Original Research

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Functional classification of hypothetical proteins from the proteome of Chlamydia pneumoniae to characterize potential drug targets

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Abstract: Chlamydia pneumoniae is an intracellular gram-negative bacterium. C. pneumoniae is non-motile and has a spherical shape and causes serious respiratory illnesses has already been linked to atherosclerosis, asthma and arthritis, along with other chronic conditions. Regardless of the fact that therapies exist to cure chlamydial infections, no drug has still proved to be value enough to eradicate the bacteria in developing nations, and an effective vaccine is far from certain. Functional characterization is critical for establishing the function of proteins during proteome analysis. Meanwhile, the function of a large number of proteins remains unknown. As a result, these molecules are referred to as fictitious proteins (HPs). C. pneumoniae has a proteome of 1,028 proteins, including 245 hypothetical proteins (HPs) that have been functionally classified by using Pfam and CDD tool. We are able to identify functions of 24 HPs having function in secretion system, flagellar synthesis and some are involved in lipopolysaccharide synthesis. The proposed study also identified the Physico-chemical properties of putative HPs and prediction of localization of HPs in the cell was done by using CELLO tool. Further analysis leads the current study to the conclusion that out of 24 HPs only 19 proteins are found to be virulent. The human proteome was also cross-referenced with these HPs to check for the similarity using NCBI BLASTp. This research implies that these hypothetical proteins are important for the organism's proliferation and pathogenicity. As a result, they can be utilized to forecast probable medication interactions.

Keywords: Chlamydia pneumoniae, Pfam, Hypothetical Proteins, Virulent, Homology.