



## wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:20 PM UTC

PDB ID : 7TEO / pdb\_00007teo  
EMDB ID : EMD-25848  
Title : Cryo-EM structure of the 20S Alpha 3 Deletion proteasome core particle in complex with FUB1  
Authors : Walsh Jr., R.M.; Rawson, S.; Schnell, H.M.; Hanna, J.  
Deposited on : 2022-01-05  
Resolution : 2.97 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](mailto: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>.

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

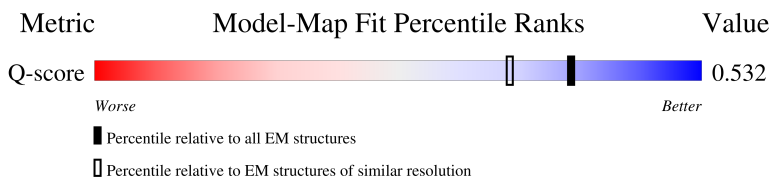
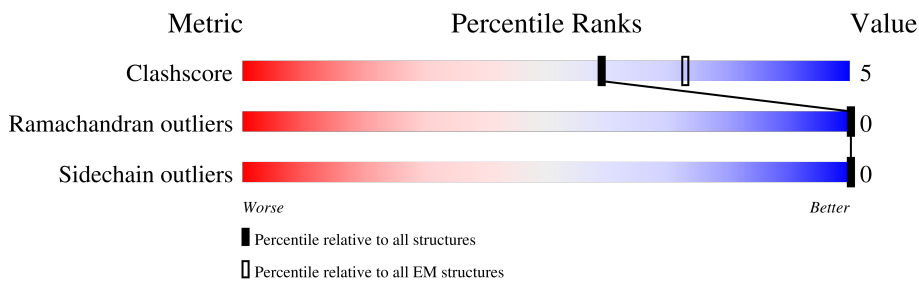
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.97 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	13205 ( 2.47 - 3.47 )

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  $\geq 3$ , 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	1	241	82% 10% 8%
1	M	241	80% 11% 8%
2	2	266	78% 8% 14%
2	N	266	79% 7% 14%


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Mol	Chain	Length	Quality of chain
3	A	252	85% 8% 7%
3	O	252	80% 13% 7%
4	B	250	90% 6% .
4	P	250	89% 7% .
5	C	254	76% 12% 13%
5	D	254	69% 13% 18%
5	Q	254	74% 13% 13%
5	R	254	74% 8% 18%
6	E	260	70% 10% 20%
6	S	260	73% 7% 20%
7	F	234	88% 11% .
7	T	234	83% 16% .
8	G	288	76% 9% 16%
8	U	288	76% 8% 16%
9	H	215	78% 13% 9%
9	V	215	78% 13% 9%
10	I	261	74% 10% 16%
10	W	261	79% 5% 16%
11	J	205	89% 10% .
11	X	205	89% 10% .
12	K	198	91% 8% .
12	Y	198	82% 16% .
13	L	287	64% 10% 26%
13	Z	287	63% 11% 26%
14	a	250	32% . 68%

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Mol	Chain	Length	Quality of chain
14	b	250	 A horizontal bar chart representing the quality of chain. The bar is divided into two segments: a green segment on the left labeled '32%' and a grey segment on the right labeled '68%'. A small yellow dot is positioned at the boundary between the two segments.

## 2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 97522 atoms, of which 48612 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 beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	1	221	Total	C	H	N	O	S	0	0
			3449	1110	1701	301	333	4		
1	M	221	Total	C	H	N	O	S	0	0
			3449	1110	1701	301	333	4		

- Molecule 2 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	2	230	Total	C	H	N	O	S	0	0
			3595	1137	1798	307	346	7		
2	N	230	Total	C	H	N	O	S	0	0
			3595	1137	1798	307	346	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
3	A	234	Total	C	H	N	O	S	0	0
			3687	1176	1841	308	354	8		
3	O	234	Total	C	H	N	O	S	0	0
			3687	1176	1841	308	354	8		

- Molecule 4 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
4	B	241	Total	C	H	N	O	S	0	0
			3694	1170	1856	303	362	3		
4	P	241	Total	C	H	N	O	S	0	0
			3694	1170	1856	303	362	3		

- Molecule 5 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	C	222	Total 3521	C 1098	H 1771	N 304	O 344	S 4	0	0
5	D	208	Total 3288	C 1025	H 1650	N 284	O 325	S 4	0	0
5	Q	222	Total 3521	C 1098	H 1771	N 304	O 344	S 4	0	0
5	R	208	Total 3287	C 1025	H 1649	N 284	O 325	S 4	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	E	207	Total 3176	C 997	H 1583	N 266	O 324	S 6	0	0
6	S	207	Total 3176	C 997	H 1583	N 266	O 324	S 6	0	0

- Molecule 7 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
7	F	231	Total 3551	C 1114	H 1778	N 307	O 348	S 4	0	0
7	T	231	Total 3551	C 1114	H 1778	N 307	O 348	S 4	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
8	G	243	Total 3776	C 1203	H 1884	N 329	O 356	S 4	0	0
8	U	243	Total 3776	C 1203	H 1884	N 329	O 356	S 4	0	0

- Molecule 9 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
9	H	196	Total 2992	C 955	H 1480	N 250	O 300	S 7	0	0
9	V	196	Total 2991	C 955	H 1479	N 250	O 300	S 7	0	0

- Molecule 10 is a protein called Proteasome subunit beta type-2.

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

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

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

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

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

- Molecule 13 is a protein called Proteasome subunit beta type-5.

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


- Molecule 14 is a protein called Silencing boundary-establishment protein FUB1.

