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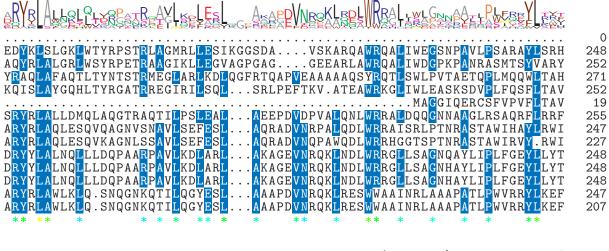
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o:Betaproteobacteriales, g:Rhodoferax, Aved.394
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o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	EKYLEKAISLOTKVNEASHTAVQLQLAHLWLAQGHNQRAEALLRDMTAMQPDNPDAWKALVAALHKQNND EELLARLLKSDIPAPERSSALLMMASTLLAKGDAAQADEMASRLVESDPLNSDAWKILLAAKQQRKLP .SIAEEMQIKEDLASRLSMVPNPVPLIREALAPP	83 59 58 12 08 75 13 69 44 10 10 10 67
o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	HAALKESGRLPKSVSSTLADDTDYVSLLASVYNSLGRFPEALRLVRRASALMRQQERTPPADLELQLAWL GEAAAAVKRIPPAVRASLEQDPDFIGLAATLQEAAGDTEGALQGVRSAMDRYAQLKKQPPVGLQLQFCWL DPTGARGVAVADLFRQRGDMIHAR MALRIASTRTIDLSPDQRLAYATE ERDGELLLAVAQAMSDAGEDTRAL AMMRTMISQNRQPDLGMMVQYSAI ERDGELLLAVAQAMSDAGEDSRAL AMMRTMISQNRQPDLGMMVQYSAI RNDAGLLYAVANAWFKRGQPAQGV AVFDRLEKRSGPLPAPVQLDHAAL GNDADLLYAVANAWFRHGLPHQGV AVYDRLAQRLAPLPPQVQLNHAVL GNDANLLYAVANAWFRHGLPHQGV AVYDRLAQRVVPLPPQAQLNHAVL GNDANLLYAVANAWFRHGLPHQGV AVYDRLAQRVVPLPPQAQLNHAVL RAEDQIPMLANTWVDIGYPEHGI LLLQQHIARQPENIQRLKLAQAAL RAEDQIPMLANTWVDIGYPEHGI LLLQQHIARQPENIQRLKLAQAAL RAEDQIPMLANTWVDIGYPEHGI LLLQQHIARQPENIQRLKLAQAAL RAEDQIPMLANTWVDIGYPEHGI SLMKRHLTDVKPATADSQLYYASL	28 29 28 60 56 23 61 17 92 57 57 57 57 50 3
o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	LLNT. NGEDRELYSLLTEVG ARPDLSMIQQDS VSELWSTW 76 LLNG. NGDERELHATLAALR VRQDLTAEQEKT SQDIWSVW 76 YM.K. ISNPVAAARLLAPLGDGSGSGAGNALLPEQQQT LQQLRMGI 70 LL.K. TRQDAELAAQMRHLY TQP.LNEQQRND LDKTRVAY 69 LL.K. TRQDAELAAQMRHLY TQP.LNEQQRND LDKTRVAY 46 LQ.R. AQQNEAVAQRLPKLL TQRNWNTSQEAQ LLNLYATH 69 RN.R. AQDDAALERQLPGLL QLPDWTPAQEAE LVQLTSEH 69 RN.R. AQDDAALERQLPGLL QLPDWTPAQEEE LLQLTSEH 63 LN.R. TQRDSELEPYLRDLL AEGKWTTAEEAE LLSTEASY 69 LN.R. TQRDSELEPYLRDLL AEGKWTTAEEAE LLSTEASY 69 LN.R. TQRDSELEPYLRDLL AEGKWTTAEEAE LLSTEASY 69 LN.R. AKQDDTLGIFLPELQ QRPDWNDEQRET MLATETDL 69	89 68 67 93 60 99 555 30 995 995 995

