Title of Article : In-silico evaluation of malaria drug targets.

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Abstract: The most severe form of malaria, a disease that affects over 300 million people annually, is caused by the single-celled parasite Plasmodium falciparum. It is most prominent in Africa and has led to the death of millions of people. Studies have also shown that the low level of resistance to this disease in children has made them susceptible to malaria. Anti-malarial drugs have been developed to target specific sites in the pathway of Plasmodium falciparum but due to the level of resistance that the organism has developed, essential drug target sites have to be identified of which Plasmodium falciparum would have low or no resistance. In a recent publication, 22 potential drug targets based on an automated metabolic pathway database called PlasmoCyc were predicted. However, in a more recent publication, a critical evaluation of the comparison of a manual reconstruction database (Malaria Parasite Metabolic Pathways) against pathways generated automatically like PlasmoCyc, MetaSHARK and KEGG (Kyoto Encyclopedia for Genes and Genomes) was done. The study shows that the automatically generated pathways/databases need an expert manual verification. We employed extraction-programming techniques to create an enhanced PlasmoCyc database and a comparison technique to identify and evaluate these drug targets in their pathways and then employed the homology modeling technique to model their structures.