Supplementary information, Figure S7 The AAA-ATPase ring conformational change between proteasome-ADP-AlFx and the resting state structures. **(A)** The AAA-ATPase ring of the resting state (left column) and proteasome-ADP-AlFx (right column) structures. The AAA-ATPase subunits follow the same color schema as in Fig. 2. The dashed lines indicate the orientation of the AAA domains in the resting state (black lines) and proteasome-ADP-AlFx (red lines) structures, and the arrows denote the direction that these domains would rotate from the resting state to the ADP-AlFx state according to these structures. The interaction interface between 19S and 20S calculated by PISA [81] is also listed (in $Å^2$). **(B)** Comparison of the AAA-ATPase ring conformations in the resting state (grey) and proteasome-ADP-AlFx (subunits with color) structures with respect to their 20S with the differences in the positions of their AAA-ATPase rings indicated in two directions

in red and black, respectively. **(C)** The top view of the AAA-ATPase ring of the resting state (left column) and proteasome-ADP-AlFx (right column) structures. The circles indicate the diameters of the AAA-ATPase pore. **(D)** Top view of the comparison as in **(B),** with the N-ring removed for better visualization. The outer boundaries of the AAA-rings of the resting state and proteasome-ADP-AlFx structures are shown in black and red hexagons, respectively. The dashed lines depict the diameters of the AAA-rings: 126.1 Å for the resting state (black) and 130.9 Å for ADP-AlFx state (red). The AAA-ring rotation is also labeled. **(E)** Location of the Rpt1 C-terminal tail (red) resolved in our resting state map. Its location relative to the entire map is shown on the upper left, a magnified view of Rpt1 (dodger blue) with its relationship to the 20S α6 subunit (sandy brown) in the middle, and the top view of the tail relative to 20S on the right. The location of the gate is indicated by the black circle.