



wwPDB EM Validation Summary Report ⓘ

Jan 11, 2024 – 02:23 PM JST

PDB ID : 8K35
EMDB ID : EMD-36844
Title : Structure of the bacteriophage lambda tail tip complex
Authors : Xiao, H.; Tan, L.; Cheng, L.P.; Liu, H.R.
Deposited on : 2023-07-14
Resolution : 3.44 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:

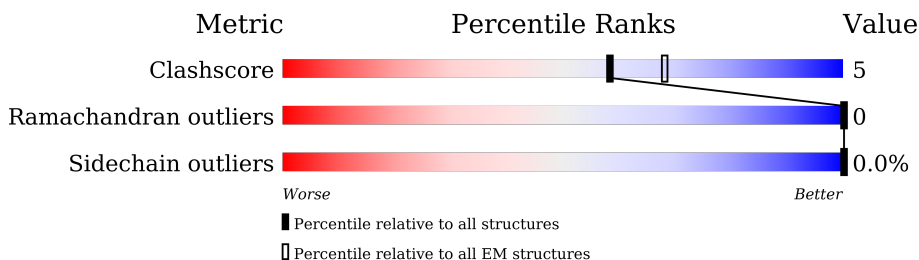
EMDB validation analysis : 0.0.1.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.44 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)
Clashscore	158937	4297
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	1132	
1	B	1132	
1	I	1132	
2	G	232	
2	J	232	
2	N	232	
3	C	109	
3	D	109	

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Mol	Chain	Length	Quality of chain
3	E	109	 94% 6%
3	F	109	 88% 12%
3	H	109	 90% 10%
3	O	109	 89% 11%
4	K	223	 34% 6% 60%
4	Q	223	 36% 6% 60%
4	x	223	 40% 6% 60%
5	L	246	 50% 12% 38%
5	R	246	 55% 7% 38%
5	T	246	 54% 9% 38%
5	U	246	 53% 9% 38%
5	V	246	 52% 10% 38%
5	W	246	 52% 10% 38%
6	M	853	 96%
6	P	853	 96%
6	S	853	 96%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 40353 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 Tip attachment protein J.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	I	851	6633	4156	1156	1301	20	0	0
1	A	851	6633	4156	1156	1301	20	0	0
1	B	851	6633	4156	1156	1301	20	0	0

- Molecule 2 is a protein called Tail tip protein L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	J	232	1801	1117	309	362	13	0	0
2	G	232	1801	1117	309	362	13	0	0
2	N	232	1801	1117	309	362	13	0	0

- Molecule 3 is a protein called Tail tip protein M.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	H	109	884	569	154	157	4	0	0
3	O	109	884	569	154	157	4	0	0
3	C	109	884	569	154	157	4	0	0
3	E	109	884	569	154	157	4	0	0
3	D	109	884	569	154	157	4	0	0
3	F	109	884	569	154	157	4	0	0

- Molecule 4 is a protein called Tail tip assembly protein I.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	x	89	Total	C	N	O	S	0	0
			652	403	116	128	5		
4	K	89	Total	C	N	O	S	0	0
			652	403	116	128	5		
4	Q	89	Total	C	N	O	S	0	0
			652	403	116	128	5		

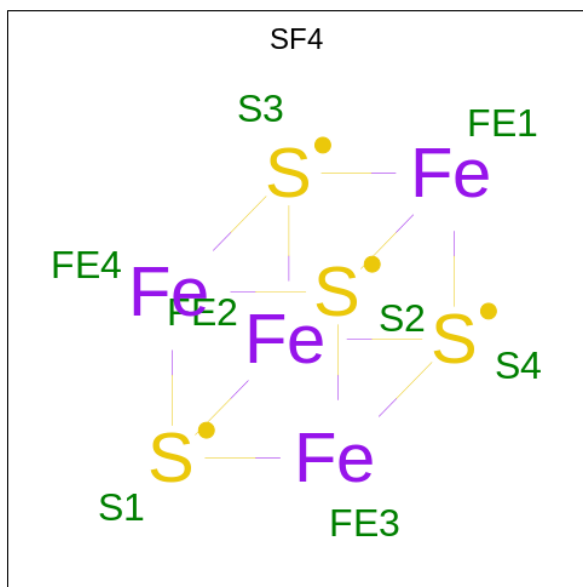
- Molecule 5 is a protein called Tail tube protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	153	Total	C	N	O	S	0	0
			1174	736	199	236	3		
5	R	153	Total	C	N	O	S	0	0
			1174	736	199	236	3		
5	T	153	Total	C	N	O	S	0	0
			1174	736	199	236	3		
5	U	153	Total	C	N	O	S	0	0
			1174	736	199	236	3		
5	V	153	Total	C	N	O	S	0	0
			1174	736	199	236	3		
5	W	153	Total	C	N	O	S	0	0
			1174	736	199	236	3		

- Molecule 6 is a protein called Tape measure protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	P	32	Total	C	N	O	S	0	0
			241	149	45	45	2		
6	M	32	Total	C	N	O	S	0	0
			241	149	45	45	2		
6	S	32	Total	C	N	O	S	0	0
			241	149	45	45	2		

- Molecule 7 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).

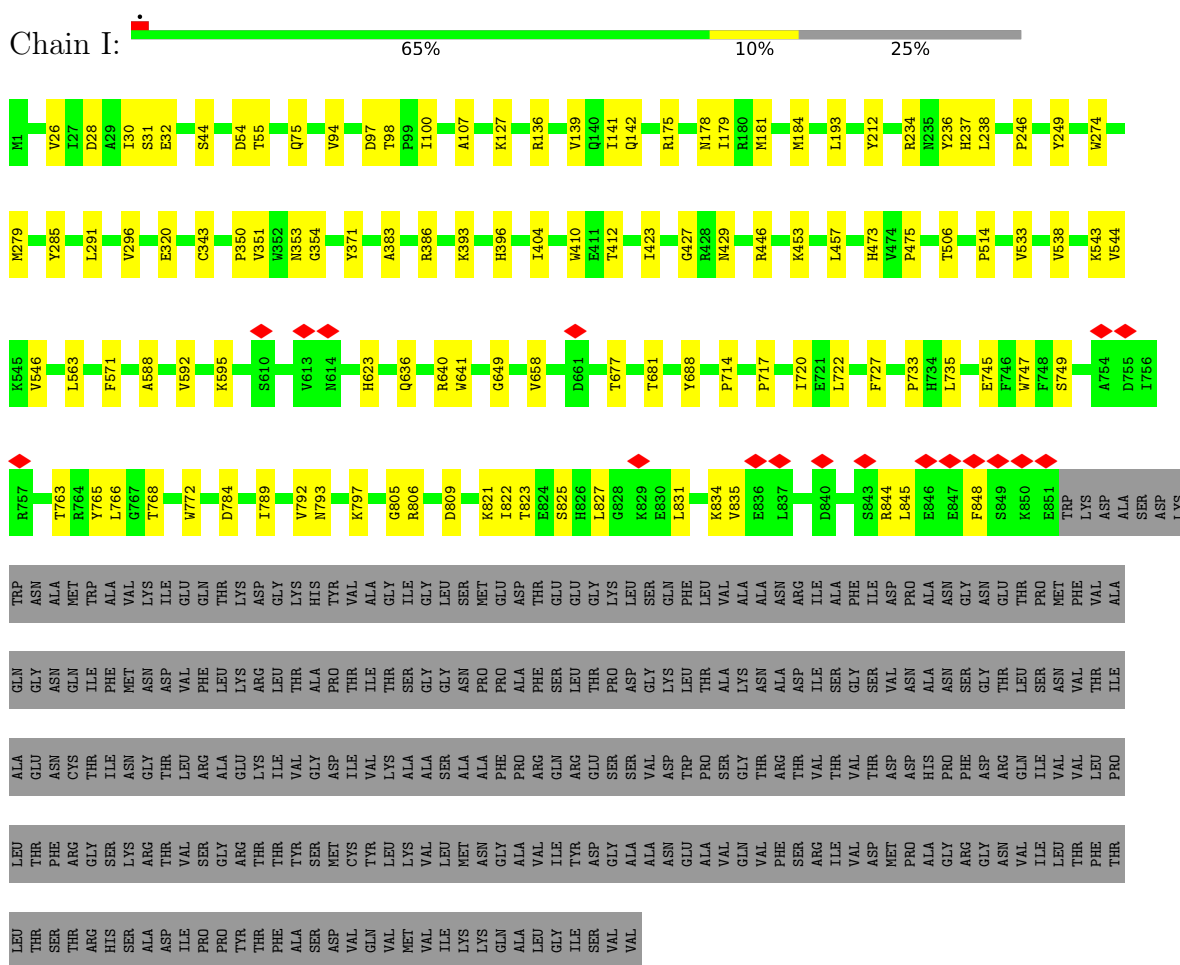


Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
7	J	1	8	4	4	0
7	G	1	8	4	4	0
7	N	1	8	4	4	0

