ADDITIONAL MATERIAL

Fig. 1. Structural alignment of the four known Hr crystal structures (with the four alpha-helical segments A-D in red) obtained using MUSTANG (31), the derived Hr fold highlighting the conservation of the Fe-coordinating and several hydrophobic residues (numbered using the *Themiste dyscritum* Hr).

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2awc Desulfovibrio vulgaris DcrH
-------VKWSEDLAN-LPSI-DTQHKRLVDYINDLYRAARR-------DMDKAREVFDALKNYAVEHFGYEERLFADYA--Y-----------PEATRHKEIHRRFVETVLKWEKQLAAG-----------DPEVVMTTLRGLVDWLVNHIMKEDKKYEAYLRERGVS
1i4y Phascolopsis gouldii Hr
GFPIPDPYVWDPSFRTFYSII-DDEHKTLFNGIFHLAID--------------DNADNLGELRRCTGKHFLNEQVLMQASQ--Y-----------QFYDEHKKEHETFIHALDNWK----------------------G-DVKWAKSWLVNHIKTIDFKYKGKI
2mhr Themiste zostericola MHr
GWEIPEPYVWDESFRVFYEQL-DEEHKKIFKGIFDCIRD--------------NSAPNLATLVKVTTNHFTHEEAMMDAAK--Y-----------SEVVPHKKMHKDFLEKIGGLS---APV---------------DAKNVDYCKEWLVNHIKGTDFKYKGKL
1hmd Themiste dyscritum Hr
GFPIPDPYCWDISFRTFYTIVIDDEHKTLFNGILLLSQA--------------DNADHLNELRRCTGKHFLNEQQLMQASQ--Y-----------AGYAEHKKAHDDFIHKLDTWD----------------------G-DVTYAKNWLVNHIKTIDFKYRGKI
Hr fold--W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
----------------------==== HELIX A ====---------------======== HELIX B ========------------------==== HELIX C ====----------------------------=== HELIX D ===--------

Iron coordination: Fe1 - H74, H78, H102; E58, D106; Fe2 (O2 binding site) - H26, H55; E59, D107.
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Fig. 2. Alignment of Hr sequences listed in Tables 1-3 in Supplementary Material, in the following order: eukaryotes, archaea and bacteria. Note that the last two bacterial sequences have uncommon interhelical inserts.

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ALVEOLATA
>Plasmodium yoelii yoelii (Alveolata; Apicomplexa) gb|AABL01004457.1 107aa
----------------------DDQHKTIFDMVNKLHDT-------AATGNRSEIGKQLDALIDYVVMHFKSEETEMQKKG--Y-----------ADFAAHKAEHDKLVGVCADLQKKFHAG-----------EAEVNQDTTRFVRDWLVNHIPKVDKLY----
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L

ANNELIDA
>Haementeria depressa (Annelida; Hirudinae) gi|47833904|gb|CN807658.1 119aa
GFEIPEPFCWDESFKV-FYEQIDQEHKGLFDAIFKLAKS-------------PSDCGALSHLAKLIDEHFAFEEGMMKKAN--Y-----------DDFENHHKAHVDFVGTLKTVS---CPV---------------AADKLHWAKEWLVNHIKTTDFKYKGKL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|157306 120aa
GFDIPEPFQWDESFLVSYDKL-DDEHKGLFQGIKSVSES-------------PSCSETLEKLVQLIKQHFLDEEEMMKAKG--F-----------DDIEAHSKAHTDFVETLKGVQ---TPV---------------TAENIKMAKEWLVNHIKGTDFKYKGKL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|100875 120aa
GFDIPEPFVWDETFKVFYNEL-DEEHKGLFQGVFNV-------------AKAPSDQGALECLAKLVDAHFKHEEEMFKAKS--Y-----------PDAESHKKAHDDFMATLKTIA---CPV---------------ANDKIHFAKNWLVNHIKGTDFLYKGKL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|81783 121aa
AYEIPSPYEWDESFRVFYDKL-DEQHKGLFKGIFDV-------------CKSPSDASALSHLKHVLTEHFKTEEGMMKDAH--F-----------SDYDNHKHIHDDFEKQLDAQH---VPI---------------PVEKVTAAKEWLVNHIKGIDFKYKTHL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|185740 123aa
GFAIPEPYIWDESFRVFYDTL-DEQHKNLFHVIFSL-------------AKSPDDPIVLKHLVKTIDEHFDHEEGLLRKAN--Y-----------ADYDVHHQEHLNFQKALKKVR---TPV---------------SDEQITWAKDWLVNHIKGTDFQYKGKL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|111854 132aa
SHPIPEPFVWDESFKVFYDKL-DGEHQGLFQAIFDV-------------GKTPNDSGVLAKLVELMDSHFAHEEREMKKAA--F-----------DGHDEHKDNHDEFLASLKKLK---TPV-------------AQESVQWAKNWLVHHIKVTDSKYSGKLHL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|86578 136aa
ASDIPSPFQWNESFRVSYDTL-DEQHKGLFKGIYDV-------------EQSPGSSQALTNLRNVIETHFRTEEKMMKDAG--Y-----------SEYDSHRKIHTDFEKDLSGYT---TTV-------------SSNQIQTAKEWLVNHIKGIDFKYKGKLSN
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|100575 134aa
AFDIPEPYKWDESFKVDYEKL-DEQHKGLFQAIFDV-------------CAAPADAAALAHLKDVIEKHFRFEEGMMTAAD--Y-----------AGYADHKKAHDGFEARLKEGQ---VPV---------------AADDVKAAKEWLVNHIKGVDFKYKTLL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|81819 134aa
AFDIPRPFKWDESFKVFYEKI-DEQHQGLFEAIYQV-------------CRHPEDAEKLKHLDDVIEKHFRDEEKMMEDAK--Y-----------EEYDEHHKIHADFEAKLDAVH---VPV---------------TRDQVKYAKEWLVNHIKGIDFKYKGKL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|174825 134aa
ALDVPEPFVWDDSFLVDYEKL-DEQHKGLFKAIFDV-------------CAAPADASAFAHLKDVIEKHFRFEEGMMEAAH--Y-----------GDLPLHKQIHESFEAALKAGQ---VPV---------------AAADIKGAKEWLVGHIKTVDFKYKTHL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|174822 134aa
AYPIPDPFQWDESF--RYDKL-DEQHKKLFTGIADV-------------QSNPADGAAISHLEDLFYKHFRFEEKMMEEVG--Y-----------ANLPAHKRMHTDFESEIKDIH---TPV---------------QGYQIFFMKDWLVNHIKGIDFQYKGKL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|81862 134aa
ALDVPEPFVWDDSFLVDYEKL-DEQHKGLFKAIFDV-------------CADPADASAFAHLKDVIEKHFRFEEGMMEAAR--Y-----------DDLLRHKHIHETFEAALKAGQ---VPV---------------AAADIKGAKEWLVGHIKFTDFKYKTHL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|81835 136aa
AEPIPAPFKWNESFRVFYDKL-DEQHKGLFKAIADV-------------EQHPSQAVAYAHLKSVMGKHFRFEEDMMKEAQ--F-----------ADLATHKGIHEDFEATLRASQ---VPI---------------SSEKVTGAKQWLVDHIKLVDFKYKGKL
>Helobdella robusta (Annelida; Hirudinae) jgi|Helro1|175368 165aa
RSHKVTDYTYEQICSNRYPKL-DDQHQQVFSEVDKL------------SENTGDEAQIKYTI-SIYKMHFDYEESQMRKAN--Y-----------ENYDDHKLLHESFLEEFRNHP---IPI---------------SIPNMEKIKSWLIAHIKTYDRKFNGKM
>Hirudo medicinalis (Annelida; Hirudinae) 120aa AAS49167.1  GI:44921619
GFEIPEPYVWDESFKV-FYENLDEEHKGLFQAIFNLSKS-------------PADNGALKHLSKVIDEHFSHEEDMMKKAS--Y-----------SDFDNHKKAHVDFQASLGGLS---SPV---------------ANDKVHWAKDWLVNHIKGTDFLYKGKL
>Theromyzon tessulatum MHr (Annelida; Hirudinae) 120aa Q9GYZ9  GI:21263690
VFEIPEPYQWDETFEV-FYEKLDEEHKGLFKGIKDLS-D------------SPACSETLEKLVKLIEDHFTDEEEMMKSKS--Y-----------EDLDSHKKIHSDFVETLKGVK---APV---------------SEENIKMAKEWLVNHIKGTDFKYKGKL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Allolobophora caliginosa (Annelida; Oligochaeta) 119aa
GFDIPEPFVWDESFKV-FYDLLDDEHKGLFKGIFDVAKA-------------PGDGGALDHLRQVVSKHFSDEEGMMEKAN--Y-----------AEVGPHKQMHTDFVAKLKGLS---TPV---------------SNDTIHFAKDDLVNHIKTTDFKYKGKL
>Neanthes (Nereis) diversicolor Hr (Annelida; Polychaeta) 119aa P80255  GI:417311
GFEIPEPYKWDESFQV-FYEKLDEEHKQIFNAIFALCGG-------------NNAGNLKSLVDVTANHFADEEAMLKASAS-Y-----------GDFDSHKKKHEDFLAVIRGLG---APV---------------PQDKINYAKEWLVNHIKGTDFGYKGKL
>Neanthes (Nereis) diversicolor MHr (Annelida; Polychaeta) 120aa P22761  GI:123030
GFEVPEPFKWDESFQV-FYDKLDEEHKQIFNAIFALGGG-------------NNADNLKKMIDVTANHFADEEAMMLASAA-Y----------KSEHPGHKKKHEDFLAVIRGLS---APV---------------PNDKLLYAKDWLVNHIKGTDFTYKGKL
>Periserrula leucophryna (Metazoa; Annelida; Polychaeta) 119aa AAQ63634.1  GI:34327785
GFDIPEPFKWDASFEV-FYKKLDDEHKAIFDSIFAVCNG-------------NNADNLKKMVDVTANHFSDEEGMMKSAN--Y-----------ADFDSHKKKHEDFLVVIRGLS---APV---------------GDDKLHYAKDWLVNHIKGIDFQYKGKL
>Riftia pachyptila (Annelida; Vestimentifera) 110aa
--EMPEPYVWDESFRV-FYDNIDDEHKGLFKGIFDCGAA-------------PADSAKLASLLQLVIDHFVDEESMMKKTN--F-----------DGLPTHNKIHTEFVDKLKSLS---CPL---------------DDATIAFAKKWLVNHIKGTD-------
>Scoloplos armiger (Annelida; Polychaeta) 110aa
--DVPEPYVWDESFKV-FYANLDEEHKGLFQGVFNVAGD-------------KGSADKLSALVAAVDKHFKNEEGMMQAKS--Y-----------ADFPAHKQAHEAFLGKIKGLK---APV---------------DDATVHFAKDWLVNHMKGTD-------
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L

BRACHIOPODA
>Lingula anatina HrA (Brachiopoda) 117aa P22764  GI:123038
-VKVPEPFAWNESFAT-SYKNIDLEHRTLFNGLFALSEF-------------NTRDQLLACKEVFVMHFRDEQGQMEKAN--Y-----------EHFEEHRGIHEGFLEKMGHWK---APV---------------AQKDIKFGMEWLVNHIPTEDFKYKGKL
>Lingula anatina HrB (Brachiopoda) 117aa P22765  GI:123044
-MKIPVPYAWTPDFKT-TYENIDSEHRTLFNGLFALSEF-------------NTQHQLNAAIEVFTLHFHDEQGQMIRSN--Y-----------VNTKEHTDIHNGFMDTMRGWQ---SPV---------------PQKALKDGMEWLANHIPTEDFKYKGKL
>Lingula reevii HrA (Brachiopoda) 117aa P23543  GI:46397821
-VKVPAPFAWNEDFAT-SYKFIDLEHRTLFNGLFALSEF-------------NTRDQLLACKEVFVMHFRDEQGQMEKAN--Y-----------EHFEEHKGIHEGFLEKMGHWK---APV---------------AQKDIRFGMEWLVNHIPAEDFKYKGKL
>Lingula reevii HrB (Brachiopoda) 117aa P23544  GI:46397822
-MKVPAPYAWNSDFAT-TYENIDSEHRTLFNGLFALAEF-------------NTLTQLNAAIEVFTLHFHDEQGQMIRSN--Y-----------VNTKEHTDIHNGFMDVMRGWR---SPV---------------PQQDLLAGMAWLANHIPTEDFKYKGKL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L

CNIDARIA
>Nematostella vectensis XP_001634535.1  GI:156388091 119aa
--------RWNESFKVFYQNLDD-EHRGLFDVVFDV-------------DAKRGDAGAVSKAASAFKGHFTTEEAEMKKGVDAGKLDGAHYKGHCTAHNKFLELF---GSFGNNLGDDEINYSMKWLVNHIKSTDFHYKGKLIQ
>Nematostella vectensis XP_001622541.1  GI:156351502 156aa
PLPIFFLNRWNESFKVFYQNLDD-EHRGLFDVVFDV-------------DAKRGDAGAVSKAASAFKGHFTTEEAEMKKGVDAGKLDGAHYKGHCTAHNKFLELF---GSFGNNLGDDEINYSMKWLVNHIKSTDFHYKGKLIQ
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L

FUNGI
>Ajellomyces capsulatus (Ascomycota; Pezizomycotina) 205aa (12-146) XP_001539786.1  GI:154277908
LQFIYLSHTTPVAMVSISDSVTK-DHKELEAFHNQIVNA----------DNDIIKTRFQNQFVWELARHSAAEELLLYPA---L---EKHLADGKERVEKDRERHQKTKEQLMEFQSMKPTDA-------------NFEPTVNSLMDNLSAHMRDEEGDNLPAL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Aspergillus clavatus (Ascomycota; Pezizomycotina) 220aa (20-154) XP_001270510.1  GI:121704493
SLPIARAVSTTPIMTGRITDTVKQDHRQLEACYDKIMHA----------TDRDDQIRFQNLFTWELARHSIGEELVVYPA---F---EKHLPDGVSMADKDRREHQTVKEKLKKFQNLDPSNP-------------EFMSTIKSLMVDLAQHIKEEETNDLVKL
>Aspergillus fumigatus (Ascomycota; Pezizomycotina ) 221aa (26-160)  XP_754309.1  GI:70999175
SHQVQAFTDWSQARRFRILDTIKHDHSEIKSFYELIVSS----------PGPEEQTKYQNQFTWELARHTVGEELVIYPA---L---EKYLDDGKELARKDRAEHQTVKEKLKAFQDMKSTDP-------------RFIPTLQSLWDDLQEHIRHEETEDIQLL
>Aspergillus fumigatus (Ascomycota; Pezizomycotina; Eurotiomycetes) 227aa (25-159) XP_747053.1  GI:70983051
TLIQNRTFAITSPTMTRLADAIKDDHRELEEAYNKILSA----------KTSDEKTRWQNQFTWELARHSIGEELIVYPL---M---EKNLPNGKEMADKDRAEHQIVKEHLYKFQSLSSEDA-------------EFEPTLKSLWSNLGQHIKEEESDDLPSL
>Aspergillus nidulans (Ascomycota; Pezizomycotina; Eurotiomycetes) 228aa (24-158) XP_681907.1  GI:67903302
TPLQQRFISQSPIAMTRIIDAIKQDHREIEDYYNKILSA----------TTEKEKIQWQNQFTWELARHSIGEELVVYPV---F---EKNLPDGRAMADKDRHEHNTVKEKLKQFQNMKPSDP-------------NFEPTLKSLMSTLSEHIQEEESQDLPKL
>Aspergillus oryzae (Ascomycota; Pezizomycotina) 221aa (23-157) BAE63202.1  GI:83773074
TLGASRGFRTTAPAATRVSEVIKNDHRELEDQYNRILSA----------KTKDEKEQWQNQFTWELARHSIGEELVVYPR---M---EKVLDNGKTMADHDRHEHQIVKEDLYKFQGLQPDDP-------------EFIPTLKTLWANLAQHIKEEETQDLPAL
>Chaetomium globosum (Ascomycota; Pezizomycotina) 197aa (1-126) XP_001219252.1  GI:116178806
---------MAASAATRVSERIKHDHDELREYYNNIKNA----------QRDDDKVKWQNQFVWELARHSVAEEIVVYPA---F---EKHIPNGMVMAEKDRSEHQQVKEKLHTFQSLAPTDP-------------TFHSTIDSLWEALAQHMQEEERDDLPAL
>Coccidioides immitis (Ascomycota; Pezizomycotina) 181aa (1-121) XP_001245291.1  GI:119189369
---------------MGLSDSVKKDHRELEDYYNQIINA----------TDDDTKIRYRNQFTWELARHSIGEELLVYPA---F--EKHLHLDGKKKADRDRQEHQVVKEQLKQFQNMEPTEP-------------NFIPTIKSLMSNLSEHIKEEEAEDLPAL
>Coprinopsis cinerea okayama (Basidiomycota; Hymenomycetes) 208aa (1-130) EAU86662.1  GI:116503767
-------MTSNPSAQHTLLQIITSDHRDIEAFYNEYLKNA---------GNKDGQTRWANQLTWTIARHSISEELVVYPQ---F--EKHLGDKGRAMAEQDRQDHQFVKDRLKLLEDMEVGSS-------------QYDATLKEIMTELKKHMASEETEDLPLL
>Coprinopsis cinerea okayama (Basidiomycota; Hymenomycetes) 228aa (17-153) EAU89470.1  GI:116506575
RYPLARTLATTAPGHVRLLQAITDDHREIEAFYDQYLKNG---------GNTDAQQRWANQLTWEIARHSISEELVVYPL---L--EKVMADQGHVLAESDRDDHQFVKDRLKKLESIEVGTT-------------AYNAILKDIMDHLKEHMRKEETEQFPQL
>Cryptococcus neoformans ( Basidiomycota; Hymenomycetes) 220aa (15-159)  XP_566714.1  GI:58258603
TRFFASPTTSSMAGNTSVADAVKHDHRELEEYYDQIIKA----------TDADTKTRYQNLFTWELARHSVGEELVVYPA---L---EKYVDGGKALADRDREEHQKVKEMLYKFQQLSPSDS-------------EFEPTIKKLMSDLAEHIKEEETEDLVKL
>Magnaporthe grisea (Ascomycota; Pezizomycotina) 239aa (34-169) XP_360008.1  GI:39940942
QRQFASASASAGSGFVKISDAIKKDHQELEQYYNEVINS----------TDQEHQQKFGNQFTWELARHSVAEELLVYPA---F---ETHLGEEGRQMAEDDRKQHHEVKILLKEFQNMRSNDS------------EYVPKLKELWAKLSLHIQEEESHDMPAL
>Neosartorya fischeri (Ascomycota; Pezizomycotina) 221aa (25-160) XP_001263153.1 GI:119490985
SHQVQAFTDWSQARRFRILDTIKHDHREIKSFYELIVSS----------TDPEEQTKYQNQFTWELARHAVGEELVVYPA---L---EKYLDDGKELARKDRAEHQTVKEKLKAFQDMKSTDP-------------RFIPTLQSLWDDLQEHIHHEETEDIQLL
>Neosartorya fischeri (Ascomycota; Pezizomycotina; Eurotiomycetes) 227aa (25-159) XP_001261781.1  GI:119483756
KLIQNRTFAITSPTMTRLADAIKDDHRELEEAYNKILSA----------KTSDEKTRWQNQFTWELARHSIGEELIVYPL---M---EKNLPNGKEMADKDRAEHQIVKEHLYKFQGLSPEDP-------------EFEPTLKSLWNNLGQHIKEEESEDLPSL
>Neosartorya fischeri (Ascomycota; Pezizomycotina) 233aa (24-158)  XP_001267572.1  GI:119501631
PIAARSVSTSPIQMIGRITDTVKQDHREIEACYQRIINA----------KDRDEQTRYQNLFTWELARHSIGEELVVYPA---F----EKHLPDGISMAEKDRREHQTVKEKLKKFQNLDPSNA------------DFIPTLKSLMGDLAEHIREEETNDLVKL
>Schizosaccharomyces pombe (Ascomycota; Schizosaccharomycetes) 203aa (9-144)  NP_595013.1  GI:19115925
VSLNFFPVRLLSYKMTRISDAIFKDHRKLQSDYQNIKSA----------NDYDTATRWQNQFVWELARHSVGEEIVVYPK---F--EKYLGEEGKEMAEKDRHEHQLVKEMLYKFQSMKANQS-------------NFIPALDELMESLQKHIDEEEQHDIPFL
>Ustilago maydis (Basidiomycota; Ustilaginomycetes) 244aa (32-170) XP_757573.1  GI:71005814
ISTNFAAAAFAMTGKD-LIKEIKVDHDNIRDLLKRFNDA-------HKAGDQDLCEALVNTIIHEAAVHSDAEELSVYKL---M-----EKLHMTQVAEKDRQDHQNVKQAMAELDTNQISDA----------GLDTFAHKVDKACKLFLEHAEEEENDQLPQL
---------W------------D--HK-LV------------------------------L------HF--E---F-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L

HETEROLOBOSEA
>Naegleria fowleri (Heterolobosea; Schizopyrenida) 119aa Q9NH76  GI:21263696
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ATTIPSPFNWDSSFCVGNNELNE-QHKKLFALINAL------------DANRSSASALKELLDFVVMHFKAEEDLFAKVN-F-SDSTSHKETHDKFVQDALGLK---T-V----GDAEIQFIKQWLVNHIKGSDMKYKGVL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Naegleria gruberi jgi|Naegr1|44819|fgeneshHS_pm.scaffold_69000005 119aa
SYPIPTPYEWSTTLDIGNAELNE-QHKKLFTLINAL------------DAKRSCGTTLKELLDYVVFHFKTEEDLFAKAG-W-SESASHKETHDKFVQDALAL----TSV----GDAEMQFIKQWLITHICASDMKYKGVI
>Naegleria gruberi jgi|Naegr1|36233|estExt_gwp_gw1.C_160163 119aa
SFPIPSPYQYDDSFCVGNAEINE-QHKKLFELINAL------------DANRTCGTTLKTLLDYVVMHFKTEEDLFAKHA-W-SESAAHKEIHDKFVQDALGL----TSV----GDAEMQFIRQWLVDHIMGSDMKYKGVI
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L

SIPUNCULA
>Golfingia vulgaris Hr1 (Sipuncula) 114aa CAG14945.1  GI:57282926
GFPIPDPYVWDPSFRT-FYTAIDDEHKTLFDGIFHLARD--------------DNKDNLGELRRCTGKHFLNEQVMMQASQ--Y-----------AGYDEHKKAHDEFIHQLDHWK-----------------------GDSNWAKTWLVNHIKTIDFKYKGKI
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Golfingia vulgaris Hr2 (Sipuncula) 113aa CAG14946.1  GI:57282928
GFPIPDPYVWDPSFRI-FYSIIDDEHKTLFNGIFHLGHD--------------DSADNLAELRRCTGKHFLNEQVLMQDSQ--Y-----------AGYAEHVRAHDGFIHQLDNWH-----------------------GDVKWAKNWLVNHIKTIDFKYKGKI
>Phascolopsis gouldii Hr (Sipuncula) 114aa P02244  GI:21264441
GFPIPDPYVWDPSFRT-FYSIIDDEHKTLFNGIFHLAID--------------DNADNLGELRRCTGKHFLNEQVLMQASQ--Y-----------QFYDEHKKEHETFIHALDNWK-----------------------GDVKWAKSWLVNHIKTIDFKYKGKI
>Phascolopsis gouldii MHr (Sipuncula) 119aa P27686  GI:232242
PFDIPEPYVWDESFRV-FYDNLDDEHKGLFKGVFNCAAD------------MSSAGNLKHLIDVTTTHFRNEEAMMDAAK--Y-----------ENVVPHKQMHKDFLAKLGGLK---APL---------------DQGTIDYAKDWLVQHIKTTDFKYKGKL
>Siphonosoma cumanense Hr (Sipuncula) 113aa P22766  GI:123040
GFPVPDPFIWDASFKT-FYDDLDNQHKQLFQAILTQGNV--------------GGATAGDNAYACLVAHFLFEEAAMQVAK--Y-----------GGYGAHKAAHEEFLGKVKGGS---ADA--------------------AYCKDWLTQHIKTIDFKYKGKL
>Sipunculus nudus HrB (Sipuncula) 119aa CAG14943.1  GI:57282922
PFPVPDPFVWDTSFQV-FYFKLDDQHRAIFETLFNSTND--------------NTPGNLQLFYIVTANHFEEEEGWMVSAS--Y-----------GGYDAHKKLHEEFLAKVRSFS---APV---------------SKENLFYAKDWLVQHIKTIDFKYKQLL
>Sipunculus nudus HrA (Sipuncula) 119aa CAF74912.1  GI:57282893
PFPVPDPFVWDTSFQV-FYFELDEKHRGIFQALFALGND--------------NNPSNLKLLYRVTANHFAEEEGFMQTAN--Y-----------GGYRSHKVLHEDFLAKLRSFK---APV---------------PDKDVYFAKDWLVQHIKTIDFKYKNLL
>Sipunculus nudus MHr (Sipuncula) 119aa CAG14944.1  GI:57282924
GFPIPDPYVWDESFKV-FYQLLDDKHKQIFQGVFDCAKD------------PSSAAKLQKLIEVTAKHFSDEENMMQQSK--Y-----------SGYPPHKKAHEEFLGKLRGLR---APL---------------DTAGLDYCKDWLVQHIKTIDFKYKGKL
>Themiste dyscritum (Sipuncula) 113aa P02246  GI:123041
GFPIPDPYCWDISFRT-FYTIVDDEHKTLFNGILLLSQA--------------DNADHLNELRRCTGKHFLNEQQLMQASQ--Y-----------AGYAEHKKAHDDFIHKLDTWD-----------------------GDVTYAKNWLVNHIKTIDFKYRGKI
>Themiste zostericola Hr (Sipuncula) 113aa P02245  GI:123042
GFPIPDPYGWDPSFRT-FYSIIDDEHKTLFNGIFHLAID--------------DNADNLGELRRCTGKHFLNQEVLMQASQ--Y-----------QFYDEHKKAHEEFIRALDNWK-----------------------GDVKWAKSWLVNHIKTIDFKYKGKI
>Themiste zostericola MHr (Sipuncula) 118aa P02247  GI:417114
GWEIPEPYVWDESFRV-FYEQLDEEHKKFKGIFDCIR-D--------------NSAPNLATLVKVTTNHFTHEEAMMDAAK--Y-----------SEVVPHKKMHKDFLEKIGGLS---APV---------------DAKNVDYCKEWLVNHIKGTDFKYKGKL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L


ARCHAEA
>Haloarcula marismortui (Euryarchaeota; Halobacteria) 617aa (9-146) YP_134671.1  GI:55376820
TDSTGEFAEWDDERYSTNIERFDEQHKRLFGLLNDLHTA------MNEGHSEEEVGDILRELERYTEYHFGDEEEFMQNCG--Y------AMDCSDCFYNHREMHEEFADKVQELREKHENGE------------YVTMEVLTVARDWLDAHIAAGDEDQNYAD
