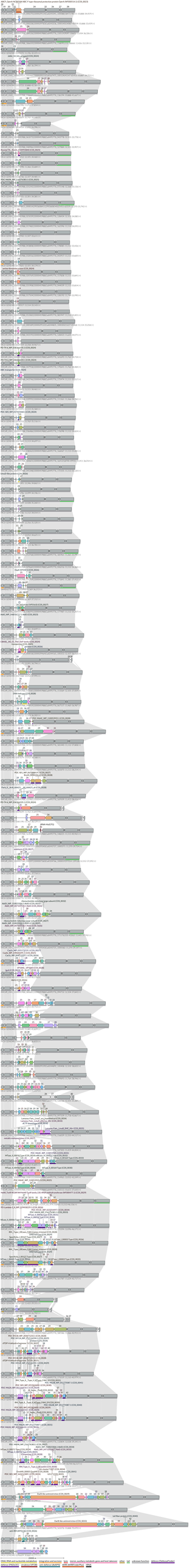

ABCF_OptrA-NCBIFAM ABC-F type ribosomal protection protein OptrA (NF000514.1) (CDS_0023)
IMGVR_UViG_3300029554_000270|3300029554|Ga0245041_100088|58473-98115: 10,888-34,459 (+)
IMGVR_UViG_3300029783_000228|3300029783|Ga0243236_1000140|54087-92709: 10,888-33,439 (+)
IMGVR_UViG_3300045988_184526|3300045988|Ga0495776_150519|9097-50605: 11,434-36,326 (+)
IMGVR_UViG_3300045988_186650|3300045988|Ga0495776_158095|152-38868: 11,426-33,530 (+)
MGV-GENOME-0290372: 11,196-32,221 (+)
Jallet_1A_hits_grouped (CDS_0024)
MGV-GENOME-0288611: 11,482-36,394 (+)
IMGVR_UViG_3300029251_000486|3300029251|Ga0167475_100134|45547-85453: 10,887-34,723 (+)
MGV-GENOME-0303723: 10,888-42,581 (+)
IMGVR_UViG_3300045988_158689|3300045988|Ga0495776_136194: 10,888-41,667 (+)
MGV-GENOME-0362396: 11,252-37,854 (+)
MGV-GENOME-0266609: 10,742-34,440 (+)
MGV-GENOME-0354954: 10,655-26,396 (+)
IMGVR_UViG_3300045988_063273|3300045988|Ga0495776_043778: 12,105-33,778 (+)
IMGVR_UViG_3300045988_048986|3300045988|Ga0495776_127884: 12,101-33,907 (+)
RosmerTA__RmrA_2734955840 (CDS_0025)
MGV-GENOME-0271412: 12,105-34,460 (+)
MGV-GENOME-0274498: 11,366-33,684 (+)
MGV-GENOME-0266736: 12,107-34,485 (+)
PDC-M69A_WP_216276383.1 (CDS_0025)
IMGVR_UViG_3300045988_031242|3300045988|Ga0495776_072148: 12,368-35,136 (+)
MGV-GENOME-0266225: 12,301-34,385 (+)
IMGVR_UViG_2903608451_000014|2903608451|2903608540|21451-62359: 12,370-35,742 (+)
IMGVR_UViG_3300045988_025039|3300045988|Ga0495776_178434: 12,101-34,080 (+)
IMGVR_UViG_3300045988_017482|3300045988|Ga0495776_162396: 11,514-34,093 (+)
MGV-GENOME-0261942: 11,507-33,611 (+)
IMGVR_UViG_3300045988_043808|3300045988|Ga0495776_178085: 11,512-33,436 (+)
IMGVR_UViG_3300045988_032056|3300045988|Ga0495776_043957: 11,513-33,820 (+)
MGV-GENOME-0337025: 12,101-34,174 (+)
serine-threonine kinase (CDS_0024)
IMGVR_UViG_3300045988_020769|3300045988|Ga0495776_157828: 11,511-33,845 (+)
IMGVR_UViG_3300045988_031908|3300045988|Ga0495776_044039: 11,513-33,854 (+)
IMGVR_UViG_3300045988_017504|3300045988|Ga0495776_128192: 11,744-33,990 (+)
MGV-GENOME-0259317: 11,514-33,143 (+)
IMGVR_UViG_3300045988_053383|3300045988|Ga0495776_085947: 11,512-33,405 (+)
IMGVR_UViG_3300029522_000189|3300029522|Ga0244835_1000302|5227-45468: 11,514-35,058 (+)
IMGVR_UViG_3300045988_043193|3300045988|Ga0495776_128423: 11,635-34,075 (+)
MGV-GENOME-0269359: 12,358-34,967 (+)
PD-T4-6_WP_036366335.1 (CDS_0024)
IMGVR_UViG_3300045988_046425|3300045988|Ga0495776_165693: 11,762-34,734 (+)
PD-T4-6_WP_036366335.1 (CDS_0024)
IMGVR_UViG_3300045988_047958|3300045988|Ga0495776_170641: 11,762-34,484 (+)
ABC transporter (CDS_0024)
IMGVR_UViG_3300045988_043746|3300045988|Ga0495776_172474: 11,511-35,017 (+)