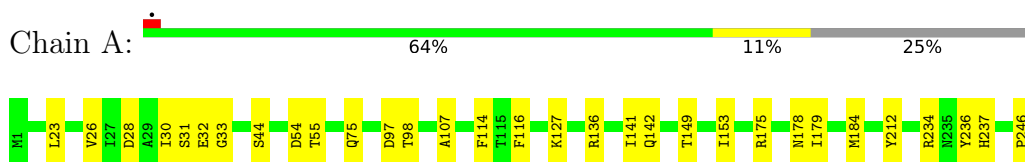
3 Residue-property plots [i](#)

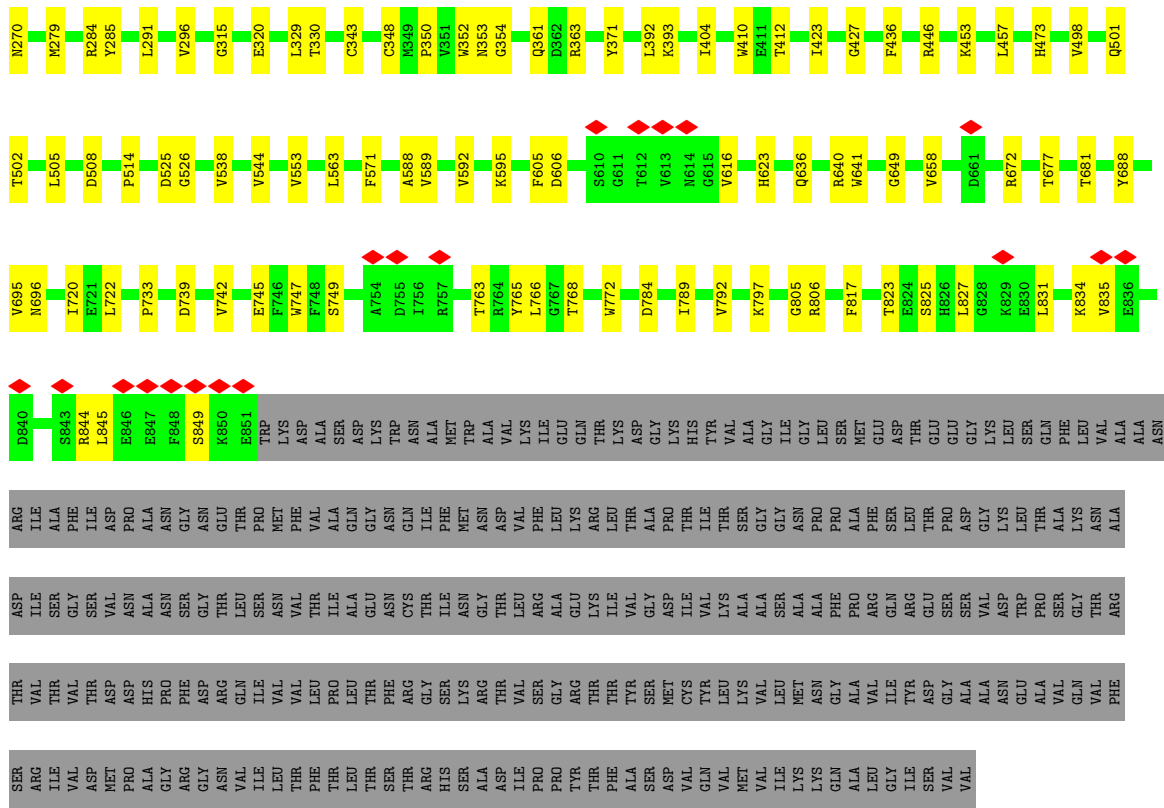
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

- Molecule 1: Tip attachment protein J

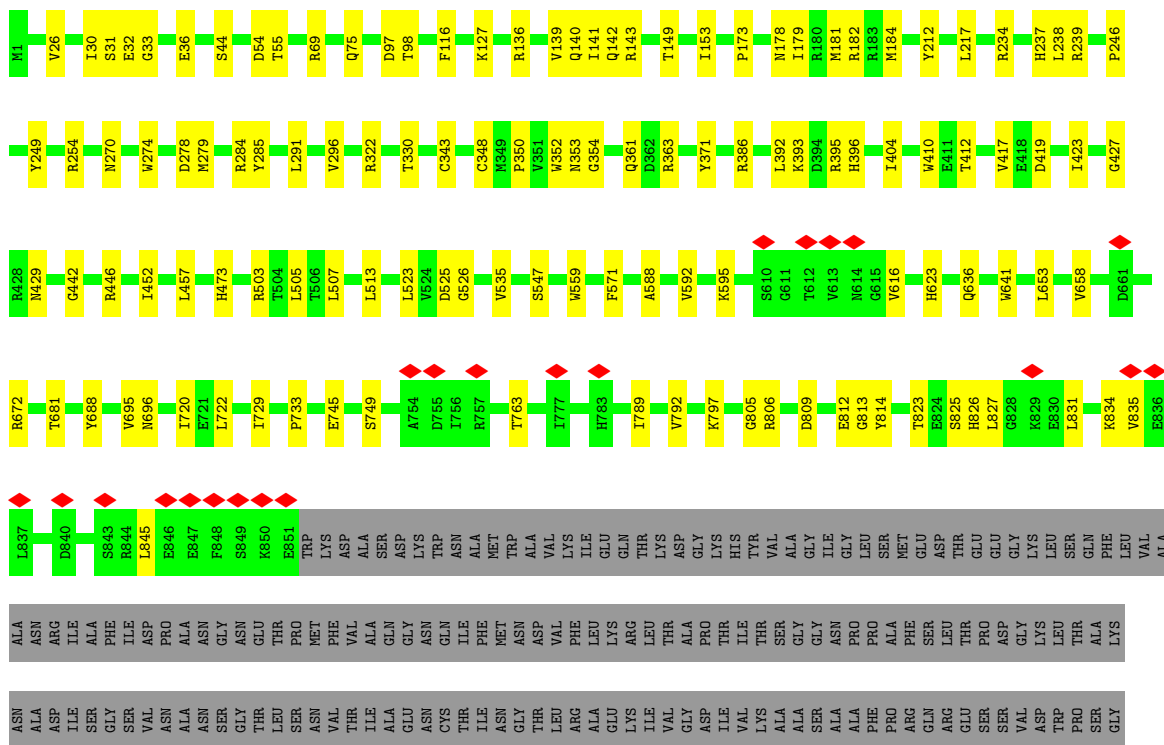


- Molecule 1: Tip attachment protein J



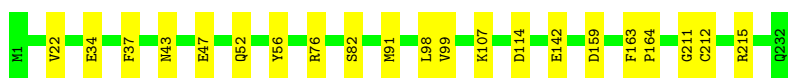
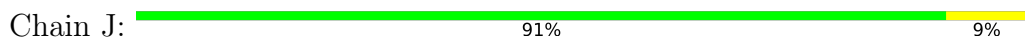


● Molecule 1: Tip attachment protein J



THR	ARG	THR	VAL	VAL	THR	ASP	ASP	HIS	PRO	PHE	ASP	ARG	GLN	ILE	VAL	VAL	LEU	LEU	PRO	LEU	THR	THR	PHE	THR	ARG	GLY	SER	LYS	ARG	THR	THR	SER	GLY	THR	THR	TYR	SER	MET	CYS	TYR	LEU	LEU	VAL	VAL	LEU	LEU	MET	LYS	LYS	GLN	ALA	ALA	LEU	VAL	ILE	TYR	ASP	GLY	VAL	VAL	GLN
VAL	PHE	SER	ARG	ILE	VAL	ASP	MET	PRO	ALA	GLY	ARG	GLY	ASN	VAL	ILE	LEU	THR	PHE	THR	LEU	THR	SER	THR	ARG	GLY	HIS	SER	ALA	ASP	ILE	VAL	PRO	SER	GLY	TYR	THR	PHE	ALA	SER	ASP	VAL	GLN	VAL	MET	VAL	VAL	ILE	LYS	LYS	GLN	ALA	ALA	LEU	VAL	ILE	TYR	SER	ASP	VAL	VAL	GLN

● Molecule 2: Tail tip protein L



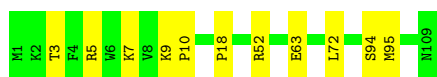
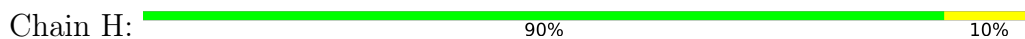
● Molecule 2: Tail tip protein L



