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Title of the Project

Structural analysis of the anti-malarial drug target arginyl-tRNA synthetase

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 malaria, includes the development and validation of novel anti-malarial drug target. Work on arginyl-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 new and potent anti-malarials.

Abstract for reviewers

Plasmodium falciparum is a parasitic protozoan that causes malaria. Small compounds inhibiting aminoacyl-trna synthetase enzymes can halt the parasite growth. This work focuses on malaria and in particular the development and validation of novel antimalarial drug targets. Work on Plasmodial protein arginyl-tRNA synthetase (PfRRS) will result in newer understanding of this target. The work include determining the subtle differences in the active site compared with the human enzyme so, overall the 3-D structures will greatly enhance the current understanding of the crucial enzymes of the protein translation machinery.

Details of Crystals:

Protein name	: Arginyl-tRNA synthetase
Source organisms	: Plasmodium falciparum
Crystals tested at home source	: Yes
Resolution at home source	: 3.5
Mosaicity	: 1
Anisotropy	: 0.04
Cell parameters	
a=	: 46
b=	: 62
c=	: 114
α=	: 90
β=	: 95
γ=	: 90
Space group	: P2
Crystallization conditions	: 10% peg6000 and 5% MPD, 0.1 M hepes 7.5
Cryo conditions	: Mother solution, glycerol
Xenon Freezing	: No
Whether for SAD / MAD dataset	: No
Heavy Atom	: Mg
Any other details	
Whether you Principal Investigator	: No

PI Name (Full name)* : Dr. Amit Prakash sharma
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Choice of Reviewers (any five):

- 1
- 2 D.M Salunke
- 3
- 4
- 5 B Gopal
- 6 S.C Mande
- 7 R. Ravishankar
- 8
- 9 A.P Sharma

* Spine caps and sample holders should be purchased by the concerned labs.

* Individual users should mention Principal Investigator.

* In order to use therobotic sample changer, Indian crystallographers should acquire SPINE standard sample holders (caps+vials). These holders are special bar-coded caps with standard loop Lengths as well as special vials (with 2 metallic pieces) for the optimal and reliable usage of the robotic sample changer.

* Users with appropriate material will be able to load up to 50 frozen samples in the robot Dewar and then screen them remotely, while users who will not have the proper ones will have to load their samples one by one manually (a terrible loss of beam time).

* It is not essential to acquire the starter kits (with baskets) as we have baskets at the beamline that we can provide. The minimal material needed is then SPINE standard caps and vials, as well of course as a shipping dewar.

* A complete sample changer information web page can be found at: www.bm14.eu under the left menu link "Run an experiment / sample changer". Or directly at:
http://ns36904.ovh.net/joomla/index.php?option=com_content&view=article&id=76&Itemid=92

* Any request for more details or clarifications can be addressed to Dinakar Salunke (dinakar@nii.res.in) or Hassan Belrhali (belrhali@embl.fr).

Confirm

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