
AMN39289.1
CP007440.1:945806-952251
Rhodoplanes sp. Z2-YC6860
FAA_hydrolase FAA_hydrolase_N adh_short Tlde1* Flagellin_C Flagellin_N ADH_zinc_N ADH_N
ARN80492.1
CP019948.1:1031154-1035938
Methylocystis bryophila
? ? Tlde1* CMD Sigma70_r4_2 Sigma70_r2
BAM86985.1
AP012603.1:1133229-1139900
Bradyrhizobium oligotrophicum S58
? HEPN ParB Tlde1* ? MIP
HCE8677678.1
DAHNDE010000006.1:144934-147432
Enterobacter cloacae
Acetylase ? Tlde1* T6SS_HCP SymE_toxin
KZD25437.1
LVYV01000001.1:657682-664020
Tardiphaga robiniae
Abhydrolase_1 Tlde1* Glyco_transf_20 NAD_binding_11 NAD_binding_2 Trehalose_PPase
MBK7464715.1
JADJNE010000044.1:149550-168098
Betaproteobacteria bacterium
? ? Tlde1* GGDEF ParBc
MBL8309473.1
JAEUPL010000005.1:201617-209614
Burkholderiales bacterium
MMR_HSR1 YifB-AAA Zn_ribbon_recom Recombinase Resolvase Tlde1* ? AP-ATPase Mrr_cat HTH
MBM3552095.1
VGDY01000056.1:18507-21921
Alphaproteobacteria bacterium
Dehyd-heme_bind Oxidored_molyb Mo-co_dimer Tlde1* ?
MBR0556965.1
JAGRRC010000001.1:3077402-3083940
Ciceribacter sp. L1K23
MarR-HTH MA PAS PAS_8 Tlde1* adh_short_C2 ?
MBS0560707.1
JAFEFJ010000111.1:2473-6931
Proteobacteria bacterium
PMT_2 Abhydrolase_1 Tlde1* Ribonuc_L-PSP HpcH_HpaI
MBV8208217.1
JAFAIN010000340.1:3116-4808
Acidobacteriota bacterium
? ? Tlde1* CENP-F_leu_zip ?
MCB1611085.1
JAGRJM010000183.1:4785-20298
Lysobacterales bacterium
? ? Tlde1 Pesticin* Thymidine-kinase STY-kinase TPR TPR TPR TPR TPR
NBR30163.1
RFZA01001161.1:1-1140
Betaproteobacteria bacterium
Tlde1* FAD_binding_2
NDA46664.1
RGPW01000083.1:5883-8220
Alphaproteobacteria bacterium
Glycos_transf_1 Glyco_transf_4 PAP2-classical Tlde1*
ODN69192.1
MCRJ01000104.1:6726-11197
Methylobrevis pamukkalensis
? DinB Tlde1* RoxA-like_Cyt-c CCP_MauG SRP54_N SRP54
PYX28242.1
QIAM01000078.1:5628-10285
Acidobacteria bacterium
HHH_8 HHH_5 DNA_pol_B_palm PHP Tlde1* ? Lactonase S1COLD
QOZ30136.1
CP030037.1:7671951-7678160
Bradyrhizobium sp. CCBAU 51753
GntR-HTH FCD GGDEF EAL DOPA_dioxygen Rieske VanA_C Tlde1*
RCZ92590.1
QOGW01000059.1:195-2709
Escherichia coli
RHS Tlde1* HEAT Pentapeptide_4
SIO56853.1
FSRD01000001.1:8247405-8250902
Bradyrhizobium erythrophlei
Acyl-CoA_dh_N Acyl-CoA_dh_M Acyl-CoA_dh_1 ? Tlde1* ? Nitroreductase-like
TKT66903.1
SZVV01000005.1:8559-14370
Rhizobiaceae bacterium LC148
Isochorismatase Sulf_transp Tlde1* M20_dimer Peptidase_M20 NmrA
WP_053982270.1
NZ_LGAK01000079.1:1-2144
Marinagarivorans algicola
? Phage_holin_3_1 Tlde1* GTA_holin_3TM ?
WP_241495965.1
NZ_LRBG01000038.1:196082-201853
Paraburkholderia monticola
Lactonase PLUG TonB_dep_Rec His-Kinase HisKA_3 ? Tlde1*
WP_084245283.1
NZ_CP007440.1:4484100-4489071
Rhodoplanes sp. Z2-YC6860
? cNMPBD CRP-HTH Ribonuc_L-PSP Ribonuc_L-PSP Ribonuc_L-PSP Tlde1* TctC
WP_245303415.1
NZ_CP021112.1:3139564-3145584
Pseudorhodoplanes sinuspersici
? RHOD-CDC25 UPF0176_N Sulfatase OmpR-HTH Tlde1*
WP_245408391.1
NZ_PDVP01000011.1:46380-51713
Zhengella mangrovi
MarC ABC_tran BPD_transp_1 Abhydrolase_1 Tlde1*
WP_110353629.1
NZ_QJJJ01000026.1:31395-37535
Methylobacterium sp. B4
HGSNAT_cat Tlde1* SnoaL_2 OsmC TonB_dep_Rec PLUG
WP_115459342.1
NZ_QRAP01000007.1:129372-133221
Enterobacillus tribolii
Acetylase DUF1493 Tlde1* LPAM_1 ?
WP_123348734.1
NZ_RJKQ01000002.1:1203156-1206531
Enterobacter sp. BIGb0383
T6SS_HCP Tlde1* ZnR ADH_N ADH_zinc_N_2 ?
WP_254797875.1
NZ_SGWD01000017.1:211526-215483
Enterobacter sp. JMULE2
DUF2955 T6SS_HCP MalT DUF445 Tlde1*
WP_132030719.1
NZ_SMAI01000003.1:322311-327758
Aquabacter spiritensis
Hist_deacetyl adh_short_C2 Tlde1* GST_C_2 GST_N_3 MFS_1
WP_244621845.1
NZ_BSPE01000033.1:74745-80093
Neomesorhizobium albiziae
ILVD_EDD ? ? Ribosomal_S6 Tlde1*
WP_169405286.1
NZ_JAADJU010000015.1:97248-99966
Rouxiella aceris
? ? Tlde1* T6SS_HCP Acetylase
WP_203428960.1
NZ_CP044125.1:118745-124412
Rhizobium sp. BG4
GvpG PhaC_N DUF3141 Tlde1* Peptidase_M24 HhH-RADC RadC