

```
1 >Globobulimina_NorI_GloG15_CONTIG49717:890-3289
2 M-----ADVA
3 PKEGEWILRPAKTNWIATLSNKNYWAFYFLVIVAICVGGIGYF--GEVAHYEVPPLCDFV
4 --G-PDGSVVISAKSINHGEVVFHLRGLMAYGSFLGDGSEGRPDYTAELHELAIGMTKH
5 YESKCLKHK-----TQHDVEALKPRVRMELR----NNAYD-LEKDVIV
6 LNSAQISAWKRIKTYRRIFAGADQG-----TSTL----TPN----MFITN
7 PTDIADLAGFFFWGAWMSAARPGEDYSYTHNWPHEPLAGNIPTAVILWSAISVLILWF
8 GLAATLFIYQQLDHENEDEEDIKT----KGQPLTTQDLET---GVVRETQVDCYKFFVLS
9 MLAFAIQVIAGVCCAIDFV---RPL-----GFS-ACYILGYNVLRSYHATFQIFWFFVA
10 WVGTTIWFLPRFQRRVPIGQKFLINLLFGGCCVVALGGAIGIPLGQTGYI-QGEMAYYFG
11 SQGWEFMELGRIFQDLLLCGFVLWILILFRGVYSYITWNT-IWSTPAWVFYGS LVMVWFL
12 FFSLKVTPKTNFIVSDFWRWMMVVMWVEVTFEVFTTVIVAFLYREMGLVSKKAAERATYI
13 AVMLFFLTATIGVGHNFYWIAKPTGVIAMGSAFSTTQVMPLILLTMDAWKFIQMRE----
14 KAELEQAKGNQKHIMRGVWLFMLGVNFWNVFGAGILGSFINLPVVNYMHSTYL TGNHAH
15 AAMWGVKGNIAIAGVLFVCVQHTVQEKYWSPKIVSVAFWSLNGGIAAQMFLSMFPAGLVHM
16 YTAMA EGLWAARTHDMYNSTIFQNLAKGRAFGGHI FLWGGLLPLVYFVVSRYFYLK-PVT
17 P-----NIDKNRKYDS-----F---WLDAAHTAPYSTKK-----
18 --LV
19 >Globobulimina_NorII_GloT15_NODE_10819:151-2556
20 MST-----DAKSY
21 PLIQDFVPSGTRNNWIATLSDKRWTFYFAIIVAICVSGIGYF--GGVAHYQNPPNCFDFV
22 --D-QNGKVVPQSMIKHGEEIFHLRGLMSYGSFLGDGSEHGVDYTAELHMMALSMGDF
23 YTAQLRQNTSR-----E---LAEHDMEAVKARVRLELR----ANTYE-EARDVVV
24 LNEAMVYAWKDLEKYHLRMHFEDGFG-----DLL----PN---ERFAK
25 KRVDSDMAAFFYWGWI SVAARPGEDYSYTHNWP HDPLVGNLPTAATILWSTLSVGVLV
26 GLGITLFIWQQRKDEIEA--DDGT----TGKPLTTQDLEL---GVVHPTQLACYKFFVLA
27 MIAFAIQVLGGIACSVVV---RPG-----GLT-LCMWIPYTVLRSYHTTFQIYWFFVA
28 WVGTTIFFLPRFQKPPAGQLFLINLLGVGCAIVAAGGLIGIPLGQGGYL-EGDMAYYFG
29 SQGWEFMELGRAFDILLGGFVLWIFILFRGVYSYITWDT-IWSTPAWLFYGS LVMVWFL
30 FFSLKVTPD TDFVVSDFWRWMMVVMWVEVTFEVFTTVIVAYLYREMGLVSKKGAERATYI
31 AVMLFFLTATIGVGHNFYWIAKPTGVIALGSAFSTTQVMPLILLTLDWKYIQVSE----
32 RAELERKKGNQKHVMKAAWL FLLGVNFWNVFGAGILGSFINMPIVNYYMHATYL TGNHAH
33 GAMFGVKGNVALAGVLFCAQHLVKEEAWSPKLLSLSFCMNGGIAAQMFLSLFPTGMYHM
34 YINMEGLYAARKFEVTQGYIFQTLAKGRAVGGHI FLWGGLLPLVYFILSRAAYLK-DAT
35 K-----NAPGKRYQS-----F---WLDSAHTAGYKVK-----
36 --VY
37 >Ga0066833_100066952
38 MTLVV-----
39 -PESVIPKAAAYDTNMAGKLANKNYWG VYGILVF AIIVLGTGYM--TGAAIFEVPPLVDFV
40 --S-ETGEVVLSTSKINHGE EIFHHRGLMSYGSMLGDGSEGRPDFTAELHIMAVSMGEF
41 YVKKHGDGQTDAG-----S---NSTYDMEAIKARVITELH----LNTWNGDDKGVIV
42 LSEAKISAWQAVRKHYRRVYYREEASVSGSEDEVSSADSAGSGRVGL---WSI---ERFAN
43 PGHADDLAAFFFWGAWCCVANRPSEDYSYTHNWPYDPLAGNTPTPEVMIWSVASL FVLFF
44 GLMITLYIYGQFP EEEEEP-----LTQQPLTTQDLEA---DIVRPTQQATYRFFVLA
45 IAAFFIQVVS GIACAIDFI---RPG-----GFS-VCQFLPFSVFRSYHTTFQIYWFFVA
46 WVGTTIFFLPRFSK-V PAAQHGLIDLLYIGCVVVALGGVIGIPLGQTGFL-EGPVAYYFG
47 SQGW EYMELGRFYQDVLLAGFVLWIVIMFRGVWPYLT LRR-AWSPPAWLFYGSIVMVAFL
48 FFSLKVTPKTNFIISDFWRWMMVVMWVEVTFEVFTTVIVSYLLVEMGLVTRKKA EKTYYI
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49 AVMLFFLTATIGVGHNFYWIAKPTGVIALGSTFSTTQILPLILVTLDAWKIMQEKS-----
50 RAEAEQKKGNQOQYVMKEVFQFVVGINFWNIIFGAGVLGSLVNLPIVNYLHSTYLTGCHAH
51 GAMFGVKGNVALAGVLFVQHLVVEEKHWSGRLINISFWCLNGGMALMMFLSLFPTGLYQL
52 FMVIKYGFWYARSAEIVHGPVFQFLLKLRPIGGHIFFEGLLPLLYFVFRGFKLK-NET
53 D-----PKSMGKDRYRS-----T---WHIDEADTKK-----

54 --EQ

55 >Ga0066844_100022823

56 MTLIA-----

57 -PESGIPKATYDTNMAGKLSNKKYWGVIIVIAIIVLGNGYM--TGAAISEVPPLVDFV
58 --S-ETGEVIMSTSKINHGEEIFHHRGLMSYGSVLGDGSEKPDFTAEALHIMAVSMGEF
59 YVEKHGQTDAG-----A---GSAYDMEAIKARVIAELH----LNTWNGDDNGVIV
60 LNEAKIFAWQAVRKYRYYRYYREEASVSGSED-----GGL---WPT---ERFAN
61 PEHADDLAAFFFWGAWCCVANRPSSESYTHNWPYDPLAGNTPTPEVMIWSVASLFFVLF

62 GLMITLYIYGQFPEDDEP-----LTQQPLTTQDLEA---DIVRPTQRATYKFFVLA
63 IAAFFIQVISGIAAIDFI---RPG-----GFS-VCEFIPFSVFRSYHTTFQIYFFFVA
64 WVGATIFFLPRFSK-VPTAQHGLIDLLYIGCIAVALGGVIGIPLGQTGYL-EGPMAYYFG
65 SQGWEYMELGRFYQDVLLAGFVLWIVIMFRGVWPFLTWKR-VWSPPAWLFYGSVIMVAFL
66 FFSKLVTPKTNFIISDFWRWVHMWVEVTFEVFTTVIVSYLLVEMGLVTRKMAEKTTYI

67 AVMLFFLTATIGVGHNFYWIAKPTGVIALGSTFSTTQILPLILITLDAWKIMQEKS-----
68 RAEAEQKKGNQMYVMKEVFQFVVAINFWNIIFGAGVLGSLVNLPIVNYLHSTYITGCHAH
69 GAMFGVKGNVALAGVLFVQHLVKEKHWSGRLNINISFWCLNGGMALMMFISLFPGLYQL
70 FMVIKYGFWYARSAEIVQGPVFQFLLKLRPIGGHIFFEGLLPLVYFIFSRWYTVK-NET
71 D-----PKSKEENMYRS-----T---WHIDESDTKK-----

72 --VQ

73 >MBS93797_Chromatiales_NP37

74 M-----

75 -----STSSQQNLALWLVNKKNLTHFMIVAGISIAGLIYL--GGATYTGAPPLVDYV
76 --S-SSGDTVISQQQIKRGKELFHIRGLMSWGSFWGDGAERGPFTADALHRTVMGMRAF
77 YGQDLEQRAG-----S---LTQHDQDAISVRVKREVVH----NNAYD-EEAGVIR
78 LNDQVVSALGDLNAHYTRMFNDPAYS-----EAY---EPS---GLISD

79 PDDLRLDTAFFFWGGWVSAADRPGETYSYTHNWPDKDAGNEPTAATFFWSVFSVFALFV
80 GVMIVLYAYGEMKEQPVDVFDQSNESQSGGQSLTTYDLEN---EYVRPTQRATYKFFVLA
81 IIVFGCQILGGVIAATDFV---RPG-----GVS-LNEIIPFNVARSYHTLLQIFWFFMC
82 WVGYTIFFLPRISK-VPPGQKSLINLLFFLCVVTGGGALVGIYMGQTGML-SDNMSYWFG
83 SQGWEFMEELGRFFQFTLLAAFALWIWIIYRAVKPWLTRRN-VWSVPSWLLYGSIMVAFL

84 FFGLLVQPEMNFAISDYWRWVHMWVEVTFEVFTTVIVGYMLVQMGLITRMMMAERVIFL
85 AVMLFLVTATIGISHNFYWIAKPTGIIALGSVFSTLQVLPLLLLTLDAWQMRQEGL-----
86 KADKNVVEGKQTIIVMEGVWLFILGVNFWNIIFGAGVFGSMINLPIVNYEHATYLTGNHAH
87 AAMFGVKGNIALGGMLFCCQHLFHKSANPKLVRTSFWSMNIGLVLMFLDLFPVGLYQT
88 WWAYTDGTWYARSSEIVTGPVFSFLTYCRTIGGAVFIWGGLLPMWFILSRGTKLRRKEE
89 E-----VEQGEWTVYEA-----D---WADQKDPALGG-----

90 ----

91 >MBT76598_Chromatiales_NP153**

92 M-----

93 -----SNANQQNLALWLVNKKNLTHFLIVATICIAGLIYL--GGATYTGAPPLVDYV
94 --S-ATGETVISQQQIKRGQELFHIRGLMSYGSFWGDGAERGPFTADALHRTVIGMRGF
95 YAQEKENSGV-----V---LDKHDHGAIASRVKLEVVH----ENTYD-ENAGIIH
96 INDAQIQAFNDLNDHYTQMFTNPDYTCYRDCANPS-----NEAF---LPS---GHISD

97 PDDLRLSAFFFWGGWVASTNRPGENYSYTHNWPGDKDAGNSPTAATFFWSVFSIFALFV
98 GVMVVLAYAYGQMKEQPVDVFDSS--RNGGQSLTTYDLEN---EYVRPTQRATYKFFVLA
