Structure of S-Adenosyl-L-Homocysteine Hydrolase from Plasmodium falciparum

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The human malaria parasite *Plasmodium falciparum* is responsible for the death of more than a million people each year. The emergence of strains of malarial parasite resistant to conventional drug therapy has stimulated searches for antimalarials with novel modes of action. *S*-Adenosy1-L-homocysteine hydrolase (SAHH) is a regulator of biological methylations. Inhibitors of SAHH affect the methylation status of nucleic acids, proteins, and small molecules. *Plasmodium falciparum* SAHH (PfSAHH) inhibitors are expected to provide a new type of chemotherapeutic agent against malaria. Despite the pressing need to develop selective PfSAHH inhibitors as therapeutic drugs, only the mammalian SAHH structures are currently available. Here, we report the crystal structure of PfSAHH complexed with the reaction product adenosine [1].

[1] Tanaka N., et al., *J. Mol. Biol.*, 2004, **343**, 1007-1017. Keywords: crystal structure, drug design, malaria