



wwPDB EM Validation Summary Report ⓘ

Jul 27, 2026 – 05:15 PM EDT

PDB ID : 10MT / pdb_000010mt
EMDB ID : EMD-75294
Title : C2 symmetry expanded and subtracted 20S Proteasome, Blm10, Fub1 Complex Halfmer
Authors : Walsh Jr, R.M.; Rawson, S.; Fermin Perez, E.; Venclovaite, U.; Hanna, J.
Deposited on : 2026-01-28
Resolution : 3.70 Å(reported)
Based on initial model : .

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.dev133
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) : 2.50

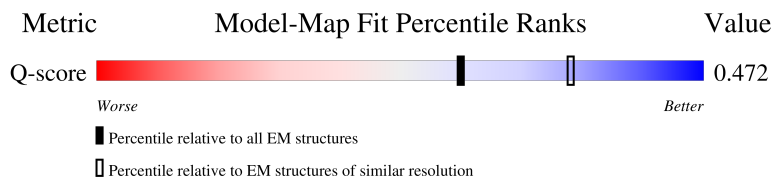
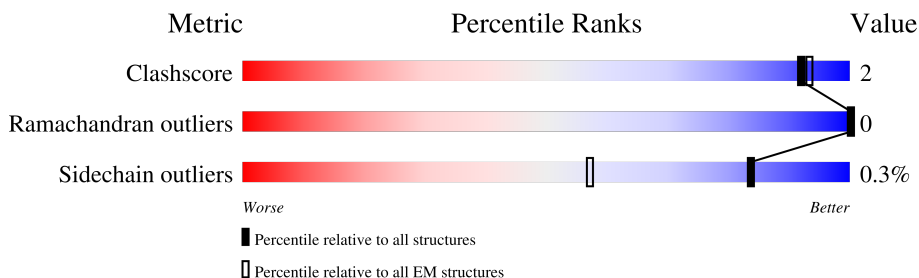
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

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



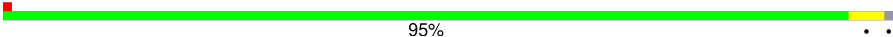
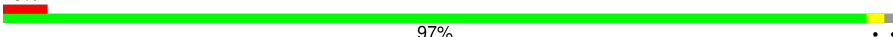
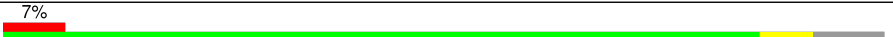
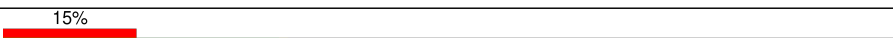
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	252	90% 6%
2	B	250	88% 5% 8%
3	F	234	94% 6%
4	G	288	82% 16%

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Mol	Chain	Length	Quality of chain
5	H	215	
6	I	261	
7	J	205	
8	K	198	
9	L	287	
10	M	241	
11	N	266	
12	C	254	
12	D	254	
13	CA	2167	
14	E	260	
15	a	250	
15	b	250	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 79518 atoms, of which 39677 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 Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	238	Total	C	H	N	O	S	0	0
			3763	1198	1881	316	360	8		

- Molecule 2 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	231	Total	C	H	N	O	S	0	0
			3555	1126	1786	292	348	3		

- Molecule 3 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	F	234	Total	C	H	N	O	S	0	0
			3615	1134	1812	313	351	5		

- Molecule 4 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	G	241	Total	C	H	N	O	S	0	0
			3756	1197	1875	327	353	4		

- Molecule 5 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	H	196	Total	C	H	N	O	S	0	0
			2992	955	1480	250	300	7		

- Molecule 6 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	I	220	Total	C	H	N	O	S	0	0
			3349	1054	1679	291	319	6		

- Molecule 7 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	J	203	Total	C	H	N	O	S	0	0
			3142	1007	1567	257	303	8		

- Molecule 8 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	K	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		

- Molecule 9 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	L	212	Total	C	H	N	O	S	0	0
			3237	1045	1593	280	312	7		

- Molecule 10 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	M	221	Total	C	H	N	O	S	0	0
			3449	1110	1701	301	333	4		

- Molecule 11 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	N	219	Total	C	H	N	O	S	0	0
			3429	1082	1717	294	329	7		

- Molecule 12 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	C	160	Total	C	H	N	O	S	0	0
			2541	790	1286	213	249	3		
12	D	188	Total	C	H	N	O	S	0	0
			2952	915	1483	253	297	4		

- Molecule 13 is a protein called Proteasome activator BLM10.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	CA	1878	Total	C	H	N	O	S	0	0
			30567	9844	15290	2532	2832	69		

There are 24 discrepancies between the modelled and reference sequences:

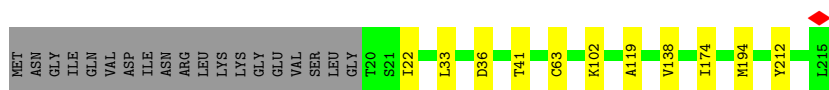
Chain	Residue	Modelled	Actual	Comment	Reference
CA	-23	MET	-	initiating methionine	UNP P43583
CA	-22	HIS	-	expression tag	UNP P43583
CA	-21	HIS	-	expression tag	UNP P43583
CA	-20	HIS	-	expression tag	UNP P43583
CA	-19	HIS	-	expression tag	UNP P43583
CA	-18	HIS	-	expression tag	UNP P43583
CA	-17	HIS	-	expression tag	UNP P43583
CA	-16	HIS	-	expression tag	UNP P43583
CA	-15	HIS	-	expression tag	UNP P43583
CA	-14	HIS	-	expression tag	UNP P43583
CA	-13	HIS	-	expression tag	UNP P43583
CA	-12	HIS	-	expression tag	UNP P43583
CA	-11	HIS	-	expression tag	UNP P43583
CA	-10	THR	-	expression tag	UNP P43583
CA	-9	ALA	-	expression tag	UNP P43583
CA	-8	ASN	-	expression tag	UNP P43583
CA	-7	ASN	-	expression tag	UNP P43583
CA	-6	ASP	-	expression tag	UNP P43583
CA	-5	ASP	-	expression tag	UNP P43583
CA	-4	ASP	-	expression tag	UNP P43583
CA	-3	ILE	-	expression tag	UNP P43583
CA	-2	LYS	-	expression tag	UNP P43583
CA	-1	SER	-	expression tag	UNP P43583
CA	0	PRO	-	expression tag	UNP P43583

- Molecule 14 is a protein called Proteasome subunit alpha type-5.

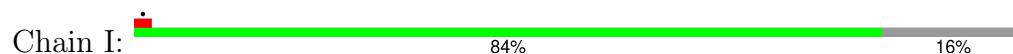
Mol	Chain	Residues	Atoms						AltConf	Trace
14	E	238	Total	C	H	N	O	S	0	0
			3686	1159	1839	310	370	8		

- Molecule 15 is a protein called Silencing boundary-establishment protein FUB1.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	a	81	Total	C	H	N	O	S	0	0
			1177	393	559	101	121	3		
15	b	81	Total	C	H	N	O	S	0	0
			1178	393	560	101	121	3		



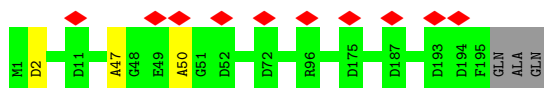
- Molecule 6: Proteasome subunit beta type-2



- Molecule 7: Proteasome subunit beta type-3



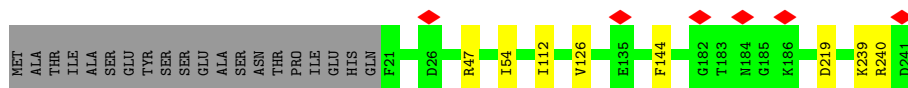
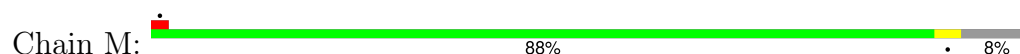
- Molecule 8: Proteasome subunit beta type-4



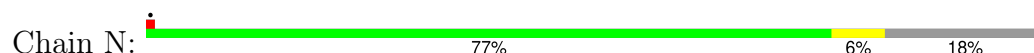
- Molecule 9: Proteasome subunit beta type-5



