Figure 2 Nucleotide-bound states of Mm. Cryo-EM class averages of the open (A), bullet (B) and closed (C) conformations of the Mm-ADP•AlF_3 complex. Each class average contains approximately 30 aligned images.

Figure 3 Surface views of the three reconstructed Mm-ADP•AlF_3 complexes with domain fitting. 3D reconstructions, displayed at a threshold of one sigma, of the open (A and D), bullet (B and E) and closed (C and F) Mm-ADP•AlF_3 complexes, with their fitted domains, viewed from the top and the side. The structures used for fitting were the domains of the thermosome crystal structure (PDB accession number 1A6D). Dotted line shows apical rotation, helices 10 and 11 are indicated.

Figure 4 Analysis of domain rotations in Mm-ADP•AlF_3 rings. Fitted coordinates of the open (A and D), partially closed (B and E) and closed rings (C and F). A, B and C show cross-sectioned side views and individual subunits are viewed from inside the cavity in D, E and F. The dashed lines in A, B and C indicate the angle between the equatorial domain and the intermediate/apical domains. The dashed lines in D, E and F show the change in angle between intermediate and apical domains. The dashed lines in the intermediate domains (lower dashed line) run along helix 14 which contains an aspartate residue required for ATP hydrolysis.

Supplementary Material

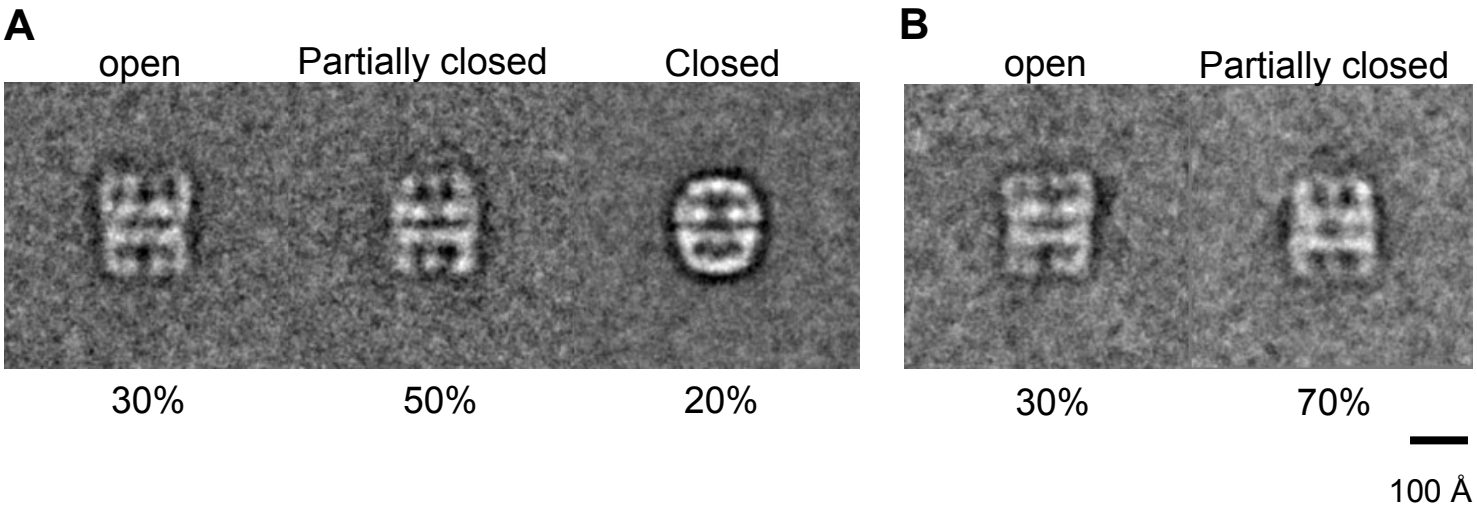
Supplementary Figure 1. Class averages of the Mm-ADP and ATP complexes. Class averages of the open, partially closed and closed complexes in 2 mM ATP (A) and the open and partially closed Mm complexes in 2 mM ADP (B). The approximate percentage of each conformation is indicated, calculated from 500 and 200 side views of Mm-ATP and ADP respectively.

Supplementary Figure 2. A native actin monomer docked into the fully closed folding chamber. In order to examine the volume available to a known group 2 chaperonin substrate, the atomic coordinates of actin (PDB accession number 2BTF) docked into the thermosome crystal structure (PDB accession number 1A6D) shown in cartoon representation in cross-section from the side (A) and the top (B). There are some side chain clashes (not shown). The

green box in (A) represents the region occupied by the disordered C-termini in the crystal structure.

Figures 2-4 and supplementary Figure 2 were generated with PYMOL (www.pymol.org).

Supplementary Figure 1



Supplementary Figure 2