVTLSIVKMFQNIIKYKDFIISILNLKQNLYLLIKINLDFKNFHKSLNF

>ABV51919.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MEITDLPYLIIGIISGIASGLFGIGGGMIIVPSMFALGASAHHAIGISVLQMIFAAVFGSYINYKKKNLN

LKDGIMIGFGGLIGASFSGMLLKALSDVALTSVFLAVSCIFFIKYAFGIKENIVQNQRSVWVKNVILFIA

GAFTGIFAISLGIGGGLLIAPILAYFLGYDSKKVVSLSLFFVIFASVSGIISFSNSGVIDSEVIHKGILV

GIASMVGVFIGIKIIEKMHISAHRKILLCVYALSILGTTHSLLNKLNLINF

>ABV51918.1 excinuclease ABC subunit A [Campylobacter jejuni subsp. jejuni 81116]

MNDTIKIIGARENNLKNIHLEIPKNKLIVFTGLSGSGKSTLAFGTLYAEGQRRYIESLSAYARQFLDKVG

KPDVDKIEGLTPAIAIDQKTTSKNPRSTVGTITEIYDYLRLLYARVGIQHCHQCGQKISSMSASDIVSEI

LKFPKGAKIIIYAPLIREKKGTYADLLENLRNKGYVRAQIDGVLVRLDEEIELAKTKKHTIKLVIDRLEI

QEDLLSRLASDIEKGLQESFGEIEIEVLNHEEINLNKHYHFSEHCACFDCKISFVPLEPLSFSFNSPKGA

CEACDGLGIRYTLDMKKIIDENLSLENGAVKIMYGFNKSYYYKFLIAFCEQNEIPIKIPFMQLNEEQKRL

VLYGNAKTIEFLWKRNRLKRTFEGVVKMAYEMLKDEKDLAEYMSEKICKDCGGHRLKPESLAVKVAKKGL

GEILDMSIEDSTAFFADEKNFSYLSEQQKLISKPILKEINERLFFLYDVGLGYLSLGRDARTISGGEAQR

IRIASQIGSGLSGVMYVLDEPSIGLHERDTAKLIKTLRNLQQKGNTLIVVEHDKMTIEEADFIVDIGPKA

GKFGGEVVFSGTYKELLKSKSETALYMNGKKQISQLQNRAQKEWLELKNVNINNIQDLSVKFPLQNLVAI

TGVSGSGKSSLILQTLLPFAQEELNRAKKVKKLGGVQIEGLEKLDKVIYLDQSPIGRTPRSNPATYTGAM

DEIRNLFAATKEAKMRGYKAGRFSFNVKGGRCEKCSGDGEIKIEMHFLPDVMVVCDTCQGKRYNDATLEI

KYKGKNISEILNMSVLEASEFFTAVPKIKQKLDTLVKVGLDYLTLGQNATTLSGGEAQRIKLAKELSRSD

TGKTLYILDEPTTGLHFEDVNKLILVLQHLVDLKNSVFVIEHNLDVIKNADYIIDMGPEGGVKGGKVIST

GSVEKVAKEHKKTRSYTGYYLDLELKNTQKS

>ABV51917.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MFDFLYNDISYLGLFIVCFLSSTLLPLASEAFVLGFIKLDFNPNLVLIVATLGNTLGSLSTYGLAYLGKQ

KILEKYFSKSLKKLENFNANFAKFGSIFAFFTFLPLVGDLFALGLGFAKYSFLKTIFFILLGKLSRYAFI

IFIANSF

>ABV51916.1 inosine-uridine preferring nucleoside hydrolase family protein [Campylobacter jejuni subsp. jejuni 81116]

MRLILDTDIGNAIAGANTDDGLALALILASKEIKLEMLSTVCGNVPSLVAYSVAKDLFKRLNLNIPVYLG

ANEALKEPSKAWRQRLDESVKNFKLEYLWENIKSPEILENINPDAIFKMGELVSKNPKEISICAIGPLTN

IAMTMKIFKDFDINLKELFIMGGSFDMPYYTKDTNFGFDPEAASIVLNSRAKITLVPYNATMQTLLTHED

LKELQGKNILCDFIVETLGVWIDYASKTRGTKGTWIHDALTIAYALDSSIADFDECYADVICDSSLARGM

SWRCFKEPKMSMGVDLSTKNCVKILKNVDNTKLLKLIKERLLKGVCYENYESITT

>ABV51915.1 major facilitator family transporter [Campylobacter jejuni subsp. jejuni 81116]

MTNQQIDGIADKNFNTPEGRKVFKKAVFSCWLGTAMEYADFALYGLAAATIFSEVFFPEQTPVIALLLSF

VTYGIGFIARPIGALFFGYLGDKHGRKNVMMSTVALMGISTTLIGFIPSYAVIGVWAPICLVILRFMQGF

GAGAELSGGTVMLGEYAPSKRRGLVSSVIALGSNSGTLLASFVWLLMVQMDEASFKEWGWRVPFMGSILI

ALFAVYIRFHVKETPVFEKQKNEMMKLRLNNEKHMKKDERSFWQRSRAFWTMVGLRIGENGPSYLAQGFI

VGYVTKILLLDKSVATTAVMIASLVGFLVIPLAGYLSDRFGRRITYRMFCLLLMIYAFPAFMLLDSKNEI

IVILTIIVGMSLASLGIFGVQAAWGVELFGVKNRYTKMAFAKELGSILSGGTAPMVASALLAYYGTWWPI

ATYFVLTAGIGFVTTFFAPETRGRDLNKIEDAI

>ABV51914.1 DNA polymerase type I [Campylobacter jejuni subsp. jejuni 81116]

MKTLTIIDTFGFFFRLYYALKGFKNSQGQASGMISGFANFIYSLKNEHKSDYIVFALDSKGKTFRSEIDP

NYKQNRTPPPPELLEQIPICIEMIEKMGFISVSQEGYEADDIIASFVRTCEDRDIFVRIITQDKDLYQLI

KDGKTSIYSPISKNDYDEAACLEKYGVKPHQIRDFLALCGDSSDNIPGVKGIGAKGAKTLLDEFGSIEGI

YENLTLVRNERSRNLLLEGKENAFLSKKLASLYENLEVQDLIEKATYPDEEPLLKILEILEHYELNTLLK

KLRQNPDNKDKNLGFKATLIQDENKLFEILNTLDKESIIAFDTETTGLDTKEAKIVGFSFCMSENEAFYV

PLTHNYLGVGEQISLQSAKKAIEVIFNHFVIGHNLKYDFKIIQNNFGLNLPQKYADTMILAWLKNPSLRV

NMDDLALRLFNYETLHFESLVKKGENFASVELEKACKYAAEDAYITLRFYLYFLKNLETPLLELAKNCEF

DFIKIIMMMEENGIKLDTNALEILMKKFENEIKNLSEEIYTLCEDRFNLNSPKQVGDILFEKLKLPSGKK

GKTGYSTDEKVLNALLDKHPVIAKILDYRELAKLYSTYCEPLLKLALKDKNSRIYSSFLQTGTATGRLSS

KDPNLQNIPAHGQYAKDYKSCFVAKDGFSFISLDYSQIELRMLAHFSEDEKLLNAFANDEDIHARTAIMI

FGESNYETRSVAKSINFGLIYGMGYKTLSQNLKIEAHLAKSYIEKYFENFTSIKKYFETVKNKAKQNGFI

TTLSGRKRYFDFENAKPMQIAMYERESINSILQGSAADVIKLAMLEINKELNEDKKLILQIHDELIFEVK

DDLCENFVKKTRDIMENIVKLKVKLKTSSSIAKNWGDLK

>ABV51913.1 putative flagellar motor proton channel [Campylobacter jejuni subsp. jejuni 81116]

MDLSTILGMVLAVTSISVGDILEGGNPLHVVHLSSFLIVMPTAAFCAMTSTHKKIVKAAYKELKVVFKGS

GVNLPERIAQLIEFAIIARRDGLLALESRTNEIENEFLKNAMMMLVDGKSFEEIHESMEIQTEQLEEHYK

ECAEYWIVFGETCPTMGLVGAVFGLILALKLLDNPQAMAAGISGAFTATVTGIFGAYALFAPWGRKMKAN

GMDLVKEQIVITEAIKGIAEGANPRDLEAKLFNFLSHDDPKISQFDKG

>ABV51912.1 chemotaxis protein MotB, putative [Campylobacter jejuni subsp. jejuni 81116]

MAKKHKCPECPAGEKWAVPYADFLSLLLALFIALWAISKTNPAKVEALKTEFVKIFDYTSTQTVKEESKT

QEKYKGAAKEESDELKSLKQMTMTQQETIKRLQAALDQSDNQVALNLPSKVEFERGSAQIVSADIQDYLK

RMAELTTYLPPQAKIEIRGYTDNSDSIIRSYELAYQRAENVLKYFIEGGANLKNISIKSYGLNNPINGNP

QALENNRVEIYFKVDTADTSTQKSVLELINKIGTKAP

>ABV51911.1 flagellar biosynthetic protein [Campylobacter jejuni subsp. jejuni 81116]

MAGEDQEKTEEPTSKKIEDARKEGNVPKSQDAAAIVTLIIGVTITLFMMSFMGERIVNLYRYYQSFIGVE

FDLRIIQAIMIKSIFEVLIILAPIVLSIMIAGVLGNIMQFGFIFTTKPIMPNLGKINPLKGLKNLFSLKK

IVESIKIILKVGIVFTIAFIVLLKFMQELPRVELYTMVAQLTWLRDRAIVLAAIVIVAFLIIAVLDVFLV

RFQYFKGLRMSKQEIKDEYKQMEGDPQVKGRIRRLQMEAARRRMVQDVAGADVVITNPTHYAVAIRYDTS

KEQAPRVVAKGVDFLALRIKQVAYENNVVVYENPPLARELYKACDVNDLIPREMFKAVAEVLGFVYNTNN

KSRLAGQVKKGN

>ABV51910.1 alkyl hydroperoxide reductase [Campylobacter jejuni subsp. jejuni 81116]

MIVTKKALDFTAPAVLGNNEIVQDFNLYKNIGPKGAVVFFYPKDFTFVCPSEIIAFDKRYQEFKNRGIEV

IGISGDNEFSHFAWKNTPVNQGGIGQVKFPLVADLTKQIARNFDVLYAEAVALRGSFLLDADGTVRHAVV

NDLPLGRNIDEMLRMVDTMLFTNEHGEVCPAGWNKGDEGMKANPKGVAEYLGKNEAKL

>ABV51909.1 ferredoxin [Campylobacter jejuni subsp. jejuni 81116]

MAVKITDICIACGSCIDECPVSAIVDDVNNPEGEDRYYVYANKCVECVGHNDQPACASACPTDGCIVWSA

VESGQPSRDNIGADMRSGDTPVFA

>ABV51908.1 nucleoside diphosphate kinase [Campylobacter jejuni subsp. jejuni 81116]

MEKTLSIIKPDAVKKGVIGKILDRFESNGLRIAAMKKVQLSKEQAENFYAVHKERPFFKDLVEFMISGPV

VVSVLEGEGAVLKNRDLMGATNPKEAKAGTIRADFAESIDANAVHGSDSLENAKIEIDFFFKPNEIC

>ABV51907.1 hypothetical protein C8J\_0308 [Campylobacter jejuni subsp. jejuni 81116]

MKIPFSKINTKEYPFKLNLENMIFEGNLVKINSKLVKINAIMQGFIYRPCDSCGTELELEIKENLELFAS

DGIFKDEANELSNTIEFFDGHIDLIEVAISELEAYLSDYFYCINCNN

>ABV51906.1 hypothetical protein C8J\_0307 [Campylobacter jejuni subsp. jejuni 81116]

MAVPKRRVSKTRAAKRRTHYKVSLPMPIKDKDGSYKMPHRANPTTKEY

>ABV51905.1 fatty acid/phospholipid synthesis protein PlsX [Campylobacter jejuni subsp. jejuni 81116]

MINIAIDAMGGDFGEKPIIEGVLKALEAKPFNAILVGNSKILKPLIPKKLEQYIQYEEASEIFSMNENAT

DALKNKETTIYKAINLLKEKKVDAVVSAGHSGASMSLATLRLGRLKGISRPAIATLMPNIINKTLLLDVG

ANTDCKAENLFQFAIMGEVYARAIMQIQKPRLALLSNGEEECKGNELTKESHQLMKKIPNFIGNAEGRDI

FNGEIDVLVCDGFDGNVILKACEGVATAIFQLLKNEVKQSFISKIGALLMKPSFKKLKKHTDWQEYGGAP

LLGVNGCVIISHGKSDSRAIKNAIFQAINFSQSHINELIENELGKYNA

>ABV51904.1 3-oxoacyl-[acyl-carrier-protein] synthase III [Campylobacter jejuni subsp. jejuni 81116]

MLKASLKSIASYIPEKILSNADLEKMVDTTDEWITRRTGIKERRIASENENTSDLGTKAALKAIKRANLK

PEDIDAILVATLSPDYFTMPSTACKIASNLGLVNISAFDISAACSGFIYLLEQAKALVESGLKKNVLIIG

AEKTSSIMDYNDRSICILFGDGAGAGVVSLDNENHILDVHTASNGNYGDLLMTQRSQKSNLCQTLSMQMK

GNEVFKIAVNTLSNDVVEILAKNNILAQEIDLFIPHQANLRIIKAVQEKLNLSDEKCVITVQKYGNTSAA

SIPMAMNDAYEEGRLKKGDLILLDAFGGGFTWGSALLKFGGENF

>ABV51903.1 hypothetical protein C8J\_0304 [Campylobacter jejuni subsp. jejuni 81116]

MIKRFDECDRMSQIIVFDKYFKTAGQVAFEPSGDIKKQTKEALAELDTLFEKIGACKGDLIQIQIWLANM

QDFDAMNEIYDAWIKNYPKPIRACVGSALAEGYLVEIQAFGKLREN

>ABV51902.1 phosphoserine aminotransferase [Campylobacter jejuni subsp. jejuni 81116]

MRKINFSAGPSTLPLEILEQAQKELCDYQGRGYSIMEISHRTKVFEEVHFGAQEKAKKLYGLNDDYEVLF

LQGGASLQFAMIPMNLSLNGVCEYANTGVWTKKAIKEAQILGVNVKTVASSEESNFNHIPRVEFSDNADY

AYICSNNTIYGTQYQNYPKTKAPLIVDASSDFFSRKVDFSNIALFYGGVQKNAGISGLSCIFIRKDMLER

SKNKQIPSMLNYLTHAENQSLFNTPPTFAIYMFNLEMDWLLNQGELDKVHEKNSQKAAMLYECIDLSNGF

YKGHADKKDRSLMNVSFNIAKNKDLEPLFVKEAEEAGMIGLKGHRILGGIRASIYNALNLDQVKTLCEFM

KEFQGKYA

>ABV51901.1 exodeoxyribonuclease VII large subunit [Campylobacter jejuni subsp. jejuni 81116]

MTPTELNLKAKALLETHFEDIVLSGEISKITLHGSGHWYFDLKDERSSIACAMFKGANLKVGFKPAVGDF

LELCGSVSLYPESGRYQFIATSMKKAGFGDLEAQFLALKERLQKEGLFDPLFKKSLPKFPKKVGIITSKT

SAALQDMLKLIHQKEYFLAKIYIFDALTQGNNAPFSLIQALKKADDMDLDVLIIARGGGSREDLFCFNDE

NLAREIFKAKTPIISAIGHEIDYVISDFVADFRAPTPSAAIDTLFYSKLDIEQSLDLMEEKLMQLWNHKI

QNYENLLLNLSKFFKFNSLPKIIDEKIKQSHNIEKQLNHLLANQMRYNELKLDKLQNAYLQHENFFNKSK

KFICIRKNGKIANLEDLKSDDIVILSSQTSQKEAKIL

>ABV51900.1 ubiquinone/menaquinone biosynthesis methyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MQKQEKIIEMFNQIAPTYDKANRILSFGADVVWRKKACQRVMSLYLKKDLKIADIACGTGDMIEIWQESA

LKMEKNILNIKGIDPSSGMLNVAKEKFPNVEFIEAGAQNLPLESQSLDILSISYGIRNVVERQKALSEFA

RVLQKGGILVVLEFTKREKGGFIAACRDFYLKNILPSIGGIISKNKSAYEYLPNSIEGFLSKEEFILELK

NAGFEMLDYKSFSFGVSSMFIAKKL

>ABV51899.1 hypothetical protein C8J\_0300 [Campylobacter jejuni subsp. jejuni 81116]

MVYEIQKNFLLSDCTLLENLKKDNIPFRNSKFETFYTQITSNHSVKFQSFCNEFYKITKFNNSILEQNQE

EKISKKKFEKARKKIIGKSIKKECFEFKFCSLKSYIDIYEEPKICILKIFFPTLDSSNEFKIPKDFKIQK

ELHHDLNSKHIVLYGFEYQNFDIEKCFKIIEKNQNFSLDFPNYINAYDGFRIFLFYLFKKLKFYWTLSLE

RKDKQSLCEFLFYSRSLYIVLSSMNTILDKNLSNILALKFKDITKKTQDILASENSNQDLLLFLSDEKIQ

DLFNDFDFFIKENSFYEGDCKDRFFKQLVALELRKKIILFRKNILKNFDLELFENSFFELAIFLEYFYRF

LEIKNLNKLYEKYCKDRDKNIFSKIINNKNKFCKLLKKSSKNLKIYKG

>ABV51898.1 transcriptional regulator, Fur family [Campylobacter jejuni subsp. jejuni 81116]

MELLQMLKKHELKATPQRLCVLKILKRHEHPNIDELYTEIKKEYPSISLATVYKNLNTLQEQGLVVEINV

LNQKTCYDIYEEEHIHVVCTKCGGIEDLSFKDAKLYEYQEHLEKKIGNLVNHLSVCAYVDSCKKCH

>ABV51897.1 1-deoxyxylulose-5-phosphate synthase [Campylobacter jejuni subsp. jejuni 81116]

MSKKFAHTQEELEKLSLKELENLAASMREKIIQVVSKNGGHLSSNLGAVELSIAMHLVFDAKKDPFIFDV

SHQSYTHKLLSGKEEIFDTLRQINGLSGYTKPSEGDYFVAGHSSTSISLAVGACKAIALKGEKRIPVALI

GDGALSAGMAYEALNELGDSKFACVILLNDNEMSISKPIGAISKYLSQAMATQFYQSFKKRIAKMLDILP

DSATYMAKRFEESFKLITPGLLFEELGLEYIGPIDGHNLGEIISALKQAKAMQKPCVIHAQTIKGKGYAL

AEGKHAKWHGVGAFDIDSGESVKKSDAKKSATEIFSKNLLDLASKYENIVGVTAAMPSGTGLDKLIEKYP

NRFWDVAIAEQHAVTSMAAMAKEGFKPFIAIYSTFLQRAYDQVIHDCAIMNLNVVFAMDRAGIVGEDGET

HQGVFDLSFLAPLPNFTLLAPRDEQMMQNIMEYAYLHQGPIAFRYPRGSFILDKEFNPCEIKLGKAQWLV

KNNSEIAFLGYGQGVAKAWQVLRALQEMNNNANLIDLIFAKPLDEELLCELAKKSKIWFIFSENVKIGGI

ESLINNFLQKYDLHVKVVSFEYEDKFIEHGKTSEVEKNLEKDVNSLLTKVLKFYH

>ABV51896.1 putative flagellar assembly protein [Campylobacter jejuni subsp. jejuni 81116]

MVNRSNVISGGASDQHVVEGYRFKVISEFDNHTGEKKHTQTPDEENANISLNDEKAVEENQAIAPTQAVM

ETQIPTFQPSFVEDLLKKTDEMSSNIIKLQMQIESQENEFNNRLNSELENAKEKFAKEGYEKAKEEFQKE

LSDFKDKYLKSIAKLDNACENLENFIEKNEKELADTAIDIAKEVILKELELNSSKIAYALAKDLIGELKG

ASAIELKVNAEDYEYLKEQFDQNAHIKISLDDAISKGSVVIISDAGNIESNLNSRLTKIKKMVNNE

>ABV51895.1 flagellar motor switch protein [Campylobacter jejuni subsp. jejuni 81116]

MIKLSEEQKMVYDDLSMPEKVAIFLIQLGEDATTSVFSHMEIDVITEISRYIAMAKNVDRSVATAVLEEF

YTLLQSNQYIKSGGLEYAKEILFRTFGPEIANKILEKLTKSMENNQNFAYLAQIKPQQLADFITKEHPQT

IALILAHMDSIHAAETLEYFSDELRAEVVIRMANLGDISPSIIKRVSAVLESKLESLTSYKVEVGGPRAV

AEVLNRLGQKASKSTITYIEQSDERLAETIKELMFTFDDIQKLSTQAIREILKVADKRDLMIGLKGASEE

LKQKFLANMSTRASEAFLEEMGFLGAVRVKDVEDAQRKVVEVVQKLAEQGLVQTGDADEMIE

>ABV51894.1 flagellar M-ring protein [Campylobacter jejuni subsp. jejuni 81116]

MDFKNMLHQIGQLYQNLTRKQRIVIAASIVVVVGFLVFLALFRGSGSNANNGYAVLVENVSPSSSAAIVA

KLEQNNIPYKLESENKILVPQDQVYRQRMFIASEGLIKDSRVGFEAFDTQAFGATNEEQRVKYQRAIEGE

LARTIETLEPIRSAVVHIAFPKDSVFTERQIPPTASVVVNVREGLKLTRKQIDGIKNIVSAAVPKLTKEN

VKISDQSGVPLDEQEAYEDDLVRAQIKFKSDQEKALEDKIIENLAPFAGGMDKVKVSVNIDFDFSKQESQ

SEIYDPNPIVRSEQTLNEERTGRKDPEIQGVPGAVSNIGPVEGLDNKGQIDTYKKNQVTTNNELSKTITN

TKKQFATVLRTSAAVTIDGKYQDVVDENGDVKSEYVPLTKEELASVESIVKNTINFSATRGDSVVVQNLP

FHRESIRVESKVKTFYNRFVEPFIPPVKYFIAAILLFIFYKKVIAPFTQKMLEDVAAQEEMQQGPNAVLD

DAEDALEKFNAARKKVEEQLGFGDNFNEDSIQYEVLLEKLRGLVSDKGEEIAALLQNLIQNDSEFGEKDM

>ABV51893.1 histidinol-phosphate aminotransferase [Campylobacter jejuni subsp. jejuni 81116]

MKFNEFLNHLSNYEPGKDIEVIAKEYGVKEVIKLASNENPFGTPPKAIECLRQNANKAHLYPDDSMIELK

STLAQKYKVQNENIIIGAGSDQVIEFAIHAKLNSKNAFLQAGVTFAMYEIYAKQCGAKCYKTQSITHDLN

EFKKLYEAHKDEIKLIFLCLPNNPLGECLDASEVTKFIKGVDEDCLVVIDAAYNEFASFKDSKKHLEPCE

LIKEFDNVLYLGTFSKLYGLGGLRIGYGIANANIINAFYKLRAPFNVSNLALKAAVAAIDDDEFTKKTLE

NNFSQMQLYKEFAKKHNIKIIDSYTNFITYFFDEKNSTDLSEKLLKKGIIIRNLKSYGLNAIRITIGTSY

ENEKFFTEFDKILR

>ABV51892.1 chorismate mutase/prephenate dehydratase [Campylobacter jejuni subsp. jejuni 81116]

MPNLEEFRNKIDTVDDKILELLNERMTYVKSIGELKQSSGGTIYRPERERAIINRLKNANLGLLDQNAIE

AIYQEIFAVSRNLEMPQTIAYLGPEGTYTHQAARSRFGAMSRYIALANIEDVFKELSNKEAKYGVVPIEN

NTEGAVGITLDCLGKYNELKIFGEIYMDIHHSFVGINENLKEIKRIYSHPQGYNQCRKFLESHELSAIEF

VPSKSTANAAYLASQDKYAAAICSKIAAKLYNVPVLFDKIEDNAANKTRFLILSDIKNPKMPNCKTSILA

HTAHKPGGLSFLLEQFKKENINLTKLESRPVKSKEFLHSFYIDFEGHIDDENVKKALKDIQEIVWLGSYL

SGEKDEI

>ABV51891.1 HAD-superfamily hydrolase, subfamily IIA [Campylobacter jejuni subsp. jejuni 81116]

MFFLDVQGTLISDHDKSLIHGAKELIDFLNAKNLPYVIITNNTKKLDFLEKLQQKGLAIKENAYIDPFSV

LKYLLKPCKVAAFGADEFVKSLENLGFELDFVNPSAVLVASYDDFKFKDFASMIEFARREVRFIAMHETS

IYKKDGRPYPGVGSIMAMLKNAIDFEYEVVGKPSIAFYKEALNLIRKQNSKIDFEDIKIISDDFRGDLLK

AKELGMKTLLVLSGKISDTKGLDTDLLDGVYPSVFEFLKELKCQI

>ABV51890.1 diaminopimelate decarboxylase [Campylobacter jejuni subsp. jejuni 81116]

MDYKQLKQEFNTPFYIYNFDFIKERFLNLKEAFKARKSQIFYAVKANSNLSLLQMLANLDSGFDCVSIGE

VKRALKAGAKAYKIIFSGVGKTKEELRQALEYDILYINLESEAEMMLLESVAKELNLKARISIRVNPNVD

AKTHPYISTGLNENKFGVEIDIARKMYLYAKNSSFLEPVGVHFHIGSQLLDISPIHEAAGIVAKLVRELK

ALQIDLKFFDIGGGLGVAYEKDECEPDLYNYAQGILAQLHGLDLTIGMEPGRYLVAKSGEFVCSVLYEKQ

NKTKRFVVVDGAMNDLIRPSLYEAYHEIILPYNQAQESLCDVVGGICESGDFFAKARSLPSTQSGDIMVI

KNTGAYGFSMSSNYNTRNKVCELALEEGQVRLIRQRENFENQIALEEKFLKA

>ABV51889.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MWIFFRFISGIYLKNFFIIFFSLLGFYCGIDLLLNFKDLPKAANLDLLYVMFLSFSAVPYVLPISLIFAL

VVSLISMIRANEFVSLYALGLSRNYVILFPFLWALFFCCIYIGLNFTSFAYANDYKRNILKNGTIMNQSG

EVFLKFNNNFVYISKINNGQNSAQNIKIFNINDLNLSSFVSAKNAHFEGESWILRDGNITLLPKNYELAN

DGLKIQDFSELKSLEGFKPKIIEGVASNSDYSISDALESFELFKAQNVNTDALKINLYKFVFTPFFAPFL

MLIMYYFFPVIARFFNLAFVTFIAFVVTLMIWGVLFLLTRLSENSVIASEIGIVVPIIILGCLSAYMYYK

HR

>ABV51888.1 peptidyl-tRNA hydrolase [Campylobacter jejuni subsp. jejuni 81116]

MILVVGLGNIGVEYENTRHNVGFMLIDLLLKESNFTNLTNSKFKGELFKIGSSLLLLKPSTYMNNSGLSV

KAVNDFYKCERMIVIHDDIDINLGALRFKKGGSSGGHNGLKSIDTLCGNDYERVRIGVGKGENVISHVLG

KFKSEEEITLSKVLEHAKKALLELIENDDLSAISSKYSLKA

>ABV51887.1 50S ribosomal protein L25 [Campylobacter jejuni subsp. jejuni 81116]

MLEGIVRESIGRKAAKALKRDGYLIANIYGKGLENINAAFKVNEFIKEVRKKTTLIFDVKVGSQTLSVVV

VDYQKDPVTAELKHVDLKVAQKGVISKYMVPVKITGTAIGLKNKGVLIQSKRRLKVKCAAENLPNFFELD

VSKLDVGDALLVRDIVVPAGVTMIDADRVAVVGVEKAR

>ABV51886.1 multidrug resistance protein, SMR family [Campylobacter jejuni subsp. jejuni 81116]

MFYKYYVNLRLHVNEKFNINIAWFLIILGGIIECFWVSGLKYSTEIWHYILTAIGVCISFTCFLKACERL

EVSITYSVFVGIGTIGVVLNEMFIFNEAVSIIKLVLIVILLLSIIALKWISKEA

>ABV51885.1 multidrug resistance protein, SMR family [Campylobacter jejuni subsp. jejuni 81116]

MEWFYLFLATACEIFGVVIMKELVSTKNKLYLLALIVCFGFSFTFLSLSMQNIAMSVAYAIWTGAGTAGG

VMIGVLFYKESKSFLKLFLITVIIACTVGLKFLS

>ABV51884.1 dethiobiotin synthetase [Campylobacter jejuni subsp. jejuni 81116]

MQIYVSGIHTDVGKTHFSAAFCANFNYDYFKLIQAGTPTDSEFIAKFSPKTKIFKEGIFLQTPASPHLGK

IKEKLDYKALDIILPKSKNLLIELAGGLFSPMDENYTMIDFVNIFKHPTILVAKYYLGSINHILLSIEAL

KQRNINLLALVMMGKKDILQDDFIKNYAKIPIINLDFFDENSILNKDFKEQMQEILQLKIP

>ABV51883.1 adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Campylobacter jejuni subsp. jejuni 81116]

MQNQILKNLDLKHIWHPCTQMKDHETLPLIPIKKAKGVWLYDFDDKAYMDCVSSWWVNLFGHCNEKIANA

IKKQVDELEHVILAGFTHEPIIKLSARLCEKVGRNFNKCFYADNGSSAIEVALKMSFHYHLNKGVKKSKF

LSLSNSYHGETLGALSVGDVALYKDTYKALLLECLSTPVPQGKDYTKELEILKDILEKNASEICAFILEP

LVQCAGNMHMYEARFIDEAIKLCHKFGVQVIFDEIAVGFGRTGTLFALHQCKQSPDFICLSKGITGGFMP

LSVVLTRDEIYNAFYDTYESQKAFLHSHSYTGNTLACAAANAVLDIFEDENILVKNQILSEFIKKEFSRL

EKFDFLGNFRTCGMISAFDILSTKYKRVGLFVFQKALEKGLLLRPLANTIYFMPPYIITKEQIVYVLESL

EQIFKEF

>ABV51882.1 8-amino-7-oxononanoate synthase [Campylobacter jejuni subsp. jejuni 81116]

MKLEKILQDLEQNHNLRTLTPLKHENKFVYKQDHKLLNLVGNDYLYLASSKELKAEFLNTLKEQDLFFSS

SSSRSLSGNFEIYEKLESFLKTKFKDKEILHFNSGYHLNISCIAALSSVSKTLFLTDKFIHASMIDGLRL

GRADFFRFHHKDMNHLESLIQKHYENYENIIVLSEALFSMDGDFSDFKTLCELKRRYDKIKLYIDEAHSV

GCFDEEGLGLVKKLALENEVDFLVFTFGKALASMGACIICDEKYKKFFINKARAFIYSTALPPINVAWTQ

FIFKKMPYFKKEREKLELLSTFFKSKLQEKNHIVLGDAYIICLLLGENKKALEISQKLQKAGFFAPAIKE

PTVPKNTARIRFSLHAGLNTEELERIIELL

>ABV51881.1 hypothetical protein C8J\_0282 [Campylobacter jejuni subsp. jejuni 81116]

MKYEFLCKNPDSKKLIVVFGGFASHSSHFSHLKSDKNVILFYDYENFDLNFDFKAFDELFLIAFSMGVCV

ANRLLKELNFKQKIAINGTNLGIDKSKGIHPAIFRKTLQNFKLENFKEALFKERKNLTKDFIFKDEKALK

IELEKLFDFALVKQEENLLWDKVYSSKKDEIFPPNALKNAFSKLIFLNEPHFAFFHFKTWDEL

>ABV51880.1 putative biotin synthesis protein [Campylobacter jejuni subsp. jejuni 81116]

MNFLKAKDYEKHAKVQDFMGLKLCEILKNLRISHFEKVFEFGCGRGELSKKLQNFITFDEYLKNDILDFK

ENSSILIFDMNEIAKQDLSKEKFDLIVSNATLQWLDLKRIIPSLRDMLNQNGILLLSTFAEQNLKEIKQS

TGFGLNYFSLNELEQIFKVYFNEVKITQELIKLSFDNALDVFRHLKLSGVNSLGFYPLNKGFLKEFEEKF

QNKLTYHPVFILCKNDIK

>ABV51879.1 molybdate transport system substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKFVVFFGILLFVSCLNAQNLSIFVASSASKAMSEVKDEFLKTHPEDKIELVFGASGKYYELLKQGREF

DLFFSADTKYAKAIYDDKNALIKPKVYVLGVLALYSLDENLLQGGVENLKEKANKITHLSIANPKVAPYG

VAAKEVLENLGLNELLKDKIVLGENISVPVLHVDSKNSDIAIVAYSLVSSINHPKGKAVIIDAKYFSPLE

QSYVITKYAKDKKLAFEFNEFIGSSKAKEIFKKYGFSTP

>ABV51878.1 hypothetical protein C8J\_0279 [Campylobacter jejuni subsp. jejuni 81116]

MNLIKGQICELLNQEDIVIVKILSKEVIFSVLMLELKSLENLKIGVSVELLFKEHELCFSASKTLLSVEN

SFLAKITKIKKGKLLYQVFFDFKGNELSSIITKEKALELEICENQEWLCFVKANDIVLRSHSA

>ABV51877.1 molybdate transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MLDPAFLQTLYLTFKLAFITTFILFFIGVFLAYLLSFVRFPFKTILQSFISLPLILPPSVLGFYLLVTFS

ANSFLGQVLKEYFNLSLVFSFEGLVFASLIFSLPFMVNPLQSAFSSINPNLLDASYSLGKSKIYTLFRVI

LPNSKAGIFSACAMSFAHTVGEFGVVMMIGGHKQGETLVASIAIYDELEILNYSLAHQYAFILFIFSFLV

LFSLYFINKKMSFQ

>ABV51876.1 molybdate transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MIRIDINHPMNTAKGRLDLNFKKDIESGKITALFGESGAGKTTLLKIIAGLIKPKLGRIEVDNELWFDSS

KNFSLALQKRKIGFVFQDYALFPNMNIKENIAYAASSKAKVSELLALMKLENLAKIYPKHLSGGQAQRVA

LARALAREPKILLLDEPLSALDFKMRANLQDELTKILEYFKISTLLVSHDLAEIYKLSHRILELKNGKII

KDFPKNEFFTHSNISAKLRLSATLLEIKKSDILVVLTLLLNQDIIKITLSEEEFLKAYQDVKIGDTLLLS

IKAFNPIIVGKLDK

>ABV51875.1 putative periplasmic beta-lactamase [Campylobacter jejuni subsp. jejuni 81116]

MKKITLFLLFLNLVFGQDKILNNWFKEYNTSGTFVFYDGKTWASNDFSRAMETFSPASTFKIFNALIALD

SGVIKTKKEIFYHYRGEKVFLSSWAQDMNLSSAIKYSNVLAFKEVARRIGIKTMQEYLNKLHYGNAKISK

IDTFWLDNSLKISAKEQAILLFRLSQNSLPFSQEAMNSVKEMIYLKNMENLELFGKTGFNDEQKIAWIVG

FVYLKDENKYKAFALNLDIDKFEDLYKREKILEKYLDELVKKVKNDG

>ABV51874.1 3-methyl-2-oxobutanoate hydroxymethyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MRKSMISFLEKKAKNEKITMVSAYDYHSARILDNSDIDIILVGDSLAMTVLGMQDTLSVTMDEMLIFTKA

VSRGAKKSFVLADMPFMSYQSSDRDAILNASRFIKESHANGVKVEGGIEIASKIKLISQSGIPVVAHLGL

TPQAVNMLGGYRVQGKDLQSAQKIIDDAKAVQDAGACMLVLECVPVKLAQKISSILEIPTIGIGSGKYCD

GQVLVYHDLLGLNKDFKAKFVKHFDKIDPQVGVEKYRDEVKSGIFPSQEHSFDYLDDELLDKLY

>ABV51873.1 pantoate--beta-alanine ligase [Campylobacter jejuni subsp. jejuni 81116]

MQVITSVKEAKQIVKDWKSHQLSIGYVPTMGFLHDGHLSLVKHAKTQDKVIVSIFVNPMQFGPNEDFSSY

PRDLERDIKMCQDNGVDMVFIPDATQMYLKNFSTYVDMNTITDKLCGAKRPGHFRGVCTVLTKFFNILNP

DIVYMGQKDAQQCVVVRHMVDDLNFDLKIQICPIIREEDGLAKSSRNVYLSKEERKASLAISQSIFLAEK

LVREGEKNTSKIIQAMKDILEKEKLIKIDYIELVDFNTMENIENITDNVLGAVAAFVGKTRLIDNFLVQG

LK

>ABV51872.1 aspartate 1-decarboxylase precursor [Campylobacter jejuni subsp. jejuni 81116]

MNITLLKSKIHRASVTEARLDYIGSISIDEKLLQASGILEYEKVQVVNVNNGARFETYTIATQEEGVVCL

NGAAARLAEVGDKVIIMSYADFNEEEAKTFKPKVVFVDENNTATKITNYEKHGAIF

>ABV51871.1 putative acetyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MLRKADIKDLNACLSLFEQSVKTLCAKDYTKDQICAWIKIDRQQWEEKFKYDEIFVYEKRGKIASFISVK

QEQKLLDLLFTHPDFVRQGLAQNLLDFILKTYLHNEIYTFASLSAKDFFLKNGFELIRENKVIKEGQNLK

KFLMKKDVVYKN

>ABV51870.1 MoeB/ThiF family protein [Campylobacter jejuni subsp. jejuni 81116]

MNDRFTRIKWLVGEEKFQKISQTKVLVCGLGGVGGICVDALYRSGFKNLTLIDADKFEITNQNRQIHSEN

IGEEKAKVFERIYKVKGIVSKIDENFLKNFDLSEFDLIIDAIDDIPAKVALAHLIDFKKQIFISSTGGAR

KLDPTRIKTTSIFKTHGDALAKKFRYELRKSGFKGNFDVVFSDEEAHCKDLGSFMGVTASFGLALASLAL

RKVLAKKS

>ABV51869.1 acid phosphatase [Campylobacter jejuni subsp. jejuni 81116]

MKEILITNDDGYESEGLKKLIKMLTKEFKAKITIVAPASEKSACSHSITLTKPLRFVKVGKRFYKLDDGT

PADCVYLALHALYKKRLPDLVISGINKGANVGEDITYSGTCAGAMEAVLQGIPAIALSQFYKKSEKELDY

KNALQITKKIIQNIFDKGFPLEKKEFLNINFPAKSKIKGIKICKAGKRVYNFEAHSNVNPRGVEYYWLAA

ANLDFEDEKNSDIALLKKGYATITPIMLDLTAYEKMKKVKKWLKANDE

>ABV51868.1 hypothetical protein C8J\_0269 [Campylobacter jejuni subsp. jejuni 81116]

MFDFFKPKAKAIKFPKEEILPRYYKMRTWSLSGVFIGYMGYYLVRNNITLSTPFIQNQLDLSKSDIGTIT

GSMLIAYGISKGAMSVISDKADPKKYMALGLILCALVNVLLGFSNSFYAYVGFVIALGVFQGMGVGPSFI

TLANWYPKKERGIYTAVWNISHNIGGGIVAPIVSLSGFALAALLGVSMADFNETYWHMNHFYVPAACAVI

ISLYVLYAVKGSPKNEGLIDITEINEMRGIKTEEIKAIETPNLSSFEIFYRYVLKNKNAWYVAWMDTFVY

MVRFGLISWLPIYLLETKGFNKEQMGIAFWLFEWAAIPSTLLAGYISDKIFKGYRMPPAIGAMVIIFFMI

IGYFTSNNLYMVIFFAAMAGCLVYIPQFLASVQTMEVVPAFAVGSCVGLRGFMSYVVGASLGTKAIGWAV

DYYGSWNAGLIMLLSACILCILCSTLCHFSAKKKYQ

>ABV51867.1 major antigenic peptide PEB3 [Campylobacter jejuni subsp. jejuni 81116]

MKKIITLFGACALAFSMANADVNLYGPGGPHTALKDIASKYSEKTGVKVNVNFGPQATWFEKAKKDADIL

FGASDQSALAIASDFGKDFNVSKIKPLYFREAIILTQKGNPLKIKGLKDLANKKVRIVVPEGAGKSNTSG

TGVWEDMIGRTQDIKTIQNFRNNIVAFVPNSGSARKLFAQDQADAWITWIDWSKSNPDIGTAVAIEKDLV

VYRTFNVVAKEGASKETQDFIAYLSSKEAKEIFKKYGWRE

>ABV51866.1 hypothetical protein C8J\_0267 [Campylobacter jejuni subsp. jejuni 81116]

MNYKKAFYSKLEDCYLGAKIKSSQNQAKNGFTNLLVIKEKYFQKIKDYLDTQKLYTDTYNKLYNFFSTYL

NETGTPFFYDTPMYKNIYARVYSNSKDTSLFYKTQNLYYVKSDTIYNPLSLQSEDKKYTLNFLTDEYEQN

ADNNKSKINFYLQNIQDDNINIKVINSKNHDGTNVFKQNPSEFSDVFLKTLKNAQINIKEEELKKLFKTY

KKQNEVDFFIHKNAKEFLKEQFDLWLFSYVNDSITEWTKEKIDEINDLKQIAFDIIDLIADFENELKAIW

LKPKFAKNVHYVFSLDTIKSHSNNADEILKSIYKDVNFNEQIAEWEELNFINDEFDIKAINDEKYKFLPF

DTKYLSEENYYKLLSAFDNLDEILNGELVKADNFQALNSLMPKYQGKIDLIYIDPPFNTGSDFDYKDKFQ

DSTWLSLMHNRLELAKEFLSDKGNFYLHLDENADYFGRILLNEFFGEMECKKITFDTNATKDEEADLFGY

KSFGNNFVLKSSTILFLKKTNSIFNKLWKPNRNSSLLNLGQLDLIGISTIETPKKITDYEYYVQIWKNGK

LCHEKIDIKDEKIYPLGDIWNDLYSFTQSEMRVSENISFYSSQKPENMLRRIIQSSSDENSVVMDFFVGS

GTTLVVSHKLNRKYLGVEMGEHFYEKYLTFNKDTKQYEYRLGLLGRMKNVIAGDIEFYAIDKKRRSSLSK

MINFKGGGAFRYYELEGYEESLENCEYKLDENSLIDYRKSRKLIKALKKGENICLDMNAYDKELDIFLTM

SNLLGLKIKNIFIDNNGIKSCKFENDEVINLENIDLIKYPKLKNLIWWEK

>ABV51865.1 hypothetical protein C8J\_0266 [Campylobacter jejuni subsp. jejuni 81116]

MKNIAILVGNSEYQNLNKLHFCRKDISSMQKILSLSKKFEIHIFENYQSEQLKSGLSKIIRELEKSKINE

LLFYYTGHGVFKEQFYYLPINFTDKQFETTSLSNNELDDMLKSLNTEMVIKIIDACQSGQQYIKESDQMS

VKKSLTQHSFKKCYFFFSSMNNQSSMGDDKGSYFTNAIIESIVTHKTDSIRYADVQSYIADCFNGKNELQ

TPFFVHQSNATEIFLSDLTSIQKFFENNDLMANNGEGIIQEIENDKIDIVEKLKTLSKKYIAKDVAQKTI

ECIFDENNINNMFNDDIKLIYDIKIEKHNDYNIDNINKLYNEIEKNKKHFFINLEYKQEAYTTTEWIPKK

KNPYDITGRFSYDEFLGKNYEEKEIQKYRNIVNSICLVDDILPIGIVISLNPKENIDNINRYLINIINFH

NNLDIVFYSNIIEYYKNNWYDWEKINTEDWIKSKESFCDKDKILDKIQIIIKNYNQKIIDNIFNILKQED

LKIRE

>ABV51864.1 hypothetical protein C8J\_0265 [Campylobacter jejuni subsp. jejuni 81116]

MAKAKQNIKKHLLLNQFIHNKSLVQKLNESYDFGNFSQAINLQFYQQEGVKNALAILSFYMKDELNSHNY

NQERRKLLDFYQGESKDLKLQKEHIARASFWMATGSGKTIVMIKLIALIHEFIKNNQLPKKPIMLLAPND

KILNQFKANITKYNNYHSNFIKIKDLKDFESIEKEASLLNEAVVYFARSDLLESEENVGKDKKAKRLNYK

NYLNKDGWYILLDEAHRGDSKTSLRKNYYHELARGFIKEDEFPKGFVFNFSATFEDEIDFITCAYNYNLQ

KFNQEGYGKNIAILNENLDFKSENNEEAKIKTILEGFIIFNAIVKTKEELFLKRSDFKYHNPLIIAVSDK

VNTQDAGIKTYFKAVHNVLKNKADIGNIALELYEKLQNQNLHFGINTLSDDFLKYIKNTNNDELRKNIFY

ASANANLECYSIKGNDKELAFKSKNSNKPFMLLNISNAKEWEKNFLLELGVESISDISQSHFENINSSQS

SINIMLGSKVFSEGWDSNRVNLISFINIGSVNAKKYVLQTIGRGVRIEPFLNIRKRLNTLKETFKIDERC

VNLACGLETLFVMASDNEAIQAIIEGIEYEFIESKHLKGFKETKLSFNLPIPKYKNETKLKSIYKISKDD

AKSLEELIKSYDEDVLILGQCLYKNFKYSTLQEFNKFIKGKESRIQLSGNKVEFNEKTILKTINSVLNSN

TKVLDKFVKLEKEITHHKNIQAKLDFETVQKINKTIKDVLNAKSEDELKADFENKKINLDELMQGIKESQ

KNKEVQNYIISAKLSTHYYNPLIIYNKNDKENKINFAISNKSEKEFLEDLESNLNLSFFEQYEWYFSKLV

ENQDEIYIPYFDEEQQKERKFYPDFIFWLKNKQSGEFDIYFIDPKGLKIEDNPRFKLKGFKMIFENKNLT

YEDKNIKVNLFFYNKNKNYVSDELKDFVKSNIEDIFK

>ABV51863.1 lipid-A-disaccharide synthase [Campylobacter jejuni subsp. jejuni 81116]

MKTFLVCALEPSANLHLKEVLKAYKKDFGEFELHGIYDESLCKEFDLNSKPLYSSHEFSAMGFIEVLPLI

FKAKKAIKELVNLTLSQTMDAVLCIDSPAFNIPFAKALKKAGSKIPRIYYILPQVWAWKKGRIPIIESHF

DILASILPFDNQFFNKSTYIGHPLLDEIKEFKNQEDINHTFSKKDDEKTIAFLPGSRRSEIRRLMPIFKE

LSQKFKGEKILCVPSFNLEKLEVYGDISEFKIESNTPKVLKKADFAFICSGTATLEAALVGTPFVLAYKA

KAIDIFIAKLFVKLKHIGLANIFCDFAGKEALNPEFLQDKVNVLNLYEAYNKYDYKAFFAKVDFLKEYLQ

FGSAKNLAKILNEI

>ABV51862.1 transcription elongation factor [Campylobacter jejuni subsp. jejuni 81116]

MQKEPMSQFGYDKLAAELKDLKDNQRPAVVIEIDTARSHGDLKENAEYHAAREKQALIESRIAELSDLLA

RAQVIDPSSYEHDSVKFGSSVVIMDLDTEKESKYTLVGICEGNLDKGYISIASPIAKAMLGKKEGDDFKV

RLPKGESEFEILSINYEPLKF

>ABV51861.1 hypothetical protein C8J\_0262 [Campylobacter jejuni subsp. jejuni 81116]

MLIGEISATHEFAKPYIELLEELALKIEIIYLEGNHDFNLSCFFKRVKIFNLQEQPIKLNLHTSKGNNLV

LNSAFIKLAHGDIFLPPLLQFTLKTLRNHYLLVFLNFLNIITRNFISNKILQNQNKKNLFYQIKDFENLA

KKRYEKYENLGFWVCEGHYHQNHQINKENIKYLNLASFAYERSFFVVEYQQEIKFREQKLRGQNV

>ABV51860.1 chemotaxis protein [Campylobacter jejuni subsp. jejuni 81116]

MFDENIVKTGSNEMELVDFRIFKQGHDKVYEGIYGVNVSKVREIIKIPSLTELPGVPDYIEGIFDLRGVV

IPVVNLAKWMQITEPESTMLKPRVIITEFSNILIGFIVHEAKRIRRINWKDIEPATFSTGSGALDKGKIT

GVTRIENDEVLLILDLESVVEDLGIYAPKTDIDFGKIEKFTGTALILDDSMTARKRVKEMMQQMGFQVVE

AKDGVEGINKLEELSQVYGESLNDTLKIIVSDVEMPQMDGFHFAARIKEDPRFKDIPIVFNSSLSNEFMN

EKGVQEAGGEGYLVKFNASDFFNEIAKVIKKHQSQEQG

>ABV51859.1 chemotaxis protein CheA [Campylobacter jejuni subsp. jejuni 81116]

MEDMQEILEDFLVEAFELVEQIDHDLVELESNPEDLELLNRIFRVAHTVKGSSSFLNFDVLTKLTHHMED

VLNKARHGELKITPDIMDVVLESIDRMKTLLNSIRDNGNDTAIGMDIEPICARLTAISEGESPVAATDSN

EKSTPQAEPEAPKQETTTPEPEVDVNQLSDSEVEAEIERLLKVRKAEDQARRAQKKQTTNAAPKPTNNTA

NKPAESGEKKVPASGSNASSMDQTIRVEVKRLDHLMNLIGELVLGKNRLLKIYDDVEERYEGEKFLEELN

QVVSQLSIITTDVQLAVMKTRMQPIAKVFNKFPRVVRDLSRELGKQIELEITGEETELDKSIVEEIGDPI

MHMIRNSCDHGVEDPATRAANGKPEKGIVQLKAYNEGNHIVVEITDDGKGLDPNGLKAKAIEKNLITERE

ADQMTDKEAFALIFKPGFSTAAKVTNVSGRGVGMDVVKTNIEKLNGVIEIDSELGKGSSFKLKIPLTLAI

IQSLLVGTQEEFYAIPLASVLETVRVPIDDIYTIEGKNVLRLRDEVLSLVRLSDVFGVKQVLESGDQTYV

VVIGVAESKLGIIVDTLVGQEEIVIKSMGDYLQNIQGIAGATIRGDGRVTLIIDVGAMMDMAKEIKVDIK

AQLESSAKKPKEQPSDYKVLIVDDSKMDRTLMQKALEPLGVSLVEATNGVEALNIIKSGEHDIDAMLIDI

EMPRMDGYTLAGEIRKYSKYRNLPLIAVTSRTSKTDRLRGVEVGMTEYITKPYSPEYLENVVRKNLKLG

>ABV51858.1 chemotaxis protein [Campylobacter jejuni subsp. jejuni 81116]

MSNEKLEQILQKQQTQMAGPDVDQREDDIIQLVGFVVGDEEYAIPILNIQEIIKPIEYTRVPSVPDYVLG

VFNMRGNVMPLIDLAQRFHLGSSKMTPQTRYIVLRGETNGTGVGGNAGFVIDRLTEAIKIHRNRIDPPPE

TLVKDKGMIYGIGKRDENILTILKVEALLKREF

>ABV51857.1 putative phosphoserine phosphatase [Campylobacter jejuni subsp. jejuni 81116]

MIKLCVFDFDATLMDGETIDILATAHGKGNQTSEITRHAMAGELDFFESLQKRVSLLKGMSYKKVLELGS

TLPLMHGAHELIQYLKSKNIQIVIFSGGFHEGIDPAMQKLGINLSFANYLHHKNDILTGLVGGEMMFSNS

KGLMLQRLKSFLNLKTDEVMCVGDGANDLAMFNESGLKIAFCAKEILRSQADICIDIKDLKEIIKVI

>ABV51856.1 transaldolase [Campylobacter jejuni subsp. jejuni 81116]

MKNFSLWCDFIENSFLDNEFLNLLSHGINGATSNPAIFKNAILNSPIYKDKILKLKGKRTKDIYEELAIS

DIQKAADKLAPLFYQKNDGFISIEIDPRLHDNTTLSLGEAKRLYSAISKENVMIKIPATKASYEVMYELM

KNGISVNATLIFSLEQSQKCFEALNAGLVEFRKNNIALKEQNTRTPQAVISIFVSRFDRLLNPKAKEQNR

IGILNANLAYNNIYSKNEPNIRALFASTGVKGDDLPKDYYIKELLFENSVNTAPLDAIEAFKGKMDFKKP

LMNFEIYTELNQIISQSEREKACNDLLSDGIEQFCIAFEDILKAL

>ABV51855.1 hypothetical protein C8J\_0256 [Campylobacter jejuni subsp. jejuni 81116]

MIYLAQTDTTVGFLSKNLEEINALKGRDKNQPCLITSAKFCELKSLARIPKSFKNLVRRSKKTTFIYPNN

QAIRIVKECKHANFLSKNGYFYSSSANKHGKEFDEEWARSVADIILDEKFFENIPSKILKLSKNKMIKIR

>ABV51854.1 carbamoyl-phosphate synthase large chain [Campylobacter jejuni subsp. jejuni 81116]

MPKRTDIKSILLIGSGPIVIGQACEFDYSGTQAAKTLKELGYRVVLINSNPATIMTDPEFADATYIEPIT

KESILSIIKKEKIDAILPTMGGQVALNVAMEVYESGLLGDVKFLGANPEAIKKGEDRQVFKECMKKIGMD

LPKSMYAYNYDEALKAVDEIGFPLMIRASYTLGGAGSGVVYNMDEFKELANTALALSPIHEILIEESLLG

WKEYEMEVIRDRADNCIMVCSIENIDPMGVHTGDSITIAPALTLTDKEYQVMRNASFAILREIGVDTGGS

NVQFAINPKNGRMIVIEMNPRVSRSSALASKATGYPIAKVATLLAVGFSLDEIKNDITGTPASFEPVIDY

IVTKIPRFTFEKFPGANTTLGTAMKSVGEVMAIGRTFKESIQKALCSLERSLSGFDRVKFEDRNDLVFKI

RNANEKRLLYVAQAFREGFSVEELYELCKIDPWFLTQIKEIVDFEEQIDMDILNNKALLRKAKTMGFSDK

MIALLVNLKDNLELSQNDIYYARMKQKIIAEFSEVDTCAGEFEALTPYLYSSINVSELTQSKNDAKDKKE

KKVMIIGGGPNRIGQGIEFDYACVHASFALKDMGIKTIMYNCNPETVSTDYDTSDILYFEPIDFEHLRAV

IEREKPDGVIVHFGGQTPLKFAKRLSAFGAKIIGTSARVIDMAEDRKKFAEFITKLGINQPKNSTATSVE

EAVLKASDIGYPVLVRPSYVLGGRAMRVVNDEAELRLYMQEAVDVSDKSPVLIDQFLDNATEIDVDAICD

GKDVYVAGIMEHIEEAGIHSGDSACSLPPCNIDEKMQEFIAQKTADIALNLGVVGLLNIQFALHNNELYM

IEVNPRASRTVPFVSKATGIPLAKVATRVMWQGNLKEALKFYDTFKVVNFDTKILRPKTPKYMSVKEAVF

PFAKLSGSDLELGPEMRSTGEVMGISKDFANSYAKSQIASFNHLPEQGVVFISLKDKDKKYTKKIAAEYV

KLGFKLMATGGTCKEILESGFECELVHKISEGRPNVEDKLKNGEIHLVINTSDNHSFKGDTKKIRENIIR

FKIPYFTNLRSALAGAKSIKAIQSKSCLDVKSLQEWLKS

>ABV51853.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKNKIFYVLVLAFLVFISFYYGGLIKQNVLRVNDFVIGNFYNIKDYLGEKISEHFNQANQIQQLKARNKE

LEDIAVKVTSFANQLNRILEDQNSTKYLPQVSLTRVISYVQLNDYKKLWLDWSKIPVGKNRGLIYQGYTA

GIAINKNGRAMALLQGDDQCVFSVYIGKSKAPGLIQGEDGRIVVKFIPKWAKINIGDEILTSGLDNIFFS

DIPVGIVNRIDDEDMYQSVEVKPYVKISIPAYLYVVDNL

>ABV51852.1 cell shape-determining protein MreB [Campylobacter jejuni subsp. jejuni 81116]

MILDQLIGFFSSDMGIDLGTANTLVLVKDKGIVINEPSVVAVERERYGSKAKILAVGKEAKDMVGKTPGN

IEAIRPMKDGVIADFDMTEKMIRYFIEKTHRRKSFLRPRIIISVPYGLTQVERKAVRESALSAGAREVFL

IEEPMAAAIGASLPIQEPKGNLVVDIGGGTTEIGVISLGGLVISKSIRTAGDKLDMSIVNYVKEKYNLII

GERTGEEIKITIGSAIQLPKELSMVVKGRDQVSGLLSRIELTSEDVREAMREYLKEIADALKMVLEMMPP

DLASDIVENGVVLTGGGALIRGLDKYLSEIVRLPVYIADEPLLAVAKGTGKALEEISLLQQLTNEE

>ABV51851.1 ATP-dependent clp protease ATP-binding subunit clpX [Campylobacter jejuni subsp. jejuni 81116]

MPRKCSFCNEVENPQRRILANENDDAFICEYCVEGAYSIIYGEEKEFKEPKQSHNTEFKDITPKELKAYL

DRYVIGQDRAKKVFSVGVYNHYKRLFKAELQDDDTELFKSNILLVGPTGSGKTLLAQTLAKFLDVPIAIC

DATSLTEAGYVGEDVENILTRLLQAADGDVQRAQKGIVFIDEIDKIARMSENRSITRDVSGEGVQQALLK

IIEGSLVNIPPKGGRKHPNQEFIQIDTSNILFVCGGAFDGLETILKRKLGDKVVGFFDDAKEENKALLEK

IEPDDLVHFGLIPELIGRLHVIASLNELNEEDMVRILTEPKNAIIKQYQKLFAIDGVNLKFEEDALRAIA

QLALERKTGARGLRSIIEEMMVDLMFELPEYKNYDIVITKEVVKDNAKALLIKRKIS

>ABV51850.1 UDP-N-acetylglucosamine acyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKKIHPSAVIEEGAQLGDDVVIEAYAYVGKDTKIGNDVVIKQGARILSDTTIGDHSRVFSYAIVGDIPQD

ISYKEEQKSGVVIGKNATIREFATINSGTAKGDGFTRIGDNAFIMAYCHIAHDCLLGNNIILANNATLAG

HVELGDFTVVGGLTPIHQFVKVGEGCMIAGASALSQDIVPFCLAEGNRASIRSLNLVGIRRRFDKDEVDR

LSRAFKTLFRQGDLKENAKNLLENQESENVKKMCHFILETKRGIPVYRGKNNA

>ABV51849.1 (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase [Campylobacter jejuni subsp. jejuni 81116]

MIDVMQIQEILPHRYPFLLVDKITELKVKEVVLGYKNISISDHVFMGHFPGHPIYPGVLILEGMAQTGGV

LAFESMEDKVDPKSKVVYFTGIDGAKFRNPVRPGDRLDYEMSVVKNRGNMWIFKGQAFVDGNLVAEAELK

AMIVDK

>ABV51848.1 hypothetical protein C8J\_0249 [Campylobacter jejuni subsp. jejuni 81116]

MLVHICCSVDSHYFIEELRKTYPDEKIIGYFYDPNIHPLSEYELRFLDVKRSCDKLGIKLYKGEYEYEKW

LNAVRGYEDEPEKGARCEICFDVRMGSSVKFAAKIGEKKLTTTLLTSPKKDLEQLKNALQKECEPYGVEF

LAPDFRKNGGTQRQFALAKKEMLYHQNYCGCIYGLKKQKQDKNFIDELMSSVNKQILPASIEARIALYKK

VVLWEKKGIKFEILREKFLNYRLLSALIKLDKKPVKSHILFYSHFKNAYTRFSLDEESLKQNLKEGFYRS

TKDEMVFVEFWRFNAFFKNKWKNFEDFLKKPLSIQAEVRWRNQVFGAYNLSPVIILEEIFPSRYEVIAKS

EIYHDNQEVLAKI

>ABV51847.1 antioxidant, AhpC/Tsa family [Campylobacter jejuni subsp. jejuni 81116]

MSLNIGDKAPQFELLNQDGVKIALKDFIGKKVILYFYPKDNTPGCTTEACDFSANYDKFGGKNAVIIGIS

PDSVTSHEKFISKFNLKHILLSDSEKEVAKAYRAWGLKKNYGKEYEGIIRSTFVIDETGKIAQIYSNVRV

KDHALKVLESL

>ABV51846.1 possible isomserase [Campylobacter jejuni subsp. jejuni 81116]

MPLVNIKLAKPSLSKEQKAELIADITELLSTKYNKSKERVVVVLEDVENYDIGFGGESVEAIKAKANK

>ABV51845.1 branched-chain amino acid aminotransferase [Campylobacter jejuni subsp. jejuni 81116]

MISADKIWMDGKLVDFKDATLHFLTHSLHYGNAVFEGTRAYKTDKGLAIFRLEDHTKRLLESAKITLLNC

PFSQKDLENAQIELLKANNFQSNVYIRPLIFLGDGVMGLYHIKAPVRVGIAAWEWGAYLGEEGLEKGIKV

KISSFARNSVKSCMGKAKASANYLNSQIAKFEAIEAGYEEALMLDEEGFIAEGTGECFFIVKDGVLITPP

NDFSLKSITQDTVLKIAHDLGITVLRQRISRDEVYTADEAFFTGTAAEITPINNIDARIIGNGLRGSVTK

KLQDAYFDVVYGRNEKYASMLTYI

>ABV51844.1 putative transmembrane protein [Campylobacter jejuni subsp. jejuni 81116]

MPADLNDYFNKKNGNSNNNGNNNRQNFNFKAPEFNFKGFGKFSPFVYGVIIIILFLIVAKPFMVINSGEM

GIKSTTGKYDPNPLEPGLHFFLPFVQKITIIDTRVRQINYASIEGSNENLSSGSGVINKNSISVLDSRGL

PVSIDVTVQYRLNPLQVPQTIATWSLNWENKIIDPVVRDVVRSVVGKYTAEELPTNRNTIAAQIEEGIRK

TIEAQPNEPVELRAVQLREIILPSKVKEQIERVQIAKQEAERTKYEVERANQEALKKAALAEGEANATII

SAKGKAMAVKIEADAQAYSNKEIANSLNTPLLNLKQIETQKEFNEALKVNQDAKIFLTPGGAVPNIWVDT

KDAKKQSAANMN

>ABV51843.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MEKLREIVLFYTTHLYLVDYMLILLVFFLFTCVLLLCVFLRHRPIAALFIIAFDIIICFLVYIYGYKLID

NEVRTRKTAITDQKMIQSSNDLIVDFNITNNSKNNFKECKITAKIFADKIPNDNIIEEYKKKFIPFRQKS

REIKDLKKNATQVQRIAFENFNYENNYTIRLVSECF

>ABV51842.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MHFTIFHIIAFIILLICFALICILIFLKVKQKEMALISYTIATIFTALLIYSIFLTINQFTTQADLSKLT

YTRDLRHESVIVSGKVQNLTKFEIRKCYLMLSILNQKQVGGEIFNDKNVRNAKMQNTSVSYTIEIIDTLP

GNTYKEFRASVPFPPSFNNPEFYHTLKCI

>ABV51841.1 putative cytochrome C-type haem-binding periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIFISFVVLATCLWAKNIAYTDEVVSLYLNKDDTKVIGRLLPTNPFEVLKSENNKVLLKIDGYVNPKA

LSVIYFNDSQRIIVAAFSKNTKLNFSQRVAGKDGKWDKVSLEIWADKKEFAKDNKEMLNRAKELFVNNCG

ICHAIHKEKEFTANAWPAIFRSMADRTGIDKKDRWLVIEYLQKNAKDFKTK

>ABV51840.1 hypothetical protein C8J\_0241 [Campylobacter jejuni subsp. jejuni 81116]

MLDRRKFLKIGASLSALPLIPSLSAGKTVEASKVSLGLVKNGEVITAAHWGILKLTIKDGKIVKSEPWEK

VTKMDNPLQHYTADMVYKSRVKYPYVRKSYLENPDNPKPELRGKDEFVRVSYDEAIKLIAKELKKTRDSK

GASAIFGGSYGWKSSGNMQNSRILLHRFLNVTGGFVGATGDYSTGASQVIMPYVVGSIEVYEQQTSWENI

LSDSKYVVIWGADPLSTLRIAWTSNEQRGLAYFEKLKNSKIKVICIDPVKTTTAKFLNAKWIAPRPNTDV

ALMMGMASHLIAKKKVNYEFLDTYTTGFDKFKDYLEGKEDGVKKDTKWASKICGIDEKTIKNLAETFYDN

PTMIMSGWGMQRAHHGEQPHWMLVTLCAMLGQIGTKGGGFGLSYHYSNGGVPTCKGGVIGGMTAGSLGIW

KNGKFKGLSKAEASSEGAEWLQNAASYSFPVARIADALLHPGKTIDHNGAKITYPDIDFIYWVGGNPLVH

HQDTNTNVKAWRKPRTVVVNEIYWTPTAKMADIIMPVTSSYERDDITMTGDYSNMHIAPMKQAVEPVGES

KDDYVIFSDICKIYGKDVFNAYTENGKKAKDFIKEYYNSALKQTQSFGEAFATPMPSFEEFWAKNEPITF

EPTAESLEWTRFSEFIEDPILNALGTDSGLIEIYSETIKNYNYDDCKAHPTWFEPIEWLGNASKEAPFHL

LTNHPRDRLHSQLCHTSLRDTYAIKDREPILINSKDAKKLGIKNGDVVRVFNKRGEVLAGAVVSDEIMQG

VVRLCEGAWYDPNENGLCKCGNANVLTMDIPTSKLANGNISHTGLVNIEKFKGELPKLTAFSAPKGAN

>ABV51839.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MQFTFEQIFIAMLLTLFAGFSTAIGSIIAFFSRKDDLRVLSLGLGFSAGVMIYISFMEILPTALKDFKNH

YDSHWAELLGLACFFGGILISLLIDKLIPEDVNPHEPKEDLSELKICPLPQKGQNPPKFHPGEKLHQINT

KALKRTGIFTALAIAIHNFPEGFATFISSLDNLTLGIAIAIAVAIHNIPEGLAVSLPIYHATGDKKKAFI

YSALSGFAEPLGAFVGALILLPFIGDLTLAISFAVIAGIMVFISLDELLPAAKTYDKAHDSLYGLIAGMA

IMALSLNLLGQ

>ABV51838.1 putative methyl-accepting chemotaxis signal transduction protein [Campylobacter jejuni subsp. jejuni 81116]

MQSINSGKSVGISAKLTLWVGILVVLILAITSAISYFDSRNNTYELLKDTQLKTMQDVDAFFKSYAMSKR

NGIQILANELTNRPDMSDEELINLIKVIKKVNDYDLVYVGFDNTGKNYQSDDQILDLSKGYDTKNRPWYK

AAKEAKKLIVTEPYKSAASGEVGLTYAAPFYDRNGNFRGVVGGDYDLANFSTNVLTVGKSDNTFTEVLDS

EGTILFNDEVAKILTKTELSINIANAIKANPALIDPRNQDTLFTAKDHQGVDYAIMCNSAFNPLFRICTI

TENKVYTEAVNSILMKQVIVGIIAIIIALILIRFLISRSLSPLAAIQTGLTSFFDFINYKTKNVSTIEVK

SNDEFGQISNAINENILATKRGLEQDNQAVKESVQTVSVVEGGNLTARITANPRNPQLIELKNVLNKLLD

VLQARVGSDMNAIHKIFEEYKSLDFRNKLENAGGSVELTTNALGDEIVKMLKQSSDFANALANESGKLQT

AVQSLTTSSNSQAQSLEETAAALEEITSSMQNVSVKTSDVITQSEEIKNVTGIIGDIADQINLLALNAAI

EAARAGEHGRGFAVVADEVRKLAERTQKSLSEIEANTNLLVQSINDMAESIKEQTAGITQINDSVAQIDQ

TTKDNVEIANESAIISSTVSDIANNILEDVKKKRF

>ABV51837.1 hypothetical protein C8J\_0238 [Campylobacter jejuni subsp. jejuni 81116]

MNLWDKKAKTYARYQNTLNTIQKQTFEYLQNLNISFQNKSIIDIGCGTGVWTLHLAKEAKEILALDSANT

MLEILQEDAKKLNLNNIKCENLSFETWMQNNPNVKFDLAFLSMSPALQNEKDYTNFLNLAKIKIYLGWAD

YRKSDFLDPIFKYFNTEFKGFYKKDLENYLLEKNIFFHKIVFDETRKVQRTKEEAIENALWHLSMNKITT

SKEAVSSFVENDIIETIESKIKLLIINNL

>ABV51836.1 hypothetical protein C8J\_0237 [Campylobacter jejuni subsp. jejuni 81116]

MVKNLIIKFGRLILDAIAAISFVVALLYSLFMMFSIGFLAGLLSLIVSFIALFLSFFVIYLVIDIRDALV

NKA

>ABV51835.1 dihydroorotase [Campylobacter jejuni subsp. jejuni 81116]

MILKNPLDMHLHLRDNQMLELIAPLSVRDFCAAVIMPNLIPPLCNLEDLKAYKMRILKACKDENFTPLMT

LFFKNYDEKFLYSAKDEIFGIKLYPVGITTNSNGGVSSFDIEYLKPTLEAMSDLNIPLLVHGETNDFVMD

RESNFAKIYEKLAKHFPRLKIVMEHITTKTLCELLKDYENLYATITLHHLIITLDDVIGGKMNPHLFCKP

IAKRYEDKEALCELAFSGYEKVMFGSDSAPHPRDTKECCGCAAGIFSAPVILPVLAELFKQNSSEENLQK

FLSDNACKIYDLKFKEDKILTLEEKEWQVPNVYEDKYNQVVPYMAGEILKFQLKH

>ABV51834.1 putative helix-turn-helix motif protein [Campylobacter jejuni subsp. jejuni 81116]

MKFENLIREILGKKRFELLKFLCENADENGFIMIKISDLEEKLHQSKPTIIATFKFLEEKKLFKRLKNGF

YQLNIGGKNDT

>ABV51833.1 diacylglycerol kinase [Campylobacter jejuni subsp. jejuni 81116]

MKPKYHFLNNARYALEGLFALFKNEMAFRIELCIIIPAIVFSFFLKVSFLEHLLLISVLILILIVEALNS

AIEACVDLITNKWHEKAKIAKDCASAAVFFSVLLALFVWGFILYSIYL

>ABV51832.1 sulfatase, putative [Campylobacter jejuni subsp. jejuni 81116]

MLRLTWLQFTFFNSLMIVLLNFNLFYFVYEKNTQNWFITFVFIVAYFALVHVICSLLFIKFFTKFFSILF

IISSFLSVYFISFYGVLIDSDMIQNVVQTDIKEVKDLLNLKLILFIVLALLLVFYVVKVKIDYYDSFKSH

LKIKIINIISGLIVVCAVLIPLSKTFLPFFRNYNEIRMYNTPFYQIYAVYRYYIRFVKAKPEFKTIANDA

YRENNHTKKLLVLVVGETARAANYSLGGYTKNDTNFYTKKDNVVFFDNFSSCGTATAVSLPCMFSISKRE

NYSSSEFQENAMDVLYKTGVDTAWFDNNSGGCKGVCDRLAYKQKLSSDLDENLLAPFKEKLNHLSDQNII

VLHLQGSHGPTYYKRYPSEFKKFTPTCDTNELSKCDNKALINTYDNTLLYTDYLLSEIIKLLKEQKSYES

SLFYLSDHGESLGENDIYLHGMPYAIAPSYQTHIPAIFWSNDENLMNLAKEHKGLKLSQDNLFSTLLGYF

DVKTSVYEPEYDLLNPKLKANP

>ABV51831.1 exodeoxyribonuclease III [Campylobacter jejuni subsp. jejuni 81116]

MKLLSWNVNGLRAICDKNALDWIAQEQIDFIGFQEIKAHEDKFPKKIYEYPFKHMYFNSAKRAGYSGVMS

LCNFDSEVKKCEFFDDEEGRVLEHRFKNIALFNIYFPNGQKDEERLNFKMKFYADFLVYLDKLLKDGFEI

IICGDVNTAHKEIDLTHPKANANTSGFLPIERAWIDDLLKLGFIDTFREINGEIKEKYSWWSYRMKARER

NVGWRIDYFFISKGLKDKLKNAFIRDDIFGSDHAPVGIEIDI

>ABV51830.1 hypothetical protein C8J\_0231 [Campylobacter jejuni subsp. jejuni 81116]

MKNTLIIFENSLSNLSKDEASDLLEDLSFNLAYKQISHNPHETKKVLNSLLVEFLTILKKLDFFDDENVT

KVIKALVKASIVDAQNSLYEYISEAELLNKQIENQKNLIKNQISDNFFEFENILQECSFCDEFSGGLNDA

ILFDIEMLGILKETAESAFLTTLEKAEDIELTSSEIAKNLVYNAICEAHFEKERILKISSIILNTAFEIA

NESMAYAKDLCLGVIKGTRDGIVLAMEKFKASLTYANFEEDVSLKSKELIGIEDDFIALLKKEIQLQNDP

CKSIVENLLEHELDNLFAKFRRLAGESREQLILVLNDIKKNPKINDFNKLTQRKLNRFKQEIFELEKIAS

EKYKDLNSKKAKKLGVRLWEKAKKFVKK

>ABV51829.1 hypothetical protein C8J\_0230 [Campylobacter jejuni subsp. jejuni 81116]

MVNLCDLKKEPQINYPTFWDYKVIFEVHVKASEIFQEILGQREYKFEHSNSSASGKYQSYLLNVYVDSKK

DRLDIFDKLKAKAKFVL

>ABV51828.1 molybdenum cofactor biosynthesis protein MoaC [Campylobacter jejuni subsp. jejuni 81116]

MKLSHLDEKNHPKMVDVSDKNITSRIATASGMIYMSQEAFDVIKNNTAKKGPVLQTAIIAAIMGAKKTSE

IIPMCHPLMLSKVETDIMEFVKECAFKLIVTVKCEGKTGVEMEALSGVSIGLLTIYDMIKAIDKSMRITD

ILLESKEGGKSGKFVRS

>ABV51827.1 hypothetical protein C8J\_0228 [Campylobacter jejuni subsp. jejuni 81116]

MAYEDEEDLNYDDYENEDEEYPQNHHKNYNYDDDDYEYDDDNNDDDFYEMD

>ABV51826.1 putative transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MSKTLNQKDIKVLGLSSLGGTLEFYDFIIFVFFANYISTNFFPKDLSSFWQMFNTYGIFAAGYLARPLGG

VILAHFGDKFGRKRMFMISILLMVIPTFTLAFIPNYESIGFLCIVLLVFIRICQGIAIGGELPGAWVFVY

EHAPQGQKRTYLGILTASVVGGILLGSLVFLIMNKIYTQEELHEWAWRIPFFLGGIFGIISAYLRKFLRE

TPVFEQMKKDKALEKFPLKEVFKKAKMGIVLSMMITWVLTGCIVVMILLMPSYMAKILQINTSIQTYLQI

GGILLICLGCIISGILADKIGIIKSCVFFSVFFGIVSLLYFNTLYRQNADFNLVACLYLLVCFFSGVMNF

CPLIMSEVFDAKIKFSGLSFSYNIAYAIAGGLTPQLAFFLHSFALDNLSNFWRFSLGIYVFFLAIIALLC

AFIFSYLNNTQRTYSQ

>ABV51825.1 hypothetical protein C8J\_0226 [Campylobacter jejuni subsp. jejuni 81116]

MKSLILPPNEFLDHYILNAEFHRFAGISKNAYKFWKNVEIGRYQGTRIIFLHRNCILEKHQQALRQCSGL

NGFVLASAFCSFTGLAPSHLVEKNNSSIYKLLELKEICGIKFVNLKKFYDFLGLNYHQHIYIEKCHFFSP

APFEKRIKITESMCVGYY

>ABV51824.1 hypothetical protein C8J\_0225 [Campylobacter jejuni subsp. jejuni 81116]

MIGDMNELLLKSVEVLPPLPDTVSKLRKYVSEANSNIETMKVAEIISSDPLMTAKLLQLANSPYYGFTRE

ITTINQVITLLGIGNIINIVTADSIRDSFKIDVSPYGLDTQNFLKTCNEEATFITNWLNDEDKKLSHLLV

PCAMLLRLGIVIFSNFLIQNHKDKDFLAFLNKNENLALAENEFLGVDHISFLGFLLHRWNFDDVLIESIC

FVRTPHAAREEVKKSAYALAITDHLFAPHDGSSPFNAKAAVALLEEAKTQGINFDLNNLLSKLPSKAKEN

LNKED

>ABV51823.1 hypothetical protein C8J\_0224 [Campylobacter jejuni subsp. jejuni 81116]

MFFNFKNKSSAQKEESKKVLEALFLQENELEEKLKKINIKPKLIIGFASYQLNLAIIGNKIQNSINEQCD

IILSNATDLLCNLDSNSNIENSPYKQNIQGISLMLFSEDMIENLCTNKIKLFSNIKDYTERKKLIEKEVL

SINIPFEAHCTNTLHYLIYDGLSQSESSLLELLYKHNLYPCALVGGGSSGNMDFSGTFIFYNGEILKNQA

LSIHVQFKSKYRFDLMKSQNFNPQSNITFTILDASLYDRTVREFIDKKTFQSINAVEALCNYFNCTFEEL

KNKMQEYTFALKIGEDYLISPMEINPDKTLFSYCDIESAQELSLLKKQILLKP

>ABV51822.1 hypothetical protein C8J\_0223 [Campylobacter jejuni subsp. jejuni 81116]

MGIAKSLVAIFFYEVENFNDFKPRYLKTFIQKYSDFKYYYLNIRAQKLEMTNEINKIILNQLKQNTSEID

KNTSIFKEIFEELENIRRSLTTISESFTNFTNYLEYNLYQSEEKMNLEKEVQSSLKNIDQLNSILDLISG

IAEQTSLLSLNAGIDAARAGKLGRGFAVIADEVRKLSENTQMGLGEMEGAIKLVIQTIQSIAKSSNSSTQ

EMNFIRDKSNEFSKIISNLINSGKEISDKLKQRSNVGEDFEKNVNQLKCYEDVLAKLNQY

>ABV51821.1 hypothetical protein C8J\_0222 [Campylobacter jejuni subsp. jejuni 81116]

MARVKTGVVRRRRHKKVLKLARGFYSGRRKHFRKAKEQLERSLVYAYRDRRRKKRDFRRLWIVRINAACR

LNDLSYSRFINGLKKAGIELDRKILADLAMNDSAAFAKIAEAAKKAL

>ABV51820.1 ribosomal protein L35 [Campylobacter jejuni subsp. jejuni 81116]

MPKMKSVKSAVKRFKVGKNKIKRGSAFRSHILTKKPAKRMRDLRTAKYVHSTNVKAVEKMLGI

>ABV51819.1 hypothetical protein C8J\_0220 [Campylobacter jejuni subsp. jejuni 81116]

MTINSANPYQNLTLSNPLQNSSALNLIKDSKALDQEGNENSLEQLSYIFNNTTYASEFGFRINEEGFFDK

DLNKIANIPESYDINIKSVRSIAKELAKQDENLNYNKIDLPYLLNSYHSSLKSINSEFLQDDNAYLSRDL

ISKLSSGFSTDNGEFLGQISRIYNNQEEIDLALSNIANLNTLMLDNKITNFHFDKAIENTSSNEILKPYL

TKNAEVSKSGLLMNFIYHDIKTQNEKEFNFFMKPATLELSSHQNLQKILKGETDIEDYIKKENEKKMSFD

LYLYVNGVDKKTSTQDKLSVFFQQYINYQKDMDLREFANSSSIFQIYIDQNRNDFDALKKQYQNQSQDTQ

RLEEANQLRSSSIENFLDRRQKQANINKILNSYMSVMV

>ABV51818.1 putative iron-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MTYNEKIISMNNDLLDHQHKELFEISKKLSLMNQRHVGTKELKIVLRELLIMINRHFSDEEAFMREIEYP

YINHHTRIHRKIILEIEEIIISEAKFVNIMTEKLNLVVQDFIFKHTAKEDSKIVKYYEEKFKK

>ABV51817.1 putative aminotransferase (nifS-like protein) [Campylobacter jejuni subsp. jejuni 81116]

MKVYLDNNATTMLDPNAYELMLPFLKDMYGNPNSLHQYGSATHPALREALDKLYAGLGANDLDDIVVTSC

ATESINWVLKGVYFDHILDKERNEVIISSVEHPAVAAAAYFLKSLGVKVIELPVNEEGVSTVEDLRKVIS

DKTALVSVMWANNETGMIFDIKAMAELAHEFGALFHTDATQAVGKIKVNLTQVGVDFASFSAHKFHGPKG

VGGLFIKKGLKLTPLLHGGEHMGGRRSGTLNVPYIVAMGEALRIANTMLDFEDSHIRRLRDKLEDQILAL

PDTTVVGKREHRVPNTILASIKGVEGEAMLWDLNKNGIAASTGSACASEALESNPIMEAIGAEHDLAHTA

LRLSLSRFNTEEEIDYAAKQIKNATQRLRAISCTYAYNPNNYK

>ABV51816.1 nifU-like protein [Campylobacter jejuni subsp. jejuni 81116]

MGKNSLIGGSIWDEYSQKVQDRMNNPQHMGEFSEEDAKARNAKLIVADFGAESCGDAVRLFWLVDEKTDK

IIDAKFKSFGCGTAIASSDTMVDLCIGKTVDEAVKITNLDVEFAMRDNPETPAVPPQKMHCSVMAYDVIK

QAAAHYKGISPEDFEDQIIVCECARVSLGTIKEVIKLNDLHSVEEITQYTKAGAFCKSCIKPGGHEKRDY

YLVDILAETRAEIDREKLKNTMKSDVAFDEMTVVGQLKAVESVLDAEIRPMLHNDGGDLEVIDIQKAEGA

AIDVYIRYLGACSGCSSGSGATLYAIETILQEELSPNIRVMPV

>ABV51815.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIIFSLCFFILYLGAQEFKFIDANISKEDEGIYALVEKYVDLNNQIKEFKKNNDENSSTFNGILSEFE

KDKKTILAKIPDMIVGQKINEEAVARFLKAKEKLLDVQKKNINKPYIYTDATLNLVYFNIVESFYSSLFE

VEKLFKNTASSEDLIATVDKAMENLQNSSNVNLDSFKSKITNPEELEKITLKERYISNAVDSYSEILKYL

RSNADLLESNYIFSLLELQVWIDRINEAIGVSFVNIGKIVISALVLVFFISLRRFFANIVYFFLVQLFYR

NKNDVDDIKVIFIENIKKPVGFLLIVYAISLCLTIATYPAPLSVNLSNFFHIVYAVLIAWLILRMLDGYG

VVLVSKLAQKSGKKEVVNLIIKILYFVIIIIALLYILAQLGFNISAIIASLGIGGLAVALAAKDIIANFF

ASILLLFDNSFNQGDWVEVSGIEGTVVETGLRKTTIRTFDNCLVFLPNSTIMGANIKNWSKRRMGRHVRM

YLGVGYDATPEKLEQCVKDLREFLHTSDLVAHDEDSALKYGDHTTKYRQNLVSINDLEGYKNACYVALSE

FADSSINIELYFYTKEIGGKDFREARQSLMLEFMRIIEKNGLTFAFPSRSIYIENLPPLDLQAKAIK

>ABV51814.1 carbonic anyhydrase [Campylobacter jejuni subsp. jejuni 81116]

MENLISGAIKFMQEDFKEHEELFESLKNKQNPHTLFIGCSDSRVIPNLITNTGPGELFVIRNIANIVPPY

RVGEDYLATTSAIEYALNSLHIKNIVVCGHSNCGGCNALYYSDEELNKIPNVKKWLTMLDPIKKDVMIFA

RDDLAMRSWLTEKLNLVNSLQNILTYPGVQEALDEGKIEVHAWYYIIETGEIYEYDFKAKIFTLIQDRKV

Q

>ABV51813.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MSLYDRDYSRSKEFENTRSSELSIFIKQTYQLFAASLLAATVGAYVGIFALASFFIQSQVTFWILFAVEI

GLLFALQWKKREAPLNLVLLFGFTFCSGLTLTPLLISVLALPAGGIIIAQAFALTTVAFAGLSVFAMNTK

KDFTVMGKALFIVLIVIVAASLLNLFFQSSIVNLAISAVAAILFSFYILYDTQNIIRGNYETPIEGAVAL

YLDFVNLFVSLLNILRSFNSR

>ABV51812.1 protein-export membrane protein secG [Campylobacter jejuni subsp. jejuni 81116]

MITLLIILQFIIVVVICIAVLLQKSSSIGLGAYSGSNESLFGAKGPAGFLAKFTFVMGILLIANTIGLGY

LYNKASKDSLAEKIKVENNNTTIPSAPIVPTTPNTNSIAPSAPQLPSDVNSSK

>ABV51811.1 ribosome recycling factor [Campylobacter jejuni subsp. jejuni 81116]

MLNEIFNKQKTQSEKSLEALKKDFTTLRTGKVNTHILDHITVDYYGTQTPLNQVATVLASDASTISITPW

EKPLLKTIESAIAAANIGVNPNNDGESVKLFFPPMTREQREENVKQAKAMGEKAKVSIRNIRKDANDAVK

KLEKDKAISEDEAKKAYDEVQKLTDTYTTKIDESVKSKESELLKV

>ABV51810.1 putative orotate phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MNLEQIYKDCGAYLEGHFLLSSGKHSQFYLQSAKVLEDPKLAAKLCDELAKIIASYKIEFDSICSPALGG

ILAGYELARACSKRFIFTERVNKEMTLRRGFEVKKGEKFIICEDIITTGGSALESAKIIESLGGIIVGFA

ALANRGFCAVENLKSPRKDNAKLPENLPLFTLGNFEFEIYDETNCPLCKKGSKAIKPGSRGN

>ABV51809.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKTKAKISSRWLRFRALLIDIFLIYVPILYLFYFLLGSKEAFLNNHFITTLCTFLFGLIQAIFLTKKAQS

PGLKAYDLYLIDIKTGKKLSFLRILLRYVIFIISFGLLFGLFVSFIRKDRLNLHDILTQSCIATKA

>ABV51808.1 ribonucleoside-diphosphate reductase beta chain [Campylobacter jejuni subsp. jejuni 81116]

MQRKRIYNPSSNETLGDRKVFDGNPHGILNFTKAKYTWALKLWDLMEANTWFPKEVDTTKDALDYRCNLT

AGEKRMYDLVWSQLISMDSFQTNNLADNINPYITAPEINAVLARQAYEEANHSKSYAVMVEAICDNTDLI

YEMEKHDETLREKNDFISSIYEELAGDVDDNKLLLAMVANQILEGVYFYSGFTAIYALARAGKMLGSAQM

IRFIQRDEITHLLLFQNMINSVRKERPDLFHDENINKIYDMFKKAGDLEIKWGKYITQNQIMGFTDDIIE

EYIHYLVDQRLSAINLDKLYNAKHPIKWVDDFSKFNDQKSNFFESKVTNYSKGSISFDDF

>ABV51807.1 putative nicotinate phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MMISKTSLALLCDFYEFTMSQGYFKNNKKDQICYFDIFFRKIPDSGSFAIFAGLEDILDFVENLSFDTED

IEFLRKQGIFDTEFLDFLSSFKFKGEIYAMREGEVIFPNEPLLCVKATTIEAQLLETFLLLSLNHQSLIA

TKTNRIVRAAKDSKILEFGSRRAQGSEAALKGARAAFIGGCIGSACTLAGKIYNIPINGTMAHSWVQMFE

NELEAFKAYVKIYPKNPVFLIDTYDCLNSGLKNAIKVFKEFGIQEGGVRIDSGNLLELSLKIRQELDQAG

LQKCKIIVSNALDEWSIKKLKEQNAPIDIFGVGERLITASSDPIFSCVYKLAALEDQGIKPKIKISENNE

KSTLPHFKKLFRVYDKNTQKILFDELYVFDENPNQDENLERKELLELVYKEKRLLKKSSLNTIQDYTKEQ

ISKLDESFLDLDRFVKFEVKLSPKLQNITEDLLKTRF

>ABV51806.1 putative acetyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MLIKFKNHSPKLGQNVFVAEGAKIIGEIEIGDESSIWFNCVLRADVNFIKIGKRTNIQDLSTVHVWHREF

DEKGKLKDAGFPTIIGDDVTIGHNCVIHACVIKNRVLIGMNAVIMDNALIEEDSIVGAGSVVTKGKKFPP

RSLILGNPAKFVRELNDEEVSFLKQSALNYVDFKNEFLKDLQ

>ABV51805.1 protein-L-isoaspartate O-methyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MNAFEQKRCQNMAEEIAQKVFINEELFNAFCQIPREIFSPLKAHAYRLDALPLANSQWISSPLTVAKMTM

ALDFKNADSILEIGCGSGYQAAILSKVIRRVFTIERIENLAKKAAQTFRELELFNINVKFDDGQNGWKNY

APYDRILFSAYATQIPEILLDQLSDDGILVAPILHNGKQFITRLRKNGTNLQKEILEECLFVPIVDGKE

>ABV51804.1 acetylornithine aminotransferase [Campylobacter jejuni subsp. jejuni 81116]

MKMDYKEQSHIIPTYKRFDIVLEKGQGVYLFDDKAKKYLDFSSGIGVCALGYNHAKFNAKIKAQVDKLLH

TSNLYYNENIAAAAKNLAKASALERVFFTNSGTESIEGAMKTARKYAFNKGIKGGQFIAFKHSFHGRTLG

ALSLTANEKYQKPFKPLISGVKFAKYNDISSVEKLVNEKTCAIILESVQGEGGINPANKDFYKALRKLCD

EKDILLIADEIQCGMGRSGKFFAYEHAQILPDIMTSAKALGCGLSVGAFVINQKVASNSLEAGDHGSTYG

GNPLVCAGVNAVFEIFKEEKILENVNKLTPYLEQSLDELIKEFDFCKKRKGLGFMQGLSLDKNVKVAKVI

QKCQENALLLISCGENDLRFLPPLILQKEHIDEMSEKLRKALKSF

>ABV51803.1 acetylglutamate kinase [Campylobacter jejuni subsp. jejuni 81116]

MQKYLEKANVLIEALPYIRKFNSKIILIKYGGSAMENEELKHCVMQDIALLKLVGLKPIIVHGGGKDISA

MCEKLGVKSEFKNGLRVSDKATTEVASMVLNHINKNLVHSLQNLGVKAIGLCGKDGALLECVKKDENLAF

VGTIQKVNSKILEELLEKDFLPIITPIGMDENFNTYNINADDAACSIAKALRAEKLAFLTDTAGLYEDFN

DKNSLISKISLEQAKILAPKIEGGMHVKLKSCIDACENGVKKVHILDGRVKHSLLLEFFTDEGIGTLVG

>ABV51802.1 acetyltransferase, GNAT family [Campylobacter jejuni subsp. jejuni 81116]

MLIRAMQKSDYEAVYKLWCEIKGFGIRSIDDSKENIENFLDRNPDLSVVAVLGEEIVGSILCGHDGRTGG

FYHVCVHKDHRKKGIAHEMTKFCLEALKAQKINKIALIAFKNNDLGNEFWKHYGFTLREDANYYDLSLNE

YNQTSFNA

>ABV51801.1 N-acetyl-gamma-glutamyl-phosphate reductase [Campylobacter jejuni subsp. jejuni 81116]

MKIKVGILGASGYAGNELVRILLNHPKVEISYLGSSSSVGQNYQDLYPNTPLNLCFENKNLDELELDLLF

LATPHEFSAKLLNENLLKKMKIIDLSADFRLKNPKDYELWYKFTHPNQELLQNAVYGLCELYKEEIKKAS

LVANPGCYTTCSILSLYPLFKEKIIDFNSVIIDAKSGVSGAGRSAKVENLFCEVNENIKAYGLASHRHTP

EIEEHLSYAAKEKITLQFTPHLVPMQRGILISAYANLKEDLQEQDIRDIYTKYYQNNKFIRLLPPQSLPQ

TRWVKSSNFADINFSVDQRTKRVIVLGAIDNLIKGAAGQAVQNMNLMFDFDEDEGLKFFANL

>ABV51800.1 hypothetical protein C8J\_0201 [Campylobacter jejuni subsp. jejuni 81116]

MEQGFSIYTPNVVFSYNEENFAQWNLEKIDSKTKDEYFFTNDNTQAIAKAKSILAQATLGSMIEWNNMHK

RMGELRNNPYESGVWLRTFGGGTSDEYNSGKYFEIQSGYDKLNEYSNFELYSGVMINYTNMNLSATDLSA

KLNGYGIGQYFSLLFNEGFYSDFVLRYIYHQNEVNANFIPGNQGRLDDNDGSHNIILSAELGYRKNYDKF

YLEPSLEFISGYVGAMDLKGDIASLKRSSYIPLVAKTAFFIGSQNQNLNFRTGLGLYADLIKTGDQILED

QASQRRYEGKKDQRMFINLGSDYKLNDKTRFSFEFEKTFFGDLNVDWSVNANLRYSF

>ABV51799.1 hypothetical protein C8J\_0200 [Campylobacter jejuni subsp. jejuni 81116]

MWIDEKDGENITDKVQDSFYGDVAQTGVGKEMGFEQNLKNTQNAKIEKVYFSGNLNLDHSDATLQNIVFS

GNIKGVDDAQKNLVIKDSLLESNIQMSNIQAEKSAIYGKVDAKKLSANNTIFKINVDFEKSKADYINSKE

SAQGTNNTLVLNFLTILAKKRV

>ABV51798.1 hypothetical protein C8J\_0199 [Campylobacter jejuni subsp. jejuni 81116]

MIFDGNIYNKEGVFKAENAKLNFQGHARIHAYVSEEQAKKLQEQGLSALTKPVSFTQEDWEDRVFCFKRA

>ABV51797.1 hypothetical protein C8J\_0198 [Campylobacter jejuni subsp. jejuni 81116]

MKLKLSFCALMAFGFSNYLFASAIDPKFYFQEYLDFASNKGKFQVGQIGFEILAKNPNQNISFNVPMIDF

STSNRGGKFQGEFTNIGQSYIVSASHMSTSSNTGEVNKGYVKQGSVLHFGGVANRIVSSSDNFTYKKENV

DFAVLKMSKINLNKSANLSKDFNFIEKDSGDGGDIYEYKDPFWDSCQSGKCDYSKGKGKLFDSSRYEYFV

REGSGIVALGFEDTNKVPIKIFDSNEINLGGFVSLAPKNTEDKRFKLQFLNYTNDKRNPFTSSSTPGDSG

SGVYVYDKIDKKWYLVGVVSTSNCNAHFTDGYTCSQVDYALINQAKINEFQNSHRVNIAQGVYTLSNQGL

MKEGQLVQGVSLISGANAGYVSYENIFGDKAKYDDRIKEMQNSKDLYFFQNGSINLNSDVDLGASVLNFE

QNSNWQITGDKWLIHGGIYADKGSSIEYNVKTKKDDFLYKMGEGELIVKSQSADAGLRMGEGKVSLEGEG

LSFGEIYMNGGTLGFKNAQNLKTDTLYMNGGTLDLSGLTLNF

>ABV51796.1 DNA modification methylase (adenine-specific methyltransferase) [Campylobacter jejuni subsp. jejuni 81116]

MKENPSFLKEQIITYLGNKRALLSFLNKGFKVAKKELGKDKFSFCDIFSGSGVVSRFAKAHSNYILANDL

EDYSKLINECYLANKDKDLLQNIKKHYKNLIQNLDFQKGFISELYAPKDDDDIKKNERVFYTFKNALYLD

TIRQKIENEIPKELRHFFIAPLIYEASVHSNTSGVFKGFYKGKDGIGKFGGEGQNALKRIKGEIELKMPI

FSNFSCEFEVMQKDASMLAKELDFFDVVYLDPPYNQHPYSSNYFMLNLIANYKKPEEISKISGIPKDWNR

STFNKPKFAQDALFELINDLKARVILLSYNCEGFVKKEIFLKRLSTLGKCRILEQKYNTFRASRNLKNRN

IHLHEQLYILVKN

>ABV51795.1 translation initiation factor IF-3 [Campylobacter jejuni subsp. jejuni 81116]

MSKEKEVLLNEEIRADEIRCVGDDGKVYGIISSDEALEIANRLGLDLVMIAADAKPPVCKIMDYGKFRYQ

QEKKQKEAKKKQKVIDIKEIKLSVKIAQNDINYKVKHALEFLEQGKHVRFRVFLKGREMATPEAGVALLE

KIWTMIENEANRDKEPNFEGRYVNMLVTPKKA

>ABV51794.1 threonyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni 81116]

MEKEVIAYLDNETIIDSQSVKNTNLKEIYFDNSKESLEVIRHSCAHLMAQAIKNLYPEAKFFVGPVIEDG

FYYDFRVESKIGEEDLVKIEKKMKELAEAKIEISKYEITKNEALAKFQNDDLKQEVLLRIPDGAVSIYKQ

GEFEDLCRGPHVPNTKFLRFFKLTRVAGAYLGGDEKREMLTRIYGTAFADKESLKEYLTIIEEAKKRDHR

KLGTELKLFTFDDEIGGGLPIWLSNGARLRSKLEHILYKIHRLRGYEPVRGPELLKADAWKISGHYANYK

ENMYFTQIDEQEYGIKPMNCVGHIKIYQSDVRSYRDLPLKFFEYGVVHRHEKSGVLHGLFRVREFTQDDA

HIFCMPSQIKEQVLEILAFVDNLMKLFDFSYEMEISTKPEKAIGDDEIWEVATKALKEALDEQGLKYGID

EGGGAFYGPKIDIKITDALKRKWQCGTIQVDFNLPSRFKLEYTDSDNEKKQPVMLHRAILGSFERFIGIL

TEHCAGEFPFFIAPTAVGIVPIGEAHIAYAKEIQKELLELNIDSEVYEKNESLSKKIRTAEKQKLPMILV

LGDDEVAKRSVALRDRRAKEQKNLSLDEFIKLVKEKMSEVHF

>ABV51793.1 undecaprenyl-diphosphatase [Campylobacter jejuni subsp. jejuni 81116]

MENLNALILGIIEGLTEFLPVSSTGHMILGTTILGIDIDEFWKSFLIIIQLGSILAVIFVFWRKLFQGLD

IWLKLAAGFFPTGVIGLFVAKYLNALFNGWVVVGMLIFGGVVFILIELAHKNKQYRINSLEEISFKQAFC

IGIFQSLAMIPGTSRSGASIIGGLLLGFNRKVAAEFSFLLAIPTMIIATAYSIYKEPELLSNANSLIPLG

IGFITAFVVAVLVIKFFLKFISKFDFIPFGIYRIILGFVFFYLYYSGILNAGSEFKL

>ABV51792.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MYKKQNLPELTLRGLILGSILTIIFTASNVYLGLKVGLTFSSSIPAVVISMAVLSLFKTSNILENNMVQT

QASAAGTLSSVIFVIPGLFMCGYWSEFPLWQTFMICLCGGGLGVLFTIPLRRAMVVESKLAYPEGRAAAE

ILKVANKDQSNKKGKQGIKEIALGSFIAAIFSLLSNGFKLAASESNFAFIWNKMAFGFSMGYSLALLGAG

YLVGLAGAIALFVGMFLAWGIFTPYLSNFEFDSAKNAVDLASSVWSSKVRLIGTGAIAIAALWTLIELLK

PVIEGIKEIVKNVKITNQEKNERTNIDLSLKSIFILFVLMVVGLFITFYSFVEDANLSIYYQMLFSFVGT

LVSVLIGFFVAAACGYMAGLVGSSSSPISGIGLIGVIISSIVFLVLGVELFQDPMLSKFAVALAIFTTSV

ILATAAISNDNLQDLKTGHLVGATPWKQQVALLVGCVFGALAIVPVLNLLYQAYGFVGAMPREGMDTSSA

LAAPQANLMSTIAQGIFHHNIEWGYMAFGVFVGILMIIIDKILRRTQKMSLPPLAVGIGIYLPPAVNIPL

VIGGILKFIVMQYLTKKYAKNSHKEEKLASCEQRGTLFASGLIVGESIFGVIIAGITVFSVSMGGSENPL

ALNLANFHDSELFALIFFVGVVLYFIKRIVKKDA

>ABV51791.1 putative transmembrane transport protein [Campylobacter jejuni subsp. jejuni 81116]

MEIFLALLGFFSLGLIVWLLLKDYTTPALAFISVSISVACILLILEQLGFGVGAALGVKGGVFDIKTLVA

FIKDGVKSVTDTAALFVFSILFFSVLNASGFFTKILNAFLSKMKANVYQVCILTVFIAAAVHLDGSGAST

FLIVIPALLPIYERLGIRKTSMLLIITSAMGVMNVIPWGGPTLRAATNIGMDANLLWHHIIPIQIVGLVL

SLLLAIWIAKIEIKRGAGAGNLSGINLNIEKSEHHNEKWFWLNLLVAIGVIGLLISGIIPSYICFMIGLA

IILPLNYPNLKTAKKVLDRASGGAMLMYITLIGAGILIGVFDKSGIMEKMGVLILNFVPDYLGAYIPLMV

GILAVPMAIIFCTDSYFYGVMPIVLSVTKAFGAEPLTIAIIMVIARNCATFISPVVPATLLGCGLAEVNI

KDHIKRSFFYIWGISIICLIFAEVAGII

>ABV51790.1 hypothetical protein C8J\_0191 [Campylobacter jejuni subsp. jejuni 81116]

MKFFKLSFLVLVAFFVVACGSSNPEDLAKNFTKDLYSGDAKSVMSYIDLSEAKSDEEKTFVSGKITQVVA

ENAAKAKRMGGVKDIQIEEKTINEDSAKIRVLVLFNNDNNQSSNVFLAKKDGKWLVLLK

>ABV51789.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MIIIKAAMFFLLKKMENGLFYLNKILYFVLILFLLIGIWGFFLNSNPSNQIIKKPHLPSLEIGDLVFRAG

IGSESFLIENLSQSPYSHIAMVVKTSPTMLIHVTTDDDKNAKNQVILSSMDDFLKLSHKIAIKRLKFDEK

TKQNIVTKALEHLGRKFIISTDKDAFYCTTFLEQSINSITPFHLQYTLIKAPFNEGLYLFPQTFFENNQS

VLIYESQNF

>ABV51788.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKSILFASALLASSMLFADSLKLEGTIAQIYDNNKTLLIDSIYGGQMAIKVLPNTEIEMDDCGIFGTDK

DGTFKDLQVGNFLESKISYGTPATPNTQAIPVARKIEIQCYKKAY

>ABV51787.1 hypothetical protein C8J\_0188 [Campylobacter jejuni subsp. jejuni 81116]

MKKWIFIVFCFILGFIIHIFYIGYTNELLFNKFIKNSNPDYTITDIYFKKGFLTSKGSFTLNHSHTQLST

KINLKFNNYFFLNKIIKGNFTNPFDFLDEVLKNNKLGTFTLKLHDNNSKIFLNIKDINLSNEGGDTIING

GYIEALMNKNLEIKNIKIHFDMINFSQFYTKFVLQNLNYEQFFNNPVQFYELNLFSDSQQEINFDYLVLD

NNKINSFYSKNQVNFNEENSTINLNIQGKSNEIDIDLKSLLGQNLNFDKTKFNITINKFLNSNFNISHFI

QKNLDLKIQNLILEKNKQNISLQGNLNINNSYQAKLQVISSDEPDEIFPWTKDYGGLNQYFLKENNNFFL

NLSYDSLANPQLKINGSEFSNMDLN

>ABV51786.1 ATPase, AAA family protein [Campylobacter jejuni subsp. jejuni 81116]

MSLALTFRPENFDDILGQYELIEIFKKFTALQKLPHSIFFGTAGSGKTTFARVVAKEFGLDFYEFDGGNF

KLEELRKILDNYKNSLYKPLIFIDEIHRLSKTQQEMLLIPMENYRLILIGASTENPYFVLSSGIRSRSML

FEFKSLGVKELETLLLRVQEKMKFSIDKEAKDFLLKSADARAMLNLLEFVLVLDEKHISLENLKKLRNTI

SSEGVSSKDTHYILASAMIKSLRGSDIDAAIYYLARLIDAGESADFIARRLVIFSSEDVGNADPNALNLA

VSTLEAVKNIGYPEARIILAQCVVYLASTIKSNASYKAINEALNYVKNNEALEIPNYLNNNHQEKQNYLY

PHDFGGWVEQKYLSKNLKFYHSKGLGEEAKLLDNLYKLKNHKA

>ABV51785.1 dihydrodipicolinate reductase [Campylobacter jejuni subsp. jejuni 81116]

MIKIGIYGAKGRMGKQIEECLKSETQAQISILYDKGGNLEELFEKSDVIIDFSSPSGTHELLNYARTMPK

PLVIGTTGLDEKILHLMQSASEVMPIFYATNMSLGVAVLNYLASKASQMLKNFDIEILEMHHRHKKDAPS

GTAMTLAQSVAKARNLELEKVRVSGRDGIIGERSKDEIAVMSLRGGDIVGRHTVGFYEDGEFLELNHTAT

SRATFAKGAIKIAIWLSKQEAKMYSINDFLGI

>ABV51784.1 amidophosphoribosyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MCAVVGVINSKNASTYAYYALFAMQHRGQEASGISVSNGKNIKTIKAKGEVSQIFNPDNLKTLEGEIAIG

HNRYSTAGNSSLNDAQPIAATSVLGDIALAHNGNLVNKEEVRSRLIQDGAIFQTNMDTENVVHLIARSKQ

ESLKDRFIESLKECIGAYCFVLASKDKLYVVRDPHGVRPLSLGRLKDGGYIVASETCAFDLIEAEFIRDV

KPGEMLIFTQGNDKFESIELFSQTPRICAFEYIYFARPDSIVEGKSVYEVRKKMGEALAKKFAYKADFVV

PVPDSGVSAAIGFAQYLQIPLEMAIVRNHYVGRTFIEPTQELRNLKVKLKLNPMRKVLEGKEIVVIDDSL

VRGTTSKKIISLLRAAGASKIHLAIACPEIKFPDTYGIDTPTFEELISANKNTEEVREYVEADTLSFLSI

EELTQSIGDERKYSLISFDGDYFIK

>ABV51783.1 flagellum-specific ATP synthase FliI [Campylobacter jejuni subsp. jejuni 81116]

MNLEKLRSKLGKENLSAIFGEITKISATSIEIRGLKTGVGDIVKLVSNENENLNTLAMVVEIKEQFSYLS

PFSFIEGFKIGDRAFISDAGMQIGVSDELLGRVVDPFMRPKDGKGAIEVSKYMPIMRAPIDAMKRGLIEE

VFPVGVKTIDALLTCGVGQKLGIFAGSGVGKSTLMGMIVKNSKAPIKVVALIGERGREIPEFIQKNLGGK

LDDTVIIVATSDDSALMRKYGAFCAMSVAEYFKEQGKDVLFIMDSVTRFAMAQREIGLALGEPPTTKGYP

PSVLSLLPQLMERTGKEEGKGTITAFFTVLVDGDDMSDPIADQSRSILDGHIVLSRELTDFGIYPPINIQ

NSASRVMSDIISPEHKLWARKFKRLNSLLKENEVLLRIGAYQKGSDKELDEAISKKEFMQKFLGQNPEES

FEFNQTLELLSQIDTPNTPLPPTQNINVGSASATLPNPNLK

>ABV51782.1 GTP cyclohydrolase I [Campylobacter jejuni subsp. jejuni 81116]

MQKKFEDCVKTILEIIGENPNREGLIKTPNRVFKAYEFLTSGYTQNVKEILNDALFESSNNEMVLVRDIE

FYSLCEHHLLPFFGRAHVAYIPNKKVVGLSKIPRLVEVFARRLQIQEQLTEQIAQALMENVDAKGVGVVI

EARHMCVEMRGVQKANSTTTTSALRGIFLKNEKTREEFFSLINSAKQVRF

>ABV51781.1 trigger factor (peptidyl-prolyl cis /trans isomerase, chaperone) [Campylobacter jejuni subsp. jejuni 81116]

MEVKAKQLDSVNATASVKIPSGMIKSEVENLAKKASKSVKMDGFRPGKVPVSAVLKRYERELTQDAEQNL

FKSAVNSALQELKKESKELVGEPYFEKFDRKDGEIIAELILSFKPEIKLDGYEKLIPEYQTPKVSKKEID

EKKDELLKRFATPEAIKTKRVLKEGDFAKFDFEGFVDDKAFEGGKAENYVLEIGSKQFIPGFEDGMVGMK

IGEEKDIKVTFPKEYGAAHLAGKDAVFKVKLHEIQELKIPELDDEMLKKLLPGEEKASVEVLDEKLKEQI

KNEKLFKLVNDELKGKFADALIEKYNFDLPKGIVEQETDMQMRAAFNTFSEKEIEELKASKEKYQEKRDS

FKEEAQKSVKLTFIIDELAKLRKIEVNDQELIQAIYFEAYRYGMNPKEHLENYKKQGALPAVKMALIEEK

LFNDIFMPKTEKSEKASKKEKEDK

>ABV51780.1 ATP-dependent clp protease proteolytic subunit [Campylobacter jejuni subsp. jejuni 81116]

MFIPYVIEKSSRGERSYDIYSRLLKDRIIMLSGEIHDELAASIVAQLLFLEAEDPTKDIYLYINSPGGVI

TSGFSIYDTMNYIKPDVCTICIGQAASMGAFLLSCGAEGKRFALPNSRIMIHQPLGGARGQATDIEIQAK

EILRLKTILNDILAKNTKQKVAKIAKDTERDFFMSAQEAKEYGLIDKVLEKSFK

>ABV51779.1 polypeptide deformylase [Campylobacter jejuni subsp. jejuni 81116]

MVRKIITYPNPRLFLNSEIVNKFDTELHTLLDDMYETMIASNGVGLAAIQVDIPLRVLLVNIFDENDEQK

KEDLLEIINPEIIPLDEEMITCTEGCLSVPDFFEEVKRYNHILLKYQDRFGEFKELEAKGFLAVAIQHEN

DHLNGHLFIEKISFAKRQKFDKEFKKKKKNHKKEK

>ABV51778.1 Mg chelatase-related protein [Campylobacter jejuni subsp. jejuni 81116]

MKKLKCISFHEGLDIIEVESTFTRGLPNLSIVGLASVAIKESVERIKATLLSCDFAFPAKKITINLSPSG

IPKKGSHFDLAIALLILLQNEELDDFFVVGELGLDGSIKSTNELFSLLLFLSAKIKKAKIVVPKSIAQKA

SMIPNLEVYGLENLNEAIEFFKEKNYENFRFSHNHPLFTSPLQIENEIFLQNMDFKLDFKDIKGQEKAKR

ACMIAALGMHNILFEGSPGSGKSMCAKRLVYIMPPQSLSEVLMQNAYMSLDSKDCEFTKIRAFRHPHHTS

TRASIFGGGTKNARIGEVALANGGVLFFDEFPHFNKQIIESLREPLEDHKIHISRVNSKITYETKFSFIA

AQNPCPCGNLFSKNLSCVCSENEIKKYKNHISAPIMDRIDLYVAMDEISKDDKTSISSKEMSEKILQAFI

FGKKRGQKEFNGKLKDEDLSRFCVLEKDAKDTLDLAISRYNLSLRSLNKILKVSRSIADLEQSLNINKTH

ILEALSFRARN

>ABV51777.1 hypothetical protein C8J\_0178 [Campylobacter jejuni subsp. jejuni 81116]

MENKSIAIFIDAENIPAKYAKSIFDIASDYGEVIIKRIYGDWTQKNIQGWREQIAEYSLIAMQQFNFAAN

KNSSDMYLITEIMSIFYEKNIDIFVIVSSDSDYTSLIQKLRENKKQVIGMGLEKSIKSYVNAFSEFFYLD

KDESKKEDILSKDYLRALINITEQLIDEKGRAEYAQIRTNMNRKYSDFHPQNYGFKNFRALIQKFLPKMK

KFEEEREKNIYFLVKKDYESYY

>ABV51776.1 hypothetical protein C8J\_0177 [Campylobacter jejuni subsp. jejuni 81116]

MKAIIDNIKILEQNAINKGLDELILMENAGLNLAKLIKKEAKKIRIQRKIKKVKILFLLGGGNNASDGLV

ALRNLKHAKAYKIGFKENTLFKKQEQILQNYAFKFCQKEPDFKKFHIIIDCILGTGSNRCLDEKTSLIIQ

KVNQSKALKIACDIPTNLGFYPCFKADITLCMGALKEILLEDFAKEFVGRIKIANLGISSKKFYPNSQAF

LLEKKDLKTIDRKINANKGNFGHIYIVANASAGTLAGLGALNFGAGLVSLVAQKSFSPLLMLKEKIENNA

SAIALGMGLENLDFLKDEILQNTPLILDANCFLSEALLWYLNRKDVVITPHPKEFIKLYKMCFDENLDIE

TLQKNRFFYARKFSQNYDCVLVLKGANPIIVQKEKLFVVNLGNQALAKGGSGDVLSGMIAAHLGFGFSAL

EAAKNATLAHGLVAKKYKFNKNSFDALKLIKGLKCL

>ABV51775.1 phosphoribosylglycinamide formyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MLVKLAVLFSGNGSNLENILEKLHKKTIGENTYEVVLCLCNKKDAFGIQRAKKFGLDTVIVDHKAYNTRE

EFDTILVQKIKESGANLTVLAGFMRILSPVFTKNIKAINLHPSLLPLFKGAHAIKESYESDMKVAGVSVH

WVSEELDGGMIIAQKAFEKRNLSFEEFEEKIHSLEHEILPLSVIEIFS

>ABV51774.1 integral membrane protein, TerC family [Campylobacter jejuni subsp. jejuni 81116]

MFEWIFSIDAWITLATLSALEIVLGIDNIIFLAILVSKLPPEHRDKGRILGLAFAMITRILLLLSLFWVM

KLVTPLFSVLGNEISGRDLVLLLGGLFLIVKSIKEIKEQISHQEESQSHFKASNKLWIVVAEIAVIDIVF

SLDSVITAVGIAQDVTIMIIAVIIAVAVMLFASKPIADFVEKYPSIKILALAFLVLIGVVLVAESFDIHI

DKAYIYTAMAFALVVQILNILDQRKEKNG

>ABV51773.1 phnA-like protein [Campylobacter jejuni subsp. jejuni 81116]

MAKDANGTELNAGDSVSVIKDLKVKGASTTLKRGTTIKNIKLTSKEGEIEARVDKFGVIVLKTEFLKKI

>ABV51772.1 Ser/Thr protein phosphatase family protein [Campylobacter jejuni subsp. jejuni 81116]

MRILLVLRGNYYAGQEEFIKNNKLQNYTLDLNALRLLSGSVKNIVSEYKILNVKNDEDLSKILLKLLEMR

MQKGEFCIINAYNETLKIYKDLAKQYRYKMYVIVFDNSLKQCQEKNLLEAKKNGYIIPYALLEKTQDLLK

KNPKKYPILDSSDWKKCLYQMPNLSKYKKIHHIGDLQGCYSVLKEYIKTIKEDEFYIFLGDYINRGIENG

KVIKFLLKICEKENVCLLEGNHERHLIKWANGELSNSKEFNENTLKDFRKEKLTPRDARKLYPHLKECLY

YKFQNKFIFCSHGGVNFIPSKPEKISFIPSHDFIYGVGGYEDSQKIANQFCNFTSDNLYQIFGHRNKEKL

PMKIAKRVFLCEGKIDDGGYLRVVTLDKKGFECIEIKNQIYKKK

>ABV51771.1 hypothetical protein C8J\_0172 [Campylobacter jejuni subsp. jejuni 81116]

MDPSQVLDLNQTSTASFDAGYSILMVVVALALVFLNGFFVLSEFSIVKVRRSKLEEMVKEKKAGAKKALE

VTSRLDTYLSACQLGITLSSLALGWIGEPAIAKMLEIPLINLGFSTVIIHTIAFIIAFSIITLLHVVLGE

LVPKSIAIAVADKAVLFIARPLHWFWILFLPCIKIFDFLAAISLKLFGIKPAKESELTHSEEEIKIIASE

SQKGGVLDEFETEIIRNAVDFSDTVAKEIMTPRKDMICLNKQKSYEENMQIICEHKHTRFPYIDGSKDTI

LGMIHIRDIIQNELSHKSQNLDTFVKPLILVPENISISKVLVMMNKERSHTALVVDEYGGTAGILTMEDI

MEEIIGEIKSEHEEDSYKKLAENIYEFQGRCDIETVEEMLVINYDEDLEQVTIGGYVFNLLGRLPIVGDR

IEDELCYYEVKKMDGNSIERVKVVKKTNKDEE

>ABV51770.1 antibiotic transport protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MFSSFFASKKWALWAYLGLFLLLFFLYIQTSLNVAINSWYSDFYNVLQKPKIELLDSNSTQKIEENLENN

TTLIQEANQRAEQNFQKANFINKGALYYYQNLLEYFFNSRAMIEKPNYSANDFYALILVFLAIAIPYVLI

ATINIYFASVYAFKWREAMTFSYLKFWKNKDDNIEGSSQRIQEDTYNFSKIVESLGLSFIKALMTLVAFI

PILWSLSDVVSKALFANLSENSSFYFLKNIDGLLVYIALLISLGGLVVSWFVGIKLPGLEYNNQKAEAAF

RKELVYAEDNRKEYAKNETMIELFTGLKFNYKRLFLHYGYFNIWLILFEQMIVIVPFLIMAPGLFAGAIG

LGIVMQINNAFDQVRSSFSVFITNWTTITQLRSIYKRLKEFEKNISYKS

>ABV51769.1 hypothetical protein C8J\_0170 [Campylobacter jejuni subsp. jejuni 81116]

MKKIILFLLCVGFAFACSEHSHTDFKDLNKTEYNSQ

>ABV51768.1 iron transport system substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIFFMFLTAFSFLGASELNIYSARHYDADFEIIKKFEEKTGIKVNHTQAKASELIKRLSLEGSNSPAD

IFITADISNLTEAKNLGLLSPVSSKYLEEFIPAHLRDKDKEWFAITKRARIIAYNKNANIDISKMKNYED

LAKAEFKGEIVMRSATAPYSKTLLASIIANDGNKEAKAWAKGVLDNLATNPKGGDRDQARQVFAGEAKFA

VMNTYYIGLLKNSKNPKDVEVGNSLGIIFPNQDNRGTHINISGIAMTKSSKNQDAAKKFMEFMLSPEIQK

ILTDSNYEFPIRNDVELSQTVKDFGTFKEDQIPVSKIAENIKEAVKIYDEVGFR

>ABV51767.1 iron transport system permease protein [Campylobacter jejuni subsp. jejuni 81116]

MYKTLKYYKLGAILLALFLVLPIFGIFAELFYILFQNFNTSDLTQFSSIKENLSHFFDYLFLKFIKDTFI

ISVGVLCLSLILGVSSAYLIANYDFYFCKILEKLLILPLAIPAYILAFVYVGIMDFQGFFHENFGFRIDF

FNHYGVIFVLAISLYPYIYLFAKTAFKSEAKEAYEVAKIMKYSEFRIFTRVALLSARPAIFSGALLVLME

TLSDYGASAYLGVDTFSAGIFKLWYDLNDSYSSSVLSGILMLFVFLIMYVDYYYKNKHHYSFNQNLALFI

KKRKLNPIKQILSCIYCFMIAFVGFILPFIWLVYWGLKDHKLFESQFYIISFQTIILALVTALITTFLAY

FLMFSSRIVKNHFFNLFILKISSLGYSIPAAALGISIIVLFVFLDKIFHMSLLGNSLLVLVFAYVIRFLA

SAIYSLEGGYNKIHLNIDEASLNLRTSYFILFFKIHTPLMKHFLFLAFIIVFIDTIKELPLSRILAPFGF

ETLSVKAFWFASDERIYDAALPSLFIVFLSLMVVVWMDKITRKDDVRN

>ABV51766.1 iron transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MLEIKNLSKNFGKIQALENINLHVKEGEFLSILGGSGSGKSTLLRIIAKLEQASSYDLFSCKGEVALMFQ

NYALFPHLNVEKNILFALYDKKDKNQILNHLLKTFEIEDLRYKKIDEISGGQAQRVAFARAIARGCKLLL

LDEPFSNLDQNLKQDLRRELKKIIENQGITAIMVTHDIEDAYCMSDQIAFLEKGKILAHANPKELYFKPD

FKSAQILPDLNIIEKKLDLEDEFFAWIASKNYIFGYAELKIGNRFEAKILQKEFLGAFYRLKLRYKNIEF

FMLLSSNYNLEEKINFDIINF

>ABV51765.1 hypothetical protein C8J\_0166 [Campylobacter jejuni subsp. jejuni 81116]

MKNLLIIGAGGVSRVATAKCAMNSDTFSKITLASRTKSKCDEIAAFIKERLGVQIETAQIDADDSNAVVE

LIKKTGAQILLNVALPYQDLSLMDACIKAGIDYVDTANYEHPDLAKFEYKEQWARNDEFKQAGILGLLGS

GFDPGVTNVFCAYAQQNLFDEISYIDILDCNAGDHGYAFATNFNPEINLREVSAKGRYWENGKWIETQPM

EIKMEWDYPEVGVKDSYLLYHEELESLVKNIKGLKRIRFFMTFGQSYLTHMKCLENVGMLGIKPVMHQGK

EIIPIEFLKTLLPDPASLGPRTKGYTNIGCVIRGKKDGKDKQVYIYNVCNHEECYKETGAQAVSYTTGVP

AMIGTKLIAKGIWQGKGVFNMEEFDAKPFMEELNSQGLPWKIIEMTPSLGE

>ABV51764.1 superoxide dismutase (Fe) [Campylobacter jejuni subsp. jejuni 81116]

MFELRKLPYDTNAFGDFLSAETFSYHHGKHHNTYVTNLNNLIKDTEFAGKDLVSIIKTSNGGVFNNAAQV

YNHDFYFDCIKPSTGCGCGGSCQSIDANLQAALEKEFGSLENFKAEFIKGATGVFGSGWFWLVYNTKNQK

LEFVGTSNAATPITEDKVPLLVVDVWEHAYYVDHRNARPAYLEKFYAHINWEFVAKAYEWALKEGMGSVS

FYANELHPVK

>ABV51763.1 hypothetical protein C8J\_0164 [Campylobacter jejuni subsp. jejuni 81116]

MKKVVLISALLGAFAANVFAANTPSDVNQTHTKAHHSKAKADKKHEAKTHKKTKEQTPAQ

>ABV51762.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MDFYSLIFLSCALGMDAFAVSLCKGFSVKKLHLKHYLIVGIYFGGFQALMPTIGYFIGITFASFIASIDH

WIAFILLSLIGLKMIKESLENENCDSNANQFGFKTMLALAIATSIDALAVGVSFAFLNVNLLLAIFLIGI

ITFILCIIALKIGNKFGIYLKNKAELLGGLVLIILGVKILIEHLFFD

>ABV51761.1 tRNA delta(2)-isopentenylpyrophosphate transferase [Campylobacter jejuni subsp. jejuni 81116]

MFFEIALIGTTASGKTYIANTLAREFDAVVLSLDSLCVYKEINIASAKPSQDDLASIKYFGVNLLSVNEH

FNVELFIREYQKAKEFALARNLPLIIVGGTGFYLKTMIDGLSEKTLESKSSLNNDEIYALLLNIDPNYKI

EKNDTYRLKKWLGIYEQTREIPSEFLKRTQKTGVLKDIEIYELAWDKEILKKRIKTRTKEMLDNGLLDEA

KILFSKFDHKLKALNSIGLKECKEYLDGEISFKELENLITIHTTQLAKRQRTFNKKFQSKALEFDKALAI

LRMKFSIEK

>ABV51760.1 4-hydroxybenzoate octaprenyltransferase, putative [Campylobacter jejuni subsp. jejuni 81116]

MNTFWIKFKDILELVVFKHSIFALPFLFSSMIVASKLANDTAWFGFKALILGIICAVSARNFAMATNRLM

DEDIDKDNPRCANRPNVSGKIGRKSVWIFIIINALIFISCSYFINTLAFYLSFPVLFVLAIYSAFKRFSS

LAHLVLGFCLGLAPIAGSVIIMGEIHIYSVILCLGVTFWTAGFDLLYSLQDMEYDKKVGLHSIPAKFGSK

ATLFISAFCHILAVLFWLLFVWEVWGIALGKIALIGVIISGIILALEHKIVHKNFAHIDRAFFTLNGYLS

IIFFIFIWIDLLWN

>ABV51759.1 hypothetical protein C8J\_0160 [Campylobacter jejuni subsp. jejuni 81116]

MELTLFKAGFEAHLECCEIENNRFLGEYLKLGAISQILKWKKLALRIDFDEGEKIIFDLLLSLKEDILRL

ENSLDKNKELIPLKQKGVIESLNFEYLNFLDTILEEDKEYYLRFDLNNQKIAIFIKAQSQTLAKIIKIKP

EDKMAFDAFVVEIQRNMIRNKKGQE

>ABV51758.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MSDDVLYLVFIIVLLIAMLAYMNIKERENNAKIAKLQNVIEDITKELHYFRKELGVKDDSEEDEDYKTSL

LKEEIMIELDKQISSKITPVLRTLKTMEHIIEDFQNEQQNRLLNLEQKAQSMAKLTPNYDTEEQKIENLF

KEGKSIEQIAKDLRIGTGNVELVLKFKKLIK

>ABV51757.1 molybdenum cofactor biosynthesis protein A [Campylobacter jejuni subsp. jejuni 81116]

MLIDQFGRKINYLRISVTQRCNFRCLYCMPKIPFDYQPKENLLSFEELFLFVKAAIDEGIEKIRITGGEP

LLRKDLSIFIKMISDYKSDIDLAITTNGFLLKDFAKDLKNAGLKRLNISLDTLDHKKAKTLAQKDVLDSV

LSGIDEALNLDLKVKLNTVALKNLNDDELISLLEFAKSKKAQIRFIEFMENTHAYGKLQGLKRDEIIQIL

SQKYQIQLIKKDEKAPVSIYKADDYEFGIIDPHSHEFCDSCNRIRLSAEGLLIPCLYFDEALSIKEAVRK

GDIKAAVEILQEVLRNKPEKNKWSVVDNETSSRAFYQTGG

>ABV51756.1 hypothetical protein C8J\_0157 [Campylobacter jejuni subsp. jejuni 81116]

MQLVESFLSIQGEGKYNGKLAIFMRFAGCNFNCLGFNVKISKNDKTLIGCDTIRAVFTKDFKESYETLNA

NELLKRVIKLKQDFDPIVVITGGEPLIHYENPEFIKFIQMLLKNKFEIHFESNGSIEIDFDRYPFYKECI

FALSVKLQNSGIKKDKRLNFKALKAFKNYAKDSFYKFVLDANTLDNSFLEINEILKEAPNQIFCMPMGEN

EQNLKKNAQKIAEFCIKNGYNYSDRIHIRLWNDKEGV

>ABV51755.1 hypothetical protein C8J\_0156 [Campylobacter jejuni subsp. jejuni 81116]

MIIRKLFEFENAHIVRFCSSKRCKSSIHGHSYKVEVLLESKYLDNAGMVYDFGLLKTYIRQIIDSFDHAI

TLFKYDDAKYLEEMKKYSSRWICLPVNVSAENFCRVFFILIDALLKQTKMVNGEQGVTLQSIIVHETRTG

YAQGFREDAYSELMPKISLQDIEFSNGIKVEWNDIDFYNKLKNEEIFINPKEI

>ABV51754.1 cytochrome c family protein [Campylobacter jejuni subsp. jejuni 81116]

MQKAKILIALSFFLLVLSACSNDEKNISKTQNTDQEVVQIEQNDEKTELSDSNLPLPVDDEAQSSDDEHE

VNPSIINSLYKQKCATCHGEKGELKPKNSTAIKTLSNKIFIQKIKMIKDKNHSFLSDEQIQNLADFINKG

K

>ABV51753.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MDQSYEFFLALHLYSLYASGFLMLFYLILTQGNFKTEFIFIRRIRLFLPIYYLFLALIIFTGCLLSAMKQ

FQMNVNIWVMIFSWILIFALAIFHFVCFKKARRFRKYATFRWISCLILPFEIFLLFLPFLIERYL

>ABV51752.1 hypothetical protein C8J\_0153 [Campylobacter jejuni subsp. jejuni 81116]

MQFLYNKQAGEEFIQLQGENFNHLKVRRVKENSELNLRNLQDNFLYNYTITNLTRNSCTLKFLNKKSQNI

KQSELNLALAIIDIKILEKTLPFLNELGVKKLHLVFTNFSQRNFKIDLERFEKIIISSCEQCGRNTKMDL

IIHQSTQEFVQKFPNAIMVDFQGEQQSHFDEKELYFIGPEGGFNNDERLLFNRKISLKSSNILKSQTAII

AIASKILL

>ABV51751.1 50S ribosomal protein L31 [Campylobacter jejuni subsp. jejuni 81116]

MKKEIHPEYVECKVSCACGNTFTTKSNKAELRVDICSNCHPFFTGSEKIVDAAGRVEKFKKKYAMQ

>ABV51750.1 tetrapyrrole methylase family protein [Campylobacter jejuni subsp. jejuni 81116]

MLYFIPTPIGNLSDISFRALELLKTCDLVFCEDTRVSKSLISLLNTKFHTDIHISKFIALHSHNEKEVLA

SIDLKIFEKNVAYLSDAGMPGISDPGKALVEFAQENNITYEILPGANAALVALVSSAFCQKEFIFIGFLA

NKGKERQKDIEKILNLPYPSIIYESPKRILSLVEQIMILDSQREIFLIKEISKKFEKKFKGNAKELSEIL

KKSNLNGEWVVVLQSKEQNFLQNTLCEKDIMDLELPLKAKAKLLSKINGKNAKEIYQKLLLSQD

>ABV51749.1 putative rRNA methylase [Campylobacter jejuni subsp. jejuni 81116]

MIVYGKQIFFYILEYHKDCINELYLAKECDKTTFSKIAKSGFKIKKLDFKTAQAYAKGGNHQGFLLDIKE

SSFANLNEIKKNDFIVMLYGISDVGNIGAITRTAYALGVGALIFIGEKLAMEGVIRTSSGAALDLPIVIS

NDALSVINELKQVGFYFYASDGSGKEIHSVKISNGKKVLVLGSEGFGLSSKIVKKCDECVGIAMKNNFDS

LNVSAAFAILCDRMLNA

>ABV51748.1 hypothetical protein C8J\_0149 [Campylobacter jejuni subsp. jejuni 81116]

MLNWKKIQELNLKEVAAKTQIELDFLEALVEKNFAVLSRFNVKGFVKILSREYELDFSDFNEEYEAYLNE

NNPTPQTKSKMITPKLDAYSQKSSNAWPFLIVLIVLVIIGSGIYYFDTLKTFFKDEQNNTSATVIDIIGQ

AQENLKSLGGNNVVVIDNNKAQETNQTESVLPSQNISLQENDKNISIENNISENNTTLLDEEKNTQIQED

TNTPKTDSLKEAHFKTSTKIWIGLIDLKSLKKTSFVKEKDFNISLDKDQLILTGAAALTMFDQENKEQKF

PAGISKRFLIKDGKITSISAAEFVKLNKGKEW

>ABV51747.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MVKKIIILTLWVNISFAISSLELAKNLVNNSSKNSQLELLFSNNSYIDNNGNCDIAKISQILKTNSLIAL

TLSNPQSLRLNFKAKADEVMFFKILSDVLTDAGYIYFIPTDLILREGNIDYTIQVESQYVLDPGTLYNLL

KENSVYINNIKRIGAYDYEYDLNFSNAVLKTNTNVNLNTPKSLEKPLKDYVLDLKNATNLIIDANDLDNW

FPKIFFLDKNLNLIKAVKSENKNNHFSELIPNGAIYAIVSDMYSLDNIRRGLKITLKK

>ABV51746.1 aminotransferase, classes I and II [Campylobacter jejuni subsp. jejuni 81116]

MFDEIRFNTIERLPNYVFAEVNAIKMAARRAGEDIIDFSMGNPDGKTPQHIIDKLCESANKDKTSGYSTS

MGIYKLRLAICNWYKRKYNVNLDPENEVVATMGSKEGFVNLARAIINPGDVAIVPTPAYPIHTQAFIIAG

GNVAKMPLAYNEKFELDENQFFENLHKTLNESIPRPKYVVVNFPHNPTTVTCEKSFYERLIATAKKERFY

IISDIAYADLTYDDYKTPSILEIEGAKDVAVETYTLSKSYNMAGWRVGFVVGNKRLVSALKKIKSWFDYG

MYTPIQVAATIALDGDQTCVDEIRATYDKRMHILLEAFENAGWKLQKPRASMFVWAKLPESKRHLKSLEF

SKQLLQRASVAVSPGVGFGEAGDEYVRIALIENENRIRQAARNIKKYLKE

>ABV51745.1 homoserine dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MKVAILGYGTVGSAVVKFLLENDKLIRARCGQSITPVIALARSPKKNALIPITHSVEEILNADVDVFVEL

MGGVDEAFKIVSEILKKEKAVVTANKAMLAYHRYEVENLAKNLAFGYEASVAGGIPIIKVLKEGLSANNI

LAIKGILNGTSNYILSSMSQKNMSFEQALQIAQNLGYAEADPTFDIEGQDAAHKLLVLSSIAYNLKAKPE

DILIEGISEIAPEDMYFANEFEFTIKLLGIAKVRENKVELRVHPTMIDKEKMLAKVDGVMNAISINGDLL

GESLYYGAGAGGEATASAVISDLMDIARDQVKAPMLGFVNTLEYELLSKDEIYTKYYLRVKVEDKIGILS

KITQLMSENNISIDSFLQKPKKNDENYSTLFFTTHLTYEKSIQNLLEILRKQDFIKTKPFMMRIE

>ABV51744.1 predicted endonuclease [Campylobacter jejuni subsp. jejuni 81116]

MGVKAYLDGILGEDKACKFLKKQGFEILKRNFHSKFGEIDIIAKKDEILHFIEVKFTQNDYEVSERLDRK

KLEKILKTIEFYHLKNGISSDFQIDLICIKNDVIQFCENISF

>ABV51743.1 thioredoxin [Campylobacter jejuni subsp. jejuni 81116]

MGKYIELTSDNFAQAKEGVALVDFWAPWCGPCRMLAPVIDELANDFDGKAKICKVNTDEQGDLAAEFGVR

SIPTLIFFKNGEVVDQLVGAQSKQAISDKLNSLL

>ABV51742.1 thioredoxin-disulfide reductase [Campylobacter jejuni subsp. jejuni 81116]

MLDVAIIGGGPAGLSAGLYATRGGLKNVVMFEKGMPGGQITSSSEIENYPGIAQVMDGISFMAPWNEQCM

RFGLKHEMVGVEQILKNSDGSFTIKLEGGKTELAKAVIVCTGSAPKRAGFKGEDEFFGKGVSTCATCDGF

FYKNKEVAVLGGGDTALEEALYLANICSKVYLIHRRDEFRAAPSTVEKVKKNEKIELITSASVDEVYGDK

MGVTGVKVKLKDGSIRDLNVPGIFTFVGLNVRNEILKQDDGKFLCSMEEGGQVSVDLKMQTSVAGLFAAG

DLRKDAPKQVICAAGDGAVAALSAMAYIESLH

>ABV51741.1 hypothetical protein C8J\_0142 [Campylobacter jejuni subsp. jejuni 81116]

MDKKQSRRNFLKASSLFALVGASAPSMVFAHTHNQNNLNSTQNYRARIFFNNSAQLDILSEAVERIFPED

DLGPGAKKLGVAIFIDNELAGNYGSGAKDYRFGPFIQGKKNQGYQYPLTRAELFKMGVNALDEEAKLRYK

KGFVELSAKQKDEVLRAFEQDKTKVSFGDKIKASDFFTELRSITITGVYADPIYGGNANMQAWRMKKFPG

AQMTYATQVLDGDKFEVIEPISLADMSH

>ABV51740.1 hypothetical protein C8J\_0141 [Campylobacter jejuni subsp. jejuni 81116]

MAKILKKTDIVVIGLGWSSSIVANECAKAGIKVVALERGGHQDTSDFLGAHDEYKYVNNAAMKQDLSKES

ICVRNNDNEIALPMRKNYAFDVGNNVGGAGVHWNGMSYRFLPYDFQIKSLTEEKYGKNKVSKEYTIQDWG

VNYDEMEPYYDKAEKMMGVSGEDKSPFSGKRKNSYPNPPLEKTTMLKKI

>ABV51739.1 hypothetical protein C8J\_0140 [Campylobacter jejuni subsp. jejuni 81116]

MVPASNSSQTYTNPDKQSLGACQYCAFCEHFGCEYGAKASPIVTTIPSALTTKNLDIKTYANVLEILHKD

GKATGVRFVNTLTLEEFIQPAEVVMLGSYVFNNAKLLMVSNIGEIYNPKTGKGTLGKNYSYQITPSVNGF

FKDPFNSYLGAGALCNWIDDFNGDNFDHSKLDFIHGASFRISQNGARPIASNPIKPGTPSWGAEFKKASI

YNYTRFTYIGAQGASIPYIGNYLSLDPTYKDAYGLPLIRVTYNFTKQDKNLYNFMLPKLKSIMQEMGAQN

IYTSPKLGDYGVVSNGWYTSTHIAGGTIMGTDKSTSVVNPYLQHWDVNNLFVVGAGNFPHNPGYNPTLTL

NALAYRASEAIIKYLKTGNC

>ABV51738.1 hypothetical protein C8J\_0139 [Campylobacter jejuni subsp. jejuni 81116]

MERRLFLKGSALGSMVAFFASSNLSAAMLKNKDLLGFKAVSASTQDKVIVPQGYEAKVLISWGDPLFSKA

KPYDENKIIDMNAVKNAHLVFGDNDDGMSFFSLSKNRGILAVNNEYINPEIMFNHHGKNLSKEDVLYEQA

SVGVSILEIKKKGDDWTVVLDSKYNRRIDANTKMQVSGAAKKEVLKNEKFVHGTFANCANGQTPWGTYIT

CEENFDDFFGSLDENLEFNDSLKRYGFNKTSLYGWEKFDERFDLAKNIDEANRFGWIVEINPFDVKSTPV

KRTSLGRFKHENAEIIVEKDGSVIVYMGDDEMNEFIYKFVSKHKYKKGADTSKILDEGTLYVGQFNGKVG

DFKGQGKWIALEYGKNGLDEKNGFKSQAQVLINTRLAASIVGATPMDRCEWIASHKQSGSKEVFATLTNN

KNRQEPNAANPRTKNVYGQILKWMPKNSHKDDDFTWEIFALAGNPDNQQGLYKGSNNITSENKFNSPDGL

KFDRDGRLWIQTDGSYSNKDEYEGMGNNCMLAANPKTGEIRRFLTGPIACELTGIAFSEDYTTMFVGIQH

PGEGLKGSTFPYGKTPRSSVMMIRKLDGGVIGS

>ABV51737.1 methyl-accepting chemotaxis signal transduction protein [Campylobacter jejuni subsp. jejuni 81116]

MKSVKLKVALIANLIAVVCLVILGVITFMFVKQAIFHEVVKAETNYVKTAKNSMESFKARNSLALESLAK

SILKHPVEQLDSQDALMRYVGKDLKNFRDAGRFLAVYIAQPNGELVVSDPDSDAKKVDFGTYGKADNYDA

RTREYYIEAVKTNKLYVTPSYIDATTNLPCFTYSTPLYKDGKFIGVLAVDVLVTDLQAEFENLPGRTFVF

DEENKVFASTDKTLLQQGYDISAIANLAKIKENFEPFEYTRPKDGSERFAVCTKVSGVYTACVGEPIEQI

EAPVYKIAFIQTAIVIFTSIISVILLYFIVSKYLSPLAAIQTGLTSFFDFINHKTKNVSTIEVKSNDEFG

QISNAINENILATKRGLEQDNQAVKESVETVSVVESGNLTARITANPRNPQLIELKNVLNKLLDVLQARV

GSDMNAIHKIFEEYKSLDFRNKLENASGSVELTTNALGDEIVKMLKQSSDFANALANESGKLQTAVQSLT

TSSNSQAQSLEETAAALEEITSSMQNVSVKTSDVITQSEEIKNVTGIIGDIADQINLLALNAAIEAARAG

EHGRGFAVVADEVRKLAERTQKSLSEIEANTNLLVQSINDMAESIKEQTAGITQINESVAQIDQTTKDNV

EIANESAIISSTVSDIANNILEDVKKKRF

>ABV51736.1 putative manganese transport system substrate-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIILFILSLGIFYTFTQAKNLEQEQNTSSNLVSVSIAPQAFFVKKIAADTLDVNVILPPNSNEHNFEF

KPSTMKKLEKSDIYFTIGLEFEKVFTDKFKQNFPKLQVVNMQKNIALIQTHDIHEHSHEHEEHEHFDPHT

WLDPILVQTMALNIYDALIQKYPQNKNLYKQNLDKFLAELDSLNLQIASKLEKLKNREFVVYHPSWTYFA

KRYNLTQIPVEILGKEPKSKDLQKLITLMKDKNLKVIFVQNGFPENAAKTLAKECDAKIYKIDHLSYDWE

NELLKTADAFSRNL

>ABV51735.1 putative manganese transport system ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MLFFEISNLNYAYDNEIILKNINLSYDNKDFLSIIGPNGAGKSTLVKLILGLLKSKNEIHFKTLQRKEIG

YVPQHTLANPNFCPRVLEIVLMGLVSKKIFGFYGKKDKEKAMQALKSVGMEKFWNKTIDSLSGGQRQRVF

IARALASECKMLILDEPTASVDNKSAIQIFELLSSLHQKGMGILLICHDINLVLAYSDKIAHLNKELFLH

TNTKEKEKSSFLKHLYENHSHFCDVEMSLNTCFCDEENCDSKKLCEQEFTRRNLKKTEFKKENFCLKFSK

ENNA

>ABV51734.1 cation ABC transporter, permease protein [Campylobacter jejuni subsp. jejuni 81116]

MLEILNFTFFQNALLGAILVSIACGIIGTLVMINRLFSMAGGITHGAFGGIGIAFYFSLPILLSTGIFTL

FLAFLVAFLAKHYEHRSDSIIAVIWAFGMAVGIILIDLSPSYNTDLMAYLFGSILAVGTQDLWLMALVDS

VVVLLIFLFYRQFEALSFDAEFAKVRGINTSFFHYLLIALMAFCIVISIRLVGLILVMALLSIPSFIAEN

FTKRLGFIMILASFLSMIFCVLGLILSYYLNLSSGACIIAVACFGFLAHLIGKFLKR

>ABV51733.1 hypothetical protein C8J\_0134 [Campylobacter jejuni subsp. jejuni 81116]

MLFPMEKIFEDYVAYMLKKVNPTQDIKVQNNGKYLISKNDEKCFMLKPDLYIENKMILDTKWKIPNDSED

EKKQGIEQSDLYQMFAYACKFKIYDIKLVYPLCEKTQDLQRKIAEKFFVFKASEHLYFKEQGQKDIKVQV

LFAPLPF

>ABV51732.1 hypothetical protein C8J\_0133 [Campylobacter jejuni subsp. jejuni 81116]

MVNNTKKLKAIDLFAGIGGIRIGFKNIFQEKLEFVFSSEIDKFACQTYFCNFNELPHGDITQINENNIPK

HNILLAGFPCQAFSIAGHRKGFNDIRGTLFFDVARIVKKHKPEIVFLENVKGFKNHDKGKTFSVVKNTLE

DMGYDVFSEVLNARNFGIPQNRERIYIVAFLKNKFKNISFNFNELKNIEIKSKLGDILEKNVDEKYTISD

KLWAGHQRRKLEHKKKGNGFGYSLFNHNSDYTSTISARYYKDGSEILIEQKNKNPRKLTPREAARLQGFP

NSFKITTSDNQSYKQFGNSVAIPVIENIAKLIHRELYNVNK

>ABV51731.1 hypothetical protein C8J\_0132 [Campylobacter jejuni subsp. jejuni 81116]

MSINDKKFDINLKFYFFMKYLVKINFSDIQIINILSHISKNKNSLYELKQYINLNTKNGINQWSYLEQII

YEIRNIIDFNVFIFALKIYSIKNFLLELAKIKQMSNIELLSKLDPLSLEYDKITIYNPYSTRVNGALLAL

TFFNHIDNNQFFHDNINKEYFLSICQLSQELRKHGLEPNQIFMLIFNESINQSIISYSGNNYENRILQKL

QSIGINQETITKKHDENDSSTEFDFFFNFNGKSYGIGAKRTLRERYKQFIKTSQTSEINVMIEITLGLDL

GEEKAKTIRNYGVYLIVSDEIYEQNKFLQNIDGVFGSSQLTLELLKTL

>ABV51730.1 hypothetical protein C8J\_0131 [Campylobacter jejuni subsp. jejuni 81116]

MNLEALCKEAGLSFYDDELVSENGRKIYRIYVQKEGGVNLDDCARLSEILSPIFDVEPPVNGEYFLEVSS

PGLERKLSKIEHFAKSIGELVKITTNEKEKFEAKIIAVDDENITLENLENKEKTTINFNDIKKARTFVEW

>ABV51729.1 ribosome-binding factor A [Campylobacter jejuni subsp. jejuni 81116]

MNPSEIKKLRTESILKELIPEALANLDDENLKNLCVVDVECKKGRYDAFVYLDKMFFNVHEQEKILSSLK

KASRALQNYCMSEQGWYRCPNFHFKFDDRLEYQNHMDALFEKIKKDKNES

>ABV51728.1 translation initiation factor IF-2 [Campylobacter jejuni subsp. jejuni 81116]

MAKIRIHEIAKELGYDSKEIIEKANELGLGIKTASNAVEPEIAAAIYEYIQTREIPEAFKKNIKTPTAKK

PKKENIKEQEKLNESEKKEPKKEEKLKQEVKKEELKVEKENVKEEEKQEIIDAHKPQSLASATLAKRRGL

VIVKKKKDEEEIQVKKEEVKNSNDISINNEERLSLKTMFSNADESLKKKKKEKKSFVASKKESTEKMNFL

DEHDFGDISLDDEDEVVLPDFSVKEQEKPQNINKKQPNFIRQAVGNSAGFGLEGGIQRRSRKKPPKKIEK

KEVEEVSSVAISKEIRVYEFADKIGKSTSEVISKLFMLGMMTTKNDFLDEDAIEILAAEFGIEINIINEA

DEFDYVKDYEEETDEKDLVTRAPVITIMGHVDHGKTSLLDYIRKSRVASGEAGGITQHVGAYMVEKNGRK

ITFIDTPGHEAFTAMRARGASITDIVIIVVAADDGVKPQTKEAINHAKAAGVPIIIAINKMDKEAANPDM

VKTQLAEMEIMPVEWGGSYEFVGVSAKTGMGIEDLLEIVLLQADILELKANPKSFAKASIIESSVQKGRG

AVATIIVQNGTLTVGSTVVAGEAYGKVRAMSDDQGKALKEIKPGECGVIVGLSEVADAGEILIAVKTDKE

AREYANKRHEYNRQKELSKSTKVSIDELGAKIKEGNLKALPVILKADVQGSLEALKASLEKLRNDEIKVN

IIHSGVGGITQSDIELASASENSIVLGFNIRPTGEVKERAKDKGVEIKTYNVIYNLLDDVKALLGGMMSP

IISEEQLGQAEIRQVINVPKIGQIAGCMVTEGVINRGAKIRLIRDGVVVYEGNVSSLKRFKDDAKEVAKG

YECGVGIEGCDDMRVGDYIESYKEVEEQASL

>ABV51727.1 hypothetical protein C8J\_0128 [Campylobacter jejuni subsp. jejuni 81116]

MKKHIPIRMCIVCKNRFEQNMLFRFKVVLGDIVPKAEHGRSGYLCQNCIEKEDKILQKAFSKICKNLNTK

ITQQGLKEIFLNGKD

>ABV51726.1 homoserine kinase [Campylobacter jejuni subsp. jejuni 81116]

MKILVPATSANLGPGFDCLGLSLKLFNETQIQKSGVFSISIGGEGSDNIFLKKNNIFVNIFYEIYEKLSG

KKDNFRFIFQNNIPLSRGLGSSSAVIVGAIASAYYMSGFKVEKERILDEALIYENHPDNIAPATLGGFVC

SLVEKNKVYSIKKEIDKDLAAVVVIPNLAMSTEQSRQALAKNLSFNDAVFNLSHASFLTACFLEKKYEFL

KFASQDKLHEINRMKNLPELFEVQKFALENKALMSTLSGSGSSFFSLAFKDDALALAKKMQTKFKDFCVQ

YLEFDDNGFEIC

>ABV51725.1 hypothetical protein C8J\_0126 [Campylobacter jejuni subsp. jejuni 81116]

MLNALSKPLMIGIYQDDKLIKTYKSEEKASEFLPKILDELLKEYDFTSLIYANGPGSYMGIKISYVSLST

LSIVKNIPLFAVSAFELNGYKPISANKNFCFVYKEGEICLEQNIPAEFFLPKNLQELKLNNDNLPFYFLD

AI

>ABV51724.1 UDP-3-O-[3-hydroxymyristoyl] n-acetylglucosamine deacetylase [Campylobacter jejuni subsp. jejuni 81116]

MKQLTLAKTVKGVGIGLHKGEPIEITLEPLEANSGIVFFRSDLNASYKASPENVINTQMATVLGDDRGFI

STIEHLMSAINAYGIDNVRIVLNANEAPVMDGSSISFCMMLDEAGVKELDAPKKIMVIKKPVEVRDGNKF

VRLTPTKEPRINYTIKFDNAVIGEQSYNFEFSKKNYIENIARARTFGFLKDVQALRSMNLALGGSLENTI

VVDENRILNPEGLRFKDEFVRHKILDAIGDLTLLGYRVFGDYISYAGSHHLNHLLTKEVLKDKDAYEIVS

LEKTTQKAYEKVFA

>ABV51723.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MAKRKGKTYLSVLILVLIAILIFFISRLSIFEKNPPQILMPDVVYTDLKKPILVHVKDDESSIKNVQIIL

HKDDNTSAMVIADEKISNLKDITLQVALPKFGYKENVKSFVLEVIAKDSSFWNFFSGNEARKQIAVLVDN

TAPKINIISNSYQIEQGGAGAVVFKADDANLDKVYIETNKGKIFKVTPYVKEGYYAALIAWDARDEEFRA

FVIATDKAGNISKERIRYYFVNRKYRVSNINLTDKFLDGKIENLANQYAPKDNNLNRYEKFKFVNETLRN

SNEKLIHEITSKVPEEKIDNFDLNLFLPLKNGMKVADFADHRYYSYNGQFVSDSYHMGLDLASVAQAPII

SNNAGKVVFAAENGIYGLNLIVYHGFGVYSLYGHCSSKNVDLDEMINKQSIIGKTGTSGLALGDHLHFGV

LVQGVETRPEQWQDKKWIENNIYNVLNDGKKIILGKN

>ABV51722.1 putative prephenate dehydrogenase [Campylobacter jejuni subsp. jejuni 81116]

MKIAIIGLGLMGGSLGLCLKENKLISCVYGMDLSKENEKDALQLGLIHELIEFKDLALCDMIFVATPVDA

IIEILQKLVDLPSNVTIIELGSTKRKIIESLPKNLIKQTLFAHPMTGTENSGPKAAFKELYKDAVCVLCD

SEIADDLHQKRAVEIFSHLGMKIVFMDSKAHDHHAAIISHLPHVISFSLANFVMKEEDKRNIVHLAGGSF

KGMSRIAKSSPQMWESIFLQNKDNLLSSIDFFQQELERCKQMIQLDKNDELREWMKQANTLREIL

>ABV51721.1 outer membrane protein, OMP85 family [Campylobacter jejuni subsp. jejuni 81116]

MKKHLISICALVAIANAATIKDIKFIGLNHLSNTSAINITGLKIGEEINPAKINTAILNLYKQNYFENIA

VENNNGILEIIVTEKPTIAKVTITGIASNDRKQVESILGIKRGTLLDEGSIKEAIERIKAYYEAKSYFDT

IVEYKKKTLENTDGLELEFIVNRGENIIIDNVHLSGAKKFSYSDIEPAVVNKEKEFMGWMWGRNDGKLKV

FELSNDSSRIADEYMKKGYLDVQVSSPYLKTYTDTYQANLTYFIKEGKPYKIKSISIENPLFDDKQNAQT

VKDLRSSAGKTINIEDIRKDVKTIETQSADLGYAFVEVYPDIQKNDQTQEATVVFKVIPHDKVYIRNVII

SGNSRTVDRVIRRELYITEGNLYNRTDLSESKNALKRTSYFDDVNIKEEKVDDTHIDLIVDVKEASTGAI

SGGIGYGSSDGILLNASLSDTNIFGSGIKSSVSVDKSDDTLSGRISLINPRVLDSQYSLGGTLYSNDYEW

DNYSEKNYGFDITVGRQFARYYNVSLTYNLEQSDIYHLSPTLLRTGYELGKSIKSSITPAITFNNTDDYY

LPRSGIIASTSLEYAGLGGDQEFISSSSKFNFYQGLQDYIGYDLIYRYKASFYKVWDEGYLPINQRIYLG

GIRSIRGFESRTVSPKNQWGDEVGGTIAFANSVELSFPLIDRIKLRGSVFFDYGMIGRKNLDEIKRMSTG

IGIEWITPIGPLQLVFAKPLNDKKGDDTNSFEFNLGTRF

>ABV51720.1 SuhB-like protein [Campylobacter jejuni subsp. jejuni 81116]

MKEFLDACLNANLQIRKYLNNIPQNDLKLCSKLGYDKNQGYELDLKCEQIFIKYLSCFGQIFSEESGLIG

KASPKQMILDPLDGSSNFVSKIPFYGTSIALMEKDQAKSAFVCNLVSQEIFAFNNNQAFKSNLSDPKYSP

LTPNLFSKIGIVEKISLHPELLDFLTKNQLKFRSLGATALSLAYASYFSFVLILGKTRIFDTAAALAIHQ

NLYIEKNENFLLLSQDKKIFDIILEFLKNN

>ABV51719.1 acetyl-CoA carboxylase carboxyl transferase subunit beta [Campylobacter jejuni subsp. jejuni 81116]

MNFADIFSKIRRQQPSIKEAPNHWVKCQSCHALMYYKEIESCFNVCPKCNYHMRISADERIKLLSDEGSF

IEYDANLEAIDPLKFVDSKSYKKRLSEGESKTGRKSSVISGECEINSLKTQLVVFDFSFMGGSLGSVEGE

KIVRAIQRAITSKTPLVIVSASGGARMQESTYSLMQMSKTSAALKLLSKEKLPYISILTDPTMGGVSASF

AWLGDLIIAEPEALVGFAGARVIKQTIGADLPEGFQKAEFLLEHGLIDAIVERGEQKQYLSDVLKFFSGK

>ABV51718.1 hypothetical protein C8J\_0119 [Campylobacter jejuni subsp. jejuni 81116]

MQVNIFCIQKSDEFKTWSEKYSKLISKYATLKEINVFNKKIALAQNLNAIEAKKSYEEAFMPYKKGYCIA

LDEKGKDLTSIEFAKLIQDKNELSFFIGGAYGLREEFNQSLDFRLSLSKLTLAHQFVKTLLLEQIYRAFC

INNNHPYHK

>ABV51717.1 dksA-like protein [Campylobacter jejuni subsp. jejuni 81116]

MKKNEIQNFKNILEERKKAILENLQSNSNEIEALHNSVPSDSVDFSVIETGSQIDFAISTNLKEELIEIE

DSLDKIKNGTYGICESCDDEIDSQRLKVKPHARYCITCRQIAEQGKKHEN

>ABV51716.1 hypothetical protein C8J\_0117 [Campylobacter jejuni subsp. jejuni 81116]

MKIKLFLLASFIYIALIFAFAWHLELGSYTLNISTYTFELPIMIWLVIPLFIYMILAVLHIAFYGFLRYL

KFKHFFKDAAKFESYTQDLLLEKDLKTTFQTKEFRAVAQLFKTIKTHEKIPHSNKINEILDLIDGLNKNE

FFNLSKFKLENNNVLYLQNEKNHLKNDANYAYSKLKNLNEIKDEFEEIAFNTLIEKASYEQIKNVKIPKK

PSEVLTLIKRFKEGNLELSAAEYEVLLSHNTLSEKDYLNAAKLSTKLLNPDAVLGIFNKIKNEKSEALRA

HLYLLAEFGLLDELREQIHNDDKKFNDFKAFLLLREKNIKIDLNQLIQ

>ABV51715.1 tRNA-dihydrouridine synthase B [Campylobacter jejuni subsp. jejuni 81116]

MIDFSKKPLFLAPMAGFSDLPFRNVVKKFGADITISEMISSNALVYESSKTLHMLERAELENPYIVQIAG

GDKEVLKKAVQMLNEMDFVDGIDFNCGCPVNKVVKQCAGSALLENLELFKNLVGVIKENNKKSLTSVKFR

LGFNEKYPEKMAKICESLGVDFVSIHGRTRKQLYSGKADYESIASAKASVSIPVIANGDINAQNAKEVYK

ITKCDGLMIGRASVGNPWIFYEIKSGKSVDEKLKKEIILTHFDEMIKHYKDQGVSIFRKHLHEYSKGHKD

ASAFRDEVNRINDAKIMQEKIESFF

>ABV51714.1 hypothetical protein C8J\_0115 [Campylobacter jejuni subsp. jejuni 81116]

MSIFSINDNSNYNSILSQSKANKESKENSKISFANAFLKQNASKLNEIQSANSQTLARSEVLNSTNTTNT

SNNTNFSISSKTSSPNYDISSEFKNSIYTLKYKQADISNNTAYGYSVDKDGYMGSDFNKAAGLPEDFKIH

KSTLDEIKKAAENDPVASSTKEYLGVSEYYTNIDMAETIKQYYNLFSNALGQSFPNDKTSFSEADINSMP

SGYAIDGFYNGYGAFKHPDAIRNDDIAIKSIADYSNVLISNIYRSQEQLNEANSIYSDSAGLISGIKPET

LGLSLEEIKNVSKGEDWQFNPDMSVYPQNEDGTYTKEDLFMSFLKAQNGQPVESPKTTLNPTIEAYNRAM

AKESFSGPAIHLDSIMTGKSDFKSFFRYWAERGIEEGDLYMYENNIPKESAMGNWALDAEIKQAIANGWK

AKPSTINSYADSIMDRLNNLLGQTRV

>ABV51713.1 hypothetical protein C8J\_0114 [Campylobacter jejuni subsp. jejuni 81116]

MILSDEKCDFLESIASFLSPKDVELVFVDSKEMQEINLEQRKQDKTTDVLSFPLENIDESLPLGSVVINV

DLAKEKAKELGHSYEEEISLLFIHAMLHLLGFDHENDNGEMREKEKELIEHFNLPKSLIVRTLG

>ABV51712.1 hypothetical protein C8J\_0113 [Campylobacter jejuni subsp. jejuni 81116]

MQGFILHTQKVKDEDLIVYILSPKMLIKAYRFYGLRHSSILSGYKIDFALEENPSFLPRLKDVLHLGFLW

IMQRDKMLIWQEFIRLLYRHLKDVEELDSFYFDLLDECVKRFEKQNPKRVIVDAYLKILEFEGRLHKDFF

CFACDEKIQNSITLLRAFLPSHSQCALGFEFEEKKLKQFYSSKNCAIFDDEEIENLYHLIKEGL

>ABV51711.1 hypothetical protein C8J\_0112 [Campylobacter jejuni subsp. jejuni 81116]

MKKAFVLVDYQNDFIDGSLGFDKALKIKENILKALNQIDFNNTHLLLTYDTHDEHYLQSKEGLNLPVKHC

IKESLGWQMPKEFEPFLQKAHKIFYKNTFGSLELANFIQKSDYEELHFAGLVSHICVFCNIILAFGAKPN

ARIILHQNLSASFDENLEKSAFDILRAYGIEIV

>ABV51710.1 hypothetical protein C8J\_0111 [Campylobacter jejuni subsp. jejuni 81116]

MINLSKKLIRQVAQANAKFGLIKDGDRVLLGLSGGKDSLALAHLLNRMQAHAPFKFELEAVTLSYGMGED

YSHLHAHCEEHGIKHSVLDSNIYEVSGDTIRENSSFCSYFSRMRRGALYTYALEKGFNKLAIAHHLDDAA

ESFFMNFIHNGALRTLAPIYQSKRGVTVIRPLIFVRERQLRDNATQNELSVIGNEFCPGMKLSEKNVKFP

HAREEAKQLLANLEKDHPKLFTSLKTAFANLHTESFWLQKA

>ABV51709.1 5'-methylthioadenosine nucleosidase / S-adenosylhomocysteine nucleosidase [Campylobacter jejuni subsp. jejuni 81116]

MKIAILGAMSEEITPLLETLKDYTKIEHANNTYYFAKYKNHELVLAYSKIGKVNSTLSASVMIEKFGAQV

LLFTGVAGAFNPELEIGDLLYATKLAQYDLDITAFGHPLGFVPGNEIFIKTDEKLNNLALEVAKELNIKL

RAGIIATGDEFICDEAKKAKIREIFNADACEMEGASVALVCDALKVPCFILRAMSDKAGEKAEFDFDEFV

INSAKISANFVLKMCEKL

>ABV51708.1 malonyl CoA-acyl carrier protein transacylase [Campylobacter jejuni subsp. jejuni 81116]

MWLWKRTWARSSSRTRTRWRRLLWWWRLRLSLMKTAFIFPGQGSQSLGMGKDFYENSIKAKELLQNASDF

CKIDFKHLLFEENEKLNQSEFTQPAIVLNSLMAYSVLLEKKPDLSSKFALGHSLGEFSALAVNGAFDFLE

ALSLVNKRGLFMQEDCAKVEAGMMVVLGLDDEKVEELCQKAQKENKQIFAANYNCDGQIVVAGLKPDLAS

YESVFKEAGAKRAMLLNMSVASHCPLLENASAKLCVELEKVLKPNFKAVISNANAKIYTSKEEALELLKA

QLISPVLYKQSIKACENEVDYFIEFGASVLKGLNKKITSKETCALTNMNDIDEFLKVI

>ABV51707.1 hypothetical protein C8J\_0108 [Campylobacter jejuni subsp. jejuni 81116]

MAIEKNSVVSMFYELKDANTNEVLESNLYSQPISFILGKGQILESLEEEVMKLDCPSNADVVIKKEKGLG

EYDENAVQTLPKEQFAGIDLKVGMELFGEGENGETVRVTVKEIGENDVTIDYNHPYAGRDLLFSLSIVDA

RAASEDEILTGIIAGSHSCGCGSGHGHDHHHGHGHGGGGCCGGGGCGCH

>ABV51706.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIFTVALLGATLLYAESSAFGAGDITSNSSYGLTSNEKLFKEKLDNLNNENIQTNARINEINERIEGL

QSTLEGINSQYAKSNSRLSQVEENNQNIENNFTSEIQKLKAYVEESRKIQEANNKQVKKVLAELSSLVDA

INANYVSKNELNDANLSVKTITPSVVVSTTDSNSTIENNNTQNTQDDKAKQIDESWKKKKNNEILELAIK

DVDKNAFEDSKAKLNFLITKQYKPARANFWLGEIEYKQKNYNNAIVYYKKSSSLSTKGDYFPKLLYHTAI

SLDKTGDTKTANGFYKALKTNYPNSPEAKASPNRK

>ABV51705.1 peptidoglycan associated lipoprotein (omp18) [Campylobacter jejuni subsp. jejuni 81116]

MKKILFTSIAALAVVISGCSTKSTSVSGDSSVDSNRGSGGSDGWDIDSKISQLNDTLNKVYFDFDKFNIR

PDMQNVVSTNANIFNTEVSGVSITVEGNCDEWGTDEYNQALGLKRAKAVKEALIAKGVNADRIAVKSYGE

TNPVCTEKTKACDAQNRRAEFKLSR

>ABV51704.1 TolB protein, putative [Campylobacter jejuni subsp. jejuni 81116]

MKKIVAIFLVFLGSLWAEDPVIDVVNSGVVLPKIIVKDNSNLSDENLKKSFYNIIVNDLKVSSNFEVVAN

ATETSNYTFEYALNKNGNTLSLNVKIKAGGSDKSEQTYTLNGLEQYPFLAHKSVKASVNALGLAPVDWMD

HKILIARNSSSKKSQIIMADYTLTYQKVIVDGGLNLFPKWGNKEQTLFYYTAYDHDKPTLYRYDLNTNKA

SKILSSGGMVVASDVSVDGSKLLVTMAPKDQPDVYLYDLNTKNLTQLTNYSGIDVNGNFIGSDDSKVVFV

SDRLGYPNIFMQDLNSNSAEQVVFHGRNNSAVSTYKDFLVYSSREPNQAGVFNIYLMSINSDYIRQLTAN

GKNLFPRFSSDGGSIVFIKYLGAQSALGVIRVNANKTFYFPLRVGKIQSIDW

>ABV51703.1 periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKNYGLSNLNSFLLALAIYISIVILVFFRLVSEVEPAIQYTDIKDSFVDIELAEPSKQVITQSNAPKEIQ

KPTEQIDIEKLFAQTTNKTVKTEDIDQKASNFNELFGNIKEIQEEKTTKIQSSAKSGASSAPKPQASELV

KQLNDSLLQEESSTQGESTKAQKIGIYDEFLGKVVRIITQRWTQYYPNSEKISVKVKIFIDENGKFGYTS

VEKSGNPLYDAKVAEFLESQKGKFITYPPQNKNISITMNLRDEAKVKND

>ABV51702.1 TonB system transport protein ExbD, putative [Campylobacter jejuni subsp. jejuni 81116]

MPFDDEKPELNITPLVDIMLVLLAILMVTAPSITYEEKINLPQGSQKNTSAPTVKSLIISINAKKEIFLN

QEKYDFISFADNLAQRKAQFNTEDPVFIRADKSLKYDDVISVLRSVKNLGFNKVALQTE

>ABV51701.1 exbB/tolQ family transport protein [Campylobacter jejuni subsp. jejuni 81116]

MNFEAIFHFFNSSSIITYIVLLWLSLYFILAFSILFARLTYLATWRNKEKESLETLLLGEKDLSRTDSIL

RKCNDTTSNHLEIYKNLASRRASAGLTWLSIIASTSPFIGLFGTVISILETFGGLGTQNSLSIIAPKISE

ALVATGCGILVAIPAYTFHLIIKRKAFELLSIIDSEIKVISSSK

>ABV51700.1 ATP synthase F1 sector epsilon subunit [Campylobacter jejuni subsp. jejuni 81116]

MNDLINFEIVTPLGVIYQGEVKSVTLPGSEGEFGVLKGHATLVSSLKSGVIDIEKADLNHELIAIDAGHA

KVDEDKICVLAKGAVWVCGSDESEIEKNLAQAKDLIKSMSSDNAALAATFSKLDNARMH

>ABV51699.1 ATP synthase F1 sector beta subunit [Campylobacter jejuni subsp. jejuni 81116]

MQGFISQVLGPVVDVDFNDYLPQINEAIVVNFESEGKKHKLVLEVAAHLGDNRVRTIAMDMTDGLVRGLK

AEALGAPISVPVGEKVLGRIFNVTGDLIDEGEEISFDKKWAIHRDPPAFEDQSTKSEIFETGIKVVDLLA

PYAKGGKVGLFGGAGVGKTVIIMELIHNVAFKHSGYSVFAGVGERTREGNDLYNEMKESNVLDKVALCYG

QMNEPPGARNRIALTGLTMAEYFRDEMGLDVLMFIDNIFRFSQSGSEMSALLGRIPSAVGYQPTLASEMG

KFQERITSTKKGSITSVQAVYVPADDLTDPAPATVFAHLDATTVLNRAIAEKGIYPAVDPLDSTSRMLDP

NIIGEEHYKVARGVQSVLQKYKDLQDIIAILGMDELSEEDKLVVERARKIEKFLSQPFFVAEVFTGSPGK

YISLEDTIAGFKGILEGKYDHLPENAFYMVGNIDEAIAKADKLKG

>ABV51698.1 ATP synthase F1, gamma subunit [Campylobacter jejuni subsp. jejuni 81116]

MSNLKEIKRKIKSVHNTQKTTNAMKLVSTAKLKKAEEAAKRSKIYAQKIDEILSEISFQINKIVHNEDDV

RLSLFHKKEQIKTVDLIFITADKGLCGGFNIKTLKAVSEMLKEYEAKNINIRLRAIGKTGIEYFNFQKIE

LLEKYFHLSSSPDYEKACEVIHAAVDDFLNGNTDEVILVHNGYKNMITQELKINHLIPVEPKSIEQTHNS

LLELEPEGTELLEDLMKTYFEYNMYYALIDSLAAEHSARMQAMDNATNNAKARVKQLNLAYNKARQESIT

TELIEIISGVESMK

>ABV51697.1 ATP synthase F1 sector alpha subunit [Campylobacter jejuni subsp. jejuni 81116]

MKFKADEISSIIKERIENFDLNLEIEETGKIISVADGVAKVYGLKNIMAGEMVEFENGDKGMALNLEESS

VGIVILGKGEGLKEGASVKRLKKLLKVPVGEALIGRVVNALGEPIDAKGVINANEYRFVEEKAKGIMARK

SVHEPLHTGIKAIDALVPIGRGQRELIIGDRQTGKTTVAVDTIISQRGQGVICIYVAIGQKQSTVAQVVK

RLEEHGAMEYTIVVNAGASDPAALQYLAPYTGVTMGEFFRDNAKHALIVYDDLSKHAVAYREMSLILRRP

PGREAYPGDVFYLHSRLLERASKLNDELGAGSLTALPIIETQAGDVSAYIPTNVISITDGQIFLETDLFN

SGIRPAINVGLSVSRVGGAAQIKATKQVSGTLRLDLAQYRELQAFAQFASDLDEASRKQLERGQRMVELL

KQPPYSPLSVEKQVVLIFAGTKGFLDDIAVSRIKEFEDGIYPFIEAKHPDIFEQIRSKKALDSDLEEKLA

KAINEFKANHL

>ABV51696.1 ATP synthase F1 sector delta subunit [Campylobacter jejuni subsp. jejuni 81116]

MENIIARRYAKAIASRADINDFYQNLCILNSAFVLPKFKNIIESNEIKKERKMEFLDSFFDIKNSSFQNF

LRLLIENSRLEYIPQIVKELERQKAFKENIFVGIVYSKEKLSQENLKDLEVKLNKKFDANIKLNNKISQD

DSVKIELEELGYELSFSMKALQNKLNEYILKII

>ABV51695.1 ATP synthase F0 sector B subunit [Campylobacter jejuni subsp. jejuni 81116]

MSKLFFIIFLLPLYAFGASNGSGEYDIIPRTINFLIFVAILYYFVATPFKNFYKNRIVKISSKLDEIQKK

LLESKAKKLDTMKKLEEAKASAAAALITAKKEAEILVQNIKKETQDELDLLQKHFEEQKDYEFRKMEKEL

VSNTLNEIFSDPNMTLKQSEIIELMMKKVS

>ABV51694.1 ATP synthase F0 sector B' subunit [Campylobacter jejuni subsp. jejuni 81116]

MFEDMHPSIMLATMAIFLAMIVILNSMLYKPLLKFMDERNDSIKNDENKVKENSQEVLGVNDELEAIHIN

TREEIQKIKQSAIAAAKEEAEQILRSKKEELERKMASFYADLAVQKKELQEHLNIHLPELKQALQNNIKK

I

>ABV51693.1 parB family protein [Campylobacter jejuni subsp. jejuni 81116]

MGLNKDRGLSSLISDMDTVYSKELGFDKNQSTMIEIDQISPNPFQPRKNFDQEALDELANSIKEFGLIQP

IIVFKKNNKFILIAGERRLRAVKALGKKEILAFIADIDENKLRELALIENIQRENLNPIELANSYKDLMQ

VHKITQENLAELIHKSRTQITNTLRLLNLDIRTQELIASGKISQGHAKVLVGLDQKDEKMLVDSIIGQKL

NVRDTEKIVKKIKNNESLPNQEFEDEIKKLKQILNRFGFDCKNKNNDFVIHLENIDKIKKLIKMLEKL

>ABV51692.1 parA family protein [Campylobacter jejuni subsp. jejuni 81116]

MSEIITIANQKGGVGKTTTAVNLAASLAVAEKKVLLIDVDPQANATTGLGFNRNNYEYNIYHVFIGRKKL

SDIILKTELPQLHLAPSNIGLVGIEQELAKGENNEKKMLLKNQIQEVIDEYDFIIIDSPPALGSITINAF

AASDSVIIPIQCEFYALEGVAMVLNTIKIIKKTINSKLRVRGFLPTMYSSQNNLSKDVVDDLKQNFKKQL

FTINGNEDDFIVIPRNVKLAESPSFGKPIILYDIKSPGSVAYQNLAYSILG

>ABV51691.1 biotin--protein ligase [Campylobacter jejuni subsp. jejuni 81116]

MKIVCVESIDSTHLFLCEQIRNGKIDGNFAIYALEQTNGVGSRENSWQSSKGNLHLSFCIKEEDLPKDLP

LASVSIYFAYLLKELLQEKGSKIWLKWPNDLYLDDKKAGGVISAKISNFIIGGMGLNLKFSPQNTALCDI

EISLKDLVSEFLQKVEKKILWKNIFSKYMLEFEKSRKFSVHHEGKVFSLENSFLYEDGSILLGDKRVYSL

R

>ABV51690.1 methionyl-tRNA formyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKKIIFMGTPSYATCILKALVENENFKLVALFTQPDKAVGRKQILTPSDTKAFLSQNYPSIPIFTPSSLK

DENIIREIKDLNPDFIVVAAYGKILPKAILDLAPCVNLHASLLPKYRGASPIQSAILNKDEKSGVCTMLM

EEGLDTGAVLESLECDIKDKNSSEVFELLANLAAKLILSTLLNFDKIIPKKQEESLATLCRKIKKEDGLI

NLQNARELYQKYLAFTPWPGVFLENGLKFLELELVDELKQNARMGEILELEKESFLLACKQGVLRIKKLQ

ESGKKALDGRTYLNGKRLKSEDSLC

>ABV51689.1 putative glutamate 5-kinase [Campylobacter jejuni subsp. jejuni 81116]

MKRIVVKVGSHVISEENTLSFERLKNLVAFLAKLMEKYEVILVTSAAISAGHTKLDIDRKNLINKQVLAA

IGQPFLISVYNELLAKFNKLGGQILLTGKDFDSRKATKHAKNAIDMMINLGILPIINENDATAIEEIVFG

DNDSLSAYATHFFDADLLVILSDIDGFYDKNPSEFSDAKRLEKITHIKEEWLQATIKTGSEHGTGGIVTK

LKAAKFLLEHNKKMFLASGFDLSVAKTFLLEDKQIGGTLFE

>ABV51688.1 GTP-binding protein, GTP1/Obg family [Campylobacter jejuni subsp. jejuni 81116]

MFIDSVKITLASGDGGKGAVSFRREKHVPLGGPDGGDGGNGGDIIFVCDNNTHTLVNFKGKRELRAQNGA

GGMGRNKNGKKGENLELIVPEGTQVIDAQTNEILLDLTKEGQRELFLKGGKGGLGNTHFKHATNQRPDYA

QPGIKGESRLVRLELKLIADVGLVGFPNVGKSTLISVVSNAKPEIANYEFTTLTPKLGLVDVDEYNSFVM

ADIPGIIEGASGGKGLGLAFLKHIERTSFLLFVLDPMRQMPLKEQFIVLRKELEKFSNELFGRKFGIMIS

KSDSVNLGEEFAEQITLNINELENYLKEINNPQSFLIKVSSLEKTGLKELKFMLLEEIKTLRNNK

>ABV51687.1 50S ribosomal protein L27 [Campylobacter jejuni subsp. jejuni 81116]

MAHKKGQGSTQNNRDSIGRRLGVKKFGGEFVRAGNIIIRQRGTATHAGNNVGMGKDHTIFALIDGFVKFE

RKDKDRKKVSVYPA

>ABV51686.1 50S ribosomal protein L21 [Campylobacter jejuni subsp. jejuni 81116]

MYAIIKHSGKQYKVSVGDELKLDHFEAESKASIEVSEVLAINDKELKVGAPFVAGAKVVLEVINHGKDKK

VVIYKKRRRKDSKLKRGFRRQFTRVVVKDIKA

>ABV51685.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKIIKILFLGLFLSLSLNAKVITTTSTKSSTGEGTGLTREDAINNAIIEAIGKMSGVSINSLKKSNTSVS

TDNSGSNIQDNYSEQISKATKGRADTYEINSVEQDANGKYTANVTIFKTTTTKKYQAPGLSADNRRSITV

FDSTPDAAKRGIGSALQQKIISDLLQSRKFNVLDRDSSGYYEMEKALIKSGDAASDEVYKLKNVLATDYI

LLFSISGLEGKQKTSNLTGKSKTEIEVIVDYRVLLFATRQIKFSNTLSMKVNLKDNSLSANEAALKQIAN

RIAGDILNAIYPLKVASVENNEVVFSQSLNQGDVYECFALGKAIKDTYTKENIGRVENKTGSIEITRTSP

KLSYAKITEGGVKVGDICRPLIGSNSGNGYTIGRDANYQTEEGGGVNLGF

>ABV51684.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKILFIGSLVMASLLYAQGSQPVEITQQDINTQNEMSDASTKDITPKSIEDFFEEFADNFGIEYGITKD

GKTFYTGKSTVAVNDTDPQFAQALQNAYQKAMLNLQSEFIRDAFGRIATSKIQNYEADNSTNAKEFDELP

KGDKVDQILNKLTQLAGAQLDKALKDLGIDTNSLSEDRKKTLLKQEFLNKTMTNAIGSMSGLVPVQTIVT

QRRGEYDVGVIAVISNKTRQLAKDMALARQSAIKGKGKAISEYLPKDTKGFLNEYGIRLVYDENGAPIIL

SYGNWGYVADPSNAKKTNILEDRAKETALTMADAAIIEFINTNLSLKDERTTGDTYEEIIKQSINVNDSS

TQEQTQNITNIIDKVNSKIKASASGKIRGIRTLKKWSYTSENGIEHVGAVRFYSYENLANTNEALNSKSN

TTKNEAKKSSSIQRSSNVVNSMDDF

>ABV51683.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKKTKILGTALIGALLFSGCAQTAYTDGKASQVKKGDALTLGLDRQDFESAAETMINSMLSDPAFANIKP

GTRKVIAIGRVVNDTPQRIDTEKLTAKITSALRKSGKFVLTSAVAAGGALDSMSEDVRELRDNDEFNQKT

IAKKGTLVSPDFSLAGKIRQDNVKLSNGKTQVEYFFLLRLTDLTSGLVYWEDEQTIDKTGSSKSVTW

>ABV51682.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKKNILFILMFLLSACAPSYQINSNQNTVILGSNLPKSLVKQFQKRINSNGYLEFEVILRSTFAKDLIYK

VDWLDKDGFVLRDVLNEDYQALRIPAGQEVILRKLASDTRAKDFRLEIKAKN

>ABV51681.1 putative lipoprotein [Campylobacter jejuni subsp. jejuni 81116]

MKIKVGLIFSGIVCLFLTACVNQVKQNTTFENALTQKYCGDDFFNQNLEKIKKNDDVIYTGLNAGLIARN

CGDFNKSNVFFDAAEESYKYDVDLENVGSKAAKFVGTTLLNDTIVDYDGSLYERIMVNIYKALNYMEEDD

YENARVEFNRALMRQDKAKEYFAKEIEKNRADLDKAKEDKNYDKNMNENSKVIEAQYDNLFKEFDTTKNF

INPYATYLASIFFFMDKDYRKAADLLREVAIIYPKNKTIKKEAKIFKEYATKIKVKKAKKYVFVVYENGF

GVVKDEFALTLPFIVDKKIISTNIALQTLKKREASFANLNINGQNTNDFVDLDNIVATEFKINMPAMIAK

ALAQTIIKTTLNVAVANNDSTGGWLSLATAVATAATNKADVRSWRGLPKSIAIATIENDGNLEIKDPQGN

ILFQKSLDKNKNALVVVRSFAPYLPASVAIMEK

>ABV51680.1 hypothetical protein C8J\_0081 [Campylobacter jejuni subsp. jejuni 81116]

MDIMIILQVIVLLGAIFIGIRLGGIAIGYAGGLGVVILGLVLGMKPGNIPWDVILIIAAAIAAISAMQQA

GGLDYMVRVTEKILRSSPKFINYLAPACGWLLTILAGTGNAVFSLMPVVVDVAKSQNIKPSVPLSLMVVS

SQIGITASPVSAAVVYMSGVLEPLGWNYPTLIGIWISTTFIACMLTAFIVSLITPMDLSKDSVYQERLKA

GLVKDAGAILHGEDKPGAKLSVGIFLITVLAVVLYATAISSNIKWIDPVVVPRDAAIMSFLLTAATLITW

LCKVEPGKILDTSVFKSGMTACVCVFGVAWLGNTFVAGHEASIKEVAGDWVKQTPAMLAVAFFFASMLLY

SQAATAKAIVPVIITALGISAANPHDSYMLVACFAAVSALFVLPTYPTLLGAVQMDDTGTTRIGKFIFNH

SFFIPGVLAIAIAVALGFVLAPMLI

>ABV51679.1 aspartate ammonia-lyase [Campylobacter jejuni subsp. jejuni 81116]

MGTRKEHDFIGELEISDEVYYGVQTFRAVENFDISHDRLKDFPRFVRALARVKKAAAMANHELGLLDKNI

QDAIIKACDKILEGGYYDQFVVDMIQGGAGTSTNMNANEVIANIGLELMGHKKGEYQYLHPNDHVNLSQS

TNDAYPTALHLALHDYLSDLAKAMEHLKKAYERKAEEFKDVLKMGRTQLQDAVPMTLGREFKTFAVMIGE

DIQRVLEARKLILEINLGGTAIGTGINSHPDYPKVVERKIREVTGFEYTVAEDLIEATQDTGAYVQISGV

LKRVATKLSKVCNDLRLLSSGPKCGLNEINLPKMQPGSSIMPGKVNPVIPEVVNQVCYFVIGADVTVTFA

CEGGQLQLNVFEPVAAYSLFNSIVMLEKAMYTLADKCIDGITANEKICSDFVYNSVGIVTALNPYIGYEN

SASIAKEAMNTGKRVADIALERGLLSKEQIDEILTPSNMLNPHMEAKK

>ABV51678.1 uracil-DNA glycosylase [Campylobacter jejuni subsp. jejuni 81116]

MEEITINIDKIKINDDWKEFLRDEFQKKYFLEIKKQYLNAINQNIIIYPPANLIFNAFNLCPLKEIKIII

LGQDPYHQPNQAMGLSFSVPKNVKIPPSLNNVFKELQNDLNITPAKSGDLSSWAKQGVLLLNSILSVEAN

KAASHSSWGWQEFSDAIIHKLSNEKSGLVFMLWGNYAKNKEILIDNAKHLILKAAHPSPLARTGFLGCKH

FSKANEFLKKVGKIPIDWKIV

>ABV51677.1 putative amino acid recemase [Campylobacter jejuni subsp. jejuni 81116]

MKTIGIIGGMSFESTITYYKTINQAINDKLKSLNSAKILLYSVNFEEIENLQSQDKWQEAAQILTQCAKK

LELAGANFIIIATNTMHKVFDEIQQNINIPILHIAKSSAKALKQENIQKIGLLGTKYTMTQDFYKKILIE

ENISVITPSDEDIKIVNDIIFNELCKGEIKQDSKEKYLNIINKLQEKGAKGVLLACTEIGLLISKNDTNI

KIFDTSLIHALDAANEALKDL

>ABV51676.1 hypothetical protein C8J\_0076 [Campylobacter jejuni subsp. jejuni 81116]

MLHALFLLAWPLVIYLSYKFIMLNINQLEKDSKL

>ABV51675.1 cytochrome bd oxidase subunit II [Campylobacter jejuni subsp. jejuni 81116]

MFFGLELEGLQIYWWLILSLLGGLLVFMFFVQGGQTLIDELSKDELEKTMLVNSLGRKWELGFTTLVLFG

GAAFAAFPLFYSTSFGGAYWAWLCILFCFILQAVAYEYRKKENNVYGSKTYEIFLKINGYLGVFLIGVAV

SSFFSGSEFILNEHNFVSWQNPLHGLELLLNPFNYLLGLALVFLARLLGAAYFMNNINDENIKIRAMKKL

MINSILFLPFFLGFLAWIFLKDGFSVDANGVVSMSANLYLYNFLNQMIFAILLAIGVILVLLGMVQGAKG

CSKAIFTLGLGTVLTVFALLSSIGLGQSAFYPSLNDLQSSLTLKNASSSYYTLSVMAYVSLLVPFVLAYI

IYVWNAMDKVKITREEIANDDHAY

>ABV51674.1 cytochrome d ubiquinol oxidase, subunit I [Campylobacter jejuni subsp. jejuni 81116]

MNELSSVDWSRAQFALTALYHFLFVPLTLGLSFMIAIMETIYVKTKNERWKKITKFWLSLFAINFAIGVA

TGIIMEFEFGTNWANYSWFVGDIFGAPLAVEGIMAFFLEATFFAVMFFGWDKVSKGFHLLSTWCVAIGSN

LSAFWILVANGWMQYPVGMSFNPDTARNEMQNFFEVALSPVAISKFLHTIGSGYVISALFVMGISAWFML

KGRHIIEAKKSLVVGASFGLVCSIFLFFSGDESAYRVTQTQPMKLAAMEGVYQGEHRAGLVPFGILNPKK

TIDNNESVFLFDITIPYALSILGNRDPNSFVPGIEDLIYGNESKGIEPMQNRIDRGKIAIQALKDYKLAK

ENNDTIAMENHKSILETHFKDFGYGYLEKPSDTIPPVALTFYSFHIMVALGSFFFLLFIVTLYLTMANDI

EKFRKVLWVCLLSIPLGYIAAEAGWIVAEVGRQPWAIQDLLPVHIAATQLGKVNVQISFWIFAVLFTALL

IAEVKIILTQIKKGFDAHAGHTPLMGKGEK

>ABV51673.1 hypothetical protein C8J\_0073 [Campylobacter jejuni subsp. jejuni 81116]

MYLKHLYFSISQIFNFYKEGFKNLTLGKTLWKIIFIKLFVMFVILKLFVFDVNFNSIFKSDKEKSTFVLK

NLTLEGK

>ABV51672.1 cytolethal distending toxin [Campylobacter jejuni subsp. jejuni 81116]

MQKIIVFILCCFMTFFLYACSSKFENVNPLGRSFGEFEDTDPLKLGLEPTFPTNQEIPSLISGADLVPIT

PITPPLTRTSNSANNNAVNGINPRFKDEAFNDVLIFENRPAVSDFLTILGPSGAALTVWALAQGNWIWGY

TLIDSKGFGDARVWQLLLYPNDFAMIKNAKTNTCLNAYGNGIVHYPCDASNHAQMWKLIPMSNTAVQIKN

LGNGKCIQAPITNLYGDFHKVFKIFTVECAKKDNFDQQWFLTTPPFTAKPLYRQGEVR

>ABV51671.1 cytolethal distending toxin, type I deoxyribonuclease-like protein [Campylobacter jejuni subsp. jejuni 81116]

MKKIICLFLSFNLAFANLENFNVGTWNLQGSSAATESKWSVSVRQLVSGANPLDILMIQEAGTLPRTATP

TGRHVQQGGTPIDEYEWNLGTLSRPDRVFIYYSRVDVGANRVNLAIVSRTQAEEVIVLPPPTTVSRPIIG

IRNGNDAFFNIHALANGGTDVGAIITAVDAHFANMPQVNWMIAGDFNRDPSTITSTVDRELANRIRVVFP

TSATQASGGTLDYAITGNSNRQQTYTPPLLAAILMLASLRSHIVSDHFPVNFRKF

>ABV51670.1 cytolethal distending toxin [Campylobacter jejuni subsp. jejuni 81116]

MKKIITLFFMFITLAFATPTGDLKDFTEMVSIRSLETGIFLSAFRDTSKDPIDQNWNIKEIVLSDELKQK

DKLADELPFGYVQFTNPKESDLCLAILEDGTFGAKSCQDDLKDGKLETVFSIMPTTTSAVQIRSLVLESD

ECIVTFFNPNIPIQKRFGIAPCTLDPNFFAEVNELMIITPPLTAATPLE

>ABV51669.1 L-lactate permease [Campylobacter jejuni subsp. jejuni 81116]

MEQILTWQQIYDPFSNIWLSALVAFLPILCFLVCLVVLKLKGYQAGFLTVILATLVALFAYKMPWNLVGA

SFIQGFTNGMWPIAWIIIAAIFLYKLSIKSGSFEIIKKSVMSITPDHRIQVILIGFCFGSFLEGAIGFGG

PVAITAALLVGLGLRPLQAAGLCLIANTAPVAFGAVGIPIIAMANLVGIEQHSVSAMVGRMLVPLSLTIP

FFIVFLMDGFKGVKETFPAILVAALSFTTTQFLSSNHLGAELPDIISAVVSLAVTTIFLKFWKPKNIFRF

DNESNFTQDNTLSFNQILKAWSPFILLIICIIIWTQPWFKALFDKDGILSYTSITLQFSNITTGILSPSV

TGIGEAKPLSLALGVDLINGKTVAQAGTAILLAAFLTIAILKIKAEDAAECFWATLKEMAIPCITIGLVV

AFAFISKNSGMSTTLGLAFAHTGDAFSFFSPIIGWIGVFLTGSDTSANLLFGTLQQVSAQKLGISEALFL

AANSVGGVVGKMISPQSIAIACAAVGLVGKESDLFKFTLKYSVAFIVLIGIWTCIIAFFLQGIIPEVIVK

>ABV51668.1 cysteine-rich domain protein [Campylobacter jejuni subsp. jejuni 81116]

MKKVYFYATCLGTAAMQQSVLNAIKLLRREGIEVIFKKNQTCCAQPSFNSGYFDESREIALYNVDLFDKD

YPIVVPSGSCAGMMSHDYKELFKNRPEFSKVKDFSSRVIELSQYLDEVLKVDYEDKGAPIKVTWHSNCHA

LRVQKSIQASKNLIKKLKNVELVELQYEEECCGFGGTFSVKEPEISNAMVRSKIKDIQNSGAKYLISGDG

GCLLNIDGTMKRMGLDIKGIHLYDFLLKRLEGERL

>ABV51667.1 iron-sulfur cluster binding protein [Campylobacter jejuni subsp. jejuni 81116]

MSQKIPHEQIVQIKLNDKQMQENLMTAMHTLQKNRLNVIDARFKDWQGLRAKAKQAKNNALMSLEERLLE

FEKNATKNGIKVHWASSDEDACEIVYEIMKEKNITKLLKGKSMASEEIGLNHYLEKKGLKAIETDLGELI

LQLNEEPPLHIVVPAIHRNRHEIGEIFKEKLGANLENDEPESLNAVAREHLRKDFEGLKLGLSGVNFAMS

REGAFWLIENEGNGRMCTTAPDIHIALCGIEKVMESFEDAATMVSLLTPSATGQFIPTYNNIITGPRKNG

DLDGPKEVHVILFDHNRSKMLAHEDYYEALRCIRCGACMNFCPVYDQIGGHAYQTTYPGPIGEVISPNIF

GIDHTGDILNFCSLCGRCSEVCPVQIPLADLIRKLRCDKIGQGKNPPLGANKVHHNALEAFAFKQFKNIA

TNGDKWRFSLSKAHYFNWAVQNFANVLPVIKKWYAFKELPQIKMDLYKEVQKLEGVSYE

>ABV51666.1 hypothetical protein C8J\_0066 [Campylobacter jejuni subsp. jejuni 81116]

MSKIDEISSKSKASILEHLKKAYKETDFTRIESIDPVEHIQTTQDMLTEMKQKMSDNKYIVENATKDTLE

EKINEIVAKYGFKSMIYGADLNLDLEQIKAEKKICFDKEIENLRSEVFHSDFSIIHARAGVSSHGVALIP

SSKTQPRMLSLAPKLCVVLLKKENVVKSLSEALNLVKKENEILPTNILFIAGPSRTADIELITVFGVHGP

QIAHIIIY

>ABV51665.1 hypothetical protein C8J\_0065 [Campylobacter jejuni subsp. jejuni 81116]

MDKLIPTWNEKYSIHDTMIDIQHQKLFELAAKIENAVYKFVQRDELKEILTELFNYMKEHFSNEEDYMQE

IHYPYLNEHKIMHKNIIHDMSYLIQNIKTTNDLKEKLYTIMSEWLLEHILHHDVMIGNWLSDQILSKQEE

ELEKINEEILYENTPTTPTAKQVKHKEYEFIYSCPCRTNHILSYTEHLDILCHKKQLRCKKCQKNLFYVK

SELKD

>ABV51664.1 hypothetical protein C8J\_0064 [Campylobacter jejuni subsp. jejuni 81116]

MFPKWDDSYSVHNAKIDEQHKKLFELAGKVEFMFDKPVYKDDVKALLAEFFNYMKDHFNDEEKYMKLIGY

PDLEEHKRIHKEIIQSMIDLIKNIKSTNDLKEKLYTVSKKWLLEHILYEDMKVEQYRRSSLASEDDGEVS

FEEVKEEKDDENAVYLYTCECVGQMHDVPFGIHQKIQLKGVKFKCKKCKEAIQFYKKYSENF

>ABV51663.1 hypothetical protein C8J\_0063 [Campylobacter jejuni subsp. jejuni 81116]

MDKKIKYFILDKFDYSYPILTKDTKCSFCENFFPIEYSSNLKTIEKECPFCNNKMDIKLKD

>ABV51662.1 hypothetical protein C8J\_0062 [Campylobacter jejuni subsp. jejuni 81116]

MKKNIVFFEVKGGSDKGEDGYRKDTMPMVNALKAKGWNAEVIFFEVGKKDEIYKYVKENFDGYVSRINPG

NLKEENEYFDMLRKLCADKLVGMPHPDAMIGYGAKDALTKLADTDLVPSDTYAYYDIKTFKENFPKSLAK

GERVLKQNRGSTGEGIWRVSVEGNVSGDSLPLNTKIKCTEAKDNHVEHRELGEFMDFCEQYIIGDNGMLV

DMTFLPRIKEGEIRLLMLYNTPVNVVHKKPAEDADAFSATLFSGAKYRYDKPEDWKTLVDMFLGELPKVR

EKLGNYDLPLIWTADFILDTDEKGNDKYVLGEINCSCVGFTSHLELADEVASNIINIVSKTKA

>ABV51661.1 signal peptide peptidase SppA, 36K type [Campylobacter jejuni subsp. jejuni 81116]

MQILKSFFKALGCGIKFINTYFKTFVLLLIVIWILMPSANSSSNLANLERIDLKGEIFDSSAVLEKIINA

KNDSNIKGVLFVVDSPGGAFAPSMELALAIKDLKIKKPVLVYASGTMASGSYLAGVGANKILANPASFIG

SIGVIMQGADLSGLANKLGIKEQTIQAGEFKSAGTFARAWNENERNFLQGLIDQSYDLFTGFVAKERALD

LNKKDQWANARVFLAAKAKELGLIDELSNYENAKKELEKLANVSNPVWKEEDKIDKFLNRLEGQTSSLIS

KSLIEIAYKTNSSFINAR

>ABV51660.1 chlorohydrolase [Campylobacter jejuni subsp. jejuni 81116]

MFIAAARYLFLCDEDFTILENQAFVFEDKILELGELDNLRKKYPKAKIIKTPKNSVILPAFINPHTHLEF

SANSTTLHFGEFLIWLKSVINSRSMLNAQAKEELILQSIKKMQKSGIGTIGEISSFGSDLDPCLKASQKG

IRVVFFNEILGTNENQVEDKKQEFLKRFENSLKFKNDFFIPAISIHSPYSTHPSLAYFALDLAKKQNLLV

STHFLESKAENIWLRESKGGFKKWLENFTLHPKPLYAPKDFAKLFKGVRTLFTHCVYLKEYEWLDKNLHS

ITHCAFSNRLLSQKSLDLKTALKSGLNIHLGTDGLSSNISLSLLDEMRANLLIHKNFDLLELASKLLQMA

TLYPARALNLNLGELKKGKIADFSVFELGECDKKQAPLQFILNAKEVDKLFIKGKECKF

>ABV51659.1 3-dehydroquinate dehydratase [Campylobacter jejuni subsp. jejuni 81116]

MKIMIIQGPNVNMLGVREVGIYGAMKMEEIHEQMKLAASQNNVELDFFQSNFEGEIVDKIQECLGTVDGI

IINAAGYTHTSVAIRDAIAAVALPTIEVHISNVYRREEFRQKSLIAPVCSGTIVGFGPFGYHLALMGIIQ

ICEQIKNLRAMQQAQQTNK

>ABV51658.1 putative 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase [Campylobacter jejuni subsp. jejuni 81116]

MLKIQGVKHFEKSRFFPFFSQNIRSFKYLALIGLGSNIEPEKKRFDMLFRVMMDDKRFKILSTSPMLINE

AFGFKEQKDFTNAVMLIQTNLHARALLKVLLYYEVKFKRKRTFKNAPRTLDLDLLYFSQKVKRDKWCEVP

HKGAKERVSVILPLGMI

>ABV51657.1 flagellar biosynthesis protein [Campylobacter jejuni subsp. jejuni 81116]

MGQLIHTFTVEDTEQIIPKVKEDYGDKALIITNKQIRPKTLNRSALYEVMVAIEESDYEEHLKKQGKSLP

AKKSSPKPSSTSLAEEKIRSQIPQEDEDVVLDFSNTRLNTNLNTVKNNDLTKKTYQDFPQNKINPHQNKT

LGFDDFKEKLSEVSNEISKVTNTPLENYTPNPNYNKKIENFEKQFEKQINKLNDKIDLLADMMWDDKAEA

RKNLMIPPEFASIYKQAKESGMLENHLEAIMKATIENMPAAMKTNKDAVQRYFHSLLRNILPCRVESDIK

KQKIMMLVGPTGVGKTTTLAKLAFRYAYGDKRYKTGIITLDTYRIGAVEQLFQYAKMMKLPIIDSIEPKD

LDEAIKSLNNCEVILVDTIGNSQYDQSKLAKTKEFLMHSNAEIDVNLVVSANTKHEDLMEIYKNFSFLNI

DTLIITKFDETKVFGNIFSLIYETNIPLSFFSTGQEVPDDLEVANSDFLVHCILEGFNKGKNNE

>ABV51656.1 putative ATP-binding protein [Campylobacter jejuni subsp. jejuni 81116]

MNNQANKLRNLMSQNGTKKSQNTHFIAITSGKGGVGKSTISANLANVLANNGYKVGLFDADIGLANLDVI

LNVRIQKNLLHVLRGECSLEDILIEVKPNLWLIPGESGDEILKYNDKNIYERFLNQASILDELDFLIIDT

GAGIGGNILNFLEMADEVIVVTVPDPAAITDAYATIKTTSKTKENLLMLFNVVKNENEALKVFENIKKVA

DANIKNPLNLEFLGHLSASKDVSGSIKKRTLFSDENTASSDELKALASKLLYRLERKVLDNVSNRSFSSF

FRKIIERF

>ABV51655.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MRPENYVAFFTVCGFFIGLAFSIISIDEAFDILIFTCFITFMFYVFVHIAIMNFIDVKKISGRIFNKHDY

EKTSNNIINDLVIREKKMDIILEKLNEEREELKKNEFKERRRNAKRAA

>ABV51654.1 RNA polymerase sigma factor, sigma-F [Campylobacter jejuni subsp. jejuni 81116]

MLKEPPKAYAQMLKKEQDELVLSYMPALRAMAFRLKERLPSSIDVNDLISIGVEEMIKLSRRYDKEQNDN

FWGFARKRVNGSMLDYLRSLDVMSRNNRKIIKDIDAIMDEYFLEHECEPDDEYLAKKLDLDVEKIKEVRT

AHAISYTLPIDEQIELYNEDNTLEKIEKEELLEKIHEVLDDLKERDQLIIQLYYYEELSLKEISEILQIS

ESRISQIHKKLLKKLRERLV

>ABV51653.1 flagellar motor switch protein [Campylobacter jejuni subsp. jejuni 81116]

MAEILSQEEIDALLEVVDDNTDTPIASNSKDEKDERNIVVYDFKRPNRVSKEQLRTIKGIHDKLARNLAS

QISSMMRSIVETKLHSVDQMTYGEFLMSLPSPTSFNVFSIKPLDGNCVLEINPSIAFPMIDRLLGGQGDS

YEASRELTDIELNLLDSILRIIMQRLKESWATVTEIYPSIEAKESSPNVVQIVSQNEIVIMVVMEIIIGN

SSGMVNICYPVVHLESILSRLANRDIMMGETSAKKSRNKELKTLIGRAEVVYEAILGKTLINVHEFLELK

QGDILRLDREADDKAIVSIDKKDVFLAQIGLHRFRKSIKILELIRTDKDEIKEILEKYEEERKAKASVYD

EPEEEDEEI

>ABV51652.1 putative flagellar motor switch protein [Campylobacter jejuni subsp. jejuni 81116]

MINDFLKMFTNECISTIEGLTGKSAEFSEYKEFDVNASDTLKAPLVYAIFNIANGGKIGILAGAVLMSAI

GEWMMGEEEITKNDKLGPDEMDAAKEAIQNIISAFSTTLGAQKDIPKMDFSIESCEFVPESVDFKDFKKL

FLYDVKIGDLEEQVSLAMDQTLHNILSGKPAETGNTSTDSNHNAEEKAIMLSEELKNINLIMDVRLPVRV

RIGNKKMLLKDVLTMDIGSVVELNQLANDPLEILIGDKRIAYGEVVIVDGNFGVQITEIGSKKERLEQLR

>ABV51651.1 hypothetical protein C8J\_0051 [Campylobacter jejuni subsp. jejuni 81116]

MDTKIIKDVEKFENIPDLEKAITFFGSARLKEDNFYYQQAKILAQKCAQNGFCVISGGGGGIMRAANEGA

FSQKNNTNSMSSVGFNIFLPHEQKLNDFVEYNITFESLAIRKMALIEKSLAFVIFPGGFGTLDELCEILT

LKQLEFKKDVPIILFGSEFWRGFDEFVRNSLLKLEVISKGDELKYKITDDLDFIINTLKEI

>ABV51650.1 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Campylobacter jejuni subsp. jejuni 81116]

MKILVAMSGGVDSTVTAYKLKNLGHEVIGCYMKLHGKPNYHEENIKKVEKVANFLQIPYHILDLQKDFKN

KVYMPFVDTYKEGKTPNPCALCNRFIKLGKLLEFAKSLGCEKLATGHYARLENNLIKTAVDESKDQSYFL

ASADKEALKYLIFPLGEMKKEDVKKFASTIEVLKSFATQKESSEICFVEDTYVQVLDQFMDTKIPGEVLD

SSGKVVGKHEGYMHYTIGKRRGFEVRGAHEPHFVLKINPKQNQIIVGTKEELKISEFKLKNINLFIDAKE

LDCEVKIRYRSKSTPCKVEIYEDKSAKITLKDPVYGLASGQMAVFYDHDKVIASGFIE

>ABV51649.1 hypothetical protein C8J\_0048 [Campylobacter jejuni subsp. jejuni 81116]

MKVKWSRDFSIKNMQLDKQHELIFEITNLANDLALKIQENNTQYKDDLKQILAKLFQYIKIHFKDEEKFM

ESIDFPLIEEHKKSHQILVEKTKELLEHSDNIVKMSQELSILTKDWILDHFANEDLWIANFTKKTLHLQE

IHYTLEQYIKLKSIKQDLRAEKTHDYICNCSLRIHAVPQTIHQELVSKENTLKCEKCGQILVHLDYFDLN

QNFEKFNAIFEDALQNHHFTTQKNDMGGG

>ABV51648.1 hypothetical protein C8J\_0047 [Campylobacter jejuni subsp. jejuni 81116]

MNFQVKTLETFNPFESLNHEQANTEQILDFRVIDFKLLCSSVKPAKTKTYERKDFDLFYADDFFVKNYNT

IVQKFLIEIYPKTQSFPFTVKLRSNSNLTHLKASINLTENFKYYPNLKFDILQNIYKIMIKQKFLILRLD

KNLFDKIDDFILSIQKSPSIKEIELEIAKGVDKIEHKSDEIIYHRDVNEECFDENINYDEGNYCKPIEKN

ELLFEYIYRILGKEGRNLRGEILHLNPIAFLDNPFIIKDESIYTEELEDRIKYFSANYGFLNKDHTGYCI

ANNLKLSQIGLKTTGSIKTNIDENINLEITNFDISDDAIKSGIVNVQASNIKVNGNVGATKLYGKNISIK

GLTHAKSEIFAQDIFITTHKGTLQADTVYIKNLENGTIIAKNVFVENCMGGKIEAENIYICNLLTDNTLY

PRKNLIITNNIKFKNNIVVSPLVSIENNSDTECENLKNLSLKIKSKLDDTISKMQNYYDYLIKNQIKIIK

LQKTKNPNAIEMKFSNLYHDIIKKYNHLSISYKKFIKLKYQIDAKLNFLNEMVYNVKIYIKAENIGEDNF

LKFYPNTNTNLELKHHINLKDYEKVLYLEKGQQVSYIKSSHNYSESDIEEIKIIFEKLEKDNS

>ABV51647.1 flagellar hook protein flgE [Campylobacter jejuni subsp. jejuni 81116]

MMNSFYNGISGVKSNSFGIDITANNIANVNTTGFKYSDAQFKDIFYTTITTQSTNPAQGGYGSGAASSQV

VFEQGSPVASDGEFDVALQGKGFFGVLGADGNAYYTRNGSFRRDANGYLVDSYGNFVLGTMNPAFTGINY

SDRVAGLMGDYLNTGTPVNNGFTVNSNNSFSIGTTASQGAIKVPVNMYLPPQVTQNVKWSGSLNTNTTTE

VVKVDLDPSKFNITKTEDGKYVVSGSVSKEDVFSAKAGDRIILNFTDDNGVKTSFEATLDENLNFKSNEL

DLKGLDENSIKLDTAQISTEQQKANKDILESPIYNADGSKSTLRVTLERVLPQEGDNIQYKAIAQIYDSN

GNAVGNPTEGNMVFDKNGALLQNNITSIANPNGGTINIDLGSPYDANKPGSGYSGIYIKEGVEKNVVTQQ

DGVAEGFFEQYNISDDGSIVAQFSNGKNAIVGKLALYNFINEQGLVAMGDNIFAATANSGDASFIMKDGQ

VVNTAKFKGGFLEQSNVDLSAELSNLIVTQKAFDASSKSITTSDQMIQKAINMKR

>ABV51646.1 putative flagellar hook assembly protein [Campylobacter jejuni subsp. jejuni 81116]

MISSSDWNLNTAATTSGTTSSGSTSGTTRTDSSSSSGIVSNPNATLDKDAFLKLLLIELQHQDPTDPMDS

DKMLTQTSQLSALEMQQNTNTTMQKMVETMQKLSDSFSTSMSTSALGAIGKMATVSDNKIKLTGADELIA

LKMYLPEDSDENGVTLEIYDSNNKLVFSEKSDAKSISQGLFTMEWPGRNNDGVYAGDGEYTVKMVYNNKN

GEKITANYGTYPIEGVVFKDGVAYAKMAGQEVPFDAIQEITDYKLGSSSSTGGSGSSGDSSGGSSDGDSS

GSGSTEDGDKEEKA

>ABV51645.1 hypothetical protein C8J\_0044 [Campylobacter jejuni subsp. jejuni 81116]

MSNLAPQNDVLNLTPSKTSNTSSSFSKTSKNKEHESSDSKNSTQDDTESFLNSLLNSIDETNEFLPDHMK

ISQKEVVSEAMNRLQKGAFDESDKISIFESASFMQILSLLDKLKTDTADVKLANLSTQLSSLIKTEANFN

ALKGASNLSELLDIAKDLGLNVKNIKVDRLLDLKATFPNLDKADFFKGAVDNVFKEIINNKISNVSKNLN

HNLENTTHTTSTHSTQKTNSKDSGSLLSQTLKNLDSILSSKESKHEKNDKVKSKIEEDTTDTKNTLKNIK

NDEFAKNLTEELNIKDKKNQDSLNKDNNLKDLNKESKDLNKDFNKELNKNQEKNNLNQENIQDQNKNLKN

NDQNLNLDKNLNKEIVKDTQNLVSNLTQKDFNLNKEPKNNNKENKDIKQNFFDQKLNFENLNKTQVVQNK

ENNANFNNNTTNKETFTQEQTKTHSENVDKNSLDELNSLVKDLNKVTQNNARNITPKETLQYFSQDLKEA

VDQYKAPITKLSITLNPNNLGEVEVTLIQRGNNLHINFNSNANAMNLFIQNQAEFKNSLVNMGFTGLEMN

FSDQGKREQNQNQGKNRSGYGFKDALDGKNESEKVNLELVLAKYF

>ABV51644.1 hypothetical protein C8J\_0043 [Campylobacter jejuni subsp. jejuni 81116]

MSKPLNEEIFIEFKSDLAERKNEVLLQVLELLETFRSDKNEKMARISSELTEILENEENLEKILNAKNLE

ELLNILIALNEDKMIKVYEDSYLKEKFPNVMVDKFLK

>ABV51643.1 GTP-binding protein typA-like protein [Campylobacter jejuni subsp. jejuni 81116]

MENIRNIAVIAHVDHGKTTMVDELLKQSGTFSEREQISERVMDSNDIEKERGITILSKNTAINYKGTKIN

IIDTPGHADFGGEVERVLKMIDGVLLLVDAQEGVMPQTKFVVKKALSLGLKPIVVINKIDKPAADPERVI

NEIFDLFVALDANDEQLDFAIVYAAAKNGYAKLDLNDESDNMEPLFKTILERVPAPSGTNDNPLQLQVFT

LGYDNFVGKIGIARIFNGVVKKNQSVMLAKADGTKVNGRISKLIGFMGLEKMDIEEAGSGDIVAIAGFEA

LDVGDSVVDPNNPMPLDPLHIEEPTLSIVFSVNDGPLAGTEGKHVTSNKIAERLEAEMKTNIAMKYESTG

EGKFKVSGRGELQITILAENMRREGFEFCMGRPEVIVKVEDGVKTEPFEHLVIDVPEEFSGAVIEKLGKR

KAEMKTMAPTGDGQTRLEFEIPARGLIGFRSQFLTDTKGEGVMNHSFLEFRPFSGAVEKRNNGALISMEN

GVALGYSLFNLQERGVLFIEPQTKVYTGMIIGEHSRPNDLDVNPIKGKNLTNVRASGSDDAIKLVPPRKL

SLERALEWIEEDELVEVTPVNVRVRKRYLDPTQRKRMEKAKS

>ABV51642.1 hypothetical protein C8J\_0041 [Campylobacter jejuni subsp. jejuni 81116]

MDLKSLENNRLYILKRLGILKFLSIIEALLVGFLAFVFIRDALIAVILAVFVGVFFFRFTAKKLKLAQKE

LQINALNLFLRRFGAKFKKQSLSQKDFLKLGLTKDLKEFKSQNCFEFKDFKIYDIQFLDENKRFFCGILL

EILSANKNPSFENEEQIYIKLQDKNFTLNHIFSKENHYLIATLSNPFFIDVKKDLESNFKDLEENLNSIK

NKLFK

>ABV51641.1 putative cytochrome c [Campylobacter jejuni subsp. jejuni 81116]

MKKHILLLGLCLSLSLSAKSVSDYKVGEELSDKEGVEYFKELSKRPVQEWPNKNLSINDVPKGKQGDLIR

YGIELLSKTESTLGPYSKLKKTSNEVNCISCHMDNDGNGLPGTKKYVIPFLNVLNNYPKLDIETMKIISV

EDRIRGMGGTDSHRFPNDSKEMKAILAYFKWLKEAYGIKDGVKLEGDFFAKMNFPNRPADPVRGKKLFEE

NCVACHGERGLGVKNDNYEQGSGHLYPSLLIYPDGGHMAMIPFLARFLKSAMPFGASADNPILSDEDALD

IAAYVNTGFVRMPITTTENRAGLDTAYSKSPSLKPEYFASPQQNLDPKEYIKVKYGPWKNPNHFPGE

>ABV51640.1 hypothetical protein C8J\_0039 [Campylobacter jejuni subsp. jejuni 81116]

MQNLNQNEQIKCPSCGSFIDISTALYAQILDKAKQEMLKQKKEFDDEVNAKRAEYIKALNDLKTQKIEQE

KLINEQVSQKLLLEKQKFEQELLTQKQNFQKEFSEKFNKEHENEMKIMQEELEKKSKELSEFLSIKAENE

RLKREQKENEERLKFQAKEEAFKEFKEQESKNLEFEREKMRLEFQKSTQEQDLKYKELETNFKSVAQKLE

DAQRRIEQGSQQLQGEAAELLIEEYIQSEYLSDEVKEVPKGVNGADCLHIVKDNFGNICGSILYESKRTK

EFNKEWLDKLKLDSIAAKSDIAVLITKTMPKDKEKTHFKEGILICTFNEFKGVLAVLRESIINAYKLKNA

LQNKDEKNHILYEYLNSKEFNTQITFILKTYQNMKEELEAEKRALQNIWKKRERAIENLSFNSTAIVSSL

NAIFSDLQGGNLIGEEGIKSLENLAKDED

>ABV51639.1 drug resistance transporter, Bcr/CflA family [Campylobacter jejuni subsp. jejuni 81116]

MQKHTKIHGFAKFKLIIILALMSSIAPLSTDMYLPALSHVEQSFQTNSFLTQLSIASFFIAFALGQLIYG

PLSDIFGRKIPALVGIFFFIVSSLFCVIIDDIYAFIALRFFEALGGCAGVVIARAIVNDLFEIKEAAGIF

ALMMVFSSLAPMLSPTFGGILLEYFSWHSIFATLFALGILLFLMILFGLKESAPHLKNKKFSHHEAMKSY

KFVLSDKRFLVYILCASFALAAMFAYITGSSFVFTQFFSLSEQKFALLFGANALGFVICANINARLVLKY

ESEKILAKALMIMFISTVILLANAFFHPNFLLFELSIFTSIAMLGFIAPNTTTLAMARFKEHSGTASAVL

GTVQFGFAGLISFVVGAINANTPIILAFVMCACVLVANMIYFLIKIKEKK

>ABV51638.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKTNNIFMALAIVLASLILAFGFNKALSDFKTLERSVSVKGLSQKEVEADTLILPIKFTRSNNNLTNLYE

ELEQDKENIIKFLKEQGVKEDEINYNSPNIIDRLSDPYSNDTQAAYRYIGTANLLIYTQNVKLGKSILEN

ISSLAKFGIVTKIDDYDIEYLYTKLNEIKPQMIEEATLNARNAAIKFAQDSNSHLGKIKKASQGQFSISN

RDKNTPYIKTIRVVSTIEYYLKD

>ABV51637.1 hypothetical protein C8J\_0036 [Campylobacter jejuni subsp. jejuni 81116]

MKEFDEKLAQYGIFTINGVENIDLIKKEIVLENISIERIDFNILQEKGIKRLIIKNSEILEIYFSKTNNF

FIYFLNCDFKCKLIAKKCIFQDQVKFIKCIFEKCVDFNASKFKSKVSFTISIFKENARFIKTEFLAKCNN

HKIIENNFKEVKFCNNVTFRRAKFESKVSFTISIFKENARFIKTEFLAKCNNHKIIENNFSETIFYNKTN

FYKAKIVSKIDFKISRFKGEIRFVETKFLSKLDNEIANNFREVVFEDKVYFNKTKINTQINFKMAKFKNN

VEFVNLHNNVSFNNVNFKGIVNFENLNINTLNFKNVIFNNIVSFDNIRFDNNCKPNFENCTFSDQFNIEH

KYIEYKFDEIEKTQEYDKLLNYRDLFRKLKSNRIAHHNLIDASELRAQELYARELELKHKENKSLKEKIE

RWQLVFYRKLCDHHTDLLLNLKWLVVVIGLFALLYFASRMIQDISLLKALNQYGVCLSIVGVFNLLCLYW

FGCIKKFDFFVYLNLIVVLWVICYMPKIIFGIVNIIGDKSYNGFENALITIYTILLALVLFSLQKTARKN

SIVPS

>ABV51636.1 hypothetical protein C8J\_0035 [Campylobacter jejuni subsp. jejuni 81116]

MKYKWIVKNAYINFKLNNLYMLINPSHKIYLKKDMCYCFEIYIKYRIFNNCILVCDMLDNWWKLISSTLH

LDKSHIKYNYLSNTFIVSDFELGIKLESNLLTKFNFEFYNGLILNQLSITNGLSLKRENYNKSLKFSNCK

FNKEFCIARINISKQIVFENIYFLENVFIEWVNFNENSCLRFFKCNFKKQCNFKYNIFYNEIDFLDIYAK

ELILEQNIFNKFLYIQNSTINNINLWKNKFKNRCYFMDSVFGNKNNENIKLNFSNAHFEDNAYFNNSEFY

SYADFHECEFDDIACFYGVKFYKAPNFSACYFKEPKAVNLINVDIDKLDFKSVEKYIEDNYKDESYKNET

KGIQDEKEIFKIQNEYRLRYAKNLKDSFRVIKDVLITQNNTLEAQEWHKLELYAKEKELEIQLSKNKNDN

LKKESKNQVYNPKDYEKINSSRLKTLKSKLMPLIFYSLLPMAHTLFLPFYLFCTIFIIIKIITKILIKIS

KLFYYFYISFRPLEWNKFIIFWKVKFNHCIKKLMTFGRKMLDFTLWFDCILLQVYRNTSNHHTNFLKILN

FTILMISSYAIFGLLFLNNMDFILSFGPMTIAAMNYIVLLMLLIIFISLTRQLYQHGAILLFLIYGLFII

SIVSFLSPIYIPAFYFLIYFVGILISYLLFICKIKLFVFISRLFAYICLIGVVILKPQLINPFVGIFSSD

KLYESKFEKRLNDLNTSAIINLASILQNDFNLHLKDQNISFTELNSAKALIIANKEKLKEILSKVYNDKY

VSDYKKVLNELENNTSNVKNIIEEIDNKNNNSVVSAQLNKFLKLNFNQEIDILYAIKSNFSISEKLSPEQ

MALFDQKDSQDKLKSVLALLKFKSSFEGILKIINQDEITENTIKSTGVLYGIILLLCIFSLQKTARKNSI

VPS

>ABV51635.1 hypothetical protein C8J\_0034 [Campylobacter jejuni subsp. jejuni 81116]

MKFEAINEKEFLNPYHRKKPILETELNEFIKTLKDYKINLENNLKNNEDSLVANALSKFFENLSFQCEVK

SIHKGNSGIDLALKKDGLTQVIIEAKLPHSREFFSPSKPNCKALHECILYYLRERKALNSSLKHIIITDF

YSFFIFKADLFEELFNKNKYFKEAFENFESKNSLFKGNTDEIYKEFEKILNGDSTLKGLFVDLKPILEQD

KLSFSKLKPLFKIFSKDCLLGEFNPNDANSLNNAFYKELLYILGLCESKQNSKLIIAKSEESKEEQGTFY

TAINSKLKEENFETILKLLILWLNRILFLKLIESNLVRFNDDKNLKFLNFKKIPDFDKLSELFFEVLAKE

KSTRKKSEFAYLPYLNSSLFEKQSIENTLEISSLSNDLKLFYYKNTVLKDDKCKAKKGQVGLLEYLFEFL

DSFDFGSDDEQSEILSQKELISSSVLGNVFEKLNGYKEGSFYTPSFITSYMCKESITKVVLDKFNAQFDL

DAKDISELRKSLRKEDKKAQKELLNSIKICDPAVGSGHFLVSALNVMLSIYDELNLFDEEFYLEVQNDEI

LITGRKGEFIEYKRPKTPKDKAHLIQQELFHTKKDIIENNLFGVDINPNSCEITKLRLWIELLKHSFYQS

FDDGNYHDLKTLPNIDINIKCGNSLVSYFETGKSLSHYPNIKERMGKYKRIVKDYKEGFYTDKSHINQEI

KNLKISFKNFCFADKFKKEMKSFNDKCEKYSKKYGNFLAVDDENLKFFVSANLTLFDFDEKEATKEFANL

KKEYDNIFNLESNHPFEWRFEFPEILDDDGNFKGFDLIIGNPPYIKENDNKDLFTNTKKLRTYQGKMDIW

YHFVGRGFDILKNNGYLAFIATNNWVTNSGAKKLRNIVLEESQILSLVDFSSFMVFDSASIQTMIMQFQK

IKPPKNYEFHFAKITTQTPIYEDVINLLKNEKTQNNEILSINLTPKKFIDKTLNFTKSDYEELFNKIQKY

GKFYLEESEVAQGIVPAIDEAFVIKDKNVFSKNEQCFIKEYYTGLSGKFYSSFTDKYLIYLSNKNYSGNL

DDLPNLKQHFQKYKEILKESKIKYKTPNKPYFYLHREREEKFFKKGEEKIISQVRCIEPIFVYSNENFYG

SRALFFIQTCRINLKYLTGVLNSKLIAFWLKHKGKIQGNLFKIDKEPLLNIPVVNINSKNEKLANKLISL

VDEILKVKEQDKNANTQELENKINSLVYKLYNLTEEEIKIIEGR

>ABV51634.1 hypothetical protein C8J\_0033 [Campylobacter jejuni subsp. jejuni 81116]

MRYLAIFAISITLSFGAANPPIQDRTGTGLVLSSHELANKIGKEVLDKGGNAIDAAVAVGYALAVVHPAA

GNIGGGGFAVIHLANGENTTLDFREMAPLKASRNMYLDSKGEVIKDASTIGYLAAGVPGTVKGMSAMLDR

YGTMKLKDLMAPAIKLAEKGYLINDRQEQTMLEAKDMFKEFPSSSKYFLKKDGSTYKSGDLFVQKDLAKT

LKLIAKEGPDAFYKGKIADLIAADMAKNKGIITKEDLAQYQAIWRKPVEGTYRGYDIISMSPPSSGGAHI

IEILNIMENANIENLGFASSKTLHIMAEAMRQAYADRSEYMGDPDFVKIPLDKLTSKEYAKEIYAKIPKD

KALPSSKVKPGLGQIHEGHNTTHYSVLDSKGNAVSITYTINASYGSGATVEGAGFLLNDEMDDFSIKPGV

PNLYGLVGGEANAIEPKKRPLSSMSPTIILKDGKVFMVVGSPGGSRIITTVLQVISNVIDHKMDISTAVE

SPRFHMQWLPDEIRTEPFGIIKDVQNNLEKMGYKITKEPYMGDVNAIMVDPKTGKIIGSMDTRKEF

>ABV51633.1 hypothetical protein C8J\_0032 [Campylobacter jejuni subsp. jejuni 81116]

MFKKIFFSFWMSLILLFIYALSCAVATFVENDFGTNAAKALVYNALWFDILHLLLLINLIGIIFIHKLLQ

RKKYASLLLHSAFIVILLGAAITRYFGIEGGMHIREGQSSDIIVTRDEFIALMLYNDEGKVVEYQSFGVA

FNPLLHNSFEKKVSMQQNKTINLKLLDYEKAPNAMSNPIIKMQISFNNESKEILLTPNYNNENVLPFRLG

GEIFALNWGPEEIKLPFSLALKDFILDRYAGSMSPSSYASDIEVIDQDKSFEYKIFMNNVLDYGGYRFFQ

SSYDQDEQGTILSVNKDPGKIPTYIGYTLLTLGFLWILFAKNSRFQKLSNYLKNQKNLLLILFCLFAFNI

KSFADENTLKLIQNIKENSAKHSMLFGSLLVQDFDGRIKPIDTLAMNYIHKITKKNDFLGLNYNQIFLGM

MMYPQHFRQIKMISVKTAKLKEILGVDKNEKYLAYDDVFDGDFYKLSNYIEEANRKKPALRDQFDKDILA

LDEKINTAFYIYSGEIFRIFPDPSQKTYTWYSPATPMPFDLKDIENIQSLLAKYFFDFEQALSTKDFSKA

DESLERLKNFQNFYGSNLIPTPTQISLELFLNHYNIFDNLTPIYLLLGSMLFILLVYEILSLKKAPKMLK

NAIFILIALSVLAHALALIFRWYVGDHAPWSNAYESMVYIAFACAFAGLVFYKRSSLALCTASIMAGISL

FVAHLGFMDPQITNLVPVLKSYWLNIHVSIITASYGFLGLCFLLGVFSLILFMLRNPKKAQIDQSILNLH

CINEMAMIIGLALLTIGNFLGGVWANESWGRYWGWDSKETWALISIIVYTMILHLRFISKFNNPYAFASA

SVIGFYSILMTYFGVNFYLSGLHSYATGDPVPVPKFLYFFIAFTVILILGAFFKRKLKSPA

>ABV51632.1 hypothetical protein C8J\_0031 [Campylobacter jejuni subsp. jejuni 81116]

