



wwPDB EM Validation Summary Report ⓘ

Jul 13, 2026 – 02:10 PM EDT

PDB ID : 10QT / pdb_000010qt
EMDB ID : EMD-75393
Title : C2 expanded and subtracted 20S Alpha 3 Deletion proteasome core particle
in complex with Blm10, Halfmer
Authors : Walsh Jr., R.M.; Rawson, S.; Fermin Perez, E.; Venclovaite, U.; Hanna, J.
Deposited on : 2026-02-02
Resolution : 3.40 Å(reported)
Based on initial model : 10MT

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

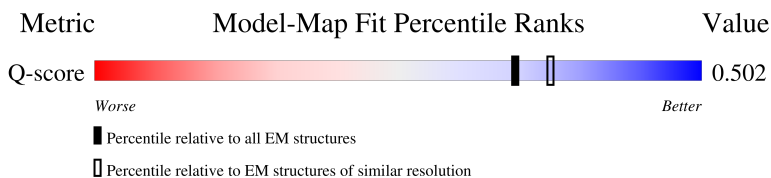
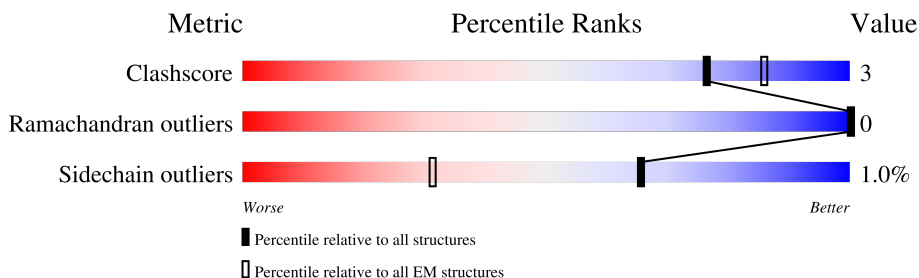
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

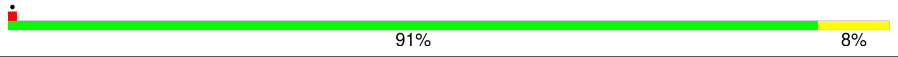
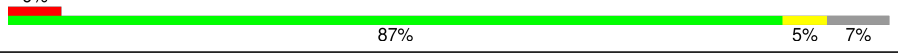
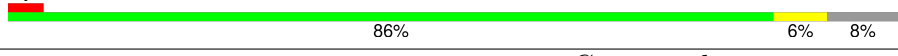
The reported resolution of this entry is 3.40 Å.

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.



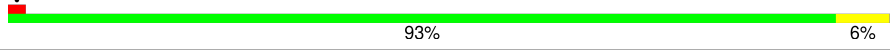
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	252	
2	B	250	
3	C	254	
3	D	254	

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Mol	Chain	Length	Quality of chain
4	E	260	
5	F	234	
6	G	288	
7	H	215	
8	I	261	
9	J	205	
10	K	198	
11	L	287	
12	M	241	
13	N	266	
14	CA	2167	

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 78939 atoms, of which 39452 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	238	Total	C	H	N	O	S	0	0
			3764	1198	1882	316	360	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	249	Total	C	H	N	O	S	0	0
			3826	1214	1919	314	376	3		

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	235	Total	C	H	N	O	S	0	0
			3698	1151	1856	322	365	4		
3	D	234	Total	C	H	N	O	S	0	0
			3687	1148	1851	321	363	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	E	241	Total	C	H	N	O	S	0	0
			3694	1163	1835	313	376	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	F	234	Total	C	H	N	O	S	0	0
			3613	1134	1810	313	351	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	G	242	Total	C	H	N	O	S	0	0
			3762	1199	1877	328	354	4		

- Molecule 7 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	H	195	Total	C	H	N	O	S	0	0
			2971	949	1468	249	298	7		

- Molecule 8 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	I	220	Total	C	H	N	O	S	0	0
			3348	1054	1678	291	319	6		

- Molecule 9 is a protein called Proteasome subunit beta type-3.

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

- Molecule 10 is a protein called Proteasome subunit beta type-4.

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

- Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	L	211	Total	C	H	N	O	S	0	0
			3229	1043	1590	279	310	7		

- Molecule 12 is a protein called Proteasome subunit beta type-6.

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

- Molecule 13 is a protein called Proteasome subunit beta type-7.

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

- Molecule 14 is a protein called Proteasome activator BLM10.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	CA	1849	Total	C	H	N	O	S	0	0
			30197	9727	15132	2501	2768	69		

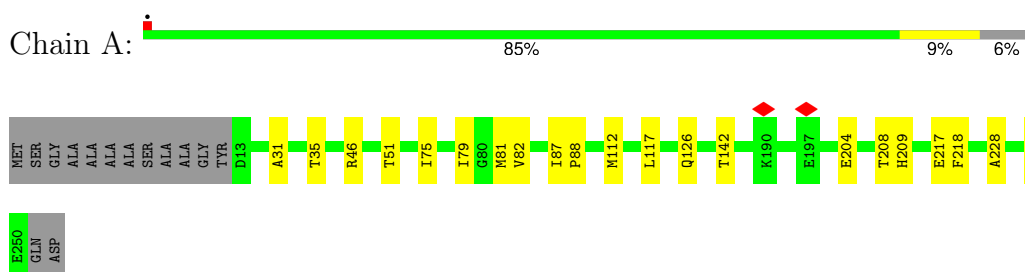
There are 24 discrepancies between the modelled and reference sequences:

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

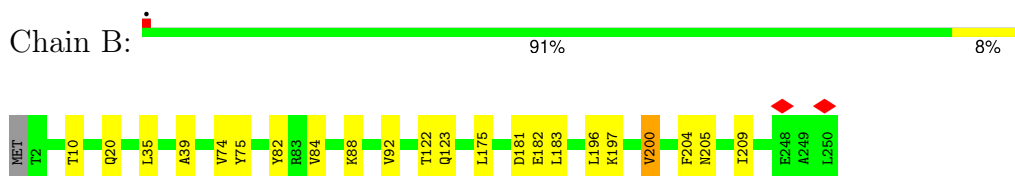
3 Residue-property plots [i](#)

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.

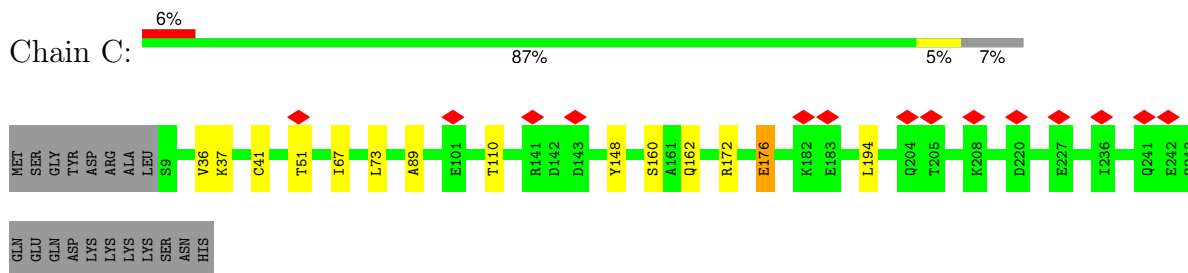
- Molecule 1: Proteasome subunit alpha type-1



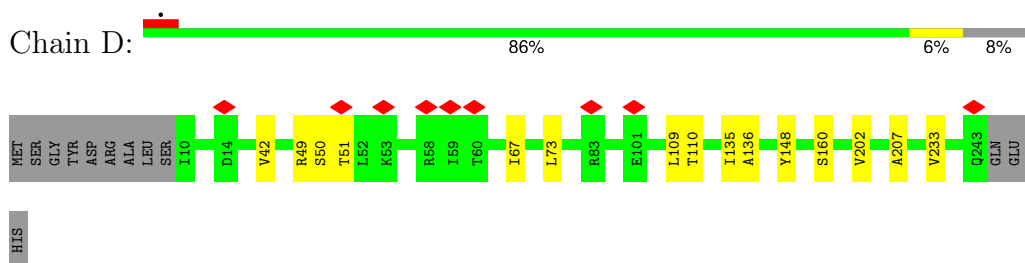
- Molecule 2: Proteasome subunit alpha type-2



