Predicted Toxin (Red Pentagon) Domain ID: D5

-- RefSeq Protein Description: hypothetical protein

-- TADB Annotation: No Hit

-- NCBI-CDD Annotation: No Hit

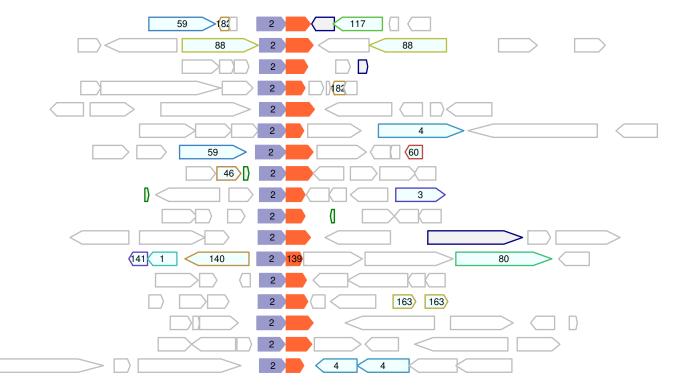
-- HHpred(Pfam) Annotation: S 4TM; SMODS-associating 4TM effector domain (80.15%)

-- HHpred(PDB) Annotation: No Hit

Bifidobacterium cuniculi DSM 20435 (TA-Like pair: WP 051920412.1 & WP 033515059.1) Curtobacterium oceanosedimentum (TA-Like pair: WP 058728014.1 & WP 058728015.1) Buttiauxella gaviniae ATCC 51604 (TA-Like pair: WP 064519104.1 & WP 064519101.1) Gordonia phage Kita (TA-Like pair: YP_009301393.1 & YP_009301394.1) Rhodococcus maanshanensis NBRC 100610 (TA-Like pair: WP 143069427.1 & WP 072749567.1) Algibacillus agarilyticus (TA-Like pair: WP 111978515.1 & WP 111978514.1) Bifidobacterium samirii (TA-Like pair: WP 125968274.1 & WP 125968275.1) Rhodococcus oryzae (TA-Like pair: WP 136911880.1 & WP 136911879.1) Pseudoalteromonas rubra (TA-Like pair: WP 138538934.1 & WP 125562112.1) Glutamicibacter creatinolyticus (TA-Like pair: WP 138926158.1 & WP 138926157.1) Corynebacterium godavarianum (TA-Like pair: WP 167496761.1 & WP 154878615.1) Candidatus Deianiraea vastatrix (TA-Like pair: WP 146820201.1 & WP 146820200.1) Rhodococcus rhodnii (TA-Like pair: WP 010840176.1 & WP 010840063.1) Canibacter oris (TA-Like pair: WP 183304953.1 & WP 183304952.1) Peptostreptococcus canis (TA-Like pair: WP 185623267.1 & WP 185623268.1) Corynebacterium imitans (TA-Like pair: WP 038591754.1 & WP 038591751.1) Pseudoalteromonas rhizosphaerae (TA-Like pair: WP 149980754.1 & WP 149980753.1)

Predicted Antitoxin (Blue Pentagon) Domain ID: D25

- -- RefSeq Protein Description: ImmA/IrrE family metallo-endopeptidase
- -- TADB Annotation: No Hit
- -- NCBI-CDD Annotation: Peptidase_M78
- -- HHpred(Pfam) Annotation: Peptidase_M78; IrrE N-terminal-like domain (99.11%)
- -- HHpred(PDB) Annotation: IRRE PROTEIN (99.28%)



^{**} For the description of flanking genes, please check this link: http://130.235.240.53/NetFlax/T8 pdfs/D25.txt