



wwPDB EM Validation Summary Report ⓘ

May 19, 2024 – 11:19 PM JST

PDB ID : 7CBM
EMDB ID : EMD-30336
Title : Cryo-EM structure of the flagellar distal rod with partial hook from Salmonella
Authors : Tan, J.X.; Chang, S.H.; Wang, X.F.; Xu, C.H.; Zhou, Y.; Zhang, X.; Zhu, Y.Q.
Deposited on : 2020-06-12
Resolution : 3.20 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

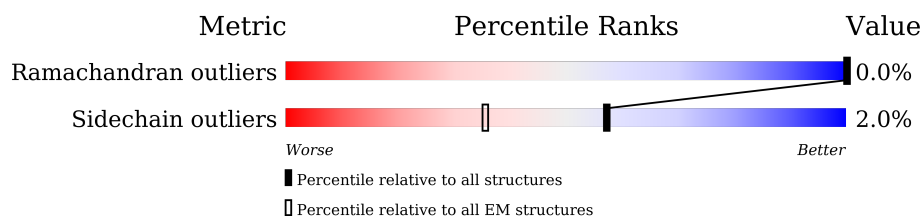
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	260	<div> <div>7%</div> <div>98%</div> <div>.</div> </div>
1	B	260	<div> <div>15%</div> <div>98%</div> <div>.</div> </div>
1	C	260	<div> <div>10%</div> <div>97%</div> <div>.</div> </div>
1	D	260	<div> <div>9%</div> <div>99%</div> <div>.</div> </div>
1	E	260	<div> <div>8%</div> <div>97%</div> <div>.</div> </div>
1	F	260	<div> <div>7%</div> <div>99%</div> <div>.</div> </div>
1	G	260	<div> <div>6%</div> <div>99%</div> <div>.</div> </div>
1	H	260	<div> <div>7%</div> <div>99%</div> <div>.</div> </div>
1	I	260	<div> <div>7%</div> <div>98%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	J	260	8% 97% .
1	K	260	. 98% .
1	L	260	5% 98% .
1	M	260	6% 98% .
1	N	260	7% 96% ..
1	O	260	7% 95% ..
1	P	260	6% 93% . 5%
1	Q	260	7% 94% . 5%
1	R	260	5% 93% . .
1	S	260	6% 93% . 5%
1	T	260	5% 97% ..
1	U	260	10% 98% .
1	V	260	10% 98% .
1	W	260	12% 98% .
1	X	260	18% 98% .
2	a	251	17% 98% ..
2	b	251	23% 98% ..
2	c	251	16% 98% ..
2	d	251	20% 97% ..
2	e	251	38% 97% ..
3	DA	403	52% 99% .
3	DB	403	51% 98% .
3	DC	403	53% 98% .
3	DD	403	54% 97% .
3	DE	403	59% 99% .

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Mol	Chain	Length	Quality of chain
3	DF	403	<div><div>67%</div><div>98%</div><div>.</div></div>
3	DG	403	<div><div>72%</div><div>99%</div><div>.</div></div>
3	DH	403	<div><div>76%</div><div>98%</div><div>.</div></div>
3	DI	403	<div><div>80%</div><div>98%</div><div>.</div></div>
3	DJ	403	<div><div>82%</div><div>97%</div><div>.</div></div>
3	DK	403	<div><div>88%</div><div>99%</div><div>.</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 87698 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Flagellar basal-body rod protein FlgG.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	B	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	C	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	D	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	E	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	F	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	G	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	H	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	I	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	J	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	K	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	L	259	Total 1941	C 1197	N 340	O 399	S 5	0	0
1	M	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	N	251	Total 1887	C 1167	N 330	O 384	S 6	0	0
1	O	252	Total 1894	C 1172	N 331	O 385	S 6	0	0
1	P	248	Total 1862	C 1151	N 327	O 379	S 5	0	0
1	Q	247	Total 1858	C 1149	N 326	O 378	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	250	Total	C	N	O	S	0	0
			1875	1159	329	382	5		
1	S	247	Total	C	N	O	S	0	0
			1858	1149	326	378	5		
1	T	253	Total	C	N	O	S	0	0
			1902	1176	333	388	5		
1	U	259	Total	C	N	O	S	0	0
			1941	1197	340	399	5		
1	V	259	Total	C	N	O	S	0	0
			1941	1197	340	399	5		
1	W	259	Total	C	N	O	S	0	0
			1941	1197	340	399	5		
1	X	259	Total	C	N	O	S	0	0
			1941	1197	340	399	5		

- Molecule 2 is a protein called Flagellar basal-body rod protein FlgF.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
2	b	248	Total	C	N	O	S	0	0
			1804	1106	324	367	7		
2	c	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
2	d	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
2	e	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		

- Molecule 3 is a protein called Flagellar hook protein FlgE.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	DA	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
3	DB	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
3	DC	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
3	DD	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
3	DE	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	DF	401	Total 2947	C 1814	N 507	O 618	S 8	0	0
3	DG	401	Total 2947	C 1814	N 507	O 618	S 8	0	0
3	DH	401	Total 2947	C 1814	N 507	O 618	S 8	0	0
3	DI	401	Total 2947	C 1814	N 507	O 618	S 8	0	0
3	DJ	401	Total 2947	C 1814	N 507	O 618	S 8	0	0
3	DK	401	Total 2947	C 1814	N 507	O 618	S 8	0	0

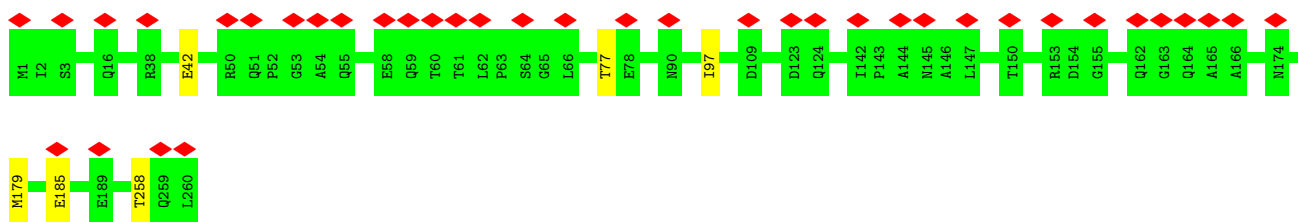
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

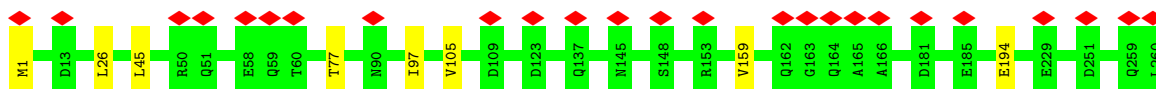
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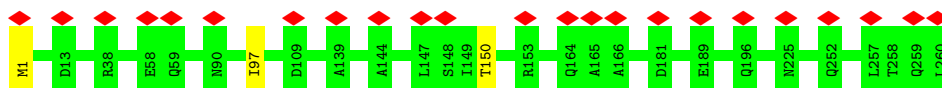
- Molecule 1: Flagellar basal-body rod protein FlgG



- Molecule 1: Flagellar basal-body rod protein FlgG

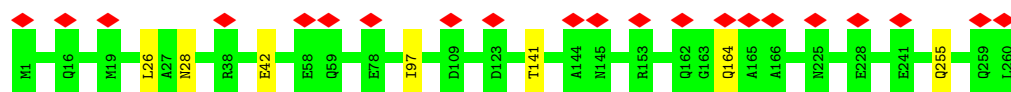


- Molecule 1: Flagellar basal-body rod protein FlgG

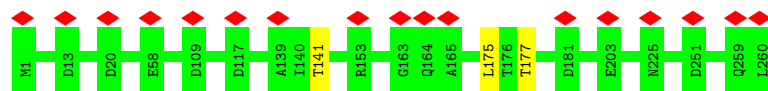


- Molecule 1: Flagellar basal-body rod protein FlgG

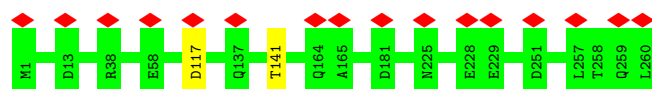




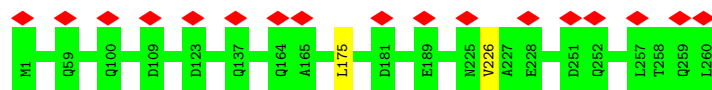
- Molecule 1: Flagellar basal-body rod protein FlgG



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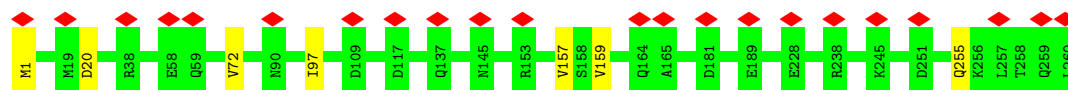
- Molecule 1: Flagellar basal-body rod protein FlgG



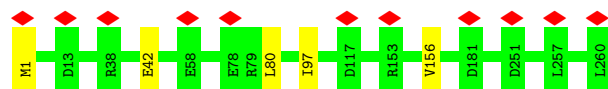
- Molecule 1: Flagellar basal-body rod protein FlgG



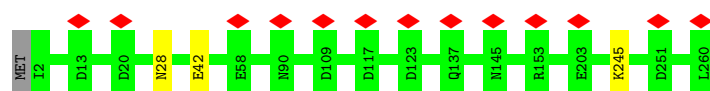
- Molecule 1: Flagellar basal-body rod protein FlgG



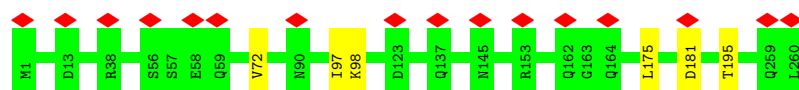
- Molecule 1: Flagellar basal-body rod protein FlgG



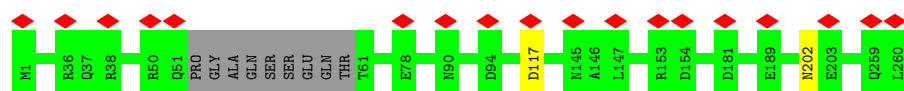
- Molecule 1: Flagellar basal-body rod protein FlgG



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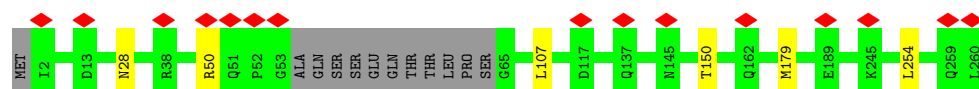
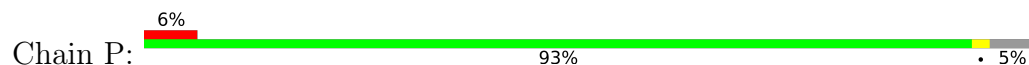
- Molecule 1: Flagellar basal-body rod protein FlgG



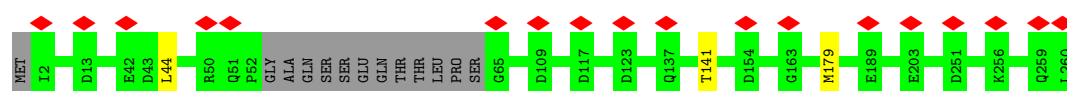
- Molecule 1: Flagellar basal-body rod protein FlgG