99 VIVFGVQIIGGVIAATDFI---RPG-----GVS-LNDIIPFQVARSYHTLLQIFWFFMC
100 WVGTYIFFLPRISK-VPPGQKALINLLFVLCVVTGGGALVGIYMGQTGML-SDSMSYWFG
101 SQGWEFMELGRRFFQFTLLAAFALWIGIYRAVKPWLTRRN-LWSVPSWLLYGGSGIMVMFL
102 FFGLLVQPEMNFAISDYWRWVHMWVEVTFEVFTTVIVGYMLVQMGLITRMAERVIFL
103 AVMLFLITATIGISHNFYWIAKPTGIIALGSVFSTLQVLPLLLLTLDAWQMRQEGL-----
104 TANKNVVEGKQTIIVMEGVWLFILGVNFWNIFGAGVFGSVVNLPIVNYEHATYLTGNHAH
105 AAMFGVKGNIALGGMLFCCQHLFHKSAWNPKLVRTSFWSLNIGLVLMFLDLFPVGLYQT
106 WIAYTEGTWYARSSEIVTGPVFSFLTYCRTIGGAVFIWGGLPLMWFILSRGFKLRRKEE
107 E----VEQGEWTVYES-----E---WAEQNNPSLGG-----
108 ----

109 >Ga0187827_100036806

110 M-----
111 -----STTSTSNQNIALWLVNKKNLTHFMIVSAICIAGLIYL--GGATYMGSPPLEDYV
112 --SASTGETVITRTQIKRGQELFHIRGLMGYGSFWGDAERGPDFSADALHRTVMGMRSF
113 YAQELADSGV-----A---PTEYDAGAIARVRGEVH----ENYYD-EVAGVIR
114 INDAQISAFSDVVDHYTAMFNDPTYS-----EAF---EPS---GFISD
115 PDDLELSAFFFWGGWVSAANRPGETYSYTHNWPNDPDAGNSPTAATFFWSVFSIFALFV
116 GVMLVLYVYGMREQDQVDVFDTSGNENNGQSLTTYDLEN---EYVRPTQRATYKFFVLA
117 MIVFLVQIIGGVLAATDFV---RPF-----GVS-MNDIIPFTVARSYHTLLQIFWFFMC
118 WVGTYIFFLPRISK-VPPGQKTLINLLFVLCIVTGGGALAGIYMGQTGML-SDSAAWFG
119 SQGWEFMELGRRFFQFTLLAAFALWIFIYRAVRPWLTKRN-LWSVPSWLLYGGSGIMVMFL
120 FFGMLVQPD MNFAISDYWRWVHMWVEVTFEVFTTVIVGYMLVQMGLITRMAERVIFL
121 AVMLFLITATIGISHNFYWIAKPTGIIALGSVFSTLQVLPLLLLTLDAWQMRQEGH-----
122 TATQNMMEGKQTIIVMEGVWLFILGVNFWNIFGAGVLGSVINLPIVNYEHATYLTGNHAH
123 AAMFGVKGNIALGGMLFCCQHLFHKAAWNPKLVRTSFWSLNIGLALMMFLDLFPVGLYQT
124 WIAYTEGTWYARSSEIVTGPVFSFLTYCRTIGGMVFIWGGLVPMVWFILSRGTKLRLKEE
125 D----VAEGEWTVYEQ-----A---WSEQNDPSLGG-----
126 ----

127 >Ga0187827_100071743*

128 M-----
129 -----STTSNQNIALWLVNKKNLTHFMIVSAICIAGLIYL--GGATYMGSPPLEDYV
130 --SASTGETVISRTQIKRGQELFHIRGLMGWGSFWGDAERGPDFSADALHRTVLGMRSF
131 YAQELENSGV-----S---PTEYDAGAIASRVRDEVH----VNNYD-EVAGVIR
132 INDAQISAFADLNEHYTAVFNDPTYS-----EAF---EPS---GFISD
133 PDDLTAFFFWGGWVSAANRPGENYSYTHNWPNDPDAGNSPTAATFFWSVFSIFALFV
134 GVMLVLYVYGMREQDQVDVFDTSAGNENNGQSLTTYDLEN---EYVRPTQRATYKFFVLA
135 MVVFLVQIIGGVVAATDFV---RPG-----GVS-LNEIIPFTVARSYHTLLQIFWFFMC
136 WVGTYIFFLPRISK-VPPGQKSLINALFVLCVVTGGGALAGIYMGQTGML-SDGAAYWFG
137 SQGWEFVELGRFFQFTLLAAFALWIFIYRAVKPWLTKRN-LWSVPSWLLYGGSGIMVMFL
138 FFGMLVQPD MNFAISDYWRWVHMWVEVTFEVFTTVIVGYMLVQMGLITRMAERVIFL
139 AVMLFLITATIGISHNFYWIAKPTGIIALGSVFSTLQVLPLLLLTLDAWQMRQEGH-----
140 TATKNMIEGKQSIIVMEGVWLFILGVNFWNIFGAGVLGSVINLPIVNYEHATYLTGNHAH
141 AAMFGVKGNIALGGMLFCCQHLFHKAAWNPKLVRTSFWSLNIGLALMMFLDLFPVGLYQT
142 WWAYTDGTWYARSSEIVTGPVFTFLTYCRTIGGMVFIWGGLVPMVWFILSRGTKLRLKEE
143 D----VAEGEWTVYEN-----A---WSDQKDPSSLGG-----
144 ----

145 >RLA57063_Gammaproteobacterium_B36_G6
146 M-----
147 -----SSQNLTGTVLTSRKNWFGVFLLVAAISVAGLIYL--GGATYTGAPPLENIE
148 --S--STGDVIISRDIHKGETVFHLRGLMSWGSFWGDGGERGPDFTADALHRTAMSMRRF
149 YELEVEANSR-----P---ATQYDKDAISVRVRELH----NNAYD--EDRGLIE
150 INDAQIFALKELNEHYTSMFMDPSYS-----EAF---DPA---GYISD
151 PTDIKNLTAFFFWGGWVSAANRPGENYSYTHNWPGDKAAGNAPTSATFMWSVFSVFALIL
152 GISAVLYVYGGEMKDQDQDMFEAEE-----GTTLTTYDLEN---EYVRPTQKATYKFFVLA
153 IIVFAVQIIAGTIIATDFV---RPG-----GMS--LNEIIPFPIARSYHTLLQIFWFFMC
154 WVGYTIFFLPRISK-VPTGQKLLIDVLFVLCITGVGSIVGIYLGQSGVL-TGDAAYWLG
155 SQGWEFMEGRFFQLTLLSSFALWIFIYRAVKPWLTAKN-MWSVPSWLLYGGSGIMVFFL
156 FFGFLIQPEMNFAIADYWRWVHMWVEVTFEVFTTVIIGYMLVQMGMITRMAERVIPL
157 AVMLFLITATIGISHNFYWIAKPTGIIALGSVFSTLQVPLLLLLTLDWQMREEGH----
158 WANKNRMAGKQNHVMEGVWLFILGVNFWNIFGAGVLGSVINLPVNYEHATYLTGNHAH
159 AAMFGVKGNIALGGMLFCCQHLFHKEAWNAKLVKTAFWSLNIGLAMMMFLDMFWVGLYQT
160 WVAFTDGTWYARSQAIATGNVFVYLT SARALGGLVFIGGLLPLVWFILSRGSKLRLKEE
161 D----VEEGEWTVYEQ-----D---WSEQNDPALGG-----
162 -----

163 >MBT4522754_Halieaceae_SI047_bin19
164 M-----
165 -----SSQNLAITLMNRKNWFTIFLIVSAISIAGLIYL--GGATYTGAPPLENFE
166 --S--STGNVVISRDQIKKGEEVFHLRGLMSWGSFWGDGAERGPDFTADALHRTAMSMRRF
167 YEQEVADRTGQ-----A---ATQYDKDAISVQVIRELH----TNTYD--EDRGLIQ
168 INDAQIFALKELNEHYTSMFTDADYY-----EAF---DPA---GYISD
169 PDDIAKLTAFFFWGGWVAAANRPGESYSYTHNWPGDKDAGNFPTSATFMWSVFSIFALIL
170 GVCIVLYVYGGQMKEEEQDMFEAEE-----GATLTTYDLEK---EYVRPTQKATYKFFMLA
171 ILVFGVQILAGIIIATDFI---RPG-----GVS--LNEILPFPVARSLHTLLQIYWFFMC
172 WVGYTIFFLPRISK-VPNGQRALINILFTLCLITGVGAIVGIFLGQTGII-TGQMAYWFG
173 SQGWEFMELGRFFQFTLLASFALWILIIYRGVKPWLTMKN-MWSVPSWLLYGGSGIMVFFL
174 FFGLLVQPD MNFAISDYWRWVHMWVEVTFEVFTTVIIGYMLVQMGMITRMAERVIPL
175 AVMLFLITATIGISHNFYWIAKPTGIIALGSVFSTLQVPLLLLLTLDWKMREEGR----
176 WADKNRIAGKQTHVMEGVWLFILGVNFWNIFGAGVFGSLINLPVNYEHATYLTGNHAH
177 AAMFGVKGNIALGGMLFCCQHLFQKPAWNAKLVRTAFWSLNIGLAMMMFLDLFWVGLYQT
178 WIAYTHGTWFARSQEIIVTGDVVFVYMTYARSLGGVFVFIGGLIPLIWFIMSRATKLRQEE
179 D----VQEGEWTVYDK-----D---WGEQNNPALGG-----
180 -----

181 >MBP20251_Gammaproteobacterium_NP964*****
182 M-----
183 -----SQNLAITLMNKNWAALFALVSAISIAGLIYL--GGATYTGSPPLENFK
184 --A--ANGDIVISREAIKGGEEVFHLRGLMSWGSFWGDGGERGPDFTADALHRTAMSMREF
185 YAQELGGSTSQYD-----T---LPQYDKDAIAARVIRELH----ANTYD--EESGFIG
186 INDAEIIYAFEELNKHYTRMFTDASYE-----EAF---SPA---GYISE
187 PDQLRDLTAFFFWGGWVSSSNRPGENYSYTHNWPGDKDAGNTPDATFMWSVFSIFALIF
188 GIGAVLYVYGGQMKQPVDVFEAGDDNGNGQQLTTYDLEN---EYVRPTQRATYKFFMLA
189 IIVFGVQILAGIIIATDFV---RPF-----GMD--LNELIPFTVARSYHTLLQIYWFFMC
190 WVGYTIFFLPRISK-PPGQKGLIDLLFALCVITGAGAIFIGIYLGQTGVI-TGSMAYWFG
191 SQGWEFMELGRFFQFTLLTSFALWILIIYRGVKPWLTTKN-MWSVPSWLLYGGSGIMVAFL
192 FFGGLMIQPEMNFAISDYWRWVHMWVEVTFEVFTTVIIGYMLVQMGLITRLMAERVIYL

193 AVMLFLITATIGISHNFYWIAKPTGIIALGSVFSTLQVLPLLLLTLDWQMRQEGN-----
194 SAEKNRVEGKQTFVMEGVWLFILGVNFWNIFGAGVFGSLINLPIVNYEHATYLTGNHAH
195 AAMFGVKGNIALGGMLFCCQHLFTRTAWNAKLVKTAFWSMNIGLAMMMFMDLFWVGLYQT
196 YVAF AEGTW MARSQEIVTGPV FVYLT SARALGGLVFIWGGLLPMMWFILSRGNKLRLKEE