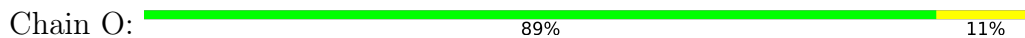
● Molecule 2: Tail tip protein L



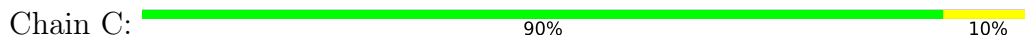
● Molecule 3: Tail tip protein M



● Molecule 3: Tail tip protein M

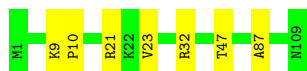


● Molecule 3: Tail tip protein M



● Molecule 3: Tail tip protein M

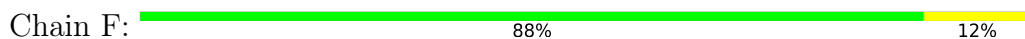




• Molecule 3: Tail tip protein M



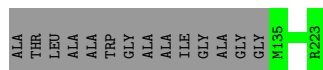
• Molecule 3: Tail tip protein M



• Molecule 4: Tail tip assembly protein I



MET	ALA	ALA	THR	HIS	THR	LEU	PRO	ASP	ARG	LEU	VAL	LEU	LEU	ALA	ALA	THR	ALA	ARG	ILE	GLN	CYS	LEU	HIS	GLU	THR	GLY	ASP	LEU	PRO	GLN	ARG	PHE	GLY	VAL	GLY	ILE	ARG	ILE	ILE	ILE	VAL	PRO	ARG	VAL	VAL	VAL	LYS	THR	GLY	ALA	ALA	GLY	ALA	LYS	SER	GLU	ALA	ALA	ILE	ILE	PHE	VAL	GLN	ILE	ALA	ALA	PRO	PRO	ALA	ALA	PHE	ALA	ARG	ILE	ALA	GLN	LYS	GLY	SER	PHE	PHE	ASP	GLY	THR	ALA	TRP	ALA	TYR				
GLN	VAL	ARG	ILE	ARG	ALA	GLY	TRP	GLY	ASP	VAL	VAL	SER	THR	THR	SER	GLY	GLY	LEU	THR	ALA	GLN	LEU	HIS	GLU	THR	GLY	ASP	LEU	PRO	GLN	ARG	ALA	VAL	VAL	ILE	ARG	HIS	ILE	ILE	VAL	PRO	ARG	VAL	VAL	LYS	THR	GLY	ALA	ALA	LYS	SER	GLU	ALA	ALA	ILE	ILE	PHE	VAL	GLN	ILE	ALA	ALA	PRO	GLY	GLN	VAL	THR	THR	GLN	LEU	GLY	ALA	ALA	ALA	PHE	ALA	ARG	ILE	ALA	GLN	LYS	GLY	SER	PHE	PHE	ASP	GLY	THR	ALA	TRP	ALA	TYR



• Molecule 4: Tail tip assembly protein I



MET	ALA	ALA	THR	HIS	THR	LEU	PRO	ASP	ARG	LEU	VAL	LEU	LEU	ALA	ALA	THR	ALA	ARG	ILE	GLN	CYS	LEU	HIS	GLU	THR	GLY	ASP	LEU	PRO	GLN	ARG	PHE	GLY	VAL	GLY	ILE	ARG	ILE	ILE	VAL	PRO	ARG	VAL	VAL	LYS	THR	GLY	ALA	ALA	LYS	SER	GLU	ALA	ALA	ILE	ILE	PHE	VAL	GLN	ILE	ALA	ALA	PRO	GLY	GLN	VAL	THR	THR	GLN	LEU	GLY	ALA	ALA	ALA	PHE	ALA	ARG	ILE	ALA	GLN	LYS	GLY	SER	PHE	PHE	ASP	GLY	THR	ALA	TRP	ALA	TYR
GLN	VAL	ARG	ILE	ARG	ALA	GLY	TRP	GLY	ASP	VAL	VAL	SER	THR	THR	SER	GLY	GLY	LEU	THR	ALA	GLN	LEU	HIS	GLU	THR	GLY	ASP	LEU	PRO	GLN	ARG	ALA	VAL	VAL	ILE	ARG	HIS	ILE	ILE	VAL	PRO	ARG	VAL	VAL	LYS	THR	GLY	ALA	ALA	LYS	SER	GLU	ALA	ALA	ILE	ILE	PHE	VAL	GLN	ILE	ALA	ALA	PRO	GLY	GLN	VAL	THR	THR	GLN	LEU	GLY	ALA	ALA	ALA	PHE	ALA	ARG	ILE	ALA	GLN	LYS	GLY	SER	PHE	PHE	ASP	GLY	THR	ALA	TRP	ALA	TYR



• Molecule 4: Tail tip assembly protein I



MET	ALA	ALA	THR	HIS	THR	LEU	PRO	ASP	ARG	LEU	VAL	LEU	LEU	ALA	ALA	THR	ALA	ARG	ILE	GLN	CYS	LEU	HIS	GLU	THR	GLY	ASP	LEU	PRO	GLN	ARG	PHE	GLY	VAL	GLY	ILE	ARG	ILE	ILE	VAL	PRO	ARG	VAL	VAL	LYS	THR	GLY	ALA	ALA	LYS	SER	GLU	ALA	ALA	ILE	ILE	PHE	VAL	GLN	ILE	ALA	ALA	PRO	GLY	GLN	VAL	THR	THR	GLN	LEU	GLY	ALA	ALA	ALA	PHE	ALA	ARG	ILE	ALA	GLN	LYS	GLY	SER	PHE	PHE	ASP	GLY	THR	ALA	TRP	ALA	TYR
GLN	VAL	ARG	ILE	ARG	ALA	GLY	TRP	GLY	ASP	VAL	VAL	SER	THR	THR	SER	GLY	GLY	LEU	THR	ALA	GLN	LEU	HIS	GLU	THR	GLY	ASP	LEU	PRO	GLN	ARG	ALA	VAL	VAL	ILE	ARG	HIS	ILE	ILE	VAL	PRO	ARG	VAL	VAL	LYS	THR	GLY	ALA	ALA	LYS	SER	GLU	ALA	ALA	ILE	ILE	PHE	VAL	GLN	ILE	ALA	ALA	PRO	GLY	GLN	VAL	THR	THR	GLN	LEU	GLY	ALA	ALA	ALA	PHE	ALA	ARG	ILE	ALA	GLN	LYS	GLY	SER	PHE	PHE	ASP	GLY	THR	ALA	TRP	ALA	TYR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54385	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	32	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.282	Depositor
Minimum map value	-0.126	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	299.2, 299.2, 299.2	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.36, 1.36, 1.36	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4

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	0/6775	0.51	0/9223
1	B	0.28	0/6775	0.51	0/9223
1	I	0.27	0/6775	0.51	0/9223
2	G	0.32	0/1836	0.52	0/2487
2	J	0.32	0/1836	0.51	0/2487
2	N	0.31	0/1836	0.52	0/2487
3	C	0.28	0/909	0.50	0/1231
3	D	0.28	0/909	0.48	0/1231
3	E	0.28	0/909	0.50	0/1231
3	F	0.28	0/909	0.50	0/1231
3	H	0.28	0/909	0.50	0/1231
3	O	0.28	0/909	0.49	0/1231
4	K	0.29	0/658	0.53	0/888
4	Q	0.28	0/658	0.54	0/888
4	x	0.28	0/658	0.54	0/888
5	L	0.25	0/1203	0.49	0/1639
5	R	0.25	0/1203	0.49	0/1639
5	T	0.32	0/1203	0.51	0/1639
5	U	0.25	0/1203	0.50	0/1639
5	V	0.25	0/1203	0.50	0/1639
5	W	0.25	0/1203	0.49	0/1639
6	M	0.30	0/243	0.48	0/323
6	P	0.30	0/243	0.49	0/323
6	S	0.30	0/243	0.50	0/323
All	All	0.28	0/41208	0.51	0/55983

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

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	A	6633	0	6479	87	0
1	B	6633	0	6479	85	0
1	I	6633	0	6479	72	0
2	G	1801	0	1715	20	0
2	J	1801	0	1715	17	0
2	N	1801	0	1715	16	0
3	C	884	0	881	8	0
3	D	884	0	881	5	0
3	E	884	0	881	6	0
3	F	884	0	881	9	0
3	H	884	0	881	9	0
3	O	884	0	881	8	0
4	K	652	0	661	13	0
4	Q	652	0	661	7	0
4	x	652	0	661	0	0
5	L	1174	0	1122	21	0
5	R	1174	0	1122	12	0
5	T	1174	0	1122	14	0
5	U	1174	0	1122	15	0
5	V	1174	0	1122	22	0
5	W	1174	0	1122	19	0
6	M	241	0	243	1	0
6	P	241	0	243	2	0
6	S	241	0	243	3	0
7	G	8	0	0	1	0
7	J	8	0	0	1	0
7	N	8	0	0	1	0
All	All	40353	0	39312	385	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 385 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:I:54:ASP:OD1	1:I:55:THR:N	2.08	0.86
1:I:745:GLU:HG2	1:I:768:THR:HG22	1.70	0.74
1:A:745:GLU:HG2	1:A:768:THR:HG22	1.70	0.73
2:N:212:CYS:HB2	7:N:301:SF4:S1	2.30	0.71
1:A:834:LYS:HE3	1:B:835:VAL:HA	1.73	0.70

