Figure S1: Electron tomography of PAN (A) A conventional transmission electron micrograph of a region used for recording a tilt series and for calculating the reconstruction volume shown in (B).
(B) A tomographic x-y slice correspond to a central section through negatively-stained PAN complexes, 1.2 nm in thickness.

Figure S2: The C-termini of model AAA$_{+}$ regulatory complexes are located in the periphery of the ATPase ring and project out of the ring-plane upon association with the protease.
(A) Cartoon illustrating the state of the *E. coli* ATPase complex HslU (in the non-associated state and upon association with HslV), as portrayed in (B).
(B) Surface rendering of bottom and side views of HslU illustrating the position and structural transition of the C-terminal resides (430-443) upon association with the protease. Left, in the non-associated state and right, upon association with HslV.
(C) Surface rendering of bottom (left) and side (right) of the C-terminal domain of p97 (301-759). The ten C-terminal residues (depicted in color) are localized on the perimeter of a cavity similar to that found in the C-terminal ring of PAN.

Figure S3: Upon association with the regulatory complex, the meshed N-terminal tails of proteasome ☐-ring dissociates and projects into the proteasome regulatory complex.
(A) Cartoon illustrating the state of the yeast 20S proteasome (in the non-associated state and upon association with PA-26), as portrayed in (B).
(B) Surface rendering of top (left) and side (right) views of the yeast 20S proteasome ☐-ring when the 20S proteasome was crystallized by itself (1RYP.pdb) and upon association with PA-26 (1Z7Q.pdb). In the nonassociated state, the ☐-ring N-terminal residues (colored) form an inward collapsed mesh gating entry into the proteasome (left). Upon association with PA-26 (right), the ☐-subunits N-terminal residues flip and project outward into PA-26. The twelve C-terminal residues of PA-26 dock into the periphery of the ☐-subunits pseudoring (colored, right).