197 D-----VEEGEWTVYDK-----D---WSAQTDP SRGG-----
198 -----

199 >MBV28360_Rhodospirillaceae_NP1106****

200 M-----
201 --SKESNGNSIHQNLALILLNKNYWITHFMIVVVISVVGLIYL--GRV TYTGAPPLVDYV
202 --S--SAGDTVISREEIKRGE EVFHLRGLMSYGSFWGDGAERGPDFSADALHRTVVTMR SF
203 YENEAKEKG-----A---VSQYDQDAIAAQVKRE VH----HNTWE--EDADLIR
204 INDAQIYA FEELNVHYTKMFSDPDYP-----EHF---M-T---GYITD
205 SEDIRALT AFFYWGGWVAAANRPGETYSYTHNWPYDPDAGNTPTSANYIWSIISILALFL
206 GIGVVLYVY GQMKS LGGEPFSGN-----GTSLTTHDLEN---EYVRPTQRATYKFFALA
207 VILFGIQVLAGIISATDFV---R PY-----GLY-LGDIIPFTVARSYHTLFQIFWFFMC
208 WVG YTIFFLPRLAK-VPNGQAF LINLLFALCII VGGGALVGIYLGQTGVL-TGPAAYWFG
209 SQGW EFMELGRA FQIILLMAFALWIAIIYRGVKPWLTKKN-LWSVPAWLLYGS GIMVAFL
210 FFGLLVTPDTNF AIADYWRWMVVMWVEVTFEVFTTVIVAYMLVQMGLVTRMMAERVIFL
211 AVILFLITATLGISHNFYWIAKPTGIIAIGSVFSTLQVLPLLLLTLDWAKMRQEGE-----
212 RANEYVAQ GKQKFLMDGVW MFILAVNFWNIFGAGVFGSLINLPIVNYFEHATYLTGNHAH
213 AAMFGVKGNIALGGMLFCCMHLFHKASWNP KLVMTSFWSLNIGLALMMFLDLFPVGVYQL
214 VAVLQ EGLWYARSYEIVQGVVFQTLTYFRSLGGAVFVIGLLPLIWFVLSRGSQLR-REV
215 E----VKDGEWSVYEK-----H---WATQEDSKLLG-----
216 -----

217 >MBL6933931_Alphaproteobacteria_S150m-G7_BlackSea

218 M-----
219 ----KSN GNSIHTNLALILLNKNYWIWHFLV VVVIGVVGLIYL--GRATYTGAPPLVDYV
220 --S--SAGDTVISREEIKKGE EVFHLRGLMSYGSFWGDGAERGP DFTADALHRTVVAMKSF
221 YEDARSKETS R-----T---VSQHDKDAIAARVKREVR----KNTWD-EDANLIQ
222 INPAQAHA FEELNDHYTKMFSDPEYP-----EFF---M-S---GYITD
223 PEDIRNLTA FFYWGGWVAAANRPGETYSYTHNWPYDPDAGNTPTSATNIWSIISILALFL
224 GIGVILYVY GQMKTLQGD PFASN-----GTSLTTHDLEN---EYVRPTQRATYKFFALA
225 VILFGLQVLAGIISATDFV---RPF-----GLY-LGDIIPFTVARSYHTLFQIFWFFMC
226 WVG YTIFFLPRLAK-VP SGQAF LINLLFALCMVVGAGSLVGIYLGQTGIL-TGPAAYWFG
227 SQGW EFMELGRA FQIILLVAFALWILIIYRGVKPWLTKKN-LWSVPAWLLYGS GIMVAFL
228 FFGLLVTPETNF AIADYWRWMVVMWVEVTFEVFTTVIVAYMLVQMGLVTRMMAERVIFL
229 AVMLFLITATLGISHNFYWIAKPTGIIAIGSVFSTLQVLPLLLLTLDWQMRQEGE-----
230 RANEYVAQ GKQRFLMDGVWLFILAVNFWNIFGAGVFGSLINLPIVNYFEHGTYLTGNHAH
231 AAMFGVKGNIALGGMLFCCMHLFHRASWNP KLIKTAFWSLNIGVALMMFLDLFPVGVYQL
232 VAVLQ EGYWYARSHEIVQGVVFQTLTYFRSIGGAVFVIGLLPLIWFILSRGFQLR-REV
233 E----VKDGEWSVYEK-----N---WATQEDPKLLG-----
234 -----

235 >MBT5374662_Rhodospirillaceae_SI074_bin107

236 M-----
237 --STQSYKSSNRGNLALILLNKNYWIWHFLIVVVIGVVGLIYL--GRLTYTGAPPLVDFT
238 --S--STGETVISLQEIKHGQEVFHLRGLMSYGSFWGDGAERGP DFTADALHRTVVAMKSF
239 YENEAKEGG-----E---LSQYDEDAIAAQVKRE VH----TNTWD-EDAGIIR
240 INAAQIYAIGELNDHYTRMFSDPDYP-----EFF---M-S---GYITD

241 PADIKGLTAFYWGVAANRPGEIYSYTHNWPYDPDAGNTPTSATYIWSIISILALFL
242 GIGVVLVYVYQMKTLQGDPFVSN-----GTSLTTHDLEN---EYVRPTQRATYKFFALA
243 VILFGLQVLGAVISATDFI---RPF-----GLY-MGDIIPFTVARSYHTLFQIFWFFMC
244 WVGYTIFFLPRLSK-VPRGQKFLINLLFMLCIIVGGGSLVGIYLGQTGIL-TGEAAYWFG
245 SQGWEFMELGRLFQIILLVAFTLWILIIYRGVKPWLTKKN-LWSVPAWLLYSGSIMVGFL
246 FFGLLVSPDTNFAVADYWRMVMVHMWVEVTFEVFTTVIVAYMLVQMGLVTRLMAERVIFL
247 AVMLFLLTATLGISHNFYWIAKPTGIIAIGSVFSTLQVLPLLLLTLDAWQMRQEGG----
248 RASEYQSQGKQTFVMEGVWLFILAVNFWNIFGAGVFGSLINLPVINYFEHATYLTGNHAH
249 AAMFGVKGNIALGGMLFCCMHLFKESSWNPGLIKIAFWSLNIGVAMMMFLDLFPVGVYQL
250 MLVFQEGFWYARSQEVVQGTVFQTLTYFRSLGGAVFIIGLLPIIWFILSRGRHLR-REV
251 N----VEDGEWSVYQK-----N---WAEQEDEKLPG-----
252 ----

253 >Ga0066848_100037855*****
254 M-----
255 ---SASAETNGRGDYALVLINKKYWVGLFLIVAASISVGLIYL--GRVTYTGAPPDANFV
256 --S-STGEVLSRQLVARGEVVFHLRGLMGYGSFWGDGAERGPDSAEALHRSVVMRTF
257 YENEIKKDR-----A---VTQFDRDAIGARVKREVEH---VNTWN-EEAGTVT
258 LNDQVFAIQELNVHYTRMFMDPEYK-----HLF---Q-T---GYITD
259 PEDIRALTAFYWGVAANRPGEVYSYTHNWPYDPAAGNYPTSAVYIWSILSIFALFL
260 GIGAVLYVYVYQMKDLGGPEFDGT-----GTSLTTSLEN---EYVRPTQRATYKFFALA
261 MILFGLQILAGIIGASDFI---RPF-----GIF-LGDLVPFTVARSYHTLFQIFWFFMC
262 WVGYTIFFLPRLSK-VPPGQKFLINLLFVGCLIVGAGALVGIYLGQTGVL-TGSTAYWFG
263 SQGWEFMELGRAQFILLGGFALWIFIYRGVVRTWLTNRN-MWSVPAWLLYSGSIMVGFL
264 FFGIFVSPETNFAIADYWRMVMVHMWVEVTFEVFTTVIVAYMLVQMGLVTRLMAERIIFL
265 AVMLFLITATIGISHNFYWIAKPTGIIALGSVFSTLQVLPLLLLTLDAWRMRQEGD----
266 RAQEYRSQKQMFVMEGAWMFILAVNFWNIFGAGVFGSLVNLPIVINYFEHATYMTGNHAH
267 AAMFGVKGNIALAGMLFCCQHLFKSSWNAKLVRTSFWSLNIGLGLMMFLDLFPVGVYQV
268 VIVLQEGLWYARSVDVVRGVSFVTLTYFRMIGGGVFLGGLLPLIWFILSRGFSLV-REV
269 E----VEEGEWVYK-----D---WAAQEDPSLRHSRPLAE-----
270 ----

271 >Ga0187827_100051115*
272 M-----
273 ---SVSAENNHGEDFALILINKKYWMGLFLIVAASISGLIYL--GRATYTGAPPDANFI
274 --S-SSGKTVLSRQLVSRGEEVVFHLRGLMSYGSFWGDGAERGPDTADALHRTVVAMRTF
275 YENELKKER-----A---VTPYDKEAIAARVRLEVH---NNTWD-EKSGTIT
276 LNDQIFAFDEVHKHYTSMFMDPNYP-----ELF---Q-T---GYITD
277 PENIRALSAFFFWGGWVSAANRPGENYSYTHNWPYDPDAGNHPTSATYIWSFLSIFALFL
278 GIGAVLYVYVYQMKVLGGPEFVEN-----GTSLTTSLEN---EYVRPTQRATYKFFALA
279 MILFGLQVLAGIISATDFI---RPF-----GIF-LGDIIPFTVARSYHALFQIFWFFMC
280 WVGYTIFFLPRLSK-VPSGQKFLINLLFLLCVITGGGALVGIYLGQTGALGTGEMAYWFG
281 SQGWEFMELGRAQFVLLVAFALWIYIIYRGVKTWLTNRN-MWSVPAWLLYSGSIMVGFL
282 FFGILVSPETNFAIADYWRMVMVHMWVEVTFEVFTTVIVGYMLVQMGLVTRLMAERIIFL
283 AVMLFLITATIGISHNFYWIAKPTGIIALGSVFSTLQVLPLLLLTLDAWRMRQEGD----
284 RAEHRAQKQMFVMEGVWMFILAVNFWNIFGAGVFGSLINLPVINYFEHATYMTGNHAH
285 AAMFGVKGNIALAGMLFCCQHLFKNSWNPGLVRTSFWSLNIGIAMMMFLDLFPVGVYQM
286 VIVLQEGLWYARSSEIVMGTWVKTLYFRMIGGGVFLGGLLPLIWFILSRGMRLV-REV
287 E----VEEGEWTVYK-----D---WAAQEDPTLRHSPGLAE-----
288 ----

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289 >0EJ69613_Magnetovibrio_blakemorei_MV-1
290 M-----
291 --SSKLNDKLRFKNLSLILLNKKFWFTHFLIVTIIISVAGLIYL--GQATYSGAPPLVHFK
292 --S--STGETVISRQLINAGERVFHLRGLMSYGSFWGDAERGPDFTADALHRMTVSMRSF
293 YAGELKAQGTQ-----D---LGQYDQDAIAARVRREVH----TNTWD--ESSDIL
294 LNEAQIFALEELNRHYTRMFTDPHY-----ELF---Q-I---GYITE
