



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:52 PM UTC

PDB ID : 8C8H / pdb_00008c8h
EMDB ID : EMD-16476
Title : Cryo EM structure of the vaccinia complete RNA polymerase complex lacking the capping enzyme
Authors : Grimm, G.; Bartuli, J.; Fischer, U.
Deposited on : 2023-01-20
Resolution : 3.84 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:

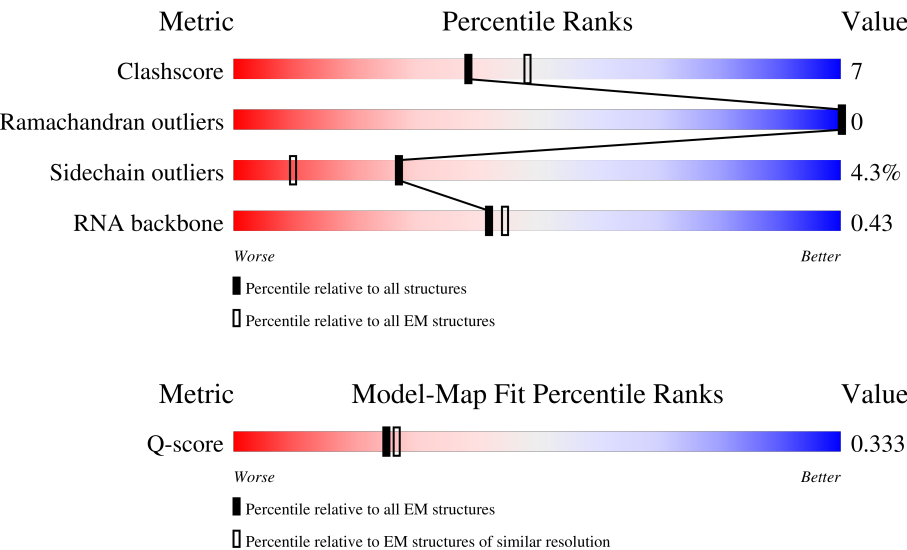
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

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

The reported resolution of this entry is 3.84 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	9033 (3.34 - 4.34)

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	B	1164	
2	E	185	
3	F	164	

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Mol	Chain	Length	Quality of chain
4	G	161	
5	I	795	
6	J	63	
7	Q	129	
7	R	129	
8	K	710	
9	U	72	
10	A	1286	
11	Y	631	
12	C	305	
13	S	259	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 41296 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 DNA-directed RNA polymerase 133 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	1129	Total	C	N	O	S	0	0
			9091	5794	1554	1695	48		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	6	ASN	ASP	conflict	UNP Q76ZP7
B	343	PHE	TYR	variant	UNP Q76ZP7

- Molecule 2 is a protein called DNA-directed RNA polymerase 22 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	184	Total	C	N	O	S	0	0
			1495	966	248	276	5		

- Molecule 3 is a protein called DNA-directed RNA polymerase 19 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	103	Total	C	N	O	S	0	0
			849	545	148	153	3		

- Molecule 4 is a protein called DNA-directed RNA polymerase 18 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	153	Total	C	N	O	S	0	0
			1192	753	198	235	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	11	SER	PRO	variant	UNP P04310

- Molecule 5 is a protein called RNA polymerase-associated transcription-specificity factor

RAP94.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	669	Total	C	N	O	S	0	0
			5603	3669	896	1017	21		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	623	CYS	TYR	variant	UNP P68438
I	624	VAL	ILE	variant	UNP P68438

- Molecule 6 is a protein called DNA-directed RNA polymerase 7 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	61	Total	C	N	O	S	0	0
			490	310	88	88	4		

- Molecule 7 is a protein called Core protein E11.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	129	Total	C	N	O	S	1	0
			1056	689	165	197	5		
7	Q	124	Total	C	N	O	S	0	0
			1013	660	158	190	5		

- Molecule 8 is a protein called Early transcription factor 82 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	91	Total	C	N	O	S	0	0
			749	476	131	133	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	401	ARG	LYS	variant	UNP P20636

- Molecule 9 is a RNA chain called chr17.trna16-GlnTTG.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	U	63	Total	C	N	O	P	1	0
			1362	608	238	452	64		

- Molecule 10 is a protein called DNA-directed RNA polymerase 147 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	1268	Total	C	N	O	S	0	0
			10188	6556	1679	1908	45		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	258	THR	SER	variant	UNP P07392
A	1006	ASN	ASP	variant	UNP P07392
A	1007	ILE	HIS	variant	UNP P07392
A	1008	THR	SER	variant	UNP P07392
A	?	-	PHE	deletion	UNP P07392
A	1010	ARG	GLU	variant	UNP P07392
A	1012	GLU	LYS	variant	UNP P07392
A	1013	THR	GLN	variant	UNP P07392
A	1015	LYS	ARG	variant	UNP P07392
A	1024	ARG	LYS	variant	UNP P07392
A	1113	ASP	CYS	variant	UNP P07392

- Molecule 11 is a protein called Nucleoside triphosphatase I.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Y	539	Total	C	N	O	S	0	0
			4347	2789	738	797	23		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	342	LYS	ARG	variant	UNP P05807
Y	347	LYS	GLY	variant	UNP P05807
Y	568	LYS	ASN	variant	UNP P05807

- Molecule 12 is a protein called DNA-directed RNA polymerase 35 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	304	Total	C	N	O	S	0	0
			2484	1608	399	464	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	212	PHE	LEU	variant	UNP P24757

- Molecule 13 is a protein called DNA-directed RNA polymerase 30 kDa polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	S	161	Total	C	N	O	P	S	
			1311	820	211	273	3	4	0
									0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	20	ALA	THR	variant	UNP P21603

- Molecule 14 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
14	B	1	Total	Zn	0
			1	1	
14	I	1	Total	Zn	0
			1	1	
14	A	2	Total	Zn	0
			2	2	

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
15	A	1	Total	Mg	0
			1	1	

- Molecule 16 is water.

Mol	Chain	Residues	Atoms		AltConf
16	B	26	Total	O	0
			26	26	
16	E	2	Total	O	0
			2	2	
16	F	1	Total	O	0
			1	1	
16	G	3	Total	O	0
			3	3	
16	I	4	Total	O	0
			4	4	
16	J	4	Total	O	0
			4	4	
16	K	1	Total	O	0
			1	1	

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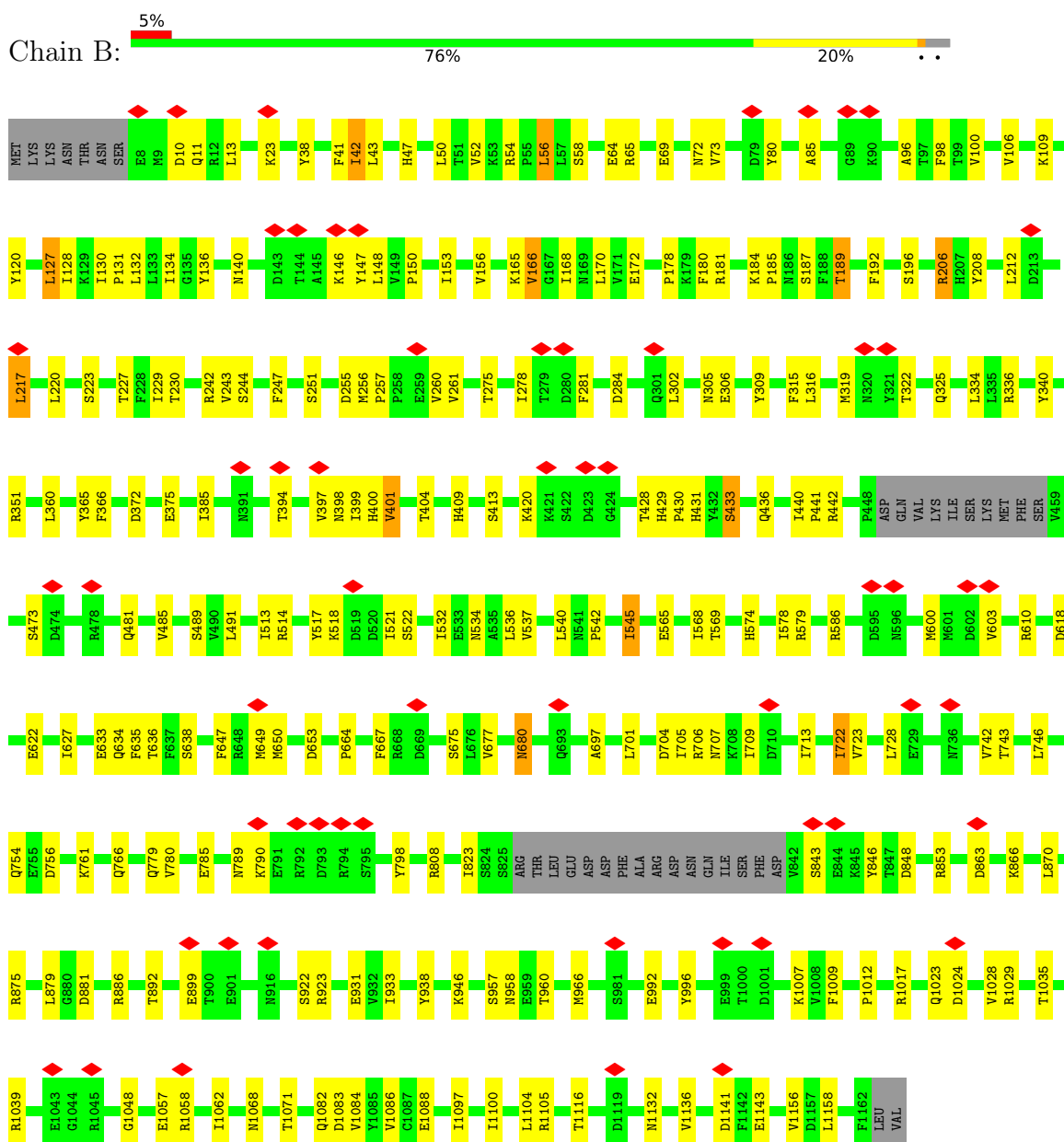
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Mol	Chain	Residues	Atoms		AltConf
16	A	17	Total 17	O 17	0
16	Y	1	Total 1	O 1	0
16	C	2	Total 2	O 2	0

