



wwPDB EM Validation Summary Report ⓘ

Apr 6, 2026 – 01:49 AM UTC

PDB ID : 9M5T / pdb_00009m5t
EMDB ID : EMD-63649
Title : Structure of the flagellar filament in short-length at 3.02 angstroms resolution
Authors : Chen, L.X.; Jiang, W.X.; Cheng, X.Q.; Dong, X.; Xing, Q.
Deposited on : 2025-03-06
Resolution : 3.02 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:

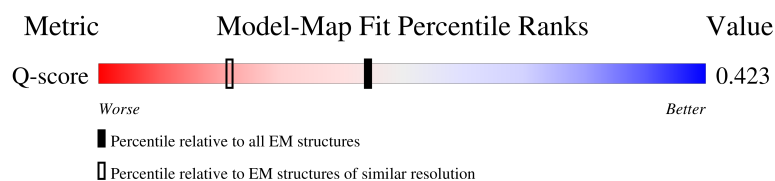
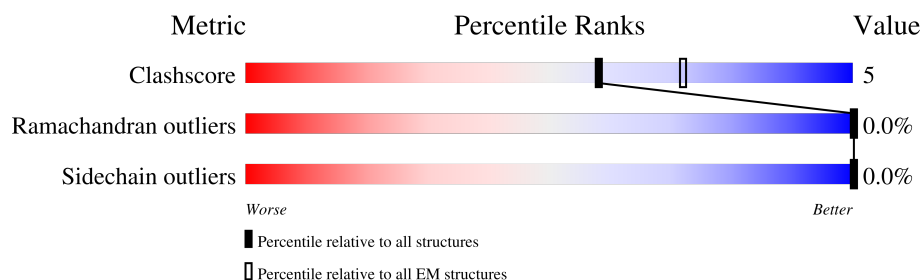
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.02 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13913 (2.52 - 3.52)

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	AA	495	 88% 12%
1	AB	495	 15% 86% 14%
1	AC	495	 15% 85% 15%
1	AD	495	 83% 17%

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Mol	Chain	Length	Quality of chain
1	AE	495	
1	AF	495	
1	AG	495	
1	AH	495	
1	AI	495	
1	AJ	495	
1	AK	495	
1	BA	495	
1	BB	495	
1	BC	495	
1	BD	495	
1	BE	495	
1	BF	495	
1	BG	495	
1	BH	495	
1	BI	495	
1	BJ	495	
1	BK	495	
1	CA	495	
1	CB	495	
1	CC	495	
1	CD	495	
1	CE	495	
1	CF	495	
1	CG	495	

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Mol	Chain	Length	Quality of chain
1	CH	495	 92% 8%
1	CI	495	 91% 9%
1	CJ	495	 94% 6%
1	CK	495	 92% 8%
1	DA	495	 91% 8%
1	DB	495	 91% 9%
1	DC	495	 95% 5%
1	DD	495	 93% 6%
1	DE	495	 91% 9%
1	DF	495	 90% 9%
1	DG	495	 91% 9%
1	DH	495	 88% 11%
1	DI	495	 92% 7%
1	DJ	495	 91% 8%
1	DK	495	 89% 11%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 159148 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 Flagellin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	AB	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	AC	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	AD	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	AE	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	AF	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	AG	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	AH	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	AI	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	AJ	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	AK	495	Total	C	N	O	S	0	0
			3623	2194	641	785	3		
1	BA	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		
1	BB	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		
1	BC	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		
1	BD	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		
1	BE	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		
1	BF	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BG	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	BH	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	BI	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	BJ	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	BK	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CA	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CB	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CC	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CD	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CE	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CF	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CG	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CH	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CI	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CJ	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	CK	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	DA	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	DB	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	DC	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	DD	494	Total 3615	C 2189	N 640	O 784	S 2	0	0
1	DE	494	Total 3615	C 2189	N 640	O 784	S 2	0	0

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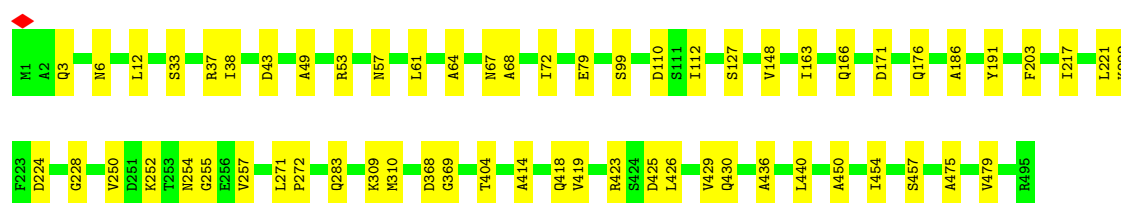
Mol	Chain	Residues	Atoms					AltConf	Trace
1	DF	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		
1	DG	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		
1	DH	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		
1	DI	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		
1	DJ	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		
1	DK	494	Total	C	N	O	S	0	0
			3615	2189	640	784	2		

3 Residue-property plots


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.

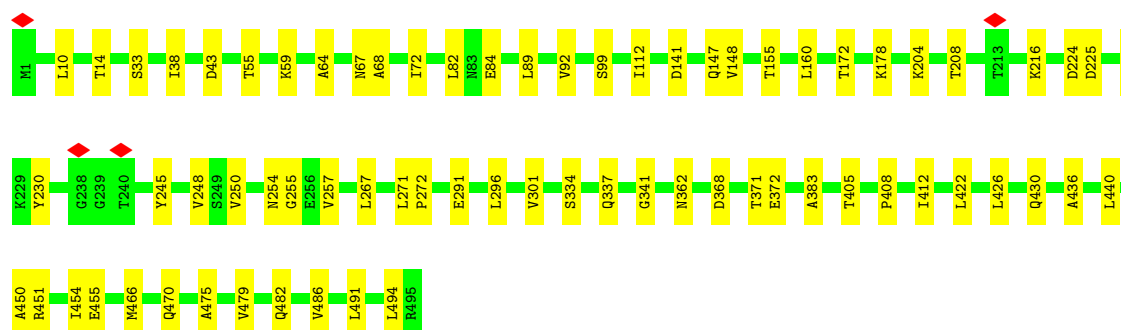
• Molecule 1: Flagellin

Chain AA:  88% 12%




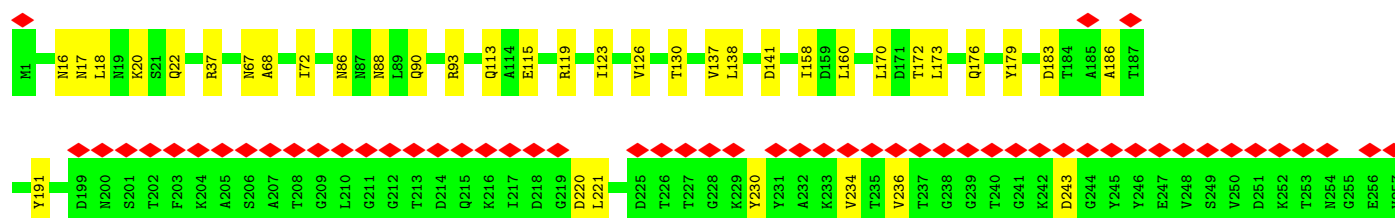
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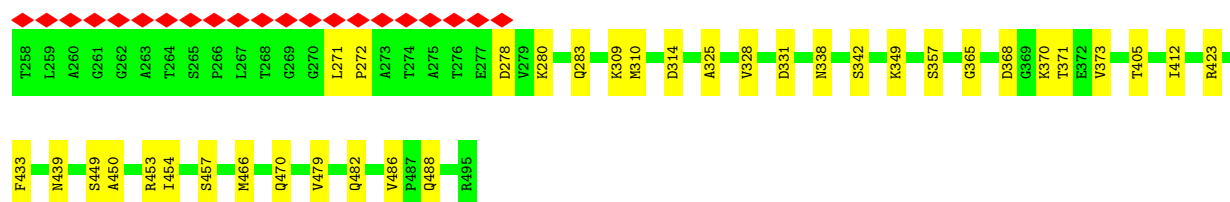
Chain AB:  86% 14%



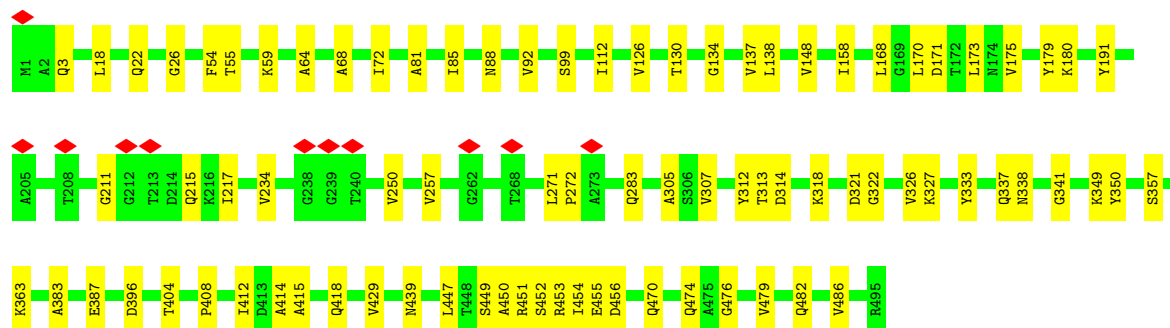
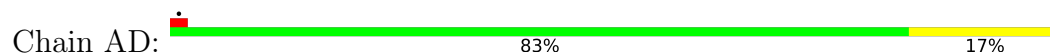
• Molecule 1: Flagellin

Chain AC:  15% 85% 15%

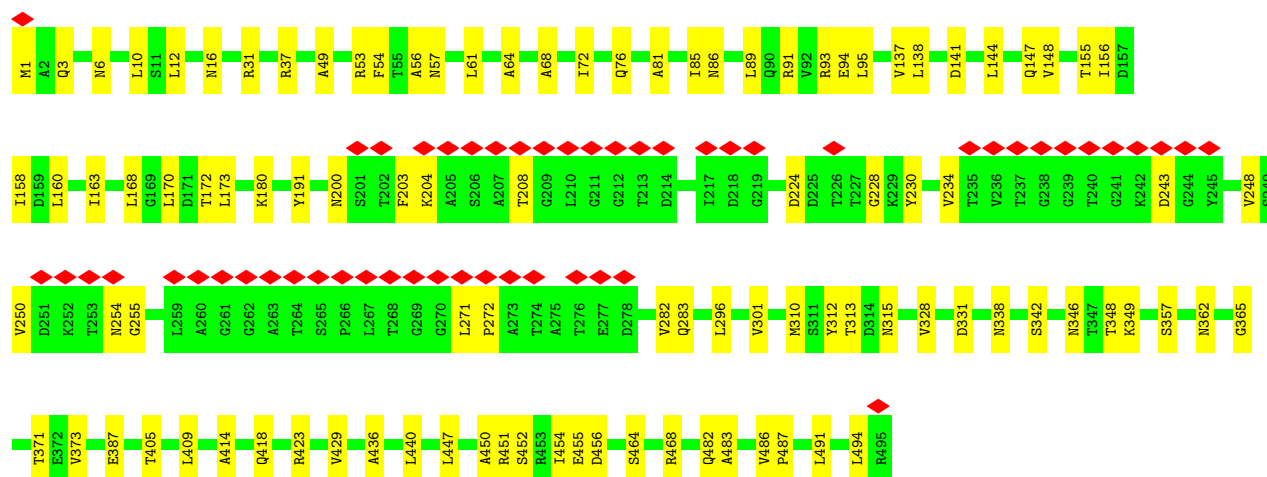
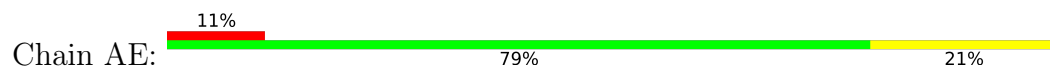




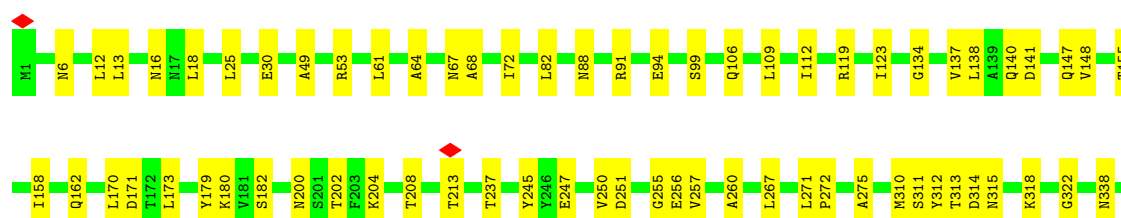
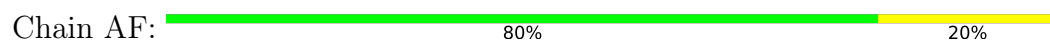
• Molecule 1: Flagellin