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o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	DERHHAFALTKLKRLDE AEPI. LRRVLER. DAND VEAVEQL AAVYASRRQWDA ALPLYRRVL ILRRANV. AANAGDVMRAMAILEAGTRMLPR. DTALRSSY AGTLLQAGEPAKALGVYKAWG SRRRADA. ARKEGDLRRCVAILEA ASRLMPR. DAALKSDL AGAWLE AGEGQRAMALYRSLL AVAQSDL. LNQRGDQAQAYDHLAPALRA. DPEATSPKLAL ARLYNGEGKSSK ALDIDLAVL SLRQFDS. LREAGNIATAYEA. IMPLVAE. RPDDITLQLAL ARLYNGEGKSK ALDIDLAVL SLRQFDT. LREAGNIATAYEA. IMPLVAE. RPDDITLQLAL ARLYASAKEYKDALAWYDYAL QERLIER. QRAEGRLEQA. VQSARAPLPEIDSSRNTPQTALQRRVQAQLLAAAAQYSDAGSLLQPLV RERLIGH. LLASQQVPQVQQAQELARQPMPFQ. TDKRSPQILAQSQKAQARLLLMVGALAEARVLLERAL RERLIGR. LLASQQVSQAQQAQELARQPMPFQ. TEKRSPQALAQGQKAQARLLLMVGALAEARVLLERAL VLRHVDQ. LRQDGSYALAQAHL. EKLLNEQ. P. NDPMLLKAQARLLTTQGDWLSALPIYRHLA VLRHVDQ. LRQDGSYALAQAHL. EKLLNEH. L. DDPMLLKAQARLLTTQGDWLSALPIYRHLA VLRHVDQ. LRQDGSYALAQAHL. EKLLNEH. L. DDPMLLKAQARLLTTQGDWLSALPIYRHLA AARQIEH. LLQRGETAQARTLA. ARAVVSGR. A. GDISTLKAQARLLLEANDSKAALLILRAIL AARQIEH. LLQRGETAQARTLA. ARAVVSGR. A. GDISTLKAQTRLLLEANDSKAALLILRAIL AARQIEH. LLQRGETAQARTLA. ARAVVSGR. A. GDISTLKAQTRLLLEANDSKAALLILRAIL * * * * * * * * * * * * * * * * * * *	249 827 826 763 752 519 765 723 698 754 754 753 701
o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	AARPNDVSLKIVYGQGLLAQRRYAEALGPLGHAAAATM.PNHGEAGLAYAEAWKGAGELKKASREFERVIP LAGAGALDFEGAVGA.AM	318 861 859 798 787 554 835 793 752 824 824 824 823 771
o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	RFARDGRVQREYGDLLLERKKYRDAARQYAEAERLGVRDDRLN.AAMGGALSANR. RWPNNAGMINLAGKLSAAKGDYKAAQRFWNAALAATPVPAEVSRPSMGARELKPADDRPAAEVLGELL. KYPRDARILNLAGQQAAQRGDYARAERFWREALALKGITPS.SIPGMPAVAVSPE. QQLEKLL. ESPMDARAWLGMAVADQADGHGHRTIADLRRAYDLRLQQVEGSR. SASG. IAPENPAVLTTLGKLYRAQGKTQLATQTFQRALSAEQSASRQLVNGPLGMRLINY.TLPTADGLGVSGIP IAPENPAVLTTLGKLYRAQGKTQLATQTFQRALSAEQSASRQLVNGPLGMRLINY.TLPTADGLGVSGIP IAPENPAVLTTLGKLYRAQGKTQLATQTFQRALSAEQSASRQLVNGPLGMRLINY.TLPTADGLGVSGIP AAPADTDVLLHAARLERSERHYAQAVALFQRAWTQEARTVGNV. SAPDIAATP. RYPDDLDVVLYAARQERSKGEYSKALALFQRAYQLALAE.GNT. AT RYPDDLDVVLYAARQERSNGEYAKALTLFQRAYQLALAE.GNT. ATDTATG. QAPNNPDVLLNAGRLEKNDRRYEQALAYFVARLVEQSPLTPT. LLSANDTA. QAPNNPDVLLNAGRLEKNDRRYEQALAYFVHARLVEQSPLTPA. LLSANDTA. QAPNNPDVLLNAGRLEKNDRRYEQALAYFVHARLVEQSPLTPA. LLSANDTA. SNPNNPDVLINAGRLEKNDRRYEQALAYFVHARLVEQSPLTPA. LLSANDTA. SNPNNPDVLIQAGRIERSDRRYHAALAYFRQALALEGRA.PS. VITTAESV. SNPNNPDVLIQAGRIERSDRRYHAALAYFRQALALEGRA.PS. VITTAESV. * ****** ****** * * ***** * * ***** * *	372 929 920 846 856 623 887 837 801 875 875 875 872 820