3 Residue-property plots

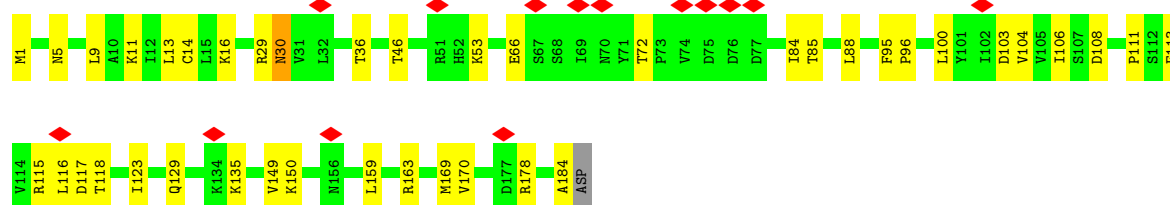
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DNA-directed RNA polymerase 133 kDa polypeptide



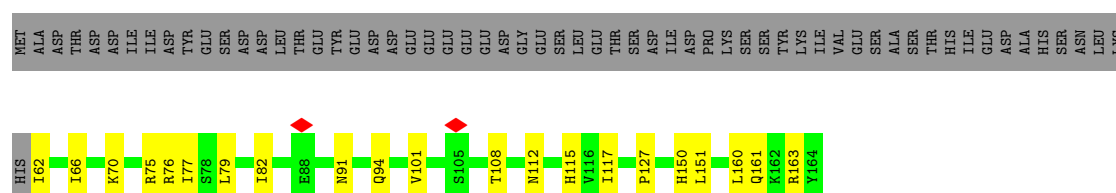
- Molecule 2: DNA-directed RNA polymerase 22 kDa subunit

Chain E: 



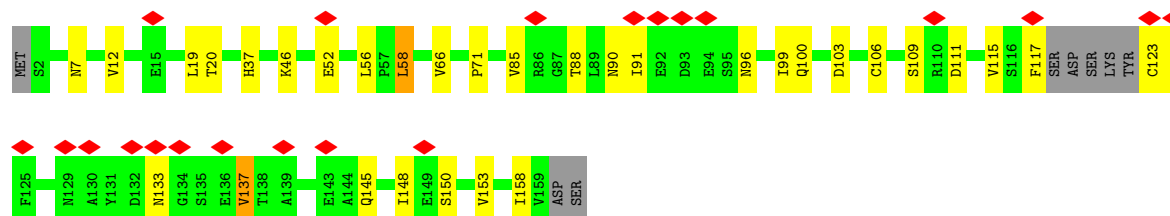
- Molecule 3: DNA-directed RNA polymerase 19 kDa subunit

Chain F: 



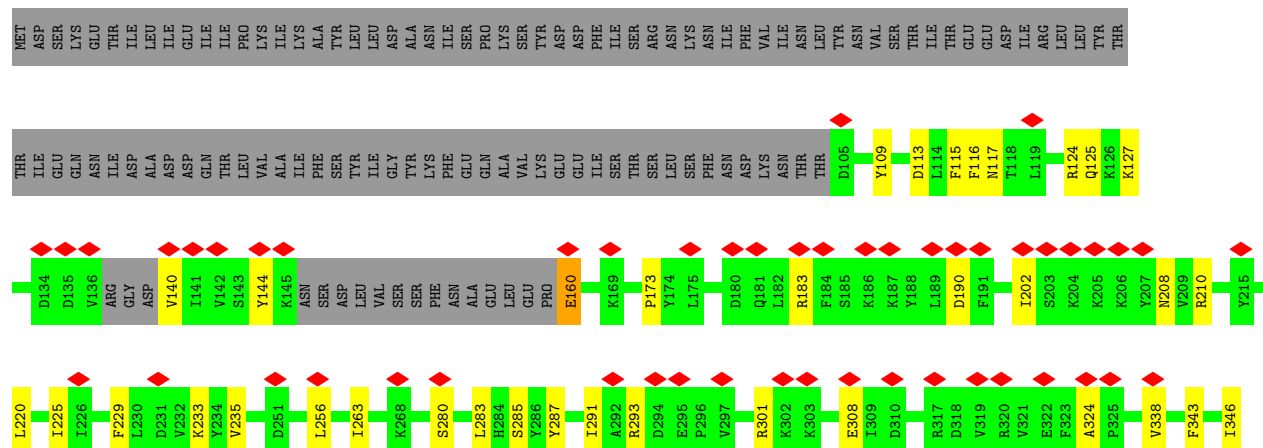
- Molecule 4: DNA-directed RNA polymerase 18 kDa subunit

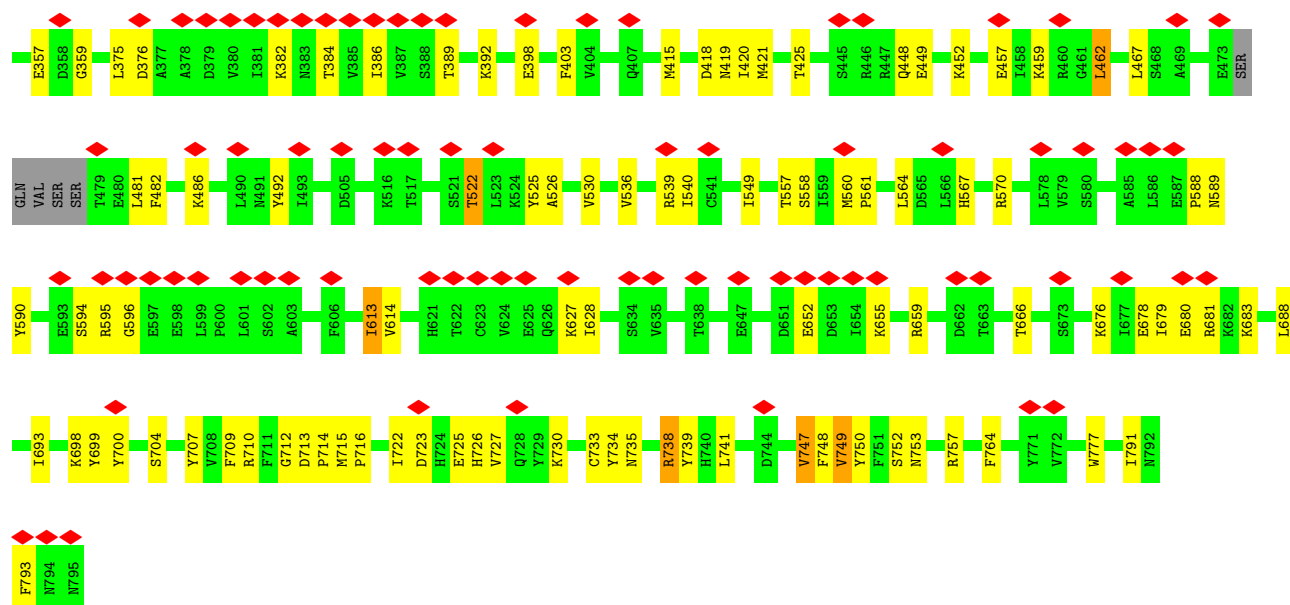
Chain G: 



- Molecule 5: RNA polymerase-associated transcription-specificity factor RAP94

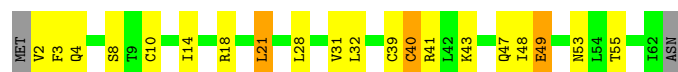
Chain I: 





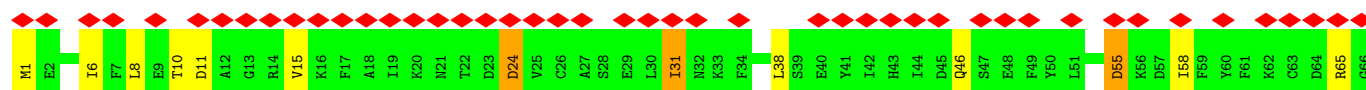
- Molecule 6: DNA-directed RNA polymerase 7 kDa subunit

Chain J: 65% 27% 5% .



