



wwPDB EM Validation Summary Report ⓘ

Nov 25, 2024 – 10:19 AM EST

PDB ID : 9D0T
EMDB ID : EMD-46461
Title : Core particle assembly intermediate 1 purified from *Saccharomyces cerevisiae*
Authors : Chen, X.; Kaur, M.; Roelofs, J.; Walters, K.J.
Deposited on : 2024-08-07
Resolution : 2.84 Å(reported)
Based on initial models : 4V7O, 7LSX

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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

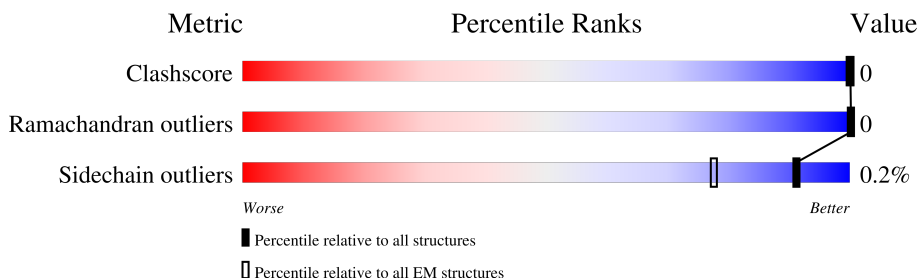
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


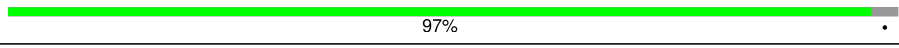
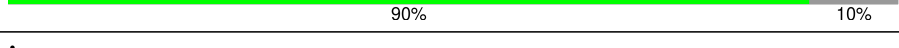
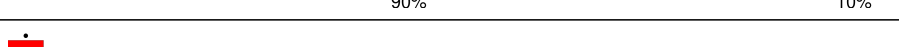




The reported resolution of this entry is 2.84 Å.

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.





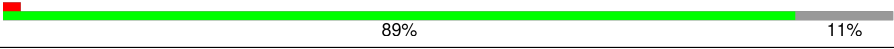

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	258	
4	D	254	
5	E	260	
6	F	234	
7	G	288	
8	I	261	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	J	205	 88% 6% 11%
10	K	198	 91% 6% 9%
11	O	2143	 89% 6% 11%
12	P	200	 44% 6% 56%

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 67179 atoms, of which 33578 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	242	Total	C	H	N	O	S	0	0
			3821	1218	1905	321	369	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	243	Total	C	H	N	O	S	0	0
			3722	1179	1870	305	365	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	232	Total	C	H	N	O	S	0	0
			3604	1139	1802	300	360	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	228	Total	C	H	N	O	S	0	0
			3596	1113	1806	315	358	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	245	Total	C	H	N	O	S	0	0
			3790	1194	1885	320	383	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	234	Total	C	H	N	O	S	0	0
			3614	1134	1811	313	351	5		

- Molecule 7 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	243	Total	C	H	N	O	S	0	0
			3777	1203	1885	329	356	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
8	I	203	Total	C	H	N	O	S	0	0
			3072	974	1531	266	296	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
9	J	183	Total	C	H	N	O	S	0	0
			2832	918	1410	226	271	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
10	K	181	Total	C	H	N	O	S	0	0
			2914	925	1461	246	276	6		

- Molecule 11 is a protein called Proteasome activator BLM10.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	O	1909	Total	C	H	N	O	S	0	0
			30998	9979	15498	2568	2882	71		

- Molecule 12 is a protein called Proteasome maturation factor UMP1,Myosin light chain kinase 2, skeletal/cardiac muscle.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	P	87	Total	C	H	N	O	S	0	0
			1439	451	714	132	137	5		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	149	GLY	-	linker	UNP P38293
P	150	ARG	-	linker	UNP P38293
P	151	ARG	-	linker	UNP P38293

Continued on next page...

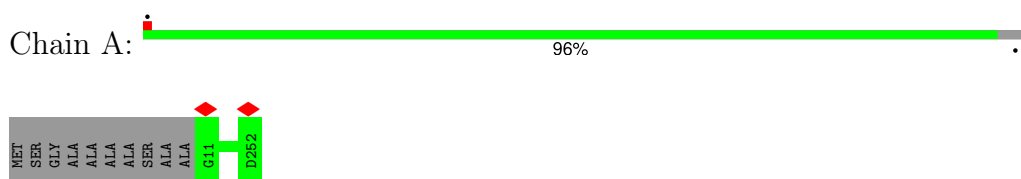
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
P	152	ILE	-	linker	UNP P38293
P	153	PRO	-	linker	UNP P38293
P	154	GLY	-	linker	UNP P38293
P	155	LEU	-	linker	UNP P38293
P	156	ILE	-	linker	UNP P38293
P	157	ASN	-	linker	UNP P38293
P	158	PRO	-	linker	UNP P38293
P	159	TRP	-	linker	UNP P38293
P	186	ASP	-	expression tag	UNP A4IFM7
P	187	TYR	-	expression tag	UNP A4IFM7
P	188	ASP	-	expression tag	UNP A4IFM7
P	189	ILE	-	expression tag	UNP A4IFM7
P	190	PRO	-	expression tag	UNP A4IFM7
P	191	THR	-	expression tag	UNP A4IFM7
P	192	THR	-	expression tag	UNP A4IFM7
P	193	ALA	-	expression tag	UNP A4IFM7
P	194	SER	-	expression tag	UNP A4IFM7
P	195	GLU	-	expression tag	UNP A4IFM7
P	196	ASN	-	expression tag	UNP A4IFM7
P	197	LEU	-	expression tag	UNP A4IFM7
P	198	TYR	-	expression tag	UNP A4IFM7
P	199	PHE	-	expression tag	UNP A4IFM7
P	200	GLN	-	expression tag	UNP A4IFM7

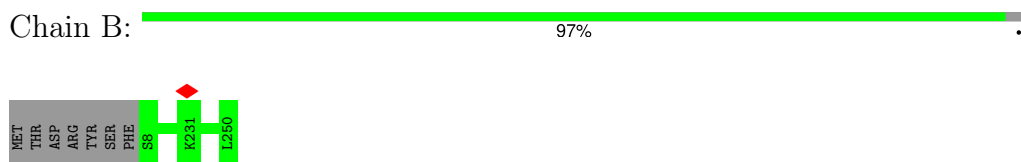
3 Residue-property plots [i](#)

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.

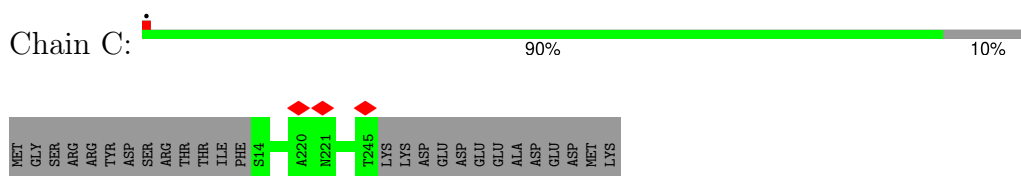
- Molecule 1: Proteasome subunit alpha type-1



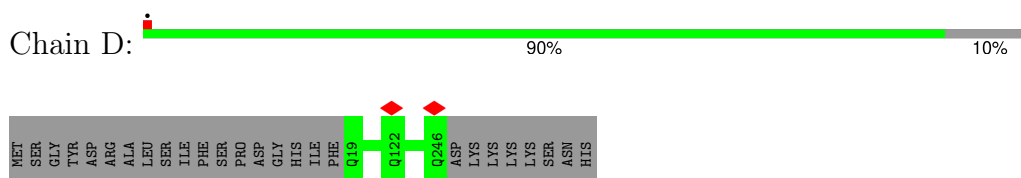
- Molecule 2: Proteasome subunit alpha type-2



