Introduction:

The following index is laid out to display examples of a *tonB* gene and a TBDT gene from each proteobacterial species to demonstrate presence of functional Ton systems. Each gene was taken from the same genome accession as the *tol-pal* loci in SI. 1, to ensure that they are not *tolA* genes, and in no case are the neighbouring *tol* genes (*tolB, pal cpoB*) present. In cases where there were multiple TonB paralogues, the first *tonB* with the expected 3-domain secondary structure was analysed. Each identified TonB sequence is displayed in FASTA format, followed by its PsiPred structural prediction, followed by the domain II analysis, where domain II is outlined in bold and separated by spaces.

Every TonB in this list was also visually inspected in the embedded UniProt Alphafold prediction model to check for the presence of an N-terminal helix, domain II, and globular domain III. In cases of poor annotation, pBLAST searches were performed using *tonB* from the closest branches on the phylogenetic tree.

Each PsiPred prediction uses the following legend:



Helix: Proline analysis was performed by first defining domain II (indicated in bold for each protein), specifically after the predicted TMH, up to 100 residues before the C-terminus.

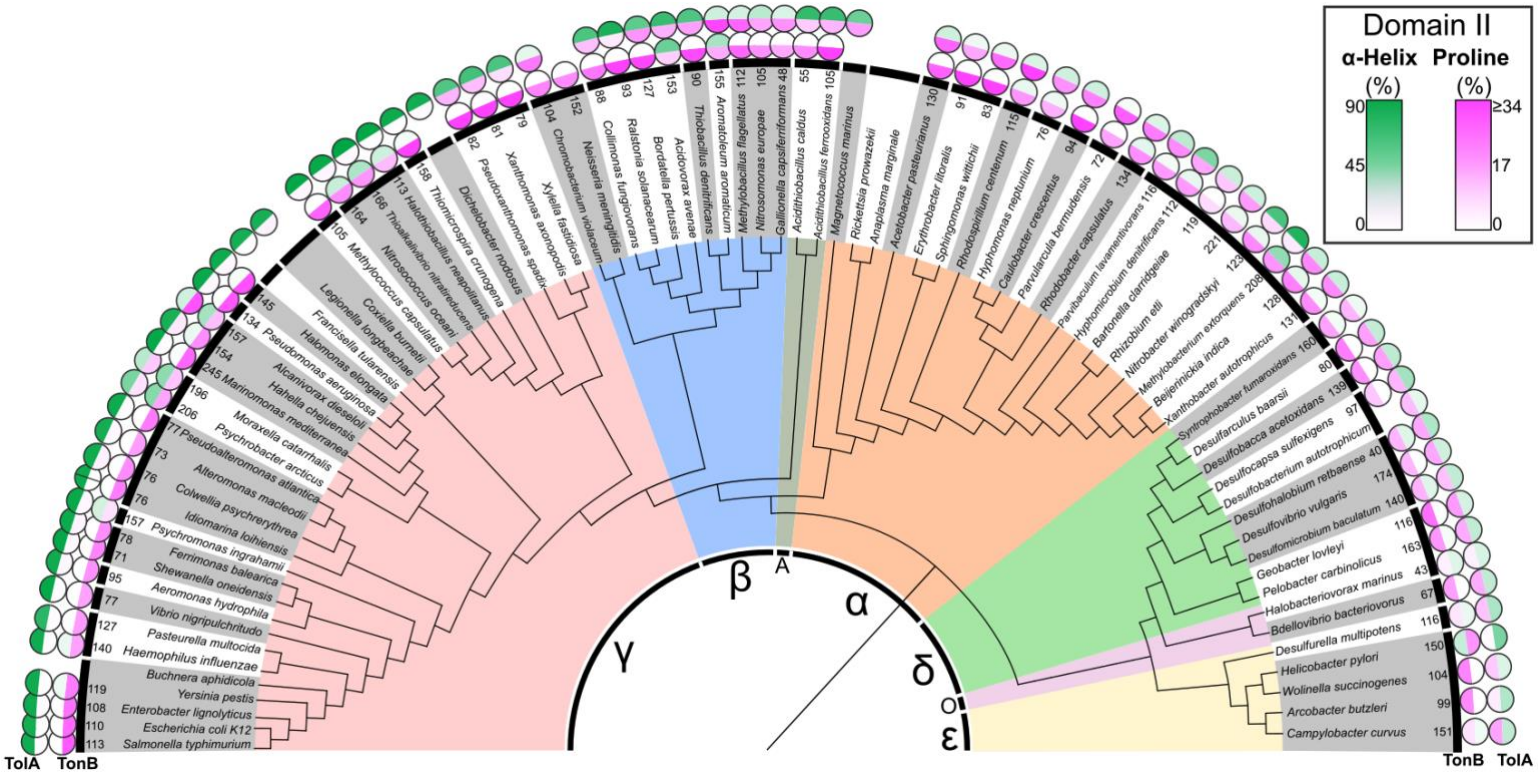

Figure S2.1 | TolA and TonB domain II length and secondary structure compositions vary amongst Proteobacteria. Genome accessions were screened for both *tonB* and TBDT genes (SS 1). Each representative TonB was structurally analysed by the same method as for TolA (SI 1). Proline content of some TonBII sequences exceeded 34%, but they are coloured the same for consistency. Phylogenetic tree adapted from Sharma *et al*., 2023. Circumferential numbers indicate respective length of TonBII per sequence analysed.

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Proteobacteria (Sharma tree)

γ-Proteobacteria

Enterobacterales

Salmonella typhimurium

>AAA27031.1 vitamin B12 transport protein [Salmonella enterica subsp. enterica serovar Typhimurium]

MIKKATLLTAFSVTAFSAWAQDTSPDTLVVTANRFQQPRSAVLAPVTIVTRQDIERWQSTSV
NDVLRRLPGVDIAQSGGARQNSSIFIRGTNSSHVLVLIDGVRLNLAGVSGSADLSQFPVSLV
QRIEYIRGPPSAIYGSDAIGGVVNIITTRDNPGTELTAGWGSNSYQNYDISTQQQLGEITRAT
LIGDYEYTKGFDVVAKGGTGMQAQPDRDGFLSKTLYGALEHTFSDRWSGFVRGYGYDNR
TDYDAYYSPGSPLIDTRKLYSQSWDAGLHFNGESIQSQLVSSYSHSKDYNYDPHYGRYDT
SATLDEMKQYNVQWTNSVVVGHGNVGAGVDWQKQTTTPGTGYVPEGYDQRNTGVYLTG
LQQLGDFTLEAAARSDDNSQFGRHGTWQTSAGWEFIEGYRFIASYGTSYKAPNLGQLYGY
YGNPNLNPEKSKQWEGAFEGLTAGVSWRISGYRNDINDMIDYDDHLQKYYNEGKARIKGIE
ATANFDTGPLTHTVSYDYVDARNAITDTPLPRRSKQMAKYQLDWDVYDFDWGMTYQYLGS
RYDSDYSAYPYRTVKMGGVSLWDLTVAYPVTSHLTVRGKIANLFDKDYETVYGYQTAGRE
YTLSGSYTF

>CAA39818.1 tonB protein [Salmonella enterica subsp. enterica serovar Typhimurium]

MTLDLPRRFPWPTLLSVGIHGAVVAGLLYTSVHQVIELPAPAQPITVTMVSPADLEPPQAVQ
PPPEPVVEPEPEPEPEPIPEPPKEAPVVIEKPKPKPKPKPKPKPVKKVEEQPKREVKPAAPR
PASPFENSAPVRPTSSTASATSKPAVSVPTGPRALSRNQPQYPARAQALRIEGRVKVKFDV
TSAGRVENVQILSAQPANMFEREVKNAMRKWRYEAGKPGSGLVVNIIFRLNGTAQIE



MTLDLPRRFPWPTLLSVGIHGAVVAGLLY
TSVHQVIELPAPAQPITVTMVSPADLEPPQAVQPPPEPVVEPEPEPEPEPIPEPPKEAPVVI
EKPKPKPKPKPKPKPVKKVEEQPKREVKPAAPRPASPFENSAPVRPTSSTA
SATSKPAVSVPTGPRALSRNQPQYPARAQALRIEGRVKVKFDVTSAGRVENVQILSAQPAN
MFEREVKNAMRKWRYEAGKPGSGLVVNIIFRLNGTAQIE

113 Domain II residues

33 Proline residues

0 α-Helix residues

Escherichia coli K12

>AAA23524.1 B12 receptor protein BtuB [Escherichia coli]

MIKKASLLTACSVTAFSAWAQDTSPDTLVVTANRFEQPRSTVLAPTTVVTRQDIDRWQSTS
VNDVLRRLPGVDITQNGGSGQLSSIFIRGTNASHVLVLIDGVRLNLAGVSGSADLSQFPIALV
QRVEYIRGPRSAVYGSDAIGGVVNIITTRDEPGTEISGGWGSNSYQNYDVSTQQQLGDKTR
VTLLGDYAHTHGYDVVAYGNTGTQAQTDNDGFLSKTLYGALEHNFTDAWSGFVRGYGYD
NRTNYDAYYSPGSPLLDTRKLYSQSWDAGLRYNGELIKSQLITSYSHSKDYNYDPHYGRYD
SSATLDEMKQYTVQWANNVIVGHGSIGAGVDWQKQTTTPGTGYVEDGYDQRNTGIYLTGL
QQVGDFTFEGARRSDDNSQFGRHGTWQTSAGWEFIEGYRFIASYGTSYKAPNLGQLYGF
YGNPNLDPEKSKQWEGAFEGLTAGVNWRISGYRNDVSDLIDYDDHTLKYYNEGKARIKGV
EATANFDTGPLTHTVSYDYVDARNAITDTPLLRRAKQQVKYQLDWQLYDFDWGITYQYLGT
RYDKDYSSYPYQTVKMGGVSLWDLAVAYPVTSHLTVRGKIANLFDKDYETVYGYQTAGRE
YTLSGSYTF

>NP_415768.1 Ton complex subunit TonB [Escherichia coli str. K-12 substr. MG1655]

MTLDLPRRFPWPTLLSVCIHGAVVAGLLYTSVHQVIELPAPAQPISVTMVTPADLEPPQAVQ
PPPEPVVEPEPEPEPIPEPPKEAPVVIEKPKPKPKPKPKPVKKVQEQPKRDVKPVESRPASP
FENTAPARLTSSTATAATSKPVTSVASGPRALSRNQPQYPARAQALRIEGQVKVKFDVTPD
GRVDNVQILSAKPANMFEREVKNAMRRWRYEPGKPGSGIVVNILFKINGTTEIQ



MTLDLPRRFPWPTLLSVCIHGAVVAGLLY
TSVHQVIELPAPAQPISVTMVTPADLEPPQAVQPPPEPVVEPEPEPEPIPEPPKEAPVVIEK
PKPKPKPKPKPVKKVQEQPKRDVKPVESRPASPFENTAPARLTSSTAT
AATSKPVTSVASGPRALSRNQPQYPARAQALRIEGQVKVKFDVTPDGRVDNVQILSAKPAN
MFEREVKNAMRRWRYEPGKPGSGIVVNILFKINGTTEIQ

110 Domain II residues

29 Proline residues

0 α-Helical residues

Enterobacter lignolyticus

>ALR74858.1 vitamin B12/cobalamin outer membrane transporter [[Enterobacter] lignolyticus]

MIKKASLLTALSVTAFSGWAQDSGSDTMVVTANRVEQPINTVLAPVSVVTRQDIDRWQSTS
VVDVMRRLPGVDVAQYGGLGQQSSLFIRGTNSSHVLILVNGIRLNQAGVSGSSDLSQFPISL
VQRIEYIRGPRSAVYGSDAIGGVVNIITTRDRDGTTLNAGIGTYGYQSYGGSTQQTLGGNTR
VTVAGDYTYTKGFDVVAEGNTGGVAQPDRDGFMSKTLYGSIEHDFSDQWGAFVRGYGYD
NRTAYDGSVFTPGVLVDTRQLYSQTWDAGLRYNNDIFHSQLTSSYSHSKDYNYDPNLGRY
DSTATLDDVKQYNLQWANSVEVGHGNIGAGVDWQKQSTEPGTSYVTDAYDIRNTGLYMTA
LQKLGDFTLEGAARSDDNSQFGQHGTWQSSAAWEFIDGYRFVASYGTAFKAPNLGQLYG
FYGNENLKPEESKQWEGAFEGLTAGVTWRVSGYRNDIDNLIDYNTDLQKYYNVGQARIKGI
EATASFDTGPLTHNIGYDYVDARDAKTNELLDRRAKQQVKYQLDWQVYDFDWSMTYHYLG
TRYDTDYSTYPSQKVKMGGVSLWDVAVSYPITSHLTVRGKIANLFDKDYETVYGYHTAGRE
YNLSGSYTF

>ALR76948.1 energy transducer TonB [[Enterobacter] lignolyticus]

MTLDLPRRFPWPTLLSVGIHGAVVAGLLYTSVHQVIELPAPAQPIMVSMVAPADLEPPQAVQ
PTPQPVAEPEPEPEVVPEPPKEAPVVIHKPKPKPKPKPKPEKKVEQPEREVKPVEPRATSS
FENATTPSRPAMNSAPATSAPVAAAPSGPRALSRNQPQYPQRAQALRIEGNVRVKFDVTP
EGRVENVEILSAQPSNLFERDVKAAMRKWRYEPGKPGTGLVMNIEFRLKGVQMN



MTLDLPRRFPWPTLLSVGIHGAVVAGLLY
TSVHQVIELPAPAQPIMVSMVAPADLEPPQAVQPTPQPVAEPEPEPEVVPEPPKEAPVVIH KPKPKPKPKPKPEKKVEQPEREVKPVEPRATSSFENATTPSRPAMNS
APATSAPVAAAPSGPRALSRNQPQYPQRAQALRIEGNVRVKFDVTPEGRVENVEILSAQPS
NLFERDVKAAMRKWRYEPGKPGTGLVMNIEFRLKGVQMN

108 Domain II residues

27 Proline residues

0 α-Helix residues

Yersinia pestis

>ABG12081.1 putative vitamin B12 receptor protein [Yersinia pestis Antiqua]

MIIKNTMTIKKYTLLTALSVTAFSGWAQGNNTTDNNDEMVVTANRFPQPKSSVLAPVDVVTR
ADIDRWQSTNINDVLRRLPGVDIAQDGGMGQRSSLFIRGTNSSHVLVLIDGVRLNQAGITGA
SDLSQIPISLVQRIEYIRGPRSAVYGSDAIGGVINILTGRDKPGTTLSAGLGSNGYQTYDGST
QQKLGEDTTVTLAGNYTYSKGYDVVAGMPGAGGPRQPDRDGFMGKMLWAGLEHQFNEQ
FNGFARVYGFDNRSDYDGYTNYSNPLALIDTRKLSSRTYDTGLRYKNGIYASQFIASYNRTK
DYNYSPLFGQHDITASLDEAEQYNLQWGNTFQLTNGMISAGADWQEQRTERKSSNQNTTA
DFTQHNTGIYLTGQQQISDVTLEGAVRSDDNSQFGWHSTWQTSAGWEFIDGYRLIGSYGT
AYKAPNLMQLYSAYGGNANLKPEESKQWEGGVEGLTGPLTWRLSAYRNDIDQLIDYSNLT
NGYFNINKATIKGVEWTGSFDTGPLSHQVTLEYLDPRNADTHEILVRRAKQQVKYQLDWQV
ADLDWSVTYQYLGQRYDKDYSTYPEETVELGGVSLWDLAVSYPVTSHLTVRGRIANLFDK
DYEMVYGYQTPGREYYFTGSYNF

>ABG13518.1 TonB protein [Yersinia pestis Antiqua]

MQLIKFFSDRRLTWSLIFSIGLHGSVVAALLYVSVEQMKIQPEIEDTPLAVTMVNIAEFAAPQP
AAAAPEPVQETPAVPEETPPVLEETPPEPEELPEPVPVPVPEPVKPKPKPVKKEVKKPEVK
KTQAPPDDKPFKSDEAALVANNAPVKSAPVASTPGLSTSAGPKALSKAKPSYPARALALGIE
GQVKVQYDIDESGRVTNVRVLEATPRNTFEREVKQVMRKWRFEAVAAKNYVTTIVFKLDGK
MEMN



MQLIKFFSDRRLTWSLIFSIGLHGSVVAALLY
VSVEQMKIQPEIEDTPLAVTMVNIAEFAAPQPAAAAPEPVQETPAVPEETPPVLEETPPEP
EELPEPVPVPVPEPVKPKPKPVKKEVKKPEVKKTQAPPDDKPFKSDEAALVANNAPVK
SAPVASTPGLSTSAGPKALSKAKPSYPARALALGIEGQVKVQYDIDESGRVTNVRVLEATPR
NTFEREVKQVMRKWRFEAVAAKNYVTTIVFKLDGKMEMN

119 Domain II residues

27 Proline residues

6 α-Helix residues

Buchnera aphidicola

No *tonB* or TBDT genes detected.

Pasteuralleles

Haemophilus influenzae

>AAC21789.1 hemin receptor (hemR) [Haemophilus influenzae Rd KW20]

MNILINKRIFLLVTLVGIQLNVTAKQNSSNSNREELLPIIVNTNDDSNKLPGRSVLKQKNIEQX
QADNAANLINILPGVNMAGGFRPGGQTLNINGMGDAEDVRVQLDGATKSFEKYQQGSIFIE
PELLRRVTVDKGNYSPQYGNGGFAGTVKFETKDARDFLQENQKIGGFLKYGNNSNNNQKT
YSTALVLQNEQKNIDLLLFGSVRNAGDYKRPDNSKILFSKNNQKTGLIKLNWQISPEHLLTLS
SVYGIHKGWEPFAAKRDILPKPSLSDIMRYGTDIAWKRKLVYRDQKDENYTLKYNYLPENNP
WINLSTQFSYSKTTQNDMRPKEASSGLVGSLGNQSWITYSDLTFDINNTSTFNIKTTVHELL
FGLQWLKNTRNTLMYDKSKVRKADYNYGYFQPYYMPSGRQYTQAFYLQDQIKWKNIIFST
GVRYDHINNIGQKNLALKYNDISAGHDYSQKNYNGWSYYLGLNYDVNHYLSLFTNFSKTWR
APVIDEQYETQFKQSSVPATSLNLEKEMINQTRVGGIITLNHLFQENDAFQFRTTYFYNRGK
NEIFKTRGVNCVGNAADTNNKVCPKIIENYRNLPGYVIQGAELEAYYQSTYLFGEITYSYVKG
KRDTSPRNPWGKTSTWIAEIPPRKATTALGFNVPKYYLTVGWRAEFVRRQDRSPLSGDPK
ASSWSLPASRGYSLHNLFLSWSPAKIKGMNVKITVDNLFNRAYNPYLGELASGTGRNIKFSL
SQKF

tonB flanked by motor genes

>AAC21917.1 tonB protein [Haemophilus influenzae Rd KW20]

MQQTKRSLLGLLISLIAHGIVIGFILWNWNEPSDSANSAQGDISTSISMELLQGMVLEEPAPE
PEDVQKEPEPEPEPGNVQKEPEPEKQEIVEDPTIKPEPKKIKEPEKEKPKPKGKPKGKPKNK
PKKEVKPQKKPINKELPKGDENIDSSANVNDKASTTSAANSNAQVAGSGTDTSEIAAYRSAI
RREIESHKRYPTRAKIMRKQGKVSVSFNVGADGSLSGAKVTKSSGDESLDKAALDAINVSR
SVGTRPAGFPSSLSVQISFTLQ



MQQTKRSLLGLLISLIAHGIVIGFILWNWN
EPSDSANSAQGDISTSISMELLQGMVLEEPAPEPEDVQKEPEPEPEPGNVQKEPEPEKQE
IVEDPTIKPEPKKIKEPEKEKPKPKGKPKGKPKNKPKKEVKPQKKPINKELPKGDENIDSS
ANVNDKASTTSAANSNAQV
AGSGTDTSEIAAYRSAIRREIESHKRYPTRAKIMRKQGKVSVSFNVGADGSLSGAKVTKSSG
DESLDKAALDAINVSRSVGTRPAGFPSSLSVQISFTLQ

140 Domain II residues

22 Proline residues

8 α-Helix residues

Pasteurella multocida

>AAK03706.1 HasR [Pasteurella multocida subsp. multocida str. Pm70]MQKQQPYPIHLGIFLMLGLPTWAFSQANLEKSTINKLETILVNESEEKNKFDENLIKTY
LSSGSYSYLSQSDISTFRGSSVGDFLSGVPGVIVGNKRNSGALSVNIRGIANENRVPVWIDK
GLQSVPSYQGYAGSSTRTYLDPDLISQVEIEKGPSLQMDATGATGGVVRVETLRWQDIIPQ
GKNWGVRLKLGTMTNTVSPPPYYTRGGYQTKYISKCLSNHTGLCQTQTYAPNARYSSHGF
DLNAYNYSLAFANKWQNADLVLAYAKRKQGNYFVGRHGQTPVIESIEFEEDSVEVKEPRVH
EEVEIGSLTFKENRSTLYRPGEEALNTSQDNTSYLAKINVYNDVHRLGLAYRHYHSRFGEIM
SSILNFRAYGALQGEGTEVKVDSYHANYSYNPTTPYVNLNVNAYFTDSDSSNFTPFIEEYGY
SLSSRHAHFLVSKQKGLSIENTSIFQLNDKPFSLKYGLAHSYERIYQPRNAQARVRAKGYPE
DAIGPLYIRDGKRKEWSAFVAANYPITSWLKADIGLRYLQSTIYDYIVRTERVNIGGAFVPNP
NGPGNIWVEKYKDVVHKQAPVKNKGMSPIVMLTFEPINGVQIYTKYAEALRSPSLFQATKG
WSMSATADNLEQLRPERAKNWEAGINLFYENLGGKDNILGFKLAYFNNRIKDYLTRSYSPK
DKVTQTINIQSAQFKGIELSAYYDMGKFYAKLAGTYYTKTKFCLTAEQAGKGEQCNSGYIYR
SNLNNAVPPRLNLHATLGTRLFEQKLDIGARYSYYSKRLVPVLSAERFVNTSSIEWAPYSLV
DLYANYNVSNNLKLTMTMDNVFNRYYLDINNMGLNTAPGRTLHLGLEYRF

tonB next to motor genes.

>AAK03272.1 TonB [Pasteurella multocida subsp. multocida str. Pm70]

MIDKSRSCIGFAISLLFHASFVSFLYWIVQKDDDSANGFAADIISTHISMEMLAATVLEEPEPE
PEPAPPVVEPELPKEEVADPTVKPEPPKEPEKPKEPEKPKEKPKEKPKEKPKKPKKEQRDL
PKSDRQIDSNSSINQQATTTGNITTNNPNLVGKGNSTDEVNAYRSALRREIEKHKRYPNRAR
MMRKQGVVTITFHLNNAGVISNARISKSSGSEELDNAALVAVNNARPIGPLPAGMPNEVSVP
VSFRITN



MIDKSRSCIGFAISLLFHASFVSFLYWIV
**QKDDDSANGFAADIISTHISMEMLAATVLEEPEPEPEPAPPVVEPELPKEEVADPTVKPEP
PKEPEKPKEPEKPKEKPKEKPKEKPKKPKKEQRDLPKSDRQIDSNSSINQQATTTGNITT
NNPNLV**
GKGNSTDEVNAYRSALRREIEKHKRYPNRARMMRKQGVVTITFHLNNAGVISNARISKSSG
SEELDNAALVAVNNARPIGPLPAGMPNEVSVPVSFRITN

127 Domain II residues

22 Proline residues

0 α-Helix residues

Vibrionales

Vibrio nigripulchritudo

Locus

>CCO59343.1 putative Outer membrane vitamin B12 receptor BtuB [Vibrio nigripulchritudo]

MKKTLLATTVASLLTHASISVAQEAAETETLVVTANRFEQSTQSTTLPVVVVTKAEIEAIQAN
DIYEVLRRLPGIQVGSNGGYGQSQSLFVRGTNSDHVLVLIDGVRTSSATTGQANIAAIPLVG
VQRVEFVRGTRAALYGSDAVGGVINIITDTSVSEAKANLGFGSNNYQKASLAVSGEIGESTS
GSFAAKFAETEGFSAQNSSGNEDADGHKVAEFAASLTHQLNNEISFKFNSTYSDGEVEYDP
ADSKKDQQLYSIVGSANYSGEKLSSKLAVSKAQDSSYYPSFNGTFQTDSQSVAFTNLYSVT
SEISVGAGVDWYKDDISETSTKYDETSRTNKSAYVSGFFDNQTFQAELAVRGDDNQRYGK
NSTWQVGLGYKVTDNHRVTANAGTAFKAPTFNDLYYPGSGNPDLKPEKSTNYELALEGRQ
SWIDWRVAAYQNKIKDMLIGWPAKNVGEAEIKGVELSGLFETGAFSHEVSLDFMDPKDKIN
DVQLSRRAKQSAKWNATYVADEWQADISYLYQGKRVDNDGKTELGAYSLVDVAASYFVTE
QLTVRGRIANLFDQNYVLAKGYNTQERSYFVNLDYKF

tonB next to motor genes.

>CCO56590.1 TonB2 [Vibrio nigripulchritudo]

MKRLFLALPVAFIVSASLFYFMAWMVSSQNGKLEESKPSVMFDLVMQEPEANVQRRQREL
PEPPKLPDQPKPLPTSTPNVAKAQVPQTLTAPKLALANLGVAVSMPSLDGIGQDQQALPLY
RVEPRYPPRAQKRRMEGYVVLSFTIDEQGRPEDINLVEVHPNKIFVREAMNALKRWKYQPK
LEGGKAVKQLDQRVKIEFKMSK



MKRLFLALPVAFIVSASLFYFMAWMVS
SQNGKLEESKPSVMFDLVMQEPEANVQRRQRELPEPPKLPDQPKPLPTSTPNVAKAQVP
QTLTAPKLALANLGVAVS
MPSLDGIGQDQQALPLYRVEPRYPPRAQKRRMEGYVVLSFTIDEQGRPEDINLVEVHPNKI
FVREAMNALKRWKYQPKLEGGKAVKQLDQRVKIEFKMSK

77 Domain II residues

12 Proline residues

0 α-Helix residues

Aeromondales

Aeromonas hydrophila

Locus

>ABK39619.1 vitamin B12 transporter BtuB [Aeromonas hydrophila subsp. hydrophila ATCC 7966]

MSKKLLAAALLPTAAFAQTTIPVNPTLVITANRVEQPISSVLAPVVVIDRAEIESRQVQSLPALL
KTLPGVQITTLGGRGHMSSLFIRGTNSNHSLVLMNGRPIAAMVAGTPDLSQIPLGNIERIEYI
RGPRAAVYGSDAIGGVINLITKTSAKNGSETHLKGGVGSNGYGQGQLRTVQALGQQTDMN
MMIGYERTDGFDVVANAQQPDRDGFDSLNGQFGLSHAFNDAWSADFNAQGYDNQTEMD
DAYQSADQSRVQAFQYDGGLKYQSGALSSRLEASYGENKLKSWLESKGESSAEPIHTGLT
RFSWINSWSGVEGLNLTGGADWQQEQLKSDTRSYGQAFNAPDRDNTGLFVVGSYRWQA
LLWELSGRTDDNKQYGRHNTWSAASGLDLDDNHNVRLSYGTAFKAPTFLDLYYPGYENPA
LKPEESKNLELGFSGRYTGWDWSLNLYRNQIQNLIACQSASSTCRPDNTDAEIRGVEVALG
LETGPLRHDLSFDYTRAEDKNDGDQQLLRRAKQKASWLTQVQLGPVDLSTELLYVGKRDD
KNFSSFPAERVELGSYTLINLGASYGVTPQFTLGGRIDNLFDRDYAPAYGYASAGTEFKLTA
DYRL

tonB next to motor genes. Two copies of *exbD*, very large *exbB* gene, predicted to form long periplasmic extension.

>ABK37434.1 outer membrane receptor-mediated transport energizer protein TonB [Aeromonas hydrophila subsp. hydrophila ATCC 7966]

MKYKLMSLGLGIALSLGILLFMATLVEPPRGEKASAEQKSIVINMQNEVTEVQVRERPIPQEP
EPLPEPPAALASTPLPMPAAAPLPSVQPSLDLVSSLSAVQVYAPGVATSPTPVASGNFHGQ
QQGAGIGAGDMLMPLQRIEPVYPYRAQQAGIEGSVTLRFSVDADGRVQDVEVVEAKPKRQ
FERAAIQAINKWRYQPRPGATDKLVQIITLKFKLES



MKYKLMSLGLGIALSLGILLFMATL
**VEPPRGEKASAEQKSIVINMQNEVTEVQVRERPIPQEPEPLPEPPAALASTPLPMPAAAPL
PSVQPSLDLVSSLSAVQVYAPGVATSPTPVASGN**
FHGQQQGAGIGAGDMLMPLQRIEPVYPYRAQQAGIEGSVTLRFSVDADGRVQDVEVVEAK
PKRQFERAAIQAINKWRYQPRPGATDKLVQIITLKFKLES

95 Domain II residues

18 Proline residues

0 α-Helix residues

Alteromondales

Shewanella oneidensis

Locus:

>AAN53891.1 TonB-dependent vitamin B12 receptor BtuB [Shewanella oneidensis MR-1]

MGTHPTKIALLIGSLCSFSIIAPVMAADDTSTAKVDEHLVVIGRSDKTPLNIAANVNVIDAAAIE
MSGATNLTDVLRGQSGIQISDNNIGTSFAMRGFSASTAVNNTLILLDGRRLNNIDIAAPSLNAI
PLNLVERVEILSGSAGVLYGDQAVGGVINIVTKSPENTGGSVQLSGGSFNTYEGRGDVSGAI
NKDWRYFLSGSYNQGDNYRQHNANETGSILGRIQYKTATDSFFVETSYYDDDRENPGSLT
VDQFKFDPRQSSNKSEYVHEMTTAARSGYQHQLNQNWALAADLDYSDTLVSSVNWGAGS
HNTRSLLMFSPKALANYSTRQGELNLVTGLDISRGKADYDSMARSNVQDMQSAYLQATVP
LSHTLSYVVGGRYARVTDELVDGNVYPNGIDLDEDATAFEFGLNYRPSAEHRFYLRGDENF
RFAKVDEQAYTPKDVFGLKPQTGRSYEAGWDWTVASQSLRVSLYRLDLEDEIVFDPSAEK
PVGGSFQGANVNADASRRYGASADWDWQVTQALQLGLEYNYIDAEFTDGLNDGKKLSWV
AEHSGRGYVSMDVAEHIQLFAEAIYTGERFVEGDNANQGEKLASYVLGNLALNYSRDAWL
ASLRIDNLFDKDYVSSGYYGGNWGDGYYSGRGRDIRLTVGYRF

tonB not near motor genes.

>AAN57525.1 TonB mediated energy transduction system energy transducer component TonB [Shewanella oneidensis MR-1]

MGQNVIVNRTGIIVVSALIPLGLFVFMAQLIHNPQPLSGQATDAPQINILMSERTPIPPKESRK
PEPPKPIPTRERITTPGESTEVVDFNPQTFTPEMPIQTTLFTQSSMSAEALPLVQVSPRYPIE
AAQNGKEGYVVVGFDITADGTVSNVRVLDANPKRIFDKEALSAVQNWKYKPKFDAGKAVP
QLNQQVQLDFKLDQKI



MGQNVIVNRTGIIVVSALIPLGLFVFMAQLIH
NPQPLSGQATDAPQINILMSERTPIPPKESRKPEPPKPIPTRERITTPGESTEVVDFNPQTFT
PEMPIQTT
LFTQSSMSAEALPLVQVSPRYPIEAAQNGKEGYVVVGFDITADGTVSNVRVLDANPKRIFDK
EALSAVQNWKYKPKFDAGKAVPQLNQQVQLDFKLDQKI

71 Domain II residues

15 Proline residues

0 α-Helix residues

Ferrimonas balearica

Locus:

>ADN77205.1 TonB-dependent receptor [Ferrimonas balearica DSM 9799]

MKYSALSVALFAAAPLAWSAPAVDVDETLIVTGDRLAQSVDSVLAPVTVIDRASIVAMQAKS
LSDILRTLPNVDVNQYGGRGQNATVTVRGATSAQSLVLIDGMRSTTSALGPLNINSFPVAEI
ERIEFIRGARASVYGSEAVAGVINIITRDGRDGTTLTAGAGSFEQVEASVRHQSQLAGGTLK
AVLAYEDEEGYNVHPVPGVNDGDKHGFTGKSALLAYDRAVTERLSLYAAARWFQNESQYD
NSSLGNPAWGAPDVRERKENRFENVDYQLEARYQGERWHSSVQAQYSDSESQDFVDTL
SYKDSPDFSHLRQYNLAWVNRVQLTDAISVGAGLDWRDEQLRGDSTYLDWATGVATPFA
DGTLSRDNTGAYALLRVEEGGHQFEASVRSDDNEQYGQHTTWQVGGRIAATESVALVASV
GTAFRAPTFYDLYYPGSGNLDLRPETAEHYELALEGAVASIDWRLGWYRQDAEDLIQFDSL
TYRPVNIGEAVIDGIEAEAAFDTGPVHHQLSYGWRDSEDRTTGNELAASARHNAKWNLSYD
WDALNLTGNLVYRGSRWGDAANTVKLDAYFLVNLAASYQLTESLALRLRLENLLDEEYVTIA
DTFSGGSYPGQERSVYGQVEYRL

tonB appears to be near a heterologous motor, where one of the two copies of ExbB has an extended periplasmic domain.

