Supporting Information

Bieniossek et al. 10.1073/pnas.0910708106

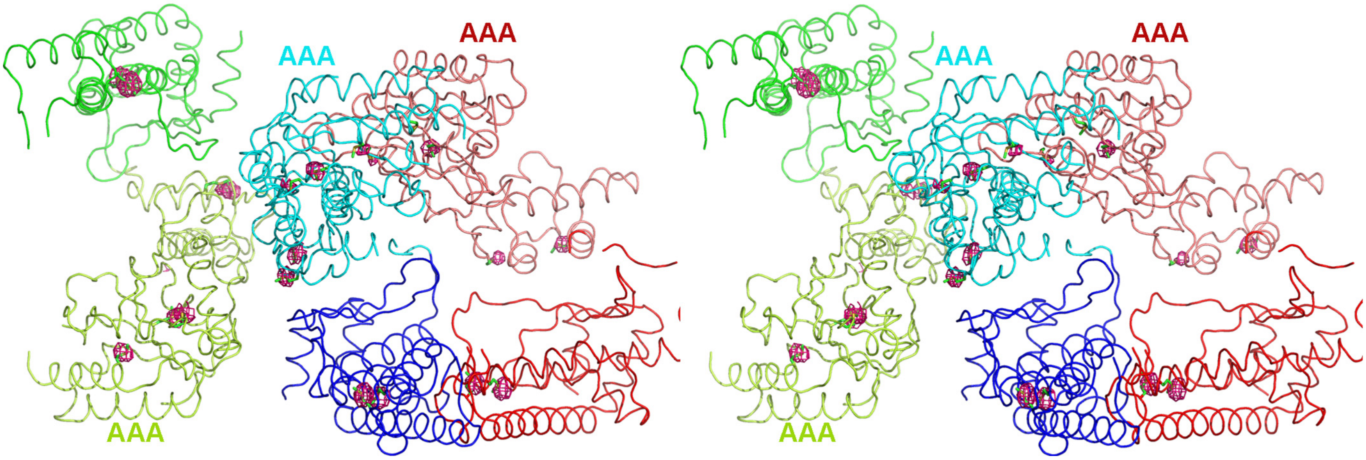


Fig. S1. Stereoview of the imaginary Fourier map revealing selenium positions in protease and AAA domains. The Cα traces of 3 independent monomers in the asymmetric unit are shown in lime/green, cyan/blue, and salmon/red for AAA/protease domains, respectively. The imaginary part of the Fourier map calculated with coefficients ($F^+ - F^-$) exp[i(φ-π/2)] is shown as pink mesh contured at 6 sigma, this is above the first noise peak (4.8 sigma). The highest signal originates from the two methionines in each protease domain.