• Molecule 1: Flagellin

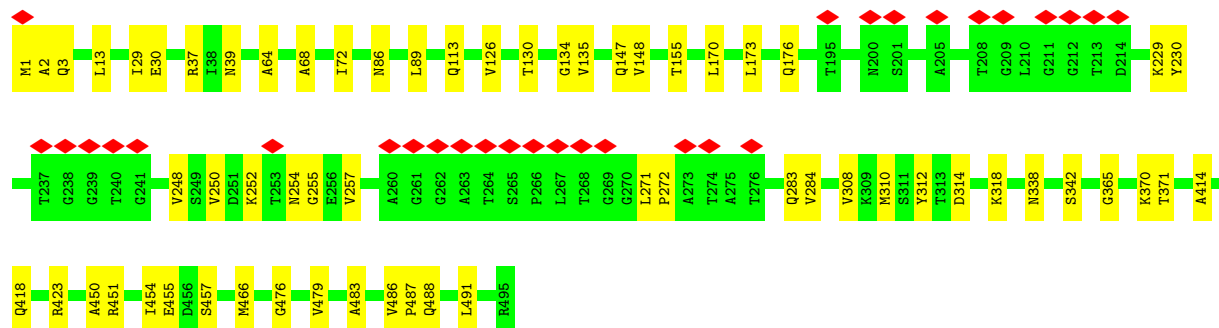
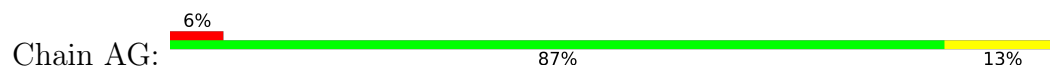


• Molecule 1: Flagellin

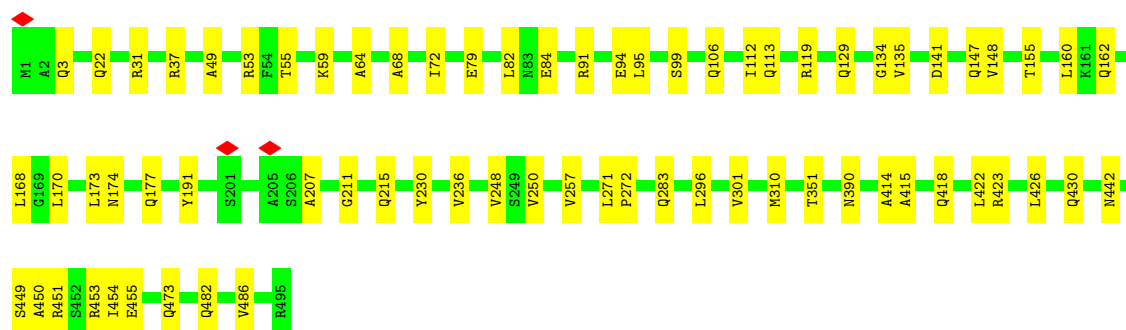
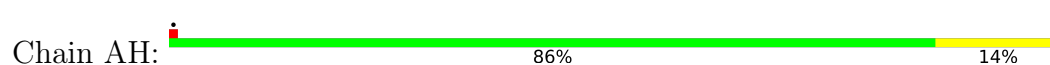




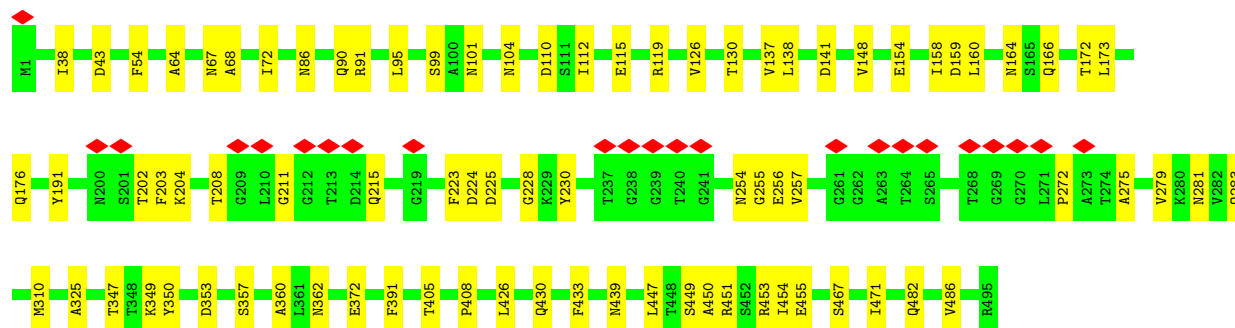
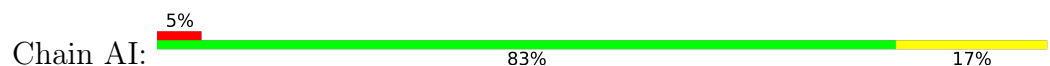
• Molecule 1: Flagellin



