



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 10:59 AM UTC

PDB ID : 9D4U / pdb_00009d4u
EMDB ID : EMD-46570
Title : Core particle assembly intermediate Capless 13S purified from *Saccharomyces cerevisiae*
Authors : Chen, X.; Kaur, M.; Roelofs, J.; Walters, K.J.
Deposited on : 2024-08-13
Resolution : 3.55 Å(reported)
Based on initial model : 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:

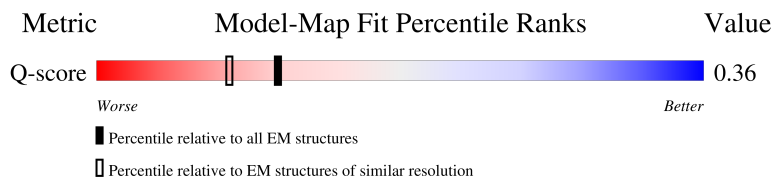
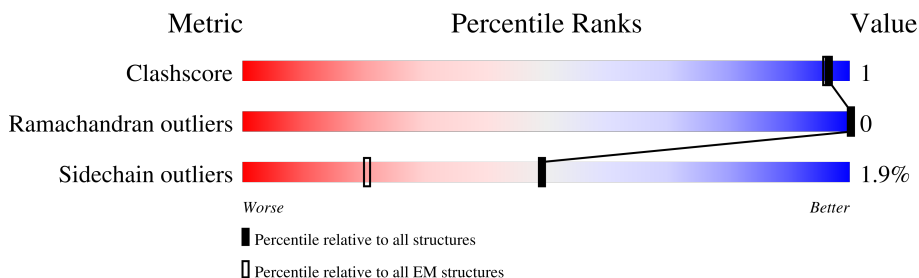
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

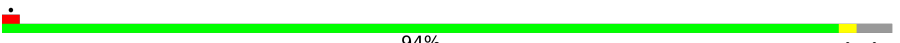
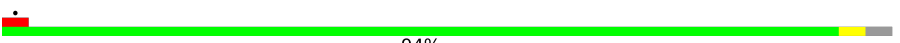


The reported resolution of this entry is 3.55 Å.

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	12819 (3.05 - 4.05)

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	 94%
2	B	250	 94%
3	C	258	 5% 86% 11%
4	D	254	 7% 87% 11%

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Mol	Chain	Length	Quality of chain
5	E	260	
6	F	234	
7	G	288	
8	I	261	
9	J	205	
10	K	198	
11	P	200	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 35217 atoms, of which 17597 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
			3791	1211	1888	317	367	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
			3723	1179	1871	305	365	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	230	Total	C	H	N	O	S	0	0
			3580	1131	1791	298	357	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	227	Total	C	H	N	O	S	0	0
			3550	1102	1781	307	356	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	228	Total	C	H	N	O	S	0	0
			3486	1098	1737	291	353	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	228	Total	C	H	N	O	S	0	0
			3464	1087	1739	295	340	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	245	Total	C	H	N	O	S	0	0
			3762	1198	1874	328	358	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
8	I	199	Total	C	H	N	O	S	0	0
			3008	954	1500	259	290	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
9	J	180	Total	C	H	N	O	S	0	0
			2771	901	1379	220	264	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
10	K	176	Total	C	H	N	O	S	0	0
			2848	905	1431	240	266	6		

- Molecule 11 is a protein called Proteasome maturation factor UMP1.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	P	75	Total	C	H	N	O	S	0	0
			1234	390	606	112	121	5		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	149	GLY	-	expression tag	UNP P38293
P	150	ARG	-	expression tag	UNP P38293
P	151	ARG	-	expression tag	UNP P38293
P	152	ILE	-	expression tag	UNP P38293
P	153	PRO	-	expression tag	UNP P38293
P	154	GLY	-	expression tag	UNP P38293
P	155	LEU	-	expression tag	UNP P38293
P	156	ILE	-	expression tag	UNP P38293
P	157	ASN	-	expression tag	UNP P38293
P	158	PRO	-	expression tag	UNP P38293
P	159	TRP	-	expression tag	UNP P38293

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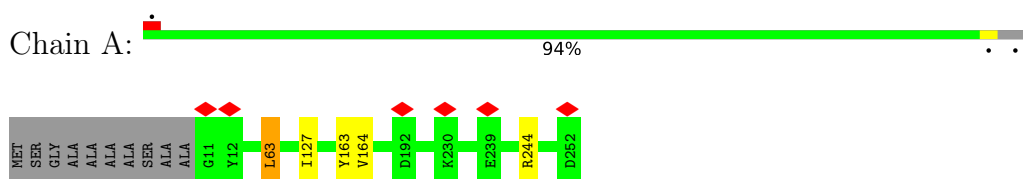
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Chain	Residue	Modelled	Actual	Comment	Reference
P	160	LYS	-	expression tag	UNP P38293
P	161	ARG	-	expression tag	UNP P38293
P	162	ARG	-	expression tag	UNP P38293
P	163	TRP	-	expression tag	UNP P38293
P	164	LYS	-	expression tag	UNP P38293
P	165	LYS	-	expression tag	UNP P38293
P	166	ASN	-	expression tag	UNP P38293
P	167	PHE	-	expression tag	UNP P38293
P	168	ILE	-	expression tag	UNP P38293
P	169	ALA	-	expression tag	UNP P38293
P	170	VAL	-	expression tag	UNP P38293
P	171	SER	-	expression tag	UNP P38293
P	172	ALA	-	expression tag	UNP P38293
P	173	ALA	-	expression tag	UNP P38293
P	174	ASN	-	expression tag	UNP P38293
P	175	ARG	-	expression tag	UNP P38293
P	176	PHE	-	expression tag	UNP P38293
P	177	LYS	-	expression tag	UNP P38293
P	178	LYS	-	expression tag	UNP P38293
P	179	ILE	-	expression tag	UNP P38293
P	180	SER	-	expression tag	UNP P38293
P	181	SER	-	expression tag	UNP P38293
P	182	SER	-	expression tag	UNP P38293
P	183	GLY	-	expression tag	UNP P38293
P	184	ALA	-	expression tag	UNP P38293
P	185	LEU	-	expression tag	UNP P38293
P	186	ASP	-	expression tag	UNP P38293
P	187	TYR	-	expression tag	UNP P38293
P	188	ASP	-	expression tag	UNP P38293
P	189	ILE	-	expression tag	UNP P38293
P	190	PRO	-	expression tag	UNP P38293
P	191	THR	-	expression tag	UNP P38293
P	192	THR	-	expression tag	UNP P38293
P	193	ALA	-	expression tag	UNP P38293
P	194	SER	-	expression tag	UNP P38293
P	195	GLU	-	expression tag	UNP P38293
P	196	ASN	-	expression tag	UNP P38293
P	197	LEU	-	expression tag	UNP P38293
P	198	TYR	-	expression tag	UNP P38293
P	199	PHE	-	expression tag	UNP P38293
P	200	GLN	-	expression tag	UNP P38293