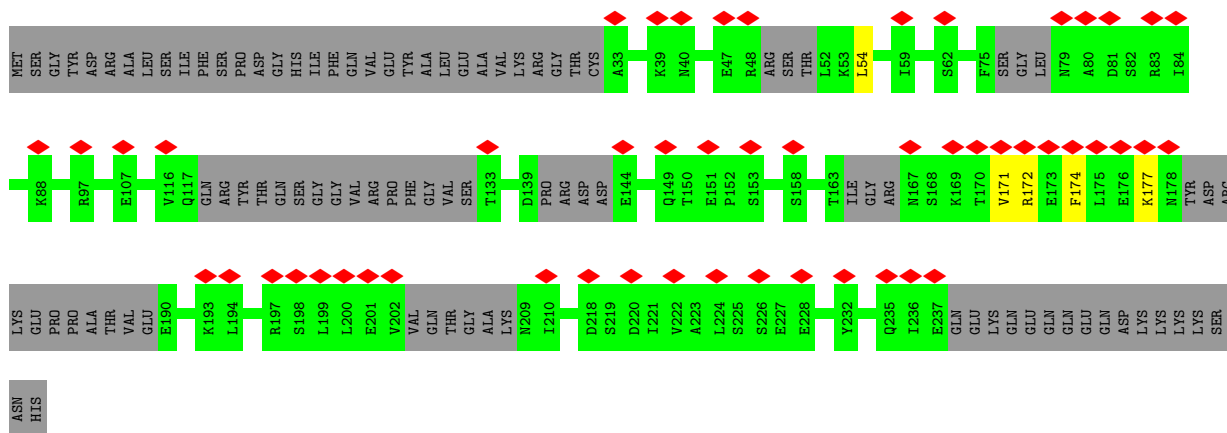
- Molecule 10: Proteasome subunit beta type-6



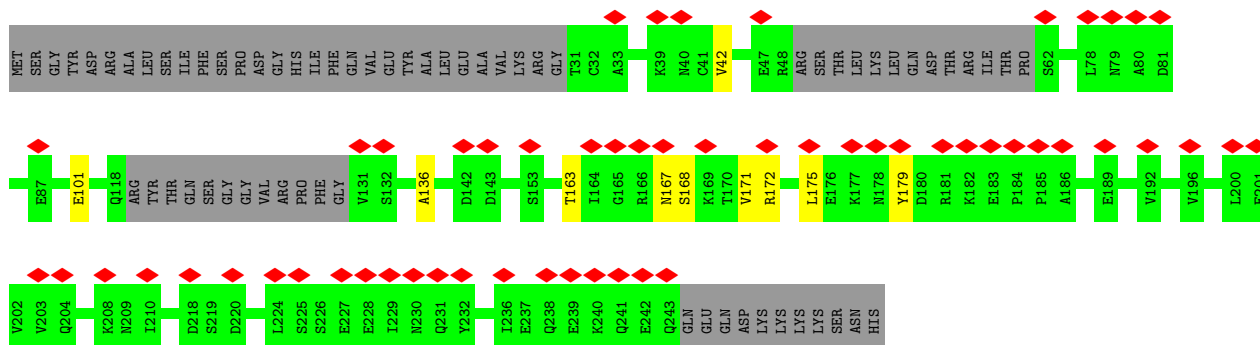
- Molecule 11: Proteasome subunit beta type-7



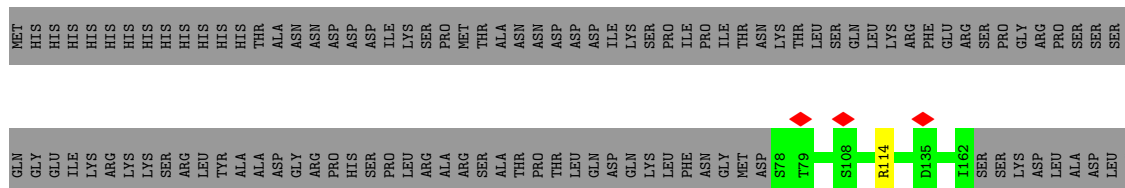
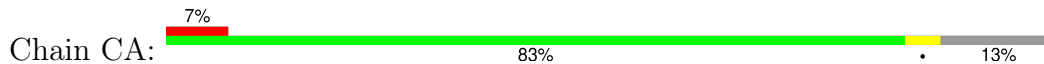
- Molecule 12: Proteasome subunit alpha type-4

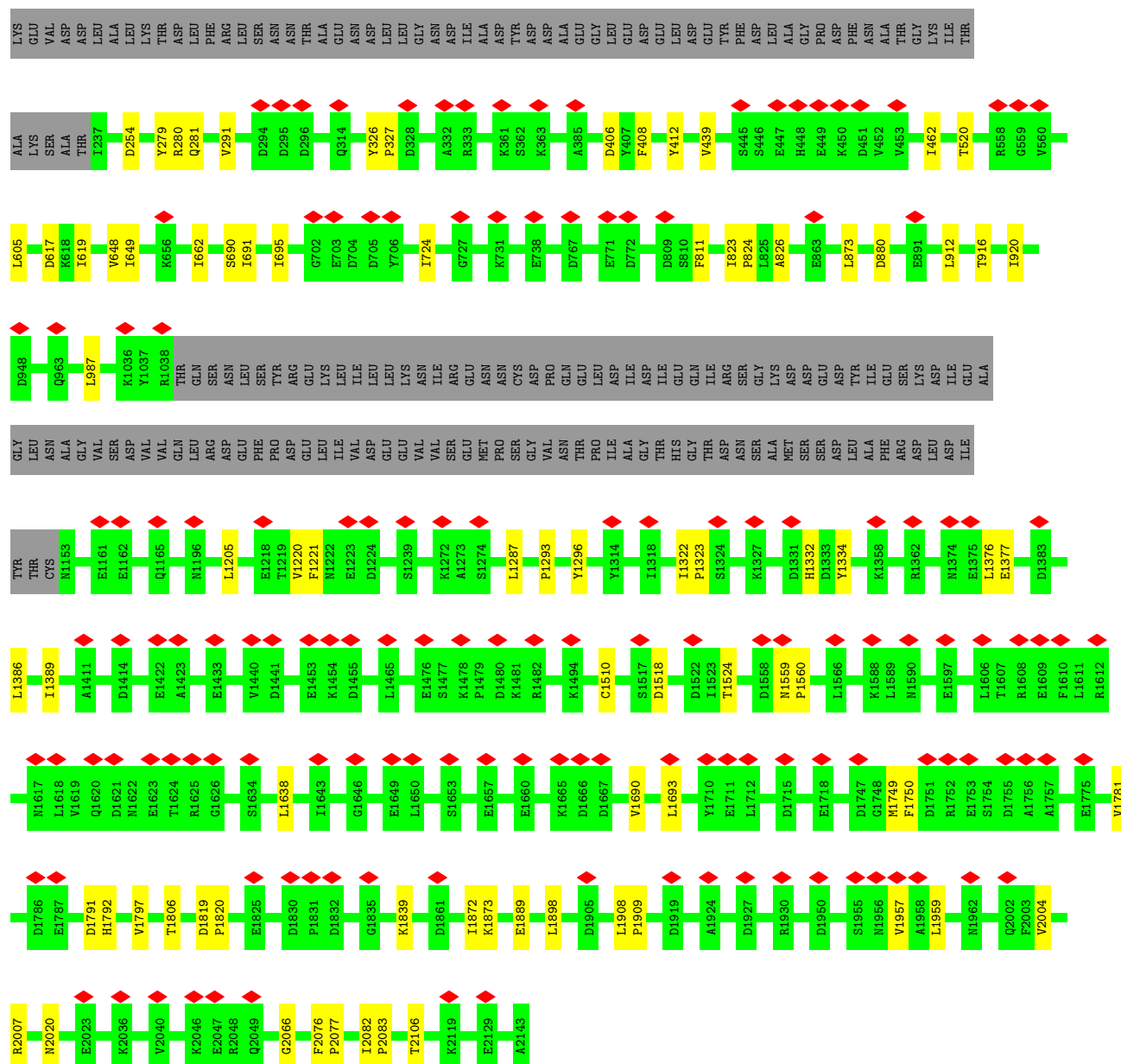


- Molecule 12: Proteasome subunit alpha type-4

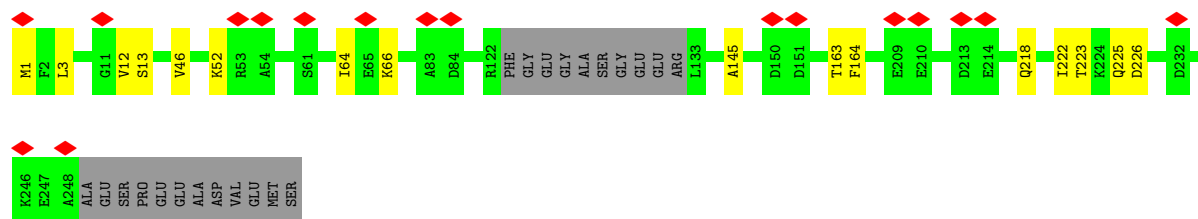
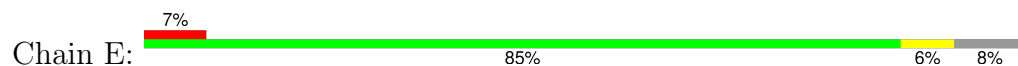


