



**INSILICO FUNCTION PREDICTION OF A HYPOTHETICAL PROTEIN FROM
*PLASMODIUM CYNOMOLGI*****ABID W, HUSSAIN Z*, ALI N AND JAVED A**

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*Corresponding author: E Mail: zahidbiotech69@gmail.comReceived 18th Oct. 2016; Revised 20th Nov. 2016; Accepted 23rd Jan. 2017 Available online 1st June 2017**ABSTRACT**

Hypothetical proteins are the proteins which are not characterized or assign no function. Hypothetical proteins are the proteins which are not experimentally identified. These proteins can be predicted insilico using bioinformatics tools. These tools use homology base detection of function which consider as gold-standard until the absence of experimental evidences. A hypothetical protein XP_004225232.1 is selected from the *plasmodium cynomolgi* for predicting its function using bioinformatics tools. Bioinformatics tools including BLAST, HHpred, CATH, PHYRE2 and FATCAT. These tools accept protein query to search for the proteins homologous to the query. Based on the analysis by these tools the protein is signal recognition particle receptor beta subunit. Signal recognition particle proteins help in the protein translocation to the endoplasmic reticulum membrane of the cell. The analysis helps in understanding the functionality and importance of the protein. Further experimental studies are needed to explain the protein functionality at chemical level.

Keywords: Hypothetical protein, HHpred, CATH, PHYRE2, FATCAT, homology**INTRODUCTION**

Proteins are the functional subunits of living system. The genomic studies and sequencing methods flooded the database with hypothetical proteins (Ian *et al.*, 2015). Conserved hypothetical proteins are the large fraction of protein which are not functionally

described or characterized at protein chemical level (Michael and Eugene, 2004). Even after several efforts only 50-60% genes are annotated or assigned with known function of the most completely sequenced genomes (Selvarajan and Piramanayagam,