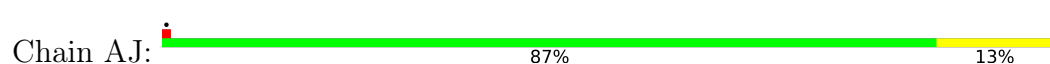
• Molecule 1: Flagellin

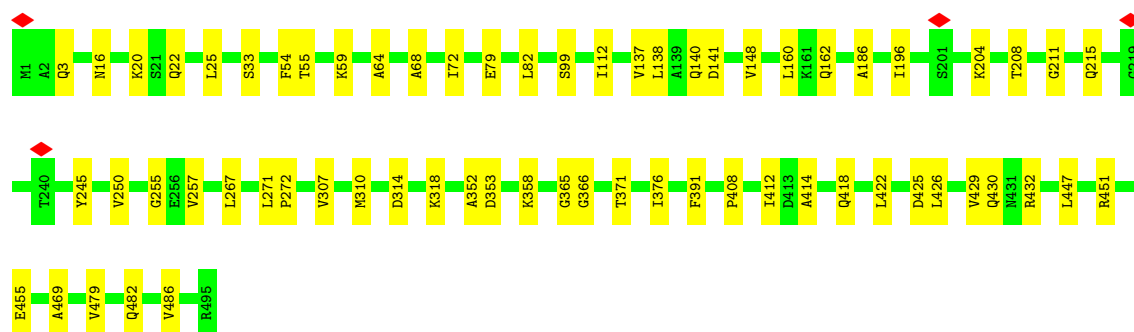


• Molecule 1: Flagellin



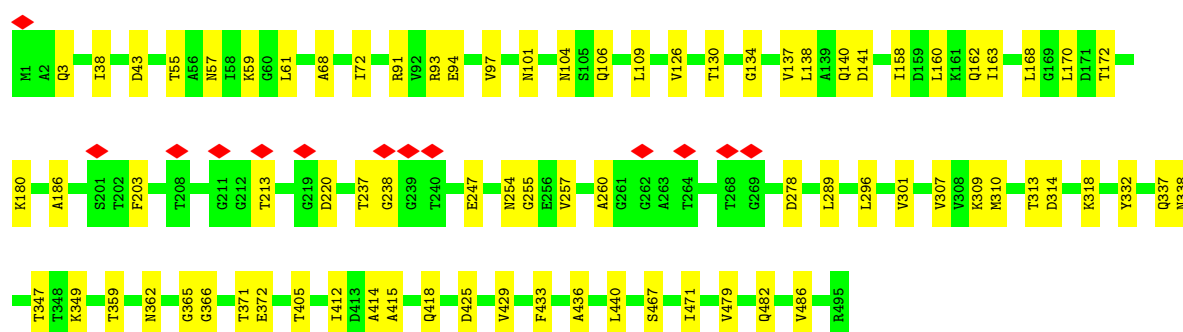
• Molecule 1: Flagellin





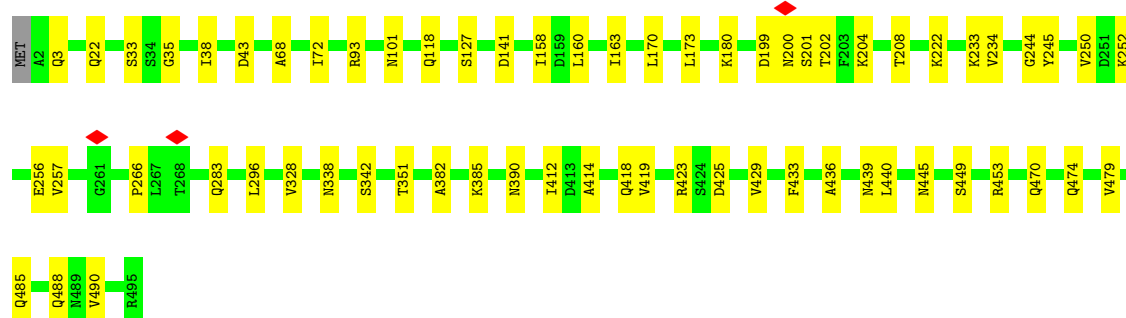
• Molecule 1: Flagellin

Chain AK: 84% 16%



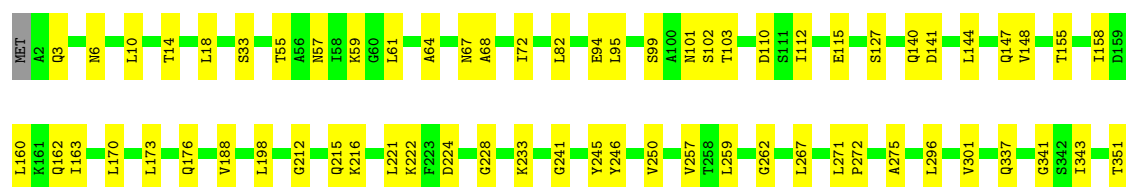
• Molecule 1: Flagellin

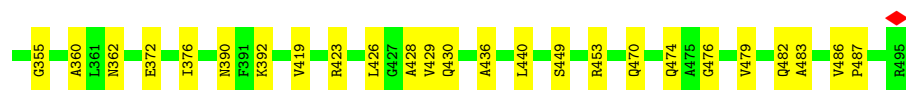
Chain BA: 87% 13%



• Molecule 1: Flagellin

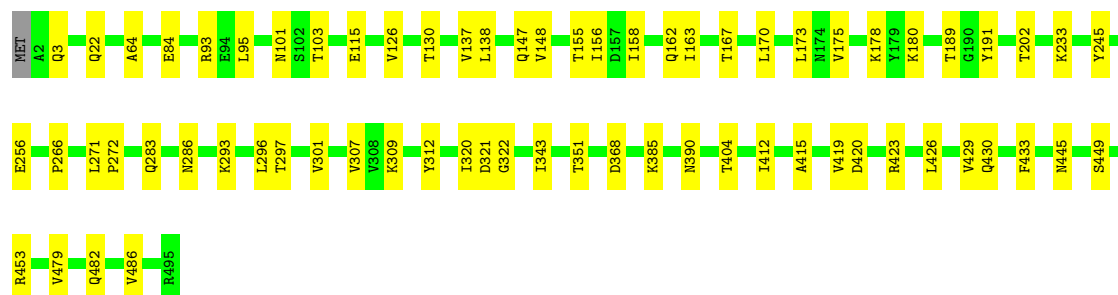
Chain BB: 82% 18%





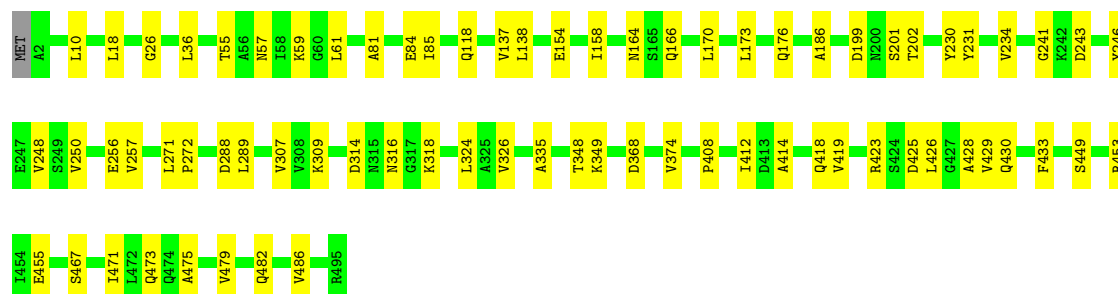
• Molecule 1: Flagellin

Chain BC: 86% 14%



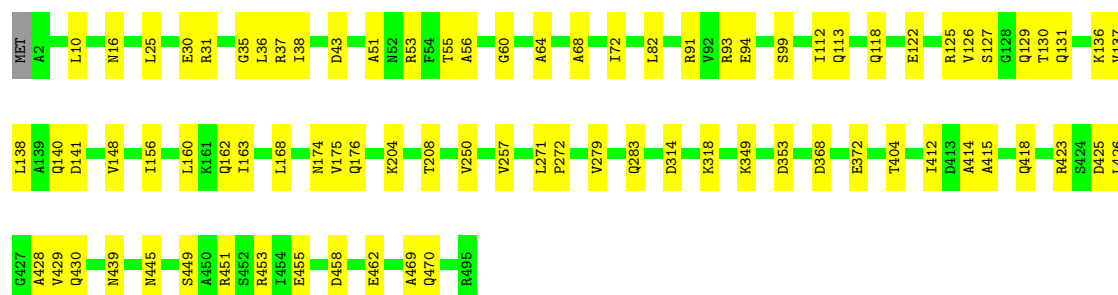
• Molecule 1: Flagellin

Chain BD: 85% 15%



• Molecule 1: Flagellin

Chain BE: 83% 17%



• Molecule 1: Flagellin

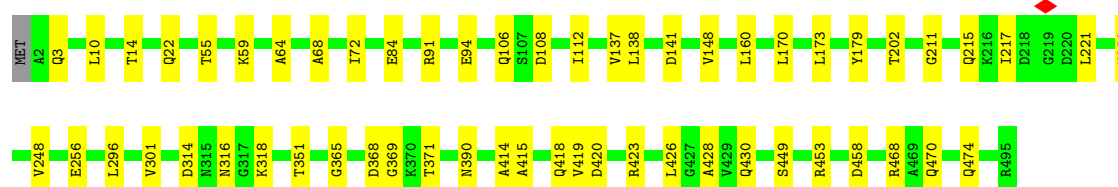
Chain BF: 86% 14%





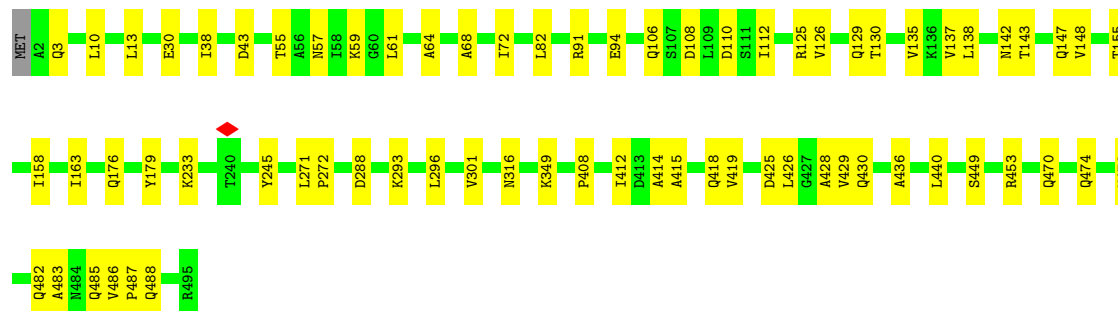
- Molecule 1: Flagellin

Chain BG: 88% 12%



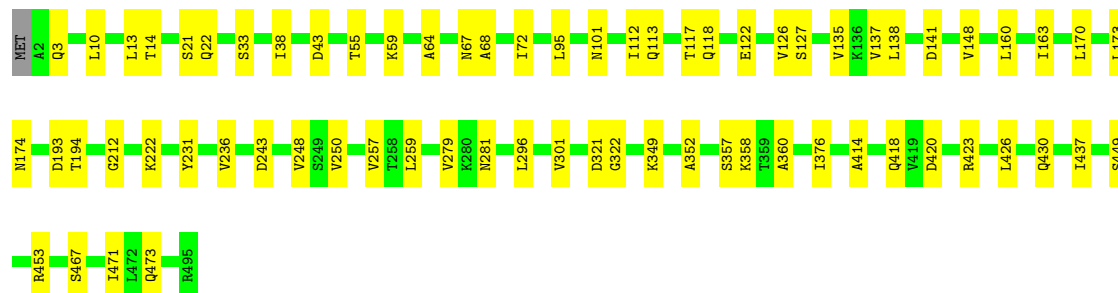
- Molecule 1: Flagellin

Chain BH: 86% 14%



- Molecule 1: Flagellin

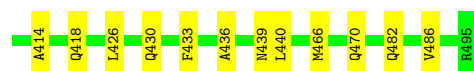
Chain BI: 86% 14%



- Molecule 1: Flagellin

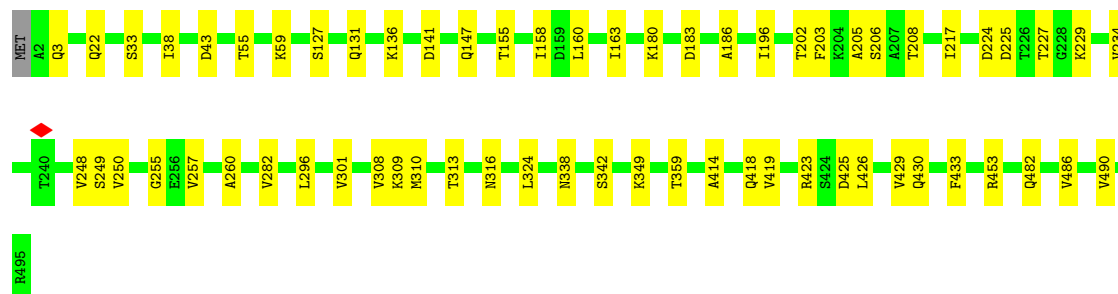
Chain BJ: 91% 9%





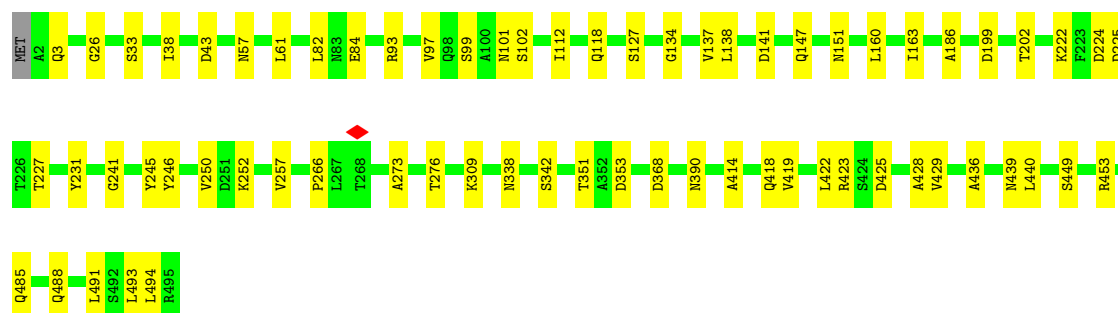
• Molecule 1: Flagellin

Chain BK: 87% 13%



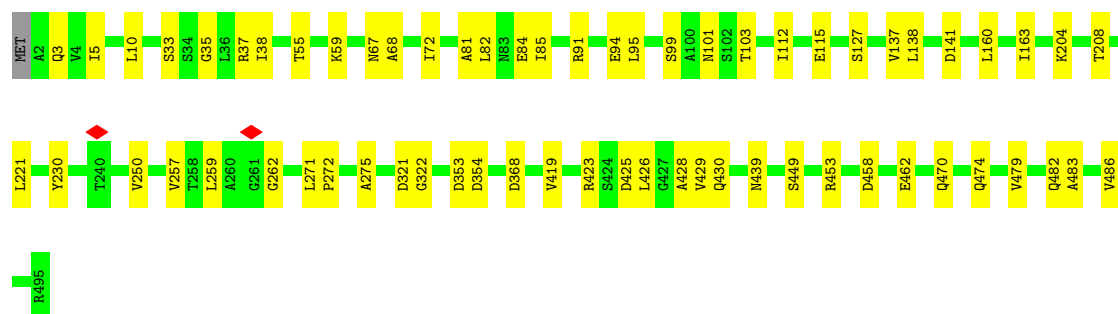
• Molecule 1: Flagellin

Chain CA: 86% 14%



• Molecule 1: Flagellin

Chain CB: 87% 13%

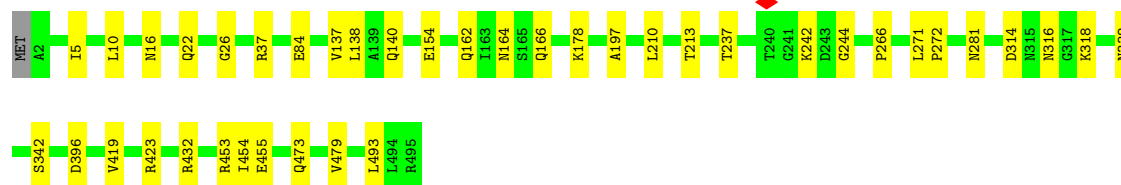


• Molecule 1: Flagellin

Chain CC: 88% 11%

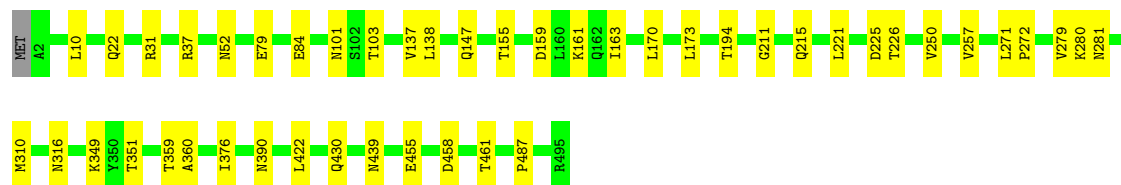


Chain CH:  92% 8%



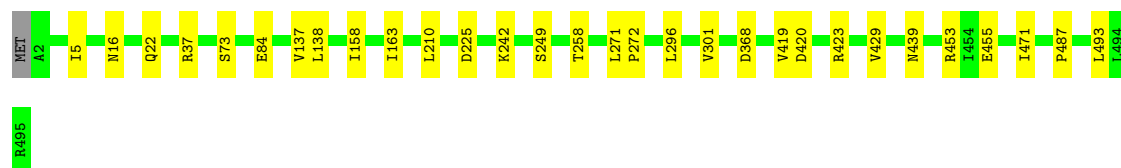
• Molecule 1: Flagellin

Chain CI:  91% 9%



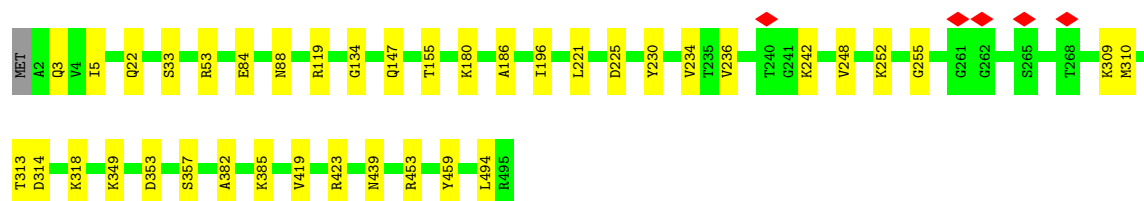
• Molecule 1: Flagellin

Chain CJ:  94% 6%



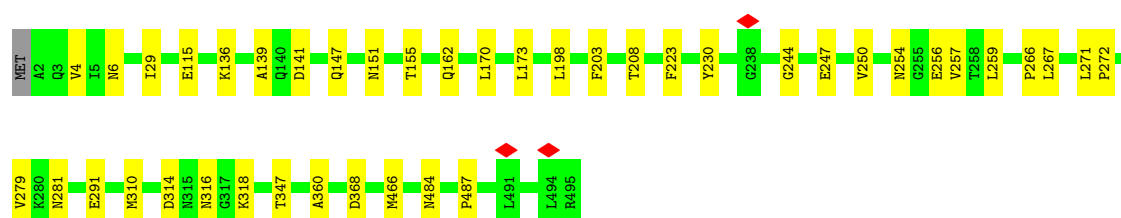
• Molecule 1: Flagellin

Chain CK:  92% 8%

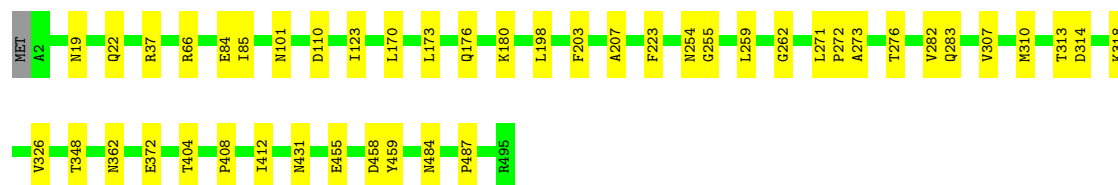


• Molecule 1: Flagellin

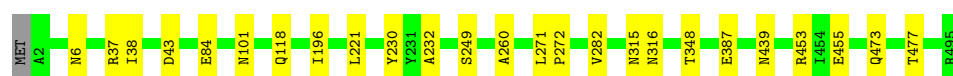
Chain DA:  91% 8%



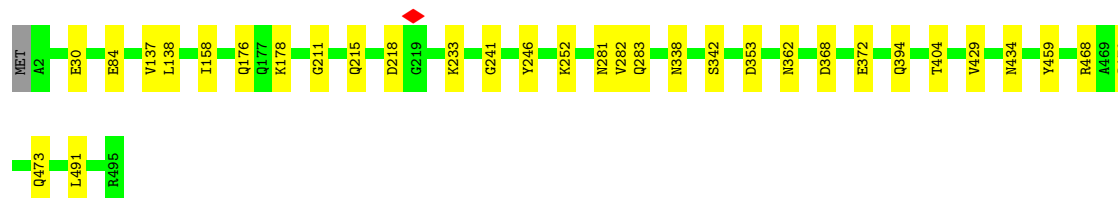
● Molecule 1: Flagellin

Chain DB:  91% 9%

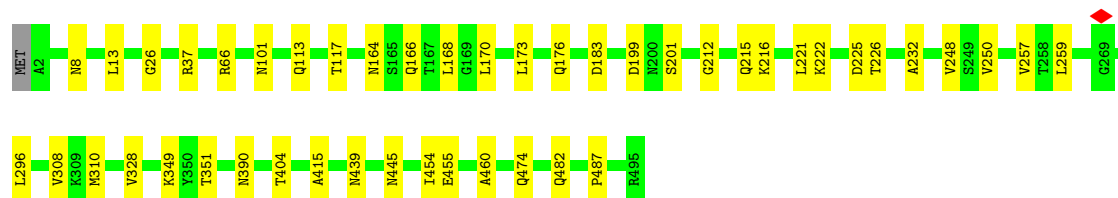
● Molecule 1: Flagellin

Chain DC:  95% 5%

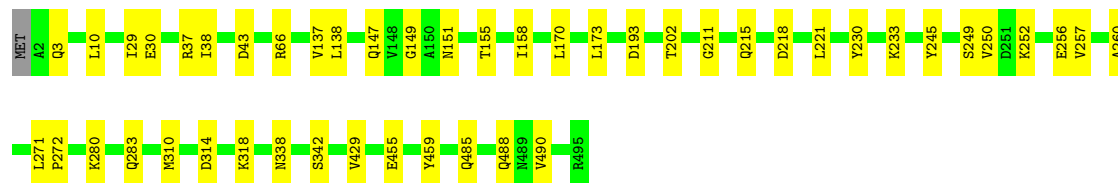
● Molecule 1: Flagellin

Chain DD:  93% 6%

● Molecule 1: Flagellin

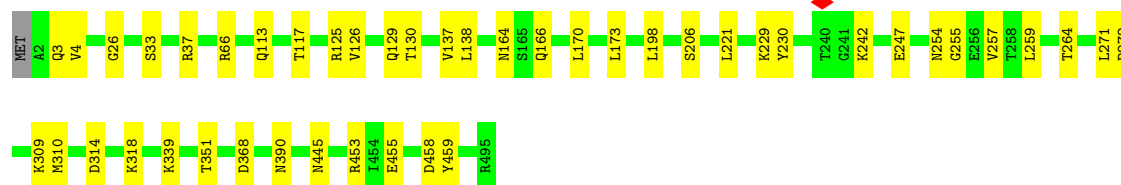
Chain DE:  91% 9%

● Molecule 1: Flagellin

Chain DF:  90% 9%

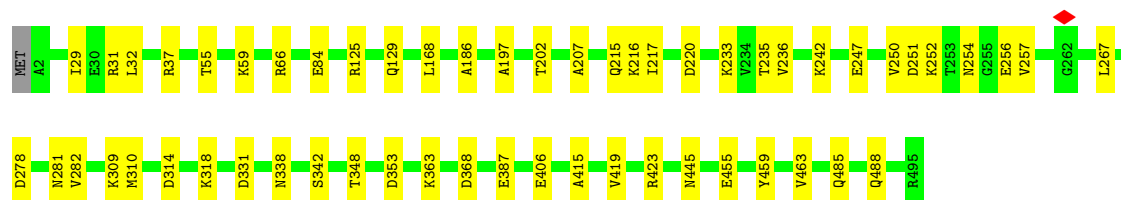
● Molecule 1: Flagellin

Chain DG:  91% 9%



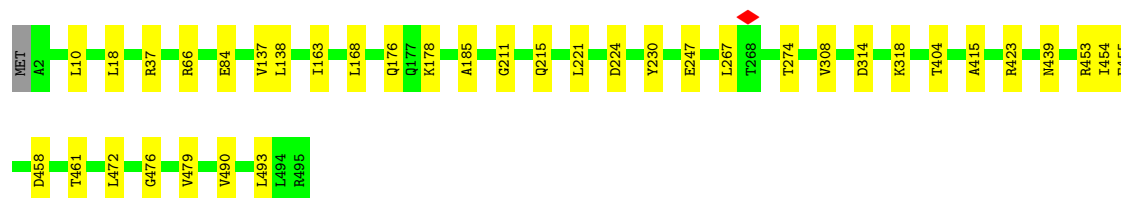
- Molecule 1: Flagellin

Chain DH:  88% 11%



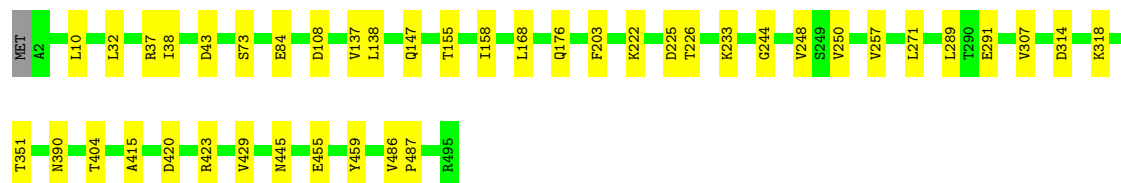
- Molecule 1: Flagellin

Chain DI:  92% 7%



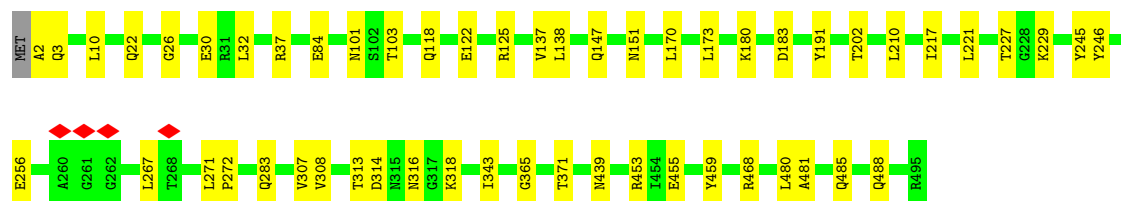
- Molecule 1: Flagellin

Chain DJ:  91% 8%



- Molecule 1: Flagellin

Chain DK:  89% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	498897	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.548	Depositor
Minimum map value	-0.282	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	408.0, 408.0, 408.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	AA	0.12	0/3646	0.25	0/4948
1	AB	0.11	0/3646	0.26	0/4948