>ADN75628.1 TonB family protein [Ferrimonas balearica DSM 9799]

MRDYLLALCLGGAITAGLFSLMAMMVTGGPGKAPSEPGPAPVSVLMADRPEQLNRRSRAL
PEPPPPLPELPQAQVVENSSATNVQMNLDLPTLSIDGPGDIQIGMPAKADLATADRQAMPL
YRVEPAYPQRALRMRAEGYVLMEFTIDEQGRPRNIRVIESEPVRLFDQAAMKALARWKYQP
KQLDGKAVSQPGQTAKLEFKLNR



MRDYLLALCLGGAITAGLFSLMAMMVT
GGPGKAPSEPGPAPVSVLMADRPEQLNRRSRALPEPPPPLPELPQAQVVENSSATNVQ
MNLDLPTLSIDGPGDIQIGM
PAKADLATADRQAMPLYRVEPAYPQRALRMRAEGYVLMEFTIDEQGRPRNIRVIESEPVRL
FDQAAMKALARWKYQPKQLDGKAVSQPGQTAKLEFKLNR

78 Domain II residues

15 Proline residues

0 α-Helix residues

Idiomarina loihiensis

Locus:

>AAV82015.1 Outer membrane protein [Idiomarina loihiensis L2TR]

MNTNTFRKSVTALAVTATLGFPAFVAAQDSGANDVERIQVTGSRIKRTDMETASPVSVFDA
EAIEASGFTTMENFIHNLPSMNGAMNGSSTNNGSGGYATANLRGLGSARTLILINGRRYAS
GDLNAVPMAMVQRVEVLRDGASTIYGSDAIAGVINFITKTDFEGAEFSAQYDLTGEGDGETT
KLSGVIGTSSGKGSVVLGLEYQNRNAIGQADRDFSRIPLAEKNGKAVFDGSTINEFGSFVPT
GEKKTYVLDPQTGEQRLFNAQKDGYNYATDSYLKSPQELFTINAVANYDITRDLRVFLEGG
YANRQSNQLLAPTGTFWGAPVDADFEYNKTGKDLSVYRRLTETGGREYTQDFSDYRMVL
GFEGYLDNGWSWDISYNYARYVDTTVEYNQANRTRFNTLLDEELCNSDEECPGIWNPFEA
DSLTDEMMDYALIANSPVVRGTTKQFMANLTGDTGSWSLPAGSIAWAAGVEKRWESYEN
QPDGAAAIGQIYSTPGIPSEGSYDVEEAYIEVDAPLLRDLPGVQSLDLSAAVRRSDYNFLDA
QTTTKFGLEYVPKDGLLVRATIAEGFRAPTIDNLNSPQVISFSRYVDPCTEYGDSSNDILDAN
CKADGLDSDFTPKTSQSATILSGNADLKPETSDSFTLGVVYQPEFMDNLNVAIDYYDIEIENG
IGAPDISLIAEQCYTSENFSSASCDLILGPEAVDTKSWPSSDYRDAQGTLAGTDATTQNISTF
ETSGIDFDVNWNDEVAGGLLNLRLDGTYLKDYNYQVQEGAAPLELAGNFGADSNFAGRIAA
FSKWRTNFTASYKVEDVAVTWISRFQSGVDDVNYDSSDLSSSVGSYIYHDMQASYFFNSE
TTFTLGIRNLFDKQPPYVSNNNDMNTLNTSYDTAGQYWYARVGFRF

tonB next to motor genes, heterologous motor observed with large *exbB* genes and two *exbbD* genes. ExbB-associated gene ExbB

>AAV82687.1 TonB-like periplasmic protein [Idiomarina loihiensis L2TR]

MVRFLVSLLLGAAVTFALFAFMAYLIGGGAQRNEAPAPTPVIDIVTSPPESDVQERRRTPPP
PPPPPEQPPETPQSEPDTSDSGMNMNMGFDVDVGGADTGLSGPGGGLSSDGDATPIVRI
EPRYPPSAARNGTEGWVQLRFTIDQQGGVTDVEVIDSEPRRVFDREARRALLRWKYKPKV
VDGKPIRQEGMTVQLDFTMDGN



MVRFLVSLLLGAAVTFALFAFMAYLIG
GGAQRNEAPAPTPVIDIVTSPPESDVQERRRTPPPPPPPPEQPPETPQSEPDTSDSGMNM
NMGFDVDVGGADTGLS
GPGGGLSSDGDATPIVRIEPRYPPSAARNGTEGWVQLRFTIDQQGGVTDVEVIDSEPRRVF
DREARRALLRWKYKPKVVDGKPIRQEGMTVQLDFTMDGN

76 Domain II residues

17 Proline residues

0 α-Helix residues

Colwellia psychrerythraea

Locus:

>AAZ28743.1 tonB-dependent vitamin B12 receptor [Colwellia psychrerythraea 34H]

MNKTIIALSISSLLYSSLSFAEQTSPTTIDKADETIVITANRSIQDKFDTLASVNIFTRENIEQIQP
LSISDLLGRVAGISINTQGTSAHKTSAFVRGTNSDHVLVLVNGVRIGSATLGSKSLASIPVQL
VERVEVIKGPRAALWGSDAIGGVIQIFTRDLAAGEGQVGIKVGSDSLYQGYGALGFGNKEH
GYTLSATAEKSDGFDVVVPDGNSQYTVDQNDDDGYDRQSIALSGTSQFTQAYALELNTQY
DQGTTEFDANTKYGGDETTYENYHFLLRNHLQLEQVYLQLGLSTSEDSTEDNYSKYNSQN
SASNANSLFTTNREQVTALAQLPLADSSEITAGFEWYTESIESNKEYDETDRDANAVFVTGR
HDIEQVKLEASVRYDKVGDIDSETTYQVAAGYQVNDQLLFSLSHGTAFKAPSFNDLYYPWQ
GNPDLISETADTSEFLARFQNDTLSAEVSIYQSDIDNLIEWAPTASGAYKPSNVAKAKILGAE
ATFTAAIYNTNNTLTLSHVDAEDKTTDHQLARRPNFSANYNFVYSLKQFDFTFDVDYQGSR
YDGANDPVKTLKAFTLLDVGLNYRLNNQVSLLAKVTNLTDKDYQTSSEYPGSERGYTLTVD
YKF

tonB next to heterologous motor with periplasmic domains. ExbB prediction.

>AAZ26539.1 putative TonB protein [Colwellia psychrerythraea 34H]

MVRFLVSILLGVVVTFGLFAFMAFLVSSGDRNKEEQQENIIVEVNTTPPKSAAEQRRRVPPP
PPPPPKAPPKQQTPEPEANNNTGGLNFNMPGVQMAGASTGLSAPGAGMGRDGDATPIVR
IEPKYPIQAARDGKEGYVILSFTINKIGGVEDVKVLEAQPKRVFDKEAKRALRKWKYKPKVVE
GKPLRQPGLTVQLDFKMGG



MVRFLVSILLGVVVTFGLFAFMAFLVS
SGDRNKEEQQENIIVEVNTTPPKSAAEQRRRVPPPPPPPPKAPPKQQTPEPEANNNTGGL
NFNMPGVQMAGASTGL
SAPGAGMGRDGDATPIVRIEPKYPIQAARDGKEGYVILSFTINKIGGVEDVKVLEAQPKRVF
DKEAKRALRKWKYKPKVVEGKPLRQPGLTVQLDFKMGG

76 Domain II residues

15 Proline residues

0 α-Helix residues

Alteromonas macleodii

Locus:

>CAI3964402.1 iron complex outermembrane recepter protein [Alteromonas macleodii]

MFSFLLDSSFSVSSKSSSGLSVSIAALPLLLTSSFSVAQGAPLNEVERYTVTAARPYYDETLS
RIFPQYEFDKSGLVAPLHTNDVLLQSPSVSLNGQGGQIQSISIRGYSRWRIQTLLDGVPIVSD
RRAGSSIGFIPPDFISTVSVLPGAASTYLGSGAIGGAVNLHFGEIQKPHLRVGYSSNQQMKA
LSYAGSTRRADNSNSLTEVSETDWNISYRSADNGEDANGGSLFDQFEQSGLFVRHRPVDS
VIKEAWTLYSDNNDIGKSSSDFPESRITTYPDNTHWLGKIAFESHLFTGNVWWHKSSLETSV
LRPESRINDSENKAFDYGFNISTDTQLKDWDLNWQLQVTGRDGVVADEREFTLTPAERALP
DTTSPSFITNAFEAELAYEVRTLDASEITTAAVADASRQWQSLSLALGARVDWQRQSDDSD
ANTFQSSTAQTNTNLSGYLGANYQLSQHWAAGMYVSSAFRNPSLTERFFAGETPRGTVLG
SLKLETEQALNMQASVAYSSEQLQGSIEVFNQKIDNYIERIMVAEDVLQYSNLDSATIEGVSY
QLSWQSHNDALDARLSGMWISGEDDLGNSIADIPANSQRLDLGVQWQAVRFFTIFAYRASK
TDIADGERALDEVFTLDMGADWQLNERVQLQASWRNLTNQQYYTSADDKAAFAQGESVQ
LAITYLL

No motors near *tonB.*

>CAI3955250.1 protein TonB [Alteromonas macleodii]

MQTTILPNANPKHLTHQSVLPFEKAPFAKRALNAATIAIAGCTVTAGLFVLMAELIKQDKVNIS
EAPPVFFEPIIYQPEDERTITKKPMVPIEQVIKTPPQKVIEIDPEPNEGPGGFEIKTHIPNTGLD
LSINLNSAQGDMQATPQFRVDPTYPPEASRDGIEGWVKLGFTISASGSVSDITVLDSEPKRV
FDRAARRALKKWKYKPKLNDGKPVSQSGMVVVLDFKLEQ



MQTTILPNANPKHLTHQSVLPFEKAPFAKRALNAATIAIAGCTVTAGLFVLMAELIK
QDKVNISEAPPVFFEPIIYQPEDERTITKKPMVPIEQVIKTPPQKVIEIDPEPNEGPGGFEIKT
HIPNTGLDL
SINLNSAQGDMQATPQFRVDPTYPPEASRDGIEGWVKLGFTISASGSVSDITVLDSEPKRVF
DRAARRALKKWKYKPKLNDGKPVSQSGMVVVLDFKLEQ

73 Domain II residues

12 Proline residues

0 α-Helix residues

Pseudoalteromonas atlantica

Locus:

>ABG40383.1 TonB-dependent receptor [Paraglaciecola sp. T6c]

MTKHADIHRKCRLSALIDESSHTKGGKNKNQVSNSIKHTLSNTLRTVMFRESVKKRIPVFQL
SMLAVTSLVAASIAEAKAAEANTAKANMFKEDRSESQVTTTDISDVIVVTGTRQAENLLTLTG
NLARINRQDIQTVSSVYPSDLLNRASGVYVQANNGMESLPSLRSPVLTGPGAGGAFLILED
GIATRAAGFANNNGLSELNLAQAQEVDIVRGPASAIYGSNAVHGVVNVINQAVRDGGDVSL
LLGPNEHYQVQGTLGNDFGAHGLSINTQLIDNGGYQDDSDFTSAKVGLRHEYRDDLNAITT
SVAGFVLDQNTAGFIASGDNGEGCFESTYADDRLFKDTQAMEKNCEDDAYRKWSSMRVA
SKWQRTLSDDRYFVLTPYVRTNDMEFRQHYLPSEAIEENSHSSFGLTSSYHWQFDPRLAL
VMGADAEWTSGELTETQQKASTFSFGKARQQGVHYDYEVDVLTLAPYVQADWQYSHALR
MSASVRFDSTHYDYKNRLADGTTQADGSPCVNGNNEPVACLYQRPADSKDDFDNVSSKIG
FNYLMNESVALFADWSQGFRAPQTTDLYRIQNQQVAGQIESEEIRSQEVGVRGLALDMNF
ELVAFYMTKDHFFFRDDDGLNVTDAETSHKGVEVGLDYPILSNVSIAVNYTYAIHQYESEHA
NSGVLKGNDIDTAPRQLGNVRLAWQPTEDSSLELEWAHVGSYYLDPSNEHEYQGHNLLQL
RGQFSLTDKVRLLARLENVLDERYASRADYAFGSYRYFGGQPRAIHLGIEARF

tonB near heterologous motor where ExbB has periplasmic domain.

>ABG41494.1 outer membrane transport energization protein TonB [Paraglaciecola sp. T6c]

MGRLIVSVLLGGVIAFVLFVVMAKLIANSSRPADKVPPAPVIDIVMSTPDDSTQTRTRVPPPP
PPPPQQPPKLEPVEPDTADANTDGLSFNMPAVDIGGASVDIGGVGAMQRDGDATPIVRIEP
KYPAQAARDGKEGWVKLSFTINEVGGVEDVDVIEADPKRVFDREAKRALRKWKYKPKVED
GKPMKQFGMKVQLDFKLDQS



MGRLIVSVLLGGVIAFVLFVVMAKLIA
NSSRPADKVPPAPVIDIVMSTPDDSTQTRTRVPPPPPPPPQQPPKLEPVEPDTADANTDG
LSFNMPAVDIGGASVDI
GGVGAMQRDGDATPIVRIEPKYPAQAARDGKEGWVKLSFTINEVGGVEDVDVIEADPKRVF
DREAKRALRKWKYKPKVEDGKPMKQFGMKVQLDFKLDQS

77 Domain II residues

18 Proline residues

0 α-Helix residues

Iteromondales

Psychromonas ingrahamii

Locus:

>ABM05027.1 TonB-dependent receptor, plug [Psychromonas ingrahamii 37]

MPRLYYTPIAFALTTLFSATSIAAAPPISEQDTRDDIVISASRVETKRIESGSSVTVLDEQYIKE
NQARTVAELLQDVPGVSVASNGGLGQATSVFIRGANSNQTLVIIDGIEVNNLGNFEGGYDFA
YLMADNIERIEVLKGSQSALWGSDAMGGVINIITKKGKAGFHPTASIEVGGNNYHKENVTLS
AAQGNSHYSLSASNMKTDGISATDTDPDDDGYKNQSVSLKAGHQFTDIFSMDTVLRYNDA
ETEYDSGYTTNSQRQAKLSSHLNLLNNQWKNRLSVAFSDSNTEDFSSWGDSKYEGKKIKT
DLQSDYYISAINGYTQRISFLAEHESDKYQSLSMTQDERIEASGVVLGYGVDWAKTIFVNVA
VRSDFNNKFDDTTTYHIDTSVWVNDGTRLHASHGTGLKNPNLGQLYGENASWGYVGNAD
LKPEKSRSWDAGVEYNFVGTDAYIDLTYFDSLYTDMHTWSGSFPNSTYINLNNKATARGIE
FTGKVKVSNKLRVNTGYTYMETNDGNGNELARRPKHAASINANYKYTPELSANIGARYVGK
RLDSDDSTLSSYTVVNISTAYQIQEHITLSARIENALDKDYQEVSGFNTDPLTAYIGFSFK

tonB near a motor where ExbB has large cytoplasmic domain.

>ABM05033.1 outer membrane transport energization protein TonB [Psychromonas ingrahamii 37]

MKIISSYFPFLIISLVFYGFIFLYLDQPKRITTLPLNSGEQSVQVQFISQPNKGQNPAEDKLAAP
TEQKIVEAKSYVTEEEVVERAKVKSKKVIKYSAKSLILSESEIKLRKQALLESFATAGTDNVAK
LKAEIFLEQLATEKILTNETEQLSKTKDQASSPQTSNGPAKKAVIKKSPSENSSSLASSTKNQ
GVLQEAIVVSGRKPVYPQRAILRNQQGRVVIKLTITKKGLPKNPKILTSSGFPLLDDAVLAFV
DQELFMPALQGEDQVMSEQLFAFRFELN



MKIISSYFPFLIISLVFYGFIFLYLD
QPKRITTLPLNSGEQSVQVQFISQPNKGQNPAEDKLAAPTEQKIVEAKSYVTEEEVVERAK
VKSKKVIKYSAKSLILSESEIKLRKQALLESFATAGTDNVAKLKAEIFLEQLATEKILTNETE
QLSKTKDQASSPQTSNGPAKKAVIKKSPSENSS
SLASSTKNQGVLQEAIVVSGRKPVYPQRAILRNQQGRVVIKLTITKKGLPKNPKILTSSGFPL
LDDAVLAFVDQELFMPALQGEDQVMSEQLFAFRFELN

157 Domain II residues

8 Proline residues

21 α-Helix residues

Pseudomonodales

Psychrobacter arcticus

Loci:

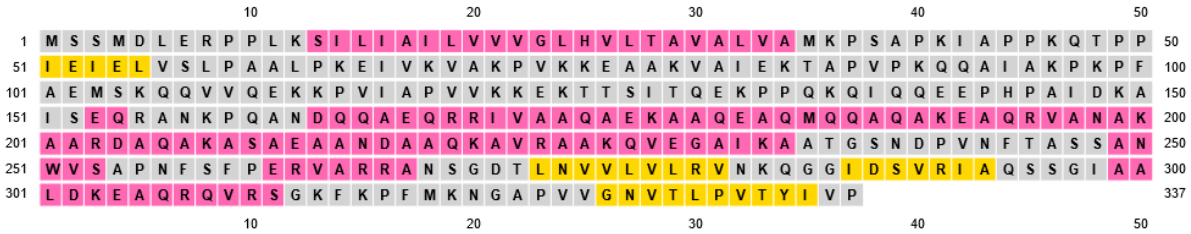
>AAZ18822.1 outer membrane receptor for transport of vitamin B [Psychrobacter arcticus 273-4]

MVLSRSSSTTYLRLCILSAFGAFAMSANAATDVNIVSDSDLPQVELDKIVVTATRTPTKTSNV
IAQTRVIDSEELQRYQGQTVTDVLKNQPGINIAQSGGMGTISNFYMRGYDSKQVLVLIDGIR
YSSISAGTSSLNLLPADQIDRIEILYGASGSSIYGSDAMGGVIQIFTKGNIVEQSNISTSVGYG
SNNHYQVGVTGQLKNDTSSLSLGVSRNKTDGFNAIADSSSSDYNADDDGFESTNASLGLQ
HKLSDSLSAGLSALYSDSTTDIDSAGTLFPNAYSDQKNGSANAFIQHQTPLTVTKFSYGQSI
DRLTSHDNNSINYQQGSQFDTTQEQARLESQINAQPGTVTIGAEWLSQKLDASDVLDFSGY
PNPAVQTAYNPDDRTVKSAFVGYQLSESYYDLQANYRVDDNSQYGNESTYNIGAAVRPLD
GVRIGASYATGFRAPTFNDLYYPGYSNPDLKPETSKNTELFVEYNKGNQISRLTGYHTDVE
DLIGGNTNTGEAKIKGLSLISDWRVNSFLFGLGYDYLDAKDKTANSANYNNDLVYRPQNSG
LIYIGYQQPTFDVRLEAKHTDSRFSDVSNQTKLDDYTLVNLSGSAYITPNLRANLRVDNLTDE
NYTLSNQFGTEYATDGTNFFTSLTYNWF

tonB next to motor.

>AAZ19512.1 outer membrane transport energization protein TonB [Psychrobacter arcticus 273-4]

MSSMDLERPPLKSILIAILVVVGLHVLTAVALVAMKPSAPKIAPPKQTPPIEIELVSLPAALPKEI
VKVAKPVKKEAAKVAIEKTAPVPKQQAIAKPKPFAEMSKQQVVQEKKPVIAPVVKKEKTTSIT
QEKPPQKQIQQEEPHPAIDKAISEQRANKPQANDQQAEQRRIVAAQAEKAAQEAQMQQAQ
AKEAQRVANAKAARDAQAKASAEAANDAAQKAVRAAKQVEGAIKAATGSNDPVNFTASSA
NWVSAPNFSFPERVARRANSGDTLNVVLVLRVNKQGGIDSVRIAQSSGIAALDKEAQRQVR
SGKFKPFMKNGAPVVGNVTLPVTYIVP



MSSMDLERPPLKSILIAILVVVGLHVLTAVA
**LVAMKPSAPKIAPPKQTPPIEIELVSLPAALPKEIVKVAKPVKKEAAKVAIEKTAPVPKQQA
IAKPKPFAEMSKQQVVQEKKPVIAPVVKKEKTTSITQEKPPQKQIQQEEPHPAIDKAISEQR
ANKPQANDQQAEQRRIVAAQAEKAAQEAQMQQAQAKEAQRVANAKAARDAQAKASAE
AANDAAQKAVRAAKQVEGAIKAATG**
SNDPVNFTASSANWVSAPNFSFPERVARRANSGDTLNVVLVLRVNKQGGIDSVRIAQSSGI
AALDKEAQRQVRSGKFKPFMKNGAPVVGNVTLPVTYIVP

206 Domain II residues

20 Proline residues

74 α-Helix residues

Moraxella catarrhalis

Loci:

>AZQ93065.1 tonB-dependent Receptor Plug domain protein [Moraxella catarrhalis]

MIKKPLVCAISATFAMPAVADNTKLGEEPTTTLKGVLVSSQTNQNTGFVSNDSKQSSDLTLS
KDKLKYRSATLGNALSGELGIHSNPFGGGSSAPVVRGQEGVRLKILQNGTDVIDVSSISPDH
VVATDTLLASKVELVRGADTLLYGLASPAGVINVVDDRIPNRMPSGAIHDKIEGETMLRYNT
NNHEKLATAGVSFGVGDRIAVRVEGLKREADDYQVPHFQADRMLDYVPGSANNSTVGMIG
VSYIHDNGHIGASYSHRKDRYGIPGHIHCDSQREHFIKWHNITKSNYYLPIYPHLMEDSDIDD
NPHTHCRHNHEDHIGEHNPTGVPINHEHHSPWIDMKTNRYDIRGEVYRPIQGLDKIKLSLTY
ADYYHDEKDAGNEQDPNNHKPSERDTTVDKGHASSIFTKKGVNGRLELYHTPTKRLSGVL
GIGYQTQKSAAGEAYLPSYFQSEAEWQKAQSQNINQYRPYLLVPNTNKSLGIFGLEQLKLN
QMTFKVAMRHERQKTPIEYDQHLLDHALQYFLSKAQLKAPDHPDLTTYKQHATSYAGSAL
WDITPNHRLSLTYSHNERIPSPMELYYQGGHLATSSFEHGNKNLVKEKSDNYELGFMHTAD
KVSYKASTYYSNFDNYIFNETIAKEGNLYIRRYNQTTAKFYGVEGSLTYQPNANHSVMFFGD
MVQGKIGALSDIKGKLVYAGRKWVYFDDDIKDMTVDDNGDYDADGGLTCALKTPEQWGQI
NDNNDCSTTINVYKNGTTTSGEEDYDRLARNPTYAPRVPPSRLGIRWQGYFGDHWSANAE
FNHVFAQNKVATSTVAIKPQFKQPEGCQRHESHCRISDYGSDNNPLMMQPRYITENKTAG
YNLLNVGLDYNNAYRNVDYTLSIRANNLLNEQIYIHNSFLPFVPQMGRNLTLGLTAKF

tonB next to motor

>AZQ92463.1 gram-negative bacterial tonB family protein [Moraxella catarrhalis]

MDNSKKIKVLAISIAAVLHGLVGFGLANMTIKPITPPPVTPPLEIEFIKEPVPEPIALNDLESPEP
PGEPVVTPEPVVEPEVATPEVIEPPEPIPEPEPLPEPIPEPEPEPEIDVEAILEQQRLQEAWV
AQQQQLAKIQEQERLEQERLENERREQERLEQERLENARREQERLDNERRAREQAQKEA
QVAAARRAAAQAAANAAKKAGNHGGGQPGQNQTVEGGINISNASWKTKPRVNNFCSARS
DIDTTLQVSFRVDAEGKISNVNLNGSTGDAKLDRQIIRQIGRGRLHPFREGNITRVGTAIYPIT
LKLQKDESCTN



MDNSKKIKVLAISIAAVLHGLVGFGLAN
**MTIKPITPPPVTPPLEIEFIKEPVPEPIALNDLESPEPPGEPVVTPEPVVEPEVATPEVIEPPE
PIPEPEPLPEPIPEPEPEPEIDVEAILEQQRLQEAWVAQQQQLAKIQEQERLEQERLENER
REQERLEQERLENARREQERLDNERRAREQAQKEAQVAAARRAAAQAAANAAKKAGN
HGGGQPGQNQTV**
EGGINISNASWKTKPRVNNFCSARSDIDTTLQVSFRVDAEGKISNVNLNGSTGDAKLDRQII
RQIGRGRLHPFREGNITRVGTAIYPITLKLQKDESCTN

194 Domain II residues

30 Proline residues

74 α-Helix residues

Pseudomonas aeruginosa

Locus:

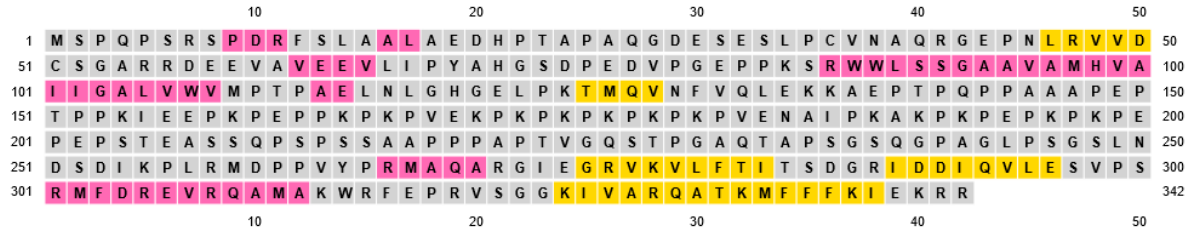
>AAG04660.1 probable tonB-dependent receptor [Pseudomonas aeruginosa PAO1]

MNRVFLTPAAVALCGASSLSLAEPVSLADQVVTATRTAQTASQSLAAVSVIDREDIERSQAR
SVPELLRQVPGVSLANNGGFGKNTTLFLRGTESDHVLVLIDGIKVGSASAGLTAFQDLPVELI
ERIEVVRGPRSSLYGSEAIGGVIQIFTRRGDGQGAKPFFSAGYGTHQTLEGSAGVSGGAGN
GWYSLGVSSFDTAGINTKRAGTAGYEPDRDGYRNLSGNLRGGYRFDNGLELDGTLLRAKS
HNDYDQVFGNSGFNANADGEQNLVGGRARFTPFDPWLVTLQAGRSEDKADAYQDGRFY
SRFDTRRDSLSWQNDLTLAEGHVLTLGYDWQKDEISSSEAFSVDSRLNKGWFAQYLGQY
GRQDWQLSLRRDDNQQFGVHDTGSAAWGYALSDALRFTVSYGTAFKAPTFNELYYPDYG
NPDLDAETSRSLEVGLSGTHGWGHWAVNAFRTNVDDLIGNDPRPAPGRPWGQPNNIDEA
RIRGVELVLGSQWLGWDWNANATFLDPQNRSGGVNDGNELPRRARRMFNLELDRRFERL
SLGASVHAEGRRYDDPANKVRLGGYATLDLRSEYRLNDEWRLQGRIANLFGADHETAYGY
NQPGQAVYLSVRYQAL

tonB not near motor.

>AAG08916.1 TonB1 [Pseudomonas aeruginosa PAO1]

MSPQPSRSPDRFSLAALAEDHPTAPAQGDESESLPCVNAQRGEPNLRVVDCSGARRDEE
VAVEEVLIPYAHGSDPEDVPGEPPKSRWWLSSGAAVAMHVAIIGALVWVMPTPAELNLGH
GELPKTMQVNFVQLEKKAEPTPQPPAAAPEPTPPKIEEPKPEPPKPKPVEKPKPKPKPKPK
PVENAIPKAKPKPEPKPKPEPEPSTEASSQPSPSSAAPPPAPTVGQSTPGAQTAPSGSQGP
AGLPSGSLNDSDIKPLRMDPPVYPRMAQARGIEGRVKVLFTITSDGRIDDIQVLESVPSRMF
DREVRQAMAKWRFEPRVSGGKIVARQATKMFFFKIEKRR



MSPQPSRSPDRFSLAALAEDHPTAPAQGDESESLPCVNAQRGEPNLRVVDCSGARRDEE
VAVEEVLIPYAHGSDPEDVPGEPPKSRWWLSSGAAVAMHVAIIGALVWV
MPTPAELNLGHGELPKTMQVNFVQLEKKAEPTPQPPAAAPEPTPPKIEEPKPEPPKPKPV
EKPKPKPKPKPKPVENAIPKAKPKPEPKPKPEPEPSTEASSQPSPSSAAPPPAPTVGQST
PGAQTAPSGSQGPA
GLPSGSLNDSDIKPLRMDPPVYPRMAQARGIEGRVKVLFTITSDGRIDDIQVLESVPSRMFD
REVRQAMAKWRFEPRVSGGKIVARQATKMFFFKIEKRR

134 Domain II residues

40 Proline residues

0 α-Helix residues

Oceanspirallales

Marinomonas mediterranea

Locus:

>ADZ90088.1 TonB-dependent receptor [Marinomonas mediterranea MMB-1]

MKKILRIALLLYSDILLADDKSVLLDTLVVTGTKTEKTVADSPVAVNVVTKKDILASNATSVAE
AIEALPGLRLKEIHGQGGDELVMQGMTGNHILVLKDGAPIHNFGISGSNLSRININDVQRIEIV
PGNASVLYGSSAMGGVVNIITNTPKEEWLSLTTTIKQNQDDKYTPSESVFQVDNGLKLDNW
TLASQWQFRNRQPYDTPPTDNSEDIAQLIAADVNEKLTYRHTKKTYSDLWFSLVREDTDRE
YDEQTPGSVLRETQQRNYRSQELGYRYKGHSWDLSLKSNAAKLTSDTDNLKTSNYLDERR
QTNSDNVLLQANKTFSTENHDITSGVSFSQIDIEQTLTETQLSATTAKTEVNDTIKGTEFFIQD
DWYVTDELELVSGIRTQWDSGFGQQTVPNIAVRWDVSPDLFIRSSAGLGYRVPNIKERYYR
FDHSSSGYEVIGNPDLEPEVAKSLNVELSYKDLTVQTFYKDITNLIDTSLDESIENGLDTYLYS
NINSALIYGASIGISHKINKVQLSANYQWTKTKDQDTGLQLDHRPTHIASLKLKRPVSLPHIKS
SNVSLSARYTGEQFYDAKKNEKSQGYLLLNANLSMHFNDQWSVSFSGKNLSDVKNESGID
YDLRPMIGRQWMLTLSYTPY

tonB next to motor with heterologous ExbD.

>ADZ89752.1 TonB family protein [Marinomonas mediterranea MMB-1]

MIKKGHWVLASTAALSLHAGAFYLAFYNPQQEGSVAPGTQGIEFGLGMVGDLGDSAETTV
AKENISEEPVVEETDVEEVEQPPEPQLEPEPEPEPEPEPEPEPEPEPEPIVASIEPEIIPEEVV
VAKQESDILIPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPE
PEPEPEPEPEPEPEPEPEPEPEPEPEPEPIQKPVVEAVITSNEPVDVPATPVPATSAPSTEG
SSSVATNSNSESLKASSGSGVSSRSGGSPGAIATYKSTLMAILAKNKKYPRASQRRGETGV
VKVAFSLDANGELVSASVRESSGYRRLDKAALKAVKRSRFPAPPSDLSKNELSFTIPILFEQ
K

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                    10                  20                  30                  40                  50
1   M I K K G H W V L A S T A A L S L H A G A F Y L A F Y N P Q Q E G S V A P G T Q G I E F G L G M V G   50
51  D L G D S A E T T V A K E N I S E E P V V E E T D V E E V E Q P P E P Q L E P E P E P E P E P E P E   100
101 P E P E P E P E P I V A S I E P E I I P E E V V V A K Q E S D I L I P E P E P E P E P E P E P E P E   150
151 P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E P E   200
201 P E P E P E P E P E P E P E P I Q K P V V E A V I T S N E P V D V P A T P V P A T S A P S T E G S S   250
251 S V A T N S N S E S L K A S S G S G V S S R S G G S P G A I A T Y K S T L M A I L A K N K K Y P R A   300
301 S Q R R G E T G V V K V A F S L D A N G E L V S A S V R E S S G Y R R L D K A A L K A V K R S R F P   350
351 A P P S D L S K N E L S F T I P I L F E Q K                                                           372
                    10                  20                  30                  40                  50
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MIKKGHWVLASTAALSLHAGAFYLAFY
NPQQEGSVAPGTQGIEFGLGMVGDLGDSAETTVAKENISEEPVVEETDVEEVEQPPEPQL
EPEPEPEPEPEPEPEPEPEPEPIVASIEPEIIPEEVVVAKQESDILIPEPEPEPEPEPEPEPEP
EPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPE
PEPIQKPVVEAVITSNEPVDVPATPVPATSAPSTEGSSSVATNSNSESLKASSGSGVSSR
SGGSPGAIATYKSTLMAILAKNKKYPRASQRRGETGVVKVAFSLDANGELVSASVRESSGY
RRLDKAALKAVKRSRFPAPPSDLSKNELSFTIPILFEQK

245 Domain II residues

66 Proline residues

5 α-Helix residues

Hahella chejuensis

Locus:

>ABC27848.1 Outer membrane cobalamin receptor protein [Hahella chejuensis KCTC 2396]

MRLVTLLLLVGSQLTGARAEELGPVVVEAKAPSADEIDAEYQTGFVKVIKREQFDSKVATVA
DVLKNETGVQVRQSGGLGSYSAVYLRGSTSKQVNVYLDGVLLNDATGGAVDLSQILLSGIE
QIEIYKGATPIQLGYSGVGGAINIKSLRFSKPIKQLALGYGSFNSRKGALTFADSVGETNYLAS
LDYLGSDNDFEMLNNNQTEFNPYDDRVERRRNADFSQFNGMLTAERSLSDRTDLQLMAQ
HFNKDQHLPDIANLESTRTSLDTDFTRLQSKLSFARNARENYTGRIFWSTQEERYDDSQSR
VGLGVQKTRANTDVVGAELYGSYSLGLHLFSATLEARKETYQEEDLTRRSQKQDFERMTY
LLGVQDEWADAEDIWLVRLSARQYFLEDETPAASMSGRVETASDSAQYHSLQAGVRYRLT
DWLSLKTNASRDVRFPQLAEKFGDRGFFIGNSELQPETALNGDIGFEVGVDSFSVSAAYFY
RDLKDAIVPSYDSRGVGRFENVGKARVSGVEVDAMYRPVPAWTFIARSTAQDTENLSDAR
DLHGKQLAGAYTYSHFLSAAWSIGRITTSVEYRHESGAYYDSAQETEVEDQNIVDVVGRWS
DGETTVEVSANNVTDEVVEAFNGFPSPGRHFFVSLMHLF

tonB next to motor.