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	A	849/1132 (75%)	822 (97%)	27 (3%)	0	100	100
1	B	849/1132 (75%)	821 (97%)	28 (3%)	0	100	100
1	I	849/1132 (75%)	822 (97%)	27 (3%)	0	100	100
2	G	230/232 (99%)	223 (97%)	7 (3%)	0	100	100
2	J	230/232 (99%)	223 (97%)	7 (3%)	0	100	100
2	N	230/232 (99%)	222 (96%)	8 (4%)	0	100	100
3	C	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
3	D	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
3	E	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
3	F	107/109 (98%)	107 (100%)	0	0	100	100
3	H	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
3	O	107/109 (98%)	107 (100%)	0	0	100	100
4	K	87/223 (39%)	86 (99%)	1 (1%)	0	100	100
4	Q	87/223 (39%)	86 (99%)	1 (1%)	0	100	100
4	x	87/223 (39%)	87 (100%)	0	0	100	100
5	L	151/246 (61%)	146 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	R	151/246 (61%)	148 (98%)	3 (2%)	0	100	100
5	T	151/246 (61%)	146 (97%)	5 (3%)	0	100	100
5	U	151/246 (61%)	148 (98%)	3 (2%)	0	100	100
5	V	151/246 (61%)	147 (97%)	4 (3%)	0	100	100
5	W	151/246 (61%)	147 (97%)	4 (3%)	0	100	100
6	M	30/853 (4%)	30 (100%)	0	0	100	100
6	P	30/853 (4%)	30 (100%)	0	0	100	100
6	S	30/853 (4%)	30 (100%)	0	0	100	100
All	All	5136/9450 (54%)	4998 (97%)	138 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	A	726/958 (76%)	726 (100%)	0	100	100
1	B	726/958 (76%)	726 (100%)	0	100	100
1	I	726/958 (76%)	726 (100%)	0	100	100
2	G	198/198 (100%)	198 (100%)	0	100	100
2	J	198/198 (100%)	198 (100%)	0	100	100
2	N	198/198 (100%)	198 (100%)	0	100	100
3	C	96/96 (100%)	96 (100%)	0	100	100
3	D	96/96 (100%)	96 (100%)	0	100	100
3	E	96/96 (100%)	96 (100%)	0	100	100
3	F	96/96 (100%)	96 (100%)	0	100	100
3	H	96/96 (100%)	96 (100%)	0	100	100
3	O	96/96 (100%)	96 (100%)	0	100	100
4	K	71/162 (44%)	71 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Q	71/162 (44%)	71 (100%)	0	100	100
4	x	71/162 (44%)	71 (100%)	0	100	100
5	L	124/196 (63%)	124 (100%)	0	100	100
5	R	124/196 (63%)	124 (100%)	0	100	100
5	T	124/196 (63%)	124 (100%)	0	100	100
5	U	124/196 (63%)	123 (99%)	1 (1%)	81	92
5	V	124/196 (63%)	124 (100%)	0	100	100
5	W	124/196 (63%)	124 (100%)	0	100	100
6	M	23/648 (4%)	23 (100%)	0	100	100
6	P	23/648 (4%)	23 (100%)	0	100	100
6	S	23/648 (4%)	23 (100%)	0	100	100
All	All	4374/7650 (57%)	4373 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	U	38	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	SF4	J	301	2	0,12,12	-	-	-		
7	SF4	G	301	2	0,12,12	-	-	-		
7	SF4	N	301	2	0,12,12	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	SF4	J	301	2	-	-	0/6/5/5
7	SF4	G	301	2	-	-	0/6/5/5
7	SF4	N	301	2	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	J	301	SF4	1	0
7	G	301	SF4	1	0
7	N	301	SF4	1	0

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.

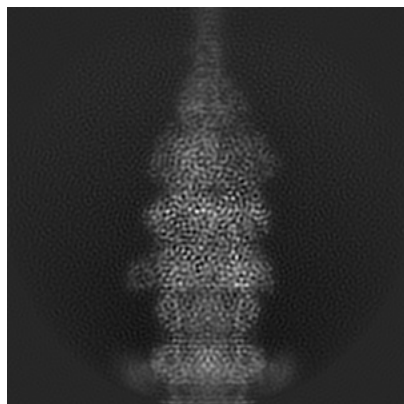
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36844. These allow visual inspection of the internal detail of the map and identification of artifacts.

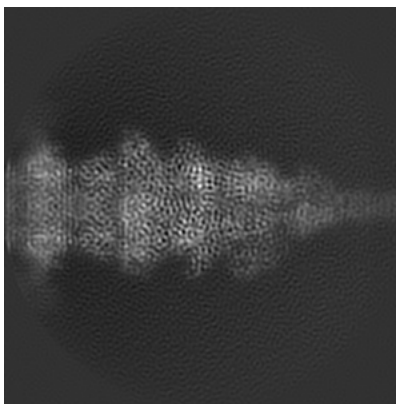
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

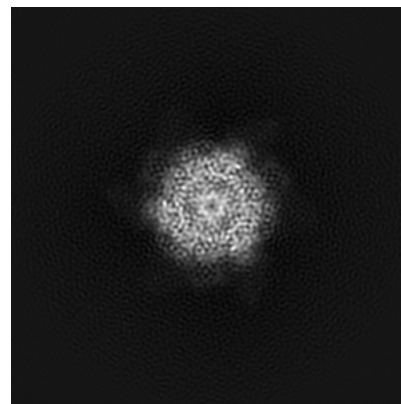
6.1.1 Primary map



X

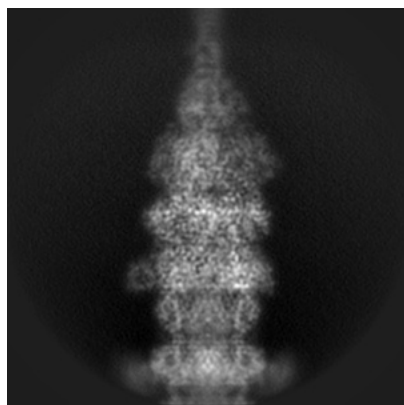


Y

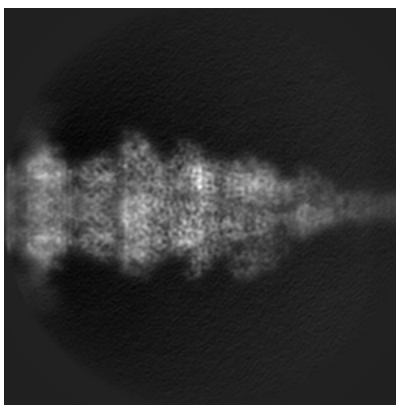


Z

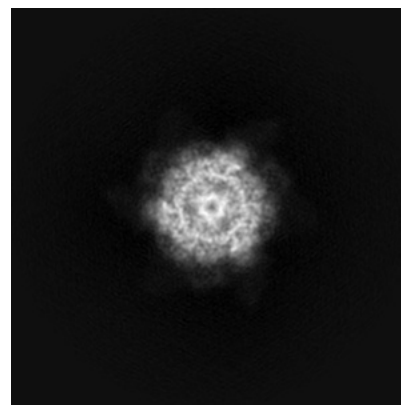
6.1.2 Raw map



X



Y

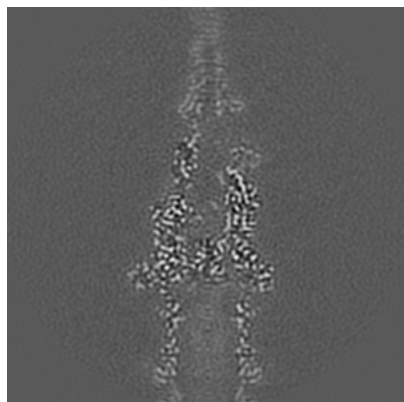


Z

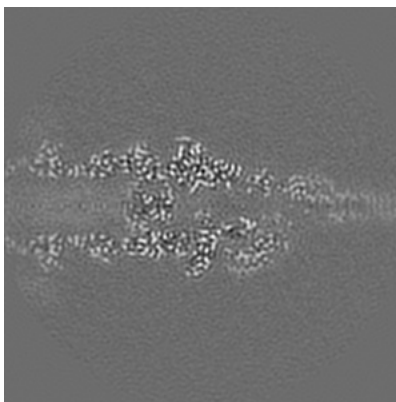
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

