



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:43 PM UTC

PDB ID : 7QH7 / pdb_00007qh7
EMDB ID : EMD-13967
Title : Cryo-EM structure of the human mtLSU assembly intermediate upon MRM2 depletion - class 4
Authors : Rebelo-Guiomar, P.; Pellegrino, S.; Dent, K.C.; Warren, A.J.; Minczuk, M.
Deposited on : 2021-12-10
Resolution : 2.89 Å(reported)
Based on initial model : 5OOL

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 : **FAILED**
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

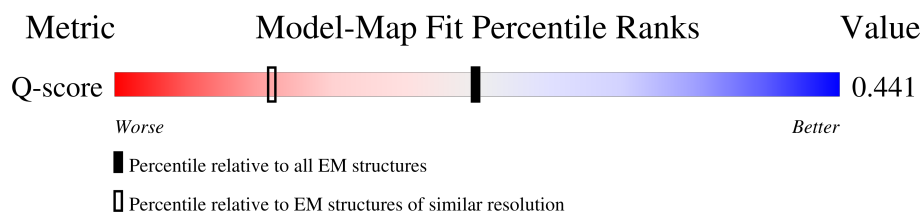
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	12148 (2.39 - 3.39)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

There are 52 unique types of molecules in this entry. The entry contains 85397 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 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	215	Total	C	N	O	S	0	0
			1671	1034	337	292	8		

- Molecule 2 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	304	Total	C	N	O	S	0	0
			2396	1539	416	430	11		

- Molecule 3 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	250	Total	C	N	O	S	0	0
			2013	1294	365	348	6		

- Molecule 4 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	95	Total	C	N	O	S	0	0
			784	498	152	134			

- Molecule 5 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	30	Total	C	N	O	S	0	0
			247	160	47	37	3		

- Molecule 6 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 7 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 8 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 9 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	201	Total	C	N	O	S	0	0
			1621	1033	302	276	10		

- Molecule 10 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 11 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	P	141	Total	C	N	O	S	0	0
			1148	719	221	203	5		

- Molecule 12 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	217	Total	C	N	O	S	0	0
			1805	1159	317	320	9		

- Molecule 13 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R	139	Total	C	N	O	S	0	0
			1143	726	228	185	4		

- Molecule 14 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 15 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	155	Total	C	N	O	S	0	0
			1274	815	232	220	7		

- Molecule 16 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	U	125	Total	C	N	O	S	0	0
			1030	660	197	171	2		

- Molecule 17 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	V	48	Total	C	N	O	S	0	0
			402	259	63	77	3		

- Molecule 18 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	W	100	Total	C	N	O	S	0	0
			801	518	150	130	3		

- Molecule 19 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	243	Total	C	N	O	S	0	0
			2035	1317	351	362	5		

- Molecule 20 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	175	Total	C	N	O	S	0	0
			1506	961	290	251	4		

- Molecule 21 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Z	115	Total	C	N	O	S	0	0
			937	598	175	161	3		

- Molecule 22 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 23 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1	49	Total	C	N	O	S	0	0
			408	263	77	66	2		

- Molecule 24 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	2	45	Total	C	N	O	S	0	0
			367	227	81	58	1		

- Molecule 25 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 26 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	5	392	Total	C	N	O	S	0	0
			3199	2067	558	563	11		

- Molecule 27 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	6	292	Total	C	N	O	S	0	0
			2460	1586	432	434	8		

- Molecule 28 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	7	287	Total	C	N	O	S	0	0
			2334	1495	397	425	17		

- Molecule 29 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	9	117	Total	C	N	O	S	0	0
			947	614	163	168	2		

- Molecule 30 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	80	Total	C	N	O	S	0	0
			672	425	124	118	5		

- Molecule 31 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 32 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	275	Total	C	N	O	S	0	0
			2214	1413	382	410	9		

- Molecule 33 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	157	Total	C	N	O	S	0	0
			1308	843	228	229	8		

- Molecule 34 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	f	17	Total	C	N	O	0	0
			142	95	26	21		

- Molecule 35 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	129	Total	C	N	O	S	0	0
			1067	690	185	190	2		

- Molecule 36 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	101	Total	C	N	O	S	0	0
			829	525	147	155	2		

- Molecule 37 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 38 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			689	426	134	127	2		

- Molecule 39 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	81	Total	C	N	O	S	0	0
			687	432	138	114	3		

- Molecule 40 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	p	125	Total	C	N	O	S	0	0
			1045	653	199	189	4		

- Molecule 41 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	101	Total	C	N	O	S	0	0
			841	527	162	149	3		

- Molecule 42 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	129	Total	C	N	O	S	0	0
			1068	679	209	172	8		

- Molecule 43 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	370	Total	C	N	O	S	0	0
			3036	1946	542	534	14		

- Molecule 44 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	111	Total	C	N	O	S	0	0
			927	595	155	167	10		

- Molecule 45 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	69	Total	C	N	O		0	0
			588	372	116	100			

