



wwPDB EM Validation Summary Report ⓘ

Nov 22, 2022 – 03:40 AM EST

PDB ID : 7TEO
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

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

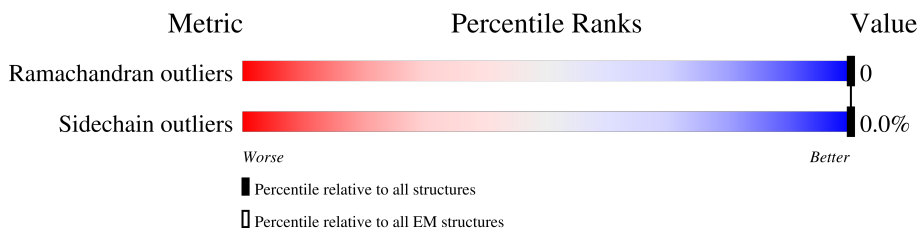
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

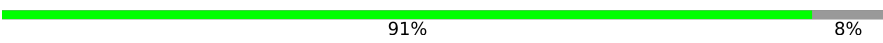
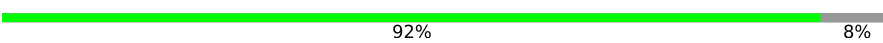


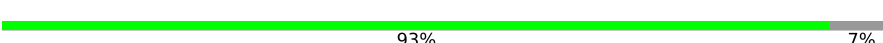

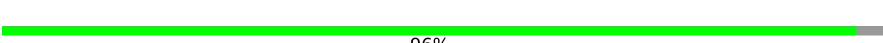
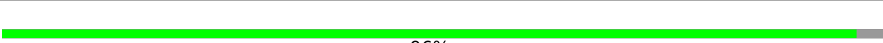

The reported resolution of this entry is 2.97 Å.

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.








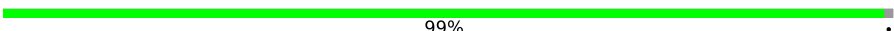







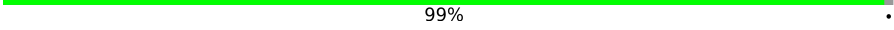
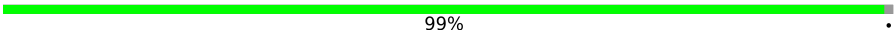
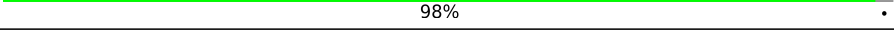
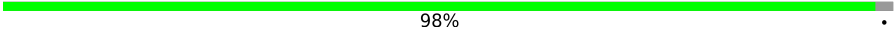




Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1	241	 91% 8%
1	M	241	 92% 8%
2	2	266	 86% 14%
2	N	266	 86% 14%
3	A	252	 93% 7%
3	O	252	 93% 7%
4	B	250	 96% .
4	P	250	 96% .
5	C	254	 87% 13%

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Mol	Chain	Length	Quality of chain
5	D	254	 82% 18%
5	Q	254	 87% 13%
5	R	254	 82% 18%
6	E	260	 80% 20%
6	S	260	 80% 20%
7	F	234	 99% .
7	T	234	 99% .
8	G	288	 84% 16%
8	U	288	 84% 16%
9	H	215	 91% 9%
9	V	215	 91% 9%
10	I	261	 84% 16%
10	W	261	 84% 16%
11	J	205	 99% .
11	X	205	 99% .
12	K	198	 98% .
12	Y	198	 98% .
13	L	287	 74% 26%
13	Z	287	 74% 26%
14	a	250	 32% 68%
14	b	250	 32% 68%

2 Entry composition

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

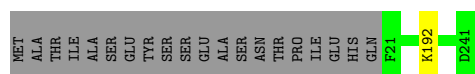
Mol	Chain	Residues	Atoms						AltConf	Trace
14	a	81	Total	C	H	N	O	S	0	0
			1177	393	559	101	121	3		
14	b	81	Total	C	H	N	O	S	0	0
			1177	393	559	101	121	3		

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.

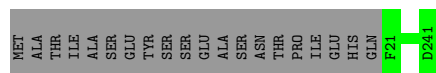
- Molecule 1: Proteasome subunit beta type-6

Chain 1:  91% 8%




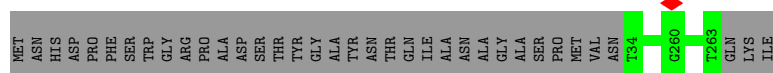
- Molecule 1: Proteasome subunit beta type-6

Chain M:  92% 8%




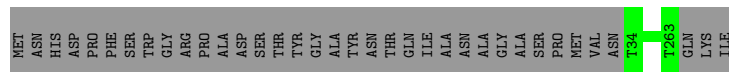
- Molecule 2: Proteasome subunit beta type-7

Chain 2:  86% 14%



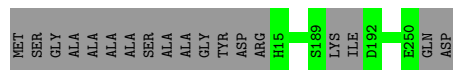
- Molecule 2: Proteasome subunit beta type-7

Chain N:  86% 14%

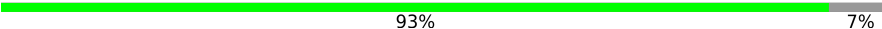


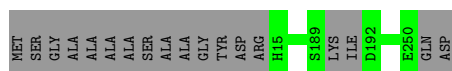
- Molecule 3: Proteasome subunit alpha type-1

Chain A:  93% 7%



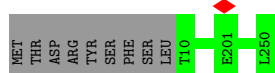
- Molecule 3: Proteasome subunit alpha type-1

Chain O:  93% 7%



- Molecule 4: Proteasome subunit alpha type-2

Chain B:  96% .



