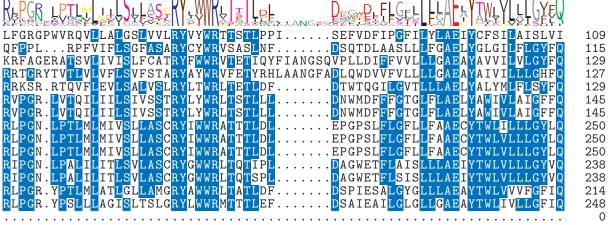
consensus

o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B

o:Rhizobiales, g:midas g 534, Hjor.155 o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 (split) o:Solibacterales, g:Paludibaculum, Skiv.396 (split) o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B consensus	MTLPTAIRSALLFFAAQLAVTIPNSPRQWLWRLFIKPVCLP. SRPLNPPSRLIARLSRKLGVIDYR MTLPTAIRSALLFFAAQLAVTIPNSPRQWLWRLFIKPVCLP. SRPLNPPSRLIARLSRKLGVIDYR MTLPTAIRSALLFFAAQLAVTIPNSPRQWLWRLFIKPVCLP. SRPLNPPSRLIARLSRKLGVIDYR MTLPTAIRSALLFFAAQLAVTIPNSPRQWLWRLFIKPVCLP. SRPLNPPSRLIARLSRKLGVIDYR MTLPTAIRSALLFFAAQLAVTIPNSPRQWLWRLFIKPVCLP. SRPLNPPSRLIARLSRKLGVIDYR MRHLLKRPFSLPKADGLAVSARVEVRPRPDPLGWLAEELGVVDRH MRHLLKRPFSLPKADGLAVSARVEVRPRPDPLGWLAEELGVVDRH MRHLKRPFSLPKADGLAVSARVEVRPRPDPLGWLAEELGVVDRH MRHLKRPFSLPKADGLAVSARVEVRPRPDPLGWLAEELGVVDRH MRHLKRPFSLPKADGLAVSARVEVRPRPDPLGWLAEELGVVDRH MNLHASLVWLAFQLQVAQPERWLAWLLRLFVLPPANQMLQAP. DPARVPNPRTWAAHTLGIAPDA	0 0 0 0 0 65 65 65 45 45 19 64 0
o:Rhizobiales, g:midas g 534, Hjor.155 o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 (split) o:Solibacterales, g:Paludibaculum, Skiv.396 (split) o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A	MNIRRM RRARFEMRLIGR KRLF  MNIRRI RRARFEMRLIGR KRLF  MNIRRI RRARFEMRLIGR KRLF  DTSEWVLRILFLPSHRAASEANETELAPGFFERLTQPLTS FITVIWERIGPAASRL  DTSEWVLRILFLPSHRAASEANETELAPGFFERLTQPLTS FVTVIWEHIGPAASRL  DTSEWVLRILFLPSHRAASEANETELAPGFFERLTQPLTS FVTVIWEHIGPAASRL  DTSEWVLRILFLPSHRAASEANETELAPGFFERLTQPLTS FVTVIWEHIGPAASRL  SVWQWVLFLFIYPPDRATRTKTP SRNTFLVLLVRTIGLLFSIAVRIVLAGVQVLRWFWQRLLS F  SVWQWVLFLFIYPPDRATRTKTP SRNTFLVLLVRTIGLLFSIAVRIVLAGVQVLRWFWQRLLS F  PWWLWLWRLFVRPKSAAGGFFSS MAATLL GLRPLGRLLVWLFKTTGMLLYAAAWPIRIAMAALDKL  RWHVWVLSLFVRPRTRVHALVQD LII GLAHTMAAI LNTIVWLVLWPLRKFTALLEWI	0 0 0 0 22 22 121 121 121 109 109 86 120

