



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:35 AM UTC

PDB ID : 8U7U / pdb_00008u7u
EMDB ID : EMD-41993
Title : Proteasome 20S Core Particle from Beta 3 D205 deletion
Authors : Walsh Jr., R.M.; Rawson, S.; Velez, B.; Blickling, M.; Razi, A.; Hanna, J.
Deposited on : 2023-09-15
Resolution : 2.16 Å(reported)
Based on initial model : 8T08

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

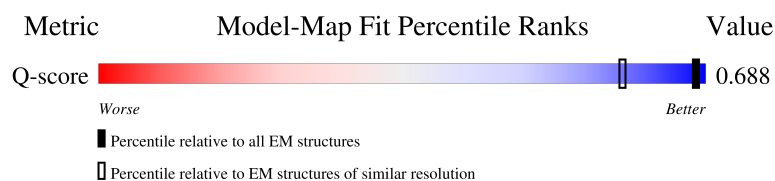
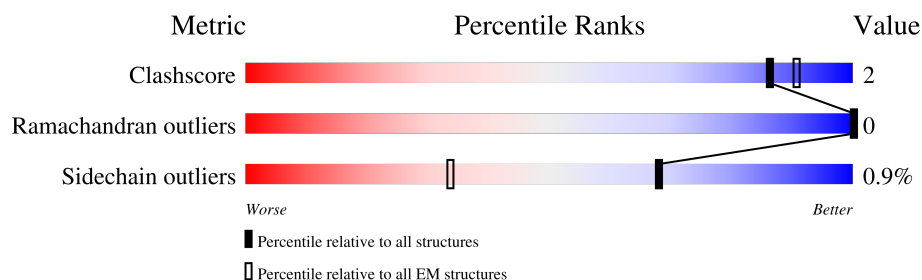
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

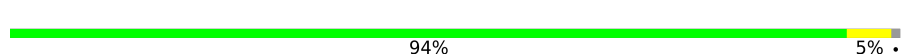
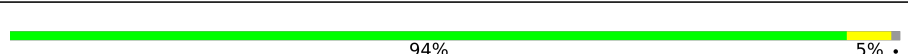
The reported resolution of this entry is 2.16 Å.

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.



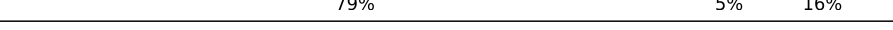
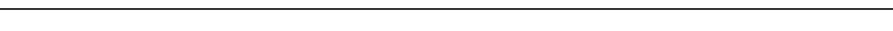
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2609 (1.67 - 2.66)

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	E	260	
1	S	260	
2	B	250	
2	P	250	

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Mol	Chain	Length	Quality of chain
3	H	215	 87% 9%
3	V	215	 87% 5% 9%
4	F	234	 91% 7%
4	T	234	 92% 6%
5	1	241	 86% 5% 9%
5	M	241	 87% 5% 9%
6	K	198	 90% 7% ..
6	Y	198	 89% 8% ..
7	G	288	 81% 15%
7	U	288	 81% 15%
8	2	266	 81% 5% 13%
8	N	266	 80% 6% 13%
9	I	261	 80% 5% 16%
9	W	261	 79% 5% 16%
10	L	287	 67% 5% 27%
10	Z	287	 67% 6% 27%
11	C	258	 88% 5% 7%
11	Q	258	 88% 5% 7%
12	A	252	 92% 5%
12	O	252	 90% 5%
13	J	204	 87% 7% 6%
13	X	204	 87% 7% 6%
14	D	254	 81% 7% 11%
14	R	254	 83% 6% 11%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 97056 atoms, of which 48422 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-5.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	E	237	Total	C	H	N	O	S	0	0
			3637	1147	1808	306	369	7		
1	S	237	Total	C	H	N	O	S	0	0
			3637	1147	1808	306	369	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	248	Total	C	H	N	O	S	0	0
			3811	1210	1911	313	374	3		
2	P	248	Total	C	H	N	O	S	0	0
			3811	1210	1911	313	374	3		

- Molecule 3 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	H	196	Total	C	H	N	O	S	0	0
			2991	955	1479	250	300	7		
3	V	196	Total	C	H	N	O	S	0	0
			2991	955	1479	250	300	7		

- Molecule 4 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	F	231	Total	C	H	N	O	S	0	0
			3550	1114	1777	307	348	4		
4	T	231	Total	C	H	N	O	S	0	0
			3550	1114	1777	307	348	4		

- Molecule 5 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	M	220	Total	C	H	N	O	S	0	0
			3436	1106	1697	300	329	4		
5	1	220	Total	C	H	N	O	S	0	0
			3436	1106	1697	300	329	4		

- Molecule 6 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	K	193	Total	C	H	N	O	S	0	0
			3098	979	1556	262	295	6		
6	Y	193	Total	C	H	N	O	S	0	0
			3098	979	1556	262	295	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	244	Total	C	H	N	O	S	0	0
			3784	1205	1888	330	357	4		
7	U	244	Total	C	H	N	O	S	0	0
			3784	1205	1888	330	357	4		

- Molecule 8 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	N	231	Total	C	H	N	O	S	0	0
			3620	1144	1812	310	347	7		
8	2	231	Total	C	H	N	O	S	0	0
			3620	1144	1812	310	347	7		

- Molecule 9 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	220	Total	C	H	N	O	S	0	0
			3347	1054	1677	291	319	6		
9	W	220	Total	C	H	N	O	S	0	0
			3347	1054	1677	291	319	6		

- Molecule 10 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	L	210	Total	C	H	N	O	S	0	0
			3210	1037	1579	278	309	7		

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Mol	Chain	Residues	Atoms						AltConf	Trace
10	Z	210	Total	C	H	N	O	S	0	0
			3210	1037	1579	278	309	7		

- Molecule 11 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	C	239	Total	C	H	N	O	S	0	0
			3756	1186	1881	315	371	3		
11	Q	239	Total	C	H	N	O	S	0	0
			3756	1186	1881	315	371	3		

- Molecule 12 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	A	239	Total	C	H	N	O	S	0	0
			3781	1203	1890	318	362	8		
12	O	239	Total	C	H	N	O	S	0	0
			3781	1203	1890	318	362	8		

- Molecule 13 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	J	192	Total	C	H	N	O	S	0	0
			2979	953	1490	245	284	7		
13	X	192	Total	C	H	N	O	S	0	0
			2979	953	1490	245	284	7		

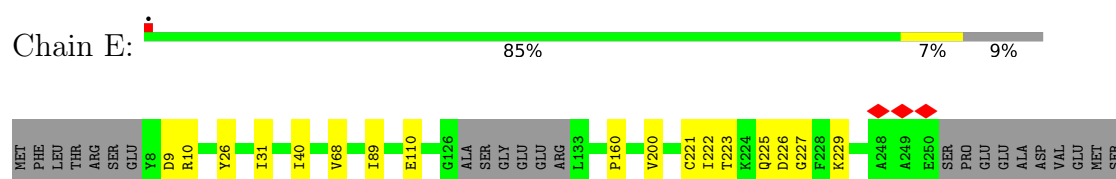
- Molecule 14 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	D	225	Total	C	H	N	O	S	0	0
			3528	1106	1766	303	349	4		
14	R	225	Total	C	H	N	O	S	0	0
			3528	1106	1766	303	349	4		

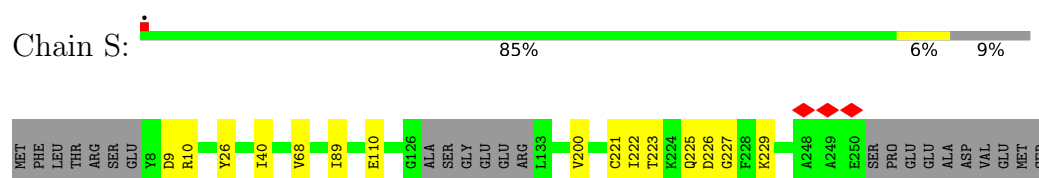
3 Residue-property plots

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.