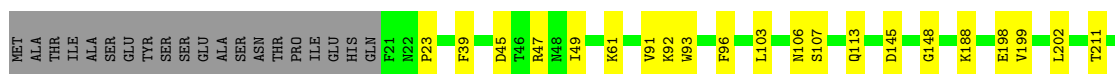
Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
14	a	81	1177	393	559	101	121	3	0	0
14	b	81	1177	393	559	101	121	3	0	0

### 3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Proteasome subunit beta type-6

Chain 1: 



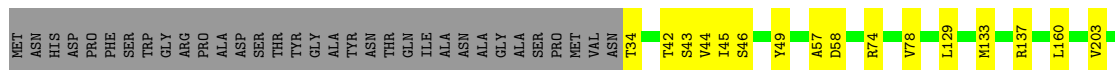
- Molecule 1: Proteasome subunit beta type-6

Chain M: 




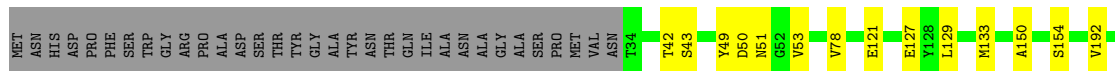
- Molecule 2: Proteasome subunit beta type-7

Chain 2: 



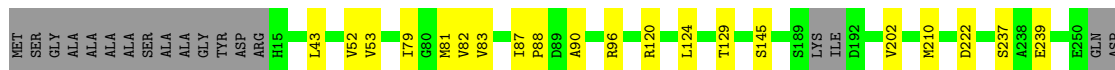
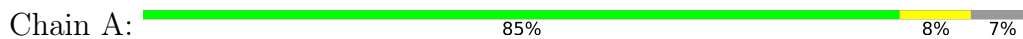
- Molecule 2: Proteasome subunit beta type-7

Chain N: 

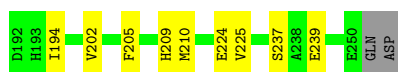
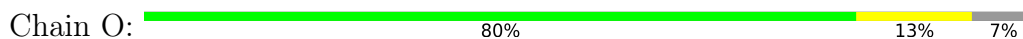




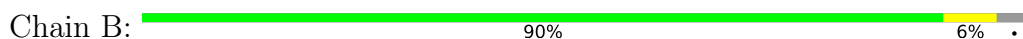
• Molecule 3: Proteasome subunit alpha type-1



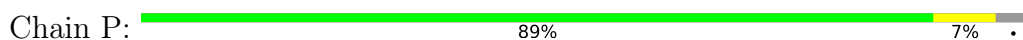
• Molecule 3: Proteasome subunit alpha type-1



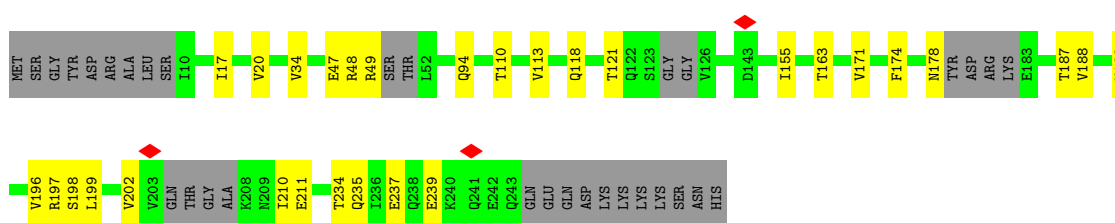
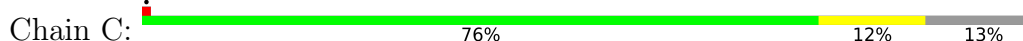
• Molecule 4: Proteasome subunit alpha type-2



• Molecule 4: Proteasome subunit alpha type-2



• Molecule 5: Proteasome subunit alpha type-4

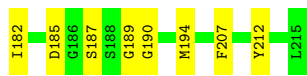
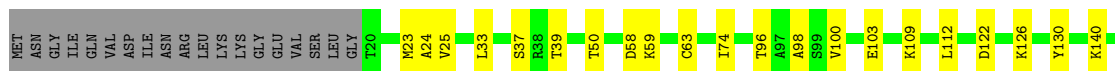


• Molecule 5: Proteasome subunit alpha type-4

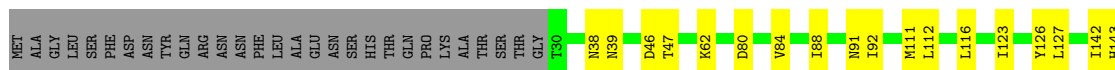




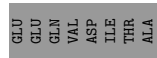
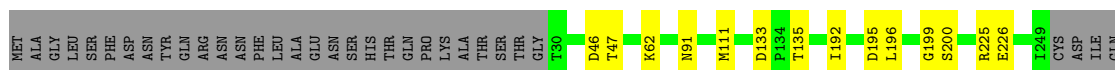
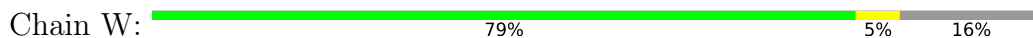




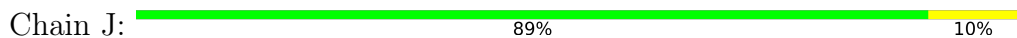
● Molecule 10: Proteasome subunit beta type-2



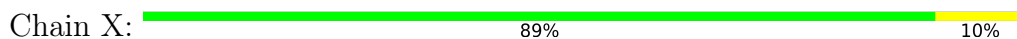
● Molecule 10: Proteasome subunit beta type-2



● Molecule 11: Proteasome subunit beta type-3



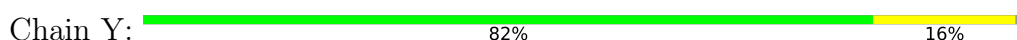
● Molecule 11: Proteasome subunit beta type-3



● Molecule 12: Proteasome subunit beta type-4



● Molecule 12: Proteasome subunit beta type-4





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

ALA GLY SER GLY PHE ILE MET P127 Q139 ASN GLN GLY THR A144 P179 ASP TRP SER GLY GLY PRO PRO ASN PRO LEU GLY ASP PRO S194 P202 ASN ARG ARG PRO A207 P208 R209 R210 E211 P229 GLY SER GLY PHE GLY SER SER GLY GLY PHE GLY SER SER GLY GLY PHE GLY SER SER GLY GLY PHE GLY SER

