Supporting Information

Śledź et al. 10.1073/pnas.1305782110

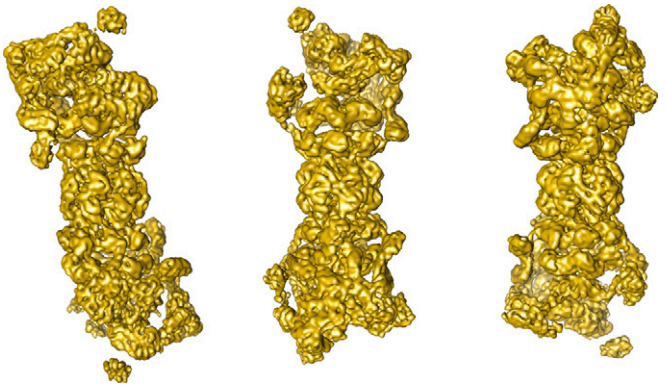


Fig. S1. Nonsymmetrized (C_1) reconstruction of ATP-γS–bound form of 26S proteasome from *Saccharomyces cerevisiae*.

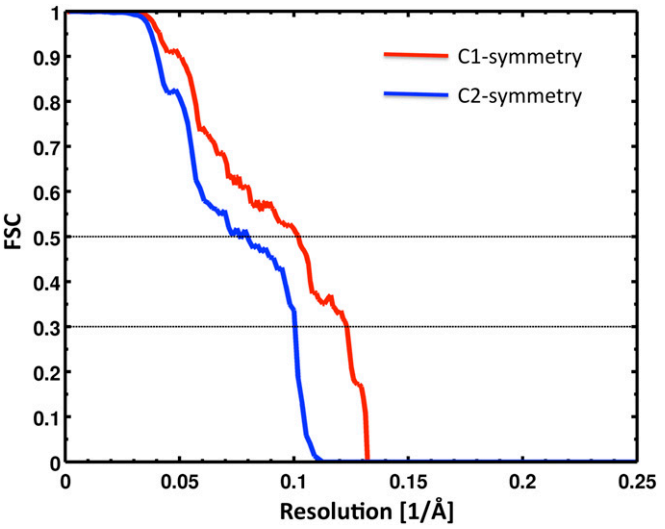


Fig. S2. Fourier-shell correlation (FSC) of C_1- and C_2-symmetrized reconstruction. To ensure the same effective particle numbers in both reconstructions, the C_2 reconstruction has been carried out with 50% randomly chosen particles.

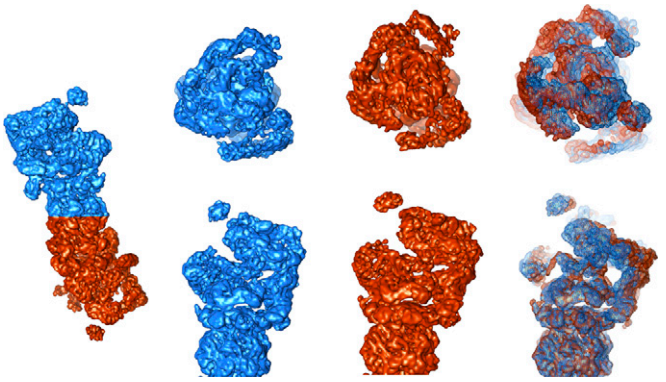


Fig. S3. Superposition of the two caps (half-proteasomes) from the ATP-γS map.

