



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 09:40 AM UTC

PDB ID : 9NH5 / pdb_00009nh5
EMDB ID : EMD-49402
Title : CRYO-EM STRUCTURE OF HUMAN U7 SNRNP WITH METHYLATED
noncleavable H2A* SUBSTRATE PRE-MRNA (core region)
Authors : Desotell, A.; Tong, L.
Deposited on : 2025-02-24
Resolution : 2.82 Å(reported)
Based on initial model : 6v4X

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

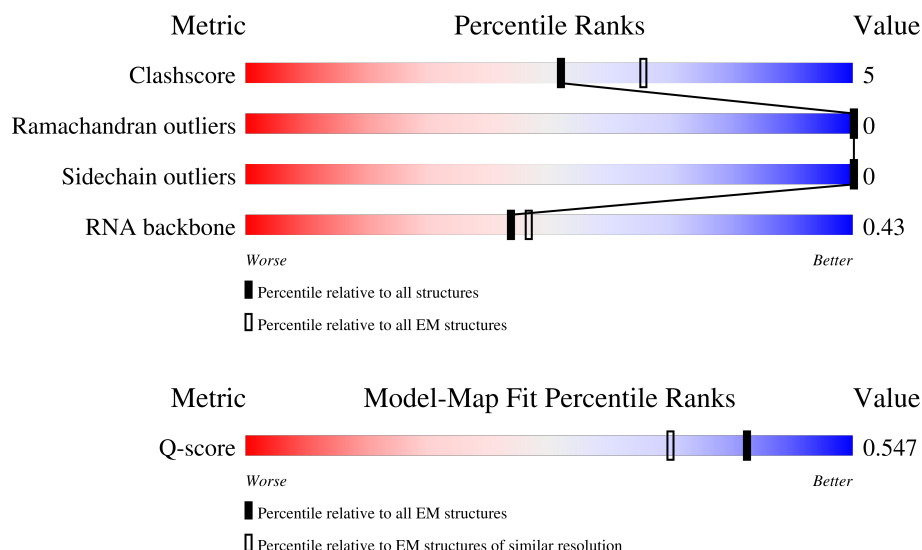
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.82 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	11795 (2.32 - 3.32)

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	146	
2	B	95	
3	F	86	

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Mol	Chain	Length	Quality of chain
4	E	92	
5	G	84	
6	C	123	
7	D	371	
8	H	684	
9	I	782	
10	J	1072	
11	K	8	
12	Z	64	
13	Y	56	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 16094 atoms, of which 0 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 Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	83	Total	C	N	O	S	0	0
			652	409	115	122	6		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P62318
A	-18	GLY	-	expression tag	UNP P62318
A	-17	SER	-	expression tag	UNP P62318
A	-16	SER	-	expression tag	UNP P62318
A	-15	HIS	-	expression tag	UNP P62318
A	-14	HIS	-	expression tag	UNP P62318
A	-13	HIS	-	expression tag	UNP P62318
A	-12	HIS	-	expression tag	UNP P62318
A	-11	HIS	-	expression tag	UNP P62318
A	-10	HIS	-	expression tag	UNP P62318
A	-9	SER	-	expression tag	UNP P62318
A	-8	SER	-	expression tag	UNP P62318
A	-7	GLY	-	expression tag	UNP P62318
A	-6	LEU	-	expression tag	UNP P62318
A	-5	VAL	-	expression tag	UNP P62318
A	-4	PRO	-	expression tag	UNP P62318
A	-3	ARG	-	expression tag	UNP P62318
A	-2	GLY	-	expression tag	UNP P62318
A	-1	SER	-	expression tag	UNP P62318
A	0	HIS	-	expression tag	UNP P62318

- Molecule 2 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	76	Total	C	N	O	S	0	0
			612	387	111	107	7		

- Molecule 3 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	74	Total	C	N	O	S	0	0
			579	375	95	104	5		

- Molecule 4 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	81	Total	C	N	O	S	0	0
			670	426	119	120	5		

- Molecule 5 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	76	Total	C	N	O	S	0	0
			594	375	107	106	6		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	77	LEU	-	expression tag	UNP P62308
G	78	GLU	-	expression tag	UNP P62308
G	79	HIS	-	expression tag	UNP P62308
G	80	HIS	-	expression tag	UNP P62308
G	81	HIS	-	expression tag	UNP P62308
G	82	HIS	-	expression tag	UNP P62308
G	83	HIS	-	expression tag	UNP P62308
G	84	HIS	-	expression tag	UNP P62308

- Molecule 6 is a protein called U7 snRNA-associated Sm-like protein LSm10.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	106	Total	C	N	O	S	0	0
			858	535	162	160	1		

- Molecule 7 is a protein called U7 snRNA-associated Sm-like protein LSm11.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	105	Total	C	N	O	S	0	0
			865	551	169	140	5		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-10	MET	-	expression tag	UNP P83369
D	-9	HIS	-	expression tag	UNP P83369
D	-8	HIS	-	expression tag	UNP P83369
D	-7	HIS	-	expression tag	UNP P83369
D	-6	HIS	-	expression tag	UNP P83369
D	-5	HIS	-	expression tag	UNP P83369
D	-4	HIS	-	expression tag	UNP P83369
D	-3	SER	-	expression tag	UNP P83369
D	-2	GLY	-	expression tag	UNP P83369
D	-1	GLY	-	expression tag	UNP P83369
D	0	SER	-	expression tag	UNP P83369

- Molecule 8 is a protein called Cleavage and polyadenylation specificity factor subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	480	Total	C	N	O	S	0	0
			3835	2450	658	699	28		

- Molecule 9 is a protein called Cleavage and polyadenylation specificity factor subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	504	Total	C	N	O	S	0	0
			4009	2549	686	751	23		

- Molecule 10 is a protein called Symplekin.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	290	Total	C	N	O	S	0	0
			2307	1473	394	428	12		

- Molecule 11 is a protein called Cleavage stimulation factor subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	8	Total	C	N	O	0	0
			76	45	17	14		

- Molecule 12 is a RNA chain called U7 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Z	30	Total	C	N	O	P	0	0
			630	282	100	218	30		

- Molecule 13 is a RNA chain called Methylated H2A* pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Y	19	Total	C	N	O	P	0	0
			405	182	75	129	19		

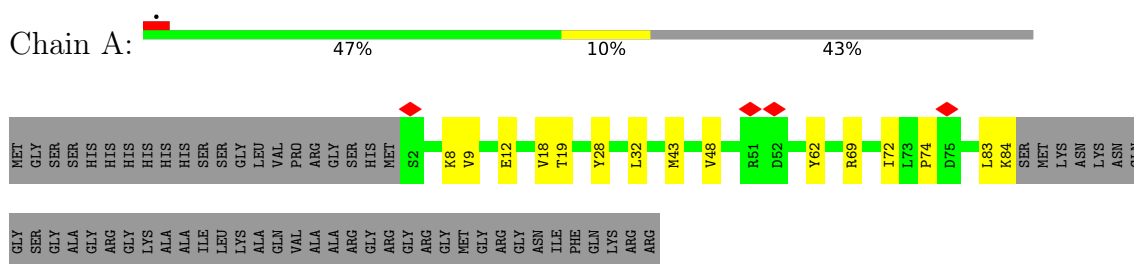
- Molecule 14 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
14	H	2	Total	Zn	0
			2	2	

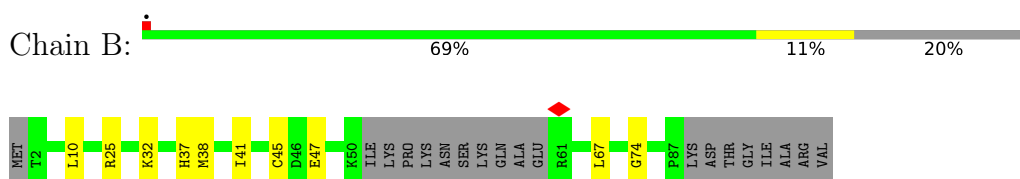
3 Residue-property plots [i](#)

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.

