

TABLE S2

	Raptor-Rag-Ragulator	Rag-Ragulator
Imaging parameters and 3D reconstruction		
Cryo-EM grids	Quantifoil R 1.2/1.3 Au 300	Quantifoil R 1.2/1.3 Au 300
Calibrated magnification	47,259	47,259
Accelerating voltage [kV]	300	300
Pixel size [Å] (super-resolution)	0.529	0.529
Total dose [e ⁻ / Å ²]	42	42
Exposure time [s]	8	8
Nominal defocus range [μm]	-1.0 to -3.5	-1.0 to -3.5
Particles in final 3D reconstruction	112,037	14,186
Resolution ('Gold-standard' at FSC 0.143) [Å]	3.18	8.67
Model refinement		
Resolution in phenix.real_space_refine [Å]	3.30	
No. atoms: protein	17043	
Ligands / ions	GTP, GDP, Mg ²⁺	
Average B factors [Å ²]: protein	76.59	
Average B factors [Å ²]: ligand/ion	19.10	
r.m.s. deviations: bond lengths [Å]	0.006	
r.m.s. deviations: bond angles [°]	0.914	
MolProbity score	2.34	
EMRinger score	2.22	
Rotamers outliers [%]	0.17	
Ramachandran angles: favored [%]	88.52	
Ramachandran angles: allowed [%]	11.48	
Ramachandran angles: outliers [%]	0	
EMDB accession code	EMD-20660	EMD-20661
PDB accession code	6U62	

Table S2. Summary of cryo-EM data collection, 3D reconstruction, and model refinement.