Supplementary Figures

Figure S1. **Image analysis reveals 6-fold symmetry in mouse lengsin.**

(a) Statistical analysis of the end views produced eigen images that demonstrate the 6-fold symmetry.

(b) Representative classes used for the final 3D reconstruction (top) and the corresponding reprojections (bottom).

Figure S2. **Fitting coordinates into the electron density.**

The atomic structure coordinates were fitted into the cryoEM electron density map for mouse lengsin, shown in transparent cyan. Polypeptide chains are represented in ribbon with chains from the upper ring shown in blue and from the lower ring in crimson, with brown ribbon indicating the position of the GSI N-terminal helix. (a) The coordinates of two polypeptide chains of StypGS, one from each ring, manually fitted to the electron density map. (b) Two energy minimized mouse lengsin homology model monomers manually fitted to the electron density map. (c) Three monomers of the mouse lengsin homology model after refinement into the electron density map using URO.

Figure S3. **Comparison of mouse lengsin with bacterial GS.**

One polypeptide chain in ribbon representation (grey) from StypGS is superposed on the homology model of mouse lengsin (maroon) viewed from two orientations. The connecting loop between the last two C-terminal helices in StypGS is shown in green. The connecting loop N-terminal to the preceding helix in StypGS is shown in yellow.

Figure S1.

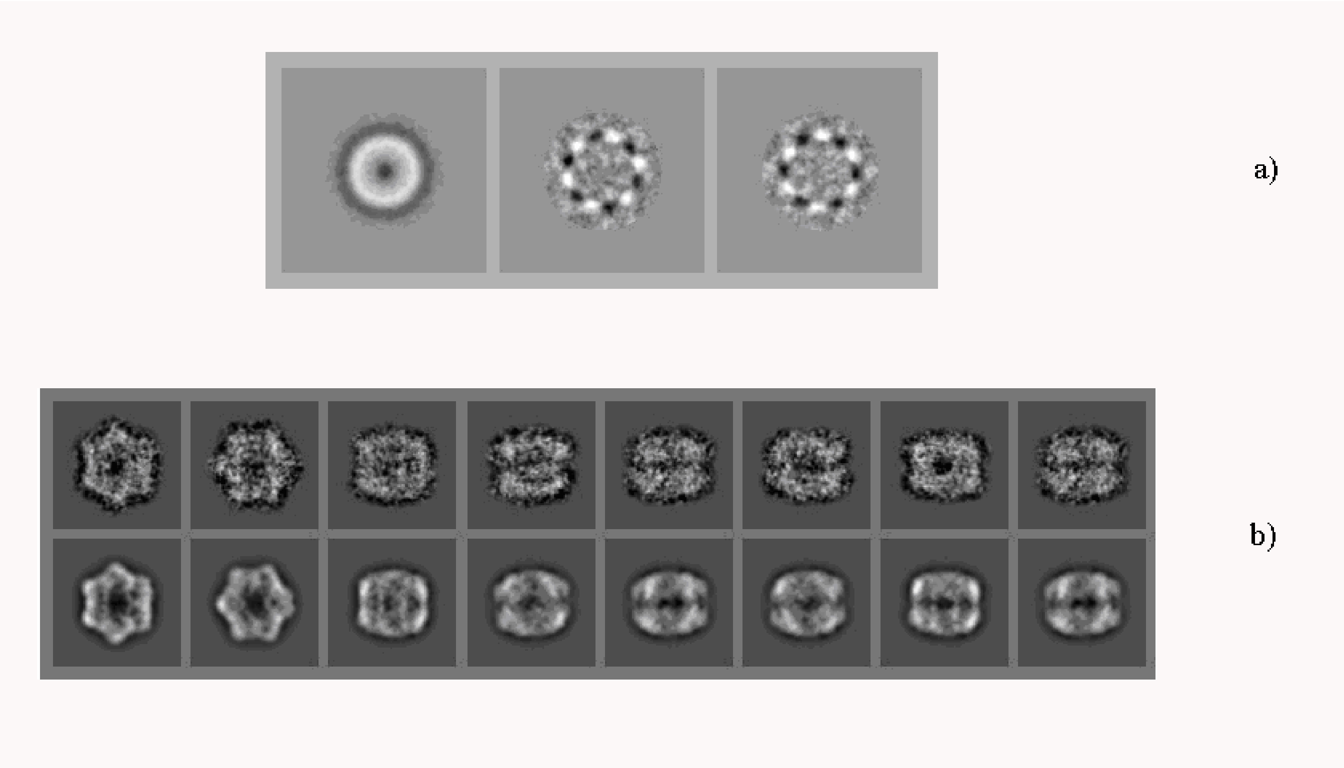

Figure S2.