- Molecule 13: Proteasome activator BLM10





- Molecule 14: Proteasome subunit alpha type-5



- Molecule 15: Silencing boundary-establishment protein FUB1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	37111	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.253	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.084	Depositor
Minimum map value	-0.053	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0137	Depositor
Map size (Å)	304.64, 304.64, 304.64	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.19	0/1919	0.34	0/2599
2	B	0.19	0/1802	0.33	0/2440
3	F	0.21	0/1831	0.33	0/2473
4	G	0.19	0/1921	0.33	0/2594
5	H	0.20	0/1541	0.32	0/2087
6	I	0.20	0/1701	0.37	0/2307
7	J	0.20	0/1605	0.35	0/2166
8	K	0.18	0/1589	0.31	0/2142
9	L	0.20	0/1681	0.34	0/2274
10	M	0.20	0/1786	0.37	0/2408
11	N	0.20	0/1741	0.37	0/2364
12	C	0.13	0/1264	0.32	0/1703
12	D	0.16	0/1486	0.37	0/2010
13	CA	0.17	0/15622	0.33	0/21165
14	E	0.19	0/1872	0.34	0/2522
15	a	0.17	0/641	0.33	0/873
15	b	0.14	0/641	0.32	0/873
All	All	0.18	0/40643	0.34	0/55000

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
12	D	0	1
13	CA	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	CA	280	ARG	Sidechain
12	D	172	ARG	Sidechain

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	1882	1881	1881	7	0
2	B	1769	1786	1784	6	0
3	F	1803	1812	1809	10	0
4	G	1881	1875	1873	3	0
5	H	1512	1480	1478	6	0
6	I	1670	1679	1676	0	0
7	J	1575	1567	1566	4	0
8	K	1561	1569	1569	2	0
9	L	1644	1593	1592	12	0
10	M	1748	1701	1700	5	0
11	N	1712	1717	1716	8	0
12	C	1255	1286	1278	3	0
12	D	1469	1483	1479	6	0
13	CA	15277	15290	15281	44	0
14	E	1847	1839	1837	10	0
15	a	618	559	556	0	0
15	b	618	560	556	1	0
All	All	39841	39677	39631	122	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.

The worst 5 of 122 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:A:129:THR:HG22	1:A:129:THR:O	2.00	0.60
11:N:192:VAL:O	11:N:192:VAL:HG13	2.03	0.59
13:CA:1781:VAL:HG12	13:CA:1781:VAL:O	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CA:2076:PHE:HB3	13:CA:2077:PRO:HD3	1.89	0.54
2:B:189:ILE:HD11	2:B:213:ILE:HD11	1.90	0.54

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	236/252 (94%)	233 (99%)	3 (1%)	0	100	100
2	B	229/250 (92%)	226 (99%)	3 (1%)	0	100	100
3	F	232/234 (99%)	228 (98%)	4 (2%)	0	100	100
4	G	239/288 (83%)	236 (99%)	3 (1%)	0	100	100
5	H	194/215 (90%)	188 (97%)	6 (3%)	0	100	100
6	I	218/261 (84%)	210 (96%)	8 (4%)	0	100	100
7	J	201/205 (98%)	196 (98%)	5 (2%)	0	100	100
8	K	193/198 (98%)	191 (99%)	2 (1%)	0	100	100
9	L	210/287 (73%)	206 (98%)	4 (2%)	0	100	100
10	M	219/241 (91%)	211 (96%)	8 (4%)	0	100	100
11	N	217/266 (82%)	210 (97%)	7 (3%)	0	100	100
12	C	144/254 (57%)	144 (100%)	0	0	100	100
12	D	182/254 (72%)	176 (97%)	6 (3%)	0	100	100
13	CA	1872/2167 (86%)	1812 (97%)	60 (3%)	0	100	100
14	E	234/260 (90%)	228 (97%)	6 (3%)	0	100	100
15	a	73/250 (29%)	72 (99%)	1 (1%)	0	100	100
15	b	73/250 (29%)	71 (97%)	2 (3%)	0	100	100
All	All	4966/6132 (81%)	4838 (97%)	128 (3%)	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	204/210 (97%)	203 (100%)	1 (0%)	81	80
2	B	192/209 (92%)	191 (100%)	1 (0%)	81	80
3	F	193/193 (100%)	193 (100%)	0	100	100
4	G	200/239 (84%)	200 (100%)	0	100	100
5	H	162/178 (91%)	161 (99%)	1 (1%)	78	79
6	I	179/214 (84%)	178 (99%)	1 (1%)	78	79
7	J	171/173 (99%)	170 (99%)	1 (1%)	78	79
8	K	173/175 (99%)	173 (100%)	0	100	100
9	L	169/235 (72%)	167 (99%)	2 (1%)	63	72
10	M	184/201 (92%)	184 (100%)	0	100	100
11	N	188/224 (84%)	188 (100%)	0	100	100
12	C	146/226 (65%)	146 (100%)	0	100	100
12	D	169/226 (75%)	169 (100%)	0	100	100
13	CA	1731/1986 (87%)	1728 (100%)	3 (0%)	87	86
14	E	199/215 (93%)	199 (100%)	0	100	100
15	a	64/207 (31%)	64 (100%)	0	100	100
15	b	64/207 (31%)	63 (98%)	1 (2%)	55	68
All	All	4388/5318 (82%)	4377 (100%)	11 (0%)	84	83

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	CA	1518	ASP
13	CA	1524	THR
15	b	127	PRO
13	CA	1791	ASP
7	J	144	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
12	C	167	ASN
13	CA	546	HIS
15	b	195	GLN
12	D	117	GLN
13	CA	146	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

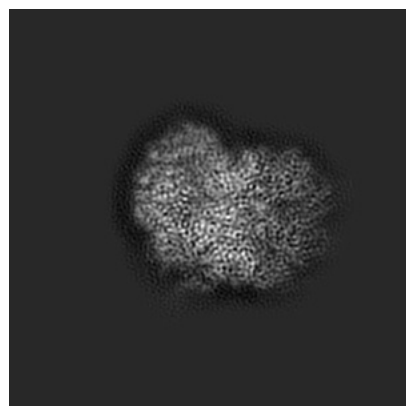
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75294. These allow visual inspection of the internal detail of the map and identification of artifacts.

