Supplementary Table 1: Cryo-EM data collection, refinement and validation statistics

	DRP1-MID49 Filaments (EMDB-EMD8874) (PDB 5WP9)
Data collection and processing	
Magnification	31,000x
Voltage (kV)	300
Per frame electron exposure (e⁻/Å²)	1.1 to 1.4
Defocus range (μm)	0.3-4
Median defocus	1.3
Pixel size (Å)	1.22
Symmetry imposed	Translational, C2
Initial particle images (no.)	489,879
Final particle images (no.)	410,639
Map resolution (Å)	4.2
FSC threshold	0.143
Map resolution range (Å)	3.8-8.2, (ResMap[74] and LocScale[72])
Refinement	
Initial model used (PDB code)	4BEJ, 4WOY, 3W6O
Model resolution (Å)	4.5 (Average)
FSC threshold	0.5
Model resolution range (Å)	4.1 to 8.2
Map sharpening B factor (Å²)	-225 (Average)
DRP1 G-domain-BSE	-200
DRP1 Stalk	-300 to -400
MID49	-150 to -200
Model composition	
Non-hydrogen atoms	57968
Protein residues	7352
Ligands	8 GMPPCP, 8 Mg
B factors (Å²)	
Protein	-58 to -626
Ligand	-145 to -169
R.M.S. deviations	
Bond lengths (Å)	0.0107
Bond angles (°)	0.98
Validation	
MolProbity score	1.43
Clashscore	2.1
Poor rotamers (%)	0.63
Ramachandran plot	
Favored (%)	93.11
Allowed (%)	98.6
Outliers (%)	1.43

References:
72. Jakobi, A. J., Wilmanns, M. & Sachse, C. Model-based local density sharpening of cryo-EM maps. *Elife* **6,** 1–26 (2017).
74. Kucukelbir, A., Sigworth, F. J. & Tagare, H. D. Quantifying the local resolution of cryo-EM density maps. *Nat. Methods* **11,** 63–65 (2014).