295 PKDIQALTAFFYWGAWVAANRPGEDYSYTHNWPYDPDAGNTPTTATFIWSAMSILGLFL
296 GIGIVLYVYQGMSMHYDPFNGNT-----GTSLTTHDLEN---NYIRPTQRGTYKFFALA
297 IVLFALQVLAGIIGATDFV---RPF-----GLF-LGDIIPFTVARSYHTLFQIFWFFMC
298 WVGYTIFFLPRLSE-APRGQTFLLINLLFTLCIIVGAGALVGIYLGQTGIL-TGDMAYWLG
299 SQGWEFMEFGRLFQIILLVAFTLWIFIIYRGVKPWLTRKN-MWSIPAWLLYGSVMVFFL
300 FFGLLVTPETNFAVADYWRWMVVMWVEVTFEVFTTVIVAYILVQMNLITRAMAERVVFL
301 AVMLFFITATVGLIAHNFYWIAKPTGVIAFGSVFSTLQVLPLLLLLTLDAWRMRQEK-----
302 RANTLRDQGKQTIVMDEVWLFILAVNFWNVFGAGVFGSVINLPVINYEHATYLTGNHAH
303 AAMFGVKGNIALAGLLFCCQHIFEKSSWNAKLIRRSFWSLNIQVAMMMFLDLFPVGVYQL
304 VDLVQNLWHARSYEIVQGDVFKLTLYFRSLGGAVFVIGGVIPLVWFILSRGRRLV-REV
305 Q----IEPNSHTDYEK-----D---WAAQEDAP-----H-
306 ----
307 >MBT38371_Deltaproteobacterium_NP36*****
308 M-----
309 -----SNSSRTIAQILQDKKTWWLHFLIVAAICVTGLVYL--GTETYTGAPPLEDYV
310 --S--ASGETVISREQIKHGQEVFHLRGLMSYGSFWGDAERGPDFTADALHRTVMSMRAF
311 YEKEMGGA-----TTVYDKDAVAARVRREVH----TNTWD--ERAGHIV
312 ISPAQTQGYNDLIVHYTAMFNPNYN-----EAF---EPA---GYISD
313 PEDLRDLSAFFFWGGWVSAANRPGEEYSYTHNWPYDPDAGNATSQTWIWSFISIFGLFL
314 GILVVLYVYQGQFKEQ-GDPFIGN-----GTSLTNDLEE---GRVRATQRATYKFFVFS
315 ILLFGAQLAGIFASMDFV---RPF-----GFS-LGDIIPFTVLRSYHTLFQIYWFFMA
316 WVGYTIFFLPRISK-VPNGQIGLINGLFALCIVTGVGALVGIYAGQTGMI-TGATAYWFG
317 SQGWEFMEIGRAFQYTLGSGFALWIYIIYRGVKPWLTTKN-IWSVPSWLLYGSIMVAFL
318 FFGLMISPEQNFAVSDYWRWMVVMWVEVTFEVFTTVIVGYILVQMGLISRMMCERVIFL
319 AVMMFLVTATLGISHNFYWIAKPTGIIAVGGVFSTLQVLPLLLLLTLDAWRGKSEAG-----
320 RARTHVTEGRQVFMMEGVWLFMLAVNFWNIFGAGVFGSLINLPVINYEHATYMTGNHAH
321 AAMFGVKGNIALGGMLFCIQHLVHKEAWSPKLVRTAFWSLQIGVALMMFLDLFPVGLYQI
322 MIVVQDGLWFARSQEILTGPVWTLTYFRSLGGTLFLLGGVPLIYFIVTRGSELK-EEA
323 D----SDEGEWTVYEK-----D---WAA-----
324 ----
325 >MBW2395684_Deltaproteobacterium_Meg19_02_Bin_150
326 M-----
327 -----SSSGRNLAQVLQDKNTWWVHFLIVTAICATGLIYL--GTQTYSGAPPLESYK
328 --S--ADGATVISREQIKHGQEVFHLRGLMSYGSFWGDAERGPDFTADALHRTVVTMRTF
329 YANELGGV-----VSQYDEDAIAARVRRELH----TNTWD--EEAGHIV
330 INAAQIQAYEDLVVHYTAMFNDPGYG-----EAF---EPA---GYISD
331 PTDLRDLTSFFFWGAWVSAANRPGQVYSYTHNWPYDPDAGNTATSQTWIWSFISIFGLFL
332 GILAILVYVYQGQFKEQ-GDPFEGD-----GTSLTNDLEE---GRVRATQRATYKFFIFS
333 IVLFGCQVLAGVFASMDFV---RPF-----GFS-LGDIIPFTVLRSYHTLFQIYWFFMA
334 WVGYTIFFLPRISK-VPNGQLFLINLLFAICCVTGAGALVGIYAGQTGMI-TGATAYWFG
335 SQGWEFMEIGRAFQYTLTSLFALWIYIIYRGVVRPWLTAKN-IWSVPSWLLYGSIMVGFL
336 FFGLMISPEQNFAVSDYWRWMVVMWVEVTFEVFTTVIVGYVLVQMGLISRMMMAERVIFL
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337 AVMMFLVTATLGISHNFYWIAKPTGIIAVGGVFSTLQVLPLLLLTLDAWRMKSEAG-----
338 RAQTNVVQGRQIFVMEGVWLFILAVNFWNIFGAGVFGSLINLPVNYEYEHATYMTGNHAH
339 AAMFGVKGNIALGGMLFCIQHLIHKEAWNEQLVRRAFWSLQGGGLGMMFLDLFPVGLYQC
340 MIVVQEGLWFARSQEILTGTWVKTLTYFRSIGGTLFIVGGVPLIYFFITSARQLK-PEA
341 D-----SDEGEWTVYEK-----D---WAA-----
342 -----
343 >MBW2230945_Deltaproteobacterium_Meg19_46_Bin_91
344 M-----
345 -----SNPSRNLAQVLQDKRTWVHFLIVA AICATGLIYL--GTETYSGAPPLESFV
346 --SSSTGKVVSREQIKKGQEVFHLRGLMGYGSFWGDGAERGPDFTADALHRTVVTMRDF
347 YADEIAATQ-----A---VTQYDTDAIAARVRREIH----TNTWD-EKAEQIL
348 INDAQVQAYRDLVVHYTRMFNDSEYG-----EAF---EPA---GYISD
349 PQDLENLTAFFYWGAWVSGANRPGQVYSYTHNWPYDPDAGNTATSQTWIWSFISILGLFL
350 GILAVLYVYGQFKEQ-GDPFEGN-----GTSLTNDLEE---GRVRATQRATYKFFVFS
351 IVLFGCQVLAMFASMDFV---RPF-----GFS-LGDIIPFTVLRSYHTLFQIYWFFMA
352 WVGYTIFFLPRISR-VPNGQLFLINALFAICMVTGAGALVGIYAGQTGMI-TGQTAYWFG
353 SQGWEFMEIGRFFQYTLSSFALWIYIIFRAVRPWLTAKN-IWSVPSWLLYSGGIMVAFL
354 FFGLMISPEQNFAVSDYWRWMVVMWVEVTFEVFTTVIVGYILVQMGLISRVMCERVIFL
355 AVMMFLVTATLGISHNFYWIAKPTGIIAVGGVFSTLQVLPLLLLTLDAWRMKSEAG-----
356 RANTNLVAGRQIHVMEGVWLFILAVNFWNIFGAGVFGSLINLPVNYEYEHATYMTGNHAH
357 AAMFGVKGNIALGGMLFCVQHLSKEAWNEKLVRTSFWSLNLGMALMMFLDLFPVGLYQC
358 MIVVQEGLWYARSQEILTGTWVKTLTYFRSIGGTLFIVGGVIPLIWFFFITSATRLE-AEA
359 D-----SDEGEWTVYEK-----D---WAA-----
360 -----
361 >MAG34007_Deltaproteobacterium_ARS120
362 M-----
363 -----SDSNRNLAQILQDKKTWVHFLIVA AICVSGLLYL--GQQTYSGAPPLESFV
364 --T-ADGQTVFSREQIKQGQEVFHLRGLMGYGSFWGDGAERGPDFTADSLHRTVLSMRAF
365 YEEELGANQS-----E---LSLYDKDAVAARVRREVH----NNTWD-EQAGQIV
366 INDAQVRAYNDLVKHYTAMFNDDPYA-----EAF---EPT---GFISD
367 PEELRSLT AFFYWGWSAANRPGQVYSYTHNWPYDPDAGNTATSQTWIWSFISIFGLFL
368 GILAVLYIYGQFKEQ-GDPFVGN-----GTSLTNDLEE---GRVRATQRATYKYFIFS
369 IVLFGCQVVAGIFASMDFV---RPF-----GFS-LGEIIPFSVLRSYHTLFQIYWFFMA
370 WVGYTIFFLPRISR-VPTGQIALINGLFALCMVTGVGALVGIYAGQTGMI-TGSTAYWFG
371 SQGWEFMEIGRFFQYTLTTSFALWIYIIFRAVKPWLTAKN-IWSVPAWLLYSGGIMVAFL
372 FFGLMISPEQNFAVSDYWRWMVVMWVEVTFEVFTTVIVGYILVQMGLISRMMCERVIFL
373 AVMMFLVTATLGISHNFYWIAKPTGIIAVGGVFSTLQVLPLLLLTLDAWRGKSEGG-----
374 RAEKNVLAGRQAFLEMEGVWLFMLAVNFWNIFGAGVFGSLINLPVNYEYEHATYMTGNHAH
375 AAMFGVKGNIALGGMLFCIQHLIHKEAWNEQLVKRAFWSLQIGVALMMFLDLFPVGLYQC
376 MIVVQEGLWFARSQEILTGSVWVKTLTYFRSIGGTLFLVGGVPLIWFILKSATQMK-AEA
377 D-----SDEGEWTVYEK-----D---WAA-----
378 -----
379 >MBM4335308_Deltaproteobacterium_K_DeepCast_100m_m2_268
380 M-----
381 -----SNTKRNLAQVLHDKKTWVHFLIVA AICLSGLVYL--GTETYTGAPPIEDYV
382 --SATTGEVVIPLATIKKGQEVFHLRGLMLYGSFWGDGAERGPDFTADALHRTGVAMRSF
383 YEQQGGGN-----LAQYDKDAIDVRVIREIK----TNTWN-ESAKQIV
384 INDAQIHAFNELKAHYTRMFNDPEYE-----EAF---KPS---GAISA
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385 PEDIEALTAFFFWGGWVSGAERPGQTYSYTHNWPYDPSTGNLPTNQTMVWSFISIFGLFL
386 GILVILYVYGQFKEE-GDPFTGN-----GTSGTTNDLEQ---GRIRATQKATYKFFVFS
387 IILFGAQVLSGMLAATDFV---TPF-----GVS-LASIIPFVSVLRSYHTLFQIYWFFMA
388 WVGYTIFFLPRISK-VPNGQLFLINLLFAICMVTGVGALVGIYMGQTGMI-TGATAYWFG
389 SQGWEFMELGRAFQYTLSSFALWIYIIYRSVRPWLTTKN-IWSVPSWLLYSGSIMVAFL