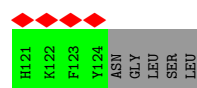
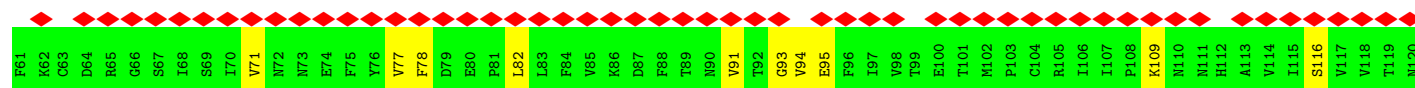
- Molecule 7: Core protein E11

Chain R: 73% 84% 14% .



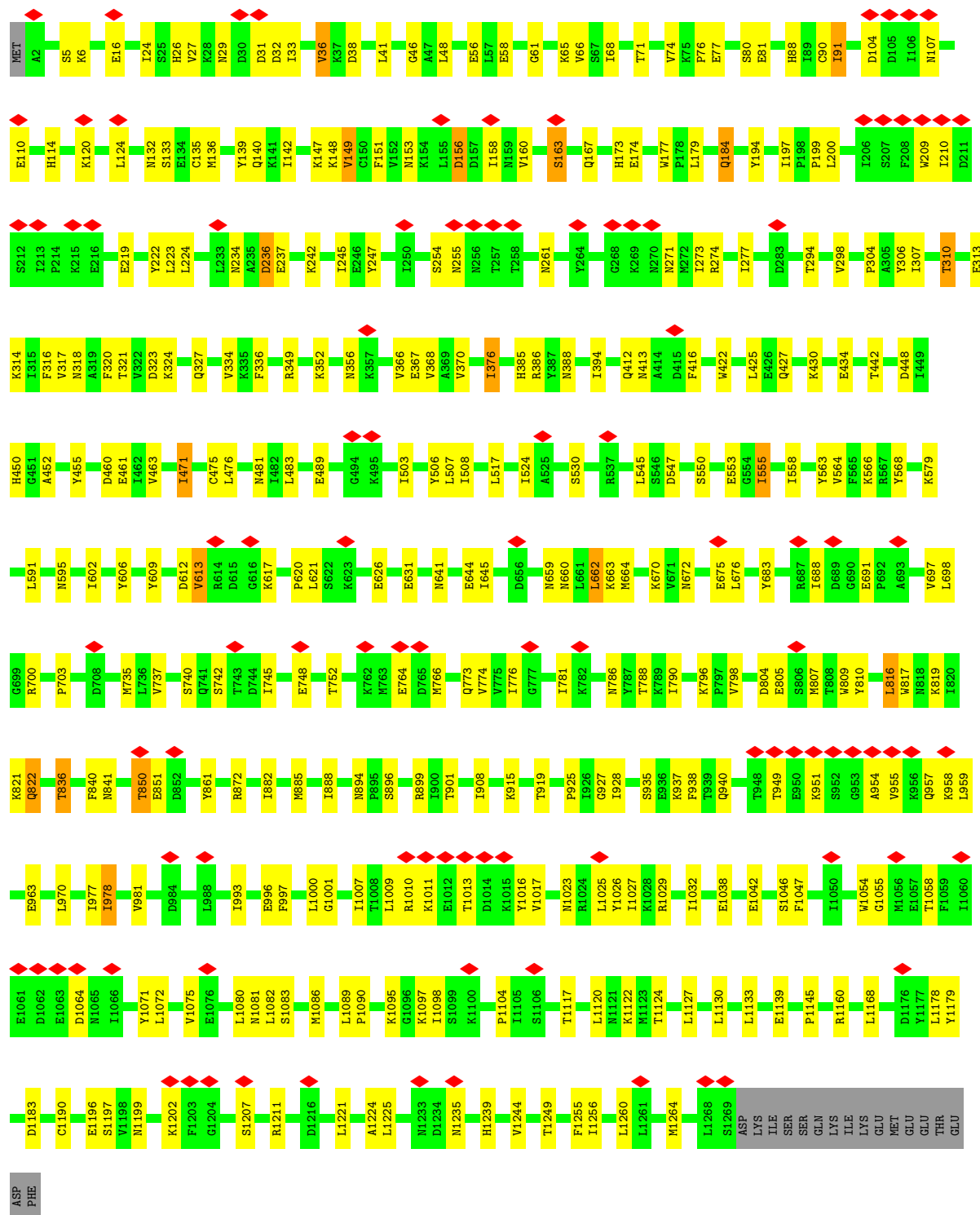
- Molecule 7: Core protein E11

Chain Q: 91% 75% 19% . .

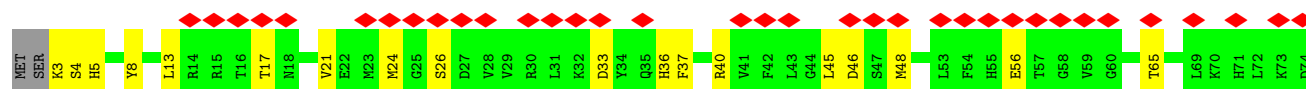


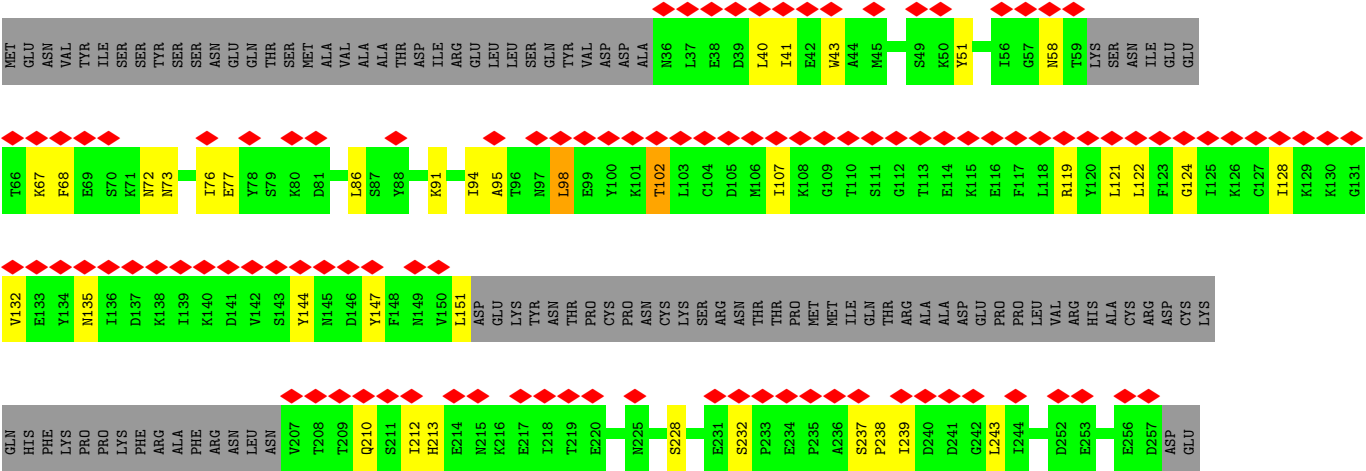
Chain K: 13% 10% 87%





• Molecule 11: Nucleoside triphosphatase I





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21338	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.345	Depositor
Minimum map value	-0.815	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.061	Depositor
Recommended contour level	0.5	Depositor
Map size ($\text{\AA}$)	382.86002, 382.86002, 382.86002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, MG, ZN

