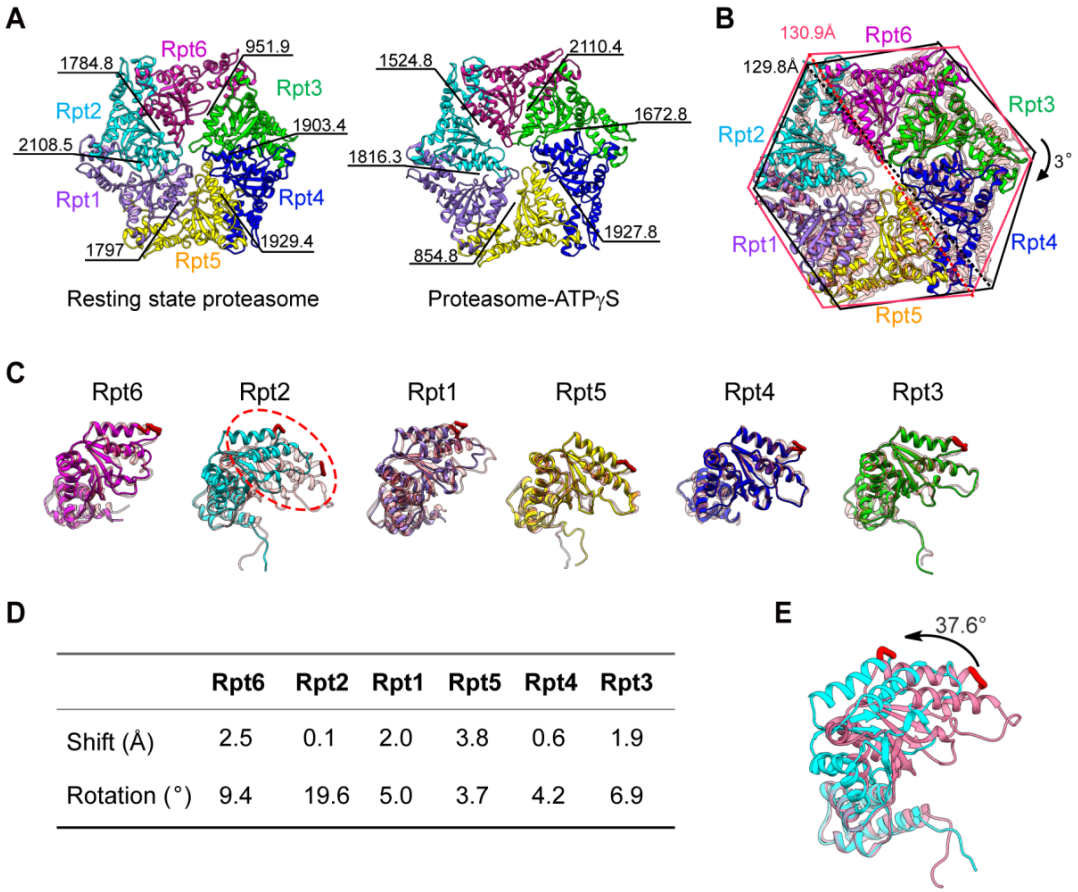

	Rpt6	Rpt2	Rpt1	Rpt5	Rpt4	Rpt3
Shift (Å)	2.5	0.1	2.0	3.8	0.6	1.9
Rotation (°)	9.4	19.6	5.0	3.7	4.2	6.9

Supplementary information, Figure S8 AAA-ATPase subunit interaction interface analysis and conformational changes of the AAA-ATPase ring from proteasome-ATPγS to proteasome-ADP-AlFx. **(A)** The AAA-ATPase ring of the resting state (left) and proteasome-ATPγS (right) structures. The interaction interface (in $Å^2$) between the neighboring AAA domains is labeled. **(B)** Superposition of the AAA-rings of proteasome-ADP-AlFx (subunits in colors) and proteasome-ATPγS (salmon, PDB ID: 4CR4) [18] with respect to their 20S. The outer boundaries of the AAA-rings of proteasome-ATPγS and proteasome-ADP-AlFx are shown in black and red hexagons, respectively. A slight increase in radius (~1 Å) and a rotation (3°) can be observed from proteasome-ATPγS to proteasome-ADP-AlFx. **(C)** Aligned AAA domains of proteasome-ADP-AlFx (in color) and proteasome-ATPγS (transparent salmon) showing the position of Rpt2 (indicated by red circle) to differ the most between the two structures. **(D)** Alignment generated global shift and rotation between the AAA domains of the two structures. **(E)** The enlarged view of the Rpt2

subunit inter domain rotation from proteasome-ATPγS to proteasome-ADP-AlFx, with the rotation angle and direction being labeled.