



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:19 PM UTC

PDB ID : 8ETI / pdb_00008eti
EMDB ID : EMD-24395
Title : Fkbp39 associated 60S nascent ribosome State 1
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-17
Resolution : 3.70 Å(reported)

This is a Full wwPDB EM Validation 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

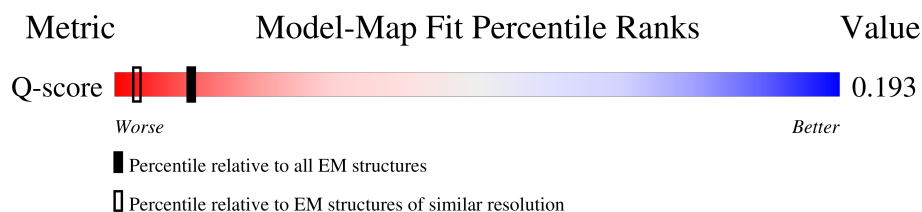
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 90456 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 RNA chain called RNA (1564-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1579	Total	C	N	O	P	0	0
			33816	15104	6144	10989	1579		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	501	G	U	conflict	GB 157310483
1	503	U	G	conflict	GB 157310483
1	2930	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	152	Total	C	N	O	P	0	0
			3229	1445	568	1064	152		

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	190	Total	C	N	O	S	0	0
			1576	999	299	272	6		

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	209	Total	C	N	O	S	0	0
			1762	1149	301	304	8		

- Molecule 5 is a protein called Ribosome biogenesis protein nsa1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	340	Total	C	N	O	S	0	0
			2686	1716	468	491	11		

- Molecule 6 is a RNA chain called RNA (125-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	81	Total	C	N	O	P	0	0
			1717	770	296	570	81		

- Molecule 7 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	254	Total	C	N	O	S	0	0
			1427	856	285	285	1		

- Molecule 8 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	332	Total	C	N	O	S	0	0
			2641	1676	488	468	9		

- Molecule 9 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	328	Total	C	N	O	S	0	0
			2571	1631	486	450	4		

- Molecule 10 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	D	391	Total	C	N	O	0	0
			1931	1149	391	391		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	170	Total	C	N	O	S	0	0
			1328	854	243	228	3		

- Molecule 12 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	239	Total	C	N	O	S	0	0
			1939	1247	355	334	3		

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	186	Total	C	N	O	S	0	0
			1464	938	264	260	2		

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	183	Total	C	N	O		0	0
			902	536	183	183			

- Molecule 15 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	113	Total	C	N	O		0	0
			564	338	113	113			

- Molecule 16 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	240	Total	C	N	O		0	0
			1190	710	240	240			

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	115	Total	C	N	O	S	0	0
			938	590	197	150	1		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	166	Total	C	N	O	S	0	0
			1401	877	291	230	3		

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	196	Total	C	N	O	S	0	0
			1557	999	297	257	4		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	147	Total	C	N	O	S	0	0
			1154	733	209	209	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	136	Total	C	N	O	S	0	0
			1057	664	205	187	1		

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	167	Total	C	N	O	S	0	0
			1395	900	262	228	5		

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	127	Total	C	N	O	0	0
			624	369	127	128		

- Molecule 25 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	W	173	Total	C	N	O	0	0
			850	504	173	173		

- Molecule 26 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	X	122	Total	C	N	O	0	0
			750	457	153	140		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 28 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	b	391	Total	C	N	O	0	0
			1939	1157	391	391		

- Molecule 29 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	d	97	Total	C	N	O	0	0
			483	289	97	97		

- Molecule 30 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	123	Total	C	N	O	S	0	0
			986	616	201	164	5		

- Molecule 31 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 32 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	h	120	Total	C	N	O	0	0
			994	626	193	175		

- Molecule 33 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	85	Total	C	N	O	S	0	0
			696	431	148	116	1		

- Molecule 34 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	j	71	Total	C	N	O	S	0	0
			563	346	121	90	6		

- Molecule 35 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	m	121	Total	C	N	O		0	0
			859	529	163	167			

- Molecule 36 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	369	Total	C	N	O	S	0	0
			2215	1369	430	415	1		

- Molecule 37 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	o	134	Total	C	N	O		0	0
			666	398	134	134			

