Full wwPDB EM Validation Report

Aug 13, 2025 – 06:15 PM EDT

PDB ID	:	9ML3 / pdb_00009ml3
EMDB ID	:	EMD-48346
Title	:	B25M05 Fab bound to HPV16 L1 pentamer
Authors	:	Hurlburt, N.K.; Singh, S.; Rodarte, J.V.; Pancera, M.
Deposited on	:	2024-12-18
Resolution	:	2.90 Å(reported)

This is a Full wwPDB EM Validation 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:

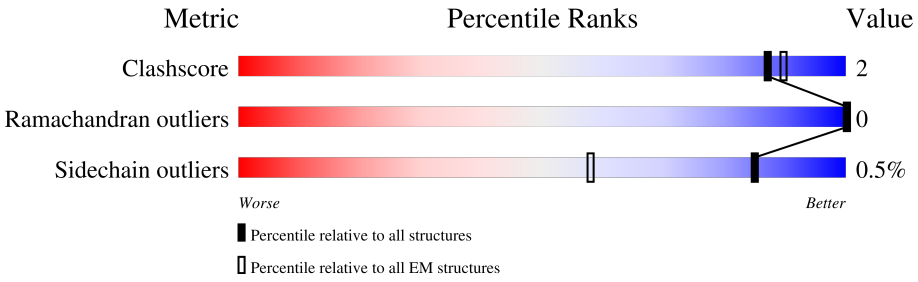
EMDB validation analysis	:	0.0.1.dev126
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.45.1

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 2.90 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 <=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	426	90% 5% 5%
1	B	426	92% 5% ·
1	C	426	93% · ·
1	D	426	93% · ·
1	E	426	94% · ·
2	H	238	5% 44% 8% 48%
3	L	216	6% 35% 14% · 49%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 35624 atoms, of which 17555 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 Major capsid protein L1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	406	Total	C	H	N	O	S	0	0
			6348	2054	3131	537	607	19		
1	B	412	Total	C	H	N	O	S	0	0
			6430	2080	3171	544	616	19		
1	C	414	Total	C	H	N	O	S	0	0
			6458	2088	3183	548	620	19		
1	D	413	Total	C	H	N	O	S	0	0
			6444	2084	3177	546	618	19		
1	E	413	Total	C	H	N	O	S	0	0
			6444	2084	3177	546	618	19		

There are 170 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	34	ALA	-	expression tag	UNP A0A451ER69
A	195	GLN	ASN	conflict	UNP A0A451ER69
A	447	GLY	PHE	conflict	UNP A0A451ER69
A	?	-	LEU	deletion	UNP A0A451ER69
A	?	-	GLN	deletion	UNP A0A451ER69
A	?	-	PRO	deletion	UNP A0A451ER69
A	?	-	PRO	deletion	UNP A0A451ER69
A	449	SER	PRO	conflict	UNP A0A451ER69
A	?	-	THR	deletion	UNP A0A451ER69
A	?	-	LEU	deletion	UNP A0A451ER69
A	?	-	GLU	deletion	UNP A0A451ER69
A	?	-	ASP	deletion	UNP A0A451ER69
A	?	-	THR	deletion	UNP A0A451ER69
A	?	-	TYR	deletion	UNP A0A451ER69
A	?	-	ARG	deletion	UNP A0A451ER69
A	?	-	PHE	deletion	UNP A0A451ER69
A	?	-	VAL	deletion	UNP A0A451ER69
A	?	-	THR	deletion	UNP A0A451ER69
A	?	-	SER	deletion	UNP A0A451ER69
A	?	-	GLN	deletion	UNP A0A451ER69

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ALA	deletion	UNP A0A451ER69
A	?	-	ILE	deletion	UNP A0A451ER69
A	?	-	ALA	deletion	UNP A0A451ER69
A	?	-	CYS	deletion	UNP A0A451ER69
A	?	-	GLN	deletion	UNP A0A451ER69
A	?	-	LYS	deletion	UNP A0A451ER69
A	?	-	HIS	deletion	UNP A0A451ER69
A	?	-	THR	deletion	UNP A0A451ER69
A	?	-	PRO	deletion	UNP A0A451ER69
A	?	-	PRO	deletion	UNP A0A451ER69
A	?	-	ALA	deletion	UNP A0A451ER69
A	?	-	PRO	deletion	UNP A0A451ER69
A	?	-	LYS	deletion	UNP A0A451ER69
A	486	LEU	ALA	conflict	UNP A0A451ER69
B	34	ALA	-	expression tag	UNP A0A451ER69
B	195	GLN	ASN	conflict	UNP A0A451ER69
B	447	GLY	PHE	conflict	UNP A0A451ER69
B	?	-	LEU	deletion	UNP A0A451ER69
B	?	-	GLN	deletion	UNP A0A451ER69
B	?	-	PRO	deletion	UNP A0A451ER69
B	?	-	PRO	deletion	UNP A0A451ER69
B	449	SER	PRO	conflict	UNP A0A451ER69
B	?	-	THR	deletion	UNP A0A451ER69
B	?	-	LEU	deletion	UNP A0A451ER69
B	?	-	GLU	deletion	UNP A0A451ER69
B	?	-	ASP	deletion	UNP A0A451ER69
B	?	-	THR	deletion	UNP A0A451ER69
B	?	-	TYR	deletion	UNP A0A451ER69
B	?	-	ARG	deletion	UNP A0A451ER69
B	?	-	PHE	deletion	UNP A0A451ER69
B	?	-	VAL	deletion	UNP A0A451ER69
B	?	-	THR	deletion	UNP A0A451ER69
B	?	-	SER	deletion	UNP A0A451ER69
B	?	-	GLN	deletion	UNP A0A451ER69
B	?	-	ALA	deletion	UNP A0A451ER69
B	?	-	ILE	deletion	UNP A0A451ER69
B	?	-	ALA	deletion	UNP A0A451ER69
B	?	-	CYS	deletion	UNP A0A451ER69
B	?	-	GLN	deletion	UNP A0A451ER69
B	?	-	LYS	deletion	UNP A0A451ER69
B	?	-	HIS	deletion	UNP A0A451ER69
B	?	-	THR	deletion	UNP A0A451ER69

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	PRO	deletion	UNP A0A451ER69
B	?	-	PRO	deletion	UNP A0A451ER69
B	?	-	ALA	deletion	UNP A0A451ER69
B	?	-	PRO	deletion	UNP A0A451ER69
B	?	-	LYS	deletion	UNP A0A451ER69
B	486	LEU	ALA	conflict	UNP A0A451ER69
C	34	ALA	-	expression tag	UNP A0A451ER69
C	195	GLN	ASN	conflict	UNP A0A451ER69
C	447	GLY	PHE	conflict	UNP A0A451ER69
C	?	-	LEU	deletion	UNP A0A451ER69
C	?	-	GLN	deletion	UNP A0A451ER69
C	?	-	PRO	deletion	UNP A0A451ER69
C	?	-	PRO	deletion	UNP A0A451ER69
C	449	SER	PRO	conflict	UNP A0A451ER69
C	?	-	THR	deletion	UNP A0A451ER69
C	?	-	LEU	deletion	UNP A0A451ER69
C	?	-	GLU	deletion	UNP A0A451ER69
C	?	-	ASP	deletion	UNP A0A451ER69
C	?	-	THR	deletion	UNP A0A451ER69
C	?	-	TYR	deletion	UNP A0A451ER69
C	?	-	ARG	deletion	UNP A0A451ER69
C	?	-	PHE	deletion	UNP A0A451ER69
C	?	-	VAL	deletion	UNP A0A451ER69
C	?	-	THR	deletion	UNP A0A451ER69
C	?	-	SER	deletion	UNP A0A451ER69
C	?	-	GLN	deletion	UNP A0A451ER69
C	?	-	ALA	deletion	UNP A0A451ER69
C	?	-	ILE	deletion	UNP A0A451ER69
C	?	-	ALA	deletion	UNP A0A451ER69
C	?	-	CYS	deletion	UNP A0A451ER69
C	?	-	GLN	deletion	UNP A0A451ER69
C	?	-	LYS	deletion	UNP A0A451ER69
C	?	-	HIS	deletion	UNP A0A451ER69
C	?	-	THR	deletion	UNP A0A451ER69
C	?	-	PRO	deletion	UNP A0A451ER69
C	?	-	PRO	deletion	UNP A0A451ER69
C	?	-	ALA	deletion	UNP A0A451ER69
C	?	-	PRO	deletion	UNP A0A451ER69
C	?	-	LYS	deletion	UNP A0A451ER69
C	486	LEU	ALA	conflict	UNP A0A451ER69
D	34	ALA	-	expression tag	UNP A0A451ER69
D	195	GLN	ASN	conflict	UNP A0A451ER69