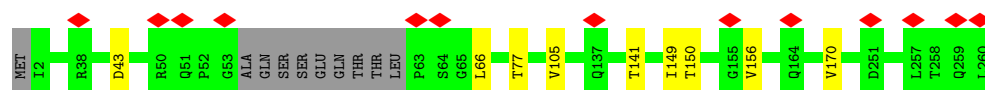
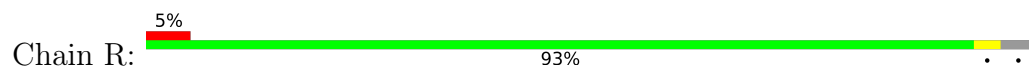
- Molecule 1: Flagellar basal-body rod protein FlgG



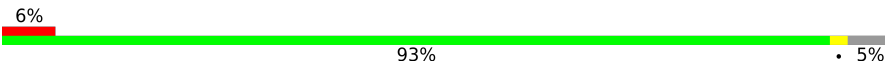
- Molecule 1: Flagellar basal-body rod protein FlgG



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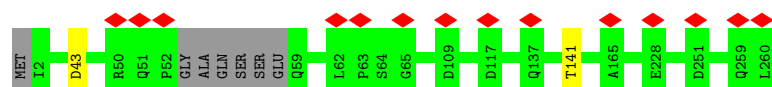
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain S: 



- Molecule 1: Flagellar basal-body rod protein FlgG

Chain T: 



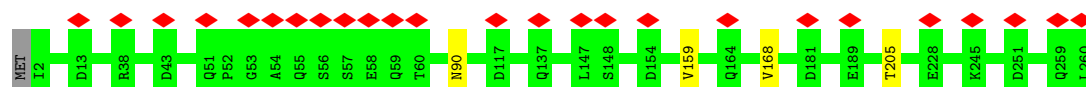
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain U: 



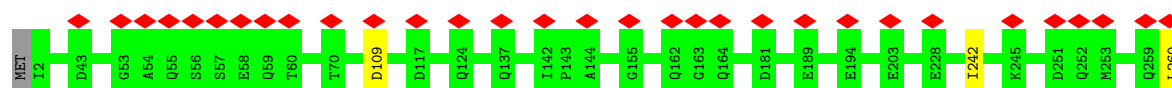
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain V: 



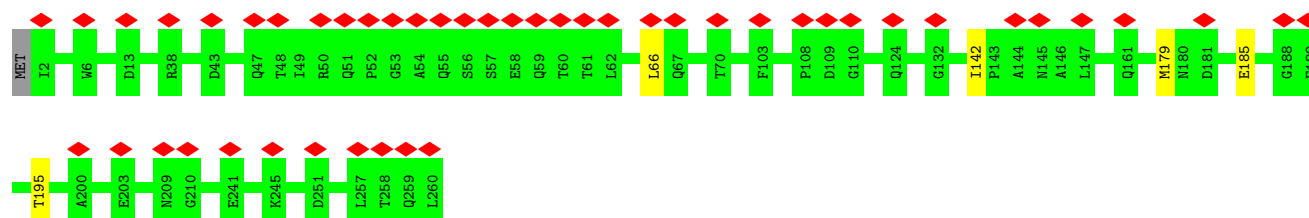
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain W: 

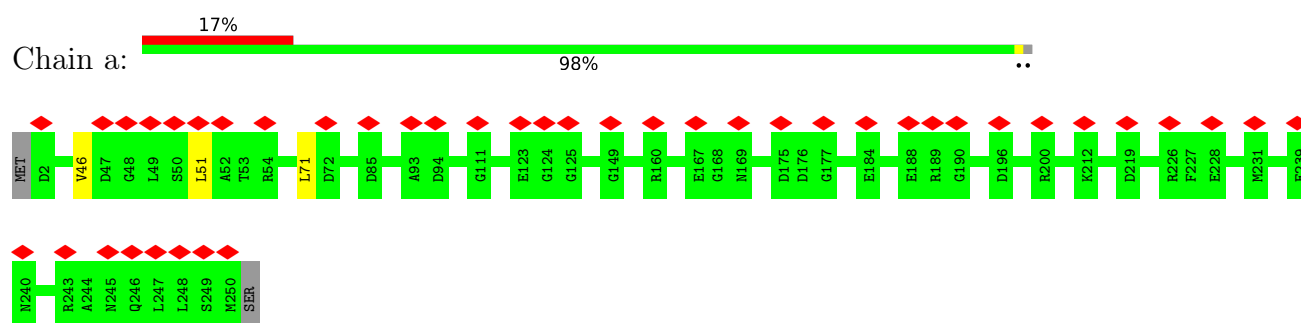


- Molecule 1: Flagellar basal-body rod protein FlgG

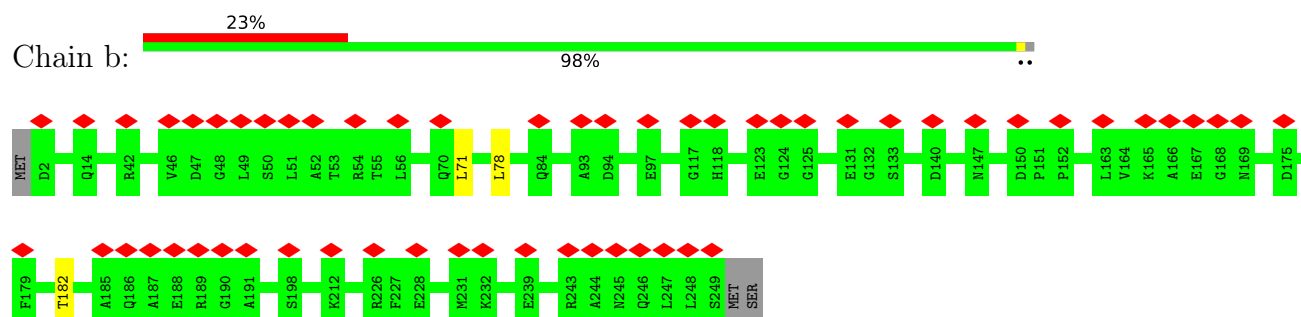
Chain X: 



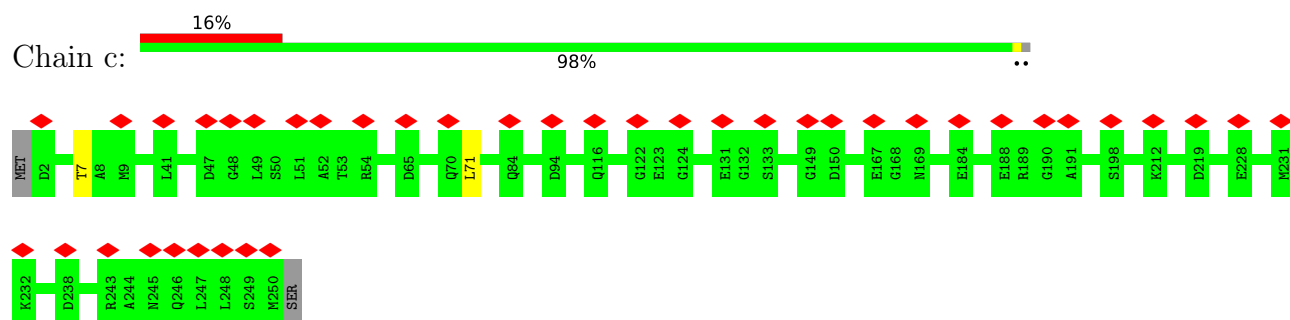
- Molecule 2: Flagellar basal-body rod protein FlgF



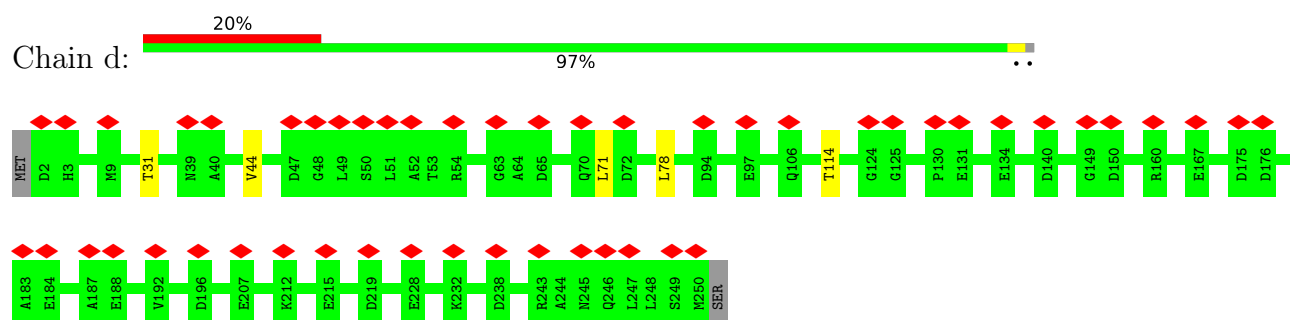
- Molecule 2: Flagellar basal-body rod protein FlgF



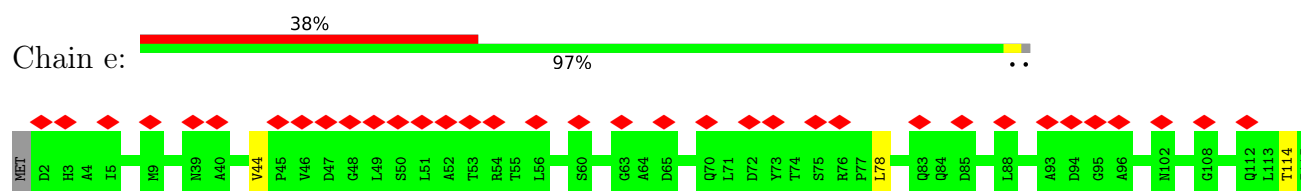
- Molecule 2: Flagellar basal-body rod protein FlgF