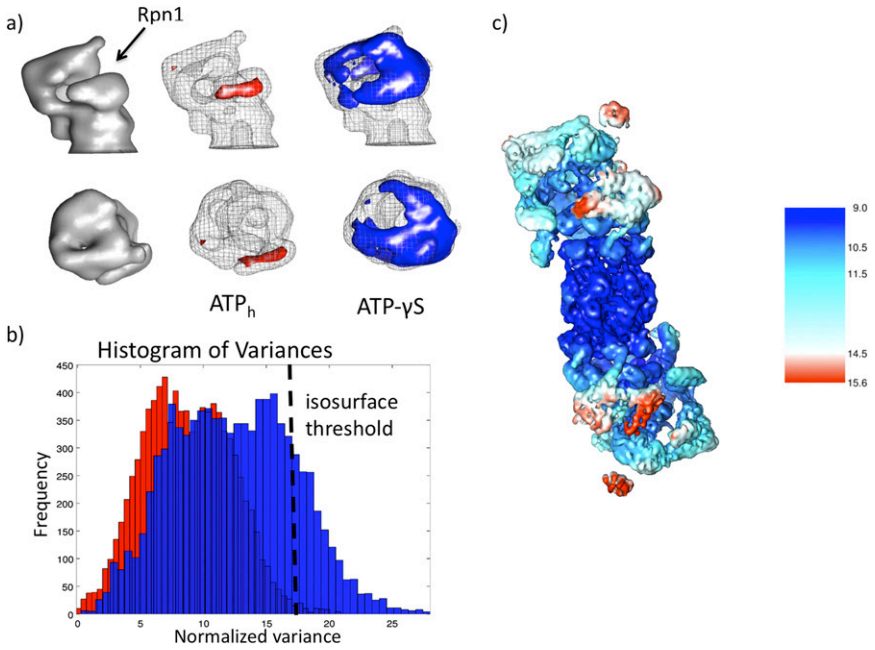


Fig. S4. (*A*) Variance maps of ATP-γS–bound and ATP-hydrolysing (ATP$_h$) maps. The variance maps were normalized to the background. (*B*) Histogram of variances for both structures. (*C*) Local resolution of ATP-γS density. The isosurface is colored according to the local resolution as indicated by the color bar (in angstroms).

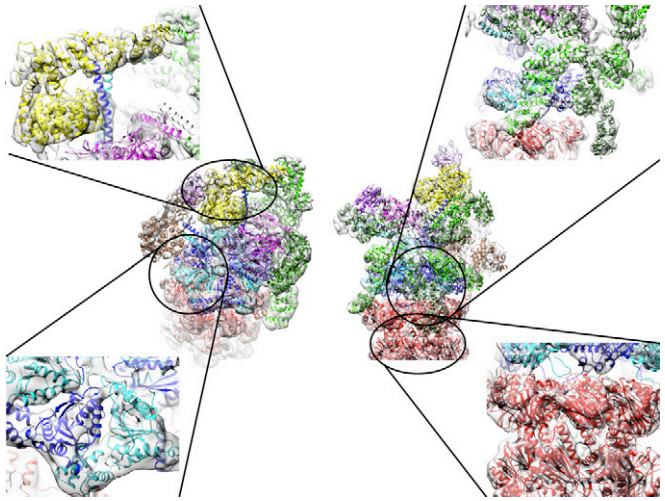


Fig. S5. Agreement between the pseudoatomic model of ATP-γS–bound proteasome and EM density. (*Upper Left*) Regulatory particle non-ATPase (Rpn) 2 subunit. (*Upper Right*) PCI (proteasome, COP9, and initiation factor 3) subunits. (*Lower Left)* AAA ATPases. (*Lower Right*) The 20S core particle.