390 FFGLMISPDQNWAVADYWRWMMVHMWVEVTFEVFTTVIVGYMLVQMGLISRMMCERVIFL
391 AVMMFLVTATLGISHNFYWIAKPTGIIAVGGVFSTLQVLPLLLLTLDAWRMKSEAV-----
392 RAKTHVAAGRQVFMMEGVWLFILAVNFWNIFGAGVFGSLINLPVNYEYHATYMTGNHAH
393 AAMFGVKGNIALGGMLFCAQHLLTKADWSEKLVKNSFWSLQIGLLMMTLDLFPVGLYQL
394 MIVFQEGLWYARSQEVITGPVWTFPTYMRSIGGTLFIVGGVPLIWL FVSRVGKLR-KET
395 PEL--ESEGWTVYEK-----D---WAA-----
396 -----

397 >Q0J32248_Gammaproteobacterium_H2_PR01

398 M-----
399 -STKAANVSTGDSNLAMWLLNKKNWFTFLIVAIISIAGLVYL--GRETYVGAPPLANFV
400 --T-SNGQVLMTTEQLARGKEIFHLRGLMLYGSFWGDGAERGPDFTADAMHRIGASMRSY
401 YEEETKRRTGAE-----S---LTGYEKDAIAQRVLREMH----NNTYN-AEAGTIV
402 LNDAQVFAFDELLQHYTRMFTDPTY-----DRM---DPI---NQVSG
403 EQNLRDLTTFYWGWSAANRPGEEYSYTHNWPYEPEVGNVPTTATFIWTFISIFALWI
404 GISVVLYVYGMKEQPVDVFSQEG---ANGHSLTSDLEN---GYVRETQRSTYKFFALA
405 MIVFGLQVLGGVSAWDFI---RPF-----GIN-LNELLPFTVSRSYHAILQIYWFMC
406 WVGYTIFFLPRLTK-VPKGQKFLINLLFFLSCVAVGAVGGIYAGQRGWI-DDTMSYWFG
407 SQGWEFIELGRFFQVWLLLGFSLWIYIIYRGVKPWISVKN-VWSVPAWLLWGSVMVFLFL
408 FFSVLMTPDSNFAISDYWRWMTVHMWVEVTFEVFTTVIVAYLLVQMGLVTRMMAERVIFL
409 AVMLFFVTAINGISHNFYWIAKPTGIIAVGSVFSTLQVLPLLLLTLDAWQMRQEGG-----
410 RAHEFRVQGKQVVMEGVWLFILGVNFWNIFGAGVFGSLITLPVNYEYHATYMTGNHAH
411 AAMFGVKGNVALAGMLFCLQHLFQKTAWNEKLVRTVFWSFQIGLALMMFLDLFPVGLYQI
412 YVVLTEGLWYARSTEVIMGPVFATLTYLRTIGGAVFIFGGLLPIIYFVLSGASRLR-KEV
413 D----VTTDEWAQYHKEYGNEGGKE---WAAQEELPKVSR-----
414 -----

415 >MBC6944429_Gammaproteobacterium_PR03

416 M-----
417 -STNAANVSTGDSNLAMWLLNKKNWFTFLIVAIISIAGLVYL--GRETYVGSPLANFV
418 --T-SSGQVMTTEQLARGKEIFHLRGLMLYGSFWGDGAERGPDFTADSMHRIGASMRSY
419 YEEETKRRTGAQ-----S---LTEYEKDAIAQRVLREMH----GNTYS-AEAGTIT
420 LNDAQVFAYDELLTHYTRMFTDATYP-----DHM---DPI---NQVSG
421 EQNLRDLTAFYWGWSAANRPGEEYSYTHNWPYEPEVGNVPTTATFIWTFISIFALWV
422 GISVVLYVYGMKEQPVDVFSQEG---ANGHSLTSDLEN---GYVRETQRSTYKFFALA
423 MIVFGLQVLGGVSAWDFI---RPF-----GIN-LNELLPFTVSRSYHAILQIYWFMC
424 WVGYTIFFLPRLTK-VPKGQNFLINLLFVMSVIVALGCVFGIYAGQRGWI-DDKMAYLFG
425 SQGWEFIELGRVFQWILLAAFSLWIYIIYRGVKPWISVKN-VWSVPAWLLWGSVMVFLFL
426 FFSVLMTPDSNFAISDYWRWMTVHMWVEVTFEVFTTVIVAYLLVQMGLVTRMMAERVIFL
427 AVMLFFVTAINGISHNFYWIAKPTGIIAVGSVFSTLQVLPLLLLTLDAWQMRQEGG-----
428 RAHEFRVQGKQVVMEGVWLFILGVNFWNIFGAGVFGSLITLPVNYEYHATYMTGNHAH
429 AAMFGVKGNVALAGMLFCLQHLFQKSAWNEKLVRTVFWSFQIGLALMMFLDLFPVGLYQI
430 YVVLTEGLWYARSTDVIMGPVFATLTYLRSIGGAVFIFGGLIPIIYFVLSGAGRLR-KEV
431 D----VTTDEWAQYHKEYGNEGGKE---WAAQEELPKVSR-----
432 -----

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433 >MBW7931464_Gammaproteobacterium_BROCD033
434 M-----
435 -STNAANVSPGDSNLAMWLLNKKNWFTFLIVAVISIAGLVYL--GQQTYSGAPPVADVF
436 --G-PNGEMIASDMLQHGKHFHIRGLMLYGSFWGDGAERGPDFTAEMHRIGASMSRSY
437 YEEEMKQRTGAS-----S---ITDYERDAIAQRVLKEMH----NNTYD-EATNKIT
438 LNDAQVFAFHELNEHYTRMFTDPTY-----ERM---EG----GQIQG
439 EETIRDLTAFWGGWVSAANRPGQEYSYTHNWPYEPEVGNVPTTATFIWTFISIFALWI
440 GISVVLYVYGQMKQPVDFVMGEG---GGHSLTSDLEN---GVRPTQRATYKFFVLA
441 MIVFGIQVFSGVIAAWDFI---KPF-----GIN-LNDLIPFSVRSYHAILQIFWFFMC
442 WVGYTIFFLPRLTK-VPKGQKSLINLLFLMSCIVAFGTVTGIYVQQRGWL-DETLGYWLG
443 SQGWEFIELGRLFQYILLAAFSLWIYIIYRGVKPWISMKN-IWSVPAWLLWGSIMVFL
444 FFSVLMTPSSNFAISDYWRWMTVHMWVEVTFEVFTTVIVAYLLVQMGLVTRVMAERVI
445 AVMLFLVTAINGISHNFYWIAKPTGIIAVGSVFSTLQVLPLLLLTLDWQMRQEGG----
446 RAHEFRVQKQVVMEGVWLFILGVNFWNIFGAGVFGSLITLPLVNYEHATYMTGNHAH
447 AAMFGVKGNVALAGMLFCMQHLVQKAAWSEKLVRMVFWFSFQIGLALMMFLDLFPVGLYQI
448 YVVLTEGLWYARSNEVVMGPVFATMTYMRTIGGSVFI FGGLLP IYFVLSRGGMR-DEV
449 D----VSSNEWADYHKEYGHEAGQE---WAAQEEPVKVA-----
450 ----
451 >MCC6201880_Gammaproteobacterium_SJ34
452 M-----
453 -ATEAVAPSGSNSNLAMWLLNKKNWFTFLIVAAISVVGLVYL--GQQTYSGAPPLVNFV
454 --T-KDGA VVFSKENIERGKELFHIRGLMAYGSFWGDGAERGPDFTAALHRTVLSMREF
455 YANEMKARNGVA-----E---LPLYEQDAIAQRVIRELH----GNTYD-ETAQHVV
456 LNEAQIYA FEELNKHYTRMFTDPTY-----DRM---DPV---NQLSG
457 ADNIRAVTAFWYGGWVSAANRPGESYSYTHNWPDPDAGNSATAATFIWTFASIFALWI
458 GISIVLYVYGQMKQPIDLFEAQN--SENSHWLTTSDLEN---GYVRPTQRATYKFFAPA
459 MIVFGCQVLAGIIGATDFL---RPF-----GIN-LNNLVPFTVARSYHTLLQIFWFFMC
460 WVGYTIFFLPRLAK-IPNGQKFLINLLFGIIVAVGALGGIYTQQRGWISDDKMAYWFG
461 SQGWEFIELGRFFQLLLLGGFTLWIYIIYRGVKPWLNRN-VWSVPAWLLYGSVMVFL
462 FFGVLMVPDSNFAISDYWRWVHMWVEVTFEVFTTVIVAYLLVQMGLVTRLMAERVI
463 AVMLFFVTALNGISHNFYWIAKPTGIIAVGSVFSTLQVLPLLLLTLDWQMRQEGN----
464 KADARRLQGKQTTVMNGVWLFILGVNFWNVFAGVFGSLITLPIVNYEHATYMTGNHAH
465 AAMFGVKGNIAIAGMLFCCQHLFPKSFNDLLIRRIFWALNIGIALMMFLDLFPVGLYQI
466 FHVVTGTWYARSTEIVMGPVFQTLTYLRMIGGAVFVLGGLLPIWVLSRGTLLR-QET
467 N----VETDEWSQYQEQYEGKEHGKE---WAAQPEPRA-----
468 ----
469 >MCC7257357_Gammaproteobacterium_SJ686
470 M-----
471 -STKAV-SNTGSSNLAMWMLNKKNWFAQFLIVAAISVVGLVYL--GQQTYSGAPPLVDFV
472 --S-STGEVVASEATIKRGKEVFHLRGLMGYGSFWGDGADRGPDFTADALHRTVVAMREF
473 YTEELKARNGTE-----T---LTAFETDAIGQRVIRELH----TNTYD-EAAGRIV
474 LTEGQIYALGELNKHYTRMFTDPTYK-----DRM---DPV---NQVSG
475 EDNLRAVSAFFWGGWVAAAANRPGEEYSYTHNWPYDPEAGNYATTATFVWTFISIFALWI
476 GIMVVLYVYGQMKLQVDFLDTQS---GNGHSLTSDLEN---GYVRPTQRSTYKFFALA
477 VIVFGLQVLAGIISATDFL---RPF-----GIN-LNELVPFTVRSYHTLLQIYWFFMC
478 WVGYTIFFLPRLTK-VPKQKFLINLLFVVAAVVAVGAVGGIYTQQRGWFGDDELSYWFG
479 SQGWEFIELGRFFQLLLLGGFTLWIYIIYRGVKPWLTMKN-IWSVPAWLLWGSVMVFL
480 FFSVLMTPSDNFAISDYWRWMTVHMWVEVTFEVFTTVIVAYLLVQMGLVTRLMAERVI
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481 AVMLFFVTAINGISHNFYWIAKPTGIIAVGSVFSTLQVLP LLLLLTLDAWQMRQEGG-----
482 RANELRVQ GKQAHVMEGVWVFILGVNFWNVFGAGVFGSLITLPLVNYEYEHATYMTLNHAH
483 AAMFGVKGNVALAGLLFCCQHLFQKSAWNDKLVSTSFWSLNIGVGLMMFLDLFPVGVYQI
484 WLVLTEGFYARSTEVITGPVFTLTYLRLMIGGALFVLGGLLPLIWFVLSRGNRLQ-KEA
485 E-----VGTDEWAQYQKEYGKEAGRE---WATQEEPRV-----
