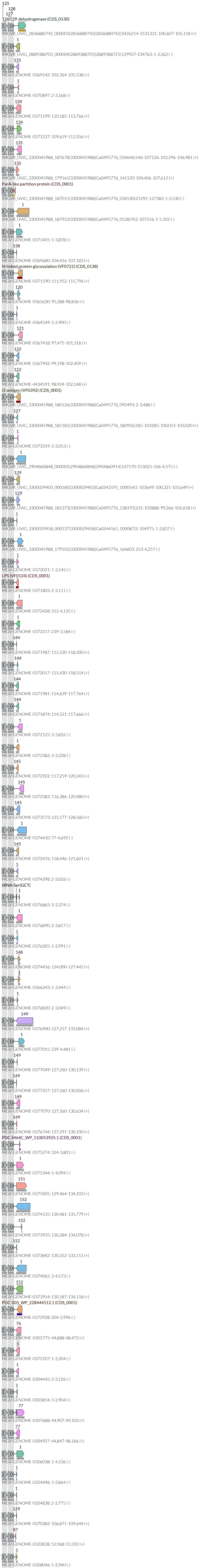
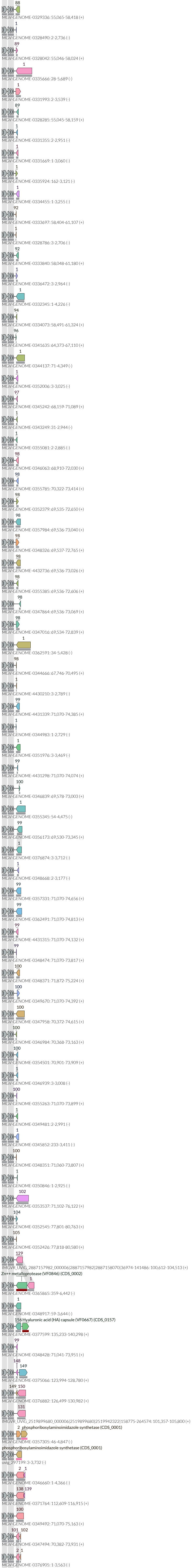
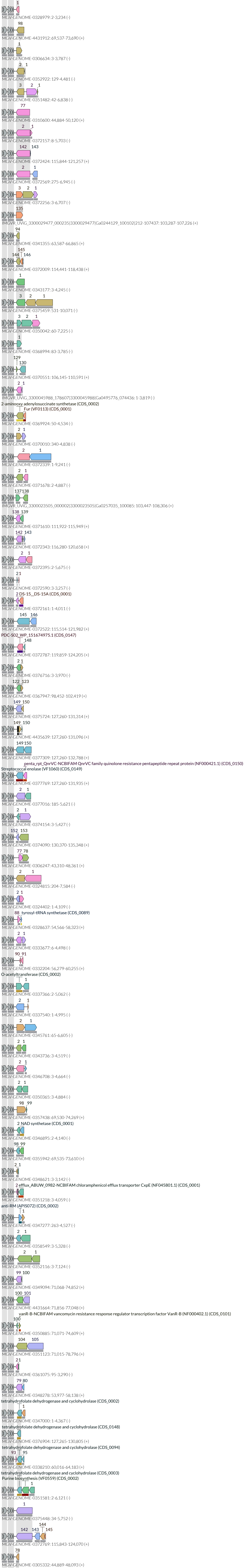
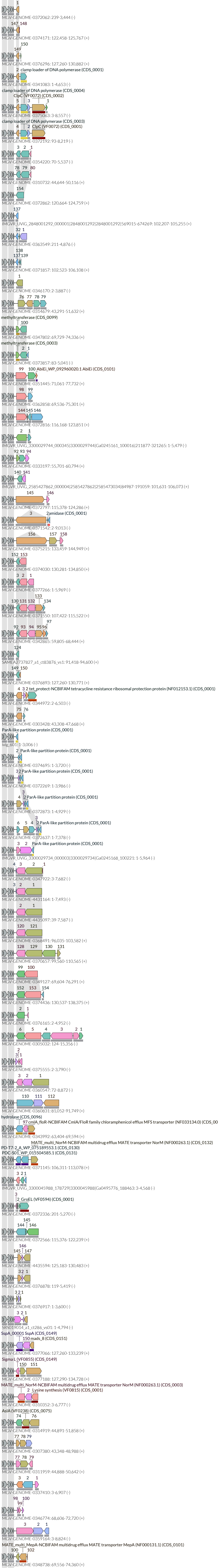
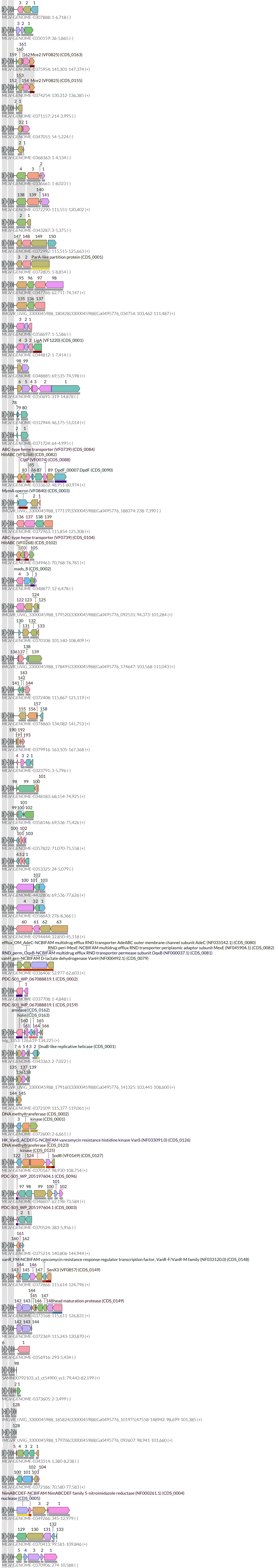
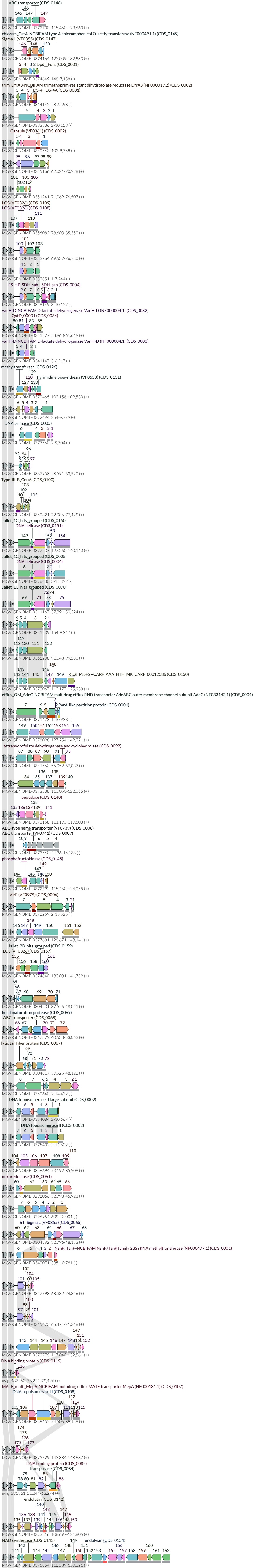

125
128
127
126
129
dehydrogenase (CDS_0130)
IMGVR_UViG_2836880742_000003|2836880742|2836880742|3426214-3531331: 100,607-105,118 (+)
1
IMGVR_UViG_2889388703_000004|2889388703|2889388725|129927-234763: 1-3,362 (-)
131
MGV-GENOME-0369142: 102,364-105,538 (+)
1
MGV-GENOME-0370897: 2-3,168 (-)
134
MGV-GENOME-0371199: 110,185-113,766 (+)
134
MGV-GENOME-0371237: 109,659-113,356 (+)
135
IMGVR_UViG_3300045988_187678|3300045988|Ga0495776_034646|146-107126: 103,296-106,981 (+)
135
IMGVR_UViG_3300045988_179161|3300045988|Ga0495776_141120: 104,406-107,612 (+)
ParA-like partition protein (CDS_0001)
IMGVR_UViG_3300045988_187015|3300045988|Ga0495776_034530|21292-127383: 1-2,530 (-)
1
IMGVR_UViG_3300045988_187952|3300045988|Ga0495776_052859|2-107256: 1-5,102 (-)
1
MGV-GENOME-0371405: 1-3,878 (-)
138
MGV-GENOME-0369680: 104,416-107,183 (+)
N-linked protein glycosylation (VF0721) (CDS_0138)
MGV-GENOME-0371590: 111,952-115,796 (+)
120
MGV-GENOME-0365630: 95,388-98,836 (+)
1
MGV-GENOME-0364549: 3-2,900 (-)
121
MGV-GENOME-0367418: 97,475-101,318 (+)
122
MGV-GENOME-0367942: 99,198-102,409 (+)
122
MGV-GENOME-4434591: 98,924-102,148 (+)
O-antigen (VF0392) (CDS_0001)
IMGVR_UViG_3300045988_180126|3300045988|Ga0495776_092493: 2-3,488 (-)
127
IMGVR_UViG_3300045988_185185|3300045988|Ga0495776_180926|185-103285: 100,051-103,020 (+)
1
MGV-GENOME-0373319: 3-3,053 (-)
1
IMGVR_UViG_2904860848_000005|2904860848|2904860914|147170-253025: 106-4,575 (-)
129
IMGVR_UViG_3300029403_000180|3300029403|Ga0243191_100054|1-103649: 100,321-103,649 (+)
129
IMGVR_UViG_3300045988_185373|3300045988|Ga0495776_138193|231-102888: 99,266-102,658 (+)
1
IMGVR_UViG_3300029458_000137|3300029458|Ga0244161_100087|2-104975: 1-2,837 (-)
1
IMGVR_UViG_3300045988_179103|3300045988|Ga0495776_164603: 253-4,257 (-)
1
MGV-GENOME-0372021: 1-3,145 (-)
LPS (VF0124) (CDS_0001)
MGV-GENOME-0371803: 2-3,111 (-)
1
MGV-GENOME-0372428: 312-4,135 (-)
1
MGV-GENOME-0372217: 239-3,584 (-)
144
MGV-GENOME-0371987: 115,530-118,300 (+)
144
MGV-GENOME-0372017: 115,430-118,514 (+)
144
MGV-GENOME-0371981: 114,639-117,764 (+)
144
MGV-GENOME-0371874: 114,521-117,666 (+)
1
MGV-GENOME-0372125: 3-3,832 (-)
1
MGV-GENOME-0372382: 3-3,228 (-)
145
MGV-GENOME-0372922: 117,259-120,343 (+)
145
MGV-GENOME-0372383: 116,386-120,480 (+)
145
MGV-GENOME-0373573: 125,177-128,560 (+)
1
MGV-GENOME-0374410: 77-4,692 (-)
145
MGV-GENOME-0372476: 118,446-121,601 (+)
1
MGV-GENOME-0374398: 2-3,026 (-)
tRNA-Ser(GCT)
1
MGV-GENOME-0376863: 3-3,374 (-)
1
MGV-GENOME-0376890: 2-3,817 (-)
1
MGV-GENOME-0376305: 1-2,991 (-)
148
MGV-GENOME-0374456: 124,000-127,443 (+)
1
MGV-GENOME-0366343: 1-3,444 (-)
1
MGV-GENOME-0376820: 2-3,049 (-)
149
MGV-GENOME-0376900: 127,257-133,084 (+)
1
MGV-GENOME-0377015: 239-4,481 (-)
149
MGV-GENOME-0377049: 127,260-130,139 (+)
149
MGV-GENOME-0377357: 127,260-130,006 (+)
149
MGV-GENOME-0377070: 127,260-130,634 (+)
149
MGV-GENOME-0376744: 127,291-130,100 (+)
PDC-M64C_WP_110053925.1 (CDS_0001)
MGV-GENOME-0375274: 324-3,801 (-)
1
MGV-GENOME-0375344: 1-4,094 (-)
151
MGV-GENOME-0375005: 129,464-134,103 (+)
152
MGV-GENOME-0374135: 130,481-135,779 (+)
152
MGV-GENOME-0373935: 130,284-134,078 (+)
152
MGV-GENOME-0373842: 130,352-133,151 (+)
1
MGV-GENOME-0374065: 3-4,573 (-)
152
MGV-GENOME-0373954: 130,187-134,118 (+)
PDC-S05_WP_228444512.1 (CDS_0001)
MGV-GENOME-0372928: 204-3,996 (-)
76
MGV-GENOME-0305775: 44,888-48,472 (+)
1
MGV-GENOME-0372107: 1-3,304 (-)
1
MGV-GENOME-0304445: 2-3,126 (-)
1
MGV-GENOME-0303814: 3-2,904 (-)
77
MGV-GENOME-0307688: 44,907-49,103 (+)
77
MGV-GENOME-0304927: 44,847-48,166 (+)
1
MGV-GENOME-0326038: 1-4,136 (-)
1
MGV-GENOME-0324496: 1-2,864 (-)
1
MGV-GENOME-0324838: 2-2,775 (-)
129
MGV-GENOME-0370382: 106,871-109,644 (+)
87
MGV-GENOME-0322838: 52,968-55,592 (+)
1
MGV-GENOME-0328046: 1-2,940 (-)

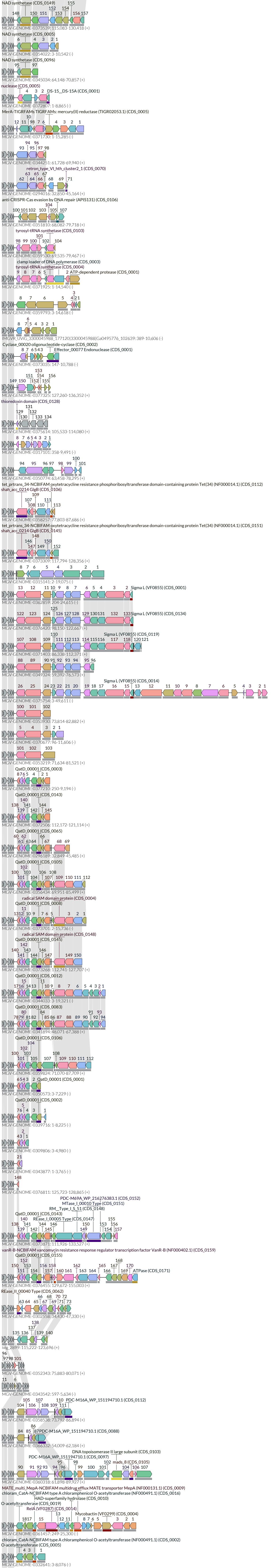

88
MGV-GENOME-0329336: 55,065-58,418 (+)
1
MGV-GENOME-0328490: 2-2,736 (-)
89
MGV-GENOME-0328042: 55,046-58,024 (+)
1
MGV-GENOME-0335666: 28-5,689 (-)
1
MGV-GENOME-0331993: 2-3,539 (-)
89
MGV-GENOME-0328285: 55,045-58,159 (+)
1
MGV-GENOME-0331355: 2-2,951 (-)
1
MGV-GENOME-0331669: 1-3,060 (-)
1
MGV-GENOME-0335924: 162-3,121 (-)
1
MGV-GENOME-0334455: 1-3,255 (-)
92
MGV-GENOME-0333697: 58,404-61,107 (+)
1
MGV-GENOME-0328786: 3-2,706 (-)
92
MGV-GENOME-0333840: 58,048-61,180 (+)
1
MGV-GENOME-0336472: 3-2,964 (-)
1
MGV-GENOME-0332345: 1-4,226 (-)
94
MGV-GENOME-0334073: 58,491-61,324 (+)
96
MGV-GENOME-0341635: 64,373-67,110 (+)
1
MGV-GENOME-0344137: 71-4,349 (-)
1
MGV-GENOME-0352006: 3-3,025 (-)
97
MGV-GENOME-0345242: 68,159-71,089 (+)
1
MGV-GENOME-0343249: 31-2,944 (-)
1
MGV-GENOME-0355081: 2-2,885 (-)
98
MGV-GENOME-0346063: 68,910-72,030 (+)
98
MGV-GENOME-0355785: 70,322-73,414 (+)
98
MGV-GENOME-0352379: 69,535-72,650 (+)
98
MGV-GENOME-0357984: 69,536-73,040 (+)
98
MGV-GENOME-0348326: 69,537-72,765 (+)
98
MGV-GENOME-4432736: 69,536-73,026 (+)
98
MGV-GENOME-0355385: 69,536-72,606 (+)
98
MGV-GENOME-0347864: 69,536-73,069 (+)
98
MGV-GENOME-0347016: 69,534-72,839 (+)
1
MGV-GENOME-0362591: 34-5,428 (-)
98
MGV-GENOME-0344666: 67,746-70,495 (+)
1
MGV-GENOME-4430210: 3-2,789 (-)
99
MGV-GENOME-4431339: 71,070-74,385 (+)
1
MGV-GENOME-0344983: 1-2,729 (-)
1
MGV-GENOME-0351976: 3-3,469 (-)
99
MGV-GENOME-4431298: 71,070-74,074 (+)
100
MGV-GENOME-0346839: 69,578-73,003 (+)
1
MGV-GENOME-0355345: 54-4,475 (-)
99
MGV-GENOME-0356173: 69,530-73,345 (+)
1
MGV-GENOME-0376874: 3-3,712 (-)
1
MGV-GENOME-0348668: 2-3,177 (-)
99
MGV-GENOME-0357331: 71,070-74,656 (+)
99
MGV-GENOME-0362491: 71,070-74,813 (+)
99
MGV-GENOME-4431315: 71,070-74,132 (+)
99
MGV-GENOME-0348474: 71,070-73,817 (+)
100
MGV-GENOME-0348371: 71,872-75,224 (+)
100
MGV-GENOME-0349670: 71,070-74,392 (+)
100
MGV-GENOME-0347958: 70,372-74,615 (+)
100
MGV-GENOME-0346984: 70,368-73,163 (+)
100
MGV-GENOME-0354501: 70,901-73,909 (+)
1
MGV-GENOME-0346939: 3-3,008 (-)
100
MGV-GENOME-0355263: 71,070-73,899 (+)
1
MGV-GENOME-0349481: 2-2,991 (-)
1
MGV-GENOME-0345852: 233-3,411 (-)
100
MGV-GENOME-0348351: 71,060-73,807 (+)
1
MGV-GENOME-0350846: 1-2,925 (-)
102
MGV-GENOME-0353537: 71,102-76,122 (+)
104
MGV-GENOME-0352545: 77,801-80,763 (+)
105
MGV-GENOME-0352426: 77,818-80,580 (+)
129
IMGVR_UViG_2887157982_000006|2887157982|2887158070|36974-141486: 100,612-104,513 (+)
Zn++ metalloprotease (VF0846) (CDS_0002)
1
MGV-GENOME-0365865: 359-6,442 (-)
1
MGV-GENOME-0348917: 59-3,644 (-)
156 Hyaluronic acid (HA) capsule (VF0667) (CDS_0157)
MGV-GENOME-0377599: 135,233-140,298 (+)
99
MGV-GENOME-0348428: 71,041-73,951 (+)
148
149
MGV-GENOME-0375066: 123,994-128,780 (+)
149 150
MGV-GENOME-0376882: 126,499-130,982 (+)
131
IMGVR_UViG_2519899680_000006|2519899680|2519942322|158775-264574: 101,357-105,800 (+)
2 phosphoribosylaminoimidazole synthetase (CDS_0001)
MGV-GENOME-0357305: 46-4,847 (-)
phosphoribosylaminoimidazole synthetase (CDS_0001)
uvig_297199: 3-3,732 (-)
2 1
MGV-GENOME-0346660: 1-4,366 (-)
138 139
MGV-GENOME-0371764: 112,609-116,915 (+)
100
MGV-GENOME-0349492: 71,070-75,163 (+)
101 102
MGV-GENOME-0347494: 70,382-73,931 (+)
2 1
MGV-GENOME-0376905: 1-3,563 (-)