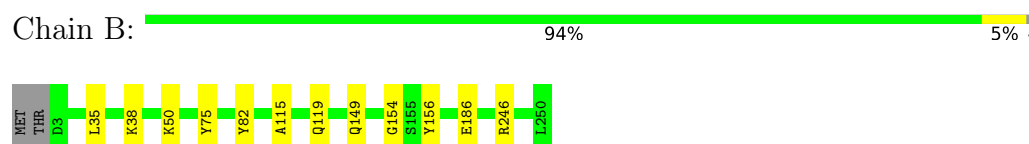
- Molecule 1: Proteasome subunit alpha type-5



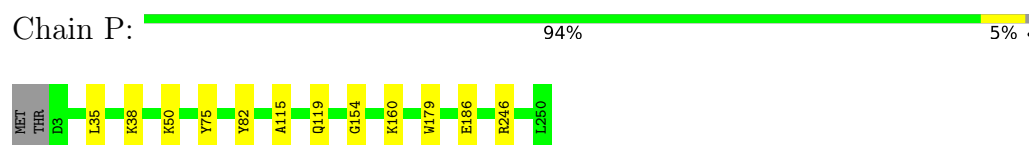
- Molecule 1: Proteasome subunit alpha type-5



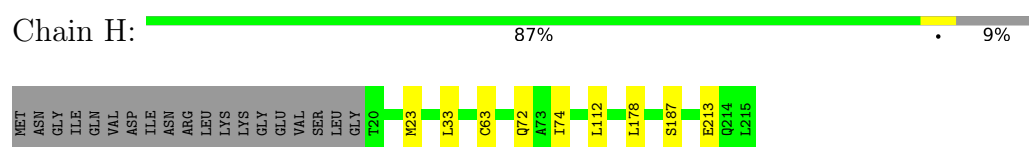
- Molecule 2: Proteasome subunit alpha type-2



- Molecule 2: Proteasome subunit alpha type-2



- Molecule 3: Proteasome subunit beta type-1



- Molecule 3: Proteasome subunit beta type-1

Chain V:  87% 5% 9%



- Molecule 4: Proteasome subunit alpha type-6

Chain F:  91% 7% .



- Molecule 4: Proteasome subunit alpha type-6

Chain T:  92% 6% .



- Molecule 5: Proteasome subunit beta type-6

Chain M:  87% 5% 9%



- Molecule 5: Proteasome subunit beta type-6

Chain 1:  86% 5% 9%



- Molecule 6: Proteasome subunit beta type-4

Chain K:  90% 7% . .

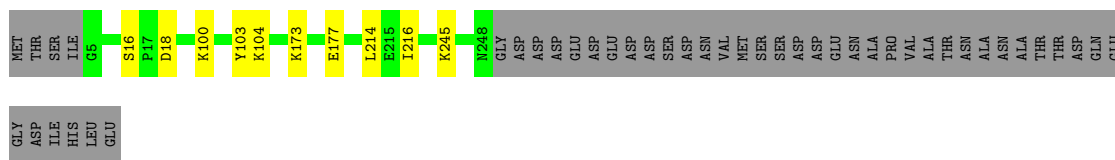


- Molecule 6: Proteasome subunit beta type-4

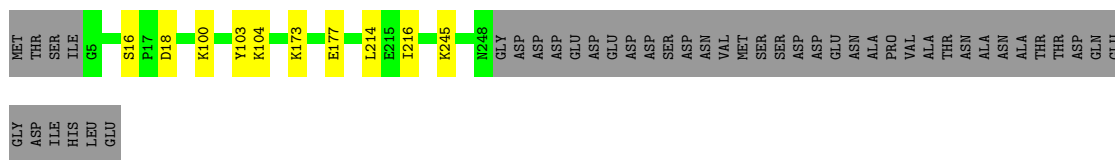
Chain Y:  89% 8% . .



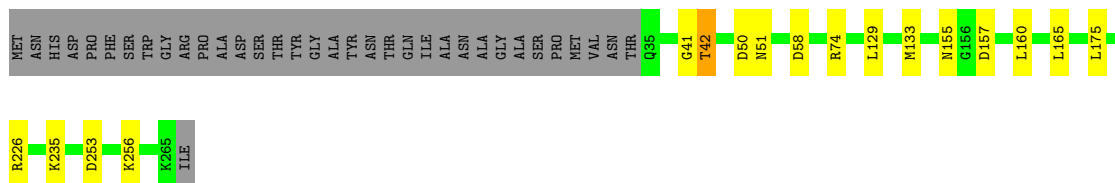
- Molecule 7: Proteasome subunit alpha type-7



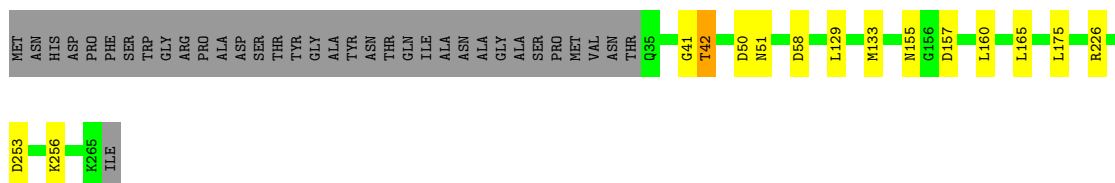
- Molecule 7: Proteasome subunit alpha type-7



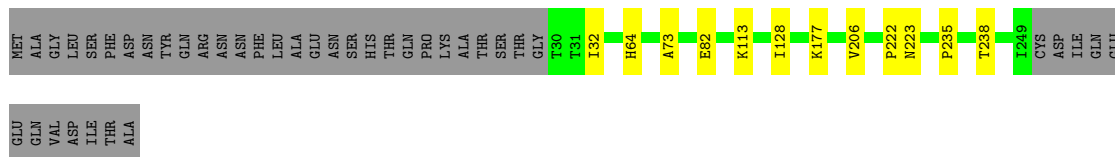
- Molecule 8: Proteasome subunit beta type-7



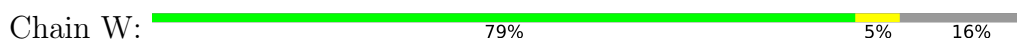
- Molecule 8: Proteasome subunit beta type-7

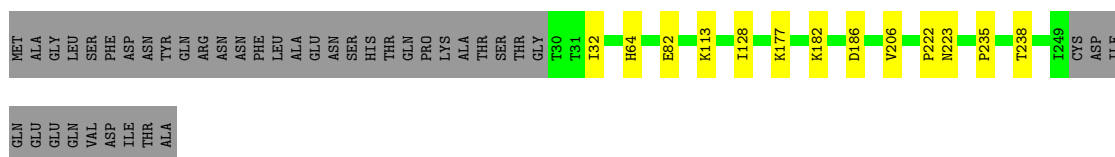


- Molecule 9: Proteasome subunit beta type-2

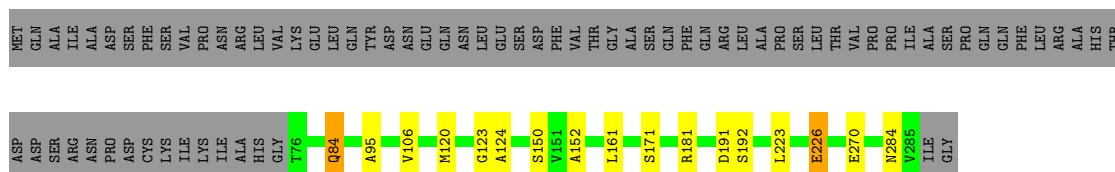


- Molecule 9: Proteasome subunit beta type-2

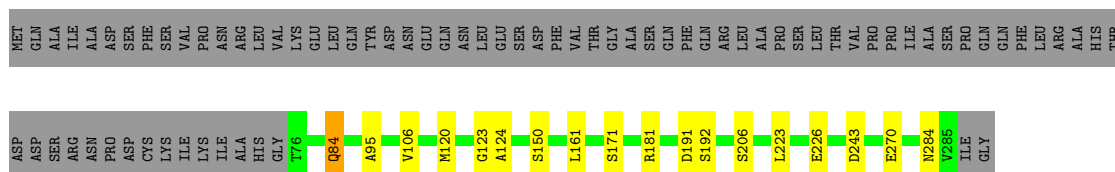




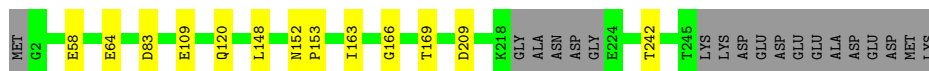
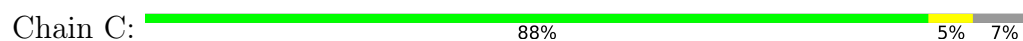
• Molecule 10: Proteasome subunit beta type-5



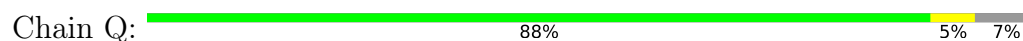
• Molecule 10: Proteasome subunit beta type-5



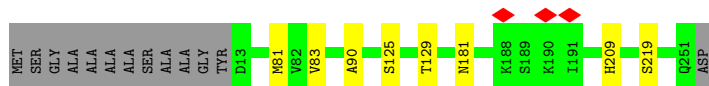
• Molecule 11: Proteasome subunit alpha type-3



• Molecule 11: Proteasome subunit alpha type-3



• Molecule 12: Proteasome subunit alpha type-1



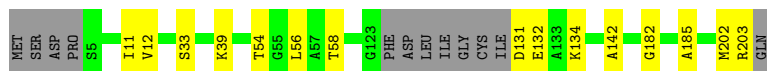
• Molecule 12: Proteasome subunit alpha type-1





