

SUPPORTING INFORMATION

Generation of Lasso Peptide-based ClpP Binders

Imran T. Malik,¹ Julian D. Hegemann,^{2,*} and Heike Brötz-Oesterhelt^{1,3,*}

¹ Department of Microbial Bioactive Compounds, Interfaculty Institute of Microbiology and Infection Medicine, University of Tübingen, Auf der Morgenstelle 28, 72076 Tübingen, Germany.

² Helmholtz Institute for Pharmaceutical Research Saarland (HIPS), Helmholtz Centre for Infection Research (HZI), Saarland University Campus, 66123 Saarbrücken, Germany.

³ Cluster of excellence "Controlling Microbes to Fight Infection"

* Correspondence: jdhegemann@googlemail.com (J. D. H.); heike.broetz-oesterhelt@uni-tuebingen.de (H. B.-O.)

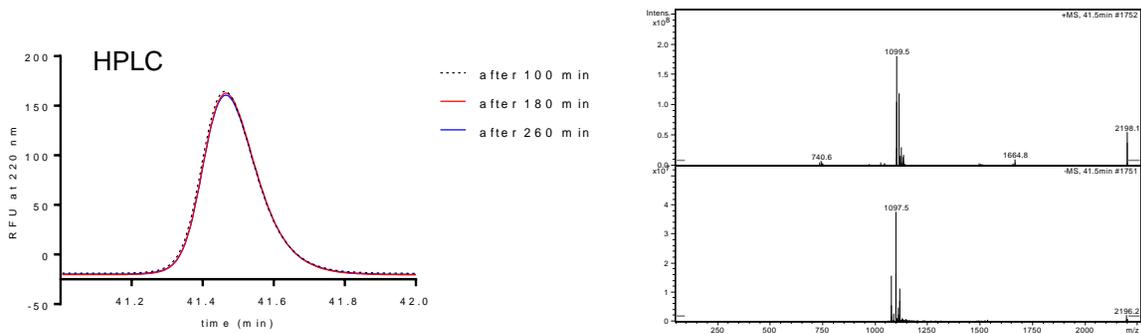


Figure S1. LC-MS analysis of SaClpP with 12IGF. SaClpP (1 μ M) and 12IGF (46 μ M) were incubated under *in vitro* assay conditions for up to 260 min and analyzed via HPLC. No reduction in 12IGF amounts could be observed. Identity of 12IGF (2196 kDa) was confirmed by mass spectrometry at a retention volume of 41.5 ml.

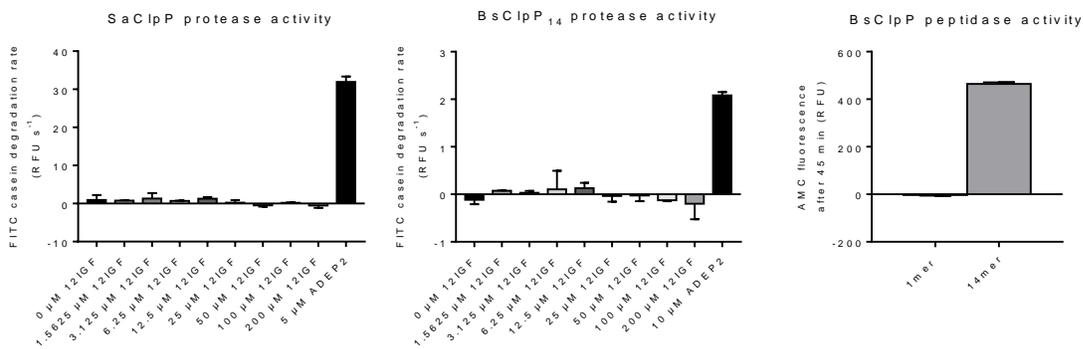


Figure S2. FITC-casein degradation by SaClpP and tetradecameric BsClpP (tetradecamer conditions applied as described in the main text) at different 12IGF concentrations and 5 μ M or 10 μ M ADEP2 as positive controls, respectively. No activation of casein degradation by 12IGF was detected. *Right panel*, the tetradecameric state of BsClpP was confirmed by stand-alone peptide hydrolysis (i. e. without addition of ADEP2 or 12IGF) with a monomeric preparation as a negative control.

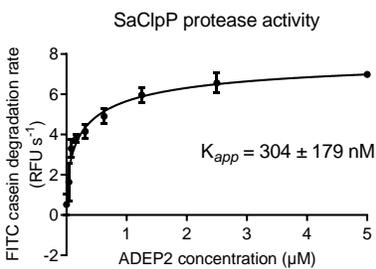


Figure S3. FITC-casein degradation by 100 nM of SaClpP at different ADEP2 concentrations.