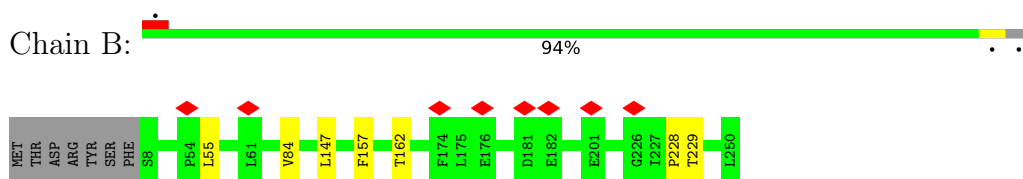
3 Residue-property plots

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

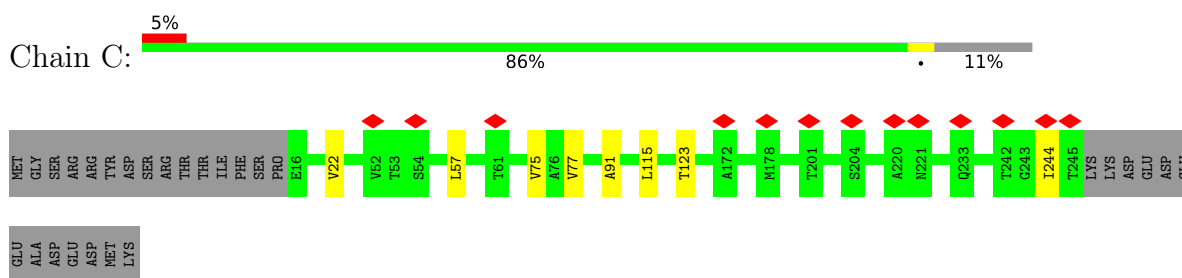
- Molecule 1: Proteasome subunit alpha type-1



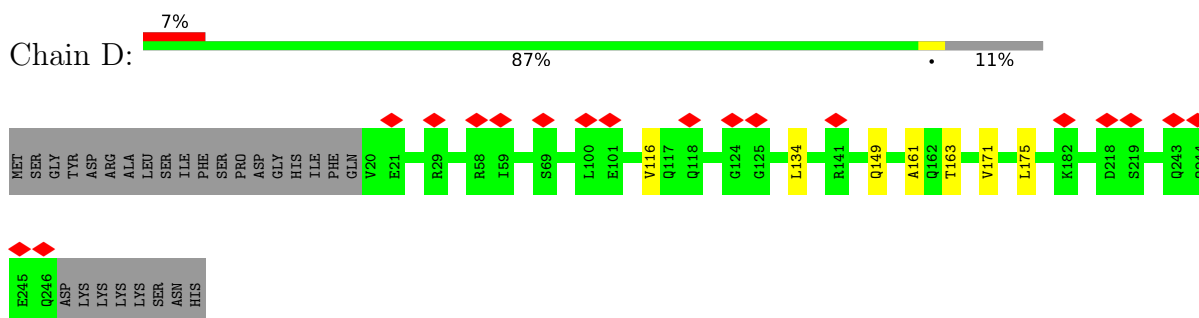
- Molecule 2: Proteasome subunit alpha type-2



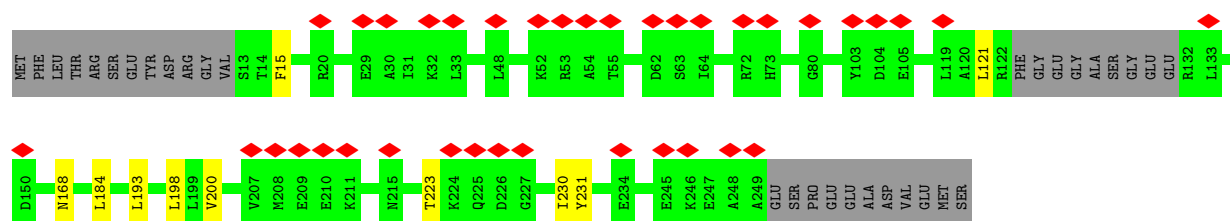
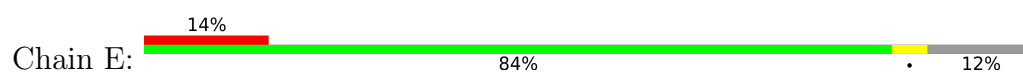
- Molecule 3: Proteasome subunit alpha type-3



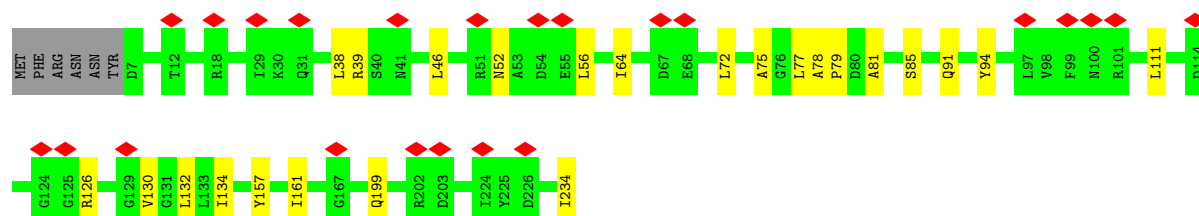
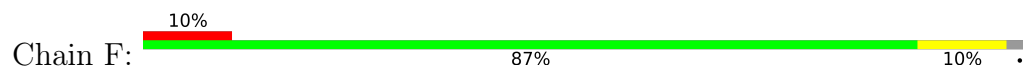
- Molecule 4: Proteasome subunit alpha type-4



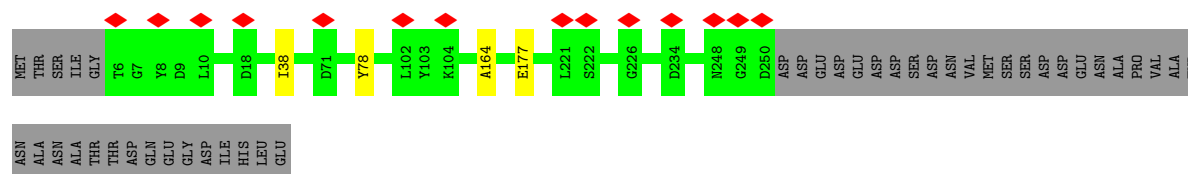
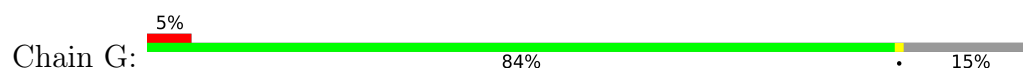
- Molecule 5: Proteasome subunit alpha type-5



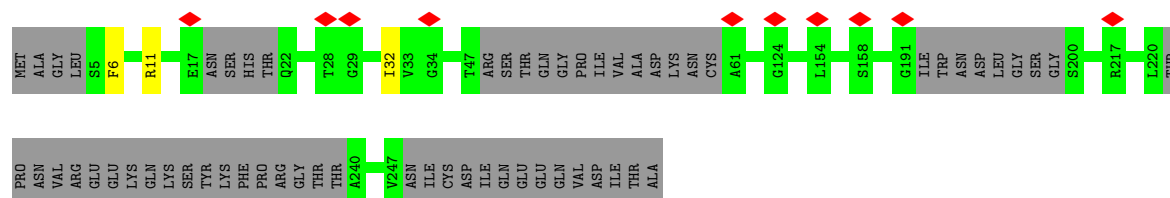
• Molecule 6: Proteasome subunit alpha type-6



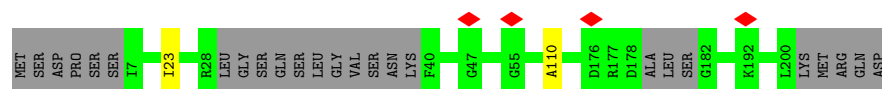
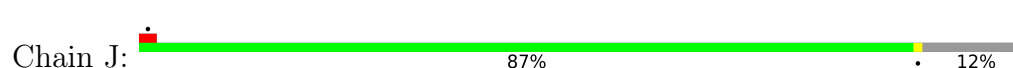
• Molecule 7: Probable proteasome subunit alpha type-7



