Predicted Antitoxin (Blue Pentagon) Domain ID: D29
-- RefSeq Protein Description: ATP-binding protein
-- TADB Annotation: No Hit
-- NCBI-CDD Annotation: AAA_21
-- HHpred(Pfam) Annotation: AAA_21 ; AAA domain, putative AbiEii toxin, Type IV TA system (98.89%)
-- HHpred(PDB) Annotation: DNA double-strand break repair rad50 (95.83%)

Predicted Toxin (Red Pentagon) Domain ID: D60
-- RefSeq Protein Description: hypothetical protein
-- TADB Annotation: No Hit
-- NCBI-CDD Annotation: No Hit
-- HHpred(Pfam) Annotation: Rota_NS35 ; Rotavirus non-structural protein 35 (67.71%)
-- HHpred(PDB) Annotation: Nonstructural protein 2 (74.87%)

Merdibacter massiliensis (TA-Like pair: WP_075878177.1 & WP_075878176.1)
Companilactobacillus suantsaicola (TA-Like pair: WP_167849802.1 & WP_135373257.1)
Fusobacterium periodonticum (TA-Like pair: WP_005965355.1 & WP_005965353.1)
Streptococcus agalactiae 2603V R (TA-Like pair: WP_000491711.1 & WP_000010056.1)
Natranaerovirga hydrolytica (TA-Like pair: WP_165868507.1 & WP_132281291.1)
Candidatus Arthromitus sp SFB mouse Japan (TA-Like pair: WP_005807578.1 & WP_005807576.1)
Enterococcus pernyi (TA-Like pair: WP_084812821.1 & WP_062804783.1)
Enterococcus columbae DSM 7374   ATCC 51263 (TA-Like pair: WP_016183475.1 & WP_016183474.1)
Oenococcus phage phi9805 (TA-Like pair: YP_009005170.1 & YP_009005171.1)
Eubacterium xylanophilum ATCC 35991 (TA-Like pair: WP_026836119.1 & WP_026836118.1)
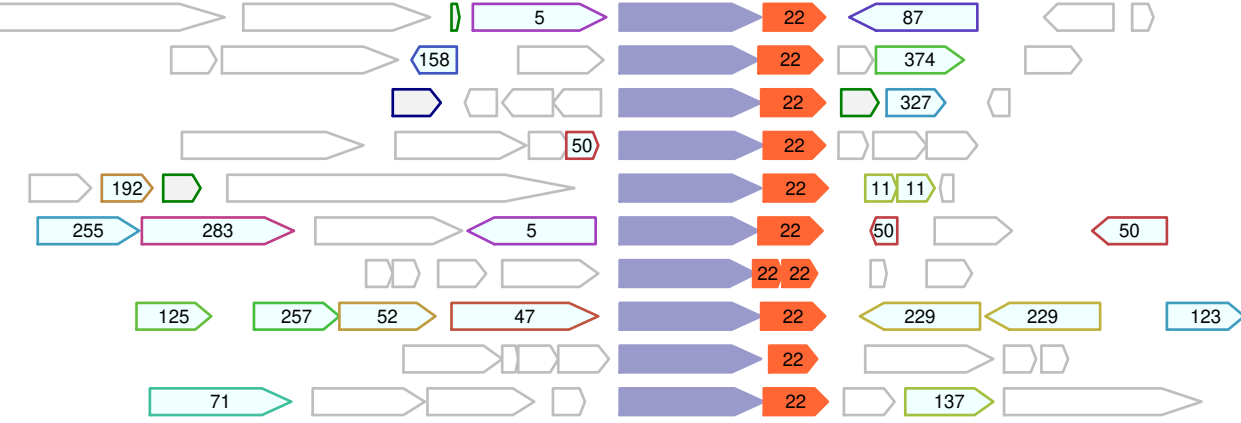
** For the description of flanking genes, please check this link: http://130.235.240.53/NetFlax/T8_pdfs/D60.txt