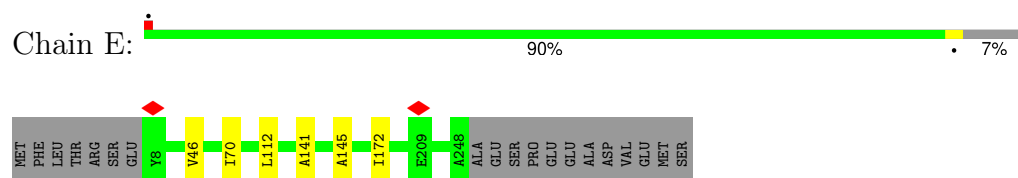
- Molecule 3: Proteasome subunit alpha type-4



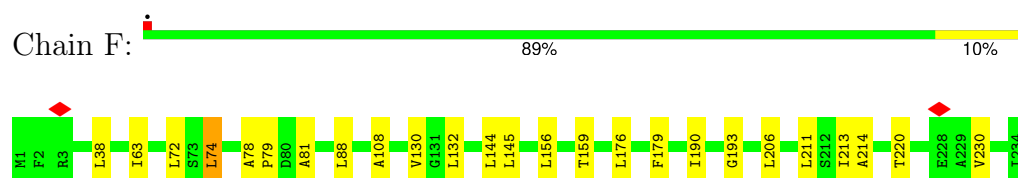
- Molecule 3: Proteasome subunit alpha type-4



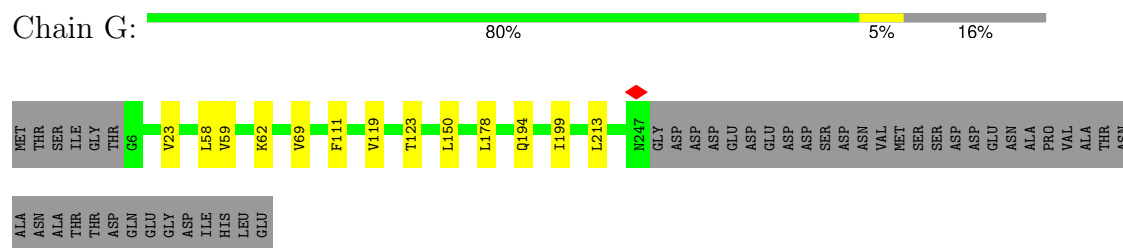
- Molecule 4: Proteasome subunit alpha type-5



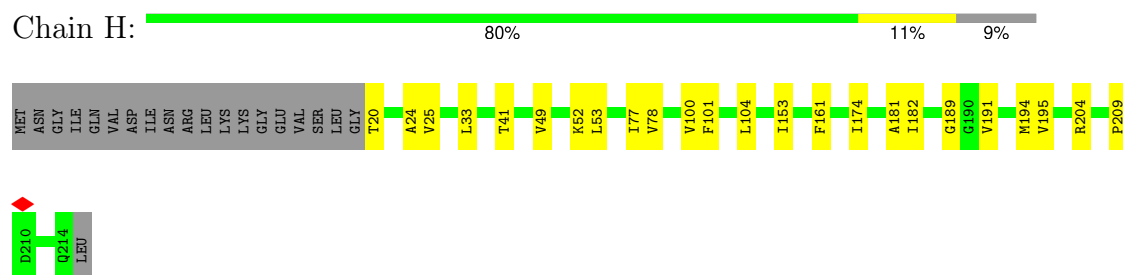
- Molecule 5: Proteasome subunit alpha type-6



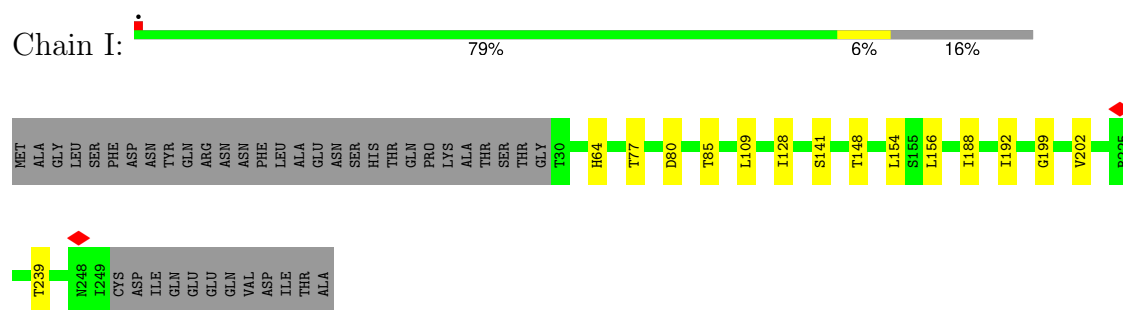
- Molecule 6: Proteasome subunit alpha type-7



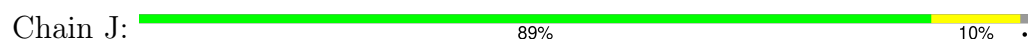
- Molecule 7: Proteasome subunit beta type-1



- Molecule 8: Proteasome subunit beta type-2



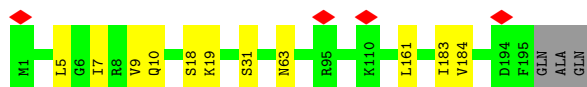
- Molecule 9: Proteasome subunit beta type-3





- Molecule 10: Proteasome subunit beta type-4

Chain K: 93% 6%



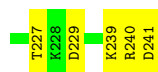
- Molecule 11: Proteasome subunit beta type-5

Chain L: 67% 6% 26%



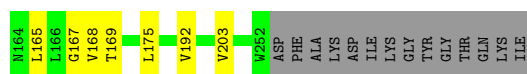
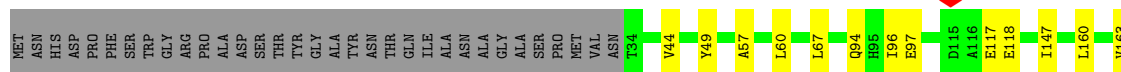
- Molecule 12: Proteasome subunit beta type-6