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Chain	Residue	Modelled	Actual	Comment	Reference
D	447	GLY	PHE	conflict	UNP A0A451ER69
D	?	-	LEU	deletion	UNP A0A451ER69
D	?	-	GLN	deletion	UNP A0A451ER69
D	?	-	PRO	deletion	UNP A0A451ER69
D	?	-	PRO	deletion	UNP A0A451ER69
D	449	SER	PRO	conflict	UNP A0A451ER69
D	?	-	THR	deletion	UNP A0A451ER69
D	?	-	LEU	deletion	UNP A0A451ER69
D	?	-	GLU	deletion	UNP A0A451ER69
D	?	-	ASP	deletion	UNP A0A451ER69
D	?	-	THR	deletion	UNP A0A451ER69
D	?	-	TYR	deletion	UNP A0A451ER69
D	?	-	ARG	deletion	UNP A0A451ER69
D	?	-	PHE	deletion	UNP A0A451ER69
D	?	-	VAL	deletion	UNP A0A451ER69
D	?	-	THR	deletion	UNP A0A451ER69
D	?	-	SER	deletion	UNP A0A451ER69
D	?	-	GLN	deletion	UNP A0A451ER69
D	?	-	ALA	deletion	UNP A0A451ER69
D	?	-	ILE	deletion	UNP A0A451ER69
D	?	-	ALA	deletion	UNP A0A451ER69
D	?	-	CYS	deletion	UNP A0A451ER69
D	?	-	GLN	deletion	UNP A0A451ER69
D	?	-	LYS	deletion	UNP A0A451ER69
D	?	-	HIS	deletion	UNP A0A451ER69
D	?	-	THR	deletion	UNP A0A451ER69
D	?	-	PRO	deletion	UNP A0A451ER69
D	?	-	PRO	deletion	UNP A0A451ER69
D	?	-	ALA	deletion	UNP A0A451ER69
D	?	-	PRO	deletion	UNP A0A451ER69
D	?	-	LYS	deletion	UNP A0A451ER69
D	486	LEU	ALA	conflict	UNP A0A451ER69
E	34	ALA	-	expression tag	UNP A0A451ER69
E	195	GLN	ASN	conflict	UNP A0A451ER69
E	447	GLY	PHE	conflict	UNP A0A451ER69
E	?	-	LEU	deletion	UNP A0A451ER69
E	?	-	GLN	deletion	UNP A0A451ER69
E	?	-	PRO	deletion	UNP A0A451ER69
E	?	-	PRO	deletion	UNP A0A451ER69
E	449	SER	PRO	conflict	UNP A0A451ER69
E	?	-	THR	deletion	UNP A0A451ER69
E	?	-	LEU	deletion	UNP A0A451ER69

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Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	GLU	deletion	UNP A0A451ER69
E	?	-	ASP	deletion	UNP A0A451ER69
E	?	-	THR	deletion	UNP A0A451ER69
E	?	-	TYR	deletion	UNP A0A451ER69
E	?	-	ARG	deletion	UNP A0A451ER69
E	?	-	PHE	deletion	UNP A0A451ER69
E	?	-	VAL	deletion	UNP A0A451ER69
E	?	-	THR	deletion	UNP A0A451ER69
E	?	-	SER	deletion	UNP A0A451ER69
E	?	-	GLN	deletion	UNP A0A451ER69
E	?	-	ALA	deletion	UNP A0A451ER69
E	?	-	ILE	deletion	UNP A0A451ER69
E	?	-	ALA	deletion	UNP A0A451ER69
E	?	-	CYS	deletion	UNP A0A451ER69
E	?	-	GLN	deletion	UNP A0A451ER69
E	?	-	LYS	deletion	UNP A0A451ER69
E	?	-	HIS	deletion	UNP A0A451ER69
E	?	-	THR	deletion	UNP A0A451ER69
E	?	-	PRO	deletion	UNP A0A451ER69
E	?	-	PRO	deletion	UNP A0A451ER69
E	?	-	ALA	deletion	UNP A0A451ER69
E	?	-	PRO	deletion	UNP A0A451ER69
E	?	-	LYS	deletion	UNP A0A451ER69
E	486	LEU	ALA	conflict	UNP A0A451ER69

- Molecule 2 is a protein called B25M05 Fab Heavy Chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	H	124	Total	C	H	N	O	S	0	0
			1925	617	951	170	183	4		

- Molecule 3 is a protein called B25M05 Fab Light Chain.

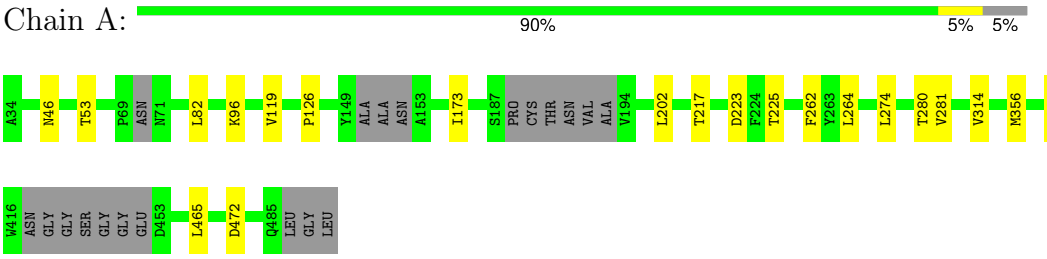
Mol	Chain	Residues	Atoms						AltConf	Trace
3	L	110	Total	C	H	N	O	S	0	0
			1575	502	765	132	174	2		

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.

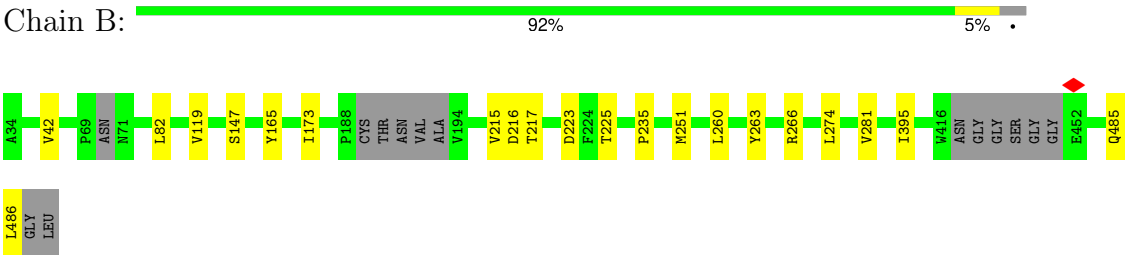
• Molecule 1: Major capsid protein L1

Chain A:



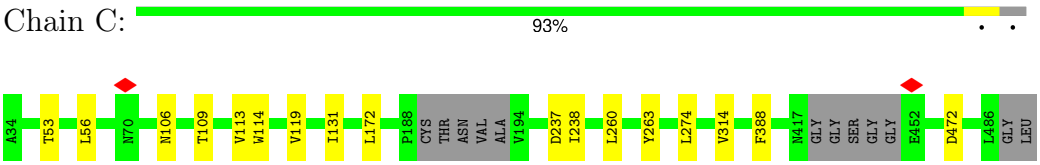
• Molecule 1: Major capsid protein L1

Chain B:



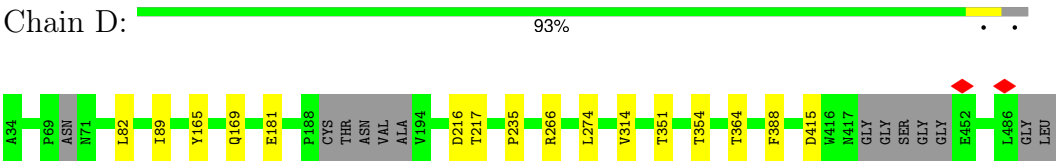
• Molecule 1: Major capsid protein L1

Chain C:



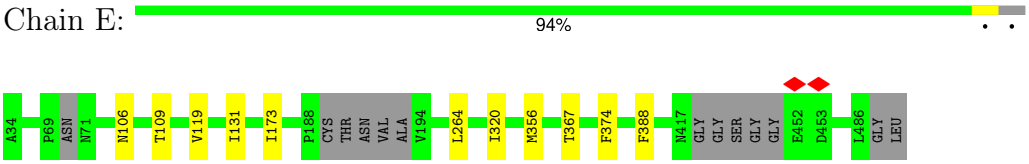
• Molecule 1: Major capsid protein L1

Chain D:



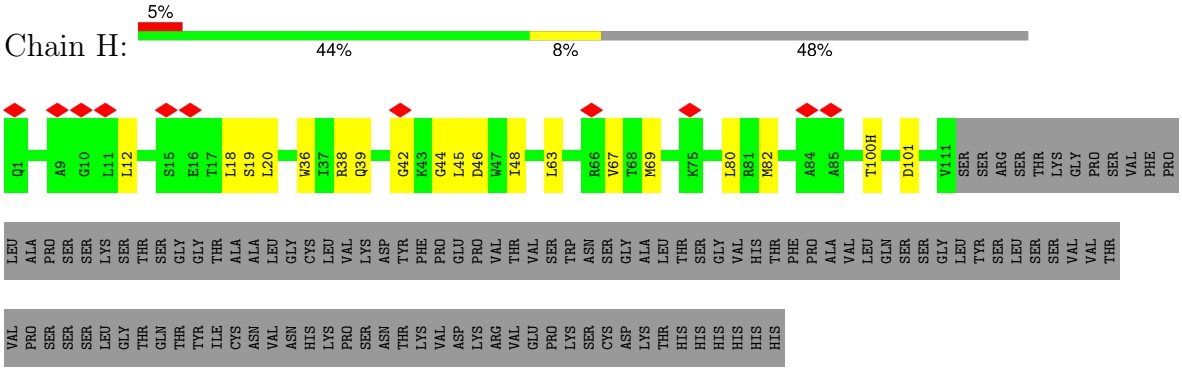
• Molecule 1: Major capsid protein L1

Chain E:



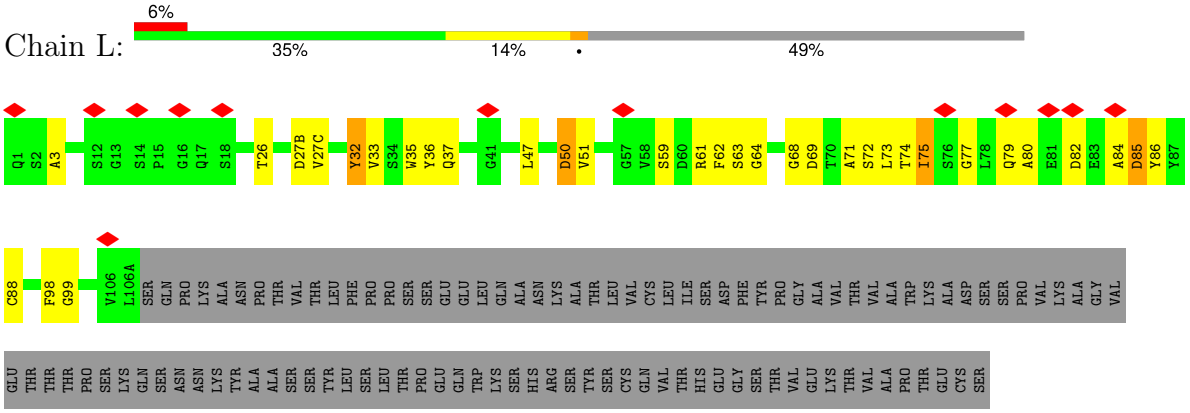
• Molecule 2: B25M05 Fab Heavy Chain

Chain H:



• Molecule 3: B25M05 Fab Light Chain

Chain L:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83711	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	36000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	7.435	Depositor
Minimum map value	-3.718	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.290	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	251.328, 251.328, 251.328	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.122, 1.122, 1.122	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	A	0.20	0/3298	0.36	0/4478
1	B	0.20	0/3342	0.35	0/4541
1	C	0.20	0/3359	0.36	0/4566
1	D	0.20	0/3350	0.36	0/4552
1	E	0.20	0/3350	0.35	0/4552
2	H	0.64	3/999 (0.3%)	0.75	9/1359 (0.7%)
3	L	1.91	11/827 (1.3%)	2.05	38/1125 (3.4%)
All	All	0.47	14/18525 (0.1%)	0.58	47/25173 (0.2%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	61	ARG	CZ-NH2	-8.26	1.22	1.33
3	L	80	ALA	CA-CB	-7.04	1.42	1.53
3	L	61	ARG	CZ-NH1	-6.77	1.23	1.32
3	L	71	ALA	CA-CB	-6.47	1.42	1.53
3	L	3	ALA	CA-CB	-6.44	1.42	1.53
3	L	84	ALA	CA-CB	-6.37	1.42	1.53
3	L	64	GLY	N-CA	-6.30	1.38	1.45
3	L	99	GLY	N-CA	-5.75	1.37	1.45
3	L	68	GLY	N-CA	-5.56	1.38	1.45
2	H	39	GLN	CA-CB	-5.41	1.47	1.53
3	L	61	ARG	CD-NE	-5.39	1.38	1.46
3	L	77	GLY	N-CA	-5.31	1.37	1.45
2	H	44	GLY	N-CA	-5.19	1.37	1.45
2	H	42	GLY	N-CA	-5.16	1.37	1.45

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	L	63	SER	CA-C-N	10.23	129.24	122.18
3	L	63	SER	C-N-CA	10.23	129.24	122.18
3	L	98	PHE	CA-CB-CG	7.05	120.85	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	L	62	PHE	CA-CB-CG	6.76	120.56	113.80
2	H	38	ARG	CA-C-N	6.29	130.75	123.15
2	H	38	ARG	C-N-CA	6.29	130.75	123.15
3	L	74	THR	CA-C-N	6.27	131.27	123.12
3	L	74	THR	C-N-CA	6.27	131.27	123.12
3	L	82	ASP	CA-CB-CG	6.24	118.84	112.60
2	H	46	ASP	CA-CB-CG	6.16	118.76	112.60
3	L	85	ASP	CA-CB-CG	6.12	118.72	112.60
3	L	75	ILE	CA-C-N	6.00	130.76	122.77
3	L	75	ILE	C-N-CA	6.00	130.76	122.77
3	L	69	ASP	CA-CB-CG	5.95	118.55	112.60
3	L	72	SER	CA-C-N	5.92	131.47	122.95
3	L	72	SER	C-N-CA	5.92	131.47	122.95
3	L	73	LEU	CA-C-N	5.85	130.44	122.19
3	L	73	LEU	C-N-CA	5.85	130.44	122.19
2	H	45	LEU	CA-C-N	5.70	131.03	123.05
2	H	45	LEU	C-N-CA	5.70	131.03	123.05
3	L	35	TRP	CA-C-N	5.52	131.24	122.62
3	L	35	TRP	C-N-CA	5.52	131.24	122.62
2	H	44	GLY	CA-C-N	5.51	130.60	123.00
2	H	44	GLY	C-N-CA	5.51	130.60	123.00
3	L	86	TYR	CA-C-N	5.47	130.72	123.00
3	L	86	TYR	C-N-CA	5.47	130.72	123.00
3	L	3	ALA	CA-C-N	5.45	128.60	120.87
3	L	3	ALA	C-N-CA	5.45	128.60	120.87
3	L	69	ASP	CA-C-N	5.44	130.66	123.05
3	L	69	ASP	C-N-CA	5.44	130.66	123.05
3	L	61	ARG	CA-C-N	5.41	129.81	122.19
3	L	61	ARG	C-N-CA	5.41	129.81	122.19
3	L	59	SER	N-CA-CB	5.38	117.82	109.48
3	L	85	ASP	CA-C-N	5.38	130.35	122.39
3	L	85	ASP	C-N-CA	5.38	130.35	122.39
3	L	79	GLN	CA-C-N	5.36	127.41	120.44
3	L	79	GLN	C-N-CA	5.36	127.41	120.44
3	L	33	VAL	CA-C-N	5.15	130.56	122.21
3	L	33	VAL	C-N-CA	5.15	130.56	122.21
3	L	32	TYR	CA-C-N	5.15	129.43	121.71
3	L	32	TYR	C-N-CA	5.15	129.43	121.71
2	H	42	GLY	CA-C-N	5.10	130.74	122.53
2	H	42	GLY	C-N-CA	5.10	130.74	122.53
3	L	37	GLN	CA-C-N	5.05	130.61	123.14
3	L	37	GLN	C-N-CA	5.05	130.61	123.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	L	36	TYR	CA-C-N	5.02	130.40	123.07
3	L	36	TYR	C-N-CA	5.02	130.40	123.07

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	3217	3131	3124	16	0
1	B	3259	3171	3165	14	0
1	C	3275	3183	3178	11	0
1	D	3267	3177	3171	11	0
1	E	3267	3177	3171	8	0
2	H	974	951	956	10	0
3	L	810	765	769	4	0
All	All	18069	17555	17534	68	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 2.

