

SUBTRACTIVE GENOMIC APPROACH TO IDENTIFY POTENTIAL DRUG TARGETS AND ACTIVE SITES IN *CHLAMYDOPHILA PNEUMONIAE*

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Abstract

Whole genome sequences of the human pathogen *Chlamydomphila pneumoniae* and four other strains of same species were analyzed to identify common drug targets. A subtractive genomic approach is applied to identify Holliday junction DNA helicase RuvB as the common non-human homologous gene among these four strains. A three-dimensional model of the Holliday junction DNA helicase RuvB protein was generated with homology modelling. The protein is analysed for identification of suitable target sites.

Keywords: *Chlamydomphila pneumoniae*, BLAST, MSA, homologous, homology modeling, active site