Chain M: 81% 10% 8%



- Molecule 13: Proteasome subunit beta type-7

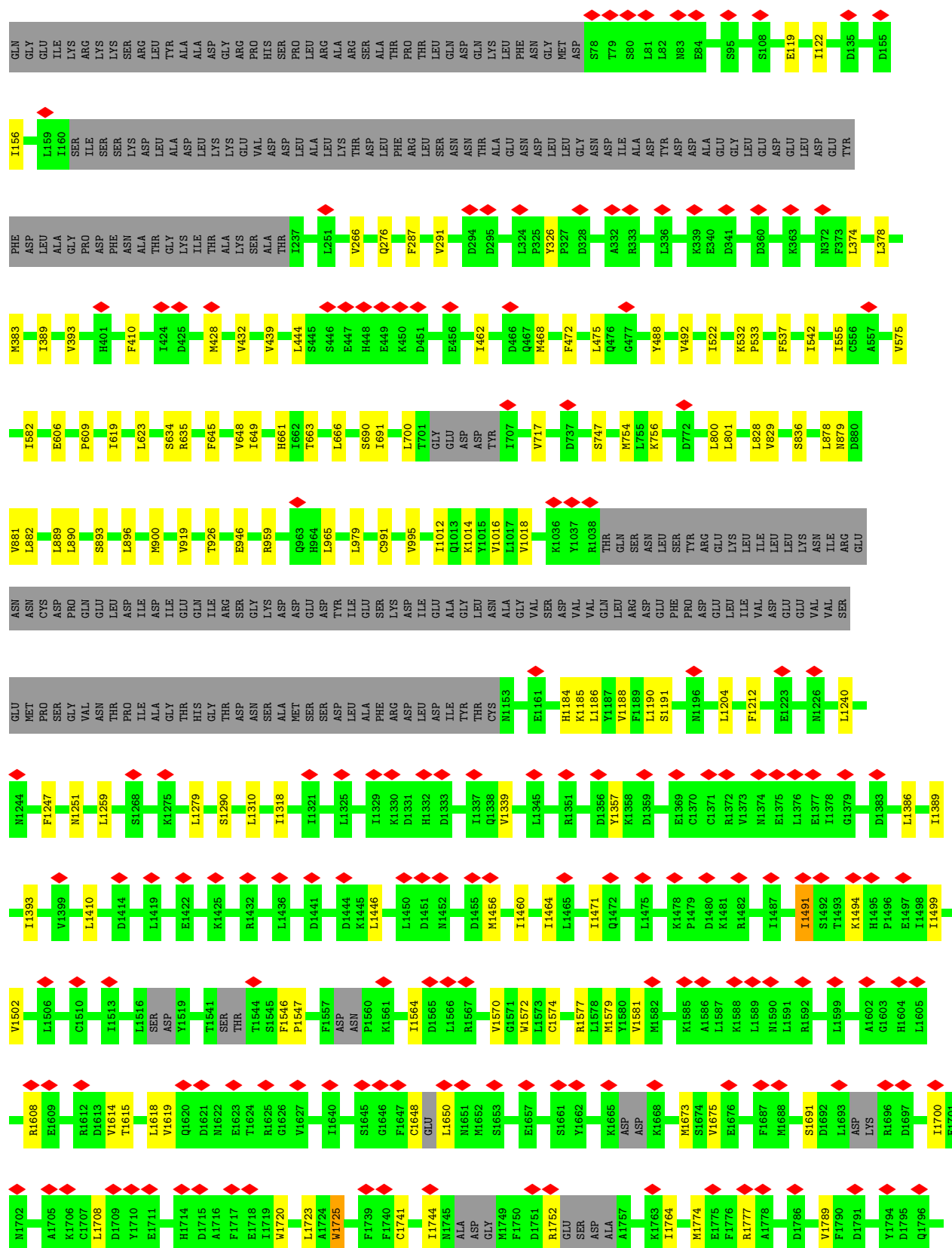
Chain N: 75% 8% 18%

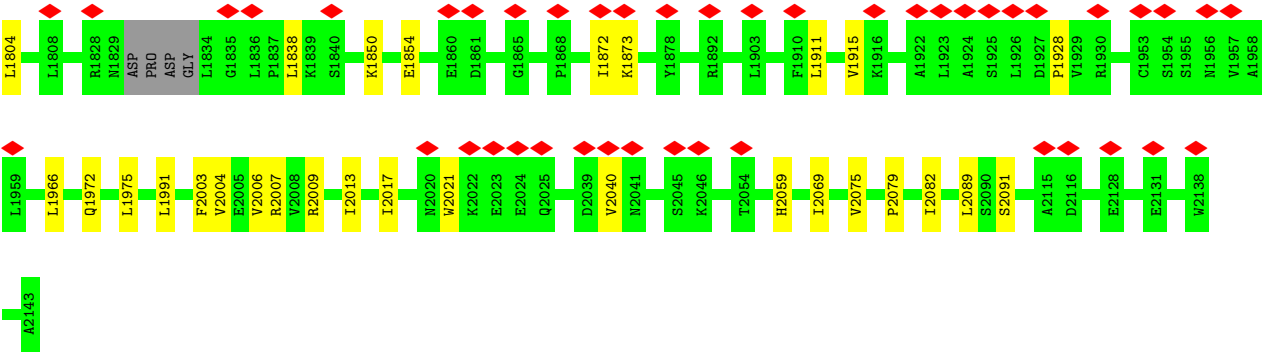


- Molecule 14: Proteasome activator BLM10

Chain CA: 10% 78% 8% 15%







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	59239	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.253	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.098	Depositor
Minimum map value	-0.055	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0138	Depositor
Map size (Å)	304.64, 304.64, 304.64	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	Depositor

5 Model quality [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	A	0.13	0/1919	0.27	0/2599
2	B	0.13	0/1944	0.30	0/2632
3	C	0.17	0/1870	0.42	0/2532
3	D	0.16	0/1864	0.39	0/2524
4	E	0.16	0/1885	0.36	0/2540
5	F	0.14	0/1831	0.30	0/2473
6	G	0.14	0/1925	0.29	0/2599
7	H	0.14	0/1532	0.29	0/2076
8	I	0.13	0/1701	0.27	0/2307
9	J	0.14	0/1605	0.29	0/2166
10	K	0.13	0/1589	0.28	0/2142
11	L	0.14	0/1676	0.28	0/2269
12	M	0.14	0/1786	0.29	0/2408
13	N	0.13	0/1741	0.29	0/2364
14	CA	0.11	0/15398	0.26	0/20843
All	All	0.13	0/40266	0.29	0/54474

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](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1882	1882	1881	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1907	1919	1917	15	0
3	C	1842	1856	1855	10	0
3	D	1836	1851	1850	10	0
4	E	1859	1835	1834	3	0
5	F	1803	1810	1809	15	0
6	G	1885	1877	1876	8	0
7	H	1503	1468	1467	14	0
8	I	1670	1678	1676	8	0
9	J	1575	1567	1566	10	0
10	K	1561	1569	1569	4	0
11	L	1639	1590	1589	11	0
12	M	1748	1701	1700	12	0
13	N	1712	1717	1716	11	0
14	CA	15065	15132	15118	93	0
All	All	39487	39452	39423	235	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 3.

The worst 5 of 235 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)
14:CA:1972:GLN:HB2	14:CA:2013:ILE:HD12	1.68	0.74
5:F:74:LEU:HD22	5:F:81:ALA:HB1	1.75	0.69
13:N:60:LEU:HD21	13:N:67:LEU:HD22	1.75	0.69
13:N:49:TYR:CE2	13:N:203:VAL:HG22	2.28	0.68
7:H:191:VAL:HG12	7:H:209:PRO:HD3	1.74	0.68

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	236/252 (94%)	230 (98%)	6 (2%)	0	100	100
2	B	247/250 (99%)	243 (98%)	4 (2%)	0	100	100
3	C	233/254 (92%)	231 (99%)	2 (1%)	0	100	100
3	D	232/254 (91%)	230 (99%)	2 (1%)	0	100	100
4	E	239/260 (92%)	239 (100%)	0	0	100	100
5	F	232/234 (99%)	229 (99%)	3 (1%)	0	100	100
6	G	240/288 (83%)	236 (98%)	4 (2%)	0	100	100
7	H	193/215 (90%)	186 (96%)	7 (4%)	0	100	100
8	I	218/261 (84%)	213 (98%)	5 (2%)	0	100	100
9	J	201/205 (98%)	196 (98%)	5 (2%)	0	100	100
10	K	193/198 (98%)	192 (100%)	1 (0%)	0	100	100
11	L	209/287 (73%)	205 (98%)	4 (2%)	0	100	100
12	M	219/241 (91%)	215 (98%)	4 (2%)	0	100	100
13	N	217/266 (82%)	214 (99%)	3 (1%)	0	100	100
14	CA	1823/2167 (84%)	1786 (98%)	37 (2%)	0	100	100
All	All	4932/5632 (88%)	4845 (98%)	87 (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	A	204/210 (97%)	203 (100%)	1 (0%)	81	81
2	B	208/209 (100%)	207 (100%)	1 (0%)	81	81
3	C	209/226 (92%)	206 (99%)	3 (1%)	59	70
3	D	208/226 (92%)	206 (99%)	2 (1%)	68	75
4	E	198/215 (92%)	198 (100%)	0	100	100
5	F	193/193 (100%)	191 (99%)	2 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	G	200/239 (84%)	199 (100%)	1 (0%)	81	81
7	H	161/178 (90%)	159 (99%)	2 (1%)	63	72
8	I	179/214 (84%)	179 (100%)	0	100	100
9	J	171/173 (99%)	169 (99%)	2 (1%)	63	72
10	K	173/175 (99%)	168 (97%)	5 (3%)	37	60
11	L	169/235 (72%)	168 (99%)	1 (1%)	78	80
12	M	184/201 (92%)	179 (97%)	5 (3%)	39	60
13	N	188/224 (84%)	187 (100%)	1 (0%)	81	81
14	CA	1707/1986 (86%)	1690 (99%)	17 (1%)	68	75
All	All	4352/4904 (89%)	4309 (99%)	43 (1%)	65	75

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	CA	374	LEU
14	CA	1491	ILE
14	CA	410	PHE
14	CA	1318	ILE
14	CA	1691	SER

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

Mol	Chain	Res	Type
14	CA	546	HIS
14	CA	1242	HIS
14	CA	664	ASN
14	CA	886	HIS
14	CA	1305	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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.

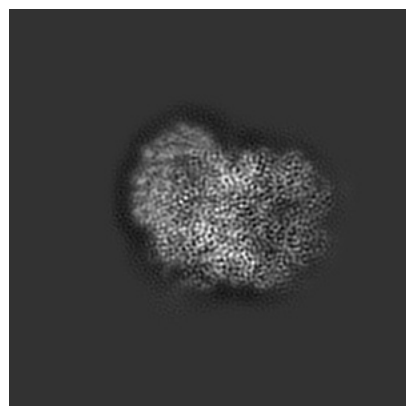
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75393. These allow visual inspection of the internal detail of the map and identification of artifacts.