logo	FGFFBXXCZZZBFPERSKEXX VXXXXBFBXXGRXFFFFZFFEZFXXIIIFYREYFEYFYYFEXB	
o:Rhizobiales, g:midas g 534, Hjor.155	TQPVSVQAQLSLAVAVIVSMILVW	45
o:Solibacterales, g:Bryobacter, Kalu.261	MQASHGSPLRKWATALAVLAALALPFAYSAVVVPLSPSEQAWAGLAMIAVAVLAG	55
o:Solibacterales, g:Bryobacter, Fred.662 (split)	.MSSTTTVTKRPVSSPSRLPRLA <mark>L</mark> ALLMTAMLLMLA <mark>TVPLDW</mark> KDQAVLGAVLFVA <mark>A</mark> LFIS	59
o:Solibacterales, g:Paludibaculum, Skiv.396 (split)	.MTASETRPVRPY <u>.</u> RGNWLSRI <mark>L</mark> VLMSVALLGLLV <mark>T</mark> VPFD <mark>W</mark> KDQAL <mark>FGL</mark> LTVVL <mark>A</mark> IWLD	57
o:Rhodospirillales, g:Komagataeibacter, QUERY	MSEVQSSAPAES <mark>W</mark> FGRFSNKILSLRGASYVVGALGLCALLA <mark>ATMVTLS</mark> LNE <mark>Q</mark> MIVA <mark>L</mark> VCVAVFFIVG	67
o:Betaproteobacteriales, g:Rhodoferax, Aved.394	SPLVLAVRQLASWKGWQNVIIQRATILASLYIIFLAITTPLSNEQQLIFGVIGLASAMVLG	83
o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged)	SPLVLAVRQLAGWKGWQNVIIQRVTILASLYIIFLAITTPLSNEQQLIFGVIGLASAMVLG	83
o:Betaproteobacteriales, g:Dechloromonas, EsbW.050		188
o:Betaproteobacteriales, g:Dechloromonas, Hade.364		188
o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub		188
o:Betaproteobacteriales, g:Nitrotoga, OdNE.187		176
o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged)		176
o:Betaproteobacteriales, g:Simplicispira, EsbW.453		152
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A	AARFDFVAPAQA <mark>L</mark> EQAL.LPVLRIRGIR <mark>W</mark> TFNMLTVLLGLIVV <mark>TTPFSM</mark> LG <mark>QLLFLL</mark> LCWAV <mark>A</mark> MVVR	186
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B		0
consensus	* * * * * * * * * * * * * * * * * * * *	
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	Rapgr aptly Lily Sulasan Language Page Flore Leaf Tyly Y La Ly E	
o:Rhizobiales, g:midas g 534, Hjor.155		109
o:Solibacterales, g:Bryobacter, Kalu.261		115

o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 (split) o:Solibacterales, g:Paludibaculum, Skiv.396 (split) o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B consensus



consensus

o:Solibacterales, g:Paludibaculum, Skiv.396 (split)

o:Betaproteobacteriales, g:Dechloromonas, EsbW.050

o:Betaproteobacteriales, g:Dechloromonas, Hade.364

o:Betaproteobacteriales, g:Simplicispira, EsbW.453

o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A

o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B

o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged)

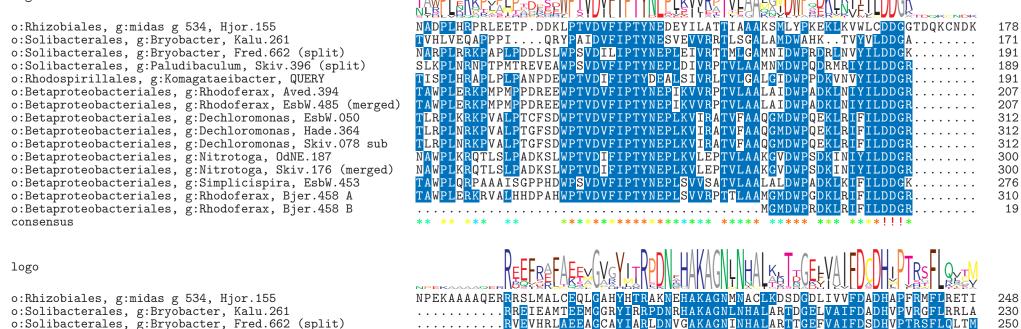
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o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged)

o:Rhodospirillales, g:Komagataeibacter, QUERY

o:Betaproteobacteriales, g:Rhodoferax, Aved.394

o:Betaproteobacteriales, g:Nitrotoga, OdNE.187



.....REEFARFAEACGARYIARPDNAHAKAGNLNYAIKHTTGDHILILDCDHIPTRAFLQISM .....RTEFSEFAKEVGVKYLTRPDNTHAKAGNINNALKYTNGKYIAIFDCDHIPTRTFLQVCM

