IMGVR_UViG_3300045988_065762|3300045988|Ga0495776_130216: 27,878-33,545 (+)

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holin (CDS_0036)

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Retron_VI__HTH (CDS_0041)

transcriptional regulator (CDS_0042)

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IMGVR_UViG_3300045988_048971|3300045988|Ga0495776_113050: 26,014-32,616 (+)

32

IMGVR_UViG_3300045988_071153|3300045988|Ga0495776_169394: 27,851-36,432 (+)

37 38 39

MGV-GENOME-0323474: 26,008-33,182 (+)

32 33 34

IMGVR_UViG_3300045988_050400|3300045988|Ga0495776_113434: 27,879-33,551 (+)

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uvig_90130: 26,001-32,853 (+)

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MGV-GENOME-0321695: 25,911-32,286 (+)

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IMGVR_UViG_3300045988_062952|3300045988|Ga0495776_130558: 27,862-33,984 (+)

37 38

MGV-GENOME-0324486: 25,917-34,069 (+)

32

PDC-M30B_WP_013406987.1 (CDS_0033)
34 35

MGV-GENOME-0321040: 27,899-33,727 (+)

37 38 43

MGV-GENOME-0319527: 26,152-31,876 (+)

30 32

MGV-GENOME-0318795: 26,008-31,786 (+)

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MGV-GENOME-0319665: 26,152-31,945 (+)

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IMGVR_UViG_3300045988_126293|3300045988|Ga0495776_121975: 25,914-41,250 (+)

32 33

RNA polymerase sigma factor (CDS_0034)

35 36 37 38

RosmerTA__RmrT_2600853143 (CDS_0039)

RosmerTA__RmrA_2600853143 (CDS_0040)
41 42

MGV-GENOME-0318255: 27,073-32,329 (+)

32

uvig_496386: 44,358-48,507 (-)

65

uvig_196875: 1-8,553 (+)

DNA helicase (CDS_0001) 2

MGV-GENOME-0336505: 1-4,734 (+)

replisome organizer (CDS_0001)
2

MGV-GENOME-0305199: 42,810-45,764 (-)

65

uvig_49679: 38,066-42,725 (-)

60 59

61

uvig_444711_: 62,610-68,348 (-)

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IMGVR_UViG_3300029336_000111|3300029336|Ga0243752_100581: 1-7,571 (+)

1

DnaC-like helicase loader (CDS_0002)
3 4 5 6 7

IMGVR_UViG_3300045988_131553|3300045988|Ga0495776_121883: 1-4,949 (+)

1 2

uvig_263250: 1-9,696 (+)

DnaD-like helicase loader (CDS_0001)

capH (CDS_0002)
3

hydrolase (CDS_0004)

penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0005)

6

PDC-M30B_WP_013406987.1 (CDS_0007)

8 9

uvig_462454: 1-9,451 (+)

GajB_00030 UrvD (CDS_0001)
2 3

transcriptional regulator (CDS_0004)

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IMGVR_UViG_3300045988_082013|3300045988|Ga0495776_090762: 27,475-40,244 (+)

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MGV-GENOME-0334239: 27,475-39,869 (+)

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uvig_145551: 27,475-41,765 (+)

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ADP-ribosylglycohydrolase (CDS_0051)

52 53

IMGVR_UViG_3300045988_077884|3300045988|Ga0495776_174560: 27,475-40,660 (+)

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ADP-ribosylglycohydrolase (CDS_0051)

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IMGVR_UViG_3300029934_000003|3300029934|Ga0169760_100204: 25,912-39,707 (+)

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ADP-ribosylglycohydrolase (CDS_0048)

49 50

IMGVR_UViG_3300045988_071098|3300045988|Ga0495776_073445: 27,475-39,273 (+)

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IMGVR_UViG_3300045988_082984|3300045988|Ga0495776_054631: 27,475-38,948 (+)

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uvig_583706: 27,484-38,960 (+)

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MGV-GENOME-0334618: 27,466-39,234 (+)

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IMGVR_UViG_3300045988_082568|3300045988|Ga0495776_073599: 27,475-39,512 (+)

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MGV-GENOME-0337111: 27,475-40,140 (+)

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MGV-GENOME-0333255: 27,475-39,273 (+)

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MGV-GENOME-0336320: 27,466-40,322 (+)

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MGV-GENOME-0332682: 27,476-38,962 (+)

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IMGVR_UViG_3300045988_067035|3300045988|Ga0495776_090463: 27,878-39,695 (+)

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IMGVR_UViG_3300045988_083843|3300045988|Ga0495776_090529: 27,476-39,520 (+)

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IMGVR_UViG_3300045988_086708|3300045988|Ga0495776_020278: 27,920-39,642 (+)

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MGV-GENOME-0334438: 27,868-39,449 (+)

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MGV-GENOME-0329199: 25,271-37,041 (+)

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IMGVR_UViG_3300045988_081936|3300045988|Ga0495776_176793: 27,481-39,059 (+)

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MGV-GENOME-0333495: 27,429-39,234 (+)

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uvig_21153: 27,929-40,962 (+)

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ADP-ribosylglycohydrolase (CDS_0052)

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MGV-GENOME-0334598: 27,429-39,869 (+)

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IMGVR_UViG_3300045988_097654|3300045988|Ga0495776_111608: 27,929-40,428 (+)

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MGV-GENOME-0335159: 27,863-39,658 (+)

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IMGVR_UViG_3300029019_000001|3300029019|Ga0169654_100119: 27,868-39,761 (+)

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MGV-GENOME-0335163: 27,635-40,118 (+)

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IMGVR_UViG_3300045988_066651|3300045988|Ga0495776_073600: 27,635-39,228 (+)

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IMGVR_UViG_3300045988_050518|3300045988|Ga0495776_090685: 27,884-40,017 (+)

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uvig_101082: 26,007-40,532 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

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MGV-GENOME-0334126: 27,878-39,066 (+)

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MGV-GENOME-0323161: 22,208-33,687 (+)

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MGV-GENOME-0334514: 27,892-39,492 (+)

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IMGVR_UViG_3300045988_053308|3300045988|Ga0495776_090566: 27,892-39,492 (+)

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IMGVR_UViG_3300045988_051914|3300045988|Ga0495776_090644: 27,927-40,196 (+)

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IMGVR_UViG_3300045988_052118|3300045988|Ga0495776_007341: 27,551-38,938 (+)

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uvig_309978: 27,475-41,322 (+)

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ADP-ribosylglycohydrolase (CDS_0051)

52 53

IMGVR_UViG_3300045988_117391|3300045988|Ga0495776_150482: 27,862-42,118 (+)

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MGV-GENOME-0335857: 26,008-39,688 (+)

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IMGVR_UViG_3300045988_069231|3300045988|Ga0495776_073566: 25,861-37,942 (+)

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IMGVR_UViG_3300045988_107792|3300045988|Ga0495776_054905: 27,872-39,269 (+)