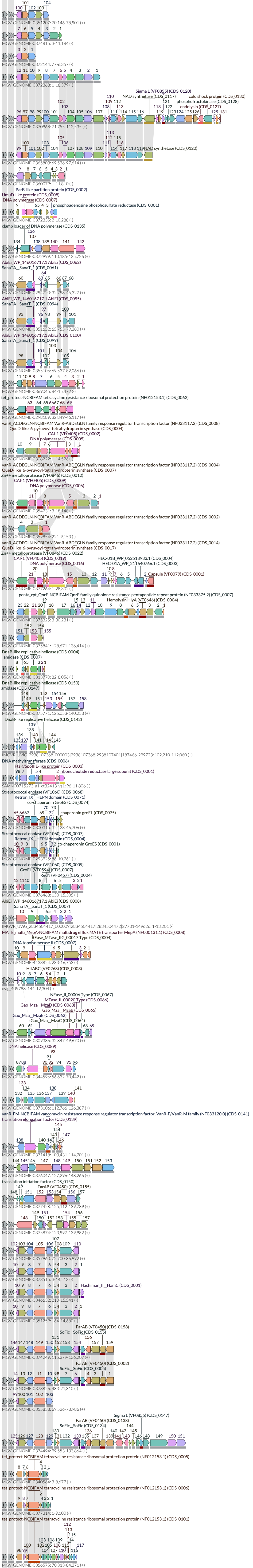

1
MGV-GENOME-0328979: 2-3,234 (-)
98
MGV-GENOME-4431912: 69,537-73,690 (+)
1
MGV-GENOME-0306634: 3-3,787 (-)
2 1
MGV-GENOME-0352922: 129-4,481 (-)
3 2 1
MGV-GENOME-0351482: 42-6,838 (-)
77
MGV-GENOME-0310600: 44,884-50,120 (+)
2 1
MGV-GENOME-0372157: 8-5,703 (-)
142 143
MGV-GENOME-0372424: 115,844-121,257 (+)
2 1
MGV-GENOME-0372569: 275-6,945 (-)
3 2 1
MGV-GENOME-0372256: 3-6,707 (-)
135
IMGVR_UViG_3300029477_000235|3300029477|Ga0244129_100102|212-107437: 103,287-107,226 (+)
94
MGV-GENOME-0341355: 63,587-66,865 (+)
145
144 146
MGV-GENOME-0372009: 114,441-118,438 (+)
1
MGV-GENOME-0343177: 3-4,245 (-)
3 2 1
MGV-GENOME-0375459: 531-10,071 (-)
3 2 1
MGV-GENOME-0350042: 60-7,225 (-)
1
MGV-GENOME-0368994: 83-3,785 (-)
129
130
MGV-GENOME-0370551: 106,145-110,591 (+)
2 1
IMGVR_UViG_3300045988_178607|3300045988|Ga0495776_074436: 1-3,819 (-)
2-aminooxy adenylosuccinate synthetase (CDS_0002)
Fur (VF0113) (CDS_0001)
MGV-GENOME-0369924: 50-4,534 (-)
2 1
MGV-GENOME-0370010: 340-4,838 (-)
2 1
MGV-GENOME-0372339: 1-9,241 (-)
2 1
MGV-GENOME-0371678: 2-4,887 (-)
137138
IMGVR_UViG_3300023505_000002|3300023505|Ga0257035_100085: 103,447-108,306 (+)
138 139
MGV-GENOME-0371610: 111,922-115,949 (+)
142 143
MGV-GENOME-0372343: 116,280-120,658 (+)
2 1
MGV-GENOME-0372395: 2-5,675 (-)
2 1
MGV-GENOME-0372590: 3-3,257 (-)
2 DS-15__DS-15A (CDS_0001)
MGV-GENOME-0372161: 1-4,011 (-)
145 146
MGV-GENOME-0372522: 115,514-121,982 (+)
PDC-S02_WP_151674975.1 (CDS_0147)
148
MGV-GENOME-0372787: 119,859-124,205 (+)
2 1
MGV-GENOME-0376716: 3-3,970 (-)
122 123
MGV-GENOME-0367947: 98,452-102,419 (+)
149 150
MGV-GENOME-0375724: 127,260-131,314 (+)
149 150
MGV-GENOME-4435639: 127,260-131,096 (+)
149 150
MGV-GENOME-0377309: 127,260-132,788 (+)
penta_rpt_QnrVC-NCBIFAM QnrVC family quinolone resistance pentapeptide repeat protein (NF000421.1) (CDS_0150)
Streptococcal enolase (VF1060) (CDS_0149)
MGV-GENOME-0377769: 127,260-131,935 (+)
2 1
MGV-GENOME-0377016: 185-5,621 (-)
2 1
MGV-GENOME-0374154: 3-5,427 (-)
152 153
MGV-GENOME-0374090: 130,370-135,348 (+)
77 78
MGV-GENOME-0306247: 43,310-48,361 (+)
2 1
MGV-GENOME-0324815: 204-7,584 (-)
2 1
MGV-GENOME-0324402: 1-4,109 (-)
88 tyrosyl-tRNA synthetase (CDS_0089)
MGV-GENOME-0328637: 54,566-58,323 (+)
2 1
MGV-GENOME-0333677: 6-4,498 (-)
90 91
MGV-GENOME-0332204: 56,279-60,255 (+)
O-acetyltransferase (CDS_0002)
1
MGV-GENOME-0337366: 2-5,062 (-)
2 1
MGV-GENOME-0337540: 1-4,995 (-)
2 1
MGV-GENOME-0345761: 65-6,605 (-)
2 1
MGV-GENOME-0343736: 3-4,519 (-)
2 1
MGV-GENOME-0346708: 3-4,664 (-)
2 1
MGV-GENOME-0350365: 3-4,884 (-)
98 99
MGV-GENOME-0357438: 69,530-74,269 (+)
2 NAD synthetase (CDS_0001)
MGV-GENOME-0346895: 2-4,140 (-)
98 99
MGV-GENOME-0355942: 69,535-73,610 (+)
2 1
MGV-GENOME-0348621: 3-3,142 (-)
2 efflux_ABUW_0982-NCBIFAM chloramphenicol efflux transporter CxpE (NF045801.1) (CDS_0001)
MGV-GENOME-0351218: 3-4,059 (-)
anti-RM (APIS072) (CDS_0002)
1
MGV-GENOME-0347277: 263-4,527 (-)
2 1
MGV-GENOME-0358549: 3-5,328 (-)
2 1
MGV-GENOME-0352116: 3-7,124 (-)
99 100
MGV-GENOME-0349094: 71,068-74,852 (+)
100 101
MGV-GENOME-4431664: 71,856-77,048 (+)
vanR-B-NCBIFAM vancomycin resistance response regulator transcription factor VanR-B (NF000402.1) (CDS_0101)
100
MGV-GENOME-0350885: 71,071-74,609 (+)
104 105
MGV-GENOME-0351123: 71,015-78,796 (+)
2 1
MGV-GENOME-0361075: 95-3,290 (-)
79 80
MGV-GENOME-0348278: 53,977-58,138 (+)
tetrahydrofolate dehydrogenase and cyclohydrolase (CDS_0002)
1
MGV-GENOME-0347000: 1-4,367 (-)
tetrahydrofolate dehydrogenase and cyclohydrolase (CDS_0148)
MGV-GENOME-0376904: 127,265-130,805 (+)
tetrahydrofolate dehydrogenase and cyclohydrolase (CDS_0094)
93 95
MGV-GENOME-0338210: 60,016-64,183 (+)
tetrahydrofolate dehydrogenase and cyclohydrolase (CDS_0003)
Purine biosynthesis (VF0559) (CDS_0002)
1
MGV-GENOME-0351581: 2-6,121 (-)
1
MGV-GENOME-0375448: 34-5,752 (-)
144
142 143 145
MGV-GENOME-0372769: 115,843-124,070 (+)
78
MGV-GENOME-0305332: 44,889-48,093 (+)

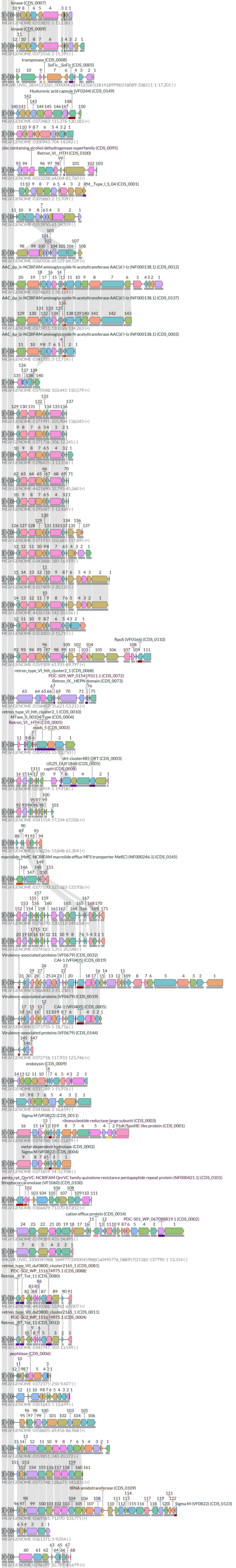

1
MGV-GENOME-0372062: 239-3,444 (-)
147 148
MGV-GENOME-0374171: 122,458-125,767 (+)
150
149
MGV-GENOME-0376296: 127,260-130,882 (+)
2 clamp loader of DNA polymerase (CDS_0001)
MGV-GENOME-0341083: 1-4,653 (-)
clamp loader of DNA polymerase (CDS_0004)
ClpC (VF0072) (CDS_0002)
5 3 1
MGV-GENOME-0375063: 3-8,557 (-)
clamp loader of DNA polymerase (CDS_0003)
4 2 ClpC (VF0072) (CDS_0001)
MGV-GENOME-0372192: 93-8,219 (-)
3 2 1
MGV-GENOME-0354220: 70-5,537 (-)
78 79 80
MGV-GENOME-0310732: 44,644-50,116 (+)
154
MGV-GENOME-0372862: 120,664-124,759 (+)
137
IMGVR_UViG_2848001292_000001|2848001292|2848001292|569015-674269: 102,207-105,255 (+)
32 1
MGV-GENOME-0363549: 211-4,876 (-)
138
137 139
MGV-GENOME-0371857: 102,523-106,108 (+)
1
MGV-GENOME-0346170: 2-3,887 (-)
76 77 78 79
MGV-GENOME-0314679: 43,291-51,632 (+)
methyltransferase (CDS_0099)
100
MGV-GENOME-0347802: 69,729-74,336 (+)
methyltransferase (CDS_0003)
2 1
MGV-GENOME-0373857: 83-5,041 (-)
99 100 AbiEi_WP_092960020.1 AbiEi (CDS_0101)
MGV-GENOME-0351445: 71,061-77,732 (+)
98 99
MGV-GENOME-0362858: 69,536-75,301 (+)
144 145 146
MGV-GENOME-0372816: 116,168-123,851 (+)
2 1
IMGVR_UViG_3300029744_000345|3300029744|Ga0245161_100016|211877-321265: 1-5,479 (-)
92 93 94
MGV-GENOME-0333197: 55,701-60,794 (+)
140 141
IMGVR_UViG_2585427862_000004|2585427862|2585473034|84987-191059: 101,631-106,073 (+)
145 146
MGV-GENOME-0372797: 115,378-124,286 (+)
3 2amidase (CDS_0001)
MGV-GENOME-0371542: 2-9,013 (-)
156 157 158
MGV-GENOME-0375215: 133,459-144,949 (+)
152 153
MGV-GENOME-0374030: 130,281-134,850 (+)
3 2 1
MGV-GENOME-0377266: 1-5,969 (-)
133
130 131 132 134
MGV-GENOME-0371550: 107,422-115,522 (+)
97
92 93 94 95 96
MGV-GENOME-0342865: 59,805-68,444 (+)
124
SAMEA2737827_a1_ct83876_vs1: 91,418-94,600 (+)
149 150
MGV-GENOME-0376893: 127,260-130,771 (+)
4 3 2 tet_protect-NCBIFAM tetracycline resistance ribosomal protection protein (NF012153.1) (CDS_0001)
MGV-GENOME-0344972: 2-6,503 (-)
75 76
MGV-GENOME-0303428: 43,308-47,668 (+)
ParA-like partition protein (CDS_0001)
ivig_601: 1-3,006 (-)
2 ParA-like partition protein (CDS_0001)
MGV-GENOME-0374695: 1-3,720 (-)
3 2 ParA-like partition protein (CDS_0001)
MGV-GENOME-0372269: 1-3,986 (-)
3
4 2 ParA-like partition protein (CDS_0001)
MGV-GENOME-0372873: 1-4,929 (-)
3
6 5 4 2 ParA-like partition protein (CDS_0001)
MGV-GENOME-0372637: 1-7,378 (-)
3 2 ParA-like partition protein (CDS_0001)
IMGVR_UViG_3300029734_000003|3300029734|Ga0245168_100221: 1-5,964 (-)
4 3 2 1
MGV-GENOME-0347922: 3-7,682 (-)
3 2 1
MGV-GENOME-4431164: 1-7,493 (-)
2 1
MGV-GENOME-4435097: 39-7,587 (-)
120 121
MGV-GENOME-0368491: 96,035-103,582 (+)
128 129 130 131
MGV-GENOME-0370657: 99,560-110,565 (+)
99 100
MGV-GENOME-0349127: 69,604-76,291 (+)
152 153 154
MGV-GENOME-0374436: 130,537-138,375 (+)
2 1
MGV-GENOME-0376165: 2-4,952 (-)
6 5 4 3 2 1
MGV-GENOME-0305032: 124-15,356 (-)
2
3 1
MGV-GENOME-0375555: 2-3,790 (-)
3 2 1
MGV-GENOME-0360547: 72-8,872 (-)
110 111 112
MGV-GENOME-0360831: 81,052-91,749 (+)
hydrolase (CDS_0096)
97 cmlA_floR-NCBIFAM CmlA/FloR family chloramphenicol efflux MFS transporter (NF033134.0) (CDS_0098)
MGV-GENOME-0343992: 63,404-69,594 (+)
MATE_multi_NorM-NCBIFAM multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0132)
PD-T7-2_A_WP_075189553.1 (CDS_0130)
PDC-S01_WP_015504585.1 (CDS_0131)
MGV-GENOME-0371145: 106,311-113,078 (+)
3 2 1
IMGVR_UViG_3300045988_178729|3300045988|Ga0495776_188463: 3-4,568 (-)
3
2 GroEL (VF0594) (CDS_0001)
MGV-GENOME-0372336: 201-5,270 (-)
145
144 146
MGV-GENOME-0372566: 115,376-122,239 (+)
146
145 147
MGV-GENOME-4435594: 125,183-130,483 (+)
3 2 1
MGV-GENOME-0376878: 119-5,419 (-)
3 2 1
MGV-GENOME-0376917: 1-3,600 (-)
3 2 1
SRS019014_a1_ct286_vs01: 1-4,794 (-)
SspA_00001 SspA (CDS_0149)
150 mads_8 (CDS_0151)
MGV-GENOME-0377066: 127,260-133,239 (+)
Sigma L (VF0855) (CDS_0149)
150 151
MGV-GENOME-0377188: 127,290-134,728 (+)
MATE_multi_NorM-NCBIFAM multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0003)
2 Lysine synthesis (VF0815) (CDS_0001)
MGV-GENOME-0310352: 3-6,777 (-)
AslA (VF0238) (CDS_0075)
74 76
MGV-GENOME-0314919: 44,891-51,858 (+)
77 78 79
MGV-GENOME-0307380: 43,348-48,988 (+)
77 78 79
MGV-GENOME-0311959: 44,888-50,642 (+)
3 2 1
MGV-GENOME-0337410: 3-6,907 (-)
98 100
99
MGV-GENOME-0346774: 68,606-72,720 (+)
3 2 1
MGV-GENOME-0359164: 3-8,824 (-)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0101)
100 102
MGV-GENOME-0348738: 69,556-74,360 (+)