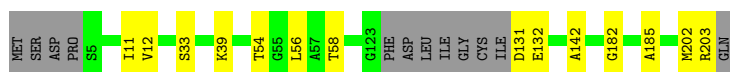
- Molecule 13: Proteasome subunit beta type-3

Chain J: 87% 7% 6%



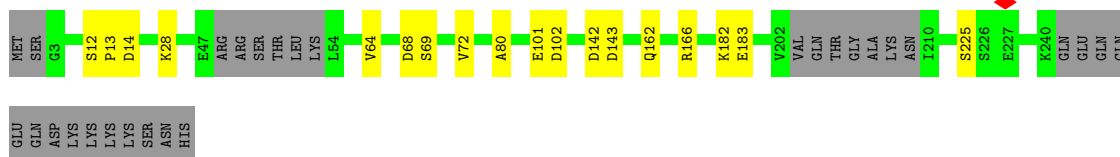
- Molecule 13: Proteasome subunit beta type-3

Chain X: 87% 7% 6%



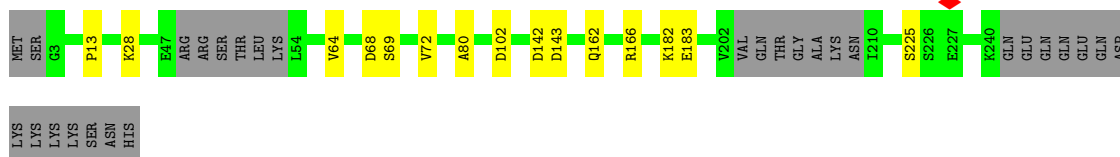
- Molecule 14: Proteasome subunit alpha type-4

Chain D: 81% 7% 11%



- Molecule 14: Proteasome subunit alpha type-4

Chain R: 83% 6% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	240235	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 ($e^-/\text{\AA}^2$)	57.00	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	47169	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	4.360	Depositor
Minimum map value	-2.318	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.134	Depositor
Recommended contour level	0.34	Depositor
Map size ($\text{\AA}$)	375.24, 375.24, 375.24	wwPDB
Map dimensions	354, 354, 354	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	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	E	0.29	0/1854	0.46	0/2498
1	S	0.29	0/1854	0.46	0/2498
2	B	0.36	0/1937	0.51	0/2622
2	P	0.36	0/1937	0.51	0/2622
3	H	0.37	0/1541	0.50	0/2087
3	V	0.37	0/1541	0.50	0/2087
4	F	0.33	0/1800	0.47	0/2433
4	T	0.33	0/1800	0.47	0/2433
5	1	0.33	0/1777	0.50	0/2397
5	M	0.33	0/1777	0.50	0/2397
6	K	0.30	0/1569	0.48	0/2115
6	Y	0.30	0/1569	0.48	0/2115
7	G	0.37	0/1936	0.50	0/2614
7	U	0.37	0/1936	0.50	0/2614
8	2	0.37	0/1839	0.56	0/2493
8	N	0.37	0/1839	0.56	0/2493
9	I	0.36	0/1701	0.52	0/2307
9	W	0.36	0/1701	0.52	0/2307
10	L	0.30	0/1668	0.49	0/2258
10	Z	0.29	0/1668	0.49	0/2258
11	C	0.33	0/1904	0.49	0/2576
11	Q	0.33	0/1904	0.49	0/2576
12	A	0.36	0/1928	0.47	0/2611
12	O	0.36	0/1928	0.47	0/2611
13	J	0.35	0/1516	0.48	0/2044
13	X	0.35	0/1516	0.48	0/2044
14	D	0.32	0/1789	0.47	0/2422
14	R	0.32	0/1789	0.47	0/2422
All	All	0.34	0/49518	0.49	0/66954

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1829	1808	1806	10	0
1	S	1829	1808	1806	9	0
2	B	1900	1911	1910	7	0
2	P	1900	1911	1910	7	0
3	H	1512	1479	1478	5	0
3	V	1512	1479	1478	6	0
4	F	1773	1777	1775	10	0
4	T	1773	1777	1775	9	0
5	1	1739	1697	1696	8	0
5	M	1739	1697	1696	8	0
6	K	1542	1556	1556	7	0
6	Y	1542	1556	1556	9	0
7	G	1896	1888	1886	6	0
7	U	1896	1888	1886	6	0
8	2	1808	1812	1811	9	0
8	N	1808	1812	1811	11	0
9	I	1670	1677	1676	7	0
9	W	1670	1677	1676	7	0
10	L	1631	1579	1578	10	0
10	Z	1631	1579	1578	9	0
11	C	1875	1881	1879	8	0
11	Q	1875	1881	1879	7	0
12	A	1891	1890	1889	5	0
12	O	1891	1890	1889	6	0
13	J	1489	1490	1488	9	0
13	X	1489	1490	1488	8	0
14	D	1762	1766	1763	10	0
14	R	1762	1766	1763	8	0
All	All	48634	48422	48382	204	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 204 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)
10:L:284:ASN:O	13:X:39:LYS:NZ	2.17	0.77
13:J:39:LYS:NZ	10:Z:284:ASN:O	2.19	0.75
10:Z:84:GLN:NE2	10:Z:223:LEU:O	2.21	0.73
13:J:203:ARG:NH1	10:Z:270:GLU:OE1	2.24	0.71
13:X:11:ILE:HG21	13:X:142:ALA:HB3	1.72	0.70

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	E	233/260 (90%)	231 (99%)	2 (1%)	0	100	100
1	S	233/260 (90%)	231 (99%)	2 (1%)	0	100	100
2	B	246/250 (98%)	240 (98%)	6 (2%)	0	100	100
2	P	246/250 (98%)	240 (98%)	6 (2%)	0	100	100
3	H	194/215 (90%)	193 (100%)	1 (0%)	0	100	100
3	V	194/215 (90%)	193 (100%)	1 (0%)	0	100	100
4	F	229/234 (98%)	224 (98%)	5 (2%)	0	100	100
4	T	229/234 (98%)	224 (98%)	5 (2%)	0	100	100
5	1	218/241 (90%)	215 (99%)	3 (1%)	0	100	100
5	M	218/241 (90%)	215 (99%)	3 (1%)	0	100	100
6	K	191/198 (96%)	188 (98%)	3 (2%)	0	100	100
6	Y	191/198 (96%)	188 (98%)	3 (2%)	0	100	100
7	G	242/288 (84%)	240 (99%)	2 (1%)	0	100	100
7	U	242/288 (84%)	240 (99%)	2 (1%)	0	100	100
8	2	229/266 (86%)	223 (97%)	6 (3%)	0	100	100
8	N	229/266 (86%)	223 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	218/261 (84%)	215 (99%)	3 (1%)	0	100	100
9	W	218/261 (84%)	215 (99%)	3 (1%)	0	100	100
10	L	208/287 (72%)	204 (98%)	4 (2%)	0	100	100
10	Z	208/287 (72%)	204 (98%)	4 (2%)	0	100	100
11	C	235/258 (91%)	232 (99%)	3 (1%)	0	100	100
11	Q	235/258 (91%)	232 (99%)	3 (1%)	0	100	100
12	A	237/252 (94%)	235 (99%)	2 (1%)	0	100	100
12	O	237/252 (94%)	235 (99%)	2 (1%)	0	100	100
13	J	188/204 (92%)	182 (97%)	6 (3%)	0	100	100
13	X	188/204 (92%)	182 (97%)	6 (3%)	0	100	100
14	D	219/254 (86%)	216 (99%)	3 (1%)	0	100	100
14	R	219/254 (86%)	216 (99%)	3 (1%)	0	100	100
All	All	6174/6936 (89%)	6076 (98%)	98 (2%)	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	E	195/215 (91%)	193 (99%)	2 (1%)	68	75
1	S	195/215 (91%)	193 (99%)	2 (1%)	68	75
2	B	207/209 (99%)	206 (100%)	1 (0%)	81	87
2	P	207/209 (99%)	206 (100%)	1 (0%)	81	87
3	H	162/178 (91%)	161 (99%)	1 (1%)	78	84
3	V	162/178 (91%)	161 (99%)	1 (1%)	78	84
4	F	190/193 (98%)	188 (99%)	2 (1%)	65	72
4	T	190/193 (98%)	188 (99%)	2 (1%)	65	72
5	1	183/201 (91%)	181 (99%)	2 (1%)	65	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	M	183/201 (91%)	181 (99%)	2 (1%)	65	72
6	K	171/175 (98%)	168 (98%)	3 (2%)	51	58
6	Y	171/175 (98%)	168 (98%)	3 (2%)	51	58
7	G	201/239 (84%)	200 (100%)	1 (0%)	81	87
7	U	201/239 (84%)	200 (100%)	1 (0%)	81	87
8	2	197/224 (88%)	196 (100%)	1 (0%)	81	87
8	N	197/224 (88%)	196 (100%)	1 (0%)	81	87
9	I	179/214 (84%)	179 (100%)	0	100	100
9	W	179/214 (84%)	179 (100%)	0	100	100
10	L	168/235 (72%)	164 (98%)	4 (2%)	43	47
10	Z	168/235 (72%)	164 (98%)	4 (2%)	43	47
11	C	201/216 (93%)	199 (99%)	2 (1%)	68	75
11	Q	201/216 (93%)	199 (99%)	2 (1%)	68	75
12	A	205/210 (98%)	204 (100%)	1 (0%)	81	87
12	O	205/210 (98%)	204 (100%)	1 (0%)	81	87
13	J	161/172 (94%)	160 (99%)	1 (1%)	78	84
13	X	161/172 (94%)	160 (99%)	1 (1%)	78	84
14	D	199/226 (88%)	196 (98%)	3 (2%)	57	64
14	R	199/226 (88%)	196 (98%)	3 (2%)	57	64
All	All	5238/5814 (90%)	5190 (99%)	48 (1%)	68	77

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	T	188	GLU
7	U	245	LYS
4	T	209	ASP
6	Y	19	LYS
10	Z	84	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
8	2	135	GLN

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Mol	Chain	Res	Type
11	Q	89	ASN
9	W	115	HIS
9	W	223	ASN
12	O	221	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.