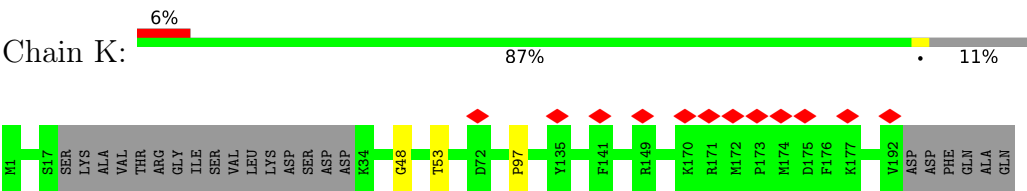
• Molecule 8: Proteasome subunit beta type-2



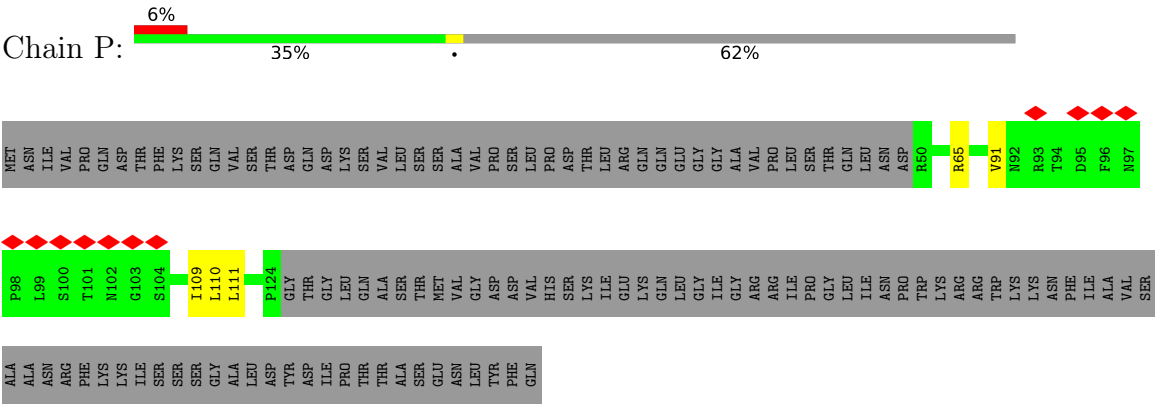
• Molecule 9: Proteasome subunit beta type-3



• Molecule 10: Proteasome subunit beta type-4



• Molecule 11: Proteasome maturation factor UMP1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	108417	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	12.256	Depositor
Minimum map value	-0.058	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.349	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	0.73	0/1941	1.26	0/2630
2	B	0.72	0/1887	1.31	0/2555
3	C	0.78	0/1816	1.33	0/2459
4	D	0.76	0/1793	1.34	0/2429
5	E	0.81	0/1772	1.34	0/2390
6	F	0.81	0/1749	1.35	0/2365
7	G	0.74	0/1927	1.34	0/2604
8	I	0.75	0/1532	1.33	0/2072
9	J	0.70	0/1419	1.26	0/1918
10	K	0.70	0/1443	1.30	0/1944
11	P	0.87	0/641	1.36	0/866
All	All	0.76	0/17920	1.32	0/24232

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	1903	1888	1881	4	0
2	B	1852	1871	1870	4	0
3	C	1789	1791	1790	3	0
4	D	1769	1781	1776	2	0
5	E	1749	1737	1732	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	1725	1739	1728	9	0
7	G	1888	1874	1868	3	0
8	I	1508	1500	1497	1	0
9	J	1392	1379	1370	1	0
10	K	1417	1431	1430	2	0
11	P	628	606	603	4	0
All	All	17620	17597	17545	27	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 1.

The worst 5 of 27 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)
11:P:111:LEU:O	11:P:111:LEU:HG	2.03	0.59
1:A:63:LEU:HD22	1:A:63:LEU:N	2.18	0.58
6:F:81:ALA:HB2	6:F:130:VAL:HG21	1.87	0.56
6:F:72:LEU:HD11	6:F:132:LEU:HD23	1.92	0.52
6:F:75:ALA:HB2	6:F:161:ILE:HG23	1.93	0.51

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%)	231 (96%)	9 (4%)	0	100	100
2	B	241/250 (96%)	225 (93%)	16 (7%)	0	100	100
3	C	228/258 (88%)	218 (96%)	10 (4%)	0	100	100
4	D	225/254 (89%)	203 (90%)	22 (10%)	0	100	100
5	E	224/260 (86%)	203 (91%)	21 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	226/234 (97%)	204 (90%)	22 (10%)	0	100	100
7	G	243/288 (84%)	227 (93%)	16 (7%)	0	100	100
8	I	189/261 (72%)	179 (95%)	10 (5%)	0	100	100
9	J	174/205 (85%)	158 (91%)	16 (9%)	0	100	100
10	K	172/198 (87%)	160 (93%)	12 (7%)	0	100	100
11	P	73/200 (36%)	69 (94%)	4 (6%)	0	100	100
All	All	2235/2660 (84%)	2077 (93%)	158 (7%)	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%)	200 (98%)	4 (2%)	48	66
2	B	202/209 (97%)	201 (100%)	1 (0%)	81	80
3	C	190/216 (88%)	187 (98%)	3 (2%)	55	69
4	D	200/226 (88%)	197 (98%)	3 (2%)	57	70
5	E	187/215 (87%)	178 (95%)	9 (5%)	23	50
6	F	182/193 (94%)	171 (94%)	11 (6%)	17	45
7	G	199/239 (83%)	198 (100%)	1 (0%)	81	80
8	I	160/214 (75%)	158 (99%)	2 (1%)	61	72
9	J	148/173 (86%)	148 (100%)	0	100	100
10	K	156/175 (89%)	156 (100%)	0	100	100
11	P	71/180 (39%)	69 (97%)	2 (3%)	38	60
All	All	1899/2250 (84%)	1863 (98%)	36 (2%)	49	67

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	157	TYR
11	P	91	VAL
6	F	199	GLN
8	I	6	PHE
5	E	121	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
7	G	147	HIS
9	J	64	ASN
10	K	146	HIS
8	I	115	HIS
5	E	23	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46570. These allow visual inspection of the internal detail of the map and identification of artifacts.

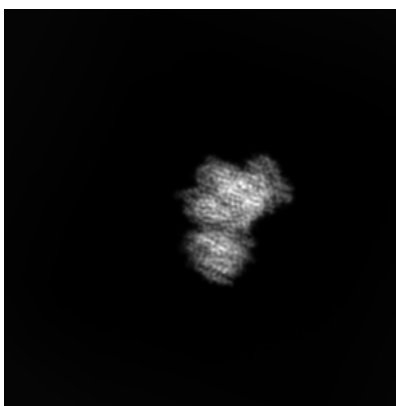
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

