CDS_0026
CDS_0024
CDS_0023
CDS_0021 CDS_0027 CDS_0029 CDS_0032
CDS_0022 CDS_0025 CDS_0028 CDS_0031
CDS_0030
IMGVR_UViG_3300045988_076257|3300045988|Ga0495776_156058 21606:29342(+)
CDS_0027
IMGVR_UViG_3300029430_000419|3300029430|Ga0243922_100401|16649-76387 21607:29655(+)
CDS_0027
IMGVR_UViG_3300029523_000272|3300029523|Ga0244821_100105|16906-79235 21606:28967(+)
CDS_0022 CDS_0028
IMGVR_UViG_3300029534_000094|3300029534|Ga0245005_100183|18263-79782 21362:28412(+)
CDS_0027
IMGVR_UViG_3300045988_066177|3300045988|Ga0495776_181365 21608:28660(+)
CDS_0028
MGV-GENOME-0334954 21362:28712(+)
CDS_0028
IMGVR_UViG_3300029426_000215|3300029426|Ga0242789_100015|123720-185608 21362:28780(+)
CDS_0028 CDS_0029
IMGVR_UViG_2814123326_000002|2814123326|2814196567|119081-182979 21362:30439(+)
CDS_0028
IMGVR_UViG_3300014519_000061|3300014519|Ga0169886_100018|130551-192809 21362:29151(+)
CDS_0028 CDS_0029
IMGVR_UViG_2513237360_000010|2513237360|2513275355|73380-135700 21362:29215(+)
CDS_0031
CDS_0030 CDS_0032
IMGVR_UViG_2844268031_000021|2844268031|2844268125|16419-80283 21360:30764(+)
CDS_0027 CDS_0028 CDS_0030
IMGVR_UViG_3300045988_066586|3300045988|Ga0495776_155507 21607:30420(+)
CDS_0027
MGV-GENOME-0372226 21607:29379(+)
CDS_0027 CDS_0028
uvig_95430 21607:30651(+)
CDS_0029
CDS_0030 CDS_0032
IMGVR_UViG_2585427818_000001|2585427818|2585468268|108327-170169 21603:29350(+)
CDS_0029
CDS_0028 CDS_0030
IMGVR_UViG_3300023506_000350|3300023506|Ga0257040_100022|65750-130317 21604:31340(+)
CDS_0027
CDS_0028
CDS_0029
SAMN00990321_a1_ct73902_vs1 21608:30324(+)
CDS_0029
CDS_0028
CDS_0027 CDS_0030
ivig_904 21606:33201(+)
multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0029)
CDS_0028
CDS_0027 CDS_0030
ivig_3356 21607:32515(+)
CDS_0020
CDS_0019
CDS_0025 CDS_0026
MGV-GENOME-0333872 21775:28602(+)
CDS_0020
CDS_0025 CDS_0026
IMGVR_UViG_3300045988_097603|3300045988|Ga0495776_020123 21142:28442(+)
CDS_0006
CDS_0005 CDS_0011 CDS_0012
MGV-GENOME-0276464 6968:15336(+)
CDS_0031
CDS_0027 CDS_0032
MGV-GENOME-0323282 22486:29431(+)
CDS_0028 CDS_0033
IMGVR_UViG_3300045988_069000|3300045988|Ga0495776_151991 22303:29453(+)
DNA polymerase/primase (CDS_0031)
CDS_0029
CDS_0030
CDS_0028
ivig_1931 22302:31975(+)
CDS_0028
IMGVR_UViG_3300045988_107874|3300045988|Ga0495776_160478 22302:30248(+)
CDS_0028 CDS_0030
CDS_0029
MGV-GENOME-0347623 21970:30331(+)
CDS_0028
CDS_0029
MGV-GENOME-0352125 21970:30226(+)
CDS_0027
MGV-GENOME-0338292 21971:29111(+)
CDS_0027
uvig_395633 21974:30273(+)
CDS_0028
CDS_0027
IMGVR_UViG_3300029391_000309|3300029391|Ga0243992_100362|76-62417 22236:29975(+)
CDS_0030
CDS_0029
transposase (CDS_0026) CDS_0031
uvig_441211_ 21801:30856(+)
transposase (CDS_0026)
CDS_0027
IMGVR_UViG_3300029424_000010|3300029424|Ga0243789_1000321 21338:28978(+)
CDS_0028
CDS_0027
MGV-GENOME-0333970 21611:29251(+)
CDS_0028
CDS_0027 CDS_0029 CDS_0035