MGV-GENOME-0286801: 11,511-34,461 (+)
IMGVR_UViG_3300045988_039992|3300045988|Ga0495776_111361: 11,366-34,782 (+)
MGV-GENOME-0272495: 11,513-35,584 (+)
PDC-S05_WP_017455060.1 (CDS_0024)
MGV-GENOME-0306222: 11,762-35,516 (+)
IMGVR_UViG_3300045988_036486|3300045988|Ga0495776_176098: 11,512-34,824 (+)
MGV-GENOME-0267880: 11,513-34,697 (+)
IMGVR_UViG_3300045988_038363|3300045988|Ga0495776_166067: 11,513-35,085 (+)
IMGVR_UViG_3300045988_184601|3300045988|Ga0495776_164125|8700-49935: 11,451-36,054 (+)
IMGVR_UViG_3300045988_045348|3300045988|Ga0495776_172105: 11,513-35,120 (+)
UmuD-like protein (CDS_0026)
MGV-GENOME-0271305: 12,346-34,862 (+)
MGV-GENOME-0265296: 12,099-34,196 (+)
MGV-GENOME-0270849: 12,028-35,260 (+)
MGV-GENOME-0264236: 11,512-34,014 (+)
MGV-GENOME-0272149: 12,356-35,520 (+)
MGV-GENOME-0271753: 12,052-34,621 (+)
MGV-GENOME-0278642: 11,513-36,781 (+)
IMGVR_UViG_3300045988_053768|3300045988|Ga0495776_185961: 11,365-35,990 (+)
IMGVR_UViG_3300045988_029660|3300045988|Ga0495776_026216: 11,512-34,384 (+)
HspX (VF0301) (CDS_0026)
IMGVR_UViG_3300045988_035709|3300045988|Ga0495776_171841: 11,385-37,452 (+)
SAMEA2737709_a1_ct1993: 12,369-36,213 (+)
MGV-GENOME-0299431: 12,369-37,312 (+)
Enh loci (VF0163) (CDS_0027)
IMGVR_UViG_3300045988_038291|3300045988|Ga0495776_177487: 11,512-35,207 (+)
AbiEi_WP_146016717.1 AbiEi (CDS_0023)
MGV-GENOME-0274429: 11,365-34,849 (+)
MGV-GENOME-0311394: 11,744-38,173 (+)
CBASS__AG_E1_ThiF ThiF family (CDS_0024)
transposase (CDS_0025)
amidase (CDS_0026)
IMGVR_UViG_3300029464_000018|3300029464|Ga0244165_100353: 12,107-36,668 (+)
MGV-GENOME-0261545: 12,091-34,794 (+)
MGV-GENOME-0327268: 12,052-37,995 (+)
IMGVR_UViG_3300045988_033585|3300045988|Ga0495776_151069: 12,105-37,009 (+)
DNA helicase (CDS_0028)
IMGVR_UViG_3300045988_098459|3300045988|Ga0495776_067557: 11,460-36,987 (+)
MGV-GENOME-0308212: 11,503-36,302 (+)
PDC-M64C_WP_110053925.1 (CDS_0028)
MGV-GENOME-0292961: 11,762-38,265 (+)
MGV-GENOME-0340063: 12,060-45,422 (+)
IMGVR_UViG_3300045988_047613|3300045988|Ga0495776_181440: 11,512-37,808 (+)
MGV-GENOME-0287674: 12,052-38,568 (+)
IMGVR_UViG_3300045988_055189|3300045988|Ga0495776_165870: 11,513-38,254 (+)
PDC-S01_WP_067088819.1 (CDS_0027)
BrxHI_00004 BrxHI (CDS_0028)
MGV-GENOME-0310342: 12,108-42,762 (+)
Paris_II__AriA_AAA21__AII_AAA21_ali (CDS_0028)
IMGVR_UViG_3300045988_122981|3300045988|Ga0495776_169509: 11,453-38,416 (+)
PD-T4-6_WP_036366335.1 (CDS_0024)
MGV-GENOME-0309649: 11,762-31,893 (+)
MGV-GENOME-0281190: 11,762-38,529 (+)
tRNA-His(GTG)
IMGVR_UViG_3300045988_163048|3300045988|Ga0495776_148221: 11,513-40,965 (+)
IMGVR_UViG_3300029340_000010|3300029340|Ga0243727_1000371: 11,370-39,724 (+)
endolysin (CDS_0027)
