

Supplementary information, Table S1 Statistics of the cryo-EM structures presented in this study.

Data collection			
EM equipment	Titan Krios (Thermo Fisher Scientific)		
Voltage (kV)	300		
Detector	Gatan K3 Summit		
Energy filter	Gatan GIF Quantum, 20 eV slit		
Pixel size (Å)	1.087		
Electron dose (e-/Å ²)	50		
Defocus range (µm)	-1.2 ~ -2.2		
Sample	Nucleotide-free	ATP-bond	
	MlaFEDB	MlaF _{EQ} EDB	
Number of collected micrographs	5,167	2,569	
Number of selected micrographs	5,110	2,481	
3D Reconstruction			
Software	Relion 3.0		
Comformation	Apo	EQ _{tall}	EQ _{close}
Number of used particles (Overall)	271,252	17,109	21,159
Resolution (Å)	2.9/ 2.7/ 2.8 ^a	4.3	3.7
Symmetry	C2/ C6/ C2 ^a	C1	
Map sharpening B-factor (Å ²)	200/ 90/ 90 ^a	150	
Refinement			
Software	Phenix		
Cell dimensions			
a=b=c (Å)	347.84	217.40	
α=β=γ (°)	90	90	
Model composition			
Protein residues	2,092	2,092	2,092
Side chains assigned	2,038	2,038	2,038
lipid	12	N/A	N/A
ADP-vanadate	N/A	N/A	N/A
ATP	N/A	2	2
R.m.s deviations			
Bonds length (Å)	0.006	0.007	0.007
Bonds Angle (°)	1.131	1.085	1.118
Ramachandran plot statistics (%)			
Preferred	87.74	88.96	87.84
Allowed	11.09	10.46	11.72
Outlier	1.17	0.58	0.44