All (68) 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)
3:L:50:ASP:O	3:L:51:VAL:HG12	1.82	0.80
1:A:53:THR:HG22	1:A:465:LEU:HD21	1.71	0.72
2:H:100(H):THR:HG21	3:L:32:TYR:HB3	1.82	0.61
2:H:12:LEU:HD11	2:H:18:LEU:HD13	1.84	0.59
1:A:119:VAL:HG11	1:A:173:ILE:CD1	2.32	0.59
1:A:46:ASN:O	1:A:46:ASN:OD1	2.23	0.57
1:A:82:LEU:HD23	1:A:217:THR:HG22	1.86	0.57
2:H:63:LEU:O	2:H:67:VAL:HG23	2.05	0.56
1:B:266:ARG:HB3	1:B:266:ARG:NH2	2.22	0.55
1:E:264:LEU:HD23	1:E:320:ILE:HD12	1.90	0.54
1:C:237:ASP:OD1	1:C:238:ILE:HG23	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:82:LEU:HD23	1:D:217:THR:HG22	1.91	0.52
1:D:415:ASP:OD1	1:D:415:ASP:C	2.53	0.52
1:C:172:LEU:HD23	1:C:263:TYR:HB2	1.91	0.52
1:B:42:VAL:HG22	1:B:395:ILE:HG12	1.93	0.51
1:A:398:THR:HG23	1:A:400:ASP:OD1	2.11	0.50
1:E:106:ASN:O	1:E:106:ASN:OD1	2.29	0.50
1:E:119:VAL:HG11	1:E:173:ILE:CD1	2.42	0.50
1:A:202:LEU:HD21	1:E:356:MET:HE1	1.93	0.49
1:A:274:LEU:HD22	1:E:131:ILE:HD12	1.94	0.49
1:D:169:GLN:NE2	1:D:351:THR:HG21	2.27	0.49
1:C:113:VAL:HG12	1:C:114:TRP:N	2.29	0.48
2:H:67:VAL:HG22	2:H:82:MET:HG3	1.96	0.48
1:C:472:ASP:O	1:C:472:ASP:OD1	2.32	0.47
1:E:109:THR:HG22	1:E:109:THR:O	2.15	0.47
1:D:364:THR:O	1:D:364:THR:HG22	2.13	0.47
1:C:106:ASN:HD22	1:C:109:THR:HG22	1.79	0.47
1:A:472:ASP:OD1	1:A:472:ASP:O	2.34	0.46
1:B:266:ARG:HB3	1:B:266:ARG:CZ	2.46	0.46
2:H:18:LEU:HD11	2:H:20:LEU:HD21	1.97	0.45
1:C:172:LEU:HD22	1:C:260:LEU:HD11	1.96	0.45
3:L:27(B):ASP:OD1	3:L:27(C):VAL:N	2.50	0.45
1:C:274:LEU:HD12	1:C:274:LEU:N	2.32	0.44
1:B:82:LEU:HD23	1:B:217:THR:HG22	2.00	0.44
1:B:281:VAL:O	1:B:281:VAL:HG13	2.16	0.44
1:C:131:ILE:HD12	1:D:274:LEU:CD2	2.48	0.44
1:D:266:ARG:HB3	1:D:266:ARG:NH2	2.32	0.43
1:A:356:MET:HE2	1:A:356:MET:HB3	1.96	0.43
1:A:280:THR:HG22	1:E:374:PHE:O	2.18	0.43
1:B:485:GLN:O	1:B:486:LEU:HB2	2.19	0.43
1:D:169:GLN:HE21	1:D:351:THR:HG21	1.82	0.43
1:D:89:ILE:HD13	1:D:388:PHE:CZ	2.53	0.43
1:B:215:VAL:HG22	1:B:216:ASP:N	2.33	0.43
1:B:251:MET:HE3	1:B:260:LEU:HD13	2.00	0.43
1:D:314:VAL:O	1:D:314:VAL:HG23	2.19	0.43
1:B:119:VAL:HG11	1:B:173:ILE:CD1	2.49	0.43
1:C:53:THR:HG21	1:C:56:LEU:HD11	2.00	0.43
1:B:274:LEU:HD12	1:B:274:LEU:N	2.34	0.43
1:D:354:THR:HG23	1:D:354:THR:O	2.19	0.42
2:H:19:SER:C	2:H:20:LEU:HD22	2.44	0.42
3:L:50:ASP:O	3:L:51:VAL:CG1	2.61	0.42
1:A:281:VAL:O	1:A:281:VAL:HG13	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:VAL:O	1:A:314:VAL:HG23	2.19	0.42
1:A:262:PHE:HZ	1:A:264:LEU:HD11	1.85	0.42
1:B:165:TYR:OH	1:B:235:PRO:HB2	2.20	0.41
1:A:223:ASP:OD1	1:A:225:THR:HG22	2.21	0.41
1:B:223:ASP:OD1	1:B:225:THR:HG22	2.21	0.41
1:B:260:LEU:HD11	1:B:263:TYR:HB3	2.01	0.41
1:C:119:VAL:HG23	1:C:388:PHE:CE1	2.55	0.41
2:H:48:ILE:HD13	2:H:48:ILE:HA	1.94	0.41
2:H:36:TRP:CD1	2:H:69:MET:HE1	2.56	0.41
2:H:48:ILE:HG21	2:H:80:LEU:HD11	2.02	0.41
2:H:101:ASP:OD1	2:H:101:ASP:C	2.63	0.41
1:A:126:PRO:HB2	1:B:216:ASP:OD2	2.21	0.41
1:E:119:VAL:HG23	1:E:388:PHE:CE1	2.56	0.41
1:D:165:TYR:OH	1:D:235:PRO:HB2	2.21	0.40
1:C:314:VAL:O	1:C:314:VAL:HG23	2.20	0.40
1:A:119:VAL:HG11	1:A:173:ILE:HD13	2.01	0.40

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	396/426 (93%)	384 (97%)	12 (3%)	0	100	100
1	B	404/426 (95%)	394 (98%)	10 (2%)	0	100	100
1	C	408/426 (96%)	393 (96%)	15 (4%)	0	100	100
1	D	405/426 (95%)	396 (98%)	9 (2%)	0	100	100
1	E	405/426 (95%)	390 (96%)	15 (4%)	0	100	100
2	H	122/238 (51%)	116 (95%)	6 (5%)	0	100	100
3	L	108/216 (50%)	97 (90%)	11 (10%)	0	100	100
All	All	2248/2584 (87%)	2170 (96%)	78 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	357/369 (97%)	356 (100%)	1 (0%)	91 97
1	B	361/369 (98%)	360 (100%)	1 (0%)	91 97
1	C	363/369 (98%)	363 (100%)	0	100 100
1	D	362/369 (98%)	360 (99%)	2 (1%)	84 95
1	E	362/369 (98%)	361 (100%)	1 (0%)	91 97
2	H	106/207 (51%)	106 (100%)	0	100 100
3	L	92/185 (50%)	86 (94%)	6 (6%)	14 40
All	All	2003/2237 (90%)	1992 (100%)	11 (0%)	85 96

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	96	LYS
1	B	147	SER
1	D	181	GLU
1	D	216	ASP
1	E	367	THR
3	L	26	THR
3	L	47	LEU
3	L	50	ASP
3	L	75	ILE
3	L	85	ASP
3	L	88	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	ASN
1	A	106	ASN

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Mol	Chain	Res	Type
1	A	167	GLN
1	A	169	GLN
1	A	195	GLN
1	A	210	GLN
1	A	380	HIS
1	B	106	ASN
1	B	110	GLN
1	B	210	GLN
1	B	341	ASN
1	C	83	GLN
1	C	106	ASN
1	C	169	GLN
1	C	273	HIS
1	C	341	ASN
1	D	71	ASN
1	D	106	ASN
1	D	169	GLN
1	D	322	ASN
1	D	341	ASN
1	D	373	ASN
1	D	387	GLN
1	E	206	ASN
1	E	341	ASN
1	E	373	ASN
3	L	37	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

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 (i)

There are no chain breaks in this entry.

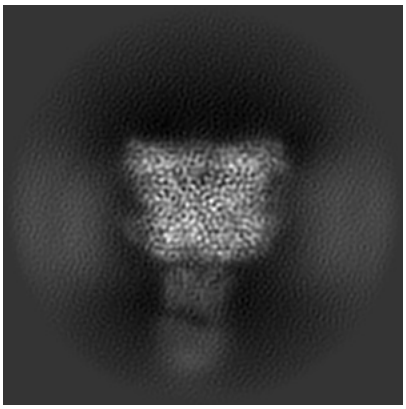
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-48346. These allow visual inspection of the internal detail of the map and identification of artifacts.

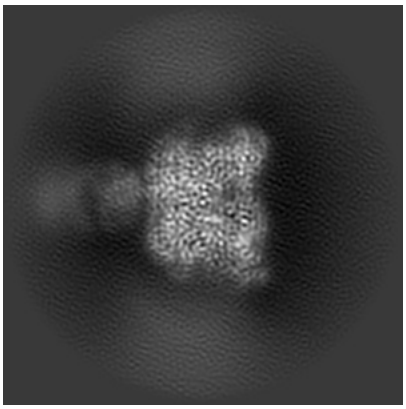
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

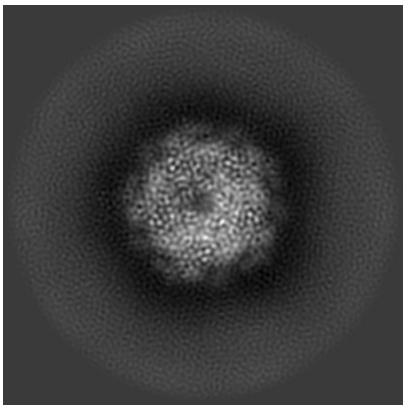
6.1.1 Primary map



X

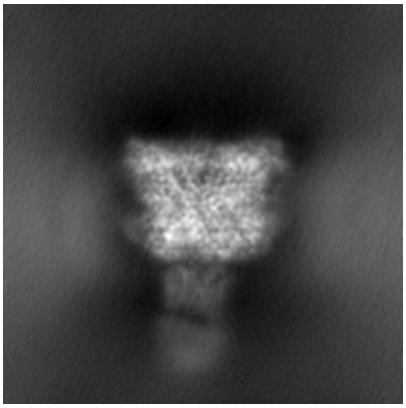


Y



Z

6.1.2 Raw map



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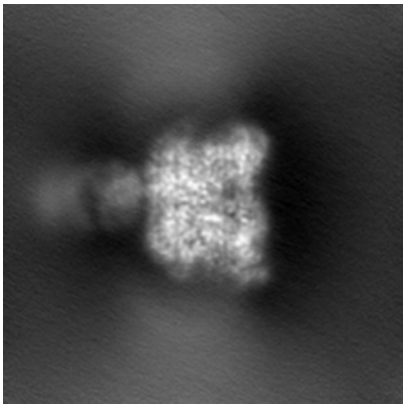
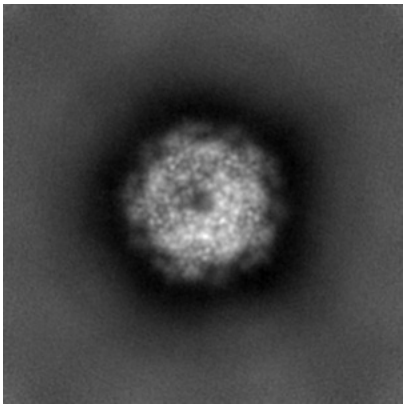