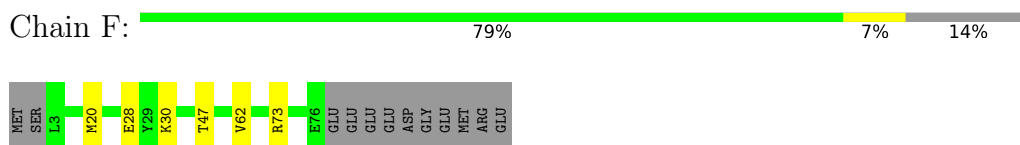
- Molecule 1: Small nuclear ribonucleoprotein Sm D3



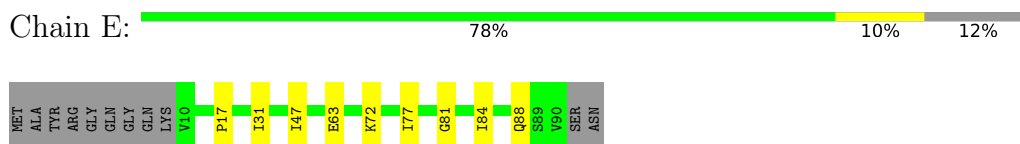
- Molecule 2: Small nuclear ribonucleoprotein-associated proteins B and B'