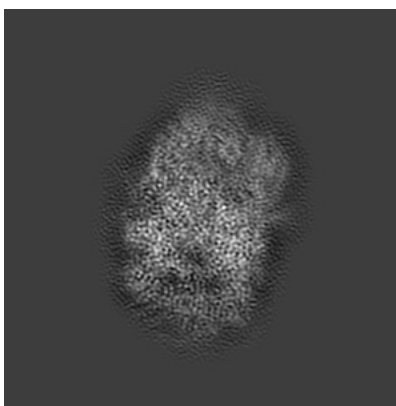
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

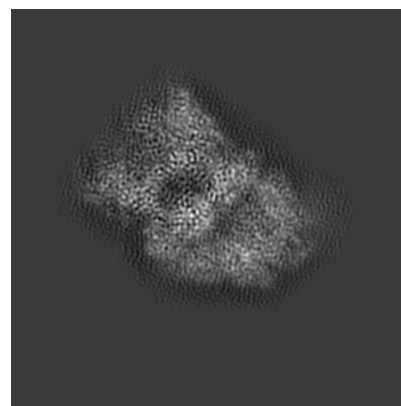
6.1.1 Primary map



X

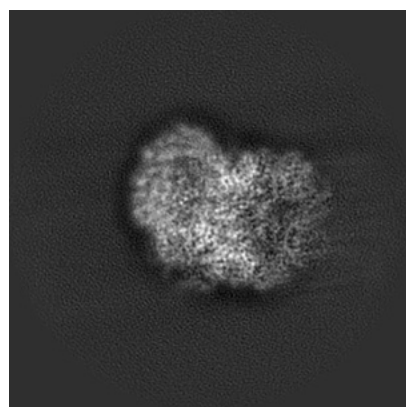


Y

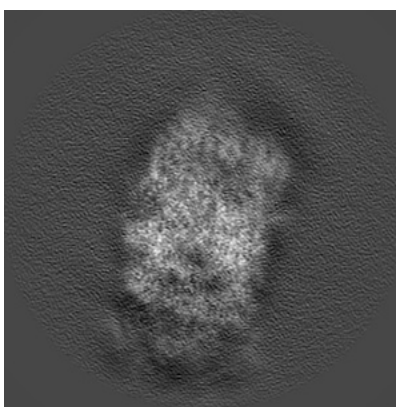


Z

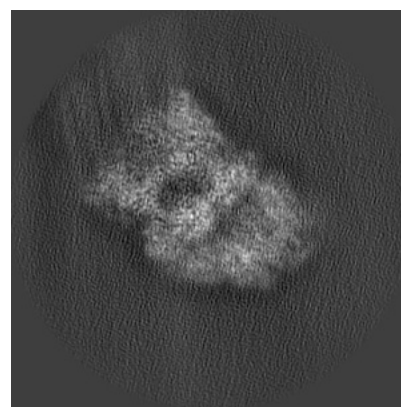
6.1.2 Raw map



X



Y

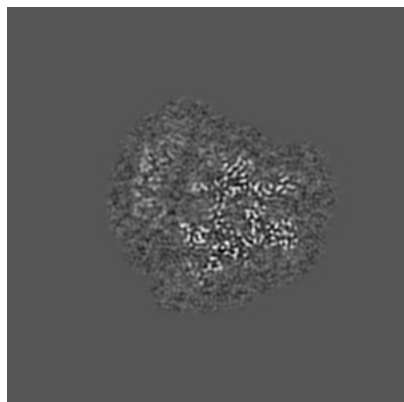


Z

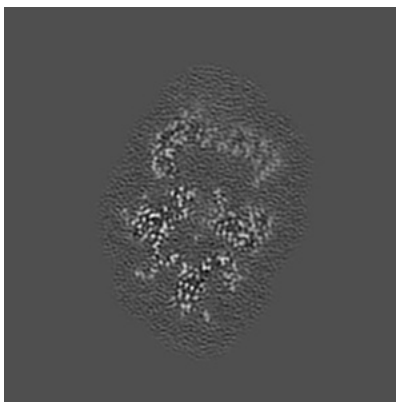
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

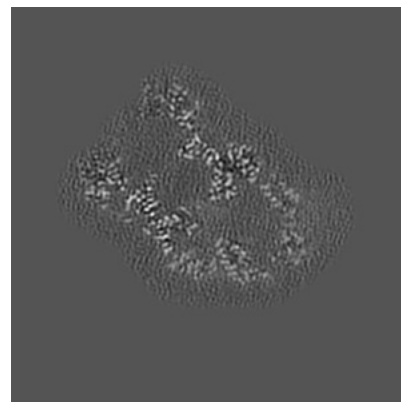
6.2.1 Primary map



X Index: 128

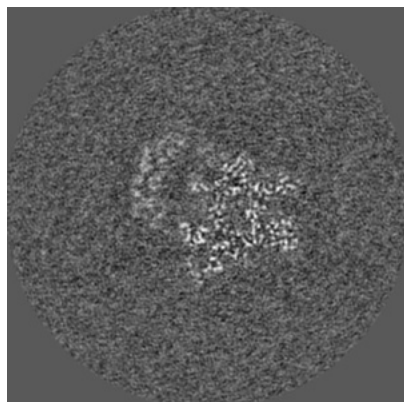


Y Index: 128

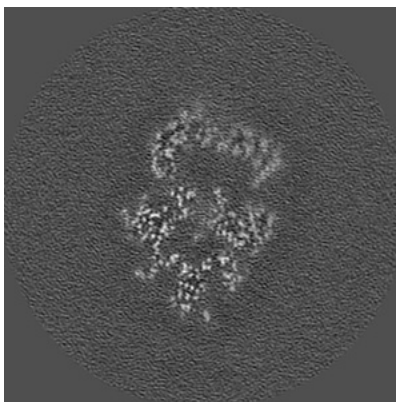


Z Index: 128

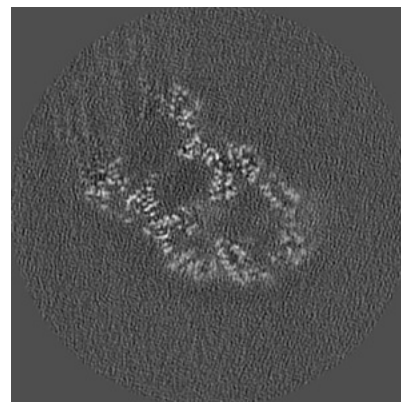
6.2.2 Raw map



X Index: 128



Y Index: 128

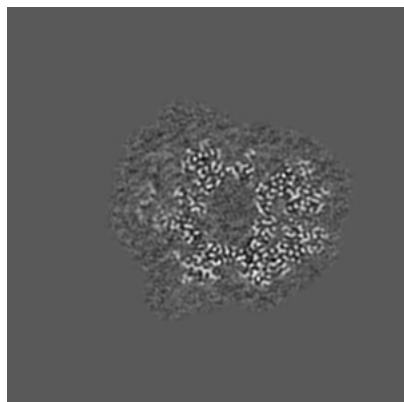


Z Index: 128

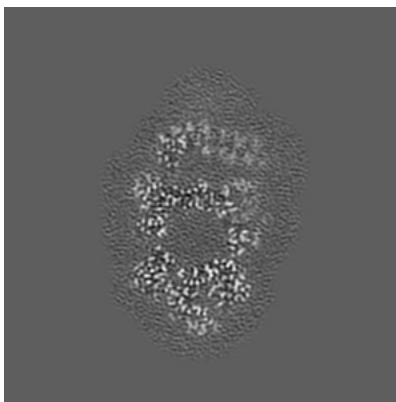
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