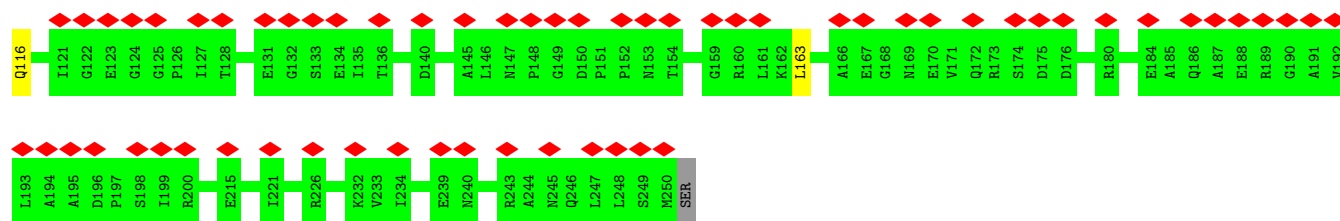


- Molecule 2: Flagellar basal-body rod protein FlgF

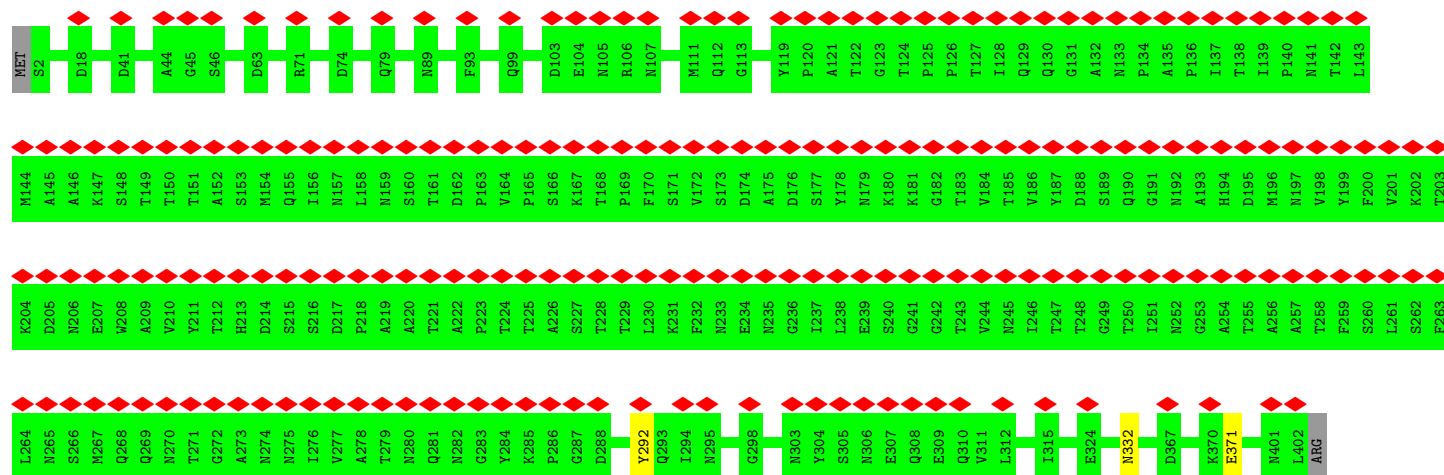


- Molecule 2: Flagellar basal-body rod protein FlgF





• Molecule 3: Flagellar hook protein FlgE

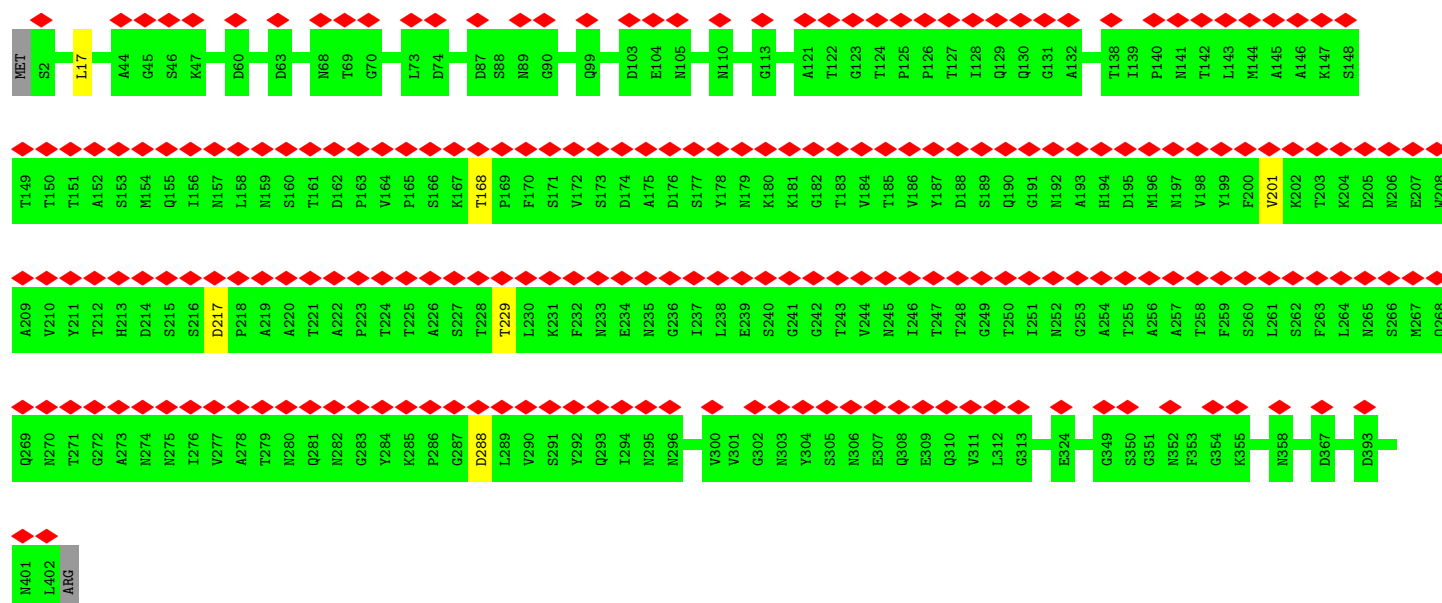


• Molecule 3: Flagellar hook protein FlgE

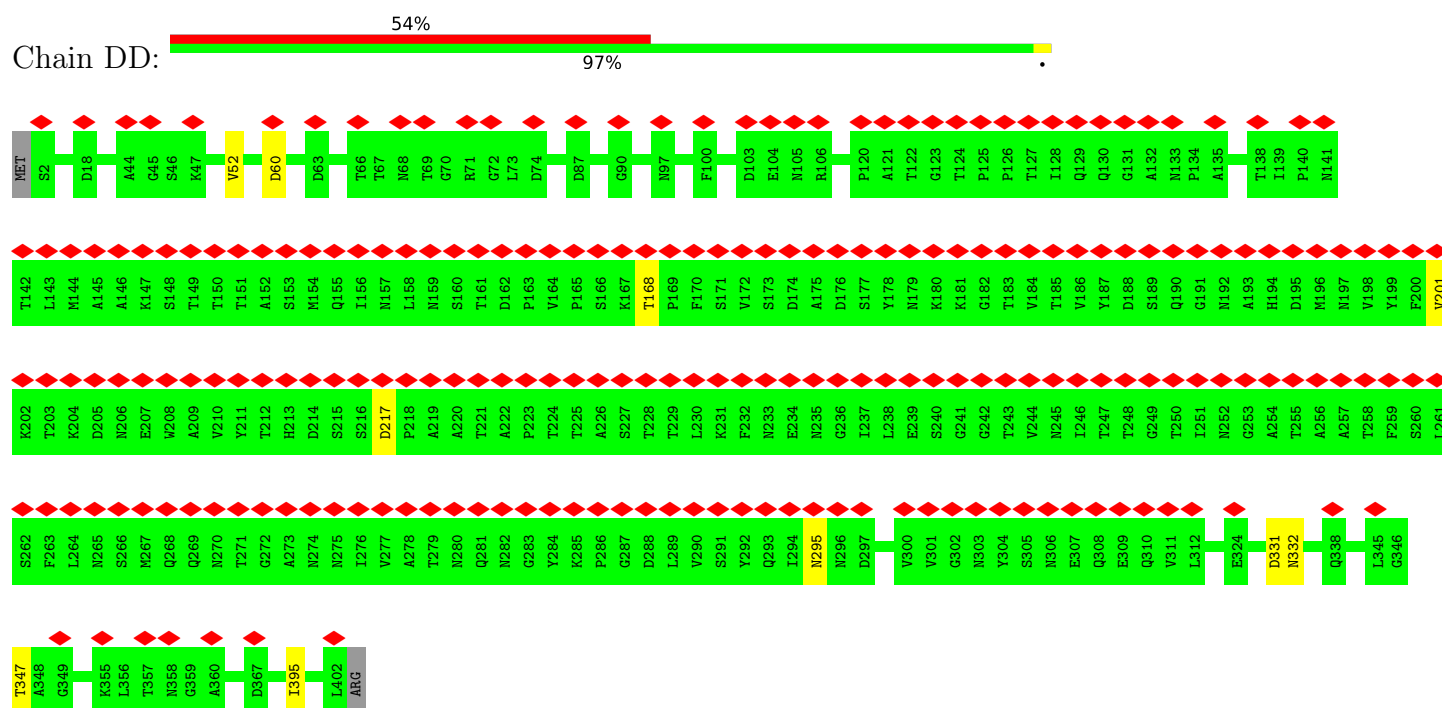


• Molecule 3: Flagellar hook protein FlgE

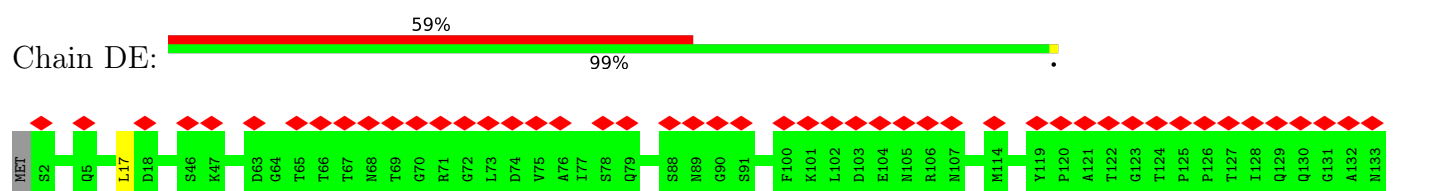


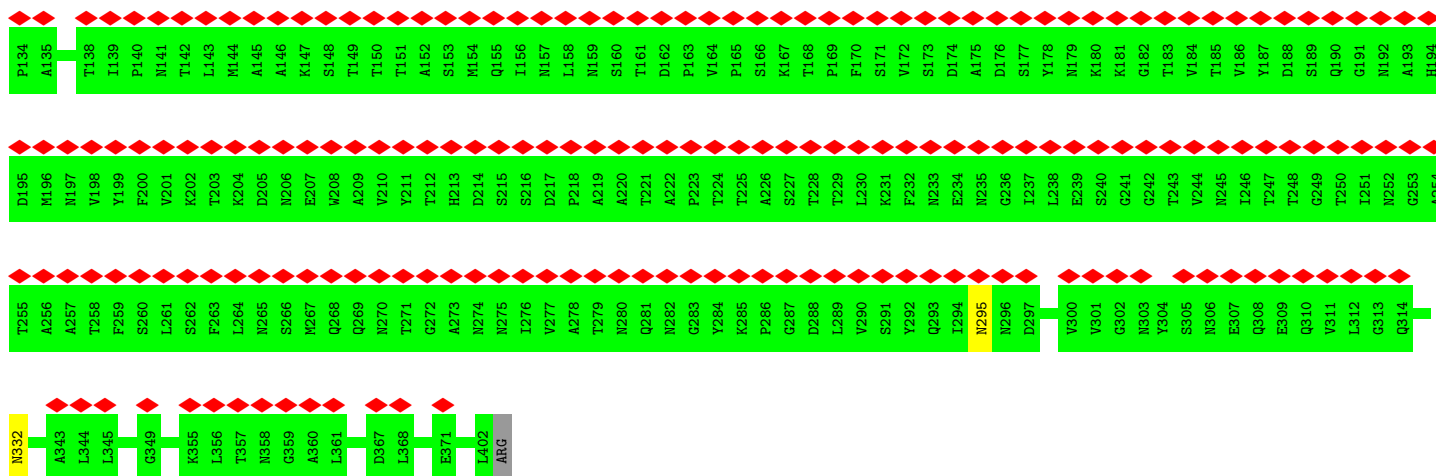


Chain DD:



Chain DE:

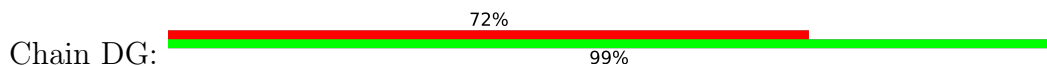


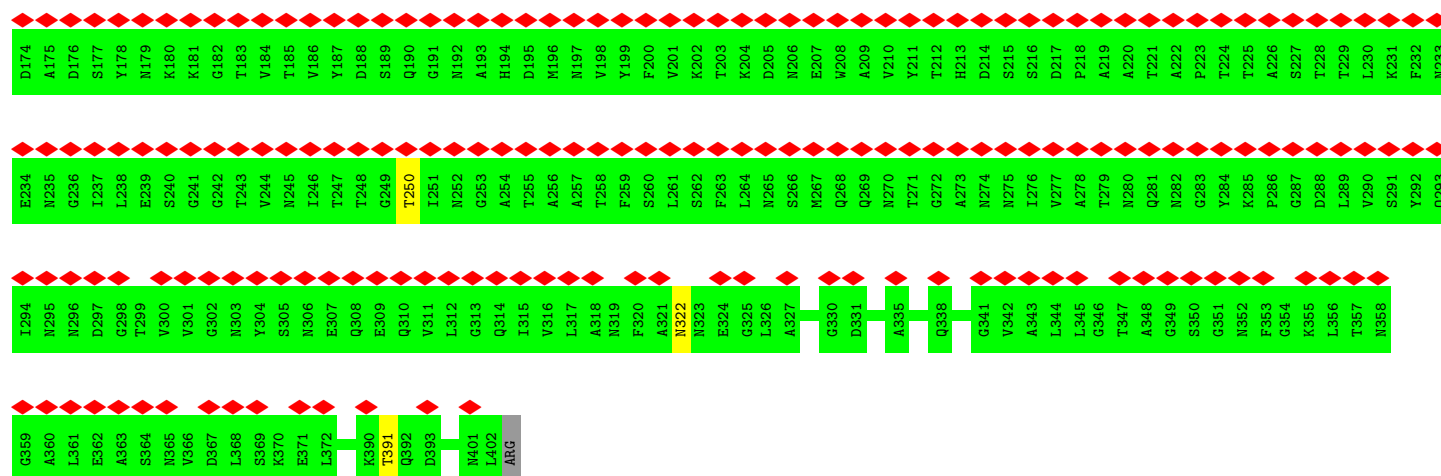


• Molecule 3: Flagellar hook protein FlgE

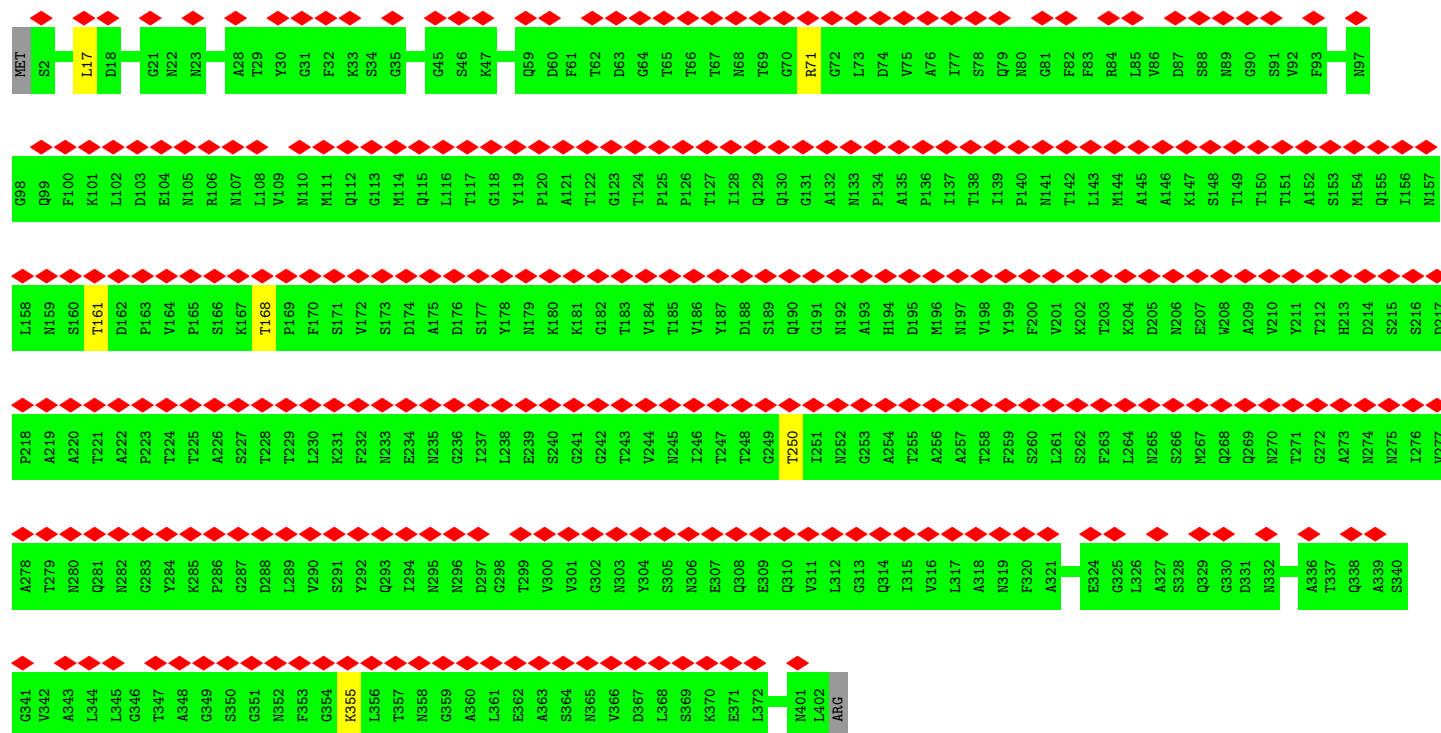
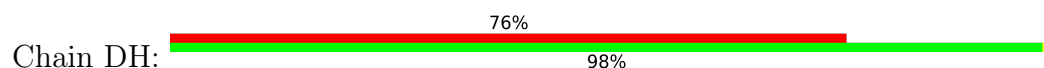


• Molecule 3: Flagellar hook protein FlgE

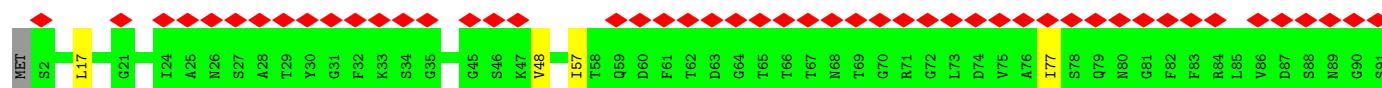


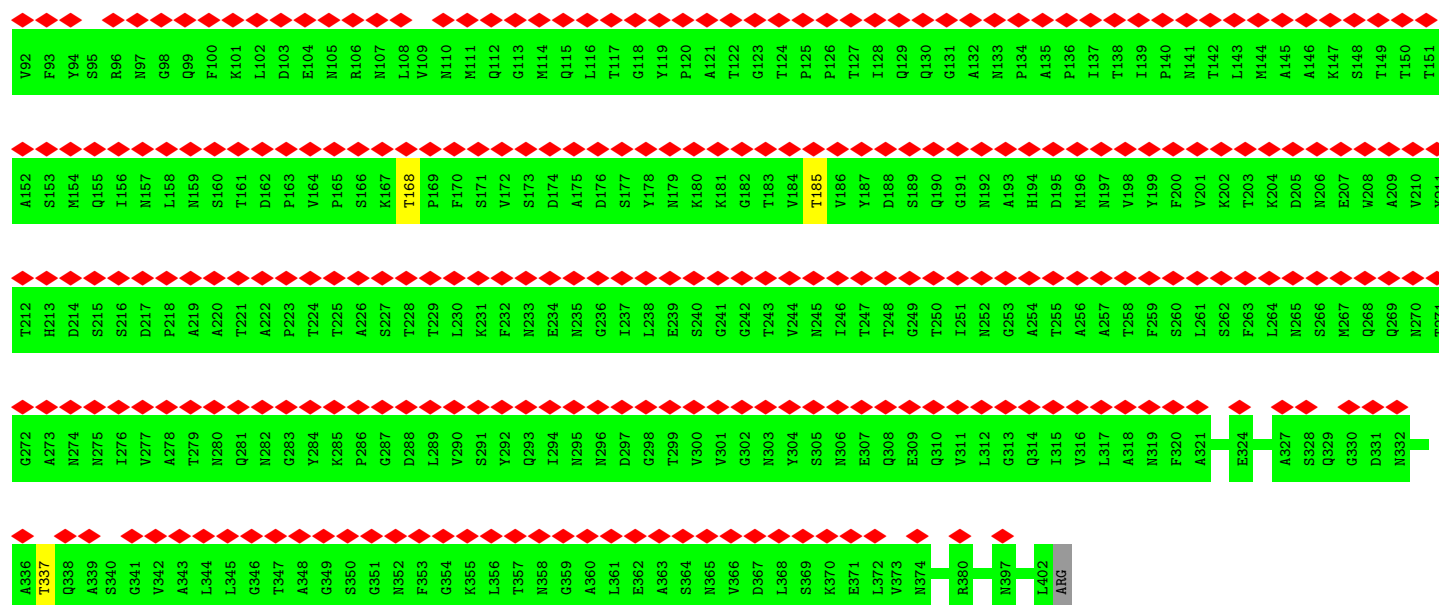


• Molecule 3: Flagellar hook protein FlgE



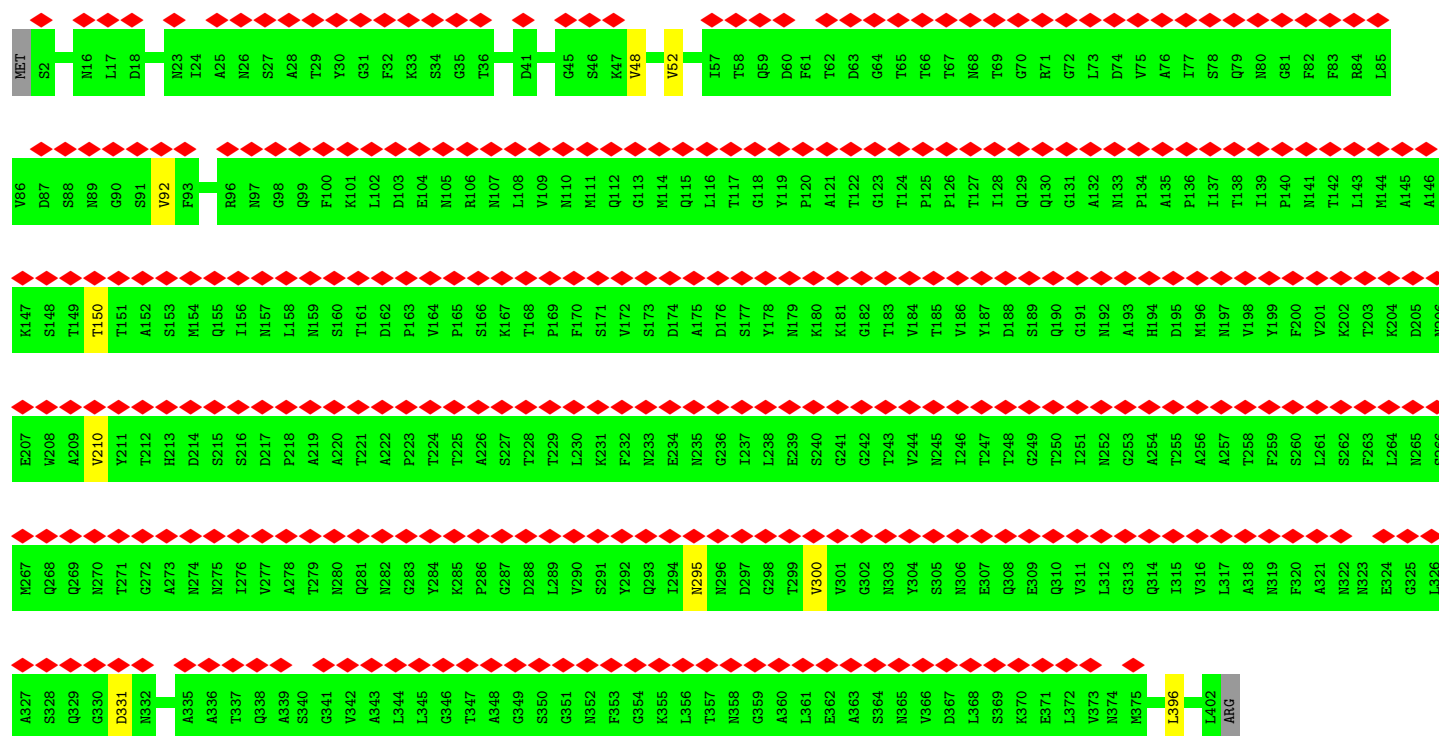
• Molecule 3: Flagellar hook protein FlgE





