Supplementary information, Table S1 Statistics of cryo-EM data collection and refinement.

	Proteasome-ADP-AlFx	**Resting state proteasome**
Data collection		
EM equipment	Titan Krios	Titan Krios
Voltage (kV)	300	300
Detector	K2 Summit	Falcon II
Pixel size (Å)	1.32	1.09
Electron dose ($e^-/Å^2$)	38	25
Exposure time (s)	7.6	1.1
Frames	38	18
Defocus range (μm)	-1.8 to -2.5	-1.8 to -2.5
Reconstruction		
Software	RELION 1.3	RELION 1.3
Raw micrographs	13,871	3,499
Final particles	178,576	26,000
Symmetry	C1	C1
Final resolution (Å)	4.2	6.3
Map-sharpening B factor ($Å^2$)	-127	-168
Refinement		
Software	Rosetta	Rosetta
Rms deviations		
Bond length (Å)	0.0037	0.0035
Bond angle (^{o})	0.92	0.92
Ramachandran plot statistics (%)		
Preferred	93.29	91.55
Allowed	6.54	8.33
Outlier	0.17	0.12