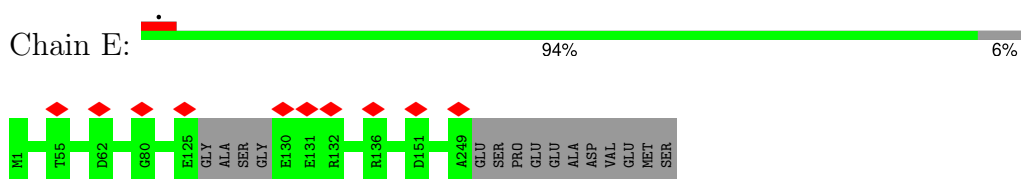
- Molecule 3: Proteasome subunit alpha type-3



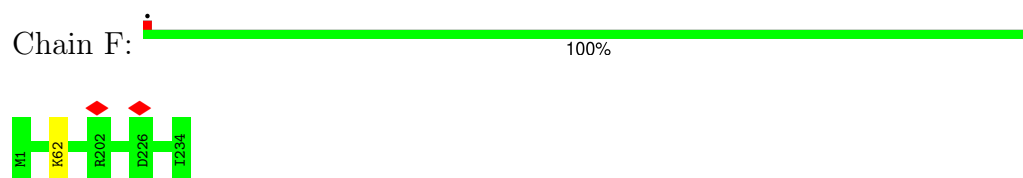
- Molecule 4: Proteasome subunit alpha type-4



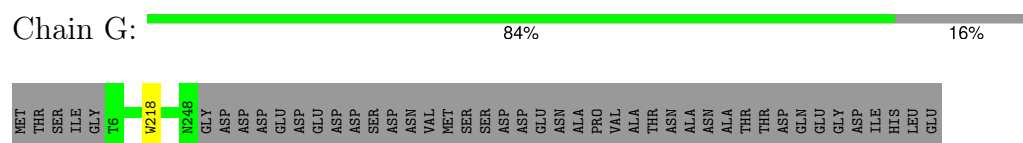
- Molecule 5: Proteasome subunit alpha type-5



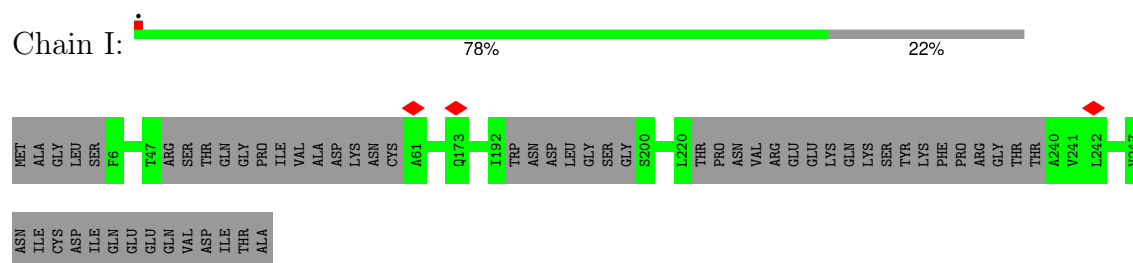
- Molecule 6: Proteasome subunit alpha type-6



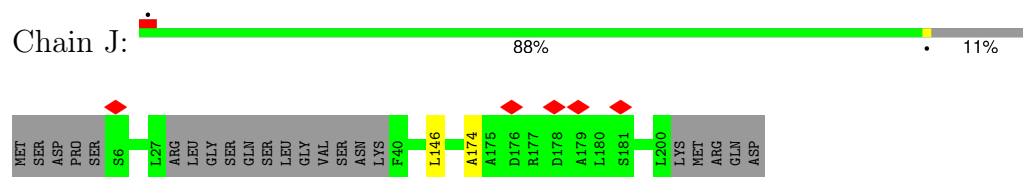
- Molecule 7: Probable proteasome subunit alpha type-7



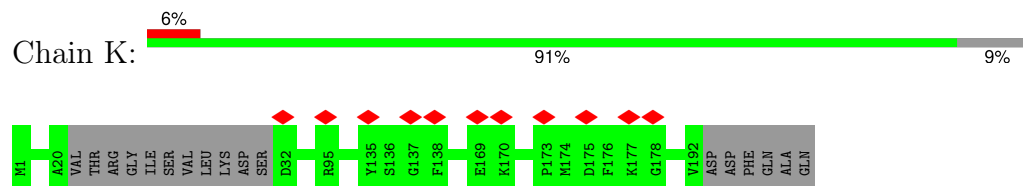
- Molecule 8: Proteasome subunit beta type-2



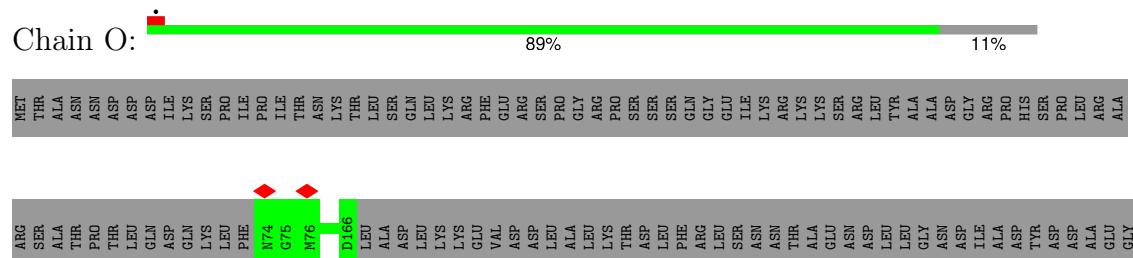
- Molecule 9: Proteasome subunit beta type-3

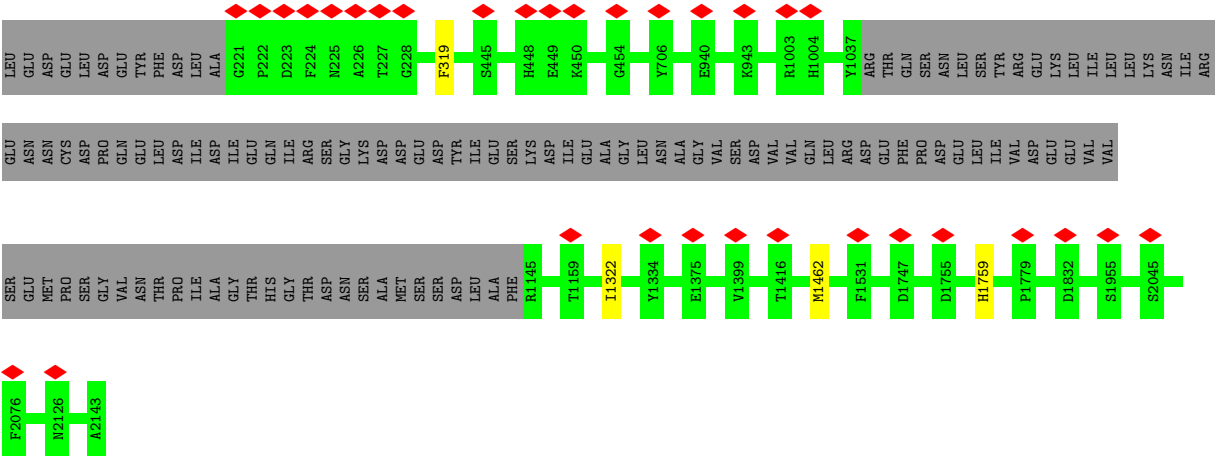


- Molecule 10: Proteasome subunit beta type-4

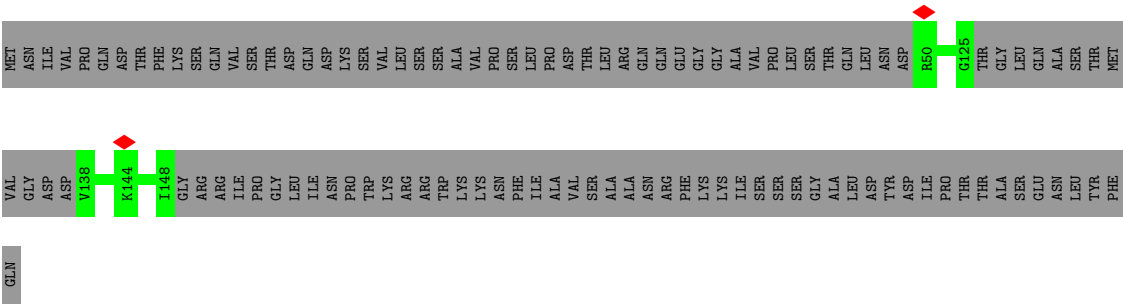


- Molecule 11: Proteasome activator BLM10





● Molecule 12: Proteasome maturation factor UMP1,Myosin light chain kinase 2, skeletal/cardiac muscle