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	B	0.12	0/9281	0.34	0/12537
2	E	0.12	0/1522	0.37	1/2069 (0.0%)
3	F	0.13	0/863	0.33	0/1158
4	G	0.10	0/1209	0.31	0/1639
5	I	0.11	0/5733	0.33	0/7754
6	J	0.16	0/494	0.42	0/663
7	Q	0.09	0/1035	0.29	0/1402
7	R	0.08	0/1081	0.29	0/1463
8	K	0.07	0/767	0.33	0/1030
9	U	0.14	0/1521	0.42	0/2368
10	A	0.12	0/10394	0.36	0/14052
11	Y	0.09	0/4429	0.30	0/5960
12	C	0.12	0/2540	0.35	0/3440
13	S	0.09	0/1302	0.34	0/1749
All	All	0.11	0/42171	0.34	1/57284 (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
10	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	14	CYS	N-CA-C	-6.19	104.94	113.18

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	147	LYS	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	B	9091	0	9146	156	0
2	E	1495	0	1548	26	0
3	F	849	0	874	15	0
4	G	1192	0	1181	18	0
5	I	5603	0	5659	87	0
6	J	490	0	530	12	0
7	Q	1013	0	998	13	0
7	R	1056	0	1056	13	0
8	K	749	0	727	9	0
9	U	1362	0	687	19	0
10	A	10188	0	10312	194	0
11	Y	4347	0	4415	67	0
12	C	2484	0	2470	37	0
13	S	1311	0	1268	31	0
14	A	2	0	0	0	0
14	B	1	0	0	0	0
14	I	1	0	0	0	0
15	A	1	0	0	0	0
16	A	17	0	0	2	0
16	B	26	0	0	0	0
16	C	2	0	0	0	0
16	E	2	0	0	0	0
16	F	1	0	0	0	0
16	G	3	0	0	0	0
16	I	4	0	0	0	0
16	J	4	0	0	0	0
16	K	1	0	0	0	0
16	Y	1	0	0	0	0
All	All	41296	0	40871	599	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 7.

The worst 5 of 599 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)
2:E:88:LEU:HD23	2:E:96:PRO:HG3	1.66	0.78
1:B:1097:ILE:HD12	1:B:1097:ILE:H	1.52	0.73
6:J:32:LEU:HD22	6:J:41:ARG:HG2	1.71	0.73
10:A:336:PHE:HB2	10:A:367:GLU:HB2	1.70	0.73
11:Y:406:ILE:O	11:Y:408:ASN:ND2	2.22	0.72

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	B	1123/1164 (96%)	1047 (93%)	76 (7%)	0	100	100
2	E	182/185 (98%)	165 (91%)	17 (9%)	0	100	100
3	F	101/164 (62%)	95 (94%)	6 (6%)	0	100	100
4	G	149/161 (92%)	139 (93%)	10 (7%)	0	100	100
5	I	661/795 (83%)	615 (93%)	46 (7%)	0	100	100
6	J	59/63 (94%)	56 (95%)	3 (5%)	0	100	100
7	Q	122/129 (95%)	118 (97%)	4 (3%)	0	100	100
7	R	128/129 (99%)	121 (94%)	7 (6%)	0	100	100
8	K	87/710 (12%)	81 (93%)	6 (7%)	0	100	100
10	A	1266/1286 (98%)	1190 (94%)	76 (6%)	0	100	100
11	Y	533/631 (84%)	502 (94%)	31 (6%)	0	100	100
12	C	302/305 (99%)	281 (93%)	21 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	S	152/259 (59%)	132 (87%)	20 (13%)	0	100	100
All	All	4865/5981 (81%)	4542 (93%)	323 (7%)	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	B	1030/1064 (97%)	990 (96%)	40 (4%)	28	53
2	E	174/175 (99%)	168 (97%)	6 (3%)	32	56
3	F	94/151 (62%)	91 (97%)	3 (3%)	34	56
4	G	136/144 (94%)	131 (96%)	5 (4%)	30	54
5	I	637/755 (84%)	611 (96%)	26 (4%)	27	52
6	J	60/62 (97%)	53 (88%)	7 (12%)	5	22
7	Q	116/121 (96%)	108 (93%)	8 (7%)	14	41
7	R	122/121 (101%)	116 (95%)	6 (5%)	22	48
8	K	87/665 (13%)	80 (92%)	7 (8%)	11	36
10	A	1139/1157 (98%)	1084 (95%)	55 (5%)	23	48
11	Y	490/573 (86%)	474 (97%)	16 (3%)	33	56
12	C	286/287 (100%)	276 (96%)	10 (4%)	32	55
13	S	146/237 (62%)	141 (97%)	5 (3%)	32	56
All	All	4517/5512 (82%)	4323 (96%)	194 (4%)	27	50

5 of 194 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	A	261	ASN
10	A	1009	LEU
10	A	366	VAL
10	A	740	SER

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Mol	Chain	Res	Type
10	A	1117	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 114 such sidechains are listed below:

Mol	Chain	Res	Type
10	A	167	GLN
13	S	55	ASN
10	A	589	ASN
12	C	260	ASN
11	Y	272	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	U	61/72 (84%)	17 (27%)	2 (3%)

5 of 17 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	U	9	G
9	U	14	A
9	U	16	U
9	U	17	G
9	U	18	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	U	18	G
9	U	20	U

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

3 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
13	SEP	S	237	13	8,9,10	1.63	1 (12%)	7,12,14	1.18	1 (14%)
13	SEP	S	232	13	8,9,10	1.63	1 (12%)	7,12,14	1.81	2 (28%)
13	SEP	S	228	13	8,9,10	1.61	1 (12%)	7,12,14	1.32	1 (14%)

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
13	SEP	S	237	13	-	0/6/8/10	-
13	SEP	S	232	13	-	2/6/8/10	-
13	SEP	S	228	13	-	4/6/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	S	232	SEP	P-O1P	3.56	1.61	1.50
13	S	237	SEP	P-O1P	3.54	1.61	1.50
13	S	228	SEP	P-O1P	3.51	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	S	232	SEP	OG-CB-CA	4.04	112.08	108.14
13	S	228	SEP	OG-CB-CA	2.91	110.98	108.14
13	S	237	SEP	OG-CB-CA	2.47	110.55	108.14
13	S	232	SEP	OG-P-O1P	2.18	112.32	106.44

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	S	228	SEP	CB-OG-P-O2P
13	S	228	SEP	CB-OG-P-O3P
13	S	228	SEP	CB-OG-P-O1P
13	S	232	SEP	CB-OG-P-O1P
13	S	228	SEP	CA-CB-OG-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

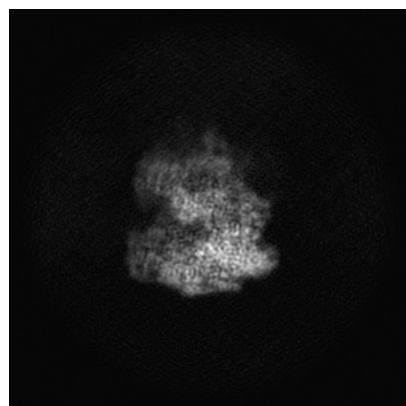
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16476. These allow visual inspection of the internal detail of the map and identification of artifacts.

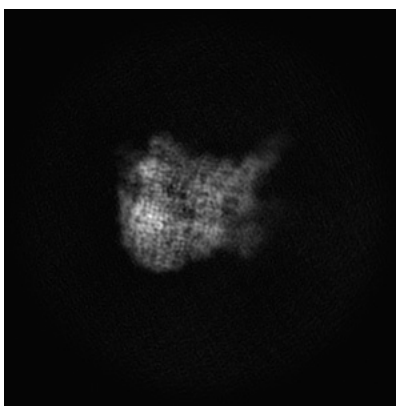
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