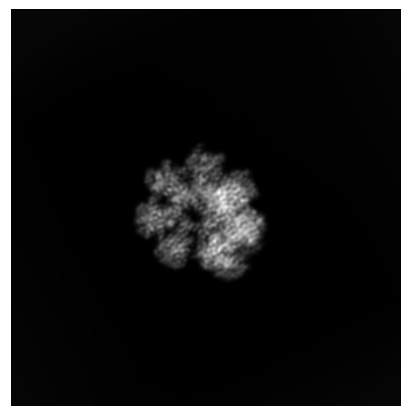
6.1.1 Primary map



X

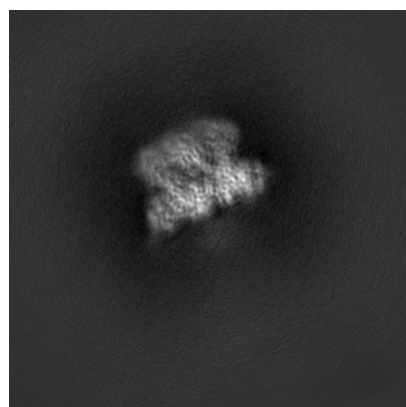


Y

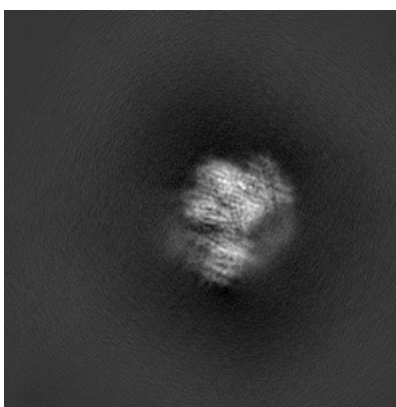


Z

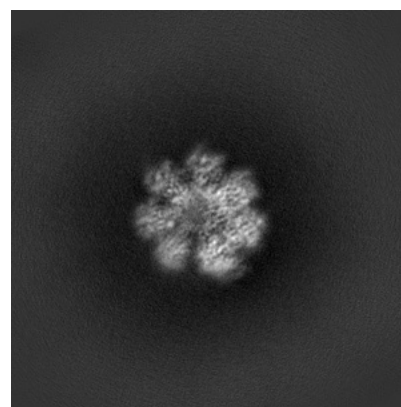
6.1.2 Raw map



X



Y

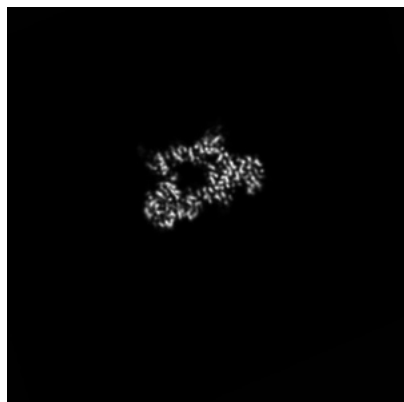


Z

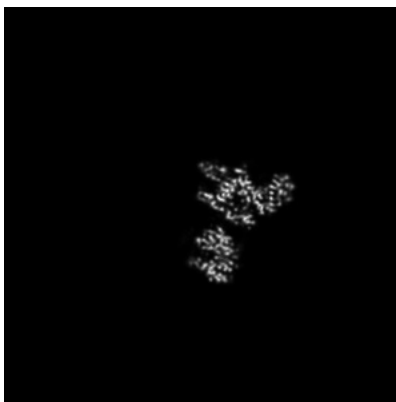
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