- Molecule 46 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	w	79	Total	C	N	O	S	0	0
			638	410	95	128	5		

- Molecule 47 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	A	1256	Total	C	N	O	P	0	0
			26670	11966	4809	8639	1256		

- Molecule 48 is a RNA chain called mitochondrial tRNA^{Val}.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B	56	Total	C	N	O	P	0	0
			1191	534	214	387	56		

- Molecule 49 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	4	37	Total	C	N	O	S	0	0
			333	212	71	47	3		

- Molecule 50 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
50	E	1	Total	Mg	0
			1	1	
50	A	49	Total	Mg	0
			49	49	

- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
51	0	1	Total	Zn	0
			1	1	
51	r	1	Total	Zn	0
			1	1	
51	4	1	Total	Zn	0
			1	1	

- Molecule 52 is water.

Mol	Chain	Residues	Atoms		AltConf
52	O	1	Total	O	0
			1	1	
52	T	1	Total	O	0
			1	1	
52	b	1	Total	O	0
			1	1	
52	i	1	Total	O	0
			1	1	
52	A	10	Total	O	0
			10	10	

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	224933	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 ($e^-/\text{\AA}^2$)	52.5	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.066	Depositor
Minimum map value	-0.017	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size ($\text{\AA}$)	381.59998, 381.59998, 381.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 53 ligands modelled in this entry, 53 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.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
47	A	25
27	6	3
40	p	3
48	B	2
16	U	1
30	a	1

The worst 5 of 35 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2545:U	O3'	2611:C	P	40.96
1	6	79:GLY	C	131:PRO	N	39.19
1	U	112:PRO	C	140:SER	N	37.93
1	A	2880:A	O3'	2896:G	P	32.37
1	A	2982:C	O3'	2994:U	P	30.68

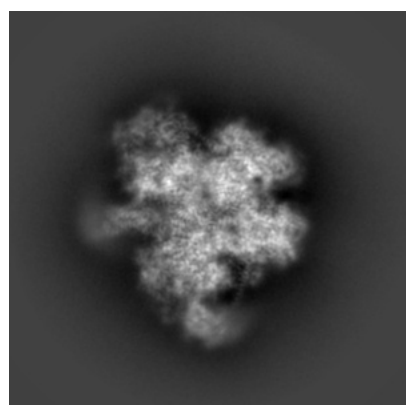
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13967. These allow visual inspection of the internal detail of the map and identification of artifacts.

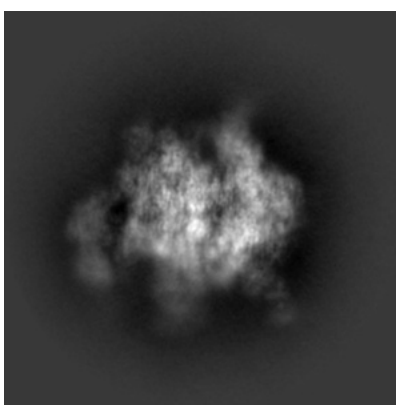
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

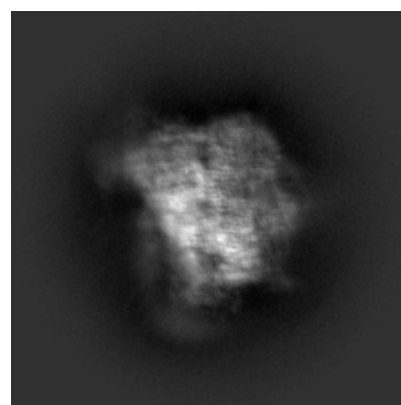
5.1.1 Primary map



X



Y

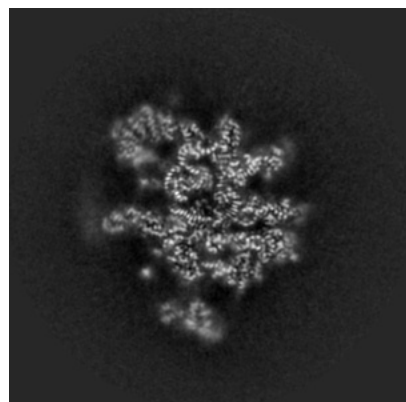


Z

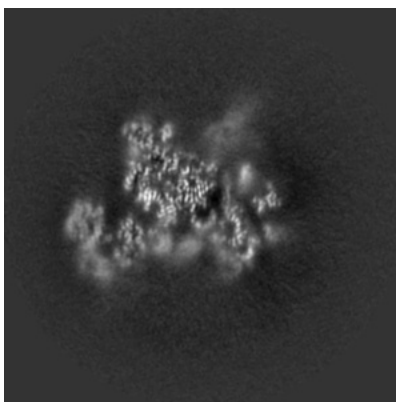
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