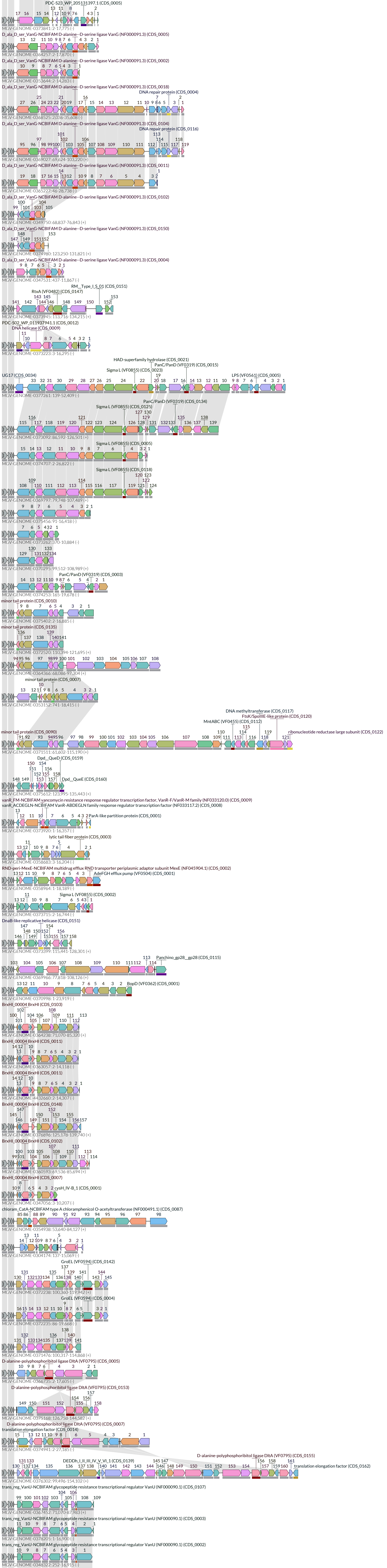

3 2 1
MGV-GENOME-0307888: 1-6,718 (-)
3 2 1
MGV-GENOME-0350159: 36-5,865 (-)
161
160
159
162 Mce2 (VF0825) (CDS_0163)
MGV-GENOME-0375954: 141,301-147,374 (+)
153
152
154 Mce2 (VF0825) (CDS_0155)
MGV-GENOME-0374254: 130,312-136,385 (+)
2 1
MGV-GENOME-0371157: 214-3,995 (-)
3 2 1
MGV-GENOME-0347055: 54-5,224 (-)
2 1
MGV-GENOME-0368363: 1-4,134 (-)
2
4 3 1
MGV-GENOME-0336661: 1-8,023 (-)
140
138 139 141
MGV-GENOME-0372290: 111,551-120,402 (+)
2 1
MGV-GENOME-0343287: 3-5,375 (-)
147 148 149 150
MGV-GENOME-0372992: 115,515-125,663 (+)
3 2 ParA-like partition protein (CDS_0001)
MGV-GENOME-0372805: 1-8,854 (-)
95 96 97 98
MGV-GENOME-0347786: 62,711-74,147 (+)
135 136 137
IMGVR_UViG_3300045988_180428|3300045988|Ga0495776_034754: 103,462-111,487 (+)
3 2 1
MGV-GENOME-0358697: 1-5,586 (-)
4 3 2 LigA (VF1220) (CDS_0001)
MGV-GENOME-0344812: 1-7,414 (-)
98 99
MGV-GENOME-0348885: 69,535-74,598 (+)
6 5 4 3 2 1
MGV-GENOME-0350691: 319-14,878 (-)
78
79 80
MGV-GENOME-0312944: 46,175-51,014 (+)
2 1
MGV-GENOME-0371724: 64-4,995 (-)
ABC-type heme transporter (VF0739) (CDS_0084)
HitABC (VF0268) (CDS_0082)
ClpP (VF0074) (CDS_0088)
85
83 86 87 89 DpdF_00007 DpdF (CDS_0090)
MGV-GENOME-0333632: 48,951-60,974 (+)
MymA operon (VF0840) (CDS_0003)
4 2 1
IMGVR_UViG_3300045988_177119|3300045988|Ga0495776_188374: 238-7,390 (-)
136 137 138 139
MGV-GENOME-0372963: 115,854-125,308 (+)
ABC-type heme transporter (VF0739) (CDS_0104)
HitABC (VF0268) (CDS_0102)
103 105
MGV-GENOME-0349461: 70,768-76,781 (+)
mads_8 (CDS_0002)
4 3 1
MGV-GENOME-0348877: 12-6,478 (-)
124
122 123 125
IMGVR_UViG_3300045988_179520|3300045988|Ga0495776_092531: 94,373-101,284 (+)
130 132
131 133
MGV-GENOME-0370108: 101,540-108,409 (+)
138
136 137 139
IMGVR_UViG_3300045988_178495|3300045988|Ga0495776_174647: 103,568-111,043 (+)
143
142
141 144
MGV-GENOME-0372408: 115,867-121,119 (+)
157
155 156 158
MGV-GENOME-0374860: 134,082-141,753 (+)
190 192
191 193
MGV-GENOME-0379916: 163,105-167,368 (+)
4 3 2 1
MGV-GENOME-0323791: 3-5,796 (-)
101
98 99 100
MGV-GENOME-0348183: 68,154-74,925 (+)
101
99 100 102
MGV-GENOME-0358146: 69,536-75,426 (+)
100 102
101 103
MGV-GENOME-0357822: 71,070-75,558 (+)
4 3 2 1
MGV-GENOME-0353325: 24-5,079 (-)
102
100 101 103
MGV-GENOME-4432806: 69,536-77,626 (+)
4 3 2 1
MGV-GENOME-0358643: 276-8,366 (-)
60 61 62 63
MGV-GENOME-0294444: 32,850-45,118 (+)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0080)
RND-peri-MexE-NCBIFAM multidrug efflux RND transporter periplasmic adaptor subunit MexE (NF045904.1) (CDS_0082)
RND_perm_OqxB-NCBIFAM multidrug efflux RND transporter permease subunit OqxB (NF000037.1) (CDS_0081)
vanH_gen-NCBIFAM D-lactate dehydrogenase VanH (NF000492.1) (CDS_0079)
MGV-GENOME-0336406: 52,977-62,603 (+)
PDC-S01_WP_067088819.1 (CDS_0002)
1
MGV-GENOME-0337708: 1-4,848 (-)
PDC-S01_WP_067088819.1 (CDS_0159)
amidase (CDS_0162)
holin (CDS_0163)
160 165
161 164 166
ivig_3353: 126,619-134,225 (+)
7 6 5 4 3 2 DnaB-like replicative helicase (CDS_0001)
MGV-GENOME-0343363: 2-7,022 (-)
135 137 139
136 138
IMGVR_UViG_3300045988_179160|3300045988|Ga0495776_141325: 103,441-108,600 (+)
144 145
MGV-GENOME-0372109: 115,377-119,061 (+)
DNA methyltransferase (CDS_0002)
3 kinase (CDS_0001)
MGV-GENOME-0372600: 2-6,661 (-)
HK_VanS_ACDEFG-NCBIFAM vancomycin resistance histidine kinase VanS (NF033091.0) (CDS_0126)
DNA methyltransferase (CDS_0123)
kinase (CDS_0125)
122 124 SodB (VF0169) (CDS_0127)
MGV-GENOME-0370167: 98,930-108,754 (+)
PDC-S05_WP_205197604.1 (CDS_0096)
101
97 98 99 100 102
MGV-GENOME-0348607: 62,198-73,584 (+)
PDC-S05_WP_205197604.1 (CDS_0003)
2 1
MGV-GENOME-0370524: 383-5,956 (-)
161
160 162
MGV-GENOME-0375214: 140,806-144,944 (+)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor, VanR-F/VanR-M family (NF033120.0) (CDS_0148)
144 146
143 145 147 SenX3 (VF0857) (CDS_0149)
MGV-GENOME-0372866: 115,614-124,796 (+)
144
145 147
142 143 146 148 head maturation protease (CDS_0149)
MGV-GENOME-0373168: 115,611-126,831 (+)
142 143 144
MGV-GENOME-0372369: 115,243-120,870 (+)
6 1
MGV-GENOME-0356916: 293-5,434 (-)
98
SAMN00792103_a1_ct54900_vs1: 79,443-82,199 (+)
2 1
MGV-GENOME-0373605: 2-3,499 (-)
128
IMGVR_UViG_3300045988_185824|3300045988|Ga0495776_101975|47558-148942: 98,699-101,385 (+)
128
IMGVR_UViG_3300045988_179706|3300045988|Ga0495776_092607: 98,941-101,660 (+)
5 4 3 2 1
MGV-GENOME-0343314: 1,380-8,238 (-)
102 104
100 101 103
MGV-GENOME-0372186: 70,580-77,583 (+)
NimABCDEF-NCBIFAM NimABCDEF family 5-nitroimidazole reductase (NF000261.1) (CDS_0004)
nuclease (CDS_0005)
3 2 1
MGV-GENOME-0349266: 345-12,979 (-)
132
129 130 131 133
MGV-GENOME-0370413: 99,581-109,846 (+)
5 4 3 2 1
MGV-GENOME-0370906: 274-10,588 (-)

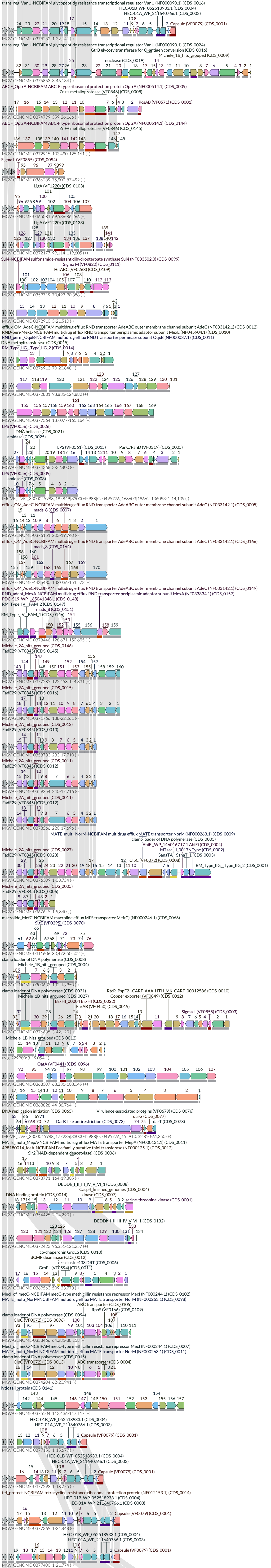

ABC transporter (CDS_0148)
MGV-GENOME-0372730: 115,450-123,663 (+)
chloram_CatA-NCBIFAM type A chloramphenicol O-acetyltransferase (NF000491.1) (CDS_0149)
Sigma L (VF0855) (CDS_0147)
MGV-GENOME-0374164: 125,009-132,983 (+)
Dpd__FolE (CDS_0001)
MGV-GENOME-0374649: 148-7,158 (-)
trim_DfrA3-NCBIFAM trimethoprim-resistant dihydrofolate reductase DfrA3 (NF000019.2) (CDS_0002)
DS-4__DS-4A (CDS_0001)
MGV-GENOME-0314142: 58-6,598 (-)
MGV-GENOME-0332336: 2-10,153 (-)
Capsule (VF0361) (CDS_0002)
MGV-GENOME-0340543: 103-8,758 (-)
MGV-GENOME-0345166: 62,021-70,928 (+)
MGV-GENOME-0351241: 71,069-76,507 (+)
LOS (VF0326) (CDS_0109)
LOS (VF0326) (CDS_0108)
MGV-GENOME-0356082: 78,603-85,350 (+)
MGV-GENOME-0353764: 69,537-76,780 (+)
MGV-GENOME-0352851: 1-7,244 (-)
FS_HP_SDH_sah__SDH_sah (CDS_0004)
MGV-GENOME-0348149: 3-10,157 (-)
vanH-D-NCBIFAM D-lactate dehydrogenase VanH-D (NF000004.1) (CDS_0082)
QatD_00001 (CDS_0084)
MGV-GENOME-0341577: 53,960-61,619 (+)
vanH-D-NCBIFAM D-lactate dehydrogenase VanH-D (NF000004.1) (CDS_0003)
MGV-GENOME-0341147: 3-6,217 (-)
methyltransferase (CDS_0126)
Pyrimidine biosynthesis (VF0558) (CDS_0131)
MGV-GENOME-0370465: 102,156-109,530 (+)
MGV-GENOME-0372494: 254-9,779 (-)
DNA primase (CDS_0005)
MGV-GENOME-0377560: 2-9,704 (-)
MGV-GENOME-0337958: 58,591-63,920 (+)
Type-III-B_CnuA (CDS_0100)
MGV-GENOME-0350321: 72,086-77,429 (+)
Jallet_1C_hits_grouped (CDS_0150)
DNA helicase (CDS_0151)
MGV-GENOME-0377237: 127,260-140,140 (+)
Jallet_1C_hits_grouped (CDS_0005)
DNA helicase (CDS_0004)
MGV-GENOME-0376630: 3-11,892 (-)
Jallet_1C_hits_grouped (CDS_0070)
MGV-GENOME-0311167: 37,391-50,324 (+)
MGV-GENOME-0351239: 154-9,347 (-)
MGV-GENOME-0366208: 91,043-99,580 (+)
RtcR_PspF2--CARF_AAA_HTH_MK_CARF_00012586 (CDS_0150)
MGV-GENOME-0372067: 112,177-125,938 (+)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0004)
ParA-like partition protein (CDS_0001)
MGV-GENOME-0371473: 1-10,933 (-)
MGV-GENOME-0378098: 127,254-142,221 (+)
tetrahydrofolate dehydrogenase and cyclohydrolase (CDS_0092)
MGV-GENOME-0341563: 55,052-67,037 (+)
MGV-GENOME-0372538: 110,050-122,066 (+)
peptidase (CDS_0140)
MGV-GENOME-0372158: 111,193-119,503 (+)
ABC-type heme transporter (VF0739) (CDS_0008)
ABC transporter (VF0741) (CDS_0007)
MGV-GENOME-0373540: 4,436-15,138 (-)
phosphofructokinase (CDS_0145)
MGV-GENOME-0372792: 115,460-124,058 (+)
VirF (VF0979) (CDS_0006)
MGV-GENOME-0373259: 2-13,525 (-)
MGV-GENOME-0377681: 128,671-143,141 (+)
Jallet_2B_hits_grouped (CDS_0159)
LOS (VF0326) (CDS_0157)
MGV-GENOME-0374840: 133,031-141,759 (+)
MGV-GENOME-0304531: 37,556-48,041 (+)
head maturation protease (CDS_0069)
ABC transporter (CDS_0068)
MGV-GENOME-0317879: 40,533-53,063 (+)
lytic tail fiber protein (CDS_0067)
MGV-GENOME-0304817: 39,925-48,123 (+)
MGV-GENOME-0350640: 2-14,432 (-)
DNA topoisomerase II large subunit (CDS_0002)
MGV-GENOME-0354084: 2-10,667 (-)
DNA topoisomerase II (CDS_0002)
MGV-GENOME-0375432: 3-11,602 (-)
MGV-GENOME-0356694: 73,192-85,908 (+)
nitroreductase (CDS_0061)
MGV-GENOME-0298066: 32,798-45,921 (+)
MGV-GENOME-0296954: 609-13,001 (-)
Sigma L (VF0855) (CDS_0065)
MGV-GENOME-0304892: 32,796-48,152 (+)
NshR_TsnR-NCBIFAM NshR/TsnR family 23S rRNA methyltransferase (NF000477.1) (CDS_0001)
MGV-GENOME-0340071: 335-10,791 (-)
MGV-GENOME-0347793: 68,332-74,346 (+)
MGV-GENOME-0345473: 65,471-71,348 (+)
MGV-GENOME-0373775: 117,040-132,561 (+)
DNA binding protein (CDS_0115)
uvig_437450: 76,221-79,426 (+)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0107)
DNA topoisomerase II (CDS_0108)
MGV-GENOME-0359455: 74,506-89,158 (+)
MGV-GENOME-0375729: 143,884-148,937 (+)
DNA binding protein (CDS_0085)
transposase (CDS_0084)
uvig_381361: 51,244-62,274 (+)
endolysin (CDS_0142)
MGV-GENOME-0373316: 108,697-121,805 (+)
NAD synthetase (CDS_0143)
endolysin (CDS_0154)
MGV-GENOME-0375864: 118,539-150,221 (+)