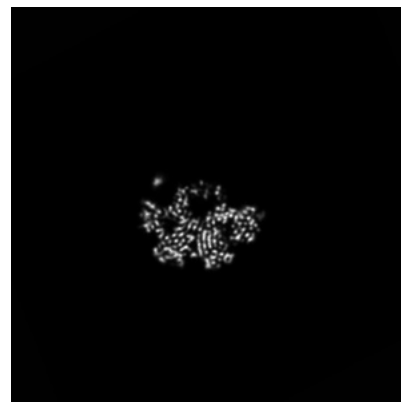
6.2.1 Primary map



X Index: 170

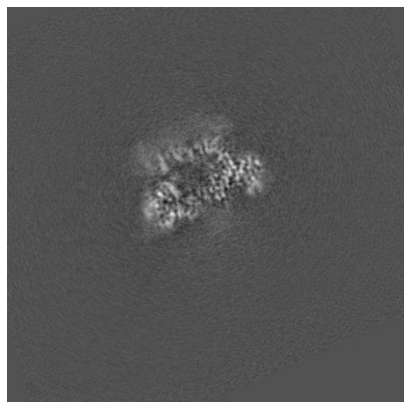


Y Index: 170

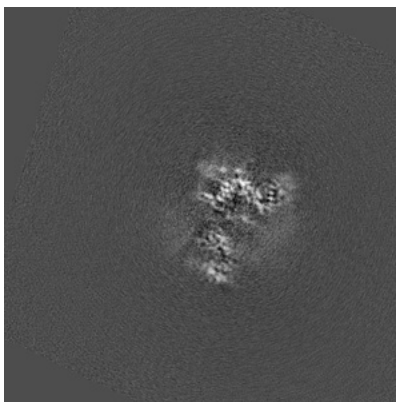


Z Index: 170

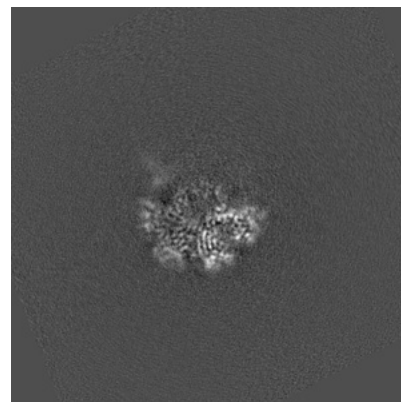
6.2.2 Raw map



X Index: 170



Y Index: 170

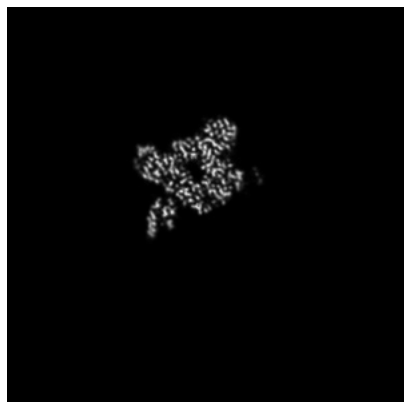


Z Index: 170

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

6.3 Largest variance slices [i](#)

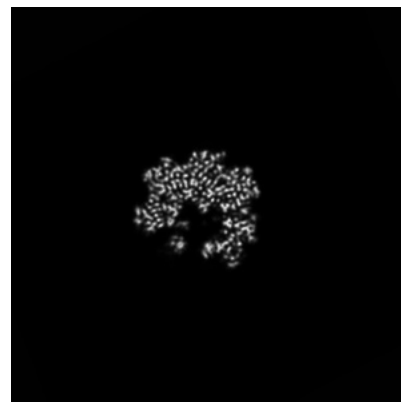
6.3.1 Primary map



X Index: 182

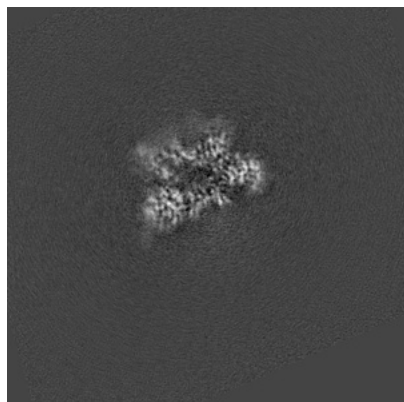


Y Index: 156

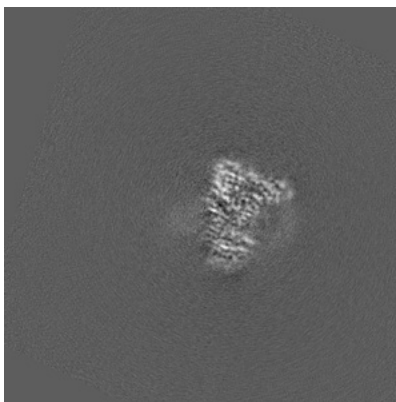


Z Index: 190

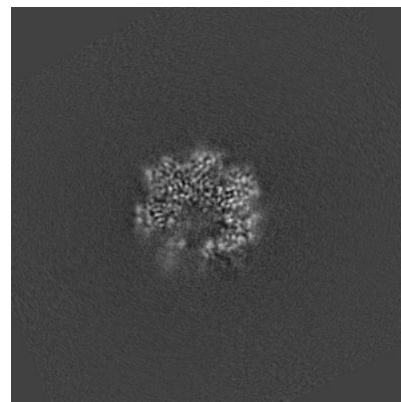
6.3.2 Raw map



X Index: 173



Y Index: 185

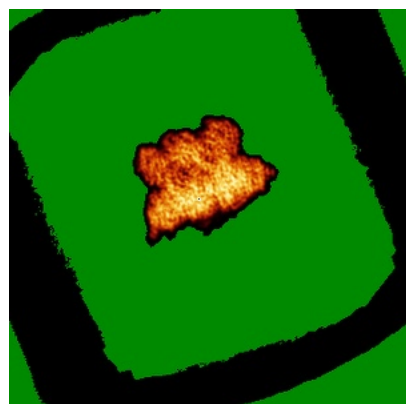


Z Index: 188

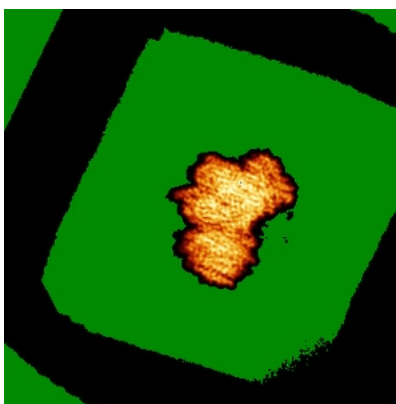
The images above show the largest variance slices of the map in three orthogonal directions.

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

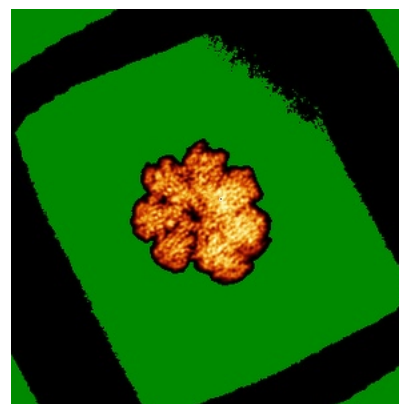
6.4.1 Primary map



X

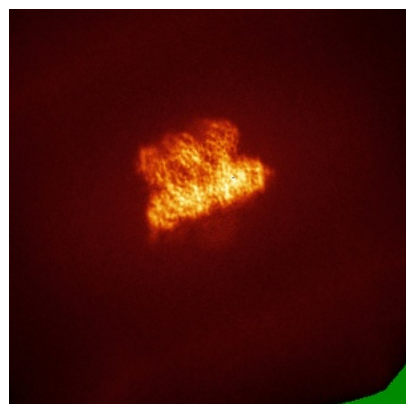


Y

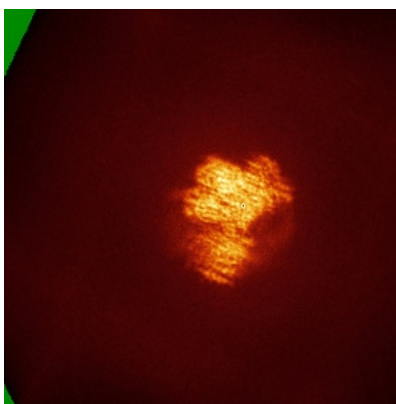


Z

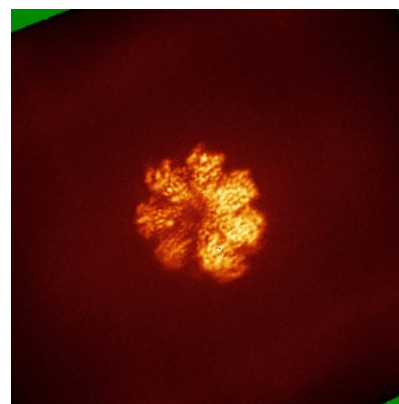
6.4.2 Raw map



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](#)

This section was not generated.

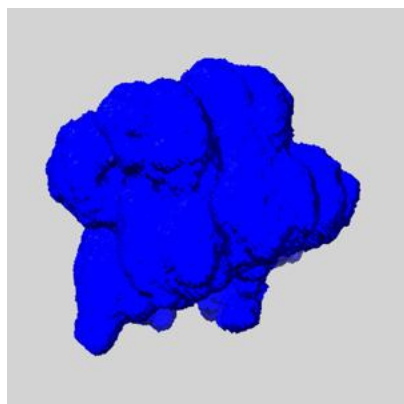
6.6 Mask visualisation [i](#)

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

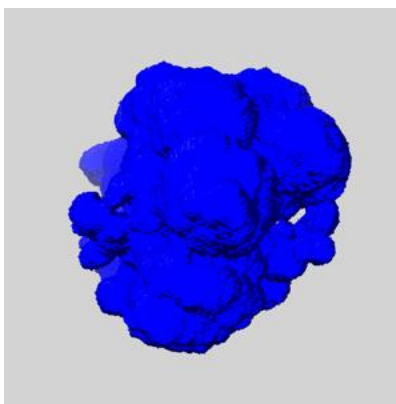
A mask typically either:

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

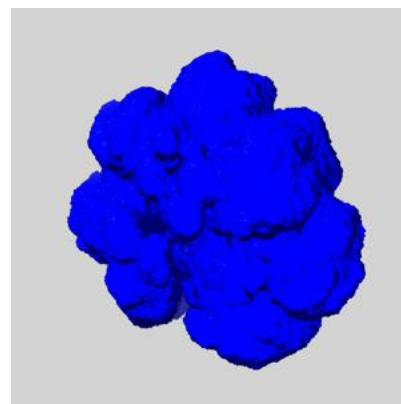
6.6.1 emd_46570_msk_1.map [i](#)