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	586158	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 ($e^-/\text{\AA}^2$)	1.034	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	23.596	Depositor
Minimum map value	-0.483	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.604	Depositor
Recommended contour level	3	Depositor
Map size (Å)	363.12, 363.12, 363.12	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	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	0.71	0/1954	0.93	0/2645
2	B	0.69	0/1887	0.95	0/2555
3	C	0.71	0/1830	0.93	0/2479
4	D	0.68	0/1814	0.96	0/2455
5	E	0.68	0/1931	0.96	0/2600
6	F	0.69	0/1831	0.95	0/2473
7	G	0.69	0/1932	0.92	0/2609
8	I	0.66	0/1567	0.90	0/2122
9	J	0.68	0/1450	0.91	0/1960
10	K	0.70	0/1479	0.92	0/1992
11	O	0.69	0/15848	0.93	0/21472
12	P	0.71	0/738	1.02	0/992
All	All	0.69	0/34261	0.93	0/46354

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	1916	1905	1905	0	0
2	B	1852	1870	1870	0	0
3	C	1802	1802	1802	0	0
4	D	1790	1806	1806	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1905	1885	1885	0	0
6	F	1803	1811	1809	0	0
7	G	1892	1885	1883	0	0
8	I	1541	1531	1529	0	0
9	J	1422	1410	1410	1	0
10	K	1453	1461	1461	0	0
11	O	15500	15498	15491	0	0
12	P	725	714	713	0	0
All	All	33601	33578	33564	1	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 0.

All (1) 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:J:146:LEU:HD23	9:J:174:ALA:HB2	2.00	0.44

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	240/252 (95%)	235 (98%)	5 (2%)	0	100	100
2	B	241/250 (96%)	238 (99%)	3 (1%)	0	100	100
3	C	230/258 (89%)	218 (95%)	12 (5%)	0	100	100
4	D	226/254 (89%)	215 (95%)	11 (5%)	0	100	100
5	E	241/260 (93%)	226 (94%)	15 (6%)	0	100	100
6	F	232/234 (99%)	223 (96%)	9 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	241/288 (84%)	230 (95%)	11 (5%)	0	100	100
8	I	195/261 (75%)	182 (93%)	13 (7%)	0	100	100
9	J	179/205 (87%)	160 (89%)	19 (11%)	0	100	100
10	K	177/198 (89%)	172 (97%)	5 (3%)	0	100	100
11	O	1903/2143 (89%)	1775 (93%)	128 (7%)	0	100	100
12	P	83/200 (42%)	82 (99%)	1 (1%)	0	100	100
All	All	4188/4803 (87%)	3956 (94%)	232 (6%)	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	207/210 (99%)	207 (100%)	0	100	100
2	B	202/209 (97%)	202 (100%)	0	100	100
3	C	192/216 (89%)	192 (100%)	0	100	100
4	D	203/226 (90%)	203 (100%)	0	100	100
5	E	204/215 (95%)	204 (100%)	0	100	100
6	F	193/193 (100%)	192 (100%)	1 (0%)	86	94
7	G	201/239 (84%)	200 (100%)	1 (0%)	86	94
8	I	164/214 (77%)	164 (100%)	0	100	100
9	J	153/173 (88%)	153 (100%)	0	100	100
10	K	160/175 (91%)	160 (100%)	0	100	100
11	O	1756/1963 (90%)	1752 (100%)	4 (0%)	92	97
12	P	82/180 (46%)	82 (100%)	0	100	100
All	All	3717/4213 (88%)	3711 (100%)	6 (0%)	91	97

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	O	1322	ILE
11	O	1462	MET
11	O	1759	HIS
7	G	218	TRP
6	F	62	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
11	O	1342	ASN
11	O	1760	GLN
12	P	68	GLN
11	O	1168	GLN
11	O	595	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

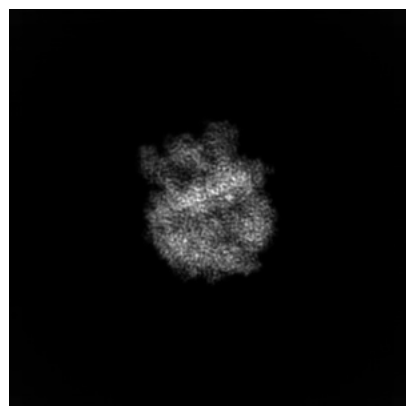
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46461. These allow visual inspection of the internal detail of the map and identification of artifacts.

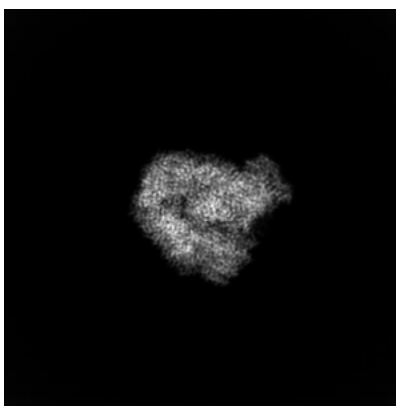
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