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Methanocaldococcus jannaschii (Euryarchaeota; Methanococci) 169aa (21-153)  NP_247732.1  GI:15668928
EIMKKEIIKWSKDFET-GIKAFDDEHKILVKTLNDIYNL------LNEGKRDEAKELLKRRVVNYAAKHFKHEEEVMEKYG--Y-----------PDLERHRKTHEIFVKTVIEKLLPKIEEG----------SENDFRSALSFLVGWLTMHIAKPDKKYGEW-
>Methanocaldococcus jannaschii (Euryarchaeota; Methanococci) 147aa (1-132) Q58157  GI:21263658
--MKKEIIKWSKDFET-GIKAFDDEHKILVKTLNDIYNL------LNEGKRDEAKELLKRRVVNYAAKHFKHEEEVMEKYG--Y-----------PDLERHRKTHEIFVKTVIEKLLPKIEEG----------SENDFRSALSFLVGWLTMHIAKPDKKYGEWF
Methanoregula boonei (Euryarchaeota; Methanomicrobia) gi|154149997|ref|YP_001403615.1 135aa
----MALISWSDELSVRVNEIDD-QHKKLISLMNNLHDA------MRAKQGKQALEATLQELAAYTVYHFQTEEKYMQKFH-Y------------PQFATHKAQHDAFVKKVSDFQKEFEANR-----------LGLSIELMNFLRDWVSNHIKSTDKQYSATF
>Methanospirillum hungatei JF-1 (Euryarchaeota; Methanomicrobia) 135aa YP_504166.1  GI:88603988
>Methanospirillum hungatei JF-1 (Euryarchaeota; Methanomicrobia) 135aa YP_502435.1  GI:88602257
----MAFLKWSESLSV-HVTEIDEQHQKLIQLINTLHDA------MLEKKGKEVLGKILDELAAYTVYHFSTEEKYMEQCG--Y-----------PGLAFHKKEHDTFVGKVESLIQDYQANK-----------LGITIELMTFLKDWVSNHIQITDKKYSDTF
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L

BACTERIA
>Acidobacteria bacterium Ellin345 (Acidobacteria; Acidobacteriales) 132aa YP_592725.1  GI:94970677
----MPFLTWETRFSV--GAAMDAEHKTWFGILNRLHDAM------AQGKGKDVQQKILIEMVAYTHTHFAHEESFLQSRN--Y-----------PDLPAHRSLHVTFTKKVRDLESKVKAGL-----------PVLSVELMDFLRDWLQNHILTHDVKYGTWM
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Acidobacteria bacterium Ellin345 (Acidobacteria; Acidobacteriales) 134aa YP_593517.1  GI:94971469
-----MTIRWKSSYSV-GVSVMDNEHRSLFNVMHELDNAL------AAGSGQLVIDTVLAKVTNWAEQHFTHEEELMLENG--F-----------PGYEAHRAEHDQARRQLETYEHDRKAG-----------KQGVPVSLLLFLDSWLRQHILKIDLQYAGYL
>Acidobacteria bacterium Ellin345 (Acidobacteria; Acidobacteriales) 142aa YP_591227.1  GI:94969179
---MWAAFAKPEDFPNLGHEAIDDEHENIARLMNELHDA---------------IHHRVALSEQRRLHHELETYVRVNNRS---EEQMMETDSYPNRESHHKAHEAMYRKLYEYEKVLQAGR-----------EDASLQGLHALRELLIRHIAQEDSRVASWH
>Acidobacteria bacterium Ellin345 (Acidobacteria; Acidobacteriales) 152aa YP_592726.1  GI:94970678
----MPDLQWKDSDSV-GIASLDAQHQGLFATAHRLRDA------MRSGRAATIQQEILAELGAYTRSHFEREERVMQICA--F-------PALCGHQHLHRSFLEQLQAIQAELRSDRSGIT---------------PDRMEFMRVWMRKHVAIEDAQYATWI
>Acidobacteria bacterium Ellin345 (Acidobacteria; Acidobacteriales) 155aa YP_592724.1  GI:94970676
----MDEVGVRDRLTF-GIPRLDSQHEQLLQLVRQMREA------DAGGKSLCELRLLAATLTLHTRMHFMDEEMFMEGAG--Y-----------PGLEAHRRRHAEFTEGLLRLQSGLLSTS-----------RSQFARIVEYELGWIHQHLEDEDNELGRWL
>Acidovorax sp. JS42 (Betaproteobacteria; Burkholderiales) 168aa YP_984586.1  GI:121592690
----MAALQWSEELAL-DLPQMDHTHQEFVALLQAVESADDVA-----------LIGAWEDLVAHTDAHFAQEDRWMQATR--F-----------AAGNCHSTQHQVVLKIMREGTDRARQGE-----------LHVLREMAAELAVWFPQHTDAMDASLAQHL
>Acidovorax sp. JS42 (Betaproteobacteria; Burkholderiales) 173aa (28-156) YP_984955.1  GI:121593059
RRPCMPFMPWTAELEL-GLPEIDDQHRQLVALTNALHDELSAA-----SPRRSAVGEIWEGLVDYTHNHFIVEEVLFQQHD--Y-----------AETPAHKAEHDGFTRKAMDLLTRFDGGQ------------EVTLEALEFLKQWLVHHICKVDRAYLPFM
>Acidovorax avenae (Betaproteobacteria; Burkholderiales) 171aa YP_968695.1  GI:120609017
----MAALQWSEGLAL-DLPLMDETHEEFVALLAAVEQAGDE-----------ALLPAWRALVAHTTEHFAREDAWMAATR--F-------ASGNCHSLQHKVVLQVMGEGTARAEAGESAVL---------------RHMAGELAVWFPQHTQTMDAALALHL
>Aeromonas hydrophila (Gammaproteobacteria; Aeromonadales) 678aa (539-672) YP_854665.1  GI:117619147
ATQDQELLHWNEAFMV-QVSSMDNQHLGLFEAMNRLYQA------VLDKSPAQLRKQRLDELLKLATQHFADEERVMEQAG--Y-----------PELRRHKQEHARLLAELDTLMQRNGTDD-----------EEFNMELLVFLKNWLLNHISKVDKQYSGTL
>Aeromonas hydrophila (Gammaproteobacteria; Aeromonadales) 809aa (673-806) YP_857472.1  GI:117618414
LDPEQGSLVWQSSHEC-GHPRIDAEHRQLFVLTNRLLEH-----MKDHQEHPALFLECMESLFDVARHHFAFEEQMLAELG--Y-----------PELAGHQQDHQLLLQKASQLMTAARAGT-----------LGNDELLNFIIQELVVGHMSQADRRYFPLM
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Alkalilimnicola ehrlichei (Gammaproteobacteria; Chromatiales) 161aa (1-127) YP_741251.1  GI:114319568
----MSYLSWSSDLDT-GIDAIDKQHRRIVEYINQLEDARSQG-------DRALIGEVLEGLVDYTQSHFAFEEQMMEDAG--Y-----------PLLRGHRRVHQLFIKQVGEYCRRFDAGE-----------DVAEELLNLLQRWLFNHIRHDDAAYVDDV
>Alkaliphilus metalliredigenes(Firmicutes; Clostridia) 137aa ZP_00800966.1  GI:77685572
------MFKWKESFNC-EVGSVDQQHQKLFQIGMQLHEIVKAK---DQLDHYDEMMEVLQELKHYTIDHFQYEEALMEKHH--Y-----------PGIADHKEAHQAFINKVIEIENQDIDEK----------QKKIGMDIIIFIANWIESHIMKVDMEYKEFF
>Alcanivorax borkumensis SK2 (Gammaproteobacteria; Oceanospirillales) 154aa (1-127)YP_691784.1  GI:110832925
-----MRLVWGPAYEL-GILVIDQQHKRIVDYINDLDRLVGQP------GAQLGVARVLYDLVDYTESHFSFEEALMERAG--Y-----------DKLDDHHSQHRKFIFHIESLLRRHEEGV-----------DVAESLLRVLEKWLFHHILEEDRAYTQQV
>Anaeromyxobacter sp. Fw109-5 (Deltaproteobacteria; Myxococcales) 132aa ZP_01667972.1  GI:121536194
-----MTVSFTRSMQI-GVPEIDQQHRELFARLGGFDDALGR-------GDRLEIEATFGFLREYALVHFECEERLMREAD--Y-----------PRLEAHRAIHRTFVERLEALSREHAERG---------PSAFLRLRARNWIVVWLTDHVGGEDVALGRHL
>Anaeromyxobacter sp. Fw109-5 (Deltaproteobacteria; Myxococcales) 133aa ZP_01668151.1  GI:121536373
------MLKWTPALAV-GIEEIDEQHQELFRRAERFVASLETA-------DRQEIGILLSYLRMYCVTHFGAEEAWMRDVR--Y-----------DGYAAHKAEHDRFVKDVLRLSDEHERRG---------GPGLEAMKVGSYLSRWLREHVTSTDTAFARFL
>Anaeromyxobacter sp. Fw109-5 (Deltaproteobacteria; Myxococcales) 135aa ZP_01669396.1  GI:121537620
---MVETHAWNEKLDV-GHEAMDHDHHLQIGLVSAFVDAVER-------GRPWMARRLADQLLAYSVAHFGSEELLMEGSA--F-----------PERDAHAGEHGAFLEQMRELQRSFSSG-----------DEALATTSALELRGALAAHMNGADRRLAAHV
>Anaeromyxobacter sp. Fw109-5 (Deltaproteobacteria; Myxococcales) 142aa ZP_01670274.1  GI:121538500
-----MPYVDSSQLPDLPLAFMNRDHAEEFRLLEELGQALEAH--GQGSGTTDEILQRLAVLAVKTREHFLHEESVMREAA--F-----------PAYLPHKMEHDRVLAEMDAEAKAFRERG----------DTKRLRRYLIDSVPRWFVAHTTSMDVVTAGF
>Anaeromyxobacter sp. Fw109-5 (Deltaproteobacteria; Myxococcales) 149aa ZP_01669455.1  GI:121537767
-----MALQWTSALSS-GVAELDAQLEELFRRVDRLLDAILAR-------DRSEASRLIAFLQHHVSDHFAAEERLMREVE--Y-----------PDAARHVAEHLAFAAQIDALAGWLAAEG---------ATARLVLRLEREVTAWLQEHVYGTDHALARFV
>Anaeromyxobacter sp. Fw109-5 (Deltaproteobacteria; Myxococcales) 195aa (44-177) ZP_01671347.1  GI:121539576
QEARLMWIQWHSGHAV-GIESVDAKQRDLLHRTNRLVETVRA-------GRTDEAVTRLELLRVAAEAQFRDEEARLRD----A---------GSRSLARHAHEHERFLSDLDELVDGVTRRG---------IVALQEVRFTSWLPRWIDIHVARTHSDLASLG
>Anaeromyxobacter dehalogenans (Deltaproteobacteria; Myxococcales) 133aa YP_467301.1  GI:86160516
------MIAWTPALAV-GIEEIDAQHQELFRRAERFVSSLG-------QTSRQEVGILLSYLRLYCVTHFGAEESWMRQVE--Y-----------PGYAQHKAEHDGFVASLMALSDEHEKRG---------GPGLQATRVSTFVERWLQDHVTSTDVEFAKFV
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Anaeromyxobacter dehalogenans (Deltaproteobacteria; Myxococcales)    133aa YP_466223.1  GI:86159438
-----MVIEWTPSLSV-GVAEIDAQHQELFRRAARLIVALR-------AGDRTEVQPLLEFLADYVIEHFEAEEREMRAAG--F-----------PEYAAHKAAHDAFRRDFEELAGEVQRSG---------ASPLAALTLHNWISDWLRRHIAGVDQELGRYL
>Anaeromyxobacter dehalogenans (Deltaproteobacteria; Myxococcales) 133aa YP_466224.1  GI:86159439
-----MGARWSPALEL-GHDVIDRQHQELFRRYESLVQALA-------RGDRAEVAPLFEFLGSYVVEHFADEERIMSETA--F-----------PGLTVHKASHDRFVREYHALRELFERAG---------PTAAIAVRAETWIADWLATHIGATDAHLARHL
>Anaeromyxobacter dehalogenans (Deltaproteobacteria; Myxococcales) 138aa YP_463433.1  GI:86156648
-----MAITWDPTLAL-GIEEIDAQHEELFRRVDALLESVQE------RRSAEETRRMLAFLDAYVVEHFGAEEALMQAHR--Y-----------PGLAAQRAEHAGFAADLAALREELERDG---------MNALLVVRVNARVATWLFEHISRSDRAFGRFL
>Anaeromyxobacter dehalogenans (Deltaproteobacteria; Myxococcales) 144aa YP_463788.1  GI:86157003
-----MALHWTSVLSI-GVPELDAEHEEMFTRMDRLHDAIL-------SGERAEVSRMIEYLREHAVRHLAAEETLMLAIG--Y-----------PDRERHLREHEAFLATVRELTRRHDANG---------PTAVLVHDVERAVASWIDGHVGIHDVALGAFA
>Anaeromyxobacter dehalogenans (Deltaproteobacteria; Myxococcales) 144aa YP_463705.1  GI:86156920
---MIEAHAWNEKLDL-GHEAMDHEHHLQIALVTALTEAIEQ-------ARPWMARQLSAQLLSYSGVHFGSEEMLMQASA--F-----------DGLADHASEHRTLLEAMREIQAALERG-----------EDDLALAFAVELRAGLAGHMAGSDRRLADHV
>Anaeromyxobacter dehalogenans (Deltaproteobacteria; Myxococcales) 146aa YP_463306.1  GI:86156521
-----MGMEWTARLAV-GIDDIDAQHQELFRRVNGLVTAMGE------RRGREELAEVVAFLRAYVDVHFAAEARLMARSR--Y-----------PGRAFHAAEHAHFRAQVEELAARIAAEG---------PESHHAVKLAGILCEWLRQHVLLTDRQLADHV
>Anaeromyxobacter dehalogenans (Deltaproteobacteria; Myxococcales) 147aa YP_463596.1  GI:86156811
----MRFVDPTQIPELPLPFMND-DHAEEVRLLEALGEALEA--HRARTGGLDVVLERLSLLAVHTREHFLREEQVMRESG--F-----------PAYPQHKGEHDRVLAEMDGEARAFREGG---------DPVRLHAYLFETVPAWFVQHIRTMDAMTARFV
>Aquifex aeolicus (Aquificae; Aquificales) 131aa NP_214180.1  GI:15606800
-----MLIRPNKVQKV-GNLFMDTVHEEEIRLLNQLYDTLMK-------KDVEKADQLMDELLVDLEDHFTTEEELMREFE--F-----------FAYPMHKAEHDTMRKRFKEVYDKWKKEK---------NPEEVVRFLKEEFVPWLKSHVARWDSTTAQQL
>Azoarcus sp. BH72 (Betaproteobacteria; Rhodocyclales) 136aa YP_932039.1  GI:119896826
----MAELVWDDARHT-LGVAEMDATHREFVELVGRLAAADDA----------SFPKLFAEFHDHTRDHFFAEDAKMKATR--F-----------NAIGEHISEHQRVLIELRSFNRNVQAGR----------MRFARAYVRENLKEWFDLHLATMDSALAAHL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Azoarcus sp. BH72 (Betaproteobacteria; Rhodocyclales) 150aa YP_935261.1  GI:119900048
MQKNTTLVTWQDNYAL-GLDEIDDQHKMLFDIMNRLWAAILR------NAEGQELGRILEDLERYTVLHFTEEETFMRSIA--Y-----------PDFDGHIAYHRKFVKQISDEKAAARSGR------------QVSLELIHFLRDWLVNHILVEDKRYAAQF
>Azoarcus sp. BH72 (Betaproteobacteria; Rhodocyclales) 160aa YP_932615.1  GI:119897402
---MAELFEWNDDYNV-GVADIDEQHLELVALINQLHDAIRS------HKASKQVRRTLDELAEYTRTHFAIEERLMRESN--Y-----------PDYESHRSYHEALIDQIRALQAKLDGGE-----------ASITFELLHFLRTWLIRHICDVDKQFGAYF
>Azoarcus sp. BH72 (Betaproteobacteria; Rhodocyclales) 162aa (1-135) YP_932470.1  GI:119897257
----MQQMEWGEQLAL-GLGRMDTTHREFVELYNLLAASEAE-----------DFINRLDAFIVHTEAHFDQENRWMEQVN--F-------------PGCHRAEHDRVLTVMRDVRERAARGD-----------AFLGRRLVEELPPWFENHVNGMDAALAFHL
>Azoarcus sp. BH72 (Betaproteobacteria; Rhodocyclales) 174aa (19-147) YP_935260.1  GI:119900047
-LENTVPITWTSDLDT-GIAVIDQQHMRIVDYINQMEHAQQKQDRGL-------VGRVLDELVDYTLSHFAFEESLQEEAG--Y-----------PYLKPHRKVHELFVRRVNEYRERFSRGE------------EIAEEIHTLLSAWLINHIKRDDADYVGAV
>Azoarcus sp. BH72 (Betaproteobacteria; Rhodocyclales) 196aa (1-128) YP_157941.1  GI:56476352
---MNPLMRKLSPSAT-HMIRTDHSHVLSVFHQYETDTSP------------QTKKALVNSACLSLEIHAQLEEEIFYPA---M----RQAMAESATVDKSVSEHEEMRRLITQLRGMEPTDPQYD-------------ETFMSLMRDVLHHAAEEETIMLPKA
>Azotobacter vinelandii (Gammaproteobacteria; Pseudomonadales) 134aa ZP_00417575.1  GI:67155948
-TPQEMLERFQDSYAL-GDETIDHTHREFLELCLAAANAGGP-----------EFAGAFKALFEHTSRHFADEEAKMQASG--Y-----------PAFGEHRANHQRILGDMDRFCQRAVAG----------RAQMARAWLNDSLPAWFDLHAKTMDSALVVYL
>Bdellovibrio bacteriovorus (Deltaproteobacteria; Bdellovibrionales) 136aa NP_970264.1  GI:42524884
--MAESFFKWDKERLTTHVDAMDHEHQKLIQIMNRLYERNEAK------ASKTELTSIVRELASWTVTHFEHEEKFFDTLA--Y-----------SQAAVHKKIHRDLIERLKGHQAEFEK------------TGVLGPAFFQFLKTWLTAHIMGIDTKYGEIA
>Bordetella avium (Betaproteobacteria; Burkholderiales) 148aa CAJ48206.1  GI:115421695
-----VAMEWHTDLEL-GYAPMDDIHEEFVDIVARLQAAPDDR-----------LAELLAELHLHLASHFGQENAWMEETA--F-----------PPRDCHIGEHDAVLKSVKDVRLLLADQ----------GNTRICRELVAALADWFPGHAAHLDSALAHWL
>Burkholderia mallei (Betaproteobacteria; Burkholderiales) 145aa ZP_00444088.1  GI:67645813
QDLSTELAPELKPELKLDDPFVDAVHTEFVQLLDAAARADDAH-----------FLQAYDVWMDHCRQHFEREERWMASTK--F-----------GPQYCHAADHNEVLKVAADVREKLARD----------AQFELGRRLLVEVAEWFDQHVRTMDSMMVSHL
>Burkholderia mallei (Betaproteobacteria; Burkholderiales) 149aa (8-135) BMA0605 YP_102393.1  GI:53725253
ELAPELKPELKPELKL-DDPFVDAVHTEFVQLLDAAARADDAH-----------FLQAYDVWMDHCRQHFEREERWMASTK--F-----------GPQYCHAADHNEVLKVAADVREKLARD----------AQFELGRRLLVEVAEWFDQHVRTMDSMMVSHL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Burkholderia pseudomallei (Betaproteobacteria; Burkholderiales) 141aa ZP_01327209.1  GI:100121156
--MQDLSTELAPELKL-DDPFVDAVHTEFVQLLDAAARADDAH-----------FLQAYDVWMDHCRQHFEREERWMASTK--F-----------GPQYCHAANHNEVLKVAADVREKLARD----------AQFELGRRLLVEVAEWFDQHVRTMDSMMVSHL
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>Burkholderia pseudomallei (Betaproteobacteria; Burkholderiales) 186aa (44-172) YP_334215.1  GI:76810098
LPMQDLSTELAPELKL-DDPFVDAVHTEFVQLLDAAARADDAH-----------FLQAYDVWMDHCRQHFEREERWMASTK--F-----------GPQYCHAADHNEVLKVAADVREKLARD----------AQFELGRRLLVEVAEWFDQHVRTMDSMMVSHL
>Burkholderia phymatum (Betaproteobacteria; Burkholderiales) 147aa ZP_01500286.1  GI:118028824
-MRDLEGFAWHDDYAL-GHQTMDETHHEFVSCVHTLLTAEDA-----------DLGDALAAFAGHAHSHFGDEDASMRETA--Y-----------RSAGCHIDEHAAVLRSLDEVRAMLAQG-----------RTDVVRSFARALVDWFPEHVRVMDQGLARWL
>Burkholderia phymatum (Betaproteobacteria; Burkholderiales) 190aa (1-123) ZP_01504458.1  GI:118033012
--------MPYVPTIT-TMIRLDHTHVVAAFHRYGSETAWWR------------KRAIVNSVCRALEIHAQLEEEIFYPA---L----ARIAPTDETLKKSRPEHDELREVIAKLRGMGPEN-------------AAYDSLFMELMRDTLHHVADEETRLLPLA
>Burkholderia thailandensis E264 (Betaproteobacteria; Burkholderiales) 141aa YP_442321.1  GI:83719963
--MQDISNELKPELKL-DDPFVDAVHTEFVQLLDAAARADDAH-----------FLQAYDAWIDHCRQHFEREERWMASTK--F-----------GPQYCHAADHNEVLKVAAAVREKVAGD----------AQFELGRRLLAEASEWFDHHVRTMDSMMVSHL
>Burkholderia vietnamiensis G4 (Betaproteobacteria; Burkholderiales) 158aa (13-142) ZP_00427022.1  GI:67549150
VRESDNSLVWSDARLL-GFTPMDDVHKEFYEVALRLVTCTDAS-----------ALAAIEEFEKHAVSHFEQEDEWMRTTN--F-----------PPRDCHIDEHEAVLKSVRDVKAAVEAG---------QAGCGLVHDIGMHLYNWFPGHADYLDSALAAWM
>Burkholderia xenovorans (Betaproteobacteria; Burkholderiales) 159aa (7-135) YP_556187.1  GI:91780980
PMKEQEIFSWNDGFKL-GYSPMDKTHEEFVEIVNTMLTCSDSK-----------LAQHLDSFVAHAEDHFSQELCWMKETD--F-----------PNTACHAEQHDAVMHSVREVREHLRTG----------GDPEAARRLAAALAEWFPGHADYLDAALAQWM
>Burkholderia xenovorans (Betaproteobacteria; Burkholderiales) 165aa (12-137) YP_555832.1  GI:91780625
PVAAEETFGWSDRFLL-GFAAMDETHREFVDRVAALKRASDAE-----------LPARLAEFAQHAVAHFAQEERWMTTTA--F-----------PAAQCHADEHAAVLRSVREVEQMLRDG----------AALTLARDLTQALIDWFPAHADYMDAALSHWM
>Burkholderia xenovorans (Betaproteobacteria; Burkholderiales) 166aa (21-147) YP_557518.1  GI:91782312
VPSGDNSFAWSDARLL-GFALMDEVHKEFYAVALNLVTCTDAT-----------AATAIDRFERHAVSHFEQEDQWMRSTN--F-----------PPRDCHIDEHAAVLKSVSEVKEAVEQG---------RAGAEMVRDLGMHLFEWFPGHADYLDSALAAWM
>Caldicellulosiruptor saccharolyticus(Firmicutes; Clostridia) 138aa ZP_00885869.1  GI:82500456
----MSQIEWKEQYTL-GDEGFDEDIKKIVERMNKILHAYEQ-----PESQKDVLEELRFLGNNLAISFSHQEYRMKKYL---Y-----------PPYFSHKREHDSFLEKYKKYREEAGKE---------GELVAAVMKIRGIIEEWLENHVIVEDKKLVAFL
>Campylobacter coli (Epsilonproteobacteria; Campylobacterales) 199aa (1-127) ZP_00367250.1  GI:57168111
-----MLPKWDSSFSV-HNAKIDDQHKKLFELAAKVEIVSDRS------VSKNEVKELLAEFFNYMKDHFNDEEKYMQLIA--Y-----------PAFEEHKKIHKEIIQTMINLIKDIKST------------NDLKEKLYIIAKKWLLEHILYEDMKVEKWR
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Campylobacter coli (Epsilonproteobacteria; Campylobacterales) 203aa (1-127) ZP_00367884.1  GI:57168753
-----MFPKWDDNYSV-HNAKIDEQHKKLFELAGKVEFMFDRP------VYKDDIKALLADFFNYMKDHFNDEEKYMKLIG--Y-----------PGLEEHKKIHKEIIQSMIDLIKNIKST------------NDLKEKLYTVSKKWLLEHILYEDMKVEQYR
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Campylobacter coli (Epsilonproteobacteria; Campylobacterales) 229aa (1-130) ZP_00367885.1  GI:57168754
--MDKLIPAWDEKYSI-NDEKIDAQHQKLFELAAKIENAVYKF------VQRDELKEILTELFNYMKDHFSNEEDYMQEIS--Y-----------PYLNEHKIMHKNIIHDMSHLIQNIKTT------------NDLKEKLYTIMSDWLLEHILHHDVMIGNWL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Campylobacter coli (Epsilonproteobacteria; Campylobacterales) 268aa (1-132) ZP_00368169.1  GI:57169041
-----MEIKWSKDFSI-KNIQLDKQHELIFEITEIANDLALKI-QDNDVQHKNDLKQILTKLFQYVKIHFKDEEKFMESID--F-----------PLIEEHRKSHQILLKKTKELLEHSND------------IVKMSFELSTLTKDWILDHFANEDLWIANFT
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Campylobacter fetus (Epsilonproteobacteria; Campylobacterales) 183aa (1-127) YP_892819.1  GI:118474426
-----MIPVWDDKYSV-GNNGIDKQHKKLFELAKKSYIYANKN------ISREDIRNIITEFFEYMKEHFRDEEIYMELIE--Y-----------PYLEQHSSIHKDIINSMSNLIKTAKN------------VNDLKENLVIIAEKWLLEHILHHDTRIEEWR
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Campylobacter fetus (Epsilonproteobacteria; Campylobacterales) 385aa  (1-143) YP_891782.1  GI:118474590
MDYNKSIFAWSKKFET-NLDKIDDQHHHLVNLINNLSKKLSNS-----NLSKNELIGLFTELFGYAKYHFHDEEQLMAENK--L---------NSEFVKDHVFNHKLFIEEVGILFAGLQS----DDEDDQENLDKTAKYILNFLINWLAFHILGQDKKMARQI
>Campylobacter jejuni (Epsilonproteobacteria; Campylobacterales) 131aa ZP_01378037.1  GI:109690967
-------MTYSEKIISMNNDLLDHQHKELFEISKKLSLMNQRH------VGTKELKIVLRELLIMINRHFSDEEAFMREIE--Y-----------PYINHHTRIHRKIILEIEEIIISEAK-----------FVNIMTEKLNLVVQDFIFKHTAKEDSKIVKVL
>Campylobacter jejuni (Epsilonproteobacteria; Campylobacterales) 133aa YP_999954.1  GI:121612294
-------MTYNEKIISMNNDLLDHQHKELFEISKKLSLMNQRH------VGTKELKIVLRELLIMINRHFSDEEAFMREIG--Y-----------PYINHHTRIHRKIILEIEEIIISEAK-----------FVNIMTEKLNLVVQDFIFKHTAKEDSKIVKYY
>Campylobacter jejuni (Epsilonproteobacteria; Campylobacterales) 144aa  YP_999771.1  GI:121613643
-----MEVKWSRDFSI-KNMQLDKQHELIFEITNLANDLALNI-QDNNTQHKNDLKQILVKLFQYIKIHFKDEEKFMESID--F-----------PLIEEHKKSHQILVEKTKELLEHSDN------------IVKMSQELSILTKDWILDHFANEDLWIANFT