Y

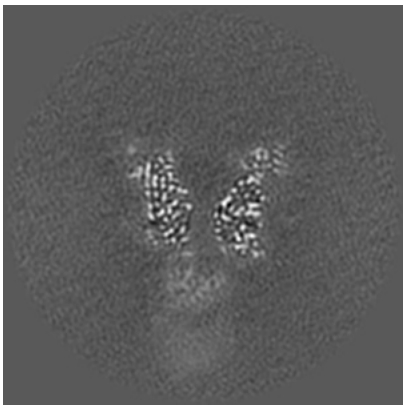


Z

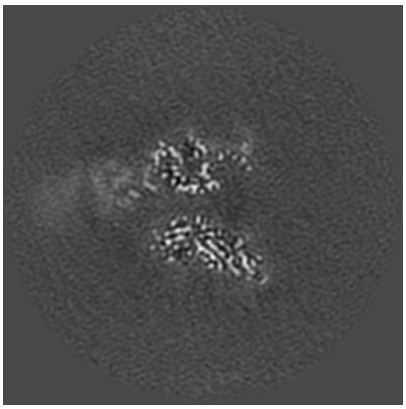
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

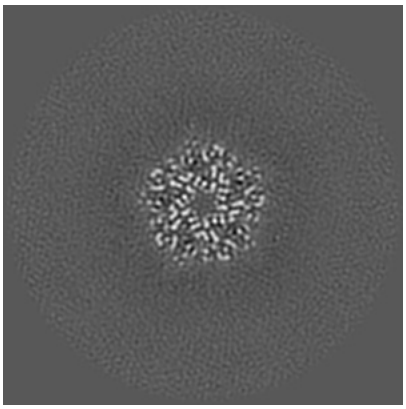
6.2.1 Primary map



X Index: 112

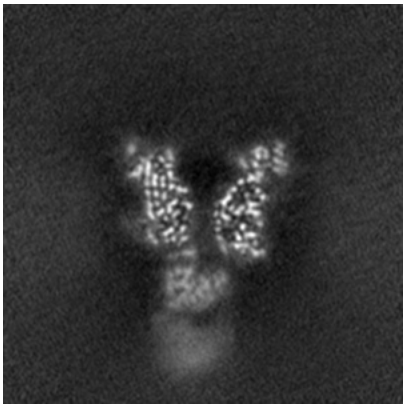


Y Index: 112

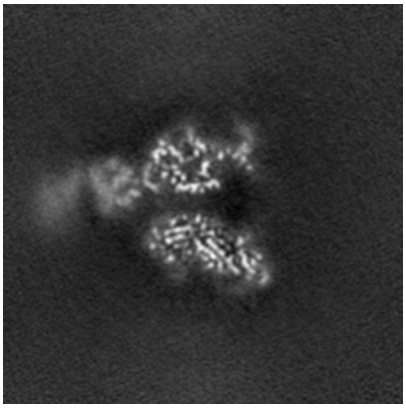


Z Index: 112

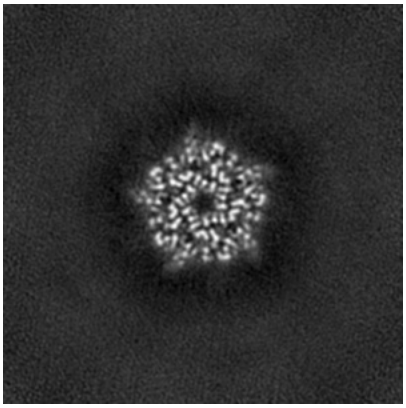
6.2.2 Raw map



X Index: 112



Y Index: 112

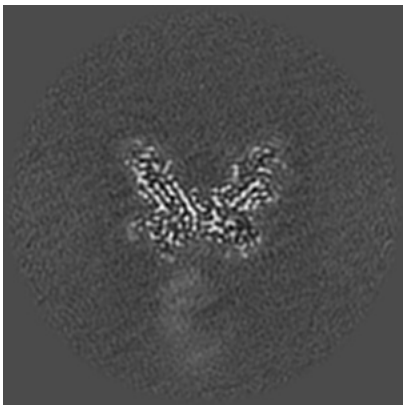


Z Index: 112

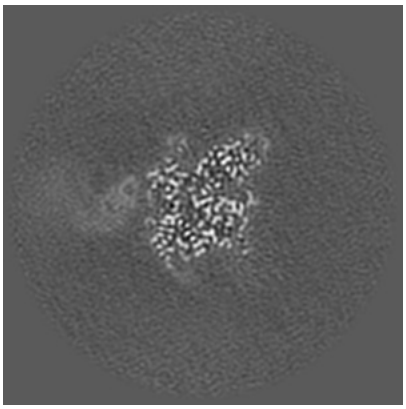
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

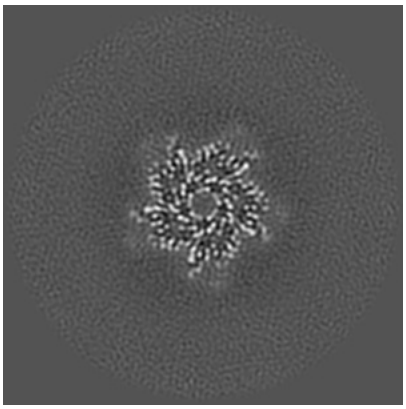
6.3.1 Primary map



X Index: 104

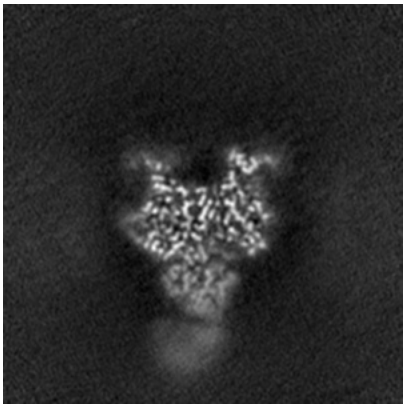


Y Index: 93

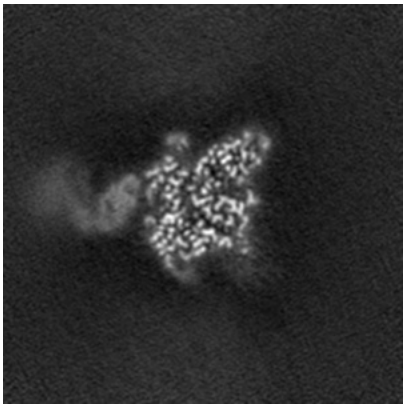


Z Index: 101

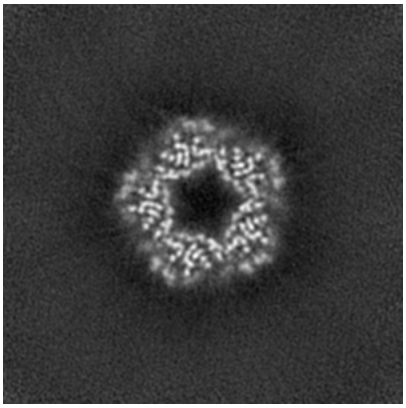
6.3.2 Raw map



X Index: 122



Y Index: 93

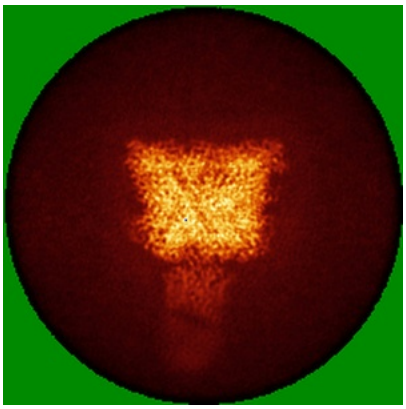


Z Index: 134

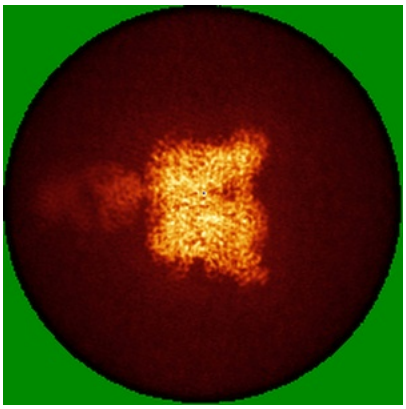
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