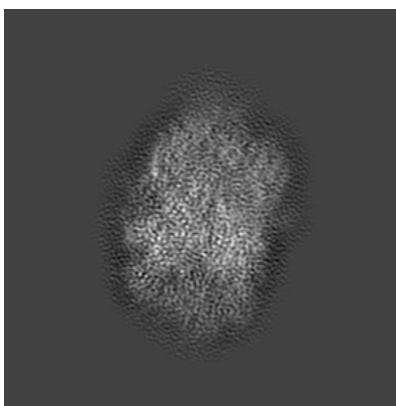
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

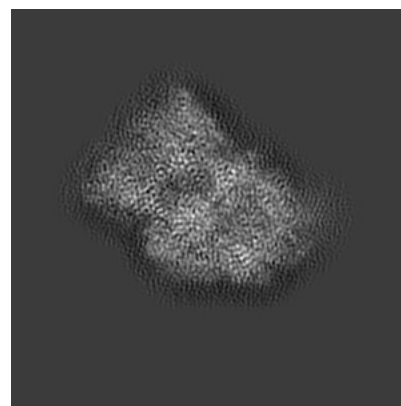
6.1.1 Primary map



X

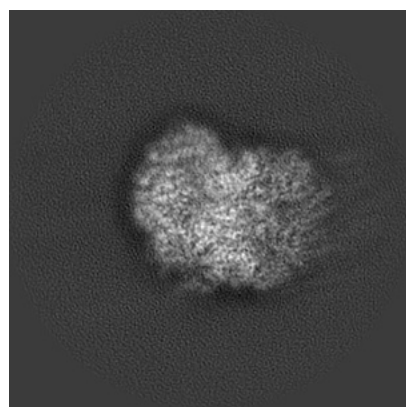


Y

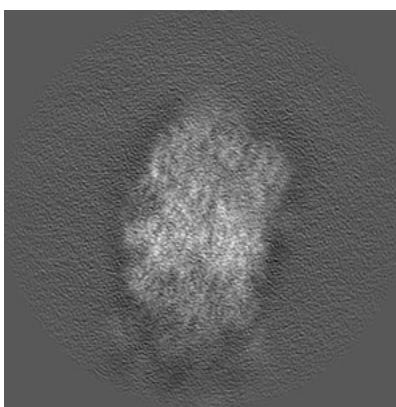


Z

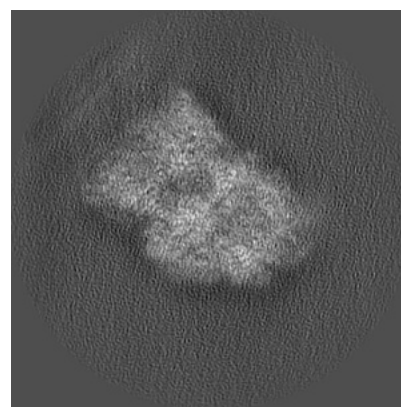
6.1.2 Raw map



X



Y

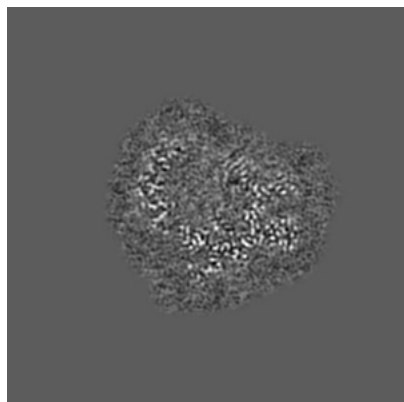


Z

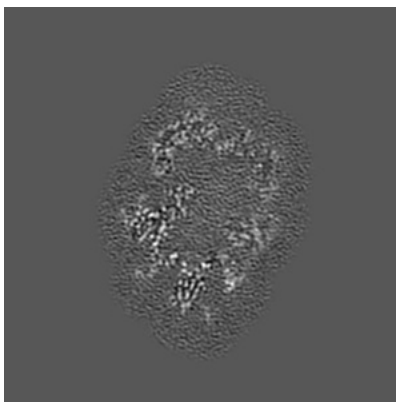
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

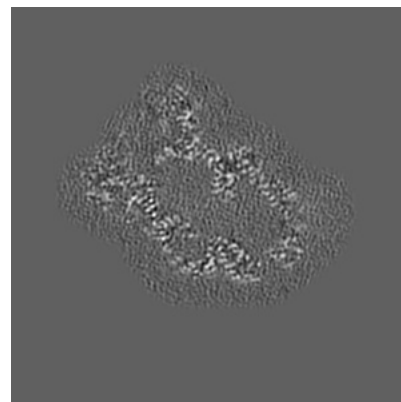
6.2.1 Primary map



X Index: 128

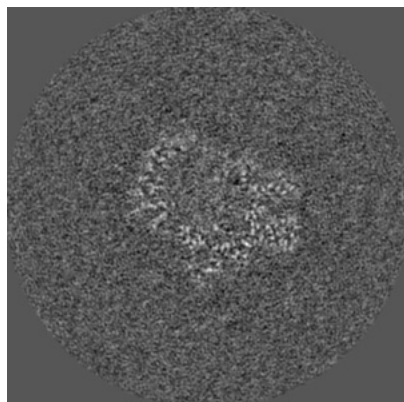


Y Index: 128

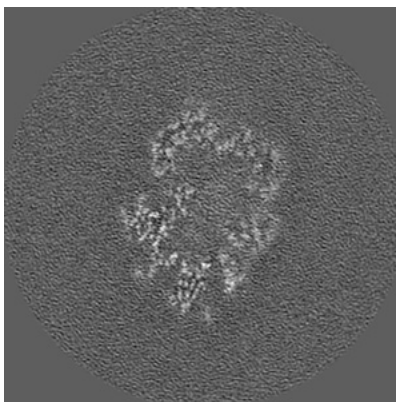


Z Index: 128

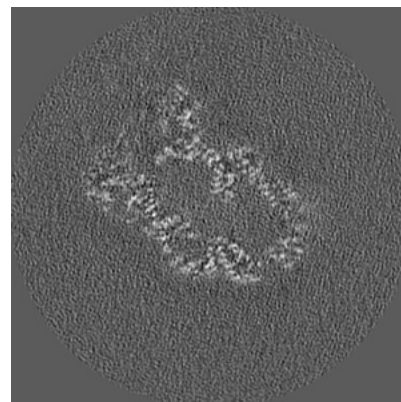
6.2.2 Raw map



X Index: 128



Y Index: 128

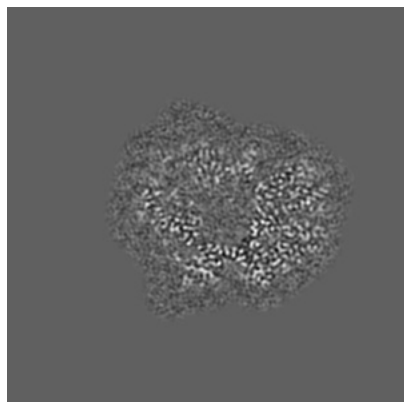


Z Index: 128

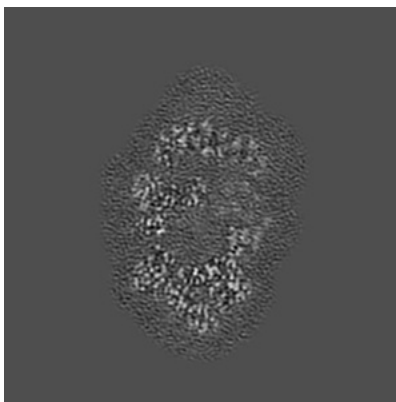
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