X



Y

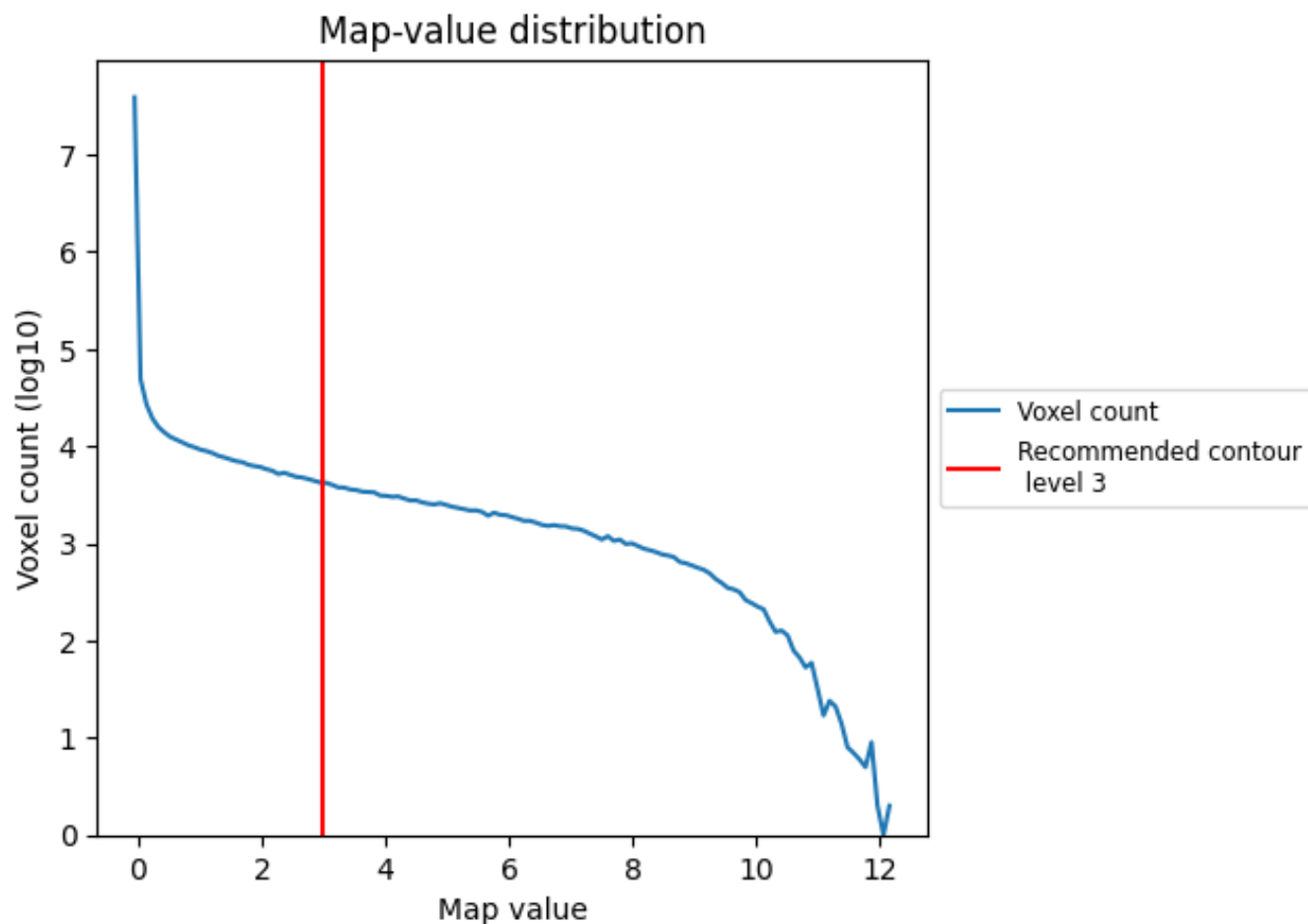


Z

7 Map analysis [i](#)

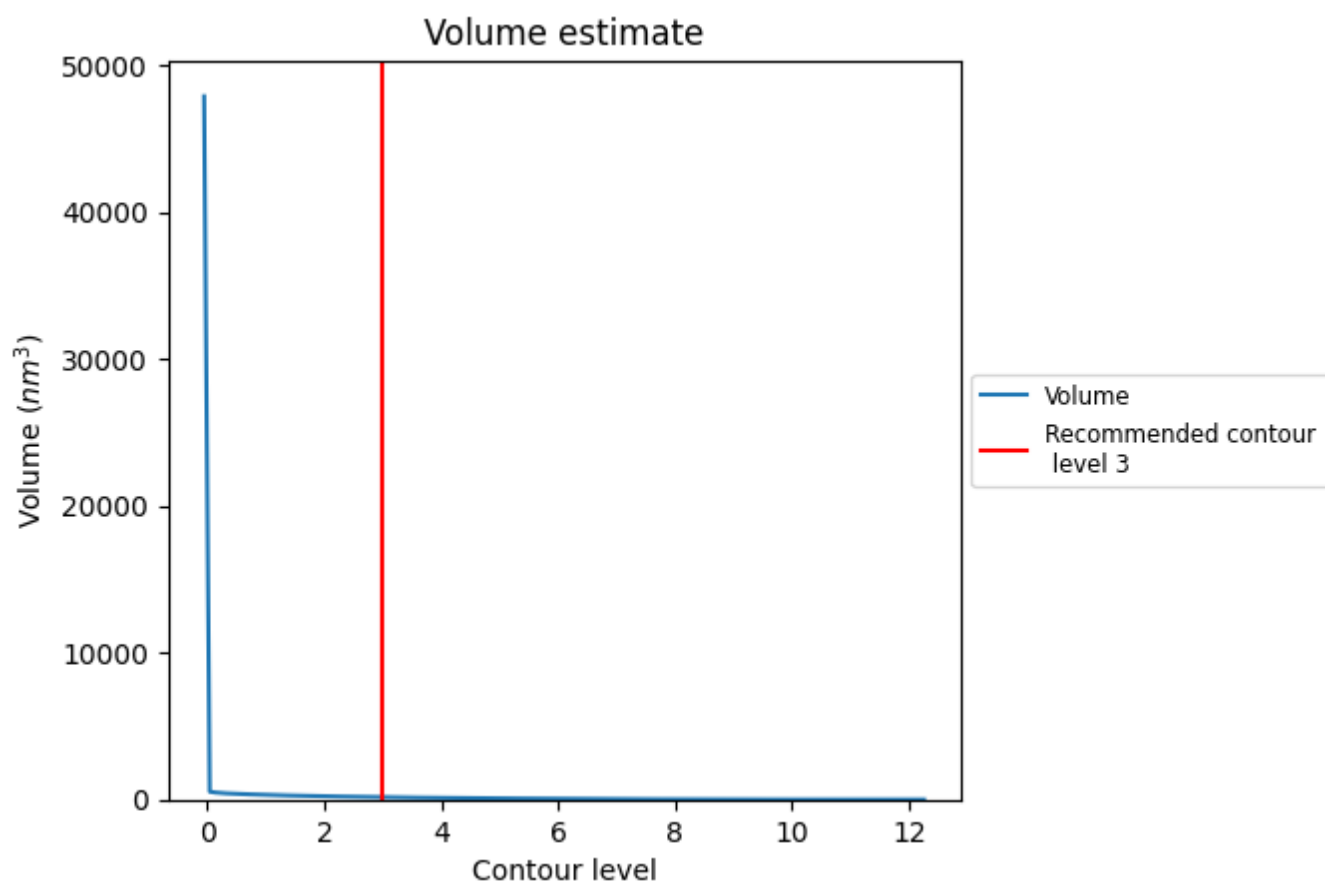
This section contains the results of statistical analysis of the map.

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.

