

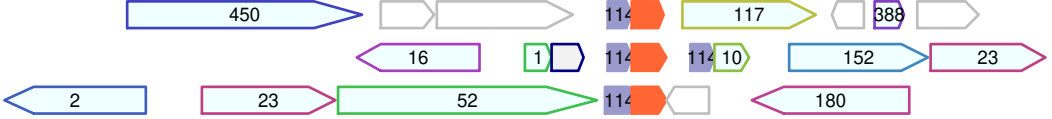
Predicted Toxin (Red Pentagon) Domain ID: D53
-- RefSeq Protein Description: type II toxin-antitoxin system RelE/ParE family toxin
-- TADB Annotation: Possible toxin ParE1; PubMed: 19016878
-- NCBI-CDD Annotation: ParE
-- HHpred(Pfam) Annotation: ParE_toxin ; ParE toxin of type II toxin-antitoxin system, parDE (97.21%)
-- HHpred(PDB) Annotation: Toxin protein parE-1, Antitoxin protein (98.97%)

Predicted Antitoxin (Blue Pentagon) Domain ID: M157
-- RefSeq Protein Description: hypothetical protein
-- TADB Annotation: No Hit
-- NCBI-CDD Annotation: No Hit
-- HHpred(Pfam) Annotation: No Hit
-- HHpred(PDB) Annotation: No Hit

Pedobacter kyungheensis (TA-Like pair: WP_143009650.1 & WP_039479981.1)

Gramella fulva (TA-Like pair: WP_107012785.1 & WP_107012784.1)

Parabacteroides acidifaciens (TA-Like pair: WP_115498388.1 & WP_115498387.1)



** For the description of flanking genes, please check this link: http://130.235.240.53/NetFlax/Mini_pdfs/M157.txt