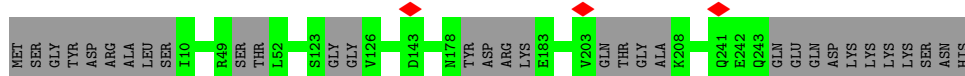
- Molecule 4: Proteasome subunit alpha type-2

Chain P:  96% .




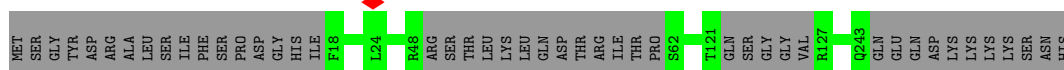
- Molecule 5: Proteasome subunit alpha type-4

Chain C:  87% 13%



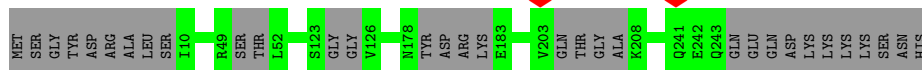
- Molecule 5: Proteasome subunit alpha type-4

Chain D:  82% 18%




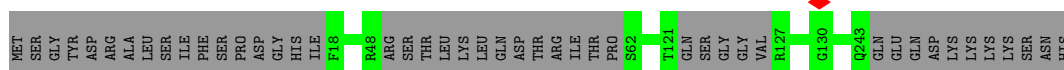
- Molecule 5: Proteasome subunit alpha type-4

Chain Q:  87% 13%



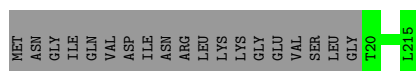
- Molecule 5: Proteasome subunit alpha type-4

Chain R:  82% 18%



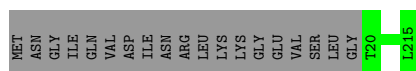
- Molecule 9: Proteasome subunit beta type-1

Chain H:  91% 9%




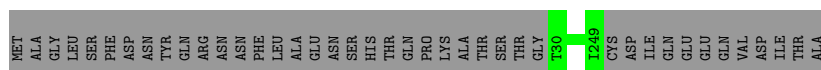
- Molecule 9: Proteasome subunit beta type-1

Chain V:  91% 9%




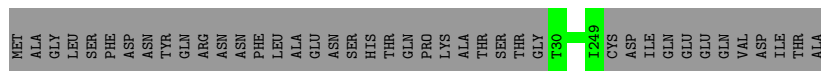
- Molecule 10: Proteasome subunit beta type-2

Chain I:  84% 16%



- Molecule 10: Proteasome subunit beta type-2

Chain W:  84% 16%



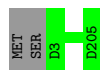
- Molecule 11: Proteasome subunit beta type-3

Chain J:  99% .



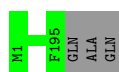
- Molecule 11: Proteasome subunit beta type-3

Chain X:  99% .



- Molecule 12: Proteasome subunit beta type-4

Chain K:  98% .



- Molecule 12: Proteasome subunit beta type-4

Chain Y:

98%

.

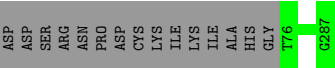
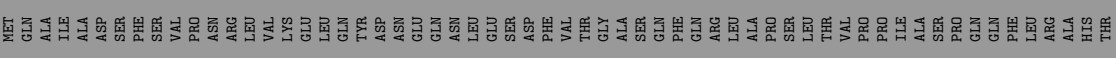


- Molecule 13: Proteasome subunit beta type-5

Chain L:

74%

26%

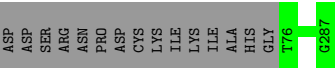
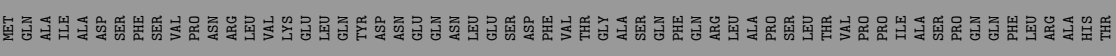


- Molecule 13: Proteasome subunit beta type-5

Chain Z:

74%

26%

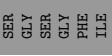
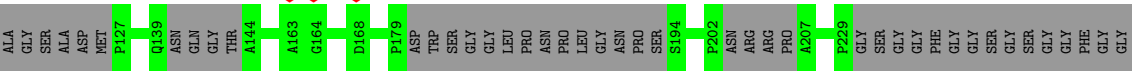
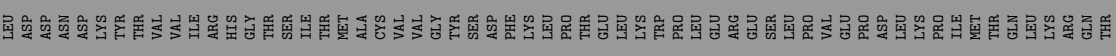
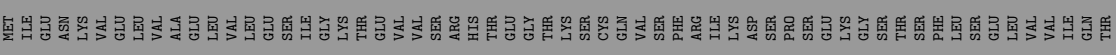


- Molecule 14: Silencing boundary-establishment protein FUB1

Chain a:

