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LSC 3 - Life Sciences Centre

2350 Health Sciences Mall

12-1pm



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"Selective proteasome inhibitors as novel anti-malarial agents"

The proteasome is a multi-component protease complex responsible for regulating key processes such as the cell cycle and antigen presentation. Proteasome inhibitors have been shown to be toxic for the malaria parasite *Plasmodium falciparum* at all stages of its life cycle, including the transmissive gametocyte stages. However, all compounds that have been tested also inhibit the mammalian proteasome resulting in toxicity. We used a recently developed substrate profiling method to uncover differences in the specificities of the human and parasite 20S proteasome cores. We designed inhibitors based on amino acid preferences specific to the *P. falciparum* proteasome, and found that they preferentially inhibit the tryptic-like subunit $\beta 2$. We determined the structure of the *P. falciparum* 20S proteasome bound to our inhibitor using cryo-EM and single particle analysis, to a resolution of 3.6 Å. These data reveal the unusually open *P. falciparum* $\beta 2$ active site and provide valuable information regarding active site architecture that can be used to further refine inhibitor design. Furthermore, we observed growth inhibition synergism with low doses of this $\beta 2$ selective inhibitor in artemisinin (ART) sensitive and resistant parasites. Finally, we demonstrated that a parasite selective inhibitor attenuates parasite growth *in vivo* without significant toxicity to the host. Thus, the *Plasmodium* proteasome is a chemically tractable target for next generation anti-malarial agents.

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