.....RTEFSEFAKEVGVKYLTRPDNTHAKAGNINNALKYTNGKYIAIFDCDHIPTRTFLQVCM

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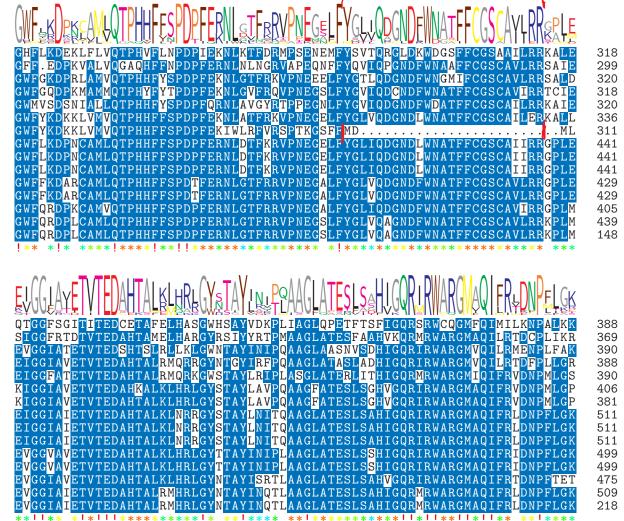
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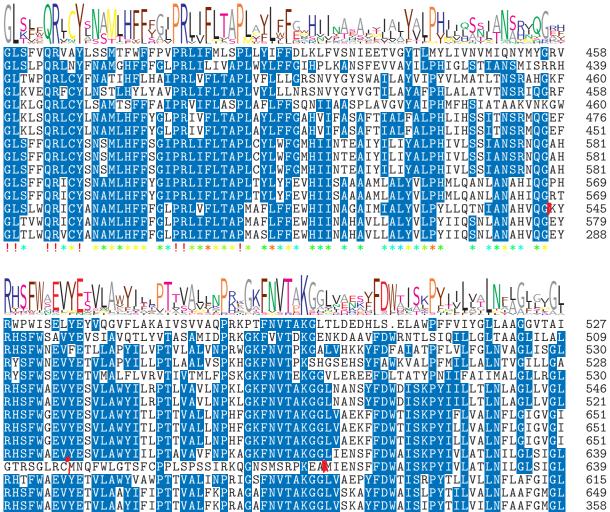
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o:Rhizobiales, g:midas g 534, Hjor.155
o:Solibacterales, g:Bryobacter, Kalu.261
o:Solibacterales, g:Bryobacter, Fred.662 (split)
o:Solibacterales, g:Paludibaculum, Skiv.396 (split)
o:Rhodospirillales, g:Komagataeibacter, QUERY
o:Betaproteobacteriales, g:Rhodoferax, Aved.394
o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged)
o:Betaproteobacteriales, g:Dechloromonas, EsbW.050
o:Betaproteobacteriales, g:Dechloromonas, Hade.364
o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub
o:Betaproteobacteriales, g:Nitrotoga, OdNE.187
o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged)
o:Betaproteobacteriales, g:Simplicispira, EsbW.453
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B
consensus
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o:Rhizobiales, g:midas g 534, Hjor.155
o:Solibacterales, g:Bryobacter, Kalu.261
o:Solibacterales, g:Bryobacter, Fred.662 (split)
o:Solibacterales, g:Paludibaculum, Skiv.396 (split)
o:Rhodospirillales, g:Komagataeibacter, QUERY
o:Betaproteobacteriales, g:Rhodoferax, Aved.394
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o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub
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consensus
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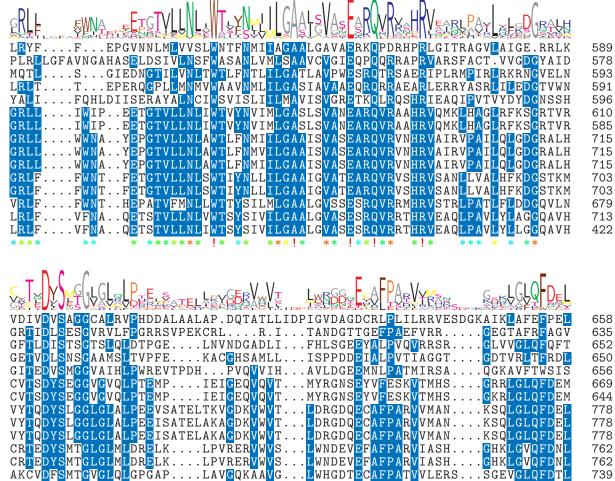
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o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged)
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o:Betaproteobacteriales, g:Dechloromonas, Hade.364
o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub
o:Betaproteobacteriales, g:Nitrotoga, OdNE.187
o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged)
o:Betaproteobacteriales, g:Simplicispira, EsbW.453
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B
consensus
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o:Rhizobiales, g:midas g 534, Hjor.155
o:Solibacterales, g:Bryobacter, Kalu.261