32%

68%

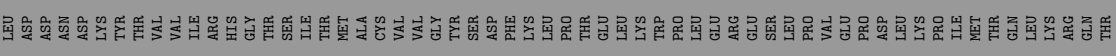
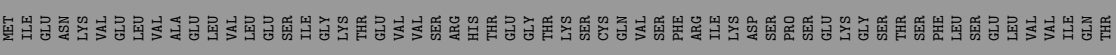


- Molecule 14: Silencing boundary-establishment protein FUB1

Chain b:

32%

68%





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 (Å)	381.59998, 381.59998, 381.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.26	0/1786	0.51	0/2408
1	M	0.26	0/1786	0.50	0/2408
2	2	0.25	0/1828	0.51	0/2480
2	N	0.25	0/1828	0.51	0/2480
3	A	0.26	0/1882	0.48	0/2549
3	O	0.27	0/1882	0.48	0/2549
4	B	0.26	0/1873	0.47	0/2536
4	P	0.26	0/1873	0.48	0/2536
5	C	0.25	0/1773	0.51	0/2396
5	D	0.25	0/1660	0.50	0/2244
5	Q	0.25	0/1773	0.51	0/2396
5	R	0.26	0/1660	0.51	0/2244
6	E	0.24	0/1612	0.47	0/2171
6	S	0.24	0/1612	0.47	0/2171
7	F	0.24	0/1800	0.50	0/2433
7	T	0.25	0/1800	0.50	0/2433
8	G	0.26	0/1932	0.47	0/2609
8	U	0.26	0/1932	0.47	0/2609
9	H	0.26	0/1541	0.48	0/2087
9	V	0.26	0/1541	0.49	0/2087
10	I	0.25	0/1701	0.49	0/2307
10	W	0.25	0/1701	0.49	0/2307
11	J	0.26	0/1605	0.48	0/2166
11	X	0.27	0/1605	0.49	0/2166
12	K	0.26	0/1589	0.50	0/2142
12	Y	0.27	0/1589	0.50	0/2142
13	L	0.27	0/1681	0.51	0/2274
13	Z	0.27	0/1681	0.51	0/2274
14	a	0.27	0/641	0.45	0/873
14	b	0.25	0/641	0.44	0/873
All	All	0.26	0/49808	0.49	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 [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 ⓘ

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%)	183 (100%)	1 (0%)	88	95
1	M	184/201 (92%)	184 (100%)	0	100	100
2	2	196/224 (88%)	196 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	200 (100%)	1 (0%)	88	95
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%)	5290 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	192	LYS
8	G	168	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
6	E	73	HIS
6	E	147	HIS
7	F	69	HIS
7	T	69	HIS

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 monosaccharides 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.

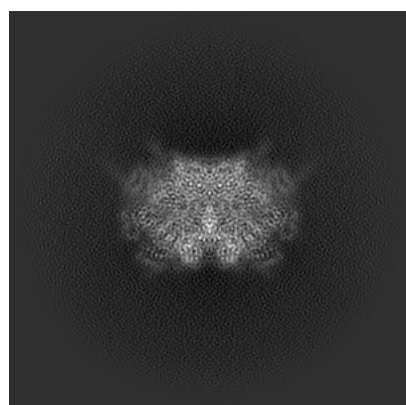
6 Map visualisation [i](#)

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.

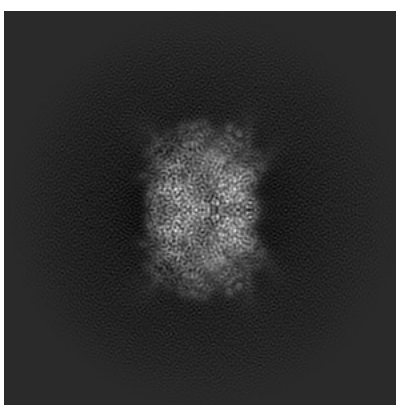
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

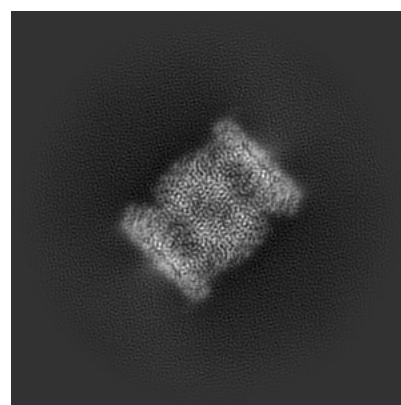
6.1.1 Primary map



X



Y

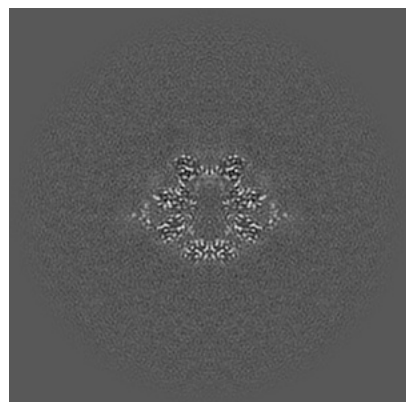


Z

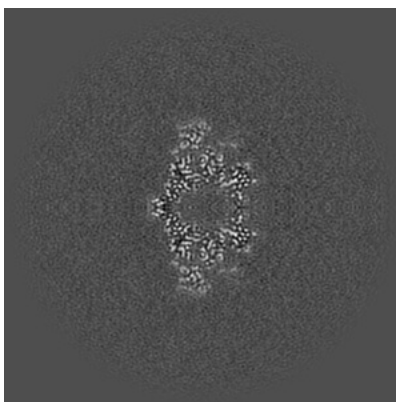
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