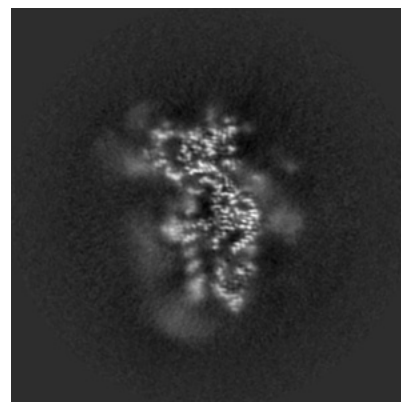
5.2.1 Primary map



X Index: 180



Y Index: 180

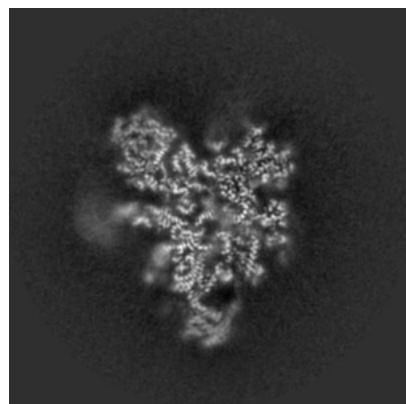


Z Index: 180

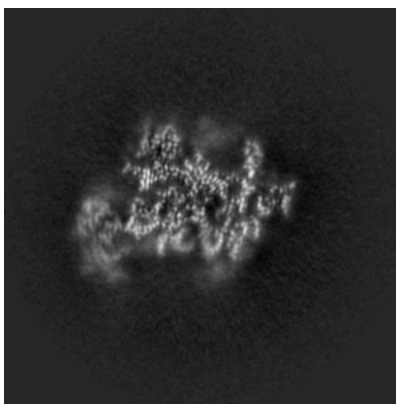
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

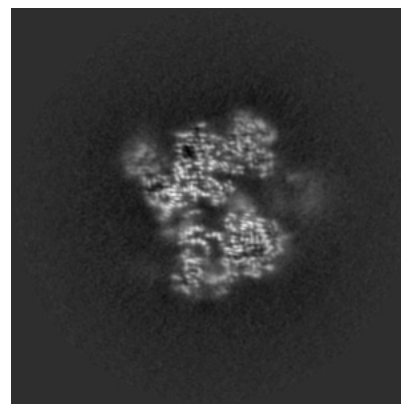
5.3.1 Primary map



X Index: 164



Y Index: 164

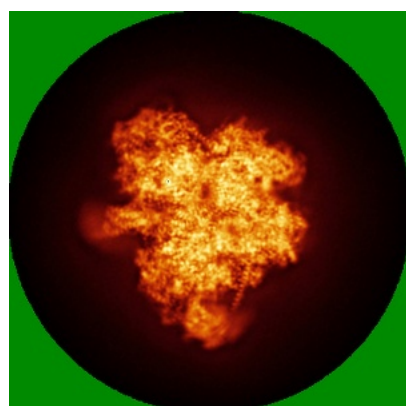


Z Index: 221

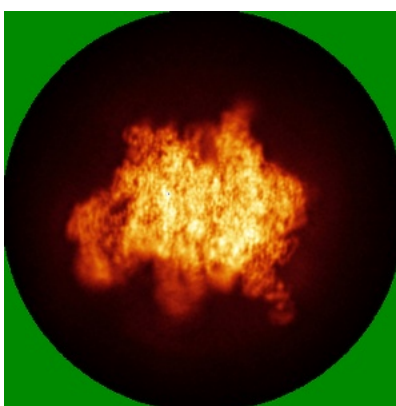
The images above show the largest variance slices of the map in three orthogonal directions.

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

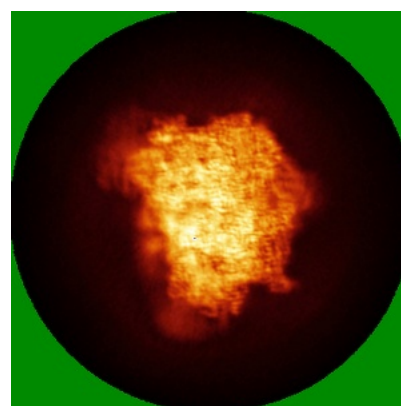
5.4.1 Primary map



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.

5.5 Orthogonal surface views

This section was not generated.