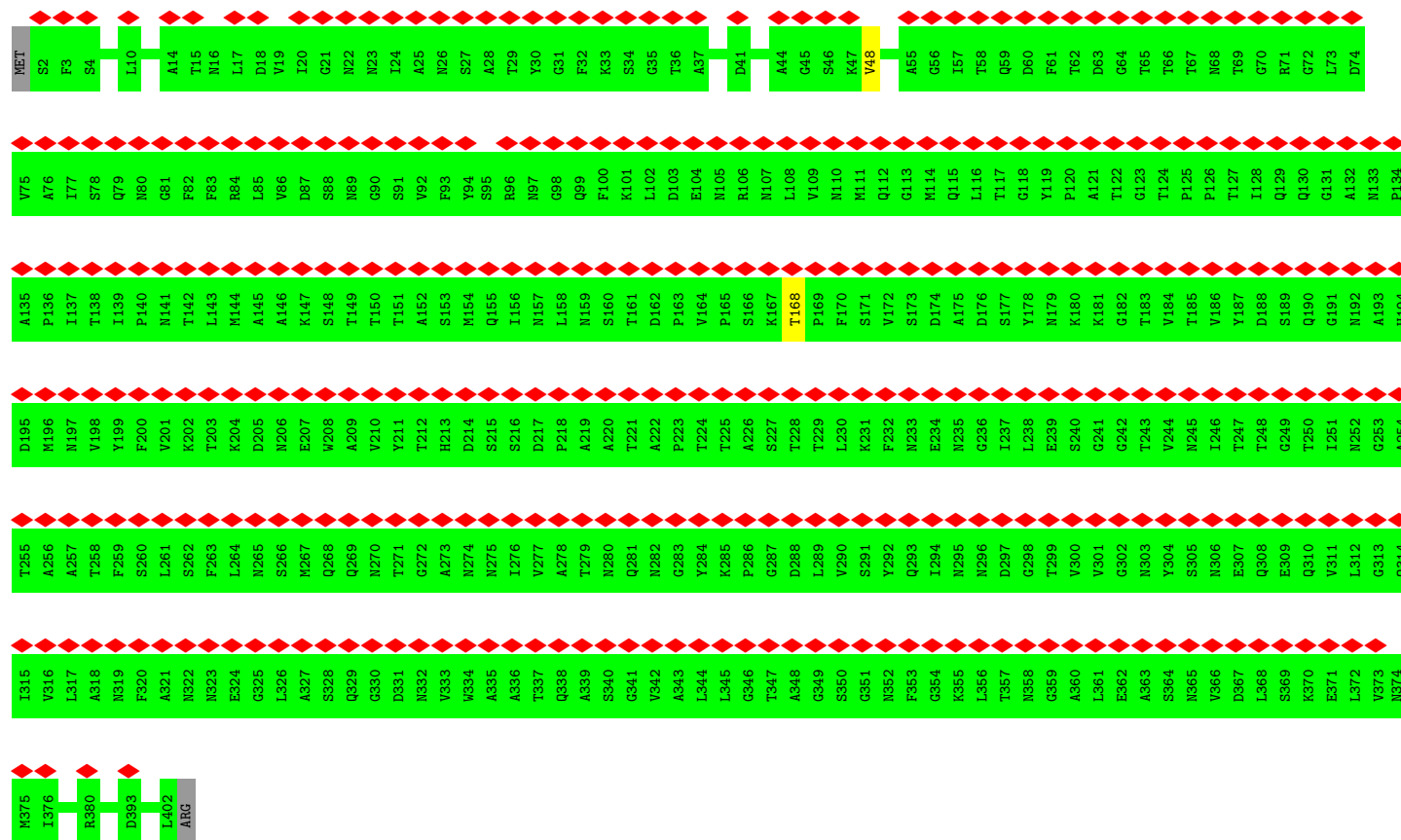
• Molecule 3: Flagellar hook protein FlgE

Chain DJ: 82% 97%



• Molecule 3: Flagellar hook protein FlgE

Chain DK: 88% 99%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	118962	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.880	Depositor
Minimum map value	-1.506	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.592	Depositor
Map size (Å)	669.184, 669.184, 669.184	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.307, 1.307, 1.307	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.28	0/1973	0.47	0/2682
1	B	0.27	0/1973	0.48	0/2682
1	C	0.28	0/1973	0.48	0/2682
1	D	0.28	0/1973	0.48	0/2682
1	E	0.28	0/1973	0.48	0/2682
1	F	0.29	0/1973	0.49	0/2682
1	G	0.28	0/1973	0.48	0/2682
1	H	0.28	0/1973	0.48	0/2682
1	I	0.28	0/1973	0.49	0/2682
1	J	0.28	0/1973	0.48	0/2682
1	K	0.29	0/1973	0.47	0/2682
1	L	0.28	0/1965	0.48	0/2672
1	M	0.29	0/1973	0.48	0/2682
1	N	0.28	0/1909	0.47	0/2593
1	O	0.28	0/1917	0.48	0/2605
1	P	0.28	0/1884	0.48	0/2559
1	Q	0.28	0/1880	0.48	0/2554
1	R	0.29	0/1898	0.49	0/2578
1	S	0.28	0/1880	0.48	0/2554
1	T	0.28	0/1925	0.47	0/2617
1	U	0.27	0/1965	0.48	0/2672
1	V	0.28	0/1965	0.47	0/2672
1	W	0.28	0/1965	0.48	0/2672
1	X	0.27	0/1965	0.48	0/2672
2	a	0.26	0/1836	0.49	0/2502
2	b	0.26	0/1828	0.48	0/2492
2	c	0.27	0/1836	0.49	0/2502
2	d	0.27	0/1836	0.49	0/2502
2	e	0.26	0/1836	0.49	0/2502
3	DA	0.26	0/2991	0.45	0/4076
3	DB	0.26	0/2991	0.46	0/4076
3	DC	0.26	0/2991	0.45	0/4076
3	DD	0.26	0/2991	0.46	0/4076
3	DE	0.26	0/2991	0.45	0/4076

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	DF	0.26	0/2991	0.46	0/4076
3	DG	0.25	0/2991	0.45	0/4076
3	DH	0.25	0/2991	0.45	0/4076
3	DI	0.25	0/2991	0.44	0/4076
3	DJ	0.25	0/2991	0.45	0/4076
3	DK	0.25	0/2991	0.45	0/4076
All	All	0.27	0/88867	0.47	0/120940

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	258/260 (99%)	247 (96%)	11 (4%)	0	100	100
1	B	258/260 (99%)	248 (96%)	10 (4%)	0	100	100
1	C	258/260 (99%)	246 (95%)	12 (5%)	0	100	100
1	D	258/260 (99%)	244 (95%)	14 (5%)	0	100	100
1	E	258/260 (99%)	246 (95%)	12 (5%)	0	100	100
1	F	258/260 (99%)	250 (97%)	8 (3%)	0	100	100
1	G	258/260 (99%)	250 (97%)	8 (3%)	0	100	100
1	H	258/260 (99%)	244 (95%)	14 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	258/260 (99%)	249 (96%)	9 (4%)	0	100	100
1	J	258/260 (99%)	246 (95%)	12 (5%)	0	100	100
1	K	258/260 (99%)	246 (95%)	12 (5%)	0	100	100
1	L	257/260 (99%)	249 (97%)	8 (3%)	0	100	100
1	M	258/260 (99%)	243 (94%)	15 (6%)	0	100	100
1	N	247/260 (95%)	240 (97%)	7 (3%)	0	100	100
1	O	248/260 (95%)	242 (98%)	6 (2%)	0	100	100
1	P	244/260 (94%)	233 (96%)	11 (4%)	0	100	100
1	Q	243/260 (94%)	237 (98%)	6 (2%)	0	100	100
1	R	246/260 (95%)	232 (94%)	14 (6%)	0	100	100
1	S	243/260 (94%)	234 (96%)	9 (4%)	0	100	100
1	T	249/260 (96%)	242 (97%)	7 (3%)	0	100	100
1	U	257/260 (99%)	243 (95%)	14 (5%)	0	100	100
1	V	257/260 (99%)	247 (96%)	10 (4%)	0	100	100
1	W	257/260 (99%)	245 (95%)	12 (5%)	0	100	100
1	X	257/260 (99%)	244 (95%)	13 (5%)	0	100	100
2	a	247/251 (98%)	240 (97%)	7 (3%)	0	100	100
2	b	246/251 (98%)	236 (96%)	10 (4%)	0	100	100
2	c	247/251 (98%)	240 (97%)	7 (3%)	0	100	100
2	d	247/251 (98%)	230 (93%)	17 (7%)	0	100	100
2	e	247/251 (98%)	235 (95%)	12 (5%)	0	100	100
3	DA	399/403 (99%)	377 (94%)	22 (6%)	0	100	100
3	DB	399/403 (99%)	376 (94%)	23 (6%)	0	100	100
3	DC	399/403 (99%)	378 (95%)	21 (5%)	0	100	100
3	DD	399/403 (99%)	370 (93%)	29 (7%)	0	100	100
3	DE	399/403 (99%)	381 (96%)	18 (4%)	0	100	100
3	DF	399/403 (99%)	383 (96%)	16 (4%)	0	100	100
3	DG	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
3	DH	399/403 (99%)	384 (96%)	14 (4%)	1 (0%)	41	74
3	DI	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
3	DJ	399/403 (99%)	379 (95%)	20 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	DK	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
All	All	11724/11928 (98%)	11213 (96%)	510 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	DH	71	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	215/215 (100%)	209 (97%)	6 (3%)	43	74
1	B	215/215 (100%)	209 (97%)	6 (3%)	43	74
1	C	215/215 (100%)	207 (96%)	8 (4%)	34	68
1	D	215/215 (100%)	212 (99%)	3 (1%)	67	86
1	E	215/215 (100%)	208 (97%)	7 (3%)	38	71
1	F	215/215 (100%)	212 (99%)	3 (1%)	67	86
1	G	215/215 (100%)	213 (99%)	2 (1%)	78	91
1	H	215/215 (100%)	213 (99%)	2 (1%)	78	91
1	I	215/215 (100%)	211 (98%)	4 (2%)	57	81
1	J	215/215 (100%)	208 (97%)	7 (3%)	38	71
1	K	215/215 (100%)	210 (98%)	5 (2%)	50	78
1	L	214/215 (100%)	211 (99%)	3 (1%)	67	86
1	M	215/215 (100%)	209 (97%)	6 (3%)	43	74
1	N	208/215 (97%)	206 (99%)	2 (1%)	76	90
1	O	209/215 (97%)	204 (98%)	5 (2%)	49	77
1	P	204/215 (95%)	198 (97%)	6 (3%)	42	74
1	Q	204/215 (95%)	201 (98%)	3 (2%)	65	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	206/215 (96%)	197 (96%)	9 (4%)	28	64
1	S	204/215 (95%)	200 (98%)	4 (2%)	55	80
1	T	210/215 (98%)	208 (99%)	2 (1%)	76	90
1	U	214/215 (100%)	209 (98%)	5 (2%)	50	78
1	V	214/215 (100%)	210 (98%)	4 (2%)	57	81
1	W	214/215 (100%)	211 (99%)	3 (1%)	67	86
1	X	214/215 (100%)	209 (98%)	5 (2%)	50	78
2	a	191/193 (99%)	188 (98%)	3 (2%)	62	84
2	b	190/193 (98%)	187 (98%)	3 (2%)	62	84
2	c	191/193 (99%)	189 (99%)	2 (1%)	76	90
2	d	191/193 (99%)	186 (97%)	5 (3%)	46	76
2	e	191/193 (99%)	186 (97%)	5 (3%)	46	76
3	DA	321/323 (99%)	318 (99%)	3 (1%)	78	91
3	DB	321/323 (99%)	313 (98%)	8 (2%)	47	77
3	DC	321/323 (99%)	315 (98%)	6 (2%)	57	81
3	DD	321/323 (99%)	311 (97%)	10 (3%)	40	72
3	DE	321/323 (99%)	318 (99%)	3 (1%)	78	91
3	DF	321/323 (99%)	314 (98%)	7 (2%)	52	79
3	DG	321/323 (99%)	318 (99%)	3 (1%)	78	91
3	DH	321/323 (99%)	316 (98%)	5 (2%)	62	84
3	DI	321/323 (99%)	314 (98%)	7 (2%)	52	79
3	DJ	321/323 (99%)	312 (97%)	9 (3%)	43	74
3	DK	321/323 (99%)	319 (99%)	2 (1%)	86	94
All	All	9580/9678 (99%)	9389 (98%)	191 (2%)	57	80

