Supplementary Information

for

Allosteric regulation of DegS protease subunits though a shared energy landscape

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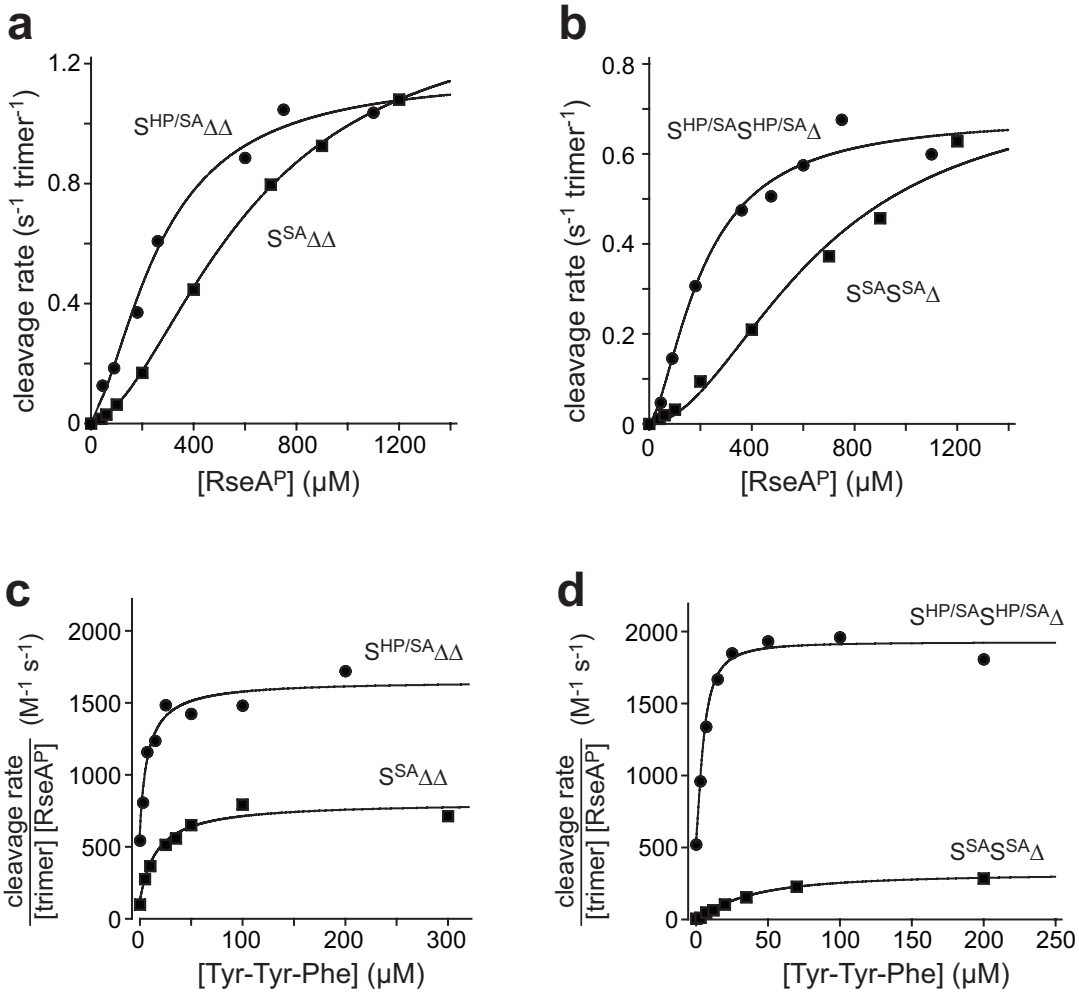
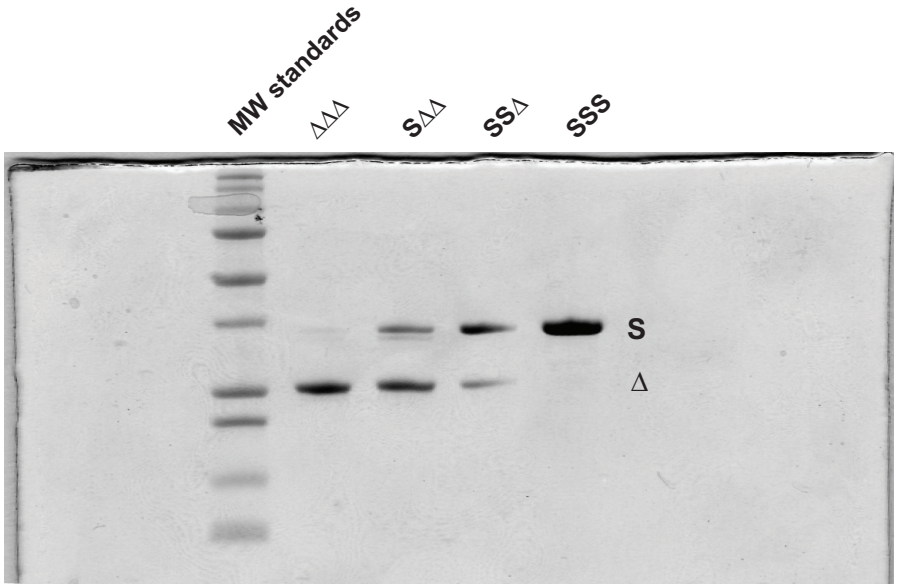
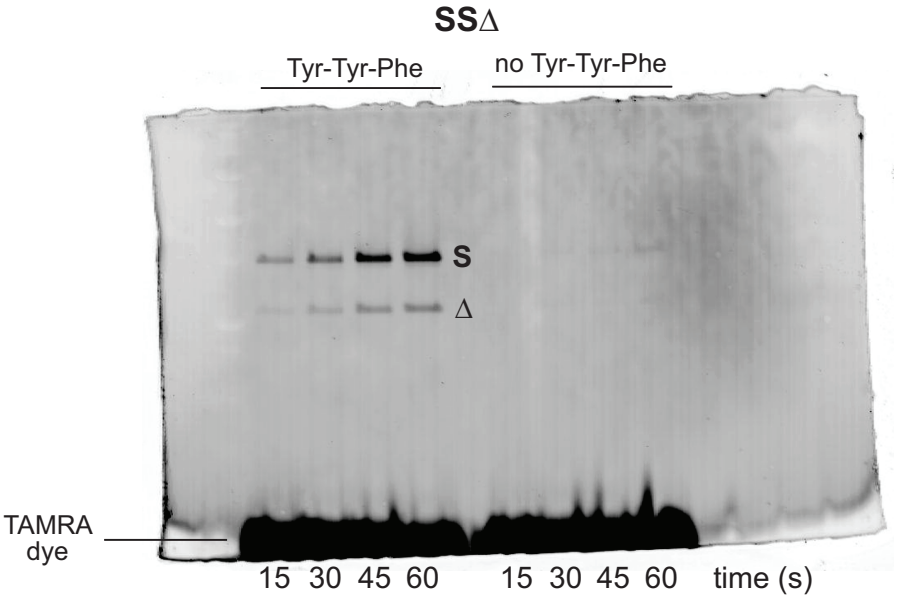
Supplementary Results