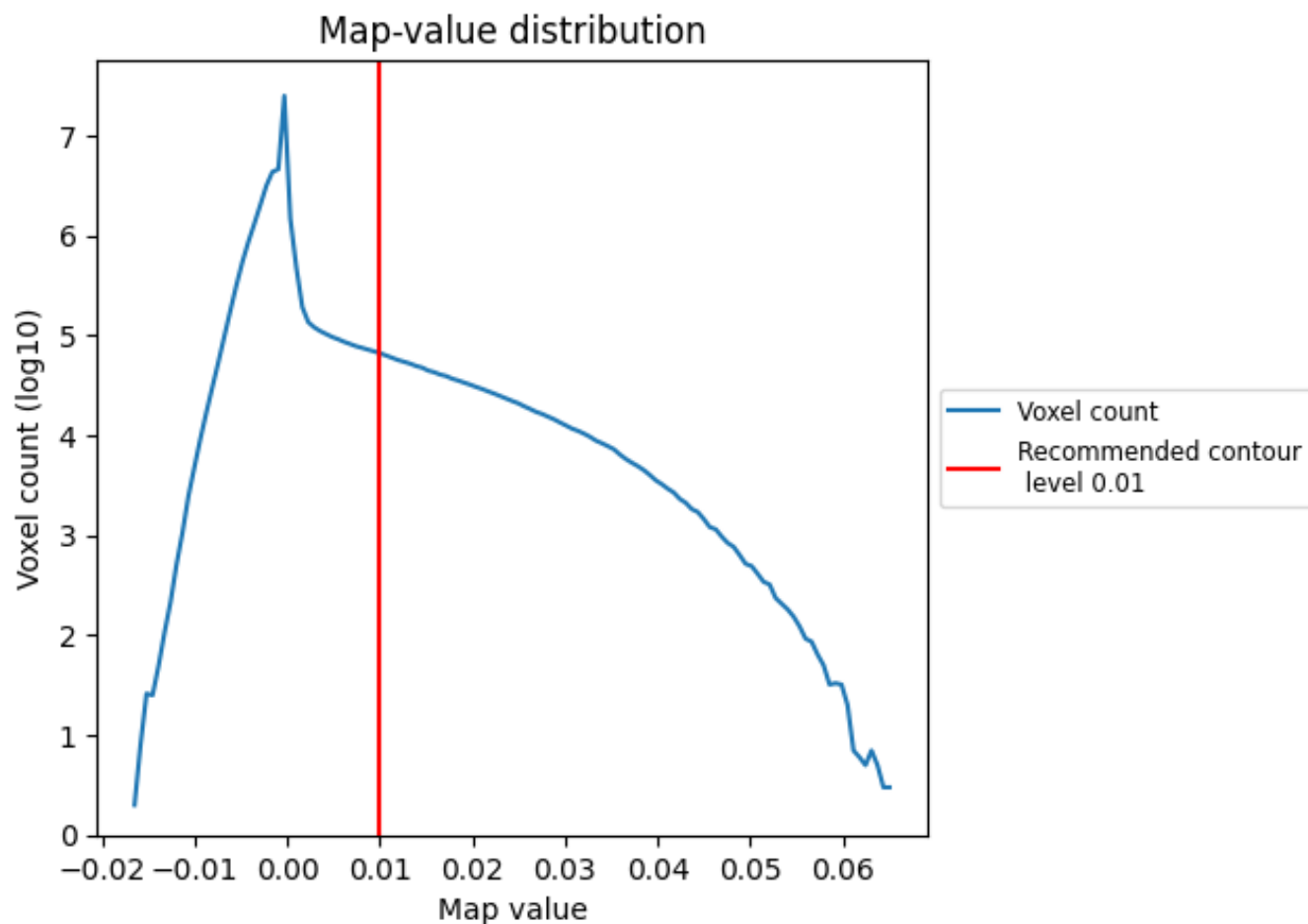
5.6 Mask visualisation

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

6 Map analysis [i](#)

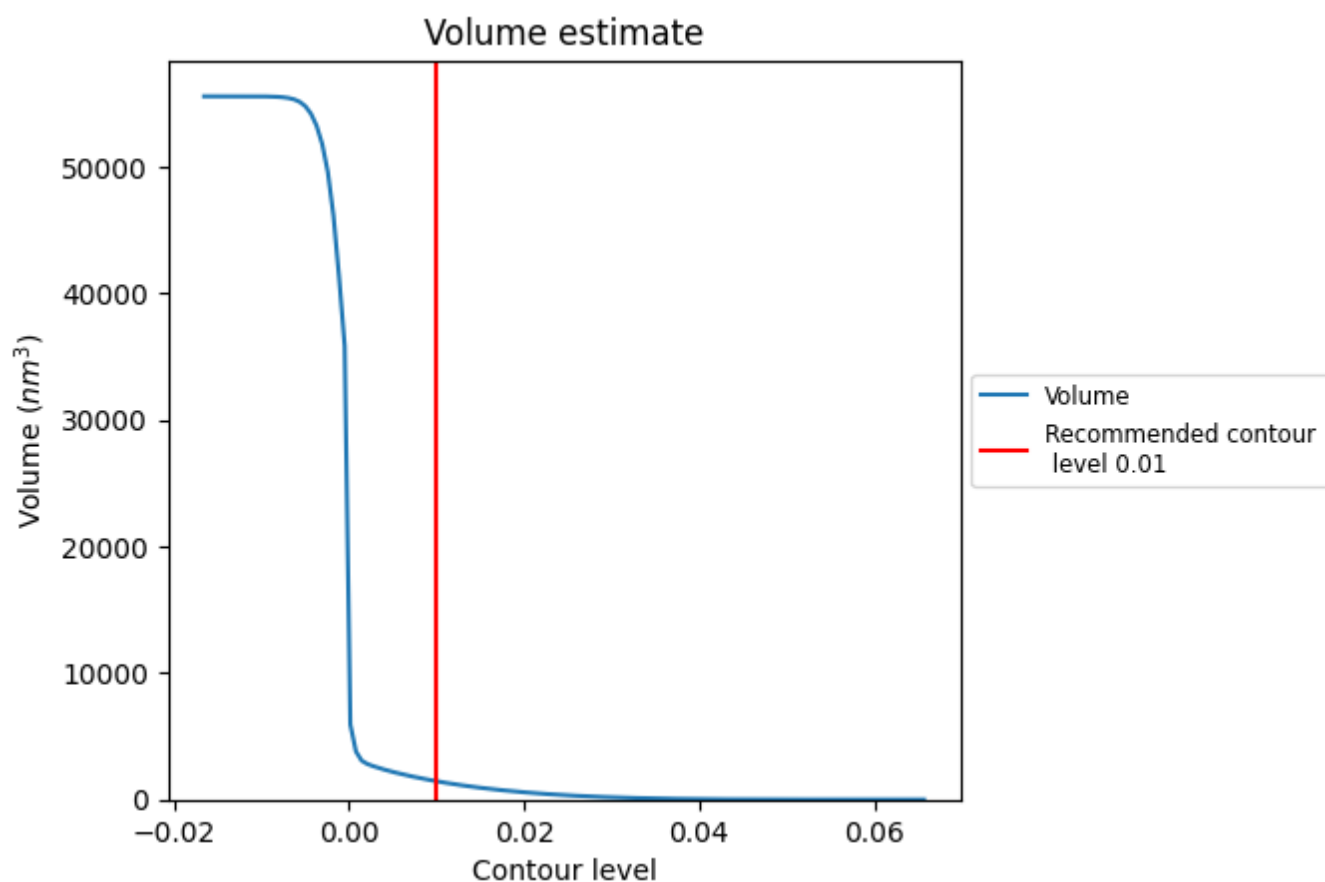
This section contains the results of statistical analysis of the map.

