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

Data collection				
EM equipment	Titan Krios			
Voltage (kV)	300			
Detector	Gatan K2			
Energy filter	Gatan GIF Quantum, 20 eV slit			
Pixel size (Å)	2.222			
Magnification	22,502			
Data set	Tilt0	Tilt30	Tilt45	Tilt55
Exposure rate (e$^-$/(s·Å^2))	2.612	2.612	2.612	2.612
Number of frames	40	46	56	70
Total Electron exposure (e$^-$/Å^2)	52	60	78	91
Defocus range (μm)	-1.0 ~ -4.0			
Total Number of images	4,606	4,186	4,158	10,111
Selected Number of images	3,250	2,888	2,745	3,516
Software	AutoEMation2			
Reconstruction				
Software	RELION2.1/RELION3.0-beta/THUNDER			
Number of used Particles	133,125	198,099	142,938	142,385
Symmetry/Final resolution (Å)	C1/8.0			
Masked regions	Core region	Nup358 region	Nup214 region	
Number of Micrographs used	12,399	12,399	12,399	
Number of extracted particles	1,721,077	1,721,077	1,721,077	
Final number of particles	616,547	387,233	552,066	
Unmasked Resolution (Å) (0.5/0.143)	8.0/6.6	9.2/7.9	9.3/7.9	
Masked Resolution (Å) (0.5/0.143)	7.3/5.4	8.4/6.7	8.8/7.6	
Local Resolution Ranges (Å)	50-4.5	50-5.0	50-6.1	
Resolution Range due to anisotropy (Å)	6.2-5.0	8.3-6.2	8.8-7.1	
Final Resolution (Å)	5.5	7.1	7.9	
Map sharpening B-factor (Å^2)	-200	-400	-400	
Accuracy of rotation (˚)	2.23	2.55	5.02	
Accuracy of translation (pixels)	0.99	1.39	1.90	
EMDB number	emd-0909	emd-0910	emd-0911	
Model building and refinement				
Model building software	Coot			
Refinement software	PHENIX			
Protein residues	16,161			
Side chains	N/A			
Validation				
CaBLAM outliers	1.97%			

PDB accession code	6LK8		
R.m.s deviations			
Bonds length (Å)	0.008	0.010	0.006
Bonds Angle (˚)	1.23	1.21	1.04
Ramachandran plot statistics (%)			
Preferred	88.66	85.33	87.70
Allowed	9.68	13.80	10.57
Outlier	1.66	0.87	1.73