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IMGVR_UViG_3300008360_000019|3300008360|Ga0114875_1000385: 27,863-39,299 (+)

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IMGVR_UViG_3300045988_069916|3300045988|Ga0495776_073443: 27,943-39,595 (+)

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IMGVR_UViG_3300045988_038556|3300045988|Ga0495776_090524: 27,872-39,281 (+)

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SRS019808_a1_ct10918: 26,008-37,621 (+)

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transcriptional repressor (CDS_0038)

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uvig_594500: 25,966-37,532 (+)

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MGV-GENOME-0305710: 9,286-27,451 (+)

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IMGVR_UViG_3300029467_000043|3300029467|Ga0244104_100385: 27,475-43,222 (+)

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ADP-ribosylglycohydrolase (CDS_0052)

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hydrolase (CDS_0054)

Jallet_2C_hits_grouped (CDS_0055)

penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0056)

57 58

uvig_384149: 36,042-47,411 (+)

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MGV-GENOME-0324645: 26,152-37,772 (+)

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transcriptional repressor (CDS_0038)

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MGV-GENOME-0328971: 25,911-36,576 (+)

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IMGVR_UViG_3300029353_000002|3300029353|Ga0243845_100541: 27,881-41,160 (+)

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transcriptional repressor (CDS_0043)

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ADP-ribosylglycohydrolase (CDS_0052)

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IMGVR_UViG_3300045988_112948|3300045988|Ga0495776_111559: 27,925-40,465 (+)

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uvig_178925: 25,909-37,921 (+)

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IMGVR_UViG_3300045988_087257|3300045988|Ga0495776_056547: 25,909-36,660 (+)

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MGV-GENOME-0334144: 25,926-36,166 (+)

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IMGVR_UViG_3300045988_104776|3300045988|Ga0495776_188139: 25,917-38,265 (+)

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MGV-GENOME-0339310: 25,917-37,664 (+)

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MGV-GENOME-0332174: 25,617-37,497 (+)

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IMGVR_UViG_3300045988_184339|3300045988|Ga0495776_163027|10437-69999: 26,171-37,316 (+)

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uvig_467052: 25,917-41,932 (+)

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VirR/VirS two component system (VF0729) (CDS_0048)

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IMGVR_UViG_3300030031_000035|3300030031|Ga0245030_100328: 25,917-37,815 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

MGV-GENOME-0334460: 27,871-39,671 (+)

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51 tRNA-Val(GAC)

IMGVR_UViG_3300045988_104380|3300045988|Ga0495776_174447: 25,926-37,182 (+)

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uvig_580437: 26,151-38,152 (+)

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MGV-GENOME-4430298: 26,154-39,327 (+)

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46 DS-30__DS-30D (CDS_0047)

IMGVR_UViG_3300029123_000258|3300029123|Ga0168800_100341|10036-69191: 26,154-37,235 (+)

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IMGVR_UViG_3300045988_063230|3300045988|Ga0495776_174394: 27,925-39,298 (+)

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IMGVR_UViG_3300045988_106771|3300045988|Ga0495776_036296: 26,010-37,198 (+)

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uvig_267544: 27,925-41,355 (+)

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vanR_ACDEGLN-NCBIFAM VanR-ABDEGLN family response regulator transcription factor (NF033117.2) (CDS_0052) HK_VanS_ACDEFG-NCBIFAM vancomycin resistance histidine kinase VanS (NF033091.0) (CDS_0053)

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MGV-GENOME-0341342: 27,871-38,860 (+)

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IMGVR_UViG_3300029847_000085|3300029847|Ga0245281_100473: 25,867-41,036 (+)

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LOS (VF0326) (CDS_0050)
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uvig_300793: 26,007-40,329 (+)

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IMGVR_UViG_3300045988_081154|3300045988|Ga0495776_073495: 25,926-38,320 (+)

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IMGVR_UViG_3300045988_104064|3300045988|Ga0495776_007373: 25,617-37,784 (+)

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IMGVR_UViG_3300045988_088221|3300045988|Ga0495776_174461: 25,506-39,271 (+)

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uvig_136608: 25,617-40,813 (+)

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4142

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ADP-ribosylglycohydrolase (CDS_0048)

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IMGVR_UViG_3300045988_077839|3300045988|Ga0495776_187901: 25,617-40,006 (+)

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MGV-GENOME-0338664: 25,617-39,424 (+)

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IMGVR_UViG_2915321476_000002|2915321476|2915321476|593947-655735: 25,912-39,038 (+)

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ADP-ribosylglycohydrolase (CDS_0047)
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ivig_17: 25,672-39,080 (+)

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ADP-ribosylglycohydrolase (CDS_0048)

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IMGVR_UViG_2843288022_000004|2843288022|2843288044|369-62521: 25,672-38,400 (+)

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ADP-ribosylglycohydrolase (CDS_0048)

MGV-GENOME-0335480: 26,154-39,579 (+)

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uvig_146055: 26,154-39,579 (+)

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MGV-GENOME-0335451: 26,154-39,566 (+)

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MGV-GENOME-0344595: 27,863-43,204 (+)

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PDC-M30B_WP_013406987.1 (CDS_0057)

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IMGVR_UViG_3300045988_076475|3300045988|Ga0495776_090402: 27,475-40,108 (+)

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uvig_381365: 27,474-40,722 (+)

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IMGVR_UViG_3300045988_128714|3300045988|Ga0495776_090411: 27,475-39,767 (+)

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MGV-GENOME-0334042: 26,088-38,842 (+)

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IMGVR_UViG_3300045988_064564|3300045988|Ga0495776_073492: 26,169-38,404 (+)

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IMGVR_UViG_3300045988_126155|3300045988|Ga0495776_073607: 27,473-39,297 (+)

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IMGVR_UViG_3300029766_000242|3300029766|Ga0242809_100038|63920-123224: 25,914-37,263 (+)

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IMGVR_UViG_3300045988_105441|3300045988|Ga0495776_073405: 25,617-38,148 (+)

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MGV-GENOME-0333117: 26,006-37,851 (+)

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IMGVR_UViG_3300045988_101234|3300045988|Ga0495776_156106: 27,905-39,466 (+)

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MGV-GENOME-0346465: 25,912-37,471 (+)

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MGV-GENOME-0331055: 25,912-38,120 (+)

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MGV-GENOME-0331042: 25,912-37,513 (+)

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uvig_255433: 23,402-35,167 (+)

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MGV-GENOME-0334294: 27,821-39,767 (+)

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IMGVR_UViG_3300045988_187063|3300045988|Ga0495776_121869|2052-63586: 27,925-39,845 (+)

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IMGVR_UViG_3300045988_067094|3300045988|Ga0495776_020321: 27,923-39,387 (+)

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IMGVR_UViG_3300045988_102571|3300045988|Ga0495776_090475: 27,821-39,767 (+)

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IMGVR_UViG_3300045988_094747|3300045988|Ga0495776_073519: 27,439-39,753 (+)