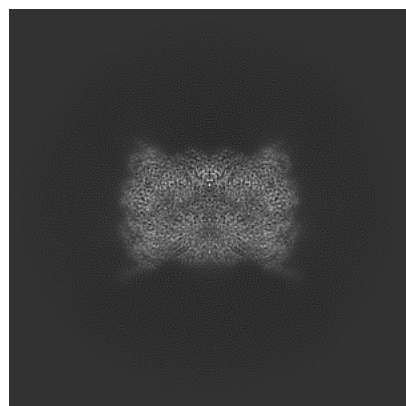
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41993. These allow visual inspection of the internal detail of the map and identification of artifacts.

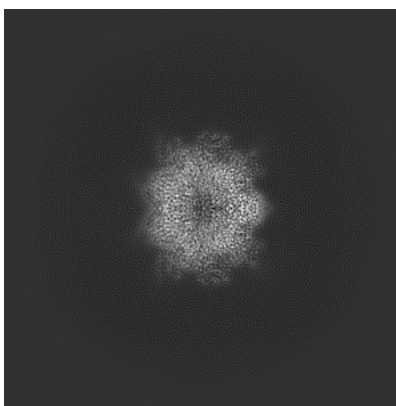
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

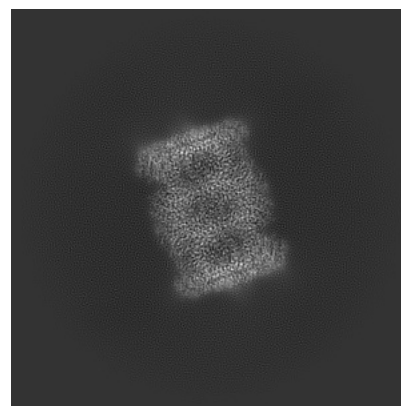
6.1.1 Primary map



X

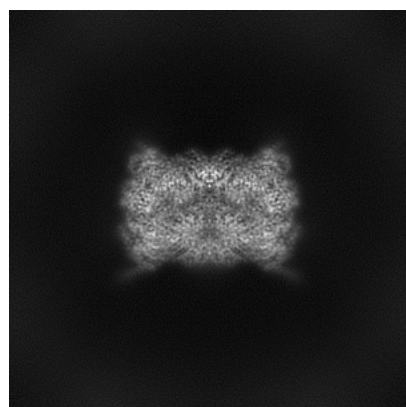


Y

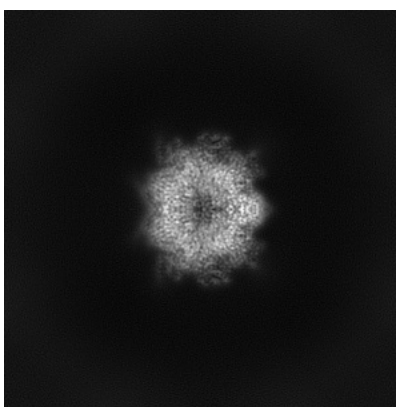


Z

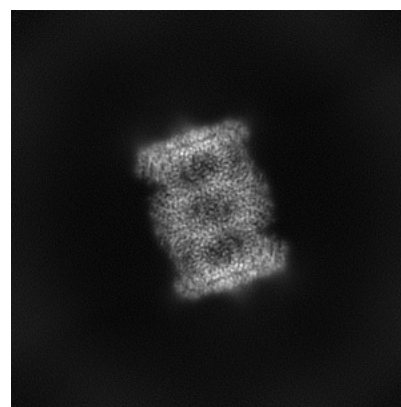
6.1.2 Raw map



X



Y

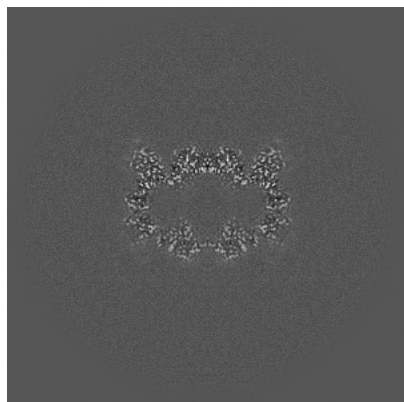


Z

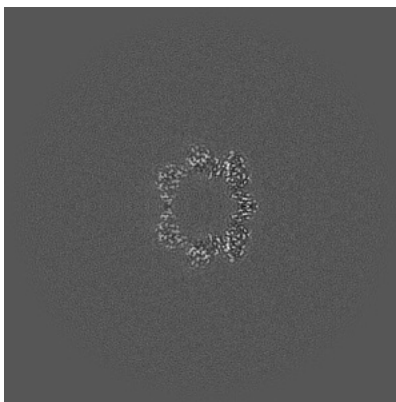
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

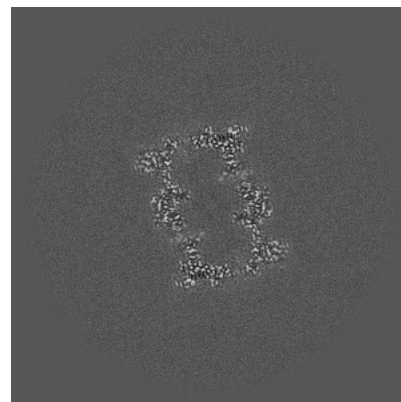
6.2.1 Primary map



X Index: 177

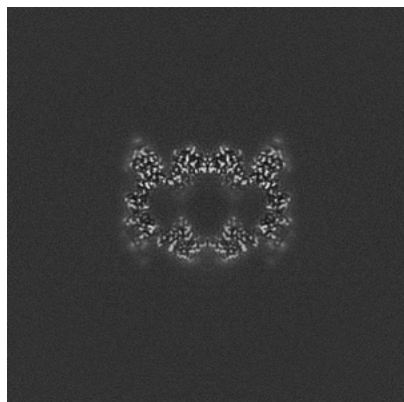


Y Index: 177

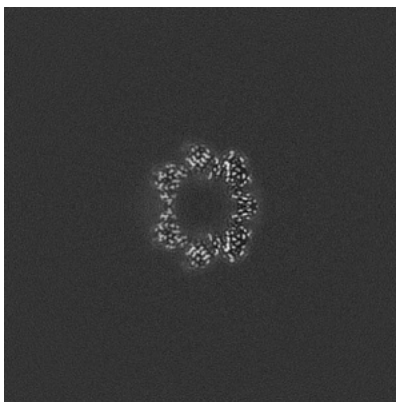


Z Index: 177

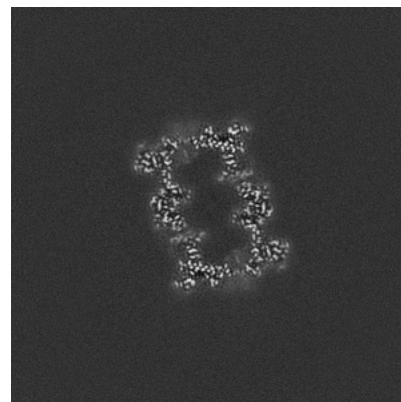
6.2.2 Raw map



X Index: 177



Y Index: 177

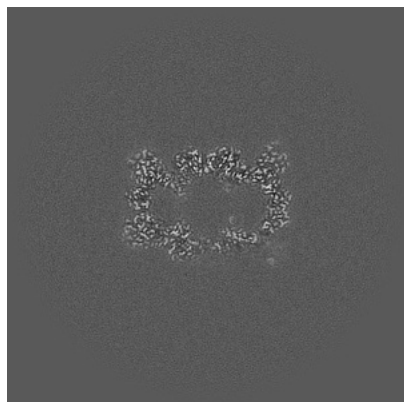


Z Index: 177

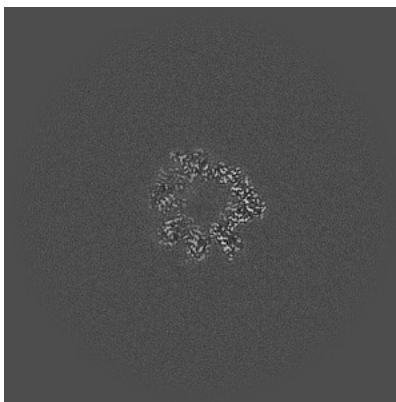
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