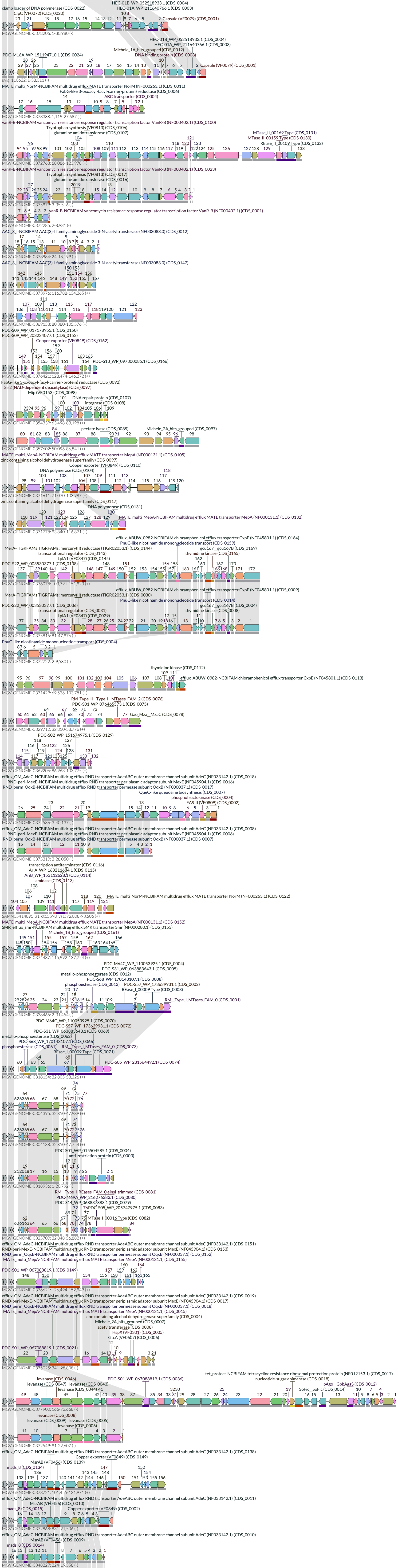

NAD synthetase (CDS_0149)
155
152 154
148 150 151 153 156 157
MGV-GENOME-0373539: 115,083-130,418 (+)
NAD synthetase (CDS_0005)
6 4 3 2 1
MGV-GENOME-0354022: 3-10,542 (-)
NAD synthetase (CDS_0096)
95 97
MGV-GENOME-0345034: 64,148-70,857 (+)
nuclease (CDS_0005)
4 3 2 DS-15__DS-15A (CDS_0001)
MGV-GENOME-0372807: 1-8,865 (-)
MerA-TIGRFAMs TIGRFAMs: mercury(II) reductase (TIGR02053.1) (CDS_0005)
10
12 11 98 7 6 4 3 2 1
MGV-GENOME-0371730: 1-15,285 (-)
94 96
93 95 97 98
MGV-GENOME-0344251: 61,728-69,940 (+)
retron_type_VI_hth_cluster2_1 (CDS_0070)
63 65 67
62 64 66 68 69 71
MGV-GENOME-0294016: 32,850-45,164 (+)
anti-CRISPR-Cas evasion by DNA repair (APIS131) (CDS_0106)
104
100 101 102 103 105 107
MGV-GENOME-0351810: 68,082-79,718 (+)
tyrosyl-tRNA synthetase (CDS_0103)
101
98 99 100 102 104
MGV-GENOME-0359530: 69,535-79,467 (+)
clamp loader of DNA polymerase (CDS_0003)
tyrosyl-tRNA synthetase (CDS_0004)
9 8 7 6 5 2 ATP-dependent protease (CDS_0001)
MGV-GENOME-0371925: 1-14,540 (-)
3
8 7 6 5 4 2 1
MGV-GENOME-0359793: 3-14,618 (-)
6
8 7 5 4 3 2 1
IMGVR_UViG_3300045988_177120|3300045988|Ga0495776_102639: 389-10,606 (-)
Cyclase_00020 oligonucleotide-cyclase (CDS_0002)
8 7 6 5 4 3 Effector_00077 Endonuclease (CDS_0001)
MGV-GENOME-0373035: 147-10,788 (-)
153
151 154 156
149 150 152 155
MGV-GENOME-0377325: 127,260-136,352 (+)
thioredoxin domain (CDS_0128)
131
129 132
130 133 134
MGV-GENOME-0375614: 105,533-114,080 (+)
8 7 6 5 4 3 2 1
MGV-GENOME-0317101: 358-9,491 (-)
100
94 95 96 97 98 99 101
MGV-GENOME-0350774: 63,458-78,295 (+)
tet_prtrans_34-NCBIFAM oxytetracycline resistance phosphoribosyltransferase domain-containing protein Tet(34) (NF000014.1) (CDS_0112)
shah_acc_0214 GlgB (CDS_0106)
109
107 111
108 110 113
MGV-GENOME-0358257: 77,803-87,686 (+)
tet_prtrans_34-NCBIFAM oxytetracycline resistance phosphoribosyltransferase domain-containing protein Tet(34) (NF000014.1) (CDS_0151)
shah_acc_0214 GlgB (CDS_0145)
148
146 150
147 149 152
MGV-GENOME-0373309: 117,794-128,356 (+)
8 7 6 5 4 3 2 1
MGV-GENOME-0315141: 2-19,075 (-)
13 12 11 10 9 8 7 6 5 4 3 2 Sigma L (VF0855) (CDS_0001)
MGV-GENOME-0362859: 204-24,615 (-)
125
122 123 124 126 127 128 129 130 131 132 133 Sigma L (VF0855) (CDS_0134)
MGV-GENOME-0376420: 98,150-122,667 (+)
110 Sigma L (VF0855) (CDS_0119)
107 108 109 111 112 113 114 115 116 117 118 120 121
MGV-GENOME-0371403: 86,338-112,371 (+)
88 89 90 91 92 93 94 95 96
MGV-GENOME-0349324: 59,392-76,573 (+)
Sigma L (VF0855) (CDS_0014)
26 25 24 23 22 21 20 19 18 17 16 15 13 12 11 10 9 8 7 6 5 4 3 2 1
MGV-GENOME-0375754: 3-49,611 (-)
100 101 102
MGV-GENOME-0353930: 73,814-82,882 (+)
5 4 3 2 1
MGV-GENOME-0370677: 96-11,606 (-)
101 102 103
MGV-GENOME-0353219: 71,634-81,521 (+)
QatD_00001 (CDS_0003)
8 7 6 5 4 2 1
MGV-GENOME-0377210: 250-9,194 (-)
QatD_00001 (CDS_0143)
140
138 141 144
139 142 145
MGV-GENOME-0372506: 112,172-121,114 (+)
QatD_00001 (CDS_0065)
60 62 66
61 63 64 67 68 69
MGV-GENOME-0296189: 32,849-45,485 (+)
QatD_00001 (CDS_0105)
102
100 103 106 108
101 104 107 109 110 111 112
MGV-GENOME-0356434: 69,951-85,499 (+)
radical SAM domain protein (CDS_0004)
QatD_00001 (CDS_0008)
11
13 12 10 9 7 6 5 3 2 1
MGV-GENOME-0373701: 2-15,736 (-)
radical SAM domain protein (CDS_0148)
QatD_00001 (CDS_0145)
142
140 143 146
141 144 147 149 150
MGV-GENOME-0373268: 112,741-127,707 (+)
QatD_00001 (CDS_0012)
15 11
17 16 14 13 10 9 8 7 6 5 4 3 2 1
MGV-GENOME-0344033: 3-19,321 (-)
QatD_00001 (CDS_0083)
80 84 91 93
78 79 81 82 85 86 87 88 89 90 92 94
MGV-GENOME-0341894: 48,071-67,388 (+)
QatD_00001 (CDS_0106)
104
102
100 103 108
101 105 107 109 110 111 112
MGV-GENOME-0359824: 71,070-87,709 (+)
6 5 4 3 2 QatD_00001 (CDS_0001)
MGV-GENOME-0350573: 3-7,229 (-)
QatD_00001 (CDS_0002)
5
7 6 4 3 1
MGV-GENOME-0339716: 1-8,225 (-)
2
4 3 1
MGV-GENOME-0309806: 3-4,980 (-)
2 1
MGV-GENOME-0343877: 1-3,765 (-)
148
MGV-GENOME-0376811: 125,723-128,865 (+)
PDC-M69A_WP_216276383.1 (CDS_0152)
MTase_I_00010 Type (CDS_0151)
RM__Type_I_S_51 (CDS_0148)
QatD_00001 (CDS_0143)
140 REase_I_00005 Type (CDS_0147) 155
138 141 144 146 150 153 156
139 142 145 149 154 157
MGV-GENOME-0373871: 111,926-133,527 (+)
vanR-B-NCBIFAM vancomycin resistance response regulator transcription factor VanR-B (NF000402.1) (CDS_0159)
QatD_00001 (CDS_0155)
152 168
150 153 156 158 162 165 167 170
151 154 157 160 161 163 164 166 169 ATPase (CDS_0171)
MGV-GENOME-0376455: 129,672-155,003 (+)
REase_II_00040 Type (CDS_0062)
66 68 70 72
63 64 65 67 69 71 73
MGV-GENOME-0302558: 34,430-47,330 (+)
138
137
135 136 139 140
ivig_2899: 115,222-123,696 (+)
96
97 98 101
MGV-GENOME-0352343: 75,883-80,071 (+)
11 6
MGV-GENOME-0343542: 597-5,634 (-)
105 107 110 PDC-M16A_WP_151194710.1 (CDS_0112)
104 106 108 109 111
MGV-GENOME-0358538: 73,792-86,894 (+)
86
84 85 87 PDC-M16A_WP_151194710.1 (CDS_0088)
MGV-GENOME-0366332: 54,009-62,184 (+)
DNA topoisomerase II large subunit (CDS_0103)
PDC-M16A_WP_151194710.1 (CDS_0097)
95 98 102 mads_8 (CDS_0105)
90 91 92 93 94 96 99 100 101 104 106 107
MGV-GENOME-0360318: 61,898-89,927 (+)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0009)
chloram_CatA-NCBIFAM type A chloramphenicol O-acetyltransferase (NF000491.1) (CDS_0016)
HAD-superfamily hydrolase (CDS_0010)
O-acetyltransferase (CDS_0019)
RelA (VF0287) (CDS_0014)
13 Mycobactin (VF0299) (CDS_0004)
18 17 15 12 11 8 7 6 5 3 2 1
MGV-GENOME-0361457: 249-25,300 (-)
chloram_CatA-NCBIFAM type A chloramphenicol O-acetyltransferase (NF000491.1) (CDS_0002)
O-acetyltransferase (CDS_0005)
4 3 1
MGV-GENOME-0332641: 3-8,076 (-)

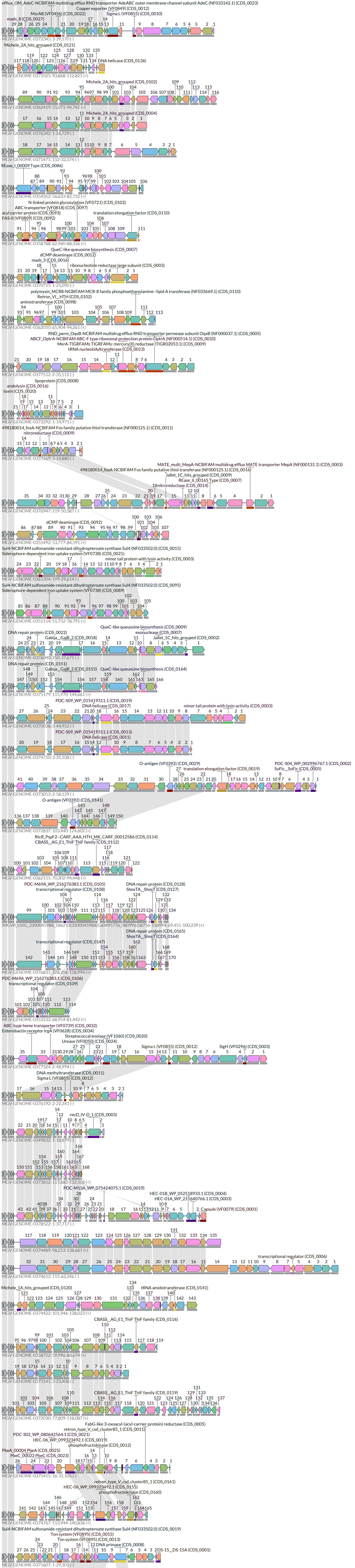

101 104
100 102 103
MGV-GENOME-0351207: 70,146-78,901 (+)
7 6 5 4 3 2 1
MGV-GENOME-0374815: 3-11,184 (-)
3 2 1
MGV-GENOME-0372144: 77-6,357 (-)
12 11 10 9 8 7 6 5 4 3 2 1
MGV-GENOME-0372368: 1-18,379 (-)
Sigma L (VF0855) (CDS_0120)
110
NAD synthetase (CDS_0117)
cold shock protein (CDS_0130)
109 112
121
phosphofructokinase (CDS_0128)
102
103
108
113
118
122
endolysin (CDS_0127)
96 97 98 99 100 101 104 105 106 107 111 114 115 116 119 123 124 125 126 129 131
MGV-GENOME-0370968: 71,755-112,535 (+)
113
105
112 115
100
103
106
111
116
99 101 102 104 107 108 109 110 114 117 118 119
NAD synthetase (CDS_0120)
MGV-GENOME-0365803: 69,536-97,614 (+)
9 8 7 6 5 4 3 2 1
MGV-GENOME-0360079: 1-11,810 (-)
ParB-like partition protein (CDS_0002)
UmuD-like protein (CDS_0008)
DNA polymerase (CDS_0007)
9 65 4 3
phosphoadenosine phosphosulfate reductase (CDS_0001)
MGV-GENOME-0372335: 2-10,288 (-)
clamp loader of DNA polymerase (CDS_0135)
136
137
134 138 139 140 141 142
MGV-GENOME-0372999: 110,185-125,726 (+)
AbiEi_WP_146016717.1 AbiEi (CDS_0062)
SanaTA__SanaT_1 (CDS_0061)
64
60 63 65 66 67 68
MGV-GENOME-0294720: 32,798-45,327 (+)
AbiEi_WP_146016717.1 AbiEi (CDS_0095)
SanaTA__SanaT_1 (CDS_0094)
97
100
93 96 98 99 101
MGV-GENOME-0351652: 65,755-79,280 (+)
AbiEi_WP_146016717.1 AbiEi (CDS_0100)
SanaTA__SanaT_1 (CDS_0099)
103
101 104 106
98 102 105
MGV-GENOME-0355106: 69,537-82,066 (+)
11 10 9 8 7 6 5 4 3 2 1
MGV-GENOME-0369045: 84-15,472 (-)
tet_protect-NCBIFAM tetracycline resistance ribosomal protection protein (NF012153.1) (CDS_0062)
63 64 65 6667 68 69
MGV-GENOME-0298189: 32,849-46,117 (+)
vanR_ACDEGLN-NCBIFAM VanR-ABDEGLN family response regulator transcription factor (NF033117.2) (CDS_0008)
QueD-like 6-pyruvoyl-tetrahydropterin synthase (CDS_0004)
CAI-1 (VF0405) (CDS_0002)
DNA polymerase (CDS_0005)
10 9 7 6 3 1
MGV-GENOME-0308222: 1-14,526 (-)
vanR_ACDEGLN-NCBIFAM VanR-ABDEGLN family response regulator transcription factor (NF033117.2) (CDS_0004)
QueD-like 6-pyruvoyl-tetrahydropterin synthase (CDS_0007)
Zn++ metalloprotease (VF0846) (CDS_0012)
CAI-1 (VF0405) (CDS_0009)
DNA polymerase (CDS_0006)
10
11 8 5 3 2 1
MGV-GENOME-0354731: 3-18,148 (-)
vanR_ACDEGLN-NCBIFAM VanR-ABDEGLN family response regulator transcription factor (NF033117.2) (CDS_0002)
4 3 1
MGV-GENOME-0359854: 221-9,153 (-)
vanR_ACDEGLN-NCBIFAM VanR-ABDEGLN family response regulator transcription factor (NF033117.2) (CDS_0014)
QueD-like 6-pyruvoyl-tetrahydropterin synthase (CDS_0017)
Zn++ metalloprotease (VF0846) (CDS_0022)
CAI-1 (VF0405) (CDS_0019)
HEC-01B_WP_052518933.1 (CDS_0004)
DNA polymerase (CDS_0016)
HEC-01A_WP_211640766.1 (CDS_0003)
20
10 8
21 18 15 13 12 11 9 7 6 5 2
Capsule (VF0079) (CDS_0001)
MGV-GENOME-0377264: 1-28,302 (-)
penta_rpt_QnrE-NCBIFAM QnrE family quinolone resistance pentapeptide repeat protein (NF033375.2) (CDS_0007)
19
15 13 11
Hemolysin HlyA (VF0646) (CDS_0004)
23 22 21 20 18 17 16 14 12 10 9 8 6 5 3 2 1
MGV-GENOME-0375325: 3-30,231 (-)
152 154
151 153 155
MGV-GENOME-0375841: 128,671-136,414 (+)
DnaB-like replicative helicase (CDS_0004)
amidase (CDS_0007)
8 65 3 2 1
MGV-GENOME-0313770: 82-8,056 (-)
DnaB-like replicative helicase (CDS_0150)
amidase (CDS_0147)
148
152 154 156
149 151 153 155 157 158
MGV-GENOME-0375771: 125,053-140,258 (+)
DnaB-like replicative helicase (CDS_0142)
139
138
136 140 144
135 137 141 143 145
IMGVR_UViG_2938107368_000003|2938107368|2938107401|187466-299723: 102,210-112,060 (+)
DNA methyltransferase (CDS_0006)
FtsK/SpoIIIE-like protein (CDS_0003)
98 7 5 4 2
ribonucleotide reductase large subunit (CDS_0001)
SAMN00715273_a1_ct32413_vs1: 96-11,806 (-)
Streptococcal enolase (VF1060) (CDS_0068)
Retron_IX__HEPN domain (CDS_0071)
co-chaperonin GroES (CDS_0074)
70 73
65 6667 69 72
chaperonin groEL (CDS_0075)
MGV-GENOME-0300315: 35,423-46,706 (+)
Streptococcal enolase (VF1060) (CDS_0007)
Retron_IX__HEPN domain (CDS_0004)
10 9 8 6 5 32
co-chaperonin GroES (CDS_0001)
MGV-GENOME-0293925: 86-10,761 (-)
Streptococcal enolase (VF1060) (CDS_0009)
GroEL (VF0594) (CDS_0007)
RecN (VF0457) (CDS_0004)
12 11 10 8 6 5 3 2 1
MGV-GENOME-0376468: 130-15,305 (-)
AbiEi_WP_146016717.1 AbiEi (CDS_0008)
SanaTA__SanaT_1 (CDS_0007)
10 9 65 4 3 2 1
IMGVR_UViG_2834504417_000009|2834504417|2834504472|27781-149626: 1-13,201 (-)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0008)
REase_MTase_IIG_00017 Type (CDS_0004)
DNA topoisomerase II (CDS_0007)
10 9 6 5 3 2 1
MGV-GENOME-4433854: 233-16,753 (-)
HitABC (VF0268) (CDS_0003)
10 9 8 7 6 5 4 2 1
uvig_409788: 144-12,304 (-)
NEase_II_00006 Type (CDS_0067)
MTase_II_00020 Type (CDS_0066)
Gao_Mza__MzaD (CDS_0063)
Gao_Mza__MzaB (CDS_0065)
Gao_Mza__MzaE (CDS_0062)
Gao_Mza__MzaC (CDS_0064)
60 61 68 69
MGV-GENOME-0309336: 32,847-49,670 (+)
DNA helicase (CDS_0089)
93
91
8788 90 92 94 95 96
MGV-GENOME-0344596: 56,632-70,442 (+)
133
134 138 141
132 135 136 137 139 140
MGV-GENOME-0373106: 112,766-126,387 (+)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor, VanR-F/VanR-M family (NF033120.0) (CDS_0141)
translation elongation factor (CDS_0139)
145
144
143 147
138 140 142 146
MGV-GENOME-0371418: 103,431-114,701 (+)
144 145 146 147 148 149 150 151 152 153
MGV-GENOME-0376047: 127,296-148,266 (+)
translation initiation factor (CDS_0150)
149
FarAB (VF0450) (CDS_0155)
148 151 152 153 154 156 157
MGV-GENOME-0377458: 125,112-139,739 (+)
149 151 154 156
148 150 152 153 155 157
MGV-GENOME-0375874: 123,997-139,982 (+)
107
102 103 104 105 106 108 109 110
MGV-GENOME-0357960: 72,700-86,992 (+)
10 9 8 7 6 54 3 2 1
MGV-GENOME-0373515: 3-14,513 (-)
10 9 8 7 6 54 3 2
Hachiman_II__HamC (CDS_0001)
MGV-GENOME-0346632: 210-15,541 (-)
10 9 8 7 6 54 3 2 1
MGV-GENOME-0351259: 164-14,680 (-)
FarAB (VF0450) (CDS_0158)
SoFic__SoFic (CDS_0155)
151 156
146 147 148 149 150 152 153 154 157 159
MGV-GENOME-0374249: 115,379-136,207 (+)
FarAB (VF0450) (CDS_0002)
SoFic__SoFic (CDS_0005)
14 13 12 11 10 98 7 6 4 3 1
MGV-GENOME-0373856: 483-21,310 (-)
99 100 101 102 103
MGV-GENOME-0355838: 69,536-78,986 (+)
Sigma L (VF0855) (CDS_0147)
FarAB (VF0450) (CDS_0138)
SoFic__SoFic (CDS_0134)
144
130 136 140 142 145
125 126 127 128 129 131 132 133 135 137 139 141 143 146 148 149 150 151
MGV-GENOME-0374494: 99,553-133,864 (+)
tet_protect-NCBIFAM tetracycline resistance ribosomal protection protein (NF012153.1) (CDS_0005)
4
8 7 6 3 2 1
MGV-GENOME-0340564: 3-8,677 (-)
tet_protect-NCBIFAM tetracycline resistance ribosomal protection protein (NF012153.1) (CDS_0006)
5
9 8 7 4 3 2 1
MGV-GENOME-0377314: 1-9,100 (-)
tet_protect-NCBIFAM tetracycline resistance ribosomal protection protein (NF012153.1) (CDS_0101)
112
113
115
103 106 109 114
100 102 105 108 111 117
98 99 104 107 110 116
MGV-GENOME-0356575: 70,313-84,371 (+)