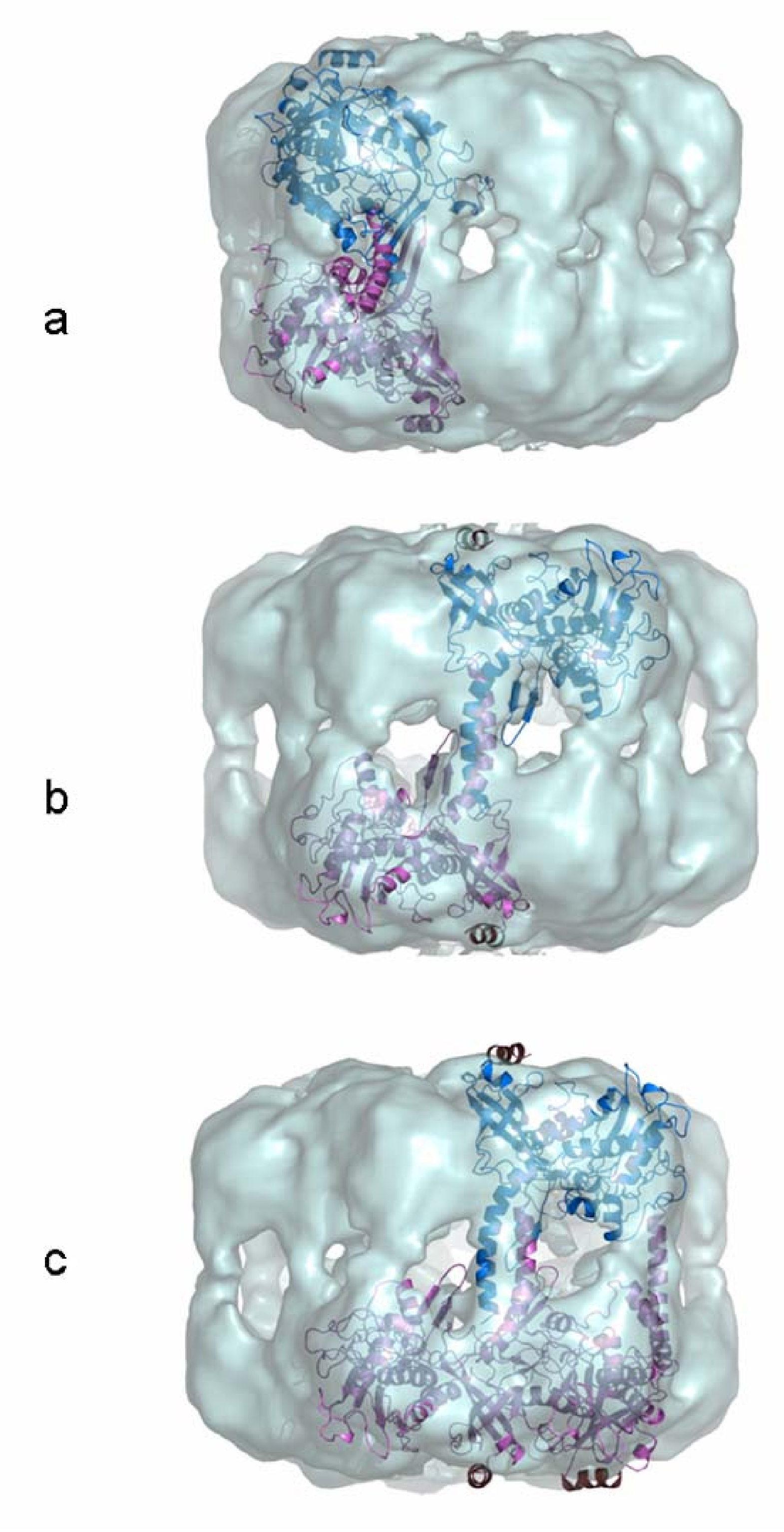

Figure S3.