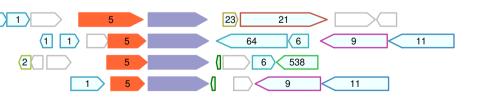
Predicted Antitoxin (Blue Pentagon) Domain ID: D95

- -- RefSeq Protein Description: site-specific integrase
- -- TADB Annotation: No Hit
- -- NCBI-CDD Annotation: Phage_int_SAM_3_DNA_BRE_C superfamily
- -- HHpred(Pfam) Annotation: Phage_integr_3; Archaeal phage integrase (97.47%)
- -- HHpred(PDB) Annotation: Int protein/DNA Complex (99.04%)

Predicted Toxin (Red Pentagon) Domain ID: M170

- -- RefSeq Protein Description: Ltp family lipoprotein
- -- TADB Annotation: No Hit
- -- NCBI-CDD Annotation: rplD superfamily_SAP
- -- HHpred(Pfam) Annotation: SAP_new25; SAP domain-containing new25 (88.16%)
- -- HHpred(PDB) Annotation: N-ADA 10 (DNA METHYLPHOSPHOTRIESTER REPAIR (95.12%)

Megamonas funiformis (TA-Like pair: WP_008538044.1 & WP_008538045.1)
Staphylococcus schweitzeri (TA-Like pair: WP_047549462.1 & WP_047549465.1)
Tepidiforma bonchosmolovskayae (TA-Like pair: WP_192498061.1 & WP_158066073.1)
Jeotgalibaca porci (TA-Like pair: WP_166063663.1 & WP_166063662.1)



For the description of flanking genes, please check this link: http://130.235.240.53/NetFlax/Mini_pdfs/M170.txt