MLKKLILGFIILLFCACNDEKIDENILSKGTKTTEQYKQDANNLDLNSYKEIAEFFKDNQNIVFSDKPVL

IIFSANNCVYCDKLKHEIQNDKEVQNILKNTYNSYYINTSYHKIHNYDNKKTSTEELSREFNIDATPTLV

FFTPKHKTLLIYPGFMSAKRLALTMEILKDEKNQKLNEDELFKTLFLAYKEKNV

>ABV51631.1 putative membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKQSLIKFILLAVFCFSTPFLLADGKIQIGIVEGVTPISMKDAEKLLGQKNVYFVDVNSKEEREVAGNIP

NAVLVDAQNWQNLLPDDFNATLIFYGSNRFTFDASNIANLSQKLGYTHVYVMLDGIESWVLSGRKVQKEQ

IEKWQNAKNLDDFKDSIHSRMYFGDVPSCRDCHGKGEDKKSIRYNNAANLDLINKNCASCHKDVDKEFKH

SIHQNISQIQLDKDGKKKKIPTCTTCHDIHNNDPLMNAMTLKQRSDFKCGECHQDKQDRYHDTFHGKAMV

LNSPGSAPKIAACYDCHGKHNILKVEDLNSTLSSLNRVQTCAQCHPNSNENFANFIAHADHSDGENYPLL

HGAYIFMTALVIGVFVFFGLHTLLWSIRLILARLSHPIEWKKAKENAHNDKILIKRFSTFHKIQHFFMAA

SFLGLAFSGLPQKFYTAPWAQTMIDLMGGPIGATIVHHISAIVMFIVFFSHIGEIILVNWKRRDLVRDPQ

TGKLDKMKILKALFGPDSLMPNWQDFKDMKAHFKWFFGMGERPQFDRWTYWEKFDYLAVFWGMFVIGLSG

LVLWFPTFFSAFLPGWMINLCSLVHSDEALLATGFIFAIHFFNTHFRADRFPMDMVIFSGTQSEAEIKQE

RNAYYQRLKESGRLESLYEKNSKFNSYKGIAKLAGYLMLITGMIFLFLMIYAFIVDLLK

>ABV51630.1 hypothetical protein C8J\_0029 [Campylobacter jejuni subsp. jejuni 81116]

MKKLISKGKVLTLLLGVGFALNVSSAENSNVLIQGEAAQDGDTKPRTLEGYVHQEDAFFKYLKEHHPMFK

YEKEGRIVGKYAISDREEEYVEFSNGPTFAQQNNLAHTSVTYRLGMESFLDFPNKFVGPKKCGECHPAQY

KAWERSRHAKTVRFPDEFEEVGNDLKKPMYNSQSTILPDGIYPDDVYAVIGTPRTKYGFIDRWLVRGTYH

VEDGNLSNMTGKIVAGGNQFSRLWSEFLTPEMTKKIAEFSPGFPTTMEQFGGNGSQVWGTNSYAAQYRKN

MLFQPASSYCETCHSFKFDFKSKEEFYKALGNTQELRKHTISKGISCEECHGAGAHLYGARGAGMPSNCE

RCHQRFSYNEEDAKKNPRKPFNAFFKSSCPACGTEGAQMYSSAHYDKGMRCSTCHDPHEVTFNDWKDGYT

KVGLKKTCTDCHDTQASFFKQGGIHSKDNCTACHMPNMMSCENFGAVQNPDKGGFDNVRASHIWKIKVDK

TAKTLNPPEGKERSPKTSGWTIARDDDGRFFLDLMWACGRTSFSDPNLMGPGASGCHSAVQSNLPKKLHF

TDQETIYDIVVGWQKPVKDGYENILKGVKEIDKAMAENPKLSVEKKSRVITLANQARAIAEKLQKDGSWG

VHGPVYSKKIVDEALVYIQEAKNILK

>ABV51629.1 L-asparaginase [Campylobacter jejuni subsp. jejuni 81116]

MAEAKPKIAILATGGTIAGSIDSAVATTGYTAGVVGVDVLIKAVPQIQDLANISGEQIANIDSSNMRDEI

WLKLAKEINKLFAEGVDGVVITHGTDTMEETAYFLNLTIKSDKPVVLVGAMRPSTAISADGPKNLYNAVA

LAADKESKGKGVMVAMNDKILSARGVVKTHSLNVDAFSSPDFGDLGYIVDGKVFFYNNVTKAHTKNAPFD

VSKLTSLPKVDILYSYSNDGSGVAAKALFEHGTKGIVVAGSGAGSIHEDQKNVLKELMKKGLDVVVSSRV

VAGRVAVSDSDKKLGFISAEDLNPQKARVLLMLALTKTSDPKKIQEYFLKY

>ABV51628.1 putative single-stranded-DNA-specific exonuclease [Campylobacter jejuni subsp. jejuni 81116]

MKIINKNEIKKILASRFEKDLHTKLCDLPLPCCLKDAYKAANRIKEAVEKNEKVAIVGDYDVDGIISCVI

MAEFFDDIGFDYIVRIPNRFKDGYGLNAEIINELDVNLIITVDNGIAALEAAKLCKEKNIDLIITDHHMP

QDVLPDAFAIINPKQKDCDFPEIEICGAQVAWYLIAALKEVCKLKYDMSKFLELLAIAIIADMMELRDLN

RALVRRGIDHINKSKRAAFRAIKHYYQKDKFALDNIGFLIAPLINSAGRMDDASISYEFLHTKDFNKALE

YLEQIVSFNESRKDEEKQLFEDSLNQIDENDSCIVVSGLNWHEGVLGIVASRLAKHFNKPAFVFSQNEEH

LKGSARSVGKIDILALISKTNSILSNYGGHKGAAGISLNSENFEQFKNKIKKECSQISESEFLDTDEILG

ILEPSEIDFEMLEILESFEPFGHKNPRPFFVLENLCVKNKKLLGKDEKHLKLILTKENKTIEALFFNFDK

EPELNQNISLLGSISKNEFRGLVTPQFVIKEIL

>ABV51627.1 CTP synthetase [Campylobacter jejuni subsp. jejuni 81116]

MKQTKYIFVTGGVLSSLGKGIAAASIATLLKNSGLKVSILKADPYINVDPGTMSPFEHGEVFVTDDGAET

DLDLGHYERFLDESLSQDNNFTTGRVYQSVIEKERRGEYLGKTIQVIPHIVGEIKDRIKKAGEGKDILIV

EIGGTVGDIEGLPFLEAIRALRLEVGKNNAMNIHLTLVPFIKAAGELKTKPTQHSVGELRRIGISPDMII

CRSEKALDRDLKDKIAISCGVEKNCVIESVDAASIYQIPLNFLKQDILSPIAEILDLKNLKPNMENWDSL

VKRVIAPSNEVKIAFVGKYVDLKESYKSLTEAIIHAGAALDTKVELKWVDSEKLENMESAEVFKDVSGIL

VAGGFGYRGVEGKIKAIQYARENKIPFLGICLGMQLALVEFARNVLKLKDANSSEFDEKCQNPVVYLIDE

FMDTNGEKQIRTAKTPLGGTMRLGAYKCDIKEKSLLAKVYNEAKSVKERHRHRYEANPKYRVDFEKHGLI

VSGESKGLIEAVELNCHPFFLAVQFHPEFTSRLEHVNPVICGFIKAAINYEDN

>ABV51626.1 probable thymidylate synthase [Campylobacter jejuni subsp. jejuni 81116]

MQITLLFHTPLSVCSHATRTCWQSFEKGDCGGEKDKELIDRVGNKFKHASTLEHLNYTFYIQGISRACLQ

EVARHRHTSPSVKSTRYTLKELRNEGEFKIGDFENASRYLVLCGNEEVDNASIKALENLRTILQKSISLD

IAKYCLPESYKTELTLTINARSLQNFISLRSSKSALWEIRNLANALFEALPQEHKFIFEHCLHKDIE

>ABV51625.1 putative transmembrane symporter [Campylobacter jejuni subsp. jejuni 81116]

MDKQFFKDFLMLSQAHTIATLAILCVVFYALKKMRDIKINFSLRMLFALLMGLGFGFALQYLANFPDAKE

ASNILWYSETKHWFAFVSSVFVAFIKMLVVPLVSICIIKVIIEIDKNIKISSLLGISLFWILFSTAIAAT

LGIFLGYSFDLGSNFAIHEGDKQIREIQTFSNIILGLIPSNIITAINKENIIAIVIFSFFIGISAKKISK

KEEYEQAFKSFHNFILTFYNIMMNMTATVIRFMPYAVVCMMANVLLSNGFEAIKTAGLFIMLIYMAMFIM

FGVHFLLLASQGLNPIKYVKKAFPVWLFAFSSRSSLGTLPMTTSTLQNKFGVNSAIANFVASIGTTTGLN

GCAGYFPALAAVFVAFATHTHIDFTFALMIVLVAVIGSLGIAGVPGSATMAASIMLAGIGFGNNFVMLSL

ILAIDPIIDMARTASNVSGAMTSALCTAKNLKALDKEIYNS

>ABV51624.1 ribonucleoside-diphosphate reductase alpha chain [Campylobacter jejuni subsp. jejuni 81116]

MKVIKRNGRTEELDVSKIKKCTSDAVKDLEGVNLSELELDAKIQFRDGISTEEIQKTLIKTAVDKIDIDC

PNWTFVAARLFLFDLYKKVNGMNRYNHLREYFQKGEKEGRILLGLKEKYDLDDLNAYIKPERDMQFTYLG

IKTLYDRYLIKDSKGMPIELPQQMFMAIAMFLAQNEFNPQEWAKKFYDLISKFELMLATPTLSNARTTRH

QLSSCYIGSTPDNIEGIFDSYQEMALLSKFGGGIGWDWSKVRAMGGSIDGHKNAAGGIIPFLKITNDIAV

AVDQLGTRKGAIAVYIEPWHMDISDFIDLRKNSGEERRRAHELFPALWINDLFMKRVRANDKWTLFDPAD

TADLCDLYGEAFEKRYEEYEKDESITKEIVEAKELWKKILLNYFETGLPFLCFKDSANRANPNAHVGIIR

SSNLCTEIFQNTEPNYYQIKVVFENGDELHFDEEQKVVIDGGYEKPAKKISTLDSIEGNKVYIVEKYKND

GKTAVCNLASINLSKVYTKEDIERVVPTAIRMLDNVIDLNFYPHRKVKDTNLKSRAIGLGVMGEAQMLAE

AKIHWGSDEHLNKIDEIMEQISFEAINASSNLALEKGSYEDFEGSNWSKGIFPIDVASPKAKALTLREGL

FDQSECDWVKLREKVKKDGMRNGYLMAIAPTSSISILVGTTQTIEPVYKRKWFEQNLSGMIPVVVPNLSL

DTWQYYTPAYELDQKILVKAAAVRGKWIDQGQSLNIFLSLDKASGGYLNEIYQLAWELGVKSTYYLRSES

PDSEKVNVADRSIECEGCQ

>ABV51623.1 adenylosuccinate lyase [Campylobacter jejuni subsp. jejuni 81116]

MVERYSREIMAKKWDMQAKYDAWLKVELAAVKAWNKLGLIDDTDCEKILKNAKFDIARIDEIEKTTKHDV

IAFLTSVSESLGEESRFVHYAMTSSDCIDTAVALQIKESLELILEDVSLLLEAIKKRALEHKNTLMVGRS

HGIHGEPITFGLVLAIWYDEISHAKELLEHAKEVISYGKISGAMGNFAHAPLEFEEEVCKNLGLKAAPVS

NQVIQRDRYAQVISAIAILASSCEQIAVAIRHFQRTEVYEAEEYFSVGQKGSSAMPHKRNPVLSENITGL

CRVLRSFVTPALENVALWHERDISHSSVERFILPDAFITADFMLMRLTNLIDKLLVYPENMMKNLNLTGG

LVFSGRVLLELPFKGISREEAYKIVQRNAMKVWADLQNGKAAINEKNESLFLLALLSDEDLRKSLSEEDI

RKCFDYNYYTKNVDAIFKRTFK

>ABV51622.1 putative ribosomal pseudouridine synthase [Campylobacter jejuni subsp. jejuni 81116]

MENLKISINEAQKLIDKKRLFCDGILVEEKNKILNGLVELIVYENNPKGVEIVFENEDFAILEKESGILS

HPNGRHCKYSLSDEIWHLWGKEACVAHRLDKETSGLILIAKNKKAQIDLKSLFEKKLVQKEYLALAHGKI

EENFIVDKAINLTKNYDDIKTRMQICKEGKQAITEFEILEYFPKINATLLLCKPLTGRQHQIRVHLHYKN

HTILGDPLYGLSKQQIESILDEKLNPKERLKLTGALRLCLHSYRLKFQYKNQNFDINSKINIKEIFNNSI

K

>ABV51621.1 fumarylacetoacetate hydrolase family protein [Campylobacter jejuni subsp. jejuni 81116]

MKFVNFIQGQKHNLGVLNSSGKIVSFTDLGIETNDMNEFIIYFDKFKHKLTDLDSKIAYEIPKENYLAPI

IEPRQDIICLGINFLDHAKESAKFKGEKFEEREYPVYFGKRCNQATPPFGDIPLHADVTSQLDYECELAF

ILSKDAYKIKAEDAKDYIFGYTIINEISARELQKRHKQFYRAKSLEGSTIMGPYITSVDEISYPPKLQLQ

SYVNDELRQNSNTQLFIFDIAYVLEELSAGMLLKAGSIISMGTPSGVGMGLNPPTFLKSGDKVRCVIENL

GELCNKIK

>ABV51620.1 cytochrome C551 peroxidase [Campylobacter jejuni subsp. jejuni 81116]

MKKIIMILYLSYANIVFAVDMITPIPNSISYDKEKAKLGKSLYMDKSLSKDGKVSCNTCHRLDQHGVDGL

EFSIGVDNQLDKPFNTPTTFNSVFNFVQFWNGRAKDLAEQATVPFFNPKEMGLSPELLLQKVNSNENYVK

TFKKLYGEVTVENIALAVAEFEKTLITPNSPFDHYLSGDQNAISAQAKKGYEDFKANGCISCHQGQNIGG

NMFQKIGIFEEYPNQEDLGRYEITKREADKMVFKVPSLRNIAKTAPYFHDGSIPTLDACVQFMAYYQLGK

FLDQETVDNIVAFLESLTGEYHDK

>ABV51619.1 MCP-domain signal transduction protein [Campylobacter jejuni subsp. jejuni 81116]

MTNKKSSFLIKFIILSTLVLAFILVLLGIIFNNYSSSKDNKDLINTVQQLEISDEKINSVFQNSFNFINY

DPSVQAIKKMQENFKKLKTFGIDISKAEEIFNAKLIQLNYFKSANSIAVNSKLYLFELAKNYFEELEQNH

ETNKNNYRTMSSMLSVLSTENILQKTTLNQLNNLMKEIKNDTKSENLQLFLKHYKMIVKQISIMQDNSSI

YENNSLMKELKQLNTFTQNAVEQSNLFKFYIALAVFGITLVLFVFFILLTLKKVIMPIHTLEKLSANLAS

KEANLHSRLNIDPKSELGQSAQYINSFISTVQNSIIEAIENAKSSHQNSQKLKNNSMMLENSSNSQHEQI

QGVKEITYVLDDHINLAGNLAQESIENMQDMHILMDKVELTLSELVNLINENNEKEQNVVANMDNLTQSA

DNIIEITSSIRDIADQTNLLALNAAIEAARAGEHGRGFAVVADEVRQLADKTSKSLLNINATVNTIVQQI

NDNKALMDLIHDSMKETSSKTNDLQQELVNSMHKLESSIESTQTMKDKSMEVKDKMLILGTNIDKVNELA

NSVKDLSCEINNISQNVLNGASKLSEKLSSFQ

>ABV51618.1 hypothetical protein C8J\_0017 [Campylobacter jejuni subsp. jejuni 81116]

MEFLELLLVLIALILIIKKPEKENLAFGLVMVAWLLMVFFYVGHKTGALLTIMNL

>ABV51617.1 putative ATP/GTP binding protein [Campylobacter jejuni subsp. jejuni 81116]

MNEINKTKNFYTLMCLAGFLIILLPVGIANFVFGYMLGDSPCTLCWGQREAMIFIGVMALFIVRYGMKGK

YLAALLIMTAVGLYQSFAHYGNHAHRDLDQGFGLAVFGIHTYFWAEVVFWAVVLLLGVIFAFAPKFNAFE

TELNGEKFRKYTKFSFAAVLISTIIVASNVFQAFVSTGIPPYVGQGDPVRFSLNPKYIIWSKEGWNGLWQ

NISFLGKRDVKAPDYAFAPASEKLGIKFDNDINNAPFAKINDELKITNEQTINFDKAINTLDYINNEFVA

SSKWDVAFLDNNFSVKEGFELDPYFSASIDPIIGIIPYMNDKFILMGSNKSFLRFAKNPNASEEDIAKQY

ADFVKGNDKFKGQGEGLGRGRLDTVRAKFNHVASMSTDGNYLYLATVPNNKDAKTFVISKVSLKDRVLSG

EFTPKANLKEGKTLGDLYVTSMTFKDGEIYALSKNHNVIAVIDPVKEEVVKTIAFPSSITNARSIFFKDG

KINILSYQDGANKLYTLN

>ABV51616.1 putative transcriptional regulatory protein [Campylobacter jejuni subsp. jejuni 81116]

MSKKALCIISGGMDSTLCAYLAKKEGYEIIALHFDYEQRTQEKERECFKQICKALKVEKSYILDVSFIKD

IGGNALTDKSIDIPKNELCISDTPPITYVPFRNGIFLSIAGSLAEKENCESIFIGVVEEDGSGYPDCTDE

FIQKAQEFINEGTSKNFKVYIKTPLVRLNKAKIVELALKENVPLELTWSCYESEDEACGECDSCLLRLRG

FEKVGFKDKIKYKS

>ABV51615.1 hypothetical protein C8J\_0014 [Campylobacter jejuni subsp. jejuni 81116]

MINIKLIEHIFKAASISRWNDYPRMANLVELDKQAHKFIIAYFIAKMEKDVDMRVIIEGGIFEFLSRVVV

TDIRPDVYHEIVRQKKAEVNAWVLSKIEPMIEDIEEGEFLKRFEAYLNGNAYAKERLILKAASYFATRWE

FNIVYQTSAFLNDIDEIKNKVEEELEDYYELIGARKIALNQKIAKIIDLSGRLRFQKRWAQTPRIPETAV

LGHMLVVAILGYFYSLKIKACDKRLENNFYCALFHDLPESLTRDIISPVKYGIDGLHDIINDYEMKLINE

RILPFVPEGLRAEFSYILGIREGRNDESNFVKNEFENRTYKNAKIELCSGSLSSFNENEFGAIDGKALKY

CDKIAAYIEAGLSISYGVKSKELESGFLGMYEFFKENPTIDGVNFFEICESLREYFKI

>ABV51614.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MKKYFQKRYTLAFFIGILAGIFGAIVKWGWEVPFPPRNPNVFWLADALERVTPPKIFLEQLGLPTDWTYM

FSGMQMPLSIFIVHVSFSIVFGVAYCMIAEKWHRITMWQGAVFGFFVYLFAHVIVMPLIAEVPPLSEIPF

DEHLSEIFGHIVWLWGMEIVRRDIRNRITKEIEE

>ABV51613.1 dihydroxy-acid dehydratase [Campylobacter jejuni subsp. jejuni 81116]

MRSDAIKKGHLKAPNRSLLRACGLKDEDFNKPFIGVANSYIDIIPGHYFLNDYAKIIKDEIRKNGCVPFE

FNTIGVDDGIAMGHEGMLYSLPSREIIANSIETVMNAHQLDALICIPNCDKITPGMLMGALRVNVPTIFV

SGGPMASGVTKKGEKISLSSVFEAVGAYEAKKISEEEFKDIECSACPSGGSCSGMFTANSMNTLCEAMGI

ALEGNGTILALSKEREELLRKAARRICEIALDERFKIRNIITQKAVRNAMVVDMAMGGSSNTVLHMLAIS

REAGVALDIKDLNFISSKVAHIAKIAPSLNSVYMDDVHKAGGVSAVMAEISSRQGHILELDALTITGESL

KERLKNAKIKDENIIRKVDNAYSKVGGLAILFGNLAEQGCVIKTAGIIGERKFKGKAVCFNSQDEAIKGI

IKGKVQKGNVCVIRYEGPKGGPGMQEMLSPTSLLMGMGLGADVALITDGRFSGATRGLSVGHISPEAAEG

GLIGLLKDGDEIEIDVDAYTIHANLSEEEITQRKKEFVLPQKEVPSRWLRMYQKLVSNASKGAVLDME

>ABV51612.1 non-haem iron protein [Campylobacter jejuni subsp. jejuni 81116]

MRQYETYKCQKCGNEVEVQNVGGGKLSCCGEEMKCITTDLTAVNLMKAFAGESMARNKYDLFADVAEEEG

WHAVARHFREAAENEKWHARAEFKAYHEIVDGKPLEVTTKNLVSAAEGENYEHTTMYPNFAKIAEDEGKK

AIARLFTAIGKVEIEHEREYLALKKMLEEEEFFNSEVEELWVCEVCGHIHRGKKAPAACPLCKAPKEYFK

REFLG

>ABV51611.1 putative non-specific DNA binding protein [Campylobacter jejuni subsp. jejuni 81116]

MKKLLFLFFALTAFLFGAVNINTATLKELKSLNGIGEAKAKSILEYRKEANFTSIDDLKKVKGIGDKLFE

KIKNDITVE

>ABV51610.1 ribonuclease HII [Campylobacter jejuni subsp. jejuni 81116]

MKTLFDTKELLNEFDINLIGIDEAGRGALAGPMMMAACKLNKKLDGLCDSKKLSEKKREELYEIIIKNSN

YLILAFSSEQIDALGLSTCLKTGLKLIKKHFKTENNFLYDGNTNLGINGIKTQIKADASILQVSAASILA

KVSKDRVMNFLAKDFPCYEFEKNKAYGTKAHKELIAKFGICKLHRKSFKLL

>ABV51609.1 glutamate synthase, small subunit [Campylobacter jejuni subsp. jejuni 81116]

MGNARGFLDFKRMDFKKIAPKERVLNFKEFTIPLDKKEQEIQGGRCMDCGVAFCHTGVMSEGKDVGCPLN

NLIPEWNDLIYRSLWEEAYERLDLTNPFPEFTGRVCPAPCEDSCVCAINGVSVSIKNNELSIIENAFKEN

LVRVNKPKQYNGKKIAIIGSGPAGLACANTLNSLGYKVSVFERSDKIGGLLMYGIPDMKLDKSIVQRRVD

LLKKSGIEFKVNENIDSKDKVSKLLKEFDALVLCTGASKPIDLDIEGRKLKGVEFALDFLTQNTKTLLKT

GKGADTAKGKNVLVIGSGDTSVDCIAVATRQGAKSIVRFERSPKRPLQRSQNNPWPLKADIFTTDYGLEE

AIAVYGKDPREYQKMTKKFLGKTHVEGVEANDLKREFKEGKAINVEIPNSKKTYKADLVLLAMGFSGCEE

AIAKNFGVKLDEKNNISTENFQTTHKKIFACGDARKGQSLVVWAIKDGIECALSLHQNLAK

>ABV51608.1 glutamate synthase, large subunit [Campylobacter jejuni subsp. jejuni 81116]

MDLENILENNQSIGLYHPKNEHDACGIAAVANIRGIASYKVICDALEILMNLEHRGGAGAEENSGDGAGI

LIQIPHDFFKTQELGFELPKKGDYAVAQMFLSPNTDAKEEAKEIFLQGLKDKKLEFLGFREVPFNPSDIG

ASALKAMPYFLQAFVKKPSKISAGLEFERVLYSTRRLIEKRAINVPKFYFSSFSSRTIVYKGMLLSTQLS

DFYLDFKDVNMKSAIALVHSRFSTNTFPSWERAHPNRYMVHNGEINTIRGNVDSIRAREGLMQSEYFENL

DEIFPIIAKPSSDSAMFDNTLEFLALNGRTLEEAFMMMVPEPWHKNENMESKKRAFYEYHSLLMEPWDGP

AAIVFTDGVIMGASLDRNGFRPSRYYLTKDDMLILSSETGALKLDEKNIKAKKRLEPGKLLLVDTARGRV

IADNEIKEHYANAKPYKKWLKNLVELEKQKSGVYKHQFLKEDEVLKLQKAFGWSYDELKMSVAAMAQNGK

EAIAAMGVDTPLAILSKTYQPLYNYFKQLFAQVTNPPLDAIREEIVTSTRIYLGSEGNLLKPDENNAKRV

KIALPVISNEELFEVKALNKFQVKEFSILYDYSKKTLEKALDELCVKIEDEVKKGVSIIILSDKGVDEKN

AYIPALLAVSGVHNHLVRKNLRTHTSLIIESGEPREIHHFACLLGYGATVINPYLVYESIQKLIANKDLN

LSYEKAVENFIKASSSGIVKIASKMGVSTLQSYNGSALFECLGLSSKVIDKYFTSTTSRIEGMDLEDFEK

ELIALHKHAFNDTHKALDSKGIHGFRSAKEEHLIDPLVIFNLQQACRNKDYKSFKKYSALVDEKQVNLRS

LMEFDFSEAISIDKVESVESIVKRFRTGAMSYGSISKEAHECLAQAMNKIGAKSNSGEGGEDEERYEIKE

GVDKNSAIKQVASGRFGVDLNYLSHAKEIQIKVAQGAKPGEGGQLMGFKVYPWIAKARHSTAGVTLISPP

PHHDIYSIEDLAQLIYDLKNANKDAKISVKLVSENGIGTVAAGVAKAGANLILVSGYDGGTGASPRTSIP

HAGIPWELGLAETHQTLILNKLRDRVRLETDGKLMNGRDLAIAALLGAEEFGFATAPLIVLGCTMMRVCH

LNTCPFGIATQDTELRDRFKGKVDDVINFMYFIAEELREYMARLGFERLDDMIGRVDKLRQKSVQGKAGK

LNLDKILKSLPTYNRTAVHFKDYKDNKLEKTIDYRILLPLCKNAVEKKEPIKLSLEVGNQSRTFATMLSS

EILKTYGKDALDEDSIHIKAIGNAGNSFGAFLLKGIKLEIIGDSNDYLGKGLSGGKIIAKISNEATFSPE

ENIIAGNACLYGATKGEVYLDGIAGERFCVRNSGALAVVLGTGVHGCEYMTGGQVVVLGDVGANFAAGMS

GGVVYIFGRHNEAHVNTELVDIKDLNAKDEKELKAVIEKHIAYTDSKKAKDILEKFDKKDFFKVMPRDYE

KMLKMLDLCKNEKDPNLAAFLKITQK

>ABV51607.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni 81116]

MTLLTNPIIISVVLMTLLCLFRFNVLLSLLISALVAGVFSHLELVDTMNILISGMKENLKTALSYILLGA

IAAAISKTNLTAYLIKIVSHFISHKKYLLLLSIALISCFSQNLIPIHVAFIPLLIPPLLSLFNKLKIDRR

AVACALTFGLTTPYMVLPVGFGLTFQDLLKDNLNANNVSVSLNDVTNTMYFAAICMIAGLFLALFVFYRK

PREYQEVEIAKVDLENLEMTRKEWGVLAGLVLTLILQILTMNLPLSGLLGFVLMVILGGVEFSKVNEVFD

DGLKMMGFIAFVILVAAGYGEVLKESGSVVDLVNSVVPWMEQSKFLAVFFMLLIGLIITMGIGTSFGTIP

IIATLFCPICLELGFSTALIIFILGVAGALGDAGSPASETTMGTTVGLNADKQHDHIKDTCIPTFIFYNG

PLLILGSIIAMFL

>ABV51606.1 hypothetical protein C8J\_0005 [Campylobacter jejuni subsp. jejuni 81116]

MKQNNQKEDRRDFLKNIGFGLLGISVLSNFSFENFLGSKALAKELPDFKIEGKKDLIYHGEKPLTAETEI

YALDSDFTKPENFFVRNNGLPPSLETIKERLHKGWTLEIDGESIINKKSYTIEDLKKKFKTYTYALTVEC

GGNGRSEVIPSTKGTQWGYGAVACGRWTGVRLKDILKDCGIKNDAVYIGYYGIDTKLNGEETSPISRGVP

ISKALQDETLIAWAYEGKDIPLVNGYPLRLVCGGYPASTSGKWLYKISVRNKIHDGEKMEGSYKVPVNPV

KPGDFNYKGEMKIIESMPIRSVITNIKNGSEIKANKKFEVRGKAWAGELEVSEVYVSNDYGVTWTKAKVE

KPLNRLAWQKWSAQISIPTKGYYEIWARAIDSQGNSQPMVLAQWNPGGYINNACHRVNVYGV

>ABV51605.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni 81116]

MKKTILILALFLSASWAQNLEINPDTGLIIDPDSPLVEANCLACHGSNLITNMHASRKAWLAAIRWMQDS

EGLWEIEPEDEEKILNYLEKYYGEKYDTRRRIPLAILLQNKTH

>ABV51604.1 DNA gyrase subunit B [Campylobacter jejuni subsp. jejuni 81116]

MQENYGASNIKVLKGLEAVRKRPGMYIGDTNIGGLHHMIYEVVDNSIDEAMAGHCDTIDVEITTEGSCIV

SDNGRGIPVDMHPTENMPTLTVVLTVLHAGGKFDKDTYKVSGGLHGVGVSVVNALSKKLVATVERNGEIY

RQEFSEGKVISEFGVIGKSKKTGTTIEFWPDDQIFEVTEFDYEILAKRFRELAYLNPKITINFKDNRVGK

HESFHFEGGISQFVTDLNKKEALTKAIFFSVDEEDVNVEVALLYNDTYSENLLSFVNNIKTPDGGTHEAG

FRMGLTRVISNYIEANASAREKDNKITGEDVREGLIAVVSVKVPEPQFEGQTKGKLGSTYVRPIVSKASF

EYLTKYFEENPIEAKAIMNKALMAARGREAAKKARELTRKKESLSVGTLPGKLADCQSKDPSESEIYLVE

GDSAGGSAKQGRERSFQAILPLRGKILNVEKARLDKILKSEQIQNMITAFGCGIGEDFDLSKLRYHKIII

MTDADVDGSHIQTLLLTFFFRFMNELVANGHIYLAQPPLYLYKKAKKQIYLKDEKALSEYLIETGIEGLN

YEGIGMNDLKDYLKIVAAYRAILKDLEKRFNVISVIRYMIENSNLVKANNEELFSVIKQFLETQGHNILN

HYINENEIRAFVQTQNGLEELVINEELFTHPLYEEASYIFDKIKDRGLEFDKDILEVLEDVETNAKKGAT

IQRYKGLGEMNPEQLWETTMDPSVRRLLKITIEDAQSANDTFNLFMGDEVEPRRDYIQAHAKDVKHLDV

>ABV51603.1 DNA polymerase III, beta subunit [Campylobacter jejuni subsp. jejuni 81116]

MKLSINKNTLESAVILCNAYVEKKDSSTITSHLFFHADEDKLLIKASDYEIGINYKIKKIRVESSGFATA

NAKSIADVIKSLNNEEVVLETIDNFLFIRQKSTKYKLPMFNHEDFPNFPNTEGKNQFDIDSSDLSRSLKK

ILPSIDTNNPKYSLNGAFLDIKTDKINFVGTDTKRLAIYTLEKANNQEFSFSIPKKAIMEMQKLFYEKIE

IFYDQNMLIAKNENFEFFTKLINDKFPDYEKVIPKTFKQELSFSTEDFIDSLKKISVVTEKMKLHFNKDK

IIFEGISLDNMEAKTELEIQTGVSEEFNLTIKIKYLLDFLTSIEEEKFTLSVNEPNSAFIVKSQGLSMII

MPMIL

>ABV51602.1 chromosomal replication initiator protein DnaA [Campylobacter jejuni subsp. jejuni 81116]

MNPNQILENLKKELSENEYENYIAILKFNEKQSKADFLVFNAPNELLAKFIQTKYGKKISHFYEVQSGNK

ASVLIQAQSAKQSSKSTKIDIAHIKAQSTILNPSFTFESFVVGDSNKYAYGACKAISQKDKLGKLYNPIF

IYGPTGLGKTHLLQAVGNASLEMGKKVIYATSENFINDFTSNLKNGSLDKFHEKYRNCDVLLIDDVQFLG

KTDKIQEEFFFIFNEIKNNDGQIIMTSDNPPNMLKGITERLKSRFAHGIIADITPPQLDTKIAIIRKKCE

FNDINLSNDIINYIATSLGDNIREIEGIIISLNAYATILGQEITLELAKSVMKDHIKEKKENITIDDILS

LVCKEFNIKPSDVKSNKKTQNIVTARRIVIYLARALTALTMPQLANYFEMKDHTAISHNVKKITEMIEND

GSLKAKIEELKNKILVKSQS

>CBM39675.1 unnamed protein product [Campylobacter jejuni subsp. jejuni 81116]

MSLEMFDKEIFDLTNKELERQCEGLEMIASENFTLPEVMEVIGSILTNKYAEGYPGKRYYGGCEFVDEIE

TLAIERCKKLFNCKFANVQPNSGSQANQGVYAALINPGDKILGMDLSHGGHLTHGAKVSSSGKMYESCFY

GVELDGRIDYEKVREIAKKEKPKLIVCGASAYARVIDFAKFREIADEIGAYLFADIAHIAGLVVAGEHPS

PFPHAHVVSSTTHKTLRGPRGGIIMTNDEELAKKINSAIFPGIQGGPLMHVIAAKAVGFKFNLSDEWKVY

AKQVRTNAQVLANVLMDRKFKLVSDGTDNHLVLMSFLDREFSGKDADLALGNAGITANKNTVPGEIRSPF

ITSGLRLGTPALTARGFKEKEMEIVSNYIADILDDINNEKLQENIKQELKKLASNFIIYERAMF

>sp|P0DPD3.1|FLIS\_CAMJ8 RecName: Full=Flagellar secretion chaperone FliS

MQNNLAYNAYSQNQAGIESPQKLIEMLYEGILRFCARAKVAIRNEDIEQRVYFVKRTTAIFIELINTLDY

EKGGEVAHYLSGLYTREIQLLSLANLENNEDRINEVINVTKGLLEAWREVHNNETVAQ

>sp|P0DPD2.1|FLAC\_CAMJ8 RecName: Full=Secreted flagellin C

MMISDATMMQQNYYLNNAQKASDKALENIAAVRAISGVDSANLAIADSLRSQSSTIDQGVANAYDAIGVL

QIADASLTNISQSADRLNELSVKMNNAALNDSQKGMLRTEATRIQESINDSFNNATYNGKNVFQTMNFVV

GSGTETTNLNPLATGGLSIDNQDSITNFMDQLGSLRSEIGSGINAITSNINASVQNSINSKAAENNLLNN

DMAKNVNDFNANYLKENAAAFVAAQSNMQLQSKIANLLQ

>sp|P0DPD4.1|CSRA\_CAMJ8 RecName: Full=Translational regulator CsrA

MLILSRKENESIIIGEGIEIKVVQTGKGYAKIGIEAPKSLMILRKELVQQVKDENLHSVVQNDIKLDDLS

KKLIK

>sp|A8FJX4.1|MIAA\_CAMJ8 RecName: Full=tRNA dimethylallyltransferase; AltName: Full=Dimethylallyl diphosphate:tRNA dimethylallyltransferase; Short=DMAPP:tRNA dimethylallyltransferase; Short=DMATase; AltName: Full=Isopentenyl-diphosphate:tRNA isopentenyltransferase; Short=IPP transferase; Short=IPPT; Short=IPTase

MFFEIALIGTTASGKTYIANTLAREFDAVVLSLDSLCVYKEINIASAKPSQDDLASIKYFGVNLLSVNEH

FNVELFIREYQKAKEFALARNLPLIIVGGTGFYLKTMIDGLSEKTLESKSSLNNDEIYALLLNIDPNYKI

EKNDTYRLKKWLGIYEQTREIPSEFLKRTQKTGVLKDIEIYELAWDKEILKKRIKTRTKEMLDNGLLDEA

KILFSKFDHKLKALNSIGLKECKEYLDGEISFKELENLITIHTTQLAKRQRTFNKKFQSKALEFDKALAI

LRMKFSIEK

>sp|A8FL01.1|QUEA\_CAMJ8 RecName: Full=S-adenosylmethionine:tRNA ribosyltransferase-isomerase; AltName: Full=Queuosine biosynthesis protein QueA

MNKDLLLSSYDYTLANELIANYPTNPKEDARLLVFDRKNKEIFHTTFKNLQDFLPNCAIFFNDTKVIKAR

IYGNKVSGGKIELFLHQPFLNSHNPLFLAQIKGRVKKDEILYFKKDLKIRVVELLNDGLRKVQFFQNDKT

LDTSNLYNLLDKIGHIPLPPYIKREDEKSDLKDYQSIFAKNLGAVAAPTASLHFSETMLENLRKKHEIYH

LTLHVGAGTFKSVECENIQEHKMHSEFFNIPQQACEIIDSKQAILGVGTTVTRTIEYYARTKTKSGFCDL

FLHPQNPPIRQNHLLTNFHLPKSTLIMLVSAFIGREQCLKLYELAIKEKYRFYSYGDAMLIL

>sp|A8FLQ4.1|SYE1\_CAMJ8 RecName: Full=Glutamate--tRNA ligase 1; AltName: Full=Glutamyl-tRNA synthetase 1; Short=GluRS 1

MYRFAPSPTGDMHIGNLRAAIFNYICARQKNMDFILRIEDTDKARNIAGKEEEIKEILNLFGISWQHYYI

QSENLKFHRQMALKLISEKKAFACFCTEEELEAKKELAKKQGKAYRYDGTCEKLADIDVLECEKPFVIRL

KKPTHTMKFTDFIKGELSFEPENIDSFVIMRTDKTPTYNFACAVDDMLENVTCIIRGEDHVSNTPKQEHI

RASLGYNKAMTYAHLPIILNEEGVKMSKREAHSSVKWLLESGILPSAIANYLIMLGNKTPCEIFTLEEAI

KWFDISKVSKAPARFDLKKLLQINREHIKMIKDDELNKILDLNKDLAQLAKFYTQEASTIKELKEKMRAI

FNTKDFGEFETECKILKELLKDIELFENYEDFKNELLSKSDLKGKKFFMPLRIILTGNIHGPELGDLYPY

IKNFIHELARI

>sp|A8FMZ3.1|SYE2\_CAMJ8 RecName: Full=Glutamate--tRNA ligase 2; AltName: Full=Glutamyl-tRNA synthetase 2; Short=GluRS 2

MHEKLTTRFAPSPTGYLHIGGLRTALYNYLYARKNGGNFLLRIEDTDLKRNSKEATKAIIEAFKWCGLEH

DGEVTYQSERFDLYKEYVKKLLDEGKAYYCYMSKEELEELRAKQEAAKERPRYDGRYREFTGTPPQGIEP

VVRIKAPQSGEIVFEDGVKGEVRFKAEDIMDDFIIARSDGTPTYNFTVVIDDALMGVSDVIRGDDHLSNT

PKQIVLYEALGFKIPKFFHVAMIHGEDGKKLSKRHGATDVMEYKEMGILPQALLNFLVRLGWSHGDDEVF

SLEDLKKLFDPYHINKSASCYNAKKLEWLNAHYIKTLPFEEINRQLKDLGFDLSVYEKAGFLLDLLRERA

KTLHDIINGAKSIVNAPQNYDENAVQKFVNENNLELLQAFANTLKDQKTGKDFEDFTNDFLEKKEAKLKD

LAQPIRIALTGSAVSPSIFEVLEFLGVDECKKRIDNFLKVRGK

>sp|A8FM94.1|THIG\_CAMJ8 RecName: Full=Thiazole synthase

MQENLKNDKLKIGKYEFDSRFILGSGKYSLELIKSAIEEAKTQIITLALRRANTGEIANILDYIPKNITL

LPNTSGARNADEALRIARLSRELGCGELIKIEVISDSRYLLPDNYETIKACELLAKEGFTPLPYMHADLY

AARAMRDAGAAAIMPLAAPIGSNKGLCAKEFIQILLNEIDLPIIVDAGIGSPSQACEAMQMGVSAVMVNT

AIAEAKDVALMAKAFSLAVNAGRAAFLAGLASVSKAKASSPLTGFLRD

>sp|A8FKT2.1|SYA\_CAMJ8 RecName: Full=Alanine--tRNA ligase; AltName: Full=Alanyl-tRNA synthetase; Short=AlaRS

MDIRKAYLDFFASKGHEITPSSPLVPDDATLLFTNAGMVPFKSIFTGEIPRPNPPRKTSCQTCIRAGGKH

NDLDNVGYTARHHTFFEMLGNFSFGDYFKEQAIAYAWEFVTEFLKLPKDRLYVTVHENDDEAFNLWQKHI

QKERIYKFGDKDNFWQMGDTGPCGPCSEIFYDQGEEHFNSSEDYMGGDGDRFLEIWNLVFMQYERSADGV

LSPLPKPSIDTGMGLERVTAIKEGKFSNFDSSLFMPIINEISKLCNKTYIYESGASFRVIADHIRSSVFL

LAQGVSFDKEGRGYVLRRILRRALRHGYLLGFKQAFMYKLVDVVCDLMGGHYTYLNEKKDFIKEQIRLEE

ERFLSTIENGIEIFNEELKNTKEIFSGEVAFKLYDTYGFPLDLTADMLREKNLKVDEEKFELLMNEQKAR

AKASWKGSGDKTASGDFKNLLEKFGENHFVGYEKAECESKILALLDEDFKEVSTLKDAGWVMLKNTPFYA

TSGGQSADSGFMAKREVLDTQKFFNLNLSFVKAGEELKVGDIVHARIDTEKREQIARHHSATHLLHHALR

EILGSHVSQAGSLVESNKLRFDFTHHKALSKEELENIEKRVNEMIINSSEAILENMPLEEAKKSGAIALF

NEKYQGNVRVLTLGESKELCGGTHVKNTAQIGSFYIVKESGVSAGVRRIEAVVSKAALEFVKNQLEELSK

VKDELKNNDILSGIKKLKNEILSLKNELKNSSKTELDSKNIQGVEICVKRIDNGDIKAMIDDFKNKFAKA

VILLIQVKDEKITLAAGVKDVPLKAGALVKEAAQILGGNGGGRDDFATAGGKDLSKINEALKQSLETIEK

AL

>sp|A8FKT3.1|Y471\_CAMJ8 RecName: Full=Maf-like protein C8J\_0471

MLILASSSISRANLLKTAKIDFRQVSFDYDENLDKNISPFLYVQKIVLEKERQFLSTLGKDFQNQNLLFA

DSIVCIDEKILTKAKDKKEAYEMLALQNGKYASILSAFLLVKPEKRVFSLSKTTLYFKNFDENALRDYVE

NDLYKGKAGCIMCEGFHQNFITHQVGNLSTALGLDIQTLKAYL

>sp|A8FNC2.1|RF2\_CAMJ8 RecName: Full=Peptide chain release factor 2; Short=RF-2

MDNYEFSELLKTLKNKVGNIASIIKPENIQTRLKEIEELENSPSFWSDVKQAGIIGKEKTKITNLLKNYE

NAFNALNDASELFDLANSENDTETLEALFNDAPKLEDTITSLEISMLLSGENDGKNAIVSIHPGAGGTES

NDWASILYRMYLRFCEREGFKVETLDFQEGEEAGLKDVSFLVKGENAYGYLKAENGIHRLVRTSPFDSAG

RRHTSFSSVMVSPELDDDIEIEIEEKDIRIDYYRASGAGGQHVNKTESAVRITHFPTGIVVQCQNDRSQH

KNKATAFKMLKSRLYELELMKQQDSANAGEKSEIGWGHQIRSYVLFPYQQVKDNRSGEAFSQVDNILDGD

IKKMIEGVLIALKAE

>sp|A8FMW9.1|RECR\_CAMJ8 RecName: Full=Recombination protein RecR

MAKGLEKFNELVESFANLPTIGKKTAIRLAYHLCINNQIDGMKLAHNIENAIRFIKPCGQCGALSENELC

EICSDEERNKNILCIVESPKDILTLEESQSYNGLYFVLDELNEEKLEKLKQIILKLNISELIFALTHSIN

SDATIFFIEDKFKGLNLTFSKIAQGIPSGVNLENVDLISLNKAMNFRTKI

>sp|A8FMU4.1|PDXA\_CAMJ8 RecName: Full=4-hydroxythreonine-4-phosphate dehydrogenase; AltName: Full=4-(phosphohydroxy)-L-threonine dehydrogenase

MKKLAISIGDINGIGLEILVRSHEELSKICTPFYFIHENLLNKASKLLNLKLFNAKIVAFKDDKDYEFNF

IKKENSLEIYSFCLPLGFKVDENFEIKAGEIDAKSGLYGFLSFKAASYFVYEKHAHALLTLPIHKKAWED

AGLKYKGHTDALRDFFKKNAIMMLGCKELFVGLFSEHIPLAKVSKKITFKNLSIFLKDFYKETHFKKIGL

LGFNPHAGDYGVIGGEEEKIMEKAIAFVNAFLHSKKDEKFFKKALKDENLQKELLLNFKGKGVYLPYPLV

ADTAFTKAGLKNCNRLVAMYHDLALAPLKALYFDKSINVSLNLPIIRVSVDHGTAFDKAYKNAKINTKSY

FEAAKFAINLSLKT

>sp|A8FMU3.1|PDXJ\_CAMJ8 RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PNP synthase

MLLGVNIDHIAVLRQARMVNDPDLLEAAFIAAKHGDQITLHVREDRRHAQDFDLENIIKFCKSPINLECA

LNDEILNLALKLKPHRVTLVPEKREELTTEGGLCLNHTKLKQSIEKLQNANIEVSLFINPSLEDIEKSKN

LKAQFIELHTGHYANLHNALFSNISHTAFALKELGQDKKNLQAQFEKELQNLELCAKKGTELGLKVAAGH

GLNYKNVKPVVKIKEICELNIGQSIVARSVFTGLQNAILEMKELIKR

>sp|A8FMQ4.1|LUXS\_CAMJ8 RecName: Full=S-ribosylhomocysteine lyase; AltName: Full=AI-2 synthesis protein; AltName: Full=Autoinducer-2 production protein LuxS

MPLLDSFKVDHTKMPAPAVRLAKVMKTPKGDDISVFDLRFCIPNKDIMSEKGTHTLEHLFAGFMRDHLNS

NSVEIIDISPMGCRTGFYMSLIGTPDEKSVAKAWEEAMKDVLSVSDQSKIPELNIYQCGTCAMHSLDEAK

QIAQKVLNLGISIMNNKELKLENA

>sp|A8FMN1.1|SYR\_CAMJ8 RecName: Full=Arginine--tRNA ligase; AltName: Full=Arginyl-tRNA synthetase; Short=ArgRS

MKSIIFNEIKKILECDFTLENPKDKNLAHFATPLAFSLAKELKKSPMLIASDLASKFQNHDCFESVEAVN

GYLNFRISKTFLNELANQALANPNDFSKGEKKQESFLLEYVSANPTGPLHIGHARGAVFGDTLTRLARHL

GYKFDTEYYVNDAGNQIYLLGLSILLSVKENILHENVEYPEQYYKGEYIADLAKEAFEKFGKEFFSEENI

PSLADWAKDKMLILIKQNLEQAKIKIDSYVSERSYYDALNATLESLKEHKGIYEQEGKIWLASSQKGDEK

DRVIIREDGRGTYLAADIVYHKDKMSRGYGKCINIWGADHHGYIPRMKAAMEFLGFDSNNLEIILAQMVS

LLKDGEPYKMSKRAGNFILMSDVIDEIGSDALRYIFLSKKCDTHLEFDISDLQKEDSSNPVYYINYAHAR

IHQVFAKAGKKIDDVMRADLQSLNQDGVNLLFEALNLKAILNDAFEARALQKIPDYLKNLAANFHKFYNE

NKVVGSINENDLLKLFSLVALSIKTAFSLMGIEAKNKMEH

>sp|A8FMF0.1|SSTT\_CAMJ8 RecName: Full=Serine/threonine transporter SstT; AltName: Full=Na(+)/serine-threonine symporter

MFSKIIQSYAKGNLIVQICIGIVLGILIGISSKEISEIANLLGILFTSALKAIAPMLVFILILTSICTKD

FSQSGAKIKNIIILYIVGTFLASACAVLANFFFPVKLVLDGVQTATNSSPTHMSEIFKDLLFKIVDNPIN

ALSSGNYLGILTWAIAGGIALKHCSNEAKQVFIDINEGVLKIVKFIVKLAPFGIFGLVANSVAQTGAQGL

LSYVKLLILLVTTMLFVTFVINALIVFFYTRKNPFPLIFICLRHSAFFAFFTRSSAANIPVNMALCAKLG

IDKEFYGISIPLGATINMAGAAVTIAILSLTAANTVGIEISLLQAFLLSIIATFAACGASGVAGGSLLLI

PLACSLFNIDYDIAMKVVAIGFIIGVIQDSVETALNSSTDVLFTAICSKNELNYNIK

>sp|A8FME4.1|SYL\_CAMJ8 RecName: Full=Leucine--tRNA ligase; AltName: Full=Leucyl-tRNA synthetase; Short=LeuRS

MAYEASLIEKKWQKIWDENEYFEPKDDLNLPKKYILSMFPYPSGRIHMGHVRNYTIGDALARYYRKIGFN

VLHPIGFDSFGMPAENAAIKHKIHPKSWTYENIAYMKKELFSLGFSFSKKRMLATSDPLYTKFEQEFFIK

MFEKGLIYTKEANVNWCEQDQTVLANEQVEDGKCWRCGHEVVQKKMPGYYVKITAYAEELLKDLEELKDK

WPNQVLTMQENWIGKSEGLEFSLNLDEESKQKTKESSLEVFTTRADTIYGVSYIALAPEHKIVQNLLSQN

LLNQDVLNKIKAIQNQSPRERQSSEKEGYFLGIYAIHPLSGEKIPLWVANFVLADYGSGAVMAVPAHDER

DFEFATKYNLAIKQVIQTQENLPYTQKSGKLIHSQEFDNLDCNEARLKIISQFEAKNIGKRVVNFKIRDW

GVSRQRYWGAPIPMIKCQSCGIVPQKLENLPITLPEDVQITGEGNPLDKHPTWKNCICPKCGKEAQKESD

TLDTFFESSWYFARFASDEKTWQEKALDEKSVKYWMSVDQYIGGIEHAILHLLYARFFQKALRDLGYLTQ

NEPFDRLLTQGMVLKDGAKMSKSKGNVVDPDEIIEKYGADTARLFILFAAPPAKELEWNDDAVEGAYRFI

CKLYDRAQNVKKGELVELKQENLNKEEKYARLKVYEALKKSFEVYHQSFAFNTLIAACMEALNALALCKN

EALEQEAFYIILNILEPIIPHVCFELSEELFKCKNFKKLELKEEIFVKDTLNLAVSINGKKRAEFEISSS

ASKEEILAFAKENTAKWLEGKSIVKEIYVEGKLVNLVIK

>sp|A8FMC8.1|FLIW\_CAMJ8 RecName: Full=Flagellar assembly factor FliW

MTLAVKCPILGFEETKNMEFSTIDEVFVRLKSLDGKDFSFVLINPYLIRPDYEFDIPTYYQELLSLTPES

NMKIFNIVAIAKSIEESTVNFLAPVVINLDNNTMVQVILDTVNYPDFFQADQIANYIKK

>sp|A8FLU6.1|SYFA\_CAMJ8 RecName: Full=Phenylalanine--tRNA ligase alpha subunit; AltName: Full=Phenylalanyl-tRNA synthetase alpha subunit; Short=PheRS

MQNFIEQIQKCENLNDLEAIRISVLGKKGILTEGFTKLKELEDEAKKEFAAKLNAQKEIFNEAYLAKFKD

LENLALEERMKQDALNFNYFDESITTGALHPVMSTMDKIIEYFIALNFSIEKGPLIEDDFHNFEALNLPK

SHPARDMQDTFYFDDKRLLRTQTSPVQIRTMLAQKPPIRMIAPGAVFRRDFDITHTPMFHQVEGLVVEEG

QKVSFANLKSVLEDFLRYMFGDVKVRFRPSFFPFTEPSAEVDISCVFCKGKGCRVCKHTGWLEVLGCGIV

DPNVYNFVGYENVSGYAFGLGVERFAMLLHQIPDLRSLFEGDLRLLEQFR

>sp|A8FLL5.1|SYC\_CAMJ8 RecName: Full=Cysteine--tRNA ligase; AltName: Full=Cysteinyl-tRNA synthetase; Short=CysRS

MRLLDSVAKEKIKLDKKDISIYLCGPTVYDDAHLGHARSSVCFDLLRRVLLANGNRVKFARNYTDIDDKI

LKKMAQSGQTLEEITEFYIKSYEEDMRVLNVLDPDFKPRATHYITAMLDLIKKLAKDGFVYTLEDGIYFD

TSKDEKYLSLSNRNLEENISRLSNEVQKRNESDFVLWKFDENFYESEFGKGRPGWHTECVAMIDSIFENT

LDIHAGGIDLLFPHHENEAAQCRCGCKRKLANIWLHNGFVKIDGEKMSKSLNNSFFIKDALKEFMGEALR

FYLLSSHYRSHFNYSLSDLENAKKRLDKFYRLKKRLDLGEISDFDVLNDIEIKSEIAKQILEILNDDLNI

SKALALLDDFISSANLELDKESKNKILKQNIKEALSELAKIFGFGFMDTTLYFQWGVSKEEREEIEKLIL

ERTEAKKNKDFNTADAIRERLSSKKITLLDTPNGTIWEKINA

>sp|A8FLH8.1|SYH\_CAMJ8 RecName: Full=Histidine--tRNA ligase; AltName: Full=Histidyl-tRNA synthetase; Short=HisRS

MINALKGMKDLLDKDAYYYEKVIKTCEEVAKNYGFTFINTPHLELCTLFKRSVGESSDIVGKEMYEFIDK

GENHVCMRPEGTAGVVRAYIEKKLDKNTSVKRWFYHGSMFRYERPQKGRLREFHQFGVESFGNASVYEDA

SIILMLVEIFSRLDIKFKLLINSLGCLKCMPKYRENLIHFLDSKEGFCEDCLRRKNLNPIRVLDCKNEHC

QSLLNDAPLLNQNLCSSCQKDFEILQSVLKENGVDFEVDSKLVRGLDYYSKTAFEFISDEIGAKAAIAGG

GRYDRLIEYLDGKSGFGVGFAMGIERIIAILEQKEEKVQREGIYLCAMDEIYIQKLLHIATNLRKEHKVL

LSYEARKLAKHLENADKNNAEIFLCMGENEAQNESLFYKNLVKKEEKMIKISDLKKVL

>sp|A8FLD3.1|SYGA\_CAMJ8 RecName: Full=Glycine--tRNA ligase alpha subunit; AltName: Full=Glycyl-tRNA synthetase alpha subunit; Short=GlyRS

MTFSQMILNLQNYWQEQGCAIMQPYDMPAGAGTFHPATFLRSLGKKPWAAAYVAPSRRPTDGRYGENPNR

LGAYYQFQVLIKPSPDNIQELYLKSLENLGFDLKSHDIRFVEDNWESPSLGAWGLGWEVWLDGMEVTQFT

YFQQVGGIAVDLVSAEITYGLERIAMYLQNVDNVYDIVWSEFNGEKIKYADVHKQSEYEFSKYNFEVSDV

KILNEQFENSYKECKNILEQGLALPAYDYCMLAAHTFNLLDARGAISVAQRQDYMLKIRELSKNCAEIYK

KNLNETE

>sp|A8FL61.1|SYDND\_CAMJ8 RecName: Full=Aspartate--tRNA(Asp/Asn) ligase; AltName: Full=Aspartyl-tRNA synthetase; Short=AspRS; AltName: Full=Non-discriminating aspartyl-tRNA synthetase; Short=ND-AspRS

MRSHYNTDLGISHVGQSVKLCGWVNSYRDHGGVIFIDLRDRSGIIQLVCDPNDSKEAHEIASNARNEFVL

IAEGTIRPRGEGLVNPKLKTGEIEVVVSKLTIENESAVPPFAIADESVNEELRLKYRFLDLRNPKLYENF

ALRSKACIAARNSLANMGFLEVETPILTKATPEGARDYLVPSRVHQGEFYALPQSPQLFKQLLMCSGFDR

YFQIAKCFRDEDLRADRQPEFTQIDVEMSFCEQKDVINVAETFLKDIFKACGKEIQTPFRQMQYKDAMEN

YGSDKPDLRFDLKFIDVIDIFAKSNNEIFANIAKDTKKNRIKAIRVPKGDTIFSKRQMQRFEEFVRKFGA

QGLAFIQVKEDGLKGPLCKFFSEEDLNELSKRCELEVGDVVFFGAGAKKTVLDYMGRFRIFLANELNLID

PNALEFLWVVDFPMFEQNDDGSYSAMHHPFTMPKNIDETDLEEISSIAYDVVLNGVELGGGSIRIHKNDI

QQKVFKLLNIDEEQQKEKFGFLLDALSFGAPPHGGIAIGLDRLIMLVTGANSIREVIAFPKTQRAQCLMT

DAPSPASNEAMRELGIKLRENIK

>sp|A8FKX4.1|EFP\_CAMJ8 RecName: Full=Elongation factor P; Short=EF-P

MASYSMGDLKKGLKIEIDGIPFKIVEYQHVKPGKGPAFVRIKIKSFIDGKVLEKTFHAGDKCEAPNLEDK

TMQYLYDDGENCQFMDTQTYEQVAISDDDVGEAKKWMLDGMMVDVLFHNGKAIGVEVPQVVELKIIETAP

NFKGDTQGSNKKPATLETGAVVQIPFHVLEGEVIRVDTVRGEYIERANK

>sp|A8FKW6.1|SYP\_CAMJ8 RecName: Full=Proline--tRNA ligase; AltName: Full=Prolyl-tRNA synthetase; Short=ProRS

MRFTKFYAPSLKEAPKDASLPSHIFLTRAGFIEQIGSGLYNFLPLGKRVLDKIKNIVKEEMDKAGAQEVN

LSFITPASLWQESGRYNVFGKELLRFKDRKENEFVLGPTHEEAMLSLVKNKITSYKQLPLHLYQIGLKFR

DEARPRFGLLRCREFLMKDGYSFHANEEDLGCEFELMYKTYSQILQRMGLDFRAVEADSGAIGGSGSKEF

MVLAKNGEDDILICENCDYAANVEAAKRAKKTCQDERPEANYASKFHTPNIKTIDSLAQFFKINAFYTIK

AVVKKAIYENESKLVVFFIRGSDDLQEIKAQNACSALELVDASEEELEKAGLVAGFIGFVGLKDIDFYID

FELENEKQMIMGANEKDYHLIGIDVVNLNKDRFKDLIEVKEGDCCAKCGAKLKQSKGIEVGHIFKLGQKY

SKAMNANFLDENGKSQPFYMGCYGIGVSRLLAVAIEASHDEKGCIWNKTLAPFVLEIIVSNLKDEKALEF

ANKLYEDLTNLGLEVLLDDRNERFGVKMNDFELMGFPYALVIGKGLENNEIELIQREGLVKELIKTDELM

EILKKKVL

>sp|A8FKN8.1|THIC\_CAMJ8 RecName: Full=Phosphomethylpyrimidine synthase; AltName: Full=Hydroxymethylpyrimidine phosphate synthase; Short=HMP-P synthase; Short=HMP-phosphate synthase; Short=HMPP synthase; AltName: Full=Thiamine biosynthesis protein ThiC

MKTQMNYAKEGVFTKEMQIVAQKENLSKDFLLENIACGKIIIPANINHKSLDPNGIGFGLRTKVNVNLGV

SNDCVDYSEEMKKVELAHKFDIEAIMDLSNYGKTSRFRDELVNVSKAMIGTVPVYDAVGFLEKDLKQIGA

KDFLDVVYHHAKSGVDFMTIHAGINSRAAHIFKQSKRLTNIVSRGGSVLYAWMMMKDAENPFFEYYDDLL

DICLKYDVTLSLGDALRPGSTHDASDGAQISELIELSLLTQRAWDVGVQVMIEGPGHMAINEIEVNMQLE

KRLCKGAPFYVLGPLVTDIGAGYDHISGAIGGAVAAASGADMLCYVTPAEHLRLPNLEDVREGIVATKIA

AHAGDIAKLPKERARDDEMSKARQEIDWEKMFKLAIDGEKAKKMFNERRPDDLNSCSMCGKMCAMNTMNQ

ILKGEDVSLA

>sp|A8FKM1.1|GPMI\_CAMJ8 RecName: Full=2,3-bisphosphoglycerate-independent phosphoglycerate mutase; Short=BPG-independent PGAM; Short=Phosphoglyceromutase; Short=iPGM

MKQKCVLIITDGIGYNKNSKFNAFEAAKKPSYEKLFKEVPNSLLKTSGLAVGLPEGQMGNSEVGHMCIGS

GRIIYQNLVRINKAIENKELEKNENLQKLLAKCKRVHIIGLYSDGGVHSMDTHFKAMLEICAKNGNEVFA

HAITDGRDVSPKSGLNFIKDLKEFCENLGVHFATLCGRFYAMDRDKRWDRVKEYYECLLGKAYKVPNLLE

YLQKSYDENVTDEFIKAAQNENYKGMREEDGIIFINFRNDRMKQLVEVLNSKDFKEFEREKIFENLLTMS

VYDDKFKLPVLFEKEKIENTLAQVISKAGLSQLHTAETEKYAHVTFFFNGGKEELLENETRVLIPSPKVK

TYDEKPQMSAFEVCDAVKKGIEKGEDFIVVNFANGDMVGHTGDFNAAIKAVEAVDTCLGEIVECAKKHDY

AFIITSDHGNCEAMQDEKGNLLTNHTTFDVFVFVQAKGVSKIKDNMGLSNIAASVLKILDLEIPKEMNEA

LF

>sp|A8FKI8.1|SYK\_CAMJ8 RecName: Full=Lysine--tRNA ligase; AltName: Full=Lysyl-tRNA synthetase; Short=LysRS

MFDNILEQQRIEKAKELKNLGINPYPHFLEKEMSLKTFKDKFSYILEQVEKRDESVNAVVAGRLKLLRIA

GKSIFANIEDEDTNLQIYFNKDSVGEELYAILKKNLEVGDIVLVKGFPFVTKTGEFSLHASEVKLATKAI

VPLPEKYHGLTDIEQRYRKRYVDMIMNAEVRKDFLVRSKVVSLIRHFFENKGFLEVETPMMHPIAGGANA

KPFVTFHNSLGVERFLRIAPELYLKRLVVGGFEAVFEINRCFRNEGMDLTHNPEFTTIEFYWAYHNYKDL

MDLTEELFALLLDKLNLGKTIEFDGKMIDFSKPFERITYKDALCKYGGLDRDLIEDKEKILTKLKVDGFE

ANEKLELGHLQAELFDNYVEEKLINPTFVIDFPISISPLSRRSDEDSQIAERFELFICGRELANGFNELN

DPLDQYERFLKQIEAKNAGDEEACEMDEDFVNALGYGMPPTAGQGIGIDRLVMLLTNKKSIRDVILFPAM

RPLKSELKEKE

>sp|A8FKH6.1|SYS\_CAMJ8 RecName: Full=Serine--tRNA ligase; AltName: Full=Seryl-tRNA synthetase; Short=SerRS; AltName: Full=Seryl-tRNA(Ser/Sec) synthetase

MLDLKNLQNNFDEVAKKLKNKKVDENILKKLAELFASLKKEKTALEEFQAFQNKFSKELATAEDKESLKA

KLSENKSKINEQSVKVNALENELEEIAHAIPNIPDECVPVGEDEDENVELKKVLNPPSFDFTPKEHFELG

ESLNWLDFVRGVKISQSRFCVLKNEGALLSRALVNYMIDFNRSHGFEFVNVPFLVNGATMFGTGQLPKFK

EDMYKVDDEDLYLISTSEIPVTNLYSGEILASETLPIKMTCYSACFRKEAGSAGRDTRGIIRQHQFEKVE

LVSITKPEQSDSVFNEMLECASDLLSSLGLAHRHLMLCTGDLGFSAAKTVDLEVWLPGQNKYREISSVSN

CRDFQARRAKIRYKNEQGKNELVHTLNGSSLAVGRTLVAIMENYQDKEGKIHIPDALKKYF

>sp|A8FKB8.1|PLSX\_CAMJ8 RecName: Full=Phosphate acyltransferase; AltName: Full=Acyl-ACP phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate acyltransferase; AltName: Full=Phosphate-acyl-ACP acyltransferase

MINIAIDAMGGDFGEKPIIEGVLKALEAKPFNAILVGNSKILKPLIPKKLEQYIQYEEASEIFSMNENAT

DALKNKETTIYKAINLLKEKKVDAVVSAGHSGASMSLATLRLGRLKGISRPAIATLMPNIINKTLLLDVG

ANTDCKAENLFQFAIMGEVYARAIMQIQKPRLALLSNGEEECKGNELTKESHQLMKKIPNFIGNAEGRDI

FNGEIDVLVCDGFDGNVILKACEGVATAIFQLLKNEVKQSFISKIGALLMKPSFKKLKKHTDWQEYGGAP

LLGVNGCVIISHGKSDSRAIKNAIFQAINFSQSHINELIENELGKYNA

>sp|A8FK33.1|RL35\_CAMJ8 RecName: Full=50S ribosomal protein L35

MPKMKSVKSAVKRFKVGKNKIKRGSAFRSHILTKKPAKRMRDLRTAKYVHSTNVKAVEKMLGI

>sp|A8FK16.1|ARGB\_CAMJ8 RecName: Full=Acetylglutamate kinase; AltName: Full=N-acetyl-L-glutamate 5-phosphotransferase; AltName: Full=NAG kinase; Short=NAGK

MQKYLEKANVLIEALPYIRKFNSKIILIKYGGSAMENEELKHCVMQDIALLKLVGLKPIIVHGGGKDISA

MCEKLGVKSEFKNGLRVSDKATTEVASMVLNHINKNLVHSLQNLGVKAIGLCGKDGALLECVKKDENLAF

VGTIQKVNSKILEELLEKDFLPIITPIGMDENFNTYNINADDAACSIAKALRAEKLAFLTDTAGLYEDFN

DKNSLISKISLEQAKILAPKIEGGMHVKLKSCIDACENGVKKVHILDGRVKHSLLLEFFTDEGIGTLVG

>sp|A8FK07.1|SYT\_CAMJ8 RecName: Full=Threonine--tRNA ligase; AltName: Full=Threonyl-tRNA synthetase; Short=ThrRS

MEKEVIAYLDNETIIDSQSVKNTNLKEIYFDNSKESLEVIRHSCAHLMAQAIKNLYPEAKFFVGPVIEDG

FYYDFRVESKIGEEDLVKIEKKMKELAEAKIEISKYEITKNEALAKFQNDDLKQEVLLRIPDGAVSIYKQ

GEFEDLCRGPHVPNTKFLRFFKLTRVAGAYLGGDEKREMLTRIYGTAFADKESLKEYLTIIEEAKKRDHR

KLGTELKLFTFDDEIGGGLPIWLSNGARLRSKLEHILYKIHRLRGYEPVRGPELLKADAWKISGHYANYK

ENMYFTQIDEQEYGIKPMNCVGHIKIYQSDVRSYRDLPLKFFEYGVVHRHEKSGVLHGLFRVREFTQDDA

HIFCMPSQIKEQVLEILAFVDNLMKLFDFSYEMEISTKPEKAIGDDEIWEVATKALKEALDEQGLKYGID

EGGGAFYGPKIDIKITDALKRKWQCGTIQVDFNLPSRFKLEYTDSDNEKKQPVMLHRAILGSFERFIGIL

TEHCAGEFPFFIAPTAVGIVPIGEAHIAYAKEIQKELLELNIDSEVYEKNESLSKKIRTAEKQKLPMILV

LGDDEVAKRSVALRDRRAKEQKNLSLDEFIKLVKEKMSEVHF

>sp|A8FJX5.1|MNTP\_CAMJ8 RecName: Full=Putative manganese efflux pump MntP

MDFYSLIFLSCALGMDAFAVSLCKGFSVKKLHLKHYLIVGIYFGGFQALMPTIGYFIGITFASFIASIDH

WIAFILLSLIGLKMIKESLENENCDSNANQFGFKTMLALAIATSIDALAVGVSFAFLNVNLLLAIFLIGI

ITFILCIIALKIGNKFGIYLKNKAELLGGLVLIILGVKILIEHLFFD

>sp|A8FJP9.1|RL21\_CAMJ8 RecName: Full=50S ribosomal protein L21

MYAIIKHSGKQYKVSVGDELKLDHFEAESKASIEVSEVLAINDKELKVGAPFVAGAKVVLEVINHGKDKK

VVIYKKRRRKDSKLKRGFRRQFTRVVVKDIKA

>sp|P22252.4|FLB\_CAMJ8 RecName: Full=Flagellin B

MGFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATLGQAINNGND

AIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTTSFNGKQLLSG

NFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSV

GTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVVIGQINYKDGDNNGQLVSAINA

VKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAI

GMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVG

SGKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVTTLKGAMAVM

DIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFASESANFSKYNILAQSGSYA

MSQANAVQQNVLKLLQ

>sp|P22251.3|FLA\_CAMJ8 RecName: Full=Flagellin A

MGFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND

ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSG

NFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSV

GTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINA

VKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAI

GMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVG

SGKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVTTLKGAMAVM

DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKANILAQSGSYA

MAQANSSQQNVLRLLQ

>sp|A8FJQ9.1|ATPD\_CAMJ8 RecName: Full=ATP synthase subunit delta; AltName: Full=ATP synthase F(1) sector subunit delta; AltName: Full=F-type ATPase subunit delta; Short=F-ATPase subunit delta

MENIIARRYAKAIASRADINDFYQNLCILNSAFVLPKFKNIIESNEIKKERKMEFLDSFFDIKNSSFQNF

LRLLIENSRLEYIPQIVKELERQKAFKENIFVGIVYSKEKLSQENLKDLEVKLNKKFDANIKLNNKISQD

DSVKIELEELGYELSFSMKALQNKLNEYILKII

>sp|A8FNZ2.1|BIOB\_CAMJ8 RecName: Full=Biotin synthase

MQIMLCAISNIASGNCSEDCKYCTQSAHVKTDIQKYRRKELSQIVLEAKMAKKNEALGFCLVTAGLGLDD

EKLEYVCEAAKAVQKEVPNLLLIACNGMASVEQLKELKKAGIFSYNHNLETSKEFFPQICTTHTWESRFQ

TNLNAKEAGLMLCCGGIYGMGESEEDRLSFRKSLQELQPFSTPINFFIANENLKLQVPRLSADEALKIVR

DTKEALPQSVVMVAGGREVVLQERQYEIFQAGAGAIVIGDYLTTKGEEPSQDIIKLKEMGFTFASECH

>sp|A8FKG2.1|Y350\_CAMJ8 RecName: Full=UPF0234 protein C8J\_0350

MASEHSFDISAALDKQELKNAFEQAKKELDSRYDLKGIKCEIDLSEKESIFKLSSSSEGKLDVLKDIVIS

KLIKRGINPNAIKELSRESGAMFRLNLKANDAIDSENAKKINKAIKDSKLKVNSSIRGEEIRVAAKQIDD

LQAVMKLVKELDLELNISFKNLK

>sp|A8FMR4.1|RNY\_CAMJ8 RecName: Full=Ribonuclease Y; Short=RNase Y

MIESLIALIAAIVGLGIGYLVAKKINDAKYEIFVEQAKAKAKAIEYEAELILKDAKNSILNAELEVKKKY

EEKTHKIQKDFNQKFDDLSKKEQKLQQEEEKLKEDKEYLCKSQKHIQDLQSDVDKLKNKYQEKLDDVLKI

LEHSTGLTQNEAKEIILKKVEENSREQIAHIVRKYEEEAKNEAKRKANFIIAQATSRFAGEFAAERLINV

INIKNDELKGRIIGKEGRNVKTLEMVLGVDIIIDDTPGAIIVSCFNLYRRAIATKVIELLVEDGRIQPAR

IEEIHEKVCKEFDSAILEEGETIVMDLGLNKIHPEIVKLIGKLKYRASYGQNALAHSLEVAHLAGIIAAE

CGGDENLARRAGILHDIGKALTHDFEGSHVDLGAELCKRYKEHPVVINAIYAHHGHEEATSIESAAVCAA

DTLSAARPGARREVLEAFLKRVSELEDIAKSKEGIKNAYAINAGREIRVIANAQLVNDDESVLLAKEIAA

EIQEKMQYPGEIKVNVIRELRAVEYAK

>sp|A8FNK1.1|Y1440\_CAMJ8 RecName: Full=UPF0271 protein C8J\_1440

MFKVDLNSDLGESFGAYKMGMDEEILKFVSSVNVACGFHAGDPCVMDKTLNLAKQNGVCIGAHPSYPDLL

GFGRRNMQISFEEAKNYALYQLGALFGFAKAKGMKIQHFKAHGALYNMAAIDENLALALCEAVASFDENI

IFLGLSNSAMNEAAKKKGLRYANEVFADRAYNDDGTLVSRKLEGALIHDENLAIKRVIKMIKESKVTSIN

GKEIDLKADSICVHGDNIKALEFVKKIKENLEKEQIQICALENFI

>sp|A8FNQ2.1|IF1\_CAMJ8 RecName: Full=Translation initiation factor IF-1

MAKDDVIEIDGTVLEALPNANFKVELDNKHVILCHIAGKMRMHYIRIMPGDKVKVELTPYSLDKGRITFR

YK

>sp|A8FJR2.1|ATPB\_CAMJ8 RecName: Full=ATP synthase subunit beta; AltName: Full=ATP synthase F1 sector subunit beta; AltName: Full=F-ATPase subunit beta

MQGFISQVLGPVVDVDFNDYLPQINEAIVVNFESEGKKHKLVLEVAAHLGDNRVRTIAMDMTDGLVRGLK

AEALGAPISVPVGEKVLGRIFNVTGDLIDEGEEISFDKKWAIHRDPPAFEDQSTKSEIFETGIKVVDLLA

PYAKGGKVGLFGGAGVGKTVIIMELIHNVAFKHSGYSVFAGVGERTREGNDLYNEMKESNVLDKVALCYG

QMNEPPGARNRIALTGLTMAEYFRDEMGLDVLMFIDNIFRFSQSGSEMSALLGRIPSAVGYQPTLASEMG

KFQERITSTKKGSITSVQAVYVPADDLTDPAPATVFAHLDATTVLNRAIAEKGIYPAVDPLDSTSRMLDP

NIIGEEHYKVARGVQSVLQKYKDLQDIIAILGMDELSEEDKLVVERARKIEKFLSQPFFVAEVFTGSPGK

YISLEDTIAGFKGILEGKYDHLPENAFYMVGNIDEAIAKADKLKG

>sp|A8FLL1.1|DDL\_CAMJ8 RecName: Full=D-alanine--D-alanine ligase; AltName: Full=D-Ala-D-Ala ligase; AltName: Full=D-alanylalanine synthetase

MKFAILFGGNSYEHEISIVSAVVLKKVINQNLEFVFCDEERRFYHIPSEKMNSKTFSTKAYKNEKELFIK

QGGFFSKGFLKENKLECECVINLIHGRDGEDGKIAALFEFYSIKFIGPRLEASVLSFNKELTKLYAKSVG

VKTLDYTMLRKNQNSKEKLSFPCIIKPARLGSSIGISIVKDEKDLEYAKDVGFEFDNDLVVEEFKNNIKE

YNLAGCMINDEFVFSIIEEPKKKEFLDFEQKYLSFSGHNELIEADLSEELKEKLKDSFKKIYNPLFKGAL

IRCDFFILDNEVYLNEINPNPGSLANYLFKDFNTTLNALADQISLEKMIKINYNFLHSINGQKGKL

>sp|A8FL05.1|RPPH\_CAMJ8 RecName: Full=RNA pyrophosphohydrolase; AltName: Full=(Di)nucleoside polyphosphate hydrolase

MENEKNYRPNVAAIVLSSSYPFECKIFIAKRSDMDNIWQFPQGGIDKGESVKNALFRELKEEIGTDEVEI

IAEYPEWLSYDFPSKIVKKMYPYDGQIQKYFLVRLKHGATININTKHPEFDDYQFVSVKQIFEMINHFKK

NIYVKVIKYFEEKGYI

>sp|A8FMM8.1|Y1116\_CAMJ8 RecName: Full=Probable transcriptional regulatory protein C8J\_1116

MGRAFEYRRASKEARWDKMSKLFPKLAKAIQVAAKEGGTDPDMNPKLRSAIATAKANNMPKDNIDAAIKR

ASGKDSADIKNIHYEGKAAHGALVIVECMSDNPTRTVANVKAIFSKNGGEVLQNGSLGFMFARKAVFHLE

KFAGDLEELELDLIDAGLEELEQNEEELVISGDYTAFGELSSAIEAKGLVLKKAGLEYIPNNPVSFSEEQ

LSDIEKLLDKLEDDDDVQAVYTNID

>sp|A8FN39.1|PPK1\_CAMJ8 RecName: Full=Polyphosphate kinase; AltName: Full=ATP-polyphosphate phosphotransferase; AltName: Full=Polyphosphoric acid kinase

MQTSPDMFINRELSWLRFNSRVLDQCSKNLPLLEKLKFIAIYCTNLDEFYMIRVAGLKQLFSAGVNASSS

DEMTPLQQLKAIRKYLHQEKELLERYFNEITSELEKENLFIKHYENLDENLKQKCDEYFFSNIFPVIVPI

AVDATHPFPHLNNLSFSLAVKICDKAHPELVKFGMIRIPRVLPRFYEVSANIYVPIESIVHQHAEEIFPG

YKLLASAAFRVTRNADMVIEEEEADDFMMILEQGLKLRRKGAFVRLQIQKDADEQIVEFLNTHMKIFHKD

VYEYSILLNLPSLWQIAGNKTFTHLLSPLYTPKTLPPFDENLSIFDAVEKEDILIIQPFESFDPVYKFIK

EASKDPEVISIRMTLYRVEKNSNIVQALIDAASDGKQVTVMVELKARFDEENNLHWAKALENAGAHVIYG

ITGFKVHAKVSQVIRKQGDKLKFYMHLSTGNYNASSAKIYTDVSYFTSKAEFARDTTSFFHILSGFSKNR

RLQTLSMSPNQIKEKVLEMIRIETSKKNEGVIVAKMNSLVDSDIIQALYEASMEGVQIDLIIRGICCLKP

DEEYSKNIRVRSIIGKYLEHARVFYFKHSEPNYFISSADWMPRNLERRLELMTPIYDERSKAKLAQFLRL

QLSDNVLAYELKNNGEYEKIPSSEKIIDSQQTLEEYVSKIYKTLKKDTDQSRATHLASKLFKEN

>sp|A8FL79.1|ERA\_CAMJ8 RecName: Full=GTPase Era

MKSGFVSIIGRTNAGKSTLINSLLEEKIALVSHKQNATRRKIKAIVMHEKNQIIFIDTPGLHESGATLNQ

LLVQSAIKSMGDCDVILFVASVFDSTKDYENFLSLNPQVPHIIALNKVDLTDNATLLKKLSEYAKFSQHF

KAIIPYSSKKKSYKKGLLDEIVKYLDKHEYFYDPEFLSASSEKELYRDFILESIYENLSDELPYSSEVLI

HRTKDTPNLLILEANIITDTNSHKGMLIGKEGATLKRIGKDARFKISKLAQKKVLLKLFVTVKKNWQKDE

EFLKKLLNDEN

>sp|A8FNC4.1|TRUD\_CAMJ8 RecName: Full=tRNA pseudouridine synthase D; AltName: Full=tRNA pseudouridine(13) synthase; AltName: Full=tRNA pseudouridylate synthase D; AltName: Full=tRNA-uridine isomerase D

MNLEEENTIFKPLYSLKHSPINAYFSKNSDDFVVRERPLYEFSGKGEHLILHINKKDLTTNEALKILSET

SGVKIRDFGYAGLKDKQGSTFQYLSMPKKFESFLSNFSHPKLKILEIFTHENKLRIGHLKGNTFFIRLKK

VLPSDALKLEQALMNLDKQGFANYFGYQRFGKFGDNYKEGFEILRGKKMKNVKMKEFLISAFQSELFNRY

LSKRVELSHFANDFSEKELIQIYKISKEEAKELKKQEQFFKLLKGEVLGHYPFGKCFLCEDLSAELERFK

ARDISAMGLLIGAKAYETGEGLALNLENEIFKDALEFKAKMQGSRRFMWGYLEELKWRYDEEKAHFCIEF

FLQKGSYATVVLEEILHKNLFE

>sp|A8FMF5.1|TRUB\_CAMJ8 RecName: Full=tRNA pseudouridine synthase B; AltName: Full=tRNA pseudouridine(55) synthase; Short=Psi55 synthase; AltName: Full=tRNA pseudouridylate synthase; AltName: Full=tRNA-uridine isomerase

MNKIFAAFKPRGLSSNAFLSTLKKKYKNKKAGYSGTLDPFAKGVLIVAFGQYTKLFRFLKKTPKTYKATL

WLGVYSLSLDDQNIKEIKNIKEFDLANLQQIIDQMQGIISYTPPQFSAKRINGTRAYELAKKGIEANLKP

CQMEVFDCKILSYNHPFLNIEITVSEGAYIRSYCELFARKLGINATLSSLERIKEGKFVYNNEKSLNVLK

YINLKPNFIKDLNKLENGAKIFVEELKFHDEGDYYIETEKYFSIINIKENTVKYLLNKVEKC

>sp|A8FNW7.2|NHAA2\_CAMJ8 RecName: Full=Na(+)/H(+) antiporter NhaA 2; AltName: Full=Sodium/proton antiporter NhaA 2

MQMIKKMVLSETFPGILLIFFTFLALLCKNSSLSVIYTDFFHANFTVGFDHFQISKSLDLWINDGLIAIF

FLCIGLELKYEILRGQLKNIRAVSLPIFGALGGMITPALIFAAINYSHDFAMKGWAIPTATDIAFAVGIL

MLLGNKIPTSLKLFLLSLAIFDDLGAIVIIALFYTDQLSALAIIICLFCIFALLLLNYYHITHLSLYVLV

GVVLWIAMLKSGVHATLAGVIISLFIPLDTKNKKPYLHEVLKDLNPWVVYFILPLFAFANAGIDIRDMHL

GSVFSPVSLGIILGLFLGKQLGVFTFCFIAIKLKLAKLPENIKYGKFYGICILTGIGFTMSLFIDGLAYK

NSDIFEHADKLAILIASFLSAIVGFIYLKIVK

>sp|A8FNW6.1|NHAA1\_CAMJ8 RecName: Full=Na(+)/H(+) antiporter NhaA 1; AltName: Full=Sodium/proton antiporter NhaA 1

MNNIVHKLKTLVLNEAFGGVLLIVCTLLALLVQNGSFSEHYREFLNLKVGFSVGEFELNKPFLLWINDGL

ISIFFFAIGLELKKEFLHGDFKNPKNIVLPFMAALGGILIPAMLFALVNIGDAYTLKGWAIPTATDTAFA

LAILMMCGKHIPSSLKIFLLSLAIFDDVGAILIIAIFYTTKLSIVAFVVAGIAILAMLVLNILGITRKSF

YFICSVILWISVLKSGVHATLAGIITAFFIPMQTKNGEAFLEEIYESLKFWLAFVILPLFAFANAGVNLS

NIDIGAIFSGVSVGIFLGLFVGKQVGVFLFSYLAIRFKFAALPQGSNLKQLYGVCILTGIGFTMSLFIDG

LAYEVSDIFNYADNLAILIASFCSGIWGFIYLKFFAARS

>sp|A8FMV9.1|PNP\_CAMJ8 RecName: Full=Polyribonucleotide nucleotidyltransferase; AltName: Full=Polynucleotide phosphorylase; Short=PNPase

MQYSIEINKNTEIFDIDKVAKQAAGAVLMRQGKSVVLATVAREEKQVEEDFLPLTVQYIEKAYAAGKIPG

GYVKRETKPSDAETLTARIIDRSLRPLFPKGYTYPTQIVVMVLSADPKVDLQVMSLNAASVALYLSDIPM

KAPVCGVRIGKIDGNFILNPNNEELQNSTLDLYVAGVKDELLMIEMRALPDQKENEIFIEAPYADVLTQT

TSQNMNELSEDEILEALNLAQKAILNGSNAYEEAFSKHKKNSQIELKNEIEHPEILAFIENNFQKQIKEA

INQMAKSERASELNKIAKEILNLEIAKDWSEESVLNTLAKVKRKLIREQILNEGKRADGRSLNEVRPISI

ETNILPNAHGSCLFTRGQTQALVVATLGGENDAQMIDLLTEKNPISERFMVNYNFPGFSVGEASPIKAPG

RRELGHGNLAKRALYPSVDENYPYVIRLVSEILESNGSSSMATVCGGSLALKAAGVPSLKLVAGVAMGLI

FEDNKHAVLTDIMGLEDHDGDMDFKVAGSKDGVTALQMDIKLGGIDQETLKQALYQAKEGRIHILNIMEE

AAKEIIVNEEVLPKLELFSVDPSKIVDIIGQAGKTIKEIIEKFGVSIDLDREKGEVKIAGSQNEQIKAAK

DYIINITSSQKGTKKGSKDKDISGFELGQEFQGIVKKIAPFGAFVELKNGVDGLLHSSKSKHLNLTENQS

LKVKISEIKNGKISVDLCE

>sp|A8FKR3.1|RPOB\_CAMJ8 RecName: Full=DNA-directed RNA polymerase subunit beta; Short=RNAP subunit beta; AltName: Full=RNA polymerase subunit beta; AltName: Full=Transcriptase subunit beta

MLDNKLGNRLRVDFSNISKQIEIPNLLQLQKKSFDYFLNLDNGESGIEKVFKSIFPIHDPQNRLSLEYVS

SEIGKPKYTIRECMERGLTYSVNLKMKIRLTLHEKDEKTGEKVGVKDIKEQEIYIREIPLMTDRVSFIIN

GVERVVVNQLHRSPGVIFKEEESSTVANKLVYTAQIIPDRGSWLYFEYDAKDVLYVRINKRRKVPVTMLF

RALGYKKQDIIKLFYPIQTIHVKKDKFLTEFNPNDFMDRIEYDIKDEKGKIVHQAGKRLTKKKAEQLIKD

GLKWIEYPVEILLNRYLANPIIDKESGEVLFDSLTLLDESKLAKIKEQKSFDIANDLANGVDAAIINSFA

QDGETLKLLKQSENIDDENDLAAIRIYKVMRPGEPVVKDAAKAFVNDLFFNPERYDLTKVGRMKMNHKLG

LEVPEYVTVLTNEDIIKTAKYLIKVKNGKGHIDDRDHLGNRRIRSIGELLANELHLGLAKMQKAIRDKFT

SLNADLDKVMPYDLINPKMITTTIIEFFTGGQLSQFMDQTNPLSEVTHKRRLSALGEGGLVKERAGFEVR

DVHATHYGRICPVETPEGQNIGLINTLSTYAKVNELGFVEAPYRKVVNGKVTNEVVYLTATQEEGLFIAP

ASTKVDAKGNIVEEFVEARQDGETILARREEVQLIDLCSGMVVGVAASLIPFLEHDDANRALMGSNMQRQ

AVPLLTASAPIVGTGMEQIIARDAWEAVKAKRGGVVEKVDNKSIFILGEDDKGPFIDHYTMEKNLRTNQN

TNYIQHPIVKKGDIVKAGQIIADGPSMDQGELAIGKNALIAFMPWNGYNYEDAIVVSERIIREDTFTSVH

IYEKEIEARELKDGIEEITKDIPNVKEEDVAHLDESGIAKIGTHIKPGMILVGKVSPKGEVKPTPEERLL

RAIFGEKAGHVVNKSLYATASLEGVVVDVKIFTKKGYEKDDRAIKSYDKEKMALEKEHHDRLLMMDREEM

LRVCALLSKAPLNSDQKIGDKNYKKGQTADISELEKINRFTLTTLIKAYSKEIQKEYDDLKNHFQNEKKK

LKAEHDEKLEILEKDDILPSGVIKLVKVYIATKRKLKVGDKMAGRHGNKGIVSTIVPEVDMPYLPNGKSV

DIALNPLGVPSRMNIGQILESHLGLIGLRLGDQIQEIFDRKQKDFLKELRAKMLEICSIPRLASEKEFIK

SLSDEELLNYARDWSKGVKFATPVFEGVNIEEFSKLFEMAKIDMDGKTELYDGRTGEKIAERVHVGCMYM

LKLHHLVDEKVHARSTGPYSLVTQQPVGGKALFGGQRFGEMEVWALEAYGAAHTLREMLTIKSDDVEGRF

SAYKALTKGENVPATGIPETFFVLTNELKSLALDVEIFDKDEDNE

>sp|A8FK31.1|HEMTB\_CAMJ8 RecName: Full=Bacteriohemerythrin

MTYNEKIISMNNDLLDHQHKELFEISKKLSLMNQRHVGTKELKIVLRELLIMINRHFSDEEAFMREIEYP

YINHHTRIHRKIILEIEEIIISEAKFVNIMTEKLNLVVQDFIFKHTAKEDSKIVKYYEEKFKK

>sp|A8FP32.1|LEUD\_CAMJ8 RecName: Full=3-isopropylmalate dehydratase small subunit; AltName: Full=Alpha-IPM isomerase; Short=IPMI; AltName: Full=Isopropylmalate isomerase

MQKFIIHKGIACPLEYANIDTDQIIPKQFLLAVSKQGFGKHLFHDLRYLDDKESVLNMDFNLNKKEYQNS

SILVSFENFGSGSSREHAPWALVDYGIRAIIAPSFADIFKNNALGNGLLTIELAKDEVLEIVDELKKSQD

KNIEISLLEKRVFFKDKIFSFDLDDFHRICLLEGLDNIALTLKHEAQIKAYEKNSKSFLV

>sp|A8FP20.1|RL4\_CAMJ8 RecName: Full=50S ribosomal protein L4

MSKVVVLNDKLEKAGELDLPSKYAEVNPHNLYLYVKSYLASLRANTAHTKGRSDVSGGGKKPWRQKGRGG

ARAGSTRTNVWVGGAVAFGPTNERNYFQKVNKKQKRLALERALADKAAKGALFTADSLAIESGKTKDANA

VIKKLGVKDALIVKDLLDEKTLLAYRNLANCYVVDVSEVNAYLVSVFNAVIIEKSALESITKEG

>sp|A8FP19.1|RL23\_CAMJ8 RecName: Full=50S ribosomal protein L23

MADITDIKTILYTEKSLNLQEQGVVVIQTSPKMTKTGLKAVLKEYFGVTPKSINSLRMDGKVKRFRGRLG

QRNDYKKFYVKLPEGVSLENTEA

>sp|A8FP18.1|RL2\_CAMJ8 RecName: Full=50S ribosomal protein L2

MAIKTYKPYTPSRRYITGLSSEDITAKPSVRSLLVKLPAHAGRNSYGRITSRHKEAGAKKLYRIIDFKRR

KFGIEGKVEAIEYDPYRNCRIALIAYKDGEKRYILQPRGLSVGDIVAAAESGLDIKPGNAMKLKNIPVGT

IVHNVELKPGKGGQMIRSAGAYAQLMGKEEKYVILRLASGEMRQVLAECMASIGEVGNEEWANVTIGKAG

RNRHRGIRPQTRGSAMNPVDHPHGGGEGKKNSGRHPVTPWGKPTKGAKTRRKKASDKLIISRRKGK

>sp|A8FP15.1|RS3\_CAMJ8 RecName: Full=30S ribosomal protein S3

MGQKVNPIGLRLGINRNWESRWFPTKANLVENIGEDYKIRAFLKRKLYYAGISQILVERTAKKLRVTVVA

ARPGIIIGKKGSDVDNLRKELQDLIGKDVNINIKEERKAGASAQLAAESVATQLEKRIAFRRAMKKVIQG

AQKAGAKGIKVSVSGRLGGAEMARTEWYLEGRVPLHTLRAKIDYGFAEARTTYGNIGVKVWIFKGEVLHK

GMQPEKTEESAPAKKPRRTRRGK

>sp|A8FP10.1|RL24\_CAMJ8 RecName: Full=50S ribosomal protein L24

MAVKLKIKKGDSVKVITGDDKGKTGKVLAVYPKTLKVVVEGCKIAKKAIKPSEKNPNGGFINKEMPMDIS

NVAKVQE

>sp|A8FP09.1|RL5\_CAMJ8 RecName: Full=50S ribosomal protein L5

MMRLKEKYNQSIKPALVKEFDIKNPMLIPVIEKVVISVGAGELAKDQKVLQNVADTISLIAGQKAVITKA

KKSVAGFKVREGFPVGVMVTLRKENMYAFLDKLISIALPRVKDFRGLSRDGFDGRGNYNFGLDEQLMFPE

VEYDKILRTHGMNISIVTTAQNDKQAQKLLELIGVPFTKGK

>sp|A8FNY3.1|ENO\_CAMJ8 RecName: Full=Enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=2-phosphoglycerate dehydratase

MLVIEDVRAYEVLDSRGNPTVKAEVTLSDGSVGAAIVPSGASTGSKEALELRDNDERFGGKGVLKAVANV

NETIADEILGLDAFNQTQLDDTLRELDGTNNYSNLGANATLGVSMATARAAAAALGMPLYRYLGGANASI

LPVPMCNIINGGAHANNNVDFQEFMIMPFGFTSFKEALRSVCEIYAILKKELANSGHSTALGDEGGFAPN

LANNTEPIDLLMTCIKKAGYENRVKIALDVASTEFFKDGKYHMEGKAFSSEDLIERYVELCAKYPICSIE

DGLAENDFEGWIKLTEKLGNKIQLVGDDLFVTNEDILREGIIKKMANAVLIKPNQIGTITQTMRTVRLAQ

RNNYKCVMSHRSGESEDAFIADFAVALNTGQIKTGALARGERTAKYNRLLEIELESDEYLGEKL

>sp|A8FNC9.1|FLGI\_CAMJ8 RecName: Full=Flagellar P-ring protein; AltName: Full=Basal body P-ring protein; Flags: Precursor

MRVLTIFLLFMTSIFAVQIKDVANTVGVRDNQLIGYGLVVGLNGSGDGTSSKFTLQSISNLLQGMNIKVD

PNDIKSKNTAAVMVTAKLPAFAKSGDKLDITVSSMGDAKSLQGGTLLLTALRGIDGEIYAIAQGSISTGG

LTPRPGGAGSHSTAATVMGGANVEREIPQNFSQNNDLTLSLKVADFKTANDIERVLNTVFGEEVAKAIDS

RTVKLKKPEDLSNVDFMARVLEQDIAYKPQSKVIIDERTGTVIAGVDVEVEPVLITHKDITIKIDPNNNA

VANQNEIDMKDGGFVDPSSNTLRINNAKSTVANIARMLNKLGATPNDIIAIMENLKRAGAINADLEII

>sp|A8FN84.1|ACPS\_CAMJ8 RecName: Full=Holo-[acyl-carrier-protein] synthase; Short=Holo-ACP synthase; AltName: Full=4'-phosphopantetheinyl transferase AcpS

MRVGCDIIAISRIEKIHSRHGKNFLDKFLSPKEQILIKNPATLAGLWAAKEAASKALGVGICELCSFFDI

EISKDEKNAPKLKYSQKITKNFNITQTSLSISHDNGFAIAIVAIV

>sp|A8FN22.1|TSAD\_CAMJ8 RecName: Full=tRNA N6-adenosine threonylcarbamoyltransferase; AltName: Full=N6-L-threonylcarbamoyladenine synthase; Short=t(6)A synthase; AltName: Full=t(6)A37 threonylcarbamoyladenosine biosynthesis protein TsaD; AltName: Full=tRNA threonylcarbamoyladenosine biosynthesis protein TsaD

MKNLILAIESSCDDSSIAIIDKNTLECKFHKKISQELDHSIYGGVVPELAARLHSEALPKILKQCKEHFK

NLCAIAVTNEPGLSVSLLSGISMAKTLASALNLPLIPINHLKGHIYSLFLEEKISLDMGILLVSGGHTMV

LYLKDDANLELLASTNDDSFGESFDKVAKMMNLGYPGGVIIENLAKNAKLKNISFNIPLKHSKELAYSFS

GLKNAVRLEILKHENLSDEIKAEIAYAFENTACDHIMDKLEKIFNLYKFKNFGVVGGASANLHLRSRLQN

LCQKYNANLKLAPLKFCSDNALMIARAAVDAYKKKEFVSIEEDILSPKNKNFSRI

>sp|A8FMS6.1|CH60\_CAMJ8 RecName: Full=60 kDa chaperonin; AltName: Full=GroEL protein; AltName: Full=Protein Cpn60

MAKEIIFSDEARNKLYEGVKKLNDAVKVTMGPRGRNVLIQKSFGAPSITKDGVSVAKEVELKDSLENMGA

SLVREVASKTADQAGDGTTTATVLAHAIFKEGLRNITAGANPIEVKRGMDKACEAIVAELKKLSREVKDK

KEIAQVATISANSDEKIGNLIADAMEKVGKDGVITVEEAKSINDELNVVEGMQFDRGYLSPYFITNAEKM

TVELSSPYILLFDKKIANLKDLLPVLEQIQKTGKPLLIIAEDIEGEALATLVVNKLRGVLNISAVKAPGF

GDRRKAMLEDIAILTGGEVISEELGRTLESATIQDLGQASSVIIDKDNTTIVNGAGEKANIDARVNQIKA

QIAETTSDYDREKLQERLAKLSGGVAVIKVGAATETEMKEKKDRVDDALSATKAAVEEGIVIGGGAALIK

AKAKIKLDLQGDEAIGAAIVERALRAPLRQIAENAGFDAGVVVNSVENAKDENTGFDAAKGEYVNMLESG

IIDPVKVERVALLNAVSVASMLLTTEATISEIKEDKPAMPDMSGMGGMGGMGGMM

>sp|A8FMS5.1|CH10\_CAMJ8 RecName: Full=10 kDa chaperonin; AltName: Full=GroES protein; AltName: Full=Protein Cpn10

MNFQPLGKRVLVKRVEETKTTASGIIIPDNAKEKPLMGEVVAVSKEITDIANGDKIVFAKYGGTEIKLDN

NEYLVLNLDDILGILK

>sp|A8FMQ3.1|GATB\_CAMJ8 RecName: Full=Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B; Short=Asp/Glu-ADT subunit B

MFEVVIGLEVHTQLNTKTKIFCSCATSFGEAPNTNVCPTCLALPGALPVLNEEAVKKAIAFGKAVNATIN

KKSVFNRKNYFYPDLPKAYQISQFDIPIVEKGELFINVKGENKRIGITRAHLEEDAGKNIHENNFSKVDL

NRAGTPLLEIVSEPELRSSDEAVAYLKKLHSIIRFLDISDANMQEGSFRCDANVSIRPKGDTKLYTRVEI

KNLNSFRFIQKAIEYEVKRQSEAWEDGTYEQEVVQETRLFDTTNLVTRSMRGKEEAAEYRYFPDPDLLPV

LLKDEFLDIKIPELPDEKKARFIDELGIKESDAEVLISSLEMSRFFESLISQNLNSKLCVNWLNTELMGL

LKGELTIENSPVDAQKLGVLIKRIEDGTISAKAAKDVLAFVFENTSVEIDEAIEKLGLKQVSDDSAIEAV

IEQILNANADKVAEYKSGKDKLFGFFVGQTMKEGKGAFNPAKVNEILKTKLG

>sp|A8FMQ2.1|GPDA\_CAMJ8 RecName: Full=Glycerol-3-phosphate dehydrogenase [NAD(P)+]; AltName: Full=NAD(P)H-dependent glycerol-3-phosphate dehydrogenase

MRIAVIGAGKWGSALHLALKENHNCFISSLHQRDLEDFVSIKEALECEYLVFALSSQGMRAWLKENFINK

GQKILIASKGIEDQSCQFLDEIFLDFVPKENFCVLSGPSFAAEVMQKLPTALMISGINQELCKKFASFFP

DFIKTYIDNDVRGAEICGAYKNVLAIASGISDGLKLGNNARAALISRGLIEMHRFGKFFGAKEETFLGLS

GAGDLFLTATSVLSRNYRVGLKLAQNQKLDSILVELNEVAEGVKTAYAIEKLAKMKGIYTPIVNEVVAIF

KGKSVQEATQSLLKQND

>sp|A8FMN8.1|RS2\_CAMJ8 RecName: Full=30S ribosomal protein S2

MVSMRDLLECGVHFGHQTRRWNPKMKKFIFGERKGIYVIDLQKTLRYFRYTYNIVRDAAAEGKTILFVGT

KKQAGGAIKEYAEKCGMPYVNHRWLGGMMTNFGTIRQSIRKLEVIEKMEEDGSIKLLTKKEALMLTRKKE

KLLAYLGGIRYMKTQPDMIFVIDTVKEKIAVQEANRLRIPVVAPLDTNCDPDLVTYPIPGNDDAIRSVQL

FCQEMAEAINEGKALREQDGEALANEEKEITDEEKKEVLDEAMSEEDFGEEQE

>sp|A8FMN7.1|EFTS\_CAMJ8 RecName: Full=Elongation factor Ts; Short=EF-Ts

MAEITAAMVKELRESTGAGMMDCKNALSETNGDFDKAVQLLREKGLGKAAKKADRLAAEGLVSVKVSDDF

TSATVSEINSETDFVAKNDQFIALTKDTTAHIQSNSLQSVEELHSSIINGVKFEEYLKSQIATIGENLVV

RRFATLKAGANGVVNGYIHTNGRVGVVIAAACDSAEVASKSRDLLRQICMHIAAMRPSYLSYEDLDMTFV

ENEYKALVAELEKENEERRRLKDPNKPEHKIPQFASRKQLSDAILKEAEEKIKEELKAQGKPEKIWDNII

PGKMNSFIADNSQLDSKLTLMGQFYVMDDKKTVEQVIAEKEKEFGGKIKIVEFICFEVGEGLEKKTEDFA

AEVAAQL

>sp|A8FM84.1|ATE\_CAMJ8 RecName: Full=Putative arginyl-tRNA--protein transferase; Short=Arginyltransferase; Short=R-transferase

MLEIGFCTLEDQCPYLKDKRSRIEYKYIENCSKEINNELIKRGWRRFGRYFSRPICKDCDECLSLRILVN

EYNFSRSERRVINKNINTKVILRTPNLSNEHLFLYDKYHRFMEEKKNWKRYDLSFKQYYNLYVDGFMNFG

YELAFYIEDKLVCVDLIDILEDGISSIYCFYDPDFSYFSLGKFSLLNEIQIAKKMNLDYIYLGYFVKKCQ

SLSYKADYTPNEILKGTKELFENEVLWEK

>sp|A8FM79.1|LEPA\_CAMJ8 RecName: Full=Elongation factor 4; Short=EF-4; AltName: Full=Ribosomal back-translocase LepA

MSVKNIRNFSIIAHIDHGKSTLADRIISECGAISDRQMSSQVMDTMDIEKERGITIKAQSVRLNYKFNNE

NFVLNLIDTPGHVDFSYEVSRSLASCEGALLVVDASQGVEAQTIANVYIALENNLEIIPVINKIDLPNAD

VEKVKHEIEHIIGIDCKDAICVSAKTGVGIKELIETIITKIPAPKTDDEAPTKALIYDSWFDNYLGALAL

VRIYEGSIAKNDEVLVMSTDKKHIVQDLFYPHPLSPIKTQSLQSGEVGVVVLGLKTVGDVQVGDTITLVK

NKAKEAIGGFEKAKAFVFAGLYPIETDKFEDLRDALDKLKLNDSSITYEPETSLALGFGFRVGFLGLLHM

EVIKERLEREFNLDLIATAPTVTYEIYQTDGELIKIQNPSELPPVNKIDHIKEPYVKATIITPSEFLGNL

ITLLNRKRGVQVKMDYITPERVLLEYDVPLNEIVMDFYDKLKSLTKGYASFDYEPIEFRVGDLVKLDIKV

AGENVDALSIIVPNEKAQSKGRELVSAMKEIVPRQLFEVAIQASIGNKIIARETVKSMGKNVTAKCYGGD

ITRKRKLLEKQKEGKKRMKAIGKVNLPQEAFLSVLKID

>sp|A8FM07.1|PUR9\_CAMJ8 RecName: Full=Bifunctional purine biosynthesis protein PurH; Includes: RecName: Full=Phosphoribosylaminoimidazolecarboxamide formyltransferase; AltName: Full=AICAR transformylase; Includes: RecName: Full=IMP cyclohydrolase; AltName: Full=ATIC; AltName: Full=IMP synthase; AltName: Full=Inosinicase

MRALLSVSDKEGIVEFGKELENLGFEILSTGGTFKLLKENGIKVIEVSDFTKSPELFEGRVKTLHPKIHG

GILHKRSDENHIKQAKENEILGIDLVCVNLYPFKKTTIMSDDFDEIIENIDIGGPAMIRSAAKNYKDVMV

LCDPLDYEKVIETLKKGQNDENFRLNLMIKAYEHTANYDAYIANYMNERFNGGFGASKFIVGQKVFDTKY

GENPHQKGALYEFDAFFRANFKALKSEASFNNLTDINAALNLASSFDKAPAIAIVKHGNPCGFAIKENLV

QSYIHALKCDSVSAYGGVVAINGTLDEALANKINEIYVEVIIAANVDEKALAVFEGKKRIKIFTQESPFL

IRSFDKYDFKHIDGGFVYQNSDEVGEDELKNAKLMSQREASKEELKDLEIAMKIAAFTKSNNVVYVKNGA

MVAIGMGMTSRIDAAKAAIAKAKEMGLDLQGCVLASEAFFPFRDSIDEASKVGVKAIVEPGGSIRDDEVV

KAADEYGMALYFTGVRHFLH

>sp|A8FLN6.1|TRUA\_CAMJ8 RecName: Full=tRNA pseudouridine synthase A; AltName: Full=tRNA pseudouridine(38-40) synthase; AltName: Full=tRNA pseudouridylate synthase I; AltName: Full=tRNA-uridine isomerase I

MKIKIIFSYDGSAFLGSATQPHKKGVQDALSGALSHLGIFSPLLMASRTDKGVHASYAVASVECGDYFTN

LEYLQKQLNKFSHPFIHIKKIEKVKDDFEVRFDVKSREYRYIFSHASYSPFMASYVHFYPKFDLGKANEL

LGFFVGKKDLKFFCKSGGDNKTTLREIFIARAYAYKDFSIFHFKANGFLRGQIRLSVASVLKVLEGKMSE

KELKEQIEAKKQYNHFLAPPNGLYLSRICY

>sp|A8FLN0.1|GLMU\_CAMJ8 RecName: Full=Bifunctional protein GlmU; Includes: RecName: Full=UDP-N-acetylglucosamine pyrophosphorylase; AltName: Full=N-acetylglucosamine-1-phosphate uridyltransferase; Includes: RecName: Full=Glucosamine-1-phosphate N-acetyltransferase

MKTSILILAAGLGTRMKSQKPKVLQELCQKSMILHILKKAFALSDDVSVVLSHQKERVEKEILEYFPKTQ

ILEQDLQNYPGTAGALRGFEPKNERVLILCGDMPLVEQTSLEALLSNNAKLNLAVFKARDPKSYGRVVIK

NDSVEKIVEFKDANTQEKEINTCNAGVYVIDSRLLKELLPLIDNNNAAKEYYLTDIVKLAKEKDVMIKAV

FVDEDEFMGINDKFELSIAENFMQEKIKKYWMQQGVIFHLPQSTFIGTDVEFMGECEVYENVRIEGKSKI

INSIIKSSSVIENSIVENSDVGPLAHLRPNCELKNTHIGNFVECKNAKLNTVKAGHLSYLGDCEIDSGTN

IGCGTITCNYDGVKKHKTIIGKNVFVGSDTQFIAPVKIEDEVIIAAGSTVSVNVEKGALFINRAEHKMIK

DYYYKKFQK

>sp|A8FLJ3.1|NAPA\_CAMJ8 RecName: Full=Periplasmic nitrate reductase; Flags: Precursor

MNRRDFIKNTAIASAASVAGLSVPSSMLGAQEEDWKWDKAVCRFCGTGCGIMIARKDGKIVATKGDPAAP

VNRGLNCIKGYFNAKIMYGEDRLVMPLLRMNEKGEFDKKGKFQQVSWQRAFDEMEKQFKKAYNELGVTGI

GIFGSGQYTIQEGYAALKLAKAGFRTNNIDPNARHCMASAVVGFMQTFGVDEPSGCYDDIELTDTIITWG

ANMAEMHPILWSRVSDRKLSNLDKVKVVNLSTFSNRTSNIADIEIIFKPNTDLAIWNYIAREIVYNHPEA

MDMKFIKDHCVFATGYADIGYGMRNNPNHPKFKESEKDTVEKENVITLDDEEATSLSYLGVKAGDKFEMK

HQGVADKNWEISFEEFKKGLAPYTLEYTAKVAKGDDNESLEDFKKKLQELANLYIEKNRKVVSFWTMGFN

QHTRGSWVNEQAYMVHFLLGKQAKPGSGAFSLTGQPSACGTAREVGTFSHRLPADMVVANPKHREISEKI

WKVPAKTINPKPGSPYLNIMRDLEDGKIKFAWVQVNNPWQNTANANHWIAAAREMDNFIVVSDCYPGISA

KVADLILPSAMIYEKWGAYGNAERRTQHWKQQVLPVGAAMSDTWQILEFAKRFKLKEVWKEQKVDNKLTL

PSVLEEAKAMGYSEDDTLFDVLFANKEAKSFNPNDAIAKGFDNTDVKGDERKIQGSDGKEFAGYGFFVQK

YLWEEYRKFGLGHGHDLADFDTYHKVRGLRWPVVNGKETQWRFNTKFDYYAKKAAPNSDFAFYGDFNKML

TNGDLIAPKDEKEHSIKNKAKIFFRPFMKAPERPSKEYPFWLATGRVLEHWHSGTMTMRVPELYRAVPEA

LCYMSEKDGEKLGLNQGDLVWVESRRGKVKARVDMRGRNKPPVGLVYVPWFDENVYINKVTLDATCPLSK

QTDFKKCAVKIYKA

>sp|A8FLH2.1|DNAK\_CAMJ8 RecName: Full=Chaperone protein DnaK; AltName: Full=HSP70; AltName: Full=Heat shock 70 kDa protein; AltName: Full=Heat shock protein 70

MSKVIGIDLGTTNSCVAVYERGESKVIPNKEGKNTTPSVVAFTDKGEVLVGDSAKRQAVTNPEKTIYSIK

RIMGLMINEDAAKEAKNRLPYHITERNGACAIEIAGKIYTPQEISAKVLMKLKEDAEAFLGESVVDAVIT

VPAYFNDAQRKATKEAGTIAGLNVLRIINEPTSAALAYGLDKKDSEKIVVYDLGGGTFDVTVLETGDNVV

EVLATGGNAFLGGDDFDNKLIDFLANEFKDETGIDLKNDVMALQRLKEAAENAKKELSSANETEINLPFI

TADASGPKHLVKKLTRAKFEGMIDSLVAETITKINEVVSDAGLKKDEIKEIVMVGGSTRVPLVQEEVKKA

FNKDLNKSVNPDEVVAIGAAIQGAVIKGDVKDVLLLDVTPLSLGIETLGGVMTKIIEKGTTIPTKKEQVF

STAEDNQSAVTINVLQGEREFSRDNKSLGNFNLEGIPPAPRGMPQIEVTFDIDANGILTVSAKDKATGKA

QEIKITGSSGLSEEEINNMVKDAELHKEEDKKRKEAVDARNAADSLAHQVEKSLSELGEKVAAADKENIQ

KALDDLRETLKNQNASKEEIESKMKALSEVSHKLAENMYKKDEPNTANDKKKKDDDVIDAEVE

>sp|A8FLE3.1|RL19\_CAMJ8 RecName: Full=50S ribosomal protein L19

MKNKYIEQFEAKQIEGKNVPDFRAGDTLKLAIRIKEGDKTRIQNFEGICIARRGNGVSETFIVRKMGANN

VGVERIFPIYSESLESITVLRRGRVRRARLFYLRDRRGKAARIKELKK

>sp|A8FLE1.1|RIMM\_CAMJ8 RecName: Full=Ribosome maturation factor RimM

MSEKDFVQVAKLGKTVGLKGYVKLHNLSDFSSQFKKDATFFIKNTKEMLKIKHYNASNSTVLFENYEDIE

KAKELINLILFQSIEKSRQTCKLKKDEFFYFDILECEVFEEDKRLGKVIDILETGASYLFEIQSDEKWVE

KKYPKIFFIPYLDKFVKNIDIEKRQIFCTQDAFLILENS

>sp|A8FLD9.1|RS16\_CAMJ8 RecName: Full=30S ribosomal protein S16

MTVIRLTRMGRTKRPFYRIVVTDSRKRRDGGWIESIGYYNPMVEPEVIKVDAERLAYWKSVGAKLSDKVA

SITSK

>sp|A8FLB7.1|FLGH\_CAMJ8 RecName: Full=Flagellar L-ring protein; AltName: Full=Basal body L-ring protein; Flags: Precursor

MKKVLFYVLPFAFFGCSATVDPQISMKPPAYVEELAPKQSNNVESAPGSLFGKGDNPLFSDKKAMNVNDL

VTVVIQESTTQSTQANKATSRTNTSNLGGGALTGSSGVVANALNKVNAYSNIGFQTNSSNNYTGTGSQSR

NESFNTTISTRVIKILSNGNYFIEGSRELLINGEKQIIQLSGVIRPYDIGQDNTIDSKYIADAKILYKTE

GEVDRSTRKPWGSKVIEAIWPF

>sp|A8FLB6.1|ISPG\_CAMJ8 RecName: Full=4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin); AltName: Full=1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase

MEYKRFKTRQIKVGNVSIGGDAPISVQSMLFTKTRDIEGSLEQISRLYFAGANIVRLACLDMADARALKE

IKAKSPLPLIVDIHFNHNLAVYCAEFIDGVRINPGNIGSKENIKEVVKACKERGIPIRIGVNHGSIEKQF

SDKFGYGVDAMLESAMYNIKLLEDLDFFDIKISMKTSDAQKTIEAYERLRPLCDYPFHLGVTEAGTKFHS

TVKSSIALGNLLLKGIGDTMRVSMTGELEEEIRVARAILQDSGVQKSGVNIISCPTCGRIQSDLLSAIKI

VEEKTKHIKEPLNISVMGCVVNALGEAKGADVAIAFGKNQGLVIRHGEVVAKLKESELVDRFLAEVEDEV

KSRAVKE

>sp|A8FL62.1|NADK\_CAMJ8 RecName: Full=NAD kinase; AltName: Full=ATP-dependent NAD kinase

MQNKIDYKNIKKIGLVTRPNVSLDKEILKLQSILSIYKVELVLFKESSEILDLPKYGLDDLFKISDFVIS

LGGDGTLISLCRKACEYDKAVLGIHAGHLGFLTDFKVDEAENFFQAFFQGEFRIEKPYLLSVFLEDKQGK

ILEKLAFNDVVISKNNQASMAHIEVFRKEKKFNEYFGDGLIVATPAGSTAYNLSANGPIVYTLAQAFILT

PVCSHSLTQRPIVLPKGFEIEIMAKDCILCIDGQENYKMNDFKSIKVGLSDKNVALIHPKNRDYFQILKE

KLHWGN

>sp|A8FL53.1|ILVC\_CAMJ8 RecName: Full=Ketol-acid reductoisomerase (NADP(+)); Short=KARI; AltName: Full=Acetohydroxy-acid isomeroreductase; Short=AHIR; AltName: Full=Alpha-keto-beta-hydroxylacyl reductoisomerase; AltName: Full=Ketol-acid reductoisomerase type 1; AltName: Full=Ketol-acid reductoisomerase type I

MAITVYYDKDCDLNLIKSKKVAIIGFGSQGHAHAMNLRDNGVNVTIGLREGSVSAVKAKNAGFEVMSVSE

ASKTADVVMILAPDEIQADIFNIEIKPNLSEGKAIAFAHGFNIHYGQIVAPKGIDVIMIAPKAPGHTVRN

EFTLGGGTPCLIAIHQDESKNAKNLALSYASAIGGGRTGIIETTFKAETETDLFGEQAVLCGGLSALIQA

GFETLVEAGYEPEMAYFECLHEMKLIVDLIYQGGIADMRYSISNTAEYGDYITGPKIITEETKKAMKGVL

KDIQNGVFAKDFILERRAGFARMHAERKNMNDSLIEKTGRNLRAMMPWISAKKLVDKDKN

>sp|A8FKR7.1|EFG\_CAMJ8 RecName: Full=Elongation factor G; Short=EF-G

MSRSTPLKKVRNIGIAAHIDAGKTTTSERILFFTGMSHKIGEVHDGAATMDWMEQEKERGITITSAATTC

FWKDHQINLIDTPGHVDFTIEVERSMRVLDGAVAVFCSVGGVQPQSETVWRQANKYGVPRIVFVNKMDRI

GANFYNVEDQIRNRLKANPVPLQIPIGAEDNFKGVIDLVTMKALVWEDDTKPTDYVEKEIPAELKEKAEE

YRTKMIEAVSETSDELMEKYLGGEELSLEEIKTGIKAGCLSLSIVPMLCGTAFKNKGVQPLLDAVVAYLP

APDEVANIKGEYEDGTEVSVKSTDDGEFAGLAFKIMTDPFVGQLTFVRVYRGCLESGSYAYNSTKDKKER

IGRLLKMHSNKREEIKVLYAGEIGAVVGLKDTLTGDTLASEKDKVILERMDFPDPVISVAVEPKTKADQE

KMSIALNKLAQEDPSFRVSTDEESGQTIISGMGELHLEIIVDRMLREFKVEAEVGQPQVAYRETIRKTVE

QEYKYAKQSGGRGQYGHVFLRLEPLEPGSGYEFVNDIKGGVIPKEYIPAVDKGVQEALQNGVLAGYPVED

VKVTVYDGSYHEVDSSEMAFKLAASMGFKEGARKAGAVILEPMMKVEVETPEDYMGDVIGDLNKRRGQVN

SMDERGGNKIITAFCPLAEMFGYSTDLRSQTQGRATYSMEFDHYDEVPKNVADEIIKKRNG

>sp|A8FKQ5.1|EFTU\_CAMJ8 RecName: Full=Elongation factor Tu; Short=EF-Tu

MAKEKFSRNKPHVNIGTIGHVDHGKTTLTAAISAVLSRRGLAELKDYDNIDNAPEEKERGITIATSHIEY

ETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHILLSRQVGVPYIVVFMNKADM

VDDAELLELVEMEIRELLSSYDFPGDDTPIISGSALKALEEAKAGQDGEWSAKIMDLMAAVDSYIPTPTR

DTEKDFLMPIEDVFSISGRGTVVTGRIEKGVVKVGDTIEIVGIKDTQTTTVTGVEMFRKEMDQGEAGDNV

GVLLRGTKKEEVIRGMVLAKPKSITPHTDFEAEVYILNKDEGGRHTPFFNNYRPQFYVRTTDVTGSIKLA

DGVEMVMPGENVRITVSLIAPVALEEGTRFAIREGGKTVGSGVVSKIIK

>sp|A8FKN0.1|ACCA\_CAMJ8 RecName: Full=Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha; Short=ACCase subunit alpha; Short=Acetyl-CoA carboxylase carboxyltransferase subunit alpha

MASYLDFEKNIQQIDEDIINAQIKGDTEAVSILKKNLEKEISKTYKNLSDFQRLQLARHPDRPYALDYIE

LILNDAHEIHGDRAFRDDPAIVCFMGYLGEKKIIVIGEQKGRGTKDKIARNFGMPHPEGYRKALRVARLA

EKFQIPILFLIDTPGAYPGIGAEERGQSEAIARNLYELSDLKIPTIAIVIGEGGSGGALAIGVADRLAMM

KNSVFSVISPEGCAAILWNDPAKSEAATKAMKVTADDLKSQGLIDDVIDEPTNGAHRNKEAAAVAIADYV

KKSLNELENIDVRELSANRMQKILKLGAYQEA

>sp|A8FKG9.1|NUSB\_CAMJ8 RecName: Full=Transcription antitermination protein NusB; AltName: Full=Antitermination factor NusB

MATRHQVRQSVISLLYAFELNSQNNVFVDEILDEKKIRNEQKNFTLNLYHGILDNLNNIDETLNSFLNDN

QITALGHVERAILRLGAYELLFTDTPSAIVINEAIELAKELANDNSPKFINGVLDALIKAKK

>sp|A8FKA0.1|RL25\_CAMJ8 RecName: Full=50S ribosomal protein L25; AltName: Full=General stress protein CTC

MLEGIVRESIGRKAAKALKRDGYLIANIYGKGLENINAAFKVNEFIKEVRKKTTLIFDVKVGSQTLSVVV

VDYQKDPVTAELKHVDLKVAQKGVISKYMVPVKITGTAIGLKNKGVLIQSKRRLKVKCAAENLPNFFELD

VSKLDVGDALLVRDIVVPAGVTMIDADRVAVVGVEKAR

>sp|A8FK85.1|PAND\_CAMJ8 RecName: Full=Aspartate 1-decarboxylase; AltName: Full=Aspartate alpha-decarboxylase; Contains: RecName: Full=Aspartate 1-decarboxylase beta chain; Contains: RecName: Full=Aspartate 1-decarboxylase alpha chain; Flags: Precursor

MNITLLKSKIHRASVTEARLDYIGSISIDEKLLQASGILEYEKVQVVNVNNGARFETYTIATQEEGVVCL

NGAAARLAEVGDKVIIMSYADFNEEEAKTFKPKVVFVDENNTATKITNYEKHGAIF

>sp|A8FK63.1|LPXA\_CAMJ8 RecName: Full=Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase; Short=UDP-N-acetylglucosamine acyltransferase

MKKIHPSAVIEEGAQLGDDVVIEAYAYVGKDTKIGNDVVIKQGARILSDTTIGDHSRVFSYAIVGDIPQD

ISYKEEQKSGVVIGKNATIREFATINSGTAKGDGFTRIGDNAFIMAYCHIAHDCLLGNNIILANNATLAG

HVELGDFTVVGGLTPIHQFVKVGEGCMIAGASALSQDIVPFCLAEGNRASIRSLNLVGIRRRFDKDEVDR

LSRAFKTLFRQGDLKENAKNLLENQESENVKKMCHFILETKRGIPVYRGKNNA

>sp|A8FK62.1|FABZ\_CAMJ8 RecName: Full=3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ; AltName: Full=(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; Short=(3R)-hydroxymyristoyl-ACP dehydrase; AltName: Full=Beta-hydroxyacyl-ACP dehydratase

MIDVMQIQEILPHRYPFLLVDKITELKVKEVVLGYKNISISDHVFMGHFPGHPIYPGVLILEGMAQTGGV

LAFESMEDKVDPKSKVVYFTGIDGAKFRNPVRPGDRLDYEMSVVKNRGNMWIFKGQAFVDGNLVAEAELK

AMIVDK

>sp|A8FK34.1|RL20\_CAMJ8 RecName: Full=50S ribosomal protein L20

MARVKTGVVRRRRHKKVLKLARGFYSGRRKHFRKAKEQLERSLVYAYRDRRRKKRDFRRLWIVRINAACR

LNDLSYSRFINGLKKAGIELDRKILADLAMNDSAAFAKIAEAAKKAL

>sp|A8FJZ4.1|TIG\_CAMJ8 RecName: Full=Trigger factor; Short=TF; AltName: Full=PPIase

MEVKAKQLDSVNATASVKIPSGMIKSEVENLAKKASKSVKMDGFRPGKVPVSAVLKRYERELTQDAEQNL

FKSAVNSALQELKKESKELVGEPYFEKFDRKDGEIIAELILSFKPEIKLDGYEKLIPEYQTPKVSKKEID

EKKDELLKRFATPEAIKTKRVLKEGDFAKFDFEGFVDDKAFEGGKAENYVLEIGSKQFIPGFEDGMVGMK

IGEEKDIKVTFPKEYGAAHLAGKDAVFKVKLHEIQELKIPELDDEMLKKLLPGEEKASVEVLDEKLKEQI

KNEKLFKLVNDELKGKFADALIEKYNFDLPKGIVEQETDMQMRAAFNTFSEKEIEELKASKEKYQEKRDS

FKEEAQKSVKLTFIIDELAKLRKIEVNDQELIQAIYFEAYRYGMNPKEHLENYKKQGALPAVKMALIEEK

LFNDIFMPKTEKSEKASKKEKEDK

>sp|A8FJZ3.1|CLPP\_CAMJ8 RecName: Full=ATP-dependent Clp protease proteolytic subunit; AltName: Full=Endopeptidase Clp

MFIPYVIEKSSRGERSYDIYSRLLKDRIIMLSGEIHDELAASIVAQLLFLEAEDPTKDIYLYINSPGGVI

TSGFSIYDTMNYIKPDVCTICIGQAASMGAFLLSCGAEGKRFALPNSRIMIHQPLGGARGQATDIEIQAK

EILRLKTILNDILAKNTKQKVAKIAKDTERDFFMSAQEAKEYGLIDKVLEKSFK

>sp|A8FJU2.1|RBFA\_CAMJ8 RecName: Full=Ribosome-binding factor A

MNPSEIKKLRTESILKELIPEALANLDDENLKNLCVVDVECKKGRYDAFVYLDKMFFNVHEQEKILSSLK

KASRALQNYCMSEQGWYRCPNFHFKFDDRLEYQNHMDALFEKIKKDKNES

>sp|A8FJU1.1|IF2\_CAMJ8 RecName: Full=Translation initiation factor IF-2

MAKIRIHEIAKELGYDSKEIIEKANELGLGIKTASNAVEPEIAAAIYEYIQTREIPEAFKKNIKTPTAKK

PKKENIKEQEKLNESEKKEPKKEEKLKQEVKKEELKVEKENVKEEEKQEIIDAHKPQSLASATLAKRRGL

VIVKKKKDEEEIQVKKEEVKNSNDISINNEERLSLKTMFSNADESLKKKKKEKKSFVASKKESTEKMNFL

DEHDFGDISLDDEDEVVLPDFSVKEQEKPQNINKKQPNFIRQAVGNSAGFGLEGGIQRRSRKKPPKKIEK

KEVEEVSSVAISKEIRVYEFADKIGKSTSEVISKLFMLGMMTTKNDFLDEDAIEILAAEFGIEINIINEA

DEFDYVKDYEEETDEKDLVTRAPVITIMGHVDHGKTSLLDYIRKSRVASGEAGGITQHVGAYMVEKNGRK

ITFIDTPGHEAFTAMRARGASITDIVIIVVAADDGVKPQTKEAINHAKAAGVPIIIAINKMDKEAANPDM

VKTQLAEMEIMPVEWGGSYEFVGVSAKTGMGIEDLLEIVLLQADILELKANPKSFAKASIIESSVQKGRG

AVATIIVQNGTLTVGSTVVAGEAYGKVRAMSDDQGKALKEIKPGECGVIVGLSEVADAGEILIAVKTDKE

AREYANKRHEYNRQKELSKSTKVSIDELGAKIKEGNLKALPVILKADVQGSLEALKASLEKLRNDEIKVN

IIHSGVGGITQSDIELASASENSIVLGFNIRPTGEVKERAKDKGVEIKTYNVIYNLLDDVKALLGGMMSP

IISEEQLGQAEIRQVINVPKIGQIAGCMVTEGVINRGAKIRLIRDGVVVYEGNVSSLKRFKDDAKEVAKG

YECGVGIEGCDDMRVGDYIESYKEVEEQASL

>sp|A8FJR0.1|ATPA\_CAMJ8 RecName: Full=ATP synthase subunit alpha; AltName: Full=ATP synthase F1 sector subunit alpha; AltName: Full=F-ATPase subunit alpha

MKFKADEISSIIKERIENFDLNLEIEETGKIISVADGVAKVYGLKNIMAGEMVEFENGDKGMALNLEESS

VGIVILGKGEGLKEGASVKRLKKLLKVPVGEALIGRVVNALGEPIDAKGVINANEYRFVEEKAKGIMARK

SVHEPLHTGIKAIDALVPIGRGQRELIIGDRQTGKTTVAVDTIISQRGQGVICIYVAIGQKQSTVAQVVK

RLEEHGAMEYTIVVNAGASDPAALQYLAPYTGVTMGEFFRDNAKHALIVYDDLSKHAVAYREMSLILRRP

PGREAYPGDVFYLHSRLLERASKLNDELGAGSLTALPIIETQAGDVSAYIPTNVISITDGQIFLETDLFN

SGIRPAINVGLSVSRVGGAAQIKATKQVSGTLRLDLAQYRELQAFAQFASDLDEASRKQLERGQRMVELL

KQPPYSPLSVEKQVVLIFAGTKGFLDDIAVSRIKEFEDGIYPFIEAKHPDIFEQIRSKKALDSDLEEKLA

KAINEFKANHL

>sp|A8FJQ3.1|FMT\_CAMJ8 RecName: Full=Methionyl-tRNA formyltransferase

MKKIIFMGTPSYATCILKALVENENFKLVALFTQPDKAVGRKQILTPSDTKAFLSQNYPSIPIFTPSSLK

DENIIREIKDLNPDFIVVAAYGKILPKAILDLAPCVNLHASLLPKYRGASPIQSAILNKDEKSGVCTMLM

EEGLDTGAVLESLECDIKDKNSSEVFELLANLAAKLILSTLLNFDKIIPKKQEESLATLCRKIKKEDGLI

NLQNARELYQKYLAFTPWPGVFLENGLKFLELELVDELKQNARMGEILELEKESFLLACKQGVLRIKKLQ

ESGKKALDGRTYLNGKRLKSEDSLC

>sp|A8FJH6.1|ILVD\_CAMJ8 RecName: Full=Dihydroxy-acid dehydratase; Short=DAD

MRSDAIKKGHLKAPNRSLLRACGLKDEDFNKPFIGVANSYIDIIPGHYFLNDYAKIIKDEIRKNGCVPFE

FNTIGVDDGIAMGHEGMLYSLPSREIIANSIETVMNAHQLDALICIPNCDKITPGMLMGALRVNVPTIFV

SGGPMASGVTKKGEKISLSSVFEAVGAYEAKKISEEEFKDIECSACPSGGSCSGMFTANSMNTLCEAMGI

ALEGNGTILALSKEREELLRKAARRICEIALDERFKIRNIITQKAVRNAMVVDMAMGGSSNTVLHMLAIS

REAGVALDIKDLNFISSKVAHIAKIAPSLNSVYMDDVHKAGGVSAVMAEISSRQGHILELDALTITGESL

KERLKNAKIKDENIIRKVDNAYSKVGGLAILFGNLAEQGCVIKTAGIIGERKFKGKAVCFNSQDEAIKGI

IKGKVQKGNVCVIRYEGPKGGPGMQEMLSPTSLLMGMGLGADVALITDGRFSGATRGLSVGHISPEAAEG

GLIGLLKDGDEIEIDVDAYTIHANLSEEEITQRKKEFVLPQKEVPSRWLRMYQKLVSNASKGAVLDME

>sp|A8FJH3.1|RNH2\_CAMJ8 RecName: Full=Ribonuclease HII; Short=RNase HII

MKTLFDTKELLNEFDINLIGIDEAGRGALAGPMMMAACKLNKKLDGLCDSKKLSEKKREELYEIIIKNSN

YLILAFSSEQIDALGLSTCLKTGLKLIKKHFKTENNFLYDGNTNLGINGIKTQIKADASILQVSAASILA

KVSKDRVMNFLAKDFPCYEFEKNKAYGTKAHKELIAKFGICKLHRKSFKLL

>sp|A8FKI7.1|FUR\_CAMJ8 RecName: Full=Ferric uptake regulation protein; Short=Ferric uptake regulator

MLIENVEYDVLLERFKKILRQGGLKYTKQREVLLKTLYHSDTHYTPESLYMEIKQAEPDLNVGIATVYRT

LNLLEEAEMVTSISFGSAGKKYELANKPHHDHMICKNCGKIIEFENPIIERQQALIAKEHGFKLTGHLMQ

LYGVCGDCNNQKAKVKI

>sp|A8FJQ1.1|OBG\_CAMJ8 RecName: Full=GTPase Obg; AltName: Full=GTP-binding protein Obg

MFIDSVKITLASGDGGKGAVSFRREKHVPLGGPDGGDGGNGGDIIFVCDNNTHTLVNFKGKRELRAQNGA

GGMGRNKNGKKGENLELIVPEGTQVIDAQTNEILLDLTKEGQRELFLKGGKGGLGNTHFKHATNQRPDYA

QPGIKGESRLVRLELKLIADVGLVGFPNVGKSTLISVVSNAKPEIANYEFTTLTPKLGLVDVDEYNSFVM

ADIPGIIEGASGGKGLGLAFLKHIERTSFLLFVLDPMRQMPLKEQFIVLRKELEKFSNELFGRKFGIMIS

KSDSVNLGEEFAEQITLNINELENYLKEINNPQSFLIKVSSLEKTGLKELKFMLLEEIKTLRNNK

>sp|A8FN77.1|PGK\_CAMJ8 RecName: Full=Phosphoglycerate kinase

MSDIISIKDIDLAKKKVFIRCDFNVPQDDFLNITDDRRIRSAIPTIRYCLDNGCSVILASHLGRPKEISS

KYSLEPVAKRLARLLDKEIIMAKDVIGEDAKTKAMNLKAGEILLLENLRFEKGETKNDENLAKELASMVQ

VYINDAFGVCHRAHSSVEAITKFFDEKHKGAGFLLQKEIDFASNLIKHPARPFVAVVGGSKVSGKLQALT

NLLPKVDKLIIGGGMAFTFLKALGYDIGNSLLEEELLEEANKILTKGKNLGVKIYLPVDVVAAPACSQDA

PMKFVPVQEIPNGWMGLDIGPASVRLFKEVISDAQTIWWNGPMGVFEIDKFSKGSIKMSHYISEGHATSV

VGGGDTADVVARAGDADEMTFISTGGGASLELIEGKELPGVKALRSKENE

>sp|A8FP35.1|LEU1\_CAMJ8 RecName: Full=2-isopropylmalate synthase; AltName: Full=Alpha-IPM synthase; AltName: Full=Alpha-isopropylmalate synthase

MKDNKIIIFDTTLRDGEQALGSSLGINQKLQIALALENLGVDVIEAGFPVSSQGDFKAVQKIASKVKNST

ICALSRVLDKDIDMAYEALKVAKHFRIHTFIATSTLHMQDKLKKDFDEILSMAKRAIIRARSYTDDVEFS

CEDAGRTPIDNLCFMVENAIKAGAKTINIPDTVGYTLPSEFANIIKILFNKVPNIDKAIISVHCHNDLGM

ATGNSLSAILQGARQIECTINGLGERAGNCALEEVVMAIKTRKDYLKGFYTDIKCENIFKTSKLVSAITN

ESIPSHKAIVGSNAFSHSSGIHQDGVLKNRQTYEIISPSAIGIHENRMLMTARSGRAMIKTCLENLGYDE

NTYNLDDVYERFLRLADKKGQVYDYDLEALMFLSYENEEENKFILEKLSVISGNIPTACVCMRIKEELKT

EACTGNGPVEAVFNCIARITNLKPALKAYSINAKSSGVDAQGQVDVDLEFKGRKFHGKGISTDVIEASAQ

AFVSAYNAIYRSLKVEERKMA

>sp|A8FNC1.1|RIMO\_CAMJ8 RecName: Full=Ribosomal protein S12 methylthiotransferase RimO; Short=S12 MTTase; Short=S12 methylthiotransferase; AltName: Full=Ribosomal protein S12 (aspartate-C(3))-methylthiotransferase; AltName: Full=Ribosome maturation factor RimO

MSKLYLMSLGCNKNLVDSEIMLGRLSAYELCDEPSKADVLIVNTCGFIDSAKKESINAILDLHEQRKKDS

LLVVTGCLMQRYREELMKELPEVDLFTGVGDYERIDEMILKKTNLFSNSTYLQSENSKRIITGSNSHAFI

KIAEGCNQKCSFCAIPSFKGKLKSREISSIIAELKDLVARGYKDFSFIAQDTSSYLFDKGEKDGLIRLID

EVEKIKGIRAARILYLYPTSASEALIKRIIASEIFINYFDMPLQHISDNMLKIMKRGANSTRLKEMLNLM

KSAPNSFLRTGFIVGHPGESEADFEELCEFVKDFGFDRISVFAYSKEEDTAAFDMEQVPFKVINKRLKII

EKIVDEVIEKSFEKEVGQKRLVVCTGKSSEGEFFIAAKDLRWDREIDGEILINESECGNLEMGQIYECEI

LQNLDKKLLAKALRKVDAN

>sp|A8FMA1.1|DAPE\_CAMJ8 RecName: Full=Succinyl-diaminopimelate desuccinylase; Short=SDAP desuccinylase; AltName: Full=N-succinyl-LL-2,6-diaminoheptanedioate amidohydrolase

MNAKEFLIELLKFKSVTPNDDGALNFIAMELSDFEAFFIEKEGIKNLLLTKKFNDEGEHLAFGGHVDVVP

AGEGWKNDPFEPLEEEGFIYARGAQDMKSGVAAFIDAVKDVSFKGRRLSLILTSDEEGEAKYGTKAVLEW

MKEKNMLPDYAVVAEPTCVKKMGDSIKIGRRGSINGKLLIRGKQGHVAYPEKCINPVHDFAPVLKLLAGF

DLDPGSAEFSPSKIVITDIRGGMGVCNVTPNDLKLMFNVRNSPDTSLEDVKSYVEKICHGLNYELELKQS

SEAFLTNIDNKIVQKMNESVQKITHEVPELNTKGGTSDARYFAKYGVKVVEFGVCNDRIHAIDERVSIEE

FEKLCLVFKDLIENF

>sp|A8FNN6.1|NUOB\_CAMJ8 RecName: Full=NADH-quinone oxidoreductase subunit B; AltName: Full=NADH dehydrogenase I subunit B; AltName: Full=NDH-1 subunit B

MAEHQVNYASGLPVVLTSVDKLVQWGRSNSLWALSYGLACCAIEMMAAGGSRYDFDRFGTIFRASPRHSE

VMIIAGTLCKKHAEFTRRLYDQMPDPKWVISMGSCANTGGMFNTYSTVQGVDRIIPVDIYVPGCAPRPES

FQFALMILQKKIRKEKASRKIAPKRLV

>sp|A8FKE9.1|LSPA\_CAMJ8 RecName: Full=Lipoprotein signal peptidase; AltName: Full=Prolipoprotein signal peptidase; AltName: Full=Signal peptidase II; Short=SPase II

MAKTFKFIFYFWGAFVLVFVLDQWVKSLTLAGLRWQSEYLDLTYALNTGVAFSMLSFLEHNLKYLHLALI

VVLFIYLFWQKTLLKTHSIAFGMMLGAGVSNLLDRFIHGGVVDMFFWHKWFNFAIFNVADVMINISVALI

LIQEIFKKRKKDDRMD

>sp|A8FLY5.1|ATPL\_CAMJ8 RecName: Full=ATP synthase subunit c; AltName: Full=ATP synthase F(0) sector subunit c; AltName: Full=F-type ATPase subunit c; Short=F-ATPase subunit c; AltName: Full=Lipid-binding protein

MKKVLFLLLACAAVAFAAETNAPVEQEAINVWIKAFSVLAAGLGLGVAALGGAIGMGNTAAATIAGTARN

PGLGPKLMTTMFIALAMIEAQVIYALVIALIALYANPFIVLQ

>sp|A8FMQ9.1|ATP6\_CAMJ8 RecName: Full=ATP synthase subunit a; AltName: Full=ATP synthase F0 sector subunit a; AltName: Full=F-ATPase subunit 6

MKDLFLFSSLLDASHTFSYFFHIGLVALIAVIVAMMATRSMQLVPRGMQNLGEAFLEGVLSMGRDTMGSE

KGARKYLPLVATLGIIVFFSNIIGIIPGFHAPTASLNLTLSLAIIVFVYYHFEGIRAQGFVKYFAHFMGP

IKLLAPLMFPIEIVSHLSRVVSLSFRLFGNIKGDDLFLMVILALVPYIAPLPAYVLLTFMAFLQAFIFMI

LTYVYLAGATVVEEGH

>sp|A8FMX4.1|MNMC\_CAMJ8 RecName: Full=tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein MnmC; Short=tRNA mnm(5)s(2)U biosynthesis bifunctional protein; Includes: RecName: Full=tRNA (mnm(5)s(2)U34)-methyltransferase; Includes: RecName: Full=FAD-dependent cmnm(5)s(2)U34 oxidoreductase

MKKAKLIFKDNTPFSLDFDDFYFNSKDGLNESKFVYTHSFEWKNQENFIIAESGFGIGLNFFLTLKRFLQ

TTPSKRPKKLFYISIEAFYIEKEQLREIYQKLGFYEEFKELLEQFLKFYPKAKEGIYRFYFEDCFLDLVF

EDITILKELDFKADIWYLDGFSPNKNSQMFDENLIFEVARLSKKNTQICTFSSASFLQKNLKKYGFRVEK

TKGFRKREMIKAYLENELEFKDKEAYFSRTFSSLKNKKVAIIGAGISSAVLAYELSLRGFEIDVFEKHLE

LGKGASGNESGILSSLILKPKVNLGEFSELSFIEASRFYRQILDLEFKGVVEFAHNDLMQERFDTQRENV

LFKISKNQAFLEEGGVIFPKNLVKNLFEKSKACIYFNHEFQAYKFENECFTLKFKNDIVKSDYAVLIYAM

GADTKDFVFYDEMKLSKVRGQVTHLKPFLNTPFPLSSKAYICPVKDDLQVIGASYDRLDASLESKEEDDK

QNIENIAEFIDKNTKLEIIGSKVGFRSYSSDRFMIVGNAYDEVFYKEEYKALLWTKNKEQKLAKISCNLY

FNFAHGSRGFSTSVLAARYLCALINNEPLYLEKKYIHAIHPARFLIRKLKKGL

>sp|A8FJU3.1|RIMP\_CAMJ8 RecName: Full=Ribosome maturation factor RimP

MNLEALCKEAGLSFYDDELVSENGRKIYRIYVQKEGGVNLDDCARLSEILSPIFDVEPPVNGEYFLEVSS

PGLERKLSKIEHFAKSIGELVKITTNEKEKFEAKIIAVDDENITLENLENKEKTTINFNDIKKARTFVEW

>sp|A8FJT1.1|RLMH\_CAMJ8 RecName: Full=Ribosomal RNA large subunit methyltransferase H; AltName: Full=23S rRNA (pseudouridine1915-N3)-methyltransferase; AltName: Full=23S rRNA m3Psi1915 methyltransferase; AltName: Full=rRNA (pseudouridine-N3-)-methyltransferase RlmH

MQVNIFCIQKSDEFKTWSEKYSKLISKYATLKEINVFNKKIALAQNLNAIEAKKSYEEAFMPYKKGYCIA

LDEKGKDLTSIEFAKLIQDKNELSFFIGGAYGLREEFNQSLDFRLSLSKLTLAHQFVKTLLLEQIYRAFC

INNNHPYHK

>sp|A8FL10.1|DNLJ\_CAMJ8 RecName: Full=DNA ligase; AltName: Full=Polydeoxyribonucleotide synthase [NAD(+)]

MKKEEYLEKVALANLWMRAYYEKDEPLASDEEYDALIRELRAFEEQNKDEISKDSPTQKIAPTIQSEFKK

IAHLKRMWSMEDVFDESEFRAWAKRAKCEKNFFIEPKFDGASLNLLYENGKLVSGATRGDGEVGEDITLN

VFEIENIPKNIAYKERIEIRGEVVILKDDFEKINEKRALLNQSLFANPRNAASGSLRQLDTSITKERNLK

FYPWGLGENTLNFTKHSEVMQFIRELGFLKDDFVRLCVNLDEVLKAYDELLALREKKPMMMDGMVVRIDD

LALCEELGYTVKFPKFMAAFKFPALEKTTRLIGVNLQVGRSGVITPVAVLEPVNLDGVVVKSATLHNFDE

IARLDVKINDFVSVIRSGDVIPKITKVFKERREGLEMEISRPKLCPTCQSELLDEGTLIKCQNIDCEDRL

VNSIIHFVSKKCLNIDGLGENIVELLYKHKKITTLESIFHLKFNDFEGLEGFKEKKINNLLNAIEQAREC

ELFRFITALGIEHIGEVAAKKLSLSFGKEWHKQSFEAYANLEGFGEQMALSLCEFTRVNRTRIDEFYKLL

NLKIEKLEIKSDGVIFGKTFVITGTLSRSRDEFKALIEKLGGKVSGSVSKKTDYVLFGEEAGSKLIKAKE

LEIKCIDESAFNELVKE

>sp|A8FMW6.1|DNAJ\_CAMJ8 RecName: Full=Chaperone protein DnaJ

MEISYYEILEITQSADKETIKKAYRKMALKYHPDRNQGDKEAEDKFKLVNEAYEVLSNDEKRAIYDRYGK

DALKGGGFGSSSSGFGGFEDLGDIFSSFFGEGFGSSSRRRKSSNDEKIPSDFIVNLKLSFKEAVFGCKKN

IDFTYKCSCKTCNGTGAKDGKLQTCPKCQGRGQVGVSQGFITFAQTCPDCQGSGEKASEKCSDCKGLGYN

ESKDSVELNIPEGIDTGMKLRVNAKGNILKNGTRGDMYVKIIAAEDDTFVRDDDDIYIEFPVFFTQAILG

QSIKVPTIRGEATLNLPKGAKDGQRFVLEKEGVKDVHSSRIGNQIVQISIKFPTSLNDEQKELLEKLSES

FGIKDGMHQEQKGLFEKIANWFKS

>sp|A8FMC3.1|RS6\_CAMJ8 RecName: Full=30S ribosomal protein S6

MKHYEVLFILKPTLTEEEVNAKLEFVKEVLTKNGAEIETVVPMGTRKLAYKIKKYERGTYFVIYFKAPTN

LIAELERVLRITEEVIRFLIVKYENKKEIAAWEKLSHGIKQSKKEIKPLDAPEIQ

>sp|A8FNU7.1|RNC\_CAMJ8 RecName: Full=Ribonuclease 3; AltName: Full=Ribonuclease III; Short=RNase III

MKNIEKLEQSLTYEFKDKNLLIHALTHKSFKKSYNNERLEFLGDAVLDLVVGEYLFHKFAKDAEGDLSKL

RAALVNEKSFAKIANSLNLGDFIFMSVAEENNGGKEKPSILSDALEAIIGAIHLEAGFEFAKTIALRLIE

KNFPQIDAKILIKDYKTKLQEITQGKIGQTPQYETVRAFGPDHLKQFEIALMLDGKELARAIAGSKKEAQ

QMAAKIALEKLGAL

>sp|A8FMV1.1|UVRC\_CAMJ8 RecName: Full=UvrABC system protein C; Short=Protein UvrC; AltName: Full=Excinuclease ABC subunit C

MTKENLENELKTLPNSAGVYQYFNQEGKLLYVGKAKNLKNRVKSYFAFTPNLHANPRNSLRIQKMIEETV

HLEFITTNSEADALILENSFIKQLHPKYNILLRDDKTYPYIYVDFEEEFPRFEITRKLVKKSKIKYFGPF

FKGARELLDALYLYYPLKQKASCKSPCIFYQISRCLAPCDKRISREKYLEILDEAMHALLNPSILIKNLE

KQMLVLAQNENYEEAAKVRDQIVTIKDLEVKVEIDIAKLEDFEVFALAFENSMLSTLRFVVQNGKIISVN

SKITPIKNDIQWDKNEIYKQLILENFSMDIPLLANVIYVYEEFEDRMLLEEILSQRFDKKISIKIPKIGE

KRRICDLAFQNALLNIEKEQKNHDFTIQKELKSYFELENLPNDIEIFDNSHLQGVANVGAMVTYSANSWD

KSKYRKFHLKHKNDYDQMREVLMRRALDFDKIPPPDLWLIDGGKALLDLAKEIIVSSGANVDILAISKEK

IDAKAHRAKGGARDKIHSLKGEFSLSINDKKLQFLQKLRDEAHRFAISFHQNTKKKQDLNSSKLVNLGLS

SGVIQKLLAYYGNFESIYKADFKDLAMLVGKKVAQKIKEN

>sp|A8FJQ2.1|PROB\_CAMJ8 RecName: Full=Glutamate 5-kinase; AltName: Full=Gamma-glutamyl kinase; Short=GK

MKRIVVKVGSHVISEENTLSFERLKNLVAFLAKLMEKYEVILVTSAAISAGHTKLDIDRKNLINKQVLAA

IGQPFLISVYNELLAKFNKLGGQILLTGKDFDSRKATKHAKNAIDMMINLGILPIINENDATAIEEIVFG

DNDSLSAYATHFFDADLLVILSDIDGFYDKNPSEFSDAKRLEKITHIKEEWLQATIKTGSEHGTGGIVTK

LKAAKFLLEHNKKMFLASGFDLSVAKTFLLEDKQIGGTLFE

>sp|A8FK86.1|PANC\_CAMJ8 RecName: Full=Pantothenate synthetase; Short=PS; AltName: Full=Pantoate--beta-alanine ligase; AltName: Full=Pantoate-activating enzyme

MQVITSVKEAKQIVKDWKSHQLSIGYVPTMGFLHDGHLSLVKHAKTQDKVIVSIFVNPMQFGPNEDFSSY

PRDLERDIKMCQDNGVDMVFIPDATQMYLKNFSTYVDMNTITDKLCGAKRPGHFRGVCTVLTKFFNILNP

DIVYMGQKDAQQCVVVRHMVDDLNFDLKIQICPIIREEDGLAKSSRNVYLSKEERKASLAISQSIFLAEK

LVREGEKNTSKIIQAMKDILEKEKLIKIDYIELVDFNTMENIENITDNVLGAVAAFVGKTRLIDNFLVQG

LK

>sp|A8FM43.1|OTC\_CAMJ8 RecName: Full=Ornithine carbamoyltransferase; Short=OTCase

MKHFLTLRDFSKEEILSLVNHASELKKEPKKLLQDKTLAMIFEKNSTRTRMAFELAITELGGKALFLSSN

DLQLSRGEPVKDTARVIGTMVDFVMMRVNKHETLLEFARYSKAPVINALSEFYHPTQVLGDLLTIKEWNK

MQNGIAKVAFIGDSNNMCNSWLIVAAILGFEFSIAIPKNYKISPEIWEFAMKQALISGAKISLSHDKFEA

LKDKDVVITDTWVSMGEENEKERKIKEFEGFMIDEKAMSVANKDAILLHCLPAYRGYEVSEEIFEKHADV

IFEEARNRLYVVKALLCFLDNQRGRE

>sp|A8FMA8.1|MURC\_CAMJ8 RecName: Full=UDP-N-acetylmuramate--L-alanine ligase; AltName: Full=UDP-N-acetylmuramoyl-L-alanine synthetase

MQNIHFIGIGGIGISALARFLKEKGFKISGSDLKESKITKELEKEGVKVSIPHHKDNILNKDLVIYSAAI

KEENPEFKHAKELGIKCLSRKEALPLILEDKRVFAVAGAHGKSTTSSILASLLDDASVIIGAILKEFGSN

MIYKESQNLVFEADESDSSFLNSNPYLAIVTNAEAEHLDHYGNEVSKLHHAYTQFLDVAKIRVINAEDEF

LKNYKNESIKLYPSKDIKNCTMCIENFKPFTSFELKDLGEFKVFGMGYHLALDASLAILAALNFLDIETI

RTRLKNYQGIKKRFDILHADENLVLIDDYGHHPTEIKATLSAAQEYAKLGGYKKITAIFEPHRYTRLAAN

LKEFAKAFEGVDELVILPVYAAGEEPIELDLKAVFPKALFVEDIKREGKFLVASKGQVFEEGLIIGFGAG

DISNKLRQKNE

>sp|A8FP40.1|RUVC\_CAMJ8 RecName: Full=Crossover junction endodeoxyribonuclease RuvC; AltName: Full=Holliday junction nuclease RuvC; AltName: Full=Holliday junction resolvase RuvC

MKILGIDPGSRNCGYAIIEANKGKNILIEAGLIKIKPNTLQYQITELCEGLDLIFKNHSFDEVAIEDIFF

AYNPKTVLKLAQFRGALSLKILQIHGDFAEYTPLQVKKAVTGKAKATKEQVAFMVKRLLGLSKDIKPLDI

TDAIAVALTHAANLRVRV

>sp|A8FNU8.1|RNH\_CAMJ8 RecName: Full=Ribonuclease H; Short=RNase H

MKHIEIYTDGSCLNNPGFGGWAYILRYKEYQKEGFGAEANTTNNRMELMAIIESLKALKEPCEISLFTDS

NLMVQSINEWLEGWIKKDFKGKKNIDLWKEYIKVAKSHKIKAFWVKAHNGHLENERCDTLAREAALKIAR

ENDEKH

>sp|A8FP33.1|LEUC\_CAMJ8 RecName: Full=3-isopropylmalate dehydratase large subunit; AltName: Full=Alpha-IPM isomerase; Short=IPMI; AltName: Full=Isopropylmalate isomerase

MAKTLYEKVFDAHVVYEGKNELPILYIDRHLIHEVTSPQAFSGLKMAKRRMARADLTLATIDHDVSTKSI

DLNACSDMAKEQITTLMQNTKEFGVRLLGLGDKNQGIVHIVGPELGFTLPGVTLVCGDSHTATHGAFGAL

AFGIGTSEVEHVMATQTLKQAKLKTMKIECKGQFQKGVYAKDLILYLIAQYGTAKGTGYAIEFCGELIRK

LSMEARMTLCNMAIEFGAKVGMIAPDEITFEYIKGKEFAPKGEEFQKYCEYWKSLRSDEGAKYDESITLD

VSKIKPQISYGTNPSQVIGIDEKIPKISDFKNQSEQKSLLDALSYVNLEQDQVIEGVKIDIVFIGSCTNG

RLEDLKIAADILKGHKIHKNVKALIVPGSMQVRKEAENLGLDKIFIEAGCEWRYAGCSMCLGMNDDKANS

GQRVASTSNRNFVGRQGKGSITHLMSPASAAACAIEGVICDNRKYLGV

>sp|A8FP22.1|RS10\_CAMJ8 RecName: Full=30S ribosomal protein S10

MERIRLKLKAYDHRVLDRTVAAIVEAVKRTGADIRGPIPMPTKIKRYTVLKSPHINKDSREQFEIRIHAR

MLDIVAATPDTVDSLTKLDLAPEVSVEVRAMGK

>sp|A8FP16.1|RL22\_CAMJ8 RecName: Full=50S ribosomal protein L22

MSKALIKFIRLSPTKARLIAREVQGMNAELAMASLKFMPNKGAKYIANAISSAVANGGFEANEVIVKSCR

VDAAAVLKRFRPRARGSASRIRKPTSHILVEVAKAEVKAEEKKTVAKKAPAAKKTTTTKAPAKKTTSTKK

ATAKKES

>sp|A8FP14.1|RL16\_CAMJ8 RecName: Full=50S ribosomal protein L16

MLMPKRTKYRKMMKGRNRGYANRGTEFTFGEFALKATEAGRINSRQIEAARIALTRFVKRQGKTWIRVFP

DKPLTKKPLETRMGKGKGAVEEWVMNIKPGRIIYEMAGVSEEMAREALTLAMHKLPFKTKFVTRESQNEI

Y

>sp|A8FP13.1|RL29\_CAMJ8 RecName: Full=50S ribosomal protein L29

MKYTEIKDKTAAELATMLKEKKVLLFTLKQKLKTMQLTNPKEISQVKKDIARINTAINALR

>sp|A8FP11.1|RL14\_CAMJ8 RecName: Full=50S ribosomal protein L14

MIQSFTRLAVADNSGAKELMCIKVLGGSKRRYATVGDVIVASVKKALPNGKVKKGQVVKAVIVRTKKEIH

RDNGSLIRFDENAAVILDNKREPIGTRIFGPVGREVRYGGFMKIVSLAPEVL

>sp|A8FP08.1|RS14Z\_CAMJ8 RecName: Full=30S ribosomal protein S14 type Z

MAKKSMIAKAARKPKFKVRAYTRCQICGRPHSVYRDFGICRVCLRKMGNEGLIPGLKKASW

>sp|A8FP07.1|RS8\_CAMJ8 RecName: Full=30S ribosomal protein S8

MINDIISDSLTRIRNAGMRKLETTKLLHSKVVEALVGIFQAKGYIESFNVIEEDKKKFINVVLKYDEKGK

SVINELKRISKPGRRVYKGKDEIKRFKNGYGTIVVSTSHGVLANDEAYKAGVGGEILCTIW

>sp|A8FP06.1|RL6\_CAMJ8 RecName: Full=50S ribosomal protein L6

MSRIGKQPIAIPAGVEVKLEGNLLKFKKGNLAKELDTKANVNVEIKDNNILFSPKGEDRQSRAYWGTYRA

LAYNIVVGLTQGFSKTLEINGVGYKAALKGKVLELSLGFSHPINYDIPEGIEIVVDKNTIAVKGSDKQVV

GQVAAQIREFRPPEPYKGKGVKYSDERIIRKAGKTSKK

>sp|A8FNY4.1|RECA\_CAMJ8 RecName: Full=Protein RecA; AltName: Full=Recombinase A

MDDNKRKSLDAALKSLDKTFGKGTILRLGDKEVEQIDSIGTGSVGLDLALGIGGVPKGRIIEIYGPESSG

KTTLTLHIIAECQKAGGVCAFIDAEHALDVKYAKNLGVNTDDLYVSQPDFGEQALEIVETIARSGAVDLI

VVDSVAALTPKAEIEGDMGDQHVGLQARLMSQALRKLTGIVHKMNTTVIFINQIRMKIGAMGYGTPETTT

GGNALKFYASVRLDVRKVATLKQNEEPIGNRVKVKVVKNKVAPPFRQAEFDVMFGEGLSREGELIDYGVK

LDIVDKSGAWFSYKDKKLGQGRENSKAFLKENPEIADEITKAIQNSMGIEGMISGSEDDEGEE

>sp|A8FNU6.1|AROC\_CAMJ8 RecName: Full=Chorismate synthase; Short=CS; AltName: Full=5-enolpyruvylshikimate-3-phosphate phospholyase

MNTFGTRLKFTSFGESHGVAVGCIIDGMPAGVKFDEEFLQNELDKRKGGSKFATPRKESDKAQVLSGVFE

GYTTGHPIAIVVFNENAHSKDYDNLKDLFRPAHADFTYFYKYGIRDHRGGGRSSARESVARVAGGAVAAM

LLREFDICVQSGVFGVGTFVSNLKEEEFDFEFAKKSEIFCLDPKLESDFKNEILNARNSKDSVGAAVFTK

VSGMLVGLGEVLYDKLDSKLAHALMGINAVKAVEIGEGINASKMRGSCHNDALKDGKFLSNHSGGILGGI

SNGENLILKTYFKPTPSIFAKQESIDKFGNNLEFELKGRHDPCVGVRGSVVASAMVRLVLADCLLLNASA

NLNNLKNAYGLK

>sp|A8FNS2.1|RS20\_CAMJ8 RecName: Full=30S ribosomal protein S20

MANHKSAEKRARQTIKKTERNRFYRTRLKNITKAVREAAANGDKNAANEALKVANKSIHAMVSRGFIKKQ

TASRRVSRLALLVNKIA

>sp|A8FNR8.1|ISPDF\_CAMJ8 RecName: Full=Bifunctional enzyme IspD/IspF; Includes: RecName: Full=2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase; AltName: Full=4-diphosphocytidyl-2C-methyl-D-erythritol synthase; AltName: Full=MEP cytidylyltransferase; Short=MCT; Includes: RecName: Full=2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase; Short=MECDP-synthase; Short=MECPP-synthase; Short=MECPS

MSEISLIMLAAGNSTRFNTKVKKQFLRLGNDPLWLYATKNLSSFYPFKKIVVTSSNITYMKKFTKNYEFI

EGGDTRAESLKKALELIDSEFVMVSDVARVLVSKNLFDRLIENLDKADCITPALKVADTTLFDNEALQRE

KIKLIQTPQISKTKLLKKALDQNLEFTDDSTAIAAMGGKIWFVEGEENARKLTFKEDLKKLDLPTPSFEI

FTGNGFDVHEFGENRPLLLAGVQIHPTMGLKAHSDGDVLAHSLTDAILGAAGLGDIGELYPDTDMKFKNA

NSMELLKQAYDKVREVGFELINIDICVMAQSPKLKDFKQAMQSNIAHTLDLDEFRINVKATTTEKLGFIG

RKEGMAVLSSVNLKYFDWTRL

>sp|A8FNR1.1|HIS7\_CAMJ8 RecName: Full=Histidine biosynthesis bifunctional protein HisB; Includes: RecName: Full=Histidinol-phosphatase; Includes: RecName: Full=Imidazoleglycerol-phosphate dehydratase; Short=IGPD

MSQKILFIDRDGTLIEEPKSDFQIDTLEKLRFEKDAIPTLLKLKNFGFKFIMVSNQDGLGTPSFPKENFE

IAHEKMLDILKSCGIEFQDIFICPHFENENCACRKPKTAMLEEYIKHELYDKEQSFVIGDRESDMILASN

LGVRGLRYGELSWKEIENEILSSFRSASYQRTTKETDIKVKVCLNGGKVSIKTGIDFFDHMLEQIAVHGG

IGLEISCKGDLEIDEHHSVEDVALALGACIKKALGDKIGIARYGFALPMDECLASCAMDFCNRPHLVYKA

KFKKSHLGALSTEMIEHFFYSLSYAMGVSLHLKVKGKNDHHKAEGLFKAFAKALKMAVKIESENLASSKG

VI

>sp|A8FNQ8.1|RL17\_CAMJ8 RecName: Full=50S ribosomal protein L17

MRHKHGYRKLGRTSSHRAALLKNLTIALVNSGKIETTLPKAKELRGYVERLITRARLGDFNAHRAVFASL

QDKNATNKLVTEIAPKFKDRNGGYTRIIKTRIRRGDAAEMAFIEFVA

>sp|A8FNQ7.1|RPOA\_CAMJ8 RecName: Full=DNA-directed RNA polymerase subunit alpha; Short=RNAP subunit alpha; AltName: Full=RNA polymerase subunit alpha; AltName: Full=Transcriptase subunit alpha

MRNITTSAYTPTEFTIENISDTVAKISAWPFEIGYGITLAHPLRRLLYTSTIGYAPTAIHIDGVAHEFDS

MRGMLEDVALFIINLKKLRFKIKGESNKEIVEFSFKGSKEIYGKDLNNDQVEVVNKDAYLATINEDAELK

FTLIVEKGIGYVPSEEIKELINDPKFIALDAFFTPVREATYDIEKVLFEDNPDYEKVVLTVTTDGQITPN

EAFQNALEAMYKQLSVFDKITNVRSVIKNQATSNELENTKLLQNITDLNLSARSYNCLEKAGVVYIGELA

LMSVSELAGLKNLGKKSLDEIKNIMESIGFPVGTSKLSDNKEILKNKIAELKAQNEG

>sp|A8FNQ6.1|RS4\_CAMJ8 RecName: Full=30S ribosomal protein S4

MARYRGPVEKLERRFGVSLALKGERRLAGKSALDKRPYAPGQHGARKGKISEYGLQLREKQKAKFMYGVS

EKQFRRLFAEAARREGNTGVLLIQLLEQRLDNVVYRMGFATTRRFARQLVTHGHVLVNGKRVDIPSFRVE

AGAKIEIIEKSKNNPQITRAIELTAQTGIVAWVDVEKDKRFGIFTRKPEREEVVIPVEERFIVELYSK

>sp|A8FNQ5.1|RS11\_CAMJ8 RecName: Full=30S ribosomal protein S11

MAKRKIVKKKVVKKNIAKGIVYISATFNNTMVTVTDEMGNAIAWSSAGGLGFKGSKKSTPYAAQQAVEDA

LNKAKEHGIKEVGIKVQGPGSGRETAVKSVGAMEGIKVTFLKDITPLAHNGCRPPKRRRV

>sp|A8FNQ4.1|RS13\_CAMJ8 RecName: Full=30S ribosomal protein S13

MARIAGVDLPKKKRIEYGLTYIYGIGLFTSRKILDKVGISYDKRVHELSEDEAAAIRKEIQENYMVEGDL

RKQVAMDIKALMDLGSFRGLRHRKGLPVRGQKTKTNARTRKGKRKTVGAKS

>sp|A8FNQ3.1|RL36\_CAMJ8 RecName: Full=50S ribosomal protein L36

MKVRPSVKKMCDKCKVVRRKGVVRIICENPKHKQRQG

>sp|A8FN57.1|SELA\_CAMJ8 RecName: Full=L-seryl-tRNA(Sec) selenium transferase; AltName: Full=Selenocysteine synthase; Short=Sec synthase; AltName: Full=Selenocysteinyl-tRNA(Sec) synthase

MNKFRTFPQINTLIEDESLKSYPFYIKAFFCKKVVAKLKENFSQDEISKDKLLLEIKKEIKTFYRKDLQS

VINASGVVIHTNLGRSVIHEELYEACKDIICNYSNVEFDLENGKRGSRYALVLEKLKMLFECEDALVVNN

NAAAVFLVLNSLCYNKEIISSRGELVEIGGSFRVPEVIKAAGVKLCEVGTSNKTHLKDYEQAISENTALI

LKTHKSNFALMGFHSEVNIKDLHELAKEKGLLSYYDLGSGWCENLNEKLIKNEPKIKKLVQECDILSFSG

DKLFGSVQAGIILGKKELIEKLKQNQLLRMLRVDKLTLSFLNESLKAYLQKDYEKIITLKLLNDDLSFIE

KKALRVQKELKFQTQLKKSKSLVGGGSMPDKSLDTYILTFQGDALKLQTRFRKENIIGRIENDEFVLDFR

TIRENELQKLILIINQMENL

>sp|A8FN42.1|RUVB\_CAMJ8 RecName: Full=Holliday junction ATP-dependent DNA helicase RuvB

MDRIVEIEKYSFDETYETSLRPSNFDGYIGQESIKKNLNVFIAAAKKRNECLDHILFSGPAGLGKTTLAN

IISYEMGANIKTTAAPMIEKSGDLAAILTNLSEGDILFIDEIHRLSPAIEEVLYPAMEDYRLDIIIGSGP

AAQTIKIDLPKFTLIGATTRAGMLSNPLRDRFGMQFRLEFYKDSELALILQKAALKLNKTCEEKAALEIA

KRSRSTPRIALRLLKRVRDFADVNDEEIITEKRANEALNSLGVNELGFDAMDLRYLELLTAAKQKPIGLA

SIAAALSEDENTIEDVIEPYLLANGYIERTAKGRIASAKSYSALKLNYEKTLFEE

>sp|A8FN28.1|MOBA\_CAMJ8 RecName: Full=Molybdenum cofactor guanylyltransferase; Short=MoCo guanylyltransferase; AltName: Full=GTP:molybdopterin guanylyltransferase; AltName: Full=Mo-MPT guanylyltransferase; AltName: Full=Molybdopterin guanylyltransferase; AltName: Full=Molybdopterin-guanine dinucleotide synthase; Short=MGD synthase

MQLNELNCVILCGGKSSRMGQDKSKLILKNQNLTQFQVEKFSKIFKNVYVSAKEDKFENHFSLIKDSLEF

EVYSPMLALYSILSNFKNEFVFVLSVDSPKVGENELLKMLPFLEQNYKIIIAKTPLHKHPLCGFYHSSLA

QTCKNFLEKNEQKIGLLFSEIKTKFVEFEDEDAFLNLNFYEEYEKFKSELR

>sp|A8FN24.1|DXR\_CAMJ8 RecName: Full=1-deoxy-D-xylulose 5-phosphate reductoisomerase; Short=DXP reductoisomerase; AltName: Full=1-deoxyxylulose-5-phosphate reductoisomerase; AltName: Full=2-C-methyl-D-erythritol 4-phosphate synthase

MILFGSTGSIGVNALKLAALKNIPISALACGDNIALLNEQIARFKPKFVAIKDSKNKHLVKHDRVFIGQE

GLEQILTECQDKLLFNAIVGFAGLKSTLKAKELGKNIALANKESLVVAGSFLKGVKFLPVDSEHAALKFL

LEGKKNIAKLYITASGGAFYRYKIKDLNQVSVKDALKHPNWNMGAKITIDSATMANKLFEIIEAYHLYDF

KEIDALIEPRSLVHAMCEFKNGASTAYFSKADMKLAISDAIFEKQDTPILEAVDFSKMPALKFHPISTKK

YPIFKLKNTFLKEPNLGVIINAANEVGVYNFLENKSGFLDIAKCIFKALDHFGVPKISSIEEVFEYDFKT

REYLRS

>sp|A8FMZ7.1|DCD\_CAMJ8 RecName: Full=dCTP deaminase; AltName: Full=Deoxycytidine triphosphate deaminase

MGLKADNWIRKMALERKMIEPFCEANIGKGVVSYGLSSYGYDIRVGREFKIFTNVNSTVVDPKNFVEENV

VDFEGDVCIVPANSFALARTIEYFKMPDDVLAICLGKSTYARCGIIVNVTPFEPGFEGHITIEISNTTPL

PAKIYANEGIAQVLFLQGDEKCDTTYKDKKGKYQAQTGITLPRILK

>sp|A8FMZ1.1|UPP\_CAMJ8 RecName: Full=Uracil phosphoribosyltransferase; AltName: Full=UMP pyrophosphorylase; AltName: Full=UPRTase

MKNIHCINHPLIEHKLGILRAKETKPFQFRMLIDEISSFLLFEASKDFSLKEIEISTPIQKTTVKKLDEK

IMICPILRAALGMLESVFKMIPDASVGFLGFVRNEETLKADFYFQKLPKDAKKRTAIVIDPMFATGGTAI

EACNFLKSQGVKKIKFISILAAPQGLKKFSQMHDDVEVFVACIDEGLNEKGYIIPGLGDAGDRVFNTL

>sp|A8FMY0.1|PYRH\_CAMJ8 RecName: Full=Uridylate kinase; Short=UK; AltName: Full=Uridine monophosphate kinase; Short=UMP kinase; Short=UMPK

MQERKRVLVKFSGEALAGENGFGIENSILKFIASEIKELIKNQIEVGIVIGGGNIIRGVSAAKGGLIKRT

SGDHMGMLATVINAIAIQEALESSGLEVRVQSAIQMEAFCETYIMRRAQRHLEKGRVVVFAAGTGNPYFT

TDTTAILRAVEIDADMVIKATKVNGVYDKDPKQFDDAVFLNTLSYDEAMQDNIKVMDDTAIALAKDNKLP

IVVCNMFEEGNLLKIIQGDTSLCSIVKNN

>sp|A8FMX9.1|RPOZ\_CAMJ8 RecName: Full=DNA-directed RNA polymerase subunit omega; Short=RNAP omega subunit; AltName: Full=RNA polymerase omega subunit; AltName: Full=Transcriptase subunit omega

MDKRIEEVAAKALEKMGNDRYRLSLVVAKRAEQLANGATPLVDFDKNKNKLADIALYEIAENKITLEGLV

ETNR

>sp|A8FMP4.1|MNMG\_CAMJ8 RecName: Full=tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG; AltName: Full=Glucose-inhibited division protein A

MFDVIVIGGGHAGVEASAAAARMGKKTLLLTTLIEQIGAASCNPAIGGLAKGHLVKELDAMGGLMGEITD

EAGIQFRILNESKGVAVQGSRAQIDMDKYRIIARNKLLKLPNLEISQEQASVLIVENDEVKGVKTNLENT

YFAKKVILTTGTFLNGLIHVGENKLQAGRVGELASVNLGNYLQTLGLKMGRLKTGTCPRVDAKSIDFSVL

EIQDGDVNPKAFSFRSKNFNPTQLPCYIARTNTTTHEIIKNNFYRAPLFTGQIEGVGPRYCPSIEDKINR

FSDKESHHLFIEPQTIDATEYYINGFSTSLPYEVQIQMLRSVKGFEDAKITRFGYAIEYDYIEPTELKHT

LELKKIKNLYCAGQINGTTGYEEAAAQGFMAGINASLSIDMKEPLILRRDEAYIGVLIDDLVVKGTKEPY

RMFTSRAEFRLLLREENAILRLGKYGYDLGLLSEQDFTYIQNIANNLQKGLEFLLSKEFTPNNQNNAFLE

SLGEDKISSIVNLQKIVARASFDIEKLKKLDPMFETMDNYSLREILNEAKYYHYISMQKAQVEKMKNLSE

LKIPENFDFKSVSGLSNEVVEKLNHHKPPTIFAASQISGITPAALDILQIYIKMQKKKA

>sp|A8FMF8.1|SSRP\_CAMJ8 RecName: Full=SsrA-binding protein; AltName: Full=Small protein B

MKIIARNKKALFDYSIIERFEAGIVLKGSEVVALRAGRANLKDSFVRIIKNEIFLLNSHISLLHTTHSFY

KHEERGARKLLMHRKQIDKLLGKVSIEGYTIVALDLYFNTKNKVKATLALAKGKNLHDKRETLKKKQADL

EARAAMKNYK

>sp|A8FMF7.1|ISPE\_CAMJ8 RecName: Full=4-diphosphocytidyl-2-C-methyl-D-erythritol kinase; Short=CMK; AltName: Full=4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase

MKAYAKANIFLKLTGFDSRKYHLLESRFILLKDLFDELELVDKESDSKKEFEIISNFKCENNIIQKAYLL

LSKRYNNELKELFSKKSLKLTKNIPVCAGLGGGSSDCASFLLLMNETLNLKLNLQELINLSIQLGSDIAF

FLSGFHSANVSGCGEIIEEFEDDIPNLKWTFPQISCQTKAVYDEFDRGIFDFQKNNNQAQIYKKLSTKEL

LQNFKNKELNDLFTPCATLYPKMKSYLQEDFFLSGSGSSVFKVDR

>sp|A8FMF1.1|PYRB\_CAMJ8 RecName: Full=Aspartate carbamoyltransferase; AltName: Full=Aspartate transcarbamylase; Short=ATCase

MRHLITTKDFNKVEIMELFKEASDFLDEKPRTFLKGKSITTIFFENSTRTLSSFESAARRLGARVLRLDV

SRSSSSKGETLYDTAANLDAMSPNAIVVRHANSGVPLILAKHIHCPVVNGGDGKHAHPTQALLDLFTIYN

HFQGDVEGKKICIVGDIKNSRVAASNIELLSRFNLDITLVAPPHFMPNTHLKKHYKLDENIIANSDIIMS

LRTQTERHNKTVYASLKDYANDFCIQKSLVKDKKLILLHPGPVNRNIDISDEMMSDERTLVLKQVKNGVA

IRMAVLKKLILENEG

>sp|A8FMD4.1|THIE\_CAMJ8 RecName: Full=Thiamine-phosphate synthase; Short=TP synthase; Short=TPS; AltName: Full=Thiamine-phosphate pyrophosphorylase; Short=TMP pyrophosphorylase; Short=TMP-PPase

MKNKLDLSLYLVASQGNKSEECFLNTLENAIKGGVSIIQLREKELNAREFYKLGLKVQKLCKAYKIPFLI

NDRVDIALALDADGVHLGQEDLEVKLARKLLGDEKIIGLSLKKLEQLEFIQGANYLGCGAIKATPTKESS

LLSLELLSQICDKSPIGVVAIGGVDKAVLDELKGINLSGVAVVRAIMDAKDAFLAAKELKRKIYENLPLK

>sp|A8FMC5.1|RS18\_CAMJ8 RecName: Full=30S ribosomal protein S18

MAEKRKYSRKYCKYTEAKVEFIDYKDTAMLKHALSERFKIMPRRLTGTSKKYQEMVEVAIKRARHVALIP

YIVDRKEVINNPFEGL

>sp|A8FMB2.1|GATA\_CAMJ8 RecName: Full=Glutamyl-tRNA(Gln) amidotransferase subunit A; Short=Glu-ADT subunit A

MITLKEALKYSKEELENLKKELNEKAKKEKKIGAYIEQFLDKDLSVSGEGVPVAIKDNISVKGWELTSAS

KILQGYIAPYDASVIVNLKANGFSPFGRCNMDEFAMGSSTASSYYGKTLNPLNFERVPGGSSGGSAAAVA

GGLALASLGSDTGGSVRQPAAFCGCVGFKPSYGRVSRYGLASYSSSLDQIGVLTQNVEDAAILYDAIAGY

DKMDSTSANIEFIKTAPNLNVNKKLKIAVIENYVNDADSEVKNALLKTIDMLKANGHEIVYKNLLDSKFD

IAAYYIIATAEASANLSRYDGVRYGKRSENIQNLKEMYVNTRSEGFGEEVKRRILLGTFVLSSGYYDAYY

IKAQKARAFIKAKYEEILQDCDLIFMPVTPTTAFKFDTQKSPMQTYLEDVYTISVNLAGLGGISVPVAKD

KEELNISAQLICKAYDEQTLLDGALSLEQMIKH

>sp|A8FM59.1|TGT\_CAMJ8 RecName: Full=Queuine tRNA-ribosyltransferase; AltName: Full=Guanine insertion enzyme; AltName: Full=tRNA-guanine transglycosylase

MEFKLKHKDGMARVCEITTAHSTFLTPVFMPVGTVGAVKSLDANDMKNELDAKIILANTYHMYLRPTSKV

VKDFGGLHGFTKFDRSFLTDSGGFQAFSLSKNSKHFNEGIEFKSHIDGSRHLFTPKSVLDTQYDFNSDIM

MILDDLVALPATKERVKISVDRTILWAKEAITYHKSMQNKGIGIGQNIFGIIQGGTDYKERKRCALSLNE

MPFDGLAIGGLSVGEENALMYETVQNLNPYLDENRPRYLMGVGTPEDLVENVERGVDMFDCVMPTRNARN

GTFFTSFGKFNIKKAEFINDHEAIDPACSCYTCCNFSRGYLNHLFKAKELTFFRLASLHNLHYYLELARK

MREAILNNSFTQFKRNFYHLRGK

>sp|A8FM10.1|MNME\_CAMJ8 RecName: Full=tRNA modification GTPase MnmE

MSDTIAAIATAHGVGSISIVRLSGERALEFALKLSHKTKLTPRHATFTKLFNQNNEIIDEAIMIYFKAPY

SFTGEDIVEFQTHGGFSVSEVLLEELVSLGARLALAGEFSKRACLNGKMTPLKALNIQDLILSKSALAAK

IIARNMQGNLGELLEKIRTDLVKTLAFVETSIDYADDDLPSDLLEQISTMCEENSKILKEIYTLSQSKKG

LIEGFKIAIVGKPNVGKSSLLNALLSYERAIVSDIAGTTRDTIEESFKLGTHLLRIIDTAGIRESKDAIE

QIGVALSKKSLEDADIILAVFDASRVQDKEDEKIFDLLANTDKKIFWILNKSDLENVFKNTQNKNFIKLS

AQKDITLLKEELQNYLNSFDSEGIMVSSLDLINACKISSEAIFRAKGLLEESSLELFAFELNLAINELAR

FTKDFQRDEILDEMFGNFCLGK

>sp|A8FM09.1|PURL\_CAMJ8 RecName: Full=Phosphoribosylformylglycinamidine synthase subunit PurL; Short=FGAM synthase; AltName: Full=Formylglycinamide ribonucleotide amidotransferase subunit II; Short=FGAR amidotransferase II; Short=FGAR-AT II; AltName: Full=Glutamine amidotransferase PurL; AltName: Full=Phosphoribosylformylglycinamidine synthase subunit II

MDKETIKAHKISDEEYAQILEILGREPNLLELGVISAMWSEHCSYKSSKKYLNGFPTKAPWVIQGPGENA

GVIDIGQGMAAVFKVESHNHPSFIEPFAGAATGVGGILRDVFTMGARVVAGLNSLKFGDIHDEKCGKHQK

YLVKGVVNGISHYGNCMGVPTIGGECAFDECFNGNILVNAFALGVCKSEDIFYAKAEGVGNPVIYVGSKT

GRDGLGGAVMASDSFNEESKSLRPTVQIGDPFSEKLLMEACLELFKTDYIVGIQDMGAAGLTSSSFEMAG

RSGSGMKLYLDKTPMRESGMTPYELMLSESQERMLICAKKGYEDKVIEIFKKWDLDAVVMGEVTNTGKME

LFWHDELVGLIPIEPLSEKAPILSRPTSEPKYLSEIKNYKFELKSSIQELFIQMLQNENINNKAFIYDQF

DSSVQTNTIKADGKLGASVIRIKENGASVAMAIECNSRLNYVNPKIGAALAVASAGRKVACTGAKPLAIS

DCLNYGNPQNPEVMWQFAQGCEGIKEACKELNTPVVSGNVSLYNETEGVSIYPSPTIVSVGVLEDANKTL

KASFEKENLSVYLLGESLGEFGGSMVMKIQDKKVSGSLKELDYKAELALWDLLYKANQNSLLECANSVGI

GGIAMTLAKMFAISSVGANLTSDFDDEKMIFDESASRAIIGLSKENEEAFLNLAKEFGVKAYKLGVSTSQ

KHFKLDSIELSKAELDKLYFESFKEQIQ

>sp|A8FLZ7.1|SECA\_CAMJ8 RecName: Full=Protein translocase subunit SecA

MFLNTLKAVFGTKNDREVKKYFKRVAQINALEGKYQNLSDDELKAEFAKFKEQILSGEKNENDILNDVFA

IVRETGKRTLNMRHFDVQLIGGMVLHDGKIAEMKTGEGKTLVATLPVVLNAMSGKGVHVVTVNDYLAKRD

AEQMSAIYNFLGFSVGVILSSQNSDIEHKQAYDCDITYGTNNEFGFDYLRDNMKFSKVEKVQREHNFVIV

DEVDSILIDEARTPLIISGPTNRTLDGYIKANEVAKQMQKGEAVLPPAKPEGDFVVDEKNRNILITEAGI

AKAEKLFGVENLYSLDNAILAHQLDQALKAHNLFEKDVHYVLRNNEVIIVDEFTGRLSEGRRFSEGLHQA

LEAKENVKIQEESQTLADITFQNYFRMYNKLAGMTGTAQTEATEFSQIYSLDVISIPTNIPIKRQDKDDL

IYKTQNEKFKAVIEEIKKANSKGQPVLVGTASIERSEVFHNMLVKEKIPHHVLNAKNHEQEALIIQDAGK

KGAVTIATNMAGRGVDIKIDDEIRALGGLYIIGTERHESRRIDNQLRGRAGRQGDPGISRFYLSLEDNLL

RIFGGDRIKNIMDRLGIEEGESIESRIVTRAVENAQKKVESLHFESRKHLLEYDDVANEQRKTIYRYRNE

LLDENYDIRAKISQNIAEYSANVMNDYILDESGSNVNFENLKAKILYECSTQISEKDFENLSVIEMQDKL

SQILENSYNEKMSRLGIKELRNIERILYLQVLDNAWREHLYQMDILKTGIGLRGYNQKDPLVEYKKESYN

LFLELVNRIKFDSIKLLFSVQFNQEEVQNLENKANEENEKLLQSSVEMGASEDNLGEAEFKKVPRNAPCP

CGSGKKFKECHGKSGPKQGILA

>sp|A8FLY0.1|ARLY\_CAMJ8 RecName: Full=Argininosuccinate lyase; Short=ASAL; AltName: Full=Arginosuccinase

MKNEMWSGRFSGASDELLKEFNASLNVDKTLFNEDIQGSIAHATMLESCGILKKEELDAIIKGLEQVKSE

IEQGKFVFDIKDEDIHMAIEKRLSEIIGSEIGGRLHTARSRNDQVATDFKLFVKKSHIELLKLLKELIQT

MLEHAKVHKKTIMPSFTHLQHAQPVSFSFYILAYAFMLMRDIKRLQNSLELADFSPLGSCACAGTSYATN

RELSAEILGFKDIMPNAMDGVSDRDFALDLLYDIAVIFTHTSRLCEEMILFSSSEFSFITISDSFSTGSS

IMPQKKNPDVCELIRGKTGRVYGNLISLLTIMKALPLAYNKDMQEDKEGLFDSVKTAKDSLIILNAMLKE

IQINKENMLNACKKGHLLATDLADYLVREKNIPFRKAHFIVGNVVAQAEAQGIDISEIKDLSKIDPVFDE

KAMELLNFEFSLNSKQSEGSSSIASVEKQIQILEGFIQNL

>sp|A8FLT4.1|RS15\_CAMJ8 RecName: Full=30S ribosomal protein S15

MALDSAKKAEIVAKFAKKPGDTGSTEVQVALLTARIAELTEHLKIYKKDFSSRLGLLKLVGQRKRLLSYL

KRKDYNSYSKLITELNLRDK

>sp|A8FLR7.1|MURA\_CAMJ8 RecName: Full=UDP-N-acetylglucosamine 1-carboxyvinyltransferase; AltName: Full=Enoylpyruvate transferase; AltName: Full=UDP-N-acetylglucosamine enolpyruvyl transferase; Short=EPT

MTYLEIEGTNHLSGNVTISGAKNAALPLIVSSILAKNEVKINNVPNVADIKTLISLLENLGAKVNFQNNS

ALLNTNTLNQTIAKYDIVRKMRASILTLGPLLARFGHCEVSLPGGCAIGQRPIDLHLLALEKMGANIQIK

QGYVVASGNLKGNEILFDKITVTGSENIIMAAALAKGKTKLLNVAKEPEVVQLCEVLKDAGLEIKGIGTD

ELEIYGTDGELLEFKEFSVIPDRIEAGTYLCAGAITNSKITLDKVNATHLSAVLAKLHQMGFETLIAEDS

ITLLPAKEIKPVEIMTSEYPGFPTDMQAQFMALALKANGTSIIDERLFENRFMHVSELLRMGADIKLNGH

IATIVGGKELNAADVMATDLRASSALILAALAAKGTSKVHRIYHLDRGYENLEEKFKGLGAKITRLEE

>sp|A8FLR4.1|FOLD\_CAMJ8 RecName: Full=Bifunctional protein FolD; Includes: RecName: Full=Methylenetetrahydrofolate dehydrogenase; Includes: RecName: Full=Methenyltetrahydrofolate cyclohydrolase

MTLLDGKALSAKIKEELKEKNQFLKSKGIESCLAVILVGDNPASQTYVKSKAKACEECGIKSLVYHLNEN

TTQNELLALINTLNHDDSVHGILVQLPLPDHICKDLILESIISSKDVDGFHPINVGYLNLGLESGFLPCT

PLGVMKLLKAYEIDLEGKDAVIIGASNIVGRPMATMLLNAGATVSVCHIKTKDLSLYTRQADLIIVAAGC

VNLLRSDMVKEGVIVVDVGINRLESGKIVGDVDFEEVSKKSSYITPVPGGVGPMTIAMLLENTVKSAKNR

LN

>sp|A8FLP0.1|TRMA\_CAMJ8 RecName: Full=tRNA/tmRNA (uracil-C(5))-methyltransferase; AltName: Full=tRNA (uracil(54)-C(5))-methyltransferase; AltName: Full=tRNA(m5U54)-methyltransferase; Short=RUMT; AltName: Full=tmRNA (uracil(341)-C(5))-methyltransferase

MSLENFGNFLTLDEKHSFIKKYFKEFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYI

IEYLDFADEKICAFMPKLLEYLRQDNKLKEKLFGVEFLTTKQELSITLLYHKNIEDIKSNLENLSNILHI

NLIARSKGKKLIFKTENLRQTLNIQDRKIFYEFNNDCFIQPNTTINEKMITWVCEILNTQKRMDLLELYC

GYGNFTLALAPFFFKVLATEISKSNINFALKNCKLNNTTNIHFARLSSEELSLAIKKEREFFRLKDIRLD

DFNFSHVLVDPPRAGLDKSVIDLIKKYENIIYISCNPITLKENLKELSLTHRVEEFALFDQFVNTPHLEC

GVFLSKV

>sp|A8FLM4.1|LPXK\_CAMJ8 RecName: Full=Tetraacyldisaccharide 4'-kinase; AltName: Full=Lipid A 4'-kinase

MSEEKNYELWLDNYFFKPNFWQKCLAFILLPLSVFYAFFAILNTFFRKKIVFKKPVISVGNLSFGGNGKT

PLCKAIAREFDGVFIVLRGYKRKSKGLFVVKNQNEILCTLTQSGDEAMEYAFEENIKGVIVSEDRVKGIE

KAFELGAKIVVLDDAFSKFHIKKFDILLESKIKPYFNFTLPSGAYRLPKFYEKRADFIALEGRDFVRYSF

VKENPKAVLVTAIAKPFRLYEHFIKARACYFFKDHYEFKKEELENLLKKHNCDTLMLTFKDFVKVKDFGF

KCQIIELNIELKDSLREKIKTYIKEFEQ

>sp|A8FLL2.1|RUVA\_CAMJ8 RecName: Full=Holliday junction ATP-dependent DNA helicase RuvA

MVVGIEGIITKKEPTFIIVKCASGLSYGIFISLFCSAKIQTQEKHEFFITQIIKEDSNKFYGFLDKDEQK

MFEMLLKVNGVGANTAMAVCSSLDVNSFYKALSLGDESVLKKVPGIGPKSAKRIIVELSDTKTKLENVSD

DKSEALAALLTLGFKQEKIISVLASAQATGTSELIKEALKKLG

>sp|A8FLI0.1|COAD\_CAMJ8 RecName: Full=Phosphopantetheine adenylyltransferase; AltName: Full=Dephospho-CoA pyrophosphorylase; AltName: Full=Pantetheine-phosphate adenylyltransferase; Short=PPAT

MTCLYPGTFDPITNGHLDVIKRALKIFDEVIVAIAKSEHKKPCYDLEKRKELALLATQNLKNVKIIAFDN

LLVDLAKELKVNTIIRGLRAVSDFEYELQIGYANHALWEDMETIYLMPSLKHAFISSSIVRSIVAHGGDV

SSLVPKEILPFLKDQSCM

>sp|A8FLH9.1|KTHY\_CAMJ8 RecName: Full=Thymidylate kinase; AltName: Full=dTMP kinase

MYVVFEGIDCVGKSTQISLLKEIYKDAIFTLEPGGTELGKHLREILLNKTHPISKRAELLLFLADRAQHF

EEILKTNQNKLIISDRSFISGMAYAKDFENDLLFALNSFALENFFPQKIIFLKGDANLIQERLSQKELDS

IEKRGIEYFLSVQDKLEKVLHFLKEKISIEILTLDAKESKEKLHQQIKEFLQ

>sp|A8FLE2.1|TRMD\_CAMJ8 RecName: Full=tRNA (guanine-N(1)-)-methyltransferase; AltName: Full=M1G-methyltransferase; AltName: Full=tRNA [GM37] methyltransferase

MKFSFVSLFPNLMEFYFQDSILARAKEKKLFKLNFYNPRDFSKNSYHKVDDYKIGGGAGLLMQAEPMYEV

LRSIQEKKENPYFIFLNPSGKTFNQKDAKRLSKKEHIVFVCGRYEGIDERVLEIFANEVFSIGDFILTGG

ELPALVMCDAILRNVNGVLGNMESLEEESFENNLLEAPAFSKPFIFEKKNKKFYTPSEFLKGNHARIASL

KTTLASCKTKFFRPDLFLEHERKK

>sp|A8FL82.1|RL9\_CAMJ8 RecName: Full=50S ribosomal protein L9

MKVLLIKDVKALGKAGEIKEVKDGYGQNFLIAKGFAKAATNEVLRKYESDKKKEAENLRFEIANLEKLKE

ELSKITLEISKPVGANGSLFGGVTKDEIAHALKEQSHIEIDKKSLECDTFKSLGLHEVSVKLGHAIHAKF

NINIKAE

>sp|A8FL58.1|MSRA\_CAMJ8 RecName: Full=Peptide methionine sulfoxide reductase MsrA; Short=Protein-methionine-S-oxide reductase; AltName: Full=Peptide-methionine (S)-S-oxide reductase; Short=Peptide Met(O) reductase

MKNIVLGGGCFWCVEAVFERLKGVIDTEVGYSGGNPNPSYESVCNGDGNIEVVKINYDEKQISLLEILTL

FFKIHDPTSIDKQGGDIGIQYRSIIFYENEEDKILAQNFIEEQQKIFSKKIVTKISRLQTYYKAENYHQH

YFINNPNQGYCQAVIAPKLQKIQSG

>sp|A8FL56.1|YQGF\_CAMJ8 RecName: Full=Putative pre-16S rRNA nuclease

MRALALDVGLKRIGVALCIDKKIALPLDAVLRKNRNQAANEIKNLLKIHEISLLIVGIPKGGSSEEEMTR

RIKHFVSLLEFDKEICFVDESGTSKEALGYGVANTRKKDGKLDSLSAFIMIKDYFAL

>sp|A8FKW8.1|HEM3\_CAMJ8 RecName: Full=Porphobilinogen deaminase; Short=PBG; AltName: Full=Hydroxymethylbilane synthase; Short=HMBS; AltName: Full=Pre-uroporphyrinogen synthase

MKLIIATRKSQLALWQSEHVAQILKNTHQIEVLLEGFKTKGDVLLDSPLAKIGGKGLFTKELEESMLRKE

AHLAVHSLKDVPSFFPRGLVLAAVSKREQSNDAMLSQNYKDFLSLPKGAKIGTTSLRRKMQLLLLRPDLE

IISLRGNVNSRIEKLKNNDFDAIILAMAGIKRLNLDKQVNFVYEFSKDELIPAASQGALGIESINDEKIL

ELLKCLNDENALIETSIEREFIATLEGGCQVPIGINAELLGDEICVRAVLGLPDGSEILKDKRMIKKNDF

KGFGESLAKEFIAKGAKELLKKAESMI

>sp|A8FKW5.1|HEM1\_CAMJ8 RecName: Full=Glutamyl-tRNA reductase; Short=GluTR

MYYCISFTHKNTDIALREKLSFSNEAKKSEFLKIISTHENIEECLVISTCNRVEIVAFVKMACAEFIVKS

LALLCDVDKDILLEKADIFEDSGAIHHLFSVASSLDSLVVGETQIAGQLKDAFAFAVKNNFCGVHLSRAV

HSAFKCAAKVRNETQISKNPISVASVAVAKAKELADLAQKKAVVIGAGEMGELAAKHLIAAGAKVIILNR

DLQKAKDLCERLGVLSEYDSLENLKKYLNQYEFFFSATNAPNAIITNSLIEELPYKRYFFDIAVPRDIDI

NENENISVFAVDDLENVVQKNLALREQEARMAYGIIGRETSEFFRYLNDLALMPIIKAIRLQAKEYADKQ

LEIALKKGYLKKSDKEEARKLIHQVFKAFLHTPTVNLKHLQGKMQSDTVINAMRYVFDLQNNLEGLNQYK

CEFDMENNDEIY

>sp|A8FKU4.1|HTPG\_CAMJ8 RecName: Full=Chaperone protein HtpG; AltName: Full=Heat shock protein HtpG; AltName: Full=High temperature protein G

MQFQTEVNQLLQLMIHSLYSNKEIFLRELISNASDALDKLNFLSVSDDKYKSLKFEPKIEIKIDKDKKTL

SISDNGIGMDKDDLINNLGTIAKSGTKSFLENLSGDAKKDSQLIGQFGVGFYSAFMVASKIEVLSKKALD

DKAYLWSSDANGYEINDANKEEQGTSITLYLKDDEFANTYKIESIIEKYSNHIQFPIFMEKEEFTPAKEG

EEEGKTELKISQINKANALWRMQKSSLKVEDYERFYEQNFHDSNKPLLYLHTKSEGKLEYNSLFFIPQNA

PFDLFRVDYQSGLKLYVKRVFISDDDKELLPTYLRFVRGIIDVEDLPLNVSREILQENQILKGVKEASVK

KILGELEKLKNNDKEKYLSFFKTFGKVLKEGLYGFGGEKDSLLKLMLYKSTKGENLRSLEEYKNDLQGEQ

KEIFYIAGNNESLLRTSPLLEEYKQKNIEVLLMDDEIDSLVTPMLEFEGLKFVAINQVEDKNELSDEEKN

TFAPLVAKFKELLKDQVEDVRLTSRLKDSPSCIVYDKNKPDFAMQQLLKQMGQEQNFKPILEINPKHAIF

TGLKNNESFSADIATLVLNMAKLSEGMGVDNPAEFNASLTKIINKAFS

>sp|A8FKT8.1|PUR7\_CAMJ8 RecName: Full=Phosphoribosylaminoimidazole-succinocarboxamide synthase; AltName: Full=SAICAR synthetase

MTKKEMLYEGKGKKLFKTDDENLLISEFKDDLTAFNAEKRGNESGKGALNCKISTEIFHLLEKNGIKTHL

VETISDTEQVVKKCKIVPIEVIVRNVATGSLTKRLGIKDGTVLPFALVEFCLKDDALGDPFINDEHCLIL

NLVQNEAQISEIKNMARKINSILTPFFDNKNLRLIDFKIELGLTKDNELVLADEISPDSCRFWDKFSNEK

LDKDRFRQDLGNVKMAYEEVLKRILN

>sp|A8FKR6.1|RS7\_CAMJ8 RecName: Full=30S ribosomal protein S7

MRRRKAPVREVLPDPIYGNKVITKFINSLMYDGKKSTATTIMYGALEAIDKKGGEKKGIDIFNDAIENIK

PLLEVKSRRVGGATYQVPVEVRPARQQALAIRWIISFARKRSERTMIDKLAAELLDAANSKGASFKKKED

TYKMAEANKAFAHYRW

>sp|A8FKR2.1|RL7\_CAMJ8 RecName: Full=50S ribosomal protein L7/L12

MAISKEDVLEYISNLSVLELSELVKEFEEKFGVSAAPVMVAGGAAAGGAAAAAEEKTEFDIVLTDGGAKK

IEVIKIVRALTGLGLKEAKDAVEQTPSTLKEGVAKAEAEEAKKQLEEAGAKVELK

>sp|A8FKQ9.1|RL11\_CAMJ8 RecName: Full=50S ribosomal protein L11

MAKKVVGEIKLQIAATKANPSPPVGPALGQQGVNIMEFCKAFNERTKDMAGFNIPVVITVYADKSFTFIT

KQPPATDLIKKAAGISKGTDNPLKNKVGKLTRAQVLEIVDKKIADLNTKDRDQAAKIIAGSARSMGVEIV

D

>sp|A8FKN5.1|RL28\_CAMJ8 RecName: Full=50S ribosomal protein L28

MARVCQITGKGPMVGNNVSHANNKTKRRFLPNLRTVRVTLEDGTTRKMRIAASTLRTLKKQNSK

>sp|A8FKM8.1|ACP\_CAMJ8 RecName: Full=Acyl carrier protein; Short=ACP

MATFDDVKAVVVEQLSIDADAVKMESKIIEDLGADSLDVVELIMALEEKFEVEIPDSDAEKLIKIEDVVN

YIDNLKK

>sp|A8FKL9.1|MURD\_CAMJ8 RecName: Full=UDP-N-acetylmuramoylalanine--D-glutamate ligase; AltName: Full=D-glutamic acid-adding enzyme; AltName: Full=UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase

MKISLFGYGKTTRAIAENLVDKFGPFDIYDDHFTETKKDTLGNLLLNPNDFDDNLSDIEIPSPGFPPKHK

LIQKAKNLQSEYDFFYDIMPKSVWISGTNGKTTTTQMATHLLSHIGAVIGGNVGTPLAELDPYAKLWILE

TSSFTLHYTHKAKPEIYALLPISPDHLSWHGSFDNYVQDKLSVLKRMNECDVVILPKIYANTPTKAHKIS

YKDEKDLAVKFGIDTEKISFKSPFLLDAIMALAIEKILLDTLSYELLNSFVMEKNKLEELKDSQNRLWVN

DTKATNESAVMAALNRYKDKKIHLIIGGDDKGVDLSNLFDFMKNFNIELYAIGISTEKMLDYAKKANLKA

YKCEVLSKAVNEISNHLRVNEVALLSPACASLDQFNSYVERGKVFKECVNKI

>sp|A8FKI5.1|GATC\_CAMJ8 RecName: Full=Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C; Short=Asp/Glu-ADT subunit C

MQIDEKLLSKLEKLSALQITKNRNETIVQLSEIVNFVEKLNELDLDSQEITVSTIKGGAPLRIDEIRNSN

VIDEVLDCAPKKQEHFFVVPKIIE

>sp|A8FKH3.1|DER\_CAMJ8 RecName: Full=GTPase Der; AltName: Full=GTP-binding protein EngA

MQSIILIGKPNVGKSSLFNRMARQRIAITSDISGTTRDTNKTQIHIHSKKAMLIDSGGLDESDELFKNVK

KNTLKVAKESDIILYLVDGKLAPDDEDRQFFYSLKKLGKPIALVVNKVDNKKDEERAWEFANFGVKEIFN

LSVTHNVGLDELYEWLEKFLHEEFLIPDEEENLEDFLEHYEEGKEFQFKEVDQNHIRVGIVGRVNVGKSS

LLNALVKQERSVVSSIAGTTIDPVNESVVHKDKVIEFVDTAGIRKRGKIQGLERFALNRTEKILSHSQIA

LLVLDAHEGFNELDERIAGLVAKHYLGVIIVLNKWDKSEMDFDKTVKELHLDRFKFLAYAPVISVSALSG

KRVHVLLDKILQIFENFTQKIQTSKLNTLIENATRSHPLPHDYGKLVKIYYAVQYDLAPPKIALIMNRPK

ALHFSYKRYLQNQIRKEFNFEGVPLVIASRKKGSKENDES

>sp|A8FKH0.1|RISB\_CAMJ8 RecName: Full=6,7-dimethyl-8-ribityllumazine synthase; Short=DMRL synthase; Short=LS; Short=Lumazine synthase

MNIIEGKLNLDSNTKIAIINARFNHIITDRLVEGAKDAFLRHGGKEENLSLILVPGAFELPYALKKAIES

KKFDAICCVGAVIRGSTPHFDYVSAETTKGIANVSLNHNIPVSFGVLTTDTIEQAIERAGSKAGNKGFEA

MTTVIEMLNLSKEL

>sp|A8FKE8.1|GLMM\_CAMJ8 RecName: Full=Phosphoglucosamine mutase

MKLFGTDGVRGKAGEFLDSFLAMRLAMAAGIYFKDKSITNNILVGKDTRRSGYMIENAIVSGLTSIGYNV

IQIGPMPTPAIAFLTEDMRCDAGIMISASHNPYYDNGIKFFDAHGNKLSEDIEKKIEEIYFDDKLIQASK

VDMEKIGQAKRIDDVIGRYIVSIKNSFPKDLTLKSLRVVLDVAHGAAYKVAPTVFKELGAEVIVMSDKPN

GLNINENCGALHPANLAAEVKRLRADVGFAFDGDADRLVVVDEKGEVANGDSLLGVLALYLKEQGKLQSS

VVATIMSNGALKEFLNKHGIELDTCNVGDKYVLEKLKVNGGNFGGEQSGHIIFSDYAKTGDGLIAALQFS

ALMLSKKKSASSILGQVKPYPQLLTNLKIAEKKDLDKIKGLKELKKDLENKNINTLFRYSGTENLIRLLL

EAKDIKLLEKEMKNVVEFFKKALNG

>sp|A8FKD7.1|TRPB\_CAMJ8 RecName: Full=Tryptophan synthase beta chain

MKKAYYGDFGGQFLPESAMFALNELEGAFLKFSKDKLFKKELNELLKTYVGRPTPLYFARNLSKKYQHEI

YLKREDLNHTGAHKINNAIAQALLAKKMGKKKIIAETGAGQHGLATATAAALLGLECEIYMGATDVQRQA

LNVYKMELLGAKIHAVQSGLKTLKEATTAAIQAWVGDIKNIFYVVGSAVGPYPYPKMVMHFQSIIGKECK

MQLQKLNKKVDYIIAAVGGGSNAAGIFYDFIKDENVKLIGIEAGGLGIDTPYHAATLNKGKTGIIHGMKT

KVLQDDLGNILPVHSVSAGLDYPGIGPLHAFLFESKRAQYHAISDEECMQALKLLCKEEGIIAAIESSHA

LAFLEKLCPTLKKKSVIVVNLSGRGDKDMQMIRDYKKGVIYG

>sp|A8FKC1.1|NDK\_CAMJ8 RecName: Full=Nucleoside diphosphate kinase; Short=NDK; Short=NDP kinase; AltName: Full=Nucleoside-2-P kinase

MEKTLSIIKPDAVKKGVIGKILDRFESNGLRIAAMKKVQLSKEQAENFYAVHKERPFFKDLVEFMISGPV

VVSVLEGEGAVLKNRDLMGATNPKEAKAGTIRADFAESIDANAVHGSDSLENAKIEIDFFFKPNEIC

>sp|A8FKB4.1|EX7L\_CAMJ8 RecName: Full=Exodeoxyribonuclease 7 large subunit; AltName: Full=Exodeoxyribonuclease VII large subunit; Short=Exonuclease VII large subunit

MTPTELNLKAKALLETHFEDIVLSGEISKITLHGSGHWYFDLKDERSSIACAMFKGANLKVGFKPAVGDF

LELCGSVSLYPESGRYQFIATSMKKAGFGDLEAQFLALKERLQKEGLFDPLFKKSLPKFPKKVGIITSKT

SAALQDMLKLIHQKEYFLAKIYIFDALTQGNNAPFSLIQALKKADDMDLDVLIIARGGGSREDLFCFNDE

NLAREIFKAKTPIISAIGHEIDYVISDFVADFRAPTPSAAIDTLFYSKLDIEQSLDLMEEKLMQLWNHKI

QNYENLLLNLSKFFKFNSLPKIIDEKIKQSHNIEKQLNHLLANQMRYNELKLDKLQNAYLQHENFFNKSK

KFICIRKNGKIANLEDLKSDDIVILSSQTSQKEAKIL

>sp|A8FKA1.1|PTH\_CAMJ8 RecName: Full=Peptidyl-tRNA hydrolase; Short=PTH

MILVVGLGNIGVEYENTRHNVGFMLIDLLLKESNFTNLTNSKFKGELFKIGSSLLLLKPSTYMNNSGLSV

KAVNDFYKCERMIVIHDDIDINLGALRFKKGGSSGGHNGLKSIDTLCGNDYERVRIGVGKGENVISHVLG

KFKSEEEITLSKVLEHAKKALLELIENDDLSAISSKYSLKA

>sp|A8FK82.1|SURE\_CAMJ8 RecName: Full=5'-nucleotidase SurE; AltName: Full=Nucleoside 5'-monophosphate phosphohydrolase

MKEILITNDDGYESEGLKKLIKMLTKEFKAKITIVAPASEKSACSHSITLTKPLRFVKVGKRFYKLDDGT

PADCVYLALHALYKKRLPDLVISGINKGANVGEDITYSGTCAGAMEAVLQGIPAIALSQFYKKSEKELDY

KNALQITKKIIQNIFDKGFPLEKKEFLNINFPAKSKIKGIKICKAGKRVYNFEAHSNVNPRGVEYYWLAA

ANLDFEDEKNSDIALLKKGYATITPIMLDLTAYEKMKKVKKWLKANDE

>sp|A8FK75.1|GREA\_CAMJ8 RecName: Full=Transcription elongation factor GreA; AltName: Full=Transcript cleavage factor GreA

MQKEPMSQFGYDKLAAELKDLKDNQRPAVVIEIDTARSHGDLKENAEYHAAREKQALIESRIAELSDLLA

RAQVIDPSSYEHDSVKFGSSVVIMDLDTEKESKYTLVGICEGNLDKGYISIASPIAKAMLGKKEGDDFKV

RLPKGESEFEILSINYEPLKF

>sp|A8FK41.1|MOAC\_CAMJ8 RecName: Full=Cyclic pyranopterin monophosphate synthase; AltName: Full=Molybdenum cofactor biosynthesis protein C

MKLSHLDEKNHPKMVDVSDKNITSRIATASGMIYMSQEAFDVIKNNTAKKGPVLQTAIIAAIMGAKKTSE

IIPMCHPLMLSKVETDIMEFVKECAFKLIVTVKCEGKTGVEMEALSGVSIGLLTIYDMIKAIDKSMRITD

ILLESKEGGKSGKFVRS

>sp|A8FK24.1|RRF\_CAMJ8 RecName: Full=Ribosome-recycling factor; Short=RRF; AltName: Full=Ribosome-releasing factor

MLNEIFNKQKTQSEKSLEALKKDFTTLRTGKVNTHILDHITVDYYGTQTPLNQVATVLASDASTISITPW

EKPLLKTIESAIAAANIGVNPNNDGESVKLFFPPMTREQREENVKQAKAMGEKAKVSIRNIRKDANDAVK

KLEKDKAISEDEAKKAYDEVQKLTDTYTTKIDESVKSKESELLKV

>sp|A8FK14.1|ARGC\_CAMJ8 RecName: Full=N-acetyl-gamma-glutamyl-phosphate reductase; Short=AGPR; AltName: Full=N-acetyl-glutamate semialdehyde dehydrogenase; Short=NAGSA dehydrogenase

MKIKVGILGASGYAGNELVRILLNHPKVEISYLGSSSSVGQNYQDLYPNTPLNLCFENKNLDELELDLLF

LATPHEFSAKLLNENLLKKMKIIDLSADFRLKNPKDYELWYKFTHPNQELLQNAVYGLCELYKEEIKKAS

LVANPGCYTTCSILSLYPLFKEKIIDFNSVIIDAKSGVSGAGRSAKVENLFCEVNENIKAYGLASHRHTP

EIEEHLSYAAKEKITLQFTPHLVPMQRGILISAYANLKEDLQEQDIRDIYTKYYQNNKFIRLLPPQSLPQ

TRWVKSSNFADINFSVDQRTKRVIVLGAIDNLIKGAAGQAVQNMNLMFDFDEDEGLKFFANL

>sp|A8FK08.1|IF3\_CAMJ8 RecName: Full=Translation initiation factor IF-3

MSKEKEVLLNEEIRADEIRCVGDDGKVYGIISSDEALEIANRLGLDLVMIAADAKPPVCKIMDYGKFRYQ

QEKKQKEAKKKQKVIDIKEIKLSVKIAQNDINYKVKHALEFLEQGKHVRFRVFLKGREMATPEAGVALLE

KIWTMIENEANRDKEPNFEGRYVNMLVTPKKA

>sp|A8FJZ8.1|DAPB\_CAMJ8 RecName: Full=4-hydroxy-tetrahydrodipicolinate reductase; Short=HTPA reductase

MIKIGIYGAKGRMGKQIEECLKSETQAQISILYDKGGNLEELFEKSDVIIDFSSPSGTHELLNYARTMPK

PLVIGTTGLDEKILHLMQSASEVMPIFYATNMSLGVAVLNYLASKASQMLKNFDIEILEMHHRHKKDAPS

GTAMTLAQSVAKARNLELEKVRVSGRDGIIGERSKDEIAVMSLRGGDIVGRHTVGFYEDGEFLELNHTAT

SRATFAKGAIKIAIWLSKQEAKMYSINDFLGI

>sp|A8FJX0.1|MOAA\_CAMJ8 RecName: Full=GTP 3',8-cyclase; AltName: Full=Molybdenum cofactor biosynthesis protein A

MLIDQFGRKINYLRISVTQRCNFRCLYCMPKIPFDYQPKENLLSFEELFLFVKAAIDEGIEKIRITGGEP

LLRKDLSIFIKMISDYKSDIDLAITTNGFLLKDFAKDLKNAGLKRLNISLDTLDHKKAKTLAQKDVLDSV

LSGIDEALNLDLKVKLNTVALKNLNDDELISLLEFAKSKKAQIRFIEFMENTHAYGKLQGLKRDEIIQIL

SQKYQIQLIKKDEKAPVSIYKADDYEFGIIDPHSHEFCDSCNRIRLSAEGLLIPCLYFDEALSIKEAVRK

GDIKAAVEILQEVLRNKPEKNKWSVVDNETSSRAFYQTGG

>sp|A8FJT9.1|KHSE\_CAMJ8 RecName: Full=Homoserine kinase; Short=HK; Short=HSK

MKILVPATSANLGPGFDCLGLSLKLFNETQIQKSGVFSISIGGEGSDNIFLKKNNIFVNIFYEIYEKLSG

KKDNFRFIFQNNIPLSRGLGSSSAVIVGAIASAYYMSGFKVEKERILDEALIYENHPDNIAPATLGGFVC

SLVEKNKVYSIKKEIDKDLAAVVVIPNLAMSTEQSRQALAKNLSFNDAVFNLSHASFLTACFLEKKYEFL

KFASQDKLHEINRMKNLPELFEVQKFALENKALMSTLSGSGSSFFSLAFKDDALALAKKMQTKFKDFCVQ

YLEFDDNGFEIC

>sp|A8FJT7.1|LPXC\_CAMJ8 RecName: Full=UDP-3-O-acyl-N-acetylglucosamine deacetylase; Short=UDP-3-O-acyl-GlcNAc deacetylase; AltName: Full=UDP-3-O-[R-3-hydroxymyristoyl]-N-acetylglucosamine deacetylase

MKQLTLAKTVKGVGIGLHKGEPIEITLEPLEANSGIVFFRSDLNASYKASPENVINTQMATVLGDDRGFI

STIEHLMSAINAYGIDNVRIVLNANEAPVMDGSSISFCMMLDEAGVKELDAPKKIMVIKKPVEVRDGNKF

VRLTPTKEPRINYTIKFDNAVIGEQSYNFEFSKKNYIENIARARTFGFLKDVQALRSMNLALGGSLENTI

VVDENRILNPEGLRFKDEFVRHKILDAIGDLTLLGYRVFGDYISYAGSHHLNHLLTKEVLKDKDAYEIVS

LEKTTQKAYEKVFA

>sp|A8FJR3.1|ATPE\_CAMJ8 RecName: Full=ATP synthase epsilon chain; AltName: Full=ATP synthase F1 sector epsilon subunit; AltName: Full=F-ATPase epsilon subunit

MNDLINFEIVTPLGVIYQGEVKSVTLPGSEGEFGVLKGHATLVSSLKSGVIDIEKADLNHELIAIDAGHA

KVDEDKICVLAKGAVWVCGSDESEIEKNLAQAKDLIKSMSSDNAALAATFSKLDNARMH

>sp|A8FJR1.1|ATPG\_CAMJ8 RecName: Full=ATP synthase gamma chain; AltName: Full=ATP synthase F1 sector gamma subunit; AltName: Full=F-ATPase gamma subunit

MSNLKEIKRKIKSVHNTQKTTNAMKLVSTAKLKKAEEAAKRSKIYAQKIDEILSEISFQINKIVHNEDDV

RLSLFHKKEQIKTVDLIFITADKGLCGGFNIKTLKAVSEMLKEYEAKNINIRLRAIGKTGIEYFNFQKIE

LLEKYFHLSSSPDYEKACEVIHAAVDDFLNGNTDEVILVHNGYKNMITQELKINHLIPVEPKSIEQTHNS

LLELEPEGTELLEDLMKTYFEYNMYYALIDSLAAEHSARMQAMDNATNNAKARVKQLNLAYNKARQESIT

TELIEIISGVESMK

>sp|A8FJP1.1|UNG\_CAMJ8 RecName: Full=Uracil-DNA glycosylase; Short=UDG

MEEITINIDKIKINDDWKEFLRDEFQKKYFLEIKKQYLNAINQNIIIYPPANLIFNAFNLCPLKEIKIII

LGQDPYHQPNQAMGLSFSVPKNVKIPPSLNNVFKELQNDLNITPAKSGDLSSWAKQGVLLLNSILSVEAN

KAASHSSWGWQEFSDAIIHKLSNEKSGLVFMLWGNYAKNKEILIDNAKHLILKAAHPSPLARTGFLGCKH

FSKANEFLKKVGKIPIDWKIV

>sp|A8FJM2.1|AROQ\_CAMJ8 RecName: Full=3-dehydroquinate dehydratase; Short=3-dehydroquinase; AltName: Full=Type II DHQase

MKIMIIQGPNVNMLGVREVGIYGAMKMEEIHEQMKLAASQNNVELDFFQSNFEGEIVDKIQECLGTVDGI

IINAAGYTHTSVAIRDAIAAVALPTIEVHISNVYRREEFRQKSLIAPVCSGTIVGFGPFGYHLALMGIIQ

ICEQIKNLRAMQQAQQTNK

>sp|A8FJG5.1|DNAA\_CAMJ8 RecName: Full=Chromosomal replication initiator protein DnaA

MNPNQILENLKKELSENEYENYIAILKFNEKQSKADFLVFNAPNELLAKFIQTKYGKKISHFYEVQSGNK

ASVLIQAQSAKQSSKSTKIDIAHIKAQSTILNPSFTFESFVVGDSNKYAYGACKAISQKDKLGKLYNPIF

IYGPTGLGKTHLLQAVGNASLEMGKKVIYATSENFINDFTSNLKNGSLDKFHEKYRNCDVLLIDDVQFLG

KTDKIQEEFFFIFNEIKNNDGQIIMTSDNPPNMLKGITERLKSRFAHGIIADITPPQLDTKIAIIRKKCE

FNDINLSNDIINYIATSLGDNIREIEGIIISLNAYATILGQEITLELAKSVMKDHIKEKKENITIDDILS

LVCKEFNIKPSDVKSNKKTQNIVTARRIVIYLARALTALTMPQLANYFEMKDHTAISHNVKKITEMIEND

GSLKAKIEELKNKILVKSQS

>sp|A8FLU4.2|AROA\_CAMJ8 RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Short=EPSPS

MKIYKLQTPVNAILENIAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIIKNLGAKIEQKDSCV

KIIPPKEILSPNCILDCGNSGTAMRLMIGFLAGISGFFVLSGDKYLNNRPMRRISKPLTQIGARIYGRNE

ANLAPLCIEGQNLKAFNYKSEISSAQVKTAMILSAFRANNVCAFSEISLSRNHSENMLKAMKAPIRVSND

GLSLEISPLKKPLKAQNIIIPNDPSSAFYFALAAIILPKSQIILKNILLNPTRIEAYKILQKMGAKLEMT

ITQNDFETIGEIRVESSKLNGIEVKDNIAWLIDEAPALAIAFALAKGKSSLINAKELRVKESDRIAVMVE

NLKLCGVEARELDDGFEIEGGCELKSSKIKSYGDHRIAMSFAILGLLCGIEIDDSDCIKTSFPNFIEILS

NLGARIDY

>sp|A8FLU3.1|ISPH\_CAMJ8 RecName: Full=4-hydroxy-3-methylbut-2-enyl diphosphate reductase; Short=HMBPP reductase

MIIELAKNYGFCFGVKRAIKKAEQIKDAATIGPLIHNNEEISRLQKNFNVKTLENIQALSNEKKAIIRTH

GITKQDLEELRKKDIEIFDATCPFVTKPQQICEQMSKEGYEVVIFGDENHPEVKGVKSYVSTKAYVVLDK

KELQNIKLPNKIAVVSQTTKKPEHFMEIVNFLILKTKEVRVFNTICDATFKNQDAIKELSLKSDVMVVVG

GKNSANTKQLFLIAKTNCEDSYLIETEEELKKEWFLDKKHCGISAGASTPDWIIQKVIAKIENFKIN

>sp|A8FL14.1|CMOA\_CAMJ8 RecName: Full=Carboxy-S-adenosyl-L-methionine synthase; Short=Cx-SAM synthase

MKDELFKQSPKKQFEFDKSVASVFDDMINRSVPFYRENLELCGNLLAKILPINASICDLGCSSANFLIFL

ANLRKDFKLFGVDNSASMVEVAKSKAKAYGLDISFFETNLCEFDFFVCDVFVANYTMQFIRPPKRQELLD

KIYKNLNSKGILIMSEKILYEDAFLSKNIIELYADYKEKQGYSKFEIAAKREALENVLIPYSQKENLNML

EKAGFKKIESIFKWANFETFIAFKD

>pdb|5TPV|C Chain C, X-ray Structure Of Wlara (tdp-fucose-3,4-ketoisomerase) From Campylobacter Jejuni

MNYTILKFKTINSKNSILNVHQKDVNCPFEIKRIFYIYDFLDDSIRGDHANLNSEFIFIALNGSCEILID

DGKTKQKIILNNKTKGLYIDKMIWKQMYNFSKDCILLVLTNTYYDEKEYIYDYKYFCELKNNIVWRGGYA

IKTMPLEHHHHHH

>pdb|5TPV|B Chain B, X-ray Structure Of Wlara (tdp-fucose-3,4-ketoisomerase) From Campylobacter Jejuni

MNYTILKFKTINSKNSILNVHQKDVNCPFEIKRIFYIYDFLDDSIRGDHANLNSEFIFIALNGSCEILID

DGKTKQKIILNNKTKGLYIDKMIWKQMYNFSKDCILLVLTNTYYDEKEYIYDYKYFCELKNNIVWRGGYA

IKTMPLEHHHHHH

>pdb|5TPV|A Chain A, X-ray Structure Of Wlara (tdp-fucose-3,4-ketoisomerase) From Campylobacter Jejuni

MNYTILKFKTINSKNSILNVHQKDVNCPFEIKRIFYIYDFLDDSIRGDHANLNSEFIFIALNGSCEILID

DGKTKQKIILNNKTKGLYIDKMIWKQMYNFSKDCILLVLTNTYYDEKEYIYDYKYFCELKNNIVWRGGYA

IKTMPLEHHHHHH

>sp|A8FM57.1|AROB\_CAMJ8 RecName: Full=3-dehydroquinate synthase; Short=DHQS

MQVEVKLKENAYKVYIDELEELEFDSKVFILSNPKISGLHLKTLLSKIKAREIFIAAVKDGEEYKNLSTM

EEILNQMFNSKLDRKSVLISFGGGVISDMGGFAASIYQRGIDFINIPTTLLACVDAAVGGKTGVNNNFGK

NLIGTFYQPKAVYCESSFLKTLSSRELAAGMAEFIKMAAMFDDSILDFIEKIDEKSFLNATCENEIFTQI

IARSIELKSRVVEQDEKESGLRMLLNYGHTFAHVIENFTDYKLYLHGEAVAIGMVMANQLALNLGFLDKM

QSQKIKDILLKFGLPISYKINNVDEFYEAFFMDKKSSNKKINFVLAGPLGKGLIKGDISKEDIIATLREF

Q

>sp|A8FKB3.1|UBIE\_CAMJ8 RecName: Full=Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE; AltName: Full=2-methoxy-6-polyprenyl-1,4-benzoquinol methylase; AltName: Full=Demethylmenaquinone methyltransferase

MQKQEKIIEMFNQIAPTYDKANRILSFGADVVWRKKACQRVMSLYLKKDLKIADIACGTGDMIEIWQESA

LKMEKNILNIKGIDPSSGMLNVAKEKFPNVEFIEAGAQNLPLESQSLDILSISYGIRNVVERQKALSEFA

RVLQKGGILVVLEFTKREKGGFIAACRDFYLKNILPSIGGIISKNKSAYEYLPNSIEGFLSKEEFILELK

NAGFEMLDYKSFSFGVSSMFIAKKL

>sp|A8FN79.1|NADD\_CAMJ8 RecName: Full=Probable nicotinate-nucleotide adenylyltransferase; AltName: Full=Deamido-NAD(+) diphosphorylase; AltName: Full=Deamido-NAD(+) pyrophosphorylase; AltName: Full=Nicotinate mononucleotide adenylyltransferase; Short=NaMN adenylyltransferase

MKIALFGGSFDPPHNGHNSVVLEALEKLDIDKLIIMPTYINPFKQSFSADEKQRFLWVKKLWGHLPKVEI

CDFETKQKRPVPSIESVKYLYKLYNPSKFYLLIGADHLEKLHLWHDFEKLNSLVEFVIANRNDIEIPKNF

KDLKTDKKIASSFIRNTLNTNEVCEEIKDEVKKYYEKLQKN

>sp|A8FLV4.1|ALR\_CAMJ8 RecName: Full=Alanine racemase

MSLIKIDQKAYEYNLRHIAKKIGSFQRLICVFKDNAYGHGAKLLAPLAKNLGVSFVAVKSEEEAQEIEEF

FENILILSHRPHGNENSRFIYALNDISQVKKYKQDIKIHLKIDTGMHRNGICVENLEHAIDLIRSSDLKL

TGMFTHFASADEMDGSFFVQKENFQKAKKIVKKYFSNLLFHSHNSAALFRGKIPEDEYCRVGLVQFGYGD

SNLKRVLSLYAHRLSQRILQKGQSIGYGGIFTAAKDMEVATYDLGYADGLFRYNGKGELVLGNGKVMLGK

MSMDSFSCENSGEEICVFKDADIWADFFHTINYEILVKLNPNIQRVLV

>sp|A8FMK7.1|GMHA\_CAMJ8 RecName: Full=Phosphoheptose isomerase; AltName: Full=Sedoheptulose 7-phosphate isomerase