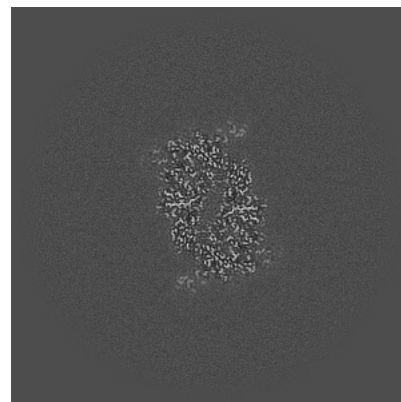
6.3.1 Primary map



X Index: 173

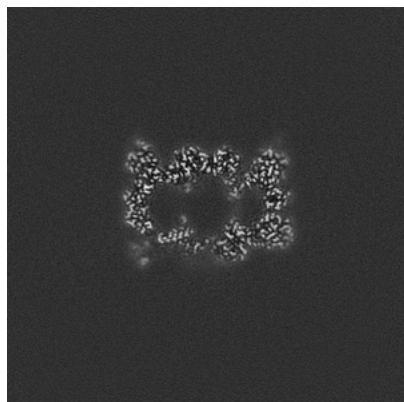


Y Index: 192

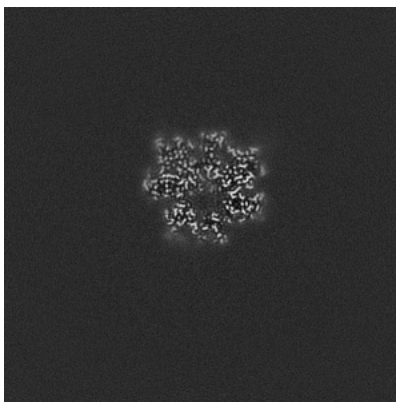


Z Index: 202

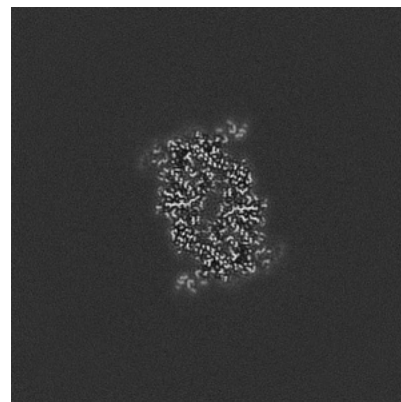
6.3.2 Raw map



X Index: 181



Y Index: 128

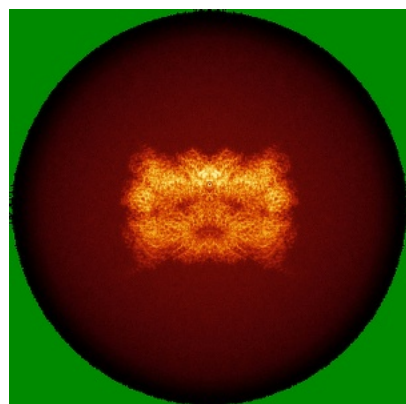


Z Index: 202

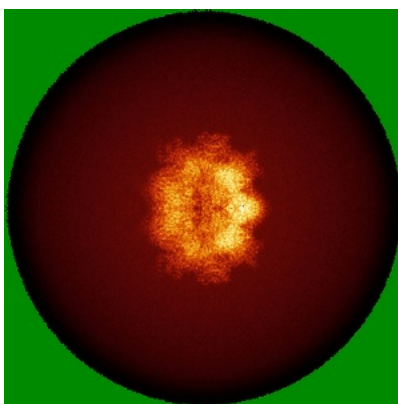
The images above show the largest variance slices of the map in three orthogonal directions.

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

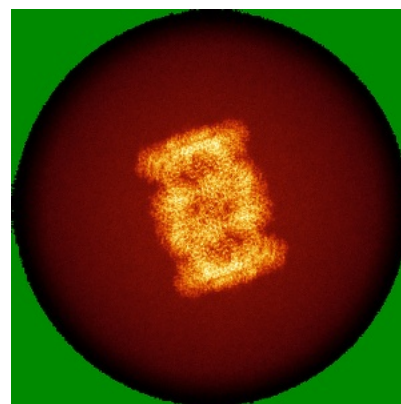
6.4.1 Primary map



X

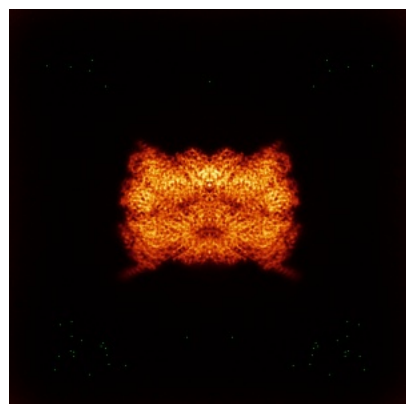


Y

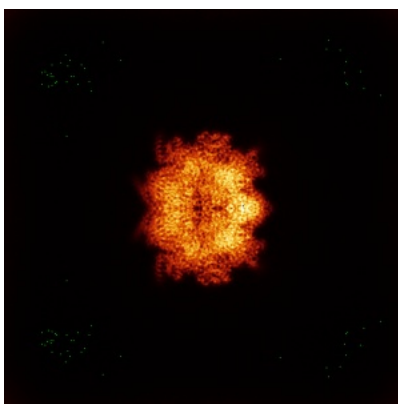


Z

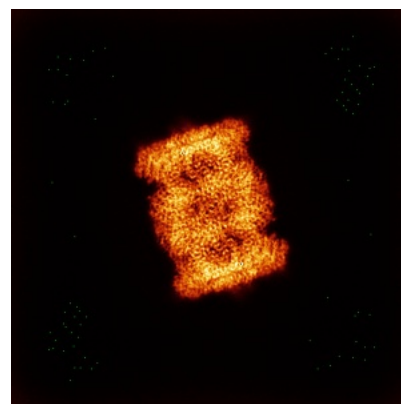
6.4.2 Raw map



X



Y

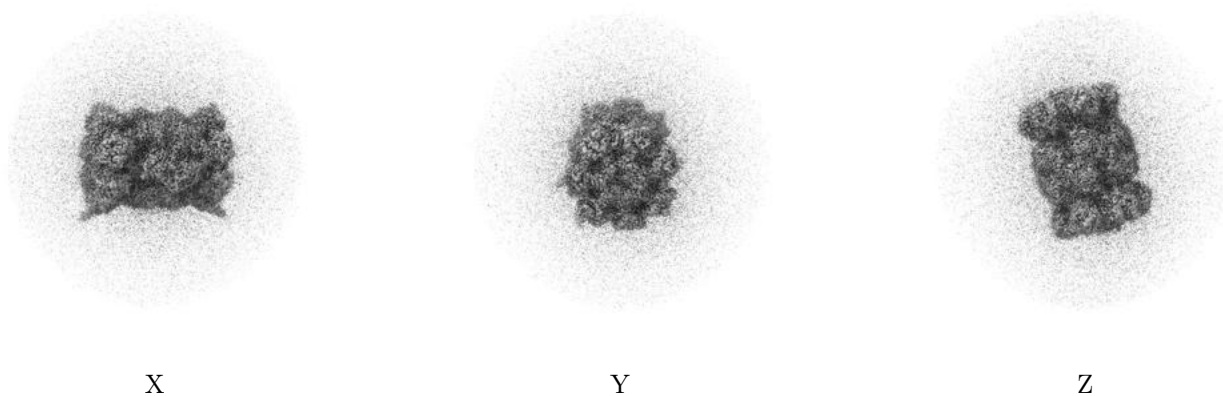


Z

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.

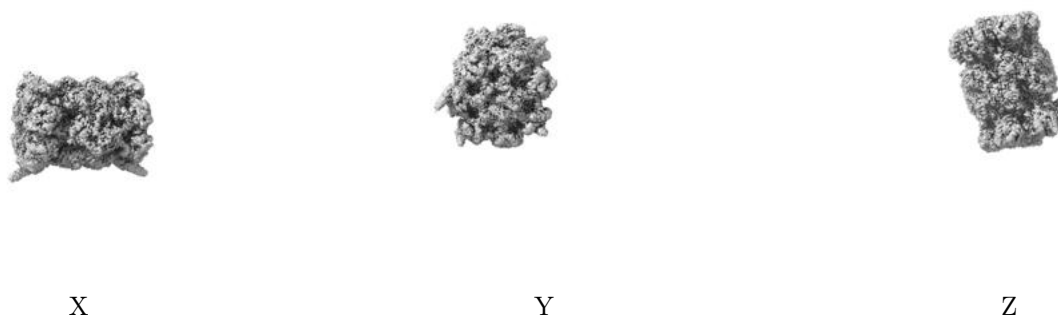
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.34. 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.