- Molecule 3: Small nuclear ribonucleoprotein F



- Molecule 4: Small nuclear ribonucleoprotein E

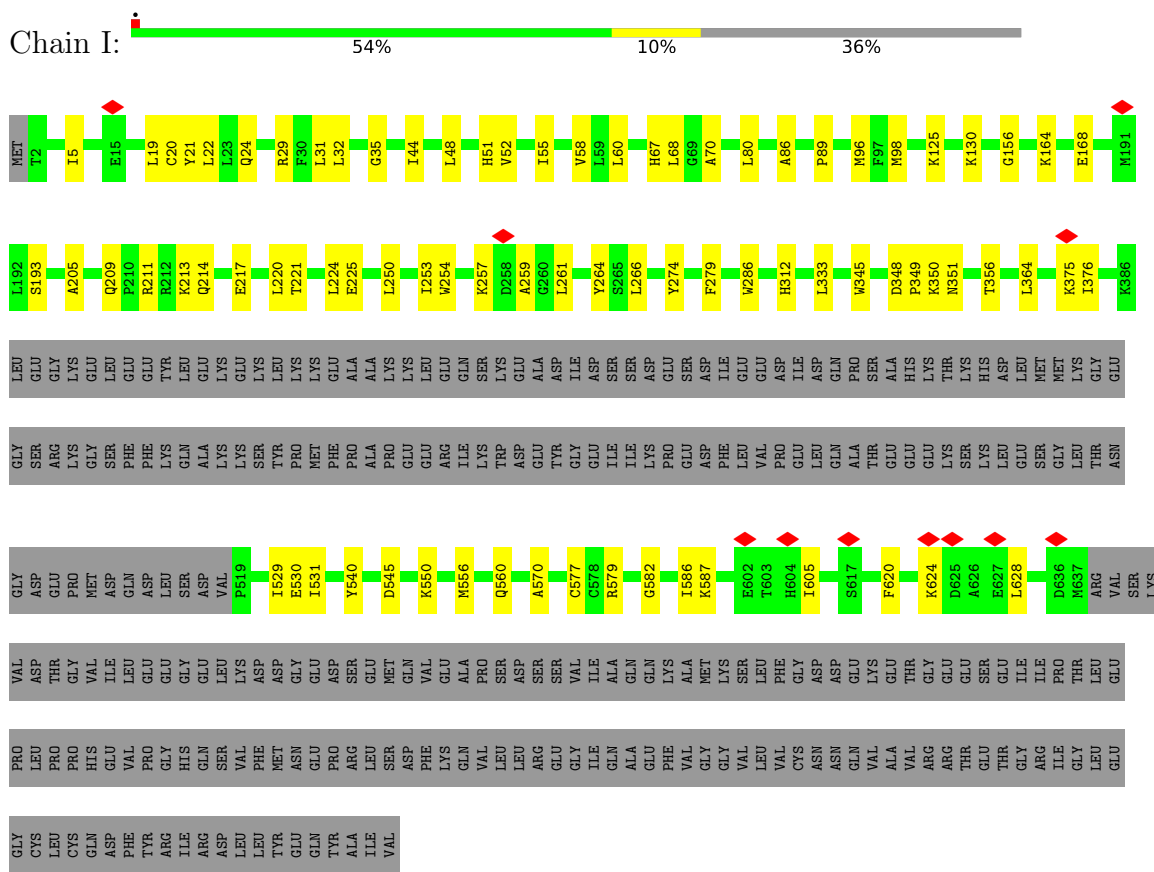


- Molecule 5: Small nuclear ribonucleoprotein G

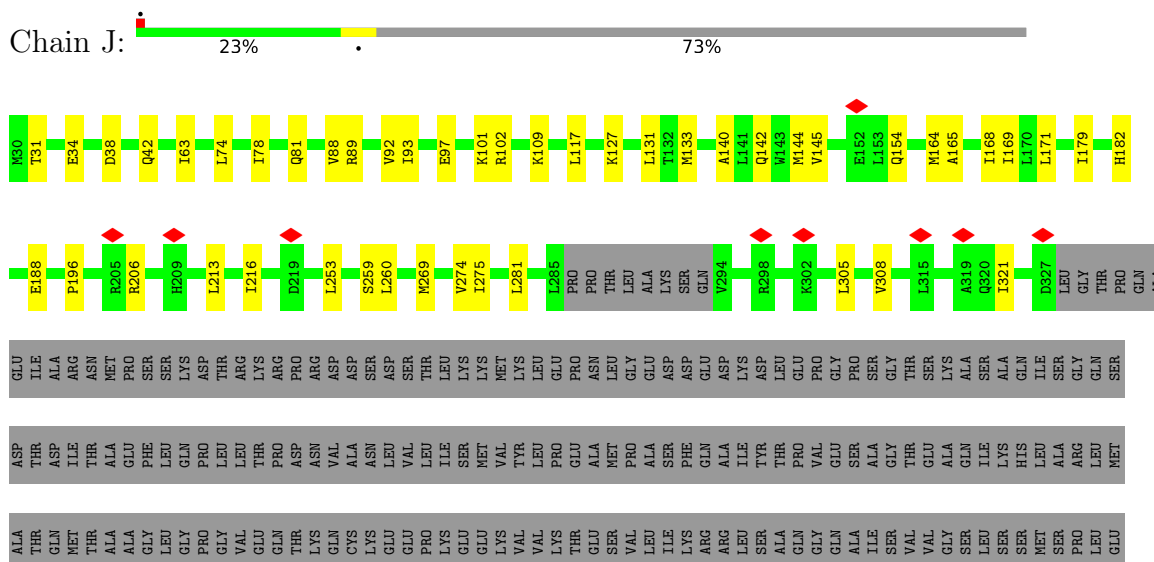


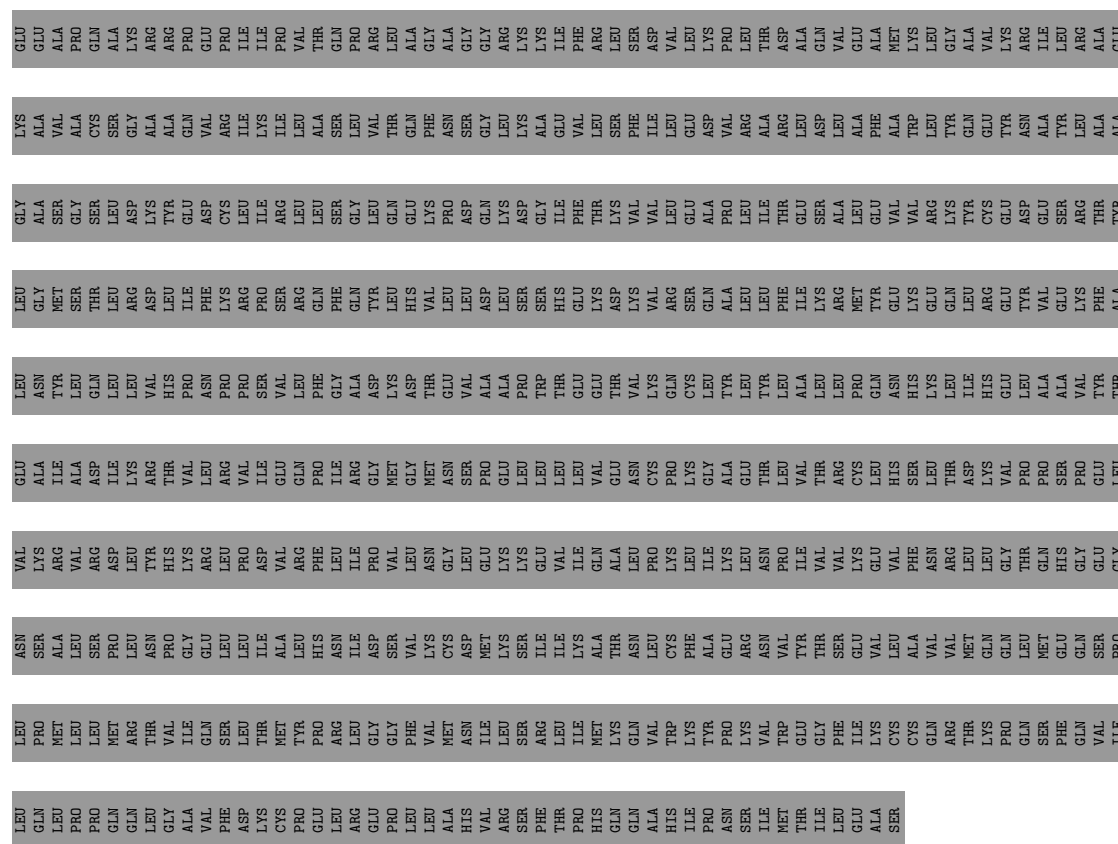
ASP	SER	ILE	LEU	SER	THR	THR	VAL	VAL	ASP	GLY	GLY	LYS	THR	ALA	ASN	LEU	LEU	GLU	THR	ARG	THR	VAL	VAL	CYS	GLU	GLU	GLY	SER	GLY	GLU	ASP	ASP	GLU	SER	LEU	LEU	ARG	GLU	VAL	GLU	LEU	ALA	ALA	GLN	ARG	TYR	GLU	ALA	LEU	THR	PRO	VAL	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 9: Cleavage and polyadenylation specificity factor subunit 2



- Molecule 10: Symplekin



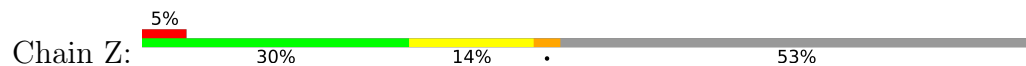


- Molecule 11: Cleavage stimulation factor subunit 3

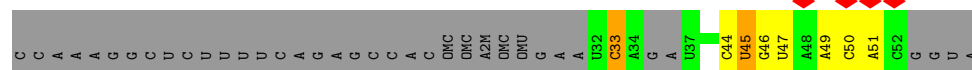
Chain K: 100%

There are no outlier residues recorded for this chain.

- Molecule 12: U7 snRNA



- Molecule 13: Methylated H2A* pre-mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	168875	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 ($e^-/\text{\AA}^2$)	58.10	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.674	Depositor
Minimum map value	-0.462	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	316.8, 316.8, 316.8	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.16	0/660	0.39	0/889
2	B	0.12	0/620	0.36	0/826
3	F	0.17	0/591	0.45	0/799
4	E	0.15	0/678	0.40	0/910
5	G	0.16	0/602	0.42	0/806
6	C	0.15	0/870	0.40	0/1179
7	D	0.18	0/881	0.47	0/1182
8	H	0.16	0/3919	0.43	0/5291
9	I	0.18	0/4088	0.44	0/5531
10	J	0.13	0/2338	0.32	0/3165
11	K	0.17	0/76	0.24	0/100
12	Z	0.13	0/701	0.33	0/1088
13	Y	0.09	0/452	0.23	0/699
All	All	0.16	0/16476	0.40	0/22465

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	652	0	670	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	612	0	634	7	0
3	F	579	0	590	5	0
4	E	670	0	696	6	0
5	G	594	0	614	11	0
6	C	858	0	865	12	0
7	D	865	0	898	14	0
8	H	3835	0	3817	38	0
9	I	4009	0	4032	51	0
10	J	2307	0	2404	25	0
11	K	76	0	71	0	0
12	Z	630	0	317	3	0
13	Y	405	0	207	7	0
14	H	2	0	0	0	0
All	All	16094	0	15815	172	0

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

The worst 5 of 172 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)
5:G:18:SER:HB3	5:G:71:GLU:HB3	1.70	0.72
10:J:253:LEU:HD11	10:J:281:LEU:HD11	1.75	0.68
6:C:8:LYS:HG3	13:Y:33:C:H1'	1.78	0.66
9:I:35:GLY:HA2	9:I:70:ALA:H	1.62	0.65
10:J:275:ILE:HD11	10:J:308:VAL:HG11	1.79	0.64

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	81/146 (56%)	79 (98%)	2 (2%)	0	100	100
2	B	72/95 (76%)	72 (100%)	0	0	100	100
3	F	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
4	E	79/92 (86%)	77 (98%)	2 (2%)	0	100	100
5	G	74/84 (88%)	74 (100%)	0	0	100	100
6	C	104/123 (85%)	100 (96%)	4 (4%)	0	100	100
7	D	99/371 (27%)	93 (94%)	6 (6%)	0	100	100
8	H	470/684 (69%)	454 (97%)	16 (3%)	0	100	100
9	I	500/782 (64%)	467 (93%)	33 (7%)	0	100	100
10	J	286/1072 (27%)	281 (98%)	5 (2%)	0	100	100
11	K	6/8 (75%)	6 (100%)	0	0	100	100
All	All	1843/3543 (52%)	1773 (96%)	70 (4%)	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	73/118 (62%)	73 (100%)	0	100	100
2	B	69/85 (81%)	69 (100%)	0	100	100
3	F	63/74 (85%)	63 (100%)	0	100	100
4	E	76/84 (90%)	76 (100%)	0	100	100
5	G	66/74 (89%)	66 (100%)	0	100	100
6	C	97/110 (88%)	97 (100%)	0	100	100
7	D	94/301 (31%)	94 (100%)	0	100	100
8	H	418/602 (69%)	418 (100%)	0	100	100
9	I	449/695 (65%)	449 (100%)	0	100	100
10	J	261/946 (28%)	261 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	K	8/8 (100%)	8 (100%)	0	100	100
All	All	1674/3097 (54%)	1674 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
9	I	185	ASN
10	J	81	GLN
10	J	64	ASN
8	H	73	HIS
9	I	133	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	Z	29/64 (45%)	9 (31%)	1 (3%)
13	Y	17/56 (30%)	4 (23%)	0
All	All	46/120 (38%)	13 (28%)	1 (2%)

5 of 13 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	Z	11	G
12	Z	14	C
12	Z	23	U
12	Z	24	U
12	Z	26	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	Z	26	G

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

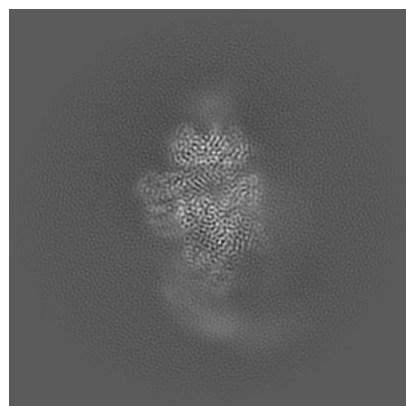
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49402. These allow visual inspection of the internal detail of the map and identification of artifacts.