o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	KHKEAVPYLERAY. RASPTPRR. LGSEAGQQRRVPPQPPAELAPARELGSPAALSPALKPA. AAIPVPSATLPSAT VGEP LPPATA.TNRGTQTAVNLPPVPAPV. ATPPV. T PAATEED SAQGSPVI.PKIAPPLAPRSMNV. PGRSPAMRPISKLDSSADTQYTQVARL DLPSPS. IAQGSPLI.PKIAPPLAPRSMNV. PGRSPAMRPISKLDSSADTQYTQVARL DLPSPS. APTL.ASEAPPDTPLALAF. SLRLSVPGT. ATDALRLELAY. NLAES. GI. TITDTLRLQLAY. NLAES. GI. DAAWLRISL TLNDERHAQ. DAAWLRISL TLNDERHAQ. DAAWLRISL TLNDERHAS.	393 981 954 860 911 680 914 855 820 893 893 893 893 884 832
o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	AMDLA KAYSKTERR EEARALLEKVERSVTQTAQRMKKWAWL GRPLPANVVNVAGRAP DAIVRP.RATAPAVGPLLAE RSGLPRPAVA YTPDPLSI P PRGAKAPTWS NPFRHHGYGRQ PSPAPSVLNKPSAPSAS SAMS TAEQIVPVQYTYPS ANQGTREPMVPQPTQIMPVQSLQQ PSPAPSVLNKPSAPSAS SAMS TAEQIVPVQYTYPS ANGGREPMVPQPTQIMPVQSLQQ PSPAPSVLNKPSAPSAS SAMS TAEQIVPVQYTYPS ANGGREPMVPQPTQIMPVQSLQQ ASLGGAKAGTVÄAPA NTVG PGDSRSFLQTPLILTYSL QLAS GADATRI ASDG PDAAT LVLRFMD AMES GT GIGTDETRI ASDG PDAAT LALRFMG AMES QQLIPDDLEDIAAPSLKAASSLGAAD VISPEHRPFLETFNT APQT QQLIPDDLEDIAAPSLKAASSLGAAD VISPEHRPFLETFNT APQT QQLIPDDLEDIAAPSLKAASSLGAAD VISPEHRPFLETFNT APQT QPNYASGYPNVV KGIATADKQKSAAATPLVP QPNYASGYPNVV KGIATADKQKSAAATPLVP * * * * * * * * * * * * * * * * * * *	973 871 970 739 955 882 851 938 938 938
o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	APSMANTAPPRDAAPYTGAPAAAAIDPKKPVLLEDQVR YSMEATSPEAADQMLSSIS	458 1077 1011 901 1039 808 976 906 866 955 955 955 933 881

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logo	PIGF PVSNIV GYRYSERIGEXY YELPTS RELITES LISYAGAR PV
o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	RFSTDASTVNAMGSCEYAPSANGS.FFFRASRTNVEETLVSATGVRPQQG. PRS 607 PRKF.LVSNFIGGLRFRPGNGPIT.LLVERDALRDSMLSFAGVRDPV. T 1231 PRSF.LVPNWVGAMRFRPANGPIT.VSLSREALRDTLLSFAGIRDSV. S 1165 PIGF.PITNVLGGVEFSPRVGPVTFRVSAERRSITNSVLSYGGLRDPNYNSALGRYALNHYGSQLASQW 1103 PIGF.KVSTAVGGVSYADRLGDMSIKLDLSRRSVTDSLLSYAGTVDDR. T 1204 PIGF.KVSTAVGGVSYADRLGDMSIKLDLSRRSVTDSLLSYAGTVDDR. T 948 GIGF.PVTNLVGGIAHSDSKDGFNYKLAVSRRPLTGNLLTYAGAHDPI T 1140 GQGF.PVSNIVGGLRQSGDIGPLGYSLELARRPMTGTLLSYAGARDPV T 1067 GQGF.PVSNIVGGLRQSGDIGPLGYSLELARRPMTGTLLSYAGARDPV T 1032 PLGF.PVQDIVGGVKTSGSIGNAYYSLDISRRPLDSSMLAYAGAKDPV T 1116 PLGF.PVQDIVGGVKTSGSIGNAYYSLDISRRPLDSSMLAYAGAKDPV T 1116 PLGF.PVQDIVGGVKTSGSIGNAYYSLDISRRPLDSSMLAYAGAKDPV T 1116 GIGF.PVQDIVGGVKTSGSIGNAYYSLDISRRPLDSSMLAYAGAKDPV T 1116 GIGF.PVQNMVGGIRKSWEANKVDYALEIFRRPQTNSLLSYAGTRDPA T 1093 GIGF.PVQNMVGGIRKSWEANKVDYALEIFRRPQTNSLLSYAGTRDPA T 1093 GIGF.PVQNMVGGIRKSWEANKVDYALEVFRRPQTNSLLSYAGTRDPA T 1041