1	AC	0.11	0/3646	0.27	0/4948
1	AD	0.10	0/3646	0.25	0/4948
1	AE	0.11	0/3646	0.26	0/4948
1	AF	0.11	0/3646	0.26	0/4948
1	AG	0.11	0/3646	0.26	0/4948
1	AH	0.11	0/3646	0.26	0/4948
1	AI	0.11	0/3646	0.25	0/4948
1	AJ	0.11	0/3646	0.26	0/4948
1	AK	0.11	0/3646	0.26	0/4948
1	BA	0.11	0/3638	0.24	0/4938
1	BB	0.11	0/3638	0.25	0/4938
1	BC	0.14	0/3638	0.31	2/4938 (0.0%)
1	BD	0.10	0/3638	0.24	0/4938
1	BE	0.12	0/3638	0.25	0/4938
1	BF	0.10	0/3638	0.24	0/4938
1	BG	0.10	0/3638	0.25	0/4938
1	BH	0.11	0/3638	0.24	0/4938
1	BI	0.11	0/3638	0.25	0/4938
1	BJ	0.10	0/3638	0.23	0/4938
1	BK	0.11	0/3638	0.25	0/4938
1	CA	0.11	0/3638	0.24	0/4938
1	CB	0.11	0/3638	0.23	0/4938
1	CC	0.10	0/3638	0.23	0/4938
1	CD	0.11	0/3638	0.24	0/4938
1	CE	0.11	0/3638	0.26	0/4938
1	CF	0.09	0/3638	0.24	0/4938
1	CG	0.07	0/3638	0.21	0/4938
1	CH	0.07	0/3638	0.20	0/4938
1	CI	0.07	0/3638	0.21	0/4938
1	CJ	0.07	0/3638	0.20	0/4938
1	CK	0.08	0/3638	0.23	0/4938
1	DA	0.08	0/3638	0.23	0/4938

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	DB	0.08	0/3638	0.21	0/4938
1	DC	0.08	0/3638	0.22	0/4938
1	DD	0.09	0/3638	0.24	0/4938
1	DE	0.08	0/3638	0.23	0/4938
1	DF	0.08	0/3638	0.23	0/4938
1	DG	0.08	0/3638	0.23	0/4938
1	DH	0.08	0/3638	0.23	0/4938
1	DI	0.08	0/3638	0.24	0/4938
1	DJ	0.08	0/3638	0.22	0/4938
1	DK	0.08	0/3638	0.22	0/4938
All	All	0.10	0/160160	0.24	2/217382 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AG	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	BC	266	PRO	CA-N-CD	-9.32	98.96	112.00
1	BC	266	PRO	N-CD-CG	-6.27	93.80	103.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AG	486	VAL	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	3623	0	3585	39	0
1	AB	3623	0	3585	46	0
1	AC	3623	0	3585	44	0
1	AD	3623	0	3585	48	0
1	AE	3623	0	3585	61	0
1	AF	3623	0	3585	66	0
1	AG	3623	0	3585	33	0
1	AH	3623	0	3585	44	0
1	AI	3623	0	3585	49	0
1	AJ	3623	0	3585	37	0
1	AK	3623	0	3585	45	0
1	BA	3615	0	3573	41	0
1	BB	3615	0	3573	57	0
1	BC	3615	0	3573	43	0
1	BD	3615	0	3573	43	0
1	BE	3615	0	3573	55	0
1	BF	3615	0	3573	42	0
1	BG	3615	0	3573	36	0
1	BH	3615	0	3573	44	0
1	BI	3615	0	3573	41	0
1	BJ	3615	0	3573	28	0
1	BK	3615	0	3573	37	0
1	CA	3615	0	3573	42	0
1	CB	3615	0	3573	43	0
1	CC	3615	0	3573	34	0
1	CD	3615	0	3573	33	0
1	CE	3615	0	3573	53	0
1	CF	3615	0	3573	28	0
1	CG	3615	0	3573	28	0
1	CH	3615	0	3573	28	0
1	CI	3615	0	3573	33	0
1	CJ	3615	0	3573	23	0
1	CK	3615	0	3573	28	0
1	DA	3615	0	3573	25	0
1	DB	3615	0	3573	29	0
1	DC	3615	0	3573	16	0
1	DD	3615	0	3573	22	0
1	DE	3615	0	3573	30	0
1	DF	3615	0	3573	30	0
1	DG	3615	0	3573	30	0
1	DH	3615	0	3573	36	0
1	DI	3615	0	3573	24	0
1	DJ	3615	0	3573	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DK	3615	0	3573	34	0
All	All	159148	0	157344	1486	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1486 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:485:GLN:OE1	1:BF:488:GLN:NE2	2.13	0.81
1:BG:230:TYR:HB2	1:BG:248:VAL:O	1.84	0.77
1:BA:22:GLN:NE2	1:BB:3:GLN:OE1	2.19	0.76
1:AI:67:ASN:HB3	1:BI:101:ASN:HD21	1.50	0.75
1:BI:67:ASN:HB3	1:CI:101:ASN:HD21	1.49	0.75

There are no symmetry-related clashes.