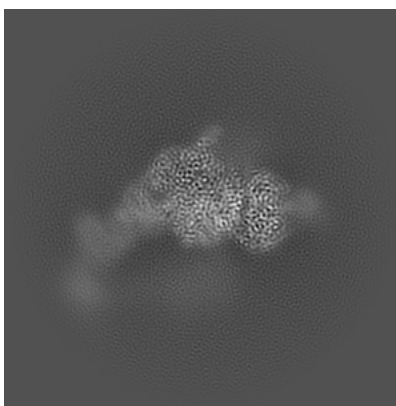
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

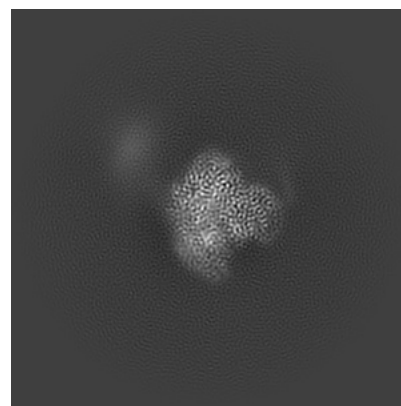
6.1.1 Primary map



X

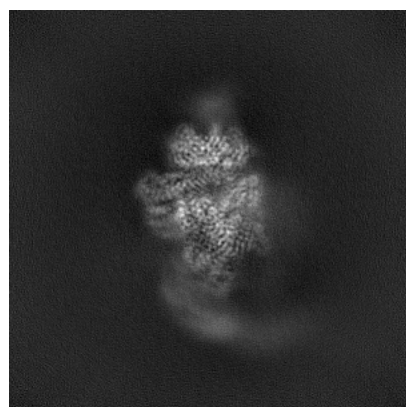


Y

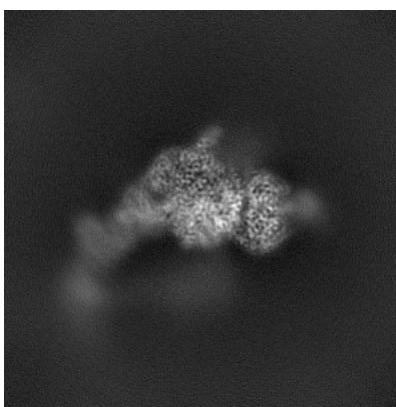


Z

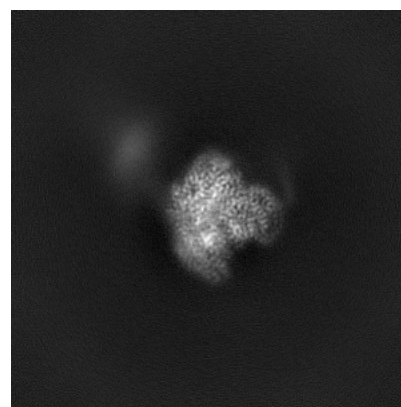
6.1.2 Raw map



X



Y

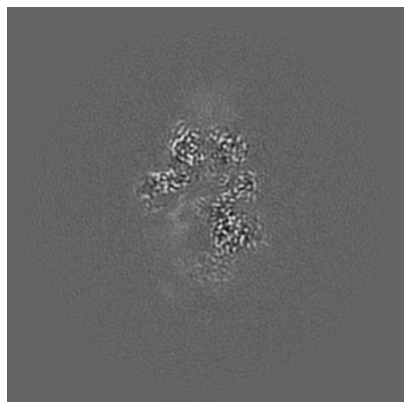


Z

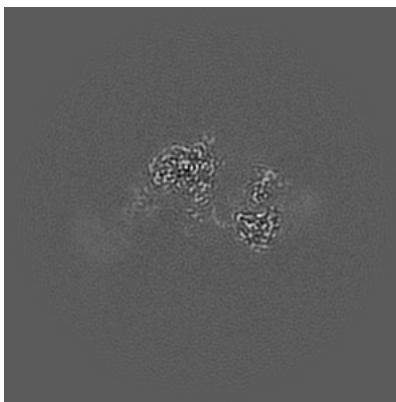
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

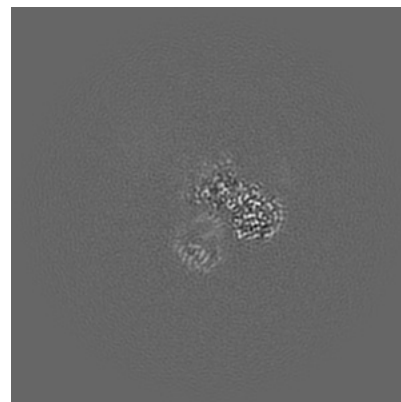
6.2.1 Primary map



X Index: 192

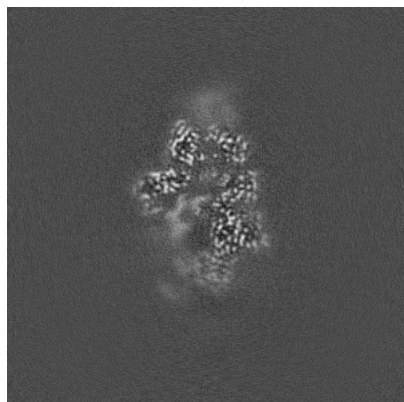


Y Index: 192

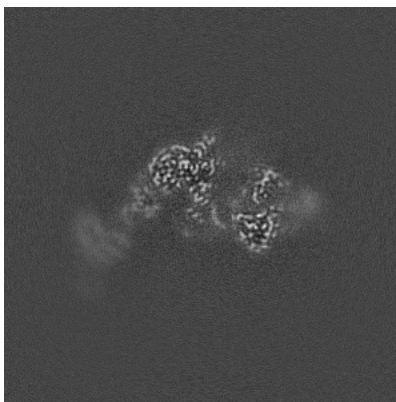


Z Index: 192

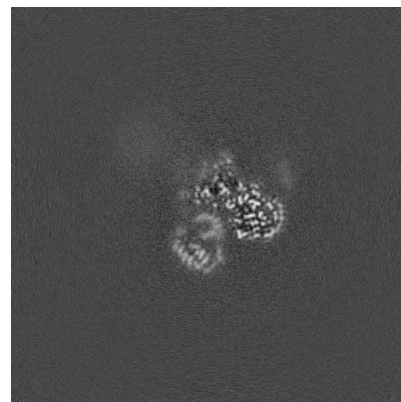
6.2.2 Raw map



X Index: 192



Y Index: 192

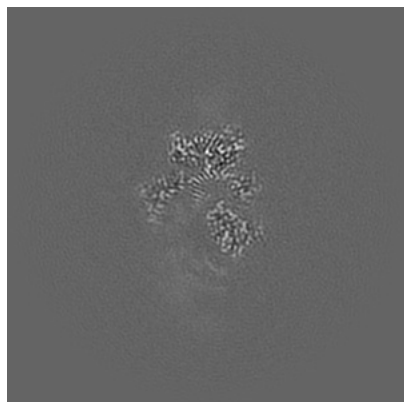


Z Index: 192

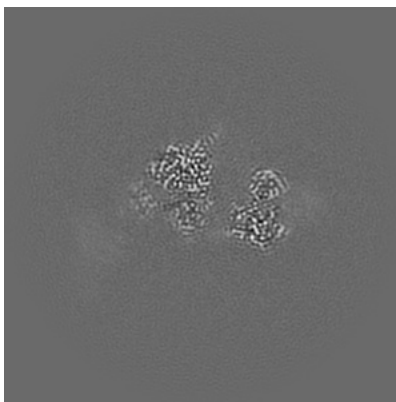
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