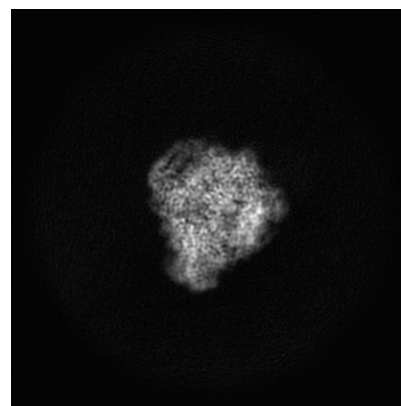
6.1.1 Primary map



X

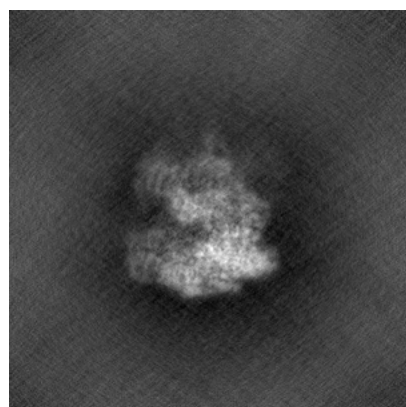


Y

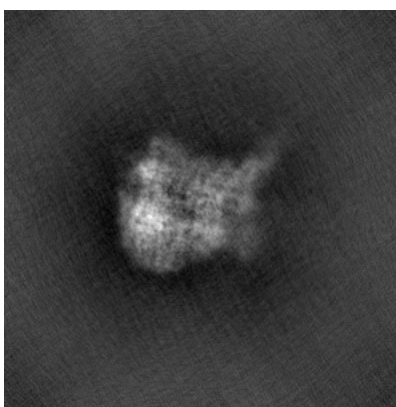


Z

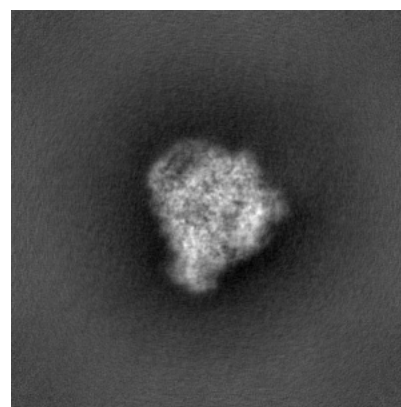
6.1.2 Raw map



X



Y

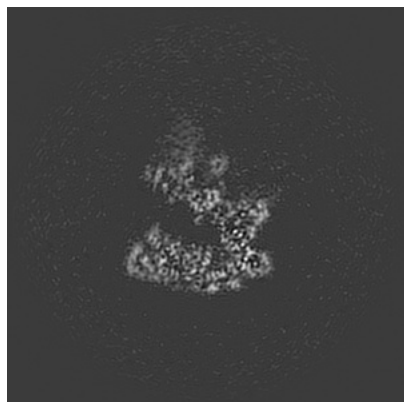


Z

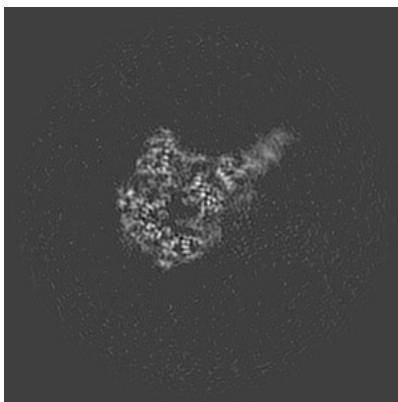
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

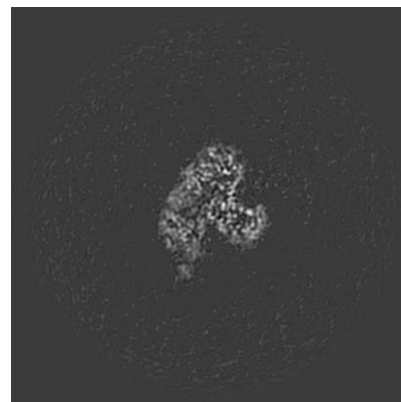
6.2.1 Primary map



X Index: 180

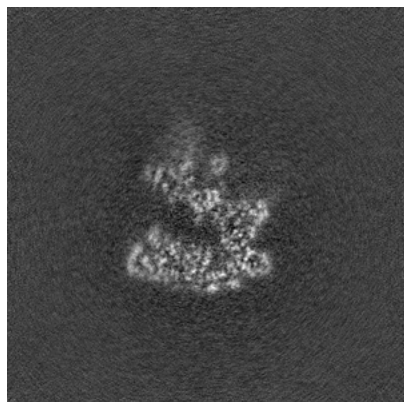


Y Index: 180

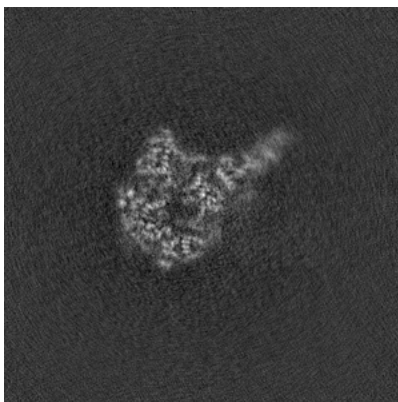


Z Index: 180

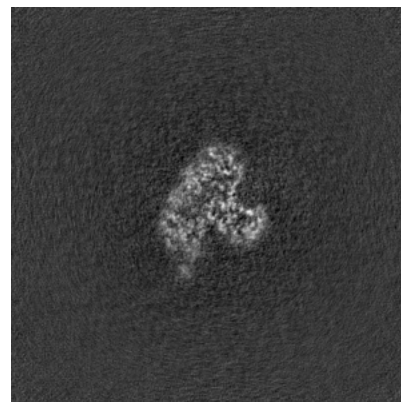
6.2.2 Raw map



X Index: 180



Y Index: 180

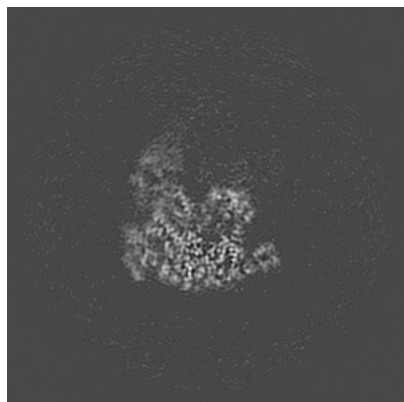


Z Index: 180

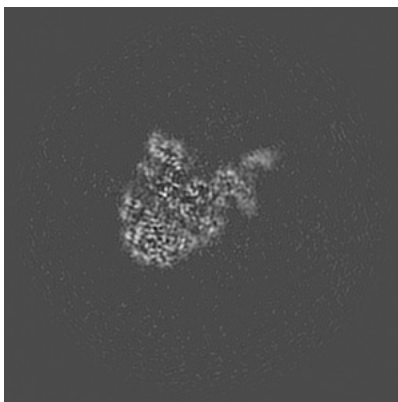
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