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uvig_136909: 25,929-42,104 (+)

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IMGVR_UViG_3300045988_091032|3300045988|Ga0495776_150510: 25,929-40,317 (+)

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IMGVR_UViG_3300045988_052081|3300045988|Ga0495776_188084: 25,929-39,123 (+)

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MGV-GENOME-0333986: 27,923-39,688 (+)

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IMGVR_UViG_3300045988_108909|3300045988|Ga0495776_150608: 27,923-39,472 (+)

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MGV-GENOME-0333656: 26,149-38,834 (+)

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IMGVR_UViG_3300045988_098299|3300045988|Ga0495776_102052: 27,847-40,988 (+)

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IMGVR_UViG_3300029780_000012|3300029780|Ga0243204_1000298: 27,475-40,258 (+)

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IMGVR_UViG_3300045988_073977|3300045988|Ga0495776_140111: 27,872-42,387 (+)

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uvig_154088: 27,473-42,521 (+)

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ADP-ribosylglycohydrolase (CDS_0052)

53 54 55

MGV-GENOME-0337473: 27,925-41,898 (+)

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IMGVR_UViG_3300045988_110879|3300045988|Ga0495776_074104: 25,233-37,465 (+)

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IMGVR_UViG_3300029690_000008|3300029690|Ga0245210_100441: 25,233-37,457 (+)

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IMGVR_UViG_3300045988_083804|3300045988|Ga0495776_055052: 27,474-39,460 (+)

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uvig_183902: 25,233-38,766 (+)

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48 49 AAC_6p_group_E-NCBIFAM aminoglycoside 6'-N-acetyltransferase, group E (NF043067.1) (CDS_0050)

MGV-GENOME-0333805: 26,155-38,588 (+)

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IMGVR_UViG_3300045988_096406|3300045988|Ga0495776_090572: 25,912-38,252 (+)

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IMGVR_UViG_3300045988_081972|3300045988|Ga0495776_090770: 27,871-40,336 (+)

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uvig_161920: 25,287-37,552 (+)

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MGV-GENOME-0332013: 25,911-38,243 (+)

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MGV-GENOME-0335253: 27,290-40,124 (+)

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uvig_285915: 27,265-41,657 (+)

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ADP-ribosylglycohydrolase (CDS_0053)

54 55

MGV-GENOME-0339327: 26,007-39,126 (+)

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IMGVR_UViG_3300045988_066930|3300045988|Ga0495776_073728: 27,298-39,188 (+)

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IMGVR_UViG_3300045988_110773|3300045988|Ga0495776_174614: 27,293-39,668 (+)

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MGV-GENOME-0331811: 25,233-37,808 (+)

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uvig_335768: 27,297-39,744 (+)

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51 52 DnaC-like helicase loader (CDS_0053)

IMGVR_UViG_3300045988_053813|3300045988|Ga0495776_111694: 28,122-40,170 (+)

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MGV-GENOME-0333782: 27,301-40,012 (+)

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uvig_63832: 27,872-43,749 (+)

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ADP-ribosylglycohydrolase (CDS_0052)

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Hsp20 heat shock protein (CDS_0056)

57

IMGVR_UViG_3300029132_000067|3300029132|Ga0168796_100334: 25,481-44,126 (+)

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capH (CDS_0049)

vanR_ACDEGLN-NCBIFAM VanR-ABDEGLN family response regulator transcription factor (NF033117.2) (CDS_0050) HK_VanS_ACDEFG-NCBIFAM vancomycin resistance histidine kinase VanS (NF033091.0) (CDS_0051)
HitABC (VF0268) (CDS_0052)

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uvig_134085: 25,481-43,345 (+)

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vanR_ACDEGLN-NCBIFAM VanR-ABDEGLN family response regulator transcription factor (NF033117.2) (CDS_0049) HK_VanS_ACDEFG-NCBIFAM vancomycin resistance histidine kinase VanS (NF033091.0) (CDS_0050)
HitABC (VF0268) (CDS_0051)
52

IMGVR_UViG_3300045988_067739|3300045988|Ga0495776_187203: 25,481-38,582 (+)

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MGV-GENOME-0343210: 27,922-41,395 (+)

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IMGVR_UViG_3300045988_053757|3300045988|Ga0495776_111717: 27,922-40,818 (+)

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IMGVR_UViG_3300045988_067092|3300045988|Ga0495776_073500: 27,922-39,525 (+)

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MGV-GENOME-0332624: 27,871-40,569 (+)

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IMGVR_UViG_3300045988_056582|3300045988|Ga0495776_054947: 27,871-40,569 (+)

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ADP-ribosylglycohydrolase (CDS_0050)

51

IMGVR_UViG_3300045988_047356|3300045988|Ga0495776_150518: 27,871-41,089 (+)

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ADP-ribosylglycohydrolase (CDS_0050)

51

uvig_166160: 27,871-40,249 (+)

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48 49 ADP-ribosylglycohydrolase (CDS_0050)

IMGVR_UViG_3300029558_000079|3300029558|Ga0245036_100331: 25,911-40,648 (+)

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ABC transporter (CDS_0047)

48

RegX3 (VF0858) (CDS_0049)
HK_VanS_ACDEFG-NCBIFAM vancomycin resistance histidine kinase VanS (NF033091.0) (CDS_0050)

uvig_250508: 25,911-37,876 (+)

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uvig_184744: 25,916-40,195 (+)

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endolysin (CDS_0047)

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MGV-GENOME-0330333: 25,916-37,372 (+)

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MGV-GENOME-0336619: 25,926-39,912 (+)

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MGV-GENOME-0334418: 27,863-39,680 (+)

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MGV-GENOME-0334117: 27,863-39,512 (+)

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uvig_176557: 25,914-38,865 (+)

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ADP-ribosylglycohydrolase (CDS_0045)

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uvig_205894: 27,863-43,405 (+)

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ADP-ribosylglycohydrolase (CDS_0051)

52 53 54 55

MGV-GENOME-0335670: 27,863-40,204 (+)

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IMGVR_UViG_3300039355_000008|3300039355|Ga0169769_00221: 26,008-37,209 (+)

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MGV-GENOME-0330959: 26,008-37,921 (+)

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MGV-GENOME-0336695: 27,863-43,368 (+)

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IMGVR_UViG_3300045988_072191|3300045988|Ga0495776_054981: 26,152-38,424 (+)

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IMGVR_UViG_3300045988_071188|3300045988|Ga0495776_151576: 25,917-39,635 (+)

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IMGVR_UViG_3300045988_184840|3300045988|Ga0495776_150562|3-57257: 25,917-38,775 (+)

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MGV-GENOME-0329389: 25,917-39,471 (+)

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MGV-GENOME-0327551: 25,917-37,998 (+)

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IMGVR_UViG_3300045988_049060|3300045988|Ga0495776_169096: 25,917-37,769 (+)

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uvig_192921: 26,065-37,618 (+)

