

## MS03-P07 | STRUCTURAL AND BIOPHYSICAL ANALYSIS OF THE PYRIDOXAL PHOSPHATE SYNTHASE FROM *PLASMODIUM VIVAX*

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Malaria is still one of the leading causes of morbidity and mortality in developing countries, especially in Africa, but also in Asia and Latin America caused by *Plasmodium* species [1]. A potential drug target and till now mostly not analysed are the structurally unique enzymes of *Plasmodium spec.* involved in vitamin B<sub>6</sub> (pyridoxal 5-phosphate) biosynthesis. Vitamin-B<sub>6</sub> is synthesized by PLP synthase complex consisting of pyridoxal biosynthesis lyase (Pdx1) and glutamine amido-transferase (Pdx2) [2]. Pdx1 exist as hexamer–dodecamer equilibrium in solution formed by two interdigitating rings, each consisting of six Pdx1 molecules and Pdx2 subunits attach to the Pdx1 oligomer [3].

To study structure-function relationship and dynamicity of the Pdx1-Pdx2 complex bacterial expression, purification and biophysical characterization of both proteins were established. Initial characterization of the recombinant proteins was performed by size exclusion chromatography and dynamic light scattering revealing that the Pdx1 protein is monodisperse and dodecameric in solution, whereas, Pdx2 appears as both monomeric and multimeric. The complex formation was analysed by Nanoparticle tracking and small-angle X-ray scattering to obtain insights about the three-dimensional structure in solution.

Further, we obtained crystals of Pdx1 and the complex applying the vapor diffusion method. Diffraction data up to 2.5 Å applying synchrotron radiation were collected and processed.

Details about structure solution, final refinement and interpretation will be presented.

[1] Guédez *et al.* 2012 *Structure*, 20, 172–184.

[2] Sangwoo Kim and Kyung-Jin Kim. *Structural Biology and Crystallization Communications*, F69 (2013), 578–580.

[3] Neuwirth *et al.* 2009, *FEBS Letters*, 583, 2179–2186.