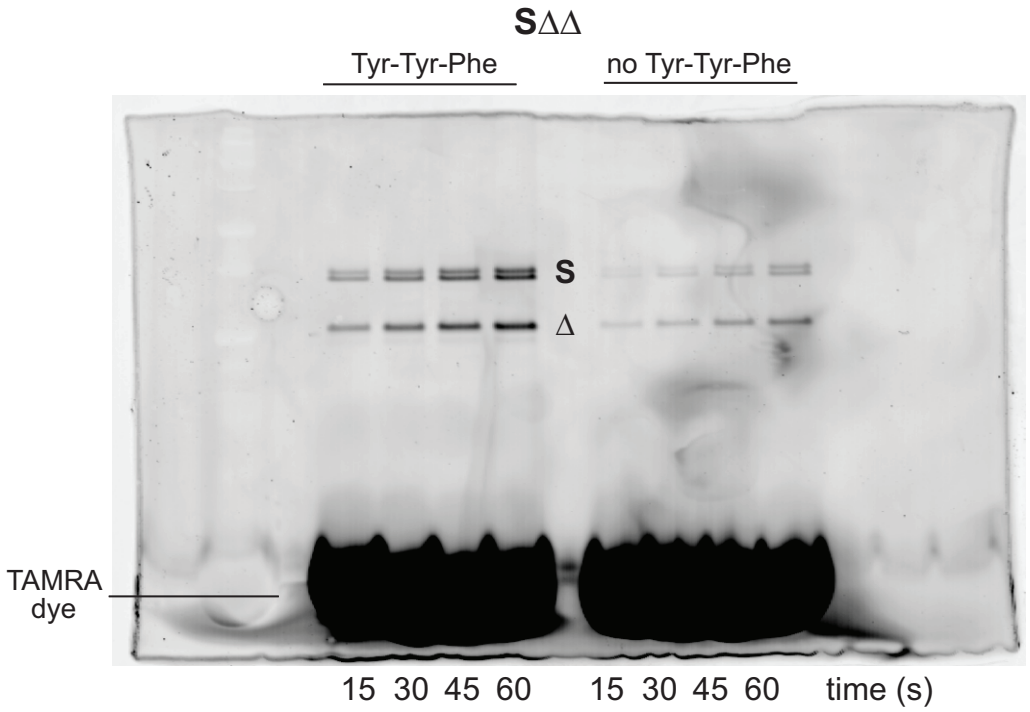
Supplementary Figure 1. The His198-Pro mutation (HP) stabilizes the active conformation of neighboring subunits. (**a,b**) Michaelis-Menten plots for $RseA^P$ cleavage by hybrid trimers (0.6 μM) containing the HP mutation in catalytically inactive S^{SA} subunits compared to otherwise isogenic trimers lacking the HP mutation. Experiments contained 150 μM Tyr-Tyr-Phe tripeptide. The lines are fits to the Hill equation, but fitting errors were too large to allow confident determination of parameters. (**c,d**) Tyr-Tyr-Phe tripeptide activation of $RseA^P$ (200 μM) cleavage by 0.6 μM concentrations of mixed trimers. Panel-c data were fitted to a hyperbolic equation, rate = basal + V_{max}•[Tyr-Tyr-Phe]/(K_{act} + [Tyr-Tyr-Phe]). Panel-d data were fitted to a Hill equation, rate = basal + V_{max}•[Tyr-Tyr-Phe]^n/(K_{act}^n + [Tyr-Tyr-Phe]^n). Fitted parameters are listed in Table 1.



