SUPPLEMENTARY ONLINE DATA

Recombinant Deg/HtrA proteases from Synechocystis sp. PCC 6803 differ in substrate specificity, biochemical characteristics and mechanism

Pitter F. HUESGEN*†1, Helder MIRANDA‡1, XuanTam LAM‡1, Manuela PERTHOLD*, Holger SCHUHMANN*, Iwona ADAMSKA*‡2 and Christiane FUNK‡

*Department of Biology, University of Konstanz, Universitätsstrasse 10, 78457 Konstanz, Germany, †Centre for Blood Research, University of British Columbia, 2350 Health Sciences Mall, Vancouver, BC, Canada, V6T 1Z3, and ‡Department of Chemistry, Umeå University, Linnaeus Väg 6, 90187 Umeå, Sweden

Figure S1 Sequence alignment of Synechocystis 6803 HtrA (SspHtrA), HhaO (SspHhoA) and HhoB (SspHhoB) in comparison to E. coli DegP (EcDegP) and DegS (EcDegS) and human HtrA2/Omi (HsHtrA2)

Orange boxes indicate the first amino acid of the constructs of HtrA, HhaO and HhoB used in the present study. α-helices and β-sheets conserved in all proteins are represented by barrels and arrows respectively. Secondary-structure elements of the protease domain are displayed in green, elements of the first PDZ domain in yellow, and elements of the second PDZ domain in orange. Residues forming the catalytic triad are highlighted in blue.
**Figure S2**  Biochemical properties of rHtrA, rHhoA and rHhoB assayed with a fluorogenic casein substrate

In both panels, data points obtained for rHtrA are represented by diamonds, rHhoA by triangles and rHhoB by circles. Open symbols connected by broken lines indicate the absence, and filled symbols connected by continuous lines the presence, of divalent ions.  

(A) Degradation kinetics at 30°C measured in 10 mM Mes, pH 5.5, and 10 mM MgCl₂ using conditions and detector-gain settings as in Figure 6(D) in the main paper. In the presence of 10 mM MgCl₂, detector saturation was reached after 20 min for rHhoA and after 30 min for rHtrA.  

(B) Effect of Mg²⁺ ion concentration on proteolytic activity measured by the initial rate of fluorescence generation in 10 mM Mes buffer, pH 6.5, supplemented with indicated concentrations of MgCl₂, and normalized to the activity observed without added MgCl₂.

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