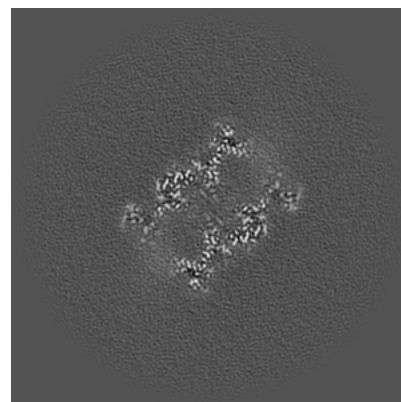
6.2.1 Primary map



X Index: 180



Y Index: 180

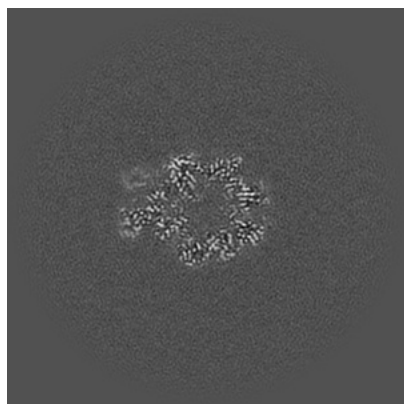


Z Index: 180

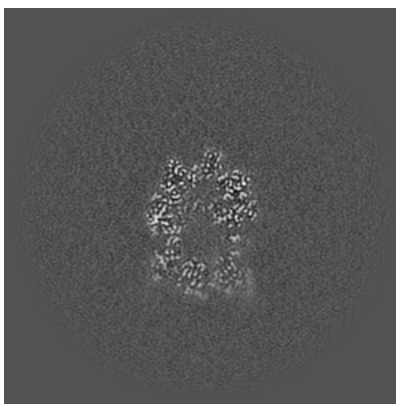
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

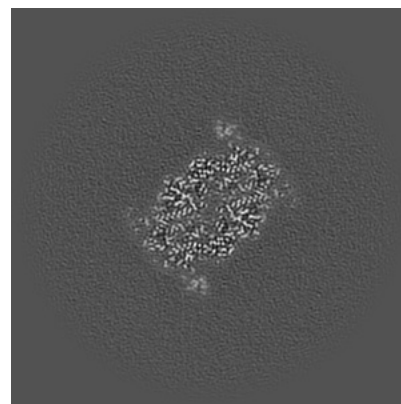
6.3.1 Primary map



X Index: 173



Y Index: 164

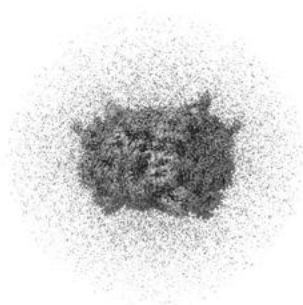


Z Index: 155

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

6.4 Orthogonal surface views [i](#)

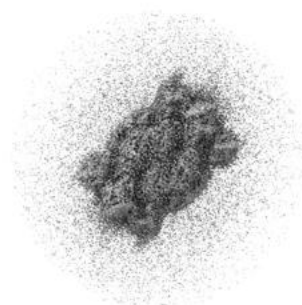
6.4.1 Primary map



X



Y



Z

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.