6.1 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.

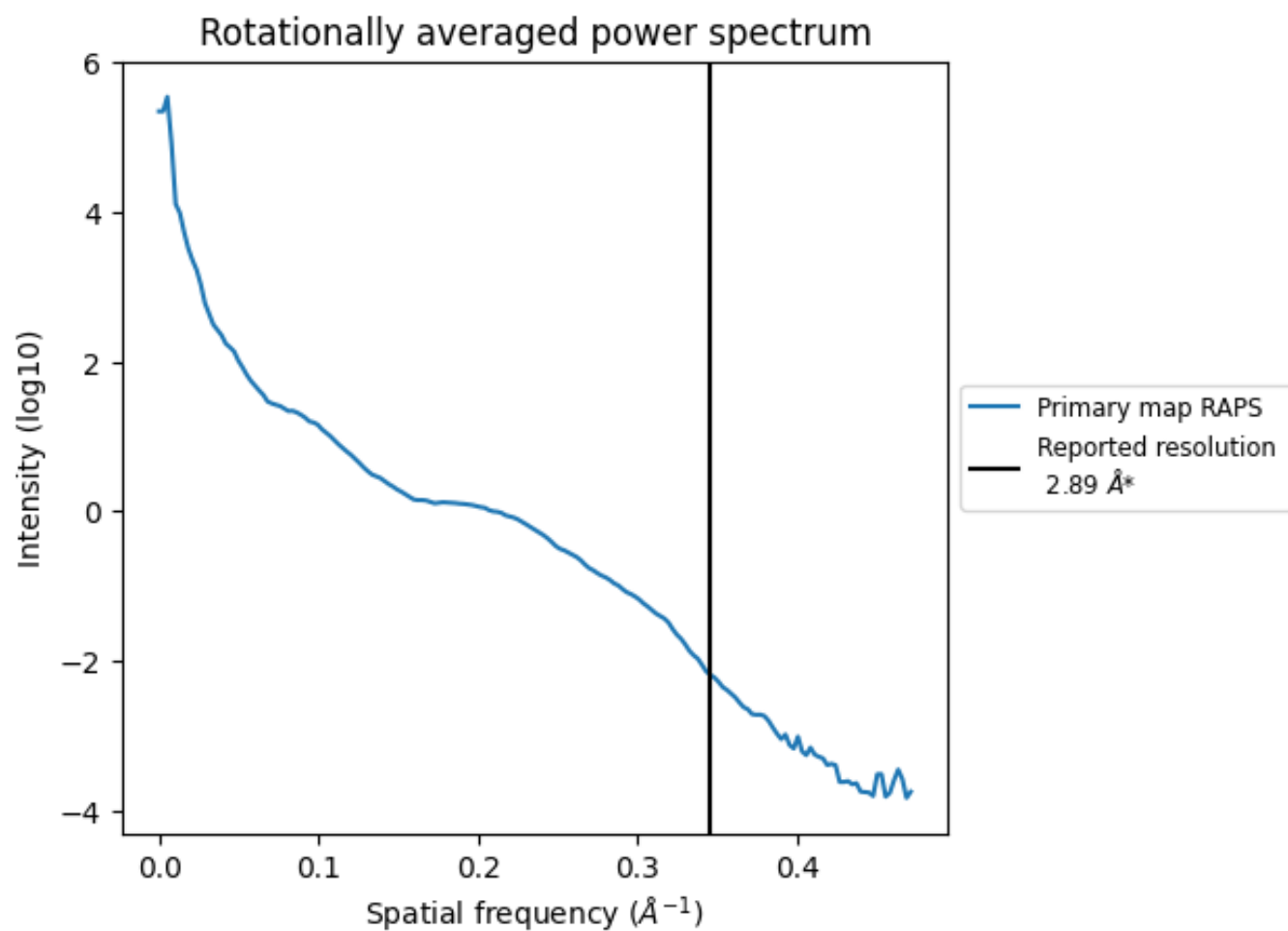
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 1452 nm^3 ; this corresponds to an approximate mass of 1312 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.