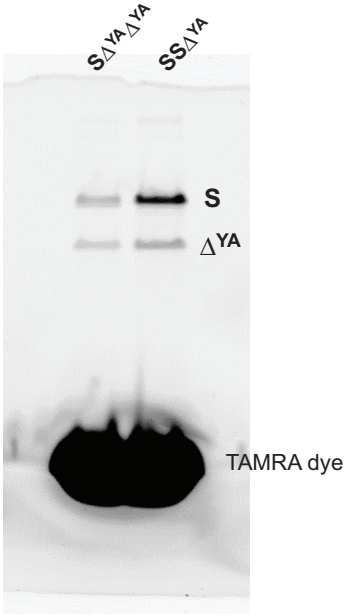
Supplementary Figure 2. Coomassie-blue stained SDS-PAGE gel from which the segment shown in Fig. 1c was taken.



Supplementary Figure 3. Fluorescence image of SDS-PAGE gel from which the segment shown in Fig. 3a was taken. The intense band at the bottom is unreacted or hydrolyzed TAMRA-FP reagent.



Supplementary Figure 4. Fluorescence image of SDS-PAGE gel from which the segment shown in Fig. 3b was taken. The intense band at the bottom is unreacted or hydrolyzed TAMRA-FP reagent.



Supplementary Figure 5. Fluorescence image of the complete lanes of the SDS-PAGE gel from which the segment shown in Fig. 4c was taken. The intense band at the bottom is unreacted or hydrolyzed TAMRA-FP reagent.