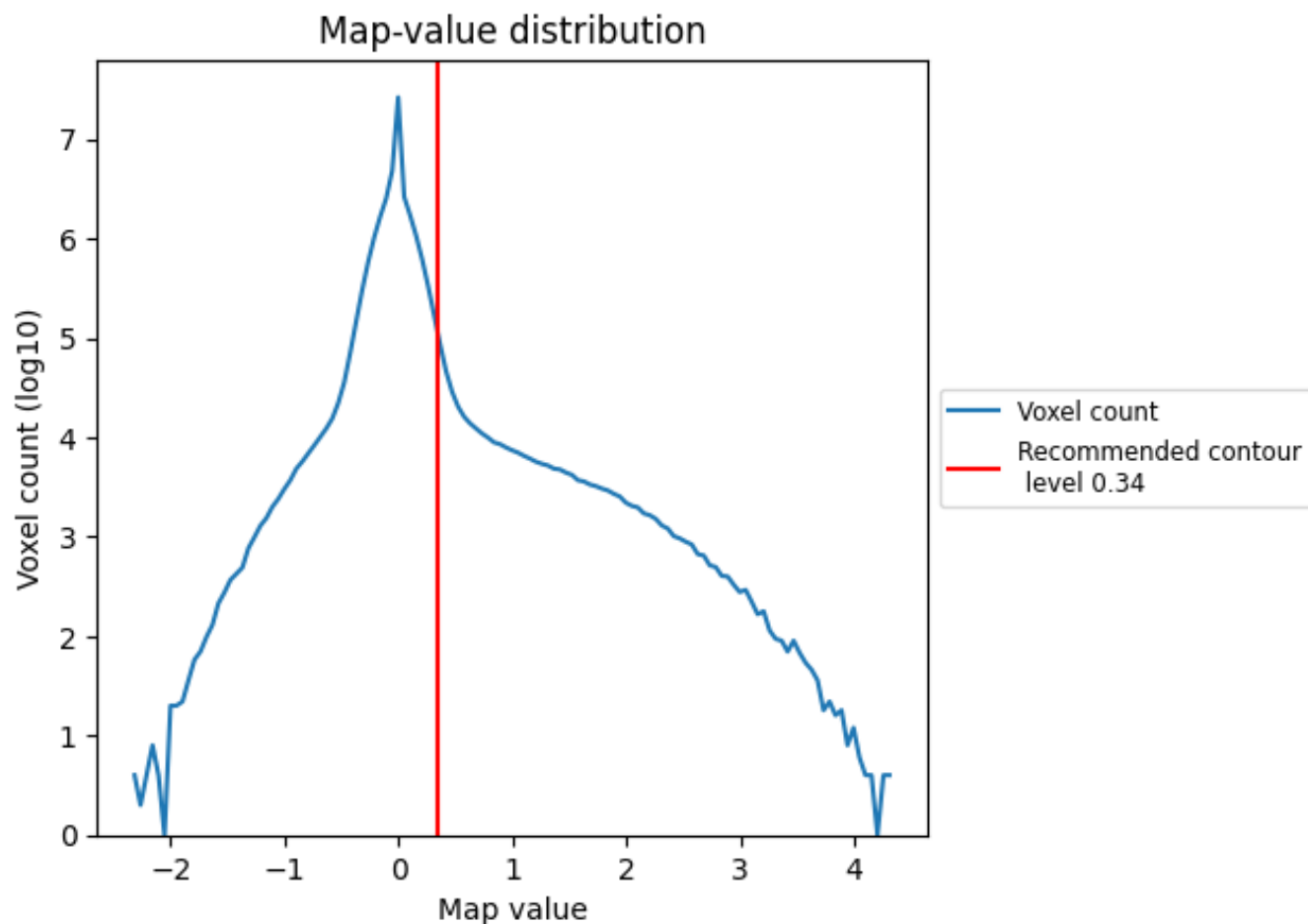
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

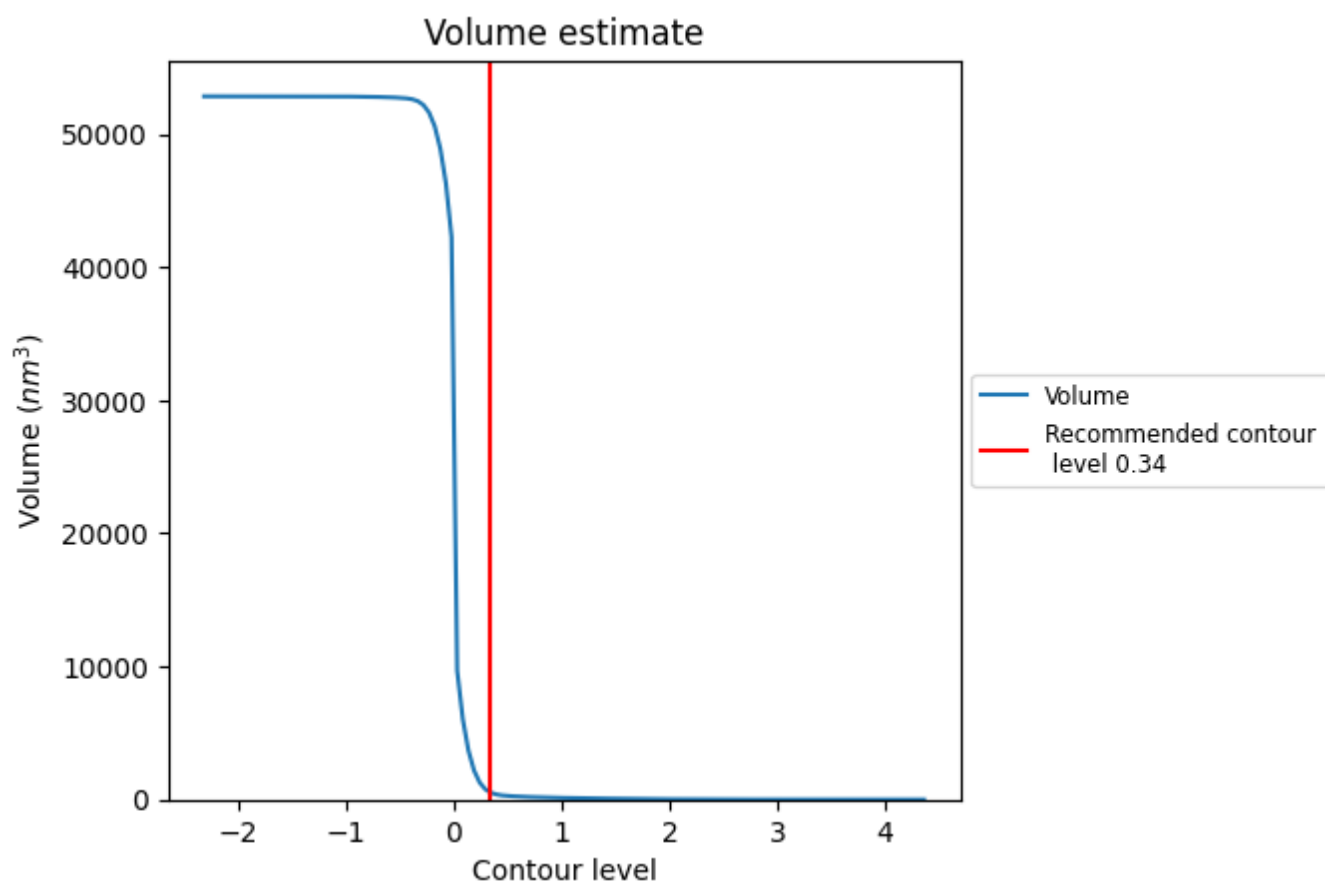
This section contains the results of statistical analysis of the map.

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.