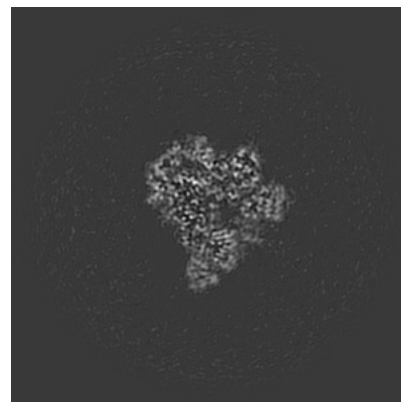
6.3.1 Primary map



X Index: 163

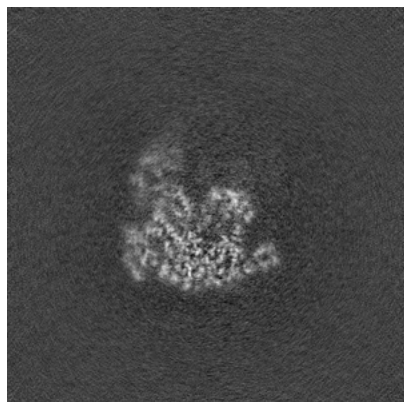


Y Index: 194

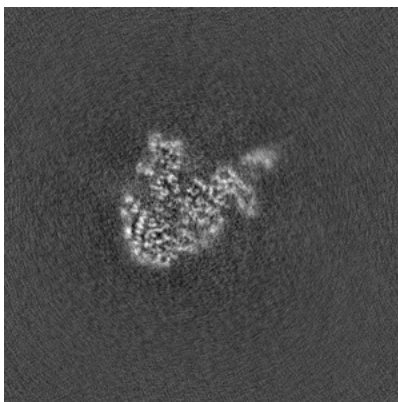


Z Index: 137

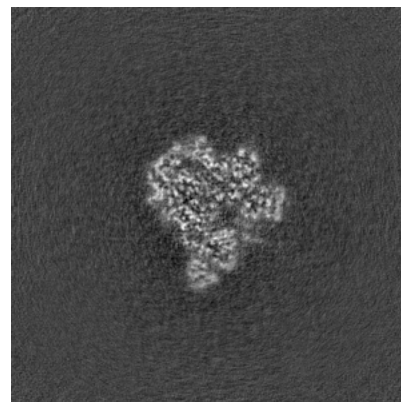
6.3.2 Raw map



X Index: 163



Y Index: 192

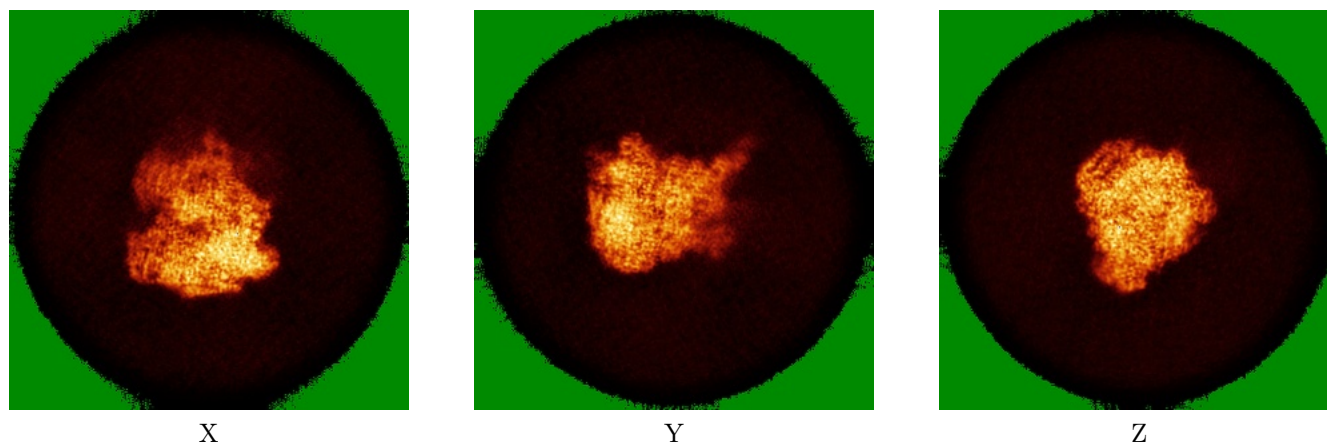


Z Index: 138

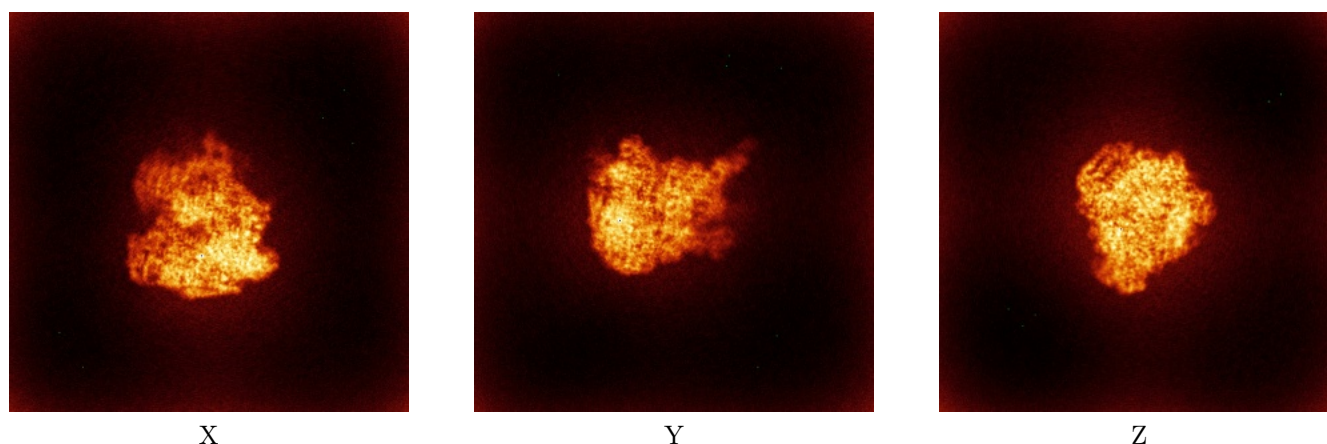
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

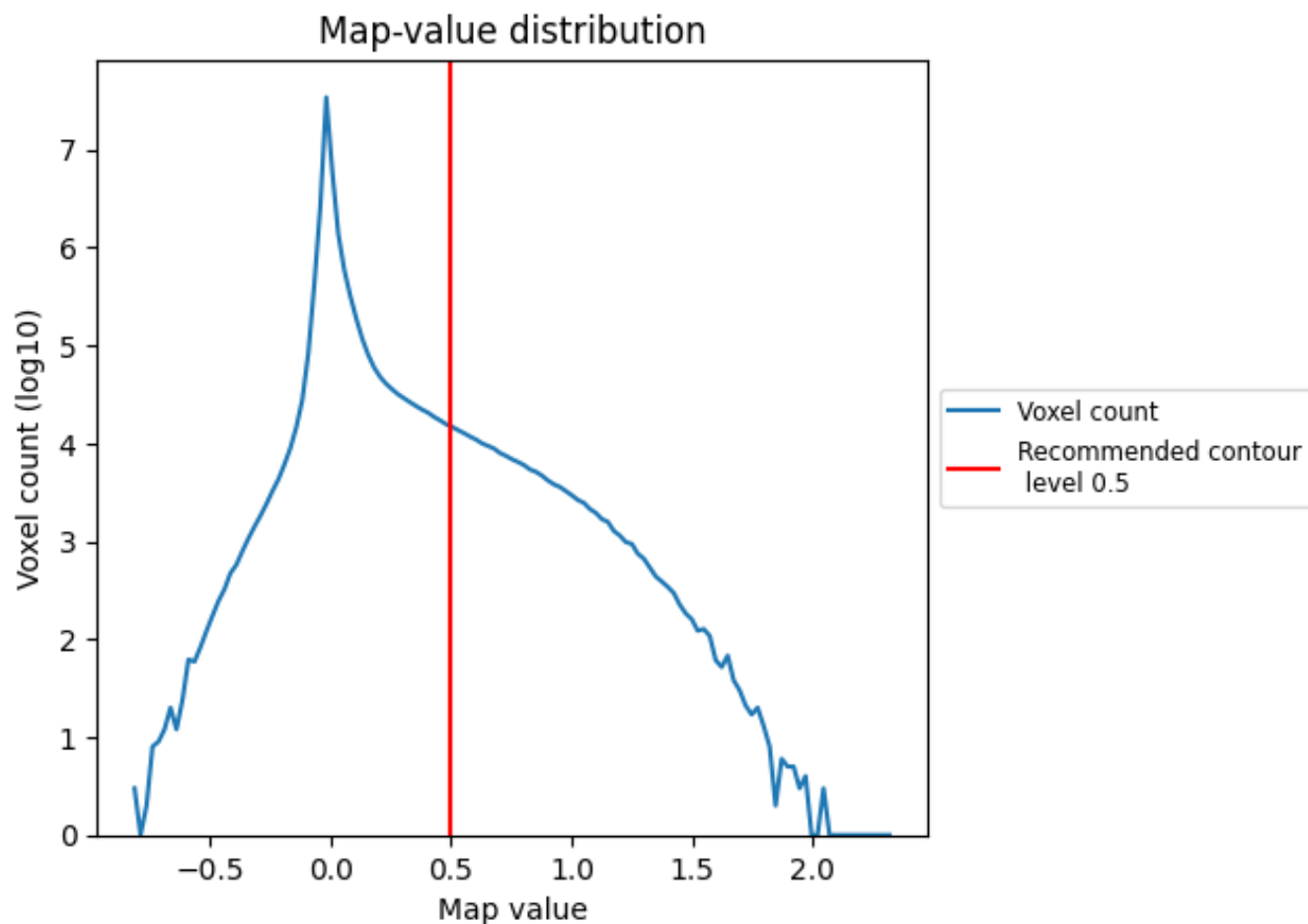
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

