CDS_0032
CDS_0033
CDS_0036
CDS_0041
CDS_0031
CDS_0037
CDS_0042
CDS_0035
CDS_0039
CDS_0034
CDS_0038
CDS_0040
CDS_0043
uvig_580441 26533:32744(+)
hemolysin (CDS_0036)
IMGVR_UViG_3300045988_062993|3300045988|Ga0495776_012555 26312:31964(+)
36
37
38
39
40
44 kinase (CDS_0045)
uvig_294492 26278:38903(+)
CDS_0041
CDS_0040
CDS_0036
CDS_0038
CDS_0045
MGV-GENOME-0316533 26958:33393(+)
CDS_0036
CDS_0040
CDS_0037
CDS_0041
IMGVR_UViG_3300045988_050665|3300045988|Ga0495776_188874 26545:32064(+)
DNA repair protein (CDS_0039)
36
37
38
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41
uvig_389252 26435:40461(+)
CDS_0038
CDS_0045
CDS_0046
MGV-GENOME-0330061 26838:33547(+)
CDS_0036
CDS_0037
CDS_0039
uvig_309061 26555:34134(+)
CDS_0036
CDS_0037
CDS_0041
MGV-GENOME-0319069 26520:33696(+)
CDS_0037
CDS_0036
CDS_0042
IMGVR_UViG_3300029471_000202|3300029471|Ga0244196_100164|10676-63969 26523:32856(+)
CDS_0036
CDS_0038
CDS_0043
CDS_0037
CDS_0039
CDS_0044
uvig_139184 26482:35522(+)
CDS_0036
CDS_0037
IMGVR_UViG_3300045988_082881|3300045988|Ga0495776_183884 26482:34010(+)
RosmerTA__RmrA_2634932349 (CDS_0037)
CDS_0036
CDS_0038
uvig_133008 26515:34606(+)
CDS_0036
CDS_0037
MGV-GENOME-0331285 26481:33196(+)
DNA repair protein (CDS_0039)
hemolysin (CDS_0036)
37
38
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41
uvig_470922 26481:39601(+)
SMODS-associating 4TM effector domain (CDS_0040)
CBASS__Cyclase_II (CDS_0038)
CBASS__E2_II (CDS_0039)
36
37
41
42
43
uvig_245194 26555:39616(+)
RosmerTA__RmrT_2600853143 (CDS_0038)
RosmerTA__RmrA_2600853143 (CDS_0039)
36
37
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uvig_231867 26555:36230(+)
RosmerTA__RmrT_2600853143 (CDS_0038)
RosmerTA__RmrA_2600853143 (CDS_0039)
hemolysin (CDS_0036)
37
40
IMGVR_UViG_3300029403_000004|3300029403|Ga0243191_100257 26560:35508(+)
38
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36
37
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41
uvig_336997 26541:34758(+)
CDS_0037
CDS_0036
CDS_0040
IMGVR_UViG_3300045988_069171|3300045988|Ga0495776_057525 26518:33276(+)
CDS_0036
CDS_0037
IMGVR_UViG_3300045988_073812|3300045988|Ga0495776_183765 26555:31606(+)
CDS_0037
CDS_0036
MGV-GENOME-0326525 26555:31352(+)
CDS_0036
CDS_0037
CDS_0038
uvig_236933 26555:37580(+)
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IMGVR_UViG_3300030442_000276|3300030442|Ga0168840_100238|1-55391 26545:35984(+)
CDS_0036
CDS_0038
CDS_0037
IMGVR_UViG_3300045988_089664|3300045988|Ga0495776_168888 26565:34268(+)
Lamassu-Fam__LmuA_effector_Hydrolase (CDS_0037)
36
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42
uvig_217815 26525:39101(+)
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hemolysin (CDS_0042)
uvig_129023 26270:34562(+)
ABC transporter (CDS_0039)
DNA repair protein (CDS_0043)
RegX3 (VF0858) (CDS_0040)
36
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IMGVR_UViG_3300029387_000103|3300029387|Ga0243994_100330 26555:44655(+)
CDS_0036
CDS_0038
CDS_0037
CDS_0039
IMGVR_UViG_3300029391_000122|3300029391|Ga0243992_100539 26555:36404(+)
Siderophore-dependent iron uptake system (VF0738) (CDS_0040)
36
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uvig_124850 26545:43450(+)
Siderophore-dependent iron uptake system (VF0738) (CDS_0040)
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uvig_283262 26481:42736(+)
Siderophore-dependent iron uptake system (VF0738) (CDS_0042)
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uvig_527933 26300:44104(+)
Siderophore-dependent iron uptake system (VF0738) (CDS_0041)
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uvig_141829 26554:43439(+)
Siderophore-dependent iron uptake system (VF0738) (CDS_0042)
RosmerTA__RmrA_2634932349 (CDS_0037)
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uvig_200802 26435:42882(+)
Siderophore-dependent iron uptake system (VF0738) (CDS_0045)
2-aminooxy adenylosuccinate synthetase (CDS_0041)
RegX3 (VF0858) (CDS_0040)
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uvig_451624 26555:49086(+)
Siderophore-dependent iron uptake system (VF0738) (CDS_0044)
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uvig_227403 26523:42525(+)
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SAMN09781718_a1_ct7660_vs1 26559:34837(+)
CDS_0036
CDS_0038
CDS_0037
CDS_0041
CDS_0042
MGV-GENOME-0335418 26555:35754(+)
CDS_0036
CDS_0037
uvig_92956 26555:35932(+)
CDS_0033
CDS_0037
CDS_0030
CDS_0036
MGV-GENOME-0324861 25319:33925(+)
CDS_0036
CDS_0037
MGV-GENOME-0320760 25319:35784(+)
RM__Type_I_REases__Type_I_REases_FAM_0.einsi_trimmed (CDS_0045)
Kiwa__KwaA (CDS_0047)
RM__Type_I_MTases__Type_I_MTases_FAM_0 (CDS_0042)
Kiwa__KwaB (CDS_0046)
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IMGVR_UViG_2915308434_000007|2915308434|2915308513|3-68883 26555:49309(+)
Siderophore-dependent iron uptake system (VF0738) (CDS_0051)
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uvig_160102 26269:52278(+)
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Han_2018_ERR1398080_NODE_203_length_62896_cov_35.639010 26555:43499(+)
major head protein (CDS_0041)
internal virion protein (CDS_0044)
DNA repair protein (CDS_0053)
peptidase (CDS_0040)
FbpABC (VF0272) (CDS_0049)
terminase large subunit (CDS_0038)
42
RegX3 (VF0858) (CDS_0050)
36
37
portal protein (CDS_0039)
43
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uvig_388493 26300:54267(+)
multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0009)
ParA-like partition protein (CDS_0002)
ParB-like partition protein (CDS_0003)
11
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4
DnaD-like helicase loader (CDS_0001)
uvig_61023 1:10858(-)
ParB-like partition protein (CDS_0003)
6
5
4
2
DnaD-like helicase loader (CDS_0001)
MGV-GENOME-0325435 1:5893(-)
DarB-like antirestriction (CDS_0001)
CDS_0002
IMGVR_UViG_3300045988_074384|3300045988|Ga0495776_134436 1:4156(-)
10000 nt
DNA, RNA and nucleotide metabolism
head and packaging
integration and excision
lysis
moron, auxiliary metabolic gene and host takeover
other
transcription regulation
unknown function
Defence
Virulence
AMR