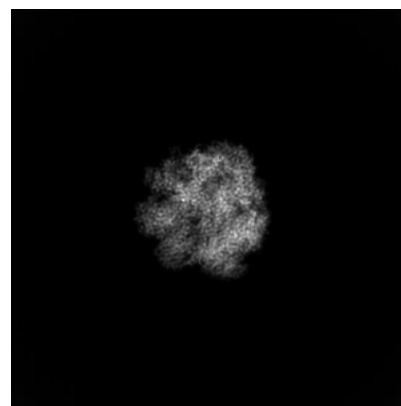
6.1.1 Primary map



X

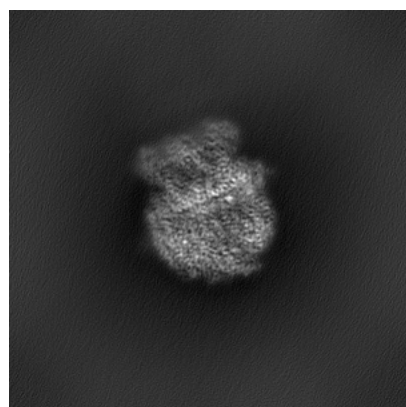


Y

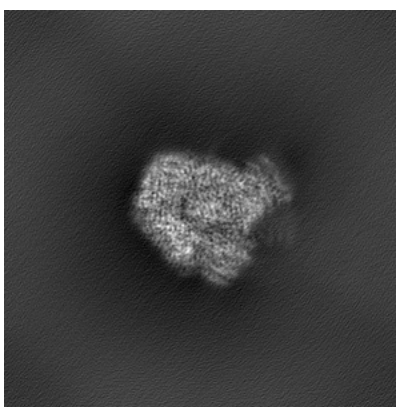


Z

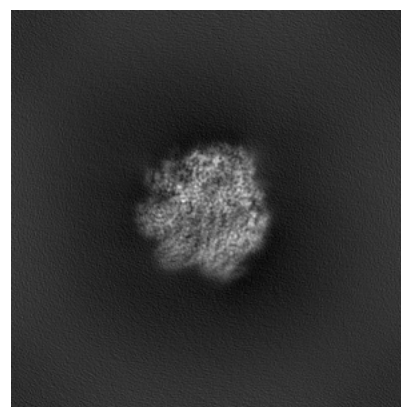
6.1.2 Raw map



X



Y

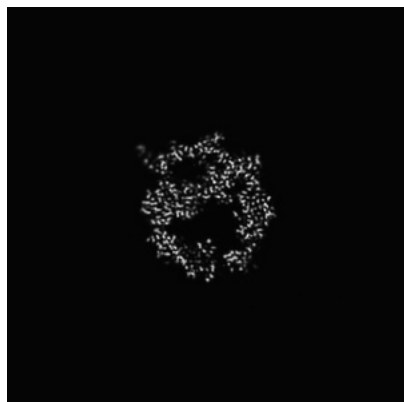


Z

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

6.2 Central slices [i](#)

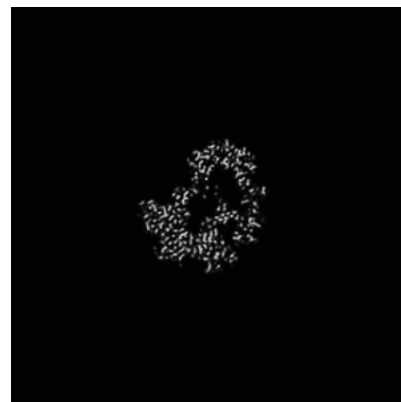
6.2.1 Primary map



X Index: 170

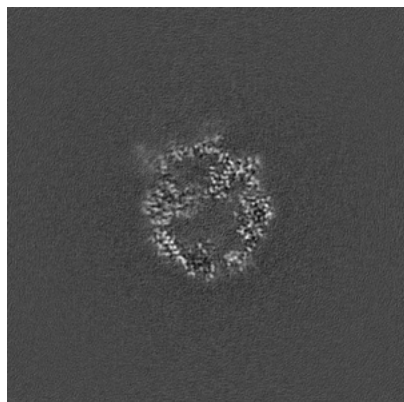


Y Index: 170

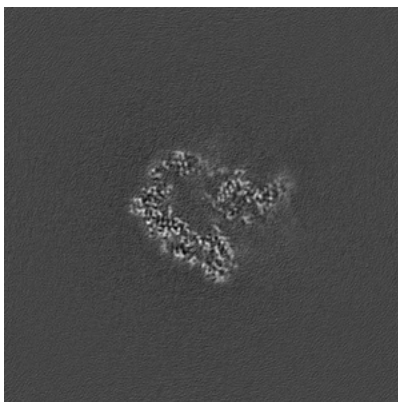


Z Index: 170

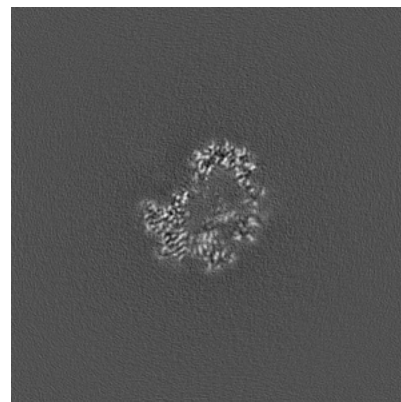
6.2.2 Raw map



X Index: 170



Y Index: 170

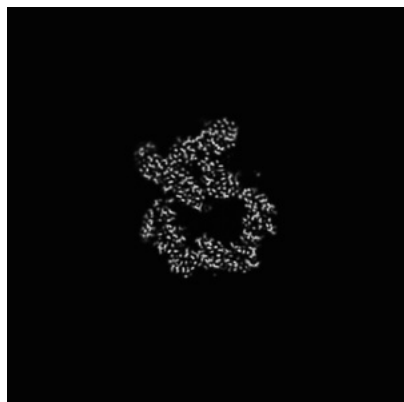


Z Index: 170

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

6.3 Largest variance slices [i](#)

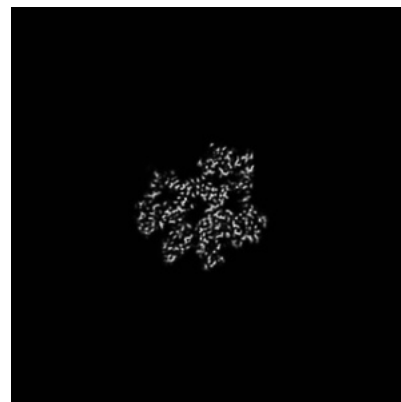
6.3.1 Primary map



X Index: 183

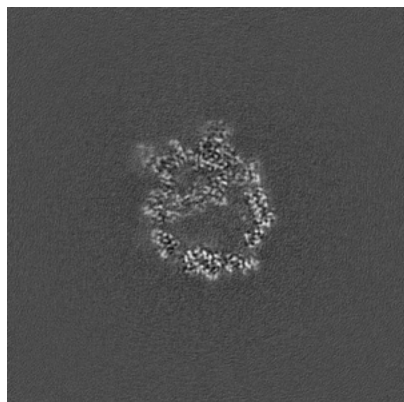


Y Index: 175

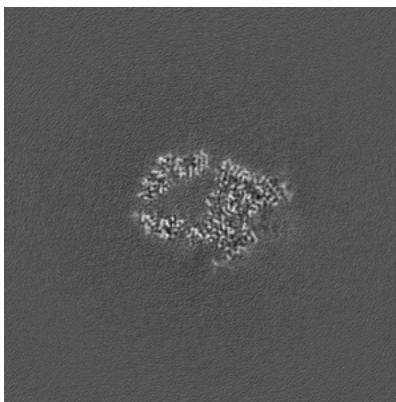


Z Index: 178

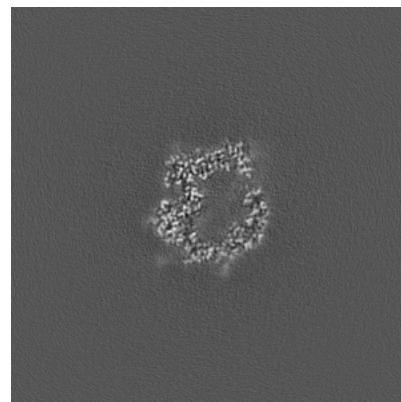
6.3.2 Raw map



X Index: 175



Y Index: 182

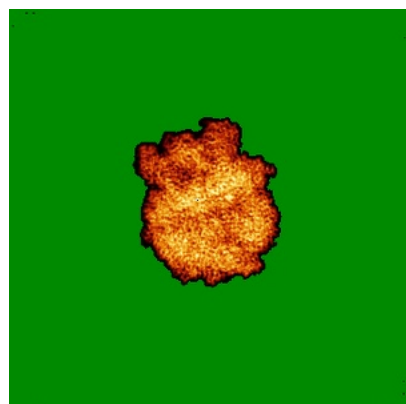


Z Index: 147

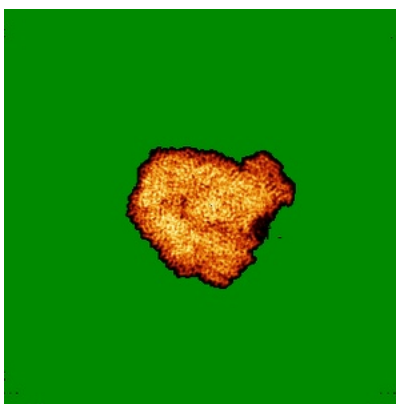
The images above show the largest variance slices of the map in three orthogonal directions.