GLY SER GLY PHE ILE

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	56059	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 ( $e^-/\text{\AA}^2$ )	53.85	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	3.742	Depositor
Minimum map value	-1.746	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.115	Depositor
Recommended contour level	0.306	Depositor
Map size ( $\text{\AA}$ )	381.59998, 381.59998, 381.59998	wwPDB
Map dimensions	360, 360, 360	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 [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	1	0.14	0/1786	0.35	0/2408
1	M	0.14	0/1786	0.32	0/2408
2	2	0.13	0/1828	0.31	0/2480
2	N	0.13	0/1828	0.31	0/2480
3	A	0.13	0/1882	0.29	0/2549
3	O	0.13	0/1882	0.31	0/2549
4	B	0.14	0/1873	0.30	0/2536
4	P	0.14	0/1873	0.31	0/2536
5	C	0.14	0/1773	0.33	0/2396
5	D	0.14	0/1660	0.33	0/2244
5	Q	0.15	0/1773	0.35	0/2396
5	R	0.15	0/1660	0.34	0/2244
6	E	0.12	0/1612	0.29	0/2171
6	S	0.12	0/1612	0.29	0/2171
7	F	0.13	0/1800	0.32	0/2433
7	T	0.13	0/1800	0.30	0/2433
8	G	0.13	0/1932	0.31	0/2609
8	U	0.14	0/1932	0.33	0/2609
9	H	0.14	0/1541	0.31	0/2087
9	V	0.14	0/1541	0.30	0/2087
10	I	0.14	0/1701	0.32	0/2307
10	W	0.14	0/1701	0.32	0/2307
11	J	0.15	0/1605	0.32	0/2166
11	X	0.15	0/1605	0.31	0/2166
12	K	0.13	0/1589	0.30	0/2142
12	Y	0.15	0/1589	0.33	0/2142
13	L	0.15	0/1681	0.34	0/2274
13	Z	0.16	0/1681	0.32	0/2274
14	a	0.16	0/641	0.32	0/873
14	b	0.10	0/641	0.30	0/873
All	All	0.14	0/49808	0.32	0/67350

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	1	1748	1701	1700	18	0
1	M	1748	1701	1700	18	0
2	2	1797	1798	1797	17	0
2	N	1797	1798	1797	12	0
3	A	1846	1841	1839	13	0
3	O	1846	1841	1839	22	0
4	B	1838	1856	1854	11	0
4	P	1838	1856	1854	14	0
5	C	1750	1771	1766	21	0
5	D	1638	1650	1646	21	0
5	Q	1750	1771	1766	21	0
5	R	1638	1649	1646	13	0
6	E	1593	1583	1579	18	0
6	S	1593	1583	1579	13	0
7	F	1773	1778	1775	16	0
7	T	1773	1778	1775	23	0
8	G	1892	1884	1883	19	0
8	U	1892	1884	1883	16	0
9	H	1512	1480	1478	22	0
9	V	1512	1479	1478	19	0
10	I	1670	1677	1676	21	0
10	W	1670	1677	1676	9	0
11	J	1575	1567	1566	12	0
11	X	1575	1567	1566	13	0
12	K	1561	1569	1569	12	0
12	Y	1561	1569	1569	21	0
13	L	1644	1593	1592	19	0
13	Z	1644	1593	1592	23	0
14	a	618	559	556	2	0
14	b	618	559	556	1	0
All	All	48910	48612	48552	445	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 445 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)
9:H:74:ILE:HD11	9:H:112:LEU:HD23	1.50	0.91
4:B:224:TYR:OH	4:B:230:ASP:OD2	1.88	0.91
12:K:25:ILE:O	12:Y:139:TYR:OH	1.90	0.90
1:M:47:ARG:NE	1:M:219:ASP:OD2	2.04	0.89
9:V:74:ILE:HD11	9:V:112:LEU:HD23	1.54	0.87

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	1	219/241 (91%)	214 (98%)	5 (2%)	0	100	100
1	M	219/241 (91%)	215 (98%)	4 (2%)	0	100	100
2	2	228/266 (86%)	223 (98%)	5 (2%)	0	100	100
2	N	228/266 (86%)	226 (99%)	2 (1%)	0	100	100
3	A	230/252 (91%)	228 (99%)	2 (1%)	0	100	100
3	O	230/252 (91%)	227 (99%)	3 (1%)	0	100	100
4	B	239/250 (96%)	239 (100%)	0	0	100	100
4	P	239/250 (96%)	239 (100%)	0	0	100	100
5	C	212/254 (84%)	209 (99%)	3 (1%)	0	100	100
5	D	202/254 (80%)	198 (98%)	4 (2%)	0	100	100
5	Q	212/254 (84%)	207 (98%)	5 (2%)	0	100	100
5	R	202/254 (80%)	201 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	E	201/260 (77%)	197 (98%)	4 (2%)	0	100	100
6	S	201/260 (77%)	200 (100%)	1 (0%)	0	100	100
7	F	229/234 (98%)	228 (100%)	1 (0%)	0	100	100
7	T	229/234 (98%)	226 (99%)	3 (1%)	0	100	100
8	G	241/288 (84%)	236 (98%)	5 (2%)	0	100	100
8	U	241/288 (84%)	236 (98%)	5 (2%)	0	100	100
9	H	194/215 (90%)	191 (98%)	3 (2%)	0	100	100
9	V	194/215 (90%)	190 (98%)	4 (2%)	0	100	100
10	I	218/261 (84%)	216 (99%)	2 (1%)	0	100	100
10	W	218/261 (84%)	214 (98%)	4 (2%)	0	100	100
11	J	201/205 (98%)	194 (96%)	7 (4%)	0	100	100
11	X	201/205 (98%)	193 (96%)	8 (4%)	0	100	100
12	K	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
12	Y	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
13	L	210/287 (73%)	207 (99%)	3 (1%)	0	100	100
13	Z	210/287 (73%)	207 (99%)	3 (1%)	0	100	100
14	a	73/250 (29%)	72 (99%)	1 (1%)	0	100	100
14	b	73/250 (29%)	73 (100%)	0	0	100	100
All	All	6180/7430 (83%)	6084 (98%)	96 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	184/201 (92%)	184 (100%)	0	100	100
1	M	184/201 (92%)	184 (100%)	0	100	100
2	2	196/224 (88%)	196 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	N	196/224 (88%)	196 (100%)	0	100	100
3	A	200/210 (95%)	200 (100%)	0	100	100
3	O	200/210 (95%)	200 (100%)	0	100	100
4	B	200/209 (96%)	200 (100%)	0	100	100
4	P	200/209 (96%)	200 (100%)	0	100	100
5	C	200/226 (88%)	200 (100%)	0	100	100
5	D	185/226 (82%)	185 (100%)	0	100	100
5	Q	200/226 (88%)	200 (100%)	0	100	100
5	R	185/226 (82%)	185 (100%)	0	100	100
6	E	172/215 (80%)	172 (100%)	0	100	100
6	S	172/215 (80%)	172 (100%)	0	100	100
7	F	190/193 (98%)	190 (100%)	0	100	100
7	T	190/193 (98%)	190 (100%)	0	100	100
8	G	201/239 (84%)	201 (100%)	0	100	100
8	U	201/239 (84%)	201 (100%)	0	100	100
9	H	162/178 (91%)	162 (100%)	0	100	100
9	V	162/178 (91%)	162 (100%)	0	100	100
10	I	179/214 (84%)	179 (100%)	0	100	100
10	W	179/214 (84%)	179 (100%)	0	100	100
11	J	171/173 (99%)	171 (100%)	0	100	100
11	X	171/173 (99%)	171 (100%)	0	100	100
12	K	173/175 (99%)	173 (100%)	0	100	100
12	Y	173/175 (99%)	173 (100%)	0	100	100
13	L	169/235 (72%)	169 (100%)	0	100	100
13	Z	169/235 (72%)	169 (100%)	0	100	100
14	a	64/207 (31%)	64 (100%)	0	100	100
14	b	64/207 (31%)	64 (100%)	0	100	100
All	All	5292/6250 (85%)	5292 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
10	W	223	ASN
12	Y	118	GLN
11	X	32	GLN
11	X	169	GLN
14	b	134	GLN