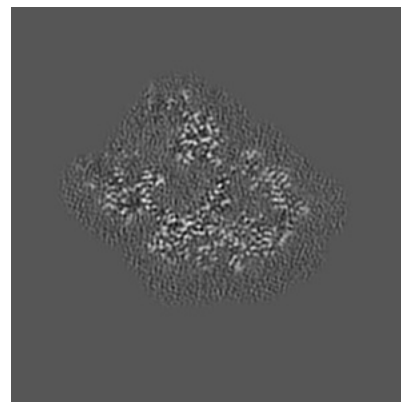
6.3.1 Primary map



X Index: 111

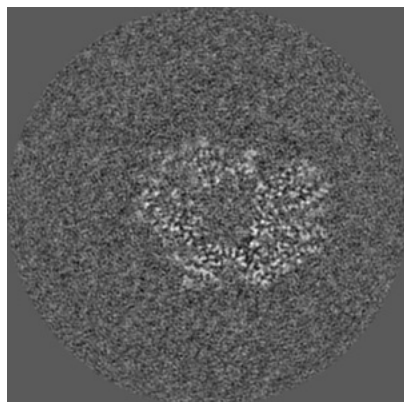


Y Index: 136

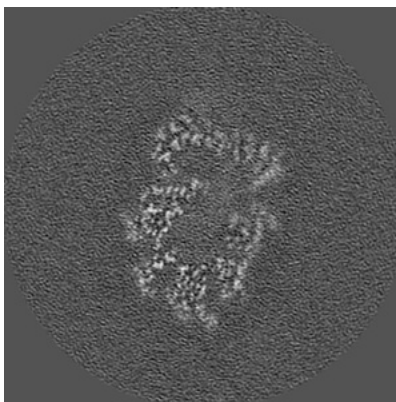


Z Index: 114

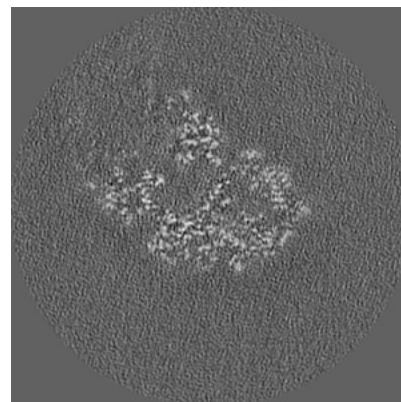
6.3.2 Raw map



X Index: 111



Y Index: 131

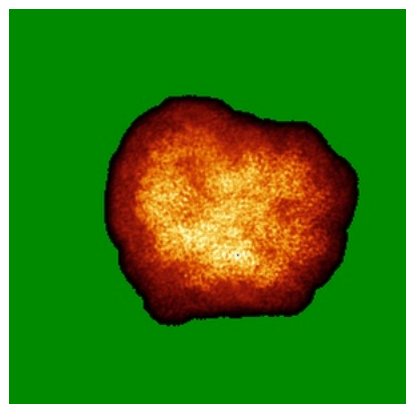


Z Index: 114

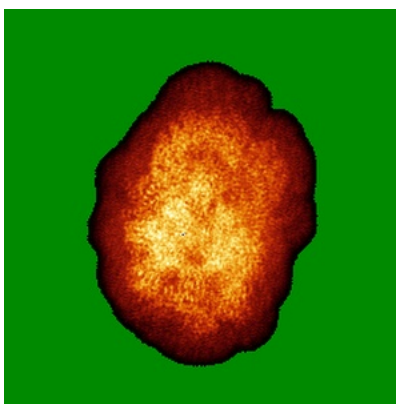
The images above show the largest variance slices of the map in three orthogonal directions.

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

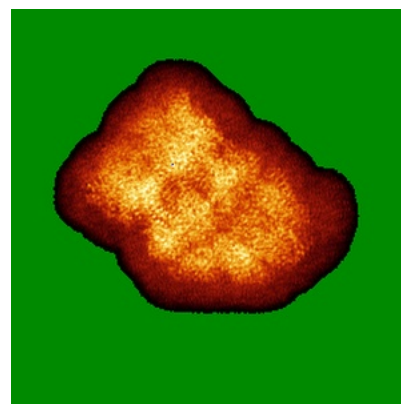
6.4.1 Primary map



X

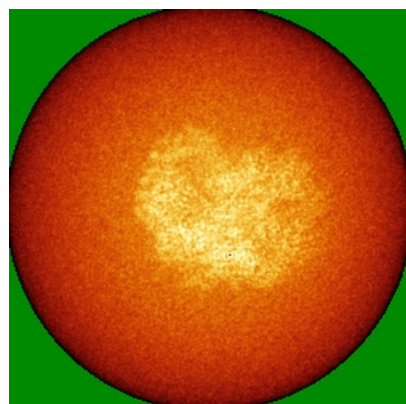


Y

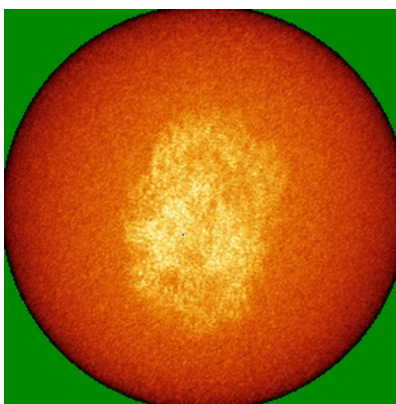


Z

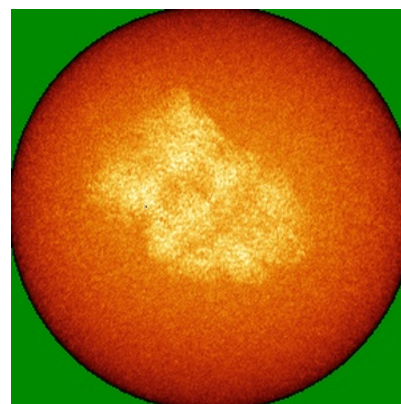
6.4.2 Raw map



X



Y

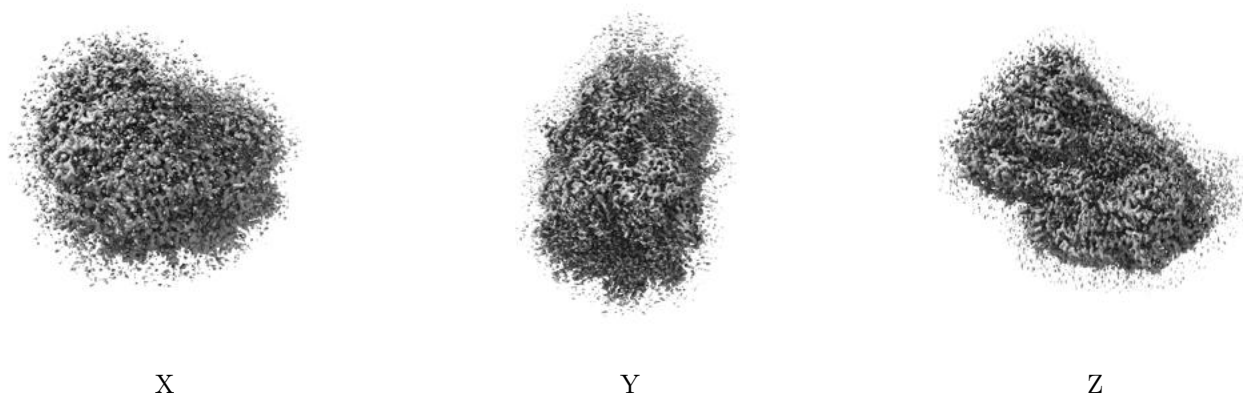


Z

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.

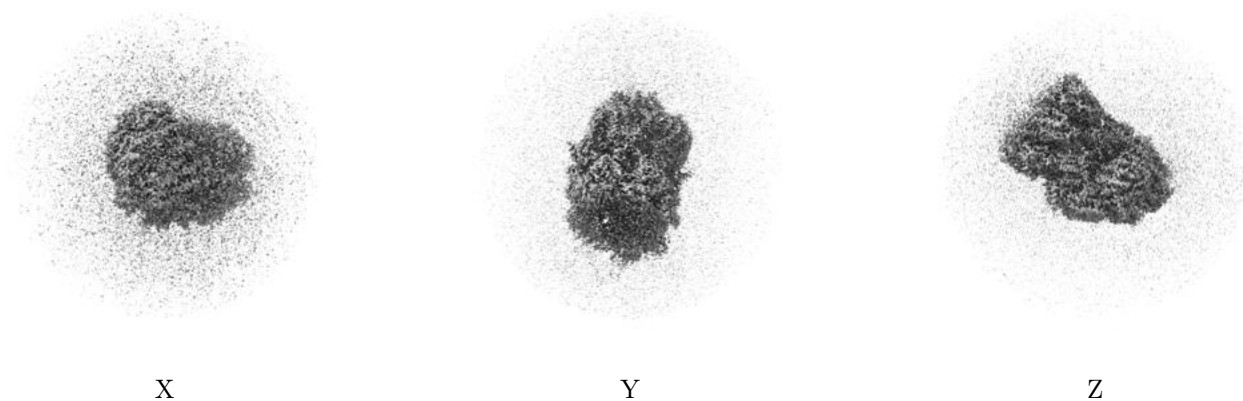
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0137. 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.