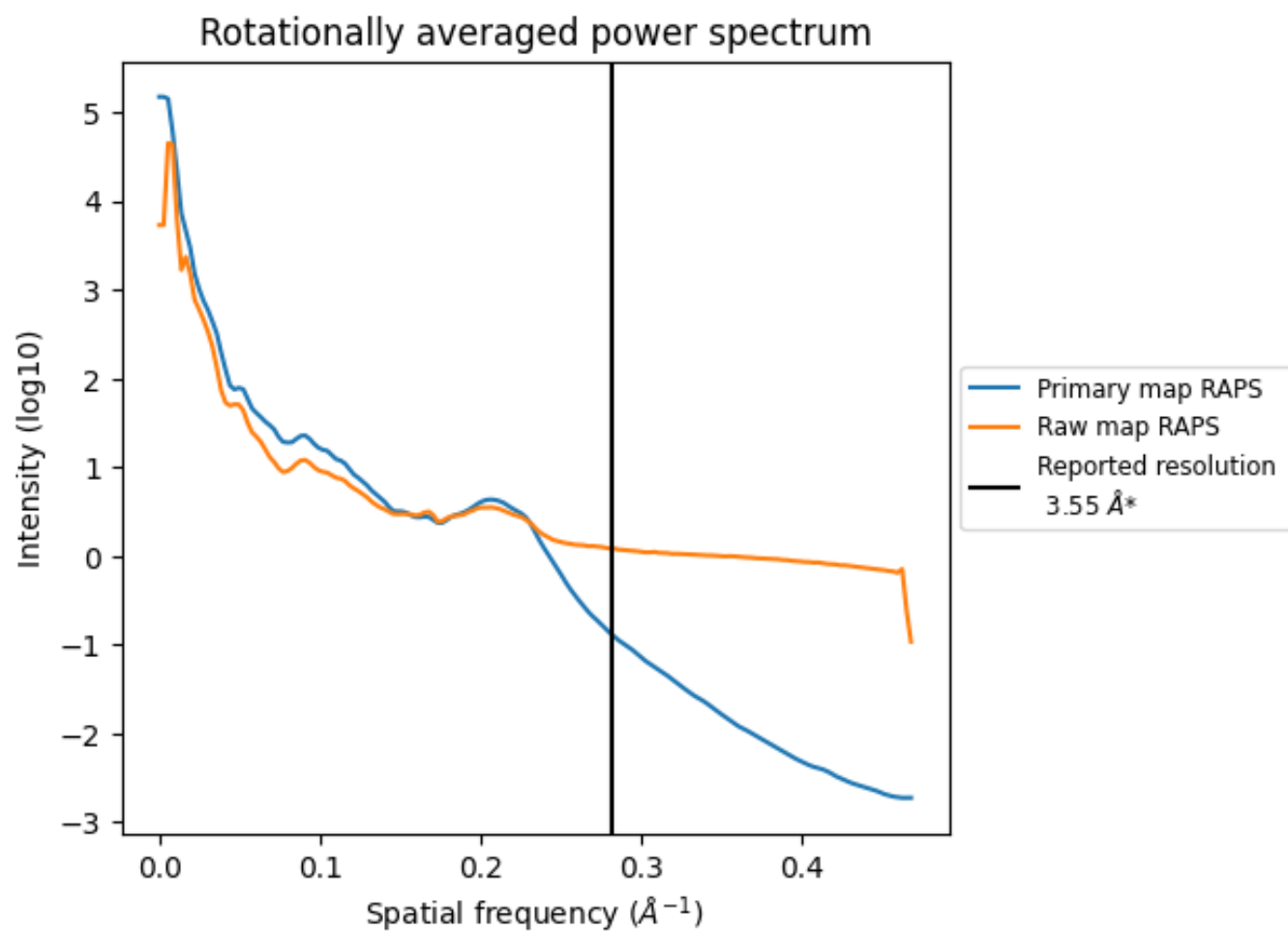
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 161 nm^3 ; this corresponds to an approximate mass of 145 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 ⓘ

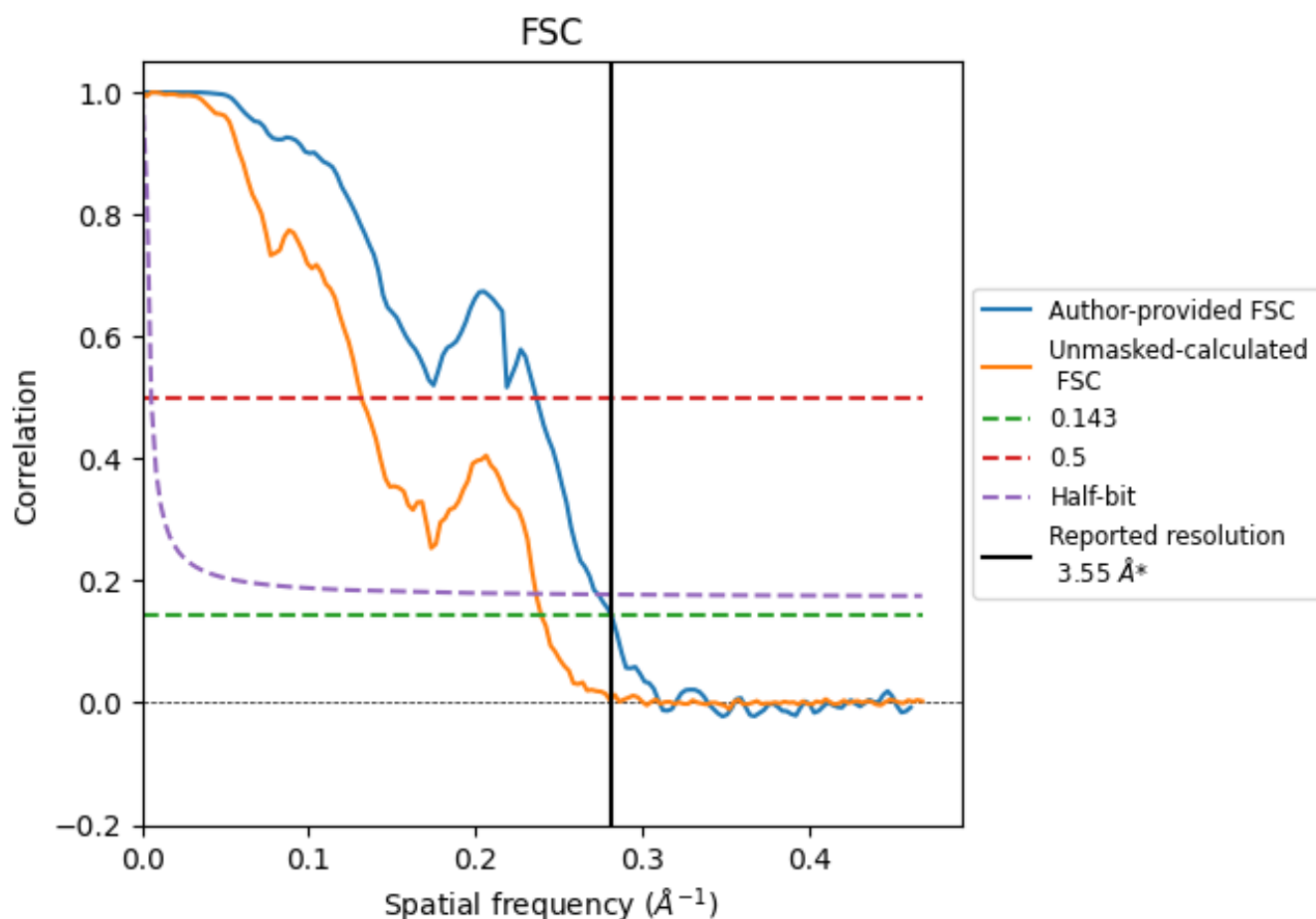


*Reported resolution corresponds to spatial frequency of 0.282 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.282 Å⁻¹

8.2 Resolution estimates [i](#)

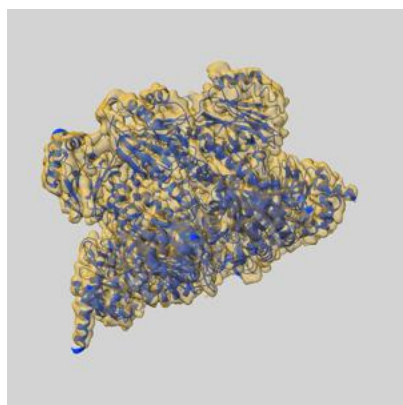
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.55	-	-
Author-provided FSC curve	3.55	4.23	3.65
Unmasked-calculated*	4.18	7.60	4.23

*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 4.18 differs from the reported value 3.55 by more than 10 %

