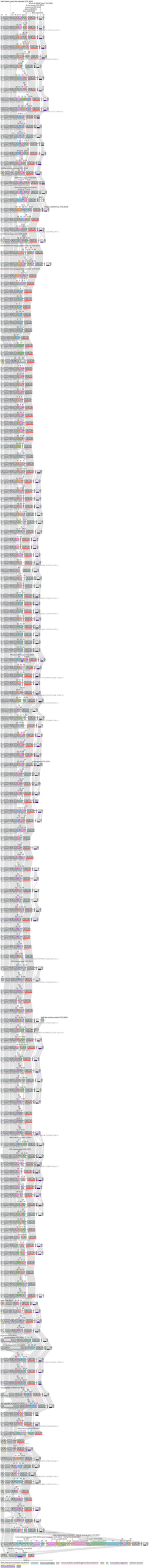

MarR family transcription regulator (CDS_0045)
MTase_II_00048 Type (CDS_0058)
Rz-like spanin (CDS_0057)
endolysin (CDS_0056)
holin (CDS_0055)
holin (CDS_0054)
tRNA-Met(CAT)
TemPhD_cluster_35164:33,139-41,603 (+)
Ma_2019_SRR1778455_NODE_250_length_47689_cov_23.373536:33,130-41,649 (+)
TemPhD_cluster_58906:34,908-43,382 (+)
TemPhD_cluster_47357_:34,085-42,965 (+)
IMGVR_UViG_2529292719_000011|2529292719|2529300014:33,361-42,364 (+)
TemPhD_cluster_47739:33,718-41,642 (+)
TemPhD_cluster_34780:35,654-44,102 (+)
TemPhD_cluster_58985:34,615-43,015 (+)
uvig_123691:33,522-42,850 (+)
IMGVR_UViG_3300028976_000001|3300028976|Ga0169648_10108:11,737-21,065 (+)
TemPhD_cluster_53250:117-7,728 (-)
uvig_376343:31,416-39,408 (+)
MGV-GENOME-0307937:34,705-42,695 (+)
TemPhD_cluster_34057:58-8,509 (-)
uvig_213829:33,778-42,613 (+)
TemPhD_cluster_53217:9,601-17,508 (+)
Holliday junction resolvase (CDS_0046)
TemPhD_cluster_31499:34,866-42,859 (+)
HNH endonuclease (CDS_0025)
TemPhD_cluster_65291:8,600-17,214 (+)
HNH endonuclease (CDS_0052)
TemPhD_cluster_47711_:32,727-41,723 (+)
TemPhD_cluster_20234:33,777-42,302 (+)
TemPhD_cluster_34945:33,554-43,000 (+)
MTase_II_00048 Type (CDS_0063)
TemPhD_cluster_34901:33,866-41,844 (+)
IMGVR_UViG_2744055167_000001|2744055167|2744121902:33,619-42,124 (+)
HTH DNA binding protein (CDS_0030)
MGV-GENOME-0261227:23,891-32,625 (+)
phosphoadenosine phosphosulfate reductase (CDS_0021)
TemPhD_cluster_65108:8,913-17,136 (+)
TemPhD_cluster_58815:33,801-43,671 (+)
phosphoadenosine phosphosulfate reductase (CDS_0012)
TemPhD_cluster_38520:1,337-8,280 (-)
TemPhD_cluster_65261:1,281-7,850 (-)
TemPhD_cluster_26543:1,381-7,455 (-)
TemPhD_cluster_65429:9,172-15,268 (+)
TemPhD_cluster_65534:1,315-7,154 (-)
TemPhD_cluster_47150:35,918-41,844 (+)
TemPhD_cluster_53475:1,388-7,438 (-)
TemPhD_cluster_31598:33,847-39,955 (+)
uvig_436758:10,207-15,710 (-)
TemPhD_cluster_65374:9,256-15,500 (+)
TemPhD_cluster_53321:1,299-7,545 (-)
MGV-GENOME-0301189:32,683-39,265 (+)
TemPhD_cluster_53343:1,281-7,478 (-)
TemPhD_cluster_53427:8,399-14,596 (+)
TemPhD_cluster_65424:9,108-15,326 (+)
TemPhD_cluster_65457:8,964-15,136 (+)
TemPhD_cluster_25085:1,382-7,386 (-)
TemPhD_cluster_53392:1,381-7,646 (-)
TemPhD_cluster_65515:8,670-14,935 (+)
TemPhD_cluster_65541:1,389-7,709 (-)
TemPhD_cluster_65540:8,417-14,736 (+)
TemPhD_cluster_65381:9,205-15,524 (+)
TemPhD_cluster_34857:35,746-41,781 (+)
TemPhD_cluster_53400:8,505-14,830 (+)
TemPhD_cluster_65425:1,306-7,783 (-)
TemPhD_cluster_47335_:34,789-42,855 (+)
TemPhD_cluster_47665_:34,026-41,769 (+)
TemPhD_cluster_31523:34,159-42,003 (+)
TemPhD_cluster_34998:34,451-42,294 (+)
TemPhD_cluster_59177:34,105-42,006 (+)
TemPhD_cluster_59234:33,750-41,873 (+)
TemPhD_cluster_47555_:33,912-42,148 (+)
TemPhD_cluster_59272:33,637-41,702 (+)
TemPhD_cluster_29030:34,446-41,743 (+)
