Predicted Toxin (Red Pentagon) Domain ID: D169
-- RefSeq Protein Description: type II toxin-antitoxin system VapC family toxin
-- TADB Annotation: VapC PAE0151; PubMed: 22539524
-- NCBI-CDD Annotation: PIN_Pae0151-like
-- HHpred(Pfam) Annotation: PIN ; PIN domain (96.66%)
-- HHpred(PDB) Annotation: VapC toxin, VapB antitoxin (96.60%)

Predicted Antitoxin (Blue Pentagon) Domain ID: M229
-- RefSeq Protein Description: tyrosine-type recombinase/integrase
-- TADB Annotation: No Hit
-- NCBI-CDD Annotation: Phage_int_SAM_1 superfamily_DNA_BRE_C superfamily
-- HHpred(Pfam) Annotation: Phage_integrase ; Phage integrase family (98.73%)
-- HHpred(PDB) Annotation: RECOMBINASE CRE/DNA Complex (99.69%)

Belnapia moabensis DSM 16746 (TA-Like pair: WP_043341653.1 & WP_043341654.1)

Gemmata massiliana (TA-Like pair: WP_162666631.1 & WP_197909461.1)

Fimbriiglobus ruber (TA-Like pair: WP_088253274.1 & WP_088253275.1)
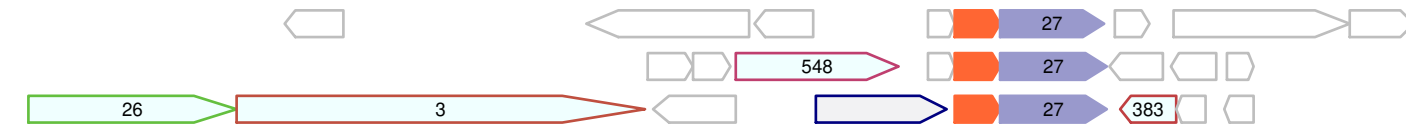
** For the description of flanking genes, please check this link: http://130.235.240.53/NetFlax/Mini_pdfs/M229.txt