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

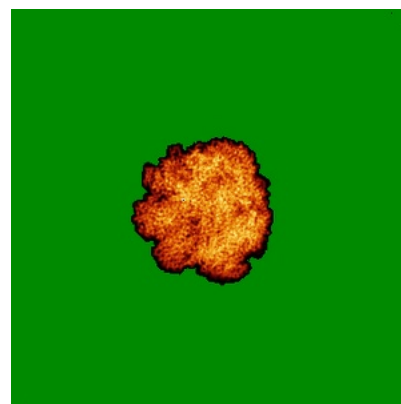
6.4.1 Primary map



X

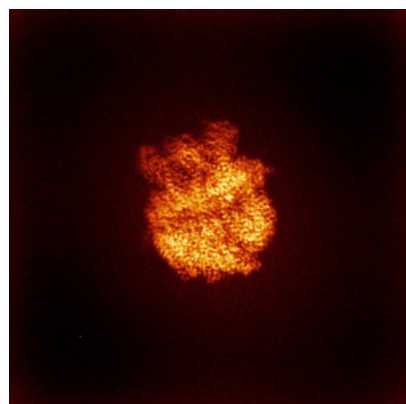


Y

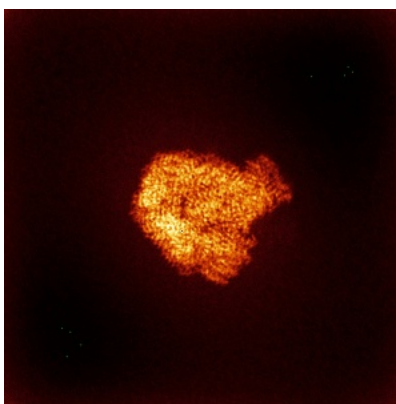


Z

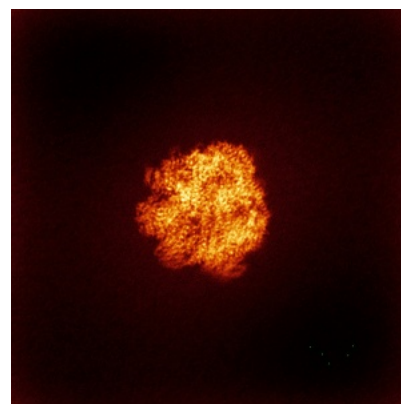
6.4.2 Raw map



X



Y

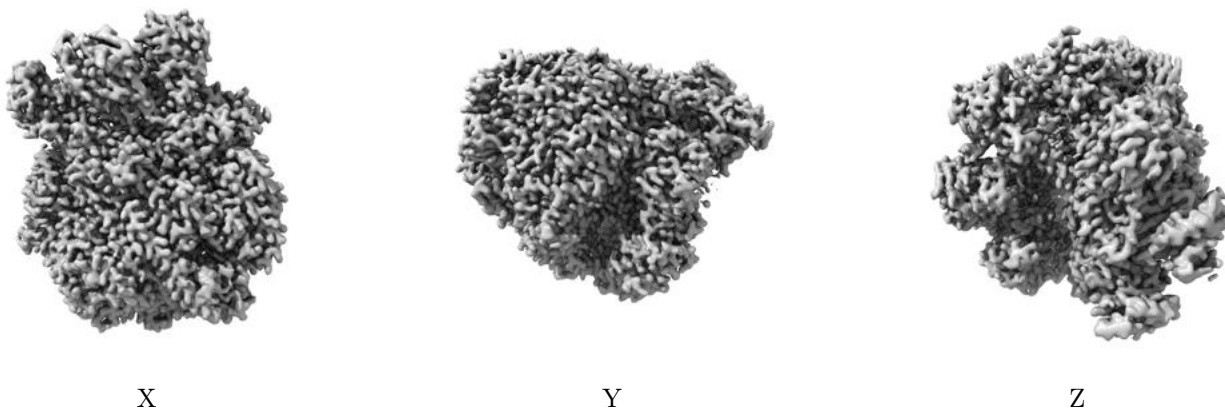


Z

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.

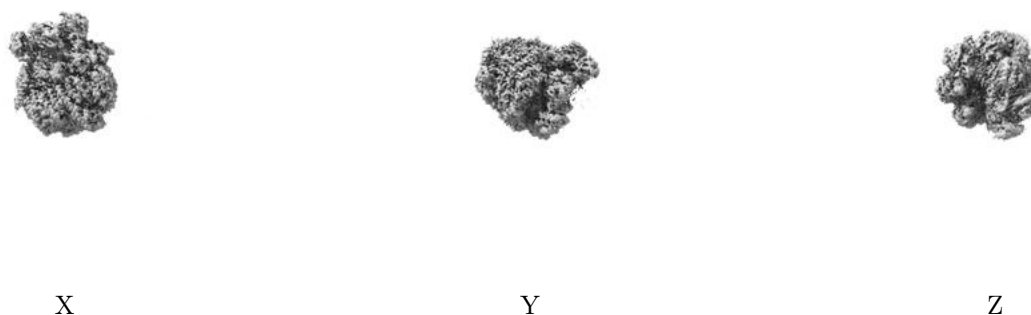
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

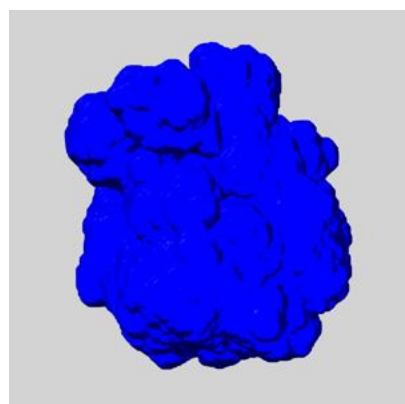
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

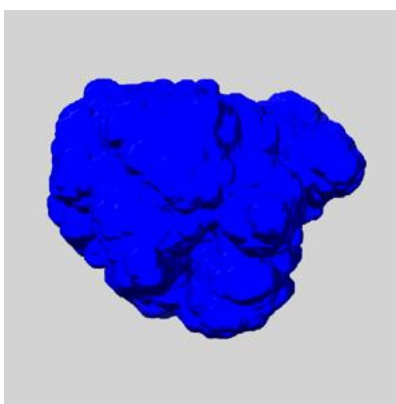
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

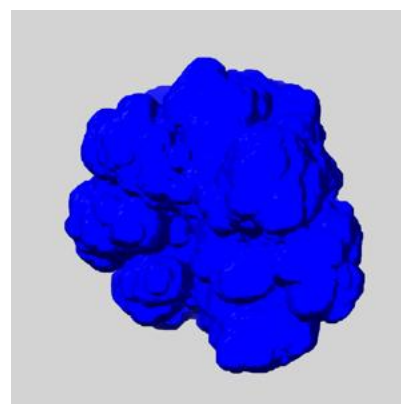
6.6.1 emd_46461_msk_1.map [i](#)