TemPhD_cluster_29029:34,446-41,743 (+)
TemPhD_cluster_47207:35,490-43,220 (+)
IMGVR_UViG_2740892231_000005|2740892231|2740960188:35,312-43,148 (+)
uvig_224040:32,259-39,714 (+)
TemPhD_cluster_23294:34,696-42,710 (+)
TemPhD_cluster_59134:34,159-41,994 (+)
IMGVR_UViG_2579778554_000001|2579778554|2579784522:33,834-41,542 (+)
MGV-GENOME-0256859:24,137-31,866 (+)
IMGVR_UViG_2537561933_000001|2537561933|2537609812:32,784-40,484 (+)
TemPhD_cluster_47410_:34,444-42,278 (+)
IMGVR_UViG_2630968533_000001|2630968533|2631001869:33,750-41,520 (+)
MGV-GENOME-0303181:33,853-41,550 (+)
TemPhD_cluster_34988:34,784-42,533 (+)
TemPhD_cluster_47293_:35,233-42,953 (+)
MTase_II_00074 Type (CDS_0052)
TemPhD_cluster_47440_:33,718-42,421 (+)
TemPhD_cluster_59019:34,992-42,953 (+)
IMGVR_UViG_3300045988_142044|3300045988|Ga0495776_029904:33,686-41,423 (+)
TemPhD_cluster_47478_:34,711-42,376 (+)
IMGVR_UViG_3300015184_000003|3300015184|Ga0183236_119762:31,584-39,347 (+)
IMGVR_UViG_2529292882_000007|2529292882|2529383995:35,137-43,497 (+)
MGV-GENOME-0308195:34,591-41,291 (+)
IMGVR_UViG_2529292906_000001|2529292906|2529362875:33,244-41,746 (+)
TemPhD_cluster_59040:34,546-42,777 (+)
TemPhD_cluster_58998:34,713-42,849 (+)
TemPhD_cluster_31554:34,104-42,070 (+)
TemPhD_cluster_31533:34,308-42,219 (+)
Rz-like spanin (CDS_0060)
TemPhD_cluster_29056:34,054-42,223 (+)
TemPhD_cluster_35130:34,159-41,753 (+)
TemPhD_cluster_35131:34,159-41,950 (+)
TemPhD_cluster_47728_:34,120-41,715 (+)
TemPhD_cluster_26541:117-7,455 (-)
TemPhD_cluster_47544_:34,164-42,366 (+)
TemPhD_cluster_40287:33,737-41,746 (+)
TemPhD_cluster_65537:8,220-14,816 (+)
TemPhD_cluster_53367:9,255-15,038 (+)
TemPhD_cluster_47469_:34,602-42,237 (+)
TemPhD_cluster_44833:8,397-14,758 (+)
TemPhD_cluster_59178:34,761-42,272 (+)
TemPhD_cluster_40449:33,281-40,691 (+)
TemPhD_cluster_47520_:34,780-42,285 (+)
TemPhD_cluster_40270:34,521-41,883 (+)
MGV-GENOME-0290443:30,285-38,070 (+)
TemPhD_cluster_47743:34,081-41,421 (+)
TemPhD_cluster_53488:8,469-14,232 (+)
TemPhD_cluster_65655:1,323-7,081 (-)
TemPhD_cluster_38572:8,454-14,451 (+)
IMGVR_UViG_2740892219_000006|2740892219|2740959034:32,206-38,473 (+)
HNH endonuclease (CDS_0053)
TemPhD_cluster_59305:33,330-41,573 (+)
IMGVR_UViG_2737471829_000005|2737471829|2737497565:30,686-38,434 (+)
TemPhD_cluster_53359:8,913-15,034 (+)
TemPhD_cluster_65491:9,063-14,970 (+)
TemPhD_cluster_34080:9,099-15,366 (+)
ParB-like partition protein (CDS_0063)
IMGVR_UViG_2541047840_000001|2541047840|2541174724:34,562-43,011 (+)
IMGVR_UViG_3300045988_149348|3300045988|Ga0495776_094697:31,785-39,175 (+)
TemPhD_cluster_59119:34,556-42,490 (+)
TemPhD_cluster_29046:33,801-42,142 (+)
uvig_576709:34,585-42,105 (+)
MGV-GENOME-0281178:28,480-36,250 (+)
MGV-GENOME-0305299:33,957-42,087 (+)
TemPhD_cluster_59205:33,978-41,900 (+)
TemPhD_cluster_29094:33,760-41,550 (+)