>ABC33592.1 Periplasmic protein TonB, links inner and outer membranes [Hahella chejuensis KCTC 2396]

MKRHIIGITVALCLHISLAAWLTSGVSTPAPAPIAAAPVSLVLSQMRIVEQQVEAKQAEAEPA
PEVEEVVEAEQPVIEEPEPEVVQETPKPVETPPEPKPEVAKVEKPKEPKKPVKKQPEPKKIV
EKVRKPQPTKKEEVAKVDPEPNKKLAENPIPSPDPHTDISTAPAIAEQPQLSSAQIVSIEQAYI
NALQLALEKNKRYPLSAKRRRQEGTSTVEFTIMKSGDIAEVRLLDSSGISRLDEAAVKALVTL
AQFHPIPDELDRNHWKMSVPIRFQLN



MKRHIIGITVALCLHISLAAWLTS
**GVSTPAPAPIAAAPVSLVLSQMRIVEQQVEAKQAEAEPAPEVEEVVEAEQPVIEEPEPEVV
QETPKPVETPPEPKPEVAKVEKPKEPKKPVKKQPEPKKIVEKVRKPQPTKKEEVAKVDPE
PNKKLAENPIPSPDPHTDISTAPAIAEQPQLSS**
AQIVSIEQAYINALQLALEKNKRYPLSAKRRRQEGTSTVEFTIMKSGDIAEVRLLDSSGISRLD
EAAVKALVTLAQFHPIPDELDRNHWKMSVPIRFQLN

154 Domain II residues

30 Proline residues

10 α-Helix residues

Alcanivorax dieselolei

Locus:

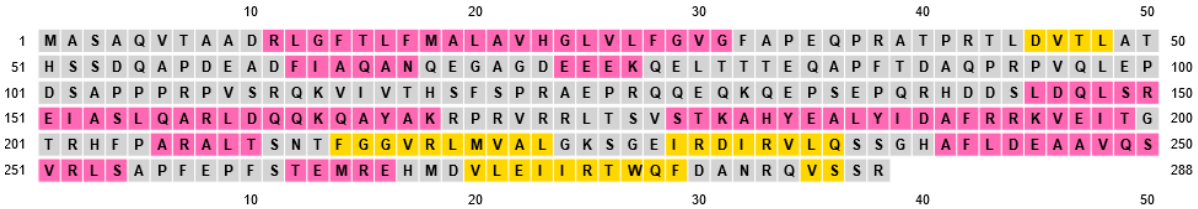
>AFT72403.1 Putative vitamin B12 transporter BtuB, tonB-dependent receptor family [Alloalcanivorax dieselolei B5]

MSRFKLTPVAAAVIGLCATASHAGENPTDPILLAQLSLPEVEPHENRLDPVVVTPSMTTQTA
RASLTPVAVIDEQTLREQQPLEMADILRAQPGVDIVGNGAFGKSTSVYMRGTGGSSTLLLLD
GVRIRPATGGTPSWQFLPPSMIDRVEVVRGPRGSLYGSDAVGGVVQVFTPDGHGDPGAW
LELGGGSFNTRSIGGGAAGEKDGTRYSMAVNRFDTDGTRLRRHGDDRGYDNTSGIVKLSH
RFGERAEIGVMGFRAEGNTEFEPGTTANREDTDYLIQVGALRGELLVSDDWLMQLQVSEA
RDENENFTDGDLTSTFNTKTRAVNLKNHFAVNDYVELIVGGEYLRDDIESTTQYSLDNRENK
AAFAQLMTTFGDLDAQASVRYDDNEAFGHKSTGGVALGYALNPHHRLRVSYGTAFRAPTF
NELYYPGFGNPDLSPEKSENKEIGIRGQYGRGFWDLSVFQNDVEDLIASELRDGKYLPYNV
NEARIRGAELQTGLDLDQWRLAMAITVLDPKDEETDELLQRRNRKSVRFDVDRDFGSVSLG
GSAVFQDHRYNDAAATQRLPGYGLLDLRASWRFAPDWTTRVSVKNVFDKEHATARNYSG
WNYLNAGRTVFVSVRYDIR

tonB not near motor.

>AFT68359.1 TonB family protein [Alloalcanivorax dieselolei B5]

MASAQVTAADRLGFTLFMALAVHGLVLFGVGFAPEQPRATPRTLDVTLATHSSDQAPDEAD
FIAQANQEGAGDEEEKQELTTTEQAPFTDAQPRPVQLEPDSAPPPRPVSRQKVIVTHSFSP
RAEPRQQEQKQEPSEPQRHDDSLDQLSREIASLQARLDQQKQAYAKRPRVRRLTSVSTKA
HYEALYIDAFRRKVEITGTRHFPARALTSNTFGGVRLMVALGKSGEIRDIRVLQSSGHAFLD
EAAVQSVRLSAPFEPFSTEMREHMDVLEIIRTWQFDANRQVSSR



MASAQVTAADRLGFTLFMALAVHGLVLFGVG
FAPEQPRATPRTLDVTLATHSSDQAPDEADFIAQANQEGAGDEEEKQELTTTEQAPFTDA
QPRPVQLEPDSAPPPRPVSRQKVIVTHSFSPRAEPRQQEQKQEPSEPQRHDDSLDQLSR
EIASLQARLDQQKQAYAKRPRVRRLTSVSTKAHYEALY
IDAFRRKVEITGTRHFPARALTSNTFGGVRLMVALGKSGEIRDIRVLQSSGHAFLDEAAVQS
VRLSAPFEPFSTEMREHMDVLEIIRTWQFDANRQVSSR

157 Domain II residues

17 Proline residues

44 α-Helix residues

Halomonas elongata

Locus:

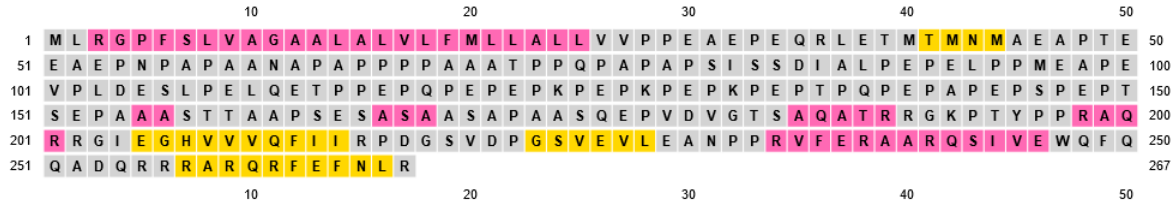
>OBX37423.1 vitamin B12 transporter BtuB precursor [Halomonas elongata]

MTTSRYFRWGLASLCLGATPLANAAPNDTDADTEQRLDPVVVSATLAPRTASQSLSSVSVI
DEATLRRQDPTDITDVLRAQPGVDVSSNGSFGKNSSVYLRGAGSQSTPLMIDGIRLRSATA
GGPSWEFLDPRMFERVEVVRGPRGSLYGADAVGGVVQLFTPEGEGEPTPRITLGGGSFD
TRRASASLSGSEDGTRYYVAASRLESDGYEIVDGEGDKGYDNTTGLMSLSHTFESGAELG
VLGLRARGNTEFDSFGTPSDTDYVQQVAGVYGELPITDTWRSRLTLSEARDERETHGGTG
ESVFDTRTRTARWENTLALGRHELVAGAEYARDDVDSTVDYDEDSRDNTAVFTQALLDFS
PLTVQAALRHDDNEAYGEETTGSLALGYELDDIHTLRASYGTAFRAPTFNDLYYPGFANPDL
DPEESESVELGLRGQLGRGFWDLAFYQTDIDDLISNIDTDGDGFVDTPENVERARIRGVELS
TGAEVLDWSLRAALTYTDPEDRETGNQLARRAKKSLRFDADRELGDWTLGGSVIAQGERY
DDAENQQRLGGFATLDLRASWDFAPGWSTRLTLENLLDKQYQTVGGYDSAGRAAFLSVSF
GG

tonB next to heterologous motor with multiple ExbB, one with large periplasmic domain.

>OBX35796.1 transport protein TonB [Halomonas elongata]

MLRGPFSLVAGAALALVLFMLLALLVVPPEAEPEQRLETMTMNMAEAPTEEAEPNPAPAAN
APAPPPPAAATPPQPAPAPSISSDIALPEPELPPMEAPEVPLDESLPELQETPPEPQPEPEP
KPEPKPEPKPEPTPQPEPAPEPSPEPTSEPAAASTTAAPSESASAASAPAASQEPVDVGTS
AQATRRGKPTYPPRAQRRGIEGHVVVQFIIRPDGSVDPGSVEVLEANPPRVFERAARQSIV
EWQFQQADQRRRARQRFEFNLR



MLRGPFSLVAGAALALVLFMLLALL
VVPPEAEPEQRLETMTMNMAEAPTEEAEPNPAPAANAPAPPPPAAATPPQPAPAPSISS
DIALPEPELPPMEAPEVPLDESLPELQETPPEPQPEPEPKPEPKPEPKPEPTPQPEPAPEP
SPEPTSEPAAASTTAAPSESASAAS
APAASQEPVDVGTSAQATRRGKPTYPPRAQRRGIEGHVVVQFIIRPDGSVDPGSVEVLEAN
PPRVFERAARQSIVEWQFQQADQRRRARQRFEFNLR

145 Domain II residues

45 Proline residues

4 α-Helix residues

Thiotrichales

Francisella tularensis

No *tonB* or TBDT genes detected.

Algorithm detected *tonB* and TBDT genes in other *Francisella* species.

Francisella sp. LA112445

Accession:

>QIW10982.1 TonB-dependent receptor [Francisella sp. LA112445]

MKKNILVKIMLSLSMFSCAYAQQNQQVNNGDTVDLGEIEVAAVKKADVGSVKKDKKKKESV
EQSANAAPPLSTSKSKNSLILSTADQLNKLQGVQIFSGSREISQNISMGGLAFNRVFVGIDGI
NNNFASFGHNSTRQLPSESLYKQVTADQSGSNIVYGNGALGGAVNFETIDPSDLLKGRSFA
TKLGVGGQTGDLGVNGNTAVAFKAGDFSYLFDIVGGRNNDIRLGNHTNLPYSASNNLQFLL
KGVWNISKIQTFKAYWLSMQNNGLYPATINDVVGEYNPPSKFNFLQQQVMLEYYLNPNNPY
VNLEAKVFYIRNHYNSNPINDGKGFAVPQDININTTGFRVTNKTFVLKQNLVYGTEFKFFNGF
NVGKNSLSFPTANQQTYSGYLQDSWDITSKLNITLGGRVNGYHSQSGNMQNGGAFFTKQ
GSISYKVIKPLKVYFAYTEGYRIPSLQDLFLGGSHPGMSFLQFVPNPNLQPEIGHNKSVGITI
NKQLTPTQSFYFNSNIFLNDVSNFIVDSKVNAASYPLKIQNINISHAQLFGYSLAFKYHNTWF
DFGTNFTYTRGESLSAYQGSGGSLVPSGSPLPIPRAKGIATLDIPIKPIDSSFQTSINYALTQN
RVPPGGEHPISSVPGYVLLNLGYKWQPKRFKGLNVSAGVDNVFNRYYQNYDGQNLVPAM
GRNFYLQASYNF

tonB next to TBDT but not motor.

>QIW10981.1 TonB family protein [Francisella sp. LA112445]

MLRTLKFTVAVVGSIFVDYSIYATLNQSKSTEWYIGETQLKSQSIEEIVKKINIVSQPKTSSKE
VAAKQLKHATKAAKKTKNTKAKLTKNKPHKQEESKVHKKSANIDVKENKAIAKITQQPKLKY
TPPKLGYPSSAIKNNEQGHVRIKANINSKGQVIGVHILQSSGFDDLDQAAIKWFEKLVFTPAK
SGFTNVATTVEQTISFNLKEQQNA



Thiomicrospira crunogena

Locus:

>ABB41558.1 TonB-dependent receptor [Hydrogenovibrio crunogenus XCL-2]

MTFKIRPLSLTLGFCLGTSTVYATPQSLDKIVVSANKAEQKTPSVTANITIITADEIEQKHYQTL
DDALKTVPGLAIKKSGGAGQQTSIFVRGASSSDRQVLILQDGIELTDPSGFGASIANIQLSSV
ERIEIIKGPQSGTWGANASAGVINIITKKGGKQASVNLKAGSFNTKQLSSTLGAGNDKVDFLV
HFNQHTTDGFSVIRKYDESQAQFENDAFKQTDVGFKLGLTPVKNHRFETTVNKTSATADYD
SGSNPDDATSNSAYDSTTRQLQYVYSGQAVNTKLFVQDHHIERTLNDTSYGTSQYEASIEE
YGGQATFDYRSTDQLTLSANSKNYRDIDKKRTFYNTGVGINNTNTLTENLVLTEALRYDDFN
RFKNATTGKIGIKNNFSTNVFISANYGTGYNVPSLYQLSTNNPEQLKPESIDGYDVTLGAYN
ATLTYFKSTTQDLITALGSWPSNYYANASGKTLNEGVEFAYQRSIDSLEADVSFNATWLNAR
NKDNQVLAYRPEQTANLTLDYYGLPQTQIGLVTRYTGTTYSADNQKGAQIGEYFVTDLTAN
YQVNRHVSLYGQVLNLLNQQYVEGVVDYPATNPVPNYVYSTGGIQAFVGVKGEL

tonB next to motor.

>ABB42216.1 TonB protein [Hydrogenovibrio crunogenus XCL-2]

MGKPGTLAFGITASIYSIIGFFLWHTFQSQQHSSQLAPIAVTTAMFVTQPEPKPEPKPEPKPE
PKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEP
KPEPKPEPKPEPKPEPKPEPKPEPKLDSQPVETPATKQPIVKKERRRPNPYSIAEQIN
AEALYINKLARHLATLAQNHYPKRAKRRHQQGEVTLQFTLHPDGHISNLSIVKPAHFESLNE
ATLNIIRHTMAYQYTPFPKEMRQRPKTIQVPIEYILR



MGKPGTLAFGITASIYSIIGFFLWHTF
QSQQHSSQLAPIAVTTAMFVTQPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPE
PKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPEPKPE
PKPEPKLDSQPVETPATKQPIVKKERRRPNPYSIAEQI
NAEALYINKLARHLATLAQNHYPKRAKRRHQQGEVTLQFTLHPDGHISNLSIVKPAHFESLN
EATLNIIRHTMAYQYTPFPKEMRQRPKTIQVPIEYILR

158 Domain II residues

58 Proline residues

5 α-Helix residues

Legionellales

Legionella longbeachae

Coxiella burnetii

No Legionellales found to have *tonB* or TBDT genes.

Methylococcales

Methylococcus capsulatus

Locus:

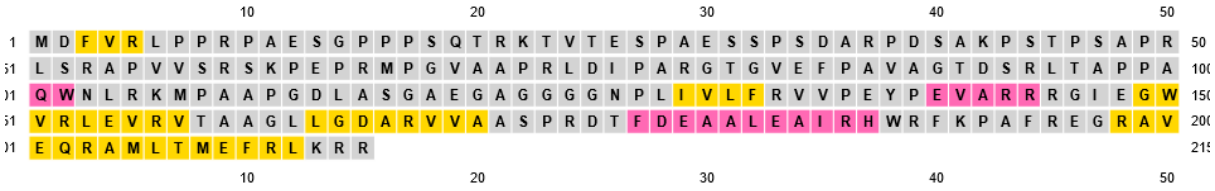
>AAU90376.1 putative TonB-dependent receptor [Methylococcus capsulatus str. Bath]

MNGAELVKHWSRFAIRCRKFMNTHSGSGLPATGVRRSRLRREAWVLAPFLFIFGSAGLRV
GSAEAAEDVVELDKITVYGEEDEVSPETEDLPEEQLEEKKAQTMDTASLFKDVPGVSLYTG
GGVSSLPAIHGMADDRVKILVNGMNITSACSNHMNPALSYVAPASVGKASIMAGVTPVSQG
GDSIGGTISVDPAAPSFAKAGQMAYTGKLGGMFRSNSDTFGNNFSGSIASEDFAFDYGGS
WAKGNNYMAGNGGPTVLPTRYLTTNMNLRASTKLDKGFFSADVTGQHIPYQGFPNQRMD
VAENDGLLGGFSYENDFDWGKLDARVYYHSTWHLMDMLSERKAGRMPMKADGSDLGYR
VRAHLPVDDVHTVRVGSEYFQQGLQDWWPGQGMHMPQDFLSINDGQRNRLGTFAEWEA
AWNKEWLTQLGVRNDMVWMNTGRVQGYDNGAFYSFWATPFNAANRSRVDHNFDATATT
AFTPDANSRYELGLSRKQRSPNLYERYAWAGPNSMITWFGDGNSYLGNLDLKPEAAYTAT
FTANWHDERQQVWSVSLTPYYTRVNDYIYGQKVAQYSNGFHGMQFVNLSHADMYGGDF
SARYAFLPESPAGSFAAKVVAAYVRGVGNDGQRSMGCPYVGTSLAGLCNNNQQFWPVN
GFLAPTSVNLYHMMPLNATVSLEHSIPAGSAVVDSAISVNLVDSKTAVAQSYAEPTTPGYVL
LNLRTSYQREHLRVDVGADNLLNKLYYHPLGGVDIVESIKAQDVVRLPAIGRSVYVSLNLEF

tonB next to motor and TBDT. Motor is heterologous, featuring ExbB with large cytoplasmic domain.

>AAU90377.1 TonB domain protein [Methylococcus capsulatus str. Bath]

MDFVRLPPRPAESGPPPSQTRKTVTESPAESSPSDARPDSAKPSTPSAPRLSRAPVVSRS
KPEPRMPGVAAPRLDIPARGTGVEFPAVAGTDSRLTAPPAQWNLRKMPAAPGDLASGAEG
AGGGGNPLIVLFRVVPEYPEVARRRGIEGWVRLEVRVTAAGLLGDARVVAASPRDTFDEAA
LEAIRHWRFKPAFREGRAVEQRAMLTMEFRLKRR



Broken. Selected the next *tonB*:

>AAU90375.1 TonB domain protein [Methylococcus capsulatus str. Bath]

MAAVPLVQTDSKSSGAESLYRPGSAILVVVSLAHLAVWWSYRQLKLLEPEERPSQPIEVSL
EMIAPAPKPAEPAAQPAPAPTAPPKPVTPPKPKPVAKPKPLTKTLPRPLPVQPERTLGDAAP
RSEPAAPPPEASSAAGGEGVPGGRSGSSVPASTPASFNANYLHNPLPEYPAFARKQRWQ
GRVTMKVHVLPSGIPAEVELQASSGHDILDESALETVRRWRFVPATKGGKAVASWVVVPLE
FSLTH



MAAVPLVQTDSKSSGAESLYRPGSAILVVVSLAHLAVWWSYRQ
LKLLEPEERPSQPIEVSLEMIAPAPKPAEPAAQPAPAPTAPPKPVTPPKPKPVAKPKPLTK
TLPRPLPVQPERTLGDAAPRSEPAAPPPEASSAAGGEGVPGGRS
GSSVPASTPASFNANYLHNPLPEYPAFARKQRWQGRVTMKVHVLPSGIPAEVELQASSGH
DILDESALETVRRWRFVPATKGGKAVASWVVVPLEFSLTH

105 Domain II residues

29 Proline residues

0 α-helix residues

Chromatiales

Nitrosococcus oceani

Locus:

>ABA57061.1 TonB-dependent receptor [Nitrosococcus oceani ATCC 19707]

MLKRTPIFVLVATACAASPLLAQDEEVTLPELEVVGQPVERAGVEAENKPFATPDTADLLRR
VPGANVNANGPIAGMVQYRGMFGPRMNVRINGTPIESGGPNWMDPPLSYAPRSLVESIEV
TRGVGSVSTGSGIGGYVEAKTKSSHFTGSEQFEFHSDVDIAGHSVDGGYNLGGILSLSNDR
HRLHFLGSRDDGGDTEFGDGTIKATEYERNTYGAGYGFKTGDHEFSADYQRLDTENSGTP
SLPMDISFIRTNRAGGKYTGFWNDIQLETRFGYSDVDHQMNNFRLRQAANFCALPAPFCQ
GDDKRLVNAGSEDFNYGLKATFALWGGDLAIGADGHAAQHNATVLDPDFAPFFVTNFNNA
QINKYGFFSEWTKEIYSNWELQLGARYDRVEMDADGVNAFPAQLADRGMGGMPAQMIQM
LRNRFNGADRGQNNNNVDWVAELSYQMNSALRWTFGAARKMRSPTYIQRYLWIPLEVNA
GLGDGNAYVGNVALDPETSHELGFGFDWQTQAAYFSPQAYYRRVDDYIQGTPAADPVVIA
VSTNAAGDATPLQFSNVDAEIYGLDADFGYRFHPRWRLDGVASYVRGKRRDINDNLYRIAP
PNLRLSLTHERIHWFTTVESVLVYRQENISDTNTLDPGNANNTNEATPGYVLVNLYGQYRLL
NQGITFTAGINNLLDKTYTNHLTGFNRVLNSDVSQGRRLPGPGRNFYAALRYEF

tonB not near motor genes.

>ABA56895.1 TonB-like protein [Nitrosococcus oceani ATCC 19707]

MLSPSAMIPTMNYPLILTLLLSVLFHGILLLGMDQLKFFPPPTPIPLPLEIILVPFKQEKIPKKPN
VLAQAGKISKSEKEERHPLAPSAPSPLAAPPRVPTSPAIQPAPAVSKQKLPPPKQTALSPLLT
QKRATPSPSKPQQIPASTSPEIPETTSPRPSARELIAALEGQLAREIQRYANQPRKRYLDSN
TTEYAATAYLDAWRKKIERVGKMNYPEEAKRRGLSGSLILVVDLNPDGTVANIVVRHSSGH
QALDKAAIRIVRLAAPFANIPANVLQGHDILSITRTWQFHSGKDFSSR



MLSPSAMIPTMNYPLILTLLLSVLFHGILLLGMDQL
**KFFPPPTPIPLPLEIILVPFKQEKIPKKPNVLAQAGKISKSEKEERHPLAPSAPSPLAAPPRV
PTSPAIQPAPAVSKQKLPPPKQTALSPLLTQKRATPSPSKPQQIPASTSPEIPETTSPRPSA
RELIAALEGQLAREIQRYANQPRKRYLDSNTTEYAATAY**
LDAWRKKIERVGKMNYPEEAKRRGLSGSLILVVDLNPDGTVANIVVRHSSGHQALDKAAIRI
VRLAAPFANIPANVLQGHDILSITRTWQFHSGKDFSSR

164 Domain II residues

32 Proline residues

28 α-Helix residues

Thioalkalivibrio nitratireducens

Locus:

>AGA32297.1 TonB-dependent receptor [Thioalkalivibrio nitratireducens DSM 14787]

MFAVLAAAMLGQSGPSAASDATLLPEITVTARGYEADTIATPQSVEILAPANAPSAAAPVGG
LFRGEPGLAVQSDGAWGQNPVLRGLKKESIVILVDGVRVNSAQPQGAIASFLDLGLLDRVE
VVKGPTSVLYGSGALGGAVNLITPEPVFSDAPAQSTRFSVGGSSADQALSGAALYRYSSPH
HGLVIGGAARDADDYRSPDGRVPRTGYSSDSLLARYAFAWSTETTLKLNLQRHEDRDVWY
PGSARTGGQPGGAGIPPMLGTVTLRSPRQTRELAEIGLDHEVLGGTLSGTIYRQEVYRQIR
AWSDVLNRDYVRNDVTFATDGARLGYLRPVGEIHLLNVGAEFWRMTGDPERYIDQPPAFE
QDNTVRRSPFRNGEIETAGFFVQDEILLGATTLVAGLRFDRTRGDADQKGFGPAPQTTGLG
KTDNTLSWSLGAIHAFSDTLNPYVNLGSAYRAADMRERFEDSARGDGFFHVGNPQLDPER
STSLEIGLKGTSGVFDYRLAAFYTRIDDYIAGRITGENHPGSGLPIKRTENLDRVVIRGLEGAL
AMPVGAFVADATFTWLRADNRQDDEPLAETPPPELRFGFGQPAERGFYWRAQTRLVARQ
DRVATKFTNGGEDETSGFATADLNLGWNFGSAGALKQASLDLNLTNLFDRRYHEHLTQGV
SGQEILAPGRSIAAQFTGRF

tonB not near motor genes.

>AGA32018.1 TonB protein [Thioalkalivibrio nitratireducens DSM 14787]

MPDESSRLTLPLFLALVLHALVILGVGFEMLPEETPAQVTLDVTWVDAPAPAPEHAEHLAPQ
AQDASGAADQERMARTPEPVGERPADPAPAGDSGLIPEPIETQLEPFDPAPERPPDPVVTR
APEVPPAPAPEEPSPTDTSQAPEQPSAALLMARGLEAARAMPAETEQTLLSRATRTRYLDT
LAARGAPEAAYLEAWIRKVERIGNLNYPDEARRRGLSGTLVLSVRLDAGGQVLDVAVAQSS
GESILDQAAIRIVELAQPFAPFTESMRESYDQLVITRTWAFRRDRVERVR



MPDESSRLTLPLFLALVLHALVILGVGFE
MLPEETPAQVTLDVTWVDAPAPAPEHAEHLAPQAQDASGAADQERMARTPEPVGERPA
DPAPAGDSGLIPEPIETQLEPFDPAPERPPDPVVTRAPEVPPAPAPEEPSPTDTSQAPEQP
SAALLMARGLEAARAMPAETEQTLLSRATRTRYLDTLAARGAPEAAY
LEAWIRKVERIGNLNYPDEARRRGLSGTLVLSVRLDAGGQVLDVAVAQSSGESILDQAAIRI
VELAQPFAPFTESMRESYDQLVITRTWAFRRDRVERVR

166 Domain II residues

30 Proline residues

43 α-Helix residues

Halothiobacillus neapolitanus

Locus:

>ACX95375.1 TonB-dependent receptor [Halothiobacillus neapolitanus c2]

MYKFPMSGRHRTGRTTLACAYLTACSFPLSALAGSPSTLPDLNITASHGAPVAFAGVPETVI
TRAEIERLQATSVLSLLENRAGINMVNQGGPGKITTASIWGMSGSQTLVLIDGVRIGSLTAGA
AYLENLPVALIDHIDIIKGPRSGQYGADAMGGVIQIFTRKGKKGIQPSFSIAGGSNKTFETSAN
VSGGNGPFDYSIGASHQGTGGFNAYTDTTGSPFAVNQPDNDGYRNNSASGRLNYTGDNG
ARLGVHWLGTNAFTDYDGSSFAGNQQRSRQQNFGLDGALMKIGIWQLRASAGRNIERQT
QYYDGKYVSEYNSRQDSFSLANDFSIGQGLLTLGADRLNDHVSSSVNYDVTSRHNNGVFA
QYATQIADLSIQTALRHDSNSQFGSANTGSVDLSWQLNPSLALTGGYGTGFHVPSFNFLYY
PGGYANPDLRPEHSRTARLGFNWQNNNGWTSSLTAFRTRTRDLIASSASTNFVPYNINQA
QSIGAEWQLGWHNADWALNSSATWISAVDRETGVSIPRQPKWSGRVDVDRKLGAWRMG
VTVRGQTATHESTFSQINNGFATADLRLSYAYSQNWHIEAKLSNVLDKQYQTAYDYHQAGR
TVLFTLRYGL

tonB not near motor genes.

>ACX95365.1 TonB family protein [Halothiobacillus neapolitanus c2]

MDHWALDQNFIDSDKRFGAALLVALVVHALFFAIYFTGDKPSPPPPRPIELTLDAPLAAKTND
ASPTPSDKINDKVTTQALASAAGEQTNTLQKPKSGKGITTTGNNGITDTPTTNAAPDAFNRL
NEAVSRSLKTGFLTSKTVNGPAGDYLSRWKRQVEAYGNDHYPEDLISQKISGQLILAVTIDK
EGHVMDIAIQHSSGNPKIDTAARRLVQLASPYPPFPPALAARFDQIVITRTWQFSSGHGLTT
R



MDHWALDQNFIDSDKRFGAALLVALVVHALFFAIYFT
GDKPSPPPPRPIELTLDAPLAAKTNDASPTPSDKINDKVTTQALASAAGEQTNTLQKPKS
GKGITTTGNNGITDTPTTNAAPDAFNRLNEAVSRSLKTGFLTSKTVNGPAGDY
LSRWKRQVEAYGNDHYPEDLISQKISGQLILAVTIDKEGHVMDIAIQHSSGNPKIDTAARRLV
QLASPYPPFPPALAARFDQIVITRTWQFSSGHGLTTR

113 Domain II residues

13 Proline

17 α-Helix residues

Cardiobacteriales

Dichelobacter nodosus

PFAM search confirmed no *tonB* or TBDT genes.

Xanthomonadales

Pseudoxanthomonas spadix

Locus:

>AER54876.1 TonB-dependent receptor [Pseudoxanthomonas spadix BD-a59]

MLLAAGSLALPEAMAQQSTAGQQMQEEPASTPTELDTVIVTGQRQAQREAIQTKRETFAVS
DVVASDDIGKLPDHNTAAALQRVPGVAVWEDQGEPREPIIRGLTSTYNRTTIDGALVSSVSE
EGRNVPLDIVPSVMADRIEVIKTVTPDQDANAIGGIINIVTRSAFSTGQPFLDATGSLGFAEQH
GDVRNDKQPYRVNFAAGRLFGADDQFGIVVSASDEQLDYDIPQVESASPSVREYTAAGAP
VDSGSALGNGIQVPTQRRLFWYNNTKNRSGLNAKLEWRPNPDFRWDTSAAYNTMEDDEE
RIENRLEPIGNVANQTATSGDFASGRQFIQLNLPDTERSIWLGRSAVEWTAAERLKVSGDVI
YSRAELDQTTTAIEFRTPTGTRARDFGFSYDTSDFYPIFTPYDQAAARDPANYRFQQYRDT
QLDSIEESQQARLDLEYDNGGLENFFKLKFGGVARFTDRELDQDRITYSTRSGFNWTLDSV
SRAGPDKLIKGRYLLSPRIDYRAANDFLNANIGNFNAALDNIGSDFTVSEDVYAGYGQATIKR
GPFTVIAGMRYERTEVDTDSTRASDDVYLPVSDSGSYHNWLPGLHLRYDATDNLVLRAAW
TNTIGRPDFADITANSSINFDGSVAVLTRGNPSLKPRESEGFDLSLEYYLDEGLVALGLFRKR
IDNEIFTLTSNVEMDLGIGRGVEMVQVQQPMNAQSAKITGAEVAWQQTLSFLPAPFDGLGF
NLNATFLDTEFAFITSAGLRETGLYMQPDVITNAALFYQYGPVEFRVSHNYLGGFLETINDTI
PNADQYWKGRHTYDASVDWQLSDRLTVFVQGQNLSDTGRREVTGPGKQYLQESADYGR
TYWVGLSGHF

tonB next to motor genes, heterologous exbD, unusual gene order.

>AER54858.1 macromolecule import protein [Pseudoxanthomonas spadix BD-a59]

MAEQLVINRYREQEGPQGLNWSRIIGYAFVIALHVAVFLLLLIPAVAPPAQKEEEQKMLVQIV
DPPPPPPPHPPPPPKQETPPPPVKELSPPKPSPVPPPPEAPPVDVPDPRPMDTYAPPAPP
APPAPSPDIGASVDISSKNMNPPRYPPAAARAGVEGTVILIIDVDANGNVTNVSVEKSSRNR
DLDRAATEAARKWRFNPGKSGGQSVAGRVRVPVDFSMGG



MAEQLVINRYREQEGPQGLNWSRIIGYAFVIALHVAVFLLLL
**IPAVAPPAQKEEEQKMLVQIVDPPPPPPPHPPPPPKQETPPPPVKELSPPKPSPVPPPPEA
PPVDVPDPRPMDTYAPPAPPA**
PPAPSPDIGASVDISSKNMNPPRYPPAAARAGVEGTVILIIDVDANGNVTNVSVEKSSRNRD
LDRAATEAARKWRFNPGKSGGQSVAGRVRVPVDFSMGG

82 Domain II residues

36 Proline residues

0 α-Helix residues

Xanthomonas axonopodis

Locus:

>AAM34966.1 TonB-dependent receptor [Xanthomonas citri pv. citri str. 306]

MSRPPHPHALSLALGLALIAWLPWQSTAADMSGGADALTMDAVQVRNPFQSQNTRAIATK
QAAPTIVDSVAADSIGQLPDFNVGDALRRVTGVSTVEYQGEPRYVTVRGLNGNYNSMLIDG
FAFASNDIGSRQALMDVLPANFVDRIDVVKSLLPENDGGAIGGVTDLVTATGFARPDGLLTA
SAKGGANLMGSRYGGRTPVGEGELKWGKRFGRDGQFAFLGAASIWRREISVPQQENGGA
LNWYNADGTRAPSAYGGTGAAVPSERRWYNYDNTRERRGVTARVDWQPDGPLSGHVSG
YTFNQHEASDRNAQVAQVQNSARLTRSGAQSGTLDNLNQLVELGQLRWKRGLSGINGELL
AELPGQWRGALRASTSRATVDNPQTWDRFQQNRLAYGFDWNGTLPAFTALDPALADDPT
RYANLNHQQERTTYAERVSDLQLELRRNMDEDSRGLGLAFGLRQVRTHMQTAFQRTTWS
GLPYSLADVLGDPTCALGCNAPMWTIDPDLADARWDAASGQARGVADITAQNSGTYTVDE
QVRAGFAQAQWRGERWRLAGGVRLEQTRFGSSGQQLSGTVWAPVSAQRTYRNWLPSLA
GQVQTSANGTLRFGASRSIGRPRLDQMALNGGVLALGSNPPTLNQGNPDLQPRRSQNLDL
GHDWTFDDGGSLLSIALFHKTIDNEIFRYGQLQNIDGEQVLVTQPRNTDRPVRMRGAELGAI
KELGPWLPALAGLSVGANVTFLDVDYPVVLGDGSRTTLSVLPQQPKQLWNLTLNYARGPL
RGTLAWSRTGELWDDRYPNYSNQQEFYRNRYQQPLDRLDLKLAWDVSPAVAVSLDVLNL
TGQGYEYRIGRHQEYVQSAWKMAPTVMLGVNVKL

tonB next to motor genes, heterologous *exbD*, unusual gene order.

