Structure of the eukaryotic replicative CMG helicase and pumpjack motion

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Supplemental Table 1. Cryo-EM data collection and refinement statistics

Data Collection			
EM equipment	FEI Titan Krios	FEI Titan Krios	FEI Titan Krios
Voltage (kV)	300	300	300
Detector	Gatan K2	Gatan K2	Gatan K2
Pixel size (Å)	1.01	1.01	1.01
Electron dose ($e^-/Å^2$)	50	50	50
Defocus range (μm)	1.5~3.5	1.5~3.5	1.5~3.5
3D Reconstruction			
Software	RELION 1.4	RELION 1.4	RELION 1.4
Number of particles used	469, 818	86,822	178, 530
Resolution (Å)	3.7	4.7	4.8
B-factor sharpening ($Å^2$)	-144	-124	-117
Model composition			
Peptide chains	11	11	11
Protein residues	2881	4931	4972
R.m.s deviations			
Bonds length (Å)	0.008	0.008	0.009
Bonds angle	1.376°	1.371°	1.412°
Ramachandran plot			
Preferred (%)	89.39	89.03	90.14
Allowed (%)	9.61	9.27	8.53
Outlier (%)	1.00	1.70	1.33
Validation			
Molprobity score	2.62 (97%)	2.71 (95%)	2.64(97%)
Rotamer outliers (%)	0.23	0.25	0.13