5 of 191 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	e	163	LEU
3	DC	229	THR
1	V	205	THR
3	DA	371	GLU
3	DD	295	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
3	DI	379	GLN
3	DK	89	ASN
3	DC	365	ASN
3	DC	322	ASN
3	DK	97	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

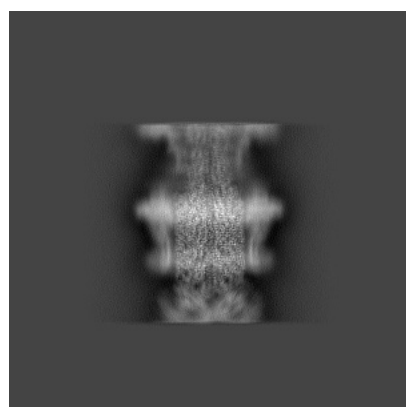
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30336. These allow visual inspection of the internal detail of the map and identification of artifacts.

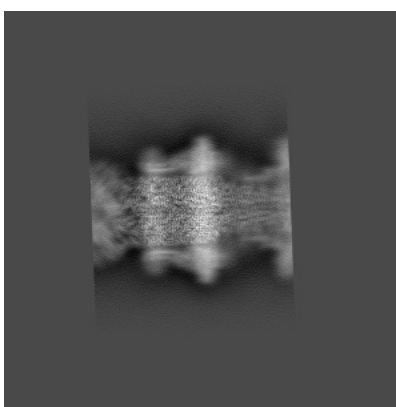
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

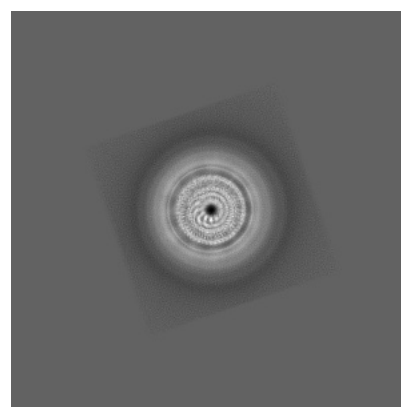
6.1.1 Primary map



X



Y

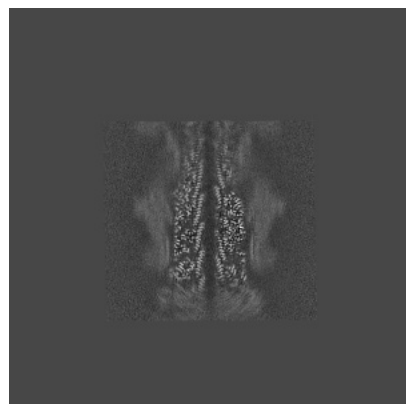


Z

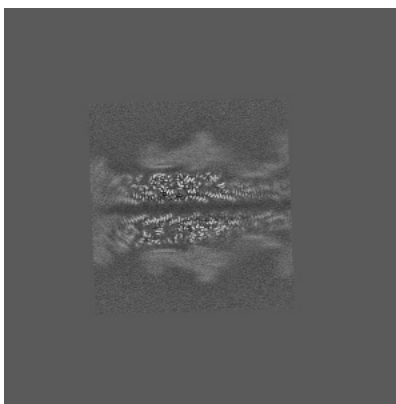
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

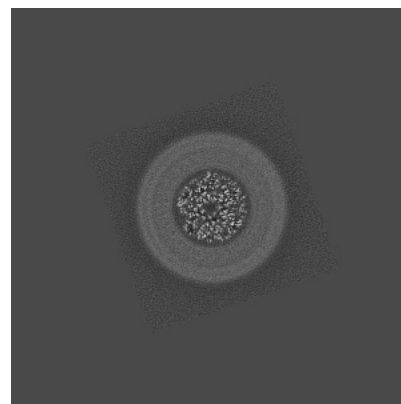
6.2.1 Primary map



X Index: 256



Y Index: 256

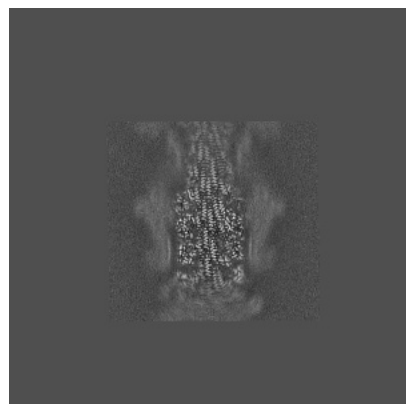


Z Index: 256

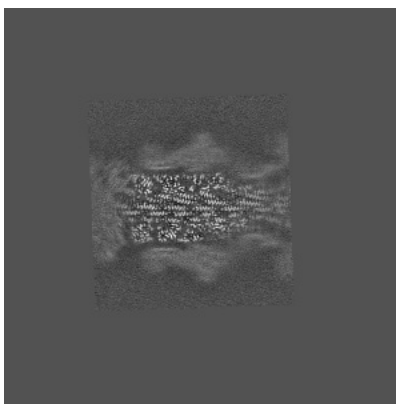
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

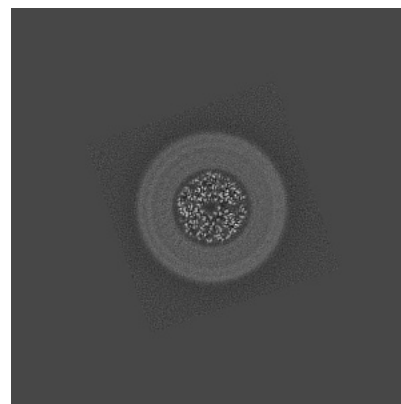
6.3.1 Primary map



X Index: 269



Y Index: 243

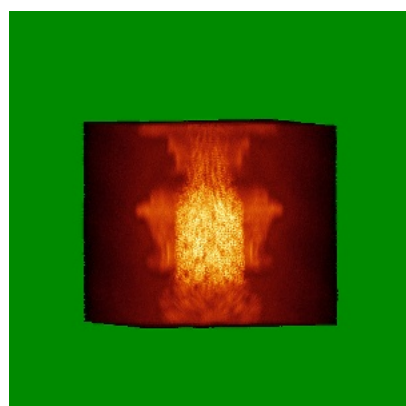


Z Index: 255

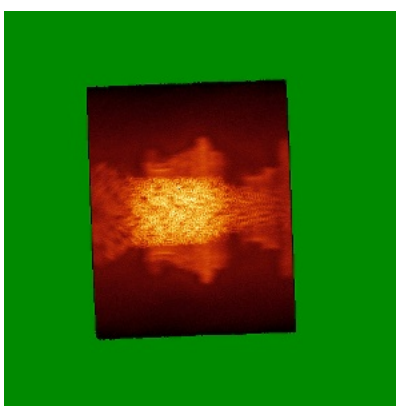
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

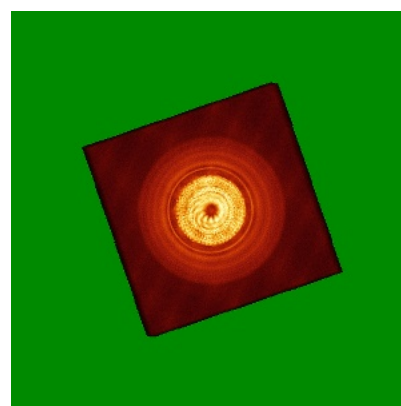
6.4.1 Primary map



X



Y

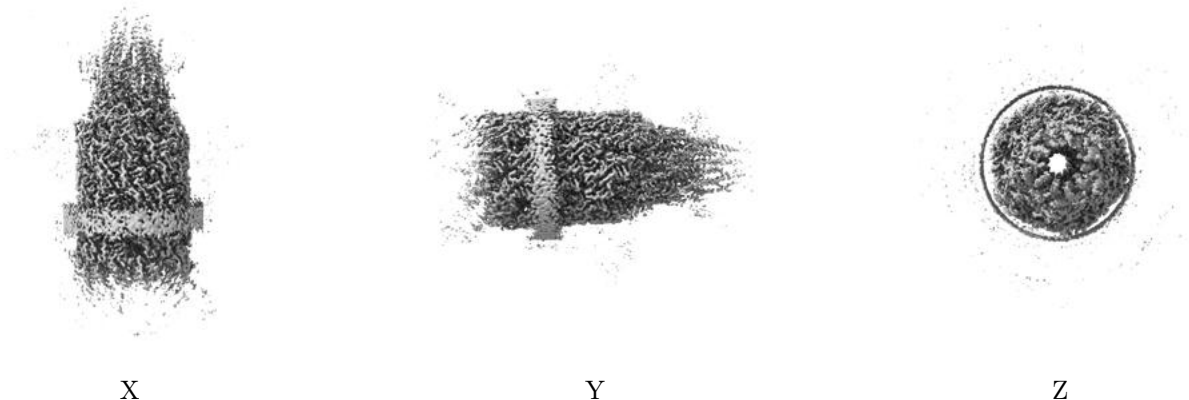


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.592. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

