holin (CDS_0023)
CDS_0022 endolysin (CDS_0028)
CDS_0021 CDS_0027
CDS_0024
CDS_0019 CDS_0025 CDS_0032
CDS_0020 CDS_0026 CDS_0031
CDS_0030
integrase (CDS_0029) CDS_0033
MGV-GENOME-0355437 16725:25692(+)
integrase (CDS_0028)
MGV-GENOME-0332263 16622:26492(+)
IMGVR_UViG_3300045988_057461|3300045988|Ga0495776_184988 18465:26942(+)
IMGVR_UViG_3300029134_000011|3300029134|Ga0168775_100575 18465:26882(+)
Nucleotidyl transferase AbiEii__AbiEii toxin, Type IV TA system (CDS_0031)
uvig_140797 18465:30790(+)
IMGVR_UViG_3300045988_079754|3300045988|Ga0495776_159234 18465:29049(+)
DNA helicase (CDS_0031)
uvig_292683 18587:31363(+)
uvig_251606 16628:26558(+)
uvig_246800 16628:25570(+)
uvig_242429 16628:24437(+)
ivig_1233 18487:28718(+)
IMGVR_UViG_2834711990_000018|2834711990|2834712047|11216-57145 16625:25931(+)
IMGVR_UViG_3300045988_049125|3300045988|Ga0495776_158653 18468:30635(+)
NinI-like serine-threonine phosphatase (CDS_0035)
MGV-GENOME-0317925 18490:33221(+)
AAA domain, putative AbiEii toxin, Type IV TA system (CDS_0033)
Trehalose-recycling ABC transporter (VF0842) (CDS_0039)
ABC transporter (CDS_0037)
SP41 (VF0694) (CDS_0040)
uvig_234257 18490:38288(+)
AAA domain, putative AbiEii toxin, Type IV TA system (CDS_0033)
RelE-like toxin (CDS_0036)
IMGVR_UViG_3300029476_000186|3300029476|Ga0244146_100335|2039-53880 18490:31964(+)
VirR/VirS two component system (VF0729) (CDS_0032)
IMGVR_UViG_3300030320_000062|3300030320|Ga0244994_100754 18796:32662(+)
MGV-GENOME-0322421 17305:27275(+)
MGV-GENOME-0292648 17290:25788(+)
IMGVR_UViG_3300007796_000293|3300007796|Ga0105889_100139|14087-61416 17308:27530(+)
uvig_516795 17353:25864(+)
uvig_278983 17290:26738(+)
uvig_382635 17305:24643(+)
MGV-GENOME-0337780 17407:24810(+)
IMGVR_UViG_3300029623_000015|3300029623|Ga0245138_1000743 17304:24697(+)
metallo-phosphoesterase (CDS_0025)
uvig_557809 17287:25390(+)
MGV-GENOME-0311150 17287:25318(+)
IMGVR_UViG_3300045988_039020|3300045988|Ga0495776_137497 17149:24460(+)
DNA primase (CDS_0025)
MGV-GENOME-0331600 17305:25578(+)
uvig_450628 17089:26304(+)
IMGVR_UViG_3300029593_000264|3300029593|Ga0245135_100245|33599-79856 17311:25006(+)
IMGVR_UViG_3300045988_038512|3300045988|Ga0495776_161768 17287:25248(+)
MGV-GENOME-0343679 17305:26069(+)
uvig_55024 17302:27440(+)
MGV-GENOME-0300905 17302:25897(+)
uvig_205510 16855:24993(+)
IMGVR_UViG_3300045988_043299|3300045988|Ga0495776_172755 16855:24390(+)
CDS_0025 transposase (CDS_0026)
IMGVR_UViG_3300014963_000811|3300014963|Ga0134523_1001255|3-48061 17287:27840(+)
RM_Type_II__Type_II_MTases__Type_II_MTases_FAM_0 (CDS_0026)
RM_Type_II__Type_II_MTases__Type_II_MTases_FAM_0 (CDS_0027)
IMGVR_UViG_3300045988_050717|3300045988|Ga0495776_169190 17287:27229(+)
replisome organizer (CDS_0025)
uvig_106247 17285:25982(+)
multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0026)
uvig_79966 17287:26890(+)
MGV-GENOME-0304404 17284:26014(+)
uvig_75755 17302:25716(+)
IMGVR_UViG_3300045988_061734|3300045988|Ga0495776_117428 17302:25919(+)
uvig_382018 17287:26191(+)
fosfomycin resistance glutathione transferase (NF000496.1) (CDS_0025)
uvig_77258 17284:27048(+)
IMGVR_UViG_3300045988_027445|3300045988|Ga0495776_136455 17368:26317(+)
IMGVR_UViG_3300045988_026176|3300045988|Ga0495776_029636 17368:26531(+)
fosfomycin resistance glutathione transferase (NF000496.1) (CDS_0025)
MGV-GENOME-0301990 17284:26279(+)
class D beta-lactamase (NF012161.0) (CDS_0026)
uvig_180351 17287:28587(+)
uvig_369242 18467:26081(+)
IMGVR_UViG_3300045988_041651|3300045988|Ga0495776_147056 16864:26186(+)
MGV-GENOME-0323725 18044:27534(+)
IMGVR_UViG_3300010262_000289|3300010262|Ga0129317_1000208|17648-63982 17909:28409(+)
MGV-GENOME-0298314 17287:25968(+)
uvig_280472 18072:25180(+)
HNH endonuclease (CDS_0026)