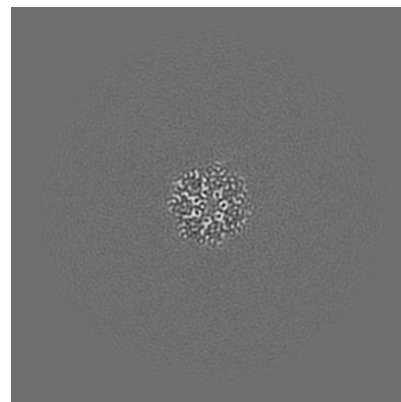
6.3.1 Primary map



X Index: 183

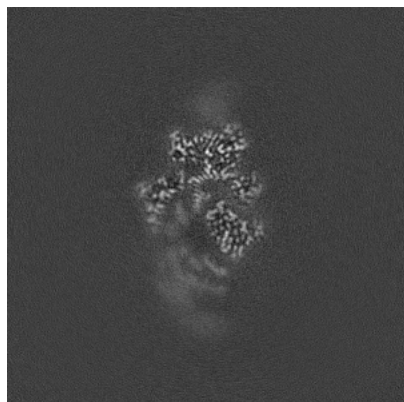


Y Index: 198

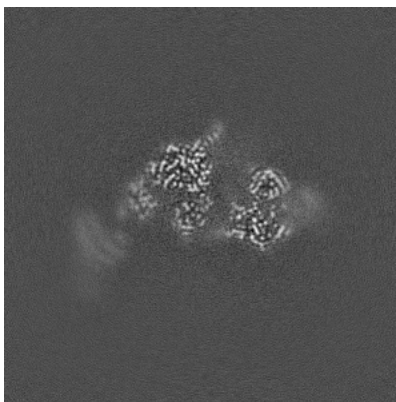


Z Index: 246

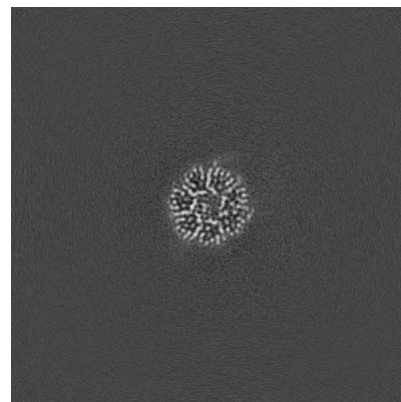
6.3.2 Raw map



X Index: 183



Y Index: 198

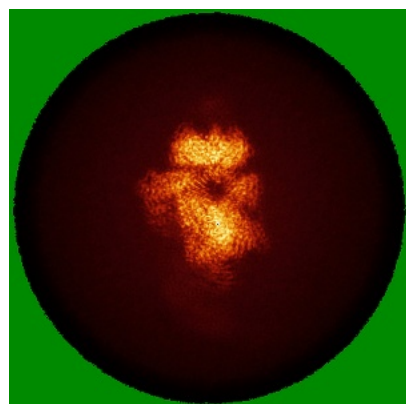


Z Index: 250

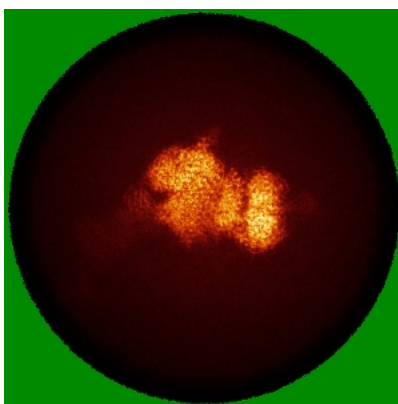
The images above show the largest variance slices of the map in three orthogonal directions.

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

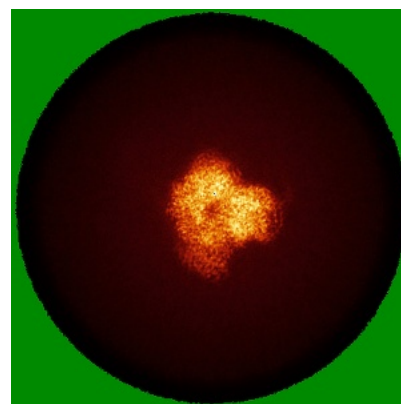
6.4.1 Primary map



X

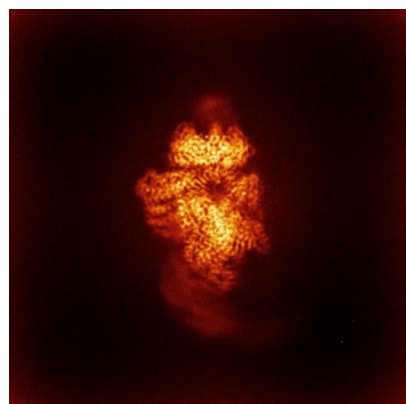


Y

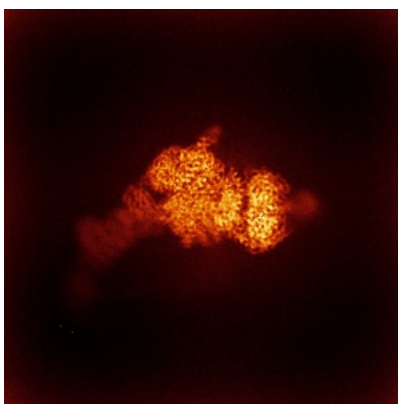


Z

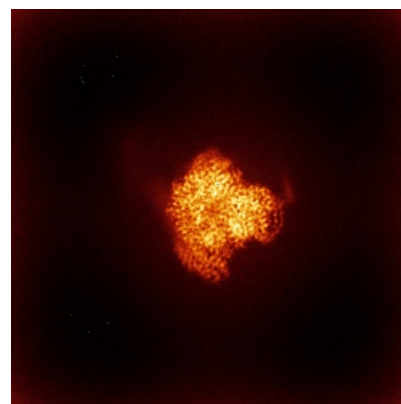
6.4.2 Raw map



X



Y

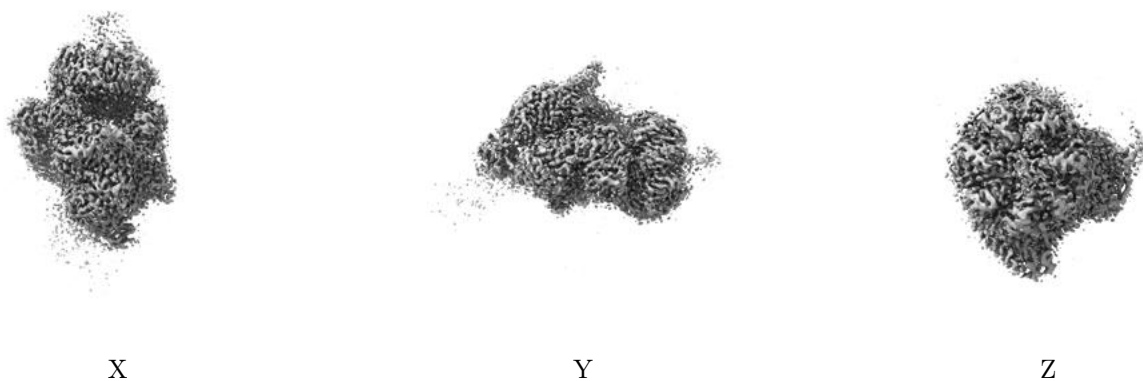


Z

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 0.06. 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.