32 3334

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MGV-GENOME-0329517: 25,234-36,871 (+)

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IMGVR_UViG_3300045988_108565|3300045988|Ga0495776_122073: 27,863-42,291 (+)

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ADP-ribosylglycohydrolase (CDS_0053)

54 55

MGV-GENOME-0340172: 25,917-44,323 (+)

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SoFic__SoFic (CDS_0056)

PDC-S07_WP_110056698.1 (CDS_0057)

uvig_206948: 27,634-45,867 (+)

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IMGVR_UViG_3300045988_034170|3300045988|Ga0495776_111563: 25,927-39,152 (+)

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uvig_139491: 25,927-39,257 (+)

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ADP-ribosylglycohydrolase (CDS_0048)

49

IMGVR_UViG_3300045988_077025|3300045988|Ga0495776_073666: 25,926-39,053 (+)

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IMGVR_UViG_3300045988_113511|3300045988|Ga0495776_174521: 27,692-40,120 (+)

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IMGVR_UViG_3300006312_000009|3300006312|Ga0099626_100304: 27,840-39,355 (+)

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uvig_524157: 25,912-40,978 (+)

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IMGVR_UViG_3300045988_106061|3300045988|Ga0495776_174369: 27,869-39,928 (+)

37 3839

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MGV-GENOME-0328769: 25,686-36,561 (+)

32 3334

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MGV-GENOME-0334467: 27,865-39,853 (+)

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IMGVR_UViG_3300045988_096014|3300045988|Ga0495776_090635: 27,866-39,783 (+)

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IMGVR_UViG_3300045988_074361|3300045988|Ga0495776_073296: 27,862-39,531 (+)

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IMGVR_UViG_3300045988_112398|3300045988|Ga0495776_090784: 27,912-39,567 (+)

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IMGVR_UViG_3300045988_121855|3300045988|Ga0495776_007701: 26,151-38,050 (+)

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IMGVR_UViG_3300029256_000004|3300029256|Ga0168827_100440: 26,250-38,094 (+)

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MGV-GENOME-0331409: 25,234-37,913 (+)

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MGV-GENOME-0332506: 25,231-38,507 (+)

32 3334

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MGV-GENOME-0338870: 27,865-42,778 (+)

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MGV-GENOME-0340152: 27,865-41,900 (+)

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IMGVR_UViG_3300045988_112914|3300045988|Ga0495776_150656: 27,851-40,668 (+)

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IMGVR_UViG_3300045988_072167|3300045988|Ga0495776_111508: 27,871-40,280 (+)

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IMGVR_UViG_3300045988_097182|3300045988|Ga0495776_054691: 26,781-38,484 (+)

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uvig_154770: 27,871-40,972 (+)

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ADP-ribosylglycohydrolase (CDS_0053)

54

IMGVR_UViG_3300045988_109019|3300045988|Ga0495776_036021: 26,011-37,658 (+)

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MGV-GENOME-0337276: 25,915-38,809 (+)

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MGV-GENOME-0333956: 25,411-37,845 (+)

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MGV-GENOME-0332466: 25,411-38,540 (+)

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MGV-GENOME-0332226: 26,007-37,533 (+)

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IMGVR_UViG_3300045988_107775|3300045988|Ga0495776_054885: 26,156-37,648 (+)

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IMGVR_UViG_3300023717_000003|3300023717|Ga0257029_10253: 27,860-39,531 (+)

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IMGVR_UViG_3300045988_110514|3300045988|Ga0495776_073695: 27,920-39,325 (+)

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MGV-GENOME-0335891: 27,926-40,731 (+)

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IMGVR_UViG_3300045988_185282|3300045988|Ga0495776_140284|3800-64761: 27,828-39,286 (+)

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IMGVR_UViG_3300045988_079100|3300045988|Ga0495776_054849: 25,617-37,609 (+)

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MGV-GENOME-0333842: 27,920-39,325 (+)

37 3839

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45 4647

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IMGVR_UViG_3300045988_075497|3300045988|Ga0495776_150279: 26,155-38,618 (+)

32 3334

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4142

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MGV-GENOME-0332396: 25,926-37,784 (+)

32 3334

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3839

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4142

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IMGVR_UViG_3300045988_116910|3300045988|Ga0495776_073681: 25,929-38,358 (+)

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404142

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MGV-GENOME-0338671: 26,154-40,871 (+)

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4243

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MGV-GENOME-0345495: 25,927-37,283 (+)

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3839

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4142

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IMGVR_UViG_3300045988_078532|3300045988|Ga0495776_073554: 25,917-38,663 (+)

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38 39

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414243

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MGV-GENOME-0333465: 26,295-38,063 (+)

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4142

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uvig_210858: 25,291-38,452 (+)

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404142

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45 46 47 48

uvig_171037: 25,287-38,257 (+)

32 3334

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404142

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ADP-ribosylglycohydrolase (CDS_0047)

48

IMGVR_UViG_3300045988_068146|3300045988|Ga0495776_073587: 25,911-39,143 (+)

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transcriptional repressor (CDS_0038)

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ADP-ribosylglycohydrolase (CDS_0048)

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MGV-GENOME-0335533: 25,911-37,302 (+)

32 3334

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transcriptional repressor (CDS_0038)

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uvig_413147: 25,911-38,909 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

transcriptional regulator (CDS_0051)
52

IMGVR_UViG_3300045988_045277|3300045988|Ga0495776_111512: 27,927-40,314 (+)

37 3839

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454647

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51 52

uvig_153907: 25,476-38,327 (+)

32 3334

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4142

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45 46

ADP-ribosylglycohydrolase (CDS_0047)

48

IMGVR_UViG_3300045988_107789|3300045988|Ga0495776_177053: 25,494-37,008 (+)

32 3334

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IMGVR_UViG_3300045988_080035|3300045988|Ga0495776_163222: 25,494-37,201 (+)

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IMGVR_UViG_3300045988_072666|3300045988|Ga0495776_187386: 25,480-37,212 (+)

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4142

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IMGVR_UViG_3300045988_090519|3300045988|Ga0495776_054610: 25,926-38,182 (+)

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IMGVR_UViG_3300045988_098300|3300045988|Ga0495776_174556: 25,916-39,282 (+)

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45 46 ADP-ribosylglycohydrolase (CDS_0047)

IMGVR_UViG_3300045988_069288|3300045988|Ga0495776_130515: 22,540-33,929 (+)

31 3233

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394041

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uvig_596863: 25,800-37,556 (+)

32 3334

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uvig_571846: 25,494-40,645 (+)

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IMGVR_UViG_3300045988_118170|3300045988|Ga0495776_033027: 27,926-43,947 (+)

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51 52 53 54 55 56 57

uvig_137797: 27,926-42,935 (+)

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uvig_557297: 25,918-42,941 (+)

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uvig_549476: 25,918-42,941 (+)

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MGV-GENOME-0337779: 27,924-41,351 (+)

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penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0053)

54 55

MGV-GENOME-0335340: 25,911-37,033 (+)