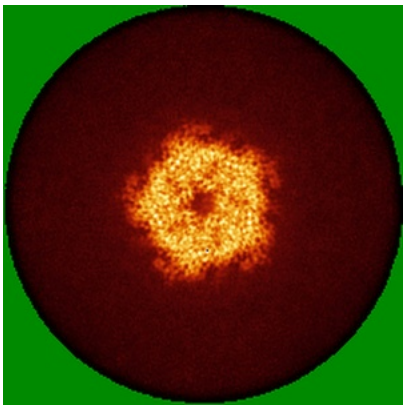
6.4.1 Primary map



X

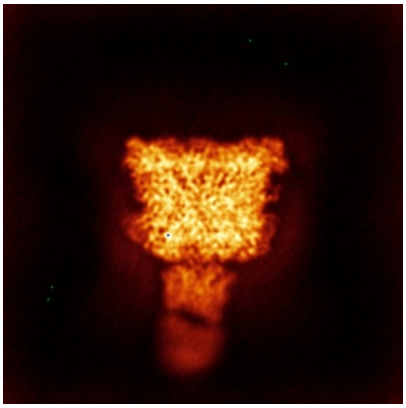


Y

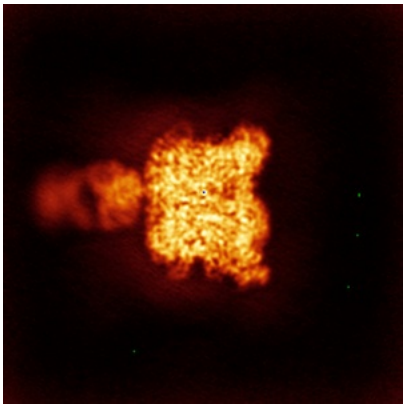


Z

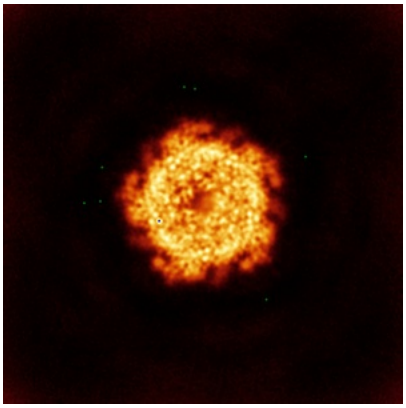
6.4.2 Raw map



X



Y

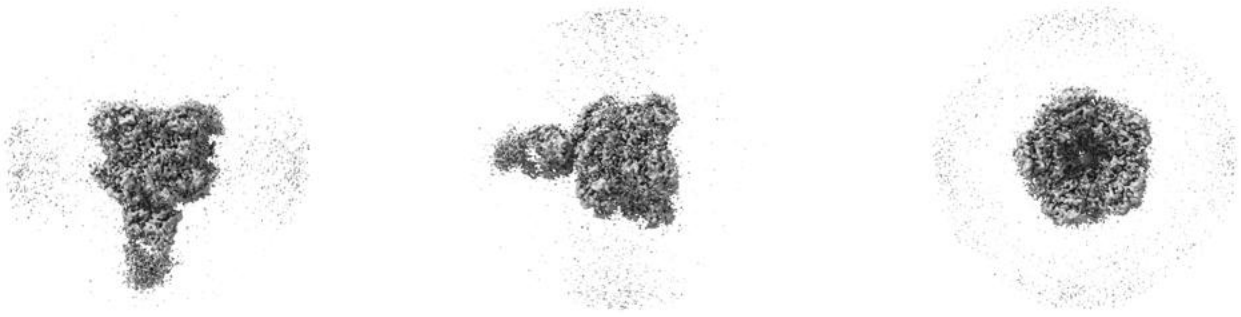


Z

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)

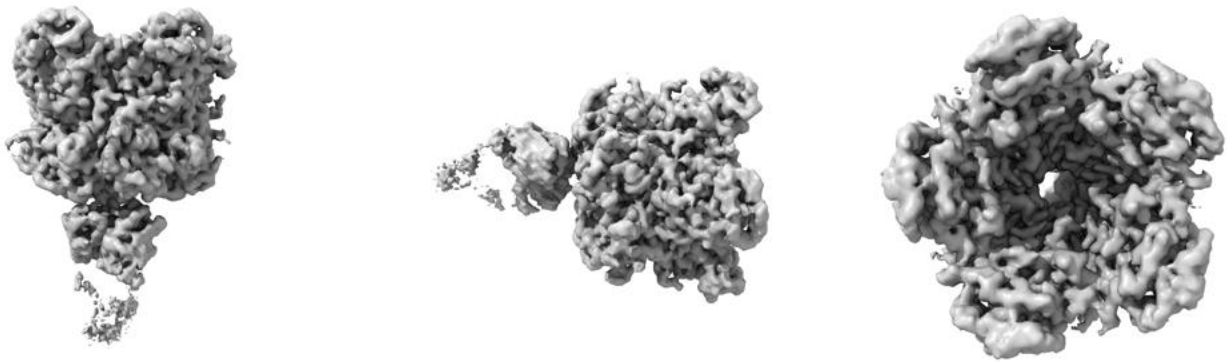
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.7. 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



X Y Z

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.

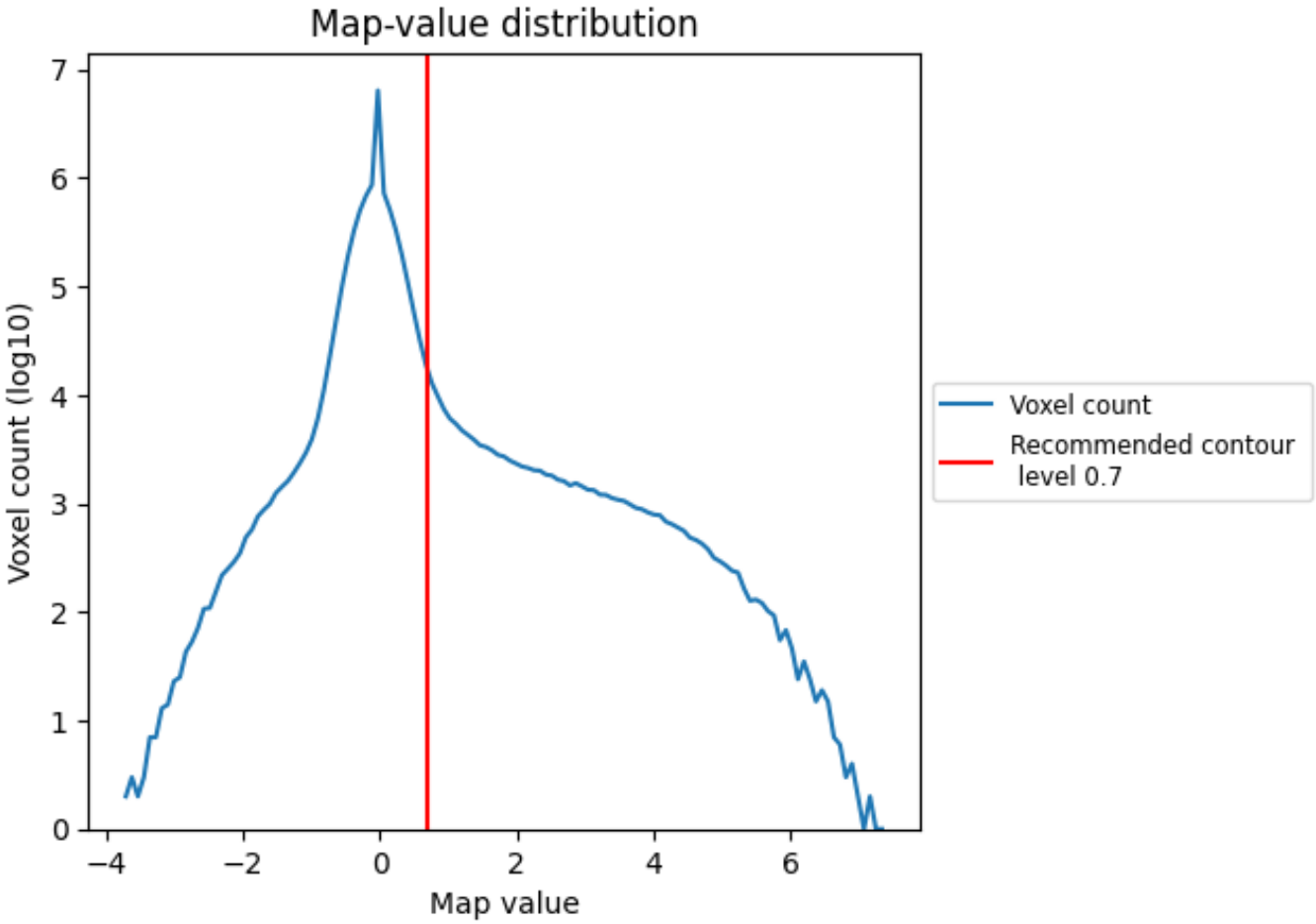
6.6 Mask visualisation (i)

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

7 Map analysis

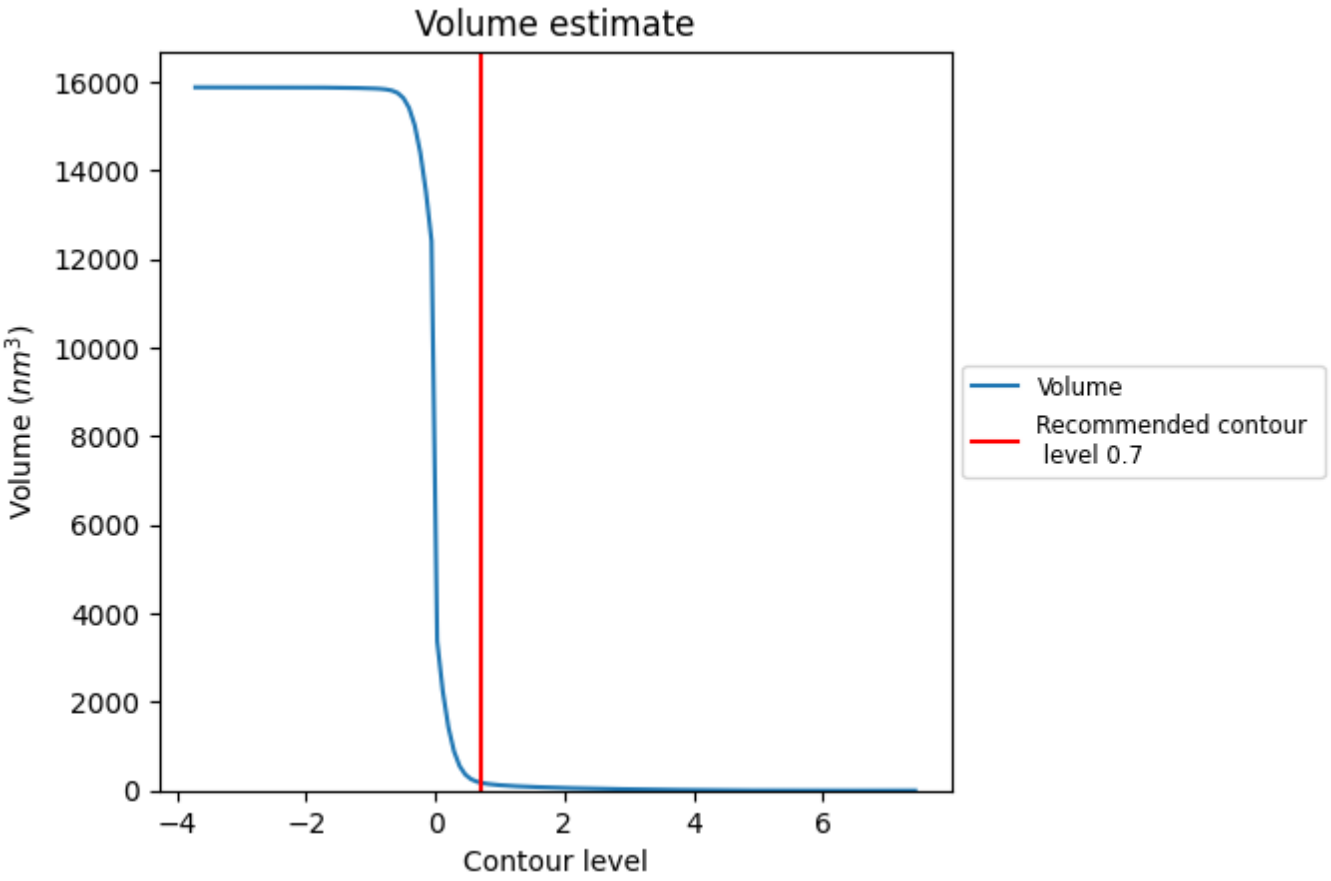
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

