

Chapter in Book

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In this paper, the *Anopheles gambiae* ABCC12 MRP protein domain sequence which contained 216 residues was obtained from the NCBI database in its fasta format (NCBI entry EAA12438.4). This MRP protein sequence was Gapped Blast using BLOSUM 62 matrix with an E-value cut-off of 0.000001 to identify the closest homologous structure as at the date of the study (Nov 2016). Additionally, the sequence was aligned with three prediction modelers, which are the Modeller v9.15 alignment script, the Swiss Model Server and the Raptor-X server for modelling based on the server's automated choice for a suitable template. The structure predicted by Raptor-X has a higher percentage (90.1%) of residues in the most favored regions as compared to Modeller and Swiss-Model (86.5%). This paper further unveils the quality of structure predicted during homology modeling and the diverse correlation as well as the significance of ABCC12 in drug design for malaria vector.