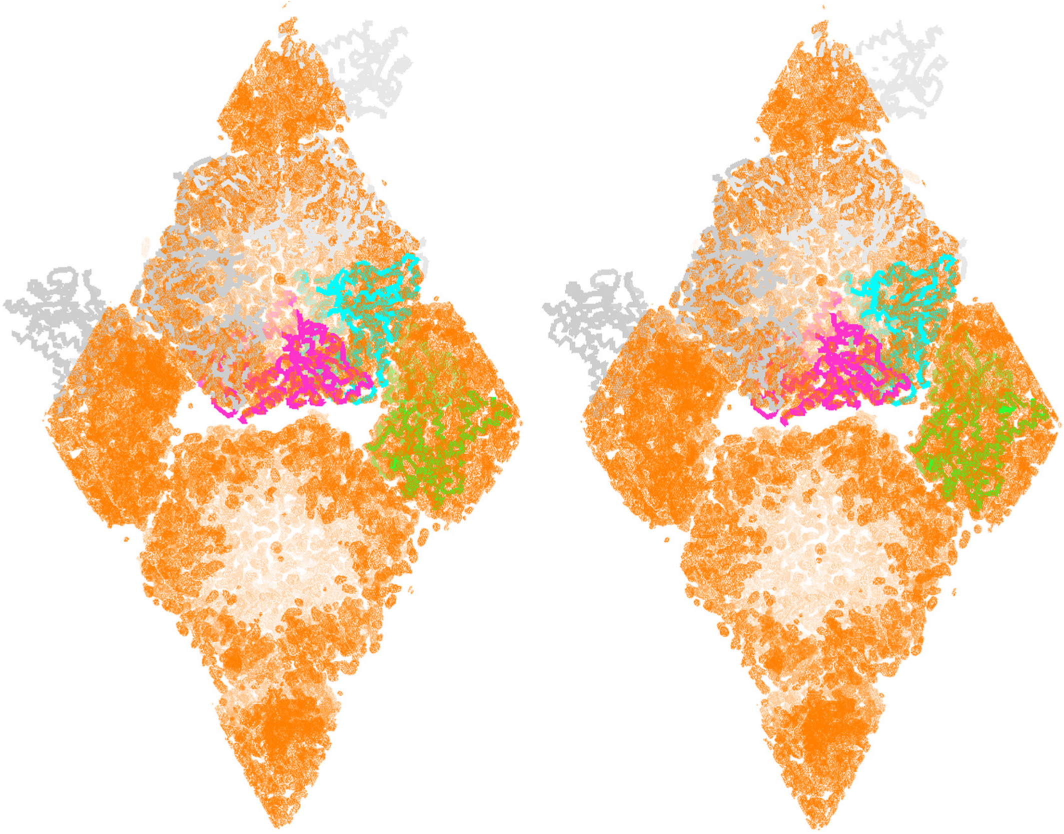
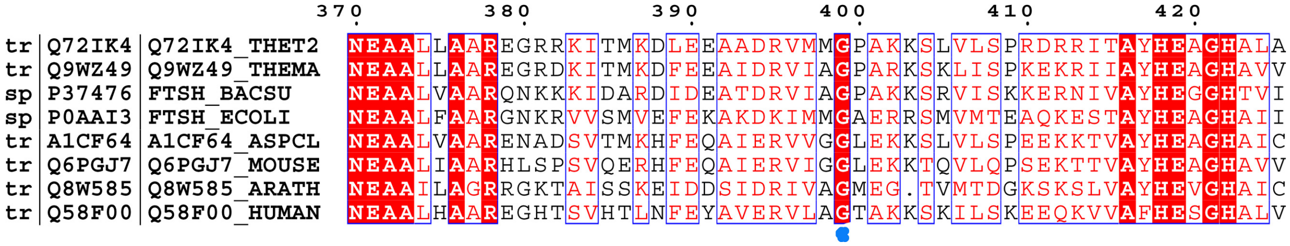


Fig. S2. Stereoview of the experimental electron density map. The 3 independent monomers are colored in magenta, green, and cyan, symmetry-mates in gray. The view is along the crystallographic 6-fold down onto the AAA domains of the magenta/cyan hexamer. The solvent-modified electron density map (orange) is contured at 1 sigma.