>AAM34900.1 TonB protein [Xanthomonas citri pv. citri str. 306]

MTEQLVIHRHDYDAGNQGLSWARIIGIAFVIALHLTALMMLLIPAVAPKAPAEKERTTMVTLV
DAPPPPPPPPPPPPPEDKPPPPVKNLSPPKPSPVPPPPEAPVVDVPEPRPSDIVTPPSPPS
PPAPPSDIGASVDISSKNMNPPKYPPAAFRAGVQGEVILIVDVDASGNVTNVSVEKSSRNRD
LDRAAMDAARKWKFNASTVNGQKAAGRVRVPVNFALN



MTEQLVIHRHDYDAGNQGLSWARIIGIAFVIALHLTALMMLL
IPAVAPKAPAEKERTTMVTLVDAPPPPPPPPPPPPPEDKPPPPVKNLSPPKPSPVPPPPEA
PVVDVPEPRPSDIVTPPSPP
SPPAPPSDIGASVDISSKNMNPPKYPPAAFRAGVQGEVILIVDVDASGNVTNVSVEKSSRNR
DLDRAAMDAARKWKFNASTVNGQKAAGRVRVPVNFALN

81 Domain II residues

36 Proline residues

0 α-Helix residues

Xylella fastidiosa

Locus:

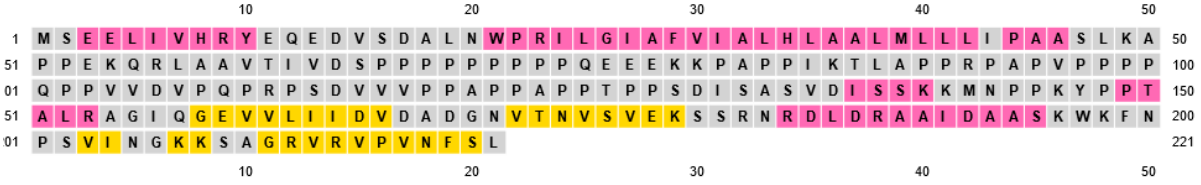
>ACA12650.1 TonB-dependent receptor [Xylella fastidiosa M12]

MKTFSRYTPALNHLALALASTLLLIATYTANATAAESEHSTNEDSKAAPHDSKTTELDRVVIT
GSRIPRAGFDTLEPATVVNRQYIDSFGFTNVADALFSQPGFNSSASVRGNQAGFGAGVSFL
GRFGLGSNRQLTLVNGRRLVTSNPPTVFGPGDGGTQVDLNVIPTSLIERTETIGVGGAPTY
GSDAISGVTNIILKKNYEGAEVNIGYGLTERGDNARYSYSALLGSNFANSRGNVTIALDADDS
AGVLGEARRYYRNGYSMQTNPNAAAIAQFQPGRQYATDGRVNPTIPFNTSNTDGIPGRVLI
RNRRRINNMTWGGLLYPSTGRYIRDASQQPRGFGPNQDQFLQFDKHGNLVSYNPGVNFGN
SSSSGGDGLDLNQTTQVTSQLDRKSVFMLGNYDVTDNISSFFEGSYYTSKALELTDQSIYN
AASFGTGNVNGSGDQSGALNFNIDNPFLSEQNRQALRNLGITDFRLSRASRDLVIGNSSTD
TRLWRAVAGLNGHFDAGGHPFTWETSLNHGEGNFDYYRTGLIQQHFINAINVTRNSAGEIV
CDSSAAGTTVDPNCVPLNLFGEGVASAAARNYVTTPTHAKAQMKQTVFNANLSGSFIDLPG
GKLGFNVGYERRREEGRFTPDEYQRLGLGRTVPTTGSHGTFTTNEYFGEILAPLVNPDAHL
PGLHRLDLTAKLRRVNNTVNGWFTAYTYGIQYEPFQGLQLRGNKTHSFRAPAIVELYTSQQ
PRYYSIPEPCTPANITAGNRPELRQRNCEAFFAYYNGVNPGTFQEAPTTQLGSVSGNPTLE
NELAKSWTAGIVFQPEWAHGLRVAADWYNIKISNVITQLDSGDITSGCFDNETFNRNDVPN
ANRFCSMITRDPSTGVASSVRGEYTNGPYINFRGWTAEINYRFDLKELRWGGSGILDLGFY
GYFPKNLKYTAAQDIPAEESVGTIDNSKRQFQWNARYLTGPWNFGVSANYKSAALYSLTNT
VETRDYLGIPSYTSYDANIGYTFDKHSSLNLAILNATDKMVAFPYVYDGLGRRYMLTFNYKF
H

tonB next to motor with two copies of *exbD*, unusual order.

>ACA11062.1 TonB protein [Xylella fastidiosa M12]

MSEELIVHRYEQEDVSDALNWPRILGIAFVIALHLAALMLLLIPAASLKAPPEKQRLAAVTIVD
SPPPPPPPPPQEEEKKPAPPIKTLAPPRPAPVPPPPQPPVVDVPQPRPSDVVVPPAPPAPP
TPPSDISASVDISSKKMNPPKYPPTALRAGIQGEVVLIIDVDADGNVTNVSVEKSSRNRDLDR
AAIDAASKWKFNPSVINGKKSAGRVRVPVNFSL



MSEELIVHRYEQEDVSDALNWPRILGIAFVIALHLAALMLLL
**IPAASLKAPPEKQRLAAVTIVDSPPPPPPPPPQEEEKKPAPPIKTLAPPRPAPVPPPPQPP
VVDVPQPRPSDVVVPPAP**
PAPPTPPSDISASVDISSKKMNPPKYPPTALRAGIQGEVVLIIDVDADGNVTNVSVEKSSRNR
DLDRAAIDAASKWKFNPSVINGKKSAGRVRVPVNFSL

79 Domain II Residues

31 Proline residues

0 α-Helix residues

β-Proteobacteria

Neisseriales

Chromobacterium violaceum TolA

Locus:

>AAQ57756.1 probable TonB-dependent receptor [Chromobacterium violaceum ATCC 12472]

MRVKTLAQAIAAIGLLGSGFAHAADDNQLERVTITGSNIKRSIKQEKALPVTILKTEDLAKQGLTTVEQVVNSIAANQ
STQGSSSAVGASSGGGSFASLRGLGNQYTLVLLDGRRMANQAIDGTSADLNAIPLSVIDRVEVLLDGASAIYGTD
AIGGVMNFITKKSMKGFSIGGSFANPQHGGGDEKRVNASYGIGDLAKDGFNVYGAVDYLKQDMIMASQRGFAST
ITPQTDTVPSVNAWPGSYYDSVKKKYVQPSAPNCRPPYSQFVNGRCREYFPLYPSIVPEVEQISGVFKATKRIGD
DHELSLQYTRTETITTAQNAPLPTAGDVTRANLTDPSQRDQLYVRAVPLGNRETEANSVTQRLMLNLEGLVAGW
DYRAGIGRSENLIKENLTSGYISKSKMQSAIDSGALDPFDLSSNNLAAWRSVSMTGQTKEAKSTIDMADAKVSKEL
FDLPAGKLGVALGAEVRHESLSTIYNKSVTRDALSTGQDKTEDSMGSRSAYAFYGEADIPVLKTLDVQLAARYDH
YSDTESSLNPKVAFKFQPDPKVMFRGSASTGFRAPSLYNIYRPNQLQLTGKPFKDTGACVNGAPLPGTNGDACT
EMQRNKRIAGNKNLQPEKSSSLSFGMVIEPTKDFTASADLWWTMIKDQISVLDESLIINNPALYADRYVRDANGNL
SYLVDDYSNLGNLSASGVDLRLSWILPKTSFGVFTAGLDGTYLAKYEYQREKNGDYFSNLGTFKDGGPTFRWQH
NLTLNWMYGPWSAILSQNYKSGYTDENPKKENHLVKPYSTWNLSASYAWNKQLTFTAGVKNLFDQEPPFSNQQ
TRTTQMNYDPRLVDPTGRSFFLKGAYKM

tonB next to motor.

>AAQ58078.1 conserved hypothetical protein [Chromobacterium violaceum ATCC 12472]

MYGGRRCAGLCPQYADDRGDCKRAAPRRPATDWKMRIVCIIISDMKSSPVLQYSALGGVL
AAHALALALLNGMAARPQTVTPPQALRMEMISLAPAEKPAVAPKAAPAPEPVKPQPQAKPA
PSKPTVQSKPALQPAKTQADAPAPAKAISAAAAPAAPTPAAEAPKSAGGKADSRDLPVTEP
LAHGGYLNNPAPAYPTVSREEGEEGTVRLRVHVSAQGLPQEVSVQSSSGFPRLDRAALAA
VKRWRFIPAKRGGEAIAYPFIVPIEFSLKSANT



MYGGRRCAGLCPQYADDRGDCKRAAPRRPATDWKMRIVCIIISDMKSSPVLQYSALGGVL
AAHALALALLN
**GMAARPQTVTPPQALRMEMISLAPAEKPAVAPKAAPAPEPVKPQPQAKPAPSKPTVQSK
PALQPAKTQADAPAPAKAISAAAAPAAPTPAAEAPKSAGGKADSR**
DLPVTEPLAHGGYLNNPAPAYPTVSREEGEEGTVRLRVHVSAQGLPQEVSVQSSSGFPRL
DRAALAAVKRWRFIPAKRGGEAIAYPFIVPIEFSLKSANT

104 Domain II residues

22 Proline residues

0 α-Helix residues

Neisseria meningitidis

Accession:

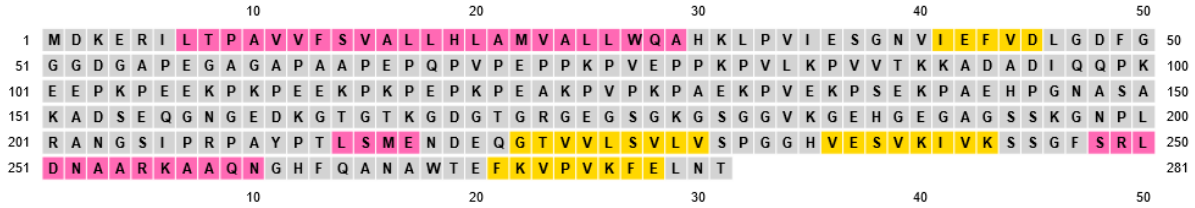
>AAF42164.1 TonB-dependent receptor [Neisseria meningitidis MC58]

MGQFMSVFRINMTAATVLAALSSSVFAAQTEGLETVHIKGQRSYNAIATEKNGDYSSFAATV
GTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSE
YNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHA
AAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRRETFYAAADWDI
NPDTVLGAGYLYQQRRLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMHSHDVFADLK
HYFGNGGYGKVGMRYSDRKADSNYTFAGSKLNNTGQADVAGLGTDIKQKAFAVDASYSR
PFALGNTANEFVIGADYNRLRSTNEQGRSTLSKSVALDGFRALPYNGILQNARAGNKGFNH
SVTEENLDETGLYAKTVFRPLEGLSLIAGGRVGHHKIESGDGKTLHKASKTKFTSYAGAVYD
IDGSNSLYASASQLYTPQTSIGTDGKLLKPREGNQFEIGYKGSYMDDRLNTRVSFYRMKDK
NAAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKWQIHAGYSYLHSQIKTASNSRDEG
IFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSSAGIHAGGYATFDAMAAYRFTPKLKL
QINADNIFNRHYYARVGSESTFNIPGSERSLTANLRYSF

tonB next to motor genes.

>AAF42075.1 TonB protein [Neisseria meningitidis MC58]

MDKERILTPAVVFSVALLHLAMVALLWQAHKLPVIESGNVIEFVDLGDFGGGDGAPEGAGA
PAAPEPQPVPEPPKPVEPPKPVLKPVVTKKADADIQQPKEEPKPEEKPKPEEKPKPEPKPE
AKPVPKPAEKPVEKPSEKPAEHPGNASAKADSEQGNGEDKGTGTKGDGTGRGEGSGKGS
GGVKGEHGEGAGSSKGNPLRANGSIPRPAYPTLSMENDEQGTVVLSVLVSPGGHVESVKI
VKSSGFSRLDNAARKAAQNGHFQANAWTEFKVPVKFELNT



MDKERILTPAVVFSVALLHLAMVALLWQA
**HKLPVIESGNVIEFVDLGDFGGGDGAPEGAGAPAAPEPQPVPEPPKPVEPPKPVLKPVVT
KKADADIQQPKEEPKPEEKPKPEEKPKPEPKPEAKPVPKPAEKPVEKPSEKPAEHPGNA
SAKADSEQGNGEDKGTGTKGDGTGRGEGSGKGS**
GGVKGEHGEGAGSSKGNPLRANGSIPRPAYPTLSMENDEQGTVVLSVLVSPGGHVESVKI
VKSSGFSRLDNAARKAAQNGHFQANAWTEFKVPVKFELNT

152 Domain II residues

30 Proline residues

0 α-Helix residues

Burkholderiales

Collimonas fungivorans

Locus:

>AMO93008.1 tonB dependent receptor family protein [Collimonas fungivorans]

MGKRARARARMYCAQKMVLTLGVALPFGAALAQTAGSTAPAATTEAPRSGSSLQLETMTV
TAQRRVEKIKDVPISVTLLKGETLDVLNSGGQDIRVLAGKVPSLNIESSNGRTFPRFYIRGYG
NTDFSTFASQPVSLIFDDVVQENAALKGFPMFDLAGVEVLRGPQGTLFGRNTPAGVVKFDS
AKPSLDKVSGYYSVSDGTHNTANVEAAVNVPLSDQWAMRFSTLVQHRDNWVTNNGGGTP
FLEGYDEQAGRLQFLYKPDGTFNALFNIHARATTGSARLFRANILEKGSDGFIAGFDPSQITT
NAINTQALHTAGGSARLSWNLDQVKLYSITGYETISSYFSRGDIDGGTPTGPGFIPFQVQTG
GGVADHKQFSQEFRVESKNEGPLNWQTGLYYFYEDVAGNSSNFDSTTQLQTSYLQNRQK
NTAYAVFGSLTYDVNDRLKLRGGLRYTEDKKDFSNEVANNVTFTGPGAISENKSNVSWDLS
ANYALTKDISTYARVATGFRAPSIAAPSSSVPITVANAETITSYEAGIKADLFNRRARANFSVY
SFDVKNQQLTAVGGNSNSIMLVNAAKTVGRGAELDLEANLSERLRVTLGGSYNYTQIRDPN
LLVAGCASCTMLNTQVRPGLFSIDGNPLPQAPKWIANVTARYGIPMGNNDELFFYTDWAYR
SKINFFLYNSTEFTGKPLLEGGLRIGYKWDGDKYEVAAFARNITNKIVAVGGIDFDNRTAFIN
DPRMFGVQFRSNF

tonB next to motor genes.

>AMO93146.1 tonB family C-terminal domain protein [Collimonas fungivorans]

MSGASPLPEPETSLRWPLALLIAGAVELTLIFLVLGTHAKPVAALLPAPVKIARLVTIADVPGE
PDPAPTAPPQKLESPKPAIKPLPQPSPKPQADAAPVESKPELQVDSTQQEAPPAALPVVQR
TQASIPAKADKPGTVRRGIVPLVRVEPDYPARALAANTEGVVVAHVTIEKDGSVSSVNIVRA
QPPKIFDPEAIRALMRWKFSQNDGGTVGEVELHFTLN



MSGASPLPEPETSLRWPLALLIAGAVELTLIFLVLG
THAKPVAALLPAPVKIARLVTIADVPGEPDPAPTAPPQKLESPKPAIKPLPQPSPKPQADA
APVESKPELQVDSTQQEAPPAALPVVQ
RTQASIPAKADKPGTVRRGIVPLVRVEPDYPARALAANTEGVVVAHVTIEKDGSVSSVNIVR
AQPPKIFDPEAIRALMRWKFSQNDGGTVGEVELHFTLN

88 Domain II residues

21 Proline residues

0 α-Helix residues

Ralstonia solanacearum

Locus:

>CAD16107.1 probable tonb-dependent receptor protein [Ralstonia pseudosolanacearum GMI1000]

MGALAGALAGVAAGPVWAQGDVQSAGMPVGELNPTVVTASRSEQKLADALPHTTVISRAD
IERSQAPDAVSLLRREAGIEIAQAGGPGAAASLFMRGAGSNQTLILIDGVRVSSGTTGTTQIE
QLMADQIDHIEIVRGNVSALYGSDAIGGVVQIFTRNGRGHAPLANAEIEYGARNTKRAQAGI
SGQLDARGDTSFALSVSALKTTGFSSINPKQAPNANPNDNAYANKSVSAQLQHRFSSDWQ
AGLTWFQTWSTVSYDNAFGAPTDDNESHNQVRAMSAYVDGKLTPDWKTRLTLSQGDDKN
LNFTNGQVQEPGRFNTRNRQASWQNDWAFLPDQMLKVGFEHLDQTIDTDAYSPPTRRVD
SGYIGYEGKFGRHQLQLNLRRDRYSDFGGASSYYAGYGFAFNPQWKAVASISNAFRAPSF
NELYYPFFGNPNLQPEKARSVEGGVEYQSTVGLVRMTAFETDYSNLITSVFDPVSGNFLAA
NVNRARVNGLETSWRGTLHGVDVRASLTIQNPQDLSANRLLARHARHFGSVSAYKSFGPF
SAGLEWNAAGERQDSARTLGGYGLLNLTGRYQITHDWALSARVENLLNKNYQLIAPYNTAS
RGVFFTLSWQQHAPQR

tonB next to motor genes.

>CAD15665.1 probable tonb transmembrane protein [Ralstonia pseudosolanacearum GMI1000]

MIHPRTLKILVVVLLMHVGVLTLIQLGLIASPLRQEPPPELQVNIIPDTPPQPVRQPEPPKPEP
AKPAPPKQVNIVKPVPQPKPAPTPAPALPPSDTAPVVPAAPPAPPAPPVEAAPAPAPAPVQ
SGPINVGINDIQCSNPPLVYPTMSQKMGEEGRTLVKITIGPEGDVVNALVATTSGSARLDRA
ALESARSLHCSPYKQNGRAMTVVANKPFVFKLDN



MIHPRTLKILVVVLLMHVGVLTLIQLGL
IASPLRQEPPPELQVNIIPDTPPQPVRQPEPPKPEPAKPAPPKQVNIVKPVPQPKPAPTPA
PALPPSDTAPVVPAAPPAPPAPPVEAAPAPAP
APVQSGPINVGINDIQCSNPPLVYPTMSQKMGEEGRTLVKITIGPEGDVVNALVATTSGSAR
LDRAALESARSLHCSPYKQNGRAMTVVANKPFVFKLDN

93 Domain II residues

36 Proline residues

0 α-Helix residues

Bordetella pertussis

Locus:

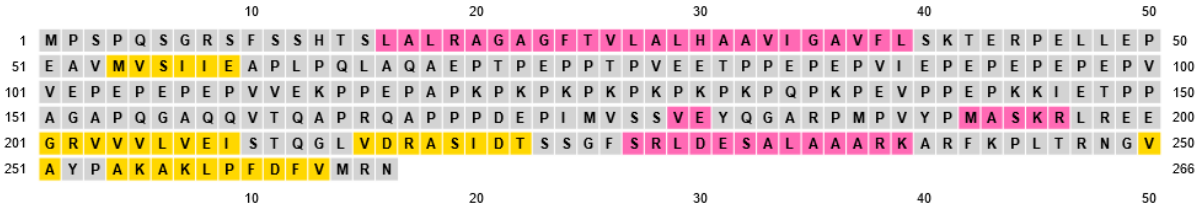
>CAE43854.1 putative outer membrane protein [Bordetella pertussis Tohama I]

MKSRSLRRCAGVLACVAPLAGHAQAGAAAGQPIPELDPVVVTAARSPQLLKNVLADASVIE
RDTLARAGQSSLAEVLAQQHGIEFADSGGPQSVTSLFMRGANSNQTLVLLNGQRINNANG
GGIALNALPPEAIERIEIMRGAASSLYGADAIGGVINIITREPGDKALSAYANAGYGTYGTSRY
DAGVSGAADGFSYSLSTGYGQSHGFNATNRRSFSYNPDKDSYYQNYATGTLGYEWRPEQ
KVVAQVYRSRINGGYDASASYDYNDRYIQDLQAYSLASENRLTRYWKSTLRAGYVEDKND
SRAEGMFEDNNTRFRTRQMQYLWQNDFTLAAGQTLTLAYEHLDQRADGQMSTATGIGNY
TETRRHVNSYTGVYLGDFGRHHVQASLRNDNNSQFGSHTTGGLAYGFDLTPNLRATVAAN
TGFRAPSFNDLYTPTSAFGYRGNPDLKPEESRNAEIGLKYQDEDSELGVVYYQTRIKNLIQV
TEDFSTVENVGRARLQGFTISGAHRFGNTRLRASLDLSNPRNEDTGKQLLRRARTVLRAGI
DHRFDRLLVGAEWYASDERYDYGFPEEKRLGGYGLVNLTAAYDLSRNMQVQVRWNNVLG
QRYTLADGYNTAGSNAFVNPSWRM

tonB next to motor genes. ExbB predicted to have an extra helix either in periplasm or membrane.

>CAE43790.1 siderophore-mediated iron transport protein [Bordetella pertussis Tohama I]

MPSPQSGRSFSSHTSLALRAGAGFTVLALHAAVIGAVFLSKTERPELLEPEAVMVSIIEAPLP
QLAQAEPTPEPPTPVEETPPEPEPVIEPEPEPEPEPVVEPEPEPEPVVEKPPEPAPKPKPKP
KPKPKPKPQPKPEVPPEPKKIETPPAGAPQGAQQVTQAPRQAPPPDEPIMVSSVEYQGAR
PMPVYPMASKRLREEGRVVVLVEISTQGLVDRASIDTSSGFSRLDESALAAARKARFKPLTR
NGVAYPAKAKLPFDFVMRN



MPSPQSGRSFSSHTSLALRAGAGFTVLALHAAVIGAVFL
SKTERPELLEPEAVMVSIIEAPLPQLAQAEPTPEPPTPVEETPPEPEPVIEPEPEPEPVV
EPEPEPEPVVEKPPEPAPKPKPKPKPKPKPKPQPKPEVPPEPKKIETPPAGAPQGAQQVT
QAPRQ
APPPDEPIMVSSVEYQGARPMPVYPMASKRLREEGRVVVLVEISTQGLVDRASIDTSSGFS
RLDESALAAARKARFKPLTRNGVAYPAKAKLPFDFVMRN

127 Domain II residues

42 Proline residues

0 α-Helix residues

Acidovorax avenae

Locus:

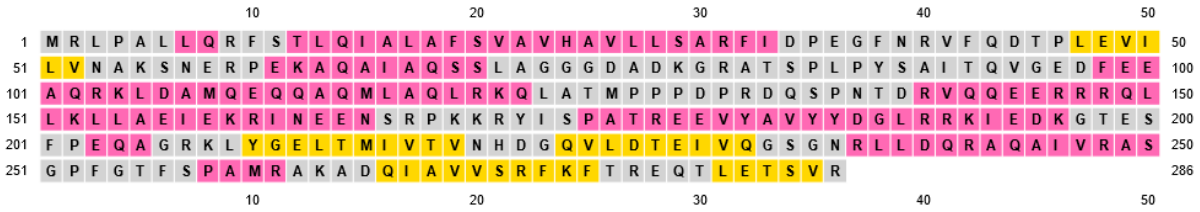
>ADX44735.1 TonB-dependent receptor [Paracidovorax avenae ATCC 19860]

MRDSMRSSPRGGLPPLALSLTLALAALSPAVHAQSDASAVVQSYDIPPGALGPALNRFAQE
AGVSLAVDASRVAGATTAGLQGRYGVEEGFAQLLQGSGYAIRKVGAGYGLAPALPAAAPA
AGGRDRTGAQAAPAQTVTAGAAAPASAAAEAAPAVRTAEGRDTLETVTVSASRSNMEAEK
APQTVQVITRAQIEQQLSLSTNSSDVLSNLIPSYTPSRGKMNGSGETLRGRTPLILVDGVPQ
SNPIRPTGREAHTIDFAMIDRVEVVQGANAINGLGATGGTINLITKRPENGALNQHVDMQAT
MPAGHGGSDSLSTKMAYSANGRQDRLDYLFSIAAEDQGLWRDAQGRGIGADNTQGDLMD
ARSYDVLGKLGYWLDDDQRLQLSINRYRIKSQAHYIGVAGDRTRGIPTTSIEGTPAGAPPFN
EVQTSAITYNHYNLAGMELSALAFSQEFEALFGGDRSATFQDPLIAPRGTLVDQSRAKSSKL
GTKVTLTKADLLDSRLKLTGGFDTLVDKGKQDLFGTGRTYVPESEYRNLSLFLQGEYRLLD
QVTLHGGVRRESADLKIDSYRTLAAYNRVAVQGGTLDFDETLYNAGIVFEPAKDWNVYASY
SEGFGMPDVGRVLRSINTPGQSVDDMKSLSPIVTQSVELGTRVKRGAWDAEASWFRSSSD
YGTRVLRVNEAFMLAREKNRIDGLEASLGWQVNRAHKARLAYSRTKGRYDSNGDGHLDA
RLDGLNIAPDRLVASWTAQWNEQLSSFVQVQRAFSRTFDNPAMNFSGYTLVDASVQYRLP
KGRLRLAVANLFNRDYITYYSQSALVEPLRYFAGRGRTLTLGYSLDF

tonB not near motor genes.

>ADX44697.1 TonB family protein [Paracidovorax avenae ATCC 19860]

MRLPALLQRFSTLQIALAFSVAVHAVLLSARFIDPEGFNRVFQDTPLEVILVNAKSNERPEKA
QAIAQSSLAGGGDADKGRATSPLPYSAITQVGEDFEEAQRKLDAMQEQQAQMLAQLRKQL
ATMPPPDPRDQSPNTDRVQQEERRRQLLKLLAEIEKRINEENSRPKKRYISPATREEVYAVY
YDGLRRKIEDKGTESFPEQAGRKLYGELTMIVTVNHDGQVLDTEIVQGSGNRLLDQRAQAI
VRASGPFGTFSPAMRAKADQIAVVSRFKFTREQTLETSVR



MRLPALLQRFSTLQIALAFSVAVHAVLLSARFI
DPEGFNRVFQDTPLEVILVNAKSNERPEKAQAIAQSSLAGGGDADKGRATSPLPYSAITQ
VGEDFEEAQRKLDAMQEQQAQMLAQLRKQLATMPPPDPRDQSPNTDRVQQEERRRQL
LKLLAEIEKRINEENSRPKKRYISPATREEVYAVYY
DGLRRKIEDKGTESFPEQAGRKLYGELTMIVTVNHDGQVLDTEIVQGSGNRLLDQRAQAIV
RASGPFGTFSPAMRAKADQIAVVSRFKFTREQTLETSVR

153 Domain II residues

12 Proline residues

73 α-Helix residues

Rhodocyclales

Aromatoleum aromaticum TolA

Locus:

>CAI07294.1 Hemin receptor precursor, TonB-dependent outer membrane uptake protein [Aromatoleum aromaticum EbN1]

MPTLRPSVVYAALACAFSSLSHADEAAHLSEVTVTAKGYASANVETPASVTAVEREEWLDR
GADNVGEALRGQPGLAVASDGAQGQNPVIRGLKKESVVLLVDGMRLNSAQPAGAIASFMS
LGLAERIEVVRGPASVLYGTGALGGAINVLLPQARFEAGVQTRAGAEFETANDGVRGTAVM
NASGGDHALMLGASLARIGDYRASDGEVDHTDYDSDSFIAQYRFRLDDSQQLRLSLQQHE
DRDVSYPGSIKPHPHPQIRSSIIHSPSQTRELVEVGYSRRGSGDTPVNVDVRVYRQEMEREI
AARAKGPFGRDFSDTEVTFATDGLDARADWLAHPDHLLSFGVNAWQMEASPERFLSSPPT
FARGRNDPFDDGRIEAIGVFMQDDMRFGRLNVLAGLRRDWVEGDADSVNNGAITRGLERS
DSATSGSLGAIFEVSKLLRPYANVSRAFRAGEMRERFESSPRSDGYYYVGNPRIEPEIATQF
EIGLKGADDDLSYALSAYRTRITDYITGRNVSGAPGTNRCPAANASACKETFNLGRATLVGV
EAEARWQAVRGQWLTAAYSRVRGENEDLDEPLFQMPADEMSLGWEGRVAAAWTADATL
RLVRKQDRVATVFAAGTENETSGFATADFGATWHGQRQRVRVALKNAFDKPYHEHLTEG
VSGMEIDSPGRSLMVSWQGQF

tonB not near motor genes.

>CAI07061.1 putative TonB protein [Aromatoleum aromaticum EbN1]

MSSRPPLRRSTPAASALRLLAKLTGGAGRDARRLQLALAVSVLLHALVLSISFTLPVRPPNR
DPGLEVVLVNARHARAPDKAEALAQANVDGGGNSDRQARPKSPLPPQEVHRDGNAPVEA
RKRVAPPAPLQRSVLTQPKVASTISRPPPRTSDAPPALAPTPSGLDLLNSAATVARLEAEIG
RQLDDYAKRPRKKFIGARTREYRFAQYVEDWRHKIERVGTLNYPEAARGRLYGSLLLVVAI
RADGSIERVEIRRSSGEPVLDEAAKRIVRLAAPFAPFPGDIRSDTDILEIARTWTFTNADKVTA
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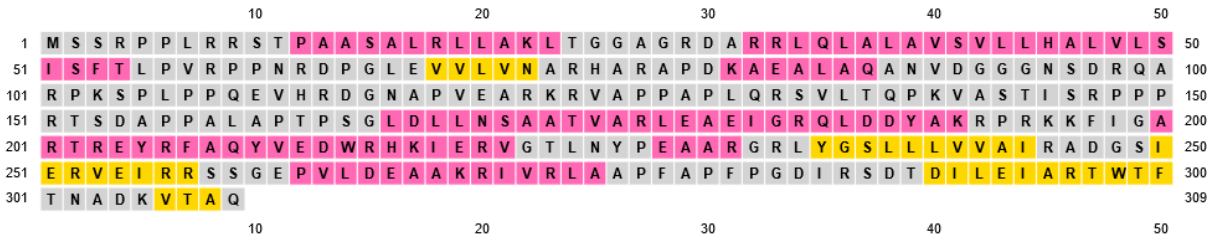


MSSRPPLRRSTPAASALRLLAKLTGGAGRDARRLQLALAVSVLLHALVLSISFT
**LPVRPPNRDPGLEVVLVNARHARAPDKAEALAQANVDGGGNSDRQARPKSPLPPQEVH
RDGNAPVEARKRVAPPAPLQRSVLTQPKVASTISRPPPRTSDAPPALAPTPSGLDLLNSA
ATVARLEAEIGRQLDDYAKRPRKKFIGARTREYRFAQ**
YVEDWRHKIERVGTLNYPEAARGRLYGSLLLVVAIRADGSIERVEIRRSSGEPVLDEAAKRIV
RLAAPFAPFPGDIRSDTDILEIARTWTFTNADKVTAQ

155 Domain II residues

22 Proline residues

43 α-Helix residues

Nitrosomonadales

Thiobacillus denitrificans

Locus:

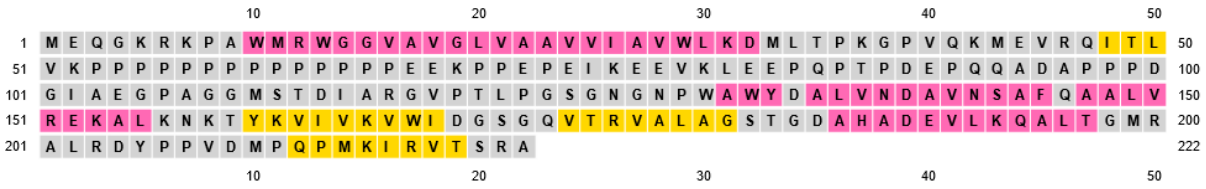
>AAZ96668.1 TonB-dependent siderophore receptor [Thiobacillus denitrificans ATCC 25259]

MKFRLSALAGALSLAFSASPVNAQTPQENPPGELDTVTVWSEYAGSFKSDTVQVGTFREA
SPLDVPQTSNVVTREVLDAQAASTLFGALRNTAGVTRSQLNGSTYDNIAIRGILVENRGNYR
LNGSLPIINLIDVPLENKERVEVLKGASSLYYGFVPPSGIVNLVTKRAGKDPVSSLALSANHY
GGANVHADVGRRFGEEQQFGARVNLLAGREDIGVDNYSGDRSLGAVAFDWQASDALSFK
LDVEHYRKDVSEQAAIKVLAPNADGTITLPAIPDARTNLAGEWQTYDADATNVLFRTDYVLS
DDWGLLLEAGHAQTNRDRRFSQFENYNLATGDGTLKIFFSPNQEYENSNYRAESFGHIPGT
WVSHDLSFGYTANQRDQNSRSGGSVSVAQNLYDPTEVPEQTAPSAPSHNPSTIEDRGWY
LFDRMSFGEKWQLMLGARASRYVSETTSTRYEADDVNPSVAIMYKPVAGVSVYGSYLEGL
EESGQAPAHRANAGELLPPALSKQKEIGVKAEVAQGVLLQAAYFDIERPSTTVDASNRFVL
NGLAQYRGIELAASGEVTRYLALIGSALFLDAEQQNAANPATFGKVPDNTPERTASLFAEYR
LPAVPGLALSGGLYYVGKRPVDNENRAFVDGYTTLSLGARHSTKLNGKRTTFQAVVDNVT
NESYWSTAGNGLLGVGAPRTLKLTAKVEF

tonB next to motor, where ExbB predicted to have two large periplasmic beta-sheet domains. Unlike previous ExbBs seen.