o:Solibacterales, g:Bryobacter, Fred.662 (split)
o:Solibacterales, g:Paludibaculum, Skiv.396 (split)
o:Rhodospirillales, g:Komagataeibacter, QUERY
o:Betaproteobacteriales, g:Rhodoferax, Aved.394
o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged)
o:Betaproteobacteriales, g:Dechloromonas, EsbW.050
o:Betaproteobacteriales, g:Dechloromonas, Hade.364
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o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B
consensus
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o:Rhizobiales, g:midas g 534, Hjor.155
o:Solibacterales, g:Bryobacter, Kalu.261
o:Solibacterales, g:Bryobacter, Fred.662 (split)
o:Solibacterales, g:Paludibaculum, Skiv.396 (split)
o:Rhodospirillales, g:Komagataeibacter, QUERY
o:Betaproteobacteriales, g:Rhodoferax, Aved.394
o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged)
                                                          GRLL
o:Betaproteobacteriales, g:Dechloromonas, EsbW.050
o:Betaproteobacteriales, g:Dechloromonas, Hade.364
                                                          GRLL
o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub
                                                          GRLL
o:Betaproteobacteriales, g:Nitrotoga, OdNE.187
                                                          GRLF
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o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B
consensus
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o:Solibacterales, g:Bryobacter, Kalu.261
o:Solibacterales, g:Bryobacter, Fred.662 (split)
o:Solibacterales, g:Paludibaculum, Skiv.396 (split)
o:Rhodospirillales, g:Komagataeibacter, QUERY
o:Betaproteobacteriales, g:Rhodoferax, Aved.394
o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged)
o:Betaproteobacteriales, g:Dechloromonas, EsbW.050
o:Betaproteobacteriales, g:Dechloromonas, Hade.364
o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub
o:Betaproteobacteriales, g:Nitrotoga, OdNE.187
o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged)
o:Betaproteobacteriales, g:Simplicispira, EsbW.453
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B
consensus
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WHNGIEHVFTAHVTLGK.

