;2:0.000,0.018,0.758,0.982;3:0.000,0.015,0.758,0.985;4:0.000,0.015,0.758,0.985;5:0.000,0.015,0.758,0.985;6:0.000,0.015,0.758,0.985;7:0.000,0.015,0.758,0.985;8:0.000,0.015,0.758,0.985;9:0.000,0.015,0.758,0.985;10:0.000,0.015,0.758,0.985;11:0.000,0.015,0.758,0.985;12:0.000,0.015,0.758,0.985;13:0.000,0.015,0.758,0.985;14:0.000,0.015,0.758,0.985;15:0.000,0.015,0.758,0.985;16:0.000,0.015,0.758,0.985;17:0.000,0.015,0.758,0.985;18:0.000,0.015,0.758,0.985;19:0.000,0.015,0.758,0.985;20:0.000,0.015,0.758,0.985;21:0.000,0.015,0.758,0.985;22:0.000,0.015,0.758,0.985;23:0.000,0.015,0.758,0.985;24:0.000,0.015,0.758,0.985;25:0.000,0.015,0.758,0.985;26:0.000,0.015,0.758,0.985;27:0.000,0.015,0.758,0.985;28:0.000,0.015,0.758,0.985;29:0.000,0.015,0.758,0.985;30:0.000,0.015,0.758,0.985;31:0.000,0.015,0.758,0.985;32:0.000,0.015,0.758,0.985;33:0.000,0.015,0.758,0.985;34:0.000,0.015,0.758,0.985;35:0.000,0.015,0.758,0.985;36:0.000,0.015,0.758,0.985;37:0.000,0.015,0.758,0.985;38:0.000,0.015,0.758,0.985;39:0.000,0.015,0.758,0.985;40:0.000,0.015,0.758,0.985;41:0.000,0.015,0.758,0.985;42:0.000,0.015,0.758,0.985;43:0.000,0.015,0.758,0.985;44:0.000,0.015,0.758,0.985;45:0.000,0.015,0.758,0.985;46:0.000,0.015,0.758,0.985;47:0.000,0.015,0.758,0.985;48:0.000,0.015,0.758,0.985;50:0.000,0.015,0.758,0.985;glycopeptide resistance transcriptional regulator VanU (NF000090.1) (CDS_0003)
DNA methyltransferase (CDS_0004)
endolysin (CDS_0006)
DNA primase (CDS_0001)
CDS_0005
CDS_0002
CDS_0007
ivig_775 1:5310(+)
ivig_3701 1:8297(+)
transcriptional repressor (CDS_0041)
Retron_VI__HTH (CDS_0044)
transposase (CDS_0045)
LPS (VF0124) (CDS_0039)
uvig_242321 16597:34741(-)
ivig_826 16602:27037(-)
CDS_0030
CDS_0029
cas13d_VI-D_1 (CDS_0028)
IMGVR_UViG_3300007353_000099|3300007353|Ga0104758_100576 16597:29951(-)
RpoS (VF0112) (CDS_0031)
IMGVR_UViG_3300029860_000345|3300029860|Ga0245305_1000344|31902-71084 16597:31520(-)
RpoS (VF0112) (CDS_0033)
uvig_32925 16872:32246(-)
amidoligase enzyme (CDS_0040)
Sigma M (VF0822) (CDS_0036)
DNA invertase (CDS_0038)
integrase (CDS_0037)
integrase (CDS_0039)
gamma-glutamyl cyclotransferase (CDS_0028)
uvig_77944 16597:33514(-)
gamma-glutamyl cyclotransferase (CDS_0029)
DNA invertase (CDS_0031)
amidoligase enzyme (CDS_0033)
integrase (CDS_0030)
integrase (CDS_0032)
amidoligase enzyme (CDS_0028)
IMGVR_UViG_2585427614_000001|2585427614|2585443446|588877-624815 16596:28276(-)
Sigma M (VF0822) (CDS_0034)
integrase (CDS_0035)
IMGVR_UViG_3300045988_172658|3300045988|Ga0495776_068534 16597:28225(-)
multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0034)
DnaC-like helicase loader (CDS_0032)
DNA helicase (CDS_0036)
uvig_191003 16597:35191(-)
multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0039)
RegX3 (VF0858) (CDS_0033)
SigE (VF0295) (CDS_0037)
LisR/LisK (VF0792) (CDS_0032)
uvig_41189 17272:37874(-)
WYL_I_II_III_IV_V_VI_1 (CDS_0029)
uvig_211098 16600:35164(-)
antitoxin from a toxin-antitoxin system (CDS_0037)
Sigma M (VF0822) (CDS_0028)
uvig_379377 16597:33137(-)
DNA transposition protein (CDS_0040)
Sigma M (VF0822) (CDS_0028)
IMGVR_UViG_3300035652_000136|3300035652|Ga0134453_00062|3-35652 16597:30963(-)
Sigma M (VF0822) (CDS_0035)
ABC transporter (CDS_0033)
transposase (CDS_0034)