>AAZ96312.1 TonB-dependent receptor, putative [Thiobacillus denitrificans ATCC 25259]

MEQGKRKPAWMRWGGVAVGLVAAVVIAVWLKDMLTPKGPVQKMEVRQITLVKPPPPPPP
PPPPPPPEEKPPEPEIKEEVKLEEPQPTPDEPQQADAPPPDGIAEGPAGGMSTDIARGVPT
LPGSGNGNPWAWYDALVNDAVNSAFQAALVREKALKNKTYKVIVKVWIDGSGQVTRVALA
GSTGDAHADEVLKQALTGMRALRDYPPVDMPQPMKIRVTSRA



MEQGKRKPAWMRWGGVAVGLVAAVVIAVWLKD
MLTPKGPVQKMEVRQITLVKPPPPPPPPPPPPPPEEKPPEPEIKEEVKLEEPQPTPDEPQQ
ADAPPPDGIAEGPAGGMSTDIARGVPTLP
GSGNGNPWAWYDALVNDAVNSAFQAALVREKALKNKTYKVIVKVWIDGSGQVTRVALAGS
TGDAHADEVLKQALTGMRALRDYPPVDMPQPMKIRVTSRA

90 Domain II residues

29 Proline residues

0 α-Helix residues

Methylobacillus flagellatus

Locus:

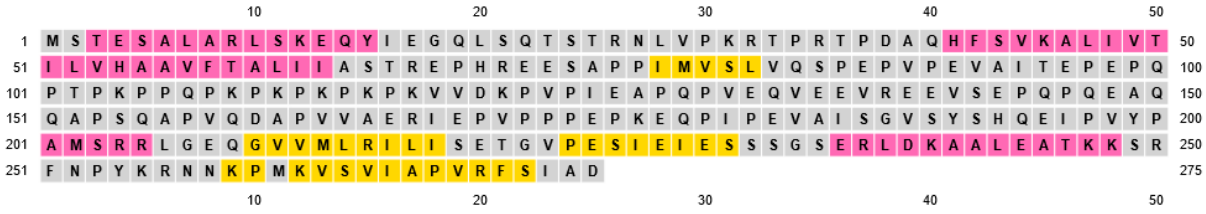
>ABE49140.1 TonB-dependent receptor [Methylobacillus flagellatus KT]

MKYSTMGVSMLALIATSGPSHAHDELPLHSTERIQKLETTSVTARRRLEKEQDVPATVSVVK
GNQLEAGRIYQLQDLPQLMPSLTAQFLHPRQSSIAIRGIGNNPANEGLEGSAGIYLDNVFLG
RPGLAVFDLLDIEQAELLRGPQGTLFGKNTTAGVLNITTRKPVFKPEYSAEASYGSRDFEQY
KVMLNQPINEMAALRIAAYKTHDDGWVKNTYDGKNLNEINRTGARGQLLLQPSESFDLRLIA
EHNEEDSSTGTLVPYRYGPWTPNAFMFLGIHPVTGQPVFGPDYSSNLPAGTPGSNATDAIT
HANGLGASNRAYDPKDYKVTLDGRQRTRTSQDALSAEANWHFNGYTLTSITAWRQWQFK
PDNDLDRTDLFAVNGGVDARHKQYSQEIRLASPLSDVFDYVAGVYYYYQDVSNREQYMTG
PDAFALTTIYPDNSAFSGSGYAKTHSYALFGQGTWHLSEKLDLTAGLRATMEKKEARVVQD
QITPLPPILSPLLDHYDTGVQHQKDESLSSLLTASYWLNDRVLGYATYSSSEKSGGFNTNGV
ASPGAVLGTEALNIDPEKANNLEFGIKSSWLDQRLVANASVFLTRVKDYQAITGTSINGTYA
GLLTNVGDLSSKGMELDLRARVSQHLSLSLSGAYTDASFDRGTAPTPAEEFNGPGGTSDS
GYGKGTRSIAGNQVNGASRWAFSSGAHLRWNPADNLEHYANAQYSWRSESYGDVNNSE
YSKIAGYGILNVSTGLRVTSGKHRWDFSLWAKNVLDKRYFLGLTNAGSNLYVGSAGQPRTI
GASLRYDF

tonB next to motor genes.

>ABE49144.1 outer membrane transport energization protein TonB [Methylobacillus flagellatus KT]

MSTESALARLSKEQYIEGQLSQTSTRNLVPKRTPRTPDAQHFSVKALIVTILVHAAVFTALIIA
STREPHREESAPPIMVSLVQSPEPVPEVAITEPEPQPTPKPPQPKPKPKPKPKVVDKPVPIE
APQPVEQVEEVREEVSEPQPQEAQQAPSQAPVQDAPVVAERIEPVPPPEPKEQPIPEVAIS
GVSYSHQEIPVYPAMSRRLGEQGVVMLRILISETGVPESIEIESSSGSERLDKAALEATKKSR
FNPYKRNNKPMKVSVIAPVRFSIAD



MSTESALARLSKEQYIEGQLSQTSTRNLVPKRTPRTPDAQHFSVKALIVTILVHAAVFTALII
ASTREPHREESAPPIMVSLVQSPEPVPEVAITEPEPQPTPKPPQPKPKPKPKPKVVDKPVP
IEAPQPVEQVEEVREEVSEPQPQEAQQAPSQAPVQDAPVVAERIEPVPPPE
PKEQPIPEVAISGVSYSHQEIPVYPAMSRRLGEQGVVMLRILISETGVPESIEIESSSGSERLD
KAALEATKKSRFNPYKRNNKPMKVSVIAPVRFSIAD

112 Domain II residues

30 Proline residues

0 α-Helix resides

Nitrosomonas europaea

Locus:

>CAD84232.1 TonB-dependent receptor protein [Nitrosomonas europaea ATCC 19718]

MYKTYAIWIGVVLFVCKDVIAQPDATGQEYSGDIPKVTMKEITVSSEALAIPNERLLLDTPTTT
GSRLGLTPRETPASINIIDRATFELRGAQTTQQILERSPGVTVSDQPGAAGTVCMRGFCGA
QITQLFNGITVQYDAVAARPIDNWITERVEVLGGPSSFLYGQGAVGGSVNYISRTANRDQQ
GHESLVLLGSWLNRRAAYGYNGRIGDTNNWLQIHAGYKGSNGYIDKTRHNSGVFSFSLLS
DLTSRISNTVAVEYQIEAREGYWGTPILNPVTAGKYDPETRFRNYNAENSVFDQQVIWVRDI
VDFRLSEATQVRNTFYWYDAYRKYRNVEVYRWNGDNTLINRSASFAVDHKQNLIGNRLEL
SHQQNLFGLPARWLAGTDIAFNDQTRFPSTESGLAVDTIDPYNFTVGDYFDNPRASGPIKD
RRNKLFTVAGYAENRLTLFPGFNLVSGIRIDSIQLDSRYFSPATATEPAAFSRNWTPVTWRA
GFVYDVTDSFNFYTQYSTAASPPAGVLTTTNLNSIRDFGLSTGRQIEGGMKFDFWGKRGTA
TIAGYYLQRKHLSTRDPDNPINAIPIGAQSSRGVEVNLGVRLSPQWSFQGNMAFVDARYDD
FNELVSGVSVSRKGNRPENVAKWVANTWLTWDFHPDFQWMLATRYVGDRYANAANTVP
VKSHVRLDTQLAWQAHRNARIIGRIMNLTDTDYIEWATSAPMYLIGAPRSYEVAVKLDF

tonB not near motor genes.

>CAD84265.1 possible TonB protein [Nitrosomonas europaea ATCC 19718]

MTKIRHKPALTGLSLVSFLVVVATHAAVLYGLWHHRFSTTTPDTITLYAQFIAPPEKQEEAAK
APKVELKAEHAPPQVKPTPPVKKVQPQPKHQLVAKTPAVTPQEYVAPPPVEEHEPEPEPEK
KTVSESVIAAKPAQMPTGPVTLSSELSVSCPDLASPAYPALSRRLGEEGKLVLQVELDETGR
IGKAKIVQSSGYSRLDNAALSAVKTWRCRPATRNGHPVPAVALQPFNFVIEGS



MTKIRHKPALTGLSLVSFLVVVATHAAVLYGLWH
HRFSTTTPDTITLYAQFIAPPEKQEEAAKAPKVELKAEHAPPQVKPTPPVKKVQPQPKHQ
LVAKTPAVTPQEYVAPPPVEEHEPEPEPEKKTVSESVIAAKPAQM
PTGPVTLSSELSVSCPDLASPAYPALSRRLGEEGKLVLQVELDETGRIGKAKIVQSSGYSRL
DNAALSAVKTWRCRPATRNGHPVPAVALQPFNFVIEGS

105 Domain II residues

20 Proline residues

0 α-Helix residues

Gallionella capsiferriformans

Locus:

>ADL54357.1 TonB-dependent receptor [Gallionella capsiferriformans ES-2]

MHQKLIIIALFGAITLPTVSFAETASLDEVVVTATRFATTSENTAVNVTVITAADIEKSAAKTLP
SLLAQHVGIQVRSTDGTPDLAVDMRGFGMTGNQNTLVLLDGQPLNDIELTSIHWSAIPLDSI
ERIEIVNGSGAVLYGGGASGGTIHIVTKHPGKGVHGIASVGAGSYGAKEWQLALSGSGERL
GMRITASGLDTANYRANNNVTQNNLEADIRGDVGQGDAFVKFGADNQTIRYPGNRSVNPN
TGVNQLLTDPRGTATPLDYGTRNGVHVSLGTAQQFEFGEFAGELSYRDTKRTAYFAAFGG
AYLDTALNLLSFTPRIKVPYQLGGAANELTVGMDLSNWNYDSSRSSAPANMGTPTTKILAG
QSDRALYLQNVNQLGADTKLTLGARSQRVSYQARDAVNPAAYASANQVRTANAYELGLRH
NLNQTLAVFGRIGRSFRIATVDEIFAQYGGPFFDSKVTMLEPQTSQDSELGLDYKSAKDKIR
ATLYQMNLNNEIHYNALTFTNMNLSPTRRYGLELEGTHAYSDSVEVGAAYSYTVAKFSNGT
YGGINVSGNNIPLVPRQRLALSTALKLTEKTSLSGSAMYVGQQHFDNDQANTFGQKMPAYT
TVDMKLTHREGAWQLAAAVNNLFNRQYYTYAVSSTFTPGVYNAYPMQGRNFSLNASYQF

tonB not near motor genes.

>ADL54217.1 hypothetical protein Galf_0172 [Gallionella capsiferriformans ES-2]

MKSRFLHNESARIAIALGLSVLAHIAILTLQPHFNAAPFAHQTTGKTLSVTLNKNSAKTPPRPS
TINLTSTLKPAITPSSPAAAATSDTHYFNTNELDQPPHTDQDQLAFNLPDPPKQIDIVMRLWI
DKSGKVVKVEPVTAELSQALISEIRSHLMNSRFSPGHRLGYPANSVVEITLHYE



MKSRFLHNESARIAIALGLSVLAHIAILTLQPH
FNAAPFAHQTTGKTLSVTLNKNSAKTPPRPSTINLTSTLKPAITPSSP
AAAATSDTHYFNTNELDQPPHTDQDQLAFNLPDPPKQIDIVMRLWIDKSGKVVKVEPVTAEL
SQALISEIRSHLMNSRFSPGHRLGYPANSVVEITLHYE

48 Domain II residues

7 Proline residues

0 α-Helix residues

Acidithiobacillales

Acidithiobacillus caldus

Locus:

TBDT gene on different contig

>OFC32715.1 TonB-dependent receptor [Acidithiobacillus caldus]

MKHPTALRCLSSAVLASLWLVPASILAATAASDGGIDIGEVSSSTNAAGTAAARAKALRESP
ENQVQITHQQIRDLVQPGGSIVTALSAAPGVQVKGYGSGNGASRYQIRINGIQVGFALAPGN
PEKNGLSVLFDGVPMNNPLAQYDGWESSETPISSIFSNIHVTQGPGNPDHRWYDSMGGTI
NLIPVEPTAKAGASLDLGGGSFATYSASTMLQTGSINGWRSELGGGYTRSAGFRTGPYHA
PNQAEAFFAKTIKDFHGGHFSAGFFFSHTQEFRSLYIPASPIPGVTTGGYGQPGELLSQGTT
GYYYTVPTSQYFKNDTAHMYLVYARLMVHLAQRLSVDNTLYFRSGYRHHYRVNDYFPHTV
NTEDFTGTTRTIGDRLAFHWNLPMNSVRFGGYYQHSRYESLYYGYNPAVLASSASKPLFAA
DYYDYWDGATAFLQDDFHPISALHITPGLQLINYHVQFVNNSEAAIPPGSTPVTYKAGNNDN
SYTKLAPSLGINYRILPGLHAFAIWAKNFQTAPAAAYGNYQQATVEVPKSPTDINSYIGGLKW
HMGAWQAQLSGFHQHLGNAVIATFLPSDLISKLDRVSAIYNGVNLLLQYGKGLGFFAGTRD
TIQHAYYPSYLPAGGSPVIDARMPGTPTLILGFDAGYRWYAANTRFAVRLSDQYASSVTTFN
NNTNLPDPTRLPGSAYNIVNLGLSADTLAFDSMIPGLKRVGVSLMIDNLLNRKYNSQGYITS
GGEYGPNSQGAILVIPGAPRAVYASFSASF

tonB not near motor genes.

>OFC35725.1 hypothetical protein BAE27_07210 [Acidithiobacillus caldus]

MKRQARGRRGFLRDLRARAPWSAYFGLSARDLDRLFPWLLLSSLGLGGIFLFVRDVGLLHV
PRVPPISSYVQIDLVSAPAEATGTPALPMPTRGPGLPVVRAPATRAPSTAQSDPKAQLAAYL
LAWERRVAEVAGASLAGHSIPQGRLIVAITIDPTGQLRRVEILRGQQHRDLVLAVESILQQAA
PFPPLPPSWQHPPQELRIVRTWNFE



MKRQARGRRGFLRDLRARAPWSAYFGLSARDLDRLFPWLLLSSLGLGGIFLFVRDV
GLLHVPRVPPISSYVQIDLVSAPAEATGTPALPMPTRGPGLPVVRAPATRAPSTA
QSDPKAQLAAYLLAWERRVAEVAGASLAGHSIPQGRLIVAITIDPTGQLRRVEILRGQQHRD
LVLAVESILQQAAPFPPLPPSWQHPPQELRIVRTWNFE

55 Domain II residues

11 Proline residues

0 α-Helix residues

Acidithiobacillus ferrooxidans

Locus:

Different contigs to *tol-pal* genes.

tonB next to motor genes.

>OAP87712.1 TonB-dependent receptor [Acidithiobacillus ferrooxidans]

MYKKLPLKPLLVAIAATGALNITVMAAAQAGVTAPTTSAPTHRIINVGRVSAGLALNTLNKVP
TKKEVFESTQSVKVIGKKQMETAGPAGGAGQALAVAPGVNTQTDSPAGASRTTISINGMKT
GWSNIAGNANDGTVMVTFDGVPMVDPAYGVWGSPEVPQMSMIKGIAVTYGPGYPVNRWF
NNIGGSINFIPLQPTAKAGASIGGFYGSFNTRGVHFNVRTGNIDGWSAILAGGMTSTGNYLT
GYGFNNPSNNYAYYAKVIKRFHGGHFSFGAYAARGVSYRPLGIPVSPNSNVTVNGTDANG
NPIPGPIYSQQTTGFYTTLPYSEYWKEAFNTSYILYSKFFDHLSRDLTLHNLLWYRHGSREH
LHYNYYTGGNSNVAMNQYYLAKSDTYGDKLYFTDRLPWNTVSFGGYFLNNKYNSLLEFYN
PTQASPINGAQVYGSLAVPNGDSHSSYMYMTDLAAFIQDDIQPVSNVRITPGLRVVTFNTNF
VNNEAAQFPLNGYNNGVNSYGTSGDRQPNSSTNFTDVEPSIGANWQITPNVAVYANYSTA
YKAPAGATGTYAHMLASSLKPQSSSQYQFGVKAYVPHDGILNDASFGANYYHLNDTNEIIPI
PVVSHLYSEFASGSSTFSGVNLYFEDDPLYNIHIFSNLSFEKAVYSNYVNPHGVSYDGMPVS
DVPAQTANIGAYYQWYHAGVVYEPRIWWQYTGAQNIYNNNTGAPTNQKLPAFGIWNAALR
VNVGHQYLFAGLHKLSVNVDVLNLLNKQYNSYQYISGGGYYGVAGQMLADPGMPRAVYVS
LEGHFA

>OAP91342.1 energy transducer TonB [Acidithiobacillus ferrooxidans]

MNTIVSDPSWAPQRPKGHFGRALLIGAVLEVVLVGGLIWGGSNTPAPKLMVKKIIAIHMVQP
APPKPKPVPPPPKPVVHPKPVPKPLPHPIPQPRPKPVVHHAPAPKPLMAKTPLPTAPVVPP
SPPVTTPPPPPPPPAPSMAAREAAIDQYAGMVRTRVQADAHVPEAVRLMHLSGTAVITFRL
TPSGRLLWARIAQSSGVGPIDKAALKSVEEGTYPPFTKNMPKHASNFNVEVHLSSHSS



MNTIVSDPSWAPQRPKGHFGRALLIGAVLEVVLVGGLIW
GGSNTPAPKLMVKKIIAIHMVQPAPPKPKPVPPPPKPVVHPKPVPKPLPHPIPQPRPKPVV
HHAPAPKPLMAKTPLPTAPVVPPSPPVTTPPPPPPPPAPSMA
AREAAIDQYAGMVRTRVQADAHVPEAVRLMHLSGTAVITFRLTPSGRLLWARIAQSSGVGP
IDKAALKSVEEGTYPPFTKNMPKHASNFNVEVHLSSHSS

103 Domain II residues

41 Proline residues

0 α-Helix residues

α-Proteobacteria

Magnetococcales

Magnetococcus marinus

Locus:

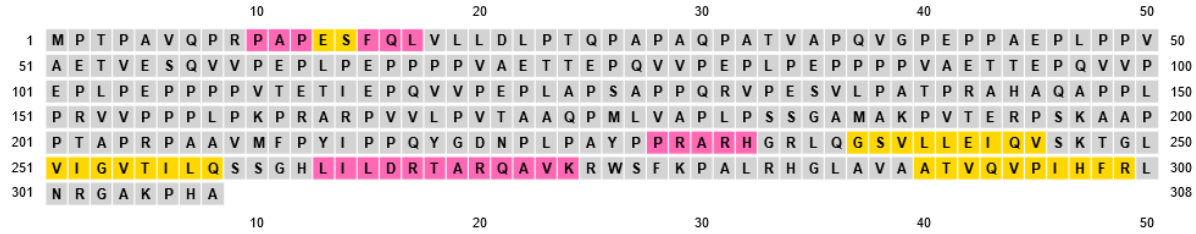
>ABK46045.1 TonB-dependent copper receptor [Magnetococcus marinus MC-1]

MKARSHLAMLSALLALPITSVQAQQSTTLAPLTVEDTLLEEDGAVILYMDNRNKGPVADGGE
LLKTIPGVSAARKGGHGLDPSIRGQNQTRLNIVLDGAFVHGGCPNRMDPPSAYGASESYNS
VTVLKGAQSVEYGAGGSGGVVLFNRQTETFDADERYRGKAGVGYRGNINALESYLDMAS
GTPSAFIRFIGNYSDGNDYKDGDNNVVRSSYTESTGNLLLGWTPDAENRVELSHEASYSSD
MLYAGAGMDAPYTRNNVTRFKFARGLHDGVMQKLEGQISYSQVAHLMDNYSLRTAPAAA
MYMQAPSTSDTLTGKLSLQFNHAGMDWKVGVDHQGNQRDAVRYRGTVGAVTNLQSYLW
PDVTTLTTGLFAQLDRPLGETNRLKAGLRYDYVRADAGKTHATPNDAMGALAKLSGHDLYT
TYYGGSTDASTEHNMGGFLRYEQGYWGNQGNFYVALSRTVRTADATERYMAANHNTSAD
SRWVGNPFIKPEKHHQLDVGTRIQWQALKSDVTLFYNRVDDYILQDHQHSAGADGNATVY
HNVEATLLGGEAAFTYNFDPHWVGGMSLAYVYGHNETSNQVLAQIAPFEAGFTLDYRADR
WDFGGKLRVVTKQTRADTDSTTATGLDTDQTPGFSTLDLYSAYRPMPNLTLKMGVNNLFD
KRYAEHLNASNSFDATQLQVNEPGRTLWFTLGTEF

tonB next to motor and TBDT genes.

>ABK46046.1 outer membrane transport energization protein TonB [Magnetococcus marinus MC-1]

MPTPAVQPRPAPESFQLVLLDLPTQPAPAQPATVAPQVGPEPPAEPLPPVAETVESQVVPE
PLPEPPPPVAETTEPQVVPEPLPEPPPPVAETTEPQVVPEPLPEPPPPVTETIEPQVVPEPL
APSAPPQRVPESVLPATPRAHAQAPPLPRVVPPPLPKPRARPVVLPVTAAQPMLVAPLPSS
GAMAKPVTERPSKAAPPTAPRPAAVMFPYIPPQYGDNPLPAYPPRARHGRLQGSVLLEIQV
SKTGLVIGVTILQSSGHLILDRTARQAVKRWSFKPALRHGLAVAATVQVPIHFRLNRGAKPH
A



Appears to have lost its TMH- no further analysis.

Rickettsiales

Rickettsia prowazekii

Anaplasma marginale

Rhodospirillales

Acetobacter pasteurianus

tonB and TBDT genes on different contig to *tol-pal*.

tonB not near motor genes.

>OAZ72116.1 Catecholate siderophore receptor Fiu [Acetobacter pasteurianus]

MSRSELSHPSSQGKGLRVAVALGVSVGLGVTESKAQAEDAAQPLQPSSSDTSIKLSAVRV
GGHAESKNESYEAGNTNSKILNISRMPASVRDTPQTINVVPQELMKQQRAFTLDQALSNVP
GITLSTGEGAGGLNGDQFRIRGLQARQDIYTDGLRDFGTYTRDVFNTESVEVIKGPSGEYF
GAGNVGGVINQSQKHAHAGNSYSYDQSFGSGPLFRGVGDINYQINDDMAIRVNGMFNKQ
DVVDRNNVTSNRYGAAVDFGVGLRSKTSWHLTWQWLNSDSKPDYGVSMIQVNGIYRPITE
YGLSRNTSYTRNFDFDRSNIHSLTSSLKSEISRWFTLTNDTRLSMYNRDYTATTPAACSGAC
ATAFLAGGNYALPYGAGGGAAYRQEGWGVQNILMGRSQFKTGFVHHDIKAGVDVNYASD
SRWPGSFTNRVNNQTIRNPQYSYSGTSVSFPSSGHGNANARDVGLFFSDRIQLTKQLSLF
GTGRWDSFSSTYYARSKAAQGRAEQKSDRWSPSASIMYSPLKNASFYFTFARSYKPVGTD
VSSLVTIKPQAGDVAQKGVNLSPQRSDLFEFGSKADFLHKRLGTTVAFFQISENNSRYYDV
NGDMETGFADSGSGRRIRGVELSANGKLTRDWQIFASYSYMDGRVTHSSTGDNGKTAPQ
VPHNTMSVWSSYDLSRQLLNPEWGTLKIGGGVQYSSGYWAGPDTANTARIPNTFLLNGML
SWDYKHYRVSFNANNITNKLNYASSFSGSRAVPALGRYFIGNIGVTF

>[OAZ72119.1](#) Vegetative cell wall protein gp1 [Acetobacter pasteurianus]

MSATTYKNIAGKVHSTTFSDWKIQQIRKARQEDTFRWGISFLIVVATTGAATLSFLHMPHTA
PAIPEPPPAAIAIDMAPEPVATPSPPTDAPPGPQQTISESDPSPVDPAKLEAPPAPVPHPPIP
VPQPEKLHKIVKKNKPTVNLKKPVPDKTPPAEKTTAPPTSKAPPAQTQAAPIEGSSSSHASQ
SPNTWQGALLARLEKYKRYPAEAMSAHQEGTPNLHFTMDRKGRVLSAHIEKSSGHSLLDS
EALALVRRAEPLPSPPDSVAGDSITLTVPIEFYMEHAQD



MSATTYKNIAGKVHSTTFSDWKIQQIRKARQEDTFRWGISFLIVVATTGAATLSFL
HMPHTAPAIPEPPPAAIAIDMAPEPVATPSPPTDAPPGPQQTISESDPSPVDPAKLEAPPA
PVPHPPIPVPQPEKLHKIVKKNKPTVNLKKPVPDKTPPAEKTTAPPTSKAPPAQTQAAPIE
GSSSSHAS
QSPNTWQGALLARLEKYKRYPAEAMSAHQEGTPNLHFTMDRKGRVLSAHIEKSSGHSLLD
SEALALVRRAEPLPSPPDSVAGDSITLTVPIEFYMEHAQD

130 Domain II residues

36 Proline residues

0 α-Helix residues

Rhodospirillum centenum

Locus:

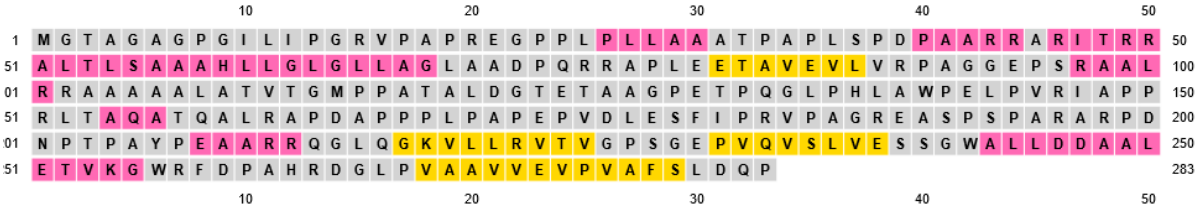
>ACI98016.1 TonB-dependent receptor, putative [Rhodospirillum centenum SW]

MKMTDTQRRVRRAALLAGAAVALAMPAMVPVHAVAQEAGALEEIVVTGSRIRAPNLVSTSP
VTAVTGEDIKAQGVTRVEDLVNSLPQAFAAQGGQVSNGSTGTATVNLRGLGSSRTLVLIDG
RRLMPGDPSVPSPDLNFIPSSLVQRVDVNTGGASAVYGSDAIAGVVNFIMERDFEGVRVDV
QHGFYMHHNENDDVQSIIRAKSASASVPTDFAVPDSNVTDGEQSEATLVIGANSADGKGNV
TAYAGYREIKAVLQGDRDFSACSLNSGDVFTCGGSGTAYPARFGNWVVDPAGPGNTFRA
RNASTDVYNFGPTNYYQRPDERYVLGAFAHYEIQPWADVYADVMYMDDRSIYQIAPGGIFA
GTFSVNCDNPFMTPTQQQQLCGANAGTQNNFTGTIARRNIEGGGRQGDMRHSAYRFVTG
VRGDITDEWNYDAYLQYGATSFNRAQTGFFQTQKIRNALIARRDANGNIVCQAAIDGSDTS
CVPYNIFKIGGVTQEALDYLETPSYATGNTEEMILSASLAGDLTNYGVVSPFATSGVGVAFGI
EYRSEYLDSASDYTAAAGLLNGSGGASLPVEGDFDTKEIYGEIRIPLVEDKPFAQSLELDAG
FRYSEYSSVGSTDAYKAGLIWSPVSDLRFRGSFQRAVRAPNILELYDPQVVQLDGSTDPCA
GLSAGDALVARCAQAFGLTAAQVLAIEENPASQYNGQNGGNPNLDPETSDTYSIGVVLTPE
FAPGLTVSFDYFDIKVEDYISGIGADLIISRCLETLDPYFCGLVNRDANGSLWLSDQGYITNTT
LNTGSLKTTGIDVNIDYSLDLEDVGLNNAGSLAFTMAGTWLDTLKTQPLPNDKAYDCTGYY
GTVCGTPNPEWRHKARLTWTTPITGLTLSTQWRYYSKAELDATSDQPGLNNPAQVAGTDL
KLGTQNYFDATITYQFLESYTLRIGANNIFDRDPPLTGSANCPTGPCNGNTWPQVYQDAMG
RYVFVGLTAKY

tonB not next to motor genes.

>ACI98096.1 protein TonB, putative [Rhodospirillum centenum SW]

MGTAGAGPGILIPGRVPAPREGPPLPLLAAATPAPLSPDPAARRARITRRALTLSAAAHLLGL
GLLAGLAADPQRRAPLEETAVEVLVRPAGGEPSRAALRRAAAAALATVTGMPPATALDGTE
TAAGPETPQGLPHLAWPELPVRIAPPRLTAQATQALRAPDAPPPLPAPEPVDLESFIPRVPA
GREASPSPARARPDNPTPAYPEAARRQGLQGKVLLRVTVGPSGEPVQVSLVESSGWALLD
DAALETVKGWRFDPAHRDGLPVAAVVEVPVAFSLDQP



MGTAGAGPGILIPGRVPAPREGPPLPLLAAATPAPLSPDPAARRARITRRALTLSAAAHLLGL
GLLAG
LAADPQRRAPLEETAVEVLVRPAGGEPSRAALRRAAAAALATVTGMPPATALDGTETAA
GPETPQGLPHLAWPELPVRIAPPRLTAQATQALRAPDAPPPLPAPEPVDLESFIPR
VPAGREASPSPARARPDNPTPAYPEAARRQGLQGKVLLRVTVGPSGEPVQVSLVESSGW
ALLDDAALETVKGWRFDPAHRDGLPVAAVVEVPVAFSLDQP

115 Domain II residues

21 Proline residues

8 α-Helix residues

Sphingomonadales

Erythrobacter litoralis

Locus:

>KEO90001.1 TonB-dependent receptor [Erythrobacter litoralis]

MMRFSLLSGAAGIAFAAIAAAPAIAGEVRGTVVDASETIALRAAQIEIEEIGRQVNSERGGTF
DFGEVPAGTYTITARYVGADPVSQRVTVPETGAVTVNFALGQSGSQILVVGQGASQASALS
RKRAADGVSDVLTRDAIGQFPDQNVAESLRRLPGINVLNDQGEGRFVAVRGLDPNLNATSV
NGVRIPSPEGDIRGVALDVISSEIIESIEVKKSLTPDMDADTIGASIEINTTSAFDRKEDLYVVK
LGGSYNELRDTLTPDLGADFAAKLTDNFGVSGGISYYNREFQTDNVEADDWTEDDGLIYAE
EVQYRDYLVERERISATLGFDARVGSSTELYLRGVFSQFDDQEFRRRLTFDLGDANVSGSG
LNPVFDDIRDPADPDDEAAIAVERDVKDRFERQRIRTVTFGGESQWGGLKAEYALAWAKSS
ERENGSVDPTIFVGEFEDSGLGVGFDYADERRPRFNVTGNTADFFDPSFYELDEIEFTALS
DAEDEEFSGRLDLGYEWFTDAGTLTVQGGAKARLREKRFNGEIEFYERDDYTLADVLGEG
PSNTLENLAPLPGLTQATDFFRDNFASFELNAVDTALDSANGDYSVEEDILAGYLLGRFEND
QWLVIGGVRYERTDNRLSGFETALFEEGQDLPGGGVADDDTVIVTPVEFERDYDHWLPSL
NIRYTPMPEFVMRFAGYRSIVRPNLEQLAPRFELDENREAVIGNPTLEPFEAWNLDASFEYY
MTGNGAITAAFFYKDIDNYVTTLVLDQPGSIFGVDYEQGETFVNGPAAEIFGIELGFYQRLDF
LPGFLDGLLVQANYTYTDASGLVADGEVGDITAAPTFREIPLPATSENTFNVALGYDKGPVS
LRLAGTYRDGFLDEVNADGPEFDRFTDSLFQLDFTARYRVTDKVQVYFDWININDAEFYAF
NRLGGRQNILQFERYNWTMKGGVRLNF

tonB on different contig, next to heterologous motor where ExbB subunit has disordered cytoplasmic domain.

>KEO91069.1 energy transducer TonB [Erythrobacter litoralis]

MAYADQQMSGNKVVSIVIVALIHVAVGYLLISGLAISAAKKIIERVDTFNVEEPPPPPEEPDEP
PPEQPQETAPPPPVAPPPPINIAPQPPQIQTQREIPPPSPPALVLPPPAPAAPPAPPPPPSQA
RGVQPRNQSRWVQRIIEDYPSRALRQEEEGTVGVRVTVGADGRVAACSVTSSSGSSILDD
AACRSMQRYARFEPALNDAGNPISGNWSTRITYQIR



MAYADQQMSGNKVVSIVIVALIHVAVGYLLIS
GLAISAAKKIIERVDTFNVEEPPPPPEEPDEPPPEQPQETAPPPPVAPPPPINIAPQPPQIQT
QREIPPPSPPALVLPPPAPAAPPAPPPP
PSQARGVQPRNQSRWVQRIIEDYPSRALRQEEEGTVGVRVTVGADGRVAACSVTSSSGS
SILDDAACRSMQRYARFEPALNDAGNPISGNWSTRITYQIR

91 Domain II residues

36 Proline residues

Sphingomonas wittichii

Locus:

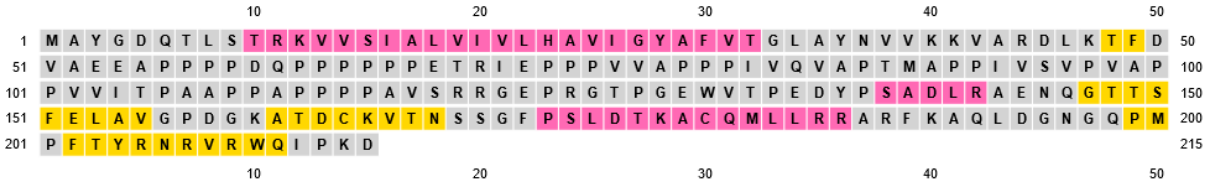
>ABQ66648.1 TonB-dependent receptor [Rhizorhabdus wittichii RW1]

MKQSLHIASIATIAFLTMIPVEAQAQEAARAAPADEAPAAGGIDDIVVTARRRAERLQDVPLA
VSAVSTAALERANIQNVAQLSRLVPSLTSVPGQGGSRSLPNFSIRGLSQQELTILADQSVST
YIGDIVAARTQGINSALFDIASVEVLRGPQGTLFGRNTTGGAIIIRPARPTDEFEGRVGVTVG
NLDTFNVEGMVNVPLSPNIAIRVAGQRQRDDGFVYDEILQRNVNDTKQEGARASILMHNDD
LESLTVYNYFHENDGGTASFLQNVRATGSLNGAAVRASRGYRPLEDLLAEQQARGIYRIAN
GSPIFTKVETHDIANTTSFDLSETIKLKNIVGYRHVKDHIFDDMDGSSNALHPQERIDRAKQF
SEEFQILGDTANLNWIAGLYYFRESGRNQGISAVGAVDPGLVEPDNVAAFPGTAYSNTDTA
ARNTSYAAFAQGTYRFGGGLSLTAGIRYNRDERQATIRNRTATACRFTRDLDNNPATPETA
VPLAQCELGVKDSFSEVTYNVSLEYKIAADKLVYIAHRHGYRTGGFGARASTEAGLRRTFR
PETVDDVEVGVKADWRMGDAFLRTNLAGYYAKYKDIQRLLTDPVAVPPTTVTTNAGRARIY
GIEADILFRPVKMIELTANYAYTNAKFTKFIYPDGTDHSNDPFARAPRNVYTLGARLLAPLDE
GQGDASVGVSYYHTGDYSGNDTYVPGYTDVKGYSLLNFDASWNRVMGSGFDVALFVNNV
TKKKYDFLLINLDSLGYTSHTPGMPRTYGATLRYHF

tonB next to motor genes.