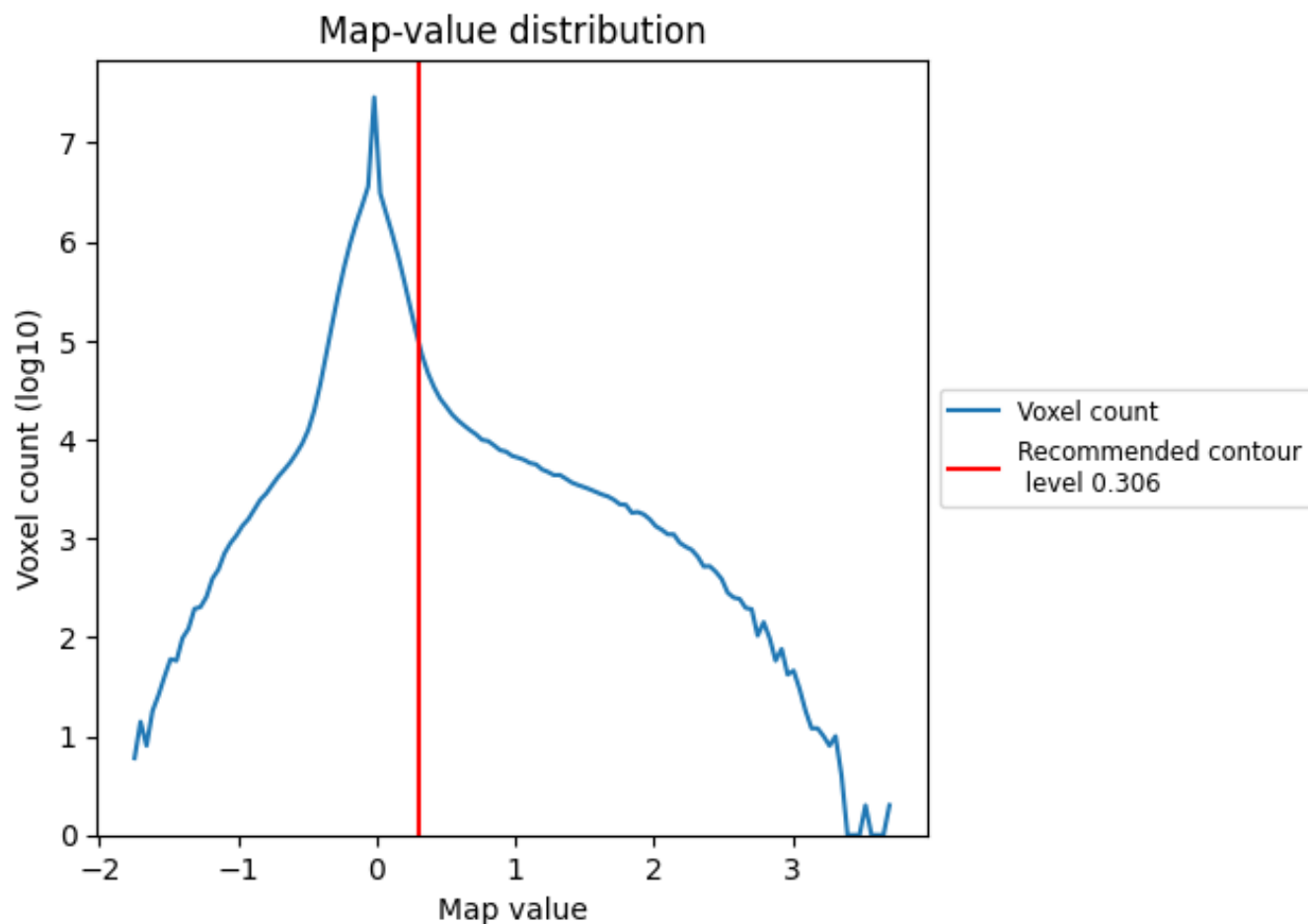
6.5 Mask visualisation

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

7 Map analysis [i](#)

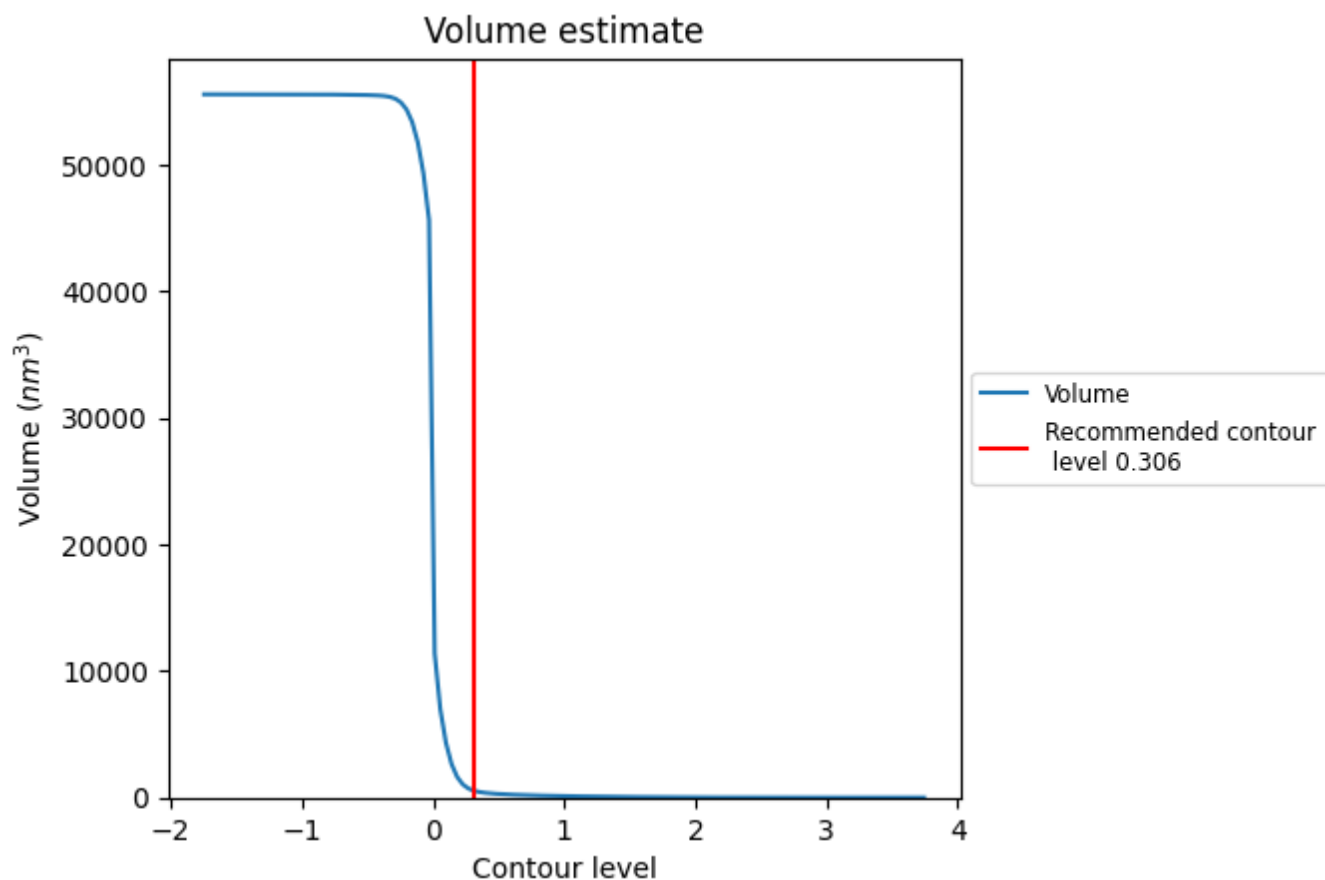
This section contains the results of statistical analysis of the map.