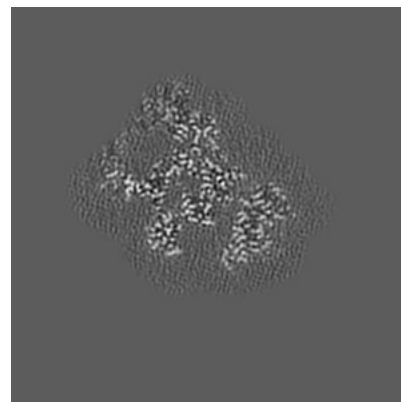
6.3.1 Primary map



X Index: 111

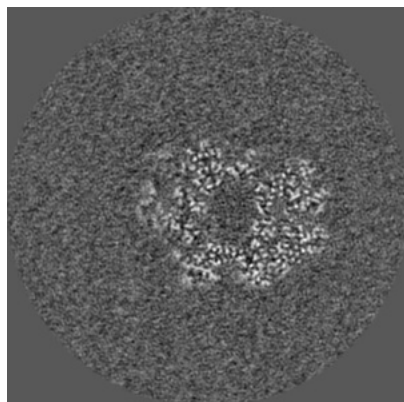


Y Index: 136

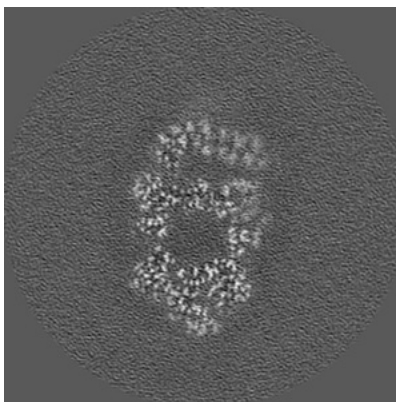


Z Index: 103

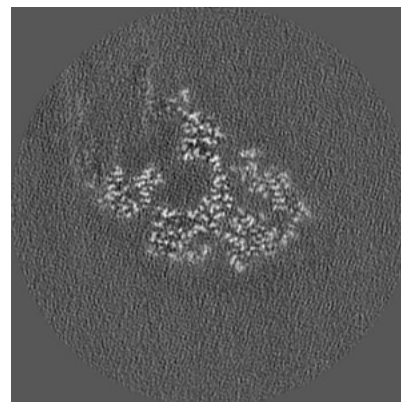
6.3.2 Raw map



X Index: 111



Y Index: 136

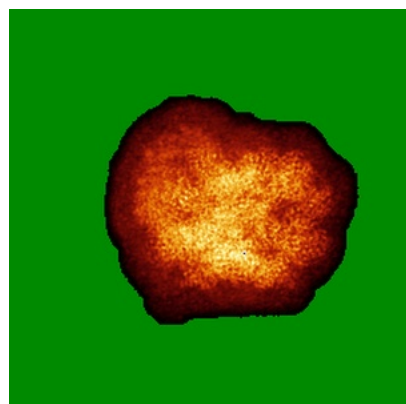


Z Index: 113

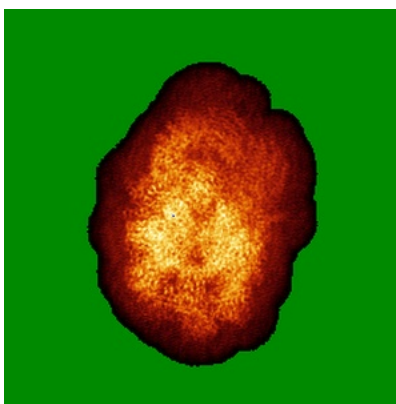
The images above show the largest variance slices of the map in three orthogonal directions.

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

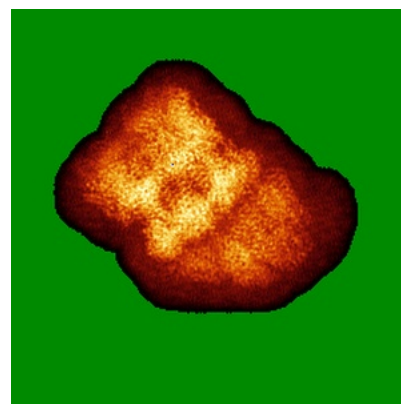
6.4.1 Primary map



X

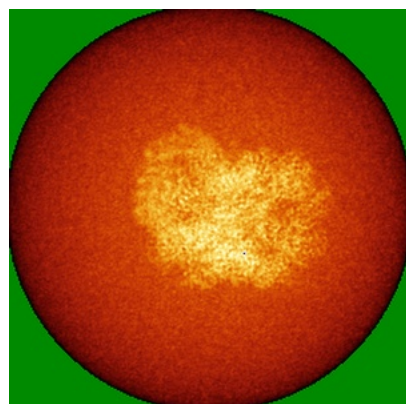


Y

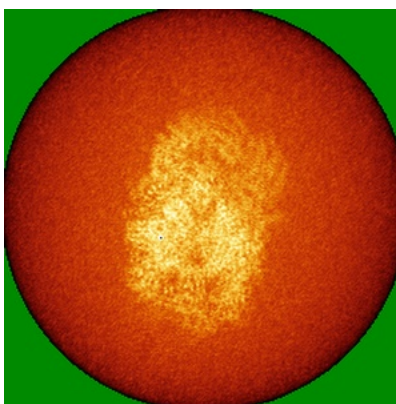


Z

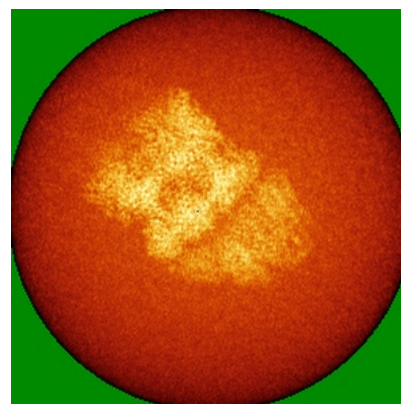
6.4.2 Raw map



X



Y

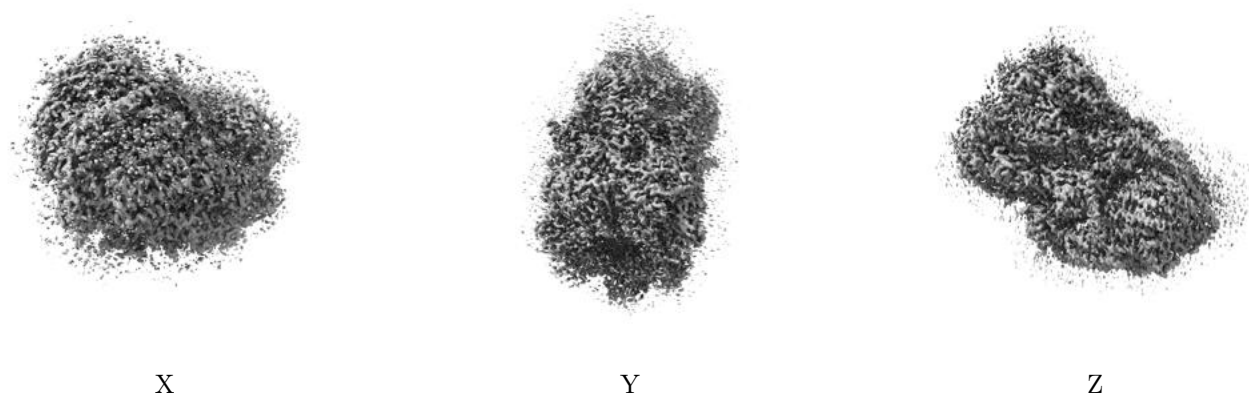


Z

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.

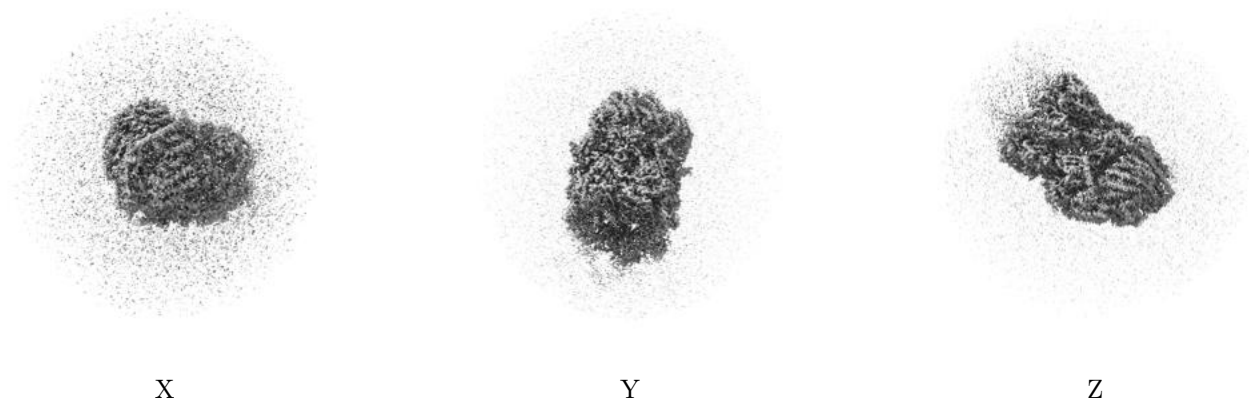
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0138. 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.