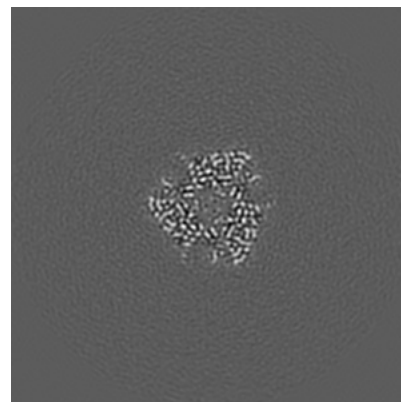
6.2.1 Primary map



X Index: 110

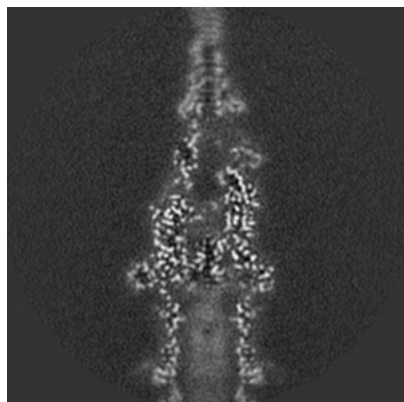


Y Index: 110

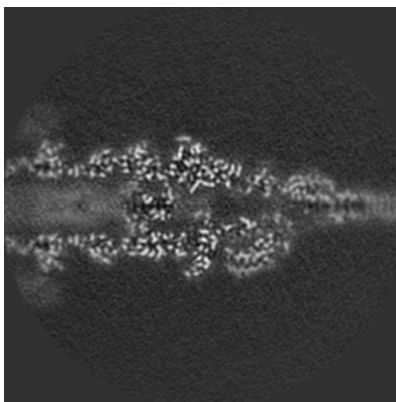


Z Index: 110

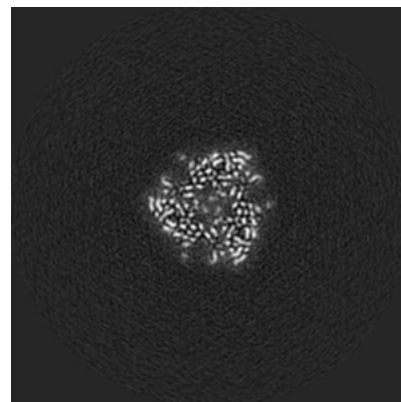
6.2.2 Raw map



X Index: 110



Y Index: 110

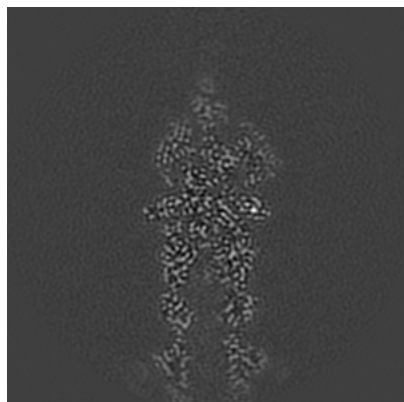


Z Index: 110

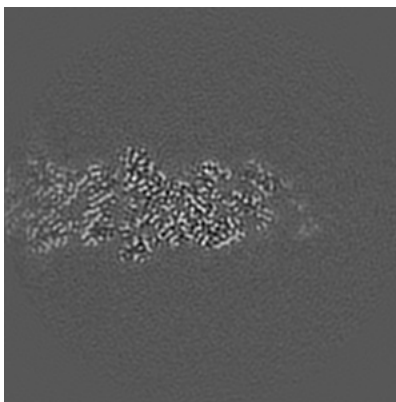
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

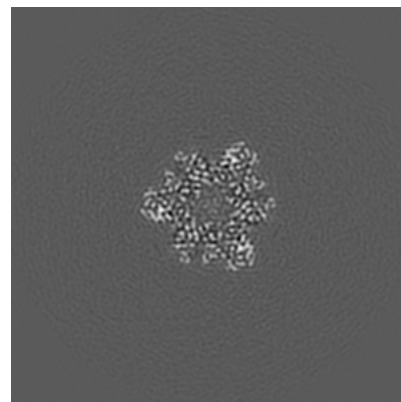
6.3.1 Primary map



X Index: 122

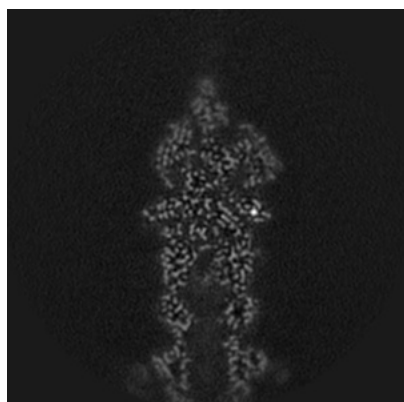


Y Index: 94

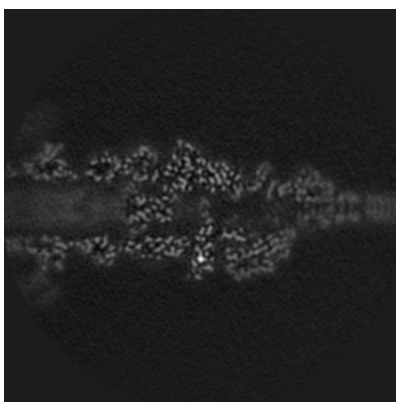


Z Index: 107

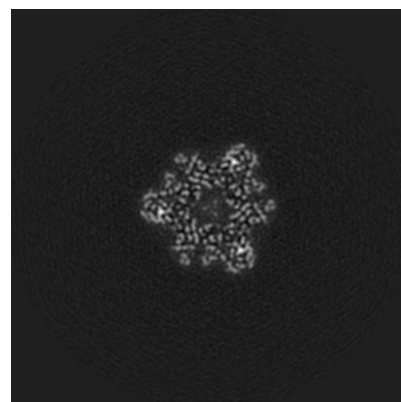
6.3.2 Raw map



X Index: 122



Y Index: 108

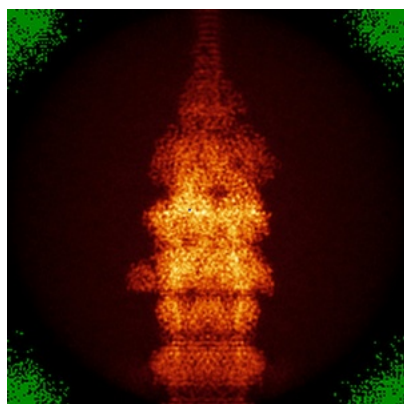


Z Index: 107

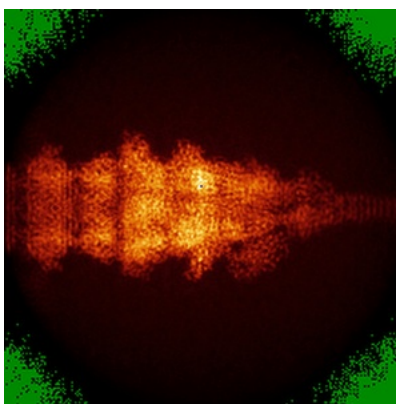
The images above show the largest variance slices of the map in three orthogonal directions.

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

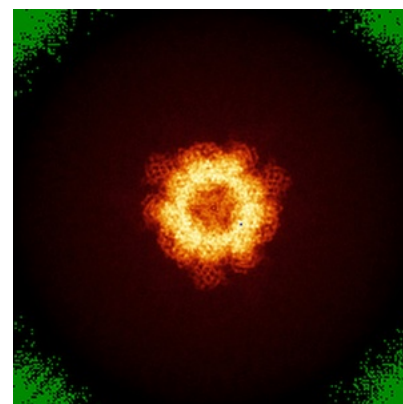
6.4.1 Primary map



X

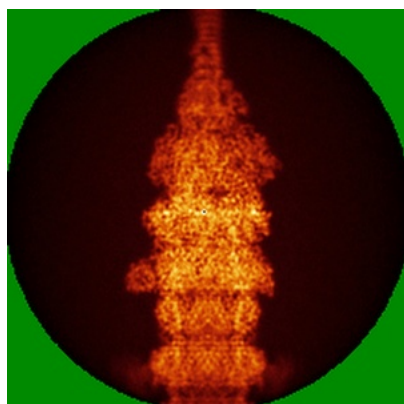


Y

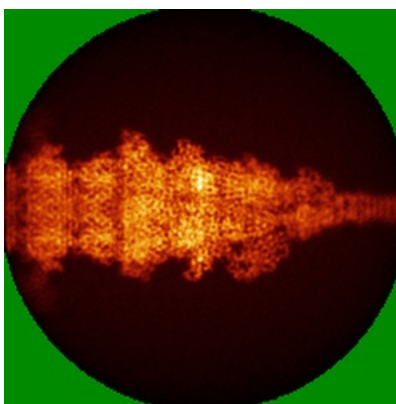


Z

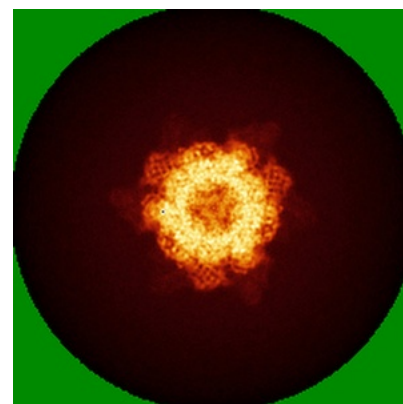
6.4.2 Raw map



X



Y

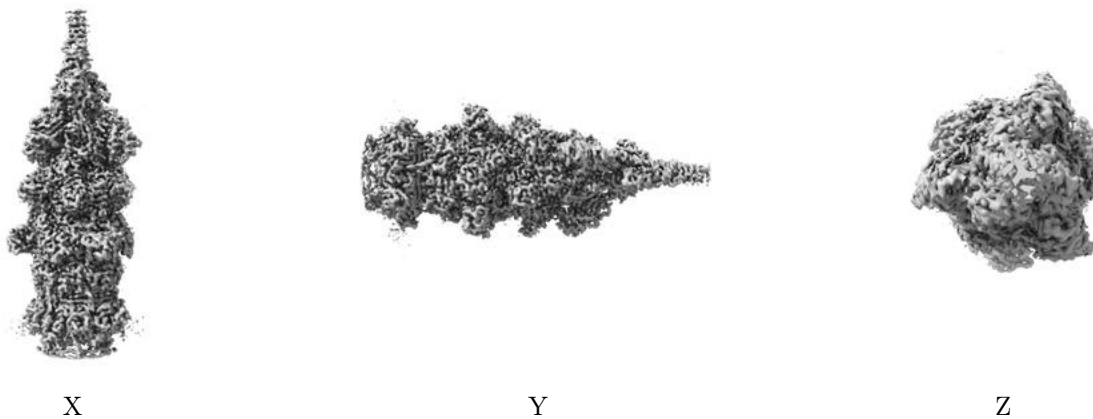


Z

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.