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.

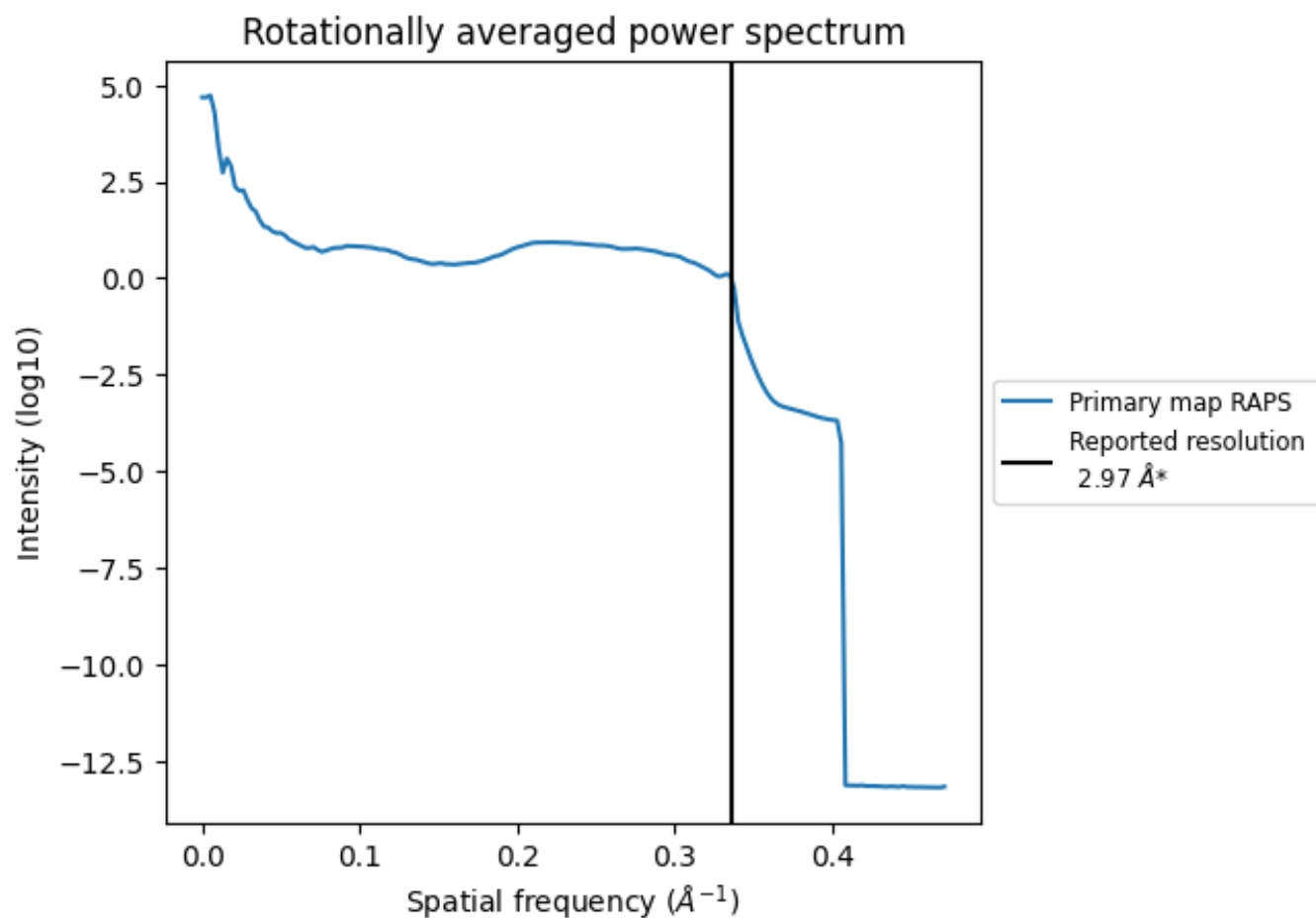
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 563 nm³; 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.337 Å⁻¹