- Molecule 38 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	r	166	Total	C	N	O		0	0
			823	490	166	167			

- Molecule 39 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	t	225	Total	C	N	O		0	0
			1115	664	225	226			

- Molecule 40 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	u	110	Total	C	N	O		0	0
			546	326	110	110			

- Molecule 41 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	v	161	Total	C	N	O	S	0	0
			1299	818	243	235	3		

- Molecule 42 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	x	303	Total	C	N	O	S	0	0
			2503	1570	460	465	8		

- Molecule 43 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	y	225	Total	C	N	O		0	0
			1107	657	225	225			

- Molecule 44 is a protein called UPF0642 protein C32H8.05.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	35	Total	C	N	O		0	0
			173	103	35	35			

- Molecule 45 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	T	23	Total	C	N	O		0	0
			175	111	31	33			

- Molecule 46 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
46	j	1	Total	Zn	0
			1	1	

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	9000	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)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.491	Depositor
Minimum map value	-0.210	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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 1 ligands modelled in this entry, 1 is 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](#)

There are no chain breaks in this entry.

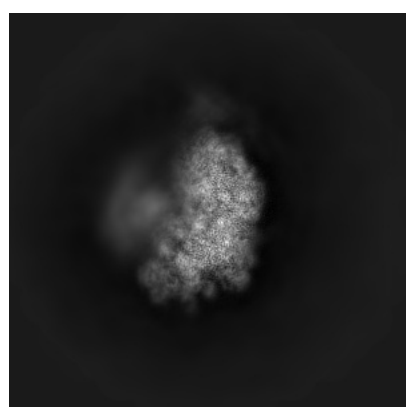
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24395. These allow visual inspection of the internal detail of the map and identification of artifacts.

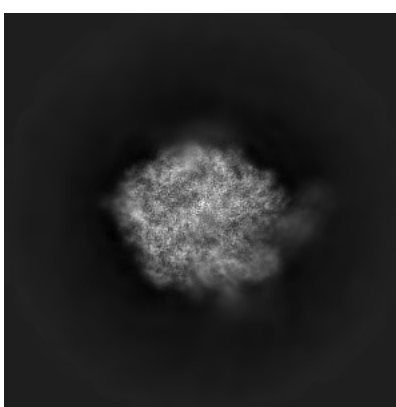
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

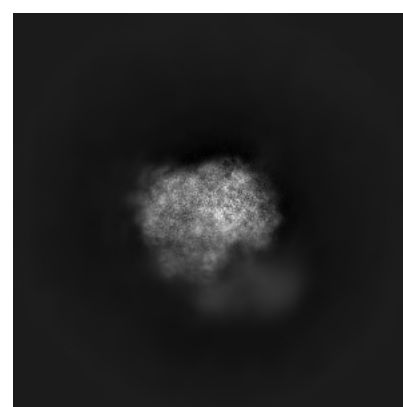
5.1.1 Primary map



X



Y

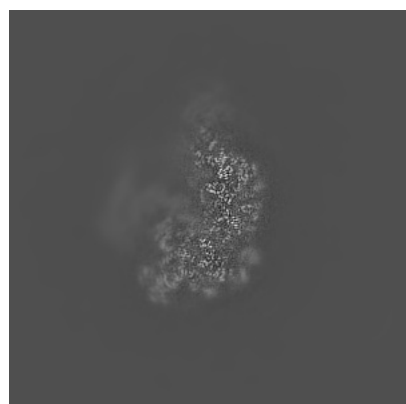


Z

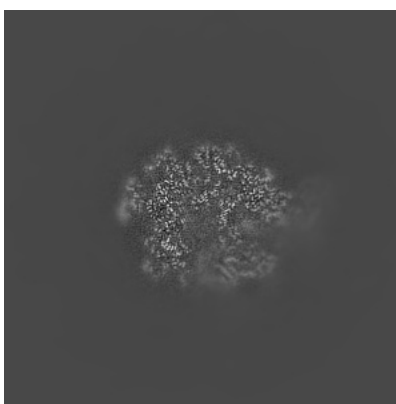
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