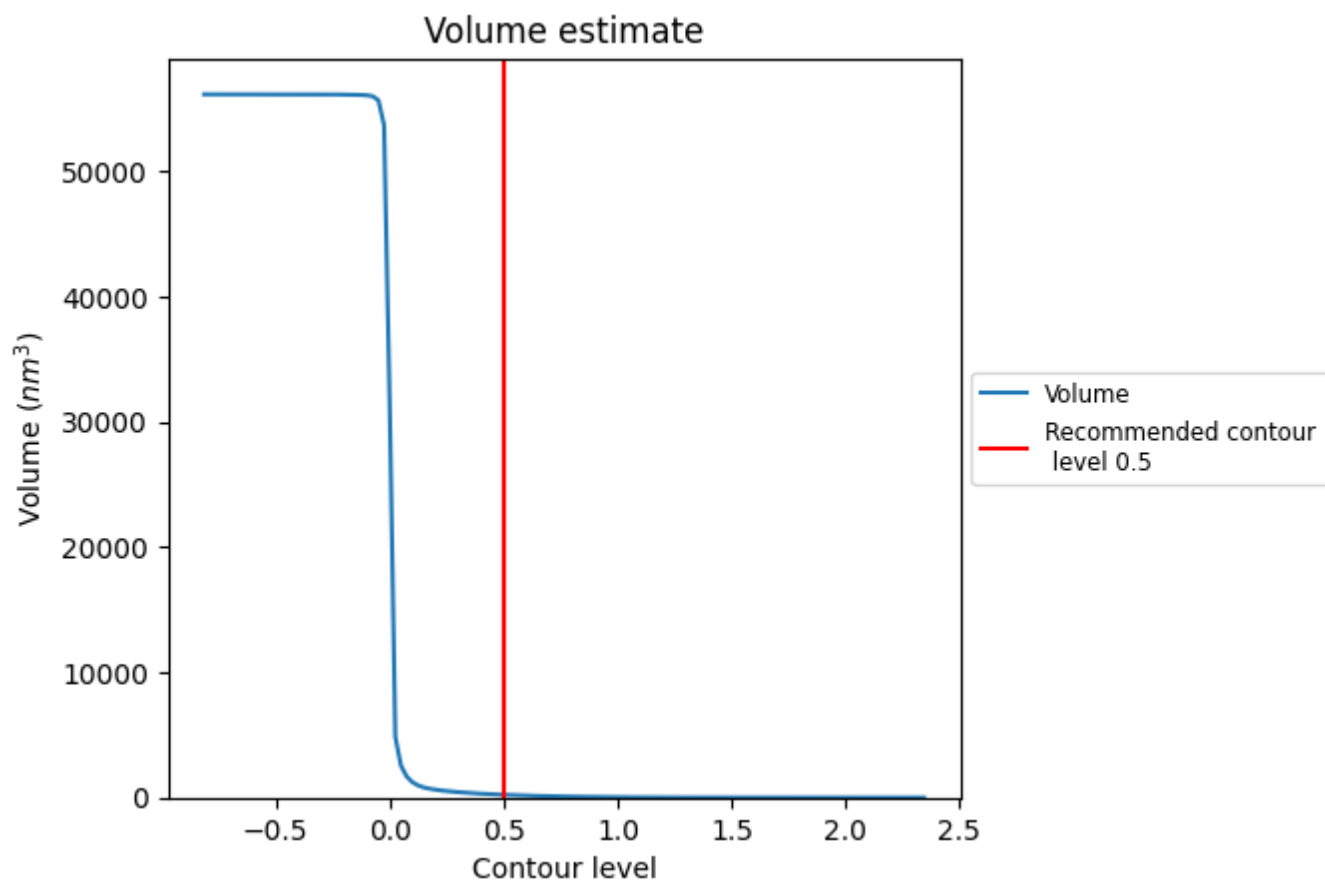
This section contains the results of statistical analysis of the map.

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.

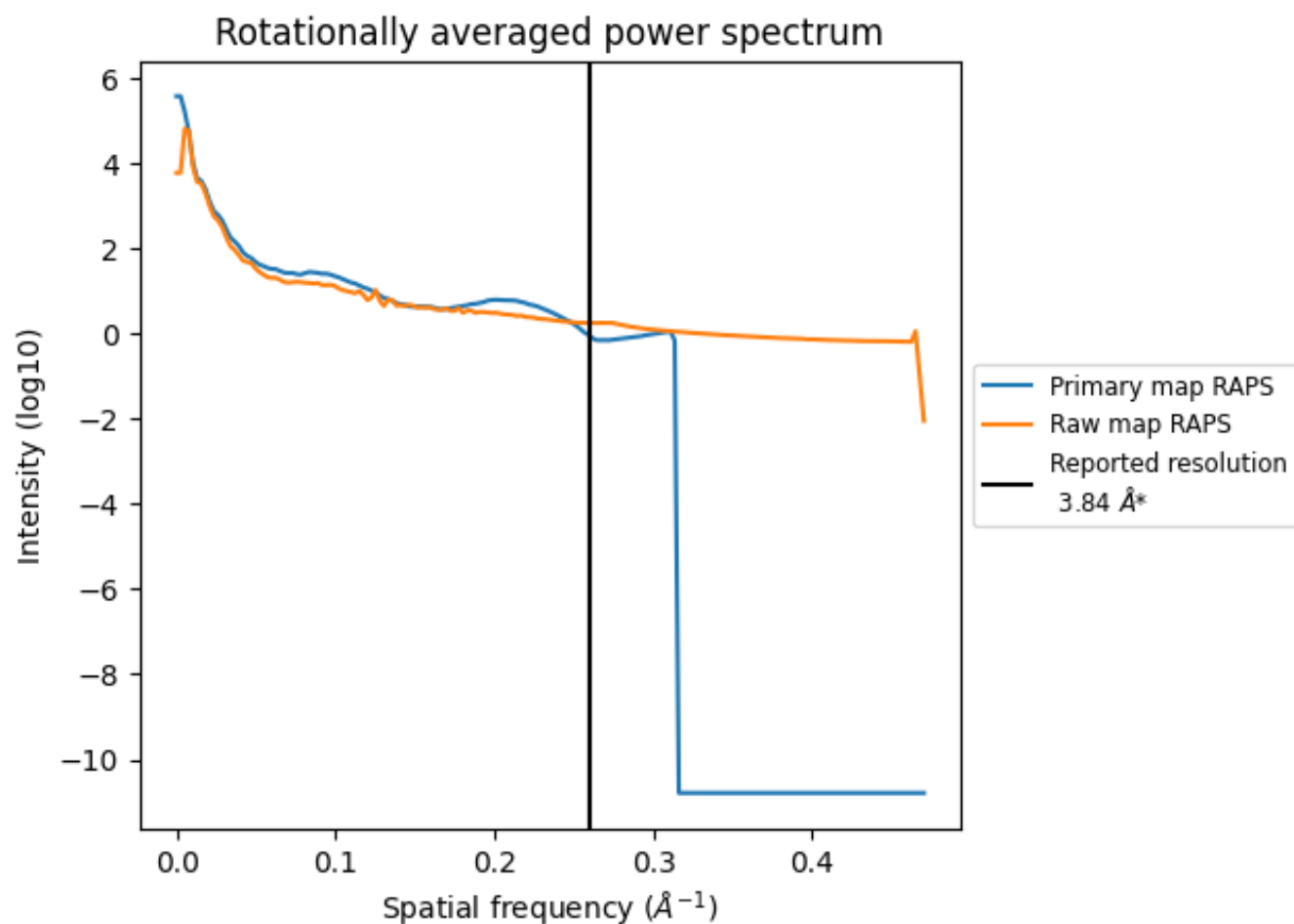
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 221 nm^3 ; this corresponds to an approximate mass of 199 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 ⓘ

