

Table S1. Cryo-EM data collection, model refinement and validation statistics of the intact basal body-hook complex in the CCW state.

	Protomers of the CCW-C ring	CCW-ring	LP ring	Proximal rod- export apparatus - 11 FliF loops
Components	FliG ₃ FliM ₃ FliN ₉ FliF ₃	FliG ₃₄ FliM ₃₄ FliN ₁₀₂ FliF ₃₄	FlgH ₂₆ FlgI ₂₆	FliP ₅ R ₁ Q ₄ FliE ₆ FlgB FlgC ₆ FlgF ₅ L1 ₅ &L2 ₅ &L3 ₁
EMDB	EMD-38546	EMD-39349	EMD-37618	EMD-37619
PDB	8XP0	8YJT	8WLE	8WLH
Data collection & processing				
Microscope	Titan Krios	Titan Krios	Titan Krios	Titan Krios
Magnification	81,000	81,000	105,000	105,000
Voltage (kV)	300	300	300	300
Electron exposure (e ⁻ / Å ²)	41	41	45	45
Defocus range (μm)	1.5 to 1.8	1.5 to 1.8	1.0 to 2.5	1.0 to 2.5
Pixel size (Å)	1.1	1.1	1.332	1.332
Symmetry imposed	C1	C34	C26	C1
Initial particles (no.)	19,627	19,627	22,192	22,192
Final particles (no.)	19,627	19,627	11,858	11,858
Map resolution (Å) (FSC = 0.143)	4.0	5.9	3.0	3.7
Refinement				
Initial model used (PDB)	3HJL, 4FHR, 5TDY, 4YXB, 4YX1, AF2	8XP0	7CBL	<i>ModelAngelo</i>
Model resolution (Å) (FSC = 0.5)	9.0	8.7	3.2	4.3
Map sharpening B factor (Å ²)	-150.8	-278.1	-112.3	-74.1
Model composition				
Non-hydrogen atoms	21,156	239,768	99,008	36,230
Protein residues	2,676	30,328	13,364	4,845
B factors (Å²)				
Protein	81.81	81.81	64.04	53.53
Ligand	N/A	N/A	N/A	N/A
R.m.s deviations				
Bond length (Å)	0.002	0.003	0.004	0.005
Bond angles (°)	0.527	0.527	0.624	0.845
Validation				
MolProbity score	2.19	2.22	2.32	2.19
Clashscore	10.97	11.70	17.56	17.25
Ramachandran plot				
Favored (%)	95.56	95.56	97.32	96.13
Outliers (%)	0.80	0.80	0.20	0.46

	Distal rod with the hook	The whole rod with export apparatus and the hook	β -collar-RBM3 subrings of the MS ring (C34)
Components	FlgG ₂₄ FlgE ₂₉	Rod, FliF ₁₁ FliP ₅ R ₁ Q ₄ FlgE ₂₉	FliF ₃₄
EMDB	EMD-37627	EMD-37628	EMD-37620
PDB	8WLP	8WLQ	8WLI
Data collection & processing			
Microscope	Titan Krios	Titan Krios	Titan Krios
Magnification	105,000	105,000	105,000
Voltage (kV)	300	300	300
Electron exposure (e ⁻ /Å ²)	45	45	45
Defocus range (μm)	1.0 to 2.5	1.0 to 2.5	1.0 to 2.5
Pixel size (Å)	1.332	1.332	1.332
Symmetry imposed	C1	C1	C34
Initial particles (no.)	22,192	22,192	22,192
Final particles (no.)	11,858	11,858	11,858
Map resolution (Å) (FSC = 0.143)	3.8	3.8	3.2
Refinement			
Initial model used (PDB)	<i>ModelAngelo</i>	<i>ModelAngelo</i>	<i>ModelAngelo</i>
Model resolution (Å) (FSC = 0.5)	4.1	4.2	3.4
Map sharpening B factor (Å ²)	-71.4	-66.0	-116.2
Model composition			
Non-hydrogen atoms	131,528	167,758	43,350
Protein residues	17,770	22,615	5,576
B factors (Å ²)			
Protein	75.07	70.41	65.75
Ligand	N/A	N/A	N/A
R.m.s deviations			
Bond length (Å)	0.005	0.005	0.004
Bond angles (°)	0.780	0.795	0.707
Validation			
MolProbity score	1.95	2.08	1.57
Clashscore	13.94	17.25	11.33
Ramachandran plot			
Favored (%)	96.20	96.19	98.75
Outliers (%)	0.39	0.41	0.00

	MS ring with the proximal rod and the export apparatus (C1)	The membrane-anchored part (CCW)	The C ring-containing basal body-hook complex (CCW)
Components	FliF ₃₄ FliE ₆ FliP ₅ FliR ₁ FliQ ₄ FlgB ₅ FlgC ₆	Rod, Export apparatus, LP ring, MS ring, Hook	Intact basal body-hook complex
EMDB	EMD-37625	EMD-37630	EMD-37679
PDB	8WLN	8WLT	8WO5
Data collection & processing			
Microscope	Titan Krios	Titan Krios	Titan Krios
Magnification	105,000	105,000	81,000
Voltage (kV)	300	300	300
Electron exposure (e ⁻ / Å ²)	45	45	41
Defocus range (μm)	1.0 to 2.5	1.0 to 2.5	1.5 to 1.8
Pixel size (Å)	1.332	1.332	1.1
Symmetry imposed	C1	C1	C34
Initial particles (no.)	22,192	22,192	19,627
Final particles (no.)	11,858	11,858	10,318
Map resolution (Å) (FSC = 0.143)	4.3	4.1	7.4
Refinement			
Initial model used (PDB)	<i>ModelAngelo</i> 7CGO AF2	7CBL, 7CGO AF2 <i>ModelAngelo</i>	
Model resolution (Å) (FSC = 0.5)	7.3	6.6	
Map sharpening B factors (Å ²)	-74.6	-52.1	
Model composition			
Non-hydrogen atoms	99,060	338,664	
Protein residues	12,996	45,376	
Ligands	N/A	N/A	
B factors (Å ²)			
Protein	67.08	69.12	
Ligand	N/A	N/A	
R.m.s deviations			
Bond length (Å)	0.008	0.006	
Bond angles (°)	1.076	0.843	
Validation			
MolProbity score	2.37	2.28	
Clashscore	19.59	18.24	
Ramachandran plot			
Favored (%)	96.11	96.50	
Outliers (%)	0.90	0.48	