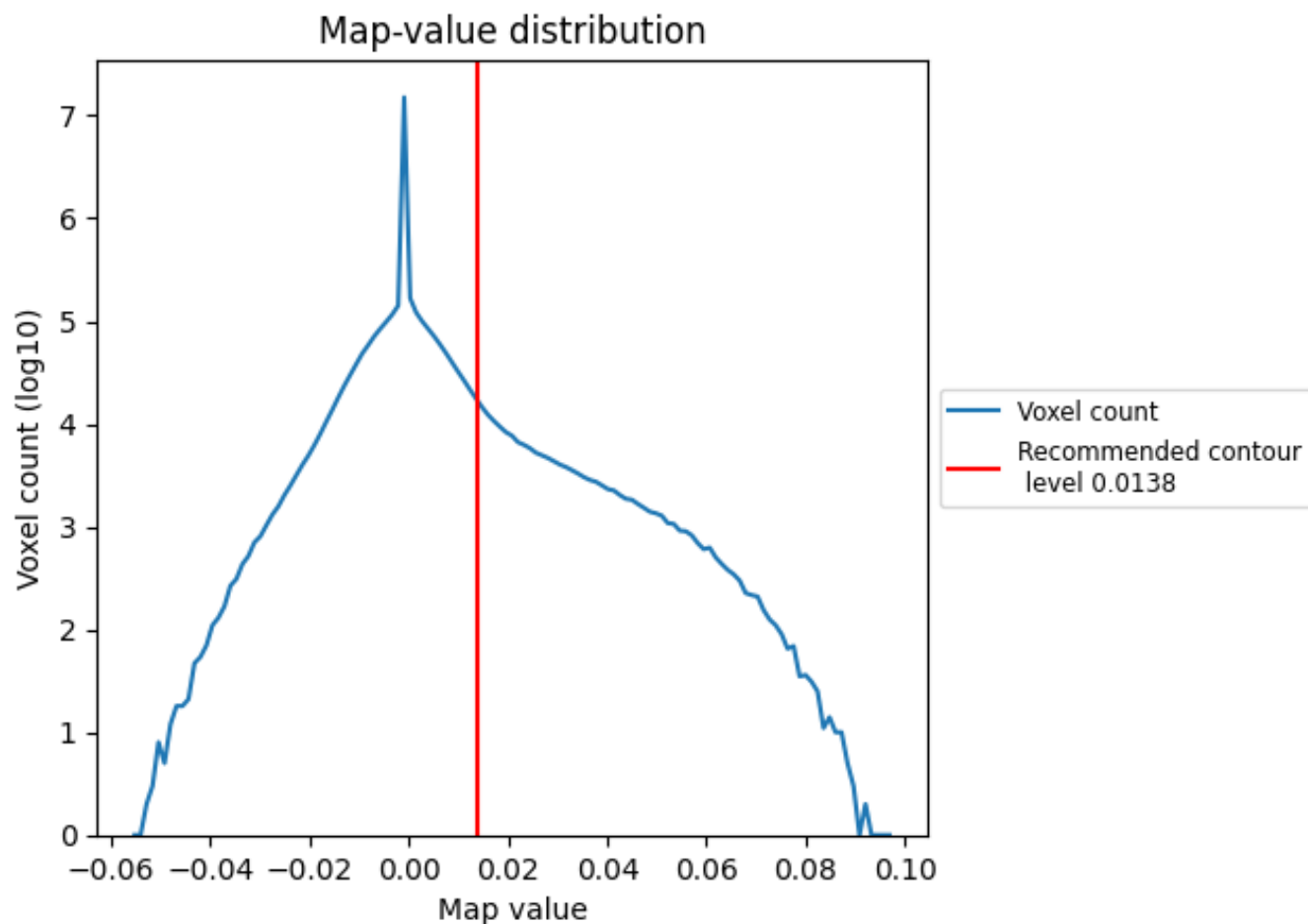
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

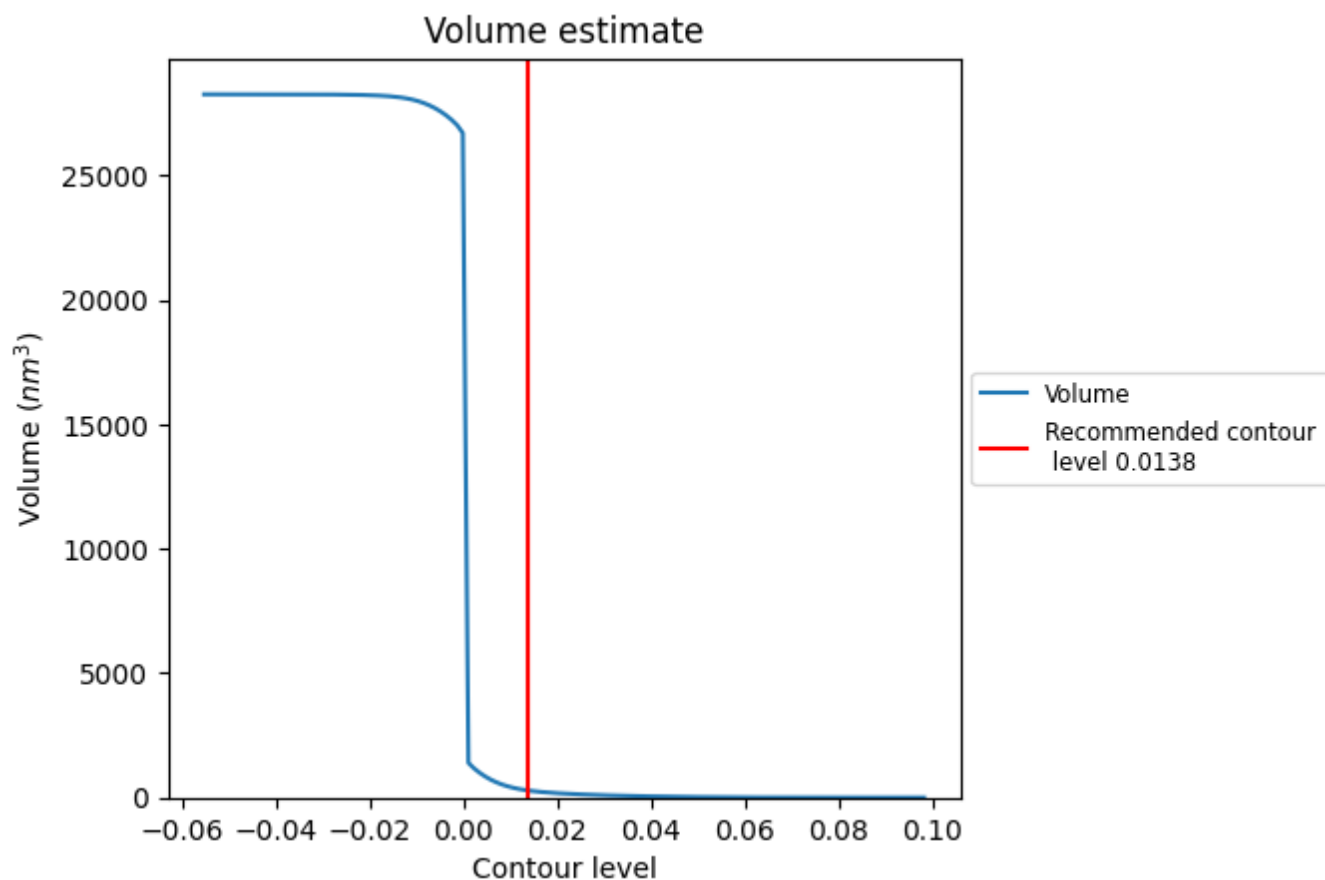
This section contains the results of statistical analysis of the map.

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.