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	AA	493/495 (100%)	491 (100%)	2 (0%)	0	100	100
1	AB	493/495 (100%)	491 (100%)	2 (0%)	0	100	100
1	AC	493/495 (100%)	492 (100%)	1 (0%)	0	100	100
1	AD	493/495 (100%)	491 (100%)	2 (0%)	0	100	100
1	AE	493/495 (100%)	492 (100%)	1 (0%)	0	100	100
1	AF	493/495 (100%)	491 (100%)	2 (0%)	0	100	100
1	AG	493/495 (100%)	491 (100%)	2 (0%)	0	100	100
1	AH	493/495 (100%)	492 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AI	493/495 (100%)	491 (100%)	2 (0%)	0	100	100
1	AJ	493/495 (100%)	491 (100%)	2 (0%)	0	100	100
1	AK	493/495 (100%)	491 (100%)	2 (0%)	0	100	100
1	BA	492/495 (99%)	487 (99%)	5 (1%)	0	100	100
1	BB	492/495 (99%)	487 (99%)	5 (1%)	0	100	100
1	BC	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	BD	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	BE	492/495 (99%)	492 (100%)	0	0	100	100
1	BF	492/495 (99%)	489 (99%)	3 (1%)	0	100	100
1	BG	492/495 (99%)	491 (100%)	1 (0%)	0	100	100
1	BH	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	BI	492/495 (99%)	489 (99%)	3 (1%)	0	100	100
1	BJ	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	BK	492/495 (99%)	487 (99%)	4 (1%)	1 (0%)	43	75
1	CA	492/495 (99%)	482 (98%)	10 (2%)	0	100	100
1	CB	492/495 (99%)	488 (99%)	4 (1%)	0	100	100
1	CC	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	CD	492/495 (99%)	487 (99%)	5 (1%)	0	100	100
1	CE	492/495 (99%)	492 (100%)	0	0	100	100
1	CF	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	CG	492/495 (99%)	491 (100%)	1 (0%)	0	100	100
1	CH	492/495 (99%)	492 (100%)	0	0	100	100
1	CI	492/495 (99%)	492 (100%)	0	0	100	100
1	CJ	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	CK	492/495 (99%)	490 (100%)	1 (0%)	1 (0%)	43	75
1	DA	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	DB	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	DC	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	DD	492/495 (99%)	489 (99%)	3 (1%)	0	100	100
1	DE	492/495 (99%)	491 (100%)	1 (0%)	0	100	100
1	DF	492/495 (99%)	490 (100%)	2 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DG	492/495 (99%)	489 (99%)	3 (1%)	0	100	100
1	DH	492/495 (99%)	492 (100%)	0	0	100	100
1	DI	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	DJ	492/495 (99%)	490 (100%)	2 (0%)	0	100	100
1	DK	492/495 (99%)	489 (99%)	3 (1%)	0	100	100
All	All	21659/21780 (99%)	21560 (100%)	97 (0%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BK	234	VAL
1	CK	234	VAL

5.3.2 Protein sidechains [i](#)

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	AA	391/391 (100%)	391 (100%)	0	100	100
1	AB	391/391 (100%)	391 (100%)	0	100	100
1	AC	391/391 (100%)	391 (100%)	0	100	100
1	AD	391/391 (100%)	391 (100%)	0	100	100
1	AE	391/391 (100%)	391 (100%)	0	100	100
1	AF	391/391 (100%)	391 (100%)	0	100	100
1	AG	391/391 (100%)	391 (100%)	0	100	100
1	AH	391/391 (100%)	391 (100%)	0	100	100
1	AI	391/391 (100%)	391 (100%)	0	100	100
1	AJ	391/391 (100%)	391 (100%)	0	100	100
1	AK	391/391 (100%)	391 (100%)	0	100	100
1	BA	390/391 (100%)	390 (100%)	0	100	100
1	BB	390/391 (100%)	390 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BC	390/391 (100%)	390 (100%)	0	100	100
1	BD	390/391 (100%)	390 (100%)	0	100	100
1	BE	390/391 (100%)	389 (100%)	1 (0%)	86	90
1	BF	390/391 (100%)	390 (100%)	0	100	100
1	BG	390/391 (100%)	390 (100%)	0	100	100
1	BH	390/391 (100%)	390 (100%)	0	100	100
1	BI	390/391 (100%)	390 (100%)	0	100	100
1	BJ	390/391 (100%)	390 (100%)	0	100	100
1	BK	390/391 (100%)	390 (100%)	0	100	100
1	CA	390/391 (100%)	390 (100%)	0	100	100
1	CB	390/391 (100%)	390 (100%)	0	100	100
1	CC	390/391 (100%)	390 (100%)	0	100	100
1	CD	390/391 (100%)	390 (100%)	0	100	100
1	CE	390/391 (100%)	389 (100%)	1 (0%)	86	90
1	CF	390/391 (100%)	390 (100%)	0	100	100
1	CG	390/391 (100%)	390 (100%)	0	100	100
1	CH	390/391 (100%)	390 (100%)	0	100	100
1	CI	390/391 (100%)	390 (100%)	0	100	100
1	CJ	390/391 (100%)	390 (100%)	0	100	100
1	CK	390/391 (100%)	390 (100%)	0	100	100
1	DA	390/391 (100%)	390 (100%)	0	100	100
1	DB	390/391 (100%)	390 (100%)	0	100	100
1	DC	390/391 (100%)	390 (100%)	0	100	100
1	DD	390/391 (100%)	390 (100%)	0	100	100
1	DE	390/391 (100%)	390 (100%)	0	100	100
1	DF	390/391 (100%)	390 (100%)	0	100	100
1	DG	390/391 (100%)	390 (100%)	0	100	100
1	DH	390/391 (100%)	390 (100%)	0	100	100
1	DI	390/391 (100%)	390 (100%)	0	100	100
1	DJ	390/391 (100%)	390 (100%)	0	100	100
1	DK	390/391 (100%)	390 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	17171/17204 (100%)	17169 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BE	470	GLN
1	CE	90	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 251 such sidechains are listed below:

Mol	Chain	Res	Type
1	BG	113	GLN
1	DD	484	ASN
1	CA	86	ASN
1	DD	106	GLN
1	DI	83	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 oligosaccharides 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 ⓘ

There are no chain breaks in this entry.

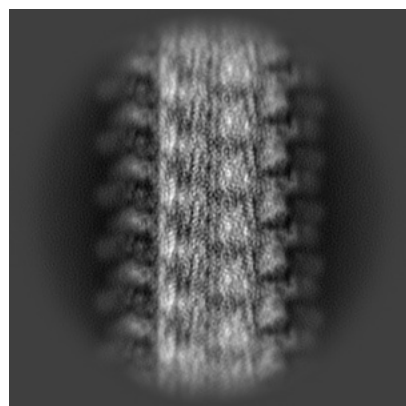
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63649. These allow visual inspection of the internal detail of the map and identification of artifacts.

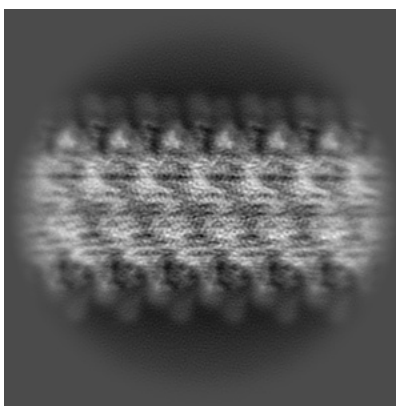
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

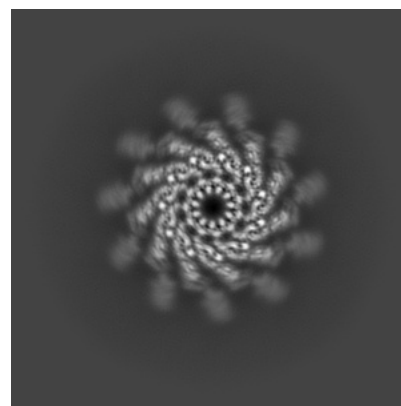
6.1.1 Primary map



X

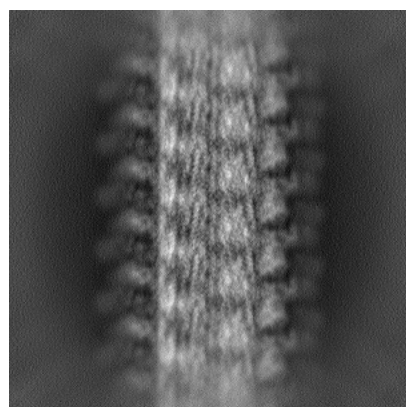


Y

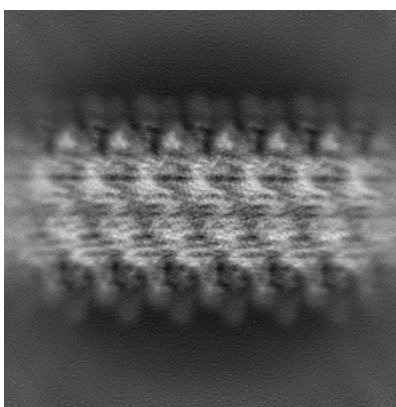


Z

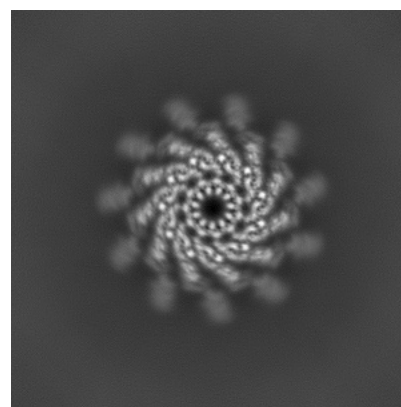
6.1.2 Raw map



X



Y

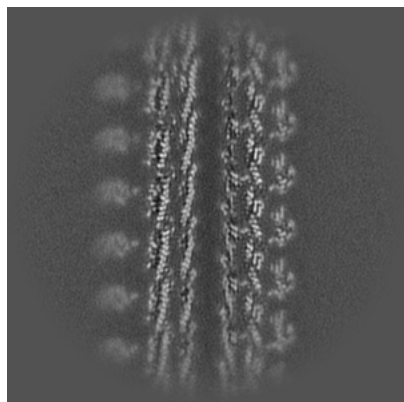


Z

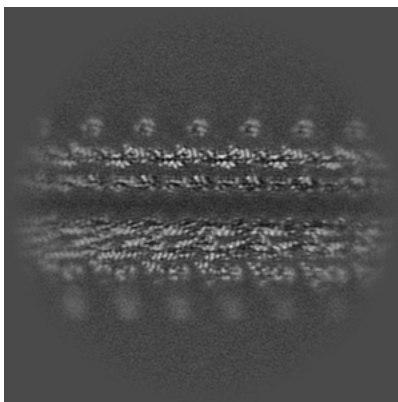
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