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IMGVR_UViG_3300045988_074529|3300045988|Ga0495776_176982: 25,930-36,608 (+)

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uvig_141010: 25,930-39,378 (+)

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4142

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gamma-glutamyl cyclotransferase (CDS_0045)

zinc containing alcohol dehydrogenase superfamily (CDS_0046)

47 48

MGV-GENOME-0336738: 25,926-40,281 (+)

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PDC-M42B_WP_087252525.1 (CDS_0048)

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MGV-GENOME-0335797: 25,926-39,605 (+)

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PDC-M42B_WP_087252525.1 (CDS_0047)

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uvig_247923: 25,618-44,677 (+)

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45 46 47 48 49 50 51 52 53

uvig_388: 25,916-40,610 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

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MGV-GENOME-0335989: 25,916-39,588 (+)

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MGV-GENOME-0338999: 27,828-43,085 (+)

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NimIJ-NCBIFAM NimIJ family nitroimidazole resistance protein (NF000262.1) (CDS_0053)

54 55 56

uvig_570824: 27,828-43,969 (+)

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ADP-ribosylglycohydrolase (CDS_0053)

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NimIJ-NCBIFAM NimIJ family nitroimidazole resistance protein (NF000262.1) (CDS_0055)

56

uvig_419399: 27,670-42,779 (+)

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ADP-ribosylglycohydrolase (CDS_0051)

52 53 54

MGV-GENOME-0340455: 27,670-41,518 (+)

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IMGVR_UViG_3300045988_119506|3300045988|Ga0495776_188079: 27,670-41,060 (+)

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MGV-GENOME-0305397: 11,373-26,640 (+)

tail length tape measure protein (CDS_0017)
18 19 24 2526 27

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313233

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IMGVR_UViG_3300045988_097233|3300045988|Ga0495776_033079: 25,911-43,223 (+)

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COG2378 CAS-I,CAS-II,CAS-III,CAS-IV,CAS-V,CAS-VI; (CDS_0048) PDC-M09B_WP_094489841.1 (CDS_0049)

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uvig_544458: 27,851-43,033 (+)

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ADP-ribosylglycohydrolase (CDS_0052)

53 54 55 56

uvig_554657: 28,781-41,444 (+)

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ADP-ribosylglycohydrolase (CDS_0052)

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uvig_268761: 25,398-44,543 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

48 49 50 51 52

uvig_230543: 25,927-48,810 (+)

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tail protein (CDS_0054)
55 56 57

IMGVR_UViG_3300029492_000075|3300029492|Ga0244090_100323: 25,927-46,257 (+)

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tail protein (CDS_0051)
52 53 54

IMGVR_UViG_3300029341_000154|3300029341|Ga0243736_1000387: 25,992-43,588 (+)

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ParB-like partition protein (CDS_0053)
5455

IMGVR_UViG_3300029789_000110|3300029789|Ga0243734_1000269: 25,992-44,816 (+)

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45 4647 48 49 50 51 52

ParB-like partition protein (CDS_0053)
transposase (CDS_0054)
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IMGVR_UViG_3300045988_132893|3300045988|Ga0495776_032989: 26,007-43,061 (+)

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PDC-M68A_WP_181373464.1 (CDS_0053)
DS-30__DS-30C (CDS_0054)
DS-30__DS-30D (CDS_0055)

IMGVR_UViG_3300029391_000359|3300029391|Ga0243992_100337|14893-77775: 25,231-40,168 (+)

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PDC-M30B_WP_013406987.1 (CDS_0048)

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IMGVR_UViG_3300029418_000004|3300029418|Ga0243993_100390: 25,234-39,448 (+)

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45 46 ADP-ribosylglycohydrolase (CDS_0047)

uvig_489425: 26,026-41,541 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

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IMGVR_UViG_3300045988_111803|3300045988|Ga0495776_090457: 25,926-39,498 (+)

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uvig_406272: 25,926-40,114 (+)

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45 46 ADP-ribosylglycohydrolase (CDS_0047)

MGV-GENOME-0337929: 25,473-37,789 (+)

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IMGVR_UViG_3300045988_106115|3300045988|Ga0495776_174301: 25,926-37,481 (+)

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uvig_254233: 25,926-37,870 (+)

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uvig_411305: 25,878-41,120 (+)

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ADP-ribosylglycohydrolase (CDS_0049)

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uvig_444348_: 25,234-42,972 (+)

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integrase (CDS_0048)
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PDC-S27_WP_184132443.1 (CDS_0050)

MTase_I_00004 Type (CDS_0051)

IMGVR_UViG_3300029390_000004|3300029390|Ga0243991_1000228: 25,234-41,601 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

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PDC-S27_WP_184132443.1 (CDS_0049)
MTase_I_00004 Type (CDS_0050)

IMGVR_UViG_3300029387_000005|3300029387|Ga0243994_100335: 25,234-42,535 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

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PDC-S27_WP_184132443.1 (CDS_0050)
MTase_I_00004 Type (CDS_0051)

IMGVR_UViG_3300029392_000310|3300029392|Ga0243989_1000269|17106-77099: 25,234-37,470 (+)

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MGV-GENOME-0332738: 27,865-38,671 (+)

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IMGVR_UViG_3300045988_102958|3300045988|Ga0495776_091032: 27,475-37,434 (+)

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IMGVR_UViG_3300029996_000054|3300029996|Ga0245029_100448: 25,917-35,765 (+)

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IMGVR_UViG_3300045988_064384|3300045988|Ga0495776_091175: 27,868-37,078 (+)

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uvig_485622: 27,926-37,757 (+)

37 3839

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uvig_91677: 27,865-36,996 (+)

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IMGVR_UViG_3300045988_062135|3300045988|Ga0495776_073348: 27,884-38,217 (+)

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MGV-GENOME-0327882: 25,234-35,232 (+)

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IMGVR_UViG_3300045988_122688|3300045988|Ga0495776_141862: 25,234-33,897 (+)

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IMGVR_UViG_3300045988_112379|3300045988|Ga0495776_026798: 25,911-34,601 (+)

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MGV-GENOME-0324317: 25,912-34,181 (+)

32 333435 36

uvig_438987: 27,905-49,470 (+)

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52 53 54 55 56 57 58 59 60 61

uvig_84191: 25,912-50,438 (+)

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MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0052) 53 54 55 56

IMGVR_UViG_3300045988_126735|3300045988|Ga0495776_163365: 25,617-39,526 (+)

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ADP-ribosylglycohydrolase (CDS_0048)

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MGV-GENOME-0341606: 25,617-39,526 (+)

32 3334

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uvig_135214: 25,617-43,890 (+)

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ADP-ribosylglycohydrolase (CDS_0048)
DNA polymerase (CDS_0049)
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IMGVR_UViG_2854081209_000001|2854081209|2854081209|467389-532186: 25,915-41,159 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