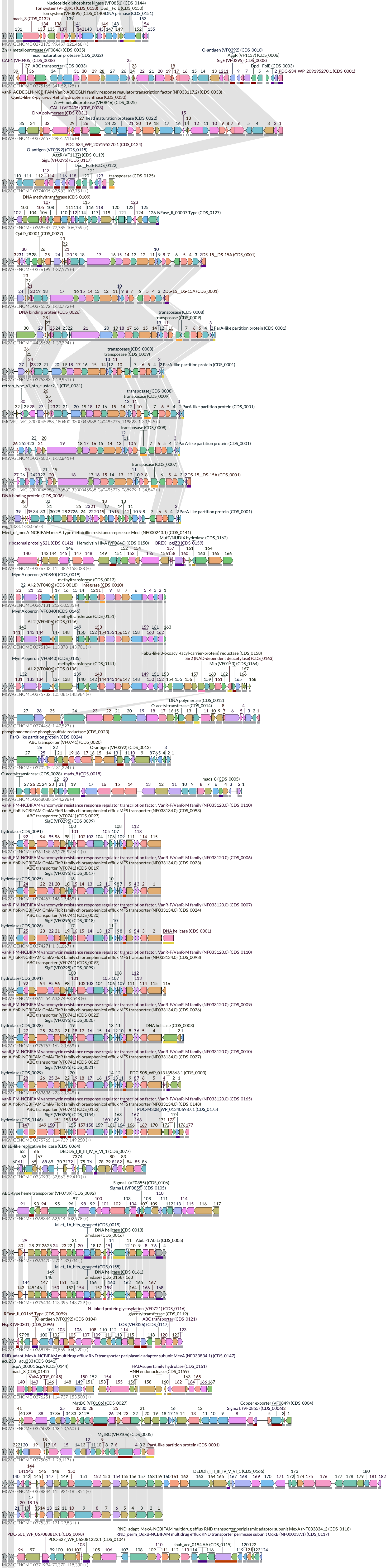

kinase (CDS_0007)
MGV-GENOME-0353831: 1-13,128 (-)
kinase (CDS_0009)
MGV-GENOME-0373556: 2-15,395 (-)
transposase (CDS_0008)
SoFic_SoFic (CDS_0005)
IMGVR_UViG_2814123265_000004|2814123265|2814189998|218089-338211: 1-17,201 (-)
Hyaluronic acid capsule (VF0244) (CDS_0149)
MGV-GENOME-0373483: 115,376-130,183 (+)
MGV-GENOME-0300943: 704-14,042 (-)
zinc containing alcohol dehydrogenase superfamily (CDS_0095)
Retron_VI_HTH (CDS_0100)
MGV-GENOME-0353228: 64,004-81,760 (+)
RM_Type_I_S_04 (CDS_0001)
MGV-GENOME-0305860: 2-15,709 (-)
MGV-GENOME-0353950: 61-14,929 (-)
MGV-GENOME-0360506: 69,529-84,539 (+)
AAC_6p_Iz-NCBIFAM aminoglycoside N-acetyltransferase AAC(6')-Iz (NF000138.1) (CDS_0012)
MGV-GENOME-0374820: 1-30,169 (-)
AAC_6p_Iz-NCBIFAM aminoglycoside N-acetyltransferase AAC(6')-Iz (NF000138.1) (CDS_0137)
MGV-GENOME-0373951: 118,026-134,263 (+)
AAC_6p_Iz-NCBIFAM aminoglycoside N-acetyltransferase AAC(6')-Iz (NF000138.1) (CDS_0003)
MGV-GENOME-0341735: 3-13,714 (-)
MGV-GENOME-0370548: 103,441-110,579 (+)
MGV-GENOME-0371991: 105,904-118,043 (+)
MGV-GENOME-0371736: 206-12,345 (-)
MGV-GENOME-0298435: 3-13,358 (-)
MGV-GENOME-4421890: 32,793-45,260 (+)
MGV-GENOME-0295047: 1-12,489 (-)
MGV-GENOME-0371910: 102,681-117,895 (+)
MGV-GENOME-0343888: 180-16,919 (-)
MGV-GENOME-0317409: 2-20,120 (-)
MGV-GENOME-4426118: 142-20,026 (-)
MGV-GENOME-0353003: 2-15,715 (-)
RpoS (VF0166) (CDS_0110)
MGV-GENOME-0359309: 61,935-89,797 (+)
retron_type_VI_hth_cluster2_1 (CDS_0068)
PDC-S09_WP_015419311.1 (CDS_0072)
Retron_IX_HEPN domain (CDS_0073)
MGV-GENOME-0318457: 35,621-53,215 (+)
retron_type_VI_hth_cluster2_1 (CDS_0010)
MTase_II_00104 Type (CDS_0004)
Retron_VI_HTH (CDS_0005)
mads_5 (CDS_0003)
MGV-GENOME-0304920: 53-13,750 (-)
drt-cluster485 DRT (CDS_0003)
UG25_DUF1848 (CDS_0005)
capH (CDS_0008)
MGV-GENOME-0316959: 1-19,918 (-)
MGV-GENOME-0341554: 57,334-67,026 (+)
MGV-GENOME-0336226: 53,848-61,304 (+)
macrolide_MefC-NCBIFAM macrolide efflux MFS transporter Mef(C) (NF000246.1) (CDS_0145)
MGV-GENOME-0377100: 125,183-133,936 (+)
MGV-GENOME-0376070: 130,512-149,658 (+)
MGV-GENOME-0374165: 1,351-20,548 (-)
Virulence-associated proteins (VF0679) (CDS_0032)
CAI-1 (VF0405) (CDS_0019)
MGV-GENOME-0366400: 2-41,338 (-)
Virulence-associated proteins (VF0679) (CDS_0019)
CAI-1 (VF0405) (CDS_0005)
MGV-GENOME-0373735: 1-18,716 (-)
Virulence-associated proteins (VF0679) (CDS_0144)
MGV-GENOME-0372718: 117,933-123,746 (+)
endolysin (CDS_0009)
MGV-GENOME-0337289: 1-15,976 (-)
MGV-GENOME-0341868: 3-16,659 (-)
Sigma M (VF0822) (CDS_0011)
ribonucleotide reductase large subunit (CDS_0003)
FtsK/SpoIIIE-like protein (CDS_0001)
MGV-GENOME-0374788: 140-23,879 (-)
metal-dependent hydrolase (CDS_0002)
Sigma M (VF0822) (CDS_0004)
MGV-GENOME-0371859: 54-12,938 (-)
penta_rpt_QnrVC-NCBIFAM QnrVC family quinolone resistance pentapeptide repeat protein (NF000421.1) (CDS_0101)
Streptococcal enolase (VF1060) (CDS_0100)
MGV-GENOME-0366439: 71,070-87,812 (+)
cation efflux protein (CDS_0014)
PDC-S01_WP_067088819.1 (CDS_0002)
MGV-GENOME-0374389: 435-34,495 (-)
IMGVR_UViG_3300045988_184977|3300045988|Ga0495776_088957|21182-137790: 1-13,314 (-)
retron_type_VII_duf3800_cluster2165_1 (CDS_0081)
PDC-S02_WP_151674975.1 (CDS_0088)
Retron_RT_Tot_11 (CDS_0080)
MGV-GENOME-4430386: 53,963-67,007 (+)
retron_type_VII_duf3800_cluster2165_1 (CDS_0011)
PDC-S02_WP_151674975.1 (CDS_0004)
Retron_RT_Tot_11 (CDS_0012)
MGV-GENOME-0342747: 503-13,549 (-)
peptidase (CDS_0006)
MGV-GENOME-0372375: 250-9,427 (-)
MGV-GENOME-0301643: 1-12,699 (-)
MGV-GENOME-0358605: 69,456-86,968 (+)
MGV-GENOME-0359851: 240-20,372 (-)
MGV-GENOME-0375748: 128,671-143,831 (+)
tRNA amidotransferase (CDS_0109)
Sigma M (VF0822) (CDS_0123)
MGV-GENOME-0369181: 71,070-103,771 (+)
MGV-GENOME-0361371: 3-9,054 (-)
MGV-GENOME-0296197: 32,797-45,679 (+)