IMGVR_UViG_3300006476_000106|3300006476|Ga0100233_100323 21972:31764(+)
CDS_0026 CDS_0032
IMGVR_UViG_3300045988_089999|3300045988|Ga0495776_157490 21143:28785(+)
CDS_0027
MGV-GENOME-0336489 21972:29522(+)
CDS_0026
CDS_0025 CDS_0027
IMGVR_UViG_3300045988_097363|3300045988|Ga0495776_174360 21509:29522(+)
Retron_VI__HTH (CDS_0030)
MGV-GENOME-0334789 21612:30542(+)
Retron_VI__HTH (CDS_0029)
CDS_0028
CDS_0027 CDS_0030
MGV-GENOME-0336520 21612:31659(+)
IMGVR_UViG_3300023720_000246|3300023720|Ga0257049_100046|17442-83474 21606:32960(+)
multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0027)
MGV-GENOME-0344541 21974:36355(+)
Lysine synthesis (VF0815) (CDS_0031)
uvig_466 22237:42373(+)
CDS_0025
CDS_0026
IMGVR_UViG_3300045988_065146|3300045988|Ga0495776_186325 21140:28132(+)
CDS_0025
CDS_0026
MGV-GENOME-0331354 21132:28169(+)
CDS_0026
CDS_0025 CDS_0027
IMGVR_UViG_3300045988_067456|3300045988|Ga0495776_020093 21143:28344(+)
CDS_0021
IMGVR_UViG_3300045988_082459|3300045988|Ga0495776_073904 19948:26696(+)
CDS_0025 CDS_0026
IMGVR_UViG_3300007524_000009|3300007524|Ga0105481_1000255 21143:28238(+)
CDS_0026
CDS_0025 CDS_0027
IMGVR_UViG_3300045988_067445|3300045988|Ga0495776_016632 21143:28340(+)
CDS_0025 CDS_0026
MGV-GENOME-0332051 21137:28143(+)
CDS_0025
CDS_0026
SAMN01915211_a1_ct17300 21143:28149(+)
CDS_0025 CDS_0026
uvig_375698 20880:27818(+)
CDS_0026
CDS_0025 CDS_0028
IMGVR_UViG_3300045988_060803|3300045988|Ga0495776_149650 21604:29299(+)
CDS_0028
MGV-GENOME-0359334 21607:29301(+)
CDS_0028
MGV-GENOME-0332967 21595:29264(+)
CDS_0026 CDS_0028
IMGVR_UViG_3300045988_093785|3300045988|Ga0495776_177103 21607:29379(+)
RT_III-AM_III-B_2 (CDS_0022)
CDS_0025
CDS_0026
IMGVR_UViG_3300045988_047689|3300045988|Ga0495776_054728 20203:28380(+)
CDS_0025 CDS_0026
MGV-GENOME-0346652 21145:28137(+)
CDS_0050
CDS_0049
MGV-GENOME-0289290 23730:31989(-)
CDS_0024
CDS_0025
uvig_177447 20062:28318(+)
CDS_0024 CDS_0025
uvig_204454 20068:28323(+)
CDS_0043 CDS_0042
MGV-GENOME-0248203 20010:28089(-)
CDS_0026 CDS_0027
MGV-GENOME-0333904 21009:28018(+)
hemolysin (CDS_0022)
CDS_0024
CDS_0025
uvig_570790 19117:27191(+)
CDS_0012
CDS_0004 CDS_0009 CDS_0013
MGV-GENOME-0225059 2747:11976(+)
VirR/VirS two component system (VF0729) (CDS_0028)
SpaH-type pili (VF0727) (CDS_0038)
phosphoesterase (CDS_0037)
integrase (CDS_0034)
uvig_173673 21609:41219(+)
CDS_0029
CDS_0028
MGV-GENOME-0346044 21609:29257(+)
multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0033)
GTP cyclohydrolase (CDS_0030)
FbpABC (VF0272) (CDS_0027)
uvig_449477 22236:38609(+)
CDS_0023
CDS_0022 CDS_0028
MGV-GENOME-0328575 21328:27322(+)
CDS_0026 CDS_0028
OTU_627 21673:29460(+)
CDS_0020
uvig_502858 18695:25105(+)
CDS_0024
MGV-GENOME-0367812 20409:26054(+)
anaerobic ribonucleotide reductase small subunit (CDS_0031)
anaerobic ribonucleoside reductase large subunit (CDS_0030)
IMGVR_UViG_3300014935_000091|3300014935|Ga0169825_100089|2-65858 21344:33611(+)