>ABQ66489.1 TonB family protein [Rhizorhabdus wittichii RW1]

MAYGDQTLSTRKVVSIALVIVLHAVIGYAFVTGLAYNVVKKVARDLKTFDVAEEAPPPPDQP
PPPPPETRIEPPPVVAPPPIVQVAPTMAPPIVSVPVAPPVVITPAAPPAPPPPAVSRRGEPRG
TPGEWVTPEDYPSADLRAENQGTTSFELAVGPDGKATDCKVTNSSGFPSLDTKACQMLLR
RARFKAQLDGNGQPMPFTYRNRVRWQIPKD



MAYGDQTLSTRKVVSIALVIVLHAVIGYAFVT
GLAYNVVKKVARDLKTFDVAEEAPPPPDQPPPPPPETRIEPPPVVAPPPIVQVAPTMAPPI
VSVPVAPPVVITPAAPPAPPPP
AVSRRGEPRGTPGEWVTPEDYPSADLRAENQGTTSFELAVGPDGKATDCKVTNSSGFPSL
DTKACQMLLRRARFKAQLDGNGQPMPFTYRNRVRWQIPKD

83 Domain II residues

29 Proline residues

0 α-Helix residues

Rhodobacterales

Hyphomonas neptunium

Locus:

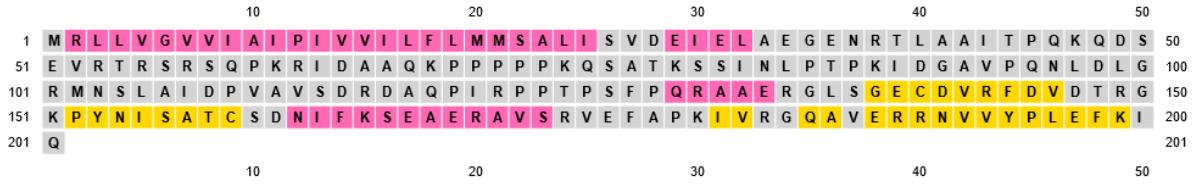
>ABI77930.1 TonB-dependent receptor [Hyphomonas neptunium ATCC 15444]

MKRANMKTHLLCSAGLLAITAMGHSLPAIAQENDTSADEVSRTLETVTVTAQFRDQQLQDV
PNSIVAFTAQDIEDAGIRSTEDFIALTPNVSFDNSFTYLNSFVVVRGVTQINNADSPVAIIVDG
VPQNNQKQFKMPLFDVEQIEVLKGPQGSLYGRNAIGGAINIVTRQPTNEIEGFVSGGLSNGS
GYRMEGGISGPVIKDQLMFRLSGSYYETDGLIENAYLGRTVDTVDHDYSIRGKLAYTPNDVF
SLDLRAAYTDARAGAAYDAVVNSQLNPDFRSGNDSNDIFAPASNLAGITEADILDLSGKASL
DMGFATATYILGYTDLTETYRSDLDFSNPDQPTFGPFGQLGQGQNLSLDLLSQELRFVSPD
ERTFRWIAGGYYLETDRSLLTRGFLDLTGSVDQFDTGIAIIDRSEDNDNTAWALFGQAEFDL
NDRTVLQLGARYDEDERNQTQGAAGPVRTRSFSAFQPKITLSYDILPDVLGYATYSTGFRS
GGFNAPGVVLDSFGDETLTNYEAGLKTGFADGNGTLNIAAFSSESEGFQFFFVDASTVSQII
SNLDKVDLRGFDADFRYRVSESFTLSGGVGYTDSEIRSIGNAQLESYLTASGVDTDAVIGSR
SPKTTDWSVSLSGQYVRPVRSGLDAVLRADYEYQGNKYWQIDNLDVRDPVNLLSLRFSLE
SDIWSASLWGKNILDEEYYADFNPAEYAGAPFDLGSQARPATYGVDFKYRF

tonB next to heterologous motor genes including ExbB with large periplasmic domain.

>ABI75541.1 TonB family protein [Hyphomonas neptunium ATCC 15444]

MRLLVGVVIAIPIVVILFLMMSALISVDEIELAEGENRTLAAITPQKQDSEVRTRSRSQPKRIDA
AQKPPPPPKQSATKSSINLPTPKIDGAVPQNLDLGRMNSLAIDPVAVSDRDAQPIRPPTPSF
PQRAAERGLSGECDVRFDVDTRGKPYNISATCSDNIFKSEAERAVSRVEFAPKIVRGQAVE
RRNVVYPLEFKIQ



MRLLVGVVIAIPIVVILFLMMSALI
SVDEIELAEGENRTLAAITPQKQDSEVRTRSRSQPKRIDAAQKPPPPPKQSATKSSINLPT
PKIDGAVPQNLDLGR
MNSLAIDPVAVSDRDAQPIRPPTPSFPQRAAERGLSGECDVRFDVDTRGKPYNISATCSDNI
FKSEAERAVSRVEFAPKIVRGQAVERRNVVYPLEFKIQ

76 Domain II residues

10 Proline residues

4 Helix residues

Rhodobacter capsulatus

Locus:

tonB next to motor genes.

>SDE40641.1 protein TonB [Rhodobacter capsulatus]

MSLALTDPPEAPGRALLWGLALSVALHAVAVSVLSQTEAAPAALVAAGAGGEDLDSLDAIA
ATFVDLAPQITLPEPEMTLPLTAPVIDIPEVRLPDPVLLPPEPPKITPPKVAEDKPTPPPPKPK
PEPRAEKPKQAKPAPAQSESRAASRAAGSGAGAQAGTGGADAQATVSAGTAKSLLSKWG
ATIRTRIERRKSYPAAAGRAAGSVGLALRVSRDGGLISAAVNRSSGHPALDAAALAAVQKA
GRFPAAPAELAKPSYAFSISVKFSR



MSLALTDPPEAPGRALLWGLALSVALHAVAVSVLSQ
**TEAAPAALVAAGAGGEDLDSLDAIAATFVDLAPQITLPEPEMTLPLTAPVIDIPEVRLPDPV
LLPPEPPKITPPKVAEDKPTPPPPKPKPEPRAEKPKQAKPAPAQSESRAASRAAGSGAG
AQAGTGGADAQAT**
VSAGTAKSLLSKWGATIRTRIERRKSYPAAAGRAAGSVGLALRVSRDGGLISAAVNRSSGH
PALDAAALAAVQKAGRFPAAPAELAKPSYAFSISVKFSR

134 Domain II residues

26 Proline residues

11 α-Helix residues

No TBDTs found in this strain as poor coverage- used a different strain.

>TKD26225.1 TonB-dependent receptor [Rhodobacter capsulatus]
MRLASRQLAAFLFCSTALSLPLAAEQADDTLWLGQIVIGYAEDGSPILAGENATHLTADDLR
GATSTSDLDGLLRVQTSVFTQKDPGNPGVSVNIRGFEGSGRVAMSLDGVPQTYRLTGHAA
QGYVFVDENLLSGIDITRGPVTGLGGSGIAGSANFRTLEVGDVLKEGQTRGGLVRLDHASN
GDTTSGMAAAAMKAGRFDALAAISRHSGESYEDGDGVEVPNTDTDISSALVKLGYDLTETQ
RLTFSLMRYETDFFATSYFQHLTNDVAKIGYHYDPGSSLIDLRVNAYAATTETDWLRGGSPF
ASSVGRNMSTKTRGLDVTNTSELRFGGWQLTSVNGIEASQDSLGGSKGGVNPTTGKARRL
SAFSENVFVQGKWEITAGLRANSYRLDGEASQGTIDIKNSSLDPKLTLAYQATDWVQPYVT
LSRAMRSPTLQETMLGGSHPGGGIGMIANPRLEAETEEGVELGFTLDRAGLFAEGDRLSG
RVNYYNMEVENYIVTSMAFTNAFGQTGAAFVNVPGRTKTEGVEIELDYDHRAFDLGLSYTH
NSSHLPSQTPGLGAGQYLPDDTVSVRLSRDFMADRLTLGAQYTHVSGGLFTDAYTSTPYQ
KDDSYELVDLFASYDVTEDAVIYAKVTNLFDEVYAPWLSASATENGQGRTLHVGTSIRF

Caulobacterales

Caulobacter crescentus

Locus:

>ACL95946.1 TonB-dependent receptor [Caulobacter vibrioides NA1000]

MGRKLWLHKVMGAASLLALATAGAAHGQVVEELVVTAQKRVENVQDVPIAISAFSANALQE
RAVGNVAQLSNLAPNVTLDGGTPFSGSPSVLSAYVRGIGSDDFAFNIDPGVGIYVDGVYLA
RTVGANQDLLDVERIEILKGPQGTLFGRNTIGGAISIVTREPGDTFKFKGDVTTGSHKLMQA
RGSADLPLAEGLSSSITFGIKSRQGYVERIPYPDARARNTTSYTAFPSSGYDTASHEGGENS
WNLRGKLKWKGELTKVVLSADYTREDGGGLANTLLATTEMVPGNFAGTSNLPGTAFDPTG
TTGFLFAGLYNFCIGATPAQIAARNAQALCGVRGTQYSPGLRVASLAGVNVDADPTNDRLP
FDSRFVSKDIDKSYATGNSFSNMVNWGVGGTVEHSLTDDVTVKSITAYRKLLWKSGTDAD
GSPLNIGQLSFNMKQWQISQELQLLGSALDKKLNYVLGGYYFKEKGSLHDYVTFDEGLLQV
DGPNQLETKNYAAFGQVDWRPSELIGVTIGGRYTKEEKLFEGGQQDLNGFNYKLFGCSDA
NGNIRPNGAFPLAPISCQVGLSYPDPSNPVRVYAPGVNKQTFSNFSPKVGVQLHPADDLMT
YVSWSKGYKTGGWTTRLTNPQLTAQPFGEEVATTWEAGFKSKLLDRRLQLNGSVFQTEY
DGIQLNFQQGTSPTIRNAGDAKIKGVELEAVAVPLEGLTINASVGYLRARYTDVLAGVLAVS
GPNVFQAGTFVGAPLPKTPEWKINLSPRYAFKLANGGSVTAIADWTYTSSIWNNAQRTYVL
KRPAVQVVNASVAYADPDGAWSVTVGGTNLTDKRYLTTGNENIAAGAVFGTYSRPREAYV
RLGVTF

tonB next to motor genes, where ExbB has a long disordered periplasmic domain.

>ACL95884.1 TonB1 protein [Caulobacter vibrioides NA1000]

MADQNTPEHRRYDPLTSEGPRRKKGFGAFGISLTVVAGLHALLFAYLAKQKFEAVFQEYSD
DATVVELPPPPPPPPPPPPPPPTNEPPPPPAVVQPRPPVAPPPDVTPPPPLPIPPVEKRVE
QTAPPVISPTPPVPSNPPARASVITRPDWARKPSGEDMARYYPDRAQRMEVSGRATISCTV
TAKGTLEGCSVVSESPADMGFGDAAIRLSRLFRMKPKTLDGAPVDGGQVTVPLVFQVPQ



MADQNTPEHRRYDPLTSEGPRRKKGFGAFGISLTVVAGLHALLFAYLAK
QKFEAVFQEYSDDATVVELPPPPPPPPPPPPPPPTNEPPPPPAVVQPRPPVAPPPDVTP
PPPLPIPPVEKRVEQTAPPVISPTPPVPSNPPAR
ASVITRPDWARKPSGEDMARYYPDRAQRMEVSGRATISCTVTAKGTLEGCSVVSESPADM
GFGDAAIRLSRLFRMKPKTLDGAPVDGGQVTVPLVFQVPQ

94 Domain II residues

42 Proline residues

0 α-Helix residues

Parvularculales

Parvularcula bermudensis

Locus:

>ADM08760.1 TonB-dependent receptor [Parvularcula bermudensis HTCC2503]

MRSKLHARLLSGAAVLALGAPAFAQDAEPALQDVIIVTGTRIDPATETGITPDAAPLQGGDIT
YLTARTPGGARLGNGELSGQMQYRGLFGERLNLRVDGQRFASGGPNLMDPVFHYAPAPL
VAAIVIDRGVSPVSAGPGLAGGADAVFKRVDYAQGDEARFGYDLTVGARSVNDSLSTGGV
VGLASDAWRVNLLGAWEKGDDTEFGDGEIGGTAFERGVYGLSAGARTALGEFTLDLRRQN
TGPSGTPPFPMDIQYFDTDFARLGYAKAFGDLHFTASVHATDIVHLMDNFSLRPAPMPGRQ
RATFADASTQGGEGSISFPAFGGDLALGLDGEQVEHDVTITNPTNTDFFVTPFPRVEMQRF
GGFAEWSGALGAINAQLGLRADRNGYDAGEASLGSALPMGPRMLATAFNDADRSGEDTT
VDAVARLWTTERGGLSWRVTLAHKQQVPGYIQRFGWLPINASGGLADGNIYVGDLALEPE
TAWIAEAGYDYASARAYLRPTVFIRQIDDYIQGVPFDGTVGVADSPVEMIATMNGDPTPLR
WANVEARLYGLDMDGGYDFDGPLRLDGVFSYVRGERRDIDDNLYRVAPLNLTLGLTWEAD
VWSATVETRAVADQEEVSLTNSEEATDGYVVLSAYGEWDLYDGVTLSAGVENLLDEVYQD
HLAGYNRNGFGDVPVGDRLPGAGRGMFVRLNMSY

>ADM09361.1 hypothetical tonB2 protein [Parvularcula bermudensis HTCC2503]

MASLLRGFVGLPLAAIVTVFLFLFMWGLIRVNELPPAEDRQQANISFTRQIQDTEIRNQKVFE
RPSLDQPPPPPPAINNATFQPSVEGVRAQAPSFDADVDIGSGFNPDRDAQPIVRIPPTNWE
RCIDDRQAGTTQRVSLEFDVTPEGQVTNVNVLDSTDRCYERYATRAAERWKYNPKIVDGE
AQPRFGVRTVIEFQIGSE



MASLLRGFVGLPLAAIVTVFLFLFMWGLIR
VNELPPAEDRQQANISFTRQIQDTEIRNQKVFERPSLDQPPPPPPAINNATFQPSVEGVRA
QAPSFDADVDI
GSGFNPDRDAQPIVRIPPTNWERCIDDRQAGTTQRVSLEFDVTPEGQVTNVNVLDSTDRC
YERYATRAAERWKYNPKIVDGEAQPRFGVRTVIEFQIGSE

72 Domain II residues

11 Proline residues

0 α-Helix residues

Parvibaculum lavamentivorans

Locus:

>ABS61808.1 TonB-dependent hemoglobin/transferrin/lactoferrin family receptor [Parvibaculum lavamentivorans DS-1]

MATINTRRLPLLSLLFATTSLAAISVAQAQDTTGTDTGEDAPKATQLDAVTSTATRNPTAIND
VAGTVSVITAEELERRNANSMQDIVRYEPGVSVSNSPTRVGAGNFTIRGIGGNRVLVLVDGF
TAPDYIDASAGGLYTRDFFDLDSMKRVEIIRGPASALYGSDGLGGVVSYVTKDPSDYLDIFD
KDWYASLKSGYDSSDESFTESATGAVRAGNVEMLGLYTRRDGHEVEPNSSYVANPIDYES
NSFLAKLVFNGPDSNKLTFTGQLDNKQADIRLLSEETGTVNRSEATDETDRYFVSAAYSHR
MPTPIADRMELKIGYTKLDRVEHTEQLRSGSTVLRLSDLHFNQEILSGDFQFGLTREWAGFT
HDFTYGVTADYTETSRPRYRTETNLITNTTTNVVGFETFPNKNFPDTETIKAGVYVQDDIGIG
RLNIIPALRFDYYSLDTKIDRMFLNSAGTNVPVDMTETEISPKLGLTFALTEEYKIFAQYAHGF
RAPPYDSANYAWQHTTFGYEIIPNPNLKPETSDGFEAGLRGKFRDGSSFSVAGFYNTYEDF
IDQVLLGVGGVPPLMQFQYQNLAEVTIYGAEAKGEYRFLPEWALIGSLAYARGEDDQTGDP
IDSVDPLKGVLGLAYEGDSWGSQLVATHAWRDTRNATPGNFEAPSYTLVDLMAYYDMSEH
LTVNAGIFNIFDEEYYFAQDVAGLASGSPLTGRYAQPGRNFGINATVRF

tonB not near motor genes, next to heme uptake TBDT. Likely specific to that TBDT.

>ABS61807.1 TonB family protein [Parvibaculum lavamentivorans DS-1]

MSMTATANGRMTDESDGSSVLVWNHRALRRPVAVSLLLHAAIFTGALAWWQGEGAPAPK
GHPDGFSVTLVNFSEPAPKAPQIQAKPVVAPAQPEVKPQPKPVVKPAVVERKVEPEPQITP
DVTPEISAAAAEPLQAAEAAAQPVQTASLAPSVSDGRGQGAAKGFEDTQGRESDKVFLTE
PRFRSPPRPPVYPRRARDLEQEGEALIRVRLDPSGNAAEVLVWKSSGFALLDKAALTAVRG
WQFEPARRGGKPVVAWVQIPVRFALN



MSMTATANGRMTDESDGSSVLVWNHRALRRPVAVSLLLHAAIFTGALAWWQ
GEGAPAPKGHPDGFSVTLVNFSEPAPKAPQIQAKPVVAPAQPEVKPQPKPVVKPAVVER
KVEPEPQITPDVTPEISAAAAEPLQAAEAAAQPVQTASLAPSVSDGRGQGAAKGFED
TQGRESDKVFLTEPRFRSPPRPPVYPRRARDLEQEGEALIRVRLDPSGNAAEVLVWKSSG
FALLDKAALTAVRGWQFEPARRGGKPVVAWVQIPVRFALN

116 Domain II residues

20 Proline residues

4 α-Helix residues

Rhizobiales

Hyphomicrobium denitrificans

Locus:

>AGK56356.1 TonB-dependent receptor [Hyphomicrobium denitrificans 1NES1]

MKAARKQGVKLMAGRILAAAWGLTLAFAVVGPASALAQESGGATTAQPPAAPNAPSPNTP
SEQTAPTQAPSTETPNQQSTTPGTENPSTVLPEVQVIQQQQKAKPKPVKQAVKPKKAPTPV
AAAPAPPPSPAAIEAAQPSEIKMSPVAGSEIPLAKVPIGVSSVTAADVQRTGDVTVQNVLET
RVPGIIVNDMQGNEFQTEVQYRGFSSSPVNGVPQGLAVYQNGVRINEAFGDIVNWDFLPS
NAISNMTVMSSNPVFGLNAIGGAISIDMRDGFNFHGAEFDVRGGSFGRIQGSGAIGAQSGN
WAMFIAAEDINDDGWRQFSPAEIHRMYADLGFKNRDAEFHVNFTGADNFVGAVTAAPVQL
LDEGWNRVYTNPQTTQNDMEMVSINGSVKATNTLTFSGVTYYRHFQQAHLDGNILEVEDC
GDGNLCLDGDPLTTSGGAEIPSSVGGGAPLGSLDRISQNTDSFGGSLQAVERAKLFDHNN
QFLLGGSIDHGHVIYGANSALGAIGPNFTISPLGIPLTGPADISPRSLTTTNDYYGLYFTDTFD
VNDRLSLTVGGRYNFARVTLEDKTGEDPFLNGSHTYQRFNPMGGATYELAKGLTFYTSYA
EANRAPTPAELACADPDNPCIIESFLTGDPPLKQVVSRTGEVGFRGESLNALTNEKINWSFG
LFRTLNQDDIISVASPTSGRGFFQNAGDTLRQGIEASISYQTQRLFLYANYAFIDPTFQSSLE
LASPNNPSPDVVPCAGDPTEKCINVRPGDRLPGVPRHRFKAGFDYWLTPKWKFGSDLIAS
SDQVFFGDEANLNKPLAGYAQVNLHTSYDITDHIQIYGLINNLFDNRYGTFGNYFNTAEGTE
ASLGTIDFIEGTEASLGTIDFTDARTIVPSMPFAAYGGMKFKF

tonB next to motor.

>AGK56470.1 TonB family protein [Hyphomicrobium denitrificans 1NES1]

MIAVVLSVLIHGSIGYAMLPALRDANSEALDMGKGTDIVLVEQGIAEEGISKLGDAMETIETAE
IKPVQAAPPPPPEQVKPDELRDVIASEESTVEQEVVKTDDPPPIKEPPPPEAVQAQSQPEQI
AVVTQQSSGEEKSGGNAKMLGLYLGQVNDHVQRAKVNPRSAIAGTVIVRFTIDVDGKLLSK
EVAKSSGSKVLDDAATAALDRAAPFPPIPPEVSIKPLAFTQPFKFVMR



MIAVVLSVLIHGSIGYAMLPALR
DANSEALDMGKGTDIVLVEQGIAEEGISKLGDAMETIETAEIKPVQAAPPPPPEQVKPDEL
RDVIASEESTVEQEVVKTDDPPPIKEPPPPEAVQAQSQPEQIAVVTQQSSG
EEKSGGNAKMLGLYLGQVNDHVQRAKVNPRSAIAGTVIVRFTIDVDGKLLSKEVAKSSGSK
VLDDAATAALDRAAPFPPIPPEVSIKPLAFTQPFKFVMR

112 Domain II residues

15 Proline residues

8 α-Helix residues

Bartonella clarridgeiae

Locus:

tonB next to hemin-related genes. Not next to motor genes.

>CBI76097.1 TonB protein [Bartonella clarridgeiae 73]

MKGASIWRISALWIGAFGGALALHIGIGAQLYFKSIYMNDIVFPPMVMLLVEPEIMHPNVNAD
SEILELGVLKQEEILKSELSKVHPEEHEIAEELESIVEKSNFTVLKPLEKSSPSKINRKVFIQKQ
LSTLNVTAKKINVKKAHSFTASRDNNTALFDNALSGQWLAKVQAQLEKQKNYIVGQRISSVQ
GVVQLEFKVSEQGDIFASRIMLSSGNQELDWLAMMTLKRVDIFPPPPREMVDKTIRVSLIFS



MKGASIWRISALWIGAFGGALALHIGIGAQLYF
KSIYMNDIVFPPMVMLLVEPEIMHPNVNADSEILELGVLKQEEILKSELSKVHPEEHEIAEEL
ESIVEKSNFTVLKPLEKSSPSKINRKVFIQKQLSTLNVTAKKINVKKAHSFTASRD
NNTALFDNALSGQWLAKVQAQLEKQKNYIVGQRISSVQGVVQLEFKVSEQGDIFASRIMLS
SGNQELDWLAMMTLKRVDIFPPPPREMVDKTIRVSLIFS

119 Domain II residues

7 Proline residues

0 α-Helix residues

TBDT detected by BLAST in many other strains.

>WP_026501097.1 TonB-dependent hemoglobin/transferrin/lactoferrin family receptor [Bartonella clarridgeiae]

MRIKRNVYKRYVTLSMLLSVYMPSFVFAQNNDKDFITKLKPIVIEKKIENPLNKATVLTDRETV
QNIDKKQINDIYDVNHLNPSINYSTDNNSFIIRGLNSNRVLTTMDGIPLPWLNDGVRGIKGGS
SAFTFNSLSTIDIVRGSDSSIHGSGALGGIIALRTLNPEDLLTKEKNWGALTKGSYNSVDKSW
HVDQAFAVRANQILLLFQGSRTEGHQRKNMGTVESYGDKRTRENPADFDKNNLLFKVHQY
LNDNHRLGFTAERFAYNKETHSLNTSTEIFLPKSVYNEKHTHRKRFSVSYDYNGNGDATFD
AFHGQFYWQKQSNNHTLNGYRIQAPKGDYLRDNFMRNTGYGFNAHSFKKLDIGSVNHKLK
FATNVFASKFHQYASGKDNCHLRGNERGCVFLGTNKSDAPDTNSHGFGLAFEDEIGFSNN
DIRFIPGIRYDWYKHIPQKTPAFEKALGSRIMPKENSSSHFSPKIRMEWDANNQVLFYTQWA
QAFRAPSVSELYLTFIKPSFYYMIGNPNLKPETSNGYDIGLQYKNMHFNGSFSVFTNEYKNFI
DVIDKGPSQEFIYARKHYINRAHVRVSGVETKAHFTLMNGFYSNVSLAYVEGKDLDKDEYLN
SIPAFKTVFGLGYEKEIWGTDVVLTLAAKRDKVEGDSDYAKVPGYGVVDILGWWKPFGEKG
PVIRAGIYNLFDQKYWNATDLPSPSPIPKRQPLPPKDYFSQPGRNFKVSYVQKF

Rhizobium etli

Locus:

>ACE91783.1 putative exported protein, TonB-dependent receptor [Rhizobium etli CIAT 652]

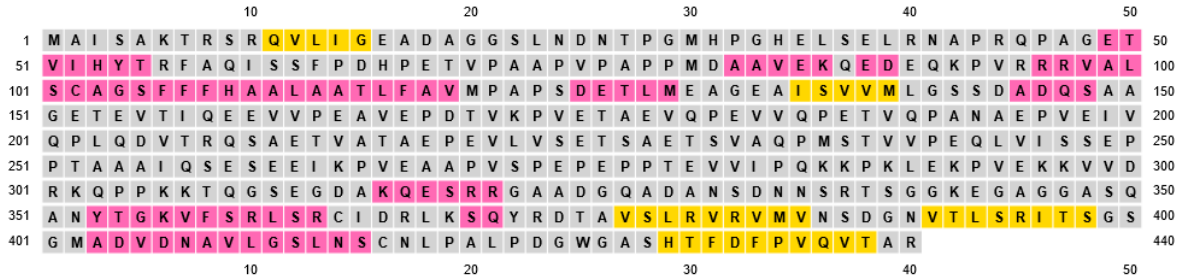
MALAFAVPGFGLPAMADPVQRPTPVAGSVIARKTGEEVRFIDVSDWRVVDINQDLLTGDVLRTNANGQLAIVFSDHTQVRLGRNSSLQVKKMAASG
DTVLELQAGTIWARAERGGQGLTVETPAAAAAIRGTDWTMTVKGDQTSMIVLEGRVSLSNPQGSVDVSEGEGAVATIGQAPHKLISVNPDDREQM
LFYLDLRDGFGLMPTSPLRADRMATERRRLLALPLEHRSIEDWLELAEVQSAFDGRQAAAASLQNIRGRKLTVAQQARVDLLDATIAGSEKRYGDA
AKLFQKALPHLDPTRRNMAQYGGYFARSLADPAHSEPPPATTTGPYGAIMQAYTAGFLENPRAALEIIKKAERRYPDDPTLPAVRAQLAQLIDDRQQ
MKEAIERSLALDPDHPMALSARAEYKAAYESDIDGALADLNHAIELAPGDSGALNSLGLLQSSRDANGEAEKAFKRAIELDPQDPLLHANLAMLYLD
QSRMKEAKREIDTAIALDPSFDIALLVRGRYYLQSGERDKSLEDLLAASTANPAHSQSQLMLAAAHYEKGDRIPSQQALDNADRLDNNDPAISAFRT
AVDIDDYDADGAIHNAQEYLRRSRARGGDYSSLGANASAGSTLNNAFRLQGLDAWGRYYGDAVFDPFKGTGYIDQSIKGSIFPFVNATSFSDDSVS
QYSVNASTYSSFIQGLLLSPHMLSGRSRSASLFDVPFIEGSLGGGINSVDGHTRRIGEAEIQGYSNETIPISFRADMTWEELALDRDYRDFGGVQTD
NKLLSADGYLTATVTPDDRVVAFVNHGKNDGALSALSSNTGFMELLFGVPFPLPLYTTEETARESTYAGVGWSHTFAYENVVNGALLYSGSKSRTS
DALDVDLDPLFIRAGVPFIIPFTDVTQETESKTYIGALSHSIGAGPLTFRYGVEGGWMDVSSTVDKTLLGVTAPPDHSESTIDIGRAYVDVLHEITPDLK
GEYALFATHLEGGGTDITRLEPRFGLAWAPVQNHWLRAAFIRQSFDTGIPTLAPIGILGLQANQFSADPQGYTDTIALQWDAEWTDRFFTSVEYQHQ
ELHDFSVDFPLISLPSDTSLPISRGSIDRAAVTANVALGNGFGLSATYAYMDSENRDPLEPIYGGPLPFIPQNSGQIALTWVNEAKVKATIAANYIGER
DGDRFGTKLDDYWSLDAHLVWEPFDKRMELEAAAYNLLDEDFEITPGVPGWGRAFKGTLKVRF

-looks like CirA with TPR fusions.

tonB on different locus.

>ACE92456.1 putative membrane protein, transduces energy to outer membrane receptors [Rhizobium etli CIAT 652]

MAISAKTRSRQVLIGEADAGGSLNDNTPGMHPGHELSELRNAPRQPAGETVIHYTRFAQISSFPDHP
ETVPAAPVPAPPMDAAVEKQEDEQKPVRRRVALSCAGSFFFHAALAATLFAVMPAPSDETLMEAGE
AISVVMLGSSDADQSAAGETEVTIQEEVVPEAVEPDTVKPVETAEVQPEVVQPETVQPANAEPVEIVQ
PLQDVTRQSAETVATAEPEVLVSETSAETSVAQPMSTVVPEQLVISSEPPTAAAIQSESEEIKPVEAAP
VSPEPEPPTEVVIPQKKPKLEKPVEKKVVDRKQPPKKTQGSEGDAKQESRRGAADGQADANSDNNS
RTSGGKEGAGGASQANYTGKVFSRLSRCIDRLKSQYRDTAVSLRVRVMVNSDGNVTLSRITSGSGM
ADVDNAVLGSLNSCNLPALPDGWGASHTFDFPVQVTAR



MAISAKTRSRQVLIGEADAGGSLNDNTPGMHPGHELSELRNAPRQPAGETVIHYTRFAQISSFPDHP
ETVPAAPVPAPPMDAAVEKQEDEQKPVRRRVALSCAGSFFFHAALAATLFAV
**MPAPSDETLMEAGEAISVVMLGSSDADQSAAGETEVTIQEEVVPEAVEPDTVKPVETAEVQPEVVQ
PETVQPANAEPVEIVQPLQDVTRQSAETVATAEPEVLVSETSAETSVAQPMSTVVPEQLVISSEPPT
AAAIQSESEEIKPVEAAPVSPEPEPPTEVVIPQKKPKLEKPVEKKVVDRKQPPKKTQGSEGDAKQE
SRRGAADGQADANSDNNSRTSG**
GKEGAGGASQANYTGKVFSRLSRCIDRLKSQYRDTAVSLRVRVMVNSDGNVTLSRITSGSGMADVD
NAVLGSLNSCNLPALPDGWGASHTFDFPVQVTAR

Confirmed TMH by TMHMM.

221 Domain II residues

26 Proline residues

14 α-Helix residues

Nitrobacter winogradskyi

Locus:

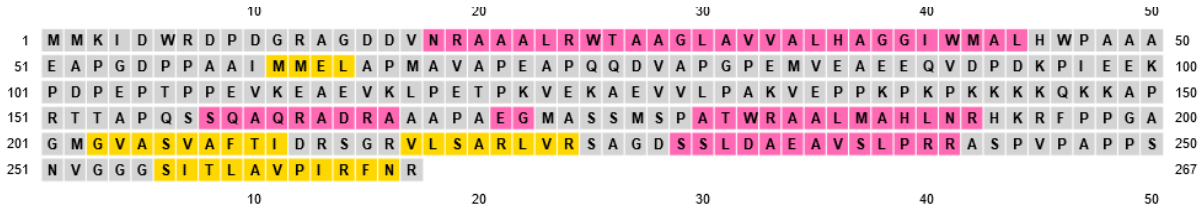
>ABA03991.1 TonB-dependent receptor protein [Nitrobacter winogradskyi Nb-255]

MAGRSVSGVAAIRMARLLASISFAALLLPSQAAFAQTAPSSAPSAGALQQSITFAIPPQSLSS
GIVAFSRAAGIDLVFDGAVPRGARTSGVSGTFTVRDGVNRLLAGTGLSARFTNARTVQIVNP
SAAGGVSGAAPSGAISLDTIDVQGETAWGPANGFVASRSATATKTDTPIIEVPQSISVVTRD
QIEIRRNQTLNETLQYTPGVFAESSGMQHSGPTFQIRGFSAVPADGPIFLNGLRTINNGDIEP
FGLERIEVMRGPASVLYGQNQPSGVIALVTKRPTEGPVHEVQLRGGSFGQKSGAFDFGGP
VTEDRTLLYRFTGLLREGGNGIDFSNDQRAFVSGAVTWRPTDATELTAFSLFQKDKGRWN
YGLPAQGTALPNPNGRIPVTRFIGEPDLDYNVTERAVVGYNLQHRATESLTFRQNLQYARE
NWDYRNATPIGLQADLRTLDRSYETLRASWDTFAIDNQAELKTTTGVLHHTVLFGVDYRWR
RYNSLGLWGGVASPIDVFAPVYGQPVLISADNYGSRQTQNFPGIYLQDQIKLDRWILTFGG
RHDWAESKTVNAFSAAVTNQNDRAFTRRAGLGYEFDSGVVPYVSYSESFMPVSGTTFDQ
VPFRPKPERSTRQASNTSRMI

tonB detected near motor genes with large periplasmic domain in ExbB. Seems to have a large disordered region.