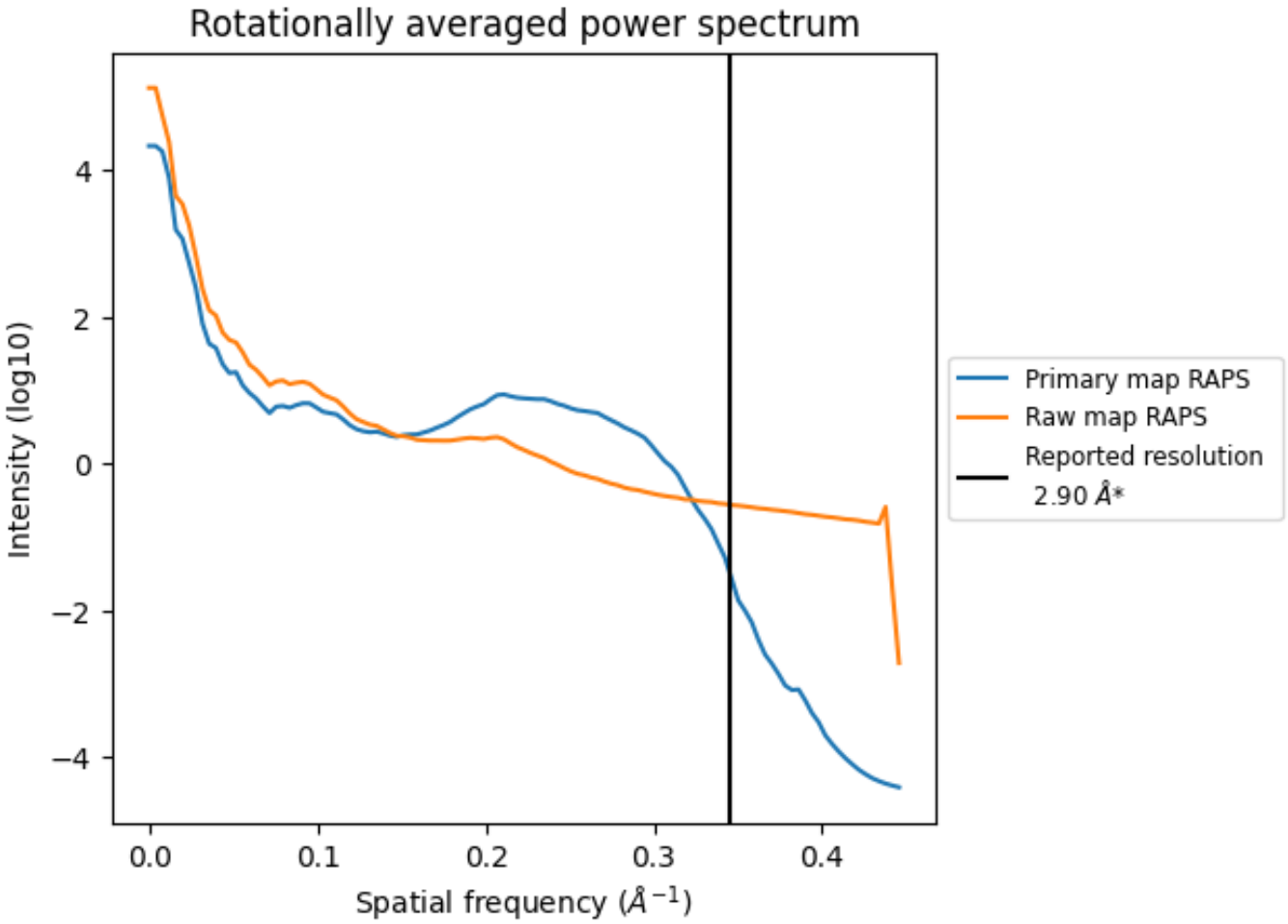
7.2 Volume estimate



The volume at the recommended contour level is 180 nm^3; this corresponds to an approximate mass of 163 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)

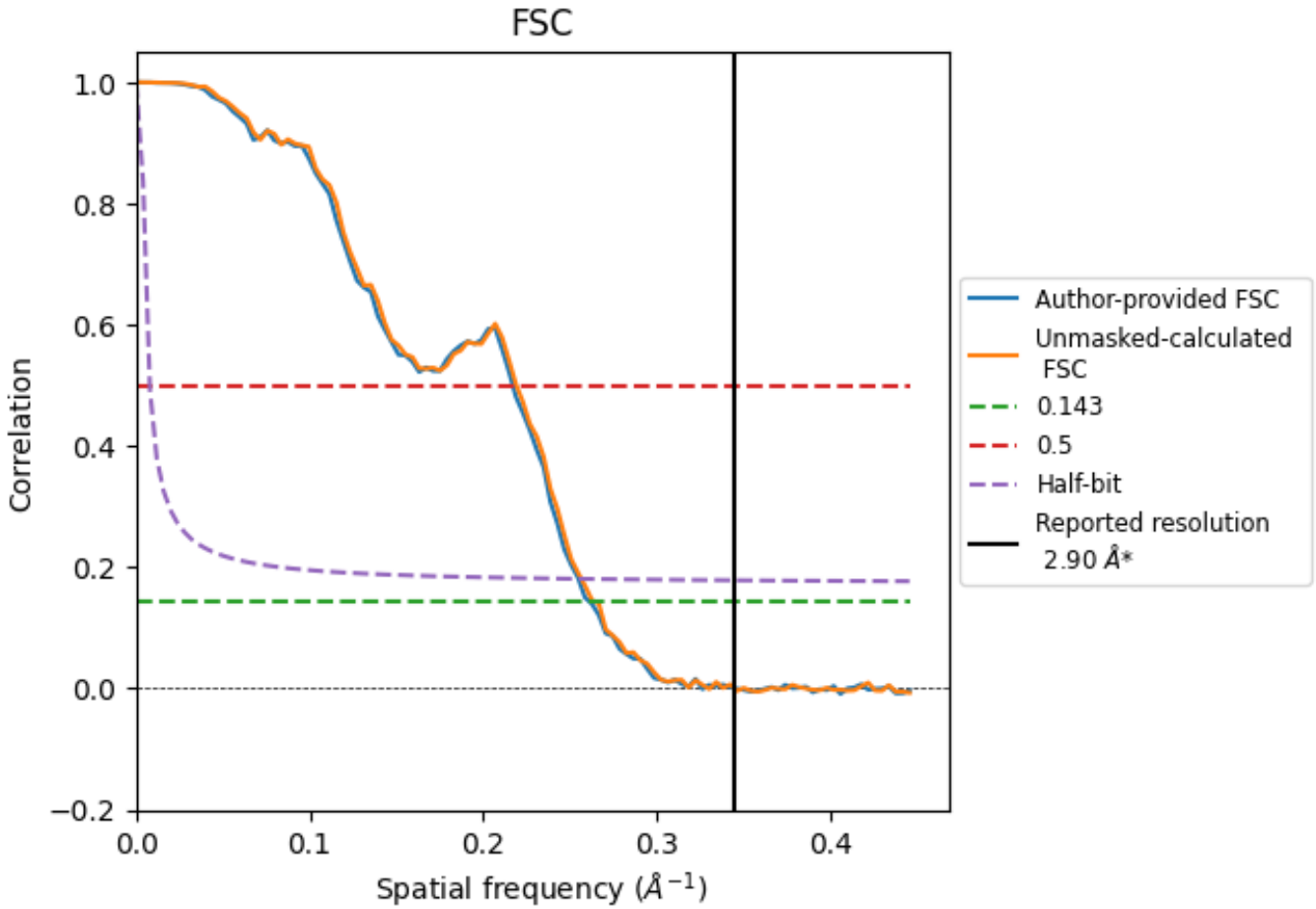


*Reported resolution corresponds to spatial frequency of 0.345 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.345 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	3.83	4.61	3.92
Unmasked-calculated*	3.78	4.56	3.90