>Campylobacter jejuni (Epsilonproteobacteria; Campylobacterales) 199aa (1-127) ZP_01068960.1  GI:86150744
-----MLPKWDNSYSV-HNAKIDEQHKKLFELAAKVEVVSDRS------VSKNEVKELLAEFFNYMKDHFNDEEKYMQLIG--Y-----------PNLEEHRKIHKEIIQTMINLIKDIKS------------TNDLKEKLYIVAKKWLLEHILYEDMKVEKWR
>Campylobacter jejuni (Epsilonproteobacteria; Campylobacterales) 202aa (1-127) ZP_01069655.1  GI:86151450
-----MFPKWDDSYSV-HNAKIDEQHKKLFELAGKVEFMFDKP------VYKDDVKALLAEFFNYMKDHFNDEEKYMKLIG--Y-----------PDLEEHKRIHKEIIQSMIDLIKNIKS------------TNDLKEKLYTVSKKWLLEHILYEDMKVEQYR
>Campylobacter jejuni (Epsilonproteobacteria; Campylobacterales) 239aa (1-132) ZP_01072240.1  GI:86154039
-----MKVKWSRDFSI-KNMQLDKQHELIFEITNLANDLALNI-QDNNTQHKNDLKQILVKLFQYIKIHFKDEEKFMESID--F-----------PLIEEHKKSHQILVEKTKELLEHSND------------IVKMSQELSILTKDWILDHFANEDLWIANFT
>Campylobacter lari (Epsilonproteobacteria; Campylobacterales) 187aa (1-127) ZP_00368466.1  GI:57240517
-----MLPKWCDKYSI-HNKEIDEQHKKLFELAANVEMISDKP------IHKGQIKFLLADFFNYMKEHFAEEEKYMEKIG--Y-----------PELVNHQKIHKSIIQSMIDLIQNIKS------------TNDLKEKLNIIASKWLLEHILREDMKIEKWH
>Campylobacter upsaliensis (Epsilonproteobacteria; Campylobacterales) 199aa (1-127) ZP_00370672.1 GI:57242735
-----MLPKWDDSFSV-HNAKIDKQHKKLFELAAKVEMVSDKA------VSKNDVKDLLAEFFNYMKDHFNDEEKYMHLIN--Y-----------PELEAHRKIHKEIIQTMINLIKDIKS------------TNDLKEKLYIVAKKWLLEHILYEDMKVQKWR
>Campylobacter upsaliensis (Epsilonproteobacteria; Campylobacterales) 233aa (1-136) ZP_00371184.1  GI:57505255
---MNKKIDWTKEFSI-NNYALDKQHELIFDIAIRANELAKEVLEHYDDSLQEELKKTIVKLFDYIKIHFKDEENYMEID--F-----------PLLEEHKASHKFLVERTKEILNYSKD------------PQNFAKELAILTKNWIVKHFCVDDKWIDTYK
>Clostridium sp. OhILAs (Firmicutes; Clostridia; Clostridiales) 131aa ZP_01361119.1  GI:106893996
------MFWWSSELET-GITSIDEQHRTIFNRAGDFLSLDSS-------TDLQEIHRAFVFLMDYCINHFTEEEQIMMDAD--Y-----------ESLEGHRAQHNHLVDRLYELGNEIKD---------TGINEELIDQFKFLVIEWLVNHINESDKHLAKFL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Clostridium sp. OhILAs (Firmicutes; Clostridia; Clostridiales) 137aa ZP_01360922.1  GI:106893798
-----MIFKWKERFET-GIEEIDKQHKRLFEIGTQIYNLASK---DDGTDHYDAIVGLIHELKDYTVYHFRYEEEQLEKAN--Y-----------SDIEAHKMEHQRFIDKLNETEAEDID----------VNQKQVLMDMIEFIINWVSGHIVGTDFKYRELL
>Clostridium sp. OhILAs (Firmicutes; Clostridia; Clostridiales) 142aa ZP_01360653.1  GI:106893528
-------MLWKDKYEL-GVSIVDEQHKELFERVQAFMQVLRS--PASWEDKVQRVNETLEFMKIYVVEHFRDEEAYQKRIE--Y-----------PGYEAHKKIHGDMVNYVVQFSDEYEK---------SGCNEQLMQQFAGKLLAWLINHVASEDQRIADYA
>Clostridium acetobutylicum (Firmicutes; Clostridia) 129aa NP_346715.1  GI:15893366
------MFVWKDEFEL-GIDKIDNEHRKLFEIANKGYELLKN---EFYVDKYDKIMDIIVELKEYAEFHFSEEEDYLASIG--Y-----------KKLFTHKLEHDSFIKKVESFNIKEID----------YDQDKYIQEMLDFVVTWIKEHILEKDREYID--
>Clostridium beijerincki (Firmicutes; Clostridia) 129aa ZP_00910041.1  GI:82747545
------MYEMKEEYKI-GIDQIDEQHKKLFELADQAYTLLKD---EFAIDKYDKIIHIMDELKDYTIFHFKSEEEYMKSIN--Y-----------KRLFTQKIEHDKFIKSLEEIDYKNID----------ENQDESLIKLLNFLNDWLTEHILKTDKLIGE--
>Clostridium beijerincki (Firmicutes; Clostridia) 129aa ZP_00911352.1  GI:82748877
------MYEFKEEFKT-GIDFIDEQHKVLFEIADKAYNLLKN---DFTTDKYDNILELVDELRDYTSFHFKAEEEYMNKIN--Y-----------KRMFTQKIEHDAFIKRINEVDFRSID----------ENQNESISTLLQLLNDWLIEHIFENDKLIGQ--
>Clostridium beijerincki (Firmicutes; Clostridia) 130aa ZP_00910329.1  GI:82747836
------MVKWKADYEV-GVKLIDEQHEKLFEIADRAYKLLTN---DFILDKYDRITEILGELKEYTIFHFKSEEEYMLSVG--Y-----------KKFLSHKVIHEDFIKSIDNLDLHEID----------LNQDESVKKILEFVVDWIDKHILNEDKFIVEN-
>Clostridium beijerincki (Firmicutes; Clostridia) 133aa ZP_00908279.1  GI:82745769
-----MDLIWDKMWSV-GVDKIDRQHKELFNRINLLVCSMKS------AKGKEEMITTLNFLEEYVIRHFNDEEEIQKKNN--Y-----------PNYEIQHKEHEIFKNNLKELRKVFET---------TGVSTLFVISEQQKMSYWWRKHVIELDKDIGKFL
>Clostridium beijerincki (Firmicutes; Clostridia) 135aa ZP_00909310.1  GI:82746807
-----MNLNWDNNLAT-GIVNIDNQHKELFDRINKLLIAMKE------GKGKDEVIGTLNFLEDYVIKHFTEEEEIQKKNN--Y-----------PKYSIQHKQHEEFKEELKELRRTFET---------TGTSALFVIKVQNRMSTWWKSHIRDLDKDLGKFL
>Clostridium cellulolyticum (Firmicutes; Clostridia) 130aa ZP_01574112.1  GI:118725472
------MIEWRDEFIL-GIEKIDEQHKKLFQIASEIYEATKN---QLITDKYDEIVRLITELKDYTVFHFTYEEEYMHSIG--Y-----------RKLLSHKVEHHDFIEKISNTDYSRID----------KDQDQYLMELLDFTVEWIANHIMKTDKAYTIK-
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Clostridium cellulolyticum (Firmicutes; Clostridia) 132aa ZP_01576604.1  GI:118728026
-----MAIKWRDSLAI-GITEIDDQHKKLFEAIDKLFTACVQ------GKGKEEVVNTIKFLEDYTIVHFNDEQEMHKKYN--Y-----------PERDAHRKIHDNFLNSFSKLKEQFEQ---------EGAGPLFISTINKQVVDWLIQHIGKADKAFAAYV
>Clostridium cellulolyticum (Firmicutes; Clostridia) 185aa (44-181) ZP_00909308.1  GI:82746805
VLMHFMNSNWDAVLST-GVDNIDRQHQELFRLINNLVSAMN------EEKSKVEIIKALDSLEEHAIRHINEEEAIQKENN--Y-----------PGLEIQQMQHEEFKECLRDIRSFLET---------REISTLFIIHMQQKIFKWCRKHMLNADKDLGEFL
>Clostridium phytofermentans (Firmicutes; Clostridia) 129aa ZP_01353421.1  GI:106886073
------MFEMKPEYMT-GITMIDEEHQKLFELADQLYDLLN---NDFIHDKFDYIVEVINGLKEYAKKHFKDEEEYMMSIN--Y-----------KRLFSHKIEHQAFLEKMEGLDLESID----------EDQKQTCLELLGFVSDWLVNHILGNDILIGK--
>Clostridium phytofermentans (Firmicutes; Clostridia) 143aa ZP_01354048.1  GI:106886715
--MFDFAFDWIKELET-GDELIDQQHKEFFRIGRDIEQLLV---RKCIGVQEQELLDIVCELREYVSYHFYTEETIMRQKG--Y-----------SNYELHVKEHLGFRKYVMEIDCPALA----------KNPYKELKAIKTMIQSWVFNHMMSEDVRMINEI
>Clostridium tetani (Firmicutes; Clostridia) 137aa NP_782896.1  GI:28211952
------MFNWKEDFSC-NIASIDAQHKKLFELANELYNLLS---LKDEYDRYDDILNTLSELQKYTVYHFGYEEDLMKSVN--Y-----------PNFECHKKQHDNFVKKVTNIDKAYID----------ENQKEVLRDLLLFIVDWIEGHILKIDMQYKELF
>Clostridium thermocellum (Firmicutes; Clostridia) 129aa ZP_00504934.1  GI:67875718
------MYEMKPEYFT-GIDFIDKEHARLFAIADEAYQLLK---NEFIPDKYDHIMNLVNELKDYTQYHFKHEEEYMESIG--Y-----------KRLLSQKVAHEDFIQKINEYTPDVID----------ENQKETLLELLDFLATWLVEHIYKQDKLIAE--
>Colwellia psychrerythraea (Gammaproteobacteria; Alteromonadales) 131aa YP_268476.1  GI:71281331
----MTQVIWQDSYSI-GIDTIDTQHKQLFDIMNKIYVAS------EEDSDIDVIMPLFDELQDYTKYHFDEEEQYFTT----L---------SQGGIEQHKSEHQFFIDELDKIKQQSLR------------IGTISLELLYFLNDWLVNHIQVEDPKYLDHD
>Colwellia psychrerythraea (Gammaproteobacteria; Alteromonadales) 192aa (59-182) YP_270886.1  GI:71279092
KQKHIKQIKWSKEYSIG-IEYIDQDHKKLLHLLNQFSIAFD------YAQCEEFEREALEELVSYTKYHFKREEKLMEDYG--Y-----------PGLAEHQEEHQAMIDKVEEYVAIYNI-----------EGHDSLKQVTNLLTYWLINHIQESDTQYRDYL
>Colwellia psychrerythraea (Gammaproteobacteria; Alteromonadales) 188aa (50-182) YP_270871.1  GI:71282489
KKSNPKQVQWREEYSV-GIAHIDDDHKKLISLLNNFSIAYD-----YAMSESFEKEALNELISYTKYHFEREEKMMEDND--Y-----------PDLIAHKAQHKVMIEQVEKFVQLYND-----------KGHDALEEIASFLTDWLINHINGTDKQYSAHL
>Colwellia psychrerythraea 34H (Gammaproteobacteria; Alteromonadales) 368aa (1-132) YP_268475.1  GI:71280761
----MKTFIWNSNYET-GVAKVDDQHQCLVEIINEYSHLLA-----NNTTTETDIELTLNKLIDYTKFHFKDEEQLMYSVG--L---------DTRHITHHEKLHRDILDEISTLLSDQVT-----------DKLSIARYILDLIIHWLVYHILGTDMNMAKQM
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Colwellia psychrerythraea (Gammaproteobacteria; Alteromonadales) 519aa (382-510)  YP_271339.1  GI:71280063
KVADKVGIQWIAEYSI-GNIEIDEQHKVLFTMINDFFHQDN----------KEAAIMLFQSLSSYIDLHFESEENLLRQIN--Y-----------PDTEEHIKKHGELREKFHLLRGKLDD-----------YDLDVHHKIAMFLYNWLAKHILKADMEYKSYA
>Colwellia psychrerythraea 34H (Gammaproteobacteria; Alteromonadales) 722aa (1-123) YP_270299.1  GI:71279208
--------------MSVGIDSLDNDHKKLIAILAQLMSAKN------EKLGQDDIDVIFERLEGYCLSHFAREEALLAKID--Y-----------KQLEAHKLSHQAFIKKIPQLKEQWFA--------KVTESEAVKDKIILFLQQWLIKHILEEDLDYVPAI
>Colwellia psychrerythraea (Gammaproteobacteria; Alteromonadales) 1328aa (1175-1306) YP_268669.1  GI:71280946
KSSPIKRIIWTNEMSIDDGGELDEDHKFMFSLLNRCQELLE------EQDDHQSAQAIITEIVQYTQDHFVNEELLMNNIN--Y-----------PYAKNHCDVHRMIAKQLSKKVLVCSD------------KEILRWLITDMSTWLVEHIMEMDKPLHKYI
>Comamonas testosteroni (Betaproteobacteria; Burkholderiales) 165aa (1-124) ZP_01520527.1  GI:118051979
----MASLEWNAALIL-DFPVMDAVHEEFVALLAQVEAAAD-----------EQLCALWDELIAHTQQHFDQEDRWMQTTG--F-----------ATGNCHSQQHKVVLAVLREGAVKGEQ-----------GDLATIRHMAAELGPWFSHHAQNMDAALALHM
>Comamonas testosteroni KF-1 (Betaproteobacteria; Burkholderiales) 179aa (37-127) ZP_01521540.1  GI:118052994
PKSTEQPPLWSEALLL-GQVPIDDEHERLAWLIERMQRASA-----------SDMAQALEAVIAHAASHFAAENELMVGTQ--F-----------PPRDCHIREHDAVLSTLRGVLRRLDC----------SDEISVAYRLADELAAWFPAHVQHLDSALSHWL
>Comamonas testosteroni (Betaproteobacteria; Burkholderiales) 211aa (37-167) ZP_01518696.1  GI:118050146
LENIMALLVWVPELDT-GIAEIDRQHRRIVDYINRLYELRS-------SPDREGLGDVIGEMIDYTVSHFVFEESLIESAG--Y-----------MFAGPHKKVHELFTRRVIEMQTRFDA------------GEDVAAELHGMLSRWLFNHIRNEDHGYVDSA
>Dechloromonas aromatica(Betaproteobacteria; Rhodocyclales) 125aa YP_284639.1  GI:71907052
-------MVWDETRHALGVPEMDGTHREFVELAYALLVASD-----------EEFPALFVRLHEHTRQHFEHEGKLMKACR--F-----------PAIGEHNSEHLRVLGELAHFSRGVAA-----------GRLGMARNYVRALPEWFATHLATMDSALAGCL
>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 127aa YP_285883.1  GI:71908296
----------MNKNLLLGVPNIDHQHRELFRSFQHLLSINS---------GDESFSEALSRLTIQIHQHFKTEEHYMAGLH--M---------PAAELAEHVLAHTQIIEDLTEIHFETMH-----------GLGVPFEEIIKRVASYVNHHVVEFDLQLKPYI
>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 128aa YP_284878.1  GI:71907291
---------MTISILKTGHAEIDRQHAELLICLAGVKEFVG------GQYAFSAGFTAIQALIGYTEDHFAFEEGLLRQWD--Y-----------PDLDAHVEQHKSLVAEVRRQWGRVEQ-----------EGADIAREVVETIEGWITDHINVEDRKFSGVV
>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 133aa YP_284887.1  GI:71907300
---MTHSPTWSDDLSV-GNYLIDGQHKRLVSLCARAADCAS----ATSPEALREFHNILNDLAKLTDEDFKDEEVLLIKNG--C-----------PNVEAHIAEHNVYREMVVNLLFDGTA------------GLLDRAKLYHVANDYLTKHIIEMDLADKAYL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 134aa YP_284625.1  GI:71907038
---MTQPREWSGALSV-CNRWIDEQHRQLIDLCNKAEACAA----LSSHEAHREFHLLLNDLATLVGNHFRDEETLLA-----I--------HESPNLDAHKAAHVSFLERLTQLLYDGAR------------GLIDSRTLHRLIADYLIEHMLEMDMQEKHYL
>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 142aa YP_286895.1  GI:71909308
-----MRIRWSSDLET-GIRAIDLQHEELIGMLNELDAAYS------GGCEQFVLDSVLQRLGAYAEFHFGTEESLMAT----L-------PRSEQHAEEHLRQHRGFIEQLSRMRAASSQ-----------DAPQTMGILIDFLNEWLYEHILKSDRNLGALL
>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 146aa YP_285962.1  GI:71908375
-MDEQQGFAWDDRYLL-GHSAMDDTHREFVALVDALLTVEA-----------DGLEAALADFARHAEAHFDQENRWMELDG--F-----------PARDCHVDEHNKVLASVREVQLELAE-----------GNVQLVRELAVALMDWFPAHADYMDSALSTWL
>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 160aa (1-126) YP_284835.1  GI:71907248
-----MPITWDSRLDT-GIDVIDAQHKRIVDYINDLEIAKI-------KGDKVLTMEVIEQLIDYTQSHFGFEESMLEEAG--Y-----------KFLKPHKKVHELFIKRVTEFTMRAAK------------GEDIADELHSMLAKWLLNHIANEDRDYSDTV
>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 161aa (10-140) YP_284552.1  GI:71906965
GEHQKSKIQWSDNLLV-GHSGIDETHREFVTLANALSESCE-----------ESAPTRLHQLEEHLMSHFDNEKLLMEKTE--F-----------PATDCHIEEHAKVFDAVVLVRERYSD---------GTASLNDIKRLAQALIDWFPGHIFYMDSALSTWV
>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 667aa (529-661) YP_287152.1  GI:71909565
SEKKNQSDWIVFESGHLVGVKIDEQHQELVRMVNKINRAIH------SRCEDASLKLMFNELVAFTEHHFSTELRFMIDFH--Y-----------PETDVHDQQHQALVAQLSNLITRFEQ--------------GDELQSLQMIKDWLLRHIEHADKPLGAYL
>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 681aa (1-129) YP_284191.1  GI:71906604
----MDAFVWNERYMT-GEAQVDEEHQELVRIINWVIEHQS------VPAQDDDIQRVLASLANYAVMHFGHEEELMEQMH--C---------DPRFIQAHVAVHQEFARQVGKMLEFQGG------------KADVEYLLRFLSSWLAHHILGIDQSMARQI
>Delftia acidovorans (Betaproteobacteria; Burkholderiales) 166aa (1-124) ZP_01580041.1  GI:118731526
----MAVLEWSGALAL-ELPAMDEVHQEFVLLLAEVEAADD-----------AQLCARWDELIAHTQVHFDQEDRWMQSTR--F-----------TSTNCHSLQHKVVMQVMREGAAKAVAG-----------DLAVIRSMAGELAAWFVHHAQTMDAALALHL
>Delftia acidovorans (Betaproteobacteria; Burkholderiales) 213aa (40-170) ZP_01578319.1  GI:118729802
LENVMALLVWVPELDT-GIAEIDRQHRRIVDYINKLYELRS-------SPDREALGDVIGEMIDYTVSHFVFEESLIESAG--Y-----------MFAGPHKKVHELFTRRVIEMQTRFDA------------GEDVAAELHGMLSRWLFNHIRNEDTGYVDSA
>delta proteobacterium MLMS-1 (Deltaproteobacteria) 135aa ZP_01288141.1  GI:94264349
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----MALFTWKEEYSV-NIKEIDDQHKQLVAMVNELHEAMM------QQRAKEVLSSILNKLVTYCGTHFALEERLMQTHG--Y-----------PEYASHKAKHDKMTAKVVSLQNDLKS-----------GKANLTIEVSQFLKDWLDKHILGTDKKYSAHL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>delta proteobacterium MLMS-1 (Deltaproteobacteria) 148aa(10-142) ZP_01288112.1  GI:94264319
LNTKMAIYSWQDEYSI-GIKEIDEQHKELVKMIDELYTAMV------KRQDQQVLGDILARLVDYCNVHFAAEEALMQSHG--Y-----------PYYRQHKEIHEKMSARVQALQKCFKA-----------GKTDLTIPTSLFIKEWLDKHILGTDQKFATFL
>delta proteobacterium MLMS-1 (Deltaproteobacteria) 296aa (150-284) ZP_01291413.1  GI:94269245
GGAIEPAVVWNEEFEV-GVEVIDRQHRELISRINRMLAAIR-----QGKGHDETISLVRFLQDYVVEHFQSEEIYMRRHH--Y-----------PDYDAHKEIHDTFVAELAGLVEELEK---------HGIQPEQVVQIHRRVINWVVDHIFLTDKALRHIK
>delta proteobacterium MLMS-1 (Deltaproteobacteria) 457aa (310-434) ZP_01290755.1  GI:94267120
GGAIEPAVVWNEEFEV-GVEVIDRQHRELISRINRMLAAIR------QGKGHGETLSLVRFLQDYVVEHFQSEEIYMRRHH--Y-----------PDYDAHKEIHDTFVAELAGLVEELEK---------HGIQPEQVVQIHRRVINWVVDHIFLTDKALRHIK
>Desulfitobacterium hafniense (Firmicutes; Clostridia) 135aa ZP_01371607.1  GI:109647704
------MLKWKDEYSI-GVEEIDEQHKHLFEIGNEIYDLLE---NYLLPDKYDKIIQIIAELKEYTVHHFQTEEELMLKIK--Y-----------PGYFKQKVAHDDFIKEVESVDFSAID----------QDQDGHTRKLLEFIFGWVLDHILKSDLGIKSFM
>Desulfitobacterium hafniense (Firmicutes; Clostridia) 139aa YP_517407.1  GI:89893920
-------MIWKEKYKV-GDPLIDSQHEELFSRVGSFVETLR--SDKPWEQKVEKVNETLEFMKDYVVTHFADEEAYQLEG---Y-----------PHFEEHQMIHKNMVAYVVAVSREYAK---------EGFKEELMQQFGGKLLAWLINHVVADDQKIAEYA
>Desulfitobacterium hafniense (Firmicutes; Clostridia) 144aa YP_516471.1  GI:89892984
---MIVMLKWKDEYSI-GVEEIDEQHKHLFEIGNEIYDLLE---NYLLPDKYDKIIQIIAELKEYTVHHFQTEEELMLKIK--Y-----------PGYFKQKVAHDDFIKEVESVDFSAID----------QDQDGHTRKLLEFIFGWVLDHILKSDAILALRV
>Desulfotalea psychrophila (Deltaproteobacteria; Desulfobacterales) 156aa YP_065523.1  GI:51245639
----MAVIKWQDTYNT-GVEHFDGEHQQIVELIDLMFFTLR------DRSGKDVTEEACKEIISYTEQHFIREEQAMRAVA--Y-----------PYLEEHIAEHSRLKAEMLKLQRGISN-----------NFPKGAAKFYRFIHKWFIIHIQEMDKKYAPYC
>Desulfotalea psychrophila (Deltaproteobacteria; Desulfobacterales) 370aa (1-140) YP_064708.1  GI:51244824
----MKTFIWDENFTT-GISDIDKQHHHIIDIINEFAFAFS-----QNSINKDFILRVSKELTTYGVDHFKTEEEIMLAAK--L---------DPRYTSKHIAAHNDFSQEIEAITANLGL-----------TDKENFRQILNFLIHWLSYHILNDDQSMARQI
>Desulfotalea psychrophila LSv54 (Deltaproteobacteria; Desulfobacterales) 374aa (1-134) YP_065775.1  GI:51245891
--MFMKTFIWDKTFTT-GISKIDEQHHHIVEVINKFVFAFS-----ENTIDKDFILHVSKELMDYAQNHFKTEEKIMLAEK--L---------DPLFISQHIDTHNAFSQQIKIFTTNPDF-----------TNHNFFRQILAFLIHWLDDHILNIDQSMARQI
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Desulfovibrio desulfuricans (Deltaproteobacteria; Desulfovibrionales) 150aa (9-142) YP_386749.1  GI:78355300
AEKHMRQLELKDSMKI-GIKELDDQHQQLTEIINELYYAYMQ------GNHRAVLCGLITRLNDYAHEHFALERQYMERFV--F---------EMPDYEQHMQEHREFFTDAIGFLLRYIE-----------EGSEITPEMLDYLQGWWKDHVMVRDKELGRFL
>Desulfovibrio desulfuricans (Deltaproteobacteria; Desulfovibrionales) 579aa (441-573) YP_386930.1  GI:78355481
STGDGQFLNWTDDLSV-NIGHLDSQHKNLVALINELAAAMK------AGKAKSVMLDTLGRLKEYTLTHFKEEEDLFDRYD--V-----------PGARDHKKIHQSLREKVLSVEQDIVS-----------GRITVSLELLEFLKEWILNHIQVVDKQYSAFL
>Desulfovibrio desulfuricans (Deltaproteobacteria; Desulfovibrionales) 722aa (584-716) YP_389304.1  GI:78357855
TADTGQLFRWTDDLSV-KISSIDEQHKGLVNLINELHEAMR------RRKSASHLIAIVGRLKDYTVYHFDTEEKLFHKHG--Y-----------PATAEHIQEHRKFVENVLAFEKDLQQ-----------GKVTVTMDVMRFLKNWLTGHIKGTDKKYSGYL
>Desulfovibrio vulgaris (Deltaproteobacteria; Desulfovibrionales) 136aa AAF23777.1  GI:6685084
-GDADVLVKWSEDLA--NLPSIDTQHKRLVDYINDLYRAAR-------RRDMDKAREVFDALKNYAVEHFGYEERLFADYA--Y-----------PEATRHKEIHRRFVETVLKWEKQLAA-----------GDPEVVMTTLRGLVDWLVNHIMKEDKKYEAYL
>Desulfovibrio vulgaris (Deltaproteobacteria; Desulfovibrionales) 137aa YP_389304.1  GI:78357855
----MATFTWDASLDV-GIPEIDAQHREMTDIIATLHEAYR------AGRERDVLAELINRINEYAQMHFATERRYMEPVAD-A----------IPNYEKHMQEHREFFSDAIGFLLRYLD-----------NGATITPELLDYLAEWWFRHIRGTDQVMGRVL
>Desulfovibrio vulgaris (Deltaproteobacteria; Desulfovibrionales) 655aa (513-635) YP_012317.1  GI:46581509
ALSGVQRLVWSEDYAC-GEPRIDASHRALLAKADSIMSSLG------GADGLNARRACILALVDAVRMHFREEERVLAAIG--Y-----------PKAGEHAVIHEALLQRGASLVAAWER-----------GGMSLDDVVITLVHGMVMRHMLDDDSAFFEHV
>Desulfovibrio vulgaris (Deltaproteobacteria; Desulfovibrionales) 689aa (550-682) YP_009395.1  GI:46578587
AGGGDKLFEWDDALNI-GVADVDPQHKVLVDLINEVYAAMK------AGADRSVLQDIVRRLREYTVKHFTYEEGVLHTSMR-Y-----------PDMQAHLKQHRAFVERIAQFEEALGS-----------GRVTLDMEMMRFLKNWLKQHIMGTDKKYVPYF
>Desulfovibrio vulgaris (Deltaproteobacteria; Desulfovibrionales) 959aa (823-953) AAB50497.1  GI:887858
TGDADVLVKWSEDLAN--LPSIDTQHKRLVDYINDLYRAAR-------RRDMDKGTEVFDALKNYAVEHFGYEERLFADYA--Y-----------PEATRHKEIHRRFVETVLKWEKQLAA-----------GDPEVVMTTLRGLVDWLVNHIMKEDKKYEAYL
>Desulfovibrio vulgaris (Deltaproteobacteria; Desulfovibrionales) 963aa (827-957) YP_012365.1  GI:46581557
TGDADVLVKWSEDLAN--LPSIDTQHKRLVDYINDLYRAAR-------RRDMDKAREVFDALKNYAVEHFGYEERLFADYA--Y-----------PEATRHKEIHRRFVETVLKWEKQLAA-----------GDPEVVMTTLRGLVDWLVNHIMKEDKKYEAYL