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tr|Q72IK4|Q72IK4_THET2  NEAALLAAREGRRKITMKDLEEAADRVMMGPAKKSLVLSPRDRRITAYHEAGHALA
tr|Q9WZ49|Q9WZ49_THEMA  NEAALLAAREGRDKITMKDFEEAIDRVIAGPARKSKLISPKEKRIIAYHEAGHAVV
sp|P37476|FTSH_BACSU    NEAALVAARQNKKKIDARDIDEATDRVIAGPAKKSRVISKKERNIVAYHEGGHTVI
sp|P0AAI3|FTSH_ECOLI    NEAALFAARGNKRVVSMVEFEKAKDKIMMGAERRSMVMTEAQKESTAYHEAGHAII
tr|A1CF64|A1CF64_ASPCL  NEAALVAARENADSVTMKHFEQAIERVVGGLEKKSLVLSPEEKKTVAYHEAGHAIC
tr|Q6PGJ7|Q6PGJ7_MOUSE  NEAALIAARHLSPSVQERHFEQAIERVIGGLEKKTQVLQPSEKTTVAYHEAGHAVV
tr|Q8W585|Q8W585_ARATH  NEAAILAGRRGKTAISSKEIDDSIDRIVAGMEG.TVMTDGKSKSLVAYHEVGHAIC
tr|Q58F00|Q58F00_HUMAN  NEAALHAAREGHTSVHTLNFEYAVERVLAGTAKKSKILSKEEQKVVAFHESGHALV
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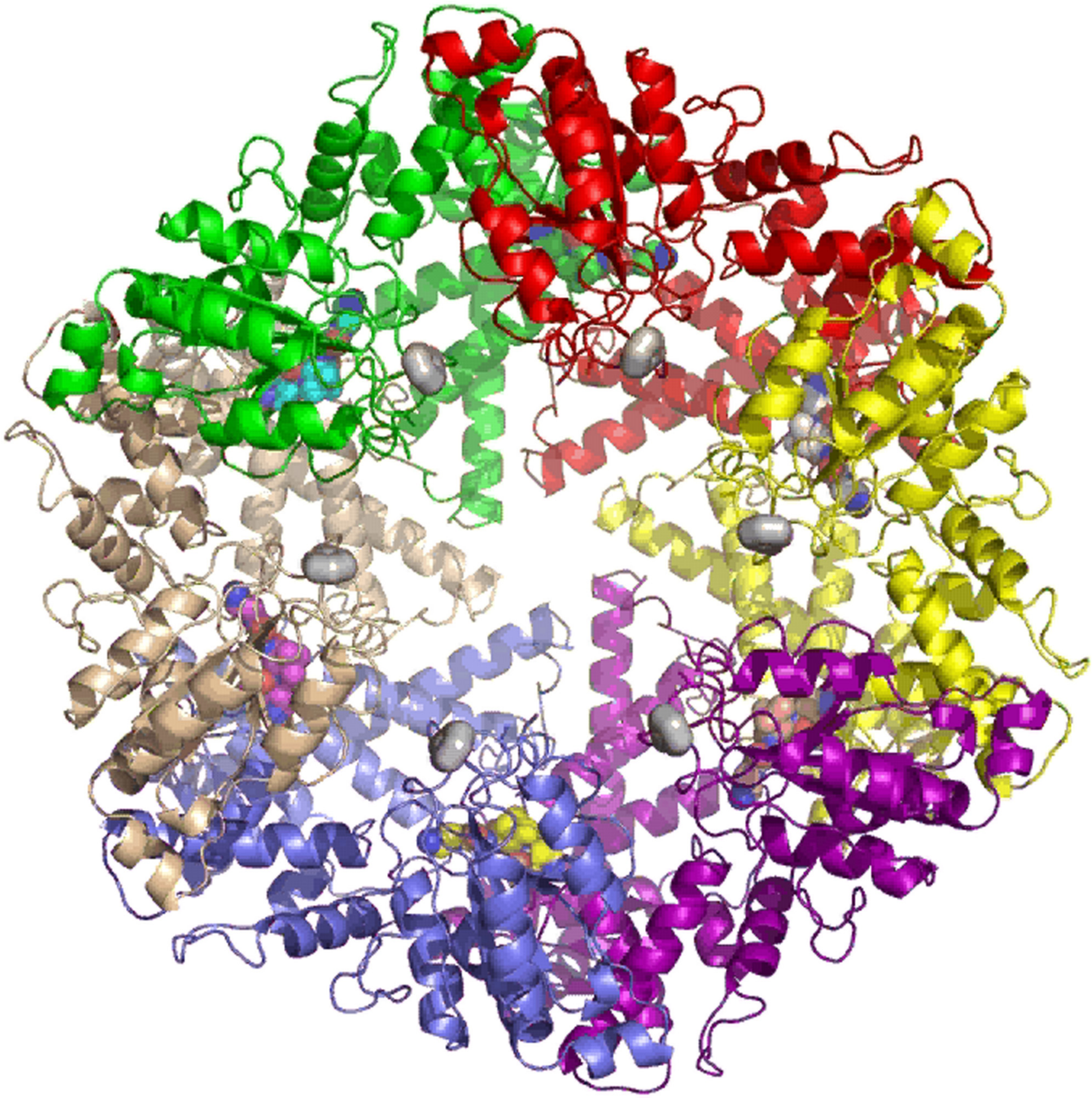
Fig. S3. Conservation of the linker glycine. Alignment of FtsH homologs from *T. thermophilus*, *T. maritima*, *Bacillus subtilis*, *E. coli*, *A. clavatus*, *Mus musculus*, *Arabidopsis Thaliana*, and *Homo sapiens.* The conserved glycine (G399 in *T. thermophilus*) is marked by a blue dot.



Movie S1. Morphing between Apo- and ADP-Bound State. The hexamer is colored according to subunits, pore residues are shown as gray sticks. TAPI and ADP are shown in space-filling representation at the endpoints. This visualization shows the trajectories of the aromatic side-chains but is unrealistic as all 6 subunits undergo simultaneously the rearrangement (1).

1. Martin A, Baker TA, Sauer RT (2005) Rebuilt AAA + motors reveal operating principles for ATP-fuelled machines. *Nature* 437:1115–1120.

Movie S1 (AVI)