48 PDC-M30B_WP_013406987.1 (CDS_0049)

ivig_43: 25,915-38,856 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

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IMGVR_UViG_3300045988_109830|3300045988|Ga0495776_188031: 25,824-40,494 (+)

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47 PDC-M30B_WP_013406987.1 (CDS_0048)

uvig_401581: 26,157-41,393 (+)

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penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0049)

50 PDC-M30B_WP_013406987.1 (CDS_0051)

MGV-GENOME-0339927: 25,914-41,932 (+)

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Jallet_2C_hits_grouped (CDS_0048)

penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0049)

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PDC-M30B_WP_013406987.1 (CDS_0052)

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IMGVR_UViG_3300029121_000057|3300029121|Ga0168811_100265: 25,911-41,714 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

48 49 50

IMGVR_UViG_3300045988_067706|3300045988|Ga0495776_121954: 27,872-41,479 (+)

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IMGVR_UViG_3300045988_084102|3300045988|Ga0495776_150378: 27,869-41,610 (+)

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ADP-ribosylglycohydrolase (CDS_0053)

MGV-GENOME-0333196: 25,271-38,638 (+)

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MGV-GENOME-0336197: 26,152-40,161 (+)

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48 PDC-M30B_WP_013406987.1 (CDS_0049)

IMGVR_UViG_3300045988_071504|3300045988|Ga0495776_181357: 25,239-39,600 (+)

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penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0047)

48 PDC-M30B_WP_013406987.1 (CDS_0049)

MGV-GENOME-0337394: 25,239-39,600 (+)

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penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0047)

48 PDC-M30B_WP_013406987.1 (CDS_0049)

uvig_465941: 25,271-46,543 (+)

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ADP-ribosylglycohydrolase (CDS_0050)

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Hsp20 heat shock protein (CDS_0054)

penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0055)

56 57

PDC-M30B_WP_013406987.1 (CDS_0058)

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IMGVR_UViG_3300045988_108362|3300045988|Ga0495776_187311: 25,271-43,487 (+)

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penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0050)

51 52

PDC-M30B_WP_013406987.1 (CDS_0053)

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uvig_324778: 25,239-45,923 (+)

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ADP-ribosylglycohydrolase (CDS_0048)

49 50 5152

capH (CDS_0053)
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hydrolase (CDS_0055)

penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0056)

57 PDC-M30B_WP_013406987.1 (CDS_0058)

IMGVR_UViG_3300045988_105478|3300045988|Ga0495776_122057: 27,875-41,693 (+)

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ADP-ribosylglycohydrolase (CDS_0053)

uvig_261062: 26,007-41,884 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

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uvig_160693: 27,635-44,092 (+)

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ADP-ribosylglycohydrolase (CDS_0053)

54 5556 PDC-M30B_WP_013406987.1 (CDS_0057)

IMGVR_UViG_3300045988_105347|3300045988|Ga0495776_163090: 27,475-42,403 (+)

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4344

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51 52 PDC-M30B_WP_013406987.1 (CDS_0053)

uvig_11453: 27,866-46,470 (+)

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454647

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ADP-ribosylglycohydrolase (CDS_0052)
Hsp20 heat shock protein (CDS_0053)

5455

PDC-M30B_WP_013406987.1 (CDS_0056)
57

MGV-GENOME-0342940: 27,866-44,482 (+)

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454647

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5152

PDC-M30B_WP_013406987.1 (CDS_0053)

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uvig_10142: 27,851-43,907 (+)

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454647

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ADP-ribosylglycohydrolase (CDS_0052)

53 54 55

IMGVR_UViG_3300029365_000006|3300029365|Ga0243866_1000529: 25,474-40,802 (+)

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transcriptional repressor (CDS_0038)

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ADP-ribosylglycohydrolase (CDS_0047)

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PDC-M30B_WP_013406987.1 (CDS_0049)

uvig_455050: 25,474-39,767 (+)

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transcriptional repressor (CDS_0038)

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ADP-ribosylglycohydrolase (CDS_0047)

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IMGVR_UViG_3300030030_000062|3300030030|Ga0245278_100555: 25,291-40,331 (+)

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404142

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47 48PDC-M30B_WP_013406987.1 (CDS_0049)

MGV-GENOME-0343910: 25,291-39,768 (+)

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404142

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45 46 PDC-M30B_WP_013406987.1 (CDS_0047)

MGV-GENOME-0335930: 25,917-39,919 (+)

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414243

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uvig_84584: 25,903-40,162 (+)

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IMGVR_UViG_3300045988_118955|3300045988|Ga0495776_181423: 25,903-39,900 (+)

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45 46 ADP-ribosylglycohydrolase (CDS_0047)

uvig_501381: 26,155-42,263 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

48 49

uvig_294490: 27,474-41,571 (+)

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MGV-GENOME-0343649: 25,617-40,063 (+)

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4142

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48PDC-M30B_WP_013406987.1 (CDS_0049)

IMGVR_UViG_3300045988_125163|3300045988|Ga0495776_149953: 25,617-40,063 (+)

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4142

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48PDC-M30B_WP_013406987.1 (CDS_0049)

uvig_230202: 25,617-45,901 (+)

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51 52 53 54

Hsp20 heat shock protein (CDS_0055)
56

IMGVR_UViG_3300045988_111999|3300045988|Ga0495776_121993: 25,888-41,101 (+)

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51 PDC-M30B_WP_013406987.1 (CDS_0052)

MGV-GENOME-4429497: 25,888-40,773 (+)

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50 PDC-M30B_WP_013406987.1 (CDS_0051)

uvig_335692: 25,888-39,603 (+)

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MGV-GENOME-0341902: 25,548-45,479 (+)

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51 52 53

SoFic__SoFic (CDS_0054)
55 56 57 BrxP_00001 BrxP (CDS_0058)

MGV-GENOME-0335819: 25,617-40,341 (+)

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IMGVR_UViG_3300045988_043097|3300045988|Ga0495776_073359: 25,617-38,679 (+)

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uvig_311977: 25,617-42,153 (+)

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ADP-ribosylglycohydrolase (CDS_0050)

51 52

IMGVR_UViG_3300045988_105764|3300045988|Ga0495776_090589: 25,548-39,695 (+)

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MGV-GENOME-0335772: 25,617-39,849 (+)

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uvig_130021: 25,617-39,849 (+)

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ADP-ribosylglycohydrolase (CDS_0050)

51

MGV-GENOME-0333974: 25,617-38,763 (+)

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MGV-GENOME-0334752: 25,534-39,676 (+)

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IMGVR_UViG_3300045988_075511|3300045988|Ga0495776_073388: 25,534-38,725 (+)

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IMGVR_UViG_3300045988_075890|3300045988|Ga0495776_166801: 25,617-40,735 (+)

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ADP-ribosylglycohydrolase (CDS_0051)

52

IMGVR_UViG_3300045988_098866|3300045988|Ga0495776_036051: 26,160-37,194 (+)

