Supplementary Figure S1. Limited structure-based sequence alignment of CT584 and orthologs in *Chlamydia*. Numbers above the sequences correspond to *C. trachomatis* CT584. The secondary structure
of CT584 and Cpn0803 are shown above and below the alignment, respectively. Residues are colored according to conservation (cyan = identical and purple = similar) as judged by the BLOSUM62 matrix. Red stars below the sequences correspond to amino acid side chains involved in the monomer-monomer (dimer) interface, while blue stars correspond to amino acid side chains involved in the dimer-dimer (hexamer) interface.

**Supplementary Figure S2.** Structural Superposition of CT548 and Cpn0803 oligomeric states. Superposition of CT584 hexamer (chains positioned and colored as in Fig. 4a) and Cpn0803 hexamer (gray) as viewed down the crystallographic c-axis. The calculated r.m.s.d. deviation was 0.547 Å over 693/852 Ca atoms within 5.0 Å. Alignment is rotated 90° about the vertical and horizontal axes with respect to a.