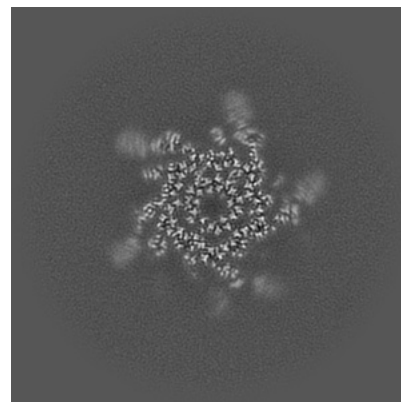
6.2.1 Primary map



X Index: 240

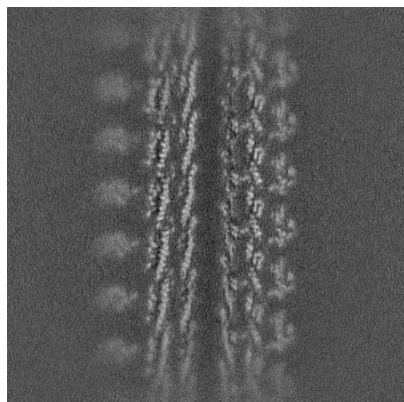


Y Index: 240

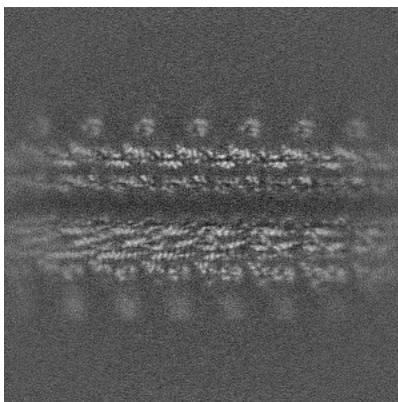


Z Index: 240

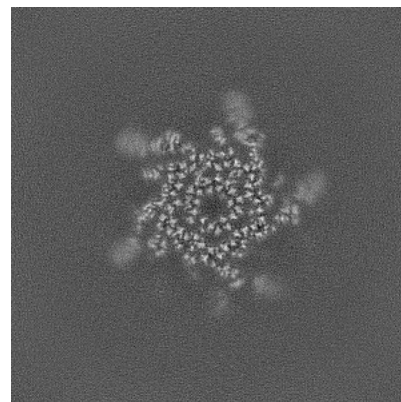
6.2.2 Raw map



X Index: 240



Y Index: 240

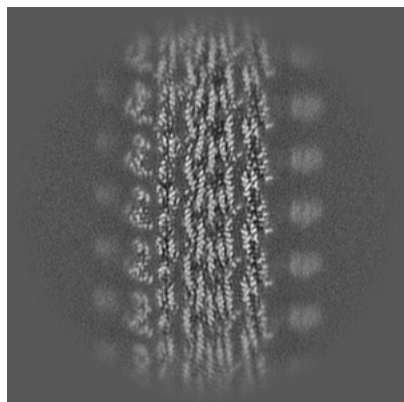


Z Index: 240

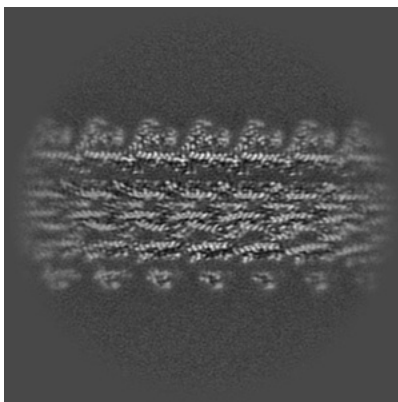
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

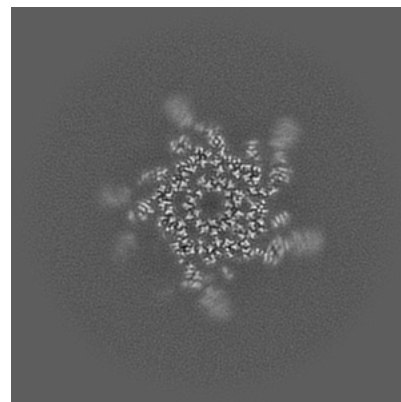
6.3.1 Primary map



X Index: 263

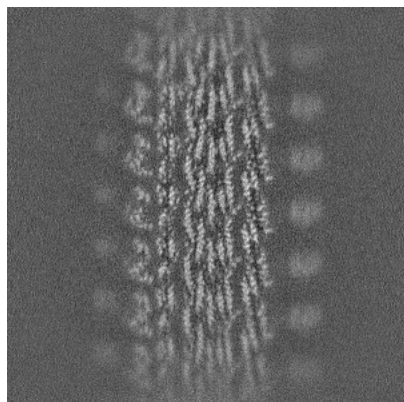


Y Index: 223

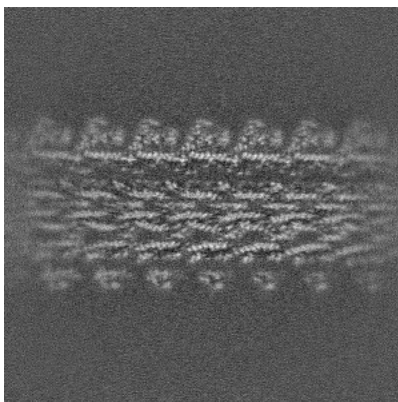


Z Index: 263

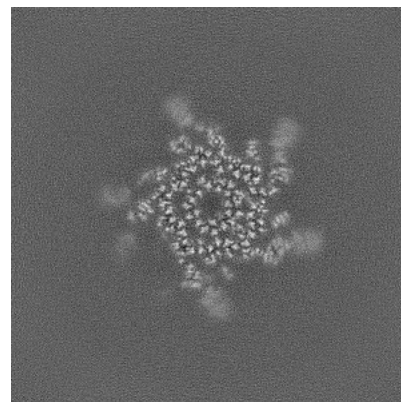
6.3.2 Raw map



X Index: 263



Y Index: 223

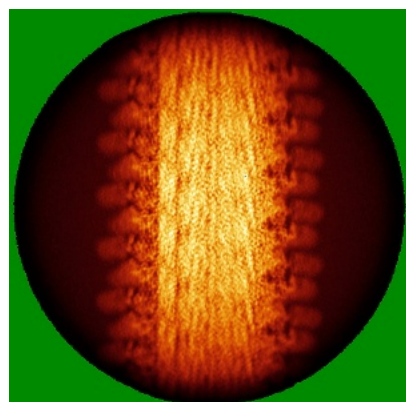


Z Index: 263

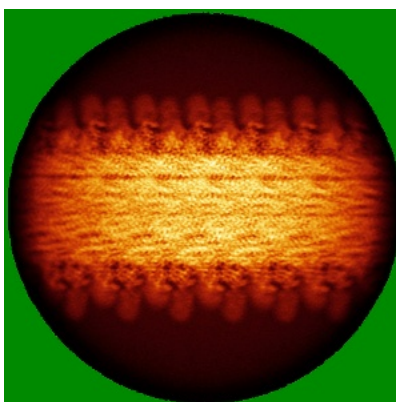
The images above show the largest variance slices of the map in three orthogonal directions.

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

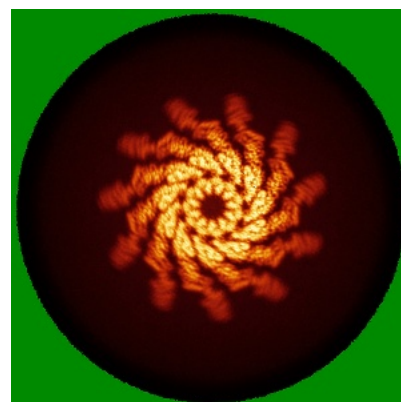
6.4.1 Primary map



X

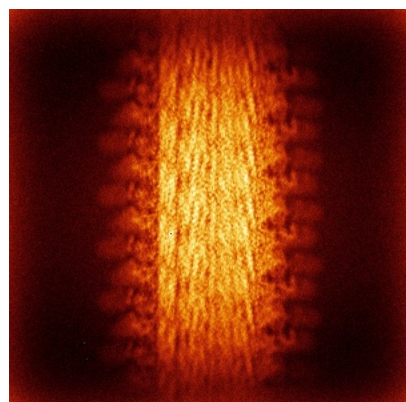


Y

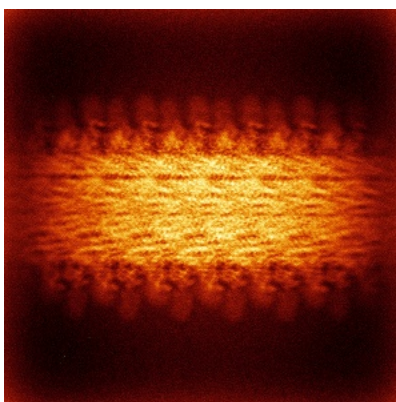


Z

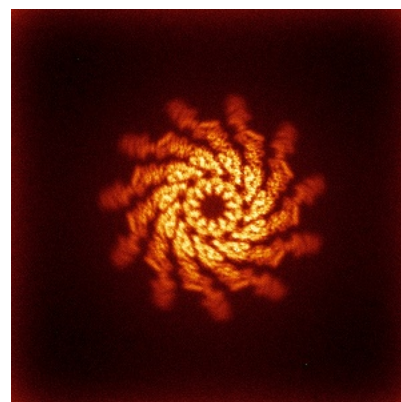
6.4.2 Raw map



X



Y

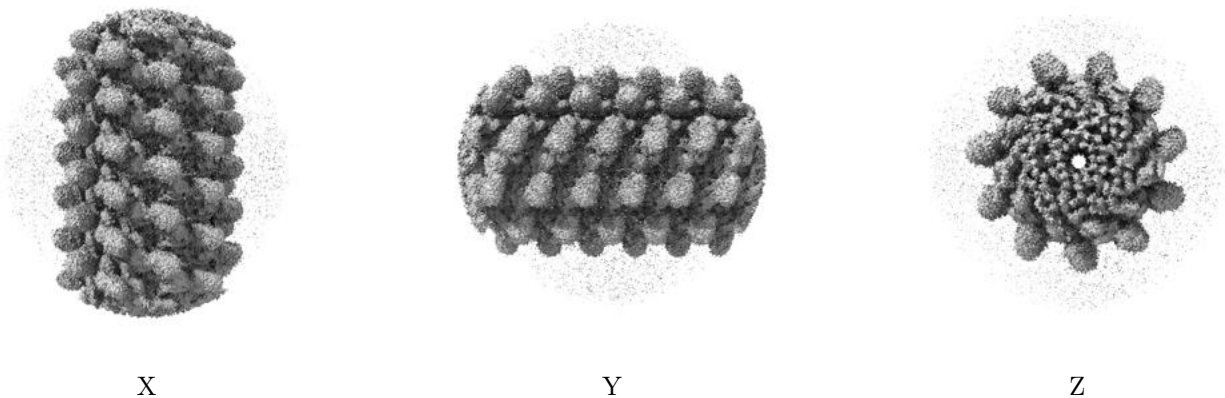


Z

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.

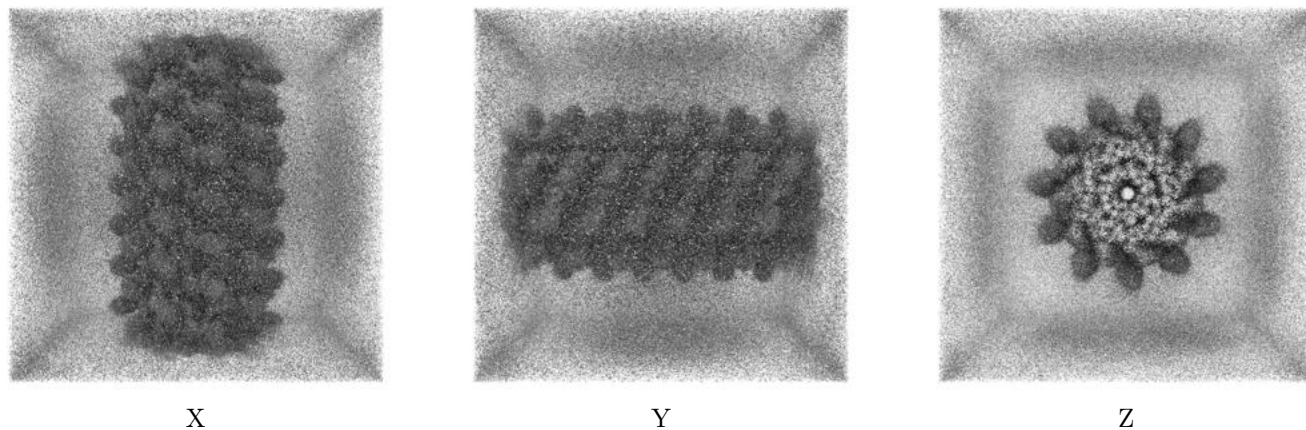
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