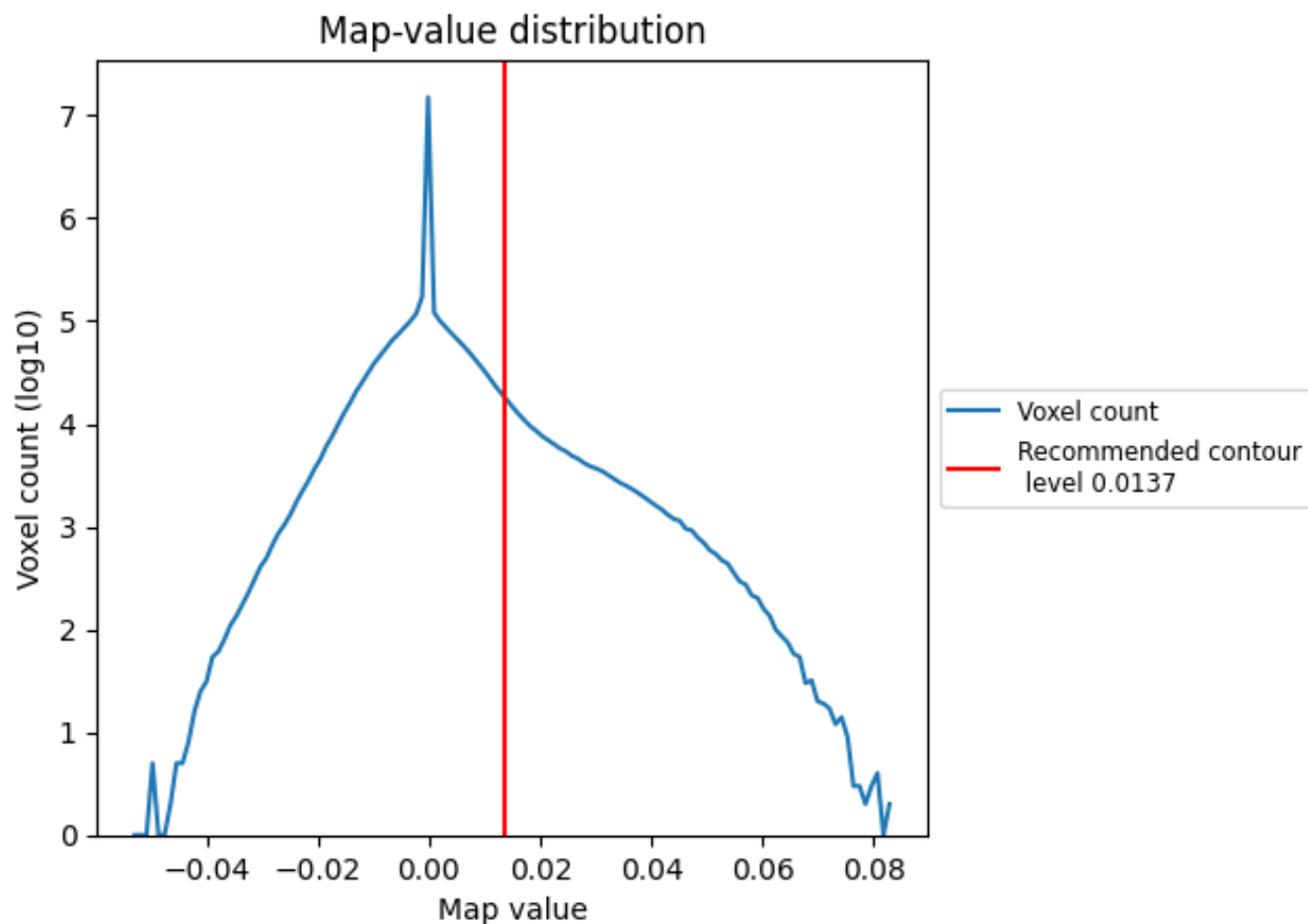
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

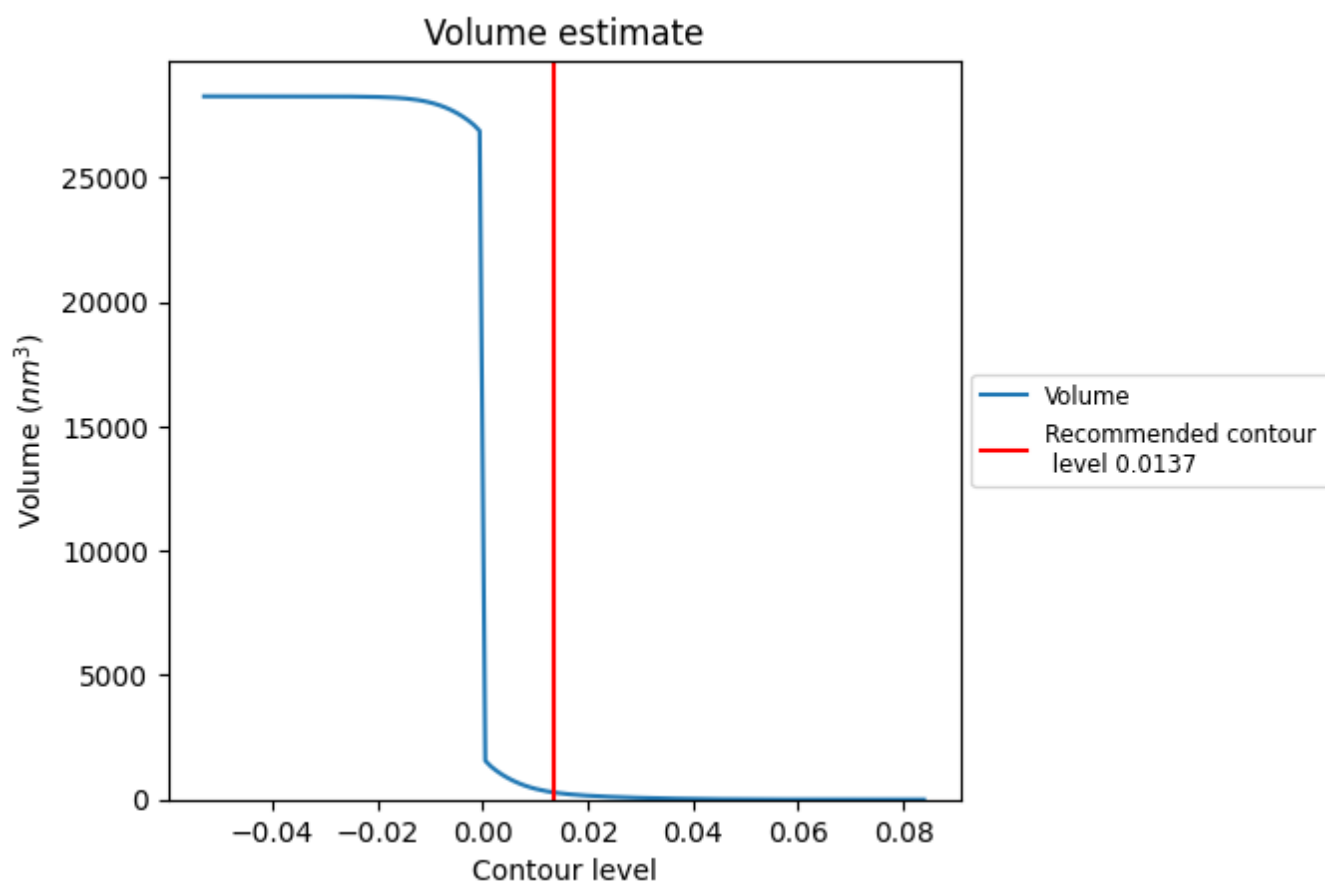
This section contains the results of statistical analysis of the map.

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.