### 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.

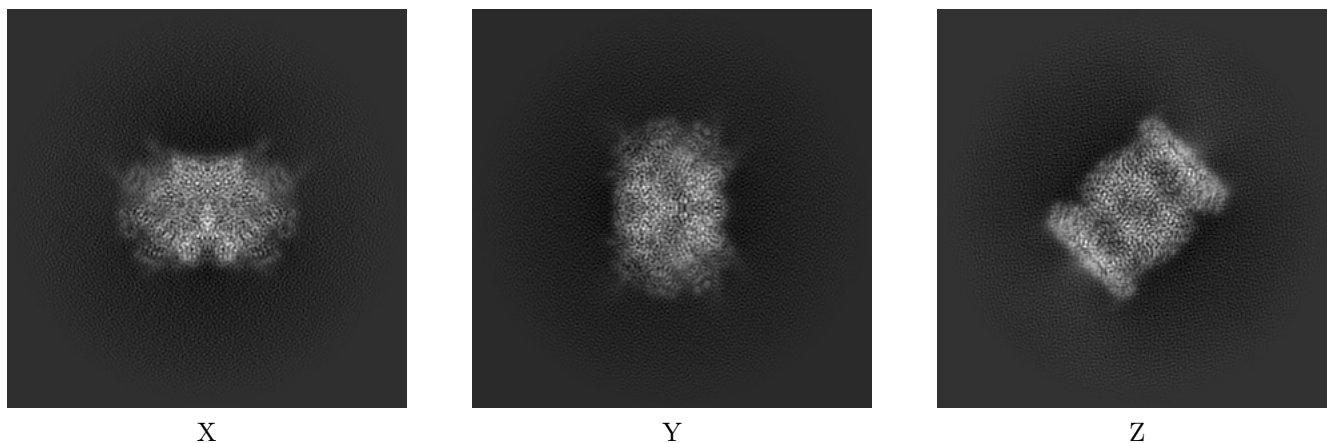
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25848. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

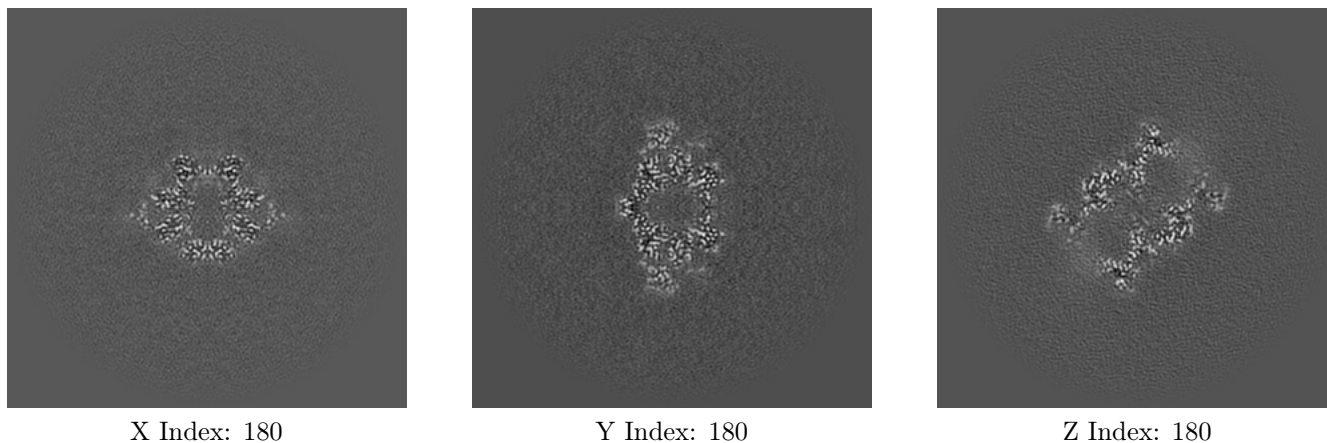
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

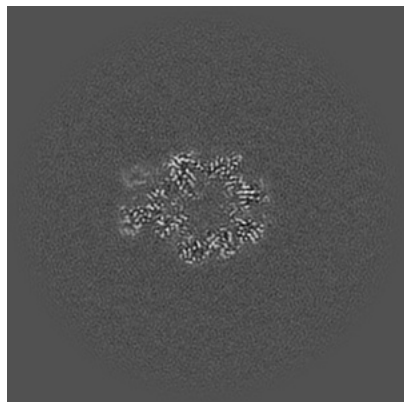
#### 6.2.1 Primary map



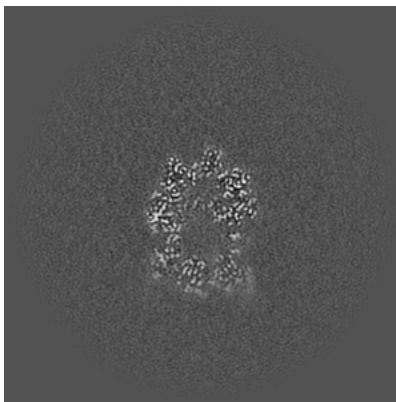
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