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IMGVR_UViG_3300045988_139377|3300045988|Ga0495776_102219: 27,476-41,388 (+)

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ADP-ribosylglycohydrolase (CDS_0050)

PDC-M30B_WP_013406987.1 (CDS_0051)

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IMGVR_UViG_3300045988_127595|3300045988|Ga0495776_090793: 27,476-40,300 (+)

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ADP-ribosylglycohydrolase (CDS_0050)

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MGV-GENOME-0335006: 27,476-40,300 (+)

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uvig_295756: 27,466-45,765 (+)

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ADP-ribosylglycohydrolase (CDS_0051)

52 53 54

Hsp20 heat shock protein (CDS_0055)
56 57 transposase (CDS_0060)

uvig_183340: 25,480-47,736 (+)

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radical SAM domain protein (CDS_0050)
51 52 53 54 55 56

IMGVR_UViG_3300029423_000004|3300029423|Ga0243802_100453: 25,906-39,331 (+)

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transcriptional repressor (CDS_0038)

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IMGVR_UViG_3300029767_000005|3300029767|Ga0243804_100513: 25,906-39,271 (+)

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transcriptional repressor (CDS_0038)

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IMGVR_UViG_3300029771_000005|3300029771|Ga0243801_100557: 25,906-39,436 (+)

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transcriptional repressor (CDS_0038)

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IMGVR_UViG_3300029414_000004|3300029414|Ga0243798_100538: 25,906-39,622 (+)

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transcriptional repressor (CDS_0038)

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44 45 PDC-M30B_WP_013406987.1 (CDS_0046)

IMGVR_UViG_3300029763_000067|3300029763|Ga0243796_100566: 25,906-42,487 (+)

32 3334

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transcriptional repressor (CDS_0038)

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hydrolase (CDS_0046)

Jallet_2C_hits_grouped (CDS_0047)

penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0048)

49 PDC-M30B_WP_013406987.1 (CDS_0050)

IMGVR_UViG_3300029420_000003|3300029420|Ga0243803_100490: 25,906-38,416 (+)

32 3334

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transcriptional repressor (CDS_0038)

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uvig_445845: 25,906-38,730 (+)

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transcriptional repressor (CDS_0038)

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IMGVR_UViG_3300029356_000003|3300029356|Ga0243797_100560: 25,906-39,257 (+)

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transcriptional repressor (CDS_0038)

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ADP-ribosylglycohydrolase (CDS_0046)

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IMGVR_UViG_3300029441_000151|3300029441|Ga0243753_1000729: 26,010-42,117 (+)

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transcriptional repressor (CDS_0038)

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translation elongation factor (CDS_0048)
49 50 51 52

uvig_447012: 26,010-40,227 (+)

32 3334

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transcriptional repressor (CDS_0038)

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uvig_517444: 26,007-44,417 (+)

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transcriptional repressor (CDS_0038)

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MTase_I_00004 Type (CDS_0048)
RM__Type_I_S_03 (CDS_0049)
REase_I_00008 Type (CDS_0050)

uvig_450222: 26,008-45,305 (+)

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transcriptional repressor (CDS_0038)

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ATP-dependent protease (CDS_0048)

49

O-acetyltransferase (CDS_0050)

co-chaperonin GroES (CDS_0051)

GroEL (VF0594) (CDS_0052)
53

IMGVR_UViG_3300029364_000262|3300029364|Ga0243886_1000191|3-66797: 26,008-44,356 (+)

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transcriptional repressor (CDS_0038)

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retron_type_VI_hth_cluster2_1 (CDS_0048)

49

GroEL (VF0594) (CDS_0050)
51

IMGVR_UViG_3300029778_000293|3300029778|Ga0243887_1000037|46834-125336: 26,008-56,064 (+)

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transcriptional repressor (CDS_0038)

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retron_type_VI_hth_cluster2_1 (CDS_0048)

49

RM_Type_IIG__Type_IIG_2 (CDS_0050)

HEC-06_WP_081759119.1 (CDS_0051)

52 53 54 55

excisionase (CDS_0056)

57

GroEL (VF0594) (CDS_0058)
59

IMGVR_UViG_3300029427_000289|3300029427|Ga0243889_1000117|23211-99790: 26,008-54,141 (+)

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transcriptional repressor (CDS_0038)

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retron_type_VI_hth_cluster2_1 (CDS_0048)

49

RM_Type_IIG__Type_IIG_2 (CDS_0050)

HEC-06_WP_081759119.1 (CDS_0051)

52 53 54 55

excisionase (CDS_0056)
57 58

uvig_556542: 27,922-48,712 (+)

38 3940

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ADP-ribosylglycohydrolase (CDS_0053)

54 555657

Hsp20 heat shock protein (CDS_0058)
59 60

zinc containing alcohol dehydrogenase superfamily (CDS_0061)

62 63 64

uvig_361590: 27,821-50,742 (+)

38 39 4041

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474849

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ABC transporter (VF0818) (CDS_0061)
62

uvig_234901: 25,618-48,237 (+)

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RM__Type_I_MTases_FAM_0 (CDS_0047)

RM__Type_I_S_06 (CDS_0048)

PDC-S15_WP_113621235.1 (CDS_0049)

REase_I_00001 Type (CDS_0050)
51 52 53 54 55 56

MGV-GENOME-0345792: 25,618-47,082 (+)

32 3334

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RM__Type_I_MTases_FAM_0 (CDS_0047)

RM__Type_I_S_06 (CDS_0048)

PDC-S15_WP_113621235.1 (CDS_0049)

REase_I_00001 Type (CDS_0050)
51 52 53 54 55

uvig_127223: 26,154-46,432 (+)

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GajA_00042 AAA (CDS_0049)

GajB_00046 UrvD (CDS_0050)

51

PDC-M68A_WP_181373464.1 (CDS_0052)

DS-30__DS-30C (CDS_0053)
DS-30__DS-30D (CDS_0054)

uvig_151388: 27,920-48,812 (+)

38 3940

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Type-III-B_CnuA (CDS_0054)

55 5657

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59 60 61 62 63

uvig_470921: 25,680-57,250 (+)

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46 47 48

Type-II_STK (CDS_0049)

Type-II_TerY (CDS_0050)

51 52

ZorA2_00004 MotA/ExbB/TolQ (CDS_0053)

ZorB1_00002 MotB (CDS_0054)
55 56 57

DNA primase (CDS_0058)
5960

excisionase (CDS_0061)
integrase (CDS_0062)

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MGV-GENOME-0351460: 25,680-56,101 (+)

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46 47 48

Type-II_STK (CDS_0049)

Type-II_TerY (CDS_0050)

51 52

ZorA2_00004 MotA/ExbB/TolQ (CDS_0053)

ZorB1_00002 MotB (CDS_0054)
55 56 57

DNA primase (CDS_0058)
excisionase (CDS_0059)

integrase (CDS_0060)

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IMGVR_UViG_3300045988_186200|3300045988|Ga0495776_149727|3-64465: 25,680-42,443 (+)