X



Y

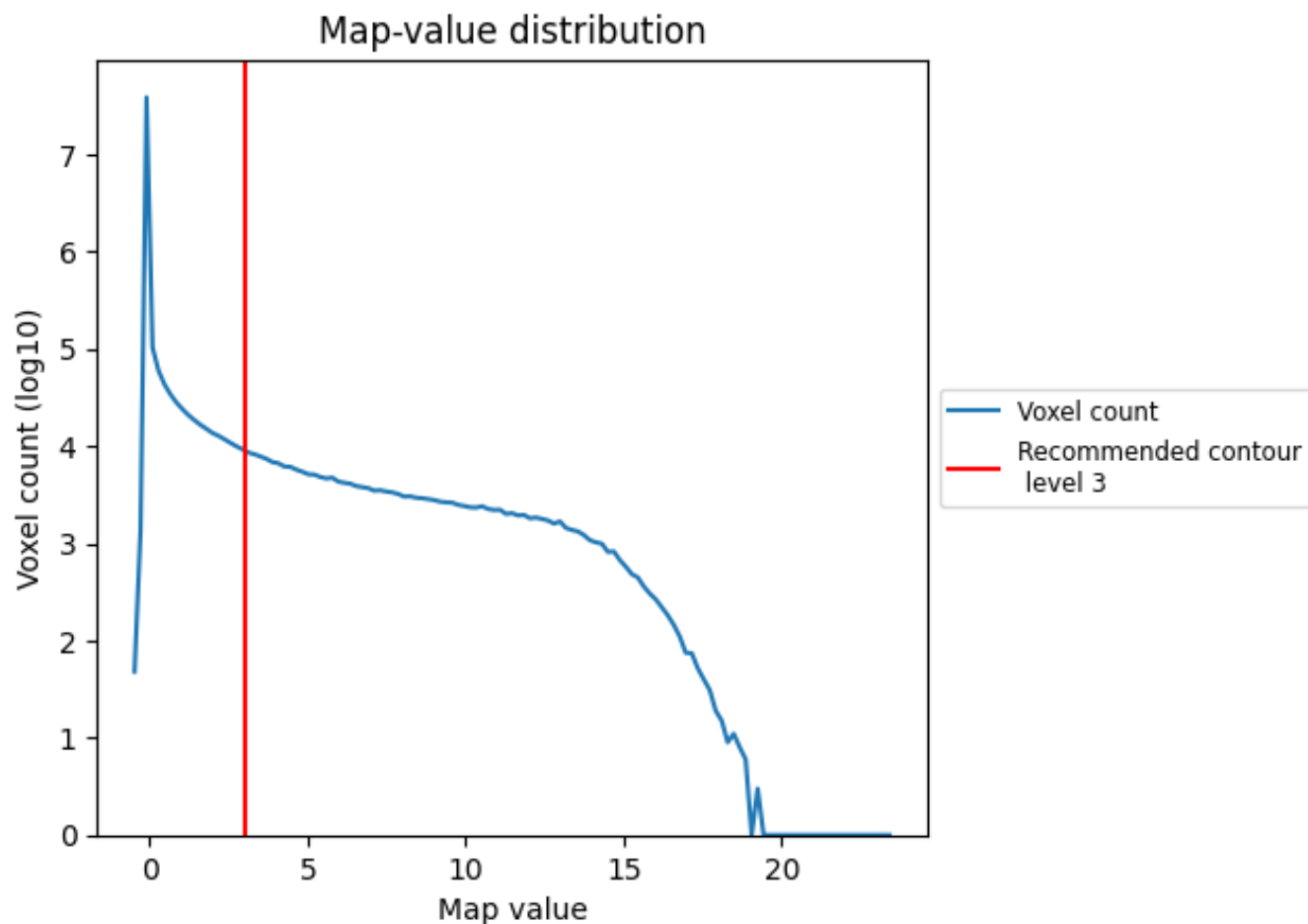


Z

7 Map analysis [i](#)

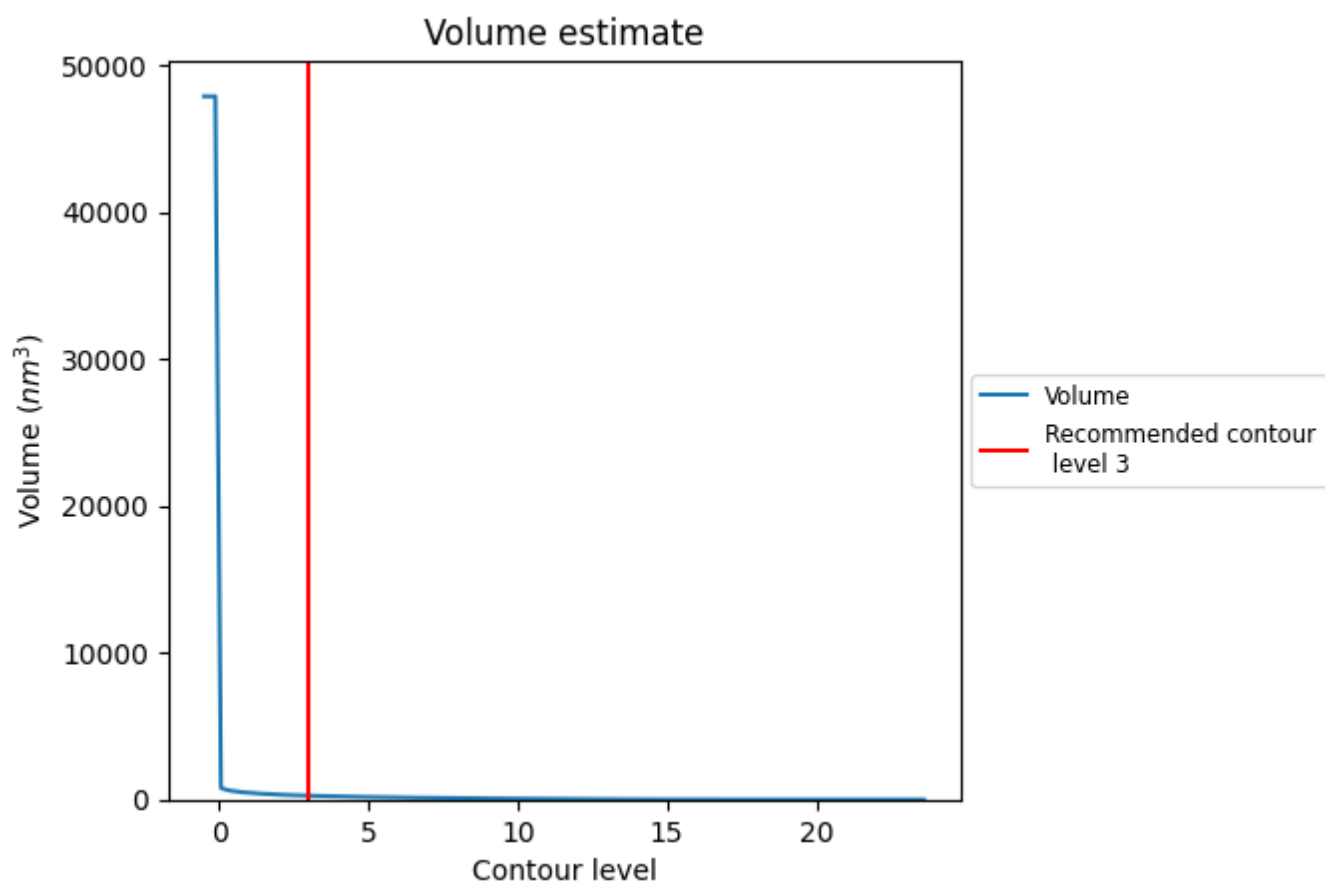
This section contains the results of statistical analysis of the map.

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.

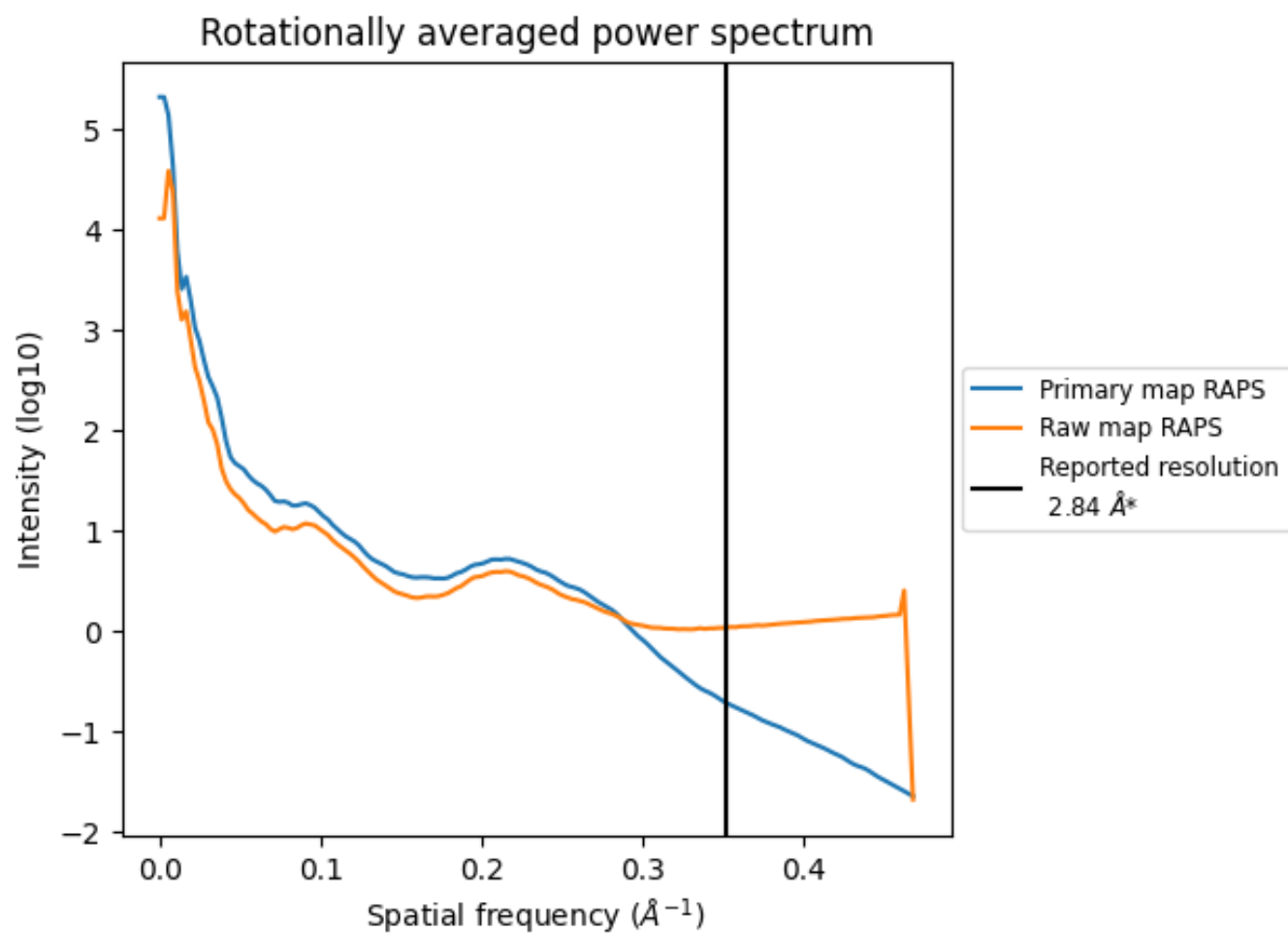
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 264 nm^3 ; this corresponds to an approximate mass of 239 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 ⓘ