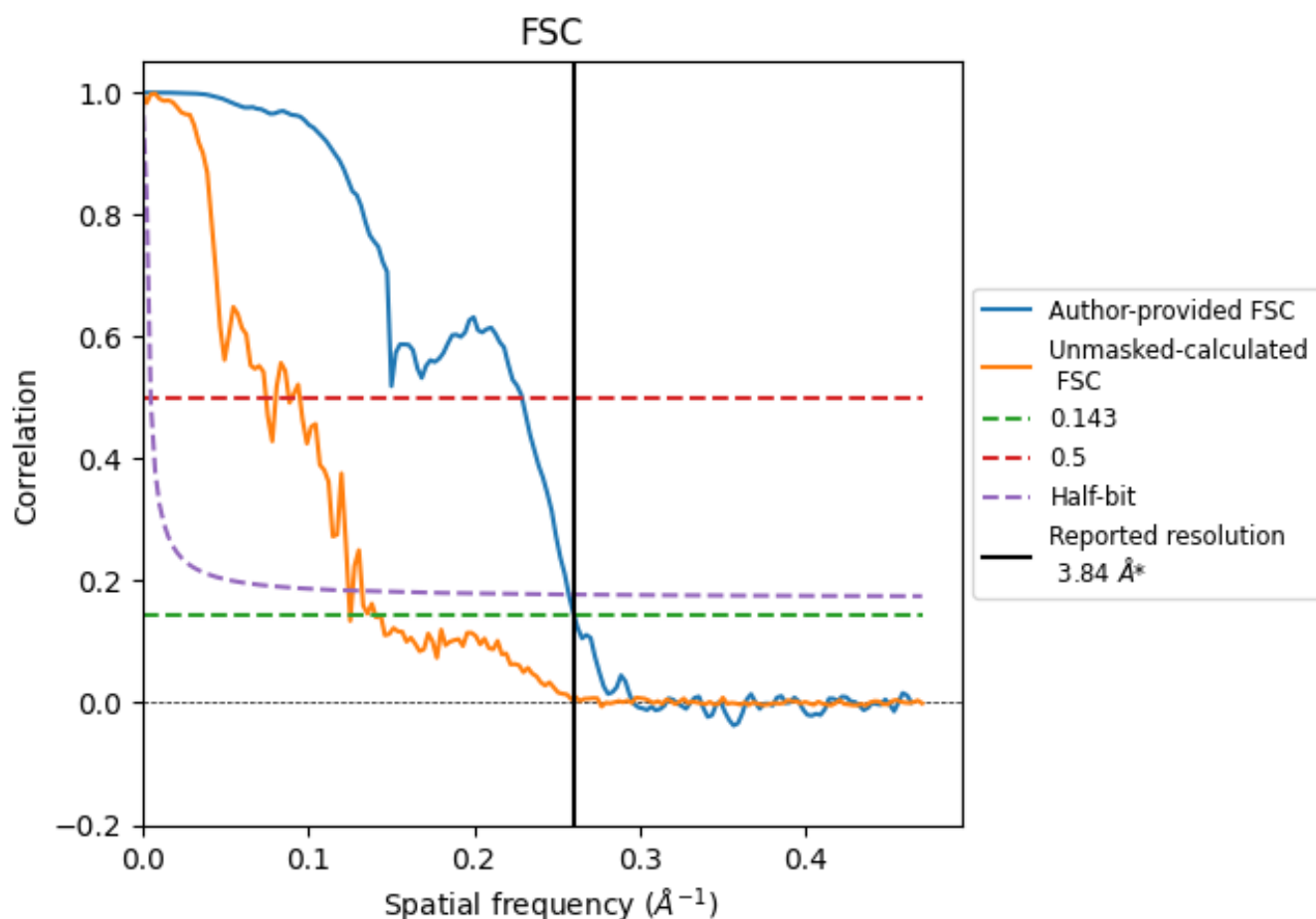


*Reported resolution corresponds to spatial frequency of 0.260 $\text{\AA}^{-1}$

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 0.260 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.84	-	-
Author-provided FSC curve	3.84	4.37	3.89
Unmasked-calculated*	7.99	13.39	8.05

*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 7.99 differs from the reported value 3.84 by more than 10 %

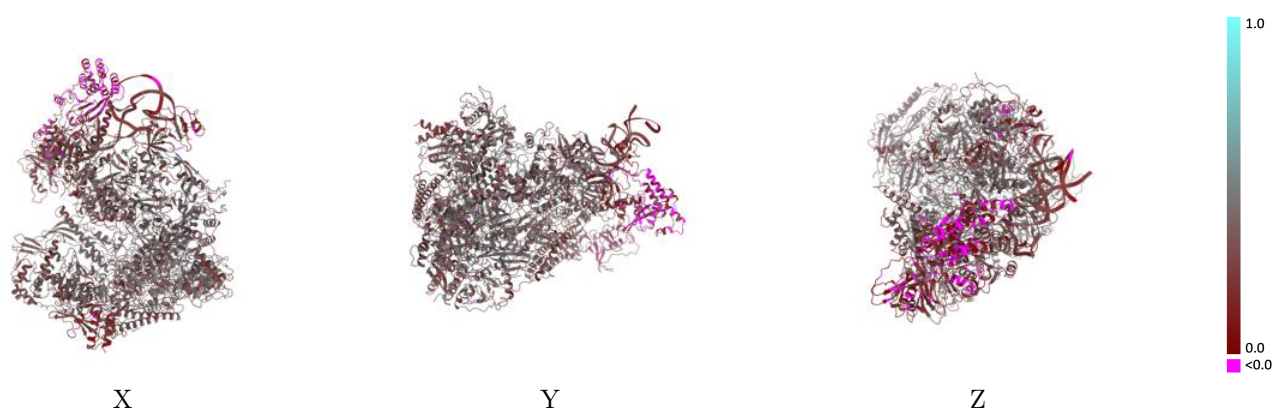
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-16476 and PDB model 8C8H. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

This section was not generated.

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

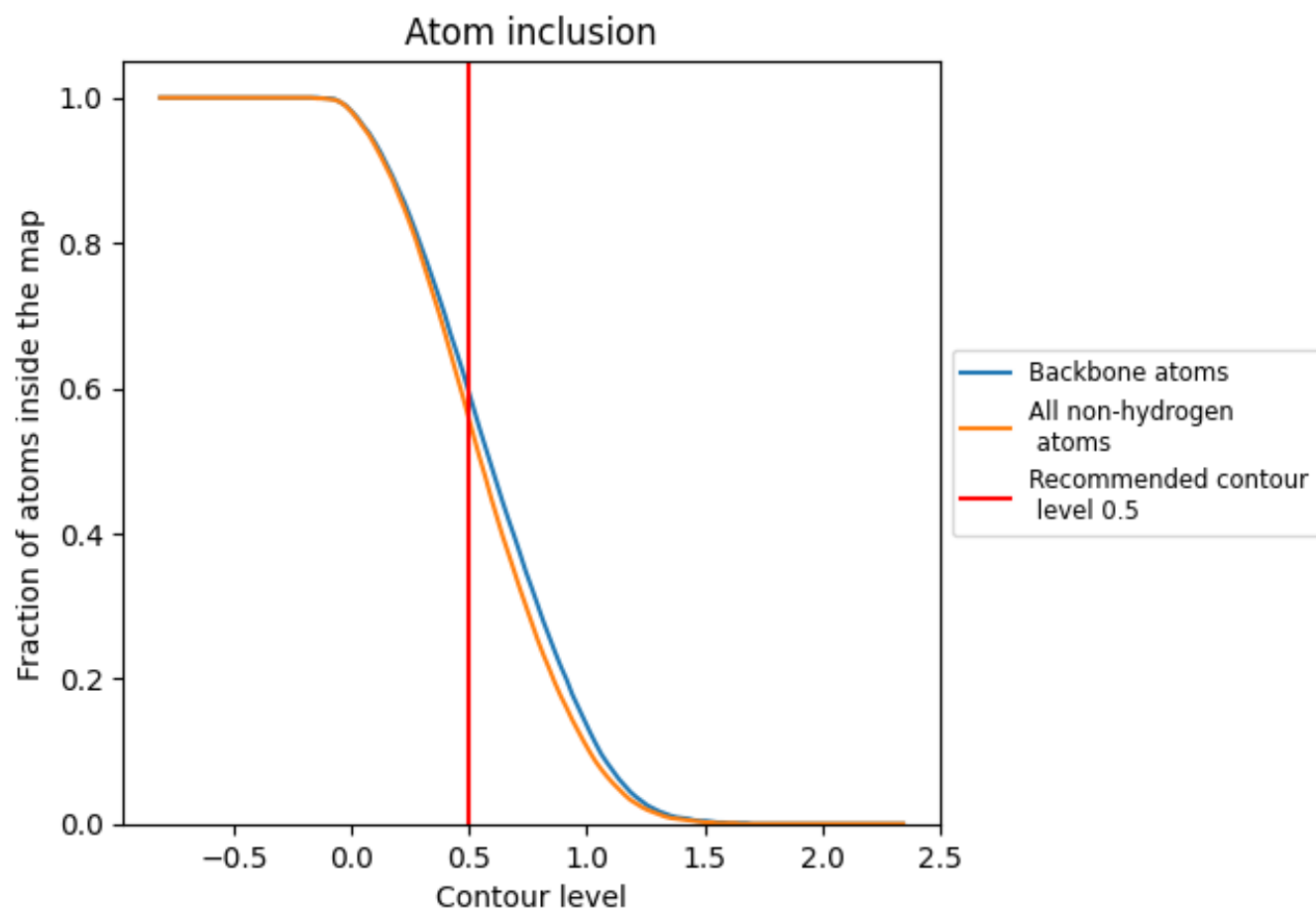


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 56% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5550	 0.3330
A	 0.6760	 0.3790
B	 0.6940	 0.3930
C	 0.6610	 0.3610
E	 0.6870	 0.3790
F	 0.7370	 0.3870
G	 0.6330	 0.3450
I	 0.5730	 0.3320
J	 0.6900	 0.3770
K	 0.0080	 0.1850
Q	 0.0810	 0.1460
R	 0.2580	 0.2560
S	 0.3100	 0.2700
U	 0.5140	 0.2520
Y	 0.1930	 0.1790