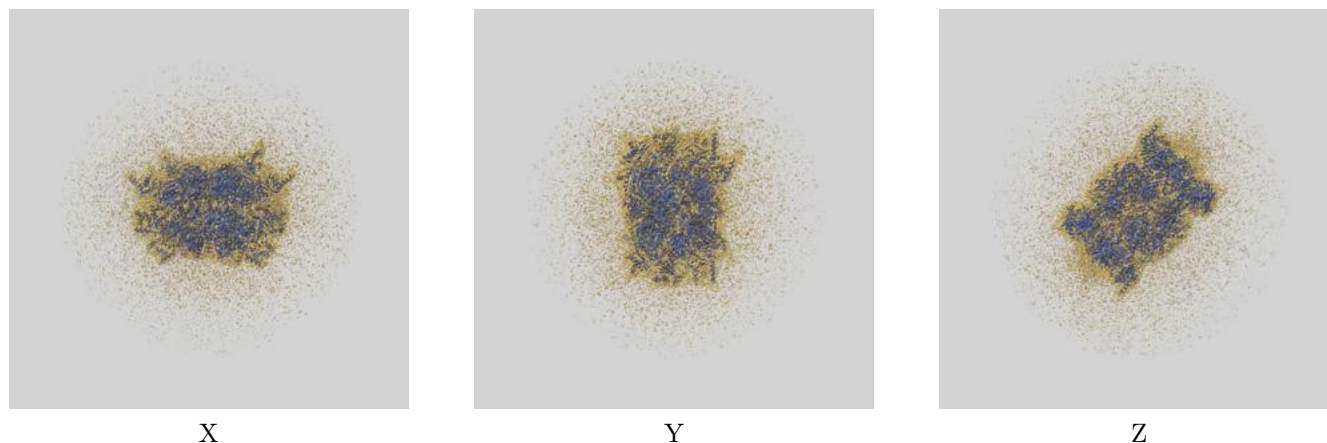
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

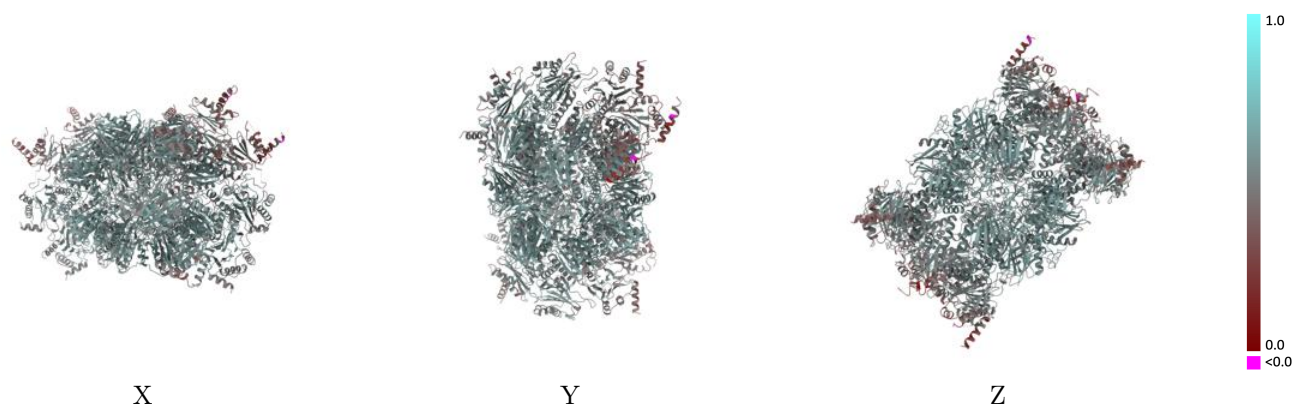
This section contains information regarding the fit between EMDB map EMD-25848 and PDB model 7TEO. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



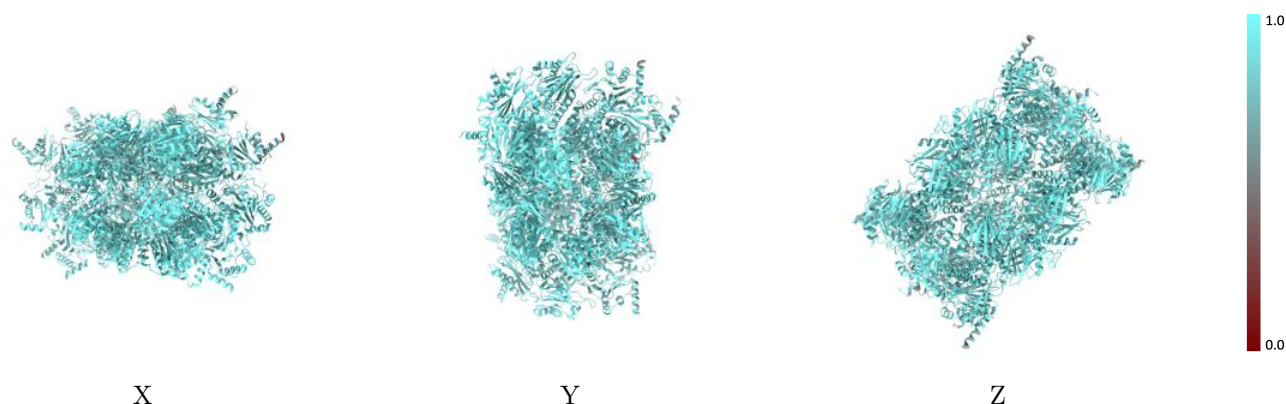
The images above show the 3D surface view of the map at the recommended contour level 0.306 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