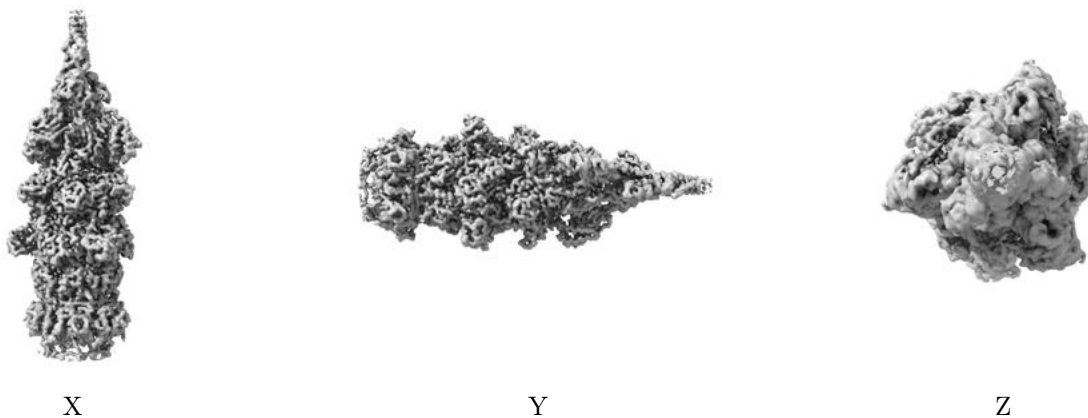
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

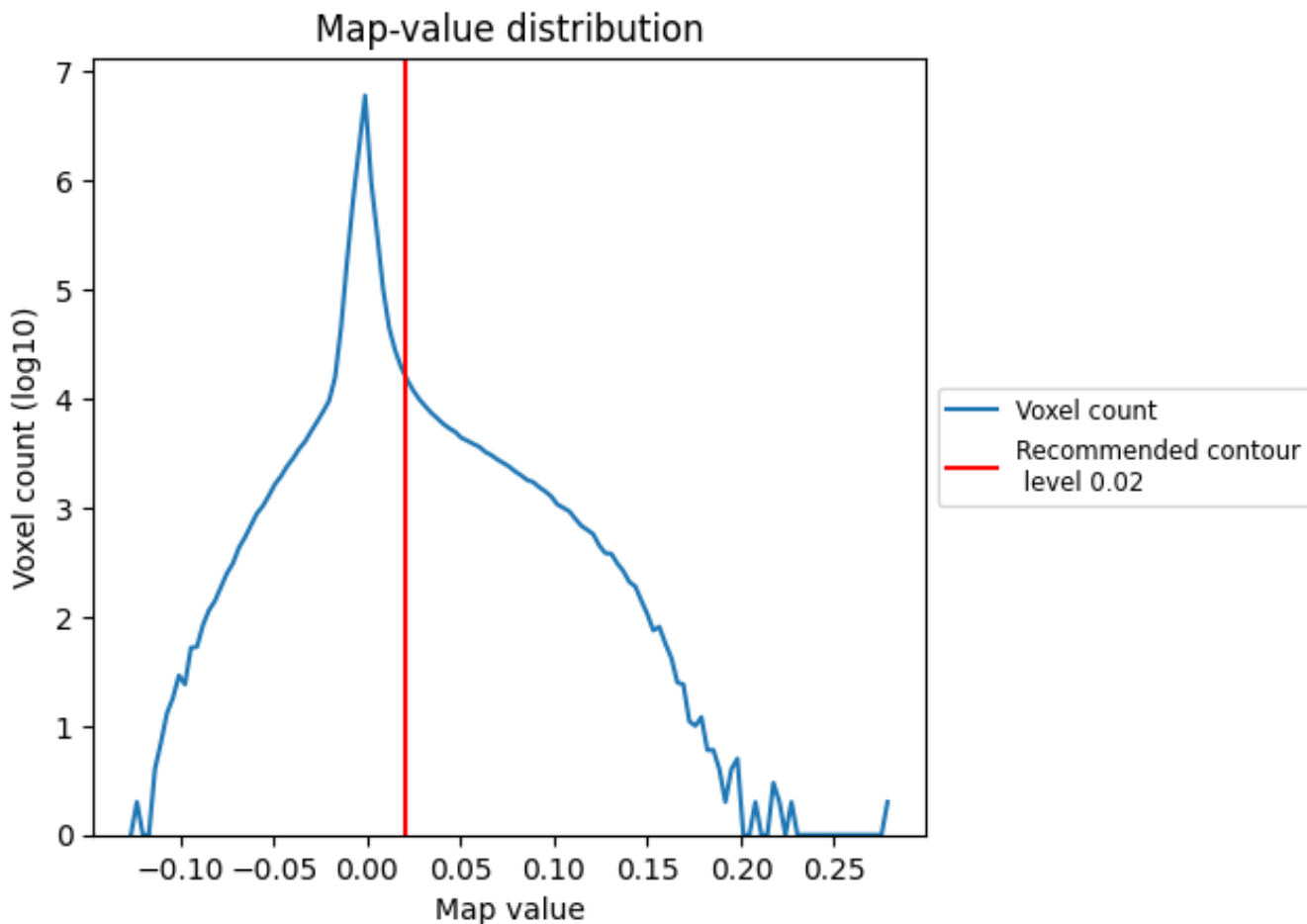
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

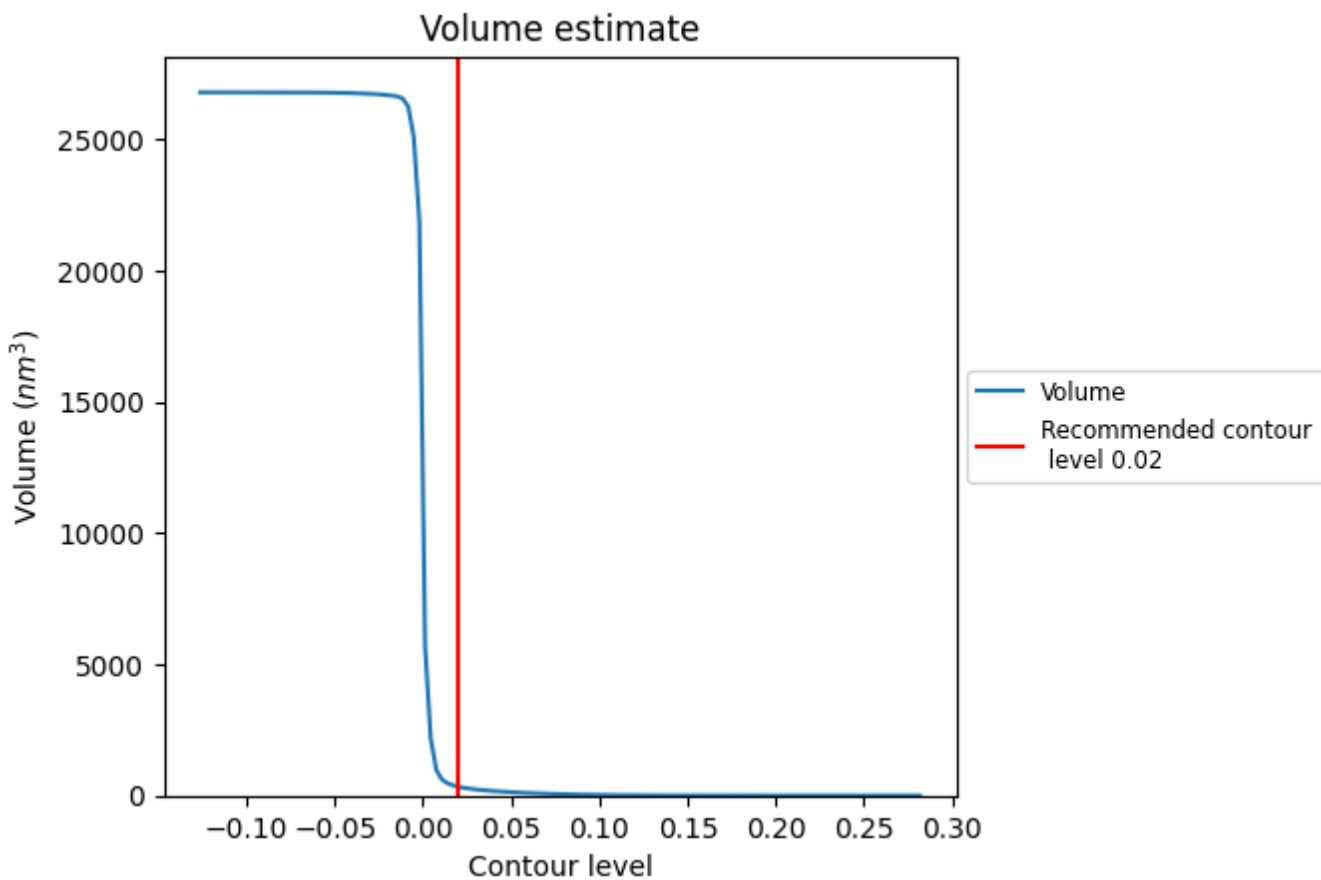
This section contains the results of statistical analysis of the map.