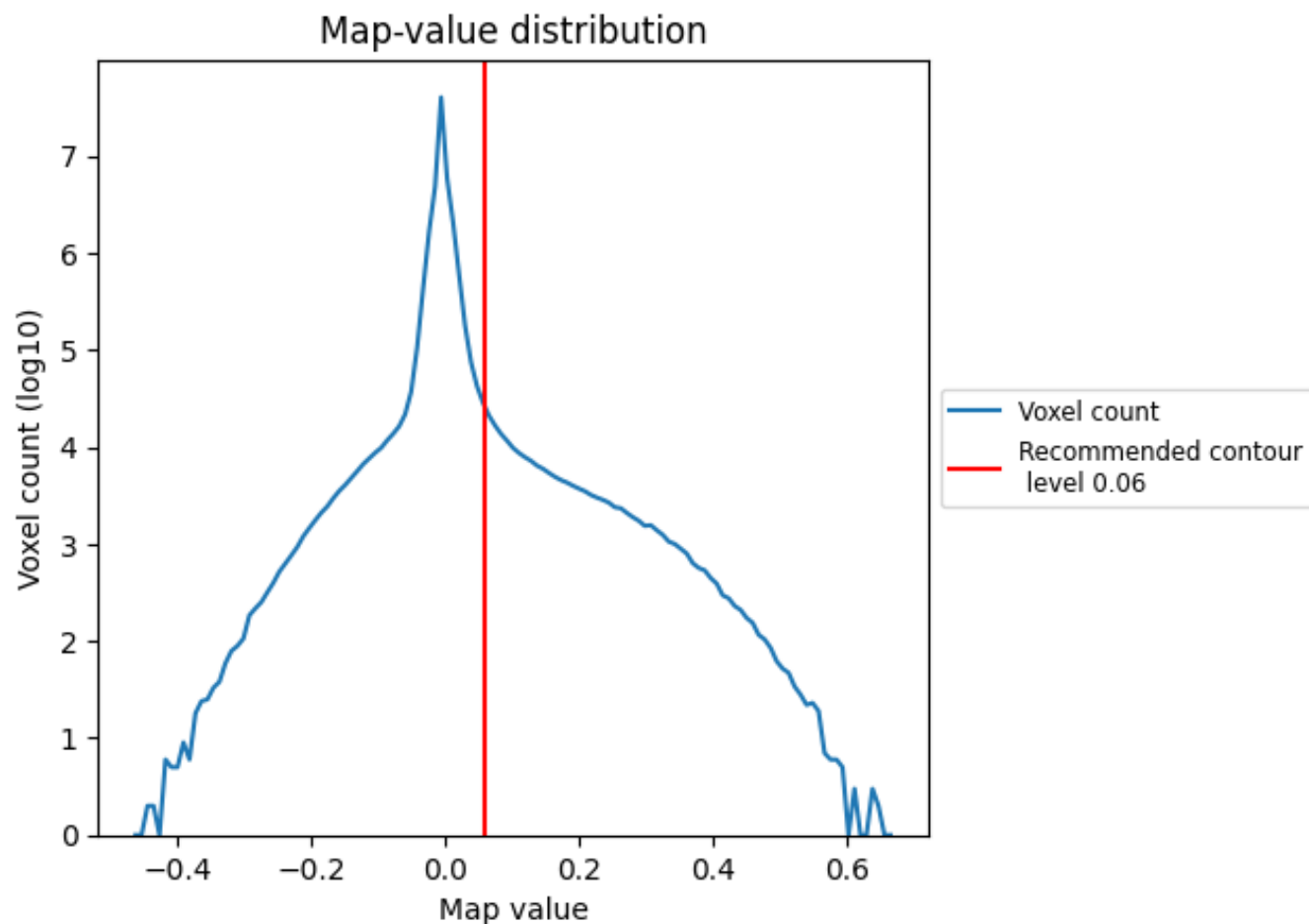
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

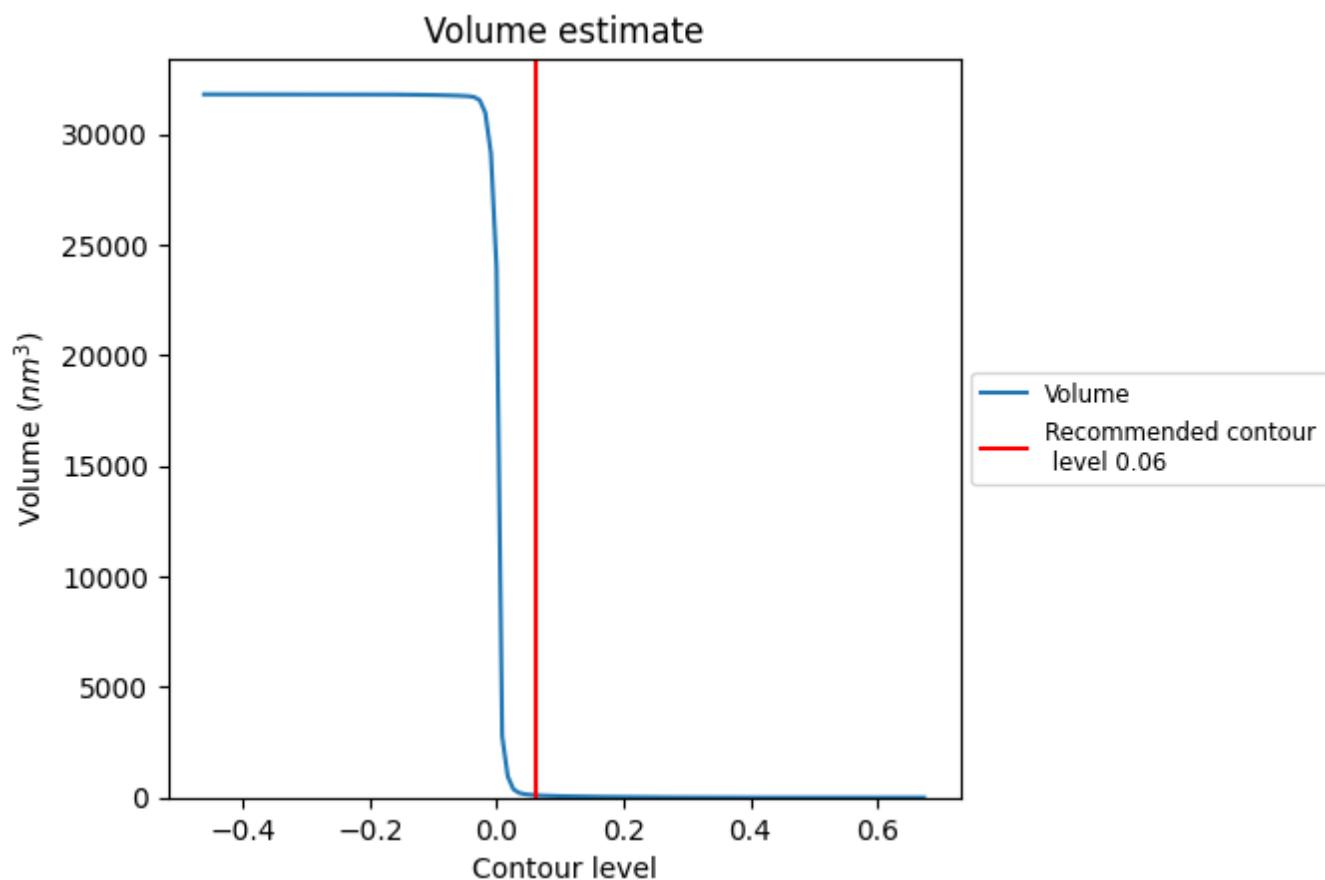
This section contains the results of statistical analysis of the map.

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.

