Retron_VI__HTH (CDS_0032)
CDS_0040
CDS_0033
CDS_0036
CDS_0039
Druantia_II__DruM (CDS_0044)
CDS_0047
CDS_0034
CDS_0037
CDS_0041
CDS_0043
CDS_0046
CDS_0035
CDS_0038
CDS_0042
CDS_0045
CDS_0048
IMGVR_UViG_3300029210_000015|3300029210|Ga0168823_100472 28725:35200(+)
CDS_0039
CDS_0040
CDS_0038
CDS_0041
IMGVR_UViG_3300045988_031138|3300045988|Ga0495776_098459 28376:35018(+)
integrase (CDS_0030)
endolysin (CDS_0029)
31
37
38
39
40
41
uvig_463342 24696:35018(+)
DNA methyltransferase (CDS_0040)
CDS_0037
CDS_0038
CDS_0041
replication initiation protein (CDS_0046)
MGV-GENOME-0293300 29080:35844(+)
DNA methyltransferase (CDS_0040)
CDS_0038
CDS_0041
IMGVR_UViG_3300045988_077555|3300045988|Ga0495776_054045 29080:35844(+)
RM_Type_II__Type_II_MTases__Type_II_MTases_FAM_0 (CDS_0055)
CDS_0051
CDS_0052
CDS_0056
uvig_482470 40747:47992(+)
CDS_0037
IMGVR_UViG_3300045988_059340|3300045988|Ga0495776_139351 28641:33227(+)
CDS_0037
IMGVR_UViG_3300045988_042977|3300045988|Ga0495776_136447 28700:35245(+)
CDS_0022
MGV-GENOME-0214831 12977:19111(+)
CDS_0048
CDS_0052
uvig_466489 38700:44924(+)
CDS_0048
CDS_0052
CDS_0053
uvig_339249 38421:44242(+)
CDS_0041
uvig_384189 32101:38203(+)
CDS_0036
uvig_328236 28498:34601(+)
CDS_0015
uvig_495915 4052:10162(-)
CDS_0024
MGV-GENOME-0224153 14583:20947(+)
CDS_0036
MGV-GENOME-0298981 26417:32820(+)
CDS_0024
MGV-GENOME-0217745 13109:19054(+)
CDS_0038
IMGVR_UViG_3300014958_000004|3300014958|Ga0134421_1000342 28806:34617(+)
CDS_0037
CDS_0039
IMGVR_UViG_3300045988_059828|3300045988|Ga0495776_016009 28466:34558(+)
DNA methyltransferase (CDS_0042)
CDS_0038
CDS_0043
MGV-GENOME-0310524 28664:35192(+)
CDS_0036
IMGVR_UViG_3300045988_052432|3300045988|Ga0495776_098314 28462:34755(+)
CDS_0038
CDS_0039
IMGVR_UViG_3300045988_054458|3300045988|Ga0495776_161760 28456:34895(+)
CDS_0036
CDS_0037
uvig_448754 28630:34834(+)
CDS_0037
CDS_0038
IMGVR_UViG_3300045988_041467|3300045988|Ga0495776_185868 28627:35055(+)
CDS_0049
CDS_0050
uvig_484063 41539:47687(+)
CDS_0037
CDS_0038
uvig_449530 28540:34758(+)
CDS_0039
CDS_0040
IMGVR_UViG_3300045988_069458|3300045988|Ga0495776_028315 31292:37703(+)
CDS_0035
CDS_0036
IMGVR_UViG_3300045988_031724|3300045988|Ga0495776_185678 26535:32686(+)
CDS_0037
CDS_0038
IMGVR_UViG_3300045988_059668|3300045988|Ga0495776_006305 28501:34761(+)
CDS_0034
CDS_0035
MGV-GENOME-0307140 24696:32287(+)
CDS_0030
CDS_0031
CDS_0038
MGV-GENOME-0278470 24004:30632(+)
CDS_0029
CDS_0030
MGV-GENOME-0265775 21865:28050(+)
DNA methyltransferase (CDS_0056)
CDS_0050
CDS_0051
DNA methyltransferase (CDS_0057)
uvig_170148 36465:42486(+)
DNA methyltransferase (CDS_0042)
CDS_0038
CDS_0043
uvig_551346 29135:35370(+)
CDS_0035
IMGVR_UViG_2811995116_000004|2811995116|2812073720|1387081-1430744 26260:32147(+)
CDS_0044
DNA methyltransferase (CDS_0049)
ivig_2691 35614:41501(+)
CDS_0037
uvig_409275 28667:34321(+)
CDS_0028
CDS_0030
CDS_0034
IMGVR_UViG_3300045988_024114|3300045988|Ga0495776_172066 24384:32980(+)
CDS_0034
IMGVR_UViG_3300045988_013006|3300045988|Ga0495776_166075 24384:32294(+)
DNA methyltransferase (CDS_0040)
CDS_0037
CDS_0036
CDS_0039
CDS_0041
MGV-GENOME-0296486 28966:35580(+)
RM_Type_II__Type_II_MTases__Type_II_MTases_FAM_0 (CDS_0040)
CDS_0039
IMGVR_UViG_3300045988_059619|3300045988|Ga0495776_097626 28966:35579(+)
CDS_0041
IMGVR_UViG_3300045988_042213|3300045988|Ga0495776_185765 28941:34970(+)
CDS_0039
IMGVR_UViG_3300045988_041299|3300045988|Ga0495776_185798 27238:33268(+)