MINLVEKEWQEHQKIAQESEILKGQIAKAGELLCECLKKGGKILICGNGGSAADAQHFAAELSGRYKKER

KALAGIALTTDTSALSAIGNDYGFEFVFSRQVEALGNENDVLIGISTSGKSPNVLEAFKKAKELNMLCLG

LSGKGGGMMNKLCDHNLVVPSDDTARIQEMHILIIHTLCQIIDEGF

>sp|A8FM88.1|MURG\_CAMJ8 RecName: Full=UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase; AltName: Full=Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase

MTIALTGGGTGGHLAIVRCLLESAIKKNIECVYIGSQNGQDKAWFENEVRFKEKFFLSSKGVVNQSKFGK

ISSLLHTLKLSKDCREIFKKYHIQAVFSVGGYSAAPASFAALFSHLPLFIHEQNSKSGSLNMLLKPFATK

FFSAFEKEISPYPVADKFFDNARIRKELKNIIFLGGSQGAQFINELALNLAPKLQEQNIKIIHQCGKNDF

EKCKKHYQSLNIQADIFDFSLNLEEKMKNADLAISRAGASTLFELCANTLPTIFIPYPYAAKNHQYFNAK

FLQDQALCQIFMQNSINLDEFFKSILKLNLENISTRLQNITQKNGADMLIQKALFDNLTFIR

>sp|A8FMH1.1|CHEY\_CAMJ8 RecName: Full=Chemotaxis protein CheY homolog

MKLLVVDDSSTMRRIIKNTLTRLGHDDVLEAEHGVEAWDLLTKNEDVKVLITDWNMPEMNGLELVKKVRA

EKKYEDMPIIMVTTEGGKAEVITALKAGVNNYIVKPFTPQVLKEKLEDVLGTGSGEGAAE

>sp|A8FLC2.1|RSMH\_CAMJ8 RecName: Full=Ribosomal RNA small subunit methyltransferase H; AltName: Full=16S rRNA m(4)C1402 methyltransferase; AltName: Full=rRNA (cytosine-N(4)-)-methyltransferase RsmH

MEIPHIPVLLNEVQEIFKNLKTGYFLDCTLGFGGHSEALLKNHPDLKFIACDQDQQALEFSKKRLKDFHN

RITFIQSNFSEVLEKISYKEELRGILADIGVSSFQLDNNERGFSVNSDFLDMRMNQNSKISAYEIINTYT

KEQLTSIFKDYGELHDAHFIAEKICLERSKNPIKSAKELYQIIGKGKQNHRKISKATLAFQAIRIEVNQE

LKVLKDFLGHLENLKPKNCILAIISFHSLEDRIVKNFFKKWSKNCICDEKIMRCECGNNHSLGQIITKKA

ISASKEELLKNSRSSCAKMRAFYFNNLDNK

>sp|A8FP27.1|RLMN\_CAMJ8 RecName: Full=Dual-specificity RNA methyltransferase RlmN; AltName: Full=23S rRNA (adenine(2503)-C(2))-methyltransferase; AltName: Full=23S rRNA m2A2503 methyltransferase; AltName: Full=Ribosomal RNA large subunit methyltransferase N; AltName: Full=tRNA (adenine(37)-C(2))-methyltransferase; AltName: Full=tRNA m2A37 methyltransferase

MKELVNILDFLPEELGEKIKPMFRVKQIYQWIYQKYANNFSDMSSLPKYLRLELAQNFHFSPVKCVKNEQ

SKDGSIKYLFELVDGLRVESVLLPMKEEKIDAEGKRISHARYTICVSSQVGCKSGCSFCLTAKGGLKRNL

SAGEIVGQILWIKKQNNIPYERRVNIVYMGMGEPLDNLKNVSKAVKILAQNDGLAISPRRQTISTSGLAK

QIKELGQMNLGVLLAISLHAVNDGLRTELMPINKAYNIAAIMDAVREFPIDQRKRVMFEYLLIDGINDKL

EHAKELVKLLNGIKAKVNLILFNPHEGSLYKRPSLENAIKFQDLLSSKGVTCTIRESKGLDISAACGQLK

ERAKEQ

>sp|A8FNB6.1|Y1355\_CAMJ8 RecName: Full=UPF0306 protein C8J\_1355

MDERILEFIKNEQLLSWAMIDEKGVYTASAFYAFDEKNLAFIIASHEDTKHIRLASENSSIALNIAKESK

IAFLKGVQAKAEFKMASKEQMKIYFSKFPFAKFDKSAKIYALELFWLKFTNNALGLSKKLEFYKK

>sp|A8FN54.1|IXTPA\_CAMJ8 RecName: Full=dITP/XTP pyrophosphatase; AltName: Full=Non-canonical purine NTP pyrophosphatase; AltName: Full=Non-standard purine NTP pyrophosphatase; AltName: Full=Nucleoside-triphosphate diphosphatase; AltName: Full=Nucleoside-triphosphate pyrophosphatase; Short=NTPase

MKIILATSNKHKVLELKEILKDFEIYAFDEVLMPFEIEENGKTFKENALIKARAVFNALDEKQKKDFIAL

SDDSGICVDVLEGNPGIYSARFSDKGDDKSNRDKLVNEMIKKGFNQSRAHYVAAIAMVGLMGEFSTHGTM

HGKVIDTEKGENGFGYDSLFIPKGFDKTLAQLSVDEKNNISHRFKALELAKIILKILNKG

>sp|A8FM27.1|CMOB\_CAMJ8 RecName: Full=tRNA U34 carboxymethyltransferase

MQENLLEKQFLNHPLYTKIQELKALNLACNFSLDDSVNLSTNSQAKDEILAITKELKPWRKGPFKIDDLF

IDTEWQSFIKFNILKPFMNEISQKCVADIGCNNGYYMFKMLEFNPAKLIGFDPSIKYRLQFELINALAKT

PIEYELLGVEDLPRYGLKFDVIFCLGVIYHRSDPIKMLKDLKAGLNKNGVVFLDTMYIEDEREIALVPNK

TYSKIPNIYFVPSISALKNWCERAGFKEFEVLATKKTDENEQRKTEWIDSFSLENFLDPKDKNLTIEGYE

APKRVYVRIGI

>sp|A8FKI9.1|GLYA\_CAMJ8 RecName: Full=Serine hydroxymethyltransferase; Short=SHMT; Short=Serine methylase

MSLEMFDKEIFDLTNKELERQCEGLEMIASENFTLPEVMEVIGSILTNKYAEGYPGKRYYGGCEFVDEIE

TLAIERCKKLFNCKFANVQPNSGSQANQGVYAALINPGDKILGMDLSHGGHLTHGAKVSSSGKMYESCFY

GVELDGRIDYEKVREIAKKEKPKLIVCGASAYARVIDFAKFREIADEIGAYLFADIAHIAGLVVAGEHPS

PFPHAHVVSSTTHKTLRGPRGGIIMTNDEELAKKINSAIFPGIQGGPLMHVIAAKAVGFKFNLSDEWKVY

AKQVRTNAQVLANVLMDRKFKLVSDGTDNHLVLMSFLDREFSGKDADLALGNAGITANKNTVPGEIRSPF

ITSGLRLGTPALTARGFKEKEMEIVSNYIADILDDINNEKLQENIKQELKKLASNFIIYERAMF

>sp|A8FM42.1|Y930\_CAMJ8 RecName: Full=UPF0763 protein C8J\_0930

MKELEKYSTCLKRIDEFSQNLGIKKKDRTIFKMKQSENENEKCLVLENGSFDSPEPWFVIDENDEIHTLL

SLQSLKNILESLKQSQKENFELRLEKAIYQQIPVDFNDVWTVAMDEIKQKAQNGTMEVSIDLEKLISKIK

QEHPNLFVDMQAMIERVNQNERL

>sp|A8FNN4.1|NUOD\_CAMJ8 RecName: Full=NADH-quinone oxidoreductase subunit D; AltName: Full=NADH dehydrogenase I subunit D; AltName: Full=NDH-1 subunit D

MQIPSKLKPYYENIAFEQEDSKMIINLGPQHPSAHGNLRLILELDGEQVVKARPCIGYMHRGMEKMAENM

IYQEFIPTTDRMDYIAASANNYAYCAAVEKLCGLEIPRRAAVIRMILLELNRIASHLLWLATHALDIGAM

SVFLYCFREREYVLDLIEKYCGARLTHSSMRIGGVMLDLPENYLEEMLVFCDKFPNDLKDYEDLLDDNRI

WRLRTENVGVVTKEQALNWGCTGVMLRGSGIKYDIRKEEPYLLYNEVEFGVPYATQGDSYARYKVYMQEF

RESLKILRQCATLYKDTPPEILATHPEYVSASKEQILTQNYSLMQHFVLITQGLKPPKGEVYVPTESPKG

ELGFFIHSDGTGRPYRLKARTPSYWHCAFFEEMLVGTYLADVVAIMGNVNIVLGEIDR

>sp|A8FKP3.1|MIAB\_CAMJ8 RecName: Full=tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase; AltName: Full=(Dimethylallyl)adenosine tRNA methylthiotransferase MiaB; AltName: Full=tRNA-i(6)A37 methylthiotransferase

MSAKKLFIQTLGCAMNVRDSEHMIAELTQKENYALTEDIKEADLILINTCSVREKPVHKLFSEVGGFEKV

KKEGAKIGVCGCTASHLGNEIFKRAPYVDFVLGARNISKITQAIKTPKFMGVDIDYDESEFAFADFRNSI

YKSYINISIGCDKHCTYCIVPHTRGDEISIPFNIIYKEAQKAVEKGAKEIFLLGQNVNNYGKRFRNEHKK

MDFSDLLEELSTIEGLERIRFTSPHPLHMDDKFLEVFANNPKVCKSMHMPLQSGSSEILKAMKRGYTKEW

YLNRALKLRELCPNVSISTDIIVAFPGESEKDFEETMDVLEKVRFEQIFSFKYSKRPLTKAATMPNQIDE

ETASRRLSTLQNRHSEILDEIVKKQENKTFKVLFEELRAGNSIAGRTDNNFLVQVEGSEELLGQFKEVKI

TNAKRMVLYGEIV

>sp|A8FMV3.1|GUAA\_CAMJ8 RecName: Full=GMP synthase [glutamine-hydrolyzing]; AltName: Full=GMP synthetase; AltName: Full=Glutamine amidotransferase

MKKADILVLDFGSQYTQLIARRLREQGVYAEILPFNVSLADIKAKEPKGIILSGGPASVYATDAYFCDKG

IFDLGLPILGICYGMQLMAHHYKATVAPAGHKEYGKANIEVKKDSALFKNLPKKQTVWMSHSDKVENLPQ

GFEVLATSENSPFCVFGNEDKKFFALQFHPEVQHSEFGKNILKNFAKYACNCESVWNMGSFAKTQAEKIR

EEVGSDKVLCAVSGGVDSSVVAALLASAIKEQVIVVFVDNGLLRSGEKEQVEFMFKNTLGIDLISIDASE

IFLSRLANVRDPEQKRKIIGNTFIEVFEEEAKKHKDVKYLAQGTLYTDIIESSVVGASKTIKSHHNVGGL

PEKMNLKLIEPLKEIFKDEVRALGLELGLSKEVVYRHPFPGPGLAIRIMGEVNRPSLELLRKADVILLEE

LKSTGWYDKTWQAFCVLLNIKSVGVMGDNRTYDNAVCIRVVDASDGMTATFSHLPYEVLENISRRIINEV

EGINRVVYDISSKPPATIEWE

>sp|A8FJJ0.1|PYRG\_CAMJ8 RecName: Full=CTP synthase; AltName: Full=Cytidine 5'-triphosphate synthase; AltName: Full=Cytidine triphosphate synthetase; Short=CTP synthetase; Short=CTPS; AltName: Full=UTP--ammonia ligase

MKQTKYIFVTGGVLSSLGKGIAAASIATLLKNSGLKVSILKADPYINVDPGTMSPFEHGEVFVTDDGAET

DLDLGHYERFLDESLSQDNNFTTGRVYQSVIEKERRGEYLGKTIQVIPHIVGEIKDRIKKAGEGKDILIV

EIGGTVGDIEGLPFLEAIRALRLEVGKNNAMNIHLTLVPFIKAAGELKTKPTQHSVGELRRIGISPDMII

CRSEKALDRDLKDKIAISCGVEKNCVIESVDAASIYQIPLNFLKQDILSPIAEILDLKNLKPNMENWDSL

VKRVIAPSNEVKIAFVGKYVDLKESYKSLTEAIIHAGAALDTKVELKWVDSEKLENMESAEVFKDVSGIL

VAGGFGYRGVEGKIKAIQYARENKIPFLGICLGMQLALVEFARNVLKLKDANSSEFDEKCQNPVVYLIDE

FMDTNGEKQIRTAKTPLGGTMRLGAYKCDIKEKSLLAKVYNEAKSVKERHRHRYEANPKYRVDFEKHGLI

VSGESKGLIEAVELNCHPFFLAVQFHPEFTSRLEHVNPVICGFIKAAINYEDN

>sp|A8FJW4.1|RL31\_CAMJ8 RecName: Full=50S ribosomal protein L31

MKKEIHPEYVECKVSCACGNTFTTKSNKAELRVDICSNCHPFFTGSEKIVDAAGRVEKFKKKYAMQ

>sp|A8FKD6.1|TRPF\_CAMJ8 RecName: Full=N-(5'-phosphoribosyl)anthranilate isomerase; Short=PRAI

MLKLKICGIKDEKNAKDLAFLNIDFFGFIFAKSPRRVSLEQARNLSAIFHEKDKKVVGVFVDENLEQILR

CIKEAKLDGIQIYRTITKEEFEILKVQNVFVWQVISVENSLDLKSEIFANLVLFDAKGILKGGNGISFDW

TLLGSYTKDFILAGGIGLDNVHKAVQTGAKILDLNSKLEDEKGLKDINKIKQILKELKK

>sp|A8FLP9.1|F16PA\_CAMJ8 RecName: Full=Fructose-1,6-bisphosphatase class 1; Short=FBPase class 1; AltName: Full=D-fructose-1,6-bisphosphate 1-phosphohydrolase class 1

MQEVISYIQKAVLEISNALKFPDTSYSQNQNFTGDTQLKFDVLSDGIITKTLSQCSSIKAIISEEKDEIL

TLNERANFIVAYDPLDGSSLMDVNFAIGSIFAIYEEKASAKNLRAALYSMYGARLELVICKDQPKLYRLN

ANNEFIFIKDLKMNEKGKINATGGTQKFWEEKHAKFIKSLFDEGYRLRYSGAMVSDINQILLKGGGIFSY

PATQDAPNGKLRAFFEVFPLAFIIEKAGGKTTNGKNHSLLELEFDKIHATTPCFFGSEYEISKLLKAYNE

>sp|A8FKQ6.1|RL33\_CAMJ8 RecName: Full=50S ribosomal protein L33

MRIKVGLKCEECGDINYSTYKNSKNTTEKLELKKYCPRLKKHTLHKEVKLKS

>sp|A8FLM3.1|NADE\_CAMJ8 RecName: Full=NH(3)-dependent NAD(+) synthetase

MDWQKITEKMCDFIQEKVKNSQSQGVVLGLSGGIDSALVATLCKRALKENVFALLMPTQISNKANLEDAL

RLCADLNLEYKIIEIQSILDAFIKQSENTTLVSLGNFAARIRMSLLYDYSALKNSLVIGTSNKSELLLGY

GTIYGDLACAFNPIGSLYKSEIYTLAKYLNLHENFIKKAPSADLWENQSDEADLGFSYAKIDEGLKALET

NDEKLLRTLDPSLIAMLKNRMQKNTFKGKMPEILEI

>sp|A8FP05.1|RL18\_CAMJ8 RecName: Full=50S ribosomal protein L18

MRANVLKRKLTLRIKRKKRIRAKISGCENFPRISVFKSNRTLYIQAIDDVKAVTLAAVDGRKLGVKANKE

GAKKIAAEFAKTLKAKKIEQAVFDRNGYVYHGVIAALAESLRENGIRL

>sp|A8FNS3.1|RF1\_CAMJ8 RecName: Full=Peptide chain release factor 1; Short=RF-1

MLASKLDPFLKRFEELNSLLSSSDILNDISKMTTLSKEQKNLEPIVLKAKEYLKTLDNIEENKALLNDPE

LGELAKEELKTLEELKPKLEEEIKILLLPKDPNDERNIFLEIRAGTGGDEASLFVGDLVKAYARYAENRG

YKLEIVSSSEGSVGGFKEIIMLVKGTGAYSRLKYEGGTHRVQRVPQTESQGRVHTSAITVAVMPEVDDIE

IEINPNDLKVDVMRSSGHGGQSVNTTDSAVRITHIPTGIVVVNQDGKSQHKNKESAMKVLKARLYEMQES

ERLAKESEARKSQVGSGDRSERIRTYNFPQNRISDHRINLTLYRLDAIMQDGLFDEIIEPLITHHQAQAL

QEQNL

>sp|A8FNR4.1|HIS6\_CAMJ8 RecName: Full=Imidazole glycerol phosphate synthase subunit HisF; AltName: Full=IGP synthase cyclase subunit; AltName: Full=IGP synthase subunit HisF; AltName: Full=ImGP synthase subunit HisF; Short=IGPS subunit HisF

MLTKRIIACLDVKDGRVVKGTQFKNHKDMGDIIELARYYSQNGIDELVFYDIAASARKERISREWVSEVA

KNINIPFCVAGGIKSEEDAAELLANGADKISINSPALNDPSLITRLAKSFGVQCVVVGIDSFKDENGNLK

VFQYTGDEKTSKHSGKSTLEWVKEVQDLGAGEIVLNMMNQDGVKNGYDLEQLKAVYKICKVPLIASGGAG

KMEHFLEAFKLGIDGALAASVFHQKLIDIKELKIYLKNQGLSIRI

>sp|A8FNR3.1|HIS4\_CAMJ8 RecName: Full=1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase; AltName: Full=Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase

MTQIIPALDLIDGEVVRLVKGDYEQKKVYKYNPLEKFKEYEKAGAKELHLVDLTGAKDPSKRQLALIEKL

AKEVNVNLQVGGGIRSKEEVKALLDCGVKRVVIGSMAIKDATLCLEILKEFGSEAIVLALDTILKEDYVV

AVNAWQEASDKKLMEVLDFYSNKGLKHILCTDISKDGTMQGVNVRLYKLIHEIFPNICIQASGGVASLKD

LENLKGICSGVIVGKALLDGVFSVEEGIRCLQNA

>sp|A8FNQ9.1|HIS1\_CAMJ8 RecName: Full=ATP phosphoribosyltransferase; Short=ATP-PRT; Short=ATP-PRTase

MQENTRLRIAIQKSGRLSKESIELLSECGVKMHIHEQSLIAFSTNLPIDILRVRDDDIPGLIFDGVVDLG

IIGENVLEENELERQSLGENPSYKLLKKLDFGYCRLSLALPQENKFQNLKDFEGLRIATSYPQLLKRFMK

ENGINYKNCMLTGSVEVAPRANLADAICDLVSSGATLQANNLKEVKVIYESRACLIQKENALSKEKQALV

DKIMLRVAGVMQARESKYIMLHAPKEKLDKIQALLPGVERPTILPLAHDEKNVALHMVSKENLFWETMEA

LKEEGASSILVLPIEKMLK

>sp|A8FNN0.1|NUOH\_CAMJ8 RecName: Full=NADH-quinone oxidoreductase subunit H; AltName: Full=NADH dehydrogenase I subunit H; AltName: Full=NDH-1 subunit H

MSDFAFFALEALIKCIIIIAIFASLAGLATYAERKVLAYFQRRIGPDMVGPFGLIQLVADMIKLFTKEDI

IPSNSQKFIFAIAPLISAICAFVSLAAIPMLPEFTLFGRVIQPIVADINVALLFVIGTSGLCFYAVFLGG

LASNNKWSILGAARGLVAIISYESVGALALIAIVMLVGSFSLVDINNYQSDGFFSWLIFKQPLAFVLFII

ALFIETNRTPLCLTENDAEIVAGYGTEYSGLRWGMFFIGEYASMIAGAILVTLLFLGGFNSFWIIPGWIM

MIVKSSFIFFWYFWARAAFPQLRPDQVMKMCYLILIPLAVLNLLITALAVLL

>sp|A8FNJ7.1|ACSA\_CAMJ8 RecName: Full=Acetyl-coenzyme A synthetase; Short=AcCoA synthetase; Short=Acs; AltName: Full=Acetate--CoA ligase; AltName: Full=Acyl-activating enzyme

MLNQNNQELFKPSKEFSRNARIKNLCEYYDLCDEAKEDFEGFWKRQALEKIEWFSPFSRVLNEDKAPFYK

WFEGGTLNVSYQCLDRHMKTRRNKAALIFEGEMGDYEVYTYRRLLHETCKAANLLKKFGVKKGDRVVIYM

PMIPETAIVMLACARIGAIHSVVFGGFSPEALRDRIIDAGAKLVVTADGAFRRGKPYMLKPAVDKALSEG

CESVEKVLIVIRNNEPIEYIKGRDYVYNELVKNESYKCEPEIMDSEDLLFLLYTSGSTGKPKGVMHASAG

YILWAQMTMEWVFDIKDYDNYWCSADVGWITGHTYVVYGPLACGATTIMHEGTPTYPNSGRWWRMIEEYQ

ISKFYTSPTAIRMLHADAPDEPRKYDLSTLEVLGTVGEPINPSAWKWFYDEIGGTKSPIVDTWWQTETGG

HMITPLPGATPLKPGCATLPLPGIFAEVIDEEGNKKDEGEDGLLCITKPWPSMIRGIWGNDERYIESYFS

QAKKDGKAVYFSGDGAFYDKNGYITITGRTDDVVNVAGHRIGTAEIESAIAKHPSVAESAVVSILDAIKG

ESLFAFVVLSPASSCDLGGAIETLKELNDILRVEIGPIAKIEKILYTPGLPKTRSGKIMRRILRTIARGE

EIKQDISTLEDSGVVETIVKLAKAEFE

>sp|A8FNJ1.1|DAPF\_CAMJ8 RecName: Full=Diaminopimelate epimerase; Short=DAP epimerase; AltName: Full=PLP-independent amino acid racemase

MKFYKYCASGNDFVITNADRKEDRSALAKELCNRYEGIGADGFIVILPHEKYDFEWEFYNNDGSRAAMCG

NGSRAAAHFVHHINKINPNMSFLTGAGVIKAKVNQDKVEVSLGKIKSVQNTFEELGKTWQLCNTGVPHLV

HFCQNLDEFDTMLCQKMRQKYNANVNFVKILDENHLKVRTYERGVEDETLACGTGMGACFYLAFLNKKVQ

NKVKITPKSGEEVGFAYKNEELFFEGKVKYCFEANYNFS

>sp|A8FNG4.1|PURA\_CAMJ8 RecName: Full=Adenylosuccinate synthetase; Short=AMPSase; Short=AdSS; AltName: Full=IMP--aspartate ligase

MSKADIIVGIQWGDEGKGKVVDKLCENYDFVCRSAGGHNAGHTIWVNGVRYALHLMPSGVLHPRCINIIG

NGVVVSPEVLIAEMAQFENLKGRLYISDRAHLNLKHHSLIDIAKEKLKGKNAIGTTGKGIGPSYADKINR

TGHRVGELLEPQRLCEALMKDFEANKTFFEMLEIEIPSAEELLADLKRFNEILTPYITDTTRMLWKALDE

DKRVLLEGAQGSMLDIDHGTYPYVTSSSTISAGALTGLGLNPKEAGNIIGIVKAYATRVGNGAFPTEDKG

EDGEKIAQIGKEIGVSTGRKRRCGWFDAVAVRYTARLNGLDALSLMKLDVLDGFEKIKICRAYEYKGMEI

DYIPSDLENVQPIYEEMDGWDKVFGIKDYDLLPENAKKYIARLEELAGVKVKYISTSPERDDTIIL

>sp|A8FMY4.1|TRMB\_CAMJ8 RecName: Full=tRNA (guanine-N(7)-)-methyltransferase; AltName: Full=tRNA (guanine(46)-N(7))-methyltransferase; AltName: Full=tRNA(m7G46)-methyltransferase

MPNFKSKKIKEINLPYSKDDVEFLWLAKNDNVSLIYTKVQEESFFLQIKKAQNGFVIKGDKHTKPSKIGY

LQKALKIFKEGFCEDIINEAFGLKNNALIEKTPFIVDNFDELLSKLQGKIYIEIGFGSGRHLLYQAKENP

NVLILGVEIYNPALTQVAKLAKVQNVNNILLIQSDARLLLSVLKSKSVEKIFLHFPVPWDKKPHRRVIGK

DFCKECARVLTQNGRFELRTDSFEYFNFTLEQFLTFPAPKFSLRKNENLEISSKYEDRWKKQEKNIYDLW

VWNFNQECKNYELNEFNLSSVEFSKEDLKKIEQNFKNITIKKDDFFLHFESIYKQDENLLLKVAFGAFNK

PEHCYLHLDKTIDFVFKEPFKIQENIKAINELKEILKVQFKI

>sp|A8FMQ7.1|METE\_CAMJ8 RecName: Full=5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase; AltName: Full=Cobalamin-independent methionine synthase; AltName: Full=Methionine synthase, vitamin-B12 independent isozyme

MKNSIISYPRIGANRELKFAIEKYFKNQSSKEELLKSAKDLRIRHWQEIQKAGIDFIPSNDFSLYDNVLD

AAVLFNIVHTKYKNLNLDALDEYFAQSRGYQGENGDVTALAMKKWFNTNYHYLVPECDNADIIALTGDKI

FKEYLEAKELGIESKPVLIGIFTLFKLIAFKDEKTQKLAKEKLLNAYIELFDKLNELKVTWLELDEPYLV

YDLSKEDIALFEEFYQELLNHKKDLKILLQSYFGDLRDIYPKLLESKFDALGLDFIEGKQSLALIQKYGF

AKDKILFAGLINGKNIYANDYAKSLKLIKELQKYTQNIVLNTSCSLLHVPYSTEFESKLDSSYLKLFAFA

KEKLQELKDLKEILNSSEENPLFRANQELFKNIPERLDEKVKARLKALKKEDFTRTPSFKERALIQKEFL

KLPLLPTTTIGSFPQSADVRSNRLAFKQEKISAQNYTEFNQQKIKECIQIQEEIGLDVLVHGEFERNDMV

EYFGENLKGFLFTQNGWVQSYGTRCVKPPVIWGDVSRTKPITLAWSKFAQSLSQKIVKGMLTGPVTILNW

SFPREDISLKESTEQIALAIRDEVLDLENAGIKIIQIDEAALREKLPLRKSDWHSEYLDWAIPAFNLVHS

GVKAKTQIHTHMCYSEFSDILKEIDAMDADVISFEASRSNLSLLDTLKAIRFKTEVGPGVYDIHSPRVPS

VEELSLTIEKILNKLPKEQIWINPDCGLKTRAYEEVIASLKNLVTATQKIREQL

>sp|A8FMN2.1|TATA\_CAMJ8 RecName: Full=Sec-independent protein translocase protein TatA

MGGWSSPSHWLIILLIVVLLFGAKKIPELAKGLGKGIKTFKDEMNNDDEVAKNTQKIEENKNTTNNTSAD

ASIDKTKKA

>sp|A8FMK8.1|HLDE\_CAMJ8 RecName: Full=Bifunctional protein HldE; Includes: RecName: Full=D-beta-D-heptose 7-phosphate kinase; AltName: Full=D-beta-D-heptose 7-phosphotransferase; AltName: Full=D-glycero-beta-D-manno-heptose-7-phosphate kinase; Includes: RecName: Full=D-beta-D-heptose 1-phosphate adenylyltransferase; AltName: Full=D-glycero-beta-D-manno-heptose 1-phosphate adenylyltransferase

MLEFLSQQKPKILIIGDFMVDNYTWCDCSRISPEAPVLVAKTLKEDKRLGGAANVYANLKSLGADVFALG

VVGDDKSGKFLQENLKGEFLIQKGRKTPFKNRIMAHNQQVLRLDEEDISAILLENELIALFDEKIKDFKA

VVLSDYAKGVLTPKVCKAVIKKAKALNIPVLVDPKGSDFSKYSGATLLTPNKKEALEALKFENLEGENLE

KGIKKLKEDFALRYSIITLSEAGIALFDEGLKIAPAKALEVYDVTGAGDSVIAVLAFCLASGIEIFKACE

LANEAAAVVVSKIGSMSVSFDEIKSFNRVDFEKKIKSKEELLTLLKQNDKKIVFTNGCFDIVHFGHIKYL

EKAKRLGDVLIVGLNSDASVKRLKGESRPVNSEFQRACMLAAFYFVDFVVIFDEDTPLELISFLKPDILI

KGADYKDKLVVGADIVSKVELIDFEEGFSTSKIIEKIKDKK

>sp|A8FMH0.1|PRMA\_CAMJ8 RecName: Full=Ribosomal protein L11 methyltransferase; Short=L11 Mtase

MQKKYYELFFIVEERYKNLFLDFAFDLGIEAIEEKDNGVYIRSHESLEELSWALEIFAQKLTTTFNLNHK

IISNLSLVEKENKDWIQEYKKGIKPILVDNVYIHTTWQEEKKNFINIKINPALAFGSGHHESTYSCVKFL

QKFSKSKLRALDLGCGSGILGIIMAKFGCNVEICDTDELAIDSSLENARLNGVDFHKAWCGSIDKANGLY

NLIVANIIADVILILEKDIKNHLEDNAILILSGILDKYSTRIKEKFQDLELIDEMQINEWCSFVYKNNKK

G

>sp|A8FMG2.1|LFTR\_CAMJ8 RecName: Full=Leucyl/phenylalanyl-tRNA--protein transferase; AltName: Full=L/F-transferase; AltName: Full=Leucyltransferase; AltName: Full=Phenyalanyltransferase

MESSNLYSKLLNAPKNAPVFLSQNLEADFIVKAYTFGLFPWTSKPVTWWCPDPRCILIPNQIHIQKNMKK

FINLYQIKLDYDFLKLITLCRDTRSQSWIDDEFITTYYKLFTQGYAHSLELYENNELIGGIYGLILGKVF

FGESMVSIKKNASKVAMIKLCDLLKPYDFIIDCQVYNQHLEFMGAHNISRKEFLNILKEKCNQESGFKNF

KDLIT

>sp|A8FMG0.1|CLPS\_CAMJ8 RecName: Full=ATP-dependent Clp protease adapter protein ClpS

MPKTQTLEQTKLSEPKMYKVILLNDDVTTMDFVIEILMNIFHQNLEKASQTMLEIHHNGSGICGIYTQEI

ALSKQKKVIDAAKLANFPLQAKVEEE

>sp|A8FM46.1|RSMG\_CAMJ8 RecName: Full=Ribosomal RNA small subunit methyltransferase G; AltName: Full=16S rRNA 7-methylguanosine methyltransferase; Short=16S rRNA m7G methyltransferase

MIFKDYDFLQNYDLKNFEEKIKIYKELLSKFNRIHNLTHLKNIDENIFDSIKILDFYDFSKAKNIADIGS

GAGFPAVFLAFLLQNNFHLFEPNPKKAAFLRTLKIECELSNLHIYKEKVQEYQNIFKADIITSRALMDVK

PLLEICKNLKDENTVFILWKGSEIYQELENIKDYEIFENNLRKYCILK

>sp|A8FM15.1|RL34\_CAMJ8 RecName: Full=50S ribosomal protein L34

MKRTYQPHGTPRKRTHGFRVRMKTKNGRKVINARRAKGRKRLAV

>sp|A8FM14.1|RNPA\_CAMJ8 RecName: Full=Ribonuclease P protein component; Short=RNase P protein; Short=RNaseP protein; AltName: Full=Protein C5

MKNFDKFSTNEEFSSVYKVGKKWHCEGVIIFYLNSYEKKIAVVASKKVGKAVVRNRSKRILRALFAKFER

YLQDGKYIFVAKNEITELSFSRLEKNLKWGLKKLECFK

>sp|A8FLY1.1|PCKA\_CAMJ8 RecName: Full=Phosphoenolpyruvate carboxykinase (ATP); Short=PCK; Short=PEP carboxykinase; Short=PEPCK

MKKFDNLGLDNIKEIFHNLSYDELNAHEKANNEGLSTDNDTFCVDTGIFTGRSPKDKYFVKQDPSSKYIA

WGKINQPITKELFDKLLTKAKQELSGKKIYVQDAFCGASLQSRKAVRFVTEIAWQAHFVKNMFIRPSQEE

LENFKADFIVYNACKCINEDYKQDGLNSEVFVIFNVEENIAVIGGTWYGGEMKKGIFSMMNYWLPLENKL

SMHCSANVGEKDDVALFFGLSGTGKTTLSTDPKRRLIGDDEHGWDDEGVFNFEGGCYAKTINLDPEHEPE

IYGAIKRNALLENVVLRADKSVDYADASKTENTRVSYPIEHIENHEPSLKAGHPKNIIFLSADAFGILPP

VSKLSKEQAMYYFLSGYTAKVAGTERGITEPQATFSACFGEPFMPLHPTVYARLLGEKIEKHEVNVYLVN

TGWSGGSYGVGKRMSIKATRACINAILDGSIAKCEFENFEVFNLAIPKALEGVESTLLNPINTWLDKNAY

TETRDKLAHMFVQNFKRYEDVKEGIEFSKFGPKI

>sp|A8FLX6.1|APT\_CAMJ8 RecName: Full=Adenine phosphoribosyltransferase; Short=APRT

MIKLTQEEQKYLLDSIRIIPDFPKKGIIFRDITTLLNNKEALNFLLKHLKERYKDYNLDFIAGTESRGFI

FASMICAKLNLPFVPIRKPGKLPFETFSCEYDLEYGSDKVELHKDAFKNIQNARVLLVDDLIATGGTAIA

SYELIQKAGAKCVEACFLMNLKDLNGANKLEKLTSVYSVLEI

>sp|A8FLR2.1|GSA\_CAMJ8 RecName: Full=Glutamate-1-semialdehyde 2,1-aminomutase; Short=GSA; AltName: Full=Glutamate-1-semialdehyde aminotransferase; Short=GSA-AT

MTNKKAFKEACKFIAGGVNSPVRAFANVQSEPKFISHGKGAYIFDIDGNSYIDYVQSWGPLLFGHCDKDI

QKACQKALHKGSSFGAPTLLETELAKLVLSDFPHLEKIRFVSSGTEATMSAIRLARGFTKKDKILKFEGC

YHGHSDSLLVSAGSGAATFNSPSSLGVLEDVAKHTLVAKYNDINSVKELFEKNKDIACVIIEPIAGNMGL

VPAKQDFLEELAKICKNNQTLLIFDEVMSGYRASYLGSYGINHIQADIITFGKVIGGGLPAAAFASRAEI

MDILSPLGGVYQAGTLSGNPLAMAAGIASLTKAKKKTKLYDKLGKLAKKLTQGMKKLADEKGLPLQACHV

GSMFGYFFTKDPVSNYQDALKSDLALFSKFHKNMLENGIYLAPSQFETGFICSKMDDKIIDTTLEAVRES

FKRI

>sp|A8FLL9.1|DAPA\_CAMJ8 RecName: Full=4-hydroxy-tetrahydrodipicolinate synthase; Short=HTPA synthase

MDKNIIIGAMTALITPFKNGKVDEQSYARLIKRQIENGIDAVVPVGTTGESATLTHEEHRTCIEIAVETC

KGTKVKVLAGAGSNATHEAVGLAKFAKEHGADGILSVAPYYNKPTQQGLYEHYKAIAQSVDIPVLLYNVP

GRTGCEISTDTIIKLFRDCENIYGVKEASGNIDKCVDLLAHEPRMMLISGEDAINYPILSNGGKGVISVT

SNLLPDMISALTHFALDENYKEAKKINDELYNINKILFCESNPIPIKTAMYIAGLIESLEFRLPLCPPSK

ENFAKIEEVMKKYKIKGF

>sp|A8FLH1.1|GRPE\_CAMJ8 RecName: Full=Protein GrpE; AltName: Full=HSP-70 cofactor

MSEQKQEFENENAENSEHLQDENLQNIEDVEQNRLQKDYDELKDKYMRANAEFENIKKRMEKEKLSAMAY

ANESFAKDLLDVLDALEAAINVECHDEISLKIKEGVQNTLDLFLKKLEKHGVALIKEEKEFDPNLHEAMF

HVDSQNHQSGEVVTVLQKGYKIADRVIRPTKVSVAK

>sp|A8FLB9.1|ACKA\_CAMJ8 RecName: Full=Acetate kinase; AltName: Full=Acetokinase

MKILVLNSGSSSIKFKFFDNKVVKASGLVEKIGEQNSKVILKNVLNNESFERELMINNHEEGLSIVNELF

KESGILADLNALDGCGHRIVHGGRNLSEHCLVDDYVLKEIDRVSIFAPLHNPAHLAGIKTMIKAAPSVAN

VAIFDTAFHRTMPDFAYMYALPYDFYDKHNIRRYGFHGTSHAFVSSRAASLLEKDKSELNVISAHLGNGA

SVCAIEKGKSVDTSMGFTPLEGLVMGTRCGDLDPAILPFISHLKGLTIEEIDTLMNKKSGVYGICGYNDF

RDIEREIEQGNDKARLALDMFCYRLVKYIGSYFAVLPKTDAIIFTGGIGENDSLVRQKVCERLAHLGIEL

DFELNKQRISGERMINHANSKVKVLVIPTDEELEIARITEELISN

>sp|A8FL83.1|ASSY\_CAMJ8 RecName: Full=Argininosuccinate synthase; AltName: Full=Citrulline--aspartate ligase

MKNEVKKVVLAYSGGLDTSIILKWLQDEYNCEVVTFTADIGQGEELEPARKKALSLGIKEENIFIKDLRD

EFVKDYVFPMFRANAIYEGEYLLGTSIARPLIAKTQAQIALQTGADAVSHGATGKGNDQVRFELGYLAFN

PDLKIIAPWREWDLNSREKLLAYAQKHGIDISKKKGKSPYSMDANLLHISYEGLVLEDPAHAPEEDMWRW

SKSPKDAPNESEIIELDFQKGDLVAINGEKLSPAGLLTKLNELGCKHGIGRLDIVENRYVGMKSRGCYET

PGGTILLKAHRALESITLDREAAHLKDELMPKYASLIYNGYWFSPERMMLQALIDESQIHANGRVKLELY

KGNVMIIGRESANDSLFNAAYCTFEEDEVYNQKDAAGFIKLNALRFIIAGKNGRKF

>sp|A8FL81.1|HSLV\_CAMJ8 RecName: Full=ATP-dependent protease subunit HslV

MFHATTILAYKGKNKSVIGGDGQVSFGNTVLKGNAVKIRKLNNGKVLAGFAGSTADAFNLFDMFENLLQS

SKGDLLKAAIDFSKEWRKDKYLRKLEAMMLVLDRNHIFLLSGTGDVVEPEDGQIAAIGSGGNYALSAARA

LAKHASLDEEELVKSSLQIAGEICIYTNTNIKTYVIEDEK

>sp|A8FL80.1|HSLU\_CAMJ8 RecName: Full=ATP-dependent protease ATPase subunit HslU; AltName: Full=Unfoldase HslU

MNLTPKEIVKFLDDYVIGQKKAKKIIAIALRNRYRRMQLSPELQDDIVPKNILMIGSTGVGKTEIARRLA

KMMGFPFIKIEASKYTEVGFVGRDVESMVRDLANAALNLVKNEQREKNKDKIDEFIENKILEKLLPPLPK

GISDEKQEEYKNSLEKMRTKLRNGDLDESTIEIEISQNMFDTNPNLPPEMGAMQDIVKVIGVGSKKVKKE

MKIKDAKNALKNEAGEKILDQESIKSEALKRAENEGIIFIDEIDKIAVSSGNSNRQDPSKEGVQRDLLPI

VEGSNIQTKIGTLKTDHILFIAAGAFHLSKPSDLIPELQGRFPLRVELDSLDDKALYEILTRPKNSLLKQ

YSQLLKTENLELEFDDEAIKEIAKIASRANEEMQDIGARRLHTVIEKLLEDLSFEADEYAGKKFVVDKKM

VEEKLGDIIENKDLARYIL

>sp|A8FL71.1|ENGB\_CAMJ8 RecName: Full=Probable GTP-binding protein EngB

MIISAKFITSLVKFDENLSSNFSEVAFLGRSNVGKSSLINSLCKQKNLAKSSATPGKTQLINFFEVTCKR

NEEKFNINFIDLPGFGYAKVSKNLKEIWNQNLDEFLKLRTSIKLFIHLIDSRHTHLEIDVNLNDYLKRFL

RPDQKILKVFTKCDKLNQSEKAKLKNEFKDSILVSNLNKFGLDSLEDIIIDQTLGLGK

>sp|A8FL60.1|KAD\_CAMJ8 RecName: Full=Adenylate kinase; Short=AK; AltName: Full=ATP-AMP transphosphorylase; AltName: Full=ATP:AMP phosphotransferase; AltName: Full=Adenylate monophosphate kinase

MKELFLIIGAPGSGKTTDASLIAQADATNITHYSTGDLLRAEVASGSELGKTIDSFISKGNLVPLDVVVN

TIVCALKAAPTKTIIIDGYPRSVEQMMEFDKVLSEQNEICLKGVIEVRVSEEVAKERVLGRNRGADDNEE

VFYNRMKVYTEPLNEILDFYQKKKLHFIIDGERTIEPIVADMKELIKKIQSI

>sp|A8FKS9.1|HEMH\_CAMJ8 RecName: Full=Ferrochelatase; AltName: Full=Heme synthase; AltName: Full=Protoheme ferro-lyase

MKLVLFLNMGGATNLQDCEVFLKNMFNDPYILGIKNRFLRKFVAWIITKARVKAMQENYKKMGGKSPLNE

LTQSLCNKLNLKQDEFKFDFVNLYVPPFATEILQKYTLNESDEIILFPLYPHHSCTTVTSSLEVLQNEIS

KQKIQAKVKTIDIFYKNELYNEMIVSHILAKKSKFDAKILIFSAHSLPQSIIDKGDLYEKHVNDHVEILK

EKLKDHFDEFILAYQSKLGPVKWLEPNTSDVLANLNDKALIYPISFCIDCSETIFELGMEYKHLAKCDYD

LISCPNDSDEFMEFILNSINSPLARKTSC

>sp|A8FKS2.1|TRPC\_CAMJ8 RecName: Full=Indole-3-glycerol phosphate synthase; Short=IGPS

MILDKIFEKTKEDLKERKLKLPYDMLGRSLASNPFFPKDVIKALKRVEKEVKIIAEVKKASPSKGVIRED

FDPLSIALNYEKNKAAAISVLTEPHFFKGSLEYLSLIRRYTQIPLLRKDFIFDEYQILEALVYGADFVLL

IAKMLSMKELKKLLEFARHLGLEALVEIHDKEDLSKAIFAGADIIGINHRNLEDFTMDMSLCEKLIPQIP

NSKIIIAESGLENKEFLEHLQNLGVDAFLIGEYFMREKDEGKALKALL

>sp|A8FKR5.1|RS12\_CAMJ8 RecName: Full=30S ribosomal protein S12

MPTINQLVRKERKKVLEKSKSPALKNCPQRRGVCTRVYTTTPKKPNSALRKVAKVRLTSGFEVISYIGGE

GHNLQEHSIVLVRGGRVKDLPGVKYHIVRGALDTAGVAKRTVSRSKYGAKRPKAGTAK

>sp|A8FKR4.1|RPOC\_CAMJ8 RecName: Full=DNA-directed RNA polymerase subunit beta'; Short=RNAP subunit beta'; AltName: Full=RNA polymerase subunit beta'; AltName: Full=Transcriptase subunit beta'

MSKFKVIEIKEDARPRDFEAFQLRLASPEKIKSWSYGEVKKPETINYRTLKPERDGLFCAKIFGPIRDYE

CLCGKYKKMRFKGVKCEKCGVEVANSKVRRSRMGHIELVTPVAHIWYVNSLPSRIGTLLGVKMKDLERVL

YYEAYIVENPGDAFYDNESTKKVEYCDVLNEEQYQNLMQRYENSGFKARMGGEVVRDLLANLDLVALLNQ

LKEEMAATNSEAKKKTIIKRLKVVENFLNSNLNANADSDEAVPNRPEWMMITNLPVLPPDLRPLVALDGG

KFAVSDVNDLYRRVINRNTRLKKLMELDAPEIIIRNEKRMLQEAVDALFDNGRRANAVKGANKRPLKSLS

EIIKGKQGRFRQNLLGKRVDFSGRSVIVVGPKLRMDQCGLPKKMALELFKPHLLAKLEEKGYATTVKQAK

KMIENKTNEVWECLEEVVKGHPVMLNRAPTLHKLSIQAFHPVLVEGKAIQLHPLVCAAFNADFDGDQMAV

HVPLSQEAIAECKVLMLSSMNILLPASGKSVTVPSQDMVLGIYYLSLEKAGAKGSHKICTGIDEVMMALE

SKCLDIHASIQTMVDGRKITTTAGRLIIKSILPDFVPENSWNKVLKKKDIAALVDYVYKQGGLEITASFL

DRLKNLGFEYATKAGISISIADIIVPNDKQKAIDEAKKQVREIQNSYNLGLITSGERYNKIIDIWKSTNN

VLSKEMMKLVEKDKEGFNSIYMMADSGARGSAAQISQLAAMRGLMTKPDGSIIETPIISNFREGLNVLEY

FISTHGARKGLADTALKTANAGYLTRKLIDVAQNVKITIEDCGTHEGVEINEITADSSIIETLEERILGR

VLAEDVIDPITNSVLFAEGTLMDEEKAKILGESGIKSVNIRTPITCKAKKGICAKCYGINLGEGKLVKPG

EAVGIISAQSIGEPGTQLTLRTFHSGGTASTDLQDRQVSAQKEGFIRFYNLKTYKNKEGKNIVANRRNAA

ILLVEPKIKTPFKGVINIENIHEDVIVSIKNKKQEVKYILRKYDLAKPNELAGVSGSIDGKLYLPYQSGM

QVEENESIVEVIKEGWNVPNRIPFASEILVEDGEPVVQNIKAGEKGTLKFYILKGDGLDRVKNVKKGDIV

KEKGFFVVIADENDREAKRHYIPRESKIEFNDSEKIDDANTIIASAPKKERKVIAEWDAYNNTIIAEIDG

VVSFEDIEAGYSADEQIDEATGKRSLVINEYLPSGVRPTLVIAGKGDKAVRYQLEPKTVIFVHDGDKIAQ

ADILAKTPKAAAKSKDITGGLPRVSELFEARKPKNAAVIAEIDGVVRFDKPLRSKERIIIQAEDGTSAEY

LIDKSKHIQVRDGEFIHAGEKLTDGVVSSHDVLKILGEKALHYYLISEIQQVYRGQGVVISDKHIEVIVS

QMLRQVKVVDSGHTKFIEGDLVSRRKFREENERIIRMGGEPAIAEPVLLGVTRAAIGSDSVISAASFQET

TKVLTEASIAGKFDYLEDLKENVILGRMIPVGTGLYGEQNLKLKEQE

>sp|A8FKR1.1|RL10\_CAMJ8 RecName: Full=50S ribosomal protein L10

MTRSEKVEIIAKLEEGFKASEAIVVCNYRGLSTKKLEELRNNARENNVKVQIVKNTLANIALNNSGKTGL

VLKDTNIYLWGEDQLSVSKVAAKFEENNDKFEIKTAYIEGEVADVAKVKALAKMPSRNELLAMLLQVWNA

PITNFTIGLNALKNKKESE

>sp|A8FKR0.1|RL1\_CAMJ8 RecName: Full=50S ribosomal protein L1

MAKIAKRLKELSQKIDSNKEYALSDAIDTIKTLKSAKFDETVEIALKLNVDPRHADQMVRGSVVLPAGTG

KKVRVAVIAKDAKADEAKNAGADIVGSDDLVEEIQKGNMNFDVLIATPNLMGLVGKVGRILGPKGLMPNP

KTGTVTMDVAQAVNNAKSGQVNFRVDKQGNIHAGLGKVSFSKEQLWDNVSTFVKAINKHKPAAAKGRYIK

NAALSLTMSPSVKLETQELLDMK

>sp|A8FKM0.1|MRAY\_CAMJ8 RecName: Full=Phospho-N-acetylmuramoyl-pentapeptide-transferase; AltName: Full=UDP-MurNAc-pentapeptide phosphotransferase

MYYLSDLSHYAFFTYISVRAGFAFFIALCLSLFLMPKFITWAKAKNASQPIYEYAPETHKTKCHTPTMGG

LIFISSAVIASLFCIKFDNIFAISALLCLILFCLIGLIDDLGKVLKKDNHSGLSPRMKLLAQIIAGLICI

LPLYFSSELSTELFIPFYKHPLFDMEIFAIVFWILVLISSSNAVNLTDGLDGLATVPSIFSLSTLGIFLY

LSGNLNYSEYLLLPKIQGLGEVVIICAALIGALMGFLWYNCYPAQVFMGDSGSLALGGFIGFLAIISKNE

ILLLLIGFVFVLETVSVILQVGSFKIFNKRVFKMAPIHHHFEKVGWVENKIIVRFWMIALLSNLLALASI

KLR

>sp|A8FKJ4.1|LGT\_CAMJ8 RecName: Full=Prolipoprotein diacylglyceryl transferase

MEFWQHIYSNFNVIAFSIFGLKVHWYGIMYVIALLLALLLAKFFVRKFQLDINEKHLDSYFIWVEIGVIL

GARLGYILIYDANTMYYITHPWQIFNPYINGEFVGIRGMSYHGAIIGFLIATLLFCKKYKTNPWIFLDLV

ALSVPLAYVFGRIGNFLNQELFGRITNVPWGIYVDGVLRHPSQLYEAFLEGIVVFIIVYLARFKQSFQGE

LILVYAGAYSLARFICEFYREPDFGIGFVLWGMSMGQILSFIMFITALLVYICIKFKKVNI

>sp|A8FKH1.1|KDSA\_CAMJ8 RecName: Full=2-dehydro-3-deoxyphosphooctonate aldolase; AltName: Full=3-deoxy-D-manno-octulosonic acid 8-phosphate synthase; AltName: Full=KDO-8-phosphate synthase; Short=KDO 8-P synthase; Short=KDOPS; AltName: Full=Phospho-2-dehydro-3-deoxyoctonate aldolase

MKKMILIAGPCVIESKDLIFKVAEQLKNFNENPNIEFYFKSSFDKANRTSINSFRGPGLEEGLKILQSVK

DEFGMKILTDIHESNQAAAVSEVADVLQIPAFLCRQTDLLVAAAKTKAKVNIKKGQFLNPSDIKYSVKKV

LQTRGIEDEGYEAAQKNGVFVAERGASFGYGNLVVDMRSLVIMREFAPVIFDATHSVQMPGAAGGSSGGK

SEFVEPLARAAAAVGIDGFFFETHINPCEALCDGPNMLNLTRLKNCVNTLLEIQNIIKENK

>sp|A8FKG8.1|PYRF\_CAMJ8 RecName: Full=Orotidine 5'-phosphate decarboxylase; AltName: Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase

MKLCVALDLSTKEECLQLAKELKNLDIWLKVGLRAYLRDGFKFIEELKKVDDFKIFLDLKIHDIPNTMAD

ACEEISKLGVDMINIHASAGKIAMQEVMTRLSKFSKRPLVLAVSALTSFDEENFFSIYRQKIEEAVINFS

KISYENGLDGMVCSVFESKIIKEHTQRNFLTLTPGIRPFGEKNDDQKRVANLTMARENLSDFIVVGRPIY

KDNNPRKICEKILQEI

>sp|A8FKF8.1|RS21\_CAMJ8 RecName: Full=30S ribosomal protein S21

MPGIKVHPNESFDEAYRKFKKQVDRNLVVTEVRARRFFEPMTEIRKKQKISARKKMLKRLYMLRRYESRL

>sp|A8FKE6.1|PLSY\_CAMJ8 RecName: Full=Glycerol-3-phosphate acyltransferase; AltName: Full=Acyl-PO4 G3P acyltransferase; AltName: Full=Acyl-phosphate--glycerol-3-phosphate acyltransferase; AltName: Full=G3P acyltransferase; Short=GPAT; AltName: Full=Lysophosphatidic acid synthase; Short=LPA synthase

MENLIIYAFIYLLGSIPFGLILAKFFAKTDIKKEGSKSIGATNVLRVVKEKNPKLAKKLAIATIILDFAK

AAIPLLILKFLHYDQALLWSVAVLAIFGHCFSIYLLFEGGKGIATGAGAMIVLLPLEVLTAFIVWVVIGK

IFKISSLASLAALLAFVISSFIFNYDLEIHTHAPVFIIAFIIVYKHLPNIKRLIFKEECKVI

>sp|A8FKD8.1|TRPA\_CAMJ8 RecName: Full=Tryptophan synthase alpha chain

MVDFRKFYKENANVAYTVLGYPNLQTSEAFLQRLDQSPIDILELGVAYSDPIADGEIIADAAKIALDQGV

DIHSVFELLARIKTKKALVFMVYYNLIFSYGLEKFVKKAKSLGICALIVPELSFEESDDLIKECERYNIA

LITLVSVTTPKERVKKLVKHAKGFIYLLASIGITGTKSVEEAILQDKVKEIRSFTNLPIFVGFGIQNNQD

VKRMRKVADGVIVGTSIVKCFKQGNLDIIMKDIEEIFKK

>sp|A8FKB9.1|RL32\_CAMJ8 RecName: Full=50S ribosomal protein L32

MAVPKRRVSKTRAAKRRTHYKVSLPMPIKDKDGSYKMPHRANPTTKEY

>sp|A8FKB7.1|FABH\_CAMJ8 RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase 3; AltName: Full=3-oxoacyl-[acyl-carrier-protein] synthase III; AltName: Full=Beta-ketoacyl-ACP synthase III; Short=KAS III

MLKASLKSIASYIPEKILSNADLEKMVDTTDEWITRRTGIKERRIASENENTSDLGTKAALKAIKRANLK

PEDIDAILVATLSPDYFTMPSTACKIASNLGLVNISAFDISAACSGFIYLLEQAKALVESGLKKNVLIIG

AEKTSSIMDYNDRSICILFGDGAGAGVVSLDNENHILDVHTASNGNYGDLLMTQRSQKSNLCQTLSMQMK

GNEVFKIAVNTLSNDVVEILAKNNILAQEIDLFIPHQANLRIIKAVQEKLNLSDEKCVITVQKYGNTSAA

SIPMAMNDAYEEGRLKKGDLILLDAFGGGFTWGSALLKFGGENF

>sp|A8FKB5.1|SERC\_CAMJ8 RecName: Full=Phosphoserine aminotransferase; AltName: Full=Phosphohydroxythreonine aminotransferase; Short=PSAT

MRKINFSAGPSTLPLEILEQAQKELCDYQGRGYSIMEISHRTKVFEEVHFGAQEKAKKLYGLNDDYEVLF

LQGGASLQFAMIPMNLSLNGVCEYANTGVWTKKAIKEAQILGVNVKTVASSEESNFNHIPRVEFSDNADY

AYICSNNTIYGTQYQNYPKTKAPLIVDASSDFFSRKVDFSNIALFYGGVQKNAGISGLSCIFIRKDMLER

SKNKQIPSMLNYLTHAENQSLFNTPPTFAIYMFNLEMDWLLNQGELDKVHEKNSQKAAMLYECIDLSNGF

YKGHADKKDRSLMNVSFNIAKNKDLEPLFVKEAEEAGMIGLKGHRILGGIRASIYNALNLDQVKTLCEFM

KEFQGKYA

>sp|A8FKB0.1|DXS\_CAMJ8 RecName: Full=1-deoxy-D-xylulose-5-phosphate synthase; AltName: Full=1-deoxyxylulose-5-phosphate synthase; Short=DXP synthase; Short=DXPS

MSKKFAHTQEELEKLSLKELENLAASMREKIIQVVSKNGGHLSSNLGAVELSIAMHLVFDAKKDPFIFDV

SHQSYTHKLLSGKEEIFDTLRQINGLSGYTKPSEGDYFVAGHSSTSISLAVGACKAIALKGEKRIPVALI

GDGALSAGMAYEALNELGDSKFACVILLNDNEMSISKPIGAISKYLSQAMATQFYQSFKKRIAKMLDILP

DSATYMAKRFEESFKLITPGLLFEELGLEYIGPIDGHNLGEIISALKQAKAMQKPCVIHAQTIKGKGYAL

AEGKHAKWHGVGAFDIDSGESVKKSDAKKSATEIFSKNLLDLASKYENIVGVTAAMPSGTGLDKLIEKYP

NRFWDVAIAEQHAVTSMAAMAKEGFKPFIAIYSTFLQRAYDQVIHDCAIMNLNVVFAMDRAGIVGEDGET

HQGVFDLSFLAPLPNFTLLAPRDEQMMQNIMEYAYLHQGPIAFRYPRGSFILDKEFNPCEIKLGKAQWLV

KNNSEIAFLGYGQGVAKAWQVLRALQEMNNNANLIDLIFAKPLDEELLCELAKKSKIWFIFSENVKIGGI

ESLINNFLQKYDLHVKVVSFEYEDKFIEHGKTSEVEKNLEKDVNSLLTKVLKFYH

>sp|A8FKA6.1|HIS8\_CAMJ8 RecName: Full=Histidinol-phosphate aminotransferase; AltName: Full=Imidazole acetol-phosphate transaminase

MKFNEFLNHLSNYEPGKDIEVIAKEYGVKEVIKLASNENPFGTPPKAIECLRQNANKAHLYPDDSMIELK

STLAQKYKVQNENIIIGAGSDQVIEFAIHAKLNSKNAFLQAGVTFAMYEIYAKQCGAKCYKTQSITHDLN

EFKKLYEAHKDEIKLIFLCLPNNPLGECLDASEVTKFIKGVDEDCLVVIDAAYNEFASFKDSKKHLEPCE

LIKEFDNVLYLGTFSKLYGLGGLRIGYGIANANIINAFYKLRAPFNVSNLALKAAVAAIDDDEFTKKTLE

NNFSQMQLYKEFAKKHNIKIIDSYTNFITYFFDEKNSTDLSEKLLKKGIIIRNLKSYGLNAIRITIGTSY

ENEKFFTEFDKILR

>sp|A8FK87.1|PANB\_CAMJ8 RecName: Full=3-methyl-2-oxobutanoate hydroxymethyltransferase; AltName: Full=Ketopantoate hydroxymethyltransferase; Short=KPHMT

MRKSMISFLEKKAKNEKITMVSAYDYHSARILDNSDIDIILVGDSLAMTVLGMQDTLSVTMDEMLIFTKA

VSRGAKKSFVLADMPFMSYQSSDRDAILNASRFIKESHANGVKVEGGIEIASKIKLISQSGIPVVAHLGL

TPQAVNMLGGYRVQGKDLQSAQKIIDDAKAVQDAGACMLVLECVPVKLAQKISSILEIPTIGIGSGKYCD

GQVLVYHDLLGLNKDFKAKFVKHFDKIDPQVGVEKYRDEVKSGIFPSQEHSFDYLDDELLDKLY

>sp|A8FK76.1|LPXB\_CAMJ8 RecName: Full=Lipid-A-disaccharide synthase

MKTFLVCALEPSANLHLKEVLKAYKKDFGEFELHGIYDESLCKEFDLNSKPLYSSHEFSAMGFIEVLPLI

FKAKKAIKELVNLTLSQTMDAVLCIDSPAFNIPFAKALKKAGSKIPRIYYILPQVWAWKKGRIPIIESHF

DILASILPFDNQFFNKSTYIGHPLLDEIKEFKNQEDINHTFSKKDDEKTIAFLPGSRRSEIRRLMPIFKE

LSQKFKGEKILCVPSFNLEKLEVYGDISEFKIESNTPKVLKKADFAFICSGTATLEAALVGTPFVLAYKA

KAIDIFIAKLFVKLKHIGLANIFCDFAGKEALNPEFLQDKVNVLNLYEAYNKYDYKAFFAKVDFLKEYLQ

FGSAKNLAKILNEI

>sp|A8FK69.1|TAL\_CAMJ8 RecName: Full=Transaldolase

MKNFSLWCDFIENSFLDNEFLNLLSHGINGATSNPAIFKNAILNSPIYKDKILKLKGKRTKDIYEELAIS

DIQKAADKLAPLFYQKNDGFISIEIDPRLHDNTTLSLGEAKRLYSAISKENVMIKIPATKASYEVMYELM

KNGISVNATLIFSLEQSQKCFEALNAGLVEFRKNNIALKEQNTRTPQAVISIFVSRFDRLLNPKAKEQNR

IGILNANLAYNNIYSKNEPNIRALFASTGVKGDDLPKDYYIKELLFENSVNTAPLDAIEAFKGKMDFKKP

LMNFEIYTELNQIISQSEREKACNDLLSDGIEQFCIAFEDILKAL

>sp|A8FK23.1|PYRE\_CAMJ8 RecName: Full=Orotate phosphoribosyltransferase; Short=OPRT; Short=OPRTase

MNLEQIYKDCGAYLEGHFLLSSGKHSQFYLQSAKVLEDPKLAAKLCDELAKIIASYKIEFDSICSPALGG

ILAGYELARACSKRFIFTERVNKEMTLRRGFEVKKGEKFIICEDIITTGGSALESAKIIESLGGIIVGFA

ALANRGFCAVENLKSPRKDNAKLPENLPLFTLGNFEFEIYDETNCPLCKKGSKAIKPGSRGN

>sp|A8FK06.1|UPPP\_CAMJ8 RecName: Full=Undecaprenyl-diphosphatase; AltName: Full=Bacitracin resistance protein; AltName: Full=Undecaprenyl pyrophosphate phosphatase

MENLNALILGIIEGLTEFLPVSSTGHMILGTTILGIDIDEFWKSFLIIIQLGSILAVIFVFWRKLFQGLD

IWLKLAAGFFPTGVIGLFVAKYLNALFNGWVVVGMLIFGGVVFILIELAHKNKQYRINSLEEISFKQAFC

IGIFQSLAMIPGTSRSGASIIGGLLLGFNRKVAAEFSFLLAIPTMIIATAYSIYKEPELLSNANSLIPLG

IGFITAFVVAVLVIKFFLKFISKFDFIPFGIYRIILGFVFFYLYYSGILNAGSEFKL

>sp|A8FJZ5.1|GCH1\_CAMJ8 RecName: Full=GTP cyclohydrolase 1; AltName: Full=GTP cyclohydrolase I; Short=GTP-CH-I

MQKKFEDCVKTILEIIGENPNREGLIKTPNRVFKAYEFLTSGYTQNVKEILNDALFESSNNEMVLVRDIE

FYSLCEHHLLPFFGRAHVAYIPNKKVVGLSKIPRLVEVFARRLQIQEQLTEQIAQALMENVDAKGVGVVI

EARHMCVEMRGVQKANSTTTTSALRGIFLKNEKTREEFFSLINSAKQVRF

>sp|A8FJQ0.1|RL27\_CAMJ8 RecName: Full=50S ribosomal protein L27

MAHKKGQGSTQNNRDSIGRRLGVKKFGGEFVRAGNIIIRQRGTATHAGNNVGMGKDHTIFALIDGFVKFE

RKDKDRKKVSVYPA

>sp|A8FM78.1|MAPA\_CAMJ8 RecName: Full=Outer membrane lipoprotein MapA; Flags: Precursor

MFKKFLIFIVPILFLSACATKQDTFAQVNQISKNSQCSSCESPGGFEAKIKGLLYISDVGIQCCANKRTL

DTGIALKKVYLHRFYDLKEGQKVLNAKGKKLFVDVNFNAVFYTYLKQELEARGIVVLDNNDQNSPYVSKI

DLEFISYGATQDAIGLHSKLVGVLQVSDINKNKKFTIRTKQDVQGFDDLKETTFYTHLLIKQMANKAASL

ISEL

>sp|A8FNH9.1|NSPC\_CAMJ8 RecName: Full=Carboxynorspermidine/carboxyspermidine decarboxylase; Short=CANS DC/CAS DC; Short=CANSDC/CASDC

MFYEKIQTPAYILEEDKLRKNCELLASVGEKSGAKVLLALKGFAFSGAMKIVGEYLKGCTCSGLWEAKFA

KEYMDKEIHTYSPAFKEDEIGEIASLSHHIVFNSLAQFHKFQSKTQKNSLGLRCNVEFSLAPKELYNPCG

RYSRLGIRAKDFENVDLNAIEGLHFHALCEESADALEAVLKVFKEKFGKWIGQMKWVNFGGGHHITKKGY

DVEKLIALCKNFSDKYGVQVYLEPGEAVGWQTGNLVASVVDIIENEKQIAILDTSSEAHMPDTIIMPYTS

EVLNARILATRENEKISDLKENEFAYLLTGNTCLAGDVMGEYAFDKKLKIGDKIVFLDQIHYTIVKNTTF

NGIRLPNLMLLDHKNELQMIREFSYKDYSLRN

>sp|A8FJV7.1|Y145\_CAMJ8 RecName: Full=UPF0102 protein C8J\_0145

MGVKAYLDGILGEDKACKFLKKQGFEILKRNFHSKFGEIDIIAKKDEILHFIEVKFTQNDYEVSERLDRK

KLEKILKTIEFYHLKNGISSDFQIDLICIKNDVIQFCENISF

>sp|A8FKV6.1|SUCC\_CAMJ8 RecName: Full=Succinate--CoA ligase [ADP-forming] subunit beta; AltName: Full=Succinyl-CoA synthetase subunit beta; Short=SCS-beta

MNIHEYQAKAIFADNGIPTLKGKVAFSVDEAVSNAKELGGSVWAVKAQIHAGGRGLGGGVKIAKNLDEVK

DYASKILGMNLATHQTGPEGKLVQKLYIESGANIVKEYYLAILFNRMAEQITIIASSEGGMDIEKVAKES

PEKIAKVGIDPQIGFKMFHGLEVARVLGLDKDEGKKLISMIAKLYKLYMDKDMNMLEINPLIKTAEGDFY

ALDAKCSFDDSALYRHPEIAELRDITEENPAEREAAEFGLSYVKLDGDVACMVNGAGLAMATMDIINYSG

AKPANFLDVGGGASPETVAKAFEIILRDKNVKVIFINIFGGIVRCDRIANGILEATKNVEVNIPIVVRLD

GTNAAEAKTILDNSNLKNIKAATNLKNGAELVKSLVG

>sp|A8FP38.1|QUEF\_CAMJ8 RecName: Full=NADPH-dependent 7-cyano-7-deazaguanine reductase; AltName: Full=7-cyano-7-carbaguanine reductase; AltName: Full=NADPH-dependent nitrile oxidoreductase; AltName: Full=PreQ(0) reductase

MRYGEKEIKEFDVENMEIWPNDAKNDYIIKITLPEFMCCCPRSGYPDFATIYLEYMPDKFVVELKAIKLY

INTFMYRNVSHEASINEIYNTLKDKLKPKWIKVVGDFNPRGNVHTVIECCSDMVVPK

>sp|A8FP17.1|RS19\_CAMJ8 RecName: Full=30S ribosomal protein S19

MARSLKKGPFVDDHVMKKVIAAKKANDNKPIKTWSRRSTITPDMIGLTFNVHNGKSFIPVYITENHIGYK

LGEFAPTRTFKGHKGSVQKKIGK

>sp|A8FP12.1|RS17\_CAMJ8 RecName: Full=30S ribosomal protein S17

MAFKREIQGVVVKIAGEKTASVLVERKVVHPRYRKIVKRFKKYLIHDERNEVKVGDTVVAVECRPLSKRK

SFRLKSVLATGVE

>sp|A8FP04.1|RS5\_CAMJ8 RecName: Full=30S ribosomal protein S5

MEKYNREEFEEVIVDIGRVTKVVKGGRRFRFTALVIVGNRKGLVGVGYGKAKEVPDAIRKAVDDAFKNIV

EVKTKGSTIAHDVEVKYNASRILLKPASEGTGVIAGGSTRPIVELAGIKDILTKSLGSNNSANVVRATIK

ALTMLKG

>sp|A8FNM9.1|NUOI\_CAMJ8 RecName: Full=NADH-quinone oxidoreductase subunit I; AltName: Full=NADH dehydrogenase I subunit I; AltName: Full=NDH-1 subunit I

MKNYYLVDEKRKTPVSTWEKISQTFRRSVKLELFVGLFVMMRELLKRNNSATIKYPFEKVKLDNRYRAVH

RLMRFIESENERCIGCGLCEKICISNCIRMETSLDENGRKKVGNYSINLGRCIYCGFCAEVCPELAIVHG

TEYENAAEQRSYFGYKQDFLTPIDKLKNQVEFEGAGSLRKDADLLVVKTPNYYDVMIERALENQDTQEQG

ENK

>sp|A8FNE5.1|RS9\_CAMJ8 RecName: Full=30S ribosomal protein S9

MATTYATGKRKTAIAKVWVKPGSGKISVNGVDLNTWLGGHEAIKLKVVQPLLVTKQETSMDIKATTLGGG

YSAQAEALRHGISRALAAMDADFRALLKPKGLLTRDSRTVERKKYGRRKARRSPQFSKR

>sp|A8FMU8.1|DCUP\_CAMJ8 RecName: Full=Uroporphyrinogen decarboxylase; Short=UPD; Short=URO-D

MIFIDACFKKPTPYTPIWMMRQAGRYLPEYMEVRKQAGDFLSLCKDYKKASEVSLQPIDILDVDAAIIFS

DILVVPLEMGMNLRFEKGEGPVFDNPISTLEDLEKLDDQNAHKKLNYVYDALKLTREKLSQNKALIGFCG

SPWTIATYMIEGSGSKNYAKCKKMLYQNPELLHKILNKLTQVLKLYLEEQIKAGANAIQIFDSWASALEY

DKFFEFSFNYMLEISNFIKSKYPNIPVILFPKGISGYLDRIDGNFDVFGVDWSTPLDLARDKLSHKYTLQ

GNMEPCRLYDKNAIKEGVEKILKTMQNKAHIFNLGHGILPDIPVENAKYFIKLVQESSAK

>sp|A8FKU3.1|CRCB\_CAMJ8 RecName: Full=Putative fluoride ion transporter CrcB

MLNTLLVVGFGGFIGAILRMFSINLVNKFFPYSISLGTLFVNVLGSFIIGLLFSYAQNKGLSPLLKSFIS

TGFLGAFTTFSTFSYQNLLLLQSGNYLHFALNIILNVFLCLFAAWLGFIIFK

>sp|A8FKF9.1|Y347\_CAMJ8 RecName: Full=UPF0323 lipoprotein C8J\_0347; Flags: Precursor

MKKIKKIIQIGMIGGLAAVAGGALAGCGSNNDNADTLNQAANAQGAFVIIEETAPGQYKIKDQYPSDETR

VVLKDLNGTERILSKEEMDALIKEEAAKIDNGTSNLTKDNGQISSGGLSLGETLLASAAGAILGSWIGSK

LFNNQNFANQQRGAFSNQSAYQRSVNSFNKAGTTSSASSAKKSGFFGGGSKATSSSSSFGS

>sp|A8FK97.1|BIOD\_CAMJ8 RecName: Full=ATP-dependent dethiobiotin synthetase BioD; AltName: Full=DTB synthetase; Short=DTBS; AltName: Full=Dethiobiotin synthase

MQIYVSGIHTDVGKTHFSAAFCANFNYDYFKLIQAGTPTDSEFIAKFSPKTKIFKEGIFLQTPASPHLGK

IKEKLDYKALDIILPKSKNLLIELAGGLFSPMDENYTMIDFVNIFKHPTILVAKYYLGSINHILLSIEAL

KQRNINLLALVMMGKKDILQDDFIKNYAKIPIINLDFFDENSILNKDFKEQMQEILQLKIP

>sp|A8FJL3.1|MNMA\_CAMJ8 RecName: Full=tRNA-specific 2-thiouridylase MnmA

MKILVAMSGGVDSTVTAYKLKNLGHEVIGCYMKLHGKPNYHEENIKKVEKVANFLQIPYHILDLQKDFKN

KVYMPFVDTYKEGKTPNPCALCNRFIKLGKLLEFAKSLGCEKLATGHYARLENNLIKTAVDESKDQSYFL

ASADKEALKYLIFPLGEMKKEDVKKFASTIEVLKSFATQKESSEICFVEDTYVQVLDQFMDTKIPGEVLD

SSGKVVGKHEGYMHYTIGKRRGFEVRGAHEPHFVLKINPKQNQIIVGTKEELKISEFKLKNINLFIDAKE

LDCEVKIRYRSKSTPCKVEIYEDKSAKITLKDPVYGLASGQMAVFYDHDKVIASGFIE

>sp|A8FJH9.1|QUEC\_CAMJ8 RecName: Full=7-cyano-7-deazaguanine synthase; AltName: Full=7-cyano-7-carbaguanine synthase; AltName: Full=PreQ(0) synthase; AltName: Full=Queuosine biosynthesis protein QueC

MSKKALCIISGGMDSTLCAYLAKKEGYEIIALHFDYEQRTQEKERECFKQICKALKVEKSYILDVSFIKD

IGGNALTDKSIDIPKNELCISDTPPITYVPFRNGIFLSIAGSLAEKENCESIFIGVVEEDGSGYPDCTDE

FIQKAQEFINEGTSKNFKVYIKTPLVRLNKAKIVELALKENVPLELTWSCYESEDEACGECDSCLLRLRG

FEKVGFKDKIKYKS

>pdb|5JXL|A Chain A, Cryo-em Structure Of The Flagellar Hook Of Campylobacter Jejuni

MRSLWSGVSGLQAHQVAMDVEGNNISNVNTTGFKYSRADFGTMFSQTVKIATAPTDGRGGSNPLQIGLGV

SVSSTTRIHSQGSVQTTDKNTDVAINGDGFFMVSDDGGLTNYLTRSGDFKLDAYGNFVNNAGFVVQGWNI

NWDDQTIDSSRTPQNIFIDPGMHIPAAKSTEVAIKANLNSGLNIGTSSRNLYALDSVHGWNTKTQRAEDE

NDTGTTQFYTTSKNSVEVTEKGVDAGALFNANGTGLNLRDGQGIWVSYADAKFTTDRANGANVFDPNLTV

AQQNNVIFWGNKDIAVTLDINLNGVRIQNDNIRSLDEAIAYINTFTAPTDTRDGTGVKAVKKADGSGIEF

VNNNADGTTDNMKNIDLTVNVGNSAGERNTINYNANTGVFSPQGGNLTTAQNDTDWIAGAAQAGQPQNVK

VVTAHKYIYSSNPVTIPPMINPDGGPAFQPNNGNRPTDPASANYWDAIQGSLKNTTERTFRTTEDLRELL

QRDARYGVDYNGSGIIDNATPTFDANDINQAVKVVVTENGNFAISNANETSTIPANAGAGAGAATTNPKN

MSFNITAYSNKQGTVSTNDAFTKIFKAFDGPLVIGNQIKESEQLKLSAFSAGLEIYDSLGSKHTLEVQFV

KQSTTQDGGNEWQMIIRVPEPAEINTTGEGPTNIIVGTARFNNDGSLANYTPKTINFSPNNGAAPNQQIK

LSFGTSGSNDGLVSSNSASTLTGQATDGYTSGNLKPDAIRVDDKGNILGEFTNGKTFAVAKIAMASVANN

SGLEEIGGNLFKVTANSGNIVVGEAGTGGRGEMKTSALEMSNVDLSRSLTELIIIQRGYQANSKTISTSD

QMLQTLIQLKQ

>pdb|4LY3|B Chain B, Crystal Structure Of Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtpd-qui3n, Dtdp-qui3nfo, And Thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LY3|A Chain A, Crystal Structure Of Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtpd-qui3n, Dtdp-qui3nfo, And Thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LY0|B Chain B, Crystal Structure Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtdp-glc And 10-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LY0|A Chain A, Crystal Structure Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtdp-glc And 10-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LXY|B Chain B, Crystal Structure Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtdp And 10-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LXY|A Chain A, Crystal Structure Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtdp And 10-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LXX|B Chain B, Crystal Structure Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtdp-fuc3nfo And 5-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LXX|A Chain A, Crystal Structure Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtdp-fuc3nfo And 5-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LXU|B Chain B, Dtdp-fuc3n And 5-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LXU|A Chain A, Dtdp-fuc3n And 5-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LXT|B Chain B, Crystal Structure Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtdp-qui3n And 5-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LXT|A Chain A, Crystal Structure Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtdp-qui3n And 5-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LXQ|B Chain B, Crystal Structure Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtdp And 5-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|4LXQ|A Chain A, Crystal Structure Wlard, A Sugar 3n-formyl Transferase In The Presence Of Dtdp And 5-n-formyl-thf

GHMIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNI

EQIIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIID

QHCFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSF

EIHNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>pdb|3N29|B Chain B, Crystal Structure Of Carboxynorspermidine Decarboxylase Complexed With Norspermidine From Campylobacter Jejuni

MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDHPFTMFYEKIQTPAYILEEDKLRKNCELLASVGEKSGA

KVLLALKGFAFSGAMKIVGEYLKGCTCSGLWEAKFAKEYMDKEIHTYSPAFKEDEIGEIASLSHHIVFNS

LAQFHKFQSKTQKNSLGLRCNVEFSLAPKELYNPCGRYSRLGIRAKDFENVDLNAIEGLHFHALCEESAD

ALEAVLKVFEEKFGKWIGQMKWVNFGGGHHITKKGYDVEKLIALCKNFSDKYGVQVYLEPGEAVGWQTGN

LVASVVDIIENEKQIAILDTSSEAHMPDTIIMPYTSEVLNARILATRENEKISDLKENEFAYLLTGNTCL

AGDVMGEYAFDKKLKIGDKIVFLDQIHYTIVKNTTFNGIRLPNLMLLDHKNELQMIREFSYKDYSLRN

>pdb|3N29|A Chain A, Crystal Structure Of Carboxynorspermidine Decarboxylase Complexed With Norspermidine From Campylobacter Jejuni

MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDHPFTMFYEKIQTPAYILEEDKLRKNCELLASVGEKSGA

KVLLALKGFAFSGAMKIVGEYLKGCTCSGLWEAKFAKEYMDKEIHTYSPAFKEDEIGEIASLSHHIVFNS

LAQFHKFQSKTQKNSLGLRCNVEFSLAPKELYNPCGRYSRLGIRAKDFENVDLNAIEGLHFHALCEESAD

ALEAVLKVFEEKFGKWIGQMKWVNFGGGHHITKKGYDVEKLIALCKNFSDKYGVQVYLEPGEAVGWQTGN

LVASVVDIIENEKQIAILDTSSEAHMPDTIIMPYTSEVLNARILATRENEKISDLKENEFAYLLTGNTCL

AGDVMGEYAFDKKLKIGDKIVFLDQIHYTIVKNTTFNGIRLPNLMLLDHKNELQMIREFSYKDYSLRN

>WP\_079254160.1 alkaline phosphatase family protein [Campylobacter jejuni]

MMSKVILVVLDGLNCKSASINMGYLNALCKENLGKFYSLECELPSMSRPLYECLLTGVKPVLSEIINNKL

SFSKQTSIFDLCKEQGLKAGGAAYHWVFELYNKKEFIPSLHRHIEDENLTLPYGHFYYEDDYLDSHLFAD

GEHLRNKYNLDFTLMHSMNIDDAGHKFGSHSIEYANKTKKVDILISEYLPTWLEQGINVIITSDHGMTEG

KSHGGLSEDEILVPFFTFGSAFSYENAKIKQDEICGSICEILGLKHDKRYNDEILKAKK

>WP\_021137667.1 ATP-binding protein [Campylobacter jejuni]

MLYKRKNIKFKNFVDLHKNLSLSKLFDFYSVFEGFEKLNILNFEDDVFTNIEQILLDDYLKTKSYFALDE

TSSYALTLLAKNNRKRFSINRKIQHFKALSTLKYLLETGIIKLEYSKEAKKIKDKRQKIKKELRSYVVQD

KIIFGNHFTRFFFYFLKPNEKLILQNRYKEVLECIKEKFELYQSFCFEQLSRELLEKKFNINGVQSYWDK

NVELDLYYQDENLCFVGEVKFKNKKICKNILNLLKSKVKSLNLTPNYYIIISKNGFSKEFDKICEQNLLL

LDLNDFKILLEE

>WP\_002878296.1 MULTISPECIES: methyl-accepting chemotaxis protein II [Campylobacter]

MGIAKSLVAIFFYEVENFNDFKPRYLKTFIQKYSDFKYYYLNIRAQKLEMTNEINKIILNQLKQNTSEID

KNTSIFKEIFEELENIRRSLTTISESFTNFTNYLEYNLYQSEEKMNLEKEVQSSLKNIDQLNSILDLISG

IAEQTSLLSLNAGIDAARAGKLGRGFAVIADEVRKLSENTQMGLGEMEGAIKLVIQTIQSIAKSSNSSTQ

EMNFIRDKSNEFSKIISNLINSGKEISDKLKQRSNVGEDFEKNVNQLKCYEDVLAKLNQY

>WP\_002878002.1 MULTISPECIES: spermidine/putrescine ABC transporter permease PotC [Campylobacter]

MNENLSLKAKIYHYAVLFLVFLFLALPLMATFLYSISTSWGVSVLPDDLTLKWYQELFHDERFLLALWHS

LLVCVGSILLSVILVFPLVFVLNYYFLKLKAFVNILIIMPFAVPPIVSCVGLLQLYADNIGGTAWILIFT

YFTIALPFIYRALDNAISNVNLNELIASNAMLGGSLMGAIFKLVLPNLRNGILVAVFLSFSFLIGEFLYA

NILVGSAYETLQVYLYNIKNQSGHYSSALVIVYFVLIFITTFIASLIKE

>WP\_002877997.1 protease HtpX [Campylobacter jejuni]

MTLIAILCLYTALLSWISYAQIRFLEREKDKQAQILSEKDYQNAADIAIENEKFKLFSNFYNLIINIAWI

GFGFLYLKELLISSNTRFENTLFLLSFLIITSILNLPLSIYKSFIKDKAHGFSNMTVKLFIKDTMKSLIL

TLIFGFLILYALLFCYDFFGTFWWIAAFIFAFCIIVIINLIYPTLIAPIFNKMKKLDDENLLKKISSLMK

QCGFSANGVYVIDASKRDKRLNAYFGGLFKSKRVVLFDTLLKALNERELLAVLGHELGHFVHKDIIKALF

NGAITMFLLFFVFANLPEFVYLESHLEGVNGGVFALLFILANIFSFLISPMLNALSRKNEFAADQHGAKV

TSKEDMKNALIALARENKAFIKTSKIYTFFYLSHPSISDRIKALS

>WP\_002877674.1 MULTISPECIES: glucose-1-phosphate adenylyltransferase [Campylobacter]

MNAIILAAGFGSRLMPLTKDQPKCMVEYKNKKIIDYEIEALKSAGINEIAVVGGYLNDVLKNYLNKYDIE

HFFINSKYDKTNMVHTFFCAKDFILKCIEEKQDLIISYADIVYFQDCVQKLINAKEELAIVVDKSWRKLW

NKRFANPLEDAETLKMTNGYIIELGKKANAYDEIEAQYIGLFKFSYQFLSEVIAFYEMLDRDILYDNKNF

ENMYMTSFLQALIEKYNNAKAVEIDGNWCEIDFMSDLKINFI

>WP\_002877672.1 MULTISPECIES: phosphoenolpyruvate synthase [Campylobacter]

MAELKFKTKAQNLKNLQTKLKKAKVLSLVLTSLEELISNEDKVLQDIQTLKANRLIIRSSSLSEDSMKNS

NAGAFLSLANIKADSKDELLKALYEVANSMPSKSDEILVQPMLENITLCGVGFSVDKDNFSPYFCLQYDE

NGSNSSITDGSSKSAKTYYHYRDYLEFKDIRLQKIIELIKELEVLYNCCFLDVEFAFAIQDDEEELFCLQ

VRPLVMHEKNNLFHSLPKEALYRFYKRFESLKESRSRVLGDKAIFGVMPDWNPAEIIGLRPKRLAFSLYK

EIITDNIWAYQRDNYGYRDLRSHPLIHSFLGIPYVDVRLSFNSFIPKKLDENIAQKLVNFYLDKLNKNHE

LHDKIEFNIVYSCYDFNSSKKLEELLNHGFNENEIKRLEFSLLELTNKIINPRSGLYLKDIQKAYKLKER

YDGIINSNFSLIDKIYWLIEECKRYGTLPFAGVARAAFVAMQLLNSLVEIDFITKEEKDDFLNSLNTVSK

NLSKQTNHLNFHNKDQFLKDFGHLRAGTYNILSPRYDEDFELYFDVDQKDSKVYLQDKAFVFSEEKTKAL

NALLREHGLEINACEFFDFLKQAIEGRELVKFEFTRLLSKAIVYIEELGKYYGIEKEDLAHLDIKSILNL

YSSLYSINPKEQFVEEINRNKKEYELTQAIKLPSLLCNADEIFSFYNHSIIPNFITQKSITAFTAKENDK

DLEGKIVLIYAADPGYDYLFTKNIAGLITCYGGANSHMAIRASELGMPAVIGVGEENFEKYLKAKKINIE

CESEQIFCL

>WP\_002877671.1 MULTISPECIES: bifunctional demethylmenaquinone methyltransferase/2-methoxy-6-polyprenyl-1,4-benzoquinol methylase UbiE [Campylobacter]

MQKLVEQVWDYTKHAKFYSYRPNYAPKTIDMLISLVGKKDIKVADIGAGTGNLSIMLLERGCKVVSVEPN

DAMREIGIERTKGEKVDWVRATGLNSTLQNSEFDWVTFGSSFNVMDRNEALEEAHRLLKSEGYFSCMWNH

RDLNDPVQKIAEDTIVEFVPNYTRGTRREDQRPIIESRKDLFDNIVYIEEDFYFHQSIENYINAWKSVKN

PYWDLEADEGNELFNKISDKISQRLPKEFSIKYTTRCWSAKKI

>WP\_002877669.1 MULTISPECIES: bifunctional demethylmenaquinone methyltransferase/2-methoxy-6-polyprenyl-1,4-benzoquinol methylase UbiE [Campylobacter]

MKQGDFTEVAKHYHNRPAYSPFLLEKLVACINDKNKNLKDLNIVEVGAGTGKLTKMLGEMFGCQISAVEP

NDNMREEGQKFTQNLSNISWHKGSGEETCMSNNQADWVIMASSFHWTDPKKSLPEFNRILTGGGYFTAIW

NPRHIVEGSVFDEIEKEIKHIVPELARVSSGTQNVKKWEEILVSTGDFTDCFFMECDYKEFWDKERYLGA

WHSVNDIQAQAGEKRWKEILEMIEAKISHMQSIEIPYKIRAWTARKA

>WP\_002877559.1 MULTISPECIES: glutathione ABC transporter substrate-binding protein GsiB [Campylobacter]

MLRFLIFAMLLFVNLEAKIPKDTLIIAVENEIARINPAYSEDHDAVINLVFSGLTRFDENMSLKPDLAKS

WDVSKDGLVYDIFLRDDVLWHDGVKFSADDVKFSIEAFKNPKNNSSVYVNFEDIKSVEILNPSHVKITLF

KPYPAFLDALSIGMLPKHLLENENLNTSSFNQNPIGTGPYKFVKWKKGEYVEFKANEHFYLDKVKTPRLI

IKHIFDPSIASAQLKNGKIDAALIDVSLLNIFKNDENFGILREKSADYRALMFNFDNEFLKDLKVRQALN

YAVDKESIVKNLLHDYAFVANHPLERSWANSKNFKIYKYDPKKAEDLLVSAGFKKNKDGNFEKEGKILEF

EIWAMSNDPLRVSLAGILQSEFRKIGVVSKVVAKPAGSFDYSKVDSFLIGWGSPLDPDFHTFRVFESSQD

SALNDEGWNFGHYHDKKVDIALQKARNTLNLEERKKYYKDFIDALYENPPFIFLAYLDFALVYNKDLKGI

KARTLGHHGVGFTWNVYEWSK

>WP\_002877556.1 MULTISPECIES: Tat proofreading chaperone DmsD [Campylobacter]

MQKLAIDIFINFLQNPPNHFLLEKLKKEEFWQNWFLKNNSKLQCTALKLLSSSNEDDKLIASDFTSLFLS

DVDYVKAPPFASFYLDENKEIYSDNSDKVKQIFAQNNFFSFFNEEPADSLINELLFISFLIKKQDDITLQ

KFLKEEFFTWFNMWSFDVINKAKTHFYKALTMLMQDFFNQLNTKF

>WP\_002877519.1 MULTISPECIES: DNA gyrase inhibitor SbmC [Campylobacter]

MAEQEDIILEKPEDGLNQPRLDESLEGFKGQEGQAPEDEEFASLPEELPQENSDSGFKFTRESAPEDVST

FEEVESQEPTPWYKDRKFMSLVGLSLGIICILVFTLFYLTFSEGKIKPDIIASKPLEQPVVMPDESYKYN

DMQRIDGMIQKANALYLKGEVEQALKVYEQVAVYNESLSNYNLGVSQMNENKFQEAFESFKKAIANGENQ

SVAAINAAVCALKLNDKEKFRYYIDLAQVYLPKEGKSKLYDYYLSLINYYKGYYPEALQMLQRTDVEPYS

DVAKYLSAKIYAKMDFDSKAIQQLNSQGNFESSLSLGLLYARIGEYAKAKVALSTAMKIERDFNQSLAAL

TLVDIKTGNYQDMLARLQNSYDNDKDRYKILDAYKIQVRLNKDLFNIAVAQNSFSKDLLKKQKDQFDLLF

YFAPYQVFDSKQAALYIKKANVTDFVDDSADAGVYLNTSKALSSTNVKIANIINYALNQKLRLANQEFQK

LIKDYPEHSILHYNLALTYAQMQNYELAYKHFSSSYHLNPKNYLAGAFAMFCAKLIDIDTTKLYNEILDN

IAADSNFKANMQKSMLFLVNNNYISMLPYLDETKKDTPLSLIFEAIVAKNNNLNNQVDVKIAKLRSELPE

DILANILYFNSLNSNLNIKEYAQNAQIHFKNLKLDYRSVFGGPSIAREFYVNLMHIAGLLNLERQKFKEL

INVSGAKDEGILQTLAYLDIFAQQYEEAYALYNSLIDDYGAKDTKTLFLAAVAAVGANNPNSAIALLQLS

KLTDKNNKESKAALGMLYQEVKNYEAAISQYKTLPNNFKSEFFTFDINNN

>WP\_002877497.1 MULTISPECIES: coproporphyrinogen III oxidase [Campylobacter]

MNLFQNLALKYSHTMMEKSLQKGFNVELLKQPKEKIPKQDKSYMLYAHVPFCHTFCPYCSFHKYYYDENL

AKVYFQNLREEIKIMKDKGFDFSSMYVGGGTTLINEEELLKTLELCKKLFNIKEISCESDPNHIDPNKLS

MFKGIIDRLSCGIQSFDDETLKKVARYNKFGSSKELQEKISKALGILPIFSIDLIFNLPGQSEKQLLNDL

EIAKNLAPQQITTYPLMKSNLTKDNIAKSLGVSIKDNEFTYYQIIREFFKDYTQNNGWSFSLEKNKLNDE

YVSSHHEYLGVGSGAFSFLDGELLINAFNLNDYAKFIQEKQNANIAKACFDKKEIIKYIFLTEIFSGKIE

IDKFNKTLNCNLEKELFIELLGLKTSGAIIKDQNALIATEFGQYLFVVLMKDFYTGMDLVRAVFRDDKRL

KNKDYIDIMKENIDPLNSASMEFKAETN

>WP\_002877326.1 MULTISPECIES: prepilin peptidase-dependent pilin [Campylobacter]

MRKAFTILELVFVIVILGILAAIALPKMSSSKDEAEVSKSLNNLKTLINDISIYTLKNDHLSSIKTMSNV

IGVENVDLGNFNGTKEVNFGVGNDKECLKLVFINKADFILMGISSNEASKNAIINAANQSHEDLENIDFT

SSSSNKACVILSKNENFKNLASKTYLLIGGM

>WP\_002877273.1 MULTISPECIES: coproporphyrinogen III oxidase [Campylobacter]

MHFYIHIPFCESKCNYCAFTSLKKNDYEKAYFKALKEDIVFQLKQFNIQSNQIKTLFIGGGTPSCVDAYN

YEDIFKILYPLLDKNVEISCEANPNSATLNWLKNMKNLGVNRISFGAQSFHPKKLHFLGRIHNQEMIIKA

LENANKVGFKNINLDLIYDTKLDNKKMLEFELLHLKQIKALITHLSAYNLTIESNTAFAKKEHFKKNAPN

LMKFFIKQLLELDFFQYEISNFSKTKSQICKHNLAYWQGKNYLACGLSAVGFYENKRFYTAKNLKNYIEN

PTFRSIEQLSSKDLNLEHLFLGLRSIVGIDETKLNQWQKDKINILLKEKKLFYKNKRYFNPNFLISDELA

LYLSS

>WP\_002877036.1 MULTISPECIES: endonuclease SmrB [Campylobacter]

MSIYFVHFLISVLPLSILMAFITPDKKYIFKSFLVVFLGFLFGYFAFFIAAQFLKTENLIFNFDFVFIGL

LLVSFIFYFWKKIEILNFILLGILSFCTALHYYFLSQDFPIFTSSLIDSEGISSLGFIALALLVCILIFF

FLKWQKNFNQKTSFMLFLLLILIESDKALANILLTLMRNSIIETHTFLVSFVGKSNYFGVFGIYVYLIFI

TFLAFLSLKIRKKNISKKQILDINYRKNEAKTSLINRYFSSVFISCVISFCIILYFFMVSSKPLTIDEPK

EILPNKNGKFIFDIALLRDNKLHRFAYISAEGKVIRFFLINKREDRDSPVAVFDACMICGDMGYIKKDGQ

LICISCNVRIFLPSVGKSGGCNPIPLKYEYDGKKITIDVKDVIAGSNYFSQIKEIEVQDPVSKTKIINTQ

APFSYSYKGITYYFSNQNNYEEFKKDPTKYVEENEAQFLIQRRNDVG

>WP\_002876769.1 MULTISPECIES: two-component system sensor histidine kinase EnvZ [Campylobacter]

MTKNYSIYTKLIILFVVTFFLVCVLFIVLLKIEGNAYNEEESLKQENLIKNLLISYENTSGVEIGAYLGN

SGFNAIQNPHLVKAIRNNGQSLFKAGGELCTLSSLKYHSNLYFDVQCKDFDGLYEENTSDRVYNLLLIGF

FSFSLLVVFMYFSVLRSLEPLKKLRRQVAEVANGEQPDFLDYQEDEVGKIAFEFQKAFKKNQELIQSRQL

FLRTIMHELKTPIGKGRIISEMIKEDRQKERLIAIFLRMDSLINEFAKIENLFSKNYNLHFKPSRFSAIL

EEAKEHLMRDDFNKVVKVDIRYDALINVDMEIFSVILKNLIDNALKYSNNGTCELFCCKECFTIKNPGKP

LAEPIEHYLEAFTREKHNQVKGMGLGLYIVSEVCKLHNFDLIYFYDDGKHCFKIFFGDKEK

>WP\_002876687.1 MULTISPECIES: hydrogenase/urease nickel incorporation protein HypA [Campylobacter]

MHELSIVESLIELCEENALNNKAYNVQEIYVKIGRLSGIEVDLFKRCFETFKENSNICKNAKLFIELAPL

EILCLKCDQVSILEENVFKCPKCQSIEYKITQGEDLHLMRLVME

>WP\_002876664.1 MULTISPECIES: peptidylprolyl isomerase [Campylobacter]

MKKFSLVAAALIAGVALNVNAATVATVNGKSISDTEVSEFFAPMLRGQDFKTLPDNQKKALIQQYIMQDL

ILQDAKKQNLEKDPLYTKELDRAKDAILVNVYQEKILNTIKIDAAKVKAFYDQNKDKYVKPARVQAKHIL

VATEKEAKDIINELKGSKGKELDAKFSELAKEKSIDPGSKNQGGELGWFDQSTMVKPFTDAAFALKNGTI

TTTPVKTNFGYHVILKENSQAKGQIKFDEVKQGIENGLKFEEFKKVINQKGQDLLNSAKVEYK

>WP\_002871813.1 MULTISPECIES: tyrosine recombinase XerS [Campylobacter]

MKYPLDCEENFEKSFLFWLAKYVKFKLNSLSNKELKNPQALAEVNFALTKGVKNIDELDALAKKARNAGL

SGVNTYFNPLKKVFEYLNFYKLYSLKQIDEELIVEVLASITGALSDASKKNYRIAVINFFDFLDKQNEED

EKAHIFDINLKNWAGIAGSKGVKLPEFMSEEELKKFLDAIENADFRNNTVRNKLIIKIIIFTGIRVSEAI

NIKMGDISEENDLYIIRIRAKGNKYRVVMIKKELIYDLLKNVSINYMSKDALLFVNKKGTPLTQSYVSRI

VEQLLFRAGIRKQKNGAHMLRHTFATLLYKKQKDLVLVQEALGHASLNTSRIYTHFDNDKLKLAAQVAKE

LSDS

>WP\_002866839.1 MULTISPECIES: DUF411 domain-containing protein, partial [Campylobacter]

MKKTILTILFLLTLTQAKEIQVYESPTCGCCDLWADYMKAKGYEVSVHKTNDFLKIKEKMGIKDEYQSCH

TGVIEGYAIEGHVPESAIVWLLENKPKDVIGISAPGMPQGSPGMEQGYSEKYPVILMKKDGSYELYGYFI

GDKKL

>WP\_002866496.1 MULTISPECIES: RsmB/NOP family class I SAM-dependent RNA methyltransferase [Campylobacter]

MQNILSSFTQEKNVCVFANTLKISIEELEKEFLKQKLKFKKINAYCYLFDAKDKAILSSMKAFNEAHFYI

QNYSSYLCALNLEVKAGQRVLDMCAAPGGKSINLANFMQNTGYLACNEMSRDRFFILQKNLKNYGVNAKV

FMKDGKNIGNLCPLKFDKILLDAPCSTFAKIGFDLEKSYKEIKNIAKTQKKLLHSALKALKIGGELVYST

CTFTKEENEEVIENALKSEFKLELLDIDLENVEAKAGQSEEFAEISKCRRILPSLDYDGFFIAKLRKLC

>WP\_002866137.1 MULTISPECIES: UDP-N-acetylbacillosamine transaminase [Campylobacter]

MRFFLSPPHMGGNELKYIEEVFKSNYIAPLGEFVNRFEQSVKDYSKSENALALNSATAALHLALRVAGVK

QDDIVLASSFTFIASVAPICYLKAKPVFIDCDETYNIDVDLLKLAIKECEKKPKALILTHLYGNAAKMDE

IVEICKENEIVLIEDAAEALGSFYKNKALGTFGEFGAYSYNGNKIITTSGGGMLIGKNKEKIEKARFYST

QARENCLHYEHLDYGYNYRLSNVLGAIGVAQMEVLEQRVLKKREIYEWYKEFLGEYFSFLDELENSRSNR

WLSTALIDFDKNELNACQKDINISQKNITLHPKISKLIEDLKNEQIETRPLWKAMHTQEVFKGTKAYLNG

NSELFFQKGICLPSGTAMSKDDVYEISKLILKSIKA

>WP\_002866045.1 MULTISPECIES: ATP-dependent metallopeptidase FtsH/Yme1/Tma family protein [Campylobacter]

MKNKKIILASFMVLCMLLGILYFKNEPKYIDENLYQSLLSQNLIQKAVIDKDEIWLKAEGENYVIIKDGI

DIKTLLAKVPVEVKKDNTLWVFFILLVFIIALFISLGYFARKKELAKYPISNKNQNHTQAQNSNINLESS

HIKPVISNITFNDVAGVDEVKMELSELVDFLQNPKKYKEFGVKMPKGVLMVGPPGVGKTLIAKAVAGEAG

VPFFYQSGSSFVEIYVGMGAKRVRELFSKAKMMAPSIVFIDEIDAVGKARGEMSNVERDSTLNQLLTQMD

GFEDNSGVIVIAATNKIELMDPALLRSGRFDRRIFLSLPDFKDRLKILEIYMKDKNNNVNLNKIAKASVG

FSGAGLETLVNEAAINALRRNSALVEESDFYAVLNKVLLGKKKILSFNDEEKKIQATYQAAKALSAYYFD

IGFEKITLIEDRFKEYEHNIRSKSELINRIKVYLAGSRAMRLIYNESYTNSQDDFLKIKELLDYMLSFDM

LEEPNLNEQKKEMDEFLNSMKDKILKLSELLLEKEKIEHDDVKNIMQV

>WP\_002853531.1 MULTISPECIES: UDP-N-acetylbacillosamine N-acetyltransferase [Campylobacter]

MARTEKIYIYGASGHGLVCEDVAKNMGYKECIFLDDFKGMKFENTLPKYDFFIAIGNNEIRKKIYQKISE

NGFKIVNLIHKSALISPSASVEENAGILIMPYVVINAKAKIEKGVILNTSSVIEHECVIGEFSHVSVGAK

CAGNVKIGKNCFLGINSCVLPNLSLADDSILGGGATLVKSQNEKGVFVGVPAKRKI

>WP\_002853468.1 MULTISPECIES: ATP-dependent metallopeptidase FtsH/Yme1/Tma family protein [Campylobacter]

MNNNTPNNKGNPQGNNFFNKNPIFIFAIFAIVMIIIFKGFFDGNGSFGGALNGNEVNKNVPYSELKKLIE

SGQINQVSIGQTTIKAISSSHNTVYTAKKVNDPELVSLLDSKNIAYGAYSETNWFTDILFSWVLPVFIFF

GIWMFLASRMQKNMGSSILGIGSSKKLVNSEKPKVKFSDVAGVEEAKEEVKEIVDFLKYPERYIKLGAKI

PKGLLLVGPPGTGKTLLAKAVAGEADVPFFSVSGSSFIEMFVGVGASRVRDLFENAKKEAPAIVFIDEID

AIGKSRAASGMMGGNDEREQTLNQLLAEMDGFGTESSPVIVLAATNRPEVLDAALLRPGRFDRQVLVDKP

DFKGRCDILKVHMKDVKISPKVKVEDIARLTAGLAGADLANIINEAALLAGRDSKKYVEQNDLVEAVERA

IAGLEKKSRRINEKEKKIVTYHECGHALIAETTKGAKRVSKVSVIPRGLAALGYTLNTPEENKFLMQKHE

LIAEVDVLLGGRAAEEVFIGEISTGASNDLERATDIIKAMISMYGMSEIAGLMVLEKQRNTFLSGGQTIK

DYSEKMAESLDDYVKKTLDERYKDVKDTLNTYKGAIETMVAALYEEETIEGNKVREIIKEFEDQNSLPTR

LQELEEVKTEVKVEE

>WP\_072225851.1 MULTISPECIES: DNA-directed RNA polymerase subunit beta/beta' [Campylobacter]

MCDMLDNKLGNRLRVDFSNISKQIEIPNLLQLQKKSFDYFLNLDNGESGIEKVFKSIFPIHDPQNRLSLE

YVSSEIGKPKYTIRECMERGLTYSVNLKMKIRLTLHEKDEKTGEKVGVKDIKEQEIYIREIPLMTDRVSF

IINGVERVVVNQLHRSPGVIFKEEESSTVANKLVYTAQIIPDRGSWLYFEYDAKDVLYVRINKRRKVPVT

MLFRALGYKKQDIIKLFYPIQTIHVKKDKFLTEFNPNDFMDRIEYDIKDEKGKIVHQAGKRLTKKKAEQL

IKDGLKWIEYPVEILLNRYLANPIIDKESGEVLFDSLTLLDESKLAKIKEQKSFDIANDLANGVDAAIIN

SFAQDGETLKLLKQSENIDDENDLAAIRIYKVMRPGEPVVKDAAKAFVNDLFFNPERYDLTKVGRMKMNH

KLGLEVPEYVTVLTNEDIIKTAKYLIKVKNGKGHIDDRDHLGNRRIRSIGELLANELHLGLAKMQKAIRD

KFTSLNADLDKVMPYDLINPKMITTTIIEFFTGGQLSQFMDQTNPLSEVTHKRRLSALGEGGLVKERAGF

EVRDVHATHYGRICPVETPEGQNIGLINTLSTYAKVNELGFVEAPYRKVVNGKVTNEVVYLTATQEEGLF

IAPASTKVDAKGNIVEEFVEARQDGETILARREEVQLIDLCSGMVVGVAASLIPFLEHDDANRALMGSNM

QRQAVPLLTASAPIVGTGMEQIIARDAWEAVKAKRGGVVEKVDNKSIFILGEDDKGPFIDHYTMEKNLRT

NQNTNYIQHPIVKKGDIVKAGQIIADGPSMDQGELAIGKNALIAFMPWNGYNYEDAIVVSERIIREDTFT

SVHIYEKEIEARELKDGIEEITKDIPNVKEEDVAHLDESGIAKIGTHIKPGMILVGKVSPKGEVKPTPEE

RLLRAIFGEKAGHVVNKSLYATASLEGVVVDVKIFTKKGYEKDDRAIKSYDKEKMALEKEHHDRLLMMDR

EEMLRVCALLSKAPLNSDQKIGDKNYKKGQTADISELEKINRFTLTTLIKAYSKEIQKEYDDLKNHFQNE

KKKLKAEHDEKLEILEKDDILPSGVIKLVKVYIATKRKLKVGDKMAGRHGNKGIVSTIVPEVDMPYLPNG

KSVDIALNPLGVPSRMNIGQILESHLGLIGLRLGDQIQEIFDRKQKDFLKELRAKMLEICSIPRLASEKE

FIKSLSDEELLNYARDWSKGVKFATPVFEGVNIEEFSKLFEMAKIDMDGKTELYDGRTGEKIAERVHVGC

MYMLKLHHLVDEKVHARSTGPYSLVTQQPVGGKALFGGQRFGEMEVWALEAYGAAHTLREMLTIKSDDVE

GRFSAYKALTKGENVPATGIPETFFVLTNELKSLALDVEIFDKDEDNE

>WP\_002878153.1 MULTISPECIES: high-affinity branched-chain amino acid ABC transporter permease LivH [Campylobacter]

MMVRIKVSHLIFLIASIVFIFVSPYIFGDYGLNIVNQIAIFIILAVSYNLINGVTGQFSLEPNGFVAIGA

YAAALVLLSADAKNDQFFLDGPSSFILAIHSNSFILALIVAGICSSLLALILAFAVFRVRGDYLAIVTLG

FGIIIKIAAINFPSITNGSRGLVDIPQFSTIYWTGGIAIVAVILILNIVYSKYGRAMKAIRDDEDAASAM

GINTFWIKTLAFSTSAFLEGVGGGLLACLLTTVSPTQFDFLLTFQLLIIIVLGGLGSTTGAIIGAILVIG

GSEWLRFLDELNIKIDSLNLDIQSTPGLRMVVFSIVLILVMLFARKGIMGYYELSDVIRGIKKRFKRSEK

>WP\_002878123.1 adenine-specific DNA-methyltransferase [Campylobacter jejuni]

MNYKKAFYSKLEDCYLGAKIKSSQNQAKNGFTNLLVIKEKYFQKIKDYLDTQKLYTDTYNKLYNFFSTYL

NETGTPFFYDTPMYKNIYARVYSNSKDTSLFYKTQNLYYVKSDTIYNPLSLQSEDKKYTLNFLTDEYEQN

ADNNKSKINFYLQNIQDDNINIKVINSKNHDGTNVFKQNPSEFSDVFLKTLKNAQINIKEEELKKLFKTY

KKQNEVDFFIHKNAKEFLKEQFDLWLFSYVNDSITEWTKEKIDEINDLKQIAFDIIDLIADFENELKAIW

LKPKFAKNVHYVFSLDTIKSHSNNADEILKSIYKDVNFNEQIAEWEELNFINDEFDIKAINDEKYKFLPF

DTKYLSEENYYKLLSAFDNLDEILNGELVKADNFQALNSLMPKYQGKIDLIYIDPPFNTGSDFDYKDKFQ

DSTWLSLMHNRLELAKEFLSDKGNFYLHLDENADYFGRILLNEFFGEMECKKITFDTNATKDEEADLFGY

KSFGNNFVLKSSTILFLKKTNSIFNKLWKPNRNSSLLNLGQLDLIGISTIETPKKITDYEYYVQIWKNGK

LCHEKIDIKDEKIYPLGDIWNDLYSFTQSEMRVSENISFYSSQKPENMLRRIIQSSSDENSVVMDFFVGS

GTTLVVSHKLNRKYLGVEMGEHFYEKYLTFNKDTKQYEYRLGLLGRMKNVIAGDIEFYAIDKKRRSSLSK

MINFKGGGAFRYYELEGYEESLENCEYKLDENSLIDYRKSRKLIKALKKGENICLDMNAYDKELDIFLTM

SNLLGLKIKNIFIDNNGIKSCKFENDEVINLENIDLIKYPKLKNLIWWEK

>WP\_002877959.1 MULTISPECIES: methyl-accepting chemotaxis protein II [Campylobacter]

MFKTIGFKVSAAIFVVLLISFIVMQVILNLDFKNTANKMSRANLDTVSTSVFQTMRMAMNLGDPEKIKEA

IEDAKSIEGISDIKIYPSKDTIDLFEMKAPQISNDKRIIEQFSNPKIQALEENVNGVVHLRLIRPLIADE

SCVACHANANVGSVIGVMDISHSLEGVQKDISKTSQSYIIIFTIALIFTLCVVLLMLKVVVGKPVLELLN

HAKELAQGSGNLKARISVKGQDEIALACGYINQFIEKTHKAVSGASHNSKNVEKQSNLLNSNAISLSDIS

SQSHKQIDQSFKLGANVGNELGELASLSNKANSANEKSFLLLEQMLKSLFNVANKVSTVSQNENELAKKV

ENMVNQAGNIQKATQMMDEIADKTNLLSLNAGIEAARAGAFGRGFSVIAEDVRQLAQNSEEFLGNVAQIT

KELLQSINEVSAELKKNAQSVQALNDDTALLVDDANEVKLCNEDARALVTQCTEKIKISQENIQNLLSRM

QENVEVSEKNEEISKILLQVADELKIVCHNLESELNQFQI

>WP\_002877869.1 MULTISPECIES: (2E,6E)-farnesyl diphosphate synthase [Campylobacter]

MNLKELFIHHLEKNLPKVESFHPFFNEALALMLKAGGKHFRAQLLLSVVQSNKPELLNQALDVALALEFI

HTYSLIHDDLPAMDNADFRRGIPTLHKSYDETTAILVGDALNTEAFLVLSHAHLKDEIKIKLIKTLAFNA

GLNGMVIGQAIDCFFEDKRLSLNELEFLHTHKTARLIAAALKMGCEICELNNEESNQIYKLGLKLGLIFQ

INDDIIDVTTSQEQSGKPTNNDTHKNSFVNLLGLEQAIKTKENLLSECEQDLEKLNEKLAQMIQNLIIQY

L

>WP\_002877783.1 MULTISPECIES: proline/glycine betaine transporter ProP [Campylobacter]

MQELTRTKKIRSIIAASSGNLVEWFDFYIYAFTATYFAHTFSTSDNPVIQQINAFGVFAAGFFMRPIGSW

LFGSLADKVGRKKSMVISVVLMALGSFMIAALPSKDTVGDLAIILLLIARLIQGLSVGGEYGIAATYLSE

LATEGKRGFYSSFQYVTLIGGQLLAVASISIMFLFFSIDDMKDYAWRILFVIGGILALGSLFVRKMMNES

ATKLHQHEDRGTLKALCKSWKPFLMVLGVTSGGSLAFYTITTYTKTFMENTGMDKMLVNNLFLGALFILM

IIQPLFGYIGDKIGHKRSLIVFCILALVGIYPIFSLIANNAQNNPSLTFMLVVLLFVILSFYTSVAGIFK

AKLFPEHVRALGTGLGYAISNAVFGGSAPWVALQFKNAGIENGFFIYIAIFTIIMLIATLYLPKKSQLN

>WP\_002877750.1 EscU/YscU/HrcU family type III secretion system export apparatus switch protein [Campylobacter jejuni]

MKKAFILIESISAITIISLIFIGIFYHYTQLYKNYENLNIFERLYKLQEELYEKPIFKTIILQTSALKPI

VLQEQFINDGIFQFQKLYFQDQNYSVYFKE

>WP\_002877685.1 potassium-transporting ATPase subunit KdpA [Campylobacter jejuni]

MLEILITLIIAFILALIFGNYLYKIASCKKTIFDFIFNPIDNLIYKICAIDRKNMTWQKYSLHLIAFNAL

VAIFSFVIFYLQDKLFLNPNLINSMKGDLNLNTVISFITNTNLQHYSGESALSLLSQNTGILLAMFVSSA

SGYSACMAFCRALCGMQMGNFYEDFTRIITRLMLPLSFILAVIFISEGVVQNYHANFSVLTLENKFQSIA

TGPVAALESIKHLGTNGGGFFGANSSMPFENPTSLTNFLQILSMMLIPSACVVAFGLMVYHRKERQGFAL

MGKEGGVIFGAMGIIFIISLLLIYFSEKMSNPNLDSLGLNANLGNLEGKEIRFGTDGSSLFSAVTTAFTT

GSVNNMHDSLNPLSISATLLNMMLNVAFGGEGVGLMNMIIYVLLTVFICALMIGRTPEFLGKKIESAQMK

LIALVILIHPLLILVLSALAVVFAKDSISNPSFHGLAQILYEFSSSAANNGSGLEGLKDDNLFWNLSTAF

AMFCGRYLVLIAQLAIAGSLLAKNTQENTANSLKTDNLTFMFVLVCIIYIFTALTFFPVLTLSSVAEYLS

LWH

>WP\_002877682.1 MULTISPECIES: two-component system sensor histidine kinase KdbD [Campylobacter]

MQRQSPEQILKKLEVKAKEEEKNKLAKLKIFLGYAAGSGKTYAMLSEARTLRDNGVDVVLGYIEPHDRPE

TMALTQGFESIANLEIPYKNIVLKEFDLDATLKRKPALVLVDELAHTNAKGLRNEKRFQDIEELLKAGID

VYTTLNIQHLESLNDLVANISKIEVKERIPDRIFDEADQVELVDIEPNKLLKRMQDGKIYKEKQAKLALE

NFFRQERLIALREIALRRLASRVNLRASEQRLINDDLAYHTGEHILVCINASNAKVIRAAARLALAFHAK

LSALYIKNPNIKEEKALEENIELAKSFDAEIISVYDDDIARQIAEYSSLSNVSKIVLGKNKDKKKFKEEI

FEAVAKKAPNIDLYLVNENQISTPKIRSKKGFDFLGFLKITGVLLLATFIAFVFHKFNTQPSNIVMIFIL

AVFASSFISDNKIFAFYSSLVSVLIYNFFFLEPIFSLKVHDSGNIITFTTMFIVGFLTAVFTRRLKLQSK

ELTKRAYRTAILLENSEKLARVKSKQELWEQLGNQALKLLNLPIIIYPINKNNILSKPLLFFNDDKQMLK

NCFSADEIAIAQWVATNKERAGVCTNTLPNANAMYLPIEDGEKTKGVIGIVLKEKRPLQDFQYEILSALL

NEAGVRTRDIFLL

>WP\_002877662.1 MULTISPECIES: putative DNA-binding protein [Campylobacter]

MTYKEIKDKTPYEILDLLEMKEPPFNPFEIAQKLGINVVKDLDLDKIDTEGQISVDEKGEPIIWINPLKN

ENRQRFTLAHELGHLANDILPSIENPIIDSYETLYRSNTYGGIETRANQFAARLLMPLRQIEDFIAECRK

TTPDLKAAEAILLIASKFEVSKQAVFHRLKNVGLIKQDYTYPF

>WP\_002877562.1 MULTISPECIES: nickel ABC transporter permease subunit NikB [Campylobacter]

MLKRLVFSIVVAFFSTFLCFVLLYFSKGSIAYANGVNSQSKEFVQRIEQNLGLDKPLLEQYKIWLFKALK

GDLGVSFLSGESVLKLIKERIFNTFILGFSALMLLFLLSVFLALLGYSYKESFIDKIITFLAFNFFALPP

FVLALLFVLIFGIFWKILPVMGSSDIGFEDDFLNRLEHLILPVLVLVLSHLALFLRIARNFINESFSQIF

IQNLYARALREKDIYFLVLKYSLSPIVAYFGGSALSFMMGTYVVESVFAYEGLGSLLFKSIIFKDYPVVL

ALIFFSVLLAAFFTFLSDIVARILNPRLRRLDFV

>WP\_002877515.1 MULTISPECIES: multidrug/spermidine transporter subunit MdtI [Campylobacter]

MLKVIKHNLGIYFMILACLDFALMGACAKILSKEMSSIEIMFFRNIIGIFFIVYLLKRSKAHKEGGHFWL

LVFRGVVGTLSLYMFFYNVSNITLGGAFAFQKTAPIFITLIAFVVFKENIGIKGWIGILIAFGGVLLIAQ

PWAHNLNHSGFDLKNSVIGITSGFLAALALTSVRELRKSYTTEQIAFSFILLGTLMPLISMISAEFFEPQ

HLDSLHLDFILAPFVMPSLTAWLIIAIMGTLGTIYQIHVTKAYGIAKQAGVVAGVSYLDVVFSMIVGIIL

GDNLPSTMVFLGIIGIIFGGLILVKNKGKK

>WP\_002877347.1 MULTISPECIES: L-cystine ABC transporter ATP-binding protein YecC [Campylobacter]

MIEVKNLQKKYGELEVLKNINTTISKGDVIAIIGPSGGGKSTFLRCINRLEPADSGEILINKQNILDKEI

DINKIRQKVSMVFQHFNLFANKNVMENLCLTPIKTGILSQEEAIKKAKILLAKVGLADKENIMPHKLSGG

QKQRIAIARSLMMNPDVILFDEPTSALDPEMIGEVLSIMKDVAKEGLTMLVVTHEMGFARNVANRIFFMD

KGKIAVDASPKEVFENPSNERLREFLNKVLNH

>WP\_002877257.1 MULTISPECIES: putative succinyldiaminopimelate transaminase DapC [Campylobacter]

MLTKRSQVLEESITLAITALANELKAKGEDIISFSAGEPDFDTPQIIKNAAISAIEKGCGKYTAVAGIPE

VLKAIQIKFKKDNNLDYETSEIITNVGAKHSLFECIECLVEKDDEVIIPSPYWVSYPEMVKFAGGKPVFV

EGLEENGFKITAEQLKKAITAKTKVLMLNSPSNPVGSIYSKEELTQIAKVLEGTQITVLSDEMYEKLRYD

GFDFVAFASVSEDALKRTVTINGLSKCGAMPGWRFGYMASKNKALISAVKRLQGQSTSNICSITQHAAIP

ALNGECDKDIEKMRQAFEKRRNLALDILKQIPNISVYKPEGAFYLFVNIQKIEKDSMNFCQKLLEQEKVA

VVPGVGFGMDGYFRLSYATSDELIKKGLERIANFIKNYK

>WP\_002877189.1 MULTISPECIES: type II secretion system protein GspL [Campylobacter]

MKIYSVILGAFLLGACSLKDQAIVDINLKSQTLMFTQKYKITQDKINAIITMSYLNPILDKTSKDDVLAL

SFTPNTLKIQNLEVFINNKKANIEKLDDEYLKYIIQNNYTDYFKVSLPNVKEETKLVTKICLDHLPCFEL

NFQKYPKSLYYRSEDVDTQYN

>WP\_002877124.1 MULTISPECIES: D-glycero-beta-D-manno-heptose-1,7-bisphosphate 7-phosphatase [Campylobacter]

MFIFFLKKLYYNVFMKTKALFLDRDGVINIDKKYVYKIEDFEFCDGIFELCRYFLARNYLLFVATNQSGI

ARRYYKESDFLKLCDYMLKEFAKQDVKIDKIYHCPHLEGCECRKPKAGMLLKAKDEFDLDMKNSIFIGDN

LSDMQAGLNANIGTLILVNEEKKEGDFFRQFKNLKEILSFFKEKDI

>WP\_002877106.1 MULTISPECIES: methyl-accepting chemotaxis protein II [Campylobacter]

MVKNGLLLTIFLSVIGVLGVIFIHIFVGAIIFVLIAVLMIYLLRQHKDEQIMIDKLLVLCRELKEGNFDN

RIIYVKTKSKKLAEIADNLNNTIDGLEAYLREINTSISCSQKGEFYRKALPEGLKGIFAHNIEFINKALA

NIEVTARSTFKNALSRTLMDLSLGNQNKDMSQISSSLNQDISMMKNVYDTVDAITHTATENGSEVDSLQS

AMGSLMDVVNSSKETVQTFVANSQNITSVVEVIRDIADQTNLLALNAAIEAARAGEHGRGFAVVADEVRK

LAERTQRSTSEISIAIQTMQQDFVNIQSGSEQVFNIVSESEERINKFSQAFKRLEENSSALGVNFGSFAK

RLILSVVKIDHILYKSNIYLNLNGAQNFNLESVDPISNLCQDERAQGVINELSSETELNLAKEFIKDNAK

KAIEESNQDYIDQKAYDAIVNDIKSLEQRSAEILAKLKI

>WP\_002877063.1 cysteine/glutathione ABC transporter ATP-binding protein/permease CydC [Campylobacter jejuni]

MLKKLFFILSKEDKNFLFFLLVFSVFVSFIETFAISLVMPFITLASDFSYFDRNKYLISLKEYLNIPVFE

IIVYFGVGLIVFYVFRALLNAYYFHLLARFSKGRYHAIAYKVFSKFLNINYEKFTQKNQSEILKSITGEV

YNLSTMISSFLLLMSEIFVVLLLYALMLLINYKITLFLSIFMVLNAFILVKILSPIIKKAGLRREEAMKN

FFEILNTNLNNFKFIKLKTKEDGVLSLFKAQSEAFSKANITNESVAAVPRIYLEGIGFCVLVFIVVFLVL

KNESDISGILSTISIFVLALYRLMPSANRIITSYHDLLYYHSSLNIIYQNLRQEEENLGEGKLSFNQELK

ICNLSFGYEGKKYLFKNLNLNIKKGEKIAFIGESGCGKSTLVDLIIGLLKPKEGQILIDKQELNASNAKN

YRQKIGYIPQNIYLFNDSIAKNITFGDAVDEEKLNKVIKQANLEHFIKNLPQGVQTKVGDGGSNLSGGQK

QRIAIARALYLEPEILVLDEATSALDTQSEAKIMDEIYKISKDKTMIIIAHRLSTITQCDKVYRLEHGKL

KEEK

>WP\_002877056.1 MULTISPECIES: glycosyltransferase [Campylobacter]

MNISIVILTFNSQKYLQEVLQSVNFANEIILIDSGSTDDSLIIAKTFKNVKIFHQDWLGFGKQKQFGVEK

ANNDWIFVLDSDEVFTEELKEEVLQIIKNPSFKAYKVARLNFFFGEAITKMGLYPDYNIRLFHKKYAKFN

EREVHESIICQEKIGKLKHHFLHYAYENIEQFIDKQNKYSSLNPKKNNLLKALINPYWTFFKLYFVKLGF

LEGKRGFIIAKLYAQYTFWKYIK

>WP\_002877021.1 MFS transporter TsgA [Campylobacter jejuni]

MNGKTYKFHPNDTKMDKKIIQITEKSGFKAAVFSMAAMTMLGSVVISSALPAINRHFEELLTQSGATLAS

SFTLAHLDILVRLVLTIPAIFVVILSPFAGILIDKFGKLKFILPAMVVWTISGVSGFFLNDIYAILTSRA

IFGMATAFIMTGASALLGDYYSRGGFNRRENALSLQGFFCAVGGAVFISIAGFVSSYSWRYPFLVYGLGI

LITLMAIIYLFEPRKFKFYNHTKIEAKTNYWQFFPIYFIGFFIMVVYYISPTQLPYYIEEHLGLDPKYIG

ISMSVSALCYGFFSLSYRYIIKFLSIKTIYVLTLFIVSCSFSLLFLVDSFFTVLIALALLGMGGGIMLVN

NTAYLFSICPENARARAYGILASCIFLGQFLSPIISQPIVRQMGLVDAFLIWSIVIFIVCIVFLFLKQKP

RIN

>WP\_002876965.1 MULTISPECIES: uridine kinase [Campylobacter]

MDFFKNGGVIWITGLAGSGKSYIAEALYKKLKEKYNNIIYLDGDELRDLLEHYGYDKQSRIDMSIKRSKF

AHFLSSQNMLVIVSAISMWNEIYEHNKKTLKNYFEIYIKCDFEELKKRDKKNLYSKNLKGEISNVVGMDI

DFDEPKSNLIIDNTYMTELDNKISYILTALKEKK

>WP\_002876954.1 MULTISPECIES: DNA replication initiation control protein YabA [Campylobacter]

MLEDDFIKERQNIRQKMLKFSRAINQGKPLDDDLRDEISSDDILRRRFKKKTPNKFLEELDEEYESKHTK

KSNIYLKEDLINVKLEEKQSLAKKFFSKMKERKKEENKKTKKIFSFGRKKINKIKNIQTKPKIQTKNDQN

PIQDKKEKKESIKSIEKIQKTEPKIQNSQTIEKRPDIKKQPDIKQSLENLQKKITPQENKQELPKPSNQA

QEKQQNDEDAQKAKNVLLEGFSNATKEDRNLNFNHLLFAALLVSFALFLFAPQIYIRNQIYYLSREIATL

RTEESVLNEENKDLKRRLENMRFQNQILDYLE

>WP\_002876900.1 MULTISPECIES: ferric iron uptake transcriptional regulator [Campylobacter]

MELLQMLKKHELKATPQRLCVLKILKRHEHPNIDELYTEIKKEYPSISLATVYKNLNTLQEQGLVVEINV

LNQKTCYDIYEEEHIHVVCTKCGGIEDLSFKDAKLYEYQEHLEKKIGNLVNHLSVCAYVDSCKKCH

>WP\_002876800.1 phosphoglycolate phosphatase [Campylobacter jejuni]

MINVFFDMDGTLIDSANAISCTVNEIRQDLNLAPLSREIIMQTINTPNIDWAKELYNIENFHHSSFKEGY

EKYFVKHYEQSVVLFEGVKELLEFLKSKNCFLAIATNAPQSSLSNILKKHQIIPYFDKILGVNLGIEPKP

HPMMLELLKSEAPYKTSVFIGDSQKDKECAKNANLPYFHAKWYQKDLKENEFSNASELKGFLEKYL

>WP\_002876785.1 LPS assembly protein LptD [Campylobacter jejuni]

MWRKFSLLLGTSIALNAAQVDIYALDAKKEGDILTANNDVIIFSDFYFITANKAIYNEKTGDVELFGDVN

ILRGQNERSHSDYAKINLNSNQADFSNFFFSNNNLEVWFQSKTSHLNDKVFESKISAVSSCNVEDPDWEI

RFSKGWLNRETNFVHLYNARLYVKNTPVFYLPYFGFSADTHRQSGLLIPKIVLKSSEGLYYEQPIYIATQ

ENWDLELDPQIRTNRGFGLYSTLRFLDSPYSTGELNFGAFRENSSYFHDENLKNQTHYGIELKYSRDDLI

KSLLSDNFQEGLWIDATYLNDVDYLNLGSRDYRDLNSLVTSKINYFLADENNFYGAYARYYIDTSKLSNN

TTLQEYPSFQYHRFLNNLFDERLRYSFDASFHNFYRPAGSYANELNLDLPISYHNAFFGDFLHFTFTERF

YASFVNYSNDPERNHEHYFRNTHDFNLYTDLSKAYENFFHTLNLGVNYILPGAKSGKITQNYLEEYDKEN

EHTSLYAVQYFYNNEGQKKLKHRISLDYLNKQNEFYELQNLLTYYFNENINLNSEVLYSYEQSRFTNVIS

QIEVNTNSKFNWMFSHAYQNDEYGKYSFIGTRANYIATPNYNLFGGIWFDTQRAHANMWELGYTYQRKCW

NYSLMYRERIDPQLTSGGITAKNQSGVYFIFNFYPLGGVKYDFSLAESENKI

>WP\_002876763.1 MULTISPECIES: N-acetylmuramoyl-L-alanine amidase AmiA [Campylobacter]

MAKIFVFLVFVFTTLFGAYENELANFDKNFIGSKSEVQVKFHHQLKSLYIQSVINEDEKTKIEILKRLII

SSNTLNLDDKSYANELKESGISEASINALRKAVIKDIKVQNISQDTEKSTFEPIKTVQKNEKKSSNEQIK

NTEKTNSKTSQAPKSSIVSKAKSDDKIYVLKSSKTNQGVEFELNADLDKDQLKSFALDEKGNYRFISDFE

GVLEGGKKEFKFDDYRLVISQFNPKTIRIVVYAKEKIPIDISFKEEKLIFSKETTSQKKTEQVSKISEKK

QDQKTEIKTKALETKKQDKKTNNEKENQEPLYVLDVDKISNAVVLNLSDDLDEKEIAVFDTKDQKFRYVV

SFKGVLEGNRKSFTFGQNVITVTQYNPKTVRVVLSAPKEFKLLKELDNKNLTLGFYAQTTNQNVNKKATQ

SSSKTLNTNYKSGKLVVIDAGHGGKDSGALSDKKGSLKEKDIVLSTALKLGNELKKRGYKVLYTRSSDKF

INLRDRTKYANDKRADLFISIHANAAPNATKAKSSEGVETFFLSPARSERSKKAAEKENQGDFEEINYFS

KQSILNFLNREKIVASNKLAIDVQKNILTQTRKKYKIVDGGVREAPFWVLVGAQMPAILIEIGYITHPNE

GKRIANKAFQDLLVKGIADGVESYFYNNR

>WP\_002876692.1 MULTISPECIES: class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI [Campylobacter]

MSKKKLVQIQRYLIIAILFLLCIALALGILVKYQNSQDVSSVKPDYFIDKQEDLISSNKDHYEIGIFQEN

EFDNNKFVSILEQKIQEIDDLNTSLNEQNLSSVEQNLSLEQNQSLEQNFIPKDTNLTQDQNLTFNEDIHL

NKISKKPKLAIIIDDMANASQVRGLKALNLKLNPSFFPPDKNHSETPKLALKFDFYMVHLPLAAINYNKP

ELDTLNPNDSKERIFKKIKQIKKDFKDLRYINNHTGSLFTSNEEAMRKLYEVLKNQNIFFVDSKTIGNSK

ANKIAKELNVPYIQRDVFLDNEDDVNYVKKQIQNAVKLAQKKGFVIAIGHPRKNTFKALEQSKDLLKSVD

LVYLSEIYGK

>WP\_002876671.1 MULTISPECIES: FMN/FAD transporter [Campylobacter]

MAKKQLSLTRLSFPIFWDLLSKYLTVIINTAMVSHYSNFIVGAMGAGNQILDLFITIFSFLSVGCSVVIA

QAIGAKDHVLARKVIHQSLFLNALLGFVCGVLILWHGEYLLYLLKIPQELLKDSEIYLHMLAICLFFDAI

GIVLAAIVRVYNMAYWVMFIGFLMDIVVICGNYYVLHYTKSELFGIGLSNIFARIVAIVALFAILFYKLK

IHLKIKEMIKLEKEVLKKVLNIGGFSAGENLLWIVQYTIAFAFVASLGEASLSVQTIYFQISMLIMLIGQ

AISIANEIIVGKLVGARYENIAYKHAWRALYFSVIASALVAFLNYLCQDFTMQILGLKEELKNLMIPLFA

LSIFLEISRTFNIVMVNSLRASGDAKFPFFSGLVFMMGVSLPVGYVLCFHFNLGILGVWIGFCADEFLRG

MVNSYRWKSKKWQGKALV

>WP\_002871921.1 MULTISPECIES: trimethylamine-N-oxide reductase TorA [Campylobacter]

MLDRRKFLKIGASLSALPLIPSLSAGKTVEASKVSLGLVKNGEVITAAHWGILKLTIKDGKIVKSEPWEK

VTKMDNPLQHYTADMVYKSRVKYPYVRKSYLENPDNPKPELRGKDEFVRVSYDEAIKLIAKELKKTRDSK

GASAIFGGSYGWKSSGNMQNSRILLHRFLNVTGGFVGATGDYSTGASQVIMPYVVGSIEVYEQQTSWENI

LSDSKYVVIWGADPLSTLRIAWTSNEQRGLAYFEKLKNSKIKVICIDPVKTTTAKFLNAKWIAPRPNTDV

ALMMGMASHLIAKKKVNYEFLDTYTTGFDKFKDYLEGKEDGVKKDTKWASKICGIDEKTIKNLAETFYDN

PTMIMSGWGMQRAHHGEQPHWMLVTLCAMLGQIGTKGGGFGLSYHYSNGGVPTCKGGVIGGMTAGSLGIW

KNGKFKGLSKAEASSEGAEWLQNAASYSFPVARIADALLHPGKTIDHNGAKITYPDIDFIYWVGGNPLVH

HQDTNTNVKAWRKPRTVVVNEIYWTPTAKMADIIMPVTSSYERDDITMTGDYSNMHIAPMKQAVEPVGES

KDDYVIFSDICKIYGKDVFNAYTENGKKAKDFIKEYYNSALKQTQSFGEAFATPMPSFEEFWAKNEPITF

EPTAESLEWTRFSEFIEDPILNALGTDSGLIEIYSETIKNYNYDDCKAHPTWFEPIEWLGNASKEAPFHL

LTNHPRDRLHSQLCHTSLRDTYAIKDREPILINSKDAKKLGIKNGDVVRVFNKRGEVLAGAVVSDEIMQG

VVRLCEGAWYDPNENGLCKCGNANVLTMDIPTSKLANGNISHTGLVNIEKFKGELPKLTAFSAPKGAN

>WP\_002867010.1 SDR family NAD-dependent epimerase/dehydratase [Campylobacter jejuni]

MKNILITGGTGFLGSNLCKRLLGEGNKIICVDNNYTGRMENIKELLENENFTFIEHDICEPLKITQKLDQ

IYNFACPASPPAYQGKHAIKTTKTSVYGAINMLELAKEHNATILQASTSEVYGDPLIHPQNEEYRGNVNS

IGIRACYDEGKRCAESLFFDYHRHEGVDIKIIRIFNTYGENMDPNDGRVVSNFICQALSGKDITIYGDGS

QTRSFCYVDDLIDIIIKVMNSSKDFQGPINTGNPSEFTIKELAQKVIEKTGSKSKIIYKDLPLDDPTQRR

PDISLAKAKFNWEPKINLDEGLEKTIKYFKEKITEFKG

>WP\_002866138.1 MULTISPECIES: N,N'-diacetylbacillosaminyl-diphospho-undecaprenol alpha-1,3-N-acetylgalactosaminyltransferase [Campylobacter]

MRIGFLSHAGASIYHFRMPIIKALKDRKDEVFVIVPQDEYTQKLRDLGLKVIVYEFSRASLNPFVVLKNF

FYLAKVLKNLNLDLIQSAAHKSNTFGILAAKWAKIPYRFALVEGLGSFYIDQGFKANLVRFVINNLYKLS

FKFAHQFIFVNESNAEFMRNLGLKENKICVIKSVGINLKKFFPIYIESEKKELFWRNLNIDKKPIVLMIA

RALWHKGVKEFYESATMLKDKANFVLVGGRDENPSCASLEFLNSGVVHYLGARSDIVELLQNCDIFVLPS

YKEGFPVSVLEAKACGKAIVVSDCEGCVEAISNAYDGLWAKTKNAKDLSEKISLLLEDEKLRLNLAKNAA

QDALQYDENNIAQRYLKLYDRVIKNV

>WP\_002854283.1 MULTISPECIES: flagellar protein export ATPase FliI [Campylobacter]

MNLEKLRSKLGKENLSAIFGEITKISATSIEIRGLKTGVGDIVKLVSNENENLNTLAMVVEIKEQFSYLS

PFSFIEGFKIGDRAFISDAGMQIGVSDELLGRVVDPFMRPKDGKGAIEVSKYMPIMRAPIDAMKRGLIEE

VFPVGVKTIDALLTCGVGQKLGIFAGSGVGKSTLMGMIVKNSKAPIKVVALIGERGREIPEFIQKNLGGK

LDDTVIIVATSDDSALMRKYGAFCAMSVAEYFKEQGKDVLFIMDSVTRFAMAQREIGLALGEPPTTKGYP

PSVLSLLPQLMERTGKEEGKGTITAFFTVLVDGDDMSDPIADQSRSILDGHIVLSRELTDFGIYPPINIQ

NSASRVMSDIISPEHKLWARKFKRLNSLLKENEVLLRIGAYQKGSDKELDEAISKKEFMQKFLGQNPEES

FEFNQTLELLSQIDTPNTPLPPTQNINVGSASATLPNPNLK

>WP\_002853498.1 MULTISPECIES: undecaprenyl phosphate N,N'-diacetylbacillosamine 1-phosphate transferase [Campylobacter]

MYEKVFKRIFDFILALVLLVLFSPVILITALLLKITQGSVIFTQNRPGLDEKIFKIYKFKTMSDERDEKG

ELLSDELRLKAFGKIVRSLSLDELLQLFNVLKGDMSFVGPRPLLVEYLSLYNEEQKLRHKVRPGITGWAQ

VNGRNAISWQKKFELDVYYVKNISFLLDLKIMFLTALKVLKRSGVSKEGHVTTEKFNGKN

>WP\_002867056.1 formate dehydrogenase accessory sulfurtransferase FdhD [Campylobacter jejuni]

MDPLFTTQILKYKGDDSFTCDDTLVREIKLEIFINDERVGALMATPVDEQALAIGYLMSENIIAKVSDIE

SIETKDDGMSVHIKAKIDKENLAKLNAEGVVISGCGRAHTANIDPEAIEASKISSDVKFSKDEILKQMST

FYTQCELYEKTGCVHTAKLFVDEKTFFIGEDIAQHNTIDKALGKARLAGVDLSQCFLMVSGRLSSEMVAK

AVMHKIPVLVSRTAPTCLGVMIARKFDLTLCGFARENKINIYSGEFRIHG

>WP\_002851949.1 MULTISPECIES: RNA polymerase-binding protein DksA [Campylobacter]

MKKNEIQNFKNILEERKKAILENLQSNSNEIEALHNSVPSDSVDFSVIETGSQIDFAISTNLKEELIEIE

DSLDKIKNGTYGICESCDDEIDSQRLKVKPHARYCITCRQIAEQGKKHEN

>WP\_002866834.1 MULTISPECIES: UDP-N-acetylmuramate dehydrogenase [Campylobacter]

MIIDFKKYSSVRIGNEFEVLVLDQICDFDGFLIGGANNLLISPKPKNIGILGDGFDFIQILDQNKDFIHL

RIGCKTKSSKMYRFAKENNLKGFEYLSKIPGTLGGLLKMNAGLKGECISQNLIKIATFQGEILRENINFD

YRFCPLNMPFFWAEFKLNFGFDILKDEALKNARSNQPSGASFGSIFKNPKNDFAGRLIEAVGLKGFSKGD

AMLSDKHANFLINKKNASFEDAFFLIELARKKVFEEFGINLENEVIII

>WP\_002867001.1 MULTISPECIES: FAD-binding protein [Campylobacter]

MGEFSRRDFIKTACISVGALAASSSGVYALDDSSKMDKDTNLPSCDVLVIGSGGAGLRAAAAVRKENPKL

SVVVATKMMPSRNATCMAEGGINGVTDFSNGDSYKLHAYDTIKGGAYLVDQDAALKFCELAGKAIFNMDF

IGTLFSRNEQGGVAQRLMGGASKKRCNYSADKTGHILMHSCLDDAISSGVKFLMDHELLDIGVMDGKCEG

VVLRDIQSGGIYPVLCKALVIATGGYTRIFYNRTSTPFIATGDGVAAALRAGLGFEDPEMIQFHPTGVAN

GGTLITEAARGEGGYLLNNRGERFMKNYHEKMELAPRDVVARAIETEIREGRGYGEGLGAYVLCDVRHLG

KEKILKDLPKIRHTAMLFENIDLVDTPVPIRPTAHYSMGGIEVAKFEDMSTKIAGIYVGGEASCISIHGA

NRLGGNSLADAVVTGHLAGIGATNYAKDASFGKGAKTHELAQKWQARFKEITNNGGNGQEMYELREELGS

QNWDNMGIFRTQEKLDLLAKNLEDIQARYEKIRIPNPNEVMNTAFTDYVELGNLILLSRCACLAARNRLE

SRGAHTREDYPKRDDKNFLKHSIVNLENDELKLSYKDVVVTEFSLDGRRVQ

>WP\_002866900.1 UbiX family flavin prenyltransferase [Campylobacter jejuni]

MKVLLGISGSSSVNLGLKLLKNLENQCELYCILTQGAKLSFKAENEVNLEEICQENFKYTHFLDDKNLSL

SVASGSFGIEKTIIAPCSISSLAKIHAGFADTLLMRAAAVALKERKKLILGVREMPFSTLNLEHMLKLSQ

MGVIIAPPIIASYSKANNLEQMENFIVGKWLDLLGIKHNLYEKWQNF

>WP\_002866571.1 filamentous hemagglutinin N-terminal domain-containing protein [Campylobacter jejuni]

MKKMSKHIVLSFAVSSLLFSQAYALPQGGKFTHGTSGTIHTSGNTVTITGKGQNHVIQWGGGFNIGQNES

VNFNGKNQNYLNIAYQKDASKIDGALNGGNNNIFLVNPMGVLIGKTGTITAGKFVASTTPLSDDNVKTFL

EKGASFSPAFDVSKQGNIINLGKINADNIVLIGNKVEIGVGAELAGQDGQTNAKTAHLIGNYVYVSVGKD

KENKNTIKIDKDGFKGTAIVEGFMQRDMTSFANDKYQFGDFGTILKSSCNGKESQNFYKAITIGGWENDK

NIQEWILFSNGWNKDELNGIFKDDLTTVRLVSDIDFGYKNAVDPVGASKYAFSGIFDGGNYTLKNILINA

QNTDKGWNTGIFGKVEGKDGNNKAKIYNLNVDGLKFSGKTNSGGAFVGQSSNADFSNIHLKNIGDLIFFD

PNSKNETSGFLYGGGFVGYAKSGSSFNRISLDNFSKIALQPEGKFSSAYIDIYLGGFAGYSEGSNFSNIL

LNNIGGVTILGSETGGNIFAGGFVGYAGDKSYFSQIDLKNIGSVQADGKTFVKHAGAGGFAGAINGTNSF

EKISLINFGDIIAKRGYVWVVNGNFKVGSGGFIGLLNPLDDKILYVDFKNILLNFDQKMQIYAKAGDGAS

SYFPDLNNWEYNFSGGFFGGLFTSKVGRANFNNIQLKFGQDVSIIAQKFRSNSNEKYQGLFYGYSVKNWN

DGIMKTDNVAIYYEKNYNTNQYNWYYQDIKDGFFGSAINDYAYKDGRSYEFYDYNVMKDMEINKQIIAIL

EKDGVVSKDYNNGYVSYYDGNAKITPEVPDFKDPVLSQNDFDPKLLQRILDDLMNGKYTYDFDTKTWTYT

DSKGVVGKDEASEITQSLNFLNAFKDTGVEQEFINLWKNSQDQNYKNYANLYEKWTQKKTAMDKIKTGEG

YFASFKEELQKYQEALAQLDKENKNYEKIKESGLVSDETLKVMYEKLLEQKEALEKQFADLSGNEGFHYK

LENEILNSQGFAINGSDVDGKAYIGNFNFKGKLASLPEKPNISIYEPDKQGGEDPANLLYCRLKFLKRL

>WP\_012006784.1 YeeE/YedE family protein [Campylobacter jejuni]

MNSFKQKYLINFWDNSRSMIALGILSAVYFGIFGGVWAVTGEMTRWGGEFLELLGMNLDGYSYYQKQNLN

GTPLTRTDGIMLIGMFIGCLVAALLANKVKFRLPASNIRIFQAIVGGILSGYGARLAFGCNLANFFTGLP

YFSLHTWLFTVFMVLGIYLGVKICNTSFFKPKAKLERVNKENLPLNKQSLRTKLYFNLGILLFIAFLVWV

FYLVFTNGNISTQNKQSLLALALIFGFVFGFVISRGQICFTSCFRDLFLFGRDNAIKGALIGMIIASLIA

FAFILQGHTSKLIELSPAVAVGAFLFGFGIVFAGGCECGWAYRAFEGQSHFMIVGIANIIGTMILALSYD

FLPKAFKEGIKINLLTEFGNLNGFFINLILFILIFAFVVFYKKYFFKNQLKGSTVKITYSLNLQGEACPY

PAIATLDVLPKLQSGEILEVLCDCPQSINSIPQDAKNRGFKVLEIDQSGPTLRFLIQKP

>WP\_002866956.1 MULTISPECIES: KR domain-containing protein [Campylobacter]

MKTAFITGASSGFGRACVEAFIQKGYKVIALARRKERLEELKNSHKDKIYTLCIDVRNQKEIFEAIENLP

KEFQEIDVLFNNAGLALGVDEFDKLNLEDINTMVDTNIKGFLYVAKVVIPILRKQKNAYIFNLGSVAGRN

PYFGGNVYCGTKAFVGQFSLALRNDLRGSNIKVTNIAPGLCKTEFSEVRFKGDIQKADAVYENTQFISAN

DIAKVVMSIINLPSHINVNEIELMPVTQTWNGFYIERDE

>WP\_002866902.1 MULTISPECIES: MetQ/NlpA family ABC transporter substrate-binding protein [Campylobacter]

MNIKKIFLSVLFTISLSFGADKTIIIGATPTPYAEILNFSKPLFQEKGWKLIVKEFNDYNIPNIALNEKD

LDANLYQHKPFLDDFNTHKGTNLSSLGAIVLVPMAIYSNSIKDIKDIPNGAKIAIPNDATNESRALDLLA

KANLIEFKSQSTLKTPIDISKNPKKLKFIELKAAQLPRALNDTDLAVITTNYALGAGLNPLKDGIFMEDK

DSLYAIVLATIKGEETSQKSLVIKEILTSDKIKNFIIEKYKGSVIPTF

>WP\_002866618.1 flagellar motor switch protein FliN [Campylobacter jejuni]

MINDFLKMFTNECISTIEGLTGKSAEFSEYKEFDVNASDTLKAPLVYAIFNIANGGKIGILAGAVLMSAI

GEWMMGEEEITKNDKLGPDEMDAAKEAIQNIISAFSTTLGAQKDIPKMDFSIESCEFVPESVDFKDFKKL

FLYDVKIGDLEEQVSLAMDQTLHNILSGKPAETGNTSTDSNHNAEEKAIMLSEELKNINLIMDVRLPVRV

RIGNKKMLLKDVLTMDIGSVVELNQLANDPLEILIGDKRIAYGEVVIVDGNFGVQITEIGSKKERLEQLR

>WP\_002866451.1 MULTISPECIES: acetolactate synthase, large subunit, biosynthetic type [Campylobacter]

MKELSGSAMICEALKEENVKIVFGYPGGAALNIYDEIYNQKYFKHILVRHEQAALHAADAYARMSGEVGV

AIVTSGPGFTNTITGLATAYSDSIPLVLISGQVANSLIGTDAFQEIDAVGISRPCVKHNYLVTCIEEFPR

ILKEAFYIARSGRPGPVHIDVPKDVSATLGLWEYPKEISMKTYKPVYKGNSKQIKKFAELLKEAKRPLFY

LGGGCISSNASEQIRELVKFTKIPAVETLMALGTLRSDDVFNLKMAGMHGSYAANMALSECDLLVSVGAR

FDDRITGKTSEFAKHATIVHVDIDPSSISKIINAHYPIVGDIKEVLKELLEELKKENFNTTFKEWHETLK

RYNELYPLSYEDSNEILKPQWVIEECAKMAPDARIITDVGQHQMWVAQFYPFNYPRQLATSGGQGTMGYS

LPAALGAKLAVGEEVVINFVGDGSVLMNIQELMTAYEYGIKTINIILNNAFLGMVRQWQSMFYKEHFSQT

DLSTQPDFIKIAQGFGCEGYEISNKEEFIQAFSQALKSDKTSLLNVKIDRFEDVLPMVPAGGAIYNMILP

KAKDRQ

>WP\_002866210.1 MULTISPECIES: MetQ/NlpA family ABC transporter substrate-binding protein [Campylobacter]

MRKGEKMTLFTKAFCVATLFTSFAWANEELKVGSSITPHADILRFIKSALQKQGYDLKIYEFNDGVIPNV

MVENGELDANYFQHEPYLKEFNQRQGTHLVKVASIHIEPMAVYSKKHKKFNPEEGQSISIPNNPTNESRA

LRIVASKGLIEVKDNELITPLDITKNPKKLKFVELKDAQLTRSLDDVDYSLINSNFAILAGLNPVKDGLY

TESKYSEYGNIIAVKEGNENLPKIKALVKALQSDEVKKFIEEKYQGALIPTF

>WP\_002866018.1 MULTISPECIES: YigZ family protein [Campylobacter]

MQTIDQIFQTQIDIKKSIFLSFLCPFKDFKFLIETLKKEHPKAVHFVYAYRVLNDFNQIVEDKSDDGEPK

GTSGMPTLNVLRGYDLINAALITVRYFGGIKLGTGGLVRAYSDAANAVINNSSLLSFELKKNISIAIDLK

NLNRFEYFLKTYSFNFTKDFKDCKAILHIKLNEKEEQEFEIFYKNFAPFEIEKL

>WP\_002857725.1 MULTISPECIES: anaerobic C4-dicarboxylate transporter [Campylobacter]

MDIMIILQVIVLLGAIFIGIRLGGIAIGYAGGLGVVILGLVLGMKPGNIPWDVILIIAAAIAAISAMQQA

GGLDYMVRVTEKILRSSPKFINYLAPACGWLLTILAGTGNAVFSLMPVVVDVAKSQNIKPSVPLSLMVVS

SQIGITASPVSAAVVYMSGVLEPLGWNYPTLIGIWISTTFIACMLTAFIVSLITPMDLSKDSVYQERLKA

GLVKDAGAILHGEDKPGAKLSVGIFLITVLAVVLYATAISSNIKWIDPVVVPRDAAIMSFLLTAATLITW

LCKVEPGKILDTSVFKSGMTACVCVFGVAWLGNTFVAGHEASIKEVAGDWVKQTPAMLAVAFFFASMLLY

SQAATAKAIVPVIITALGISAANPHDSYMLVACFAAVSALFVLPTYPTLLGAVQMDDTGTTRIGKFIFNH

SFFIPGVLAIAIAVALGFVLAPMLI

>WP\_002851673.1 MULTISPECIES: TerC family protein [Campylobacter]

MFEWIFSIDAWITLATLSALEIVLGIDNIIFLAILVSKLPPEHRDKGRILGLAFAMITRILLLLSLFWVM

KLVTPLFSVLGNEISGRDLVLLLGGLFLIVKSIKEIKEQISHQEESQSHFKASNKLWIVVAEIAVIDIVF

SLDSVITAVGIAQDVTIMIIAVIIAVAVMLFASKPIADFVEKYPSIKILALAFLVLIGVVLVAESFDIHI

DKAYIYTAMAFALVVQILNILDQRKEKNG

>WP\_002826913.1 MULTISPECIES: NYN domain-containing protein [Campylobacter]

MENKSIAIFIDAENIPAKYAKSIFDIASDYGEVIIKRIYGDWTQKNIQGWREQIAEYSLIAMQQFNFAAN

KNSSDMYLITEIMSIFYEKNIDIFVIVSSDSDYTSLIQKLRENKKQVIGMGLEKSIKSYVNAFSEFFYLD

KDESKKEDILSKDYLRALINITEQLIDEKGRAEYAQIRTNMNRKYSDFHPQNYGFKNFRALIQKFLPKMK

KFEEEREKNIYFLVKKDYESYY

>WP\_032603130.1 MULTISPECIES: TonB-dependent receptor [Campylobacter]

MKFKKSLLCFLILSGALLKAEEKYQLNDVVVSASGFEQDLVDAPASISIITKEELEKKPIKDIGEAIGDI

PGVDVTMNKTGTYDFSIRGFGSSYTLVLIDGKRQSVANGFYDNGFSGSESGYLPPLSMIERIEVIRGPAS

TLYGSDAVGGVINIITKKNPDKTEANIEFNTLLQQHSNHYGNAGGFNAYVATPLIEDTLSISARLKYYDK

AASDLKWPTPVWNNSQQRPDNYQIASHSPGAFTSLGFGSRLNWTVDDKNNIYFDIERYINEISVNSTSSR

AIKSERQLFKDNIVLNHDGNYDFGSTNSYLQYGSTKDKELHSQIWVGEGKVVLPWNLGQYGNLVNTFGAR

IDYEMLKNDQASAGSQIRGKNLDQTTVALYGENEYFITDDLIFTTGLRYIYSDLFDSEFTPRVYLVYHLN

DNIAFKGGVSKGYKTPAAKELTNGYYNYSNDNAYFGNPDLKPEESINYELGVDFRIFDFAHYSITGFITD

FTNQISSEDLTGMQNGINCSNGTVCTRPINLGKTQTKGIEFAFNTKTYNGFSLNSSYTFMDNRYKDGQKN

WFGGDRIENLPRHIAMLKLNYERGKFSSYIKTRARLDTIAKAKGGGNGSLPWQKYKPFYIVDLGINYKIN

KQSSLSFVVQNLFDKNFFDPQVTKWAGANPAGYANRYQDYTEGRSFWLSYKYDF

>WP\_012006762.1 MULTISPECIES: 4Fe-4S dicluster domain-containing protein [Campylobacter]

MQDFVYIKNDVLIPLPDAIEILDQANDKEVLVCNDKNQKAQIYAPEINFYLKNSQDEILEQSKNVLTLYK

ARASVYDLGLDLEQSKEVQNRLILADSDTQTVEFLKEHGFKVIALSSVEILAVFGSVGELCAVVKNQGEE

VEIDFDFLLFKAEDLSAVRKDFTRQSGCYNLLNFENLEVLLEFLQSKSPKYHYKTYISYNASVCQYHERR

SEHCAKCAEICPTVAILKDDEKKHLEFSQVDCLGCGGCISVCPSGSLDYAPMPRESFFTLCEFYKDKKIL

IIPKKMSLENLNLALPKDVLPFMIEGEKWLSSMHFLALLQNSGANLVFYTDFVSRGSNEAIVLLNTFFER

KFQKKAIFVAKDEKELQNVLKEQEFIQDLKYDFHNNTLTTRENFAKRMQEMIKNEDFGSIESGEWLRYGK

VEINPNTCTLCLSCVGACNVGALIADKQENALKFNASLCTTCGYCELSCAEKDTLKLFRSGMEFRASYFE

YQTMAKDELFACIECGKEFATKKAVEKIANLMKPKFGNDENKIKTLYCCADCKAKVMIKAMGFAGQN

>WP\_012006670.1 MULTISPECIES: MFS transporter [Campylobacter]

MSKNVKNLDTSFFGHPKPLLSLSLTELWERFSFYGIRPLLYLFMIASFEKSGMNLKPEEASAIMGIFASC

LYLAALPGGWLADNYLGQKRAILLGALTIAFGHLCIAFSYFNNKIIFVGMVFLVIGTGLFKTCASVMVGM

LYKKNDARRDSGFTLFYMCFNFGAFVAPLICGFLQKEYGWHFGFGAGGIGMLLAVIIFYLKTMPDLKEFD

EKVGIDSTWDRPSKKSKNAFYIIIVSGIVLLGAIFLILGGFIKLDAQVINKNIILTILACAGIYFLYLFA

FTSLKIEEKRNLIIFIVLFLAAALFWSVYEQQYTSFNFFAEKLTDKTILNYEIPTIWFQSLGGLFVILFA

PFSAFIWTICAKNNKEISSIIKFALGLLGAALAFLIMALASNHAISLNGDANTLRENLENSSQIILVSPW

WLVSSFLLMVLGELCLSPVGLSIMTKIAPNLIKSQVMGLWFVASALGNALAGFIGGKASEENIAYLPNLF

YQCMWILLGAVIILLILKKPINKILKN

>WP\_002867075.1 MULTISPECIES: ATP-binding protein [Campylobacter]

MKVLNFFYENHPKFEVSYERKNQISKPNIIIKGPRFCGKKTLIFNFLSQFKASEILFLDLYDTRFEKQSL

ERLADFLNENLQIKILCLYNLDFIPNLEKIKIPIILSTNIKDLNINGFEELELDYFDFEEFISVSKKNLP

INNLVGLFLQSGRSKFGEKNILLRQSFTLLELEILKYLALNLGQQISISKIFIELKKRLKTSKDSVYQAI

KKLENTYVIYTLKHDEKKLQKIYFKDFGLRNNLCISKDFSHLFENLVLSELFKFKEEFFYNKYFNFYSQI

SKIAYISSPTLDIDLIKLRAKKILPKALELGIFHVIFITLSSEDNFFEQGVKFEVISFDKFSLGF

>WP\_002866546.1 U32 family peptidase [Campylobacter jejuni]

MIIPEIVAPAGNFTKLKIALAYGADAVYAGVNNFSLRSRTAREFNYESFEEAIKYTHERGKKIYVTLNGF

HLSSQIEGLKRHILKLREMKPDAFIVASVGAMRLVKELAPEISLHVSTQANILNYLDAQVYKDMGAKRVV

IARELGLKDAKALKENCDIELEAFVHGSMCFAYSGRCLISSVQSGRMSNRGSCANDCRFNYELYAKNPEN

GTLFRLEEDENGTHVFNSKDLNLCSYIEKIMQENCISAFKIEGRTKSEYYVALTTRTYKMAIQDALEGKF

ESSKYEKEIATLKNRGFTDGYLVSRPLEKTDTQNHNTSIEEGSHQVHAISEDGSFFKCKGKIVLNTPYEI

LAPLGDVIQTCDNELGKIYQKEDRYFIEFKKLIAKNNKEFSEIHSGNEHEIQLPNKISALSFLRKEI

>WP\_002865998.1 MULTISPECIES: filamentous hemagglutinin N-terminal domain-containing protein [Campylobacter]

MKKLNKLSLSLVVGSLLFTQSYALPSGGKFTHGTSGSISVSGGTMNISGSKTNSVIQWGGGFNIANGETV

NFKGNGYNYLNIVYGSKSSHIDGTLEGGTNNIFLINPNGIVVGKDGSINANRVFLSASSIGDKEMKEFAK

DGKISAFEGNPLTTASPVIKSNAGNVINLGTITAGERVVMVGNQVSNMKYGSTDYGKFIFTNKKEQSNTV

YLDVYSNDIFVIRGPASNTIKKEDSVMLSIRPNKGSTGPGGDPTDTIGYKETSDLVAKDNISNEVLNSIF

NDLKFNSSVDISDLSKFYKDGKILTADELTSINQSMDFITALYGQTQDSNNATFANALKEVLGNSYGNLG

KANQAIIKTKEILSQIPKITEQQKNIQKAYDQAVDAYNEAVKKYNAALSGVTGSNASETITALKTVLDKA

YNDLKNAEANLESTTASNNSSLKSSNETLASVSIDGYKLTVNGEYLADYKTVNKPNDNNSGSNNGNDGTD

SGDINNGNNNGSNNNPNDTIGQQEPDIATALLMQTTDEDPNINEDDKQASIDEASTQESGNACIVSDNFK

AGNPCSR

>WP\_002856595.1 MULTISPECIES: acetyl-CoA carboxylase biotin carboxylase subunit [Campylobacter]

MNQIHKILIANRAEIAVRVIRACRDLHIKSVAVFTEPDRECLHVKIADEAYRIGTDAIRGYLDVARIVEI

AKACGADAIHPGYGFLSENYEFAKACEDAGIIFIGPKSEVIHKMGNKNIARKLMAKNGIPIVPGTEKLNS

YSMEEIKIFAEKIGYPVILKASGGGGGRGIRVVHKEQDLENAFESCKREALTYFNNDEVFMEKYVVNPRH

IEFQILGDNYGNIIHLCERDCSIQRRHQKVIEIAPCPGISDNLRKTMGVTAVAAAKAVGYTNAGTIEFLL

DDYNRFYFMEMNTRIQVEHPITEEITGIDLIVRQIRIAAGEILDLEQSDIKPRGFAIEARITAENVWKNF

IPSPGKIGEYYPALGPSVRVDSHIYKDYTVPPYYDSMLAKLIIKATSYDLAVNKLERALKEFVIDDIRTT

IPFLIAITKTREFRRGYLDTSFIETHMQELLEKTEDRHQENKEEVIAAIAATLKKIRESRE

>WP\_002854819.1 MULTISPECIES: 4Fe-4S dicluster domain-containing protein [Proteobacteria]

MSMTAPKDTPVWVDEHRCKACNICVSYCPAGVLAMRDDVHAVLGQMIEVVHPESCIGCTECETHCPDFAI

MVAKRDEFKFAKLTAEAKDRAVAVKNNKYKKLA

>WP\_012006685.1 MULTISPECIES: MetQ/NlpA family ABC transporter substrate-binding protein [Campylobacter]

MKIKSLFIVSILTLSLNANALETITVAATPVPHAEILEQVKPDLEKQGYKLEIKEFTDYVLPNLAVDNGE

ADANFFQHTPYLEEFNKNKGTKLIKVAAIHIEPMAVYSKKYKSLDDIKEGVKIAIPNDPTNESRALDIIA

KKGLVKFKDKALKTPLDIIDNPKKIKFVELKPAQLPRALDDVDFAVINSNYALSANLNPAKDSVFIEDKE

SPYANILVVRVGHENDPKIKALTQALQSDKIKQFIIEKYNGSVLPAF

>WP\_002932343.1 PAS domain S-box protein [Campylobacter jejuni]

MKDFFKDQFFKALEKNTIFSRADVQGNLIFVSDKLCQISGYSKKELIGKKHSIFKHPDVEECYIEELLKK

LSYKKPYQVIFKNIDKLGKTFYLETLLIPILDKNNELIEIVAFSHDVSNSFKLNEELALNHAKLRELSIN

LENTVKNHQQEFIQLGKKFEKKMQIALEKNEKDIKIVYEEILKSSLEQMISDIAHQWRQPLNELGIAMFQ

MKQNLKDEKGFAEIYSQSKDMIKNMSETIDVFRTLFNKGVEQCVFIKETLNKALEIAFETIEKNHVNINI

VSKSDYEVLAYENGLIRVFLNLILNSIEAFKNKKRKIITITFSKFGKNYLKITIKDNAGGIDKENLDKIF

QPYFTTKHPSQGIGVGLYISRQIIESFQGKIKVKNGKDGACFEVFLKLKERVE

>WP\_002867091.1 MULTISPECIES: RloB domain-containing protein [Campylobacter]

MGTDDLRKKRNTKTRDREAKRKKNEIILIVCEGEKTEKNYLNQLKDFFRLSNVSINIISSKKPNPSQIVE

FTKEKNKDYSYNKVYCVFDKDTHSDFDKARQECEKYKFEAITSNPCFEFWILLHFTYTTKSFSTNSPCNE

LIESDLKKHIKDYKKDYNFTSIIKQNLSTAIANAQKANKEAEKNNYTSSYTFMDKLALKFQELNSARINQ

>WP\_002866779.1 MULTISPECIES: autotransporter domain-containing protein [Campylobacter]

MKKNASSKILLSLGVATLLYSGAFAAEITFNGDSDLDKYFDINEKDNVATFKNENYKNKQDVTFNISTSA

FDDAPEDTKINIDLGNNSLTLKNQMDYQGKTAALVKNFNVDAKDFKTTDIGLSYFNAGIINANFTMEGSG

KDFDLGNIDKNKASSLLIFNGSRENTNDTVNGSLTVNGDFSTTNSAIVSMKSDTFKVNGTATLKEAGLGF

LSQSYSNLDVNDFIALRAKDIKTDTLNEDTNAGALILKTASSYINENLLNGDDYAAYLDVTDDKKYGGAF

VDYKLSLKNCGGDKCLVINGGATAAAKNLTNQIAVDLEAITRIIDGLDNEQAKKALQEQKTELEKLQQEA

MQNGGKIDDEKYIDLVNKNSNLNLSANDKASILVLRSITEQLGSIGADLASREGVKLALQIKKDTDNTGK

SVSNFNSASSAVNTTMNISNDVSIGSRVAMLNNPFGTYASKMNGLKFAALDSDMRPSYVNEYTNSVWANA

FGGANIIDGDSGAMYGATVGVDKQANDNVLWGAYFTYANAKIKDNNLEQKSDNFQLGMYSTINIAPQWEL

NLKAYAQVSPTKQDNVQVDGAYNSDYTSKFLGLSANAGRVFDLSDNTLFIKPFAGVNYYFSYTPSHTENG

AIAKDIDSMKNNSVSVEVGAEFRKYMNENSYIFVTPKIEQFVINSGDDYTANLAVNNAFFTSVEANNKKK

TYGQIIVGGNVDFTNQLSMNLGFGAKQILAGKVDNKNETYLSGQVGLKYKF

>WP\_002866332.1 cytochrome c [Campylobacter jejuni]

MQKAKILIALSFFLLVLSACSNDEKNISKTQNTDQEVVQIEQNDEKTELSDSNLPLPVDDEAQSSDDEHE

VNPSIINSLYKQKCATCHGEKGELKPKNSTAIKTLSNKIFIQKIKMIKDKNHSFLSDEQIQNLADFINKG

K

>WP\_002866200.1 MULTISPECIES: PAS domain-containing protein [Campylobacter]

MSREIFLQEDSLITSKTDLKGKIVYANDDFLKYAGYTMGEVLNKPHNIVRHEEMPKTVFKYLWDYMKEGK

EIFAYVKNKTKDNNYYWVFANVTPSIDINNNIIGYYSVRRMPNKSAISTIESLYSDLLRVEQQQGLNKGV

EMLKNFCKDADKTYNELIFSLQEAK

>WP\_002861827.1 MULTISPECIES: PAS domain-containing protein [Campylobacter]

MFGAKKNNTEIIEQLEKKCNGLGDILRSIGNTMAVIEFTTDGVILEANQNFLTTMKYSLSEIKGKHHSMF

CLPEVVNSSAYSDFWKDLRDGKARSGLFRRIAKGGIDVYLEANYLPISDNNGHVYKIIKFANDITQRHYE

MLDLRNTIAAANRSMAIIEFKPDGTIITANENFLRTMDFNIDEIKGKHHSMFCDSNYRHSKDYVQFWEDL

REGKFQSGKYIRYGRNNKKVYLEASYNPVKNDDGKIYKVIKFATDISEQVKKDQEKLRLISELAEKNDNL

TQDGDRVIENTVSNVQNIADMMSQSSNLVSSLNQQSDEIKSIIQTISDIADQTNLLALNAAIEAARAGEH

GRGFAVVADEVRNLAERTGHSVNEITTTINSIRNVTSQVVESIKSGLEDVNQSVELAKEARECMEKIRES

SAEVAKAMS

>WP\_002857015.1 MULTISPECIES: MetQ/NlpA family ABC transporter substrate-binding protein [Campylobacter]

MNLFKIIILACILNLSSLFAQNITIGATPNPFGSLLELMKDDFKNKGYELKIVEFSDYILPNRALEEKEL

DANLYQHKPFLEEYNLKKGSNLIATTPVLIAPVGVYSKKIKNLENLKEGARVAIPNDATNESRALELLEK

AKLIELNKNTLKTPLDINKNPKKLKFIELKAAQLPRALDDVDIAIINSNFALGAGLNPSKDTIFREDKNS

PYVNYVVVRSEDKNSEKTKVIDEILRSDKFKAIINEHYKDILIPAF

>WP\_002866665.1 MULTISPECIES: prephenate dehydratase [Campylobacter]

MPNLEEFRNKIDTVDDKILELLNERMTYVKSIGELKQSSGGTIYRPERERAIINRLKNANLGLLDQNAIE

AIYQEIFAVSRNLEMPQTIAYLGPEGTYTHQAARSRFGAMSRYIALANIEDVFKELSNKEAKYGVVPIEN

NTEGAVGITLDCLGKYNELKIFGEIYMDIHHSFVGINENLKEIKRIYSHPQGYNQCRKFLESHELSAIEF

VPSKSTANAAYLASQDKYAAAICSKIAAKLYNVPVLFDKIEDNAANKTRFLILSDIKNPKMPNCKTSILA

HTAHKPGGLSFLLEQFKKENINLTKLESRPVKSKEFLHSFYIDFEGHIDDENVKKALKDIQEIVWLGSYL

SGEKDEI

>WP\_002851617.1 MULTISPECIES: peptidoglycan-associated lipoprotein Pal [Campylobacter]

MKKILFTSIAALAVVISGCSTKSTSVSGDSSVDSNRGSGGSDGWDIDSKISQLNDTLNKVYFDFDKFNIR

PDMQNVVSTNANIFNTEVSGVSITVEGNCDEWGTDEYNQALGLKRAKAVKEALIAKGVNADRIAVKSYGE

TNPVCTEKTKACDAQNRRAEFKLSR

>WP\_002816247.1 MULTISPECIES: adenosylmethionine--8-amino-7-oxononanoate transaminase [Campylobacter]

MQNQILKNLDLKHIWHPCTQMKDHETLPLIPIKKAKGVWLYDFDDKAYMDCVSSWWVNLFGHCNEKIANA

IKKQVDELEHVILAGFTHEPIIKLSARLCEKVGRNFNKCFYADNGSSAIEVALKMSFHYHLNKGVKKSKF

LSLSNSYHGETLGALSVGDVALYKDTYKALLLECLSTPVPQGKDYTKELEILKDILEKNASEICAFILEP

LVQCAGNMHMYEARFIDEAIKLCHKFGVQVIFDEIAVGFGRTGTLFALHQCKQSPDFICLSKGITGGFMP

LSVVLTRDEIYNAFYDTYESQKAFLHSHSYTGNTLACAAANAVLDIFEDENILVKNQILSEFIKKEFSRL

EKFDFLGNFRTCGMISAFDILSTKYKRVGLFVFQKALEKGLLLRPLANTIYFMPPYIITKEQIVYVLESL

EQIFKEF

>WP\_002866599.1 MULTISPECIES: bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase RibD [Campylobacter]

MSNFKIQGRQMKEFYMNLALNEAWKYQFLTYPNPAVGCVILDKNGKILAIKAHEKAGLAHAELNAIAHAF

KSLRPEISLPKEANALHEFICKNHQGVFKDSIAFVTLEPCSHQGKTPPCAKLFSELGFKKIFISVKDENK

IASGGAEFLKKQGIEIEFDILKEEGKKLLKPFLKWQKEQFKLFKLALSMNGSPFGKIVSNELSRTYAHKI

RAVIDLLVVGGETIRKDHPILDARLCKAKAPNLCILSRQNIDNFDKNIPLFKVPNRQIYTQIPSEAKFLM

YEGGENFLKTFKDEIDMFLIFQSSSLNDEKNVTIPLNFKPLYRNFLGSDTYGIYEL

>WP\_002866415.1 NADP-dependent isocitrate dehydrogenase [Campylobacter jejuni]

MQITYTLTDESPALATYSFLPIVKAFLSRAHIGVKTSDISLSGRILATFSEYLKEEQRCEDALELLGELV

KRSDANLIKTPNISASIPQLKAAIKELQDKGYMLPNYPDEPKNDEELQIKTKYQKVLGSAVNPVLRQGNS

DRRSTKAVKDYAKNNPYRVVEFNPNSKTRVSYMKEGDFFSNEKAVLIDQDCVANIEFASVDGKKEILKEG

LKLEKNEILDATFMDVQKLQEFYAKEIKASKDDDVLFSLHLKATMMKISDPILFGYAVKVFFKELFIEFQ

DEFEKLGINPNNGLSELLSKIENSSKKDEILKKYNEILAKSADISMVNSDKGITNLHVPSDVIVDASMPA

MLKNGARLWDKEGKEKDTNAVIPDQTYATIYEAVIEDLHKNGTLNPSKLGSVSNVGLMAKKAQEYGSHDK

TFVAKEEGTFKIVSEGKVLLEHKVRKGDIYRANQAKFDAVLNWIDLGIERSELSGAEAIFWLDSKRASNK

IMITLVQNRLKEKGKNIAILTPKEACLRSLELIREGKDVISITGNVLRDYLTDLFPILELGTSAKMLSVV

PMLNGGAMFETGAGGSAPKQVEQLVEENHLRWDSLGEFLALQASLEFYANKCSNHKAKILAECLDEAIGE

WLENNKAPSRKVKEDDNRTSHFYLAMYFANYLARQASDMELQSFFKDIALELSSNEEKIRAEFNNAQGVK

VDLGGYYKFDDEKANKIMRPSATFNAILEKIGQR

>WP\_002852232.1 MULTISPECIES: trimeric intracellular cation channel family protein [Campylobacter]

MEINALTITTLYIIGISAEGMTGALAAGRHKMDLFGVIFIALVTAIGGGSIRDVLLGHYPLTWVKHPEYI

ILICFCALVATKIPRVVTKLETLFLTLDAIGLVVFSILGAQIAIDQNHGFIIAVAAAVITGVFGGILRDI

LCMRIPLVFQKEIYAGIAIIAGAIYYSLIIWLELNALVCTLLTLFIGVFARLLAIKYQWSLPIFSYNEEK

>WP\_002866953.1 MULTISPECIES: bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase [Campylobacter]

MSFMQEYNKLVEERAALGIPPLPLNANQTKELCKLLENENNEELANLLENRVNPGVDDAALVKCEFLNSI

LKGKISAPNIDKKRALRMLGTMLGGYNVKVLIDALKDENIAKDAAEVLKNIIFVHDNFHTIAELSKNNPH

AREVLQSWANADWFNKKEKLPQVIKCIVFKVAGETNTDDLSPAGDAFTRSDIPLHANAMLKVRQAGSLEK

IKELKKSGREVVYVGDVVGTGSSRKSAINSIQWHLGKEIEGVPNKHSGGIVMGSTIAPIFFNTAQDSGAL

PIICDVINLEMGDEFEIHPYEGKIIKNGSTIAEFTLSPNTLLDEVRAGGRIPLIIGRGLCAKAREFLGME

SENIFTKPEQPKSSSGGYTLAQKMLGRACGVEGVRPGMYIEPMTLTVGSQDTTGPMTRDEIKELASLGFN

ADFVMQSFCHTAAYPKVSDSNLHKTLPNFMTSRGGVSLKPGDGVIHSWLNRFVLPDTVGTGGDSHTRFPI

GISFPAGSGLVAFAAVTGSMPLNVPESVLVRFSGELQAGVTLRDLVNAIPYYAIKQGQLTVEKKNKKNIF

AGKILEIEGLPNLKVEQAFELSDASAERSAAACSVDLSIESVSEYIKSNISLIEAMIEAGYENKATLVRR

AEKMREWLKNPTLLRADKDAKYAYIIDINLNDIKEPILACPNDPDDVATLSEILADNKRPKNIDEVFVGS

CMTNIGHYRALGEILKDKGILKTRLWVVPPTKMDKAQLTNEGYYSIFGAAGARIEVPGCSLCMGNQARVN

DGAVVFSTSTRNFDNRMGMGAKVYLGSAELAAVCAILGKIPSKEEYLQIVSEKLSDEHKANIYRYLNFNE

IENFKLEN

>WP\_002860618.1 MULTISPECIES: ribosome recycling factor [Campylobacter]

MIMLNEIFNKQKTQSEKSLEALKKDFTTLRTGKVNTHILDHITVDYYGTQTPLNQVATVLASDASTISIT

PWEKPLLKTIESAIAAANIGVNPNNDGESVKLFFPPMTREQREENVKQAKAMGEKAKVSIRNIRKDANDA

VKKLEKDKAISEDEAKKAYDEVQKLTDTYTTKIDESVKSKESELLKV

>WP\_012006622.1 peptidylprolyl isomerase [Campylobacter jejuni]

MAIEKNSVVSMFYELKDANTNEVLESNLYSQPISFILGKGQILESLEEEVMKLDCPSNADVVIKKEKGLG

EYDENAVQTLPKEQFAGIDLKVGMELFGEGENGETVRVTVKEIGENDVTIDYNHPYAGRDLLFSLSIVDA

RAASEDEILTGIIAGSHSCGCGSGHGHDHHHGHGHGGGGCCGGGGCGCH

>WP\_002866293.1 MULTISPECIES: PhoX family phosphatase [Campylobacter]

MERRLFLKGSALGSMVAFFASSNLSAAMLKNKDLLGFKAVSASTQDKVIVPQGYEAKVLISWGDPLFSKA

KPYDENKIIDMNAVKNAHLVFGDNDDGMSFFSLSKNRGILAVNNEYINPEIMFNHHGKNLSKEDVLYEQA

SVGVSILEIKKKGDDWTVVLDSKYNRRIDANTKMQVSGAAKKEVLKNEKFVHGTFANCANGQTPWGTYIT

CEENFDDFFGSLDENLEFNDSLKRYGFNKTSLYGWEKFDERFDLAKNIDEANRFGWIVEINPFDVKSTPV

KRTSLGRFKHENAEIIVEKDGSVIVYMGDDEMNEFIYKFVSKHKYKKGADTSKILDEGTLYVGQFNGKVG

DFKGQGKWIALEYGKNGLDEKNGFKSQAQVLINTRLAASIVGATPMDRCEWIASHKQSGSKEVFATLTNN

KNRQEPNAANPRTKNVYGQILKWMPKNSHKDDDFTWEIFALAGNPDNQQGLYKGSNNITSENKFNSPDGL

KFDRDGRLWIQTDGSYSNKDEYEGMGNNCMLAANPKTGEIRRFLTGPIACELTGIAFSEDYTTMFVGIQH

PGEGLKGSTFPYGKTPRSSVMMIRKLDGGVIGS

>WP\_002866051.1 MULTISPECIES: magnesium transporter CorA family protein [Campylobacter]

MLELHENLKKILQAKNLETFYSEIYGQKIFVYVGLNLETWLFNDEKIYKLQDEEFKLSSIEEFSNFIKSI

LEDFKVQNTHFQNLLEHKEGIILKGGFVKNFYKKSFVLRQKINKNLKQINLLSEAFNLLLSEQAQYKKHL

KILNLSISILSKNTKEHLVRVDTLYTLTSAIKNEKMNKSIYLLSILSSIFLPLNLIVGFFGMNTNNLFFK

DSPYGTLYIFSLICCILIVGFIFYHSKKTKEFDLDEGKKAKKQTK

>WP\_002865934.1 MULTISPECIES: thiol:disulfide interchange protein DsbA/DsbL [Campylobacter]

MKFPVKLARSIVVCAFLAGISASALSEGKEYIILKNPIANADNSLIEIFSYRCTHCYDHHKFNTMGKVKE

KLPNLTYKFYPVSSMGDYGRQANEIFAFAAFKDGVNKIDPTDKNSLTHKVAKAYFNAYFKKKQRWENGKN

PEAFYSVGLKAMNVSKADLENFLKTPEAAELLKSYEIANPISQNYGTPAFVVNGKYQIIPSAINSPEALI

EITKELSKQK

>WP\_002865931.1 MULTISPECIES: thiol:disulfide interchange protein DsbA/DsbL [Campylobacter]

MRKFFCKFVLTLVFCSSFALANNSFITLNPSLPNSENSVIEAFSYKCIHCYNHHKFGTLEKLREAFPNLH

FKLYPVSLMNGEFSKEMNELFAFAQYKDEQNGKDASYSDSLSHKLADVYFVSYFLNKQRNFSNLDEFYDI

GLKAMNVNKNEVLNFLNTPKAKEILSEFQRANDIAKTYGTPAFVVNGKYQINPSAINSMQDLEDLVKKLS

NMK

>WP\_002852081.1 MULTISPECIES: GatB/YqeY domain-containing protein [Campylobacter]

MTLKEQILNDIKEAMKQKDDFKRDSLRTLNAAFKQIEVDERIELDNERIYKIIASEIKKRKDAIELYLKA

NREDLAQKEQNEISLFEIYLPKQLSDEELTLALKQLIEELGVSSLKEQGLVMKEAKIKLGASVDGKRLNL

ALKELLQ

>WP\_002880964.1 MULTISPECIES: endolytic transglycosylase MltG [Campylobacter]

MTIPFLSTINKANISTTKNTTIYKIFFFIRNFFLIFILGIFYYLTQPLKSNSVVFIPQGSISQIITYLKQ

NKYQMSSIDKYILFFLGHPQSGWINIGTKDLNRAEFLHKLTIAKAALQTITLIPGETSVIFLEQAAKQLE

LDKDMLLKEFQAQAPYDEGVFLPETYKIPKGITENLLIQMLLNHAEISNKKTSEKIFGDYNPKKWHQYII

IASVIQKEAANDNEMPIVASVIYNRLKKGMKLQMDGTLNYGIYSHVKVTPQRIRQDNSSYNTYKFTGLPK

EAVCNVSLAAIRAAIFPLKTDYLYFVRDKNTGVHIFSTNIDDHNKAINLQKGK

>WP\_002866859.1 NADH-quinone oxidoreductase subunit J [Campylobacter jejuni]

MIENLAFVFFSVVVLGFFGIAVLSKNMLYSLSALAGGMVFLSGFYFLLDAEFLGVIQIIVYSGAVLGLYS

FAIMFFDASKEFKEQLKAKKSFFTLVVLSAILLLAMLIGFKYQNISTDLPLNDPALFDFNKQLALAIFSK

YLLAFEFIAILLLIALVCAIVLTRKELTKEKQ

>WP\_002866405.1 MULTISPECIES: phosphoribosylformylglycinamidine synthase, purS protein [Campylobacter]

MEVIVNISLKNGVLDPQGKAVEKALHSLNFNSVKEVKIAKQIKISLDEKDEKLAKEQVKKMCEELLVNSI

IEDYELVIEKE

>WP\_002860004.1 MULTISPECIES: RNA-binding S4 domain-containing protein [Campylobacter]

MRVDKFLNVVNITKRRAISEDMCKSGVVGINGVIVKASKEVKVGDIITLHFTEYTQKYKVLAIPSTKSIP

KNAQNEYVVKL

>WP\_002857627.1 multidrug efflux system transcriptional regulator CmeR [Campylobacter jejuni]

MNSNRTPSQKVLARQEKIKAVALELFLTKGYQETSLSDIIKLSGGSYSNIYDGFKSKEGLFFEILDDICK

KHFHLIYSKTQEIKNGTLKEILTSFGLAFIEIFNQPEAVAFGKIIYSQVYDKDRHLANWIENNQQNFSYN

ILMGFFKQQNNSYMKKNAEKLAVLFCTMLKEPYHHLNVLINAPLKNKKEQKEHVEFVVNVFLNGINSSKA

>WP\_002866271.1 MULTISPECIES: acetyl-CoA carboxylase biotin carboxyl carrier protein [Campylobacter]

MTKEEIKELVNLFAEANISKIKIKEQDGFEIELERDMCCDVPAPVCPPVPAPQPINVSVVNEAQPSQSAK

SNKPSINSPMVGTFYQAPSPGAAPFVKVGSTVKKGDTIAIIEAMKIMNEIEAEFDCRIAEILVADGQPVE

FGMPLFAVEKL

>WP\_002851874.1 MULTISPECIES: YraN family protein [Campylobacter]

MGVKAYLDGILGEDKACKFLKKQGFEILKRNFHSKFGEIDIIAKKDEILHFIEVKFTQNDYEVSERLDRK

KLEKILKTIEFYHLKNGISSDFQIDLICIKNDVIQFCENISF

>WP\_002856815.1 MULTISPECIES: S41 family peptidase [Campylobacter]

MMELILKTKRFFAGLAGFATTFILCLFLTSHLQAKVDQKEEQVQKRLEALDKLTKTLAIVEQYYVDDQNI

SDLVDKSLSGLLSNLDAHSSFLNEKDFNDMKIQTNGEFGGLGITVGMKDGALTVVSPIEGTPADKAGIKS

GDIILKINDEATLGINLNDAVDKMRGKPKTQITLTIFRKGATKPFDVTLTREIIKIESVYAKMIENENIL

YLRVTNFDKNVVDVASKELKKYPNVKGVILDLRNNPGGLLNQAIGLVNLFVDKGVIVSQKGRIASENQEY

KADPKNKISNASLVVLVNGGSASASEIVSGALQDLKRGVIVGENTFGKGSVQQIIPINKTEALRLTIARY

YLPSGRTIQAVGVKPDIEVFPGKVNTQEDGFSIKESDLKQHLESELEKIDKNKKEDKQENKDNKNLISQK

QINDDAQLKSAIDTIKILNIKQGQ

>WP\_079254161.1 thiamine biosynthesis protein ThiF [Campylobacter jejuni]

MMRVKFNGKELDTDFKTSLEFFENISKNENDVWIINGFATKENIALNENDELFCIEKNTLPPKDALDAMM

RARHTPKLHDKLKNGRVAVCGLGGLGSHIVINLARSGVGYLKLIDFDVIEPSNLNRQAYRVSDLGKFKTE

ALKEQISEINPYISVEICTLKIDEDNLESLFKDIDIVCEAFDSAIAKAMIAQNFHRFYKDGILICASGLA

GYGDSNSIQTRKIAKNFYVCGDLVNGAKVGNGLMAPRVNICAGHQSNLVLELLANKE

>WP\_072238644.1 MULTISPECIES: cadmium-translocating P-type ATPase [Campylobacter]

MIMKCEHCKLDYKQAQMIEYKGKFFCCKGCESVWEILHESGLDEFYEKLGNQTLSPVNFQNEMKNYDEFI

TKTKEGFSEIYLMIHGIECAACVWLNEKILTKQEGILELDINHLSHKARIVFDEQSISLVQILRLIESIG

YKASAYDASKASKKADLLKREFYSKLVVAIACVMNIMWIAVAKYAGLFSGMDKDTKDILNFAEFILCSPV

LFYTGSHFYKSAFKTLKMHSLNMDVLVISGASLAYVYSLWAMFFRVGEVYFDSVAMIICFVFIGKYLEMF

SKKRALDTIDGLNDFLQNEVLVFNGKEFAPKKVQKVCLGDRILLKTGDKILIDGICKSGEMSVDTSSLNG

ESIPKLIQKEDEIFSACMVLDGSVEYEATKLYKDSKLSQIIQLLELASSKKAKLESLVNSLSAYFSRTVL

LIAFICFAFWFFYKEESFEISLVNAIAVLIIACPCALALATPVSNLVALGRALKKHILFKSSSVIEDLSK

CDCVVFDKTGILTKIELELKEVFLDKVLDLNELYNFVKLSKHPISQNIASYLKQKGAKDLNLNFKKHSSI

QAKGLSAELNEELLLGGSSKFLQEKSIATKEFDNTHFIFAKEGKILAFFEFDSVLREGAKELIAYLKKEK

KELMILSGDHQKAVEKIARKLEIQNYQASCLPEDKMKAIENLSKNYKVLFVGDGVNDALALKYASVSMTL

REGSDLAIESSDVLLLKNDLLSLKKAIKLSKNTFKIIKQNLAFSLFYNACTIPLAFLGMINPLFAAISMS

FSSIIVVLNALRIKE

>WP\_012006755.1 DUF814 domain-containing protein [Campylobacter jejuni]

MKYTELLQLQTFFSQFKKIDFIKRINDNILELSFDRERFIFDLTRAMSAIYTAKFNAKNYNAPFDFMLKK

YFSNAFIKEVKVLEGNRILCFSVKANKAYKSYESKIYFEFTGKNTNVILTDEKDLIIEALRHIDKSYRVV

KPNVILEPLKPYKMDENFEEIKDFKDYFSCKFTSIYESKIKQIKNLKLAQVDKKIQNLQELFSSLDEENS

LLLKALEYRKRADVLFANLSVLKDYEREFKLDDFEGKELEFKLEFSPKQSANLYYKNAKKLEQKAKNLNI

QRQNLKEKLDFTLSLKELLLQAKSEIELEILLPKKNSKKNQDHKQEDLVANFYYNEFKICVGKNEKGNEF

LLKNAKKDDLWLHVRDIPSAHTLIVSNKQKISLDVIEFAARLCVSFSKLKKGSYWVDYTLKNFVKVQQKA

FVNYTNFKSINITKD

>WP\_010891887.1 MULTISPECIES: nitrate reductase cytochrome c-type subunit [Campylobacter]

MMKKKLVLLGSAAVVFFAACAMNSGVSSEQIGLRKASLENENKVNLVEANFTTLQPGESTRFERSYENAP

PLIPHAIEDLLPITKDNNMCLSCHDKAIAADAGATPLPASHYYDFRHNKTTGDMISDSRFNCTQCHVPQS

DAKPLVGNSFKPEFKNEQLKSRSNLIDVINEGVK

>WP\_002869046.1 endonuclease III domain-containing protein [Campylobacter jejuni]

MTGARIFTKLLNLDLNYHDFDWLENQGLSEFELLISVILTQNTNWKNVLKALENLKKENIVSLEQINTLS

NLELATLIKPSGFYNTKAKRLKGLVESIINTYENLENFKTNVSREWLLNIKGLGFESVDSILNYLCKREI

LVVDNYSLRLAFCLGYEFENYEELREFFQSGIESEQENLCKILGRKCELYELYQIFHALIVAFAKQSFKG

QKLSPKGEEWIKILKEDL

>WP\_002868803.1 MULTISPECIES: prepilin peptidase [Campylobacter]

MIFFIIILGACLGSFCTSLASRIIEKKPFFISRSFCFSCDTKLKYYEIIPIFSYIFLKAKCQTCKCHLPI

SLLINEILGIILLILAYSLSQNFYDFLFLSLFLFNLFLLSLIDIKLKAVPQILLWSAFLFAFFYAFRESE

ILHFLIFKEFSGGFLLNAFSFGGFVFLLKSLVFFLMNFRKKDEILENLGDADIIIMSCIGGILGFEYGFL

VLLIASILTLPFFIFFKIKAIKEQELAMIPFLNIAFVAVLFYKNLGLF

>WP\_002866993.1 MULTISPECIES: 3'-5' exonuclease [Campylobacter]

MSSQQIDQIISILNKQSKPYDWVMQEFAKVEELKNFDLDLETFELLGLGLTLNKDNIFTLKTRTTKIKDE

IFCIVDIESTGGVSKGEILEIGAVKIQNSKEIGRFQSFVKVKEIPENITELTGITYEMVENAPSLAKVLS

DFRLFLKDSIFVAHNVRFDYSFISKALNECGFGILLNRRICTIEFAQCCIESPKYKLEVLKEFLGVENTH

HRALDDALAAAEIFKYCLGKLPYHIKTTEELINFTKTARIKQK

>WP\_002866667.1 LptF/LptG family permease [Campylobacter jejuni]

MWIFFRFISGIYLKNFFIIFFSLLGFYCGIDLLLNFKDLPKAANLDLLYVMFLSFSAVPYVLPISLIFAL

VVSLISMIRANEFVSLYALGLSRNYVILFPFLWALFFCCIYIGLNFTSFAYANDYKRNILKNGTIMNQSG

EVFLKFNNNFVYISKINNGQNSAQNIKIFNINDLNLSSFVSAKNAHFEGESWILRDGNITLLPKNYELAN

DGLKIQDFSELKSLEGFKPKIIEGVASNSDYSISDALESFELFKAQNVNTDALKINLYKFVFTPFFAPFL

MLIMYYFFPVIARFFNLAFVTFIAFVVTLMIWGVLFLLTRLSENSVIASEIGIVVPIIILGCLSAYMYYK

HR

>WP\_002866347.1 MULTISPECIES: ATP-binding protein [Campylobacter]

MKKLKCISFHEGLDIIEVESTFTRGLPNLSIVGLASVAIKESVERIKATLLSCDFAFPAKKITINLSPSG

IPKKGSHFDLAIALLILLQNEELDDFFVVGELGLDGSIKSTNELFSLLLFLSAKIKKAKIVVPKSIAQKA

SMIPNLEVYGLENLNEAIEFFKEKNYENFRFSHNHPLFTSPLQIENEIFLQNMDFKLDFKDIKGQEKAKR

ACMIAALGMHNILFEGSPGSGKSMCAKRLVYIMPPQSLSEVLMQNAYMSLDSKDCEFTKIRAFRHPHHTS

TRASIFGGGTKNARIGEVALANGGVLFFDEFPHFNKQIIESLREPLEDHKIHISRVNSKITYETKFSFIA

AQNPCPCGNLFSKNLSCVCSENEIKKYKNHISAPIMDRIDLYVAMDEISKDDKTSISSKEMSEKILQAFI

FGKKRGQKEFNGKLKDEDLSRFCVLEKDAKDTLDLAISRYNLSLRSLNKILKVSRSIADLEQSLNINKTH

ILEALSFRARN

>WP\_002866274.1 DUF4910 domain-containing protein [Campylobacter jejuni]

MDKLDFRNQDFSQTGKAMYELACELFPIPRSITGQGFRASLEILNKTLGGGILKFHSIKSGTKVFDWIVP

DEWNAKEAYIITPEGEKICDFKKHNLHLLNYSEAIDQEIELEELQDHLYSIEEMPDAIPYVTSYYKRRWG

FCLTHNERKKLKKGKYKVYIDAKHDENGVLDYADFILPSTQNSKDEILISTYLCHPSMANNELSGPVVAI

FLAKWLLNLKERKYNYRFVIIPETIGSIVYLSKHLEHLKKHVKAGFVLSCIGDDHAYSLIHTPKENTLSD

KVALHTLKNKENFKAFSFLNRGSDERQYNAPLANLGIVGVCRTRYGDYDGYHNSKDDLNFISEKGLMGGL

QSMQEIILNLEINAIYENTIVCEPNLGKRGLYHTINKGVKQKPISADFLAYCDGQNDIIDIANILNMQAY

EFKELLEKIKFYGLVK

>WP\_002866196.1 MULTISPECIES: cytochrome bc complex cytochrome b subunit [Campylobacter]

MAQIRKANGLVDWLDQRLAVHKLLDVLMVKYWIPKQINFLWAMGVILTTLFAVLFITGLLLVMYYKPDTA

LAFDSVNKTIMQEVDYGWLWRHMHGVAASVVFLIIYIHMLTGIYYGSYKKGREMIWVSGMLLFVVFSAEA

FSGYMLPWGQMSYWAAQVITNLFGGIPFIGPELVIWIRGDYAVSDPTLTRFFMLHVCLLPIVIIAIIAFH

FYSLRIPHVNNEISEELDFDLEAEKYMAGDTKGSKVIPFWPGFLSKDFMYISFFMIFFFYLVCFKFEFAM

DPINFDPANALKTPAHIYPEWYFLWSYEVLRGFFFDIAGIKAFDIGLAAFGIAQVIFFLLPWLDRSDVVK

PAHERPLFFIWFWILLIDLIVLTVYGKLPPTGVNAWVGFYASIVFLLLLIVVLPVITIMERKGAKQ

>WP\_002856798.1 MULTISPECIES: LptF/LptG family permease [Campylobacter]

MKLSLRYVLNQFLSTNLSIFFVLFAIVSMVFFIQLAKLTSSIEISFLDLLKLYGFMLPRILIFTLPISFF

ISLTLALFRLSKENESIVLFTLGFSPMILAKFFLKIASLISAFMLVVALVMIPIVFELQDNFVNYKSTQV

KFNYKTGEFGQKFLDWMIFIEKQDSDKYENIIMYRPKHKADDKEQLIIAKEAHVQRKDDSFAFSLNQGKM

YNFEQGQSIFSGEFDTLVVNTQFNTDNLQTKKFYEYWNDLNENPQRAREFVIYTTIALFPLASTLFALCF

GLVTYRYEKGYVYLGMFGVIAIYFGLLSSFSQPPILACLGIFSLSLFVSAYCFKKMILSRY

>WP\_002854656.1 MULTISPECIES: pyridoxal phosphate-dependent aminotransferase [Campylobacter]

MFDEIRFNTIERLPNYVFAEVNAIKMAARRAGEDIIDFSMGNPDGKTPQHIIDKLCESANKDKTSGYSTS

MGIYKLRLAICNWYKRKYNVNLDPENEVVATMGSKEGFVNLARAIINPGDVAIVPTPAYPIHTQAFIIAG

GNVAKMPLAYNEKFELDENQFFENLHKTLNESIPRPKYVVVNFPHNPTTVTCEKSFYERLIATAKKERFY

IISDIAYADLTYDDYKTPSILEIEGAKDVAVETYTLSKSYNMAGWRVGFVVGNKRLVSALKKIKSWFDYG

MYTPIQVAATIALDGDQTCVDEIRATYDKRMHILLEAFENAGWKLQKPRASMFVWAKLPESKRHLKSLEF

SKQLLQRASVAVSPGVGFGEAGDEYVRIALIENENRIRQAARNIKKYLKE

>WP\_002854264.1 MULTISPECIES: flagellar biosynthesis protein FlhF [Campylobacter]

MGQLIHTFTVEDTEQIIPKVKEDYGDKALIITNKQIRPKTLNRSALYEVMVAIEESDYEEHLKKQGKSLP

AKKSSPKPSSTSLAEEKIRSQIPQEDEDVVLDFSNTRLNTNLNTVKNNDLTKKTYQDFPQNKINPHQNKT

LGFDDFKEKLSEVSNEISKVTNTPLENYTPNPNYNKKIENFEKQFEKQINKLNDKIDLLADMMWDDKAEA

RKNLMIPPEFASIYKQAKESGMLENHLEAIMKATIENMPAAMKTNKDAVQRYFHSLLRNILPCRVESDIK

KQKIMMLVGPTGVGKTTTLAKLAFRYAYGDKRYKTGIITLDTYRIGAVEQLFQYAKMMKLPIIDSIEPKD

LDEAIKSLNNCEVILVDTIGNSQYDQSKLAKTKEFLMHSNAEIDVNLVVSANTKHEDLMEIYKNFSFLNI

DTLIITKFDETKVFGNIFSLIYETNIPLSFFSTGQEVPDDLEVANSDFLVHCILEGFNKGKNNE

>WP\_002866637.1 MULTISPECIES: protoporphyrinogen oxidase HemJ [Campylobacter]

MTEWINDYYFWIKWVHYLAFVSWMAGLFYLPRLFVYHAEHKDNKGFVEIVKIQERKLYFYIQTPAMIVTL

ITGSLMLHAHKEVLMVGAGFMHVKLTCVTLLIIFHIHNYYCLKALANDTSAKSGKYFRIYNEFPTIMFII

IALMMVIRPF

>WP\_002866333.1 MULTISPECIES: 7-carboxy-7-deazaguanine synthase QueE [Campylobacter]

MQLVESFLSIQGEGKYNGKLAIFMRFAGCNFNCLGFNVKISKNDKTLIGCDTIRAVFTKDFKESYETLNA

NELLKRVIKLKQDFDPIVVITGGEPLIHYENPEFIKFIQMLLKNKFEIHFESNGSIEIDFDRYPFYKECI

FALSVKLQNSGIKKDKRLNFKALKAFKNYAKDSFYKFVLDANTLDNSFLEINEILKEAPNQIFCMPMGEN

EQNLKKNAQKIAEFCIKNGYNYSDRIHIRLWNDKEGV

>WP\_002856712.1 MULTISPECIES: thiol peroxidase [Campylobacter]

MSTVNFKGNPVKLKGNSVEVGADAPKVNLKAKDLSVIEIGAAGKTQIILSVPSLDTPVCATEAREFNKKV

ASYNGAEVIVVSMDLPFAMGRFCSTEGIENLSVASDFVAKEFGEKYGVLINEGALEGLLARAVFVIKEGK

VAYKELVNEITEMPDIAKLDAFFGGSSCCGGCGCH

>WP\_002867060.1 multicopper oxidase CueO [Campylobacter jejuni]

MNRRNFLKFNALTLASMGVAYANPMHDMHSMHKNHSINHDLDTSFINFAPKNLKLLDPKQFPQGEILKAL

PLLKNESKEKNIFRATLEIKENHIELIKGKKTLFYTYNGLVPAPKIEVFEGDKLEILVKNKLKEATTIHW

HGVPVPPDQDGSPHDPILAGKERIYHFEIPQDSAGTYWYHPHPHYTTSKQVFMGLAGAFVIKAKKDALSH

LKEKDLMISDLRLDENAQIPNNNLNDWLNGREGEFVLINGQFKPKIKLATNERIRIYNATAARYLNLRIQ

GAKFILVGTDGGLIEKAIYKEELFLSPASRVEVLIDAPKDGNFKLESAYYDRDKMMVKEEPNTLFLANIS

LKKENVELPKNLKIFKPSEEPKEFKEIIMSEDHMQMHGMMGKSESELKIALASMFLINGKSYDLKRIDLS

SKLGVVEDWIVINKSHMDHPFHIHGTQFELISSKLNGKVQKAEFRALRDTINVRPNEELRLRMKQDFKGL

RMYHCHILEHEDLGMMGNLEVKE

>WP\_002877339.1 MULTISPECIES: class II fumarate hydratase [Campylobacter]

MEYRVEHDTMGEVKVPNDKYWGAQTERSFENFKIGCEKMPKVLIYAFANLKKSLALVNNKLGKLDDAKKN

AIVQACDEIIAGKFDDNFPLAIWQTGSGTQSNMNMNEVIANRATEIMGGDFRKEKLVHPNDHVNMSQSSN

DTFPTAMSIVAVEQVEKKLIPALDELIATFEKKVKEFDGIIKIGRTHLQDATPLTLAQEFSGYLSMLLHS

KEQIIASLPTLRELAIGGTAVGTGLNAHPELSQKVSEELTQLIGTKFVSSPNKFHALTSHDAINFTHGAM

KGLAANLMKIANDIRWLASGPRCGLGELIIPENEPGSSIMPGKVNPTQCEAVTMVAVQVMGNDAAIGFAA

SQGNFELNVFKPVIIYNFLQSLDLLADSMHSFNIHCAVGIEPNRAKIDHNLHNSLMLVTALNPHIGYENA

AKVAKNAHKKGISLKESAMELGLVGEEDFNKFVDPTKMIGPKA

>WP\_002877023.1 type I DNA topoisomerase [Campylobacter jejuni]

MKKNLIIVESPAKAKTIGNFLGKDYEVIASKGHIRDLPKSSFGIKIEDDEFIPEYRITSDHSALVKELKS

KAKDAKEVYLATDEDREGEAIAYHIAKAIGKDENTLPRIVFHEITKNAIENALKNPRKLDMHSVNAQQTR

RLLDRIVGYKLSPLLGQKIQRGLSAGRVQSAALKIIVDREKEIRAFVPLEYFSIDMIFQKDLDAELVEFD

KAKIEKLTITNKDRAKLILEACKNEAYAISDIESKERKIAPPPPFMTSTLQQSASNRLGFNPKKTMMIAQ

KLYEGVNTHEGVMGVITYMRTDSLNLAKEAIENARKFIQTNFGKDYLPSKANVYTTKAKGAQEAHEAIRP

TNLSFTPEIAAKFLDKDELKLYTLIYNRFLACQMNPAISQTQNVFVKNDRALFKISGRKILFDGYYKVYG

DMDKDKILPNLKIGENLKIQNLEMNSHFTEPPSRYSEAGLVKKLESLGIGRPSTYAPTISILTSRDYVKI

DKKQLIPSDVAFNVTEVLEKNFSDIVDSKFTSNLENTLDEIAEDKADWQETLKEFYYPFMRKIEEGKTKI

ASQKTVTKLGESCPDCGGELAIRKGRFGEFVACLNFPKCKYSRNLKSESKNESENTAAKAKANGTGITCP

SCQKGEIVERFSKRGKFYGCSAYPKCNFISKYKPSEEKCEECGETLVIKELKKGTFLECLKCKIKKEMKD

>WP\_002852246.1 MULTISPECIES: hydroxyisourate hydrolase [Campylobacter]

MFSIKKTLLILASVPMFLSATEYQLSTHVLDITSGQPAPKVKVELYKLEANQQWKKVSEEFTEENGRIGD

LLPYEKAENRAFGIYKLKFFTKDYYTSHKINTFYPFVEVSFELSKDQKHYHVPITLSPFGYSTYRGS

>WP\_019108971.1 MULTISPECIES: RluA family pseudouridine synthase [Campylobacter]

MAYIKIKLSNNGKKAFQVLMENLKISINEAQKLIDKKRLFCDGILVEEKNKILNGLVELIVYENNPKGVE

IVFENEDFAILEKESGILSHPNGRHCKYSLSDEIWHLWGKEACVAHRLDKETSGLILIAKNKKAQIDLKS

LFEKKLVQKEYLALAHGKIEENFIVDKAINLTKNYDDIKTRMQICKEGKQAITEFEILEYFPKINATLLL

CKPLTGRQHQIRVHLHYKNHTILGDPLYGLSKQQIESILDEKLNPKERLKLTGALRLCLHSYRLKFQYKN

QNFDINSKINIKEIFNNSIK

>WP\_002893398.1 MULTISPECIES: translation initiation factor IF-2 [Campylobacter]

MAKIRIHEIAKELGYDSKEIIEKANELGLGIKTASNAVEPEIAAAIYEYIQTREIPEAFKKNIKTPTAKK

PKKENIKEQEKLNESEKKEPKKEEKLKQEVKKEELKVEKENVKEEEKQEIIDAHKPQSLASATLAKRRGL

VIVKKKKDEEEIQVKKEEVKNSNDISINNEERLSLKTMFSNADESLKKKKKEKKSFVASKKESTEKMNFL

DEHDFGDISLDDEDEVVLPDFSVKEQEKPQNINKKQPNFIRQAVGNSAGFGLEGGIQRRSRKKPPKKIEK

KEVEEVSSVAISKEIRVYEFADKIGKSTSEVISKLFMLGMMTTKNDFLDEDAIEILAAEFGIEINIINEA

DEFDYVKDYEEETDEKDLVTRAPVITIMGHVDHGKTSLLDYIRKSRVASGEAGGITQHVGAYMVEKNGRK

ITFIDTPGHEAFTAMRARGASITDIVIIVVAADDGVKPQTKEAINHAKAAGVPIIIAINKMDKEAANPDM

VKTQLAEMEIMPVEWGGSYEFVGVSAKTGMGIEDLLEIVLLQADILELKANPKSFAKASIIESSVQKGRG

AVATIIVQNGTLTVGSTVVAGEAYGKVRAMSDDQGKALKEIKPGECGVIVGLSEVADAGEILIAVKTDKE

AREYANKRHEYNRQKELSKSTKVSIDELGAKIKEGNLKALPVILKADVQGSLEALKASLEKLRNDEIKVN

IIHSGVGGITQSDIELASASENSIVLGFNIRPTGEVKERAKDKGVEIKTYNVIYNLLDDVKALLGGMMSP

IISEEQLGQAEIRQVINVPKIGQIAGCMVTEGVINRGAKIRLIRDGVVVYEGNVSSLKRFKDDAKEVAKG

YECGVGIEGCDDMRVGDYIESYKEVEEQASL

>WP\_002892992.1 MULTISPECIES: tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD [Campylobacter]

MKNLILAIESSCDDSSIAIIDKNTLECKFHKKISQELDHSIYGGVVPELAARLHSEALPKILKQCKEHFK

NLCAIAVTNEPGLSVSLLSGISMAKTLASALNLPLIPINHLKGHIYSLFLEEKISLDMGILLVSGGHTMV

LYLKDDANLELLASTNDDSFGESFDKVAKMMNLGYPGGVIIENLAKNAKLKNISFNIPLKHSKELAYSFS

GLKNAVRLEILKHENLSDEIKAEIAYAFENTACDHIMDKLEKIFNLYKFKNFGVVGGASANLHLRSRLQN

LCQKYNANLKLAPLKFCSDNALMIARAAVDAYKKKEFVSIEEDILSPKNKNFSRI

>WP\_002877914.1 MULTISPECIES: glutamate synthase large subunit [Campylobacter]

MDLENILENNQSIGLYHPKNEHDACGIAAVANIRGIASYKVICDALEILMNLEHRGGAGAEENSGDGAGI

LIQIPHDFFKTQELGFELPKKGDYAVAQMFLSPNTDAKEEAKEIFLQGLKDKKLEFLGFREVPFNPSDIG

ASALKAMPYFLQAFVKKPSKISAGLEFERVLYSTRRLIEKRAINVPKFYFSSFSSRTIVYKGMLLSTQLS

DFYLDFKDVNMKSAIALVHSRFSTNTFPSWERAHPNRYMVHNGEINTIRGNVDSIRAREGLMQSEYFENL

DEIFPIIAKPSSDSAMFDNTLEFLALNGRTLEEAFMMMVPEPWHKNENMESKKRAFYEYHSLLMEPWDGP

AAIVFTDGVIMGASLDRNGFRPSRYYLTKDDMLILSSETGALKLDEKNIKAKKRLEPGKLLLVDTARGRV

IADNEIKEHYANAKPYKKWLKNLVELEKQKSGVYKHQFLKEDEVLKLQKAFGWSYDELKMSVAAMAQNGK

EAIAAMGVDTPLAILSKTYQPLYNYFKQLFAQVTNPPLDAIREEIVTSTRIYLGSEGNLLKPDENNAKRV

KIALPVISNEELFEVKALNKFQVKEFSILYDYSKKTLEKALDELCVKIEDEVKKGVSIIILSDKGVDEKN

AYIPALLAVSGVHNHLVRKNLRTHTSLIIESGEPREIHHFACLLGYGATVINPYLVYESIQKLIANKDLN

LSYEKAVENFIKASSSGIVKIASKMGVSTLQSYNGSALFECLGLSSKVIDKYFTSTTSRIEGMDLEDFEK

ELIALHKHAFNDTHKALDSKGIHGFRSAKEEHLIDPLVIFNLQQACRNKDYKSFKKYSALVDEKQVNLRS

LMEFDFSEAISIDKVESVESIVKRFRTGAMSYGSISKEAHECLAQAMNKIGAKSNSGEGGEDEERYEIKE

GVDKNSAIKQVASGRFGVDLNYLSHAKEIQIKVAQGAKPGEGGQLMGFKVYPWIAKARHSTAGVTLISPP

PHHDIYSIEDLAQLIYDLKNANKDAKISVKLVSENGIGTVAAGVAKAGANLILVSGYDGGTGASPRTSIP

HAGIPWELGLAETHQTLILNKLRDRVRLETDGKLMNGRDLAIAALLGAEEFGFATAPLIVLGCTMMRVCH

LNTCPFGIATQDTELRDRFKGKVDDVINFMYFIAEELREYMARLGFERLDDMIGRVDKLRQKSVQGKAGK

LNLDKILKSLPTYNRTAVHFKDYKDNKLEKTIDYRILLPLCKNAVEKKEPIKLSLEVGNQSRTFATMLSS

EILKTYGKDALDEDSIHIKAIGNAGNSFGAFLLKGIKLEIIGDSNDYLGKGLSGGKIIAKISNEATFSPE

ENIIAGNACLYGATKGEVYLDGIAGERFCVRNSGALAVVLGTGVHGCEYMTGGQVVVLGDVGANFAAGMS

GGVVYIFGRHNEAHVNTELVDIKDLNAKDEKELKAVIEKHIAYTDSKKAKDILEKFDKKDFFKVMPRDYE

KMLKMLDLCKNEKDPNLAAFLKITQK

>WP\_002877769.1 MULTISPECIES: apolipoprotein N-acyltransferase [Campylobacter]

MKLKLNFLPYFSFIPKKLNTNSIIFKIIKVFFIAILLSNSIYLSFFENIFTQTISPFLAIWGLVLLLKSK

NSKQYFWIGFFVGILWFWWIGLSSIYFNLNYLVPIIPIIIGFIYGLLFRLCYLLKFDFLRLCGIFCISFI

HPLGFDWLNWGIFTVYGFFDPSYRGIICIFLIAYFIYEGYISRYYKIAIVLILFFSGFQYNEKQAQTLNL

NYKLINTNISQDQKFLQENLKSNSDILIQDILQAINEKKELVILPETAFAFDLKNTKYELILKELSYKIT

IITGAFHVEKEHTYNSTYIFKKGNVYILNKHFLVPFGEEIPFFKDLTKKYFLKNIEEFSKGPIQSKYKLD

NQIITNAICYEATKEQNYQNSQIIIALSNNAWFNNSSEYKLQQLLMKFYASKYGVSVYHATNGKENIVIL

PKKLLSKDWKNLSKEIFNDKK

>WP\_002877596.1 MULTISPECIES: glutamate-5-semialdehyde dehydrogenase [Campylobacter]

MRNLLENIKKNSQKLLNLTPKDKEKIILKLAQILRENFKIILEANKKDMANFTKSGAMKDRLLLDEKRIL

ALCEGLEKIAHIEDPIGKISKGWKNYAGLNIQKISIPLGLICVIYEARPSLSAEIAALMIKSSNACVFKG

GSEAKFTNEAIFTLVNKVLKEFDLQDCFAMFTQRDEILQILAFDDLIDVIIPRGSSNMIQEIANNTKIPL

IRQDKGLCHAFVDQSANLDMALKIILNAKCQRVSVCNALETLLIHEKIAKNFISLLIPEFEKFKVKIHAH

ENALAYFNNSNLEVFKADENTFDTEWLDFALSVKLVKDCDEAIEHINKHSSLHSETIISNDASNIAKFQR

LINSSCIYANASTRFSDGGEFGFGGEVGISTSKLHARGPMGVEDICTYKYIISGEGQIRE

>WP\_002877328.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKFFLTILFFITSIFALELDFSVGENGKSLDDNNTVLIFGGIQGDEPGGFHAASLLLSDYNITKGKIIVA

PNLAFDSIIKRSRGNNGDLNRKFASISPKDPDYKTVQRIKELILLPEVSMVINLHDGWGFYKPTYIDAMQ

NPKRWGNSSVIDTSEINASKYPDLENIATQTVNSVNSSLADPKHAYHLKNTKTQELGDTEMLKALTYFVI

SNHKAAFANEASKNLPVNLRAYYHLLAIENYLKTAGIEFSRDFELTPKGVDKAINRELEVKLFNDRILLS

LKNPRKVINYVPFPVNKELNYNTSNELTAVIAEGNSFYIQYGNRFQTRLYPEYLEFSDAFNEVTFQVDGN

ETTVPFGTKVKVKENFLIPKIANVRVNIIGFDHGKDESGILVHKKNMQTQYSLDMAGKIYRVEFYELRGA

NLQQLLEANTNSKLIKNAKNLDLNTLKMARSKDKFLGSILVEFE

>WP\_002866765.1 MULTISPECIES: phosphatidate cytidylyltransferase [Campylobacter]

MFNTTRIISALVMIGAIIIIALIDQFFINFIVFAVLLYLSFSEAKKLFALENISIIPLAIAFILGSLSHK

ALLFGILALLLVIGYLVYKKASLKSALIYIYPSLPILALWQVYLDQGMFALFWLIIIVAACDSGAYFIGK

LMGKTPFSPTSPNKTLEGVIGGLICASVIGTILGVFVYSFWLSLLCSFFVAIFAVIGDLLESYFKREAGV

KDSGDLIPGHGGVLDRIDAVIIAAFVMVALL

>WP\_002866751.1 MULTISPECIES: mcrBC 5-methylcytosine restriction system component [Campylobacter]

MEKIFEDYVAYMLKKVNPTQDIKVQNNGKYLISKNDEKCFMLKPDLYIENKMILDTKWKIPNDSEDEKKQ

GIEQSDLYQMFAYACKFKIYDIKLVYPLCEKTQDLQRKIAEKFFVFKASEHLYFKEQGQKDIKVQVLFAP

LPF

>WP\_002866748.1 MULTISPECIES: ribosome maturation factor [Campylobacter]

MNLEALCKEAGLSFYDDELVSENGRKIYRIYVQKEGGVNLDDCARLSEILSPIFDVEPPVNGEYFLEVSS

PGLERKLSKIEHFAKSIGELVKITTNEKEKFEAKIIAVDDENITLENLENKEKTTINFNDIKKARTFVEW

>WP\_002866744.1 MULTISPECIES: homoserine kinase [Campylobacter]

MKILVPATSANLGPGFDCLGLSLKLFNETQIQKSGVFSISIGGEGSDNIFLKKNNIFVNIFYEIYEKLSG

KKDNFRFIFQNNIPLSRGLGSSSAVIVGAIASAYYMSGFKVEKERILDEALIYENHPDNIAPATLGGFVC

SLVEKNKVYSIKKEIDKDLAAVVVIPNLAMSTEQSRQALAKNLSFNDAVFNLSHASFLTACFLEKKYEFL

KFASQDKLHEINRMKNLPELFEVQKFALENKALMSTLSGSGSSFFSLAFKDDALALAKKMQTKFKDFCVQ

YLEFDDNGFEIC

>WP\_002866739.1 MULTISPECIES: acetyl-CoA carboxylase carboxyltransferase subunit beta [Campylobacter]

MNFADIFSKIRRQQPSIKEAPNHWVKCQSCHALMYYKEIESCFNVCPKCNYHMRISADERIKLLSDEGSF

IEYDANLEAIDPLKFVDSKSYKKRLSEGESKTGRKSSVISGECEINSLKTQLVVFDFSFMGGSLGSVEGE

KIVRAIQRAITSKTPLVIVSASGGARMQESTYSLMQMSKTSAALKLLSKEKLPYISILTDPTMGGVSASF

AWLGDLIIAEPEALVGFAGARVIKQTIGADLPEGFQKAEFLLEHGLIDAIVERGEQKQYLSDVLKFFSGK

>WP\_002866602.1 MULTISPECIES: DUF4261 domain-containing protein [Campylobacter]

MTIDLNHNFTSFVLLDEVDFNFSELKSILEDKFNIKIADENFTKEGVIFSYENMLITLNLIKNPIPNHEA

EYYANFNFMWKDALEQTKKHKAHLLIAVLSQDQSKLEQAKMFTKIAALCLDNKHALGFYTGAVVLEPSFY

IENAKMLDDNRLPVYNWIYVSVYPSENGVNAYTYGLRNFDKLELEVCDLNIEEKELFFCIYDIVLHILTY

DINLKDKDILKFEDGKEIKFIKSQGISVENESLKIIF

>WP\_002866553.1 MULTISPECIES: RluA family pseudouridine synthase [Campylobacter]

MQEKAYKLLALQEKISNREAKDLIDKGCVFSHGKKVVVARALMSDKARFNVIKTKNPQIIFEDDKIIAIN

KPYAYVSEDLEKKFNAKLLNRLDKETSGVILLCKDEDFRKLCIEEFKKHRVYKSYIAVLDGVLAEEVEVN

EPIFTIKAKGGALSKVSKDGLSALSIITPIMMQSKKTLAKIVIQTGRTHQIRVHAKFIKHGVVGDEKYAK

ISSDRMYLHSYEIKIFDYYFKAELDNSFAKVGFEIKNLDF

>WP\_002866416.1 MULTISPECIES: malate dehydrogenase [Campylobacter]

MKITVIGAGNVGSSVAYALILREIANKIVLVDINEDLLYAKELELTQSIAALNLNIDLLCTKDYTHTKNS

DIVLFSAGFARKDGQSREELLQLNTSIMLDCAKKIKDFTEDPLFIILTNPVDFLLNTLYESGIFSSKKII

AMAGVLDNARFKYELAKKLNVKMSSVDTRLIGFHNDDMVLVKSYASVKNKNISEFLNEEEFDDLENEVKT

GGAKVIKHLKTSAYLAPASACIRMLESIRSGEFLPMSVILHGEFGVQNKALGVMARLGLEGVIEIMKMDL

SLQEKDKLEKSLIKYQYKGE

>WP\_002866083.1 MULTISPECIES: NAD-dependent protein deacylase [Campylobacter]

MKNIMILSGAGLSAPSGLKTFRDNDGLWEEYDVMEVCSATGFRKNPKKVLDFYDARRAQLQNVKPNHAHE

KIAQLKEKWGKNLFVITQNVDDLLERAGCKDVIHLHGFLPELRCLKCEGIFNIGYEKFTDKQCPKCKSKD

LRHNIVMFEEQAPAYATLYSLLHQTSLFISIGTSGAVLPVGQYASMCEKSILNIYEKDVNLERYFDKIYI

EDIISAIDKITLDIENFMKDGNV

>WP\_002866073.1 MULTISPECIES: thiamine phosphate synthase [Campylobacter]

MWDKKIIAISDRKCVEIDFLKQIEKLAKAKVDAIVLREKDLSEFEYYDLAKEVLSICVKQKVTCFLHFFD

RECLKLGHRYFHAPLSLLRKEPKLIKYFHILGTSVHSKEELLEAMSYKVNYAFVGHIFESSCKVGLEPKG

IDFLKSLLEFSQIPLYAIGGINTQNIENFKDINIAGVCMREILMKEKDLKKYLLECRQNLR

>WP\_002866070.1 MULTISPECIES: undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase [Campylobacter]

MTIALTGGGTGGHLAIVRCLLESAIKKNIECVYIGSQNGQDKAWFENEVRFKEKFFLSSKGVVNQSKFGK

ISSLLHTLKLSKDCREIFKKYHIQAVFSVGGYSAAPASFAALFSHLPLFIHEQNSKSGSLNMLLKPFATK

FFSAFEKEISPYPVADKFFDNARIRKELKNIIFLGGSQGAQFINELALNLAPKLQEQNIKIIHQCGKNDF

EKCKKHYQSLNIQADIFDFSLNLEEKMKNADLAISRAGASTLFELCANTLPTIFIPYPYAAKNHQYFNAK

FLQDQALCQIFMQNSINLDEFFKSILKLNLENISTRLQNITQKNGADMLIQKALFDNLTFIR

>WP\_002865916.1 MULTISPECIES: DJ-1 family protein [Campylobacter]

MSKKVLIPLAQGFEEAEFIGIADVLKRARELNPDLEVVIASLNSELLVKGANDISIKADCSIEDVDIENL

DAIALAGGFEGMMNLKNSNVILNIIKQLHSKNKIVAAICASPIVLNEAGVLEGEFACYPSCEVGLNGNRV

NKAVVVNKNVITSAGPATAILFGLELAKKLCGDEIYQKLYEGMLLPLTK

>WP\_002856495.1 MULTISPECIES: RluA family pseudouridine synthase [Campylobacter]

MQTFLVDENSRLDVFLAKKLNQSRNQVALLIEKDCVQVNDKIQDKNSFKLKNGDIISIASLKLCNEIKPQ

FEVDFDIDVLYEDEDLLVLNKPSNLVVHGASSVKNATLVDWLIEKKYTLSNLGGEIRAGLVHRLDKDTSG

AILIAKNNFTHQKLSEQLADKSMGRIYLALIDLPLKEDKIIVEKFLMRSPSNAIKKIAIDKENKFSKNAK

SAFINIVKTENLTLMAAKLFTGRTHQIRAHLASLNRHILGDSLYGYKGKYDCRIMLHAYFLYFIHPKTKE

QIFVKAPLMEDFKNIMFKQINLGENDEKISLGFLLEFFNSFA

>WP\_002854639.1 MULTISPECIES: hemerythrin [Campylobacter]

MFPKWDDSYSVHNAKIDEQHKKLFELAGKVEFMFDKPVYKDDVKALLAEFFNYMKDHFNDEEKYMKLIGY

PDLEEHKRIHKEIIQSMIDLIKNIKSTNDLKEKLYTVSKKWLLEHILYEDMKVEQYRRSSLASEDDGEVS

FEEVKEEKDDENAVYLYTCECVGQMHDVPFGIHQKIQLKGVKFKCKKCKEAIQFYKKYSENF

>WP\_079254166.1 MULTISPECIES: 3-isopropylmalate dehydratase large subunit [Campylobacter]

MTMAKTLYEKVFDAHVVYEGKNELPILYIDRHLIHEVTSPQAFSGLKMAKRRMARADLTLATIDHDVSTK

SIDLNACSDMAKEQITTLMQNTKEFGVRLLGLGDKNQGIVHIVGPELGFTLPGVTLVCGDSHTATHGAFG

ALAFGIGTSEVEHVMATQTLKQAKLKTMKIECKGQFQKGVYAKDLILYLIAQYGTAKGTGYAIEFCGELI

RKLSMEARMTLCNMAIEFGAKVGMIAPDEITFEYIKGKEFAPKGEEFQKYCEYWKSLRSDEGAKYDESIT

LDVSKIKPQISYGTNPSQVIGIDEKIPKISDFKNQSEQKSLLDALSYVNLEQDQVIEGVKIDIVFIGSCT

NGRLEDLKIAADILKGHKIHKNVKALIVPGSMQVRKEAENLGLDKIFIEAGCEWRYAGCSMCLGMNDDKA

NSGQRVASTSNRNFVGRQGKGSITHLMSPASAAACAIEGVICDNRKYLGV

>WP\_075888381.1 MULTISPECIES: ferrous iron transporter A [Campylobacter]