IMGVR_UViG_3300007360_000397|3300007360|Ga0104766_1000019|97054-139528: 12,312-37,292 (+)
MGV-GENOME-0301455: 12,301-37,714 (+)
MGV-GENOME-0295437: 12,110-40,309 (+)
MGV-GENOME-0286715: 12,102-38,380 (+)
ribonucleotide reductase large subunit (CDS_0032)
AbiEii_WP_110023304.1 AbiEii (CDS_0025)
AbiEi_WP_047105540.1 AbiEi (CDS_0026)
MGV-GENOME-0314890: 11,445-43,325 (+)
ribonucleotide reductase large subunit (CDS_0027)
AbiEii_WP_110023304.1 AbiEii (CDS_0025)
AbiEi_WP_047105540.1 AbiEi (CDS_0026)
IMGVR_UViG_3300045988_185666|3300045988|Ga0495776_171176|335-43262: 11,445-37,742 (+)
IMGVR_UViG_3300029343_000130|3300029343|Ga0243725_1000582: 11,370-39,147 (+)
Cas2c_WP_035173219.1 (CDS_0027)
Cas4c_WP_149685095.1 (CDS_0025)
Cas1c_WP_008519397.1 (CDS_0026)
MGV-GENOME-0317258: 12,109-42,333 (+)
VP1840__VP1840 (CDS_0028)
tgvA (CDS_0024)
MGV-GENOME-0311166: 11,514-40,178 (+)
AbiGi (CDS_0026)
IMGVR_UViG_3300045988_080681|3300045988|Ga0495776_094752: 12,104-37,843 (+)
MGV-GENOME-0328235: 11,451-44,753 (+)
MGV-GENOME-0302737: 11,616-40,266 (+)
MGV-GENOME-0322420: 11,485-45,829 (+)
MGV-GENOME-0300212: 11,477-36,833 (+)
MGV-GENOME-0290614: 11,761-39,233 (+)
IMGVR_UViG_3300029539_000006|3300029539|Ga0244892_100408: 12,102-38,832 (+)
IMGVR_UViG_3300045988_092953|3300045988|Ga0495776_099893: 11,764-38,946 (+)
MGV-GENOME-0340588: 11,513-41,457 (+)
IMGVR_UViG_3300045988_062166|3300045988|Ga0495776_128566: 12,105-35,389 (+)
IMGVR_UViG_3300045988_137462|3300045988|Ga0495776_097339: 11,758-42,867 (+)
Lamassu-Fam__LmuC_acc_hypothetical (CDS_0034)
Lamassu-Fam__LmuA_effector_Mrr (CDS_0033)
dCTP deaminase (CDS_0030)
Lamassu-Fam__LmuB_SMC_Mrr (CDS_0035)
IMGVR_UViG_3300045988_142561|3300045988|Ga0495776_156029: 12,350-44,517 (+)
metallo-endopeptidase (CDS_0027)
IMGVR_UViG_3300045988_063542|3300045988|Ga0495776_147305: 11,459-44,004 (+)
PDC-M64C_WP_110053925.1 (CDS_0031)
MTase_II_00058 Type (CDS_0024)
mREase_IV_00003 Type (CDS_0032)
MTase_II_00164 Type (CDS_0033)
MGV-GENOME-0312887: 12,052-45,805 (+)
MTase_II_00058 Type (CDS_0024)
MTase_II_00164 Type (CDS_0030)
IMGVR_UViG_3300045988_100013|3300045988|Ga0495776_154965: 12,052-42,249 (+)
PDC-M64C_WP_110053925.1 (CDS_0025)
IMGVR_UViG_3300045988_058331|3300045988|Ga0495776_150513: 10,655-37,650 (+)
NshR_TsnR-NCBIFAM NshR/TsnR family 23S rRNA methyltransferase (NF000477.1) (CDS_0029)
Han_2018_ERR1398226_NODE_56_length_51319_cov_474.156465: 11,513-46,136 (+)
PD-Lambda-2_A_WP_029458229.1 (CDS_0026)
PDC-M13C_WP_023354497.1 (CDS_0034)
PDC-M69A_WP_216276383.1 (CDS_0033)
MTase_II_00058 Type (CDS_0031)
MTase_II_00058 Type (CDS_0030)
NEase_II_00006 Type (CDS_0024)
IMGVR_UViG_3300045988_097763|3300045988|Ga0495776_170394: 12,096-46,571 (+)
RM_Type_I_REases_FAM_0.einsi_trimmed (CDS_0028)
DNA helicase (CDS_0029)