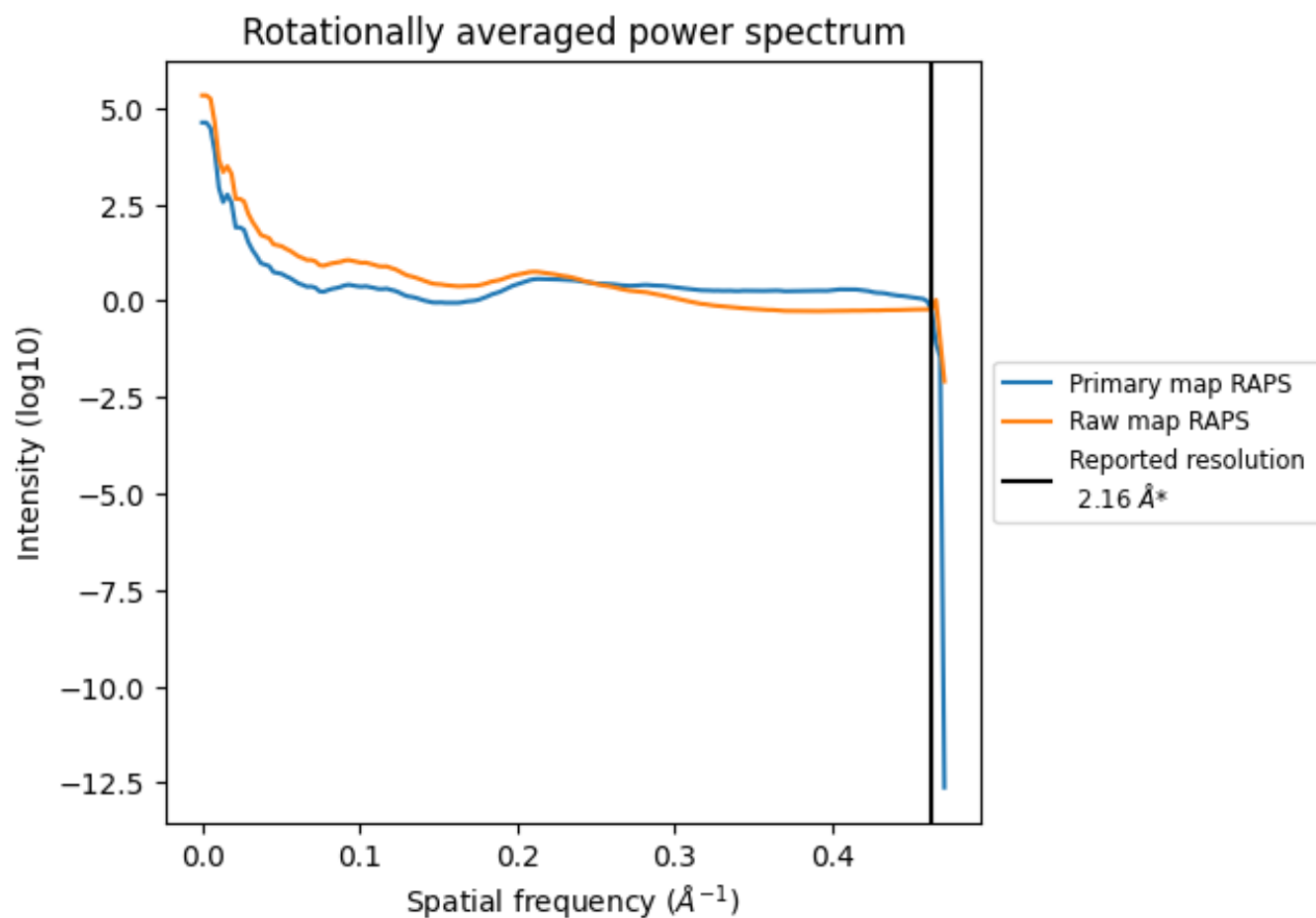
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 531 nm^3 ; this corresponds to an approximate mass of 479 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 ⓘ

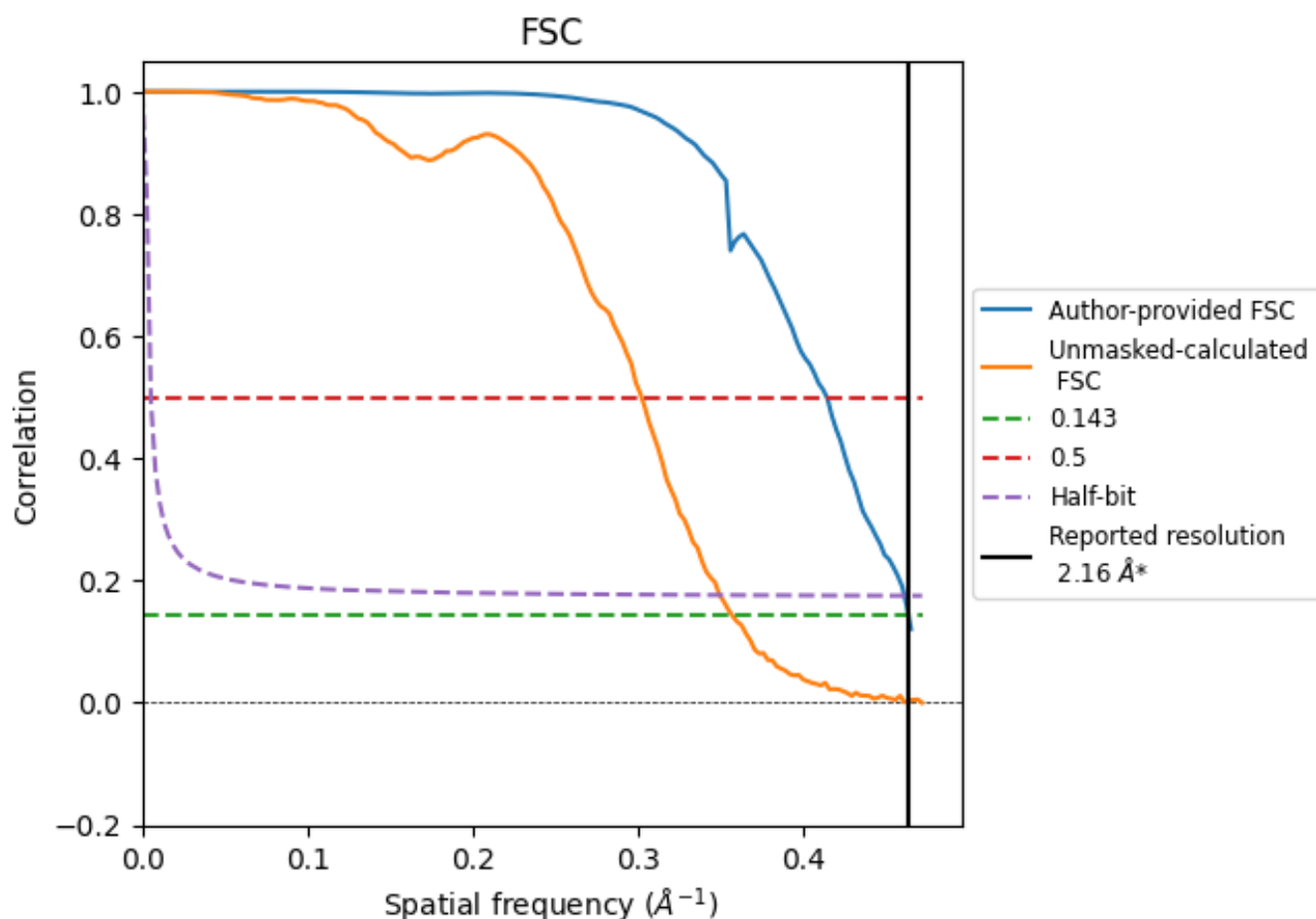


*Reported resolution corresponds to spatial frequency of 0.463 Å⁻¹

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 0.463 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

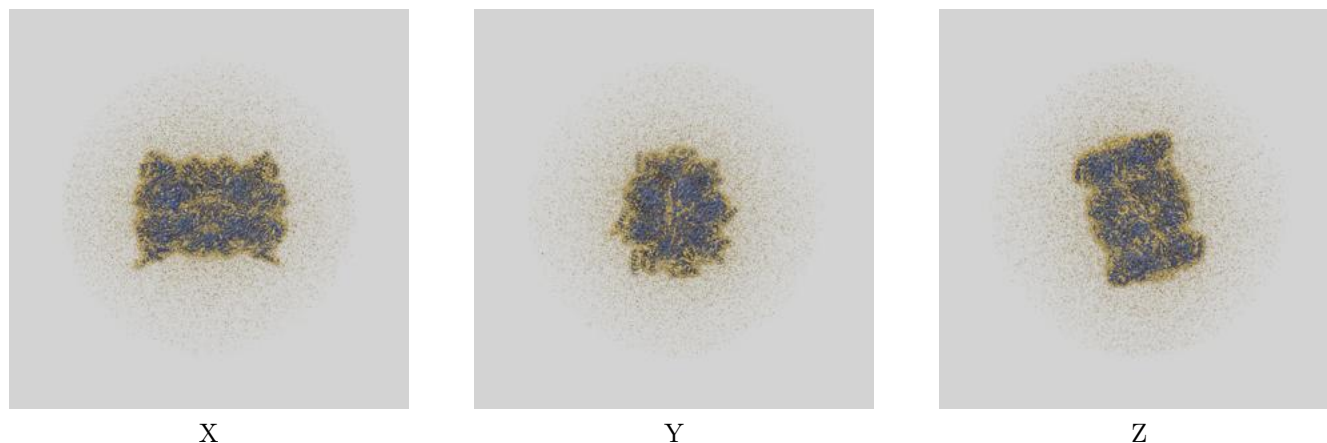
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.16	-	-
Author-provided FSC curve	2.16	2.41	2.17
Unmasked-calculated*	2.80	3.31	2.86