MMKRFRLGFYLSFLTLLLSACSVSQMNSLASSKEPAVNESLPKVESLKSLSDMSNIAFEWEPLYNENIKG

FYLYRSSDENPDFKLVGTIKDKFQTHYVDTKLEPGTKYRYMMKSFNEQGQISEDGKVIEVSTAPRLEAVP

FVQAVTNLPNRIKLIWRPHPDFRVDSYIIERTKGDDKEFKKIAEVKNRLNAEYIDSDLKPNENSSYRIIA

VSFNGIKSEPSQVVSSTSKALPPQVEHLSASTDGSNKIILTWDAPTYEDFSYYKVYSTSSSFLPFSVLAK

TDKNSYEDIVEGAGKSKYYKVTMVDKDGLESPMPKDGVEGKTLGNPLAPSIILAQSTSEGINLEWSDNDT

RAVEYEVRRYGGEQNAVFKGIKEKRLKDVKALPGVEYSYEVIAIDSAGLRSEPSSKVKAAQ

>WP\_072238677.1 MULTISPECIES: ABC transporter permease [Campylobacter]

MLKLLILKRIFLDYIFDGFKQALFLLFNADESVISAIKTTLLSSSISIVLALLIGFPLGFILGFFDFKFK

RFIKLIIDTSLSFPTVAVGLILYALISSRGPLGEFGLLFTIKALILGQFILALPIVIALFSNLIENMNKK

HFLLIKSFHLSPLKLVLTMIYELRFALISVVALAYGRIVAEVGVAMIVGGNIKYDTRTITTAISLETNKG

EFASGIALALVLILIAFCLNFITHKLKRT

>WP\_072238666.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKQGSVLHFGGVANRIVSSSDNFTYKKENVDFAVLKMSKINLNKSANLSKDFNFIEKDSGDGGDIYEYKD

PFWDSCQSGKCDYSKGKGKLFDSSRYEYFVREGSGIVALGFEDTNKVPIKIFDSNEINLGGFVSLAPKNT

EDKRFKLQFLNYTNDKRNPFTSSSTPGDSGSGVYVYDKIDKKWYLVGVVSTSNCNAHFTDGYTCSQVDYA

LINQAKINEFQNSHRVNIAQGVYTLSNQGLMKEGQLVQGVSLISGANAGYVSYENIFGDKAKYDDRIKEM

QNSKDLYFFQNGSINLNSDVDLGASVLNFEQNSNWQITGDKWLIHGGIYADKGSSIEYNVKTKKDDFLYK

MGEGELIVKSQSADAGLRMGEGKVSLEGEGLSFGEIYMNGGTLGFKNAQNLKTDTLYMNGGTLDLSGLTL

NF

>WP\_072238665.1 MULTISPECIES: hypothetical protein [Campylobacter]

MYFKKEGKMKNTLIIFENSLSNLSKDEASDLLEDLSFNLAYKQISHNPHETKKVLNSLLVEFLTILKKLD

FFDDENVTKVIKALVKASIVDAQNSLYEYISEAELLNKQIENQKNLIKNQISDNFFEFENILQECSFCDE

FSGGLNDAILFDIEMLGILKETAESAFLTTLEKAEDIELTSSEIAKNLVYNAICEAHFEKERILKISSII

LNTAFEIANESMAYAKDLCLGVIKGTRDGIVLAMEKFKASLTYANFEEDVSLKSKELIGIEDDFIALLKK

EIQLQNDPCKSIVENLLEHELDNLFAKFRRLAGESREQLILVLNDIKKNPKINDFNKLTQRKLNRFKQEI

FELEKIASEKYKDLNSKKAKKLGVRLWEKAKKFVKK

>WP\_072238664.1 MULTISPECIES: acetylglutamate kinase [Campylobacter]

MIMQKYLEKANVLIEALPYIRKFNSKIILIKYGGSAMENEELKHCVMQDIALLKLVGLKPIIVHGGGKDI

SAMCEKLGVKSEFKNGLRVSDKATTEVASMVLNHINKNLVHSLQNLGVKAIGLCGKDGALLECVKKDENL

AFVGTIQKVNSKILEELLEKDFLPIITPIGMDENFNTYNINADDAACSIAKALRAEKLAFLTDTAGLYED

FNDKNSLISKISLEQAKILAPKIEGGMHVKLKSCIDACENGVKKVHILDGRVKHSLLLEFFTDEGIGTLV

G

>WP\_072238662.1 MULTISPECIES: oligopeptide transporter, OPT family [Campylobacter]

MMYKKQNLPELTLRGLILGSILTIIFTASNVYLGLKVGLTFSSSIPAVVISMAVLSLFKTSNILENNMVQ

TQASAAGTLSSVIFVIPGLFMCGYWSEFPLWQTFMICLCGGGLGVLFTIPLRRAMVVESKLAYPEGRAAA

EILKVANKDQSNKKGKQGIKEIALGSFIAAIFSLLSNGFKLAASESNFAFIWNKMAFGFSMGYSLALLGA

GYLVGLAGAIALFVGMFLAWGIFTPYLSNFEFDSAKNAVDLASSVWSSKVRLIGTGAIAIAALWTLIELL

KPVIEGIKEIVKNVKITNQEKNERTNIDLSLKSIFILFVLMVVGLFITFYSFVEDANLSIYYQMLFSFVG

TLVSVLIGFFVAAACGYMAGLVGSSSSPISGIGLIGVIISSIVFLVLGVELFQDPMLSKFAVALAIFTTS

VILATAAISNDNLQDLKTGHLVGATPWKQQVALLVGCVFGALAIVPVLNLLYQAYGFVGAMPREGMDTSS

ALAAPQANLMSTIAQGIFHHNIEWGYMAFGVFVGILMIIIDKILRRTQKMSLPPLAVGIGIYLPPAVNIP

LVIGGILKFIVMQYLTKKYAKNSHKEEKLASCEQRGTLFASGLIVGESIFGVIIAGITVFSVSMGGSENP

LALNLANFHDSELFALIFFVGVVLYFIKRIVKKDA

>WP\_072238660.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MMLEIKNLSKNFGKIQALENINLHVKEGEFLSILGGSGSGKSTLLRIIAKLEQASSYDLFSCKGEVALMF

QNYALFPHLNVEKNILFALYDKKDKNQILNHLLKTFEIEDLRYKKIDEISGGQAQRVAFARAIARGCKLL

LLDEPFSNLDQNLKQDLRRELKKIIENQGITAIMVTHDIEDAYCMSDQIAFLEKGKILAHANPKELYFKP

DFKSAQILPDLNIIEKKLDLEDEFFAWIASKNYIFGYAELKIGNRFEAKILQKEFLGAFYRLKLRYKNIE

FFMLLSSNYNLEEKINFDIINF

>WP\_072238651.1 MULTISPECIES: tRNA 5-methoxyuridine(34)/uridine 5-oxyacetic acid(34) synthase CmoB [Campylobacter]

MSRIKMQENLLEKQFLNHPLYTKIQELKALNLACNFSLDDSVNLSTNSQAKDEILAITKELKPWRKGPFK

IDDLFIDTEWQSFIKFNILKPFMNEISQKCVADIGCNNGYYMFKMLEFNPAKLIGFDPSIKYRLQFELIN

ALAKTPIEYELLGVEDLPRYGLKFDVIFCLGVIYHRSDPIKMLKDLKAGLNKNGVVFLDTMYIEDEREIA

LVPNKTYSKIPNIYFVPSISALKNWCERAGFKEFEVLATKKTDENEQRKTEWIDSFSLENFLDPKDKNLT

IEGYEAPKRVYVRIGI

>WP\_072238642.1 MULTISPECIES: type II asparaginase [Campylobacter]

MKKLLLCVLVFLSIGACMAEAKPKIAILATGGTIAGSIDSAVATTGYTAGVVGVDVLIKAVPQIQDLANI

SGEQIANIDSSNMRDEIWLKLAKEINKLFAEGVDGVVITHGTDTMEETAYFLNLTIKSDKPVVLVGAMRP

STAISADGPKNLYNAVALAADKESKGKGVMVAMNDKILSARGVVKTHSLNVDAFSSPDFGDLGYIVDGKV

FFYNNVTKAHTKNAPFDVSKLTSLPKVDILYSYSNDGSGVAAKALFEHGTKGIVVAGSGAGSIHEDQKNV

LKELMKKGLDVVVSSRVVAGRVAVSDSDKKLGFISAEDLNPQKARVLLMLALTKTSDPKKIQEYFLKY

>WP\_072238640.1 MULTISPECIES: ribonuclease J [Campylobacter]

MNMDENKEINKNEQNPNSNSKNNKRYKYKNRRKKLADSLQNENDTPKIDQNSNKEISENSENKTEKKKKK

NRNLPSKLTGNEDWQIALAECIEANRVSHENRLHPLKYNNSSEHKIRITPLGGLGEIGGNISVFETNKDA

IIVDIGMSFPDGTMHGVDIIIPDFDYVRKIKDKIRGIVITHAHEDHIGAVPYFFKEFQFPIYATPLALGM

ISNKFEEHGLKAERKWFRPVEKRRVYEIGEFDIEWIHITHSIIDASALAIKTKAGTIIHTGDFKIDQTPI

DGYPTDLGRLAHYGEEGVLCLLSDSTNSYKEGYTKSESSVGPTFDQIFSRTKGRVIMSTFSSNIHRVYQA

ITYGLKYGRKVCVIGRSMERNLYTTMELGYIKLDRKIFIDADEVSKYKDNEVLIVTTGSQGETMSALYRM

ATDEHKFIKIKPTDQVIISAKAIPGNEASVSAVLDYLLKAGAKVAYQEFSEIHVSGHASIEEQKLMLTLT

KPKFFLPVHGEYNHITKHKETAMKCGIPERNIYLMSDGDQVELCQKYVKRIKTVKTGKVFVDNQINKQIA

DDVVIDRQKLADSGIVVIIAQIDKTTKTLINKPRVFSYGLVADKHDHAFSKDMAEVLGQFFINVKDEVLN

DPRFLENQIRQVLRKHIFRKIKKYPTIVPTIFVM

>WP\_072238638.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKMRYCFILFLSLVLSSNLLANNFSQKKVIKIEKSADSFEVIDLNQNVANPNLNQQKALFDSSTLIEKKS

QITKDEDIDFAIVLTSRKNFGYFLDGFRVSDKEFSTLFAKNLIQSLKLNWVNSAANGIYQSPKTLSYFSP

KDAKLINVSPFLTQEKDKAKMYAKFTDYVVVVNLQDFYVNITNYFITTSKEGVANVNFKIISTSNGKILA

AKNAELNLTLKDQDAKQNYQDIVNQMPKMLASVIDNEIKKLKLTIN

>WP\_072238637.1 MULTISPECIES: ABC transporter permease [Campylobacter]

MMLAKMIFNSIFKNKIQKFLAFLTCFLATLLLSTMLNITLSIGDEVTKQLKSYGSNILVLPKGSSLSIEI

GNELYEPLKNKNYLEEKNLYMIKDIYWRNNITALAPFLEGKITIENSQQKALIYGTYFQKAIKIKDDDDF

ITGIKSLYPYLAVQGEWAKDDSNEIMLGEDFAKNNKLKLGDTIELTGENNQSKEAKIVGILLHANPKMSN

KIIAPLNLAQDLLNKQGLYSSAEVRAFTIPESALSEKVRRMGEEKLDQLEYDKWYCSAYVGSIASQISDG

LPGADAKALNAISDAQSLVVKKIQSLMGITCIICLIVASIAISSLMSSEIHRRKKEIGLLKVLGANTFQI

YLIFASENLIVALFAALFGFIFGTALSQIISLSIFGYFIDIAFIALPLSFIFAGLIALLGCLLPIKNITQ

LSAAGVLYGR

>WP\_072238635.1 MULTISPECIES: radical SAM/SPASM domain-containing protein [Campylobacter]

MLHILINFINFGKMFTLGNIMKFKKIYIELSDICGLKCDFCPSRKGIRGVMSEEKFQNLAHEISNKAELF

TFHLLGDPLLLPNLENYLKIAKSEAMKLEITTSGFYLNSKNQALLLGYENIHQINISLMSFLSQSKISLE

QYFKPILELCKKHLEQKSLSFINLRLWNLDANFKAPKSNLKIYEFLAKEFEVKIDTNLSKNRLQRHILLH

QNKLFKWPNLKDEPLYKKGKCHALKEQIGILSDGSLVPCCLDAKADINLGNVFENNFDKLFKSPRIKMMK

KAFEEDKRIEKLCQTCEFFKARLGD

>WP\_072238634.1 MULTISPECIES: NADH dehydrogenase [Campylobacter]

MMRKYSDKKNAQTQNYYKDRFYHAPHAVKSDVNESVFKDDFEVLKTQVEILNSFVELDFWVIEIKKEDNV

KTLQMLKTLGYLSFTEASAIDFVADKNGFEVFYQLLNLEKKLRVRIKTFVGVKERLQSVAHVFKGANWSE

REIYDMFGIFIINHPNLKRILMPDDWFGHPLLKTYPLKGDEFARWYEIDKIFGKEYREVVGEEQRDSGFA

DDKDTLNFARLYHEVPKGSQKKEISFKQEYQEDEGVAFVKKVKRDEAKILEKRR

>WP\_072238632.1 MULTISPECIES: SLC13 family permease [Campylobacter]

MIMVFLIISSIIVAIILGYITRHNVGIFAMIFAYIIGAFFMDLAPKKIIAFWPISIFFVIFAVSLFYNFA

TVNGTLEKLAGHLMYRFANHPYLLPFVIFVVSAIIAALGAGFYTVLAFMAPLTFLLCDKIGLSKIAGAMA

INYGALGGANFMTSQSGIIFRGLMENSGIEANEAFVNSSIIFAFTIILPIVVLSFFVFNAFKNNIKISVI

SKPDSFDYKQKTTLILMFMMIVVVLIFPVLNIIFPHNETISYFNKKIDIAMIAMIFVAIALFLKLADEKQ

VVALIPWGTLIMICGVGMLISIAVEAGVIKLFSDLVENEINVIFIPLIMCAIAAFMSLFSSTLGVVTPAL

FPIVPSIAASSGLSEALLFSCIVVGAQASAISPFSSGGSLILGSCPDKYKEKLFKDLLIKAVPIGFIAAI

LATIIMSFIL

>WP\_072238630.1 MULTISPECIES: carboxy-S-adenosyl-L-methionine synthase CmoA [Campylobacter]

MMKDELFKQSPKKQFEFDKSVASVFDDMINRSVPFYRENLELCGNLLAKILPINASICDLGCSSANFLIF

LANLRKDFKLFGVDNSASMVEVAKSKAKAYGLDISFFETNLCEFDFFVCDVFVANYTMQFIRPPKRQELL

DKIYKNLNSKGILIMSEKILYEDAFLSKNIIELYADYKEKQGYSKFEIAAKREALENVLIPYSQKENLNM

LEKAGFKKIESIFKWANFETFIAFKD

>WP\_072238629.1 MULTISPECIES: hypothetical protein [Campylobacter]

MTMKITLFLSLIGIFFAACEQTKSVEYYQNHPEEAKKRSLECRHKAIISQDCVNAYRVGFPKDEWEDENI

SNP

>WP\_072238628.1 MULTISPECIES: hypothetical protein [Campylobacter]

MMKINSLNKINFIKSTDLLYAQRTGISKEDELFNNLTADFKLSKPFDYQIAFFKHNEIYHCFLAPVYKLK

KSRFCFPEPLIFQALFDERFIEESDYCVLNLYDQTLYLYFYQEGKFINLKKIENFNPSNMDLFFKQNRFI

ELLKHYESKLLLYQDLDTIKHYFSSQIKCLNLNDILDKNSLLKLSSYSIKNLDQNCNFIKHNKIKISISF

KIILIFIFSFSLSMMILLFKDFIEYKQNKEIQNKNFIIQEEISKLKQDKQKLLTNIQDLNFTLSNKISST

QQQFHILSTITKEINLDKNKAIILNQIISWLNSNELKITNLEFKQTKIILSFIDENHFKKALENLNLTFK

ILDKNEETFNIILEVIHE

>WP\_072238622.1 MULTISPECIES: pyridoxamine 5'-phosphate oxidase [Campylobacter]

MMDLKEIAQFLDDNVPAFLATLGTCGNPRVRPIQSPLLVRDKIYFCTANTKGLFKHIKNYNGIEFCSCAK

DGTFLRLRANAVFEPNLEVKKMMFEKYPYLVNLYETPQNPKFEVFYLDHLSARMQFMNGEFKLFKA

>WP\_072238621.1 MULTISPECIES: thiaminase II [Campylobacter]

MMLFSNLIKENQKIWNAYLHHDFVKKLEDKSLKQENFLFYLKQDYIYLLNYAKCYARLALNSNTAKELRF

AMKFQNYIVEGEMELHRAILSLGINADELNIKDESLVNIAYSRYMLSVGENGDFLDMLVALSACAIGYAK

IGAEIINRLKNENLKDHPYKEWILTYGSENFQNEAKEFEDFVNSYTSSVSAQKFQKLSEIFHTATRLEVA

FWEHSLRMELNL

>WP\_072238620.1 MULTISPECIES: hypothetical protein [Campylobacter]

MGGIVLLVLVNKFQELQMKDKSLEEIDLLKLIICALSFISVCTALILFLLLPTLKNYKQANLRENSQLAI

LKAAKSKFDFSEDKISTLRSENNKSLEQFEQNFNIGNFDIFLQKYFQNVKIQETKPKKQEKYLKNRLAIK

ATMNNPRRLYDFIDALKNYNNLIKLDYPLNLKAGEQGISIDLTLKVYSS

>WP\_050552456.1 MULTISPECIES: hypothetical protein [Campylobacter]

MQEYTFALKIGEDYLISPMEINPDKTLFSYCDIESAQELSLLKKQILLKP

>WP\_041176357.1 MULTISPECIES: glycosyltransferase family 2 protein [Campylobacter]

MEKNPLVSIIIPCYNAENFIENCINSIINQTYINYEIICVDDGSTDNTLKILKNLSINNSRLKAYSINHT

GIPSVVKNYGLKLAKGEFLLILDSDDMITEYFLEKGIKYFQDNPVDIILYPIKFMFSNNNYKIIGGIYNN

SLNISDVNYLGATNKIISGRDAFRFNIYNKLIGFPFYKKTIDKIINFNEESFNGDEYSFREHLLQAKKIA

FIDTEFYVYNFNQESITKKIGVHHWDTWKTWFNLEKLAQKHNYEKKLIKKINKIRYSIYYELCIKFNKTE

YLFSQNEKNIILNKILENKNHLSRINSIFDFLFYKCKDEKGKYIKFINKYTFYYKKIKGNNVFFEFKTNK

>WP\_032603539.1 MULTISPECIES: DegT/DnrJ/EryC1/StrS family aminotransferase [Campylobacter]

MMFFLNLKQINDRFNTEFITKFKEILESGWYILGKQCEKFENNFAKYCGVKHCIGVANGLDALRLIIKAY

DFKENDEIIVPANTYIASILAITDNKCKPILIEPDINTYNINPDLIEEKITKKTKAIMVVHLYGQVCDME

KIQLLANKYNLKIIEDCAQAHGAIYKDKRVGNLGDAAGFSFYPGKNLGALGDAGCICTNDDNFASKIRAL

ANYGSHKKYENLYTGLNSRLDEIQAAFLDIKLKYLDEDNNKRKNIANFYLQNIKNENIILPSNKFDHVWH

LFVVKTKLRDELQHYLNNHDIQTIIHYPIPPHKQKCYKDLNHLKLPITENIHQEVLSLPISPTMKENDFK

KVADILNKWKV

>WP\_032603128.1 MULTISPECIES: hypothetical protein [Campylobacter]

MRLCFSLFAFFIRNLLRLQFLKLNLLRIDNEI

>WP\_032603127.1 MULTISPECIES: DUF374 domain-containing protein [Campylobacter]

MGKSFKIHCLTYIIFILQWLIFLSCKKHYKGEKVDRKASVILFWHGKLALMPFAFRHYRQKNKKAYVMIS

HHKDGEQIAKIIKLFGLDTVRGSTSRGASSALRAAFKVLEQNDDIVITPDGPRGPYHSISDGSIILAQKK

ELKIRILNYEANRFWEFKSWDKMILPKPFSKITYSLSEPLDILSLDKEKAKEFLMEQFDKINLADQFKE

>WP\_032588912.1 MULTISPECIES: sodium:proton antiporter [Campylobacter]

MILTLLTNPIIISVVLMTLLCLFRFNVLLSLLISALVAGVFSHLELVDTMNILISGMKENLKTALSYILL

GAIAAAISKTNLTAYLIKIVSHFISHKKYLLLLSIALISCFSQNLIPIHVAFIPLLIPPLLSLFNKLKID

RRAVACALTFGLTTPYMVLPVGFGLTFQDLLKDNLNANNVSVSLNDVTNTMYFAAICMIAGLFLALFVFY

RKPREYQEVEIAKVDLENLEMTRKEWGVLAGLVLTLILQILTMNLPLSGLLGFVLMVILGGVEFSKVNEV

FDDGLKMMGFIAFVILVAAGYGEVLKESGSVVDLVNSVVPWMEQSKFLAVFFMLLIGLIITMGIGTSFGT

IPIIATLFCPICLELGFSTALIIFILGVAGALGDAGSPASETTMGTTVGLNADKQHDHIKDTCIPTFIFY

NGPLLILGSIIAMFL

>WP\_012006802.1 MULTISPECIES: NADPH-dependent 7-cyano-7-deazaguanine reductase QueF [Campylobacter]

MRYGEKEIKEFDVENMEIWPNDAKNDYIIKITLPEFMCCCPRSGYPDFATIYLEYMPDKFVVELKAIKLY

INTFMYRNVSHEASINEIYNTLKDKLKPKWIKVVGDFNPRGNVHTVIECCSDMVVPK

>WP\_012006800.1 MULTISPECIES: hypothetical protein [Campylobacter]

MVNKNIPKDLTQNLINKKELGFNDNAFKATTLENKIYAIPFASSLPVVYYNMDLVKQAEWNKELPKTWDE

LFDLAQKINSLNGKSGVYFGETDTWLILALSLERGGKLINEKGKVDFNNKAWQETFKLLSDFHTLAKMPA

IKRSEAISSFYAGNLGILIQTSAALTQTEKSINFPLKLSKFPGVQSGGELPVGGSVVMLTNDKNKEAALK

YIHFVTGEANAYVPQYTGYMTSNLLANAKLKDFYNKNPNYTIAPSQIELMGNWPSFPGDNALKATNTLWN

YAEKLLMGTSTNYEEIAKQAQEEINALLP

>WP\_012006789.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MIEISNLFFNYQNKEVLKIKNLKLDTSKINILMGANGSGKSTFLRILKFLEGDFSKNISYFGNFKLNNKQ

KREIYLLFPEPILLNRSVRANFLFTLKTYGIKEDIEERIKESLMCLNLNESLLNKYPNELSSGQSQKIAF

AIALSVRAKYYLLDEPSAFLDKNTTLLFKKAILKMHENFNTGFLIASHDKHFLDSLAQKKLYLHSGEILE

FENTNVFELENQGVKFCNFIDFSNCKKYKDFKKPPSKIAIDPYKISFFNSKNIPKNNYEFILEKCYIIAL

RSRKSDVFIRVSCMDKILEFALEKQEFLKFDLKLYEELSLYFYEDAICFLN

>WP\_012006761.1 MULTISPECIES: MFS transporter [Campylobacter]

MLNNVLPLSFIVGTRFFGLFIVLPVLSLYALKLEGANEFLVGLLVGVYALTQMILQMPFGILSDKIGRKK

TMLIGLIIFIIGSLICSFAENIYTMLLGRMLQGAGAIGAVATAMISDFITEENRGKAMAVMGSFIGLSFA

ASMVISPLMSAKWGLSSLFDLSAALSLLCIILLYTVVPKENKITHENEKTPFFHLIKQKNLALMNLTNFM

QKMLMSIAFLSIPIILVKHLGFASDKLWIVYSASMVAGFIAMGFAGSLGEKRGLAKQILLLGIVFFILSY

LFFAFSNSIVFFIIAVVIFFIGFNLHEPIMQSCASKFCKVHEKGAALGLFNAFGYGGSFIGGIIGGIFLH

LDALNLLAIILVILALIWLVALFFLKNPADFKNLYLPLETPLSFSTFSENLGVVDIYKNSKNLVVKFDSK

LINKEELEGKIKI

>WP\_012006757.1 MULTISPECIES: nucleotidyltransferase [Campylobacter]

MLNKELEIFKKNLSSYTQSCRKFFLKQGAFSLYHSKNMDNFIKKAYDIVLKDYFDDFSPPSDNIPFCVLA

SKAYANNSLCFNESISLIFVYKDIKAFHLKPMIKAFIEILNDAHLQIDSVILEFNGLYNASNELKTSIIQ

TRFICGSRILFKGIKTKFESILKENKNDFAKLLLENFKEFDIPFIKQEFNILKDFGGLNHLRSLESLLVL

FKTSPKNYALNFIDEKNLSELRLAGDFLLSLKSAMNLLSAKDEDEFLLINVHDLSELMYKKAKKHFGANE

LLVQKALQSMHTIGFYTHFLAKQIQDGLNHTLKQEYKFKTLVEVLEYLLKLEDKQVIFDLNLVFALRRLK

YSKKDIEKALILFEKIFYKRHSFCVLKLLLDSGILKDLCKPFWTVRFLSDEEGNYSFDEQVFLMLSEFEK

YEDELEILQKLKTDEKMILKLVILLSAIESENEISLAGIYRAYCSKFDLKNEILEWGLKIFKNNNALKDL

VEKEDIYNPIVVSSLVSKLENLENLELLYTLTWLKAKALNYNAFYFRVLDKLLENAKQGFEDENLLEESA

RRVKKELTLKRSKIFLEQDEILQDKIIHIKSNLFIIKNTFEDIVMISKLAKENDFKFWFSNETNLSLQIV

APLHFNIAIILSSLTNLNLIFMNFFELFDDKIYLRFEYDNIISDEQKLKLCELLNSNLSGFNLKKIKKPI

IKKDELKLDLNYSKMYAKLGLNTKDQQGLMAYLMNVFNELELVLCAAKIQTIRQRTRNIFIFQKNEKLEH

SEQKLVNLLISE

>WP\_012006741.1 MULTISPECIES: hypothetical protein [Campylobacter]

MILAGIIFIFNLILAYLSIDISKLDSVAEQLKIGMFSSIFVLSLTLFIFAFRQNRNINKIYQKIFYMQND

FLNFQKKIDVDSVLDLLKEKFETTGQNLTKTSHEKDRYLHLLEENLYQLGNISNAMRCLNEGYNKEINSL

ILNALNSQKDQIRLELNEALEHHKSIIGTSHGKVLQFEASVAIVNNDELENFLLANLLSYFGIESTCFKN

LSFDVNDFHLIFIKDKILNENVKKNYDFIVMGRHKNTHYEYFLTLPFEKKDLENILQNKLDKVCTLKFKT

PYQNNVLLFKQNDFDATLFFNIIEKQCDKNVCINSFSQLKQELSKETYRLILLDYELIKFDLEQMRNLLS

AYKKQHPQSHIIFFSKEKVGDFDCVSEVLSDVSRNDLITLLRKYLPKA

>WP\_012006735.1 MULTISPECIES: protein YibB [Campylobacter]

MIDNEITIVTAFYDIGRKDIKNFERDNDKYLSYFEFLAGIKNKMIIYTQENIKEKILDTRKKHNLEDKTI

IITKELQEFDEQGYKKIIDTFRNYDQSINRKNPNNIECISPMYCYLMYLKPFFVCDAIQRGLTDENIMWL

DFGFNHGGNFFVDKDQFNFYLQKQNSIDENKINLFSIKNDDKQTLANIYFSMETFLMGGIIFAKSKNWLL

FKHHMQKCIKYFTSFGIIDDDQIMLLWCARNYRKNYNIIKVYFWFDSLYHFIPQNIAKKLKINTNQIKYY

KIIKEKLKEDFNNKNIKNIFINLIKYCYFKFINKNHKVL

>WP\_012006709.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKSCLYFTFIVLFLTACSTKNLTSLHHENLEQKNENQHYAKLEYEQNVSILPQFAYDINFDAKRYKKYFF

NPWHDSFKNYKGQNIFWSFPLYLNSKNTYYFFNKQIIPLSWFKNATNNANIQEFGKLNQKALIIQNTIIK

NLPTQRAILKNPFFENEGIPFDYASDGILNAGTPVLISHFSKDKRYAFVLGEAGFGFVESKNLEFFSNDR

AKIYENLNFITPLKEKFPIYSEDGKFFFESRIGAIYPYYKEDKNYFYGKIGSKKYKISKKDVSKFPLQFN

DKNLKNQLSQVLNLPYGWGGYNFERDCSLLTRDIFSAFGLYLPRNSAAQKNSFNHFDISTLSNSQKKDFL

NRFGKAYLSLLYLPGHIMLYVGQIADNNIAIHNIWGLRKDTTQRLLISSSVITSLEIGKNEILEDNLLLS

RLKEISFINLNEQEKEQIKSYLENIQNK

>WP\_012006708.1 MULTISPECIES: amino acid ABC transporter permease [Campylobacter]

MSLFTQKNKNFKPLKPLSKSKIITNLILLILFLILFCYCSFSISAYHFDFSVIATYKEKFLQGFLNTLII

SFFSLLLSIILGGVFCAFSLSSIVFLRFLSTFYIELIRGTPLLVQVLLMYYIIANNLGLDNRYVAGVIIL

SCFSAAYLAEIFRAGILSISISQLESARALGLKEMQVFAYVIFPQALKNILAPLSGQFANLIKDSSLLSV

IAVNELTQSAQEINSYTFATLEAYVILAITYLILTLPISIFSRYLERKCQK

>WP\_012006707.1 MULTISPECIES: AEC family transporter [Campylobacter]

MFVFIPLFTIFILLAGGYFAKRIGVLKQKQARTFLDFAIIFALPCLIFDKAYHLNFDFSLIIFIFIGLFS

CILAAFFAILIGKVFHFSKVTLVSMFLLSCFGNTIFVGMPIVAGIFNDPQFSAEVIFYDALATTLPISLF

GPFILSLGNGEKVSLLANVKKILSFPPFLALLFGFLCKLITLPEFIFSPIRLFGASATPVALFAIGLGLG

FMAIKTSYKPTIVVIFAKMILAPLFFVFCLKIFNLELKDSTIVAIIESAAPTMTLAGAMVMKAKLDSNLA

VSAVAFGVLFAFISMPILIWALL

>WP\_012006702.1 MULTISPECIES: sodium-dependent transporter [Campylobacter]

MSSKFSKIGFILAVAGSAVGLGNAWKFPTLVGQSGGSAFILLYIILTLGVGFVIFLAELSIGKISEKDPV

NAYEKLAPSNKKAWSYVGFTMVGAILIVSFYTLVIGWIVKYVFLSITGNLPMDLEVSKAQFGFFTSEDFL

SQFICFTLVFLCVFYIVSKGVKNGIEKLNVWMMPSLFILLILMLVYAISKDGFMMAVKFLFVPDFSKINT

SNVLEALGLAFFSLSLGVGTIITYSASLPDKTNFITSTLNIIFINLLVGLLMGLVVFTFIFEFGYNPNQQ

GPGLVFISLATLFEKIGVIGCIFGAAFFISLIFAGITSAVSMIEPFAFYLINTFGMSRKKALILIGIVVY

ILGMLCILSSLKSTQFGFFGMSFFDLLDSISSKVIMPLGGILAAIFVGFVMKKEALKILFEPYMRGIFFE

LWYVFLRFISPLAVVIVMIAAFLK

>WP\_012006693.1 MULTISPECIES: DNA translocase FtsK [Campylobacter]

MLAPSMGEWVYKANLFLFGEFGYYYPFSLLILNYLYYKKNYKIENFKRRELFGFSLAFFSTLLLFSVFYR

GFGYILEIVYGFFSIILGHTGSGIFALLLLLFSLILLFPKFAKEILKIELDFTYLLKVEQAFKSLLMRVF

GGENEKEDIGKSEPMVPKLNILQDNIYENSQINEKEKTNNLEQIIKDSNINASKNSITTAKENFEKLKNQ

ILDETIEIDKQSLKESRSFVYEHSQQVRNFAQKASKMSISLDEDFNFISEEEVDMIPERFLKPKKLEDIK

QIDTNKNLDEPSYKRKNIEIPVSKQEVKPKIFTKELELRENLIKKEKLEQEYKAYQNEILENKVKQEIKK

LEEYDAINSSDIIEGNKYSFNSPKTIKTETEESNKINENKNPDKTDNIFEFAPIVEELNHPYIEPTPIKN

INEIVIEEKNTLDFIQNTETKIDDKKTNDQEIKLQKAVLAKEIAINQALLREIEQGEVEKPKDFTLPPLD

FLANPKEHRQEINESEIDKKIYNLLEKLRRFKIGGDVISTYVGPVVTTFEFRPSADVKVSRILNLQDDLT

MALMAKSIRIQAPIPGKDVVGIEVPNDEIQTIYLREILQSEVFKNAKSPLTIALGKDIVGNAFVTDLKKL

PHLLIAGTTGSGKSVGINSMLLSLLYRNSPKTLRLMMIDPKMLEFSIYNDIPHLLTPVITDPKKAVNALS

NMVAEMERRYRLMADAKTKNIENYNEKMKELGEEELPFIVVIIDELADLMMTAGKDVEFYIGRLAQMARA

SGIHLIVATQRPSVDVVTGLIKANLPSRISYKVGQKIDSKVILDAMGAESLLGRGDCLFTPPGTSSIVRL

HAPFASEFEIEKIVDFLKDQQSVEYDESFLKDQQSAGVTTNESFDGEVDELYEEAKRVILEDGKTSISYL

QRRLKIGYNRSANIIEQLTQNGVLSEPDAKGQREIL

>WP\_012006668.1 MULTISPECIES: aspartate--tRNA ligase [Campylobacter]

MRSHYNTDLGISHVGQSVKLCGWVNSYRDHGGVIFIDLRDRSGIIQLVCDPNDSKEAHEIASNARNEFVL

IAEGTIRPRGEGLVNPKLKTGEIEVVVSKLTIENESAVPPFAIADESVNEELRLKYRFLDLRNPKLYENF

ALRSKACIAARNSLANMGFLEVETPILTKATPEGARDYLVPSRVHQGEFYALPQSPQLFKQLLMCSGFDR

YFQIAKCFRDEDLRADRQPEFTQIDVEMSFCEQKDVINVAETFLKDIFKACGKEIQTPFRQMQYKDAMEN

YGSDKPDLRFDLKFIDVIDIFAKSNNEIFANIAKDTKKNRIKAIRVPKGDTIFSKRQMQRFEEFVRKFGA

QGLAFIQVKEDGLKGPLCKFFSEEDLNELSKRCELEVGDVVFFGAGAKKTVLDYMGRFRIFLANELNLID

PNALEFLWVVDFPMFEQNDDGSYSAMHHPFTMPKNIDETDLEEISSIAYDVVLNGVELGGGSIRIHKNDI

QQKVFKLLNIDEEQQKEKFGFLLDALSFGAPPHGGIAIGLDRLIMLVTGANSIREVIAFPKTQRAQCLMT

DAPSPASNEAMRELGIKLRENIK

>WP\_012006666.1 MULTISPECIES: hypothetical protein [Campylobacter]

MSLLKNSSYILTLLSLFGFLLTWQRTVFSLFFLIPIFLTLFWEFFLFLKLRKNIIKEATLIKGSLFYRIS

MGDFYLYIFSFFLAIFGLISLFLNFLNLEKIDFVFIFIILPLLMIFLKKELHLQFVDNAYNDFRIVVIAS

FFTALFYAFYGLFFTYNEILNLELFSRKIIAYKSASFVYFDFLSEFLHFISNLKFFIFSYFGYLGFRVLN

FIFDFFNFFMFCSLLAFVFNFVLKIKIKIIVLFLCFIMVLGSYFLKEQRNNALKSEQEQILLWMNNFDFL

KDNNLSLIQKEKDLFEKDLKDLREIFKKNAFEIGIWWFSKEKEDLEKRINESLK

>WP\_012006658.1 MULTISPECIES: ferrochelatase [Campylobacter]

MKLVLFLNMGGATNLQDCEVFLKNMFNDPYILGIKNRFLRKFVAWIITKARVKAMQENYKKMGGKSPLNE

LTQSLCNKLNLKQDEFKFDFVNLYVPPFATEILQKYTLNESDEIILFPLYPHHSCTTVTSSLEVLQNEIS

KQKIQAKVKTIDIFYKNELYNEMIVSHILAKKSKFDAKILIFSAHSLPQSIIDKGDLYEKHVNDHVEILK

EKLKDHFDEFILAYQSKLGPVKWLEPNTSDVLANLNDKALIYPISFCIDCSETIFELGMEYKHLAKCDYD

LISCPNDSDEFMEFILNSINSPLARKTSC

>WP\_012006655.1 MULTISPECIES: tRNA 2-selenouridine(34) synthase MnmH [Campylobacter]

MLSEVEFAEFQKENFSLLIDARSPREFLHSHLIGALNFYALNDEEYQEIGTIYKKNQALAKARGASYICQ

NTAKHILKITQNFRIGEKVGIYCSRGGLRSKSIAVILSELGFRVVRLKGGFKAYRTFVTHYFENEINFDF

FTLCGNTGCGKTELLEQLPQAINLEKIANHLGSSFGDILGKQPTQKAFEAELFHNMQNLENFAFIESESR

KIGDIILPLKFYEKMQKAFKIYCFCSLENRVKRIQKIYQEKMTPLKFQQCVQKISPYISLNLRQDLLQSY

ERKEWQRLITMLLEYYDKTYKKPDKIDLELNTDDILKAKEEILRYFKLKNYILI

>WP\_012006654.1 MULTISPECIES: HIT domain-containing protein [Campylobacter]

MQYLYAPWRSEYFEKEKSICPFCDCANKIKSDEDLGVIFRAKHCFGVMNRYPYSVGHFMVIPYVHEEHIE

NLSDEIWQEMSHFVRLGVKILKEQIHANGVNIGMNLSKDAGAGIAPHCHYHLVPRWAGDTNFITTIGETR

VCGTNIEQVYQKLVLAFKNAQ

>WP\_012006653.1 MULTISPECIES: hypothetical protein [Campylobacter]

MYRYLLFVLAAFFLAACGSSKINVVYPDYTKYKSNDFDLRVMKAYNYEYYKQYKEARDEFLSLYQDYNNT

NFLENAFLLTLANNLDKQAELNNLAKPYLNQNDNLKRLSALYALNSNDINNAQKLMKELLTKKDSDPRNL

ELYGDILVKKNDLKNATKYYRSAYNQVQNEEILFKLIGIYAILNDTLNIKNVLEFSRKTNGCTLKTCVLL

AKIYFDEKNIEALKSIYKELYQLTKNKSFALALVELLNSQGKTEEALKISLQYDLDDDIKLALYQNLKRF

DDAKKMSLALYHKTKNKEYLLRAAVFEFEAANEAKKITPKVIDSVKEKFEQAIDKDSNALYLNYYGYLLI

DYDLDVKKGIELVKLALEKDPQNLYYLDSLAWGYYKLGDCRQAWEILKQTLDDKEFANSDESKAHIKAIK

ACVKP

>WP\_012006651.1 MULTISPECIES: hypothetical protein [Campylobacter]

MDFNSVLFSIGDKLPKDATSTVMLKKKFDRLNEDKQKEVVAQLPMIKLKSPALVFWVGTFLFGAFGVGRF

MIGDWVLGLIRLGITIVAMICGVLMITYSALGIIYGLLWLVNWIWWIVDMFLVGKKLRKQNFEKIANIIQ

>WP\_012006650.1 MULTISPECIES: membrane protein [Campylobacter]

MFLLDFLISLSFIFEISALVLSFYFKNSRIFFLTLVLLGAKLPYFYTSFFQANLFVALFLPMIFTLFCLG

KHHALILSKKNIASITTLIFIGVLSIILPRNTTFNSAGLEFHFITLNFFKPVSELGFLFFLVGLILIFIK

IFKTKEYYLIIAFFAAYFQFLFQEGAGIRYFEFASLVFCFYLLNHAYKLAFFDILTKLPNEKSLTRFTKG

KNNYIIALLHFNELKDTKESYAKLILKQIAKILKRFRAKIFIVENDFILIFNDKNQALNHLAFLESTLKN

TEFNLENENFKPDFKLIWQESEENLDKNLQSLRARLLD

>WP\_012006649.1 MULTISPECIES: ATP-binding protein [Campylobacter]

MKELFQKIWQNELQFLNFDAKFQDKNKLDTAECAIILSVNKDNYERYFLLKEFQELCKKIDLRVDIFSIQ

NAQICILNLFKSGFIPKQDLLKALKILEKISKNTEIFDFISQEKVQSIDQKALFQNDFKELNTINLELQK

LSFDENLKSRLQKTLEKFQNLEFNIAITGVMNAGKSSLLNALLKEDFLGVSNIPETANLTVLSYGKSEEA

KIYFWDKKEWQNILESSHFNADLKEFIDKLDKSVNIQDFIKDKPLIQNIALCELKNFSSAKNKISALIKK

IEIKSHLDFLKNNISIVDTPGLDDVVVQREIVTNEYLRESDFLIHLMNASQSLTQKDADFLVHCLLNSRL

SKFLIVLTKADLLSKKDLEEVIVYTKESLKSRLVDLDENLVEKIDFLCVSAKMASDFYKSLAPKESLQKS

GMQEFENYLFNELYAGEKSKIALRAYKKELHLELKNILSEYEMQNRLIKENKQGVSEENQKLLLELQKQN

TLLKEAQDEISNSVAKLKNIDSGIDNLVLLLVKKLKERLIDEFKYLKNNAQKLNLSRILNIVDITTKDGI

NDILREIKFENIKKIEELKTNLSLKYDFLKDDFDNGFEGFKDGISKNIDSIFQSEKFALLRLKIEKLSNL

KSDLYELETNLDTVIFDTFKEFKMSEILNSLNINGAFFEFLNDKLKHYEKNQKSKLESLEKVLQSLKNQD

ANILNSFEENLEKIEKLKQLEMGLLNAD

>WP\_012006641.1 MULTISPECIES: histidinol-phosphate aminotransferase [Campylobacter]

MKFNEFLNHLSNYEPGKDIEVIAKEYGVKEVIKLASNENPFGTPPKAIECLRQNANKAHLYPDDSMIELK

STLAQKYKVQNENIIIGAGSDQVIEFAIHAKLNSKNAFLQAGVTFAMYEIYAKQCGAKCYKTQSITHDLN

EFKKLYEAHKDEIKLIFLCLPNNPLGECLDASEVTKFIKGVDEDCLVVIDAAYNEFASFKDSKKHLEPCE

LIKEFDNVLYLGTFSKLYGLGGLRIGYGIANANIINAFYKLRAPFNVSNLALKAAVAAIDDDEFTKKTLE

NNFSQMQLYKEFAKKHNIKIIDSYTNFITYFFDEKNSTDLSEKLLKKGIIIRNLKSYGLNAIRITIGTSY

ENEKFFTEFDKILR

>WP\_012006636.1 MULTISPECIES: carbamoyl-phosphate synthase large subunit [Campylobacter]

MPKRTDIKSILLIGSGPIVIGQACEFDYSGTQAAKTLKELGYRVVLINSNPATIMTDPEFADATYIEPIT

KESILSIIKKEKIDAILPTMGGQVALNVAMEVYESGLLGDVKFLGANPEAIKKGEDRQVFKECMKKIGMD

LPKSMYAYNYDEALKAVDEIGFPLMIRASYTLGGAGSGVVYNMDEFKELANTALALSPIHEILIEESLLG

WKEYEMEVIRDRADNCIMVCSIENIDPMGVHTGDSITIAPALTLTDKEYQVMRNASFAILREIGVDTGGS

NVQFAINPKNGRMIVIEMNPRVSRSSALASKATGYPIAKVATLLAVGFSLDEIKNDITGTPASFEPVIDY

IVTKIPRFTFEKFPGANTTLGTAMKSVGEVMAIGRTFKESIQKALCSLERSLSGFDRVKFEDRNDLVFKI

RNANEKRLLYVAQAFREGFSVEELYELCKIDPWFLTQIKEIVDFEEQIDMDILNNKALLRKAKTMGFSDK

MIALLVNLKDNLELSQNDIYYARMKQKIIAEFSEVDTCAGEFEALTPYLYSSINVSELTQSKNDAKDKKE

KKVMIIGGGPNRIGQGIEFDYACVHASFALKDMGIKTIMYNCNPETVSTDYDTSDILYFEPIDFEHLRAV

IEREKPDGVIVHFGGQTPLKFAKRLSAFGAKIIGTSARVIDMAEDRKKFAEFITKLGINQPKNSTATSVE

EAVLKASDIGYPVLVRPSYVLGGRAMRVVNDEAELRLYMQEAVDVSDKSPVLIDQFLDNATEIDVDAICD

GKDVYVAGIMEHIEEAGIHSGDSACSLPPCNIDEKMQEFIAQKTADIALNLGVVGLLNIQFALHNNELYM

IEVNPRASRTVPFVSKATGIPLAKVATRVMWQGNLKEALKFYDTFKVVNFDTKILRPKTPKYMSVKEAVF

PFAKLSGSDLELGPEMRSTGEVMGISKDFANSYAKSQIASFNHLPEQGVVFISLKDKDKKYTKKIAAEYV

KLGFKLMATGGTCKEILESGFECELVHKISEGRPNVEDKLKNGEIHLVINTSDNHSFKGDTKKIRENIIR

FKIPYFTNLRSALAGAKSIKAIQSKSCLDVKSLQEWLKS

>WP\_012006633.1 MULTISPECIES: nicotinate phosphoribosyltransferase [Campylobacter]

MMISKTSLALLCDFYEFTMSQGYFKNNKKDQICYFDIFFRKIPDSGSFAIFAGLEDILDFVENLSFDTED

IEFLRKQGIFDTEFLDFLSSFKFKGEIYAMREGEVIFPNEPLLCVKATTIEAQLLETFLLLSLNHQSLIA

TKTNRIVRAAKDSKILEFGSRRAQGSEAALKGARAAFIGGCIGSACTLAGKIYNIPINGTMAHSWVQMFE

NELEAFKAYVKIYPKNPVFLIDTYDCLNSGLKNAIKVFKEFGIQEGGVRIDSGNLLELSLKIRQELDQAG

LQKCKIIVSNALDEWSIKKLKEQNAPIDIFGVGERLITASSDPIFSCVYKLAALEDQGIKPKIKISENNE

KSTLPHFKKLFRVYDKNTQKILFDELYVFDENPNQDENLERKELLELVYKEKRLLKKSSLNTIQDYTKEQ

ISKLDESFLDLDRFVKFEVKLSPKLQNITEDLLKTRF

>WP\_012006630.1 MULTISPECIES: bifunctional ADP-dependent NAD(P)H-hydrate dehydratase/NAD(P)H-hydrate epimerase [Campylobacter]

MKAIIDNIKILEQNAINKGLDELILMENAGLNLAKLIKKEAKKIRIQRKIKKVKILFLLGGGNNASDGLV

ALRNLKHAKAYKIGFKENTLFKKQEQILQNYAFKFCQKEPDFKKFHIIIDCILGTGSNRCLDEKTSLIIQ

KVNQSKALKIACDIPTNLGFYPCFKADITLCMGALKEILLEDFAKEFVGRIKIANLGISSKKFYPNSQAF

LLEKKDLKTIDRKINANKGNFGHIYIVANASAGTLAGLGALNFGAGLVSLVAQKSFSPLLMLKEKIENNA

SAIALGMGLENLDFLKDEILQNTPLILDANCFLSEALLWYLNRKDVVITPHPKEFIKLYKMCFDENLDIE

TLQKNRFFYARKFSQNYDCVLVLKGANPIIVQKEKLFVVNLGNQALAKGGSGDVLSGMIAAHLGFGFSAL

EAAKNATLAHGLVAKKYKFNKNSFDALKLIKGLKCL

>WP\_012006620.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKVKWSRDFSIKNMQLDKQHELIFEITNLANDLALKIQENNTQYKDDLKQILAKLFQYIKIHFKDEEKFM

ESIDFPLIEEHKKSHQILVEKTKELLEHSDNIVKMSQELSILTKDWILDHFANEDLWIANFTKKTLHLQE

IHYTLEQYIKLKSIKQDLRAEKTHDYICNCSLRIHAVPQTIHQELVSKENTLKCEKCGQILVHLDYFDLN

QNFEKFNAIFEDALQNHHFTTQKNDMGGG

>WP\_012006613.1 MULTISPECIES: dihydroxy-acid dehydratase [Campylobacter]

MRSDAIKKGHLKAPNRSLLRACGLKDEDFNKPFIGVANSYIDIIPGHYFLNDYAKIIKDEIRKNGCVPFE

FNTIGVDDGIAMGHEGMLYSLPSREIIANSIETVMNAHQLDALICIPNCDKITPGMLMGALRVNVPTIFV

SGGPMASGVTKKGEKISLSSVFEAVGAYEAKKISEEEFKDIECSACPSGGSCSGMFTANSMNTLCEAMGI

ALEGNGTILALSKEREELLRKAARRICEIALDERFKIRNIITQKAVRNAMVVDMAMGGSSNTVLHMLAIS

REAGVALDIKDLNFISSKVAHIAKIAPSLNSVYMDDVHKAGGVSAVMAEISSRQGHILELDALTITGESL

KERLKNAKIKDENIIRKVDNAYSKVGGLAILFGNLAEQGCVIKTAGIIGERKFKGKAVCFNSQDEAIKGI

IKGKVQKGNVCVIRYEGPKGGPGMQEMLSPTSLLMGMGLGADVALITDGRFSGATRGLSVGHISPEAAEG

GLIGLLKDGDEIEIDVDAYTIHANLSEEEITQRKKEFVLPQKEVPSRWLRMYQKLVSNASKGAVLDME

>WP\_011812682.1 MULTISPECIES: cytochrome c biogenesis protein [Campylobacter]

MFKKIFFSFWMSLILLFIYALSCAVATFVENDFGTNAAKALVYNALWFDILHLLLLINLIGIIFIHKLLQ

RKKYASLLLHSAFIVILLGAAITRYFGIEGGMHIREGQSSDIIVTRDEFIALMLYNDEGKVVEYQSFGVA

FNPLLHNSFEKKVSMQQNKTINLKLLDYEKAPNAMSNPIIKMQISFNNESKEILLTPNYNNENVLPFRLG

GEIFALNWGPEEIKLPFSLALKDFILDRYAGSMSPSSYASDIEVIDQDKSFEYKIFMNNVLDYGGYRFFQ

SSYDQDEQGTILSVNKDPGKIPTYIGYTLLTLGFLWILFAKNSRFQKLSNYLKNQKNLLLILFCLFAFNI

KSFADENTLKLIQNIKENSAKHSMLFGSLLVQDFDGRIKPIDTLAMNYIHKITKKNDFLGLNYNQIFLGM

MMYPQHFRQIKMISVKTAKLKEILGVDKNEKYLAYDDVFDGDFYKLSNYIEEANRKKPALRDQFDKDILA

LDEKINTAFYIYSGEIFRIFPDPSQKTYTWYSPATPMPFDLKDIENIQSLLAKYFFDFEQALSTKDFSKA

DESLERLKNFQNFYGSNLIPTPTQISLELFLNHYNIFDNLTPIYLLLGSMLFILLVYEILSLKKAPKMLK

NAIFILIALSVLAHALALIFRWYVGDHAPWSNAYESMVYIAFACAFAGLVFYKRSSLALCTASIMAGISL

FVAHLGFMDPQITNLVPVLKSYWLNIHVSIITASYGFLGLCFLLGVFSLILFMLRNPKKAQIDQSILNLH

CINEMAMIIGLALLTIGNFLGGVWANESWGRYWGWDSKETWALISIIVYTMILHLRFISKFNNPYAFASA

SVIGFYSILMTYFGVNFYLSGLHSYATGDPVPVPKFLYFFIAFTVILILGAFFKRKLKSPA

>WP\_004304140.1 MULTISPECIES: valine--tRNA ligase [Campylobacter]

MYDKNLEKEYYQICEERGYFEIDGNKTIQEKDKNFCIMMPPPNVTGVLHIGHALTFTLQDIMTRYKRMDG

YKVLYQPGLDHAGIATQNVVEKQLLAQGIKKEELGREKFIEKVWEWKEQSGGKILDQMRTLGITPAWSRL

RFTMDEGLVNAVKKAFVELYDKRLIVRGNYMINWCTHDGALSDIEVEYKENKGKLYHIKYFLKDSDEFLV

VATTRPETFFGDTAVMVHPDDERYTKFVGKEVILPISKKAIKIIADEHVEKEFGTGVVKVTPAHDMNDYE

VGLRHNLDFISVFNEKGILNEHCLEFQGLERLEAREKIVAKLESLGFIEKIEEHNNQIGYCYRCNNIVEP

YISKQWFVKKEIAQESIEKVALGESKFYPNHWINSFNAWMKDLRDWCISRQLWWGHQIPVYYCECSHEWA

SQHTPKTCPKCQSQNFKQDEDVLDTWFSSGLWAMSTLGWGNENWGKDKIWSENDLEDFYPNSLLITGFDI

LFFWVARMMFQSTNALHQLPFKDIYLHALVKDEQGRKMSKSLGNVIDPNESIKEYSADILRFTLALLAIQ

GRDIKLSNDKLLQVRNFTNKIYNATNYLLLNESKFEDLENITLHSELAKYIYAKFQTCVKDVRENLDNYR

FNDAANTLYKFFWDDFCDWGIELSKAEKSSVKELGSIFKEALKLLNPFMPFISEYLYHKLSDTELKTSPS

IMISKYPKFKEQDKNIEKIFSLLIESIVGIRRAKSLIDLGNSKIEKAYIKFNDKKIKDEIKAYMNFIMML

AKCEQIEFSEEKLPKAICDVSENLEIFITLENVDLSGILTRLENQKNKLEKESFKLNSMLSNEKFIANAP

KEVVEQNKEALENLKIQLEKISVELQNLRG

>WP\_004304137.1 MULTISPECIES: ABC transporter permease [Campylobacter]

MNEENISIISAFFSRISQFFNEFSWQDIKEVSLSSITSFSENYENILKPALNETIYMSLMAVLFGFLLAI

IPGILLAIWDKNGIKENKIAYSILDFITNILRAFPFLILIVVLLPLSKIIVGTSIGTNAAIVPLAIGIAP

YLAKMLESAFKEIDKGIIEAAKSYGASNIQIIFKVIFSEALPAIISGITLTLIFTIGFSALAGTVGGGGL

GDVAIRYGYERFNKEVMIQTVVILLILVQLVQILGNLFYTWAKNSKTTYIIATLLILLGISIVININNDE

NFFWQVIVFILFLGSLLYKGFEK

>WP\_002937560.1 MULTISPECIES: methyl-accepting chemotaxis protein [Campylobacter]

MTNKKSSFLIKFIILSTLVLAFILVLLGIIFNNYSSSKDNKDLINTVQQLEISDEKINSVFQNSFNFINY

DPSVQAIKKMQENFKKLKTFGIDISKAEEIFNAKLIQLNYFKSANSIAVNSKLYLFELAKNYFEELEQNH

ETNKNNYRTMSSMLSVLSTENILQKTTLNQLNNLMKEIKNDTKSENLQLFLKHYKMIVKQISIMQDNSSI

YENNSLMKELKQLNTFTQNAVEQSNLFKFYIALAVFGITLVLFVFFILLTLKKVIMPIHTLEKLSANLAS

KEANLHSRLNIDPKSELGQSAQYINSFISTVQNSIIEAIENAKSSHQNSQKLKNNSMMLENSSNSQHEQI

QGVKEITYVLDDHINLAGNLAQESIENMQDMHILMDKVELTLSELVNLINENNEKEQNVVANMDNLTQSA

DNIIEITSSIRDIADQTNLLALNAAIEAARAGEHGRGFAVVADEVRQLADKTSKSLLNINATVNTIVQQI

NDNKALMDLIHDSMKETSSKTNDLQQELVNSMHKLESSIESTQTMKDKSMEVKDKMLILGTNIDKVNELA

NSVKDLSCEINNISQNVLNGASKLSEKLSSFQ

>WP\_002933370.1 MULTISPECIES: DegT/DnrJ/EryC1/StrS aminotransferase family protein [Campylobacter]

MNFINLQAQYLAYKDEINAEIESVLSSSSFIGGAKLNEFEQNLAHFLGVKHAIGCSSGTSALYLALRALD

IGKDDEVIVPSFTFIATAEVVALVGAKPVFVDINLSNYNLDFEAVQKAITPKTKAVIAVSMFGQMSDLRA

LEEILKDKNITLIEDGAQSFGASFKGEKSCSIAKISCTSFFPSKPLGAYGDGGAIFCHDDEIAKKIRILL

NHGQTQRYKHEFIGINGRLDTLQAAILNVKLKYLEKELDKRQKLAQTYNANLKNCQIPQIDPNAFSAYAQ

YSVLVEDRASVLQKFEKANIPYAIHYPTPLHKQPCFSEFSNLELKNSEYASEHILSLPFSPFLSEEEQEQ

VICIFKD

>WP\_002922699.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKWIFIVFCFILGFIIHIFYIGYTNELLFNKFIKNSNPDYTITDIYFKKGFLTSKGSFTLNHSHTQLST

KINLKFNNYFFLNKIIKGNFTNPFDFLDEVLKNNKLGTFTLKLHDNNSKIFLNIKDINLSNEGGDTIING

GYIEALMNKNLEIKNIKIHFDMINFSQFYTKFVLQNLNYEQFFNNPVQFYELNLFSDSQQEINFDYLVLD

NNKINSFYSKNQVNFNEENSTINLNIQGKSNEIDIDLKSLLGQNLNFDKTKFNITINKFLNSNFNISHFI

QKNLDLKIQNLILEKNKQNISLQGNLNINNSYQAKLQVISSDEPDEIFPWTKDYGGLNQYFLKENNNFFL

NLSYDSLANPQLKINGSEFSNMDLN

>WP\_002922696.1 MULTISPECIES: membrane protein [Campylobacter]

MFYLNKILYFVLILFLLIGIWGFFLNSNPSNQIIKKPHLPSLEIGDLVFRAGIGSESFLIENLSQSPYSH

IAMVVKTSPTMLIHVTTDDDKNAKNQVILSSMDDFLKLSHKIAIKRLKFDEKTKQNIVTKALEHLGRKFI

ISTDKDAFYCTTFLEQSINSITPFHLQYTLIKAPFNEGLYLFPQTFFENNQSVLIYESQNF

>WP\_002911887.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLTQKDIIKKIKTIFIRSFLYLIIKISKNKKINKRLKVLRYIDLRKGNSITQIINKMIKHLFKNTIIKAY

>WP\_002895094.1 MULTISPECIES: aspartate/glutamate racemase family protein [Campylobacter]

MKTIGIIGGMSFESTITYYKTINQAINDKLKSLNSAKILLYSVNFEEIENLQSQDKWQEAAQILTQCAKK

LELAGANFIIIATNTMHKVFDEIQQNINIPILHIAKSSAKALKQENIQKIGLLGTKYTMTQDFYKKILIE

ENISVITPSDEDIKIVNDIIFNELCKGEIKQDSKEKYLNIINKLQEKGAKGVLLACTEIGLLISKNDTNI

KIFDTSLIHALDAANEALKDL

>WP\_002893140.1 MULTISPECIES: methionine import ATP-binding protein MetN [Campylobacter]

MIKIKNLKKYYGKELVINDVSLEIKKGEIYAIVGHSGAGKSTLLRCINGLENYQEGSLKVFDQEIKDLSQ

KKSKELRVLRKDIGMIFQNFALMERKNVFENVAMPLRTHYTQCKFHAKLFNKEYMSEKEIAQKVNSLLEI

VGLDHKNKSYPRELSGGQKQRVAIARALALNPKILLSDEATSALDPNTTKNILELISKINAEFGITVVLV

THEMDVVKDIAQKALLLEHGQIIGSGAIDELFLRPNAKMKEFLGESDFLPEHGLNIKLYFPKEVAQNSVI

THMARTLNIDFNIVWGKIEKLNGKALGNLVININEKDKDKVLDYIEKSGVLWEVAS

>WP\_002892246.1 MULTISPECIES: sigma-54-dependent Fis family transcriptional regulator [Campylobacter]

MNLVIVEDDINMRKSLEIALAEYEEFNIKSYKSATEALKKIDENTDLIITDINMPGIDGIEFVKACENKY

DFIIMTGNATLSRAIEAVRLGVKDFLTKPFDVDTLVEAIKRAKIIREKTADKKSKKNEKKEENKDFFSTS

PNLEKTLNLSQKAAKTDASVMFFGESGVGKEVFSRYIHTHSKRSNKPFVAINMAAIPANLIESELFGFEK

GAFTDANATKIGLFEMANEGTLFLDEIGEMPYEIQAKLLRALQEKEITRLGSTKSIKIDVRIISATNANL

DEKIKNGEFRSDLYYRLNTVPINIPPLRERKEEILGIAQKVLEDTCKEYDFKEKQLSQEAKNALLEYDFP

GNIRELISVVQRACILSENDEISSEDLFLEARSIKKDVKNLEKELICEVLLSVDYDKDQASQILGMDIKI

LNEKIKKYQIKDR

>WP\_002878300.1 MULTISPECIES: hypothetical protein [Campylobacter]

MTINSANPYQNLTLSNPLQNSSALNLIKDSKALDQEGNENSLEQLSYIFNNTTYASEFGFRINEEGFFDK

DLNKIANIPESYDINIKSVRSIAKELAKQDENLNYNKIDLPYLLNSYHSSLKSINSEFLQDDNAYLSRDL

ISKLSSGFSTDNGEFLGQISRIYNNQEEIDLALSNIANLNTLMLDNKITNFHFDKAIENTSSNEILKPYL

TKNAEVSKSGLLMNFIYHDIKTQNEKEFNFFMKPATLELSSHQNLQKILKGETDIEDYIKKENEKKMSFD

LYLYVNGVDKKTSTQDKLSVFFQQYINYQKDMDLREFANSSSIFQIYIDQNRNDFDALKKQYQNQSQDTQ

RLEEANQLRSSSIENFLDRRQKQANINKILNSYMSVMV

>WP\_002878146.1 MULTISPECIES: lipid A/FlgG phosphoethanolamine transferase EptC [Campylobacter]

MLRLTWLQFTFFNSLMIVLLNFNLFYFVYEKNTQNWFITFVFIVAYFALVHVICSLLFIKFFTKFFSILF

IISSFLSVYFISFYGVLIDSDMIQNVVQTDIKEVKDLLNLKLILFIVLALLLVFYVVKVKIDYYDSFKSH

LKIKIINIISGLIVVCAVLIPLSKTFLPFFRNYNEIRMYNTPFYQIYAVYRYYIRFVKAKPEFKTIANDA

YRENNHTKKLLVLVVGETARAANYSLGGYTKNDTNFYTKKDNVVFFDNFSSCGTATAVSLPCMFSISKRE

NYSSSEFQENAMDVLYKTGVDTAWFDNNSGGCKGVCDRLAYKQKLSSDLDENLLAPFKEKLNHLSDQNII

VLHLQGSHGPTYYKRYPSEFKKFTPTCDTNELSKCDNKALINTYDNTLLYTDYLLSEIIKLLKEQKSYES

SLFYLSDHGESLGENDIYLHGMPYAIAPSYQTHIPAIFWSNDENLMNLAKEHKGLKLSQDNLFSTLLGYF

DVKTSVYEPEYDLLNPKLKANP

>WP\_002878143.1 MULTISPECIES: cyclic pyranopterin monophosphate synthase MoaC [Campylobacter]

MKLSHLDEKNHPKMVDVSDKNITSRIATASGMIYMSQEAFDVIKNNTAKKGPVLQTAIIAAIMGAKKTSE

IIPMCHPLMLSKVETDIMEFVKECAFKLIVTVKCEGKTGVEMEALSGVSIGLLTIYDMIKAIDKSMRITD

ILLESKEGGKSGKFVRS

>WP\_002878014.1 MULTISPECIES: murein biosynthesis integral membrane protein MurJ [Campylobacter]

MKSLVFKNFIINALGILFSRILGLARDVLIALFLGAGLYSDIFFVALKMPAFFRRIFAEGAFGQSFLPNF

VKAKKKGAFCVSVMMQFSLIVFLFCLLVSFFSSFFTKLFAFGFNADTIALAAPLVAINFWYLFFIFLVTF

LGAILNYRQKFFITSFSAALFNLSIVIAAFFVDKNAPQNTLYYFSYATVLSGVAQLILHLLVLKNNPVIR

AMALSIKFKKAKAKLQGFYGNFFHGVLGSSATQFSSLLDTTIASFLMSGSISYLYYANRVFQLPLALFAI

ALTQVSFPKILKHLKSGQENLALKFMQRALAFLSILLIASSIIGSAFALEISKLLFERGNFTHEDSVITA

YVLIAYLIGLLPFGLQKLFSLWLYAKFKQKTAAWIAVKSLIISALCSMAFIFLIKDESLKVIAVALSSSI

SAFYLLGANIKEFGFKKFFALISIKICLLVIVALIVFTILLILIKPYILSFFIGIFTSFKGVF

>WP\_002877813.1 MULTISPECIES: rod shape-determining protein MreC [Campylobacter]

MKNKIFYVLVLAFLVFISFYYGGLIKQNVLRVNDFVIGNFYNIKDYLGEKISEHFNQANQIQQLKARNKE

LEDIAVKVTSFANQLNRILEDQNSTKYLPQVSLTRVISYVQLNDYKKLWLDWSKIPVGKNRGLIYQGYTA

GIAINKNGRAMALLQGDDQCVFSVYIGKSKAPGLIQGEDGRIVVKFIPKWAKINIGDEILTSGLDNIFFS

DIPVGIVNRIDDEDMYQSVEVKPYVKISIPAYLYVVDNL

>WP\_002877809.1 MULTISPECIES: transaldolase [Campylobacter]

MKNFSLWCDFIENSFLDNEFLNLLSHGINGATSNPAIFKNAILNSPIYKDKILKLKGKRTKDIYEELAIS

DIQKAADKLAPLFYQKNDGFISIEIDPRLHDNTTLSLGEAKRLYSAISKENVMIKIPATKASYEVMYELM

KNGISVNATLIFSLEQSQKCFEALNAGLVEFRKNNIALKEQNTRTPQAVISIFVSRFDRLLNPKAKEQNR

IGILNANLAYNNIYSKNEPNIRALFASTGVKGDDLPKDYYIKELLFENSVNTAPLDAIEAFKGKMDFKKP

LMNFEIYTELNQIISQSEREKACNDLLSDGIEQFCIAFEDILKAL

>WP\_002877805.1 MULTISPECIES: phosphoserine phosphatase SerB [Campylobacter]

MIKLCVFDFDATLMDGETIDILATAHGKGNQTSEITRHAMAGELDFFESLQKRVSLLKGMSYKKVLELGS

TLPLMHGAHELIQYLKSKNIQIVIFSGGFHEGIDPAMQKLGINLSFANYLHHKNDILTGLVGGEMMFSNS

KGLMLQRLKSFLNLKTDEVMCVGDGANDLAMFNESGLKIAFCAKEILRSQADICIDIKDLKEIIKVI

>WP\_002877789.1 MULTISPECIES: bifunctional 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase/2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Campylobacter]

MSEISLIMLAAGNSTRFNTKVKKQFLRLGNDPLWLYATKNLSSFYPFKKIVVTSSNITYMKKFTKNYEFI

EGGDTRAESLKKALELIDSEFVMVSDVARVLVSKNLFDRLIENLDKADCITPALKVADTTLFDNEALQRE

KIKLIQTPQISKTKLLKKALDQNLEFTDDSTAIAAMGGKIWFVEGEENARKLTFKEDLKKLDLPTPSFEI

FTGNGFDVHEFGENRPLLLAGVQIHPTMGLKAHSDGDVLAHSLTDAILGAAGLGDIGELYPDTDMKFKNA

NSMELLKQAYDKVREVGFELINIDICVMAQSPKLKDFKQAMQSNIAHTLDLDEFRINVKATTTEKLGFIG

RKEGMAVLSSVNLKYFDWTRL

>WP\_002877773.1 MULTISPECIES: 4-diphosphocytidyl-2C-methyl-D-erythritol kinase [Campylobacter]

MKAYAKANIFLKLTGFDSRKYHLLESRFILLKDLFDELELVDKESDSKKEFEIISNFKCENNIIQKAYLL

LSKRYNNELKELFSKKSLKLTKNIPVCAGLGGGSSDCASFLLLMNETLNLKLNLQELINLSIQLGSDIAF

FLSGFHSANVSGCGEIIEEFEDDIPNLKWTFPQISCQTKAVYDEFDRGIFDFQKNNNQAQIYKKLSTKEL

LQNFKNKELNDLFTPCATLYPKMKSYLQEDFFLSGSGSSVFKVDR

>WP\_002877704.1 MULTISPECIES: hypothetical protein [Campylobacter]

MERIVCLLIFLSFKLFAQDEFIFWAELSSKNFILFHQNQNLSLAMTQSENVEEQWVCEISYSDQDIKVLP

RTSLGLIDDNMPKTIKFNFLNSHKDELSDCFIGAKISVKDIVNTDLLRAQSETYIKILPLRFTVEFGEQN

AIIYYLKKK

>WP\_002877649.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKILLTLIFSVVVLFGRGEISVFGGQDENMQKELQKLPQEEQKIYQNIPPSDENNDFESNVDDPFVAKGS

LVLTNDEYPSRVYVGEVFPITIYARTTENTKFDFNISVEKTNLSFLNPDAKWEFINNEYKTTLWFEAKNS

NASLSKISIKLLRNNEAFQEADINLNPIKFENTLSNKDFSHLVASSLEIKKVKASYFDDANIIMMVELNA

TNTNLKSFFIEGIQKQGIENLKGDFNASSAFYYAILPLSKTNFEFSYFNKDSKKLENINLKLKISDDEIS

TQSDLNPVNKDLNIYKQYTLWFLAVLFGALFVWRKNYIILALAVVCFALSFLVDTNTQNAIIKAGSRAKI

LPTEPSTYFYTANADEKVEVLGKRQNYIKVLFSDGKIGWVNKDDLQKN

>WP\_002877518.1 MULTISPECIES: tryptophan--tRNA ligase [Campylobacter]

MRVLTGLQPSGDLHIGNYFGAIKQMVDAQEKSQMFMFIANYHAMTSSQDGEKLKQNSLKAAAAFLSLGID

PQKSVFWLQSDVKEVMELYWILSQFTPMGLLERAHSYKDKVAKGLSASHGLFSYPVLMAADILLFDTQIV

PVGKDQIQHVEIARDIALKVNNEWGEIFTLPEAKVNEEVAVVVGTDGAKMSKSYQNTIDIFSSEKTLKKQ

ISSIVTDSTALEDPKDHENCNIFKIAKLFLDESGQKELQIRYEKGGEGYGHFKMYLNELVNAYFKEAREK

YNELLEKPSHLKEILDFGATKARKIAQEKMQKIYEKIGL

>WP\_002877513.1 MULTISPECIES: 2-dehydro-3-deoxyphosphooctonate aldolase [Campylobacter]

MKKMILIAGPCVIESKDLIFKVAEQLKNFNENPNIEFYFKSSFDKANRTSINSFRGPGLEEGLKILQSVK

DEFGMKILTDIHESNQAAAVSEVADVLQIPAFLCRQTDLLVAAAKTKAKVNIKKGQFLNPSDIKYSVKKV

LQTRGIEDEGYEAAQKNGVFVAERGASFGYGNLVVDMRSLVIMREFAPVIFDATHSVQMPGAAGGSSGGK

SEFVEPLARAAAAVGIDGFFFETHINPCEALCDGPNMLNLTRLKNCVNTLLEIQNIIKENK

>WP\_002877433.1 MULTISPECIES: TIGR02757 family protein [Campylobacter]

MKNFIHLKAKLDFLANQKNTNHSLFETPDPLQIAKIHNDEFIALICALFAYGNAKNIVNFLKKLDFSLLN

LQEKQIKKELKNLKYRFQNEKDIQEIFITLSRLKNESSLYELFYQAYQERENTTDAILAFMQKIKTLNSY

SSYGYDFFFGKIWQNTPTSPLKRYNMYLRWMVRKDELDLGLFTKIHTKDLLIPLDTHAHKISLTLGLLKR

KIYDYKSVLELTQNLKKLDANDPIKYDFALYRLGQSKEIDKFKE

>WP\_002877372.1 MULTISPECIES: ferrous iron transport protein B [Campylobacter]

MKKIKIALVGQPNVGKSLLINALCKANMKVGNFSGVTIEKASAKTFYKNYEFEVIDLPGTYSLDGYSEEE

KITRHFLNQNDYDVIVNVLDATNLERNLILSAELLSLNKKMLLALNMCDEAKKEGIELDTSVLSQEFQSQ

VVEISAKTKENLELLLQKIIILFESKFIPRSQFYTPLCEKSPEKEDLLYFINELSKKIITHKKEERNLTK

KIDALLIHKFFGLPIFLFLMWLLFQLTFSLGQIPMDYIESGFNTLGEFVKNNISNTFIASALADGIIAGV

GAVILFLPNIMILFLGIALLETTGYMSRVAFLLDGILHKFGLHGKSFIPLITGFGCSVPAFMATRTLKNK

RDRLLTLFVINFMSCGARLPVYVLFIGAFFPSEKAGNYLFGIYILGAILGLCAAKFLRMTAFRGLDEPFV

MEMPKYRMPNWHLVWFMVYNKAKMYLKKAGTFILLASLLIWFASNFPKSEENLNDFNAQERAIEQSYLGQ

FGKGIEPIFKPLELDWKLSVSLISGLAAKEVMISTMGVLYSLGKDVDETNNDLKGIIAKNIPIPSAVAFI

LFVMIYNPCFAATIVFSKESGKLKYTLFLFLFTCTSAYIVAFIGLYIAKILLN

>WP\_002877364.1 MULTISPECIES: selenocysteine-specific translation elongation factor [Campylobacter]

MKSVIIGTAGHIDHGKTSLIKALNGFEGDSLKEEQERQITINLSFSNLKLKDKNISFIDVPGHKDLVKTM

VSGAFGFSICLFVVDINEGLKEQSLEHLEILKILDIKNIILVLSKCDLCENIEQKSVEILEELKNLDYPI

LKVFHTSIKNNQGIEELKNYLYTIENKENNEELIFHYYIDRVFSLKGIGTVVTGSLNEGSITLNEKIICL

DTQKELIVKNIQNHDTNLEQIKACNRVALSLNCDYKELKKGYLLSKKGYFKAFKECDALVKAKNLQNSKM

IFCVGSRQIECKINILKKLENDEFFVHFSFDKNVFLSFDEAFILLQNNRVIGGGKVLNPLSEPLKKEQKN

KFLMFLKNKDFKAAFSFLKDAHKYGFGLLSSYQRFKLSHQKALKLAKELNQVFVDEKNLNVYHLQSLEEI

KNFIKFILEKNPYAMLSAHSLALRITWASENFCELGLKEMSNLLDFQNGIYFKKGIDFEKLQEKNNNQMY

EILKKQGIKPEAPYNLYDFLELDRKSGDNILKKLTQKGLVVRLSHNLFIEKQALEKLMQECLNLLKNQSL

DVQSMKEYFNLSRKYAIAYLEYLDKFPQVNKEAEKRFLTNI

>WP\_002877346.1 MULTISPECIES: phenylalanine--tRNA ligase subunit beta [Campylobacter]

MIITKSWLNDWLELEEISSDKIAKTLNSIGIEVDRVGALKAPDKVVVGYVKEKIKHENSDKLSICQVDIG

SETLQIVCGAANVDAGQFVAVATKGAIMPNGMEIKEAKLRGVDSCGMLCSSLELGFEKINEGIMLLDESI

GKLELGRALNTYEIFNDELIEVELTPNRGDCLSIYGIARDLATALNLNLKEPKPFKESENVLGIGRILRL

AAEKELNGLYNYRAIELKEEIQTNLLLSLRLAQIEGLGKNSIENLLNYATHSTGVLFNAYDLSSFSEKDE

EFTINLSKQVHGETKVSCKDKLLSFSGIFQNNESRCKDDSKIIIIEANYTDPLVIADAKIYHKDQDEKML

YRSFRGSEPKLNLGMDFLLSIFEQIPNLVIYSSSQQILTDKELPIIPISIESIGDIIGQNVDKDEVLKIL

KKLGFELILSGEGLINVKAPLHRPDIKNLSDICEEVVRIIGIDNIASKGLEFIEKNRLNSAYKNYIEFLN

LRKRAVASGYFESLHYVLDNEEELKRLGFDSVKLKLINPITAELNTLRTTLLNHLLNAASLNAKNSKKII

KLFELGAVFNVNNQELNRIAFIHSGLKEEAKISNKAKPESVQFYDFLLDIKNIIGDFKLKSSKYNILSPY

EQADIYLSDIKVGFIGRLHLKIENERDLPKTYICELDLDLIRQDFKIAKPYSKFPAITRDLSVLIPKGFE

YNQIKNCIEELNLEILENFRLVDIYSDENLKEFYSITISFSFRDINKTLEDNQVNECMDKILNTLKNLGL

DLR

>WP\_002877345.1 MULTISPECIES: 30S ribosomal protein S1 [Campylobacter]

MSEVNKKVQGGVDDYLEEEDFGQLLEAFDKSREEATTEGVIVEIKNDEVYVDIGKKSEGILALSEIQDDN

SKLLFNVGDSIKVAVMGSRGGRSLLSHKKALRKEKVIEFIKNYQENQDDIFTVKVVGKNKGGLIVVDEND

VEFFLPKSQYGFKETNNIIGKTFKVKIIKIDKDEQSIIVSRKKTLDDERRKRKELINNVAQQEDLIEGIV

KKITTYGMFVDVGGVDGLVHYSEISYKGPVNPGTLYKEGDKVPVKVIKYDKERKHLSLSIKAALPDPWSE

IKDTLDVGDTIKVIVSNIEPYGAFVDLGNDIEGFLHISEISWDKNIKNPKDYINKGQEIDVEVIEINPNE

RRLRVSLRNLLSRPFDEFMKSYKIADVVEGEITSVTSFGAFVKLGGIEGLLHNEDASWDRNDKCKDKFSQ

GDKIKVKIIKIDEENQKISLSTKELSSSPVQEYAKIHKVGDIVKGAIRDIKDFGVFVELSKNVDALIHKE

DISTSMLENLKIGDDIEAAIVFIDEKKNRIRLSVKNLVRMKEREVLNEINNDDKVTLGDIIKDQLA

>WP\_002877290.1 MULTISPECIES: tungsten ABC transporter substrate-binding protein [Campylobacter]

MKKIISLALALALSASAAELKMATTTSTDNTGLLDALKPLYEKESGNTLKWVAVGTGAALKMGEDCNADV

LFVHSPKAEKEFMKKGFGVDRTPVMYNDFIIIADKSLASKFKGKNLKESLELIKNEKLTFISRGDKSGTD

NKEKSLWKNLGGVPEKQSWYQQSGQGMLASIKIAEEKKGVILTDRGTYIKYEANEKGNPNLVIVNEGDDS

LKNFYSVIATNPKHCKNVNYTEASKFIKWVTSDKTLNFIADFKLLNKPLFVIDAKTRKD

>WP\_002877280.1 MULTISPECIES: hypothetical protein [Campylobacter]

MNNYIHLEELDLKANYADLEKELENLSKKECLRIEIDKGLENSLKELEDLMEKLPEQQTQTLFEQCTKNA

MDAVTGHFGLASTILNAKDGGNVTTLHNFEKGIVATEEDLQKLTKYQQGYKRDSNYDKIKDNIRDNSPKI

VRSEYTGEEMERGAGKNKAQLDHVISLKEIDRDPNMHLFLDDAIRAEIANHPDNLKWLDASANASKGDRD

LMEWGKEIDPKTGKTNFEKYGIDEKKAEKIYNTAKSNLKKKVIKEKIVKYSNEVLSTGAKDSMKIFVYSA

FGVVLKDFIEAVVIELKTTFREFGKENIKEIFKRFARRMEKVWEKIKAKWKDIFKGSLEAGIQAFFSNLL

VFIINTIFTTLKKIVQIIRAGFTSLYQAVKIIINPPKNIPKDEIYFEASKIFVSGMISAISMLGSEMIHK

FLLSIPGFNVFLSLPIPFTDETIGDALSLCISAAGGAVLSTIAIFYMDKWRSNSKIGNLQIQIVTQKNLI

VQYKIAKTWFALNDAYHIVKNETLATIQQIKKDNQIREQSSQEVETAIEEFENCNITKKLYKKLNQTKEN

>WP\_002877276.1 MULTISPECIES: tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA [Campylobacter]

MNKDLLLSSYDYTLANELIANYPTNPKEDARLLVFDRKNKEIFHTTFKNLQDFLPNCAIFFNDTKVIKAR

IYGNKVSGGKIELFLHQPFLNSHNPLFLAQIKGRVKKDEILYFKKDLKIRVVELLNDGLRKVQFFQNDKT

LDTSNLYNLLDKIGHIPLPPYIKREDEKSDLKDYQSIFAKNLGAVAAPTASLHFSETMLENLRKKHEIYH

LTLHVGAGTFKSVECENIQEHKMHSEFFNIPQQACEIIDSKQAILGVGTTVTRTIEYYARTKTKSGFCDL

FLHPQNPPIRQNHLLTNFHLPKSTLIMLVSAFIGREQCLKLYELAIKEKYRFYSYGDAMLIL

>WP\_002877269.1 MULTISPECIES: hypothetical protein [Campylobacter]

MIKAFSLLEFVFIILILGIVFNLGSLYLKKDNLLEGAIQILNDIQYTQSLAMMQEGIRVDELAIAKREWF

KSKWQIYFIKSAATGYDQTYTIFLDKNGDGNANLGKTEINIDREIAVDVINHNKLMNSGQSGVISKDDEK

TTQRFNITKRFGIEKVEFKGSCSGFTRLVFDEMGRVYSPLKNANYAYEKTLAKNNSDCIIRLLSKKHALC

IVIDTLSGYAYIPDFKTLKSQFVNIKNKNYECSKI

>WP\_002877200.1 MULTISPECIES: membrane protein [Campylobacter]

MEHKKALFCIFAIIHLFFWIIFSSLNHFKLDTFLSYEIAFFSVLLIIFASYLNYKKVIIKKSKNYEKNFN

FISSLFIKKKQNLSKIIHFKVLKDDLKPNVKEKIHFFAMFFTLFKLMAYVILVAGFLFLHRQDKLDIFAY

ICGISSLLVCVFIFILYIKKYESKKNY

>WP\_002877194.1 MULTISPECIES: MFS transporter [Campylobacter]

MSPKKIIKSMTALFAGMAFLFAGNALIVSSIGVILKENGESSLAVGVVSSCFFVGALVGTISAHKIISRI

GHIRSFGLFGAIFGISAMLHTVSENLIFWAVLRFFIGICYYGLLMVIESWLNEKSKNAIRSRILGFYEIV

FYLAFGIGVLIIALNLSKHSVFILSATLILLSSLPLNLIKIKEPVLPASSPISIPKIFDIAPLAIVTSFI

AGMLINGFFSMASLFILLQGFDTKAVSYFIFCGVLGGFIAQTIIGTISDKLGRKFAIITCASIGFITMLI

FIFFKLHLYMQYFLGITLGIGIFCLYALALARANDVLVSKNKGVELGRGVLFCYSLGSLFGPLILGFLMQ

YFEIKGFIWFYIISLAFLILFAINKPNILNKKFKKKPGNMVIFDD

>WP\_002877190.1 MULTISPECIES: glutamate--tRNA ligase 1 [Campylobacter]

MYRFAPSPTGDMHIGNLRAAIFNYICARQKNMDFILRIEDTDKARNIAGKEEEIKEILNLFGISWQHYYI

QSENLKFHRQMALKLISEKKAFACFCTEEELEAKKELAKKQGKAYRYDGTCEKLADIDVLECEKPFVIRL

KKPTHTMKFTDFIKGELSFEPENIDSFVIMRTDKTPTYNFACAVDDMLENVTCIIRGEDHVSNTPKQEHI

RASLGYNKAMTYAHLPIILNEEGVKMSKREAHSSVKWLLESGILPSAIANYLIMLGNKTPCEIFTLEEAI

KWFDISKVSKAPARFDLKKLLQINREHIKMIKDDELNKILDLNKDLAQLAKFYTQEASTIKELKEKMRAI

FNTKDFGEFETECKILKELLKDIELFENYEDFKNELLSKSDLKGKKFFMPLRIILTGNIHGPELGDLYPY

IKNFIHELARI

>WP\_002877188.1 MULTISPECIES: methionine--tRNA ligase [Campylobacter]

MRYITTPIYYVNDVPHLGHAYTTIIADTLARFYRLQGHETRFLTGTDEHGQKIEEAAKLRNSTPQEYADK

ISFEFKKLWDEFEITYDIYARTTDTRHIEFVKAMFLKMWQKGDIYKDEYEGHYCISCESFFTQSQLINDC

SCPDCGKNTTILKEESYFFKLSKYQDKILQWYEEKDPILPKNKKNELINFVQSGLKDLSITRTSFDWGIK

LPQEINDDKHIIYVWLDALFIYISSLDFQSKGENAKFWPAHVHLVGKDILRFHAIYWPAFLMSVDLPLPK

FIGAHGWWTKEGEKMSKSKGNVVKPKEVVDAYGSEAFRYFLLREVPFGNDGDFSENMLINRINAELSNEF

GNLLNRIIGMSTKYSQGNILKEGVLKYYNTELNQAKEHLNLAVEFLENLQCNRYLEELFKALSVANLAIS

KYEPWNLIKENKHEQANALVALCANILAKTSLLLSPTLPKSCEKVALALNFEISSTNYAKMILDNELLDF

KANPCEALFPKVEKALLKQEIKEEPKKEESPKIKIDDFAKIEIKVAKVLDCQNIEGSEKLLKFQLELDDK

EIRQVLSGIAKHYKASDLIGKQVCIISNLKKAKIFGHESDGMILSAKSGDKLVLITPEQLVQNGSLVG

>WP\_002877184.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKLLFTSFCCFASLMASDAINCDNIKNNKTLLNESSNLDYLNIASSCKESLKNQDFTKKLYAISNEIRGS

NSSCNGVAYLPKLQQFDFLLLKIAIDPITYQKTLDTPENLEKKYDILKSYFRYWAYQSIGNFRLYKAFWQ

EYNNAIEPLEKYFESNFNFDKGSNIYYTSNALNEFLNWAVGETKIYKDISPLAKIMSNKNYSVSYIQDFI

FSNNPSQDDLTIALQAALLNQREKEILELLIRFGARIDEGYESAIFYALENYENTNFLIQNGANVNQANA

FGKTPLFYAIEFNRLDIIKLLLDNGANVNQKYINNNEKLALSANIGSNTPYFITFCALEHTSKNVLMHAA

AYGNVEILKLLISKGANLNAVDDLGFNALDFALAAGKKENADYLKSLGLKANENLFYGGSLE

>WP\_002877159.1 MULTISPECIES: Fe(3+) ABC transporter substrate-binding protein [Campylobacter]

MKKIFFMFLTAFSFLGASELNIYSARHYDADFEIIKKFEEKTGIKVNHTQAKASELIKRLSLEGSNSPAD

IFITADISNLTEAKNLGLLSPVSSKYLEEFIPAHLRDKDKEWFAITKRARIIAYNKNANIDISKMKNYED

LAKAEFKGEIVMRSATAPYSKTLLASIIANDGNKEAKAWAKGVLDNLATNPKGGDRDQARQVFAGEAKFA

VMNTYYIGLLKNSKNPKDVEVGNSLGIIFPNQDNRGTHINISGIAMTKSSKNQDAAKKFMEFMLSPEIQK

ILTDSNYEFPIRNDVELSQTVKDFGTFKEDQIPVSKIAENIKEAVKIYDEVGFR

>WP\_002877145.1 MULTISPECIES: leucyl aminopeptidase [Campylobacter]

MKFELNDKKLDAIKADFELVFIQDKNLKIFNKEKDFFKLNNYKGEGALLDLNNKKLYLELKSLAYEDIRL

SLCTAYKTLEKLNIKSVKLPSIIGDCVVRSFASLVEGVLFGAYKFDKYKSEKKTRTLERFIISSEELNGK

KFNKDEAKIGLERGEILANATNFTKNIVNEIPEIYTPLKMAEDAQNLAKENKNITCKIYDEKFLAKEKMN

AFLAVNRASVHPPRLIHLSYKATNAKKRVVFVGKGLTYDSGGLSLKPADFMLTMKADKSGAAAAMGIIKA

VAELALDLEVHCILGATENMIGGNAYKPDDVLISREGVSIEVRNTDAEGRLVLADCLSFAQDLKPDLLID

MATLTGACVVGLGEFTSAIMGNNEELQNDFYLSSKKSGEYTTILHFNPHLRELIKSNIADVSNTASSRYG

GAITAGLFLDKFIRKEYKDKWLHLDIAGPAYTEKSWGYSSFGAGGAGVRMCVNYLIQILRKAK

>WP\_002877126.1 MULTISPECIES: cbb3-type cytochrome oxidase assembly protein CcoS [Campylobacter]

MNSIIMMMIGVSILAFFIILATLLWGIKNKQFDDDYKFTTLNDDEDSLRDAIELERRKKEALNKKRLS

>WP\_002877123.1 MULTISPECIES: ADP-glyceromanno-heptose 6-epimerase [Campylobacter]

MKIAITGGAGFIGSQLALNLQEKHEILIIDKMRSSATFENGNLQSFGHFKNLLEFDGELFAGDINDEKVL

KKIKDFRPEIIFHQAAISDTTVFDQTKVLQTNLNTFKDFIELSIDLNAKLIYASSASVYGDAKSPQTVGK

DEKPKNPYAFSKLMMDKLAKKYYDKAHLVGLRYFNVYGKGEFYKNKTASMVLQFGHQILAGKNPCLFEGS

DQIYRDFTYIKDVISANLIALDSKCGVYNVGSGKARTFQDIVDILQKELKTDLPCEYIPNPYVKSYQFHT

EAKLDQTWDYRPKFTLEEGIKDYLGEIKRLFEKEVNA

>WP\_002877121.1 MULTISPECIES: bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase [Campylobacter]

MLEFLSQQKPKILIIGDFMVDNYTWCDCSRISPEAPVLVAKTLKEDKRLGGAANVYANLKSLGADVFALG

VVGDDKSGKFLQENLKGEFLIQKGRKTPFKNRIMAHNQQVLRLDEEDISAILLENELIALFDEKIKDFKA

VVLSDYAKGVLTPKVCKAVIKKAKALNIPVLVDPKGSDFSKYSGATLLTPNKKEALEALKFENLEGENLE

KGIKKLKEDFALRYSIITLSEAGIALFDEGLKIAPAKALEVYDVTGAGDSVIAVLAFCLASGIEIFKACE

LANEAAAVVVSKIGSMSVSFDEIKSFNRVDFEKKIKSKEELLTLLKQNDKKIVFTNGCFDIVHFGHIKYL

EKAKRLGDVLIVGLNSDASVKRLKGESRPVNSEFQRACMLAAFYFVDFVVIFDEDTPLELISFLKPDILI

KGADYKDKLVVGADIVSKVELIDFEEGFSTSKIIEKIKDKK

>WP\_002877119.1 MULTISPECIES: phosphoheptose isomerase [Campylobacter]

MINLVEKEWQEHQKIAQESEILKGQIAKAGELLCECLKKGGKILICGNGGSAADAQHFAAELSGRYKKER

KALAGIALTTDTSALSAIGNDYGFEFVFSRQVEALGNENDVLIGISTSGKSPNVLEAFKKAKELNMLCLG

LSGKGGGMMNKLCDHNLVVPSDDTARIQEMHILIIHTLCQIIDEGF

>WP\_002877117.1 MULTISPECIES: hypothetical protein [Campylobacter]

MFASNKKFILFSLLCPLPLVIILFTLLYIRDPFWFFHPPYFRKETYMKDMRMQARGLILYKDFDSAIIGT

SMLENTSAKEANKKLGGNWINLSLGGSTFALRAVILDYLFKHKDIKNIIYSLDIRALNELETPKDKNFIS

LYNDKTIDLFKLYLSSRFINCAIFFSKKEKCIGKDNLDTLTNWFLENKNHFGGIEYWSKEWWHDKNFQNE

ILQAQNFQPNFDIDISHFKNYTKKYLLSFIKKYQKTQFYLIIPSYSRLNYRKLSYGEYYNKDSVLFSNYY

AILSWIIQETQKYPNVKIYGFDDLDYADNIKNYKDPAHYNTDMNSMQLNAIRDNTHILNTQNIVKYLNTM

ERKIKEFDLTPFVEYIKNQNF

>WP\_002877116.1 MULTISPECIES: MBOAT family protein [Campylobacter]

MLFSSFTFIFAFLPLTLVGFYILKALQYYTSAKIFLILASLFFYAYFKIDYIFILTFSTLVNFFLANLIL

RKENNRAGYTLLYLGIIFNLCLLAIFKYTDFFLENFNLFSKLAHLDFNIPLPHILLPLGISFFTFQQIAF

LVDCYKKSNIEDLLENKKVDFIDYCLFISFFPQLIAGPIVHHKEMMPQFHSLLNKEKALIDWKLIAKGLF

IFSIGLFKKVYIADSFASWANAGFTVVQNGNFLNIFEAWATSLSYTFQLYFDFSGYCDMAIGLALFFGIA

LPVNFNSPYKALNIADFWRKWHITLGRFLKDYLYIPLGGNRFGKFINLRNLFIVAFLSGVWHGAGWGFVI

WGILHAIAMISHRIYSFWAKGKTFLNSKIYKIISWFITFNFINIAWIFFRSENLQGAINLLKSMFGVIWV

ELPLKFKAGLLFKKIGGNDTMVGFILVSFILCICFKNSINMLQDFKSSFKNSLIVMFLFYIALITLIATP

YTEFIYFNF

>WP\_002877108.1 MULTISPECIES: arsenic transporter [Campylobacter]

MLAFFIFLSTLVLLFWRPWNLPIWVFSSLGAFFVFIFQLVDFKDAYFVFSLVWDSSLTLVGLIILSFSLE

ALGFFDFIASKILHFSREKNQEKIYISTKKLMLFLLIFVFFLSAFFANDGAILIITPIIIALFSTLKDCK

NHAFILSSFLLSLSFLCDASSNALVISNLTNIITANYFKIEFLEFAKNMFLPNFFVLLSTIVMVFVLYVR

VLPKRLEFKLVKKEQISSKLFFLCIVFLFLFVISFFIGEIFDIKISFFALLWAGIFWLIVLKIQGKKSIK

ILFEAPYGVLLFSFGLYMVVFALHKIGVSEILVKSYTFLMQDKSGIFGVALISAFGSSVFNNLPMVLIGD

LALKEYFENFSFDSLMIYAHLLGVNIGPKLTPIGSLATLLWLGVLARKGINISFWQYCKFGFLITLPVLV

FSLFALIV

>WP\_002877107.1 MULTISPECIES: tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG [Campylobacter]

MFDVIVIGGGHAGVEASAAAARMGKKTLLLTTLIEQIGAASCNPAIGGLAKGHLVKELDAMGGLMGEITD

EAGIQFRILNESKGVAVQGSRAQIDMDKYRIIARNKLLKLPNLEISQEQASVLIVENDEVKGVKTNLENT

YFAKKVILTTGTFLNGLIHVGENKLQAGRVGELASVNLGNYLQTLGLKMGRLKTGTCPRVDAKSIDFSVL

EIQDGDVNPKAFSFRSKNFNPTQLPCYIARTNTTTHEIIKNNFYRAPLFTGQIEGVGPRYCPSIEDKINR

FSDKESHHLFIEPQTIDATEYYINGFSTSLPYEVQIQMLRSVKGFEDAKITRFGYAIEYDYIEPTELKHT

LELKKIKNLYCAGQINGTTGYEEAAAQGFMAGINASLSIDMKEPLILRRDEAYIGVLIDDLVVKGTKEPY

RMFTSRAEFRLLLREENAILRLGKYGYDLGLLSEQDFTYIQNIANNLQKGLEFLLSKEFTPNNQNNAFLE

SLGEDKISSIVNLQKIVARASFDIEKLKKLDPMFETMDNYSLREILNEAKYYHYISMQKAQVEKMKNLSE

LKIPENFDFKSVSGLSNEVVEKLNHHKPPTIFAASQISGITPAALDILQIYIKMQKKKA

>WP\_002877100.1 MULTISPECIES: inverse autotransporter beta-barrel domain-containing protein [Campylobacter]

MRGIFYIIALFSLLNADELTEALAKNNNQNSWEHFDYENTKEAPKIQEENVDFKSTFDSLLSKTLENNNG

IDKTDGNLDFQNENAQVKNLSSLYEGENNSLLFQKELFVAQDNYNYSWGLINRYEKDDFLFGVNGFIDKQ

KEQKDTKSFGTEFGYSKFIKAYSNYYIPNEAEKNLQLGMSFVIPTYTAFAFDISKDNDKTNYQVSYSPYS

VFSLNLLRRDYSARETVDDTVVQVGFSFNFNESFLKQFRKKDNTLEEVNRYDFLQRTH

>WP\_002877092.1 MULTISPECIES: 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [Campylobacter]

MKNSIISYPRIGANRELKFAIEKYFKNQSSKEELLKSAKDLRIRHWQEIQKAGIDFIPSNDFSLYDNVLD

AAVLFNIVHTKYKNLNLDALDEYFAQSRGYQGENGDVTALAMKKWFNTNYHYLVPECDNADIIALTGDKI

FKEYLEAKELGIESKPVLIGIFTLFKLIAFKDEKTQKLAKEKLLNAYIELFDKLNELKVTWLELDEPYLV

YDLSKEDIALFEEFYQELLNHKKDLKILLQSYFGDLRDIYPKLLESKFDALGLDFIEGKQSLALIQKYGF

AKDKILFAGLINGKNIYANDYAKSLKLIKELQKYTQNIVLNTSCSLLHVPYSTEFESKLDSSYLKLFAFA

KEKLQELKDLKEILNSSEENPLFRANQELFKNIPERLDEKVKARLKALKKEDFTRTPSFKERALIQKEFL

KLPLLPTTTIGSFPQSADVRSNRLAFKQEKISAQNYTEFNQQKIKECIQIQEEIGLDVLVHGEFERNDMV

EYFGENLKGFLFTQNGWVQSYGTRCVKPPVIWGDVSRTKPITLAWSKFAQSLSQKIVKGMLTGPVTILNW

SFPREDISLKESTEQIALAIRDEVLDLENAGIKIIQIDEAALREKLPLRKSDWHSEYLDWAIPAFNLVHS

GVKAKTQIHTHMCYSEFSDILKEIDAMDADVISFEASRSNLSLLDTLKAIRFKTEVGPGVYDIHSPRVPS

VEELSLTIEKILNKLPKEQIWINPDCGLKTRAYEEVIASLKNLVTATQKIREQL

>WP\_002877089.1 MULTISPECIES: ComEC family protein [Campylobacter]

MSLWNSFFYSFKEFHYLFLSVVIIFIFNILLEYNNFLKFKNQKHYFINNALLTHQYTKYNKKNKKYWVLK

LQTENFTFYTTSFKDLNLSKNQLLSLRIITHNINFKDYLSKSFYVPSYDFEKLKEKEYNPIISYFLNQHT

NEKIKEFYGALFFALPISLELRNDVNYYGIAHLIAISGYHIGLLFSLIFFILAPIYSFFQKIYFPYRNLR

LDLSILIFTLLLAYACLIGFIPSFVRSLIMAFWVFYLLCKNIKIINFFTLFCSILLCISLYPRLLFSIGF

LFSILGVFYIFLYMHHFANKFNNLINIILLNIWTFFAMVLPVLYFFPLISYQQILGIILSGIFVIFYPLV

LFLHLINYGDLLNFILDEFFKFKIYGTNIYIPFWIFISYLIASLISVRFKYLAFLCIFANFIPFIMIVI

>WP\_002877059.1 MULTISPECIES: polysaccharide biosynthesis protein [Campylobacter]

MAKNEGYICVFDCESVPDVELIRKTLGFEGSDLEVSLKALQWQKEQSGSEFLPLPYHKIISICAVLSDNF

GKFIKVNKIDGQNEKEMIANFFNFIENYEPKLVSFNGKNFDMPVLVLRALKYNLKAATYLDTQSDKWNNY

KTRFSELKHCDLLESLGSNGRGIKLDTLCSMVGLPGKYDVHGDEVMKLFCENELEKIHEYCESDVLNTYM

LFLKYELIKANVSEEDYIDFLSYMRDFLRAKKSDRSYTEVFAKACESEISKVQS

>WP\_002877039.1 MULTISPECIES: iron permease [Campylobacter]

MKIFKIIFLIISIFLSSSAFARVDDYINEANLIKDMLKQSIETYKKGDNLGAKKLSEDAYFQHFENMEGP

IGRNIGRKAITMERKFVNLRRMYKDEAPLTQINALIDSLYYDLDEVAPILQNGYRLKAEASDTNYDKAKA

EKSSLEANAKREADAEALIAQMMGVDKKDLAQSSLTTQASTPANNDTSKLTDDNASADLQAAAAMDARLQ

FILDNISTKFSQAANAFKEKNYQASKDFLNDALFSDYRNTKVEILVNKFTKAGNDQKIQQAIRTLIRQIN

DAKIDEKGLRDGLDNIEEQIFDVFLQIPNSELSSLQISGFNDETKGKDYAKVSNDIKLALDEILKNYDGF

SASIVDDLQGIYLDIFEASGMENKIGAVDSGLKLKIESLFSKGVALIKASADKKELEATFNDLEQLIASS

VDKIQDSTPYSLFIWALGIILREGLEALIIVVAIVSYLVQSGNKNRLNIAYSALFTGVILSFVTAFGVSW

LFKENAGQSRELIEGITMLIAVLLLFYVGFWLLSNAQNKKWTSFIKQGAIDAISNNSAKTLWITVFLAVY

REGAETVLFYQALLFDAKTSTDFSAVFGGLGLGILILIVLYFLLKAGAIRIPVKQFFYITSYIIFYMVFV

FTGKGIAELIEGKVIIPSLIPMNFEPILWLGIYPYYETLIPQFIVLIMLIIGILITKQISKKGVKS

>WP\_002877031.1 MULTISPECIES: lipoprotein-releasing ABC transporter permease subunit LolE [Campylobacter]

MVDKFFLNELFKSISFSYQRLFIIVLSVFIGALTCSAFLNIYFDIDTKLSKELKAYGANVMISPKQDENF

ISNAEYEKIKENLKARALTPFLYDFLNLGSTSGVVLGTDFRALKITKPFLEVKEGSFSLNDFDENSAFLG

VNLAKQLGLKTGNELQIYNPNNGKSIKLTIKGILSSNDEFDSIVLAPLSVVQNLSDRAGINYANAVVYGN

FDEVKAKTQAISNEFIDAKPISSVSLSEGLVLGKIKALMFLIILVVLIIVTTSVNTTLSSIIFSRKKEIA

LRLALGAKKSEIFKLFASECFIVSFFASLIGAFCGIFLANVFGYLIFNSSIDFRFIAVFIALIISLIFAF

LAAFFPIKRALKINVCENLKGE

>WP\_002877012.1 MULTISPECIES: 50S ribosomal protein L22 [Campylobacter]

MSKALIKFIRLSPTKARLIAREVQGMNAELAMASLKFMPNKGAKYIANAISSAVANGGFEANEVIVKSCR

VDAAAVLKRFRPRARGSASRIRKPTSHILVEVAKAEVKAEEKKTVAKKAPAAKKTTTTKAPAKKTTSTKK

ATAKKES

>WP\_002877006.1 MULTISPECIES: hypothetical protein [Campylobacter]

MTMLDIFEIVFITAVVIIGFFGIIYFLNKER

>WP\_002876996.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLKELLEIKKEMEPVIHEANVKLNVLAREVIVRKKEYEIYGPMVDRVYLDNAIYVKVMSSGRDVKTDNVT

IKNGFYMVFVAPEKESTKDIKNKLKVAYEGLDNKFIATLIRSCQRFKEIINKTQATLAKASKMNVVVKTN

LGEASAALKFNITIEYTKENQKLTRENSKSAGSFRDTKTYINLVVEKNTESQICEKLLDDVEKYFIGGG

>WP\_002876992.1 MULTISPECIES: uracil-DNA glycosylase [Campylobacter]

MEEITINIDKIKINDDWKEFLRDEFQKKYFLEIKKQYLNAINQNIIIYPPANLIFNAFNLCPLKEIKIII

LGQDPYHQPNQAMGLSFSVPKNVKIPPSLNNVFKELQNDLNITPAKSGDLSSWAKQGVLLLNSILSVEAN

KAASHSSWGWQEFSDAIIHKLSNEKSGLVFMLWGNYAKNKEILIDNAKHLILKAAHPSPLARTGFLGCKH

FSKANEFLKKVGKIPIDWKIV

>WP\_002876863.1 MULTISPECIES: putative sulfate exporter family transporter [Campylobacter]

MKTSFLAHSVAIVRSNFKGLLFTACIVIFAMYLSSVQSIKDTTHLAATAFAIIIGVLLSPWFFKYQHHFQ

AGVHFSAKKLLRLGIVLYGFNITLTELLSVGLKGFLLSAIVIFFVFMIALFVGMKIFKLDKETSMLVGAG

SAICGAAAVLALESSLKSDPFKGILAVGTVVIFGLVFMFLYPIAFSLNLFPFFDQNAMGVFMGATLHEVA

NVAGAAEMAKDMAGFEQGASNVAVIIKMMRVILLVPFLLIVTYFFAKNQHSSSGKTAKSITIPYFAFAFL

GMIVLNTYLASKESILGIATSDIISLGKTLCTLCIVFAMAALGLQIDFKKFLKSGSRVFGLAFVLGLVLI

FGGYFLTLAFKGILW

>WP\_002876816.1 MULTISPECIES: cysteine desulfurase, NifS family [Campylobacter]

MKVYLDNNATTMLDPNAYELMLPFLKDMYGNPNSLHQYGSATHPALREALDKLYAGLGANDLDDIVVTSC

ATESINWVLKGVYFDHILDKERNEVIISSVEHPAVAAAAYFLKSLGVKVIELPVNEEGVSTVEDLRKVIS

DKTALVSVMWANNETGMIFDIKAMAELAHEFGALFHTDATQAVGKIKVNLTQVGVDFASFSAHKFHGPKG

VGGLFIKKGLKLTPLLHGGEHMGGRRSGTLNVPYIVAMGEALRIANTMLDFEDSHIRRLRDKLEDQILAL

PDTTVVGKREHRVPNTILASIKGVEGEAMLWDLNKNGIAASTGSACASEALESNPIMEAIGAEHDLAHTA

LRLSLSRFNTEEEIDYAAKQIKNATQRLRAISCTYAYNPNNYK

>WP\_002876768.1 MULTISPECIES: hydrogenase maturation peptidase HycI [Campylobacter]

MKFLVLGIGNIMFADEGLGVHLCKQLEKNYKFTHPEFTLDFIDGGTLALQLSYIIARYDRLIVLDCIEAQ

DASIGDIFFFPYDAMPNKISWSGSAHEIEMLQTLQYMELAGDLPKTHILACVPKRIEAMSFKLSDELIQG

AKIMEKTLLDFLTKEGFAYEKIADFSLQELADISYKNY

>WP\_002876765.1 MULTISPECIES: bifunctional tRNA (5-methylaminomethyl-2-thiouridine)(34)-methyltransferase MnmD/FAD-dependent 5-carboxymethylaminomethyl-2-thiouridine(34) oxidoreductase MnmC [Campylobacter]

MKKAKLIFKDNTPFSLDFDDFYFNSKDGLNESKFVYTHSFEWKNQENFIIAESGFGIGLNFFLTLKRFLQ

TTPSKRPKKLFYISIEAFYIEKEQLREIYQKLGFYEEFKELLEQFLKFYPKAKEGIYRFYFEDCFLDLVF

EDITILKELDFKADIWYLDGFSPNKNSQMFDENLIFEVARLSKKNTQICTFSSASFLQKNLKKYGFRVEK

TKGFRKREMIKAYLENELEFKDKEAYFSRTFSSLKNKKVAIIGAGISSAVLAYELSLRGFEIDVFEKHLE

LGKGASGNESGILSSLILKPKVNLGEFSELSFIEASRFYRQILDLEFKGVVEFAHNDLMQERFDTQRENV

LFKISKNQAFLEEGGVIFPKNLVKNLFEKSKACIYFNHEFQAYKFENECFTLKFKNDIVKSDYAVLIYAM

GADTKDFVFYDEMKLSKVRGQVTHLKPFLNTPFPLSSKAYICPVKDDLQVIGASYDRLDASLESKEEDDK

QNIENIAEFIDKNTKLEIIGSKVGFRSYSSDRFMIVGNAYDEVFYKEEYKALLWTKNKEQKLAKISCNLY

FNFAHGSRGFSTSVLAARYLCALINNEPLYLEKKYIHAIHPARFLIRKLKKGL

>WP\_002876677.1 MULTISPECIES: carbamoyltransferase HypF [Campylobacter]

MCHLGYKIKISGLVQGVGFRPLVYELALKSKLFGEVRNDGFGVEIILACTQKECENFIENLKNHLPPLAR

IDQLIITQISISNYENFSITPSLENTKSTPMLSDFALCKECKKEFFDEKNPRFLYPFITCTHCGPRFSII

KSLPYDRFNTSMQELLMCEFCKSEYEDPKNRRFHAQPISCPKCKINVFLKNPKGEILAKDQEAFMQSAKF

LKEGKILAIKGIGGFHLMCDAFNEEALKTLRLRKNRPKKPFALMCKDLQSAKELAFIDEKEEALLGGVLA

PIVILKAKKAFSLIAPDVDKIGIMLAYTPLHLLLFEYFKGSLVATSANLSGESIIKDEFNLCKKLDKVFD

FYLDYDREIINASDDSIAQVVNGETMFLRTSRGLNPFYLERNFNKKGTFLALGAELKNEFVIFYENKLLI

SPYIGDLKSLDAHERFFKLLEFFKQNYDLKFDAILCDKHPHFSYAKEFEERIKISHHYAHFCAAYFEYEE

NFAKDEKALAFICDGTGYGEDGKIWGGEVFVGNLKEYERIAHFENFTLINSDIKNIQNLALSLIFHYDLE

DKAKDFLAKIPKIKLKNLKKIYSHSNLQTSSLGRIIDAFGSIVFNLEKSSYEAQVGLMCEAFYDKNLDFS

YKLFVEKGQVNFKNLILGALQDEKTKAITGMFNALANFIIDFSKDYDLKVLLSGGVFQNKTLLEILKAKN

FDFFIPLKYPCNDSSIALGQMVHFLNLEK

>WP\_002876670.1 MULTISPECIES: MBOAT family protein [Campylobacter]

MTYFSLEFSILMIAFFAIYWTFKNDYKIQNILILIFSYIIYILINPYFALVLFIYTFFIHYFALLIFVRR

KRYIFATCMAFIILNLCFFKYFPSIKGSVDEILNFFGLEFLNIDLVLPIGISFYTFTSITYLVEVYQKRR

LESFLNLATFLSFFPTLLSGPIMRSSFFFEQAYQKREFKHANLIIILLVFGIVKKVLIANYLGIYAKSIL

DFPQSYNFIQLLSAIYAYAIQIYCDFSGYVDLVCAFALMLGFTLPPNFNMPYLAKNLKDFWARWHISLST

FIRDYIYIPLGGNRKGMPRTIVNILIAFILSGMWHGNTLAFIVWGLLHGIGIVFIHLLALSKFSLQKIPA

LGRFLTFQFVCFTWIFFYYSKNLEDAIEYFKACYYNFFQIPSYNDIYMLVAFGVLFMVYPLFINFKEYCI

KILNLTPFLLKPFIIAFILLLVFAFMPDGIPDFIYSSF

>WP\_002876662.1 MULTISPECIES: bifunctional riboflavin kinase/FAD synthetase [Campylobacter]

MLNIFTTISKINITSLAIGCFDGMHLGHLKLVKCLDENGALLVINKFKGQFLCSNRQKEEISGKKVIEVD

FESIKSLDGKDFLSFLKKEFVNLKFIVVGYDFSFGKNRAYNAKDIEFLSGIKTIIVDEFSIGGIGVHASL

IKDFLSKANLQKAKEFLGRDYSIKGKMIKGQGLGSKELFATINLDCKGYFLPQNGVYATLLKSQRKIYKS

VSFLGIRSSDENFAIESHILEELGEKFTQGEFFELEFISFLRENQKFQDLKKLKNQIAKDIEQAKELLRK

NDER

>WP\_002872302.1 MULTISPECIES: porin family protein [Campylobacter]

MNKKLLSIIASTTLFSNLALADENSGFFIGTDAAWMHAQVKSELKHKNTKRNFNGDISGNIPSFGLKLGY

RLNENHRIYAGYNYSDEFSDFIKTPKIQIEGDFTTHKFFTGYDFTPKLFEKTRAVLGVYGGYARTDLTLK

TSFLSLSQNFDGYFYGAKIGALYDLTPHNEIELGFKAEQIHYNSRNFYQNKVGSNFYDPKQTNYGVYLGY

NYKF

>WP\_002872103.1 MULTISPECIES: protein-disulfide oxidoreductase DsbI [Campylobacter]

MSCIKMKDNCRKFSLSKWQDTRKPWLILIIVTIGLTCIAHFLFQEYLFMEPCEQCVYIRFDMLVMAIGGM

IALINPTNNIIKIFSYSLAFYGIWLGLEHCLTLNHIHEVVHSENPFAGVDGCREIPIYPFNLPLHEWAPS

WFLPTGECGMDTPVVPENAYNHLNAFQKFFIGTPPDFENGLYSNGWYLIPSLKFMNMAICCLIAFLCCFI

VLFAMFIAYVLDKNKLNAKIFALVIVILVLVLKFIGEPKNPNQNIASLNHLNQVV

>WP\_002871815.1 MULTISPECIES: glutamine amidotransferase [Campylobacter]

MKKILFIDNYDSFSYTIIYYLKELGFECKVIKNDAFKKAKELEKFDFTHLIISPGPHSPKESKLSLKAIK

YFKKNKKILGICLGHQCIAEIFGGRVSKMQNPMHGKISKLYFKKDPIFKGIKKEIEICLYHSLHISSMPK

KCKILAHNSENIIMAIKHKKYPIYGLQFHPEAVLTQKGKKILKNFMKL

>WP\_002869960.1 MULTISPECIES: replicative DNA helicase [Campylobacter]

MQQEYYDLDLERAILSSCIMSEEAYASIAGDISPKDFSLKAHQDIFKAVIACSNNKEPISVSFLRKHKKI

DEQILAEILATPSMIDLPAYVNELREKSVKRQLLSFAHLLPTRINEDRAVSEIADEIGKEIFSITNRVNS

RDIKDVDMVISELFEEFKKQKTLENKGIIGLDTGFEGLNKMTKGFKGGELIIIAARPGMGKTTLCLNFID

KILRQKKGVALFSLEMPATQIMQRMLSSKTSIPLQKILTADLNDDEWERLGDACNDYSQKKLYIYDSGYA

TIADVRAILRRLKSQDESIGLCVIDYIGLMMSNSNFNDRHLQVSEISRGLKLLARELDMPIIALSQLNRG

LEQRANKRPLMSDLRESGAIEQDADAILFVYRDEVYREQEEKERENKAKAEGKAYQRLFIPNPMQENAEI

IVGKNRNGPVGTIEVVFLKEKSCFVDKPIGYETTEFTG

>WP\_002868575.1 MULTISPECIES: Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase GatCAB subunit B [Campylobacter]

MFEVVIGLEVHTQLNTKTKIFCSCATSFGEAPNTNVCPTCLALPGALPVLNEEAVKKAIAFGKAVNATIN

KKSVFNRKNYFYPDLPKAYQISQFDIPIVEKGELFINVKGENKRIGITRAHLEEDAGKNIHENNFSKVDL

NRAGTPLLEIVSEPELRSSDEAVAYLKKLHSIIRFLDISDANMQEGSFRCDANVSIRPKGDTKLYTRVEI

KNLNSFRFIQKAIEYEVKRQSEAWEDGTYEQEVVQETRLFDTTNLVTRSMRGKEEAAEYRYFPDPDLLPV

LLKDEFLDIKIPELPDEKKARFIDELGIKESDAEVLISSLEMSRFFESLISQNLNSKLCVNWLNTELMGL

LKGELTIENSPVDAQKLGVLIKRIEDGTISAKAAKDVLAFVFENTSVEIDEAIEKLGLKQVSDDSAIEAV

IEQILNANADKVAEYKSGKDKLFGFFVGQTMKEGKGAFNPAKVNEILKTKLG

>WP\_002867099.1 MULTISPECIES: hypothetical protein [Campylobacter]

MDKKIKYFILDKFDYSYPILTKDTKCSFCENFFPIEYSSNLKTIEKECPFCNNKMDIKLKD

>WP\_002867098.1 MULTISPECIES: chlorohydrolase [Campylobacter]

MFIAAARYLFLCDEDFTILENQAFVFEDKILELGELDNLRKKYPKAKIIKTPKNSVILPAFINPHTHLEF

SANSTTLHFGEFLIWLKSVINSRSMLNAQAKEELILQSIKKMQKSGIGTIGEISSFGSDLDPCLKASQKG

IRVVFFNEILGTNENQVEDKKQEFLKRFENSLKFKNDFFIPAISIHSPYSTHPSLAYFALDLAKKQNLLV

STHFLESKAENIWLRESKGGFKKWLENFTLHPKPLYAPKDFAKLFKGVRTLFTHCVYLKEYEWLDKNLHS

ITHCAFSNRLLSQKSLDLKTALKSGLNIHLGTDGLSSNISLSLLDEMRANLLIHKNFDLLELASKLLQMA

TLYPARALNLNLGELKKGKIADFSVFELGECDKKQAPLQFILNAKEVDKLFIKGKECKF

>WP\_002867094.1 MULTISPECIES: MFS transporter [Campylobacter]

MQALNQEKFNSLSDIKIILVLCLGVFGILSTELGMMGIIPIVSQNFSVSISDAGWSVSIFALVITFCAPI

VPLLCANFNPKKLMLICLAVFILSSLTSAFVSEFWQLLILRAIPAFFHPIYIALALSMVANLVEDKKEIP

KATAKIFAAVSAGMVLGVPMTSYFGGNFSFKMAMLFFVFLNTLSFIATLFFVPDFKKVNSVKISKQLLIL

RYPLLWISILCVICINAGIWGFYSYFSDFLHSVGKMNFTLISIVLAIYGFSNIIGNYIAGKTLVKNANFT

LILTPLIMIGFYILLFSFYSEIILIIFAFILGILAGVMNNGTHFMISYPFPKAANFSNGLFISVANIGLS

TGTAICGLVISLSDTRYIIVNTIVLLILGIIMIFVRSRIEKMKLRF

>WP\_002867092.1 MULTISPECIES: DNA methyltransferase [Campylobacter]

MQNKIDKITDILRRDDGISGAMHYTEQIGWILFLKFLDDYETNLKDLAFLDGKDYKSILEEKFSWSVWAA

PKKDGKLDVKNALSGSDLLEFVNKELFPYLKNFKNNDDFKSIEYKIGGIFEFIDNRIANGHTLREVINII

DEISFNKEDEVFALGEVYEKLLKDMGSDGGNSGEFYTPRPLIKTMVEVIDPKPKERIYDPSCGSCGFLVE

SFLHILYKDRTKGKKANLSVEELEFLKNDALFGKEKTPLSYAMGVMNMILHEISSPNIIKTNTLSKKITD

ITEKDKYEVILANPPFGGKEKEQIQENFPIKSNATELLFLQHILKSLKNNGRCAIIVPEGVLFQNSNAFV

SVKKDLLDDFNLECVLSLPSGVFLPYSAVKTNVLFFSKGKKCICEGDGVYYYELIPPYKLTKNKPLEYAH

FKEFLKCYKERKITANSWLVSKKELEERNYDLSAKNPNVKEEKILRTSEEILNSLEENLKTQQEYLNELK

SILK

>WP\_002867090.1 MULTISPECIES: ATP-binding protein [Campylobacter]

MLIEFRVENFLSIQDEQILSMMASKDNTFFDSHTNGDKKLALLKSSVIYGANASGKSNIVKALQTMKTIV

ISSANTQRGDKLPITPFLLGDEDDKPTKFEIIFIQNDTKYQYGFILNSEKILEEWLLTFDENNTEQNWFE

RIYNKKEGRYNYSFGDQFLADEIYKQLWENSTRDNALFLSVAIQLNNEQLKPVFDFFNLKLQIANSNGWG

NGKSITINEYKKDKELVNSFFKIADLDIEGVEIKTSDIDENSLPSNLQNIPQELKEKIIQEVKNIQNLKN

VKILEDISFIHLSQKNQIKFLNFNDESDGTRKFFNIAGIWIDSLKKGNILIIDELNTHLHPLMTKFLVNL

FHNEDLNKSNAQLIFTTHDTSILNQDIFRRDQIWFCEKQNKATKLYPLSDFEESEERRDKTNLENDYLLG

RFGALPYFKEILSSWSDNGN

>WP\_002867088.1 MULTISPECIES: NAD(P)-dependent alcohol dehydrogenase [Campylobacter]

MQYKILENNRIASKGYAMLSKDAKFTPFEFSRHAIGDNDILIKILYAGICHSDIHTARSEWGEATYPCVP

GHEIAGEVIAVGKNVSKFKVGDYAGVGCMVNSCGECDACKRSQEQFCENGKTIFTYNSCDVFHGNENTYG

GYSNNIVVSEKFAICVPKNAPMHKVAPLLCAGITTYSPLKFSKIKEGSSVAIAGFGGLGMMAVKYAVKMG

AKVSVFARNENKKADALAMGVSSFYTSTDKNAVKERFDLIISTIPTPYNPAIYLDLLKFGGEMAIVGLPP

VEDKVNIGINELVHKAGKKVYGSLIGGIAETQEMLDFSLKHEIYPETELITPQEIDKAYENLTSGKAKFR

YVIDMTKE

>WP\_002867087.1 MULTISPECIES: biotin transporter BioY [Campylobacter]

MLELIGELSLQNYMGEWLEMARKPAFFQKSCLNSKAKYELKYKNGVPYVEIENFCSKENEISSIKGKAKI

VSNRQLAVRFNIFMNLFNKVNYEIIFIDSEYKVAIVGSPDKKYLWILARNIIDEKSIKELLDIAKQRGFS

VSDVIFDKY

>WP\_002867084.1 MULTISPECIES: allophanate hydrolase [Campylobacter]

MSIKIIEASINSSLQDFGRKKFAKFGIARSGAMDEDALRMANILLGNKQDEAGVELCLKGGKYEFLDGNY

FVLSGAEFEAKLNNQKIKTYKVYKANKGDILELGLAKIGFRGYLCVAGGFEIKSFLNSKSSDAKMGVGFF

EGRALQKDDILNTHNTFIPFNLEARECENPLFKSHKEPIIRVILGTNEDAFTQKGIDTFLNTSYKVGSKS

DRMAIYAESSKSIEHKNSADIISDPAVFGSIQVPKSGIPIILMAGRQSTGGYTKIGTVIENDLSLLAQAK

LGSSFKFQSISMQEALELYKQREMKFKAMDQKINLDFENLI

>WP\_002867082.1 MULTISPECIES: LamB/YcsF family protein [Campylobacter]

MFKVDLNSDLGESFGAYKMGMDEEILKFVSSVNVACGFHAGDPCVMDKTLNLAKQNGVCIGAHPSYPDLL

GFGRRNMQISFEEAKNYALYQLGALFGFAKAKGMKIQHFKAHGALYNMAAIDENLALALCEAVASFDENI

IFLGLSNSAMNEAAKKKGLRYANEVFADRAYNDDGTLVSRKLEGALIHDENLAIKRVIKMIKESKVTSIN

GKEIDLKADSICVHGDNIKALEFVKKIKENLEKEQIQICALENFI

>WP\_002867037.1 MULTISPECIES: pilus (MSHA type) biogenesis protein MshL [Campylobacter]

MIRLILINILFCHYLYALDCQKRLFDISINEKLSIQESLDELAKYCSFSIIVKDKIAKEKLETLQNSVNI

HQMSLDEIFNFFIKEHDLSYDFDGKILRISGINTKIFKISYITSIREGQSITKASVDAKPRQSEYSGSFD

DAEDNMIKSMEKFDFWQNIEKEIIVLLKNSHEDYEAKTPIINPNAGLIIVTGTNSQLKSVKNYLQKLENR

LKKQVIIDVSILAVSLNESHSSGINWQNFNIGLNSQVNNENSFIQFQNGQGFVKNLGLRANLNFDSIINF

LSQNGKTSVLSNPKLMALNNQQAIISVGDTINYQVKESSKGTENGTTVSESYNNYSIFVGILLNILPEIS

DDGKIMLRINPSLSDFKYPEDNKRQKEPRTIAPDTIQKKLSSVVQVENNQTLILGGLISHDKSNEKNSIN

FLSKIPILGSLFKGEVLNSKVTEIVFIITPSIVDSVNAPSLKDLGFKHYE

>WP\_002867036.1 MULTISPECIES: hypothetical protein [Campylobacter]

MQERIKELELRYKYFLLKKYLKYLLLVILISVIAFCFFVLMQKYNKQKNIYLQAIEHKKHLEQKILQAQI

LQEKNKISREKLYKELEEVKAVQENTHISKIEIDSKILNISDLKKSFYQNPSYEKALNLAKKYFDIKAYQ

KTIFWTLKANELDKQKQDSWLIFAQAKRALGEEKEAQSALDAYINYYGLMELDGK

>WP\_002867028.1 MULTISPECIES: 23S rRNA (adenine(2030)-N(6))-methyltransferase RlmJ [Campylobacter]

MNDEFISVKDFFNHNEKRKKFLQKQEIKPPKEKTKKTKETKLYTNIESGKYKGKKLLLPSLTTTRSTKSI

VKSCVFNVIREDLRSKIFIEAFGGSALIAAEALSNYALKAYAIELDIKAYKIALENAKNIDPNLEVIHAN

TFEILPKLIENSKNEIILYLDPPFDIREGFSDIYEKIYHFLENLDLKTLNLIIFEHHSTIKTPEKIQNFQ

KVKEKKFGSTSLSFYSS

>WP\_002867024.1 MULTISPECIES: tRNA pseudouridine(13) synthase TruD [Campylobacter]

MNLEEENTIFKPLYSLKHSPINAYFSKNSDDFVVRERPLYEFSGKGEHLILHINKKDLTTNEALKILSET

SGVKIRDFGYAGLKDKQGSTFQYLSMPKKFESFLSNFSHPKLKILEIFTHENKLRIGHLKGNTFFIRLKK

VLPSDALKLEQALMNLDKQGFANYFGYQRFGKFGDNYKEGFEILRGKKMKNVKMKEFLISAFQSELFNRY

LSKRVELSHFANDFSEKELIQIYKISKEEAKELKKQEQFFKLLKGEVLGHYPFGKCFLCEDLSAELERFK

ARDISAMGLLIGAKAYETGEGLALNLENEIFKDALEFKAKMQGSRRFMWGYLEELKWRYDEEKAHFCIEF

FLQKGSYATVVLEEILHKNLFE

>WP\_002867005.1 MULTISPECIES: phospho-N-acetylmuramoyl-pentapeptide-transferase [Campylobacter]

MYYLSDLSHYAFFTYISVRAGFAFFIALCLSLFLMPKFITWAKAKNASQPIYEYAPETHKTKCHTPTMGG

LIFISSAVIASLFCIKFDNIFAISALLCLILFCLIGLIDDLGKVLKKDNHSGLSPRMKLLAQIIAGLICI

LPLYFSSELSTELFIPFYKHPLFDMEIFAIVFWILVLISSSNAVNLTDGLDGLATVPSIFSLSTLGIFLY

LSGNLNYSEYLLLPKIQGLGEVVIICAALIGALMGFLWYNCYPAQVFMGDSGSLALGGFIGFLAIISKNE

ILLLLIGFVFVLETVSVILQVGSFKIFNKRVFKMAPIHHHFEKVGWVENKIIVRFWMIALLSNLLALASI

KLR

>WP\_002867004.1 MULTISPECIES: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Campylobacter]

MKQKCVLIITDGIGYNKNSKFNAFEAAKKPSYEKLFKEVPNSLLKTSGLAVGLPEGQMGNSEVGHMCIGS

GRIIYQNLVRINKAIENKELEKNENLQKLLAKCKRVHIIGLYSDGGVHSMDTHFKAMLEICAKNGNEVFA

HAITDGRDVSPKSGLNFIKDLKEFCENLGVHFATLCGRFYAMDRDKRWDRVKEYYECLLGKAYKVPNLLE

YLQKSYDENVTDEFIKAAQNENYKGMREEDGIIFINFRNDRMKQLVEVLNSKDFKEFEREKIFENLLTMS

VYDDKFKLPVLFEKEKIENTLAQVISKAGLSQLHTAETEKYAHVTFFFNGGKEELLENETRVLIPSPKVK

TYDEKPQMSAFEVCDAVKKGIEKGEDFIVVNFANGDMVGHTGDFNAAIKAVEAVDTCLGEIVECAKKHDY

AFIITSDHGNCEAMQDEKGNLLTNHTTFDVFVFVQAKGVSKIKDNMGLSNIAASVLKILDLEIPKEMNEA

LF

>WP\_002867003.1 MULTISPECIES: 3-oxoacyl-ACP reductase FabG [Campylobacter]

MKFSGKNVLITGASKGIGASIAKTLAGFGLKVWINYRSKPELADALKDEIIASGGVAAVIKFDASKEDEF

ENGVKTIVESDGELGYLVNNAGVTNDKLALRMKLEDFSSVVDTNLSSAFLGCREALKTMSKKRFGAVVNI

ASIVGEMGNAGQVNYSASKGGMIAMTKSFAKEGASRNLRFNCVTPGFIKSDMTEVLSDEIKQTYQDNIPL

KRFAEPEEVANCVAFLLSDYASYVTGDVLKINGGLYM

>WP\_002866999.1 MULTISPECIES: heterodisulfide reductase subunit B [Campylobacter]

MQKEYAFFPGCVLSQAAKESKISLEAIAPILGWKLNEIKGWSCCGASQAQCVDPIATLVANARNIALAEE

MKMPMLTTCSTCMLTLTKAKNTLDKGAKERINTFLAQGGMKYQGSTPITSLLWELYEDLDNLKSKVKKPL

SNLKVALFYGCHSLRPEDAFGKKESSTNPKSFESVVEVLGAKIVPFEKRLDCCGFHASYPAEKSVKKMSS

QIVNNASENQADCVVTPCPLCQMQLDIYQERFQDYTSSKARLPMIHLSQLVGLALGLSKEMVGLDYNIID

ASKIA

>WP\_002866997.1 MULTISPECIES: beta-ketoacyl-[acyl-carrier-protein] synthase II [Campylobacter]

MKRVVVTGIGMINALGLDKESSFKAICNGESGVNKITLFDATDFPVQIAAEVKNFDPLEVVDGKEVKKID

RFIQLGIKAAREAMQDAGFSEELDKEEFGIVSAAGIGGLPNIEKNSIICSERGPRKISPFFIPSALVNML

GGLISIEHGLKGPNISCVTACAAGTHAIGEAYKSIALGNAKKMLVIGAEAAICPVGIGGFASMKALSTRN

EDPQHASRPFDKERDGFVMGEGAGALVFEEYEEAKKRGATIYAELIGFGESADAHHITSPTLDGPLRAMK

KALNMAGNPKVDYINAHGTSTPVNDKNETAAIKELFGNNIPLISSTKGQTGHCLGAAGAIEAVISVMALR

DGVVPPTINQLVKDDECDLDYVPNISRKVDLKVVMSNSFGFGGTNGCVVFKKVD

>WP\_002866995.1 MULTISPECIES: NUDIX hydrolase [Campylobacter]

MAFKNLKELSFEKSNYIKPKRFAYESNGKFCTWDFIESKDSVSVLLYHKELESFIFVRQFRIPLWYHQMH

DKDYVKDDNMGYTIELCSGLVDKKLSLEEIAKEECIEELGYAPKNLEKIGDFYTGFGSGVSKQSFYFAEV

DEKDKISSGGGVDDEEIEAVYVKVQDFEKKCKNIIRTPLLDFAYMWFLKEKWEKY

>WP\_002866989.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLFLLKKIFPQLFISIILEDKKNIVKASIYRGNKLISSNEKTFDKSENLLEYIKNLSKHFLFYHTALFLD

AKEQGLIPSTNIQDCEHFNIGKISLQHILFNNALVYTATEHVEYYSELFEEYRGLDFLYSPFALLYYNIQ

KEKQPDDQILLYGFKQGHLLAIIVAKGNTILYGDFKIFEQELGLELELPSEDNQEIENNNDDTEVTLDNF

NEALNNKFDLLDQENNLETLDNNDNFNLDELNQFSNDMELCRYIITSIEKFYNDDKYAGVFINGILLYSE

SDINISAIDFLESETFLEIKTKQINTLDLMIELMQKELK

>WP\_002866986.1 MULTISPECIES: transcription termination/antitermination protein NusA [Campylobacter]

MEKIADIIESIANEKNLNLENVREKVATALINTAKRIYGQEYEFFVDPKNLNLYQKITIVADNDERLQNK

SESFIALSKAKSEAPDVEIGDELTYECSLENLGRTAVNTLHKELEYHIQKLLEQTIFEKYKNKVGQMVFG

TVVRVDNEENTFIEIDELRAFLPRKNRIKGEKFKIGDVAKAVIRRVYTDKGIKIELSRTSPKFLECLLEA

EVPEIKDGYVNIIGCARIPGERAKIILQANGANIDPVGATVGVKGVRINAVSKELHNENIDCIEFTNESE

ILISRALAPAIVNSVKIEDKKAIVSLNSEQKSKAIGKNGINIRLASMLSGYEIELNELSSSQLNNAISNE

EAMKNLQDLFKI

>WP\_002866985.1 MULTISPECIES: MFS transporter [Campylobacter]

MNYIELLKNNKNIRILASVQFIVYFGAWFSQTGVFTLLVELNAPTWATATSAMLAFLPGVLLAPINGVIV

EKNKPKKLLLNMISIELISIFCLIFVTSLSMLWLLFILIFIRLCVASIYFQAEMSLLAKILTPQELKLAN

EMHSVIWAISYTAGMASAGIFIYFLGVKTAFLFDCMLILIGISFLVRLSIPDFHQKTQSRFFIMIKEGFF

YVLNNKIIFHLILLHAFIGLTAYETLVTLLAQHQYKEVLSAALVIGFLNAVRACSLAIGPMVLSKFINDK

NLFYMYLGQGFGIILWALTQFNFYISFLGLIGAGFFTSALWAYTYTMIQKNADKEYHGRVIAYTDMIYLS

FSAIISMLMGFLFEIDLSLELITGLLGMIFIFAAFYWKWFYKKYL

>WP\_002866984.1 MULTISPECIES: dehypoxanthine futalosine cyclase [Campylobacter]

MKRLDKKEALDLLHHASLTELGEMAYRRKLELHPEKITTFVVDRNINYTNVCCIDCSFCAFYRHHKEDDA

YILSFEEIDKKIEELEAIGGTQILFQGGVHPKLKIEWYEELVSWIKEHYPNITVHGFSAVEIAYIAKASK

ISITEVLQRLQAKGLFSIPGAGAEVLSDRVRDIIAPNKCDTATWLEVHRQAHKIGMKSTATMMFGTVEND

EEIIDHFEHLRKLQDETGGFRAFILWSFQSDNTALIQKHPEIMKQSSNKYLRLLALARLYLDNFKNLQSS

WVTQGSLIGQLALKFGANDLGSTMMEENVVSAAGASYRMNQDEMIRLIRSLGENPAKRNTAYEILERF

>WP\_002866983.1 MULTISPECIES: insulinase family protein [Campylobacter]

MQYLESRGVKIPFIFEKNSDFPIVVLKLVFRNCARSYDEIAGLAKMFSRILNEGVDDKFFKDLEFRAINL

EASSGFESLEINLSCLKENFDFALKSLEKLLLKPRIEEKTLQKLKINALGELASKNSNFDYLAKNLLNAQ

IFKCKEFQSPNDGDEKSIETLSLKDLQNFYKNFIHLSDLVVILGGDLEEKQAKEDLLKLLSKLQIGKKNT

PKKYELSKNIKDEILVRPESEQAYIYFATPFFADFKDKDLYLAKIALFVLGQGGFGSRIMEEIRVKRGLA

YSAYAMLDMNMSFSRVFGYLQTKNESAKEAKKIVKELFEDFIKNGMTQNELDQAKNFLIGSTPLRYESLS

KRLSIAFNEFYQGLNLGYYKEELKLMEKVKLETINAYIKKHQELLNISFASIQNEN

>WP\_002866982.1 MULTISPECIES: ATP-dependent DNA helicase RecG [Campylobacter]

MKIKESDFEFFKKLKIRSAIDLALLLPKKIENLNPSKNPKENEICTQKITIKSVSSRKNQLFGLGFCEEW

QENISFVFFHPRAWHFGVCKVGKELIFNAKLSRFNHTWQFNNPKILTSFEGFSPKYQILGLKDTKIAAFI

HKYLNYENLKESGIEDKYIHFLLNLHAYDEKSFFMFENLQNFSKDLKYIEIYNFLKRLKAKQTHFKAHQI

NVFNIANWLKDLPFSLTKDQLNALKDIEKDLHSKEAKRRVIMGDVGCGKTLVLLGAALMVYPKQAILMAP

TSILAYQLYEEAKKFLPDFMNILFIKGGKKEKDLEQNIQKANLIIGTHALIHLESHNAVLVMIDEQHRFG

SAQREKIHSLNKQEFAPHFIQFSATPIPRTLSMIQSELLNFSFIKQMPFKKDITTYCIQNEGFSKLSEKI

KEEISKNHQIIIIYPLVSASDNIPYLSLEQAKEYWQSHYEKVFVTHGKDKQKDEILERFRDEGNILLSTT

VVEVGISLPRLSMIVIVGAERLGLATLHQLRGRVGRVGLKSTCYLYTKLKEIPSRLKEFASTLDGFKIAE

LDLKNRLSGDLLDGFMQHGNEFKFFDFSKDEEILEKVKKDLAKKLPN

>WP\_002866980.1 MULTISPECIES: Crp/Fnr family transcriptional regulator [Campylobacter]

MKDYLELLSSVGKLKKIQKNSILFYEGEEAKKFFILLKGKIRIYKSTASDKEITLHYFNPPNFIAEMPAF

KKLNYPANAIFEEDGEILEIDFINFQNLCSENKEFNFLLISSLFDKIKILEKKLSQNALDLRTRLLKYLL

ENEKNLDTISQKQIAIDLNVRAQSLSRVLKELKISELIDTKKGRIEILNKDMIMKELW

>WP\_002866974.1 MULTISPECIES: DNA-directed RNA polymerase subunit beta' [Campylobacter]

MSKFKVIEIKEDARPRDFEAFQLRLASPEKIKSWSYGEVKKPETINYRTLKPERDGLFCAKIFGPIRDYE

CLCGKYKKMRFKGVKCEKCGVEVANSKVRRSRMGHIELVTPVAHIWYVNSLPSRIGTLLGVKMKDLERVL

YYEAYIVENPGDAFYDNESTKKVEYCDVLNEEQYQNLMQRYENSGFKARMGGEVVRDLLANLDLVALLNQ

LKEEMAATNSEAKKKTIIKRLKVVENFLNSNLNANADSDEAVPNRPEWMMITNLPVLPPDLRPLVALDGG

KFAVSDVNDLYRRVINRNTRLKKLMELDAPEIIIRNEKRMLQEAVDALFDNGRRANAVKGANKRPLKSLS

EIIKGKQGRFRQNLLGKRVDFSGRSVIVVGPKLRMDQCGLPKKMALELFKPHLLAKLEEKGYATTVKQAK

KMIENKTNEVWECLEEVVKGHPVMLNRAPTLHKLSIQAFHPVLVEGKAIQLHPLVCAAFNADFDGDQMAV

HVPLSQEAIAECKVLMLSSMNILLPASGKSVTVPSQDMVLGIYYLSLEKAGAKGSHKICTGIDEVMMALE

SKCLDIHASIQTMVDGRKITTTAGRLIIKSILPDFVPENSWNKVLKKKDIAALVDYVYKQGGLEITASFL

DRLKNLGFEYATKAGISISIADIIVPNDKQKAIDEAKKQVREIQNSYNLGLITSGERYNKIIDIWKSTNN

VLSKEMMKLVEKDKEGFNSIYMMADSGARGSAAQISQLAAMRGLMTKPDGSIIETPIISNFREGLNVLEY

FISTHGARKGLADTALKTANAGYLTRKLIDVAQNVKITIEDCGTHEGVEINEITADSSIIETLEERILGR

VLAEDVIDPITNSVLFAEGTLMDEEKAKILGESGIKSVNIRTPITCKAKKGICAKCYGINLGEGKLVKPG

EAVGIISAQSIGEPGTQLTLRTFHSGGTASTDLQDRQVSAQKEGFIRFYNLKTYKNKEGKNIVANRRNAA

ILLVEPKIKTPFKGVINIENIHEDVIVSIKNKKQEVKYILRKYDLAKPNELAGVSGSIDGKLYLPYQSGM

QVEENESIVEVIKEGWNVPNRIPFASEILVEDGEPVVQNIKAGEKGTLKFYILKGDGLDRVKNVKKGDIV

KEKGFFVVIADENDREAKRHYIPRESKIEFNDSEKIDDANTIIASAPKKERKVIAEWDAYNNTIIAEIDG

VVSFEDIEAGYSADEQIDEATGKRSLVINEYLPSGVRPTLVIAGKGDKAVRYQLEPKTVIFVHDGDKIAQ

ADILAKTPKAAAKSKDITGGLPRVSELFEARKPKNAAVIAEIDGVVRFDKPLRSKERIIIQAEDGTSAEY

LIDKSKHIQVRDGEFIHAGEKLTDGVVSSHDVLKILGEKALHYYLISEIQQVYRGQGVVISDKHIEVIVS

QMLRQVKVVDSGHTKFIEGDLVSRRKFREENERIIRMGGEPAIAEPVLLGVTRAAIGSDSVISAASFQET

TKVLTEASIAGKFDYLEDLKENVILGRMIPVGTGLYGEQNLKLKEQE

>WP\_002866972.1 MULTISPECIES: tRNA1(Val) (adenine(37)-N6)-methyltransferase [Campylobacter]

MSDLITLAQLSQGYRYNSDSLILADFILKQGIKGAVFDVGAGCGIIGILLKKNIANLSLSLIDIQKENIK

LIEKNLKSNQIQGDIFHDDFNQFQSIKKFDFIVCNPPFYRQGAYKSEDQHKAISKFQEFLPLHSFLTKAN

SMLKPNGTLYFCYEALALDEICFILKDIKIKITKLCFVHTHQNKKARLVLIQVKKGSKSPCEILPPFFVY

ENEILSKQMQEIHLRFRLKSYDI

>WP\_002866971.1 MULTISPECIES: YkgJ family cysteine cluster protein [Campylobacter]

MIFDKNFSYAFDENACEKCGGKCCTGESGNIFASKEELEALRKHLNLESKEFAEKYLRKVGFKMSFKEVE

FEDGFACIFFDTQKRNCSIYDFRPKQCRTFPFWEYFKTHQKELEKECIGICYLF

>WP\_002866957.1 MULTISPECIES: tRNA (uridine(54)-C5)-methyltransferase TrmA [Campylobacter]

MSLENFGNFLTLDEKHSFIKKYFKEFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYI

IEYLDFADEKICAFMPKLLEYLRQDNKLKEKLFGVEFLTTKQELSITLLYHKNIEDIKSNLENLSNILHI

NLIARSKGKKLIFKTENLRQTLNIQDRKIFYEFNNDCFIQPNTTINEKMITWVCEILNTQKRMDLLELYC

GYGNFTLALAPFFFKVLATEISKSNINFALKNCKLNNTTNIHFARLSSEELSLAIKKEREFFRLKDIRLD

DFNFSHVLVDPPRAGLDKSVIDLIKKYENIIYISCNPITLKENLKELSLTHRVEEFALFDQFVNTPHLEC

GVFLSKV

>WP\_002866952.1 MULTISPECIES: methylated-DNA--[protein]-cysteine S-methyltransferase [Campylobacter]

MFKVYYKMPLCYLSLHSDGKFLTRVDFCDNKRSEKNCSLLDLVKYELDLYFTHKLRKFSIPVLIQGTDFE

SKVYKALMKIPYGKIATYKDIAEKINHPKAFRAVGNANSKNQIPIFIPCHRVIASNGIGGYNGGLEIKRF

LLENEGVNLK

>WP\_002866951.1 MULTISPECIES: hypothetical protein [Campylobacter]

MQISNLGELLNATLIHEGSVLSVEGFAINLNELKAGFAFFNNDKKEITQAVKKGAYAIITENDITIEDKD

IFYFRVENLEQALVRFLRFFCEDKECEFLLFKSYELSLCKAFYFNILKGNIFADFEKLIKAKKGEIFCYC

EENYLNKLCAYSHSLKDANFTLLSRSSFFFTTLICENLYFKNLNLPFFYANSFAKIISFLKEKSQKIIFD

FNKIDDFKIYFIDDKFEITPFGSSSQAFIVSNNQNTFEFWKEKFKNIKDFKIASKNSLFCDFSYNQLSDL

RKLKNFKYCLILENYDIFEQEFENKENQTPSLF

>WP\_002866948.1 MULTISPECIES: fructose 1,6-bisphosphatase [Campylobacter]

MQEVISYIQKAVLEISNALKFPDTSYSQNQNFTGDTQLKFDVLSDGIITKTLSQCSSIKAIISEEKDEIL

TLNERANFIVAYDPLDGSSLMDVNFAIGSIFAIYEEKASAKNLRAALYSMYGARLELVICKDQPKLYRLN

ANNEFIFIKDLKMNEKGKINATGGTQKFWEEKHAKFIKSLFDEGYRLRYSGAMVSDINQILLKGGGIFSY

PATQDAPNGKLRAFFEVFPLAFIIEKAGGKTTNGKNHSLLELEFDKIHATTPCFFGSEYEISKLLKAYNE

>WP\_002866947.1 MULTISPECIES: YggT family protein [Campylobacter]

MVIDSFIISIFQVLQIVINIYTWIIIIAALLSWVNPDPYNPIVQILYKLSYPAYTLVRKIPTRIGNIDLA

PLIIVLALQFLGIFLGNILRSIL

>WP\_002866944.1 MULTISPECIES: phosphatidylserine decarboxylase [Campylobacter]

MSFSKESSRLFGFVAGIKFPKMIQKVINENYVKYFNIDMSEFKSPCEYESLNALFTRTLHIPRKLEEGFI

SPSDGKILECGSTFLANEEHFAFSIKGHTYSIEELLKDSFEKDELKNGLDYVNIYLSPKDYHRYHSPCDM

QILSATYTSGALYSVNEKHLERISNLYVKNERVSLKCQNEKGIFWLVFVGAQNVGKMRFNFDTSIQTNAK

ISHNFTRKYENLNFKKGEELGNFELGSTIVLISQKGILNFNLKAGQGIKFGEKIAD

>WP\_002866943.1 MULTISPECIES: flagellar hook-length control protein FliK [Campylobacter]

MINTQLASQIVNTQKNDLKVDNSASKDKTNLKDNPKEALAQALKQNLGLSKDASSEEILAKFVQNETGTK

LKELVNKLLDQINAQKNPDSPVLKQGKNLNLAPNFANELKTLSTELAKSDTFTQVLDRLNQILKPASEIK

NNNLAPLFKNSGVFLEAKLKDALNEELLPKSFHSLLSTIKGLSSEKLSVQIAQLANTNLSPKDTLKELKN

IINSSKNENKQILNQSSFKALLNLSSKLENFKNYISKNPSHAQEKITPIANKILKELNSIKNDFFKALNK

PENLMIKDPNILKQTATAFEKLENTLKNILGNQASKIQDKENILENLLSNKENMKEEKLNHNTKNQDEEK

HIKASKEETLTDDTKTDIKQDSKNEENSHAKETDIKEDENLDSDIKTHEEDTQDTKNDIQNNETENKPDN

DIKNSTPNQEKIKDGKQEKSKENIKENPKFYETKTENKTSINTNTNTSNPNTNNTQNLNNSQNIQSNNNQ

TMQNIFKNQEFIKQNIVKNLAFNVENLDLEQVQDLSKNLNNLSRRLNESLKELEPYTQNAKLNQAELKNL

EHKLNLSTKDLAQIKPKTEQDIAESLHHDVKSTLLQISNLAKNEGNEAVYNQANRLLAQIEINQLMSLAN

DSINTYLPFSWDDLNDSKIMFRRGKKDKFFAQIKLEFAKLGDLEILISLNNEKYIDINIMAENIEFRKTI

YENAHELKRNINKAGLLSANFFVGDIIRSKFDTRNMKNLDLEMGMDKKV

>WP\_002866937.1 MULTISPECIES: molybdopterin molybdenumtransferase MoeA [Campylobacter]

MKNIFETLKDLEDQISCLDESELISLEKAKDRILAKDLYARKNLPSFDNAALDGYAFNYTDINEALEIKG

TIFAGDKNFYTVAKNECYKIMTGAKMPKNADTILMLEDEYIEENKLIIKKAPKQYNAYRYKGEELKKGEI

LLQKGTKLNDKHIALLASQGLYKIEVIRKIRIGIFSSGNELKEPWQECDEESIYNTNALSLLTMLQNTSY

LGIIKDNFKSTKEALENTNFDLLITSGGASVGEADFMEKALDELGFTPLFKGLKARPARPTKLYRKGKNF

VLILPGNPMAAYLSCFIFAKKIIALLSGNLDNPLKFHATMGMDLKLKSGRNNLILGNLEKDIFTPFNENK

FGSGMILPLIKSEFLLISEENTSELKKGDEITLLKI

>WP\_002866936.1 MULTISPECIES: UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Campylobacter]

MTYLEIEGTNHLSGNVTISGAKNAALPLIVSSILAKNEVKINNVPNVADIKTLISLLENLGAKVNFQNNS

ALLNTNTLNQTIAKYDIVRKMRASILTLGPLLARFGHCEVSLPGGCAIGQRPIDLHLLALEKMGANIQIK

QGYVVASGNLKGNEILFDKITVTGSENIIMAAALAKGKTKLLNVAKEPEVVQLCEVLKDAGLEIKGIGTD

ELEIYGTDGELLEFKEFSVIPDRIEAGTYLCAGAITNSKITLDKVNATHLSAVLAKLHQMGFETLIAEDS

ITLLPAKEIKPVEIMTSEYPGFPTDMQAQFMALALKANGTSIIDERLFENRFMHVSELLRMGADIKLNGH

IATIVGGKELNAADVMATDLRASSALILAALAAKGTSKVHRIYHLDRGYENLEEKFKGLGAKITRLEE

>WP\_002866935.1 MULTISPECIES: hypothetical protein [Campylobacter]

MQINNSLNSLSQYVKVNSNEENQNSKNQEQNALAQDPAVEVNISKEAKEKSNTSNQNNSQAPAQALNAQN

NTQQDSSSDSEDKLTELTQKLAEIQAKIVELTAKMSKANEDQIKSIESQIATLNAQASTIQAQIQELQSQ

QA

>WP\_002866906.1 MULTISPECIES: ATP-dependent helicase [Campylobacter]

MPLSKLNNEQYLAATADFGRNLVIASAGTGKTSTIVARISYLLSKGVAPQKIMLLTFTNKASKEMIGRLG

KFFDKNITSKILAGTFHSTAYTLLRNADKNIALKQASELKTLLKSVYEKRTFRHLSDIKPYQSSYLYDLY

SLFQNKAHNQDFYTWFCQNYEDQSIYAEIYEDILKEYDNEKKRFNYVDFNDLLINLKELLKEEKYEFDEI

LVDEYQDTNTLQSSLIEAFHSKSLFCVGDYDQSIYAFNGADINIIGGFKDRFKDAKIFSLNKNYRSSRSI

LALANKVILNNERLYPKELIVTRNDEFKAPSLLTFEELFDQYQNIAKMILTSGVSLEEIAVIFRNNSSAD

GVEVALREQGIASVRKGSGSFFESLEVKAFSSMLALVVNPKDIMAFIHLVQYTKGVGGVLAKEIFDALLK

LGHGNLIKGFLDPDKNVNLQNHQKRNYQLGLFADLEELASETRFKFESEFDAHPILRLSKINDLCARNLE

KIYLFLKKAMEIKHSLTLVNLICENSFYREICEELATKRATNKAGQVDLLRKSENLEKIETKFNVLKELT

KNYSDIYKYYNFLTLGASEMSSGKGVNLLSVHASKGLEFDLVFVIDLAQGRFPNQKLMGMGGSLEEERRL

FYVAVTRAKNILYLSYAKYDKNKKTSFAPSRFLIEAGLCKGELTID

>WP\_002866905.1 MULTISPECIES: hypothetical protein [Campylobacter]

MNLKIFSIIVSILIAVIVILGGTYYYLFEYSKPKNYTLNTNTYTEQKSYTNNYDNSYSPSIQTNNSSSDI

NINNNTIQKQETNLLDENQSLNNDTFNTSISENNQSLNNDTNTSNNINTNENKQILDTDKEKLKQENKQA

KIEALKKEISKQQKILERERAVKKELQSNKSNKNKYLNTAREYLSIGKNSRLEPELSTENMKVYILDGKF

LSQYRINLLKDMLSVIQDNAKDYYLSIFVKMLPKGEMKLTIYNKEIIFSDMKKAYKYISLDRLSPYLNNP

KELNEHVAREEILERLKLQIKKDGKGSDFSKHIKSLKTGLNTAQYFFPFCEIIEISSIK

>WP\_002866899.1 MULTISPECIES: thymidylate kinase [Campylobacter]

MYVVFEGIDCVGKSTQISLLKEIYKDAIFTLEPGGTELGKHLREILLNKTHPISKRAELLLFLADRAQHF

EEILKTNQNKLIISDRSFISGMAYAKDFENDLLFALNSFALENFFPQKIIFLKGDANLIQERLSQKELDS

IEKRGIEYFLSVQDKLEKVLHFLKEKISIEILTLDAKESKEKLHQQIKEFLQ

>WP\_002866898.1 MULTISPECIES: histidine--tRNA ligase [Campylobacter]

MINALKGMKDLLDKDAYYYEKVIKTCEEVAKNYGFTFINTPHLELCTLFKRSVGESSDIVGKEMYEFIDK

GENHVCMRPEGTAGVVRAYIEKKLDKNTSVKRWFYHGSMFRYERPQKGRLREFHQFGVESFGNASVYEDA

SIILMLVEIFSRLDIKFKLLINSLGCLKCMPKYRENLIHFLDSKEGFCEDCLRRKNLNPIRVLDCKNEHC

QSLLNDAPLLNQNLCSSCQKDFEILQSVLKENGVDFEVDSKLVRGLDYYSKTAFEFISDEIGAKAAIAGG

GRYDRLIEYLDGKSGFGVGFAMGIERIIAILEQKEEKVQREGIYLCAMDEIYIQKLLHIATNLRKEHKVL

LSYEARKLAKHLENADKNNAEIFLCMGENEAQNESLFYKNLVKKEEKMIKISDLKKVL

>WP\_002866897.1 MULTISPECIES: serine O-acetyltransferase [Campylobacter]

MNFWGIIKEDFSQPKAQDPAFNSCIELFFNYPGVWAVVNYRFAHFFYIRNFKRIARMISGISQFLTGVDL

HPGAELGRRVFIDHANGVVIGQTAIIEDDVLIYQGVTLGGTSLEKGAKRHPTIKKGVIIGSGAKVLGNIT

IGENAKIGSNAVVVKDVGANLTAVGIPAYIIEERKNKNIRAIDANCDDKLEKLEKKILELENLILKQPES

QK

>WP\_002866894.1 MULTISPECIES: tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE [Campylobacter]

MSDTIAAIATAHGVGSISIVRLSGERALEFALKLSHKTKLTPRHATFTKLFNQNNEIIDEAIMIYFKAPY

SFTGEDIVEFQTHGGFSVSEVLLEELVSLGARLALAGEFSKRACLNGKMTPLKALNIQDLILSKSALAAK

IIARNMQGNLGELLEKIRTDLVKTLAFVETSIDYADDDLPSDLLEQISTMCEENSKILKEIYTLSQSKKG

LIEGFKIAIVGKPNVGKSSLLNALLSYERAIVSDIAGTTRDTIEESFKLGTHLLRIIDTAGIRESKDAIE

QIGVALSKKSLEDADIILAVFDASRVQDKEDEKIFDLLANTDKKIFWILNKSDLENVFKNTQNKNFIKLS

AQKDITLLKEELQNYLNSFDSEGIMVSSLDLINACKISSEAIFRAKGLLEESSLELFAFELNLAINELAR

FTKDFQRDEILDEMFGNFCLGK

>WP\_002866888.1 MULTISPECIES: META domain-containing protein [Campylobacter]

MKKTLQIALAAAFFAGCASTSVTSSTSKGNNELVQNQLFKIEKIIVNGKTFDPKNAEESPNISFENNKFY

GYSGCNRFFGSYQTKADTLQIEGDRVASTQMLCHPMDVMDFENSFLSNFKGTFKISNENGKLVLSNDEMK

IFFK

>WP\_002866887.1 MULTISPECIES: agamatine deiminase [Campylobacter]

MIKSIPEWSEQEYLMLSLPHEKSDWNPYLEEILQSYKEFVKAVSEFQKVLLIAPKQSDFENFKDIKNVEY

FKCDTNDTWIRDFGAIDIVENGRFKALDFTFNAWGNKFQSELDNAVNSKLFKEKFKEELKKVDFILEGGS

IDFNGEGVMLTSSHCLLNENRNSHLNKTQIDTKLKEIFGLKQIIWLENGFIKGDDTDHHIDTLARFIDKN

TIAHCICEDEEDEHYLPLQKMKEELKKTGFDLIELPIPKPLYYEGRRLGATYANFVFINNALIVPFYKDK

NDEIIAKRLSKALPNHKIIGVDARVFLRQNGSLHCSCQNRFKGLR

>WP\_002866885.1 MULTISPECIES: apolipoprotein acyltransferase [Campylobacter]

MKIALIQQKFHSNKEQTIKKTCEFIEEASKQGAELICLGELHQSEYFCQSENVDFFDYANDYEKDVKFWA

NIARKNQIVLITSLFEKRSAGLYHNTAVVFEKDGSIAGKYRKMHIPDDPCFYEKFYFTPGDLGFEPINTS

LGKLGVLICWDQWYPEAARIMALKGAEILIYPTAIGWFDKDKDEEKQRQLNAWLGVQKGHAIANGLYVVA

INRVGFEKDVSGVEEGIRFWGNSFVFGPQGEELCLLDSQNECVKIIEIDKKRSENVRRWWPFLRDRRIEY

FADLTKRFID

>WP\_002866882.1 MULTISPECIES: helicase [Campylobacter]

MLDKLEKILAYDNVFLSGGAGVGKSFLTNELIKSYRKQKKLAIALGSSALSAFNIGGVTLHSFFCLGYCD

DMMKLSALDRNQKQKEKLTKLKELLKTIELIIIDEISMVSASVFEMIGFRLKNSQFNGKILVVGDFFQLP

PVIKEKKETLFNHSYYAFSSFFWQDLNFKNIKLSQPKRTQNMEFYNYLSLIRQGFLDEKILSFFESLRID

YKELENLEDDYTLLCGINKKVNNINQEKLSKLETPLVCFKAQVKKEDKRIKDEELDSWVGSLNILEELNI

KIGARIIFCVNNWDKNYYNGEQGIIEDILYEEEKIYISIIKNNGMKILLEPYTFFMEELEQSGKDFVVNI

LASVTQFPIKLAYAITIHKSQGMSIEKLVCDIDHIFENGQLYVALSRATNPNTLKIYSTKKINFGFYFAN

ILKIDSNVIEFYKKHNFLDLEIQEQII

>WP\_002866881.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKIFLSVFLALSLNAQNLEIDKIRTDLYSKSGANVLKKVEISLEFDGNNLKENENKLIDAVNTVISGFF

YEDIFTEIGKNNFKKTLEKFLDKKYKIKLDDIYIISLSGVEKFDLEEFKRFLESTEAKEKGMGSEVKKAL

ENLEVPKTQVPGVEKIPTPSVPNLEAKQVEQLFKDSDEENKNDNGEINIDNLNTPKMTPDIEEKIKRDLI

ANPPQIFKENNASKPYHLPQTGYDIKLDENSTQN

>WP\_002866880.1 MULTISPECIES: outer membrane lipoprotein chaperone LolA [Campylobacter]

MKKTFLIFFIFIGQLFALDLNFNTFSSDFIQIVKSKNSTLSYSGHFILSKDQAYWSYDTPSKKEIYINKN

QVTIVEHDLEQVIFSHLDNIPNLNEIFKKASLIDKDKLVAKYDNINYTIKLNQEQIQSISYKDEFENDVI

INLNNQIKNPKINSDVFKAKIPQNYDIVR

>WP\_002866879.1 MULTISPECIES: protein translocase subunit SecA [Campylobacter]

MFLNTLKAVFGTKNDREVKKYFKRVAQINALEGKYQNLSDDELKAEFAKFKEQILSGEKNENDILNDVFA

IVRETGKRTLNMRHFDVQLIGGMVLHDGKIAEMKTGEGKTLVATLPVVLNAMSGKGVHVVTVNDYLAKRD

AEQMSAIYNFLGFSVGVILSSQNSDIEHKQAYDCDITYGTNNEFGFDYLRDNMKFSKVEKVQREHNFVIV

DEVDSILIDEARTPLIISGPTNRTLDGYIKANEVAKQMQKGEAVLPPAKPEGDFVVDEKNRNILITEAGI

AKAEKLFGVENLYSLDNAILAHQLDQALKAHNLFEKDVHYVLRNNEVIIVDEFTGRLSEGRRFSEGLHQA

LEAKENVKIQEESQTLADITFQNYFRMYNKLAGMTGTAQTEATEFSQIYSLDVISIPTNIPIKRQDKDDL

IYKTQNEKFKAVIEEIKKANSKGQPVLVGTASIERSEVFHNMLVKEKIPHHVLNAKNHEQEALIIQDAGK

KGAVTIATNMAGRGVDIKIDDEIRALGGLYIIGTERHESRRIDNQLRGRAGRQGDPGISRFYLSLEDNLL

RIFGGDRIKNIMDRLGIEEGESIESRIVTRAVENAQKKVESLHFESRKHLLEYDDVANEQRKTIYRYRNE

LLDENYDIRAKISQNIAEYSANVMNDYILDESGSNVNFENLKAKILYECSTQISEKDFENLSVIEMQDKL

SQILENSYNEKMSRLGIKELRNIERILYLQVLDNAWREHLYQMDILKTGIGLRGYNQKDPLVEYKKESYN

LFLELVNRIKFDSIKLLFSVQFNQEEVQNLENKANEENEKLLQSSVEMGASEDNLGEAEFKKVPRNAPCP

CGSGKKFKECHGKSGPKQGILA

>WP\_002866878.1 MULTISPECIES: ABC transporter permease [Campylobacter]

MNKSVLKYLLFKYLRFDKEQPFINLSMLLAFLGVCVGLCVLLVAMAIMNGFDKEFEKRFFVMNYPITILP

KFYAPVNDEFIDELRKTFPNLLFSPYISTQVVVKGDNRFEGGVLFGVNFNDEKKINEVVAKALRDENLSG

FDILVGSALIDEFGLHKNDKLSLIFSNLNPSGFSLVPQTKRFDVKARFTSGLAFYDKAYMYTDVDALKKV

LGMPKNPNYDGIHVYSDNAFKDVEKIKSYLKDDYAVVGWWEQNKNFFSALELEKRALFIVLMLIILVASL

NIVSSLLMIVMNRRSEIALLLALGASKNEVKKSFFALGMLIGGGGMIVGVVLAFFALWLLGNFDIVTLPA

DVYGTSKLPLDLSLMDFSLTIVGALIIIALSSFYPAKKATQINILDTLRNE

>WP\_002866876.1 MULTISPECIES: MBL fold hydrolase [Campylobacter]

MFNFITTLLKTNLYFLEEKTTSKSSNQTHIISLKQSDDEFLNLLFSFLVPQNDEDKNFIEKTRTKIKRNE

HNIALIKNPNFNALIDTGFLDTIDTLKEKLHTHKTDFKDITHIILTHAHPDHIGALMSEENLFPKAQILI

DKKEYDFWIKSDRQEIKNTLLKLKNIEFINHSKDLIFQNSGIKAIPAYGHTPGQNAIIIDDKIVFWGDLL

HLYDIQIPKPKIAIKFDIDQNEAIQTREKLLKEFKERKLKVIGTHVPFIEPKFLD

>WP\_002866875.1 MULTISPECIES: MFS transporter [Campylobacter]

MRKSKFGTKEIKILGLSSLGGTLEFYDFIIFVFFAEYIANVFFPKDMSEFWALLNTYGAFAAGYLARPLG

GIVMAHFGDKFGRKNMFMLSILLMVLPTFVLAFIPGYETLGFLAPVLLILIRIFQGIAIGGELPGAWVFV

REHCQEKQKAFFLSCLNSAMALGILLGSIVFLIINAFFSIEEIAAYAWRIAFFVGGIFGIISIYLRRFLQ

ETPVFKQMKKESSLSSFPLRDLFKEKDIVKNLFSSMMMTWVLTGCVIVLVLLMPKFMPSILNLSGVEGSY

LQILGILGIALGGAFMGYLVDKFGLFKICIFFSLTFVFFSFLYFYALYELKNLVLVCILYSIVCFLGGIN

VFAPILMSEVFRAKIRFSGISFSYNIAYAISGGITPQLVFWLNTLASKNENPFLYGMSIYMIFLALLAIC

AVFIVKDKIKF

>WP\_002866874.1 MULTISPECIES: multidrug ABC transporter permease/ATP-binding protein [Campylobacter]

MPFIIELLKQNKLKLISFLLFSFITSAVGVLTLVFINDYLLKNAQNIPIFYFIVLLLIFFISSTIVELGL

SIFGQNFIFKMQRRVVKQILDTPLLRVAKVGKARILASLGSDVRNISFGLLRLPDFLQSSILILCTSVYL

CYLSPQIFVLCVVWIMVIFITNNFLMMKVYQYFRKARENDDALQNNYQNILDGHKELLINRDRAKLYYED

EFENNARLKKKNSTLGNLFNNLSNNWTNVTLLALVGVEFYLALKFEWASVADATTIALSILFLRTPLVSM

IGSFPTLLLAKIALDKIAKLELDDYIEGFKKTHYISEWKKISFRNTQFAYEENFHLNPVNIELKKGELVF

LIGKNGSGKSTFCMLLTGLFKPSKGGIYVDDTLIDDKKLDEYRSLISAVFSDFHLFTKTLNKENFASEEK

IAFWLEFLELKDKTSVKDNELTLTKLSTGQKKRLAMLIALLEERDILVLDEWAADQDPVFRRFFYKKLLP

LLKEQGKTIFAITHDDAYFDSADRIFLAQNGEISELKGENIKELAKNLVEKFD

>WP\_002866873.1 MULTISPECIES: globin [Campylobacter]

MTKEQIQIIKDCVPILQKNGEDLTNEFYKIMFNDYPEVKPMFNMEKQISGEQPKALAMAILMAAKNIENL

ENMRSFVDKVAITHVNLGVKEEHYPIVGACLLKAIKNLLNPDEATLKAWEVAYSKIAEFYIDIEKKLYDK

>WP\_002866872.1 MULTISPECIES: dimethyl sulfoxide reductase subunit C [Campylobacter]

MTSFNHILSEMPLVLFTILAQAVIGLSLVYAPAFINGYKNYANLKSFGLALGIAMMVAFIPSFFHLNDIT

HIFNVLNRMGVFYANNEWHIGWMNNEILFVSLVCALGFLLYLKTSNWVFYLTLICGILGLFFMSGAYGSM

QESVPTWDFKITLLYFFASAIFLGAIVYYCFFENSEHERKMSFFTGLIGIGLLSTAIVLQTLHVGQTWIM

GLVNPFELLGGTYDWFISLSFAFLGLGIVTWYLHNYLHEKFKSKFFAYFALLCAFLGVFTTRMLFYGLIS

TQIMLGHS

>WP\_002866868.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MKVRNLNISLKNNLLLKDINLDIKTGKTLMILGQSGVGKSLLGKALVRLLDSNFTISFDELSFHNSCIFN

FNKEELRNFRSKVALVLQDAELSLYPYLDIGNLCHLVLKTHTKLKQKERKDYAFSYFQKLGFENLDRLWH

SYANELSLGMARRVSLALALLNQPQILICDEITASLDKENASKIISILEELKNTTALVCITHDLNLVNSL

ADEILMLEKNSSNLYSLNEFLRYYNA

>WP\_002866864.1 MULTISPECIES: NADH-quinone oxidoreductase subunit D [Campylobacter]

MQIPSKLKPYYENIAFEQEDSKMIINLGPQHPSAHGNLRLILELDGEQVVKARPCIGYMHRGMEKMAENM

IYQEFIPTTDRMDYIAASANNYAYCAAVEKLCGLEIPRRAAVIRMILLELNRIASHLLWLATHALDIGAM

SVFLYCFREREYVLDLIEKYCGARLTHSSMRIGGVMLDLPENYLEEMLVFCDKFPNDLKDYEDLLDDNRI

WRLRTENVGVVTKEQALNWGCTGVMLRGSGIKYDIRKEEPYLLYNEVEFGVPYATQGDSYARYKVYMQEF

RESLKILRQCATLYKDTPPEILATHPEYVSASKEQILTQNYSLMQHFVLITQGLKPPKGEVYVPTESPKG

ELGFFIHSDGTGRPYRLKARTPSYWHCAFFEEMLVGTYLADVVAIMGNVNIVLGEIDR

>WP\_002866861.1 MULTISPECIES: NADH-quinone oxidoreductase subunit H [Campylobacter]

MSDFAFFALEALIKCIIIIAIFASLAGLATYAERKVLAYFQRRIGPDMVGPFGLIQLVADMIKLFTKEDI

IPSNSQKFIFAIAPLISAICAFVSLAAIPMLPEFTLFGRVIQPIVADINVALLFVIGTSGLCFYAVFLGG

LASNNKWSILGAARGLVAIISYESVGALALIAIVMLVGSFSLVDINNYQSDGFFSWLIFKQPLAFVLFII

ALFIETNRTPLCLTENDAEIVAGYGTEYSGLRWGMFFIGEYASMIAGAILVTLLFLGGFNSFWIIPGWIM

MIVKSSFIFFWYFWARAAFPQLRPDQVMKMCYLILIPLAVLNLLITALAVLL

>WP\_002866855.1 MULTISPECIES: tetratricopeptide repeat family protein [Campylobacter]

MRILFLILLSFLNAFAFELVLNTGRENNQAFAVLHASNDLEFTCQKFITEAKVHFECDIAGMVDNKLKDQ

SFSAFDLKFIQEAQKIKMIILPKIQARMFDTSQNIYIDKELSSSSSHKSKAFTFIFTPELVRVKDYDGLD

FNINFPHESLPYVGALDLNSDPVVIPQSADINTYLRIKKEYDKANYNQVVIDAQNAINRYRGSIFASEFI

LYKLRAQNKLYTQDPSMRDQQILEKMIDDAKNWTRTFTSDKNFSEVLHIMLRTYIALAQRADVEYTMSIL

DNEQPNNYFTQLSKLDYADYIYNLNEKEKAVNIYENTYFNTKNLDLAARAAMSLAKNLLSNEQVNKAIEY

INTILKANPEYFGKDIPRSLELAKLFNQKGQFDISASIYEDAFAKMSKLDPSYEETLKDLALVLSHTNRS

SDAKKYLDLYMDDYLDGKYLDEIKKASDEVFFALGDNNASFLHQRYTDLMKQYANKDENIANKALDEDVA

LYYKEGNFSAILAYKDLIESKKIPNATQFLEKAAINDLKNAIKADNCINAANIFMRFSAYDIGQKIENKK

QMLACLIRTSNVEQALDYIDKNYNEDSIFYGLQKASILFDNKQYPQVIKISKDIANSRILKSDDENFKAY

YLQFLSLLRLNDYNQAIKILQILESFPMNFSMVEAYDALLSYANDHNMQTTILTYAPKAIDYQNFKGINL

FSPNLEFIYLDALTKINKNEESLAVLTDLLKLKLSDEDRARALYIQALTYERMQNVQAEKESLKQCLEIK

SASNWQNLCKSKNQILNQ

>WP\_002866838.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKLGLALAALVALNVSAFAGVITIHDSNLVKVSGGDDTYAKIALDNAKEGMKNQFNTDNLEIYAIESIK

KDDPEHYNVIQRGSFKVMKQEIAKGKTVYYNEFLVVDRKTNWAAEWDIECDHLDRPIKLSNNVNCRSGIS

TRRYNFK

>WP\_002866837.1 MULTISPECIES: DNA ligase [Campylobacter]

MRFIFLICCACLVFANEILLLSKFDKQDFNSKDFNAYLMSEKLDGVRGIWDGKYLKTRQNYKIKTPDFFT

KNFPPFAIDGELWIARNKFDEISALIRSGDSNLTLWKEVTYNIFDVPNACEEFQISTCTLKNRLAVLEEY

LQKYPSAYIKIIPQIPVENQNNLNQFYESIIKNQGEGIVIRKNLSPYEKGRSKNAMKLKPYDDAECELVG

FRKGKGKFENQVGALLCKMPNGQIIKIGSGLKDEDRKNPPKIGSIVTYKFNGLTKNSLPRFPVFLRIRDE

NP

>WP\_002866835.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKITIAHSPDADDIFMYMAIKFGWIGNDFAYENTALDIQTLNEFALKNEFDATAISFGLYPLIASEYAL

LRTAVSFGEGYGPKLIKKKDTHLKRNFKVALSGANTTNALIFRMKYPEARIIYKNFLDIENAVLSGEVDA

GVLIHESILEFDQSLCVEAELWDIWLEFAKENLPLPLGGMALRRSLPLSDAIKIERDLTYAVKIADANRK

ILAPMLMERKLIRVNEEKLDTYLNLYANKNSISMNQTQLLAVDTLFKLGYDYKFYDKIIHVNDYLIPSEY

EEARNS

>WP\_002866826.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MLKINNLNKKFGNNEILKNINLEIKEGEFLTLVGESGSGKSTLLRIIAGLEEPSQGEILNLNNQDISKQN

PRDRNFAMVFQSYALYPHLSVRENLAMPIKARAKFIHKLPLASFYIKSYKEFKTHLEEKIEQVATKLKIT

HLLDKKPKQLSGGQCQRVALGRAIIREPNIFLMDEPLSNLDAKLRIHTRAELSAMHRELNKTFIYVTHDQ

SEAMTMSDRIAFLVDGELLQVASPDEMYNNPNHLKVAQFIGTPTINTLCVELKSYGFALINKNLSKHKSL

AIRAENCFIDPHSQIKAKIYNIENMGNEYLIYTKLLKNDNNFILSLNTQEGKKLQLDSVVGINFDYSKAF

IFDEEGKRMDIKLYNLSFAA

>WP\_002866824.1 MULTISPECIES: carbohydrate ABC transporter permease [Campylobacter]

MFRILRHLILGILSLFFIFPFVWMVITSFKPENEIFSNAFHFFPQNFTLIENYTKAFKENDLLHFLFNGF

FVCFAILLIQIIIAYPCAYALSKYKFKGQKFLLVIIVCSLLIPTQAICVPWYILMYYFGVLDSYLALILP

FSISVFGIFLIRQFINCIPNDIIYAARMDGLNEFSILCKIILPLTTPALISFGIFSIVAHWNDYFWPLIA

VSSPQYFTPTLGVISFKNNEAGTDYGTLMAASTIVVAPLIIGFLLAQKRFIQGIANTGIK

>WP\_002866821.1 MULTISPECIES: HAD family hydrolase [Campylobacter]

MIFFDFDGVLVDSLKLWEQACQFSAKKLGFKGIFPQKPYAKLNPVAHKEIGRILGFNPLEFEKIADEYFL

EHIHTLVFFDKTKELLKDLSLDFKLSILSASNENLVRILLEKEQILKYFTNLHCTSSIPKAQTLKKFKQN

HSIMIGDCISDIEAALEADVYSIGVLWGWQDKIMLEKANILVNNHAQLKNAIRSFYEIHPFN

>WP\_002866819.1 MULTISPECIES: preprotein translocase subunit SecY [Campylobacter]

MNRALTNKILITLAFLFAYRVLAYVPVPGVNADVIAEFFNNNQNNALGLFNVFSGGAAERFSIISLGIMP

YITASIIMELLAATFPNIGKMKKERDSMQKYMQIIRYATIVITLVQSIGVAIGLQSLHGRGGAGAIMVED

LNMFIALCAISMLAGTMLLMWLGEQITQRGIGNGISLIIFAGIVSGIPRAISGTVGQINSGEMNFLTAFA

IFALILITIGVIIYVELGERRIPISYSRKVVMQNQNKRIMNYIPIKLNLSGVIPPIFASAILMFPTTILQ

TSTNPYLQAINDFLNPNGYLFHVLTFLFVIFFAYFYASIVFNAKDIAENLKKQGGFIPGIRPGEGTSSYL

NEVASRLTLSGSIYLGLVATLPWVLVKFMGVPFHFGGTSVLIVVQVALDTMRKIEAQIYMSKYQTLSAVG

L

>WP\_002866814.1 MULTISPECIES: 23S rRNA (adenine(2503)-C(2))-methyltransferase RlmN [Campylobacter]

MKELVNILDFLPEELGEKIKPMFRVKQIYQWIYQKYANNFSDMSSLPKYLRLELAQNFHFSPVKCVKNEQ

SKDGSIKYLFELVDGLRVESVLLPMKEEKIDAEGKRISHARYTICVSSQVGCKSGCSFCLTAKGGLKRNL

SAGEIVGQILWIKKQNNIPYERRVNIVYMGMGEPLDNLKNVSKAVKILAQNDGLAISPRRQTISTSGLAK

QIKELGQMNLGVLLAISLHAVNDGLRTELMPINKAYNIAAIMDAVREFPIDQRKRVMFEYLLIDGINDKL

EHAKELVKLLNGIKAKVNLILFNPHEGSLYKRPSLENAIKFQDLLSSKGVTCTIRESKGLDISAACGQLK

ERAKEQ

>WP\_002866811.1 MULTISPECIES: LPS biosynthesis protein [Campylobacter]

MENNINNILLKLDKNRHFCFLKDNINYENKKDIAIFRGAVYQKHRKEFFDSYFGRTFCDIGDTSKQPSQW

EKNFLNKKEQMKYKFIISLEGNDVASNLKWAMNSNSLVLAPKITCETWFMEGTLKPNYHFALIDNENLSA

VIEYFKSRPKDALEIINNAHQYIKKFLDKKKEFHIGILVLTKYFYYSRQLELNKKRDILELIK

>WP\_002866809.1 MULTISPECIES: 3-isopropylmalate dehydrogenase [Campylobacter]

MKTYKVAVLAGDGIGPLVMKEALKILTFIAQKYNFSFEFNEAKIGGASIDAHGVALSDETLKLCEQSDAI

LFGSVGGPKWDNLPIDQRPERASLLPLRKHFNLFANLRPCKIYESLTHTSPLKNEIIQKGVDILCVRELT

GGIYFGKQDLGKESAYDTEIYTKKEIERIAHIAFESARIRKKKVHLIDKANVLASSILWREVVANVAKDY

QDINLEYMYVDNAAMQIVKNPSIFDVMLCSNLFGDILSDELAAINGSLGLLSSASLNDKGFGLYEPAGGS

APDIAHLNIANPIAQILSAALMLKYSFKEEQAAQDIENAISLALAQGKMTKDLNAKSYLNTDEMGDCILE

ILKENDNG

>WP\_002866808.1 MULTISPECIES: 2-isopropylmalate synthase [Campylobacter]

MKDNKIIIFDTTLRDGEQALGSSLGINQKLQIALALENLGVDVIEAGFPVSSQGDFKAVQKIASKVKNST

ICALSRVLDKDIDMAYEALKVAKHFRIHTFIATSTLHMQDKLKKDFDEILSMAKRAIIRARSYTDDVEFS

CEDAGRTPIDNLCFMVENAIKAGAKTINIPDTVGYTLPSEFANIIKILFNKVPNIDKAIISVHCHNDLGM

ATGNSLSAILQGARQIECTINGLGERAGNCALEEVVMAIKTRKDYLKGFYTDIKCENIFKTSKLVSAITN

ESIPSHKAIVGSNAFSHSSGIHQDGVLKNRQTYEIISPSAIGIHENRMLMTARSGRAMIKTCLENLGYDE

NTYNLDDVYERFLRLADKKGQVYDYDLEALMFLSYENEEENKFILEKLSVISGNIPTACVCMRIKEELKT

EACTGNGPVEAVFNCIARITNLKPALKAYSINAKSSGVDAQGQVDVDLEFKGRKFHGKGISTDVIEASAQ

AFVSAYNAIYRSLKVEERKMA

>WP\_002866803.1 MULTISPECIES: molybdopterin containing oxidoreductase [Campylobacter]

MKQNNQKEDRRDFLKNIGFGLLGISVLSNFSFENFLGSKALAKELPDFKIEGKKDLIYHGEKPLTAETEI

YALDSDFTKPENFFVRNNGLPPSLETIKERLHKGWTLEIDGESIINKKSYTIEDLKKKFKTYTYALTVEC

GGNGRSEVIPSTKGTQWGYGAVACGRWTGVRLKDILKDCGIKNDAVYIGYYGIDTKLNGEETSPISRGVP

ISKALQDETLIAWAYEGKDIPLVNGYPLRLVCGGYPASTSGKWLYKISVRNKIHDGEKMEGSYKVPVNPV

KPGDFNYKGEMKIIESMPIRSVITNIKNGSEIKANKKFEVRGKAWAGELEVSEVYVSNDYGVTWTKAKVE

KPLNRLAWQKWSAQISIPTKGYYEIWARAIDSQGNSQPMVLAQWNPGGYINNACHRVNVYGV

>WP\_002866800.1 MULTISPECIES: glutamate synthase subunit beta [Campylobacter]

MGNARGFLDFKRMDFKKIAPKERVLNFKEFTIPLDKKEQEIQGGRCMDCGVAFCHTGVMSEGKDVGCPLN

NLIPEWNDLIYRSLWEEAYERLDLTNPFPEFTGRVCPAPCEDSCVCAINGVSVSIKNNELSIIENAFKEN

LVRVNKPKQYNGKKIAIIGSGPAGLACANTLNSLGYKVSVFERSDKIGGLLMYGIPDMKLDKSIVQRRVD

LLKKSGIEFKVNENIDSKDKVSKLLKEFDALVLCTGASKPIDLDIEGRKLKGVEFALDFLTQNTKTLLKT

GKGADTAKGKNVLVIGSGDTSVDCIAVATRQGAKSIVRFERSPKRPLQRSQNNPWPLKADIFTTDYGLEE

AIAVYGKDPREYQKMTKKFLGKTHVEGVEANDLKREFKEGKAINVEIPNSKKTYKADLVLLAMGFSGCEE

AIAKNFGVKLDEKNNISTENFQTTHKKIFACGDARKGQSLVVWAIKDGIECALSLHQNLAK

>WP\_002866798.1 MULTISPECIES: DUF655 domain-containing protein [Campylobacter]

MKKLLFLFFALTAFLFGAVNINTATLKELKSLNGIGEAKAKSILEYRKEANFTSIDDLKKVKGIGDKLFE

KIKNDITVE

>WP\_002866793.1 MULTISPECIES: 7-cyano-7-deazaguanine synthase [Campylobacter]

MSKKALCIISGGMDSTLCAYLAKKEGYEIIALHFDYEQRTQEKERECFKQICKALKVEKSYILDVSFIKD

IGGNALTDKSIDIPKNELCISDTPPITYVPFRNGIFLSIAGSLAEKENCESIFIGVVEEDGSGYPDCTDE

FIQKAQEFINEGTSKNFKVYIKTPLVRLNKAKIVELALKENVPLELTWSCYESEDEACGECDSCLLRLRG

FEKVGFKDKIKYKS

>WP\_002866792.1 MULTISPECIES: disulfide bond formation protein B [Campylobacter]

MNEINKTKNFYTLMCLAGFLIILLPVGIANFVFGYMLGDSPCTLCWGQREAMIFIGVMALFIVRYGMKGK

YLAALLIMTAVGLYQSFAHYGNHAHRDLDQGFGLAVFGIHTYFWAEVVFWAVVLLLGVIFAFAPKFNAFE

TELNGEKFRKYTKFSFAAVLISTIIVASNVFQAFVSTGIPPYVGQGDPVRFSLNPKYIIWSKEGWNGLWQ

NISFLGKRDVKAPDYAFAPASEKLGIKFDNDINNAPFAKINDELKITNEQTINFDKAINTLDYINNEFVA

SSKWDVAFLDNNFSVKEGFELDPYFSASIDPIIGIIPYMNDKFILMGSNKSFLRFAKNPNASEEDIAKQY

ADFVKGNDKFKGQGEGLGRGRLDTVRAKFNHVASMSTDGNYLYLATVPNNKDAKTFVISKVSLKDRVLSG

EFTPKANLKEGKTLGDLYVTSMTFKDGEIYALSKNHNVIAVIDPVKEEVVKTIAFPSSITNARSIFFKDG

KINILSYQDGANKLYTLN

>WP\_002866789.1 MULTISPECIES: FAA hydrolase family protein [Campylobacter]

MKFVNFIQGQKHNLGVLNSSGKIVSFTDLGIETNDMNEFIIYFDKFKHKLTDLDSKIAYEIPKENYLAPI

IEPRQDIICLGINFLDHAKESAKFKGEKFEEREYPVYFGKRCNQATPPFGDIPLHADVTSQLDYECELAF

ILSKDAYKIKAEDAKDYIFGYTIINEISARELQKRHKQFYRAKSLEGSTIMGPYITSVDEISYPPKLQLQ

SYVNDELRQNSNTQLFIFDIAYVLEELSAGMLLKAGSIISMGTPSGVGMGLNPPTFLKSGDKVRCVIENL

GELCNKIK

>WP\_002866787.1 MULTISPECIES: adenylosuccinate lyase [Campylobacter]

MVERYSREIMAKKWDMQAKYDAWLKVELAAVKAWNKLGLIDDTDCEKILKNAKFDIARIDEIEKTTKHDV

IAFLTSVSESLGEESRFVHYAMTSSDCIDTAVALQIKESLELILEDVSLLLEAIKKRALEHKNTLMVGRS

HGIHGEPITFGLVLAIWYDEISHAKELLEHAKEVISYGKISGAMGNFAHAPLEFEEEVCKNLGLKAAPVS

NQVIQRDRYAQVISAIAILASSCEQIAVAIRHFQRTEVYEAEEYFSVGQKGSSAMPHKRNPVLSENITGL

CRVLRSFVTPALENVALWHERDISHSSVERFILPDAFITADFMLMRLTNLIDKLLVYPENMMKNLNLTGG

LVFSGRVLLELPFKGISREEAYKIVQRNAMKVWADLQNGKAAINEKNESLFLLALLSDEDLRKSLSEEDI

RKCFDYNYYTKNVDAIFKRTFK

>WP\_002866786.1 MULTISPECIES: sodium:dicarboxylate symporter [Campylobacter]

MDKQFFKDFLMLSQAHTIATLAILCVVFYALKKMRDIKINFSLRMLFALLMGLGFGFALQYLANFPDAKE

ASNILWYSETKHWFAFVSSVFVAFIKMLVVPLVSICIIKVIIEIDKNIKISSLLGISLFWILFSTAIAAT

LGIFLGYSFDLGSNFAIHEGDKQIREIQTFSNIILGLIPSNIITAINKENIIAIVIFSFFIGISAKKISK

KEEYEQAFKSFHNFILTFYNIMMNMTATVIRFMPYAVVCMMANVLLSNGFEAIKTAGLFIMLIYMAMFIM

FGVHFLLLASQGLNPIKYVKKAFPVWLFAFSSRSSLGTLPMTTSTLQNKFGVNSAIANFVASIGTTTGLN

GCAGYFPALAAVFVAFATHTHIDFTFALMIVLVAVIGSLGIAGVPGSATMAASIMLAGIGFGNNFVMLSL

ILAIDPIIDMARTASNVSGAMTSALCTAKNLKALDKEIYNS

>WP\_002866785.1 MULTISPECIES: CTP synthetase [Campylobacter]

MKQTKYIFVTGGVLSSLGKGIAAASIATLLKNSGLKVSILKADPYINVDPGTMSPFEHGEVFVTDDGAET

DLDLGHYERFLDESLSQDNNFTTGRVYQSVIEKERRGEYLGKTIQVIPHIVGEIKDRIKKAGEGKDILIV

EIGGTVGDIEGLPFLEAIRALRLEVGKNNAMNIHLTLVPFIKAAGELKTKPTQHSVGELRRIGISPDMII

CRSEKALDRDLKDKIAISCGVEKNCVIESVDAASIYQIPLNFLKQDILSPIAEILDLKNLKPNMENWDSL

VKRVIAPSNEVKIAFVGKYVDLKESYKSLTEAIIHAGAALDTKVELKWVDSEKLENMESAEVFKDVSGIL

VAGGFGYRGVEGKIKAIQYARENKIPFLGICLGMQLALVEFARNVLKLKDANSSEFDEKCQNPVVYLIDE

FMDTNGEKQIRTAKTPLGGTMRLGAYKCDIKEKSLLAKVYNEAKSVKERHRHRYEANPKYRVDFEKHGLI

VSGESKGLIEAVELNCHPFFLAVQFHPEFTSRLEHVNPVICGFIKAAINYEDN

>WP\_002866780.1 MULTISPECIES: Holliday junction branch migration DNA helicase RuvB [Campylobacter]

MDRIVEIEKYSFDETYETSLRPSNFDGYIGQESIKKNLNVFIAAAKKRNECLDHILFSGPAGLGKTTLAN

IISYEMGANIKTTAAPMIEKSGDLAAILTNLSEGDILFIDEIHRLSPAIEEVLYPAMEDYRLDIIIGSGP

AAQTIKIDLPKFTLIGATTRAGMLSNPLRDRFGMQFRLEFYKDSELALILQKAALKLNKTCEEKAALEIA

KRSRSTPRIALRLLKRVRDFADVNDEEIITEKRANEALNSLGVNELGFDAMDLRYLELLTAAKQKPIGLA

SIAAALSEDENTIEDVIEPYLLANGYIERTAKGRIASAKSYSALKLNYEKTLFEE

>WP\_002866777.1 MULTISPECIES: ammonia-forming cytochrome c nitrite reductase subunit c552 [Campylobacter]

MKKNILRLGIVVLVLLIAGVLWLNNDINQKKEDEANKNAIAANADFSLLSDDDPNFEKWGKVFPEQLKMY

LTVEKEEPKATEFGGNLAYSKLIRFPQLTILWAGYPFSLDFNEERGHFWVQIDQMKTARNNKDFLNAHGL

AAFKGQPAACMNCHSGWTPWLIKNVAKGDFTAFNSTNYWTMIKNIPAVDGIVENSPEHAGPHGGKRMGVT

CADCHNPNDMSLRLTRPAAINALVSRGYEKDPVQGVKATREEMRTLVCSQCHVEYYFKPTGEKVKVMGET

IVDDSSKKWWNGTQKNYDEYEFWRDGNKAKEIETDGIVLTFPWSEWKKGQPFRIEMLDDYYDKVRGVFGA

DFTHKLTGAQIIKIQHPESELYSGGVHAANGVSCVDCHMPYVREGAKKVTQHNITSPLRDINSACKSCHK

QSEDYLKAQVLDIQNSVAHDQRTAEYAIVSLIMDTKKLRDELGNMEKFQSDGKADTKKISEELKEVLELH

RKAQMRADFVNAENSTGFHNPREASRMLLQAVDMARMGQTKLVEIAAANGIKDFKTSNLGFEDIQKFNPG

ELYYKVDVNNHKAGERYYADEKDVNGNPPKELLEHDKELAPYNYQVIDKK

>WP\_002866775.1 MULTISPECIES: type II toxin-antitoxin system RelE/ParE family toxin [Campylobacter]

MKIVPTPKFKNELRHIVNFIKLDSSFYAKEFLNDINSICKNLSFMPYKNRKSLSFDNENIRDLIFKGYII

PYLIDKSKNEIVILGIYKSNLWD

>WP\_002866772.1 MULTISPECIES: iron ABC transporter ATP-binding protein [Campylobacter]

MIKLKNITKFYDNKAIISDLSLDFHKGKITSIIGANGAGKSTLLALASRLIKPSSGEIYIDGMKLKDYKE

QILAQKISILKQQNNINLRLKVEELVAFGRFPHSQGRLNANDKIKINEALEYMGLSNLRNEFLDTLSGGQ

KQRAFIAMIIAQDTEFIMFDEPLNNLDMKHSVQIMQLMKNLVKDFNKSIAVVLHDINFASIYSDEIIALK

DGKLLKQGSKDEIINQENLKQIYDMDIPVSQIDGKKICIYF

>WP\_002866771.1 MULTISPECIES: iron ABC transporter permease [Campylobacter]

MRKKMLILSFLTLGMIGIFILVGLNGFDEYALKSRFLQIAAIIIVAICIAVSTVIFQTLCNNKILTPAII

GLDSLYMLLQSALIFSFGAANLSVYKNDINFLITLVCMVVFSLGLYKILFSSDRSIYLIMLLGLVFGTLF

STLSSFFEVLIDPDEFMVIQGRMFASFDNIAFDILILAYIISFLSFIWIFRYMKFLDPLNLGKDLAINLG

INYQKISKQLMIIIAILTSISTALVGPITFLGLLVANITYELFKTAKHSILLSACILISILALLGGVFFV

SRVFDYNATISVVINFLGGIYFIYLVLKGNKL

>WP\_002866753.1 MULTISPECIES: ABC transporter substrate-binding protein [Campylobacter]

MKKIILFILSLGIFYTFTQAKNLEQEQNTSSNLVSVSIAPQAFFVKKIAADTLDVNVILPPNSNEHNFEF

KPSTMKKLEKSDIYFTIGLEFEKVFTDKFKQNFPKLQVVNMQKNIALIQTHDIHEHSHEHEEHEHFDPHT

WLDPILVQTMALNIYDALIQKYPQNKNLYKQNLDKFLAELDSLNLQIASKLEKLKNREFVVYHPSWTYFA

KRYNLTQIPVEILGKEPKSKDLQKLITLMKDKNLKVIFVQNGFPENAAKTLAKECDAKIYKIDHLSYDWE

NELLKTADAFSRNL

>WP\_002866752.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MLFFEISNLNYAYDNEIILKNINLSYDNKDFLSIIGPNGAGKSTLVKLILGLLKSKNEIHFKTLQRKEIG

YVPQHTLANPNFCPRVLEIVLMGLVSKKIFGFYGKKDKEKAMQALKSVGMEKFWNKTIDSLSGGQRQRVF

IARALASECKMLILDEPTASVDNKSAIQIFELLSSLHQKGMGILLICHDINLVLAYSDKIAHLNKELFLH

TNTKEKEKSSFLKHLYENHSHFCDVEMSLNTCFCDEENCDSKKLCEQEFTRRNLKKTEFKKENFCLKFSK

ENNA

>WP\_002866742.1 MULTISPECIES: M23 family peptidase [Campylobacter]

MAKRKGKTYLSVLILVLIAILIFFISRLSIFEKNPPQILMPDVVYTDLKKPILVHVKDDESSIKNVQIIL

HKDDNTSAMVIADEKISNLKDITLQVALPKFGYKENVKSFVLEVIAKDSSFWNFFSGNEARKQIAVLVDN

TAPKINIISNSYQIEQGGAGAVVFKADDANLDKVYIETNKGKIFKVTPYVKEGYYAALIAWDARDEEFRA

FVIATDKAGNISKERIRYYFVNRKYRVSNINLTDKFLDGKIENLANQYAPKDNNLNRYEKFKFVNETLRN

SNEKLIHEITSKVPEEKIDNFDLNLFLPLKNGMKVADFADHRYYSYNGQFVSDSYHMGLDLASVAQAPII

SNNAGKVVFAAENGIYGLNLIVYHGFGVYSLYGHCSSKNVDLDEMINKQSIIGKTGTSGLALGDHLHFGV

LVQGVETRPEQWQDKKWIENNIYNVLNDGKKIILGKN

>WP\_002866728.1 MULTISPECIES: ATP synthase epsilon chain [Campylobacter]

MNDLINFEIVTPLGVIYQGEVKSVTLPGSEGEFGVLKGHATLVSSLKSGVIDIEKADLNHELIAIDAGHA

KVDEDKICVLAKGAVWVCGSDESEIEKNLAQAKDLIKSMSSDNAALAATFSKLDNARMH

>WP\_002866727.1 MULTISPECIES: ATP synthase subunit gamma [Campylobacter]

MSNLKEIKRKIKSVHNTQKTTNAMKLVSTAKLKKAEEAAKRSKIYAQKIDEILSEISFQINKIVHNEDDV

RLSLFHKKEQIKTVDLIFITADKGLCGGFNIKTLKAVSEMLKEYEAKNINIRLRAIGKTGIEYFNFQKIE

LLEKYFHLSSSPDYEKACEVIHAAVDDFLNGNTDEVILVHNGYKNMITQELKINHLIPVEPKSIEQTHNS

LLELEPEGTELLEDLMKTYFEYNMYYALIDSLAAEHSARMQAMDNATNNAKARVKQLNLAYNKARQESIT

TELIEIISGVESMK

>WP\_002866726.1 MULTISPECIES: ATP synthase subunit delta [Campylobacter]

MENIIARRYAKAIASRADINDFYQNLCILNSAFVLPKFKNIIESNEIKKERKMEFLDSFFDIKNSSFQNF

LRLLIENSRLEYIPQIVKELERQKAFKENIFVGIVYSKEKLSQENLKDLEVKLNKKFDANIKLNNKISQD

DSVKIELEELGYELSFSMKALQNKLNEYILKII

>WP\_002866723.1 MULTISPECIES: methionyl-tRNA formyltransferase [Campylobacter]

MKKIIFMGTPSYATCILKALVENENFKLVALFTQPDKAVGRKQILTPSDTKAFLSQNYPSIPIFTPSSLK

DENIIREIKDLNPDFIVVAAYGKILPKAILDLAPCVNLHASLLPKYRGASPIQSAILNKDEKSGVCTMLM

EEGLDTGAVLESLECDIKDKNSSEVFELLANLAAKLILSTLLNFDKIIPKKQEESLATLCRKIKKEDGLI

NLQNARELYQKYLAFTPWPGVFLENGLKFLELELVDELKQNARMGEILELEKESFLLACKQGVLRIKKLQ

ESGKKALDGRTYLNGKRLKSEDSLC

>WP\_002866722.1 MULTISPECIES: GTPase ObgE [Campylobacter]

MFIDSVKITLASGDGGKGAVSFRREKHVPLGGPDGGDGGNGGDIIFVCDNNTHTLVNFKGKRELRAQNGA

GGMGRNKNGKKGENLELIVPEGTQVIDAQTNEILLDLTKEGQRELFLKGGKGGLGNTHFKHATNQRPDYA

QPGIKGESRLVRLELKLIADVGLVGFPNVGKSTLISVVSNAKPEIANYEFTTLTPKLGLVDVDEYNSFVM

ADIPGIIEGASGGKGLGLAFLKHIERTSFLLFVLDPMRQMPLKEQFIVLRKELEKFSNELFGRKFGIMIS

KSDSVNLGEEFAEQITLNINELENYLKEINNPQSFLIKVSSLEKTGLKELKFMLLEEIKTLRNNK

>WP\_002866721.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKIIKILFLGLFLSLSLNAKVITTTSTKSSTGEGTGLTREDAINNAIIEAIGKMSGVSINSLKKSNTSVS

TDNSGSNIQDNYSEQISKATKGRADTYEINSVEQDANGKYTANVTIFKTTTTKKYQAPGLSADNRRSITV

FDSTPDAAKRGIGSALQQKIISDLLQSRKFNVLDRDSSGYYEMEKALIKSGDAASDEVYKLKNVLATDYI

LLFSISGLEGKQKTSNLTGKSKTEIEVIVDYRVLLFATRQIKFSNTLSMKVNLKDNSLSANEAALKQIAN

RIAGDILNAIYPLKVASVENNEVVFSQSLNQGDVYECFALGKAIKDTYTKENIGRVENKTGSIEITRTSP

KLSYAKITEGGVKVGDICRPLIGSNSGNGYTIGRDANYQTEEGGGVNLGF

>WP\_002866720.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKILFIGSLVMASLLYAQGSQPVEITQQDINTQNEMSDASTKDITPKSIEDFFEEFADNFGIEYGITKD

GKTFYTGKSTVAVNDTDPQFAQALQNAYQKAMLNLQSEFIRDAFGRIATSKIQNYEADNSTNAKEFDELP

KGDKVDQILNKLTQLAGAQLDKALKDLGIDTNSLSEDRKKTLLKQEFLNKTMTNAIGSMSGLVPVQTIVT

QRRGEYDVGVIAVISNKTRQLAKDMALARQSAIKGKGKAISEYLPKDTKGFLNEYGIRLVYDENGAPIIL

SYGNWGYVADPSNAKKTNILEDRAKETALTMADAAIIEFINTNLSLKDERTTGDTYEEIIKQSINVNDSS

TQEQTQNITNIIDKVNSKIKASASGKIRGIRTLKKWSYTSENGIEHVGAVRFYSYENLANTNEALNSKSN

TTKNEAKKSSSIQRSSNVVNSMDDF

>WP\_002866719.1 MULTISPECIES: DUF1425 domain-containing protein [Campylobacter]

MKKNILFILMFLLSACAPSYQINSNQNTVILGSNLPKSLVKQFQKRINSNGYLEFEVILRSTFAKDLIYK

VDWLDKDGFVLRDVLNEDYQALRIPAGQEVILRKLASDTRAKDFRLEIKAKN

>WP\_002866718.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKIKVGLIFSGIVCLFLTACVNQVKQNTTFENALTQKYCGDDFFNQNLEKIKKNDDVIYTGLNAGLIARN

CGDFNKSNVFFDAAEESYKYDVDLENVGSKAAKFVGTTLLNDTIVDYDGSLYERIMVNIYKALNYMEEDD

YENARVEFNRALMRQDKAKEYFAKEIEKNRADLDKAKEDKNYDKNMNENSKVIEAQYDNLFKEFDTTKNF

INPYATYLASIFFFMDKDYRKAADLLREVAIIYPKNKTIKKEAKIFKEYATKIKVKKAKKYVFVVYENGF

GVVKDEFALTLPFIVDKKIISTNIALQTLKKREASFANLNINGQNTNDFVDLDNIVATEFKINMPAMIAK

ALAQTIIKTTLNVAVANNDSTGGWLSLATAVATAATNKADVRSWRGLPKSIAIATIENDGNLEIKDPQGN

ILFQKSLDKNKNALVVVRSFAPYLPASVAIMEK

>WP\_002866711.1 MULTISPECIES: toluene tolerance protein [Campylobacter]

MKKIFLILTLFFNAFALQLDEISSTMQKNIDASLKLLQDSKEDKKQAANGIFKLFDSIIDYKLMAKLSLS

KNYSKLTPKEQEKFTTAFETSLKKSFTDKLSLYKDQVLKVKNGELKNEKRYFLTTSTVVDGEEKNIIFKF

YNDNNNWLIYDVDVLGVSIVQTYRSQFGDILANQGFDALLQKLESIVIE

>WP\_002866708.1 MULTISPECIES: non-canonical purine NTP pyrophosphatase [Campylobacter]

MKIILATSNKHKVLELKEILKDFEIYAFDEVLMPFEIEENGKTFKENALIKARAVFNALDEKQKKDFIAL

SDDSGICVDVLEGNPGIYSARFSDKGDDKSNRDKLVNEMIKKGFNQSRAHYVAAIAMVGLMGEFSTHGTM

HGKVIDTEKGENGFGYDSLFIPKGFDKTLAQLSVDEKNNISHRFKALELAKIILKILNKG

>WP\_002866705.1 MULTISPECIES: L-seryl-tRNA(Sec) selenium transferase [Campylobacter]

MNKFRTFPQINTLIEDESLKSYPFYIKAFFCKKVVAKLKENFSQDEISKDKLLLEIKKEIKTFYRKDLQS

VINASGVVIHTNLGRSVIHEELYEACKDIICNYSNVEFDLENGKRGSRYALVLEKLKMLFECEDALVVNN

NAAAVFLVLNSLCYNKEIISSRGELVEIGGSFRVPEVIKAAGVKLCEVGTSNKTHLKDYEQAISENTALI

LKTHKSNFALMGFHSEVNIKDLHELAKEKGLLSYYDLGSGWCENLNEKLIKNEPKIKKLVQECDILSFSG

DKLFGSVQAGIILGKKELIEKLKQNQLLRMLRVDKLTLSFLNESLKAYLQKDYEKIITLKLLNDDLSFIE

KKALRVQKELKFQTQLKKSKSLVGGGSMPDKSLDTYILTFQGDALKLQTRFRKENIIGRIENDEFVLDFR

TIRENELQKLILIINQMENL

>WP\_002866702.1 MULTISPECIES: hypothetical protein [Campylobacter]

MSKITLILSFFIALFMSACTNATFIQSFIQTSNEGIFIRSQKQQSFKISFQNPSQLRTTLDRDLALKLKN

LGLKEVKENADYEILINLVDMKKHSYAQKITTSARFFYDFDPLESDGEWMVENYYTMQVNLQINSKNHNS

QKTSLLARTAYLGNKERCQLSLENKIINQIVSFFYF

>WP\_002866701.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLFGFDDKREFIPQIYRYLNNQELMLTFLTQYNASVDSALKIPLLYAKNTKSLKMIFGNFLHNIMHVSFG

KIQNINIKLNTYAFYFQKRKSLIFNTKISKNIDLLRLLRIYLYGICFDAQILFSSYVYDKVSFQNNGKNI

DQDGDLIIIDKKFAILPLCKEINAHNLKIENEIHGLLNLIKENNFEKFYIVCPRNKNFTHFIEIKHFLCD

LNKTMLKLVPYKISNQIIRRK

>WP\_002866699.1 MULTISPECIES: ankyrin repeat domain-containing protein [Campylobacter]

MTTLSLEEEKRFEELCKMAFNFARNNECENLKIMIEAGLNANLKTHKGDSLLMLAAYNNSYESAKMLLEK

GAKVDEKNDRGQTPLAGVCFKGYLPMCELLVKYGANIDENNGLGMTPYTFAIMFGRKDVAEFLLKKSKNN

FLKKTSLKILKFIKKF

>WP\_002866698.1 MULTISPECIES: DNA-binding protein [Campylobacter]

MDEGQKQQFIKLTYFLGEVLGEQYEIVFHVITEDGAYIAAIANNHISGRSLDSPLTAFASELMQNKKYLE

KDFLCDYKALVGKSKLIRGSTFFIKNHDKLVGILCINHDTSIMRDLICKMIDLEKIGDMGDILGNISFSQ

NDSSIETLSHSIEDILVQSVDSSYLNSNYQLSITQKEEIAEKLYEKGIFNIKGAVPIVAKFLKISEPSVY

RYLKKFKK

>WP\_002866662.1 MULTISPECIES: flagellar basal body M-ring protein FliF [Campylobacter]

MDFKNMLHQIGQLYQNLTRKQRIVIAASIVVVVGFLVFLALFRGSGSNANNGYAVLVENVSPSSSAAIVA

KLEQNNIPYKLESENKILVPQDQVYRQRMFIASEGLIKDSRVGFEAFDTQAFGATNEEQRVKYQRAIEGE

LARTIETLEPIRSAVVHIAFPKDSVFTERQIPPTASVVVNVREGLKLTRKQIDGIKNIVSAAVPKLTKEN

VKISDQSGVPLDEQEAYEDDLVRAQIKFKSDQEKALEDKIIENLAPFAGGMDKVKVSVNIDFDFSKQESQ

SEIYDPNPIVRSEQTLNEERTGRKDPEIQGVPGAVSNIGPVEGLDNKGQIDTYKKNQVTTNNELSKTITN

TKKQFATVLRTSAAVTIDGKYQDVVDENGDVKSEYVPLTKEELASVESIVKNTINFSATRGDSVVVQNLP

FHRESIRVESKVKTFYNRFVEPFIPPVKYFIAAILLFIFYKKVIAPFTQKMLEDVAAQEEMQQGPNAVLD

DAEDALEKFNAARKKVEEQLGFGDNFNEDSIQYEVLLEKLRGLVSDKGEEIAALLQNLIQNDSEFGEKDM

>WP\_002866661.1 MULTISPECIES: flagellar assembly protein FliH [Campylobacter]

MVNRSNVISGGASDQHVVEGYRFKVISEFDNHTGEKKHTQTPDEENANISLNDEKAVEENQAIAPTQAVM

ETQIPTFQPSFVEDLLKKTDEMSSNIIKLQMQIESQENEFNNRLNSELENAKEKFAKEGYEKAKEEFQKE

LSDFKDKYLKSIAKLDNACENLENFIEKNEKELADTAIDIAKEVILKELELNSSKIAYALAKDLIGELKG

ASAIELKVNAEDYEYLKEQFDQNAHIKISLDDAISKGSVVIISDAGNIESNLNSRLTKIKKMVNNE

>WP\_002866660.1 MULTISPECIES: 1-deoxy-D-xylulose-5-phosphate synthase [Campylobacter]

MSKKFAHTQEELEKLSLKELENLAASMREKIIQVVSKNGGHLSSNLGAVELSIAMHLVFDAKKDPFIFDV

SHQSYTHKLLSGKEEIFDTLRQINGLSGYTKPSEGDYFVAGHSSTSISLAVGACKAIALKGEKRIPVALI

GDGALSAGMAYEALNELGDSKFACVILLNDNEMSISKPIGAISKYLSQAMATQFYQSFKKRIAKMLDILP

DSATYMAKRFEESFKLITPGLLFEELGLEYIGPIDGHNLGEIISALKQAKAMQKPCVIHAQTIKGKGYAL

AEGKHAKWHGVGAFDIDSGESVKKSDAKKSATEIFSKNLLDLASKYENIVGVTAAMPSGTGLDKLIEKYP

NRFWDVAIAEQHAVTSMAAMAKEGFKPFIAIYSTFLQRAYDQVIHDCAIMNLNVVFAMDRAGIVGEDGET

HQGVFDLSFLAPLPNFTLLAPRDEQMMQNIMEYAYLHQGPIAFRYPRGSFILDKEFNPCEIKLGKAQWLV

KNNSEIAFLGYGQGVAKAWQVLRALQEMNNNANLIDLIFAKPLDEELLCELAKKSKIWFIFSENVKIGGI

ESLINNFLQKYDLHVKVVSFEYEDKFIEHGKTSEVEKNLEKDVNSLLTKVLKFYH

>WP\_002866656.1 MULTISPECIES: 3-phosphoserine/phosphohydroxythreonine aminotransferase [Campylobacter]

MRKINFSAGPSTLPLEILEQAQKELCDYQGRGYSIMEISHRTKVFEEVHFGAQEKAKKLYGLNDDYEVLF

LQGGASLQFAMIPMNLSLNGVCEYANTGVWTKKAIKEAQILGVNVKTVASSEESNFNHIPRVEFSDNADY

AYICSNNTIYGTQYQNYPKTKAPLIVDASSDFFSRKVDFSNIALFYGGVQKNAGISGLSCIFIRKDMLER

SKNKQIPSMLNYLTHAENQSLFNTPPTFAIYMFNLEMDWLLNQGELDKVHEKNSQKAAMLYECIDLSNGF

YKGHADKKDRSLMNVSFNIAKNKDLEPLFVKEAEEAGMIGLKGHRILGGIRASIYNALNLDQVKTLCEFM

KEFQGKYA

>WP\_002866655.1 MULTISPECIES: RidA family protein [Campylobacter]

MIKRFDECDRMSQIIVFDKYFKTAGQVAFEPSGDIKKQTKEALAELDTLFEKIGACKGDLIQIQIWLANM

QDFDAMNEIYDAWIKNYPKPIRACVGSALAEGYLVEIQAFGKLREN

>WP\_002866654.1 MULTISPECIES: 3-oxoacyl-ACP synthase III [Campylobacter]

MLKASLKSIASYIPEKILSNADLEKMVDTTDEWITRRTGIKERRIASENENTSDLGTKAALKAIKRANLK

PEDIDAILVATLSPDYFTMPSTACKIASNLGLVNISAFDISAACSGFIYLLEQAKALVESGLKKNVLIIG

AEKTSSIMDYNDRSICILFGDGAGAGVVSLDNENHILDVHTASNGNYGDLLMTQRSQKSNLCQTLSMQMK

GNEVFKIAVNTLSNDVVEILAKNNILAQEIDLFIPHQANLRIIKAVQEKLNLSDEKCVITVQKYGNTSAA

SIPMAMNDAYEEGRLKKGDLILLDAFGGGFTWGSALLKFGGENF

>WP\_002866653.1 MULTISPECIES: 4Fe-4S dicluster domain-containing protein [Campylobacter]

MAVKITDICIACGSCIDECPVSAIVDDVNNPEGEDRYYVYANKCVECVGHNDQPACASACPTDGCIVWSA

VESGQPSRDNIGADMRSGDTPVFA

>WP\_002866649.1 MULTISPECIES: excinuclease ABC subunit UvrA [Campylobacter]

MNDTIKIIGARENNLKNIHLEIPKNKLIVFTGLSGSGKSTLAFGTLYAEGQRRYIESLSAYARQFLDKVG

KPDVDKIEGLTPAIAIDQKTTSKNPRSTVGTITEIYDYLRLLYARVGIQHCHQCGQKISSMSASDIVSEI

LKFPKGAKIIIYAPLIREKKGTYADLLENLRNKGYVRAQIDGVLVRLDEEIELAKTKKHTIKLVIDRLEI

QEDLLSRLASDIEKGLQESFGEIEIEVLNHEEINLNKHYHFSEHCACFDCKISFVPLEPLSFSFNSPKGA

CEACDGLGIRYTLDMKKIIDENLSLENGAVKIMYGFNKSYYYKFLIAFCEQNEIPIKIPFMQLNEEQKRL

VLYGNAKTIEFLWKRNRLKRTFEGVVKMAYEMLKDEKDLAEYMSEKICKDCGGHRLKPESLAVKVAKKGL

GEILDMSIEDSTAFFADEKNFSYLSEQQKLISKPILKEINERLFFLYDVGLGYLSLGRDARTISGGEAQR

IRIASQIGSGLSGVMYVLDEPSIGLHERDTAKLIKTLRNLQQKGNTLIVVEHDKMTIEEADFIVDIGPKA

GKFGGEVVFSGTYKELLKSKSETALYMNGKKQISQLQNRAQKEWLELKNVNINNIQDLSVKFPLQNLVAI

TGVSGSGKSSLILQTLLPFAQEELNRAKKVKKLGGVQIEGLEKLDKVIYLDQSPIGRTPRSNPATYTGAM

DEIRNLFAATKEAKMRGYKAGRFSFNVKGGRCEKCSGDGEIKIEMHFLPDVMVVCDTCQGKRYNDATLEI

KYKGKNISEILNMSVLEASEFFTAVPKIKQKLDTLVKVGLDYLTLGQNATTLSGGEAQRIKLAKELSRSD

TGKTLYILDEPTTGLHFEDVNKLILVLQHLVDLKNSVFVIEHNLDVIKNADYIIDMGPEGGVKGGKVIST

GSVEKVAKEHKKTRSYTGYYLDLELKNTQKS

>WP\_002866646.1 MULTISPECIES: anthranilate phosphoribosyltransferase [Campylobacter]

MILLIDNYDSFVFNVKSMLEQLSNDEILVRRNDEISLSEIKNLNPTHIILSPGPKHPSQSGICLEIFKAR

LNIPVLGICLGHQALALAFDSLVVKMQEPMHAKNSLIKQCRENELFSNLPLNFSVMRYHSLEVKQLSDEL

EILALDEKGVIMALGHKNLPYYGVQFHPESYFSEYGLQLFSNFLKQDIKKSQKQENPLSFYLQKMSENHF

LQSDDFEQICKIIMSKDYEILQVAALLILITEKSLNEKSLSAFVRQILRYSQTFSDESEMIDICGTGGDG

FKSINVSTTSAFILAALGVKVAKHGNRAISSSSGSTDVLEALSITTPNTLESVLKQLNNQGLSFLHAPFF

HPLVGELKEIRSRLGVRTVFNVLGPLLHPNLKLKYQLMGNYHAPVHRLLIEVLKNLGRKKALVVRGNDGM

DELSICDESKIYELCEGEILEYSICPEQFGFKRAFHSEIIGSSAYDNAKDLKDILSGRMQGAKFDLVVLN

AMFALYTANKASSPLVAKDMILEAIYSGKVIEYFKEYQAYAKA

>WP\_002866619.1 MULTISPECIES: TIGR00730 family Rossman fold protein [Campylobacter]

MDTKIIKDVEKFENIPDLEKAITFFGSARLKEDNFYYQQAKILAQKCAQNGFCVISGGGGGIMRAANEGA

FSQKNNTNSMSSVGFNIFLPHEQKLNDFVEYNITFESLAIRKMALIEKSLAFVIFPGGFGTLDELCEILT

LKQLEFKKDVPIILFGSEFWRGFDEFVRNSLLKLEVISKGDELKYKITDDLDFIINTLKEI

>WP\_002866612.1 MULTISPECIES: UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase [Campylobacter]

MKLKLENSFITDNTLECEKECFFLQTTQNAKFHAQALEKGAKIIDVNECKKLLKIDEKIQIIGITGTNGK

TTTAAAIYSILLDLGYKCGLCGTRGAFINDEQIDEKSLTTSPILKTLEYLQIATQKKCDFFIMEVSSHAL

VQNRIEGLKFVAKIFTNITQDHLDFHGTFENYKEAKELFFTDESLKFINKDALAIKFNVRNAFTYGIENP

ALYQIKAYSLEEGISAIATNKNQTFHIDSPLLGLFNLYNLLVASACVNELVKPDLKDLEKAISGFGGVCG

RVEQVAKGVIVDFAHTPDGIEKVLDTLKNKKLIVVFGAGGDRDKTKRPLMGTIVEHFAKIAIITSDNPRS

EEPKTIMEEILSGFAKKEKVLMIEDRKEAIKKALELKENDDLVVILGKGDETTQEIKGIKYPFSDKVVVN

EILKNQG

>WP\_002866610.1 MULTISPECIES: DNA primase [Campylobacter]

MITKESIENLSQRLNIVDIIENYIEVKKQGSSFVCICPFHADKNPSMHINPTKGFYHCFACKAGGDAFKF

VMDYEKLSFADAVEKVASLSNFTLSYTKEKQENKKELKSILPSLNAYFKDNLKHHKEVLTYLYQRALNDK

DIAKFELGFAGASEDSIRLLQNQKIPLEDAMSVGALKKDENNEFYASFIWRITFPIYDHKDLLVGFGGRT

LNPNVPAKYVNSPQNILFDKSRIFYAFNIAKENIAQKKEIIVCEGYMDAIAFHKAGFNNAVAVLGTALTE

HHLPLIRRYDAKVILCFDNDEAGLKAATRSAFLLSTNKIDGKVAILQGGKDPAELVAKNESTKLHDILDE

GIELGEFYIRRLISTHSIISALDKQKALETIQKFTFNLEPLVANSYTSLVSNLLKVDEKFIVLSQNSKKT

IQTPLISQNKYNFPKEKIHIAELELIAFLKQHPDICNDFKQISDSVCFKHKILLDKILEKKGYEDSDIRE

FESKNIRKNLNYSEFLLGICKVNLAFLNNVKIKNSTLALKKQLFTLIDKNLNLLIKNLNTEELNNFLKEY

LSFLKYEKNEEILQQSFRNLNGIFSNKNFTAYDLGFSAQDNDEPF

>WP\_002866598.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLAFFKGLGIGFLCLLLFVAGVVFNVEFLGKKDSNHDLYFSRNIEVSNTLKPDILYANINFWANENLSSK

ITLDNSEKAEIANTFNQILERSKKENFCSGGSFSLEPNFSYKDGIQTPKGQRFDAILECEFKENQLADFN

KLLNDINSIIAKNNFISVSTPAIQTKFSKDTLNNNKENLYKELLKTSYEYEKTYSLDLNKTCVLKNLQVN

TNVNIAPRMLNAKSDNIELSSPIISEKEQILSAKALFICK

>WP\_002866594.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MLKIQDLSFAYHQKDLLKNIHLELKNQAFIGILGPNGSGKSTLLKLILKNLSPNKGEISLFNTNIKDFSL

KEFAKICGFVPQKSELNTPLKVIDVLLMSKYANLKHAFSSYSKEDILEIKEFAKDLRLENFLERSILSLS

GGEFQRMLLARALLKKPKILFLDEPTSALDLNYAIELLSLCEKLVKEKNIAVVAILHDLNLASMFCDKIL

FLKEGEIKYFGTSKELFTQEILKEIYDLNCEIIYKNSKPYILALKEKK

>WP\_002866591.1 MULTISPECIES: TonB-dependent receptor [Campylobacter]

MHPNKKAFKLSLFALLLITNLNAQESNEAINLQKVVVSATGFEQDADSNLRNVISIEGKDLQNKGYVSLE

QALERISGISFVNFGLGRNIDMRGQGDKSNIAVKVMIDGRAINVLDNSHGVTPLDSINLDNVERIEIIPG

GGSVLYGSGTRGGVINIITKKQKSDAFAINLKSSAYDHGGLGGNLGINGAKQINENLAFSFDIQSFNLDG

YQEGYNEKGYFINTKTYIDINDNSDLTLGYDYFKSKNTSSGYLTKAQAQSDPTQKGNSDNITQINRPEIS

LDYHYYFDDIWEFNLEAFWQNQKIDYLKDEISMMGTTAYQNGSGFEDTLTGISLKNKLNYANNSYFIFGY

EFTNHDAKRKSLVYYSVPGVINYHRMTTLMDMTKQSHSIFALNSHNFNEFFTLSGGARYEFSTYDTDRSY

RNEMSMNIPRPPSDSTTLFDTNKNTNNFAFEITPNFKYSDTGNLYLKYERGFVSPAPAQFVNRNKTGNGI

PPYYSSNLKAEIFDTFELGIDDFWWDFYGFNLTLFYTLSKDEISYLGNPHSTSGSWWKYYNIDQTRRLGV

ELSLSQNFLDDDLIFRESLTYLDAKISKGVNDGMRIPYVSKIKATAGLEYAWNKNFSNFIDLTYFSRAKD

GGTIDENTGKMSKNSWIRDYFLTDIGMKYNYKKLQILAGIRNLFDKRYYTYQDSINDQYLVGNGRNYYVE

FKYAF

>WP\_002866590.1 MULTISPECIES: HugZ family heme oxygenase [Campylobacter]

MNFESIISHMNDHHKSNLVDLCKKFGGIEQVQDVFLKSVDFNGLDLVYNDKENLRVEFPKKADENTIKDT

IISLCMSAKSEQNFSGVEKELNEFMLSFNSVALATLNANAEVVCSYAPFVSTQWGNYIYISEVSEHFNNI

KVNPNNIEIMFLEDESKAASVILRKRLRYRVNASFLERGERFDQIYDEFEKQTGGEGGIKTIRKMFDFHL

VKLEFKKGRFVKGFGQAYDIENGNVAHVGASGNPHKFPHKH

>WP\_002866588.1 MULTISPECIES: sulfate adenylyltransferase [Campylobacter]

MKSARKNKNITIDQNEFGILSLIKEGLLGTCTHLMNEKEVNEIIKSGKFKGESFPYPLSFAPKNAEEALN

DIKSGDRIDLILDEKVVGHIDFKSRFKNNKNFSDIFSPNTCSLEDMGTTCISGKIEIYNSQIKKIKENFQ

QIKNNLNAQKITAIVSSFDPLHRAHERMFRWTIDKADLVVIFLVESFDANGFEFELKEAYLKKFIQNYLP

PDRIFIFPLKNINIFHAHLNPGLESIIAKSLGCTKLVVGQNHTGLGMFYDDNQPKTILDDFSKDYGIEVI

VLPEFVFCDQCRMIVSTRSCPHGCHHHLHYNSQSLKDLLRAGIIPPAIFMRKEVSSVILTSLFPNRLKNM

QKIYNELFPTDGILEYKNDEEFYQKLLEIHQMSYMV

>WP\_002866584.1 iron-sulfur cluster carrier protein ApbC [Campylobacter jejuni]