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.

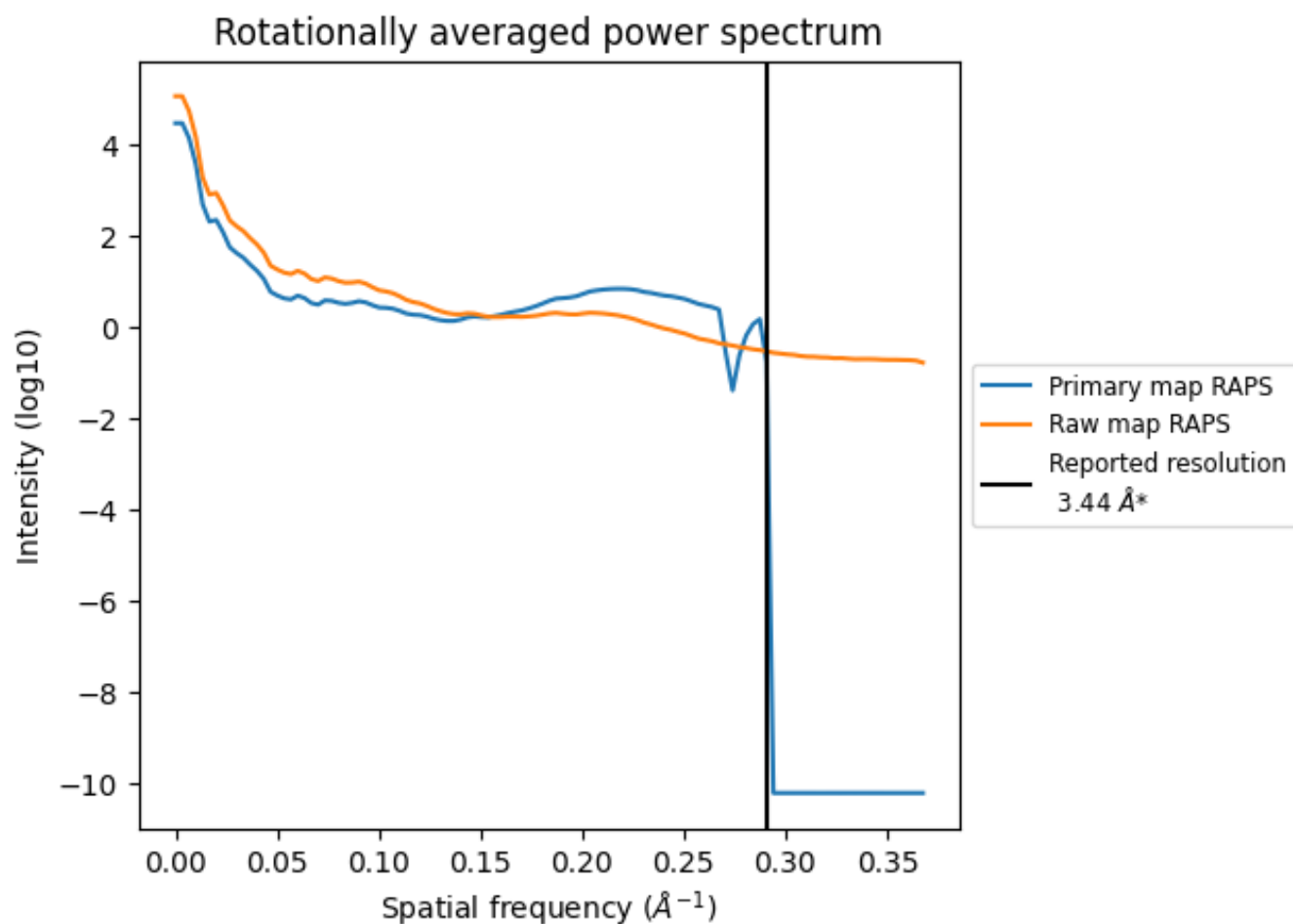
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 340 nm^3 ; this corresponds to an approximate mass of 307 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 [i](#)

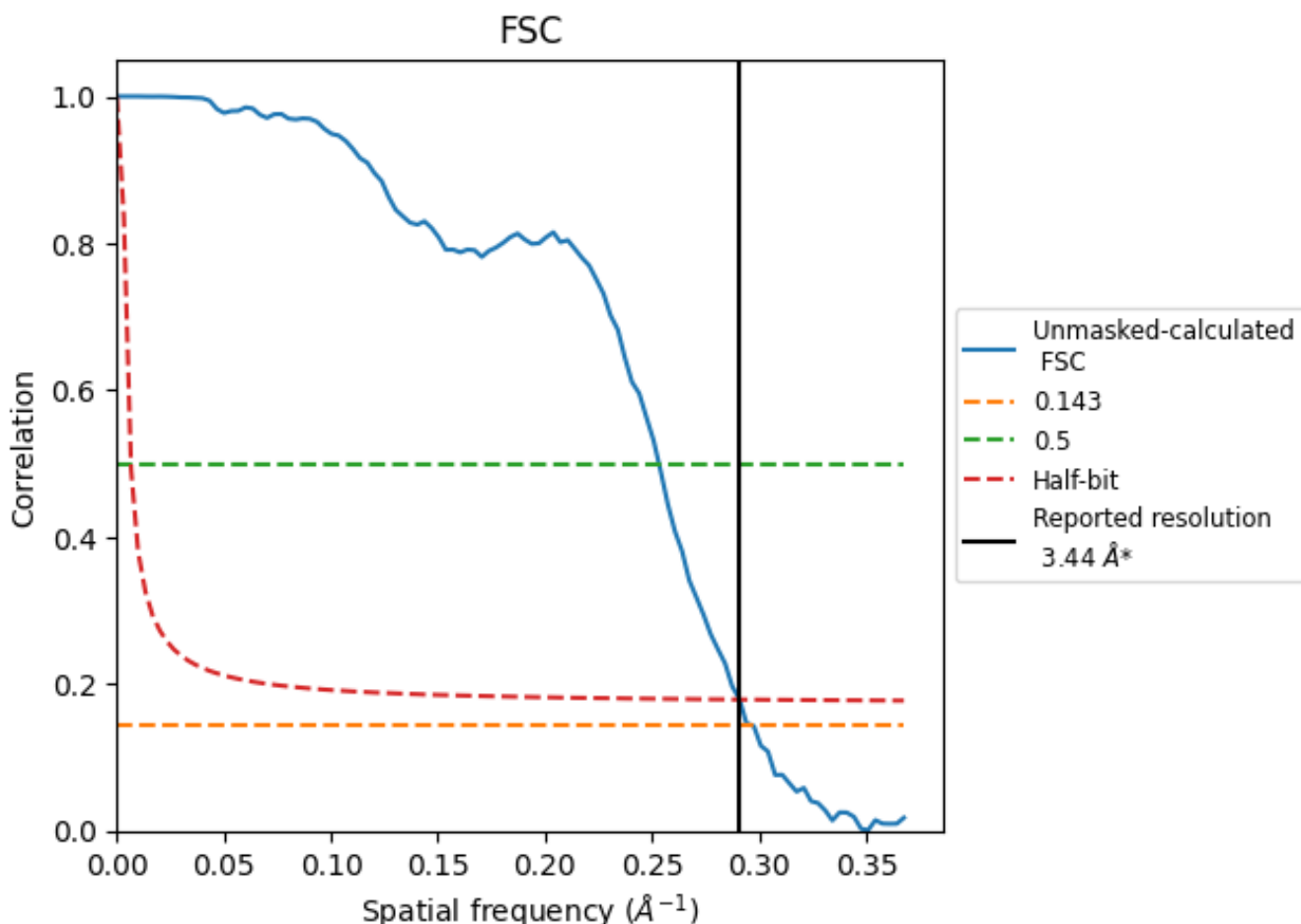


*Reported resolution corresponds to spatial frequency of 0.291 Å⁻¹

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 0.291 \AA^{-1}

8.2 Resolution estimates [i](#)

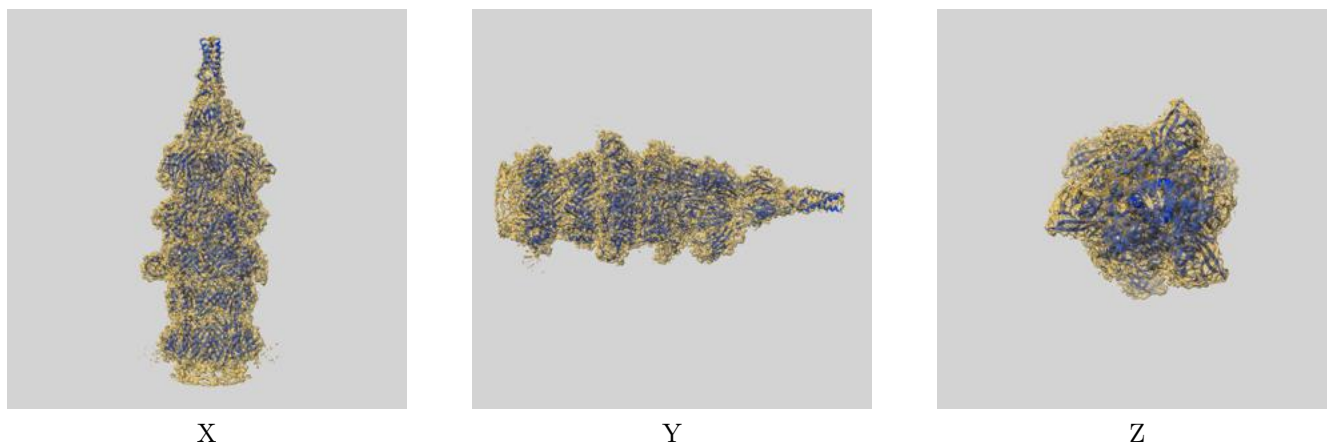
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.44	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.37	3.95	3.44