>ABA03971.1 TonB protein [Nitrobacter winogradskyi Nb-255]

MMKIDWRDPDGRAGDDVNRAAALRWTAAGLAVVALHAGGIWMALHWPAAAEAPGDPPA
AIMMELAPMAVAPEAPQQDVAPGPEMVEAEEQVDPDKPIEEKPDPEPTPPEVKEAEVKLPE
TPKVEKAEVVLPAKVEPPKPKPKKKKQKKAPRTTAPQSSQAQRADRAAAPAEGMASSMSP
ATWRAALMAHLNRHKRFPPGAGMGVASVAFTIDRSGRVLSARLVRSAGDSSLDAEAVSLP
RRASPVPAPPSNVGGGSITLAVPIRFNR



MMKIDWRDPDGRAGDDVNRAAALRWTAAGLAVVALHAGGIWMAL
HWPAAAEAPGDPPAAIMMELAPMAVAPEAPQQDVAPGPEMVEAEEQVDPDKPIEEKPD
PEPTPPEVKEAEVKLPETPKVEKAEVVLPAKVEPPKPKPKKKKQKKAPRTTAPQSSQAQ
RADRAA
APAEGMASSMSPATWRAALMAHLNRHKRFPPGAGMGVASVAFTIDRSGRVLSARLVRSA
GDSSLDAEAVSLPRRASPVPAPPSNVGGGSITLAVPIRFNR

123 Domain II residues

25 Proline residues

9 α-Helix residues

Methylobacterium extorquens

Locus:

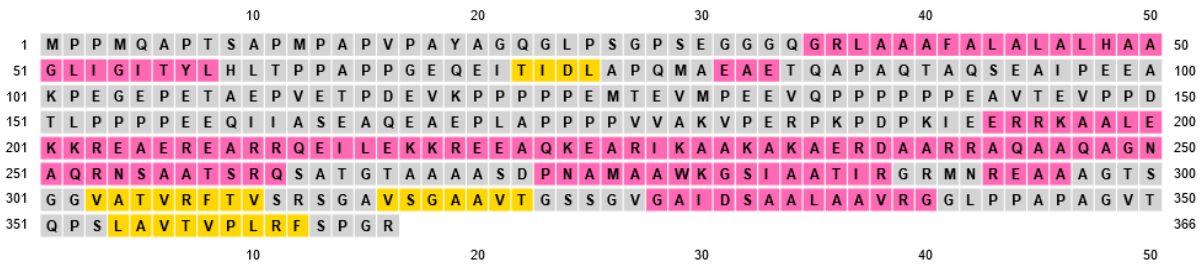
>SOR31005.1 putative TonB-dependent siderophore receptor (putative ferrichrome outer membrane transporter) [Methylorubrum extorquens]

MGSVRTLVGVRALRTMALTGASLMALTLAAAAQQATARLEELSVEGSGRGAGATGGPPAQ
RGADGRAAPEDPRGPVAGYVATRSVTATKTNTPLIETPQAITVIGREQIEAQGAQTLTQATQ
YTAGIYSGVYGADERVDFFTLRGFVASDYGIYKDGLQLLNYGFGTLKTETFGLERIEVLRGP
AAVLFGAGNPGGLVNQVTKRPTLAPFGYVEIAGGSFGQVYGAFDVGGPADDSGHLFYRLT
GIGRQGGTQVEGADSDRAYIAPAFTWRPDAGTTFTVLTSYQRDSTAVTANFLPYAGTVRPN
ASGLRIDRSLNVGDPRINSFQREQVFAGYEFEHAVDDVWTVRQNFRYSFSDATQNSYIGQL
GYADLPQTQLARYQFQYSDKVSLFQVDNQAEARFSDGLVAHDVLFGIDYKNYSLYDNQAS
LFPAPNLSIINPLYGQIVGRPLPYQVDVNSFRQLGFYAQDQIKLTDRLSLIGGLRYDIANSDVL
RKLAPDTSTSRTDTALTGRIALLYNFDPGIAPYVAYSTSFQPQIGVDAITGGSLSPDRGEQIE
VGLKIEPVGERFSLNIAAFDLVRDNPPFPVIVGFGSTQLGTVRSRGIEGQFVASLAEGLNVVA
AVTHYDLEYTRVRDAALGDLVGKTPTNVPETFASVFADYTIPLGDWRGFGFGGGVRYVGR
SYADQLNNLKVPDYVLFDATVHYNWERWRMAITAANLGDRRFVTSCQSANSCFYGEARRV
LASVSYRW

tonB next to motor pseudogenes.

>SOR30983.1 putative TonB family protein [Methylorubrum extorquens]

MPPMQAPTSAPMPAPVPAYAGQGLPSGPSEGGGQGRLAAAFALALALHAAGLIGITYLHLT
PPAPPGEQEITIDLAPQMAEAETQAPAQTAQSEAIPEEAKPEGEPETAEPVETPDEVKPPPP
PEMTEVMPEEVQPPPPPPEAVTEVPPDTLPPPPEEQIIASEAQEAEPLAPPPPVVAKVPERP
KPDPKIEERRKAALEKKREAEREARRQEILEKKREEAQKEARIKAAKAKAERDAARRAQAA
QAGNAQRNSAATSRQSATGTAAAASDPNAMAAWKGSIAATIRGRMNREAAAGTSGGVAT
VRFTVSRSGAVSGAAVTGSSGVGAIDSAALAAVRGGLPPAPAGVTQPSLAVTVPLRFSPGR



MPPMQAPTSAPMPAPVPAYAGQGLPSGPSEGGGQGRLAAAFALALALHAAGLIGITYL
**HLTPPAPPGEQEITIDLAPQMAEAETQAPAQTAQSEAIPEEAKPEGEPETAEPVETPDEVK
PPPPPEMTEVMPEEVQPPPPPPEAVTEVPPDTLPPPPEEQIIASEAQEAEPLAPPPPVVAK
VPERPKPDPKIEERRKAALEKKREAEREARRQEILEKKREEAQKEARIKAAKAKAERDAA
RRAQAAQAGNAQRNSAATSRQSATGT**
AAAASDPNAMAAWKGSIAATIRGRMNREAAAGTSGGVATVRFTVSRSGAVSGAAVTGSSG
VGAIDSAALAAVRGGLPPAPAGVTQPSLAVTVPLRFSPGR

208 Domain II residues

38 Proline residues

72 α-Helix residues

Beijerinckia indica

Locus:

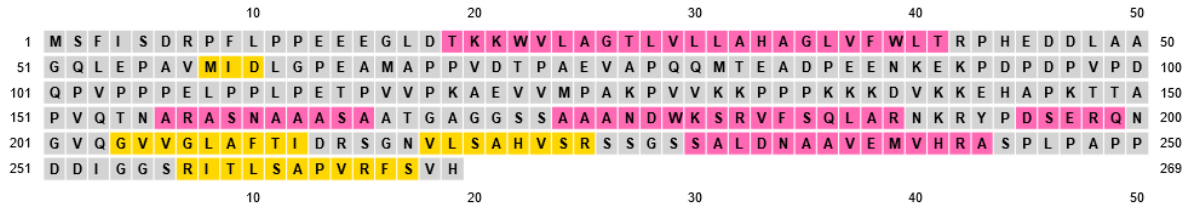
>ACB93894.1 TonB-dependent siderophore receptor [Beijerinckia indica subsp. indica ATCC 9039]

MKRDEFEIFEGSAANTPATELYIKAKARPPLKNAVVGLASLMLGGGAATAQESTNLALEQIE
VEAGNASNNGSAYNPRSTGLDRLPEPILDTAQSINVIPQQLLRDQQTTTMVEALRNVPGISI
NSAEGGTQGDNINIRGFSARNDIYRDGIREPAWYSRDSFSVENIDVYKGPSSFIFGRGSTG
GVINVVSKLPVFTNFTDFSLSGNTAPGVRSTIDVNRTFGDIAARIIILGTDWDTAGRNFIGTKR
VGAAPSIAFRFTEQTKLTLSYIYQHDDNVPDYGIPIVPGSIFGTSYGKPAPVSRGTYYGQQTP
GFNDTEKVDAHIVTAKLEHEFNKDWMLTNGTRFSNVDRFLRARAPQWVASTSAIYAQPVG
GTALTSLAGVPIGSLYSIDNNHFQNHTINSMISNLTNVVGHEETWGLKHTIQMGLDLSKEDR
YNARQATNNTTAATTNQRINLLYPDPYPFGNNFGPNTTLTRTEARDIGMYVSDQVKFNDYF
ELKGGFRYDFYKAWQFTANSSRADGSLSQNGTTPFNLSSTNNFASWNGSALFHPAPNATL
YYSFGTSVNPLAEYTTITNGGQNLGATTNESHEVGAKIDLFDSRLSLTGAAFMITQNNAVETI
DATTSPPTVALVGKTRVKGIEVGATGEVTPGWNVFAGYTYLDGRLLQSQQYANFVGNVVQ
NVPRNQASFSTTYQVTPDWKIGTSVYFVDSRWTNVQHAGWVPSYWRWDLMTSYQVTEN
FSLQANLFNVLNTTNYESIAGAGFAVPGVGRSLQLTARLHW

tonB next to motor genes, where ExbB has a long disordered periplasmic domain.

>ACB93889.1 TonB family protein [Beijerinckia indica subsp. indica ATCC 9039]

MSFISDRPFLPPEEEGLDTKKWVLAGTLVLLAHAGLVFWLTRPHEDDLAAGQLEPAVMIDL
GPEAMAPPVDTPAEVAPQQMTEADPEENKEKPDPDPVPDQPVPPPELPPLPETPVVPKAE
VVMPAKPVVKKPPPKKKDVKKEHAPKTTAPVQTNARASNAAASAATGAGGSSAAANDWK
SRVFSQLARNKRYPDSERQNGVQGVVGLAFTIDRSGNVLSAHVSRSSGSSALDNAAVEMV
HRASPLPAPPDDIGGSRITLSAPVRFSVH



MSFISDRPFLPPEEEGLDTKKWVLAGTLVLLAHAGLVFWLT
RPHEDDLAAGQLEPAVMIDLGPEAMAPPVDTPAEVAPQQMTEADPEENKEKPDPDPVPD
QPVPPPELPPLPETPVVPKAEVVMPAKPVVKKPPPKKKDVKKEHAPKTTAPVQTNARAS
NAAASAATGA
GGSSAAANDWKSRVFSQLARNKRYPDSERQNGVQGVVGLAFTIDRSGNVLSAHVSRSSG
SSALDNAAVEMVHRASPLPAPPDDIGGSRITLSAPVRFSVH

128 Domain II residues

28 Proline residues

10 helix residues

Xanthobacter autotrophicus

Locus:

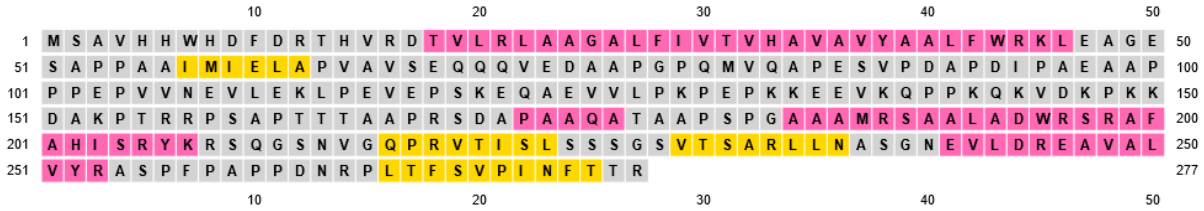
>TLX43811.1 TonB-dependent hemoglobin/transferrin/lactoferrin family receptor [Xanthobacter autotrophicus]

MALRPQRAGVCIWTRRILCSGVAACALLSGMAGVARAQSATAATAQSESDGEISLDTITVAA
SLTPERTIDALAAISVVRPEDLEQLMPARTQDVFLGMPGTTVIQNGNSTQASINIRGMQDFG
RVAVFVDGARQNFTQLGHGTGAGSFFLEPGLLADVDVVRGPVSNIYGSGAIGGVVTMRTK
DADDIIKKGQTWGVEASSDFGSNGPMGFGALFAAARVGQNVDLFLGGTYRAQNDYKDGN
GDVVPGTGYDTWTGIAKATFRPADFHEVKFTGLNYNADYTTYNTALVNGALPSTATQYGST
VLNQTATASWNYTNPNDNVFDWRSTLYWNKVKQDQIKVAGTASSITGAIGNPRYFTINTVG
FDANNTSRFVWNDIRNAITIGGDYFHDDVDNIDDYGFGEGYNPSGERGVGGAFVQWKANY
SSWLEAQGAVRYDTYSLNGDGVSTDGQRFSPKFTLGITPWNWLTFYGTYAEGYRAPAVTE
TLVNGAHPPNIPLVFCPDGSYGVFCFVPNPYLQPEVGKNKELGLNIRFDDIFVKGDKFRGKA
NIYRNDVDDYIELVGYQMTRYGTYANYQYQNIAQARLQGFELESNYDAGAWFAGFNVTVS
DGENTETGGPLSNTMPNNVAGTLGARFLDRKLTVSVRWQWVAAVTEADMPADAPYEPTP
SFNLVNVYLGYQPSENVLASVSVENLLNEQYTQYQQFLPSAGLTVRGGLKIRFGADTIAAAT
PSPVFK

tonb next to motor genes with ExbB with long disordered periplasmic domain.

>TLX43694.1 TonB family protein [Xanthobacter autotrophicus]

MSAVHHWHDFDRTHVRDTVLRLAAGALFIVTVHAVAVYAALFWRKLEAGESAPPAAIMIELA
PVAVSEQQQVEDAAPGPQMVQAPESVPDAPDIPAEAAPPPEPVVNEVLEKLPEVEPSKEQ
AEVVLPKPEPKKEEVKQPPKQKVDKPKKDAKPTRRPSAPTTTAAPRSDAPAAQATAAPSP
GAAAMRSAALADWRSRAFAHISRYKRSQGSNVGQPRVTISLSSSGSVTSARLLNASGNEV
LDREAVALVYRASPFPAPPDNRPLTFSVPINFTTR



MSAVHHWHDFDRTHVRDTVLRLAAGALFIVTVHAVAVYAALFWRKL
**EAGESAPPAAIMIELAPVAVSEQQQVEDAAPGPQMVQAPESVPDAPDIPAEAAPPPEPVV
NEVLEKLPEVEPSKEQAEVVLPKPEPKKEEVKQPPKQKVDKPKKDAKPTRRPSAPTTTA
APRSDAPAAQAT**
AAPSPGAAAMRSAALADWRSRAFAHISRYKRSQGSNVGQPRVTISLSSSGSVTSARLLNAS
GNEVLDREAVALVYRASPFPAPPDNRPLTFSVPINFTTR

131 Domain II residues

26 Proline residues

5 α-Helix residues

δ-Proteobacteria

Syntrophobacterales

Syntrophobacter fumaroxidans

Locus:

>ABK16192.1 TonB-dependent receptor [Syntrophobacter fumaroxidans MPOB]

MFLLLLPGLLLPAVAVAADAAEKVAPAESRTGSSEIGYTAAEGAPAPGHADETAKKDHPLDP
IVVTATRTEKSIVDVPAATSVVTREDIESRNIQKVDEAMNLVPGLFDKRAKGLDTTGRVTLRG
LPDQKRTLVLLDGQPLNNGYTGHVDWNSINPEDVQQIEVARGPFSSLYGGNAMGGVVNIIT
RMPEKREFTVKGGYGSDNYWSTYGSYGDKLFDRLRLLASFGYKSSDGYPSGLVVKKPSG
SGGTPARGAVPTTDTYGNPAFIIGDTGDNSWWTQSGGLKLSYDVCEEAKVFFSYRNNQYG
YGYDNPNSYLTNAMGDTIWSGPVNFRGNTLSFTEGSFLSGGGGILQNLYNGGLETRLFGD
SVLKLSGGLIDMPTNWYVTPSSSTATRSGGPGTISETPTRAYHADAQLSIPVLEKHMLIVGT
AFRHDEANNQEHALTDWTDTGSKADLTYEAKGADNIFSFYSQAEIALFRDVTLYAGLRGDY
WETFDGMADQVGVAGYPQYYDSKGEFSVNPKGSVVYKPLDGTTFRASVGTAFRPPNVYE
LYRTWVTSYGTVYQGNPKLDPESSFSWDIGVEQKIGQSTVLKLTYFNNTIDDFIYFRTVTPTL
LVQTNAGKAETDGFELEAETRPWECLKLFTSFTYTHSEMLDNPANPLTEGKQLPGVPRYM
FSAGGEVKYRRLSFTAIGRYVSKQYSSDQNLDTVSGVYGSYDAYFVGEFAARYKLTDWATI
DFAVNNIFDNNYYSYYKAPGRQFFGGVTARF

tonB not near motor.

>ABK16191.1 TonB family protein [Syntrophobacter fumaroxidans MPOB]

MRLWQNLTISILGHLGVACVLWATPLAIYRPPPWMEVRLISPADFHGRAEIPCDGNGAGEG
GPAADDNIHAAPKEVCAVKQLPPPEQRPEEPKLEPPVRNRSVKKEKPPAKPKGASRVVPLA
AIRADAQRPADPAESSAGEGAAAAGSHASIGPGTFASGTPSGGSVDAGAGAGSLSPGGPG
EGVVDARFGAANGPRFHRLVKPRYPSVARQLGKEGTVVLRVTIDEKGRAIHVEVLTRAGSG
FEEEAILAVRESTFTPARLNGHAVKSRAVLPIRFALTNSG



MRLWQNLTISILGHLGVACVLWA
**TPLAIYRPPPWMEVRLISPADFHGRAEIPCDGNGAGEGGPAADDNIHAAPKEVCAVKQLP
PPEQRPEEPKLEPPVRNRSVKKEKPPAKPKGASRVVPLAAIRADAQRPADPAESSAGEG
AAAAGSHASIGPGTFASGTPSGGSVDAGAGAGSLSPGGPGE**
GVVDARFGAANGPRFHRLVKPRYPSVARQLGKEGTVVLRVTIDEKGRAIHVEVLTRAGSGF
EEEAILAVRESTFTPARLNGHAVKSRAVLPIRFALTNSG

160 Domain II residues

25 Proline residues

6 α-Helix residues

Desulfobacca acetoxidans

Locus:

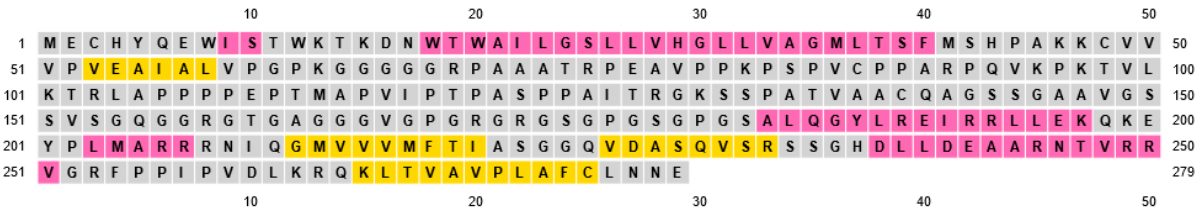
>AEB08475.1 TonB-dependent receptor [Desulfobacca acetoxidans DSM 11109]

MKRILFLLICLVLHPGIGLAQETASSEGVNPEETTNVAALGQSTSTSEDVQKVDEIIITATGTE
EQLKKTSVSSTVITAPEIEKRQVTRVEEMLRSVPGVVVNQTGSQGGNTSLFMRGGNSNMS
QVLLNGIRLNNAGGTYDWANLTVDNVERIEVVRGPMSSLYGADAMTGVTNLITKKGVGPPT
FTYSGAWGAHSEKGQFISENRFSLMGSAKDRFGYSIGFSRIDDQGILPINNRFGSNVLNGR
FDLDPTEKLSFTFSTLFIDTYFGYPTEYGDRVDPAPDPNQNQTRTDLLFGLTTKYSPYSWW
ENELTLSTYHRDWSYDDAFDPVDIFGGSVFHPIEDRSSLDYRSNLRFNFSDRIGTTTTIGLAA
FTERLKQSYESFGVWPYSSETRAHRRSVDFYFQEQISFWERLFLTAGMRLEDNTAFDGTE
FSPRASAAFRITETDTTLRAAGGRAIKAPTFSEQYYQSTTAVGNPNLKPEKNTSWEVGVDQ
YALNDRLKFGLTYFENHFTDLIAYITRAWPATSFYGNISDARVRGLETSLTAKPLPYLTLSAS
YTYLLSQVLSTGGEDLGLNYEVGKPLVRRPKHTVSFTINYDHKPFNVNLNGLYVGKRDDFY
YITDPFFVTHTGRVFNPSYLLFNLAATYDIAENLRYAKKMQLQARIGNLFDQNYQETYNYSS
PGFNFVTGLRFVF

tonB next to motor genes.

>AEB08240.1 TonB family protein [Desulfobacca acetoxidans DSM 11109]

MECHYQEWISTWKTKDNWTWAILGSLLVHGLLVAGMLTSFMSHPAKKCVVVPVEAIALVPG
PKGGGGGRPAAATRPEAVPPKPSPVCPPARPQVKPKTVLKTRLAPPPPEPTMAPVIPTPAS
PPAITRGKSSPATVAACQAGSSGAAVGSSVSGQGGRGTGAGGGVGPGRGRGSGPGSGP
GSALQGYLREIRRLLEKQKEYPLMARRRNIQGMVVVMFTIASGGQVDASQVSRSSGHDLLD
EAARNTVRRVGRFPPIPVDLKRQKLTVAVPLAFCLNNE



MECHYQEWISTWKTKDNWTWAILGSLLVHGLLVAGMLTSF
**MSHPAKKCVVVPVEAIALVPGPKGGGGGRPAAATRPEAVPPKPSPVCPPARPQVKPKTV
LKTRLAPPPPEPTMAPVIPTPASPPAITRGKSSPATVAACQAGSSGAAVGSSVSGQGGRG
TGAGGGVGPGRGRGSGPGSG**
PGSALQGYLREIRRLLEKQKEYPLMARRRNIQGMVVVMFTIASGGQVDASQVSRSSGHDLL
DEAARNTVRRVGRFPPIPVDLKRQKLTVAVPLAFCLNNE

139 Domain II residues

27 Proline residues

0 α-Helix residues

Desulfarculales

Desulfarculus baarsii

Locus:

>ADK85828.1 TonB-dependent receptor [Desulfarculus baarsii DSM 2075]

MKRLLALLCLFCCPPCWPTAAMAAAPPPDGDIVVFSAADIQRMSVRTIQDLLNLAPGVKAG
DSSVSIRGDSAVAVYLDGMSLINNISAHKSVNWGLVSLEDVELIKVIKGGGAVSFGDNSSGG
VIVITSKKAARAKAGVEVEAGNHDYWKTSANVSQRAGAWGVSANGELESTDGFRPNDDEK
HRRAGFKLSYAPEAWLAWAGPDGQAPTLALDYGHTERGNPGLPGYATPHARSRDEALGL
SLNLGAKGYKSTSSFTNFQNEFENTDTAADTMLRGWTVQEDLRKSYDLPLLGRTAFGALIS
HTAASGNKIAGVDEQAYSLFANKKLGLKPLPLSLAMGLRANAYSQFDGALNPELRLSWTRG
PARLEAGFQMTNNTPSIRQRYYETTSTRPNPDLGSESSANYSLGASYQPLKWLGGNATVF
RNNIDDRITYMRVGGVGRYENVGRSHLSGVDASLSITPWAWLSLRPSYTYLEAIDDTSGLW
LPAKPRHKLMIDLQLRPLDGLMLGLTVAHCSEVFTNAANSAIAPAYEEIDLRGEYQYKNARV
YFRVENLADADYLYADGYPAPPRTWLVGLGWDF

tonB next to heterologous motor genes where one copy of ExbB has a large periplasmic domain.

>ADK85655.1 TonB family protein [Desulfarculus baarsii DSM 2075]

MSATMTKRRGGRWVGASLALGGAALVNVLVFCAAPLLQQPQHAAAEMPTYELTTFMPIKP
PAEEEPEPTPPPPPPKLETKVVRLDVSATDVTLVKPELTFEVNPKLAVGPAVAPPGPGRFD
MGQVDQLPMAYGRVPPEYPYLARRRGIEGAVKIRFLVDTQGRVMHLQVLAADPKGVFEES
VLRTVQRWRFKPGVKDGAPVETWVETAVRFTLDGK



MSATMTKRRGGRWVGASLALGGAALVNVLVFCAAPL
LQQPQHAAAEMPTYELTTFMPIKPPAEEEPEPTPPPPPKLETKVVRLDVSATDVTLVKPE
LTFEVNPKLAVGPAVAPPG
PGRFDMGQVDQLPMAYGRVPPEYPYLARRRGIEGAVKIRFLVDTQGRVMHLQVLAADPKG
VFEESVLRTVQRWRFKPGVKDGAPVETWVETAVRFTLDGK

80 Domain II residues

18 Proline residues

0 α-Helix residues

Desulfobacterales

Desulfocapsa sulfexigens

Locus:

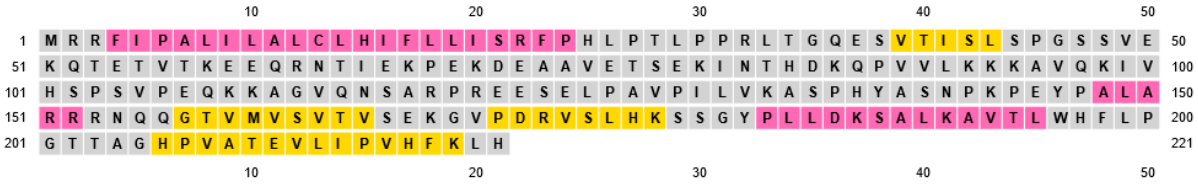
>AGF77330.1 outer membrane cobalamin receptor protein [Desulfocapsa sulfexigens DSM 10523]

MTKRYYPLLCAQLFTIAVVPGISAAETNSTTLMEEVVVTASRTEESRATVSSNISIISEDDIRQ
SASDNVADLLAEQSIATIKKYPGTLTSIALRGFSTDTHGNDLQGHVLVLLDGRRAGTGNLAKI
LTKNVARIEVIRGPGAVQYGSAGMGGVVNVITKRATDNSIFTEAYGGSFDTAEGSIGGSFLK
DGVDFTGSYTYGTTGDYDTGNDEHYRNSGINYETGMSTNLGYSFSELNRIGLIFTRFEVDE
AGTPGFLNRNDLDDYSNKENYSADLNFEGQCPLTESRIFARYFFGQDENSWMDPTVSNPS
GWNDGQLSKNKTDQQGAQFQLSRALGLATLTAGFDWLDYEVENSWTPNTTEYSNSAIFLL
SRLSFLEDRLSANIGLRYDWYDVAVTNPAGHNADDSHFTPQFGVAWMVSDTLKLRAQYGE
AFMMPSADQMSADYSSFGSRVVGNPGLSPEKSATWEGGVDYGQNGFTGSLTYFHTDFKD
KIVSDPLLDGSRSWKNLGDATISGIEAEFAYDIGLPLGLAWEVRPYLNMTILTRYDDEQSGE
DLQNISATNYSAGVVVNDGDGIFCRLNTAYSGSQNIKDYESDFPYRNGTLDSHIVTDLTASY
RFYEDSRLGSFTLRGELQNIFDQDYAYVKGYPMPGRGFYAGLRWDF

tonB next to motor genes.

>AGF77335.1 TonB family protein [Desulfocapsa sulfexigens DSM 10523]

MRRFIPALILALCLHIFLLISRFPHLPTLPPRLTGQESVTISLSPGSSVEKQTETVTKEEQRNTI
EKPEKDEAAVETSEKINTHDKQPVVLKKKAVQKIVHSPSVPEQKKAGVQNSARPREESELP
AVPILVKASPHYASNPKPEYPALARRRNQQGTVMVSVTVSEKGVPDRVSLHKSSGYPLLDK
SALKAVTLWHFLPGTTAGHPVATEVLIPVHFKLH



MRRFIPALILALCLHIFLLISRFP
**HLPTLPPRLTGQESVTISLSPGSSVEKQTETVTKEEQRNTIEKPEKDEAAVETSEKINTHDK
QPVVLKKKAVQKIVHSPSVPEQKKAGVQNSARPRE**
ESELPAVPILVKASPHYASNPKPEYPALARRRNQQGTVMVSVTVSEKGVPDRVSLHKSSGY
PLLDKSALKAVTLWHFLPGTTAGHPVATEVLIPVHFKLH

97 Domain II residues

9 Proline residues

0 helix

Desulfobacterium autotrophicum

Locus:

>ACN14007.1 TonB-dependent outer-membrane uptake protein [Desulforapulum autotrophicum HRM2]

MTRMPDLKRLAEARHPEASKQMHGLKVFLQPISIVLLLILAATGTAIPGEGYTQTEEQEQER
RITLDPVLVTARGRQSLASETPGGVGVVDQEEISESNSISLTNAAARIPGVDKSSDSAWGSA
MTIRGLGRNAVIFLVDGCRVNTSTDINARFGLVNPLDIEQIEVLKGPISALYGSGSTGGVVNII
TRKGKFTQTPTWTGEITNTIASNPQGNDSYGLATYNSKNVWVSASAGFRDHASYESGSGE
KIDNSQFEDSTLNASLGLRENPLNTTQFQVQHLRGEEIGIPGKGLALPTGPDVTYPDVNRTL
VNLTHTLTPDTPLISESSINLFYQKIERRVRLDHFPGGPLTELRPQADHDTWGAKWQNTLTP
RAHTIVAGVDVWNWKISNSNRYREFASGLTGVDASLADVEQFSGGVFMEDEWRIGKTVSL
NLGARLDYISAESQDLYNWITPPTPSTPVTLVQSGRSYSDTSWNAHGGVTWKFMPDWTMT
FITASAFRAPDLMERFKYINLGGGVELFGNPDLDPERSIFLEYGLKHTTDRFTISASAYVNFL
DDLITETVVDDTTHEMMNVDKARIHGGEIDVACYLTPSLTATATLAYIYGKNTRTDEPLAFIAP
LNGLAGLRYDGTSRFWGTIEMEWAADQNRTPDATPSGKGWERFNLHMGKKFTALGKNQE
LILGIDNLFDRDTTNYLSTSRSMELKEPGINFFCTWKIII

tonB next to motor genes.

>ACN13127.1 TonB [Desulforapulum autotrophicum HRM2]

MRLKEPDPEIVKKEPEKKRPDSESKGKKDTLKNIKQPPRSAPQRVAHDFPTLDFKVNPNLP
TTPQAPVFPMEQVAFSPQVMDRIYTGADIDNSLVPKVHIPPVYPFQAKRRGIEGWVKVRFL
VNPKGEVEDISILDSSPKNVFDQSVLNALPRWKFTPGTVEGVAVKTRVETTIRFELEN



No TMH- analysis halted. No other *tonB* genes detected.

Desulfovibrionales

Desulfohalobium retbaense

Locus:

tonB next to motor genes.

>ACV67330.1 TonB-dependent receptor [Desulfohalobium retbaense DSM 5692]

MRSVLAAALCVAVVCVGTSVGAQNATQLSEIVVTATAAPATEQDVPVSTQIVDREAIERSGA
RDLEGLLQREMAADFEIQPGGYSSFGIRGFESYESLGAGFDSGVLVLLDGTRIATGTLSLIPL
DLVQRVEIVHGPGSALYGGSAMGGVVNVITRTGGQETAGQVGVGYGSWEEKTAHVGVSG
CSSEETFGYVLAGSKRTRDDYAIGGGKTYPNTAIDMQSWGGKLTAGPGQQHQLHGVYLES
RNNDLGSPGPLDDNVAENYIDDTLRHLLVTYQGESTDGKQSWRLQPFHSEHEYAFYSNDM
SKYITQMAGVRGQYNHQTARLGTLSLGAEYTQIQDERSGSLVYEPNSEYDVTAVFAEHRFG
SGPWDLWVGARYDHYRARIEKTSELKNVETGTETYDALTWRVGGKYWLTANLGLHAAVG
TAFRPPMAKELTGKFTSYGTTYIGNPNLKSEHSVTYETGMEWGGQHGRIEGTVFHTKYTDK
IEGPSFGETGKYVNIDGWTVQGLELQGQTAFDWSEMLIVRPHATARYYTKREQEDSGGSS
QTIFQLPEYEGQIGLAVDLGAKLSLDSWLEIRGPWEGKNVGRQTEFAVFGSRISYRPVVDL
QVYLDVENLFDKRYSYKNGYPMPGRSVAAGIEYTF

>ACV68205.1 TonB family protein [Desulfohalobium retbaense DSM 5692]

MDERHCWVALLLLSCVLHGLVLDLDLFRIPSVAQKGDPVSLETVPPHQQTSDALALTAEMP
ATEADKPHQSAADKRRSLLAQYVHKVRQRIERHKFPPTAGNCSDLIGKAKYAFTITGEGCFT
NVHLIHSSGVARLDKTALLAIRRASGEVKRPPVTGSRPLFLQVTVKYQHGL



MDERHCWVALLLLSCVLHGLVLDLDL
FRIPSVAQKGDPVSLETVPPHQQTSDALALTAEMPATEAD
KPHQSAADKRRSLLAQYVHKVRQRIERHKFPPTAGNCSDLIGKAKYAFTITGEGCFTNVHLI
HSSGVARLDKTALLAIRRASGEVKRPPVTGSRPLFLQVTVKYQHGL

40 Domain II residues

5 Proline residues

4 α-helix residues

Desulfovibrio vulgaris

Locus:

>AAS94584.1 TonB-dependent receptor [Nitratidesulfovibrio vulgaris str. Hildenborough]

MGKRLMAALALAAMVCAGTAHAEDAPPASGGATLLEEEVVVSAPIIEGNEVTRYAGQYTEV
TQEQITDLNAQDMSSALRRTPGVNISRYNPVGSFGGAEGGGVFIRGMGSSRPGSEIMTMY
DGVPRYNPVFSHPLLDMLPMDPAQSIRVYKGVQPTEFGNAFSAIDVIPKRMTEDGYRTRLF
TSYGSYNTFTQGVEHGGKQGGVDYYAGQSVRLSDGHREHSDGQIENYFGRLGYDLYENW
NVSWFGNVTRNVARDPGSSLSTGNDGRFYTDDVLNVITLANDYGDADGHIKVYWNNGYAN
WAGQKGNADTTISDWDLYGLRAREAFRAWEGGEVTAGFDYDVMSGKALFENDNGTSSEF
EREDFVLFSPYAAVSHEFGSRDDFYAIPSAGMRFYTHNEFGDQVAPHTGLVFGYRDTELHA
GYARGVNYPGLNVAVFSENVIPPIMGGPFRDDWKNLDPELVDHFEAGVSQKLWGKVKADL
TAFWDEGTDRYAVVQGTPKRFRNIESFTIQGLEGTLTYTPFADLSVYAGATWLDTFPSDLP
YAPEWTFSAGLNWRFLQHFRLSLDAQYVTGEQVLSQGRTENAVNASEVDPYHVVNGRIAY
VFDYAPWEIKEAEVYLALENITDSDYEYRPGYRMPGSSATVGLSVTF

tonB near motor genes and ExbB with a large periplasmic domain.