MKEQILEKLKTVKYPGFEKDIVSFNFVKDIKIQDDGVFIDIEIVSANPEVANEIRKNATEALSSLALKNI

ELNIITPKIPEEKSNSRSGKNIAPQVKNFIMVSSGKGGVGKSTTTVNLAISMAKMGKRVGILDADIYGPN

IPRMLGETKTQPEVVGQRLKPILTHGVYMMSMGVLIEEGQGLMWRGAMIMKAIEQLLADVIWPELDVLFL

DMPPGTGDAQITSAQSIPITAGVCVSTPQTVSLDDSKRALDMFNKLHIPIAGVIENMSGFLCPDNGKEYD

IFGKGTAEDMAKAYKSEVLAQIPIEMIVREGGDEGKPVSFYHPESVSSKRYLTAAEKIWGFIEKINNEGG

ADNSAIQPVMNGKSACSH

>WP\_002866582.1 MULTISPECIES: bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP diphosphatase HisIE [Campylobacter]

MQNFKELNEKIAWQKVDHLLPVIIQDAKTCEVLMLGFMNNEALEKSLESGKVVFFSRTKQRLWMKGEESG

NFLNIVDLSLDCDNDTLLILANPVGSTCHTGDISCFEKISKNADFVFLARLEKLINARKNADENTSYTAK

LFKSGTKRIAQKVGEEGVETALAATVKDKEELICEAADLMYHLSVLLADANLSFSDVISKLKERHKA

>WP\_002866580.1 MULTISPECIES: 1-(5-phosphoribosyl)-5-((5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase [Campylobacter]

MTQIIPALDLIDGEVVRLVKGDYEQKKVYKYNPLEKFKEYEKAGAKELHLVDLTGAKDPSKRQLALIEKL

AKEVNVNLQVGGGIRSKEEVKALLDCGVKRVVIGSMAIKDATLCLEILKEFGSEAIVLALDTILKEDYVV

AVNAWQEASDKKLMEVLDFYSNKGLKHILCTDISKDGTMQGVNVRLYKLIHEIFPNICIQASGGVASLKD

LENLKGICSGVIVGKALLDGVFSVEEGIRCLQNA

>WP\_002866579.1 MULTISPECIES: bifunctional histidinol-phosphatase/imidazoleglycerol-phosphate dehydratase [Campylobacter]

MSQKILFIDRDGTLIEEPKSDFQIDTLEKLRFEKDAIPTLLKLKNFGFKFIMVSNQDGLGTPSFPKENFE

IAHEKMLDILKSCGIEFQDIFICPHFENENCACRKPKTAMLEEYIKHELYDKEQSFVIGDRESDMILASN

LGVRGLRYGELSWKEIENEILSSFRSASYQRTTKETDIKVKVCLNGGKVSIKTGIDFFDHMLEQIAVHGG

IGLEISCKGDLEIDEHHSVEDVALALGACIKKALGDKIGIARYGFALPMDECLASCAMDFCNRPHLVYKA

KFKKSHLGALSTEMIEHFFYSLSYAMGVSLHLKVKGKNDHHKAEGLFKAFAKALKMAVKIESENLASSKG

VI

>WP\_002866578.1 MULTISPECIES: histidinol dehydrogenase [Campylobacter]

MQILVYDNLDEKQKEEALKRPAISAKDEISKIVSSIVKEVQEKGDEALIEQALKFDKAEISNIKITQEEI

TQVSNRLDKDLQDAILVAYENIKKFHEAQIPHEIALETTKGVKCEVLTRPIEKVGLYIPGGLAPLFSTVL

MLAIPAKIAGCEKIVLASPAKINDAVLFCAKLCGVDEIYQMGGAGAIAALAYGTQSVLKVDKIFGPGNAF

VTEAKRQVSSDINGATIDMQAGPSEVLVIADDLANEKFVASDLLSQAEHGADSQVILVCLSQDFAKKASD

EVQSQLELLPRKELASKSIANSRIIIAKDLNQALEISNLYAPEHLIIQTQNPRELLKGVKHAGSVFLGAY

SPESMGDYASGTNHVLPTYGLTKTHSSLGLADFSKRMTVQELSKEGFLALGKSVEILAQNEHLDAHKNAV

TFRLESLK

>WP\_002866573.1 MULTISPECIES: ShlB/FhaC/HecB family hemolysin secretion/activation protein [Campylobacter]

MRKILVVLVLLQVFSHAEELNNNKIRELIESSPEANEPQNKNLKNTLKNQKSPVNFKEQNTTNITNSQTD

QNEAKVFVREYVLHIDNKDLTFKKLRISEKEIQDAIAEYRNQELSLQNLKDITNIIAYYCQVSGYPSATA

YIPPQDLSSNKVQINIAFGTLGKVIIKNNSGVRDYALESKLNKNLKGKVITTKNVENEIYKINEIYGIQT

NANLQSGDGYGESDVIIEVNKGDSATLTLYSNNYGTKETGRFRAGMSQSLNNIARQGDNLNFYLQDSDEN

QIDYGINYSTFIGNLKITPFATQGHYVLGGIYRNLGFYGDSMNVGVNFSYPVFLYTEYSLYLVSGFTHKK

IKDYYLDGLVSNEKASNSVNLGIEGTYKGLENNVLSYTLNFTYGNVENDGDSSGFNGVNLGNFGKMNLNL

SNEYQFQERLTHIFQLNYQKVIGGAVLDSSESVSLGGPYGVRAYLEGEGSADNVVSGTLGIRFQTPLEGL

YLTPFYDIGYSWYENKEYQSENHYFMDAMGMQILYTRSANFYVKMDAARAVHRFKHDGEHRARVYVSLGK

YF

>WP\_002866516.1 MULTISPECIES: GTPase Era [Campylobacter]

MKSGFVSIIGRTNAGKSTLINSLLEEKIALVSHKQNATRRKIKAIVMHEKNQIIFIDTPGLHESGATLNQ

LLVQSAIKSMGDCDVILFVASVFDSTKDYENFLSLNPQVPHIIALNKVDLTDNATLLKKLSEYAKFSQHF

KAIIPYSSKKKSYKKGLLDEIVKYLDKHEYFYDPEFLSASSEKELYRDFILESIYENLSDELPYSSEVLI

HRTKDTPNLLILEANIITDTNSHKGMLIGKEGATLKRIGKDARFKISKLAQKKVLLKLFVTVKKNWQKDE

EFLKKLLNDEN

>WP\_002866514.1 MULTISPECIES: hypothetical protein [Campylobacter]

MNKIEVFLQNLNPREKFLFISFICLCALFLAFKIHDHFLENIFQKTLVEHNYLALNEAKIENSHLKEIGI

KLTKQIKTEEEKLKYYKEKLHLFSYDKDFFNKKINNLSKNLTINEIKFSQENKNFIHYNYVSLSLNGDFK

DLLNFIQNLENLPIALKIDKIKLYNTQGLKLKLDLMFKFVNL

>WP\_002866513.1 MULTISPECIES: MFS transporter [Campylobacter]

MTKQEIQKLDTNFLGHPKPLFSLSMVELWERFAFYGIRSLLVLFMATTISKGGLGISTEYASAIYGIFAG

CLYLAALPGGWITDNYLGQKKALFLGSFIIALGHISIALSILSTPIFFLGLTFIVIGTGFFKTSASVTVG

MLYKQNDTRCDTGYTIFYIGINIGAFIAPLICGFVQAKWNYHLGFGIGGLGMLISLLILYFKATPELEEF

HKNCTLKQNWEQPFKKSKNLTLILSISLLSIIGFFLIFINLADINPIILSKKLLIVILLCLVIYFIYLFV

FKTLNKREKQQLTILIVLFFVATFFWSTFEQKPTAYNLFAQDFTNRNIFDWKIPTNWFQSFNPIFIIILA

PIASYIWIFLEKKNIYFSSIGKFTLGILFAGIGFMMMTFASQNLINNNGLPISMVWIIISIFFLTLGELC

VSPVGLSIMAKVAPDLIKNQIMGLWFVASALGNFVAGLIGGNVNIKNIDQLPNIFGQCMWMLFVVALLLF

IAKKPIYKILNEKNKQLSN

>WP\_002866509.1 MULTISPECIES: penicillin-binding protein 2 [Campylobacter]

MRMRLVVGFILLFFIFLLSRVYYLSIKSNVYYEELAKQNAIKTEFLPPVRGQITDRNGTLLAINDLGFSI

SIKPYLSIKKSNKGILDKELSELTNLFPDLNASKLAEIYKRNDSYYNQDFIKVVDFIPYDEIIPHYSELN

LNKTIKIDPVVKRKYPFGKLASHIIGYVGKANLQDVQENEIAKLSNYTGKSGIERYYNDILQGEKGTRVY

KVNALNQEVEQLSYTPAMSNDIELTIDIELQSYLTSLFEGNAGAAIIMNVNDGSILAAGSFPEYDLNPFV

TGISFKDWDELSNSLDHPFTNKLINGYYPPGSVVKMGVGLSFLNSKNISPSTQYVCNGSIELGGRFFRCW

NRSGHGPVDLKHAIKYSCDVYFYNGSLQVGIDQISETLSRIGFGAKTGVDLPSEFVGTLPSKEWKMQRYR

QSWFQGDTLNTAIGQGNFLATPMQIARYTAQIAKGGEVIPHFLKSIENNNNTTIENQMDENKKEIFTLFE

KSQLPYIRDAMYAVANEQGGTSYRYLHNLDVKVAAKTGTAQVVGFSQTDKNRVDEKQFEYYTRSHAWLTS

YAPYSKPKYVVTVLLEHGGRNITSGATVAKIYQKMIELGYFK

>WP\_002866506.1 MULTISPECIES: GTP-binding protein [Campylobacter]

MIISAKFITSLVKFDENLSSNFSEVAFLGRSNVGKSSLINSLCKQKNLAKSSATPGKTQLINFFEVTCKR

NEEKFNINFIDLPGFGYAKVSKNLKEIWNQNLDEFLKLRTSIKLFIHLIDSRHTHLEIDVNLNDYLKRFL

RPDQKILKVFTKCDKLNQSEKAKLKNEFKDSILVSNLNKFGLDSLEDIIIDQTLGLGK

>WP\_002866503.1 MULTISPECIES: lytic transglycosylase [Campylobacter]

MKKNLLCFLICFNFLFAQINTPEFYERQMNVLRNLDINPSFISDLIFVQTQQDIKSKHAQTLIDSMQNFS

KVTPMIRKILSQQEVPDEILYLAMVESGLKTHSVSNAKAVGVWQFMQPTARNLGLRIDAYVDERRDPVKS

TYAATNYLKELKEEFGKWYLALLAYNCGNGKLRQAIKQAGSDDLSVLLNPDKKYLSLETRNFIRKILTLA

FLANDRDFLLDKDASLMNYALSNEFAKVDVPSSASLKEIAKNLNMDLATFKKYNPQFKHNFTPPGKGYYM

YIPLNKVAFFDKNFKAEKLAKVDTTIPMTRTYTVKSGDSLYKIAKNYNISVDEIREFNKIAKNHLSINQK

LIIPIKENKNANKNNYTKVVSR

>WP\_002866502.1 MULTISPECIES: TatD family deoxyribonuclease [Campylobacter]

MFLNLDFQDGLRIVDTHCHLDSEAFKDDLDETLNRAFKNGIEKIIIPGADIKDLPYAATIAHKYKNIFFA

VGVHPYEIDNYDEKILRQYLYDEKCVAVGECGLDYFRFKSDLAEEIQKEKENQKKIFIAQLELAIEFKKP

VIIHSREANHDTYEILHGYSKDLVGGVLHCFNASEHLLTLFEDGFYFGIGGVLTFKNAKKLVEILPKIPK

DRLLLETDAPYLTPEPYRGKRNEPLLTQFVANKMCEVLNLSRKELLEICFNNSEKLFFKGY

>WP\_002866501.1 MULTISPECIES: diguanylate cyclase response regulator [Campylobacter]

MNKKILIIDDNKMLGKLLAKKIQMTLDYEVDIAFGFAEAKELMNNDYFLAFVDLCLPDAPNGEVVDYVIE

KKIPAIVLTASGDKATKEKFMDKDILDYIFKESETCIDEIISSIVKLNQYAKTKVILAMSKLPERNEIKK

ILTQRQFNVLAAAHGEEAMSYLNDNNDVKLIIADVNMPVISGFELLIQVRERFSDDELGVILLGDHNDSF

EANSFKNGVNEYLFKPLSKESFNCRLDHCLSYMDDKKFLSTYNVLDPVSGVKNYNALIDGIDDYFNEIAT

KDEEFAFAFLDIDNLQMINDEYGREVGDEVIKICANEIVNETKGRDLVGRYSAEKICILLKNISQERAIK

IFSRIRVNIKKAGVLVNLDEVFFTASIGVVFGKSGDKIDSLVDKASKILSQAKDNGKDRVEVCS

>WP\_002866499.1 MULTISPECIES: NAD(+) kinase [Campylobacter]

MQNKIDYKNIKKIGLVTRPNVSLDKEILKLQSILSIYKVELVLFKESSEILDLPKYGLDDLFKISDFVIS

LGGDGTLISLCRKACEYDKAVLGIHAGHLGFLTDFKVDEAENFFQAFFQGEFRIEKPYLLSVFLEDKQGK

ILEKLAFNDVVISKNNQASMAHIEVFRKEKKFNEYFGDGLIVATPAGSTAYNLSANGPIVYTLAQAFILT

PVCSHSLTQRPIVLPKGFEIEIMAKDCILCIDGQENYKMNDFKSIKVGLSDKNVALIHPKNRDYFQILKE

KLHWGN

>WP\_002866480.1 MULTISPECIES: DUF459 domain-containing protein [Campylobacter]

MSVVRFFFILIIVLGLVVVVMNQSISSYIEQKYHFAFYPHNDLLKEANGFKIKLEQIRAILSNEPLPQTN

EETTNQESKSTDENLSKIDKVLNTLENDENTSHKETNLTLIQDANISFIDNTKLELQNGDEFLFIGDSLM

QGVAIALNRDLRNLNLKVTDLSKQNTGLSYKSYFDWSKATNEAFVKNSNIKYLVVLLGANDPWDIKKGGN

YHRFGSPSWIDIYTNRVDEIIKIAKKHKAKVFWFEIPPVKKEDLNKKIQVLNKIYSDEILKNKEIFINTK

LFFSVNDEYSAYIKDENNRSIKVRTDDGVHFTPSGAREMSKLLLEHIKLKEENASK

>WP\_002866479.1 MULTISPECIES: TolC family protein [Campylobacter]

MRVIFSIFLAFFLSACGAKLSLPKEVDLTQEQMKDLNLTYDWYRSYDNAKLNEFLNFVLLNNSDINIARK

TLLSALARADLINYDLYPTLSGNLGFGGDKDLNSGKQSKNFNNSLNLSYELDIYGKLRDSASASEFSAKA

SAYDLENLKISMINTALNDVFELAYFNDVDKLLRAYLSNLEQMKELYSYKYKLGKIEELDLLNIEQSLLR

AKQNLLSNDQNRNLLIKNLQDLLAKQEGFAYIEYFKTLSLNDFKTLSPDFNIPLKALAYRADVRSKLNSL

KSAFKDYSSMQKSILPSISLGGALSGSDKKIDDSFKFEILSGNVKISLPFLDYGRVKQNIKISQFTYEQL

LISYEQALQSAMNEFALNYKDYQSNTLLLQNLQNINIKQELITKAYYEKYILGKSELKDYLDANNTLNST

QQEFLRARFNLLKTINSYYQITALSFNDENLEFPKY

>WP\_002866478.1 MULTISPECIES: macrolide ABC transporter permease/ATP-binding protein MacB [Campylobacter]

MIFLKNICKNIGENAILKNVSLSIEKGEFVAIIGQSGSGKTSLLNIIGTLDTPSSGTYIFDEYEVTKLNN

DEKARLRREKIGFIFQRYNLLSLLSAKENVSLPAVYAGKKLQERSQNAKKLLNDLELAHKLDSKPNELSG

GQQQRVSIARALMNGGELILADEPTGALDSKSGIMVLEILQKLNAQGHTIVLVTHDPKIAAQAKRVIEIK

DGEILSDTKKEKAQEKLTLKTMSKEKKTLTLLKNQAFECFKIAYSSILAHKLRSVLTMLGIIIGIASVVC

VVALGLGSQAKVLESIARLGTNTIEIRPGRGFGDLRSGKTRLNFSDLETLRSLEYLEAVDAHSNTSGVAT

YTNISLSARAEGVGVNNFAIEGLRIDAGRILNNDDVKNSTNVAVLDFNAKKNLFPDEKSENILGRVVLFN

SQPFKIIGVLQKDTDKPIEDNVVRLYIPYTTLMNKLTGDRNLREIIVKVKDDVSSTLAENAIIRILEIKR

GQKDFFTFNSDTFKQAITANKRTTTILTACVAVIALIVGGIGVMNIMLVSVSERTREIGIRMAIGARRED

IMMQFLIEAVVICTIGAILGVILSIFVIFAFNTLSTDFPMILNAYSVLLGLLSSMFIGVVFGFFPARNAA

NLNPISALSKE

>WP\_002866477.1 MULTISPECIES: efflux RND transporter periplasmic adaptor subunit [Campylobacter]

MKKKIVLIILIAILGSVGAYFIFFNNDEKISYLTQKIQKKDISQTIEAVGKVYAKDQVDVGAQVSGQIIK

LYVDVGTHVKQGDLIAQIDKDKQQNDLDITKAQLESAKANLESKKVALEIASKQYQREQKLYAAKASSLE

NLETQKNNYYTLKANVAELNAQVVQLEITLKNAQKDLGYTTITAPMDGVVINVAVDEGQTVNANQNTPTI

VRIANLDEMEVRMEIAEADVSKIKVGTELDFSLLNDPQKTYHAKIASIDPADTEVSDSSTSSSSSSSSSS

SSSSSNAIYYYAKFYVPNKDDFLRIGMSIQNEIVVASAKAVLAVPTYAIKSDPKGYYVEILENQKAVKKY

VKLGIKDSINTQILEGVNENEELIVSSSADGLAPKVKLRF

>WP\_002866476.1 MULTISPECIES: amidohydrolase [Campylobacter]

MQKLVENLALKYYDKVVDLRHQIHMHPELEFEEENTAHLVCKILDEFGIKYQKNIAKTGILATIEGKKKS

QKKPKCVLLRADMDALPVQEKTNLSYASKIDGKMHACGHDGHTAGLLGAALILNELKDEFCGTIKFMFQP

AEEGSGGAKPMIESGVLENPYVDAVFGCHLWGSLLENTAQIVSGEMMAGTDIFDLEFIGRGGHGAHPHTC

IDPIIMATQFVNNIQSVVSRRLAPYEAGVITVGQICAGTTYNVIPTNAYLKGTVRFLNDKTQDILKSSLE

EVAAATAKSNGGDYKLKYTKEFPPLINDEKAALIARKAFAKVLGEENIIVSSKPDMGAEDFAFLTRERMG

AYVFVGISKDLNHPALHHSSTFCWDDENLKVLMQGDVMMALEFLNL

>WP\_002866473.1 MULTISPECIES: 1-aminocyclopropane-1-carboxylate deaminase [Campylobacter]

MNFIKTISPIQKINFNGFEFYIKRDDLLGEINGNKARKLAFYIHQRYPKNQSFISYGGSQSNALAALSIF

AKQRSYKLVFACEKISTFLKNNPCGNYALALENGVDFVENIHSLSLKQFAFSLCKKDDIFIEQGIANLEA

QYGYMELAQEIQMQSQSLKLDFDIFLPSGTGTSAAFLAKYSKFKVFTCACVGDIKYLKKQILTLDPSYDF

SNLEFLTSDKKYHFAKPYKEFYELYMDLKLKCNIEFDLLYDILGLSIALKQEWKKPLLYIHQGGILGNST

MLERYKFKKLV

>WP\_002866472.1 MULTISPECIES: membrane protein [Campylobacter]

MKNESKEDSNFWIAYADLMAGLLFVFILLIGAIVVKYVLTQSDLKEIKDNLNKQEARLEESKEELRNKEA

IVFKLSSDLNNASSALNLANSQKAELEANITNYKQLSKDLNLTLDNKDKQILILLGQLEKKDEELKNLQE

DFQKAKEKVQNLGLIRENLSKELQSKLDNNITIDEKTGSISLPAEVLFDKDSYVLKNEAKASLRKILSEY

FDAILEDPKIFSNIENIIIEGHTDSDGSYIYNLDLSQKRAYEVMNFIYTFYKSDKLQKLLMASGRSFSDP

VFVNGVEDKDKSRRIEIKFSIKNDNALKDVEKFFEFH

>WP\_002866471.1 MULTISPECIES: membrane protein, partial [Campylobacter]

MDIKSDEISELVLPEGKDARGSLVYFKIIFIPAFLYILILLGYFNVIDFKVELHTVIMTGVIFFTALIFA

RHSAEYAYSIFEQQKDEFKQALKRHIMRHFLAIGKDTKSNANFDDFAYTYIKGARNENFASIGSAIFPMM

GILGTFISIAFSMPNFSSSDTAALEQEIADLLSGVGTAFYVSIYGIFLALWWMFFEKYGKSKIDRLLNRQ

KNATSGFFWTKEELDQRYLTESLQHFEKIGAIFKQVSNDDFFAELDHAIDRKFGIFQDMLNVEEKAIRLS

SEHIKQTMGELSKAQRDQRDLGKLYSEMLNGIGLLNQNLKEINTRMSEQYNRLLDISSDKIHHLDKTLSA

FDEKVERFGKNFELYEKAMLESQEKVFEGFKASLFEGMHKFKEVYEEEKSIDAKIKMMDELKKEMKALDE

ETSQMMSKLSGDENQNKENETKQIEDFSESKTEENQDEIQAEISKQESNDELKNEDKENK

>WP\_002866470.1 MULTISPECIES: class II fructose-bisphosphate aldolase [Campylobacter]

MGVLDIVKAGVISGDELNKVYDYAKAEGFAIPAVNVVGTDSINAVLEAAKKVNSPVIIQFSNGGAKFYAG

KNCPNGEVLGAISGAKHVHLLAKAYGVPVILHTDHAARKLLPWIDGLIEANAQYKKTHGQALFSSHMLDL

SEESLEENLSTCEVYLQKFDALGVALEIELGCTGGEEDGVDNTGIDNSKLYTQPEDVALAYERLGKISDK

FSIAASFGNVHGVYKPGNVSLQPEILKNSQKFVKDKFALNSDKPINFVFHGGSGSELKDIKDAVSYGVIK

MNIDTDTQWAFWDGVREYELKNRAYLQGQIGNPEGDDKPNKKYYDPRVWLRSGEESMVKRLEIAFEDLNC

INKN

>WP\_002866467.1 MULTISPECIES: endonuclease III [Campylobacter]

MKRNLEIKELFLKHFDKPVTELKFSNLYELLVCVMLSAQCTDKRVNLITPDLFKAYPDIKSLANANLSSL

KTYIQTCSFFNNKAQNLIKMAKAVCENFDGEIPLEEEKLKSLAGVGQKTAHVVLIEWCGANFMAVDTHVF

RVSHRLGLSKAKTPEATEEDLTGIFKDNLNYLHQAMVLFGRYTCKAKKPLCKECFLNHLCKSKDKELK

>WP\_002866466.1 MULTISPECIES: DNA/RNA non-specific endonuclease [Campylobacter]

MKIFIFLLAISLNIFALESYKPSADFSSYFNNINCSQILDKFFYLNCYDYKLKGTKAVAYKVEASNLKDK

QIKKRPRFEDDTNIPKKYRTTWSDYKNSGYTRGHTAPNASFSFSKAAQNSVFLMSNITPQIAQINNKIWN

EIEQRERNLAFKFQSIEVLNLVLYDKEPLYIKNRIAIPSFYVKIIKTPKFKECYQVPNHEVNDENIKQYQ

INCDKF

>WP\_002866465.1 MULTISPECIES: hypothetical protein [Campylobacter]

MRRLSILLTILIVINITACDSKTENYYKNHPSEAKEKAKECKESGTLSEDCINALKVGVKPTNEESKYSP

NTPKKSDNQILEALKQNDLKKEKTTKDINQSSENNESIIIPPITETPSEIYPSKTTENNQSSIFSDDVNI

TQEKLP

>WP\_002866462.1 MULTISPECIES: TlyA family RNA methyltransferase [Campylobacter]

MRFDFFVSKRLNISRNKALELIENEEVLLNGKSFKASFDVKNFLENLKKTQDLNPEDILLTDGLKLDLLS

EIYVSRAALKLKNFLEENDIEIKHKNCLDIGSSTGGFVQILLENQALKITALDVGNNQLHLSLRTNEKII

LHENTDLRAFKSEEKFELITCDVSFISLINLLYYIDNLALKEIILLFKPQFEVGKNIKRDKKGVLKDDKA

ILKARMDFEKECAKLGWLLKNTQKSSIKGKEGNVEYFYYYIKN

>WP\_002866457.1 MULTISPECIES: hypothetical protein [Campylobacter]

MSDFLSFTLENIRNGGAFMAWLESRRLEWAPLMAARLKYLLEGRTFVLMCDEQRSWYEEYFLKNINSKAA

RPMLPFVSLNSLCKKKVQSSEDIALLNDLLDISFPNGYVYFYIGSAFDNKSLIAKSRDDSLLWLFDEQLQ

DSFYLNSKDKDLDIKLISLYQLFDVSLDAILFSRVQLG

>WP\_002866452.1 MULTISPECIES: UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase [Campylobacter]

MKLSEIAEFLSLEYKGEDIEISALNSLLKANFTELTYCDGEKNTKDIPHTGAAAILVSKEYENLVPKDTK

ALITQSPHLSFAFLSKLFAKPLISTAKEKVQNIAKSARIMPNVYIGDNVNIGENVIIMAGAYIGDNVSIG

DESIIHPNVVIYNDTKIGKKCHLLANCVIGSDGFGYAHNKNGEHYKIYHNGNVVLEDFVEVGACTTIDRA

VFDSTIIKAGTKVDNLVQIGHNCNIGQNCIIVAQTGISGSSELGRNVIMGGQSATSGHLKIGDFSTIAAR

GGVSKNLEGGRVYGGFPIMLQKDWLKLQAKIAIKFKEKSQD

>WP\_002866450.1 MULTISPECIES: YafY family transcriptional regulator [Campylobacter]

MKEYDKLSIRLVQILSKFNNGESLSAQELAQEFNVDTRTIQRDLNERLTFMPIKKENGRYVLESFALGKL

SFKDIQNFATLSGIAKLYPKLDQGFIVDLLSHRVNKVLMVKNEGFQKVDYELFKDLSVAILKHNVLIFFY

KEKERQIKPYKLVNYKGIWYLLGDENDKLKHFNLDKISKFRTKNENFIPNEKLEEQIQNDPNIWLGESKE

VILKLDKNAKEYFFRKEILSNYQIIDEDETSYTLSTQVSYEDEILHLVKQWIPYIKILAPIELKTRLENI

LKSYLNNLSK

>WP\_002866439.1 MULTISPECIES: DUF2860 domain-containing protein [Campylobacter]

MKKYLFSCVLASILTQSATAVEFQEGFSGNLSIGVGARDIKSNISTLANSDYLSSYNADNSDSSFIPFIG

VELYYGNLIDNDRIFIKNYNGRDISGIALGYERAYLERFSTSFSVISSLREKAYANPYATGNREETDVDR

YGFKISQLYESDFGKFTTSYLFSKNKYDKDTIAQSSLKREGYYHEFELNYNYSLLNLGLNYDYNDADGKA

QSYSRYGFSIGTNLAFANDYIFTPNLNLSKYEAVGTDPIFHKKQDGNIVKLNLKVVKNQFLGYNGLYGFA

NYGIEKRNSDIGFYDETYQIVLTGIGYKF

>WP\_002866437.1 MULTISPECIES: pyridine nucleotide-disulfide oxidoreductase [Campylobacter]

MKKIDLIVVGAGPTGIGCAVEAKLKNKEVLILEKSNNICQTLMQFYKDGKRVDKAYKGCEGTNHGHVPFE

DGTKESTIETFQNALKEHNIEVEFGSEVESVKNENGVFLVSTAKGVYECKNIIVAIGRMGKPNKPDYKLP

MTLTKIINFNANSVLANEKILVVGGGNSAAEYAVDLANSNQVSLCYRKKEFTRLNDINLKDIHEAGNSGK

VELKLGIDINEVEDDNGKAKVNFTDGTSDIYDRIIYAIGGSTPLDFLQKCGINVDDKGVPLMDENKQSNV

KGIFVAGDIATKNGASIVTGLNDAVKILSVL

>WP\_002866435.1 MULTISPECIES: FUSC family protein [Campylobacter]

MNKIEMLKQHFKEIAKLNSSEQVWQMPFFAALGVGIVLGLSVFFGKLNYGLIAMIGALSFLYVPNTPLYH

RMAVVMCCSFGIVSSFFLGILTHFLPAIFAFIPIGLVAMGSSILIRYYNIGAPGYFFFVFSCVLGAYSPF

EAKDFIFLVGLVFLGAMVANLMALLYSIVVIYGFKNALPSEIPPREYICFDAVFVDSLIMGSFVAFSIFI

GTFLELERSYWIAISCTAIMQGVTLNSIWIKQIQRIIGTALGVCFAWWLLSKQFHDIELVLLMMSLFFIG

QFLVNRNYALAMIFFTPYATYLSKAANFMSENADTLILARLIDVVIGSILGLLGGFVIYKPYLRVHFERI

AKYIFRIKRKA

>WP\_002866434.1 MULTISPECIES: amidohydrolase [Campylobacter]

MKIDTHAHIFLKKLNTVANARYKPDYDASFKDYKANLDHYGFDKGVLVQPSFLGVDNEFLLQSIEKDENI

KAIVVVDEGIKFDELKKLKERKACGVRLNLIGKELPNFKTMVWTQFFENLSKLKMQIEIQRDLDNNLVDI

VKNLIPYGCNIVIDHLARANANLTNLEDLICLKNSRIFFKISGFYRAKIDYVNNEQAVKFAKKIYEILKE

YFPLSNFVFGSDWPHTNFEANVNFSSALAAFNEVVVSKKEQEQILGDNACALFDF

>WP\_002866431.1 MULTISPECIES: DUF2891 domain-containing protein [Campylobacter]

MEKFIKQFSFIALENIFRELPNKITHSFNDINDIKPPKLMYPIFYGSYDWHSSVHSHWLLVKILKDFSHF

APKDEIIKALDSQFSKEKAEGELKYLQNPAHKGFERPYGWGWFLKLALEINLLAKENDKAKIWAKNLEGI

ADFFVKEFKEFLPKMDYPIRVGTHFNSSFALYFALEYARFKKDQELEYCIIQSAKKWFLNDKNMQALEPC

GDEFLSPVLMEAVLLSAVLPKNDFVKFFKVYLPNLEAKEPVTLFTPVSVSDRSDGKIAHLDGLNLSRAWC

FKILSNFCDENLKILLRNNAIEHFDKAIAHIEDDYLGSHWLGSFALLAMDVDIL

>WP\_002866430.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKQWLSDFKLALIQEDVNKLENLLDELDMKAFIKNLTKESPSEDFLKENANDLFYQVQALLQEAVMLIEQ

KKKTKAVEIQKFQKALTYFKS

>WP\_002866429.1 MULTISPECIES: flagellar cap protein FliD [Campylobacter]

MAFGSLSSLGFGSGVLTQDTIDKLKEAEQKARIDPYTKKIEENTTKQKDLTEIKTKLLSFQTAVSSLADA

TVFAKRKVVGSISDNPPASLTVNSGVALQSMNINVTQLAQKDVYQSKGLANDSGFVNANLTGTTDLTFFS

NGKEYTVTVDKNTTYRDLADKINEASGGEIVAKIVNTGEKGTPYRLTLTSKETGEDSAISFYAGKKDAQG

QYQSDPEAENIFSNLGWELDKTTQTIDPAKDKKGYGIKDASLHIQTAQNAEFTLDGIKMFRSSNTVTDLG

VGMTLTLNKTGEINFDVQQDFEGVTKAMQDLVDAYNDLVTNLNAATDYNSETGTKGTLQGISEVNSIRSS

ILADLFDSQVVDGTTEDANGNKVNTKVMLSMQDFGLSLNDAGTLSFDSSKFEQKVKEDPDSTESFFSNIT

KYEDINHTGEVIKQGSLNQYLDSSGTGNKGLDFKPGDFTIVFNNQTYDLSKNSDGTNFKLTGKTEEELLQ

NLANHINSKGIEGLKVKVESYDQNGVKGFKLNFSGDGSSDFSIKGNATILQELGLSDVNITSKPIEGKGI

FSKLKATLQEMTGKDGSITKYDESLTNDIKSLNTSKDSTQAMIDTRYDTMANQWLQYESILNKLNQQLNT

VTNMINAANNSNN

>WP\_002866428.1 MULTISPECIES: menaquinone biosynthesis decarboxylase [Campylobacter]

MKEFIQILKENDLLRVIEEPVDVDLEIAHLAYIEAKKGEKGKALLFKNPIDKKLNKQYKFPVLMNTFCNE

KALNLAFGRDYEEVAEEISKLTKLHIPTSFKAKMDFFMNLLSFKNIPPKRLKKNKALYDYEILNSLEELP

ILKTWEDDAGKFITMGQVYIQNLDKTQNNLGMYRLQMSDKNELLIHWQIHKDGANFYHEYKNVGFKKMPV

SIAIGGDPLYIWCSQAPLPKGIFELLLYGFIKKTPAKLTPCENGIFVPYDSDVVIEGYVDLEEFKIEGPF

GDHTGFYTPAELFPVMKVEKIYAKKDAIYQATVVGKPPLEDKIMGLGTERIFLPLLQTSVPDLIDYNMPE

NGVFHNLILAKIDAKYPAHAQQIMHAFWGVGQMSFVKHAIFVDKNAPSLKDYDALIPYMLDRFNTKKILI

SEGICDQLDHASPNSCFGGKAGLDACEEIQVEELEILEDEKLLELFKTKVELLNLKQFYKESKSPIVCIL

LDKKEKIEQSFDKLLEFKKHFRILVFLDAENKLENSYMLVWRVVNNIDAKRDIFIKEERLGVDASAKGEA

EGYLRAWPKQTDCTKSVIEDLILRNILENNPDLFNKFEIF

>WP\_002866427.1 MULTISPECIES: hydroxymethylbilane synthase [Campylobacter]

MKLIIATRKSQLALWQSEHVAQILKNTHQIEVLLEGFKTKGDVLLDSPLAKIGGKGLFTKELEESMLRKE

AHLAVHSLKDVPSFFPRGLVLAAVSKREQSNDAMLSQNYKDFLSLPKGAKIGTTSLRRKMQLLLLRPDLE

IISLRGNVNSRIEKLKNNDFDAIILAMAGIKRLNLDKQVNFVYEFSKDELIPAASQGALGIESINDEKIL

ELLKCLNDENALIETSIEREFIATLEGGCQVPIGINAELLGDEICVRAVLGLPDGSEILKDKRMIKKNDF

KGFGESLAKEFIAKGAKELLKKAESMI

>WP\_002866426.1 MULTISPECIES: membrane protein [Campylobacter]

MNYKLSLSPLFVLEIIASILFIVFFGFGNFLFFILLSMIFGVILLGIFWKNMLEFQMGGLKDMLTQFSFV

IAGFLLIFPGIITSVFGIFVFFFGIALKLMTKSKYQYTKQEYQNSNEEIIDVEIIEDRK

>WP\_002866423.1 MULTISPECIES: polyprenyl synthetase family protein [Campylobacter]

MQKIDELIKQFLEELGYEPILNMLSNVKSGKKLRSKLLLAIADESEIAFKICAAIELIHLASLLHDDIID

ESELRRGARSVNAEFGTKNALMLGDILYSKAFYELSKMDARFTSIISDAVVKLAIGELMDVDLGEKFNIN

KEAYLKMIYNKTAVLIEASARCGAILAGLYEKDFAEYGKNLGLAFQMIDDILDIKSDEKILGKPAMNDFK

EGKTTLPYIYLYENLQEQDRIYLQTLFKKDLNENEKEWLKTKFEEQKALEKAILEAKTYAKKASKAIEKY

DNNKLNDIIKAMIDREF

>WP\_002866422.1 MULTISPECIES: 2-oxoglutarate:acceptor oxidoreductase [Campylobacter]

MKYQLRFGGEGGQGVITAGEILAEAAIKEGRQAFKASTYTSQVRGGPTKVDIIIDDKEILFPYAVEGEVD

FMLSTADKGYKGFRGGVKEGGIIVVEPNLVHPESEDYKKWQIFEIPIITIAKDEVGNVATQSVVALAIAA

YMSKCIDLDVLKDTMLHMVPAKTRDANAKAFDLGIKYATQAKPHS

>WP\_002866421.1 MULTISPECIES: 2-oxoglutarate ferredoxin oxidoreductase subunit beta [Campylobacter]

MAFNYDEYLRVDKMPTQWCWGCGDGVVLKCIIRAIEKLGWNMDDVCLVSGIGCSGRMSSYVNCNTVHTTH

GRAIAYATGIKLANPSKHVIVVSGDGDTLAIGGNHTIHGCRRNIDLTHVVINNFIYGLTNSQTSPTTPKG

FYTVTAQFGNIDPNFDACELTKAAGASFVARGNVIEANKLENLIYKALAHKGYSFVDVFSNCHINLGRKN

KMGEAVAMLDWIKSRVVDKAKFESMDFEERKDKFPTGILHEDNSQPEYCHAYEEVRRAAKEKRMVDLGAL

K

>WP\_002866410.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLGIYLLIAALSFLALYFAVKKLTLNIDEQTLLEPIKMDIYPKFCDLIDEKIREFKENVQNANLALKNSD

QKDEFLEKLGDLSRELTFIQTMNLSNKNDSIWQNELFSFLKELENLLLEYLEKGEEEAENLREFLMNEFE

KLKG

>WP\_002866409.1 MULTISPECIES: rhodanese-like domain-containing protein [Campylobacter]

MIENIPASLWTKQDLNAYQIFDVRTPLEWEEGILPNAQCVALYDNQGLLNAKFLDEFQSKRDESKKLAFI

CRSGHRSMVAAEFIAERLGLESINLDGGMLALKGY

>WP\_002866407.1 MULTISPECIES: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Campylobacter]

MIYKKIKALYFWIFFVLSVALVVFCFCFTKSQNTLWKIRKIWAKFQRYTISYKQEIIGTFNPQAQMILMN

HQSALDIIALEELYPKNLCWIAKKELGEIPIFKVAMKKPKLLCIDRKNPRDLVRVLKEAKERISEDRVLA

IFPEGTRSKNEKMLKFQSGAKILSEKLNLKVQPILIVDSVKILDTKSFSASSGVLKIICMDLVDTNDDKW

LENTRKKMQELLDQERAKLC

>WP\_002866406.1 MULTISPECIES: phosphoribosylformylglycinamidine synthase I [Campylobacter]

MKVAIIRFPGTNCEFDTAYAFEKLGVKTQIVWHEEKEFDTDLVVLPGGFSYGDYLRCAAIAKLAPAMQGV

FNHAKKGGYILGICNGFQILLESGLLKGAMKHNNNLSFISKNQNLRVVSNDNAFLKNFKKDEIINLPIAH

GEGNYYADEATLKELQDKDLITLKYEPNPNGSVFDIAGICDENKKIFGLMPHPERACEKVLGNDIGLKML

KGFLF

>WP\_002866403.1 MULTISPECIES: maf-like protein [Campylobacter]

MLILASSSISRANLLKTAKIDFRQVSFDYDENLDKNISPFLYVQKIVLEKERQFLSTLGKDFQNQNLLFA

DSIVCIDEKILTKAKDKKEAYEMLALQNGKYASILSAFLLVKPEKRVFSLSKTTLYFKNFDENALRDYVE

NDLYKGKAGCIMCEGFHQNFITHQVGNLSTALGLDIQTLKAYL

>WP\_002866402.1 MULTISPECIES: alanine--tRNA ligase [Campylobacter]

MDIRKAYLDFFASKGHEITPSSPLVPDDATLLFTNAGMVPFKSIFTGEIPRPNPPRKTSCQTCIRAGGKH

NDLDNVGYTARHHTFFEMLGNFSFGDYFKEQAIAYAWEFVTEFLKLPKDRLYVTVHENDDEAFNLWQKHI

QKERIYKFGDKDNFWQMGDTGPCGPCSEIFYDQGEEHFNSSEDYMGGDGDRFLEIWNLVFMQYERSADGV

LSPLPKPSIDTGMGLERVTAIKEGKFSNFDSSLFMPIINEISKLCNKTYIYESGASFRVIADHIRSSVFL

LAQGVSFDKEGRGYVLRRILRRALRHGYLLGFKQAFMYKLVDVVCDLMGGHYTYLNEKKDFIKEQIRLEE

ERFLSTIENGIEIFNEELKNTKEIFSGEVAFKLYDTYGFPLDLTADMLREKNLKVDEEKFELLMNEQKAR

AKASWKGSGDKTASGDFKNLLEKFGENHFVGYEKAECESKILALLDEDFKEVSTLKDAGWVMLKNTPFYA

TSGGQSADSGFMAKREVLDTQKFFNLNLSFVKAGEELKVGDIVHARIDTEKREQIARHHSATHLLHHALR

EILGSHVSQAGSLVESNKLRFDFTHHKALSKEELENIEKRVNEMIINSSEAILENMPLEEAKKSGAIALF

NEKYQGNVRVLTLGESKELCGGTHVKNTAQIGSFYIVKESGVSAGVRRIEAVVSKAALEFVKNQLEELSK

VKDELKNNDILSGIKKLKNEILSLKNELKNSSKTELDSKNIQGVEICVKRIDNGDIKAMIDDFKNKFAKA

VILLIQVKDEKITLAAGVKDVPLKAGALVKEAAQILGGNGGGRDDFATAGGKDLSKINEALKQSLETIEK

AL

>WP\_002866400.1 MULTISPECIES: gfo/Idh/MocA family oxidoreductase [Campylobacter]

MKIGIIGLGKMGQNHLNELSKNSHFKLNALFDLCKNPNLNIFDDIFYDDLDKFLNQNNDIIIIATPTNSH

LAIAKKVFKQCKCVLIEKPLALNLKEIDEISNLAKEYSVKVGVGFCERFNPAVLALKKELENEEIISINI

QRFSPYPQRISDVGILQDLAVHDLDLLCFLSKQEITKTNLLKKYTQDQTRESESIILCELEKCIASIHQS

WNSTQKLRKIHLITKNHFYEANLNDFSLLKDGNFIELTQQSPLFSEHEALLKLIDNQANHLASTSDAYKV

QEILERFA

>WP\_002866388.1 MULTISPECIES: exodeoxyribonuclease III [Campylobacter]

MKLLSWNVNGLRAICDKNALDWIAQEQIDFIGFQEIKAHEDKFPKKIYEYPFKHMYFNSAKRAGYSGVMS

LCNFDSEVKKCEFFDDEEGRVLEHRFKNIALFNIYFPNGQKDEERLNFKMKFYADFLVYLDKLLKDGFEI

IICGDVNTAHKEIDLTHPKANANTSGFLPIERAWIDDLLKLGFIDTFREINGEIKEKYSWWSYRMKARER

NVGWRIDYFFISKGLKDKLKNAFIRDDIFGSDHAPVGIEIDI

>WP\_002866385.1 MULTISPECIES: HDOD domain-containing protein [Campylobacter]

MIGDMNELLLKSVEVLPPLPDTVSKLRKYVSEANSNIETMKVAEIISSDPLMTAKLLQLANSPYYGFTRE

ITTINQVITLLGIGNIINIVTADSIRDSFKIDVSPYGLDTQNFLKTCNEEATFITNWLNDEDKKLSHLLV

PCAMLLRLGIVIFSNFLIQNHKDKDFLAFLNKNENLALAENEFLGVDHISFLGFLLHRWNFDDVLIESIC

FVRTPHAAREEVKKSAYALAITDHLFAPHDGSSPFNAKAAVALLEEAKTQGINFDLNNLLSKLPSKAKEN

LNKED

>WP\_002866382.1 MULTISPECIES: 50S ribosomal protein L20 [Campylobacter]

MARVKTGVVRRRRHKKVLKLARGFYSGRRKHFRKAKEQLERSLVYAYRDRRRKKRDFRRLWIVRINAACR

LNDLSYSRFINGLKKAGIELDRKILADLAMNDSAAFAKIAEAAKKAL

>WP\_002866376.1 MULTISPECIES: mechanosensitive ion channel family protein [Campylobacter]

MKKIIFSLCFFILYLGAQEFKFIDANISKEDEGIYALVEKYVDLNNQIKEFKKNNDENSSTFNGILSEFE

KDKKTILAKIPDMIVGQKINEEAVARFLKAKEKLLDVQKKNINKPYIYTDATLNLVYFNIVESFYSSLFE

VEKLFKNTASSEDLIATVDKAMENLQNSSNVNLDSFKSKITNPEELEKITLKERYISNAVDSYSEILKYL

RSNADLLESNYIFSLLELQVWIDRINEAIGVSFVNIGKIVISALVLVFFISLRRFFANIVYFFLVQLFYR

NKNDVDDIKVIFIENIKKPVGFLLIVYAISLCLTIATYPAPLSVNLSNFFHIVYAVLIAWLILRMLDGYG

VVLVSKLAQKSGKKEVVNLIIKILYFVIIIIALLYILAQLGFNISAIIASLGIGGLAVALAAKDIIANFF

ASILLLFDNSFNQGDWVEVSGIEGTVVETGLRKTTIRTFDNCLVFLPNSTIMGANIKNWSKRRMGRHVRM

YLGVGYDATPEKLEQCVKDLREFLHTSDLVAHDEDSALKYGDHTTKYRQNLVSINDLEGYKNACYVALSE

FADSSINIELYFYTKEIGGKDFREARQSLMLEFMRIIEKNGLTFAFPSRSIYIENLPPLDLQAKAIK

>WP\_002866374.1 MULTISPECIES: orotate phosphoribosyltransferase [Campylobacter]

MNLEQIYKDCGAYLEGHFLLSSGKHSQFYLQSAKVLEDPKLAAKLCDELAKIIASYKIEFDSICSPALGG

ILAGYELARACSKRFIFTERVNKEMTLRRGFEVKKGEKFIICEDIITTGGSALESAKIIESLGGIIVGFA

ALANRGFCAVENLKSPRKDNAKLPENLPLFTLGNFEFEIYDETNCPLCKKGSKAIKPGSRGN

>WP\_002866373.1 MULTISPECIES: RDD family protein [Campylobacter]

MKTKAKISSRWLRFRALLIDIFLIYVPILYLFYFLLGSKEAFLNNHFITTLCTFLFGLIQAIFLTKKAQS

PGLKAYDLYLIDIKTGKKLSFLRILLRYVIFIISFGLLFGLFVSFIRKDRLNLHDILTQSCIATKA

>WP\_002866370.1 MULTISPECIES: aspartate aminotransferase family protein [Campylobacter]

MKMDYKEQSHIIPTYKRFDIVLEKGQGVYLFDDKAKKYLDFSSGIGVCALGYNHAKFNAKIKAQVDKLLH

TSNLYYNENIAAAAKNLAKASALERVFFTNSGTESIEGAMKTARKYAFNKGIKGGQFIAFKHSFHGRTLG

ALSLTANEKYQKPFKPLISGVKFAKYNDISSVEKLVNEKTCAIILESVQGEGGINPANKDFYKALRKLCD

EKDILLIADEIQCGMGRSGKFFAYEHAQILPDIMTSAKALGCGLSVGAFVINQKVASNSLEAGDHGSTYG

GNPLVCAGVNAVFEIFKEEKILENVNKLTPYLEQSLDELIKEFDFCKKRKGLGFMQGLSLDKNVKVAKVI

QKCQENALLLISCGENDLRFLPPLILQKEHIDEMSEKLRKALKSF

>WP\_002866368.1 MULTISPECIES: N-acetyl-gamma-glutamyl-phosphate reductase [Campylobacter]

MKIKVGILGASGYAGNELVRILLNHPKVEISYLGSSSSVGQNYQDLYPNTPLNLCFENKNLDELELDLLF

LATPHEFSAKLLNENLLKKMKIIDLSADFRLKNPKDYELWYKFTHPNQELLQNAVYGLCELYKEEIKKAS

LVANPGCYTTCSILSLYPLFKEKIIDFNSVIIDAKSGVSGAGRSAKVENLFCEVNENIKAYGLASHRHTP

EIEEHLSYAAKEKITLQFTPHLVPMQRGILISAYANLKEDLQEQDIRDIYTKYYQNNKFIRLLPPQSLPQ

TRWVKSSNFADINFSVDQRTKRVIVLGAIDNLIKGAAGQAVQNMNLMFDFDEDEGLKFFANL

>WP\_002866365.1 MULTISPECIES: hypothetical protein [Campylobacter]

MIFDGNIYNKEGVFKAENAKLNFQGHARIHAYVSEEQAKKLQEQGLSALTKPVSFTQEDWEDRVFCFKRA

>WP\_002866362.1 MULTISPECIES: threonine--tRNA ligase [Campylobacter]

MEKEVIAYLDNETIIDSQSVKNTNLKEIYFDNSKESLEVIRHSCAHLMAQAIKNLYPEAKFFVGPVIEDG

FYYDFRVESKIGEEDLVKIEKKMKELAEAKIEISKYEITKNEALAKFQNDDLKQEVLLRIPDGAVSIYKQ

GEFEDLCRGPHVPNTKFLRFFKLTRVAGAYLGGDEKREMLTRIYGTAFADKESLKEYLTIIEEAKKRDHR

KLGTELKLFTFDDEIGGGLPIWLSNGARLRSKLEHILYKIHRLRGYEPVRGPELLKADAWKISGHYANYK

ENMYFTQIDEQEYGIKPMNCVGHIKIYQSDVRSYRDLPLKFFEYGVVHRHEKSGVLHGLFRVREFTQDDA

HIFCMPSQIKEQVLEILAFVDNLMKLFDFSYEMEISTKPEKAIGDDEIWEVATKALKEALDEQGLKYGID

EGGGAFYGPKIDIKITDALKRKWQCGTIQVDFNLPSRFKLEYTDSDNEKKQPVMLHRAILGSFERFIGIL

TEHCAGEFPFFIAPTAVGIVPIGEAHIAYAKEIQKELLELNIDSEVYEKNESLSKKIRTAEKQKLPMILV

LGDDEVAKRSVALRDRRAKEQKNLSLDEFIKLVKEKMSEVHF

>WP\_002866361.1 MULTISPECIES: undecaprenyl-diphosphatase [Campylobacter]

MENLNALILGIIEGLTEFLPVSSTGHMILGTTILGIDIDEFWKSFLIIIQLGSILAVIFVFWRKLFQGLD

IWLKLAAGFFPTGVIGLFVAKYLNALFNGWVVVGMLIFGGVVFILIELAHKNKQYRINSLEEISFKQAFC

IGIFQSLAMIPGTSRSGASIIGGLLLGFNRKVAAEFSFLLAIPTMIIATAYSIYKEPELLSNANSLIPLG

IGFITAFVVAVLVIKFFLKFISKFDFIPFGIYRIILGFVFFYLYYSGILNAGSEFKL

>WP\_002866358.1 MULTISPECIES: DUF4878 domain-containing protein [Campylobacter]

MACGSSNPEDLAKNFTKDLYSGDAKSVMSYIDLSEAKSDEEKTFVSGKITQVVAENAAKAKRMGGVKDIQ

IEEKTINEDSAKIRVLVLFNNDNNQSSNVFLAKKDGKWLVLLK

>WP\_002866353.1 MULTISPECIES: ATPase AAA [Campylobacter]

MSLALTFRPENFDDILGQYELIEIFKKFTALQKLPHSIFFGTAGSGKTTFARVVAKEFGLDFYEFDGGNF

KLEELRKILDNYKNSLYKPLIFIDEIHRLSKTQQEMLLIPMENYRLILIGASTENPYFVLSSGIRSRSML

FEFKSLGVKELETLLLRVQEKMKFSIDKEAKDFLLKSADARAMLNLLEFVLVLDEKHISLENLKKLRNTI

SSEGVSSKDTHYILASAMIKSLRGSDIDAAIYYLARLIDAGESADFIARRLVIFSSEDVGNADPNALNLA

VSTLEAVKNIGYPEARIILAQCVVYLASTIKSNASYKAINEALNYVKNNEALEIPNYLNNNHQEKQNYLY

PHDFGGWVEQKYLSKNLKFYHSKGLGEEAKLLDNLYKLKNHKA

>WP\_002866350.1 MULTISPECIES: trigger factor [Campylobacter]

MEVKAKQLDSVNATASVKIPSGMIKSEVENLAKKASKSVKMDGFRPGKVPVSAVLKRYERELTQDAEQNL

FKSAVNSALQELKKESKELVGEPYFEKFDRKDGEIIAELILSFKPEIKLDGYEKLIPEYQTPKVSKKEID

EKKDELLKRFATPEAIKTKRVLKEGDFAKFDFEGFVDDKAFEGGKAENYVLEIGSKQFIPGFEDGMVGMK

IGEEKDIKVTFPKEYGAAHLAGKDAVFKVKLHEIQELKIPELDDEMLKKLLPGEEKASVEVLDEKLKEQI

KNEKLFKLVNDELKGKFADALIEKYNFDLPKGIVEQETDMQMRAAFNTFSEKEIEELKASKEKYQEKRDS

FKEEAQKSVKLTFIIDELAKLRKIEVNDQELIQAIYFEAYRYGMNPKEHLENYKKQGALPAVKMALIEEK

LFNDIFMPKTEKSEKASKKEKEDK

>WP\_002866342.1 MULTISPECIES: serine/threonine protein phosphatase [Campylobacter]

MRILLVLRGNYYAGQEEFIKNNKLQNYTLDLNALRLLSGSVKNIVSEYKILNVKNDEDLSKILLKLLEMR

MQKGEFCIINAYNETLKIYKDLAKQYRYKMYVIVFDNSLKQCQEKNLLEAKKNGYIIPYALLEKTQDLLK

KNPKKYPILDSSDWKKCLYQMPNLSKYKKIHHIGDLQGCYSVLKEYIKTIKEDEFYIFLGDYINRGIENG

KVIKFLLKICEKENVCLLEGNHERHLIKWANGELSNSKEFNENTLKDFRKEKLTPRDARKLYPHLKECLY

YKFQNKFIFCSHGGVNFIPSKPEKISFIPSHDFIYGVGGYEDSQKIANQFCNFTSDNLYQIFGHRNKEKL

PMKIAKRVFLCEGKIDDGGYLRVVTLDKKGFECIEIKNQIYKKK

>WP\_002866338.1 MULTISPECIES: iron ABC transporter permease [Campylobacter]

MYKTLKYYKLGAILLALFLVLPIFGIFAELFYILFQNFNTSDLTQFSSIKENLSHFFDYLFLKFIKDTFI

ISVGVLCLSLILGVSSAYLIANYDFYFCKILEKLLILPLAIPAYILAFVYVGIMDFQGFFHENFGFRIDF

FNHYGVIFVLAISLYPYIYLFAKTAFKSEAKEAYEVAKIMKYSEFRIFTRVALLSARPAIFSGALLVLME

TLSDYGASAYLGVDTFSAGIFKLWYDLNDSYSSSVLSGILMLFVFLIMYVDYYYKNKHHYSFNQNLALFI

KKRKLNPIKQILSCIYCFMIAFVGFILPFIWLVYWGLKDHKLFESQFYIISFQTIILALVTALITTFLAY

FLMFSSRIVKNHFFNLFILKISSLGYSIPAAALGISIIVLFVFLDKIFHMSLLGNSLLVLVFAYVIRFLA

SAIYSLEGGYNKIHLNIDEASLNLRTSYFILFFKIHTPLMKHFLFLAFIIVFIDTIKELPLSRILAPFGF

ETLSVKAFWFASDERIYDAALPSLFIVFLSLMVVVWMDKITRKDDVRN

>WP\_002866336.1 MULTISPECIES: saccharopine dehydrogenase [Campylobacter]

MKNLLIIGAGGVSRVATAKCAMNSDTFSKITLASRTKSKCDEIAAFIKERLGVQIETAQIDADDSNAVVE

LIKKTGAQILLNVALPYQDLSLMDACIKAGIDYVDTANYEHPDLAKFEYKEQWARNDEFKQAGILGLLGS

GFDPGVTNVFCAYAQQNLFDEISYIDILDCNAGDHGYAFATNFNPEINLREVSAKGRYWENGKWIETQPM

EIKMEWDYPEVGVKDSYLLYHEELESLVKNIKGLKRIRFFMTFGQSYLTHMKCLENVGMLGIKPVMHQGK

EIIPIEFLKTLLPDPASLGPRTKGYTNIGCVIRGKKDGKDKQVYIYNVCNHEECYKETGAQAVSYTTGVP

AMIGTKLIAKGIWQGKGVFNMEEFDAKPFMEELNSQGLPWKIIEMTPSLGE

>WP\_002866335.1 MULTISPECIES: tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA [Campylobacter]

MFFEIALIGTTASGKTYIANTLAREFDAVVLSLDSLCVYKEINIASAKPSQDDLASIKYFGVNLLSVNEH

FNVELFIREYQKAKEFALARNLPLIIVGGTGFYLKTMIDGLSEKTLESKSSLNNDEIYALLLNIDPNYKI

EKNDTYRLKKWLGIYEQTREIPSEFLKRTQKTGVLKDIEIYELAWDKEILKKRIKTRTKEMLDNGLLDEA

KILFSKFDHKLKALNSIGLKECKEYLDGEISFKELENLITIHTTQLAKRQRTFNKKFQSKALEFDKALAI

LRMKFSIEK

>WP\_002866330.1 MULTISPECIES: 23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB [Campylobacter]

MIVYGKQIFFYILEYHKDCINELYLAKECDKTTFSKIAKSGFKIKKLDFKTAQAYAKGGNHQGFLLDIKE

SSFANLNEIKKNDFIVMLYGISDVGNIGAITRTAYALGVGALIFIGEKLAMEGVIRTSSGAALDLPIVIS

NDALSVINELKQVGFYFYASDGSGKEIHSVKISNGKKVLVLGSEGFGLSSKIVKKCDECVGIAMKNNFDS

LNVSAAFAILCDRMLNA

>WP\_002866323.1 MULTISPECIES: polyisoprenoid-binding protein [Campylobacter]

MKKVLLSSLVAVSLLSTGLFAKEYTLDKAHTDVGFKIKHLQISNVKGNFKDYSAVIDFDPASAEFKKLDA

TIKIASVNTENQTRDNHLQQDDFFKAKKYPDMTFTMKKYEKIDNEKGKMTGTLTIAGVSKDIVLDTEIGG

VVKGKDGKEKIGFSLNGKIKRSDFKFATSTSTITLSDDINLNIEVEANEK

>WP\_002866308.1 MULTISPECIES: thioredoxin [Campylobacter]

MLKKLILGFIILLFCACNDEKIDENILSKGTKTTEQYKQDANNLDLNSYKEIAEFFKDNQNIVFSDKPVL

IIFSANNCVYCDKLKHEIQNDKEVQNILKNTYNSYYINTSYHKIHNYDNKKTSTEELSREFNIDATPTLV

FFTPKHKTLLIYPGFMSAKRLALTMEILKDEKNQKLNEDELFKTLFLAYKEKNV

>WP\_002866307.1 MULTISPECIES: membrane protein [Campylobacter]

MKQSLIKFILLAVFCFSTPFLLADGKIQIGIVEGVTPISMKDAEKLLGQKNVYFVDVNSKEEREVAGNIP

NAVLVDAQNWQNLLPDDFNATLIFYGSNRFTFDASNIANLSQKLGYTHVYVMLDGIESWVLSGRKVQKEQ

IEKWQNAKNLDDFKDSIHSRMYFGDVPSCRDCHGKGEDKKSIRYNNAANLDLINKNCASCHKDVDKEFKH

SIHQNISQIQLDKDGKKKKIPTCTTCHDIHNNDPLMNAMTLKQRSDFKCGECHQDKQDRYHDTFHGKAMV

LNSPGSAPKIAACYDCHGKHNILKVEDLNSTLSSLNRVQTCAQCHPNSNENFANFIAHADHSDGENYPLL

HGAYIFMTALVIGVFVFFGLHTLLWSIRLILARLSHPIEWKKAKENAHNDKILIKRFSTFHKIQHFFMAA

SFLGLAFSGLPQKFYTAPWAQTMIDLMGGPIGATIVHHISAIVMFIVFFSHIGEIILVNWKRRDLVRDPQ

TGKLDKMKILKALFGPDSLMPNWQDFKDMKAHFKWFFGMGERPQFDRWTYWEKFDYLAVFWGMFVIGLSG

LVLWFPTFFSAFLPGWMINLCSLVHSDEALLATGFIFAIHFFNTHFRADRFPMDMVIFSGTQSEAEIKQE

RNAYYQRLKESGRLESLYEKNSKFNSYKGIAKLAGYLMLITGMIFLFLMIYAFIVDLLK

>WP\_002866306.1 MULTISPECIES: cytochrome c [Campylobacter]

MKKLISKGKVLTLLLGVGFALNVSSAENSNVLIQGEAAQDGDTKPRTLEGYVHQEDAFFKYLKEHHPMFK

YEKEGRIVGKYAISDREEEYVEFSNGPTFAQQNNLAHTSVTYRLGMESFLDFPNKFVGPKKCGECHPAQY

KAWERSRHAKTVRFPDEFEEVGNDLKKPMYNSQSTILPDGIYPDDVYAVIGTPRTKYGFIDRWLVRGTYH

VEDGNLSNMTGKIVAGGNQFSRLWSEFLTPEMTKKIAEFSPGFPTTMEQFGGNGSQVWGTNSYAAQYRKN

MLFQPASSYCETCHSFKFDFKSKEEFYKALGNTQELRKHTISKGISCEECHGAGAHLYGARGAGMPSNCE

RCHQRFSYNEEDAKKNPRKPFNAFFKSSCPACGTEGAQMYSSAHYDKGMRCSTCHDPHEVTFNDWKDGYT

KVGLKKTCTDCHDTQASFFKQGGIHSKDNCTACHMPNMMSCENFGAVQNPDKGGFDNVRASHIWKIKVDK

TAKTLNPPEGKERSPKTSGWTIARDDDGRFFLDLMWACGRTSFSDPNLMGPGASGCHSAVQSNLPKKLHF

TDQETIYDIVVGWQKPVKDGYENILKGVKEIDKAMAENPKLSVEKKSRVITLANQARAIAEKLQKDGSWG

VHGPVYSKKIVDEALVYIQEAKNILK

>WP\_002866266.1 MULTISPECIES: peptidase M23 [Campylobacter]

MRKNILIFFCFFLFVDISLANAINEKTKSLEENKRIQEQLNKKLEDLASDILNGEKSLKDLSLQIESLNS

QTSKLEASAKAQNQELNTLTSQNEDLLKSKSNMEGKLISLMAKDFAYDLPIPQGYIESEESFMAFEILGS

LNKVLNEEIFKISKDYEGVSRLIDDKQAQINKINESLKDYNAQLAKLQSLKQKQISEINKQKTDRAIYAK

KLDDLQAQQEELRKTLNQLKIINDKEDANSNKNDTKIVKNNQKIRQLGSSYQGSSVKRYTGKKTIAPLDS

FTVKQKFGNYVDPVYNLKIFNENVVLRSNKSDAVVKNVLDGKIVFAKDTSMLARVVIVEHDNGIHTIYAH

LDKIAPNIKVGKNIKKGAVVGRIKNDLTFEVTQKNFHINPLELISLN

>WP\_002866264.1 MULTISPECIES: nitronate monooxygenase [Campylobacter]

MNLQPLQIGKHTIKYPIFQGGMGLGISWDRLASAVSLNGGLGIISSVGTGYYEERKYASKELNAKPYGSE

NFYSRKGLQALINNARKVCGDAPLGCNILCASNDYARIARDACEVGFNVIVSGAGLPTNLPEFTADFPDV

ALVPIISSAKALKIICKRWQSRYNRLPDAVVLEGPKSGGHQGFTYEQCLDPNYQLEKLIAPVVEEAKNWG

SFPVIAAGGIWDKKDIENAISLGASGVQMGTRFIGTFECDASEEFKSVLLASKEEDIELIKSPVGYPARG

VRTNLLNLVDKRIGPKINCISNCVAPCGRGKEATKVGYCIADRLFDAWSGKKETGLFFTGANGYRLDKLI

SVKELMEKLVNGE

>WP\_002866259.1 MULTISPECIES: nickel-dependent hydrogenase large subunit [Campylobacter]

MSQKIIVDPITRIEGHLRVEVVVDDNNVVKEAYAGSTLWRGIETIVKGRDPRDAGFMTQRICGVCTFSHY

KAGIVAVENALGITPPLNALLTRTLMNAALFLHDHIVHFYQLHGLDWADVVSALSADVKKASDEAFKYTS

NPYATGADKLLEVQQRLKTFVDKGNLGPFANAYYGHPTYRLTPEQNLIVLSHYLECLRIQRIIAQCMAIF

GAKNPHPQSLTVGGVTCVMDLLDPARMGEYMVKFQEVQDFVNRAYYPDLVMAGKAYAHEASVLNDIGVNN

LYTFKEFQIGRDEWLFESGIIKNGDLSKVYEVEEDKITEEATHSWYADNEPLHPYDGKTNPNYTGLVDGE

SVDHHGNNVHSKVFDTKGKYSWIKAPRYEGNPMQVGPLANIVVNYAKGNPNVVPVVDEFLKETGLPLNAV

FSTLGRTAARCIEAKIVANNALKAFNNLVENLKVDQSTCAPYVIDNSKEYKGRYMGHVPRGTLSHWCRIK

NGVIENWQAVVPSTWNASPKDANGIGGSYEQCLIGLKIADVKQPLEIIRKIHSYDPCIACAVHVMDAKGN

NLSEYKVNVNL

>WP\_002866258.1 MULTISPECIES: Ni/Fe-hydrogenase, b-type cytochrome subunit [Campylobacter]

MQNKEEKLQRKAEYEFSIGLRLTHWVRAIAIVILIGTGYYLSYVFQSPISNGEPVNFMQAKYRLVHQAVG

FVLIACIIFKVYLFFCDKVSAKERRSVWDIFNIKLWIEQVKFYIFLGKHPHLKGVYNPLQFVTYFFFYLV

MLGIILTGLILYTHTYHEGLGGLLYHILRPLEAAMGGLADVRTYHRILMWVIMIFVPVHIYMAIFNAVKG

KDGAMDAIISGYKYIKEEKH

>WP\_002866246.1 MULTISPECIES: hypothetical protein [Campylobacter]

MHGKIAIYMDSTGRGTVTNSANTFFDFNRQIWNDKKSMPSVGMLVEFRTLSSEKKAEDGKPVQTSKTITG

IKPSKFQEFKEGDFITEHDFWKTDNDDELEDLQNSRRSAYITELYRTTDFDTIEKIPLSFTIPQAIQKYF

AHEILSVETLQANLQDEKEIPCILDYLILKRFLFKAYDTLIFMDNSIDQTQFSALKSIMMHLENSYKQMI

ADQKPNITKIFNETFLSLQCHYQALVATIDTRNNRLASLEAQMKTLQSEINLKSNAANADPEKLKARQER

LTKLQKEAEYYRTTLKRLDAIREDFYKKNYNIFENAFKLSREKLFKKIVTGLNLCATIMDVKIWHLSLKS

SGVKNSYFTMSNIENSFCSLSFAEHYLSRLNKSALNPFDQKLLVYIQKITKEQRKKFLVVTSDLDLLCKL

KIENFSQNPYYLVKYAPKKVNYQSLMRDNTFDIVYIDEKHVWENVADIILQGKHFDKSGKTKFKLI

>WP\_002866245.1 MULTISPECIES: GMP synthase (glutamine-hydrolyzing) [Campylobacter]

MKKADILVLDFGSQYTQLIARRLREQGVYAEILPFNVSLADIKAKEPKGIILSGGPASVYATDAYFCDKG

IFDLGLPILGICYGMQLMAHHYKATVAPAGHKEYGKANIEVKKDSALFKNLPKKQTVWMSHSDKVENLPQ

GFEVLATSENSPFCVFGNEDKKFFALQFHPEVQHSEFGKNILKNFAKYACNCESVWNMGSFAKTQAEKIR

EEVGSDKVLCAVSGGVDSSVVAALLASAIKEQVIVVFVDNGLLRSGEKEQVEFMFKNTLGIDLISIDASE

IFLSRLANVRDPEQKRKIIGNTFIEVFEEEAKKHKDVKYLAQGTLYTDIIESSVVGASKTIKSHHNVGGL

PEKMNLKLIEPLKEIFKDEVRALGLELGLSKEVVYRHPFPGPGLAIRIMGEVNRPSLELLRKADVILLEE

LKSTGWYDKTWQAFCVLLNIKSVGVMGDNRTYDNAVCIRVVDASDGMTATFSHLPYEVLENISRRIINEV

EGINRVVYDISSKPPATIEWE

>WP\_002866244.1 MULTISPECIES: hypothetical protein [Campylobacter]

MGKRNNIKMTKNASAVINELMDKPHYKPLKTLFFCKDFLSSFPLAKQRLIAKIYVKNHILNIITLHPAAY

QELNHDDSKIYIKFLIKAYGQKYPLSGFVDIKDIKIFSQKYTYAVNKNKNDEKLSKNSYLELSKGEFKNC

FEDEKLFKKFEDLRELIKKGSNLD

>WP\_002866239.1 MULTISPECIES: radical SAM protein [Campylobacter]

MKILFGPVSSRRFGRSLGIDLSPSKKQCNFDCVYCELDPKKAQEKQDEIISIDKIISEVKVVLEKNVEFD

FLTLTANGEPSLYPHLNELILSLRSIAKDKKLLILSNGTAVLDEDKFNALLKLDVVKFSLDSAVAKTFYR

IDRALKNIDLEKMIEKMADFRARFNGDLIMEILVVKDLNDNEEEFEALNQALKKIMPLRVDLSTIDRPPA

YAVKKVSEEKLLELSKLIDSTPVLLAKRHYEGEKLSFNEEELLKMLHLRSQSEIDIEVKFDEQSKTLLNQ

LIKEKKVKILDLAGVKFYKA

>WP\_002866222.1 MULTISPECIES: hemerythrin [Campylobacter]

MLPKWDNSYSVHNAKIDEQHKKLFELAAKVEVVSDRSVSKNEVKELLAEFFNYMKDHFNDEEKYMQLIGY

PNLEEHRKIHKEIIQTMINLIKDIKSTNDLKEKLYIVAKKWLLEHILYEDMKVEKWRSSSLSTDDGGDVS

FEAAEDEDNEHPQFYLYTCNCPGKIHDVPYSIHQKIELQGHKFTCKTCKQAIKFYKKHS

>WP\_002866221.1 MULTISPECIES: sensor histidine kinase [Campylobacter]

MAKKVIRQILLIYLTTTGIFLTIFFALWYQKLYEELVVLKGATLRENHRNIVISILNSRFTPIDISAKNI

AQSTALKFAIFDAKKIVFSNIDFDLRKAKIELKGRGICDNKVFFLAPMSADHYFLRHASNEEVNTNDGLQ

ILIQGEDVSKDLFWIRTKVFGFAIMAFCILGLISYILVKIALKPLEDKISTLNRFIKDSTHELNTPLSVI

LMSIEQLEHQNLGDNAKFTRIKLAAKSLSQVYSDLVFYNFPNTLETEKQKFDLRILLEERLEYFKVFFEQ

KKITLKLDLNQANIFAPKSQISKLIDNLISNAIKYNKKGGVISIILKANFLSIADTGCGISKSNLNHIFD

RYTRFNTDQGGFGIGLSLVKKVCDDNDIKIICESVENQGSVFKLNW

>WP\_002866220.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKIFYGVIAFVVVLLIAIYTILFTSFGNNIVANIAQKKIKESAGLDVNITHFNLRFSSLELQANIANMA

DFNLKGALSPFKLGFDLDYLISLNQNYAKNLGLNLNQNLSFVGKIQGKASDFTLDGKGYLLGSNVLLNAR

MYNYSPIALNLDAQNLKIEEILHLLSYPSYAKGFLNAQAKISAQNLKPDGNIIIKLDTNYINYEAIKKDF

SLDLPLNSNPKAEILANVKEDKIYAVSKIYNDYLNLQTQKTLYDISKNALSTDFNLSIPSLVKLETLTKT

RLNGNLGVIGQTSVVNNALSSLNAQVIGLGGEVKASLKNNKIFADINEASLEKLLALAGYGALVSGNLNA

KLLNADLDFSNFDLEAKINNAKLNTNELKKIAKIELPNTIFSFDAKANAKNSNIAYNALLASNLLNIKKL

QGSYNLKNSELNTDLNAFIDDLSQFSAIAGQKLQGKADLAAKAHIIGTQIQNLNANANLADGVIKADSNG

KKLDLNIDKLDLSKLFVIAGMPNYASGIVNAKINLDNIDFNNLNGKANLEAKGILNATTLSKILNKNFPN

NTSYDLNTKINFKNNIAQFDSVLNSSLADLTKLQGSFDISKMLLNSDFNLKINDFSKLGFLLDRKLKGKA

EFNGKVGFDKSLNFVVNSPNLFEGRLQSTLKDNLLLADLNGVDLSSLAQGLDFMDVYQGKADVKANYNLL

SEEGEVNLDMKEGKLKPNLITNALKILTLKDITNDVYRTANAKALIKKENIKLDLNMQADRSYILVQSGA

LNSKSGALNLPFDIKLDRANFKGSITGTTENPKVNLNAGSVLNSIKNVVGGGVSDGAKSTGDKVDKAVNK

LLNKIF

>WP\_002866217.1 MULTISPECIES: FAD-binding oxidoreductase [Campylobacter]

MKKEFEQYFKRFLGEENAYFDEIHKRAYSYDATKKHYLPDGVLFPRNEEDIAQILKFCNENNIIVIPRGS

GSGFTGGALAVNGGVVLAFEKHMNKILEIDLENLVAVVQPGVINIHLQKEVAKYGLFYPPDPASMEYSSL

GGNVSENAGGMRAAKYGITKDYVMALRAVLSSGEIIRAGKRTIKDVAGYNLAGILIASEGSLAVLSELTL

KLIPLPKFKKTAFAIFPSVKSAMNAVYKSLASGVNPVSMEFLDNLSIRAVESKFNKGLPIEAGAILIADV

DGNVREAIDEDLRNLEHYFLEAGASEFKIAKDEQETADIWFARRNCSQSIAMYGTLKLNEDITVPRSKLP

ALLEGIDEISKKYGFKIPCFGHTGDGNVHTNVMVPDKNDKEQVKKGYEAVEEIFKLTVKLGGTLSGEHGI

GLSKAPFMNLAFSEAEMNLMRNIKKAFDPNNILNPFKMGL

>WP\_002866215.1 MULTISPECIES: DedA family protein [Campylobacter]

MQDMIDTLIKYGYIVLFFYSLGGGMVGILAAGVLSSQGKMDLSFCIALAFIANTIGSTLLFILGKYYKKD

IMPYFKKHRRKLALAMMKTKQHGIILLVTQKFIYGLKTFIPIAAGMAKYNFIKFFIINTLASLAWAIVLG

FAAYTFGYVIEAIFDKLSLYPYAAPLFLLFLAGIIWLYLSKFSKK

>WP\_002866214.1 MULTISPECIES: TlpA family protein disulfide reductase [Campylobacter]

MKIKKILLLVAISCLFVACGNDKEKQQNDVNLSTEASINQSDDMNFKLNLIDGGSISVKKENAVLNFNDE

DKATLFVFFTTWCTPCIAEIPHLNKLQEKYNNDFNIVGVLLEDKSNDEIQKFIEQHKISYKVANGENNYL

LAKALGGVNGIPTMFLYNKHSKLINQYLGLIPEEMLEIDIQKAIL

>WP\_002866183.1 MULTISPECIES: DUF3373 domain-containing protein [Campylobacter]

MKTKFSLILSACLLSSSLFAKNTDDEITKLQKQLAQIQAELAEIRKEREAQAKQNEAVKAELADLNDRAD

ETEFQAALSKVKFGLEFSTAVSNTNYKVGGQDYSANNKWMNELHLNMNADINDKTKFYGRLSMAKNWSQM

GWSGSPLDLDAGRNTRSSGPVLYVDRAYLDYYITPEWIATIGRQPGTDGPGSNLRNNALRQSTYPALAIN

ALGDAAVITYKPESLQDHKVAIRAAYGKTYQWDEESGKVRDWMSDQKDADANLYYAAVEGELPIEGMGDN

LIIFNVAHMTDFALPIPGSTTLLGDDDGVINLGNLTLANIHFENYKAFGTNFNYFVSLGYSNGANAHTLS

ANPTVQSQLEINEKDGYAVHVGGRYDFTKALKVGYEFFWGSRYWYTMSRPSINDPLNIRMTRGTAHDFYV

IYQLDRYQFLRLSYTNIQNIWGNRGLPFGGAKKDKARADNIMLMYNVKF

>WP\_002866182.1 MULTISPECIES: DedA family protein [Campylobacter]

MQEIISFIVETASAWGYLGIIILMTLESCFIPFPSEVVMIPAGYLAHKGKLDITLCILSGTLGSVLGALI

NYYICFFWGKNFVLKWGKYFGINEVKFAKFEEFFNKHGEFSTFTCRLLPGIRQYISMPAGLVKMKLVNFI

LFTALGSAIWVAILVFLGYYIGQNEELIKTYLTQILIIIIVFVILASLIYIKIKKPFKKA

>WP\_002866181.1 MULTISPECIES: L-lactate dehydrogenase [Campylobacter]

MAKIGIVGLGYVGASSAYSIVTQGICSELYLYDIKQDLALAHARDLEDMSAIHFSYTKIFHVPNLENLAS

CDIIILAFRKESLKELPSRLVELQNNILELKDIVLTLKNANFKGKYIVATNPNDTITYYTQVLSQLPKNH

VFGSGTNLDSSRLKKFLAKDLNINSKDIFACMIGEHGDSQFAALSNASVLGQNLLDFYKQKLGKDLDIQK

LEKAVISEGYFIYERKGRTEFGIGTSCANLAKAILEDRKSLHPVSVVFDDMAFSMPAIIGKDGIEKVFEL

KFNEKEKIKLENSKQQIKNAIQSVKDKI

>WP\_002866180.1 MULTISPECIES: membrane protein [Campylobacter]

MEKPDIQRLTNFLIVYTKTLLGAGTYTARVAKCVGRIAEVYGYEININFFFHHITLNVVDMDDNSIQRTY

VIPNHHAHVNFKLIFDLSALSWAIYDHKYDLEKAKVVFEQISQQKKHSYLLNLLFVSMANSAFCRLFGGD

FGAGNLVFFATFVGLLLRYILTKAKIDLRIQYILCSFISSWFVFFGLDMGYTNTSDVALGSSILYLIPGV

FFINSVIDILKDHILMGLSRIISVGILICCIALGIYMTLSISDFGILR

>WP\_002866179.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLCPVCNVDLVMSDRSGVEIDYCPKCRGVWLDRGELDKIIERSVPNTANFNQASRQESRYNDSAYHQHND

YYKKKKKESWLGELFDF

>WP\_002866178.1 MULTISPECIES: cation transporter [Campylobacter]

MYKFLSHEPLANKSCHHNHEEHSHEHHHSHADARSVDKKILKISLLMTFSMMLVQFIYSILSNSLALLSD

TLHMFSDVFALALSFLAIIAVEKWQDHQKTFGYFRLEVLVAFINALTIILSALFIIYEAIEKFINPKEID

AKTMIIVAILGFLVNGINALMMFKGANLENVNMKSAFLHMMSDLLGSLAVIIGGIVVYFSGIVYIDTILA

IVLSILLLRWAIILLKQSANVLLESSPVDIEKVRQVLLLNPSVDEVVDLHITQITNKMLVASMHLKVRVC

DLKEFEKLSQDLSHKLLHEFEIGHITIQPIRSENEI

>WP\_002866176.1 MULTISPECIES: copper-translocating P-type ATPase [Campylobacter]

MEELRIKIGKMTCVNCSNAIERACKKIDGVKDASVSYVNSSGVFLLEDQEKRKDIIAKIKNLGFEILEDE

QSLNAYKVKKHLELRKNLLLSIVLSVIIMYFEMFVKSSFSQNIQMALSFFGIFYCGRDFFSHAFLGLKSK

NLDMNTLVALGTLSAFVYSFLVYLQIFKEEDLYFSGAMMIISFVLLGKYLESKAKFKAQDYQRILENIDT

KKTKILLEDESIKEISSSFVKSGDVLLVKEGESIVADGVVLLGSAELDMSFLNGEFLPVLKKEGDEVQAG

AVVLNGTLRIKANKKAMDSTLEQIKNLVFEAGNIKSPLANLADQISKYFVGGIIFFAFLVFVFWALKADL

NTAFLHACAVLLISCPCALGLATPIALVVASSNAAKNFILIKNPAALEKLALVKYAFFDKTGTLTKENLS

IFKHNLSKDDFDKLCQIESLSSHPIAKALHKDQIFDLKGEGRVIVGSGIKYKEDSDIYLAGSAKFLHENE

IDTKESDIFFDTFKEYVRVYFAKNKKCLGGVLLSNALKDGAKELVLNLKKQNLKTFILSGDHVKNVEKIA

KELQIDEFYAQLKSEEKLRIIQKFKKTLFVGDGINDAAALSAATVSMSFSKANELAKKTGDFILIKDDLS

AIFKCFKLAKKTRSIIKLNLFWAFIYNVLCIPIAAGFVPFITLSPHIAALAMCFSSITVVLNSLRLKRI

>WP\_002866163.1 MULTISPECIES: glycosyltransferase family 2 protein [Campylobacter]

MPQLSIIIPLFNSCDFISRVLQSCINQTLKDIEILIIDDKSKDNSLNMVLEFAKKDPRIKIFQNEENLGT

FASRNLGVLHSSSDFIMFLDSDDFLTPDACEIAFKEMKKGFDLLCFDAFVHRVKTKQFYRFKQDEVFNQK

EFLDFLSKQRHFCWSVWAKCFRKDMILKIFEKVKIDERLSYGEDVLFCYIYFMFCEKIAVFKTCIYHYEF

NPNGRYENKNQEILNQNYQDKKKSNEIIKRLSREFLFDEFHQKLFEVLEREEKSLCMRANKI

>WP\_002866160.1 MULTISPECIES: glycosyl transferase [Campylobacter]

MKFFIINLKIAKDRKEYMQNLCLKHNLDYEIIQAVDGKELDSDFVKNISDFSLSEKYLGRTLSLGEIGCA

LSHKKCFERMFELNLNECLILEDDAYFDEKLNYILSLKDKFPKDLELFLLGHYRQVYLDDGFRIESPFSL

RYDYKIDDFYHAKRLVGGGNGTHGYYINKNGALKMYKYLEKIIFPYDHCTSNDNIINVYALYPVVITTDE

IFGAQTYVQDDNKRRYRKRSKISKYIKKIKNKIIFFIPSLKKLRKYE

>WP\_002866158.1 MULTISPECIES: DUF2972 domain-containing protein [Campylobacter]

MKKSKSIQIIKQQGIAEFIKYKKIKIYTKYEKKFNINIFTPYLLKFCKPLKDDYKFILFSYGVSGHWAFK

SFLKYCELDDFVLYQNNYSYYKEYKNFNKKNYYVEIASYQSIQPKYKHISKILNKNKPVVILTRDPISRL

KTMVNHGFYKIEELGKNELKNFYINEDIFENLDRIRYTDKNGYNANLKKPDLSSIYFIVNEELSFSYFSN

INLIKNKNILYVDTKSISKDNAFATIKTLAKELNFKEPNDNDEYKFKQKFWNELYYLLPYRLIVNNDILI

IVSDENKVFLDNDKHYNEIKDDLIDIKKELVNPKSKLFDKISINIENKNWIIVKDDKALINDLREYFEKF

MIILEKKANERLENMVKEEDVLNYLKEHQDLGKKLKNILDYELQHIKEHRPGIINSWEYYKKFLEIF

>WP\_002866155.1 MULTISPECIES: glycosyltransferase family 2 protein [Campylobacter]

MAKISILTPCFNHEKYVSYFLQSVLEQSFSDFELIIVDDCSNDNSTKEIQKFKDPRIKLIKHEFNKGINA

TLNTAFENSNGEYIVFCASDDILEKNALEIIYKTFKDNDIIAVYPNLICIDENNEILGNLYPLKQRNKVE

LLYYLFMRYNCLTSVGLSLKRDVFEKLYPLPNSMCNYQDMKMHIDILNIGEIKILETQLIRYRRTRSKTN

ISAHNSITTTRENLETEMLLDTYLKFDNIFLLEQIFHKEINKTNIKPYQETLPFFLGIMALESENIYKKY

WGYHKIMEFYKNDANAKILYEKYNFTFKDYLQLAKKCDTGDIFIKKYRKYKKISNFLIIVCFFLILCIII

ITIY

>WP\_002866152.1 MULTISPECIES: WxcM-like domain-containing protein [Campylobacter]

MIKNCKILNLRAIRDNRGSLIALENNKEVPFEIKRVYYIFDTDPNFPRGAHAHKNLEQVLIMMSGSCDII

LNDGKNYEKICLNRPDIGLYIGKNMWREMKNFSYGAKLLVLASDFYDEKEYIRNYDEFLRNINDT

>WP\_002866149.1 MULTISPECIES: dTDP-glucose 4,6-dehydratase [Campylobacter]

MYILVTGGAGFIGSNFLLYFFEKNPNAKIINLDFLTYASDISNLNKLKNNPNYVFIQGDISDVSLVGEIF

SKYKINAVINFAAESHVDNSIKNPDIFIKTNIYGTWNLLNSAYKTWFLEPFLKKDEFKQSFFYQISTDEV

YGSLGENGKFTEDNAYAPNSPYSASKASADMLVRSYHHTYGLNAVISNCSNNYGPFQHDEKLIPTIIRNA

LNETPIPIYGDGKNIRDWLYVKDHCVAIESIYKYAFEKIKENNSFFDVFNIGTNEEWQNIDIANKICSYL

DNVLPKNTSYKEQITFVKDRAGHDRRYAIDSTKLQRVIGWKAQENFNSGLDKTIQWYIKKYKG

>WP\_002866148.1 MULTISPECIES: glucose-1-phosphate thymidylyltransferase [Campylobacter]

MKGIILAGGSGTRLYPSTLTLCKQLLPIYDKPMIYYPMSVLMLAKIKEVLIISTPKDIDRFKELFKDGSF

LGMQIQYKIQERPEGLAQGLILAQDFIQNDDIALILGDNIFYGQGFSDILENAKDDLKKGFASIFSYHVK

DPERFGVVEMDQNGNVLSLEEKPKNPKSNHVATGLYFYNNDAIDIAKNVKPSARGELEITDVNIEYLRLN

KLKSQHLGRGFAWIDTGTHDSLIEASSFVQTIELRQGYKIACLEEIAYNNNWIDNEILEKRALLLSKSNY

GQYLYKILSQGK

>WP\_002866145.1 MULTISPECIES: lipopolysaccharide heptosyltransferase I [Campylobacter]

MKIAIVRLSALGDIIQSAVVLQFIKNFKKDIEIHWFVDEKFEGILKNHPLIDKLYALPLKDKKILKSLKI

LLKARKNNYNAVIDLQGLIKSAIVSRILSRNNFGFDKNSLKESFAHNFYNQKLELDYNENVFVRYLSLTS

FMLNTDFNVKNLAFKQDIFSVDENLKQLLNNKLKLDKNEKNILIHVGSSVENKIYPKTKLAILCKLLINE

FQQAKIWLAWGNVKEYEFAKEVLNLSGIDETHIELAPKFNLEELMAFTKMMDLIIGNDSGPTHLAFALNK

ASITIFGATPSYRNAFQTHINKIIDAGKKIQNTKHIDKSDFCITRIEEEDIFKLAKGLLNEK

>WP\_002866139.1 MULTISPECIES: peptide-binding protein [Campylobacter]

MLKKEYLKNPYLVLFAMIILAYVFSVFCRFYWVWWASEFNEYFFNNQLMIISNDGYAFAEGARDMIAGFH

QPNDLSYYGSSLSALTYWLYKITPFSFESIILYMSTFLSSLVVIPTILLANEYKRPLMGFVAALLASIAN

SYYNRTMSGYYDTDMLVIVLPMFILFFMVRMILKKDFFSLIALPLFIGIYLWWYPSSYTLNVALIGLFLI

YTLIFHRKEKIFYIAVILSSLTLSNIAWFYQSAIIVILFALFALEQKRLNFMIIGILGSATLIFLILSGG

VDPILYQLKFYIFRSDESANLTQGFMYFNVNQTIQEVENVDLSEFMRRISGSEIVFLFSLFGFVWLLRKH

KSMIMALPILVLGFLALKGGLRFTIYSVPVMALGFGFLLSEFKAIMVKKYSQLTSNVCIVFATILTLAPV

FIHIYNYKAPTVFSQNEASLLNQLKNIANREDYVVTWWDYGYPVRYYSDVKTLVDGGKHLGKDNFFPSFA

LSKDEQAAANMARLSVEYTEKSFYAPQNDILKTDILQAMMKDYNQSNVDLFLASLSKPDFKIDTPKTRDI

YLYMPARMSLIFSTVASFSFINLDTGVLDKPFTFSTAYPLDVKNGEIYLSNGVVLSDDFRSFKIGDNVVS

VNSIVEINSIKQGEYKITPIDDKAQFYIFYLKDSAIPYAQFILMDKTMFNSAYVQMFFLGNYDKNLFDLV

INSRDAKVFKLKI

>WP\_002866136.1 MULTISPECIES: UDP-N-acetyl-alpha-D-glucosamine C6 dehydratase [Campylobacter]

MIFYKSKRLAFFLTSDIVLILLSVYLAFSLRFSGDIPSIFYHGMMVSAIILLVLKLSFLFVFRIYKVAWR

FFSLNEARKIFIALLLAEFCFFLIFYFFSDFFNPFPRSAIVIDFVLSYMFIGTLRISKRMLVDFKPSKMK

EEETPCIVVGATSKALHLLKGAKEGSLGLFPVGVVDARKELIGTYCDKFVVEEKEKIKSYVEQGVKTAII

ALRLEQEELKKLFEELVAYGICDVKIFSFTRNEARDISIEDLLARKPKDLDDSAVAAFLKDKVVLVSGAG

GTIGSELCKQCIKFGAKHLIMVDHSEYNLYKINDDLNLYKEKITPILLSILDKQSLDEVLKTYKPELILH

AAAYKHVPLCEQNPHSAVINNILGTKILCDSAKENKVAKFVMISTDKAVRPTNIMGCTKRVCELYTLSMS

DENFEVACVRFGNVLGSSGSVIPKFKAQIANNEPLTLTHPDIVRYFMLVAEAVQLVLQAGAIAKGGELFV

LDMGKPVKIIDLAKKMLLLSNRNDLEIKITGLRKGEKLYEELLIDENDAKTQYESIFVAKNEKVDLDWLN

KEIENLQICEDISEALLKIVPEFKHNKEGI

>WP\_002866135.1 MULTISPECIES: membrane protein [Campylobacter]

MYIKDIQRFEDNRYRARAYMSYILTRNLPNKLPDIHLETIKTALDKIAHEVVVFDALYILDISGMQIENA

ISLNKAHEIGQGEDRSTRSYFYRAVKLKRCVLSDPYPSVLNNELCVTASIPIYDDKNNLLFVVCIDIKLE

DILKIIQAGKFEFVFTQFSRLVYFCFALVLFVITCFLFQKGFFSLFDNQAIGIEHMFESTIAITLALAIF

DLAKTLIEQEVLGRTKKEEGGIQKTMVRFLGSIIIALAIEALMLVFKLAIGDLSQMIYAIYLIGGVSLLL

LGLSVYLFTVKYKNNNI

>WP\_002866133.1 MULTISPECIES: 50S ribosomal protein L11 methyltransferase [Campylobacter]

MQKKYYELFFIVEERYKNLFLDFAFDLGIEAIEEKDNGVYIRSHESLEELSWALEIFAQKLTTTFNLNHK

IISNLSLVEKENKDWIQEYKKGIKPILVDNVYIHTTWQEEKKNFINIKINPALAFGSGHHESTYSCVKFL

QKFSKSKLRALDLGCGSGILGIIMAKFGCNVEICDTDELAIDSSLENARLNGVDFHKAWCGSIDKANGLY

NLIVANIIADVILILEKDIKNHLEDNAILILSGILDKYSTRIKEKFQDLELIDEMQINEWCSFVYKNNKK

G

>WP\_002866123.1 MULTISPECIES: tRNA pseudouridine(55) synthase TruB [Campylobacter]

MNKIFAAFKPRGLSSNAFLSTLKKKYKNKKAGYSGTLDPFAKGVLIVAFGQYTKLFRFLKKTPKTYKATL

WLGVYSLSLDDQNIKEIKNIKEFDLANLQQIIDQMQGIISYTPPQFSAKRINGTRAYELAKKGIEANLKP

CQMEVFDCKILSYNHPFLNIEITVSEGAYIRSYCELFARKLGINATLSSLERIKEGKFVYNNEKSLNVLK

YINLKPNFIKDLNKLENGAKIFVEELKFHDEGDYYIETEKYFSIINIKENTVKYLLNKVEKC

>WP\_002866112.1 MULTISPECIES: M23 family peptidase [Campylobacter]

MVKNKFTITITDINGSRHFYLNQIIKKIVFYTIAFIVLFLVFSGFYIKYLDSKLSDISEKREELLKKSKE

LELSNSQMQKSIEEKTQQYAAIEDKIASFEEALGLEAENNLTISARLDNLQLTNEQQLGILGQIPNGWPI

ENKGITGNFGWREHPLLKRREFHPGIDLRAEIGTPIYAPASGVVEFSGYSDNGYGYNVILLHNFGFKTVF

AHMMRKEVVKAGQFVSKGQLIGYSGNTGLSTGPHLHYEVRFINKTLEPLYFLNLQRKNMNDFFNQERRVP

WQSLIKAVSAQHPALAQKQQ

>WP\_002866072.1 MULTISPECIES: ATP-binding protein [Campylobacter]

MKKYVLSLALLGSLLGASELKYQEFDGFKNPESIFVDKNYVYVSNVGEKLEPLAKDNDGFISKLDKNGKV

LEYKFLTHLNAPKGMMEIGKTLYVVDIDVLRGFDLKTKKEIFNLPIKGAIFLNDIEKLDDNTLLVSDTGT

GLILKVDLKTKQYDELLKLDLAKFGGPNGLYLDRKKHKLFIAGYHPDGVSGGVVMAYDLNTKELSIIKNE

KESYDGIVPYKDGLLVSSWGNNLNGYIYNLDNVKSVKLELPLMKGPADIFIEGNILWIPKMAEGKIFKVE

LNK

>WP\_002866071.1 MULTISPECIES: MFS transporter [Campylobacter]

MASFKKIFWINVIIVIIVAFNLRAPITAVGPIIDIIKDKYYLNSTVAGILTSLPLIAFGSISFIVGYFSP

IRAIVFGIFLIFLGEIIRSYFGVYGLFLGMLAMGCGIAIANVLLPSFIKEKFPKKMASIMGIYSLVLSIS

SIMGIALAIPLLSVFDLAGAMFFWAIFSFIALVVYYPQAKNGRFFRIKKKAHKKINLFTNLTTWKITLFM

GFQSFLAYSLFFWYVQIVVEKGFDKEFSTSMVLFAQLVAAPVSLFGPLLLGKLRQNLHTFYIAGLCSMYV

IAFGILFIFDSKISIIISAFIMGFPWGGVFGIALLFIAQKSSNAQIAARLSALAQGFGYLIAAQGQWIIG

FLHDKFENFSFAILMLVFVGILVNIFGYLSYKSQIIK

>WP\_002866068.1 MULTISPECIES: arginyl-tRNA-protein transferase [Campylobacter]

MLEIGFCTLEDQCPYLKDKRSRIEYKYIENCSKEINNELIKRGWRRFGRYFSRPICKDCDECLSLRILVN

EYNFSRSERRVINKNINTKVILRTPNLSNEHLFLYDKYHRFMEEKKNWKRYDLSFKQYYNLYVDGFMNFG

YELAFYIEDKLVCVDLIDILEDGISSIYCFYDPDFSYFSLGKFSLLNEIQIAKKMNLDYIYLGYFVKKCQ

SLSYKADYTPNEILKGTKELFENEVLWEK

>WP\_002866067.1 MULTISPECIES: adenylosuccinate lyase [Campylobacter]

MQIVQTLETINVNTDDISVFQYFKDLITKNFTKVIGRKNKIFSFFEENEIPQRRYFLKVLDQKYRKSTNE

GIENLQDAHFKTFRLIFEQNNMLKPMLFIKIDFVAGRILMKLSSNEKLFITYIRNYFQDHYIEYNEMTNI

LILEYKNENTLELFEAFADESEHLKYCVNFEVDREEYKKFRQNIHNKENMKWKFNALAKLFSNYFNTLEC

TPQNDLSEIRQKYLILVKLYHPDFHQGKSAIEKAYAREQFEKIQIAYDNLKALYKNNT

>WP\_002866062.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKIYFMLAIAGIFAGCVPSANSATKNSSANSTPPSQDVIVQKVDKDDVRDIIREEKMLAPDASETELSF

TAVGEGIAPMNTVSTAQALALAKRAAITDAYRQLASKLYGVKVNGKDTVKDAMLRSSTITAQVNGLIKNA

SIIDENFNQGLYRVNLELKIDADKWKELFAY

>WP\_002866046.1 MULTISPECIES: tRNA (N(6)-L-threonylcarbamoyladenosine(37)-C(2))-methylthiotransferase MtaB [Campylobacter]

MKEKVFFKTFGCRTNIYDTELLKSYVKDYEIINDENKAQIIVVNSCTVTNGADSGIKSYVNTMQKKGIKV

ILTGCGAVSKGKELLDKKQVFGVLGASNKDKINEFLGAKTSFYELGNLNFIDKDIVCEYENHTKAFVKIQ

EGCDFACSYCIIPSVRGKSRSVDEKALLKQVEILGANGYSEIVLTGTNIGSYGLKNGTSLGKLLQKMGQI

SGIKRIRLGSLEPAQIDESFLEILDETWLERHLHIALQHTSEKMLRIMRRRSHTDNDLKLFNTIASKGYA

LGTDFIVAHPGESEEVWQEALKKFKEFPLTHIHAFIFSPRNNTHSATMKDVINGTLAKERLNILKSIVEK

NNYEFRKKNQVPLEVLVENQKDGFFEGYDQFFNKIKIKSDKDIAKEWIFISQYEAQEKSNFANLKG

>WP\_002866043.1 MULTISPECIES: LysR family transcriptional regulator [Campylobacter]

MKIKDMEIFLDLLNTQSPTHTANNFSITQPNVSIVIKNLENKFDGILFERLGKKLLPTPKALELGKNWLK

IIQAYYQSLEKLNDESMLLGEIKIASTQSISEHFLAPILFDFKAEFKNIEIHSQTQNSKECLNLLKNGNI

EFAIIEAELDPALVEYENLEINFWQDDELIVATSDKKLNEKEFYIDELLEQKWILREAGSGLRDKFLNEI

GASSKKLNIFLELDRMAAIKELVLQKKAISIFSKKSIEKELKNSTLYEIKLKNIDLKRKFYTLKRKNYNF

NRALEKFEKIFKS

>WP\_002866038.1 MULTISPECIES: ornithine carbamoyltransferase [Campylobacter]

MKHFLTLRDFSKEEILSLVNHASELKKEPKKLLQDKTLAMIFEKNSTRTRMAFELAITELGGKALFLSSN

DLQLSRGEPVKDTARVIGTMVDFVMMRVNKHETLLEFARYSKAPVINALSEFYHPTQVLGDLLTIKEWNK

MQNGIAKVAFIGDSNNMCNSWLIVAAILGFEFSIAIPKNYKISPEIWEFAMKQALISGAKISLSHDKFEA

LKDKDVVITDTWVSMGEENEKERKIKEFEGFMIDEKAMSVANKDAILLHCLPAYRGYEVSEEIFEKHADV

IFEEARNRLYVVKALLCFLDNQRGRE

>WP\_002866037.1 MULTISPECIES: oxygen-independent coproporphyrinogen III oxidase [Campylobacter]

MRDYKAFVKYSKAGPRYTSYPTAVEFNTNFKYEEYIEILKKQDRSLSLYFHLPFCRSACYFCGCNVIYTA

KEESKERYLTYIFKELDILNTILDTKREVVQMHFGGGTPTFFSAKQLQNLILKIRSVFGNFSKDAEISCE

IDPRFLNEEQATVLTQNGFNRISFGVQDFDEKVQKEIHRIQPFELTQNALNLVRSKGIKSVNMDLIYGLP

YQNLQSFTQTLEKVMLLNPDRLAIFNYAHVPWLKKNMRKFDENTLPSPDVKLEILEFCEKFLSKNGYKMI

GMDHFAKENDELFKALENGTLHRNFQGYTTKGGADLVGVGLTSIGEGQRHYAQNFKDMSSYEAALDRGVL

PFERGVALSDDDELRKAVIMELMANFKLDIKSIEKEFCIDFQEYFKEDLKALEEYKDFINFDENFIKVNE

TGVLLIRNIAMCFDAYMKNISEDKKVFSKTV

>WP\_002866034.1 MULTISPECIES: MFS transporter [Campylobacter]

MEKSLLFHFRRIGVEFIIFSVYAVFSISWAATGSLMPLISNDLALNTQQATLITSMIVVAKIFGASFTAF

LVYKFGLKKGYFLGCILMSSGIFLSFVDSYSGILVIRFLTGLGSACALVCLVPIAQQWFEKKALHFVISF

NITSNLVGITLGLILAESISNYFGNWRDSLSFYAWINLILLILWLFVGKDENKKEEKKNNAKDLIYALKS

RVTWGMIIFYIGPILFLNSLFTFLPTFYAQYAGFSKELADFAKKEIPALANFAIIFGPYLGLFFKRKNIS

FKIMLLSGGACIFICGFCMLFLQNLVLIQIFAVLSGIFYSMWFPFFFNLPSELKNSNPNQTAYIMSAFWS

ITFVILSFNLWVVSWSVDKTHSFTLGFVYIFALIFISAILAQFVLPRRENFIQGEK

>WP\_002866032.1 MULTISPECIES: peroxide stress protein YaaA [Campylobacter]

MKILFSPSESKNENCVKNPINENSFIFKELFPYRMEALKHYEEFIKNASLQNLQELFGIKNENEIDKFKH

DLKQAPTQEAILLYTGVSYEYLNFKALDKKSQAYILENTLIFSNLFGVVRANDTLPFYKFKQGAKIGNFA

IEKFYKEHFSKALDEYLENEEILDLRAGFYDKFYTPKKKFYTYKFVKNGKVISHFAKAYRGILLSISAKN

QVKNNKELLANLPSNLKLKEIQIKGLKEEIVLEILD

>WP\_002866031.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKGIFLSIGIAVLFSACGNSIDEKTVKKYENQLNQTVKQEIASLSQDSGIKIEFSDFKCNADGDFIACL

SSNFKTLAKDNKDEYQELFQAKNIKIRSNEIYKGEANASISIKEYYNDLFKNQKSIQSNLVFENFKLGEK

VVSDINASLFQQDPKISSFINKLSSDSYTLSFDNSINKQENNYLDNLDIKFYNAKLNFNTNLNINLKEDL

LNYLDSKGIKFNTQTLAMDEQAINELLNMANYEQASDFSNTIQKYIILNNFKIDSTLKTEGVFSSYIATA

KENLQTLKAQSQNEEQALIFDKALAILNNITQNDDYKLNLDLKFKNIPVSDYSTQGIDSIEKLSINNQDA

TEALKIILPFIMFSMLMGGASF

>WP\_002866030.1 MULTISPECIES: aminoacyl-histidine dipeptidase [Campylobacter]

MQNVIENFKQLCKIPHCSYETEQMKEFLSSYAKDKGFKVSVDKAGNIRAIKGKPKICLQSHYDMVCMGDA

PNLEVYEENGFLRAKNSSLGADNGIGIAIMMSAMAEFKNLECLFTNDEEVGLMGVNSLEHTLESKMLLNL

DHESDDEIMIGCAGGVDIEASLPFNTLRKKGKIYELYAQNFKGGHSGINIVRNEKSSIKEMAKFIQENKG

EIISFEGGERINSIPKHAKALVHFKNEVKSNNWIKCDFKEEGEFEICDQSNKLLSLINSFTHGVRAYDEN

LGIVQTSINLATLRMQDKQIKFALFARSNILDGLKQVEFETLEFFKAFDFKVRSFNFYPPWEGKPNALSD

MVFKALKKISPNAKVSAIHAGLECGIIEKKQELLCASIGPNIHNPHSTDEHCEIASVEKISKVVFEVLKD

NA

>WP\_002866029.1 MULTISPECIES: nuclease [Campylobacter]

MRINYKKLFNLRKLLSDPKKLFSVLIFTLVVVFIQNYIAQNSSFEGKVVRIIDGDTIEVNHENKLTRIRF

FGIDAPELKQSFGKQSKEALSRILSGKQVEIIYKNKDTYGRIVAIVKLNNVDINRFLVSKGYAWADTYYS

NAYIKEQENAKKNHLGLWKEGNPIEPYKWRKHNKF

>WP\_002866028.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKYTLMILLVLGISGCFVNERGISNRFYDDCKEYYDGSGTYHKVCPKNWVDIKMTP

>WP\_002866027.1 MULTISPECIES: hypothetical protein [Campylobacter]

MAKKDNFEEYAQLEEYASAEDISRVRAELLTCPELNTSLTGTIIEIDKNYAKSILITTSEMVADDQGLIF

DAFIFAAANYVAQASINKEFSVIIGSKCFFYAPLKLGDVLELEAHALFDETSKKRDVKVVGHVKEIKMFE

GTIQVVSTDEHIFKLKRPPLNTVKPTENQEQGAKINNPEAVAAALMASVGGK

>WP\_002866014.1 MULTISPECIES: redox-regulated ATPase YchF [Campylobacter]

MSLSVGIVGLPNVGKSTTFNALTKAQNAQSANYPFCTIEPNKAMVEVPDLRLNELAKIVKPEKIMHSLIE

FVDIAGLVKGASKGEGLGNKFLSNIRETEVILHIVRCFDEENITHVEGGVDPLRDVEIINTELILADIEQ

LSKKIEKLTKEAKANQKGAKESLELANSLLDHLNKGLAASSYPEKESEIYQALIKELRLLSAKEVIYGAN

VNENGISEDNDYVKALKEYAKKNDHEVIKLCAKIEEELVGLSDEESHEFLSSLGVNESGLDQIIRTAFAK

LGLISYFTAGVVEVRSWTIKKGWKAPKAASVIHNDFEKGFIKAEVISYEDYIQYKGENGAKEAGKLRLEG

KDYIVLDGDVMHFRFNV

>WP\_002866013.1 MULTISPECIES: argininosuccinate lyase [Campylobacter]

MKNEMWSGRFSGASDELLKEFNASLNVDKTLFNEDIQGSIAHATMLESCGILKKEELDAIIKGLEQVKSE

IEQGKFVFDIKDEDIHMAIEKRLSEIIGSEIGGRLHTARSRNDQVATDFKLFVKKSHIELLKLLKELIQT

MLEHAKVHKKTIMPSFTHLQHAQPVSFSFYILAYAFMLMRDIKRLQNSLELADFSPLGSCACAGTSYATN

RELSAEILGFKDIMPNAMDGVSDRDFALDLLYDIAVIFTHTSRLCEEMILFSSSEFSFITISDSFSTGSS

IMPQKKNPDVCELIRGKTGRVYGNLISLLTIMKALPLAYNKDMQEDKEGLFDSVKTAKDSLIILNAMLKE

IQINKENMLNACKKGHLLATDLADYLVREKNIPFRKAHFIVGNVVAQAEAQGIDISEIKDLSKIDPVFDE

KAMELLNFEFSLNSKQSEGSSSIASVEKQIQILEGFIQNL

>WP\_002866012.1 MULTISPECIES: phosphoenolpyruvate carboxykinase (ATP) [Campylobacter]

MKKFDNLGLDNIKEIFHNLSYDELNAHEKANNEGLSTDNDTFCVDTGIFTGRSPKDKYFVKQDPSSKYIA

WGKINQPITKELFDKLLTKAKQELSGKKIYVQDAFCGASLQSRKAVRFVTEIAWQAHFVKNMFIRPSQEE

LENFKADFIVYNACKCINEDYKQDGLNSEVFVIFNVEENIAVIGGTWYGGEMKKGIFSMMNYWLPLENKL

SMHCSANVGEKDDVALFFGLSGTGKTTLSTDPKRRLIGDDEHGWDDEGVFNFEGGCYAKTINLDPEHEPE

IYGAIKRNALLENVVLRADKSVDYADASKTENTRVSYPIEHIENHEPSLKAGHPKNIIFLSADAFGILPP

VSKLSKEQAMYYFLSGYTAKVAGTERGITEPQATFSACFGEPFMPLHPTVYARLLGEKIEKHEVNVYLVN

TGWSGGSYGVGKRMSIKATRACINAILDGSIAKCEFENFEVFNLAIPKALEGVESTLLNPINTWLDKNAY

TETRDKLAHMFVQNFKRYEDVKEGIEFSKFGPKI

>WP\_002866011.1 MULTISPECIES: biotin attachment protein [Campylobacter]

MAKKFIDVMDTSFRDGFQSVYGARVLMDDFFPAVEAAKEAGITHFEFGGGARFQSLYFYLNEDAFAMMDR

FRAIVGKDANLQTLARGVNTVTLDTGSSELIDLHAKLFAKHGTTTIRNFDALNDVNNLKFSGECIVKYGL

KHEITITLMDLPSNCKGAHDVPFYEKILKEILAAEIPFHSICFKDASGTSNPNKIYETIKMARKILPQDT

HIRLHTHETAGVSIACYLAALEAGVDGIDLAAAPVSGGTSQPDILTMMHALKDKDYDLGGFEEEKILKYE

EVLKDCLKEYFLPPEATMVNPLIPFSPMPGGALTANTQMMRDNNILDKFPQVIHAMREVVEKGGFGTSVT

PVSQFYFQQAFNNVMFGPWKKIAEGYGKMVLGYFGKTPVAPDANIIELASKQLNLEPTTELAINIADKDE

SKSIAYTKTLLEKEGIETSEENIFVAAACKEKGIAFLKGEAKVNVRKLASMPKPMSVDENKFTVAVNGNK

YHVEVSYGFDKDVNVKSVKKVEENKNIISSNSTSSVDAENEVLAGISGNVFKIYVNEGEEVKSGQAIMVL

EAMKMEIEVNAPKDGIISELCIKIGDTVNEGEVLAIYKN

>WP\_002866010.1 MULTISPECIES: sodium-dependent transporter [Campylobacter]

MRTYFSKIGFVLAVAGGAVGLGNAWKFPTLSAENGGFVFVLLYLFFTLTIGFSIFLAEVAMGRLSKSDLA

NAYSNLAIKYGNRWRYGGVFMLGGIFVLSFYLVIMGWVLKYTVVSLYYLPKTLDEAASNFQNLITTNLTS

SVFFFILSFFLTLLIVSKGLIKGIEKLNVVIMPSLFLMLVFMLFYCMGFKQGFANAFSYLFYPDFSHFKF

SSIAEALGLAFFTLCLGIGCIVTYSSALDKKTNFIKSSVYIVLINLLISFIMGLIVFTFIFEFGADPHTQ

GAGIVFVSLMSLFNQLGALGYIFAFCFFLALFFAGITSAVSMIEPLTFYMINNYQISRVKALFLIGLFVF

VFGICCILSLNLNFFSMFSFFGKDFFTLLDKLTSNFLLPLGAIVCSIFVGFFMNKKQIYKIFSKFISRKI

FLIWLFFIRFISPIAIILVMCYQIFV

>WP\_002866001.1 MULTISPECIES: acyl-[ACP]--phospholipid O-acyltransferase [Campylobacter]

MQKKSFLKIYGLIPFLLIAFINAFVDLGHKIIIQNTIYKAYEGSEQLFLNAIVNALILLPFILMLSPSGF

LADKYPKNIVMKISAIFNVILTLIICICYYSGAFWMAFIFTFIMGAQAAIYSPSKYGFIKELVGKDFLAM

GNGVINAVSIMAILAGMALFSLSFESLYSSAYNQTDEILKEVAPLGIVLILFSCIEVFFAWRLPKLKQTN

KDLVFNKKDYIRGKLLINNLKLVFKNKTIWLCIIGFSFFWAISQLYLVSFPVFAKNELFIENTFYVQISL

AFSGIGVILGSLVAGKFSKNYIELGLIPLGALGMFLMAFLMPYFISLLSYSFLFFFFGFCGALFIIPLNT

LIQFHAKENELGQILAGNNFFQNIAMLGFLLLATLFAKFEINVVYLFYFITLVTFIGSFYILLKLPFSLV

RILLSIAFLQRYRLLVEGFENIPEKGGALLLGNHISFIDWAVVQMAIPRKIYFVMERSIYSKWYIKIFLD

KFGIIPVSSTGSKTSLELIAKHIKESNLVCLFPEGTLSRHGQLNEFKAGFELACEYLSEDDGKIIPFYIR

GLWGSAFSRSDEEFSARNRTLNKRKIAIAFGKAMPLHSKKDEVKAKVFELSFMAWKSQCEAMHTIARAWI

DTAKKNLNQIAIIDTLAGDISYRKMLTLSLILNFFIKRKSKELNINPQRGSYAPKEEAIGILLPASFASS

LTNLSVLIAEKIAVNLNFTAGEKALKAAIKNAQISQIYTSKIFLEKLANKGINLNFDTNIHLIYFEDIVE

DFKMQKTKIFSMMLAVSIIPSFILKSIFTPLKNNLAIAAILFSSGSEGSPKGVMLNNRNILSNIAQISDV

LCTRNNDVILSSLPPFHAFGLTVTTILPLLEGIKSITFSDPTDALGVAKAVAKNNVTIMCGTSTFLGIYA

RNKKLDALMFESLRIVVSGAEKLKNEVRTAFEMKFKKSIFEGYGATETTPVASVNLPNRFDADYWLIHRA

NKEGSVGMPLPGTAVHIVDPNNYENLKTNEDGLILIGGHQVMVGYLNDKEKTDEVIKEIDGIRWYNTGDK

GHLDEDGFLYIVDRYSRFAKIGGEMISLGAIEEEIAKFIDTEVVKFCATSLEDEKKGEQIALLIECNNEI

FERVCEAIKNSNIPTLFKPRYYFQIEKIPLLGSGKVDLKKVKELAKNLAL

>WP\_002865995.1 MULTISPECIES: insulinase family protein [Campylobacter]

MIAYEKIQLKNKLEVYALPVNKNSDVISVDIFYKVGSRNEIMGKSGIAHMLEHLNFKSTKNLKAGEFDEI

VKGFGGVDNASTGFDYTHYYIKCAKKNLDKALELFAELMANLNLKDEEFQPERAVVLEERRWRTDNNPLG

YLYFRLFNHAFMYHPYHWTPIGFFKDIENWSIEDIKEFHSIYYQPKNAILLVSGDIESKEVFELSKKHFE

KIKNTRTIPKIHTKEPKQDGVKRIYLHKNSDTELLALAYKIPNFKHKDIPALNALSELLGSGKSSLMSEI

LIDKLNLINDYYAYVNDCIDENLFIFICNCNPNVNAEKVEKELLKIIDKLKMGKISQKDLQRVKNNVKSD

FIFSLNNASAVANIYGSYLARGDIDPLLNYEKDIQNLELKDLISCAKKYFIQENSTTVILRKDSNG

>WP\_002865985.1 MULTISPECIES: cupin domain-containing protein [Campylobacter]

MKIIQWNRAEFSPKEVKINVLIDNEKGKEIQILLAKDSVMKEHKAPFAIHVQVLSGKIWFEVEKEKFELN

VLDMISLEANVAHSLGGLENSIIRLSLNKSDSVQRVNAVLKKP

>WP\_002865984.1 MULTISPECIES: MBL fold metallo-hydrolase [Campylobacter]

MNLSFKTFDISNVQRSKAKKVQGKKYEIFLNENEQSLITPKVSFKEILRYYYLYPKNAIPSFKLPFFKPD

LSGFSTPHITWLGHSSLFISFKEYKILIDPVFNTHASPISFINKAFKNTPVYNVNDFNEIFAVIITHSHF

DHLDAKSIKALKEKARFFITPLKVGNYLKSYGVSEKKIIELDWWSGVEFGDLKIIATPAQHSSSRGDGKN

KTLWASFVMEFLSVDKRVFFSADGGYFTHFKKIGEYFGSFDLACLESGQFNIAWPYSHSFPDQILKEAKD

LNAKAVMPIHWGRFLVGTHAWNEVIKFLYENLDLPLITPKMGEAYEIGAKFKQDFWWKEG

>WP\_002865982.1 MULTISPECIES: nucleotide exchange factor GrpE [Campylobacter]

MSEQKQEFENENAENSEHLQDENLQNIEDVEQNRLQKDYDELKDKYMRANAEFENIKKRMEKEKLSAMAY

ANESFAKDLLDVLDALEAAINVECHDEISLKIKEGVQNTLDLFLKKLEKHGVALIKEEKEFDPNLHEAMF

HVDSQNHQSGEVVTVLQKGYKIADRVIRPTKVSVAK

>WP\_002865981.1 MULTISPECIES: hypothetical protein [Campylobacter]

MDFIKFLNHFQPISKSSQQASVYKSFKLNLKPKILNEKDENSSSFQDQKTDVAQTMLQRLEDEKVFNQKV

SDKVKKAERGMTTIYFRDPITNNLVRSALSSTAINKMGIEFDKEDMTKRLDGSYILNGKAENFVAGWYAD

IAYTRAYVASDRNNDGYLEDYELEDTKSGFVAQETNLGLFVQSYTQLNGSVDTLFGFEKDFREMRPDDTK

DTDYAGRTIGLELDKMIRKDGDFDGELSFSETGMQAVKTKAPNSGWTESVGILTLTKFDQTNTMEIKDIL

DKLGKGVKYDDLSEDEKSLLKMQLSDKIFDEVEDKETGNKKLVFNLDKFKIFYEGFVDLFKQRSVKMLGL

KPEDATKLNYDNLGEIVNEMKQTYFDTNSTSYGKIADLIKIWA

>WP\_002865979.1 MULTISPECIES: cysteine--tRNA ligase [Campylobacter]

MRLLDSVAKEKIKLDKKDISIYLCGPTVYDDAHLGHARSSVCFDLLRRVLLANGNRVKFARNYTDIDDKI

LKKMAQSGQTLEEITEFYIKSYEEDMRVLNVLDPDFKPRATHYITAMLDLIKKLAKDGFVYTLEDGIYFD

TSKDEKYLSLSNRNLEENISRLSNEVQKRNESDFVLWKFDENFYESEFGKGRPGWHTECVAMIDSIFENT

LDIHAGGIDLLFPHHENEAAQCRCGCKRKLANIWLHNGFVKIDGEKMSKSLNNSFFIKDALKEFMGEALR

FYLLSSHYRSHFNYSLSDLENAKKRLDKFYRLKKRLDLGEISDFDVLNDIEIKSEIAKQILEILNDDLNI

SKALALLDDFISSANLELDKESKNKILKQNIKEALSELAKIFGFGFMDTTLYFQWGVSKEEREEIEKLIL

ERTEAKKNKDFNTADAIRERLSSKKITLLDTPNGTIWEKINA

>WP\_002865974.1 MULTISPECIES: cytochrome d ubiquinol oxidase subunit II [Campylobacter]

MFFGLELEGLQIYWWLILSLLGGLLVFMFFVQGGQTLIDELSKDELEKTMLVNSLGRKWELGFTTLVLFG

GAAFAAFPLFYSTSFGGAYWAWLCILFCFILQAVAYEYRKKENNVYGSKTYEIFLKINGYLGVFLIGVAV

SSFFSGSEFILNEHNFVSWQNPLHGLELLLNPFNYLLGLALVFLARLLGAAYFMNNINDENIKIRAMKKL

MINSILFLPFFLGFLAWIFLKDGFSVDANGVVSMSANLYLYNFLNQMIFAILLAIGVILVLLGMVQGAKG

CSKAIFTLGLGTVLTVFALLSSIGLGQSAFYPSLNDLQSSLTLKNASSSYYTLSVMAYVSLLVPFVLAYI

IYVWNAMDKVKITREEIANDDHAY

>WP\_002865973.1 MULTISPECIES: cytochrome ubiquinol oxidase subunit I [Campylobacter]

MNELSSVDWSRAQFALTALYHFLFVPLTLGLSFMIAIMETIYVKTKNERWKKITKFWLSLFAINFAIGVA

TGIIMEFEFGTNWANYSWFVGDIFGAPLAVEGIMAFFLEATFFAVMFFGWDKVSKGFHLLSTWCVAIGSN

LSAFWILVANGWMQYPVGMSFNPDTARNEMQNFFEVALSPVAISKFLHTIGSGYVISALFVMGISAWFML

KGRHIIEAKKSLVVGASFGLVCSIFLFFSGDESAYRVTQTQPMKLAAMEGVYQGEHRAGLVPFGILNPKK

TIDNNESVFLFDITIPYALSILGNRDPNSFVPGIEDLIYGNESKGIEPMQNRIDRGKIAIQALKDYKLAK

ENNDTIAMENHKSILETHFKDFGYGYLEKPSDTIPPVALTFYSFHIMVALGSFFFLLFIVTLYLTMANDI

EKFRKVLWVCLLSIPLGYIAAEAGWIVAEVGRQPWAIQDLLPVHIAATQLGKVNVQISFWIFAVLFTALL

IAEVKIILTQIKKGFDAHAGHTPLMGKGEK

>WP\_002865972.1 MULTISPECIES: cytolethal distending toxin subunit B family protein [Campylobacter]

MKKIICLFLSFNLAFANLENFNVGTWNLQGSSAATESKWSVSVRQLVSGANPLDILMIQEAGTLPRTATP

TGRHVQQGGTPIDEYEWNLGTLSRPDRVFIYYSRVDVGANRVNLAIVSRTQAEEVIVLPPPTTVSRPIIG

IRNGNDAFFNIHALANGGTDVGAIITAVDAHFANMPQVNWMIAGDFNRDPSTITSTVDRELANRIRVVFP

TSATQASGGTLDYAITGNSNRQQTYTPPLLAAILMLASLRSHIVSDHFPVNFRKF

>WP\_002865971.1 MULTISPECIES: cytolethal distending toxin subunit A [Campylobacter]

MKKIITLFFMFITLAFATPTGDLKDFTEMVSIRSLETGIFLSAFRDTSKDPIDQNWNIKEIVLSDELKQK

DKLADELPFGYVQFTNPKESDLCLAILEDGTFGAKSCQDDLKDGKLETVFSIMPTTTSAVQIRSLVLESD

ECIVTFFNPNIPIQKRFGIAPCTLDPNFFAEVNELMIITPPLTAATPLE

>WP\_002865970.1 MULTISPECIES: L-lactate permease [Campylobacter]

MEQILTWQQIYDPFSNIWLSALVAFLPILCFLVCLVVLKLKGYQAGFLTVILATLVALFAYKMPWNLVGA

SFIQGFTNGMWPIAWIIIAAIFLYKLSIKSGSFEIIKKSVMSITPDHRIQVILIGFCFGSFLEGAIGFGG

PVAITAALLVGLGLRPLQAAGLCLIANTAPVAFGAVGIPIIAMANLVGIEQHSVSAMVGRMLVPLSLTIP

FFIVFLMDGFKGVKETFPAILVAALSFTTTQFLSSNHLGAELPDIISAVVSLAVTTIFLKFWKPKNIFRF

DNESNFTQDNTLSFNQILKAWSPFILLIICIIIWTQPWFKALFDKDGILSYTSITLQFSNITTGILSPSV

TGIGEAKPLSLALGVDLINGKTVAQAGTAILLAAFLTIAILKIKAEDAAECFWATLKEMAIPCITIGLVV

AFAFISKNSGMSTTLGLAFAHTGDAFSFFSPIIGWIGVFLTGSDTSANLLFGTLQQVSAQKLGISEALFL

AANSVGGVVGKMISPQSIAIACAAVGLVGKESDLFKFTLKYSVAFIVLIGIWTCIIAFFLQGIIPEVIVK

>WP\_002865968.1 MULTISPECIES: lactate utilization protein C [Campylobacter]

MSKIDEISSKSKASILEHLKKAYKETDFTRIESIDPVEHIQTTQDMLTEMKQKMSDNKYIVENATKDTLE

EKINEIVAKYGFKSMIYGADLNLDLEQIKAEKKICFDKEIENLRSEVFHSDFSIIHARAGVSSHGVALIP

SSKTQPRMLSLAPKLCVVLLKKENVVKSLSEALNLVKKENEILPTNILFIAGPSRTADIELITVFGVHGP

QIAHIIIY

>WP\_002865932.1 MULTISPECIES: aryl-sulfate sulfotransferase [Campylobacter]

MRLSKTLCMALLAGSTLLAPNALMAMGGPSGAKIDWQIQGQIGAIKMNPYGLSPLTAIIMDNGYVLSDIK

VTIVPKPNGQTISYNVNSKMAKTYGGIPIFGLYPSYLNTVKVSYTKTANGKSQKVIDEIYKITTPGVSIE

PSGSTDQRGTPFENVKVLKMDPKFSDRLYLVNNAPGKQSGKGSQSVWNNPVGGAMEWDENSNVFIIDTKG

EIRWYFDNDKLMNWDNIYNRGIMMGFHQNKDGALTWGFGQRYVKYDILGREIFNRKLPAAYIDFSHAMDN

MQNGHYLLRVASANTLRPDGKHVRTVRDTIVEVDENGNVVDDWRLYEILDPYRSTIIKALDQGAVCLNID

ASKAGKTLSDEELAKMDESDKFGDIAGTGIGRNWAHVNSVDYDPSDDSIIISSRHQSAVVKIGRDKKIKW

ILGAHKGWNKEFQKYLLQPVDKNGKKIVCDDDYSKCPGYENDNGGFDFTWTQHTGWRIDSKSNKRYIYIS

VFDNGDARGAEQPAFASQKYSRAVIYKIDQQNKTVEQIWEYGKNRGNEWFSPVTSLTQYEPDKDSIMVYS

ATAGMAFDLSKGVSLGEPKPEIDEFNWGAKEPSVQIQFSGSGTGYQAMPFSVDQAFNLKK

>WP\_002865930.1 MULTISPECIES: cytochrome CBB3 [Campylobacter]

MNKFSIVLTLLLCGSCALALDPNLEKTKSATGIDLPTAKWNLPKALNEDGTIDETKMPKNSEYSKMVILG

NKILNETSKYVGPQAKDPKKRFAGNNLSCSSCHANGGSVQNQSGFVGIWARFPQYNARGDKVITLADRIN

GCFERSMNGKRMPSDTPEMKAMLTYMQWLSQGVPVGAKIEGQGLKKIDFISRAADPKKGKAIYMDKCAVC

HQENGLGLKNEDSAGAYYLYPPLWGDDSYNTGAGMYRLIKAASYIKENMPQGAPDLSLEDAYDVAAYMNS

QARPIKANRDKDFPDRKVKPLDMDVGPYDDSFSTTQHRYGPYTNMIKK

>WP\_002865929.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKCILFFFSLYSLSFANIYEKLNDFAYEKKPNKDFKIQEVKLVQFSQENKDCLELLIEAGQVRILNSYN

SCQKLSKDESFQKFLNEDFLKLYKNNGYLINENLQNLKNTMQDIMIYYKLRYSFSKDVKDMSKNKNLDIL

NIDEKDGGTLLYKINNQACVGIELTRHDSRMAMKIYGIENLDKECKLFIQSPSFKDLSYTKKDFKWYYLE

>WP\_002865928.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKIYHLSHTDLDGYACQFIVNFYFKNVRFYNSNYGKEINENFNSIIGDIEKDENFGKAIILITDLNLNLN

QCEEFEKICKEKNIKIFLLDHHQSGEECAQKYSWYLLDSKRCATKIVYDFFSKICTPVLELSKFVDVVNA

VDIWLSEDENFELGKVFLGLIANAKEINRVMFKESQIDYMFFLLDKAWKFIGKENANILLDNATHFIKKD

YFARKNDDTLSNLISYFVVEKLSELKENFSIEYEGHKGILTSNIGNTSVIGNDFLVKNPDYDFFIDVSSR

KTLSFRANGKIDVSLMAKNLVGGGGHKNASGGLFATFKDGANYNYIKAQIIDLIKSKELKKENNESKQ

>WP\_002865927.1 MULTISPECIES: flagellar biosynthesis protein FlhA [Campylobacter]

MAKNKIVDLVFPFLGPLIAPVLKAKSLTIVGFLVCILAIIIVPLPSPILDFFLALSIALSVLIILISIYI

PKPTDLTTFPTLILIITLFRLSLNIATTRMILSEGQNGPEAVSEIIAAFGEFVVGGNMVIGVIVFCILVL

INFMVVTKGSTRVSEVQARFTLDAMPGKQMAIDADLNAGLIDEQTARARRQEVIAEANFYGAMDGSSKFI

KGDAVAGIIITIINIIGGFLIGSFQHDMALSDAASTYTILTIGDGLVSQIPGLITSTATAIIITRASKDE

ENFAEGTLTQLLSEYRTLLIVGFVLFIFALVPGLPTLSLGFMALVFLSLGYLTKQVKEGKIDITTVKKSK

PSAAAASQSGAGGTTAAPAKKSEEEILKEEEHKINDILKVEILELELGYGLIKLAENELTERIRSMRRSI

AESLGFLMPKIRIRDNLRLKPNEYSFKLKGVSIASAEIYPDKYLAMDSGFITEEIEGIATKEPAFNSDAL

WIDANLKDEATLNGYIVIDPASVISTHMSELIKAHASELLTRQEVQNLLDKIKNDYPIIVEGALGVAPVS

LIQKILKDLLKHHIPIKDMLTILESVSDIAEVSKSFDMIIEHVRASLARMITNMYLDDKGNLDIFILDSA

SSAVLMENVQFRDGSYHLPLSVAQTGTLVDTLRAEVAAVANGRIKPFILCVEPQLRKFIADICYNFSINI

VVLSFAEIAENTNFNTEGIIRIEL

>WP\_002865918.1 MULTISPECIES: 3-phosphoshikimate 1-carboxyvinyltransferase [Campylobacter]

MKIYKLQTPVNAILENIAADKSISHRFAIFSLLTQEENKAQNYLLAQDTLNTLEIIKNLGAKIEQKDSCV

KIIPPKEILSPNCILDCGNSGTAMRLMIGFLAGISGFFVLSGDKYLNNRPMRRISKPLTQIGARIYGRNE

ANLAPLCIEGQNLKAFNYKSEISSAQVKTAMILSAFRANNVCAFSEISLSRNHSENMLKAMKAPIRVSND

GLSLEISPLKKPLKAQNIIIPNDPSSAFYFALAAIILPKSQIILKNILLNPTRIEAYKILQKMGAKLEMT

ITQNDFETIGEIRVESSKLNGIEVKDNIAWLIDEAPALAIAFALAKGKSSLINAKELRVKESDRIAVMVE

NLKLCGVEARELDDGFEIEGGCELKSSKIKSYGDHRIAMSFAILGLLCGIEIDDSDCIKTSFPNFIEILS

NLGARIDY

>WP\_002865912.1 MULTISPECIES: tRNA (cytidine(34)-2'-O)-methyltransferase [Campylobacter]

MFNIVLVHPRIPQNTGSIGRMCFNAGFKLHIIKPTVFDISQKAVRRAGLDYWDKLEPIIWENLEEFLNEN

MIYKNRFFFATTKSQKAYFDAEFQKNDFLFFGSESYGLPMELMQLNWENAITIPMKSYGRSLNLATSVGI

ISYEALRQNFSNFVS

>WP\_002865911.1 MULTISPECIES: alanine racemase [Campylobacter]

MSLIKIDQKAYEYNLRHIAKKIGSFQRLICVFKDNAYGHGAKLLAPLAKNLGVSFVAVKSEEEAQEIEEF

FENILILSHRPHGNENSRFIYALNDISQVKKYKQDIKIHLKIDTGMHRNGICVENLEHAIDLIRSSDLKL

TGMFTHFASADEMDGSFFVQKENFQKAKKIVKKYFSNLLFHSHNSAALFRGKIPEDEYCRVGLVQFGYGD

SNLKRVLSLYAHRLSQRILQKGQSIGYGGIFTAAKDMEVATYDLGYADGLFRYNGKGELVLGNGKVMLGK

MSMDSFSCENSGEEICVFKDADIWADFFHTINYEILVKLNPNIQRVLV

>WP\_002865908.1 MULTISPECIES: hypothetical protein [Campylobacter]

MRKIIFILAFAFVIVILYIIFDFYIIKDSKKITKADFSTPLTCDLNVKDCTYSFNNKEVLISLNPKPLQS

LDVTNLKIVNLGNYNNLGIKIYGLNMYMGEIKPKIHRLNSTDYESKIVLAACVLDTMRFRVEFMDNNKPI

GFYFDFELKK

>WP\_002865907.1 MULTISPECIES: SCO family protein [Campylobacter]

MKKNIILFIVIVAIILGVIFFIKNHQNSYDFILKSDLKEETTLKDFKGDKLIIYFGYTYCPDVCPATLSL

AGKALKQINNPKAHLLFISLDPNRDNNLSNTNEWLRYFYPKADALIAKDEKTLQKITKQYNVQYQKIDLN

DSFMGYSITHSNMLYLIDEKGHFYKEISDLNPQEILRELRIFLNSQ

>WP\_002865905.1 MULTISPECIES: hypothetical protein [Campylobacter]

MNNFKEIAKLVRKYKERNNALYEFLDKEDVGEYFRSLISLSELKQDKTTMLAILRRLIDLKEENLVQEWK

KNNFKEDKIIELKHKFYEEVRKFYEKEHQNLINEIKEKKLLNNFYQSLIQGVHNIGLIMNIFEISWTKEI

IEKNNKILSTQFPNLDDAMEFLRKNHLYQKTPEGEICERSYGVLVRIGNLWKFVPYARFFENEILKLEFA

FENMIDQLKIFASSEEEKAYIEYFEKLKLAFCEKDEDRVIKAWQEAEFAWMKVKSPLQVGHPLEYYEDNY

THAVALEWDIRIEDENDFDVLKFGSEIKESFEHVYKNIGLEDCELEKEVLSNIEKTQLYICTPMIFYGAE

LKGLFSAQVVPNDEFVSSKAGKKIFAFINFVYENAKTKPFMKISSEVFDKEFLDFGRNILFYQEKIWKRV

YEVSTIGHEFGHIFFIANDTEKTMNQSGFFKNIEEYKATTGGLINFFYHEQDDLIMPVFHELIKRAIGLI

SWQRVDEVRPYYTEGLIHLSLLFESEVLIFENNNLKINFDLGHYEKFKELTLKNYHELAKHYALRLDAKE

FLSRFCEIKDNIFLPIMPKCKEFVKFYYDLYEKIGNEIDNSGEFERYKKK

>WP\_002865900.1 MULTISPECIES: chemotaxis protein B [Campylobacter]

MKLILIGSSTGGPNQLKFLLKDIDIKNTCVVIAQHMSASFIPSFVGQFNKEAFSEVCLLNDKEILSNKIY

ICPKNTILSGNLNIVAAWQDVASSFKPSVDLLFHSAVSLVKTNKILAIILTGMGDDGAKGLFELYKTGVR

CLCENEADSVVYGMPKRAKDMNPHLKPMSLKEIKKEIVNFIDQD

>WP\_002865894.1 MULTISPECIES: ribosome biogenesis GTPase Der [Campylobacter]

MQSIILIGKPNVGKSSLFNRMARQRIAITSDISGTTRDTNKTQIHIHSKKAMLIDSGGLDESDELFKNVK

KNTLKVAKESDIILYLVDGKLAPDDEDRQFFYSLKKLGKPIALVVNKVDNKKDEERAWEFANFGVKEIFN

LSVTHNVGLDELYEWLEKFLHEEFLIPDEEENLEDFLEHYEEGKEFQFKEVDQNHIRVGIVGRVNVGKSS

LLNALVKQERSVVSSIAGTTIDPVNESVVHKDKVIEFVDTAGIRKRGKIQGLERFALNRTEKILSHSQIA

LLVLDAHEGFNELDERIAGLVAKHYLGVIIVLNKWDKSEMDFDKTVKELHLDRFKFLAYAPVISVSALSG

KRVHVLLDKILQIFENFTQKIQTSKLNTLIENATRSHPLPHDYGKLVKIYYAVQYDLAPPKIALIMNRPK

ALHFSYKRYLQNQIRKEFNFEGVPLVIASRKKGSKENDES

>WP\_002865893.1 MULTISPECIES: shikimate kinase [Campylobacter]

MMKAKNIVFIGFMGSGKSTLARALAKDLDLVFLDSDFLIEQKFNQKISEIFAQKGEIFFREQEQKMADFF

SSCEKTCIATGGGFVNVSNLEKVGFCIYLKASFEYLKKRLDKDEISKRPLFYDEIKAKKLYNERLSKYEL

KANFILNIENKNIDELLSEIKKVIK

>WP\_002865890.1 MULTISPECIES: serine--tRNA ligase [Campylobacter]

MLDLKNLQNNFDEVAKKLKNKKVDENILKKLAELFASLKKEKTALEEFQAFQNKFSKELATAEDKESLKA

KLSENKSKINEQSVKVNALENELEEIAHAIPNIPDECVPVGEDEDENVELKKVLNPPSFDFTPKEHFELG

ESLNWLDFVRGVKISQSRFCVLKNEGALLSRALVNYMIDFNRSHGFEFVNVPFLVNGATMFGTGQLPKFK

EDMYKVDDEDLYLISTSEIPVTNLYSGEILASETLPIKMTCYSACFRKEAGSAGRDTRGIIRQHQFEKVE

LVSITKPEQSDSVFNEMLECASDLLSSLGLAHRHLMLCTGDLGFSAAKTVDLEVWLPGQNKYREISSVSN

CRDFQARRAKIRYKNEQGKNELVHTLNGSSLAVGRTLVAIMENYQDKEGKIHIPDALKKYF

>WP\_002865886.1 MULTISPECIES: malate:quinone oxidoreductase [Campylobacter]

MSQQEFDVLVIGAGISGAALFYELARYTNIKNIALIEKYNTAATLNSKGTSNSQTIHCGDIETNYTLEKA

RKVKRTADMIVKYGLMQNAQNNFMFSHQKIALAVGDIECDYMKKRYEEFKELYPYIKFFDKAKIKQIEPK

VVLGEDCNQDRPENICAMGVESGEVFTTVDFGKMSINLIEQAQKQNKNTFVAFNQEIVHIEKKDDIFILK

TSNHQEYHAKSVVVNAGAHSLYLAHKMNLGMDKSCWPVAGSFYLTKQKLLNGKVYMVQNPKLPFAALHGD

PDLLADMNTRFGPTALVIPKLERYHGLKSVPEFFEALKLDKTVLKVTFNMFKDATIRNYIFYNYLFELPF

IDKSLFVKDAKKIVPSLKTSDIYYAKGFGGVRPQVIDKTKGELMLGEASITETPGIIFNMTPSPGATSCL

GNAERDAKLICNYLGMEFNEDKFSSELL

>WP\_002865885.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKIFLTLFCLIFLCACGTKRQYFEPEQTNGDLSHNGNLKSKIVDWNLVSAKLSNNTAILKNNISIDKFK

LPKNYILIAYQDGEYFTADDNGNLKIFDNSYNEIYNFQFDASVVGVASNGDDLALVLANNTIVLANRSLG

IKFSQTLTSAPAQDSRTANPIFLDNIIVYPTLDGKILILSRNNLQVIKDVVISAENFFNNVIHLSVIGDK

LIAATAKKIIVVSPARTLYLDADIKDVALSDDGIFILEKDGTIIKTDYNLRKIAEKKFEFAIFVKSNIYN

NYLYIFEKTGYLIKMNLNLDNTQVFKLSEAVDKISFMGNGKFYYGDKILDLL

>WP\_002865884.1 MULTISPECIES: hypothetical protein [Campylobacter]

MGLKDNLKAVKNELNTEEQFIENFIKGERFIRKYKFYISAVVIILVAWFAGNFIISKINDYKTKEANEIY

ANLIQDPSNKNLLEQLKNKNTNLYAIFLLKENINDFNNTALQNELKQIYNNAQTNTLLKNIIALSLGDKS

IFLKNYDKLLEAYKLLEQNKIEEANVLLSQIKENSSLNQIAKNLKHYQGITQ

>WP\_002865883.1 MULTISPECIES: colicin V biosynthesis protein [Campylobacter]

MNFYWFDAFILGFTLLLGLKGIINGLIKEIFGLLGIIGGVFIASKYATQAAEFIQSTFYKIENQSLAGFA

GFLAILIIFWIVCLLAGNFLSKLIKLSGLGFLDRIGGFIFGGAKIFLIFAILVFCVARIDFLNDKLDNFA

KNSYTLNLLKETGSFIMNQPLTENSLDHASEKLQDIVSDLNNTQKGE

>WP\_002865882.1 MULTISPECIES: serine hydroxymethyltransferase [Campylobacter]

MSLEMFDKEIFDLTNKELERQCEGLEMIASENFTLPEVMEVIGSILTNKYAEGYPGKRYYGGCEFVDEIE

TLAIERCKKLFNCKFANVQPNSGSQANQGVYAALINPGDKILGMDLSHGGHLTHGAKVSSSGKMYESCFY

GVELDGRIDYEKVREIAKKEKPKLIVCGASAYARVIDFAKFREIADEIGAYLFADIAHIAGLVVAGEHPS

PFPHAHVVSSTTHKTLRGPRGGIIMTNDEELAKKINSAIFPGIQGGPLMHVIAAKAVGFKFNLSDEWKVY

AKQVRTNAQVLANVLMDRKFKLVSDGTDNHLVLMSFLDREFSGKDADLALGNAGITANKNTVPGEIRSPF

ITSGLRLGTPALTARGFKEKEMEIVSNYIADILDDINNEKLQENIKQELKKLASNFIIYERAMF

>WP\_002865881.1 MULTISPECIES: shikimate dehydrogenase [Campylobacter]

MKFLAVIGDPISHSKSPRMHNNAINALGLDSIYTRYHLRNANCLREDFFKLGLSGANITLPFKEKALDIA

DVKDDFARNIGSANTLCLKEDKIYAYNTDALGFLEAIKDFDNIKKALILGAGGTALALAYALKQKGVEVY

IANRSKERFKDFLAYPTYLYKNLQDFDFDLVINSTSAGLKDENLPCDRELLDRILPKAKFAFEVIYGRET

PFYRLCKEYHLKIKDGLDMLLWQGVFAFELFFEIRDKREMIKNAMQQALILK

>WP\_002865879.1 MULTISPECIES: ATP-binding protein [Campylobacter]

MQINLLNDFIKAYENTYSVSFDDSFKGRIQELCKELNEPFMHASYALENELKELVFSLDKNVNIAIIGQF

SSGKSSLLNLILGCDCLPTGVVPVTFKPTFLRYAKEYFLRVEFEDGSDIITNIEKLAFYTDQRNEVKQAK

SLHIFAPIPLLEKITLVDTPGLNANENDTLTTLDELKNIHGAIWLSLIDNAGKKSEEDAIKANLELLGEN

SICVLNQKDKLSTEELDNVLNYAKSVFLKYFNELIAISCKEAKDEQSYEKSNFQSLLDFLTQLDTTALKE

KFVKRKILNLCEILEDENQLFVGIFDRLLNQFQNYEKHLLLAYENFLKEIEILNHQILEQLKSISERISS

EIFASVKEKDAYFYKESKGFLKKDLYTRYDYKAPYISSDDAFLAMFYNSDVMSKEFKKIKNELYKSFEEI

KMKLKDFINILEREILLFKAEFSNIQKDHIFQSDKNFSELRAFCNASDEYFLKDFKELLFKSILELDLFF

EKLNLKAFTNYENATKLSLAFFSRKINESRVLYELDSSEFVLFYPKKSEIYERVLNELNVYEFEALLINK

PILTKIAKNFLEQSQNLIQEKNKFLDLKKAELQKRRAQILNVRESIKED

>WP\_002865877.1 MULTISPECIES: oxidoreductase [Campylobacter]

MQDNIIDRRSFFKLGLLGGSVVAASTIGGGAVLKAAELTHSHQASQGKSNKVRGRMFFQTQTEFDTLSAA

CERIYPKDEQGEGAIGLGVPYFIDNQLASAYGYNDREYMQGPFMEGKAEQGYQTPMQRKDIFLEGVHALE

ENAQKRYKKSFSLLKGGDQDKILSDFEKGKIQTTGFKSSYFFTLLRDMTVAGVLADPIYGGNDNKNGWRM

MQYPGAQMSYVDKIASDEFFNIEPMSLADMES

>WP\_002865876.1 MULTISPECIES: GMC family oxidoreductase [Campylobacter]

MAEVLKKVDVVTVGAGWTGGIVAAELTKAGLNVLSLERGHMQSTENFNFIHDEWRYGINYGLMQDCSKDT

VTFRHDPSGLALPYRKMGSFLLGNNVGGAGVHWNGWTFRFMPYDFEIQTLSKQRYGNKLGNDYTLQDWGV

TYKDMEPYYDRFEKTCGVSGEPNPLAEKMGAFRSSPYPQEPLENTKMLKRFESAAKSSNLHTYRLPASNS

KGGYTNPDGQDLAPCQYCAYCERFGCEYGAKASPLNTVIPKAMSTGKYTIRTYSNVTQILKKDGKVTGVK

FVDTRTMKEYIQPADIVVLTSYMFNNAKLLMVSNIGEQYDPKTGKGTLGRNYCYQMNMGTTAFFDEQFNT

FMGSGALGTTSDDFNGDNFDHSKEKFLHGAMIYSVQLGTRPIQSAPLPAGAPTWGAEFKKALNYNFTRAI

TVGGQGASLPHKNNYLSLDPTYKDAFGMPLLRLTYNFTDQDRALHKFITDKTAEVAKRMQGVKSIKKGAY

LKDYSVVPYQSTHNTGGTTMGADRETSVVNTYLQHWDADNLFVVGAGNFQHNSGYNPTDTVGALAYRCAE

GILKYHKSGKSLA

>WP\_002865087.1 MULTISPECIES: ribonucleoside-diphosphate reductase subunit alpha [Campylobacter]

MKVIKRNGRTEELDVSKIKKCTSDAVKDLEGVNLSELELDAKIQFRDGISTEEIQKTLIKTAVDKIDIDC

PNWTFVAARLFLFDLYKKVNGMNRYNHLREYFQKGEKEGRILLGLKEKYDLDDLNAYIKPERDMQFTYLG

IKTLYDRYLIKDSKGMPIELPQQMFMAIAMFLAQNEFNPQEWAKKFYDLISKFELMLATPTLSNARTTRH

QLSSCYIGSTPDNIEGIFDSYQEMALLSKFGGGIGWDWSKVRAMGGSIDGHKNAAGGIIPFLKITNDIAV

AVDQLGTRKGAIAVYIEPWHMDISDFIDLRKNSGEERRRAHELFPALWINDLFMKRVRANDKWTLFDPAD

TADLCDLYGEAFEKRYEEYEKDESITKEIVEAKELWKKILLNYFETGLPFLCFKDSANRANPNAHVGIIR

SSNLCTEIFQNTEPNYYQIKVVFENGDELHFDEEQKVVIDGGYEKPAKKISTLDSIEGNKVYIVEKYKND

GKTAVCNLASINLSKVYTKEDIERVVPTAIRMLDNVIDLNFYPHRKVKDTNLKSRAIGLGVMGEAQMLAE

AKIHWGSDEHLNKIDEIMEQISFEAINASSNLALEKGSYEDFEGSNWSKGIFPIDVASPKAKALTLREGL

FDQSECDWVKLREKVKKDGMRNGYLMAIAPTSSISILVGTTQTIEPVYKRKWFEQNLSGMIPVVVPNLSL

DTWQYYTPAYELDQKILVKAAAVRGKWIDQGQSLNIFLSLDKASGGYLNEIYQLAWELGVKSTYYLRSES

PDSEKVNVADRSIECEGCQ

>WP\_002864548.1 MULTISPECIES: inorganic phosphate transporter [Campylobacter]

MQKDNLIAFVIFIISTIAFVIWGFGYISQHQLILFILASIFGIFMAFNIGGNDVANSFGTSVGAKTVTIK

QALIIAAVFELSGAIFAGAEVTKTIRSGIVIFPNSLDPMLFVIIMLAALLSSGVWIFIATKKGLPVSTTH

SIVGGIVGASIMMGLLKFDGIQTLSMVKWSEILRIAISWIASPLLGGIVAYIIYSYIDKKILKPSEKLND

DLKNIKKERKKFKEEYFLNLKTKSQEEQIKELSAIALDEEEQENNFYRNKMKEFKDQEKDIDIYSILKTH

MPIIACIAAAIISAMFLFKGLNNVSTLDILQNFWIIGIIGTISYVVTFAIVKIVKKTELNKTTDRIFSWF

QIFTASSFAFSHGANDIANAIGPFAAILDVLKNGTINATSPVPFAALAMFGVALVVGLWFLGKEVITTVG

SKLATIRPTTGFSAELGASIVILLATQFGIPVSSTHILIGAILGIGVYNKNANWIMMKPIGLAWIITLPA

AGIMAALVFLGFKLSLGI

>WP\_002858909.1 MULTISPECIES: restriction endonuclease subunit S [Campylobacter]

MTNLPQGWEVKTLSEIGEIVTGSTPSKSNLDFYGKDYPFFKPSDFEQGYFLENAGDNLSKLGFGKARQLP

PKTILVVCIGSLGKVALTKVIGSCNQQINAIIPHKNIISEYIYYYCISSKFQSILFSKAPQTTLAILNKT

EFSKLEIIYPKDIKEQERIVGILDFAFSKIDENIKKAKENLANIDELMQSALQKAFNPLNDNTKENYQLP

QSWEWKSLGDTSNYGKTSQVKPSQLKGNDWILELEDIEKESGVLLQKVLFQDRQSKSNKIKFNKGDILFG

TLRPYLKKVIIADDNGACSSEIMPFSTGNSITNHFIYYYLFANFLHDRISSLTYGARMPRLGTKDGKSLQ

IPLPPLQEQEQIAEHLDFVFEKAKALKELYTKELKDYEELKQSLLDKAFKGEL

>WP\_002858903.1 MULTISPECIES: flavodoxin family protein [Campylobacter]

MKNILLLNGAKEFGNSKGQLNLTLHNHALEILKTLGYEVDQTHIDQRYDPKEEIQKFIKADAVIYQMPAW

WMGEPWIVKKYIDEVFGLGAGVLFKNDGRTHENPSKNYGKGGLDHGKKYMFSLTWNAPLEAFNDKNEFFE

GKGVDMVYWHLHKAHEFIGMKALPTFMCNDVVKNPQVEKYLNEYELHLKKIF

>WP\_002858902.1 MULTISPECIES: EamA/RhaT family transporter [Campylobacter]

MTRTKYLYILLVLAMFLWGSSWPTSKILSAYADTSVITFWRFFFVLLGSLMVLGFLRIPLSLEKSILKWV

LIAGILNGLYTFVFFIAIKHGLAGKGGVLVTTMIPIFSYLIFMIAILFQKDKKSTHKIIKSEILGLFLGL

LSGFCLLNLGSLEDLFGKFNILFLTCSFIWALIAVFNHKAKGVHPLAINFYINLISVLMFSWVLFDVKSY

EIFHFEFKFWISMFVVAFLSTIIGTSIYYYGIHILGSVKANSFVLITPASALICSYFILDEVPNALTLLG

CALAIGAIYFINIYGKKA

>WP\_002857311.1 MULTISPECIES: hybrid sensor histidine kinase/response regulator [Campylobacter]

MEDMQEILEDFLVEAFELVEQIDHDLVELESNPEDLELLNRIFRVAHTVKGSSSFLNFDVLTKLTHHMED

VLNKARHGELKITPDIMDVVLESIDRMKTLLNSIRDNGNDTAIGMDIEPICARLTAISEGESPVAATDSN

EKSTPQAEPEAPKQETTTPEPEVDVNQLSDSEVEAEIERLLKVRKAEDQARRAQKKQTTNAAPKPTNNTA

NKPAESGEKKVPASGSNASSMDQTIRVEVKRLDHLMNLIGELVLGKNRLLKIYDDVEERYEGEKFLEELN

QVVSQLSIITTDVQLAVMKTRMQPIAKVFNKFPRVVRDLSRELGKQIELEITGEETELDKSIVEEIGDPI

MHMIRNSCDHGVEDPATRAANGKPEKGIVQLKAYNEGNHIVVEITDDGKGLDPNGLKAKAIEKNLITERE

ADQMTDKEAFALIFKPGFSTAAKVTNVSGRGVGMDVVKTNIEKLNGVIEIDSELGKGSSFKLKIPLTLAI

IQSLLVGTQEEFYAIPLASVLETVRVPIDDIYTIEGKNVLRLRDEVLSLVRLSDVFGVKQVLESGDQTYV

VVIGVAESKLGIIVDTLVGQEEIVIKSMGDYLQNIQGIAGATIRGDGRVTLIIDVGAMMDMAKEIKVDIK

AQLESSAKKPKEQPSDYKVLIVDDSKMDRTLMQKALEPLGVSLVEATNGVEALNIIKSGEHDIDAMLIDI

EMPRMDGYTLAGEIRKYSKYRNLPLIAVTSRTSKTDRLRGVEVGMTEYITKPYSPEYLENVVRKNLKLG

>WP\_002857112.1 MULTISPECIES: sodium:proton antiporter [Campylobacter]

MNKFLVLLFLPLVAFANSSEAAANANLFGAFTLIPPLVAIALAFITKDVILSLFAGVLSGTFLLSLSANI

FKAQHLAFVNFYNTAVESFSKIISYILGSTSDPVNAGIILQILCIGGLVALITKMGGAKAVALKFAKRAK

SAVSAQVNTWFLGLLIFFDDYANLLIVGPIMRPLADKFKISREKFAFIIDSTAAPVAGIAVISTWIGLEV

SLIKTAYEHIGISDISAFGIFVETIPYRFYNIFMLFFVVMTAIMGREFGSMYKAEVRARTTGQIAPLPKS

GTLDTAELEDQFLAPKEGIKIRAFDAIVPIFTLIILAILGFYFNGLSTLEGEELAKASANPLSFETFRAA

FGNADSSVVLFQAALFAAIVAIFIGVRRKIFNLKEAVETWIYGWKTMIFTIVLLLFAWSLSSIVKDLGTS

LFITSLLADKLPEFILPATIFAFASAISFAIGTSYGTMGILMPLAVPLAHEIAKINGMDANAMHHYMVIN

ISCVLTGAIFGNHCSPISDNVILSSMSAKCDHMEHVRTQIPYALFICGISLIAGYIPVSLGLSVWFVLPL

NFILIALLLRLIGKKVP

>WP\_002857099.1 MULTISPECIES: penicillin-binding protein 1A [Campylobacter]

MKILKYIFSFFTLLFIAGFIYVAYLFTSADTEGYTFKEYKPPLTTQIYDRNGKLVANIFEQHRFYAPYEE

LPPRLIEALVAIEDTSFFEHNGVNIDAIFRAAVKIIKSGGKTMEGASTLTQQFIKNTELTPERTITRKIR

EALLAYKMETILTKEQILERYLNFIFFGHGYYGVKTASLGYFHKNLNELSLKEIAMLVGMPKAPSSYDPT

KHLDLSISRANNVISRMYNLGWISKADYDTAIKEIPQVYDDTLTQNAAPYVVDEVIKQLSPNIKDLKTGG

YKIILNIDLDVQNMAQNALKFGYDEIVKRDKDANLSTLNGAMVVVNHQSGDVLALVGGVDYEKSNYNRAT

QSMRQPGSSFKPFVYQVAINLGYSPMSEIADISRIFEGGAGNNEDWKPKNEGGKFLGLITLKEALTRSRN

LATINLALDMGLDVLYSKLMEFGFKDIPPNLSIVLGSFGISPLEYSKFYTMFGNYGTIKDPQIIRQVQDK

TGKTIMEFNSNERKVSDEAQSFLVLDMMRNVVEKGTGRNARVKDIEIAGKTGTTNKSVDAWFCGLTPEIE

AIIWYGNDNNKPMRYTEGGARTAAPVFREFLTQYIEKFPDTTRKFSIPNGVYRGNYKGESAYYTTKSPLP

KANMKFNESEIIF

>WP\_002857018.1 MULTISPECIES: membrane protein [Campylobacter]

MRRNLSAYKAKFNGAYVFLGFFFLIYQILGSTFVYAPLLYGIFFCYMFCLLEERERTFSKLDFRWYFSLF

FLFFTDITYNFFIFSSWLAFFIFYYLCADWIKTNLKIGKFIPVVFVLCAYGIILFLDMILSYIGDEKIKI

LGWAYIVSVFIECCLAYVFFKGKI

>WP\_002856841.1 MULTISPECIES: K(+)-transporting ATPase subunit B [Campylobacter]

MSKKQNKLITKEILNNAIKGAFLKFDPRFMVKNPVMFMVEVGLILTLILSIFPTLFNGNSDERIYNILIT

FILFITLLFANFAESIAEGRGKAQAATLRQSKKDSKARRIKSDGSEEMLNSSELKIGDIVLVKAGELIPN

DGEIIEGAASVDESAITGESAPVMREAGGDFSSVTGGTTVLTDFLKIKILVGAGESFLDKMINLVEGAAR

QKTPNEIALNTLLIVLSLSFLVVVVSLYPFMQFLGVSLPISWLVALLVCLIPTTIGGLLSAIGIAGMDRV

TRFNVIALSGKAVESCGDVDTMILDKTGTITFGNRLANEFYEVQGISKEEMIKACVLSSLKDETPEGKSI

VALAQKMGYELEGNDIKEFIEFSAQNRMSGVDLQDNTKIRKGAFDAIRAYISEMNGKIPSDLETKVMEIS

NLGGTPLVVCKNEKILGVIYLKDTVKPGLKERFDELRKMGIKTLMCTGDNPLTAATIAKEAGLDGFIAEC

KPEDKIEAIKKEQAQGKIVAMTGDGTNDAPALAQADVGIAMNSGTQAAKEAANMIDLDSNPTKILEVVEI

GKGLLITRGSLTTFSMANDIAKYFTILPAMFSVVLPQMQILNIMHLATPQSAILSALIFNAIIIPLLIPI

AMRGVKFKPMKSEHLLLRNLSIYGLGGMIAPFIGIKIIDIPTAWILRILGV

>WP\_002856121.1 MULTISPECIES: 50S ribosomal protein L15 [Campylobacter]

MNLTKAAGSTHKTKRIGRGQGSGMGKTATKGGKGQTARKGYNEKRGFEGGQQPLQRRLPKVGFTSKIQKP

YVINVEKITAVKELSEITFDSIKSVHKISKSVNKIKLIGASAKDLVSKIKDENISVTGSK

>WP\_002855930.1 MULTISPECIES: recombination protein RecR [Campylobacter]

MAKGLEKFNELVESFANLPTIGKKTAIRLAYHLCINNQIDGMKLAHNIENAIRFIKPCGQCGALSENELC

EICSDEERNKNILCIVESPKDILTLEESQSYNGLYFVLDELNEEKLEKLKQIILKLNISELIFALTHSIN

SDATIFFIEDKFKGLNLTFSKIAQGIPSGVNLENVDLISLNKAMNFRTKI

>WP\_002855605.1 MULTISPECIES: 16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase RsmA [Campylobacter]

MVKAKKQYGQNFLIDKSVLAKIIQAIPKEMNNIIEIGPGLGDLTQELLKISQVKAYEIDNDLIPILKKKF

QKELECGKFNLIHQDASEAFNPSLDEKPYFLVANLPYYVASHIILKALEDKNCLGLIVMVQREMAEKFCA

KEGNSEFSSLGVLSAMICERKMLFDVDPQCFNPPPKVMSAVMSLIKTKDFDELCEIENFKNFLKDCFKAP

RKQLLGNLKTYKAKVLEVLSTLGLKENIRPHEICVDSYLKIYDKLKDEYGRKQRDK

>WP\_002855515.1 MULTISPECIES: cupin domain-containing protein [Campylobacter]

MQELEKAGIHGSFKGDSKFFSKNVKVSMMFKSNEWRNFSGALVEFEASARSAWHTHPQGQTLIVTEGEII

TKVPGQKAFIAKKGDVISCPIGVKHFHGATNTSSGAHIALTGEKEGKNVEWLELVSDEEYENALKEARE

>WP\_002854990.1 MULTISPECIES: flagella export chaperone FliS [Campylobacter]

MQNNLAYNAYSQNQAGIESPQKLIEMLYEGILRFCARAKVAIRNEDIEQRVYFVKRTTAIFIELINTLDY

EKGGEVAHYLSGLYTREIQLLSLANLENNEDRINEVINVTKGLLEAWREVHNNETVAQ

>WP\_002854923.1 MULTISPECIES: protein-disulfide reductase DsbD [Campylobacter]

MRIFGIILLSFCLCFASILSLNEAFNVKSNSYNNSISIDIELGKDIYLYSNKLKLYINEKDISSLINLPQ

SSTRGNENVYYQKLNLALPNLLLEHFAKNTTNLIKLEFQGCSEQGLCYNPQTWYFDLISKKDAFEISKPY

KTQKTDKKTKIESEESSIANFLATDNFFWILLSFFGYGLLLSLTPCILPMIPILSSLIVAKSNAKFSKKY

SFFLSFIYVFFMSLAYAIAGVIASFLGASIQGILQKPIILILFALIFIAFAFAMFGAFRFELPLRFQTFI

HKKSEKGKGVLGIAIMGFLSALIVGPCVAAPLAGALIYIANTGNALLGGSALFIMSFGMGIPLLFIGLGL

GFIKPGFWMEKVKIFFGFVMLAMAIWILSRIIEENYILIAYGILGVFFSVFMGIFEKSFTIISKIKKSIL

ILILAYSLSIFLGGLFGAKNFLNPLNFNTISASKSALSYDYINNFEQLKQEIQTNTKPIMLDFTASWCEN

CKLLDELTFSDERIIQKMQNYKLIKVDVSENNNEQIKTMKEFNVFGPPVLIFFENGKEKLKITGFISADD

LLKKLEP

>WP\_002854721.1 MULTISPECIES: signal peptide peptidase SppA [Campylobacter]

MQILKSFFKALGCGIKFINTYFKTFVLLLIVIWILMPSANSSSNLANLERIDLKGEIFDSSAVLEKIINA

KNDSNIKGVLFVVDSPGGAFAPSMELALAIKDLKIKKPVLVYASGTMASGSYLAGVGANKILANPASFIG

SIGVIMQGADLSGLANKLGIKEQTIQAGEFKSAGTFARAWNENERNFLQGLIDQSYDLFTGFVAKERALD

LNKKDQWANARVFLAAKAKELGLIDELSNYENAKKELEKLANVSNPVWKEEDKIDKFLNRLEGQTSSLIS

KSLIEIAYKTNSSFINAR

>WP\_002854542.1 MULTISPECIES: SPOR domain-containing protein [Campylobacter]

MENQKNEFDDIILEKSNKSEKVKKILLRVIALVILFLAIMIVMKLINGSGDENTQNQSVLPSEPIATQDN

NNDTSFESMPITDNTSAEDQFEALRKQFQDEQNTTQNTTTSSSNNNDTTNFAMPDQEVPAEPTATTSENT

TPQASTPKQEVTQTAKPKEEAKKQTAVKKEKESTKQIPKKEQNANDLFKNVDAKPVHPSGLASGIYVQIF

SVSNLDQKSKELASVKQKGYDYKLYKTTVGGKEITKVLIGPFEKADIAAELAKIRKDIAKDAFSFTLK

>WP\_002854541.1 MULTISPECIES: biotin--[acetyl-CoA-carboxylase] ligase [Campylobacter]

MEKGLKVKIVCVESIDSTHLFLCEQIRNGKIDGNFAIYALEQTNGVGSRENSWQSSKGNLHLSFCIKEED

LPKDLPLASVSIYFAYLLKELLQEKGSKIWLKWPNDLYLDDKKAGGVISAKISNFIIGGMGLNLKFSPQN

TALCDIEISLKDLVSEFLQKVEKKILWKNIFSKYMLEFEKSRKFSVHHEGKVFSLENSFLYEDGSILLGD

KRVYSLR

>WP\_002854461.1 MULTISPECIES: 4-hydroxy-tetrahydrodipicolinate reductase [Campylobacter]

MIKIGIYGAKGRMGKQIEECLKSETQAQISILYDKGGNLEELFEKSDVIIDFSSPSGTHELLNYARTMPK

PLVIGTTGLDEKILHLMQSASEVMPIFYATNMSLGVAVLNYLASKASQMLKNFDIEILEMHHRHKKDAPS

GTAMTLAQSVAKARNLELEKVRVSGRDGIIGERSKDEIAVMSLRGGDIVGRHTVGFYEDGEFLELNHTAT

SRATFAKGAIKIAIWLSKQEAKMYSINDFLGI

>WP\_002854385.1 MULTISPECIES: lysine--tRNA ligase [Campylobacter]

MFDNILEQQRIEKAKELKNLGINPYPHFLEKEMSLKTFKDKFSYILEQVEKRDESVNAVVAGRLKLLRIA

GKSIFANIEDEDTNLQIYFNKDSVGEELYAILKKNLEVGDIVLVKGFPFVTKTGEFSLHASEVKLATKAI

VPLPEKYHGLTDIEQRYRKRYVDMIMNAEVRKDFLVRSKVVSLIRHFFENKGFLEVETPMMHPIAGGANA

KPFVTFHNSLGVERFLRIAPELYLKRLVVGGFEAVFEINRCFRNEGMDLTHNPEFTTIEFYWAYHNYKDL

MDLTEELFALLLDKLNLGKTIEFDGKMIDFSKPFERITYKDALCKYGGLDRDLIEDKEKILTKLKVDGFE

ANEKLELGHLQAELFDNYVEEKLINPTFVIDFPISISPLSRRSDEDSQIAERFELFICGRELANGFNELN

DPLDQYERFLKQIEAKNAGDEEACEMDEDFVNALGYGMPPTAGQGIGIDRLVMLLTNKKSIRDVILFPAM

RPLKSELKEKE

>WP\_002854134.1 MULTISPECIES: YihY/virulence factor BrkB family protein [Campylobacter]

MKNFFTILLNLRDKEILNYAAALSFYTVLSLIPILFVCFSVFTQISSFKAYYEKAKQVIFAFLIPTQQDV

VATYIDTFLKNSVNLGIVGLIAMAFTSLAFFSGYDFVINRITKNEPKGLWQSISSYWTLLTLVPLGLGLS

FYISGFIQQTLDDYKIGFNFFEILPFVIIWGLFFISYSSSVHKGTLKSLALVSFGAGAIWYIGKNLFVYY

VVYNKTYASVYGSFSTILFFFIWIYISWIIYLFGLKLYYFLNYNHNEGNKIRKNTKKS

>WP\_002854131.1 MULTISPECIES: ribbon-helix-helix domain-containing protein [Campylobacter]

MKRNVKTYSFRMPLELKERLDNLSKNLSKPKSAIVKEAIEAYLNEVEDFSFAVNALEELKDGDYQKASKK

IDKIVKNLQEDSNDNELGDFDFAIEALEELKDGDYQKASKKIDKIVKNLKQTK

>WP\_002853850.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKILVSVLSSCLLASALSAVSFKEDSLKVSFEGYKTKDMIGTKGEFKNVEYKFSKNTKDLASYLKGAKA

TIKPSNAFMGEGNDIITNNITKVFFPALLGDTDIKVVFQDVIAGENKGVISAKITMDKKSTIVPLTYTIK

DNKFEAKGQLDLHTFKNGSKALKALSDVAAGHGGISWPLVDISFNADLAE

>WP\_002853829.1 MULTISPECIES: ribonuclease Y [Campylobacter]

MIESLIALIAAIVGLGIGYLVAKKINDAKYEIFVEQAKAKAKAIEYEAELILKDAKNSILNAELEVKKKY

EEKTHKIQKDFNQKFDDLSKKEQKLQQEEEKLKEDKEYLCKSQKHIQDLQSDVDKLKNKYQEKLDDVLKI

LEHSTGLTQNEAKEIILKKVEENSREQIAHIVRKYEEEAKNEAKRKANFIIAQATSRFAGEFAAERLINV

INIKNDELKGRIIGKEGRNVKTLEMVLGVDIIIDDTPGAIIVSCFNLYRRAIATKVIELLVEDGRIQPAR

IEEIHEKVCKEFDSAILEEGETIVMDLGLNKIHPEIVKLIGKLKYRASYGQNALAHSLEVAHLAGIIAAE

CGGDENLARRAGILHDIGKALTHDFEGSHVDLGAELCKRYKEHPVVINAIYAHHGHEEATSIESAAVCAA

DTLSAARPGARREVLEAFLKRVSELEDIAKSKEGIKNAYAINAGREIRVIANAQLVNDDESVLLAKEIAA

EIQEKMQYPGEIKVNVIRELRAVEYAK

>WP\_002851986.1 MULTISPECIES: metal ABC transporter permease [Campylobacter]

MLEILNFTFFQNALLGAILVSIACGIIGTLVMINRLFSMAGGITHGAFGGIGIAFYFSLPILLSTGIFTL

FLAFLVAFLAKHYEHRSDSIIAVIWAFGMAVGIILIDLSPSYNTDLMAYLFGSILAVGTQDLWLMALVDS

VVVLLIFLFYRQFEALSFDAEFAKVRGINTSFFHYLLIALMAFCIVISIRLVGLILVMALLSIPSFIAEN

FTKRLGFIMILASFLSMIFCVLGLILSYYLNLSSGACIIAVACFGFLAHLIGKFLKR

>WP\_002851979.1 MULTISPECIES: restriction endonuclease subunit M [Campylobacter]

MKENPSFLKEQIITYLGNKRALLSFLNKGFKVAKKELGKDKFSFCDIFSGSGVVSRFAKAHSNYILANDL

EDYSKLINECYLANKDKDLLQNIKKHYKNLIQNLDFQKGFISELYAPKDDDDIKKNERVFYTFKNALYLD

TIRQKIENEIPKELRHFFIAPLIYEASVHSNTSGVFKGFYKGKDGIGKFGGEGQNALKRIKGEIELKMPI

FSNFSCEFEVMQKDASMLAKELDFFDVVYLDPPYNQHPYSSNYFMLNLIANYKKPEEISKISGIPKDWNR

STFNKPKFAQDALFELINDLKARVILLSYNCEGFVKKEIFLKRLSTLGKCRILEQKYNTFRASRNLKNRN

IHLHEQLYILVKN

>WP\_002851919.1 MULTISPECIES: chromosome partitioning protein ParB [Campylobacter]

MGLNKDRGLSSLISDMDTVYSKELGFDKNQSTMIEIDQISPNPFQPRKNFDQEALDELANSIKEFGLIQP

IIVFKKNNKFILIAGERRLRAVKALGKKEILAFIADIDENKLRELALIENIQRENLNPIELANSYKDLMQ

VHKITQENLAELIHKSRTQITNTLRLLNLDIRTQELIASGKISQGHAKVLVGLDQKDEKMLVDSIIGQKL

NVRDTEKIVKKIKNNESLPNQEFEDEIKKLKQILNRFGFDCKNKNNDFVIHLENIDKIKKLIKMLEKL

>WP\_002851632.1 MULTISPECIES: DUF4492 domain-containing protein [Campylobacter]

MYLKHLYFSISQIFNFYKEGFKNLTLGKTLWKIIFIKLFVMFVILKLFVFDVNFNSIFKSDKEKSTFVLK

NLTLEGK

>WP\_002859761.1 MULTISPECIES: (Fe-S)-binding protein [Campylobacter]

MMKKVYFYATCLGTAAMQQSVLNAIKLLRREGIEVIFKKNQTCCAQPSFNSGYFDESREIALYNVDLFDK

DYPIVVPSGSCAGMMSHDYKELFKNRPEFSKVKDFSSRVIELSQYLDEVLKVDYEDKGAPIKVTWHSNCH

ALRVQKSIQASKNLIKKLKNVELVELQYEEECCGFGGTFSVKEPEISNAMVRSKIKDIQNSGAKYLISGD

GGCLLNIDGTMKRMGLDIKGIHLYDFLLKRLEGERL

>WP\_002853400.1 MULTISPECIES: acyl-CoA thioesterase [Campylobacter]

MKMRVYYEDTDAGGVVYHSNYLKFCERARSEIFFNKKVDIFDASKGHFLLAKANCNFLKPAKLGDMIEIK

TKILEVKNASVEILQEIYKDEILLFKMELTLAFIKNEKPARMDMQLKKLFEELF

>WP\_002851165.1 MULTISPECIES: type II secretion system F family protein [Campylobacter]

MKFYEVEFLKNNQNYTKTIKAENLNTAQAKALSKNWKIIDIKEIQKSNFQRLKDENFILFFKELALLCEV

GLSVQEAIRELYFMHSCKIMKKILDNLILAQNLNQAFENANFGLNRAELALIKTAEKTGKISEVFSQISK

LREKSLESQKQLKKAFRYPTLVFLSIIGAFLFLMLFVVPNFKDLFENLGASLPFITHVMLEIYNFLDDYG

IFCIFLFVIFIVMLILAYKNFHSFAFSCDFLFLKVPLISRLIIYNQNYYFFMVFSLLLKNGISISKAFDL

AIIGLENKFLIFQYKKLFSFIDSGLELSQAFKKIDIFDSLVFSMLSVAMKSGRLEVLSEEIAKYYQQKSE

NLMDRFLIFLEPMMTLFVALLVLFLALGIFLPMWELSSGVNFN

>WP\_012006716.1 (Fe-S)-binding protein [Campylobacter jejuni]

MKFSQISDACVKCGKCIPVCTIHEENRDEITSPRGFLDLLAAYKEGSLELDKEAKKVFESCFLCTNCVEV

CPSKLRVDNAIEEVRYDIAKKFGIAWYKKLIFFFLRRRKILDLVAKLGYVFQSCAFKIQNENENTGMKAR

FSMPFVKKGRLLTSFNKKSFLNSNPKFINNDGEKTIGFFVGCLANYFYIDTANAVLKIAKELKINVDLMK

EQVCCGAPQFFTGDFKSVEVLAKKNIEYFEKKLEKLDAIIVPEATCSAMLKIDYEHFFIMQNDLDWAKRA

KCVSSKIYMASEYFYKFTSLEEILKTKNKFNYSITYHDPCHARKMQGVFKEPRELLKTNYHFVEMSNSNT

CCGFGGVSMQTDYYDRALSVGLKKAQMIDESKASVVSAECSACRMQISNALEQNSSKVVFVSPLELIAKA

L

>WP\_002866843.1 NlpC/P60 family protein [Campylobacter jejuni]

MRHIFFIITIIFFISGCSFYQNLNYTRPIYNTNKETKLKTIAHEWKKTPYVLGGTSKKGADCSGFTQSAL

AQLNIRIPRTTKTQLGSGRKVSKSKLQTGDLVFFKTGRGPNGMHVGIYMSKGKFIHLSTKGGVKEVELNN

SYWKARYIGARRY

>WP\_002866641.1 MULTISPECIES: Ppx/GppA family phosphatase [Campylobacter]

MAKKTAVVDLGSNSIRMVIFEKTSRYGFYTTCEYKRKVRLGENAYNNGKILQEEAMQRAEDALAFFKQCA

LKHKCKKIFIVGTSALRDAPNSKNFIKRIKDNLSLNIRCIDGKSESYLGGLAALNLLSPFKDGTTLDIGG

GSSELCLIKNNRIISCISLDIGTVRLKELFYDTGKMDSLEEFIKPILEQIPKEFCNQNLIAIGGSLRAIS

NSIMQKNSYPLKNLHDFRYMLDEEKGHILKIFNSNLDSLINFGIKKDRFDTIKEGIFIFLKIAEKIKAKQ

VITSGVGIREGVYLQDLLRPKITFPPNFNPSLKCLQDKFLQSKQKNKTPHFALQIFTTLKNLHKLNDNYK

HTLLNAAKLCHIGEYLNFYFANEHSAHFVLGGLNYGFSHKEKALIASIIKLNGKKVNPYNLEPYKQLLPN

IHTISWLNFILCLAKTLSTNEDKIDFAFANNTLYIYQENKILNLPKDELKKIAKPATIALAINQKI

>WP\_002853412.1 MULTISPECIES: DUF2603 domain-containing protein [Campylobacter]

MKELEKYSTCLKRIDEFSQNLGIKKKDRTIFKMKQSENENEKCLVLENGSFDSPEPWFVIDENDEIHTLL

SLQSLKNILESLKQSQKENFELRLEKAIYQQIPVDFNDVWTVAMDEIKQKAQNGTMEVSIDLEKLISKIK

QEHPNLFVDMQAMIERVNQNERL

>WP\_002852959.1 MULTISPECIES: ComF family protein [Campylobacter]

MRCINCGAFALLCFCELCELELSEFSLNVRKLDNNFKVYSFYKYHEIQHLLHSKHYFYGYFVYKMLAKLS

FAKFKDFFDPRMTINVIALDDKVEDMLYSHSAILARYLKTKFVKPVFNVLKAQNSVKYSGKSLEFRQKHK

RNYKLLKTIHEPVILVDDIVTTGSSLLEAKKVLEENKISVLFALVLADAKV

>WP\_002851668.1 MULTISPECIES: BAX inhibitor (BI)-1/YccA family protein [Campylobacter]

MSLYDRDYSRSKEFENTRSSELSIFIKQTYQLFAASLLAATVGAYVGIFALASFFIQSQVTFWILFAVEI

GLLFALQWKKREAPLNLVLLFGFTFCSGLTLTPLLISVLALPAGGIIIAQAFALTTVAFAGLSVFAMNTK

KDFTVMGKALFIVLIVIVAASLLNLFFQSSIVNLAISAVAAILFSFYILYDTQNIIRGNYETPIEGAVAL

YLDFVNLFVSLLNILRSFNSR

>WP\_002866185.1 MULTISPECIES: YebC/PmpR family DNA-binding transcriptional regulator [Campylobacter]

MGRAFEYRRASKEARWDKMSKLFPKLAKAIQVAAKEGGTDPDMNPKLRSAIATAKANNMPKDNIDAAIKR

ASGKDSADIKNIHYEGKAAHGALVIVECMSDNPTRTVANVKAIFSKNGGEVLQNGSLGFMFARKAVFHLE

KFAGDLEELELDLIDAGLEELEQNEEELVISGDYTAFGELSSAIEAKGLVLKKAGLEYIPNNPVSFSEEQ

LSDIEKLLDKLEDDDDVQAVYTNID

>WP\_002867064.1 type II CRISPR-associated endonuclease Cas1 [Campylobacter jejuni]

MSYDEAFKTLLISSNAKLNLELNHLVIKQDENIAKLFLKDINIIVLESLQVSLSSALFNAFARHKIILLT

CDETHSINGVFTPFLGHFQSAKIAKEQMNVSAQKKAILWQKIIKNKILNQAFVLKKHNKIGQSNELINLA

KKVSLNDSKNIEAVAAALYFKTLFGVSFSRDELCFENSALNYGYAIIRACIIRAVCISGLLPWLGIKHDN

IYNSFALCDDLIEVFRASVDDCVLKLKGESEFLSKDDKRALIGNLQSKINFDGQNYPLNRAINHYVANFK

NALLYEDELKIVKFDD

>WP\_002866558.1 YggS family pyridoxal phosphate-dependent enzyme [Campylobacter jejuni]

MTLEQILEKTKNVRLVAASKYVDASTIEKLFDQGIVEFGENQVQALAQKKENLDEKKLDIKWHFIGTLQS

NKINLLIKQKPILWHSCNGIKIAKAMDKRLDYKLNTLLEINSANENSKSGLDPNQAVEEYLQIQEECSNL

NLCGVMSIGSHSQDKESIIKSFETTFKIYEILQKHGAKICSMGMSNDFEIAIKCGSNLVRLGSILFKNLK

>WP\_002855439.1 MULTISPECIES: cytochrome-c oxidase, cbb3-type subunit II [Campylobacter]

MFSWLEKNPFFFAVAVFVVIAYAGIVEVLPNFAENARPIEGKKPYTVLQLAGRAVYIKDSCNACHSQLIR

PFKSETDRYGMYSVSGEFAYDRPFLWGSKRTGPDLARVGNYRTADWHENHMWDPTSVVPDSIMPSYKHMF

KNNADIETAYAEALTVKKVFNVPYDTENGTKLGSWEDAQAEVKAEAQAIVDQMKNQEVKDAFAKGEIKEI

VALIAYLNSLK

>WP\_002855339.1 MULTISPECIES: ribosome silencing factor [Campylobacter]

MQERIDLIVKILDEKKAEDIKTIDMSEQEYFVKYVIIAATLGERHALSLIDELKTQLKAKGEEFLNIDSS

EEWSVIDLGDILIHLLTPEHRGIYNIEELLENLKKGRV

>WP\_002854950.1 MULTISPECIES: succinate dehydrogenase/fumarate reductase iron-sulfur subunit [Campylobacter]

MKIIIDRFNGKEKYEQSYDIDDKDIQGKTLLSLLLFIKKTKDITLNFTASCQSAICGACAVRVNGHSYLA

CDTKMQDLLKEYDNPSSIRISPLGNFRVISDLIVDWEPSIENLRKIRPAMVAKNEFSAEKGCKQSQEEFD

RISKQWDCILCGSCASECNKLEADSSDYMQPFVFTHAWRAAADSRGKDPMLHVKPSVMNGLWLCVHCQEC

ADRCPKGISSVSDIANLRVMAIKKGLNEGLGPDHAEAFYKDLVEGSGRLNEIYLALRSEGVIGSMGKTDI

AFKLMRAGKMNPMHVFGEDEIEGHKDLVKMIKAAQEAAVKE

>WP\_002851405.1 MULTISPECIES: cytochrome-c oxidase, cbb3-type subunit I [Campylobacter]

MHPGNVLNYDYTVARYFMFATILFGIVGMAIGTLIAFQMAYPNLNYLAGEYATFSRLRPLHTSGVIFGFM

LSGIWATWYYIGQRVLKVSMAESRFLMAVGKLHFWLYMLTMVLAVISLFMGVTTSKEYAELEWPLDILVV

LVWVLWGVSIFGLIGIRREKTLYISLWYYIATFLGIAMLYLFNNMEVPTYFVTGMGKWWHSVSMYAGTND

ALVQWWYGHNAVAFVFTVGIIAQIYYFLPKESGQPIFSYKLSLFAFWGLMFVYLWAGGHHLIYSTVPDWM

QTMGSVFSVVLILPSWGSAINILLTMKGEWSQLRESPLIKFMILASTFYMFSTLEGPILSIKSVNALAHF

TDWIPGHVHDGTLGWVGFMTMAALYHMTPRVFKRELYSKSLMEAQFWIQTTGIVLYFASMWIAGITQGMM

WRATDEYGNLLYSFIDTVVAIVPYYWIRAIGGLLYLIGFFMFTYNIYKTIACGRVLDKEPKSASPMAA

>WP\_002854334.1 MULTISPECIES: sulfite exporter TauE/SafE family protein [Campylobacter]

MEITDLPYLIIGIISGIASGLFGIGGGMIIVPSMFALGASAHHAIGISVLQMIFAAVFGSYINYKKKNLN

LKDGIMIGFGGLIGASFSGMLLKALSDVALTSVFLAVSCIFFIKYAFGIKENIVQNQRSVWVKNVILFIA

GAFTGIFAISLGIGGGLLIAPILAYFLGYDSKKVVSLSLFFVIFASVSGIISFSNSGVIDSEVIHKGILV

GIASMVGVFIGIKIIEKMHISAHRKILLCVYALSILGTTHSLLNKLNLINF

>WP\_002851757.1 MULTISPECIES: 6-carboxytetrahydropterin synthase [Campylobacter]

MIIRKLFEFENAHIVRFCSSKRCKSSIHGHSYKVEVLLESKYLDNAGMVYDFGLLKTYIRQIIDSFDHAI

TLFKYDDAKYLEEMKKYSSRWICLPVNVSAENFCRVFFILIDALLKQTKMVNGEQGVTLQSIIVHETRTG

YAQGFREDAYSELMPKISLQDIEFSNGIKVEWNDIDFYNKLKNEEIFINPKEI

>WP\_002851494.1 MULTISPECIES: citrate synthase [Campylobacter]

MSNSVTITDNRNGKSYEFPIYDGTTGPSVVDMSSFYKQTGMFSYDEGLTSTATCKSKITYIDGENGILMH

RGYPIEWLAENKLYLDVVHLLLYKELPDATRLEAFRYEMKKRSFIHEGMHRLFDSFPDNAHPMAVLQGAV

SSLSAFYPDHLNMNVKEEYMEMAARIVAKIPTIVATAYRYKHGFPMAYPNLDRGFTENFLYMLRTYPYDH

VELKPIEVKALDTVFMLHADHEQNASTSTVRAVGSTHAHPYACIAAGIGALWGHAHGGANEGVIRMLEQI

GSVDRVDEFIKRAKDKNDPFRLMGFGHRVYKNFDPRAKVLKKLRDQLIDELGIDTNLIKVATRIEEIALS

DDYFVQRGLYPNVDFHSGLILKALGIPNEMFATLFVIGRTPGWIAQWIEQKEQESLKIVRPRQLYLGETS

KI

>WP\_002777281.1 MULTISPECIES: QacE family quaternary ammonium compound efflux SMR transporter [Campylobacter]

MNIAKKELFVAWFFLIAAIVFEVLGTSFLKMENQILGYIFMALFIAFSYFFMGKAIKKIQVGIAYAVWEL

LGIILILLVSFIVFKESLTLTQILGIVLSIVGIIMINIGEVKE

>WP\_012006780.1 MULTISPECIES: thiamine-phosphate kinase [Campylobacter]

MNKEDFIIKAFLNEKNGDDGAIIDDWCFSKDLFFENVHFKREWFSLEQIATKAMLVNISDAISMNAVPKY

ALLGLALPKNLSENEIKALQKGFLKTARKFNIKIIGGDTISNDKIDISLTIISKINDKAVFRKGLKKGHL

LAYTGKLGRSLKGLEILQNGGTLKPNHVFIKPKLRASFFYEVAPLISCAMDISDGLSKDLSRLLALNKCG

ISWFKKLDDYTLYSGEEYEILFAFDEKERQNIKTIAKKHGVKLNIFGKAVKGKYEFRGREHHF

>WP\_012006756.1 glutamine--fructose-6-phosphate transaminase (isomerizing) [Campylobacter jejuni]

MCGIVGYIGNNEKKQIILNGLKELEYRGYDSAGMAVMQEGELSFFKAVGKLENLANKCTDFESQGYGFAI

GHTRWATHGKPTEINAHPHLGQYSCVIHNGIIENYKEIKDKLEKEGVSFLSQTDTEVIVQLFEFYARNLG

VFEAWQKTIKELRGAFATLLVTKKDPNHVYFAKNAAPLIIGKNANKEWYFSSGDAPLIGSCDEVMYLEDL

SLGYASKDELVVYENDVLKSLSFSKLSGDKAYAKKDGFRFFMEKEIYEQSRVMSEVLMGRIQGDEVVFDE

LNNEDLSQVDEITLCACGTSYHAAMASAYLFERIAKVKAKVEIASEFRYREAIIKKDSLFIVISQSGETA

DTLEALKIAKEQGAKTFAICNVDNSNIVRLAHLSLLTRAGIEKGVASTKAFATQVLTLWMLAIFMAQKRN

LNVSAEIKALLHTPNCVSVKQALHEKIHRLSKRYLDGHGFFFIGRDVFYPLALEGALKLKELSYLHAEGY

PAGEMKHGPIALADSKLYTIALMPKHMLYEKTKSNVEELIARDSTVLSISPLEFDLSDDFIKTNEQDHYM

CEFFEMMIITQLLAMEISIRLGNDVDMPRNLAKSVTVE

>WP\_002877060.1 UDP-glucose 4-epimerase GalE [Campylobacter jejuni]

MKILISGGAGYIGSHTLRQFLKTDHEICVLDNLSKGSKIAIEDLQKIRTFKFFEQDLSDFQGVKALFERE

KFDAIVHFAASIEVFESMQNPLKYYMNNTVNTTNLIETCLQTGVNKFIFSSTAATYGEPQTPVVSETSPL

APINPYGRSKLMSEEVLRDASMANPEFKHCILRYFNVAGACMDYTLGQRYPKATLLIKVAAECAAGKRNK

LFIFGDDYDTKDGTCIRDFIHVDDISSAHLSALDYLKENESNVFNVGYGHGFSVKEVIEAMKKVSGVDFK

VELAPRRAGDPSVLISDASKIRNLTSWQPKYDDLGLICKSAFDWEKQC

>WP\_002866938.1 MULTISPECIES: signal peptidase I [Campylobacter]

MEILKKLYKFSQSWTGTVVIVLLVIFFFIQAFVIPSGSMKNTLLVGDFLFVKKFSYGIPTPHIPWLEIPV

LPDFNKDGHLIKAQGPQRGDIVVFRNPRNEKEHFVKRCVGTGGDRIVYANKTLYVRMHEGDEFMKEHYPN

DLVTLGGQIYVKEPYKQKGIHYDPKKDIESDILRFLSIGDFAMSPTYIKELGNHIGFSGGNAYVFDVPEN

EYFMMGDNRDYSYDSRFWGSVPYRLIVGKPWFVYFSWDKDKNVRWERIGRFVDTLENDEQYIHDHDDEDK

LS

>WP\_002866140.1 MULTISPECIES: glycosyltransferase [Campylobacter]

MQKLGIFIYSLGSGGAERVVATLLPILSLKFEVHLILMNDKISYEIPECQIHFLECSKPSENPILKFLKL

PFLALKYKKLCRNLGIDTEFVFLNRPNYIALMARMFGNKTRLVINECTTPSVMYAKNNFNSLANKFLISL

LYPKADLILPNSKGNLEDLVQNFSINPKKCEILYNAIDLENIEQKALEDVALKDKFILSVGRLDKGKNHA

LLIRAYARLKTDLKLVILGEGVLKDELLALIKELNLEEKVLLLGFDNNPYKYMAKCEFFAFASVFEGFSN

VLIESLACSCAVVCTDHKSGARELFGDDEFGLLVEVDNENSMFQGLKTMLEDDKLRKAYKNKAKTRAKAF

DKVKIARDALKYLLG

>WP\_002857493.1 MULTISPECIES: branched-chain-amino-acid transaminase [Campylobacter]

MISADKIWMDGKLVDFKDATLHFLTHSLHYGNAVFEGTRAYKTDKGLAIFRLEDHTKRLLESAKITLLNC

PFSQKDLENAQIELLKANNFQSNVYIRPLIFLGDGVMGLYHIKAPVRVGIAAWEWGAYLGEEGLEKGIKV

KISSFARNSVKSCMGKAKASANYLNSQIAKFEAIEAGYEEALMLDEEGFIAEGTGECFFIVKDGVLITPP

NDFSLKSITQDTVLKIAHDLGITVLRQRISRDEVYTADEAFFTGTAAEITPINNIDARIIGNGLRGSVTK

KLQDAYFDVVYGRNEKYASMLTYI

>WP\_002856787.1 MULTISPECIES: molybdopterin-guanine dinucleotide biosynthesis protein B [Campylobacter]

MKQLIMAFSGPSNSGKTTLITKIADNFLQQNLKVLIIKHDPADKAQFDFNGKDSFKFFQSGAEVMVLSPT

RTTFFSHENRDILKALKLAPNFDICLVEGLKTLDLPRISVFCKEIDESYFTFSNAIASYEKISHPYLTWL

DLNDIQAICRYILKNAKNLQGEL

>WP\_002855252.1 MULTISPECIES: LPS export ABC transporter ATP-binding protein [Campylobacter]

MSKLEIVNLEKIIKKTKIIHGISLEVNSGEVVGLLGPNGAGKTTTFYMICGLISPSSGKVLLDGLDVTKD

PLNKRARSGIGYLPQESSIFKDLSVEDNLLLAAQIFYKDKKILHDKVEQMLELLSIEPIRLRKGLSLSGG

ERRRCEIARSLMCEPKFLLLDEPFAGVDPIAVAEIQTLIKELKRLGIGVLITDHNVRETLAICDRAYVIR

SGSLLASGNADEIATNKDVKKYYLGAEFKLLD

>WP\_002852324.1 MULTISPECIES: prepilin-type N-terminal cleavage/methylation domain-containing protein [Campylobacter]

MNKAFTLLELVFVILILGILSSLSLSFINTTKDEVKILKLKMDYEMLSSALALMRSQMRLKNLNFPEILD

NAQNNQAKEKLFYCLNDCDYSLLDTPIYSDFKSWIKIGKNHYRFALNAKEMVEFIYDSKEGLLKCIGSSR

CKDLI

>WP\_012006732.1 WxcM-like domain-containing protein [Campylobacter jejuni]

MNYTILKFKTINSKNSILNVHQKDVNCPFEIKRIFYIYDFLDDSIRGDHANLNSEFIFIALNGSCEILID

DGKTKQKIILNNKTKGLYIDKMIWKQMYNFSKDCILLVLTNTYYDEKEYIYDYKYFCELKNNIVWRGGGM

L

>WP\_002859058.1 MULTISPECIES: fluoride efflux transporter CrcB [Bacteria]

MLNTLLVVGFGGFIGAILRMFSINLVNKFFPYSISLGTLFVNVLGSFIIGLLFSYAQNKGLSPLLKSFIS

TGFLGAFTTFSTFSYQNLLLLQSGNYLHFALNIILNVFLCLFAAWLGFIIFK

>WP\_002854882.1 MULTISPECIES: HAD-IB family hydrolase [Campylobacter]

MKLVLFDLDDTLIQGDSAKLWLKFCVEKGFLPQEYLEKIVFYQKQYQEKKLDMDEFMTFFLQSVKGKNED

RISSLVDEFIKIYIKPYEKAKELIIKYQDQRCIIISATAEFLVRKIASFLGVRESIAIKCERVGDKFSGK

AYGVYSFKEGKVLRLKEYLGKDYEKWMKDSYFFSDSINDLPLLESVSKAFVCNGDEKILKIAKERKYEIL

TF

>WP\_072238676.1 sodium/proline symporter PutP [Campylobacter jejuni]

MIKERLMEVVQINTPIAVMFVAYALLMLYIGFYFYKQNKNSEDYFLGGRTMGPVISALSAGASDMSGWLL

MGLPGALYVSGFIDSYIAIGLTIGASLNWIFVAKRLRIYTSVIANSLTIPDYFETRFDDDKHILRIVCAV

VILIFFTFYVSSGLVSGAKLFESTFGIRYDYALTTGTIIIVAYTFLGGYKAVCWTDMIQGLLMMMALIIV

PLVMLYHLGGFGEAMNIVREIKPQALSMGEGVGVISIISALAWGLGYFGQPHILVRFMSIRSTKDIPMAT

FIGIAWMAVCLLSACMIGILGIAYVHKFELSLQDPEKIFIVMSQLLFNPWIAGILLSAILAAIMSTASSQ

LLVSSSTIAEDFYKKIFREDAPSHVVLNLGKLGVLLVAVIAFLISTDKNSSVLSIVSYAWAGFGASFGSV

MLFSLFWSRMTRVGAILGMITGAATVVLWKNFANSGLYEIVPGFLAASVVIIIASLFTNVRSGTKAAYEK

MLKEL

>WP\_002856169.1 MULTISPECIES: TlpA family protein disulfide reductase [Campylobacter]

MKKILTLFLISLAFFLNACSKEEEIQNDFMFEEYHKGDKIVLNSVNGGSKTLIRTDKGFVVEGEEGKVLM

FDFFGTFCTPCKEEALDLSKLWKNNSSKFIIIGLTHFEDVSDETVKKFADDYGAYYFLSNGGSNDRIIAQ

ILKDIDYQNMEQLPFKVVLKNGIYQKISDYWNNNAPTNFYLGKIPTELMQEDLNKIYKGK

>WP\_002851267.1 MULTISPECIES: TlpA family protein disulfide reductase [Campylobacter]

MKKSLLILSILFLLNACSFENSKDTGKVGEKSAEISAKDTLGKAVKLADDNTSLKVLVFFQNGCPSCLKE

LPSLDEFIQNHPNKISVYAINSIDNANVVKVLAEQFDFKNVKVLKDDLKITNDRYAVFATPTTIIIKDGM

IKDRILGEKPWEFFESKLISLL

>WP\_075888380.1 MULTISPECIES: NAD(P)H-dependent glycerol-3-phosphate dehydrogenase [Campylobacter]

MMRIAVIGAGKWGSALHLALKENHNCFISSLHQRDLEDFVSIKEALECEYLVFALSSQGMRAWLKENFIN

KGQKILIASKGIEDQSCQFLDEIFLDFVPKENFCVLSGPSFAAEVMQKLPTALMISGINQELCKKFASFF

PDFIKTYIDNDVRGAEICGAYKNVLAIASGISDGLKLGNNARAALISRGLIEMHRFGKFFGAKEETFLGL

SGAGDLFLTATSVLSRNYRVGLKLAQNQKLDSILVELNEVAEGVKTAYAIEKLAKMKGIYTPIVNEVVAI

FKGKSVQEATQSLLKQND

>WP\_072238617.1 MULTISPECIES: 16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH [Campylobacter]

MILEIPHIPVLLNEVQEIFKNLKTGYFLDCTLGFGGHSEALLKNHPDLKFIACDQDQQALEFSKKRLKDF

HNRITFIQSNFSEVLEKISYKEELRGILADIGVSSFQLDNNERGFSVNSDFLDMRMNQNSKISAYEIINT

YTKEQLTSIFKDYGELHDAHFIAEKICLERSKNPIKSAKELYQIIGKGKQNHRKISKATLAFQAIRIEVN

QELKVLKDFLGHLENLKPKNCILAIISFHSLEDRIVKNFFKKWSKNCICDEKIMRCECGNNHSLGQIITK

KAISASKEELLKNSRSSCAKMRAFYFNNLDNK

>WP\_002856979.1 MULTISPECIES: potassium-transporting ATPase subunit KdpC [Campylobacter]

MLRTLLSFFVVMLILCTLIYPFALNTVAKFIFPYQSSGSLVDKEGRPTLDISKAVGSKLLGQDFNKPYFL

HSRASVSNYNTSDTNESSVSSGGFNYAMSNPALKERVQKDLQKFLDENPQITKEQIPLDLLSASGSGLDP

HISLQAALVQIPRISQSSKITKEELEKIIQENTESKFLGIFGEEKVNVLAVNIAIAKAMKKE

>WP\_002855878.1 MULTISPECIES: flagellar type III secretion system protein FliR [Campylobacter]

MEFVNYLGDKNVVTFMLLLARMSGLIVFFPFFSHNSIPMVIKSTIVLFLTMYLYPLARLESLHLDSFFVL

QLISEVIFGMIAGLMLQIIFAIIMMAGEQIAFTMGFTMASILDPSSGTSMPITSQILNLLALMFFLAFDG

HHLMLLFLSHSLGYISLGGFYPHENLMHYLNMGMFNIFIIGFTMSFPILGISLLADVIFGLLMKTMPQFN

LLVIGYPIKIALGFVVLIAILLVMMQYFKNLILELFTHMQTLFFS

>WP\_002855629.1 MULTISPECIES: flavodoxin FldA [Campylobacter]

MSVAVIYGSAMGNTEGAANTIASKLGISDVFNISDIDAAKMNSYDKLICGTSTWGSGDLQDDWDGFDFSG

LSLGGKTVAVFGMGDSESYSDTFCGGMGKLAQNLKDAGANLVGEVSTDGYTFEASDAVVDGKFVGLALDN

DNQEDQTESRIDAWVEQIKPYFA

>WP\_002855031.1 MULTISPECIES: inorganic diphosphatase [Campylobacter]

MDLSKIKIGDIPNKINAVIEIPYGSSIKYEIDKDSGAIMVDRVMASAMFYPANYGFIANTLADDGDPVDI

LVLNEYPIQAGAVIPCRLIGVLIMEDESGMDEKLLAVPNSKIDARYDNIKTYTDLPQATLNKIKNFFETY

KILEPNKWVKVQDFKDEKAAIEILEKAIKNYK

>WP\_032595244.1 MULTISPECIES: biosynthetic arginine decarboxylase [Campylobacter]

MMDYGIDIWGNENFIIKNGKVCINHEKKPAIIDIVKELRDDGYKGPLLLRFPHLIQKQIENIYGNFNKAR

KEFGYKGGFNAVYPLKVNQYPGFVKNLVKLGKDYNYGLEAGSKAELLLAMAYNNEGAPITVNGFKDRELI

NIGFIAAEMGHNITLTIEGLNELEAIIDIAKERFKPKPNIGLRVRLHSAGVGIWAKSGGINSKFGLTSTE

LIEAVNLLKENKLLEQFTMIHFHLGSQITEIHPLKKALNEAGNIYTELRKMGAKNLKAINLGGGLAVEYS

QFKNEKSRNYTLREYANDVVFILKNIAEQKKDLEPDIFIESGRFVAANHAVLIAPVLELFSQEYAENKLI

LKKQNPKLIDELYDLYKSIKPSNALEYLHDSIDHLESILTLFDLGYVDLQDRSNAEILTHLITKKAILLL

GDKQNPADLLAIQDEVQERYLVNFSLFQSIPDFWGLEQNFPIMPLDRLDEEPTRSASIWDITCDSDGEIS

YSKDKPLFLHDVDVEKENYFLGFFLVGAYQEVLGMKHNLFTHPTEAIISINEKGYEVEGIIEAQSILDAL

EDLDYDIHAIMDILNERISNSKLVNDKQKKHILGELYLFLNDNGYLKSIGV

>WP\_012006673.1 excinuclease ABC subunit UvrB [Campylobacter jejuni]

MLELTSKFKPSPDQQEAIKGIVKSIKKGNKYQTLLGVTGSGKTFTMANVIKELNIPTLIMSHNKSLCAQL

YSEFKGFFSKNHVEYFISYYDYYQPEAYIPRTDVFIEKDSSTNEDLERLRLSTTASLLSYEDVVCIASVS

ANYGLGNPNEYIGMVLIFELGMQISQKELLKKLVDMGYKRNDNFFDRADFRVQGDIIDIYPAYYEDEVVR

LEFFGDELDAMYHYNVLENKKGKDLKRFILYPTSQFSVGETRLKQAIKDIKAELNERLAYFEHENKLVEY

QRLKQRVEFDLEMLTSTGMCKGVENYARHLTGLKEGDTPYTLFDYFAIKDRKFLVIVDESHVSLPQFRGM

FAGDRSRKQTLVDYGFRLPSALDNRPLMFDEFIHKNCQFLFVSATPAPLELELSKENIFHQIMRPTGLLD

PLIELKDSDNQVEILFDEAKKVIQRNERVLVTVLTKKLAEELTRYYLELGIKVKYMHSDIDAIERNEIIR

GLRSGAFDMLIGINLLREGLDLPEVSLIAIMDADKEGFLRSTTSLIQTMGRAARNVNGKVLLFCKKITKS

MQEAMDTTNERRKLQMAYNKKYNITPTSVKRHIEESLKNEEDLGEIYRKGKKLEKMPASERAKLVKELRK

QMLEAAKALEFEKAAAIRDEINKLRDL

>WP\_002872967.1 MULTISPECIES: quinone-dependent dihydroorotate dehydrogenase [Campylobacter]

MAYEMIKPLLFKLNPEHAHALVEYSLRALSASFPGALSFLAHKYIVDDESLRQNLLGLDFNNPVGLAGGF

DKNATMIRPLSALGFGFLEVGTFTPKPQEGNEKPRLFRLVKQESIQNAMGFNNEGAEKIALRLAKTYPFV

LPLGVNIGKNKITPNDKALEDYFTLFRDFKDLCDYFIVNISSPNTKNLRELQNDDFLNTLLEEAKKITSK

PILIKIAPDMKIDDALNLCENAIKKGADGFILANTSVDYSLLDNNRTFGGISGRLITEKSGIFFKEVAKI

LFGKTLLIASGGIDSADIAYERIKNGANLVQVYTALIFKGPSLVKNINQNLIELLRKDGFLHISEAVGVN

LK

>WP\_002860591.1 MULTISPECIES: 5'-methylthioadenosine/adenosylhomocysteine nucleosidase [Campylobacter]

MMKIAILGAMSEEITPLLETLKDYTKIEHANNTYYFAKYKNHELVLAYSKIGKVNSTLSASVMIEKFGAQ

VLLFTGVAGAFNPELEIGDLLYATKLAQYDLDITAFGHPLGFVPGNEIFIKTDEKLNNLALEVAKELNIK

LRAGIIATGDEFICDEAKKAKIREIFNADACEMEGASVALVCDALKVPCFILRAMSDKAGEKAEFDFDEF

VINSAKISANFVLKMCEKL

>WP\_002858466.1 MULTISPECIES: NADH-quinone oxidoreductase subunit NuoK [Campylobacter]

MIEKYFFIAILMFVIGLVGILKRQNLIMLFISSEILLNSANLALVAASKMHNDLNGQVFALFIMGVAACE

VAVGVALCVLWYRRKGTLELKSLKEVEA

>WP\_002857634.1 MULTISPECIES: protein-methionine-sulfoxide reductase catalytic subunit MsrP [Campylobacter]

MIITPENLYKKRRDFLKLGAGALISSSVLASKLSALNFTSDTNPNKLEISDEELATNYVNFYEFSTDKKK

AVSLAQNFNTQNWKIDISGEIEKPLTLSMEDILKFPLEERIYRFRCVETWSMVVPWVGFELRRLIEMAKP

TSEAKFVKFTTLLDKSQFPDQDALFPTIDYPYVEGLRMDEAMHPLTLLAVGMYKKALKPQNGAPIRLVVP

WKYGFKSIKSIVKIEFTKEQPKSTWESYAPSEYGFYANVNPNVSHPRWSQANERALGDFFTKPTLMFNGY

EKEVASLYKNMDLKVNF

>WP\_002851780.1 MULTISPECIES: protein-L-isoaspartate(D-aspartate) O-methyltransferase [Campylobacter]

MNAFEQKRCQNMAEEIAQKVFINEELFNAFCQIPREIFSPLKAHAYRLDALPLANSQWISSPLTVAKMTM

ALDFKNADSILEIGCGSGYQAAILSKVIRRVFTIERIENLAKKAAQTFRELELFNINVKFDDGQNGWKNY

APYDRILFSAYATQIPEILLDQLSDDGILVAPILHNGKQFITRLRKNGTNLQKEILEECLFVPIVDGKE

>WP\_002776342.1 MULTISPECIES: HypC/HybG/HupF family hydrogenase formation chaperone [Campylobacter]

MCLSIPSEILEIDELNNALVQTLGVKRKVNLDLIDEPLKQGDYVLIHVGVAMEKIDKEAALESIKTYQEI

VEKMNSGEIKSDEGDLGLNEFHR

>WP\_002870612.1 MULTISPECIES: enoyl-[acyl-carrier-protein] reductase FabI [Campylobacter]

MIMKGKKGLIVGVANNKSIAYGIAKACFDQGAELAFTFLNDALKKRVEPIAQEFNSNFVYELDVNNNEHL

DSIAEKIKKDLGEIDFVVHAVAFAPKEALENSFLETSKEAFDIAMQTSVYSLLSLTRALLPILKDKGSIL

TLSYLGGVKYVPHYNVMGVAKAALESSVRYLARDLGVKGIRVNAISAGPIKTLAASGIGDFRMILKYNEI

NSPLKRNVSIEDVGNSAMYLLSDLANGVTGEIHYVDAGYNIMGMGDVEKNEEGQTVLCWDNQKG

>WP\_002854829.1 MULTISPECIES: flagellar hook-basal body protein [Campylobacter]

MQNGYYQATGGMVTQFNKLDVITNNLANINTSGYKRDDVVIADFKRIFKETQDELPIENHTRDASRFVNT

TIDGIPQVSQEYTDFSLGSLKATNNPLDLAMTREDAFYLVQTKDGEVRLTKDGNFQLDDEGYLVNKQGYK

VLSSDYFNNPQNAGIRIPNGAVQISVDKNGSIEVDGAQNARLFVAQVDDIRALQKDGDNVYKIDDLTRIR

DLENSNAIRQGFSQGSNVNPVTEMVGLIEANRMVEMYQKVMTAHMDDLNQEAINKLAAVK

>WP\_072238685.1 MULTISPECIES: quinol dehydrogenase ferredoxin subunit NapH [Campylobacter]

MMKYLIARRIVQLGILALFSFKATDFILQGNLSSSRFFNTIPLSDPFAVLQIILASWSIDLMALIGALII

FFIYGLLLGRVFCSWVCPVNLITDFAAFVRNKLTLNNKFLILPKNLRYFVLVLVLVLSFVFSLPVFESFS

YIGMIHRGIIFATSSWIFVAFILFCIDTFLSPRAICSHFCPLGAFYAFISRFALLKIKHDSDKCTKCYEC

IRICPEKQVLWMVGKESTSVKSGECIRCARCIEVCNDDALNFNIFDLRNK

>WP\_012006635.1 methyl-accepting chemotaxis protein [Campylobacter jejuni]

MQSINSGKSVGISAKLTLWVGILVVLILAITSAISYFDSRNNTYELLKDTQLKTMQDVDAFFKSYAMSKR

NGIQILANELTNRPDMSDEELINLIKVIKKVNDYDLVYVGFDNTGKNYQSDDQILDLSKGYDTKNRPWYK

AAKEAKKLIVTEPYKSAASGEVGLTYAAPFYDRNGNFRGVVGGDYDLANFSTNVLTVGKSDNTFTEVLDS

EGTILFNDEVAKILTKTELSINIANAIKANPALIDPRNQDTLFTAKDHQGVDYAIMCNSAFNPLFRICTI

TENKVYTEAVNSILMKQVIVGIIAIIIALILIRFLISRSLSPLAAIQTGLTSFFDFINYKTKNVSTIEVK

SNDEFGQISNAINENILATKRGLEQDNQAVKESVQTVSVVEGGNLTARITANPRNPQLIELKNVLNKLLD

VLQARVGSDMNAIHKIFEEYKSLDFRNKLENAGGSVELTTNALGDEIVKMLKQSSDFANALANESGKLQT

AVQSLTTSSNSQAQSLEETAAALEEITSSMQNVSVKTSDVITQSEEIKNVTGIIGDIADQINLLALNAAI

EAARAGEHGRGFAVVADEVRKLAERTQKSLSEIEANTNLLVQSINDMAESIKEQTAGITQINDSVAQIDQ

TTKDNVEIANESAIISSTVSDIANNILEDVKKKRF

>WP\_012006626.1 methyl-accepting chemotaxis protein [Campylobacter jejuni]

MKSVKLKVALIANLIAVVCLVILGVITFMFVKQAIFHEVVKAETNYVKTAKNSMESFKARNSLALESLAK

SILKHPVEQLDSQDALMRYVGKDLKNFRDAGRFLAVYIAQPNGELVVSDPDSDAKKVDFGTYGKADNYDA

RTREYYIEAVKTNKLYVTPSYIDATTNLPCFTYSTPLYKDGKFIGVLAVDVLVTDLQAEFENLPGRTFVF

DEENKVFASTDKTLLQQGYDISAIANLAKIKENFEPFEYTRPKDGSERFAVCTKVSGVYTACVGEPIEQI

EAPVYKIAFIQTAIVIFTSIISVILLYFIVSKYLSPLAAIQTGLTSFFDFINHKTKNVSTIEVKSNDEFG

QISNAINENILATKRGLEQDNQAVKESVETVSVVESGNLTARITANPRNPQLIELKNVLNKLLDVLQARV

GSDMNAIHKIFEEYKSLDFRNKLENASGSVELTTNALGDEIVKMLKQSSDFANALANESGKLQTAVQSLT

TSSNSQAQSLEETAAALEEITSSMQNVSVKTSDVITQSEEIKNVTGIIGDIADQINLLALNAAIEAARAG

EHGRGFAVVADEVRKLAERTQKSLSEIEANTNLLVQSINDMAESIKEQTAGITQINESVAQIDQTTKDNV

EIANESAIISSTVSDIANNILEDVKKKRF

>WP\_002866858.1 NADH-quinone oxidoreductase subunit L [Campylobacter jejuni]

MQNLALISLFSPFVAFLFASCFALSEKKQFVGIICSLLVALSAFCSLYLLFCNEAFNVSLFEWFAGVNFG

FDIDAISLTMMSVVGIVATCVHFYSIFYMAHDEGFNKFFAYLGLFVFSMLFLVMSDNFLGLFVGWEGVGL

CSWLLIGFWYKNDTYSFAANEAFIMNRIADLGMLLGIFWLYLQAGTLKYDEVFSMAQSLDHNALILIATC

LFIGAMGKSAQFPFHTWLADAMAGPTPVSALIHAATMVTAGVYLVIRASTLYDLVPEVSYIIALLGAFVA

IFAASMALVARDLKRIIAYSTLSQLGYMFVAAGLGAYGIALFHLATHAFFKSLLFLGAGNVMHAMNDKLD

IEKMGGLFKPLKFTAILMCIGSLALAGIYPFAGFFSKDLILGYSFISFHHGIFLVLLIAAFLTAFYSFRL

LMLVFFTPARHNEHPHEASKIALLAMSPLMVLAIVAGFFEHSFFEYLSTKLVFIDAQNQIVMICASVAAI

LGVILAIFAYKNSWFKESIEENKIHKLLSNDYFIPQFYHQFIVSKYESLCAILKHCDLYIFDRIVEKIAL

YSQIISQKMIMPNSLNLMLRFLVAAFVILLILVWMV

>WP\_002866849.1 STAS domain-containing protein [Campylobacter jejuni]

MNANFKFQNNTLFIFGIWDKTSIYKLKIKDFLALIQSKEVIFDFKDLKAIDTAGVRFFLALENDLKDKNI

KITKEGLNSRFQTLFELCEKNYQRLSKTKKSHKNFSEYFIDLGKLSLELLKILIKFTNFTGAFFTSLFLC

LKNPKNFRFIAFLYHIENSAFKALPIVILTALLVGVVLAYQAAYQLAQFGANIFIVDLMGISATRELAPL

IAAIVIAGRSASSYTAQIGVMKITDEIAAMNTMGFRSFEFIIIPRVMALVVAMPLIVAISDAISIIGGMM

VAKLNLDISFAEFLRRFREAVDIKHIFIGLAKAPIFGFLIGLIACFRGFEVKNTTQSIGIYTTKSVVNAI

FWVIAFDALFSVVLTSAGI

>WP\_002866282.1 imidazole glycerol phosphate synthase subunit HisF [Campylobacter jejuni]

MLKTRIIPCVLLKNSQLVKSIEFKNFRTIGHLTSTMRIYNARNVDELIILDIDASKSGEIDFESIEDLAK

ECFMPLTIGGGIKTLEDIQKILNLGADKISINSKALEDKDFISKAANRFGSQCIVCSIDVKRKGEQFCVY

DRGNLLEKSPLELALEYEKKGAGELLLTSVDFEGKAKGYDLELLKIFQNKLKIPLIVNGGLGKPSDGVKA

LNLGVDALAGAYIFHFSKYTPKDVKEELAKQGFAVRLL

>WP\_002853517.1 MULTISPECIES: DUF1751 domain-containing protein [Campylobacter]

MLTIFLIFLNILCYFLISYDYYNILGLNILFFNGAYWQLLSSMFLHGNLTHLILNMIVLFQFGRILETYL

GALRFIFIYFIGGLLCSLLSVFYVYFDFKYFGENINVIGASGAICVLMGFYAVLDKNSTKGLIVAILLMS

FAPLLMGVNVAWYGHIFGFMCGYILAKIKEVK

>WP\_002852142.1 MULTISPECIES: flagellar basal-body rod protein FlgG [Campylobacter]

MMRSLHTAATGMVAQQTQIDVTSNNIANVNTAGFKKSRAEFADLMYQVMKYAGTSTSATTLSPSGIEVGV

GVRPTAVTKVFTEGNLKSTSTDGLDMAIAGNGFFQIQLPDGTIGYTRNGQFTKDNEGNIVNSDGYRLLPE

MTIPEGATAINVATDGTVSVMLPGEQQETQIGQVELVQFINPAGLHSMGDNLYLETGASGAPVAGIAGQD

GLGTIRHGFIELSNVQLVEEMTDLITGQRAYEAGSKAITTSDDMLGIVNQLKR

>WP\_002812870.1 MULTISPECIES: RIP metalloprotease RseP [Campylobacter]

MRSLLLLIVILILGIKFYSIEFLATVLVISFLIFFHELGHFLAARSLGVKVEVFSIGFGKSLIEREFKGT

NYRLSALPLGGYVKLKGQDDMRPGFENLDKDSYSILSPLKKIYILFAGPFFNLILAFFLYIIIGNLGLNK

LAPQIGNIAPNSAAQEIGLQKNDTILEINGVKIQSFDEISKHLSLEPLKILIDREGKNLEFTLTPKIGQG

YNDFGQIVEKPQLGVSPNGTSTLVKHQGLESFKYAIQESFQASTLIIKGIIKLISGEVEAKNLGGIITMT

EITSKAAQNSFTLLLFITALISINLGILNLLPIPMLDGGHILFNLYEMIFRRKVPQRAFEYLSYAGMAIL

LSLMLFATYNDISRIAGE

>WP\_012006612.1 DNA topoisomerase (ATP-hydrolyzing) subunit B [Campylobacter jejuni]

MQENYGASNIKVLKGLEAVRKRPGMYIGDTNIGGLHHMIYEVVDNSIDEAMAGHCDTIDVEITTEGSCIV

SDNGRGIPVDMHPTENMPTLTVVLTVLHAGGKFDKDTYKVSGGLHGVGVSVVNALSKKLVATVERNGEIY

RQEFSEGKVISEFGVIGKSKKTGTTIEFWPDDQIFEVTEFDYEILAKRFRELAYLNPKITINFKDNRVGK

HESFHFEGGISQFVTDLNKKEALTKAIFFSVDEEDVNVEVALLYNDTYSENLLSFVNNIKTPDGGTHEAG

FRMGLTRVISNYIEANASAREKDNKITGEDVREGLIAVVSVKVPEPQFEGQTKGKLGSTYVRPIVSKASF

EYLTKYFEENPIEAKAIMNKALMAARGREAAKKARELTRKKESLSVGTLPGKLADCQSKDPSESEIYLVE

GDSAGGSAKQGRERSFQAILPLRGKILNVEKARLDKILKSEQIQNMITAFGCGIGEDFDLSKLRYHKIII

MTDADVDGSHIQTLLLTFFFRFMNELVANGHIYLAQPPLYLYKKAKKQIYLKDEKALSEYLIETGIEGLN

YEGIGMNDLKDYLKIVAAYRAILKDLEKRFNVISVIRYMIENSNLVKANNEELFSVIKQFLETQGHNILN

HYINENEIRAFVQTQNGLEELVINEELFTHPLYEEASYIFDKIKDRGLEFDKDILEVLEDVETNAKKGAT

IQRYKGLGEMNPEQLWETTMDPSVRRLLKITIEDAQSANDTFNLFMGDEVEPRRDYIQAHAKDVKHLDV

>WP\_002866039.1 porphobilinogen synthase [Campylobacter jejuni]

MFKRFRRLRLNENLRAMVRENSLSVNDLIYPLFVVNGTGIKKEISSMPDVFQMGLDEILKECQNVVNLGI

KAIILFGVLENEKKDSCGSDALDDKGLVARSIREIKKNFPDLFIISDLCFCEYTDHGHCGIIDPKTKSVD

NDATLEISAKQALVHARAGVDMIAPSGMMDGIITTLRKALDKEGFENLPIMAYSTKFASSYYGPFRDVAE

SAPSYGDRKSYQMDFANGKEALEESLEDEAQGADILMVKPALAYLDVVKEISLHSNLPLCVYNVSGEYAM

LKAAKNAGVIDYEKVLYETMIAFKRAGAKLIITYHAKELAKMLKGEK

>WP\_002851290.1 MULTISPECIES: flagellar biosynthetic protein FliQ [Campylobacter]

MDESTLVALGVQTFKITLLLSLPMLLAGLIAGLVISIFQATTQINEMTLSFVPKIILVVVILIFLMPWMT

TTMIDFTENILNQIPTFIK

>WP\_012006759.1 phosphoribosyltransferase [Campylobacter jejuni]

MIFYSYEEFKEDVKILAKEIKKDFNPDALLAIARGGMSLGHSLAVALKTRQLFALNSIHYDDTKKLDTIE

IFNIPDLSKHKKILLIDDIVDSGESLAEIKKVLLEKFPHIKLKIATIFYKKTALLEPDFKVKEATEWVDF

YWDINLD

>WP\_002854361.1 MULTISPECIES: MotA/TolQ/ExbB proton channel family protein [Campylobacter]

MNFEAIFHFFNSSSIITYIVLLWLSLYFILAFSILFARLTYLATWRNKEKESLETLLLGEKDLSRTDSIL

RKCNDTTSNHLEIYKNLASRRASAGLTWLSIIASTSPFIGLFGTVISILETFGGLGTQNSLSIIAPKISE

ALVATGCGILVAIPAYTFHLIIKRKAFELLSIIDSEIKVISSSK

>WP\_079254165.1 ABC transporter ATP-binding protein [Campylobacter jejuni]

MMKKELIKINNLNKEFGKVKALNNINLSVYEGEWLAIMGPSGSGKSTLLNILSLMDTPSSGEYILDNENL

EQMDEEQKITLRREKIGLVFQQFHLIPYLNALENVMLSQYYHSSVDEEDTKMVLEKVGLSHRLTHLPSQL

SGGEQQRVCIARALINNPELLLADEPTGNLDEANEQIVLQTLQKLKNEGKTIVLITHNPDLAKFADRTLI

LQHGVLK

>WP\_002866696.1 MULTISPECIES: PLP-dependent transferase [Campylobacter]

MNSKTKLIHCGRGDQGAEVRSVNPTLMRASTILFKDHATWQKYRELRKTDRVLSYGARGTTTNFELEKLI

CTLEGGYRAQLFPTGLAALAMVLLNYASKDAHFLITDAIYGPVRTICELFLDKMGVEIDFLKADASDVEE

KIKPNTKLILCESPGSILYEVIDLPKLCKIAHAHNIPVAIDNTYSSGYFLNPLELGVDISVIAATKYLSG

HSDVTMGIVVINEKEWKNFDKLPEALGFTTSPDDAYLVLRGMRTLDVRMKAHEKSADEIVEFLQSRKEIK

TIFYPKLKSHPNHEIFMRDHKGANGMITIEFTEGYSKDDAIKFVDKLEYFSIGASWGGYESLATVTTPPR

TATDWSARGPFVRFHIGLEDTKDLIADLTQAFDSIKK

>WP\_002853664.1 MULTISPECIES: TrkA family potassium uptake protein [Campylobacter]

MKNLNYGIIGLGKFGSVVADELIAGGHTVIVADKDEEALKSIQNPPSYAYILDSTNISALKEAGFHDVEV

VIVSIGENVEKSILTLMALKDIGVKNIIAKATSNIHGQILSKLGATKVIYPEKESAKRLVKEFLTKDADY

EVFDLSANTIRAIKINIDEKLAGNSLKHVAQNMKVISYKKLNSDWEILPDLETTTVYSGDVVILLGTVKE

LREFEH

>WP\_002852622.1 MULTISPECIES: type II toxin-antitoxin system Phd/YefM family antitoxin [Campylobacter]

MLSFKQDEIYTATEVVRNFSPIMEKLKKSESGKIVILKNNKFEAVMLSMKEFERLQNAMQLLENIYKNQK

A

>WP\_012006695.1 MULTISPECIES: sensor histidine kinase [Campylobacter]

MLKTKNIFIVFFVVLALIFGFIFYTFTNSYLNFLLIKQYEQKIKSLDDVLKFSLLEHLNDANIKDFAKDT

RADFIILNNDMKISSVKNPDFFSNLKEGEILNFNSKKILTKSFIYKGYKYIIIVYPRFLDLELFWTKIAI

GFGVCLLFVFILMLLLGRRIEKNFNKILDFLDSIGDHKVVILEKGMFKEFNLLNEKLLKTKDKILKNTQK

NKKQSDKITLKNTQLASVISAISHELKNPLSVIDLSLEMLKDEKLEDKKLKKELLEKISRQSIKLNALTH

KLNFVFNLNSEALQMQEFDLFFLCEKITKNPGFERVVLQGKSTKVKADEFLIEQVIINLLSNALKYSQKE

VILTARDQKIIVQDFGKGIEEDKIKLITKKFYKIDVKSDNSFGLGLFLVKKILNIHKSYLEISSTLGYGS

SFSFKLSQG

>WP\_002866331.1 16S rRNA (cytidine(1402)-2'-O)-methyltransferase [Campylobacter jejuni]