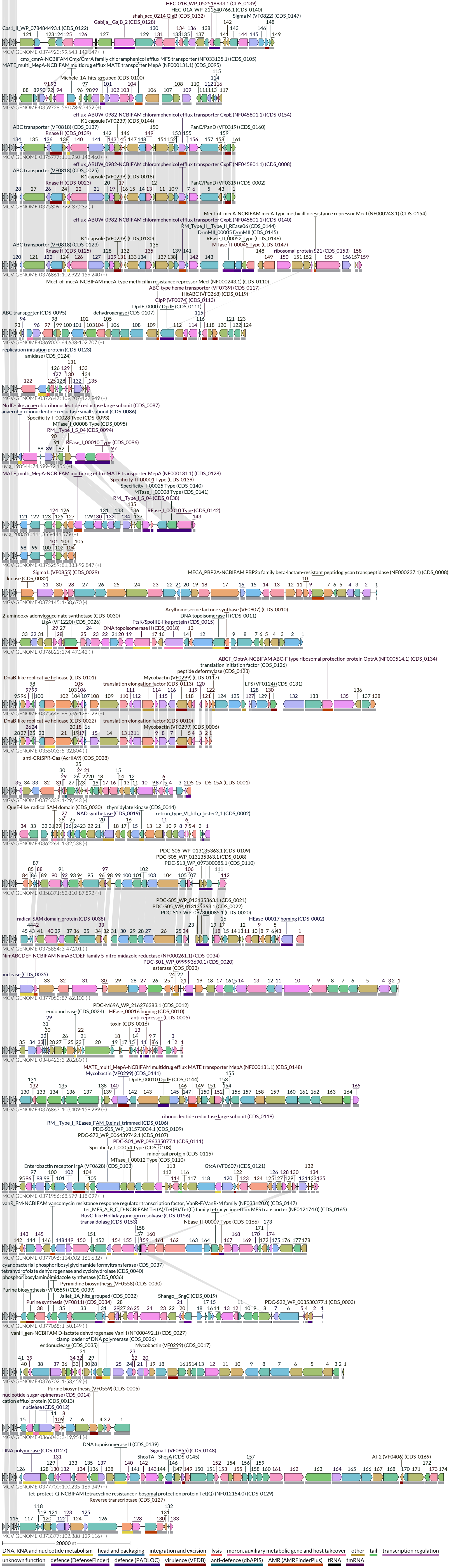

PDC-S23_WP_205131397.1 (CDS_0005)
MGV-GENOME-0373841: 2-17,775 (-)
D_ala_D_ser_VanG-NCBIFAM D-alanine--D-serine ligase VanG (NF000091.3) (CDS_0005)
MGV-GENOME-0364257: 2-17,870 (-)
D_ala_D_ser_VanG-NCBIFAM D-alanine--D-serine ligase VanG (NF000091.3) (CDS_0002)
MGV-GENOME-0353644: 2-14,283 (-)
D_ala_D_ser_VanG-NCBIFAM D-alanine--D-serine ligase VanG (NF000091.3) (CDS_0018)
DNA repair protein (CDS_0004)
MGV-GENOME-0368525: 2,036-35,608 (-)
D_ala_D_ser_VanG-NCBIFAM D-alanine--D-serine ligase VanG (NF000091.3) (CDS_0104)
DNA repair protein (CDS_0116)
MGV-GENOME-0369027: 69,624-103,220 (+)
D_ala_D_ser_VanG-NCBIFAM D-alanine--D-serine ligase VanG (NF000091.3) (CDS_0011)
MGV-GENOME-0365227: 46-28,738 (-)
D_ala_D_ser_VanG-NCBIFAM D-alanine--D-serine ligase VanG (NF000091.3) (CDS_0102)
MGV-GENOME-0349750: 68,837-76,843 (+)
D_ala_D_ser_VanG-NCBIFAM D-alanine--D-serine ligase VanG (NF000091.3) (CDS_0150)
MGV-GENOME-0374980: 123,250-131,821 (+)
D_ala_D_ser_VanG-NCBIFAM D-alanine--D-serine ligase VanG (NF000091.3) (CDS_0004)
MGV-GENOME-0347531: 437-11,867 (-)
RM__Type_I_S_01 (CDS_0151)
RtxA (VF0482) (CDS_0147)
MGV-GENOME-0373945: 113,716-134,215 (+)
PDC-S02_WP_011937941.1 (CDS_0012)
DNA helicase (CDS_0009)
MGV-GENOME-0373223: 3-16,295 (-)
HAD-superfamily hydrolase (CDS_0021)
PanC/PanD (VF0319) (CDS_0015)
Sigma L (VF0855) (CDS_0023)
UG17 (CDS_0034)
LPS (VF0561) (CDS_0005)
MGV-GENOME-0377261: 139-52,409 (-)
PanC/PanD (VF0319) (CDS_0134)
Sigma L (VF0855) (CDS_0125)
MGV-GENOME-0373092: 86,592-126,501 (+)
Sigma L (VF0855) (CDS_0005)
MGV-GENOME-0374707: 2-26,822 (-)
Sigma L (VF0855) (CDS_0118)
MGV-GENOME-0369797: 79,748-107,489 (+)
MGV-GENOME-0375456: 91-16,418 (-)
MGV-GENOME-0373262: 370-10,884 (-)
MGV-GENOME-0370295: 99,512-108,989 (+)
PanC/PanD (VF0319) (CDS_0003)
MGV-GENOME-0374253: 165-19,678 (-)
minor tail protein (CDS_0010)
MGV-GENOME-0375402: 2-16,885 (-)
minor tail protein (CDS_0135)
MGV-GENOME-0372520: 110,394-121,695 (+)
MGV-GENOME-0364366: 68,086-97,334 (+)
minor tail protein (CDS_0007)
MGV-GENOME-0353152: 741-18,415 (-)
DNA methyltransferase (CDS_0117)
FtsK/SpoIIIE-like protein (CDS_0120)
MntABC (VF0455) (CDS_0112)
minor tail protein (CDS_0090)
ribonucleotide reductase large subunit (CDS_0122)
MGV-GENOME-0371511: 61,602-115,190 (+)
Dpd__QueD (CDS_0159)
Dpd__QueE (CDS_0160)
MGV-GENOME-0375612: 123,995-135,443 (+)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor, VanR-F/VanR-M family (NF033120.0) (CDS_0009)
vanR_ACDEGLN-NCBIFAM VanR-ABDEGLN family response regulator transcription factor (NF033117.2) (CDS_0008)
ParA-like partition protein (CDS_0001)
MGV-GENOME-0373920: 1-16,357 (-)
lytic tail fiber protein (CDS_0003)
MGV-GENOME-0358683: 3-16,204 (-)
RND-peri-MexE-NCBIFAM multidrug efflux RND transporter periplasmic adaptor subunit MexE (NF045904.1) (CDS_0002)
AdeFGH efflux pump (VF0504) (CDS_0001)
MGV-GENOME-0358964: 1-18,189 (-)
Sigma L (VF0855) (CDS_0002)
MGV-GENOME-0373715: 2-16,744 (-)
DnaB-like replicative helicase (CDS_0151)
MGV-GENOME-0373399: 115,441-128,301 (+)
Panchino_gp28__gp28 (CDS_0115)
MGV-GENOME-0369966: 77,818-108,126 (+)
BopD (VF0362) (CDS_0001)
MGV-GENOME-0370998: 1-23,919 (-)
BrxHI_00004 BrxHI (CDS_0103)
MGV-GENOME-0364238: 71,070-85,320 (+)
BrxHI_00004 BrxHI (CDS_0011)
MGV-GENOME-0363057: 2-14,118 (-)
BrxHI_00004 BrxHI (CDS_0011)
MGV-GENOME-4432660: 2-14,307 (-)
BrxHI_00004 BrxHI (CDS_0148)
MGV-GENOME-0376896: 125,178-139,740 (+)
BrxHI_00004 BrxHI (CDS_0102)
MGV-GENOME-0360593: 69,536-85,694 (+)
BrxHI_00004 BrxHI (CDS_0007)
cysH_IV-B_1 (CDS_0001)
MGV-GENOME-0347056: 3-10,207 (-)
chloram_CatA-NCBIFAM type A chloramphenicol O-acetyltransferase (NF000491.1) (CDS_0087)
MGV-GENOME-0354938: 53,640-84,127 (+)
MGV-GENOME-0304174: 137-15,069 (-)
GroEL (VF0594) (CDS_0142)
MGV-GENOME-0372238: 100,360-119,942 (+)
GroEL (VF0594) (CDS_0004)
MGV-GENOME-0372235: 86-19,668 (-)
MGV-GENOME-0371476: 100,317-114,868 (+)
D-alanine-polyphosphoribitol ligase DltA (VF0795) (CDS_0005)
MGV-GENOME-0366735: 2-17,605 (-)
D-alanine-polyphosphoribitol ligase DltA (VF0795) (CDS_0153)
MGV-GENOME-0375168: 126,758-144,582 (+)
D-alanine-polyphosphoribitol ligase DltA (VF0795) (CDS_0007)
translation elongation factor (CDS_0014)
MGV-GENOME-0374941: 2-27,185 (-)
D-alanine-polyphosphoribitol ligase DltA (VF0795) (CDS_0155)
DEDDh_I_II_III_IV_V_VI_1 (CDS_0139)
translation elongation factor (CDS_0162)
MGV-GENOME-0376302: 99,496-154,102 (+)
trans_reg_VanU-NCBIFAM glycopeptide resistance transcriptional regulator VanU (NF000090.1) (CDS_0107)
MGV-GENOME-0367452: 71,070-87,983 (+)
trans_reg_VanU-NCBIFAM glycopeptide resistance transcriptional regulator VanU (NF000090.1) (CDS_0003)
MGV-GENOME-0378205: 1-16,900 (-)
trans_reg_VanU-NCBIFAM glycopeptide resistance transcriptional regulator VanU (NF000090.1) (CDS_0002)
MGV-GENOME-0348322: 252-16,915 (-)


trans_reg_VanU-NCBIFAM glycopeptide resistance transcriptional regulator VanU (NF000090.1) (CDS_0016)
HEC-01B_WP_052518933.1 (CDS_0004)
HEC-01A_WP_211640766.1 (CDS_0003)
2 Capsule (VF0079) (CDS_0001)
MGV-GENOME-0378282: 1-32,141 (-)
trans_reg_VanU-NCBIFAM glycopeptide resistance transcriptional regulator VanU (NF000090.1) (CDS_0024)
GtrB glycosyltransferase for O-antigen conversion (CDS_0016)
Michele_1B_hits_grouped (CDS_0009)
nuclease (CDS_0019)
MGV-GENOME-0375863: 3-46,134 (-)
ABCF_OptrA-NCBIFAM ABC-F type ribosomal protection protein OptrA (NF000514.1) (CDS_0009)
Zn++ metalloprotease (VF0846) (CDS_0008)
RcsAB (VF0571) (CDS_0001)
MGV-GENOME-0374799: 359-26,166 (-)
ABCF_OptrA-NCBIFAM ABC-F type ribosomal protection protein OptrA (NF000514.1) (CDS_0144)
Zn++ metalloprotease (VF0846) (CDS_0145)
MGV-GENOME-0372915: 103,490-125,161 (+)
Sigma L (VF0855) (CDS_0094)
MGV-GENOME-0366289: 75,900-87,492 (+)
LigA (VF1220) (CDS_0103)
MGV-GENOME-0365081: 69,536-86,266 (+)
LigA (VF1220) (CDS_0133)
MGV-GENOME-0372177: 99,114-119,605 (+)
Sul4-NCBIFAM sulfonamide-resistant dihydropteroate synthase Sul4 (NF033502.0) (CDS_0099)
Sigma M (VF0822) (CDS_0111)
HitABC (VF0268) (CDS_0109)
MGV-GENOME-0359719: 70,493-90,388 (+)
MGV-GENOME-0372910: 3-21,510 (-)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0012)
RND_peri-MexE-NCBIFAM multidrug efflux RND transporter periplasmic adaptor subunit MexE (NF045904.1) (CDS_0010)
RND_perm_OqxB-NCBIFAM multidrug efflux RND transporter permease subunit OqxB (NF000037.1) (CDS_0011)
DNA methyltransferase (CDS_0015)
RM_Type_IIG__Type_IIG_2 (CDS_0014)
MGV-GENOME-0376913: 70-20,848 (-)
MGV-GENOME-0372881: 93,835-124,882 (+)
MGV-GENOME-0377364: 137,077-165,164 (+)
LPS (VF0056) (CDS_0026)
DNA helicase (CDS_0021)
amidase (CDS_0025)
LPS (VF0561) (CDS_0015)
PanC/PanD (VF0319) (CDS_0005)
MGV-GENOME-0374368: 3-32,800 (-)
LPS (VF0056) (CDS_0009)
amidase (CDS_0008)
IMGVR_UViG_3300045988_185849|3300045988|Ga0495776_168603|18662-136093: 1-14,139 (-)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0005)
mads_8 (CDS_0007)
MGV-GENOME-0376151: 203-19,740 (-)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0166)
mads_8 (CDS_0164)
MGV-GENOME-4435480: 132,036-151,573 (+)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0149)
RND_adapt_MexA-NCBIFAM multidrug efflux RND transporter periplasmic adaptor subunit MexA (NF033834.1) (CDS_0157)
PDC-S19_WP_165041348.1 (CDS_0148)
RM_Type_IV_FAM_2 (CDS_0147)
mads_8 (CDS_0151)
RM_Type_IV_FAM_1 (CDS_0146)
MGV-GENOME-0378446: 128,671-150,695 (+)
Michele_2A_hits_grouped (CDS_0146)
FadE29 (VF0845) (CDS_0145)
MGV-GENOME-0377285: 122,458-144,331 (+)
Michele_2A_hits_grouped (CDS_0015)
FadE29 (VF0845) (CDS_0016)
MGV-GENOME-0371766: 188-22,061 (-)
Michele_2A_hits_grouped (CDS_0012)
FadE29 (VF0845) (CDS_0013)
MGV-GENOME-0358733: 233-17,710 (-)
Michele_2A_hits_grouped (CDS_0011)
FadE29 (VF0845) (CDS_0012)
MGV-GENOME-0359254: 240-17,716 (-)
Michele_2A_hits_grouped (CDS_0011)
FadE29 (VF0845) (CDS_0012)
MGV-GENOME-0373566: 220-17,696 (-)
MATE_multi_NorM-NCBIFAM multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0009)
clamp loader of DNA polymerase (CDS_0005)
AbiEi_WP_146016717.1 AbiEi (CDS_0004)
MTase_II_00176 Type (CDS_0002)
SanaTA__SanaT_1 (CDS_0003)
Michele_2A_hits_grouped (CDS_0027)
FadE29 (VF0845) (CDS_0028)
ClpC (VF0072) (CDS_0008)
RM_Type_IIG__Type_IIG_2 (CDS_0001)
MGV-GENOME-0376309: 1-38,754 (-)
Michele_2A_hits_grouped (CDS_0005)
FadE29 (VF0845) (CDS_0006)
MGV-GENOME-0367645: 1-9,840 (-)
macrolide_MefC-NCBIFAM macrolide efflux MFS transporter Mef(C) (NF000246.1) (CDS_0066)
SigE (VF0295) (CDS_0070)
MGV-GENOME-0311606: 33,472-50,502 (+)
clamp loader of DNA polymerase (CDS_0008)
Michele_1B_hits_grouped (CDS_0004)
MGV-GENOME-0300633: 132-13,950 (-)
clamp loader of DNA polymerase (CDS_0031)
RtcR_PspF2--CARF_AAA_HTH_MK_CARF_00012586 (CDS_0010)
Michele_1B_hits_grouped (CDS_0027)
Copper exporter (VF0849) (CDS_0012)
BrxHI_00004 BrxHI (CDS_0022)
FarAB (VF0450) (CDS_0019)
Sigma L (VF0855) (CDS_0003)
MGV-GENOME-0372685: 3-42,120 (-)
Michele_1B_hits_grouped (CDS_0012)
uvig_229980: 3-19,054 (-)
OatA (VF0441) (CDS_0096)
MGV-GENOME-0368307: 63,331-103,049 (+)
MGV-GENOME-0363828: 44-36,764 (-)
DNA replication initiation (CDS_0065)
Virulence-associated proteins (VF0679) (CDS_0076)
darG (CDS_0077)
darT (CDS_0078)
DarB-like antirestriction (CDS_0073)
IMGVR_UViG_3300045988_177236|3300045988|Ga0495776_155910|32,850-61,350 (+)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0011)
4918 0014_fosA-NCBIFAM Fos family putative thiol transferase (NF000125.1) (CDS_0003)
Sir2 (NAD-dependent deacetylase) (CDS_0006)
MGV-GENOME-0373791: 164-19,305 (-)
DEDDh_I_II_III_IV_V_VI_1 (CDS_0008)
Casp4_finished_genomes (CDS_0004)
DNA binding protein (CDS_0014)
kinase (CDS_0007)
serine-threonine kinase (CDS_0001)
MGV-GENOME-0354425: 2-24,290 (-)
DEDDh_I_II_III_IV_V_VI_1 (CDS_0132)
MGV-GENOME-0372423: 96,351-121,257 (+)
co-chaperonin GroES (CDS_0010)
dCMP deaminase (CDS_0012)
drt-cluster433 DRT (CDS_0006)
GroEL (VF0594) (CDS_0011)
MGV-GENOME-0369563: 509-23,778 (-)
MecI_of_mecC-NCBIFAM mecC-type methicillin resistance repressor MecI (NF000244.1) (CDS_0102)
MATE_multi_NorM-NCBIFAM multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0098)
ABC transporter (CDS_0105)
RpoS (VF0166) (CDS_0109)
clamp loader of DNA polymerase (CDS_0094)
ClpC (VF0072) (CDS_0096)
MGV-GENOME-0358466: 64,285-88,158 (+)
MecI_of_mecC-NCBIFAM mecC-type methicillin resistance repressor MecI (NF000244.1) (CDS_0007)
MATE_multi_NorM-NCBIFAM multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0011)
clamp loader of DNA polymerase (CDS_0015)
ClpC (VF0072) (CDS_0013)
ABC transporter (CDS_0004)
MGV-GENOME-0374204: 62-20,941 (-)
lytic tail protein (CDS_0141)
MGV-GENOME-0375504: 113,436-147,117 (+)
HEC-01B_WP_052518933.1 (CDS_0004)
HEC-01A_WP_211640766.1 (CDS_0003)
2 Capsule (VF0079) (CDS_0001)
MGV-GENOME-0377150: 1-15,677 (-)
HEC-01B_WP_052518933.1 (CDS_0004)
HEC-01A_WP_211640766.1 (CDS_0003)
2 Capsule (VF0079) (CDS_0001)
MGV-GENOME-0377293: 1-18,775 (-)
tet_protect-NCBIFAM tetracycline resistance ribosomal protection protein (NF012153.1) (CDS_0014)
HEC-01B_WP_052518933.1 (CDS_0004)
HEC-01A_WP_211640766.1 (CDS_0003)
2 Capsule (VF0079) (CDS_0001)
MGV-GENOME-0377369: 1-21,848 (-)
HEC-01B_WP_052518933.1 (CDS_0004)
HEC-01A_WP_211640766.1 (CDS_0003)
2 Capsule (VF0079) (CDS_0001)
MGV-GENOME-0377400: 1-21,774 (-)