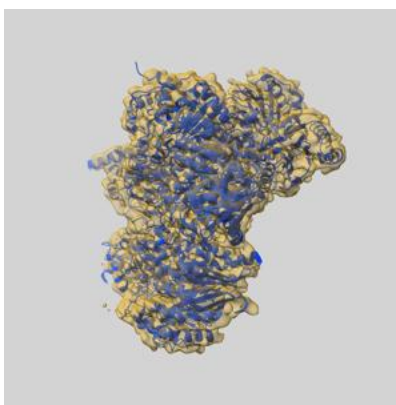
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-46570 and PDB model 9D4U. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

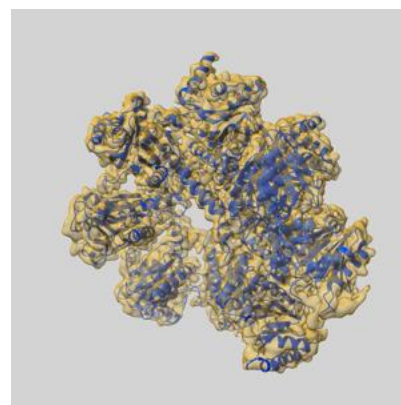
9.1 Map-model overlay [i](#)



X



Y



Z

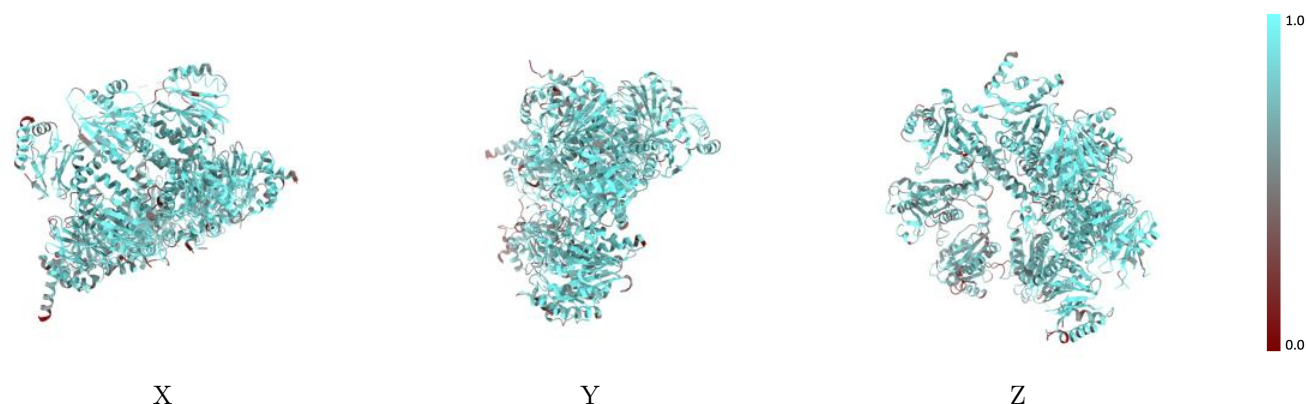
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



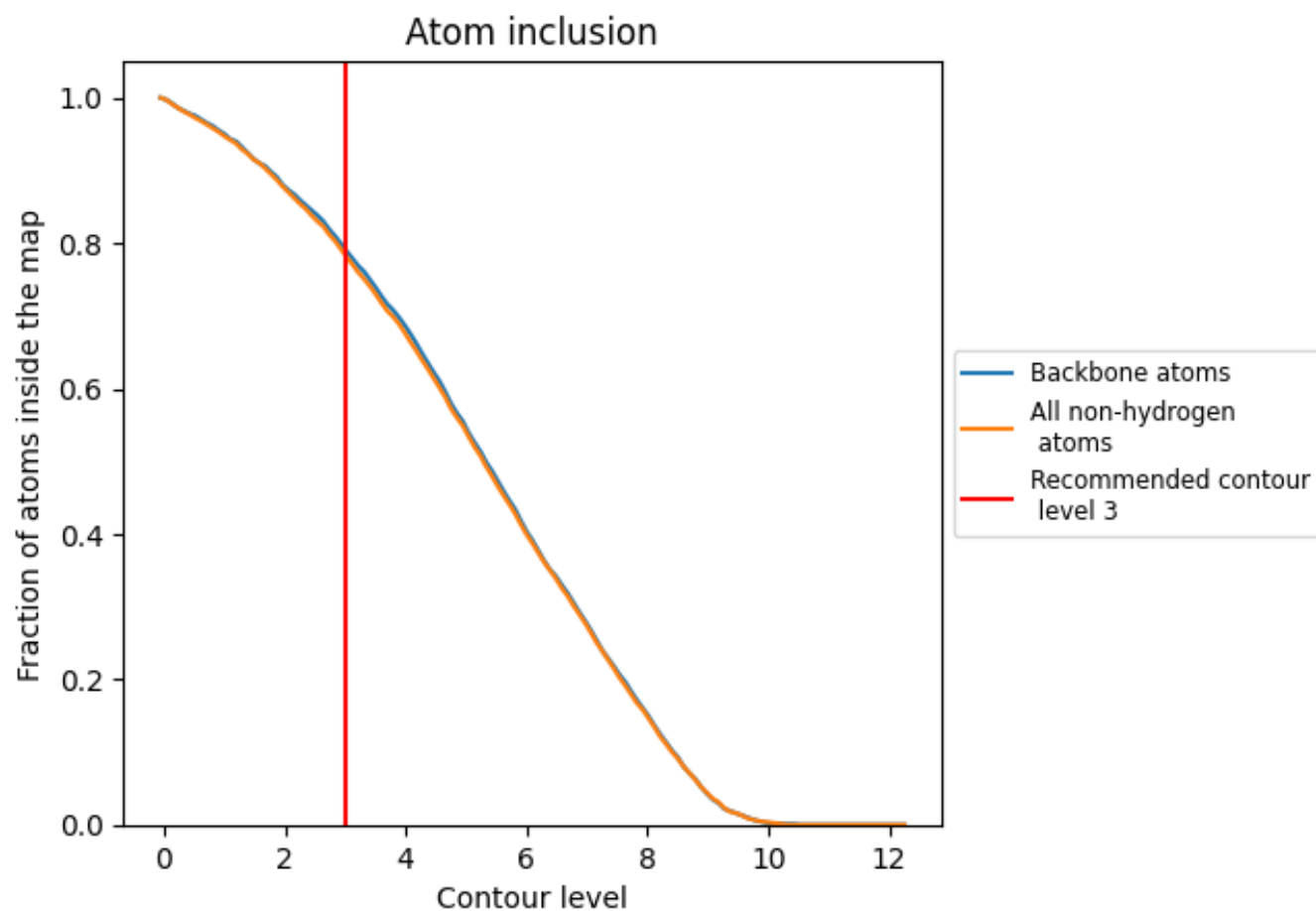
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 79% of all backbone atoms, 78% 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> 0.7830	<div></div> 0.3600
A	<div></div> 0.8440	<div></div> 0.4120
B	<div></div> 0.8250	<div></div> 0.3770
C	<div></div> 0.8180	<div></div> 0.3800
D	<div></div> 0.7690	<div></div> 0.3500
E	<div></div> 0.6700	<div></div> 0.2550
F	<div></div> 0.7500	<div></div> 0.3090
G	<div></div> 0.8020	<div></div> 0.3680
I	<div></div> 0.8140	<div></div> 0.3920
J	<div></div> 0.8570	<div></div> 0.4240
K	<div></div> 0.7820	<div></div> 0.3480
P	<div></div> 0.6930	<div></div> 0.3370

1.0

0.0

<0.0