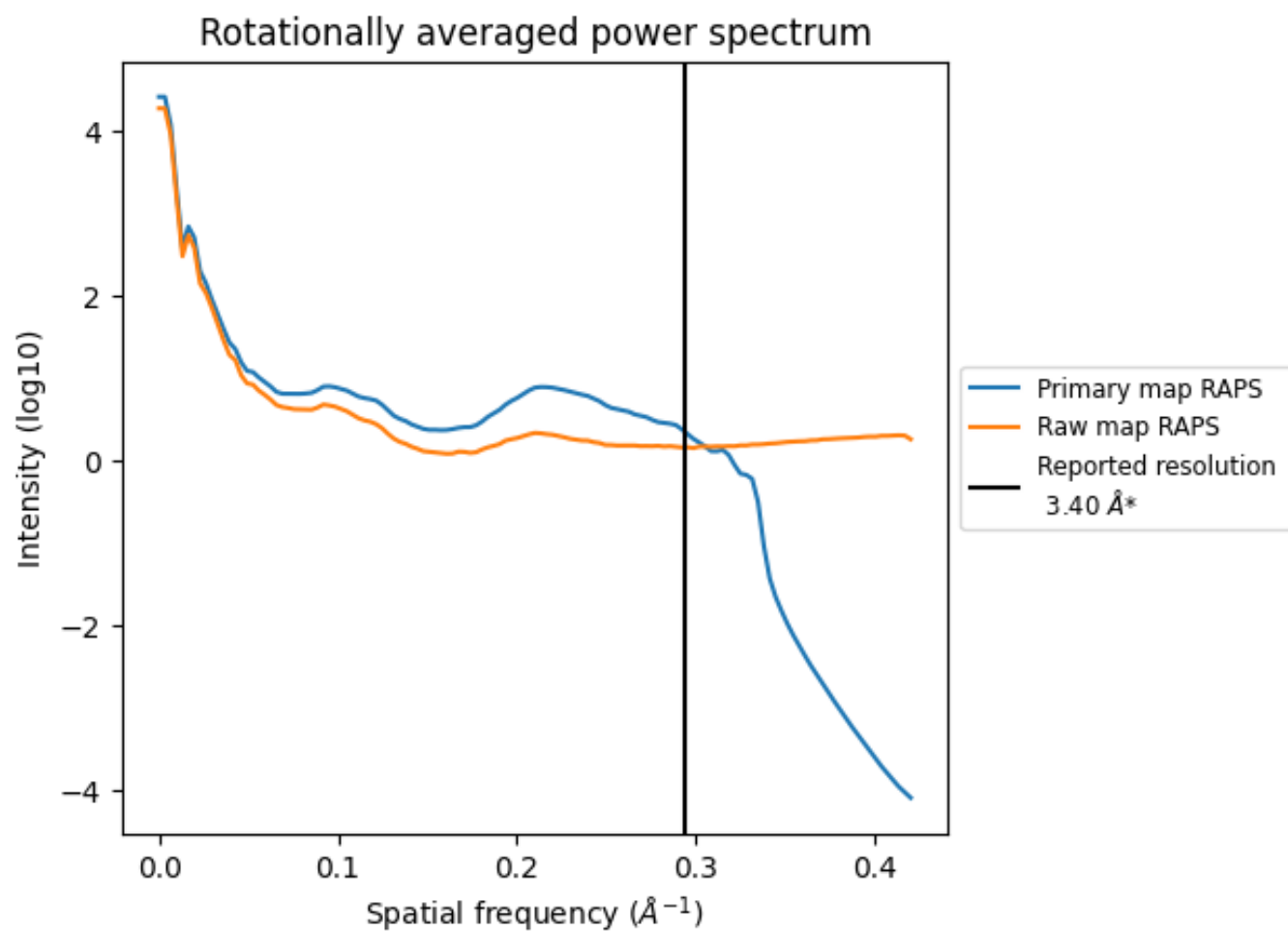
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 284 nm³; this corresponds to an approximate mass of 257 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 ⓘ

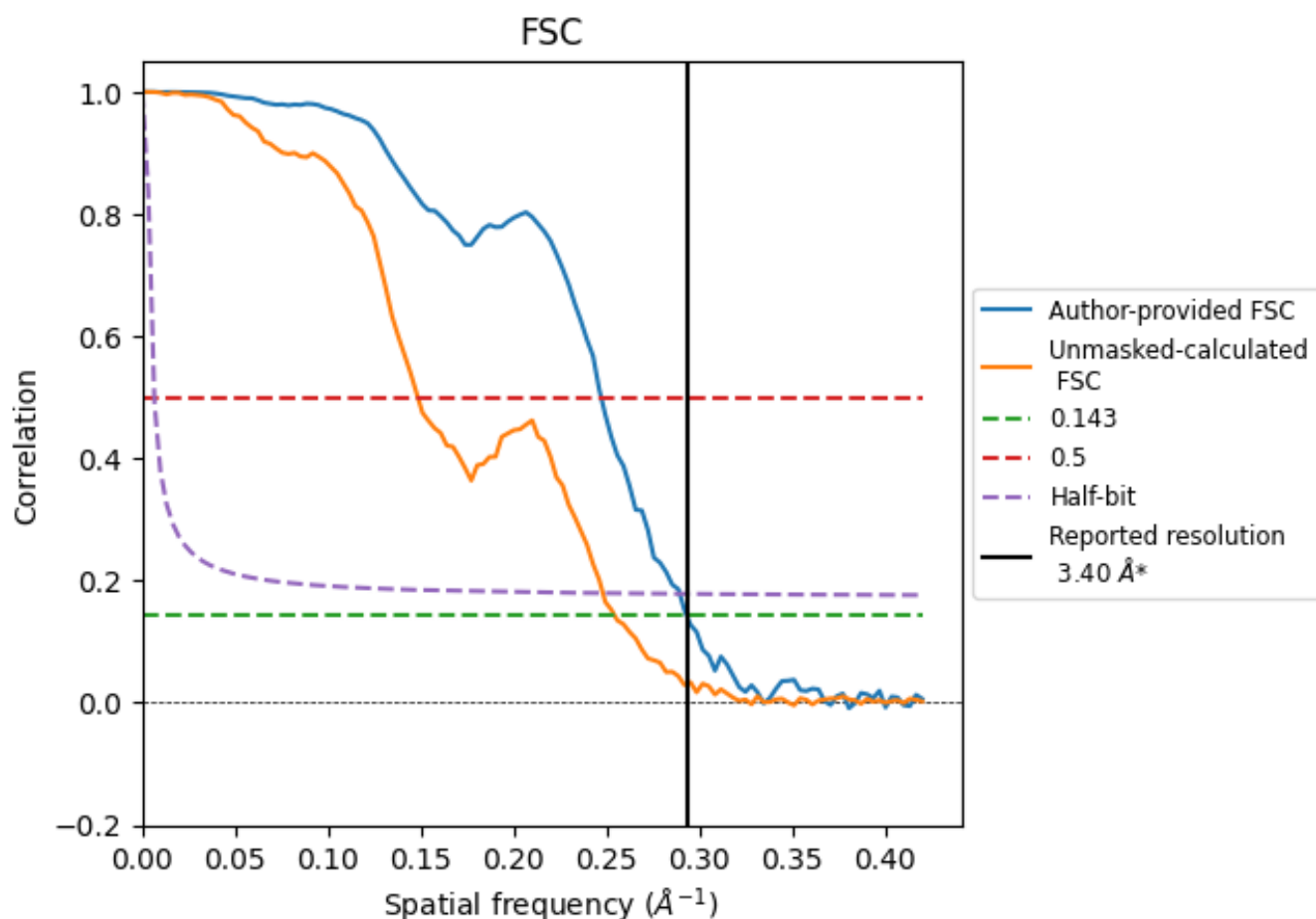


*Reported resolution corresponds to spatial frequency of $0.294 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

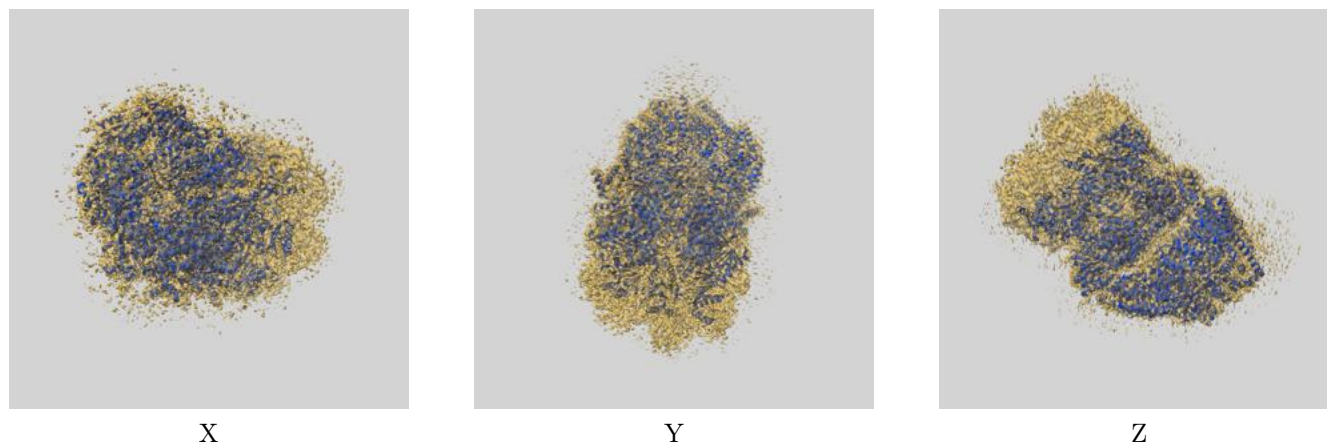
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.41	4.05	3.45
Unmasked-calculated*	3.93	6.73	4.03