Specificity_I_00127 Type (CDS_0027)
MTase_I_00005 Type (CDS_0026)
MTase_I_00003 Type (CDS_0036)
MGV-GENOME-0313699: 12,031-46,166 (+)
RM_Type_I_REases_FAM_0.einsi_trimmed (CDS_0028)
DNA helicase (CDS_0029)
Specificity_I_00127 Type (CDS_0027)
MTase_I_00005 Type (CDS_0026)
MTase_I_00003 Type (CDS_0035)
MGV-GENOME-0343437: 12,031-45,147 (+)
IMGVR_UViG_3300045988_107289|3300045988|Ga0495776_161787: 11,634-42,717 (+)
MGV-GENOME-0299041: 11,616-38,134 (+)
MGV-GENOME-0236912: 11,422-29,355 (+)
MGV-GENOME-0214840: 10,510-26,702 (+)
MGV-GENOME-0250285: 11,656-33,618 (+)
IMGVR_UViG_3300045988_112779|3300045988|Ga0495776_180586: 11,366-42,951 (+)
PDC-M11B_WP_204471233.1 (CDS_0028)
PDC-M11A_WP_212116594.1 (CDS_0029)
amidase (CDS_0034)
dTDP-4-dehydrorhamnose 3 (CDS_0025)
MGV-GENOME-0318205: 11,510-42,917 (+)
PDC-M11B_WP_204471233.1 (CDS_0028)
dTDP-4-dehydrorhamnose 3 (CDS_0025)
PDC-M11A_WP_212116594.1 (CDS_0029)
IMGVR_UViG_3300045988_131972|3300045988|Ga0495776_171019: 11,510-40,979 (+)
RM_Type_II__Type_II_MTases_FAM_29 (CDS_0031)
PDC-M62B_WP_051775087.1 (CDS_0041)
PDC-S05_WP_091962608.1 (CDS_0030)
PDC-M62A_WP_001166610.1 (CDS_0024)
Septu__PtuB (CDS_0032)
MGV-GENOME-0320191: 12,028-49,073 (+)
RM_Type_II__Type_II_MTases_FAM_29 (CDS_0030)
PDC-M62B_WP_051775087.1 (CDS_0040)
PDC-S05_WP_091962608.1 (CDS_0029)
PDC-M62A_WP_001166610.1 (CDS_0024)
Septu__PtuB (CDS_0031)
MGV-GENOME-0319511: 12,028-48,759 (+)
PDC-M62B_WP_051775087.1 (CDS_0031)
PDC-M62A_WP_001166610.1 (CDS_0024)
IMGVR_UViG_3300045988_135853|3300045988|Ga0495776_132804: 12,028-39,345 (+)
PDC-M69A_WP_216276383.1 (CDS_0027)
AbiEii_WP_110023304.1 AbiEii (CDS_0034)
MTase_II_00072 Type (CDS_0024)
AbiEi_WP_047105540.1 AbiEi (CDS_0033)
MTase_II_00058 Type (CDS_0025)
transposase (CDS_0028)
IMGVR_UViG_3300029342_000011|3300029342|Ga0243726_1000389: 10,744-46,517 (+)
RM_Type_II__Type_II_REase06 (CDS_0030)
drt-cluster7 DRT (CDS_0034)
DrmMII_00005 DrmMII (CDS_0028)
amidase (CDS_0041)
PDC-S01_WP_163212389.1 (CDS_0024)
UG17 (CDS_0035)
IMGVR_UViG_3300045988_158725|3300045988|Ga0495776_157588: 11,458-50,475 (+)
DarB-like antirestriction (CDS_0029)
MGV-GENOME-0347454: 10,886-61,299 (+)
IMGVR_UViG_3300045988_089062|3300045988|Ga0495776_142098: 11,512-51,705 (+)
DarB-like antirestriction (CDS_0033)
tail fiber protein (CDS_0040)
IMGVR_UViG_3300045988_088346|3300045988|Ga0495776_165076: 10,888-70,470 (+)
anti-RM (APIS136) (CDS_0026)
MGV-GENOME-0306115: 12,105-34,552 (+)
MGV-GENOME-0296609: 30,860-45,771 (+)
20000 nt
DNA, RNA and nucleotide metabolism
integration and excision
lysis
moron, auxiliary metabolic gene and host takeover
other
tail
unknown function
defence (DefenseFinder)
defence (PADLOC)
virulence (VFDB)
anti-defence (dbAPIS)
AMR (AMRFinderPlus)
tRNA