>Desulfuromonas acetoxidans (Deltaproteobacteria; Desulfuromonadales) 132aa ZP_01311722.1  GI:95928977
----MTFVTWNDDFLL-HVDQFDEHHKHLVDLLNETYEKFV------NKTVDLSLEKLFDELIDYATYHFSAEEYWMQAKQ--Y-----------PGYEEHKKEHAYFTKRVVEMHRDFVA-----------GNTSLGLEVLTFIKNWVANHILNSDAEYGRFI
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Desulfuromonas acetoxidans (Deltaproteobacteria; Desulfuromonadales) 133aa ZP_01311940.1  GI:95929196
----MAFIEWNQNFAV-NVDQFDDHHRHLIDLLNKTHDQIT------RRLEKEKLGLVLVELIEYAKYHFRAEEVWMKNLD--Y-----------PKLKQHCAEHHYFINRVQEMCEDYNS-----------GNTALAQELLSFMKNWLSSHILGTDREYSRFI
>Desulfuromonas acetoxidans (Deltaproteobacteria; Desulfuromonadales) 142aa ZP_01313281.1  GI:95930546
----MATITWKSCYET-GNPTFDAEHRALVNALNDLYEAIR------KKQGDEVLASLLSTLNLYIRKHFQHEEQAMLKHH--Y-----------PGMEAHIKAHRAFKKTVNDYQEQVLT-----------GYTGLASDLYKYLRDWLLNHIVKTDGQFGEFL
>Desulfuromonas acetoxidans (Deltaproteobacteria; Desulfuromonadales) 199aa (35-159) ZP_01313282.1  GI:95930547
KGRRVYVVEWKDAYSN-GIDEVDDQHKHLFFLVKCLRLETI--------------EKTLDDLADYVFSHFSTEQGLMDESE--Y-----------PDRDRHRQIHDQFVSTVAECIADDAP-----------WDDERLHDLRKFLNKWLIGHIMTDDQQFGRWY
>Desulfuromonas acetoxidans (Deltaproteobacteria; Desulfuromonadales) 368aa (1-131) ZP_01313679.1  GI:95930950
----MDVIVWNKNFET-GLAEVDKQHRHLVEITNRFGQILS-----DKNALCKEMEEIFTELVSYTQYHFSEEEHLMESTG--I-------------DSRHIAYHKNEHASFLQSVLHLYG--------ESKLGRDTGKPLFEFLMNWLVYHILGSDRTFGEQV
>Desulfuromonas acetoxidans (Deltaproteobacteria; Desulfuromonadales) 371aa (7-134) ZP_01312822.1  GI:95930083
-MIYMDVIVWNENFET-GLDDVDQQHRHLVEITNRFGRILF-----DKNALCKEMEEIFAELVSYTQYHFSEEENLMETIG--I-------------DERHVDYHKNEHASFLQSVLHLYG--------ESKLGRDTGKPLFEFLMNWLVYHILGSDRSFGEQC
>Desulfuromonas acetoxidans (Deltaproteobacteria; Desulfuromonadales) 591aa (2-127)ZP_01313525.1  GI:95930793
HLDKIEIFPWDKNFDT-GILEIDRQHQRLVELLNLLVSHLA------FQSQAPTLNTIFDELKSYALIHFKTEEEIWHKA---L--------DDDPWVIDHQETHAQFVVEVKRLKGEKSD----------RCFDDVVADIVAFLTNWLALHIIDTDKRLAKAV
>Desulfuromonas acetoxidans (Deltaproteobacteria; Desulfuromonadales) 1174aa (1032-1164) ZP_01313825.1  GI:95931099
SINNVLQLSWSDKFCC-GHETIDEQHMGLFALGNELIEAFL------MRQDKRLVDDKLEELYKNTCDHFSFEEQLLEEVH--Y-----------PNVVEHRQEHRHMEEKLVSLIEIYQQ-----------NRADYSELLHYISIDLISGHLLCTDNDYFAYL
>Endoriftia persephone (Gammaproteobacteria) ref|NZ_AASF01001681.1
--------VWKESYSV-GIAQIDDEHRRLIELLNKFQAA------YKYHMGEEFEQQALKALVDYTKYHFKNEESLMQKYD--Y-----------PDFNGHVEQHRAMIAEVDSFVRQYEEK-----------GHEALEGVVLYLQGWLIKHINGTDKQYSSFL
>Geobacter sp. FRC-32 (Deltaproteobacteria; Desulfuromonadales) 132aa ZP_01390530.1  GI:110602439
----MQLVKWDNTLTL-GVEPFDDHHKHLVCLLNETYDLFI------AGEKPSSLEEVIDELIDYATYHFSSEELWMVKLN--Y-----------PKQEEHKKQHEEFSSRVVNFQRDLIQ-----------KGSTSTLEVLSFLQRWLVEHIKHSDGEYSRFI
>Geobacter sp. FRC-32 (Deltaproteobacteria; Desulfuromonadales) 135aa ZP_01387533.1  GI:110599293
----MSLITWNQSLSV-NVKQFDEQHKKLIDLINKLHDAMK------AGKGKDVLGEILQSLVDYTKQHFAAEEALLQKHG--Y-----------GDYEKHKKEHNLLVMQVADIQKKLKE-----------GSPVLTQTVMTFLKDWLSNHIQREDQKYGPFL
>Geobacter lovleyi (Deltaproteobacteria; Desulfuromonadales) 135aa ZP_01593656.1  GI:118745688
----MALLLWGPMLEV-GVKEIDTQHRKLVDLANELSDAQM------AGKAKDVLGKTLSELVRYTVTHFSTEERLMDQHK--Y------PAAQKGVKVDHKQQHKDLVKTVSDFKAKFDK-----------GDAALSQEIMHFLRDWLTKHIMNTDKAFARDL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Geobacter lovleyi (Deltaproteobacteria; Desulfuromonadales) 137aa ZP_01594022.1  GI:118746066
-----MGITWREDLAI-GVDQIDDQHKELLARFDLLLSSCK------EGKGREEVLHLLTFLDDYVISHFSDEEKLQKQSG--F-----------PEYESHHAEHVSFIARLAELKERMRS--------EGGVQIDHVLDTNKLLLDWLLRHISVRDRALGRHL
>Geobacter lovleyi (Deltaproteobacteria; Desulfuromonadales) 147aa (1-130) ZP_01593713.1  GI:118745747
MSSYSPLNTFGYVATQ-HLMPYDSRQARLISVLDAIIATAD-------QVPSAELEQQIEDLLGNVLGQTASENVHMFTID--Y-----------LAYEDHKLDHFRICTTIAGIRCKAAR-------------ALCIDDDLQTLRKLLSLHIDKHDQMLEQYL
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>Geobacter lovleyi (Deltaproteobacteria; Desulfuromonadales) 147aa ZP_01592161.1  GI:118744164
-----MGIYWRKELEI-GVIEIDKQHQSLVESFNAFLLACR------NGKGSSELLELLKFLDEYALHHFHTEEAIQKAAA--Y-----------PEYESHRLQHLGFTKKIKDLKEQLTL--------NEPPQINHLIATNTVLLDWFIKHISGSDSHFGRHL
>Geobacter lovleyi (Deltaproteobacteria; Desulfuromonadales) 518aa (379-512) ZP_01593682.1  GI:118745715
HFKLANALVWDDSFAT-GVHRYDEQHKVLFRMVNDLHDAMQ------QKRTKEAIGEILRGLADYTVNHFADEEKVFAQTR--Y-----------PDEANHKLLHKALVDQVVALIGKFQS-----------GETVLSQDVITFLQKWLIDHIKGQDKKYGPHL
>Geobacter lovleyi (Deltaproteobacteria; Desulfuromonadales) 768aa (620-753) ZP_01594207.1  GI:118746259
ASRSIIRLAWKAEYLS-GEPGIDAEHQQLFRMANQLFEQAA-----SQKSDPAGFNAALDDLLQHVTSHFDNEEALLRRIG--Y-----------SELEEHVRQHSQLKEQAVSLRQVADK-----------REISTGELVDFLAIRVVHEHLLEADRNYFPLL
>Geobacter metallireducens (Deltaproteobacteria; Desulfuromonadales) 135aa YP_386060.1  GI:78224313
----MALITWNDSLSV-KVKQFDDQHKKLVEMLNQLFDAMK------AGKGSLVVGDILKQLIAYTQTHFAAEERLMTQYG--Y-----------ADLEIHKKEHNALVVQVLDLQKQFQD-----------GKAVLTQNVMTFLRDWLSKHIQGDDKKYGVFF
>Geobacter metallireducens (Deltaproteobacteria; Desulfuromonadales) 155aa (12-146) YP_383801.1  GI:78222054
TFQFRESCMWTDDLAV-GIDEIDSQHKALFEQLDKLLDACV------AGGEREEVVTMLCFLDQYVVAHFSAEEKLQQEYG--Y-----------PGYEKHRAEHEEFMRRINRFVEEVAA---------AAPTRDLVLRVNQTLIDWLKFHILAVDKEMSEFL
>Geobacter sulfurreducens (Deltaproteobacteria; Desulfuromonadales) 131aa NP_953971.1  GI:39998020
-----MAIGWRDDLLT-GVVEVDDQHKELFRRFGELLTACN------QGKGGEEVLRLFNFLDDYVVKHFAAEERIMRQHG--Y-----------PDYLEHKQQHQGFTRRLEELKRQFRD---------EGAGLSLVITTNHVMIEWLSRHIEKMDKEIAKYV
>Geobacter sulfurreducens (Deltaproteobacteria; Desulfuromonadales) 134aa NP_952095.1  GI:39996144
------MVVWKDEYLI-GVEQVDRQHRELFARFHRLMDALT------GGTARHELLETIAFLESYAENHFREEESLQQECH--Y-----------PDAGFHRMAHETFRRQLGDITASLAE---------QGVTNLLVIETGRTLFQWLVDHVCGMDREFASYL
>Geobacter sulfurreducens (Deltaproteobacteria; Desulfuromonadales) 135aa NP_951461.1  GI:39995510
----MALISWSDSLSV-KVKQFDDQHKKLVDMVNQLFDAMKA------GKGNQVMGDILKSLIQYTQTHFAAEERIMKQYG--Y-----------PDFEAHKKEHNALVMQVLDLQKQFQE-----------GKAVLTQNVMTFLRDWLSKHIQGDDKKYGVYL
>Geobacter sulfurreducens (Deltaproteobacteria; Desulfuromonadales) 139aa NP_953680.1  GI:39997729
--------MWTDDLTV-GIWEIDTQHRALFAQLEKLLDACMV------GRELEEVMEMIVFLDGYVDTHFEAEERLQREGG--Y-----------PEYEKHRAEHLIFRTNLERLKAELVE---------SGATRDLVLRVNQVLIDWLKTHIRNVDAAMSEFL
>Geobacter sulfurreducens (Deltaproteobacteria; Desulfuromonadales) 145aa (11-142) NP_951317.1  GI:39995366
NKASQKFIVWQDSYSV-GVPKLDGQHKKIIDLINEVYDYLQG------RTGLLDLGRILDDLSTYTQNHFADEEQLLRLAK--Y-----------PEYEEHKKHHDWMMQRTRSIRSEYRE-----------KREDLSWELMDFLKKWWLSHIQSNDARYVPYV
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Geobacter uraniumreducens (Deltaproteobacteria; Desulfuromonadales) 135aa ZP_01143645.1  GI:88938143
----MALITWNDSYSV-KVKQMDEQHKKLVEMINQLHDAMKV------GQGKQVVGDVLNALVSYTKTHFANEESLMKTYG--Y-----------PGYEDQKKAHANLVGQVGDIQKKFLD-----------GNAPLSQDVMTFLKEWLVKHIQGADQKYGLYF
>Geobacter uraniumreducens (Deltaproteobacteria; Desulfuromonadales) 138aa ZP_01140038.1  GI:88934395
-----MSIEWNNNLAT-GVAEIDNQHKELFSRFDSLLSACNE------GKGRDEVLRLLLFLDDYIKSHFAAEERLQLRHN--Y-----------PGYDAHKAQHTRFTEDVDRLESQFRR---------EGATLPLVIQTNQTLVAWLIQHISRIDMEFAAFL
>Helicobacter hepaticus (Epsilonproteobacteria; Campylobacterales) 184aa (1-128) NP_859535.1  GI:32265503
-----MLPEWSDDFSV-HHQIIDEQHQKLFALAHRAYNIANN-----NKSLASDVKNILIEFFDYMKTHFKDEEEYMKAIG--F-----------PQLEEHKKIHRQIVNDMAGMVKNVHS------------VDVLKEMIATIAKDWLLTHILQEDMCYEKYR
>Helicobacter hepaticus (Epsilonproteobacteria; Campylobacterales) 187aa (1-127) NP_859536.1  GI:32265504
-----MLPRWSDDFSV-HHQIIDEQHQKLFALAHRAYKAANG------HVAVNDIKNILIEFFDYMKTHFKDEEEYMKAIG--F-----------PQLEEHKKIHRQIVNDMAGMVKNVHS------------VDVLKEMIATIAKDWLLTHILQEDMRIEKYR
>Hydrogenobacter thermophilus (Aquificae; Aquificales) 131aa BAF34936.1  GI:116234997
------MVIKRADLPQVANSIMNALHEDEIEIINELYEACQK-------GNMERIDELMELLLYDIEEHFLTEEELMREAEF-F------------AYPMHKAEHDGMRKEVKALMESWKK---------NREAQEISNFIKDRLVPWLILHIARWDSTTAIHL
>Idiomarina baltica (Gammaproteobacteria; Alteromonadales) 566aa (429-560) ZP_01041958.1  GI:85710897
LAQQEKLIEWSSQFDV-GIEEINRQHQRLIYIANELYRIQQR------GGDRQAVERLLSSLINYTATHFSYEELLMERHD--Y-----------PDLDAHKHHKHQQLVQQVVDFRNRIER------------GDQVVGELLEFVKRWLLQHIQHSDKAYQAHL
>Idiomarina loihiensis (Gammaproteobacteria; Alteromonadales) 832aa (695-826) YP_154567.1  GI:56459286
LSEQDVLIEWSPKLDV-GIEEINRQHQRLIYIANELYRLKLR------DGDQHALQRLVDSLINYTATHFNYEELLMERNG--Y-----------PDLENHKLKHRDLVQDVMRFKHRVDS------------HEDVIDELLEFVKAWLMNHIMKSDMAYKGHL
>Janthinobacterium sp. J3 (Betaproteobacteria; Burkholderiales)  149aa BAC56750.1  GI:28201215
-MDEKTEFAWDDSYLL-GHHAMDTVHREFVDLLQAALTAPNA-----------ELPHALADIARHAEGHFAQENEWMVSQE--F----------P GGDCHIDEHNKVLASIYDVQEKVIQ-----------GDIAIGRKLAQALSEWFPDHASFMDSALAAWL
>Janthinobacterium lividum (Betaproteobacteria; Burkholderiales) 132aa ABK64032.1  GI:118161348
----MGKSHWKDEMAL-GVPVIDEAHEALFQELARLGQLSDQ-----------RFSVAFRELIAAVERDFREEEDLMEQIA--F-----------PSLANHREQHARVLSGLHHAWAAVDE-----------GDLEQGRHALSLLPQWLIFHQATMDLALAAAL
>Kuenenia stuttgartiensis (Planctomycetes; Planctomycetacia) 129aa CAJ72144.1  GI:91202505
-----------MFDYSVKIAEFDGHHKQLIGMINDLDDAMRQ------GKGKIVVGDILKKLINYTGFHFAAEEKIFKQHD--Y-----------PEYVEHKDKHDKMTAKVLALQNDYNA-----------GKVSLTVEVSKFLTDWLNKHIKETDQRYSEHL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Kuenenia stuttgartiensis (Planctomycetes; Planctomycetacia) 872aa (734-866) CAJ71928.1  GI:91204275
TLNSLPIFYWRNEYCI-NIQKIDYHHKQLLAKANKLCEAIDS------KKETPILDASISFLIDFVLYHFAEEENLLREHY--Y-----------NDYESHRMKHQRLIEDIMKIKKQISN-----------EDMEMNMEALDLFKDWIIDHILTEDRKYGPYL
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 124aa YP_865096.1  GI:117924479
-----------MRMIELGVDFMDAQHQSFVTELSQLAPQPDS-----------ALLLAFPGLVEALTDHFSQEELLMQRCG--F-----------GASQEHRGEHQRLLGQCAMLARFAKR----------GGAPDILAFMRSDLPKWFETHLLTMDAALARHA
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 134aa YP_866138.1  GI:117925521
---MPPFLDLPENCRL-NQPDIDLQHSILFALINAVETNNSI-----------ELEVVFKSLVEYVDVHFSYEEKTMLPES--Y-----------GFYHQHLAQHRMFEKKVSEMRSRLTS--------GDQAQEVLRQELRLFLHDWLVDHINGIDRQLFATA
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 160aa (1-130) YP_867250.1  GI:117926633
----MKTLSINPAFVT-GLDEIDLQHAFFVDLLARLTPALRN------SKSLPRQVRLLQEIQLFAAFHFHSEENLYREHG--L---------SDHQLTHHQKRHGELLGALNHYIFQLEQ------------EKETVESILAVLGDWFAFHAVEEDGYAVTTL
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 249aa (5-142) YP_866733.1  GI:117926116
IIPCKSGTLNFEQDLKLNVPSIDKQHEQLFLLAIGVSHAIQA------GADEESIRVSALELEAYVQEHLSFEERLLASNN--Y-----------PQLNSHKLAHSRFVKTNSELQKSLES-------CSAGTCIKQAPKLFDMLTEWLSDHILRVDRMAVDFM
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 253aa (6-142) YP_867005.1  GI:117926388
VPCKAGPLTFEQNLKL-NIPAIDQQHEQLFRLAIGINETLQS------GATEDAVRMNALELEAYVQEHLVYEEKLLSSNH--Y-----------PQQKSHRLAHARFVATSHKIQDELAR-------CSGPACIAKAPQLFDLLTTWLCDHIMNVDRLAVDFM
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 320aa (182-316) YP_864332.1  GI:117923715
KIGAAGPCEFPLLGIS----LVDQQHRQLFQLMYALQAQIEN--------RDNRVDLMIMALNNYANKHLADEEALLQRYA--Y-----------PRLADHQKLHIKLREDLVQRAHAVKQ------AADDNEKFKRAEELRDFIQEWLVSHIGSEDRKHCDYL
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 779aa (647-777) YP_864533.1  GI:117923916
KDTQPNLMPWNSHLVI-GVAQMDKEHSQLVALINQLYHTILE------GGSSKQGQPVLEALMRYTQDHFKHEEALLKQMH--Y-----------PDLQAHMAEHRALIEQVQHFQQDFER-----------GQASINLRLVGFLKDWLSNHILGSDKPYGTYV
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 871aa (733-865) YP_866360.1  GI:117925743
GSENEQVFVWRDAFAI-GVHEMDTHHKKLVEIANSIIEIIGS------NIGKESLMKSMDALIAYTEYHFQAEEKMMEAYG--Y-----------ADLEHHHHLHVKLVSQVVEFQNMVEE-----------KDDYLGLDFEGFFSDWLIQHILNEDRRYAMHL
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 926aa (788-921) YP_867064.1  GI:117926447
ANAIEPKIRWLSSYEV-GIETIDSDHKRLVGMMNQLYAAMKT------GSSSQVMEELFDGLINYSVVHFQREERLFEQHR--Y-----------PDAAGHSKRHEAFKTYVLGKRDEFVA----------GSNIHLSQDIFTYLEEWLINHIIHDDMAYVPYL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 927aa (789-921) YP_867464.1  GI:117926847
VGAYAPAIAWRNEYSV-GVQLLDADHKQLINLINELSIAVKD-------DRENFLQHVYERLVNYATTHFAREERMMAEIG--Y-----------SALPSQKAEHERFLSTVGSKRDILLN----------GADPKVATEIIDFLKDWLVGHIMKSDMAYKPAF
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 941aa (802-935) YP_866832.1  GI:117926215
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CGTGEEFFPWNDILLT-NVKEVDIQHKELVRMVNALHQEITS-----GQGGKQKLRTMVDGLIAYTVNHFKDEEAFMRRNH--F-----------PGLQAHLPEHIKFTDAVVELVAQVDK-----------GEAYIDMDLTGLLRDWLVNHIMGTDRKYAEHF
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 994aa (856-988) YP_864243.1  GI:117923626
TINDQKMIDWEDALDV-GVKVLNADHLKLMNYINDLHAAMRD------GKGKDKLATILAGLIEFTHTHFAREEGLMKKHG--Y-----------DRYAQQKEEHVNLIAQLGEKKKQFDE-----------GSATVALDLLAFLQNWLIDHIKGEDMRYKTFF
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 997aa (863-995) YP_865500.1  GI:117924883
SIDRSTFLKWNDGYST-GNAQIDGEHQQLMNIINELYIKLWS------GEKNPDYNPILLRLDGYTRDHLRREEELLASKS--A-----------PGLDGHKSIHREFIKKLEAFKLAFDQ-----------GNVGLSMEMMAFLKNWLSQHIVKVDKVIFKKI
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 1032aa (894-1031) YP_864127.1  GI:117923510
VDAEPIAVVWKPNMSV-GVQIFDQDHRRLVSYINRLELAHRA------GQSKTALERVLRALTDYTLIHFRREEKMMTESN--Y-----------PGVQAHKAQHTKLEDQVADYNRRMLQ-----------EESHITEEVLTFLKGEFLDHIMRTDHEYSDHF
>Magnetospirillum gryphiswaldense (Alphaproteobacteria; Rhodospirillales) 149aa (1-127) CAE12026.1  GI:33945221
------MFDFTDDLSV-GNEAIDADHRAFFEVARLIHESVHG------GKHDLIILSALLMLDEYVEGHFYREEKAMKAVG--Y-----------PRLAGHRHRHRVFRGRVRAIVEAYRE-----------GTMSVADNLSTLVVQWLRSHITNDDLQYKTWI
>Magnetospirillum gryphiswaldense (Alphaproteobacteria; Rhodospirillales) 159aa (1-136) CAJ30087.1  GI:78033471
------MFDFTDDLSV-GNEAIDADHRAFFEVARLIHESVHG------GKHDLIILSALLMLDEYVEGHFYREEKAMKAVG--Y-----------PRLAGHRHRHRVFRGRVRAIVEAYRE-----------GTMSVADNLSTLVVQWLRSHITNDDLQYKTWI
>Magnetospirillum gryphiswaldense (Alphaproteobacteria; Rhodospirillales) 524aa (197-329) CAJ30107.1  GI:78033490
SVPVKPDFGWSKAIET-GRNDIDSQHRGIIDIMNDLNEVPDT-----EDGDGTKVERALIALKDYVKIHFSHEEQLMDSFD--Y-----------DDRKRHKKLHSAFVAKIETLKAGSLT------------SPDVRRKLLGIVYNWLMSHITCVDRIMIAQL
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 122aa YP_419883.1  GI:83309619
---MGMIAIWDNRYSV-GHARVDAEHRQVISLLNEIDVARSV------GAPPVVVEMALETLLRTIVAHFARDEVPQGDHMA-I------------IASARRLLDGWRGGKPEALERRALV----------------------NLARRWIGHMGRREASLPSQR
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 127aa YP_421315.1  GI:83311051
------MATWLDEQWKSGDPAIDAEHQKLHQMISSMSAVIRN------DPGLGLAIEAVDVLTERIRIHFRMEGLAAR-----L---------NAAAAEQLKLDHQRLLRLLTPLYDALRR-----------GSAEQAKLLLSDFLSQLDAHDREMDIPLFQK-
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 129aa YP_419932.1  GI:83309668
----MSIIAWTEAMSV-DNPALDKDHQKLIRMINELDQSAPD------------FLELFNAVLDYTTGHFDREETHLDAIG--F-----------PGLDAHRVQHDDFADQVAAMLKEYRE----------RPFDAGDTRLKDFLWSWLKGHILIEDQRYAAWT
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 132aa YP_420778.1  GI:83310514
------MPAWTESLSV-GVPVLDEHHRHLFHLLATLDGMAGG------SVGQDAVRSVFDDLNGYIAYHFAEEEAMMARAD--F-----------PFLELHRHSHQTIAMRVADMSAELSM----------ANVERVIRELHDFLVGWLVHHIEIEDFEYRPFL
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 134aa YP_420912.1  GI:83310648
----MSLIEWDPSFSV-GSARMDADHQKLISLLNRLYDAWHG------GESIAELGWLFDELLAYADTHFAAEEMALKSRN--Y-----------PRLEKQQEDHLRLKESVMAFRDRHLA---------GEMPDALTTEMTAFLKAWLLEHILGEDMQYRSYF
>Magnetospirillum magneticum(Alphaproteobacteria; Rhodospirillales) 135aa YP_419589.1  GI:83309325
----MAYLQWTENLSV-GIPRMDEHHKKLVELINQVFDAMSG-------DAASAVDSVLADLLDYTRYHFSEEEKLLAACA--Y-----------PDLAEHQEVHRSMVKEVLDMRSRHLA----------DPASVTASETLDFLSKWLMRHIIGKDLRYRPYA
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 136aa YP_423659.1  GI:83313395
---MTAQISWSDDLLI-NVAAIDSDHKKLFDLMSEIFATSAH--------GADAINRAIGALAKYTKEHFAREEASMAKTN--Y-----------PGLSKQMYEHEHLVFTLESMMDRLMI----------SGPEAIDADLAKFLMSWLGDHIMDFDLKYAEYL
>Magnetospirillum magneticum(Alphaproteobacteria; Rhodospirillales) 138aa YP_423534.1  GI:83313270
-----MSIAWNEALAI-GDPIIDADHRRMIELIARLEVAAGL------EIDCAGIGRTLRDLTDLCREHFAREEALQHAVG--F-----------PETESHRTAHEMLMKRLDAVLAHFTD-------GCDEVRSGIVRTLGDSLATWLVSHIVNSDMEFKPYV
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales)138aa YP_420035.1  GI:83309771
----MSTDFWVDALSV-GVDEFDRAHRQHLNTIGEIEVALSE-------NRRSDAVGLLTHLLQILTVHQAEELDLLVRTS--Y-----------PGVDQIREVQAANLARLHRLKDQVEG---------QTSQLADARRVATEMRMAFVDYLLKGDINFKSHL
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 140aa YP_422017.1  GI:83311753
-----MAIAWEETLKV-GDIEIDADHKELIGLINDFEAKAKA----PEGVDKHVIQVTLERLQLYAYDHFAREEYIQAVAK--Y-----------DGLEENKRQHAALRKTLGDYIAKFNA-------GEYADLKVAAGEMSGFLNHWLMNHILETDLKMKGKM
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 140aa YP_423499.1  GI:83313235
SGNALWQYRWSEEFAL-GDPLVDAQHRAFFEEAAALRAALAS------EEPKDEIVAYCSAFITNLRTHFADEERLMARIG--F-----------PALPIHQQEHERLLARTESVVAEIHA----------ADCLLDCLLGAHALMEALVEHVTQQDMRIKTFV
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 142aa YP_421602.1  GI:83311338
------MANWQEHMRT-GIDVVDDDHQELFALVGQFETASKT---ASGQVDGAEIGRILERLQAYVNEHFEREETAQLESG--Y-----------EGYAENKRQHDELRRTLETFLGKHRR-------GEWGDLKVATESMRSFLAIWLSEHIMKTDRKMRGRI