RM_Type_II__Type_II_MTases__Type_II_MTases_FAM_0 (CDS_0039)
MGV-GENOME-0272961 23901:30744(+)
CDS_0039
CDS_0037
CDS_0040
MGV-GENOME-0290256 29077:34010(+)
CDS_0043
CDS_0037
CDS_0041
CDS_0042
MGV-GENOME-0300153 29048:35924(+)
DNA methyltransferase (CDS_0041)
CDS_0042
IMGVR_UViG_3300029427_000005|3300029427|Ga0243889_1000452 29710:36097(+)
DNA methyltransferase (CDS_0038)
CDS_0039
IMGVR_UViG_3300045988_013004|3300045988|Ga0495776_179774 26789:33643(+)
CDS_0037
IMGVR_UViG_3300045988_011475|3300045988|Ga0495776_148853 26550:33503(+)
CDS_0041
Druantia_II__DruM (CDS_0043)
CDS_0042
IMGVR_UViG_3300045988_077038|3300045988|Ga0495776_097536 28968:35798(+)
CDS_0038
endolysin (CDS_0044)
Han_2018_ERR1398090_NODE_164_length_46357_cov_5.784869 28675:35294(+)
CDS_0038
CDS_0040
IMGVR_UViG_3300045988_052179|3300045988|Ga0495776_138057 28589:35454(+)
22
23
24
25
26
30
31
MGV-GENOME-0226290 14958:21104(+)
CDS_0038
CDS_0042
CDS_0039
CDS_0041
DNA ligase (CDS_0048)
CDS_0049
MGV-GENOME-0300491 28657:35422(+)
CDS_0026
CDS_0025
MGV-GENOME-0221026 13953:20391(+)
CDS_0038
CDS_0040
CDS_0037
CDS_0039
CDS_0043
uvig_302629 31273:38454(+)
DNA methyltransferase (CDS_0025)
CDS_0020
CDS_0026
MGV-GENOME-0265122 14805:21664(+)
RM_Type_II__Type_II_MTases__Type_II_MTases_FAM_0 (CDS_0027)
CDS_0032
MGV-GENOME-0215305 13592:21277(+)
RM_Type_II__Type_II_MTases__Type_II_MTases_FAM_0 (CDS_0026)
MGV-GENOME-0209614 12812:20289(+)
CDS_0028
MGV-GENOME-0213767 13251:20830(+)
CDS_0043
Druantia_II__DruM (CDS_0042)
CDS_0044
CDS_0049
IMGVR_UViG_3300045988_064404|3300045988|Ga0495776_097977 29102:36752(+)
CDS_0048
CDS_0054
ivig_1298 36322:44318(+)
CDS_0045
uvig_229812 34991:42730(+)
Druantia_II__DruM (CDS_0042)
CDS_0041
IMGVR_UViG_3300029123_000009|3300029123|Ga0168800_100584 28825:36470(+)
CDS_0039
IMGVR_UViG_2876114868_000004|2876114868|2876114868|221462-265695 26631:33906(+)
CDS_0039
MGV-GENOME-0297254 28800:35814(+)
Mom-like DNA modification protein (CDS_0044)
CDS_0043
CDS_0045
MGV-GENOME-0288979 27589:34637(+)
Druantia_II__DruM (CDS_0039)
CDS_0038
IMGVR_UViG_3300045988_041513|3300045988|Ga0495776_185860 28584:36294(+)
Druantia_II__DruM (CDS_0039)
CDS_0038
MGV-GENOME-0301042 28584:36294(+)
CDS_0047
IMGVR_UViG_3300029819_000008|3300029819|Ga0245024_100570 33385:39535(+)
CDS_0034
MGV-GENOME-0273678 24010:29921(+)
CDS_0052
uvig_460042 36667:43543(+)
CDS_0041
MGV-GENOME-0295921 29125:35021(+)
CDS_0034
MGV-GENOME-0275645 23999:29643(+)
transposase (CDS_0052)
CDS_0048
transposase (CDS_0051)
uvig_382127 36235:44129(+)
CDS_0038
IMGVR_UViG_3300045988_046066|3300045988|Ga0495776_053992 28567:33927(+)
Druantia_II__DruM (CDS_0043)
Druantia_II__DruM (CDS_0042)
45
40
41
44
DNA methyltransferase (CDS_0046)
uvig_592001 28963:38558(+)
DNA methyltransferase (CDS_0039)
CDS_0040
IMGVR_UViG_3300045988_031643|3300045988|Ga0495776_148320 27101:35193(+)
CDS_0038
CDS_0040
CDS_0037
CDS_0039
CDS_0043
CDS_0044
IMGVR_UViG_3300045988_047681|3300045988|Ga0495776_015858 28696:36078(+)
multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0038)
QueC-like queuosine biosynthesis (CDS_0040)
Druantia_II__DruM (CDS_0049)
35
36
37
anaerobic ribonucleoside reductase large subunit (CDS_0039)
41
42
43
48
uvig_293321 28502:42593(+)
5000 nt
DNA, RNA and nucleotide metabolism
integration and excision
lysis
moron, auxiliary metabolic gene and host takeover
other
transcription regulation
unknown function
Defence
AMR