

VGAATA---QEASTIXEMVIGAEDAPVTXXEYASWTCIHXXFHDEAL---LKX-YIDTGKV-X-XREVFYDR-GLWAX---ARCXG---XFFGI-D-X-QX-W-----GE	86	SIP2_5_Bin10_scaffold_17_c1_94
TDTAV---AEPNGVIEMSIGAEDAPVTIVEYASFTCPHCANWHQVWADLKADYIDSGKVKFVLREVFYDRPGLWAGMVARCAGP-VRYFGITDMLFDEQSDWTSG--GQ	104	SIP_5_Bin0_scaffold_23_c1_94
TDTAV---AEPNGVIEMSIGAEDAPVTIVEYASFTCPHCANWHQVWADLKADYIDSGKVKFVLREVFYDRPGLWAGMVARCAGP-VRYFGITDMLFDEQSDWTSG--GQ	104	SIP_700_Bin9_scaffold_4_c1_286
-----QDAETLPDIAQGAEDAPLTIVEYASFTCGHCANFHANVYPQLKAEYIDTGKVRVFVQRDVYFDQPGLWAGILARCGG-DKFFPVSGMLFDEQEQLAG--GE	99	SIP_700_Bin1_scaffold_5_c1_369
-----QDAETLPDIAQGAEDAPLTIVEYASFTCGHCANFHANVYPQLKAEYIDTGKVRVFVQRDVYFDQPGLWAGILARCGG-DKFFPVSGMLFDEQEQLAG--GE	99	SIP_5_Bin7_scaffold_70_c1_41
AEAETETVAETSSEITEMTLGNPDAPVKVVEYASFTCSHCGAFHREGFKELKANYIDTGKVHFTYREVFYDRAALWASMVARCGGE-EKFFGITDLIYKGQRDWMGG--GQ	108	SIP_5_Bin13_scaffold_54_c1_126
AEAETETVAETSSEITEMTLGNPDAPVKVVEYASFTCSHCGAFHREGFKELKANYIDTGKVHFTYREVFYDRAALWASMVARCGGE-EKFFGITDLIYKGQRDWMGG--GQ	108	SIP_5_Bin3_scaffold_9_c1_14
VGAASA---QEASTITEMVIGAEDAPVTLIEYASYTCIHCANFHKGVPYQLKENYIDTGKVLIYREVFYDRYGLWASMIARCGGP-EKFFGISDLIYKGQSDWTRA--GE	105	SIP_700_Bin13_scaffold_24_c1_341
VGAASA---QEASTITEMVIGAEDAPVTLIEYASYTCIHCANFHKGVPYQLKENYIDTGKVLIYREVFYDRYGLWASMIARCGGP-EKFFGISDLIYKGQSDWTRA--GE	105	SIP_700_Bin8_scaffold_26_c1_341
VGAASA---QEASTITEMVIGAEDAPVTLIEYASYTCIHCANFHKGVPYQLKENYIDTGKVLIYREVFYDRYGLWASMIARCGGP-EKFFGISDLIYKGQSDWTRA--GE	105	SIP_5_Bin37_scaffold_14_c5_70
VGAASA---QEASTITEMVIGAEDAPVTLIEYASYTCIHCANFHKGVPYQLKENYIDTGKVLIYREVFYDRYGLWASMIARCGGP-EKFFGISDLIYKGQSDWTRA--GE	105	SIP_5_Bin25_scaffold_178_c1_52
LGAANAQT-AEASTVVEMQLGNPDAPVTVIEYASYTCPHCATFHTGNYKQLKADYIDTGKINFIYREVFYDRFGLWASSIARCAGTPEAFFGITDMLYATQSEWARAGGGM	110	SIP_5_Bin8_scaffold_220_c1_7
LGAANAQT-AEASTVVEMQLGNPDAPVTVIEYASYTCPHCATFHTGNYKQLKADYIDTGKINFIYREVFYDRFGLWASSIARCAGTPEAFFGITDMLYATQSEWARAGGGM	110	SIP_700_Bin0_scaffold_1857_c1_3
VGAANAQT-TEGSGITEMVMGDENAPVTMIEYASFTCPHCATFHNDTFKKLKADYIDSGKVKFYREVFYDRYGLWASMVARCAGGQ-EKFFGIADLIYKSQSEWTRA--GA	107	SIP_5_Bin1_scaffold_2025_c1_5
FGAANAT--EAGSSILEMTLGAEDAAIQMTEYASYTCPHCRTFHKDVQKLKADYIDTGKLRFTYREIYFDRYGLWGSIVARCGGA-DKFFAISDLLYTKQSEWTK---GE	105	P00272-Rubredoxin-2_alkG-Pseudomonas_oleovorans
SLEKLPSADVKGKTQPPRS-----DAQGGK-AYLKWICITCGHIYDEAL-----GE	45	Q9WWW4-Rubredoxin-1_alkG-Pseudomonas_putida
SAEIALDVATEGGRKPRVT-----NLQSGA-AFLKWICITCGHIYDEAL-----GE	45	Q0VKZ2-Rubredoxin-2_alkG-Alcanivorax_borkumensis
TGASTPSANNKAKAKPARAKSSKDSTGKETTFRKWICITCGHIYDEAL-----GE	50	WP_138436252.1-Rubredoxin-Marinobacter_shengliensis
TDASTPSTKNKAKTKPTSSKSAKDSTHTD-TYRKWVCITCGHIYDEAL-----GE	49	WP_161463810.1-Rubredoxin-Halomonas_titanicae
TDASTPSAQNKTKPKPTPSTSPKDDSTQKD-TYRKWVCITCGHIYDEAL-----GE	49	WP_089423380.1-Rubredoxin-Sulfitobacter_pseudonitzschiae
VEAAPQPPSKAAK-----PFVKWICITCGHIYDEAL-----GE	34	WP_084394766.1-Rubredoxin-Henriciella_pelagia
AAAPPPAPVAQAGT-----AYRKWLITCGHIYDEAL-----GE	34	WP_015486580.1-Rubredoxin-Thalassolituus_oleivorans
--AAQPTAAKKKKATLGKVESVSDDKG--PLRKWVCITCDHIYDEAL-----GE	45	Q9HTK8-Rubredoxin_rubA2-Pseudomonas_aeruginosa
-----RKWQCVCVCGFIYDEAL-----GE	18	Q9HTK7-Rubredoxin_rubA1-Pseudomonas_aeruginosa
-----KKWQCVCVGLIYDEAK-----GE	18	