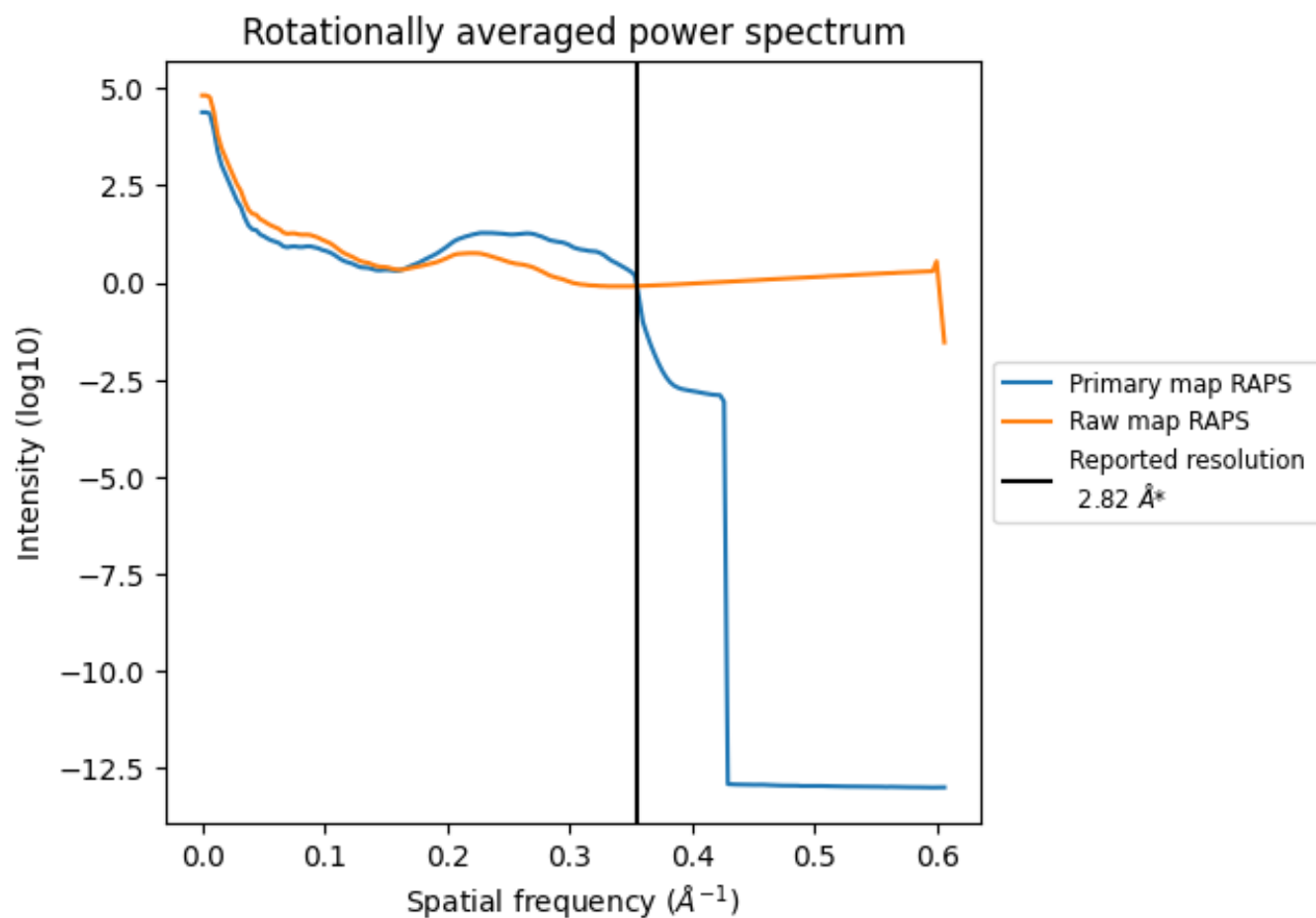
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 109 nm³; this corresponds to an approximate mass of 98 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 ⓘ

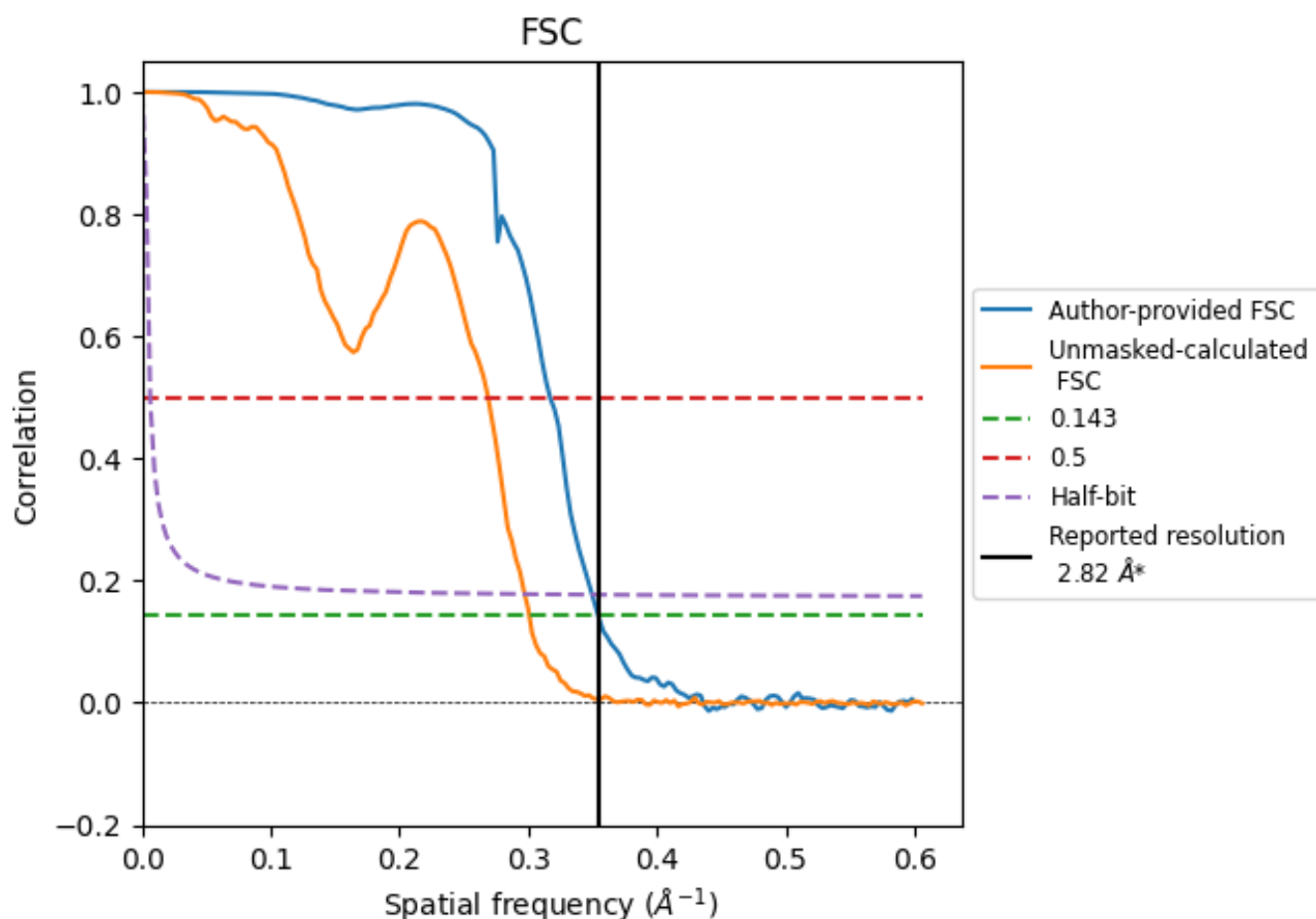


*Reported resolution corresponds to spatial frequency of 0.355 Å⁻¹

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 $0.355 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

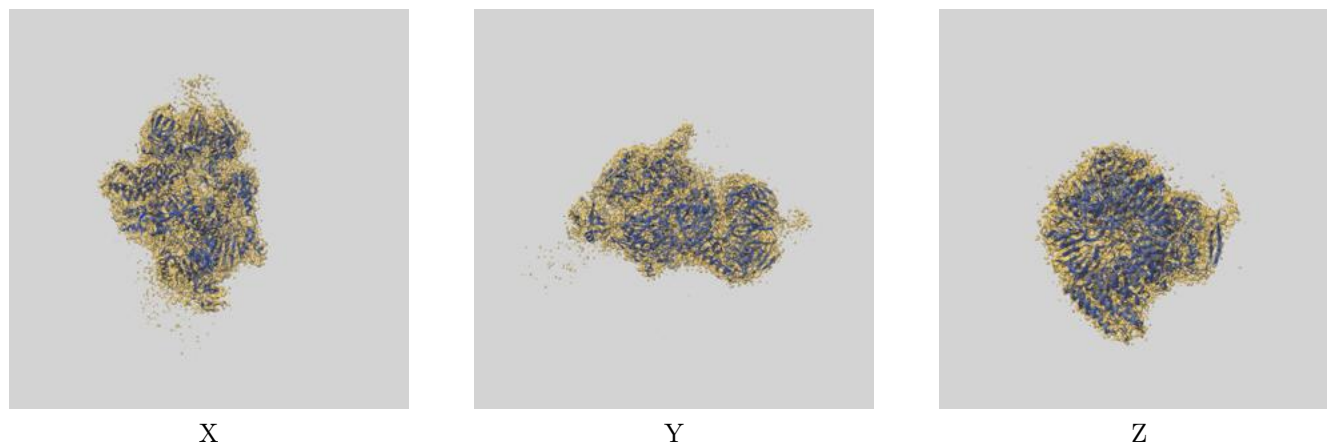
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.82	-	-
Author-provided FSC curve	2.82	3.15	2.86
Unmasked-calculated*	3.32	3.72	3.36