IMGVR_UViG_3300029486_000123|3300029486|Ga0244145_100758 16599:31066(-)
replisome organizer (CDS_0031)
IMGVR_UViG_2868558209_000012|2868558209|2868558231|184874-218841 16666:28348(-)
CDS_0029
CDS_0030
CDS_0028
uvig_523554 16813:24992(-)
Avs_IV__Avs4A (CDS_0028)
ivig_742 16596:35379(-)
cas13d_VI-D_1 (CDS_0029)
IMGVR_UViG_3300045988_163087|3300045988|Ga0495776_184600 16597:35236(-)
MGV-GENOME-0290538 16597:35116(-)
cas13d_VI-D_1 (CDS_0030)
uvig_486396 16597:36331(-)
IMGVR_UViG_3300029737_000342|3300029737|Ga0245199_100143|64542-105958 16596:33754(-)
IMGVR_UViG_3300023505_000130|3300023505|Ga0257035_100459 16597:34193(-)
IMGVR_UViG_3300045988_167482|3300045988|Ga0495776_147717 16597:33166(-)
IMGVR_UViG_3300045988_160442|3300045988|Ga0495776_162455 16597:32627(-)
cas13d_VI-D_1 (CDS_0030)
IMGVR_UViG_3300045988_169785|3300045988|Ga0495776_147672 16599:32606(-)
IMGVR_UViG_3300045988_166396|3300045988|Ga0495776_187834 16597:34534(-)
MGV-GENOME-0288953 16597:34750(-)
MGV-GENOME-0289308 16597:34800(-)
MGV-GENOME-0289963 16600:34884(-)
IMGVR_UViG_3300045988_163520|3300045988|Ga0495776_169891 16595:35086(-)
MGV-GENOME-0289632 16597:34835(-)
MGV-GENOME-0273513 16597:33290(-)
WYL_I_II_III_IV_V_VI_1 (CDS_0049)
uvig_117392 16597:43729(-)
WYL_I_II_III_IV_V_VI_1 (CDS_0046)
IMGVR_UViG_3300029098_000161|3300029098|Ga0169171_100163|52506-102030 16597:41862(-)
IMGVR_UViG_3300029605_000348|3300029605|Ga0245145_100377|29138-78882 16600:42082(-)
uvig_41489 16597:41611(-)
WYL_I_II_III_IV_V_VI_1 (CDS_0043)
IMGVR_UViG_3300045988_161412|3300045988|Ga0495776_148187 16597:40052(-)
uvig_389790 16599:39321(-)
MGV-GENOME-0310146 16597:36743(-)
IMGVR_UViG_3300029934_000224|3300029934|Ga0169760_100126|32989-77993 16597:37342(-)
IMGVR_UViG_3300045988_167345|3300045988|Ga0495776_155087 16597:36743(-)
MGV-GENOME-0295068 16597:34631(-)
MGV-GENOME-0308183 16597:35994(-)
MGV-GENOME-0305564 16597:37008(-)
MGV-GENOME-0308421 16594:35850(-)
IMGVR_UViG_3300007312_000016|3300007312|Ga0104941_100456 16597:28641(-)
Retron_VI__HTH (CDS_0040)
IMGVR_UViG_3300045988_169527|3300045988|Ga0495776_041123 16597:30127(-)
HitABC (VF0268) (CDS_0037)
tail protein (CDS_0031)
uvig_107922 16597:39219(-)
MntABC (VF0455) (CDS_0041)
Thoeris_II__ThsA_new_petit (CDS_0031)
transposase (CDS_0044)
transcriptional regulator (CDS_0033)
transposase (CDS_0028)
IMGVR_UViG_2902120641_000002|2902120641|2902120649 16594:37231(-)
transpeptidase-like D-Ala-D-Ala carboxypeptidase VanY-D (NF000471.1) (CDS_0041)
HAD-superfamily hydrolase (CDS_0040)
ATP-dependent protease (CDS_0038)
SRS050941_a1_ct328_vs01 17272:40746(-)
vancomycin resistance response regulator transcription factor VanR-B (NF000402.1) (CDS_0033)
RNA polymerase sigma factor (CDS_0045)
FbpABC (VF0272) (CDS_0029)
DNA invertase (CDS_0042)
LisR/LisK (VF0792) (CDS_0032)
35 integrase (CDS_0034)
uvig_195542 16597:42122(-)
ParA-like partition protein (CDS_0043)
ParB-like partition protein (CDS_0042)
uvig_528465 16600:35503(-)
radical SAM domain-containing protein (CDS_0034)
uvig_308688 16597:39671(-)
DNA methyltransferase (CDS_0036)
Druantia_II__DruM (CDS_0041)
IMGVR_UViG_3300029379_000431|3300029379|Ga0243906_1000097|86833-125836 16604:34317(-)
integrase (CDS_0028)
uvig_276877 15133:31042(-)
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