
CryoEM structures reveal how the bacterial flagellum rotates and switches direction

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Supplementary Tables

Supplementary Table 1

	CCW C-ring (EMDB: EMD-41100) (PDB:8T8O)	MS-ring (EMDB: EMD-41101) (PDB:8T8P)	CW C-ring (EMD-43256) (PDB:8VIB)	CW C-ring with extra density (EMD-43258) (PDB:8VID)
Data Collection				
Microscope	Thermo Fisher FEI Titan G4	Thermo Fisher FEI Titan G4	Thermo Fisher FEI Titan G4	Thermo Fisher FEI Titan G4
Detector	Gatan K3	Gatan K3	Gatan K3	Gatan K3
Magnification	105,000x	105,000x	105,000x	105,000x
Voltage (kV)	300	300	300	300
Electron exposure (e ⁻ /Å ²)	51.557	51.557	56.323	59.242
Defocus range (μm)	-1.0 to -2.0	-1.0 to -2.0	-1.0 to -2.1	-0.9 to -2.3
Pixel size (Å)	0.818	0.818	0.818	0.818
Total micrographs taken	34,381	34,381	35,552	26,130
Data Processing				
Micrographs used for processing	34,275	34,275	35,552	26,130
Symmetry imposed	C34	C11	C34	C34
Initial particle images	295,031	295,031	43,741	59,404
Final particle images	51,268	16,411	7,201	11,106
Map resolution (Å)	3.98	3.42	4.6	5.9
FSC threshold	0.143	0.143	0.143	0.143
Model Refinement				
Initial model used (PDB)	Ab-initio	PDB: 8FTF ¹⁰	PDB: 8T8O	PDB: 8T8O
Model resolution (Å)	3.9 (masked), 3.9 (unmasked)	3.4 (masked), 3.5 (unmasked)	4.6 (masked), 10 (unmasked)	5.9 (masked), 10 (unmasked)
Model composition				
Total atoms	205,020	69,025	151,198	151,198
Protein residues	30,396	9,009	30,362	30,362
Validation				
RMSD Bond lengths (Å)	0.007	0.009	n/a	n/a
RMSD Bond angles (°)	0.984	0.916	n/a	n/a
Rotamer outliers (%)	1.04	0.21	n/a	n/a
Ramachandran plot			n/a	n/a
Favored (%)	95.06	96.53	n/a	n/a
Allowed (%)	4.94	2.86	n/a	n/a
Disallowed (%)	0	0.61	n/a	n/a

Supplementary Table 1. Cryo-EM data collection, processing, model refinement, and validation statistics.

Supplementary Data Table 2

Subunit	Residues	Domain Name	Name(s) in literature	Location	Refs
FliF	FliF ₁₋₁₅	FliF _N	FliF N-terminus	cytoplasm	
	FliF ₁₅₋₅₀	TM1	TM1	M-ring	
	FliF ₅₀₋₁₀₆	RBM1	RBM1	S-ring	5
	FliF ₁₀₇₋₁₂₄	none (linker)	none	S-ring	
	FliF ₁₂₅₋₂₂₈	RBM2	RBM2	S-ring	5
	FliF ₂₂₈₋₂₇₃	RBM3a	RBM3a	S-ring	5
	FliF ₂₇₃₋₃₇₉	β -collar	β -collar	S-ring	5
	FliF ₃₇₉₋₄₃₇	RBM3b	RBM3b	S-ring	5
	FliF ₄₃₈₋₅₀₁	TM2	TM2	M-ring	
	FliF ₅₀₂₋₅₁₃	none (linker)	none	cytoplasm	
	FliF ₅₁₄₋₅₆₀	FliF _C	FliF _C	C-ring	34,36
FliG	FliG ₁₋₆₇	FliG _{D1}	FliG _N	C-ring	34,36
	FliG ₆₈₋₇₂	FliG _{L1}	Helix _{NM}	C-ring	38
	FliG ₇₃₋₉₉	FliG _{D2}	Helix _{NM} , H ₆ & H ₇ , G _N α 4	C-ring	34,36,38
	FliG ₁₀₀₋₁₀₆	FliG _{L2}	loop _M	C-ring	38
	FliG ₁₀₇₋₁₈₆	FliG _{D3}	FliG _M , ARM _M , FliG _M , domain I	C-ring	30,38
	FliG ₁₈₇₋₁₉₅	FliG _{L3}	loop _C , helix _{MC}	C-ring	35,38
	FliG ₁₉₆₋₂₃₃	FliG _{D4}	ARM _C , FliG _{CN}	C-ring	35,38
	FliG ₂₃₄₋₂₄₂	FliG _{L4}	none	C-ring	
	FliG ₂₄₃₋₃₃₁	FliG _{D5}	FliG _C , FliG _{CC} , domain II	C-ring	30,33,35
FliM	FliM ₁₋₁₆	FliM _N	FliM _N , FliM ₁₆ (residues 1-16)	C-ring	73
	FliM ₁₇₋₃₀	FliM _N	none	C-ring	
	FliM ₃₁₋₅₀	FliM _{L1}	none	C-ring	
	FliM ₅₁₋₂₃₀	FliM _{mid}	FliM, FliM _{mid} , FliM _M	C-ring	32,74
	FliM ₂₃₁₋₂₅₆	FliM _{L2}	none	C-ring	
	FliM ₂₅₇₋₃₃₀	FliM _C	FliM _C , SpoA domain	C-ring	39
FliN	FliN ₁₋₄₄	FliM _N	none	C-ring	
	FliN _{45/59/63-137}	FliN _C	FliN, SpoA domain	C-ring	39,42

Supplementary Table 2. Domain nomenclature of FliF, FliG, FliM, and FliN. Residues that belong to structurally defined domains in the assembled C-ring are indicated. A subset of the historical name(s) for these regions of sequence are indicated. Select literature citations are included to illustrate settings where other names are used. As the mapping of domain names is meant to assist in comparison to past structural work, these citations focus on the nomenclature used in comparator structures for C-ring analysis rather than the first use of the domain name in the literature. RBM, ring-building motif; TM, transmembrane.