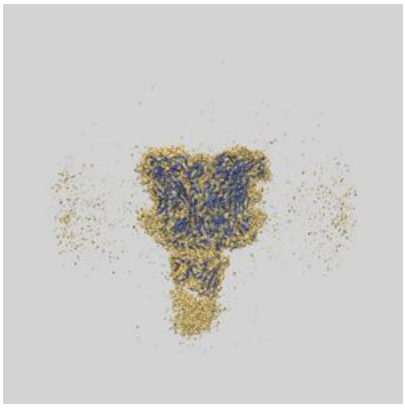
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.83 differs from the reported value 2.9 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.78 differs from the reported value 2.9 by more than 10 %

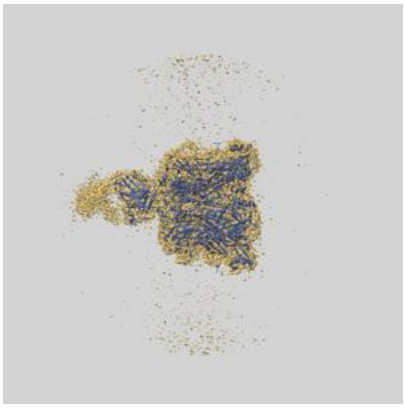
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-48346 and PDB model 9ML3. Per-residue inclusion information can be found in section 3 on page 8.

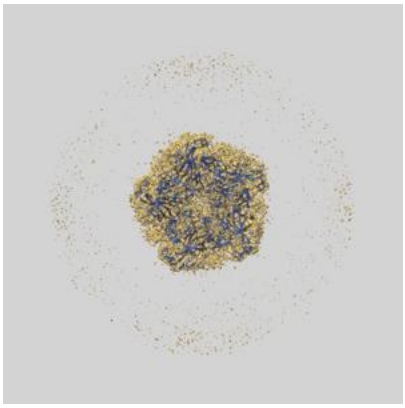
9.1 Map-model overlay



X



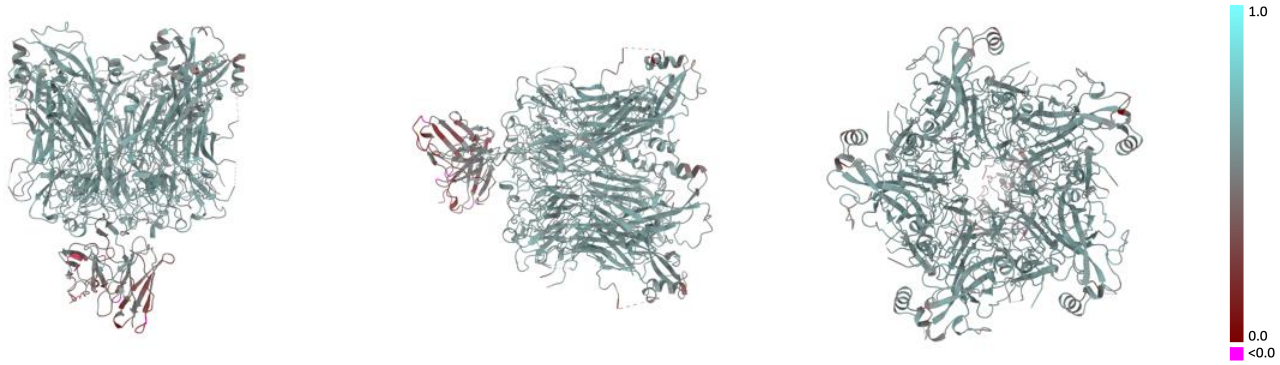
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.7 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.

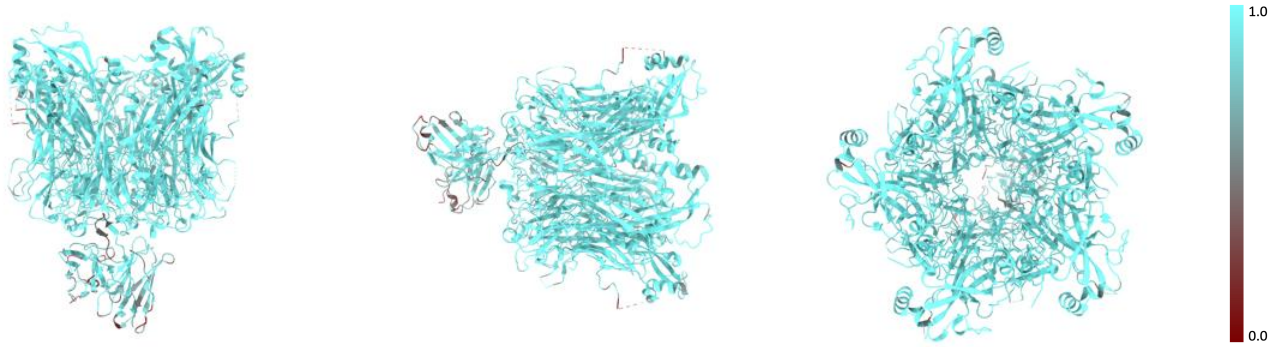
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

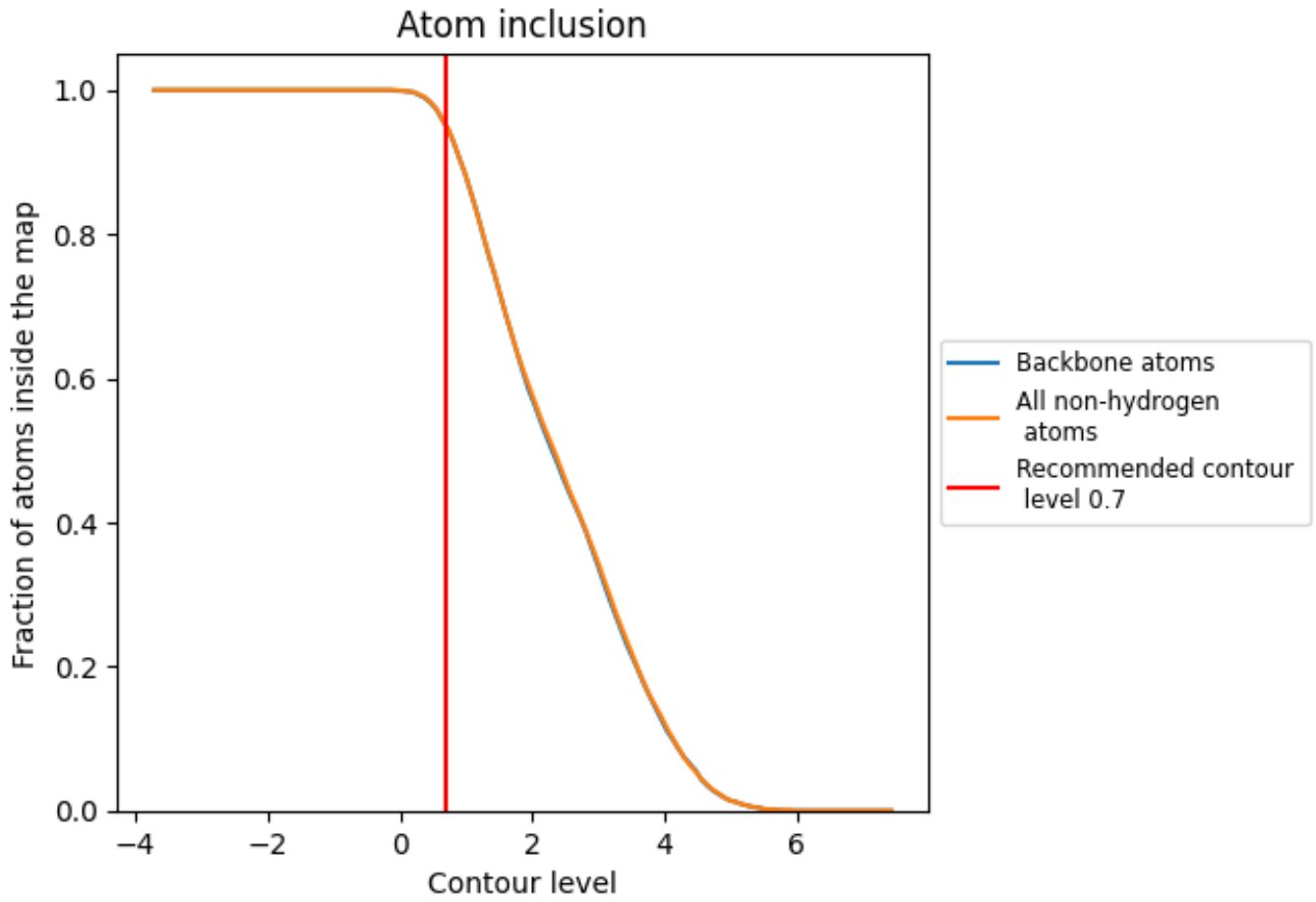
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.7).

9.4 Atom inclusion (i)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9500	0.5570
A	0.9670	0.5720
B	0.9640	0.5730
C	0.9660	0.5760
D	0.9690	0.5770
E	0.9600	0.5670
H	0.8180	0.4170
L	0.7900	0.4050