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 143aa YP_421612.1  GI:83311348
----MTVIEWSNELKL-GVPAMDAEHRHLLKLTNDFLTAARE------NAAFARLTLILGELIARTRIHFQAEETLLDRAG--Y-----------PGLAGHRAEHGRLLVEAQRLYERFQT-LDAAPEHDDLASRTLTLEAAKFLQRWLVDHILADDRPYRPYV
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 144aa YP_423628.1  GI:83313364
------MLIWRDAMAI-GQPEIDRARKHVIGRINDFERALGA------HGPHTALGLFLTGLYEETSTAFGREEKIQRECS--F-----------PFTEMHHREHAAILEKVELLKEQYDE------LDARGNFTPLLRELAGLAKEWITAHIVQSDLKLRPYW
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 146aa YP_420100.1  GI:83309836
MIPRHAVIRWGEPLLL-GVGFVDHDHCEAVEMINRLAAAAPT-----------ERLDLARAFAHHCVEHFAREEEMMVKTGF-F------------ALDPHRDEHIRVVAQLEEVIRALEA------------GDPCDDYFTVELPQWFLEHRATMDYVTSGFA
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 147aa YP_422454.1  GI:83312190
----------MATSYTIGHKPLDDDHDRMIAAWRELEGSRTL----------EAAKAAAAVLMAEAGEHFAREEMFMLQCG--Y-----------PDRVRHMALHAEMASGLRRVLLSPLM--------GGSPHDDFVLAVRSLMDKWVMVHILGEDAKLAPYA
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 148aa (7-148) YP_423329.1  GI:83313065
VSWGNEKIEWSDDLLL-QAEQDDEDHREMFALMNRVFSAARL--------GADVVTSAVADLCLFTREHFTREQHSMESAG--Y-----------PDCEAHRYDHEYLIFQLDVLIDRLML----------SGPELVAEELVDLLKRWLCDHILTYDSAFVEFL
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 156aa( 8-142) YP_423198.1  GI:83312934
AGDPMTSIAWSEAFSV-GNSLLDSDHRILFDLLTQLFDATDT------GQSRDVVGSVLSALSEYAEHHFRREEALLAASG--Y-----------PDIEIHRAEHRRLEDHVRDISGRYRA----------GERGVLDEQVVELLKKWLTQHIQVTDKSYKPWV
>Magnetospirillum magneticum(Alphaproteobacteria; Rhodospirillales) 157aa (5-138) YP_420298.1  GI:83310034
GAARGAIPEWTPEMSV-GNDTLDSDHKAFFDIARLLYDSLAD-----KRDQGLIIASTLLILEEYVDGHFLREEKALKAVG--Y-----------TQLSEHHHKHRKFQARVRAISETYQS-----------GTKSAADDLPDLVVKWLTHHILNEDMQYKRWI
>Magnetospirillum magneticum(Alphaproteobacteria; Rhodospirillales) 161aa (1-132) YP_423764.1  GI:83313500
-----MTIAWREAMSV-GDETIDADHRHLVDMINVFEAAVVG------KIDHKRVARVLLGLVEYTGAHFKREEEIQVLIR--Y-----------PYHDSHRHGHRDVLKQLTGIAQQYTQ-------ATGTARDEMIRGLGGFLREWLVDHIIQSDLRMKPYV
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 169aa (31-162) YP_420741.1  GI:83310477
-----MTIAWREAMSV-GDETIDADHRHLVDMINVFEAAVVG------KIDHKRVARVLLGLVEYTGAHFKREEEIQVLIR--Y-----------PYHDSHRHGHRDVLKQLTGIAQQYTQ-------ATGTARDEMIRGLGGFLREWLVDHIIQSDLRMKPYV
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 171aa (13-148) YP_420348.1  GI:83310084
MNQTNPLPEWTDDLSV-NVEIIDEDHQAFFRLAALMSDVTST----PDNDQPYLIETSINILEEYIEGHFLREQKAMAKAD--Y-----------AYLVEHIAAHDAFADRVTRIIQDYRQ----------TGSIEKIGTLAHLVTDWLNNHIRVVDAQYKGIL
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 171aa (21-158) YP_422163.1  GI:83311899
TRSEGIMLVWREAMST-GHSEIDKAQRQLIAHINEFETALRK------SGPDVAMGLFLSGLYDQVAINFGREEQIQRESS--F-----------PFLDAHHREHGNLLGRLASIQNHYQS------ANHRADQGALLRDLTALIRDWVSHHMVQSDVMLRRYL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 179aa (31-160) YP_422102.1  GI:83311838
KAERLHWDFWSEELAI-GHAAIDDDHKRILAGIERLAKAFQL------GDGDAALSDGLALIVDYSRHHFEREERMLAAAG--Y-----------AHLEHHRARHQSFCDYVAHASKADGG--------------IDHGALLSYLVDWWVGHIASEDKLYRPAL
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 275aa (1-134) YP_420086.1  GI:83309822
----MAMLELTDDLRI-GHPVIDADHQRLIEIINEFLEHSKA------ADNSQVLHETLKSLLAYGRDHFSREERIQRQCL--Y-----------PLQPGHFHEHKALLDQVREIARAYFI------AKTKPLNESSVLEVNELLKAWLIGHVKKFDTGMRDWV
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 282aa (1-129) YP_421898.1  GI:83311634
-----MGVTWSERMSV-GVPLLDSDHKTLIGLINHLQRSIGD------DEEHASVGSVLQALEEYAAHHFAREEAMMDVCR--Y-----------PLLSRHHGTHAEFTKKVTDLKGRYDLD----------RTGVRARECLAFLNSWLIDHICTTDMNYRSWV
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 499aa (1-131) YP_422973.1  GI:83312709
------MIVWRDAMSV-GAPALDADHKRLIDLINLTEQWIGQ-------DNWRQVATITEELLRYVDEHFRREEAVMAAIK--Y-----------SELEQHKKAHETLAHKAKLLHDKFKA------ATLEEDLKTCSQVLIRVLTDWLVTHILKEDMKYKGSV
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 502aa (14-150) YP_420234.1  GI:83309970
CWGCAMAVQWQEAMSI-GVADLDAEHRAMLELLNSLEAGLEG-------GDDDGVADAMRDLVGLMSEHFSREEDLLSGIG--C-----------PSFYAHRDGHDAIADRIHLLRRRYLV------AVDSGARRDVASALLNFTRISLLDHILTEDHAMGRRM
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 665aa (527-659) YP_422630.1  GI:83312366
DQSDVKLLNWDNALNM-GIGNIDRHHREMFDEVNRLYAKMSQ------GNGAEAGQGMITLIDTVMGSHFREEEEVMSRNS--Y-----------PHLDEHRRHHRDFLDRAKSHKGAVQS-----------GDPTAAAKMFEYVATWLTNHIQMEDGKLANYL
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 795aa (656-788)) YP_423519.1  GI:83313255
EKKDMVLLHWDRDLEA-GVTSIDRYHQEKFEHINEFYRQMMS------EDGGKAAIALLSEIDRSIQGHFGEEEALMAKCG--Y-----------GDGEAHRRSHKAFQERIRALRTGIET-----------NHPEAVSQLFDYVSDWFPDHIRNEDMALALFL
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 807aa (668-800) YP_419583.1  GI:83309319
DKADMRILEWENALNT-GESSIDRHHREMFDQVNRFYGEMMSG------NGDAAIQGILGLVPAAFVPHFKEEEELMTRHA--Y-----------PGIDEHRRRHREFMDKFEGLKRAVET-----------GKDGANGQLFQFVAGWLKDHIRHEDGKIAAFL
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 810aa (673-803) YP_423156.1  GI:83312892
DKKDMKLLVWDGALNT-GVASVDRHHQAMYDQVNEFYRQMMS------GDGSRAAAAMLAELNRSIQDHFTEEEALMDKTR--Y-----------PAAEDHRRNHQAFLDRLAGMKTGLET-----------NRAEAPAEMFEYVSTWLRGHIGNDDRALGLHL
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 870aa (733-864) YP_422458.1  GI:83312194
QVVSSTDLVWRDEYSV-NIQRIDNHHRRLFEMSNRLIEAVRL------SKGKAEIGEALDFLMGYAMYHFSEEEALLERYG--Y-----------PEGAGHASRHRRLMAQARELEEHLAS------------AAISADEVLTFLQDWIVNHILMEDRRYAPFI
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Magnetospirillum magneticum (Alphaproteobacteria; Rhodospirillales) 906aa (778-900) YP_421045.1  GI:83310781
GEHARVLIKWHDEYSV-GVQRIDSHHRRLFEIGNSVLDMMER------KSPDAEVAETMGLLREYARFHFSEEEGLLIRYK--Y-----------PDLSSHRARHNRLLEQLTELQAAVAE-----------GRGYNEAEVLTFLQEWIVGHTLAEDRKSAIYL
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 120aa ZP_00053268.2  GI:46202398
--------------------MDAEHRVQVGLISALERAVEA------RAPQAEIQALVEQLIDYTDVHFMSEQLLMRLAA--Y-----------PDIHGHEAEHDGLMEQLRRIQSGFDL-----------GDSDVVMAETQVLRNLLIEHIRTHDLVFAQYV
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 120aa    GI:23014047
-----MIAIWDNRYTV-GNALADAEHRQVISLLNEIDVARSV------GAPPEVIGKALETLVRSIESHFAGDQPPQREHAA-I------------IMSARRLLTSWQSRAPGAIERRALI----------------------NLARRWFDHMGRNERVMTSQR
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 122aa ZP_00054990.2  GI:46201470
-------------------MIDEQHRRLFALAGRLTLDASA-----NDKDEAGGEAVLADLLDYTHSHFRDEEEFMRLIQ--Y-----------PGLRVHQQAHASIFAGVDQLLARMRT----------VDRQIMRREIGYFISEWLVRHVLHDDLQYTRYI
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 127aa ZP_00053732.1  GI:23013881
------MATWLEDQWKSGDSTIDTEHLKLHEMIRSMTAVMRN------DPGTGLAQEAVDVLTERLRIHFRMEESLAAKAN------------PEAIDTLKQDHQRLLRLLTPVRDAVQS-----------GSAEKAKSLMTDFAEQLDKHDREIDIPLFRK-
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 132aa ZP_00053735.1  GI:23013885
------MAEWTESLSV-GVPKLDEHHRHLFHLLDRIDGLAEA------GLAQDDVRSVFDELNNYIAYHFSEEEAMMERAG--F-----------PFLDLHRHSHQTIAMRVAEMSATLSV----------ANVERVVRELHDFLAGWLVHHIEIEDFEYRPFM
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 134aa ZP_00054355.1  GI:23014545
MIARHAVIRWGEPLLL-GVGFVDRDHCEAVEMINRLAAASGA-----------ERLELARAFAHHCAEHFAREEEMMVKTG--F-----------FALEPHRDEHMRVLGQLDEVIRSLEG------------GDSCAEYFAVDLPQWFLEHRATMDYVTSGFA
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 134aa ZP_00051444.1  GI:23010917
----MSLIEWDPSFSV-GSARMDADHQKLISLLNRLYDAWHG------GEDIAELGWLFDELLAYADTHFAAEEMALKSRN--Y-----------PRLEKQEQDHVRLKDSVIAFRDRHLA---------GETPDALTTEMTAFLKAWLLEHILGEDMQYRSYF
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 135aa ZP_00207881.1  GI:46200880
----MAYLQWTENLSV-GIARMDEHHKKLVDLINQVFDAMSG-------DASAAVDSVLADLLDYTRYHFAEEEKLLAACA--F-----------PDLEEHQAVHRSMVKEVMEMRSRHLA----------DPASVTASETLDFLSKWLMRHIIGKDLRYRPFA
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 135aa ZP_00052929.2  GI:46202606
--------------MRTGIDVVDDDHQELFALVGQFETASKT---ASGLVDGAEIGRILERLQTYVIEHFEREETAQLETG--Y-----------EGYEENKRQHDELRRTLEKFLDKHNK-------GEWGDLKVATESMRSFLSIWLSEHIMKTDRKMRGRI
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 136aa ZP_00055246.1  GI:23015471
-----MSIAWSEALAV-GDPSIDADHRRMIELIAQLEAAVCS------EIDCAAVGRTLQDLADLCRLHFAREEELQASVG--F-----------PETESHRTAHEMLLKRLDAILAHFAD-------GCDEVRTGIIRTLGDSLATWLVSHIVNNDMEFKPYV
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 139aa (1-122) ZP_00054325.1  GI:23014513
---------MAATYSI-GQPALDDDHDRMIAAWRELEASRTL----------DAAKTAAAVLMSEAAEHFAREEQFMLQCG--Y-----------PDRVRHTAMHAEMASGLRRVLLSPLM--------GGGKHEDFVGAVRNLMDRWVRVHILGEDTKLAPYA
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 140aa ZP_00052752.1  GI:23012741
-----MAIAWDEALKV-GDIEIDADHKELIGLINDFEAKAKA----PEGVDKHVIQVTLERLQLYAYDHFAREEYIQAVAK--Y-----------EGLEENKRQHAALRTTLGTYIEKFNA-------GQYADLKVAAGEMSAFLNHWLMNHILETDLKMKGKM
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 142aa ZP_00055707.1  GI:23015944
------MFLWNMSMET-GIETVDQGRKRVLAAMADFFQGMDD------------PALNQQILAARTGAIFNAMKTAFAAENA-Y-----LAEREAPDQEKHQANHAALSAAFIDLCRKLIP------KIKNHKQAQQVCLEIYQLVDDAIFHHITKEVGNYRDL
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 144aa ZP_00055499.1  GI:23015731
---------MLIWRDAMAIGQADIDHARKHVIGRINDFERA----LGAHGAHTAMGLFLTGLYEETSTAFGREEKIQRECS--F-----------PFTEPHHREHAAILEKLELLKERYDET------DARGDFTPLLRDLAGLAKEWITVHIVQSDLKLRPYW
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 146aa (7-138) ZP_00055962.2  GI:46201047
VSWGNHKIEWSNDLLL-HMEQEDGDHREMFVLMNRIFSAAQ--------IGADMVTQAVADLCLFTREHFLREQHGMERAG--Y-----------PDREAHRYDHEYLIFQLDVLIDRLMLS----------GPECVAEELVDLLKRWLCDHILTYDQAFAAYL
>Magnetospirillum magnetotacticum Alphaproteobacteria; Rhodospirillales) 150aa ZP_00052625.1  GI:23012573
KAERLHWDFWSEELAI-GHAVIDDDHKRILAGIERLAKAFQ------LGDGDEALRDGLALIVDYSKSHFEREERMLAAAG--Y-----------PHLEHHRARHQSFSDYVAHASEADGGI--------------DHGALLSYLVDWWVGHIASEDKLYRPAL
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 158aa (1-140) ZP_00056082.1  GI:23016325
----MRTMVWSEHFAL-GHDRIDREHRRLLELSAQIEARAE------TTTDLDDILPLCRDFFRLLVAHCFYEEQLLRK----L-----PRDRFGSHVDEHCRGHARLIKQAQTVLTGQVPS-------------GFESLQGFFGAYFELMHDLLVDDTELVGS
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 159aa (1-136) ZP_00053162.2  GI:46202468
MNQTNPLPEWTDDLSV-NVEIIDEDHQAFFRLAALMNDVTA----TPDNDQLYLIETSINILEEYIEGHFLREQKAMAKAD--Y-----------AYLVEHIAAHDAFADRVTRIVQDYRQT----------GNIEHIGALAHLVTDWLNIHIRGVDAQYKGIL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 179aa (31-160) YP_422102.1  GI:83311838
KAERLHWDFWSEELAI-GHAAIDDDHKRILAGIERLAKAFQ------LGDGDAALSDGLALIVDYSRHHFEREERMLAAAG--Y-----------AHLEHHRARHQSFCDYVAHASKADGGI--------------DHGALLSYLVDWWVGHIASEDKLYRPAL
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 272aa (1-131) ZP_00053965.2  GI:46202007
------MLELTDDLRI-GHPVIDADHQRLIEIINEFLEHSN-------EVNPQILHETLKSLLAYGREHFAREEGIQRQCL--Y-----------PYQQGHSNEHKSLLDQVREIARAYFVA------KTKPLNATSVQDVNELLKAWLIGHVKKFDTSMRDWV
>Magnetospirillum magnetotacticum Alphaproteobacteria; Rhodospirillales) 274aa (1-121) ZP_00054151.2  GI:46201886
--------------MSVGVPLLDSDHKTLLGLINHLQRSIG------DDEEHAAVGSVLQALEEYAAHHFAREEAMMDACR--Y-----------PLLTRHHGTHAQFTEKVLGLKSRYDQD----------QTGVRARECLAFLNSWLIDHICTTDMNYRSWM
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 500aa (1-131) ZP_00054349.2  GI:46201789
------MIVWRDAMSV-GAPALDADHKRLIDLINLTEQWIG------QDNWRQVATVTDELLRYVDEHFRREESVMAAIK--Y-----------PEIEQHKKAHETLAQKARLLHEKFKAA------TQDEDLKTCSQVLIRVLTDWLVTHILKEDMKYKASI
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 699aa (560-692) ZP_00056481.1  GI:23016728
DKKDMKILVWEGALNT-GVASVDRHHQKMYDQVNEFYRRMM------SGDGFAAAIAMLDELNRSIRDHFNEEEALMSKAN--Y-----------PGADEHRRNHRAFLERLASLETSLDAN-----------HPEAASQMFDYVSTWLREHISKDDKALGNHL
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 807aa (668-800) ZP_00056272.1  GI:23016517
DKNDMKILVWDNALNT-GESSIDRHHREMFDQVNRYYGEMM------SGNGDVAVQGILSLVPTTFVPHFKEEEDLMSRRG--Y-----------PGIDEHRGRHREFLDAFESHKRAVEAG-----------KDGASGALFQFAATWLKDHIHYEDGKIAAFL
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 808aa (670-808) ZP_00055928.1  GI:23016169
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DKKDMTLLHWDATAET-GEATVDKHHRDLFELVNKAYRQMM------SGEGSQMAVPLLAELDRTMRSHFTEEESLMSRSA--Y-----------AEIETHRRSHHAFFERVDPLRAAIAAG-----------SAEAGGELFDYVATWLSQHIRKDDKALAAFL
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 870aa (733-864) ZP_00054329.1  GI:23014517
QVVSGGDLIWREEYSV-NIQRIDNHHRRLFEMSNRLIAAVR------LGKGTAEMSEALDFLKGYATYHFSEEETLLERYG--Y-----------PEEAGHAAKHRRLLAQLHELTERLATT------------TVTAGDVATFLQDWIVNHILIEDRRYAPFI
>Magnetospirillum magnetotacticum (Alphaproteobacteria; Rhodospirillales) 889aa (751-883) ZP_00055643.1  GI:23015878
GEHARVLIKWHEEYSV-GVQRIDSHHRRLFEIGNSVLDMME------RKTDDAEVAETMGLLREYARFHFSEEEGLLIRYK--Y-----------PELSAHRVRHARLLEQLTELQAAVAEG-----------RGYNEAEVLTFLQEWIVGHTLAEDRKSAIYL
>Marine gamma proteobacterium HTCC2207 (Gammaproteobacteria) 174aa (29-166) ZP_01224113.1  GI:90416181
ALKRLLDKALALKLDSALKSETKSPEPEALGEFETEEEAKT------SQSDSTKIELLMQTLLLDTVTHFKLEEQCMEQ----Y---------EFPAREAHSQEHRLVLQWMDREHSLWSRD------CNIETINHLSIYAADRFPKWLLNHIVTMDTVMASYI
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Marinobacter aquaeolei (Gammaproteobacteria; Alteromonadales) 662aa (5-138) YP_960352.1  GI:120556001
VPNAFEIFPWNRNFET-GIDDIDQQHRVLVNILNRLAWHFA------SDTSELTPDQILDELLTYAAFHFEYEEAIWNQT----L-------GEAAMARNHHDAHQMFFAQVEELRNSREPQ------------EEVLTRLFDFLTRWLAFHILESDRRMALTA
>Mariprofundus ferrooxydans (Proteobacteria; Mariprofundus) 143aa ZP_01451258.1  GI:114775690
MQDQVWQLEWNDKLSV-GIDDIDVEHRHFIELINGLNRAIL------DRMDISEIRRRMQLILDDAAQHFAHEEALFAAWH---Y----------PDADEHAKYHRQATAAFQEIMARLSDK----------HTESEWIEAGLKVKQLLVEHLITEDMKYRDYF
>Mariprofundus ferrooxydans (Proteobacteria; Mariprofundus) 373aa (3-132) ZP_01451244.1  GI:114775676
----MVAFQWDSNFIT-GVADVDQQHMHLVDLINRLGEHLA-----GNDIALDYIEEIYQELAAYAHYHFQCEEELMQEVG---L--------DQRHQDFHRKEHLDFLHEVTSMHDGISAD-----------SPDTSSYLMEFLTHWLAYHILGADQNMARQM
>Mesorhizobium sp. BNC1 (Alphaproteobacteria; Rhizobiales) 134aa YP_665917.1  GI:110347099
----MALIEWKSHYSV-GVDAVDHEHRELIDLINQLHENLL------AGSPDLMVTAFLGEIFRAISAHFALEERFMREHG---Y----------DQFAEHKQAHEQLLDEIRDIMDGYEAD-----------PEGTSQQLSDRLDAWFTLHFRTHDARLHHRL
>Methylococcus capsulatus (Gammaproteobacteria; Methylococcales) 131aa YP_113225.1  GI:53805087
----MALMTWTAAEFGTNVGFADDQHKTIFDMVNKLHDTAA-------TGNRSEIGKQLDALIDYVVMHFKSEETEMQKKG---Y----------ADFAAHKAEHDKLVGVCADLQKKFHAG-----------EAEVNQDTTRFVRDWLVNHIPKVDKLYGPCL
>Myxococcus xanthus (Deltaproteobacteria; Myxococcales) 185aa (7-139) YP_635509.1  GI:108758665
TQVVCFLVHAECSGMGSPFDILIDQHRELEERLERLASGVE----------PDELRGLTAELLALLRLHSRLEERCLYPVMAG-V-------EGRESCREQTEDHLTMRELMAELEELPSGH-------------PEWQARLLTLEDLAVAHFQEEENARLPQL
>Oceanospirillum sp. MED92 (Gammaproteobacteria; Oceanospirillales) 121aa ZP_01167458.1  GI:89094519
------------MPLTSELIWQDQQHQVLFDLIDEIKADHV-------------SKSTFVRLHDYAEHHFCIEEAYMKALE---Y----------PEYENHLLAHNKFRTELKTMLDEHHSY-----------DAMLRDALSDFLSEWLKRHIFGVDKKLETFI
>Oceanospirillum sp. MED92 (Gammaproteobacteria; Oceanospirillales) 129aa ZP_01165824.1  GI:89092872
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>Oceanospirillum sp. MED92 (Gammaproteobacteria; Oceanospirillales) 135aa ZP_01166597.1  GI:89093650
-MANQLNPSVIPQVAL--DFMNE-DHGEAVELVNQLLIAIE-------SDSSTKVSELLKAFFEHNQEHFAREEEQMIRVN---F----------PPYSCHKGEHERVLEEMKTVISEWEAS---------EDRSALQSYLTDTVANWLVNHISTMDTVTAMFV
>Pelobacter carbinolicus (Deltaproteobacteria; Desulfuromonadales) 135aa YP_355938.1  GI:77918123
----MALIQWNTSLSV-NIAEIDTQHQRLISMINELNDAML------QGRGKDVLGKIIAGLVSYTATHFATEEKYFDRHG---Y----------PASNAHKQEHRDFTAKVSEFKQGFDEG-----------RLGLSVSVMNFLGDWLRNHIKGSDMDYSPFL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Pelobacter propionicus (Deltaproteobacteria; Desulfuromonadales) 138aa YP_902721.1  GI:118581471
-----MGIRWRESLAI-GIEEIDSQHRELVEQFARLLAACE------QGRGEDELKSMLDFLDRYVRRHFSDEEILQQRYR---Y----------PAYQGHRNEHQNFIARIGSLQQQIAAR---------GVEVAHLVETNQLLYAWFVKHISSADRVLGSFL
>Pelobacter propionicus (Deltaproteobacteria; Desulfuromonadales) 143aa YP_901724.1  GI:118580474 FUGUE Z=22.4
----MSLMEWDGTYSI-GIKELDDHHQHLFMLINRAFDGYN------RGMGDAAVKKLLDELLEYATYHFSAEEMRMGEDA---Y----------PGIEEHYRQHKLFVNKVAELMELYKAV-----------GSSILTSTLMFMNTWLTRHILQHDREYARYC
>Pelobacter propionicus (Deltaproteobacteria; Desulfuromonadales) 518aa (380-512) YP_902711.1  GI:118581461
HFRLSNALEWDASFAT-GIGTFDDEHKTLFRMVNDLHDAMQ------QKRSKEAIGQILDGLADYTVNHFAGEERAFSRTG---Y----------PEEAQHRELHRKLVDQVVELQGRFRDG-----------QALLTQDVITFLQNWLVNHIKGVDKKYGPHL
>Polaromonas naphthalenivorans (Betaproteobacteria; Burkholderiales; Comamonadaceae) 152aa (6-133) YP_982345.1  GI:121605016
PLDASGSLQWSDQFLL-GYTPIDEVHQEFVDLMGQMQRAED-----------AALPALLAQFSVHLQHHFEMENEWMVSTE---F----------PPRECHMDEHAAVMQSVEEVQALLAQG-----------DVAICRDLVAQLAQWFPQHADQLDSALAHWM
>Polaromonas naphthalenivorans (Betaproteobacteria; Burkholderiales; Comamonadaceae) 155aa (3-YP_973791.1  GI:121583360
KSSAAVAYFWEDKLLI-GHEQMDDEHQAFAHIIQALLKAPD-----------NAIASCLADVIAHATQHFAQEDEWMCNLD---F----------PARQCHMDEHAAVLRSAAGVKLRVHAG-----------DHQAARLFSQELAAWLPPHVQHLDSALAAWI