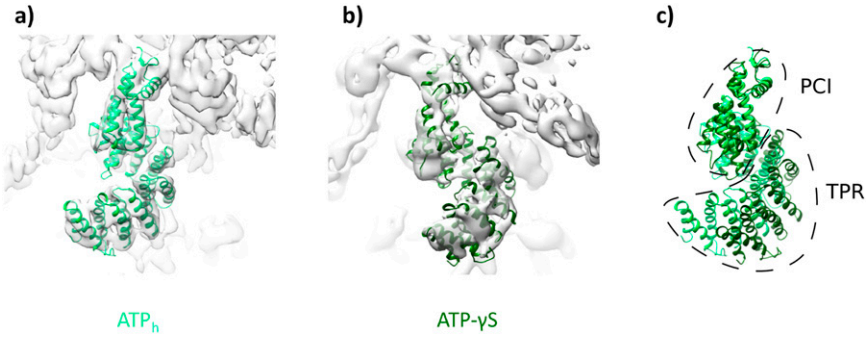


Fig. S6. Conformational changes of Rpn6 upon transition between the nucleotide states. (*A*) Rpn6 and corresponding EM density in ATP$_h$ structure. (*B*) Rpn6 and corresponding EM density in ATP-γS–bound structure. (*C*) Superposition of two models of Rpn6.

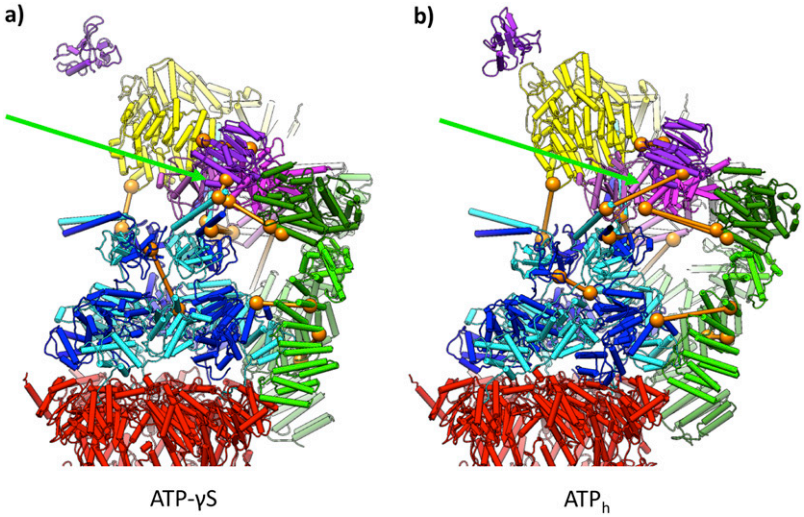


Fig. S7. Site-specific cross-links that display a large difference in length between ATP-γS–bound (*A*) and ATP$_h$ (*B*) structures. The arrow indicates the cross-link between Rpn10:K30 and regulatory particle AAA-ATPase (Rpt) 5:K45, which were 44 Å apart in the ATP$_h$ structure, whereas the distance is only ∼10 Å in the ATP-γS–bound structure (Cα-Cα distances).