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

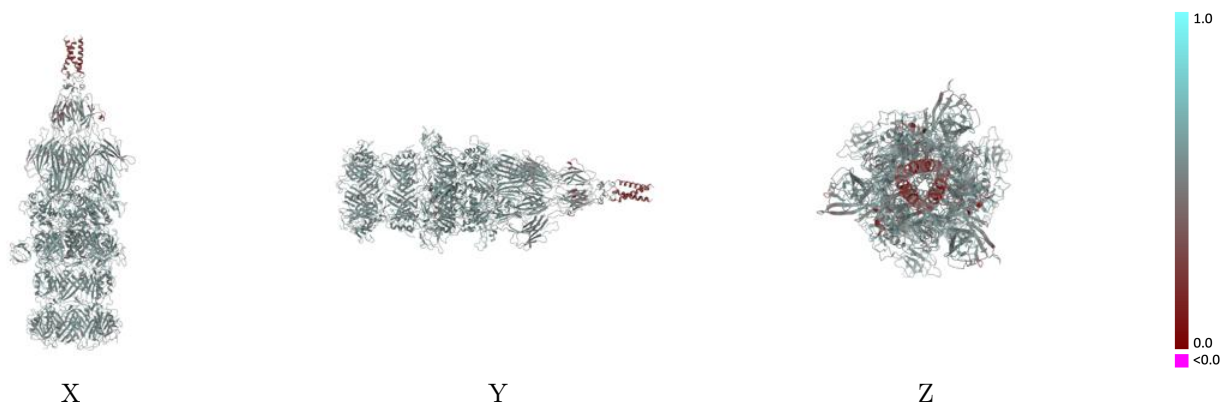
This section contains information regarding the fit between EMDB map EMD-36844 and PDB model 8K35. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



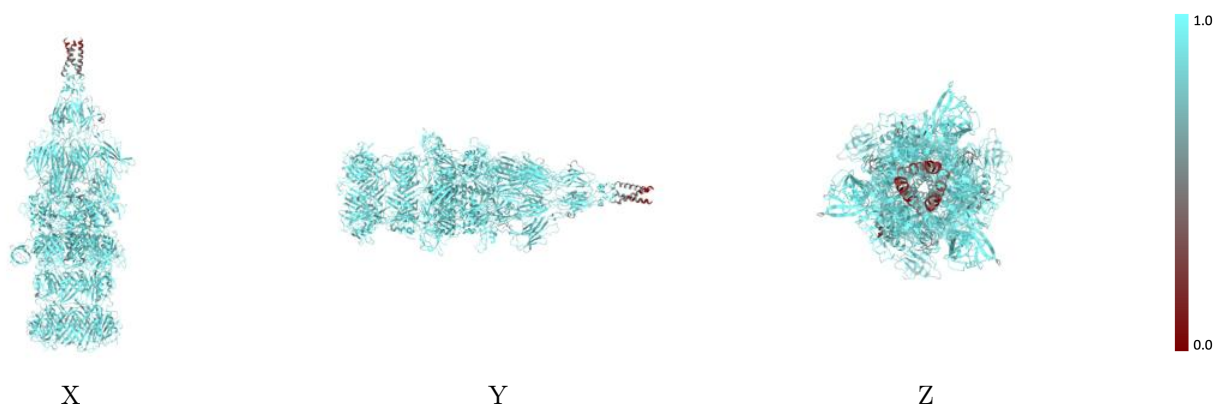
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



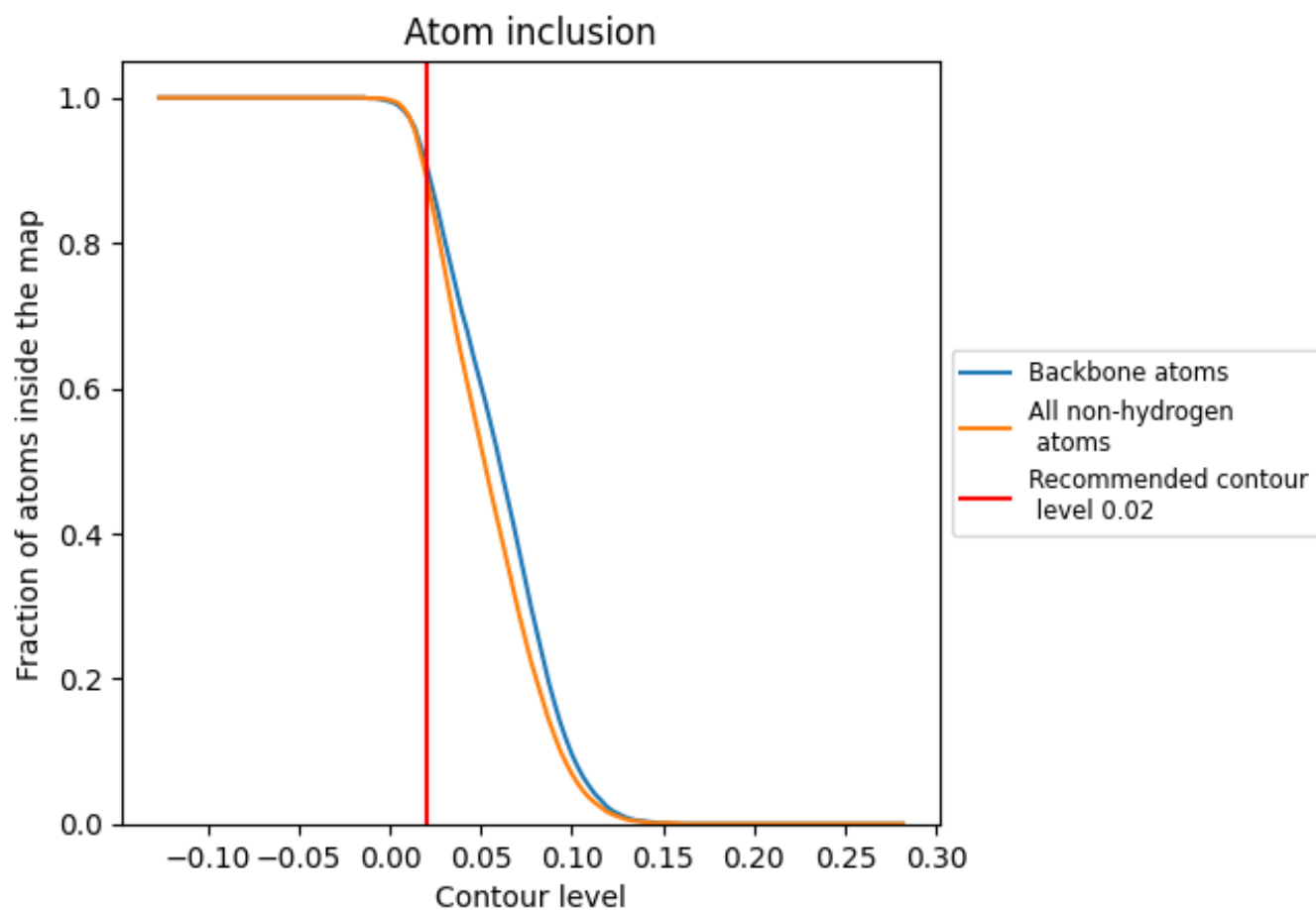
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 89% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8940	 0.5390
A	 0.8810	 0.5260
B	 0.8810	 0.5270
C	 0.9230	 0.5580
D	 0.9270	 0.5580
E	 0.9290	 0.5640
F	 0.9310	 0.5630
G	 0.9320	 0.5560
H	 0.9200	 0.5600
I	 0.8810	 0.5280
J	 0.9350	 0.5570
K	 0.9200	 0.5570
L	 0.8690	 0.5370
M	 0.8930	 0.5350
N	 0.9360	 0.5550
O	 0.9310	 0.5620
P	 0.9020	 0.5330
Q	 0.9060	 0.5530
R	 0.8700	 0.5410
S	 0.9060	 0.5350
T	 0.8690	 0.5370
U	 0.8700	 0.5410
V	 0.8700	 0.5380
W	 0.8630	 0.5410
x	 0.9190	 0.5550