>Polaromonas naphthalenivorans (Betaproteobacteria; Burkholderiales; Comamonadaceae) 168aa (1-125) YP_981479.1  GI:121604150
----MSNLEWSDALAL-NLPVMDDTHREFVELLAVVETASD----------ETLLSHWRTLVDHTDDHFGREDQWMQATR---F----------SSTNCHSVQHKVVLQVMREGITHALAG-----------DLGAIRQMARELAIWFPQHAQTMDAALALHL
>Pseudomonas aeruginosa (Gammaproteobacteria; Pseudomonadales) 153aa NP_250364.1  GI:15596870 YP_791573.1  GI:116049622
----MAHLVWQDDLNT-GIQVIDNQHKRIVEMINHLHDAQQ------GKEHAAIAEVIEELVDYTLSHFAFEETLMEDAG---Y----------QFSRAHKKIHELFIRRVSEYRVRFQAG-----------EDVGDELKGLLSRWLFNHIRNDDAGYVDAV
>Pseudomonas resinovorans (Gammaproteobacteria; Pseudomonadales) 146aa (1-127) NP_758575.1  GI:27228525
-MDEKTEFAWDDSYLL-GHHAMDMVHREFVDLLQAALTAPN-----------AELPNVLADIARHAEGHFAQENEWMESQG---F----------PGGDCHIDEHNKVLASIYDVQEKVIQG-----------DIAIGRKLAKALSEWFPDHASFMDSALAAWL
>Pseudomonas resinovorans (Gammaproteobacteria; Pseudomonadales) 165aa BAB32774.1  GI:13094185
-MDEKTEFAWDDSYLL-GHHAMDMVHREFVDLLQAALTAPN-----------AELPNVLADIARHAEGHFAQENEWMESQG---F----------PGGDCHIDEHNKVLASIYDVQEKVIQG-----------DIAIGRKPGESPVRVVPRPCVFYGFCSRSVA
>Pseudomonas syringae pv. syringae (Gammaproteobacteria; Pseudomonadales) 160aa (1-133) YP_235578.1  GI:66045737
-MLPAPGSRPGDMTLNIFEALRES-HDRQRSYADALIQTSG---------DSAEREKAYKQLKEELQAHETAEERFFYIP----L---MAHDNGVDLSRHAISEHHEMDEMMEELDETEMSS-------------PAWLATAKKLSEKVHHHLKEEEQKFFQMA
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Ralstonia eutropha (Betaproteobacteria; Burkholderiales) 146aa (1-131) YP_727244.1  GI:113868755
---------MDAKDQLSSAGLPDHLHLGEPVTDATHAEFVQ-LLAAVAGADDAGFLAAMDEWIDHTRHHFAQEEQWMEAMG---F----------GPRHCHAGEHQQVLAVAAAVRDKVHTD-----------EFQLGRRLVAELSGWFDHHVKSMDAMMVEHM
>Ralstonia eutropha (Betaproteobacteria; Burkholderiales) 157aa (24-140) YP_295043.1  GI:73540523
MPPAAPAPSMDSKSQLSSDGLPADLHLGEPVTDATHAEFVQ-LLAAVAGADDAGFLAAMDEWIDHTRHHFAQEESWMEAMG---F----------GPRHCHAGEHQQVLAVAKAVRDKVASD----------GELELGRRLAAELSGWFDHHVKSMDAMMVEHM
>Ralstonia metallidurans (Betaproteobacteria; Burkholderiales) 160aa (9-147) YP_584783.1  GI:94311573
PYAGLSAEGLPDDLRL-GEPVTDATHAEFLQLLAAMEKADD-----------AGFLAAFEEWIEHTRHHFEQEEQWMEAMQ---F----------GPRFCHSNEHQGVMSVAKAVRDKIVEE-RADPEGPGKGALSLGRRLTGELSGWFDNHVKSMDTMMVEHM
>Ralstonia pickettii (Betaproteobacteria; Burkholderiales) 138aa (1-124) ZP_01663990.1  GI:121531385
----MPVIEWSEALQL-GDAATDANHVEFCALLNAVADATD-----------AEFIGALDAFIDHTEHHFAEENAWMDAAD---F----------PPRHCHRGEHDNVLALCREVHKRAAAG-----------DMDLGRRLVAELPAWFAQHVDVMDRMMTTYL
>Ralstonia pickettii (Betaproteobacteria; Burkholderiales) 158aa (1-131) ZP_01661972.1  GI:121529360
----MNKAEIPVAQRAVLSMLLD-DHREVKKLFKTFQQEKD----------EATREQIVREACEKLTVHTQLEEEVFYP-----YVRDNGGEAFKDLVDEAVVEHATAKDLIQQLNGMHAGD-------------DLFAAKFTVLAEYVSHHVEEEETELFPKL
>Ralstonia solanacearum (Betaproteobacteria; Burkholderiales) 137aa NP_518898.1  GI:17545496
----MPVIQWSEALHL-GDAATDANHAAFCTLLNAVADASE-----------ADFVSALDAFIAHTEVHFAEENAWMEAAD---F----------PPLHCHRNEHDNVLALCREVRRRAADG-----------DMALGRRLVTELPEWFAQHVDVMDRMMTTWL
>Reinekea sp. MED297 (Gammaproteobacteria; Reinekea) 150aa (1-130) ZP_01113653.1  GI:88798066
-----MTIKWTSALEI-GIPVIDAQHHRIVEYINQVEHVQK-------THSREELLDVLDELVDYTISHFAFEESLMEEAG---Y----------PAANAHSKVHRLFAKRVEAFQKRARAG------------EDITEELLHVLKAWLVNHIQRDDQDYSADV
>Reinekea sp. MED297 (Gammaproteobacteria; Reinekea) 151aa ZP_01113654.1  GI:88798067
-----MKMQWTDEYEI-GIGVIDGQHQRIVEYINRIDDFEQ------SGDQEAMNDVLASLVDYTLSHFAFEEALMEDVG---Y----------QELAEHKLTHDSFRRQIERLKARHDQG------------EKVAVELSEMLLTWLLKHIMTDDQSYAPQV
>Rhodoferax ferrireducens (Betaproteobacteria; Burkholderiales) 277aa (146-273) YP_522715.1  GI:89900244
IHHFSTRIEWRDQYKI-GDQAIDEQHRELFKRAAYVLAATS----------HEGQVISAMRLLQYMRTHLSHEEEMMRRLH---Y----------PKLKVHTQEHLEMLARLNIISLRIAN------------ENLVKSDLEELLGDWFLTHMETADTELARFA
>Rhodoferax ferrireducens (Betaproteobacteria; Burkholderiales) 498aa (364-496) YP_525259.1  GI:89902788
VAVNLVQLVWHPAYES-GQAELDAQHRALFGHVNNILAALL------LERPVDEVAALIDTLIGDVAKHFEDEEKIILAAG---F----------PGAAAHAAMHRELIAHAGYLVSRFKT-----------RDLDRGEPFQFLAHDLVARHILGEDREFFPHL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Rhodoferax ferrireducens (Betaproteobacteria; Burkholderiales) 840aa (688-822) YP_524860.1  GI:89902389
APKSHVHLRWKAAFAS-GNPVIDQEHETLFRLANTLLDEAA-----LRRQQPAAFEAAFEALLAHVVEHFAHEEAILLAHG---F----------AGMADHARQHQVLLARAHALHLSALA--------ADAGDATEGELVKFLVTELVAGHMLHTDSAFFPLF
>Rhodopseudomonas palustris BisA53 (Alphaproteobacteria; Rhizobiales) 504aa (358-480) NP_946988.1  GI:39934712
PGERRPDILWHETYAC-GEPTIDAQHRELFDLANVILGPEI------EMLEPARLSELVELLLTRVAEHFQYEQAVLEASG---Y----------DECGLHRMEHDHLLIRARQVSEAVVS-----------GHQSLGELRAFLVNSVILGHMLKDDRRFFPLF
>Rhodopseudomonas palustris BisA53 (Alphaproteobacteria; Rhizobiales) 507aa (354-487) YP_780986.1  GI:115524075
VDRSEPGLHWSRAYES-GDALIDSQHRELFVLANALFDPSL-----KPEAAPRELTLALDRLLSHVAKHFADEEAELSARH---F----------RGLSGHQAAHATLLRDADDLKNEVRS-----------GLRTLGDLREFIVNEVVAQHMLTADLEFFPLF
>Rhodopseudomonas palustris BisB18 (Alphaproteobacteria; Rhizobiales) 470aa (1-131) YP_532029.1  GI:90423659
----MVPFQWNALFET-GNARIDRQHRTLFELTNDLARAVQ------NGEKLPEISALVLKLRDYAATHFCDEEQLMRCSALA-I----------QEKTRHACAHRSFIKKVEDLAARRDL-----------SNVEAVSEFLQFLVTWLVTHILKLDHRMTKAL
>Rhodospirillum rubrum (Alphaproteobacteria; Rhodospirillales) 148aa (1-130) YP_426742.1  GI:83592990
----MVEITWSEKMSV-GNSALDWDHKTLLDLLNRFHGVAA------GQVNPSEVPALFTELVRYTEYHFQIEERLMRLAG---Y----------AELDKHKEMHAALVSRLLAFQSQYLE----------APERFNFTAMADFLSDWLVRHILREDMKMGEVL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Rhodospirillum rubrum (Alphaproteobacteria; Rhodospirillales) 176aa (23-157) YP_428293.1  GI:83594541
GAAPWRPLIWLDVYSV-GDPLLDDDHRRLMEEINHLGAALI----NQIAPVSEALIAPLKRLAHQEAEHNLREEAILAQLG---Y----------PGLEDHRAEHRQLESGLGALVESLIP-----------QGPIEPEILADLLKDWFVRHVLGQDMRYKTYV
>Rhodospirillum rubrum (Alphaproteobacteria; Rhodospirillales) 209aa (1-130) YP_427169.1  GI:83593417
----MAPHSWSNRYAT-GLRAIDDDHRGLFELVDALEEHHE------KASGSSLVAATIAALQVYAAEHFAREERFMRKAH---F----------PDFERHHRIHEDFRALVDALARFQGQ----------SPDSVDLGRVTRFLNRWIGEHILVKDMEYLPYV
>Rhodospirillum rubrum (Alphaproteobacteria; Rhodospirillales) 262aa (133-260)YP_426610.1  GI:83592858
DLPHPAPRPWDRSLDT-GNARIDSHHRALSRLATRFHRLDG-------RADTGHLANLLHGLNTLMRLHFRTEETLWP----------------ESDPHHALAHSHFLETLDHAGRRLLE-----------GEMSPSAFARDVLDHWLVDHIRAADQPRFRVL
>Rhodospirillum rubrum (Alphaproteobacteria; Rhodospirillales) 316aa (9-126) YP_427592.1  GI:83593840
GQGDLSLFNWSEERRL-GVRLMDRDHQVVCHQAGLLAAGVD-------RGDGAAMAAGARFLQDYIPRMFEREDRLMANT-------------NHPERGAHQDAHRQLLVGLMTRTSGPIE---------------TAASVLAAVETWIRGHIDAHDRPLARHV
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Rhodospirillum rubrum (Alphaproteobacteria; Rhodospirillales) 736aa (591-723) YP_425723.1  GI:83591971
DGEDHALVTWSDDLAT-GDAHVDEDHRKLMALVNSVYGHVK------QGEAGAALEASFGELKRYSIEHFAEEEAFMATVN---F----------PQAETHRRQHQHFLGRSDALFEAYRR-----------GADTAAVELMGLLGSWWETHIRIYDTELAHFV
>Shewanella sp. ANA-3 (Gammaproteobacteria; Alteromonadales) 529aa (392-523) YP_868383.1  GI:117919191
QAQSKQFVKWGPELDI-GMPEINRQHQRLVSLINELHRTLS------EAYGLEAIKRIVQGLVDYTANHFSYEEELFARFG---Y----------PQTVAHKEKHAQLVGQVLDFQKRVAR------------GEDVADELMAFLKAWLVNHIQKSDKEYTQFL
>Shewanella sp. MR-4 (Gammaproteobacteria; Alteromonadales) 529aa (392-523) YP_735348.1  GI:113971555
EAQSKLFVKWGPELDI-GMPEINRQHQRLVSLINELHRTLS------EAYGLEAIKRIVQGLVDYTANHFSYEEELFARFG---Y----------PQTVAHKEKHAQLVDQVLDFQKRVGR------------GEDVADELMAFLKAWLVNHIQKSDKEYTQFL
>Shewanella sp. MR-7 (Gammaproteobacteria; Alteromonadales) 529aa (392-523) YP_735348.1  GI:113971555
EAQSKLFVKWGPELDI-GMPEINRQHQRLVSLINELHRTLS------EAYGLEAIKRIVQGLVDYTANHFSYEEELFARFG---Y----------PQTVAHKEKHAQLVSQVLDFQKRVAR------------GEDVADELMAFLKAWLVNHIQKSDKEYTQFL
>Shewanella sp. PV-4 (Gammaproteobacteria; Alteromonadales) 530aa (393-518) ZP_00835633.1  GI:78365347
DTRRDKLIEWSDALDL-NLAEINRQHKTLVHLINELYYLLN------NNYGLASIKRVVQGLIDYTANHFKYEETLFEQFG---Y----------PQDKQHTDSHHQLVGKVLAFQRRVEQ------------GEDIGDELMAFLKSWLSQHIQKEDKAYVDCF
>Shewanella sp. W3-18-1 (Gammaproteobacteria; Alteromonadales) 526aa (389-520) YP_964765.1  GI:120600191
QALSKLFVTWGPELDI-GMPEINRQHQRLVSLINELHRTLS------EDYGLEAIKRIVQGLVDYTANHFSYEEELFERFG---Y----------PQSESHKEKHGQLVGQVLDFQTRVGK------------GEDVADELMSFLRSWLVNHIQKSDKEYTTFL
>Shewanella amazonensis (Gammaproteobacteria; Alteromonadales) 518aa (381-512) YP_926430.1  GI:119773690
IRHENAFVSWGPSLDI-GMAEVNRQHQRLITLINELHRAIN------EGYGLAAIKRIVQGLVDYTANHFSYEEELFARFD---Y----------PQSQDHEDEHKKLVTQVLDFQRRVGR------------GENVSDELMAFLKAWLINHIQGSDKQYAPYL
>Shewanella baltica (Gammaproteobacteria; Alteromonadales) 529aa (392- ZP_00582180.1  GI:68542450
QAQNKLFVKWGPELDI-GMPEINRQHQRLVSLINELHRTLN------EEYGLEAIKRIVQGLVDYTANHFAYEEELFARFG---Y----------PQTDSHKEKHGKLVGQVLDFQKRVVK------------GEDVADELMTFLKAWLVNHIQKSDKEYTAFL
>Shewanella oneidensis (Gammaproteobacteria; Alteromonadales) 529aa(392- NP_719421.1  GI:24375378
QAQNKLFVKWGPELDI-GMSEINRQHQRLVSLVNELHRTLS------EAYGLEAIKRIVQGLVDYTANHFSYEEELFARFG---Y----------PQTNGHKEKHAQLVGQVLDFQKRVAR------------GEDVADELMAFLKSWLVNHIQKSDKEYAQFL
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Shewanella putrefaciens (Gammaproteobacteria; Alteromonadales) 526aa (389-520) ZP_00815671.1  GI:77816487
QALSKLFVTWGPELDI-GMPEINRQHQRLVSLINELHRTLS------EDYGLEAIKRIVQGLVDYTANHFSYEEELFERFG---Y----------PQSESHKEKHGQLVGQVLDFQKRVGK------------GEDVADELMSFLRSWLVNHIQKSDKEYTTFL
>Shewanella woodyi (Gammaproteobacteria; Alteromonadales) 159aa (1-132) ZP_01539832.1  GI:118071638
----MDPFQWDKNFAT-GIDNVDFQHKKLVDLINRFGHQLA-----CDELIMEDINQVLQELWLYTQEHFQDEERLMHEKG---I--------DPRHLTMQKQAHRYFLHEVQLMQASISI-----------DQPEVLKYLLDFLTQWLAYHILGDDKNMARQI
>Solibacter usitatus (Acidobacteria; Solibacteres) 133aa YP_827140.1  GI:116624984
------MFDWKPQFAV-GIPSIDAQHQKLFAIARELYEAMS------AGRGKASLALILDRLVRYTATHFAHEERLMRI-----Y--------EYPDFVRHKAQHDALTKQVLGFQKEFDA-----------GMVSMTVQLLQFLKNWLENHIQVSDFEYGPCL
>Solibacter usitatus (Acidobacteria; Solibacteres) 141aa YP_823672.1  GI:116621516
----MSLFKWSKGHSV-YLPEIDAEHRNLCQMAAELHKIAL------AGGKSEQLKPILLNLLEAADEHFRHEERLMKVVH---Y----------SAFEWHKRQHDTVRKRLRQTIKRVEA-----------GETEACTDFLKFLGTWLVDHMTVTDRMMGAFI
>Solibacter usitatus (Acidobacteria; Solibacteres) 166aa (1-130) YP_826389.1  GI:116624233
---MTSSLVWSASTAV-FVTEIDDEHREIFDAISQVREALE------SRGSMPAIHKLAERLMGCLAEHFAHEERLMRAAR---Y----------GSTHWHQRSHRAARRRVEQFVGRLKE-----------GDTAAGHELVEYMTCWLTDHASVADRMMGSAL
>Sphingomonas sp. SKA58 (Alphaproteobacteria; Sphingomonadales) 154aa (1-123) ZP_01303096.1  GI:94496520
--------MADATIFHRLKQDHD-SHRQLFKKMDEAQGDDD------------RLKKLFDQFKVEATAHAAAEEETLYATM---L-----ARPDLREDAQHSVSEHKEIDDYLEEMEEQDF------------NGKEWRETFAQLKKRYLHHIDEEEEEMFPDA
>Sphingomonas wittichii (Alphaproteobacteria; Sphingomonadales) 183aa (25-159)  ZP_01607194.1  GI:118759500
NAVRKIFVQAPTMMAGEWDDALAAEHRAVLELFDQIQATEE--------GHATRRSLLLTQIGHALAKHAMEEENAVYATLR--I------HGQVADADRLNGDHGYVKQYLFELGQMAPE-------------HPLFLSKIGDFRSMLEEHMRSEEETVFPKL
>Stenotrophomonas maltophilia (Gammaproteobacteria; Xanthomonadales) 153aa (1-127) ZP_01642673.1  GI:119875611
----MALLVWQDDLNI-GIDVIDQQHRRIIEMLNHLHVAQT-------SMQRAAVGEVIDEVVDYTMSHFAFEEELMEEAG---Y----------PFCAAHKRVHEVFIKRVAEYRLRFQA-------------EDISDELRTMLSRWLFNHIRGDDQAYADQV
>Symbiobacterium thermophilum (Actinobacteria; Symbiobacterium) 147aa (9-145) YP_075222.1  GI:51892531
AGGKEMALRWYSALETG-IEEIDGQHRQLFEQIDRLLESAK------SGAGQDACLRILDFLGGYVVEHFATEERYMERYG---Y----------PKKAEHKQQHAELVEYYRKMRARVEA---------EGAKPTLIIQLQHSLVEWLNNHILKSDRDLGDFL
>Syntrophomonas wolfei (Firmicutes; Clostridia) 130aa YP_754830.1  GI:114567676
------MIRWKDEYSVG-VEHIDEQHRKLFEIAGRAYDLLK---DELVVDKYDRIVAILGELKDYSVFHFNSEEEYMKSIG---Y----------RKFLSHKVIHDDFIEKINGIDLDKVD----------ENQDKYLLDILDFIVRWIDGHILGQDKQYMQS-
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Thermoanaerobacter tengcongensis (Firmicutes; Clostridia) 133aa NP_621951.1  GI:20806780
------MIKWTESLSVG-NETIDSQHKELIQKINDVLEACN------RQHGKEKVVEVMQFLKDYTVKHFKDEENLMKKYQ---Y----------PMYEEHKKIHEDLVKKVEDLDERIKR---------EGVSLSVVMTVNKTLVDWFVNHISKEDKKVGEYI
>Thermosynechococcus elongatus (Cyanobacteria; Chroococcales) 136aa NP_682783.1  GI:22299536
---MLQRFEWTDRLSTG-VPMVDIQHKELVTAINDLADAIE------QGRGASRIKQLIVFMKYYAEWHFENEESCANK-----Y-------RCPLAEVNHR-AHQQFIQLFEELQQQYRH---------SQADESVAVMIHGKLADWLVNHIMKIDKEIGQHI
>Thermosynechococcus elongatus (Cyanobacteria; Chroococcales) 149aa NP_682162.1  GI:22298915
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----MDGLAWQAAFVSG-LAEVDEEHQALLEMLQQLRSAIA------AGATFSQVKPQLLACARETERHLQHEETLMATAN-------------HPLYLSHRAAHQNLLRDLSGLLEEVHG-----------HPENLTPETIEAIGTLVVRHICEEDLPMLYLL
>Thiobacillus denitrificans (Betaproteobacteria; Hydrogenophilales) 195aa (10-146) YP_314491.1  GI:74316751
TTGRQTARRSVASLRESVLDMLKDDHKRVKKAFRDFEKIDP-------HEDPERAAELVEQTCSELEVHAQLEEEIFYPAVRENI---SEADLVTEAEVEHKSAKQLIADIRSLSPEDEKY----------------AASFTVLGEYVKHHIREEEQEMFKQL
>Thiomicrospira denitrificans (Epsilonproteobacteria; Campylobacterales) 1004aa (1-125) YP_393480.1  GI:78777165
-MKTIDIFPWSNHFNTE-IKIIDEQHKKLVIILNRLATHIA------YSDTDDDLNDIFDELIDYTSYHFETEEAIWHK-----Y------LPNDELDASHKVVHKTFVDTVLRLKNEQNR----------ESLSELAQEALGFLASWLASHILETDRHMAYIV
>Treponema denticola (Spirochaetes; Spirochaetales) 137aa NP_971622.1  GI:42526524
---MDDFVSWDASYDLG-IEYVDKQHRRLVELINELYHACL----GEKGELEEKFKHVMKELVEYVMIHFKDEEKIMEEIN---Y----------PNIKEHKQHHENFVKKILQSVNDYRN-----------GKQFVPNTFVRFLRDWLFNHILISDKEWAKFY
>Treponema denticola (Spirochaetes; Spirochaetales) 143aa NP_971908 GI:42526810
-MSEIKGFEWEDSLSVG-YNTIDLHHKKLLTIMGQFKDLFDL----PQEEYKLKIGKILKNLSDYTYYHFEEEEKVMKEYG---Y----------PYLKEHAEIHKSFIKKIREAIVPLAS-----------GNIETGLQFYDFLGRWLVEHIAGADHDWAEYI
>Verminephrobacter eiseniae (Betaproteobacteria; Burkholderiales) 168aa (15-143) YP_997683.1  GI:121609876
PRRGHDGPHLDHDGWLLGYAPMDRLHEEFLALVHALAQAPE-----------HAVAAALDALALNARAHFGAEDQWMAASA---F----------PARACHIDEHAAVMRSIEGVQRRVAR-----------ADFGAARPLADALLQWFPGHADYLDSALAHWL
>Vibrio cholerae (Gammaproteobacteria; Vibrionales) 372aa (1-132) NP_230861.1  GI:15641229
----MQSFKWDQYFETG-LEEVDEQHQSLVNIVNRYSSLLA-----ENHVSLDEIRLALFELSRYSEYHFKEEEKLMREVG---I--------SALHLEEHIQVHRTFMSEVFSMQAFIHD-----------VDDRSAVQLLEFLIHWLAYHILGIDQNMARQV
>Vibrio parahaemolyticus (Gammaproteobacteria; Vibrionales) 381aa NP_797668.1  GI:28898063
----MNSFRWDIYFETG-IEDVDDQHQYLVEFINKYGKLLT-----RNTISIADIQSALFELSRYAEFYFKEEENLMREVG---I--------HHEHLQKHIQVHRTFMGDIVSMQSFINE-----------DNRQSAEQLLDFLIHWLAYHILGIDQNMAKQI
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L
>Vibrio splendidus (Gammaproteobacteria; Vibrionales) 383aa (21-146) ZP_00990126.1  GI:84387104
PKGSMNLFNWDKNFETG-IGVVDEQHQYLVGFINHYGNLLS--------------ENTISIDEINEFHFKEEESLMRDCGV--Y---------ELHIEEHIKVHRVFMQDIYSMQAFILE-----------EDQVSARQLLDFLIHWLTYHILGIDQNMARQM
>Vibrio vulnificus (Gammaproteobacteria; Vibrionales) 371aa (1-132) NP_761216.1  GI:27365688
----MNSFKWDKNFETG-IADVDEQHQYLVGFINRYGELIS-----ENTISIQDIQMALFELSRYAEFHFKEEENLMRNAGV--Y---------HEHLQYHIKIHRAFMSDIMGMQSFISE-----------ENKKSAEQLLHFLIHWLAYHILGIDQNMARQV
>Wolinella succinogenes (Epsilonproteobacteria; Campylobacterales) 168aa NP_907673.1  GI:34557858
--MPERILQWKEEYSIG-EEEIDSQHKRLFEIAAGAFSIVS------PSERAAKVKETIRRLVEYTRFHFDEEERFMKEEL---Y----------PHLDTHKELHEEIIISMNAFMRRIPE----------MKIQELEKELAFSIQSWFIDHITQKDKQIQAWL
>Xanthomonas axonopodis (Gammaproteobacteria; Xanthomonadales) 153aa (1-127) NP_642798.1  GI:21243216
----MALLVWQDDLNTG-IEVIDHQHRRIVDMINQLHVAQT-------SLQQLAVAEVIDELIDYTLSHFAFEEELMQEAG---Y----------PFSQAHQRVHAVFGKRVGEYRLRFQA------------GEDVSDELRNMLSRWLFNHIRGDDQAYAPQV
>Xanthomonas campestris (Gammaproteobacteria; Xanthomonadales) 153aa (1-127) NP_637705.1  GI:21231788
----MALLIWQDDLNTG-IEVIDHQHRRIVEMINHLHVAQT-------SLQRLVVSDVIDELIDYTLSHFAFEEELMEEAG---Y----------PFSHAHQRVHAVFAKRVGDYRLRFQA------------GEDISDELRNMLSRWLFNHIRGDDQAYAPQV
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI-------------------------------------WLV-HI---D--Y---L

>Dechloromonas aromatica (Betaproteobacteria; Rhodocyclales) 187aa (18-176) YP_286170.1  GI:71908583
SALSDITAHWLTTGALPPELVTGHKLIDFEHRFLVSAIANLRKVCIDHETFADCSGCGHESQLRCENQLIGLLGDIFSFILDHFKTEESIMRDSLMLMVDRDMCQAHMEDHAEIAAKVQEIVSSLDQLHVVSRIRELEKLLARWITNHIALHDLLLARWI
---------W-----------------D--HK-LV----------------------------------------L------HF--E--LF---------------HK--H--FI----------------------------WLV-HI---D--Y---L
>Magnetococcus sp. MC-1 (Proteobacteria; Magnetococcus) 174aa (14-149) YP_867131.1  GI:117926514
-------MSQPTGLVRTGIGPIDRDHLHLWDLFQTLLEKDLRED---------EALAVLKELLAYTRYHFGREERLMQEIG---L--------TGEPRQAHIHEHAIFVKRVENFLELLQNRAAPKTTGLQAMVEEIQKMHQLPTLPQLDPAKRVVAFLVDWILNHTSGMDVELANHT
---------W------------D--HK-LV------------------------------L------HF--E--LF-----------------------HK--H--FI--------------------------------------------------WLV-HI---D--Y---L
```

Fig. 3. A Bayesian phylogenetic tree of 3 protozoan and 42 metazoan sequences. The Hr sequences are identified by the fist three letter of the genus name and the first three letters of the species name (see Fig. 2 in Supplemental Material). The cnidarian *N. vectensis* Hr is marked with a dot.