MLYFIPTPIGNLSDISFRALELLKTCDLVFCEDTRVSKSLISLLNTKFHTDIHISKFIALHSHNEKEVLA

SIDLKIFEKNVAYLSDAGMPGISDPGKALVEFAQENNITYEILPGANAALVALVSSAFCQKEFIFIGFLA

NKGKERQKDIEKILNLPYPSIIYESPKRILSLVEQIMILDSQREIFLIKEISKKFEKKFKGNAKELSEIL

KKSNLNGEWVVVLQSKEQNFLQNTLCEKDIMDLELPLKAKAKLLSKINGKNAKEIYQKLLLSQD

>WP\_002853920.1 MULTISPECIES: sensor histidine kinase [Campylobacter]

MNKSSIFYTITFIFIFAGVSVILGFLWLIEYDQQNYTRELNTKYSLIANARLLNFAGVISEKEFEEQTKN

YNKMDEITEAKQIRKILFRGDVLARVEVNNGLIEIISYNRQVYLNIIYDGKVYLYKDQDYQTYRYFIIKA

IAVAVICILVLLYIYIFKKLKPLKRLKKQIDKFAQGKLNDIEDVSTGVDEISQVSEAFYQAIVQIRKLNQ

SRQFFLRNIMHELKTPITKGLLTLEMIEDNKYKERLNGVFTRLEILINEFAAIEQITSGAAFINRKKYNI

LDVLDEAKEIAMRDDSNIRIFMEESFFVNVDFKLFTTAIKNMIDNGIKHSEDGFVQIDIIDDYICFKNRG

PELNNTLEYYTQAFTQGSKQKSSFGLGLYIVNTILETHGMKLDYLYEDGVNLFYFRNLKSVIVKE

>WP\_002852488.1 MULTISPECIES: sensor histidine kinase [Campylobacter]

MNESILKSLDSNEKETLQKGLESLIEQTYVIENEYKTLNENYNSLRAMVDEIIEVLPSALWILDKEKNII

LQNQEALKNPKLLSIISLDKIRDELEFEGRFYAVKIIAHNEKTIVSATDISDEKRNERLASMGSVAAHLA

HEIRNPIGSISLLASTLFARSELKNKHIVLEIQKAIARVERIVNSTLLFTKGVHINALNFNLLELKEECE

SAINSYNFTSQIDFEISFLDKQICADKALLGLVLQNLIYNAIDAIEESECEKPMIKILASYDNEKICIRV

YDNGCEIKDEKLVFEAFKTTKLKGNGLGLSLSKEIINAHKGELSFQSDPKNFYFTLPLV

>WP\_002778629.1 MULTISPECIES: thioredoxin [Campylobacter]

MGKYIELTSDNFAQAKEGVALVDFWAPWCGPCRMLAPVIDELANDFDGKAKICKVNTDEQGDLAAEFGVR

SIPTLIFFKNGEVVDQLVGAQSKQAISDKLNSLL

>WP\_012006677.1 MULTISPECIES: DUF2972 domain-containing protein [Campylobacter]

MQNLLLYIKNNLTPTLAQILLQALKNSNNEKFFTFVLKNIETICTWLNSSEFKNRYLSIKHPYPPLINPN

FIEIDASRHCAELAWDLNLPLPKHYKFIYISPHGVGAAAFLRYLNQCCDVTCFASWVLPPDAKERYCLNY

MCLNDNTITQYAINISEINLPYFDKYLSLLDFNSKIICGVRDPIGILKHNWGRDWSKVLRNYPSEFNLTY

DWRYYIDYLTHQNHKIKIDINELQQGVFIISYLLKYFNKDNVYYLDMEEIRQSKAFDTMNLLAINFNFTP

PHKDKLDLFKIKEFRGYIRYLFPITLYANSKDINNTFYLNTPKNNKNFNIDKTSSIPIILDRKHINHEKI

DIIQEIIKNDLCNDMGVYIDKNDFKQLEQNNLLFSTIKHYLYDFLYQIKITIDETESKMMKEKDVIDYFI

KNKSLVYTFFNIFENDLNHLKQKFPNIINSWTYYKEFEKCVKS

>WP\_002870410.1 MULTISPECIES: DUF448 domain-containing protein [Campylobacter]

MKKHIPIRMCIVCKNRFEQNMLFRFKVVLGDIVPKAEHGRSGYLCQNCIEKEDKILQKAFSKICKNLNTK

ITQQGLKEIFLNGKD

>WP\_002869004.1 MULTISPECIES: peptidylprolyl isomerase [Campylobacter]

MIKTIDTSKVNEYKFALIETEKGTMKLKLFGDEAPQTVCNFATLANEGFYKDLNFHRVIPNFVIQGGCPH

GNGIGGPGYEIICECDDQEHKHERGTLSMAHAGRDTGGSQFFICHSPQAHLDGVHTVFGQIDPKDEESLE

VLDSIRQGDKILDIKICDKI

>WP\_002866934.1 EamA/RhaT family transporter [Campylobacter jejuni]

MGVFLVLLGGIFWAISGVLAEYLFKNNYSVDWVCFYRLLSTGLILIFLSFKAQKILVFTNLKESLSICMF

GFFGLLLTQFGYFKAIYYTDAGTATMIQYCAPLIIMLYLCFKNKKFPKLIEIFALILIIFALFLLATKGD

IEAVVLNYWGIFWAVIGAFGVAFYSLSAREVILKYGLFWIMGWASLFASFVFLLILQFDKGLIHYAFNLK

AFFSMGGIVFIGTIGAFCLYLKGVEYIGALRASMIASIEPVAAALMSFLFLKTRYSLLDIFAFVLIILSV

ILNAKKTKAS

>WP\_002866510.1 aminopeptidase P family protein [Campylobacter jejuni]

MSIYKQRVLELRRLMKENNIDAYLILSADPHLSEYLPEYYKNRVFISGFKGSVGTVLITQEEGFLWVDGR

YWLQAQKELEGSGILLQKQDVKNTFTKWLEKNLSEDQILGIDFALLPLSLQKDLQINCKANLKHIDLISP

LWKDRPTLPQEKIYEHELEYCSYSRKEKLALVRQKMKNLNVTSHLISSLDDIAWLTNLRGNDVNYNPVFL

SHLLILEDKALLFVDQKKVNSELEKKLNLDGFWLKNYDEIIMELEKLANTNLLIEPSKMTALLINSLDKS

VKIIQEINPSTHLKAVKNTKEIAHIQDAMIEDGVALCKFFAWLEEAIENKELISELDIDAKASEFRAQSK

HYISDSFATIAGFNENAAYPHYKATKESFAYLKKDGLLLIDSGGQYKNGTTDITRVVPIGKANAEQIHDY

TLVLKAHIAISSAIFPKDIAMPLLDAITRAPLWKEQIDYIHGTGHGVGYFLNVHEGPQVLSYLSPVLEKT

KAKEGMLTSIEPGIYKVGKWGIRLENLVIHTKVENPKNKDFGEFLYFKPVTLCPFEISCIDTKMLDEKEK

EWLNNYHKEVFEKLSPKLGDYPKALVWLEKRTKAIF

>WP\_002859818.1 MULTISPECIES: tetratricopeptide repeat-containing protein [Campylobacter]

MMKNTVTEASIYEAQGLKDEALEIYKNILKEDPDNQNAIDAVRRLSGFRSKHKDLNTQMLDFFINMKSDE

EINEFKRWLIKI

>WP\_002858657.1 MULTISPECIES: UDP-2,3-diacylglucosamine diphosphatase [Campylobacter]

MLIGEISATHEFAKPYIELLEELALKIEIIYLEGNHDFNLSCFFKRVKIFNLQEQPIKLNLHTSKGNNLV

LNSAFIKLAHGDIFLPPLLQFTLKTLRNHYLLVFLNFLNIITRNFISNKILQNQNKKNLFYQIKDFENLA

KKRYEKYENLGFWVCEGHYHQNHQINKENIKYLNLASFAYERSFFVVEYQQEIKFREQKLRGQNV

>WP\_002857630.1 MULTISPECIES: class I SAM-dependent methyltransferase [Campylobacter]

MNLWDKKAKTYARYQNTLNTIQKQTFEYLQNLNISFQNKSIIDIGCGTGVWTLHLAKEAKEILALDSANT

MLEILQEDAKKLNLNNIKCENLSFETWMQNNPNVKFDLAFLSMSPALQNEKDYTNFLNLAKIKIYLGWAD

YRKSDFLDPIFKYFNTEFKGFYKKDLENYLLEKNIFFHKIVFDETRKVQRTKEEAIENALWHLSMNKITT

SKEAVSSFVENDIIETIESKIKLLIINNL

>WP\_002857542.1 MULTISPECIES: thioredoxin-dependent thiol peroxidase [Campylobacter]

MSLNIGDKAPQFELLNQDGVKIALKDFIGKKVILYFYPKDNTPGCTTEACDFSANYDKFGGKNAVIIGIS

PDSVTSHEKFISKFNLKHILLSDSEKEVAKAYRAWGLKKNYGKEYEGIIRSTFVIDETGKIAQIYSNVRV

KDHALKVLESL

>WP\_002852985.1 MULTISPECIES: AraC family transcriptional regulator [Campylobacter]

MNKILSLPEDLKQLKGVNYKKIKSCTFAKYTQTDTSHSTFVNVGSHLLTFVRKGYKILHTASKDYKINSY

ETLFLKAGSYTLSNVGLSKGVYEAYLFFFDNAFLIELIYKYKDFFKLDQKFQNYEIFWVKNDKILQGILE

SFSPHFEENTQILDPIVSLKFEEIFLHLLLNKNIYFISFLSGILKEFRLDLSQLFEYCGREFLSVNEMSN

FAKLDLATFSKEFKKCFGQSPKKWLDEKRLQKAKILLKFSKKNINEIANECAFSSVAWFIERFKEKYEQT

PKQYQKTKNLYFLSKN

>WP\_002852144.1 MULTISPECIES: KH domain-containing protein [Campylobacter]

MVENFLREYAKLIADYPEQIDTQKIELSENFFEIVLFAHKVDTGKLIGKNGKMINAIKTVISAYKSKDAS

SYRVTVKALE

>WP\_002780599.1 MULTISPECIES: QacE family quaternary ammonium compound efflux SMR transporter [Campylobacter]

MYIFIIVLSALLDIVANLLLKKSDGFKHKIWGLAAIVNAILAFFLLSFSLKYVPLSIAYSTWGAIGIIGT

CLGGWILYKEKLNKIGILGIIIVIIAVFLLNY

>WP\_002779573.1 MULTISPECIES: type II toxin-antitoxin system HicB family antitoxin [Campylobacter]

MKDLDYYLNLPYEIIIKKLDEKDGGGYFARYKDFPYIMGDGENEIEALKDLKEAFKGALEVMLEKGDYIK

EPIDNEAKIRINITLPKSLVEAIDTISDNRSKFLADLANSAIKSYKIST

>WP\_032603618.1 [acyl-carrier-protein] S-malonyltransferase [Campylobacter jejuni]

MKTAFIFPGQGSQSLGMGKDFYENSIKAKELLQNASDFCKIDFKHLLFEENEKLNQSEFTQPAIVLNSLM

AYSVLLEKKPDLSSKFALGHSLGEFSALAVNGAFDFLEALSLVNKRGLFMQEDCAKVEAGMMVVLGLDDE

KVEELCQKAQKENKQIFAANYNCDGQIVVAGLKPDLASYESVFKEAGAKRAMLLNMSVASHCPLLENASA

KLCVELEKVLKPNFKAVISNANAKIYTSKEEALELLKAQLISPVLYKQSIKACENEVDYFIEFGASVLKG

LNKKITSKETCALTNMNDIDEFLKVI

>WP\_002867452.1 MULTISPECIES: putative selenoprotein [Campylobacter]

MNFKKFKYYYEKAERFFHPLVGLSSYDKYLEHMKQKHPGKIPKTRGEFFKECLDKKYNSGGLNKC

>WP\_002867048.1 carbamoyl-phosphate synthase (glutamine-hydrolyzing) small subunit [Campylobacter jejuni]

MKAYIYLENDIFLSAKAFGKSGTFFGELVFNTSLTGYQEIISDPSYAGQFIVFSMPEIGIVGTNENDNES

KEIFASGVLMRELSSSFSNFRAKESLQDYLEKHGKIGIYELDTRYLVKMIRNNGNLRAVISTEISNKEDL

KIALEKSAKIDEVNFVKEVSTKKNYSHKQGVWNASFQKFNDAKRSEKKVAVIDYGVKTNILNELVEVGFE

VEVYPYNVKADELITLYKKGEIQGVFLSNGPGEPRILKQEIAEIKKLAEAKIPMLGICLGHQLLSNAFGY

ATYKMKFGQHGANHPVINLDTKTVEITAQNHNYNVPEELAQVAHITHRNLFGDNVEGVRYKDYPIISVQH

HPESSSGPHESKYIFKEFMNLM

>WP\_002866069.1 MULTISPECIES: putative lipid II flippase FtsW [Campylobacter]

MVADKRLFYLSCILITIGIVFSYSLTAFTVLFLDYSEFHFFIRQLFFGISGILIMFFISRLDPDKALSKK

IILAILIISFIFIIILPFLPSVLATASGGAKRWIRLGPLSISPVEFFKIGLIYFLAWSYTRRIDDSKKAI

RHEALILLPYCILASIVIGYIYITQNDLGQSVISFFLILALAFFAGASKRLFAFGTLIIMMIGIMVIFSN

QRRIQRIASWWGNIQDAFLPMLPDWLANALRVSSNSEPYQISHSLNAIAHGGMFGEGLGLGTFKLGFLSE

VHTDFVLSGITEEIGLLGLGVICYIYLWMILRIFRIAGRCEAKQDFIFCSGIALLLLFSFFMNAFGIISL

TPLKGVAVPLLSYGGSSMWAICIGIGYVLMISKKVKL

>WP\_002853472.1 MULTISPECIES: DUF2165 domain-containing protein [Campylobacter]

MQQKCFCISKMIRFSKIIILLTVASLAGIVVFGNVTDYNSNFQFVSHVMSMDTKPDYLGNAIVYRAITSP

VIHHIGYIAIILFETFITLTALKGAYDMFKARNLDAQSFHNAKIFGIISLTCCCILWFFAFQVVAAEWFG

MWMSKVWNGLPDATRLVTYMFLALIFISLKNDD

>WP\_002816243.1 MULTISPECIES: DUF452 domain-containing protein [Campylobacter]

MKYEFLCKNPDSKKLIVVFGGFASHSSHFSHLKSDKNVILFYDYENFDLNFDFKAFDELFLIAFSMGVCV

ANRLLKELNFKQKIAINGTNLGIDKSKGIHPAIFRKTLQNFKLENFKEALFKERKNLTKDFIFKDEKALK

IELEKLFDFALVKQEENLLWDKVYSSKKDEIFPPNALKNAFSKLIFLNEPHFAFFHFKTWDEL

>WP\_002812869.1 MULTISPECIES: DUF535 domain-containing protein [Campylobacter]

MNKKFSYPIPNFTDRRKSIIFWRYLRFQARKILYFPQVRLLEKTLNEEKNKHLKDFFSQRPYACYNAIRR

FCDKSFKANERVKTLIYDVDKGLTCFKFLPEEQMIFSFDEDFELFLGYNHNVYEEGFWAFSLKFKKYTIS

QCNFCFTLENNLLLSCIQGYKYKDFNILEINKILTKKCHGLRPVALLIECSKMLCEILKLQATLGVHEKN

QIRSQKGKEKGYFVDYQKIWLENGGELIKIDKHKYYKLHHSQKNLEEIPSQKRSMYKKRFAMLEEIKVNL

DKTLDIQD

>WP\_022552310.1 DUF3800 domain-containing protein [Campylobacter jejuni]

MNNMKEFKIFCDESNHLFYKDNPTLCSRVMVLGALKVPSSEIIKINKTIKYLKHKYKYNKEIKWTKLNLS

QKGFYDELLEFFFSSVYMWFKAVLIPNKTILQHDIYNQGDHDLFYYKMYYQALHNLIDIDTKIKIYLDYK

DTKSGDKIKGLEKVLFNKFKQSVNIKIFTIQSHESNIVQLVDLLIGAISYKARNDIEHVSEIKNYIINKI

ETLANIELDAGTPPWENKFNIFRIQLSKGEQ

>WP\_021137666.1 aminotransferase class V-fold PLP-dependent enzyme [Campylobacter jejuni]

MYLQISDLKKELILKKGILHFDFTASALALKCVEKEISKILPTYANTHSDSSLNSFKTQQIYEQARKDIK

KSLSLDENFALIACGTGSSSAIKKFQELIGIYIPPLVKERYFTQIDKNTLPLVIVGPYEHHSNELSFREG

LCECIRIPLDKNGEIDFDFLEKTLQKNKKRKIIASFSLASNVTGILSDYKRISEMVRKFKGIVAFDASSF

IPYKNISCQYYDALFISSHKLIGGIGGSGLLAIKKDLCGNKPSFAAGGTVGYVSRTSQCYLCNEEALEEG

GTPGILQLIRASLAFKIKDSIGVKNIEKKEEILKDYFFEKLKTIPNLILYAKNLKTRLPIFAFNIKGISP

FDIAYELSKKYHIETRAGCACAGPYGHDLLGLKDNQKLKTKPGWLRISLHYTHEKENIDYFFNALNKTIV

KLSH

>WP\_012006754.1 DUF2920 domain-containing protein [Campylobacter jejuni]

MIVSKTYEIDSCDDVELGIKRESKLEFKLWYDDEKTPEALVFVVQGVGADCNDIYLKFIVEYLLKNFNLA

FVGVNYHCIGNRPQTGSTFYLDDIDKLILKASCEAVDIKLPYDVDKIQDYKQMSEIFHFVNNQIVEGKQK

GNFMPNYFLNLHVSLQPAKNEYQNFGIMQAQDLLNVALYLKKNTPFDTMGGGIPVIMIGGSHGGYLAHLT

AKIAPWLVDGVIDNSSGAKFLWRVVGFGKEIDFMQYSEFATFDFFHHIKTHCSTKTFWTSNSSSPRFFSP

ARRKIRNLLEEDHLLEQSKCLKTCFISYHSLYDEYVSLKEKTMLYEELEKLGFDVTLHSITKESQVDGKF

IKNLNHGMGIPVKLLIKKELPLMLEKIKQNSKKDCKEKCISYPCEDLLYQFSEKDDKISLKIDKI

>WP\_012006753.1 DUF115 domain-containing protein [Campylobacter jejuni]

MTILEKNIQALLSGVNEPLGNKLLNFIQNKTCSRFNIDENLNIYDKTHNVFMYENLEEELNFFYQSILEK

TPRYPFICIYGIGNALLIKNLAKHYKHLFVFESEIELFILALSTIDLSEELCSGKIYLVDIQEKKINLQL

RILFDQNDVFLWLNLYEMFINNNFYKKYYYEEILNTDKIAYENINLVIRNLDPDSKISLSCYENFYKNIS

LMLKNIPLKRIINERKGLFDNCIVVCAGPSLQKQIPLLRQYQKKFVIFCVDGAYPLLVKNNIIPDYVLNL

DFEEYPLKFFEEVDAENKTLFILAASTHPSVVEYLYKKQIPLSIALNDNLPYQNLHIDEFGYLEFGTHVG

HACYALAIALKFKNIIIIGQDLSFDQRGNSHFDSFDLGSDIDATLDIPTLKRIAYGGIGEVLTHLAWDDY

RKKLEDLFARNLEVNFFNATEGGAKIEFTKELDFKSCCKQFANLNNKSNKYLPKTLTTNRGAKILNKILA

TFKREKQNTLICLEHAIRLNDVLKIILASDRKFPIDFLKNTYESIKKFEIFLEENSFLNDGVLKGVIFHK

GKLLSEVIVSKIEDEREYLLIYLTFYKQWLEIFICRFQLKCDIYNFLV

>WP\_012006749.1 DUF115 domain-containing protein [Campylobacter jejuni]

MKFNLNQKELFNKNIEALDNIPLKESLKEIKSSKFKLILGKDILDINLQNTSDNTFLYENVIDELNTMLN

TYNDKYLLYPVLYFYGFGNGILFKALLQNKNHQHIVVFEKDIEIIWTMFHILDFSNELQKNNLIIINTNI

LSEFDLLNFYKKANSIFLQFSRIYFLELISNYYERYNEEILKLNDTILSTIKISIIQYGNDSIDNLMGIK

HFIYNLSKLLTHPHSEIFLKKRYKLSDTAIIVSTGPSLTKQLPLLKQYANKATIFCADSAYPILAKHNIK

PDYVCMLERDDIVSKCFDNDFKEFDKGILFILASVVHKEVIEFLERNNREYMLVPRAYDFFYYLNLAKYF

QPIDGMVSVAHMNYWLAKFLSHKNIIFIGQDLAYSKDQSSHAKDFIHEKLHEGHFQKDENLFTSIAYGGK

GEVESSYFWKLFREIFEKWISHDNNFINIYNCTEGGARIKGTIEKPFLWACENLLGKDLNKPFPKLNPLN

INKQNELMLKAYNKIYKSIYHCKDFNKKLLQEYNEIKELYLTLENLQIEESKELLNFIIQKIDTIKYQID

DAKNMQDLYEILGPLLVQFELNLARIYVLNPKTPEDSFNKSLIWIKEHLEWIEMIYGHIQAQENALFENI

IPLEQKLKERKMQKYLRRIKNANK

>WP\_012006746.1 DUF2920 domain-containing protein [Campylobacter jejuni]

MLINQTFEIDSCDDVELGIKRTSKLEYRISYDDEKDIKAIVFIVGGFGANANISFLDFDREYIAKKFDVV

AVHVFYHCFCHRRSNVEKYSAITMFTKEDVSNLSQALLDIGIKIDVDIQNAHQCYELLNQNITTLKSQGR

LVQNYQAKLSSTFIPPNGDYQNFGIMPAIDHINALKDLVKRFPKFADLPKIYGGGSYGGYLSLLIAKIAP

WYVDGVIDNSGTVLPLLECIIGRKLNKPEFIYNDPNTLIEMFIKTYWIREDENSSYFIANENYMIRSLLN

SSHLTIQANINKNIIFISYHSLKDEFNTAKDKQTLFLAYKELGYDATLYLIKDESEIDGRFIKDLKHGMR

ISNKALFRKELPLMLEKLQGRKSFMQENSISYPCRDQKFIFEDDKDKFTLIIT

>WP\_012006667.1 MULTISPECIES: RNB domain-containing ribonuclease [Campylobacter]

MKEFLNSLSYGISSHEVNNEFKQILRELLTNHIIKEHKNKYYLNNGFAFGVLDISSKGTGFLQCFDESFK

KDLLIENKNLKGANYKDIVAVKLLPLKKKRPSAKVILVLKRANETSLVITKRYGEAVLGMNIKTGLSTTL

KASQKSLKALPLGTILKIENENNNIIEVLGHIDDESVDEKISLALFNKNNEFSDACIKEALANGDSVDAS

MYENRMDLRALPFCTIDPIHAKDFDDAIYFDIQKREIYVAIADVSEYVYAYSAIDKEARNRGFSIYFPHI

AIPMLPRPLSENICSLKPHLDRLAYCFKIALDHENKVIKEELFEGIINSKRRFNYDEVDEILIQKPDLKE

LSWLYELFEITKNLRKMRLKNAFEFRTEELRMNLDENLSLKSTVFEKDTPSHNLIEDCMLLANKAAAKLI

DIGVFRNHLSADARKIDKLLNELRELGIDVNFKPNLPELIRDIQALADELNLRAEVDKLIIKAQKKAEYS

SVNAGHFGLGFDKYSHFTSPIRRYSDLILHRLLKAKQKNDEKLFNYLLLNIESTCENLSTLEREADKVAF

DFMDRKFARWAAKNIGKKFKALVVQNDGVCIAKLDDEIKGADIILYDTRVNLLESVEVQIMEADIVMAKI

YAKITQRLIKEENV

>WP\_012006661.1 DUF969 domain-containing protein [Campylobacter jejuni]

MEWLLLASIPLIVLGFALKINPFLVVTSVGIYAGLVSGFDFIKVVSDIGKSFVDNRYVAIIWLILPLLAV

LERKGLREQAKNLISKIKVASTGRILMCYFVFRQVTAALGLLSLGGHAQMIRPLIAPMAEAAAKLKFKNL

THKDSQKIKAFSAGTDNVAVFFGEDIFIAVHSILFIKAFYESNGIIVEPLHLSVWAIPTGILALIIHCSR

LYLFDKRLEKTYKGLSDDKS

>WP\_012006614.1 DUF1440 domain-containing protein [Campylobacter jejuni]

MKKYFQKRYTLAFFIGILAGIFGAIVKWGWEVPFPPRNPNVFWLADALERVTPPKIFLEQLGLPTDWTYM

FSGMQMPLSIFIVHVSFSIVFGVAYCMIAEKWHRITMWQGAVFGFFVYLFAHVIVMPLIAEVPPLSEIPF

DEHLSEIFGHIVWLWGMEIVRRDIRNRITKEIEE

>WP\_002878012.1 MULTISPECIES: DUF342 domain-containing protein [Campylobacter]

MALDEKIIAYTENPARELLSVASRTNLSLNELDFSLLAFSTQYRFGDLEWEKISEKELTLFDKDEIFLKN

DLQIKQEYKIEIFHGINQSKASQAVKLVANKNLTKIVAQIDFTNLDFHEKLALELLQNIYKKMLKLKFLI

GIRIFDFKKNLMSFCNQHKNTPLNKTIQITVAQGIDPIESQDESLILTYKEKTKNYTIDEKRSGIIVVDE

NEVVLKHAKFKQGKEGKDLNLHTLKVLAANENKVKFSCSSAFKQVEQDGYTEYIALKKGYVVQDGEKFDI

ANELDFNGVDFKNIGIIRAGLDKNVKINIKFLSEVKDAVNSGVGIECEELNVVGSVGSNTQLNATKMKIE

GTTHSKAKIQAKQAYIKTHRGFAEAEILNIDLLEGGTIKAKEVRIKKSLGGNIQADKIYIENLESNNSCV

FFENTTIERINGDNNKFHAKIKTLDKNYDEEFAILGEQISKLNHKINKIRQYILSSKNGILSVEKKITEL

KNQGQNVPVQYEKALKDFSLQNLELNKLQNEEKELLERKKSLQLELINLQKMLFEATFINKSGKWTDMNE

IKFSLLEPKEDIFYSSFVNESAKFIGIKKVIQNNQESIEIHKKLDYEEKDIAWLSASKE

>WP\_002858582.1 MULTISPECIES: DUF4149 domain-containing protein [Campylobacter]

MKAVNLFLLASIIGVELILGIVVAPTIFFPQNLIGEGVLSHFQSGLMMTQIFIKMGYLLIFVSVVNFLYE

IYSLIKDEMKFQIKFSKFMLSLLILILSLIFVFYFTNTIIELQNLGENATKTQEFISIHNASEVVIKIIL

IMQVFLYFLSFKIAKK

>WP\_002857453.1 MULTISPECIES: GNAT family N-acetyltransferase [Campylobacter]

MLRKADIKDLNACLSLFEQSVKTLCAKDYTKDQICAWIKIDRQQWEEKFKYDEIFVYEKRGKIASFISVK

QEQKLLDLLFTHPDFVRQGLAQNLLDFILKTYLHNEIYTFASLSAKDFFLKNGFELIRENKVIKEGQNLK

KFLMKKDVVYKN

>WP\_002856328.1 MULTISPECIES: DUF815 domain-containing protein [Campylobacter]

MDWNKTYAAIYRARKDYLKPIFEIDPITLKDLVGMESQKKALYENTLNFIQDKGANHALLWGSKGTGKSS

LIKAIFNEFKDQGLRLVELNKEDLFALVDIIDEIRLENFKFILFCDDFSFEKGDDSYKFLKPLLEGSIEK

APNNVIIYASSNRRHLLSESIADNLDTQIAHTELHLSDAAEERLSLSDRFGLWLSFYQGNLEEYLKMIDF

YFKDYSCDKELLHAKAKEFATLRASRSGRTAKQFYLAFKENFK

>WP\_002852251.1 MULTISPECIES: DUF3972 domain-containing protein [Campylobacter]

MQTYLELEEFCKLVHLNEDVVKGMMANGALNFKEEEGKIYIEAHQGTFSVVPSSAKSQTAMVNSMTLAGE

SFVEKTIGTILNLHEKVLDAKDETLEALKNENKFLKDALYSMQELYDEDRKTIETLNNELKHAREEIEFL

KRKYKLMWSKTAEIFGAKTEPDLEMNKNLEKPIENMEQ

>WP\_002851269.1 MULTISPECIES: DUF507 domain-containing protein [Campylobacter]

MRIKLPHIPYIANKMMLDIANSSFVEIKDQLEKLKVCIIEVLEKDILNERKLDERVKELLEQQEDEMELM

QVDRKNMFWLVKKKLAPEFNVILDSEDRHNHLAHQILEELVENDYINFIVSENRVKNLIFSSIESYLKIY

EKLEDEVYEKISNYKTKPIPGSEEYDLIFEKLYQEELRKKGMF

>WP\_002800608.1 MULTISPECIES: DUF2130 domain-containing protein [Campylobacter]

MQNLNQNEQIKCPSCGSFIDISTALYAQILDKAKQEMLKQKKEFDDEVNAKRAEYIKALNDLKTQKIEQE

KLINEQVSQKLLLEKQKFEQELLTQKQNFQKEFSEKFNKEHENEMKIMQEELEKKSKELSEFLSIKAENE

RLKREQKENEERLKFQAKEEAFKEFKEQESKNLEFEREKMRLEFQKSTQEQDLKYKELETNFKSVAQKLE

DAQRRIEQGSQQLQGEAAELLIEEYIQSEYLSDEVKEVPKGVNGADCLHIVKDNFGNICGSILYESKRTK

EFNKEWLDKLKLDSIAAKSDIAVLITKTMPKDKEKTHFKEGILICTFNEFKGVLAVLRESIINAYKLKNA

LQNKDEKNHILYEYLNSKEFNTQITFILKTYQNMKEELEAEKRALQNIWKKRERAIENLSFNSTAIVSSL

NAIFSDLQGGNLIGEEGIKSLENLAKDED

>WP\_072224426.1 MULTISPECIES: DUF4006 domain-containing protein [Campylobacter]

MMENNNRCVFSLSGVTGMLIATVLLLAILVVLTIWGLKAQQEVMQKPYSLKDVQSVKMFGSKEQDHRSIK

EAQ

>WP\_012006750.1 MULTISPECIES: DUF115 domain-containing protein [Campylobacter]

MQTNEIFKKNLEAMQGSTYEKLKYKLKNFQELRNFSFHIGKDPIDINIIDKKHLKKIYQNPIKELEENLK

LYQEQYTNYPFLFFYGLGNGILYKALLKNTLHKRIIIIEKELDIIFITLNLIDFSEDLFKGRIIITHTLD

YNNNIAELIFGLTEISLFLKTYQINLHSPFYRIYQEDIKKINNINLQTIKYLTLKKGTDPLDAMVGIEQA

IWNLPEMFKHYSYKELLDKRKNLSKNAIIVSTGPSLTKQLSLLKQYANKAIIFCADSSYPILAKHNIKPD

YVLSLERIPLTSEFFNNDFGEFDKDILFILPGLTHPNSIKYLKKFKKDYMLVARHLPFALSLDLKEYGYI

GGGMSVAHSAYELAILLKCENIILIGQDLAYSKEGKSHTDDYINLALHEKDFERNKGHFTTIAYGGEGEV

ESSEVWTLFRKIFENYAINNQKYIKTYNCTEGGARIKGTIEKPFAEICKEILTKDIKKPLKKLKKKTKKE

QFDKMLKSYRKIKTNIQLALNFQKECKKTLRKIQKITQKNKYINLENIVKDIDIIREKLSHKKYFFLHEI

LGPTLHHEESLIAPIYTQSVHNESQRQNKILSWIYANESLIETIIDLIESQNTRLKKAIIPLQDELEKRS

LI

>WP\_012006748.1 DUF115 domain-containing protein [Campylobacter jejuni]

MNKDLFLKNTRALFEVDQILAYKLRSLEKIDFKILQNENGINFIKDDIALYKNPNQELLESLTLFKSEYE

KYPVLFFYGFGNGMFYKALCENKNHKHIIVFEDELEILALAFHLFDFSKELKNEKLILFYTPEVTTAQLT

TLFIYENIQKSVKIFNLYIHNNFYEKFYTQKIKNLNYKLMETIKYVVLNKGNDPYDSIIGIKHTLNNIPK

LLSHGIFQDFLKKRKRKVKNAIIVSTGPSLTKQLPLLKQYANKATIFCADSAYPILAKHNIKPDYVCMLE

RDDIVSKCFDNDFKEFDKGILFILASVVHKEVIEFLERNNREYMLVHRPLHFAVSLNLKEFGYIGVGASV

ANMAYELAASLRHENIIFIGQDLAYAKDGSSHPREHIYGNQGEKLRGEIYTLAYGGEKQVRTQLTWNLFR

QAFEKDIFWAKEKLKINTYNCTEGGARIEGAIEKPFQEVCETLLKENLKKPFDKPKILEKNKIKNKFLQT

QKLLIKNVKQSEEFIKKCQNELKKLDFELSKSQLNSQTLIKIKKNLLFFFNEFKRLKLFNELTQAIYYHN

ECEIMYYEVLNDLEQDKKIEDFLTNQKKWWLQSFEYLNTQNQIIKETLKKYKNDDI

>WP\_002932559.1 MULTISPECIES: DUF1090 domain-containing protein [Campylobacter]

MKKILVLLSLCAFAFGASECDRKIDRINKEISFSKAHNDTARTLSLELALKQVQNDCAKDPMFYDKKLEA

KKLKEQEVEKIEKELDALKEQKDYMSKAEYKAKKEALKEQKEKIKKEIKEYIDNL

>WP\_002866852.1 PDZ domain-containing protein [Campylobacter jejuni]

MKKILIICMLFTLSFGIERPKFEDFLAGYERNKASMLNYEGMPAFALSENLLAVLKQPNTKLNKYVKYDP

FLNLYLVRTDFSLIPTPMGDEEKLTRNDWVGIWDPNKPYIGHIKYLAQNIDEKDQLDFNSKIGLLGTPCC

EMMGIALNNSSFIGNRYLKHFMKYNDAYWGDIGVDFVVRENKIYVNNVRKNPQFLINDQVISVDGLPAND

LRKLNEKILFADRGSTLYFQVLRDNMDLNISTEVFAKDLSKFNLPDSKPKPKITNFTSNLGLTVNTSLVV

TKIDPKSKASNAGFMVGDKILRVNNIILNNFKELQNILSAGNDFSILIERKSTKLPLSNFNNELGGNANS

GGDGKFQFFIRLTK

>WP\_002866674.1 DUF2972 domain-containing protein [Campylobacter jejuni]

MQFNIKNIDLILEKDIIKKYRRQIIKWIQTKEFEENYSHFLYPPLLNPNNVDYCQISPEVSWELNLPLPP

FYRFVYWGSHGCGNTAFGVFLAKYGGYNFYSTNENDGRKAYISLFKDMISKRHLLKKDKFGYLAIRNYVD

GNEHEKFHFLIHSSSAINLVRDPISCLKHYIGMKRYYNKSIRRFNLTFNPKDIFKELVGYSCGNEIKKTP

SLEAIESWIDFRYKCFHDGQLIQEMKNIKETIVIDMREIVGKNSFNTMQNIARYYKLKTKFYDDGTMQEK

VAEYEGILPLTLYVHPSDIKDFYYDNNLKSIDGIDIFITTHYWLPFNGFVPYETQSRFEGVVFPEKVEDI

TKYILNYQHDKIIICVRKGDFKKIKKSNKLYKAIQQYIIKLIPYIEKQKDIEEKKKIHERDILEFFNKNK

TLCAKFKNILDIHLSYIKLNRPDIVGSWNYYQEFEKIYKRLHT

>WP\_002866129.1 MULTISPECIES: DUF455 domain-containing protein [Campylobacter]

MQKEFFQELQDILYEKNITIKFHSFQNFYEDFKSHKFIFNHEHQSIFKKNTSQQITLLHPTRIRRPKFVN

STHALAKIIHSVAHIEFNAINLALDASYRFKNLPLQFYYDWLEVADEEIKHFKLLNSALEELGYKYGDFP

VHDNLESALEATKDSLSFRMGIVHRGLEAKGLDANPFVVQKLQSSNHSIKNLLMEYLEIILNDEIKHVKK

GDTWWKFANQNKYDFIELCKTFKQFSLAGKKLNIQARIKAGFTQEECEVIEKFYS

>WP\_002859481.1 MULTISPECIES: DUF1882 domain-containing protein [Campylobacter]

MISPMDMSLIKIIGDHYYIRRDKIVNKITHRGRLFFDKFERVDAPLNLNVMREHAAKKIVVAHDLITKDN

KVENIVFDYNGFNAERFYHRAQLILREEGFINFTAYKTKTPGHLHLYIHKGHTALNEGYSLASKLSMMFA

SKMPVEWKVFPSMDVPREFNILILPYEVYQKERGSSWSKHM

>WP\_002858607.1 MULTISPECIES: DUF979 domain-containing protein [Campylobacter]

MISLDLLYYIVGILFLVFGILSFSNQAKDIKSRISGGVFWISYSFTFLLAGVLPHFVMGCIVILLALIAG

FNLLKPAKIEVSKEEKEYEIKHANIYKNKLFIPALMVPLITLIGTFLFPYLSFFENKNATLMALIIGIII

SSVVACFMFKASPKRAVKDAAHTMDHISWAALLPQILATLGVVFVSTGMGDQVSKLLSSYISLDNAFIAV

AVYCIAMALFTIVMGNAFAAFPVITAAIALPILIIQMHANPAIIGAIGMLSGFCGTLMTPMAANFNIVPA

ALLNLDDKNGVIKAQFMSGLVLLVANIFLMYFLAFRF

>WP\_002856967.1 MULTISPECIES: copper chaperone PCu(A)C [Campylobacter]

MKKILLLGALFAVNLWAVNDIEVKNAFVKQTPPHAQNSAIFLTIFNNTDKDIALISAKSDISEVSELHTH

IHKDGKMMMQKIPEIIIKAHSSTELKSGGYHIMLLKLKKPIIKDTKVNLDLKFNNHKIIELKNIDSKEF

>WP\_002855201.1 MULTISPECIES: DUF465 domain-containing protein [Campylobacter]

MLHEYRELMSELKGKDAHFDKLFDRHNELDDMIKDAEEGRTSLSSMEISTLKKEKLHVKDELSQYLANYK

K

>WP\_002851753.1 MULTISPECIES: DUF2393 domain-containing protein [Campylobacter]

MEKLREIVLFYTTHLYLVDYMLILLVFFLFTCVLLLCVFLRHRPIAALFIIAFDIIICFLVYIYGYKLID

NEVRTRKTAITDQKMIQSSNDLIVDFNITNNSKNNFKECKITAKIFADKIPNDNIIEEYKKKFIPFRQKS

REIKDLKKNATQVQRIAFENFNYENNYTIRLVSECF

>WP\_002855637.1 MULTISPECIES: DUF2325 domain-containing protein [Campylobacter]

MSVLVIGADEITPIRAVLHDLGAKKIEHWDARNENRVNRKPIPCDTECIVMLTSFLNHNTMKKIKNEAKK

RKIPLVCAKRSVSCVYCEYCKIFNLNKEFSCYKG

>WP\_002854834.1 MULTISPECIES: DUF2018 domain-containing protein [Campylobacter]

MDFFDEMFNKTPKEKFIEIIQNGNLGALEKVFEEFFADHIAMVELLEKQGLTEMDVKNFILENGDFIEER

QNDIYIELGAKILGHEG

>WP\_002853958.1 MULTISPECIES: DUF4230 domain-containing protein [Campylobacter]

MEMILFVLVMILLVLLFVVLFRQYKSPKIEEKSTQSFSDIMQLKSIGELSVFQVFSKEIVTKKDSAFNGI

WKNLLGWSLSERQIALIFEFEITFLYDLRDKNFDILPLGDDAYKIIMPECRYKHSIIDMKFYDEKNAKFL

PFLLPDSINSTGISFSESDKNKLIKEAKDEVKDLSLNLIQNLESKIHKSAKDTLEAIAKGFGAKRVEFEF

KDNTQKLDVN

>WP\_072238645.1 glycosyltransferase family 4 protein [Campylobacter jejuni]

MMKISFIIATLNSGGAERVLVTLANALCKEHEVSIIKFHTGESFYKLENEVKVTSLEQFRFDTLYHKIAS

RFKKFFALRKALKESKADVFISFLDTTNIACILANIGLKTPLIISEHSNEAYLKPKTWRFLRRVSYPFCD

ALSVLGSSDKVYYERFVKRVKLLLNPCHFSDEIPFDSSFEKENLVLFIGRLDHNKNPVMFLKAIAHLDKN

LQENYKFVIAGDGELRQELEYKVKSLGIKVDFLGRVENVKALYEKAKVLCLCSFVEGLPTVLIESLYFEV

CRISSSYYNGAKDLIKDNHDGLLVGCDDEIALAKKLELVLNDENFRKELVNNAKQRCKDFEISNIKEEWL

KLIVEVKNA

>WP\_012006777.1 glycosyltransferase family 2 protein [Campylobacter jejuni]

MIKISILIPSFNSILYIKECLESVINQSLKEIEILCIDAYSDDGTLEVLQKYALKDKRIKIILSDKKSLG

YQINLGLEQVQGKYFTIVESDDYAHLLMCEKLWVLSQSYNCDMIKADIIGFYDKKRVKKFQNEAICYDKN

LYGKILYFDDKIEILKNSWNMNQSGIYKMDFIRKFNIRANETLGASYQDLGLWFLMVVFAKNIYFHNEGL

YFYRQDNPNASMQSKDKVYCVCDEYKFIENFLELHLGKNQYFKDVFLYRKFKSYWWNIRRIDTKFRLEFF

EYFAKDFEKELTDLNDKFFTYGELKEFRKIIKNPKKFYDFYRSPFFKIIKFLARIKNTFKRYLNYAR

>WP\_012006772.1 glycosyltransferase family 8 protein [Campylobacter jejuni]

MRKNIHIFFTINDVYSGYLSACMISILDSLDRDYIPYFYIIDGGISEKNKNKLKFLNIGREFYVEFIAVN

QDLFKNLPNSSQSHISNETNYRFLVSTIKPNLDKCIFLDVDLVAVGDISKLWEICIDDYYMAAVSDQAPL

HSESWTLKLPLPYDYLYVNTGVTLINLKKWREDNIQELLFQNSAQYAEILQFPDQDTLNITLYKKIKYLS

HIYNAMPVQTYYNEKQKQEAFSNPQIIHWAGYKKPWKFPDAPYAEMFWHYARQTPFYEEILFKNITQNSL

NIIQNSIQGAVERVKAHLSYKLGKEILSVKENKLKVLILPFALILIYVKHKISNLIFKLILISNPNLKSL

PLNHYSDYQEALKIQNYLSYKLGNLLIKYPFTFVFRVASVYKEWKKNVKR

>WP\_012006738.1 M23 family peptidase [Campylobacter jejuni]

MKALWILLSLTLWLFGAQNLELIKGQALFLELDKKNFLSLKNNDKNIPTFAHPKNQEKILAIFSLPYKNP

PQNTKLIAFYKDKKEEIFIKTLEGNYKSEKLQVENKKIFPPKTVQERIAKELKEANAIYSSYTPKALFNG

AFNIPLNSFITSDFGKARTFNEKVASYHSGTDFRAATGTPIYAANSGIVKIAKDRYFAGNSVVIDHGFGI

YSQYYHLSKINVKVGQKIKKGELIGLSGASGRVSGPHLHFGILAGGKQVDPLDFVSKFNAIFQ

>WP\_002893128.1 MULTISPECIES: CCA tRNA nucleotidyltransferase [Campylobacter]

MQISKISLKNNSDLQFIAEFLKPYTKRAYLVGGSVRDLFLGLKICDYDIELYDIKLKDFEKIMQKLGAQG

FGKSFFVYKFKNYDLALARTENKISYGHKGFEVQICNDEKLGAKRRDFTINSMMINLFNDEFLDFYGGLK

DLGAGFLRHIDKQSFQEDSLRVLRAVVFASRFNFKITSESLKLMQSMDITDLSKDRINAELYKFFKSPRL

DVGYRYLQELGLEKQVFGFESVFKSLEFQNLLRQSREFVKSDALFLYLYLNFFNLEKDIFFKRTKLKKEY

LKYANQAFYLDDISDFELAKIAFEMPLKEWLGLWSKKRIEQAKRLGLYENKFESKILAKDFINAGFCGKI

LGLKLQEARENELKEYIKGLVK

>WP\_002880961.1 MULTISPECIES: penicillin-binding protein 2 [Campylobacter]

MQEYKKNRVSKVAFAYCMALLFMIIFISSTFFLTSKRHIPNTEKDQYALALRGSIITKDNFTITSSKQIY

RAEIDLRSINKDKFDLFLKLFQIYSGISNDQVADIKKRMQNQKKRSYNFVLLQNLDSKQASYLKDLAKKL

YIQGFFKAFTNNSGRVETRGLNIIEHEEDRIYMSKDSFTPIIGYTKMILDPESGILKNIGVKGLEKYYDE

CLSPVQNEKIQGLKDIGGNIILNLNSLQQKKINGCDLYLNLSLKLQKSIEKAIDQRNEDLKANEIIVGVM

ESKTGRILALASSRRYDPQNRGKDLSVLNASAIEYGYEAGSVIKPFIFTTALRLGKIKMDEVINTYGGSY

KLGRFTIKDDHKMDKMTMEEVIRYSSNIGMIQIAKRLNNIEIVSGLKIFKFGEKSGIDLPYEQKGEIPNP

KRLRDIEKSVLSYGYGLKTTFIQLLAAYNVFNNDGFYITPRLAEKFYQNGRFTNLDDDVKKEKILSSEAA

KTMQNVLINVIEKGTGKKAITQGIIAGGKTGTARIAERQGYTSNRYNASFFGFANDLNHAYTIGVLVRHP

TKPYSYYAAQSALPMFKDVVDILINEEFLTPIQDNNQTSTNN

>WP\_002866911.1 MULTISPECIES: WD40 repeat domain-containing protein [Campylobacter]

MKKFLFILSLFCVLSYAYELKLNANITALKLDKQNLYIGTDKGEILQYNIKDKSLKELLSLPKIKNYYGD

DFAKIYNIDVFKHTLLILSEGDFGAKNLSFYKENLQIKKLEENSIIKAFFINENTYLLISIGSEIELIDK

SLKNIKKFNFSHSSLNDAVLNEDKSRLVAGFESGEVELFDLKNWKMLKNYDKMHKDNIYQVDFKNNVILS

CGTDRRIGVVKNEEQNFLQKDFLIYTCALSPNGELAVYSDNEAGVSEVFSTSDFKPVKTFNNENLMSEFI

IFLNNKDFIISGFGDSIMFRSIDE

>WP\_002866624.1 MULTISPECIES: flagellar hook protein FlgE [Campylobacter]

MMNSFYNGISGVKSNSFGIDITANNIANVNTTGFKYSDAQFKDIFYTTITTQSTNPAQGGYGSGAASSQV

VFEQGSPVASDGEFDVALQGKGFFGVLGADGNAYYTRNGSFRRDANGYLVDSYGNFVLGTMNPAFTGINY

SDRVAGLMGDYLNTGTPVNNGFTVNSNNSFSIGTTASQGAIKVPVNMYLPPQVTQNVKWSGSLNTNTTTE

VVKVDLDPSKFNITKTEDGKYVVSGSVSKEDVFSAKAGDRIILNFTDDNGVKTSFEATLDENLNFKSNEL

DLKGLDENSIKLDTAQISTEQQKANKDILESPIYNADGSKSTLRVTLERVLPQEGDNIQYKAIAQIYDSN

GNAVGNPTEGNMVFDKNGALLQNNITSIANPNGGTINIDLGSPYDANKPGSGYSGIYIKEGVEKNVVTQQ

DGVAEGFFEQYNISDDGSIVAQFSNGKNAIVGKLALYNFINEQGLVAMGDNIFAATANSGDASFIMKDGQ

VVNTAKFKGGFLEQSNVDLSAELSNLIVTQKAFDASSKSITTSDQMIQKAINMKR

>WP\_002866604.1 energy transducer TonB [Campylobacter jejuni]

MKTLFLNHKYQASYITFIVFIPLLFVIFHSNDFFKMEIKNEDSFSLAIKQFTQTNPTNETKPTESIIEPI

KPKPQPKVIKKTPEKIQKKIKKTPPHPIPNKTPIAPTQEVKTFTKTTDTNVKPKITQLTQGKDNHPVLKE

IQKAIQQAQFYPRQAKKMRMQGTVKVEFLWKENKTLADLKIIESSGYDLLDKSALESIRKASLNFPQYNG

DLRITLPIIYDFKTLRG

>WP\_002866284.1 N-acetyl sugar amidotransferase [Campylobacter jejuni]

MKFCKKCVMPDTKPDLHFDEEGICDACRSQEAKNQKINWQEREKEFFELVKKYKKHPVYDCVIGVSGGKD

STFQVVKMLELGLNPLCVCFEPSVPTKIGRKNLDNLNHLGVDLIHIKRDPKVYQKLAREAFIRTGDNEWQ

NHLGIFTSVPRIAVNFGVPLIIWGESPQIEYGGPASSKNKNILDREWLEEFGGLLGNRISDMIGVEGITQ

KDVYFYTYPINEELQRVGVTGLFLGYYFKWDYKKILEISKKYGFLTLDHPVETTYENFENLDCYSNHVHD

YLKYCKYGFGRATDNACLDIRLGYISREEGVRLVQKYDGKPPKKAIKKYLEFSGFSEEEFQKIVDSFTNK

KIFKRDENGKFIRDYDGSLVRKDECVLK

>WP\_002866141.1 MULTISPECIES: glycosyltransferase family 2 protein [Campylobacter]

MPKLSVIVPTFNRQVLLEKAIKSIQNQDFKDLEIIVSDDNSSDDTKSVVQNLQKDDDRIKYFLNQNYKQG

PNGNKNNGLDQASGEFVTFLDDDDELLSGALSTLMQKANEGYAHVFGNCLIEKEGNLSKEFSGKGLEKDS

EISKKDFLMAKFSGEFFSVFKKSLLENKRFNEEFYGNEATLWVNLYKEKSFYIHKAFRIYRIFRQDSVTL

GASKNAHRVYLGYLELAKILENELRMSKDKDYKKTCASYYKMAAYYAKLAKNYKALYKCLFKSLSIKINA

PALILLILSIIPNNMIEKLSKIRVALCKN

>WP\_002860666.1 MULTISPECIES: carboxymuconolactone decarboxylase family protein [Campylobacter]

MQLRQKAREIFEKFFGKVEEKLLFTSDKEFFTNHINFTFGESFVKANLDTQKYFLITLASTLAVGGKIEF

KALLQGAIKNDISPIVIKEVIYQATPYVGFARVCDFLSLCNKVFKKLNIALVLTPQGTTTQENRKIKGRE

IQNAIFSEANITKMIETTPEDKAFINDFLSANCFGDYYTRMGLDLKTRELLTLVYLISLGGLENQVKAHI

QGNLNMEQSRKDLLNIIAALIPYIGYPKALNALNLLDDIKK

>WP\_002854691.1 MULTISPECIES: MinD/ParA family protein [Campylobacter]

MNNQANKLRNLMSQNGTKKSQNTHFIAITSGKGGVGKSTISANLANVLANNGYKVGLFDADIGLANLDVI

LNVRIQKNLLHVLRGECSLEDILIEVKPNLWLIPGESGDEILKYNDKNIYERFLNQASILDELDFLIIDT

GAGIGGNILNFLEMADEVIVVTVPDPAAITDAYATIKTTSKTKENLLMLFNVVKNENEALKVFENIKKVA

DANIKNPLNLEFLGHLSASKDVSGSIKKRTLFSDENTASSDELKALASKLLYRLERKVLDNVSNRSFSSF

FRKIIERF

>WP\_002852845.1 MULTISPECIES: M23 family peptidase [Campylobacter]

MKKLLLLFIFVVQSFAALSVEELTWDNGDTLLKFLQRNSIPMSLYYGLDREDQELASDIAYKIKYQVLKD

ENNNIEQVLIPISDDLQIHIYKDKDGQYTLAFTPVSYQKEDRILHLTIKSSAYQDVYEESGSSTLARAMV

RAFRGSINFRNIQKGDEVTLYYEQKRRMGKLWGDINIKMAMVEINKSAREVFSYNDIFYDRDGKELESFL

LTKPVNYTRISSPFTTARYHPILKRYRAHLGIDYAAPTGTPVKSAGKGVVTFIGTKGGYGNVIQIKHDSG

YMTLYAHLSRFAKIKNGQKVNQGQVIAYVGSTGMSTGPHLHFGVYLNNKAINPASVVKIAKSELSGKAKE

NFKHIIAGYEQVVKEALASNQPNPPKEEDFENYIEF

>WP\_012006691.1 bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC [Campylobacter jejuni]

MKTILLAISGSIAFYKSYELISLFKKEGFRVKVLLSNSLLKFASKMSFEALADEILCEENESWQNSNNHI

AFSKDVDLVLFAPASVNSINKLAFGIADNLFIQTLIAANKPLIIAPAANTNMFHHFSTQNSLKILKENKA

LIIEPICKVLACKDEGVGALAEVKDIFNITKRELLKEKFWCNKSVVITGGGTRERIDDVRCVSNFSSGKM

AKVIADAFYFLGARVKLLSSVEFDTPYELCKFESSKDLKELLDKNLSHDFLIMTAAVSDFIPQSVKGKIK

KNEHLQGLNLHLSLNEDLLKTCKFQGKKIGFKMEFDSQNALENAKKSLKDKQLDMVCLNIIDQKNYFGSD

QNELYFITLNNENKSTLQSKEKLAFELVKWCEKL

>WP\_002857391.1 MULTISPECIES: molybdate ABC transporter permease subunit [Campylobacter]

MLDPAFLQTLYLTFKLAFITTFILFFIGVFLAYLLSFVRFPFKTILQSFISLPLILPPSVLGFYLLVTFS

ANSFLGQVLKEYFNLSLVFSFEGLVFASLIFSLPFMVNPLQSAFSSINPNLLDASYSLGKSKIYTLFRVI

LPNSKAGIFSACAMSFAHTVGEFGVVMMIGGHKQGETLVASIAIYDELEILNYSLAHQYAFILFIFSFLV

LFSLYFINKKMSFQ

>WP\_002791314.1 MULTISPECIES: 50S ribosomal protein L25 [Campylobacter]

MLEGIVRESIGRKAAKALKRDGYLIANIYGKGLENINAAFKVNEFIKEVRKKTTLIFDVKVGSQTLSVVV

VDYQKDPVTAELKHVDLKVAQKGVISKYMVPVKITGTAIGLKNKGVLIQSKRRLKVKCAAENLPNFFELD

VSKLDVGDALLVRDIVVPAGVTMIDADRVAVVGVEKAR

>WP\_012006778.1 KpsF/GutQ family sugar-phosphate isomerase [Campylobacter jejuni]

MNTLEIAKEVFEKEAQAILDLATNLDENFNQAVNLMLNTKGRCIVSGMGKSGHIGAKIAATLASTGTPSF

FIHPGEALHGDLGMLTSEDVLIAISNSGETEEILKIIPAIKKREIPLIVMCGKKNSTLVKQGDIFLNIAV

EKEACPLQLAPMSSTTATLVMGDALAAALMKVRNFKPDDFALFHPGGSLGRKLLTKVKDLMVSSNLPIVH

PDTEFNDLIDVMTSGKLGLCVVLENEKLIGIITDGDLRRALKASDKPRFDFRAKEIMSTNPKVVDADAMA

SEAEEIMLKHKIKEIVVSKENKVVGIIQLYAIGNV

>WP\_002867041.1 outer membrane beta-barrel domain-containing protein [Campylobacter jejuni]

MKKIFLCLGLASVLFGADNNVKFEITPTLNYNYFEGNLDMDNRYAPGIRLGYHFDDFWLDQLEFGLEHYS

DVKYTNTNKTTDITRTYLSAIKGIDVGEKFYFYGLAGGGYEDFSNAAYDNKSGGFGHYGAGVKFRLSDSL

ALRLETRDQINFNHANHNWVSTLGISFGFGGKKEKAVEEVADTRPAPQTKCPVEPREGALLDENGCEKTI

SLEGHFGFDKTTINPTFQEKIKEIAKVLDENERYDTILEGHTDNIGSRAYNQKLSERRAKSVANELEKYG

VEKSRIKTVGYGQDNPRSSNDTKEGRADNRRVDAKFILR

>WP\_002866064.1 efflux RND transporter periplasmic adaptor subunit [Campylobacter jejuni]

MKKILFLLLVFNCAFGEEIYASFNVEASKQSKLALESIGLVQKIPVEIGQKVSKGELLLTLDQESEKIAL

QNAQNSYQLALVEYENTKSKMQKIKAVENVIDKQSYEDMKAKFDAANLNLNKAKINIAYYKNIMTKKELR

APYDAIIANKFIQVGEGVGGVAQPLIEIFSYPQSKLILSFDEKYKDKVKLGDDFFYKIDQNGTELKGKIS

LIYPSIEVKTRKIYAEVQTTNLTPGLFGEGRIITKD

>WP\_002866033.1 amidohydrolase [Campylobacter jejuni]

MNLIPEILDLQGEFEKIRHQIHENPELGFDELCTAKLVVQKLKEFGYEVYEEIGKTGVVGVLKKGNSDKK

IGLRADMDALPLQECTNLPYKSKKENVMHACGHDGHTTSLLLAAKYLASQNFNGTLNLYFQPAEEGLGGA

KAMIEDGLFEKFDSDYVFGWHNMPFGSDKKFYLKKGAMMASSDSYSIEVIGRGGHGSAPEKAKDPIYAAS

LLVVALQSIVSRNVDPQNSAVVSIGAFNAGHAFNIIPDIATIKMSVRALDNETRKLTEEKIYKICKGIAQ

ANDIEIKINKNVVAPVTMNNDEAVDFASEVAKELFGEKNCEFNHRPLMASEDFGFFCEMKKCAYAFLENE

NDIYLHNSSYVFNDKLLARAASYYAKLALKYLK

>WP\_002857601.1 efflux RND transporter periplasmic adaptor subunit [Campylobacter jejuni]

MKLFQKNTILALGVVLLLTACSKEEAPKIQMPPQPVTTMSAKSEDLPLSFTYPAKLVSDYDVIIKPQVSG

VIENKLFKAGDKVKKGQTLFIIEQDKFKASVDSAYGQALMAKATFENASKDFNRSKALFSKSAISQKEYD

SSLATFNNSKASLASARAQLANARIDLDHTEIKAPFDGTIGDALVNIGDYVSASTTELVRVTNLNPIYAD

FFISDTDKLNLVRNTQSGKWDLDSIHANLNLNGETVQGKLYFIDSVIDANSGTVKAKAIFDNNNSTLLPG

AFATITSEGFIQKNGFKVPQIAVKQNQNDVYVLLFKNGKVEKSSVHISYQNNEYAIIDKGLQNGDKIILD

NFKKIQVGSEVKEIGAQ

>WP\_012006722.1 Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase GatCAB subunit A [Campylobacter jejuni]

MITLKEALKYSKEELENLKKELNEKAKKEKKIGAYIEQFLDKDLSVSGEGVPVAIKDNISVKGWELTSAS

KILQGYIAPYDASVIVNLKANGFSPFGRCNMDEFAMGSSTASSYYGKTLNPLNFERVPGGSSGGSAAAVA

GGLALASLGSDTGGSVRQPAAFCGCVGFKPSYGRVSRYGLASYSSSLDQIGVLTQNVEDAAILYDAIAGY

DKMDSTSANIEFIKTAPNLNVNKKLKIAVIENYVNDADSEVKNALLKTIDMLKANGHEIVYKNLLDSKFD

IAAYYIIATAEASANLSRYDGVRYGKRSENIQNLKEMYVNTRSEGFGEEVKRRILLGTFVLSSGYYDAYY

IKAQKARAFIKAKYEEILQDCDLIFMPVTPTTAFKFDTQKSPMQTYLEDVYTISVNLAGLGGISVPVAKD

KEELNISAQLICKAYDEQTLLDGALSLEQMIKH

>WP\_002854550.1 MULTISPECIES: Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase GatCAB subunit C [Campylobacter]

MQIDEKLLSKLEKLSALQITKNRNETIVQLSEIVNFVEKLNELDLDSQEITVSTIKGGAPLRIDEIRNSN

VIDEVLDCAPKKQEHFFVVPKIIE

>WP\_038402202.1 ShlB/FhaC/HecB family hemolysin secretion/activation protein [Campylobacter jejuni]

MLEQSPYKEDANLKNYNNTLKVKDGVIIIDHSNTSDDNNSKTINTKKNTQKDNNNTQKNQPNLSNDNTLK

TKTPNSNTPSLKNTSKEESIHKVSFSFHITNKNINFKDLGLDEQVLQEALNDYKKESISVQDLQDIANII

SYYVQVSGYPAATAYIPQQELKDQIQINITLGVLGKYVVQNNSSVRDYAIESKLPNHKGEIITTKLVEDA

VYKVNEMYGIQTLASLKAGDNPGETDVVIETTPSDSFVSVLFYGDNYGIKESGRYRGGASMSFNNIAHQG

DSLNAYLQRSDEAQTNYGISYTTFLGNLKITPSYSKGNYALGGIWREFDFIGTSENLGIDLKYPLWITTY

NSFYLTSSYYHKKLSDSKFDILTFDKSSDTISFGIEGVYNGISNDSFSYSANVSYGNVKDEGMTIVGIGT

SKVGGVEFGKFAKLNVNLNNAYFFNDTFTHLFSLNYQQVINGATLDSSETISLRGPYGVRAYNNGDGEGD

NAVVASFGLRMATPLKDFYITPFYDIGYSWYENDSYTNYMDAYGLQLLYNKTGNFYVKLDLARALKKYKL

DDDYSSKAYVSFGKYF

>WP\_072238625.1 flagellar hook-length control protein FliK [Campylobacter jejuni]

MMSNLAPQNDVLNLTPSKTSNTSSSFSKTSKNKEHESSDSKNSTQDDTESFLNSLLNSIDETNEFLPDHM

KISQKEVVSEAMNRLQKGAFDESDKISIFESASFMQILSLLDKLKTDTADVKLANLSTQLSSLIKTEANF

NALKGASNLSELLDIAKDLGLNVKNIKVDRLLDLKATFPNLDKADFFKGAVDNVFKEIINNKISNVSKNL

NHNLENTTHTTSTHSTQKTNSKDSGSLLSQTLKNLDSILSSKESKHEKNDKVKSKIEEDTTDTKNTLKNI

KNDEFAKNLTEELNIKDKKNQDSLNKDNNLKDLNKESKDLNKDFNKELNKNQEKNNLNQENIQDQNKNLK

NNDQNLNLDKNLNKEIVKDTQNLVSNLTQKDFNLNKEPKNNNKENKDIKQNFFDQKLNFENLNKTQVVQN

KENNANFNNNTTNKETFTQEQTKTHSENVDKNSLDELNSLVKDLNKVTQNNARNITPKETLQYFSQDLKE

AVDQYKAPITKLSITLNPNNLGEVEVTLIQRGNNLHINFNSNANAMNLFIQNQAEFKNSLVNMGFTGLEM

NFSDQGKREQNQNQGKNRSGYGFKDALDGKNESEKVNLELVLAKYF

>WP\_012006723.1 CinA family protein [Campylobacter jejuni]

MKHLLYLIGDELTINEKFKNYIYRTYEEKFKEINEIRIQNKTDKDLPFLLENLLNQYDFITLFTSPLHYA

TVAKILATLNDDNLILKDDTLVPDKAEFSKNSFVCNFSNSKINVVKINPSEKLPNLLGHIKLNFAYFCIF

GMDDESAILLLQTLTKSYEISIKSTKLLDNLVLIKATCANFGKLDGFLNSVKNLFGQKVFLGKDPIHFIS

SKLLEKKLKISFAESCTGGLCASTLTKISGVSEIFEGSIVSYSNRIKHEWLGISKSVLENNGEYSERCVY

FMLKGIFKTANPDFALAISGVVGEKDEGKIKSGTIYIGAMFRDGTFIQETLYLDGDREFMQEQAVLATFC

LLLKLKPEIFEI

>WP\_012006719.1 AcrB/AcrD/AcrF family protein [Campylobacter jejuni]

MFKLAINRPITVLMFFLALMIFGLISAFSMSVNLFPNVSIPLIKITSKVNGDLNFVESKVTKEIENALSE

IDGVKTITSAAYDNFSVSVVEFKLGKNLEVAANDVRDKIGTLSLPSKPEIEKISSDSGSAISLFLYSKDK

LQLMREINDKIKPFLQRVEGVGKIEAKGFLEPQIRIELKPNELRKYNLNALDVANIIKSQNFKQALGELN

NNQDNYIIKGYFEATNLEELSNLRIKTGVFLSDIANISSLYEDEKQSALYEGKEGVLLELGKITNYNTLE

MIKNVKNALPILEKQIPKDISINMLYDKSLNIHKHLSQVIFDMVLGIFLTLVIVFLFLRNLSATLIACIA

IPTSIISTFFIIDLLGYDLNRLTFIALTLSIGIFIDDAIVVIENIAKKLKTYPPLQAAFLGINEIGFSVL

SISIVLLCVFIPISYMNSISGLFFNALGISVASGIVISFLVSVFLIPSIGARFLNPKENKFYEKTEAFFE

KIEQKYENLLYKILQNKVKFILATLVFTGLSFALATRIGLDFLPMEDDSEIQVLLESKKDLSLEAMKEKS

LNLLEKIKNDSNVKYAFLLVGYDDAKDATKAKIYVKLKNLDERNLRQSAIVSLYRQKFQDESLKIKILEL

PKIEGAGIDDPVQFLILGDDLNTLKEAASQAKEILGTNARIVDISDNANATKDEVALHINKEKAKLLDVN

PQYIAGVLGYSFSQLSVGSMDRGNSKDDIILSFAPEFKKDIEALKRISIKNNQGINLELSSVVDFIYSKD

LKTINRYNKNRSVKITAGVNDLSLGAVQKLLLDNMDKILNNNPSLSYAFSGFINLLGETVQGFAMAVALA

FVLIYLVLAALYESFILPLIIMITMPLAFGGASIGLFITGHNFSLFVLIAIILLFGMVGKNAILLVDVAN

KKCHEGLDPDKALLIAGKSRLRAILMTTFAMIFAMLPLALSRGAGYEANSPMAIAIIFGLISSTLLTLLV

VPALFKFCFKLDSKLRKIYEREKLN

>WP\_002876672.1 MULTISPECIES: M48 family peptidase [Campylobacter]

MARQSSSLKSFIYKDECYFYSKKCIKTLRLRLNEKGEFVLSIPYFCTFKSVYEFLDKSSSWMNEAKIRFE

KKVLKDDELIFLAKKYKIIFDENAKKIYFDKDKIICQNKAKLDLFLRQNAKKIFTFYLKKWSKKTGLFYT

HLSIKNMKTRWGSCNHNKAYINLNLKLIQKSLRAIEYVILHEICHLKFPNHSKEFYTFIEHFMSDFRQRE

KEFLS

>WP\_002869083.1 MULTISPECIES: low molecular weight phosphotyrosine protein phosphatase [Campylobacter]

MKKILFICLGNICRSPMAEFIMKDLVKKANLEKEFFINSAGTSGEHDGEGMHYGTKNKLAQLNIEHKNFT

SKKLTQKLCDESDFLITMDNSNFKNVLKNFTNTQNKVLKITDFSPSLNYDEVPDPWYSGNFDETYKILSL

ACKNLLVFLSK

>WP\_002867061.1 molybdopterin synthase sulfur carrier subunit [Campylobacter jejuni]

MIKVEFLGPINKENLELEVKNLKELKEILQKDESLKEWLELCAVSLNDEIIFDENTKLKDGDKIALLPPV

CGG

>WP\_002867040.1 HAD family hydrolase [Campylobacter jejuni]

MNKTILFDLDGTLIDSTDAILNSFQGAFKALGLTSKNNEEIKNLIGYPLEQMFRMLYPDKVNLSKEFVLA

YREIYAQIYLEQTTLLPKAKEALELGSEIADLGIVTTKGGKFTPILLDYLGVKKFFKTLITLEDVTNPKP

SSEPIILALKRLNKTQENAYMIGDTILDIQAAISANITPLALACGYGNENELKAYSMVFLNAYEAVNYIA

RLN

>WP\_002867035.1 type II/IV secretion system protein [Campylobacter jejuni]

MESRMDKIFQAYIDNEISLDEICTKFNITSWDFFKKLANFCNLHFVDLDEDNDFIYEGIPFSLLLKFKFL

LIKNNDGFMIIRSKPCSLELLEQVKTFMICEKIDTAIADELKIAKILNQIRIQEEIKRLSIKLRLEWQEN

HKRDDQSCISQIFDFLLHEILSFHASDIHIEARNDDALIRFRVDGILREFAIFEKDIYEALVFHVKFLAC

LNLAESRKTQDGSFELDFENERYDFRVSCLPLIYGESVVIRILKHDKEILDLHKLNLGDKNLEILKKILH

RPNGMILLTGPTGSGKSTTLYACLNELKSIEKKIISAEDPIEYKIPLVQQILLNSKVGVEFNSVLRAILR

QDPDIIMIGEIRDEESLDIALKASLTGHLLLSTLHTNDALSTIDRLLDMQAKSYLIASALSLVIAQRLVR

KLCPWCKQKSKKHYIEFEGEFFEPKGCERCHHSGFFGRELIAECLEINEDLACAIRENQDKTILMELAKK

YGFQTMFEQGLKKAKEGLTSIDELLRVVR

>WP\_002867009.1 UDP-glucose/GDP-mannose dehydrogenase family protein [Campylobacter jejuni]

MKIGIIGTGYVGLPTGVGLAELGNDVICIDREKSKIDALNDGILTIYEDNLEELFHKNVKEGRLKFTTSM

QEGIKDADLVIIAVGTPPHPVTKEADMKYIHAAATELADYLTGYTVIATKSTVPVGTGDDIESLISKKNP

NAEFDVLSLPEFLREGFAVYDFFNPDRIIVGTNSQRAKAVIEKLYEPFKGKSELLFVNRRSSETIKYASN

AFLAIKIHYINEMANFCEKAGADILEVARGMGLDTRIGNRFLNPGPGYGGSCFPKDTLAMAFMGKQNDID

LTLINAAIKGNEERKNHMSERILNSIKDIKNPKIAVLGLAFKDGTDDCRESPAVDIVFKLLEQKVQICAY

DPKAMDLAKQILGDRIDYANSMYEAIKDADAIAILTEWKEFSSLDLKKAYDLLNHKKIIDLRNLLDKNEA

IKLGFEYQGVGR

>WP\_002866979.1 amino acid ABC transporter permease [Campylobacter jejuni]

MDFDFILVQAPAFLTAAWLTIKLSFFGIIFSLIIGLFCILMSYFKIKILENICKLYIEFSRNTPLLIQLF

FLYYALPKFNIHLEQIPPLDLICLSVEETLRPSFACAIVGLSFLGGSYMAESLRAGFEAIRKQQFEAGLS

LGFSKFGNLRYVILPQALAISMPSISANIIFLIKETSVVSIIALPDLVNLMKSLNSLTYKTDELLFLLFM

GYLCIILPLSFILLKFEKRLLHA

>WP\_002866925.1 MULTISPECIES: alpha/beta hydrolase [Campylobacter]

MAQTQLSYKNKTYQISYEILGDLSLPQILILHGWGANKELMKQSFCPFLKDFCQIYMDLAGFGNSSVEEI

LNTQDYANITELFLKQKKLDVCFFMGHSFGGKVSTLLAKEKDTLILLSSAGILAKKSLKVRFKIRIFKIL

KLFGLGKFYRYFASKDGVNLSPMMYETFKKVVDEDFSEIFAKQKAKSLIFWGKSDEATPLYCGEKMHELL

KNSTFYPLEGDHFFFLKHSAFIAQKIKEI

>WP\_002866847.1 MCE family protein [Campylobacter jejuni]

MENRANYFFVGLFVFGVFFASLGFILWLGGYSKEESFKYYEIHTQESVAGLGIKAPVRLLGVEVGSVEEI

SIYNQDELGVNIRIKVKNNTPIKEDTFATLQLQGITGLKFIQLQGGSKNSKDLVSIHGKLPVIPFKESFL

ATIDRQSEHIFSLVKTADDKSKELLSEKNLKNLEILLQNLAELSANLNANSKNLSLNLSNASLKIGKMAD

NISLSAQNFNSSLKNIKESTMILKNFIKKADEKLNTYDDIKASLMQNLELFKRVLIESNILIENLQNSPA

DLIFKETKPKLGPGEK

>WP\_002866831.1 cation:proton antiporter [Campylobacter jejuni]

MHQSVIDPQGLIDLKILIVIALCLLFSPHIAKILRLPLSATEIILGAVIAYFGFIGKSENFALLANVGFY

YLMFIAGMEVNLRAFFNMDKEVAKKSFFYIFLLYALSSLIVWIFGLSLVFVIIIPVMSVGLLSLLFKDFG

KECYWLNIAMIVATLAEVISIVLLTIAGAFLREGTGIIDVAQSILYLNIFLGLCLLGFKMLGVLFWWYPQ

LKVVLMPWEDKNEKDIRFCMAIFILIIVAMVITKLEIVLGSFIAGSFIATFFDHKKDLEHKLSTFGHGFL

IPIFFIHIGSTFDLKMILDYKIVLQAFLLMFVMVGLRILCASVFLKRIGFKNMILFGLSHSMPLTLLIAT

ATLGYSGKVIDEKLYSALILTALFEAIIVMSMIKFLSNSKK

>WP\_002866825.1 sugar ABC transporter permease [Campylobacter jejuni]

MKNSLATFCFISPAVLLMLLFLILPIIWVIILSFSDYQLGNGDFHFVGLINYKALLKDPVFFTSVKNTLI

YALIVLPLSVLGGLALALLIESKNSAKSFYRAVFFLPVMATLIAMSMVWEYILHPDIGIFNKILALFGVN

TINWLSNKDTVLYTLAGIGVWQQLGYNMILFTAGLMSIPTSVYEAAKLDGLNKTQILFKITLPLLLPILF

FVLIISSIKAFQVFDTVQVLTNGGPNHSSEVLLFTIYQEAFMFFRTNYASAISVIFLLFILILTLLKIKF

LDKKD

>WP\_002866794.1 MULTISPECIES: HD family hydrolase [Campylobacter]

MINIKLIEHIFKAASISRWNDYPRMANLVELDKQAHKFIIAYFIAKMEKDVDMRVIIEGGIFEFLSRVVV

TDIRPDVYHEIVRQKKAEVNAWVLSKIEPMIEDIEEGEFLKRFEAYLNGNAYAKERLILKAASYFATRWE

FNIVYQTSAFLNDIDEIKNKVEEELEDYYELIGARKIALNQKIAKIIDLSGRLRFQKRWAQTPRIPETAV

LGHMLVVAILGYFYSLKIKACDKRLENNFYCALFHDLPESLTRDIISPVKYGIDGLHDIINDYEMKLINE

RILPFVPEGLRAEFSYILGIREGRNDESNFVKNEFENRTYKNAKIELCSGSLSSFNENEFGAIDGKALKY

CDKIAAYIEAGLSISYGVKSKELESGFLGMYEFFKENPTIDGVNFFEICESLREYFKI

>WP\_002866694.1 MmgE/PrpD family protein [Campylobacter jejuni]

MFYSEILADFIFNLKYENIPNTVVQRAKELMLDSLGTAIAASKEECVLNAFKAFENLSTDKNTPIWVNDQ

KLVPIYAAMLDGIASHALDFDDTHTEAILHASAILTPLCLSYGFHVNKDAKKIIKAFIVGWEIAARVGIA

SKGTFHKRGFHTTAIAGIFGSVSASAILLDLNKEQIINALGLAGSFASGVNEFLSNGSNSKVLHIANAIK

NGIMVAHFAKNNMSGPLSIFEGRDNIFKCFGIEEECDKTELSKALGEIWQTMQVSIKPYPSCHFAHGLID

CAIALKNDGLKADEIKSIHCFVDEVPISFICDPLEAKYTPNSAYEAKFSMPFLMALGFFDGKITLDSYEN

LKREEVLEFAKKISYEKRKSQGFPKYFPGHLEASLQDGRIIQKDVFINKGNFDNPLSFEELKAKFLANAQ

IYLDNAKANKILDQIINLENLNHFSF

>WP\_002866685.1 MULTISPECIES: phosphomannomutase/phosphoglucomutase [Campylobacter]

MLDVIFREYDIRGLYGKELNEKSVKAIGFCLGQTMLNKGCKNVSVGYDARYSANELFNYLVSGLNKAGIK

IYDIGLVPTPLGYFSLYEGLKFDANVMITGSHNPKDYNGFKITINKESFFGVELKEFSKEVYKHLDDEIE

ENLEVEKYDILSLYVKFMCEQFSFLKDFNYKFGVDCTNGAAGVVIKPLIKALNLKAHVMFAEPDGQFPNH

APDPTEEENLSAIREFLNQNQDYSLAFAFDGDADRMVALSKTHVFCGDELCYLFAKNIPNPRILGEVKCS

KNLFDEVAKFGTIFMGKTGHSNIKKMMKEKDIDLAAEVSGHIFFKHRYFGYDDGIYAFLRALELVYKGFD

LESMIKALPKLYTTPEIKIPVNEEEKFKLVEEFQKEIEKGALKGVKSLCEIDGARIDFGDGWALLRASNT

SPYLITRFEATSLERAKELESMVFTLFDDIKARLKN

>WP\_002866673.1 class I SAM-dependent methyltransferase [Campylobacter jejuni]

MKCYICGSESNIQREGKVRDSLKINILECKDCGLVFLDKQETDDEYYKASGMRKDFKNSVEVLTLNQNLS

LTDNERRIDFIKQNFSKDINLLDFGSGLGHFLILAKENHFLNICGVELEERVKSVYFDHNITLYENLDYI

QNDSLDVVTLFHCIAHIHDPIMLLKKLSEKLKKNGKIIIETPNANDALLDIYKNKGFSNFTYQKCMLYHF

NKYSLYQIARKSSLDIDFIKHIQRYPLSNTLYWLNNNLPAGQKYWGSIIDNKNLQNAYEATLASIGATDT

LFAQFSKI

>WP\_002866650.1 MULTISPECIES: DedA family protein [Campylobacter]

MFDFLYNDISYLGLFIVCFLSSTLLPLASEAFVLGFIKLDFNPNLVLIVATLGNTLGSLSTYGLAYLGKQ

KILEKYFSKSLKKLENFNANFAKFGSIFAFFTFLPLVGDLFALGLGFAKYSFLKTIFFILLGKLSRYAFI

IFIANSF

>WP\_002866635.1 MULTISPECIES: TolC family protein [Campylobacter]

MNKIISISAIASFTLLISACSLSPNLNIPEANYSIDNKLGALSWEKENNSSITKNWWKDFDDENLNKVVD

LALKNNNDLKLAFIHMEQAAAQLGIDFSSLLPKFDGSASGSRAKTAINAPSNRTGEVSYGNDFKMGLNLS

YEIDLWGKYRDTYRASKSSFKASEYDYEAARLSVISNTVQTYFNLVNAYENENALKEAYESAKEIYRIND

EKFQVGAVGEYELAQARANLESMALQYNEAKLNKENYLKALKILTSNDLNDILYKNQSYQVFNLKEFDIP

TGISSTILLQRPDIGSSLEKLTQQNYLVGVARTAFLPSLSLTGLLGFESGDLDTLVKGGSKTWNIGGNFT

LPIFHWGEIYQNVNLAKLNKDEAFVNYQNTLITAFGEIRYALVARKTIRLQYDNAQASEQSYKRIYEIAK

ERYDIGEMSLQDYLEARQNWLNAAVAFNNTKYSYANSIVDVIKAFGGGFEQSEDTSKNIKEESKNLDMSF

RE

>WP\_002866623.1 MULTISPECIES: DUF342 domain-containing protein [Campylobacter]

MNFQVKTLETFNPFESLNHEQANTEQILDFRVIDFKLLCSSVKPAKTKTYERKDFDLFYADDFFVKNYNT

IVQKFLIEIYPKTQSFPFTVKLRSNSNLTHLKASINLTENFKYYPNLKFDILQNIYKIMIKQKFLILRLD

KNLFDKIDDFILSIQKSPSIKEIELEIAKGVDKIEHKSDEIIYHRDVNEECFDENINYDEGNYCKPIEKN

ELLFEYIYRILGKEGRNLRGEILHLNPIAFLDNPFIIKDESIYTEELEDRIKYFSANYGFLNKDHTGYCI

ANNLKLSQIGLKTTGSIKTNIDENINLEITNFDISDDAIKSGIVNVQASNIKVNGNVGATKLYGKNISIK

GLTHAKSEIFAQDIFITTHKGTLQADTVYIKNLENGTIIAKNVFVENCMGGKIEAENIYICNLLTDNTLY

PRKNLIITNNIKFKNNIVVSPLVSIENNSDTECENLKNLSLKIKSKLDDTISKMQNYYDYLIKNQIKIIK

LQKTKNPNAIEMKFSNLYHDIIKKYNHLSISYKKFIKLKYQIDAKLNFLNEMVYNVKIYIKAENIGEDNF

LKFYPNTNTNLELKHHINLKDYEKVLYLEKGQQVSYIKSSHNYSESDIEEIKIIFEKLEKDNS

>WP\_002866560.1 peptide chain release factor N(5)-glutamine methyltransferase [Campylobacter jejuni]

MTIKNALMEAKSSLKGYENEAVFILCEYLKKDKAWLFLNQDIQIDHEPYFELIKRFKSGEPFEYIFEKVD

FWGLEFKIKKGVLIPRYDSEILLFQILNLCKKNTFNGILEIGFGSGILSIVLAKELGLKITACDINPKAL

ELALENAKLHKVDHLIDFKLCNFKQIKENYDFIFSNPPYIKNSYPIDIWVQKEPKEALFGGEKGYEILEE

IIHFSLDKKVKFLACEFGYDQKEILEKILYQNNFIVDFFKDEQDYNRAFIAKFTNMRYDKK

>WP\_002866265.1 MULTISPECIES: bifunctional (p)ppGpp synthetase/guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [Campylobacter]

MKPIDEELLLEQLIDNVKNCKDLEAAKALLFEICGHDAILEKAVDYCIFCHEGQFRKSGEPYAVHPILVA

TLVGFLSENKSNILAALLHDVIEDTNCTEEELREQFGSEVLKLVLGLTKIIEIREDNLISSKSKKSLTKS

ALTFRNMLLASIEDVGVLIVKLCDRLHNMLTLDILREDKQKRISEETLVVYAPIAHRLGISSIKNYLEDL

SFKYLMPDEYKLIDNYINSNNQEMQLGLNEFISKIELLFLSNGFRQGSFEIQKRIKHSYSIYLKMQRKGI

GIEEVLDLLGVRILVEKVSDCYLALGILHTHFNPLVSRFKDYIALPKQNGYQTIHTTLFDAKSIIEAQIR

TFDMHKIAEFGIAAHWKYKEDGSVVAPRLDWLTDISMQSINNLENAEDYNAIELYEYAKDSLYVEDVAVY

SPKGEIFTLPRGATVLDFAYEVHTKVGLHAKSAYVNRIKVPLLTELKNGDIVRVVTSNDKFYRCSWIDSV

KTGKAKASIREFCKQKIREINLASSINMLSFIFGVDKNRIETWIEKENLARRIRQVATDSAYLKDIVNGL

KKYAKKSYWFDKYEIKEQKIGNFTLYCNHKIANVDFDFCCHPKRGDAVLAFVKGGNAIVHHKLCDRADKM

IDNNQDMVFIKWDSNIPKSYKLIFSLENKKGVLAEFLAFLAKMQINLLTINLSSDLNSAVDYFEITMEIP

DNINPDSVKDRLKSRCKILDFTSLNDAYKEG

>WP\_002866194.1 MULTISPECIES: class I SAM-dependent methyltransferase [Campylobacter]

MLEKQMIKFILSKWNYGNFRIVFWDQEEFHVGNQSAKFSLIFKEKIPFLKLFSDTSLVFAKHYMESKLEI

EGDYDEIAKVLYYFSNKRFLKNTEDILSKIAQKQESKNIKSHYDIGNDFYKLWLDDTMSYSCAYFKEPNN

TLYEAQINKIEHTLKKLDLKEGEKLLDIGCGWGWLSIMAAQKYGVKVVGITISEEQCKKAKERVKELGLE

DKIEIRLQNYQDLEFENYFDKVVSVGMFEHVGKENLGLYFMKVKQVLKPGGSMLLHSILAMFEGKTNAWI

DKYIFPGGYLPSLREVVSAMSEWDFHLLLAESLRMHYAKTLDLWDENFNKVLDKVREKYDEEFIRMWDLY

LRSCASAFRVGSVDLFQFLITKEINNNLSLTKDYIYK

>WP\_002866128.1 MULTISPECIES: MarC family protein [Campylobacter]

MGSELYLMFFAAITLLAILNPFGNLTQFLAMSDGLPLMLRKKLFRTILYTAFTIVLVFLLSGPLFMNYIF

RVSLDDLRVSGGLVLIIMAIKNLLFSTKIATKDFSSYQDMDDKEILRQSLIPMAFPMLVGPGTLASVIVI

AEDGGLDVALGGVMIAFIFMFILFHFAATIEKIVGKLILHVFSRIAQVFIAAMGFKMIIVGLKDIFNL

>WP\_002866089.1 carbon-nitrogen hydrolase family protein [Campylobacter jejuni]

MSKIAALQFPTLALSESRLDYYLKASKDNGANLVVLGEYVINSFFTELLHMPKNMIKEQSEAKKESLIKL

AKKYELEIIAPYVSVEAKSYKKLCLKVTPNGVKSYEQQILMPYEHWNEEKFFSNKTSSELKIFTFNYEKL

KCALLFGFEAHFDIFWQQIMTKKIDLVIVPSACTFESKQRWEELLKTRAFLNSTSILRVNRIGKTKDEWN

FYGDTLFINAFGEIESKLGSEEEMLIIEPKKSDEARKLWGFEKIIKEFKN

>WP\_002865913.1 sodium:alanine symporter family protein [Campylobacter jejuni]

MNLDIMLDFANKASDIIANKIVPNTDIIMVVLLIVCGLYYSFLTRFVQFRMLSSVFKILTEKNEGHTKEH

ISPFQALMISTASRVGIGNIAGISLALATGGAGALFWMWVMAFFGGASAFAESTLAQVYKSKDDTGGFKG

GPAYYIKKALGSHFFGAFFAFILIITYAYGFNGLQSQTMTSSFKVYYDMFNPNAAVDFASSSWPMIIGIV

LTIFGVWMFFSHHTKIGKISSLIVPFMALAYVLLAVIAVLMNFDKIPSVVHMILQSAFDFKAIFGGFAGS

ALVIGIKRGLFSNEAGMGSAPNAAAAALTSHPAKQGVIQAFSVLIDVVVCTSSGFLVLFSMAYLGLGESK

IDGGMPLVQEAMREYYGSFGIHFITIAIVLFAITSLIGNYYYAQANVKYLTNSKFVMNLFRITAVAMIFI

GSQMNLKLAWNLADLTMAFMATTNIISLLLLGGIVNKVLKDFNTQQKSGIDPKFNASKLGIKNAECWD

>WP\_002865878.1 MULTISPECIES: sel1 repeat family protein [Campylobacter]

MRIFLALFLFFNSLFALSELEEGLKLYEANKFDKAYEIFKNLCEKDISKACFSLAFMHESAKGVSKDLNQ

AYKFYDKACKLGLANACSNMALLLQNQGYKNEALLAFNKACTLGESLSCNNIALFYEKEKDGQMASSFYK

RSCDLKNARACYQLGSLYDKGELVKASVKSALAFYSKSCTLGFGEACYLLGRYNQLEKQDLTKAKRYFGM

ACDQKHQEACAAYKELNSKDIELY

>WP\_002862129.1 MULTISPECIES: ATP-binding protein [Campylobacter]

MSKIIPFREEIFHQINQILESQKAFIFLWGKSGSGKSVLLQRLAKKYNVDFINENFKDQSFLKEKIEFLI

SQGQSLIILDEVGMYDYAMLESIRIYSDSISFVLSSHKKLNILKKEHFKSRLSACFELKNISLLELDDYI

KLKFGMNFSNKCLKFLQKISQGNLRYIDKTLKSFYEINSFFDKNKSQEYILKLSALENGLLR

>WP\_002860995.1 MULTISPECIES: HlyC/CorC family transporter [Campylobacter]

MDPSQVLDLNQTSTASFDAGYSILMVVVALALVFLNGFFVLSEFSIVKVRRSKLEEMVKEKKAGAKKALE

VTSRLDTYLSACQLGITLSSLALGWIGEPAIAKMLEIPLINLGFSTVIIHTIAFIIAFSIITLLHVVLGE

LVPKSIAIAVADKAVLFIARPLHWFWILFLPCIKIFDFLAAISLKLFGIKPAKESELTHSEEEIKIIASE

SQKGGVLDEFETEIIRNAVDFSDTVAKEIMTPRKDMICLNKQKSYEENMQIICEHKHTRFPYIDGSKDTI

LGMIHIRDIIQNELSHKSQNLDTFVKPLILVPENISISKVLVMMNKERSHTALVVDEYGGTAGILTMEDI

MEEIIGEIKSEHEEDSYKKLAENIYEFQGRCDIETVEEMLVINYDEDLEQVTIGGYVFNLLGRLPIVGDR

IEDELCYYEVKKMDGNSIERVKVVKKTNKDEE

>WP\_002858931.1 MULTISPECIES: ABC transporter permease [Campylobacter]

MILFKFLIILAPLIFLFLCALFAPFLAPFDILSTHLENLHQAPNFTYILGTDFLGRDLFSRLLFALRNSL

IIGVGGSLLSIIFALCYLFLARCFFYVFWMRILEFFLALPAFLLMMFFQSMITSDVFLMIFLIALIHWCF

IARIIESELKRLENLDFYKANIVLGRTKFRAFFKDLIPALKTLIFTLFIFNIVHAIATEATLSFFGLGLG

FEIPTLGTLLSESSKAVFIGAWWMILFPLLSLLLLFLPLLWLGNFLQKIWGIRS

>WP\_002858782.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MHNEMNLKEVLIRFKPFYKRYWKQFAIAIFGMILASGGTAGSFYALEPILNYIFVEKNEALLYTVPFLLV

LMYFFKNLGTYLQSFYVSFIGTDMLRVLRARVLKNVLRLDMDFFKRYRSGELVSRCTNDINALQSIVSNI

IPDFFRELLTAIGLLAVVLYQSPTLAFFALVILPLAIFPLVWFAKKLKKYARNIQETNSDLLSYLGEIFS

NIELIKANDNEKKESDKFAKHNDTLCKLNLKSARIDALTSPLMDMMGSVGVAVVIIVGGREVINGSMSVG

SFISFVSALFAIYTPLKRLSSLYGKLQGAVAASERTFYLLDLEPQIKGGSKELKNIEKISFENVEFAYEN

PHKSVLKGVNFDFVKGQMLALVGTSGGGKSSIINLLMYFYEKQKGKILLNQEDISTFTIESLHAKIGLVT

QNIYLFNDSFAANIAYSEELEEEKVIQALKLANAYEFVKEMGGIWAEVKEHGKNLSGGQKQRIAIARALY

KNPDVLIFDEATSALDNESEKAIVKTIENLKQDRLILVVAHRLSTIENADKIVVLDKGKVLAIGKDEELL

QTCSLYQKFKSKEKTKPSFS

>WP\_002857365.1 MULTISPECIES: chemotaxis protein CheV [Campylobacter]

MFDENIVKTGSNEMELVDFRIFKQGHDKVYEGIYGVNVSKVREIIKIPSLTELPGVPDYIEGIFDLRGVV

IPVVNLAKWMQITEPESTMLKPRVIITEFSNILIGFIVHEAKRIRRINWKDIEPATFSTGSGALDKGKIT

GVTRIENDEVLLILDLESVVEDLGIYAPKTDIDFGKIEKFTGTALILDDSMTARKRVKEMMQQMGFQVVE

AKDGVEGINKLEELSQVYGESLNDTLKIIVSDVEMPQMDGFHFAARIKEDPRFKDIPIVFNSSLSNEFMN

EKGVQEAGGEGYLVKFNASDFFNEIAKVIKKHQSQEQG

>WP\_002857315.1 ATP-binding protein [Campylobacter jejuni]

MEKLKNFLILKNIEDTQIYKELKCAKNEALILRELCRNYVVSISSINAFTLLSTIFGNDKYLYLDALEDL

KKLIERGFVNQNSSFFKSLENNKTQTLTLALLQSELSLSEYFLEFLEAKPRLNFEKQEAYADYLEYLKDE

FARIQLYERLSFIQKSAYNSEIKNQIKLYEKHIKERLKKSKFYNVLADIFKEYNLEHKEQIIFLALLKEE

YALSNESSISREMNSLLSLISENDLERHKNKKLLQENAPLLNLIEYDEYLNAFGDISKSFFIIDEILQRI

INFEPKQSKKIKIESVLKDQDIFELIEPSTDINDIIMPENTKELLENILKQQDKKVLERLHSWGIKSNKN

IEAKIIFYGPAGTGKTMSALAMAKSMKKSVLSFDCSKILSKWVGESEQNVRKIFDTYKNIVQTCKQSPIL

LLNEADQFLSTRVDGSSGSDKMHNQMQNIFLEQIERFSGVIIATTNFLESLDSAFSRRFDYKIEFQKPDF

KDRLKIWEKFLPKKALFEKDFDINILSNYELSGAQILMVVKNTALKVAVSKDGVFKMQDFIESIQKELNS

SFDKSKIVGF

>WP\_002856871.1 MULTISPECIES: MOSC domain-containing protein [Campylobacter]

MKIQSLQIGKIKNYKNFQSAFIKDTYLEETQIDFLGILDDQIADKIHHGGYHKAIFANSCQNYPIWERFL

NKKLNFGSMGENLSIDGLCEQNVCIGDIHQISNAILQVSEPRKPCVKISKIHNNSNFTHEIFKTGLSGWY

YKVLQVGQIRKYENIKILEKNSTSLSVFELNQLFYSPHQALRQNPILLDKLEKLNSLISQNWHETIHKRL

KNTYDISYMDSL

>WP\_002856526.1 MULTISPECIES: iron ABC transporter permease [Campylobacter]

MLNLNTHSKILVIIGLLVAYIIASFTALCLGDENLNPKELFSYIFSQDEILRQIIIDGRLPRIIMAILIG

MLLASSGAITQNVFSNPIADPYIIGIASAATFGAVLAYLLKLNDYYYGILGFVCSAFFALGVFKISSKAS

IATLLIIGIAASSFLGAFTSFFTYLIGEDSFKIVAWLMGNIGNASWFRVGILILPLIFCLFYFYAHKNEL

NILLSGDDEARNLGVNAQKLKINLLIVSSLAVSFAVAFSGLIGFVGLIIPHTIRLLLKNYDNALVIPLCT

AFGGLFLLICDTLARTLLAPVQIPIGILTAFFGAPIFLYLALSARRFL

>WP\_002855813.1 MULTISPECIES: RDD family protein [Campylobacter]

MKENLQDRLERENLKIASFGKRVLAFLIDDMVISLIVFIIFYDRLIQAKDLFETTQIIGNFYLGFILLHF

SYQAIFTYLYGASLGKILCKIIILDENLLDKPNLIQSCIRSAIRQVSAMAFMLGFAWALSNDLRKAWEDY

LARTIVVDVA

>WP\_002854219.1 MULTISPECIES: peroxiredoxin [Campylobacter]

MIVTKKALDFTAPAVLGNNEIVQDFNLYKNIGPKGAVVFFYPKDFTFVCPSEIIAFDKRYQEFKNRGIEV

IGISGDNEFSHFAWKNTPVNQGGIGQVKFPLVADLTKQIARNFDVLYAEAVALRGSFLLDADGTVRHAVV

NDLPLGRNIDEMLRMVDTMLFTNEHGEVCPAGWNKGDEGMKANPKGVAEYLGKNEAKL

>WP\_002854047.1 MULTISPECIES: DedA family protein [Campylobacter]

MEEFLKNLLYQYKDLAYIIIFLWCILEGELALILAGIFAHQGHVNLGFVIFIAGLGGFVGDQIYFYIGRY

NKRYIQKKLKTQRRKFAVAHLLLQRFGWPIIFIQRYMYGFRTIIPMSIGITRYSAKKFAIINLFSAWVWA

SITILLAWYFGEQIWKMVTWAEEHWYYAAIIIIAFLSLLLFGFKQMEKAILKDKRKKS

>WP\_002853205.1 MULTISPECIES: DNA-binding response regulator [Campylobacter]

MAAKILLLEDDLSLSEIIEEFLNDEGYEVFLCDNAQEALDMAYERYFDLWILDVKVPLGDGFSLLKELRK

SGKQTPAIFMTSLNTTNDLKQGFDAGCDDYIKKPFELAELSIRVKALLKRAFSHKNEDFEDLGDGFRFEF

TTQILYHNNKALTLPSKEIKLLSLLLKNKNNFLSTERIFEELWDYDEEPSELSLRAYVKNLRKILGKEKI

INQRGRGYCYG

>WP\_002853086.1 MULTISPECIES: rRNA pseudouridine synthase [Campylobacter]

MRINKFISHNTRYSRREADELIKQGLVKINNKIALLSDEVKFDDKVFVKGKRVQKRTQFSVIIYHKQKGE

IVSKKDDRGRKTIYDTLPRQFSTWLSVGRLDYASEGLLLLTDSPVIADALMHSDLEREYYLKVKGTVSKQ

VIEAMQNGLEIKNEKKGAHAKTKITSMSFAPFIDFEIFGSSGGYTKLRVVINEGKNRELRRFFGHFDLEV

MDLKRVAFGALDLGMLKAGKHRYLENGEYEKLRDFLKFNEIRY

>WP\_002852947.1 MULTISPECIES: TolC family protein [Campylobacter]

MFEKYLKSAIFLALYPLAMLASNLHEFIALSQNNESYLIKQMQSEQANLDKEQAFRNYLPSLSLNSAYVA

NNKDRFIIDPQESLFAKVSLNFLLFDGGAREANLRALESREKLSLLDKEQNKNYLALNAITLYFNTLSLE

KILLANQQKVSFLKSTFERLQKFYDAGLSPKDELESIKAKYHLSLLELSQNELKLANIQKEIKILSDTDF

KVQGNAFLENPQQEKSQNYEVMIAKEQINLAKESVNLAKAEYFPKFYIQDNFNFYKNNYNPKVPAPFANL

ADQFLEKYSQGNQFILGMEWKIFDFNARAKEVEKERLNVQIANANARFSERKNKEELNYLDKSLKVLQEQ

ILALNLSLNAANLAFESVDKKYQAGLVSYVEYLQALEVKFKAQSDLELAKNEFEITKANYYFNAGIDLNS

KVKE

>WP\_002851789.1 MULTISPECIES: tRNA threonylcarbamoyladenosine biosynthesis protein TsaB [Campylobacter]

MIGIYQDDKLIKTYKSEEKASEFLPKILDELLKEYDFTSLIYANGPGSYMGIKISYVSLSTLSIVKNIPL

FAVSAFELNGYKPISANKNFCFVYKEGEICLEQNIPAEFFLPKNLQELKLNNDNLPFYFLDAI

>WP\_002851697.1 MULTISPECIES: ParA family protein [Campylobacter]

MSEIITIANQKGGVGKTTTAVNLAASLAVAEKKVLLIDVDPQANATTGLGFNRNNYEYNIYHVFIGRKKL

SDIILKTELPQLHLAPSNIGLVGIEQELAKGENNEKKMLLKNQIQEVIDEYDFIIIDSPPALGSITINAF

AASDSVIIPIQCEFYALEGVAMVLNTIKIIKKTINSKLRVRGFLPTMYSSQNNLSKDVVDDLKQNFKKQL

FTINGNEDDFIVIPRNVKLAESPSFGKPIILYDIKSPGSVAYQNLAYSILG

>WP\_002831397.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MAYLKIKNFKKAYGDKIIFEDINFSAKKGEFITLLGPSGCGKSTLLRCIAGLSQINGGKISLNDKDLTKL

SPQKRNIGMVFQNYALFPNLNVFENIAFGLKIKKMDKKDIEKRVKKMLKLVELEEYAKTYPHKLSGGQMQ

RVALARSLVTKPDLLLLDEPLSALDAKIRKHLRVQIKEIQKELELTTIFVTHDQEEALELSDRIILMNKG

KIIQNSNANNLYLLPESHFVASFIGNYNILSPKELDNLGLKHDFKKDIALRPETIEISNEGLEAKIKEKS

LLGNIIRYRVRVQEIEFKVDTLNFSTHSTYEAGDKIALKFNLSLAKELK

>WP\_002826355.1 MULTISPECIES: chemotaxis protein CheW [Campylobacter]

MSNEKLEQILQKQQTQMAGPDVDQREDDIIQLVGFVVGDEEYAIPILNIQEIIKPIEYTRVPSVPDYVLG

VFNMRGNVMPLIDLAQRFHLGSSKMTPQTRYIVLRGETNGTGVGGNAGFVIDRLTEAIKIHRNRIDPPPE

TLVKDKGMIYGIGKRDENILTILKVEALLKREF

>WP\_002867063.1 molybdopterin molybdenumtransferase MoeA [Campylobacter jejuni]

MLMSYEESLKILHSHIKTYEKIEKIALTECLGRILAQDIKAPKNQPEFPTSAMDGYAIKFEDQDKPLKIL

GLTPAGTMPQFSVQNGTCVKTFTGSLMSEGSDTLVPVENVRVENDTLFIEKKVPQAFAVRAVGENYKKDE

ILLKKGTKLNYSEIALLAELGFFHISVFIKPIVGVLSSGSEIKDLGEALENPAQIRSSNHIAIANLAKNL

NCDTRVFPLLKDDEKATFSTLESALQSCDILITTGGVSMGDFDFLKKAVKEYEIIIDKADIKPGRHIKIA

KANEKFIIALPGFPYSAMVMFNLYAREILNSWLLQPKDYICKAFLQGSYKKKTPYLEFVACNVEFKNGRI

LANLEGKKEGSSAIINNLNNKAALMVVPKECEILENESLVDIIFMP

>WP\_002866703.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKLSLILACSASLFAASNSEISDFYSKSIKAQFPNATVSVSNRQKVGNTGFESVIVSVELNGQKQENIL

FTKDSLITPDLIDLKTGISYAQEYEMKKFQEARENFTKNAKAVAQKETMVIALGDKNKPAIYVFSDPECP

YCREHLAQIDDELKNYQVNYILTPVHGKSAFEKSALIYKEAKKAKNDKEKIAILNKYYDANIKNYPKVSD

TELKEVFSLYEKYRSLGLSATPTIIK

>WP\_002857514.1 MULTISPECIES: orotidine-5'-phosphate decarboxylase [Campylobacter]

MKLCVALDLSTKEECLQLAKELKNLDIWLKVGLRAYLRDGFKFIEELKKVDDFKIFLDLKIHDIPNTMAD

ACEEISKLGVDMINIHASAGKIAMQEVMTRLSKFSKRPLVLAVSALTSFDEENFFSIYRQKIEEAVINFS

KISYENGLDGMVCSVFESKIIKEHTQRNFLTLTPGIRPFGEKNDDQKRVANLTMARENLSDFIVVGRPIY

KDNNPRKICEKILQEI

>WP\_079254163.1 MULTISPECIES: selenide, water dikinase SelD [Campylobacter]

MQYKNQNLTHFVKAAGUAAKLSPGGLKTILNFMQKTPALLSDIGNNEDASVYQISPDLALVQTLDFITPI

VDSAYHFGAIAAANALSDVFAMGAEVINALNIVGFDTCNHDINILKELLEGANDKVQECNALVVGGHTIE

STELFFGLSVTGKVHPSKFIANNTAKVGDCIILTKPLGTGILSTALKAQMLNQKHLDIMLKSMMELNYKA

SQIALKFHPSAMSDVTGFGLLGHLKEMLNKNISFEIFESELPFLDGVKEYFNMGLIPAGAYKNLEFIKEL

IPDLNEEKLLLCDPQTSGGLLISISEKESLECLKKLEDENIQAKIIAKVVNKQENDIIIS

>WP\_074469321.1 MULTISPECIES: cell division protein FtsA [Campylobacter]

MILNILGIDLGSTQTCAIIAQKDEDGLKIIGFSKSKTNGVKKGAITNIELASKSIEEAVRSAEMMSGVHY

DKVVVSISGAYTKSVDSIGVVNIPNHEIGIKEIHRAVSTAKHTANLPSGYEIIHVLPYNFKVNDLEHVDD

PLGMSGNRLEVSTHIVISQESHIKNLKKAVELADLRVDNIVLSGYASAIACLDDSEKELGAVLIDMGGAI

CDMVVHTGNSIRYNDCLQIGSINITQDLSMALHTPLKEAEKIKLNYAALSQQPNTLIQIPSMGDERKVNE

VSLDIISNVIYARAEETLMILAKILSDNRYANAIGGGVVLTGGMTKLAGIDELAPATFDNRSVRLATARK

DLITGFSEIFNDPENTCAIGLCLYGAGYFTPYELDSNEKLRYKGEIENFNRQIKQDIVLQKDAESEIKSD

FFDENLQENDTIAIQEQLDFKEPKEKKPSVFSNIWHKIMNQF

>WP\_072238654.1 MULTISPECIES: hypothetical protein [Campylobacter]

MVIFCAALALLLFLGMIAYLITSDGKKTIKKQKTSQKQHVAEKTKKFDTDLDKMIIAASDVKLTDIELKE

LAKLYVQTHKLGSKTSKELDEATKKKLEFVSALAANINASAQTVSYLNKELKKISGSYKKEIDAYEHMGL

AKRKIKEDK

>WP\_072238616.1 MULTISPECIES: phosphate acetyltransferase [Campylobacter]

MMANLYLMRSRSDELNTIISTNLLKNYSKIYKNIAIYCPVIYIHRVPVLQGWLEEFNINQTVKSAYGFTF

REAMEEFSKDPHNFFNVILEEYEELKRKYDFVLVNSFCEFGILDGFDLSIKLAKNLNTPIAAIINDEDKL

IAQKYFDHALDGRNYVLINENFNFEEVQKLEEYDFITPHRFKYELIKQSVKNKKTVVLPESNDERILKAA

EILLKSKVVDLILLGDEEKIKQDAARLSLDLSTIQIMNPLNSEYNQEFTSILYEARKSKGMSLEEAKMLV

QDKTYFGTLLIHTGKADAMVSGASTTTAETIRPALQLIKTKEGISSVSGIFFMGLEDQVLAFADCAVNPS

PTAEQLATSAYVSAMTAKSFGLEPRIALLSYSSGDSGKGESVDLVKEALKIAKEKYPELNIDGPMQFDCA

YDPKTAAKKMPNSKIAGHANVYIFPDLNAANICYKAVQRTANALAIGPILQGLKKPVNDLSRGCLVDDIV

DTVILSAIQAQ

>WP\_022552263.1 MULTISPECIES: transcriptional regulator, putative [Campylobacter]

MLELSKAFFKTTPKNMKAIKVDGYSMVPMLLPDSWVVFEETHKYQGDGLYILNFDNQLMVKLLQLDPISK

VLDIISVNKDYKSYSLDLKDSQVELIIQGKVLRFII

>WP\_011812694.1 MULTISPECIES: hypothetical protein [Campylobacter]

MSMKKIILFLLCVGFAFACSEHSHTDFKDLNKTEYNSQ

>WP\_009881789.1 MULTISPECIES: 50S rRNA methyltransferase [Campylobacter]

MENNLQVNIFCIQKSDEFKTWSEKYSKLISKYATLKEINVFNKKIALAQNLNAIEAKKSYEEAFMPYKKG

YCIALDEKGKDLTSIEFAKLIQDKNELSFFIGGAYGLREEFNQSLDFRLSLSKLTLAHQFVKTLLLEQIY

RAFCINNNHPYHK

>WP\_002865962.1 MULTISPECIES: membrane protein insertion efficiency factor [Campylobacter]

MICLKILRFYQKFLSPLKPAACRYYPSCSEYALWQFQKKNFFLAFFSTFFRILRCNPFFKGGFDYPRVSK

NFYPMNLCFKPIFLAKKQLCFLYIPYKNKSFYLIKIIFKRTNQ

>WP\_002861483.1 MULTISPECIES: lytic transglycosylase [Campylobacter]

MIKKILVFLFIFSSLNATQYSIEKLKKEENSLAKDYYIYRLLEKNKISKKDAQDLNSHIFRYIGKIKSEL

EKIIPLKPYINPKYAKCYTYTANTILDANLTCQSVRLNSLVFIASLNSKDRTTLAQTFKNQRPDLTNLLL

AFNTSDPMSYIVQKEDINGFFKLYNYSKKYDLDLNTSLVNKLPNHIGFKDFAQNIIIKKENPKFRHSMLE

INPENVSEDSAFYLGVNALTYDKTELAYDFFKKAAQSFKSQSNKDNAIFWMWLIKNNEEDLKTLSQSSSL

NIYSLYAKELTNTPFPKIESLNPSKKKNNFNMQDPFAWQKINKQIRDANASQLDVLAKEFDTQETLPIYA

YILERKNNFKKHYFIMPYYDNIKDYNKTRQALILAIARQESRFIPTAISVSYALGMMQFMPFLANHIGEK

ELKIPNFDQDFMFKPEIAYYFGNYHLNYLESRLKSPLFVAYAYNGGIGFTNRMLARNDMFKTGKFEPFLS

MELVPYQESRIYGKKVLANYIVYRHLLNDSIKISDIFENLIQNKANDLNKS

>WP\_002860322.1 MULTISPECIES: tRNA cyclic N6-threonylcarbamoyladenosine(37) synthase TcdA [Campylobacter]

MMNDRFTRIKWLVGEEKFQKISQTKVLVCGLGGVGGICVDALYRSGFKNLTLIDADKFEITNQNRQIHSE

NIGEEKAKVFERIYKVKGIVSKIDENFLKNFDLSEFDLIIDAIDDIPAKVALAHLIDFKKQIFISSTGGA

RKLDPTRIKTTSIFKTHGDALAKKFRYELRKSGFKGNFDVVFSDEEAHCKDLGSFMGVTASFGLALASLA

LRKVLAKKS

>WP\_012006779.1 30S ribosomal protein S12 methylthiotransferase RimO [Campylobacter jejuni]

MSKLYLMSLGCNKNLVDSEIMLGRLSAYELCDEPSKADVLIVNTCGFIDSAKKESINAILDLHEQRKKDS

LLVVTGCLMQRYREELMKELPEVDLFTGVGDYERIDEMILKKTNLFSNSTYLQSENSKRIITGSNSHAFI

KIAEGCNQKCSFCAIPSFKGKLKSREISSIIAELKDLVARGYKDFSFIAQDTSSYLFDKGEKDGLIRLID

EVEKIKGIRAARILYLYPTSASEALIKRIIASEIFINYFDMPLQHISDNMLKIMKRGANSTRLKEMLNLM

KSAPNSFLRTGFIVGHPGESEADFEELCEFVKDFGFDRISVFAYSKEEDTAAFDMEQVPFKVINKRLKII

EKIVDEVIEKSFEKEVGQKRLVVCTGKSSEGEFFIAAKDLRWDREIDGEILINESECGNLEMGQIYECEI

LQNLDKKLLAKALRKVDAN

>WP\_002866901.1 flagella basal body P-ring formation protein FlgA [Campylobacter jejuni]

MKIIFLTFFIVINYIQAASLEEIKTALAKEFRNNFPKIIISQIDLKITSLPKDFDQYEFLRIANGRFNQA

QGFLRAEFKTPQNIQKNVFFRYFIQANLEVLKSERTIKRGDKLGAFDYKSVLIDFDKVPLNALTLDDVDN

LVAKSNINKNAILRANMFKTTALIRRNDPIIGVLSEANVDVLIELVALQSANMGERIRAKNKEGKVMQGI

VVGKNRMIIQ

>WP\_002799607.1 MULTISPECIES: translational GTPase TypA [Campylobacter]

MENIRNIAVIAHVDHGKTTMVDELLKQSGTFSEREQISERVMDSNDIEKERGITILSKNTAINYKGTKIN

IIDTPGHADFGGEVERVLKMIDGVLLLVDAQEGVMPQTKFVVKKALSLGLKPIVVINKIDKPAADPERVI

NEIFDLFVALDANDEQLDFAIVYAAAKNGYAKLDLNDESDNMEPLFKTILERVPAPSGTNDNPLQLQVFT

LGYDNFVGKIGIARIFNGVVKKNQSVMLAKADGTKVNGRISKLIGFMGLEKMDIEEAGSGDIVAIAGFEA

LDVGDSVVDPNNPMPLDPLHIEEPTLSIVFSVNDGPLAGTEGKHVTSNKIAERLEAEMKTNIAMKYESTG

EGKFKVSGRGELQITILAENMRREGFEFCMGRPEVIVKVEDGVKTEPFEHLVIDVPEEFSGAVIEKLGKR

KAEMKTMAPTGDGQTRLEFEIPARGLIGFRSQFLTDTKGEGVMNHSFLEFRPFSGAVEKRNNGALISMEN

GVALGYSLFNLQERGVLFIEPQTKVYTGMIIGEHSRPNDLDVNPIKGKNLTNVRASGSDDAIKLVPPRKL

SLERALEWIEEDELVEVTPVNVRVRKRYLDPTQRKRMEKAKS

>WP\_002867054.1 MULTISPECIES: sulfurtransferase-like selenium metabolism protein YedF [Campylobacter]

MKIDCRNLSCPQPIVETKNALEKLQENEILEIVLNSIISKNNVVKFLNSLNLNPIIDENAQEFCIKVQKK

NFNSSEVNIHDYNVLFLKTDKVGEGELGQNLLVGFLSTLKNLDHAPSKILCVNESVLINVDENHKAHLAM

KELENLGIEIISCGACLEFFNKSKELKIGNIGNAYEILNELFGKAKIITL

>WP\_022552433.1 formate dehydrogenase subunit alpha [Campylobacter jejuni]

MSSVGENIKLTRRSFLKMAALSSLATPLLARSETLREASADELKEAYEGSKKVKTVCTACSVGCGIIAEV

QNGVWVRQEIAQDHPVSSGGHCCKGSDMIDMVRSHVRLKYPMKKENGEWKRISYEQALSEIGEKLAAYRK

ENPESVMFLGSAKMSNEQAYYVRKFAAFFGTNNVDHQARIUHSATVAGVANTFGYGAMTNHLGDIQRSKC

IIIIGANPAVNHPVGFRHFLKAKEKGAKLIVVDPRFTKSAAKADIYARIRPGTDIAFMYGMLKIIFDEGL

EDTKYLDERVFGIDKIREEAAKWTAEEVENVTGISKELLVQITHEVAKNKPTTLIWAMGLTQHTVGTSNT

RLAPIVQMVLGNIGKFGGGVNILRGHDNVQGASDMACLSENLPGYYPLNEATWRYYAKIWGVDYEWLLGN

FVSKDWMHKTGLSLARWWAAALNGKDGNDAIDNAGTPLKALVVMGNGITSTAQQVKVKEGLEALELLVLA

DPFVNEAGIIAERKDGIYLLPAATQFETSGSVTATNRSGQWRFKVVDPLYESMEDQEILFELAKKLGFYE

DFTKTLRDEKGEIVWPENATREIAKAVRSIGLNGWSPERLKKHTLYWDKFDEVTLEGKDEVAGEYYGLPW

PCWSDKHPGSPVLYNTDIEVAKGGMGFRNNFGLEYEGESLLAKNAPLNSPIDTGYPQITKDNIEKVLGIT

LSAQEKEKMGSTWSYDDSNIIATKCIEKGIVPYGNAKARAVVWTFKDKIPLHREPLHSPRNDLVQKYPSF

EDQKALYRVDTKFVSVQQAKDYSKEFPLNLVTARLVNLNGAGMENRASMYLTRLTPEMFCEINPELAKEQ

DIKAGDMIWVHSPEGTKIHVRVKVNPGVAKDMIFLPFHFTGVMQGVDLTHNFPKGTKPYASGESANTVTN

YGYDIMCQIPETKGGLCRISKDGK

>WP\_002877135.1 MULTISPECIES: twin-arginine translocase TatA/TatE family subunit [Campylobacter]

MGGWSSPSHWLIILLIVVLLFGAKKIPELAKGLGKGIKTFKDEMNNDDEVAKNTQKIEENKNTTNNTSAD

ASIDKTKKA

>WP\_002866455.1 twin-arginine translocase subunit TatC [Campylobacter jejuni]

MFEELRPHLIELRKRLFISVACIVVMFIVCFALRSYILDILKAPLIAVLPEVAKHVNVIEVQEALFTAMK

VSFFAAFIFSLPVIFWQFWKFVAPGLYDNEKRLVVPFVSFASIMFALGACFCYFVVVPLAFKFLINFGLN

EDFNPVITIGTYVDFFTKVVVAFGLAFEMPVIAFFFAKIGLIDDSFLKRHFRIAILVIFVFSAFMTPPDV

LSQFLMAGPLCGLYGLSILIVQKVNPAPKDKESDE

>WP\_002855100.1 MULTISPECIES: twin-arginine translocase subunit TatB [Campylobacter]

MSFGEIIVILVVAILVLGPDKLPEAIVQIAKILKAVKRNIDDAKSSIEKEIRINDLKEEAKKYKDEFSST

NENIRKKLSFEEFDDLKRDILDKTKVDLTFDSRDDNTKNNLSGQNLNTEEKPNLSKLETQDKTEK

>WP\_011812746.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLEFPKNKVVFMEILDFILIVIFVFLMIVLVIGFNRQMMQKNKEREERFKKYKKGEQNE

>WP\_010891900.1 MULTISPECIES: hypothetical protein [Campylobacter]

MMMKIVFKGKSSEYEIQRSCFCVDAFVIKDKIEERDGVDFITSNVDLLEFSDDSFTFEEIVKHFNICDTE

DMIIVEDFDMKSNKDNQNQEDDIEHNILKSEKIIHENTKQTSMQFKNLKFFSRIFKNENFLSDFKESKQE

VVTIKKHEKLEIFKNLSQEDQEISFVKIEILNYDSNEDSLSFNLDIFPSGMSYKYGILKGSMHIILQGKT

SSTMLFPFLKSMIYKNKSENSSEKIFTLMINQKKHYKLIANLS

>WP\_002859753.1 MULTISPECIES: RNA polymerase sigma factor FliA [Campylobacter]

MNSKKDEEMLKEPPKAYAQMLKKEQDELVLSYMPALRAMAFRLKERLPSSIDVNDLISIGVEEMIKLSRR

YDKEQNDNFWGFARKRVNGSMLDYLRSLDVMSRNNRKIIKDIDAIMDEYFLEHECEPDDEYLAKKLDLDV

EKIKEVRTAHAISYTLPIDEQIELYNEDNTLEKIEKEELLEKIHEVLDDLKERDQLIIQLYYYEELSLKE

ISEILQISESRISQIHKKLLKKLRERLV

>WP\_002859649.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLEFTLNFNDYGLKMGILTKLELDYEIDDIEKFLQFFRTMCDRFEPLIIKLGSDSVRYKEAIKELETLAH

NTAWAARRLNLEEVTDFCVFCEEMMAQANRFNGPASDEFTDWMLLMSDQFEKYCRSYENDDSVLAVFNPL

IVNVPNIISK

>WP\_002859498.1 MULTISPECIES: hypothetical protein [Campylobacter]

MMAKFRIQYSAGFGHYTQNHKGFGPTIYIEEVVEFDNGKDYFDYIDFYKTYSKSDDTYFHISFLEDRPLS

DKEITIRNEYRKMRDENCKKAKEEFIANNELDVEHLPTHHD

>WP\_002859022.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKILKDLAMELKLARTLINEKPKNISLEKIEEAIEKEGQKFFYFDKDNTHKQLIALVNHFEKKGVSIYHR

TVKYGLDDNDFMYEVHIL

>WP\_002854628.1 MULTISPECIES: hypothetical protein [Campylobacter]

MMKSLILPPNEFLDHYILNAEFHRFAGISKNAYKFWKNVEIGRYQGTRIIFLHRNCILEKHQQALRQCSG

LNGFVLASAFCSFTGLAPSHLVEKNNSSIYKLLELKEICGIKFVNLKKFYDFLGLNYHQHIYIEKCHFFS

PAPFEKRIKITESMCVGYY

>WP\_002852636.1 MULTISPECIES: tRNA pseudouridine(38-40) synthase TruA [Campylobacter]

MMKIKIIFSYDGSAFLGSATQPHKKGVQDALSGALSHLGIFSPLLMASRTDKGVHASYAVASVECGDYFT

NLEYLQKQLNKFSHPFIHIKKIEKVKDDFEVRFDVKSREYRYIFSHASYSPFMASYVHFYPKFDLGKANE

LLGFFVGKKDLKFFCKSGGDNKTTLREIFIARAYAYKDFSIFHFKANGFLRGQIRLSVASVLKVLEGKMS

EKELKEQIEAKKQYNHFLAPPNGLYLSRICY

>WP\_002851307.1 MULTISPECIES: CcoQ/FixQ family Cbb3-type cytochrome c oxidase assembly chaperone [Campylobacter]

MEHLSIVFDVIKNLITFDLATVQKHEWEIFQGYGFFALVMFLSIVLYAYWYHLYRTEKKGERNYENYANL

ALKDDIDDSVLESKRSA

>WP\_079254164.1 methyl-accepting chemotaxis protein [Campylobacter jejuni]

MLKITKIKRKIMNSIKIKLSLIANLIAIFALIVLGIVSFYFTKTSLHESALKNQTDLLKVTQSTVEDFRS

TNQSFTRALEKDITNLPYQSLITEENIINNVGPILKYYRHSINALNVYLGLNNGKVLLSQKSNDAKMPEL

RDDLDIKTKDWYQEALKTNDIFVTPAYLDTNLKQYVITYSKAIYKDGKIIGVLGVDIPSEDLQNLVAKTP

GNTFLFDQKNKIFAATNKELLNPSIDHSPVLNAYKTHGDYNFFTYGLDGKERLGTCTKVFAYTACITESA

DIINKPIHKAAFIQAIVVIIVVVFSVILLYFIVSKYLSPLAAIQTGLTSFFDFINHKTKNVSTIEVKSND

EFGQISNAINENILATKRGLEQDNQAVKESVETVSVVESGNLTARITANPRNPQLIELKNVLNKLLDVLQ

ARVGSDMNAIHKIFEEYKSLDFRNKLENASGSVELTTNALGDEIVKMLKQSSDFANALANESGKLQTAVQ

SLTTSSNSQAQSLEETAAALEEITSSMQNVSVKTSDVITQSEEIKNVTGIIGDIADQINLLALNAAIEAA

RAGEHGRGFAVVADEVRKLAERTQKSLSEIEANTNLLVQSINDMAESIKEQTAGITQINESVAQIDQTTK

DNVEIANESAIISSTVSDIANNILEDVKKKRF

>WP\_079254162.1 endonuclease MutS2 [Campylobacter jejuni]

MMNDTKEELISKLDLNSYLEEFKALFARDKEIFLQGDSNLHFKRIHELCEVEFPTMPELSNLDKALVHLS

KQGILHLDEIFEFVKIFRYFEKLKKIKLGTNLDSWLQKIEFASGALELCLNFDEKGELKESLDERLVNLN

TALRLKNESIIAEFKKFCYTKALMPYLIDTQIHLINNLEALLVRGGFNHAIKAKIIGRSSGGGFYIVPLS

VENLQNDIEKIKNQKEEIYYEYAKNFSAFLAKNLPFLKFINTAFDLFDHYSARVLFAKKRDFEFVLCDQS

TDLVLKNFAHPALKNPKSVSLEFKKQVLIITGVNAGGKSMLLKSMLSAAFLAKHLLPMHIKASESKIGTF

KEFDAIIEDPQNVKNDISTFAGRMLHFSRLFSKKNLLLGIDEIELGTDFEEAACLYSVLISKLIANNLKI

IITTHHKRLAMLLAKNEQVELIAALYNEELSRPKYEFLKGTIGKSYAFETALRYQIPPNLVSEAKKLYGE

DKENLEELVGKNINLELELKAKLENVEKKEQKVDEILLSLKDQKEKNEQEFRTSLRNLEFKFHKAIEEAK

KTIQLKDTKDKQRSLNKANELKKEIILPSMEQNEELRVGDFVKYEKIKGKIISISKNDAMVESDGIKLRV

PLKLLKKSGAMPKKVAKTSISISKPSNLSVTLDLHGLRSDEAISRLDKFISDALLAGFDEVLVYHGIGTG

KLAFAVREFLKTHKSVKGFNDAPINQGGFGAKVVRL

>WP\_079254159.1 hypothetical protein [Campylobacter jejuni]

MFYTFFVILKQGEKMLKQIAFGGIALTATGYGIKKLYEKLSKPERKFDTHAIVPSCKDMINTEEYKLKRE

VEVEQKKNQIQEFLCECMECYSGFSKYFNSKEFLEFEQNFTSKNNHKTEFLLSSYKDQMIKVIDYAKKFE

CLSAFLETQSEKNDLAVVKMISESMERKTQRFYLQTKFQTFPQYIFPSVWSSPMWNKQWE

>WP\_079254158.1 proline--tRNA ligase [Campylobacter jejuni]

MMRFTKFYAPSLKEAPKDASLPSHIFLTRAGFIEQIGSGLYNFLPLGKRVLDKIKNIVKEEMDKAGAQEV

NLSFITPASLWQESGRYNVFGKELLRFKDRKENEFVLGPTHEEAMLSLVKNKITSYKQLPLHLYQIGLKF

RDEARPRFGLLRCREFLMKDGYSFHANEEDLGCEFELMYKTYSQILQRMGLDFRAVEADSGAIGGSGSKE

FMVLAKNGEDDILICENCDYAANVEAAKRAKKTCQDERPEANYASKFHTPNIKTIDSLAQFFKINAFYTI

KAVVKKAIYENESKLVVFFIRGSDDLQEIKAQNACSALELVDASEEELEKAGLVAGFIGFVGLKDIDFYI

DFELENEKQMIMGANEKDYHLIGIDVVNLNKDRFKDLIEVKEGDCCAKCGAKLKQSKGIEVGHIFKLGQK

YSKAMNANFLDENGKSQPFYMGCYGIGVSRLLAVAIEASHDEKGCIWNKTLAPFVLEIIVSNLKDEKALE

FANKLYEDLTNLGLEVLLDDRNERFGVKMNDFELMGFPYALVIGKGLENNEIELIQREGLVKELIKTDEL

MEILKKKVL

>WP\_002873309.1 MULTISPECIES: 2-iminoacetate synthase ThiH [Campylobacter]

MQDYMQYLPHMQEIKSEILNKVLTQVQSYDESQFSAKDVKNALNQTHLSIEHLKALLSSAAEDFIEELAF

KSAKVKQKYFGNSISLFTPLYLSNYCNSKCVYCGFQKGNKIARAKLSEAEIHEEMQAIAKSGLEEILMLT

GEGREFASVEYIANACKIAREYFKVVGVEIYPMNEDEYKILHEKGCDYVTVFQETYNALKYSKIHLAGEK

RIFPYRFNAQERALKAGMRGVAFGALLGIDDFRKDALATALHAHFLQQAYPHAEISISVPRLRPIINNAK

IHPKDVSEKRLLQVLCAYRLFLPFAGITISSRERIGFRDEVIKLGATKMSAGVSVGIGEHKGEKKGDEQF

EISDDRSVDEILAMLKRSNLQAVMSDSIYVG

>WP\_002866908.1 MULTISPECIES: periplasmic nitrate reductase subunit alpha [Campylobacter]

MNRRDFIKNTAIASAASVAGLSVPSSMLGAQEEDWKWDKAVCRFCGTGCGIMIARKDGKIVATKGDPAAP

VNRGLNCIKGYFNAKIMYGEDRLVMPLLRMNEKGEFDKKGKFQQVSWQRAFDEMEKQFKKAYNELGVTGI

GIFGSGQYTIQEGYAALKLAKAGFRTNNIDPNARHCMASAVVGFMQTFGVDEPSGCYDDIELTDTIITWG

ANMAEMHPILWSRVSDRKLSNLDKVKVVNLSTFSNRTSNIADIEIIFKPNTDLAIWNYIAREIVYNHPEA

MDMKFIKDHCVFATGYADIGYGMRNNPNHPKFKESEKDTVEKENVITLDDEEATSLSYLGVKAGDKFEMK

HQGVADKNWEISFEEFKKGLAPYTLEYTAKVAKGDDNESLEDFKKKLQELANLYIEKNRKVVSFWTMGFN

QHTRGSWVNEQAYMVHFLLGKQAKPGSGAFSLTGQPSACGTAREVGTFSHRLPADMVVANPKHREISEKI

WKVPAKTINPKPGSPYLNIMRDLEDGKIKFAWVQVNNPWQNTANANHWIAAAREMDNFIVVSDCYPGISA

KVADLILPSAMIYEKWGAYGNAERRTQHWKQQVLPVGAAMSDTWQILEFAKRFKLKEVWKEQKVDNKLTL

PSVLEEAKAMGYSEDDTLFDVLFANKEAKSFNPNDAIAKGFDNTDVKGDERKIQGSDGKEFAGYGFFVQK

YLWEEYRKFGLGHGHDLADFDTYHKVRGLRWPVVNGKETQWRFNTKFDYYAKKAAPNSDFAFYGDFNKML

TNGDLIAPKDEKEHSIKNKAKIFFRPFMKAPERPSKEYPFWLATGRVLEHWHSGTMTMRVPELYRAVPEA

LCYMSEKDGEKLGLNQGDLVWVESRRGKVKARVDMRGRNKPPVGLVYVPWFDENVYINKVTLDATCPLSK

QTDFKKCAVKIYKA

>WP\_012006731.1 protein translocase subunit SecD [Campylobacter jejuni]

MRNSKINYRLIIFIAVFIFGVAFSLPSFLQSERGAKINLGLDLQGGLYMLLGVDNEEAVKSKIKSIASSL

SYSFNKENILNDGLNTHDDILEFTLLDNADIAKVENLLKEIKGINIQSENMHYKISFTSEEVKNIENFAL

LQAVETIRNRLDQFGLAEPTVAKQGDDKILVELAGIKTKEDELRAKERITKAAHLQLMEVDDSKMGQAST

MSDAEAASYGLILVSDSRNPNLKYTLKSIPILDGSMLTDARVGISDKSNYPVINFTLNAEGSKKFADYTG

ANVGKRLAIVLDNKVYSAPSINERIGGGSGQISGAFTQEEARDVAVALRSGALLAPVKLLEQRSIGPSLG

ADSIKMSMIALIGASVFIVIFMMMYYGVVGIFANIAMLVNVLVVVAVMAMFGATLTLPGMAGLVLTVGMA

VDANVIINERIRELLRDGVNIRASIEQGYKNAMSAIIDSNITSLVTSVALYAYGTGAVKGFAVTLGIGIV

VSMITAILGTHGMFDYFMQRIEKSNNTRFWFGYRRR

>WP\_002857190.1 MULTISPECIES: 3-deoxy-7-phosphoheptulonate synthase class II [Campylobacter]

MWTKNSWKNYPIKQQPIYPDQEEMNRVLARLEKLPPLVFAGEVRNLQKSLARVCKKEAFLLQGGDCAESF

ENFGAVNIRDMFKILLQMAIVLTFAGGCPVVKIGRIAGQFAKPRSSDFEELNGISLPSYRGDIINGFEFS

EQARIPDPHRMLEAYYQSATTLNLLRGFAKGGLADLHEVHRWNLGFLKKSELHKQYTDISEKISQALAFM

EACGINTSNTPSLREVSVYTSHEALLLPYEEALTRVDSLSGEIYDCSAHMLWIGERTRALDEAHVHFLRG

VKNPLGVKIGPSASADDIIALANVLNPNNEEGRLNIIIRMGADKIINNLPKIFSKLKSEGLNLVYSIDPM

HGNTVKAGNFKTREFDKIMQEVRSFFEIAISEGVYPGGVHLEMTGKDVTECTGGASNVTAQSLEDRYETQ

CDPRLNADQALELAFLIADLVKKARK

>WP\_002853635.1 MULTISPECIES: protein translocase subunit SecF [Campylobacter]

MQFFSEKKIYDFMRMRFAAISLSFILFFGSIYLLWDRGLQYGIDFSGGTLVQLKYENAAPITQIREILEK

QGTFQNLSVTEFGSNEEVTIRFLGSNDNVSNDIGEHISTLLKDTGKFEVRRADVVGPKVGDELRNKGLMA

IAVSLIAILIYIALRFEWRFALAAIISEIHDVVITLGAISLFKIDVNLDTLAAVLTVLGYSLNDTIIIFD

RIREGIKTSKKTELAPIINESVSATLSRTVLTSGLTLATVVILYFFGGEMIQGFSLALIVGIIAGTLSSI

FVASPTLLWFKFSVLEFRNKEIEKAKRKQDKERNRAMYEKGTV

>WP\_002854405.1 MULTISPECIES: N utilization substance protein B [Campylobacter]

MATRHQVRQSVISLLYAFELNSQNNVFVDEILDEKKIRNEQKNFTLNLYHGILDNLNNIDETLNSFLNDN

QITALGHVERAILRLGAYELLFTDTPSAIVINEAIELAKELANDNSPKFINGVLDALIKAKK

>WP\_002873362.1 MULTISPECIES: YajQ family cyclic di-GMP-binding protein [Campylobacter]

MASEHSFDISAALDKQELKNAFEQAKKELDSRYDLKGIKCEIDLSEKESIFKLSSSSEGKLDVLKDIVIS

KLIKRGINPNAIKELSRESGAMFRLNLKANDAIDSENAKKINKAIKDSKLKVNSSIRGEEIRVAAKQIDD

LQAVMKLVKELDLELNISFKNLK

>WP\_002866386.1 MULTISPECIES: MFS transporter [Campylobacter]

MSKTLNQKDIKVLGLSSLGGTLEFYDFIIFVFFANYISTNFFPKDLSSFWQMFNTYGIFAAGYLARPLGG

VILAHFGDKFGRKRMFMISILLMVIPTFTLAFIPNYESIGFLCIVLLVFIRICQGIAIGGELPGAWVFVY

EHAPQGQKRTYLGILTASVVGGILLGSLVFLIMNKIYTQEELHEWAWRIPFFLGGIFGIISAYLRKFLRE

TPVFEQMKKDKALEKFPLKEVFKKAKMGIVLSMMITWVLTGCIVVMILLMPSYMAKILQINTSIQTYLQI

GGILLICLGCIISGILADKIGIIKSCVFFSVFFGIVSLLYFNTLYRQNADFNLVACLYLLVCFFSGVMNF

CPLIMSEVFDAKIKFSGLSFSYNIAYAIAGGLTPQLAFFLHSFALDNLSNFWRFSLGIYVFFLAIIALLC

AFIFSYLNNTQRTYSQ

>WP\_072238648.1 UDP-N-acetylmuramate--L-alanine ligase [Campylobacter jejuni]

MMQNIHFIGIGGIGISALARFLKEKGFKISGSDLKESKITKELEKEGVKVSIPHHKDNILNKDLVIYSAA

IKEENPEFKHAKELGIKCLSRKEALPLILEDKRVFAVAGAHGKSTTSSILASLLDDASVIIGAILKEFGS

NMIYKESQNLVFEADESDSSFLNSNPYLAIVTNAEAEHLDHYGNEVSKLHHAYTQFLDVAKIRVINAEDE

FLKNYKNESIKLYPSKDIKNCTMCIENFKPFTSFELKDLGEFKVFGMGYHLALDASLAILAALNFLDIET

IRTRLKNYQGIKKRFDILHADENLVLIDDYGHHPTEIKATLSAAQEYAKLGGYKKITAIFEPHRYTRLAA

NLKEFAKAFEGVDELVILPVYAAGEEPIELDLKAVFPKALFVEDIKREGKFLVASKGQVFEEGLIIGFGA

GDISNKLRQKNE

>WP\_072238646.1 bifunctional folylpolyglutamate synthase/dihydrofolate synthase [Campylobacter jejuni]

MQRLMNNIMKVENFLAQKSINYDKIDRFLMFRMYEKYKKYFKNIPIIQLIGTNGKGSTGRYLTQLLENLN

YKIGHYTSPHIFSFNERFYLDGKIANDEELEQAHIRLEEIFKQDLQKLSYFEYATFLAMILFQKCDFIVL

EAGVGGEYDATSVFERRMNIFTRIGFDHIQILGNSLEDIARTKLKVMAPVALISDEQEQNVLNLAKKIAF

LKKANLQVSSLNPFLKEKFEIYCKKFVLPCFLKHNLKLALKACEILTSQEKTLEALKKLQGLNLQGRCQE

ISPNFFVDVGHNPMAAKAMLDKFQGEKINLIYNAYLDKDIFQILNTLKPIIDTIQIYKYKSAERKLADDE

IYSIASKLGIQCKEFVKLEENKKNLVFGSFMLVENFLKEWCGKK

>WP\_002856927.1 MULTISPECIES: Holliday junction branch migration protein RuvA [Campylobacter]

MVVGIEGIITKKEPTFIIVKCASGLSYGIFISLFCSAKIQTQEKHEFFITQIIKEDSNKFYGFLDKDEQK

MFEMLLKVNGVGANTAMAVCSSLDVNSFYKALSLGDESVLKKVPGIGPKSAKRIIVELSDTKTKLENVSD

DKSEALAALLTLGFKQEKIISVLASAQATGTSELIKEALKKLG

>WP\_002852281.1 MULTISPECIES: Holliday junction resolvase RuvX [Campylobacter]

MRALALDVGLKRIGVALCIDKKIALPLDAVLRKNRNQAANEIKNLLKIHEISLLIVGIPKGGSSEEEMTR

RIKHFVSLLEFDKEICFVDESGTSKEALGYGVANTRKKDGKLDSLSAFIMIKDYFAL

>WP\_012006769.1 UDP-N-acetylglucosamine 2-epimerase (hydrolyzing) [Campylobacter jejuni]

MKKILFITGTRADYSKIKSLMYRVQNSSEFELCIFATGMHLSKNFGYTVKELYKNGFKNIYEFINYDKYY

QTDKALATTIDGFSRYVNELKPDLIVVHGDRIEPLAAAIVGALNNILVAHIEGGEISGTIDDSLRHAISK

LAHIHLVNDEFAKKRLMQLGEDEKSIFIIGSPDLELLNDNKISLNEAKKYYDINYENYALLMFHPVTTEI

TSIKNQADNLVKALIQSNKNYIVIYPNNDLGFELILQSYEELKNNPRFKLFPSLRFEYFITLLKNADFII

GNSSCILKEALYLKTAGILVGSRQNGRLGNENTLKVNANSDEILKAINTIHKKQDLFSAKLEILDSSKLF

FEYLQSGEFFKLSTQKVFKDIII

>WP\_002866219.1 riboflavin synthase [Campylobacter jejuni]

MFNGLIREIAKVQSYQNNTLSLKAKYRPNLGDSIAINGACLSVTKLYEGGFEVELSRESRTHIAIENLKD

KVHIEPALRYGDRIDGHLMQGHIDFIGTLEKIQKDENGVDFYISLPKEAMKFMAEKGSIAVDGVSLTINE

ILKNGIRLTIIPITFKETLFKDYQVGRKINIESDLLARYIYAQLQGKNKGLSWEEVERISYLY

>WP\_002860160.1 MULTISPECIES: thymidylate synthase (FAD) [Campylobacter]

MQITLLFHTPLSVCSHATRTCWQSFEKGDCGGEKDKELIDRVGNKFKHASTLEHLNYTFYIQGISRACLQ

EVARHRHTSPSVKSTRYTLKELRNEGEFKIGDFENASRYLVLCGNEEVDNASIKALENLRTILQKSISLD

IAKYCLPESYKTELTLTINARSLQNFISLRSSKSALWEIRNLANALFEALPQEHKFIFEHCLHKDIE

>WP\_002867006.1 UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase [Campylobacter jejuni]

MKISLFGYGKTTRAIAENLVDKFGPFDIYDDHFTETKKDTLGNLLLNPNDFDDNLSDIEIPSPGFPPKHK

LIQKAKNLQSEYDFFYDIMPKSVWISGTNGKTTTTQMATHLLSHIGAVIGGNVGTPLAELDPYAKLWILE

TSSFTLHYTHKAKPEIYALLPISPDHLSWHGSFDNYVQDKLSVLKRMNECDVVILPKIYANTPTKAHKIS

YKDEKDLAVKFGIDTEKISFKSPFLLDAIMALAIEKILLDTLSYELLNSFVMEKNKLEELKDSQNRLWVN

DTKATNESAVMAALNRYKDKKIHLIIGGDDKGVDLSNLFDFMKNFNIELYAIGISTEKMLDYAKKANLKA

YKCEVLSKAVNEISNHLRVNEVALLSPACASLDQFNSYVERGKVFKECVNKI

>WP\_002853622.1 MULTISPECIES: ABC transporter permease [Campylobacter]

MKFFKTHLSLILPLLFMMFAFEFILITNATLKHYEELVNKDYNIIVVSKTELDQNVVKTKVPFFAGLESL

DPKDLIDRLKNDVSEKNLKVLKDSLPKFYTLKLNSLPDQNELNSIKNQLLNIVGVSKVETFSKTHDKIYS

LLILMKFVFWLFLFIIILLAFVLFLKQMRIWLYEHTDRIEIMCLFGAPFWFRSFMLYKVVVVDCFIAFVI

LLAFFTQIFDLSIIQESLKAVDIIFPPINFILHLTLIFLATLFICLLCVNTVMFKVKR

>WP\_012006758.1 NCS2 family permease [Campylobacter jejuni]

MDFFKLKENNTSFKTEVIAGLTTFLAMVYIIPVNSSIVGNTGMPIEALITATALITIVASAFNAFFANTP

VAMSVGMGLNAYFTFAVCLGQKIPWQSALGAVFISSIIFLLLSFTHFRLWVIRNIPKDLRLAICAGIGCF

IAFLGLSQMGVIMHNKDTLVSIGNFKSPHMLFGIFTLALIIFFWAIKLRGAFIFGVLASSIIAWIFHLDN

ASFPVQIFSLPNFSMENGLGAIFLQLDIKSALNITMIPIILTFFITQLFDSIGTITGVGERGKIFDDPKN

GEKKLSKTLMADATGSALGAMTGTSTVTAFVESTTGVESGGRTGLTALVVAICFAFTLFLLPLFKAIPAN

AIYPVLVMVGILMFMEVKNIDFKDSAIAVASFFTIIMMPFTYSITTGFAFGFLSYLLVRIFKREWDKINL

GIIVLSLLSLGNFLLMALQ

>WP\_002866495.1 MULTISPECIES: DNA-processing protein DprA [Campylobacter]

MASEILPDEFLELFKDLKKPPKKLHYKGNLSLLKQDKIAIIGSRRMSVYTKNCVFSLASMLKNAHLCVVS

GGALGVDITASMAAMPNTIGIFANGLDQIYPRTNEKIIKQIYENALALSEYEDDYLPKNYDFLLRNRLVI

ALSKAVVVAQADIKSGSMQSAKLALELNKPLYVLPQRLGESTGTNLLLKENKAKLICDFKEFVSEFASID

INQDEFLEFCKKGVSVDEALKIYGQKVYEYELEGKISIEGLFIRVLA

>WP\_002857401.1 MULTISPECIES: N-acetyltransferase [Campylobacter]

MLIRAMQKSDYEAVYKLWCEIKGFGIRSIDDSKENIENFLDRNPDLSVVAVLGEEIVGSILCGHDGRTGG

FYHVCVHKDHRKKGIAHEMTKFCLEALKAQKINKIALIAFKNNDLGNEFWKHYGFTLREDANYYDLSLNE

YNQTSFNA

>WP\_002853673.1 MULTISPECIES: histidine phosphatase family protein [Campylobacter]

MKKIYIIRHAKASKSGDIDDFERKLTKSGKEDLKKLFKNLALHEIHPDLVLSSPAVRTAKTAKKIAKFYN

FDKNKICFDERLYLCNVENLLKILQDIDDEFNEVFLVGHNPGLMELGELLSSLCLASFPTSSILCLEFDI

KEFKNLKKHSGKLVFFEHVRKLKEEKDLGF

>WP\_002779137.1 MULTISPECIES: RidA family protein [Campylobacter]

MSNYPKAIGPYSAYREANGLLFISGQLPINPASGEIESSDIKEQTKQSLKNIGAILEENGISYDKVIKTT

CFLADINDFVAFNEIYAEFFKAPYPARSAFAVKDLPKKAKVEIEIIAQKG

>WP\_002778525.1 MULTISPECIES: MerR family transcriptional regulator [Campylobacter]

MAYTIKKVEKETKISAHTLRFWAKKGLFPFVQKDENSVKYFSKSDIEWAKWIEWLRISGMPIEQVKHYIK

LCSLGIKTAKERQEMLKQTKKKLQNQIKTLKESEKVLSKKIKIYEEMLANEVDGFNPESKDYQPCDKFCK

ES

>WP\_012006736.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MELLRAENLSHSFDYPLFEGLNLALNTKDCIAIQGSSGCGKSTLLHIFSSLLIPKKGEVFFKGSSLYQID

ENERLKIRRYDFGIIFQTHYLFKGFSALENIELASVLSGQNLDEKILKRLGIDTLLHQKIGKLSGGQQQR

VSIARVLCKKPKIIFADEATGNLDFDNAKNVIELLISYVKENDAALFFVTHDNKLASFCDKTYTINANGI

C

>WP\_012006694.1 MULTISPECIES: flagellar hook-associated protein FlgL [Campylobacter]

MRITNKLNFTNSVNNSMGGQSALYQISQQLASGLKIQNSYEDASTYIDNTRLEYEIKTLEQVKESTSRAQ

EMTQNSMKALQDMVKLLEDFKVKVTQAASDSNSQTSREAIAKELERIKESIVQLANTSVNGQYLFAGSQV

ANKPFDSNGNYYGDKNNINVVTGAGTESPYNIPGWDLFFKADGDYKKQISTNVSFTDNRWDLNKDPDKTK

YLTGDSKWQQLIGQGYVKDNGLDPDKDFEYDDKLDFPPTTLYVQGTKPDGTSFKSAVLVKPEDTLEDVME

NIGALYGNTPNNKVVEVSMNDSGQIQITDLKQGNNKLDFHAVAFTPQADDRAELTGIIDAAKQEGISMDE

VTNRVMQAATAAPSNGDITKLNSPVTVTINNQQFTIDLKQTDFIKSKMTDTDGNATNGADYDNVYFEKNG

NTVYGNVSQVIKGSNAYATDSTKLSEVMAGDSLNGTTLNLKVNSKGGNSYDVTINLQTSTVSYPDPNNPG

QTISFPITHTDPATGNSGVVTGSNDITYGQINDIIGMFAADKIPTQSITATNGKVDANGYNNLQQLMKDS

QATVDVSMDYKGRISVTDKLSSGTNIEISLSDSQSGHFPQPPFSTTSSVTNGPNFSFSANNSLVIDEPNV

DIIKDLDSMIDAVLKGNMRADSESEDPRNTGMQGALERLDHLADHISKLNTTMGAYHNTIEDVNTRSTFL

SVNVQSIKSNVIDVDYGEAMMNLMQVQLAYQASLKASTTISQLSLLNYM

>WP\_009881977.1 MULTISPECIES: cytochrome c [Campylobacter]

MKKIFISFVVLATCLWAKNIAYTDEVVSLYLNKDDTKVIGRLLPTNPFEVLKSENNKVLLKIDGYVNPKA

LSVIYFNDSQRIIVAAFSKNTKLNFSQRVAGKDGKWDKVSLEIWADKKEFAKDNKEMLNRAKELFVNNCG

ICHAIHKEKEFTANAWPAIFRSMADRTGIDKKDRWLVIEYLQKNAKDFKTK

>WP\_002932912.1 MULTISPECIES: hypothetical protein [Campylobacter]

MRIKFISFILIFFTIFAFAKEQNLDDFEQEYQNYQVNDPLSGYNKAMTSFNVALYDYGLRPVLKGYNAIT

PEFIRLGARNFFDNLLAPLRFVGNVLQFKFEEAGEEFKRFTANTIMGFGGLMDVASKMGLKKHPADLGTV

LAHWGVGSGFHIVLPILGPSNLRDTLTLPATWYASFTAYIDPTWASIAISAYGFGNELSFRLDEIDEIYH

NTPNLYPFLRDAYEQRRNELSK

>WP\_002878020.1 MULTISPECIES: threonine synthase [Campylobacter]

MKLVESRNVKNVSSFKEALINPNAPEGGLYSPLNLPIFEGEKYANLSYKDFALKLIESFGFGEEELFKKA

LKSYESFDDKNTPISLQKISEKTYINELWHGPTRAFKDMALQPFGVLLSEFSKDKNILIICATSGDTGPA

TLKSFENAKNVKVACMYPKGGTSGVQELQMRALDKDNLKVFAIDEDFDAAQRTLKELLFSKDFQNEIKAL

NYELCAANSVNFGRILFQIIYHYYASLKLFNEFLEEVQIIVPSGNFGNALGAFYAKKMGAKISKIKIASN

ANNILSEFFNQGVYDLREKSLKKTISPAMDILISSNIERLLFAKFKDKRTKELMNLLKNERYFKLEKEEL

QSLQEDFEADFCTDEECMQFIKQSKILIDPHTATCFKMLDPLKPSIITSTAEWTKFTPSMIKALYDRDSK

NEKEDLKFIAKEFNVQVKDEILTLFDLKNSDEKVFEARNIKKEILDWMQK

>WP\_002877495.1 MULTISPECIES: lipoprotein signal peptidase [Campylobacter]

MAKTFKFIFYFWGAFVLVFVLDQWVKSLTLAGLRWQSEYLDLTYALNTGVAFSMLSFLEHNLKYLHLALI

VVLFIYLFWQKTLLKTHSIAFGMMLGAGVSNLLDRFIHGGVVDMFFWHKWFNFAIFNVADVMINISVALI

LIQEIFKKRKKDDRMD

>WP\_002877447.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLETKKSFWPYGILLSLLAIIIACIVTIFIASHHPVYEDDFYFDSYQNVENNYNQIQKQQVNFDKFFKVN

FQNDKITFIGKRKIPSYEVDQNSYVANFKISALQNINSDDLKVQALLTRPFTKNFDQKLEGQVKNGILSI

ALPKLDKGRWELKLKFYANQETVGFFSYELNAQ

>WP\_002877436.1 MULTISPECIES: pyruvate:ferredoxin (flavodoxin) oxidoreductase [Campylobacter]

MGKIMKTMDGNEAAAYAAYAFTEVAGIYPITPSSPMADYTDMWAAAGKKNLFGVPVKIVEMQSEAGAAGS

VHGSLQAGALTTTYTASQGLLLKIPNMYKIAGQLLPCVIHVAARSLAAQALSIFGDHQDIYAARQIGFAM

LCSHSVQETMDLAGVAHLAAIKGRVPFLHFFDGFRTSHEIQKVEVMDYAHFDRLLDREALLEFRNNALNP

ENPKTRGTAQNDDIYFQTREVSNRFYDALPDVVNEYMQEISKITGREYKPFTYYGHKEPERVIVAMGSVT

QALEEVVDYLNAKGEKVGILKVYLYRPFSLKYFFDVMPKSVKKIAVLDRTKEPGSLGEPLYLDVKSAFYG

RENAPVIVGGRYGLSSKDVDPAQMIAVFENLKLDNPKDGFTVGIVDDVTHTSLSTGEKISLGDESTIECL

FYGLGADGTVGANKNSIKIIGDKTDFYAQAYFAYDSKKSGGYTRSHLRFSKKPIRSTYLVSTPHFIACSV

AAYLEIYDVLAGIRKGGTFLLNSIWNAEETIRQLPDAVKKTLAEKEVNFYIINATKLARDIGLGNRTNTI

MQSAFFKLAKIIPYEDAQKYMKELAYKSYSKKGDAIVEMNYKAIDVGADGLVKVEVDPNWKNLELKEKEQ

TNAYKGTEFVEKIVKPMNAAKGDDLPVSAFLGYEDGSFEHGTTEYEKRGVGVMVPRWIEANCIQCNQCAS

VCPHAVIRPFLINDEEMANAPRGVKDHALEAKGTKGEKLSFKIQVSPLDCTGCELCVHECPTKEKSLVMV

PLQEEMDFGEQENADYLFKEITYKDDILNKETTKGAQFAQPLFEFHGACPGCGETPYITLITRLFGERMI

VANATGCSSIYGGSAPSTPYRKSVKNGHGPAWGNSLFEDNAEFGLGMKIATENTRHRIEHIMNESMQEVP

NALSALFKDWIANKDNGAMSVEIKDKMIPILEQNKNIKAVQDILELKQYLSKKSHWIFGGDGWAYDIGYG

GLDHVLASGENVNILVLDTEVYSNTGGQSSKSSRTGAVAQFAAAGKPIQKKDLGQIAMTYGYIFVAQVNS

TANYTHLIKAITAAEAYDGPSLVICYSPCIAHGIKGGLGYSGEQGELATKCGYWPLYTFDPRLEEQGKNP

LTLTGKEPDWDLYEQFLMNEVRYNSLKKANPEHAAELFERNKKDAQRRYRQLKRIAMADYSNEVES

>WP\_002877171.1 MULTISPECIES: hypothetical protein [Campylobacter]

MSMINSTLPIQMKVLAKSGYGHYTLLLNHKKIQTKSMIELEIGAEYLAELYMQNGGVIQFKHLSKRPNFK

PFEEGLALIIAILEDKISYKKFIIQNLLDCKDIERYQILKEMLFASFENIYHIPFIFENKSCLFQMRKRA

KYLEIYLYFSVFGALKILIDSQGISVFTPFAKVQKFLNEHLDFNVSQENKIEPLFVFKRLFDFKG

>WP\_002876956.1 MULTISPECIES: acetate kinase [Campylobacter]

MKILVLNSGSSSIKFKFFDNKVVKASGLVEKIGEQNSKVILKNVLNNESFERELMINNHEEGLSIVNELF

KESGILADLNALDGCGHRIVHGGRNLSEHCLVDDYVLKEIDRVSIFAPLHNPAHLAGIKTMIKAAPSVAN

VAIFDTAFHRTMPDFAYMYALPYDFYDKHNIRRYGFHGTSHAFVSSRAASLLEKDKSELNVISAHLGNGA

SVCAIEKGKSVDTSMGFTPLEGLVMGTRCGDLDPAILPFISHLKGLTIEEIDTLMNKKSGVYGICGYNDF

RDIEREIEQGNDKARLALDMFCYRLVKYIGSYFAVLPKTDAIIFTGGIGENDSLVRQKVCERLAHLGIEL

DFELNKQRISGERMINHANSKVKVLVIPTDEELEIARITEELISN

>WP\_002873265.1 MULTISPECIES: DNA polymerase III subunit beta [Campylobacter]

MKLSINKNTLESAVILCNAYVEKKDSSTITSHLFFHADEDKLLIKASDYEIGINYKIKKIRVESSGFATA

NAKSIADVIKSLNNEEVVLETIDNFLFIRQKSTKYKLPMFNHEDFPNFPNTEGKNQFDIDSSDLSRSLKK

ILPSIDTNNPKYSLNGAFLDIKTDKINFVGTDTKRLAIYTLEKANNQEFSFSIPKKAIMEMQKLFYEKIE

IFYDQNMLIAKNENFEFFTKLINDKFPDYEKVIPKTFKQELSFSTEDFIDSLKKISVVTEKMKLHFNKDK

IIFEGISLDNMEAKTELEIQTGVSEEFNLTIKIKYLLDFLTSIEEEKFTLSVNEPNSAFIVKSQGLSMII

MPMIL

>WP\_002870481.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKFKVKNVNCMNCVNLIKNSLEDEFGNIEVDLEQKILSLNLEENQVSNFTKEFQDLGFEIIERL

>WP\_002869613.1 MULTISPECIES: hypothetical protein [Campylobacter]

MNNFVLYSLYFIYSAFFLNKHRRIIKGKILHQKEHENIANYLENAYIKKYFENKLDDIQIKKTRNINGKK

IIWQFWYQGIDNAPCIIKKCFKSVQKYKGNYEVVLLDKDNIKDYLIFPDFIYQKIDDKKFGEKTITIFSD

LLRVSLLNNYGGIWLDAGMFLSGEIQKEILDQDFFIFHRSTKKPQDYKNWINFNYNFFSWDEKFKVNIVN

GFILSNKNNEIMKIMQDILINYWKYENKLVYYFMFQILFDTLKKKYLNLNLYITNDTDIHLLQYHAKDKY

SDKLWNDIKNKTSIHSLKIFKKIRKHSMIDKILFKDTI

>WP\_002869155.1 MULTISPECIES: dihydroorotase [Campylobacter]

MILKNPLDMHLHLRDNQMLELIAPLSVRDFCAAVIMPNLIPPLCNLEDLKAYKMRILKACKDENFTPLMT

LFFKNYDEKFLYSAKDEIFGIKLYPVGITTNSNGGVSSFDIEYLKPTLEAMSDLNIPLLVHGETNDFVMD

RESNFAKIYEKLAKHFPRLKIVMEHITTKTLCELLKDYENLYATITLHHLIITLDDVIGGKMNPHLFCKP

IAKRYEDKEALCELAFSGYEKVMFGSDSAPHPRDTKECCGCAAGIFSAPVILPVLAELFKQNSSEENLQK

FLSDNACKIYDLKFKEDKILTLEEKEWQVPNVYEDKYNQVVPYMAGEILKFQLKH

>WP\_002869049.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKAYVLIWTIFLILLISLWMSLTLNISSYTPKIIQDSYYYLQAQILSHNATQFSKYFLYQAKQENKECL

DNIYFNYAKALIKIKYFYPIAQCVNFKFSNFNPDANLNKDGVIIAHISIALNRDKNVNDEILLTKSIIIY

PKENFWNLKN

>WP\_002868731.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLVHICCSVDSHYFIEELRKTYPDEKIIGYFYDPNIHPLSEYELRFLDVKRSCDKLGIKLYKGEYEYEKW

LNAVRGYEDEPEKGARCEICFDVRMGSSVKFAAKIGEKKLTTTLLTSPKKDLEQLKNALQKECEPYGVEF

LAPDFRKNGGTQRQFALAKKEMLYHQNYCGCIYGLKKQKQDKNFIDELMSSVNKQILPASIEARIALYKK

VVLWEKKGIKFEILREKFLNYRLLSALIKLDKKPVKSHILFYSHFKNAYTRFSLDEESLKQNLKEGFYRS

TKDEMVFVEFWRFNAFFKNKWKNFEDFLKKPLSIQAEVRWRNQVFGAYNLSPVIILEEIFPSRYEVIAKS

EIYHDNQEVLAKI

>WP\_002868630.1 MULTISPECIES: hypothetical protein [Campylobacter]

MAIFNKGGISPTSSSSSETTVISSGARIEGKFYFASMLHVDGELSGIIHSESIVVIGKNGNLKGELQADK

IVVNGYFEGQLEANSLEILAGGVVNGDISTQKISIENGGRFNGTSKIKEDTIKLIENNNEE

>WP\_002867737.1 MULTISPECIES: lipid-A-disaccharide synthase [Campylobacter]

MKTFLVCALEPSANLHLKEVLKAYKKDFGEFELHGIYDESLCKEFDLNSKPLYSSHEFSAMGFIEVLPLI

FKAKKAIKELVNLTLSQTMDAVLCIDSPAFNIPFAKALKKAGSKIPRIYYILPQVWAWKKGRIPIIESHF

DILASILPFDNQFFNKSTYIGHPLLDEIKEFKNQEDINHTFSKKDDEKTIAFLPGSRRSEIRRLMPIFKE

LSQKFKGEKILCVPSFNLEKLEVYGDISEFKIESNTPKVLKKADFAFICSGTATLEAALVGTPFVLAYKA

KAIDIFIAKLFVKLKHIGLANIFCDFAGKEALNPEFLQDKVNVLNLYEAYNKYDYKAFFAKVDFLKEYLQ

FGSAKNLAKILNEI

>WP\_002867455.1 MULTISPECIES: hypothetical protein [Campylobacter]

MIRNFFIGMSFLGILFLAFYALYDKKKESVFSLNTCQPLTCDLNLQDCVFSFNKKNIEVSAYPKPIKIFN

KTTIKIKNFPHYSNLKIKIYSLNSYIGDIIPKFNIVNGDILINFIGRSITDDSRFRVEFLNNNAPTGFFF

DFDVTMQKNFQTGNTH

>WP\_002867086.1 MULTISPECIES: transcriptional regulator [Campylobacter]

MTKENSQCNFEECGFNYTLALINGKYKMSILYCLFRYEIVRYNELKRFLSSISFKTLTNTLRELENDGLI

IRKEYAQIPPKVEYSLSKRGQSLIPILQAMCKWGEKDKKEKNA

>WP\_002867077.1 MULTISPECIES: glucose-6-phosphate isomerase [Campylobacter]

MLNNTLFFKQSEIHTISSYANRINDEVKSGDIGYYHLIDTSLSLIDESLAFIKDKEHIKNIVLVGMGGSS

CGVKALRDMLFNEKSNQRELFILDNTSSHSFNKTLEKIKLEESLFLIISKTGSTIEVVSLFKLLIEHFKL

DMQELKKYFVFITDKDSKLHQEGENLGIKCFFIPANVGGRFSILSAVGIVPLCFCGYNAKALLEGAKACF

EDFFTHKKDEILQKAYHYCTHKNANINVLFSYSDAFKGFNEWYIQLIAESLGKKQGYKRIGLTPIALIGA

RDQHSFLQLIMDGPKNKTVTFLKIKDAQKAPIIPDIHFKFLDSLSNKVNLHELLNAQCDATMHALIAENL

SVDVIELEKLDAWHAGYLMYYYELFTSTCGVMLGINTYDQPGVEVGKLILKNILNS

>WP\_002867071.1 MULTISPECIES: dephospho-CoA kinase [Campylobacter]

MKNAFFVTASIACGKSTFIEIANSLGFKSISADKIAHEILDENALELEKIFSPFSLKNLLTKEKKIDRKI

LGEIVFNNKEAKKILENFTHPKIRAKILEQMQILDKENKAFFVEIPLFFESGAYENLGKVIVIYTPKELS

LKRIMQRDKLSLEAAKARLDSQIDIEEKLKKADFIIKNTNSYADFRQECVKVIQEISKGKM

>WP\_002867022.1 MULTISPECIES: peptide chain release factor 2 [Campylobacter]

MDNYEFSELLKTLKNKVGNIASIIKPENIQTRLKEIEELENSPSFWSDVKQAGIIGKEKTKITNLLKNYE

NAFNALNDASELFDLANSENDTETLEALFNDAPKLEDTITSLEISMLLSGENDGKNAIVSIHPGAGGTES

NDWASILYRMYLRFCEREGFKVETLDFQEGEEAGLKDVSFLVKGENAYGYLKAENGIHRLVRTSPFDSAG

RRHTSFSSVMVSPELDDDIEIEIEEKDIRIDYYRASGAGGQHVNKTESAVRITHFPTGIVVQCQNDRSQH

KNKATAFKMLKSRLYELELMKQQDSANAGEKSEIGWGHQIRSYVLFPYQQVKDNRSGEAFSQVDNILDGD

IKKMIEGVLIALKAE

>WP\_002866981.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKFETINQESIAKLMEIFYEKVRKDKDLGPIFNNAIGTSDEEWKEHKAKIGNFWAGMLLGEGDYNGQPLK

KHLDLPPFPQEFFEVWLGLFEESLNMVYNEEMKAVILQRAQMIASHFQNMLYKYGGH

>WP\_002866976.1 MULTISPECIES: 50S ribosomal protein L10 [Campylobacter]

MTRSEKVEIIAKLEEGFKASEAIVVCNYRGLSTKKLEELRNNARENNVKVQIVKNTLANIALNNSGKTGL

VLKDTNIYLWGEDQLSVSKVAAKFEENNDKFEIKTAYIEGEVADVAKVKALAKMPSRNELLAMLLQVWNA

PITNFTIGLNALKNKKESE

>WP\_002866966.1 MULTISPECIES: bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase [Campylobacter]

MKTSILILAAGLGTRMKSQKPKVLQELCQKSMILHILKKAFALSDDVSVVLSHQKERVEKEILEYFPKTQ

ILEQDLQNYPGTAGALRGFEPKNERVLILCGDMPLVEQTSLEALLSNNAKLNLAVFKARDPKSYGRVVIK

NDSVEKIVEFKDANTQEKEINTCNAGVYVIDSRLLKELLPLIDNNNAAKEYYLTDIVKLAKEKDVMIKAV

FVDEDEFMGINDKFELSIAENFMQEKIKKYWMQQGVIFHLPQSTFIGTDVEFMGECEVYENVRIEGKSKI

INSIIKSSSVIENSIVENSDVGPLAHLRPNCELKNTHIGNFVECKNAKLNTVKAGHLSYLGDCEIDSGTN

IGCGTITCNYDGVKKHKTIIGKNVFVGSDTQFIAPVKIEDEVIIAAGSTVSVNVEKGALFINRAEHKMIK

DYYYKKFQK

>WP\_002866959.1 MULTISPECIES: threonine ammonia-lyase [Campylobacter]

MLELNKIYKAKQQISGFVNKTPFIYSSFLSDICQSEIYLKNENLQITGAYKIRGAYNKIANLSAEQKQHG

VIAASAGNHAQGVAISAKKFGIKAVIVMPESTPLLKVSATKALGAEVILKGDNFDEAYVFATSYAKENNL

SFIHPFEDEFVMAGQGTLMLEMLDEISDLDMIIAPVGGGGLISGIASAAKQINPNIKIIGVGAKGAPAMY

ESFHAKKIKNAKSVRTIADGIAVRDANPINFNIILECVDDFIQVDDEEIANAVLFLLEKHKIIVEGAGAA

SVATLLHQKINTQNHKKIGVVLSGGNIDAQMLNIIIEKGLFKSYRKMQIHVTLVDKPGALLHLTDSLKIA

NANIVKIDYDRFSTKLDYGDAMISITLETKGKEHQEEIRKILTQKAFNFYESF

>WP\_002866926.1 MULTISPECIES: D-alanine--D-alanine ligase [Campylobacter]

MKFAILFGGNSYEHEISIVSAVVLKKVINQNLEFVFCDEERRFYHIPSEKMNSKTFSTKAYKNEKELFIK

QGGFFSKGFLKENKLECECVINLIHGRDGEDGKIAALFEFYSIKFIGPRLEASVLSFNKELTKLYAKSVG

VKTLDYTMLRKNQNSKEKLSFPCIIKPARLGSSIGISIVKDEKDLEYAKDVGFEFDNDLVVEEFKNNIKE

YNLAGCMINDEFVFSIIEEPKKKEFLDFEQKYLSFSGHNELIEADLSEELKEKLKDSFKKIYNPLFKGAL

IRCDFFILDNEVYLNEINPNPGSLANYLFKDFNTTLNALADQISLEKMIKINYNFLHSINGQKGKL

>WP\_002866924.1 MULTISPECIES: UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase [Campylobacter]

MLINALYFVNSLFFNFCIAFYLMSALQWYSYKFKRVFFHYHKPLWHLYFLFIPYFLFLAFPLYSLAYFAL

IHTPILYFWSKGIDKKLVFTSKVKWFFVFVFVYNAIFAILALRFSFLFNLFSLPFALFSLKIYEFFTNLY

YKKQAKAKLRANENLKIILITASFGKTSIKNFLYELLKDDFKSYKTPRSVNTLLGIVADINTNLSQDTQI

YIAEAGARLKGDIDEITRFLQPHISIVGEIGNAHLEYFKSVENIRSTKLEALNSKRLEKAFLHSSTQKEE

DKLISLYDDKLSLIHSSLEGLEFKIDIENKSYDFKSQILGDFNAQNLCVCILCAHYLGIKLEKIQKQVLN

INSVEHRLQVLSREPKFIIDDGFNGNFKGMSTSYELCKSYKGRKVLVSPGIVEVSEEENIKLAKIINECF

DLAIISAQINAEIFKKELKIKTIILKEKSQLVQTLAKETKNGDLILFSNDAPSFM

>WP\_002866913.1 MULTISPECIES: hypothetical protein [Campylobacter]

MNLEDLAKKTISEVSSIMEEQRRQNEILKEQELNRKTEIKDELPPMEFVCEELDTPQDLEDKISMAKFEE

EQKIQNNIEISTQENKEFKKEEPFLQSEILNPSVITEVQTLNEDIFLKHLRERILVLFEGLNSIKKDDLE

NRLNLTINFLEFLLANIEDKLKK

>WP\_002866912.1 MULTISPECIES: oxidoreductase [Campylobacter]

MNNLSSVLILVKEEYINDLKKAISEIPFCSVELCENEKIIVVIESENLEDELNSYKMLEKLPNIISINMV

FSYQDLNDDIQKAINSGAIETIEKNENAENIRYYGSVFNQFS

>WP\_002866909.1 MULTISPECIES: ferredoxin-type protein NapG [Campylobacter]

MKGRREFFVSAFKAACLCTGGGFLANLALKADDNYALRPPGAEDEARFLSKCIRCGLCVKACPYDTLKLA

SLLDSPKNGTPFFKAREIPCYLCKDIPCIRECPTDALDKKHLEQGIESLKMGIAIVDSASCVAHWGIQCD

ACYRACPLIDRALKLELKRNERTAKHAFLLPSVDHEVCVGCGLCELACITEKPAIRVLPREYVLGKAGSH

YVKGWDEKDEGRIKNADTSKHFDAKKATNYLNDGEL

>WP\_002866871.1 MULTISPECIES: dimethylsulfoxide reductase, chain B [Campylobacter]

MKLEENSQFGFMLDQSKCVGCRTCSLSCKDYKNMPVGVNFRRVFETEGGNWTAKEDGSFEQSVFAYYTSI

SCNHCSNPSCLKACPTGATMKIKWGIVAIDDSMCIGCKACAMACPYGAPQFNHESGHMSKCDGCYERLKE

GKNPICVDSCPFRALKAGDITKLREEHGNLASITPLPDASITHPNLCIVPEKHSLPSGNKSAIFHLPQNY

QGVKNDII

>WP\_002866856.1 MULTISPECIES: NADH-quinone oxidoreductase subunit N [Campylobacter]

MLNNFLNLELLNISLSYPFLFLITTAIVLLLCSGFWKFHRSFYIGISSLSLIVSAFLILNNANAQGLEAK

AFLATLNNDIVSFYAFLVILCFSFLYLLMQKEENQGEFYALFLFMIASLLLMVSSSNLVLIFIGLESSSL

ALYTLIAMRGSDNAISSAIKYFSVAAVGAGFFVMAVAFIYLKTGTLDLSANLALKNEFQKDPMLLGAGVM

IFVLCAIKLSLAPFHFWLKDVYYAAHTNLVAFISVVPKVAMLVVVIRLFDFLNNTGFEYIIIVLAIFSML

IGAFAALSQNNIKKMFAYSSVVHSSLVLVACIPLLKEQNFDGILLAIFGYWTLFAFANYAVFMILSNYEN

NSYESLNGLLVKKPLIVFCLSISVLSLAGIPPFGVFWGKFMILNTAILNGYWYLALFVALSSVIMLYAYL

KILIHALFMKNDRVYNIKFSFIQNFILACCVCVSTFAILLML

>WP\_002866836.1 MULTISPECIES: AMIN domain-containing protein [Campylobacter]

MKTRILAIFFIFTSLLYADENPFKTDQNITLVAPPEFQKEEVKFNSSARILKSITFNYINLDGSEDKIDL

DVNKSIDWHDTYTISRFKSPDPSKVLDVSVTIPEKNSSKQESNSTANVEIPLQVAKIYDFISYAVYKNKI

KLNTSDEMITDFSVGNPSKIVIDFRSNLISPTKNIRLSNSIFKRIDFGSHKGYYRLVIYLDGTYNYNIQK

DATGYMINLL

>WP\_002866832.1 MULTISPECIES: 3'(2'),5'-bisphosphate nucleotidase CysQ [Campylobacter]

MLNLDKFLEIAINASNQASKAILEERKNFKTWEKEDKSPLTSADLASNKILNDILGSTDIKILSEEKLLS

KEECEELKTFWLIDPLDGTSGFLKGSDEFCVMISLVHDNRPVLSLIQNPSKGDIFYAHAKTKVYKNDKPL

QIDQQEYEKNKYKALLSVNHLSKEDEDFAKEHQLEAINIGSGLKFCAILEARAGVYKRFEKLNIWDIVAG

DFLINQNGGFMGDFSKKYILYNPLNYKSSPFICVSSRNFLQDFL

>WP\_002866817.1 MULTISPECIES: 50S ribosomal protein L4 [Campylobacter]

MSKVVVLNDKLEKAGELDLPSKYAEVNPHNLYLYVKSYLASLRANTAHTKGRSDVSGGGKKPWRQKGRGG

ARAGSTRTNVWVGGAVAFGPTNERNYFQKVNKKQKRLALERALADKAAKGALFTADSLAIESGKTKDANA

VIKKLGVKDALIVKDLLDEKTLLAYRNLANCYVVDVSEVNAYLVSVFNAVIIEKSALESITKEG

>WP\_002866799.1 MULTISPECIES: ribonuclease HII [Campylobacter]

MKTLFDTKELLNEFDINLIGIDEAGRGALAGPMMMAACKLNKKLDGLCDSKKLSEKKREELYEIIIKNSN

YLILAFSSEQIDALGLSTCLKTGLKLIKKHFKTENNFLYDGNTNLGINGIKTQIKADASILQVSAASILA

KVSKDRVMNFLAKDFPCYEFEKNKAYGTKAHKELIAKFGICKLHRKSFKLL

>WP\_002866784.1 MULTISPECIES: single-stranded-DNA-specific exonuclease RecJ [Campylobacter]

MKIINKNEIKKILASRFEKDLHTKLCDLPLPCCLKDAYKAANRIKEAVEKNEKVAIVGDYDVDGIISCVI

MAEFFDDIGFDYIVRIPNRFKDGYGLNAEIINELDVNLIITVDNGIAALEAAKLCKEKNIDLIITDHHMP

QDVLPDAFAIINPKQKDCDFPEIEICGAQVAWYLIAALKEVCKLKYDMSKFLELLAIAIIADMMELRDLN

RALVRRGIDHINKSKRAAFRAIKHYYQKDKFALDNIGFLIAPLINSAGRMDDASISYEFLHTKDFNKALE

YLEQIVSFNESRKDEEKQLFEDSLNQIDENDSCIVVSGLNWHEGVLGIVASRLAKHFNKPAFVFSQNEEH

LKGSARSVGKIDILALISKTNSILSNYGGHKGAAGISLNSENFEQFKNKIKKECSQISESEFLDTDEILG

ILEPSEIDFEMLEILESFEPFGHKNPRPFFVLENLCVKNKKLLGKDEKHLKLILTKENKTIEALFFNFDK

EPELNQNISLLGSISKNEFRGLVTPQFVIKEIL

>WP\_002866741.1 MULTISPECIES: outer membrane protein assembly factor BamA [Campylobacter]

MKKHLISICALVAIANAATIKDIKFIGLNHLSNTSAINITGLKIGEEINPAKINTAILNLYKQNYFENIA

VENNNGILEIIVTEKPTIAKVTITGIASNDRKQVESILGIKRGTLLDEGSIKEAIERIKAYYEAKSYFDT

IVEYKKKTLENTDGLELEFIVNRGENIIIDNVHLSGAKKFSYSDIEPAVVNKEKEFMGWMWGRNDGKLKV

FELSNDSSRIADEYMKKGYLDVQVSSPYLKTYTDTYQANLTYFIKEGKPYKIKSISIENPLFDDKQNAQT

VKDLRSSAGKTINIEDIRKDVKTIETQSADLGYAFVEVYPDIQKNDQTQEATVVFKVIPHDKVYIRNVII

SGNSRTVDRVIRRELYITEGNLYNRTDLSESKNALKRTSYFDDVNIKEEKVDDTHIDLIVDVKEASTGAI

SGGIGYGSSDGILLNASLSDTNIFGSGIKSSVSVDKSDDTLSGRISLINPRVLDSQYSLGGTLYSNDYEW

DNYSEKNYGFDITVGRQFARYYNVSLTYNLEQSDIYHLSPTLLRTGYELGKSIKSSITPAITFNNTDDYY

LPRSGIIASTSLEYAGLGGDQEFISSSSKFNFYQGLQDYIGYDLIYRYKASFYKVWDEGYLPINQRIYLG

GIRSIRGFESRTVSPKNQWGDEVGGTIAFANSVELSFPLIDRIKLRGSVFFDYGMIGRKNLDEIKRMSTG

IGIEWITPIGPLQLVFAKPLNDKKGDDTNSFEFNLGTRF

>WP\_002866740.1 MULTISPECIES: inositol monophosphatase [Campylobacter]

MKEFLDACLNANLQIRKYLNNIPQNDLKLCSKLGYDKNQGYELDLKCEQIFIKYLSCFGQIFSEESGLIG

KASPKQMILDPLDGSSNFVSKIPFYGTSIALMEKDQAKSAFVCNLVSQEIFAFNNNQAFKSNLSDPKYSP

LTPNLFSKIGIVEKISLHPELLDFLTKNQLKFRSLGATALSLAYASYFSFVLILGKTRIFDTAAALAIHQ

NLYIEKNENFLLLSQDKKIFDIILEFLKNN

>WP\_002866735.1 MULTISPECIES: rRNA maturation RNase YbeY [Campylobacter]

MILSDEKCDFLESIASFLSPKDVELVFVDSKEMQEINLEQRKQDKTTDVLSFPLENIDESLPLGSVVINV

DLAKEKAKELGHSYEEEISLLFIHAMLHLLGFDHENDNGEMREKEKELIEHFNLPKSLIVRTLG

>WP\_002866734.1 MULTISPECIES: tRNA 2-thiocytidine(32) synthetase TtcA [Campylobacter]

MINLSKKLIRQVAQANAKFGLIKDGDRVLLGLSGGKDSLALAHLLNRMQAHAPFKFELEAVTLSYGMGED

YSHLHAHCEEHGIKHSVLDSNIYEVSGDTIRENSSFCSYFSRMRRGALYTYALEKGFNKLAIAHHLDDAA

ESFFMNFIHNGALRTLAPIYQSKRGVTVIRPLIFVRERQLRDNATQNELSVIGNEFCPGMKLSEKNVKFP

HAREEAKQLLANLEKDHPKLFTSLKTAFANLHTESFWLQKA

>WP\_002866688.1 MULTISPECIES: phosphoglycerate kinase [Campylobacter]

MSDIISIKDIDLAKKKVFIRCDFNVPQDDFLNITDDRRIRSAIPTIRYCLDNGCSVILASHLGRPKEISS

KYSLEPVAKRLARLLDKEIIMAKDVIGEDAKTKAMNLKAGEILLLENLRFEKGETKNDENLAKELASMVQ

VYINDAFGVCHRAHSSVEAITKFFDEKHKGAGFLLQKEIDFASNLIKHPARPFVAVVGGSKVSGKLQALT

NLLPKVDKLIIGGGMAFTFLKALGYDIGNSLLEEELLEEANKILTKGKNLGVKIYLPVDVVAAPACSQDA

PMKFVPVQEIPNGWMGLDIGPASVRLFKEVISDAQTIWWNGPMGVFEIDKFSKGSIKMSHYISEGHATSV

VGGGDTADVVARAGDADEMTFISTGGGASLELIEGKELPGVKALRSKENE

>WP\_002866684.1 MULTISPECIES: holo-ACP synthase [Campylobacter]

MRVGCDIIAISRIEKIHSRHGKNFLDKFLSPKEQILIKNPATLAGLWAAKEAASKALGVGICELCSFFDI

EISKDEKNAPKLKYSQKITKNFNITQTSLSISHDNGFAIAIVAIV

>WP\_002866651.1 MULTISPECIES: nucleoside hydrolase [Campylobacter]

MRLILDTDIGNAIAGANTDDGLALALILASKEIKLEMLSTVCGNVPSLVAYSVAKDLFKRLNLNIPVYLG

ANEALKEPSKAWRQRLDESVKNFKLEYLWENIKSPEILENINPDAIFKMGELVSKNPKEISICAIGPLTN

IAMTMKIFKDFDINLKELFIMGGSFDMPYYTKDTNFGFDPEAASIVLNSRAKITLVPYNATMQTLLTHED

LKELQGKNILCDFIVETLGVWIDYASKTRGTKGTWIHDALTIAYALDSSIADFDECYADVICDSSLARGM

SWRCFKEPKMSMGVDLSTKNCVKILKNVDNTKLLKLIKERLLKGVCYENYESITT

>WP\_002866648.1 MULTISPECIES: hypothetical protein [Campylobacter]

MFQNIIKYKDFIISILNLKQNLYLLIKINLDFKNFHKSLNF

>WP\_002866647.1 MULTISPECIES: anthranilate synthase component I [Campylobacter]

MFVKNVNFYYRQILEKFENSYFAEDLTKVIIGIDCDYLDANELSFSEFKAKYYEALSKNKICDFAGFFGV

FSANFVSLFEKIPLSSKKNYDFPLFLFANAKAYLIYEKNSKMFFKFGASKYFEYLKDDIEPIKTKQKNDF

EILNSLEDEKNDFLKMCEKAKEYLLSGDIFQVVLSKQLCIKHQVNAFDYYESLSTLNPSAYMFYFPSKYG

VVLGSSPEFLLKIKKREIYLAPIAGTRNLENNCDLLALEKDLLSDEKELSEHKMLVDLARNDASKFGTQT

RVENLFSIIKNKFVMHIVSEVYANMKEDASIFDVIEAVFPAGTLSGAPKIRALEIISELEDCDRGVYGGA

VGFLNFNEDITLAILIRCAFFTQDKAYLASGAGIVLQSESQKEYAEICAKRRALLVAFENLKKENQ

>WP\_002866645.1 MULTISPECIES: N-(5'-phosphoribosyl)anthranilate isomerase [Campylobacter]

MLKLKICGIKDEKNAKDLAFLNIDFFGFIFAKSPRRVSLEQARNLSAIFHEKDKKVVGVFVDENLEQILR

CIKEAKLDGIQIYRTITKEEFEILKVQNVFVWQVISVENSLDLKSEIFANLVLFDAKGILKGGNGISFDW

TLLGSYTKDFILAGGIGLDNVHKAVQTGAKILDLNSKLEDEKGLKDINKIKQILKELKK

>WP\_002866611.1 MULTISPECIES: NifU family protein [Campylobacter]

MMPFSDEELINPVKASLEKSLPMLERDGGGLEFLGIKNGVVYVHLIGACKGCASSGTTLKYGLERQLKID

IHPEITIINLNGGADEFAKL

>WP\_002866595.1 MULTISPECIES: ABC transporter substrate-binding protein [Campylobacter]

MKKILIIMSLFLITLNAKERLVVLDPASIETLFMLKAEDQIVGIATLQHSNIYPKDQTSKLTSVGTFSNP

SLEKIVALKPSLVILSSYSLNLEEGLKNFGIKSINLKAERLEDITKNITTLGQITKKEKEAEFLKQEFTQ

NLKKLSDKPLNKSAIYLYSSNPLMAFNDNSLIADILRLIGIKNLSPQSQISRPVISAEYILKQNPDILIL

GINAKNNLLDTNALLKNTKAVKTGSIYFNKDTHILLRLSPKIIDRIQEFKTKLENNNF

>WP\_002866587.1 MULTISPECIES: response regulator [Campylobacter]

MKVLIIENEIYLAQSISIKLSDAGYSCEIINSFDEYNGEKYYDIVLLSTNTNNFLKAVGQFKHSIIILLI

SYISTDTVSNPLKLGASDYIQKPFMIEELIRKIKHYQDFRKLSILNKAYQSYIKSRLETIKIPEYNYKKL

KLPLILKSNKQSSADAFVFNYANECDITLSFIDLTSTNSVEKVMKLPTENNLLFLSNFQALKATEKEKLL

DFIQNKNVILHTNSNTDDLKINCINLNDNEKNIDSNEILTIDEYVKYVIINYQNIFPDTDLSKKLGISRK

SLWEKRKKYEISKKK

>WP\_002866583.1 MULTISPECIES: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase [Campylobacter]

MINTKEDFLLLIKQIEQKSGYKKPKAFGIARLDRGQLNKNKILQASFALINYEQNFGSAAIMLEAFMQRG

VEIDFNASEFVQTLKLEDIDFALSCFKPFLEEEGHQNIDLLKIIKDKFKDDEFAFVCLFEDKEPLSVESV

YLKLYLLSTKKVPLRSINLNGAFGLLSNVAWSDDKPIELEYLRANEMRLKMSNQYPKIDFVDKFPRFLAH

IIPEDNTRILESSKVRMGASLAAGTTIMPGASYVNFNAGTTGACMVEGRISSSAIVGEGSDVGGGASILG

VLSGTSGNAISVGKACLLGANSVTGIPLGDNCIVDAGIAVLEGTKFLLKDAEELAKLNPYFNFDKEIYKG

LELKGLNGLHFRQDSISGAMIVALNKKAVKLNEALH

>WP\_002866577.1 MULTISPECIES: ATP phosphoribosyltransferase [Campylobacter]

MQENTRLRIAIQKSGRLSKESIELLSECGVKMHIHEQSLIAFSTNLPIDILRVRDDDIPGLIFDGVVDLG

IIGENVLEENELERQSLGENPSYKLLKKLDFGYCRLSLALPQENKFQNLKDFEGLRIATSYPQLLKRFMK

ENGINYKNCMLTGSVEVAPRANLADAICDLVSSGATLQANNLKEVKVIYESRACLIQKENALSKEKQALV

DKIMLRVAGVMQARESKYIMLHAPKEKLDKIQALLPGVERPTILPLAHDEKNVALHMVSKENLFWETMEA

LKEEGASSILVLPIEKMLK

>WP\_002866547.1 MULTISPECIES: 5-(carboxyamino)imidazole ribonucleotide mutase [Campylobacter]

MNFVSILMGSKSDYETMKEAAKTLESFGVKYELIISSAHRSPKRTKEYIANAEEKGAKVFIAAAGMAAHL

AGAVAAYTTKPVLGVPMPGSNLASMDSLFSTVQMPSGIPVGTLAIGKAGAINAAYLAMQILAIYDVDLAQ

KLKEDRLEKEKKLVSDSKEVEVLL

>WP\_002866541.1 MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Campylobacter]

MLTWMQHHKKYLVVTIWVSTIAFVGAGFLGWGAYDFNLNRSSSVATVGNEKIGFSEFDTRYRQILSYYNQ

ISNGALTPENAEQLGIKNIALSSLVEDKLLLNFAKDLGIGVNENEILQKLANTREFQDPTGDFNKTIYYE

LLNANNLTPKDYETQLANEVITDKLNQIFNIPSKDEELKMLASSYFMQDALSIAKIDYDKKNIKINEEDL

KKLWNEHKEDYKTKKIYEISTYFLSVSNEKIDDKELEKFYNQDENKLKYKDFAGKVMDFQSAKNEVAKDY

ALIQLKNVANAKFLDLKNGKDNFQKDQNISESDVYYPIDLLNKAKNGDVLRPAPYNNGYIIVKLNKVDPI

RNKTFEEAREEVLPMYLSEQARKNLEEKAKNSLVNFKGDDIGFVSRDSSRESVKLSDKILNDSEFAYFLM

NVFNTDQNSSYVIINDNKAILYKINKQKLDMNSDKFEQYKTMLEQNLRNLKANELKQELVDELKKIYPIK

IYYKGN

>WP\_002866447.1 MULTISPECIES: hypothetical protein [Campylobacter]

MFSKIFSSLSLANAFKGFLFKRISSPMQSARIISMVLDIKNAFNDSKDQASSICKTLDLIVNFKKEHPQD

FNELFEILKDLIQEYEQNPNEIKQNLKEILK

>WP\_002866408.1 MULTISPECIES: molecular chaperone HtpG [Campylobacter]

MQFQTEVNQLLQLMIHSLYSNKEIFLRELISNASDALDKLNFLSVSDDKYKSLKFEPKIEIKIDKDKKTL

SISDNGIGMDKDDLINNLGTIAKSGTKSFLENLSGDAKKDSQLIGQFGVGFYSAFMVASKIEVLSKKALD

DKAYLWSSDANGYEINDANKEEQGTSITLYLKDDEFANTYKIESIIEKYSNHIQFPIFMEKEEFTPAKEG

EEEGKTELKISQINKANALWRMQKSSLKVEDYERFYEQNFHDSNKPLLYLHTKSEGKLEYNSLFFIPQNA

PFDLFRVDYQSGLKLYVKRVFISDDDKELLPTYLRFVRGIIDVEDLPLNVSREILQENQILKGVKEASVK

KILGELEKLKNNDKEKYLSFFKTFGKVLKEGLYGFGGEKDSLLKLMLYKSTKGENLRSLEEYKNDLQGEQ

KEIFYIAGNNESLLRTSPLLEEYKQKNIEVLLMDDEIDSLVTPMLEFEGLKFVAINQVEDKNELSDEEKN

TFAPLVAKFKELLKDQVEDVRLTSRLKDSPSCIVYDKNKPDFAMQQLLKQMGQEQNFKPILEINPKHAIF

TGLKNNESFSADIATLVLNMAKLSEGMGVDNPAEFNASLTKIINKAFS

>WP\_002866352.1 MULTISPECIES: amidophosphoribosyltransferase [Campylobacter]

MCAVVGVINSKNASTYAYYALFAMQHRGQEASGISVSNGKNIKTIKAKGEVSQIFNPDNLKTLEGEIAIG

HNRYSTAGNSSLNDAQPIAATSVLGDIALAHNGNLVNKEEVRSRLIQDGAIFQTNMDTENVVHLIARSKQ

ESLKDRFIESLKECIGAYCFVLASKDKLYVVRDPHGVRPLSLGRLKDGGYIVASETCAFDLIEAEFIRDV

KPGEMLIFTQGNDKFESIELFSQTPRICAFEYIYFARPDSIVEGKSVYEVRKKMGEALAKKFAYKADFVV

PVPDSGVSAAIGFAQYLQIPLEMAIVRNHYVGRTFIEPTQELRNLKVKLKLNPMRKVLEGKEIVVIDDSL

VRGTTSKKIISLLRAAGASKIHLAIACPEIKFPDTYGIDTPTFEELISANKNTEEVREYVEADTLSFLSI

EELTQSIGDERKYSLISFDGDYFIK

>WP\_002866343.1 MULTISPECIES: phosphoribosylglycinamide formyltransferase [Campylobacter]

MLVKLAVLFSGNGSNLENILEKLHKKTIGENTYEVVLCLCNKKDAFGIQRAKKFGLDTVIVDHKAYNTRE

EFDTILVQKIKESGANLTVLAGFMRILSPVFTKNIKAINLHPSLLPLFKGAHAIKESYESDMKVAGVSVH

WVSEELDGGMIIAQKAFEKRNLSFEEFEEKIHSLEHEILPLSVIEIFS

>WP\_002866340.1 MULTISPECIES: transporter [Campylobacter]

MFSSFFASKKWALWAYLGLFLLLFFLYIQTSLNVAINSWYSDFYNVLQKPKIELLDSNSTQKIEENLENN

TTLIQEANQRAEQNFQKANFINKGALYYYQNLLEYFFNSRAMIEKPNYSANDFYALILVFLAIAIPYVLI

ATINIYFASVYAFKWREAMTFSYLKFWKNKDDNIEGSSQRIQEDTYNFSKIVESLGLSFIKALMTLVAFI

PILWSLSDVVSKALFANLSENSSFYFLKNIDGLLVYIALLISLGGLVVSWFVGIKLPGLEYNNQKAEAAF

RKELVYAEDNRKEYAKNETMIELFTGLKFNYKRLFLHYGYFNIWLILFEQMIVIVPFLIMAPGLFAGAIG

LGIVMQINNAFDQVRSSFSVFITNWTTITQLRSIYKRLKEFEKNISYKS

>WP\_002866334.1 MULTISPECIES: 4-hydroxybenzoate octaprenyltransferase [Campylobacter]

MNTFWIKFKDILELVVFKHSIFALPFLFSSMIVASKLANDTAWFGFKALILGIICAVSARNFAMATNRLM

DEDIDKDNPRCANRPNVSGKIGRKSVWIFIIINALIFISCSYFINTLAFYLSFPVLFVLAIYSAFKRFSS

LAHLVLGFCLGLAPIAGSVIIMGEIHIYSVILCLGVTFWTAGFDLLYSLQDMEYDKKVGLHSIPAKFGSK

ATLFISAFCHILAVLFWLLFVWEVWGIALGKIALIGVIISGIILALEHKIVHKNFAHIDRAFFTLNGYLS

IIFFIFIWIDLLWN

>WP\_002866280.1 MULTISPECIES: pseudaminic acid cytidylyltransferase [Campylobacter]

MKNLCIIPARGGSKRIPRKNIIDFLGKPLIAYSIENALNSGIFDEVILSSDDEEIIEVALKYGAKAPFVR

DKNLSDDYASSTAVVQNAIEILQSQNQIYDNVCCLYATAPLLNKDILKQAYEKFIQNQSKFLFAATEFEY

PIQRAFYLNENNQVYMFDEKHYKSRSQDLTKAYHDAGAFYFGTSKAWLEEDFMFKPHSGVFVLPRNLVCD

IDTMQDLEFAKILYKANHESTF

>WP\_002866270.1 MULTISPECIES: glutamate--tRNA ligase [Campylobacter]

MHEKLTTRFAPSPTGYLHIGGLRTALYNYLYARKNGGNFLLRIEDTDLKRNSKEATKAIIEAFKWCGLEH

DGEVTYQSERFDLYKEYVKKLLDEGKAYYCYMSKEELEELRAKQEAAKERPRYDGRYREFTGTPPQGIEP

VVRIKAPQSGEIVFEDGVKGEVRFKAEDIMDDFIIARSDGTPTYNFTVVIDDALMGVSDVIRGDDHLSNT

PKQIVLYEALGFKIPKFFHVAMIHGEDGKKLSKRHGATDVMEYKEMGILPQALLNFLVRLGWSHGDDEVF

SLEDLKKLFDPYHINKSASCYNAKKLEWLNAHYIKTLPFEEINRQLKDLGFDLSVYEKAGFLLDLLRERA

KTLHDIINGAKSIVNAPQNYDENAVQKFVNENNLELLQAFANTLKDQKTGKDFEDFTNDFLEKKEAKLKD

LAQPIRIALTGSAVSPSIFEVLEFLGVDECKKRIDNFLKVRGK

>WP\_002866238.1 MULTISPECIES: uroporphyrinogen decarboxylase [Campylobacter]

MIFIDACFKKPTPYTPIWMMRQAGRYLPEYMEVRKQAGDFLSLCKDYKKASEVSLQPIDILDVDAAIIFS

DILVVPLEMGMNLRFEKGEGPVFDNPISTLEDLEKLDDQNAHKKLNYVYDALKLTREKLSQNKALIGFCG

SPWTIATYMIEGSGSKNYAKCKKMLYQNPELLHKILNKLTQVLKLYLEEQIKAGANAIQIFDSWASALEY

DKFFEFSFNYMLEISNFIKSKYPNIPVILFPKGISGYLDRIDGNFDVFGVDWSTPLDLARDKLSHKYTLQ

GNMEPCRLYDKNAIKEGVEKILKTMQNKAHIFNLGHGILPDIPVENAKYFIKLVQESSAK

>WP\_002866237.1 MULTISPECIES: hypothetical protein [Campylobacter]

MVVDNTQKTSNAIFSTTTKVKEKNTSADEFQATLNEVKNKEEKEEEKTSSSKFTNEDIDLGAVREDFRSY

AWQKMREDQYKKNEETLLNKLFATIDAGNATNNTKA

>WP\_002866195.1 MULTISPECIES: cytochrome c [Campylobacter]

MREIKIFLVVVVFTALVYWGVEPYAHSVMKPHVAPANFDFAVEDTTFAKGIVEAKELALKDAQASGDAKR

IESANKELEKAKEELSKVETLWADVAKIDFAKGDAKKGKEFFENNCFACHGVKEDGITANITDSSMGVIP

PDLSAAGAIFDEKFLAALIMHPALALKVDHKFGDAFIMTAYNKDTSGESEEATNANIANVIAYLKDVSVK

FEANEDATIKKDVEAKYAKMENSAQKVALMEKDIKFAKDKATFIEACGRCHDMKYDSFFTPSNQNDLKTY

LGSVPPDLSMMIRSRGEQYLHDFINNTQKLLPGTAMPRVGLTEAAQAKVVSYIDQVGDSKKEERKTTGIY

VMIFFVILSIFAIGWKRSVWSKLH

>WP\_002866193.1 MULTISPECIES: elongation factor Ts [Campylobacter]

MAEITAAMVKELRESTGAGMMDCKNALSETNGDFDKAVQLLREKGLGKAAKKADRLAAEGLVSVKVSDDF

TSATVSEINSETDFVAKNDQFIALTKDTTAHIQSNSLQSVEELHSSIINGVKFEEYLKSQIATIGENLVV

RRFATLKAGANGVVNGYIHTNGRVGVVIAAACDSAEVASKSRDLLRQICMHIAAMRPSYLSYEDLDMTFV

ENEYKALVAELEKENEERRRLKDPNKPEHKIPQFASRKQLSDAILKEAEEKIKEELKAQGKPEKIWDNII

PGKMNSFIADNSQLDSKLTLMGQFYVMDDKKTVEQVIAEKEKEFGGKIKIVEFICFEVGEGLEKKTEDFA

AEVAAQL

>WP\_002866189.1 MULTISPECIES: guanylate kinase [Campylobacter]

MQGFILLISGPSGAGKSTLLKKLFDEFEDELYFSISSTTRKPREGEKNGIHYHFISHEEFQKGIDGDHFL

EWAKVHENFYGTSLKHTQDALDNGKIVVFDIDVQGFKIARQKMADKIVSVFITTKNKDELKKRLIKRNTD

TIIQLEKRLQNASDEMKELSDYDYLIINDELKQSYEALRAILIAHKFRTKGQNLGQIQNIWNEGE

>WP\_002866187.1 MULTISPECIES: arginine--tRNA ligase [Campylobacter]

MKSIIFNEIKKILECDFTLENPKDKNLAHFATPLAFSLAKELKKSPMLIASDLASKFQNHDCFESVEAVN

GYLNFRISKTFLNELANQALANPNDFSKGEKKQESFLLEYVSANPTGPLHIGHARGAVFGDTLTRLARHL

GYKFDTEYYVNDAGNQIYLLGLSILLSVKENILHENVEYPEQYYKGEYIADLAKEAFEKFGKEFFSEENI

PSLADWAKDKMLILIKQNLEQAKIKIDSYVSERSYYDALNATLESLKEHKGIYEQEGKIWLASSQKGDEK

DRVIIREDGRGTYLAADIVYHKDKMSRGYGKCINIWGADHHGYIPRMKAAMEFLGFDSNNLEIILAQMVS

LLKDGEPYKMSKRAGNFILMSDVIDEIGSDALRYIFLSKKCDTHLEFDISDLQKEDSSNPVYYINYAHAR

IHQVFAKAGKKIDDVMRADLQSLNQDGVNLLFEALNLKAILNDAFEARALQKIPDYLKNLAANFHKFYNE

NKVVGSINENDLLKLFSLVALSIKTAFSLMGIEAKNKMEH

>WP\_002866154.1 MULTISPECIES: hypothetical protein [Campylobacter]

MIKICIAGKNNIAVNSLQFILKNYFEADQIVVIPNKNDKGIDSWQKSLLKFALDNNIKIVTLDEIYNIEQ

IIFFSLEFDQIIKIENFKSDRLFNIHFSALPKYKGVFTSITPILNNELESGVTLHRIDNGIDTGNIIDQH

CFPIDINDTARDLYFNYLKYGESIFKKNIQTIINNSYKDLKQTNINSSYFSRKDINLVHKINFKKTSFEI

HNQIRAFIFQEYQLPIINNSKIIKSILANEFIGYNVFEEFENYFIISGIDGFKIIAQKLNKL

>WP\_002866122.1 MULTISPECIES: ATP-dependent DNA helicase [Campylobacter]

MNLFEDLNDSQKQAVSHIDGAMLILAGAGSGKTKTITTRLAYLIGEVGIPSHNTLTLTFTNKAASVMRHR

ALNFLQGNHNPLLCTFHKFGLLFLKLHFERLERKNSFIVIDTDDTKKIIKDLIHDKNKDNVYDIIKYISY

CKNEGKRVSNVFEDLNLLKEHNFEKYQNEYKFANYYRAYEEYLLKQNFVDFDDLLLLSNLILENDINFAK

EQSLLYNYITVDEYQDTNTLQYKILKNLCCMHENITVVGDDDQSIYSWRGAKIENILNFQNDFKNVKLVK

LEQNYRSVGTILQAANNLISHNEQRLGKTLICTKDTGENIKILKNENEKDEGLYIAQEVKKLLNSGVEAK

EIAVLFRVNALSRAIEEAFMKEKISYKLLSGMRFYERLEIKDLISYLRLILNPNDDLSFRRIINRPKRSI

GEKALKNLEEYAKKRQISLFDALCESDGGVGILTTKKAQNEANIFIQNIHTLKSYDNAKKVFDNIEELFK

IKDYFSEQDDGDERIRNLDEFYANLREKLKEDPEASLEDLLSEISLLSDQDNLDEECVCLMSIHASKGLE

FDYVFIIGFDEGFFPLNSEENLEEERRLAYVAITRAKKFLTISVANSRFYHGSRANINPSRFLEESKLIN

EKSKNQNIQKTSFCKGDLVKHKIFGIGRVVEVNKSGKEEKLNINFGGIMRVIMASFVEKAV

>WP\_002866058.1 MULTISPECIES: aspartate-semialdehyde dehydrogenase [Campylobacter]

MSKKQKIAIVGATGAVGEELLNVLDELDFPVESILPLASAKSVGSEVEFKGKAYKVKELTENVFKENPID

IAFFSAGGSVSEKYAKFAVESGAVVIDNTSHFRMEKDVPLVVPECNPEDIKDWKKTGIIANPNCSTIQMV

QVLKPLNDAFNLKRVDVSTYQAASGAGKEGMQELVEAMQSFFAFKLDEFEPQTFPYTLALNLIPQIDVFM

DNDYTKEELKMVNETQKILHKNLEVSATCVRVPVLRSHSEAITMHFEKEIDVKKAKEILEKAPSVVVIDD

PKNKKYPMPLMTSDTNETYVGRIRADVYDKKILHLWCVADQIRVGAATNAVRIAQKWLELKNK

>WP\_002866056.1 MULTISPECIES: branched-chain amino acid ABC transporter substrate-binding protein [Campylobacter]

MKKLTLTLSVLTMVNCLYAKDINIGVVLPLTGTVAAYGQDVFNGIELANKLQPKLSNGDVIKLITIDTKG

DKLETSNGVNRLIATDKVLGIIGEATTPNTIQAISIAEEKKIPLIAPVASGDKLLDKKKYASRVCFKDNF

QGDKFATYVSKDLGLKNAVIIIDQSNVYSLGLARAFENSFKNNGGKIIKKLVINSGDKDFRAVVSQLKSL

NPDFVYMPIYHPEAALIARQARQIGFDKLLAAGDGVNNQTFIDLGGSAVNGVIFTDSFDYNNPSTQLGKD

FVAAYEKVKGTKELPAFSAMGADAYFVMLNAMNACVDNLSSECINSKIHQTKDFQAVGGVISIDESGNAI

RSVVIKEIQNQKQNYKTIINP

>WP\_002866054.1 MULTISPECIES: cytochrome c biogenesis protein [Campylobacter]

MKNIIKSIGDLRVSVVLFLLFALFCALATFIESAYGTPTAWAMVYDTFWFEYIQLLLGINLLCGMFRYKM

FGLKKLPLMIFHISFLFILVGSAMTRYAGFEGILPIREHTQNSLIESSKTSLRISAIKDGERYSAVNDRY

IGNLPFANSFKLKLNLGDDQAVLKYKDLILNAHYTYKENNNSNPLLVLMLSQKGSQGVDVKFEKGEVKNI

EGVNFAFMNDNVKAPFVKIDENLTLSSSENLHFLSMLDGQNLDLKIGEKANAKERRLYEINDISFVVKAA

SLHAQEALEGSNRPQDESFWLWFKSAWLEVGRTMLISTFGEPQNWKNSLLLHFKDFALSNENKNLELTGS

NALKLELSYKNESKEFYIFEYNKPIMIELAGQKFFISWALSYEQLPFDIYLRDFVLDRYPGSMSPASYAS

EITVKNNNENFDYRIFMNNVLDYDGYRFYQSSYDQDEKGTVLSVNKDPGKIPTYIGYFLLCLGMFMNFLN

PHSRFRTLARLINKDTLKHASVIIFILLLSFGSEKTFAQDLNLTLPVVNTNHAKALATLIVQKSADGRMV

PFDTLSREILEKIHQSDSYKGQNSNAVMLSMLVDVDKWQMEPFILMPQNQAVRDAIANILEIPSTKYISY

KDFFDENNRYKLQKYVENANRKNPNARGVFDKEIIKLDERANVVNLVFSGELFKFIPVQNNPNNVWLAPF

SAVTTLKGDEGHIVLALIQNYFSAVENAFKDGNWTRADEGLKFIKEYQEKIGYKVMPSKTKVEMEIFSNK

AEIFVKLAPVYLIAGFLLLILVFSKMVVPNLKISFIFKVVYVLNVLAFVIHTVGLGLRAYLSGHAPWSNG

YESMVYIAWALSLSGIFFSRKSPIALSLTSILSGVVLMVAHLSEMNPQITNLVPVLNSYWLSIHVSVITA

SYGFLGLCALLGIFTLFLMCFLKKDGKYNLNILRNITEATRINEMAMIFGLCLLTVGNFLGAIWANESWG

RYWSWDSKETWALVSILVYAAILHLRMIPKYCNQFVFALWSMFAYWVIIMTYFGVNYFLTGLHSYAAGEA

AQIPNYVYWGFALMVVLALFARRKRNFVGKL

>WP\_002866050.1 MULTISPECIES: tRNA guanosine(34) transglycosylase Tgt [Campylobacter]

MEFKLKHKDGMARVCEITTAHSTFLTPVFMPVGTVGAVKSLDANDMKNELDAKIILANTYHMYLRPTSKV

VKDFGGLHGFTKFDRSFLTDSGGFQAFSLSKNSKHFNEGIEFKSHIDGSRHLFTPKSVLDTQYDFNSDIM

MILDDLVALPATKERVKISVDRTILWAKEAITYHKSMQNKGIGIGQNIFGIIQGGTDYKERKRCALSLNE

MPFDGLAIGGLSVGEENALMYETVQNLNPYLDENRPRYLMGVGTPEDLVENVERGVDMFDCVMPTRNARN

GTFFTSFGKFNIKKAEFINDHEAIDPACSCYTCCNFSRGYLNHLFKAKELTFFRLASLHNLHYYLELARK

MREAILNNSFTQFKRNFYHLRGK

>WP\_002866049.1 MULTISPECIES: potassium transporter TrkA [Campylobacter]

MNNILIIIDGILAKHFLERLCFEKGLGYFFTVVCQNSEKNNLNISSEYIDLHYFDPTSTARLENIMSKDF

KQAFIYMQDEFETKKSYEALRSLNPNLEIEIMDFWGLSVNDTHANLADARMTLSRRFMDFLPDIALTAQY

IGLGVGEIMEVKIPAGSIFAYRHISSIQQKRWRIVLIYRNSKIYFVKPSFVLEPNDSILIVGDPVVLQSI

FHNIRGKAGQFPMPFGSNVFALIDMKNMNQNMQERVLDTTLKLTQKSNAKRFFIHVINPKLGVMYEKLKK

LSEDKEGVFFDYFNTDFKQISTWLQNNDVGLVVTDIKNFEKEKQAFFDLKIPIMKVGEASFDELKEAIIL

SADESELENNANVITDLSKQLDFGVILYYYNPNSQNTTDMEEYFRSLSKLYDKNIQIINKNDENPLLNLQ

YREDLLQFVSFQKELLNRDFGRNLSTNLNRHYYKMRQNYQLFIPVE

>WP\_002866048.1 MULTISPECIES: 3-dehydroquinate synthase [Campylobacter]

MQVEVKLKENAYKVYIDELEELEFDSKVFILSNPKISGLHLKTLLSKIKAREIFIAAVKDGEEYKNLSTM

EEILNQMFNSKLDRKSVLISFGGGVISDMGGFAASIYQRGIDFINIPTTLLACVDAAVGGKTGVNNNFGK

NLIGTFYQPKAVYCESSFLKTLSSRELAAGMAEFIKMAAMFDDSILDFIEKIDEKSFLNATCENEIFTQI

IARSIELKSRVVEQDEKESGLRMLLNYGHTFAHVIENFTDYKLYLHGEAVAIGMVMANQLALNLGFLDKM

QSQKIKDILLKFGLPISYKINNVDEFYEAFFMDKKSSNKKINFVLAGPLGKGLIKGDISKEDIIATLREF

Q

>WP\_002866047.1 MULTISPECIES: membrane protein [Campylobacter]

MKKIIILTFFVVFAFGDVNRTIINNINEKINTLNTVISASIWNIRYENFIKYQDINDELIILNLNLKKTS

DIHQQEELKRKIANLEEQLSLLKEYKDLNFAQSLSAPDNIETLSKLTNPLAIIGAFSHIKKLKGEKEEYI

FKFNDFKNLVDKIREKNSELKELVGLKPSVENIEALKASDKKLEEFEQALNFASVSYSVYEKKIDEELSR

VSAEIKVQSLRAVNILVAIVIVIAIAFMLKFIAKKYIKDSERYYTATKIINFININIIFLILLFAYIENI

TYLVTILGFASAGLAIAMKDMFMSMLGWCVIIFGGSFRVGDRVKVFQNDTTYIGDIIDISFLRITLYEEL

TLETYNKNRRSGRIIFIPNNYVFTNLLANYTHHGMKTVLDGIDISVTFDSNLDKAQEIVENIVTRHAKGY

TELARKNIARLQHEYSIKNPKVEPRFFMFFEHWGMRISAWYMTNAYAALVLRSTISKEIIKEFNKHKDIK

IAYPSQNLYLGNLNQNHFEQHHENMHFHARNKD

>WP\_002866020.1 MULTISPECIES: hypothetical protein [Campylobacter]

MDYNVFLLNIQDKINQEDFFNLKLKFEQLQNKKEALSNLVFLRLQDPIKPLIMSMICGFLSLGWLAIDRF

MIKDYALGILRIILSLFPCVLFLILGISYENDSNLDISEIFFGLFGIFLLLGIIWWGVDLFLVYKKIKKQ

NYNKIIEFIFNYQKI

>WP\_002866019.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MVEVKNLTMRFANQLLFENVNLKLVRGQRYGLIGANGAGKSTFLKILSGEIESSSGEIVFDEGLKIAVLG

QDQFAFENYTIKDAVMCANKRLYEALKEKEKLYMSEEFTDEINERLGELEIITAEEDPNYDCETRCEKIL

SSLKIKDFDALMSTLQSADKFKVLLAQVLFLGADVLFLDEPTNNLDLEAISWLENELLRHEGTLVVISHD

RHFLNKICTRILDVDFKQIRDFAGNYDDWYMASTLLAKQAELKRDKTLKEREELENFIRRFSANASKAKQ

ATSRAKALEKLELEEIKISSRRDPSIVFRTNREIGNEVLEFKGIGKAYDKQLFSNLELKIEKNDKIALIG

ANGVGKSTLAKIIAHAISPDTGSMHLGATIELGYFPQDTSNLICENLKLYEWLMSEKFKDLDEIRKCLGR

MLFSGSDQEKMAASLSGGEKHRLMLSRLMLERPNFLLLDEPDNHLDLESIIALGEALYNFKGVVLCISHD

RELVSAFANRIWHLENGKLTDFRGTYQEFLGENDG

>WP\_002866017.1 MULTISPECIES: membrane protein [Campylobacter]

MEKIKNYKLIIILLSLDLLALLYGISTLSISADEADIYFGEQGKSLIFSHSLLYYISHFGTFIFGQNDFG

LRLPFLFFHFLSCLLLYLLALKYTKTKIDAFFSLLLFVLLPGTVASALLVNAASLVIFLTLAILCAYEYE

KKWLFYILLIIVLFVDKSFNILFLTFFFFGIYKRNAILFTLSLVLFGASISFYGFDTGGRPRGYFLDTLG

IFAACFSPLVFVYFFYTIYRLTFQKYKNLLWFLMSVTFVFCLLLSLRQKLFLDDFLPFCVICTPLLIKTL

MQSYRVRLPVFRLRYKIFIECSIIFLIFCYFLIVANQLLYYFINNPNRHFANNYHFAKELALELKKQDVL

ELATAPSLQKRLRFYGIKNSNKFYLKALKQADKHDMDKKIVKVKLGKYEKVYQILNYD

>WP\_002865990.1 MULTISPECIES: NAD(+) synthetase [Campylobacter]

MDWQKITEKMCDFIQEKVKNSQSQGVVLGLSGGIDSALVATLCKRALKENVFALLMPTQISNKANLEDAL

RLCADLNLEYKIIEIQSILDAFIKQSENTTLVSLGNFAARIRMSLLYDYSALKNSLVIGTSNKSELLLGY

GTIYGDLACAFNPIGSLYKSEIYTLAKYLNLHENFIKKAPSADLWENQSDEADLGFSYAKIDEGLKALET

NDEKLLRTLDPSLIAMLKNRMQKNTFKGKMPEILEI

>WP\_002865989.1 MULTISPECIES: tetraacyldisaccharide 4'-kinase [Campylobacter]

MSEEKNYELWLDNYFFKPNFWQKCLAFILLPLSVFYAFFAILNTFFRKKIVFKKPVISVGNLSFGGNGKT

PLCKAIAREFDGVFIVLRGYKRKSKGLFVVKNQNEILCTLTQSGDEAMEYAFEENIKGVIVSEDRVKGIE

KAFELGAKIVVLDDAFSKFHIKKFDILLESKIKPYFNFTLPSGAYRLPKFYEKRADFIALEGRDFVRYSF

VKENPKAVLVTAIAKPFRLYEHFIKARACYFFKDHYEFKKEELENLLKKHNCDTLMLTFKDFVKVKDFGF

KCQIIELNIELKDSLREKIKTYIKEFEQ

>WP\_002865923.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MALIDLIEASKKFGDKIVLNEANFSANEGEKIAIIGKNGEGKSTFLKTLLGTLPLDSGRVIRQNGKSIAM

LSQSVDFNANLSVKEAIKQELAEIYNALEEYEILHKKLEEDPSNKDYLKKIDTLMTLIDSKDAWNIESKI

IRVLKEFSLLEYENRIISTLSGGEIRRVGLCILLLKNPDILLLDEPTNHLDVYMTSFLEELLKNSKMCVI

FISHDRYFIDAIAHKCVEVEQGKLSIFKGGYANYLEKKTQILQSLAKSHETLLKQLKSEEEWLRRGVKAR

LKRNEGRKERIFKMREEAKKNPGAIKRLKLEISRAALNFNGEKTINRKKMLFELKNISKNINNKNLFKDF

STRILQGERIAIVGRNGCGKSTLLKILLGQIKQDCGEIKRGELKIGYFDQARSLVNSDKSLLEIFCPNGG

DRVEVRGKNMHVYGYLKNFLFPKEFLDKSVALLSGGEKNRVALALLFTKEYDVLILDEPTNDLDIATINI

LEEYLLSFEGAILLVSHDRYFVDKIATKLYAFEGDGYINILHTLYTEYLENEKEIEELDNFALELQTQEQ

NNNQKEKSSKKLSYKENEILKNHPEKIDFLEQKIAKLNQDLSDPNVYQEIGINKLYQELEVMQKELEILE

NEYFLVLEKSENL

>WP\_002865921.1 MULTISPECIES: DNA-binding response regulator [Campylobacter]

MLKFKILIIEDDIDLNELLVLKLKSSGYEVISLVDFFGVEDLLDNEQIDLLIVDRNLPSGDSLEKIQDLR

EQGYKEAVIFLTAKALHQDLLEGFESGCDDYVCKPFDFNELLLRIKAILKRHKKEEEKLSFGDFILDLAN

YEFFYKNQKLEISNLDYELLKCFFENPNTLLTRQFLSESVWKDDTTSDKTINIALTRLRNKFPKLKDHII

SVRGVGYKLC

>WP\_002865915.1 MULTISPECIES: amino acid ABC transporter permease [Campylobacter]

MNQKNIRIFVFFVIIILWGYFSFPIEILKIQDPSGVVSYGYTENAKAYLKSYLITLLLTACAVIIGVIIG

FSLAILRFSKFKTLNFIIDEYIDIIRGTPVILQLMIFAFVIFTFIDNLYAAILALGLNSSAYIAEIVRSG

INSVDKGQMEAARAMGLDYKTSMKEIILPQATKNILPALANEFISLFKETSVVGFISVIDITMQSQSLQA

VLYNPKPIIFTGLVYYVSVKIFSYFAKKLELRMNKND

>WP\_002865903.1 MULTISPECIES: major cell-binding factor [Campylobacter]

MVFRKSLLKLAVFALGACVAFSNANAAEGKLESIKSKGQLIVGVKNDVPHYALLDQATGEIKGFEVDVAK

LLAKSILGDDKKIKLVAVNAKTRGPLLDNGSVDAVIATFTITPERKRIYNFSEPYYQDAIGLLVLKEKNY

KSLADMKGANIGVAQAATTKKAIGEAAKKIGIDVKFSEFPDYPSIKAALDAKRVDAFSVDKSILLGYVDD

KSEILPDSFEPQSYGIVTKKDDPAFAKYVDDFVKEHKNEIDALAKKWGL

>WP\_002865902.1 MULTISPECIES: polar amino acid ABC transporter ATP-binding protein [Campylobacter]

MIELKNVNKYYGTHHVLKNINLSVKEGEKLVIIGPSGSGKSTTIRCMNGLEEVSSGEVVVNNLVLNHKNK

IEICRKYCAMVFQHFNLYPHMTVLQNLTLAPMKLQKKSKKEAEETAFKYLKVVGLVDKANVYPATLSGGQ

QQRVAIARSLCTKKPYILFDEPTSALDPETIQEVLDVMKEISHQSNTTMVVVTHEMGFAKEVADRIIFME

DGAIVEENIPSEFFSNPKTERARLFLGKILKN

>WP\_002865901.1 MULTISPECIES: chemotaxis protein methyltransferase [Campylobacter]

MEKKITPSELELNEFIKIINEMSGIDLTDKKNILALKLNKFLEGTNTKNFSEFLGKLKSNRQLKQETLDF

VTIGETYFLRELAQLKEIIYYAKSLEKRVNILSAPCSSGEEVYSLALLAAQNFIKDMYILGIDINSSVIE

KAKLGKYQGRTLQRLSESEKRRFFLESEDKFYTINKNELCTCKFELCNVFEEKFSRLGKFDIIASRNMII

YFDHESKLKLMERFHRILNDKGRLYVGNADLIPETIYFKKIFSPRGVYYEKV

>WP\_002865899.1 MULTISPECIES: adenine phosphoribosyltransferase [Campylobacter]

MIKLTQEEQKYLLDSIRIIPDFPKKGIIFRDITTLLNNKEALNFLLKHLKERYKDYNLDFIAGTESRGFI

FASMICAKLNLPFVPIRKPGKLPFETFSCEYDLEYGSDKVELHKDAFKNIQNARVLLVDDLIATGGTAIA

SYELIQKAGAKCVEACFLMNLKDLNGANKLEKLTSVYSVLEI

>WP\_002865887.1 MULTISPECIES: pyruvate kinase [Campylobacter]

MLKKTKIVATVGPASEKEEILRQMIINGVNVFRLNFSHGTHEYHKKNLDTIRRVAKELHTRIGILQDISG

PKIRTGELKEPFELKKGDRLDFYRETILGEKIAQNHYKISINQKSILDMLKIDEYIYLYDGSIRAKVVSI

DNQKIETIIENDGFLNSNKGINFPNTKINIDVITQKDKNDLLWGIKNEVDFLAISFVQNAHDIDEVREIL

AQNNAKISIFAKIEKFDAVENIDEIIKSSDGIMVARGDLGIEVPYYKVPNIQKEIIQKANNASKPVITAT

QMLFSLAKSKTATRAEISDVANAVLDGTDAVMLSEESAVGIDPANAVDIMCQTIIETEKRYPYNKFNDFN

DLDNTDKIMRSSAHLATDLNADAIFSLTSSGKSAIKIARYRPNIEIIAVGHSEKTLNSLSIVWGVNPAIL

VNKSNELTELLKDSVRSSVEKGFMDEDKCYLLTAGFPTGVEGTSNLIRILNKEQIAYYLQ

>WP\_002865584.1 MULTISPECIES: hypothetical protein [Campylobacter]

MDLKSLENNRLYILKRLGILKFLSIIEALLVGFLAFVFIRDALIAVILAVFVGVFFFRFTAKKLKLAQKE

LQINALNLFLRRFGAKFKKQSLSQKDFLKLGLTKDLKEFKSQNCFEFKDFKIYDIQFLDENKRFFCGILL

EILSANKNPSFENEEQIYIKLQDKNFTLNHIFSKENHYLIATLSNPFFIDVKKDLESNFKDLEENLNSIK

NKLFK

>WP\_002864610.1 MULTISPECIES: MFS transporter [Campylobacter]

MENFNRTLLVCWFGVFTTSMGLSQIAPILPFYIKELGHVDTSEIAFYSGLAFGITPLFMAVFSPLWAFLG

AKYGYKNMLLRASFGMSVLTLWLSFAHSALEVVFVRGLTGIISGFTSAAVVFIAVIAPKEKVAYALGTLS

TASISGSLLGPLFGGFVAEFFSISAVFDVVAFLIACSFVTIYFFIHGRKIQKEAKKNTQKVKENKTLIIV

LFITTFVIQFGTFGVMPILSIYVEQIHQGGNLALWAGIVVAANGISNLFFAPKLGKIADKIGPSKIIFGA

LIFCGICFYLQAVASNVYTLIFVRLLIGVGLGGLLPCVNALLKKSVSAKNLSVIFGFNQTCQFLGNFCGA

FGGGLMASHFSVEFVFTFVCLIFIINAFIFLAFEKKYIFSNQGL

>WP\_002862267.1 MULTISPECIES: hypothetical protein [Campylobacter]

MAFMNFSGFFYARNDLRLFKIEKKNELKSFFYKDYTLSSYKDALNLNNEIFFYQSLKEGLFKENDEILVS

NLGKKIILFRNFTQNCDNFNEAKLKQILLLFFLLLASVFFASLAMINEFGAIDLVFLMICLLLLVMGVIN

LGLLFKQIRILKSFSKEEMKEFLSQRMKKYTKV

>WP\_002862245.1 MULTISPECIES: imidazole glycerol phosphate synthase subunit HisH [Campylobacter]

MKIIIIDTACANLASLKFCLDRLGFNATISRDLKELESADKLFLPGVGTAKEAMKNLEQFNLIDFIKNTK

KPLLGICLGMQILGNFSEELNQETLKLIDFTTQKFKAKEGFTFPHMGWNQVHSSHALFKGLEGAYFYFVH

SYCVGLGEYTIADCEYSQKFSASVMKDNFYGVQFHPERSSEAGEILISNFIKDIG

>WP\_002862181.1 MULTISPECIES: acetyl-coenzyme A synthetase [Campylobacter]

MLNQNNQELFKPSKEFSRNARIKNLCEYYDLCDEAKEDFEGFWKRQALEKIEWFSPFSRVLNEDKAPFYK

WFEGGTLNVSYQCLDRHMKTRRNKAALIFEGEMGDYEVYTYRRLLHETCKAANLLKKFGVKKGDRVVIYM

PMIPETAIVMLACARIGAIHSVVFGGFSPEALRDRIIDAGAKLVVTADGAFRRGKPYMLKPAVDKALSEG

CESVEKVLIVIRNNEPIEYIKGRDYVYNELVKNESYKCEPEIMDSEDLLFLLYTSGSTGKPKGVMHASAG

YILWAQMTMEWVFDIKDYDNYWCSADVGWITGHTYVVYGPLACGATTIMHEGTPTYPNSGRWWRMIEEYQ

ISKFYTSPTAIRMLHADAPDEPRKYDLSTLEVLGTVGEPINPSAWKWFYDEIGGTKSPIVDTWWQTETGG

HMITPLPGATPLKPGCATLPLPGIFAEVIDEEGNKKDEGEDGLLCITKPWPSMIRGIWGNDERYIESYFS

QAKKDGKAVYFSGDGAFYDKNGYITITGRTDDVVNVAGHRIGTAEIESAIAKHPSVAESAVVSILDAIKG

ESLFAFVVLSPASSCDLGGAIETLKELNDILRVEIGPIAKIEKILYTPGLPKTRSGKIMRRILRTIARGE

EIKQDISTLEDSGVVETIVKLAKAEFE

>WP\_002862151.1 MULTISPECIES: adenylosuccinate synthetase [Campylobacter]