o:Solibacterales, g:Bryobacter, Kalu.261 o:Solibacterales, g:Bryobacter, Fred.662 o:Solibacterales, g:Paludibaculum, Skiv.396 o:Rhodospirillales, g:Komagataeibacter, QUERY o:Betaproteobacteriales, g:Rhodoferax, Aved.394 o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged) o:Betaproteobacteriales, g:Simplicispira, EsbW.453 o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged) o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub o:Betaproteobacteriales, g:Dechloromonas, EsbW.050 o:Betaproteobacteriales, g:Dechloromonas, Hade.364 o:Betaproteobacteriales, g:Nitrotoga, OdNE.187 o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged) consensus	QELVGLVMDNRVTGGGRAVLLERWDVFVEGGLGTRTGQNVESNPFRHATGGLGYSLIAAPPEETVSLLRA NRVWGGVIANTFSA.QGNWGGAKTGFYTSFGFQTLTGQQVQSNTRVEGNLGMYFKVLENPSGKLTA KQVWGGVVANNASL.RADFGSEDQGFYLGGGYQTLRGKNVATNTRLDVMLGGYKRVLV.KSNGALTV GQEWGGVVTNHFHG.QVEATLGNTILYGGGGYAIQTGKNTRSNNEREAGIGANTLVWH.NANMLVRI GTIWGGVTATGGRA.ELGLEDGRFGVFGYGSYHYVGGKGVVDNNRYEGGAGAYYKVAQ.DANMELTA GTIWGGVTATGGRA.ELGLEDGRFGVFGYGSYHYVGGKGVVDNNRYEGGAGAYYKVAQ.DANMELTA GQIWGGVVATGVSA.RVATDLGPYSTSMSASYALLTGLNVRNNTRLQLRMAADRDVWQ.SSHSVNL GAVWGGVVATSVGG.RVSADVGAFGLSASTSFAVLNGRNVDDNQRFAWRLALDRDLYR.STAQQVNL GAVWGGVVATSVGG.RISADVGAFGLSASTSFAVLNGRNVDDNQRFTWRLALDRDLYR.STAQQVNL GEVWGGIRANGINL.WAGWDVGQLGLYGSIGAHLLTGKNVPQNSRFATRVGADWMVTK.KEDMRIAV GEIWGGIAYTGVGG.RVAHTFGQFNTFASAEYGLLRGKNVLDNNRLALRTGIDKDVLH.RENMWVNL GEIWGGIAYTGVGG.RVAHTFGQFNTFASAEYGLLRGKNVLDNNRLALRTGIDKDVLH.RENMWVNL ###################################
logo	* **!** * * * * * * * * * * * * * * * *

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

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o:Solibacterales, g:Bryobacter, Kalu.261
o:Solibacterales, g:Bryobacter, Fred.662
o:Solibacterales, g:Paludibaculum, Skiv.396
o:Rhodospirillales, g:Komagataeibacter, QUERY
o:Betaproteobacteriales, g:Rhodoferax, Aved.394
o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged)
o:Betaproteobacteriales, g:Simplicispira, EsbW.453
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged)
o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub
o:Betaproteobacteriales, g:Dechloromonas, EsbW.050
o:Betaproteobacteriales, g:Dechloromonas, Hade.364
o:Betaproteobacteriales, g:Nitrotoga, OdNE.187
o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged)
consensus
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	CYSYTYWTYDEN LSEFT EUHUTYS OSY-S-RLPLPYEWS R NGKLS	
	SFAVDYFGFDKDLFGFTGVSRAGGRVPGFDGGPVTWAPGRRCTGGYYFSPDRFVSQTGRLEVKCQTSRWFE	747
	GFNLTGIHYEKNLRYFTLGHGGYFSPQQYMLANVPVQWRGLYNQKVQ	1343
	GGFATGMTYDKNLRFFTFGHGGYFSPQRYILFSVPVAWRGVWNRQFE	
	GVSLTYFGYANNQDFYTYGQGGYFSPQSYYSATVPIRYAGQ.HKRLD	
	GVSVTALGYDKNLRYFTLGHGGYFSPQRYFALNFPVEWSGR.TGQLS	
	GVSVTALGYDKNLRYFTLGHGGYFSPQRYFALNFPVEWSGR.TGQLS	
	GLALSAWRFGHDLSEFSWGHGGYYSPNSYVSLALPLEWSGR.KGALT	
	GVSVSGVQFARDLSGFTWGHGGYYSPKSSTTLTLPLEWNGR.NNAWS	1178
)	GVSVSGAQFARDLSGFTWGHGGYYSPKSSTTLTLPLEWNGR.HKAWS	
	GAAVTYWTYDQDLSNYT	
	GVAVTYWTYDQDLSNYTFGQGGYYSPQSYSAISLPIFWTGR.NGKLA	
	GAAVTYWTYDQDLSNYT	
	GFTLTYWRYKENESFYTFGHGGYYSPQSYTSVNLPVEWSGR.SGKLS	
	GFTLTYWRYKENESFYTFGHGGYYSPQSYTSVNLPVEWAGR.SGKLS	1152
	* *** ** ** ** **	