*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 2.80 differs from the reported value 2.16 by more than 10 %

9 Map-model fit [i](#)

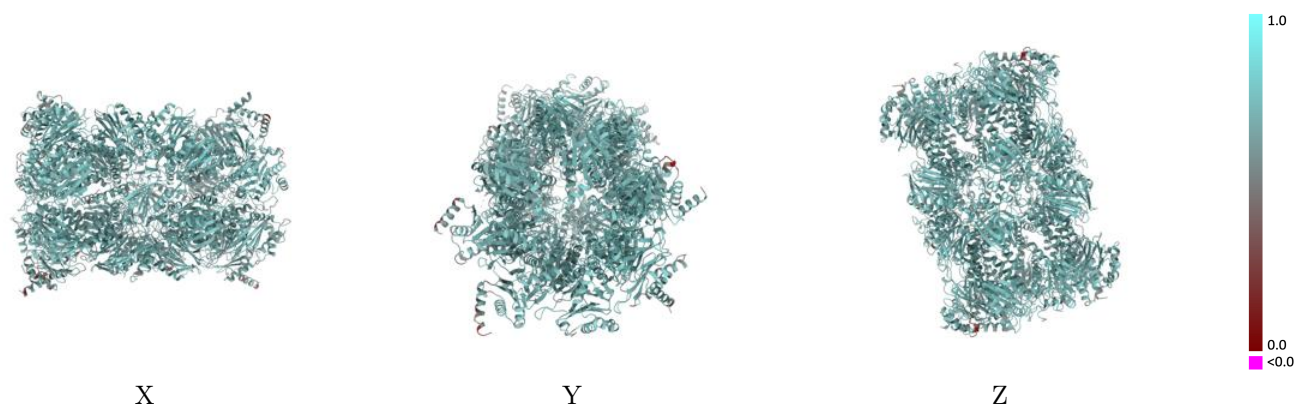
This section contains information regarding the fit between EMDB map EMD-41993 and PDB model 8U7U. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



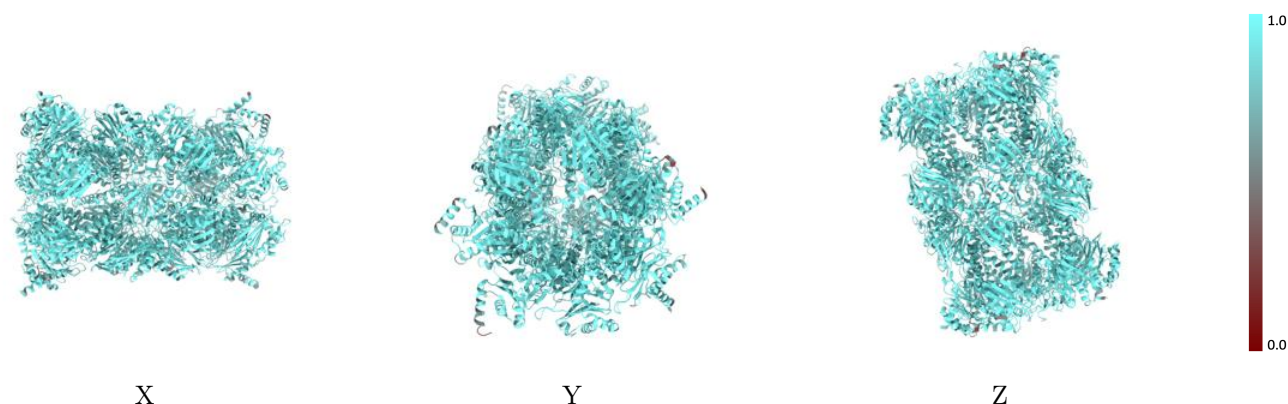
The images above show the 3D surface view of the map at the recommended contour level 0.34 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



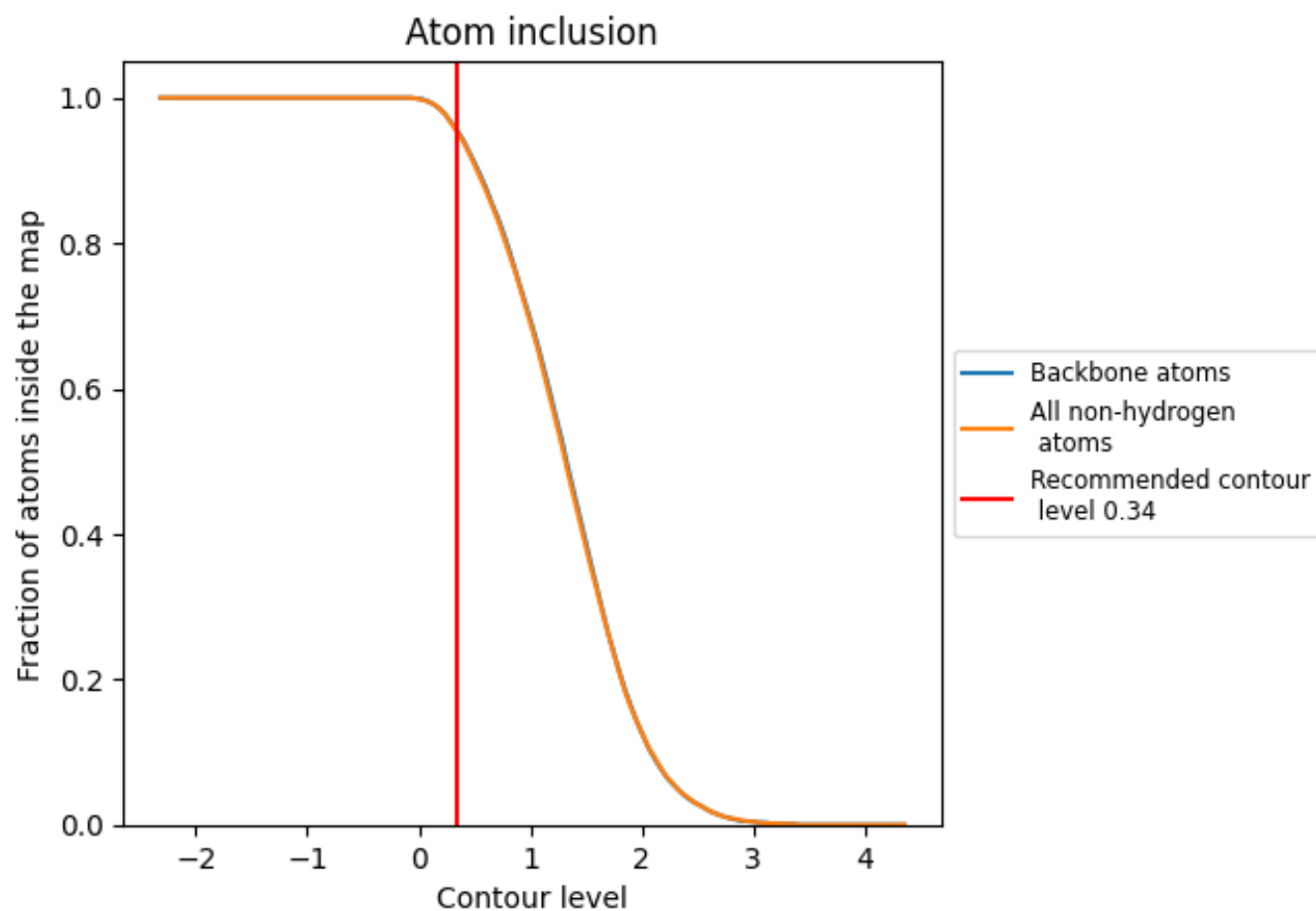
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.34).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% 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 (0.34) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9540	 0.6880
1	 0.9550	 0.6890
2	 0.9800	 0.7210
A	 0.9470	 0.6810
B	 0.9530	 0.6840
C	 0.9440	 0.6700
D	 0.9370	 0.6630
E	 0.9210	 0.6540
F	 0.9650	 0.6910
G	 0.9500	 0.6870
H	 0.9760	 0.7170
I	 0.9780	 0.7040
J	 0.9520	 0.6880
K	 0.9580	 0.6980
L	 0.9540	 0.6810
M	 0.9550	 0.6900
N	 0.9800	 0.7230
O	 0.9460	 0.6820
P	 0.9530	 0.6840
Q	 0.9440	 0.6700
R	 0.9350	 0.6640
S	 0.9200	 0.6550
T	 0.9650	 0.6920
U	 0.9500	 0.6880
V	 0.9760	 0.7180
W	 0.9780	 0.7050
X	 0.9520	 0.6900
Y	 0.9580	 0.6980
Z	 0.9540	 0.6800