6.3 Rotationally averaged power spectrum ⓘ

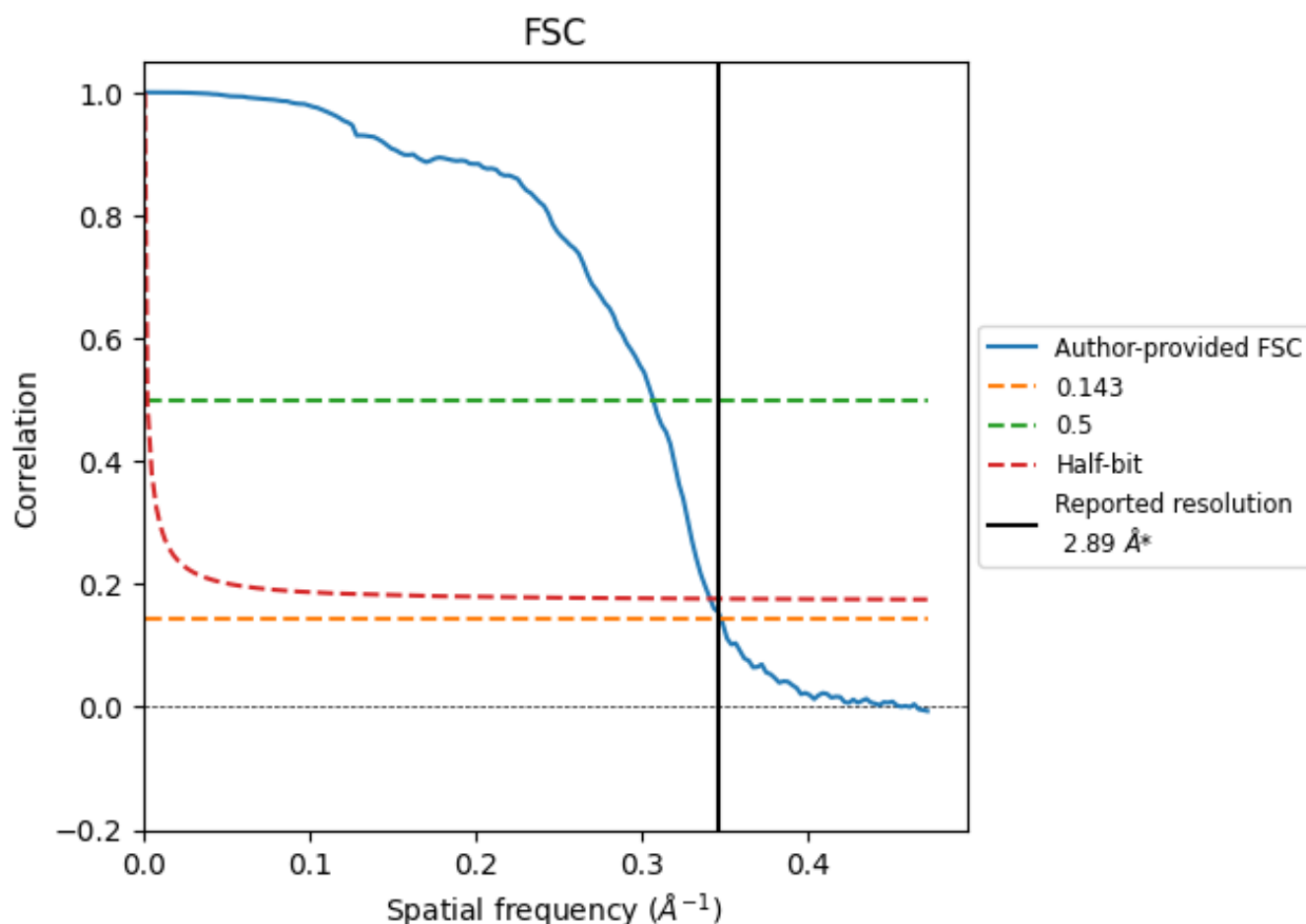


*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

7 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.