Lsa family ABC-F type ribosomal protection protein (NF000167.2) (CDS_0030)
DNA polymerase (CDS_0032)
uvig_111589 21609:41131(+)
Lsa family ABC-F type ribosomal protection protein (NF000167.2) (CDS_0030)
IMGVR_UViG_3300029026_000066|3300029026|Ga0169630_100073 21603:37816(+)
multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0033)
AAA domain, putative AbiEii toxin, Type IV TA system (CDS_0035)
SodC (VF0170) (CDS_0030)
multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0037)
Ma_2019_SRR413685_NODE_87_length_89451_cov_7.750548 21607:56545(+)
multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0031)
AAA domain, putative AbiEii toxin, Type IV TA system (CDS_0033)
SodC (VF0170) (CDS_0028)
multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0035)
uvig_542284 21608:45586(+)
CDS_0029
CDS_0028
CDS_0027 CDS_0030
uvig_160747 21839:33854(+)
CDS_0027
MGV-GENOME-0359462 21839:30896(+)
CDS_0031
CDS_0030
CDS_0028
CDS_0029 CDS_0035
MGV-GENOME-0333455 21970:29596(+)
CDS_0024
MGV-GENOME-0333587 20704:29190(+)
CDS_0024
IMGVR_UViG_3300045988_094032|3300045988|Ga0495776_073586 19554:29190(+)
Paris_I__AriB_DUF4435_I__AriB_DUF4435_I_ali (CDS_0026)
Paris_I__AriA_AAA15__AriA_AAA15_ali (CDS_0025)
CDS_0027
CDS_0020 CDS_0028
IMGVR_UViG_3300029726_000211|3300029726|Ga0245201_100138|2439-64618 18678:29511(+)
minor tail protein (CDS_0016)
CDS_0021 CDS_0022
IMGVR_UViG_3300045988_070893|3300045988|Ga0495776_056539 17832:26006(+)
FbpA/Fbp68 (VF0595) (CDS_0035)
guanylate kinase (CDS_0037)
uvig_238885 21971:41761(+)
ivig_2778 21970:35262(+)
phospho-2-dehydro-3-deoxyheptonate aldolase (CDS_0027)
Pyrimidine biosynthesis (VF0558) (CDS_0029)
FbpA/Fbp68 (VF0595) (CDS_0032)
guanylate kinase (CDS_0034)
uvig_90743 21974:43025(+)
CDS_0057
MGV-GENOME-0217235 26939:31023(-)
ABC transporter (CDS_0028)
ABC transporter (CDS_0027) CDS_0030
CDS_0021 CDS_0029
uvig_274501 21145:31277(+)
uvig_164059 21604:35108(+)
uvig_540149 21607:40905(+)
multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0034)
ivig_4444 21847:32567(+)
DarB-like antirestriction (CDS_0036)
MazEF__MazF (CDS_0030)
uvig_542551 22136:41231(+)
metal-dependent phosphohydrolase (CDS_0037)
uvig_452347 22132:35388(+)
Retron_XII__RT_12 (CDS_0037)
IMGVR_UViG_2840324701_000001|2840324701|2840324701|33054-402512 22302:37109(+)
MGV-GENOME-0342868 22302:35380(+)
Thoeris__ThsB_Global (CDS_0039)
IMGVR_UViG_3300045988_097426|3300045988|Ga0495776_181678 22303:37736(+)
aminoglycoside 6-nucleotidyltransferase (NF033084.2) (CDS_0041)
amidase (CDS_0045)
holin (CDS_0046)
transcriptional regulator (CDS_0042)
multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0031)
uvig_441024_ 21607:49232(+)
10000 nt
DNA, RNA and nucleotide metabolism
head and packaging
integration and excision
lysis
moron, auxiliary metabolic gene and host takeover
other
tail
transcription regulation
unknown function
Defence
Virulence
AMR