486 -----

487 >CBE69502_Candidatus_Methylomirabilis_oxyfera_DAM0_2437

488 M-----SPN
489 -PSGTAAGKKNERTFAQVLLIKKYWWLHALIVTAISTIGLIAL--GVWTYAGAPPLVNFV
490 --S-KSGDVVIAEHSMNRGKQVFHLKGLMLYGSFWGDGAERGPDFTAELHRTFVSMGKY
491 YEMQIEKEQGR-----P---ATQDEKDG IAGKV KREIH----QNGYD-AAAGVIR
492 LNDAQIFAYNELVDHYTKMFTDPTYE-----EAFQKGRIQ---SYVSN
493 PEDIKGLAGYFFWGGWVAGANRPGEIYSYTHNWPYDPDAGNLPTYATYIWSFLSILVLF
494 GTMLVLYVYGEMKSLPGEPFN GRD-----WSLTTVDLENKGDAYVRPTQRATYKFFAFA
495 VILFLVQVLAGILGAEDFV---GGGPGEAI-LGA-FGLVIPFSVRSYHAI VQIYWFFMA
496 WVG YTLFFLPRISK-VPNGQRFLINLLFALCVLVGAGALFGIYAGHTGML-TDDMAYWFG
497 SQGWEFLELGRFWHLMLASFCLWVYIIFRAVKPWITSQN-LWSVPAWLFYGS GIMVLF
498 FFGMFMTPSQNFAISDYWRWMNIHMWVEVTFEVFTTCIVGYMLVQMGLVNRAMAERVI FL
499 AVMMFLVTALIGISHNFYWIAKPTGIIALG SVFSTMQVLP LLLLITLDAWKMR TERT----
500 KAHEHLSEGKQRFVMDGVWTFILAVNFWNIFGAGVMGSLINLPVNYEYEHGTYLTNNHAH
501 GAMFGVKGNIAIAGMLFACQHLFQRSAWNEKLIKTVFWSLQVGI VMMMLMDMFPVGLYQL
502 AHIFQYGFYGRQQS FVTNEVWHTLTWLR SIGGVVFLFGGVLP LCFWILSRAGRMV-REA
503 AV---VEEGEWTIYDREKAK----EREAWAASDEAF-----
504 -----

505 >WP_107560883_Candidatus_Methylomirabilis_limnetica

506 M-----SPN
507 -PNEAVSKAKMHR TFAQALLIKKYWWLHALIVTAISVIGLIAL--GVWTYAGAPPLVNFV
508 --SSTTGEVVIPEWEMNRGKQVFFL KGLMTYGSFWGDGAERGPDFTAELHRTSLSMGTH
509 YRNEIAKTR-----A---VTQDDEMIKTRVAREIH----TNLYD-SAAGVIR
510 LNDAQIFAYHELNTHYTRMFTDRTYV-----EAFQNGRIE---SYIKN
511 PADIKALTGFFFWGGWVSGANRPGEVYSYTHNWPYDPAVGNFPTYATYIWSFLSIFVLF
512 GTMLVLYVYGEMKTLPGEPFN GRD-----WSLTTVDLENKGDAYVRPTQRATYKFFAFA
513 VILFLVQILAGIISAEDFI---GGGPVDAM-LGM-VGLTIPFSVARGWHLIVQIYWFFMA
514 WVG YTIFFLPRISK-VPNGQRFLINLLFTLCVIVGAGALFGIYLGHTGFFANDEMAYWFG
515 SQGWEFLELGRFWHLMLISFCLWVFIIFRAVKPWLT SQN-MWSVPAWLFYGS AIMVLF
516 FFGMFMT PQQNFAISDYWRWMNIHMWVEVTFEVFTTCIVGYMLVQMGLVNRAMAERVI FL
517 AVMMFLVTALIGISHNFYWIAKPTGIIALG SVFSTMQVLP LLLLITLDAWKMR TERV----
518 KAHEAVAEGKQRFVMDGVWTFILAVNFWNIFGAGVMGSMINLP IINYYEYEHGTYVTSNHAH
519 GAMFGVKGNIAIGGMLFACQHLFQRSAWNEKLIKTVFWSLQIGLVMMMMMDMFPVGLYQV
520 AAI IQHGFYGRQQS FITNEVWHTLTL LRAIGGAVFLFGGVLP LTFWILSRGTRMV-REA
521 AT---VEEGEWTIYDKEKAK----EREAWAASDEAF-----
522 -----

523 >CBE69496_Candidatus_Methylomirabilis_oxyfera__DAM0_2434

524 MR-----
525 -SSSSSGMGKTNRTFGQALLIKKYWWLHALIVTVISVIGLVAL--GVWTYTSAPPLTNYV
526 -LS-STGETVIPEWQIQRGKQVFHLKGLMTYGSFWGDGGERGPDFTAELHHTYVSMSKF
527 YENEIAKER-----P---VTQADRD MISVRVKREIH----ENGYD-AAANIIR
528 INPAQVFAYQELITHYTRMFTDATYE-----EAFMKGRIE---NHISS

529 PEDLKALAGYFFWGGWVSGANRPGFDYTYTHNWPPDPLVGNTPTFETYLWSFISIFVLFC
530 GTMLVLYVYGEMKVLPGEPFNGRD-----WSLTTVDLENKGDAYVRPTQRATYKFFAFA
531 VILFLVQVLAGILSAEDFV---GGPGSAIATTV-LGFTIPFTVTRGWHTIVQIYWFFMA
532 WVGYTLLFFLPRISK-VPNGQRFLINLLFTLCLIVGAGALFGIYLGHGTGYM-TDDMAYWFG
533 SQGWEFLELGRFWHILMLASFCLWVYIIFRAVKPWITSQN-LWSVPAWLFYGGSGIMVFLFL
534 FFGMFMTPSQNFAIADYWRWMNIHMWVEVTFEVFTTCIVGYMLVQMGLVNRAMAERVI FL
535 AVMMFLVTALIGISHNFYWIAKPTGIIALGSVFSTMQVLP LLLITLDAWKMRTERT-----
536 KAHENIAEGKQRFVMDGVWTFILAVNFWNIFGAGVFGSLINLPVNYEYHGTYLTGNHAH
537 AAMFGVKGNIAIAGMLFACQHLFQRSAWNEKLIKGI FWSLQVGLVLMMLDLFPVGLYQV
538 ATVFKEGLWAARAQAHVTDVSWITLTMRTIGGAVFLFGGVLPLVYFILSRAGRMV-REA
539 SV---VEEGEWTIYDREKAK-----EREAWAAGDEAF-----
540 -----
541 >WP_107560884_Candidatus_Methylomirabilis_limnetica
542 M-----SPH
543 -PSTPVSKAKVYRTFAQALLIKKYWWLHALIVGLISVVGLIAL--GWTYASAPPLVNFV
544 AVS-NSGTVVIPEWEIQRGKQVFFLKGLMTYGSFWGDGGERGPDYTAELHHTSVSMRKY
545 YSAEIVKSR-----P---LTQDDLGMIDSRVKREIH----TNLYD-EKAGVIA
546 LNDAQIFAYQELITHYTRTFTDATYE-----EAFMKGRIE---NHISN
547 PADLKALASFFWGGWVSGANRPGEDYSYTHNWPPDQSVNNYPTFPTYLWSFISIFVLFA
548 GTMLVLYIYGEMKTLPGEPFNGRD-----WSLTTVDLENKGDAYVRPTQRATYKFFAFA
549 VILFLVQILAGILSAEDFV---GGPGSFLATSV-LGFTIPFTVTRGWHLIVQIYWFFMA
550 WVGYTLLFFLPRISK-VPNGQRFLINLLFTLCVIVGAGALFGIYFGHTGWFANDEMAYWFG
551 SQGWEFLELGRFWHILMLSSFCLWVFIIFRAVRPWLTSQN-MWSVPAWLFYGGSGMMVFLFL
552 FFGLFMTPTQNFAIADYWRWMNIHMWVEVTFEVFTTCIIGYMLVQMGLVNRAMAERVI FL
553 AVMMFLVTALIGISHNFYWIAKPTGIIALGSVFSTMQVLP LLLITLDAWKMRTERI-----
554 KAHEAVAEGKQRFVMDGVWTFILAVNFWNIFGAGIMGSMINLPVNYEYHGTYLTGSHAH
555 AAMFGVKGNIAIAGMLFACQHLFQRSAWNEKLIKTI FWSLQIGLSLMIGLDLFPVGLYQV
556 ATVFKEGLWAARAQSHVTDVSWVTLTWLRTIGGAI FLFGGVLPLAWFILSRGTRMV-REA
557 AT---VEEGEWTIYDKEKAK-----ERESWAASDEAF-----
558 -----
559 >MBI3325094_Nitrospinae_NC_groundwater_833_Pr1_B
560 MS-----SSTS
561 -RASRSHNGSRRTFAQILLVKRYWWLHLLIVAAISTVGLVAL--GTWYTGSPPLADVF
562 --SSTTGRTVIPLDQIQRGKEVFHLKGLMDYGSFWGDGATRGPDFTADALHRTVVYMRSF
563 YENEMKDR-----P---VTQFERDGI AARVQRELH----ANAWD-ETAGVIR
564 INDAQIHAYRELIGHYTRMFTDSTYP-----EAFQLGRIT---GYISD
565 PADLKALAAFFWGGWVSAADRPGESYSYTHNWPYDPAAGNTPTFATMFWSVASILGLFL
566 GIMLVLYVYGQMKTLPGDPFNGAN-----GGTLTIDLENKGDAYVRPTHRSTYKFFAFA
567 VILFLVQVLAGILSAEDYV---RGGPGTAA-LNL-LGMTIPFTVTRSWHLILQIYWFFMC
568 WVGYTIFFLPRLSR-VPNGQRFLINLLFAVCVLV GAGALFGIYLQGTGRL-SDRVAYWFG
569 SQGWEFLELGRFWHILMLSAFVLWVGIIFRAVKPWITSQN-LWSVPAWLFYGGSGIMVAFL
570 FFGMLMTPGQNFAISDYWRWMNIHMWVEVTFEVFTTCIIGYMLVQMGLVSRLVAERII FL
571 AVMMFLVTALIGISHNFYWIAKPSGIIALGSVFSTMQVLP LVLITLDAWRMRAEKF-----
572 RANEYLVOGKQQFVMDGVWMFILAVNFWNIVGAGVFGSLINLPVNYFEHSTYLTANHAH
573 AAMFGVKGNVALGGMLFCCQHLFQRASWNAKLVKTVFWALNGGLVLMFFDLFPVGVYQL
574 SVVFTHGFYARSQEVVTPVFTTLTWLRTLGGVVFLFGGVLPLVWFILSRARRLV-REV
575 E-----VQEGEWTVYDKEKKGK-----D---WAAQEEPIPSA-----
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577 >MBI2962797_Deltaproteobacterium_NC_groundwater_687_Ag
578 M-----QKSN
579 -VNRNRGSSKSRNFGTWLLAKPNWFIQFAIVSGISIVGLIAL--GSWTYSGAPPRVAMV
580 --SAASGEPVVPPIEQIRRGQELFHIRGLMSWGSFWGDGAERGPDFTADALHRTVVGMRSF