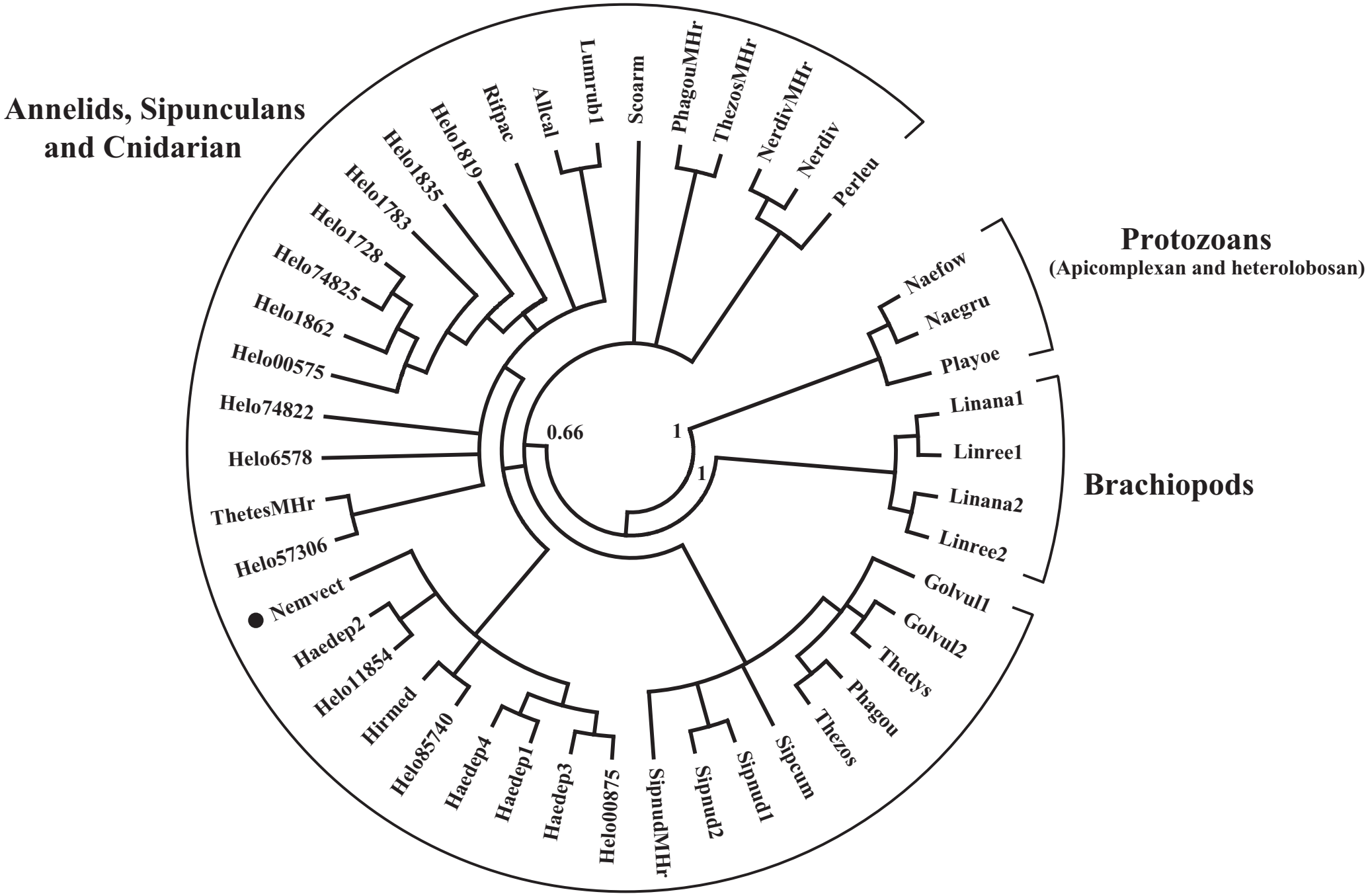
Annelids, Sipunculans
and Cnidarian
Protozoans
(Apicomplexan and heterolobosan)
Brachiopods
Lumrub1
Scoarm
PhagouMHr
ThezosMHr
NerdivMHr
Nerdiv
Perleu
Allcal
Rifpac
Helo1819
Helo1835
Helo1783
Helo1728
Helo74825
Helo1862
Helo00575
Helo74822
Helo6578
ThetesMHr
Helo57306
Nemvect
Haedep2
Helo11854
Hirmed
Helo85740
Haedep4
Haedep1
Haedep3
Helo00875
SipnudMHr
Sipnud2
Sipnud1
Sipcum
Thezos
Phagou
Thedys
Golvul2
Golvul1
Linree2
Linana2
Linree1
Linana1
Playoe
Naegru
Naefow
0.66
1
1

Fig. 4. A Bayesian phylogenetic tree of 16 fungal, 3 protozoan and 42 metazoan sequences. The Hr sequences are identified by the fist three letter of the genus name and the first three letters of the species name (see Fig. 2 in Supplemental Material). The cnidarian *N. vectensis* Hr is marked with a dot.

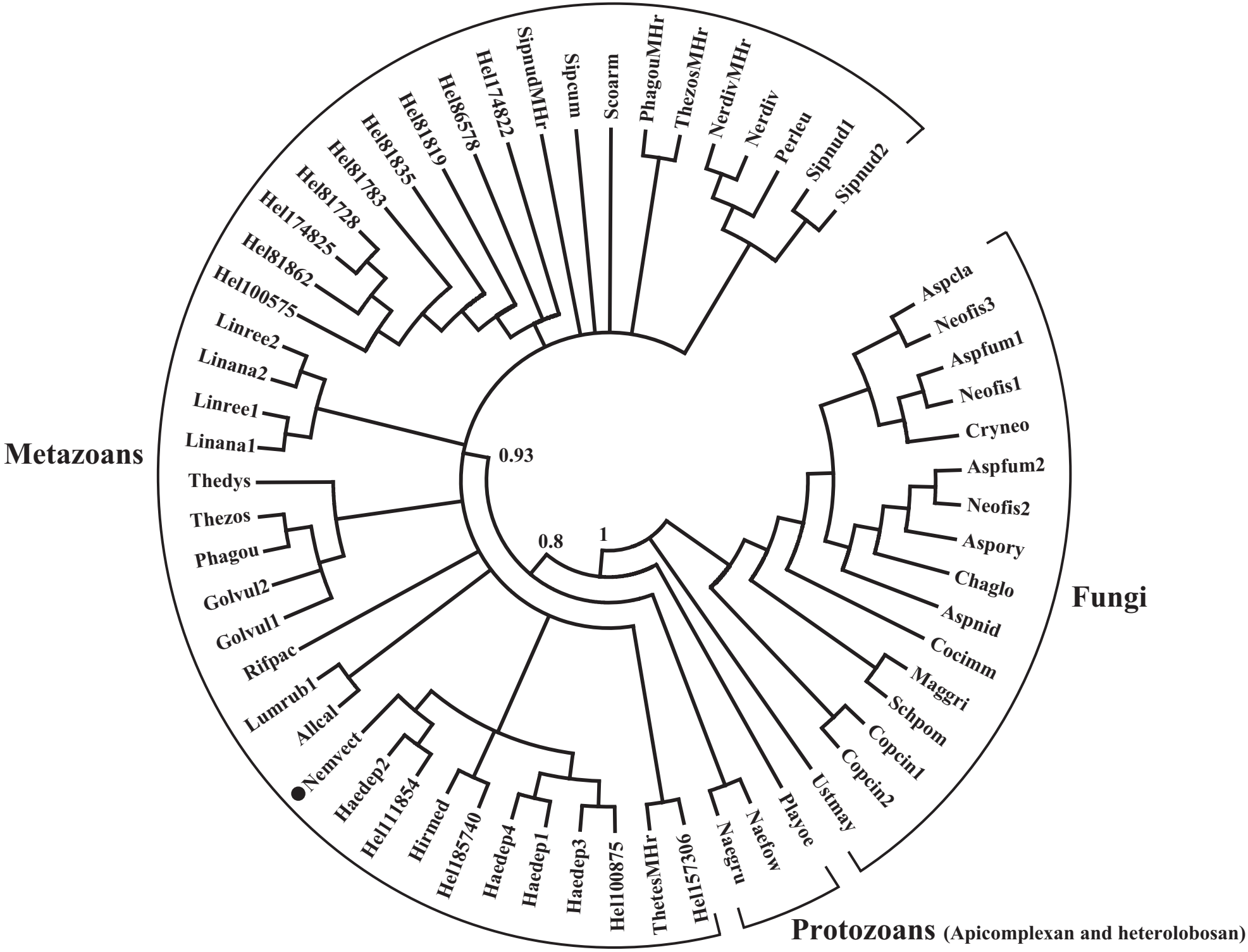
Metazoans
Fungi
Protozoans (Apicomplexan and heterolobosan)
0.93
0.8
1
Sipnud2
Sipnud1
Perleu
Nerdiv
NerdivMHr
ThezosMHr
PhagouMHr
Scoarm
Sipcum
SipnudMHr
Hel174822
Hel86578
Hel81819
Hel81835
Hel81783
Hel81728
Hel174825
Hel81862
Hel100575
Linree2
Linana2
Linree1
Linana1
Thedys
Thezos
Phagou
Golvul2
Golvul1
Rifpac
Lumrub1
Allcal
Nemvect
Haedep2
Hel111854
Hirmed
Hel185740
Haedep4
Haedep1
Haedep3
Hel100875
ThetesMHr
Hel157306
Naegru
Naefow
Playoe
Ustmay
Copcin2
Copcin1
Schpom
Maggri
Cocimm
Aspnid
Chaglo
Aspory
Neofis2
Aspfum2
Cryneo
Neofis1
Aspfum1
Neofis3
Aspcla

Table 1. Putative hemerythrins in eukaryote genomes.

Taxon	Identifier	Size and Hr domain (aa)
Alveolata		
Plasmodium yoelii yoelii	gb|AABL01004457.1	132
Annelida		
Hirudinae		
Haementeria depressa	gi|47833904|gb|CN807658.1	119
Helobdella robusta	jgi|Helro1|157306	120
	jgi|Helro1|100875	120
	jgi|Helro1|81783	121
	jgi|Helro1|185740	123
	jgi|Helro1|111854	132
	jgi|Helro1|100575	134
	jgi|Helro1|81819	134
	jgi|Helro1|174825	134
	jgi|Helro1|174822	134
	jgi|Helro1|81862	134
	jgi|Helro1|81835	136
	jgi|Helro1|175368	136
	jgi|Helro1|86578	165
Hirudo medicinalis	AAS49167.1 GI:44921619	120
Theromyzon tessulatum	Q9GYZ9 GI:21263690	120
Oligochaetea		
Allolobophora caliginosa	Ref 10	119
Polychaeta		
Neanthes (Nereis) diversicolor	P80255 GI:417311	119
	P22761 GI:123030	120
Periserrula leucophryna	AAQ63634.1 GI:34327785	119
Riftia pachyptila	This work	110?
Scoloplos armiger	This work	110?
Brachiopoda		
Lingula anatina	P22764 GI:123038	117
	P22765 GI:123044	117
Lingula reevii	P23543 GI:46397821	117
	P23544 GI:46397822	117
Cnidaria		
Nematostella vectensis	XP_001634535.1 GI:156388091	119
	XP_001622541.1 GI:156351502	156, 2-117
Fungi		
Ascomycota		
Ajellomyces capsulatus	XP_001539786.1 GI:154277908	205, 12-146
Aspergillus clavatus	XP_001271296.1 GI:121706066	220, 26-160
	XP_001270510.1 GI:121704493	220, 21-160
Aspergillus fumigatus	XP_754309.1 GI:70999175	221, 26-160
	XP_747053.1 GI:70983051	227, 31-160
Aspergillus nidulans	XP_681907.1 GI:67903302	228, 24-158

Aspergillus oryzae	BAE63202.1 GI:83773074	221, 33-157
Coccidioides immitis	XP_001245291.1 GI:119189369	181, 1-121
Magnaporthe grisea	XP_360008.1 GI:39940942	239, 34-169
	XP_001261781.1 GI:119483756	227, 31-160
Neosartorya fischeri	XP_001263153.1 GI:119490985	221, 25-160
	XP_001267572.1 GI:119501631	233, 25-160
Neurospora crassa	XP_955932.1 GI:85076485	232, 33-167
Schizosaccharomyces pombe	NP_595013.1 GI:19115925	203, 11-144
Basidiomycota		
Coprinopsis cinerea okayama	EAU86662.1 GI:116503767	208, 1-130
	EAU89470.1 GI:116506575	228, 17-153
Cryptococcus neoformans	XP_566714.1 GI:58258603	220, 15-159
Ustilago maydis (zeae)	XP_757573.1 GI:71005814	244, 41-170
Heterolobosa		
Naegleria fowleri	Q9NH76 GI:21263696	119
Naegleria gruberi	jgi|Naegr1|44819|fgeneshHS_pm.scaffold_69000005	119
	jgi|Naegr1|81770|estExt_fgeneshNG_pg.C_680095	119
	jgi|Naegr1|83311|estExt_fgeneshNG_pm.C_680002	119
	jgi|Naegr1|83016|estExt_fgeneshNG_pm.C_100003	119
	jgi|Naegr1|36233|estExt_gwp_gw1.C_160163	119
Sipuncula		
Golfingia vulgaris	CAG14945.1 GI:57282926	114
	CAG14946.1 GI:57282928	113
Phascolopsis gouldii	P02244 GI:21264441	114
	P27686 GI:232242	119
Siphonosoma cumanense	P22766 GI:123040	113
Sipunculus nudus	CAG14943.1 GI:57282922	119
	CAF74912.1 GI:57282893	119
	CAG14944.1 GI:57282924	119
Themiste dyscritum	P02246 GI:123041	113
Themiste zostericola	P02245 GI:123042	113
	P02247 GI:417114	118

Table 2. Putative hemerythrins in archaeal genomes

Taxon	Identifier	Size and Hr domain (aa)
Euryarcheota		
Halobacteriales		
Haloarcula marismortui	YP_134671.1 GI:55376820	617, 12-146
Methanococcales		
Methanocaldococcus jannaschii	Q58157 GI:21263658	147
	NP_247732.1 GI:15668928	169, 21-154
Methanomicrobiales		
Methanoregula boonei	gi|154149997|ref|YP_001403615.1	135
Methanospirillum hungatei	YP_504166.1 GI:88603988	135
	YP_502435.1 GI:88602257	135
No. genomes with Hr/Total	4/43	

Table 3. Identified and putative hemerythrins in bacteria[1].

Taxon	Identifier	Size and Hr domain	Oxygen requirement and habitat [2]
Acidobacteria			
Acidobacteria bacterium Ellin 345	YP_592725|GI:94970677 YP_593517|GI:94971469 YP_591227|GI:94969179 YP_592726|GI:94970678 YP_592724|GI:94970676	132, 1-128 134. 1-128 142, 1-131 152, 1-129 155, 1-129	Ae, Tr
Solibacter usitatus	YP_827140.1 GI:116624984 YP_823672.1 GI:116621516 YP_826389.1 GI:116624233	133, 1-127 141, 1-129 166, 1-130	
No. genomes with Hrs/Total	2/3		
Actinobacteridae (high G+C, Gram+) *Symbiobacterium thermophilum*	YP_075222.1 GI:51892531	147, 9-143	MAe, Tr
No. genomes with Hrs/Total	1/39		
Aquificales			
Aquifex aeolicus	NP_214180.1 GI:15606800	131, 1-129	Ae, Sp
Hydrogenobacter thermophilus	BAF34936.1 GI:116234997	131, 1-129	
No. genomes with Hrs/Total	2/3		
Cyanobacteria (Blue green algae)			
Chrooccocales *Thermosynechoccus elongates*	NP_682783.1 GI:22299536 NP_682162.1 GI:22298915	136, 1-132 149, 1-129	Sp
No. genomes with Hrs/Total	1/20		
Firmicutes (Low G + C, Gram +)			
Clostridia			

Alkaliphilus metalliredigenes	ZP_00800966.1 GI:77685572	137, 1-131	?
