

Crystal Structure of Prostaglandin F_{2α} Synthase from *Leishmania Major*

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Leishmania major is the causative agent of leishmaniasis. A gene encoding prostaglandin F_{2α} synthase, catalyzing NADPH-dependent reduction of 9,11-endoperoxide PGH₂ to PGF_{2α} was identified from *L. major* (*LmPGFS*)[1]. In the previous study, we have crystallized prostaglandin F_{2α} synthase from *Trypanosoma brucei* (*TbPGFS*) using citrate as a precipitant and successfully solved the ternary structure of NADP⁺/citrate/*TbPGFS*[2]. We also attempted to solve the inhibitor complex of *TbPGFS*, but a citrate molecule strongly binds to the active site.

In this study we have successfully crystallized *LmPGFS* using PEG instead of citrate and determined the structure of *LmPGFS* in the unliganded form by the molecular replacement method at 1.8 Å resolution. Comparing the structure of *LmPGFS* with *TbPGFS*, we found that the overall structure and the catalytic residues are almost the same without the extra α-helix between β4 and α4. The structural analysis of inhibitor complex is in progress to develop drug preventing a miscarriage.

[1] Kabututu Z., *et al.*, *Int. J. Parasitol.*, 2003, **33**. [2] Kilunga B. K., *et al.*, *J. Biol. Chem.*, *in press*.

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