

Predicted Antitoxin (Blue Pentagon) Domain ID: D26

-- RefSeq Protein Description: ribbon-helix-helix protein, CopG family

-- TADB Annotation: No Hit

-- NCBI-CDD Annotation: No Hit

-- HHpred(Pfam) Annotation: RHH_7 ; Transcriptional regulator, RHH-like, CopG (83.27%)

-- HHpred(PDB) Annotation: MNT REPRESSOR MUTANT WITH C-TERMINAL (90.40%)

Predicted Toxin (Red Pentagon) Domain ID: M54

-- RefSeq Protein Description: type II toxin-antitoxin system RelE/ParE family toxin

-- TADB Annotation: Possible toxin ParE1 ; PubMed: 19016878

-- NCBI-CDD Annotation: ParE_toxin

-- HHpred(Pfam) Annotation: ParE_toxin ; ParE toxin of type II toxin-antitoxin system, parDE (96.40%)

-- HHpred(PDB) Annotation: Inosine-guanosine kinase (97.60%)

Erwinia tracheiphila PSU 1 (TA-Like pair: WP_016192195.1 & WP_016192194.1)

Candidatus Accumulibacter aalborgensis (TA-Like pair: WP_186407814.1 & WP_186407815.1)



For the description of flanking genes, please check this link: http://130.235.240.53/NetFlax/Mini_pdfs/M54.txt