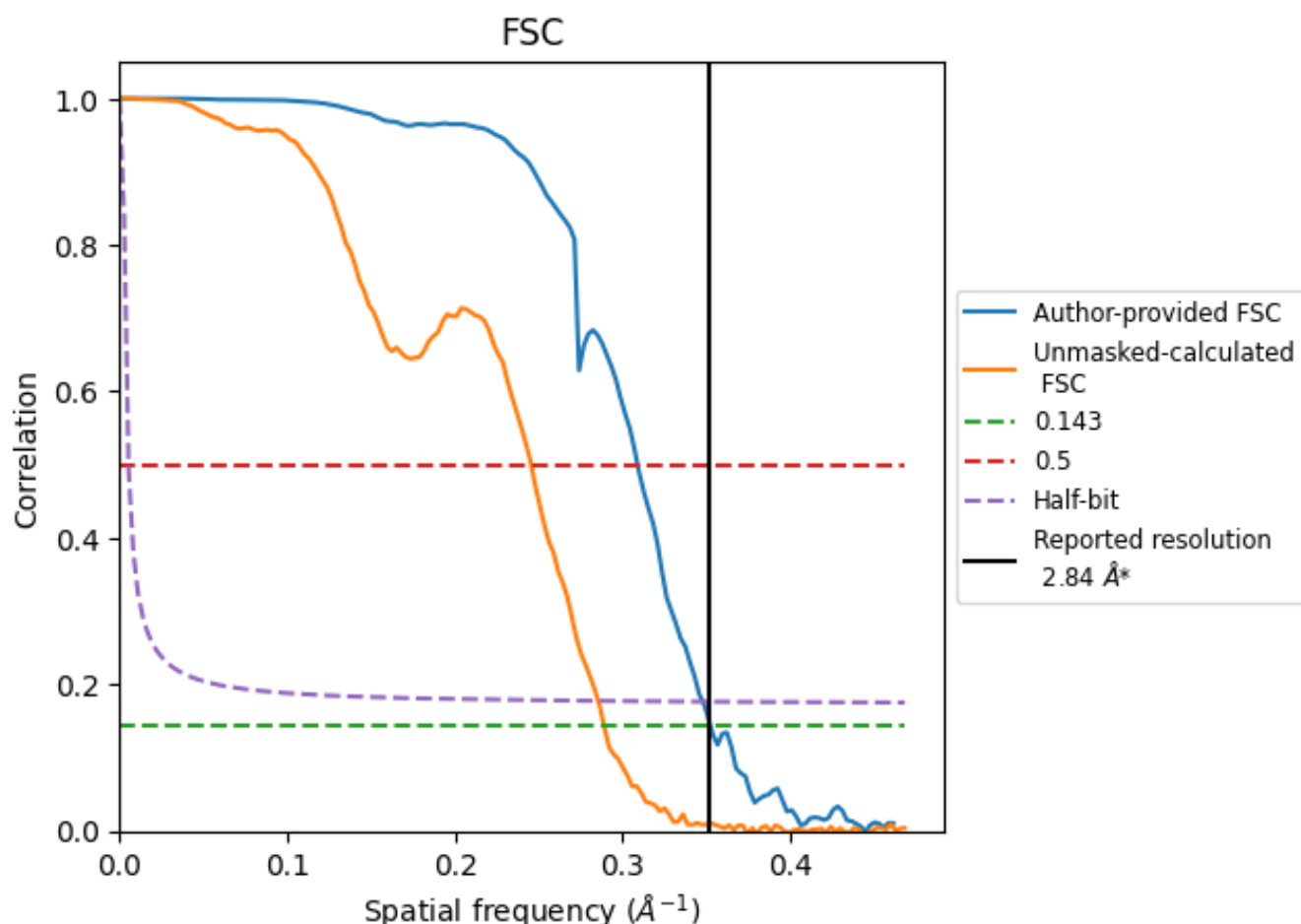


*Reported resolution corresponds to spatial frequency of 0.352 \AA^{-1}

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 0.352 \AA^{-1}

8.2 Resolution estimates [i](#)

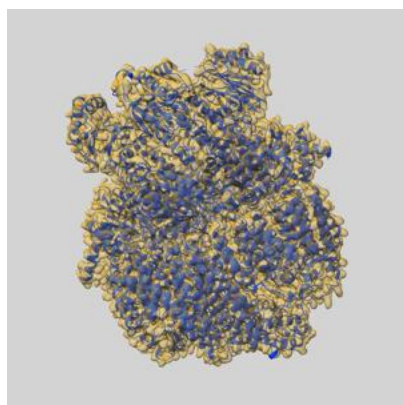
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	2.84	3.24	2.88
Unmasked-calculated*	3.46	4.07	3.50

*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 3.46 differs from the reported value 2.84 by more than 10 %

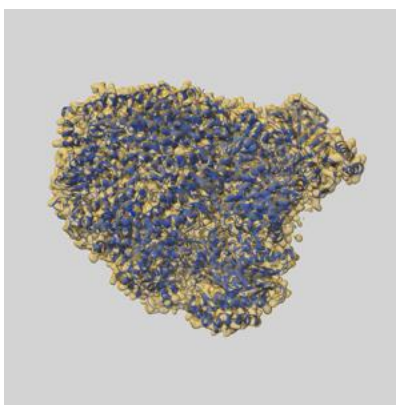
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-46461 and PDB model 9D0T. Per-residue inclusion information can be found in section [3](#) on page [7](#).