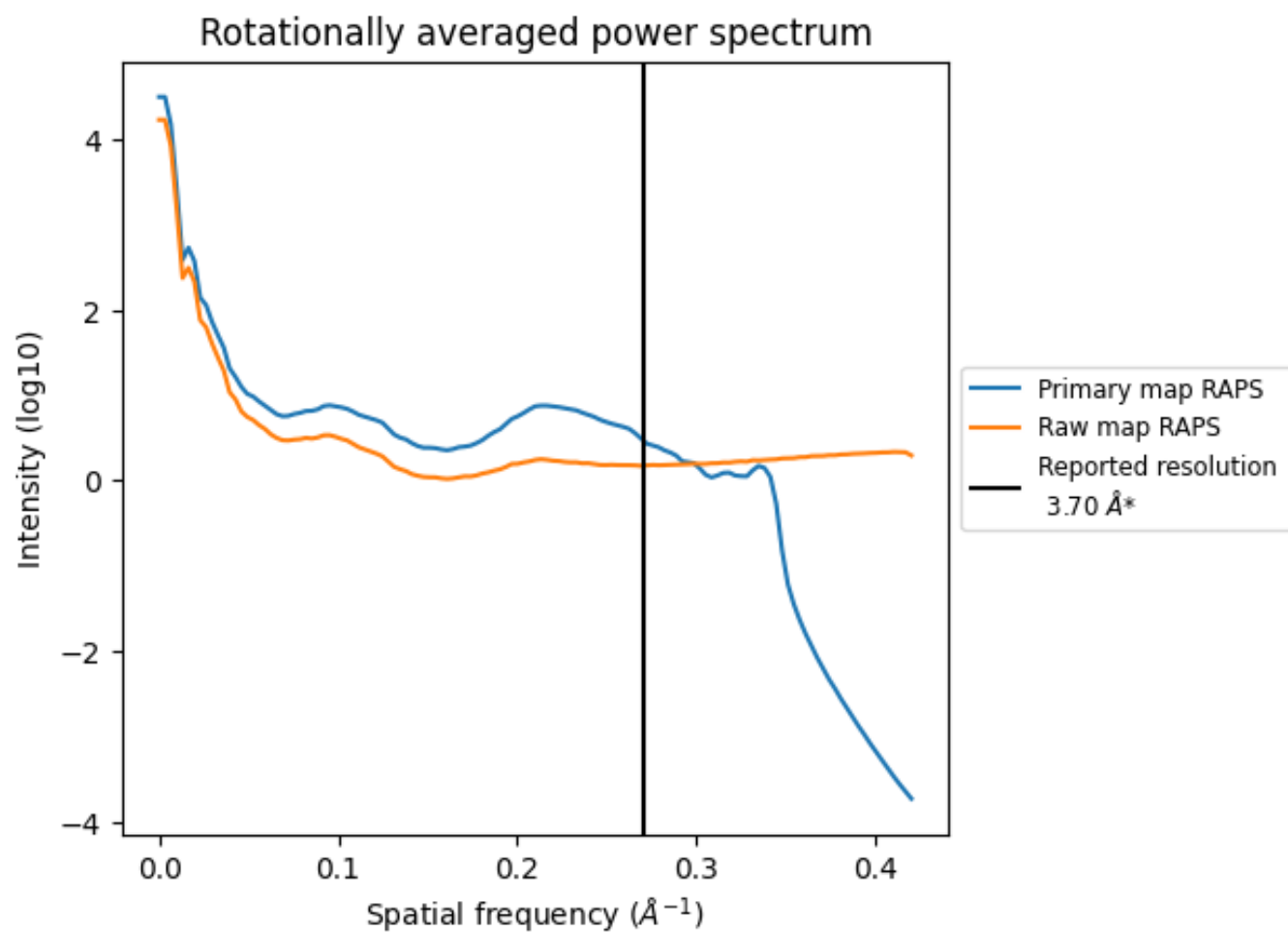
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 283 nm³; this corresponds to an approximate mass of 256 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 ⓘ

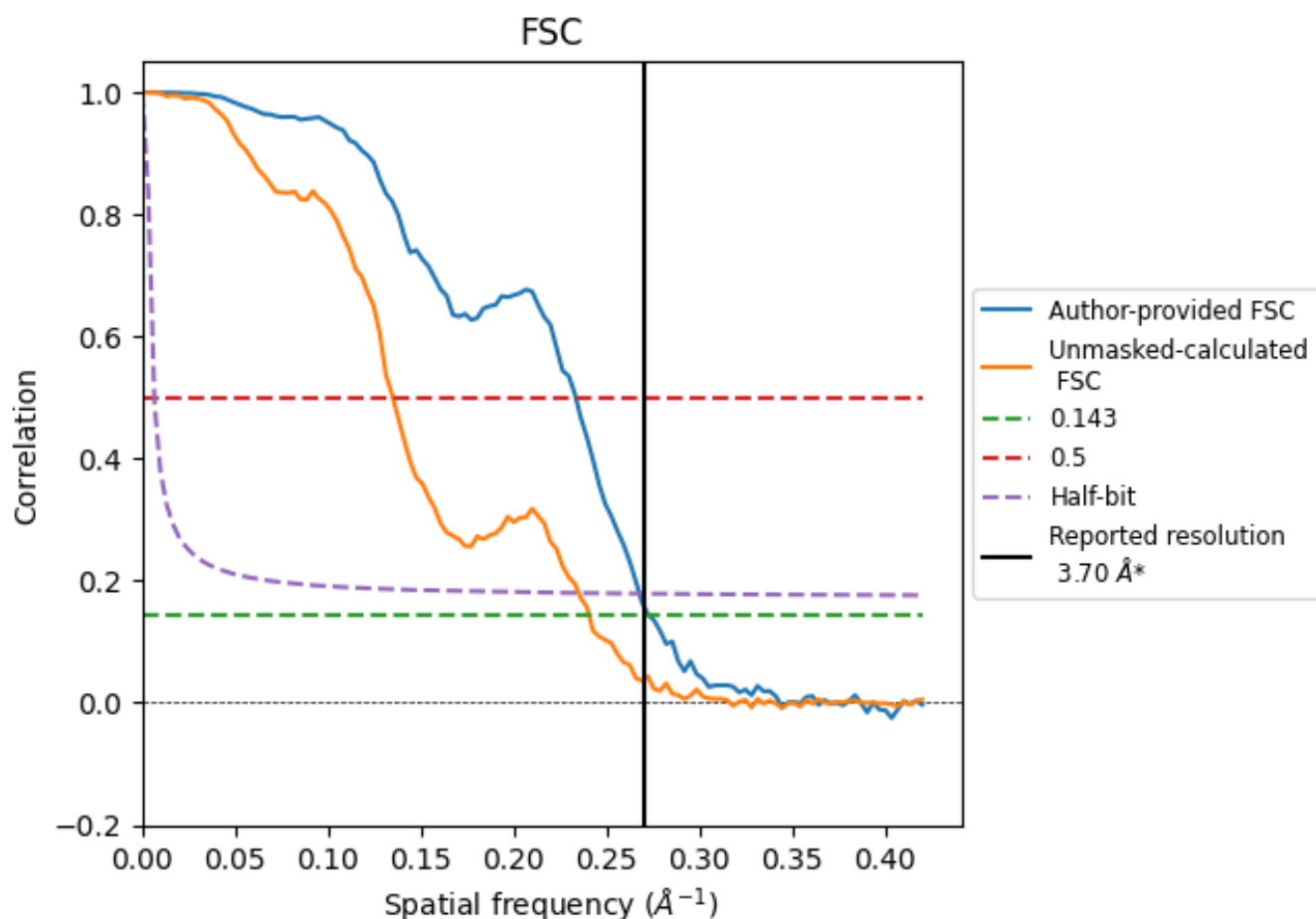


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

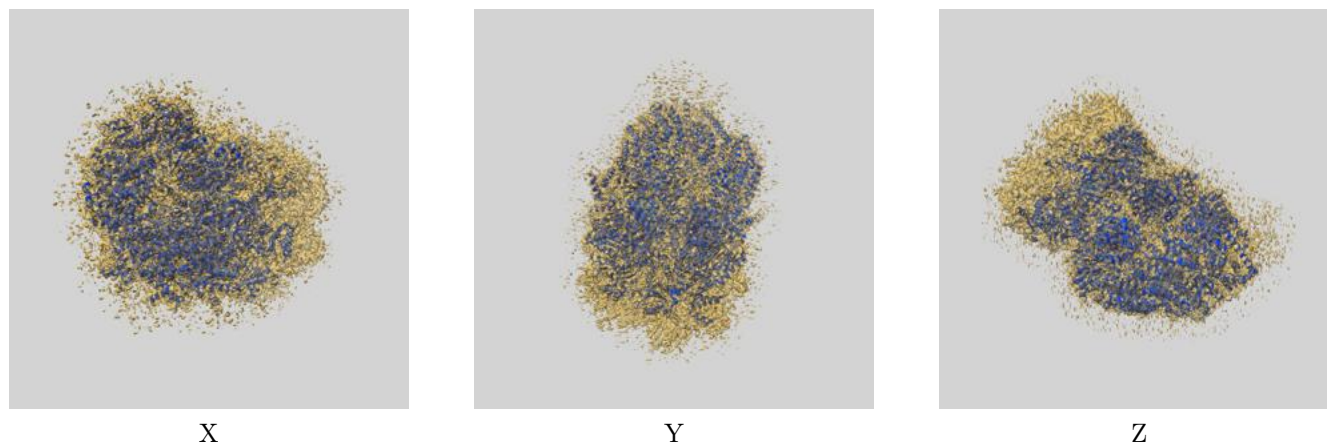
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.66	4.28	3.73
Unmasked-calculated*	4.15	7.41	4.25

