Summary and Conclusions
Conclusions

P-loop NTPases comprise one of the largest protein families with members present in all kingdoms of life. Numerous subgroups of the family are involved in diverse cellular functions. The functional roles of a number of families belonging to P-loop NTPases superfamily are still unknown in eukaryotes. The repertoire of the P-loop NTPase has not been identified and classified in *P. falciparum*. The challenge of studying and classifying these NTPases further increases in *P. falciparum* due to low sequence similarity and unique features of the genome such as extended insertions and repeats. In the present study, a systematic classification of the P-loop NTPases in *P. falciparum* genome is carried out, that provided information on their function, classification, phylogenetic and orthologous relationships amongst various protein families and organisms. Variations in critical residues within the conserved regions as well as long insertions are observed in the P-loop NTPase domain for most of the *P. falciparum* NTPases suggesting that the parasite has evolved constantly to sustain inspite of the mutations/variations in these imperative regions. The study provided an understanding of the P-loop NTPases, especially in terms of their structural and functional relationships. The proteins with similar functional roles are observed to have similar sequence and structure pattern of P-loop domain. Based on this, putative functional roles for 14 hypothetical proteins are predicted. This is one of the key findings of the study pertaining to the fact that most of *P. falciparum* proteins are not homologous to any other eukaryotic protein and have been annotated as hypothetical proteins. Therefore, elucidation of putative roles of these proteins that are unique to the parasite may provide leads to identify novel drug targets. The sequence orthology based studies are found to be useful in identifying P-loop NTPases either similar to prokaryotic origin or restricted to *Plasmodium* species. Such P-loop NTPases involved in important physiological pathways may lead to identification of new drug targets. It must be emphasized that the current study demonstrates the possible achievements of a computational analysis and is a preliminary investigation. Experimental evidence to explore the role of these genes is thus required. It becomes mandatory in the case of *P. falciparum*
where new functional roles have been predicted for a significant number of hypothetical proteins inspite of very low levels of sequence similarity. Overall the study provides us new leads in investigating the functions and biology of *P. falciparum* P-loop NTPases