HEC-01B_WP_052518933.1 (CDS_0004)
HEC-01A_WP_211640766.1 (CDS_0003)
clamp loader of DNA polymerase (CDS_0022)
ClpC (VF0072) (CDS_0020)
Capsule (VF0079) (CDS_0001)
MGV-GENOME-0378206: 1-30,980 (-)
HEC-01B_WP_052518933.1 (CDS_0004)
HEC-01A_WP_211640766.1 (CDS_0003)
Michele_1A_hits_grouped (CDS_0012)
PDC-M16A_WP_151194710.1 (CDS_0024)
DNA binding protein (CDS_0008)
Capsule (VF0079) (CDS_0001)
uvig_110632: 1-38,011 (-)
MATE_multi_NorM-NCBIFAM multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0011)
FabG-like 3-oxoacyl-(acyl-carrier-protein) reductase (CDS_0006)
ABC transporter (CDS_0004)
MGV-GENOME-0373388: 1,119-27,687 (-)
vanR-B-NCBIFAM vancomycin resistance response regulator transcription factor VanR-B (NF000402.1) (CDS_0100)
Tryptophan synthesis (VF0813) (CDS_0106)
glutamine amidotransferase (CDS_0107)
MTase_II_00169 Type (CDS_0131)
MTase_II_00159 Type (CDS_0130)
REase_II_00109 Type (CDS_0132)
MGV-GENOME-0372763: 68,086-123,978 (+)
vanR-B-NCBIFAM vancomycin resistance response regulator transcription factor VanR-B (NF000402.1) (CDS_0023)
Tryptophan synthesis (VF0813) (CDS_0017)
glutamine amidotransferase (CDS_0016)
MGV-GENOME-0375979: 3-35,516 (-)
vanR-B-NCBIFAM vancomycin resistance response regulator transcription factor VanR-B (NF000402.1) (CDS_0001)
MGV-GENOME-0372285: 2-8,931 (-)
AAC_3_I-NCBIFAM AAC(3)-I family aminoglycoside 3-N-acetyltransferase (NF033083.0) (CDS_0012)
MGV-GENOME-0373884: 24-18,199 (-)
AAC_3_I-NCBIFAM AAC(3)-I family aminoglycoside 3-N-acetyltransferase (NF033083.0) (CDS_0147)
MGV-GENOME-0373976: 116,788-134,265 (+)
MGV-GENOME-0369153: 80,380-105,576 (+)
PDC-S09_WP_017178955.1 (CDS_0150)
PDC-S09_WP_203234077.1 (CDS_0152)
Copper exporter (VF0849) (CDS_0162)
PDC-S13_WP_097300085.1 (CDS_0166)
MGV-GENOME-0376421: 128,474-146,272 (+)
FabG-like 3-oxoacyl-(acyl-carrier-protein) reductase (CDS_0092)
Sir2 (NAD-dependent deacetylase) (CDS_0097)
Mip (VF0153) (CDS_0098)
DNA repair protein (CDS_0107)
integrase (CDS_0108)
MGV-GENOME-0354339: 63,498-83,198 (+)
pectate lyase (CDS_0089)
Michele_2A_hits_grouped (CDS_0097)
MGV-GENOME-0357602: 50,096-86,841 (+)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0105)
zinc containing alcohol dehydrogenase superfamily (CDS_0097)
Copper exporter (VF0849) (CDS_0110)
DNA polymerase (CDS_0104)
MGV-GENOME-0371611: 71,070-103,987 (+)
zinc containing alcohol dehydrogenase superfamily (CDS_0117)
DNA polymerase (CDS_0131)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0132)
MGV-GENOME-0371778: 93,840-116,871 (+)
efflux_ABUW_0982-NCBIFAM chloramphenicol efflux transporter CxpE (NF045801.1) (CDS_0164)
PnuC-like nicotinamide mononucleotide transport (CDS_0159)
MerA-TIGRFAMs TIGRFAMs: mercury(II) reductase (TIGR02053.1) (CDS_0144)
gcu167__gcu167B (CDS_0169)
transcriptional regulator (CDS_0143)
thymidine kinase (CDS_0165)
LplA1 (VF0347) (CDS_0145)
PDC-S22_WP_003530377.1 (CDS_0138)
MGV-GENOME-0376078: 103,791-151,923 (+)
efflux_ABUW_0982-NCBIFAM chloramphenicol efflux transporter CxpE (NF045801.1) (CDS_0009)
MerA-TIGRFAMs TIGRFAMs: mercury(II) reductase (TIGR02053.1) (CDS_0030)
PnuC-like nicotinamide mononucleotide transport (CDS_0014)
PDC-S22_WP_003530377.1 (CDS_0036)
gcu167__gcu167B (CDS_0004)
transcriptional regulator (CDS_0031)
thymidine kinase (CDS_0008)
LplA1 (VF0347) (CDS_0029)
MGV-GENOME-0375815: 81-47,976 (-)
PnuC-like nicotinamide mononucleotide transport (CDS_0004)
MGV-GENOME-0372722: 2-9,580 (-)
thymidine kinase (CDS_0112)
efflux_ABUW_0982-NCBIFAM chloramphenicol efflux transporter CxpE (NF045801.1) (CDS_0113)
MGV-GENOME-0371429: 69,536-103,781 (+)
RM_Type_II__Type_II_MTases_FAM_2 (CDS_0076)
PDC-S01_WP_076465573.1 (CDS_0075)
Gao_Mza__MzaC (CDS_0078)
MGV-GENOME-0329712: 32,850-58,776 (+)
PDC-S02_WP_151674975.1 (CDS_0129)
MGV-GENOME-0369206: 86,963-103,775 (+)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0018)
RND-peri-MexE-NCBIFAM multidrug efflux RND transporter periplasmic adaptor subunit MexE (NF045904.1) (CDS_0016)
RND_perm_OqxB-NCBIFAM multidrug efflux RND transporter permease subunit OqxB (NF000037.1) (CDS_0017)
QueC-like queuosine biosynthesis (CDS_0007)
phosphofructokinase (CDS_0004)
FAS-II (VF0809) (CDS_0002)
MGV-GENOME-0372536: 3-40,137 (-)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0008)
RND-peri-MexE-NCBIFAM multidrug efflux RND transporter periplasmic adaptor subunit MexE (NF045904.1) (CDS_0006)
RND_perm_OqxB-NCBIFAM multidrug efflux RND transporter permease subunit OqxB (NF000037.1) (CDS_0007)
MGV-GENOME-0375319: 3-28,050 (-)
transcription antiterminator (CDS_0116)
AriA_WP_163211684.1 (CDS_0115)
AriB_WP_153112628.1 (CDS_0114)
amidase (CDS_0113)
MATE_multi_NorM-NCBIFAM multidrug efflux MATE transporter NorM (NF000263.1) (CDS_0122)
SAMN05414895_a1_ct15598_vs1: 72,808-93,606 (+)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0152)
SMR_efflux_smr-NCBIFAM multidrug efflux SMR transporter Smr (NF000280.1) (CDS_0153)
Michele_1B_hits_grouped (CDS_0161)
MGV-GENOME-0374437: 115,992-137,754 (+)
PDC-M64C_WP_110053925.1 (CDS_0004)
PDC-S31_WP_063883643.1 (CDS_0005)
metallo-phosphoesterase (CDS_0012)
PDC-S68_WP_170143107.1 (CDS_0008)
phosphoesterase (CDS_0013)
PDC-S57_WP_173639931.1 (CDS_0002)
REase_I_00009 Type (CDS_0003)
RM__Type_I_MTases_FAM_0 (CDS_0001)
MGV-GENOME-0338465: 2-31,454 (-)
PDC-M64C_WP_110053925.1 (CDS_0070)
PDC-S57_WP_173639931.1 (CDS_0072)
PDC-S31_WP_063883643.1 (CDS_0069)
metallo-phosphoesterase (CDS_0062)
PDC-S68_WP_170143107.1 (CDS_0066)
phosphoesterase (CDS_0061)
RM__Type_I_MTases_FAM_0 (CDS_0073)
REase_I_00009 Type (CDS_0071)
PDC-S05_WP_231564492.1 (CDS_0074)
MGV-GENOME-0318154: 32,805-53,226 (+)
MGV-GENOME-0304395: 32,850-47,989 (+)
MGV-GENOME-0304138: 32,850-47,754 (+)
PDC-S01_WP_015504585.1 (CDS_0004)
anti-restriction protein (CDS_0003)
MGV-GENOME-0318936: 1-20,792 (-)
RM__Type_I_REases_FAM_0.einsi_trimmed (CDS_0081)
PDC-M69A_WP_216276383.1 (CDS_0080)
PDC-S14_WP_068837883.1 (CDS_0079)
PDC-S05_WP_205747975.1 (CDS_0083)
MTase_I_00016 Type (CDS_0082)
MGV-GENOME-0325709: 32,848-56,882 (+)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0151)
RND-peri-MexE-NCBIFAM multidrug efflux RND transporter periplasmic adaptor subunit MexE (NF045904.1) (CDS_0153)
RND_perm_OqxB-NCBIFAM multidrug efflux RND transporter permease subunit OqxB (NF000037.1) (CDS_0152)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0155)
PDC-S01_WP_067088819.1 (CDS_0149)
MGV-GENOME-0376621: 126,494-152,949 (+)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0019)
RND-peri-MexE-NCBIFAM multidrug efflux RND transporter periplasmic adaptor subunit MexE (NF045904.1) (CDS_0017)
RND_perm_OqxB-NCBIFAM multidrug efflux RND transporter permease subunit OqxB (NF000037.1) (CDS_0018)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0015)
zinc containing alcohol dehydrogenase superfamily (CDS_0004)
Michele_2A_hits_grouped (CDS_0007)
acetyltransferase (CDS_0008)
HspX (VF0301) (CDS_0005)
GtcA (VF0607) (CDS_0006)
PDC-S01_WP_067088819.1 (CDS_0021)
MGV-GENOME-0375025: 341-28,808 (-)
tet_protect-NCBIFAM tetracycline resistance ribosomal protection protein (NF012153.1) (CDS_0017)
levanase (CDS_0046)
PDC-S01_WP_067088819.1 (CDS_0036)
nucleotide-sugar epimerase (CDS_0018)
levanase (CDS_0047)
levanase (CDS_0043)
pAgo__GbbAgaS (CDS_0012)
levanase (CDS_0044)
SoFic__SoFic (CDS_0014)
MGV-GENOME-0377900: 166-73,668 (-)
levanase (CDS_0008)
levanase (CDS_0009)
levanase (CDS_0005)
levanase (CDS_0006)
MGV-GENOME-0372549: 91-22,607 (-)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0138)
Copper exporter (VF0849) (CDS_0149)
MsrAB (VF0456) (CDS_0139)
mads_8 (CDS_0134)
MGV-GENOME-0373721: 101,455-131,971 (+)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0011)
MsrAB (VF0456) (CDS_0010)
mads_8 (CDS_0015)
Copper exporter (VF0849) (CDS_0002)
MGV-GENOME-0372868: 831-21,506 (-)
efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0010)
MsrAB (VF0456) (CDS_0009)
mads_8 (CDS_0014)
MGV-GENOME-0348227: 224-19,358 (-)


efflux_OM_AdeC-NCBIFAM multidrug efflux RND transporter AdeABC outer membrane channel subunit AdeC (NF033142.1) (CDS_0023)
Copper exporter (VF0849) (CDS_0012)
MsrAB (VF0456) (CDS_0022)
Sigma L (VF0855) (CDS_0010)
mads_8 (CDS_0027)
MGV-GENOME-0372345: 3-39,170 (-)
Michele_2A_hits_grouped (CDS_0121)
DNA helicase (CDS_0136)
MGV-GENOME-0371025: 93,868-112,825 (+)
Michele_2A_hits_grouped (CDS_0102)
MGV-GENOME-0362419: 55,071-94,742 (+)
Michele_2A_hits_grouped (CDS_0004)
MGV-GENOME-0376342: 1-26,729 (-)
MGV-GENOME-0371471: 112-32,374 (-)
REase_I_00009 Type (CDS_0086)
MGV-GENOME-0354352: 56,633-82,732 (+)
N-linked protein glycosylation (VF0721) (CDS_0102)
ABC transporter (VF0818) (CDS_0097)
acyl carrier protein (CDS_0093)
translation elongation factor (CDS_0110)
FAS-II (VF0809) (CDS_0092)
MGV-GENOME-0358788: 62,960-88,336 (+)
QueC-like queuosine biosynthesis (CDS_0007)
dCMP deaminase (CDS_0012)
mads_3 (CDS_0016)
ribonucleotide reductase large subunit (CDS_0003)
MGV-GENOME-0370715: 1-25,092 (-)
polymyxin_MCR8-NCBIFAM MCR-8 family phosphoethanolamine--lipid A transferase (NF033669.1) (CDS_0110)
Retron_VI_HTH (CDS_0102)
aminotransferase (CDS_0098)
MGV-GENOME-0362010: 65,904-94,261 (+)
RND_perm_OqxB-NCBIFAM multidrug efflux RND transporter permease subunit OqxB (NF000037.1) (CDS_0005)
ABCF_OptrA-NCBIFAM ABC-F type ribosomal protection protein OptrA (NF000514.1) (CDS_0010)
MerA-TIGRFAMs TIGRFAMs: mercury(II) reductase (TIGR02053.1) (CDS_0009)
tRNA nucleotidyltransferase (CDS_0013)
MGV-GENOME-0377512: 2-35,512 (-)
lipoprotein (CDS_0008)
endolysin (CDS_0016)
toxin (CDS_0020)
MGV-GENOME-0373292: 1-14,971 (-)
498180014_fosA-NCBIFAM Fos family putative thiol transferase (NF000125.1) (CDS_0011)
nitroreductase (CDS_0009)
MGV-GENOME-0372767: 3-14,880 (-)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0003)
498180014_fosA-NCBIFAM Fos family putative thiol transferase (NF000125.1) (CDS_0016)
Jallet_1C_hits_grouped (CDS_0009)
REase_II_00165 Type (CDS_0007)
nitroreductase (CDS_0014)
MGV-GENOME-0376947: 119-50,387 (-)
dCMP deaminase (CDS_0092)
MGV-GENOME-0355492: 53,777-84,591 (+)
Sul4-NCBIFAM sulfonamide-resistant dihydropteroate synthase Sul4 (NF033502.0) (CDS_0015)
Siderophore-dependent iron uptake system (VF0738) (CDS_0021)
minor tail protein with lysin activity (CDS_0003)
MGV-GENOME-0361304: 199-29,614 (-)
Sul4-NCBIFAM sulfonamide-resistant dihydropteroate synthase Sul4 (NF033502.0) (CDS_0095)
Siderophore-dependent iron uptake system (VF0738) (CDS_0089)
MGV-GENOME-0351114: 51,752-78,791 (+)
QueC-like queuosine biosynthesis (CDS_0009)
DNA repair protein (CDS_0022)
exonuclease (CDS_0007)
Gabija__GajB_2 (CDS_0018)
Jallet_1C_hits_grouped (CDS_0002)
MGV-GENOME-0376040: 250-37,671 (-)
DNA repair protein (CDS_0151)
Gabija__GajB_2 (CDS_0155)
QueC-like queuosine biosynthesis (CDS_0164)
MGV-GENOME-0375179: 115,970-144,661 (+)
PDC-S09_WP_015419311.1 (CDS_0019)
DNA helicase (CDS_0017)
minor tail protein with lysin activity (CDS_0003)
MGV-GENOME-0370038: 3-44,952 (-)
PDC-S09_WP_015419311.1 (CDS_0013)
DNA helicase (CDS_0011)
MGV-GENOME-0374710: 3-35,108 (-)
O-antigen (VF0392) (CDS_0029)
translation elongation factor (CDS_0019)
PDC-S04_WP_002996767.1 (CDS_0002)
SoFic__SoFic (CDS_0005)
MGV-GENOME-0373053: 2-58,129 (-)
O-antigen (VF0392) (CDS_0141)
MGV-GENOME-0372837: 103,440-124,602 (+)
RtcR_PspF2--CARF_AAA_HTH_MK_CARF_00012586 (CDS_0114)
CBASS__AG_E1_ThiF ThiF family (CDS_0112)
MGV-GENOME-0362115: 70,302-94,448 (+)
PDC-M69A_WP_216276383.1 (CDS_0105)
DNA repair protein (CDS_0128)
transcriptional regulator (CDS_0108)
ShosTA__ShosT (CDS_0127)
IMGVR_UViG_3300045988_186253|3300045988|Ga0495776_0809965875B_158994:69,451-100,239 (+)
DNA repair protein (CDS_0165)
transcriptional regulator (CDS_0147)
ShosTA__ShosT (CDS_0164)
MGV-GENOME-0376831: 128,206-158,994 (+)
PDC-M69A_WP_216276383.1 (CDS_0106)
transcriptional regulator (CDS_0109)
MGV-GENOME-0353132: 68,954-81,442 (+)
ABC-type heme transporter (VF0739) (CDS_0032)
Enterobactin receptor IrgA (VF0628) (CDS_0034)
Streptococcal enolase (VF1060) (CDS_0020)
Urease (VF0050) (CDS_0024)
Sigma L (VF0855) (CDS_0012)
SigH (VF0296) (CDS_0003)
MGV-GENOME-0377324: 2-48,994 (-)
DNA methyltransferase (CDS_0011)
Sigma L (VF0855) (CDS_0012)
MGV-GENOME-0376192: 2-22,341 (-)
recD_IV-D_1 (CDS_0003)
MGV-GENOME-0349832: 1-18,879 (-)
MGV-GENOME-0373812: 117,683-132,508 (+)
PDC-M13A_WP_075424075.1 (CDS_0019)
HEC-01B_WP_052518933.1 (CDS_0004)
HEC-01A_WP_211640766.1 (CDS_0003)
Capsule (VF0079) (CDS_0001)
MGV-GENOME-0378522: 1-37,717 (-)
MGV-GENOME-0374489: 98,253-138,681 (+)
transcriptional regulator (CDS_0006)
MGV-GENOME-0377612: 115-62,246 (-)
Michele_1A_hits_grouped (CDS_0120)
tRNA amidotransferase (CDS_0141)
MGV-GENOME-0374422: 101,946-138,023 (+)
CBASS__AG_E1_ThiF ThiF family (CDS_0116)
MGV-GENOME-0358722: 59,996-86,674 (+)
MGV-GENOME-0373141: 3-23,046 (-)
CBASS__AG_E1_ThiF ThiF family (CDS_0119)
MGV-GENOME-0372030: 77,809-118,087 (+)
FabG-like 3-oxoacyl-(acyl-carrier-protein) reductase (CDS_0005)
retron_type_V_csd_cluster85_1 (CDS_0011)
PDC-S02_WP_080642564.1 (CDS_0021)
HEC-06_WP_099323492.1 (CDS_0019)
phosphofructokinase (CDS_0012)
PbeA_00004 PbeA (CDS_0025)
PbeC_00022 PbeC (CDS_0023)
MGV-GENOME-0375415: 16-31,105 (-)
retron_type_V_csd_cluster85_1 (CDS_0161)
HEC-06_WP_099323492.1 (CDS_0155)
phosphofructokinase (CDS_0160)
MGV-GENOME-0374767: 113,944-140,836 (+)
Sul4-NCBIFAM sulfonamide-resistant dihydropteroate synthase Sul4 (NF033502.0) (CDS_0019)
Ton system (VF0895) (CDS_0015)
Ton system (VF0895) (CDS_0013)
DNA primase (CDS_0008)
DS-15__DS-15A (CDS_0001)
MGV-GENOME-0375607: 1-29,305 (-)