*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 3.93 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

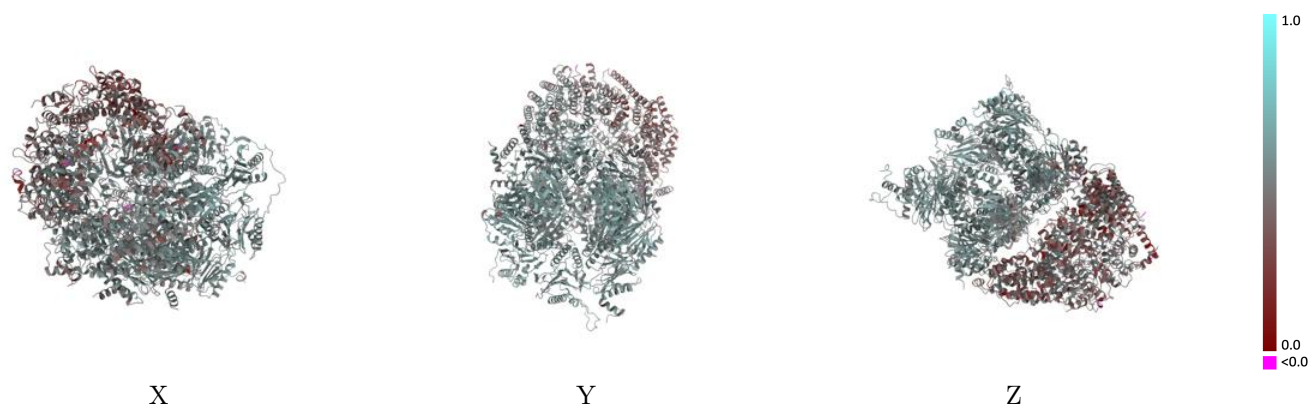
This section contains information regarding the fit between EMDB map EMD-75393 and PDB model 10QT. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



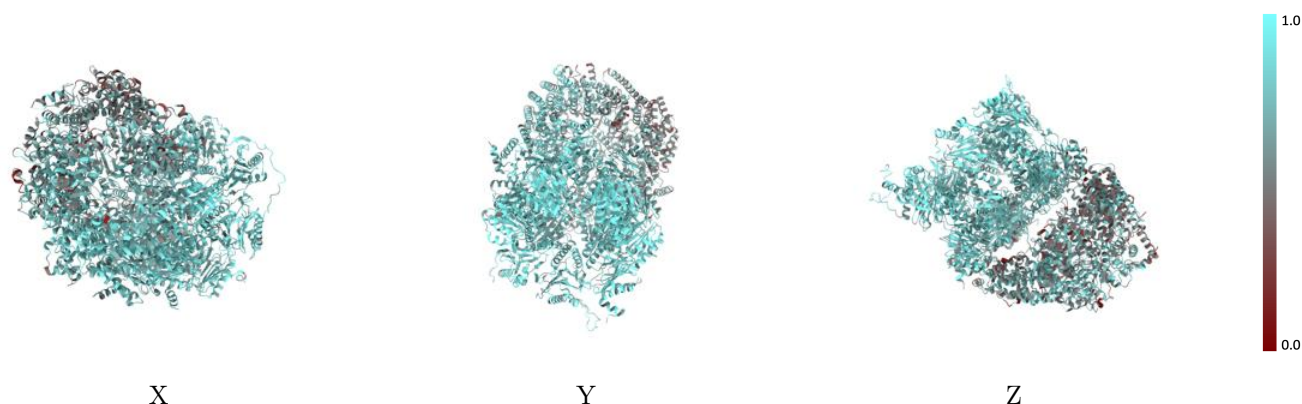
The images above show the 3D surface view of the map at the recommended contour level 0.0138 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



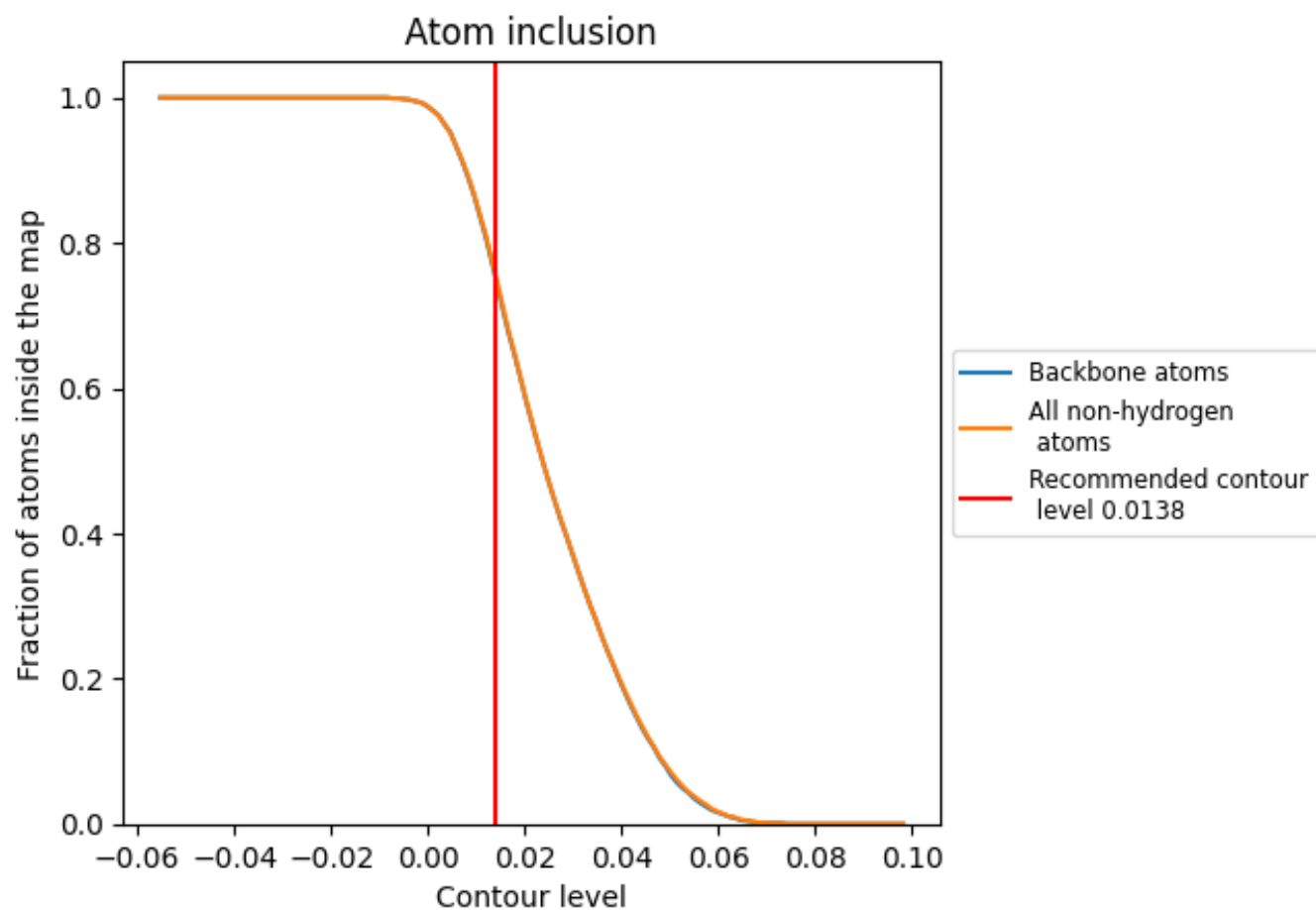
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0138).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 76% 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 (0.0138) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7600	 0.5020
A	 0.8370	 0.5370
B	 0.8250	 0.5490
C	 0.7600	 0.5010
CA	 0.6660	 0.4370
D	 0.7650	 0.5150
E	 0.8040	 0.5430
F	 0.8460	 0.5480
G	 0.8310	 0.5420
H	 0.8560	 0.5580
I	 0.8540	 0.5520
J	 0.8550	 0.5620
K	 0.8200	 0.5410
L	 0.8520	 0.5540
M	 0.8310	 0.5480
N	 0.8510	 0.5550

