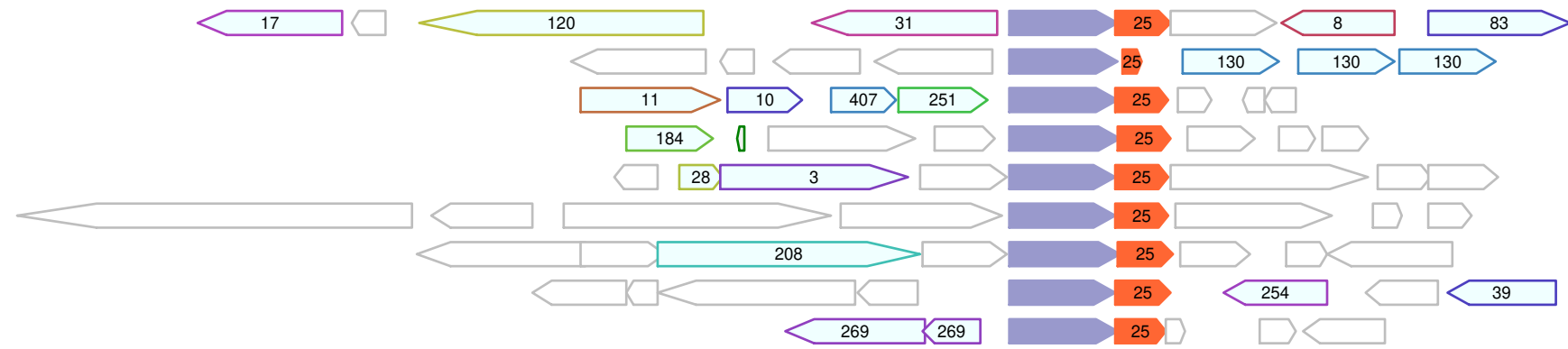


Predicted Antitoxin (Blue Pentagon) Domain ID: D29
-- RefSeq Protein Description: ATP-binding protein
-- TADB Annotation: No Hit
-- NCBI-CDD Annotation: AAA_21
-- HHpred(Pfam) Annotation: AAA_21 ; AAA domain, putative AbiEii toxin, Type IV TA system (98.89%)
-- HHpred(PDB) Annotation: DNA double-strand break repair rad50 (95.83%)

Predicted Toxin (Red Pentagon) Domain ID: D62
-- RefSeq Protein Description: hypothetical protein
-- TADB Annotation: No Hit
-- NCBI-CDD Annotation: No Hit
-- HHpred(Pfam) Annotation: DUF4276 ; Domain of unknown function (DUF4276) (92.83%)
-- HHpred(PDB) Annotation: No Hit

- Calothrix membranacea FACHB 236 (TA-Like pair: WP_190624116.1 & WP_190624117.1)
- Chondromyces apiculatus DSM 436 (TA-Like pair: WP_044237756.1 & WP_044237753.1)
- Desulfonatronovibrio magnus (TA-Like pair: WP_045213600.1 & WP_045213598.1)
- Tuwongella immobilis (TA-Like pair: WP_162660447.1 & WP_162660448.1)
- Candidatus Methylobacter oryzae (TA-Like pair: WP_127028559.1 & WP_127028560.1)
- Fimbrioglobus ruber (TA-Like pair: WP_088251575.1 & WP_088251576.1)
- Polyangium spumosum (TA-Like pair: WP_153817670.1 & WP_153817671.1)
- Desulfocarbo indianensis (TA-Like pair: WP_082205282.1 & WP_152961325.1)
- Candidatus Marithrix sp Canyon 246 (TA-Like pair: WP_069471169.1 & WP_069471170.1)



** For the description of flanking genes, please check this link: http://130.235.240.53/NetFlax/T8_pdfs/D62.txt