1269

1013 1205

1132

1097

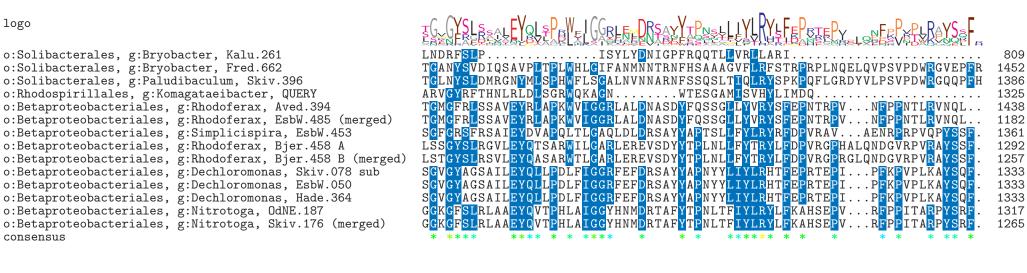
1181

1181 1181

1158

1106

1316 WDVT<mark>GSV</mark>GYQVFH<mark>E</mark>HSSPFFPTSSL<mark>LQ</mark>SG<mark>A</mark>QYIADSYMQNATASDYLSEETVDRAY<mark>YPG</mark>DSIASLTGGFN YKLEGSLGIQNFRENTAAYFPGSTSLQTAWETAAATANSAAG....GPAGVTWKTSYPGQTK....... YKLEGSLGIQNFRENTAAYFPGSTSLQTAWETAAATANSAAG....GPAGVTWKTSYPGQTK....... WLV<mark>R</mark>AA<mark>VS</mark>VSHSSSAASDF<mark>FP</mark>GNPG<mark>LQ</mark>LQAGGLGT...............LPV**Y**A<mark>G</mark>SRS...... 1295 WL<mark>LRASVS</mark>ASRSDSHQAD<mark>YFP</mark>GNAVLQSQAQTQGS........DPVYA<mark>GG</mark>GG......S 1223 WLLRASVSASRSDSHAADYFPGNALLQSQAQSLVS......DPVYSGGGGG......P 1188 YYLRGSVSFSRSNSDESDYFPTRHDLQMVAG......NQKFSGGPG...... 1267 YYLRGSVSFSRSKSDESDYFPTRHDLQMAAG.......NQKFSGGPG....... YYLRGSVSFSRSNSDESDYFPTRHDLQMAAG.......DQKFSGGPG....... 1267 YLARGSTSFAWTNEKRMPYYPTNSALQSDAVTSGN......NVDLGFYPGGDG....... YLARGSTSFAWTNEKRMPYYPTNSALQSDAVTSGN......NVDLGFYPGGDG.......



logo

	Lay	
o:Solibacterales, g:Bryobacter, Kalu.261		809
o:Solibacterales, g:Bryobacter, Fred.662	LY.	1454
o:Solibacterales, g:Paludibaculum, Skiv.396	LGY	1389
o:Rhodospirillales, g:Komagataeibacter, QUERY		1325
o:Betaproteobacteriales, g:Rhodoferax, Aved.394		1438
o:Betaproteobacteriales, g:Rhodoferax, EsbW.485 (merged)		1182
o:Betaproteobacteriales, g:Simplicispira, EsbW.453		1361
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 A		1292
o:Betaproteobacteriales, g:Rhodoferax, Bjer.458 B (merged)		1257
o:Betaproteobacteriales, g:Dechloromonas, Skiv.078 sub		1333
o:Betaproteobacteriales, g:Dechloromonas, EsbW.050		1333
o:Betaproteobacteriales, g:Dechloromonas, Hade.364		1333
o:Betaproteobacteriales, g:Nitrotoga, OdNE.187		1317
o:Betaproteobacteriales, g:Nitrotoga, Skiv.176 (merged)		1265
consensus		

X non-conserved

 $\leq 250\%$ conserved