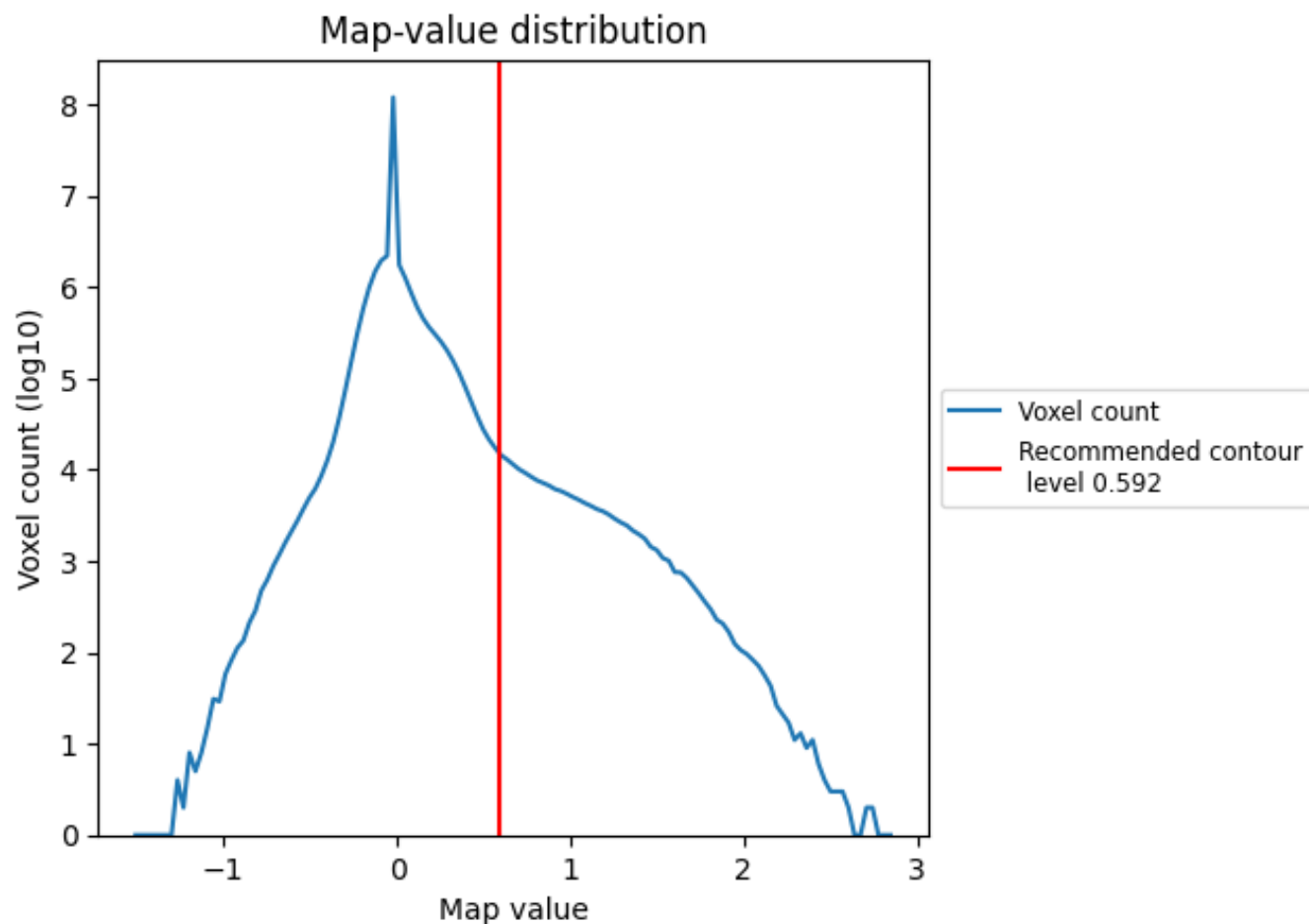
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

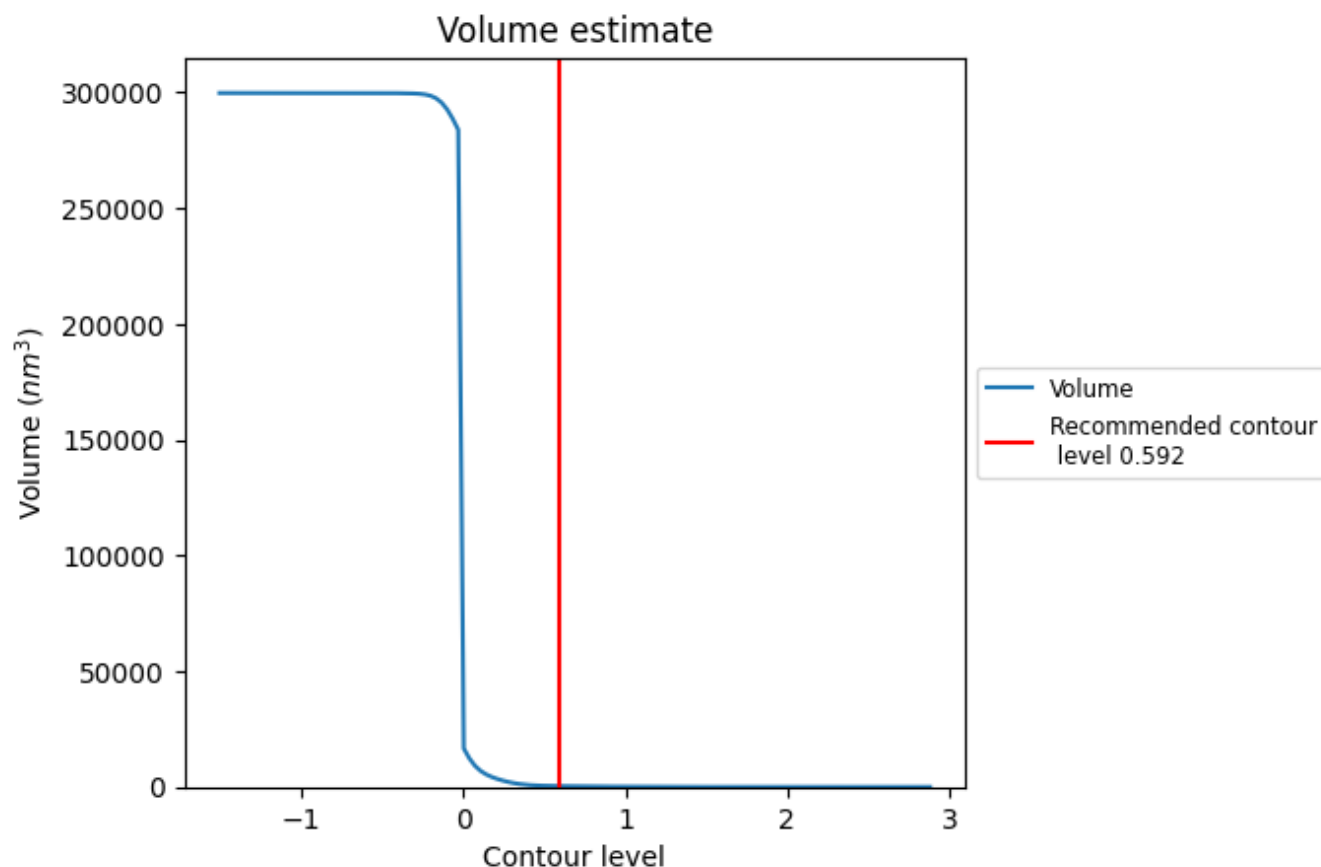
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

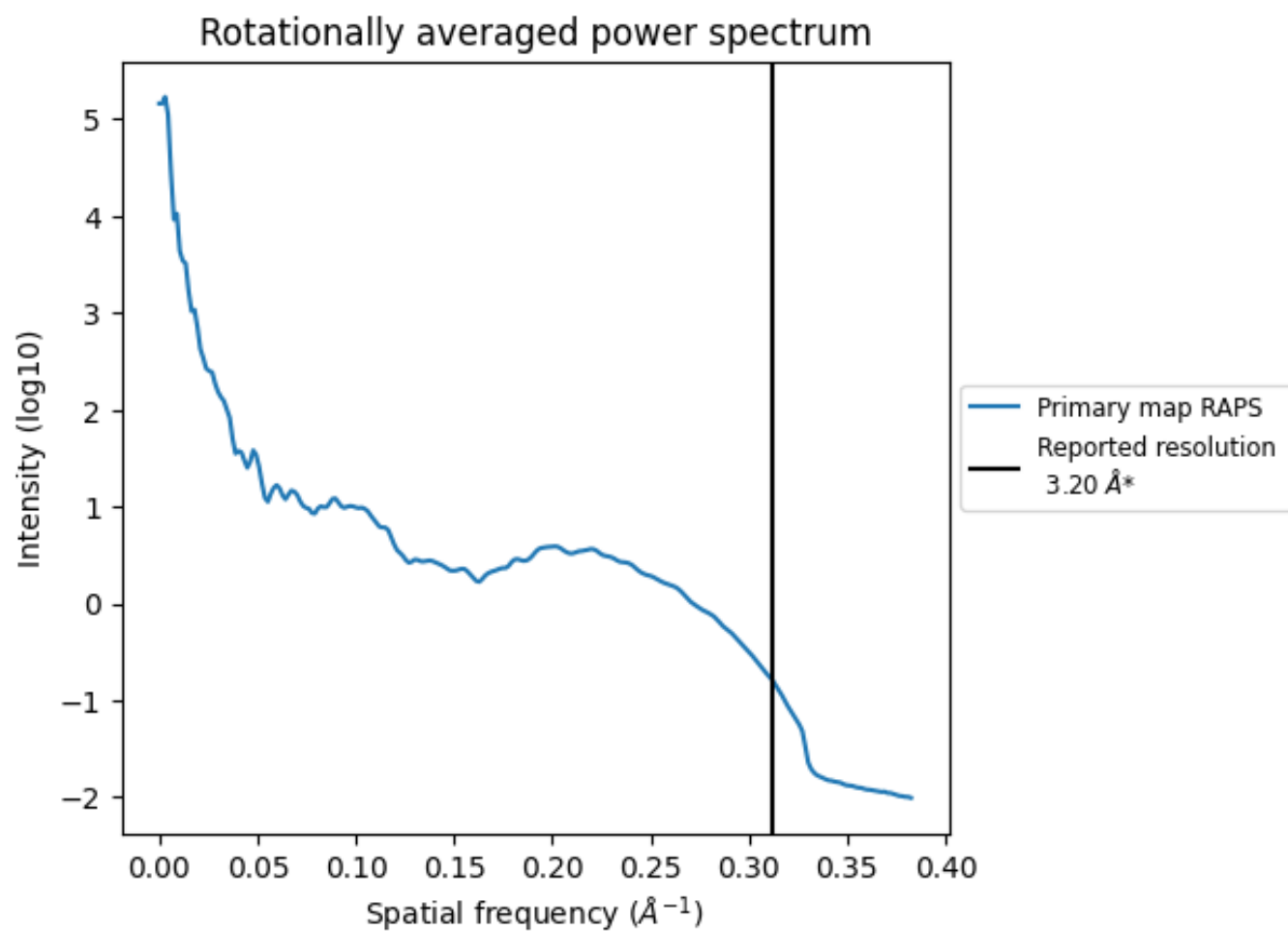
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 363 nm³; this corresponds to an approximate mass of 327 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