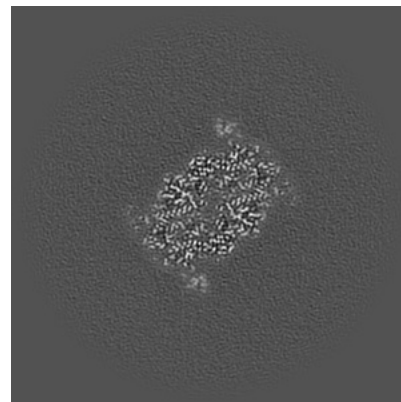
### 6.3.1 Primary map



X Index: 173



Y Index: 164

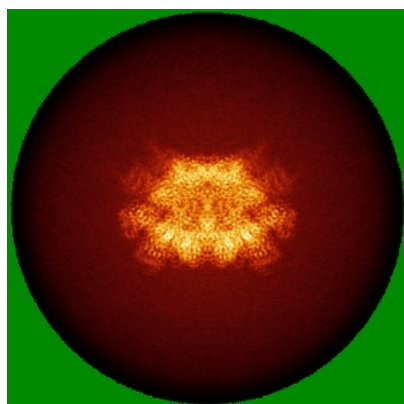


Z Index: 155

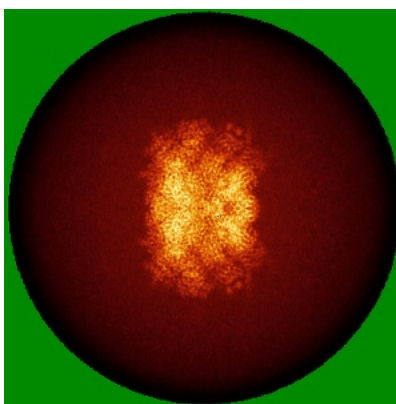
The images above show the largest variance slices of the map in three orthogonal directions.

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

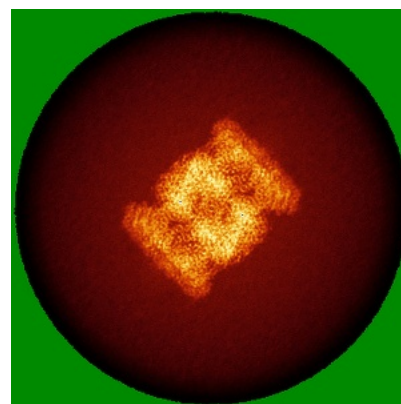
### 6.4.1 Primary map



X



Y

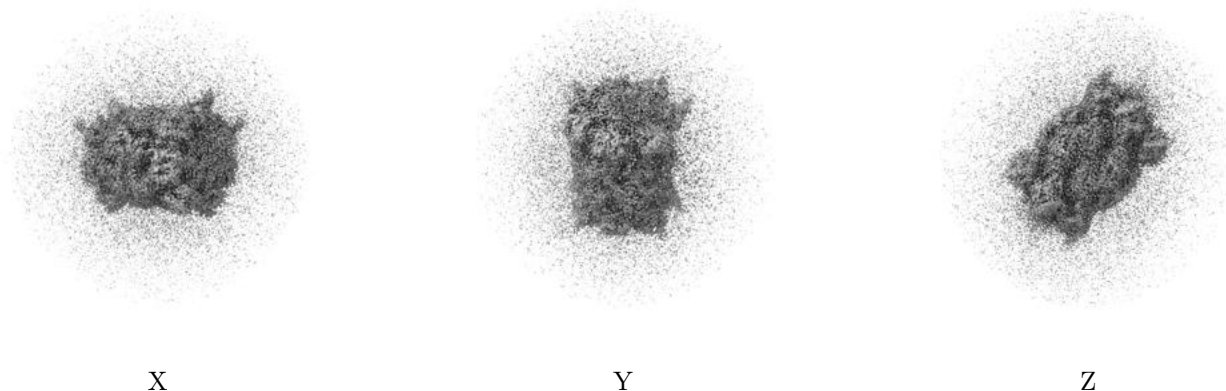


Z

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 0.306. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

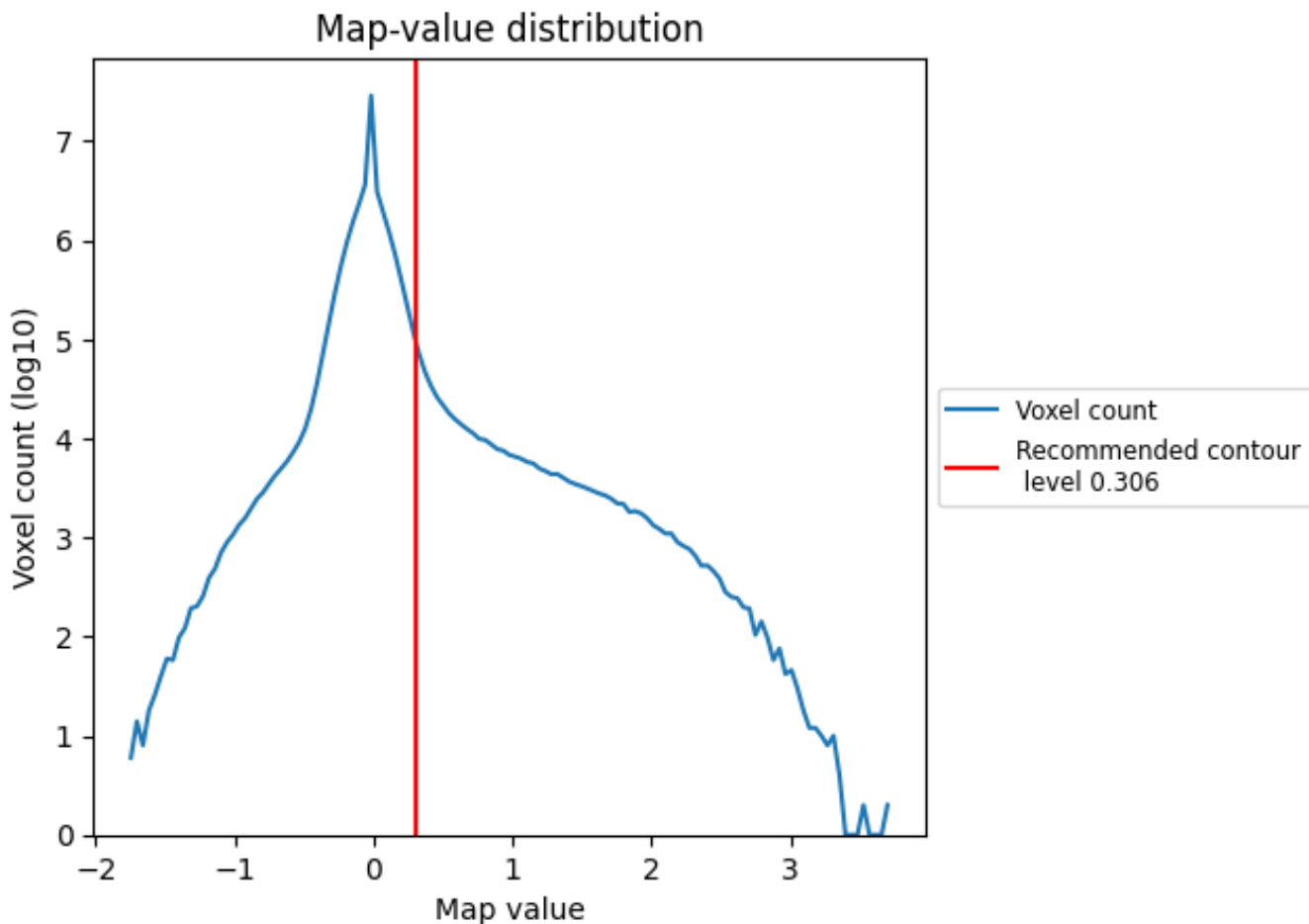
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