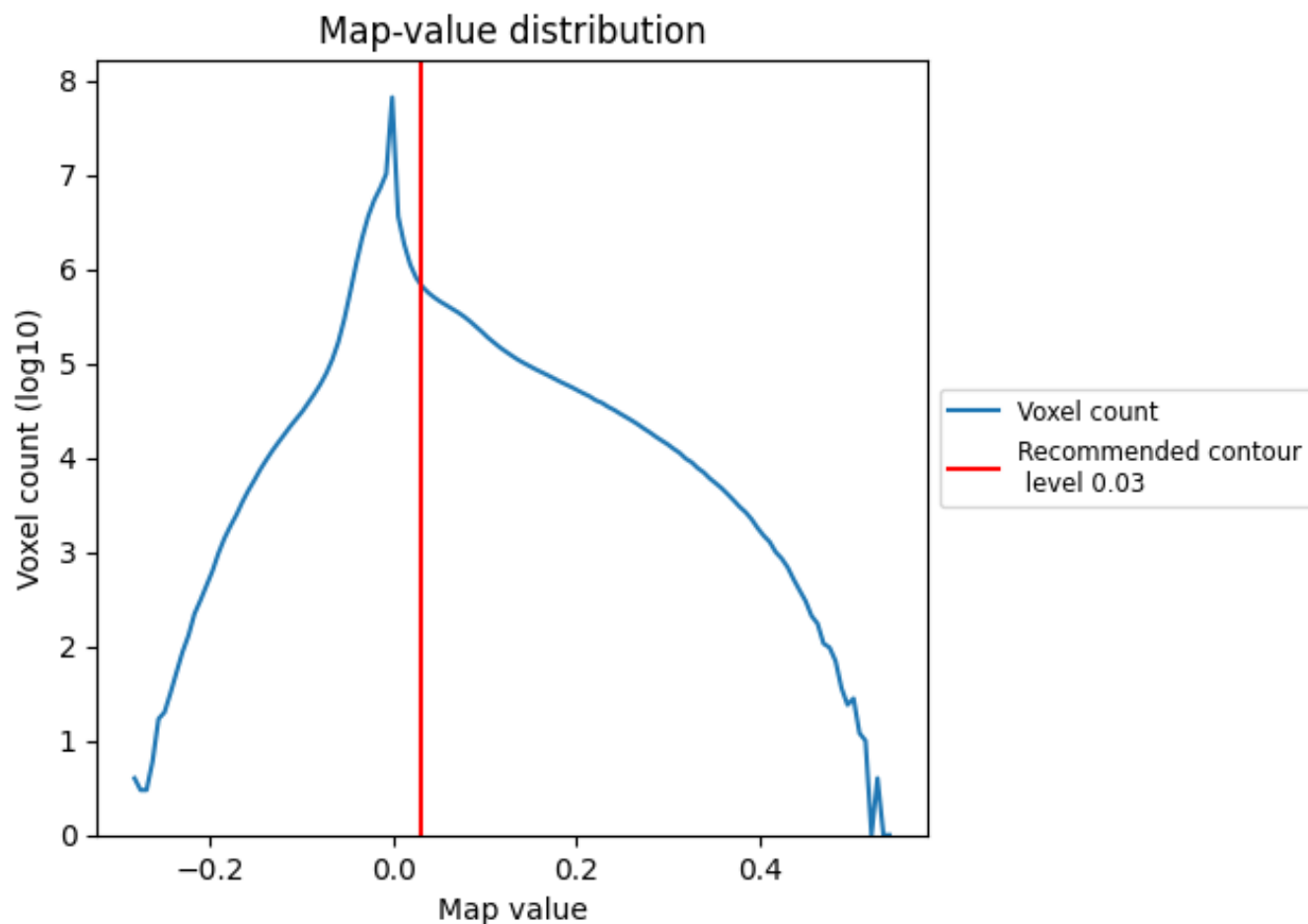
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

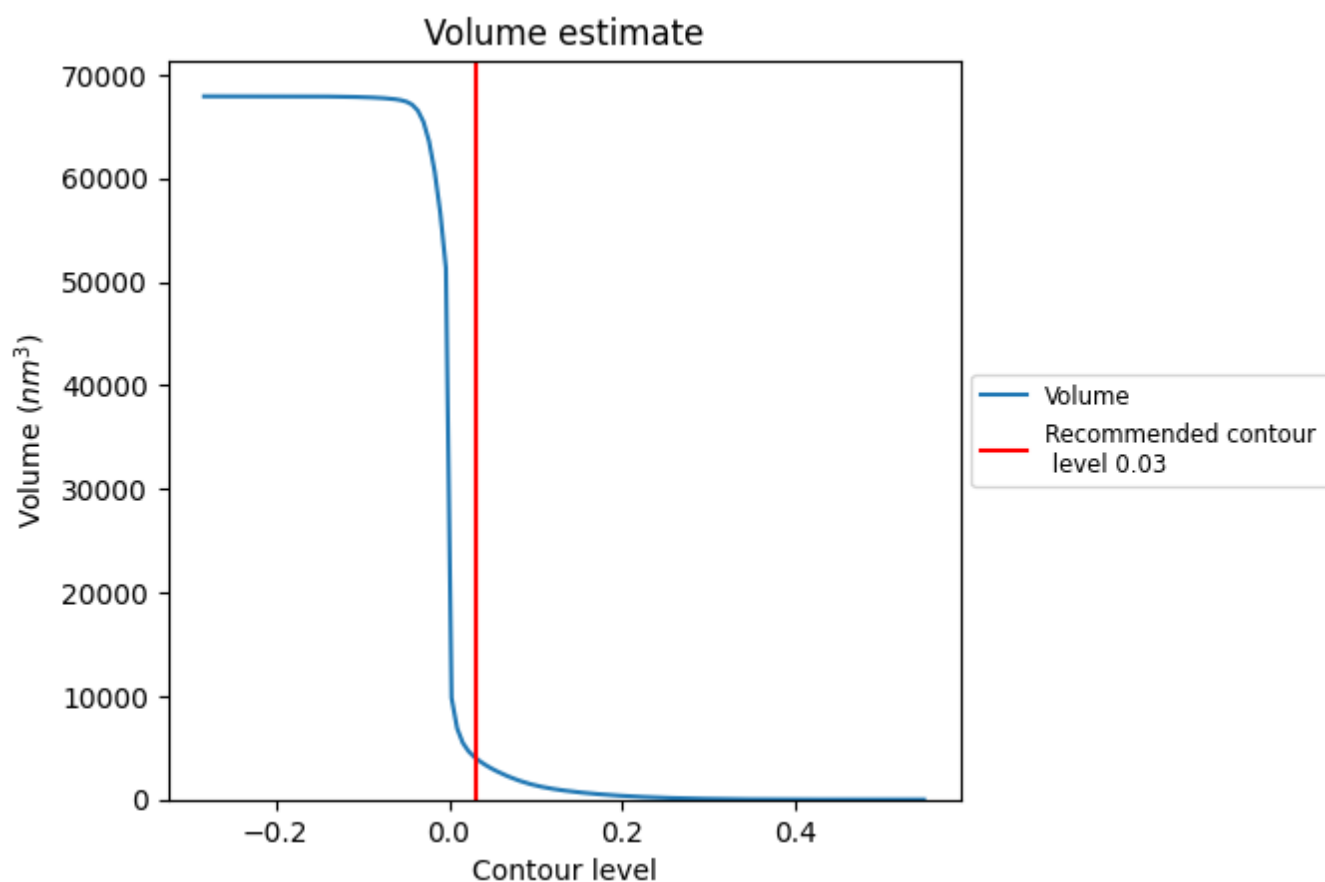
This section contains the results of statistical analysis of the map.

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.

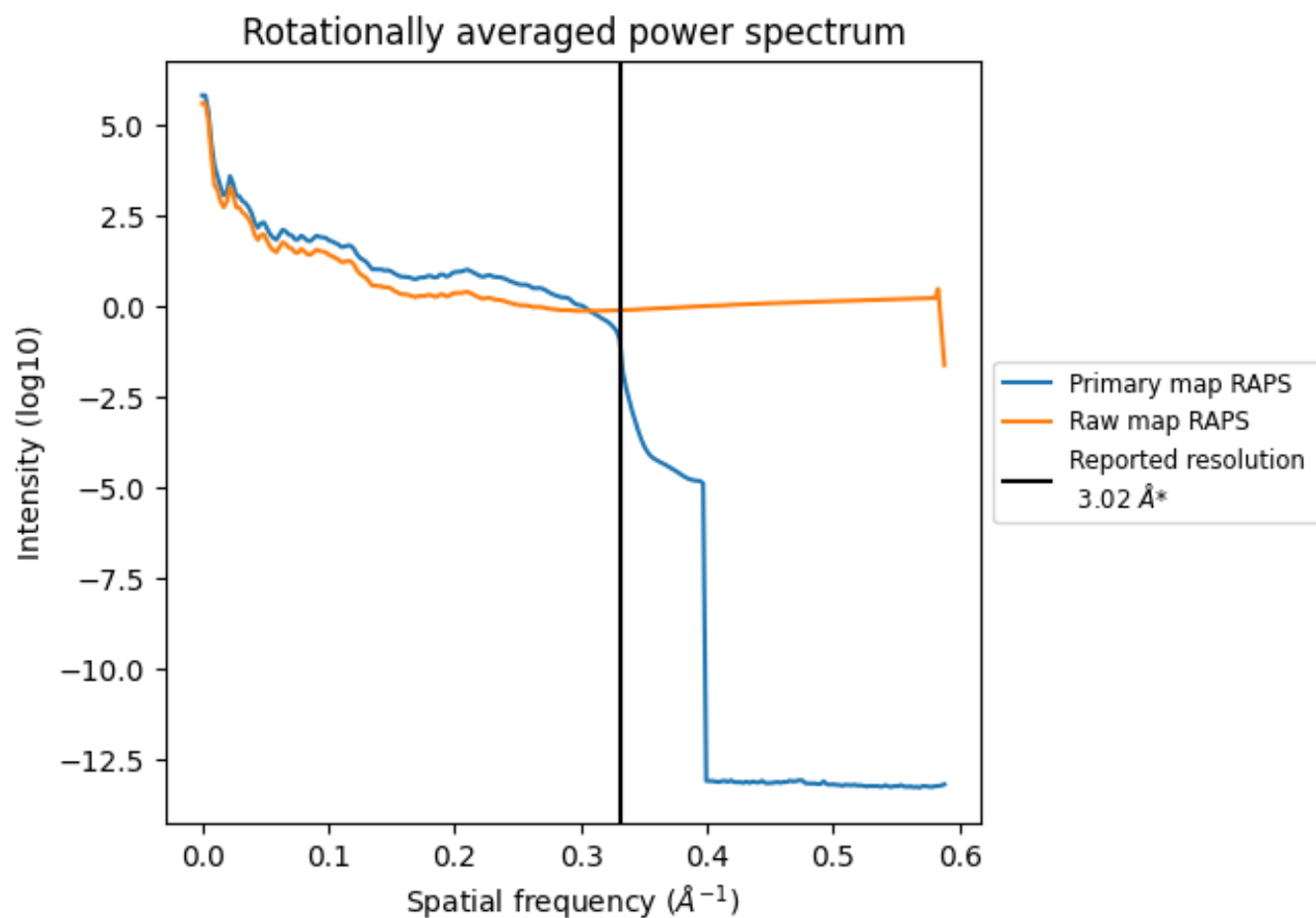
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4064 nm³; this corresponds to an approximate mass of 3671 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 ⓘ

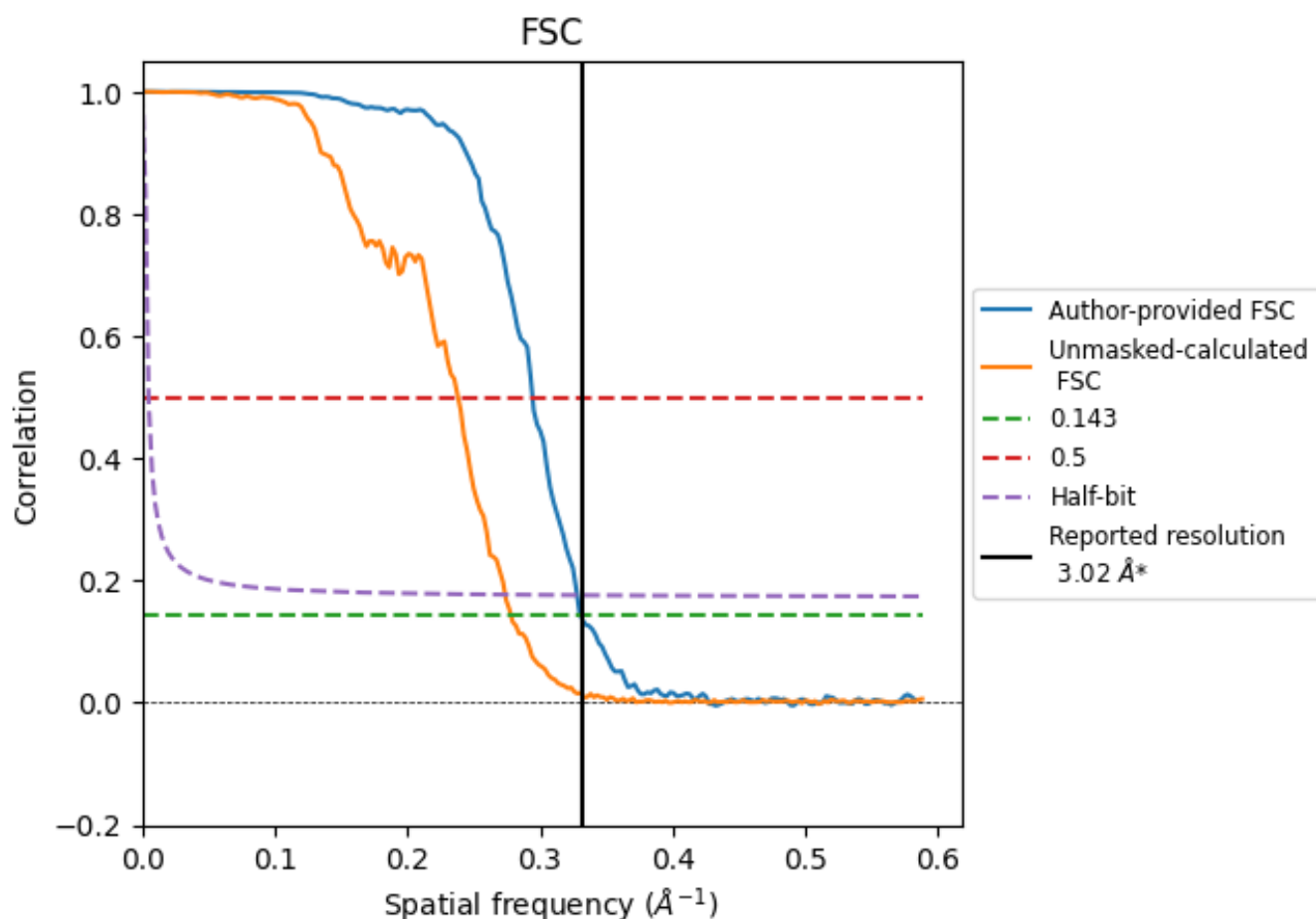


*Reported resolution corresponds to spatial frequency of 0.331 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.331 \AA^{-1}