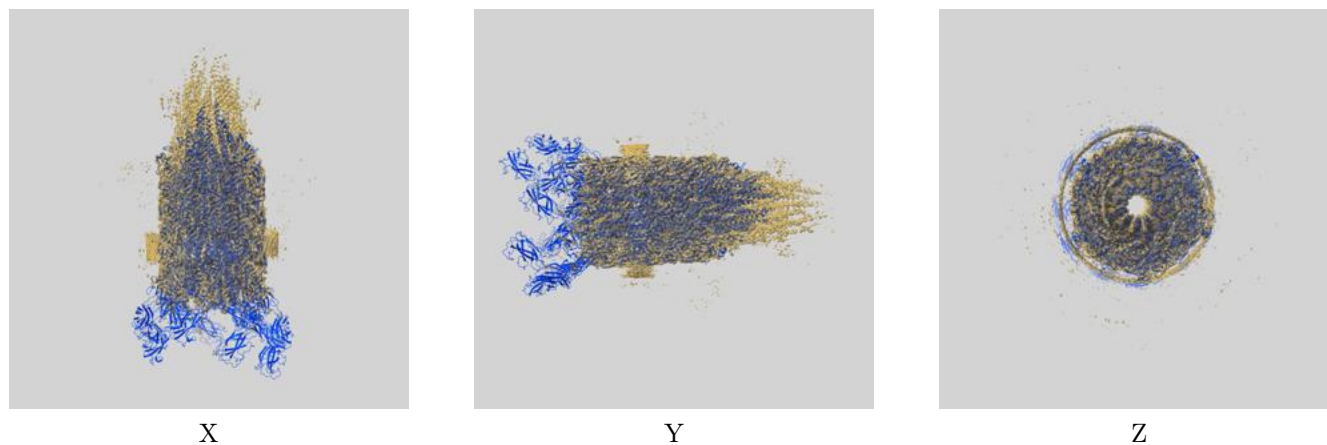
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

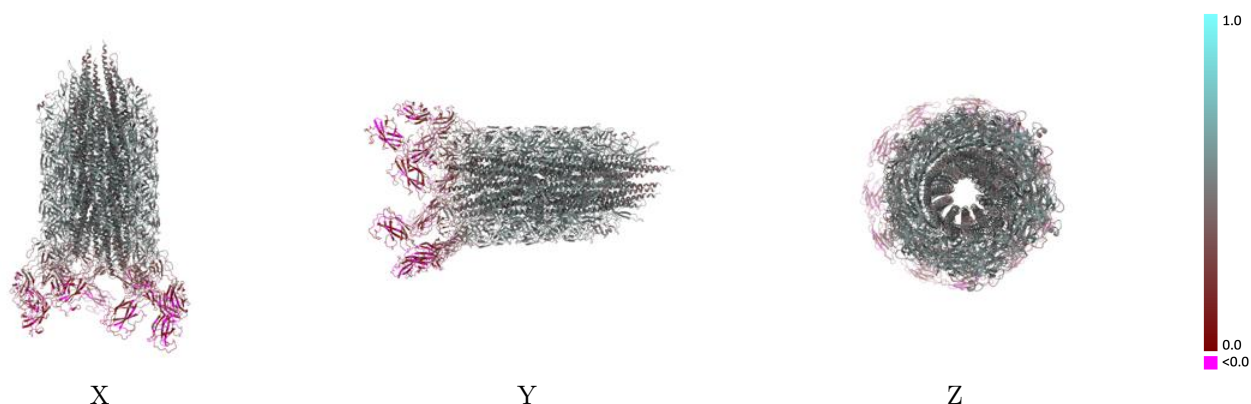
This section contains information regarding the fit between EMDB map EMD-30336 and PDB model 7CBM. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



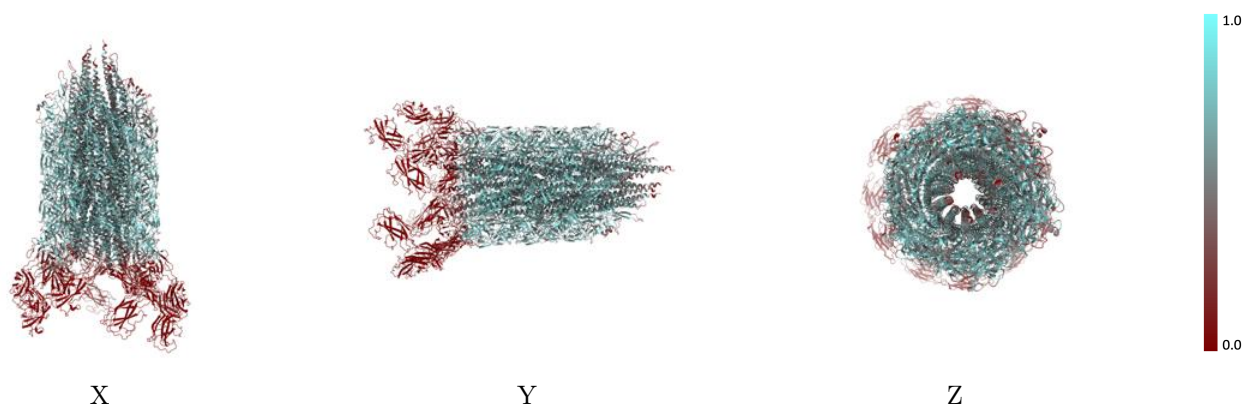
The images above show the 3D surface view of the map at the recommended contour level 0.592 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



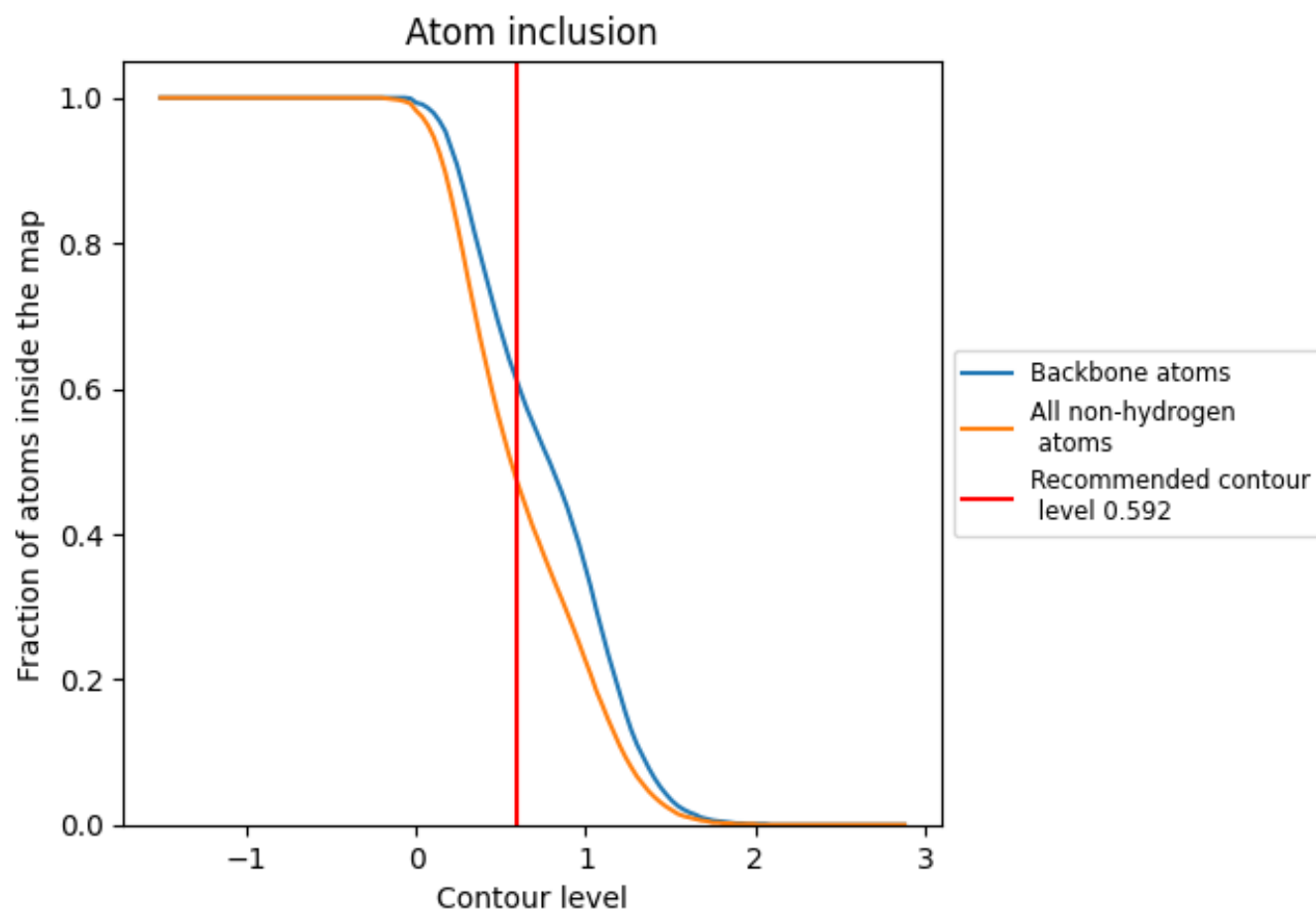
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.592).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 48% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ













The table lists the average atom inclusion at the recommended contour level (0.592) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4750	 0.4250
A	 0.6340	 0.5010
B	 0.5900	 0.4870
C	 0.6340	 0.4940
D	 0.6110	 0.4920
DA	 0.3370	 0.3380
DB	 0.3410	 0.3600
DC	 0.3260	 0.3530
DD	 0.3290	 0.3260
DE	 0.2990	 0.3280
DF	 0.2400	 0.3140
DG	 0.2120	 0.2970
DH	 0.1840	 0.2910
DI	 0.1510	 0.2550
DJ	 0.1410	 0.2460
DK	 0.0930	 0.2160
E	 0.6090	 0.4930
F	 0.6410	 0.5000
G	 0.6390	 0.5030
H	 0.6510	 0.5060
I	 0.6300	 0.5050
J	 0.6280	 0.5060
K	 0.6580	 0.5090
L	 0.6360	 0.5140
M	 0.6610	 0.5140
N	 0.6150	 0.5090
O	 0.6150	 0.5000
P	 0.6380	 0.5040
Q	 0.6340	 0.5080
R	 0.6520	 0.5100
S	 0.6600	 0.5070
T	 0.6310	 0.5090
U	 0.6080	 0.4970
V	 0.6140	 0.4960
W	 0.6080	 0.4980



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Chain	Atom inclusion	Q-score
X	 0.5640	 0.4770
a	 0.5640	 0.4810
b	 0.5460	 0.4600
c	 0.5810	 0.4830
d	 0.5570	 0.4870
e	 0.4510	 0.4710