MSKADIIVGIQWGDEGKGKVVDKLCENYDFVCRSAGGHNAGHTIWVNGVRYALHLMPSGVLHPRCINIIG

NGVVVSPEVLIAEMAQFENLKGRLYISDRAHLNLKHHSLIDIAKEKLKGKNAIGTTGKGIGPSYADKINR

TGHRVGELLEPQRLCEALMKDFEANKTFFEMLEIEIPSAEELLADLKRFNEILTPYITDTTRMLWKALDE

DKRVLLEGAQGSMLDIDHGTYPYVTSSSTISAGALTGLGLNPKEAGNIIGIVKAYATRVGNGAFPTEDKG

EDGEKIAQIGKEIGVSTGRKRRCGWFDAVAVRYTARLNGLDALSLMKLDVLDGFEKIKICRAYEYKGMEI

DYIPSDLENVQPIYEEMDGWDKVFGIKDYDLLPENAKKYIARLEELAGVKVKYISTSPERDDTIIL

>WP\_002862071.1 MULTISPECIES: nicotinate-nicotinamide nucleotide adenylyltransferase [Campylobacter]

MKIALFGGSFDPPHNGHNSVVLEALEKLDIDKLIIMPTYINPFKQSFSADEKQRFLWVKKLWGHLPKVEI

CDFETKQKRPVPSIESVKYLYKLYNPSKFYLLIGADHLEKLHLWHDFEKLNSLVEFVIANRNDIEIPKNF

KDLKTDKKIASSFIRNTLNTNEVCEEIKDEVKKYYEKLQKN

>WP\_002862042.1 MULTISPECIES: aminofutalosine synthase MqnE [Campylobacter]

MKNLITKLENEERLNQEEANALWDLDLFTLGKYAHKKRTKLHGKKVYFNINRHINPTNICADTCKFCAFS

AHRKNPNPYLMTHEEIMKIVDETVKRETKEVHIVSAHNKDTTWQWYLEIFKMIKEKYPNLHVKAMTAAEI

DFLHRRFKMSYEEVIEKMLEYGVDSMPGGGAEIFDEEVRKKICHGKVSSENWLKIHKLWHEKGKQSNATM

LFGHIEERHHRIDHMLRLRDLQDQTGGFNAFIPLVWQRDNSFIQTDKIMDSEEILKTIAIARLVLDNIKN

IKAYWATMTLNLAMVAQEFGANDLDGTIEKESIQSAGGAKSAKGTSLKTFIDMIKTSNLIPVERDSLYNE

LKTY

>WP\_002861955.1 MULTISPECIES: DNA-binding response regulator [Campylobacter]

MINVLMIEDDPDFAQLLSEYLAQFNIKITNFENPKSALNVGVQGYDCLILDLTLPGIDGLEVCREIRQKS

NIPIIISSARGDLSDKVVGLQIGADDYLPKPYDPKEMYARIMSLIRRTKRVEHANNENINSAFKIDERRH

EITYEDKVLTLTPAEFEILEYLIQQHGYSVSREQLVSRCKNLKDKDSKSLDVIIGRLRVKIGDSSKSPKH

IFSVRGIGYKLIG

>WP\_002861720.1 MULTISPECIES: glutamine ABC transporter substrate-binding protein [Campylobacter]

MKKILLSVLTAFVVVVLAACGGNSDSKTLNSLDKIKQNGVIRIGVFGDKPPFGYVDEKGNNQGYDIALAK

RIAKELFGDENKVQFVLVEAANRVEFLKSNKVDIILANFTQTPQRAEQVDFCLPYMKVALGVAVPKDSNI

TSVEDLKDKTLLLNKGTTADAYFTQNYPDIKTLKYDQNTETFAALMDKRGDALSHDNTLLFAWVKDHPDF

KMAIKELGNKDVIAPAVKKGDKELKEFIDNLIIKLGQEQFFHKAYDETLKAHFGDDVKADDVVIEGGKI

>WP\_002861719.1 MULTISPECIES: MFS transporter [Campylobacter]

MQKKYKNIIYASLGGILEFYDFVLFAFFLDIFAKVFFPQNDAFWMQINAYIAFGAAYLARPFGSIVMAHF

ADRYGRKNIFYISMLLMVLPSFALAFLPSYESIGIFATLILFTIRILQGLAVGTEVSGAWIYVSEFVKGR

QIPLALGFISATLTIGLLLGNIATLGIRSYFTPEEVQSYAWRIPFIIGGFFGILALFLRNKLSETPEFVK

VQNEKKILSFPLFEALKTHKMSMLVCFLMTMVLTSGVATLMILPKYFESLLAMSKTSALWVQNFAILAVI

FGALFQGFLASKWGSYRICSIFSIAFIIFGMLFSFYDEKFLFYFLLACFTQGIITFAPVFMTQIFKSELK

FSGLSFAYNISYAILGFLTPFVVNAFYKEYLGIYLAIVGSCSLFCVFLLKRVFARSKIKELSIVF

>WP\_002861386.1 MULTISPECIES: glycine--tRNA ligase subunit alpha [Campylobacter]

MTFSQMILNLQNYWQEQGCAIMQPYDMPAGAGTFHPATFLRSLGKKPWAAAYVAPSRRPTDGRYGENPNR

LGAYYQFQVLIKPSPDNIQELYLKSLENLGFDLKSHDIRFVEDNWESPSLGAWGLGWEVWLDGMEVTQFT

YFQQVGGIAVDLVSAEITYGLERIAMYLQNVDNVYDIVWSEFNGEKIKYADVHKQSEYEFSKYNFEVSDV

KILNEQFENSYKECKNILEQGLALPAYDYCMLAAHTFNLLDARGAISVAQRQDYMLKIRELSKNCAEIYK

KNLNETE

>WP\_002861208.1 MULTISPECIES: amino acid ABC transporter permease [Campylobacter]

MLELLNTDTLLRLWQGLFVTLEISFISIIITSIGGLFLGILMSFKNTYIYAFCRLGLEFVRVMPLLVWLF

VVYFGFPRWFGWDLSSVSAAIIVFSIWGCFEMMDLVRVSLQSIPKHQYESASSLGLNTVQSFVYIIIPQA

MRRLTPMSMNLLTRMIKSTTFAYLIGAVELVKVGQQIIEFHNRNDFAPFIIYGLIFFIFFILCYPITLYS

RKLEKKWS

>WP\_002861166.1 MULTISPECIES: hypothetical protein [Campylobacter]

MQISSSYNSYDYYSSKPSFDKTNQSDSTQKDEKNLSENKDDKEKNGEQTQMVNGVELSQKEVAQVRELQS

IDRNVKAHEAAHQAAGGGLAGAASFTYTRGPDNQMYATAGEVPISMQKGNTPEETIANARQIAAAAMAPA

DPSPQDYKVAANATKMEFEARAEAMKLKAEEAKEKEEENKEKDDKNSENSLEKTDKDSKNNDKNSNFDKD

FKNFVARTYQQNSQNNDIKFNIAS

>WP\_002861157.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKYILLASSMLILAACGGTSSNFVNVSMPNFKPQVPTKVEPIDSGVSIALEPINIEQNNNYSDYFENSV

LKIRIEKEIDLLKRNLEEQIKTIAQLKGYKIVTTNPDYTLKSSISIYTEEKNAQKTSNFMSGDYVKSNLG

INFKGKIDFIDAHNPQNSTNLSSSTKLDSLVALNYPIKNDDGVNMFKTTISTVPTQLNKGLEQPAFEIDK

SFLAFYKNTLNTLYNNLPKATDIGKTIPNTNSGFNSFDGDATFEESLPQTNSNQNNTIENTPTQNIPTNP

SSTNQNNQSKNQDGVEIFE

>WP\_002861057.1 MULTISPECIES: acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase [Campylobacter]

MKKIHPSAVIEEGAQLGDDVVIEAYAYVGKDTKIGNDVVIKQGARILSDTTIGDHSRVFSYAIVGDIPQD

ISYKEEQKSGVVIGKNATIREFATINSGTAKGDGFTRIGDNAFIMAYCHIAHDCLLGNNIILANNATLAG

HVELGDFTVVGGLTPIHQFVKVGEGCMIAGASALSQDIVPFCLAEGNRASIRSLNLVGIRRRFDKDEVDR

LSRAFKTLFRQGDLKENAKNLLENQESENVKKMCHFILETKRGIPVYRGKNNA

>WP\_002860962.1 MULTISPECIES: DNA (cytosine-5-)-methyltransferase [Campylobacter]

MVNNTKKLKAIDLFAGIGGIRIGFKNIFQEKLEFVFSSEIDKFACQTYFCNFNELPHGDITQINENNIPK

HNILLAGFPCQAFSIAGHRKGFNDIRGTLFFDVARIVKKHKPEIVFLENVKGFKNHDKGKTFSVVKNTLE

DMGYDVFSEVLNARNFGIPQNRERIYIVAFLKNKFKNISFNFNELKNIEIKSKLGDILEKNVDEKYTISD

KLWAGHQRRKLEHKKKGNGFGYSLFNHNSDYTSTISARYYKDGSEILIEQKNKNPRKLTPREAARLQGFP

NSFKITTSDNQSYKQFGNSVAIPVIENIAKLIHRELYNVNK

>WP\_002860943.1 MULTISPECIES: protein TolB [Campylobacter]

MKKIVAIFLVFLGSLWAEDPVIDVVNSGVVLPKIIVKDNSNLSDENLKKSFYNIIVNDLKVSSNFEVVAN

ATETSNYTFEYALNKNGNTLSLNVKIKAGGSDKSEQTYTLNGLEQYPFLAHKSVKASVNALGLAPVDWMD

HKILIARNSSSKKSQIIMADYTLTYQKVIVDGGLNLFPKWGNKEQTLFYYTAYDHDKPTLYRYDLNTNKA

SKILSSGGMVVASDVSVDGSKLLVTMAPKDQPDVYLYDLNTKNLTQLTNYSGIDVNGNFIGSDDSKVVFV

SDRLGYPNIFMQDLNSNSAEQVVFHGRNNSAVSTYKDFLVYSSREPNQAGVFNIYLMSINSDYIRQLTAN

GKNLFPRFSSDGGSIVFIKYLGAQSALGVIRVNANKTFYFPLRVGKIQSIDW

>WP\_002860433.1 MULTISPECIES: S-ribosylhomocysteine lyase [Campylobacter]

MPLLDSFKVDHTKMPAPAVRLAKVMKTPKGDDISVFDLRFCIPNKDIMSEKGTHTLEHLFAGFMRDHLNS

NSVEIIDISPMGCRTGFYMSLIGTPDEKSVAKAWEEAMKDVLSVSDQSKIPELNIYQCGTCAMHSLDEAK

QIAQKVLNLGISIMNNKELKLENA

>WP\_002860276.1 MULTISPECIES: hypothetical protein [Campylobacter]

MQVNTFSNIASMAQTQVSNKKADDAKENTKDKNVQSANSSKDVDKNTLEKLNALGGKGITQIYLVQFQQQ

TMNAVIGSSNAQTGLDSLLNGANLDTAKSILTNIDFASLGYSGKNPLDMNTDELQQLVSEDGFFGVENTA

NRIADFVIKGGGDDVEKLKKGLEGMKKGFEQAEKMWGGELPQISQDTIDAALKKVSDRIDELGGKTLDLQ

A

>WP\_002860199.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKILIFCIGLFLGACGYVPTSKIANNIFDEKVYVNVELSQQDPKNSIYVADTLKEMVISKLGRKLALKH

EADDVINVKMNNLEFIPLAYDKNGYVISYKAKLNLDFNVVFKDGSSQAFSTSGSYNFEISPNSIISDSAR

YEAIRAASSEAFDEFISVIAIKGQKRDSKY

>WP\_002859889.1 MULTISPECIES: ribulose-phosphate 3-epimerase [Campylobacter]

MYVAPSLLSANFLKLEEEVKAIEAAGADLLHIDVMDGHFVPNLTFGPCVIEKISTISKLPLDVHLMVKDV

SKFIDLFIPLKPKFISFHMESEVHPIRLCEYIRSQGIHPAIVLNPHTPIDSIKHMLEFVDMVLLMSVNPG

FGGQKFLPLVHEKIKELRQMIDKKNAKVFIEVDGGVNGLNASDLEESGADILVAGSYIFSSNDYKTAISS

LKLEF

>WP\_002858915.1 MULTISPECIES: arsenical-resistance protein [Campylobacter]

MLGFIDRFLTLWIFLAIFLGLILGIIFPNIALFWNLFEYKSVNVVLTLCLILMMYPPLAKVDYAKLSKVF

DSKKVILLSMILNWFIGPLLMFILAFIFLKDEPLYMQGVIIIGLARCIAMVVVWSDLAKGDREYTSALVA

MNSIFQILFFSTLAYIYLDFLPKLLGQSTLATSLDIDFSALSKNVLIYLGIPFLMGFITRTLLLKYKSKR

WYENTFLPKISPITLITLLATIIIMCSYKANEVFHLPLEALKIAFVLTLYFIFMFFLTWFISKKNHLSYP

KTCSLCFSASGNNFELAIIICIATFGLHSEQAFASIIGPLVEVPVLILLVKWALGKSLNSKKMNQAS

>WP\_002858390.1 MULTISPECIES: ATP synthase subunit A [Campylobacter]

MKDLFLFSSLLDASHTFSYFFHIGLVALIAVIVAMMATRSMQLVPRGMQNLGEAFLEGVLSMGRDTMGSE

KGARKYLPLVATLGIIVFFSNIIGIIPGFHAPTASLNLTLSLAIIVFVYYHFEGIRAQGFVKYFAHFMGP

IKLLAPLMFPIEIVSHLSRVVSLSFRLFGNIKGDDLFLMVILALVPYIAPLPAYVLLTFMAFLQAFIFMI

LTYVYLAGATVVEEGH

>WP\_002857723.1 MULTISPECIES: F0F1 ATP synthase subunit B' [Campylobacter]

MFEDMHPSIMLATMAIFLAMIVILNSMLYKPLLKFMDERNDSIKNDENKVKENSQEVLGVNDELEAIHIN

TREEIQKIKQSAIAAAKEEAEQILRSKKEELERKMASFYADLAVQKKELQEHLNIHLPELKQALQNNIKK

I

>WP\_002857621.1 MULTISPECIES: tRNA (N6-isopentenyl adenosine(37)-C2)-methylthiotransferase MiaB [Campylobacter]

MSAKKLFIQTLGCAMNVRDSEHMIAELTQKENYALTEDIKEADLILINTCSVREKPVHKLFSEVGGFEKV

KKEGAKIGVCGCTASHLGNEIFKRAPYVDFVLGARNISKITQAIKTPKFMGVDIDYDESEFAFADFRNSI

YKSYINISIGCDKHCTYCIVPHTRGDEISIPFNIIYKEAQKAVEKGAKEIFLLGQNVNNYGKRFRNEHKK

MDFSDLLEELSTIEGLERIRFTSPHPLHMDDKFLEVFANNPKVCKSMHMPLQSGSSEILKAMKRGYTKEW

YLNRALKLRELCPNVSISTDIIVAFPGESEKDFEETMDVLEKVRFEQIFSFKYSKRPLTKAATMPNQIDE

ETASRRLSTLQNRHSEILDEIVKKQENKTFKVLFEELRAGNSIAGRTDNNFLVQVEGSEELLGQFKEVKI

TNAKRMVLYGEIV

>WP\_002857583.1 MULTISPECIES: membrane protein [Campylobacter]

MLNWKKIQELNLKEVAAKTQIELDFLEALVEKNFAVLSRFNVKGFVKILSREYELDFSDFNEEYEAYLNE

NNPTPQTKSKMITPKLDAYSQKSSNAWPFLIVLIVLVIIGSGIYYFDTLKTFFKDEQNNTSATVIDIIGQ

AQENLKSLGGNNVVVIDNNKAQETNQTESVLPSQNISLQENDKNISIENNISENNTTLLDEEKNTQIQED

TNTPKTDSLKEAHFKTSTKIWIGLIDLKSLKKTSFVKEKDFNISLDKDQLILTGAAALTMFDQENKEQKF

PAGISKRFLIKDGKITSISAAEFVKLNKGKEW

>WP\_002857569.1 MULTISPECIES: hypothetical protein [Campylobacter]

MQVNYRTISSYEYDAISGQYKQVDKQVEDYSSSGKSDFMDILNKADEKSSGDALNSSNSFQSNAQNSNSN

LSNYAQMSNVYAYRFRQNEGELSMRAQSASVHNDLVQQGANEQSKNNTLLNDLLNAI

>WP\_002857551.1 MULTISPECIES: tautomerase [Campylobacter]

MPLVNIKLAKPSLSKEQKAELIADITELLSTKYNKSKERVVVVLEDVENYDIGFGGESVEAIKAKANK

>WP\_002857480.1 MULTISPECIES: DUF493 domain-containing protein [Campylobacter]

MVNLCDLKKEPQINYPTFWDYKVIFEVHVKASEIFQEILGQREYKFEHSNSSASGKYQSYLLNVYVDSKK

DRLDIFDKLKAKAKFVL

>WP\_002857440.1 MULTISPECIES: chemotaxis protein [Campylobacter]

MFGSKINHSDLQKLEEENKNLAHKIEKFQSENLELKNKITSLEQAALESKLKTDLLNVLLTGVLKNITIV

QGDMLENVNKAEVISSYSKTSLAEMDELNHIANSINASLGDITESANKTRDVAGTLHRSVDEITNVINLI

KDVSDQTNLLALNAAIEAARAGEHGRGFAVVADEVRKLAEKTQKATTEVEMNINLLKQNANEMYTQSEQV

EKISIDSNAHIMSFSEKFTHLVNEAHSTNSNAVGIASEAFVSLAKLDHIAFKLNGYKEIFSKSGKQLADH

TSCRLGKWLASTGKERFGQNKSFLKINEPHEKVHENMNNAITIANTEDISKDITQHSIINKCEVAENASL

DLFNVFKEMLDESDH

>WP\_002857432.1 MULTISPECIES: diacylglycerol kinase [Campylobacter]

MKPKYHFLNNARYALEGLFALFKNEMAFRIELCIIIPAIVFSFFLKVSFLEHLLLISVLILILIVEALNS

AIEACVDLITNKWHEKAKIAKDCASAAVFFSVLLALFVWGFILYSIYL

>WP\_002857332.1 MULTISPECIES: ArsR family transcriptional regulator [Campylobacter]

MKFENLIREILGKKRFELLKFLCENADENGFIMIKISDLEEKLHQSKPTIIATFKFLEEKKLFKRLKNGF

YQLNIGGKNDT

>WP\_002857306.1 MULTISPECIES: HIT family protein [Campylobacter]

MIYENDLIYIEKEEAQVPWLKIFTKEIYKEFSDCPLELQKELFEKILLCEKAMIEFYKPEKINIASFANY

VPRVHFHVMARFKEDAFFPECMWGKQQREAIKLDLPKFEEFVKFLNSKIF

>WP\_002857271.1 MULTISPECIES: hypothetical protein [Campylobacter]

MAKDANGTELNAGDSVSVIKDLKVKGASTTLKRGTTIKNIKLTSKEGEIEARVDKFGVIVLKTEFLKKI

>WP\_002857098.1 MULTISPECIES: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase [Campylobacter]

MIIELAKNYGFCFGVKRAIKKAEQIKDAATIGPLIHNNEEISRLQKNFNVKTLENIQALSNEKKAIIRTH

GITKQDLEELRKKDIEIFDATCPFVTKPQQICEQMSKEGYEVVIFGDENHPEVKGVKSYVSTKAYVVLDK

KELQNIKLPNKIAVVSQTTKKPEHFMEIVNFLILKTKEVRVFNTICDATFKNQDAIKELSLKSDVMVVVG

GKNSANTKQLFLIAKTNCEDSYLIETEEELKKEWFLDKKHCGISAGASTPDWIIQKVIAKIENFKIN

>WP\_002857007.1 MULTISPECIES: formyltetrahydrofolate deformylase [Campylobacter]

MISVLKICTKDQKGLIYRISDVIFKYHINIVKNDEFVGEGMFFFRALLEGEFDKEAFIGTLEAMLGQEAL

IELCEKRKKDIVVFATKESHCLGDLLIKHYSNELEANIKAVISNHNSLKDLVEKFEIPYHFISAENLDRK

EQENQILKCLEQYKFDYLVLAKYMRILSPDFVRHFEGKIINIHHSFLPAFIGANPYKQAFERGVKIIGAT

AHFVNNNLDEGPIITQAVLPVNHEFTWQDMQQAGRNIEKDVLSKALDLVFEDRIFIHNNKTIIF

>WP\_002856966.1 MULTISPECIES: HrcA family transcriptional regulator [Campylobacter]

MKSRDKKDLILDSIIQTYLLDNVPIGSNELNLNLCIPASTIRVYLKRLSDEGLITQLHISSGRIPTILTM

QNYWQSFWKKEQDQDINIKSENFLKELSKEFEIYCLVYGGRSLVLKEVLDLNAKFIVLDFKEEELVLKYE

KEAWNFLQSLIGLDLFSIEKIALRVHFMDLVEKIASLRQNLICYRSNEERAYQIYQNDEFVKLLDCGVHR

YFKESLEFEPLFKEGFMGLKVDAQFLGEDVNIILAGSVYTDYKKILQYIKEAA

>WP\_002856855.1 MULTISPECIES: hypothetical protein [Campylobacter]

MSDIRDEFEQDMDKKKEILLSCQNSKNLNSCYNCDEIFNCQTRKNYVDAVYNSMSKGKTEGGFDF

>WP\_002856760.1 MULTISPECIES: molecular chaperone DnaK [Campylobacter]

MSKVIGIDLGTTNSCVAVYERGESKVIPNKEGKNTTPSVVAFTDKGEVLVGDSAKRQAVTNPEKTIYSIK

RIMGLMINEDAAKEAKNRLPYHITERNGACAIEIAGKIYTPQEISAKVLMKLKEDAEAFLGESVVDAVIT

VPAYFNDAQRKATKEAGTIAGLNVLRIINEPTSAALAYGLDKKDSEKIVVYDLGGGTFDVTVLETGDNVV

EVLATGGNAFLGGDDFDNKLIDFLANEFKDETGIDLKNDVMALQRLKEAAENAKKELSSANETEINLPFI

TADASGPKHLVKKLTRAKFEGMIDSLVAETITKINEVVSDAGLKKDEIKEIVMVGGSTRVPLVQEEVKKA

FNKDLNKSVNPDEVVAIGAAIQGAVIKGDVKDVLLLDVTPLSLGIETLGGVMTKIIEKGTTIPTKKEQVF

STAEDNQSAVTINVLQGEREFSRDNKSLGNFNLEGIPPAPRGMPQIEVTFDIDANGILTVSAKDKATGKA

QEIKITGSSGLSEEEINNMVKDAELHKEEDKKRKEAVDARNAADSLAHQVEKSLSELGEKVAAADKENIQ

KALDDLRETLKNQNASKEEIESKMKALSEVSHKLAENMYKKDEPNTANDKKKKDDDVIDAEVE

>WP\_002856736.1 MULTISPECIES: 3-deoxy-manno-octulosonate cytidylyltransferase [Campylobacter]

MIIIPARLKSSRFHEKILCDIGGVPMFVATARRVSSVDEVCIALDDEKVLSIAKEYGLNAVLTSKDHESG

TDRINEACKKLALKDDEIIINVQADEPFIECENLLKFKEFASSCLDKKAFMASCYKKITQEEAMDPNLVK

VLCDKEGYALYFSRAKIPYERENYEESFKGHLGIYAYSVKALREFCSLSSSALERAEKLEQLRAIENGKK

IKMLEISTTSMGIDTKEDYERALKIYLEK

>WP\_002856715.1 MULTISPECIES: anaerobic C4-dicarboxylate transporter [Campylobacter]

MDFLTSLSEGGQFAIQIIIVLICLFYGAKKGGIALGLLGGIGILMLVFAFHIKPGKPAIDVMLTILAVVV

ASATLQASGGLDVMLQIAERILRRNPKFLTILAPFVTCFLTILCGTGHVVYTIMPIIYDIAIKNGIRPER

PMAAASISSQMGIIASPVSVAVVSLTALLLNANHKLAGFDGYINLLQITIPSTLFGVLCIGIFSWFRGKD

LDKDEVFQEKLKDPEFKKYVYGDSKTLLGVKLPKSNWVAMWIFLGAIALVALLGVFDFLRPNWGQVVKNG

IPQVDALGNPKMDVLSMVSVIQMFMLLAGSLIIIFTKTDAKKIGSNEIFKSGMIALVAVFGISWMADTMF

AVHTPMMKAALGDIVKEHPWTYAVMLLLISKFVNSQAAAISAFVPLALGIGVEPGVIVAFAAACYGYYIL

PTYPSDLATIQFDRSGTTHIGKFVINHSFILPGLIGVITSCIAGYFIAMAAGYL

>WP\_002856631.1 MULTISPECIES: serine/threonine transporter [Campylobacter]

MNTPKWTSHDTRWVLSLFGTAIGAGVLLLPISAGLGGLIPLLVILVLAFPMTYLAHRNLCRFVLSSSNPK

DDITFVAESYFGKGGGFLITLLYFFAILPILLVYSANLTTTLLEFLINQFNFNADLTHAARWWVSFLIVG

VLVLISILGENVVTKAMSFLVFPFIIFLFIFSLLLIPQWNSSLFTNVDFSVISTSNFWVTLWLVIPVMVF

SFNHSPIISSLACYCKKEYGDYAEPRARKIISLAIILMVFVVMFFVFSCALTFTPEDFASAKDQNINILT

FIANKFPEVSLLAYVGPIVALVAISKSFLGHYLGSQEGLNGILYKASNGKIQGKFAQTLTAIITFAIAWL

VAYKNPSVIGIIEAIGGPVLAILLFLMPLYCIYRFDILARFRNKFLDLFILVMGIVAISAAIHDLL

>WP\_002856602.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKAKLTLLALLGATVLLAKDMVVPASELPNNAKEFISKNFKTAQIGLVKKDIDSYDVILNDGTEIDFMIN

GDWKEVDGKYKALPHTILPSVMKKVSATQPNAQILEIDKEINGYKFKFNNNMKVYTDMQGNVLGQKLD

>WP\_002856563.1 MULTISPECIES: tyrosine--tRNA ligase [Campylobacter]

MDIKKILAEVKRGCAELIDEERIENLIKNYYEKGENFFIKAGFDPTAPDLHLGHSVVLTKMAFLQKHGAI

VQFLIGDFTGQIGDPSGKSATRKKLDKEQVLINAKTYETQVFKVLDKEKTQIKFNSTWLNELGAAGIVEL

TSTFSVARMLERDDFTKRFKEQSPISICEFLYPLLQGYDSVALKSDIEMGGTDQKFNLLMGRQLQRVYNI

GKEQAVIMMPLLEGLDGVNKMSKSLNNYIGVTEKANDMYAKILSISDELMFRYYELLSQKSLEEIAQIKK

DIEQGNLHPKKAKENLALEITERFHSKEEANNAKSEFDRIHSQNALPSDMAEFEIQGKIWLAKALVECGL

ESSTSAARRSISANAVSVNSQKVSDEQMHLEQGEYILQIGKRKFAKLKVKE

>WP\_002856539.1 MULTISPECIES: ribose-phosphate pyrophosphokinase [Campylobacter]

MRGYKIFSGSANVEFARQVSKYLSLPLSDAGVKRFSDGEISVQIDESVRGKDVFIIQSTCAPTNDNLMEL

LILTDALRRSSANSITAIIPYFGYARQDRKANPRVPITAKLVANLIQAAGIDRVATIDLHAGQIQGFFDI

PVDNLYGSIVFNDYIKAKHFKNAIIGSPDIGGVARARSVAKHLGLDIVIVDKRREKANESEVMNIIGDVK

DKEVILVDDIIDTAGTIVKAAEALKEKGAKSVMACCTHAVLSGKAYERIASGALDELVVTDTIPLKEQLP

NIKVLSVTPVFAEVIRRVYHNESVNSLFI

>WP\_002856474.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKILLSFAFFASLASANTINAIAVVVDKEPITTYDIDQTMKALKIDRNKALGVLINEKMEISQMKQLGI

VVNDLELDDAINKMLAQNKTTLNAFKANLKSKNQSYEQFRTNFKKDLEKRKLYEKIASMAKTDFSDDGAK

KFFEQNKDKFTFYTQINANIYLSNNPQTLENIKNTKKTILKPQNASLNTSNADPRLLGLLSQIPVGGFSP

VLNGKNGYELYEVKSKDGTQTPEYEQVKNEVLNAYVSEQRQNFIQDYFDKLRSKINIEYLR

>WP\_002856400.1 MULTISPECIES: thiamine phosphate synthase [Campylobacter]

MKNKLDLSLYLVASQGNKSEECFLNTLENAIKGGVSIIQLREKELNAREFYKLGLKVQKLCKAYKIPFLI

NDRVDIALALDADGVHLGQEDLEVKLARKLLGDEKIIGLSLKKLEQLEFIQGANYLGCGAIKATPTKESS

LLSLELLSQICDKSPIGVVAIGGVDKAVLDELKGINLSGVAVVRAIMDAKDAFLAAKELKRKIYENLPLK

>WP\_002856386.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MPNLIQANKLTLGYDELVIKEASFAFKDDDFVFITGKSGSGKSTLLKSFYGDLEPISGKLEVCGSLMNKI

GNLELLKLRQRIGIIFQDYKLVQEYSVEKNVMLPLMIKGYSKKVCHDQAAKLLKHVNLTFKADKLPNQLS

GGEQQRVAMARALAHNPKLLLCDEPTGNLDEYSSDIIWTLLKSARELLGTCVIVVTHRIPSNLRVDYRRF

NIENGKMNEIF

>WP\_002856298.1 MULTISPECIES: uroporphyrinogen-III synthase [Campylobacter]

MKIYLLNETPFKGVENLILNEIIFYDFSIDLSLYDALICTSKNALKALQNAKITLNFKLNLYAVGQSTAQ

YAKNLGFKKIKIPSKAYGKDLFLEFKEELKTQKCLYLRAKNIVSTLNLDLKNVGVDLDEVIVYENVFKKG

DKKLTHPAIFIFTSPLSVENFLKFYSLKEEDKVVVIGQSTAKKLLNFKNLYICENQSLLECVKLAKTLV

>WP\_002856264.1 MULTISPECIES: deoxycytidine triphosphate deaminase [Campylobacter]

MGLKADNWIRKMALERKMIEPFCEANIGKGVVSYGLSSYGYDIRVGREFKIFTNVNSTVVDPKNFVEENV

VDFEGDVCIVPANSFALARTIEYFKMPDDVLAICLGKSTYARCGIIVNVTPFEPGFEGHITIEISNTTPL

PAKIYANEGIAQVLFLQGDEKCDTTYKDKKGKYQAQTGITLPRILK

>WP\_002856145.1 MULTISPECIES: tRNA (guanosine(46)-N7)-methyltransferase TrmB [Campylobacter]

MPNFKSKKIKEINLPYSKDDVEFLWLAKNDNVSLIYTKVQEESFFLQIKKAQNGFVIKGDKHTKPSKIGY

LQKALKIFKEGFCEDIINEAFGLKNNALIEKTPFIVDNFDELLSKLQGKIYIEIGFGSGRHLLYQAKENP

NVLILGVEIYNPALTQVAKLAKVQNVNNILLIQSDARLLLSVLKSKSVEKIFLHFPVPWDKKPHRRVIGK

DFCKECARVLTQNGRFELRTDSFEYFNFTLEQFLTFPAPKFSLRKNENLEISSKYEDRWKKQEKNIYDLW

VWNFNQECKNYELNEFNLSSVEFSKEDLKKIEQNFKNITIKKDDFFLHFESIYKQDENLLLKVAFGAFNK

PEHCYLHLDKTIDFVFKEPFKIQENIKAINELKEILKVQFKI

>WP\_002856038.1 MULTISPECIES: ATP-dependent Clp protease adaptor ClpS [Campylobacter]

MPKTQTLEQTKLSEPKMYKVILLNDDVTTMDFVIEILMNIFHQNLEKASQTMLEIHHNGSGICGIYTQEI

ALSKQKKVIDAAKLANFPLQAKVEEE

>WP\_002856010.1 MULTISPECIES: putative motility protein [Campylobacter]

MVSDVSMGNANLMTAVNTSVLKKSMDTNEALMNELIEGMEGVSQASAPQVSSSSGLDIYA

>WP\_002855944.1 MULTISPECIES: Na+/H+ antiporter NhaA 2 [Campylobacter]

MQMIKKMVLSETFPGILLIFFTFLALLCKNSSLSVIYTDFFHANFTVGFDHFQISKSLDLWINDGLIAIF

FLCIGLELKYEILRGQLKNIRAVSLPIFGALGGMITPALIFAAINYSHDFAMKGWAIPTATDIAFAVGIL

MLLGNKIPTSLKLFLLSLAIFDDLGAIVIIALFYTDQLSALAIIICLFCIFALLLLNYYHITHLSLYVLV

GVVLWIAMLKSGVHATLAGVIISLFIPLDTKNKKPYLHEVLKDLNPWVVYFILPLFAFANAGIDIRDMHL

GSVFSPVSLGIILGLFLGKQLGVFTFCFIAIKLKLAKLPENIKYGKFYGICILTGIGFTMSLFIDGLAYK

NSDIFEHADKLAILIASFLSAIVGFIYLKIVK

>WP\_002855898.1 MULTISPECIES: L-serine ammonia-lyase [Campylobacter]

MSNLSIFKIGVGPSSSHTLGPMLAGNLFCKKVAKKLDEIDRVEVTLYGSLSLTGKGHLSDKAVIWGLNGL

EAKNLSAAIQDEVNKNAIENAQIDFCGEKKLCFNYEKDLIFSKDFLPLHENGMKIKAYDCKGGLVDEETY

YSVGGGFVLTAAQLEKKGKNSNQNKKKKLDIELNNAKEALELCDKRDWDLAELSYRYELQFHTKEEIRAY

CLEIWEVMQEVYYNGTHPNEDYLPGKLHLKRRAKGLKERVAMTADPMGIIDFISLYAIAIAEENASGAKV

VTAPTNGACAVIPAVMLYLKNHTIGFSDEKAIEFLLTAMLIGSFYKKNASISGAEAGCQAEIGSASSMAA

AAMATVLGANAFKACNAAEMAMEHHLGLTCDPVAGLVQIPCIERNAFGAIKAISAARMAMTRKSTPMVSL

DEVIETMYETGKDMNYKYKETSLGGLATNLKTVC

>WP\_002855880.1 MULTISPECIES: signal transduction histidine kinase [Campylobacter]

MKEIVLSENALITSKTDLKGNIIYANNDFLKYAGYKVDELLYKSHNIVRHEDMPRTVFKCLWDYIQKGDE

IFAFVKNKAKDGNFYWVFANVSASFDTNGNIINYYSVRRAPNRKSLSIIEEVYKILLEKEQKSGINAGVS

ALMDIVSSYKMTYNELIFNLQENN

>WP\_002855735.1 MULTISPECIES: potassium transporter [Campylobacter]

MKQFGLDRRTFKILLAGYIIIALFGALLLHSSWAHTTPIDFLDAFFTSTSAVSMTGLVVKNTAVDFTLAG

QIIILALVQIGGLGYMGIGLFVYILIRKKVGFSARNLLKESLFYPSMDGLFKFFKKVLLFIFTIELIGAI

LLTMRFALEMNFKKALWFGIFHSISAFNNSGFTIFEHGLIAYKHDIAINLIITSLIIIGGLGYFVLVELY

FFQRKKLQNLSLHTKMVVVASIFLIFSSTLIIFAFEYSNPQTIGHFSFFDKILSSYFIAINYRTAGFSTL

DMGHLHDASLFFGSLFMVIGGAPGGTAGGMKVTTVMVLLLYAYWSIRDGRVRIFGHEIPRETISKAFIIA

VGSAVYIVIAVILLSLLESKFDFIALLFETSSAFATVGISVGNGGTLSLCALFSDPSKVIIIIMMLSGRI

GVFAFLLSVFKQDKAIHLKFPEGKVNL

>WP\_002855727.1 MULTISPECIES: hypothetical protein [Campylobacter]

MQNYKKLGIEHFYKKDFKTAKMYFSMAYEKRKNKRLLNFICLCDLALKSPKEASLLFDFYIEHYKISSID

KDLEEILSTIEFKKQENKQENEFEDGHALNYQDFLKSEEELGFQKSFENIINSTKLVIDNRDDFLDFLEK

LLDNGYKDMTLNYIENVMPHFWANDRFIKLQEKLIGFKSEIKT

>WP\_002855349.1 MULTISPECIES: hypothetical protein [Campylobacter]

MDKNQEKEIISYMRELLNSNEKLDCGTAFKIAKKFNVNIEKIGQLADENHMRIDNCELGQFGHLDFEKAK

IEVLKKIEPSLDEKRRIFCKDARDIAKEGCGLKSMRSALKAYKVDVKYCQLGCFKEKKGKQFIVRTKTWI

ENADGDLLFGRGKTELLELIGQTGSLLHASKLMGINYKKAWMHLQTLQKNSQEILVSTRQGRSKESGTKL

TPRALELMENYSILQKDIEEYANKRFKELFLKGKK

>WP\_002855147.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKFKEFSLRFLFKVSEQPVLVKDLLEANALFNDGMLVDPSKLNFNFKILNSYIYFGVFCAVVLLPLLLI

THYFLTKLDFHISIVSAVMVTACVFIGYDIFKVYTRKIISKKIIQKAWALHFPYFAYEKYSIMAGEIYKE

ALKEEIPKANLEQYVLDKIIHSK

>WP\_002855137.1 MULTISPECIES: adenylate kinase [Campylobacter]

MKELFLIIGAPGSGKTTDASLIAQADATNITHYSTGDLLRAEVASGSELGKTIDSFISKGNLVPLDVVVN

TIVCALKAAPTKTIIIDGYPRSVEQMMEFDKVLSEQNEICLKGVIEVRVSEEVAKERVLGRNRGADDNEE

VFYNRMKVYTEPLNEILDFYQKKKLHFIIDGERTIEPIVADMKELIKKIQSI

>WP\_002855129.1 MULTISPECIES: HslU--HslV peptidase proteolytic subunit [Campylobacter]

MFHATTILAYKGKNKSVIGGDGQVSFGNTVLKGNAVKIRKLNNGKVLAGFAGSTADAFNLFDMFENLLQS

SKGDLLKAAIDFSKEWRKDKYLRKLEAMMLVLDRNHIFLLSGTGDVVEPEDGQIAAIGSGGNYALSAARA

LAKHASLDEEELVKSSLQIAGEICIYTNTNIKTYVIEDEK

>WP\_002855117.1 MULTISPECIES: DNA polymerase III subunit delta' [Campylobacter]

MFISKIIISEDFLGIKEEMINNFGIKKLRFFMPQNEFLLDDARAVEKESYIAETEEKIIVLMADSYRIEA

QNFLLKLLEEPPKNIKFLIVIPSKNLLLPTIKSRLICEKRKVEKEVKKLDLDLKRMDLRMLFDFLQKNEN

LDKNELMDQIALLAKECVKYKDFNAEELEFFYESYELAKLNSKSGVLLATLLLNYYTKK

>WP\_002855099.1 MULTISPECIES: ribosome maturation factor RimM [Campylobacter]

MSEKDFVQVAKLGKTVGLKGYVKLHNLSDFSSQFKKDATFFIKNTKEMLKIKHYNASNSTVLFENYEDIE

KAKELINLILFQSIEKSRQTCKLKKDEFFYFDILECEVFEEDKRLGKVIDILETGASYLFEIQSDEKWVE

KKYPKIFFIPYLDKFVKNIDIEKRQIFCTQDAFLILENS

>WP\_002855028.1 MULTISPECIES: polyphosphate kinase 2 [Campylobacter]

MQENNSPKTQAVVKKNEIYVSVKRKKSTIEYEKDLKNLQIELLKFQNHVKAKGLKVLILIEGRDAAGKGG

AIKRLIEHLNPRGCRVVALEKPSDVEKTQWYFQRYIAHLPSAGEIVIFDRSWYNRAGVEPVMGFCTPQQH

KDFLREVPLFENMISNSDIIFFKFYFSVSKDEQKKRFEKRRSDPLKQYKLSPVDQKSQELWDKYTLAKYS

MLLASNTPTCPWTIISSDDKKKARLNLLRFILSKVEYPNKKTGDFSKIDAKLVRSGEEEIRKMEANLEKL

DSKKADEKIKDLD

>WP\_002854995.1 MULTISPECIES: type I glutamate--ammonia ligase [Campylobacter]

MGKFVNNIDDFFKFCKQNEVLFVDFRFTDMIGTWHHITYNLHAINEETFQTGIPFDGSSIHGWQPIEKSD

MILKPDAQSAFLDPFTADPTIIVFCDVYDIYKGQMYEKCPRSIAKKAMEHLKNSGIADTAYFGPENEFFV

FDSVKIVDTTHCSKYEVDTEEGEWNDDREFTDSYNTGHRPRNKGGYFPVQPIDSLVDIRSEMVQTLEKVG

LKTFVHHHEVAQGQAEIGVNFGTLVEAADNVQIYKYVVKMVAHLNGKTATFMPKPLYGDNGNGMHVHMSL

WKDGVNLFYDKDGYSGLSQTAINYIGGILKNARSVAAFTNPSSNSYKRIVPGFEAPCILTYSCQNRSASC

RVPYGIGKNSARIEIRFPDSTANPYLAFVSLLMAGLDGIKNKTIPVGPMDENLFDLTLDEIREKGIEQLP

HTLRGSLEALIRHNSYLKPVMSDIFIDDYQHLKFETQVWPVEARPTAYEFKTCYSC

>WP\_002854935.1 MULTISPECIES: aspartate kinase [Campylobacter]

MLIVQKYGGTSVGTLERIEAVANRVIQSAQQGNQLVVVVSAMSGVTNTLIEQAEYFSKTPNGKDMDMLLS

SGERVTSALLSIALNEKGYPAISFSGRKAGIITDSVFTKARIHHIDTKAIKSELQNGKIVVIAGFQGVDE

EGNVTTLGRGGSDLSAVAVAGALNADLCEIYTDVDGVYTTDPRIEPKAKKLDKISYEEMLELASLGAKVL

QNRSVELAKKLNVNLVTRSSFNNNEGTMITKEDGMEQALVSGIALDKNQARVTLRNVEDKPGIAAEIFSV

LANENINVDMIIQNVGVDGATNLGFTVPQNELELAKNAMQKILSSKTTIESDSAVVKVSIVGVGMKSHSG

VASKAFKALADEGINIGMISTSEIKISMIVHEKYGELAVRALHECYGLDK

>WP\_002854905.1 MULTISPECIES: tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE [Campylobacter]

MKEFILAKDEIKTMLQIMPKEGVVLLQGDLASGKTSLVQAWVKFLGLDARVDSPTFSTMQKYENHDICIY

HYDIYQEGLEGLLANGLFENFFEKGLHLVEWGGENLKKTLMKFGISTIQIKISIKDDKRKYEIYE

>WP\_002854879.1 MULTISPECIES: flagellar basal body rod protein FlgB [Campylobacter]

MINPFKSKELVTGALAGRNLRNQLINANLANVDTPFYKARDIEFETALVNRANEIFKKNDNKELQLAVTE

EGHQKPWKFPDPSKSTIYLRDGHLARNDANTVDLDVETTEMSKNTVMITALDGVLRRQSNIFSSILDASS

KLS

>WP\_002854849.1 MULTISPECIES: flagellin [Campylobacter]

MMISDATMMQQNYYLNNAQKASDKALENIAAVRAISGVDSANLAIADSLRSQSSTIDQGVANAYDAIGVL

QIADASLTNISQSADRLNELSVKMNNAALNDSQKGMLRTEATRIQESINDSFNNATYNGKNVFQTMNFVV

GSGTETTNLNPLATGGLSIDNQDSITNFMDQLGSLRSEIGSGINAITSNINASVQNSINSKAAENNLLNN

DMAKNVNDFNANYLKENAAAFVAAQSNMQLQSKIANLLQ

>WP\_002854824.1 MULTISPECIES: 50S ribosomal protein L19 [Campylobacter]

MKNKYIEQFEAKQIEGKNVPDFRAGDTLKLAIRIKEGDKTRIQNFEGICIARRGNGVSETFIVRKMGANN

VGVERIFPIYSESLESITVLRRGRVRRARLFYLRDRRGKAARIKELKK

>WP\_002854816.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLELITQKDQDFLQNIENLDEEYIQKFINKKISEIAIAIETAAENADKAKDRTQKAKNLNTDSDWQTYIP

IFGRWLGETSEEKKEIKSNMILEVAELQNESMNQMTTILKEVVIFFTSSFCIATRMNQALSLIIAQGFVK

SDGKVIRLSKAAKEQFQQIQKFTLSFIEDHEKHKDTINNIQVELDKKNQIDDEQYKLIEKHYQEFIQYKN

YNDKIVQEQECKINELKDILNKRKNVFTNSISILALIVSVASIVLYFIGR

>WP\_002854797.1 MULTISPECIES: RNA pyrophosphohydrolase [Campylobacter]

MENEKNYRPNVAAIVLSSSYPFECKIFIAKRSDMDNIWQFPQGGIDKGESVKNALFRELKEEIGTDEVEI

IAEYPEWLSYDFPSKIVKKMYPYDGQIQKYFLVRLKHGATININTKHPEFDDYQFVSVKQIFEMINHFKK

NIYVKVIKYFEEKGYI

>WP\_002854780.1 MULTISPECIES: acetyl-CoA carboxylase carboxyl transferase subunit alpha [Campylobacter]

MASYLDFEKNIQQIDEDIINAQIKGDTEAVSILKKNLEKEISKTYKNLSDFQRLQLARHPDRPYALDYIE

LILNDAHEIHGDRAFRDDPAIVCFMGYLGEKKIIVIGEQKGRGTKDKIARNFGMPHPEGYRKALRVARLA

EKFQIPILFLIDTPGAYPGIGAEERGQSEAIARNLYELSDLKIPTIAIVIGEGGSGGALAIGVADRLAMM

KNSVFSVISPEGCAAILWNDPAKSEAATKAMKVTADDLKSQGLIDDVIDEPTNGAHRNKEAAAVAIADYV

KKSLNELENIDVRELSANRMQKILKLGAYQEA

>WP\_002854663.1 MULTISPECIES: hypothetical protein [Campylobacter]

MELTLFKAGFEAHLECCEIENNRFLGEYLKLGAISQILKWKKLALRIDFDEGEKIIFDLLLSLKEDILRL

ENSLDKNKELIPLKQKGVIESLNFEYLNFLDTILEEDKEYYLRFDLNNQKIAIFIKAQSQTLAKIIKIKP

EDKMAFDAFVVEIQRNMIRNKKGQE

>WP\_002854626.1 MULTISPECIES: cytolethal distending toxin subunit A [Campylobacter]

MQKIIVFILCCFMTFFLYACSSKFENVNPLGRSFGEFEDTDPLKLGLEPTFPTNQEIPSLISGADLVPIT

PITPPLTRTSNSANNNAVNGINPRFKDEAFNDVLIFENRPAVSDFLTILGPSGAALTVWALAQGNWIWGY

TLIDSKGFGDARVWQLLLYPNDFAMIKNAKTNTCLNAYGNGIVHYPCDASNHAQMWKLIPMSNTAVQIKN

LGNGKCIQAPITNLYGDFHKVFKIFTVECAKKDNFDQQWFLTTPPFTAKPLYRQGEVR

>WP\_002854624.1 MULTISPECIES: membrane protein [Campylobacter]

MHFTIFHIIAFIILLICFALICILIFLKVKQKEMALISYTIATIFTALLIYSIFLTINQFTTQADLSKLT

YTRDLRHESVIVSGKVQNLTKFEIRKCYLMLSILNQKQVGGEIFNDKNVRNAKMQNTSVSYTIEIIDTLP

GNTYKEFRASVPFPPSFNNPEFYHTLKCI

>WP\_002854440.1 MULTISPECIES: aspartate ammonia-lyase [Campylobacter]

MGTRKEHDFIGELEISDEVYYGVQTFRAVENFDISHDRLKDFPRFVRALARVKKAAAMANHELGLLDKNI

QDAIIKACDKILEGGYYDQFVVDMIQGGAGTSTNMNANEVIANIGLELMGHKKGEYQYLHPNDHVNLSQS

TNDAYPTALHLALHDYLSDLAKAMEHLKKAYERKAEEFKDVLKMGRTQLQDAVPMTLGREFKTFAVMIGE

DIQRVLEARKLILEINLGGTAIGTGINSHPDYPKVVERKIREVTGFEYTVAEDLIEATQDTGAYVQISGV

LKRVATKLSKVCNDLRLLSSGPKCGLNEINLPKMQPGSSIMPGKVNPVIPEVVNQVCYFVIGADVTVTFA

CEGGQLQLNVFEPVAAYSLFNSIVMLEKAMYTLADKCIDGITANEKICSDFVYNSVGIVTALNPYIGYEN

SASIAKEAMNTGKRVADIALERGLLSKEQIDEILTPSNMLNPHMEAKK

>WP\_002854114.1 MULTISPECIES: GTP cyclohydrolase II [Campylobacter]

MKIKISEIANLPSKWGNFQIQSFKENDKEHLCIFKNTPKDTLNLRIHSECLTGDALGSLKCDCGEQLEFS

LKYIEKNGGMVIYLRQEGRGIGLFNKVNAYALQDKGFDTIKANHQLGFKADERTYEIVEFILKHYEISKV

NLLTNNPEKLESIKEKIITRIPILIEPNRFNVEYLNIKQTQMGHLK

>WP\_002854065.1 MULTISPECIES: chorismate dehydratase [Campylobacter]

MIFGKIDYINLLPLHIYLKKYPLPNGYKANMEYKKGVPSKLNKDLFYRRIDAAIISSIESARKKYKNLDL

GICANKRVLSVLVEKNTSNAKDPSSATSNALAKVLKQDGKVIIGDKALKLYLKDPSKYIDLCAKWHEKTG

LPFVFARFSCVQKKALYKQILKKFPKTKIKIPYYILQNYAKTRDLDIKDVRYYLDEVIYHKISTKEKTAL

KRFVKACKALNLA

>WP\_002854063.1 MULTISPECIES: malate dehydrogenase [Campylobacter]

MNLKEEALKYHLGGKIDIVPSKPMATSYDLSLAYSPGVAEPCLEIAKDNELAYTYTNKANLVAIVSDGSA

VLGLGNIGAQASKPVMEGKACLFKKFANVNAYDIEINVHSIEEIVNFCKALAPTVGGINLEDIAAPKCFE

IEAALQDLGIPVMHDDQHGTAIISTAGLMNAMEISGKKFKDIKVVVSGAGAAGIASAKMYRNLGVENIIL

VDSKGVISKDRNDLTPQKLEFAVDSKEKTLKEVLKGADVFLGLSAPKILDDEMVLSMAKDPVIFALANPI

PEVMPEDVARLRKDAIVGTGRSDYPNQINNVLGFPFIFRGALDVRASKITENMKVAAAKALADLAKLPVS

DAVKKAYNLSTLEFGRDYVIPKPFDERVKAAVSTAVAAAAVKDGVAKVKNFDEKAYFESLK

>WP\_002853959.1 MULTISPECIES: cytochrome c [Campylobacter]

MIIRWLFISSIFVVALFGINLKSFFTYTFDANKQYDMEKAKALYFQNKCNTCHGDNAEKSVIGSRILKDM

SPEDIKGALIGYTLDSSSSTTASQMAFYARNLSHEDIDNIIAYIKGGNFALDLQVKDLLEEEPAQKTKHN

IFLK

>WP\_002853905.1 MULTISPECIES: branched-chain amino acid ABC transporter substrate-binding protein [Campylobacter]

MKKSLILASILSLSLSAAEVKIGVVLPLSGATAAYGQSALEGIKLANSMQSTLSNGDKVSLAIIDTKGDK

LESSSGANRLVSQDKVIGLIGEMVTANTLQVMRVAEDNKIPLIAPAATGDRLLDKKIYSSRVCFMDSFQG

SSLAKYVFSKLNYKSAVIVVDQSTDYSLGLAKAFEKQYKSNGGQILRILRVNSGDKDFRAIVAQVKSLNP

EFIFLPLYYSEASLFARQSKLAGLNIPMGSADGVADQTFISLAGDASEGYIFTDSFDANNPTTKLSKEFI

SVYEKAKGTKEVPNFSAMGADAYFVMLNAMNACVENLTSKCVNEKIHQTKNYQGVSGVISIDQTGNATRS

VVVKEIKNQKQNYKDIINP

>WP\_002853792.1 MULTISPECIES: hypothetical protein [Campylobacter]

MFKTIVCFLALNLSLFAVGFDLKPIKSELVKVDDIYGYIKDSDDIKLYSSGVVVQHFSNSQSIIARASVI

DKKNGLAKLEFSVFSALKQDALPLPNVLPKVGDEVVLNFLYDRGLVIAPDEQTYNELVREFPQIYFTHID

IFGAQLIRTATLSPKRSDFRQFCDDNAVGILVVALENQAEVVDCQDFNKLYEVPISKPTSVQVPFYSRIG

GYKSNFFDFNSQEIGNYYRYYDALINLPKVQ

>WP\_002853760.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKIKFLSIITILSLSLNADIIISADNLPSVSKEFLQHNFKAPIGIVQKDKNSYEVYLSDGTELEFDIDGA

WKEIENKAFPFDLDFLPQNLANIIKNEFPNIKAREIERKINHYKIKLDNDVKILIDFNGTILHKEIDD

>WP\_002853752.1 MULTISPECIES: NAD(P)H-dependent oxidoreductase [Campylobacter]

MKKELEIFSTRYSCRNFKNEKLKKEDLNSILEIARLSPSSLGLEPWKFIVVQDEKRKEELSKICNQQKHV

KDCAALIIIISRLDFLDYFEEKLRKRDMSETEMQKRLDTYMPFLKSLNQEQKISYAREQAHIALASILYS

ANALNIASCTIGGFDKEKLDSYLSLDIQKERSSLVVALGYCNDKKNPQKNRFSFDEVVKFI

>WP\_002853705.1 MULTISPECIES: transcription termination factor Rho [Campylobacter]

MEKEKKQHQRTHVPVEGYKIEELKLLDLENLVKIANECEIENPREFRRQELIFEILKAQTKKGGFILFTG

ILEISSEGYGFLRGMDSNLSDSVNDAYVSNSQIRKFALRVGDIVTGQVREPKDQEKYYALLKIEAINYLP

LQEAKERPLFDNLTPIFPTEKIKLEYDAMKLTGRVLDLFTPIGKGQRGLIVAPPRTGKTELMKELATAIA

KNHPEMHLIVLLVDERPEEVTDMQRCVKGEVFSSTFDLPAYNHVRVAELVIEKAKRMVETGKDVIILLDS

ITRLARAYNTATPSSGKVLSGGVDANALHKPKRFFGAARNIENGGSLTIVATALIDTGSRMDDVIFEEFK

GTGNSEIVLDRNIADRRIYPAINIIKSGTRKEELLQGVANLQKIWAIRSAISQMDDVEALKFLYSKMLKT

KDNVELLSIMNE

>WP\_002853683.1 MULTISPECIES: ATP synthase subunit C [Campylobacter]

MKKVLFLLLACAAVAFAAETNAPVEQEAINVWIKAFSVLAAGLGLGVAALGGAIGMGNTAAATIAGTARN

PGLGPKLMTTMFIALAMIEAQVIYALVIALIALYANPFIVLQ

>WP\_002853451.1 MULTISPECIES: RNA polymerase sigma factor RpoD [Campylobacter]

MNAKTQEAELEELFQENAKDYITYEKLVKYLTKQPSASTAKKVQALMKKHKVQLFSAAEIAQMKNIEDAK

RLQEEKQKLQDTSLENEFDLANENDLLEWSRSDSPVRMYLREMGQIALLNKDEEIEISKKIELGEDIIID

AFCSVPYLIDFILDYKEPLINRERRVKELFKSFDDEEKSDDKLDELDIDEDEENETELESDEENTKKNSK

KEDERTLKVIEKFKALEKAKKDWLKTSKDKESGDELLDKLSIAFKKNILKEKLMDLGPTSKLISEIVKSM

ETALKSDEEFDKELKRLEYRLPMFSDELKKRHADILKDITKLSKEEITERALETTMVSTYMEIKKLFQTK

EASEKSFDLEKSRLKEILEQIKRGKKISDEAKGRMAKSNLRLVVSIAKRYTNRGLPFLDLIQEGNIGLMK

AVDKFEYKRGYKFSTYATWWIRQAISRAIADQARTIRIPIHMIETINQINKIIREHLQKDGKEPDVSVIA

KEVGLSVDKVKQVIKITKEPISLEAPIGNEDDGKFGDFVEDRNSLSPMDHILKDDLKEQIDEVLDQLNDR

EKAVIRMRFGLMDDESDRTLEEIGKELNVTRERVRQIESSAIKKLKHPKVGRKLKNYIEGWK

>WP\_002853180.1 MULTISPECIES: hypothetical protein [Campylobacter]

MTKNEEKALRVKYLRNLEKFFNGAISALKKEDFDKTKFEERMLKNAKFFEKNPAVNLNSTYAKNLEFFVN

ACLDFSKEKSELLNLANALDKQKKQGEKKEKHKNYLKDYE

>WP\_002852542.1 MULTISPECIES: bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase [Campylobacter]

MTLLDGKALSAKIKEELKEKNQFLKSKGIESCLAVILVGDNPASQTYVKSKAKACEECGIKSLVYHLNEN

TTQNELLALINTLNHDDSVHGILVQLPLPDHICKDLILESIISSKDVDGFHPINVGYLNLGLESGFLPCT

PLGVMKLLKAYEIDLEGKDAVIIGASNIVGRPMATMLLNAGATVSVCHIKTKDLSLYTRQADLIIVAAGC

VNLLRSDMVKEGVIVVDVGINRLESGKIVGDVDFEEVSKKSSYITPVPGGVGPMTIAMLLENTVKSAKNR

LN

>WP\_002852252.1 MULTISPECIES: organic solvent tolerance protein OstA [Campylobacter]

MVARQIILLLVCVSVTWATQIEVKALNFYSDENKGESILSGNVEVIRGDDILNSEKLIIYTDKNRKPIRY

EAMQNARFKIVLKGKTYKGSGDKFIYNVIKDTYEINGHAYINELGSNQKLFGDKIIVDRKANIYRVESKD

QKPARFVFDLKDK

>WP\_002852070.1 MULTISPECIES: sodium-dependent transporter [Campylobacter]

MQRQTWSSTLTYILTVAGATIGFGATWRFPYLVGENGGGAYVLVFCIAMIIIGIPVILVENVIGRKAMTN

SVDAFKQKWQSIGYMGLLGSFGIMAYYMVLGGWVLVYIWELTLGNFSLANVVSKEFTHQFFNDKIAFNPL

GVGIFTTVFVIINYIILKRGIIDGIEKSVKFLMPLLFICLIIVVGRNLTLDGAMAGVKFYLEPDFSKILS

PKLLIDVLGQVFFALSLGFGVMITLSSHLNKNENMAKTAIYTGVLNTIIAVLAGFMIFPALFSAGLAPDS

GPSLVFETLPIAFSHIHFGTIVCILFFVLLLIAALTTSLPIYQVIISVLEEKFKYSKNLSINLTLGFIFI

LGNLPCILTYGPWRDIVIIKGKNIFDSFDFISGNILFVLTAFFCCIYVGWILGKQESLKELSNNNTLKSS

WFGIWFYYVKYIVPLIILIIFIYGILN

>WP\_002851965.1 MULTISPECIES: hypothetical protein [Campylobacter]

MAYEDEEDLNYDDYENEDEEYPQNHHKNYNYDDDDYEYDDDNNDDDFYEMD

>WP\_002851840.1 MULTISPECIES: zinc transporter ZupT [Campylobacter]

MQFTFEQIFIAMLLTLFAGFSTAIGSIIAFFSRKDDLRVLSLGLGFSAGVMIYISFMEILPTALKDFKNH

YDSHWAELLGLACFFGGILISLLIDKLIPEDVNPHEPKEDLSELKICPLPQKGQNPPKFHPGEKLHQINT

KALKRTGIFTALAIAIHNFPEGFATFISSLDNLTLGIAIAIAVAIHNIPEGLAVSLPIYHATGDKKKAFI

YSALSGFAEPLGAFVGALILLPFIGDLTLAISFAVIAGIMVFISLDELLPAAKTYDKAHDSLYGLIAGMA

IMALSLNLLGQ

>WP\_002851763.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKNIVFFEVKGGSDKGEDGYRKDTMPMVNALKAKGWNAEVIFFEVGKKDEIYKYVKENFDGYVSRINPG

NLKEENEYFDMLRKLCADKLVGMPHPDAMIGYGAKDALTKLADTDLVPSDTYAYYDIKTFKENFPKSLAK

GERVLKQNRGSTGEGIWRVSVEGNVSGDSLPLNTKIKCTEAKDNHVEHRELGEFMDFCEQYIIGDNGMLV

DMTFLPRIKEGEIRLLMLYNTPVNVVHKKPAEDADAFSATLFSGAKYRYDKPEDWKTLVDMFLGELPKVR

EKLGNYDLPLIWTADFILDTDEKGNDKYVLGEINCSCVGFTSHLELADEVASNIINIVSKTKA

>WP\_002851300.1 MULTISPECIES: capsule polysaccharide transporter [Campylobacter]

MEENKTLLEKIKDLSIFDSFKIVWFIMIFVVIYYTLIAAPRYVSTMILDVRSTSGESAQTSGILSLLSST

STASEDLNYLKGYIESSDMLKILDEKIKLKNLYQEQHIDLPFKIWDSSSIESYLKYYQARVKVHTDETTK

LLKVEVEGFTPKSAHLIAQAIMQESEKFINEISHKAAREQMAFAENEVQKYKERYQKAQNDLIAFQNKYG

VFDPLKQAETKASLVAQIEANLAQKEAKLLTLQSYMNDAAPEVVALKAEIEAIKKQLLREKSKISANNSS

QKLNDLAAKFQDLTIEATFAQKAYEAALKAYESARIEALRKIKQLVIIQSPDIPESAKYPERIYDILTAF

IVLSLIFGIVKFIKMIIEEHKY

>WP\_002851179.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MIKLINLTKSYPLFSGGRHYVFKNFTFEFPENCSIGLMGYNGAGKSTLMRLLSGAELPDSGKIITNKKLS

WPLGLNGAFQGSLTARDNAKFVARVYGYKGKELQEKVKFVEDFAELGKFFDEPMKTYSSGMSARIAFGLS

MAFDFDYYLIDEAGAVGDPAFREKSVKLYRERLSKSKVIMVSHNVAEIKEWCDKIIYMKNGQITVYDDVD

EGIAVYQGKV

>WP\_002877660.1 MULTISPECIES: peptidase [Campylobacter]

MQMQEVIEKLKDILASEGKCNLKTKDIAKELGIHPDTFNSMKFRNSIPYPQILNFLNQRNISINYFFYGS

SPKDQLECENKYKILKLYKTNASLGGGGINDLIDSSDLIIDEKVLNFFGSKECEFITCYGESMEPIIKDG

SICVIDRNKTFKNKSICVINTRDGLFIKQVLKQDDGVILHSLNPLYEDIFYKNGDFLLIGVVIGELSRL

>WP\_002862131.1 MULTISPECIES: hypothetical protein [Proteobacteria]

MCFSTLFAQDNFEEYFKLIDKENRINFNTLQNPFVNPTFEKLRHIKITAIMLDKVKIYDRWYKKGDMIDD

AIIHEINTKEIKFQYDNLEIAIQINKNDKININ

>WP\_002851537.1 MULTISPECIES: Tat pathway signal protein [Proteobacteria]

MKNRREFLKKSAFALGAAGVLGSTTLALAKDEERKDLVKGKSKKKEVLFQRSANWENYYIKAE

>WP\_002851332.1 MULTISPECIES: 50S ribosomal protein L17 [Proteobacteria]

MRHKHGYRKLGRTSSHRAALLKNLTIALVNSGKIETTLPKAKELRGYVERLITRARLGDFNAHRAVFASL

QDKNATNKLVTEIAPKFKDRNGGYTRIIKTRIRRGDAAEMAFIEFVA

>WP\_012006730.1 bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase [Campylobacter jejuni]

MKAKGSELIPVLTIAGSDCSGGAGIQADLKTFSAHNLFGMSVVLSVVAENTARVISVHDIPTQSVDEQIL

AVFEDIVPKATKIGMIGSCELMSCVAKNLSEFKPQNVVIDPVMFAKNGYALMPQENCDFFKQTIVKFADI

LTPNIPEAEFLCGFKIANEEQMIKAAKHLCSLGAKAVLLKGGHSEENANDVLYDGKEIYILKGERIETKN

THGTGCTLSSAIASNLAKGKDLFYAVSEAKEYVRNAIYYSLNLGKGCGPTNHFFKFLDEK

>WP\_002854660.1 MULTISPECIES: succinate dehydrogenase/fumarate reductase cytochrome b subunit [Campylobacter]

MRELIEGYLGKSIEGKKSKMPAKLDFIQSASGLFLGLFMWVHMLFVSTILVSEDFFNSVVHFLELKFVYD

NPVMSYLTSFLAACVLVVFFVHALLAMRKFPINYRQYQILRTHSKKMNHSDTSLWWVQAFTGFIMFFLGS

AHLIFIVTNADKISGDMSGDRVVSHFMWLFYAVLLVCVELHGSIGLYRLCVKWGWFEGKNVKESRKKLKT

AKWIISIFFLVLGVLSLAAFIKIGYENYQNQTQTTAMIKNYNGANYEYTI

>WP\_002782323.1 MULTISPECIES: SIMPL domain-containing protein [Campylobacter]

MKTNNIFMALAIVLASLILAFGFNKALSDFKTLERSVSVKGLSQKEVEADTLILPIKFTRSNNNLTNLYE

ELEQDKENIIKFLKEQGVKEDEINYNSPNIIDRLSDPYSNDTQAAYRYIGTANLLIYTQNVKLGKSILEN

ISSLAKFGIVTKIDDYDIEYLYTKLNEIKPQMIEEATLNARNAAIKFAQDSNSHLGKIKKASQGQFSISN

RDKNTPYIKTIRVVSTIEYYLKD

>WP\_012006783.1 DNA-binding response regulator [Campylobacter jejuni]

MSQECKELIILVVEDEIKTRESLINVLSERFSKVIGAQNGDEGLKKFKPDLVITDIAMPIMDGLDMTREI

KEISDDVPIVVLSAYSEKERLLRSIDIGIDKYLIKPVDIEELFKVLDCLVGEKIEANMLVKISEEYQFNK

TKRTLIHNGKEIVLTKKELAFISLLLKQPGVLVLHEDIKKNVWIGEHVSDTAVRTFIKRVRDKVGEDFIK

NVPSLGYKININK

>WP\_002853404.1 MULTISPECIES: N-acetyltransferase [Campylobacter]

MSEFKIIDLRQEDLDILQEMIIEFAKYEDMLDFLQCTKEKLEHSLLKNKFARAFLLKENEKTIGYMIYFY

TFSSFWGSGGIYLEDIYIREDFRKKGYGKAVFKFLGEICKKENLKRLDWVCLNDNILGINFYESLNAKHL

KQWRNYRLSGENLEKLCDL

>WP\_002783539.1 MULTISPECIES: N-acetyltransferase [Campylobacter]

MQNTIIQKAVNKDLNSILEITKDALNAMKTMNFHQWDENYPNEIVFQEDIQAQELYVFKENDEILGFICI

NEKFEPEFYKQVIFNKNYDDKAFYLHRLAVKQNAKGKGVAQKLLNFCENFALENHKASLRADTHSKNFPM

NSLFKKLDFNFCGNFDIPNYQDPFLAYEKILNQKAF

>WP\_002851172.1 MULTISPECIES: nucleoid-associated protein, YbaB/EbfC family [Campylobacter]

MFENMDFSKMGELLNQVQEKAKNIELELANREFSAKSGAGLVKVSANGKGEIIDVSIDDSLLEDKESLQI

LLISAINDVLAMVAQNRSSMANDVLGGFGGMKL

>WP\_002867029.1 flagellar hook-associated protein FlgK [Campylobacter jejuni]

MGIFGTLYTGVTGLKASEVQIATTGNNISNANATFYTRQRVVQTTNGYITTGGVQVGTGTAVESIVRLHD

EYSYYKLKGASTQLEYTKYMASTLQEIAQRFPDLQNTGILQDLENYNKAWNDFASNPNENATKIALVKAS

QTLTESVNNTFATLDKIQKKVNDDIKNTVDEINRIGEEIATINKQIYGQEALPTEHANELRDRRDELELT

LSKLVSAVASKNEINQDNRLDTTITDPGHQYNLSIEGFSIVDGINFHPLKLDYDDKNKSYSIYYETPDEK

VRDLTAKISGGQLGAQLDLRGRNYSKSEGKYEDGIIQGYMDSLDTFAKTMINETNNLYASSAKSSVTSDY

LSGLKGDIPLVNYDRTIQPGSFDIVIYDDKGDKKLTKTITIDVNTTMNDIMRQINANTDDNNDHNANNDV

DDHINASFSYDAKTGDGLFQINAKSGFKVAIEDKGTNFAGAFSIGGFFSGTDASNMKVKDSILNDPSTVR

ASLSGVDSGNDMANKIIQLQYEKVNFYNEDGTIDNLTMEEYYRKLTGKIASDGENNNVVNSSNETLYNSV

YSEYQSKSGVNTNEELAALIQYQSSYGAAAKIVSTVDQMLDTLLGLKS

>WP\_002866164.1 lipopolysaccharide heptosyltransferase II [Campylobacter jejuni]

MKIFIHLPTWLGDAVMASPALYAIKEHFKNTQFILYGSLVSTALFREFPNSKIIIENKQTRYKQALSLRK

ELGKIDLSFAFRSAFSSKIILHILKTKQRYFFDKNKHKEEHQVLKYLYFIENSLSIKAHFKDLKLPFKLK

FQNPLILKNGKKILGLNPGASFGSAKRWDASYFAKVALNFSQSHEILIFGAGKAEQELCNEIYQILKEQN

IKVKNLCNKTTIKTLCQNIAFCDLFITNDSGPMHISTVYKIKTVAIFGPTKFTQTSPWQNQNAKLVHLDL

ACMPCMQKTCPLKHHKCMKDLKPEKVIEEIKKLSTP

>WP\_002859072.1 MULTISPECIES: 2-oxoglutarate synthase subunit alpha [Campylobacter]

MREVIATGNVLIAKAAIDCGCKFFGGYPITPSSEIAHELSHMLPANDGTFIQMEDEISGISVAIGAAMSG

VKSMTASSGPGISLKAEQIGLAFIAEIPLVIVNVMRGGPSTGLPTRVAQGDLFQAKAPTHGDFASIAIAP

ASLEEAYTETIRAFNLAEKYMTPVFLLMDETVGHMNGKAVLPDLKDIKIYNRKKFEGDKKDYKPYAAGEN

EPATLNPFFTGYRYHVTGLHHGDIGFPTEDGVIVKKNMERLIGKIKNNQEDICTYEEYMLDDAEFLIIAY

GSVSRSAKEAIQRLREQGIKVGLFRPITLYPVAEKKIAEVVSKFKKVMVSELNMGQYLEEIERVTSRRDF

ISLHRANGRPITPSEIIAKVKENI

>WP\_002797470.1 MULTISPECIES: phosphate ABC transporter, permease protein PstA [Campylobacter]

MKKLFKKRQKASKSFKRLCKMGLYINLIFLCIFLGSVAYLGFPAFKQTYIFVEANRNSPAYDLLSRAEQR

KIRTGQITEKSWLLANSEVDQYMKQKYNRLSEKQRTLVDDLVQKGEIELKFNSNFFLNGDSKSPENSGIL

SSVVGTLLVMLVCMVVSVPIGVAAAIYLEEFAPQNILTHFIEVCINNLASIPSILFGLLGLGVFINLFGM

PRSSALVGGLTLAIMSLPIIIVSTKAALKSVDINMKNAAYALGMTKVQMVKGIMLPLAMPMILTGSILTL

AQAIGETAPLMIIGMIAFIPDVASSIFDPTSVLPAQIYSWSAMPERAFLERTAAGIIVLLGLLVVLNLSA

ILLRKYFQGKLK

>WP\_002866676.1 adenylyl-sulfate kinase [Campylobacter jejuni]

MVIAVIPARSGSKGIKNKNLVLLNNQPLIYYTIKAALNSKCISKVLVSSDSEEILSYAKSQNVDILKRPI

ELAQDDTTSDKVLLHALEFYKDYEDVIFLQPTSPLRTNIHIDEAFKIYKNSDANALISVTECDNKILKAF

ICDNKGDLKGICDDEYPFMPRQKLPKTYMSNGAIYILSIKDFLNKPSFLQSKTKYFLMNKISSLDIDNLE

DLKQVENIQKMKGCVVWISGLAGAGKTTISSGLYKKLKEKYNNSVLLDGDELRKIFKHTGYTREERLESA

KKISSLCSFLAKNDIIVICATISLFEEIYLLNRNTIENYFEVFVDCPMEELILRDQKGLYSGALKGEIKD

VVGVDIKYAKPNAHYIIDNSSKTDLEKKINNLYNEVELFFNKER

>WP\_002860448.1 MULTISPECIES: serine endoprotease DegQ [Campylobacter]

MKKIFLSLSLASALFAASINFNESTATANRVNPAAGNAVLSYHDSIKDAKKSVVNISTSKTITRANRPSP

LDDFFNDPYFKQFFDFDFPQRKGKNDKEVVSSLGSGVIISKDGYIVTNNHVVDDADTITVNLPGSDIEYK

AKLIGKDPKTDLAVIKIEANNLSAITFTNSDDLMEGDVVFALGNPFGVGFSVTSGIISALNKDNIGLNQY

ENFIQTDASINPGNSGGALVDSRGYLVGINSAILSRGGGNNGIGFAIPSNMVKDIAKKLIEKGKIDRGFL

GVTILALQGDTKKAYKNQEGALITDVQKGSSADEAGLKRGDLVTKVNDKVIKSPIDLKNYIGTLEIGQKI

SLSYERDGENKQASFILKGEKENPKGVQSDLIDGLSLRNLDPRLKDRLQIPKDVNGVLVDSVKEKSKGKN

SGFQEGDIIIGVGQSEIKNLKDLEQALKQVNKKEFTKVWVYRNGFATLLVLK

>WP\_012006770.1 hypothetical protein [Campylobacter jejuni]

MSREIQEFIEKLKDWKNNFSIQDYDYTKYNCEVADIAKWQKENNVNELINFWNEKIKEDYFELKHPLYNK

ILTRAVFSCNIHNFFNWVFFIDIKNKNPFLLGQVNSCINFILVKNSIIILDEGWSNLYIGAIDHARDFIC

GSCLDLKYKGIGFGFTLQNTRPAHFFNHILNGFINIDNTKPVYGKNIFFKPKFLLYTEQKDLVYFYPTTK

MNTNLVPMFNYVYQESIRDFITLIDKDIFKEKYDLTIWLGLPGERRNWVEQIEGVANILKHCNKYFKKIK

VYIDGMTGYDGQIQDFPENKMLFNKIVNTTRELFLQEYNKNIIFTFEELQKLVDISTENEEKIIVFKSLA

GYDYRTKICYCRDCNIAISDGGTTTFVPFIIFKKPGIIFCGHLNHINYANCILNDKRLQKVTGKDMFLQV

DRKTYFNFSFHLSYEHIYNLAAEVLEELSAVGKLKVKNLKMHRLDVPPVELIAKQYELEQKLNIKFSIEN

VALFSELEKKIDTLALNNTAIINNANNTTLLIQNKDQYIHNLEQNIQNLNHQILFKTAKARIQNHLSYKL

GQALIINSKSILGYIRMPYVLSYIKDKHRQEQKAYEEKIKDNPNLALPPLETYPDYNEALKEKECFTYKL

GEALIKADKEWYKAGYVKFYFKDVPRLKREFGKR

>WP\_012006643.1 hypothetical protein [Campylobacter jejuni]

MRLLVLFFLILPLYSVELISFNIYDRNDRVDLMLSFDNAYNGKISQKKEKNLTLLTFSDLTYSKDELKEL

NSQLVDKISISSKNNNTYIMLQNKQNINLELSSIIDKFGVRIRAIEQGKANIESVPTTTANNSQELMPKP

KSTSLEGYDYTNYILVMLILVILLIVLWWFKKTMVYKNNNVSRDFTMIFQRFLDKNNQLVVFDHANKRYT

MIIGNSNVLLESVEIPEEQIIKHTEKTEKNFDSFFEENKKRIQNLIEQRQKGKKS

>WP\_041176288.1 hypothetical protein [Campylobacter jejuni]

MKHCLALCFIFFLCACSVKNQNFSSQSLMVLIASPMIKINDAAFLKKENNALNLEVYKLGQAFFELKIKD

KICINAVCYDKKVFNQKFFKNVYYDDILNDILKANALWQGKNLEKTDCGFEQNLKAKNYEIFYQVCDNKV

SFFDKISHTKIILTHIQN

>WP\_002921317.1 hypothetical protein [Campylobacter jejuni]

MVKKIIILTLWVNISFAISSLELAKNLVNNSSKNSQLELLFSNNSYIDNNGNCDIAKISQILKTNSLIAL

TLSNPQSLRLNFKAKADEVMFFKILSDVLTDAGYIYFIPTDLILREGNIDYTIQVESQYVLDPGTLYNLL

KENSVYINNIKRIGAYDYEYDLNFSNAVLKTNTNVNLNTPKSLEKPLKDYVLDLKNATNLIIDANDLDNW

FPKIFFLDKNLNLIKAVKSENKNNHFSELIPNGAIYAIVSDMYSLDNIRRGLKITLKK

>WP\_002876968.1 MULTISPECIES: hypothetical protein [Campylobacter]

MFYRDSYKVKKYKNILSKNVTILESKKHFWDIKFKIKARIYPPFKQHLISFFGIKQTFWDFWDIWDFLHF

KLGKIKSHFCKL

>WP\_002876674.1 MULTISPECIES: hypothetical protein [Campylobacter]

MTLDFDFIYNADNDIFEYLLRFYAKNYNYILSKEENTYHFSIDADEENLKTFCDSLNFMSHSVFLKKFDV

KAGHGFNPCMPEDKEFSRFSYITHLNSNAYQEKKLLNKNEWGVFCECEFSSNLSEFEKINEENFNTFLNL

AFDLLSQEKKIYLKDKNGIYEFSLFKNEFIGDFLLPCDIKAINSVFVCSNENLKFLASLEKPLMKLRLNA

MFRKNHNLDFNDFKIRLARDLFCFALGLKLFENEYKFLSVKKIEEYQKDFYISALDEQVVVLEGFEFINA

KARELIFSKEDKNMARISYLVSRYKEKAFILELSKDYEDILLVNKELNLLKLSLPKHSKELYEEIKKDEI

GARLLENFSKEFPLLDENFELQNNFYSLLGLVGRVLNLGKNLQESVSELLKIADESKMPRGVKIDYRLKE

DKSFDYTRTLRSAMSFMLAGVDSANIAYGAVESLAYFLRDTYDELREKKQSDLALISGSLFEHKSLLKNT

LKHLKNCQLSDVPLRV

>WP\_002868686.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKFFLLVFCFVNLALAQVYKGELYFYHLQDKEIFAIVYDNAPMTPLFDRDKNQTSSSFLIIDDINGNLEI

PLVKTNDFWQDERKKYKINSSKMLTYDNKNFQGENLGTTTLELVETQDGIRIKRSLDFIGFNDDFKEFHP

VHKSVFSFEQIRQKPIFLQDGKISFEEWYYFYEDGMSRAILELNNFVYDINAHAFVKLNDLYNTKNQKFQ

NLLHEKLKNTCDECFEDLQNLQFNNNFLLNNGKLKICYLPFEGHFLDENICVEFNEDELKEFKK

>WP\_002866842.1 hypothetical protein [Campylobacter jejuni]

MLLNTPCRGIVDTNFESKRINITSTLKFQEKKEKVEAKAEKEEANKDNSDSTNTDTNKKDKLLDISA

>WP\_002866121.1 hypothetical protein [Campylobacter jejuni]

MLETILKNENFIHTMQKHCYEVISHLIEENIEFSIVANTNFIDFNPELPKELDVKQNPYALFALGGYTFE

SIQLNKDFIQFHAGFGNDDFDSFVKVDLGAITQIQIENNILFVNFSLYKREDSKNLQKSKNIFLNNPKNK

DIFKK

>WP\_002862076.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKRVRTKIRANFRRRVKRTLKGSLKEKLAGTILLCAIVPLAVLGYLFIVIIGTFFNTARARQGVRALDHF

VNASLFNGYAWESVSSHAWRERNRKKWARIVIKITDFFQKDHCKRANKREQPVVDFILSRNLDKQTIGK

>WP\_002859817.1 MULTISPECIES: hypothetical protein [Campylobacter]

MVFLIPLLIIIGVIFGIDYVYFKNQDLKAQVKKEQKELNSSLEKEKKEYIEKLFKTK

>WP\_002858872.1 MULTISPECIES: hypothetical protein [Campylobacter]

MSKALEYLIVIGLVVAAAITAWSVLTVNHLHIG

>WP\_002858698.1 MULTISPECIES: hypothetical protein [Campylobacter]

MIKILEQTIKALKLNLKPYDLSMLTRKKSYICAKDQNNILFMYTGKTKFLMKDALFLENLAQQININNKY

FFSMASLCSKAKNHLEMKGFNIYVAL

>WP\_002858498.1 MULTISPECIES: hypothetical protein [Campylobacter]

MTYSFIQPRKKPIFTLFDKIWLGLFGFSILFILLVYFTYTIKIALINSSIDDEKQQVIVLQNQTKQNEML

YEILFDQSQIAKNFNTQNQIVKESLRNLFDIIVKTDNITLESVEQDEYSLKLIGVTPTREMFTLLLETPL

KSIFDQSYTTYYRLDNGWYRFVSISKQIPGVADER

>WP\_002858150.1 MULTISPECIES: hypothetical protein [Campylobacter]

MIPNTNEIAKQTLIALKERKLKPTPENYTEIFEELSLKYGITSSNKAKLDKYKTLLLPIYQQELNSKTIR

SLEELISFLISVLNRQSGKQFSEFFDFLYTISKTLQISKDKKIRDLAKVTSIRISKTMDSESIYLLTKKW

KELERNYDENDLEEQARKYGISKYDDYDSVIKKLLVKLEERSYEHFSELLCLGLNPSLVEDLKIQGFIQN

LTQKPFVIGEENFKNELMEFINHRIMVDNMYVQKNLNFFNDNLKKIYELLVLLNKSNEKNMDFINTLKPD

ENGEVKLSFEDLKLKFKQLGEKITSLNNQIEFTQSLEEREAWSVLKELDKMDENFNKYKVNYSLALFSIV

NYRFIMEKYGMGSLNEIFVRFKKILKDSCSEFDELWMIDEKSYLIVSPGKSKDEITQLVNTNLKTIENFR

FIYKQDIITPKIHVAYLDKQSKPSINILDELIKQIAAVNEQHNES

>WP\_002857548.1 MULTISPECIES: hypothetical protein [Campylobacter]

MIKIAFFITFVISFLTAQSPVNFKEDNNITKEQNIFKEQPPKRIKIPTH

>WP\_002856886.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKYITISILSILLLILLAVVFTLLWQFKANVNFIPQFAKDTNTQPSIQTQNQDLSWQEELAKWPTRDFT

PAAEKFTLYFDADTSELKEKNKYYQLIVGKYDIYSMFCLRQTLNSFNVKYFLLKSGDSPEIFLDTGNEKL

IDDIIKELKKYKINTEVKEIWL

>WP\_002855905.1 MULTISPECIES: hypothetical protein [Campylobacter]

MPVSPLGNVNYINQNMAYPATQASNELAKEGFAATLNMAEFNEKEKTLNKLEKVNETHEIKEEIKEKAEQ

EEKKKKHNQEAKTSDDEKNEEDESKDPNFKDAQSIHRLDISI

>WP\_002854947.1 MULTISPECIES: hypothetical protein [Campylobacter]

MADNLKQVIVNVNAKDFIVKCSEEFANFLEDDIALISGGTKKIELKRFVDAFVKKSYENYILERELKKLI

KAINEELPTK

>WP\_002854546.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKIPFSKINTKEYPFKLNLENMIFEGNLVKINSKLVKINAIMQGFIYRPCDSCGTELELEIKENLELFAS

DGIFKDEANELSNTIEFFDGHIDLIEVAISELEAYLSDYFYCINCNN

>WP\_002853612.1 MULTISPECIES: hypothetical protein [Campylobacter]

MYERKDLRVLKIIQKAREFGDGDLLNEALVKQLIDADFCEINEKEKEELATLLNSLINAKDKALLSN

>WP\_002853267.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLIIGHKLLKNLDFSFIESVEEVKDNKVYCIVYDEKLISYLSQNDFEFAILVQNKDEIFLANALGAKFLL

CNDKKLAKFASKVAEFYVFDSRVLMIVDKLENFKKFYKLKIDGIILKDNIDNFPKN

>WP\_002853000.1 MULTISPECIES: hypothetical protein [Campylobacter]

MDFLDSLKSIKKEMQANTNTSKLAKKSSKSGASVKNLEKLAKDIREKNQETNIDKEMQEIFLKQEKLQDE

FSEFIKNTDIKKI

>WP\_002851904.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKVVLISALLGAFAANVFAANTPSDVNQTHTKAHHSKAKADKKHEAKTHKKTKEQTPAQ

>WP\_002851454.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKILQDGFFLAIFFFVLLPSRVFALDAVLFNENILSQKVSNEINLIGKELYQKSNIFIGVMVGDKTEIE

TLLNKQKELPQSYILLLLSKNSHKVDIVGSKGALALIDKEAVLSPYPGTGSILPILATNKGDIYNAAILN

GYADIVDRVAKSLGLQLEHSIGNANRDTINILRILIYGFICFALLYYAQRRIKRKKNVRN

>WP\_002839177.1 MULTISPECIES: hypothetical protein [Campylobacter]

MIFWAFLVVIGAIYFGNMFFGQYSLDTLLSLENTKEELNKKIILLKEQNAKAQKDYFELKGLYPNEN

>WP\_002826012.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKISLECKDLIIEKTLELFLKDHLVMKKNCDFIISDEKIHTAKPLFIISKNSPFLSIPFSKEALFESLNE

FDNALKAAALQLALEQKRLLEEKIDAIALEFKKDYENKIDLAIKDLKNKLVKALNDE

>WP\_002824650.1 MULTISPECIES: hypothetical protein [Campylobacter]

MSKPLNEEIFIEFKSDLAERKNEVLLQVLELLETFRSDKNEKMARISSELTEILENEENLEKILNAKNLE

ELLNILIALNEDKMIKVYEDSYLKEKFPNVMVDKFLK

>WP\_002783105.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKCFNAKFMFVGILAVFLSACSSGIPKCSDQDVQNVLTEIILEHNFGRFSEVDRKKLKFTYSGFMSDLTD

KESKTQYCKAQVKANGSIDSRPYKWDAWIEYFARYTDDGMVYVEITR

>WP\_002776553.1 MULTISPECIES: hypothetical protein [Campylobacter]

MFFKKKISQKQKEKPKIPINDVILDDRLCKFKNKVQKISKDEASASLLARQLSRLVRANKF

>WP\_012006639.1 MFS transporter [Campylobacter jejuni]

MFDFFKPKAKAIKFPKEEILPRYYKMRTWSLSGVFIGYMGYYLVRNNITLSTPFIQNQLDLSKSDIGTIT

GSMLIAYGISKGAMSVISDKADPKKYMALGLILCALVNVLLGFSNSFYAYVGFVIALGVFQGMGVGPSFI

TLANWYPKKERGIYTAVWNISHNIGGGIVAPIVSLSGFALAALLGVSMADFNETYWHMNHFYVPAACAVI

ISLYVLYAVKGSPKNEGLIDITEINEMRGIKTEEIKAIETPNLSSFEIFYRYVLKNKNAWYVAWMDTFVY

MVRFGLISWLPIYLLETKGFNKEQMGIAFWLFEWAAIPSTLLAGYISDKIFKGYRMPPAIGAMVIIFFMI

IGYFTSNNLYMVIFFAAMAGCLVYIPQFLASVQTMEVVPAFAVGSCVGLRGFMSYVVGASLGTKAIGWAV

DYYGSWNAGLIMLLSACILCILCSTLCHFSAKKKYQ

>WP\_002851895.1 MULTISPECIES: recombination protein RecO [Campylobacter]

MQGFILHTQKVKDEDLIVYILSPKMLIKAYRFYGLRHSSILSGYKIDFALEENPSFLPRLKDVLHLGFLW

IMQRDKMLIWQEFIRLLYRHLKDVEELDSFYFDLLDECVKRFEKQNPKRVIVDAYLKILEFEGRLHKDFF

CFACDEKIQNSITLLRAFLPSHSQCALGFEFEEKKLKQFYSSKNCAIFDDEEIENLYHLIKEGL

>WP\_002826016.1 MULTISPECIES: flagellar protein FlgN [Campylobacter]

MLKQRLDEVNAILAKLIALTEEDIENIKVAKHESVTPSVEEKNKLIAEFITAKKQLDVALVELNNSSTKG

LSELLDDEDKQKLDLLKKNLQNLHSKNKEYAKFVLIVKDFLDGLVNKMFNINDGTNNAYGDKKTNPESIF

KINV

>WP\_002854837.1 MULTISPECIES: basic amino acid ABC transporter substrate-binding protein [Campylobacter]

MKKILSIALVALVGLFLGACSDSKNKESNASVELKVGTAPNYKPFNYKENSKLTGFDTDLVEEIAKKNGI

KIVWVETNFDGLIPALKAGKIDMIASAMSATDERRQSVDFTKPYYMSKNLYLKLKNNDSLQTKNDLEGKK

IGVQLGTLQENTAKAIKNAQVQSNKDLNIAVLALKNNKIDAIVADQDTAKGFLAENPELVSFYQETDGGE

GFSFAFDKNKQKDIIEIFNKGIDEAKTDGFYDTLIKKYELE

>WP\_002878197.1 hypothetical protein [Campylobacter jejuni]

MKYKWIVKNAYINFKLNNLYMLINPSHKIYLKKDMCYCFEIYIKYRIFNNCILVCDMLDNWWKLISSTLH

LDKSHIKYNYLSNTFIVSDFELGIKLESNLLTKFNFEFYNGLILNQLSITNGLSLKRENYNKSLKFSNCK

FNKEFCIARINISKQIVFENIYFLENVFIEWVNFNENSCLRFFKCNFKKQCNFKYNIFYNEIDFLDIYAK

ELILEQNIFNKFLYIQNSTINNINLWKNKFKNRCYFMDSVFGNKNNENIKLNFSNAHFEDNAYFNNSEFY

SYADFHECEFDDIACFYGVKFYKAPNFSACYFKEPKAVNLINVDIDKLDFKSVEKYIEDNYKDESYKNET

KGIQDEKEIFKIQNEYRLRYAKNLKDSFRVIKDVLITQNNTLEAQEWHKLELYAKEKELEIQLSKNKNDN

LKKESKNQVYNPKDYEKINSSRLKTLKSKLMPLIFYSLLPMAHTLFLPFYLFCTIFIIIKIITKILIKIS

KLFYYFYISFRPLEWNKFIIFWKVKFNHCIKKLMTFGRKMLDFTLWFDCILLQVYRNTSNHHTNFLKILN

FTILMISSYAIFGLLFLNNMDFILSFGPMTIAAMNYIVLLMLLIIFISLTRQLYQHGAILLFLIYGLFII

SIVSFLSPIYIPAFYFLIYFVGILISYLLFICKIKLFVFISRLFAYICLIGVVILKPQLINPFVGIFSSD

KLYESKFEKRLNDLNTSAIINLASILQNDFNLHLKDQNISFTELNSAKALIIANKEKLKEILSKVYNDKY

VSDYKKVLNELENNTSNVKNIIEEIDNKNNNSVVSAQLNKFLKLNFNQEIDILYAIKSNFSISEKLSPEQ

MALFDQKDSQDKLKSVLALLKFKSSFEGILKIINQDEITENTIKSTGVLYGIILLLCIFSLQKTARKNSI

VPS

>WP\_002868256.1 hypothetical protein [Campylobacter jejuni]

MKKTILILALFLSASWAQNLEINPDTGLIIDPDSPLVEANCLACHGSNLITNMHASRKAWLAAIRWMQDS

EGLWEIEPEDEEKILNYLEKYYGEKYDTRRRIPLAILLQNKTH

>WP\_002866863.1 hypothetical protein [Campylobacter jejuni]

MIYDNALCFLDMPSLKNKNLCEKIGVNSINISCLEDKNLKAKFYKCEIASLSFVLALLCKLSDEGHFCDL

DEGYLSAESCFGEEEAGEVLSFLKEAKYLIVDKNIHSYKDSENIKYFLNFLSIKYELKILDSDEEECDFK

KAKLNTLKELDNYDGLVLFRANLQDKNLHCSKQFLQIAKCKDQSEVEILAKDFSLKTKLCLDENLQGTIA

FLNYENNGFDFTPIRIKEAK

>WP\_002866815.1 hypothetical protein [Campylobacter jejuni]

MIVCAGGNENFSFAKAIGIGLVESAFHLGQLCFKEKPSKLIFIGTCGLYDKGKILEIYKSSHAFNVEFSK

ISHAFYTPAKYEIYLEKENVSRETIKINSSNYICQNSKAAKEFSKLGFFAENMEAFSVLSVAKNLNIDAE

CILCATNFCNENAHEDFIKNHQKAKEKLEEYLKKYHYI

>WP\_002866738.1 hypothetical protein [Campylobacter jejuni]

MKIKLFLLASFIYIALIFAFAWHLELGSYTLNISTYTFELPIMIWLVIPLFIYMILAVLHIAFYGFLRYL

KFKHFFKDAAKFESYTQDLLLEKDLKTTFQTKEFRAVAQLFKTIKTHEKIPHSNKINEILDLIDGLNKNE

FFNLSKFKLENNNVLYLQNEKNHLKNDANYAYSKLKNLNEIKDEFEEIAFNTLIEKASYEQIKNVKIPKK

PSEVLTLIKRFKEGNLELSAAEYEVLLSHNTLSEKDYLNAAKLSTKLLNPDAVLGIFNKIKNEKSEALRA

HLYLLAEFGLLDELREQIHNDDKKFNDFKAFLLLREKNIKIDLNQLIQ

>WP\_002866682.1 hypothetical protein [Campylobacter jejuni]

MDREVFYIAGYDPKSYRFYYDLFKKNLKDYSHAFNIEADLSKIEKKEQFPFFKISCEGVQTKYHFLTWND

IVKKNWSENYKDALADCYSFFRIYTITGLFIKFGKESIYQLITGYYPFFYVLFSLLFSLVLAFGSFAFLQ

NYMHFSLAIIIGCFLGFLLNHFLFKLGKKLAVFWIARICAFCATWQDKKTGTMQERIKLFANVIIDKLKR

NESKQDYELILVAHSVGTIVCIEVLECILRQNLDLSLLRKLKILTLGECIPLVSYQKKADEFRKKLEFVS

RFDLKWYDYTSIIDGACFPQVDFFRTSGVNAKFTPPFLSAKFHTLYEKHEYKKIKRDKNKAHFLYLYSIS

VKGDYDFFSFIIMPKFLEEKVKI

>WP\_002866442.1 hypothetical protein [Campylobacter jejuni]

MGIILGILNLIAGFVAIVLMCSLYFIVFMVFVGMAILIFLSMQPYPYNIIFCAIYLITILALVLWRKT

>WP\_002866278.1 hypothetical protein [Campylobacter jejuni]

MQNTVDLIKQFFINIDRADIDENMENLLSEDIIDSIDIMSLVAEIEKFYKKPLKAEFIKAENFESFKTIQ

DMINQAFK

>WP\_002866190.1 hypothetical protein [Campylobacter jejuni]

MKILLLNENPVVSRLVSLSAKKMSYDFEELNAYSENLGNYDVIVVDSDTPAPLKILKEKCDRLIFLAPRN

QNVDIDAQILQKPFLPTDFLNLLNNKDTNKHTSIDLPILSNDENPYADISLDLDNLNLDDLPDENSLDIN

SEGMEDLSFDDDAQDDNANKALETQNLEDENLEQETTKEQTQEDIQTDLDLTLEDGGSQKEDLSQEHTAL

DTEPSLDELDDKNDEDLEIKEDDKNEEIEKQELLNDSKANTLEMQEELNESQDDNANKALETQNLEDENL

EQETTKEQTQEDIQTDLDLTLEDGGSQKEDLSQEHTALDTEPSLDELDDKNDEDLEDNKELQANISDFDD

LPVVEEQEKEMDFDDIPEDAEFLGQAKDNEESEENLEEFSPVVEEDVQDEMDDFISNLSTQDQIKEELAQ

LDELDYGIDSDNSSKVLEDFKDEPILDDTELGTNEEEVVVPNLNISDFDALKESDIQEALGEEIVEKNEE

PIVSNATKDDNSEEIVNELSQSIAGAITSSIKDDTLKAALKGMNMNININISFKED

>WP\_002866087.1 hypothetical protein [Campylobacter jejuni]

MSRFFLYLLIILILALITFVLREKLGKKTKPFFGVLLVIFIVLAVFFEFENTQKSHLRTDIIVAFNQNKN

ILCKDINVSKAYFNYEFGTGSFISKDNNQSFNSLIIDIKDCRLNDE

>WP\_002857540.1 hypothetical protein [Campylobacter jejuni]

MNDFFDFFHKFILKTENLNLEILTKNNKYFLIPNEVCRYKKSPFGLLG

>WP\_002876927.1 MULTISPECIES: tRNA 2-thiouridine(34) synthase MnmA [Campylobacter]

MKILVAMSGGVDSTVTAYKLKNLGHEVIGCYMKLHGKPNYHEENIKKVEKVANFLQIPYHILDLQKDFKN

KVYMPFVDTYKEGKTPNPCALCNRFIKLGKLLEFAKSLGCEKLATGHYARLENNLIKTAVDESKDQSYFL

ASADKEALKYLIFPLGEMKKEDVKKFASTIEVLKSFATQKESSEICFVEDTYVQVLDQFMDTKIPGEVLD

SSGKVVGKHEGYMHYTIGKRRGFEVRGAHEPHFVLKINPKQNQIIVGTKEELKISEFKLKNINLFIDAKE

LDCEVKIRYRSKSTPCKVEIYEDKSAKITLKDPVYGLASGQMAVFYDHDKVIASGFIE

>WP\_002868040.1 MULTISPECIES: tRNA (guanosine(37)-N1)-methyltransferase TrmD [Campylobacter]

MKFSFVSLFPNLMEFYFQDSILARAKEKKLFKLNFYNPRDFSKNSYHKVDDYKIGGGAGLLMQAEPMYEV

LRSIQEKKENPYFIFLNPSGKTFNQKDAKRLSKKEHIVFVCGRYEGIDERVLEIFANEVFSIGDFILTGG

ELPALVMCDAILRNVNGVLGNMESLEEESFENNLLEAPAFSKPFIFEKKNKKFYTPSEFLKGNHARIASL

KTTLASCKTKFFRPDLFLEHERKK

>WP\_002825654.1 MULTISPECIES: GTP cyclohydrolase I FolE [Campylobacter]

MQKKFEDCVKTILEIIGENPNREGLIKTPNRVFKAYEFLTSGYTQNVKEILNDALFESSNNEMVLVRDIE

FYSLCEHHLLPFFGRAHVAYIPNKKVVGLSKIPRLVEVFARRLQIQEQLTEQIAQALMENVDAKGVGVVI

EARHMCVEMRGVQKANSTTTTSALRGIFLKNEKTREEFFSLINSAKQVRF

>WP\_002866517.1 HslU--HslV peptidase ATPase subunit [Campylobacter jejuni]

MNLTPKEIVKFLDDYVIGQKKAKKIIAIALRNRYRRMQLSPELQDDIVPKNILMIGSTGVGKTEIARRLA

KMMGFPFIKIEASKYTEVGFVGRDVESMVRDLANAALNLVKNEQREKNKDKIDEFIENKILEKLLPPLPK

GISDEKQEEYKNSLEKMRTKLRNGDLDESTIEIEISQNMFDTNPNLPPEMGAMQDIVKVIGVGSKKVKKE

MKIKDAKNALKNEAGEKILDQESIKSEALKRAENEGIIFIDEIDKIAVSSGNSNRQDPSKEGVQRDLLPI

VEGSNIQTKIGTLKTDHILFIAAGAFHLSKPSDLIPELQGRFPLRVELDSLDDKALYEILTRPKNSLLKQ

YSQLLKTENLELEFDDEAIKEIAKIASRANEEMQDIGARRLHTVIEKLLEDLSFEADEYAGKKFVVDKKM

VEEKLGDIIENKDLARYIL

>WP\_032603143.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKETTDVFLNKIIEDEKLRNDFINKILKNSEFMEEFERMVDLHINDKISILTDIDQEKSQIGGLE

>WP\_002877673.1 MULTISPECIES: gamma-glutamyl-gamma-aminobutyrate hydrolase [Campylobacter]

MFIGITQRLIYNESYHEERECLALDWGKLFNKDLFKNFTPLPLSYEIDFSHYKHLIKAVILSGGNDLSFY

SPNVLSKKRDLYEKQVIEICLKEKIPLLGICRGAQMIAHYFNSHISPCENHIGKHEVFFSKEKFISNSFH

NFAIEKLGEDLVELCLAKDNTIEAFKHKYENIFGIMWHIERENGLNNIQILKEWFSLIKE

>WP\_002877661.1 MULTISPECIES: hypothetical protein [Campylobacter]

MDRVSADIRQGVNKRFINAICNHNNELVLEYLKNGMSVTKECMGKEPMFYAVTHNNFGAILLLLKYGAIL

DKEYLEESNKNFSKEALEFLASLL

>WP\_002876971.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKILKNKYFILWMIGFFAIVCLCLYFNLEVKIIASAISAYAVSISLVLNAYSIFEKTRADKFNLTMQLLS

KWDEKHFIEARDYTREQQNIKEKKEMKKY

>WP\_002857436.1 MULTISPECIES: QacE family quaternary ammonium compound efflux SMR transporter [Campylobacter]

MEWFYLFLATACEIFGVVIMKELVSTKNKLYLLALIVCFGFSFTFLSLSMQNIAMSVAYAIWTGAGTAGG

VMIGVLFYKESKSFLKLFLITVIIACTVGLKFLS

>WP\_002857302.1 MULTISPECIES: QacE family quaternary ammonium compound efflux SMR transporter [Campylobacter]

MNEKFNINIAWFLIILGGIIECFWVSGLKYSTEIWHYILTAIGVCISFTCFLKACERLEVSITYSVFVGI

GTIGVVLNEMFIFNEAVSIIKLVLIVILLLSIIALKWISKEA

>WP\_002787630.1 MULTISPECIES: low molecular weight phosphatase family protein [Campylobacter]

MKLAFICIHNSCRSQMAEALARHKAEKMGIDIEVFSAGSDTSKGVNSQAIRLMREIYQIDMKKHYSKLID

SLPQNLDIVVSMGCGVACPSLKSRYYFDFGLKDPSGSYDDEFRKIIQILDYKITALLQAIKTNSLKDFTC

>WP\_012006765.1 phosphonopyruvate decarboxylase [Campylobacter jejuni]

MLNMEFFGEALKTIGCFQFSGVPCSYLSPMINYAINENSFIMSNNEGDAIAIATGISLANMEKKDNFGVV

LMQNSGLSNALSPLTSLNYTFEIPILGFVSLRGERDDQDRNTDEPQHELLGTITDRLLETCNIAYDFLSP

DYNQAIRQLQIAHKYLKQQKSYFFIVKNNTFEKCSLKNFNIPVKNIGREIIQQENSLAEFQPKRIEILEC

IANFSYKNNIALFATTGKTGRELYEIRDTENQLYMVGSMGCVSSLALGVSLQNSKKIIAIDGDSALLMRM

GALTTNAYYTKNNNKGNFCHILLDNESHDSTGGQFNLSPFINFPQIAHFCGYEKIFIINSLDDLIQALDF

FIARKEGGAVFIYVKILKGSKGKLGRPKITPKEVALRIAQFLNRKSDE

>WP\_010891930.1 MULTISPECIES: cytochrome c nitrite reductase small subunit [Campylobacter]

MIILRRKILKKTSNLFTIFLVLLFVFFAVGFYTFYNAKGTSYLSNASESCNNCHIMNEVYNEYMAGPHSQ

KVKGEPRATCVDCHLPHNFVAKWIAKAQSGLGHAYAFTFKLDELPTNLSATEKSRKMVQENCIRCHADFA

QTAINATTNPHADKSLNCASCHKDVGHKHGI

>WP\_002866671.1 N-acetylneuraminate synthase [Campylobacter jejuni]

MKEIKIQNIIINEEKAPLVVPEIGINHNGSLELAKIMVDAAFSAGAKIIKHQTHIVEDEMSKAAKKVIPG

NAKISIYEIMQKCALDYKDELALKEYTEKLGLVYLSTPFSRAGANRLEDMGVSAFKIGSGECNNYPLIKH

IAAFKKPMIVSTGMNSIESIKPTVKILLDNEIPFVLMHTTNLYPTPHNLVRLNAMLELKKEFSCMVGLSD

HTTDNLACLGAVALGACVLERHFTDSMDRSGPDIVCSMDTKALKELIMQSEQMAIMRGNNESKKAAKQEQ

VTIDFAFASVVSIKDIKKGEVLSMDNIWVKRPGLGGISAAEFENILGKKALRDIENDTQLSYEDFA

>WP\_002851470.1 MULTISPECIES: TonB system transport protein ExbD [Campylobacter]

MLKLPKNEGLNIVPFIDIMLVLLAIVLSISTFIAHGKIQISLPSSENATNISNNEKKLLITIDEKNTFYL

NDKLADLNEVQNAIFSLDKKTIVELKSDKNAKFESFVKIIDFLKAKEHENFQILTEKNK

>WP\_002851166.1 MULTISPECIES: TonB-system energizer ExbB [Campylobacter]

MEFLKDYIDLIIFLILGIMAFIAFWCVVERMLFFRKINFKNYENQEQFDDAISENLTTIYIIYSNAPYIG

LLGTVIGIMVTFYEMGLAGNIDVKSIVVGLSLALKATALGLLVAIPALMAYNALLRKVSLLSNAYKANKN

A

>WP\_012006617.1 gamma-glutamyltransferase [Campylobacter jejuni]

MRYLAIFAISITLSFGAANPPIQDRTGTGLVLSSHELANKIGKEVLDKGGNAIDAAVAVGYALAVVHPAA

GNIGGGGFAVIHLANGENTTLDFREMAPLKASRNMYLDSKGEVIKDASTIGYLAAGVPGTVKGMSAMLDR

YGTMKLKDLMAPAIKLAEKGYLINDRQEQTMLEAKDMFKEFPSSSKYFLKKDGSTYKSGDLFVQKDLAKT

LKLIAKEGPDAFYKGKIADLIAADMAKNKGIITKEDLAQYQAIWRKPVEGTYRGYDIISMSPPSSGGAHI

IEILNIMENANIENLGFASSKTLHIMAEAMRQAYADRSEYMGDPDFVKIPLDKLTSKEYAKEIYAKIPKD

KALPSSKVKPGLGQIHEGHNTTHYSVLDSKGNAVSITYTINASYGSGATVEGAGFLLNDEMDDFSIKPGV

PNLYGLVGGEANAIEPKKRPLSSMSPTIILKDGKVFMVVGSPGGSRIITTVLQVISNVIDHKMDISTAVE

SPRFHMQWLPDEIRTEPFGIIKDVQNNLEKMGYKITKEPYMGDVNAIMVDPKTGKIIGSMDTRKEF

>WP\_002866272.1 UDP-N-acetylglucosamine 4,6-dehydratase (inverting) [Campylobacter jejuni]

MFNGKNILITGGTGSFGKTYTKVLLENYKPNKIIIYSRDELKQFEMASVFNAPCMRYFIGDIRDNERLSA

AMRDVDFVIHAAAMKHVPIAEYNPMECIKTNIHGAQNVIDACFENGVKKCIALSTDKACNPINLYGATKL

ASDKLFVAANNIAGNKQTRFSVTRYGNVVGSRGSVVPFFKKLISEGAKELPITDTRMTRFWISLEDGVKF

VLSNFERMHGGEIFIPKIPSMKITDLAHALAPHLSHKIIGIRAGEKLHEIMISSDDSHLTYEFENYYAIS

PSIKFVDKDNDFSINALGEKGQKVKDGFSYSSDNNPLWASEKELLEIINHTEGF

>WP\_002876679.1 MULTISPECIES: hydrogenase accessory protein HypB [Campylobacter]

MCKDCGCSINSSHTHGHHHDHHHENPSLKEGKTIEVISKILSKNDEEAKHNRAHFNEANTLCINLMSSPG

SGKTTLLESTIKALKNELKIAVIEGDLETNNDALRVKNAGALAYQITTGQSCHLDAFMVHEALHHLAIDD

VDLLFIENVGNLVCPASYDLGEHLNVVLLSVTEGSDKPQKYPVMFKKADIVLITKVDLAHHFDFDLKEAT

KLIKELNPRADIITLDAKNGTNMELWYKVLKLKKELF

>WP\_002872053.1 cytochrome c oxidase accessory protein CcoG [Campylobacter jejuni]

MQGHITNYTKKRYFVYLIASIIIFALPFIRINENHFFLLSFDHSKLNLFFISFLTQEFYLMPFVLIFLFL

FIFFITTLGGRIWCAWSCPQTIFRVIYRDIIQTKFLKIRKNINNKQKEYEGQYFKKFLGVIIFYFISLVA

VSNLLWYFIPPEDFFNYIQNPGEHLLLLGILFCASLLFTLDITYLQEKFCVYICPYARIQSVMFDHDTMQ

VIYDEKRGGLIYDGHTKLHKKPPEGECIGCEACVSICPTHIDIRKGMQLECINCLECADACSKVQSKFNR

PSLINWTSAKAIETRSKVHYLRFRTIAYFIVLLIALLALIIMGSKKESMLLNINRSSELYNISNVKGELV

ISNAYTFLFQNTDSKPHEYYFTANLEGINDGIEIIRPNKPFKLKAGEQVKKIVVIRATKNLANNDKKDVI

FPLHIKAYAKDNEKISVFRKSIFVYPKSTLIKDKNELK

>WP\_002866285.1 pseudaminic acid synthase [Campylobacter jejuni]

MQIGNFNTDKKVFIIAELSANHAGSLEMALQSIKAAKEAGADAIKIQTYTPDSMTLNSNKEDFIIKGGLW

DKRKLYELYESAKTPYEWHSQIFETAQNEGILCFSSPFAKEDLEFLKRFDPIAYKIASFEANDENFVRLI

AKEKKPTVVSTGIATEEELFKICEIFKEEKNPDLIFLKCTSAYPTAIEDMNLKGIVSLKEKFNVEVGLSD

HSFGFLAPVMAVALGARMIEKHFMLDKNIESEDSKFSLDFDEFKAMVDAVRQAESALGDGKLDLDEKALK

NRVFARSLYASKDIKKGEMFSEENVKSVRPSFGLHPKFYQELLEKKATKDIKFGDALKESDFR

>WP\_002866273.1 UDP-4-amino-4,6-dideoxy-N-acetyl-beta-L-altrosamine transaminase [Campylobacter jejuni]

MLTYSHQNIDQSDIDTLTKALKDEILTGGKKVNEFEEALCEYVGVKHACVLNSATSALHLAYTALGVKEK

IVLTTPLTFAATANAALMAGAKVEFIDIKNDGNIDEKKLEARLLKDSENIGAISVVDFAGNSVEMDEISN

LAKKYNIPLIDDASHALGALYKSEKVGKKADLSIFSFHPVKPITTFEGGAVVSDNEELIAKIKLLRSHGI

IKKRLWDSDMVELGYNYRLSDVACALGINQLKKLDHNLEKREKIASFYDKEFEKNPYFSTIKIKNYKKSS

RHLYPILLFPEFYCQKEELFESLLHAGIGVQVHYKPTYEFSFYKKLLGEIKLQNADNFYKAELSIPCHQE

MNLKDAKFVKDTLFSILEKVKKGYCG

>WP\_002859283.1 MULTISPECIES: methylenetetrahydrofolate reductase [NAD(P)H] [Campylobacter]

MCSFSFEVFPPRKDENIKNLHAILDDLGQLSPNFISVTFGAGGSINSQNTLEVASLIQEEYQIPSIVHLP

CIHSSKEKITQILQKCKEKNLNQILALRGDICENLEKSKDFSYASDLISFIKKQEYFEIYAACYPEKHNE

SKNFIEDIHHLKTKVNAGTDKLITQLFYDNEDFYTFKQNCALAGIDIPIYAGIMPITNKRQVLKISQLCG

AKIPPKFVKILEKYENNALALEDAGIAYACDQIVDLITSGVDGIHLYTMNKSKAAIKIYEAVKHLLKEEL

HA

>WP\_002857589.1 MULTISPECIES: molybdate ABC transporter substrate-binding protein [Campylobacter]

MKKFVVFFGILLFVSCLNAQNLSIFVASSASKAMSEVKDEFLKTHPEDKIELVFGASGKYYELLKQGREF

DLFFSADTKYAKAIYDDKNALIKPKVYVLGVLALYSLDENLLQGGVENLKEKANKITHLSIANPKVAPYG

VAAKEVLENLGLNELLKDKIVLGENISVPVLHVDSKNSDIAIVAYSLVSSINHPKGKAVIIDAKYFSPLE

QSYVITKYAKDKKLAFEFNEFIGSSKAKEIFKKYGFSTP

>WP\_002855824.1 formate dehydrogenase subunit gamma [Campylobacter jejuni]

MRKVFVTLLLSVASLFAYGSERMGQDTQIWDFHRITNIPNYDTFGKLWTTLQGEYIATIALIAVIAVLSA

FALHYMVIGPKQFSHDGKKIYAFTLFERLFHFIAAISWVILVPTGFVMMFGATFGGGLFVRVCKNLHAFA

TVLFIISIIPMFLWWIKRMLPASYDIRWMMIVGGYLSKVKRPVPAGKFNFGQKSWYYIAVFGGFLMIITG

GFMYFLDFNSTAIQGLFGLTQIELLRISAIVHNFLGIVCAVFFGVHIYMAVFAIKGSIHSMISGYKEEEE

VYILHSYWYKELSNKKQIEPSFSYDPNVKI

>WP\_002852529.1 MULTISPECIES: flagellar biosynthetic protein FliP [Campylobacter]

MKKILLFLLLSMSLFAAEATIPTVNLSLSAPNTPNQLVTTLNIVIVLTILALAPSIVFVMTSFLRLIVVF

SFLRQAMGTQSMPPNTILVTLALILTFFIMEPVATKSYNEGIKPYLAEKIGYEEAFIKGAKPFKDFMLKN

TREKDLALFYRIRNLPNPKTIDDVPLTVLVPAFMISELKTAFEIGFLIYLPFLVIDMVVSSVLMAMGMMM

LPPTMISLPFKLLIFVLVDGWNLLVQRLVESFVT

>WP\_002776558.1 MULTISPECIES: magnesium and cobalt transport protein CorA [Campylobacter]

MLYIYIKTQNALVQRINFNLDSQELPQNILWIDLLHPSVAEIAFISSEFNLEFPTKEEREEIELSAKYWE

DNATITINAHFLVRDLKSDEEDRNLIKLRTEIVTFATAKNILFTIRYNEFSTFEEIQARILASPKNFEDG

FDIIDKMFEVRVEKDADLLEWIDKEARRLRTSVLEKKDEYSYDEMLKDISSLQELNMRVRDSLFDKRRAM

TSLLKSDKIDKDIKQNLTIVLKDLNSLVEFSVSQLNILDNIQTILASQINIEQNKIIKIFTVATVAMMPP

TLIGTVYGMNFKFMPELELHYAYPIVLGVMVISIILPLVVFKKKGWL

>WP\_012006774.1 UDP-glucose 4-epimerase GalE [Campylobacter jejuni]

MKNILVVGGAGYIGSHTLKHLLDNNYNCIVMDNLIYGHKQAIDKRAKFIHADLLDTFSLTNVFKQEKIDA

VVHFAAFAYVGESVVNPAKYYQNNVVGTINLLNAMLENNVKDIVFSSTCATYGEPQYTPIDEKHPQNPIN

AYGRTKLMIEQVFADYEKAYGLRHISLRYFNAAGASKDGLIGESHEPETHLIPLVLKAIKGEIPAINIFG

NDYDTEDGTCIRDYIHVEDLALAHRLALENLHKFSGCINLGTGIGTSVKEIISAAEVVSGKKCPINYAPR

RAGDPARLYADNKKAKEILSWEAKYTDIKDIIKSAWVWENNRKY

>WP\_012006726.1 endopeptidase La [Campylobacter jejuni]

MQIEEIQNYPANLPVLVEDELFLYPFMITPIFINDLSNMKALDLAIKNDSMLFVAPSKLENGRNFDEIYN

CGVIGTIMRKVPLPDGRVKILFQGYAKGKIIEQISNKPLEAKIELIKEDFLEGTKKEALLEVLKEKVKNL

ANISHYFSPDLLRTIEEGFDASRICDLILNTVRIKKQVAYEFFVLTDLEQKLVKLIDLIAQEIEANKIQK

EIKNKVHSRIDKVNKEYFLKEQLRQIQKELGSDTQKEDEVREYQKRLELKKKFMHEDAYKEIKKQIEKFE

RIHQDNSEASMIQTYIETALDIPFEKISKKKLDIKEVSKQLNHDHYALNKPKERIEEYFAVRELLEKRKI

AEKDGAKVILCLYGPPGVGKTSLANSVSKALKRELIRIALGGLEDVNELRGHRRTYIGAMPGRITQGLIE

AKQINPVIVLDEIDKLNRSFRGDPSAVLLEILDPEQNSKFRDYYLNFNIDLSKVIFIATANDISNIPAPL

RDRMEFIELSSYTPSEKFHIMKKYLIPDELKKHGLKSNELSIDDETIELIISDYTRESGVRNLRRKVAEL

CRKSAKKLLLENIKKVIINTKNLNEFLDKKVFEIEKNNGENQVGQVNGLAWTSVGGDVLKVEAVKIKGKG

ELTLTGSLGDVMKESARIAFSMIKVLIDEGKIKIPKKIIIDPKVNVYDSYNIHIHVPDGATPKDGPSAGI

TISTAIASIFSDKKVKADVAMTGEIDLKGKVLPIGGLKEKLIAAYKADIKTALIPRKNYERDLKDIPSEV

RDNMEIIAVDTFSDVLEYTLI

>WP\_002877875.1 type I methionyl aminopeptidase [Campylobacter jejuni]

MIELKKPDEIEKLRIANQIVAKTLNFLENEIKIGMSLKQIDKMAEDYILSLGAKPSFKGLYGFPGAICTS

LNQVCIHGIPDDKIIKEGDILGLDVGSLIDGYYGDAARTIAIGEVSPTDKALISCAKDALYHAIDIIHDG

MRFKELSAALGEFIHTRGFVPLRGYCGHGIGRKPHGEPEILNYLEKGASAKSGPKIKNGMVFCIEPMICQ

KDGTPKHYNGKWDAGSIDGLNAAHYEHCVAVINGRAEILSMI

>WP\_002868484.1 MULTISPECIES: type I glyceraldehyde-3-phosphate dehydrogenase [Campylobacter]

MAVKVAINGFGRIGRCVARIILERNDIELVAINDTTDIELTKYLFKYDTVHGEFKGSVDSEGDDLVVNGK

KIKVFKSRNVKDLDFAKHGAQIVLECTGAHLTMAKCQEFIDMGVQKVIMSAPAKDDTPTYVLGVNSELYK

GESIISNASCTTNCLGPVCRVLQDNFGIEKGLMTTIHAYTNGQSIIDAKAKDKRRSRAAAQNIIPTSTGA

AKAMKLVMPELNGKLHGQSMRVPVIDVSSVDLTAQLSRKVSKDEINEAFRKAATTNLKGILMVDDDERVS

SDFITCSYGAIVASDLTQVIADDFIKVIAWYDNEWGYSSRLVDMAVYIANKA

>WP\_002866327.1 thioredoxin-disulfide reductase [Campylobacter jejuni]

MLDVAIIGGGPAGLSAGLYATRGGLKNVVMFEKGMPGGQITSSSEIENYPGIAQVMDGISFMAPWNEQCM

RFGLKHEMVGVEQILKNSDGSFTIKLEGGKTELAKAVIVCTGSAPKRAGFKGEDEFFGKGVSTCATCDGF

FYKNKEVAVLGGGDTALEEALYLANICSKVYLIHRRDEFRAAPSTVEKVKKNEKIELITSASVDEVYGDK

MGVTGVKVKLKDGSIRDLNVPGIFTFVGLNVRNEILKQDDGKFLCSMEEGGQVSVDLKMQTSVAGLFAAG

DLRKDAPKQVICAAGDGAVAALSAMAYIESLH

>WP\_002865906.1 cysteine synthase A [Campylobacter jejuni]

MKVHEKVSELIGNTPIIHLKKFGINVFVKCEFLNPSHSIKDRAAFEMIKDALDSKKINQDTTIVEATSGN

TGISLAMICADLGLKFIAVMPESMSLERRKMITLFGARLELTPVNLGMKGAVDKANEILLNTPNSFMVSQ

FENISNKNAHRKNTALEILRDLDNELDIFVAGFGTGGTISGVGEILKEKLEKVHIVGVEPLNSPLLSKGE

AGSHKIQGIGANFIPAILNKEIIDEVITVSNEDAINTAKELAKSGLMVGISSGANVFAASMLAKKFPDKR

ILTMLNDTAERYLSTDLFA

>WP\_002784291.1 MULTISPECIES: phosphate ABC transporter permease subunit PstC [Campylobacter]

MLKEKIIKFALFLCAFVSVIVSFAIMLTILIEALKFFQKESVVTFLFSSQWAADAAFMNADGTSKQGVFG

ALSLFWGTFYISLIAMLTALPLGVMCAIYLGVFAGKKSKNYLKPILEIIAGIPTVVFGFFAAIVVAPFIV

WFFSLFGIQASFQSALGAGFIMGIMIVPIVASLSQDCIEAVSEKRINGAYALGMTKKEVVFAVILPEAIP

GIVAACLLGLSRALGETMIVVMAASLRPNLTMNFLEDMTTVTVKIVEALSGDQAFDSSLALSAFSLGLVL

FIITLIINMFSVYLINRFHKRKNL

>WP\_002856854.1 MULTISPECIES: molybdopterin adenylyltransferase [Campylobacter]

MDTINIGVLTLSDRASSGIYEDKATAEIERVLNSYIKNDIIYHKELIPDDYDLIIKKLLYLADEKKCDLI

VTSGGTGPALRDVTPEATEAVCDKMMPGFGELMRLESLKYVPTAILSRQSAGIRNKSFIINLPGNPKAIK

ECLEPVFPAIPYCIDLIEGAYIEANDEVIKVFRPKKKCQN

>WP\_002857293.1 MULTISPECIES: hypothetical protein [Campylobacter]

MDKAKIVQNLNALFKQRAEFYSYFDENIAKINNTEVFDFKNAKNLNPEEVYKQFYHFDYAIRKLLPAIYK

AYEITDADLDKDF

>WP\_002852415.1 MULTISPECIES: hypothetical protein [Campylobacter]

MNQNNNKTLKNELEDLQYELSIVLEAMLLYAGVKREKLENAIEAYIDNIDNVLENSNKEGVDEILEVVEF

LKNKYKDFFQ

>WP\_002852327.1 MULTISPECIES: hypothetical protein [Campylobacter]

MFDEKIINTMTDKVNELIEKYNEVCEANEALRNELVSVKAQNEAKSNQIMRLEEELKSRNIESEDIYKKI

EAVLGR

>WP\_002783228.1 MULTISPECIES: OXA-61 family class D beta-lactamase OXA-193 [Campylobacter]

MKKITLFLLFLNLVFGQDKILNNWFKEYNTSGTFVFYDGKTWASNDFSRAMETFSPASTFKIFNALIALD

SGVIKTKKEIFYHYRGEKVFLSSWAQDMNLSSAIKYSNVLAFKEVARRIGIKTMQEYLNKLHYGNAKISK

IDTFWLDNSLKISAKEQAILLFRLSQNSLPFSQEAMNSVKEMIYLKNMENLELFGKTGFNDEQKIAWIVG

FVYLKDENKYKAFALNLDIDKFEDLYKREKILEKYLDELVKKVKNDG

>WP\_012006697.1 phosphoglycerate dehydrogenase [Campylobacter jejuni]

MKKKIIVCDAILDKGVDILRKAEDIELIEAAKVPKDELMQMLSDVEVAITRSSTDVDINFLNHAKKLKAL

VRAGVGVDNVDIPECSKRGVIVMNVPTANTIAAVELTMTHLLTSARSFVNAHNFLKIERKWEREKWYGIE

LMNKTLGVIGFGNIGSRVAIRAKAFGMKILAYDPYISASKITDLDMEQAKNLDEILEKSDFITIHTPKTK

ETNGMIGKQEIAKMKDGIRLINCARGGLYTEEALYEGLKSGKIAWLGIDVFDKEPATNHPLLDFENISVT

SHLGANTLESQDNIAREACEQALSAARGVAYPNALNLPIKTEDLPPFVAPYIELVSKMAFLAVQIDKNPI

KSIKLEAEGIIGEYANSMLTFAAVGALGGILGEKINYVNAEFVAKEKGVELSCETLPNSGYNNKLSVKII

TENSNISVSGTVFNENEQRIVGLNGFKTDFKPKGKMIIFKNKDIPGVIAKISSVLAAKNINIADFRLGRD

GFGYALAVVLIDEKVQKEVLDELKQLEACVFVQYVEI

>WP\_002865961.1 membrane protein insertase YidC [Campylobacter jejuni]

MNNSNNIFQQKRILLAVVISFLFFVVYDYFFIPKQPLKIEQNITQQNQQNTSINNTPNIQNTTTNTPSAA

LVSQDSVISKVQSKHFEAQIDSFGRISAFYLKDKKYQNEKGEFINLVSKENSPYPLEMRFSDPSINSEAF

KIPYVANASNLFVDENGSQVLKLTQNLSGLKIEKDITFYPKGNYEIEVKLSKNANYFISPGYRPNIAVDS

YTVHGALVMDNKETIETYKDGDVEKDESANNVVMTSAFDRYYATFFYNFDKPLNVAISKDANKNPIVFAY

SDNEFKAGGYIGSKEHVILRSIDPRLEAVVEYGWFTFIAKPMFEFLNFLHQYIGNWGWAIVVMTLIVRII

LFPLTYKSMISMNKLKDLAPKMKDIRERYKGDPQKMNMHMMELYKKHGANPMSGCLPILLQIPIFFAIYR

VLLNAIELKAAPWAFWIHDLSVMDPYFILPILMGVTMFLQQLITPMTIQDPMQAKIMKFLPVIFTFFFIT

FPAGLTLYWFVNNLCSLVQQWVINKIFAKEHHKKQAEHEK

>WP\_002825273.1 MULTISPECIES: co-chaperone GroES [Campylobacter]

MNFQPLGKRVLVKRVEETKTTASGIIIPDNAKEKPLMGEVVAVSKEITDIANGDKIVFAKYGGTEIKLDN

NEYLVLNLDDILGILK

>WP\_012006674.1 primosomal protein N' [Campylobacter jejuni]

MQRSDIRYYELAICGLYLDNLTFHSFDEIKPLTQVLVDLKTKKNLKAIVLKECQKPDFKTVEIKEITKYF

LTPLQFELANFIVYYYASKLGFVLGFFETSPKYECQKMFFKDTPKLSNQQQNALSFLQKENNSLLFADTG

SGKTEIYISLIKECLEQGKQALLLMPEIALTPQMKKRLEVYFKDNFFLWHSKISKKKKQEYLERFCKGEV

LLVAGARSALFLPFRNLGLIVVDEEHDNSYKASNQPFINARDLALFLGQKNNIKVVLGSATPSLTSFYKQ

KSFRLKGTFFESKKHFLYDENELGITPMLLSELEKSLKHQKQAIVFLPTRANFRQIICKDCGETIKCPFC

SIAMSMHKKKNVLKCHYCNYTSLIEQNCPSCKGEMLEARKMGTAELLELLQNALPLAKIAKFDSDEITSV

KKLNTILKDFNENKIDILIGTSMLAKGHDYHSVDLSVILGLDEYLLRPSFRASEETLALAMQVAGRAGRK

GEARVLLQTKNRAFFERYIEDYDAFLKDELENRKDLYPPFKRLLRVLIEDKDQKNAQKLCEKLAYQFKNI

KQVELVGYGICGVEMLHEKYRFYLLLRSENYKALVAIENYILQFKNVSADIDPIDFI

>WP\_002851903.1 MULTISPECIES: 16S rRNA (uracil(1498)-N(3))-methyltransferase [Campylobacter]

MQFLYNKQAGEEFIQLQGENFNHLKVRRVKENSELNLRNLQDNFLYNYTITNLTRNSCTLKFLNKKSQNI

KQSELNLALAIIDIKILEKTLPFLNELGVKKLHLVFTNFSQRNFKIDLERFEKIIISSCEQCGRNTKMDL

IIHQSTQEFVQKFPNAIMVDFQGEQQSHFDEKELYFIGPEGGFNNDERLLFNRKISLKSSNILKSQTAII

AIASKILL

>WP\_002855278.1 MULTISPECIES: succinate--CoA ligase subunit alpha [Campylobacter]

MSILVNKNTKVIVQGFTGKEATFHAEQCMAYGTNIVGGVTPHKGGQTHLGKPVFDTVADAVKATKADVSL

IFVPAFAVGDSVIEAADAGIKLAVVITEHTPVKDMMFAKQYANKKGMKIIGPNCPGIITSEECKLGIMPG

FIFKKGCVGLISKSGTLTYEAANQVVQGGYGISTAVGIGGDPIIGLAYKELLSEFQKDDETKAIVMIGEI

GGSLEVEAAKFIKENISKPVVAFIAGATAPKGKRMGHAGAIVGSADESAAAKKEALKSYGIHVVDSPALI

GEEIQKILG

>WP\_012006644.1 cytochrome c biogenesis protein CcsA [Campylobacter jejuni]

MKVKSLLIASLVAFSSLNAASLIDEAKNSGLVALPKDQKGVDEILKQNGVKASEFTLEKVELGKKLYFEP

RLSKSGIISCNTCHNVGLGGTDGISTAIGHKWTANPHHLNSPTVYNAVLNNTQFWDGRAGTLADQAKGPI

QADPEMATPAKLAVEKISSLPEYVSEFKKIYGKSGVNFDNIADAIANFERTLITPSRFDKFLEGDEKALT

KEEQKGLKLFIDKGCVACHNGVNLGGNMQAFEVAGKYKFANLGDFKGDANGMVKTPTLRNVAETAPYFHN

GAIWNLKDAIKEMGSVQLGIKISDKEAKSIETFLKSLTGTKPAIVYPQLPISTEKTPKPEL

>WP\_012006615.1 cytochrome b6 [Campylobacter jejuni]

MKKIIMILYLSYANIVFAVDMITPIPNSISYDKEKAKLGKSLYMDKSLSKDGKVSCNTCHRLDQHGVDGL

EFSIGVDNQLDKPFNTPTTFNSVFNFVQFWNGRAKDLAEQATVPFFNPKEMGLSPELLLQKVNSNENYVK

TFKKLYGEVTVENIALAVAEFEKTLITPNSPFDHYLSGDQNAISAQAKKGYEDFKANGCISCHQGQNIGG

NMFQKIGIFEEYPNQEDLGRYEITKREADKMVFKVPSLRNIAKTAPYFHDGSIPTLDACVQFMAYYQLGK

FLDQETVDNIVAFLESLTGEYHDK

>WP\_002865956.1 5'-nucleotidase SurE [Campylobacter jejuni]

MKEILITNDDGYESEGLKKLIKMLTKEFKAKITIVAPASEKSACSHSITLTKPLRFVKVGKRFYKLDDGT

PADCVYLALHALYKKRLPDLVISGINKGANVGEDITYSGTCAGAMEAVLQGIPAIALSQFYKKSEKELDY

KNALQITKKIIQNIFDKGFPLEKKEFLNINFPAKSKIKGIKICKAGKRVYNFEAHSNVNPRGVEYYWLAA

ANLDFEDEKNSDIALLKKGYATITPIMLDLTAYEKMKKVKKWLKANDE

>WP\_002859743.1 MULTISPECIES: cytochrome c [Campylobacter]

MKKHILLLGLCLSLSLSAKSVSDYKVGEELSDKEGVEYFKELSKRPVQEWPNKNLSINDVPKGKQGDLIR

YGIELLSKTESTLGPYSKLKKTSNEVNCISCHMDNDGNGLPGTKKYVIPFLNVLNNYPKLDIETMKIISV

EDRIRGMGGTDSHRFPNDSKEMKAILAYFKWLKEAYGIKDGVKLEGDFFAKMNFPNRPADPVRGKKLFEE

NCVACHGERGLGVKNDNYEQGSGHLYPSLLIYPDGGHMAMIPFLARFLKSAMPFGASADNPILSDEDALD

IAAYVNTGFVRMPITTTENRAGLDTAYSKSPSLKPEYFASPQQNLDPKEYIKVKYGPWKNPNHFPGE

>WP\_002852762.1 MULTISPECIES: cytochrome c [Campylobacter]

MKKLLVVSALACLGVSAFAADGATLFKKCAVCHGANADKVYLNKVPALKTLSSAERLQYMKEYSEGKRNA

YGQGAIMKLNLKGLTEEDFKAIEAHIETLK

>WP\_002866459.1 DNA ligase (NAD(+)) LigA [Campylobacter jejuni]

MKKEEYLEKVALANLWMRAYYEKDEPLASDEEYDALIRELRAFEEQNKDEISKDSPTQKIAPTIQSEFKK

IAHLKRMWSMEDVFDESEFRAWAKRAKCEKNFFIEPKFDGASLNLLYENGKLVSGATRGDGEVGEDITLN

VFEIENIPKNIAYKERIEIRGEVVILKDDFEKINEKRALLNQSLFANPRNAASGSLRQLDTSITKERNLK

FYPWGLGENTLNFTKHSEVMQFIRELGFLKDDFVRLCVNLDEVLKAYDELLALREKKPMMMDGMVVRIDD

LALCEELGYTVKFPKFMAAFKFPALEKTTRLIGVNLQVGRSGVITPVAVLEPVNLDGVVVKSATLHNFDE

IARLDVKINDFVSVIRSGDVIPKITKVFKERREGLEMEISRPKLCPTCQSELLDEGTLIKCQNIDCEDRL

VNSIIHFVSKKCLNIDGLGENIVELLYKHKKITTLESIFHLKFNDFEGLEGFKEKKINNLLNAIEQAREC

ELFRFITALGIEHIGEVAAKKLSLSFGKEWHKQSFEAYANLEGFGEQMALSLCEFTRVNRTRIDEFYKLL

NLKIEKLEIKSDGVIFGKTFVITGTLSRSRDEFKALIEKLGGKVSGSVSKKTDYVLFGEEAGSKLIKAKE

LEIKCIDESAFNELVKE

>WP\_002853034.1 MULTISPECIES: exodeoxyribonuclease VII small subunit [Campylobacter]

MSFEENLKHANESLEKLNNQELALDESVKIYKEGLESIKKARLELEKAKLEVEQIDE

>WP\_002852880.1 MULTISPECIES: ubiquinol-cytochrome c reductase iron-sulfur subunit [Campylobacter]

MATSESRRSFMGFAFGSVAAVGGVFSLVAMKKTWDPLPSVKAAGFTTVDLSGMQDGELRTIEWRKKPIFI

LKKDASMPKDEKRDVVVDNAAYTVVIGLCTHLGCIPAYQPSEQLFKCACHGGEFDTSGKNVFGPPPKPLE

IPPFKIDGTKLVLGEEGPEYKKMIAEA

>WP\_002856408.1 MULTISPECIES: IMP dehydrogenase [Campylobacter]

MKIVKRALTFEDVLLRPGYSEVLPKEVKIHTKLTKNITLNMPLISAAMDTVTEHRAAIMMARLGGLGVIH

KNMDIASQVREVKRVKKSESGVIIDPIFVSPKASVAEALEIMAEYRISGVPVVDEDKKLIGILTNRDLRF

ESDFSNLVENVMTKMPLITAPKGCTLDDAEKIFSTNKVEKLPIVDEQGRLEGLITIKDLKKRKEYPDANK

DNFGRLRVGAAIGVGQMDRVNALVEAGVDVVVLDSAHGHSKGIIDTVKAIKAKYPNLDLIAGNIATAAAA

KALCEAGVDAVKVGIGPGSICTTRIVSGVGVPQISAIDECVEEANKFGVPVIADGGIKYSGDIAKALAVG

ASSVMIGSLLAGTDESPGELFTYQGRQYKSYRGMGSLGAMQKGSSDRYFQQGTAQDKLVPEGIEGRVPYV

GSIRSVVHQLLGGLRSSMGYVGAKDIEDFQKRAEFVEITTAGLKESHVHDVTITHEAPNYKVNHQ

>WP\_002854049.1 MULTISPECIES: UMP kinase [Campylobacter]

MQERKRVLVKFSGEALAGENGFGIENSILKFIASEIKELIKNQIEVGIVIGGGNIIRGVSAAKGGLIKRT

SGDHMGMLATVINAIAIQEALESSGLEVRVQSAIQMEAFCETYIMRRAQRHLEKGRVVVFAAGTGNPYFT

TDTTAILRAVEIDADMVIKATKVNGVYDKDPKQFDDAVFLNTLSYDEAMQDNIKVMDDTAIALAKDNKLP

IVVCNMFEEGNLLKIIQGDTSLCSIVKNN

>WP\_002866689.1 triose-phosphate isomerase [Campylobacter jejuni]

MIFAVNLKCNHTRASFKIYAEILNKTMGAKCDDIIVFPPSVAFLENENNFIQGAQNFYPCVNGAFTGELG

KEHLDEFGIKCVLIGHSERRALGDEEFIKAKFDFAKEHGYKIVFCIGENLDTKNSGKTLEFLKKQLEIID

LNYEKLIIAYEPIYSIGTGVSAQSTDIAKVLEFLASLTKAPLLYGGSVNENNIKEILSVKHCGGVLIGSA

ALKVENFIKLIKG

>WP\_002867070.1 phosphoribosylformylglycinamidine cyclo-ligase [Campylobacter jejuni]

MKISYEDAGVSIDNGNAFVEAIKPLVKETFNDNVVGGIGSFAGAFRMPSGFKKPVILGATDGVGTKLRLA

IDAKKYDTIGQDLVAMCVNDLICNFATPLFFLDYYATVKLEVEVAKAVVSGIAKGCKMANCALIGGETAE

MPGMYAKDDFDLAGFAVGMAEEDEIDRSKFVKNGDILLALPSSGLHSNGYSLARKVLFESLKLKFDDKIE

GKNLIDILLEPTRIYVRDFLTLKPYISALAHITGGGLVENLPRVLPSGMGATIRKHHLKTPEIFYTIGQA

VEESEMYRSFNMGVGLVMVVDPSNVSKVLENSDAFIIGEICINEGIVLE

>WP\_002866117.1 methionine adenosyltransferase [Campylobacter jejuni]

MYLFTSEVVSAGHPDKCADIIADTIVDILLKNDKNSRVASEVFVAGNKVVIGGEVKSNHKLSKADYDNLV

KDVLKNIGYDGAGHFSKEQCLHPDEVDVMVFLNEQSPDINQGVDQEDGETGAGDQGIMFGFASCEAEEYM

PAAISYARMLCDRVYAYAKANPHELGVDIKTQVTIDYGTKANFENCEPQSIHTIVVSAPCVESMKIEDLR

SLVMKLILDSNLPKELFDPNKTRILINPTGKYVNHSSLHDSGLTGRKLIVDSFGGYSPIGGGAQSSKDYT

KVDRSGLYAGRWLAKNIVAAGLAKKCIVQLSYAIGVAKPTSVSVDCMGTNTSVNDDVLSDFVMQNFSLTP

NWIRDKFHLDKPSKETFLYADVAARGQVGQKDYPWEKLDALEQFKKLL

>WP\_002852211.1 MULTISPECIES: acetolactate synthase small subunit [Campylobacter]

MRRVLSVIVLNEHGVLSRIVGLFSGRGYNIDSLTVAPLENKEFSRINIVTSGNERTFEQIVKQLHKLIPT

YKVIESEEFIDKEMALVKIPLNENLGGLDAVLKAYNGTIANSNENFLFLMVADDANRIDNFLKTIKKYNP

SDIVRSGSVLMEIK

>WP\_002851622.1 MULTISPECIES: gamma carbonic anhydrase family protein [Campylobacter]

MLIKFKNHSPKLGQNVFVAEGAKIIGEIEIGDESSIWFNCVLRADVNFIKIGKRTNIQDLSTVHVWHREF

DEKGKLKDAGFPTIIGDDVTIGHNCVIHACVIKNRVLIGMNAVIMDNALIEEDSIVGAGSVVTKGKKFPP

RSLILGNPAKFVRELNDEEVSFLKQSALNYVDFKNEFLKDLQ

>WP\_002858914.1 MULTISPECIES: transcriptional regulator [Campylobacter]

MQKFLTIISAINDESRVLILHHLLRYKELCVCDLQELLNMGQSRLSRHLKILKDAGFLYVKRKGTWAYYG

INNELLKLHSDLFENIKNLDIDNIVLEQNTCENDK

>WP\_002854645.1 MULTISPECIES: tryptophan synthase subunit alpha [Campylobacter]

MVDFRKFYKENANVAYTVLGYPNLQTSEAFLQRLDQSPIDILELGVAYSDPIADGEIIADAAKIALDQGV

DIHSVFELLARIKTKKALVFMVYYNLIFSYGLEKFVKKAKSLGICALIVPELSFEESDDLIKECERYNIA

LITLVSVTTPKERVKKLVKHAKGFIYLLASIGITGTKSVEEAILQDKVKEIRSFTNLPIFVGFGIQNNQD

VKRMRKVADGVIVGTSIVKCFKQGNLDIIMKDIEEIFKK

>WP\_002854230.1 MULTISPECIES: transcriptional repressor [Campylobacter]

MLIENVEYDVLLERFKKILRQGGLKYTKQREVLLKTLYHSDTHYTPESLYMEIKQAEPDLNVGIATVYRT

LNLLEEAEMVTSISFGSAGKKYELANKPHHDHMICKNCGKIIEFENPIIERQQALIAKEHGFKLTGHLMQ

LYGVCGDCNNQKAKVKI

>WP\_002853007.1 MULTISPECIES: thiamine biosynthesis protein ThiS [Campylobacter]

MIINGQKLELKELKFMDFIKEKGLKIELIALELNGEIIPKSEFENLILKENDKAEIVSFVGGG

>WP\_002851700.1 MULTISPECIES: rod shape-determining protein [Campylobacter]

MILDQLIGFFSSDMGIDLGTANTLVLVKDKGIVINEPSVVAVERERYGSKAKILAVGKEAKDMVGKTPGN

IEAIRPMKDGVIADFDMTEKMIRYFIEKTHRRKSFLRPRIIISVPYGLTQVERKAVRESALSAGAREVFL

IEEPMAAAIGASLPIQEPKGNLVVDIGGGTTEIGVISLGGLVISKSIRTAGDKLDMSIVNYVKEKYNLII

GERTGEEIKITIGSAIQLPKELSMVVKGRDQVSGLLSRIELTSEDVREAMREYLKEIADALKMVLEMMPP

DLASDIVENGVVLTGGGALIRGLDKYLSEIVRLPVYIADEPLLAVAKGTGKALEEISLLQQLTNEE

>WP\_002778123.1 MULTISPECIES: pantoate--beta-alanine ligase [Campylobacter]

MQVITSVKEAKQIVKDWKSHQLSIGYVPTMGFLHDGHLSLVKHAKTQDKVIVSIFVNPMQFGPNEDFSSY

PRDLERDIKMCQDNGVDMVFIPDATQMYLKNFSTYVDMNTITDKLCGAKRPGHFRGVCTVLTKFFNILNP

DIVYMGQKDAQQCVVVRHMVDDLNFDLKIQICPIIREEDGLAKSSRNVYLSKEERKASLAISQSIFLAEK

LVREGEKNTSKIIQAMKDILEKEKLIKIDYIELVDFNTMENIENITDNVLGAVAAFVGKTRLIDNFLVQG

LK

>WP\_002886243.1 MULTISPECIES: accessory colonization factor AcfC [Campylobacter]

MKKIITLFGACALAFSMANADVNLYGPGGPHTALKDIASKYSEKTGVKVNVNFGPQATWFEKAKKDADIL

FGASDQSALAIASDFGKDFNVSKIKPLYFREAIILTQKGNPLKIKGLKDLANKKVRIVVPEGAGKSNTSG

TGVWEDMIGRTQDIKTIQNFRNNIVAFVPNSGSARKLFAQDQADAWITWIDWSKSNPDIGTAVAIEKDLV

VYRTFNVVAKEGASKETQDFIAYLSSKEAKEIFKKYGWRE

>WP\_002862038.1 MULTISPECIES: AI-2E family transporter [Campylobacter]

MQNGKFFLISFILVILFLLLYLFKGFLLVIIIASLMAVATSNINAKFLNLTKGHKFLASILTTTCMVLLF

FAPFVYAMIELAKALKNFDINLVTQTLDYVKNYQFTLPESFNFLEPKIKEFLASIDLNSISKQILSYASS

FTKSGAKFLIDMVLICVFYFFANLYGTELVIYLKSIIPIDKKELDDVLSEVGNVMAVVLYSMVIVAIFQG

ALFGLITMFYGYDGILMGVIFAVSSLIPAIGGALIYVPVSLYEFASNNLNSALVIFIYSVIVISFIADTL

IKPLIIKWINKKLVKTPTKINELLIFLAMIAGISTFGFWGIILGPAILTFFVSTLRMYVILKDKNLI

>WP\_012006745.1 major outer membrane protein [Campylobacter jejuni]

MKLVKLSLVAALAAGAFSAANATPLEEAIKDVDVSGVLRYRYDTGNFDKNFVNNSNLNNSKQDHKYRAQV

NFSAAIADNFKAFVQFDYNAADGGYGANGIKNDQKGLFVRQLYLTYTNEDVATSVIAGKQQLNTIWTDNG

VDGLVGTGIKVVNNSIDGLTLAAFAVDSFMAAEQGSDLVGANGSAFKVDSIGNLYGAAAVGSYDLAGGQF

NPQLWLAYWDQVAFFYALDASYSTTIFDGINWTLEGAYLGNSLDSELDKTYANGNLFALKGSIEVNGWDA

SLGGLYYGDKEKASTVVIEDQGNIGSLLAGEEIFYTTGSRLNGDTGRNIFGYVTGGYTFNETVRVGADFV

YGGTKTEAANHLGGGKKLEAVARVDYKYSPKLNFSAFYSYVNLDQGVNTNESADHSTVRLQALYKF

>WP\_002859296.1 MULTISPECIES: DnaJ family protein [Campylobacter]

MNSLYETLGVSKNASADEIKKAYRRLARKYHPDINKEKGAEEKFKEINAAYEILSDEKKRAQYDQYGDSM

FGGQSFHDFSRNTGGVNLDDILKDLFGGGFGGRSRGGFNGFSSKGFSSGFGGFGGFEEENLDSNLELHIP

FEKAVKGGEHSFNFQGETIKFKIPHGIKEGEKLRIRSKGKQSRNGARGDLIIIVKIEESPIYTREDDDLY

QKVDISLKTALFGGKINIKTLKEGKEEATINITPNSKNNQKIRLKGYGVQNRKSDIYGDMYLILNVVLPN

LDTLDEKFIELLKEKLP

>WP\_002854779.1 MULTISPECIES: indole-3-glycerol-phosphate synthase [Campylobacter]

MILDKIFEKTKEDLKERKLKLPYDMLGRSLASNPFFPKDVIKALKRVEKEVKIIAEVKKASPSKGVIRED

FDPLSIALNYEKNKAAAISVLTEPHFFKGSLEYLSLIRRYTQIPLLRKDFIFDEYQILEALVYGADFVLL

IAKMLSMKELKKLLEFARHLGLEALVEIHDKEDLSKAIFAGADIIGINHRNLEDFTMDMSLCEKLIPQIP

NSKIIIAESGLENKEFLEHLQNLGVDAFLIGEYFMREKDEGKALKALL

>WP\_002854376.1 MULTISPECIES: nucleoside-diphosphate kinase [Proteobacteria]

MEKTLSIIKPDAVKKGVIGKILDRFESNGLRIAAMKKVQLSKEQAENFYAVHKERPFFKDLVEFMISGPV

VVSVLEGEGAVLKNRDLMGATNPKEAKAGTIRADFAESIDANAVHGSDSLENAKIEIDFFFKPNEIC

>WP\_002851945.1 MULTISPECIES: penicillin-binding protein activator LpoB [Campylobacter]

MKKTKILGTALIGALLFSGCAQTAYTDGKASQVKKGDALTLGLDRQDFESAAETMINSMLSDPAFANIKP

GTRKVIAIGRVVNDTPQRIDTEKLTAKITSALRKSGKFVLTSAVAAGGALDSMSEDVRELRDNDEFNQKT

IAKKGTLVSPDFSLAGKIRQDNVKLSNGKTQVEYFFLLRLTDLTSGLVYWEDEQTIDKTGSSKSVTW

>WP\_002866657.1 exodeoxyribonuclease VII large subunit [Campylobacter jejuni]

MTPTELNLKAKALLETHFEDIVLSGEISKITLHGSGHWYFDLKDERSSIACAMFKGANLKVGFKPAVGDF

LELCGSVSLYPESGRYQFIATSMKKAGFGDLEAQFLALKERLQKEGLFDPLFKKSLPKFPKKVGIITSKT

SAALQDMLKLIHQKEYFLAKIYIFDALTQGNNAPFSLIQALKKADDMDLDVLIIARGGGSREDLFCFNDE

NLAREIFKAKTPIISAIGHEIDYVISDFVADFRAPTPSAAIDTLFYSKLDIEQSLDLMEEKLMQLWNHKI

QNYENLLLNLSKFFKFNSLPKIIDEKIKQSHNIEKQLNHLLANQMRYNELKLDKLQNAYLQHENFFNKSK

KFICIRKNGKIANLEDLKSDDIVILSSQTSQKEAKIL

>WP\_002866581.1 imidazole glycerol phosphate synthase cyclase subunit [Campylobacter jejuni]

MLTKRIIACLDVKDGRVVKGTQFKNHKDMGDIIELARYYSQNGIDELVFYDIAASARKERISREWVSEVA

KNINIPFCVAGGIKSEEDAAELLANGADKISINSPALNDPSLITRLAKSFGVQCVVVGIDSFKDENGNLK

VFQYTGDEKTSKHSGKSTLEWVKEVQDLGAGEIVLNMMNQDGVKNGYDLEQLKAVYKICKVPLIASGGAG

KMEHFLEAFKLGIDGALAASVFHQKLIDIKELKIYLKNQGLSIRI

>WP\_002857192.1 MULTISPECIES: histidine triad nucleotide-binding protein [Campylobacter]

MQEKTIFELIVEGKLPCNKVLESDDFLAFHDIAPKAPIHILIIPKKHFKDFQEFDPELMAKMTSFIQELA

VLLGVDKSGYRLVTNCGKNSGQEVFHLHFHMLGGFELPKEKTKKENPQALF

>WP\_002854922.1 MULTISPECIES: phosphoribosylaminoimidazolesuccinocarboxamide synthase [Campylobacter]

MTKKEMLYEGKGKKLFKTDDENLLISEFKDDLTAFNAEKRGNESGKGALNCKISTEIFHLLEKNGIKTHL

VETISDTEQVVKKCKIVPIEVIVRNVATGSLTKRLGIKDGTVLPFALVEFCLKDDALGDPFINDEHCLIL

NLVQNEAQISEIKNMARKINSILTPFFDNKNLRLIDFKIELGLTKDNELVLADEISPDSCRFWDKFSNEK

LDKDRFRQDLGNVKMAYEEVLKRILN

>WP\_002787379.1 MULTISPECIES: hydrogenase expression/formation protein HypE [Campylobacter]

MKNISLAHGGGGEEMNELLTKLFKIFDNEILNANNDAAILGNLALSTDSFVLSPIFLDEEVNIGKLCVCG

SINDVLMVGAKPKYLSLGLILEEGFELEKLERILKSIKEECEKCGVMLVCGDTKVVPKGKADEIYINTTA

LGEIISKKESKNIKAGLSILLSGDIGRHGASVLIKRNELEADVKSDCKALDKEVLELLEKDIKVVAMRDA

TRGGLSAVLNEWAKQSGNDLLIFEEKIIVQDEVLGLCELFGYEAYELANEGTFILCVEKEDELKALEILK

KYNVNASIIGEVLEEKKARVILQNAYGAKRFLESPKGELLPRIC

>WP\_002877962.1 bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/inosine monophosphate cyclohydrolase [Campylobacter jejuni]

MRALLSVSDKEGIVEFGKELENLGFEILSTGGTFKLLKENGIKVIEVSDFTKSPELFEGRVKTLHPKIHG

GILHKRSDENHIKQAKENEILGIDLVCVNLYPFKKTTIMSDDFDEIIENIDIGGPAMIRSAAKNYKDVMV

LCDPLDYEKVIETLKKGQNDENFRLNLMIKAYEHTANYDAYIANYMNERFNGGFGASKFIVGQKVFDTKY

GENPHQKGALYEFDAFFRANFKALKSEASFNNLTDINAALNLASSFDKAPAIAIVKHGNPCGFAIKENLV

QSYIHALKCDSVSAYGGVVAINGTLDEALANKINEIYVEVIIAANVDEKALAVFEGKKRIKIFTQESPFL

IRSFDKYDFKHIDGGFVYQNSDEVGEDELKNAKLMSQREASKEELKDLEIAMKIAAFTKSNNVVYVKNGA

MVAIGMGMTSRIDAAKAAIAKAKEMGLDLQGCVLASEAFFPFRDSIDEASKVGVKAIVEPGGSIRDDEVV

KAADEYGMALYFTGVRHFLH

>WP\_002857452.1 MULTISPECIES: beta-hydroxyacyl-ACP dehydratase [Campylobacter]

MIDVMQIQEILPHRYPFLLVDKITELKVKEVVLGYKNISISDHVFMGHFPGHPIYPGVLILEGMAQTGGV

LAFESMEDKVDPKSKVVYFTGIDGAKFRNPVRPGDRLDYEMSVVKNRGNMWIFKGQAFVDGNLVAEAELK

AMIVDK

>WP\_002840050.1 MULTISPECIES: iron-sulfur cluster assembly scaffold protein NifU [Campylobacter]

MGKNSLIGGSIWDEYSQKVQDRMNNPQHMGEFSEEDAKARNAKLIVADFGAESCGDAVRLFWLVDEKTDK

IIDAKFKSFGCGTAIASSDTMVDLCIGKTVDEAVKITNLDVEFAMRDNPETPAVPPQKMHCSVMAYDVIK

QAAAHYKGISPEDFEDQIIVCECARVSLGTIKEVIKLNDLHSVEEITQYTKAGAFCKSCIKPGGHEKRDY

YLVDILAETRAEIDREKLKNTMKSDVAFDEMTVVGQLKAVESVLDAEIRPMLHNDGGDLEVIDIQKAEGA

AIDVYIRYLGACSGCSSGSGATLYAIETILQEELSPNIRVMPV

>WP\_002866283.1 imidazole glycerol phosphate synthase subunit HisH [Campylobacter jejuni]

MIALIDYKTGNLNSVAKAFEKIGATNFIAKNPKDLQKADKLLLPGVGSFKEAMKNLKELGFIEALKEQVL

VQKKPILGICLGMQLFLERGYEGGVCEGLGFIEGEVVKFEEDLNLKIPHMGWNELEILKQEPLYQDIEDK

SDFYFVHSFYVRCKDEFVSAKAQYGHKFVASLQKDHIFATQFHPEKSQNLGLKLLENFVRL

>WP\_012006786.1 type II CRISPR RNA-guided endonuclease Cas9 [Campylobacter jejuni]

MARILAFDIGISSIGWAFSENDELKDCGVRIFTKAENPKTGESLALPRRLARSARKRLARRKARLNHLKH

LIANEFKLNYEDYQSFDESLAKAYKGSLISPYELRFRALNELLSKQDFARVILHIAKRRGYDDIKNNGDE

EKSEILKAIKQNEEKLVNYQSVGEYLYKEYFQKFKENSKEFINVRNKKESYERCITQSFLKDELKLIFQK

QREFGFSFSKKFEEEVLSVAFYKRALKDFSHLVGNCSFFTDEKRAPKNSPLAFMFVALTRIINILNNLKN

TEGILYTKDDLNALLNEVLKNGTLTYKQTKKLLGLSDDYEFKGEKGTYFIEFKKYKEFIKALGEHNLSQD

DLNEIAKDITLIKDEIKLKKALAKYDLNQNQIDSLSKLEFKDHLNISFKALKLITPLMLEGKKYDEACNE

LNLKVAINEDKKDFLPAFNETYYKDEVTNPVVLRAIKEYRKILNALLKKYGKVHKINIELAREVGKNHSQ

RAKIEKEQNENYKAKKDAEIECEKLGLKINSKNILKLRLFKEQKEFCAYSGEKIKLSDLQDEKMLEIDHI

YPYSRSFDDSYMNKVLVFTKQNQEKLNKTPFEAFGNDSTKWQKIEVLAKNLPEKKQKRILDKNYKDKEQK

DFKDRNLNDTRYIARLVLNYTKDYLDFLPLSDDENTKLNDTQKGSKVHVEAKSGMLTSALRHTWGFSAKD

RNNHLHHAIDAAIIAYANNSIVKAFSDFKKEQESNSVELYAKKISELDYKNKRKFFEPFSGFRQKVLDKI

DEIFVSKPERKKPSGALHEETFRKEEEFYQSYGGKEGVLKALELGKIRKVNGKIVKNGDMFRVDIFKHKK

TNKFYAVPIYTMDFALKVLPNKAVARSKKGEIKDWILMDENYEFCFSLYKDSLILIQTKDMQEPELVYFN

AFTSSTVSLIVSKHDNKFETLSKNQKILFKNANEKEVIAKSIGIQNLKVFEKYIVSALGEVTKAEFRQRE

DFKK

>WP\_002852567.1 MULTISPECIES: phenylalanine--tRNA ligase subunit alpha [Campylobacter]

MQNFIEQIQKCENLNDLEAIRISVLGKKGILTEGFTKLKELEDEAKKEFAAKLNAQKEIFNEAYLAKFKD

LENLALEERMKQDALNFNYFDESITTGALHPVMSTMDKIIEYFIALNFSIEKGPLIEDDFHNFEALNLPK

SHPARDMQDTFYFDDKRLLRTQTSPVQIRTMLAQKPPIRMIAPGAVFRRDFDITHTPMFHQVEGLVVEEG

QKVSFANLKSVLEDFLRYMFGDVKVRFRPSFFPFTEPSAEVDISCVFCKGKGCRVCKHTGWLEVLGCGIV

DPNVYNFVGYENVSGYAFGLGVERFAMLLHQIPDLRSLFEGDLRLLEQFR

>WP\_002866764.1 1-deoxy-D-xylulose-5-phosphate reductoisomerase [Campylobacter jejuni]

MILFGSTGSIGVNALKLAALKNIPISALACGDNIALLNEQIARFKPKFVAIKDSKNKHLVKHDRVFIGQE

GLEQILTECQDKLLFNAIVGFAGLKSTLKAKELGKNIALANKESLVVAGSFLKGVKFLPVDSEHAALKFL

LEGKKNIAKLYITASGGAFYRYKIKDLNQVSVKDALKHPNWNMGAKITIDSATMANKLFEIIEAYHLYDF

KEIDALIEPRSLVHAMCEFKNGASTAYFSKADMKLAISDAIFEKQDTPILEAVDFSKMPALKFHPISTKK

YPIFKLKNTFLKEPNLGVIINAANEVGVYNFLENKSGFLDIAKCIFKALDHFGVPKISSIEEVFEYDFKT

REYLRS

>WP\_002857553.1 MULTISPECIES: DNA-binding response regulator [Campylobacter]

MRILVIEDEISLNKTIIDNLNEFGYQTDSSENFKDGEYFIGIRHYDLVLANWTLPDGDGAELVNTIKHKS

PRTSVMIMSSKTDKETEIKALKAGADDFVKKPLDFDILLARIEARLRLGGTNVIKIEDLVIDPDEEKITY

KGQDIELKGKPFEVLTHLARHSDQIVSKEQLLDAIWEEPELVTPNVIEVAINQIRQKMDKPLNISTIETV

RRRGYRFCFPKKS

>WP\_002853196.1 MULTISPECIES: DNA-binding response regulator [Campylobacter]

MTNILMIEDDLELAEITAEYLEKFDMKVDIAHEPYIGLSKLALKEYQLIILDLSLPGLDGLEVCEEIRKK

YDTPIIVSSARHDITDKVNALELGADDYLPKPYNPKELQARIKSHLRRISNTKSAIAKSVKDLVYDQYKH

IITMKGQELTLTNAEFDILSYLIKKEGGVVSREELVYNCSSISEDSSNKSIDVIISRIRQKMGDDPKTPK

YIHSIRGIGYKLTQ

>WP\_002866820.1 phosphodiesterase [Campylobacter jejuni]

MKFIHLTDIHYGDKKEAIYSREPSAMMRLAIEDINKNHSDADFVFITGDLTHKGSLESYTLLKQDLTKLN

MPYYLILGNHDDRANALEIFNNLKQDENGFIQYEIQCNDNNVFLVLDTIKLKSHGGEYCQKRQIWLKNAL

ERNQNKNIFICLHHAPFKTGLRAMDFIGLDEKHSLELYKLFNSYKNIKHLFFGHYHSTLCGRWKDISFSS

LKGINHQVKFDLNSNEILLEFRNPEYAVVLLNNEVLNIHYNDFTFDKNLIFHEK

>WP\_002866134.1 MULTISPECIES: two-component system response regulator [Campylobacter]

MKLLVVDDSSTMRRIIKNTLTRLGHDDVLEAEHGVEAWDLLTKNEDVKVLITDWNMPEMNGLELVKKVRA

EKKYEDMPIIMVTTEGGKAEVITALKAGVNNYIVKPFTPQVLKEKLEDVLGTGSGEGAAE

>WP\_002858951.1 MULTISPECIES: phosphatidylglycerophosphatase A [Campylobacter]

MQKLFLTFFYSGSIKKASGTFGTIAALIPAFFILKYLGINTLFLLSILIFVASIRVIDDYEKKTGIHDDK

HIVIDEVAGVFLACAIAASVENSIVNFILAFVLFRLFDITKPSIIGKIDKKVKGGLGVMLDDMLAGLFAG

LLSAVIYGFLLKFNLVFWDINLKDLF

>WP\_002776307.1 MULTISPECIES: phosphate ABC transporter ATP-binding protein [Campylobacter]

MIAKTTNLNLFYGKKQALFDINMQIEQNKITALIGASGCGKSTFLRCFNRMNDKIAKIDGLVEIEGKDVK

NQDVVALRKNVGMVFQQPNVFVKSIYENISYAPKLHGMIKNKDEEEALVVDCLQKVGLFEEVKDKLKQNA

LALSGGQQQRLCIARALAIKPKLLLLDEPTSALDPISSGVIEELLKELSHNLSMIMVTHNMQQGKRVADY

TAFFHLGELIEFGESKEFFENPKQEKTKAYLSGAFG

>WP\_012006710.1 molecular chaperone DjlA [Campylobacter jejuni]

MTLVLIILVVLVFYWYYKTWGKQDFLNSATRGAKGFAKGFARGVMEERMDEFKRRMNYYVIALLAKIAKS

DGRVSENEAEMIKDLLDANAKDEKERAFLKASFNEHKENLSDAFYVAKDFLKEVPLPKNERFNVLRVLVF

MALIDADFNAKKREILEQIAKAFDIAKSELDAFIASLSNLKSTKKELSLDEAFAILELPNNADLNAVKKQ

YRNLAKKYHPDILNANNVSEEELKIGVEKFQKINEAYEKVKKYLER

>WP\_002867076.1 DNA starvation/stationary phase protection protein [Campylobacter jejuni]

MSVTKQLLQMQADAHHLWVKFHNYHWNVKGLQFFSIHEYTEKAYEEMAELFDSCAERVLQLGEKAITCQK

VLMENAKSPKVAKDCFTPLEVIELIKQDYEYLLAEFKKLNEEAEKESDTTTAAFAQENIAKYEKSLWMIG

ATLQGACKM

>WP\_002853599.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MILELKQISKSFGSVKAINETSFKINEGEIFALIGPNGAGKTTLFNIITGNYKPSSGSVEFLGERIDHLK

PHKIVHLGIARTFQNIRLFSSMNVLENVLIGFNKQMKYNIFEAFLHLGRFGKIEQVFKEKAYAILEELGI

AEFAYEKATSLSYGQQRKVEIARAMATQPRLLLLDEPAAGMNSSESDELAELIFKLRKDYKISVLLIEHD

MKFVNKLCDRVLVLDYGKTIFEGKLCDAVNHKEVIAAYLGDFDANS

>WP\_002853544.1 MULTISPECIES: acyl-CoA thioesterase [Campylobacter]

MRDMGEPKLKIVAMPSDTNPAGNIFGGWILSQIDLAGAIAARELSPERVVTISMDKVVFKEPVFIGDIIS

CYSKVVNVGNTSISVEVEVTAQRVDSQGCTSCINVTSALVTYVSVTRDGKKKPISEELKRIHGFLNA

>WP\_002852965.1 MULTISPECIES: ABC transporter ATP-binding protein [Campylobacter]

MLIVKDLHVYYGLIEAVKGIDFKVETGHIVSLIGSNGAGKTSTLNALLNSVKRTGEVNFLGYDTKRHLTH

TLVQKGIALVPEGRRVFINLSVEENLKIGAFNNAENYEHLREQMYKLFPRLASKKHALAGTLSGGEAQML

AISRALMSEPKLLMLDEPSLGLAPKIVGEVFDIIVRLKEEGITILLVEQNAYSALKISDYAYVLENGRIV

MENEAKNLIGDDEIRKKYLGL

>WP\_002851424.1 MULTISPECIES: DNA recombination/repair protein RecA [Campylobacter]

MDDNKRKSLDAALKSLDKTFGKGTILRLGDKEVEQIDSIGTGSVGLDLALGIGGVPKGRIIEIYGPESSG

KTTLTLHIIAECQKAGGVCAFIDAEHALDVKYAKNLGVNTDDLYVSQPDFGEQALEIVETIARSGAVDLI

VVDSVAALTPKAEIEGDMGDQHVGLQARLMSQALRKLTGIVHKMNTTVIFINQIRMKIGAMGYGTPETTT

GGNALKFYASVRLDVRKVATLKQNEEPIGNRVKVKVVKNKVAPPFRQAEFDVMFGEGLSREGELIDYGVK

LDIVDKSGAWFSYKDKKLGQGRENSKAFLKENPEIADEITKAIQNSMGIEGMISGSEDDEGEE

>WP\_002866092.1 isoleucine--tRNA ligase [Campylobacter jejuni]

MDYKETLLLPSTTFAMRANLAELEPQRFKKWFEQNYAYEKMKENRKNAKKSFTLHDGPPYANGHIHIGHA

LNKILKETIIKTHYFKGESVRFTPGWDCHGLPIEQQVEVKLGEKKKSLSKKEIREFCRQHASEFVDIQRE

EFKNLGIIADWDKPYLTMKFEFEAAIYRTLCEIAKKGLLCERSKPVFWSWAAKSALAEAEVEYQDKEDYS

IFVAFDLDVKACEKLGVSKASAVIWTTTPWTLVANQAIALNPNENYVITKEGLIFASALLKSMVEKGLTS

GEIQKELNAKEFEKLEAINPLNGRKSVLIMGEHVLMDGGSGLVHTAPGHGEDDYYACLKYGIEVLMPVDD

GGCYDETLRAKELLPSHLLEEFIGLHIFKANEKILELLGEKLLHSSKFIHSYPFCWRTHKPVIYRATKQW

FILMDEPKLQGKTLRECAKEQLLKTTFYPQSGVKRIGSMVENRPDWCISRQRDWGTPIAFFRDKNTKEVI

FDDELFDFVAAIFEKHGADAWWEFEIKDLIPTNSKYKAENLEKVYDILDVWFDSGSTFNAVLNSGLYDAG

EKRASMYLEGSDQHRGWFQSSLLVGTAINESAPYESILTHGFTTDEKGQKMSKSKGNVIAPEYVAKTYGV

EILRLWILLSDYSSDLKISDNILKQVGEQYRKIRNTIRFLLANTNDLKDLEVKEFSFIDKWILSRATKVF

KASKEAFFAYEFAKGFSLLLNFLSADLSGIYLDISKDRLYCDSENAQRRKSAQVAMALIAKELLNLLAPN

LSYSVDEALEHANVLIKGDAKDVFDLSLTQDFDYDFGIDDTFLMSAREKFFEQIDILKKDKIIKSTLELN

LNISFNKFPNEELADWFMVSQISNENEEILAEFEVENEKFKITKASLCKCPRCWKLQSKDEETPCLRCEE

VLKGIQC

>WP\_012006727.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKGIFLLVFLSIFFSACSTKNDEGLYNLSASEWYKQIIKDLQDKDLEKADDHYNGMASEHVADPLLETT

LIILAQAHMDEEEYKLAEFYLDEYNKKFGNSRNADYIRYLKIKAKFDAFAVPNRNQALMLESQKEIDTFL

KDYPYTEYEPLVQTMLTKFNLAVFYLNSTIENLYQRIGHDESAQIYKQRLQESEFYQQSIIKPELPWYRS

IFERF

>WP\_002876767.1 MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Campylobacter]

MIDYHQIESRLSALEKLPSLKDNDSITKALEKSGFSRRDFMKWAGAMTAFLALPASFTPMVAKAAELADR

LPVVWLHMAECTGCSESLLRSDTPTIDSLIFDYISLEYHETVMAAAGWQAEENLESAIQKHKNKYILMVE

GGIPMGDTEHFLTIGAHGKTGYELSKMASENALAIFAIGTCSSFGGIQAARPNPSNAQPLSKVTSKTVIN

VPGCPPSEKNIVGNVLHYLLFGELPALDVYNRPKWAYGLRIHDLCERRGHFDAGEFVHAFGDEGAKQGFC

LYKVGCKGPYTFNNCSRERFNQHTSWPIQAGHGCIGCSEPDFWDTMGPFEEPMASRKFDTVFGLGADSVS

DKIGIGVLTLTGVAIAAHAVISSMQKDKE

>WP\_002876088.1 MULTISPECIES: microcin C ABC transporter ATP-binding protein YejF [Campylobacter]

MLKVCNLSKFYELKKHWYLKKERHIIFDNINFSLNENDNLIILGKSGAGKSTLARILCFLEDPSEGEVWY

ENLNLHKLDKNKQRLLRKQIQYCFQDQKMALNPYKKIKNLIQDGLENFNLQKNDDLILEFFDFFSLKKQI

LKQKPYELSGGEATRVGLIRALVLNPKLLILDEITSALDIKTSKEILTFLYDYQQKNNISYIFITHQSDL

FYKFNHKKLKL

>WP\_002869571.1 MULTISPECIES: catalase [Campylobacter]

MKKLTNDFGNIIADNQNSLSAGAKGPLLMQDYLLLEKLAHQNRERIPERTVHAKGSGAYGEIKITADLSA

YTKAKIFQKGEITPLFLRFSTVAGEAGAADAERDVRGFAIKFYTKEGNWDLVGNNTPTFFIRDAYKFPDF

IHTQKRDPRTHLRSNNAAWDFWSLCPESLHQVTILMSDRGIPASYRHMHGFGSHTYSFINDKNERFWVKF

HFKTQQGIKNLTNQEAAELIAKDRESHQRDLYNAIENKDFPKWKVQVQILAEKDIEKLGFNPFDLTKIWP

HSLVPLMDIGEMILNKNPQNYFNEVEQAAFSPSNIVPGIGFSPDKMLQARIFSYPDAQRYRIGTNYHLLP

VNRAKSEVNTYNVAGAMNFDSYKNDAAYYEPNSYDNSPKEDKSYLEPDLVLEGVAQRYAPLDNDFYTQPR

ALFNLMNDDQKTQLFHNIAASMEGVDEKIITRALEHFEKISPDYAKGIKKALEK

>WP\_002869238.1 MULTISPECIES: hypothetical protein [Campylobacter]

MITLSSFNRYFGNNPLQTLTKIRDESIENAKI

>WP\_002869114.1 MULTISPECIES: membrane protein [Campylobacter]

MLENPIPNSIIITTIAVVLAFSALAVFLIKKTKENK

>WP\_002868437.1 MULTISPECIES: cyclic pyranopterin monophosphate synthase [Campylobacter]

MLIDQFGRKINYLRISVTQRCNFRCLYCMPKIPFDYQPKENLLSFEELFLFVKAAIDEGIEKIRITGGEP

LLRKDLSIFIKMISDYKSDIDLAITTNGFLLKDFAKDLKNAGLKRLNISLDTLDHKKAKTLAQKDVLDSV

LSGIDEALNLDLKVKLNTVALKNLNDDELISLLEFAKSKKAQIRFIEFMENTHAYGKLQGLKRDEIIQIL

SQKYQIQLIKKDEKAPVSIYKADDYEFGIIDPHSHEFCDSCNRIRLSAEGLLIPCLYFDEALSIKEAVRK

GDIKAAVEILQEVLRNKPEKNKWSVVDNETSSRAFYQTGG

>WP\_002868356.1 MULTISPECIES: C4-dicarboxylate ABC transporter [Campylobacter]

MFITATAPNPLVLYFLSPLEIKSTPNASTFAKDKLKELVKMKNSEKIMLSVFVSLLLLWAGALGLFFWNF

S

>WP\_002866940.1 MULTISPECIES: glutamate-1-semialdehyde 2,1-aminomutase [Campylobacter]

MTNKKAFKEACKFIAGGVNSPVRAFANVQSEPKFISHGKGAYIFDIDGNSYIDYVQSWGPLLFGHCDKDI

QKACQKALHKGSSFGAPTLLETELAKLVLSDFPHLEKIRFVSSGTEATMSAIRLARGFTKKDKILKFEGC

YHGHSDSLLVSAGSGAATFNSPSSLGVLEDVAKHTLVAKYNDINSVKELFEKNKDIACVIIEPIAGNMGL

VPAKQDFLEELAKICKNNQTLLIFDEVMSGYRASYLGSYGINHIQADIITFGKVIGGGLPAAAFASRAEI

MDILSPLGGVYQAGTLSGNPLAMAAGIASLTKAKKKTKLYDKLGKLAKKLTQGMKKLADEKGLPLQACHV

GSMFGYFFTKDPVSNYQDALKSDLALFSKFHKNMLENGIYLAPSQFETGFICSKMDDKIIDTTLEAVRES

FKRI

>WP\_002866730.1 MULTISPECIES: biopolymer transporter ExbD [Campylobacter]

MPFDDEKPELNITPLVDIMLVLLAILMVTAPSITYEEKINLPQGSQKNTSAPTVKSLIISINAKKEIFLN

QEKYDFISFADNLAQRKAQFNTEDPVFIRADKSLKYDDVISVLRSVKNLGFNKVALQTE

>WP\_002866652.1 MULTISPECIES: MFS transporter [Campylobacter]

MTNQQIDGIADKNFNTPEGRKVFKKAVFSCWLGTAMEYADFALYGLAAATIFSEVFFPEQTPVIALLLSF

VTYGIGFIARPIGALFFGYLGDKHGRKNVMMSTVALMGISTTLIGFIPSYAVIGVWAPICLVILRFMQGF

GAGAELSGGTVMLGEYAPSKRRGLVSSVIALGSNSGTLLASFVWLLMVQMDEASFKEWGWRVPFMGSILI

ALFAVYIRFHVKETPVFEKQKNEMMKLRLNNEKHMKKDERSFWQRSRAFWTMVGLRIGENGPSYLAQGFI

VGYVTKILLLDKSVATTAVMIASLVGFLVIPLAGYLSDRFGRRITYRMFCLLLMIYAFPAFMLLDSKNEI

IVILTIIVGMSLASLGIFGVQAAWGVELFGVKNRYTKMAFAKELGSILSGGTAPMVASALLAYYGTWWPI

ATYFVLTAGIGFVTTFFAPETRGRDLNKIEDAI

>WP\_002866625.1 MULTISPECIES: flagellar basal body rod modification protein FlgD [Campylobacter]

MISSSDWNLNTAATTSGTTSSGSTSGTTRTDSSSSSGIVSNPNATLDKDAFLKLLLIELQHQDPTDPMDS

DKMLTQTSQLSALEMQQNTNTTMQKMVETMQKLSDSFSTSMSTSALGAIGKMATVSDNKIKLTGADELIA

LKMYLPEDSDENGVTLEIYDSNNKLVFSEKSDAKSISQGLFTMEWPGRNNDGVYAGDGEYTVKMVYNNKN

GEKITANYGTYPIEGVVFKDGVAYAKMAGQEVPFDAIQEITDYKLGSSSSTGGSGSSGDSSGGSSDGDSS

GSGSTEDGDKEEKA

>WP\_002866505.1 MULTISPECIES: hypothetical protein [Campylobacter]

MAIKIFGILIALFTITFTILSLQDPYSLNLQTNALNFKNIEAKNLKAYESNTSTIKAYYKANSWVRYADR

DEFNDFITLNLDFNLSANRLEFFNKDMSKVLFEGNVTYIGANNVKIISQEVEYEPKNKVLYTNTDFKALI

NGSIINGNTLNYDVKNKILNIQGVNAWLQDK

>WP\_002866504.1 MULTISPECIES: 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase [Campylobacter]

MTELIFLDVDGCLTDGKIIYTSNGEFIKEFDVKDGAAIEAWLKLGKKIAIITGRNCPCVEKRAKDLKIEI

LYQGIKDKLACAKEILQKLNLDFSQCAAIGDYFNDKALLESVGLSFKPKDGHKDLNVDIVLSKKGGKAAV

AQMIEILVEKNHLEEEWNKLWL

>WP\_002866497.1 MULTISPECIES: peptide-methionine (S)-S-oxide reductase [Campylobacter]

MKNIVLGGGCFWCVEAVFERLKGVIDTEVGYSGGNPNPSYESVCNGDGNIEVVKINYDEKQISLLEILTL

FFKIHDPTSIDKQGGDIGIQYRSIIFYENEEDKILAQNFIEEQQKIFSKKIVTKISRLQTYYKAENYHQH

YFINNPNQGYCQAVIAPKLQKIQSG

>WP\_002866493.1 MULTISPECIES: ketol-acid reductoisomerase [Campylobacter]

MAITVYYDKDCDLNLIKSKKVAIIGFGSQGHAHAMNLRDNGVNVTIGLREGSVSAVKAKNAGFEVMSVSE

ASKTADVVMILAPDEIQADIFNIEIKPNLSEGKAIAFAHGFNIHYGQIVAPKGIDVIMIAPKAPGHTVRN

EFTLGGGTPCLIAIHQDESKNAKNLALSYASAIGGGRTGIIETTFKAETETDLFGEQAVLCGGLSALIQA

GFETLVEAGYEPEMAYFECLHEMKLIVDLIYQGGIADMRYSISNTAEYGDYITGPKIITEETKKAMKGVL

KDIQNGVFAKDFILERRAGFARMHAERKNMNDSLIEKTGRNLRAMMPWISAKKLVDKDKN

>WP\_002866218.1 MULTISPECIES: laccase [Campylobacter]

MGRSRKNFLSLLENDKVVIFCAFDKDYNVFRAKVYSENLFYHLGFKDIKKCVFMDQIHSHKVIIYEKNLK

NLSCDGLISKEKNIALCVLSADCLPLILYHESGIIAALHSGRKGSFENILKECVDQITMQNSHLDKNKFH

LFILPGICAKNYEIDGEILEFAKKEFKEFVQDDKLDLKALVKFQAQNLGIENIKDCGICSFDDESFFSYR

RDKTPKRFVSVVYLKD

>WP\_002866132.1 MULTISPECIES: phosphatidylserine decarboxylase [Campylobacter]

MKDFIAKDGYLSLIILSLIFIFVWIFYSFSILLLALIVICIFLFRAPKRELVCSDEKAIFAPMDGRVTKI

ENIHHKDLGECVEITIKNALYDAGNFNTPFAMSIIDIRLRHGLFLCSELKSAKMMNERAFILAKVKENKT

IALRIYAGSFDRKLKLDNISHDLKAGDRMGFLINGSISLLLPKDTRIHIGLNDEIKAGSLLGYFA

>WP\_002866076.1 MULTISPECIES: thiazole synthase [Campylobacter]

MQENLKNDKLKIGKYEFDSRFILGSGKYSLELIKSAIEEAKTQIITLALRRANTGEIANILDYIPKNITL

LPNTSGARNADEALRIARLSRELGCGELIKIEVISDSRYLLPDNYETIKACELLAKEGFTPLPYMHADLY

AARAMRDAGAAAIMPLAAPIGSNKGLCAKEFIQILLNEIDLPIIVDAGIGSPSQACEAMQMGVSAVMVNT

AIAEAKDVALMAKAFSLAVNAGRAAFLAGLASVSKAKASSPLTGFLRD

>WP\_002862275.1 MULTISPECIES: ribonuclease 3 [Campylobacter]

MKNIEKLEQSLTYEFKDKNLLIHALTHKSFKKSYNNERLEFLGDAVLDLVVGEYLFHKFAKDAEGDLSKL

RAALVNEKSFAKIANSLNLGDFIFMSVAEENNGGKEKPSILSDALEAIIGAIHLEAGFEFAKTIALRLIE

KNFPQIDAKILIKDYKTKLQEITQGKIGQTPQYETVRAFGPDHLKQFEIALMLDGKELARAIAGSKKEAQ

QMAAKIALEKLGAL

>WP\_002860439.1 MULTISPECIES: 5-formyltetrahydrofolate cyclo-ligase [Campylobacter]

MEKTDFRALQKIRLFKHSKLNFKQDYKIFKECLKIIKLFKAKNILIFIPLHYEPNLIKFRHILNKNYKLF

VPFMQDKSLKIVKLRLPFIKKRFGVLEPIDSFFKAKIDLAIVPVIGVDKNLKRIGHGQGFYDRFFENLNY

KPHIIFVQSIDALSQNNLTQKHDISGKLYINPYKKYYKKERKNDRITYRTYSRYSRTRYRIFSCKKNQ

>WP\_002860421.1 MULTISPECIES: polyphosphate kinase [Campylobacter]

MQTSPDMFINRELSWLRFNSRVLDQCSKNLPLLEKLKFIAIYCTNLDEFYMIRVAGLKQLFSAGVNASSS

DEMTPLQQLKAIRKYLHQEKELLERYFNEITSELEKENLFIKHYENLDENLKQKCDEYFFSNIFPVIVPI

AVDATHPFPHLNNLSFSLAVKICDKAHPELVKFGMIRIPRVLPRFYEVSANIYVPIESIVHQHAEEIFPG

YKLLASAAFRVTRNADMVIEEEEADDFMMILEQGLKLRRKGAFVRLQIQKDADEQIVEFLNTHMKIFHKD

VYEYSILLNLPSLWQIAGNKTFTHLLSPLYTPKTLPPFDENLSIFDAVEKEDILIIQPFESFDPVYKFIK

EASKDPEVISIRMTLYRVEKNSNIVQALIDAASDGKQVTVMVELKARFDEENNLHWAKALENAGAHVIYG

ITGFKVHAKVSQVIRKQGDKLKFYMHLSTGNYNASSAKIYTDVSYFTSKAEFARDTTSFFHILSGFSKNR

RLQTLSMSPNQIKEKVLEMIRIETSKKNEGVIVAKMNSLVDSDIIQALYEASMEGVQIDLIIRGICCLKP

DEEYSKNIRVRSIIGKYLEHARVFYFKHSEPNYFISSADWMPRNLERRLELMTPIYDERSKAKLAQFLRL

QLSDNVLAYELKNNGEYEKIPSSEKIIDSQQTLEEYVSKIYKTLKKDTDQSRATHLASKLFKEN

>WP\_002860329.1 MULTISPECIES: ATP-dependent Clp protease ATP-binding subunit ClpX [Campylobacter]

MPRKCSFCNEVENPQRRILANENDDAFICEYCVEGAYSIIYGEEKEFKEPKQSHNTEFKDITPKELKAYL

DRYVIGQDRAKKVFSVGVYNHYKRLFKAELQDDDTELFKSNILLVGPTGSGKTLLAQTLAKFLDVPIAIC

DATSLTEAGYVGEDVENILTRLLQAADGDVQRAQKGIVFIDEIDKIARMSENRSITRDVSGEGVQQALLK

IIEGSLVNIPPKGGRKHPNQEFIQIDTSNILFVCGGAFDGLETILKRKLGDKVVGFFDDAKEENKALLEK

IEPDDLVHFGLIPELIGRLHVIASLNELNEEDMVRILTEPKNAIIKQYQKLFAIDGVNLKFEEDALRAIA

QLALERKTGARGLRSIIEEMMVDLMFELPEYKNYDIVITKEVVKDNAKALLIKRKIS

>WP\_002860289.1 MULTISPECIES: glycerol-3-phosphate acyltransferase [Campylobacter]

MENLIIYAFIYLLGSIPFGLILAKFFAKTDIKKEGSKSIGATNVLRVVKEKNPKLAKKLAIATIILDFAK

AAIPLLILKFLHYDQALLWSVAVLAIFGHCFSIYLLFEGGKGIATGAGAMIVLLPLEVLTAFIVWVVIGK

IFKISSLASLAALLAFVISSFIFNYDLEIHTHAPVFIIAFIIVYKHLPNIKRLIFKEECKVI

>WP\_002859562.1 MULTISPECIES: DNA-binding protein HU [Campylobacter]

MTKADFISLVAQTAGLTKKDATTATDAVISTITDVLAKGDSISFIGFGTFSTQERAAREARVPSTGKTIK

VPATRVAKFKVGKNLKEAVAKASGKKKK

>WP\_002859311.1 MULTISPECIES: phosphoribosylamine--glycine ligase [Campylobacter]

MKIMILGSGAREYSIALALRRVDKNLEFYFAPGNGATESLGTNLNLKDPVVLATYAKEKGFDLCIVGSES

FLAEGVVDIFKQQGLAIFGPSKAAAMLETSKSFMKSFLKKYRIKTAKFLNTNDIEKAKNFIYSLTPPIVV

KADGLCAGKGVIIAKTHEEAIEETAKMLSGESFGDAGKLVVIEEFLDGYELSIFAVCDGNDFVLLPAAQD

HKKLLDNDQGPNTGGMGAYAPSSLANESLLRKVQKDIILPTLAGMKKEGAEFCGVLFIGAMIVGNKPYVL

EFNVRFGDPECEVLMPLIEDPLELILAATQRRLRHAKIKIKKEFAVGVVCASENYPYKSSPKSEITVNNI

PENSHISYAGVSLEDGKLMADGGRVLVCVGTGKSIEEAQKNAYKLCDNVNFKGKQYRKDIAHQVLK

>WP\_002859150.1 MULTISPECIES: pyrroline-5-carboxylate reductase [Campylobacter]

MLYILANGSMATALAYGLKDDYEICIVGRSIEKLQALAKEGFKTLLYKDFNIEGKDVILAFKPYALENIA

QMLKGQARILISVLANVDFEKLQTIKAQNYVRIIPNTAAKYKASTTPYILKNSHFENEILDILKTFGSAY

KLDNEIQMNAAMAISGCAPAFLALIAESIANAGVYEGLSKELSLNLTRSLFKSSSALLEHEHPAIIKENI

CSPGGVTIKGIKILEQKGIRGSFFEAINASSAK

>WP\_002859122.1 MULTISPECIES: CDP-diacylglycerol--serine O-phosphatidyltransferase [Campylobacter]

MNNRPQLIYILPNLFTAASAFLGVISIIASIHGNYYTALIYIILSLICDGLDGRVARLTNSTSKFGVEFD

SLADLVAFGVAPAVLFYMAIGYDFGKLGSLITAFFVVFGAIRLARFNVTTGTYEPSVFIGLPIPTAAVVS

AIWTYAFISYDFLKPYGVVFLVLQAILGLLMVSNIRYPSFKKLDFNRSSVLKVLIILIIIFSFLYLYPLE

SLVILASLYVLYGIIRVLYTIIVSKFKIRNQE

>WP\_002858952.1 MULTISPECIES: peptide chain release factor 1 [Campylobacter]

MLASKLDPFLKRFEELNSLLSSSDILNDISKMTTLSKEQKNLEPIVLKAKEYLKTLDNIEENKALLNDPE

LGELAKEELKTLEELKPKLEEEIKILLLPKDPNDERNIFLEIRAGTGGDEASLFVGDLVKAYARYAENRG

YKLEIVSSSEGSVGGFKEIIMLVKGTGAYSRLKYEGGTHRVQRVPQTESQGRVHTSAITVAVMPEVDDIE

IEINPNDLKVDVMRSSGHGGQSVNTTDSAVRITHIPTGIVVVNQDGKSQHKNKESAMKVLKARLYEMQES

ERLAKESEARKSQVGSGDRSERIRTYNFPQNRISDHRINLTLYRLDAIMQDGLFDEIIEPLITHHQAQAL

QEQNL

>WP\_002858674.1 MULTISPECIES: 50S ribosomal protein L32 [Campylobacter]

MAVPKRRVSKTRAAKRRTHYKVSLPMPIKDKDGSYKMPHRANPTTKEY

>WP\_002858660.1 MULTISPECIES: transcription elongation factor GreA [Campylobacter]

MQKEPMSQFGYDKLAAELKDLKDNQRPAVVIEIDTARSHGDLKENAEYHAAREKQALIESRIAELSDLLA

RAQVIDPSSYEHDSVKFGSSVVIMDLDTEKESKYTLVGICEGNLDKGYISIASPIAKAMLGKKEGDDFKV

RLPKGESEFEILSINYEPLKF

>WP\_002858659.1 MULTISPECIES: peptidyl-tRNA hydrolase [Campylobacter]

MILVVGLGNIGVEYENTRHNVGFMLIDLLLKESNFTNLTNSKFKGELFKIGSSLLLLKPSTYMNNSGLSV

KAVNDFYKCERMIVIHDDIDINLGALRFKKGGSSGGHNGLKSIDTLCGNDYERVRIGVGKGENVISHVLG

KFKSEEEITLSKVLEHAKKALLELIENDDLSAISSKYSLKA

>WP\_002858547.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLVNKFKIILLFFIIFTSSYAQNLNTNDTIDSILNQNKNHSALTSYVLKKDLKNLEKKLEKNQNIGIRIY

GDSHMAADFFPRVIRGYLIRSNSIGFAYPLQPKYQQNLNLVYSYKNFEILNSRNPANAGHNFPLGGIIAK

AKIKGAKINLDTTLDKKKFKIGFLFKAKQNTNAFSIKDAKNQSYELRTTQINKWSYKELELDLPLQISAL

QKDAELGGYFITNKDNNVFLDTIAINGAKSDLWLSWNQTVVKKELGLLHNDLIILAYGSNDALFKGFEKQ

KFKNNLKKWISILKTYNKNAVIMLISPPTVVQKQGKNYKLAPDFFTIRKALYEVAKEEKTLIFDMHQFMQ

DSGGKNKWIEQKLSLNDVHLTIKGYELMAKKLLEDLKNIIDY

>WP\_002858139.1 MULTISPECIES: dihydroorotase [Campylobacter]

MIIKNAKIYGDSLQDIEIKEGKITNIGSNLQGEEILDAKGMTLLPSFVDLCVSLKNDKFSLANLELLENE

CLKGGISSIVLRDCMDFDEESFALFLQNLAQRKMQIFSSVRVKDANGKLKNLATLLNKGACALELDSSLD

ANTLKVSSQYAFMKDSPIFVRCYDKDFDDNGVMNDCEMSFELGLIGMSKIAETSQIAKMKELAKFYKNKV

IFDLLSLKDSLVLLDEKDLKLVSIHHLIKDDSACEDFNTAAKLMPPLRSKEDVLALREALKEGKISFLTS

LHSAKSISLKDLAFDEAAFGIHSVCEFISLCYTFLIKEGFLNWQELCRFTSKNPSEFLGLNSGVIEVGKE

ANLVLFDENEEIFAPKSSLYSEDKLFGKIKMHIIKGKNILEK

>WP\_002858085.1 MULTISPECIES: signal recognition particle-docking protein FtsY [Campylobacter]

MFNFFKKGLAKTLENIVGVKGENKKITKDLLEEILLEADVSYEIVEEIIYYLPPQNEVKKEDLKRVMGSY

FLYEKKETNQEKPFVELILGVNGAGKTTSIAKLAYLYKNQNQKVILGACDTFRAGAIEQLKLWAQKVDVD

IVLTAQGHDPSAVAFDTISKAKAKDFDRVIIDTAGRLQNQKNLAHELEKIVRISNKALEGAPHRKILVLD

GTQGNAGILQAKAFNELVKLDGVIITKLDGTAKGGALFSIARELELPIFYVGVGEQMTDLQEFNASAYLD

TLLDPIFE

>WP\_002857328.1 MULTISPECIES: molybdenum-pterin-binding protein [Campylobacter]

MNLIKGQICELLNQEDIVIVKILSKEVIFSVLMLELKSLENLKIGVSVELLFKEHELCFSASKTLLSVEN

SFLAKITKIKKGKLLYQVFFDFKGNELSSIITKEKALELEICENQEWLCFVKANDIVLRSHSA

>WP\_002857279.1 MULTISPECIES: flagellar biosynthesis protein FlhB [Campylobacter]

MAGEDQEKTEEPTSKKIEDARKEGNVPKSQDAAAIVTLIIGVTITLFMMSFMGERIVNLYRYYQSFIGVE

FDLRIIQAIMIKSIFEVLIILAPIVLSIMIAGVLGNIMQFGFIFTTKPIMPNLGKINPLKGLKNLFSLKK

IVESIKIILKVGIVFTIAFIVLLKFMQELPRVELYTMVAQLTWLRDRAIVLAAIVIVAFLIIAVLDVFLV

RFQYFKGLRMSKQEIKDEYKQMEGDPQVKGRIRRLQMEAARRRMVQDVAGADVVITNPTHYAVAIRYDTS

KEQAPRVVAKGVDFLALRIKQVAYENNVVVYENPPLARELYKACDVNDLIPREMFKAVAEVLGFVYNTNN

KSRLAGQVKKGN

>WP\_002856929.1 MULTISPECIES: hypothetical protein [Campylobacter]

MNKYLEQLVLLSKIDQEIDSYEPKIDSINRTLKDAELKIGKINTDLEKIDEEIKDIENQKVQNNAHISEF

SAKIKELSKKSGAVKTEKEANALKIEEDIAKEQLDAANDEIVRLDKILENKETYKKELEEEKIKQEQNIN

EIRVSIKSEMEVLEKDRMSVYDKKTKLVGEMNQKVLSFYEKIRKWAKNTAVVPVKKQACYGCFMKIYDKT

YLSVVKGEEIVTCPHCGRILYKEQEEQN

>WP\_002856884.1 MULTISPECIES: flagellar hook-basal body complex protein FliE [Campylobacter]

MNNINDLRLNNNISNTNKSQNSTGIGDEFAKMLKNEIDDLNKAQESGEAAMTDIATGQVKDLHQAAIAIT

KAESSMKFMLEVRNKAISAYKEITRTQI

>WP\_002856751.1 MULTISPECIES: membrane protein [Campylobacter]

MEEFYPYTLTIHLLCAILFIGYLFVDVFVLGVVKKKNPNFDKSLFSATGVKIMPFVVLLLFLSGGALAGF

HFKPLNLLFAVKIILAFGILSLVVFSLFCHFILKKKNPLGAFIHPFVFVLCIAIVILAKLMNYFFIPC

>WP\_002856547.1 MULTISPECIES: 30S ribosomal protein S20 [Campylobacter]

MANHKSAEKRARQTIKKTERNRFYRTRLKNITKAVREAAANGDKNAANEALKVANKSIHAMVSRGFIKKQ

TASRRVSRLALLVNKIA

>WP\_002856489.1 MULTISPECIES: enolase [Campylobacter]

MLVIEDVRAYEVLDSRGNPTVKAEVTLSDGSVGAAIVPSGASTGSKEALELRDNDERFGGKGVLKAVANV

NETIADEILGLDAFNQTQLDDTLRELDGTNNYSNLGANATLGVSMATARAAAAALGMPLYRYLGGANASI

LPVPMCNIINGGAHANNNVDFQEFMIMPFGFTSFKEALRSVCEIYAILKKELANSGHSTALGDEGGFAPN

LANNTEPIDLLMTCIKKAGYENRVKIALDVASTEFFKDGKYHMEGKAFSSEDLIERYVELCAKYPICSIE

DGLAENDFEGWIKLTEKLGNKIQLVGDDLFVTNEDILREGIIKKMANAVLIKPNQIGTITQTMRTVRLAQ

RNNYKCVMSHRSGESEDAFIADFAVALNTGQIKTGALARGERTAKYNRLLEIELESDEYLGEKL

>WP\_002856024.1 MULTISPECIES: ribose 5-phosphate isomerase B [Campylobacter]

MLREKIYIASDHAGFELKEKICVFLKEKNIIFNDLGTNTCASCDYPDYAHLLAEKIDERSFGILICGSGI

GISIAANRHKNIRCALCHESLSAELARRHNDANVLALGGRLIGVELAIDIIEKFIQTPFEEGRHMQRIQK

IEVKI

>WP\_002855748.1 MULTISPECIES: DNA-directed RNA polymerase subunit alpha [Campylobacter]

MRNITTSAYTPTEFTIENISDTVAKISAWPFEIGYGITLAHPLRRLLYTSTIGYAPTAIHIDGVAHEFDS

MRGMLEDVALFIINLKKLRFKIKGESNKEIVEFSFKGSKEIYGKDLNNDQVEVVNKDAYLATINEDAELK

FTLIVEKGIGYVPSEEIKELINDPKFIALDAFFTPVREATYDIEKVLFEDNPDYEKVVLTVTTDGQITPN

EAFQNALEAMYKQLSVFDKITNVRSVIKNQATSNELENTKLLQNITDLNLSARSYNCLEKAGVVYIGELA

LMSVSELAGLKNLGKKSLDEIKNIMESIGFPVGTSKLSDNKEILKNKIAELKAQNEG

>WP\_002855562.1 MULTISPECIES: rubrerythrin [Campylobacter]

MRQYETYKCQKCGNEVEVQNVGGGKLSCCGEEMKCITTDLTAVNLMKAFAGESMARNKYDLFADVAEEEG

WHAVARHFREAAENEKWHARAEFKAYHEIVDGKPLEVTTKNLVSAAEGENYEHTTMYPNFAKIAEDEGKK

AIARLFTAIGKVEIEHEREYLALKKMLEEEEFFNSEVEELWVCEVCGHIHRGKKAPAACPLCKAPKEYFK

REFLG

>WP\_002855280.1 MULTISPECIES: hypothetical protein [Campylobacter]

MCQEKHTHTHSQKHLKAVCNRLSRTIGHLSAIKRMVENDKDCSEILIQLAAVKAEVNNTAKVVLKEHLAH

CMVHAVEENDIQSIEELNKAIDMFMK

>WP\_002855271.1 MULTISPECIES: elongation factor Tu [Campylobacter]

MAKEKFSRNKPHVNIGTIGHVDHGKTTLTAAISAVLSRRGLAELKDYDNIDNAPEEKERGITIATSHIEY

ETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHILLSRQVGVPYIVVFMNKADM

VDDAELLELVEMEIRELLSSYDFPGDDTPIISGSALKALEEAKAGQDGEWSAKIMDLMAAVDSYIPTPTR

DTEKDFLMPIEDVFSISGRGTVVTGRIEKGVVKVGDTIEIVGIKDTQTTTVTGVEMFRKEMDQGEAGDNV

GVLLRGTKKEEVIRGMVLAKPKSITPHTDFEAEVYILNKDEGGRHTPFFNNYRPQFYVRTTDVTGSIKLA

DGVEMVMPGENVRITVSLIAPVALEEGTRFAIREGGKTVGSGVVSKIIK

>WP\_002855235.1 MULTISPECIES: flagellar basal body rod protein FlgC [Campylobacter]

MAYLSDFDISGYGLSAQRFRMNVISSNIANANTTRTAEGGPYRRREVIFKATDFDKLLNEQINKDNNFLK

YENPLNDPSSPEEAKPAIQSVVVDKVVRDDKDFRMKYDPSHPDANAEGYVAYPNVNPVIEMADLIEATRA

YQANVSAFTSAKTIAQSAIDLLRG

>WP\_002855217.1 MULTISPECIES: hypothetical protein [Campylobacter]

MFKISPYLICIFFIFSNVLASEPTFDYTYKFILKKDERASVQIKEIGYEDKVQNFDFYWTLFDNTNIIVH

SKFRKYPRQFVMSLRRNLDWVTQTLIPDYTNPHIDRARLILEFSGYNKGLATFTVYIEDKESRLMVEFLD

PRKKALQNPPQNNQVVPMINFNEPQVKPLTSKENNNSN

>WP\_002854985.1 MULTISPECIES: preprotein translocase subunit SecE [Campylobacter]

MEKLITYFKLSKAELRKVIFPLKEQVRNAYITVFVVVAVISLFLALVDWLMSSIVSAIV

>WP\_002854974.1 MULTISPECIES: 50S ribosomal protein L28 [Campylobacter]

MARVCQITGKGPMVGNNVSHANNKTKRRFLPNLRTVRVTLEDGTTRKMRIAASTLRTLKKQNSK

>WP\_002854966.1 MULTISPECIES: ArsC family transcriptional regulator [Campylobacter]

MKLYGIKNCNSVKKAMDALTQKGIVFDFMDIKKINQDILYTWLKQKSFEELINTAGLTSKKLGLNKEKVK

NLNEKELEKIVLENPSCIKRPIIEYEQNIYIGKEYEKML

>WP\_002854928.1 MULTISPECIES: 50S ribosomal protein L1 [Campylobacter]

MAKIAKRLKELSQKIDSNKEYALSDAIDTIKTLKSAKFDETVEIALKLNVDPRHADQMVRGSVVLPAGTG

KKVRVAVIAKDAKADEAKNAGADIVGSDDLVEEIQKGNMNFDVLIATPNLMGLVGKVGRILGPKGLMPNP

KTGTVTMDVAQAVNNAKSGQVNFRVDKQGNIHAGLGKVSFSKEQLWDNVSTFVKAINKHKPAAAKGRYIK

NAALSLTMSPSVKLETQELLDMK

>WP\_002854831.1 MULTISPECIES: acyl carrier protein [Campylobacter]

MATFDDVKAVVVEQLSIDADAVKMESKIIEDLGADSLDVVELIMALEEKFEVEIPDSDAEKLIKIEDVVN

YIDNLKK

>WP\_002854820.1 MULTISPECIES: 50S ribosomal protein L7/L12 [Campylobacter]

MAISKEDVLEYISNLSVLELSELVKEFEEKFGVSAAPVMVAGGAAAGGAAAAAEEKTEFDIVLTDGGAKK

IEVIKIVRALTGLGLKEAKDAVEQTPSTLKEGVAKAEAEEAKKQLEEAGAKVELK

>WP\_002854726.1 MULTISPECIES: DNA polymerase I [Campylobacter]

MKTLTIIDTFGFFFRLYYALKGFKNSQGQASGMISGFANFIYSLKNEHKSDYIVFALDSKGKTFRSEIDP

NYKQNRTPPPPELLEQIPICIEMIEKMGFISVSQEGYEADDIIASFVRTCEDRDIFVRIITQDKDLYQLI

KDGKTSIYSPISKNDYDEAACLEKYGVKPHQIRDFLALCGDSSDNIPGVKGIGAKGAKTLLDEFGSIEGI

YENLTLVRNERSRNLLLEGKENAFLSKKLASLYENLEVQDLIEKATYPDEEPLLKILEILEHYELNTLLK

KLRQNPDNKDKNLGFKATLIQDENKLFEILNTLDKESIIAFDTETTGLDTKEAKIVGFSFCMSENEAFYV

PLTHNYLGVGEQISLQSAKKAIEVIFNHFVIGHNLKYDFKIIQNNFGLNLPQKYADTMILAWLKNPSLRV

NMDDLALRLFNYETLHFESLVKKGENFASVELEKACKYAAEDAYITLRFYLYFLKNLETPLLELAKNCEF

DFIKIIMMMEENGIKLDTNALEILMKKFENEIKNLSEEIYTLCEDRFNLNSPKQVGDILFEKLKLPSGKK

GKTGYSTDEKVLNALLDKHPVIAKILDYRELAKLYSTYCEPLLKLALKDKNSRIYSSFLQTGTATGRLSS

KDPNLQNIPAHGQYAKDYKSCFVAKDGFSFISLDYSQIELRMLAHFSEDEKLLNAFANDEDIHARTAIMI

FGESNYETRSVAKSINFGLIYGMGYKTLSQNLKIEAHLAKSYIEKYFENFTSIKKYFETVKNKAKQNGFI

TTLSGRKRYFDFENAKPMQIAMYERESINSILQGSAADVIKLAMLEINKELNEDKKLILQIHDELIFEVK

DDLCENFVKKTRDIMENIVKLKVKLKTSSSIAKNWGDLK

>WP\_002854647.1 MULTISPECIES: ferredoxin [Campylobacter]

MSLLITKDCVCCDACREECPDEAIYENSPIYVIDPDLCSECVNDFSEPACIVACPYECIIPDPDNVETIE

ELKLKHRDREF

>WP\_002854600.1 MULTISPECIES: prolipoprotein diacylglyceryl transferase [Campylobacter]

MEFWQHIYSNFNVIAFSIFGLKVHWYGIMYVIALLLALLLAKFFVRKFQLDINEKHLDSYFIWVEIGVIL

GARLGYILIYDANTMYYITHPWQIFNPYINGEFVGIRGMSYHGAIIGFLIATLLFCKKYKTNPWIFLDLV

ALSVPLAYVFGRIGNFLNQELFGRITNVPWGIYVDGVLRHPSQLYEAFLEGIVVFIIVYLARFKQSFQGE

LILVYAGAYSLARFICEFYREPDFGIGFVLWGMSMGQILSFIMFITALLVYICIKFKKVNI

>WP\_002854524.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLKILEYSITHFCEHILRLRIEAAQDISGELYGASIPIMGKSEGECNFYLFFPKEFLKKIAEILINDEKF

KEDDWCDLTKECANQIIGYAKNLLNDAKGDDEYKLGIPEYLGKVDFSEIVLDEALTYKFENCYFRIGYCK

>WP\_002854351.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKIKKIIQIGMIGGLAAVAGGALAGCGSNNDNADTLNQAANAQGAFVIIEETAPGQYKIKDQYPSDETR

VVLKDLNGTERILSKEEMDALIKEEAAKIDNGTSNLTKDNGQISSGGLSLGETLLASAAGAILGSWIGSK

LFNNQNFANQQRGAFSNQSAYQRSVNSFNKAGTTSSASSAKKSGFFGGGSKATSSSSSFGS

>WP\_002854333.1 MULTISPECIES: flagellar motor protein MotB [Campylobacter]

MAKKHKCPECPAGEKWAVPYADFLSLLLALFIALWAISKTNPAKVEALKTEFVKIFDYTSTQTVKEESKT

QEKYKGAAKEESDELKSLKQMTMTQQETIKRLQAALDQSDNQVALNLPSKVEFERGSAQIVSADIQDYLK

RMAELTTYLPPQAKIEIRGYTDNSDSIIRSYELAYQRAENVLKYFIEGGANLKNISIKSYGLNNPINGNP

QALENNRVEIYFKVDTADTSTQKSVLELINKIGTKAP

>WP\_002854302.1 MULTISPECIES: fumarate reductase iron-sulfur subunit [Campylobacter]

MSRKLTIKAFKYNPLSKISKPHFVTYELEETPFMTVFVCLTLIREKMDADLSFDFVCRAGICGSCAMMIN

GVPKLACKTLTKDYPDGVIELMPMPAFRHIKDLSVNTGEWFEDMCKRVESWVHNEKETDISKLEERIEPE

VADETFELDRCIECGICVASCATKLMRPNFIAATGLLRTARYLQDPHDHRSVEDFYELVGDDDGVFGCMS

LLACEDNCPKELPLQSKIAYMRRQLVAQRNK

>WP\_002854278.1 MULTISPECIES: 6,7-dimethyl-8-ribityllumazine synthase [Campylobacter]

MNIIEGKLNLDSNTKIAIINARFNHIITDRLVEGAKDAFLRHGGKEENLSLILVPGAFELPYALKKAIES

KKFDAICCVGAVIRGSTPHFDYVSAETTKGIANVSLNHNIPVSFGVLTTDTIEQAIERAGSKAGNKGFEA

MTTVIEMLNLSKEL

>WP\_002854273.1 MULTISPECIES: dihydroneopterin aldolase [Campylobacter]

MQSHIKIKFHFKCIIGILDFERRKKQKIIIKLKAKANEFLNYAEVITKIKTWYKKEEFYTLEESLDFVSL

NLKKDFPNLTNLNIKIFKPHIIKNATVGVKLKKKY

>WP\_002854249.1 MULTISPECIES: phosphate acyltransferase [Campylobacter]

MINIAIDAMGGDFGEKPIIEGVLKALEAKPFNAILVGNSKILKPLIPKKLEQYIQYEEASEIFSMNENAT

DALKNKETTIYKAINLLKEKKVDAVVSAGHSGASMSLATLRLGRLKGISRPAIATLMPNIINKTLLLDVG

ANTDCKAENLFQFAIMGEVYARAIMQIQKPRLALLSNGEEECKGNELTKESHQLMKKIPNFIGNAEGRDI

FNGEIDVLVCDGFDGNVILKACEGVATAIFQLLKNEVKQSFISKIGALLMKPSFKKLKKHTDWQEYGGAP

LLGVNGCVIISHGKSDSRAIKNAIFQAINFSQSHINELIENELGKYNA

>WP\_002854234.1 MULTISPECIES: type III pantothenate kinase [Campylobacter]

MLLCDIGNSNANFLDDNKYFTLSIDQFLEFKNEQKIFYINVNEHLKEHLKNQKNFINLEPYFLFDTIYQG

LGIDRIAACYTIEDGVVVDAGSAITIDIISNSIHLGGFILPGIANYKKIYSHISPRLKSEFNTQVSLDAF

PQKTMDALSYGVFKGIYLLIKDAAQNKKLYFTGGDGQFLANYFDHAIYDKLLIFRGMKKIIKENPNLLY

>WP\_002854204.1 MULTISPECIES: tryptophan synthase subunit beta [Campylobacter]

MKKAYYGDFGGQFLPESAMFALNELEGAFLKFSKDKLFKKELNELLKTYVGRPTPLYFARNLSKKYQHEI

YLKREDLNHTGAHKINNAIAQALLAKKMGKKKIIAETGAGQHGLATATAAALLGLECEIYMGATDVQRQA

LNVYKMELLGAKIHAVQSGLKTLKEATTAAIQAWVGDIKNIFYVVGSAVGPYPYPKMVMHFQSIIGKECK

MQLQKLNKKVDYIIAAVGGGSNAAGIFYDFIKDENVKLIGIEAGGLGIDTPYHAATLNKGKTGIIHGMKT

KVLQDDLGNILPVHSVSAGLDYPGIGPLHAFLFESKRAQYHAISDEECMQALKLLCKEEGIIAAIESSHA

LAFLEKLCPTLKKKSVIVVNLSGRGDKDMQMIRDYKKGVIYG

>WP\_002854193.1 MULTISPECIES: fumarate reductase flavoprotein subunit [Campylobacter]

MNIQYSDALVIGGGLAGLRAAIEVAKSGQSVTLLSICPVKRSHSAAVQGGMQASLANGAKGEGDNEDLHF

ADTVKGSDWGCDQEVARMFAQTAPKAVRELAAWGVPWTRVTKGPRTVVINAQKTVIEEKEEAHGLINARD

FGGTKKWRTCYIADATGHCMLYGVANEAIKHQVKIIDRMEAVRIIHDGKKCLGVIARDLTNGQLIAYIAR

GTMIATGGYGRIYKQTTNAVICEGTGAAIALETGLCRLSNMEAVQFHPTPIVPSGILLTEGCRGDGGILR

DVDGYRFMPDYEPEKKELASRDVVSRRMMEHIRKGKGVKSPYGDHLWLDISILGRAHVEKNLRDVQDICK

TFNGIDPADEGPKGWAPVLPMQHYSMGGIRTKPTGESQWLNGLFACGEAACWDMHGFNRLGGNSCAETVV

AGMIVGDYFADYCKNNGEVIDTNVVKDFLTKEYQYLKSLVDKEGKHNVFEIKNRMKEIMWDKVAIFRTGE

GLKEAVDELEKLYKDSQDVKVHCKELDCANPELEEAYRVPRMLKIALCVAYGALLRTESRGAHYREDYPK

RDDLNWMKRTNTFWVEGETLPRIEYEELDIMKMEIPPAFRGYGAKGNIIENPLSEKRQAEVDAIREKMEA

EGKGRYEIQNALMPYELQAKYKAPNQRIGVDYE

>WP\_002854170.1 MULTISPECIES: flagellar motor protein MotA [Campylobacter]

MDLSTILGMVLAVTSISVGDILEGGNPLHVVHLSSFLIVMPTAAFCAMTSTHKKIVKAAYKELKVVFKGS

GVNLPERIAQLIEFAIIARRDGLLALESRTNEIENEFLKNAMMMLVDGKSFEEIHESMEIQTEQLEEHYK

ECAEYWIVFGETCPTMGLVGAVFGLILALKLLDNPQAMAAGISGAFTATVTGIFGAYALFAPWGRKMKAN

GMDLVKEQIVITEAIKGIAEGANPRDLEAKLFNFLSHDDPKISQFDKG

>WP\_002854112.1 MULTISPECIES: acetyl-CoA carboxylase biotin carboxylase subunit [Campylobacter]

MEIKSILIANRGEIALRALRTIKEMGKKAICVYSEADKDALYLKYADASICIGKARSSESYLNIPAIITA

AEIAEADAIFPGYGFLSENQNFVEICAKHNIKFIGPSVEAMNLMSDKSKAKQVMQRAGVPVIPGSDGALA

GAEAAKKLAKEIGYPVILKAAAGGGGRGMRVVENEKDLEKAYWSAESEAMTAFGDGTMYMEKYIQNPRHI

EVQVIGDSFGNVIHVGERDCSMQRRHQKLIEESPAILLDEKTRTRLHETAIKAAKAIGYEGAGTFEFLVD

KNLDFYFIEMNTRLQVEHCVSEMVSGIDIIEQMIKVAEGYALPSQESIKLNGHSIECRITAEDSKTFLPS

PGKITKYIPPAGRNVRMESHCYQDYSVPPYYDSMIGKLVVWAEDRNKAIAKMKVALDELLISGIKTTKDF

HLSMMENPDFINNNYDTNYLARH

>WP\_002853757.1 MULTISPECIES: membrane protein [Campylobacter]

MIEFILRDMFFAAVAGFGFAYACNPPLKTLILSALLAAIAHGLRFTLVEYFHFQTLAIATFVASFCIGCL

GIALAKIIKTPAEIIAFPALIPMIPGIYAYKAILYLISFIRSDDLKAKSEFLVQFFDYFFTTVSVTLALA

IGVSVTLLIFFEQSFMMTRHAKKH

>WP\_002853654.1 MULTISPECIES: rod shape-determining protein RodA [Campylobacter]

MFRLDRRILTHFDYMQPILFLPIILISFFLIFEANPFLAEKQFVYACVGLFAFMVFFFFPIRKFIWIIPV

AYWINIFLLLSVDIFGVEKLGAKRWLEIPFTHFTIQPSEIFKPSFILMLAYLIYQNPPPKNGYKLKQFIK

LSFYIILPFLLIAKEPDLGSAMVLLLVGFGVLFIMGVHYKIWLSIVIAISVSSPIIYTHLLKPYQKQRIH

DFISEKPSYQVAQSMIAIGNGGLTGKSQDEATQTHFKFLPISTSDFIFAYMIERFGFIGGLTLIIFYILL

IFHLLSLNYKLKDDYFARVAINCVALFIFIYAAVNISMTIGFAPVVGIPLPFFSYGGSSFTIFMIFFGIL

QHLITFRYFWTDIKAK

>WP\_002853464.1 MULTISPECIES: DNA-directed RNA polymerase subunit omega [Campylobacter]

MDKRIEEVAAKALEKMGNDRYRLSLVVAKRAEQLANGATPLVDFDKNKNKLADIALYEIAENKITLEGLV

ETNR

>WP\_002853455.1 MULTISPECIES: 30S ribosomal protein S2 [Campylobacter]

MVSMRDLLECGVHFGHQTRRWNPKMKKFIFGERKGIYVIDLQKTLRYFRYTYNIVRDAAAEGKTILFVGT

KKQAGGAIKEYAEKCGMPYVNHRWLGGMMTNFGTIRQSIRKLEVIEKMEEDGSIKLLTKKEALMLTRKKE

KLLAYLGGIRYMKTQPDMIFVIDTVKEKIAVQEANRLRIPVVAPLDTNCDPDLVTYPIPGNDDAIRSVQL

FCQEMAEAINEGKALREQDGEALANEEKEITDEEKKEVLDEAMSEEDFGEEQE

>WP\_002853356.1 MULTISPECIES: membrane protein [Campylobacter]

MEFLAFIFLIIIFLFVVFIIVTRYEKKIKLLNQNIQNMKEDIADLKETTQKNRSLIEKNRSNIENIIK

>WP\_002853349.1 MULTISPECIES: ribonuclease P protein component [Campylobacter]

MKNFDKFSTNEEFSSVYKVGKKWHCEGVIIFYLNSYEKKIAVVASKKVGKAVVRNRSKRILRALFAKFER

YLQDGKYIFVAKNEITELSFSRLEKNLKWGLKKLECFK

>WP\_002853332.1 MULTISPECIES: amino acid ABC transporter permease [Campylobacter]

MNESVGFVEHLRQILTSWGLYDENSISPFAVWKFLDALDNKDAFINGFIYTLEVSILALLIATIFGTIGG

VMATSRFKIIRAYTRIYVELFQNVPLVIQIFFLFYALPVLGIRLDIFTIGVLGVGAYHGAYVSEVVRSGI

LAVPRGQFEASASQGFTYIQQMRYIIVPQTIRIILPPMTNQMVNLIKNTSVLLIVGGAELMHSADSYAAD

YGNYAPAYIFAAVLYFIICYPLAYFAKAYENKLKKAHLTR

>WP\_002853290.1 MULTISPECIES: amino acid ABC transporter permease [Campylobacter]

MENVFNAQNIEFLMQGLFLTLKIALATCIISIVFGTFLAITKNYGDRLSKFLAACYIDIFRNTPLLLWML

AACFVLPVFFGQFPQAFWGTIGFSLYTSSVMAEIIRGGLNSIPKGQFEAAYSQGFGKFFTLFYIILPQTF

RKIIPALLSQIVTTVKDTAYLAGLGIAELTYNSKTILAKLTSFEEILAMIGVVAGIYFIICFSLSMLVRY

YAKKTAYIS

>WP\_002853247.1 MULTISPECIES: membrane protein [Campylobacter]

MFTNWLVLTILICATIYLIVMLFYYKTLLNKEKTSKDFIKNNLDDTEIVIRKLQIQLQRSLGNIDILTEE

LNKIKADLTSLRTRNSQYRLENDKLRQRIKELEAKIEALL

>WP\_002853239.1 MULTISPECIES: potassium transporter [Campylobacter]

MDNFLEIFLITVAIAIVLNVIFKKFEIPTIIGYIAAGEIISEIYHLSGKGEITHIAEFGIVFLMFTIGLE

FSFKHLMAMKQEVFLNGSLQMLTCGFVFMLLAIGILGLGDKSATIVGFALALSSTAVVLKILNDNGDINE

QYGRKALGILLFQDIAVIPLLLLVDIFSSNNQNIEKLLFTSLISALILITLLFFIGKYLVDRIFRLIIHT

SSQEIFISTVLFMVIGASFLANYFGFSYSLGAFIAGALIAETKYKHKIEADLIPFRDLLLGLFFITVGMQ

IQLDVVAQNWFLIIVLTLLVMALKFGIVFGFLFLYTKKRVALKTAFAIAQIGEFALAIFSLLQAKNMLDI

KTSQILIVVSILTMIITPFILNNIRKITNVVEDIALNTNAVQNIDSNIKLKNHLVVFGYGRLGQEVVQKI

KNTGVPYLVLESDLNLVELGVSRGENVVFANAAQEETLKIANIEECAVAIITVTNEAKLEILCQVLANYP

KPIDTIIHVNGTLKKMLFSSIDENIRIIRSEKVIARNLVQEALECRIHKNT

>WP\_002853230.1 MULTISPECIES: MerR family transcriptional regulator [Campylobacter]

MEQHYDEPVYLISVVAKVLSIHPQTLRQYEREGLIEPSRTDGKIRLYSQRDIDRIKLILRLTRDMGINLA

GVDVILKLKNQLHEFENLIDELRLELSKQQDKEAASKAVVKHKNSFDLIFYEKK

>WP\_002853150.1 MULTISPECIES: 3-isopropylmalate dehydratase small subunit [Campylobacter]

MQKFIIHKGIACPLEYANIDTDQIIPKQFLLAVSKQGFGKHLFHDLRYLDDKESVLNMDFNLNKKEYQNS

SILVSFENFGSGSSREHAPWALVDYGIRAIIAPSFADIFKNNALGNGLLTIELAKDEVLEIVDELKKSQD

KNIEISLLEKRVFFKDKIFSFDLDDFHRICLLEGLDNIALTLKHEAQIKAYEKNSKSFLV

>WP\_002853032.1 MULTISPECIES: 30S ribosomal protein S18 [Campylobacter]

MAEKRKYSRKYCKYTEAKVEFIDYKDTAMLKHALSERFKIMPRRLTGTSKKYQEMVEVAIKRARHVALIP

YIVDRKEVINNPFEGL

>WP\_002853004.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKIFLIGMILNHFVFAAPLDEVFKDIEVSGTVRYRYDIKKEKKYNKKTHRYQNKTQTEITIK

>WP\_002852982.1 MULTISPECIES: flagellar assembly factor FliW [Campylobacter]

MTLAVKCPILGFEETKNMEFSTIDEVFVRLKSLDGKDFSFVLINPYLIRPDYEFDIPTYYQELLSLTPES

NMKIFNIVAIAKSIEESTVNFLAPVVINLDNNTMVQVILDTVNYPDFFQADQIANYIKK

>WP\_002852952.1 MULTISPECIES: branched-chain amino acid ABC transporter permease [Campylobacter]

MDSTLFLQQLVNGLSLGSMYALIAVGYTMVYGVLRLINFAHGDIMMVGAYAALFCMTNLNVPFLGALSLA

MIFAACVGIATDRIAYKPLRQAPRISLLITAIGISFFLQNLFNMLFTSTPRTFTPPSYFEESVNFGGVIT

TYGSLMVPALTFVILIAVLWILYKSKYGIAIRALAFDIQTVNLMGIDANRIIAIVFALGSALAAVGGVFW

AANYYSVEPTMGTLIGLKAFAAAVLGGIGSVVGAVLGGLIIGFTEVVVVAFFPDLSGFKDAFAFIFLVFI

LLFRPTGILGINFEKSRF

>WP\_002852941.1 MULTISPECIES: hypothetical protein [Campylobacter]

MFKKFLIFIVPILFLSACATKQDTFAQVNQISKNSQCSSCESPGGFEAKIKGLLYISDVGIQCCANKRTL

DTGIALKKVYLHRFYDLKEGQKVLNAKGKKLFVDVNFNAVFYTYLKQELEARGIVVLDNNDQNSPYVSKI

DLEFISYGATQDAIGLHSKLVGVLQVSDINKNKKFTIRTKQDVQGFDDLKETTFYTHLLIKQMANKAASL

ISEL

>WP\_002852919.1 MULTISPECIES: membrane protein [Campylobacter]

MLEKIFESLLVRSRIVTILPVIFGLIGAFVLFFIASYDVLKVIFYTYNYFFDAGSNVDLHEDVVALIIGA

VDLYLMALVLFIFSFGVYELFISEIEEFKQTKQSKVLEVHSLDQLKDKLAKVIIMVLVVNFFQRVLQMKF

ATPVDMAFLAGSILALCVGLYFLHKGGH

>WP\_002852861.1 MULTISPECIES: SsrA-binding protein [Campylobacter]

MKIIARNKKALFDYSIIERFEAGIVLKGSEVVALRAGRANLKDSFVRIIKNEIFLLNSHISLLHTTHSFY

KHEERGARKLLMHRKQIDKLLGKVSIEGYTIVALDLYFNTKNKVKATLALAKGKNLHDKRETLKKKQADL

EARAAMKNYK

>WP\_002852856.1 MULTISPECIES: membrane protein [Campylobacter]

