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Report:

Malaria, a disease caused by the parasite *Plasmodium falciparum*, is among the most widespread infectious diseases in the world, afflicting several hundred million and killing nearly 2 million people every year. *Plasmodium falciparum* invades erythrocytes and consumes nearly all of its host´s hemoglobin as asource of nutrients during growht and development. Two aspartic proteases have been implicated in the initial steps of the hemoglobin degradation process. The two proteases have sequence homology to mammalian aspartic proteases, such as cathepsin D and renin.

To provide a structural framework for subsequent structure-based design, we produced crystals of one of the aspartic proteases, plasmepsin II, in complex with pepstatin A, a general inhibitor to this class of bacterial proteases. As a part of this experimental visit we collected one native data set to 2.6 Å of this particular complex. The data quality was sufficient to solve the structure by molecular replacement using a previously solved plasmepsin structure as search model (Silva, A. M., *et al.*, 1996, *PNAS*, 93:100034-10039).