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Supplemental Information

Cryo-EM Reveals How Human Cytoplasmic Dynein Is Auto-inhibited and Activated

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Table S1. Cryo-EM data collection and processing summary, Related to Figure 1.

Data Collection and processing					
	Dynein-(1)	**Dynein-(2)**	**Dynein-(3)**	**DDB-(1)**	**DDB-(2)**
Institution	MRC-LMB	MRC-LMB	DLS	MRC-LMB	CEITEC
Detector	Falcon II	K2 summit	K2 summit	Falcon II	Falcon II
Frames	34	25	20	34	7
Exposure (sec)	2	20	8	2	2
Dose (ē/Å2)	54	40	40	54	54
Micrographs	6746	2649	3781	2634	3058
Pixel size (Å)	1.32	1.43	1.06	1.32	1.34
Raw particles	312, 198	187, 830	214, 543	75, 052	41, 222
Final particles	233,227 (motor) / 102,309 (tail)			78,671	
Resolution	3.8Å (motor) / 8.4Å (tail)			8.7Å / 12Å (masked tail)	

Refinement summary	
Model composition of all proteins	
Non-hydrogen atoms	46214
Amino acid residues	5852
Ligands (ADP/ATP)	6/2
Refinement statistics	
Resolution	257.28 - 3.80
sharpening B-factors ($Å^2$)	-100
Rfactor*	0.339
Overall FSC†	0.820
Correlation coefficient	0.922
Mean B-factor ($Å^2$)	157.1
Rms deviations	
Bond length (Å)	0.0060
Bond angle (°)	1.1182
Chiral volume ($Å^3$)	0.0699
Validation	
MolProbity score	2.13 (100^{th} percentile)
Clashscore, all atom	19.17 (97^{th} percentile)
Good rotamers	95.22%
Ramachandran plot	
Favored	94.87%
Outliers	0.10%
Cβ deviations >0.25Å	0.50%

*Rfactor = $(\Sigma||F_{obs}|-|F_{calc}||)/\Sigma|F_{obs}|$, in which $|F_{obs}|$ is the amplitude of simulated reflections from EM map and $|F_{calc}|$ is the amplitude of calculated reflections from the coordinates.

† Fourier Shell Correlation, $FSC_{overall} = \Sigma(N_{shell} FSC_{shell}) / \Sigma(N_{shell})$, where FSC_{shell} is the FSC in a given shell, N_{shell} is the number of 'structure factors' in the shell. $FSC_{shell} = \Sigma(F_{model} F_{EM})/(\sqrt{(\Sigma(|F|^2_{model}))}\sqrt{(\Sigma(|F|^2_{model}))})$.