IMGVR_UViG_3300045988_060024|3300045988|Ga0495776_117286 17284:25887(+)
IMGVR_UViG_3300045988_043526|3300045988|Ga0495776_137900 17284:24969(+)
uvig_261618 17284:25296(+)
MGV-GENOME-0323490 17284:27006(+)
MGV-GENOME-0307006 17284:25705(+)
uvig_38418 17287:27853(+)
IMGVR_UViG_3300045988_046264|3300045988|Ga0495776_117413 17305:26729(+)
integrase (CDS_0025)
uvig_449531 17290:25825(+)
MGV-GENOME-0303196 16855:24992(+)
tail protein (CDS_0025)
MGV-GENOME-0306518 17386:28771(+)
DNA invertase (CDS_0025)
MGV-GENOME-0299104 17305:26635(+)
IMGVR_UViG_3300045988_043176|3300045988|Ga0495776_171976 17305:26419(+)
uvig_77665 17305:26600(+)
endolysin (CDS_0025)
endolysin (CDS_0024)
uvig_594664 17290:26017(+)
IMGVR_UViG_3300045988_020954|3300045988|Ga0495776_185775 16686:23957(+)
uvig_51346 17368:27619(+)
uvig_314019 17284:31959(+)
IMGVR_UViG_3300045988_063637|3300045988|Ga0495776_029678 17303:27728(+)
RNA polymerase sigma factor (CDS_0029)
Sortase B (VF0789) (CDS_0026)
IMGVR_UViG_3300045988_107291|3300045988|Ga0495776_163836 17386:31845(+)
integrase (CDS_0028)
uvig_162495 17386:29607(+)
PlcR-PapR quorum sensing (VF0660) (CDS_0026)
MntABC (VF0455) (CDS_0028)
SenX3 (VF0857) (CDS_0029)
RegX3 (VF0858) (CDS_0030)
ivig_3378 17305:31377(+)
MGV-GENOME-0312080 17468:29521(+)
uvig_443642_ 17305:34257(+)
IMGVR_UViG_3300045988_043398|3300045988|Ga0495776_172120 18482:26924(+)
IMGVR_UViG_3300045988_030842|3300045988|Ga0495776_054065 17386:26539(+)
MGV-GENOME-0297833 17155:25986(+)
IMGVR_UViG_3300045988_044870|3300045988|Ga0495776_183766 16722:24459(+)
MGV-GENOME-0350301 16628:22576(+)
IMGVR_UViG_3300029872_000012|3300029872|Ga0245317_100685 15776:22800(+)
DNA methyltransferase (CDS_0027)
uvig_458125_ 17404:32877(+)
RM_Type_II__Type_II_MTases__Type_II_MTases_FAM_0 (CDS_0029)
endonuclease (CDS_0030)
Gao_Mza__MzaD (CDS_0026)
MADS__mad1 (CDS_0034)
Gao_Mza__MzaE (CDS_0028)
Gao_Mza__MzaC (CDS_0025)
Gao_Mza__MzaB (CDS_0036)
MGV-GENOME-0329376 17287:38288(+)
IMGVR_UViG_3300045988_115690|3300045988|Ga0495776_158415 17287:35046(+)
IMGVR_UViG_7000000332_000148|7000000332|SRS015133_WUGC_scaffold_4781 17287:37175(+)
metallo-protease (CDS_0025)
MGV-GENOME-0319837 15689:24536(+)
VirR/VirS two component system (VF0729) (CDS_0037)
uvig_517850 18551:37951(+)
IMGVR_UViG_3300045988_087894|3300045988|Ga0495776_073924 18468:38600(+)
tail tube protein (CDS_0029)
baseplate wedge subunit (CDS_0036)
IMGVR_UViG_650377989_000001|650377989|650378050|216953-281644 17287:44056(+)
VirR/VirS two component system (VF0729) (CDS_0035)
GTP-binding domain (CDS_0031)
SspBCDE__SspD (CDS_0032)
metallo-endopeptidase (CDS_0028)
FbpABC (VF0272) (CDS_0040)
transposase (CDS_0039)
ABC transporter (VF0818) (CDS_0043)
IMGVR_UViG_3300008722_000222|3300008722|Ga0113880_1000277 17305:45114(+)
multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0027)
Siderophore-dependent iron uptake system (VF0738) (CDS_0044)
Sigma M (VF0822) (CDS_0042)
uvig_522562 17305:48218(+)
ABC transporter (CDS_0030)
D-lactate dehydrogenase VanH (NF000492.1) (CDS_0035)
DNA methyltransferase (CDS_0042)
uvig_328068 17407:43025(+)
Ma_2019_SRR413723_NODE_185_length_63844_cov_9.120554 16725:43025(+)
PfiAT__PfiT (CDS_0031)
uvig_271497 17389:47430(+)
Lamassu-Fam_LmuC_acc_hypothetical (CDS_0035)
transcriptional repressor (CDS_0043)
Lamassu-Fam_LmuB_SMC_Mrr (CDS_0036)
DNA invertase (CDS_0041)
integrase (CDS_0042)
endonuclease (CDS_0033)
IMGVR_UViG_3300045988_117077|3300045988|Ga0495776_149981 18490:39947(+)
FbpABC (VF0272) (CDS_0027)
RegX3 (VF0858) (CDS_0026)
holin (CDS_0023)
uvig_160969 16605:42685(+)
10000 nt
DNA, RNA and nucleotide metabolism
integration and excision
lysis
moron, auxiliary metabolic gene and host takeover
other
tail
transcription regulation
unknown function
Defence
Virulence
AMR