..TDFVGVQFDSI

772

481

CTCLDYSMTGLGLRVPHGLV....LAPDERLHVG...LWHNGIEHVFTAHVALAK..

CTCLDYSMTGLGLRVPHGLV....LTKDDRVHVG..

consensus

o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A

o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B

o:Rhizobiales, g:midas g 534, Hjor.155 o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 (split) o:Solibacterales, g:Paludibaculum, Skiv.396 (split) o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B consensus	KGREYYVLADLMYGDSDALPRFLASRRTHKDIFRGSAQFMAWGLLEPFRSFSYL.TRDMYQSWR TPEEHRRLVDLMFGPDDSWVQPQYPEDRIL.LSFWNL.LTTPWRATRQRSCE.GAGRRVIP SLLEHEALVRVIFGRADSWVNWGAGRHDDRLL.WSFGRV.LWVALRGIAGNAIVFATSEPLDSRRNAVLV STAQREGLTRIIFGAADSWLTGHNAAEQDRPM.RSFWMI.FKISMRGLMLVPRGAMADHRGVRLTP NIQVEAAVVRFVFGRADAWLQWNNY.EDDRPL.RSLWSL.ILSIKALFRRKGQMIAHSRPKKKP SLEQSINFVQCTFARADSWAVWGDKREHDTPL.RGLVEV.FFLGLGGLKMFGGIIVRVULRRGNEAPKP. SLEQSINFVQCTFGRADAWIRKNDGRPDDKPM.EGFREV.CSLGLRGYLRIFQRVRQSLFNKLQSVTQHF SIADERRLVQCTFGRADAWIRKNDGRPDDKPM.EGFREV.CSLGLRGYLRIFQRVRQSLFNKLQSVTQHF SIADERRLVQCTFGRADAWIGKNDGRPNDKPL.EGFREV.CSLGLRGYLRIFQRVRQSLTNNLHSVAQHI SIADERRLVQCTFGRADAWIGKNDGRPNDKPL.EGFREV.CSLGLRGYLRIFQRVRQSLTNNLHSVAQHI SIEQEANFVQCTFARPDAWSNWSDEQGVDRPL.QSLKEI.AIFGFKGYRSLWRNLGKGFTRQHQSLRGWL TKRQQIDLVQCTFARPDAWSNWSDEQGVDRPL.QSLKEI.AIFGFKGYRSLWRNLGKGFTRQHQSLRGWL TKRQQIDLVQCTFARPDAWSNWSDEQGVDRPL.QSLKEI.AIFGFKGYRSLWRNLGKGFTRQHQSLRGWL TKRQQIDLVQCTFARPDAWSNWSDEQGVDRPL.HGLLEI.ARASINGYKRFALALRDLLRDNARKRAEK TLQEEINLVQCTFARPDAWKHWNTTQEVDKPL.HGLLEI.ARASINGYKRFALALRDLLRDNARKRAEK TLQEEINLVQCTFARPDAWKHWNTTQEVDKPL.HGLLEI.ARASINGYKRFALALRDLLRDNARKRAEK ** **********************************	721 693 720 714 717 736 711 846 846 846 830 830 830 807 840 549
o:Rhizobiales, g:midas g 534, Hjor.155 o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 (split) o:Solibacterales, g:Paludibaculum, Skiv.396 (split) o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453	TRGEAAPEAD AAPQPAVAPALAPAAVAAPAPAAATLAALLRETTGRDAGEAAPQAAAPEPEKPEPAPEPV AS.DSL.VP.VP.SEE.VSR. AVGDQQNFDFFMQ.SLHSSA SWSERKRLKEFIS GEASPGIVIQA F VS .IALPVERREP.TTSQGQQKQEG K ISRAAS .VAAP KRKSTGTARPA L KS .VAAP KRKSTGTARPA L KS .VEKFESPASP.TRLSSKVISQ L .VEKFESPASP.TRLSSKVISQ L .VEKFESPASP.THLSSKVISR L .VEKFESPASP.THLSSKVISR L .GRPMI .GRPMI .GRPMI .RLPMR	791 708 739 741 745 754 729 867 867 867 835 835 812

....SIQPLPDSP.....SSS.....

....SAPATP<mark>ATP</mark>......VTRP......

852

	ENDECADE LAACINESSRGAAFSINDDDR I VATE LOAAAF IIVAAEFDDQVEEDF LOACKREEERAKFGARGA	
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o:Rhodospirillales, g:Komagataeibacter, QUERY		745
o:Betaproteobacteriales, g:Rhodoferax, Aved.394		754
o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged)		729
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o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A		852
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B		562
consensus		

# logo

	RIRAA	
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o:Solibacterales, g:Bryobacter, Fred.662 (split)		739
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o:Betaproteobacteriales, g:Dechloromonas, Hade.364		867
o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub		867
o:Betaproteobacteriales, g:Nitrotoga, OdNE.187		835
o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged)		835
o:Betaproteobacteriales, g:Simplicispira, EsbW.453		812
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A		852
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B		562
consensus		

 $\overline{X}$  non-conserved  $\overline{X}$   $\geq 50\%$  conserved