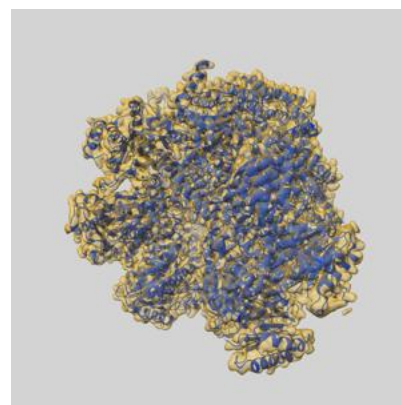
9.1 Map-model overlay [i](#)



X



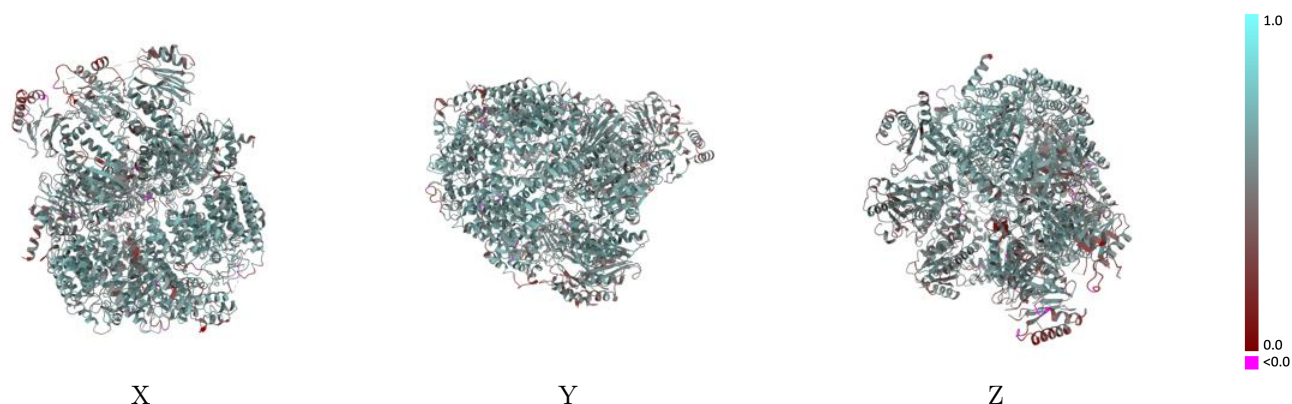
Y



Z

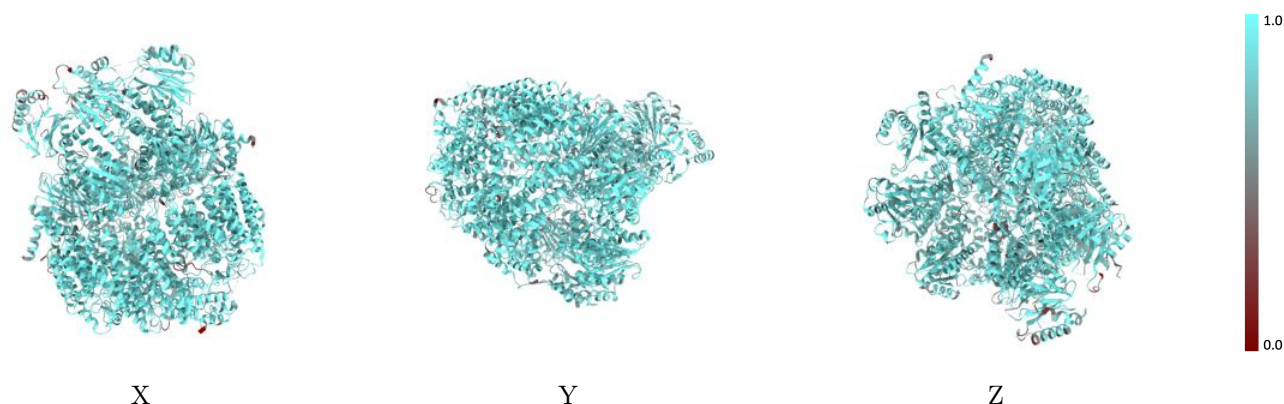
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



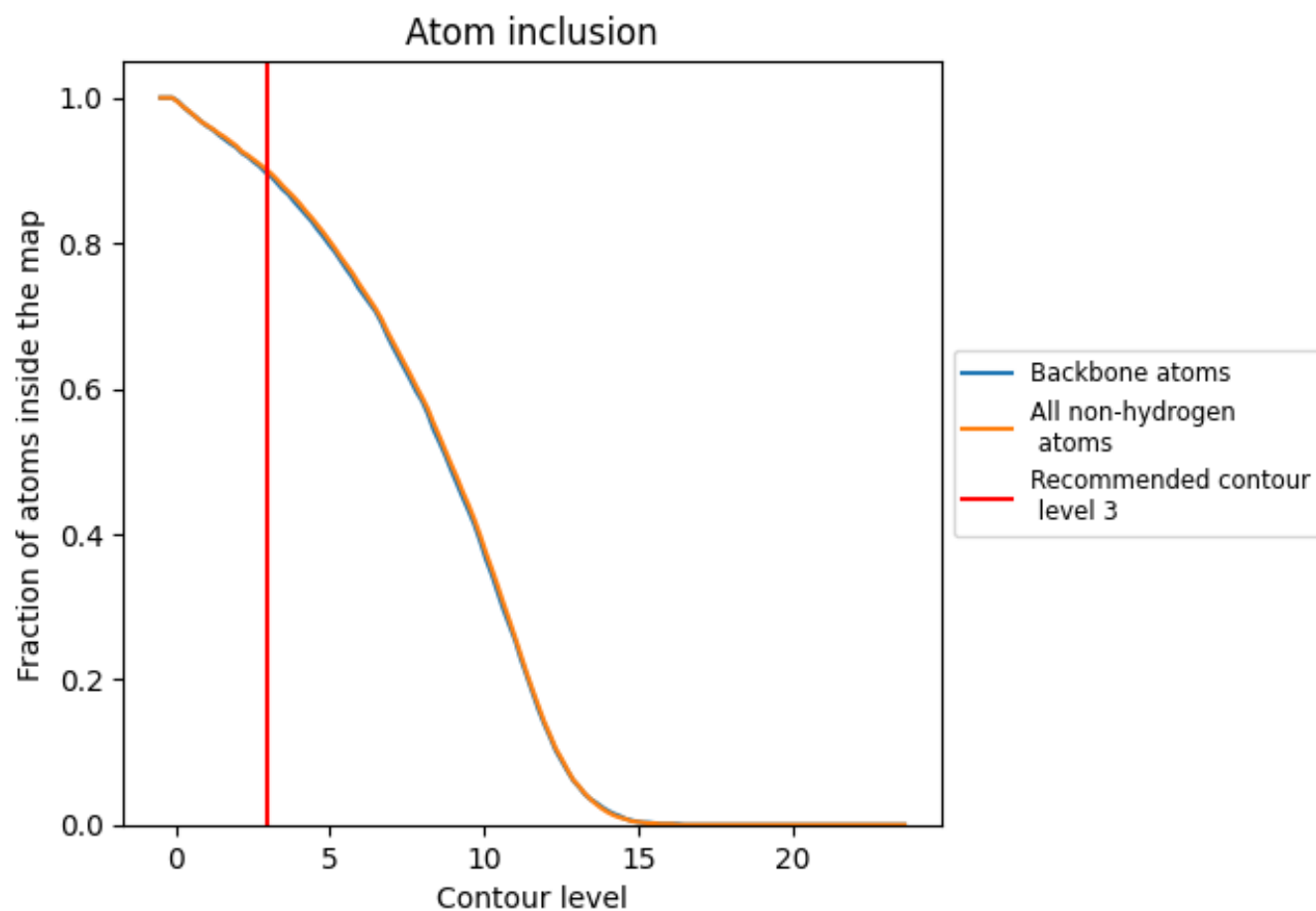
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 90% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8990</div>	<div><div></div>0.5410</div>
A	<div><div></div>0.9230</div>	<div><div></div>0.5730</div>
B	<div><div></div>0.9230</div>	<div><div></div>0.5660</div>
C	<div><div></div>0.9030</div>	<div><div></div>0.5350</div>
D	<div><div></div>0.8910</div>	<div><div></div>0.5190</div>
E	<div><div></div>0.8440</div>	<div><div></div>0.4740</div>
F	<div><div></div>0.8990</div>	<div><div></div>0.5200</div>
G	<div><div></div>0.9110</div>	<div><div></div>0.5480</div>
I	<div><div></div>0.8810</div>	<div><div></div>0.4990</div>
J	<div><div></div>0.8560</div>	<div><div></div>0.4820</div>
K	<div><div></div>0.8200</div>	<div><div></div>0.4470</div>
O	<div><div></div>0.9250</div>	<div><div></div>0.5690</div>
P	<div><div></div>0.8570</div>	<div><div></div>0.4890</div>

1.0

0.0

<0.0