581 YERQMEKER-----P---LTQSDKDAITVRVQREIK----QNGYD-AAAGVIR
582 INDAQIHAYEELQTHYKRVFTDPTYP-----AKF---RLD---NYITD
583 PEDLRALTGYFFWGGWVAGAARPGETYSYTHNWPYDPEAGNPTMPTVLWSFLSILALFA
584 GAMLVLYVYGEMKALPGDPFNGAN-----GGTLTTIELEK-GYDFVRPTQRATYKFFAFA
585 VILFLVQVLGILSAEDFV---GGGPGEAI-VQV-FGISLPFTVVRAYHTILQIYWFFMC
586 WVGYTIFFLPRLSK-VPNGQRFLINLLFTLCVIVGAGALFGIYFGQMGYL-SDTAAYWFG
587 SQGWEFLELGRFHWILMLASFVLWITIIIFRGVWPWITKQN-MWSVPAWLFYGGSGIMVMFL
588 FFLGATTTSNFAIADYWRWMTVHMWVEVTFEVFTTCIVGYMLVQMGLLNRAMAERVI FL
589 AVMMFLITATVGISHNFYWIAKPTGIIALGSVFSTLQVLP LLLITLDAWRMRNEKI-----
590 RAGEHLVEGKQKQFVMEGVWLFVLAVNFWNIVGAGVFGSLINLPVINYFEHGTYLTGNHAH
591 AAMFGVKGNVALAGLLFCCQHLFPRLAWNEALLRRTFWSLQIGIVLMMTLDLFPVGLYQL
592 AAVLTHGYWYARTNEFVTGPVFATLTWMRVIGGVVFLFGGVLPLVWFVLSRGPKMV-REL
593 E----VEEGEWTVYDK-----D---WAAHEEEILRALK-----
594 ----
595 >MCC6766257_Deltaproteobacterium_SJ478
596 M-----HTD
597 -VKARTRNSRTRQNLGKWM LAKPNWLTQFAIVTAVSLLGLIAL--GTWTYGSAPPRVPFV
598 --SASTGKEVIPLSDILRGQELFHIRGLMSWGSFWGDGAERGPDFTA EALHHTVVSMSRSF
599 YEAQAASGG-----T---SSQTDRAIAVRVQREIK----ENGYD-EAAGVIR
600 INDAQIRAYQDLQTHYARVFTDPTYP-----AKF---RLA---NYITD
601 PNDLRALSAYFFWGGWVSGAKRPGEPYSYTHNWPYDPDAGNVPTTPTVMWSFLSILVLF A
602 GAMLVLYVYQG MKELPGDPFNGAN-----GGTLTTAELER-GYEFVRPTQRATYKFFAFA
603 VILFLAQVLGILSAEDFV---SGGPGTAI-VKV-LGVPFSFTVTRAWHTILQIYWFFMC
604 WVGYTIFFLPRLSR-VPNGQRFLINLLFALCVIVGAGALFGIYFGHMGYM-SDTASYWLG
605 SQGWEFMELGRFHWILMLASFVLWIAIIYRGVWPWITKQN-MWSVPAWLFYGGSGIMV LFL
606 FFLGATPSGNFAITDYWRWMTVHMWVEVTFEVFTTCIVAYLLVQMGLLNRSMAERVI FL
607 AVMMFLITAIIVGISHNFYWIAKPTGIIALGSVFSTMQVLP LLLMTLDAWRMRNEKL-----
608 RAGEHRAQGKQKQFVMEGVWLFILACNFWNIVGAGVFGSLINLPVINYFEHGTYLTHNHAH
609 AAMFGVKGNIALAGVLFCCQHLFPRAAWNEKLLRTSFWSLQAGLVLMMLVLDLFPVGLYQM
610 AAVVTHGFYARTNDFVTGPVWVKLTWLRITIGGVIFLFGGVLPLLWFILSRGRVLV-REL
611 E----LEEGEWTVYEK-----D---WAAHEEEIEHALTS-----
612 ----
613 >OQY65997_Polyangiaceae_bacterium_UTPR01
614 M-----HTD
615 VVKARGRTSRSRQNI GKWMLAKPNWLTQFAIVTAVSVTGLVAL--GMWTYGSAPPRVPFV
616 --SASTGKEVIPLADIVRGQEIFHIRGLMSWGSFWGDGAERGPDFTA EALHHTVVSMSRSF
617 YESAASKDR-----P---LAQADRDAIAMRVQREIK----DNGYD-EAAGVIR
618 INDAQIRAYEELQTHYTRVFTDPTYP-----AKF---RLA---NYITD
619 PNDLRAITAYFFWGGWVSGAKRPGETYSYTHNWPYDPEAGNVPTMPAVLWSFLSILVLFV
620 GTMLVLYVYGM RDLPGSPFNGAH-----GGTLTTSELER-GYEFVRPTQSATYKFFAFA
621 VILFLIQVLGILSAEDFI---GGGPGEAI-VKV-FGLALPFTVVRAWHTILQIYWFFMC
622 WVGYTIFFLPRLSH-VPKGQRFLINLLFAVCVIVGAGALFGIYFGHMGYL-SDTAAYWLG
623 SQGWEFVELGRFHWILMLSAFVLWIAIIIFRGVWPWITKQN-MWSVPAWLFYGGSGIMV LFL
624 FFLGATPTGNFAITDYWRWMTVHMWVEVTFEVFTTCIVAYLLVQMGLMNRAMAERVI FL
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625 AVMMFLVTALVGISHNFYWIAKPTGIIALGSVFSTMQVLP LLLMTLDAWRMRNEKL-----
626 RAAEHREAGKQQFVMEGVWLFILACNFWNIVGAGVFGSLINLP IVNYFEHGTYVTGNHAH
627 AAMFGVKGNIALAGVLFCCQHLFPRAAWNEKLIKTSFWSFQIGLVLMMTL DLFVPVGLYQM
628 AAVVQHGFWFARTNEFVTGPV FVTLTYLRVIGGMVFLFGLLPLLW FILSRGPRLV-REL
629 D-----IEEGEWTVYGK-----D---WAAHEEEI LSALK-----

630 -----
631 >MCC6850618_Deltaproteobacterium_SJ588

632 M-----NAN
633 -VRTRTWSNRTRQN LGKWL LAKPNWLTQFAIVTSVSVLGLVAL--GTW TYGSAPPRVPFV
634 --SATTGKEVIPLADLARGQELFHLRGLMSWGSFWGDGAERGP DFTA EALHRTVVSMSRF
635 YEESAQNQ-----PSPEAAQADRDAITVRVQREIK----HNGYD-EAAGVIR
636 INDAQIQAYQDLQAHYTRVFTDPTYP-----ARF---RLA---NYITD
637 PNELRALTAFFFWGGWVSGAKRPGETYSYTHNWPYDPDAGNFPTT PAVVWSFSLV LFA
638 GAMLVLYVYGQMKDLP GDFPNGAK-----GGTLTTYELER-GYEFVRPTQRATYKFFAFA
639 LILFLVQVLAGILSAEDFV---SGGPG EAI-VKV-LGLSLPFTVVR AWHITLQIYWFFMC
640 WVGYTIFFLPRLSR-VPKGQRFLINLLFALS VTVGAGVLFGIYFGHMGYL-TDSAAYWLG
641 SQGWEFMELGRLWHIMMLGAFVLWIGIIFRGV RPWITKAN-MWSVPAWLFY GSGIMVFLFL
642 FFGLGATPYQNFAITDYWRWMTVHMWVEVTFEVFTTCIVAYLLVQMGLMNRAMAERVI FL
643 AVMMFVVTA VVGISHNFYWIAKPTGIIALGSVFSTMQVLP LLLMTLDAWRMRNEKL-----
644 RAAEHQAAGRQTFVMEGVWLFV LACNFWNIVGAGVFGSLINLP IVNYFEHGTYVTGNHAH
645 AAMFGVKGNIALAGVLFCCQHLFPRASWNEKLIKTSFWSFQIGLVLMMTL DLFVPVGLYQM
646 AAVVTHGFWYARTNEFVTGPVWVILT WLRITIGGVIFLFGLLPMLW FILSRGLKLV-REL
647 E-----LEEGEWTVYDK-----D---WAAHEEEI VHALK-----

648 -----
649 >OFW12443_Acidobacteria_RIFCSLOW02_02_FULL_67_21

650 MV-----NHRN
651 RPNGTGNGSKTQQNFGKWL LAKRNWVQFTVVAGISLVGLLAL--GVW TYAGAPPLTRFV
652 --SSATGETV VPLDGIQRGREVFHLRGLMAWGSFWGDGAERGP DFTADALHRTNVAMKAY
653 YEQGIAKER-----P---VTQTDRDAIAVRVQREIK----ANGYD-EAADVIR
654 VNDAQIYALRELEAHYTRMFTDPTYS-----EAF---TLD---GYITD
655 PDDLKALAAFFYWGGWVAGAARPGETYSYTHNWPYDPEVGNLPTMPTV VWSFSLV LFA
656 GAMLVLYVYGQMKDLP GDFPNGAN-----GGTLTTIELEK-GYDFVRPTQRATYKFFAFA
657 MVLFLVQVLAGIISAEDFV---QGGPGQAI-ISL-FGISIPFTVAR SWHTILQIYWFFMC
658 WVGYTIFFLPRLSR-VPKGQRFLINLLFAMS VIAGAGVLFGIYFGQM GYM-SDTASYWFG
659 SQGWEFLEMGRFWHIAILAA FVLWIAIIFRGV RPWITRQN-LWSVPAWLFY GSGIMVAFL
660 FMSLGATTSGNFAIEDYWRW MNVHMWVEVTFEVFTTCIVGYMLVQMGLLN RAMAERVI FL
661 AVMMFLVTAIVGISHNFYWIAKPTGIIALGSVFSTLQVMPLLLITLDAWRMRSEKI-----
662 RAGEHQQEGRQKFVMEGVWLFILAVNFWNIVGAGVFGSLINLP IVNYFEHGTYLTGNHAH
663 AAMFGVKGNIALGGMLFCCQHLFPRAAWNEKLIKNSFWSLQIGIVLMMTL DLFVPVGM YQL
664 AAVLTHGFWYARTNEFVTGPVFTTLT WMRVIGGMVFLFGLLPLMWFILSRGRVLV-REL
665 E-----VEEDEWTVYEK-----D---WAAHEEEI LRALK-----

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667 >MBI2828937_Acidobacteria_NC_groundwater_629_Ag_B

668 M-----
669 -NNNRHNSRTRQNFGKWL LAKPNWVQFSVVAGISLAGLLAL--GTW TYMGAPPYTSFV
670 --SASTGETVIPYATVARGKEVFHLRGLMSWGSFWGDGAERGP DFTADALHRTVVSMSRSY
671 YENELSRDR-----P---VTQADKDAISVRVQREIHENTRENGYD-EQADVIR
672 INDAQIQAYRDLIVHYTRMFTDPSYP-----EKF---NLD---GFISD

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673 PDDLRLTAFFYWGGWVAGANRPGETYSYTHNWPYDPAAGNNPTMATVLWSFLSILALFA