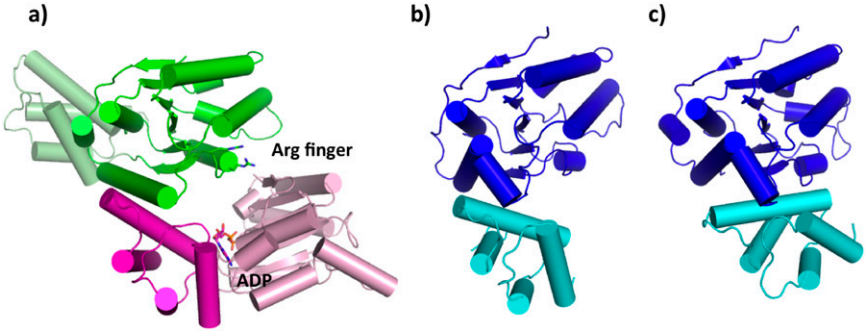
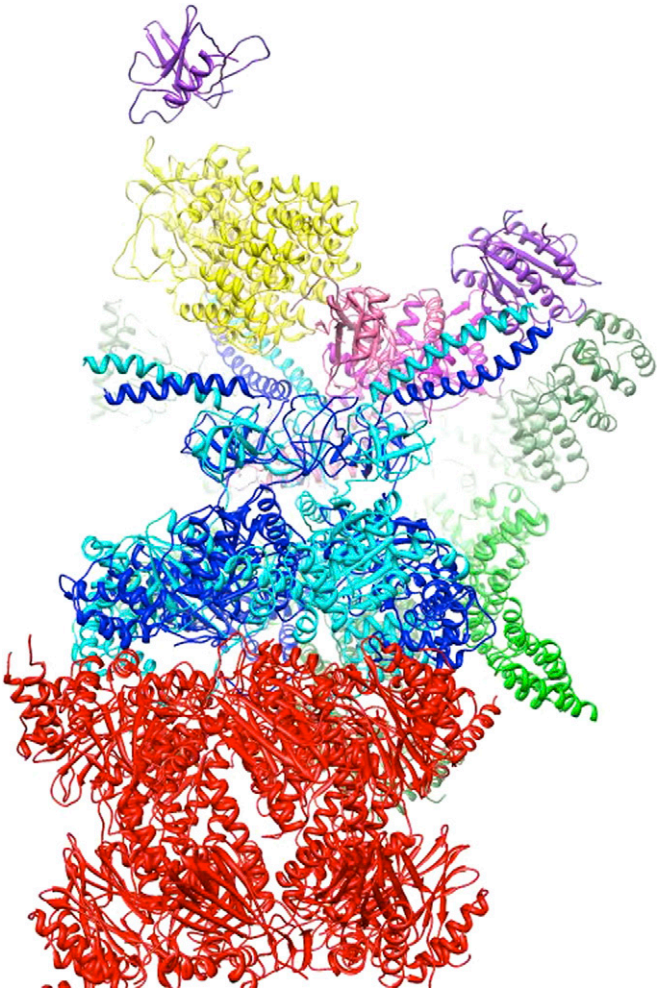
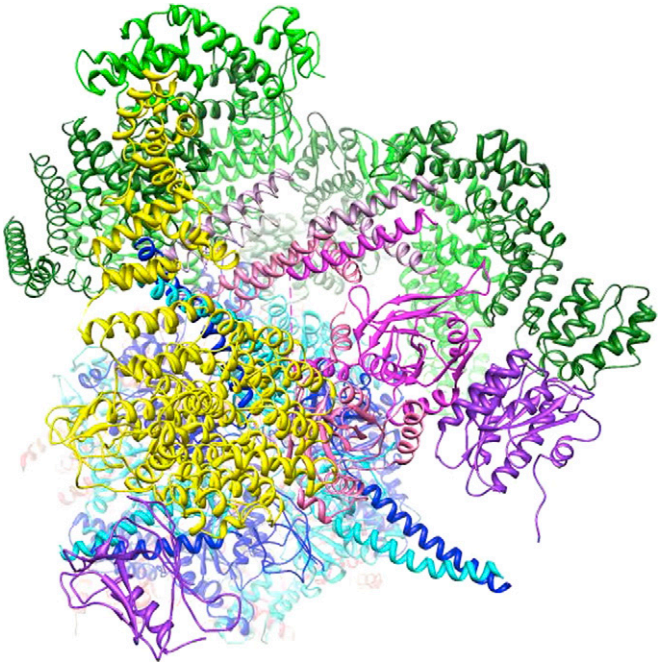


Fig. S8. Comparison of intersubunit module (ISM) structures. (*A*) ISM in the crystal structure of proteasome-activating nucleotidase-ADP (PDB ID code: 3H4M). (*B*) An open ISM$_{1–5}$ from the ATP$_h$ structure. The large AAA domain has been aligned to the same position as in *A*. (*C*) The closed ISM$_{6–3}$ seen from the ATP$_h$ structure. Again, the large AAA domain has been aligned to the same position as in *A*.



Movie S1. Morph between ATP_h and ATP-γS–bound structures as seen from the side.

Movie S1



Movie S2. Morph between ATP_h and ATP-γS–bound structures as seen from the top.

Movie S2