*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 4.15 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

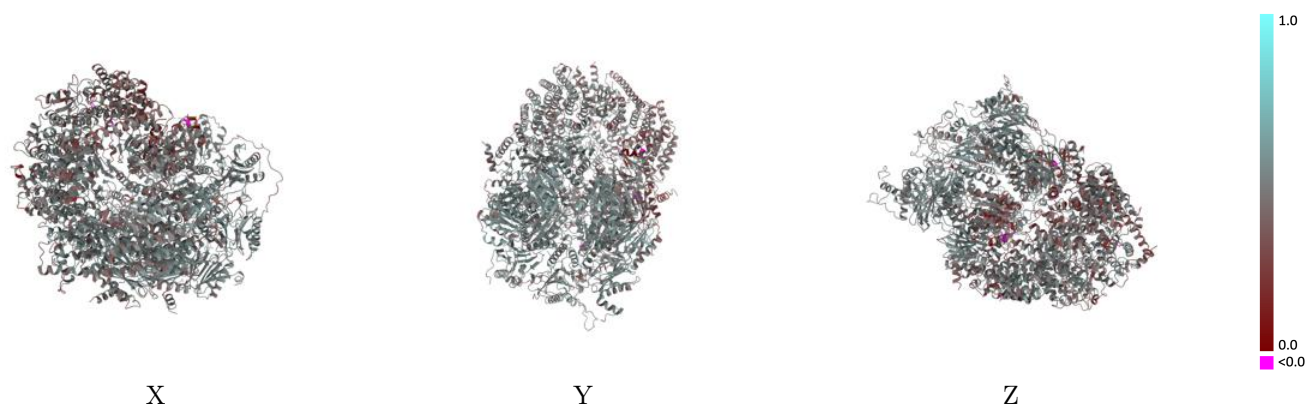
This section contains information regarding the fit between EMDB map EMD-75294 and PDB model 10MT. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



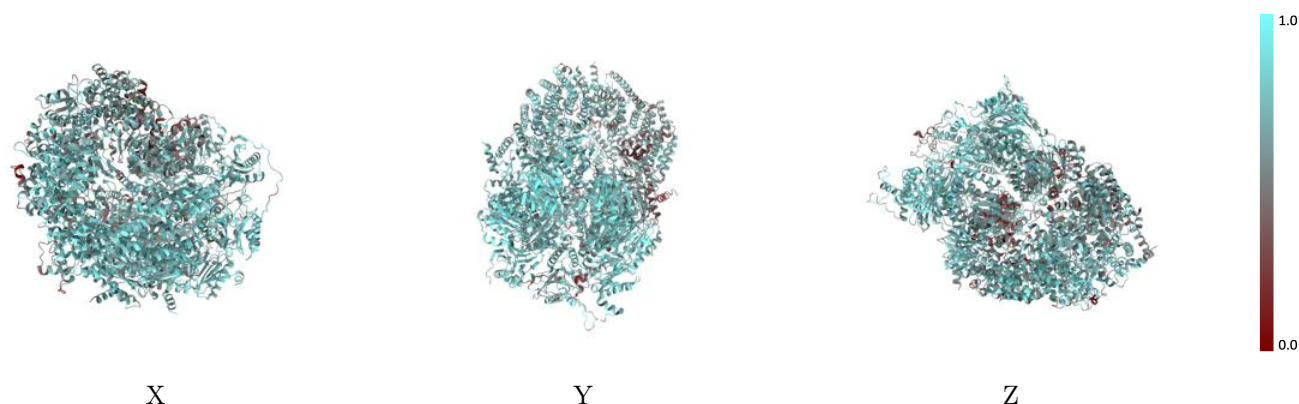
The images above show the 3D surface view of the map at the recommended contour level 0.0137 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



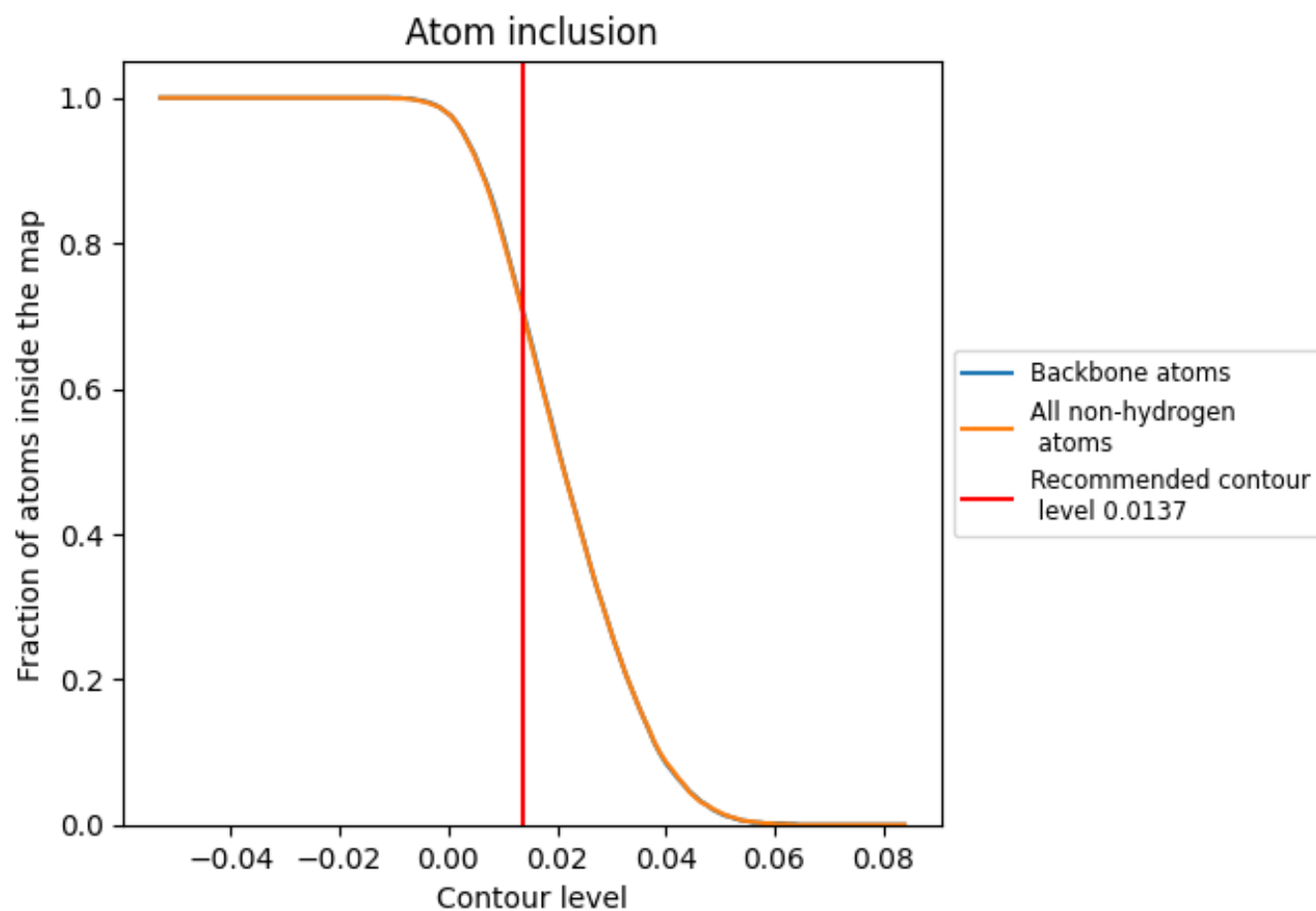
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0137).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 70% 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 (0.0137) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7050	0.4720
A	0.7560	0.4950
B	0.7470	0.4900
C	0.5020	0.3620
CA	0.6940	0.4540
D	0.5130	0.3520
E	0.7090	0.4730
F	0.7950	0.5120
G	0.7670	0.5020
H	0.7950	0.5160
I	0.7800	0.5090
J	0.7660	0.5130
K	0.7330	0.4840
L	0.7790	0.5100
M	0.7750	0.5110
N	0.7810	0.5150
a	0.6650	0.4730
b	0.4740	0.4340

1.0

0.0

<0.0