MS6-P2 Crystal structure of *Plasmodium falciparum* calmodulin / peptide complex

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Calmodulin, a ubiquitous calcium binding protein is present in all eukaryotic cells. It regulates the action of more than 100 proteins by interacting with them in a calcium dependent way. Both of its lobes contain two calcium binding EF-hand motifs. Ca^{2+} binding of the protein causes a global conformational change and exposure of hydrophobic patches on both domains capable for binding target proteins. Though the bound segments of the target possess basic amphiphilic helix conformation, the target orientation, distances of their anchoring residues and orientations of the calmodulin lobes varies within the complexes. Some calmodulin antagonist compounds were reported to inhibit *Plasmodium falciparum*, suggesting *P. falciparum* calmodulin could be a possible target of anti-malarial treatment. Structures of calmodulin and apocalmodulin from several species are known, but that of *P. falciparum* has not been published. Though calmodulin is a highly conserved protein, its structure explores differences between vertebrate and *P. falciparum* calmodulin.

We solved the structure of calmodulin from *P. falciparum* in complex with a model target peptide (melittin, a component of bee venom) and refined the structure to 2.4 Å resolution. The structure contains four calmodulin/melittin complex units showing two main binding modes of the peptide: there are some differences in the orientations of calmodulin lobes and binding patterns for the peptide. It is the flexibility of the middle short coil segment within the melittin helix that facilitates different binding modes to calmodulin. The structure suggests that interactions with the two calmodulin lobes are formed independently.

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Keywords: calcium signalling, protein/peptide complex, flexible binding, Plasmodium falciparum

MS6-P3 The molecular bases of δβ T-cell mediated antigen recognition

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αβ and γ**δ** T-cells are disparate T-cell lineages that, via their use of either αβ or γ**δ** T-cell antigen receptors (TCRs) respectively, can respond to distinct antigens. Here we characterise a new population of human T-cells, term **δβ** T-cells, that express TCRs comprising a TCR-**δ** variable gene fused to a Joining-α/Constant-α domain, paired with an array of TCR-**β** chains. We characterised the cellular, functional, biophysical and structural characteristic feature of this new T-cells population that reveal some new insight into TCR diversity. We provide molecular bases of how **δβ** T-cells can recognise viral peptide presented by Human Leukocyte Antigen (HLA) molecule. Our findings highlight how components from αβ and γ**δ**TCR gene *loci* can recombine to confer antigen specificity thus expanding our understanding of T-cell biology and TCR diversity.

Keywords: immunology, new T cell receptor, HLA