7.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

7.2 Resolution estimates [i](#)

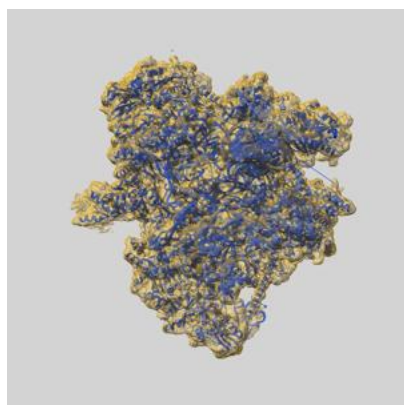
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	2.88	3.26	2.93
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

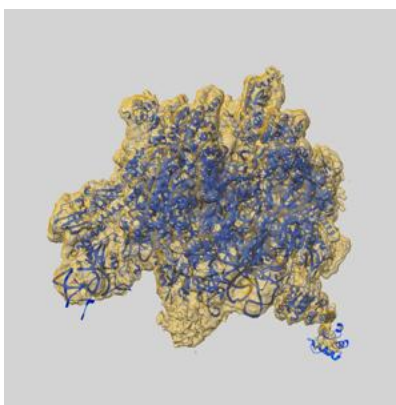
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13967 and PDB model 7QH7. Per-residue inclusion information can be found in section ?? on page ??.

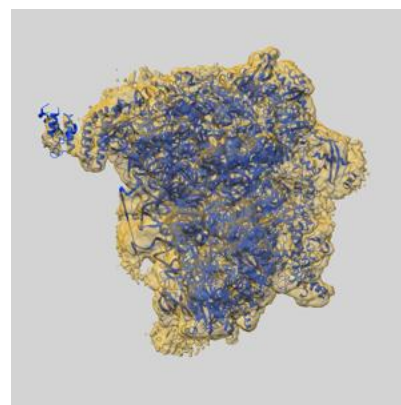
8.1 Map-model overlay [i](#)



X



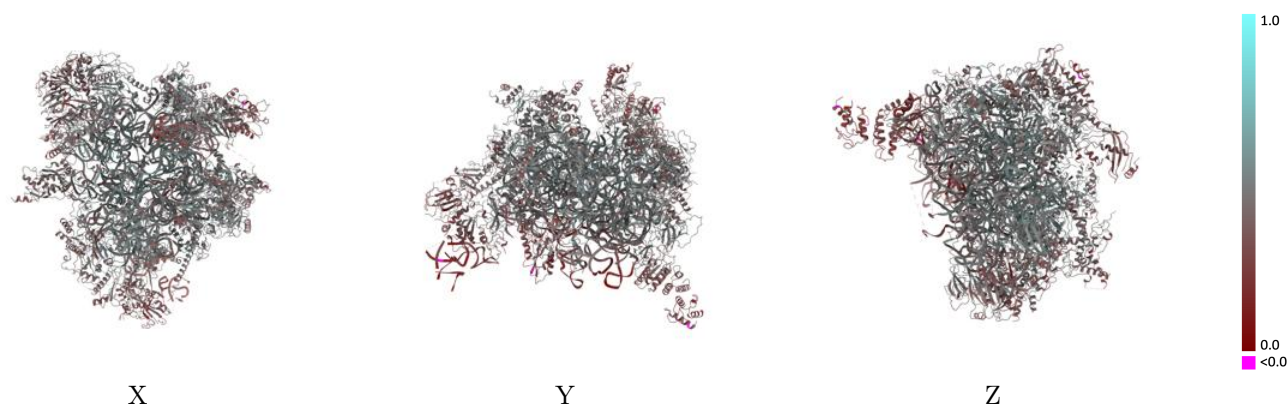
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 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.