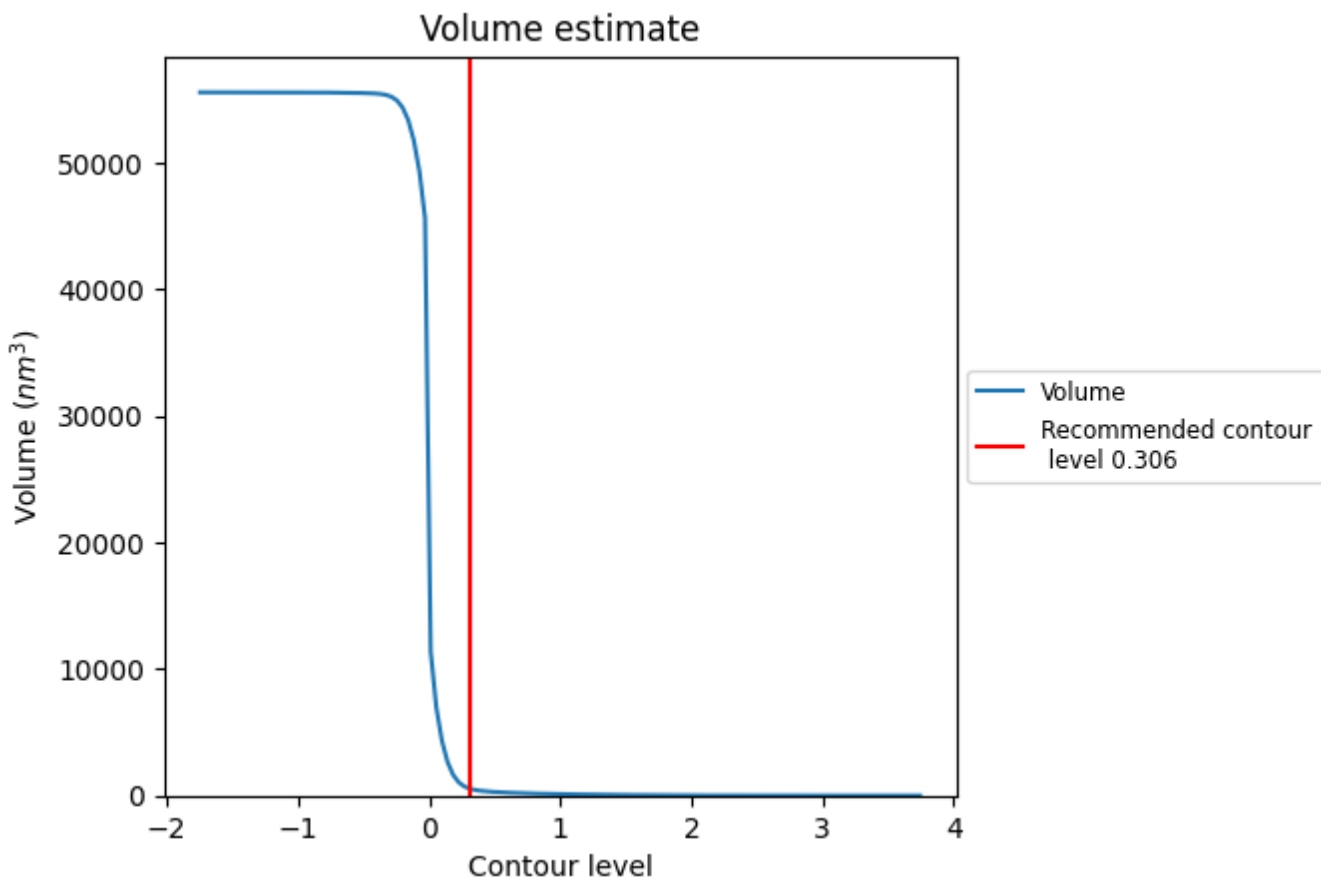
This section contains the results of statistical analysis of the map.