674 GAMLVLYVYGQMKELPGDPFNGAN-----GGTLTTFELEK-GYDFVRPTQRATYKFFAFA
675 VILFVVQVLGILSAEDFV---SGGPGMAI-TSV-LGISLPFSVVRWHTLLQIYWFFMA
676 WVGYTIFFLPRLSR-VPKGQRFLINLLFTLCVVAGAGVLFGIYFGQMGYM-SDTMSYWFG
677 NQGWEFLEMGRFWHIAILGAFALWIFIIFRGVWPWLTKQN-MWSVPAWLFYGSIMVFLFL
678 FMSLGATMGGNFAITDYWRWMNVHMWVEVTFEVFTTCIVGYMLVQMGLLNRAMAERVIFL
679 AVMMFLVTAIVGISHNFYWIAKPSGIIALGSVFSTLQVLPLLLITLDAWRMRNEKV-----
680 RAGEHLQEGKQKFVMEGVWLFILAVNFWNIVGAGVFGSLINLPVINYFEHSTYLTDGNHAH
681 AAMFGVKGNVALAGLLFCCQHLFPRAQWNEKLIRTSFWSLQSGIVLMMTLDLFPAGLYQL
682 AAVLTHGFYARTNDFVTGPVWVTLTWLRTIGGVVFLFGGVLPLTWVLSRGRSLL-REV
683 E-----IEEGEWTYDR-----D---WASHEEEILQVLKS-----
684 --RE
685 >CBL43845_Gammaproteobacterium_HdN1_NorZ2
686 MST-----
687 -NSLLGGSIRAKKNIALWLVSCKNWILQFLIVAICTGGLLYL--GAQTYISAPPIVNFV
688 --N-DKGDTVFSEQQIMDGKHWWSIRGLMAYGSFWGDGAERGPDFTADSLHRSVVAMREF
689 YAKEKKAELGVD-----A---LPVYETDAIAARVIRELH----NNAYD-EEAGIVR
690 LNPAQEYAFAEVREHYRKMFNATYS-----EAF---HPQ---GLISD
691 PEQITSLTSFFFWGGWASAANRPGETYSYTHNWPDPGAGNAPTATWIWSFLSILALFL
692 CIVVLYVYGQMRPELIDVFGTST---ENPFALTTHDLEN---GYVRPTQKATYKFFALA
693 MILFGVQIFAGIAAAWDFV---KPF-----GIS-LNDFLPFTASRSFHAIQIYVFFVC
694 WVGYTIFFLPRLSK-LPSSQRTMINSLFAMIVIVGLGTLIGVYLSTMGFL-DGWVAYWFG
695 TMGWEFMEMGRFFQLFLLVTFDFWYIIYRGVKNWLTRKN-IWSVPAWLLYGSIMVFLFL
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697 AVMLFLITAVIGISHNFYWIAKPTGIIALGSIFSTLQVLPMLLLTLDWAKMRQELG-----
698 RAHDLRQQGRQVHVMEGVWLFILGVNFWNIVGAGVFGSLINLPVINYEHATYLTGNHAH
699 AAMFGVKGNIAIAGMLFCLQHMFKSAWSETRIKGIFWSLQIGLVLMVLDMPVGLYQV
700 WLTLDGLWHARSSEVILGPVFASFYTLRVIGIAVFVLLGGALPLIWFVLSRGRTLQ-QET
701 E----VAEGEWTAYED-----D-EPWVAVKK-----
702 ----
703 >Ga0257115_100087344_SI112_100m_VIRAL
704 MTHLL--SLIVLIIALMGFLYLISWVFKIINKIIDIFKIKEEKMTTEFKNGEYIITTKDD
705 -SETVRSVLSFKDSVSALLLNKKYWFHFVIVSIIISILGLVYM--GGATYMGAPPVPTYV
706 --A-SNGEVIITEAEIMKGQEIFHLRGLMNYGSFWGDGAERGPDFTAETLHTMAVAMKGY
707 YAEQLKPGSVTQDDKLRKWKFD---ISEYDEGAIETRVKKELEH----NNTYT-EERNRVV
708 LNDAQIYGIEYVRWYEQMFTNADHP-----EAF---HPI---GYITD
709 KTDLNNLAFFYWGSWTSAADRPGDDFSYTSNWPYDPQAGNEPPPSLMMWSFLSIFILWI
710 GIMLVLYVYGQMRTPGGPFDMGA----RGPTLTADLES---GYVRPTQLATYKFFALS
711 IVMFGLQVLGILGAMDFV---NPF-----AHK-LANILPFNILRSYHTLLQIYWFFVA
712 WVGYTIFFLPRLSE-VPKHQEFLLINLLFGICVTVGVGGIVGVYLGQAGYM-TGWAAYWFG
713 SQGWEFMELGRFFQMLLLGGFSLWIYIIYRGVKNWITKKT-FWSVPAWLLWGSIMVFFL
714 FFGVLFATIDSNWAIADFWRMVVMWVEVTFEVFTTVIVGYILVQMGLVTKVMAERVIYL
715 AVILFLITATIGVAHNFYWIAKPESVIALGSVFSTLQILPLLLLTLDWQMRKEGI-----
716 GAYQSRDEGKQTFIMEGVWLFVIAVNFVNIVGAGIFGSLINLPVINYEHATYLTGNHAH
717 AAMFGVKGNVALAGILFVCQHLFTTESWNDKIIKYAFWSLNIGVVLMMFLDLFPAGLYQL
718 SIVLEDGFWLARAQETINGTVFQTLTYFRSIGGAVFVT-GVVALIWFILSRSMHLK-SET
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725 YANQIKPGSVTQDDRLREWRFR---ISDYDEGAIEARIAKELH----VNTFN-EDTNTVI
726 LNDAQTDSFEYINWYYTQMFTNADHP-----EAF---YPT---NYISD
727 KQQLKELSAFFFWGAWTSAADRPGDAFSYTSNWPYDPAAGNTPPPGLMMWSFLSIGILLI
728 GIMIVLYVYQGMRLEPGSPFKLNP----TGKILTPDLEA---GYVRPTQKSTYKFFAVA
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738 K---
739 >St16_OMZ_317E_VIRAL
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741 -RNNMKQDKEFKGTVAHMLLSKKYWFAHFVWVSVISIMGLLYM--GGATYMGAPPVPDYK
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744 LNDAQVFSFEYINWYYTQMFTNADHP-----EAF---HPL---NYITD
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748 WVGYTIFFLPRLSK-VPKGQNTLINILFTICVIVGLGGVFGVYLGQAGYM-TGWAAYWFG
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758 M-----
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761 YRVQ--SPL-----D---PKPFELAGIEQMVKNEIK----KNRYQ-TRSNQTE
762 LTPAQVFAVSEINTFYQRVFLDPEFH-----EAF---KPA---GYLTD
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764 GLGAVMYYYGQFEQLTEEYYAKGA-----SEMVTEEKVRS---FRPTPTQRATFKFFFVA
765 ILLFFIQVLAGVLT VHDFVGFTSFF-----GLD-LQALLPVTISR SWHVQISLYWISAC
766 WVGISFFILPILAKGEPKGQLKLINLLFAIFFVLVAGSLVGIYLGPMNML--GSLSRWLG
767 HQGWEFVELGRLYQYMLLAVFALWAVIVYRGLKGVMAKAK-PWELPNWL VYAVVCILILL
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771 AALMGVYGNLSIAGILFALRYLVQPTSWNPQLVKLSFWSINLGLVFMVVLDFPAGIHQL
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773 P-----FVLNRFHQERKEM----E-----
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775 >WP_130276701_Cecemia_calidifontis
776 M-----
777 -----KPDTKFLNYIMKQKNWWLPFMVIFVISIVGLLFI--AYQTYEEAPPIPHYV
778 --D-EKGEEIITQEILRGQEVFHRYSALMEYGSFMFGDGALRGPDFTAQALNERAKSMFRF
779 YQESLNENG-----S---RSEFESEGILRKVQKEIK----ENTYD-ENNNQVN
780 ISFAQVAAIRDLEGFYQEMFLNPDFH-----EAF---KPT---GYISD
781 PTEIKDLSAFFFWGSWVCSVERPGEKYSYTHNWPYDEFAGNVATPSTLIWSIVGLLGLVL
782 GLGIVLYYYGQFEQLSEEYYAKGA-----SEMVTEEKLQQ---YKPTPTQRATFKFFYVA
783 VILFLIQVLAVLTVHDFVGFTKFF-----GWD-IQEVLPVTISRSHVQLSLFWISAC
784 WVGISFFILPLLAKSEPKGQLFLINLLFGIFFVMVGGSFVGFIFMGPMGML--GDYSRWLG
785 HQGWEFVELGRLYQYFLLAIFALWAIIVYRGVKNTLRPGM-PWGLPNWLVSIVCILLLL
786 LSGFVARPETNFVIADFWRWVVMVHMWVEAFFEVFTTIIVGYMMVMMGLVNRQAVVKVYI
787 AALLFLGSGLLGISHNFYWNAKPVGTLALGSVFSTLQVVPLILLTLEAWRMQRMPYL-L-
788 STKQKERHRSSLFAMPGVFLFIIGVTFWNFFGAGVFGLIINLPIANYEHGTYLTVNHGH
789 AALMGVYGNLSIAAILFALRFLKPEAWNTQLVKTAFWWSINIGLLLMVTLDFPAGIHQL
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797 YGQQVASGSTD-----E---LSQIEKDGISVRVKRELK----ANRYD-RERNIVV
798 LTEGQAYAAGR LAEYYNSKF-KGDHK-----EAF---KPA---GYITD
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805 ATLLFLGSGLLGISHNFYWNAKPAALMAMGSVFSTLQVIPLVLLTLEVWKFVRVPGYSF-
806 GPSTNSAVTGSSFGFSEAFLLIAVNFWNFFGAGVFGLIINLPIMNYYEHGTYLTVNHGH
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