Supplemental Information

Table S1. CryoEM image collection, map reconstruction, and model refinement

	Apo-TRiC	**PFD-βTub-TRiC**	**TRiC-βTub State I**	**TRiC-βTub State II**	**TRiC-βTub State III**	**TRiC-βTub State IV**
CryoEM image collection and map processing						
Voltage (kV)	300	300	300	300	300	300
Total electron exposure ($e^-/Å^2$)	37	36	37	37	37	37
Defocus range (μm)	-0,5~-2.5	-0.5~-3.5	-0.5~-3.5	-0.5~-3.5	-0.5~-3.5	-0.5~-3.5
Pixel size (Å)	1.0	1.02	1.1	1.1	1.1	1.1
Symmetry imposed	C1	C1	C1	C1	C1	C1
Particle images (no.)	662,744	194,013	110,984	42,804	94,955	24,233
Map resolution (Å) FSC threshold (0.143)	3.1	3.9	3.0	3.3	2.9	3.6
EMDB ID	32822	32823	26089	26120	26123	26131
Model refinement						
Initial model used (PDB code)	NA	6NR8	7LUM, 6I2I	7LUM, 6I2I	7LUM, 6I2I	7LUM, 6I2I
Model composition						
Non-hydrogen atoms		67039	33714	34563	35180	35877
Protein residues		8727	4377	4481	4561	4650
Ligands		ADP:4	MG: 8 ADP: 8 AF_3: 8 H_2O: 8	MG: 8 ADP: 8 AF_3: 8 H_2O: 8	MG: 8 ADP: 8 AF_3: 8 H_2O: 8	MG: 8 ADP: 8 AF_3: 8 H_2O: 8
R.m.s. deviations						
Bond lengths (Å)		0.003	0.014	0.012	0.010	0.006
Bond angles (°)		0.790	1.137	1.233	1.049	0.767
Validation						
MolProbity score		2.12	1.6	1.61	1.57	1.65
Clashscore		18.09	4.7	4.54	4.52	6.22
Rotamer outliers (%)		0.08	0.08	0.32	0.00	0.13
Ramachandran plot						
Favored (%)		94.66	94.83	94.39	95.02	95.62
Allowed (%)		5.25	5.03	5.45	4.78	4.30
Outliers (%)		0.09	0.14	0.16	0.20	0.09
PDB ID		7WU7	7TRG	7TTN	7TTT	7TUB