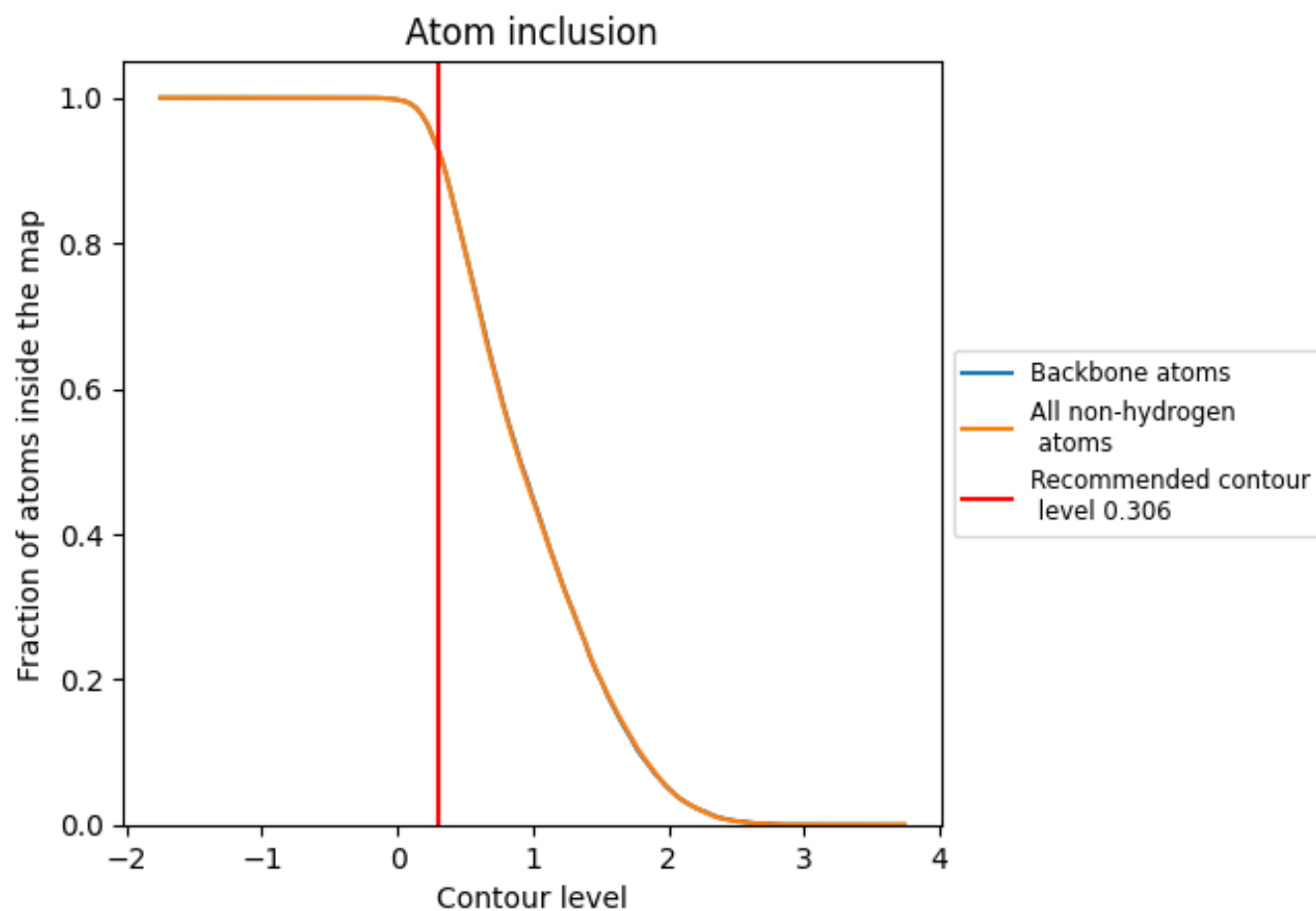
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.9274	 0.5320
1	 0.9475	 0.5560
2	 0.9489	 0.5690
A	 0.9504	 0.5350
B	 0.9271	 0.5380
C	 0.8489	 0.4300
D	 0.8740	 0.4460
E	 0.8818	 0.4610
F	 0.9367	 0.5320
G	 0.9393	 0.5350
H	 0.9542	 0.5640
I	 0.9629	 0.5750
J	 0.9632	 0.5790
K	 0.9594	 0.5680
L	 0.9571	 0.5740
M	 0.9515	 0.5620
N	 0.9534	 0.5700
O	 0.9531	 0.5340
P	 0.9293	 0.5380
Q	 0.8425	 0.4280
R	 0.8665	 0.4400
S	 0.8825	 0.4640
T	 0.9287	 0.5300
U	 0.9436	 0.5330
V	 0.9582	 0.5630
W	 0.9653	 0.5790
X	 0.9600	 0.5760
Y	 0.9555	 0.5670
Z	 0.9627	 0.5700
a	 0.8432	 0.5100
b	 0.8647	 0.5210