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

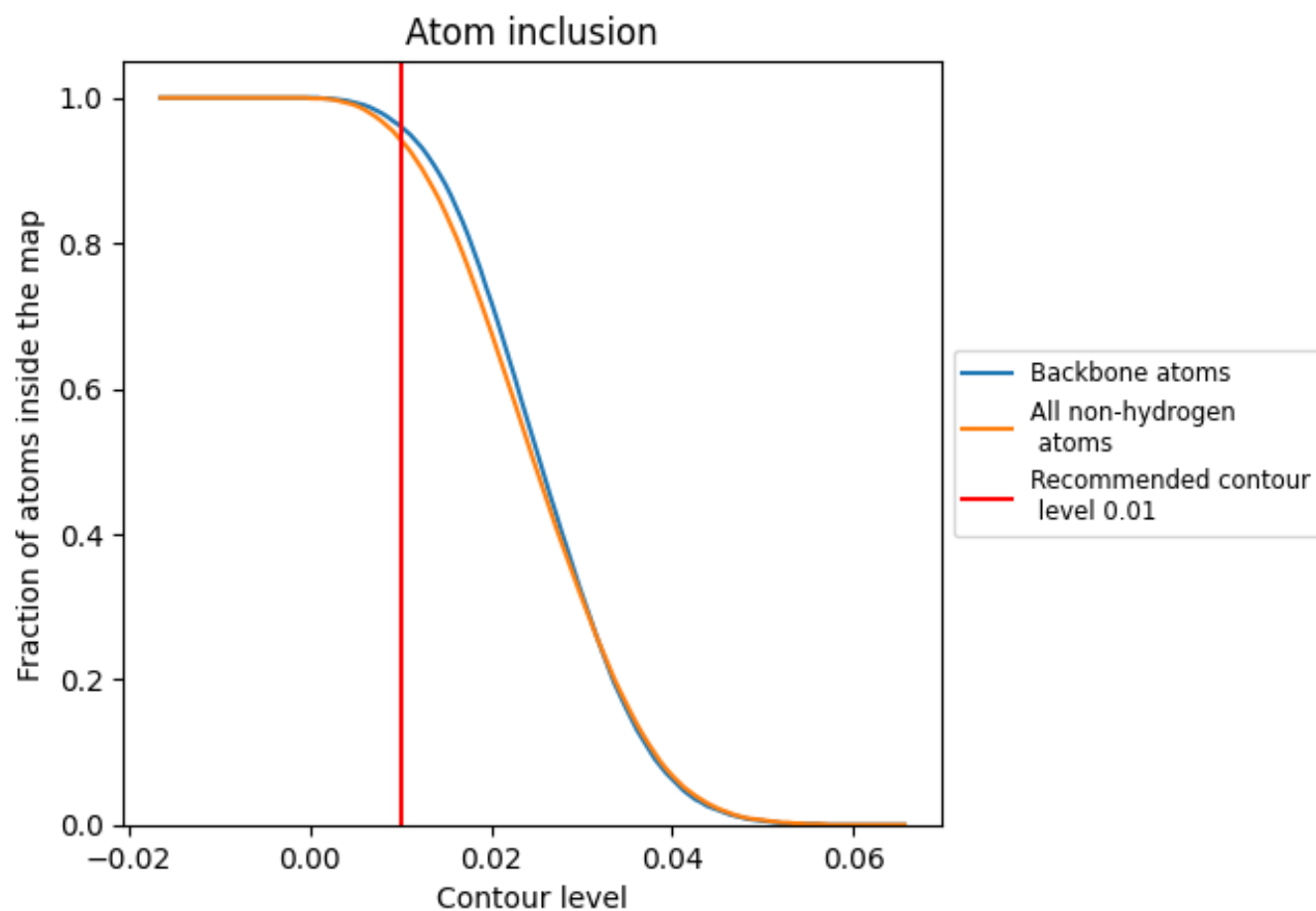


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

8.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9420	 0.4410
0	 0.9410	 0.4630
1	 0.9020	 0.1990
2	 0.9720	 0.5350
3	 0.9660	 0.5030
4	 0.8710	 0.4360
5	 0.9220	 0.4080
6	 0.9420	 0.3680
7	 0.9410	 0.3960
9	 0.9470	 0.4510
A	 0.9910	 0.4620
B	 0.7760	 0.2050
D	 0.9490	 0.4560
E	 0.9500	 0.4730
F	 0.9420	 0.4960
H	 0.9210	 0.4220
I	 0.9460	 0.3800
K	 0.9600	 0.4840
L	 0.9260	 0.4540
M	 0.9400	 0.4800
N	 0.8940	 0.3230
O	 0.9590	 0.4800
P	 0.9570	 0.3590
Q	 0.9220	 0.4550
R	 0.9340	 0.4890
S	 0.9440	 0.4830
T	 0.9330	 0.4900
U	 0.9720	 0.4880
V	 0.9520	 0.4270
W	 0.9490	 0.4400
X	 0.9300	 0.4420
Y	 0.9550	 0.4580
Z	 0.9270	 0.4720
a	 0.9340	 0.4790
b	 0.9590	 0.4940



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Chain	Atom inclusion	Q-score
c	 0.9530	 0.4440
d	 0.9790	 0.3490
f	 0.9290	 0.3930
g	 0.9610	 0.4780
h	 0.9580	 0.4170
i	 0.9550	 0.5160
j	 0.8990	 0.4510
o	 0.9200	 0.4500
p	 0.7690	 0.3750
q	 0.9180	 0.3970
r	 0.9630	 0.4520
s	 0.9370	 0.4570
u	 0.9010	 0.3510
v	 0.7070	 0.3000
w	 0.2320	 0.2320