### 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.

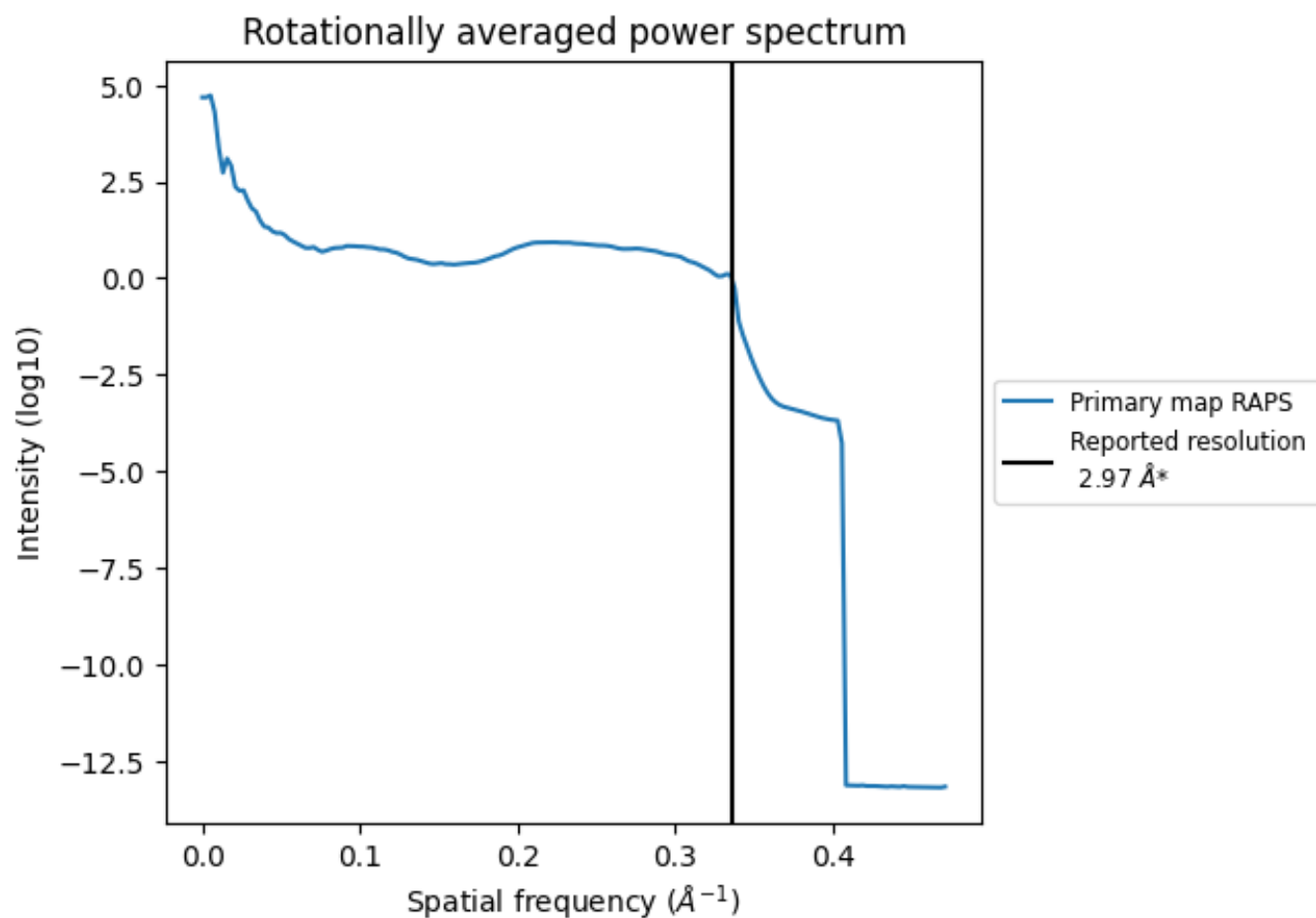
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 563 nm<sup>3</sup>; this corresponds to an approximate mass of 508 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)



\*Reported resolution corresponds to spatial frequency of 0.337 Å<sup>-1</sup>

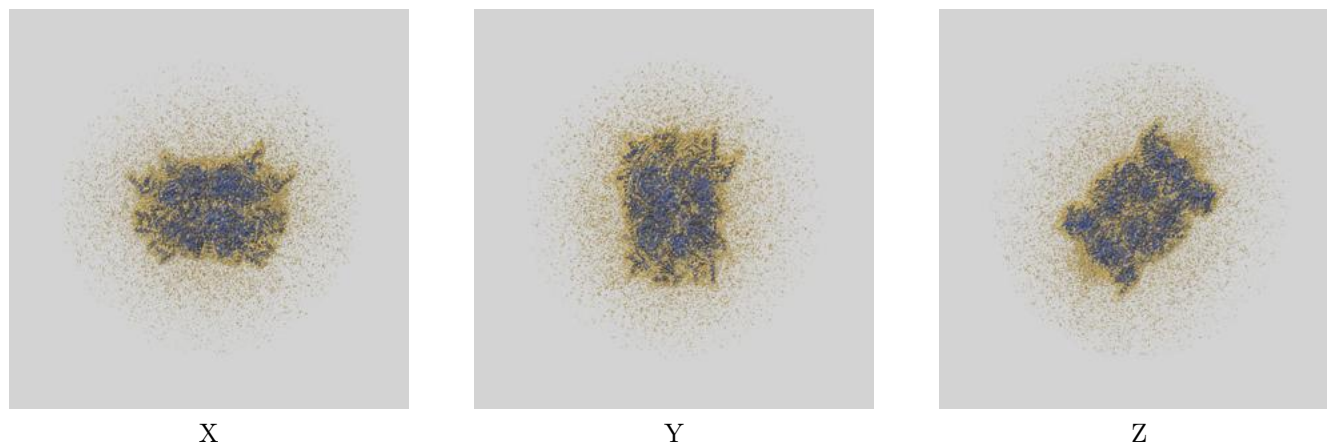
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

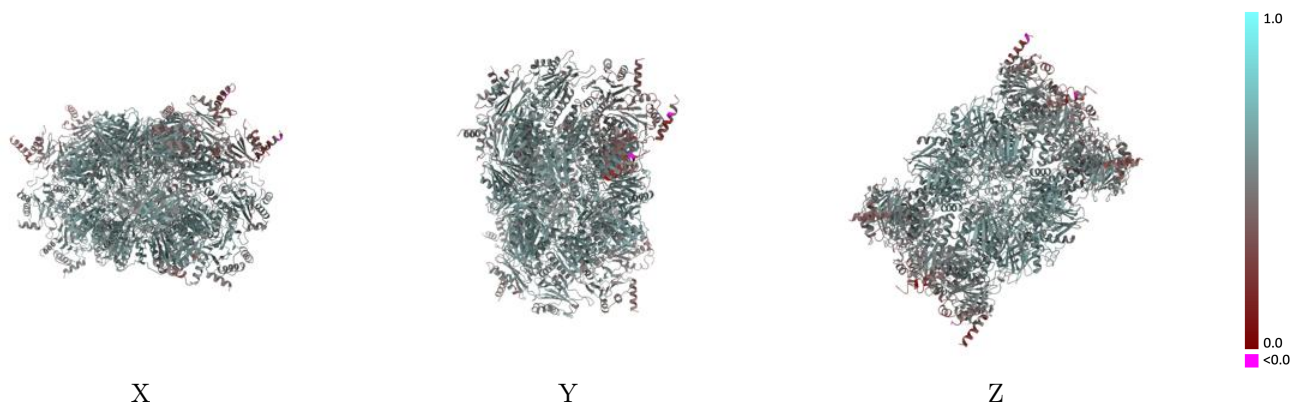
This section contains information regarding the fit between EMDB map EMD-25848 and PDB model 7TEO. Per-residue inclusion information can be found in section 3 on page 8.