MIYILEFFKGASLALMLFGALFFFFKYNSFFYLCLGIIPGLLLSLIFVLLIENHKLKNENKLR

>WP\_002852854.1 MULTISPECIES: carbon storage regulator [Campylobacter]

MLILSRKENESIIIGEGIEIKVVQTGKGYAKIGIEAPKSLMILRKELVQQVKDENLHSVVQNDIKLDDLS

KKLIK

>WP\_002852641.1 MULTISPECIES: hypothetical protein [Campylobacter]

MSKIKRSIKKAVALGYQKEKNSAPKVLASGKGESAAKIISLAKEHGVPIKEDEDLIEILSKLDLGDEIPP

NMYKAVAEVFAFIYQMANKTPKN

>WP\_002852609.1 MULTISPECIES: transcriptional regulator [Campylobacter]

MLFTKASEYALLSLIYISQKETPQDVDSLALELDIPKSFLAKILQTLAKDGLLKSFKGAKGGFVLIKEPS

QYTIKEIVNSAEKKDISVFECSGGTCPNNKEENCTLMPMLVNLQNKVDEFLDSITLEDIMKNNGKK

>WP\_002852579.1 MULTISPECIES: 30S ribosomal protein S15 [Campylobacter]

MALDSAKKAEIVAKFAKKPGDTGSTEVQVALLTARIAELTEHLKIYKKDFSSRLGLLKLVGQRKRLLSYL

KRKDYNSYSKLITELNLRDK

>WP\_002852565.1 MULTISPECIES: isoprenyl transferase [Campylobacter]

MNELKHLAVVMDGNRRWARAKGFLAKLGYSQGVKTMQKLMEVCMEENISNLSLFAFSTENWKRPKDEIDF

IFELLDRCLDEALEKFEKNNVRLRAIGDLSRLEDKVREKITLVEEKTKHCDALCVNLAISYGARDEIIRA

AKRVIEKKLELNEENLTQNLDLPLDVDLMLRVGNAKRLSNFLLWQCSYAEIYFSETLFPSLTKREFKRII

KEFRNRERTFGK

>WP\_002852485.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKIVLMFFLFSISLFGADFITLKEYSKMLYENPRGISCKECHGADGSEQILGYYMKNGIKTAYKVPSIQN

LSFENFKNSLNQSKDAKSIMPNYSLTNDEIVTLYNYIKQFSKEEK

>WP\_002852414.1 MULTISPECIES: membrane protein [Campylobacter]

MSNILKEEKNHLENSNSKRQKIIRKTLEAADGLSLGISMVVAVFIGVGIGYLLKKFTPYPWLFWLGVFWG

ISAAILNVYKAYKVQVKSYEEFKERDELIKEKIQKEKNK

>WP\_002852274.1 MULTISPECIES: 30S ribosomal protein S16 [Campylobacter]

MTVIRLTRMGRTKRPFYRIVVTDSRKRRDGGWIESIGYYNPMVEPEVIKVDAERLAYWKSVGAKLSDKVA

SITSK

>WP\_002852256.1 MULTISPECIES: non-heme ferritin [Campylobacter]

MLSKEVVKLLNEQINKEMYAANLYLSMSSWCYENSLDGAGAFLFAHASEESDHAKKLITYLNETDSHVEL

QEVKQPEQNFKSLLDVFEKTYEHEQFITKSINTLVEHMLTHKDYSTFNFLQWYVSEQHEEEALFRGIVDK

IKLIGEHGNGLYLADQYIKNIALSRKK

>WP\_002852227.1 MULTISPECIES: RlpA-like lipoprotein [Campylobacter]

MQIKTITLKLSAVSLGALFFSGCLGTSFFSSLDNAQVYYPSNDFKSSPSSSGTKGTMKPYTINGKTYYPT

VVAVGETADGIASWYGPGFHGKKTSNGETYNQNALTAAHKTLPMNTILKVTNLNNNRQVTVRVNDRGPFV

NNRIIDLSKGAASQIDMIASGTAPVRLEVIGFGSSNSGNNIVHSNVNYGNSGEIANNGQIYEGGNFMVQI

GAFKNPAGAQTIAARYKTYRTYSSTIRTSSVDGLNRVFLTGFRSEDEARDFAASGAFAGAFVVRE

>WP\_002852104.1 MULTISPECIES: 3,4-dihydroxy-2-butanone-4-phosphate synthase [Campylobacter]

MKFVSVEQAIKDLQAGKMLVMVDAEDRENEGDLIFPAQFSTQEKVNFMIKEARGVVCVALDETLAKKFEL

PLMVPKNTSNHETAFTITVDAKDATTGVSAYERNMTIQIFADDNAKASDFVRPGHINPLIAKKGGVLERT

GHTEGTVDLCKLAGLKGACVICEIVKDNGDMARREDLEIFCQKHDLNMIAVSDLIEYRLKHESLIKLEEK

SQSVLAGFKAEKFIFSDHNQTQHIAFCFKDIKKCENVKFHISGSDFELLTSDKFSKLLEQIKFLSENGGV

IVFMQGEKSSTTQYKNYGIGAQILRYFGIEEIKLLSQSCDKDYIGLEGFGLNLKACNFN

>WP\_002852071.1 MULTISPECIES: cell division protein FtsZ [Campylobacter]

MSEFLVEEMQHNKGAKIKVIGCGGGGGNMINHMVKMGLNDLDLIAANTDAQAISISLAKTKIQLGEKKTK

GLGAGMLPEVGAESARESFEEIKASLSQSDIVFIASGFGGGTGTGATPVIAQAAKEIGALTVSVVTMPFA

FEGKQRKKLAESGLLELKKESDSILVIQNEKLLSIIDKKAGIKDAFRLVDDILARAVKGMVSILLDNGDI

NVDFADVRTIMSHRGLALMGVGSASGENAIEEALSNAIESPLLDGMDIKGAKGVILHFKTSSNCSLFEIS

AAANSIQEIVDENAKIIFGSTTDDSMEDRVEVTIIATGFEDKDTVAKKSTEEAQASKKNPYLSLKKVSGG

YDEEIMAQIETPTFLRRQMD

>WP\_002852005.1 MULTISPECIES: ATP synthase subunit beta [Campylobacter]

MQGFISQVLGPVVDVDFNDYLPQINEAIVVNFESEGKKHKLVLEVAAHLGDNRVRTIAMDMTDGLVRGLK

AEALGAPISVPVGEKVLGRIFNVTGDLIDEGEEISFDKKWAIHRDPPAFEDQSTKSEIFETGIKVVDLLA

PYAKGGKVGLFGGAGVGKTVIIMELIHNVAFKHSGYSVFAGVGERTREGNDLYNEMKESNVLDKVALCYG

QMNEPPGARNRIALTGLTMAEYFRDEMGLDVLMFIDNIFRFSQSGSEMSALLGRIPSAVGYQPTLASEMG

KFQERITSTKKGSITSVQAVYVPADDLTDPAPATVFAHLDATTVLNRAIAEKGIYPAVDPLDSTSRMLDP

NIIGEEHYKVARGVQSVLQKYKDLQDIIAILGMDELSEEDKLVVERARKIEKFLSQPFFVAEVFTGSPGK

YISLEDTIAGFKGILEGKYDHLPENAFYMVGNIDEAIAKADKLKG

>WP\_002851996.1 MULTISPECIES: membrane protein [Campylobacter]

MDFYSLIFLSCALGMDAFAVSLCKGFSVKKLHLKHYLIVGIYFGGFQALMPTIGYFIGITFASFIASIDH

WIAFILLSLIGLKMIKESLENENCDSNANQFGFKTMLALAIATSIDALAVGVSFAFLNVNLLLAIFLIGI

ITFILCIIALKIGNKFGIYLKNKAELLGGLVLIILGVKILIEHLFFD

>WP\_002851936.1 MULTISPECIES: peptide deformylase [Campylobacter]

MVRKIITYPNPRLFLNSEIVNKFDTELHTLLDDMYETMIASNGVGLAAIQVDIPLRVLLVNIFDENDEQK

KEDLLEIINPEIIPLDEEMITCTEGCLSVPDFFEEVKRYNHILLKYQDRFGEFKELEAKGFLAVAIQHEN

DHLNGHLFIEKISFAKRQKFDKEFKKKKKNHKKEK

>WP\_002851900.1 MULTISPECIES: hemerythrin [Campylobacter]

MTYNEKIISMNNDLLDHQHKELFEISKKLSLMNQRHVGTKELKIVLRELLIMINRHFSDEEAFMREIEYP

YINHHTRIHRKIILEIEEIIISEAKFVNIMTEKLNLVVQDFIFKHTAKEDSKIVKYYEEKFKK

>WP\_002851849.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKSILFASALLASSMLFADSLKLEGTIAQIYDNNKTLLIDSIYGGQMAIKVLPNTEIEMDDCGIFGTDK

DGTFKDLQVGNFLESKISYGTPATPNTQAIPVARKIEIQCYKKAY

>WP\_002851836.1 MULTISPECIES: ATP synthase subunit alpha [Campylobacter]

MKFKADEISSIIKERIENFDLNLEIEETGKIISVADGVAKVYGLKNIMAGEMVEFENGDKGMALNLEESS

VGIVILGKGEGLKEGASVKRLKKLLKVPVGEALIGRVVNALGEPIDAKGVINANEYRFVEEKAKGIMARK

SVHEPLHTGIKAIDALVPIGRGQRELIIGDRQTGKTTVAVDTIISQRGQGVICIYVAIGQKQSTVAQVVK

RLEEHGAMEYTIVVNAGASDPAALQYLAPYTGVTMGEFFRDNAKHALIVYDDLSKHAVAYREMSLILRRP

PGREAYPGDVFYLHSRLLERASKLNDELGAGSLTALPIIETQAGDVSAYIPTNVISITDGQIFLETDLFN

SGIRPAINVGLSVSRVGGAAQIKATKQVSGTLRLDLAQYRELQAFAQFASDLDEASRKQLERGQRMVELL

KQPPYSPLSVEKQVVLIFAGTKGFLDDIAVSRIKEFEDGIYPFIEAKHPDIFEQIRSKKALDSDLEEKLA

KAINEFKANHL

>WP\_002851769.1 MULTISPECIES: glutamate 5-kinase [Campylobacter]

MKRIVVKVGSHVISEENTLSFERLKNLVAFLAKLMEKYEVILVTSAAISAGHTKLDIDRKNLINKQVLAA

IGQPFLISVYNELLAKFNKLGGQILLTGKDFDSRKATKHAKNAIDMMINLGILPIINENDATAIEEIVFG

DNDSLSAYATHFFDADLLVILSDIDGFYDKNPSEFSDAKRLEKITHIKEEWLQATIKTGSEHGTGGIVTK

LKAAKFLLEHNKKMFLASGFDLSVAKTFLLEDKQIGGTLFE

>WP\_002851738.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKIFTVALLGATLLYAESSAFGAGDITSNSSYGLTSNEKLFKEKLDNLNNENIQTNARINEINERIEGL

QSTLEGINSQYAKSNSRLSQVEENNQNIENNFTSEIQKLKAYVEESRKIQEANNKQVKKVLAELSSLVDA

INANYVSKNELNDANLSVKTITPSVVVSTTDSNSTIENNNTQNTQDDKAKQIDESWKKKKNNEILELAIK

DVDKNAFEDSKAKLNFLITKQYKPARANFWLGEIEYKQKNYNNAIVYYKKSSSLSTKGDYFPKLLYHTAI

SLDKTGDTKTANGFYKALKTNYPNSPEAKASPNRK

>WP\_002851727.1 MULTISPECIES: membrane protein [Campylobacter]

MRPENYVAFFTVCGFFIGLAFSIISIDEAFDILIFTCFITFMFYVFVHIAIMNFIDVKKISGRIFNKHDY

EKTSNNIINDLVIREKKMDIILEKLNEEREELKKNEFKERRRNAKRAA

>WP\_002851726.1 MULTISPECIES: translation initiation factor IF-3 [Campylobacter]

MSKEKEVLLNEEIRADEIRCVGDDGKVYGIISSDEALEIANRLGLDLVMIAADAKPPVCKIMDYGKFRYQ

QEKKQKEAKKKQKVIDIKEIKLSVKIAQNDINYKVKHALEFLEQGKHVRFRVFLKGREMATPEAGVALLE

KIWTMIENEANRDKEPNFEGRYVNMLVTPKKA

>WP\_002851715.1 MULTISPECIES: hypothetical protein [Campylobacter]

MSDDVLYLVFIIVLLIAMLAYMNIKERENNAKIAKLQNVIEDITKELHYFRKELGVKDDSEEDEDYKTSL

LKEEIMIELDKQISSKITPVLRTLKTMEHIIEDFQNEQQNRLLNLEQKAQSMAKLTPNYDTEEQKIENLF

KEGKSIEQIAKDLRIGTGNVELVLKFKKLIK

>WP\_002851710.1 MULTISPECIES: flagellar motor switch protein FliM [Campylobacter]

MAEILSQEEIDALLEVVDDNTDTPIASNSKDEKDERNIVVYDFKRPNRVSKEQLRTIKGIHDKLARNLAS

QISSMMRSIVETKLHSVDQMTYGEFLMSLPSPTSFNVFSIKPLDGNCVLEINPSIAFPMIDRLLGGQGDS

YEASRELTDIELNLLDSILRIIMQRLKESWATVTEIYPSIEAKESSPNVVQIVSQNEIVIMVVMEIIIGN

SSGMVNICYPVVHLESILSRLANRDIMMGETSAKKSRNKELKTLIGRAEVVYEAILGKTLINVHEFLELK

QGDILRLDREADDKAIVSIDKKDVFLAQIGLHRFRKSIKILELIRTDKDEIKEILEKYEEERKAKASVYD

EPEEEDEEI

>WP\_002851686.1 MULTISPECIES: hypothetical protein [Campylobacter]

MIYLAQTDTTVGFLSKNLEEINALKGRDKNQPCLITSAKFCELKSLARIPKSFKNLVRRSKKTTFIYPNN

QAIRIVKECKHANFLSKNGYFYSSSANKHGKEFDEEWARSVADIILDEKFFENIPSKILKLSKNKMIKIR

>WP\_002851681.1 MULTISPECIES: F0F1 ATP synthase subunit B [Campylobacter]

MSKLFFIIFLLPLYAFGASNGSGEYDIIPRTINFLIFVAILYYFVATPFKNFYKNRIVKISSKLDEIQKK

LLESKAKKLDTMKKLEEAKASAAAALITAKKEAEILVQNIKKETQDELDLLQKHFEEQKDYEFRKMEKEL

VSNTLNEIFSDPNMTLKQSEIIELMMKKVS

>WP\_002851662.1 MULTISPECIES: superoxide dismutase [Fe] [Campylobacter]

MFELRKLPYDTNAFGDFLSAETFSYHHGKHHNTYVTNLNNLIKDTEFAGKDLVSIIKTSNGGVFNNAAQV

YNHDFYFDCIKPSTGCGCGGSCQSIDANLQAALEKEFGSLENFKAEFIKGATGVFGSGWFWLVYNTKNQK

LEFVGTSNAATPITEDKVPLLVVDVWEHAYYVDHRNARPAYLEKFYAHINWEFVAKAYEWALKEGMGSVS

FYANELHPVK

>WP\_002851653.1 MULTISPECIES: prephenate dehydrogenase [Campylobacter]

MKIAIIGLGLMGGSLGLCLKENKLISCVYGMDLSKENEKDALQLGLIHELIEFKDLALCDMIFVATPVDA

IIEILQKLVDLPSNVTIIELGSTKRKIIESLPKNLIKQTLFAHPMTGTENSGPKAAFKELYKDAVCVLCD

SEIADDLHQKRAVEIFSHLGMKIVFMDSKAHDHHAAIISHLPHVISFSLANFVMKEEDKRNIVHLAGGSF

KGMSRIAKSSPQMWESIFLQNKDNLLSSIDFFQQELERCKQMIQLDKNDELREWMKQANTLREIL

>WP\_002851635.1 MULTISPECIES: membrane protein [Campylobacter]

MDQSYEFFLALHLYSLYASGFLMLFYLILTQGNFKTEFIFIRRIRLFLPIYYLFLALIIFTGCLLSAMKQ

FQMNVNIWVMIFSWILIFALAIFHFVCFKKARRFRKYATFRWISCLILPFEIFLLFLPFLIERYL

>WP\_002851603.1 MULTISPECIES: 50S ribosomal protein L31 [Campylobacter]

MKKEIHPEYVECKVSCACGNTFTTKSNKAELRVDICSNCHPFFTGSEKIVDAAGRVEKFKKKYAMQ

>WP\_002851549.1 MULTISPECIES: 30S ribosomal protein S17 [Campylobacter]

MAFKREIQGVVVKIAGEKTASVLVERKVVHPRYRKIVKRFKKYLIHDERNEVKVGDTVVAVECRPLSKRK

SFRLKSVLATGVE

>WP\_002851306.1 MULTISPECIES: cytochrome CBB3 [Campylobacter]

MQWLNLEDNVNLLSLIGAILIILITLVIVGRMFKQMKEKKGESELSEHSWDGIGEYKNAVPTGWAVVFFL

TIVWAIWYFLWGYPLNSFSSIGQYNEEVATHNTKFEEKFKNLSPEDKIAMGQNIFLVQCSACHGITGDGI

NGKAQNLNIWGSEEGIINVIKHGSKGMNFPGGEMLGAADLGVAEEDIPAIAAYVAKDLSAIKKTANENLV

AKGKEAYATCAACHGEDGKGQDGMFPDLTKYGSAAFVVDVLHSGKAGFIGTMPSFPTLNDIQKEAVGEYV

ISLSRGE

>WP\_002851302.1 MULTISPECIES: 50S ribosomal protein L6 [Campylobacter]

MSRIGKQPIAIPAGVEVKLEGNLLKFKKGNLAKELDTKANVNVEIKDNNILFSPKGEDRQSRAYWGTYRA

LAYNIVVGLTQGFSKTLEINGVGYKAALKGKVLELSLGFSHPINYDIPEGIEIVVDKNTIAVKGSDKQVV

GQVAAQIREFRPPEPYKGKGVKYSDERIIRKAGKTSKK

>WP\_002851277.1 MULTISPECIES: ribonuclease HI [Campylobacter]

MKHIEIYTDGSCLNNPGFGGWAYILRYKEYQKEGFGAEANTTNNRMELMAIIESLKALKEPCEISLFTDS

NLMVQSINEWLEGWIKKDFKGKKNIDLWKEYIKVAKSHKIKAFWVKAHNGHLENERCDTLAREAALKIAR

ENDEKH

>WP\_002851264.1 MULTISPECIES: formate dehydrogenase iron-sulfur subunit [Campylobacter]

MSKVNFANLEKERLKFFCDNERCIDCNGCAVACDEAHELPIHIRRRRVITLNEGIQGKEVSTSISCMHCD

DAPCSIVCPVDCFYIRADGIVLHDKEICIGCGYCLYACPFGAPQFPKDSVFGNKGIMDKCTMCAGGPEAT

NSEKERELYGQNRIAEGKVPVCAAMCSTKALLVGESSKIEEIYHNRLMNRNYGIPNPSESLEWKIAYTGK

ERL

>WP\_002851157.1 MULTISPECIES: thioredoxin [Campylobacter]

MGIFRIQAYFFALIIALFFVACDSGENFKALNSDKTYNFAYNGFEKSLKLNDKAQNFALVFFTKDCGVCK

EQIPILQNLAKNYDFNIFVVLGDANDANDAKAWADEKGLSNLAMFYEKRAAKYLSSAIGEIYGVPVLSFF

KEGKMDEKFIGLTPYSILEKEIKKVKS

>WP\_002851098.1 MULTISPECIES: transcription termination/antitermination protein NusG [Campylobacter]

MSTHKWYAIQTYAGSEMAVKRAIENLVKDNGIEEQLKEIVVPTEDVIEFKNGKEKISERSLYSGYVFALL

DLNTELWHRIQSLPKVGRFIGESKKPTPLTEKDINLILEKVHNRAAPKPKISFEEGENVRITEGPFANFT

AIVEEYDMVRGLLKLNVSIFGRSTPVEILYSQVEKII

>WP\_002866228.1 glycine--tRNA ligase subunit beta [Campylobacter jejuni]

MSELLIEIGTEELPAIPLLKELANIEKKWKNVLEEYRLVNDFKFYYTPRRLVFFHENFAEKQEDSFAEFI

GAPKNVAYKDGVLTPAGQSFLQKAGISENELTFKEIKGKEVLYHQKAIKGLQSQEILGEMIEKFLKSLSF

GKSMRWGANSFEFIRAIRSIACILNDELVNFQSYGVKSAKKTFIHRSVSYDLQDFNNAKEYFELLEKNYI

ILDPNKRKEKILEQFKLIESQKNIQIGEDEELLAEVVAITEYPNALLGSFEEEFLEIPGEVIITSMRENQ

RYFAVFNDKGLSNHFIVVSNAVCKDYSKIIHGNERVLRARLSDAMFFYQNDLQNGLKPEKLAKMTYLEGL

GTMQDKSLREIKIAEILCQMLHNDKIENISTALKYAKADLATQMVYEFTDLQGIMGSYYAQKMGLDYEIC

LAIKEQYLPNSEQAPLPSTEFSSIVALANKLDTLIGLFSIGKIPSGTKDPYALRRAANGIIKIALNLNKE

FDIQILLEKLSSHYKSFDMQILKDFIFERLYTFYTVNASFVKAVLSSQNTDLIHINQSVNALIELSKKDN

FNENFATFKRLANIATKNPHKVDESLFVQEAESKLYKAFQEKTKANSLQEKLENLFALKPFIDEFFNQVM

INAEDEKLKNNRQALVYEIYAEFLKIADLKELSL

>WP\_002858852.1 MULTISPECIES: tRNA(Ile)-lysidine synthetase [Campylobacter]

MQIKDEILALLKRGKNLLAFSYGSDSSVLFYLLMQEKIDFDLVMINYKTRKNSDLEELKAKELALKFHKK

IFIKHAPKFQSNFEKKARDFRYDFFEKICLEQGYDHLILAHHLNDQFEWFLMQLSRGAGLAEILGMQECE

KRSNYTLLRPLLFISKDEISSFLKEKDIFYFHDESNENEKYFRNYIRKNFSNAFVSEFHQGLKRSFSYLD

EDRKKLYDFENIKEIQGLLICPKNESLIARAVKMKGLLLSTAQRKELLKGDCVLGGKIALAYKNEQAIVF

EYETCQKLPKNFKEECRIAKIPRLLRAYLYNHKIDISSLSF

>WP\_002826104.1 MULTISPECIES: peptide-methionine (R)-S-oxide reductase [Campylobacter]

MKELNEEEKKVILNKGTEAPFSGKYNDFYEKGIYQCKQCGASLYKSEDKFKSGCGWPSFDDEIKGAVKRI

PDKDGIRTEIVCANCNGHLGHVFEGEGFSAKNVRHCVNSISLEFVKTKD

>WP\_002866275.1 AAC(3) family N-acetyltransferase [Campylobacter jejuni]

MKYFLEHNDKKYSDKDLIDAFYQLGIKRGDILCVHTELFNFGVPLLSRNEFLQTILNCFFEVIGKEGTLI

MPTFTYSFCKNEVYDKLNSKCTVGTLNEFFRKQQGVKRTNDPIFSFAIKGAKEELFLKNTTSCFGENSVY

DTLVKENGKIILLGTKIAGYTFTHFIEEKIKVPYRYFKEFKGKIILENKMPKEIVINYYVRDLEENSNLD

VYKQIEILKQNDNFKLQQFSNSCIVLINSKAYLEDTMQALNQNLKCLLMEP

>WP\_002866438.1 MATE family efflux transporter [Campylobacter jejuni]

MSSIFSTLSPFRLFVKCAVPNVISMAFISFYYIVDGIFVGKYLGSDALAALALIIPFIMMSFALADMIAI

GSAVQISMYLGLGKKNLARKIFSSSMLIIFIISCFIGILEYFLGPVLIDCLNVSDEIKTMAKECMFVFAL

FAPFTMLSFALDNYLRICGKTAYSMVMNVIIALSNIVLDFIFIVELGWGLFSAALATCLGLVLGGIFGIF

PFLFQNLELKISSLYMNLKIFKNILYNGSSEFFGNISGSLYSIFANFVLLKISDTQAVAAFSIVLYIDSF

IIMLIIAMGDAMQPALSYNYAKKDFSRIKAIIKVVFFAGGFLSLFSIVLILIFGENLITLFTKENNQEFK

TFAYTALMLFAFNYFFAWFNVLSGSFLTAFNKASFSLVLSLAQNLFIPLFFLLFLSYFIGLNGVWLSPFF

AEFCVLILAWIFLKRIFKDLSL

>WP\_002877469.1 carboxynorspermidine decarboxylase [Campylobacter jejuni]

MFYEKIQTPAYILEEDKLRKNCELLASVGEKSGAKVLLALKGFAFSGAMKIVGEYLKGCTCSGLWEAKFA

KEYMDKEIHTYSPAFKEDEIGEIASLSHHIVFNSLAQFHKFQSKTQKNSLGLRCNVEFSLAPKELYNPCG

RYSRLGIRAKDFENVDLNAIEGLHFHALCEESADALEAVLKVFKEKFGKWIGQMKWVNFGGGHHITKKGY

DVEKLIALCKNFSDKYGVQVYLEPGEAVGWQTGNLVASVVDIIENEKQIAILDTSSEAHMPDTIIMPYTS

EVLNARILATRENEKISDLKENEFAYLLTGNTCLAGDVMGEYAFDKKLKIGDKIVFLDQIHYTIVKNTTF

NGIRLPNLMLLDHKNELQMIREFSYKDYSLRN

>WP\_002878094.1 MULTISPECIES: 2-oxoglutarate translocator [Campylobacter]

MARGVIKTGLGEHLAYHFISILGKKTLGIAYSIAFCETILAPVTPSNTARAGAIINSIVQVIARSFKSTP

EDGTQNKIGTYLSLVNYQEPILFHQLCLLQLQLQILWCFIFSLR

>WP\_002870200.1 MULTISPECIES: lipopolysaccharide assembly protein LapB [Campylobacter]

MDFFFVEYRDPLVGLIILTILVFVVAVANYIWKIFANKDEEQKLEKFIKKFEMDNAHKELLRNSSLSFGN

LSFLAEIFTKSGEFEKATQIYLIALEKCKDKQEREFIFLSLAKVYFKAGFLERAKEVLLQALKLRPRNIQ

ALKLLKIVYLKLRSYKENLELLECLFELNEDVQKEHDFIKALELCTFNITDEEKKKKLLEFKIEDNPMLG

RLVFEKYHMFLGQNFFDICDLLYRENEAFNLENQDFLEFFYALGKISKHDDTHQFVFKNSNFKMLKILKD

NSFNAGLEFSYRCSECKNVMPLFFYHCPVCYEFNTCKIIYEVKNNETH

>WP\_002866973.1 MULTISPECIES: 30S ribosomal protein S12 [Campylobacter]

MPTINQLVRKERKKVLEKSKSPALKNCPQRRGVCTRVYTTTPKKPNSALRKVAKVRLTSGFEVISYIGGE

GHNLQEHSIVLVRGGRVKDLPGVKYHIVRGALDTAGVAKRTVSRSKYGAKRPKAGTAK

>WP\_002866620.1 MULTISPECIES: 2-oxoglutarate translocator, partial [Campylobacter]

MGLGEISIMIFLSLAFLYTHYFFASITAHISAMFFVFYSAGLALGAPPLLYAFIMIASGNVMMALTHYAT

GTAPVIFGTGYVTLKKWWSIGFVISIVDIVVMIAVGLFWWKILGFY

>WP\_002854522.1 MULTISPECIES: membrane protein [Campylobacter]

MPADLNDYFNKKNGNSNNNGNNNRQNFNFKAPEFNFKGFGKFSPFVYGVIIIILFLIVAKPFMVINSGEM

GIKSTTGKYDPNPLEPGLHFFLPFVQKITIIDTRVRQINYASIEGSNENLSSGSGVINKNSISVLDSRGL

PVSIDVTVQYRLNPLQVPQTIATWSLNWENKIIDPVVRDVVRSVVGKYTAEELPTNRNTIAAQIEEGIRK

TIEAQPNEPVELRAVQLREIILPSKVKEQIERVQIAKQEAERTKYEVERANQEALKKAALAEGEANATII

SAKGKAMAVKIEADAQAYSNKEIANSLNTPLLNLKQIETQKEFNEALKVNQDAKIFLTPGGAVPNIWVDT

KDAKKQSAANMN

>WP\_002852633.1 MULTISPECIES: phosphopantetheine adenylyltransferase [Campylobacter]

MTCLYPGTFDPITNGHLDVIKRALKIFDEVIVAIAKSEHKKPCYDLEKRKELALLATQNLKNVKIIAFDN

LLVDLAKELKVNTIIRGLRAVSDFEYELQIGYANHALWEDMETIYLMPSLKHAFISSSIVRSIVAHGGDV

SSLVPKEILPFLKDQSCM

>WP\_002851856.1 MULTISPECIES: 2-oxoglutarate translocator [Campylobacter]

MALLGLSLVLISGVLTFGEVLAEKAAWNTLVWFSALVMMATLLGKLGVTQFLAEA

>WP\_002851459.1 MULTISPECIES: 30S ribosomal protein S9 [Campylobacter]

MATTYATGKRKTAIAKVWVKPGSGKISVNGVDLNTWLGGHEAIKLKVVQPLLVTKQETSMDIKATTLGGG

YSAQAEALRHGISRALAAMDADFRALLKPKGLLTRDSRTVERKKYGRRKARRSPQFSKR

>WP\_002851265.1 MULTISPECIES: hypothetical protein [Campylobacter]

MIKKFILLVFISSVVFGAEQDCEQYFEARKAQIELQTREFDEARQSLEAYKASFEALQKERLENLEKKEA

EVNATLAKIEELKLENARLVEEQQKILNSINDKTQGRVKEIYSQMKDAAIADVLSQMDAEDASKIMLSLE

SRKISGVLSKMDPKKASELTLLLKNLDNNASN

>WP\_012006747.1 UDP-4-amino-4,6-dideoxy-N-acetyl-beta-L-altrosamine N-acetyltransferase [Campylobacter jejuni]

MIKLKNFTELNPQEIELIFKWRNHPDISQFMKTKHIDFEEHLRFLKNLHQDSSKKYFLVFQDEQIIGVID

FVNITTKSCEFGLYAKPDLKGVGQILMNEIIKYAFENLKVNTLKAYVFKDNHKALKLYQQNHFTIYDEDK

NIFYIKLKNYNYKKQFAKRISKLDRGGGKYKY

>WP\_002934480.1 UDP-4-amino-4,6-dideoxy-N-acetyl-beta-L-altrosamine N-acetyltransferase [Campylobacter jejuni]

MQDYRCNILLKNYINLNYIEKEKIRKYRNQPEVKKYLYQTHFISKLEHKNFIKKLKYNTKKSYFCVILDN

QIIGNINFYIRENEIDFGFYANPFSKILGIGRILEQIGIYYAFKIINVPILSLEVFSNNTQVINLHRKFG

FSIVQEFFIKKQKILKMSLKQSDCKALLS

>WP\_002866597.1 A/G-specific adenine glycosylase [Campylobacter jejuni]

MQKKELEKLQENLLLWYEKNGRKTLPWRNLQSQNCDESLKHIDRAYGVYISEIMLQQTQVKSVLERFYFP

FLKKFPTLESLANANEDELLKAWQGLGYYTRARNLKKAALECVDKFGAKLPKEVEDLKKLSGIGVYTAGA

IACFGYDQKVSFVDGNIRRVLSRLFALENPSMKELEKGAKELLNVNHAFDHNQALLDVGALVCVSKNAKC

GICPLYDFCQGKFHTELYPRAKKILYESLNLNLFLFEFNKKFAIQKSQDKLYKGMYNFPFFKEGEYKLSK

DMSFVGEFKHGYTKYKLNIKVYHQILNNENKNYEFKTLKELESTALSVLSLNALKLIKL

>WP\_002866521.1 RNA polymerase sigma-54 factor [Campylobacter jejuni]

MLKQKITQAPKTKISQTLRSWLPILQANIEDLKENLDKFAEDNPFLNVQDSIQTHDKGKNYFDSFYKHNI

NSAFVDSKGLAKKSVYELLNEQILPPLFPTNKSQELAKKIIECLNEEGYFEYDEEFLKEYSLEEIERVRA

RFKFLDPVGVGAKDYKEAFLFALENMELDEDIDEFCRMLIMDFENIQNYTKEPLYKEALAVLKRFSTPPF

LEYFEDSRIIVPDIFVYKENGEIKVKINDDYYPEISIQTDGLEHDFLSHYIKEAKNLVDALAMRKATLYK

IGLMIVEYQYDFFMGKEIKPMTFKDLALDLERNASTISRAVANKYLSCERGLIPLRDFFAFALDEEGETS

NVGVKEFVANLVKNEDRNKPLSDSKILELIKEEFKVDIGRRTITKYRKHLNIASSTDRKKLYELEG

>WP\_002866404.1 chaperone protein ClpB [Campylobacter jejuni]

MANIQNFLTDNMLSNLESAASLAIHSKNNEVAPLHLLWALSVDSTSILNQILNKLNISKEALELEIKSRI

SKLATSSNVNRENIRFSNELINSLENAKGLMSANGDSYLSVDTWLISESQKSPTKEILAQFLDLREFQKE

LESLRAGRKIDSKTSDETLDSLNKFGIDLTLKASEGKLDPVIGREEEIERLMQILIRKTKNNPILLGEPG

VGKTAIVEALAQRIIKKDVPKSLQNKKVIALDMSALIAGAKYRGEFEDRLKAVVNEVIKSENIILFIDEI

HTIVGAGASEGSMDAANILKPALARGELHTIGATTLKEYRKYFEKDAALQRRFQPVNVGEPSVNEALAML

RGIKEKLEIHHNVTINDSALVAAAKLSKRYIADRFLPDKAIDLIDEAAAELKMQIESEPSSLRKVRKDIE

TLEVENEALKMENDEKNQKRLDEIAKELANLKEKQNALNSQFENEKSVFDGISAKKKEIDLLKNEASLAK

ARGEFQKAAELEYGKIPSLEKEVEILEDKWKKMSENGVLLKNQVDEDLVAGILSKWTGISVQKMLTSEKQ

KFLEVEKHLKESVIGQDKALSALARAIKRNKAGLNADNKPIGSFLFLGPTGVGKTQSAKALAKFLFDDEK

AMIRFDMSEFMEKHSVSRLLGAPPGYIGHEEGGELTEAVRRKPYSVLLFDEVEKAHKDVFNVLLGILDDG

RATDSKGVTVDFKNTIIILTSNIASSAIMNLSGKEQEDVVKNELKNFFKPEFLNRLDDIITFNPLGKDEA

YEIVKLLFKDLQMSLENKGIKASLSENAALLIAKDGFDPDFGARPLRRAIYDLIEDKLSDMILADELHEN

DSIIIDAKDDEIIIKKA

>WP\_002866281.1 UDP-2,4-diacetamido-2,4,6-trideoxy-beta-L-altropyranose hydrolase [Campylobacter jejuni]

MKVLFRSDSSSQIGFGHIKRDLVLAKQYDDVSFACLPLKGSLIDEIPYPVYELSSESIYELINLIKEEKF

ELLIIDHYGISVDDEKLIKLETGVKILSFDDELKPHHCDILLNVNAYAKASDYEGLVPFKCEVRCGFSYA

LIREEFYQETKENREKKYDFFICMGGTDIKNLSLQIASELPKTKIISIATSSSNPNLKKLQKFAKLHSNI

RLFIDHENIAKLMNESNKLIISASSLVNEALLLKANFKAICVAKNQEKLANWLAQKGYEVEYKY

>WP\_002816240.1 MULTISPECIES: malonyl-[acyl-carrier protein] O-methyltransferase BioC [Campylobacter]

MNFLKAKDYEKHAKVQDFMGLKLCEILKNLRISHFEKVFEFGCGRGELSKKLQNFITFDEYLKNDILDFK

ENSSILIFDMNEIAKQDLSKEKFDLIVSNATLQWLDLKRIIPSLRDMLNQNGILLLSTFAEQNLKEIKQS

TGFGLNYFSLNELEQIFKVYFNEVKITQELIKLSFDNALDVFRHLKLSGVNSLGFYPLNKGFLKEFEEKF

QNKLTYHPVFILCKNDIK

>WP\_002876781.1 DNA-deoxyinosine glycosylase [Campylobacter jejuni]

MSKFLTHPFEPFFDKDSKILILGSFPSVKSRQDGFYYQHSRNRFWPILETLFDVKLENITEQQAFLRKKH

IALWDVLQSCKIKNSDDKTISYAKANDLSLILSQAKIQAIFTTGQSAYKFFVKFHPRLEAIALPSTSPAN

LNFSFEQLLQNYEIIKKFTK

>WP\_002851566.1 MULTISPECIES: 50S ribosomal protein L29 [Proteobacteria]

MKYTEIKDKTAAELATMLKEKKVLLFTLKQKLKTMQLTNPKEISQVKKDIARINTAINALR

>WP\_002780988.1 MULTISPECIES: CRISPR-associated endonuclease Cas2 [Campylobacter]

MIEDKFMRVLLMFDVPTKSKKEQKLASKFRNNLIKLGYFMLQFSVYMRICKGLSSAKSSIENVKKILPPY

GNVRALIITEKQFDKMELLLGGIVFNEKVNNETNLTLFDIDSHGEFKYKNSNNEEIQLNKKQEKYHQQNL

FEF

>WP\_012006796.1 Na+/H+ antiporter NhaA 1 [Campylobacter jejuni]

MNNIVHKLKTLVLNEAFGGVLLIVCTLLALLVQNGSFSEHYREFLNLKVGFSVGEFELNKPFLLWINDGL

ISIFFFAIGLELKKEFLHGDFKNPKNIVLPFMAALGGILIPAMLFALVNIGDAYTLKGWAIPTATDTAFA

LAILMMCGKHIPSSLKIFLLSLAIFDDVGAILIIAIFYTTKLSIVAFVVAGIAILAMLVLNILGITRKSF

YFICSVILWISVLKSGVHATLAGIITAFFIPMQTKNGEAFLEEIYESLKFWLAFVILPLFAFANAGVNLS

NIDIGAIFSGVSVGIFLGLFVGKQVGVFLFSYLAIRFKFAALPQGSNLKQLYGVCILTGIGFTMSLFIDG

LAYEVSDIFNYADNLAILIASFCSGIWGFIYLKFFAARS

>WP\_002866417.1 succinyl-CoA ligase subunit beta [Campylobacter jejuni]

MNIHEYQAKAIFADNGIPTLKGKVAFSVDEAVSNAKELGGSVWAVKAQIHAGGRGLGGGVKIAKNLDEVK

DYASKILGMNLATHQTGPEGKLVQKLYIESGANIVKEYYLAILFNRMAEQITIIASSEGGMDIEKVAKES

PEKIAKVGIDPQIGFKMFHGLEVARVLGLDKDEGKKLISMIAKLYKLYMDKDMNMLEINPLIKTAEGDFY

ALDAKCSFDDSALYRHPEIAELRDITEENPAEREAAEFGLSYVKLDGDVACMVNGAGLAMATMDIINYSG

AKPANFLDVGGGASPETVAKAFEIILRDKNVKVIFINIFGGIVRCDRIANGILEATKNVEVNIPIVVRLD

GTNAAEAKTILDNSNLKNIKAATNLKNGAELVKSLVG

>WP\_002866666.1 haloacid dehalogenase [Campylobacter jejuni]

MFFLDVQGTLISDHDKSLIHGAKELIDFLNAKNLPYVIITNNTKKLDFLEKLQQKGLAIKENAYIDPFSV

LKYLLKPCKVAAFGADEFVKSLENLGFELDFVNPSAVLVASYDDFKFKDFASMIEFARREVRFIAMHETS

IYKKDGRPYPGVGSIMAMLKNAIDFEYEVVGKPSIAFYKEALNLIRKQNSKIDFEDIKIISDDFRGDLLK

AKELGMKTLLVLSGKISDTKGLDTDLLDGVYPSVFEFLKELKCQI

>WP\_012006680.1 periplasmic protein [Campylobacter jejuni]

MKKVILTSAMLCSVLFGVQEYEANLAGHIIIDSKSTVKPPKDAPDFFKTYGKFANITREEKIGTFKSKGN

RETDFYLPFKNQPIQGHSGIKYIPKKDVFWVISDNGLGKKYNSYDAMLYAHEFKFDFKNSKYELLKTVFF

KDSDKKYPYPITTETTKERYLSGVDFDTESIQVINDEFYIGDEFGPYLLHFDKNGNLKEVFDVYVEGKKL

ISPDNPSLKFSDKPDGENEKFNIKRSKGFEAMASSKDGSKLYLLLEGSIYNNNAYENEKGKEYLRIIEFD

VKNKKFTGKTYKYFLEDKSHSIGDFNMIDDKYGIIIERDQKEGTKDKVCKEGEDTKHCFNNVAQFKRNYK

VKLDDKTHEAQKISYIDLLNIKDRNKISKKPLVNDKFVFPFETIEGVDIVDDSHIVIENDNNFPYSSSRE

PNKTDDNEFILLEVKDFLKSK

>WP\_002866550.1 Nif3-like dinuclear metal center hexameric protein [Campylobacter jejuni]

MKLSEIYNFLDQLSPFDIQESWDNSGILLGDRDSEISTVYLSLDIDENIIKEASENSLIITHHPLIFKGL

KDLYDKTYPRAFIKEMICKNISLISMHTNYDLSHLNTYFTEEILGFKISFKDEFLIYVENSMSFEALCDW

VKKKLNLQILRVSDCGKKDIKRIAICTGSGGDLISKVDADCFLSGDFKYHQALEALSNQISLIDLGHFES

ERYFSQCLAKDLKNLPLQAIITVSKNPFQYF

>WP\_002865969.1 iron-sulfur cluster-binding protein [Campylobacter jejuni]

MSQKIPHEQIVQIKLNDKQMQENLMTAMHTLQKNRLNVIDARFKDWQGLRAKAKQAKNNALMSLEERLLE

FEKNATKNGIKVHWASSDEDACEIVYEIMKEKNITKLLKGKSMASEEIGLNHYLEKKGLKAIETDLGELI

LQLNEEPPLHIVVPAIHRNRHEIGEIFKEKLGANLENDEPESLNAVAREHLRKDFEGLKLGLSGVNFAMS

REGAFWLIENEGNGRMCTTAPDIHIALCGIEKVMESFEDAATMVSLLTPSATGQFIPTYNNIITGPRKNG

DLDGPKEVHVILFDHNRSKMLAHEDYYEALRCIRCGACMNFCPVYDQIGGHAYQTTYPGPIGEVISPNIF

GIDHTGDILNFCSLCGRCSEVCPVQIPLADLIRKLRCDKIGQGKNPPLGANKVHHNALEAFAFKQFKNIA

TNGDKWRFSLSKAHYFNWAVQNFANVLPVIKKWYAFKELPQIKMDLYKEVQKLEGVSYE

>WP\_002876774.1 molecular chaperone DnaJ [Campylobacter jejuni]

MEISYYEILEITQSADKETIKKAYRKMALKYHPDRNQGDKEAEDKFKLVNEAYEVLSNDEKRAIYDRYGK

DALKGGGFGSSSSGFGGFEDLGDIFSSFFGEGFGSSSRRRKSSNDEKIPSDFIVNLKLSFKEAVFGCKKN

IDFTYKCSCKTCNGTGAKDGKLQTCPKCQGRGQVGVSQGFITFAQTCPDCQGSGEKASEKCSDCKGLGYN

ESKDSVELNIPEGIDTGMKLRVNAKGNILKNGTRGDMYVKIIAAEDDTFVRDDDDIYIEFPVFFTQAILG

QSIKVPTIRGEATLNLPKGAKDGQRFVLEKEGVKDVHSSRIGNQIVQISIKFPTSLNDEQKELLEKLSES

FGIKDGMHQEQKGLFEKIANWFKS

>WP\_002865991.1 MBL fold metallo-hydrolase [Campylobacter jejuni]

MQIIKQACGAYETNCYILFSEHGEIIIDPGFDALNFIKKHVKNPLAILNTHGHYDHVWDNEKVKQAYQIP

IYIHKNDAFMLEDPFNQGFMPSKADYLIDDENIISIGGLDFKFHFLPGHTPGCTMIEIVGKNIMFSGDFL

FYRSIGRWDFPYSDANLMKQSLEKVMTYKEDFKLLPGHGQETTLKEEQVHLPSWLRYF

>WP\_012006645.1 multidrug efflux RND transporter permease subunit [Campylobacter jejuni]

MFSKFFIERPVFASVVAIIISLAGAIGLTNLPIEQYPSLTPPTVKVSATYTGADAQTIASTVASPIEDAI

NGADNMIYMDSTSSSSGTMSLTVYFDIGTDPDQATIDVNNRISAATAKMPDAVKKLGVTVRKTSSTTLAA

ISMYSSDGSMNAVDVYNYITLNVLDELKRVPGVGDANAIGNRNYSLRIWLKPDLLNKFGITATDVISAVN

DQNAQYATGKIGEEPVTQKSPYVYSITMQGRLQNPSEFENIILRTNNDGSFLRLKDVADVEIGSQQYSSQ

GRLNGNDAVPIMINLQSGANALHTAELVQAKMQELSKNFPKGLTYKIPYDTTKFVIESIKEVVKTFVEAL

ILVIIVMYMFLKNFRATLIPMIAVPVSLLGTFAGLYVLGFSINLLTLFALILAIGIVVDDAIIVVENIDR

ILHENEQISVKDAAIQAMQEVSSPVISIVLVLCAVFVPVSFISGFVGEIQRQFALTLAISVTISGFVALT

LTPSLCALFLRRNEGEPFKFVKKFNDFFDWSTSVFSAGVAYILKRTIRFVLIFCIMLGAIFYLYKAVPNS

LVPEEDQGLMISIINLPSASALHRTISEVDHISQEVLKTNGVKDAMAMIGFDLFTSSLKENAAAMFIGLQ

DWKDRNVSADQIIAELNKKFAFDRNASSVFIGLPPIPGLSITGGFEMYVQNKSGKSYDEIQKDVNKLVAA

ANQRKELSRVRTTLDTTFPQYKLIIDRDKLKHYNLNMQDVFNTMNATIGTYYVNDFSMLGKNFQVNIRAK

GDFRNTQDALKNIFVRSNDGKMIPLDSFLTLQRSSGPDDVKRFNLFPAAQVQGQPAPGYTSGQAIEAIAQ

VAKETLGDDYSIAWSGSAYQEVSSKGTASYAFALGMIFVFLILAAQYERWLIPLAVVTAVPFAVFGSFLL

VYLRGFSNDIYFQTGLLLLIGLSAKNAILIVEFAMEERFKKGKGVFEAAVAAAKLRFRPIIMTSLAFTFG

VLPMIFATGAGSASRHSLGTGLIGGMIAASTLAIFFVPLFFYLLENFNEWLDKKRGKVHE

>WP\_012006611.1 chromosomal replication initiator protein DnaA [Campylobacter jejuni]

MNPNQILENLKKELSENEYENYIAILKFNEKQSKADFLVFNAPNELLAKFIQTKYGKKISHFYEVQSGNK

ASVLIQAQSAKQSSKSTKIDIAHIKAQSTILNPSFTFESFVVGDSNKYAYGACKAISQKDKLGKLYNPIF

IYGPTGLGKTHLLQAVGNASLEMGKKVIYATSENFINDFTSNLKNGSLDKFHEKYRNCDVLLIDDVQFLG

KTDKIQEEFFFIFNEIKNNDGQIIMTSDNPPNMLKGITERLKSRFAHGIIADITPPQLDTKIAIIRKKCE

FNDINLSNDIINYIATSLGDNIREIEGIIISLNAYATILGQEITLELAKSVMKDHIKEKKENITIDDILS

LVCKEFNIKPSDVKSNKKTQNIVTARRIVIYLARALTALTMPQLANYFEMKDHTAISHNVKKITEMIEND

GSLKAKIEELKNKILVKSQS

>WP\_002871934.1 Bcr/CflA family drug resistance efflux transporter [Campylobacter jejuni]

MQKHTKIHGFAKFKLIIILALMSSIAPLSTDMYLPALSHVEQSFQTNSFLTQLSIASFFIAFALGQLIYG

PLSDIFGRKIPALVGIFFFIVSSLFCVIIDDIYAFIALRFFEALGGCAGVVIARAIVNDLFEIKEAAGIF

ALMMVFSSLAPMLSPTFGGILLEYFSWHSIFATLFALGILLFLMILFGLKESAPHLKNKKFSHHEAMKSY

KFVLSDKRFLVYILCASFALAAMFAYITGSSFVFTQFFSLSEQKFALLFGANALGFVICANINARLVLKY

ESEKILAKALMIMFISTVILLANAFFHPNFLLFELSIFTSIAMLGFIAPNTTTLAMARFKEHSGTASAVL

GTVQFGFAGLISFVVGAINANTPIILAFVMCACVLVANMIYFLIKIKEKK

>WP\_002867072.1 diaminopimelate epimerase [Campylobacter jejuni]

MKFYKYCASGNDFVITNADRKEDRSALAKELCNRYEGIGADGFIVILPHEKYDFEWEFYNNDGSRAAMCG

NGSRAAAHFVHHINKINPNMSFLTGAGVIKAKVNQDKVEVSLGKIKSVQNTFEELGKTWQLCNTGVPHLV

HFCQNLDEFDTMLCQKMRQKYNANVNFVKILDENHLKVRTYERGVEDETLACGTGMGACFYLAFLNKKVQ

NKVKITPKSGEEVGFAYKNEELFFEGKVKYCFEANYNFS

>WP\_002866830.1 biotin synthase [Campylobacter jejuni]

MQIMLCAISNIASGNCSEDCKYCTQSAHVKTDIQKYRRKELSQIVLEAKMAKKNEALGFCLVTAGLGLDD

EKLEYVCEAAKAVQKEVPNLLLIACNGMASVEQLKELKKAGIFSYNHNLETSKEFFPQICTTHTWESRFQ

TNLNAKEAGLMLCCGGIYGMGESEEDRLSFRKSLQELQPFSTPINFFIANENLKLQVPRLSADEALKIVR

DTKEALPQSVVMVAGGREVVLQERQYEIFQAGAGAIVIGDYLTTKGEEPSQDIIKLKEMGFTFASECH

>WP\_002866639.1 phosphoglucosamine mutase [Campylobacter jejuni]

MKLFGTDGVRGKAGEFLDSFLAMRLAMAAGIYFKDKSITNNILVGKDTRRSGYMIENAIVSGLTSIGYNV

IQIGPMPTPAIAFLTEDMRCDAGIMISASHNPYYDNGIKFFDAHGNKLSEDIEKKIEEIYFDDKLIQASK

VDMEKIGQAKRIDDVIGRYIVSIKNSFPKDLTLKSLRVVLDVAHGAAYKVAPTVFKELGAEVIVMSDKPN

GLNINENCGALHPANLAAEVKRLRADVGFAFDGDADRLVVVDEKGEVANGDSLLGVLALYLKEQGKLQSS

VVATIMSNGALKEFLNKHGIELDTCNVGDKYVLEKLKVNGGNFGGEQSGHIIFSDYAKTGDGLIAALQFS

ALMLSKKKSASSILGQVKPYPQLLTNLKIAEKKDLDKIKGLKELKKDLENKNINTLFRYSGTENLIRLLL

EAKDIKLLEKEMKNVVEFFKKALNG

>WP\_002866608.1 chorismate synthase [Campylobacter jejuni]

MNTFGTRLKFTSFGESHGVAVGCIIDGMPAGVKFDEEFLQNELDKRKGGSKFATPRKESDKAQVLSGVFE

GYTTGHPIAIVVFNENAHSKDYDNLKDLFRPAHADFTYFYKYGIRDHRGGGRSSARESVARVAGGAVAAM

LLREFDICVQSGVFGVGTFVSNLKEEEFDFEFAKKSEIFCLDPKLESDFKNEILNARNSKDSVGAAVFTK

VSGMLVGLGEVLYDKLDSKLAHALMGINAVKAVEIGEGINASKMRGSCHNDALKDGKFLSNHSGGILGGI

SNGENLILKTYFKPTPSIFAKQESIDKFGNNLEFELKGRHDPCVGVRGSVVASAMVRLVLADCLLLNASA

NLNNLKNAYGLK

>WP\_002866424.1 glutamyl-tRNA reductase [Campylobacter jejuni]

MYYCISFTHKNTDIALREKLSFSNEAKKSEFLKIISTHENIEECLVISTCNRVEIVAFVKMACAEFIVKS

LALLCDVDKDILLEKADIFEDSGAIHHLFSVASSLDSLVVGETQIAGQLKDAFAFAVKNNFCGVHLSRAV

HSAFKCAAKVRNETQISKNPISVASVAVAKAKELADLAQKKAVVIGAGEMGELAAKHLIAAGAKVIILNR

DLQKAKDLCERLGVLSEYDSLENLKKYLNQYEFFFSATNAPNAIITNSLIEELPYKRYFFDIAVPRDIDI

NENENISVFAVDDLENVVQKNLALREQEARMAYGIIGRETSEFFRYLNDLALMPIIKAIRLQAKEYADKQ

LEIALKKGYLKKSDKEEARKLIHQVFKAFLHTPTVNLKHLQGKMQSDTVINAMRYVFDLQNNLEGLNQYK

CEFDMENNDEIY

>WP\_002857482.1 MULTISPECIES: aspartate 1-decarboxylase [Campylobacter]

MNITLLKSKIHRASVTEARLDYIGSISIDEKLLQASGILEYEKVQVVNVNNGARFETYTIATQEEGVVCL

NGAAARLAEVGDKVIIMSYADFNEEEAKTFKPKVVFVDENNTATKITNYEKHGAIF

>WP\_002837927.1 MULTISPECIES: elongation factor 4 [Campylobacter]

MSVKNIRNFSIIAHIDHGKSTLADRIISECGAISDRQMSSQVMDTMDIEKERGITIKAQSVRLNYKFNNE

NFVLNLIDTPGHVDFSYEVSRSLASCEGALLVVDASQGVEAQTIANVYIALENNLEIIPVINKIDLPNAD

VEKVKHEIEHIIGIDCKDAICVSAKTGVGIKELIETIITKIPAPKTDDEAPTKALIYDSWFDNYLGALAL

VRIYEGSIAKNDEVLVMSTDKKHIVQDLFYPHPLSPIKTQSLQSGEVGVVVLGLKTVGDVQVGDTITLVK

NKAKEAIGGFEKAKAFVFAGLYPIETDKFEDLRDALDKLKLNDSSITYEPETSLALGFGFRVGFLGLLHM

EVIKERLEREFNLDLIATAPTVTYEIYQTDGELIKIQNPSELPPVNKIDHIKEPYVKATIITPSEFLGNL

ITLLNRKRGVQVKMDYITPERVLLEYDVPLNEIVMDFYDKLKSLTKGYASFDYEPIEFRVGDLVKLDIKV

AGENVDALSIIVPNEKAQSKGRELVSAMKEIVPRQLFEVAIQASIGNKIIARETVKSMGKNVTAKCYGGD

ITRKRKLLEKQKEGKKRMKAIGKVNLPQEAFLSVLKID

>WP\_002831283.1 MULTISPECIES: uracil phosphoribosyltransferase [Campylobacter]

MKNIHCINHPLIEHKLGILRAKETKPFQFRMLIDEISSFLLFEASKDFSLKEIEISTPIQKTTVKKLDEK

IMICPILRAALGMLESVFKMIPDASVGFLGFVRNEETLKADFYFQKLPKDAKKRTAIVIDPMFATGGTAI

EACNFLKSQGVKKIKFISILAAPQGLKKFSQMHDDVEVFVACIDEGLNEKGYIIPGLGDAGDRVFNTL

>WP\_002781436.1 MULTISPECIES: translation initiation factor IF-1 [Campylobacter]

MAKDDVIEIDGTVLEALPNANFKVELDNKHVILCHIAGKMRMHYIRIMPGDKVKVELTPYSLDKGRITFR

YK

>WP\_002867055.1 methyl-accepting chemotaxis protein [Campylobacter jejuni]

MFKSLNIGLKLIFSVATVVVIGLVILISLITKQVSQNITKNTEDILASITKEYATQTQGIFGEMIALNKS

ISGTLTEMFRSTSKEDLDIDNITNIITNTFDNSAYSNFTYLYLIDPPEYFKEESKFFNTQSGKFVMLYAD

EEKDNKGGIKAIQASDEIANLQVVQDILKKAKYGENKVYIGRPIKMNLEGQDFDAVNVAMPIFDRKNQVV

GVIGMTLDFSAIATYLLDPKSQKYNGELRILLNSDGLVAIHPNKNLVLKNLKDVNPNKGAQETYKAMSEG

KNGVFNYIAFDGDDSYAAINSFKVQDSSWTVLVTAPKYSVFEPLKKLQLIIIGASFIFIFVVLGVVYYCV

RKIVASRLPVILSSLESFFRFLNHEKIEPKAIEIRANDELGAMGRIINENIEKIQISLEQDQNAVDESVQ

TAREIEKGNLTARITKNPINPQLVELKNVLNRMLDVLQSKIGSNMNEINRVFDSYKALDFSTEVLDAKGE

VEITTNILGKEIKKMLVASSNFAKDLANQSEELKNSMQKLADGSNAQASSLEQSAAAVEEINSSMQNVSG

KTVEVASQADDIKNIVNVIKDIAEQTNLLALNAAIEAARAGEHGRGFAVVADEVRQLAERTGKSLSEIEA

NINILVQSVNEVAESVKEQTAGITQINDAIAQLETVTKENVEVANVTNNITNEVNQIAAAILEDVDKKRF

>WP\_002851336.1 hypothetical protein [Campylobacter jejuni]

MDERILEFIKNEQLLSWAMIDEKGVYTASAFYAFDEKNLAFIIASHEDTKHIRLASENSSIALNIAKESK

IAFLKGVQAKAEFKMASKEQMKIYFSKFPFAKFDKSAKIYALELFWLKFTNNALGLSKKLEFYKK

>WP\_012006804.1 crossover junction endodeoxyribonuclease RuvC [Campylobacter jejuni]

MKILGIDPGSRNCGYAIIEANKGKNILIEAGLIKIKPNTLQYQITELCEGLDLIFKNHSFDEVAIEDIFF

AYNPKTVLKLAQFRGALSLKILQIHGDFAEYTPLQVKKAVTGKAKATKEQVAFMVKRLLGLSKDIKPLDI

TDAIAVALTHAANLRVRV

>WP\_012006752.1 flagellin A [Campylobacter jejuni]

MGFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND

ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSG

NFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSV

GTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINA

VKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAI

GMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVG

SGKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVTTLKGAMAVM

DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKANILAQSGSYA

MAQANSSQQNVLRLLQ

>WP\_012006751.1 flagellin B [Campylobacter jejuni]

MGFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATLGQAINNGND

AIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTTSFNGKQLLSG

NFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSV

GTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVVIGQINYKDGDNNGQLVSAINA

VKDTTGVQASKDENGKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAI

GMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQGSGFSRGSGFSVG

SGKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVTTLKGAMAVM

DIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFASESANFSKYNILAQSGSYA

MSQANAVQQNVLKLLQ

>WP\_012006742.1 UvrABC system protein C [Campylobacter jejuni]

MTKENLENELKTLPNSAGVYQYFNQEGKLLYVGKAKNLKNRVKSYFAFTPNLHANPRNSLRIQKMIEETV

HLEFITTNSEADALILENSFIKQLHPKYNILLRDDKTYPYIYVDFEEEFPRFEITRKLVKKSKIKYFGPF

FKGARELLDALYLYYPLKQKASCKSPCIFYQISRCLAPCDKRISREKYLEILDEAMHALLNPSILIKNLE

KQMLVLAQNENYEEAAKVRDQIVTIKDLEVKVEIDIAKLEDFEVFALAFENSMLSTLRFVVQNGKIISVN

SKITPIKNDIQWDKNEIYKQLILENFSMDIPLLANVIYVYEEFEDRMLLEEILSQRFDKKISIKIPKIGE

KRRICDLAFQNALLNIEKEQKNHDFTIQKELKSYFELENLPNDIEIFDNSHLQGVANVGAMVTYSANSWD

KSKYRKFHLKHKNDYDQMREVLMRRALDFDKIPPPDLWLIDGGKALLDLAKEIIVSSGANVDILAISKEK

IDAKAHRAKGGARDKIHSLKGEFSLSINDKKLQFLQKLRDEAHRFAISFHQNTKKKQDLNSSKLVNLGLS

SGVIQKLLAYYGNFESIYKADFKDLAMLVGKKVAQKIKEN

>WP\_012006678.1 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) [Campylobacter jejuni]

MEYKRFKTRQIKVGNVSIGGDAPISVQSMLFTKTRDIEGSLEQISRLYFAGANIVRLACLDMADARALKE

IKAKSPLPLIVDIHFNHNLAVYCAEFIDGVRINPGNIGSKENIKEVVKACKERGIPIRIGVNHGSIEKQF

SDKFGYGVDAMLESAMYNIKLLEDLDFFDIKISMKTSDAQKTIEAYERLRPLCDYPFHLGVTEAGTKFHS

TVKSSIALGNLLLKGIGDTMRVSMTGELEEEIRVARAILQDSGVQKSGVNIISCPTCGRIQSDLLSAIKI

VEEKTKHIKEPLNISVMGCVVNALGEAKGADVAIAFGKNQGLVIRHGEVVAKLKESELVDRFLAEVEDEV

KSRAVKE

>WP\_002876783.1 polyribonucleotide nucleotidyltransferase [Campylobacter jejuni]

MQYSIEINKNTEIFDIDKVAKQAAGAVLMRQGKSVVLATVAREEKQVEEDFLPLTVQYIEKAYAAGKIPG

GYVKRETKPSDAETLTARIIDRSLRPLFPKGYTYPTQIVVMVLSADPKVDLQVMSLNAASVALYLSDIPM

KAPVCGVRIGKIDGNFILNPNNEELQNSTLDLYVAGVKDELLMIEMRALPDQKENEIFIEAPYADVLTQT

TSQNMNELSEDEILEALNLAQKAILNGSNAYEEAFSKHKKNSQIELKNEIEHPEILAFIENNFQKQIKEA

INQMAKSERASELNKIAKEILNLEIAKDWSEESVLNTLAKVKRKLIREQILNEGKRADGRSLNEVRPISI

ETNILPNAHGSCLFTRGQTQALVVATLGGENDAQMIDLLTEKNPISERFMVNYNFPGFSVGEASPIKAPG

RRELGHGNLAKRALYPSVDENYPYVIRLVSEILESNGSSSMATVCGGSLALKAAGVPSLKLVAGVAMGLI

FEDNKHAVLTDIMGLEDHDGDMDFKVAGSKDGVTALQMDIKLGGIDQETLKQALYQAKEGRIHILNIMEE

AAKEIIVNEEVLPKLELFSVDPSKIVDIIGQAGKTIKEIIEKFGVSIDLDREKGEVKIAGSQNEQIKAAK

DYIINITSSQKGTKKGSKDKDISGFELGQEFQGIVKKIAPFGAFVELKNGVDGLLHSSKSKHLNLTENQS

LKVKISEIKNGKISVDLCE

>WP\_002866893.1 phosphoribosylformylglycinamidine synthase subunit PurL [Campylobacter jejuni]

MDKETIKAHKISDEEYAQILEILGREPNLLELGVISAMWSEHCSYKSSKKYLNGFPTKAPWVIQGPGENA

GVIDIGQGMAAVFKVESHNHPSFIEPFAGAATGVGGILRDVFTMGARVVAGLNSLKFGDIHDEKCGKHQK

YLVKGVVNGISHYGNCMGVPTIGGECAFDECFNGNILVNAFALGVCKSEDIFYAKAEGVGNPVIYVGSKT

GRDGLGGAVMASDSFNEESKSLRPTVQIGDPFSEKLLMEACLELFKTDYIVGIQDMGAAGLTSSSFEMAG

RSGSGMKLYLDKTPMRESGMTPYELMLSESQERMLICAKKGYEDKVIEIFKKWDLDAVVMGEVTNTGKME

LFWHDELVGLIPIEPLSEKAPILSRPTSEPKYLSEIKNYKFELKSSIQELFIQMLQNENINNKAFIYDQF

DSSVQTNTIKADGKLGASVIRIKENGASVAMAIECNSRLNYVNPKIGAALAVASAGRKVACTGAKPLAIS

DCLNYGNPQNPEVMWQFAQGCEGIKEACKELNTPVVSGNVSLYNETEGVSIYPSPTIVSVGVLEDANKTL

KASFEKENLSVYLLGESLGEFGGSMVMKIQDKKVSGSLKELDYKAELALWDLLYKANQNSLLECANSVGI

GGIAMTLAKMFAISSVGANLTSDFDDEKMIFDESASRAIIGLSKENEEAFLNLAKEFGVKAYKLGVSTSQ

KHFKLDSIELSKAELDKLYFESFKEQIQ

>WP\_002866860.1 NADH-quinone oxidoreductase subunit I [Campylobacter jejuni]

MKNYYLVDEKRKTPVSTWEKISQTFRRSVKLELFVGLFVMMRELLKRNNSATIKYPFEKVKLDNRYRAVH

RLMRFIESENERCIGCGLCEKICISNCIRMETSLDENGRKKVGNYSINLGRCIYCGFCAEVCPELAIVHG

TEYENAAEQRSYFGYKQDFLTPIDKLKNQVEFEGAGSLRKDADLLVVKTPNYYDVMIERALENQDTQEQG

ENK

>WP\_002866768.1 molybdenum cofactor guanylyltransferase [Campylobacter jejuni]

MQLNELNCVILCGGKSSRMGQDKSKLILKNQNLTQFQVEKFSKIFKNVYVSAKEDKFENHFSLIKDSLEF

EVYSPMLALYSILSNFKNEFVFVLSVDSPKVGENELLKMLPFLEQNYKIIIAKTPLHKHPLCGFYHSSLA

QTCKNFLEKNEQKIGLLFSEIKTKFVEFEDEDAFLNLNFYEEYEKFKSELR

>WP\_002866743.1 UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [Campylobacter jejuni]

MKQLTLAKTVKGVGIGLHKGEPIEITLEPLEANSGIVFFRSDLNASYKASPENVINTQMATVLGDDRGFI

STIEHLMSAINAYGIDNVRIVLNANEAPVMDGSSISFCMMLDEAGVKELDAPKKIMVIKKPVEVRDGNKF

VRLTPTKEPRINYTIKFDNAVIGEQSYNFEFSKKNYIENIARARTFGFLKDVQALRSMNLALGGSLENTI

VVDENRILNPEGLRFKDEFVRHKILDAIGDLTLLGYRVFGDYISYAGSHHLNHLLTKEVLKDKDAYEIVS

LEKTTQKAYEKVFA

>WP\_002866114.1 leucine--tRNA ligase [Campylobacter jejuni]

MAYEASLIEKKWQKIWDENEYFEPKDDLNLPKKYILSMFPYPSGRIHMGHVRNYTIGDALARYYRKIGFN

VLHPIGFDSFGMPAENAAIKHKIHPKSWTYENIAYMKKELFSLGFSFSKKRMLATSDPLYTKFEQEFFIK

MFEKGLIYTKEANVNWCEQDQTVLANEQVEDGKCWRCGHEVVQKKMPGYYVKITAYAEELLKDLEELKDK

WPNQVLTMQENWIGKSEGLEFSLNLDEESKQKTKESSLEVFTTRADTIYGVSYIALAPEHKIVQNLLSQN

LLNQDVLNKIKAIQNQSPRERQSSEKEGYFLGIYAIHPLSGEKIPLWVANFVLADYGSGAVMAVPAHDER

DFEFATKYNLAIKQVIQTQENLPYTQKSGKLIHSQEFDNLDCNEARLKIISQFEAKNIGKRVVNFKIRDW

GVSRQRYWGAPIPMIKCQSCGIVPQKLENLPITLPEDVQITGEGNPLDKHPTWKNCICPKCGKEAQKESD

TLDTFFESSWYFARFASDEKTWQEKALDEKSVKYWMSVDQYIGGIEHAILHLLYARFFQKALRDLGYLTQ

NEPFDRLLTQGMVLKDGAKMSKSKGNVVDPDEIIEKYGADTARLFILFAAPPAKELEWNDDAVEGAYRFI

CKLYDRAQNVKKGELVELKQENLNKEEKYARLKVYEALKKSFEVYHQSFAFNTLIAACMEALNALALCKN

EALEQEAFYIILNILEPIIPHVCFELSEELFKCKNFKKLELKEEIFVKDTLNLAVSINGKKRAEFEISSS

ASKEEILAFAKENTAKWLEGKSIVKEIYVEGKLVNLVIK

>WP\_002866040.1 ribosomal RNA small subunit methyltransferase G [Campylobacter jejuni]

MIFKDYDFLQNYDLKNFEEKIKIYKELLSKFNRIHNLTHLKNIDENIFDSIKILDFYDFSKAKNIADIGS

GAGFPAVFLAFLLQNNFHLFEPNPKKAAFLRTLKIECELSNLHIYKEKVQEYQNIFKADIITSRALMDVK

PLLEICKNLKDENTVFILWKGSEIYQELENIKDYEIFENNLRKYCILK

>WP\_002865994.1 4-hydroxy-tetrahydrodipicolinate synthase [Campylobacter jejuni]

MDKNIIIGAMTALITPFKNGKVDEQSYARLIKRQIENGIDAVVPVGTTGESATLTHEEHRTCIEIAVETC

KGTKVKVLAGAGSNATHEAVGLAKFAKEHGADGILSVAPYYNKPTQQGLYEHYKAIAQSVDIPVLLYNVP

GRTGCEISTDTIIKLFRDCENIYGVKEASGNIDKCVDLLAHEPRMMLISGEDAINYPILSNGGKGVISVT

SNLLPDMISALTHFALDENYKEAKKINDELYNINKILFCESNPIPIKTAMYIAGLIESLEFRLPLCPPSK

ENFAKIEEVMKKYKIKGF

>WP\_002864738.1 MULTISPECIES: flagellar L-ring protein [Campylobacter]

MKKVLFYVLPFAFFGCSATVDPQISMKPPAYVEELAPKQSNNVESAPGSLFGKGDNPLFSDKKAMNVNDL

VTVVIQESTTQSTQANKATSRTNTSNLGGGALTGSSGVVANALNKVNAYSNIGFQTNSSNNYTGTGSQSR

NESFNTTISTRVIKILSNGNYFIEGSRELLINGEKQIIQLSGVIRPYDIGQDNTIDSKYIADAKILYKTE

GEVDRSTRKPWGSKVIEAIWPF

>WP\_002854652.1 ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE [Campylobacter jejuni]

MQKQEKIIEMFNQIAPTYDKANRILSFGADVVWRKKACQRVMSLYLKKDLKIADIACGTGDMIEIWQESA

LKMEKNILNIKGIDPSSGMLNVAKEKFPNVEFIEAGAQNLPLESQSLDILSISYGIRNVVERQKALSEFA

RVLQKGGILVVLEFTKREKGGFIAACRDFYLKNILPSIGGIISKNKSAYEYLPNSIEGFLSKEEFILELK

NAGFEMLDYKSFSFGVSSMFIAKKL

>WP\_002851478.1 MULTISPECIES: 30S ribosomal protein S14 type Z [Campylobacter]

MAKKSMIAKAARKPKFKVRAYTRCQICGRPHSVYRDFGICRVCLRKMGNEGLIPGLKKASW

>WP\_002826014.1 MULTISPECIES: flagellar P-ring protein [Campylobacter]

MRVLTIFLLFMTSIFAVQIKDVANTVGVRDNQLIGYGLVVGLNGSGDGTSSKFTLQSISNLLQGMNIKVD

PNDIKSKNTAAVMVTAKLPAFAKSGDKLDITVSSMGDAKSLQGGTLLLTALRGIDGEIYAIAQGSISTGG

LTPRPGGAGSHSTAATVMGGANVEREIPQNFSQNNDLTLSLKVADFKTANDIERVLNTVFGEEVAKAIDS

RTVKLKKPEDLSNVDFMARVLEQDIAYKPQSKVIIDERTGTVIAGVDVEVEPVLITHKDITIKIDPNNNA

VANQNEIDMKDGGFVDPSSNTLRINNAKSTVANIARMLNKLGATPNDIIAIMENLKRAGAINADLEII

>WP\_002779472.1 MULTISPECIES: elongation factor G [Campylobacter]

MSRSTPLKKVRNIGIAAHIDAGKTTTSERILFFTGMSHKIGEVHDGAATMDWMEQEKERGITITSAATTC

FWKDHQINLIDTPGHVDFTIEVERSMRVLDGAVAVFCSVGGVQPQSETVWRQANKYGVPRIVFVNKMDRI

GANFYNVEDQIRNRLKANPVPLQIPIGAEDNFKGVIDLVTMKALVWEDDTKPTDYVEKEIPAELKEKAEE

YRTKMIEAVSETSDELMEKYLGGEELSLEEIKTGIKAGCLSLSIVPMLCGTAFKNKGVQPLLDAVVAYLP

APDEVANIKGEYEDGTEVSVKSTDDGEFAGLAFKIMTDPFVGQLTFVRVYRGCLESGSYAYNSTKDKKER

IGRLLKMHSNKREEIKVLYAGEIGAVVGLKDTLTGDTLASEKDKVILERMDFPDPVISVAVEPKTKADQE

KMSIALNKLAQEDPSFRVSTDEESGQTIISGMGELHLEIIVDRMLREFKVEAEVGQPQVAYRETIRKTVE

QEYKYAKQSGGRGQYGHVFLRLEPLEPGSGYEFVNDIKGGVIPKEYIPAVDKGVQEALQNGVLAGYPVED

VKVTVYDGSYHEVDSSEMAFKLAASMGFKEGARKAGAVILEPMMKVEVETPEDYMGDVIGDLNKRRGQVN

SMDERGGNKIITAFCPLAEMFGYSTDLRSQTQGRATYSMEFDHYDEVPKNVADEIIKKRNG

>WP\_002777888.1 MULTISPECIES: NADH-quinone oxidoreductase subunit B [Campylobacter]

MAEHQVNYASGLPVVLTSVDKLVQWGRSNSLWALSYGLACCAIEMMAAGGSRYDFDRFGTIFRASPRHSE

VMIIAGTLCKKHAEFTRRLYDQMPDPKWVISMGSCANTGGMFNTYSTVQGVDRIIPVDIYVPGCAPRPES

FQFALMILQKKIRKEKASRKIAPKRLV

>WP\_002855429.1 MULTISPECIES: flagellar basal body protein FliL [Campylobacter]

MDEELENEETKKKKGGSLVIIIVILLFVLLLSIMGVIAWLISSSSSDESEVKEAPKEEAKADKPKVSAPT

QRGSDFANIGPMYPLDPFTLNLLSDSGSRYVKCTIELEQNSELLKPELDKKVPVIRDIIIRTLTAKTFEE

VSTQKGKERLKDELVGKINEILTDGFIKNVYFTDFVVS

>WP\_002855210.1 MULTISPECIES: elongation factor P [Campylobacter]

MASYSMGDLKKGLKIEIDGIPFKIVEYQHVKPGKGPAFVRIKIKSFIDGKVLEKTFHAGDKCEAPNLEDK

TMQYLYDDGENCQFMDTQTYEQVAISDDDVGEAKKWMLDGMMVDVLFHNGKAIGVEVPQVVELKIIETAP

NFKGDTQGSNKKPATLETGAVVQIPFHVLEGEVIRVDTVRGEYIERANK

>WP\_002919844.1 MULTISPECIES: DNA polymerase III subunit delta [Campylobacter]

MYRKELQILLSKDSIPNFFFLYGADNFQSELYAEFIKEKYKPDETLKLFFEEYNFTRASDFLSAGSLFSE

KKLLEIKTSKKIPTKDLKVLVDLCKNNADNFFLLELYDESSKQSDIEKIFSPHFVRFFKANGAKEGVELL

SIKAKQLGVEITQNALFTLFTSFDENLYLAASELNKFSGLRVDEKTIEQYCYSLNTGSFESFFEKILKKQ

DFKSELEKILDNFNEIALTNSLYNSFYRLFKIALYAKVNGKIDFKDLLGYTPPPQVGQNLSSQAFSLKIE

QYKEIFTLLLKSEYELKTNSKLVKKEFLISNLLKLARILKS

>WP\_002876969.1 MULTISPECIES: hypothetical protein [Campylobacter]

MMMNYFETLQTFIENNRIDEGIIMEHFAHMLKDILERYDCYLNSDDFKKNNPLGLKKLIKLKNRCNTYIS

>WP\_002859291.1 MULTISPECIES: molecular chaperone GroEL [Campylobacter]

MAKEIIFSDEARNKLYEGVKKLNDAVKVTMGPRGRNVLIQKSFGAPSITKDGVSVAKEVELKDSLENMGA

SLVREVASKTADQAGDGTTTATVLAHAIFKEGLRNITAGANPIEVKRGMDKACEAIVAELKKLSREVKDK

KEIAQVATISANSDEKIGNLIADAMEKVGKDGVITVEEAKSINDELNVVEGMQFDRGYLSPYFITNAEKM

TVELSSPYILLFDKKIANLKDLLPVLEQIQKTGKPLLIIAEDIEGEALATLVVNKLRGVLNISAVKAPGF

GDRRKAMLEDIAILTGGEVISEELGRTLESATIQDLGQASSVIIDKDNTTIVNGAGEKANIDARVNQIKA

QIAETTSDYDREKLQERLAKLSGGVAVIKVGAATETEMKEKKDRVDDALSATKAAVEEGIVIGGGAALIK

AKAKIKLDLQGDEAIGAAIVERALRAPLRQIAENAGFDAGVVVNSVENAKDENTGFDAAKGEYVNMLESG

IIDPVKVERVALLNAVSVASMLLTTEATISEIKEDKPAMPDMSGMGGMGGMGGMM

>WP\_002852001.1 MULTISPECIES: 3-dehydroquinate dehydratase [Campylobacter]

MKIMIIQGPNVNMLGVREVGIYGAMKMEEIHEQMKLAASQNNVELDFFQSNFEGEIVDKIQECLGTVDGI

IINAAGYTHTSVAIRDAIAAVALPTIEVHISNVYRREEFRQKSLIAPVCSGTIVGFGPFGYHLALMGIIQ

ICEQIKNLRAMQQAQQTNK

>WP\_002851915.1 MULTISPECIES: preprotein translocase subunit SecG [Campylobacter]

MITLLIILQFIIVVVICIAVLLQKSSSIGLGAYSGSNESLFGAKGPAGFLAKFTFVMGILLIANTIGLGY

LYNKASKDSLAEKIKVENNNTTIPSAPIVPTTPNTNSIAPSAPQLPSDVNSSK

>WP\_002851887.1 MULTISPECIES: carbonic anhydrase [Campylobacter]

MENLISGAIKFMQEDFKEHEELFESLKNKQNPHTLFIGCSDSRVIPNLITNTGPGELFVIRNIANIVPPY

RVGEDYLATTSAIEYALNSLHIKNIVVCGHSNCGGCNALYYSDEELNKIPNVKKWLTMLDPIKKDVMIFA

RDDLAMRSWLTEKLNLVNSLQNILTYPGVQEALDEGKIEVHAWYYIIETGEIYEYDFKAKIFTLIQDRKV

Q

>WP\_002851803.1 MULTISPECIES: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase [Campylobacter]

MLKIQGVKHFEKSRFFPFFSQNIRSFKYLALIGLGSNIEPEKKRFDMLFRVMMDDKRFKILSTSPMLINE

AFGFKEQKDFTNAVMLIQTNLHARALLKVLLYYEVKFKRKRTFKNAPRTLDLDLLYFSQKVKRDKWCEVP

HKGAKERVSVILPLGMI

>WP\_002851758.1 MULTISPECIES: ribonucleotide-diphosphate reductase subunit beta [Campylobacter]

MQRKRIYNPSSNETLGDRKVFDGNPHGILNFTKAKYTWALKLWDLMEANTWFPKEVDTTKDALDYRCNLT

AGEKRMYDLVWSQLISMDSFQTNNLADNINPYITAPEINAVLARQAYEEANHSKSYAVMVEAICDNTDLI

YEMEKHDETLREKNDFISSIYEELAGDVDDNKLLLAMVANQILEGVYFYSGFTAIYALARAGKMLGSAQM

IRFIQRDEITHLLLFQNMINSVRKERPDLFHDENINKIYDMFKKAGDLEIKWGKYITQNQIMGFTDDIIE

EYIHYLVDQRLSAINLDKLYNAKHPIKWVDDFSKFNDQKSNFFESKVTNYSKGSISFDDF

>WP\_002793551.1 MULTISPECIES: 50S ribosomal protein L33 [Proteobacteria]

MRIKVGLKCEECGDINYSTYKNSKNTTEKLELKKYCPRLKKHTLHKEVKLKS

>WP\_002866159.1 hypothetical protein [Campylobacter jejuni]

MQIKLDNLNSYIPKDIVDNIEKYDNEHFYKINHIIKSKHKGFFDFDEKSKNPTSPLNPWAYIRVKNEALT

LKASLKSILPAIQRGIIGYNDCNDGSEEIILEFCKQYPSFIPVKYPYEVQIENPQSEENKLYSYYNYVAS

FIPQGEWLIKIDVDHIYDAKRLYKSFYIPKKDYDIVVYSKMDFLINDEDAFIVKYKNLNAIINNKSNDHW

LIKNNHLKWAESMHEDRYCIEYLDVKKLKIYQTEFLNYHFPYFKRSLDKNKIELIPIDDFSIKEYKDIIS

PDMVTKEKLLYLKKYIKENQ

>WP\_002866078.1 MULTISPECIES: hypothetical protein [Campylobacter]

MYHLLDFSTCKCENEKFDLAYKIFKQDFIEVPLYLAGCIYIDPQSHKKHKGKEKIFWHITTRENKQNKTR

EFDSQRACRINWIKQIIINHTHPEIKAFYYKEKRAIRFYLWLYNHNFIVILQKLGRSSSFLVTSFYIDKG

YNKNIYEKRYRNYINGNDIELKNCEWF

>WP\_002877369.1 MULTISPECIES: adenylosuccinate lyase [Campylobacter]

MTGISVFDHRLLADSWSTQEMRAIFCEQNRIQKWLDVEAALAKAQAKLKIIPKKAADEIAKKAHYKFMDM

DFIFAEFKKTKHPLVPTVRGLEKACDNNLGEYVHFGVTTQDIIDTGLVLQFKEAMTLVKSELKAIAKALA

KLAKTHKNTAMMGRTLALQALPITFGHKVAIWLSELERHFERILELEKRLYVGSIVGAVGTKASLSDECN

EVEKLTLENLGLDVPNISWQPARDRFIELGFVLGNINATFNKIAHEILILSHNEIDEVAEPFGKGQVGSS

TMPHKRNPAVSENAVTISNAFKANLAILSDIERHEHERDGQVWKMEWKLLPEMFLMLSVVLANMKFALSD

LEVKKDKMLKNLNTLNGFVLAERVMFALSDHYGKQHAHEIVYENAMLGIEKQKTFKEVLLADKRVSKVLK

EKEIDALLDATTYVGYAPKLVDEFLAKIKNSAILK

>WP\_002851453.1 MULTISPECIES: 50S ribosomal protein L5 [Campylobacter]

MMRLKEKYNQSIKPALVKEFDIKNPMLIPVIEKVVISVGAGELAKDQKVLQNVADTISLIAGQKAVITKA

KKSVAGFKVREGFPVGVMVTLRKENMYAFLDKLISIALPRVKDFRGLSRDGFDGRGNYNFGLDEQLMFPE

VEYDKILRTHGMNISIVTTAQNDKQAQKLLELIGVPFTKGK

>WP\_002851353.1 MULTISPECIES: 30S ribosomal protein S8 [Campylobacter]

MINDIISDSLTRIRNAGMRKLETTKLLHSKVVEALVGIFQAKGYIESFNVIEEDKKKFINVVLKYDEKGK

SVINELKRISKPGRRVYKGKDEIKRFKNGYGTIVVSTSHGVLANDEAYKAGVGGEILCTIW

>WP\_002866554.1 signal recognition particle protein [Campylobacter jejuni]

MFELVSESFKSAINKLRFVDDEKALKNALETLKKALLKADVHHKVTKELLTLIEEDVKQNGIGQKQFLNA

IKVNLENILSVNGKNQGFVFASKPPTVVLMAGLQGGGKTTSTIKLANYLKLRNKKVLVAACDLQRLAAVE

QLRQLCEANEIELFFIENEKDPIRVAKEALKKAESSMVDVLLVDTAGRLAIDEALMNELKAVKDVLNPDE

IFYVADAMSGQDGVKTAASFNEALNISGVILSKFDADTKGGVALGIAKQIGIPLRFIGVGEKVADLEVFI

PDRIVSRIMGEGDLATLAEKTAAIIDEKEAKKLNQKIKKGEFNFNDFLNQMESIKKLGSMKSLIGMIPGL

GGMANAVKDIDLDNSKEIIRIKAMISSMTPKERENPDLLNNARKRRIAEGAGLSQVEVNRFLKQFSNAAK

LAKRFSGKKGMESLTQMMSQARRQF

>WP\_002856384.1 MULTISPECIES: 50S ribosomal protein L23 [Campylobacter]

MADITDIKTILYTEKSLNLQEQGVVVIQTSPKMTKTGLKAVLKEYFGVTPKSINSLRMDGKVKRFRGRLG

QRNDYKKFYVKLPEGVSLENTEA

>WP\_002851509.1 MULTISPECIES: 30S ribosomal protein S19 [Campylobacter]

MARSLKKGPFVDDHVMKKVIAAKKANDNKPIKTWSRRSTITPDMIGLTFNVHNGKSFIPVYITENHIGYK

LGEFAPTRTFKGHKGSVQKKIGK

>WP\_002851138.1 MULTISPECIES: 30S ribosomal protein S3 [Campylobacter]

MGQKVNPIGLRLGINRNWESRWFPTKANLVENIGEDYKIRAFLKRKLYYAGISQILVERTAKKLRVTVVA

ARPGIIIGKKGSDVDNLRKELQDLIGKDVNINIKEERKAGASAQLAAESVATQLEKRIAFRRAMKKVIQG

AQKAGAKGIKVSVSGRLGGAEMARTEWYLEGRVPLHTLRAKIDYGFAEARTTYGNIGVKVWIFKGEVLHK

GMQPEKTEESAPAKKPRRTRRGK

>WP\_002856574.1 MULTISPECIES: 30S ribosomal protein S4 [Campylobacter]

MARYRGPVEKLERRFGVSLALKGERRLAGKSALDKRPYAPGQHGARKGKISEYGLQLREKQKAKFMYGVS

EKQFRRLFAEAARREGNTGVLLIQLLEQRLDNVVYRMGFATTRRFARQLVTHGHVLVNGKRVDIPSFRVE

AGAKIEIIEKSKNNPQITRAIELTAQTGIVAWVDVEKDKRFGIFTRKPEREEVVIPVEERFIVELYSK

>WP\_002854670.1 MULTISPECIES: flagellar motor switch protein FliG [Campylobacter]

MIKLSEEQKMVYDDLSMPEKVAIFLIQLGEDATTSVFSHMEIDVITEISRYIAMAKNVDRSVATAVLEEF

YTLLQSNQYIKSGGLEYAKEILFRTFGPEIANKILEKLTKSMENNQNFAYLAQIKPQQLADFITKEHPQT

IALILAHMDSIHAAETLEYFSDELRAEVVIRMANLGDISPSIIKRVSAVLESKLESLTSYKVEVGGPRAV

AEVLNRLGQKASKSTITYIEQSDERLAETIKELMFTFDDIQKLSTQAIREILKVADKRDLMIGLKGASEE

LKQKFLANMSTRASEAFLEEMGFLGAVRVKDVEDAQRKVVEVVQKLAEQGLVQTGDADEMIE

>WP\_002867023.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKKILTSALALGAMTLIIGCGDGDLVELKNNGNDQAMFDLGNQEIMKKYPNYKLYDYTSVRAISDFKDPE

GKIKEMKRDLEIDKTPYSNYVFLLNPNDKKDYKVVSVYCDKDFKKRIYCSVNDAFRFYAR

>WP\_002831077.1 MULTISPECIES: glutathionylspermidine synthase [Campylobacter]

MQLLQVDKLQKDYLENIGFSWHTDEDGSDYISNKLVCVKESEANAYYEAVNELYDMFIAAAQEVIDNDRF

DELGIPFNLIDAIKMSWENEVHWHLYGRFDLAGGLDGKPIKLIEFNADTPTALFESAILQWALLKQNGMD

ESAQFNSIYESLMDNFKRLITLDESVEGFEEHYQGWKILFSSVAGSKEEEITTKLLSHIANEAGFQTNFS

FVDEVEFSEEGIFKEGENYEYWFKLIPWEDIAIEEGELAMLLTQIMRNQRAIILNPAYTLLFQSKGILKI

LWELYPNHPLLLETKDTPLEGKNYVKKPVFGREGANISIIKDGKTLHENVGPYGNNKAIYQEYVEFNSCE

NEYYQAGVFFAYEGCGLGFRKGGLVLDNYSKFVGHIIKD

>WP\_002826386.1 MULTISPECIES: glutamate racemase [Campylobacter]

MKIGVFDSGVGGLSVLKSLYEARLFDEIIYYGDTARVPYGVKDKDTIIKFCLEALEFFEQFQIDMLIIAC

NTASAYALDALRAKAHFPVYGVIDAGVEATIKALHDKNKEILVIATKATIKSEEYQKRLLSQGYTNINAL

ATGLFVPMVEEGIFEGDFLQSAMEYYFKNITTPDALILACTHFPLLGRSLSKYFGDKTKLIHSGDAIVEF

LKERENIDLKNHKAKLHFYASSDVESLKNTAKIWLNL

>WP\_002826203.1 MULTISPECIES: ATP-binding protein [Campylobacter]

MQIDASKNQSFSMDYTTKSGKHLALSMYDNQSVSYANNEEGKTLNLKRQYGFSFTFEGSKLTQNDLDEIK

NAMKEVEPMIKDFLANSKVGELKPKEIIESAMQMANVLPTPNDENHQNAIMNNFTNKLSDLLKQNQTDDK

DINASMLEDSKKLLDEVLEQMKKQLEKQQEKAKENQDKTDDSLNLYA

>WP\_002826100.1 MULTISPECIES: leucyl/phenylalanyl-tRNA--protein transferase [Campylobacter]

MESSNLYSKLLNAPKNAPVFLSQNLEADFIVKAYTFGLFPWTSKPVTWWCPDPRCILIPNQIHIQKNMKK

FINLYQIKLDYDFLKLITLCRDTRSQSWIDDEFITTYYKLFTQGYAHSLELYENNELIGGIYGLILGKVF

FGESMVSIKKNASKVAMIKLCDLLKPYDFIIDCQVYNQHLEFMGAHNISRKEFLNILKEKCNQESGFKNF

KDLIT

>WP\_002825501.1 MULTISPECIES: 50S ribosomal protein L2 [Campylobacter]

MAIKTYKPYTPSRRYITGLSSEDITAKPSVRSLLVKLPAHAGRNSYGRITSRHKEAGAKKLYRIIDFKRR

KFGIEGKVEAIEYDPYRNCRIALIAYKDGEKRYILQPRGLSVGDIVAAAESGLDIKPGNAMKLKNIPVGT

IVHNVELKPGKGGQMIRSAGAYAQLMGKEEKYVILRLASGEMRQVLAECMASIGEVGNEEWANVTIGKAG

RNRHRGIRPQTRGSAMNPVDHPHGGGEGKKNSGRHPVTPWGKPTKGAKTRRKKASDKLIISRRKGK

>WP\_002825033.1 MULTISPECIES: phosphate-binding protein [Campylobacter]

MKKILSLSVASLALCGALNAADLKIAGSSTVYPFTSFVAEEYASIKNTKTPIVESLGTGGGFKVFCEGTT

DISNASRPMKLSEFETCKKAGVTDIVGIMIGYDGIVLAQNKTNAPLNITKKELFLALAKEIPQNGKLIPN

PYTNWNQINKNLPNRKISVYGPPSSSGTRDTIEELVMSDVSKKIPEYKGEYKTIRQDGAYIPSGENDNLI

VSKLTIDKDAFGIFGYSFLVSNSDKINAANIDGVTPSEESIADEKYELARSLFIYINAKKNPKEAFEFAK

IYMSDDLAKSGGELEKIGLVPLSDDKLKASQKHVEDRKILNDELVKAGKVF

>WP\_002824979.1 MULTISPECIES: hypothetical protein [Campylobacter]

MRRVDLRKSKELFEDLAQIIKEAKQGEVLVVLFEIGDFSPVEKSFSFVKEQGCELLNSLKFNQVDWTIVI

KKERV

>WP\_002824972.1 MULTISPECIES: NADH dehydrogenase subunit A [Campylobacter]

MSHIDASHPYFGIFLMLVLASVIFFGLVFLASKIGNNFAAKNRKKLGLGIYECGPIPVKQANKINSQFFI

IALIFILLDIEVVFLFPWALIFKDLGWFGLLEVFVFIVLLGVGFLYAYKKGAFAWQSIK

>WP\_002824739.1 MULTISPECIES: flagellar motor switch protein FliN [Campylobacter]

MSDDIEFNIHHGLLQSYEDILDITVDFVSELGTTNMSVAELLKLEVGSVIDLEKPAGESVELYINKRIFG

KGEVMVYEKNLAIRINEILDSKTVLQYFKKEI

>WP\_002822505.1 MULTISPECIES: hypothetical protein [Campylobacter]

MRKILFASLLPIIALADCASLMAKYEAPEPESKTMKQVERWINKKVSDPADAAVLKECMIARAADNPNQV

SVAGK

>WP\_002819467.1 MULTISPECIES: membrane protein [Campylobacter]

MDILKLAIKDFLSLKFLKFALIPLIFSLILMLFLGVLGFSALLDYFNSLFSVGEDSFWAWFYALHFVQIL

ITIISFLFSGFIVVFASVFLALFITSFLTPFIAKEINQKYYHYDNTNEVSTLKTIFEIFKIFIKFIGILL

LCTLALFLPFINIFVYYLAFYYLFHKLLMIDVTSTILDKESFKNFHSDFSPLEFKFSTLCFYLLSSVPLL

GLFLQVFFVIFLTHLSYQRILKLKAKA

>WP\_002816248.1 MULTISPECIES: ATP-dependent dethiobiotin synthetase BioD [Campylobacter]

MQIYVSGIHTDVGKTHFSAAFCANFNYDYFKLIQAGTPTDSEFIAKFSPKTKIFKEGIFLQTPASPHLGK

IKEKLDYKALDIILPKSKNLLIELAGGLFSPMDENYTMIDFVNIFKHPTILVAKYYLGSINHILLSIEAL

KQRNINLLALVMMGKKDILQDDFIKNYAKIPIINLDFFDENSILNKDFKEQMQEILQLKIP

>WP\_002816245.1 MULTISPECIES: 8-amino-7-oxononanoate synthase [Campylobacter]

MKLEKILQDLEQNHNLRTLTPLKHENKFVYKQDHKLLNLVGNDYLYLASSKELKAEFLNTLKEQDLFFSS

SSSRSLSGNFEIYEKLESFLKTKFKDKEILHFNSGYHLNISCIAALSSVSKTLFLTDKFIHASMIDGLRL

GRADFFRFHHKDMNHLESLIQKHYENYENIIVLSEALFSMDGDFSDFKTLCELKRRYDKIKLYIDEAHSV

GCFDEEGLGLVKKLALENEVDFLVFTFGKALASMGACIICDEKYKKFFINKARAFIYSTALPPINVAWTQ

FIFKKMPYFKKEREKLELLSTFFKSKLQEKNHIVLGDAYIICLLLGENKKALEISQKLQKAGFFAPAIKE

PTVPKNTARIRFSLHAGLNTEELERIIELL

>WP\_002816233.1 MULTISPECIES: GTPase [Campylobacter]

MIRIDINHPMNTAKGRLDLNFKKDIESGKITALFGESGAGKTTLLKIIAGLIKPKLGRIEVDNELWFDSS

KNFSLALQKRKIGFVFQDYALFPNMNIKENIAYAASSKAKVSELLALMKLENLAKIYPKHLSGGQAQRVA

LARALAREPKILLLDEPLSALDFKMRANLQDELTKILEYFKISTLLVSHDLAEIYKLSHRILELKNGKII

KDFPKNEFFTHSNISAKLRLSATLLEIKKSDILVVLTLLLNQDIIKITLSEEEFLKAYQDVKIGDTLLLS

IKAFNPIIVGKLDK

>WP\_002812871.1 MULTISPECIES: CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [Campylobacter]

MNLPNILAIFRMVLAPLLFFLLIHKFENIHQSWINYFAALTFSLAALSDFFDGYIARTWKQTTKLGGILD

PLADKMLVLAAFLGLLLTGKANEWVIYIILVREFFITGFRVVMISENLNVNASFAGKLKTAFQMTAIGFL

IMEWIGGEILLYIALILTLYSGFEYIYTYIKAQKKGEK

>WP\_002812868.1 MULTISPECIES: 30S ribosomal protein S6 [Campylobacter]

MKHYEVLFILKPTLTEEEVNAKLEFVKEVLTKNGAEIETVVPMGTRKLAYKIKKYERGTYFVIYFKAPTN

LIAELERVLRITEEVIRFLIVKYENKKEIAAWEKLSHGIKQSKKEIKPLDAPEIQ

>WP\_002806309.1 MULTISPECIES: ATP-dependent Clp protease proteolytic subunit [Campylobacter]

MFIPYVIEKSSRGERSYDIYSRLLKDRIIMLSGEIHDELAASIVAQLLFLEAEDPTKDIYLYINSPGGVI

TSGFSIYDTMNYIKPDVCTICIGQAASMGAFLLSCGAEGKRFALPNSRIMIHQPLGGARGQATDIEIQAK

EILRLKTILNDILAKNTKQKVAKIAKDTERDFFMSAQEAKEYGLIDKVLEKSFK

>WP\_002801091.1 MULTISPECIES: lauroyl acyltransferase [Campylobacter]

MKNSDRIYLSLYYILKFFVTFMPECILHFLALIVARITFYLNKKHRKIIDTNLQICFPQYTQKERDKLSL

KIYENFAQFGIDCLQNQNTTKEKILNKVNFINENFLIDALALKRPIIFTTAHYGNWEILSLAYAAKYGAI

SIVGKKLKSEIMYEILSQSRTQFDIELIDKKGGIRQMLSALKKERALGILTDQDCVENESVRLKFFNKEV

NYQMGASLIAQRSNALIIPVYAYKEDGKFCIEFFKAKDSQNANLEELTLYQAQSCEEMIKKRPWEYFFFH

RRFASYNQGIYS

>WP\_002800974.1 MULTISPECIES: 50S ribosomal protein L27 [Campylobacter]

MAHKKGQGSTQNNRDSIGRRLGVKKFGGEFVRAGNIIIRQRGTATHAGNNVGMGKDHTIFALIDGFVKFE

RKDKDRKKVSVYPA

>WP\_002800301.1 MULTISPECIES: permease [Campylobacter]

MQVFFSTFKEFLYLFVELSVLFIGINILVAFLNAKYSNFFEKHLKQDNFQTRLKAIFFGSLTPFCSCSSI

PLLNAFLKAKVPLSVCMAYLITSPLINPIIIVVFIVSFGIKISFIYIGFLYAIILFISFLLSKFDTSKFL

NNDFLENEFNEKSSCCSTKKCCSSKTHINLKQICIDSLKEYKKILPYALAGTFIGALIHGVFPSNFFEIY

LKDYGILGVFIAAFIGVLLYMNCTAMIPVALVLTQTGIPLGIMMSFLIAGSGCSLPELILLKRNFKTSFL

ILFALLIILIAILFGILMFFI

>WP\_002800121.1 MULTISPECIES: 30S ribosomal protein S13 [Campylobacter]

MARIAGVDLPKKKRIEYGLTYIYGIGLFTSRKILDKVGISYDKRVHELSEDEAAAIRKEIQENYMVEGDL

RKQVAMDIKALMDLGSFRGLRHRKGLPVRGQKTKTNARTRKGKRKTVGAKS

>WP\_002799865.1 MULTISPECIES: hypothetical protein [Campylobacter]

MDFENQLNAIVETIAERKTLVNTEEATKMTFIMPFLKTLGYDVFNPSIVVPEYTADIGTKKGEKVDYAIF

KDSKPFILIEAKNHTENLDNHNNQLVRYFNTNPSIKFAILTNGIEYRFFTDIEQQNLMDKIPFLVVNLEK

LKPRDIKDLKRFICTDLNLDEILSIAMEKKYYRSIQEIFKSEIENPSDEFTSFFAKQMTEKRMTSAVLEE

FKNYIKKSFKEIINDLAYEKITSIKNNLQNINDDENDEQIDESKDIVTTEEELQGFYIVKSILASVSANL

EDVSYKDTLSYFSILYQGKVTKWICRLYFNTSKKSISFPDGASYNIEKLEDIYQYKADIIKAFESRK

>WP\_002787417.1 MULTISPECIES: ABC transporter permease [Campylobacter]

MKEKFLAFLSILPFFIVFTFFMIAPLIWIVFNAFYVEEDEIYSLANFIHIFESKFYLQSIINSLQISFIS

SIFGLLIGLLASYSLFVLAPSKICKFLFSLNTMISNFSGVPLAFAFIIVLGSNGVVNVFLKNLGIEPFVS

VYANFGVNIVYVYFQIPLAILLLLPAFKSLENSHLNACKMLGGGNFLYWLKIALPLLAPALFGVFVILFA

NAFGAYATIYALSSGNFNVAPVRIAALIAGDINLDPYMASALSIIITIIMLVVTFIANFLSKKYHFKVL

>WP\_002786346.1 MULTISPECIES: preprotein translocase subunit YajC [Campylobacter]

MAENSILTSLLPLVVLFAIFYFLVIRPQQKQAKAHKQMLESLQKGDKIITNGGLICEVVKPEEDFIKVKL

NEDNVTAKISREFIAKKIDA

>WP\_002785902.1 MULTISPECIES: hydrogenase formation protein HypD [Campylobacter]

MNFIDEFRDKESILALKKLIEQELKNPINIMEICGGHTHSIMKYALPSILPKEINFIHGPGCPVCVMPRV

RIDTAIKLASMKDTIFCTLGDLLRVPGSEISLLDLRAKGADVRALYSPLEVLEIAKQNLNKNIIFFAIGF

ETTTPMSALLLQKVIEEKINNVFFHINHITVPAPVEAIMNDENVKINAFLGPSHVSVITGYGIYEPLAAK

FKTPIAVSGFEPVDILESVLNIIKQSNEGTFKVYNQYKRAVSKEGNVKAQNLVKKYFRVCDFEFRGLGLI

KDGGLELKEEFSAYDASKKFDCTVQSKNESKACICGQILRGLAKPYDCKVFGKACTPRSPIGSCMVSGEG

ACAAYYKYSKVNV

>WP\_002785535.1 MULTISPECIES: 50S ribosomal protein L18 [Campylobacter]

MRANVLKRKLTLRIKRKKRIRAKISGCENFPRISVFKSNRTLYIQAIDDVKAVTLAAVDGRKLGVKANKE

GAKKIAAEFAKTLKAKKIEQAVFDRNGYVYHGVIAALAESLRENGIRL

>WP\_002785057.1 MULTISPECIES: hydrolase [Campylobacter]

MKKAFVLVDYQNDFIDGSLGFDKALKIKENILKALNQIDFNNTHLLLTYDTHDEHYLQSKEGLNLPVKHC

IKESLGWQMPKEFEPFLQKAHKIFYKNTFGSLELANFIQKSDYEELHFAGLVSHICVFCNIILAFGAKPN

ARIILHQNLSASFDENLEKSAFDILRAYGIEIV

>WP\_002784057.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKVDNFLNTYSMNSALLDRAAKARSLESSIKINDNDIVTKSKEDEALKEQTDAFEAFFLKQVLDVSLKSQ

NSLFGKDASDEIYSSMYNDTMSKALSGGMGFSKLLYDFLKERG

>WP\_002783229.1 MULTISPECIES: 3-methyl-2-oxobutanoate hydroxymethyltransferase [Campylobacter]

MRKSMISFLEKKAKNEKITMVSAYDYHSARILDNSDIDIILVGDSLAMTVLGMQDTLSVTMDEMLIFTKA

VSRGAKKSFVLADMPFMSYQSSDRDAILNASRFIKESHANGVKVEGGIEIASKIKLISQSGIPVVAHLGL

TPQAVNMLGGYRVQGKDLQSAQKIIDDAKAVQDAGACMLVLECVPVKLAQKISSILEIPTIGIGSGKYCD

GQVLVYHDLLGLNKDFKAKFVKHFDKIDPQVGVEKYRDEVKSGIFPSQEHSFDYLDDELLDKLY

>WP\_002781429.1 MULTISPECIES: 50S ribosomal protein L36 [Campylobacter]

MKVRPSVKKMCDKCKVVRRKGVVRIICENPKHKQRQG

>WP\_002780697.1 MULTISPECIES: 30S ribosomal protein S21 [Campylobacter]

MPGIKVHPNESFDEAYRKFKKQVDRNLVVTEVRARRFFEPMTEIRKKQKISARKKMLKRLYMLRRYESRL

>WP\_002779987.1 MULTISPECIES: 50S ribosomal protein L3 [Campylobacter]

MEYIVEKIGMSRTITNPSIAVTLLRVVNAKVCEVEGGKALVAYPKGKASNKCVAGQQKKYNLSAEYNRFA

TLEVANTEAGDLDETPLNEAKILKVSFNTKGRGYSGVMKRHNFAGGPASHGSRFHRRHGSIGNREWPGRV

QPGMKMAGHYGNTKVTVKNEVVSYDAENKILVVKGAVPGYNGAMGKIRIAK

>WP\_002779544.1 MULTISPECIES: 30S ribosomal protein S11 [Campylobacter]

MAKRKIVKKKVVKKNIAKGIVYISATFNNTMVTVTDEMGNAIAWSSAGGLGFKGSKKSTPYAAQQAVEDA

LNKAKEHGIKEVGIKVQGPGSGRETAVKSVGAMEGIKVTFLKDITPLAHNGCRPPKRRRV

>WP\_002779495.1 MULTISPECIES: hypothetical protein [Campylobacter]

MKNIVFHSDGFGDLLVCFKALYAIKQLYPEYKLFLLTNGLMESDFLEKIPFIDEVLIYKDDFLEKIQSKN

PVIFITTRRQGLYFKKLKFLNVQKCIVFPHLISIISKNLTTPLPFFRAKKHMSEIVLKLVRMINTRHFDK

NFNQIDFSKIKNLLPYDARLSDNFFKQIDTKYEKIIGINAFSNNSEYRGFNFFIKDWIGLARQLSLKYPK

FLFILLNFSTNSIQYNIDQNANLKVFCNNKNIASLVSISQKLDFLITVDTGNLHLCDILQIPTLAFTSSL

AAYRFGGGSYGGRFDKLIVKPAWQKEYRKIYEIFTKKAENNLENL

>WP\_002779471.1 MULTISPECIES: 30S ribosomal protein S7 [Campylobacter]

MRRRKAPVREVLPDPIYGNKVITKFINSLMYDGKKSTATTIMYGALEAIDKKGGEKKGIDIFNDAIENIK

PLLEVKSRRVGGATYQVPVEVRPARQQALAIRWIISFARKRSERTMIDKLAAELLDAANSKGASFKKKED

TYKMAEANKAFAHYRW

>WP\_002779452.1 MULTISPECIES: 50S ribosomal protein L11 [Campylobacter]

MAKKVVGEIKLQIAATKANPSPPVGPALGQQGVNIMEFCKAFNERTKDMAGFNIPVVITVYADKSFTFIT

KQPPATDLIKKAAGISKGTDNPLKNKVGKLTRAQVLEIVDKKIADLNTKDRDQAAKIIAGSARSMGVEIV

D

>WP\_002779441.1 MULTISPECIES: 50S ribosomal protein L16 [Campylobacter]

MLMPKRTKYRKMMKGRNRGYANRGTEFTFGEFALKATEAGRINSRQIEAARIALTRFVKRQGKTWIRVFP

DKPLTKKPLETRMGKGKGAVEEWVMNIKPGRIIYEMAGVSEEMAREALTLAMHKLPFKTKFVTRESQNEI

Y

>WP\_002779438.1 MULTISPECIES: 50S ribosomal protein L14 [Campylobacter]

MIQSFTRLAVADNSGAKELMCIKVLGGSKRRYATVGDVIVASVKKALPNGKVKKGQVVKAVIVRTKKEIH

RDNGSLIRFDENAAVILDNKREPIGTRIFGPVGREVRYGGFMKIVSLAPEVL

>WP\_002779437.1 MULTISPECIES: 50S ribosomal protein L24 [Campylobacter]

MAVKLKIKKGDSVKVITGDDKGKTGKVLAVYPKTLKVVVEGCKIAKKAIKPSEKNPNGGFINKEMPMDIS

NVAKVQE

>WP\_002779428.1 MULTISPECIES: 30S ribosomal protein S5 [Campylobacter]

MEKYNREEFEEVIVDIGRVTKVVKGGRRFRFTALVIVGNRKGLVGVGYGKAKEVPDAIRKAVDDAFKNIV

EVKTKGSTIAHDVEVKYNASRILLKPASEGTGVIAGGSTRPIVELAGIKDILTKSLGSNNSANVVRATIK

ALTMLKG

>WP\_002779353.1 MULTISPECIES: 30S ribosomal protein S10 [Campylobacter]

MERIRLKLKAYDHRVLDRTVAAIVEAVKRTGADIRGPIPMPTKIKRYTVLKSPHINKDSREQFEIRIHAR

MLDIVAATPDTVDSLTKLDLAPEVSVEVRAMGK

>WP\_002779321.1 MULTISPECIES: 50S ribosomal protein L13 [Campylobacter]

MTKITKPNEVKREWIVLDAEGKRFGRLLTEVATILRGKNKPCFTPNVDCGDYVIIINASKAVFTGANKAE

DKLYHRHSGYFGSVKSEKFGDLLEKNPAKLYKLAVRGMLPKTNLGRAMLKKLKIYAGSEHPHTAQIAKEG

K

>WP\_002779270.1 MULTISPECIES: dihydroneopterin aldolase [Campylobacter]

MEFLELLLVLIALILIIKKPEKENLAFGLVMVAWLLMVFFYVGHKTGALLTIMNL

>WP\_002779262.1 MULTISPECIES: hypothetical protein [Campylobacter]

MINPIQQSYVANTALNTNRIDKETKTNDTQKTENDKASKIAEQIKNGTYKIDTKATAAAIADSLI

>WP\_002779147.1 MULTISPECIES: hypothetical protein [Campylobacter]

MTLNELKDGQKAIIVNLNAHKELKNRLLSFGFIKNKNLKKIHSSLKNATIMVELDTSCVILRSDEAKTIE

VNLI

>WP\_002778908.1 MULTISPECIES: hypothetical protein [Campylobacter]

MLKIILVLSILSSFAFANSCANYEQELKKCNSLKNSHERKMCRLGLFAKCKKG

>WP\_002778842.1 MULTISPECIES: iron transporter [Campylobacter]

MIKKVLSVVAAAAVISTNLFAGEVPIGDPKELNGMEIAAVYLQPIEMEPRGIDLAASLADIHLEADIHAL

KNNPNGFPEGFWMPYLTIAYELKNTDTGAIKRGTLMPMVADDGPHYGANIAMEKDKKGGFGVGNYELTFY

ISNPEKQGFGRHVDEETGVGKWFEPFKVDYKFKYTGTPK

>WP\_002778820.1 MULTISPECIES: 50S ribosomal protein L21 [Campylobacter]

MYAIIKHSGKQYKVSVGDELKLDHFEAESKASIEVSEVLAINDKELKVGAPFVAGAKVVLEVINHGKDKK

VVIYKKRRRKDSKLKRGFRRQFTRVVVKDIKA

>WP\_002778650.1 MULTISPECIES: ribosome-binding factor A [Campylobacter]

MNPSEIKKLRTESILKELIPEALANLDDENLKNLCVVDVECKKGRYDAFVYLDKMFFNVHEQEKILSSLK

KASRALQNYCMSEQGWYRCPNFHFKFDDRLEYQNHMDALFEKIKKDKNES

>WP\_002778401.1 MULTISPECIES: transcriptional regulator [Campylobacter]

MTKKSKRDMAYELDIDVSTLYNWRKYKPNLYRIVMLGFKFDELLENSKKTHEELLHIEQTIQDEIAKFK

>WP\_002777995.1 MULTISPECIES: 50S ribosomal protein L35 [Campylobacter]

MPKMKSVKSAVKRFKVGKNKIKRGSAFRSHILTKKPAKRMRDLRTAKYVHSTNVKAVEKMLGI

>WP\_002776864.1 MULTISPECIES: 50S ribosomal protein L34 [Campylobacter]

MKRTYQPHGTPRKRTHGFRVRMKTKNGRKVINARRAKGRKRLAV

>WP\_002776559.1 MULTISPECIES: ABC transporter substrate-binding protein [Campylobacter]

MSKKFFLSLGLVALLFSNSQAIDENLIKAAQAEGRVNSLAMPDTWANWKDTWADLKNLYGIEHSDTDMSS

AQEIAKFKAEKKNASGDIGDVGASFGEIAVKQGVAQPFKTSYWDQIPTWAKDKDGNWLLAYTGTIAFIVN

KDVVKDIPKTWQDLLKGNYKITVGDVSVAAQAVSAVLAANYALGGDEKDLSPALAFFNTLAKQGRLVNND

VSIANLEKGEVEVGLVWDFNGLGYRDKVGKDRYEVLIPADGSVISGYTTIINKYAKHPNAAKLAREFILS

DKGQINLAKGYARPIRIDHITLPDDIKAKLLPSEQYKNARAIKDQKAWEKSAKELPQLWQEKVIVDMK

>WP\_002776146.1 MULTISPECIES: flagellar protein FlaG [Campylobacter]

MEISKANGQMDTALANISQRTSETQASLNIQTDRSQGQEGDDGQQRGVSEKLADITKKLNEQMDSLDTNV

RFGYSDKIGSMYISVTEKSTGREIRQIPSEEAMRLAEYFRDVIGMIFDKES

>WP\_002854538.1 diaminopimelate decarboxylase [Campylobacter jejuni]

MDYKQLKQEFNTPFYIYNFDFIKERFLNLKEAFKARKSQIFYAVKANSNLSLLQMLANLDSGFDCVSIGE

VKRALKAGAKAYKIIFSGVGKTKEELRQALEYDILYINLESEAEMMLLESVAKELNLKARISIRVNPNVD

AKTHPYISTGLNENKFGVEIDIARKMYLYAKNSSFLEPVGVHFHIGSQLLDISPIHEAAGIVAKLVRELK

ALQIDLKFFDIGGGLGVAYEKDECEPDLYNYAQGILAQLHGLDLTIGMEPGRYLVAKSGEFVCSVLYEKQ

NKTKRFVVVDGAMNDLIRPSLYEAYHEIILPYNQAQESLCDVVGGICESGDFFAKARSLPSTQSGDIMVI

KNTGAYGFSMSSNYNTRNKVCELALEEGQVRLIRQRENFENQIALEEKFLKA

>WP\_002851559.1 capsule polysaccharide transporter [Campylobacter jejuni]

MLNVIYALFFRELKTRFGKNRYLGYIWVVGEPMSIVLLVTIIGTIVREYHHQVMPEGISIFMFLISGIMP

FFMFRSIVTQLMNGTQANLALFAYKPVKPIHVFIARTLLEFCIYFVIFIIILFFAGWFFRLDVFPVHLLG

VLFCIFLLICSAFALGICFAIIWHFVEPLRTLLAYFSIVFYWTSGIIFPTWLTPRPLLDIFYYNPLLHIF

ELLRFNFFENYPLQDEYSYFYAIFWILLVLFIGLFIYYYNRQALTAVKKE

>WP\_002851485.1 sugar ABC transporter substrate-binding protein [Campylobacter jejuni]

MKKILILLFSCILCFGAVDVSQIISAEDQGSATTSIDQNLSSNYDIANKENNLTKIHQILVFGAHLFNGN

FKNYNQRVYNPDYKIAVGDQISLKIWGAVEFSQVLVVDSQGNIFIPKVGAVNLLGVKNSALVSVIKARVN

KIYKSNVFVYADMNAYQNVSVFVTGNVNAPGLYQGLSSDSVIQYLDKAGGINLEYGSFRDIQILRNNSVI

KNIDLYDFLLKGQMDLFPFRSGDVILVGNVQNYAFVNGDVQRPFRFELSNDIKTLADLARVSGAKPIVTN

AIVKSYGEDHKLDVSAYNKMQFSKVLLRTGDEVEFHPEYVSENITISVNGEHNGLKTLVVGKGTTLEDIS

KLIKANPQSNMQALQVFRKSVARTQKELINAQLKELETLALTSGSVTAQGAAIRAQQAKTILEFIQRAKQ

VEPKGQIVIDNPKSYNSVILEDGDTINVPSKNNLIIVQGEVSLPGAFVYDKGKDLRYYINLAGGYGERAD

TSKVLVIRSNGKAEKYHSGIDMKRGDSVLVLPKVDSENLQIFSMLTQILYQIAIATNVVLNL

>WP\_002851377.1 dUTPase [Campylobacter jejuni]

MTNIEILENMLKLQQKLNDETNGLNWENGYTKEGKLISWRRCIYMECAELIDSFTWKHWKNISSLTNWEN

VRIEIVDIWHFILSLLLEEYRDKNNKDFKAIATEVNAVSVFQDFCKEEEYPNEGDIYGILNDIELIIHKC

SGFGFNLGELLSTYFTLAIKCGLNLEILYKTYIGKNVLNIFRQNNGYKDGSYKKTWNGKEDNEVLAQILE

QELDFDTIYKKLEECYKKA

>WP\_002877301.1 mannosyl-glycoprotein endo-beta-N-acetylglucosamidase [Campylobacter jejuni]

MKPIIIFLSLFLIPLFAADDLKSGFGEEYYKLDIDQKRQIFFTKMNEMFDQSFKKIEQERAFIEAFFKDA

YKTGFRTSNQINLEKLITIKNKYRIENLYDFAEYKKRIQKIPKSMGIAQALVESATGTSRFAREANNLFG

EWTWGEKGLIPDLRHPDKKHKIKIFDSLQDSVDSYVLNLNRHFAYEKFRDARAKFESEGKEITGLEAIKT

LDSYSERKGYYINLITKIIKRYNLEKYDTNSNNT

>WP\_002866945.1 metallophosphoesterase [Campylobacter jejuni]

MIFLIFSFIVLLIFGLANVYIYKRLIKKITLFKYFYKIFAFIFIVLFLAQAVFLIFRRDEYLSDTWYEIL

AMLYAPTYCLFFMTLAWDFIKLILALMGKRDKKYNLILRLIFEFSLIVLSVFLIYISINNALKTPEVKSV

DVEIPNLKQDLKIAMLTDIHLGKNLHENFLDKLITKVNLQSPDMVVIVGDLIDTNPKDLKNYISKLNDFN

STYGTFYALGNHEYYHGINEVLDLLRKHANMKILVNQNLDLGFINIAGLGDLAGLNKGLYAPDLARIKVD

LNTSKASILLTHQPKTALLYDLSDFDLVLSGHTHGGQIFPFMFLVKLQQGFVHGLYNLGEKTKLYVSSGA

GFWGPSLRVFAPSEIVILNLKGKK

>WP\_012006799.1 ABC transporter substrate-binding protein [Campylobacter jejuni]

MKKIFFTLALFGALNLAQAKTELVVSYAYPWFKDLHEKLKEDFEKQNPDIEIRFLAPAQNYEEQSARLLR

EKMINKFPDVSFNSYSYYLHW

>WP\_012006790.1 allophanate hydrolase [Campylobacter jejuni]

MFSVHFSGSKALLLRFEQEISPQINAYVLSTEQRIQKALKEGEIYGIDELVSAYASLLIYFNPCILSLNS

LLDFLEKIKKDIKLAEQNSSLCIEVPLCYDEEFGLDLEFVCKHNQISKEELISLHTKPYYLVFMLGFMAG

FPYLGGLDERLFTPRLSSPRAKIEAGSVGIADKQTGVYPISSPGGWQIIARTPLEFFDKEDEKNPTLLKA

GMFLKFKAISKDEFFDIQEQVAKKVYQREIYEYKNH

>WP\_012006787.1 C4-dicarboxylate ABC transporter [Campylobacter jejuni]

MPIFMICSTLLAVIVVAYYILKKYNPIFVFFLSGIILLIFAFYITGTPIPKAPSREHASFLNVLLDSYAF

ITATFKSQLSGVGLIIMSVAGFAAYMKHINASAKLAFLANKPLGKIKNKYLILSGTFVVGMALKIVISSY

AGLLLLLLACIYPVLISLKIRPITAVCVLSLIALDYGPKDGNSINMADMVGQSDNVVGLFLNYQIYSVIA

YVVVIAILIPFYFAWIDKRDKEKGVLNDEVEIPQIIDPRCPTFYILFPWLPVVFLFTAYFFTIKLDVVTA

NFVSISLVFLVEFARHRNARKLGEDMMVILKAMAEIFISVVSIIIAAGVFAEGIKALGGVNILANAVSNL

GTGNFAWFGILLSIAILSFLVYFATVIMGSGIAAFNAFGKLAPDIATKLGVAPITLVLPIEIASCLGRAA

SPIAGGIIALAGFAKVAPMDIIKRTTPLLLIAMLVNVLVAFYLAQTNPLPKEQNTTKIAVSLNNK

>WP\_012006773.1 UDP-galactopyranose mutase [Campylobacter jejuni]

MKKVKNLIVGCGLSGAILAERLASKGQEVLIIDKREHIGGNIYDYKDQESNITVHKYGPHVFHTSIKGVW

EYLSRFTKWHYFMYRVKAFIDGREVNIPFNLDTLHKVFPEYLAKELEQKLVSKFAFNSKIPILELKNAND

KDLEFLAEYIYKKVFLGYTVKQWGVKPEELDFSVSARVPVYISRDDRYFVDTYQAIPKDGYTKMIENIIN

HSLIEVQLNTDFKNIKKDIEYERLFYTGAIDEFFDYKFGKLPYRSLNIVFETFDKEYMQSCPQINYPENY

DFTRSVEYKYYLDEKSSKTILSYEFPCEYEEGKNERYYPIPNDENQKLYEKYLKESAKLNNVYFLGRLGD

YKYYDMDKTVERVLKFYKEKL

>WP\_012006764.1 alcohol dehydrogenase [Campylobacter jejuni]

MSDFRYYNPVKINFNVSYEHIIDSLKTDSILLLTSKSFYKKGLTKILEDKLGDRLKGVIYDILPNPEINY

AELIKKDYRNYKEIIAFGGGSVLDMAKYFSVSGDVIRNGGNLDISNSCSFIPIFAIPTTAGTSSELTKWA

TLWDTPNNIKFSLSDENLYCKEAFYDPNLFLNIPRELTIYTALDALSHSIESIWNKNSNAISTNHAIKAI

ELILEYLPRLQNDLNSKELRLKIILASIYAGLAFSNTQTALAHAISYPITMKLGISHGLACSFTIPILLQ

CIDDVKINKLLSIYKEKIISLFHILNISTNLKSYGITKQFIEDIFDNLNSRAKNGMFDLELTKKRFLLCI

K

>WP\_012006763.1 capsule polysaccharide transporter [Campylobacter jejuni]

MRFSTKIKKEFSGKNVLLLQGPVGNFFHHLAMKMKKNQTKVFKLNFNGGDFFFYPSGTRCKCDEKDLENF

YRDFFQSKKIDAILMYNDCRIIHAKAIKVAKELEIEVWIFEEGYLRPYCITLEKDGVNANSSLPRDKNFY

LSQDIFTKESIKEILGGFKFMAFDAFLYWLFAFILAPFFNNKLHHRTLYPFEFLFWFRSLYRKYLYKITE

KKLNEKIYNLEKKYFLAILQVYSDTQIKYHYKKSIEHFIEQTILSFANHARAKSYLVFKHHPMDRGYKNY

SKLINDLSQKYHVEGRVLYVHDTHLPVLLRKALGCITINSTVGLSAILEGCPTKVCGNAFYDFEGLSYPK

KLQFFWREAHAYKPNPILVCNFKKYLLQTNQFNGNFYKNFFLDK

>WP\_012006760.1 membrane protein [Campylobacter jejuni]

MFAKLLKFFISRPKSTFFGTLFICLFLNFFAFKLSVDASAESLLLEDDADLKTFREISKHYKSDNFLLLA

FKPYDEKPFSNENLAKLKKLHEELEKAPLVERVFSIINAPLLQSSQNTDLKELLKNIPNIESQDINRTKA

QNEILNSPFYKNNIISKDGKVTGLIIYLKPDTVYNNLIEKRDLASDEKEKDQIRLAIKEHQDKQKVITKQ

SLDTIKSIVRNYEKNKDTLYLGGVSMIADDMIAYIKSDLVLYGVSLVFLLGLALYYFFRSWRFVFLPLFI

CFISLSAASGVFALLNFQITVISSNYVALVLIITLSVVVHLITHFIESTQNHPKAKVERIVLETLLAKAN

PSLYAIVTTMIGFFSLILSNIEPIIKLGIMMSIGIGLALIFSYLFLASILVLLKPKNYHKKEFKFNLLAF

CAKTALDPKKRRMIYGISVLAIILALIGILKLRVENSFVNYFKDGSEIKKGLLVIDKNLGGTLPLEVIIR

FPNNKNDQNTSDTLDSFESEFENLATQETYWFDSKKTRIAKKVHEFLENKEFVGSVLSLNSLLTLGENIN

DGKELDDFALAFLNENLPAKFKQDLLSPFVSIENNELRFSMRIVDSDPNLRRNEFLIDLKKQLNELVKND

GVEVQITGIMVLYNNMLQSLFSSQFDTLIFVILAIFILFIIVFRDLKFSVAAILVNVIPLSVVFALMGLL

GIPLDMMSITIAAIAIGIGVDDAIHYIYRFREEIKNKSLEEAIMISHLSIGSALYYTTISIVLGFSVMVS

SNFIPTIYFGILTVFVMILLLSGSLFLLPSFLITIYSKKTKFPNQYKEHILKQ

>WP\_012006740.1 hypothetical protein [Campylobacter jejuni]

MKKIIFLFGLSLASLEALSFDELIYKDEVKPSFDCSKVKDDGKSDDELMICNEIGVRNEFENKKLALADN

IYSSLYQNISKKADKKMKKDFKAISKKMLKERKICIKNMQNTKAGENPILPLLNASDCMQEAYIKALLEL

MQRAKKDTKTKEVLEQIFKNKVDKYENLLTQSLNTNKDLQDFIDSLAKEDLIDSRAKFKF

>WP\_012006737.1 C4-dicarboxylate ABC transporter [Campylobacter jejuni]

METLSQTLAERKPPLYKRIIKSLGFWVIIGIIAGIVLGYIDKELAIASKPGVDYFIGALKVLIGPIIFVT

LVLGIISLESLKKVGSIGAKAVIYFEVVSTLALAIGIFMANVMQPGHGMNLDPSQLDTKSVQKYISQTTE

VSASSEIMHILKDAMPTDIITPFTEGKTIQVLVIAIITALIISLMRIEDKQAIQRVFEVAQNFVFKILQI

IMYFSPIAAFSAMAVLIAQYGIGSLINLAYLLLVMLISCLVFIFGILGLICYFAKVNIFKFMRFISREVL

IVFATSSSESALAPLMRKLEKAGLSKATVGLVLPTGYSFNLDCTNIYLAMSLIFLAQAFNVNLSLAHEIS

ILIVLMIASKGAVGVTGSGFIVLGSTLAALGDMEISEANATLAQVLPVTAIGILLGVDKFMSEMRAVGNL

CGNSVAALIVAIWDKQIDWEKFRYAMDNPEKFHNAGMN

>WP\_012006721.1 type I restriction-modification protein subunit M [Campylobacter jejuni]

MIEEILKDSDYKLDLFSKKAIAELETKIIAKTNKNNQIIYYTNCLIRDKEIKLTPEEIVRQLYIDKLLNE

YNYPKDMIKIEFGVHFGREVKRADIVIMDKIQITVPYIIIEVKKPKLKDGKEQLKSYCNATGATMAVWCN

GKEISYYHRKDPNYFESIPNIPASNQTLPDLLKVKFTFDDLIKEDILKSQKRSLKNLVTEMEDEVLANAG

VDVFEECFKLIFIKLFDELEGVRDRTKSLEFRNYGGSDSELKQKIEKLFDKAKKKWEGVFNNDEKIKLSP

SHLSVCVSSLQNVKLFNSNLEVIDDAFEYLVNKSSKGEKGQYFTPRYVIDMCVKMLNPKKDESMIDTASG

SCGFPIHTCFYVWRSIYKERGIEASHLFTAQEKISECQDYVKEKVFGIDFDEKSVRVSKMLNLIAGDGHT

NVLYLNSIDFDRWDEWVKDDEDWQDVYFEGFKRLKNLRVTKNQNRDFNFDVLMANPPFAGDIKESRILAR

YELGKKENGKPQSKVGRDILFIERNLDMLKPGGRMAIVLPQGRFNNSSDKYIREFIAQKARILAVVGLHG

NVFKPHTGTKTSVLFLQKWDDKLCPKCEDYNIFFATMNEPSKDNSGEKIYYPLLDSHDHLVVKHDLFHPH

LEGDEPIKQKDESQEEFDKRIQEYRLNVEKYKDLQKDGIAEAFIEFAKAENLSFWKE

>WP\_012006687.1 hypothetical protein [Campylobacter jejuni]

MKKILILSLVAASFLNAEILVYGPGGPAPVLKELALKFEEKTKEKVIVTAGPTPAWIDKAKENADLIFSG

NTSMMDDFAKKFPSLSLENLSVLNVRPSGIIVRPNNPKNIKNFEDILKDGVNVMVVDGAGQVGLYEDMAL

KSAKRENLVKLRKNIKIYAKNSKAAVDEWNNNPNIDALIIWSHWAKALGDDKALFIKDKNAVIYRAAEIA

PTKKGLENKKALEFVDFIKSKEAQKVWKKYTWKEVK

>WP\_012006659.1 Na/Pi-cotransporter [Campylobacter jejuni]

MQEERNSLKYFKFISWSIFILVLIFILIRYDELANLLAGVAILLIGMTNLGIGFKAFSGGLLEKILAKST

DTKIKSILFGTLSTLIMQSSTLVSIITISFLSAGLISLGAGIGIIFGANLGNTASSWLIVGLTNIKISML

AIPLLIIGVLFFFQKDSVLKGLGNIFIGIGFFFLGVDYIKSGFENFKHIIDLSRFDFAGFKGVFVFLGLG

ALLTGVIQSSTATMAIIVAALLAGQISLENSLAATLGTSVGGVVTAVLASLSTNIEGKKLAFANCIFNFG

IAFLIVLIFPYFIHFLNFLSIVLNIEDIALKVALFHTLFNLIGVVLFSFFTPQIVLFLNKIVKAPKDKNK

DKPLYLDSSLVKFSDTAIKALRKESEHLYNNTYAIVAHAIGFSRKDIQSDKSFKEILENKKWFSKNVDLD

YLYQTRIKVLFEAIIDFSTKAQVYINDETKNHKIFTFKMAAKNLAETTKNLKIIQANIKKYSSSSNEFLA

LEYNKIRSNLGELLRSIEELRVVEDREKLYLIIKNLQKGKEILKEIDTLTLGNVEHLISVRKITTAEGIS

ILNDTTFAAKIAEELIGAVEVIFSKDISN

>WP\_012006637.1 DEAD/DEAH box helicase [Campylobacter jejuni]

MAKAKQNIKKHLLLNQFIHNKSLVQKLNESYDFGNFSQAINLQFYQQEGVKNALAILSFYMKDELNSHNY

NQERRKLLDFYQGESKDLKLQKEHIARASFWMATGSGKTIVMIKLIALIHEFIKNNQLPKKPIMLLAPND

KILNQFKANITKYNNYHSNFIKIKDLKDFESIEKEASLLNEAVVYFARSDLLESEENVGKDKKAKRLNYK

NYLNKDGWYILLDEAHRGDSKTSLRKNYYHELARGFIKEDEFPKGFVFNFSATFEDEIDFITCAYNYNLQ

KFNQEGYGKNIAILNENLDFKSENNEEAKIKTILEGFIIFNAIVKTKEELFLKRSDFKYHNPLIIAVSDK

VNTQDAGIKTYFKAVHNVLKNKADIGNIALELYEKLQNQNLHFGINTLSDDFLKYIKNTNNDELRKNIFY

ASANANLECYSIKGNDKELAFKSKNSNKPFMLLNISNAKEWEKNFLLELGVESISDISQSHFENINSSQS

SINIMLGSKVFSEGWDSNRVNLISFINIGSVNAKKYVLQTIGRGVRIEPFLNIRKRLNTLKETFKIDERC

VNLACGLETLFVMASDNEAIQAIIEGIEYEFIESKHLKGFKETKLSFNLPIPKYKNETKLKSIYKISKDD

AKSLEELIKSYDEDVLILGQCLYKNFKYSTLQEFNKFIKGKESRIQLSGNKVEFNEKTILKTINSVLNSN

TKVLDKFVKLEKEITHHKNIQAKLDFETVQKINKTIKDVLNAKSEDELKADFENKKINLDELMQGIKESQ

KNKEVQNYIISAKLSTHYYNPLIIYNKNDKENKINFAISNKSEKEFLEDLESNLNLSFFEQYEWYFSKLV

ENQDEIYIPYFDEEQQKERKFYPDFIFWLKNKQSGEFDIYFIDPKGLKIEDNPRFKLKGFKMIFENKNLT

YEDKNIKVNLFFYNKNKNYVSDELKDFVKSNIEDIFK

>WP\_012006621.1 energry transducer TonB [Campylobacter jejuni]

MKNYGLSNLNSFLLALAIYISIVILVFFRLVSEVEPAIQYTDIKDSFVDIELAEPSKQVITQSNAPKEIQ

KPTEQIDIEKLFAQTTNKTVKTEDIDQKASNFNELFGNIKEIQEEKTTKIQSSAKSGASSAPKPQASELV

KQLNDSLLQEESSTQGESTKAQKIGIYDEFLGKVVRIITQRWTQYYPNSEKISVKVKIFIDENGKFGYTS

VEKSGNPLYDAKVAEFLESQKGKFITYPPQNKNISITMNLRDEAKVKND

>WP\_012006618.1 membrane protein [Campylobacter jejuni]

MKEFDEKLAQYGIFTINGVENIDLIKKEIVLENISIERIDFNILQEKGIKRLIIKNSEILEIYFSKTNNF

FIYFLNCDFKCKLIAKKCIFQDQVKFIKCIFEKCVDFNASKFKSKVSFTISIFKENARFIKTEFLAKCNN

HKIIENNFKEVKFCNNVTFRRAKFESKVSFTISIFKENARFIKTEFLAKCNNHKIIENNFSETIFYNKTN

FYKAKIVSKIDFKISRFKGEIRFVETKFLSKLDNEIANNFREVVFEDKVYFNKTKINTQINFKMAKFKNN

VEFVNLHNNVSFNNVNFKGIVNFENLNINTLNFKNVIFNNIVSFDNIRFDNNCKPNFENCTFSDQFNIEH

KYIEYKFDEIEKTQEYDKLLNYRDLFRKLKSNRIAHHNLIDASELRAQELYARELELKHKENKSLKEKIE

RWQLVFYRKLCDHHTDLLLNLKWLVVVIGLFALLYFASRMIQDISLLKALNQYGVCLSIVGVFNLLCLYW

FGCIKKFDFFVYLNLIVVLWVICYMPKIIFGIVNIIGDKSYNGFENALITIYTILLALVLFSLQKTARKN

SIVPS

>WP\_002898677.1 iron ABC transporter permease [Campylobacter jejuni]

MFFKHILSLKVLIALLLFFGMISLFIGVISINVKDILNLNSTQLEIITLTRIPRLIAILLTGMSLSICGL

IMQQLTQNKFVSPTTAGTMDCAKFGILISLIFFAGASFFTQAIIASVFALLGSFIFIQILRKIKLKDVIF

VPLIGLMFGGIISAITTFFAYALNYIQNIQGWLQGSMANVMQGNYELLYISLPLFILAYFLAHKITIVGM

GEDVALNLGISYNGILFLGLMIVSIITSLVIVSVGIIPFLGLIIPNLVALYLGDNLRKNLIYIALCGALF

LLVCDIISRLVIFPFEMPLSITTGVLGSLIFIFLLLKRKVYA

>WP\_002878198.1 type II restriction endonuclease [Campylobacter jejuni]

MKFEAINEKEFLNPYHRKKPILETELNEFIKTLKDYKINLENNLKNNEDSLVANALSKFFENLSFQCEVK

SIHKGNSGIDLALKKDGLTQVIIEAKLPHSREFFSPSKPNCKALHECILYYLRERKALNSSLKHIIITDF

YSFFIFKADLFEELFNKNKYFKEAFENFESKNSLFKGNTDEIYKEFEKILNGDSTLKGLFVDLKPILEQD

KLSFSKLKPLFKIFSKDCLLGEFNPNDANSLNNAFYKELLYILGLCESKQNSKLIIAKSEESKEEQGTFY

TAINSKLKEENFETILKLLILWLNRILFLKLIESNLVRFNDDKNLKFLNFKKIPDFDKLSELFFEVLAKE

KSTRKKSEFAYLPYLNSSLFEKQSIENTLEISSLSNDLKLFYYKNTVLKDDKCKAKKGQVGLLEYLFEFL

DSFDFGSDDEQSEILSQKELISSSVLGNVFEKLNGYKEGSFYTPSFITSYMCKESITKVVLDKFNAQFDL

DAKDISELRKSLRKEDKKAQKELLNSIKICDPAVGSGHFLVSALNVMLSIYDELNLFDEEFYLEVQNDEI

LITGRKGEFIEYKRPKTPKDKAHLIQQELFHTKKDIIENNLFGVDINPNSCEITKLRLWIELLKHSFYQS

FDDGNYHDLKTLPNIDINIKCGNSLVSYFETGKSLSHYPNIKERMGKYKRIVKDYKEGFYTDKSHINQEI

KNLKISFKNFCFADKFKKEMKSFNDKCEKYSKKYGNFLAVDDENLKFFVSANLTLFDFDEKEATKEFANL

KKEYDNIFNLESNHPFEWRFEFPEILDDDGNFKGFDLIIGNPPYIKENDNKDLFTNTKKLRTYQGKMDIW

YHFVGRGFDILKNNGYLAFIATNNWVTNSGAKKLRNIVLEESQILSLVDFSSFMVFDSASIQTMIMQFQK

IKPPKNYEFHFAKITTQTPIYEDVINLLKNEKTQNNEILSINLTPKKFIDKTLNFTKSDYEELFNKIQKY

GKFYLEESEVAQGIVPAIDEAFVIKDKNVFSKNEQCFIKEYYTGLSGKFYSSFTDKYLIYLSNKNYSGNL

DDLPNLKQHFQKYKEILKESKIKYKTPNKPYFYLHREREEKFFKKGEEKIISQVRCIEPIFVYSNENFYG

SRALFFIQTCRINLKYLTGVLNSKLIAFWLKHKGKIQGNLFKIDKEPLLNIPVVNINSKNEKLANKLISL

VDEILKVKEQDKNANTQELENKINSLVYKLYNLTEEEIKIIEGR

>WP\_002877438.1 DNA helicase II [Campylobacter jejuni]

MSQFEPFLALEASAGSGKTFALSVRFVALILKGARINEILALTFTKKAANEMQKRIIETFLNLEKENKTS

ECNELCKLLGKDKEELISLRDVKKEEFLRTELKISTFDAFFGKILRVFALNLGLSSDFTMSEERLDVREI

FLKLLKKDELKDLAYYINLVDEKENFFNELEKFYENAYFQNLPKIPNPSKAYINKAYSELRSYCLGLTHV

KNYKNLCDNFKSEVLDLSVFMQSSFMTKFESTKYLQDLESTNLHFSAKRMELINALNTYAIELENYKIAN

LMNLLNHYSEAKNIFHKDKNTLNFQDVSKKVYELITSEFKDMIYFRLDGFISHLLIDEFQDTSVIQYQIL

RPLIAELVSGEGVKKNRTFFYVGDKKQSIYRFRKGKKELFDLLKQEFSQIKSDSLNTNYRSKELLVDFVN

ETFKEKIKDYKEQFALESKKGGFVRIVESKEQKVKNQAQEIKEKTLETLFEQINFLRSKNISYDDICILC

WKNSDADMVLDFLREQKIPAFTQSNVLLENKASVRLVLEYAKYCIFGDEFYLVFLKELLGFEPRKITLDF

SKNAMENVLFLIKELKLDLNDIALIQFIEYAKTKENFLKLLFEPCTLKIVSEQNMGISIMSVHKSKGLEF

DHVILLDSLSKNNSNNEDIMLEYDINQGWQLHIKDKIRELTKEPIYTLFKENITRANYEDDINKLYVAFT

RAKESLIIVKRSEESVNGNYPSYFKGGFLNIYSQERGFLESKEQILSVKKESIQALQKFEKISPQEVQSE

EKLDSKELYFGNAFHFFMQNLKLPKGENFQMLTQRCKSKFRHFLDESDFEKLFKRIEILLKNTQFQNLIG

DGKLLKEQALSFNGEIKQLDLLALKDEEAFIIDYKTGLAMQDKHKEQVRTYKIAISEILKKDKVRAFIVY

CLENEIQILEI

>WP\_002876948.1 3-deoxy-D-manno-octulosonic acid transferase [Campylobacter jejuni]

MIFFYYFLTWTAFLFCAVFILLLSFLKSKYKTSLKSRFFLYKNLHQEKADVHFHACSYGEVRSIKTLVLK

FDSRITTITQTGFEYAKEFCKKVNYLAFENFLPFWFKPCKVLVIFEAEYWLMLVFMAHIYKTKIILLNAR

ISDKSYHSYQRFSFFYKKIFSYIDEVFAQSELDKVRLESLGAKNVKIFKNIKANLEIKNNKIYAKPKEKL

IIFASTHKDEEELLLDHFKLEENEKLIIAPRHPERFKEVENLLLNKGLEFEKFSSLKDENKKFAKKILLL

DALGELVNFYAISDVVVLGGSFIEGIGGHNPIEVAYFDNVLISGKFIHNQKALFEEVENVYFCENLKDLN

DKIHYLNLKVKISKKENLDLIIQTIQKGIDARKSL

>WP\_002871814.1 aminodeoxychorismate synthase component 1 [Campylobacter jejuni]

MTLENYAIFGKYFYHDLKHTLKAFNHKESKKCFKFIEKYKNDFYILMLADYELYRYFQDKNFTSKKAYLS

VFAFKKRKKFQKEDIDEEKFIPEFINFLDQDNYKENFIKVKEAISKGRVYQINLTQNFKFHSKMDSFELF

KLLLSRQDTEFKAFIKDETREILSFSPELFFKTKKRKIFTKPMKGTIKRDKDPIKDEENKTFLQNDTKNL

SENVMICDLLRNDLSKIITKKSLKTKLFEIQSHPTLHQMTSSVQGKLKKNISLYQIFKALFPCGSITGAP

KLESIKFIEELEQRDRGIYCGTIGLIHKNKNKFSVAIRTLEKQDEIYTYSTGSGLVWDSKFKDEFEELKL

KSAILNPCDFHLFETMYFKNSQILFLKEHLLRLINSALKFNFNTHKLFKDFYNILNQKSSYKEYQNFTLF

KLDEKIFHKKHSLFYNFPLPFKNPHKEGILKLILYKDGRYEFQQSALKQNSNDILLLSDDKINSKSDNLY

HKSSLRTFYNQHSYKWQQNLCYDIAFFNEKDELCEGSRTNLILEKNTQFYTPQIQSGMLNGVYRNFLINL

GLIKEKALFKQDLFEAENIYCINSVRGLKKVKLQ

>WP\_002867089.1 DEAD/DEAH box helicase [Campylobacter jejuni]

MQNLYSEDDTRVKFIDAKLYDSSWNEENIKRNYYFTDGRKLLGGKRAQRKFADYLLRYEGNNLAIIEAKK

FSKDPLDGLSQGIEYAKILNVPFVYSSNGEKIYEYDIRSHSGKYIDKFPSPKELFDRIYGNVKEWQYRLL

TQNVMYIPQKELRYYQKIAIDKVIEAIINNKNRILLTLATGTGKTTIAFNLCYRLLEARWNKENKDQKPK

ILFLCDRVSLRDQALGEFNPIESDCKAISAEEIKKNDGKIITNANVFFGIYQSLAANSKEQENTQEEQES

KFYLQYPKDFFDLIIIDECHRGGANEEGSWRAVLEYFSYATQLGLTATPKKEENIDTYEYFGESVYDYSL

KSGIEDGFLTPYKVKLIKTTLSDGYTYNPDDLIQGELEKGFYKQSEFERNIFLPNYNDFIAKKILELINP

MDKTIIFCANQAHANEVKRAIDKYKSVKRDDYCVRVTSDEGKIGLDYLKQFQDNDKSFPVILTSSKMLTT

GVDAKNVRNIVLLANIGSMVEFKQIIGRGTRVYEGKDFFTILDFVGATKLFYDPKWDGEKIKELKEQNKQ

EKITKEQIKQTKEESKEKKSVTIHLKGTKLKVLDITTSYVGAQGKPLSTKEFLEFLIGKLGEYYDDEAKL

REIWSDQKNRERFLKALANDGVDEDALKDLRKIFQKDCDIYDVLAHLSFNAEIKTRQERVLQVENGEFLK

RFQKEKAIKFIEFLLNRYQEYGIKDFDDGLKPLIELSSLGNVRELADEFGGLEILKQSFDDLQREIYAR

>WP\_002867078.1 UTP--glucose-1-phosphate uridylyltransferase [Campylobacter jejuni]

MLQTCIFPAAGYGTRFLPATKTLPKEMLPILTKPLIHYGVDEALEAGMENMGFVTGRGKRALEDYFDISY

ELEHQISGTKKEYLLDEIRSLINRCTFTFTRQNQMKGLGDAVLKGKPLVGDEAFGVILADDLCVNEEGLN

VMAQMVKIYEKYRCTIIAVMEVPKEQVSNYGVIFGNFVEENLIMVNSMIEKPSPDEAPSNLAIIGRYILT

PDIFGILENTKAGKNGEIQLTDALLTQATNGMVLAYKFQGKRFDCGSVEGFVEATNYFYEKSKC

>WP\_002867062.1 molybdenum cofactor biosynthesis protein MoaE [Campylobacter jejuni]

MKHFTLYQGSLDIPKIYSQWYEFAKDKNCGALLTFCGIVREEGGIEALSFDIYEPLLKKWFDEWQKRVDF

DDISLLFAHSIGDVAVHESSYFAGILSKQRKLGLKLLNEFVEDFKASAPIWKYDVINKERIYAKERSTKL

CGAGLLKG

>WP\_002867052.1 1-pyrroline-5-carboxylate dehydrogenase [Campylobacter jejuni]

MIQKALALAEELQGQIEANISNSEKEFHAKMQKLLNNPKNKVMLIELLDRSFRCKDKNASFELIEYTLSK

YGIADFFSTFEKFLLFSFLNFGKFAPNLSVPFFVKHLREDTKAMVLDANASVLEPHIKKRKEQDKITLNV

NLIGEEVLGEAESKYRMQKYEEALKSSYITYISIKITTIFSQINIIDFDYSKEEVVKRLDYLYALALEEE

KKQGVSKFINLDMEEFRDLELTVAAFMESVAKFDIKAGIVLQAYIPDSYEYLKKLFSFSKERVLKGMKPI

KIRFVKGANMESEETIASQKGWELPTFYKKIDTDSNYNKMLDFILEGDNHKYINIGIASHNIFEIAYAYT

RISEAGALDSFTFEMLEGMSLQCSYELSKMHDLILYAPVCDEAHFNNAIAYLVRRLDENTSEDNFMRYFF

NLKVGDENWKAQKELFLKSLEGIKTLDNTTHRKQDRNKESNIISSYESKKFSNESDTDFILAQNRAWAKE

IKAKYENLKDYDVYPVIGELDFKAENLNVLEVKDKIEDRVIGKAYLAGEKEIKQALEVAKNSKFTQKSHD

EIYQILAKSAKLMRERRGDLIGLAALEVGKTFLEIDPEVSEAIDFIEFYPHSLEELKKQNPKVKFTPKGI

GVTIAPWNFPIGISVGTIAAPLAAGNVVIYKPSSLSTLTGYMLCKCFWDAGIPKDALIFLPSKGSDISKY

LLVDEAIKFSILTGGEDTAYAMLKANPTLLLSAETGGKNATIVSKFADRDSAIKNIIHSAFSNSGQKCSA

TSLLVLEEEVYNDEEFKKTLVDAASSMAVGNPFEFKNKLGTLADKPSSKVQKALDELQPYEEWALKPKFL

ENNPYLMTPGIKYGTKKGDFTHMNELFVPILSVMKAKDLKEAIDIVNSTGYGLTAGFESLDEREWEYFHT

HIEAGNIYINKPTTGAIVLRQPFGGVKKSAIGLGRKVGIYNYITQFLEIKQEDFDDHLIEDKFSKKLAQI

DLKEAQDFMNDLIKMSQSYAYHYKNEFSVSKDYVNIRGEDNLFSYTKIKNMVLRLCGNESLKDVLGVILG

ANIANIDLSISYDEQDISMIERIVQSIGAKVLFLKENKENFIKSIKEYERVRYLAKPDVNDEIYKEAAKL

AKIIIREKPLLNGRFELLNYFNEKALSISFHRYGNLGIRAIS

>WP\_002867049.1 hypothetical protein [Campylobacter jejuni]

MKSKYNSVVKVRKQQLDKAESNLNQAKQRQLEHEKAYELSRQECESLGVLPKSGSIAELRSNLSMAQVGR

EALARAKEKVELSKKEMNHYQFLYQKAHLDYEKMKALETEEIKQKQKEFAKAEEKFLDEIAISRFFKGEK

DD

>WP\_002867047.1 membrane protein [Campylobacter jejuni]

MSIDFLAIISVAFLSSFGHCYSMCGGFNLLFINLNSKSNNLFLLTFIYHLFRIFAYIALGIIFGTFGNIL

AINAKVQSLSFFILGIFMMILGFALIFRGNMLSFIENNVFFDSFIKKIIKKSKNFKGLKSAIFLGFSNGF

VPCGLVYFFIANAMSKQNIFKGILVMMIFGISTLPAMLFFSKISQFFSDFLKNLFNYLSYGVIVCYGMNL

AYIGFKAFQ

>WP\_002867032.1 membrane protein [Campylobacter jejuni]

MGFEHLNTIYYFILFFVALFAGFIDSIVGGGGLITLPALIACGIPAHLSLATNKLQSVFGSFTATLTYFK

STTLPHLAWGVFFTTLGAAIGSYSVLFVKDEQLKLIILIFLTLTFLYTALRPNLGKHESEPKIKNIKIFH

LICGLTLGFYDGFLGPGTGSFWIFACVMLLGFNMRKASINTKILNFTSNIIALAIFLWQYELLWAVGLLM

GVGQVLGAYLGSKLVLKTNGKFIKTLFLIVVGATIIKVAWDYFS

>WP\_002867011.1 capsular polysaccharide biosynthesis protein [Campylobacter jejuni]

MKYSVIVPVDLDLRPFDILKKVKSILKRSSNEVEIVFGHNDRGSIFDKYLKKICTKKNNVKLVSGKFYTK

LICQSLLRNRAVEQCSSEFIYLMDVDYLFDEALSDECINDIKNDKNPFIILPCLYLSRKGSREIFKFSRE

EMFEKYISFRKDLFISLASPSGGSIFMKKEDYFAVGGFDEDFVGRGGEDFEFMIKLALYKNVIKPTKDLM

INKFYKAPLLSEGFRKYLTFNGLPYFFEKKVAFHIYHGRNRLRGYFRQYDKNSNLLQEKIKLASNLEDTG

VSLIEFYEQLCKKYDVSIDKYAVLFDAYKPKLFSFERFMLFLRRL

>WP\_002866992.1 phosphomethylpyrimidine synthase [Campylobacter jejuni]

MKTQMNYAKEGVFTKEMQIVAQKENLSKDFLLENIACGKIIIPANINHKSLDPNGIGFGLRTKVNVNLGV

SNDCVDYSEEMKKVELAHKFDIEAIMDLSNYGKTSRFRDELVNVSKAMIGTVPVYDAVGFLEKDLKQIGA

KDFLDVVYHHAKSGVDFMTIHAGINSRAAHIFKQSKRLTNIVSRGGSVLYAWMMMKDAENPFFEYYDDLL

DICLKYDVTLSLGDALRPGSTHDASDGAQISELIELSLLTQRAWDVGVQVMIEGPGHMAINEIEVNMQLE

KRLCKGAPFYVLGPLVTDIGAGYDHISGAIGGAVAAASGADMLCYVTPAEHLRLPNLEDVREGIVATKIA

AHAGDIAKLPKERARDDEMSKARQEIDWEKMFKLAIDGEKAKKMFNERRPDDLNSCSMCGKMCAMNTMNQ

ILKGEDVSLA

>WP\_002866967.1 amino acid ABC transporter substrate-binding protein [Campylobacter jejuni]

MKKIILIFISFFALNLSAKDLVVGMELGYPPFEMSDKTGRASGISVDFLEAFAKKNGYKLVVKNIAWDGL

IPALKTAKIDLIMSSMTITDERKKVVDFSIPYAKANLAILTPLNSDITNIKDLDKKGKVLALKRGSTGHL

YAVKNLKNATINLFDKENAAILEVIQGKADGFFYDQLTIYRTWQKHQDTTRAILVPFQENPEFWGIAVQK

GNAELKKELDEFIAESKKDGLFDSLGEKYLKDVKDTFKKNNLEFFF

>WP\_002866958.1 CoA-binding protein [Campylobacter jejuni]

MNEKETISYIINASKNIAIFALSPDKTKASYRVAEFLQRKNYKIFPIYPKEEFILNEKVYRNLDQIEEKI

DTLILFRKGEVALEILPKLVEKNIKNLWLQLGISNETAKEECKKLDINFIQNRCIMLEYPYFKTKEK

>WP\_002866886.1 cation transporter [Campylobacter jejuni]

MSLQKKATFVASLCAIVLALVKFIVGLTSGSVAVLSSAIDSLMDFAISAFNFLALKKSSQKANENYNFGF

SKIEALMGLLEGVFIVGVGIFIFYESILKIYYKEEIKDLNSSIYVMIFALIMTFFLVLFLNYVAKKTKSL

IIESDALHYKTDCLTNACTLGALVLIYFTNLHIIDAIFGIVISLYTAFSAFKIIKKALAFLMDEALPKKQ

VDKICTLISNNPEIISYHELKTRKTPSCNYLSVHLVFCPIISLLNAHKISDEIEEGVRKMFENEKWDIQI

HLDPYDDAEQERQRQ

>WP\_002866862.1 NADH dehydrogenase subunit G [Campylobacter jejuni]

MTVKINGIDCAFEEGEYILNIARRNDIFIPAICYLSGCSPTLACRMCMVEADGKKVYSCNTKAKEGMIVE

SDLQNLWDERNEIMQAYCINHPLECGVCDKSGECELQNFTHKSRVNVQKHWIKDTHKPHKHWGMINYDPA

LCIVCERCITVCKDKIGESALKTVPRGGDSVDNSFKESMGKDAYAIWTKFQKSLIGPANGDTLDCSFCGE

CTSVCPTGALIGSKFQYTSNIWELKRIPASNPHSSDCELMYYDIKQSGISNQKEKIYRVSNDFAFASLNK

AARFAFDTQNEADKDEKAFKELVELFEKNEIKNIKFNSFITNEEALILQNLKKKFNLSLINEEALKFKEF

LQEFIANSGEFYSANTQDITKSDFLVVAGTLLRYDAPTLSYKINNALVINKGSGLYFHPMEDMGIAKYSK

NFISHIHKSGDEEQILYFLLQKFSQDEGIKTHLAEFFVSENKEIEESINEEVVEQVIEKDEEGNEIQKEV

KKVVPKKVKKIIEVQRSVFAKNLGIDEDKLEDLLLKKANFTLVVGNDFYFHKNAKKLAKLLALIQNTTPF

KVFLNPTHTNTLGVAMICDLDKNTQEGKTLGYNEKGDFSFSYEEHANLASASLNQQEGTFLNYDKRVVPT

NAALEFKGYFLNDLANALGFDEEYTINYTKRLPINKGFSPIDFDHLDNFYTNAGDCKRGYELNLECFKQV

AKKEFISPNFENLNPKEDEILLYSANPSYQFGRFSNRASAINEVIFLGVSENLAKEKNLKDKDLVKLKIK

DKELSLSVRVDKDIKNGAFLPYFDEKLDTLSFFDERFVVANLEKLGASHE

>WP\_002866857.1 NADH-quinone oxidoreductase subunit M [Campylobacter jejuni]

MLNYLIFFPLISAFVVLLLNRGGIKVFSVVVSFMILALNLDIFADFLQGVSFDYNLSFKILKFFSFHVGV

DSIALILMLLSSLMIFLSFLFLKLEQKALVSCIFFLEFAIMGLFSAKDGLLFYVFWEFSLLPLLYIMGVY

GKDFRAGVKFFIYAFAGSILMLIALIYQAYLNYQLLNIFTFDLEIWKNNASAVNFTEQLLLFGAFFIAFA

IKAPLFPLHTWAPKVYVNSPVLVSVMLVVFKMAPFGFLLFCLPLFPDASVYFMPLIVALCIVSIVYNALI

AYRAENIKELIAYSSISHLGVMILGIFSLNALGISGAVFYMFAHGIVTGALFLMVELLYQRYHTYDISFY

HSLAKKAPLFSIFFMLILLASVSLPLTVSFVGEFLILLGIAKINLFYALLAGLVIILGAIYMFAVFRKIF

FMQKQSFIENFSLRLREIVALVCIIVMIFGLGLMPNILLKPIQKDVDNLIKTMNIRAVEQNTLDFLSKIG

EANVK

>WP\_002866848.1 sulfate ABC transporter ATP-binding protein [Campylobacter jejuni]

MVIKAQNIITKFGEKIVHDGVSFEIKKNEIFGILGGSGSGKSVLLKQMLMLEHFDGGEYEILGYKLKNID

EEDALALRKKWGVVFQFAALFSFFNVYENIAIPLKEYTHLDENSIQELVLMKLKMVGLNESVLKQFPSEL

SGGMQKRVAIARALALDSKLLFLDEPTSGLDPHSSREFDDLVLELKKSFDLNIILVTHDKESMKNLLDRF

IILENKKVGFCGTYEELRLQNERLFKKFME

>WP\_002866846.1 hypothetical protein [Campylobacter jejuni]

MLKQIFYIFTFIFILCGCSLKHETINKNENIILKDEGIDSNIFFKKTGKILKIRNANTPLYLNSRAIVYI

DNGFSNKYAHYFWGDLPSNLYSFLILSKFEQSNIFTTLLSSTSSLNADYALESRINSFEQILSNNENYAQ

ISISVNFINLENNQIIAHKIFNTKEKIEKKDIRSTYNAFQKALNKIGNEIIFWVNSNLS

>WP\_002866813.1 radical SAM protein [Campylobacter jejuni]

MLNTTKLLENKLFQERYIKPNIDWYFSYLNGKRGMSRIYKTPYAILMKKFFLQKYFEKRIKKRIIDIPYL

ELVLTTKCTMRCQSCNNLMQYFSQNNQYTCTFEGIKKSLEILLSKVDSIARIRIIGGEPLLFKDLPKLID

YLNCQKKILTFSLVTNGTIDFKDELINKLKHSKKVRKITISNYKNSPNLKIPLKQEDIIKKLIKNKIPYS

LDSNKENSTWFDPEKIYKRGRNKEEIIKNYYYCKMPCVSLMTSEGENLKGKELASNGAIFVCPVSSSLSR

LKGLNEFEGDFLNLDDNIEKFFEFYIKDFYKACDYCRDFSKPYKRIPIAIQTNKTLKLEKED

>WP\_002866776.1 membrane protein [Campylobacter jejuni]

MINKNKLFRQVHIYLSLFFLPCALLFALTGIAYIFGINQDVGLKVEQYQLSKVIESGKEREALIEYLKTN

GLKVPSNTNIIKSKDKGITIGGAHYSANITQNSTNEYNITLKTRSLLGDMIMLHKDKGAWYFSVLSVGFG

ITLFMLYISGLMITLFANKKDRSKQFAVLGVGVVVTLLLAYLSL

>WP\_002866773.1 enterochelin ABC transporter substrate-binding protein [Campylobacter jejuni]

MKKSLVFAFFAFFLSLILTACNSNSNENNASSTTKTNTATMKVLPISMSDEGDSFLVKDSLGENKIPKNP

SKVVILDLGILDTFDALKLNDKVAGVPAKNLPKYLQQFKNKPSVGGVQQVDFEAINALKPDLIIISGRQS

KFYDKLKEIAPTLFVGLDNANFLSSFENNVLSVAKLYGLEKEALEKISDIKNEIEKAKSIVDEDKKALII

LTNSNKISAFGPQSRFGIIHDVLGINAVDENIKVGTHGKSINSEFILEKNPDYIFVIDRNIIVGNKERAQ

GILDNALVAKTKAAQNKKIIYLDPEYWYLASGNGLESLKTMILEIKNAVK

>WP\_002866769.1 phospholipase [Campylobacter jejuni]

MRKIALFLSLCVFIWASDLQQALEYEKQGDYKKAMEIYKKLALKNSSVLISQEQNNSSQATQTQNSITIK

KEEKQDFSRLALANYLGENESFNPLGISSYKMNYFLPLAYSFNSLGTNNNKSEAKFQLSVKKRLFENLLG

LDEKYYIAYTQTSWWQIYEHSSPFRETNYQPEFFIDFPLYLKDYEFFNNLRVGILHESNGKGDENLQSRS

WNRIYVSTAILYNKFLFVPRLWYRIPESKKDDDNPAILHYMGNFDVNLGYLGDDYFINLMLRNNLKFHDN

KGAIQVDLGYDIFNNGIYWYLQYFNGHGESLIDYNKHLQRLSTGFLISY

>WP\_002866737.1 tRNA-dihydrouridine synthase [Campylobacter jejuni]

MIDFSKKPLFLAPMAGFSDLPFRNVVKKFGADITISEMISSNALVYESSKTLHMLERAELENPYIVQIAG

GDKEVLKKAVQMLNEMDFVDGIDFNCGCPVNKVVKQCAGSALLENLELFKNLVGVIKENNKKSLTSVKFR

LGFNEKYPEKMAKICESLGVDFVSIHGRTRKQLYSGKADYESIASAKASVSIPVIANGDINAQNAKEVYK

ITKCDGLMIGRASVGNPWIFYEIKSGKSVDEKLKKEIILTHFDEMIKHYKDQGVSIFRKHLHEYSKGHKD

ASAFRDEVNRINDAKIMQEKIESFF

>WP\_002866697.1 C4-dicarboxylate ABC transporter [Campylobacter jejuni]

MLGIVFSLFSVFLLVFMLYKKINAHMALLLSGLLLLSLAALFGLSPHIVAKGSLNLGFFDIFQVFNQTMS

STLAGLGLTLMTIAGFSAYMDHVGASYALFKVFEKPLKAVKSPYVLLIVAYFIVQFLVLFIPSHAGLALL

LMVTMYPILVRSGVSKLSALSVIAICQYIDHGPGSGNVIMASKVAEVDPAIYFVHYQLPTTLPIIIAVGI

AIYLCNKFFDKKDNFVFNAQEIEKELNENEGKEKELKKPPRIYAILPIIPLVLILGFSSVLDSILVLMGI

SSAEEVKAVASTAIKMNVPVAMVISTFVAIIFEMIRYKSIVETLNSIMIFFKGMGHLFVITISLIVCGQV

FASGLLSVGFVDTLIEFCKNAGFGVLAIIIAVSILLAVCAFLMGSGNAAFFSFAPLIPNIAKHFGVETIT

MIAPIQIMTGFGRCVSPIAPAILAISAIAKVSPFAVVKRTAIPMLVAAIVNVIMTYIYL

>WP\_002866691.1 oxidoreductase [Campylobacter jejuni]

MAKLSNEELKNILEGRIKKLENSILKEDKVVNEESVKILAKHLSLGNEIPALAQRFFQIAPKTKLVWLHL

CECTGCSESLLRSELPSFDELIFDFFSLEYHETLMAANGTKAEELLEHVLEEDFILAVEGGVAAIDTFFL

TIGAQGESGYEILEKLAAKAKAIFAVGTCSSYGGIQAAYPNPSKTCGISEVLSQKVVNIPGCPPSDINII

ATLSFFALFGVLPELDEQNRPVWAYGKCLHDMCERKAKFESGIFAEHFDDEAAKNGACLFKVGCKGPYTY

NNCPKVKFNAKTSWPVAAGHGCIACSEKNFWDEFGNYEKPMANIFSYAKLCNEELKQEFFLEEQIKILEQ

IDFEFESNIKLILQNIAKNKLGALLVENYKKSFEKNYAFIEQNFDENPMPSKDFWKYLEISFILVKGAFL

KDKNDFLIAAKNYAFKHASPYDFKLNMNAEKPKLDVSKSFRMTLIYLCGGLDFEGVAYSILKAFEDNIAK

ISSLKAS

>WP\_002866683.1 cytochrome P450 [Campylobacter jejuni]

MSECPFFPKPYKNKASTLLTFLLKRRSWLDGLYERSYKMQTGYVKMPNFDLYVINDTKEVKRMMVDEVRE

FPKSAFLHELLSPLLGESIFTTNGEVWKKQRELLRPSFEMTRINKVFNLMSEAVADMMDRFSKYPNHAVI

EVDEAMTFITADVIFRTIMSSKLDEEKGKKILNAFVTFQEQSVHTAMRRMFRFPKWLSYILGDRKRAKAG

DVIRQVLSDIIKPRYDMADNAEFEDILGSLLLVVDADTNKRFSFEEILDQVAMLFLAGHETTASSLTWTL

YLLSLYPKEQEKAYEEITQVLQGGAIEISHLRQFKYLTNIFKESLRLYPPVGFFAREAKKDTQVRDKLIK

KGSGVVIAPWLIHRHEEFWTNPHGFNPSRFEGEYKKDAYLPFGVGERICIGQGFAMQEAILILANILKTY

KLELEEDFVPDVVGRLTVRSANGMRIKFSKREL

>WP\_002866680.1 capsular polysaccharide biosynthesis protein [Campylobacter jejuni]

MQKERFFMFGFSLWKRHFIKPFFKAKDNEIIFLNSIKSLLRYKLKDDDKFFIWGKRIDYNTLKSTLIKKA

QDENLLHFTPKISLVEDGFIRSISLGSDLTRPFSLIVDDKGLYIDPNKPSKLEELLQNEIFDENILNRAK

NIIKILLENRFSKYNGLKHENLKINAKIGQKVILIPAQVEDDASMILGGFGLSTLDLLKEVRAKNQDAYI

IFKPHPDVLSGNRVGLKDETLILEFCDEIVKDCSIDSAIKIADEIHTITSTSGFDALLRAKKVFTYGMPF

YAGWGLTKDKYKCKRRTRKLSLEELVAGVLITYPRYINPKTKTLCEIEVCLDIMLNLQKDYFSKKHIKLA

IDFKTFMLRKIRRFYEFLAKK

>WP\_002866675.1 polysaccharide deacetylase [Campylobacter jejuni]

MKAIMYHYVRYSDKDFPFFRYLSVENFCKQLDFFEKHYGFVQFNDFLEVCNKPFKTQIFEKIKNKILLTF

DDGFLDHFKFVMPELLKRNTFGLFFISTGVYQRKKALDVHRIHYLIGRYGGEVLVKLSNDLLDANMLENI

PYFKEKTYTKQNNDFYTNEFKKLFNYYIKYEFRESILDKIVKLCNENDEDIFKNLYMNKDQLKTMHKNGM

ILGSHSVNHRVFSKLNNEEQEKEIHDSFSFLEKTIGNLNAKIFCYPYGGFHTFTDFTQKILNNANCNFSF

NVESRDVILNDLINYPQALPRYDCNEFDFGKASCG

>WP\_002866658.1 hypothetical protein [Campylobacter jejuni]

MVYEIQKNFLLSDCTLLENLKKDNIPFRNSKFETFYTQITSNHSVKFQSFCNEFYKITKFNNSILEQNQE

EKISKKKFEKARKKIIGKSIKKECFEFKFCSLKSYIDIYEEPKICILKIFFPTLDSSNEFKIPKDFKIQK

ELHHDLNSKHIVLYGFEYQNFDIEKCFKIIEKNQNFSLDFPNYINAYDGFRIFLFYLFKKLKFYWTLSLE

RKDKQSLCEFLFYSRSLYIVLSSMNTILDKNLSNILALKFKDITKKTQDILASENSNQDLLLFLSDEKIQ

DLFNDFDFFIKENSFYEGDCKDRFFKQLVALELRKKIILFRKNILKNFDLELFENSFFELAIFLEYFYRF

LEIKNLNKLYEKYCKDRDKNIFSKIINNKNKFCKLLKKSSKNLKIYKG

>WP\_002866607.1 ATP-binding protein [Campylobacter jejuni]

MKALALFSGGLDSMLAMKLITAQGIEVKALNINIGFGSTSDKSEIMKKRAAMIGADFEMIDVRNSYLQEV

LFNPQYGYGKHFNPCIDCHAFMFKTALAMLKEENASFIITGEVLGQRPMSQRSDAMAKVKKLALDEEDLI

LRPMCAKNLPLTKPEREGWVDREKLEGISGRSRKRQLELAAKFGLEDFESPGGGCLLTLDNFAKKIRDFI

EFDKDMQVNDAQLLKYGRHLRLPNGAKMIIGRNELENTLLKGLKTPKYEVIELGDLIGAYSLVDEKISEK

DLELALKIALTYTKHEVGKSYELKFKNQAYTSIAFENKADINQFFIS

>WP\_002866545.1 chemotaxis protein [Campylobacter jejuni]

MTQEELDALMNGDVDLDSETEAEVKTEESNTEEDALMLEDVKIADYKPNPSVVWPPPPPNQEHKVVHQLD

DVTKDSELKATEMMDKLESINNFFADSESLLKEINKAIEKNIDIFSKLNEKFPNVESFSEALELNNQAKK

SSKQIVGNLQSGQDEVMMAMDAMQYQDIHRQKIERVINVMRALSRYMSSLFEGKIDDKKRVSSAVHIEGD

STADVVSNDDIEALIASLGQK

>WP\_002866518.1 50S ribosomal protein L9 [Campylobacter jejuni]

MKVLLIKDVKALGKAGEIKEVKDGYGQNFLIAKGFAKAATNEVLRKYESDKKKEAENLRFEIANLEKLKE

ELSKITLEISKPVGANGSLFGGVTKDEIAHALKEQSHIEIDKKSLECDTFKSLGLHEVSVKLGHAIHAKF

NINIKAE

>WP\_002866414.1 hypothetical protein [Campylobacter jejuni]

MKKKILYIVVFFVVLILALFIVLKNGIVISSIQFDFLKLEQLYIKLDKKLIVRAKNITINETQNSEISSQ

THSSDNASTEILKITKNLKYLYAFVEEIDIQNLNIKDNHVRILFKDNEFFIDNDLLFLKLTLQRQNKELI

ADIKKLLLKDYDLNIDGNLSINTKSEFYYFQGRASGELLDFNASISYKDKNLAYKIEDLNIRNIMEIFKR

VNKRIELPQSLNLWVAYRAKGEFYHLDYLQGFIDFAKDNYYLDNISASGYVNNVKVRLDDKMNAIEIPKL

DLNLNKQKLDFVFNKAFYNGADLSSSKVYLYDLFDEKKAGIYLRIKSDNLKFDEKLAKALEDYHFSLPFY

QKSGKIKSDLELKIDFHDKGEISYSGILALENASISLADFNITKAFVKLNQNDLNIENASVKNSFLEADF

NAKFDLQKQQGNFNTQISRLYFDNGELLDLKNQNVEVKLDYSQNVNISIPQWNLILNFKDGLEANLNNPK

ILFSFSPLLKKFGFIDAKNVYYKTLNFEDFNASVNDAYFKNNLLINGQTPYENDSFDIVKNKGIMEIHTQ

SDTASAKISSDNKEIHLKNLSYIYKKDSNSSNSTFDISTNTQNISFGGANVALILPDSNKTLAFDRVEAD

LKGNALDLKGSRGNAKFDLYYSSNDLNLNVSNIDDNYLNEFLQKQAVQDGVFNLSIKGSGLEYFDGQIDF

KNTYVKDLRGINQLISFIDTVPSLLMFKSPTFNQKGLSLHDGKIIFNRKKDLLSVSAINLNGDSVDIYGL

GSANLRLNTVDFSLELKTLKSASEAISKVPILNYVILGKNQEISTNLKIDGSIDDPKFHTEILTDALKTP

FNLIKNIIQLPANLLN

>WP\_002866359.1 citrate transporter [Campylobacter jejuni]

MEIFLALLGFFSLGLIVWLLLKDYTTPALAFISVSISVACILLILEQLGFGVGAALGVKGGVFDIKTLVA

FIKDGVKSVTDTAALFVFSILFFSVLNASGFFTKILNAFLSKMKANVYQVCILTVFIAAAVHLDGSGAST

FLIVIPALLPIYERLGIRKTSMLLIITSAMGVMNVIPWGGPTLRAATNIGMDANLLWHHIIPIQIVGLVL

SLLLAIWIAKIEIKRGAGAGNLSGINLNIEKSEHHNEKWFWLNLLVAIGVIGLLISGIIPSYICFMIGLA

IILPLNYPNLKTAKKVLDRASGGAMLMYITLIGAGILIGVFDKSGIMEKMGVLILNFVPDYLGAYIPLMV

GILAVPMAIIFCTDSYFYGVMPIVLSVTKAFGAEPLTIAIIMVIARNCATFISPVVPATLLGCGLAEVNI

KDHIKRSFFYIWGISIICLIFAEVAGII

>WP\_002866328.1 homoserine dehydrogenase [Campylobacter jejuni]

MKVAILGYGTVGSAVVKFLLENDKLIRARCGQSITPVIALARSPKKNALIPITHSVEEILNADVDVFVEL

MGGVDEAFKIVSEILKKEKAVVTANKAMLAYHRYEVENLAKNLAFGYEASVAGGIPIIKVLKEGLSANNI

LAIKGILNGTSNYILSSMSQKNMSFEQALQIAQNLGYAEADPTFDIEGQDAAHKLLVLSSIAYNLKAKPE

DILIEGISEIAPEDMYFANEFEFTIKLLGIAKVRENKVELRVHPTMIDKEKMLAKVDGVMNAISINGDLL

GESLYYGAGAGGEATASAVISDLMDIARDQVKAPMLGFVNTLEYELLSKDEIYTKYYLRVKVEDKIGILS

KITQLMSENNISIDSFLQKPKKNDENYSTLFFTTHLTYEKSIQNLLEILRKQDFIKTKPFMMRIE

>WP\_002866326.1 hypothetical protein [Campylobacter jejuni]

MDKKQSRRNFLKASSLFALVGASAPSMVFAHTHNQNNLNSTQNYRARIFFNNSAQLDILSEAVERIFPED

DLGPGAKKLGVAIFIDNELAGNYGSGAKDYRFGPFIQGKKNQGYQYPLTRAELFKMGVNALDEEAKLRYK

KGFVELSAKQKDEVLRAFEQDKTKVSFGDKIKASDFFTELRSITITGVYADPIYGGNANMQAWRMKKFPG

AQMTYATQVLDGDKFEVIEPISLADMSH

>WP\_002866277.1 formyl transferase [Campylobacter jejuni]

MKKFENIYIIGTGKVAKECQKIASGFFKQEVIFVKNIENLDDFFKNLKNCLIISANNFYIFKKECIQNNA

IINYHNALLPFHKGCNAHIWSIWENDKKTGITWHMVEESIDTGAILTQKEIKLDDNFTALSLLNTQHNLA

MASFKEAVENLENKALKAQISKKGYHKKLALPNEGYLDLTWDKEKISRFLRAMDCGVLSGAPKARLKILG

EEKEILFYEINELDLILNLSDNTLLKITKE

>WP\_002866276.1 amino acid adenylation protein [Campylobacter jejuni]

MTTHIYDFLEKSLIKFSEKTAFVEPFAKERKEITYKNFDLFSKKLASEILRNLGNDNPIQVPVLIILPKG

IDCLISFFGVALSGNFYTLLDEKSPKERVEKVIEVLKPKLFITSKNLNFNLNLPTLYTQDFEGFDINESL

LKNAKEKHIDTNLLYVFFTSGSTGIPKGVSIAHKSVIDYTFWVCETFKFDENEILANQAPFYFDNSILDI

FSSVKSGATLHLLPNHLFAFPNKILECLEKEKVSTIFWVPSVLIYFANTEALNNFSLNTLKKILFCGEIM

PNKQLNIWRKHLPNALFANLYGPTEITDVCSFYIINRTFKDEELLPIGKACKNTELLVFDENMNFISPKQ

IGVKGELFVRGTSLSLGYYNDKEKSKQAFIQNPLHDNYLDLLYKTGDIVSYNKFGELLCYGRADNQIKYM

GHRIELGEIESVINSHESVKNSACIFKEDIICFYESKDELDLKAFLKDKLPSYMIPKNFIKIDKFKLNQN

GKIDRKILNEKI

>WP\_002866236.1 MFS transporter [Campylobacter jejuni]

MQNYKKALFALALSAFCMGVTEFVMAGVLIDVEAYFSVDAKTAGYLTTLYAIGVVIGAPLITIPLSHFHR

HTQLLINLGIFALANFIIFFSQNFYLTAFARFIAGTQHGVFFVIATLAVSAIVPNDKKSSALAIMVTGLT

VALVTGVPLGTFIGHYFGFKFIFLLIFIITSLAFFGVWHMMPKNLHPSPTSLKNLIPAFSHQNLLKTYTI

TICSCGAQFVLYTYLQKLLVEISGFKVQDTAYILLLYGICAICGNLWGGKIVDKKGAIFSLRLILSIQVL

VFLSVFLTMHSKILIIFSVALIGFFAFSTIPALKMLSIAKAKRHTYKVIDSTVSVNEAAFNVGIALASFL

GGIVLAGLGIEFNALFSALFVSPALIFALLFAKDKLNYKKFQRKSLKKI

>WP\_002866232.1 pyridoxine 5'-phosphate synthase [Campylobacter jejuni]

MLLGVNIDHIAVLRQARMVNDPDLLEAAFIAAKHGDQITLHVREDRRHAQDFDLENIIKFCKSPINLECA

LNDEILNLALKLKPHRVTLVPEKREELTTEGGLCLNHTKLKQSIEKLQNANIEVSLFINPSLEDIEKSKN

LKAQFIELHTGHYANLHNALFSNISHTAFALKELGQDKKNLQAQFEKELQNLELCAKKGTELGLKVAAGH

GLNYKNVKPVVKIKEICELNIGQSIVARSVFTGLQNAILEMKELIKR

>WP\_002866231.1 exopolyphosphatase [Campylobacter jejuni]

MLGIDLGSNTLRAVQMDEKLNKLKEYEFVIGAAKNLNQSGEISKEAIQRLKNALSILAKEQDLSKARAVA

TAAFRKASNTNEIFAHLKEEFGIDFKLIDAKSEAKISVLGMQSGLRRLKIWGEFAYCDLGGASCELSFRK

SFKSFDFGIISFYEKNCHSYYKSCISYKKLIKKYPKFIINIKDKKLKIHFLIANPYLKHLAFMAFDEVAM

IKKELRSLGVKTVVLNSGVPTTLSALKQNINYEKYEATRVNGKKLCHKDFLNYAIKLFHMEEKKAIKEVG

MMRKNYLSAGCLLFYALFDKHKLLVIDEGLREGVCLASMKNIKF

>WP\_002866230.1 hypothetical protein [Campylobacter jejuni]

MKFSDFFHAWLHESYYKNAVSIGKNGDFFTAVSVGNLFSTLLAKHFLNLIDKKILQPPLELVEIGANEGY

LSRDFLAALLELRPEIFSQISFFVIEPHEKLKNLQKKTLEGVEFTHKNSLKECHFKNAFFFCNELFDSFT

CELIDHDKMAFVENFKLIFKNMDENLITKCKALNLTKGELSLELENFFKDLDQACERFIFAGFDYGTLNP

QNFSLRIYQKHEVFSPFEVSLKDFFGKSDLTYNVNFTHLQKLIKEYDFKPLAFKKQSLALMDFGFEDLLE

YTKNKNIKTYESFLSQAKILFFNFDEKFHFFEFQKN

>WP\_002866174.1 DNA polymerase III subunit gamma/tau [Campylobacter jejuni]

MLQALAIKYRPKTFDELIGQKTVSVSLKYALNHNRLAHAYLFSGLRGSGKTSSARIFSRALVCEQGPSDT

PCGTCKHCLAALEGKHIDIIEMDAASNRGLEDIQALIEQTKYTPSMARFKIFIIDEVHMLTPQAANALLK

TLEEPPSYVKFILATTDPLKLPATVLSRTQHFRFKQIPQSEILNHLKEILLKENVKFEEEALKFIARSGN

GSLRDTLTLLDQAIIFCQNEISISKITDMLGFLDPQKIKAFYQAILTKDKEKVFAYLEELQDYEASSVID

EMLFYLKESFFAKSTEFSILIYERFFRILSKAKNMLCDDDGFTLCVMAFMMMEASHLKEIDAQIQEIKQE

NTTNITPRITPAPIIPNLEKKIEKNAYEILLDSIYDRDFDLAECFKQSTKFISFENNTLNISSNAQGQNR

DTLNKGFKLIQELFKAKFGENAKINVQKALTIDENKLQSLTQELPNNENKNIDIQSSINMLKEGAKKFDP

QEDLKEALKDCFGEPSIEN

>WP\_002866125.1 ATP-dependent Clp protease ClpA [Campylobacter jejuni]

MKYQENLQKYLDNAKNLSLINHHEFVTCEHVLFALLKLSIDFKDIFEEFSDGDLELLETELKNYISQNNQ

VIKQEIEPTISVVLDEILLSSKNKNNEIKIIDFLEKLIQDSRSYSSYLLKKHNINLTKIQELQNHENIQN

LSNHTSNLTLLAQNGKIDPLIGRKFELERMMQILSRRKKNNPILVGEAGVGKTAIVEGLALAIAEKKVPK

NLQNAKIFSLDMASILAGTKYRGDFEKRIKEILNELEKIPNAILFIDEIHTIVGAGSTGESHTDFSNLLK

PALSNGTLKCIGATTFMEYKNTFDKNKPLSRRFAKINVDEPSQEESLQILKGLKNKYEEFHHIKLNDEIL

QYAVIWGKKFFNDKFLPDCAIDLIDELGASFALNPKAKKNANLKDLENVLAKMTHHHKMFEFDQNKALMN

LKTNLKAKIFGQDEVIDSLVSSLKQSFAGFKNSNTPRGVFLFTGSSGVGKTEFCKALAEFLGLNLERFDM

SEYAEKHAISKLIGSPAGYIGFEEGGLLSNAIRKNPFSLVLFDEIEKAHPDLSNTFLQIFDNAELTDNSG

LKVDFKNTIIIMTSNLGLKESNELGFLSKNEEKSNRAIKDFFAPEFINRIDKILHFNDLNDAILVKIIEK

ELDEISKNLNNIKLSVDDKVKIYLAKKAYNKEFGVRLLKRIISEEIGEKISDEILFGKLKKGGIAKIKLG

KNGKLEFIF

>WP\_002866120.1 oligoendopeptidase F [Campylobacter jejuni]

MLEWDLSALFHDKEALQNFTQDQIQQSLNFKKNYENKLYALNANEFLQALKDYENLNQALGKIMTYAYLL

FAKNTQNGSFYAQYEEECKKIEENLLFFELEFCELAPEKSQEFTTFCKDYDFYLSNLLQNKRYNLSKNEE

RIMLYLSNTGANAFSRLFDESMSALKIPFEGKKLSEEEILSKMYDEDRKTRKKAAKKFSKVLQKNSRLLS

FIINMIKTERKNISLLRGYENAEISRHISNQISQKSVDSLIASAQKHFNLVSQFYKRKKQILGYDELKDY

DRYAPIGKEASFDFKTSKNIVLEAFQAFSPQFYDIAKNAFNQGWIDVYPQENKQGGAFSHSATSDAHPFV

LLNYTDKRRDLFTLAHELGHTIHQKLSYNVSYLNQNTPLTTAETASVFAEMLVFDFIKDKLKKEELLSLY

ANKIEDIFATFYRQINFTCFERRLHAQENELSTEEINKIWMEESQKMFQDSVKLTKNYASWWSYIPHFIH

SPFYCYAYAYAQLLVLALYGLYKSKKCENFKELYIKMLSLGGSVSPKELVGMFGFDIEDENFWEIGIKEI

QKLINEFMELQSC

>WP\_002866118.1 serine/threonine transporter SstT [Campylobacter jejuni]

MFSKIIQSYAKGNLIVQICIGIVLGILIGISSKEISEIANLLGILFTSALKAIAPMLVFILILTSICTKD

FSQSGAKIKNIIILYIVGTFLASACAVLANFFFPVKLVLDGVQTATNSSPTHMSEIFKDLLFKIVDNPIN

ALSSGNYLGILTWAIAGGIALKHCSNEAKQVFIDINEGVLKIVKFIVKLAPFGIFGLVANSVAQTGAQGL

LSYVKLLILLVTTMLFVTFVINALIVFFYTRKNPFPLIFICLRHSAFFAFFTRSSAANIPVNMALCAKLG

IDKEFYGISIPLGATINMAGAAVTIAILSLTAANTVGIEISLLQAFLLSIIATFAACGASGVAGGSLLLI

PLACSLFNIDYDIAMKVVAIGFIIGVIQDSVETALNSSTDVLFTAICSKNELNYNIK

>WP\_002866082.1 lysine transporter LysE [Campylobacter jejuni]

MFDSFLSGVFLGFGVSVPFGPVNILILTYALKAFKNSIAVGLGAFSIDMLYLFLLQFGLLNFLDNVIFMR

FLAIFGFCFLTYMAYLMLRKKKESLNLEHKEFKESLLKSYIKGIILNGSNPYVIGFWLSATGIVLSNQHT

YSTILGLVVAILFWIGALAFVVAKYSYLFSAKVIRIINIVSALIIEYFALSLLYKTFIG

>WP\_002866077.1 type I restriction endonuclease subunit S [Campylobacter jejuni]

MNLNQTLQEKYPHLEVSVLKLSEVKKNIDFRIDDSFWTMKLIYNNKLNYKKIGECLLKSQYGISINMNEE

GDGIPIYRMNDIDNMLCNFEVKKYALIDKNELQTFRLNYGDVLFNRTNSYEFVGRTGIFYNNRENFVFAS

YLVRLVCNKEILLPEYLTVFLNTHIGKKEIRRRARPSINQANVNPEELKEIKIPIFPMEFQLEIQNLVKD

SHKALEESKELYKKAEETLYLELGLDPKNPLQSLLDSKTNNPTKSLNISIHTLKESFLKTGRLDSEYYQS

KYEDIEKMIRSYKDGFCNLKDLVNDISSGFAFSSDDYQDVGELVLIRINNIKNATLDLSNVIYLKNEAYN

LSPKDKIKKGDILISMSGSIGLSCVVRDDISAMVNQRILKISIKNFNSDVLVLLLNSFICKMQFERIGTT

GGVQTNLSSIDMQNILIPKIDSTTQEKIAKYIQESFNLRKKSKQLLDNAKIKVEEQIQGKI

>WP\_002866063.1 DNA gyrase subunit A [Campylobacter jejuni]

MENIFSKDSDIELVDIENSIKSSYLDYSMSVIIGRALPDARDGLKPVHRRILYAMQNDEAKSRTDFVKSA

RIVGAVIGRYHPHGDTAVYDALVRMAQDFSMRYPSITGQGNFGSIDGDSAAAMRYTEAKMSKLSHELLKD

IDKDTVDFVPNYDGSESEPDVLPSRVPNLLLNGSSGIAVGMATNIPPHSLNELIDGLLYLLDNKDASLEE

IMQFIKGPDFPTGGIIYGKKGIIEAYRTGRGRVKVRAKTHIEKKTNKDVIVIDELPYQTNKARLIEQIAE

LVKERQIEGISEVRDESNKEGIRVVIELKREAMSEIVLNNLFKSTTMESTFGVIMLAIHNKEPKIFSLLE

LLNLFLTHRKTVIIRRTIFELQKARARAHILEGLKIALDNIDEVIALIKNSSDNNTARDSLVAKFGLSEL

QANAILDMKLGRLTGLEREKIENELAELMKEIARLEEILKSETLLENLIRDELKEIRSKFDVPRITQIED

DYDDIDIEDLIPNENMVVTITHRGYIKRVPSKQYEKQKRGGKGKLAVTTYDDDFIESFFTANTHDTLMFV

TDRGQLYWLKVYKIPEGSRTAKGKAVVNLINLQAEEKIMAIIPTTDFDESKSLCFFTKNGIVKRTNLSEY

QNIRSVGVRAINLDENDELVTAIIVQRDEDEIFASGGEENLENQEIENLDDENLENEESVSTQGKMLFAV

TKKGMCIKFPLAKVREIGRVSRGVTAIKFKEKNDELVGAVVIENDEQEILSISAKGIGKRTNAGEYRLQS

RGGKGVICMKLTEKTKDLISVVIVDETMDLMALTSSGKMIRVDMQSIRKAGRNTSGVIVVNVENDEVVSI

AKCPKEENDEDELSDENFGLDLQ

>WP\_002865993.1 7-alpha-hydroxysteroid dehydrogenase [Campylobacter jejuni]

MNTEFQGKTLVISGGTRGIGKAIVYEFAKVGVNIAFTYNSNAQIADEMVQDLEKNYKIKARAYEFNILEP

ETYKELFEKIDADFDRVDYFISNAIISGRAVVGGYTKFMKLKPKGINNIFTATVNAFVVGAQEAAKRMEK

VGGGSIISISSTGNLVYIENYSGHGTAKAAVEAMARYAATELGEKNIRVNVVSGGPIETDALRAFTNYEE

VKQATINLSPLNRMGQSEDLAGACLFLCSSKASWVTGHTFIVDGGTTFK

>WP\_002865992.1 hypothetical protein [Campylobacter jejuni]

MELDQILLYAFIFLNLFAFFGLFLGNKKKNQFNDKKFYKICPCKKMAENGSLSTICIYSAVGGFFYSVLS

IGFVGFGNWTLNFIFLLALLSVFLGWKLKLD

>WP\_002856575.1 single-stranded DNA-binding protein [Campylobacter jejuni]

MFNKVVLVGNLTRDIEMRYAQSGSAIGASAIAVTRRFTTNGEKREETCFIDISFYGRTAEVANQYLTKGS

KVLIEGRLRFEQWSDQNGQNRSKHSIQVENMEMLGNSNAPQQGGNFGNNSFSNNNYSGNYENQSYDPYMS

ENQNFNKAKTNPTPQRNQNPQHEEKLKEIDIDAYDSDDTNLPF

>WP\_012006803.1 flagellar hook protein FlgE [Campylobacter jejuni]

MMRSLWSGVSGLQAHQVAMDVEGNNISNVNTTGFKYSRADFGTMFSQTVKIATAPTDGRGGSNPLQIGLG

VSVSSTTRIHSQGSVQTTDKNTDVAINGDGFFMVSDDGGLTNYLTRSGDFKLDAYGNFVNNAGFVVQGWN

INWDDQTIDSSRTPQNIFIDPGMHIPAAKSTEVAIKANLNSGLNIGTSSRNLYALDSVHGWNTKTQRAED

ENDTGTTQFYTTSKNSVEVTEKGVDAGALFNANGTGLNLRDGQGIWVSYADAKFTTDRANGANVFDPNLT

VAQQNNVIFWGNKDIAVTLDINLNGVRIQNDNIRSLDEAIAYINTFTAPTDTRDGTGVKAVKKADGSGIE

FVNNNADGTTDNMKNIDLTVNVGNSAGERNTINYNANTGVFSPQGGNLTTAQNDTDWIAGAAQAGQPQNV

KVVTAHKYIYSSNPVTIPPMINPDGGPAFQPNNGNRPTDPASANYWDAIQGSLKNTTERTFRTTEDLREL

LQRDARYGVDYNGSGIIDNATPTFDANDINQAVKVVVTENGNFAISNANETSTIPANAGAGAGAATTNPK

NMSFNITAYSNKQGTVSTNDAFTKIFKAFDGPLVIGNQIKESEQLKLSAFSAGLEIYDSLGSKHTLEVQF

VKQSTTQDGGNEWQMIIRVPEPAEINTTGEGPTNIIVGTARFNNDGSLANYTPKTINFSPNNGAAPNQQI

KLSFGTSGSNDGLVSSNSASTLTGQATDGYTSGNLKPDAIRVDDKGNILGEFTNGKTFAVAKIAMASVAN

NSGLEEIGGNLFKVTANSGNIVVGEAGTGGRGEMKTSALEMSNVDLSRSLTELIIIQRGYQANSKTISTS

DQMLQTLIQLKQ

>WP\_012006795.1 transketolase [Campylobacter jejuni]

MDIQILQEQANTLRFLSADMVQKANSGHPGAPLGLADILSVLSYHLKHNPKNPTWLNRDRLVFSGGHASA

LLYSFLHLSGYDLNLEDLKNFRQLHSKTPGHPEISTLGVEIATGPLGQGVANAVGFAMAAKKAQNLLGSD

LIDHKIYCLCGDGDLQEGISYEACSLAGLHKLDNFILIYDSNNISIEGDVGLAFNENVKMRFEAQGFEVL

SINGHDYEEINKALEQAKKSTKPCLIIAKTTIAKGAGELEGSHKSHGAPLGEEVIKKAKEQAGFDPNISF

HIPQASKIRFESAVELGDLEEAKWKDKLEKSGKKELLERLLNPDFSKIAYPDFKGKDLATRDSNGEILNV

LAKNLEGFLGGSADLGPSNKTELHGMGDFIEGKNIHFGIREHAMAAINNAFARYGIFLPFSATFFIFSEY

LKPAARIAALMKIKHFFIFTHDSIGVGEDGPTHQPIEQLSTFRAMPNFLTFRPADGVENVKAWQIALNAD

IPSAFVLSRQKLKALNEPIFGDVKNGAYLLKESKDAKFTLLASGSEVWLCLESANELEKQGFACNVVSMP

CFELFEKQDKTYQERLLKGEVIGVEAAHSNELYKFCHKVYGIESFGESGKDKDVFEHFGFSVSKLINFIL

SK

>WP\_012006785.1 hypothetical protein [Campylobacter jejuni]

MEALMDLEKLRLARSLYYQCLGELFVFSFSEERLSKLQEYLKTMQECLFDENLKSNFDILLKHLDDENSI

QAFFKEYDLLFLSLKNSIPTTFSYIEEGFENSNPLLCVRQILVKSKIRRNEKFFKESEDSVGFCLLLMSE

FLRQNEDDLAKELFEKVINKSIDEFLGDVFMNKNANLYKEIASIAMAFMEFERLCFEVEKPAKINSKKVQ

NDLSRSEFLRREANKQRRTREKSQGIS

>WP\_012006781.1 hypothetical protein [Campylobacter jejuni]

MKKLELRIFRFDKTKDYEAYYKPYIYDNYENFASFYDLLLQVQDDDIYFDFDKDEDTYIVVNKQIIPLFT

PLEKIAKEFDFSLCIEPLSTKRAIKDLIIDKNDFLDKYKYLEKFGNEEDKKLYAKYDYLYYASEILDYLP

EYMGDGVFYLASKMIEKYPEKKIEILKTLADKEKGIFYHLESKNEILETTIKNLQNEILNLGLFDKNILH

FDLPKTNAFDNEIKELKEIKHNFQDFNIAFYGFNACDTLKSKLKAKFISYENSIKNNGFSLLNLNPTLSY

KIAADIVLDAYDSGADFMVVKEEKDFYLFDTCAKKLMQTSGREFEDFYILSRFEFLALIEGIQAPSLKNH

TLKVSLI

>WP\_012006776.1 hypothetical protein [Campylobacter jejuni]

MQDKKVGIVIPIYNVEKYLDECLQSVIDQTYTNLSIVLVNDGSNDNSLSIAKKYALQDERIIIIDKKNGG

LSSARNTGIDFFANQYTLQFEKEEQELLKFQIINENYLDICSIYRKNTMLDKNFEIPQIDYIIFLDSDDF

WKSNCIEECVKRINNVDIVWFGHDLLIEIPLKKKTKNQMQFFDYNQEQIITSLDWLKQVNSEYKPLFWFA

WQGMINFSFLMKIRLKFINGIIHEDNHFGILLFSMAKYIYVYPETLYVYRVRSGSIMTQNDRTKVASNSY

LYPLYLKANKNYELFKRYQAALSCVLSCVKVAEFIEENKAENLILIEIKKVFIPMLLDRAVVILFLEKDP

LNLSAYLNSLESYFKEFKLSGAESFKYELSYRLGYLFLNNYRSIKGLLTLIPKMKKEIQDYYLEKQNFKN

NIKYFPFIEFVSQLDENPSLKRIKNHYSYKVGKIFAWILKYFGVR

>WP\_012006771.1 hypothetical protein [Campylobacter jejuni]

MLKDNKIVGVVIPVYNCEKYLIECLESVVNQSYYYLKIILINDGSTDRSLEILKKYAIRDDRIIVVDQIN

SGQGVARNVGMDLFKNKIKLQFYRNEQNLSVFNVNNQNNYNIKYIYIKQNQSSRQFNLSIDYIIFLDSDD

FWELNCIEECIKHMSNVDIVWFDYKLHYDLEYKYAVTLFDLYKFQKDMIISSEKWLKLSFKNEISEFWFT

WQGMINFKKLDDLNIYFKKGILYEDQVFGILLFGQVNSIYVLVKTLLNYRIRLNSSMNYDRETKQYSSYF

NGLSKTNINNIKKSFEYDINITNKYLQIARICNTYLTINKIIQNKNIFHLFKQVFLNKYLERSVQIFNFK

EDPLGIKHTLAGEIDKEIDNFFILPPQDKLSHIPIVFSCDANYFSYLTVVLQSIKEKSSENYNYDIYILH

NKLDKSLTQKLINYIQAENFSIKFVDISRILNLLKSQIQFYTALFFSEATYYRFFIPKIFKEFKKIIYLD

TDIIVKQDLNLLYSIDFDKPLAAAKCMIFSQVKQADHRITKLKMKQPENYFQAGVMVYNIQKCLKMDFTQ

KCLNKLQELKDPPLVDQDVLNAVFEGDIHYISLKWNCLWNVSYRIPNFKILYSKDFLKDYQEAERDPYII

HYCDYFKPWNSPHLPKADIWWHYARQTPFYEEILFKNITQNSLNIIQNSIQGAVERVKAHLSYKLGKEIL

SVKENKLKVLILPFALILIYVKHKISNLIFKLILISNPNLKSLPLNHYSDYQEALKIQNYLSYKLGNLLI

KYPFTFVFRVASVYKEWKKNR

>WP\_012006739.1 4-hydroxythreonine-4-phosphate dehydrogenase [Campylobacter jejuni]

MKKLAISIGDINGIGLEILVRSHEELSKICTPFYFIHENLLNKASKLLNLKLFNAKIVAFKDDKDYEFNF

IKKENSLEIYSFCLPLGFKVDENFEIKAGEIDAKSGLYGFLSFKAASYFVYEKHAHALLTLPIHKKAWED

AGLKYKGHTDALRDFFKKNAIMMLGCKELFVGLFSEHIPLAKVSKKITFKNLSIFLKDFYKETHFKKIGL

LGFNPHAGDYGVIGGEEEKIMEKAIAFVNAFLHSKKDEKFFKKALKDENLQKELLLNFKGKGVYLPYPLV

ADTAFTKAGLKNCNRLVAMYHDLALAPLKALYFDKSINVSLNLPIIRVSVDHGTAFDKAYKNAKINTKSY

FEAAKFAINLSLKT

>WP\_012006728.1 hypothetical protein [Campylobacter jejuni]

MSKAFTLFELIISLILFTFITSLLSKSLMDFYHLNFTALHTNNLITQAHLNLLKIEKLIQNCINITFSQN

TLKCLLKDELISLKDNKLYLINSALILENNHTLYSPHSDFKTQLQNRKDLYNDNEHISYAYKINKIEKIS

ILENGISTNFTGSFIPLQAQLVIKLQNEELIYEIKPKFNEQLNQQGLISKNISSFNLQNNKLKICLKRQT

KYCLEKRILL

>WP\_012006712.1 hypothetical protein [Campylobacter jejuni]

MDKLITWNEKYSIHDTMIDIQHQKLFELAGKVESAVYKFVKREELKEILTELFNYMKEHFDNEEQYMQEI

HYPYLNEHKIMHKNIIRDMSYLIQNIKTTNDLKEKLYTIMSEWLLEHILHHDVMIGKWIKAHNKNTKEEE

TKQEELTEDSQEKLEFIYSCPCKTTHALSYNEHLDILYHNKNLKCKNCQQTLFYFKNPI

>WP\_012006690.1 hypothetical protein [Campylobacter jejuni]

MSIFSINDNSNYNSILSQSKANKESKENSKISFANAFLKQNASKLNEIQSANSQTLARSEVLNSTNTTNT

SNNTNFSISSKTSSPNYDISSEFKNSIYTLKYKQADISNNTAYGYSVDKDGYMGSDFNKAAGLPEDFKIH

KSTLDEIKKAAENDPVASSTKEYLGVSEYYTNIDMAETIKQYYNLFSNALGQSFPNDKTSFSEADINSMP

SGYGVSGTQWMDFNDPSNRMNITGLKDFSNSLISNVYKTHEQAKEADDLWVDSGYMIDGLLPKTLGLSLE

EIKNVSKGEDWQFKPDMSFYPKNEDGTYTKEDLFMSFLKAQNGQPVESPKTTLNPKVEAYNRAMAKESFS

TTSVDIGDIMTGKVDFASLFKYLASKNGKLEGQLYMYENNISKESAMGNWALDAEIKQAIANGWKAKPST

INSYADSIMDRLNNLLGQTRV

>WP\_012006689.1 hypothetical protein [Campylobacter jejuni]

MSIFSINDNSNYNSILSQSKANKESKENSKISFANAFLKQNASKLNEIQSANSQTLARSEVLNSTNTTNT

SNNTNFSISSKTSSPNYDISSEFKNSIYTLKYKQADISNNTAYGYSVDKDGYMGSDFNKAAGLPEDFKIH

KSTLDEIKKAAENDPVASSTKEYLGVSEYYTNIDMAETIKQYYNLFSNALGQSFPNDKTSFSEADINSMP

SGYGVSGTQWMDFNDPSNRMNITGLKDFSNSLISNVYKTHEQAKEADDLWVDSGYMIDGLLPKTLGLSLE

EIKNVSKGEDWQFKPDMSFYPKNEDGTYTKEDLFMSFLKAQNGQPVESPKTTLNPKVEAYNTAMTKESFS

TTSVDLTDIMTGKVDFASLLKYELDRGRIAGELYMYEKGMSPKQALGNWALDAEIKQALANGWKASSESI

NSYVGSIMDRLNNLIGQTRA

>WP\_012006684.1 hypothetical protein [Campylobacter jejuni]

MGVENIYTLPLNGVPYISGSVAFDGEAKDNKLILESNTKIDLHNSQYFSDEEGKDIYDKRITRLMGAFGI

NSNLQNNKVLIDSANIVLHGPDGEYTTRSTFEILGALADVNNLKKYNISKNSVIIKNLNLDLMVNSQNKI

TFYDAVLFGEIYGGRTLQGNAEKNSIEVYHFNSLDHLNKNIKTHASLNLYGGYSNDGEANGNKIVFRLKK

PLKISDNFYGKNYYNLYGGFATEGANFNVIDIQNDLTYEKVPQNYSDKFTVYAARTLSGKANNNILSIKD

SVISLPLYAFITSETTLDGIDYIADESNNNEVNFENIKSSKNLSLMINAKNVSNNKINYNLIQSLTEASS

LGKGSKIILKATQNANNNLIKLKDCSSAAVESSCIIKADKESAFNKIIINNTAFSTASDKRQGYVGLIAG

VSANSHDNIMELVNLNIDEYKNQDAIFLAPSGTSDISNFKSYNNTLYLGGELNFFKDVNIDLLSGSVFHE

VNKKGKIITQILPHQEDFSKNNRLIIDTQDVKSEVVNNFENFTFILPNKIKNPILTIEKLINLPANGSME

ILTKNKPTKGKYILIQSDVGIYDGDNRLLNQQELENLLEKMKNNKNKFNYNKIEKLAKSTLKNVNFSFEV

SDDAKIIYINIL

>WP\_012006669.1 DNA repair protein RecN [Campylobacter jejuni]

MINRIFMKENLGFKKAELEISKGLTVFTGLSGAGKSVLFKGILSAFSLSESEAKIVEIELDDKLDLESFG

IESEEENVFKLLKEKNTKYFINNQSIAKKSLQNLSKTFIKYLSAKENNEFGNEKFLNLLDALEMQENTNF

VSFLEDFKKDFNAYSQISNELNVILEEEKKVEELKELARVQIEKISSINPKIGEYEELLIFKKKLSKKDK

LEEAWSKAERIFELEKVVIEALNLSEVDPSFFSECLNELRVICENQKMEDLDFDVETLLDRIENLSYLIK

RYENIENALEVLKQKKHELEHYENLSFEKKELEKKFQELKQKLEEKAQILTQTRKKNLKKLEKCLNNYLK

DLYMKDASLTLKENEKISISGKDEIMLDINLAHLKNLSSGELNRLRLAFIATECKILNAGKGILFLDEID

ANLSGKEAMSIAKVLEELSKFYQIFAISHLPQLSSKAHNHFLVEKNGEESKVKKLDQEERIKELARMVSG

ELVSDEAIEFAKTLFKN

>WP\_012006646.1 2-hydroxyacid dehydrogenase [Campylobacter jejuni]

MKIVCLDAATLGDYDLSVFEKFGSLQIYTTTNKEQTIERLKDANVAMTNKVVIDKDVIDACKNLKLILET

ATGVNNIDIEYAKEKGIIVKNAAGYSTMSVVQHTFAFMFAFLNQVLYYDKWSKEGKWCESPIFTDYSRIL

NTLSGKKHGIIGLGAIGKEVAKISKAFGAEIYYYSTSGANKNVDFIHLELKDLLKTCDIISIHAPLNEKT

KNLLTFEELKLLKDNAILINVGRGGIINENDLAKIIDEKNIRVGLDVLEIEPMMKNHPLLSIKNKENLII

TPHVAWASKEALNALMDIVYNNLKEWIENGK

>WP\_012006638.1 caspase family protein [Campylobacter jejuni]

MKNIAILVGNSEYQNLNKLHFCRKDISSMQKILSLSKKFEIHIFENYQSEQLKSGLSKIIRELEKSKINE

LLFYYTGHGVFKEQFYYLPINFTDKQFETTSLSNNELDDMLKSLNTEMVIKIIDACQSGQQYIKESDQMS

VKKSLTQHSFKKCYFFFSSMNNQSSMGDDKGSYFTNAIIESIVTHKTDSIRYADVQSYIADCFNGKNELQ

TPFFVHQSNATEIFLSDLTSIQKFFENNDLMANNGEGIIQEIENDKIDIVEKLKTLSKKYIAKDVAQKTI

ECIFDENNINNMFNDDIKLIYDIKIEKHNDYNIDNINKLYNEIEKNKKHFFINLEYKQEAYTTTEWIPKK

KNPYDITGRFSYDEFLGKNYEEKEIQKYRNIVNSICLVDDILPIGIVISLNPKENIDNINRYLINIINFH

NNLDIVFYSNIIEYYKNNWYDWEKINTEDWIKSKESFCDKDKILDKIQIIIKNYNQKIIDNIFNILKQED

LKIRE

>WP\_012006625.1 hypothetical protein [Campylobacter jejuni]

MSINDKKFDINLKFYFFMKYLVKINFSDIQIINILSHISKNKNSLYELKQYINLNTKNGINQWSYLEQII

YEIRNIIDFNVFIFALKIYSIKNFLLELAKIKQMSNIELLSKLDPLSLEYDKITIYNPYSTRVNGALLAL

TFFNHIDNNQFFHDNINKEYFLSICQLSQELRKHGLEPNQIFMLIFNESINQSIISYSGNNYENRILQKL

QSIGINQETITKKHDENDSSTEFDFFFNFNGKSYGIGAKRTLRERYKQFIKTSQTSEINVMIEITLGLDL

GEEKAKTIRNYGVYLIVSDEIYEQNKFLQNIDGVFGSSQLTLELLKTL

>WP\_012006624.1 hypothetical protein [Campylobacter jejuni]

MSIFSINDNSNYNSILSQSKANKESKENSKISFANAFLKQNASKLNEIQSANSQTLARSEVLNSTNTTNT

SNNTNFSISSKTSSPNYDISSEFKNSIYTLKYKQADISNNTAYGYSVDKDGYMGSDFNKAAGLPEDFKIH

KSTLDEIKKAAENDPVASSTKEYLGVSEYYTNIDMAETIKQYYNLFSNALGQSFPNDKTSFSEADINSMP

SGYAIDGFYNGYGAFKHPDAIRNDDIAIKSIADYSNVLISNIYRSQEQLNEANSIYSDSAGLISGIKPET

LGLSLEEIKNVSKGEDWQFNPDMSVYPQNEDGTYTKEDLFMSFLKAQNGQPVESPKTTLNPTIEAYNRAM

AKESFSGPAIHLDSIMTGKSDFKSFFRYWAERGIEEGDLYMYENNIPKESAMGNWALDAEIKQAIANGWK

AKPSTINSYADSIMDRLNNLLGQTRV

>WP\_002877994.1 DNA polymerase III subunit alpha [Campylobacter jejuni]

MSQFTHLHLHTEYSLLDGANKLKELALTLKEQGATSVAMTDHGNMFGAIDFYQTMKAQGLKPIIGMEAYL

HNHDELDDKSSRQRFHLCLYAKNEIGYQNLMYLSSQSYIKGLYYYPRINKKLLEDHSEGLICSSACLQGE

VNWHLNTYSERNVRFGAKGYEAAKEAALWYKKVFKDDFYFEIMRHGIGDQRMIDDDIIRLSKELNIKIIA

TNDTHYTFKERAAAHEVFMCIAMGKKLNDPDRMRHSVHEFYVKSPEQMSELFADIPEAIENTQEIAQKCN

LELNLGNPTPPNFKFTREYAKDHNITLPEETKEFSFDNDDIVFEELCKKGLEERLKFIDESKHEEYKQRL

EVEINIIKNMKFSGYMLIVHDFIKVAKDKGIPVGPGRGSAAGSLVSYCLRITDLDPIPYSLLFERFLNPE

RVSMPDIDVDFCQDRRAEVIDYVIDKYGADKVAQVITFGKLLAKGVIRDVARVCDMSIQDADELAKLVPE

ELKITLDAAYEKEPKIKEFIDRHPKGPEVWEYARALEGLNRNAGMHAAGVVISNESLWKKTPLFRQSKND

ERHLVTQYSKDHLEDVDLIKFDFLGLKTLTVINNAIKLIKKRYNKDIIWETIDVNDSKVYKTIQSGNTLG

IFQIESGGMQSLNARLKPERFEDIIAVLALYRPGPMESGMLDDFIDRKHGLKSIEYPFDSLEKVLEPTYG

VIVYQEQVMQIVQIIGGFSLGGADVVRRAMGKKDPEKMKKLKTDFADGAEKQGYDRAKAEDLWELIVKFA

GYGFNKSHSAAYALITFQTAYLKTYYPSEFMAALLTSEENNVDKIAVYIDEMKKMNIKLLPPSINKAIRE

FSALEQDGKDAIIYGLGAIKSVGIPAVENLLEARQDGEFKDINDFLGKIDPTKINRRTLESLIKAGAFDE

FGFTRKALFDNMENLSEASRKMAEVRKNAASSLFGEEELTSGVQVNFTPKNEEFEVMEKLGYEKEILGIY

VSGHPLDRFYEQINAIDYVKSLDFESLKNNGEILSIGKIEDFKSMMSKNNKRYGRIEILDYYSSFDATVF

ESNVEEIENIIKDENLKNNAYGFVLGFKAEGGEKPSFFLKAIKDLQSLEDGEIKAIKKFGAKKDFKNKEE

NHFTAEPKEFEKNIIELDLTRLNRELIYEIHEIARNAHNPNEKNNKKLVLKVISAGSCLLYHTDFIISDS

IVEEISNKYA

>WP\_002877967.1 hypothetical protein [Campylobacter jejuni]

MKIEAIDLQSALTEASRSLECSVMDLEYEIIQHPRKGFFGFGRKKAIIEAKAKKRILKKNPKKEFASSKN

HKPETHEPKQENKIEIKNEKNKIQKEKYTVKSDEIFDSFHRESKGVRNTQDILDEIRIQLVKLLESSQFK

IELSELRMYNEDCVLIRLDGEDAALMIGKEAHRYKAISYLLHNWINLKYNLLVRLEIAQFLENQIQGMQL

YLQSVIEKIKIHGRGQTKPLDGVLIKIALEQLRAEFPDKYVGIKQNNDQRFVVINDFFKKDE

>WP\_002877873.1 recombination protein RecR [Campylobacter jejuni]

MKSDLEIFKKHLGEIQGVNEFKANQICSQINDANDFIGALQVLDMSLKKIEKSILERIDENSDDMQKRTL

DATASQLIQNCSFMGTALFGNIFNVYVGKKLFEFEIANPLLILQTSNYEGVLAYIQDKRDEIKIILSELA

TTITMGETMDNTGIYNSTMDFKNLFK

>WP\_002877766.1 transcription-repair coupling factor [Campylobacter jejuni]

MQASFYEYLQNPKICELLLCKDEKQADLLAQVSRFKGLKTFVLPDFRAQFGDDLRAFSKELFDLCKILNA

YHKEEEKKILISPLNTVLKKLPSKKHLQNYHIDKKQNFNLKCFEDEISRLGYEFVDIVQDKGEISIRADI

IDIFCINEENPIRILLFGEEIESIRYFDLQSQKSIPNELEHFEICPFLKYFDKENYEIFKDKLEDFQSDT

LIHDINSLGFWCIDDFFDYLELDFLACEKFDINEYEKDVSFVNAKILPQAKKFKELQSSYNKDFFEFHKN

KKITLLAKNEALFKALELEDTQNIYFVKSDLRLNLISPEELIISLNQKEKQKTRKKASLIIDELKNGDYI

VHEDYGVGKFLGLEMIVISGAKKEFVAIEYQNSDKLLLPVENLYLIDKYLGVSGSIPSLDKLGKTSFIKL

KEKLKTKLLAIASEIVIMAAKRSLVQAKKITVDLSRQADFITSAGFIYTSDQEKACHEILQDFQSGKVMD

RLLSGDVGFGKTEVAMNAIYPVVKSGFCAFLFAPTTLLSHQHYKTLKKRFDPFDIKVFKLDRFTSSAEKK

QVLQNLKENKACVVVGTHALLSVECENLALVIIDEEHKFGVKQKEKLKEITQNSHILSMSATPIPRSLNQ

ALSSIKSYSVLQTPPEDRMDVRTFVKENDDALLKEAIARELRRGGQIFYIHNHIASIEQCKKHLLELFST

LRILILHSKIDAKVQEEEMLKFENKEYDLLLSTSIVESGIDLPNANTIIVEKSDRFGMADLHQLRGRVGR

SDKQGYCYFLIEDKNAITKDALKRLVSLESNSFLGAGSVLAYHDLEIRGGGNLLGVDQSGHIEQIGYSLY

LKMLEDELNALSKNEVDQKENKLDLKLNVNAFLNSELISEDRLRLELYRRLSKCEQVHEVYEIEGEIEDR

FGKLDIYTKQFLSLIIIKILALNKFKSISNYEQNIQFTALNDEKELIKAKSKDDDDILEAILTHLRKA

>WP\_002877440.1 ornithine carbamoyltransferase [Campylobacter jejuni]

MKLRIFSSSRQIREYYNQKKQQNALLDSAIHIGEFLDKVCLSNFHKASSYESLLLMQEACLKSKDLEKKL

GISVEFFAFLKNNEYLFSFFKELSLEKKSIEDLKNNDYYATYNEHLEILDEVYKNYLALLEKNSFYDDLS

LPKNYTLNKDFLDEYEAIVYDLQGFLSKFEENLLSEISQIKEVVLSFKTSKFNLEYLLKLDFLKTFDLKI

NTYYEINLSKQEILKEEIFKTKNSKIKLKSFELRALQCAFVMDEISHFVRKGLKPENIVVITPDESFCEF

LRLFDKDNMLNFASGISIKESLFYQKFQALYESASSASFVYKNQEDYFEDTQMIFDYHNTLLHSLKLDFI

EFKKYFDEKCDFEYFEKLLALFLENEKQELVYLIRKELYFIKDLLKNQSLTLKELIHLFFMQISQLSLSD

VGGGKVTVMGLLESRGLCFDGVILVDFNEEFIPKRSVNELFLNNEVRKKAGLISYDRRENLQRFYYESLM

KNALEVSICFVENEEKSKSRFLDELDFDFFYETHIHQKAYLNALKLDYEGIKPNLTPIKAPILKHNPFEF

ALSFSRFNLLENQKRTYYYRYILNLAEPRVLSEESKAKNQGNFIHKMLEIYYKNYANNDFDIKVFANLLD

KEYQKYNISELDLEVFKLKFIQFAKNEKEHFSKGFYVAHTELELNNILKLGTDSIKLKGTIDRIDSSKEG

NLIIDYKSGKVPSNSYQLAFYQALYDENANVGFYDLNSMQILHQKAKSLDELRERLKDLVLMSKEEIEFE

NEQDEHCPYKLIYKKELK

>WP\_002866774.1 hypothetical protein [Campylobacter jejuni]

MSLEFSKETQHFLTNYCKDNNLSEKEVLELALSYLEHKIRIDGYKKDIELYKQDKLKTLDFDETFNDIRK

DLE

>WP\_002866605.1 hypothetical protein [Campylobacter jejuni]

MKIDTSASLTHSLTNNVDKKELSVLKKEDQDKIPVQDLSSLNSDGVKIVFENKQGELIALNLSDENYSSL

QKNFGSYTNYVARNDGSIRLNGEANQFVSNWFESVKDNFGSLNSNLNNKQQSVKLNFNTSTLQQSMQNLG

FKTSDEKISDDANIEEKLNFFIDKDVNKDGKVDDSDVKEPSMREILSDIKEASGGGANAMKTIDPQKINK

KDDKENNIKEKEDEDLLQKAQEKGLSALSADEQAKLEASNPEEFEKLKQKSLQELSQNLSKDFQNKIENQ

EAQIVDKRV

>WP\_002866519.1 argininosuccinate synthase [Campylobacter jejuni]

MKNEVKKVVLAYSGGLDTSIILKWLQDEYNCEVVTFTADIGQGEELEPARKKALSLGIKEENIFIKDLRD

EFVKDYVFPMFRANAIYEGEYLLGTSIARPLIAKTQAQIALQTGADAVSHGATGKGNDQVRFELGYLAFN

PDLKIIAPWREWDLNSREKLLAYAQKHGIDISKKKGKSPYSMDANLLHISYEGLVLEDPAHAPEEDMWRW

SKSPKDAPNESEIIELDFQKGDLVAINGEKLSPAGLLTKLNELGCKHGIGRLDIVENRYVGMKSRGCYET

PGGTILLKAHRALESITLDREAAHLKDELMPKYASLIYNGYWFSPERMMLQALIDESQIHANGRVKLELY

KGNVMIIGRESANDSLFNAAYCTFEEDEVYNQKDAAGFIKLNALRFIIAGKNGRKF

>WP\_002866458.1 dihydropteroate synthase [Campylobacter jejuni]

MKFFKINPNTDFNLLCSFINPHKMGQKIMSEKTKIHFIFIKDISTPAANILKQDALRVGAELITHKEVIT

AKITHSNVLLMASKEQIQKLIVKEKLQDFGLKNLALFLQKDFLKPKKAELMAVINVNEDSFNAKSRVSEE

DFEKRLNDFLALKPEYIDIGAVSSRPGSEYCGKEEEFKRLKKVLDLIYEKNYYEQAIFSLDSFDEYCLEY

ALNKGFKLINDITSLRNLNLAKLASKYEAKYCLMHMQNNPNNMQDNPFYEDLLDEMTLFFKEKLELLESF

GVKESILDVGIGFGKSAGHNMILIKHLEHFLQFNKPLLIGASRKSVINAYFQSEIKDRLAGTLYLHLKAF

ENGASIIRVHDLYEHKQLFALAQAMDNIGV

>WP\_002866213.1 DNA repair protein RadA [Campylobacter jejuni]

MAKNKALFECQACGNQQSKWLGKCPDCGAWDSFVELKAEQIKVLKELAQVSMKTSEAVCIEDVELEHFTR

YSTDDNELDLVLGGGLVEGSLVLIGGSPGVGKSTLLLKIASNLAKQGKKVLYVSGEESKAQIKLRADRLE

ANTPNLFLLTELCLENILEELHKKDYSILIIDSIQTLYSNKITSVAGSITQVREITFELMRVSKAYNIST

FIIGHITKEGAIAGPRVLEHMVDVVLYFEGDATKEIRLLRGFKNRFGGTNEVGIFEMTAKGLISAKDLAN

RFFTRGKAISGSALGVVMEGSRALVLEVQALVCESSYPKRSATGYEKNRLDMLLALLERKLEIPLGHYDV

FVNISGGVKVSETAADLAVVAAIISSFKNRPLSKDSIFIGELSLNGEIREVFSLDTRLKEAKMQKFKNAI

VPSKPLEDIGLKCFVAKELSQVLEWM

>WP\_002866119.1 aspartate carbamoyltransferase [Campylobacter jejuni]

MRHLITTKDFNKVEIMELFKEASDFLDEKPRTFLKGKSITTIFFENSTRTLSSFESAARRLGARVLRLDV

SRSSSSKGETLYDTAANLDAMSPNAIVVRHANSGVPLILAKHIHCPVVNGGDGKHAHPTQALLDLFTIYN

HFQGDVEGKKICIVGDIKNSRVAASNIELLSRFNLDITLVAPPHFMPNTHLKKHYKLDENIIANSDIIMS

LRTQTERHNKTVYASLKDYANDFCIQKSLVKDKKLILLHPGPVNRNIDISDEMMSDERTLVLKQVKNGVA

IRMAVLKKLILENEG

>WP\_002866081.1 succinyl-diaminopimelate desuccinylase [Campylobacter jejuni]

MNAKEFLIELLKFKSVTPNDDGALNFIAMELSDFEAFFIEKEGIKNLLLTKKFNDEGEHLAFGGHVDVVP

AGEGWKNDPFEPLEEEGFIYARGAQDMKSGVAAFIDAVKDVSFKGRRLSLILTSDEEGEAKYGTKAVLEW

MKEKNMLPDYAVVAEPTCVKKMGDSIKIGRRGSINGKLLIRGKQGHVAYPEKCINPVHDFAPVLKLLAGF

DLDPGSAEFSPSKIVITDIRGGMGVCNVTPNDLKLMFNVRNSPDTSLEDVKSYVEKICHGLNYELELKQS

SEAFLTNIDNKIVQKMNESVQKITHEVPELNTKGGTSDARYFAKYGVKVVEFGVCNDRIHAIDERVSIEE

FEKLCLVFKDLIENF

>WP\_002865967.1 hypothetical protein [Campylobacter jejuni]

MDKLIPTWNEKYSIHDTMIDIQHQKLFELAAKIENAVYKFVQRDELKEILTELFNYMKEHFSNEEDYMQE

IHYPYLNEHKIMHKNIIHDMSYLIQNIKTTNDLKEKLYTIMSEWLLEHILHHDVMIGNWLSDQILSKQEE

ELEKINEEILYENTPTTPTAKQVKHKEYEFIYSCPCRTNHILSYTEHLDILCHKKQLRCKKCQKNLFYVK

SELKD

>WP\_002865910.1 hypothetical protein [Campylobacter jejuni]

MLKRLALLITLSSLMLYASDLVKIYLNQGLDAVGVAIEKELTQKDFWLSEIGDKNISLGYYDDNVAIVLT

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NLLDKVQGKTGGGIWIHGYPLDGSRLDEFKTRGCIALFNNNLEKFAQVVQDKKVFVMTEEKEKIRAKKDQ

IASLLADLFTWKLAWTNSDTNTYLSFYDEQEFKRFDKMKFEQFASMKKSIFSRKEDKKIKFSDINISPYP

NLENETMYRISFYEDYYTKNYQFRGDKILYVKIDSKGKMKILAEQ