TemPhD_cluster_44791:9,038-15,161 (+)
TemPhD_cluster_44761:1,382-7,506 (-)
IMGVR_UViG_2541047728_000005|2541047728|2541169738:33,999-41,764 (+)
HNH endonuclease (CDS_0051)
uvig_531573:31,329-39,767 (+)
HNH endonuclease (CDS_0039)
MGV-GENOME-0267217:25,167-33,528 (+)
IMGVR_UViG_2681813146_000002|2681813146|2681858354:33,807-41,812 (+)
uvig_429698:34,803-42,510 (+)
uvig_429141:34,903-43,238 (+)
TemPhD_cluster_47371_:34,586-42,666 (+)
TemPhD_cluster_59535:33,158-40,987 (+)
TemPhD_cluster_47689_:33,553-41,877 (+)
TemPhD_cluster_40220:33,616-41,941 (+)
TemPhD_cluster_65518:1,303-7,981 (-)
TemPhD_cluster_28962:33,992-40,757 (+)
TemPhD_cluster_23302:33,839-40,772 (+)
TemPhD_cluster_59144:34,135-42,240 (+)
TemPhD_cluster_40129:33,870-42,165 (+)
TemPhD_cluster_65478:1,335-7,972 (-)
TemPhD_cluster_65511:8,417-14,876 (+)
TemPhD_cluster_65228:9,561-16,342 (+)
MGV-GENOME-0307091:34,448-42,883 (+)
toxin (CDS_0031)
TemPhD_cluster_61727:24,122-31,333 (+)
TemPhD_cluster_14594:24,918-32,669 (+)
TemPhD_cluster_22697:25,148-33,130 (+)
TemPhD_cluster_50392:25,150-32,836 (+)
tail protein (CDS_0021)
tail fiber protein (CDS_0022)
MGV-GENOME-0222935:16,662-25,875 (+)
tail fiber protein (CDS_0021)
MGV-GENOME-0220084:15,545-25,526 (+)
IMGVR_UViG_3300045988_155859|3300045988|Ga0495776_116914:34,018-42,365 (+)
TemPhD_cluster_18352:33,912-42,243 (+)
TemPhD_cluster_65330:9,002-15,825 (+)
tail collar fiber protein (CDS_0022)
MGV-GENOME-0223382:16,662-26,089 (+)
tail collar fiber protein (CDS_0022)
MGV-GENOME-0228913:16,662-27,062 (+)
TemPhD_cluster_65306:1,381-7,396 (-)
IMGVR_UViG_2802429253_000004|2802429253|2802452538:35,016-42,640 (+)
HNH endonuclease (CDS_0009)
TemPhD_cluster_38856:1,381-9,495 (-)
TemPhD_cluster_66021:7,883-12,511 (+)
TemPhD_cluster_40559:33,589-39,863 (+)
IMGVR_UViG_2698536573_000004|2698536573|2698570673:30,857-38,668 (+)
TemPhD_cluster_59490:33,475-41,065 (+)
IMGVR_UViG_2778261458_000002|2778261458|2778311971:34,358-41,199 (+)
IMGVR_UViG_2585427870_000005|2585427870|2585474084:31,392-39,174 (+)
TemPhD_cluster_65734:8,279-13,802 (+)
TemPhD_cluster_53490:1,325-7,424 (-)
TemPhD_cluster_39821:34,168-41,913 (+)
TemPhD_cluster_47516_:34,426-42,272 (+)
IMGVR_UViG_2913186981_000002|2913186981|2913186994:31,380-39,889 (+)
major head protein (CDS_0064)
internal virion protein (CDS_0069)
transcriptional regulator (CDS_0056)
head-tail adaptor (CDS_0061)
tail protein (CDS_0067)
protease (CDS_0063)
internal virion protein (CDS_0070)
tail protein (CDS_0068)
endolysin (CDS_0071)
IMGVR_UViG_3300029841_000009|3300029841|Ga0245272_100538:33,723-62,502 (+)
MTase_II_00030 Type (CDS_0050)
TemPhD_cluster_27084:32,627-39,180 (+)
10000 nt
DNA, RNA and nucleotide metabolism
connector
head and packaging
lysis
moron, auxiliary metabolic gene and host takeover
other
tail
transcription regulation
unknown function
defence (PADLOC)
tRNA