### 9.1 Map-model overlay [i](#)



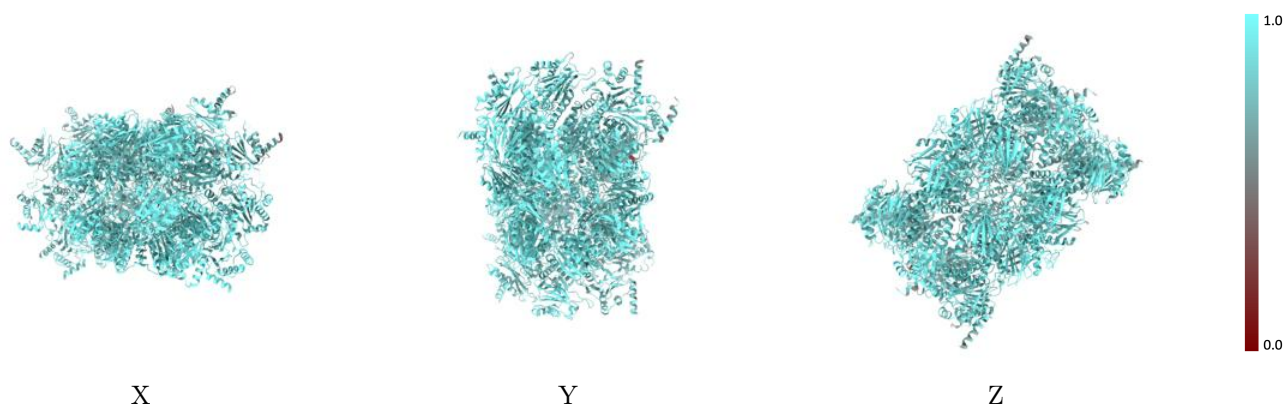
The images above show the 3D surface view of the map at the recommended contour level 0.306 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



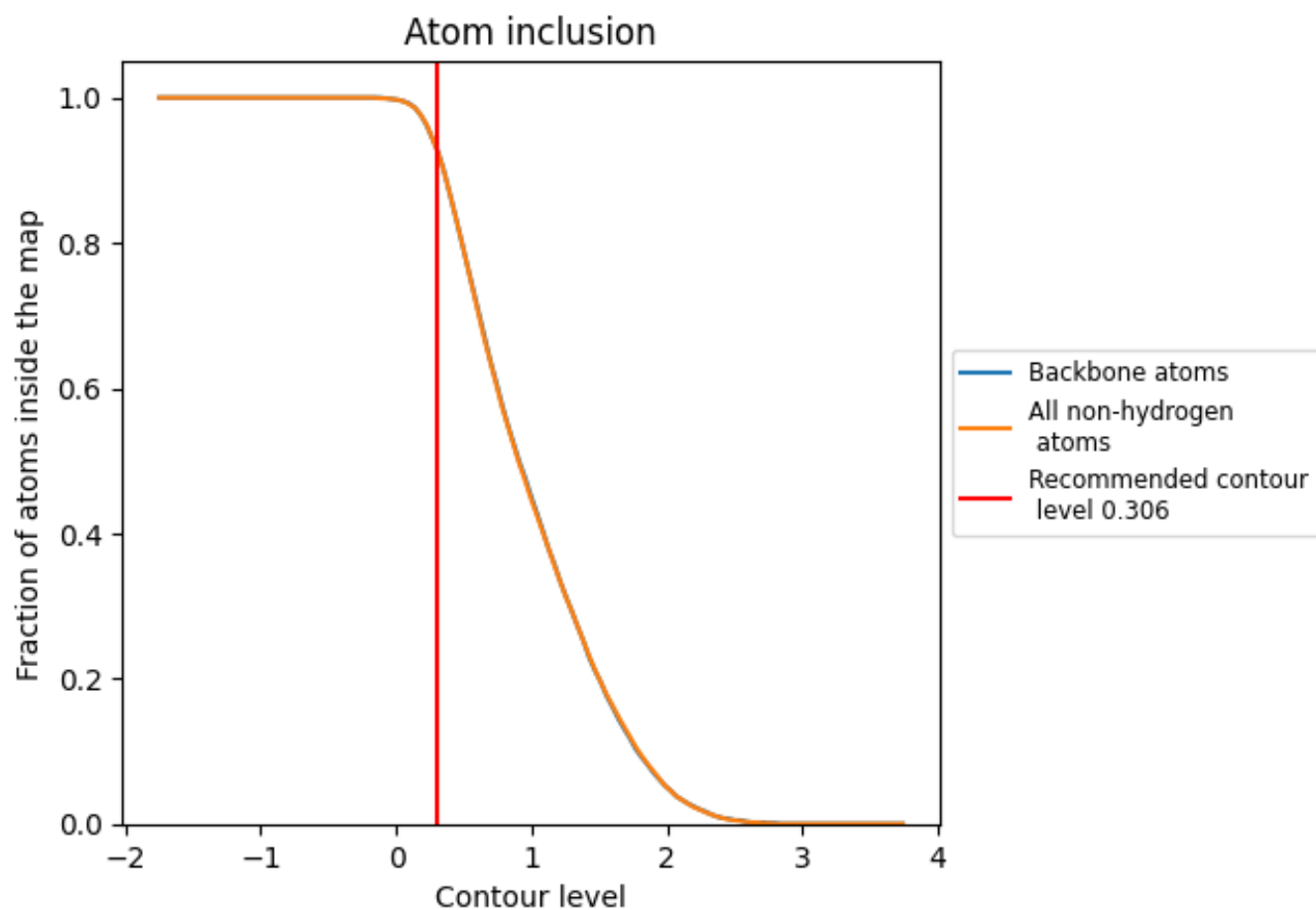
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.306).































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.306) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9270	 0.5320
1	 0.9480	 0.5560
2	 0.9490	 0.5690
A	 0.9500	 0.5350
B	 0.9270	 0.5380
C	 0.8490	 0.4300
D	 0.8740	 0.4460
E	 0.8820	 0.4610
F	 0.9370	 0.5320
G	 0.9390	 0.5350
H	 0.9540	 0.5640
I	 0.9630	 0.5750
J	 0.9630	 0.5790
K	 0.9590	 0.5680
L	 0.9570	 0.5740
M	 0.9520	 0.5620
N	 0.9530	 0.5700
O	 0.9530	 0.5340
P	 0.9290	 0.5380
Q	 0.8430	 0.4280
R	 0.8670	 0.4400
S	 0.8820	 0.4640
T	 0.9290	 0.5300
U	 0.9440	 0.5330
V	 0.9580	 0.5630
W	 0.9650	 0.5790
X	 0.9600	 0.5760
Y	 0.9560	 0.5670
Z	 0.9630	 0.5700
a	 0.8430	 0.5100
b	 0.8650	 0.5210