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excisionase (CDS_0049)

integrase (CDS_0050)

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uvig_151742: 27,922-46,743 (+)

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51 52

ADP-ribosylglycohydrolase (CDS_0053)
Hsp20 heat shock protein (CDS_0054)

55 56 57 58 59 60

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IMGVR_UViG_3300029129_000008|3300029129|Ga0168797_100330: 27,244-43,032 (+)

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PDC-M30B_WP_013406987.1 (CDS_0056)

57 58

uvig_42750: 11,340-39,084 (+)

tail length tape measure protein (CDS_0017)
24 2526

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LPS (VF0124) (CDS_0040)

GtcA (VF0607) (CDS_0041)

FbpABC (VF0272) (CDS_0042)

4344

ABC transporter (VF0818) (CDS_0045)

ABC transporter (VF0818) (CDS_0046)

LPS (VF0124) (CDS_0047)
48

Adherence; porin (VF0713) (CDS_0049)

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IMGVR_UViG_3300045988_118494|3300045988|Ga0495776_056470: 27,920-36,099 (+)

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41 42

IMGVR_UViG_3300045988_112263|3300045988|Ga0495776_026616: 25,629-34,152 (+)

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IMGVR_UViG_3300045988_105447|3300045988|Ga0495776_074080: 25,926-35,042 (+)

32 3334

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PDC-M30B_WP_013406987.1 (CDS_0036)

uvig_70218: 25,917-43,216 (+)

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MutT/NUDIX hydrolase (CDS_0053)

54

SoFic__SoFic (CDS_0055)

PDC-S07_WP_110056698.1 (CDS_0056)

57

uvig_319718: 27,862-56,921 (+)

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56 57 58 59 60 61

transcriptional regulator (CDS_0062)
63 64 65 66 67 PDC-S27_WP_184132443.1 (CDS_0068)

uvig_417895: 26,418-50,867 (+)

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COG2378 CAS-I,CAS-II,CAS-III,CAS-IV,CAS-V,CAS-VI; (CDS_0051)

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58 59 60

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62 63

Sak-like ssDNA annealing protein (CDS_0064)
transposase (CDS_0065)
66
67

uvig_236472: 26,171-49,278 (+)

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MGV-GENOME-0345638: 26,171-47,752 (+)

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transcriptional repressor (CDS_0054)
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uvig_282993: 25,732-46,892 (+)

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ADP-ribosylglycohydrolase (CDS_0047)

48 49 50

Hsp20 heat shock protein (CDS_0051)
52 53

zinc containing alcohol dehydrogenase superfamily (CDS_0054)

55 56

uvig_547768: 26,007-46,075 (+)

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ADP-ribosylglycohydrolase (CDS_0048)

49 50

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Hsp20 heat shock protein (CDS_0052)

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uvig_131025: 25,506-52,765 (+)

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drt-cluster433 DRT (CDS_0052)

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57 58 59 60

MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0061)

62 63 64

uvig_136304: 25,617-52,499 (+)

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ADP-ribosylglycohydrolase (CDS_0051)

52 53 54

vanR_ACDEGLN-NCBIFAM VanR-ABDEGLN family response regulator transcription factor (NF033117.2) (CDS_0055)

56 57 58

MntABC (VF0455) (CDS_0059)

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64 65 66 67

mads_8 (CDS_0068)
69

uvig_203744: 26,007-52,089 (+)

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47 48 49 50 51 52 53

MazF-like growth inhibitor (CDS_0054)
55 56 57 58 59

VirR/VirS two component system (VF0729) (CDS_0060)

61 62 63

uvig_164839: 25,911-52,459 (+)

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MutT/NUDIX hydrolase (CDS_0049)

SoFic__SoFic (CDS_0050)
51 52 53 54

FabG-like 3-oxoacyl-(acyl-carrier-protein) reductase (CDS_0055)

56 57

DNA polymerase (CDS_0058)
59 60

transposase (CDS_0061)

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uvig_170432: 27,863-52,160 (+)

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DarTG__DarG (CDS_0056)

57 58 59 60 6162

hydrolase (CDS_0063)

Jallet_2C_hits_grouped (CDS_0064)

penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0065)

6667

PDC-M30B_WP_013406987.1 (CDS_0068)

69

uvig_160832: 27,926-50,411 (+)

38 3940

41
42

43
4445

46
47

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49

50

51
52

ADP-ribosylglycohydrolase (CDS_0053)

54

DarTG__DarG (CDS_0055)
56 57 58 59 6061

hydrolase (CDS_0062)

Jallet_2C_hits_grouped (CDS_0063)

penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0064)

65 PDC-M30B_WP_013406987.1 (CDS_0066)

uvig_399374: 26,103-50,544 (+)

32 3334

35
36

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38 39 40 41

42
43 44

ADP-ribosylglycohydrolase (CDS_0045)

46 47

DarTG__DarG (CDS_0048)
49 50 51 52

PDC-M69A_WP_216276383.1 (CDS_0053)

capH (CDS_0054)
55

hydrolase (CDS_0056)

Jallet_2C_hits_grouped (CDS_0057)

penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0058)

59 PDC-M30B_WP_013406987.1 (CDS_0060)

uvig_254435: 27,475-47,367 (+)

36 37 38

39
4041

42
4344

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51

ADP-ribosylglycohydrolase (CDS_0052)

53

COG0640 Csa3_1_CAS-I-II-III-IV-V-VI (CDS_0054)

5556

excisionase (CDS_0057)
integrase (CDS_0058)

Jallet_2C_hits_grouped (CDS_0059)

penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0060)

61

PDC-M30B_WP_013406987.1 (CDS_0062)

64

IMGVR_UViG_3300045988_106286|3300045988|Ga0495776_111886: 27,294-39,815 (+)

37

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4142

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44

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46 47 48 49 50

MGV-GENOME-0336035: 27,294-39,815 (+)

37

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4142

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46 47 48 49 50

MGV-GENOME-0336007: 27,293-40,614 (+)

36

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4041

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45 46 47 48 49 50 51

IMGVR_UViG_3300045988_045234|3300045988|Ga0495776_054589: 27,265-38,165 (+)

36

37
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41
42 43 44 45 46

MGV-GENOME-0316843: 19,309-30,623 (+)

tail protein (CDS_0022)
23 24 25 26 30

uvig_168505: 19,492-30,850 (+)

UG17 (CDS_0025) 30

MGV-GENOME-0320524: 19,318-31,209 (+)

30 3132

MGV-GENOME-0311923: 18,634-28,581 (+)

23

tail fiber protein (CDS_0024)
25 26 27 28 30

MGV-GENOME-0324272: 18,216-29,165 (+)

21 25 26 29

MGV-GENOME-0332535: 54,821-60,429 (-)

PDC-M30B_WP_013406987.1 (CDS_0081)
82

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 (DefenseFinder) defence (PADLOC) virulence (VFDB) AMR (AMRFinderPlus) tRNA