Supplementary Table 1: 33-fold FliF Cryo-EM data collection, refinement and validation statistics

	33-fold FliF Whole map (EMD-10143) (PDB-6SCN)	33-fold FliF RBM3/β-collar (EMD-10145) (PDB-6SD1)	33-fold FliF $RBM2_{inner}$ (EMD-10146) (PDB-6SD2)
Data collection and processing			
Magnification	165,000	165,000	165,000
Voltage (kV)	300	300	300
Electron exposure (e–/Å^2)	48	48	48
Defocus range (μm)	0.5–4	0.5–4	0.5–4
Pixel size (Å)	0.822	0.822	0.822
Symmetry imposed	C3	C33	C21
Initial particle images (no.)	449142	449142	449142
Final particle images (no.)	175233	77849	84797
Map resolution (Å)	3.1	2.6	2.9
FSC threshold	0.143	0.143	0.143
Map resolution range (Å)	2.9-5.0		
Refinement			
Initial model used (PDB code)	*Ab initio*	*Ab initio*	*Ab initio*
Model resolution (Å)	3.1	2.6	2.9
FSC threshold	0.143	0.143	0.143
Model resolution range (Å)			
Map sharpening *B* factor (Å^2)	-72	-62	-104
Model composition			
Non-hydrogen atoms	60582	39377	13566
Protein residues	7875	4984	1848
Ligands	0	0	0
B factors (Å^2)			
Protein	130	53	59
Ligand	N/A	N/A	N/A
R.m.s. deviations			
Bond lengths (Å)	0.007	0.003	0.009
Bond angles (°)	0.817	0.442	0.770
Validation			
MolProbity score	2.0	1.7	2.4
Clashscore	13.0	7.1	6.7
Poor rotamers (%)	0.8	0.0	5.6
Ramachandran plot			
Favored (%)	94.3	95.7	92.7
Allowed (%)	4.9	4.3	7.3
Disallowed (%)	0.8	0.0	0.0

Supplementary Table 2: 34-fold FliF Cryo-EM data collection, refinement and validation statistics

	34-fold FliF Whole map (EMD-10147) (PDB-6SD3)	34-fold FliF RBM3/β-collar (EMD-10148) (PDB-6SD4)	34-fold FliF $RBM2_{inner}$ (EMD-10149) (PDB-6SD5)
Data collection and processing			
Magnification	165,000	165,000	165,000
Voltage (kV)	300	300	300
Electron exposure (e–/Å^2)	48	48	48
Defocus range (μm)	0.5–4	0.5–4	0.5–4
Pixel size (Å)	0.822	0.822	0.822
Symmetry imposed	C2	C34	C22
Initial particle images (no.)*	449142	449142	449142
Final particle images (no.)	140606	140606	87107
Map resolution (Å)	3.3	2.8	3.1
FSC threshold	0.143	0.143	0.143
Map resolution range (Å)	3.1-7.4	2.7-3.6	3.0-3.9
Refinement			
Initial model used (PDB code)	EMD-10143	EMD-10143	EMD-10143
Model resolution (Å)	3.3	2.8	3.1
FSC threshold	0.143	0.143	0.143
Model resolution range (Å)			
Map sharpening *B* factor (Å^2)	-67	-85	-103
Model composition			
Non-hydrogen atoms	63144	40562	14212
Protein residues	8212	5134	1936
Ligands	0	0	0
B factors (Å^2)			
Protein	139	41	51
Ligand	N/A	N/A	N/A
R.m.s. deviations			
Bond lengths (Å)	0.008	0.009	0.006
Bond angles (°)	0.824	0.657	0.617
Validation			
MolProbity score	2.3	1.9	2.0
Clashscore	12.3	5.7	7.1
Poor rotamers (%)	1.2	0.8	1.4
Ramachandran plot			
Favored (%)	88.5	89.7	91.7
Allowed (%)	10.8	9.6	8.3
Disallowed (%)	0.7	0.7	0.0

* Particle numbers quoted are post-2D clean-up

Supplementary Table 3: 32-fold and 35-fold FliF Cryo-EM data collection, refinement and validation statistics

	32-fold FliF RBM3/β-collar (EMD-10560) (PDB-6TRE)	35-fold FliF RBM3/β-collar (EMD-10561)
Data collection and processing		
Magnification	165,000	165,000
Voltage (kV)	300	300
Electron exposure (e–/Å^2)	48	48
Defocus range (μm)	0.5–4	0.5–4
Pixel size (Å)	0.822	0.822
Symmetry imposed	C32	C35
Initial particle images (no.)*	449142	449142
Final particle images (no.)	33026	42165
Map resolution (Å)	3.3	4.5
FSC threshold	0.143	0.143
Map resolution range (Å)	3.2-6.0	4.1-6.6
Refinement		
Initial model used (PDB code)	EMD-10143	
Model resolution (Å)	3.3	
FSC threshold	0.143	
Model resolution range (Å)		
Map sharpening *B* factor (Å^2)	-106	
Model composition		
Non-hydrogen atoms	38176	
Protein residues	4832	
Ligands	0	
B factors (Å^2)		
Protein	70	
Ligand	N/A	
R.m.s. deviations		
Bond lengths (Å)	0.009	
Bond angles (°)	0.87	
Validation		
MolProbity score	3.1	
Clashscore	18.4	
Poor rotamers (%)	11.3	
Ramachandran plot		
Favored (%)	89.7	
Allowed (%)	10.3	
Disallowed (%)	0.0	

* Particle numbers quoted are post-2D clean-up

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