Tata Institute of Fundamental Research
Survey No. 36/P, Gopanpally Village, Serilingampally, Ranga Reddy Dist., Hyderabad – 500 046

Students' Annual Webinar

*Pf*RALP1: Structural characterization and identification of peptide/protein-based inhibitors

Akash Narayan

*Pf*RALP1 binds to an unknown receptor at the surface of human red blood cells (RBCs) during invasion and plays an essential role in the growth and development of malaria parasite. Initial studies have shown that *Pf*RALP1 is immunogenic, localises at moving junctions and contains bZIP as well as coiled-coil domains.[1,2] In this endeavour, characterisation and functional studies of recombinantly expressed fragments of *Pf*RALP1 have been carried out to find out the functionally active region(s) responsible for the invasion process. Taken together, the efforts are on to identify the potential functional region(s) of *Pf*RALP1 which is/are the natural binding site(s) and would possibly be targeted to inhibit parasite invasion into RBCs.

References:

[1] Haase, S.; Cabrera, A.; Langer, C.; Treeck, M.; Struck, N. et al. Characterization of a conserved rhoptry-associated leucine zipper-like protein in the malaria parasite *Plasmodium falciparum*. *Infect. Immun.* **2008.** *76*(3), 879–887.
[2] Ito, D.; Hasegawa, T.; Miura, K.; Yamasaki, T.; Arumugam, T. U.; Thongkukiatkul, A. et al. RALP1 Is a rhoptry neck erythrocyte-binding protein of *Plasmodium falciparum* merozoites and a potential blood-stage vaccine candidate antigen. *Infect. Immun.* **2013.** *81*(11), 4289–4298.

Friday, Apr 29th 2022

4:00 PM