>AAS96863.1 TonB domain protein [Nitratidesulfovibrio vulgaris str. Hildenborough]

MNGWWDRGTGIAVAQHLVLVGFLLFGLASGGDGKLEGDGVGGGSQLMELSLGGPGMPV
SKPARAAQATQPPPAARPPAAQTPTTRPRPDEATAVSPRKRRVEAKPRPKKETPRREVAQ
RAPVPRAEEKRTVDTQPTQTTSTTTAPESSHEGDSAVANTAHAGVPGTGTTPGSGGPEKG
MAYGTGGGTGGGSTAHAGTGGEGLGGTGAGTGGYDRGPRAVYTPRPPYPREALHKGAE
GVVMVRLLLDPSGRVVQSRIAGGDMADIFAETTLETVERWRFKPCGRQGRNVSCEVEIPVE
FRIDR



MNGWWDRGTGIAVAQHLVLVGFLLFGLA
**SGGDGKLEGDGVGGGSQLMELSLGGPGMPVSKPARAAQATQPPPAARPPAAQTPTTR
PRPDEATAVSPRKRRVEAKPRPKKETPRREVAQRAPVPRAEEKRTVDTQPTQTTSTTTA
PESSHEGDSAVANTAHAGVPGTGTTPGSGGPEKGMAYGTGGGTGGGSTAHAGTGGEG
L**
GGTGAGTGGYDRGPRAVYTPRPPYPREALHKGAEGVVMVRLLLDPSGRVVQSRIAGGDM
ADIFAETTLETVERWRFKPCGRQGRNVSCEVEIPVEFRIDR

174 Domain II residues

22 Proline residues

0 α-helix residues

Desulfomicrobium baculatum

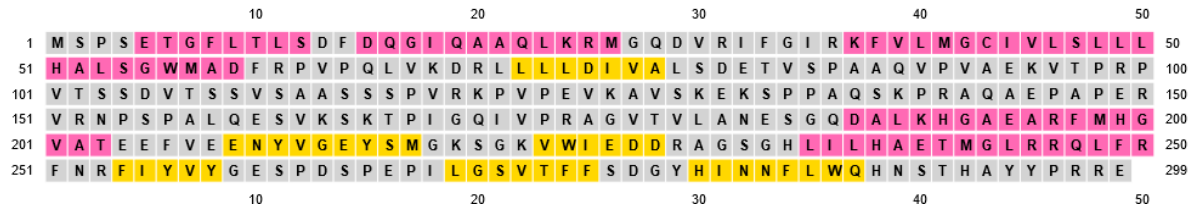
Locus:

>ACU90676.1 TonB-dependent receptor plug [Desulfomicrobium baculatum DSM 4028]MVPHGSQSVAERDDHGSGNGTSPHNASGRSEGSADQWQALLTDQGDVVYQLEPV
NVLGDKHQSGKATIEGAELQSLPSHTGSITEAIKGFSNVQFSNEDTSSLTGGEIRPPRVSIAG
AKPYENNFLIDGMSVTNTLNPSGLDADGDGIGPNDLHVNGGDQTIFYDSSLVDTVTVYTSN
VPAKYGGFVGGVVGAELIDPRIDRWHAVFSGGHSRSEWFDLRGVNEDSTTSANQPRFRTY
ALRAGADGPLTDNVALLVAASQRRSVIPLKMETPEDSFYDKDQKRSSENFFTKLLFTPDDDL
KLTLDATYAPYSEERWKPLYENSDWKTQNEAFRLAGSATLGGTWGELGGRVAYSRNGYS
RDSMSNLRETYAGTGVPEEDWYYRGGLGDAKVVNRGIDAGLDVDLSTFKTGDLSWGLSS
GLTLSNVTTDMWNEEARMEILTLPSSGKWTQVFTTYPESDQRRTLNTLGWYVQAEMEWS
RFTLTPGLRVDYDDFSHNTDISTRLKMELDTMGDGALRVVAGVNRYYGGQLRAYAFDRYR
PSSSLLIRYNTDPDNLPPVKVSDDQSYEAKGLDTPYSDELMGGLLGDVAGFEYGLEFVHRD
HRKQIISKAREEDVYELTNDGKSTYDGISLTLARSFETKRFGSHSLSLGVSQSRTKTFNGAF
DSEIDEYEESNGYEYDYDRVFYEGELVDRSSLPPDDYNAPAVVTLRWMGLFFDDRFRVNC
VSRWRDSTSGLKNDARTFDETPYGTAEKKKTTSSSKWLDEDGLYHDAYKTGIISGSLVTDV
SLELDVVKEELFTMSLMLDVFNVFAADGHVGVSQIGSGDVPAPRSEYGRGYYAGVRCEF

tonB not near motor genes.

>ACU90059.1 hypothetical protein Dbac_1971 [Desulfomicrobium baculatum DSM 4028]

MSPSETGFLTLSDFDQGIQAAQLKRMGQDVRIFGIRKFVLMGCIVLSLLLHALSGWMADFRP
VPQLVKDRLLLLDIVALSDETVSPAAQVPVAEKVTPRPVTSSDVTSSVSAASSSPVRKPVPE
VKAVSKEKSPPAQSKPRAQAEPAPERVRNPSPALQESVKSKTPIGQIVPRAGVTVLANESG
QDALKHGAEARFMHGVATEEFVEENYVGEYSMGKSGKVWIEDDRAGSGHLILHAETMGLR
RQLFRFNRFIYVYGESPDSPEPILGSVTFFSDGYHINNFLWQHNSTHAYYPRRE



MSPSETGFLTLSDFDQGIQAAQLKRMGQDVRIFGIRKFVLMGCIVLSLLLHALSGWMAD
**FRPVPQLVKDRLLLLDIVALSDETVSPAAQVPVAEKVTPRPVTSSDVTSSVSAASSSPVRK
PVPEVKAVSKEKSPPAQSKPRAQAEPAPERVRNPSPALQESVKSKTPIGQIVPRAGVTVL
ANESGQDALKHGAEARFMH**
GVATEEFVEENYVGEYSMGKSGKVWIEDDRAGSGHLILHAETMGLRRQLFRFNRFIYVYGE
SPDSPEPILGSVTFFSDGYHINNFLWQHNSTHAYYPRRE

140 Domain II residues

18 Proline residues

13 α-Helix residues

Bacteriovoracles

Geobacter lovleyi

Locus:

>ACD95195.1 TonB-dependent receptor [Trichlorobacter lovleyi SZ]

MTVQQLSLLALLLTLTAQTARAEHLLLDEIIVRADKESPKEESLSVREVRESPARDMGEALK
QVEGINIVHKGAIANDVVLRGFQKDNINVLVDGVRLHGACPSRMDPPSFHYDFAEIEQVRIIK
GPYDLSNPGGLGGLIDAQTKRPGKGFGGELSLGYGDWHGTNAAATASYGTERYDALMGY
AYKYSDVPQSGNGKLLTQIYPATSPNRYKNTAIDSKAYEINTGWGKLGLNPTANSRTELSYT
YQDADHVLYPYLKMDADYDRTDRMNWSYRIQNLSALLQDLKLQVYWDRVEHLMDDRSRF
SSSTSPRFYSMQTDASTQTYGAKLQAELKLGPGSLKSGLDYYNRNWDATNRRAMYFNYR
DLAMIPDVTIENFGLFGEYTLPLGGKLSLTGGVRGDLTRAKADRANTMVTAGSSKEFSTISA
NLQLNYTPFKELVIFTGLGRGTRTPDQQELFLDLPGNPAWRGNQGLKATVNHQADLGAKY
ATDRFYVNASIFYSDLQDYVNFYQASATLKSYQNIHASIWGAELGSQVSLPADLFLRGTLSY
TEGRNISGNRPLSEMPPLKGTISIRYDNGSFFAELLETLSREQDRIDSSLNEQKTAGWVTTD
LKAGYQYKGFSVTGGINNILDTQYYSHLSYLRDPFVSGVGYRVPENGRNVYLTMAYKF

tonB not near motor genes.

>ACD96479.1 TonB family protein [Trichlorobacter lovleyi SZ]

MSAAHQSRKTRSIRLYLSVSLLLHGLFFVAAIVLLPPLVQAPPKEPALVMTHLVSLPTPNAGK
ETTSPAPALPVINRPTPKSQPQPQPPPPKSVAPTTFSSNPPLKPSEPAPQAPPAPTFSAQQ
TKAGVASKPETGSQPAVQTSTTTGGNRIAPQEMAFGSASGPAFRRQAVPVYPALAKRRNK
EGVVLLRLSISETGQLTQLEVLEDPGYGFGEAAQEAVRNSSFTPARHNGKPVAVRAVLPIRF
SLR



MSAAHQSRKTRSIRLYLSVSLLLHGLFFVAAIV
LLPPLVQAPPKEPALVMTHLVSLPTPNAGKETTSPAPALPVINRPTPKSQPQPQPPPPKS
VAPTTFSSNPPLKPSEPAPQAPPAPTFSAQQTKAGVASKPETGSQPAVQTSTTTGG
NRIAPQEMAFGSASGPAFRRQAVPVYPALAKRRNKEGVVLLRLSISETGQLTQLEVLEDPG
YGFGEAAQEAVRNSSFTPARHNGKPVAVRAVLPIRFSLR

116 Domain II residues

29 Proline residues

0 α-Helix residues

Pelobacter carbinolicus

Locus:

>ABA87714.1 cobalamin uptake ligand-gated TonB-dependent outer membrane channel [Syntrophotalea carbinolica DSM 2380]

MVKIPSLALVGLLMLSATASASDVTTLEPVVVTATKIETPTREVASSITVVTAEEIEEKQQRTV
LEALRDVPAVDVVQSGGDGQQTSVFMRGANSEHTLVLIDGIEVNDPISPSKAFNFANLTTD
NVERIEILRGPASALYGSDAIGGVINIITKKGQGKPSITLSAEGGSFETHHETVSLSGGTQLVN
YALSASYLDSNGITAARWSDGNHERDGYENLTTSLRLGLTPTKNFDLDFILRYMETDTDIDN
SAGPLGDDPNYTTEEEKLFFRTQAGLYLFDDLWEQKLGFSITDYDRSTRDDTDAAHPLDWV
RSSYQSTLYKVDWQHNLYLHKTNTLTLGIEHEEEEGKNKFLSESAYGPWNTYYPRQKTRTT
GYYVQDQFKLWNRFFTTLGLRLDDHEEFGRRVTYHVASSYIFDSTGTKIRATWGTGFKAPS
LVQLYDTNFGGNPDLNPEKSEGWDVGIDQNLWQDRLTISLTYFENSFEDLIVNEYLGWGPT
GAIYLYKNVDSANSKGIELLLTCRPLETLTITAGYTYTDTENEDSHDQLLRRPRNKFTADINY
RFLEKGNVNLSMIYVGKREDSFYNNATWASGRVELASYTLFNLGASYEVTKWLTLSGRIEN
LLNEHYEETWGYDTAGIAGYMGAKLTF

tonB next to TBDT gene, not near motor genes.

>ABA87713.1 periplasmic energy transduction protein, TonB-related protein [Syntrophotalea carbinolica DSM 2380]

MLSQETFLPWIILSLGIHITALTLWPLPPSWEATRPGPIAVDLRYSTQPGGNNQPNKTPGPG
THGPKAIMPPKVLHPHPKPAPPHKSSRPITPPAPIKKAAPHRTPRKSQSQKSAPAAISAPEQ
QPEKSLEPPSDQPESDLADTSMENLNGAASATDDTNASHASLSPASGTGTDNTGYGSGEN
SGTNGGGGGDGIIRATPLGYGENPPMPYPRSARRRGWEGEVLLKVDVSAHGRVLAVHIEQ
SSGYGILDDTALGAVSEWRFRPARVNGSTRPDTVIVPIHFRLDAP



MLSQETFLPWIILSLGIHITALTLWP
LPPSWEATRPGPIAVDLRYSTQPGGNNQPNKTPGPGTHGPKAIMPPKVLHPHPKPAPPH
KSSRPITPPAPIKKAAPHRTPRKSQSQKSAPAAISAPEQQPEKSLEPPSDQPESDLADTS
MENLNGAASATDDTNASHASLSPASGTGTDNTGYGSGENSGTNG
GGGGDGIIRATPLGYGENPPMPYPRSARRRGWEGEVLLKVDVSAHGRVLAVHIEQSSGYG
ILDDTALGAVSEWRFRPARVNGSTRPDTVIVPIHFRLDAP

163 Domain II residues

29 Proline residues

5 α-helix residues

Desulfurellales

Desulfurella multipotens

Locus:

TBDT found on different scaffold.

>SDC20763.1 iron complex outermembrane recepter protein [Desulfurella multipotens]

MKRVWLVCLFLTILSNYAFADDSKNLEAVNVSATPIVEPTKQTEQTVFSGLEVTKQGMDLG
GTQAQTSVYNAINILPDVSIENADSSGLYAEGTNVRIRGVRGYLGAMTVEGIPNYGGNPMG
PRDYIYNMQNFKAIKVYESAMPASLGVGVGNRGGAIELVPLWPLKTTQFKMQQTYGSYELY
ENFFRFDSGNIDKTNTRFSVSYSYGIANKWRGPGEIGPRNNVNFMLDQPVGDVFDAKVFFN
YNFVKQNLYRALTYAQIDDTNLDYNSSKTSVASKDINYFGYNHGDFQNTDFFSILTIKPTNIF
DVVLKPYYSKENTHIWQGISPQNIVQKRTRDIDRKGIIAQFDLNVNHFKVSSGMQYEVSNMD
IYSQNYAILGDNLSYRGYGVFATTGDTYIKSPFLQVAFEDQKFKAQAGIKYFRFNDSASQGY
VTSKTAPYSLVRAPDLDRKERLYDIWLPNVGLSYKFSDEFELYANYGRNFIRPYAYMPLINL
YNTNRQAFQKAHITLNDLFDGYNIERSDNIDLGARIRGSWFDLLPTFFYSKQKDLLTTVYDP
RVKLNYQQNIGKATGYGFELAFNAYVNDYLTFFFNPSFTRLTYDNDISYQGSLIGCKDKQIV
DVPKWLIKSGFIVNYDKWQFIPSVIYVGSRYADAGHTQEVASYATLNAQINYTLKNIYKMHEL
KLSLQLNNILNKKYIAVINSMDDALAGNTSFYPGEPFNASLTASLTF

tonB next to acyl-co-A thioesterase gene, not near a motor.

>SDC93247.1 outer membrane transport energization protein TonB [Desulfurella multipotens]

MEKFYTKKTFTSSLALSIFVNVIFFALGIKLLSGFYKPIKKPIEVVLLGISQPKTDDKILHVKNKT
LAQKKQNILITQESIPKEKINNKVFPKQEIQKTGNLKTADKTDKIEKTNNAIVHTDTISNNESNT
KSSKGSAVQTTQNIQTTQTTNSFQSVSKEDYAFLRKLIEEHLKYPYLARRNSYEGTVVISFIID
NGIIKDIEIVKSSGYSILDKSAIEAIKKIEPLVKLDKNVKIVIPINFKLNNS



MEKFYTKKTFTSSLALSIFVNVIFFALGIKLL
SGFYKPIKKPIEVVLLGISQPKTDDKILHVKNKTLAQKKQNILITQESIPKEKINNKVFPKQEI
QKTGNLKTADKTDKIEKTNNAIVHTDTISNNESNTKSSKGSAVQTTQNIQTT
QTTNSFQSVSKEDYAFLRKLIEEHLKYPYLARRNSYEGTVVISFIIDNGIIKDIEIVKSSGYSILD
KSAIEAIKKIEPLVKLDKNVKIVIPINFKLNNS

116 Domain II residues

5 Proline residues

7 α-Helix residues

Oligoflexia

Bacteriovoracles (cont.)

Halobacteriovorax marinus

Locus:

>WP_096908354.1 TonB-dependent siderophore receptor [Halobacteriovorax marinus]MKLSFIVATLLCFNLQAQTNILVSAEKISLDKDQTVSDVDVIDAAEIEASGESSLVDL LADRASLYINSNGGFAKATSLFLRGADSSYTLIEIDGVEYNDRSSVGGAAILEHIDLSNIEKVEI LKGAQSVLYGSDAMAGVIKITTKTPGKYVGANASIGYGSYDNKRASFSTSQKGKTMNYVLG MSFQDVEGFSSYNEKRAPFAERDGMNNLTATFKGVKKLGSTDQLMFNVRGVKAQSDFDA STSDKLDYMGRDEQLIAGVSYKKRIGDYWIPELSITYNKSDRLSNSFSLSRLVAETKKVELKN PLYINESITILNGLEYEDIEASIENINNKKNYNSYATYLDSHLQRGAFKLQAGLRWSKEKSLSD QIVWKGGASYRLFENTFAKLNASTGYKSPSLYQLFSSFGNEQLRATKSKSYDFTLEQRFSA FVLSGTIFQNEYENVIDFDSTLNKYTNTFKSETKGVELGLDISTEKFDLSSSATILRAFNKSAG SDGIYLARRPREKYYLGLKYKFNEKLSLSNNYNYVGRRENSDFDTVVLSSYLLVGLNLNYEI SNDQAVLLKIDNALDKEYEQIHGFGTAGRSFFLRYNFKL

tonB not near motor genes.

>WP_096908355.1 energy transducer TonB [Halobacteriovorax marinus]

MNSSLIFGIFISLVFHSLLVIDLSIKSEAEVTMMMSSSKSSFKVNLNKEKKSPKRKGIGQNKKV SNEVKADESNLAKTSVHVANQFKPQYPYRSRLFSEEGIVFVNVKIDKSAKVIDASIAKSSGFK RLDNAALEAARKSFFTVTQKGRESVVEYVLEFNFKLNEGE



MNSSLIFGIFISLVFHSLLVIDLS
IKSEAEVTMMMSSSKSSFKVNLNKEKKSPKRKGIGQNKKVSNE
VKADESNLAKTSVHVANQFKPQYPYRSRLFSEEGIVFVNVKIDKSAKVIDASIAKSSGFKRLD NAALEAARKSFFTVTQKGRESVVEYVLEFNFKLNEGE

43 Domain II residues

1 Proline residues

4 α-helix residues

Bdellovibrionales

Bdellovibrio bacteriovorus

Locus: (different to tol-pal locus)

>ASD62360.1 outer membrane receptor protein [Bdellovibrio bacteriovorus]

MKYSVLLACLFLGLAAHAQEAVPSFETVVEDVVFNTSNKVVIDEKTIKDSRAPNITSLLSSQA
NITVVSTPFQPNSIFIRGGDSGHVMIIVDGVPFYDASTVQRTFNLNSLDIKSVRRIEIIKGGQTV
LYGGQALSGVIKIDTIPQEIKSQSSLQGQLGTQNFRDVTVGHTEALNDNNALVLRGHGAWR
DAESPVLDSTETYSRNNWNAEGAYVWKGAVDGNLKALFLQDFNTSPTTDRTTNQVMDTE
DLEMFTRQIGGSTYMKFNELPFEPRLALSMQNSLRTYEWPVVPVQNPTGTDQKYGANLRT
ARLDLTPYKSEKISVAAGLSYLYEDFTYRDKGVESVNTFSEQRGVFAKADYEFHPGFSLAV
GGRVENWADQDAVSTYQIGLTVFEHTKLEVASGYKIPSLFQLYSSYGNPDLKAERAVQYSL
MQEFEISESQSASITFFRSDFTDLIQISGSFPSIQYENVSKTETRGVDISYTIRPWTGGTFIAT
YGYQEPRNVDTGTWLLRRPLVNGSLKYIQNHDKHTAALELVGAGERMDNGAPISMTAYAS
TSIPGYVTANAAYSYQWNDNINVFTRLNNLTDHRYEETYSFYSEGFSGSLGAEYLF

tonB not next to motor genes.

>ASD62361.1 energy transducer TonB [Bdellovibrio bacteriovorus]

MRRSKGLKLKLWILLSVILHLLAVTALQWGASPVSPDLGTVVDLTVTSPAGVSGLPPAPPAA
VSKPAPTVPSESVKSEAPETTANADAGAAGGGGDSTTPVGFSEITRLPKVKREFKAQYPEE
AKKAAVDGPVILEILIDREGKVRHVQVLSGPGHGLNESAVEALKKFEFQPAFKGEESVAVKI
RYTYRFKLEVN



MRRSKGLKLKLWILLSVILHLLAVTALQW
GASPVSPDLGTVVDLTVTSPAGVSGLPPAPPAAVSKPAPTVPSESVKSEAPETTANADAG
AAGGGGD
STTPVGFSEITRLPKVKREFKAQYPEEAKKAAVDGPVILEILIDREGKVRHVQVLSGPGHGLN
ESAVEALKKFEFQPAFKGEESVAVKIRYTYRFKLEVN

67 Domain II residues

11 Proline residues

0 α-helix residues

ε-Proteobacteria

Campylobacterales

Helicobacter pylori

Locus:

>ABF84926.1 iron-regulated outer membrane protein [Helicobacter pylori HPAG1]

MFLRSYPKLRYALCFPLLAETCYSSDHTLGKVTTQAKRIFTYNNEFKVTSKELDQRQSNEVK
DLFRTNPDVNVGGGSVMGQKIYVRGVEDRLLRVTVDGAAQNGNIYHHQGNTVIDPGMLKS
VEVTKGAANASAGPGAIAGVIKMETKGAADFIPRGKNYAASGAVSFYTNFGDRETFRSAYQ
NAHFDIIAYYTHQNIFYYRSGATAMKNLFNPTQADKEPGTPSEQNNALIKMNGYLSDRDTLT
FSWNMTRDNATRPLRSNAIGLAYPCEAPFSPDGAQGCPNVLDSFTRYMYHSINSANNLSL
QYKREAGNSFGDPRLDFTLYTSIRNAQFDPLFDPNGVYAKFPTSQASAWERENYPCVEGA
YCTPSFSDVDKPSSQPRDLFLNNTGLNLKVAHVIDEATDSLFEYGFNYQNLSVFDARIPKSE
LYRPNQVYTDDKGQKQIACSLVDNNPNDPTLCQRGKANGNIYGGYVQANYSPHKIITFGAG
VRWDAYTLYDKDWNHRYTQGFSPSAALVLSPIEPLSLKITYSQVTRGVMPGDGVYMRQND
LRYAKNIKPEVGSNAEFNIDYSSQYFSGRAAAFYQALDNFISQYAQNLIVTNLSQAIRIYGYE
VGGTFRYKGVSLNVGVSRTWPTTRGYLMADSYELAASTGNVFIIKLDYTIPKTGINLAWLSR
FVTGLDYCGFDIYLPDYGTAEKPKTPTDLAKCGSKLGLVHMHKPGYGVSNFYINWSPKTKS
RWKGLLLSAVFNNVFNKFYVDQTSPYVMSPDMPGTDAVKRAIAEPGFNARFEVAYKW

tonB next to motor genes.

>ABF85355.1 siderophore-mediated iron transport protein [Helicobacter pylori HPAG1]

MKISPSPQKLSKVSTSVSFLISFALYAIGFGYFLLREDAPEPLAQAGTTKVTMSLASINTNSNT
KTNAESAKPKEEPKEKPKEEPKKEEPKKETKPKPKPKPKPKPKPEPKPKPEPKPKPEPK
PEPKVEEVKKEEPKEEPKKEEAKEEAKEKSAPKQVTTKDIVKEKDKQEESNKTSEGATSEA
QAYNPGVSNEFLMKIQTAISSKNRYPKMAQIRGIEGEVLVSFTINADGSVTDIKVVKSNTTDIL
NHAALEAIKSAAHLFPKPEETVHLKIPIAYSLKED



MKISPSPQKLSKVSTSVSFLISFALYAIGFGYFLL
**REDAPEPLAQAGTTKVTMSLASINTNSNTKTNAESAKPKEEPKEKPKEEPKKEEPKKETK
PKPKPKPKPKPKPKPEPKPKPEPKPKPEPKPEPKVEEVKKEEPKEEPKKEEAKEEAKEK
SAPKQVTTKDIVKEKDKQEESNKTSEGATSE**
AQAYNPGVSNEFLMKIQTAISSKNRYPKMAQIRGIEGEVLVSFTINADGSVTDIKVVKSNTTDI
LNHAALEAIKSAAHLFPKPEETVHLKIPIAYSLKED

150 Domain II residues

27 Proline residues

26 α-Helix residues

Wolinella succinogenes

Locus:

>CAE10216.1 TONB-DEPENDENT OUTER MEMBRANE RECEPTOR [Wolinella succinogenes]

MKNSIVLWGSLGLASVLMADSSVYELGRVEINEKSDISKNPSLEIVTQETIRETEAKSVVDAL
QSVPGIYTDYAGARGETKVRLRGFSSTRVPLYIDGIPIYVPYDHNIDLGRFKTYDIGEIDVSKG
YVSPMYGANTMGGAINLVTRRPTKEFEGEVGAGIFSGKGQEQYLTLGTKQELFYGLISASN
VQRDYYKLSGDYEEAGHQQGKKRSNSESKDQKVNLKVGYTPNDTDEYSFNYIVQRGEKE
QPWFAMERRKNSDGSWKDGSGMYNRNWDWADWDKTSYYLITKTAIKEHYLKTRWYYDT
FYNKIFFRGTPGSPTQNIITETSEYDDNTFGGMVEGDLQLAKGHLLKLFVSQKYDNHKDKNY
VDSSNTRYADLKDEGKTTSLGAEYSWLMSDQWTWTLGGSYDKNEVTKAEYRNSAGTQIL
GEFPKYETNAFNPQTILSYKAKEGLTFYGSISKKSNMPTLKDRYSSKFGDYVLNPGLDSERS
TTYELGSNWAVNENHYAKTALFLTKTKDYIASYSGVSNSDSTLGCVGANCKQMQNFDQEE
HKGVELTLDSYWSDQFKSTLSYVYIDASIEDSQTKDAKYTTDTPDHTLYASVTYSPFYSINIT
PVVRYESERYLSVDGSDKSTPHTLVDLRVAYRPVKSFEVAAGVKNMFDKNYYISYGYPQE
GRNYYLNVRYSF

tonB not near motor genes, near TBDT gene.

>CAE10218.1 hypothetical protein WS1128 [Wolinella succinogenes]

MPPMSERRYSQVGWSFSIVLHGAIWLFWAFLGVTPPVIEERKISLPLGMILSQEPSPLLSAP
TPAPPPVMPLESSEPLEIPKPSLKNPAPHPKPLVKNRDKMAIEPKVTPLMSQERESISTDSLL
SPAPLAVMEGVRETKEVEEEAYLFEQIRQIIQKNRSYPERARRRNIEGEVVVEFCLTPRGEV
KDLVLVQSSGSAILDQHSLRLIEESKEQFPRPKESIKIELPIGYRLL



MPPMSERRYSQVGWSFSIVLHGAIWLFWAF
LGVTPPVIEERKISLPLGMILSQEPSPLLSAPTPAPPPVMPLESSEPLEIPKPSLKNPAPHP
KPLVKNRDKMAIEPKVTPLMSQERESISTDSLLSPAPLAVME
GVRETKEVEEEAYLFEQIRQIIQKNRSYPERARRRNIEGEVVVEFCLTPRGEVKDLVLVQSS
GSAILDQHSLRLIEESKEQFPRPKESIKIELPIGYRLL

104 Domain II residues

22 Proline residues

0 α-Helix residues

Arcobacter butzleri

Locus:

>ABV66603.1 TonB-dependent receptor protein [Aliarcobacter butzleri RM4018]

MKPIKKTITYSICLSMSLLSQTFAQETTLLDEIKVSTENSNYSTQNDNYYKTKSQSATKTDTPI
RETPQSVQVVSNEIIKELNAVKIEDVLDYTSGVSRQNNFAGMWDNFSIRGFAGNENTGMSL
LKNGFADNRGFNAPRDTANIESIEFLKGPSGSLYGNSEPGGTINIVTKQPKFTSEHSIKTDVG
SYDFYRMALDSTAPINDNLAYRLNVATEKKGSFRDHIESQRYVVAPSLLYSINDDTFVSYMG
EFIEQKAPFDRGIALIDGKNVMNPKNFLGNPDDGDVTLKNQTHQLKLEHYFSDSWSSRMGV
AYKNNSLKGFGSEVTPATKITTDSINLRTRYRDYSSDDIQFQVDLQNVTDIKDATNTLLFGVE
TYRFEQDSILYTNKDTVRVDNIRSNPTYTVLKTGLGSLSTDKYEEQKGVALFVQDEIAYKDF
RFLTGLRYDEVRMDNVNHLDSSSVKQNDYAVSPRVGITYLIDDMWSVYTTSGTSFRPNTGT
DIDGKTFESERSVSIETGLKFESEDKKTGGTLSLYQIEKKNVLTKDPNDDLFSIAAGKVKSKGI
EFDFNGKITDNIKANFNYTYTDAKVVEDSTYEGKELLNIPKHTSSVLLMWEDTLSLNSSYGIG
TGVTYVGRKAGNVNNDFYLPDYTTAKIVSYYKVNKELNFSLNIDNLFDKEYIASSYDRSWLT
VGNPRTATLSMTYKF

tonB next to motor genes.

>ABV66968.1 TonB-dependent receptor protein [Aliarcobacter butzleri RM4018]

MNRYLNSFFITSGVYFIAAFFLFFVFADMLITPPAKEEIVTKISLNSVSIVEPQPVVEPTPEPIVE
PQPVIEKPKPVKNKPEKPKKEHKKPVEKIVQKEEVTEVVAAVPPPTKTPPKEEVSAPSINQN
QIDTIETKYLAKVRATIEKNKIYPKAAKRLNQTGKVNVNFDILKSGEIRNVKVLGKSSFAKLDE
ASIELLIKISNFDEIPEELKKSVWNVTIPIDYSIN



MNRYLNSFFITSGVYFIAAFFLFFVFAD
MLITPPAKEEIVTKISLNSVSIVEPQPVVEPTPEPIVEPQPVIEKPKPVKNKPEKPKKEHKKP
VEKIVQKEEVTEVVAAVPPPTKTPPKEEVSAPSINQ
NQIDTIETKYLAKVRATIEKNKIYPKAAKRLNQTGKVNVNFDILKSGEIRNVKVLGKSSFAKLD
EASIELLIKISNFDEIPEELKKSVWNVTIPIDYSIN

99 Domain II residues

20 Proline residues

0 α-Helices

Campylobacter curvus

Locus:

>EAT99645.1 TonB-dependent heme/hemoglobin receptor family protein [Campylobacter curvus 525.92]

MNKICKFSIICTALLSLSNAAQNESEDLTFDTLEVSAKSVSNAEKSFATPGAVSSRDDVKSKT
QSIDSIVRAMPGSYTQVDQSQGSVSVNIRGLTGLGRVNTMVDGVTQTYFGTSSDSGGFHN
FTGNLGTSAFGALIDQNFLVGIDIERGTFSGPNTGLMGSANFRTIGVDDVITEGKPFGFLGRY
SYGSNKVGPSYMGAIAARHRFENGTSLGFVFGYSGKKTSQNYTVGGGGKISDKQPDLDGD
GVPDVPPSLDTDDLVQKPKSYLFKTEYAHEDSSAILSYRNLNNYLAKRKINNDSYQLNYRYD
PSSDLVDVKFLAAYNRSKQNYDKGASISWGTLKNGMKFYNKSSQFDLSDTMKFNPASELFI
TTSAGINLLTNKYTKQTGDSDYKTLTTNYAVPTGEQKAVSYYLNNAFSYDIFEFDANFNLQK
WQTKGRKGKCALSNPLCSQKEAGEFKTDDTYLNASLMASAKLHDLFSPFVSYSRTSRPLN
VQELFASGTVYEDINTALRPEKTQTWQIGFNSYKHGLFADDDVFGLKAVYYRSKVKDFIYDR
LLMFDTPDTTMFLARLNDKAKFRGFELELTYDIGYFYTNLSYTRQKTTYLPSDSSALDWTNG
PASGQSQFSELPKDYATLDIGTRLFGEKLTFGSLIKYTGKAKRIYPKAEFTPSPNNQNPLFKK
LQTQELPKIPTVIDLYASYEPIKNLTLKFEVQNLTDKNYMDALYTYNSSYSSQVFNDDIVLFN
NSARGRTFLMSFEYRY

tonB next to motor, where ExbB has large periplasmic domain. Also near TBDT.

>EAT99643.1 energy transduction protein TonB [Campylobacter curvus 525.92]

MTRRRFLLPFAFLLSLSVHIFIVFLFMQSAPSQNNGGYIGESGEFQSVRIVSSLPIGELMDTAI
NSQKQTQLQTPPEQETSEGSLSDTDVKSQITVKKSKVFSKKQTVKRLPEKEKKSNEKRETT
EDQTQKDKDTGDSQVDSVSANSVASAPVQGSGDKLSSPNDGNSQSTGASWQGAVMSHL
NKHKKYPNEALAKKQEGKVLLLVKIAEDGAVLECKIKKGSGVALLDEEALNLFKRASPLPKP
PQSVLKGKREITFSIPIDYNIKKFLERDLLRNGG



MTRRRFLLPFAFLLSLSVHIFIVFLFMQ
**SAPSQNNGGYIGESGEFQSVRIVSSLPIGELMDTAINSQKQTQLQTPPEQETSEGSLSDTD
VKSQITVKKSKVFSKKQTVKRLPEKEKKSNEKRETTEDQTQKDKDTGDSQVDSVSANSV
ASAPVQGSGDKLSSPNDGNSQSTGASWQGAV**
MSHLNKHKKYPNEALAKKQEGKVLLLVKIAEDGAVLECKIKKGSGVALLDEEALNLFKRASP
LPKPPQSVLKGKREITFSIPIDYNIKKFLERDLLRNGG

151 Domain II residues

7 Proline residues

6 α-Helix residues