Nucleoside diphosphate kinase (VF0851) (CDS_0144)
Ton system (VF0895) (CDS_0138) Dpd_FolE (CDS_0150)
Ton system (VF0895) (CDS_0140) DNA primase (CDS_0151)
mads_3 (CDS_0132)
MGV-GENOME-0373175: 99,457-126,468 (+)
Zn++ metalloprotease (VF0846) (CDS_0035)
head maturation protease (CDS_0032)
CAI-1 (VF0405) (CDS_0038)
ABC transporter (CDS_0033)
O-antigen (VF0392) (CDS_0010)
AggR (VF1137) (CDS_0006)
SigE (VF0295) (CDS_0008)
Dpd_FolE (CDS_0003)
PDC-S34_WP_209195270.1 (CDS_0001)
MGV-GENOME-0375165: 341-52,128 (-)
vanR_ACDEGLN-NCBIFAM VanR-ABDEGLN family response regulator transcription factor (NF033117.2) (CDS_0033)
QueD-like 6-pyruvoyl-tetrahydropterin synthase (CDS_0030)
Zn++ metalloprotease (VF0846) (CDS_0025)
CAI-1 (VF0405) (CDS_0028)
DNA polymerase (CDS_0031)
head maturation protease (CDS_0022)
MGV-GENOME-0372657: 298-52,116 (-)
PDC-S34_WP_209195270.1 (CDS_0124)
O-antigen (VF0392) (CDS_0115)
AggR (VF1137) (CDS_0119)
SigE (VF0295) (CDS_0117)
Dpd_FolE (CDS_0122)
transposase (CDS_0125)
MGV-GENOME-0374005: 82,983-103,751 (+)
DNA methyltransferase (CDS_0109)
NEase_II_00007 Type (CDS_0127)
MGV-GENOME-0369547: 77,785-106,769 (+)
QatD_00001 (CDS_0027)
DS-15_DS-15A (CDS_0001)
MGV-GENOME-0376199: 1-37,575 (-)
DS-15_DS-15A (CDS_0001)
MGV-GENOME-0375372: 1-30,772 (-)
DNA binding protein (CDS_0026)
transposase (CDS_0008)
transposase (CDS_0009)
ParA-like partition protein (CDS_0001)
MGV-GENOME-0435526: 1-39,394 (-)
transposase (CDS_0008)
transposase (CDS_0009)
ParA-like partition protein (CDS_0001)
MGV-GENOME-0375383: 1-29,951 (-)
retron_type_VI_hth_cluster2_1 (CDS_0031)
transposase (CDS_0008)
transposase (CDS_0009)
ParA-like partition protein (CDS_0001)
IMGVR_UViG_3300045988_18040|3300045988|Ga0495776_119823: 1-33,545 (-)
transposase (CDS_0008)
ParA-like partition protein (CDS_0001)
MGV-GENOME-0375807: 1-32,841 (-)
transposase (CDS_0007)
DS-15_DS-15A (CDS_0001)
IMGVR_UViG_3300045988_178580|3300045988|Ga0495776_088979: 1-34,842 (-)
DNA binding protein (CDS_0036)
ParA-like partition protein (CDS_0001)
ivig_1323: 1-33,056 (-)
MecI_of_mecA-NCBIFAM mecA-type methicillin resistance repressor MecI (NF000243.1) (CDS_0141)
ribosomal protein S21 (CDS_0142)
Hemolysin HlyA (VF0646) (CDS_0150)
MutT/NUDIX hydrolase (CDS_0162)
BREX_pglZ3 (CDS_0159)
MGV-GENOME-0376733: 115,382-158,028 (+)
MymA operon (VF0840) (CDS_0019)
methyltransferase (CDS_0013)
AI-2 (VF0406) (CDS_0018)
integrase (CDS_0010)
MGV-GENOME-0367131: 212-30,535 (-)
MymA operon (VF0840) (CDS_0145)
methyltransferase (CDS_0151)
AI-2 (VF0406) (CDS_0146)
MGV-GENOME-0375104: 113,378-143,701 (+)
FabG-like 3-oxoacyl-(acyl-carrier-protein) reductase (CDS_0158)
Sir2 (NAD-dependent deacetylase) (CDS_0163)
MymA operon (VF0840) (CDS_0135)
Mip (VF0153) (CDS_0164)
methyltransferase (CDS_0141)
AI-2 (VF0406) (CDS_0136)
MGV-GENOME-0375732: 103,081-148,984 (+)
DNA polymerase (CDS_0012)
O-acetyltransferase (CDS_0014)
MGV-GENOME-0374466: 1-47,527 (-)
phosphoadenosine phosphosulfate reductase (CDS_0023)
ParB-like partition protein (CDS_0024)
ABC transporter (VF0741) (CDS_0020)
O-antigen (VF0392) (CDS_0012)
MGV-GENOME-0370235: 2-31,224 (-)
O-acetyltransferase (CDS_0028)
mads_8 (CDS_0018)
mads_8 (CDS_0005)
MGV-GENOME-0368080: 2-44,298 (-)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor, VanR-F/VanR-M family (NF033120.0) (CDS_0110)
cmlA_floR-NCBIFAM CmlA/FloR family chloramphenicol efflux MFS transporter (NF033134.0) (CDS_0093)
ABC transporter (VF0741) (CDS_0097)
SigE (VF0295) (CDS_0099)
hydrolase (CDS_0091)
MGV-GENOME-0361168: 63,278-92,601 (+)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor, VanR-F/VanR-M family (NF033120.0) (CDS_0006)
cmlA_floR-NCBIFAM CmlA/FloR family chloramphenicol efflux MFS transporter (NF033134.0) (CDS_0023)
ABC transporter (VF0741) (CDS_0019)
SigE (VF0295) (CDS_0017)
hydrolase (CDS_0025)
MGV-GENOME-0374457: 146-29,469 (-)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor, VanR-F/VanR-M family (NF033120.0) (CDS_0007)
cmlA_floR-NCBIFAM CmlA/FloR family chloramphenicol efflux MFS transporter (NF033134.0) (CDS_0024)
ABC transporter (VF0741) (CDS_0020)
SigE (VF0295) (CDS_0018)
hydrolase (CDS_0026)
DNA helicase (CDS_0001)
MGV-GENOME-0374271: 1-31,667 (-)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor, VanR-F/VanR-M family (NF033120.0) (CDS_0110)
cmlA_floR-NCBIFAM CmlA/FloR family chloramphenicol efflux MFS transporter (NF033134.0) (CDS_0093)
ABC transporter (VF0741) (CDS_0097)
SigE (VF0295) (CDS_0099)
hydrolase (CDS_0091)
MGV-GENOME-0361554: 63,274-93,548 (+)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor, VanR-F/VanR-M family (NF033120.0) (CDS_0009)
cmlA_floR-NCBIFAM CmlA/FloR family chloramphenicol efflux MFS transporter (NF033134.0) (CDS_0026)
ABC transporter (VF0741) (CDS_0022)
SigE (VF0295) (CDS_0020)
hydrolase (CDS_0028)
DNA helicase (CDS_0003)
MGV-GENOME-0375757: 162-33,669 (-)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor, VanR-F/VanR-M family (NF033120.0) (CDS_0010)
cmlA_floR-NCBIFAM CmlA/FloR family chloramphenicol efflux MFS transporter (NF033134.0) (CDS_0027)
ABC transporter (VF0741) (CDS_0023)
SigE (VF0295) (CDS_0021)
PDC-S05_WP_013135363.1 (CDS_0003)
hydrolase (CDS_0029)
MGV-GENOME-0363636: 223-33,249 (-)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor, VanR-F/VanR-M family (NF033120.0) (CDS_0165)
cmlA_floR-NCBIFAM CmlA/FloR family chloramphenicol efflux MFS transporter (NF033134.0) (CDS_0148)
ABC transporter (VF0741) (CDS_0152)
PDC-M30B_WP_013406987.1 (CDS_0175)
SigE (VF0295) (CDS_0154)
hydrolase (CDS_0146)
MGV-GENOME-0375765: 114,739-149,250 (+)
DnaB-like replicative helicase (CDS_0064)
DEDDh_I_II_III_IV_V_VI_1 (CDS_0077)
MGV-GENOME-0330933: 32,863-59,410 (+)
Sigma L (VF0855) (CDS_0106)
Sigma L (VF0855) (CDS_0105)
ABC-type heme transporter (VF0739) (CDS_0092)
MGV-GENOME-0368344: 62,914-102,978 (+)
Jallet_1A_hits_grouped (CDS_0019)
DNA helicase (CDS_0013)
amidase (CDS_0016)
AbiLi-1 AbiLi (CDS_0005)
MGV-GENOME-0363470: 2,701-33,034 (-)
Jallet_1A_hits_grouped (CDS_0155)
DNA helicase (CDS_0161)
amidase (CDS_0158)
MGV-GENOME-0375434: 113,395-143,729 (+)
N-linked protein glycosylation (VF0721) (CDS_0116)
REase_II_00165 Type (CDS_0099)
glycosyltransferase (CDS_0119)
O-antigen (VF0392) (CDS_0104)
ABC transporter (CDS_0121)
HspX (VF0301) (CDS_0096)
LOS (VF0326) (CDS_0117)
MGV-GENOME-0368785: 70,859-104,220 (+)
RND_adapt_MexA-NCBIFAM multidrug efflux RND transporter periplasmic adaptor subunit MexA (NF033834.1) (CDS_0147)
gcu233_gcu233 (CDS_0141)
SspA_00001 SspA (CDS_0144)
HAD-superfamily hydrolase (CDS_0161)
mads_8 (CDS_0142)
HNH endonuclease (CDS_0159)
VakA (CDS_0145)
MGV-GENOME-0376251: 114,737-153,500 (+)
MgtBC (VF0106) (CDS_0027)
Copper exporter (VF0849) (CDS_0004)
Sigma L (VF0855) (CDS_0006)
MGV-GENOME-0375023: 138-53,560 (-)
MgtBC (VF0106) (CDS_0005)
ParA-like partition protein (CDS_0001)
MGV-GENOME-0375067: 1-28,117 (-)
DEDDh_I_II_III_IV_V_VI_1 (CDS_0166)
MGV-GENOME-0378844: 115,921-185,854 (+)
MGV-GENOME-0375332: 171-29,831 (-)
RND_adapt_MexA-NCBIFAM multidrug efflux RND transporter periplasmic adaptor subunit MexA (NF033834.1) (CDS_0118)
PDC-S01_WP_067088819.1 (CDS_0098)
RND_perm_OqxB-NCBIFAM multidrug efflux RND transporter permease subunit OqxB (NF000037.1) (CDS_0117)
PDC-S27_WP_062081222.1 (CDS_0104)
shah_acc_0194 AA (CDS_0115)
MGV-GENOME-0371994: 70,370-118,330 (+)


HEC-01B_WP_052518933.1 (CDS_0139)
HEC-01A_WP_211640766.1 (CDS_0140)
shah_acc_0214 GlgB (CDS_0132)
Sigma M (VF0822) (CDS_0147)
Gabija__GajB_2 (CDS_0128)
Cas1_II_WP_078484493.1 (CDS_0122)
MGV-GENOME-0374923: 99,543-142,147 (+)
cmx_cmrA-NCBIFAM Cmx/CmrA family chloramphenicol efflux MFS transporter (NF033135.1) (CDS_0105)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0095)
Michele_1A_hits_grouped (CDS_0100)
MGV-GENOME-0359728: 56,078-90,452 (+)
efflux_ABUW_0982-NCBIFAM chloramphenicol efflux transporter CxpE (NF045801.1) (CDS_0154)
K1 capsule (VF0239) (CDS_0144)
ABC transporter (VF0818) (CDS_0137)
PanC/PanD (VF0319) (CDS_0160)
Rnase H (CDS_0139)
MGV-GENOME-0375777: 111,950-148,460 (+)
efflux_ABUW_0982-NCBIFAM chloramphenicol efflux transporter CxpE (NF045801.1) (CDS_0008)
ABC transporter (VF0818) (CDS_0025)
K1 capsule (VF0239) (CDS_0018)
Rnase H (CDS_0023)
PanC/PanD (VF0319) (CDS_0002)
MGV-GENOME-0375309: 722-37,232 (-)
MecI_of_mecA-NCBIFAM mecA-type methicillin resistance repressor MecI (NF000243.1) (CDS_0154)
efflux_ABUW_0982-NCBIFAM chloramphenicol efflux transporter CxpE (NF045801.1) (CDS_0140)
RM_Type_II__Type_II_REase06 (CDS_0144)
DrmMII_00005 DrmMII (CDS_0145)
REase_II_00052 Type (CDS_0146)
MTase_II_00045 Type (CDS_0147)
K1 capsule (VF0239) (CDS_0130)
ABC transporter (VF0818) (CDS_0123)
Rnase H (CDS_0125)
ribosomal protein S21 (CDS_0153)
MGV-GENOME-0376861: 102,922-159,240 (+)
MecI_of_mecA-NCBIFAM mecA-type methicillin resistance repressor MecI (NF000243.1) (CDS_0110)
ABC-type heme transporter (VF0739) (CDS_0117)
HitABC (VF0268) (CDS_0119)
ClpP (VF0074) (CDS_0113)
DpdF_00007 DpdF (CDS_0111)
dehydrogenase (CDS_0107)
ABC transporter (CDS_0095)
MGV-GENOME-0369000: 64,638-102,707 (+)
replication initiation protein (CDS_0123)
amidase (CDS_0124)
MGV-GENOME-0372647: 109,207-122,949 (+)
NrdD-like anaerobic ribonucleotide reductase large subunit (CDS_0087)
anaerobic ribonucleotide reductase small subunit (CDS_0086)
Specificity_I_00028 Type (CDS_0093)
MTase_I_00008 Type (CDS_0095)
RM__Type_I_S_04 (CDS_0094)
REase_I_00010 Type (CDS_0096)
uvig_198544: 74,699-92,156 (+)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0128)
Specificity_II_00001 Type (CDS_0139)
Specificity_I_00025 Type (CDS_0140)
MTase_I_00008 Type (CDS_0141)
RM__Type_I_S_04 (CDS_0138)
REase_I_00010 Type (CDS_0142)
uvig_208398: 111,355-141,579 (+)
MGV-GENOME-0375259: 81,383-92,847 (+)
Sigma L (VF0855) (CDS_0029)
MECA_PBP2A-NCBIFAM PBP2a family beta-lactam-resistant peptidoglycan transpeptidase (NF000237.1) (CDS_0008)
kinase (CDS_0032)
MGV-GENOME-0372145: 1-58,670 (-)
Acylhomoserine lactone synthase (VF0907) (CDS_0010)
2-aminooxy adenylosuccinate synthase (CDS_0030)
DNA topoisomerase II (CDS_0011)
LigA (VF1220) (CDS_0026)
FtsK/SpoIIIE-like protein (CDS_0015)
DNA topoisomerase II (CDS_0018)
MGV-GENOME-0376822: 274-47,342 (-)
ABCF_OptrA-NCBIFAM ABC-F type ribosomal protection protein OptrA (NF000514.1) (CDS_0134)
translation initiation factor (CDS_0126)
peptide deformylase (CDS_0123)
DnaB-like replicative helicase (CDS_0101)
Mycobactin (VF0299) (CDS_0117)
translation elongation factor (CDS_0113)
LPS (VF0124) (CDS_0131)
MGV-GENOME-0375646: 69,536-128,029 (+)
DnaB-like replicative helicase (CDS_0022)
translation elongation factor (CDS_0010)
Mycobactin (VF0299) (CDS_0006)
MGV-GENOME-0355003: 5-32,804 (-)
anti-CRISPR-Cas (AcrIIA9) (CDS_0028)
2DS-15__DS-15A (CDS_0001)
MGV-GENOME-0375339: 1-29,543 (-)
QueE-like radical SAM domain (CDS_0030)
thymidylate kinase (CDS_0014)
NAD synthetase (CDS_0019)
retron_type_VI_hth_cluster2_1 (CDS_0002)
MGV-GENOME-0362264: 1-32,538 (-)
PDC-S05_WP_013135363.1 (CDS_0109)
PDC-S05_WP_013135363.1 (CDS_0108)
PDC-S13_WP_097300085.1 (CDS_0110)
MGV-GENOME-0358371: 52,810-87,892 (+)
PDC-S05_WP_013135363.1 (CDS_0021)
PDC-S05_WP_013135363.1 (CDS_0022)
PDC-S13_WP_097300085.1 (CDS_0020)
radical SAM domain protein (CDS_0038)
HEase_00017 homing (CDS_0002)
MGV-GENOME-0375854: 3-47,201 (-)
NimABCDEF-NCBIFAM NimABCDEF family 5-nitroimidazole reductase (NF000261.1) (CDS_0034)
PDC-S01_WP_099993690.1 (CDS_0020)
esterase (CDS_0023)
nuclease (CDS_0035)
MGV-GENOME-0377053: 87-62,103 (-)
PDC-M69A_WP_216276383.1 (CDS_0012)
endonuclease (CDS_0024)
HEase_00016 homing (CDS_0010)
anti-repressor (CDS_0005)
toxin (CDS_0016)
MGV-GENOME-0348423: 3-28,280 (-)
MATE_multi_MepA-NCBIFAM multidrug efflux MATE transporter MepA (NF000131.1) (CDS_0148)
Mycobactin (VF0299) (CDS_0141)
DpdF_00010 DpdF (CDS_0144)
MGV-GENOME-0376867: 103,409-159,299 (+)
ribonucleotide reductase large subunit (CDS_0119)
RM__Type_I_REases_FAM_0_einsi_trimmed (CDS_0106)
PDC-S05_WP_181573034.1 (CDS_0109)
PDC-S72_WP_006439742.1 (CDS_0107)
PDC-S01_WP_096335077.1 (CDS_0111)
Specificity_I_00054 Type (CDS_0108)
minor tail protein (CDS_0115)
MTase_I_00012 Type (CDS_0110)
Enterobactin receptor IrgA (VF0628) (CDS_0103)
GtcA (VF0607) (CDS_0121)
MGV-GENOME-0371956: 68,579-118,097 (+)
vanR_FM-NCBIFAM vancomycin resistance response regulator transcription factor VanR-F/VanR-M family (NF033120.0) (CDS_0147)
tet_MFS_A_B_C_D-NCBIFAM Tet(A)/Tet(B)/Tet(C) family tetracycline efflux MFS transporter (NF012174.0) (CDS_0165)
RuvC-like Holliday junction resolvase (CDS_0156)
transaldolase (CDS_0153)
NEase_II_00007 Type (CDS_0166)
MGV-GENOME-0377096: 114,002-161,632 (+)
cyanobacterial phosphoribosylglycinamide formyltransferase (CDS_0037)
tetrahydrofolate dehydrogenase and cyclohydrolase (CDS_0040)
phosphoribosylaminoimidazole synthetase (CDS_0036)
Pyrimidine biosynthesis (VF0558) (CDS_0030)
Purine biosynthesis (VF0559) (CDS_0039)
Jallet_1A_hits_grouped (CDS_0032)
Shango__SngC (CDS_0019)
Purine synthesis (VF0811) (CDS_0034)
PDC-S22_WP_003530377.1 (CDS_0003)
MGV-GENOME-0377068: 1-50,149 (-)
vanH_gen-NCBIFAM D-lactate dehydrogenase VanH (NF000492.1) (CDS_0027)
clamp loader of DNA polymerase (CDS_0026)
endonuclease (CDS_0035)
Mycobactin (VF0299) (CDS_0017)
MGV-GENOME-0376702: 1-53,205 (-)
Purine biosynthesis (VF0559) (CDS_0005)
nucleotide-sugar epimerase (CDS_0014)
cation efflux protein (CDS_0013)
nuclease (CDS_0012)
MGV-GENOME-0366043: 3-19,951 (-)
DNA topoisomerase II (CDS_0139)
Sigma L (VF0855) (CDS_0148)
DNA polymerase (CDS_0127)
ShosTA__ShosA (CDS_0145)
AI-2 (VF0406) (CDS_0169)
MGV-GENOME-0377700: 130,255-169,349 (+)
tet_protect_Q-NCBIFAM tetracycline resistance ribosomal protection protein Tet(Q) (NF012154.0) (CDS_0129)
Reverse transcriptase (CDS_0127)
MGV-GENOME-0373377: 102,388-129,174 (+)
20000 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)
anti-defence (dbAPIS)
AMR (AMRFinderPlus)
tRNA
tmRNA