Caldicellulosiruptor saccharolyticus	ZP_00885869.1 GI:82500456	138, 1-131	An, Sp
Clostridium sp. OhILAs	ZP_01361119.1 GI:106893996 ZP_01360922.1 GI:106893798 ZP_01360653.1 GI:106893528	131, 1-127 137, 1-132 142, 1-132	An, Aq
Clostridium acetobutylicum	NP_346715.1 GI:15893366	129	An, Aq
Clostridium beijerincki	ZP_00910041.1 GI:82747545 ZP_00911352.1 GI:82748877 ZP_00910329.1 GI:82747836 ZP_00908279.1 GI:82745769 ZP_00909310.1 GI:82746807	129 129 130 133 135	An, M
Clostridium cellulolyticum	ZP_01574112.1 GI:118725472 ZP_01576604.1 GI:118728026 [ZP_00909308.1 GI:82746805	130 132 185, 44-179	
Clostridium phytofermentans	ZP_01353421.1 GI:106886073 ZP_01354048.1 GI:106886715	129 143, 1-135	An, M
Clostridium tetani	NP_782896.1 GI:28211952	137, 1-131	An, Aq
Clostridium thermocellum	ZP_00504934.1 GI:67875718	129	An, M
Desulfitobacterium hafniense	ZP_01371607.1 GI:109647704 YP_517407.1 GI:89893920 YP_516471.1 GI:89892984	135, 1-131 139, 1-132 144, 1-134	An, M
Syntrophomonas wolfei	YP_754830.1 GI:114567676	130	An, Aq
Ruminococcus gnavus	ref|NZ_AAYG01000020.1	120	An, HA
Ruminococcus torques	ref|NZ_AAVP01000029.1	120	An, HA
Thermoanaerobacter tengcongensis	NP_621951.1 GI:20806780	133	An, Aq
No. genomes with Hrs/Total	14/21		
No. genomes with Hrs/Total	14/75		
Planctomycetes			
Kuenenia stuttgartiensis	CAJ72144.1 GI:91202505 CAJ71928.1 GI:91204275	129 872, 734-866	An
No. genomes with Hrs/Total	1/4		

Proteobacteria (Purple bacteria)			
Alphaproteobacteria			
Rhizobiales			
Mesorhizobium sp. BNC1	YP_665917.1 GI:110347099	134, 1-129	Ae, M
Rhodopseudomonas palustris BisA53	NP_946988.1 GI:39934712 YP_780986.1 GI:115524075	504, 358-480 507, 354-487	F, M
Rhodopseudomonas palustris BisB18	YP_532029.1 GI:90423659	470, 1-124	F, M
No. genomes with Hrs/Total	3/25		
Rhodospirilalles			
Magnetospirillum gryphiwaldense	CAE12026.1 GI:33945221 CAJ30087.1 GI:78033471 CAJ30107.1 GI:78033490	149, 1-127 159, 1-136 524, 197-329	
Magnetospirillum magneticum	YP_419883.1 GI:83309619 YP_421315.1 GI:83311051 YP_419932.1 GI:83309668 YP_420778.1 GI:83310514 YP_420912.1 GI:83310648 YP_419589.1 GI:83309325 YP_423659.1 GI:83313395 YP_423534.1 GI:83313270 YP_420035.1 GI:83309771 YP_422017.1 GI:83311753 YP_423499.1 GI:83313235 YP_421602.1 GI:83311338 YP_421612.1 GI:83311348 YP_423628.1 GI:83313364 YP_420779.1 GI:83310515 YP_420100.1 GI:83309836 YP_422781.1 GI:83312517 YP_422454.1 GI:83312190 YP_423329.1 GI:83313065 YP_421350.1 GI:83311086 YP_423198.1 GI:83312934 YP_420298.1 GI:83310034 YP_423764.1 GI:83313500 YP_420741.1 GI:83310477 YP_420348.1 GI:83310084 YP_422163.1 GI:83311899 YP_422102.1 GI:83311838 YP_420086.1 GI:83309822 YP_421898.1 GI:83311634 YP_422973.1 GI:83312709	122 127 129 132 134 135 136 138 138 140 140 142 143 144 144 146 146, 1-139 147, 1-132 148, 7-148 149, 11-141 156, 8-142 157, 5-138 161, 1-132 169, 9-135 171, 18-148 171, 27-158 179, 40-160 275, 1-134 181, 1-129 499, 1-131	MAe, Aq

	YP_420234.1 GI:83309970 YP_422630.1 GI:83312366 YP_423519.1 GI:83313255 YP_419583.1 GI:83309319 YP_423156.1 GI:83312892 YP_422458.1 GI:83312194 YP_421045.1 GI:83310781	501, 19-150 665, 529-659 795, 658-788 807, 672-800 810, 673-803 870, 740-864 906, 774-900	
Magnetospirillum magnetotacticum	ZP_00052849.2 GI:46202650 ZP_00053268.2 GI:46202398 ZP_00054990.2 GI:46201470 ZP_00053732.1 GI:23013881 ZP_00055446.1 GI:23015677 ZP_00053735.1 GI:23013885 ZP_00054355.1 GI:23014545 ZP_00051444.1 GI:23010917 ZP_00207881.1 GI:46200880 ZP_00052929.2 GI:46202606 ZP_00055246.1 GI:23015471 ZP_00054325.1 GI:23014513 ZP_00052752.1 GI:23012741 ZP_00055707.1 GI:23015944 ZP_00055084.1 GI:23015304 ZP_00055499.1 GI:23015731 ZP_00055962.2 GI:46201047 ZP_00052625.1 GI:23012573` ZP_00056082.1 GI:23016325 ZP_00053162.2 GI:46202468 YP_422102.1 GI:83311838 ZP_00053965.2 GI:46202007 ZP_00054151.2 GI:46201886 ZP_00054349.2 GI:46201789 ZP_00056481.1 GI:23016728 ZP_00056272.1 GI:23016517 ZP_00055928.1 GI:23016169 ZP_00054329.1 GI:23014517 ZP_00055643.1 GI:23015878	114 120 122 127 131 132 134 134 135 135 136 139 140 142, 1-133 144, 1-132 144, 1-129 146, 7-138 150, 1-131 158, 1-140 159, 1-138 179, 31-160 272, 1-131 274, 1-121 500, 1-130 699, 563-692 807, 668-800 808, 672-808 870, 736-864 889, 754-883	MAe, Aq
Rhodospirillum rubrum	YP_426742.1 GI:83592990 YP_428293.1 GI:83594541 YP_427169.1 GI:83593417 YP_426610.1 GI:83592858 YP_427592.1 GI:83593840 YP_425723.1 GI:83591971	148, 1-130 176, 23-157 209, 1-130 262, 133-262 316, 9-126 736, 590-732	F, M
No. genomes with Hrs/Total	4/6		
Sphingomonadales			
Sphingomonas sp. SKA58	ZP_01303096.1 GI:94496520	154, 1-122	Ae, Aq
Sphingomonas wittichii	ZP_01607194.1 GI:118759500	184, 25-159	Ae, Aq

No. genomes with Hrs/Total	2/6		
No. genomes with Hrs/Total	9/75		
Betaproteobacteria			
Burkholderiales			
Acidovorax sp. JS42	YP_984586.1 GI:121592690 YP_984955.1 GI:121593059	168, 1-124 173, 28-160	Ae, Tr
Acidovorx avenae	YP_968695.1 GI:120609017	171, 1-124	Ae, M
Bordetella avium	CAJ48206.1 GI:115421695	148, 1-124	Ae, HA
Burkholderia mallei	YP_102393.1 GI:53725253	149, 7-135	HA
Burkholderia pseudomalllei	YP_334215.1 GI:76810098	186, 44-172	An, Tr
Burkholderia phymatum	ZP_01500286.1 GI:118028824 ZP_01504458.1 GI:118033012	147, 1-127 190, 1-123	HA
Burkholderia thailandensis	YP_442321.1 GI:83719963	141, 1-127	Ae, Tr
Burkholderia vietnamiensis	ZP_00427022.1 GI:67549150	158, 13-142	F, M
Burkholderia xenovorans	YP_556187.1 GI:91780980 YP_555832.1 GI:91780625	159, 7-135 165, 12-140	Ae, M
Comamonas testoreni	ZP_01520527.1 GI:118051979 ZP_01518696.1 GI:118050146	165, 1-124 211, 37-160	Ae, M
Delftia acidovorans	ZP_01580041.1 GI:118731526 ZP_01578319.1 GI:118729802	166, 1-124 213, 40-170	Ae, M
Janthinobacterium sp. J3	BAC56750.1 GI:28201215	149, 1-127	?
Janthinobacterium lividum	ABK64032.1 GI:118161348	132	?
Polaromonas naphthalenivorans	YP_982345.1 GI:121605016 YP_973791.1 GI:121583360 YP_981479.1 GI:121604150	152, 6-133 155, 3-130 168, 1-125	Ae, Aq
Ralstonia eutropha	YP_727244.1 GI:113868755 YP_295043.1 GI:73540523	146, 1-131 157, 1-140	F, M
Ralstonia metallidurans	YP_584783.1 GI:94311573	160, 9-147	F, Sp
Ralstonia picketi	ZP_01663990.1 GI:121531385 ZP_01661972.1 GI:121529360	131 158, 1-130	

Ralstonia solanacearum	NP_518898.1 GI:17545496	137	Ae, M
Rhodoferax ferrireducens	YP_522715.1 GI:89900244 YP_525259.1 GI:89902788 YP_524860.1 GI:89902389	277, 138-272 498, 366-496 840, 691-822	F, M
Verminephrobacter eiseniae	YP_997683.1 GI:121609876	168, 22-143	
No. genomes with Hrs/Total	20/26		
Hydrogenophilales			
Thiobacillus denitrificans	YP_314491.1 GI:74316751	195, 10-146	F, M
Rhodocyclales			
Azoarcus sp.EbN1	YP_932039.1 GI:119896826 YP_935261.1 GI:119900048 YP_932615.1 GI:119897402 YP_932470.1 GI:119897257 YP_935260.1 GI:119900047	136 150, 1-132 160, 1-130 162, 1-122 174, 19-148	F, Tr
Dechloromonas aromatica	YP_284639.1 GI:71907052 YP_285883.1 GI:71908296 YP_284878.1 GI:71907291 YP_284887.1 GI:71907300 YP_284625.1 GI:71907038 YP_286895.1 GI:71909308 YP_285962.1 GI:71908375 YP_284835.1 GI:71907248 YP_284552.1 GI:71906965 YP_286170.1 GI:71908583 YP_287152.1 GI:71909565 YP_284191.1 GI:71906604	129 127 128 133 134 142, 1-130 146, 1-127 160, 1-126 161, 10-140 187, 24-176 667, 534-661 681, 1-129	F, M
No. genomes with Hrs/Total	24/33		
Gammaproteobacteria			
Aeromonadales			
Aeromonas hydrophila	YP_854665.1 GI:117619147 YP_857472.1 GI:117618414	678, 540-672 809, 680-807	F, M
Alteromonadales	9 other genomes - no Hr		
Colwellia psychoerythrae	YP_268476.1 GI:71281331 YP_270871.1 GI:71282489 YP_270886.1 GI:71279092 YP_268475.1 GI:71280761 YP_271339.1 GI:71280063 YP_270299.1 GI:71279208	131 188, 52-182 192, 52-182 368, 1-132 519, 389-509 722, 1-123	F, Sp

	YP_268669.1 GI:71280946	1328, 1180-1310	
Idiomarina baltica	ZP_01041958.1 GI:85710897	566, 427-560	Ae, Aq
Idiomarina loihiensis	YP_154567.1 GI:56459286	832, 603-826	Ae, Sp
Marinobacter aquaeole	YP_960352.1 GI:120556001	662, 8-136	F, Aq
Shewanella sp. ANA-3	YP_868383.1 GI:117919191	529, 390-524	F, M
Shewanella sp. MR-4	YP_735348.1 GI:113971555	529, 394-523	F, M
Shewanella sp. MR-7	YP_735348.1 GI:113971555	529, 394-523	F, Aq
Shewanella sp. PV-4	ZP_00835633.1 GI:78365347	528, 395-524	F, M
Shewanella sp. W3-18-1	YP_964765.1 GI:120600191	526, 387-520	F, M
Shewanellla amazonensis	YP_926430.1 GI:119773690	518, 383-513	F, M
Shewanella baltica	ZP_00582180.1 GI:68542450	529, 394-523	F, Aq
Shewanella oneidensis	NP_719421.1 GI:24375378	529, 394-523	F, M
Shewanella putrefaciens	ZP_00815671.1 GI:77816487	526, 391-520	F, M
Shewanella woodyi	ZP_01539832.1 GI:118071638	159, 1-131	F, M
No. genomes with Hrs/Total	14/23		
Chromatiales			
Alkalilimnicola ehrlichei	YP_741251.1 GI:114319568	161, 1-127	F, Aq
Methylococcales			
Methylococcus capsulatus	YP_113225.1 GI:53805087	131	Ae, M
Oceanospirillales	4 other genomes - no Hrs		
Alkanivorax borkumensis	YP_691784.1 GI:110832925	154, 1-127	Ae, Aq

Oceanospirillum sp. MED92	ZP_01167458.1 GI:89094519 ZP_01165824.1 GI:89092872 ZP_01166597.1 GI:89093650	121 129 135	Ae, Aq
Pseudomonadales			
Acinetobacter baumannii	ref|NC_009085.1		Ae, M
Azotobacter vinelandii	ZP_00417575.1 GI:67155948	134	Ae, M
Pseudomonas aeruginosa	NP_250364.1 GI:15596870	153, 1-127	Ae, M
Pseudomonas mendocina	ZP_01526847.1 GI:118058386	155, 1-125	
Pseudomonas resinovorans	NP_758575.1 GI:27228525 BAB32774.1 GI:13094185	146, 1-127 165, 1-127	
Pseudomonas syringae	YP_235578.1 GI:66045737	160, 1-133	Ae, M
No. genomes with Hrs/Total	6/14		
Reinekea			
Reinekea sp. MED29	ZP_01113653.1 GI:88798066 ZP_01113654.1 GI:88798067	150, 1-126 151, 1-126	Aq
Vibrionales			
Vibrio cholerae	NP_230861.1 GI:15641229	372, 1-132	F, Aq
Vibrio parahaemolyticus	NP_797668.1 GI:28898063	381, 1-132	F, Aq
Vibrio splendidus	ZP_00990126.1 GI:84387104	383, 14-146	F, Aq
Vibrio vulnificus	NP_761216.1 GI:27365688	371, 1-132	F, Aq
No. genomes with Hrs/Total	4/11		
Xanthomonadales			
Stenotrophomonas maltophilia	ZP_01642673.1 GI:119875611	153, 1-127	
Xanthomonas axonopodis	NP_642798.1 GI:21243216	153, 1-127	Ae, HA
Xanthomonas campestri	NP_637705.1 GI:21231788	153, 1-127	Ae, HA

No. genomes with Hrs/Total	3/5		
Unclassified gammaproteobacteria			
Marine gamma proteobacterium	ZP_01224113.1 GI:90416181	174, 29-166	Aq
No. genomes with Hrs/Total	34/104		
Deltaproteobacteria			
Bdellovibrionale			
Bdellovibrio bacteriovorus	NP_970264.1 GI:42524884	136	Ae, M
Desulfobacterales			
Desulfotalea psychrophila	YP_065523.1 GI:51245639 YP_064708.1 GI:51244824 YP_065775.1 GI:51245891	156, 1-129 370,1-132 374, 1-130	An, Sp
Desulfovibrionales	One other genome - no Hrs		
Desulfovibrio desulfuricans	YP_386749.1 GI:78355300 YP_386930.1 GI:78355481 YP_389304.1 GI:78357855	150, 1-143 579, 441-573 722, 580-722	An, M
Desulfovibrio vulgaris	YP_389304.1 GI:78357855 YP_012317.1 GI:46581509 YP_009395.1 GI:46578587 AAB50497.1 GI:887858 YP_012365.1 GI:46581557	137 655, 520-646 689, 548-682 959, 810-955 963, 827-957	An, M
Desulfuromonadales			
Desulforomonas acetoxidans	ZP_01311722.1 GI:95928977 ZP_01311940.1 GI:95929196 ZP_01313281.1 GI:95930546 ZP_01313282.1 GI:95930547 ZP_01313679.1 GI:95930950 ZP_01312822.1 GI:95930083 ZP_01313525.1 GI:95930793 ZP_01313825.1 GI:95931099	132 133 142, 1-129 199, 35-159 368, 1-131 371, 7-132 591, 8-132 1174, 1030-1174	An
Geobacter sp. FRC-32	ZP_01390530.1 GI:110602439 ZP_01387533.1 GI:110599293	132 135	An, M
Geobacter lovleyi	ZP_01593656.1 GI:118745688 ZP_01594022.1 GI:118746066 ZP_01592161.1 GI:118744164 ZP_01593682.1 GI:118745715 ZP_01594207.1 GI:118746259	135 137 147, 1-131 518, 372-512 768, 620-740	

Geobacter metallireducens	YP_386060.1 GI:78224313 YP_383801.1 GI:78222054	135 155, 12-146	An, Aq
Geobacter sulfurreducens	NP_953971.1 GI:39998020 NP_952095.1 GI:39996144 NP_951461.1 GI:39995510 NP_953680.1 GI:39997729 NP_951317.1 GI:39995366	131 134 135 139 145	An, M
Geobacter uraniumreducens	ZP_01143645.1 GI:88938143 ZP_01140038.1 GI:88934395	135 138	MAe, M
Pelobacter carbinolicus	YP_355938.1 GI:77918123	135	An, Aq
Pelobacter propionicus	YP_902721.1 GI:118581471 YP_901724.1 GI:118580474 YP_902711.1 GI:118581461	138 143 518, 380-508	An, M
No. genomes with Hrs/Total	7/7		
Myxococcales			
Anaeromyxobacter SP.Fw109-5	ZP_01667972.1 GI:121536194 ZP_01668151.1 GI:121536373 ZP_01669396.1 GI:121537620 ZP_01670274.1 GI:121538500 ZP_01669455.1 GI:121537679 ZP_01671347.1 GI:121539576	132 133 135 142, 1-135 149, 1-129 195, 44-177	
Anaeromyxobacter dehalogenans	YP_467301.1 GI:86160516 YP_466223.1 GI:86159438 YP_466224.1 GI:86159439 YP_463433.1 GI:86156648 YP_463788.1 GI:86157003 YP_463705.1 GI:86156920 YP_463306.1 GI:86156521 YP_463596.1 GI:86156811	133 133 133 138 144, 1-129 144, 1-129 146, 1-130 148, 1-135	An, Tr
Myxococcus xanthus	YP_635509.1 GI:108758665	185, 11-139	
Unclassified deltaproteobacteria			
Deltaproteobacterium MLMS-1	ZP_01288141.1 GI:94264349 ZP_01288112.1 GI:94264319 ZP_01291329.1 GI:94268940 ZP_01290755.1 GI:94267120	135 148, 10-142 296, 150-283 457, 320-450	Aq
No. genomes with Hrs/Total	14/18		

Epsilonproteobacteria			
Campylobacter coli	ZP_00367964.1 GI:57168833 ZP_00367250.1 GI:57168111 ZP_00367884.1 GI:57168753 ZP_00367885.1 GI:57168754 ZP_00368169.1 GI:57169041	112 199. 1-123 203, 1-128 229, 1-130 268, 1-134	Mae, M
Campylobacter fetus	YP_892819.1 GI:118474426 YP_891782.1 GI:118474590	183, 1-127 385, 1-143	MAe, M
Campylobacter jejuni	YP_999771.1 GI:121613643 ZP_01068960.1 GI:86150744 ZP_01069655.1 GI:86151450 ZP_01072240.1 GI:86154039 NP_281267.1 GI:15791444 ZP_01067851.1 GI:86149621 YP_178071.1 GI:57237059	144, 1-132 199, 1-127 202, 1-132 239. 1-132 240, 1-132 242, 1-132 254, 1-132	MAe, M
Campylobacter lari	ZP_00368466.1 GI:57240517	187, 1-132	MAe, M
Campylobacter upsaliensis	ZP_00370672.1 GI:57242735 ZP_00369894.1 GI:57241954 ZP_00371184.1 GI:57505255	199, 1-127 202, 1-127 233, 1-127	MAe, M
Helicobacter hepaticus	NP_859535.1 GI:32265503 NP_859536.1 GI:32265504	184, 1-128 187, 1-128	
Thiomicrospira denitrificans	YP_393480.1 GI:78777165	1004, 1-128	An, Aq
Wolinella succinogenes	NP_907673.1 GI:34557858	168, 1-132	MAe, HA
No. genomes with Hrs/Total	8/13		
Unclassified proteobacteria			
Magnetococcus sp. MC-1	YP_866138.1 GI:117925521 YP_867250.1 GI:117926633 YP_867131.1 GI:117926514 YP_866733.1 GI:117926116 YP_867005.1 GI:117926388 YP_864332.1 GI:117923715 YP_864533.1 GI:117923916 YP_866360.1 GI:117925743 YP_867064.1 GI:117926447 YP_867464.1 GI:117926847 YP_867464.1 GI:117926847 YP_864243.1 GI:117923626 YP_865500.1 GI:117924883 YP_864127.1 GI:11792351	134 160, 1-130 174, 1-149 249, 10-150 253, 12-247 320, 196-316 779, 646-778 871, 740-860 926, 787-921 927, 787-918 927, 787-918 994, 856-985 997, 863-995 1032, 890-1026	F, Aq
Mariprofundus ferrooxydans	ZP_01451258.1 GI:114775690 ZP_01451244.1 GI:114775676	143 373, 3-131	Aq

No. genomes with Hrs/Total	2/2		
Spirochaetes			
Treponema denticola	NP_971622.1 GI:42526524 NP_971908 GI:42526810	137 143	An, HA
No. genomes with Hrs/Total	1/5		
No. genomes with Hrs/Total	115/440		

[1] Based on NCBI Taxonomy Database (www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi and www.ncbi.nlm.nih.gov /sutils/genom_table.cgi).

[2] From www.ncbi.nlm.nih.gov/genomes/lproks/cgi. Abbreviations: Ae – aerobe; An – anaerobe; Aq – aquatic; F – facultative; HA – host associated; M – multiple habitats; MAe – microaerophilic; Sp – specialized; Th – thermophilic; Tr - terrestrial.

Table 4. Hemerythrin sequences with alterations at the seven iron-coordinating positions.

Name	Accession No.	Remarks	FUGUE Z score
Anaeromyxobacter sp. Fw109-5	ZP_01669455|GI:121537679 ZP_01671347|GI:121539576	Leu/His in helix A Gln/His in helix A and in helix B	18.7 18.5
Anaeromyxobacter dehalogenans	YP_463433|GI:86156648	Gln/His in helix C	19.0
Azoarcus sp.EbN1	YP_157941|GI:56476352	Ser/His in helix C	7.2
Burkholderia phymatum	ZP_01504458|GI:118033012	Ser/His in helix C	6.8
Caldicellulosiruptor saccharolyticus	ZP_00885869|GI:82500456	Ile/His in helix A	20.8
Campylobacter coli	ZP_00367964|GI:57168833	No helix D	15.8
Campylobacter upsaliensis	ZP_00371609|GI:57505683	No helix A	11.9
Clostridium beijerincki	ZP_00910041|GI:82747545 ZP_00911352|GI:82748877 ZP_00908279|GI:82745769 ZP_00909310|GI:82746807 AALO01000013|EAP60047.1	Gln/His in helix C Gln/His in helix C Gln/His in helix C Gln/His in helix C Gln/His in helix C	17.3 19.3 21.3 17.7 21.3
Clostridium cellulolyticum	[ZP_00909308|GI:82746805	Gln/His in helix C	21.3
Clostridium thermocellum	ZP_00504934|GI:67875718	Gln/His in helix C	19.4
Dechloromonas aromatica	YP_284887|GI:71907300	Asp/His in helix B	20.8
Desulfitobacterium hafniense	ZP_01371607|GI:109647704 YP_516471|GI:89892984	Gln/His in helix C Gln/His in helix C	17.2 21.1
Geobacter lovleyi	ZP_01593713|GI:118745747	Gln/His in helix B	7.9
Geobacter uraniumreducens	ZP_01143645|GI:88938143	Gln/His in helix C	26.7
Janthinobacterium lividum	ABK64032|GI:118161348	Asp/His in helix B	24.4
Kineococcus radiotolerans	AAEF02000092|EAM73238.1	Ile/His in helix C; Glu/Asp in helix D	8.1
Lumbricus rubellus	CF426790	Asn/His in helix C	20.9
Magnetococcus sp. MC-1	YP_867464|GI:117926847 YP_864243|GI:117923626	Gln/His in helix C[1] Gln/His in helix C[1]	19.8 23.4
Magnetospirillum magneticum	YP_419883|GI:83309619 YP_421315|GI:83311051 YP_420912|GI:83310648 YP_423659|GI:83313395 YP_420035|GI:83309771 YP_422017|GI:83311753 YP_421602|GI:83311338 YP_420779|GI:83310515 YP_422781|GI:83312517	Arg/His and Asp/His in helix C Leu/His in helix C Gln/His in helix C Gln/His in helix C Ile/His and Gln/His in helix C; Tyr/His in helix D Asn/His in helix C Asn/His in helix C Asn/His in helix A; Asn/His in helix B Arg/His in helix A; Ala/His in helix B	14.8 16.1 18.1 19.2 17.6 17.0 20.5 19.6 6.8

	YP_421350|GI:83311086 YP_422163|GI:83311899	Val/His and Gln/His in helix C; Tyr/His in helix D Gln/His in helix A; Asn/His and Gln/Glu in helix B	21.0 20.6
Magnetospirillum magnetotacticum	ZP_00052849|GI:46202650 ZP_00053886|GI:23014047 ZP_00053732|GI:23013881 ZP_00055446|GI:23015677 ZP_00051444|GI:23010917 ZP_00052929|GI:46202606 ZP_00052752|GI:23012741 ZP_00055707|GI:23015944 ZP_00053639|GI:46202172 ZP_00055499|GI:23015731	Missing helix A Arg/His and Thr/His in helix C Leu/His in helix C Met/His in helix C Gln/His in helix C Asn/His in helix C Asn/His in helix C Arg/His in helix A; Ile/His in helix B Missing helix D Ala/His in helix B	13.1 23.2 18.8 17.7 18.8 17.6 17.6 8.0 9.1 18.1
Marine γ-proteobacterium	ZP_01224113|GI:90416181	Glu/His in helix A	17.6
Myxococcus xanthus	YP_635509|GI:108758665	Gln/His in helix C	8.2
Novosphingobium aromaticivorans	YP_497813|GI:87200556	Ser/His in helix C; Glu/Asp in helix D	6.5
Pseudomonas mendocina	ZP_01526847|GI:118058386	Glu/His in helix C; Glu/Asp in helix D	6.6
Pseudomonas resinovorans	BAB32774|GI:13094185	No His or Asp in helix D	17.5
Pseudomonas syringae	YP_235578|GI:66045737	Ala/His in helix C	6.9
Ralstonia pickettii	ZP_01661972|GI:121529360	Ala/His in helix C; Glu/Asp in helix D	6.5
Rhodospirillum rubrum	YP_427592|GI:83593840	Met/His in helix B[2]	20.4
Shewanella woodyi	ZP_01539832|GI:118071638	Gln/His in helix C	16.1
Sphingomonas sp. SKA58	ZP_01303096|GI:94496520	Glu/His in helix C[3]	6.9
Sphingomonas wittichii	ZP_01607194|GI:118759500	Leu/His in helix C	8.4
Thiobacillus denitrificans	YP_314491|GI:74316751	Lys/His in helix C	7.9
Vibrio parahaemolyticus	NP_797668|GI:28898063	Tyr/His in helix B[4]	19.1

[1] Methyl-accepting chemotaxis sensory transducer.
[2] Response regulator receiver domain protein (CheY).
[3] But there is a His next to the Glu (see alignment in Fig. 2 Supplemental Information).
[4] GGDEF family protein.

Table 5. Numbers of alterations to the His resIdues coordinating the two Fe atoms in the four helices of bacterial Hrs.

Alteration	A	B	C	D	Total
Gln / His	2	2	20	0	24
Asn / His	1	2	5	0	8
Lys, Arg / His	2	0	3	0	5
Ala, Val, Leu, Ile, Met, Tyr / His	2	5	9	2	18
Glu, Asp / His	1	2	4	0	7
Ser, Thr / His	0	0	3	0	3
Others	0	0	0	2	2
Helix missing	2	0	0	2	4
Total	10	11	44	6	71