*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 3.32 differs from the reported value 2.82 by more than 10 %

9 Map-model fit [i](#)

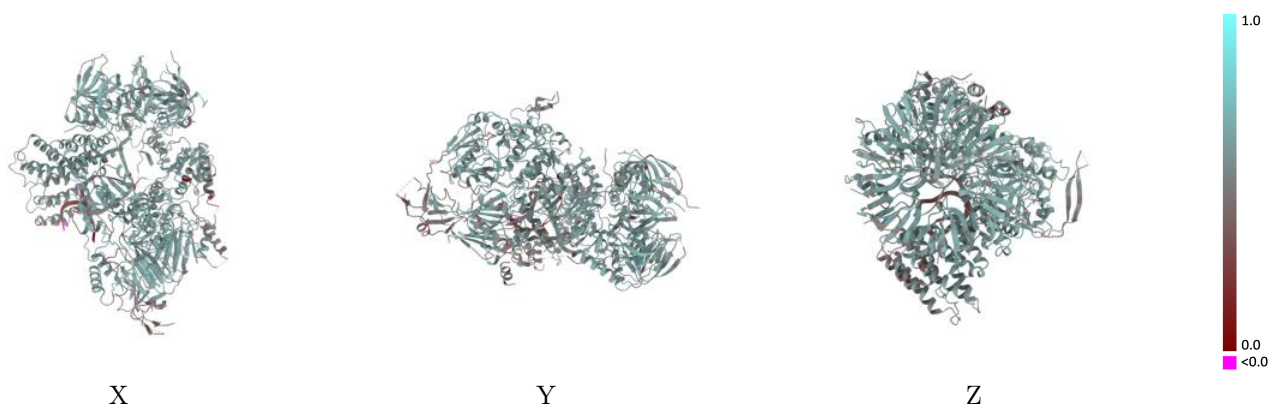
This section contains information regarding the fit between EMDB map EMD-49402 and PDB model 9NH5. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



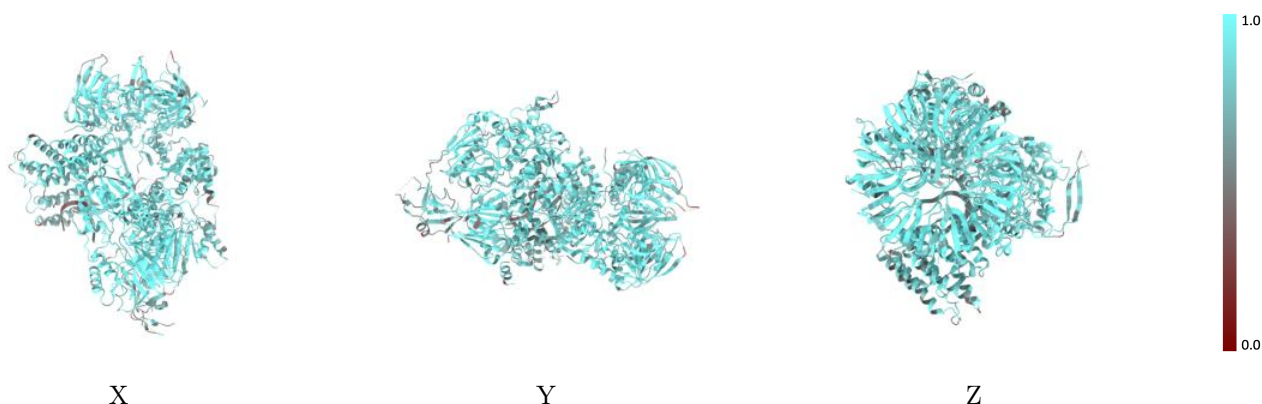
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



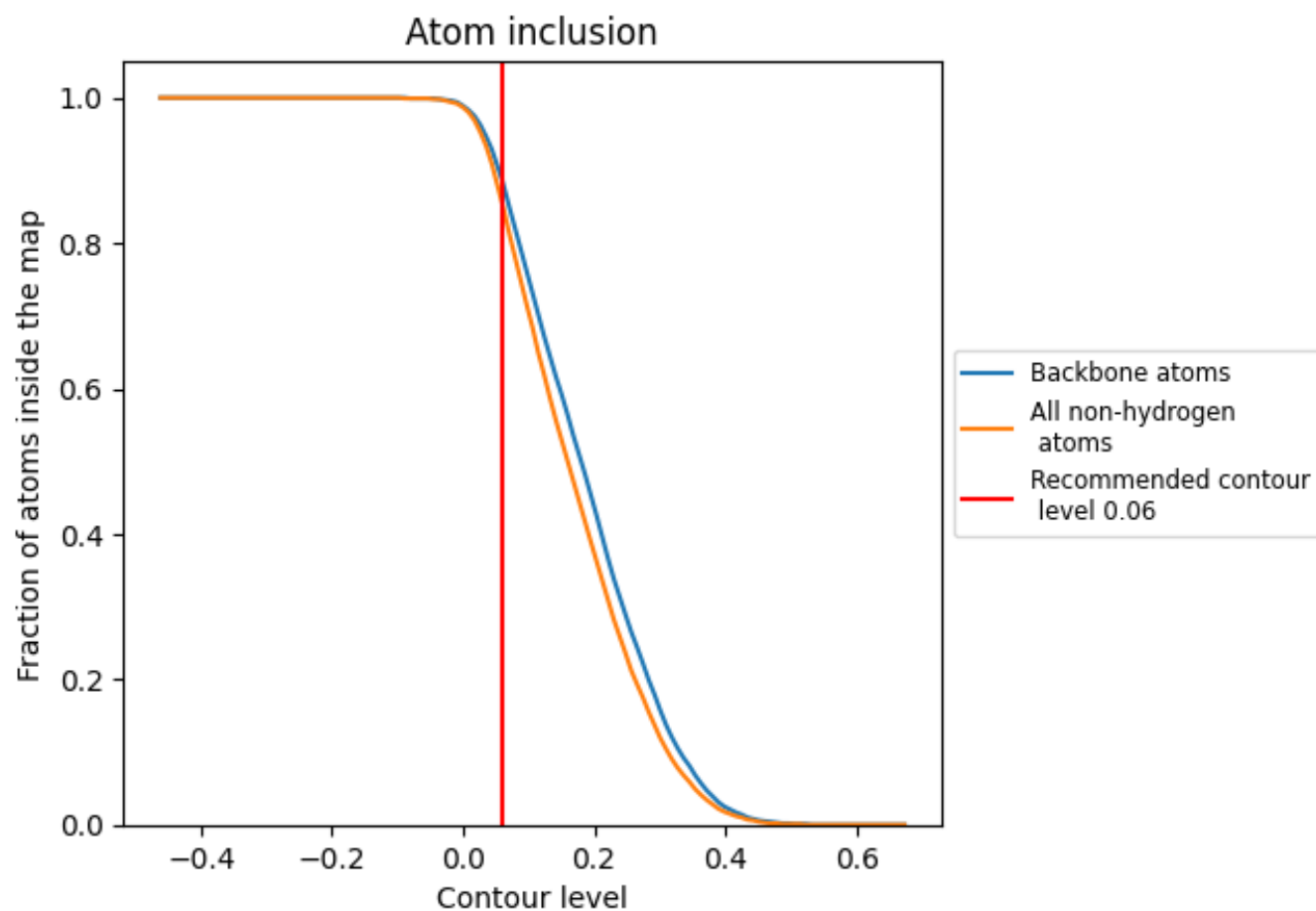
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 85% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8540	 0.5470
A	 0.8550	 0.5510
B	 0.8660	 0.5650
C	 0.9110	 0.5840
D	 0.8780	 0.5560
E	 0.8810	 0.5700
F	 0.9090	 0.5790
G	 0.8910	 0.5870
H	 0.8480	 0.5480
I	 0.8760	 0.5570
J	 0.8220	 0.5350
K	 0.8170	 0.5280
Y	 0.6690	 0.3980
Z	 0.7630	 0.4480

