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Indian Consortium of Macromolecular Crystallography
(Funded by the Department of Biotechnology
Government of India)

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Proposal Details

Title of the Project:

Structural analysis of the antimalarial drug target prolyl trna synthetase inhibitor complexes.

Abstract for lay readers:

Aminoacyl tRNA synthetases (aaRSs) drive protein translation in cells and hence these are essential enzymes across life. Inhibition of these enzymes can halt growth of an organism by stalling protein translation. Therefore, small molecule targeting the aaRS active sites is an attractive avenue from the perspective of developing anti-malarials. The current work on prolyl tRNA synthetase from plasmodium falciparum, the causative agent of severe malaria will result in newer understanding of this target. This knowledge will help in the development of newer antimalarials.

Abstract for reviewers:

Malaria is caused by a parasitic protozoan, plasmodium falciparum. This work focuses on malaria and in particular the development and validation of novel antimalarial drug targets. Work on Plasmodial protein prolyl-tRNA synthetase (PfPRS) in complex with newer HF based derivatives will result in newer understanding of this target-inhibitor complex. This will guide towards developing better and more potent and less toxic drug like molecules.

Details of Crystals:

Protein name	:	PfPRS
Source organisms	:	Plasmodium falciparum
Crystals tested at home source	:	Yes
Resolution at home source	:	3.6
Mosaicity	:	1.1
Anisotropy	:	0.05
Cell parameters:		
a=	:	81
b=	:	89
c=	:	86
α=	:	90
β=	:	97
γ=	:	90
Space group	:	p21
Crystallization conditions	:	1.5 M LiSo4 and hepes 100 mM ph 7.5
Cryo conditions	:	glycerol 20%
Xenon Freezing	:	No
Whether for SAD / MAD dataset	:	No
Heavy Atom	:	Mg
Any other details		