Figure: S1

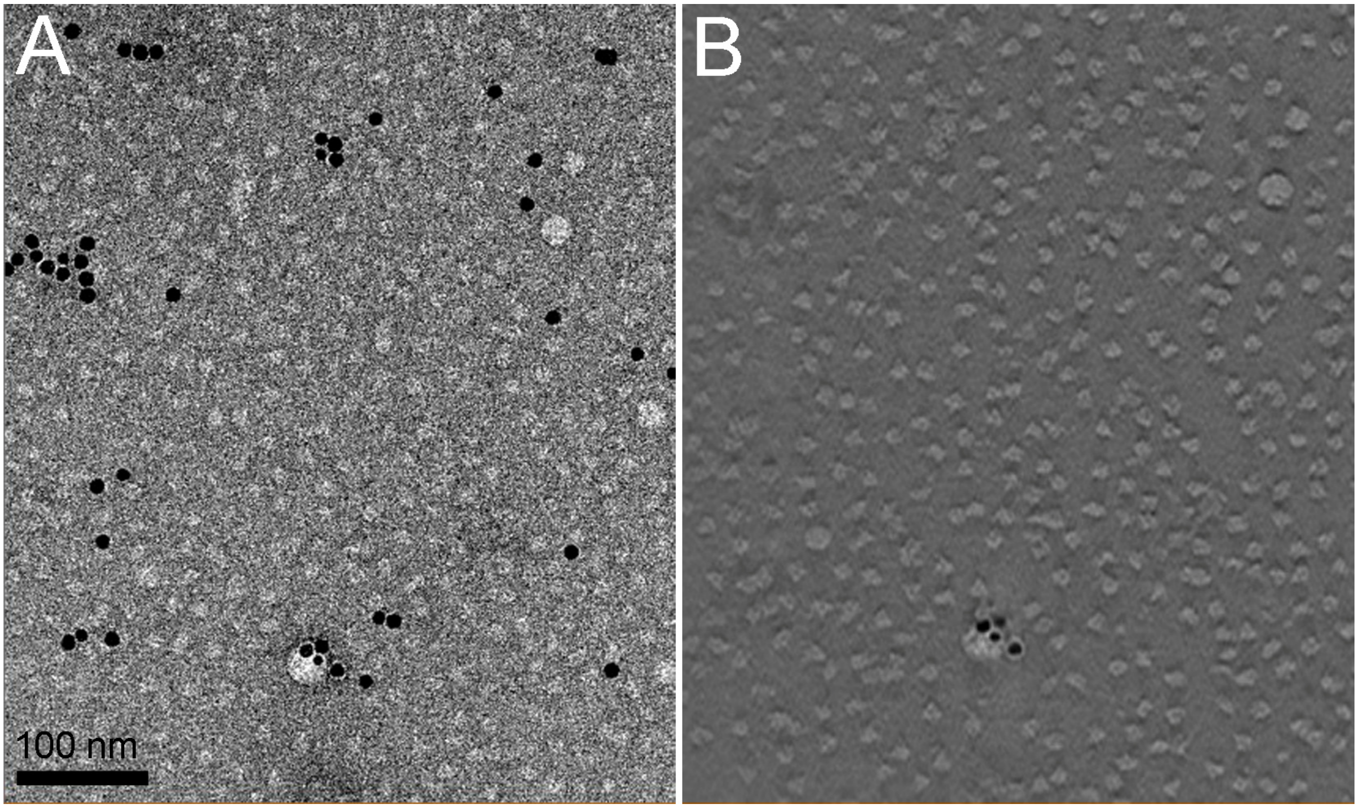

Figure: S2

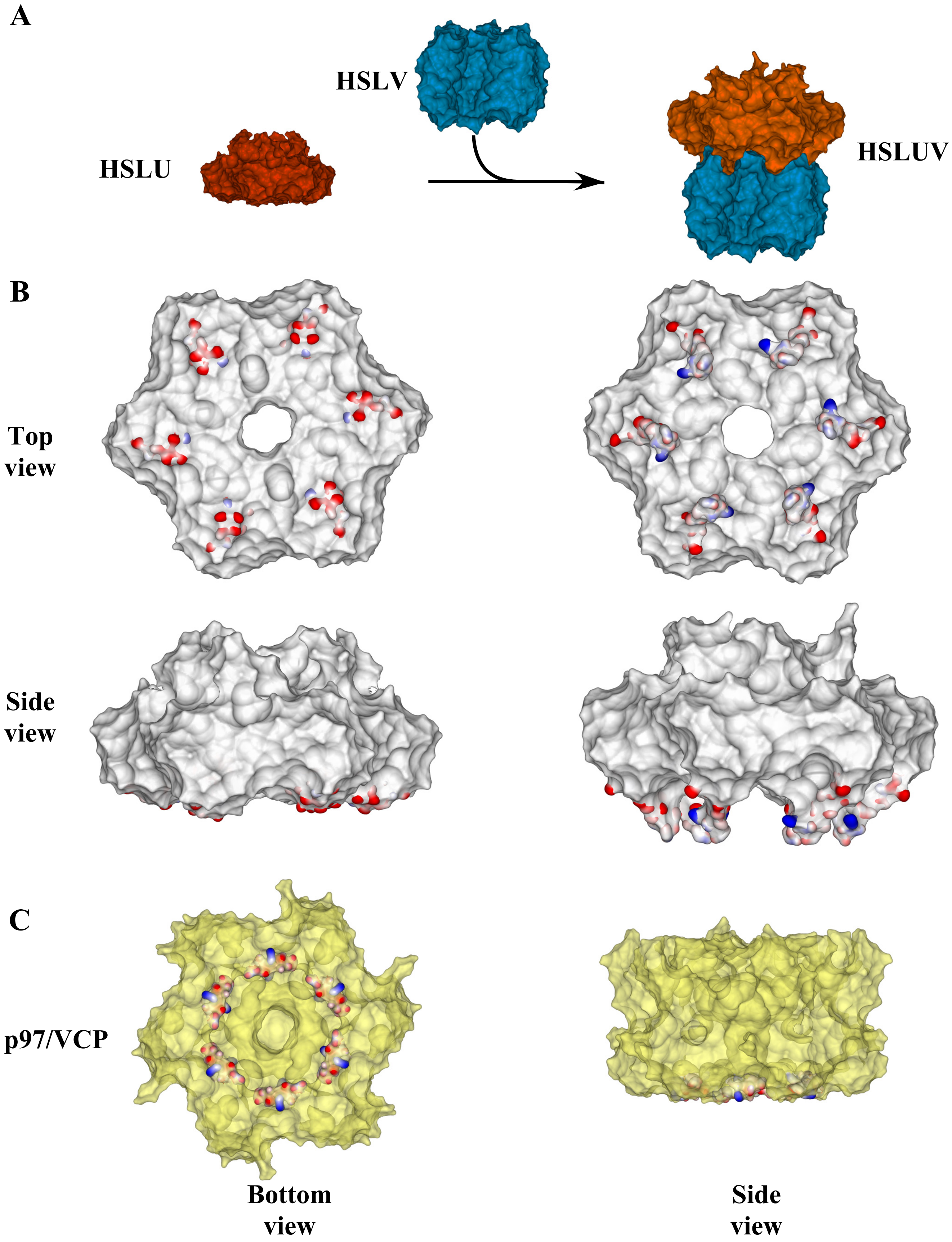
A
HSLV
HSLU
HSLUV
B
Top view
Side view
C
p97/VCP
Bottom view
Side view

Figure: S3