8.2 Resolution estimates [i](#)

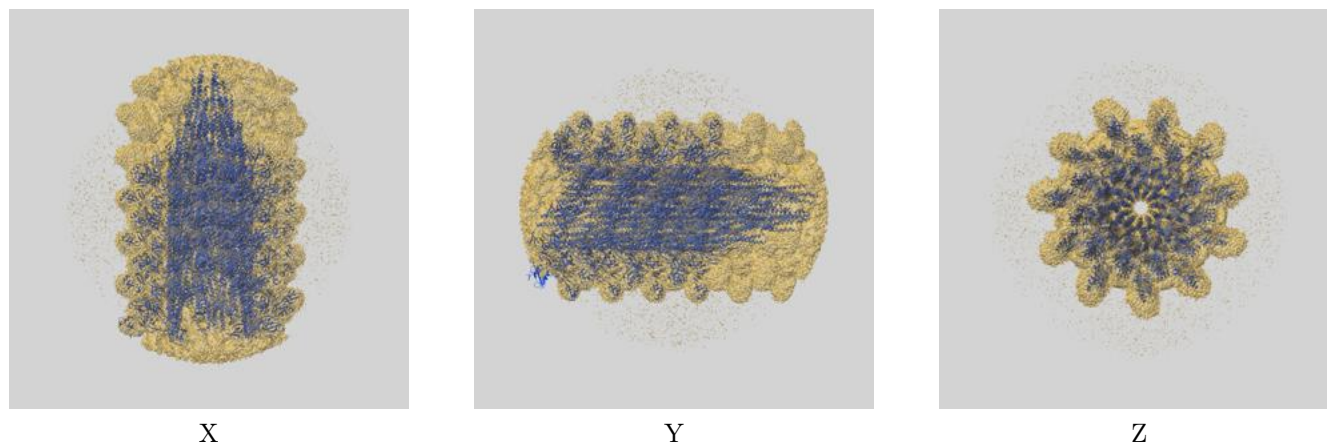
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.02	-	-
Author-provided FSC curve	3.02	3.40	3.05
Unmasked-calculated*	3.60	4.20	3.65

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.60 differs from the reported value 3.02 by more than 10 %

9 Map-model fit [i](#)

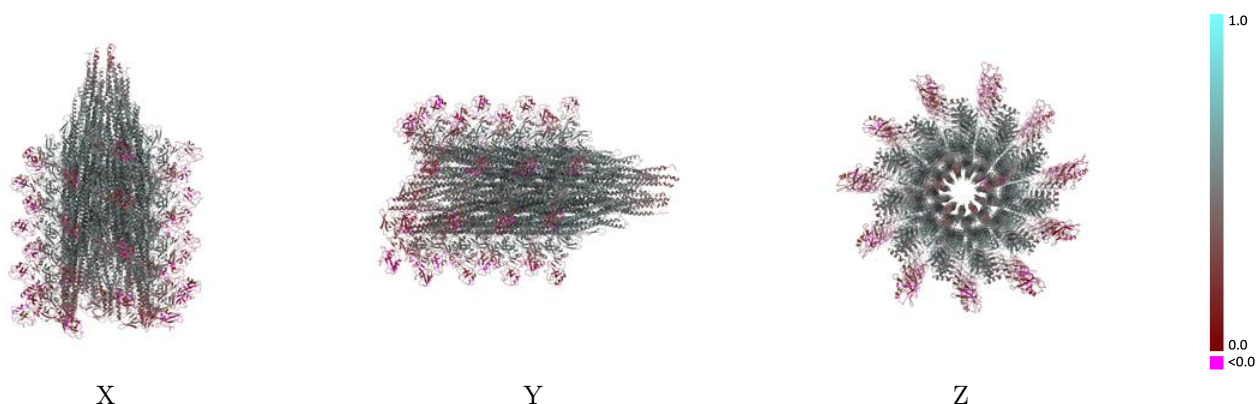
This section contains information regarding the fit between EMDB map EMD-63649 and PDB model 9M5T. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



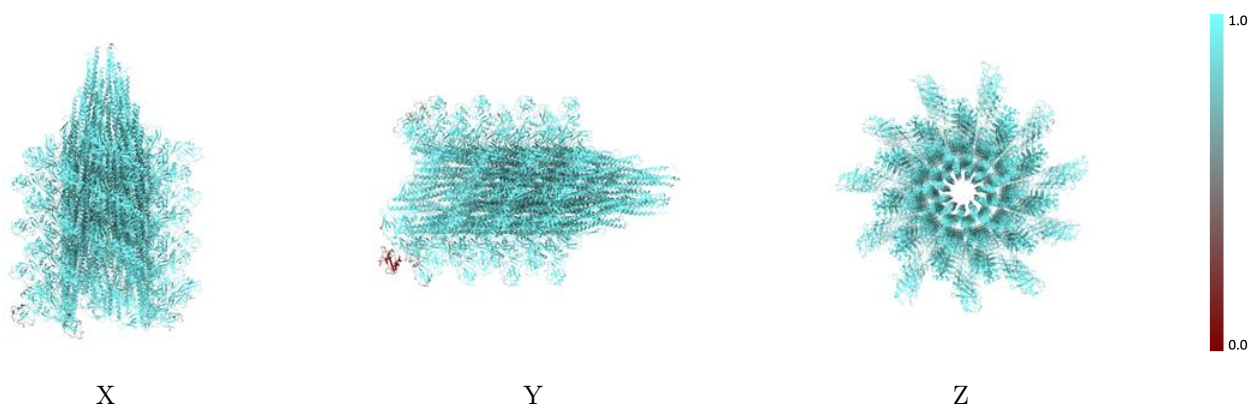
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



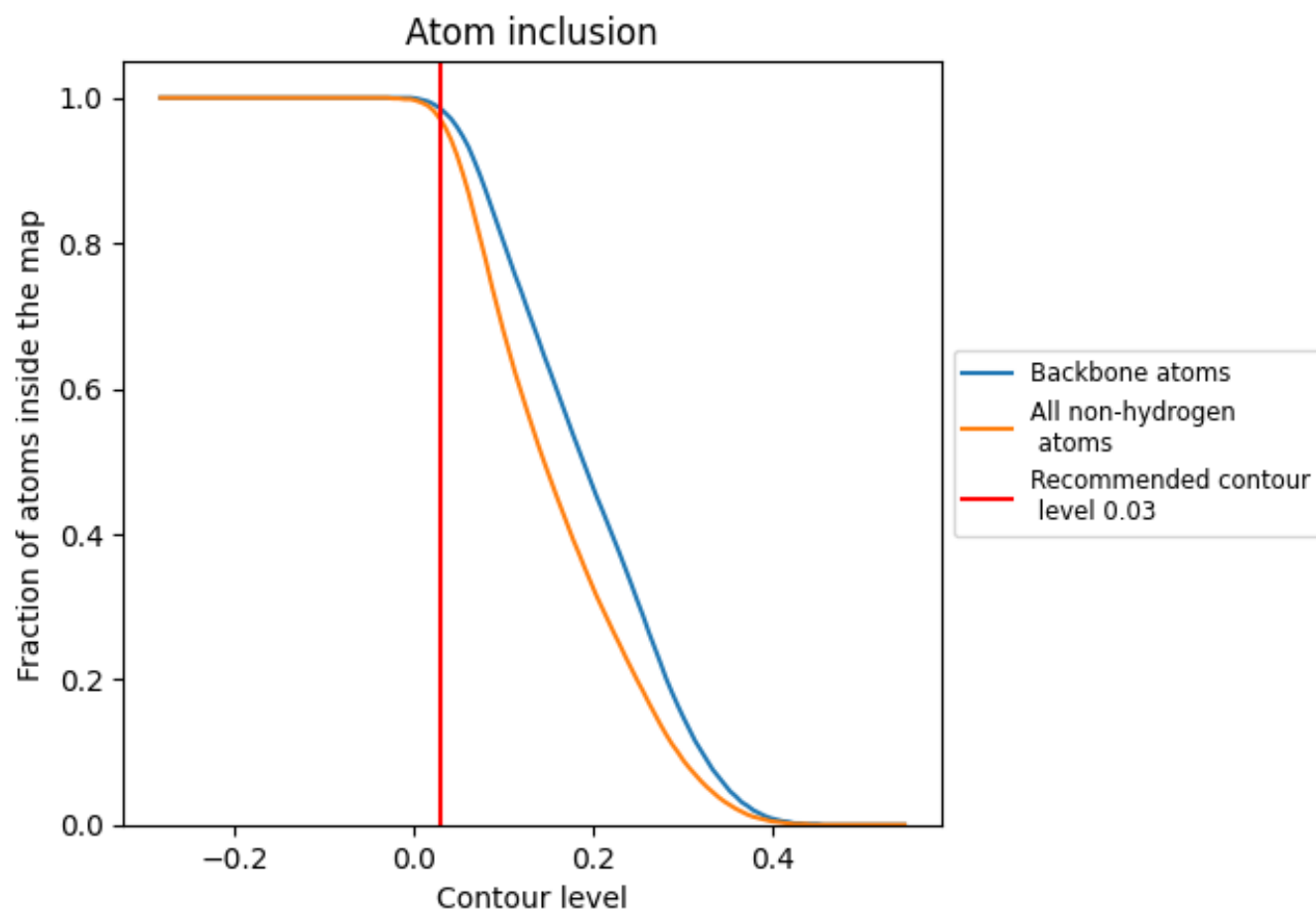
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.4230
AA	 0.9700	 0.4080
AB	 0.9590	 0.3740
AC	 0.8210	 0.3040
AD	 0.9580	 0.3790
AE	 0.8700	 0.3120
AF	 0.9730	 0.3680
AG	 0.9120	 0.3270
AH	 0.9720	 0.3890
AI	 0.9300	 0.3550
AJ	 0.9730	 0.4030
AK	 0.9480	 0.3720
BA	 0.9770	 0.4490
BB	 0.9850	 0.4430
BC	 0.9820	 0.4210
BD	 0.9830	 0.4320
BE	 0.9800	 0.4070
BF	 0.9800	 0.4200
BG	 0.9820	 0.4180
BH	 0.9830	 0.4360
BI	 0.9810	 0.4340
BJ	 0.9840	 0.4500
BK	 0.9770	 0.4310
CA	 0.9810	 0.4480
CB	 0.9820	 0.4550
CC	 0.9860	 0.4490
CD	 0.9820	 0.4470
CE	 0.9840	 0.4450
CF	 0.9830	 0.4450
CG	 0.9870	 0.4550
CH	 0.9860	 0.4600
CI	 0.9860	 0.4570
CJ	 0.9840	 0.4680
CK	 0.9740	 0.4590
DA	 0.9710	 0.4150



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Chain	Atom inclusion	Q-score
DB	 0.9840	 0.4550
DC	 0.9840	 0.4610
DD	 0.9830	 0.4420
DE	 0.9840	 0.4500
DF	 0.9770	 0.4260
DG	 0.9880	 0.4570
DH	 0.9820	 0.4310
DI	 0.9850	 0.4550
DJ	 0.9810	 0.4340
DK	 0.9800	 0.4540