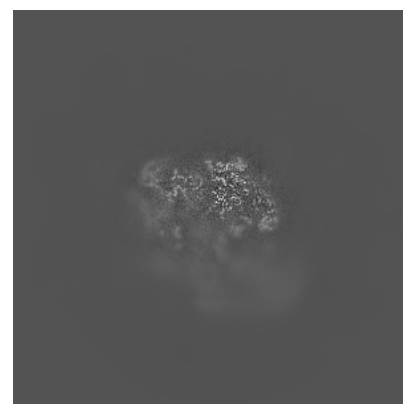
5.2.1 Primary map



X Index: 256



Y Index: 256

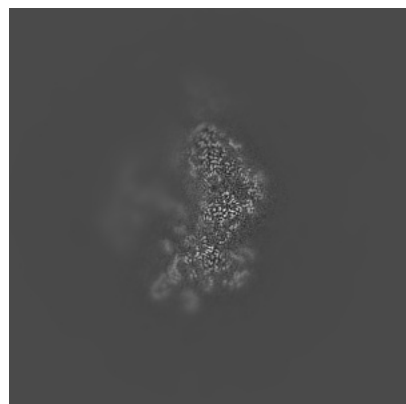


Z Index: 256

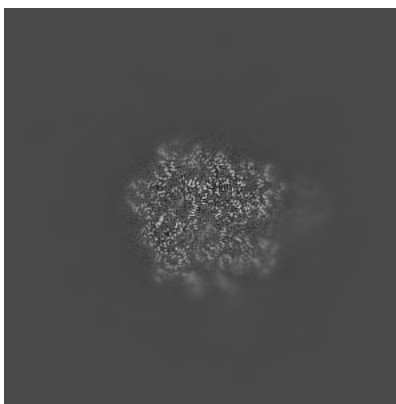
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

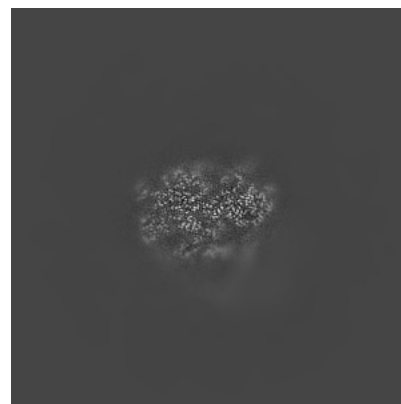
5.3.1 Primary map



X Index: 267



Y Index: 272

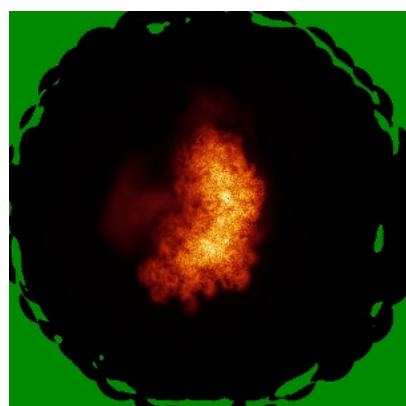


Z Index: 208

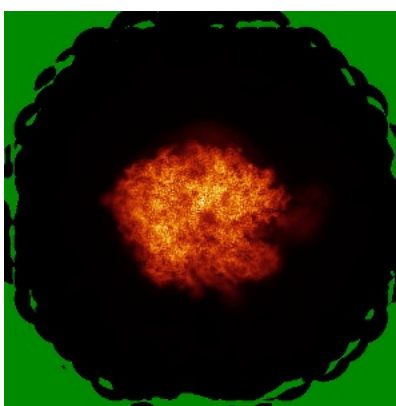
The images above show the largest variance slices of the map in three orthogonal directions.

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

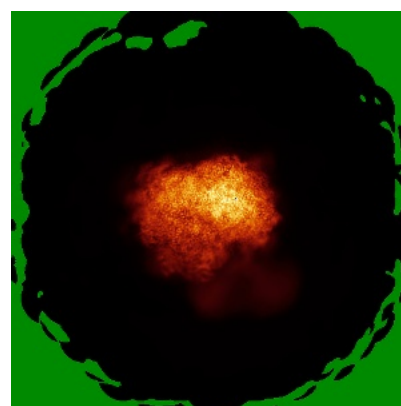
5.4.1 Primary map



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.

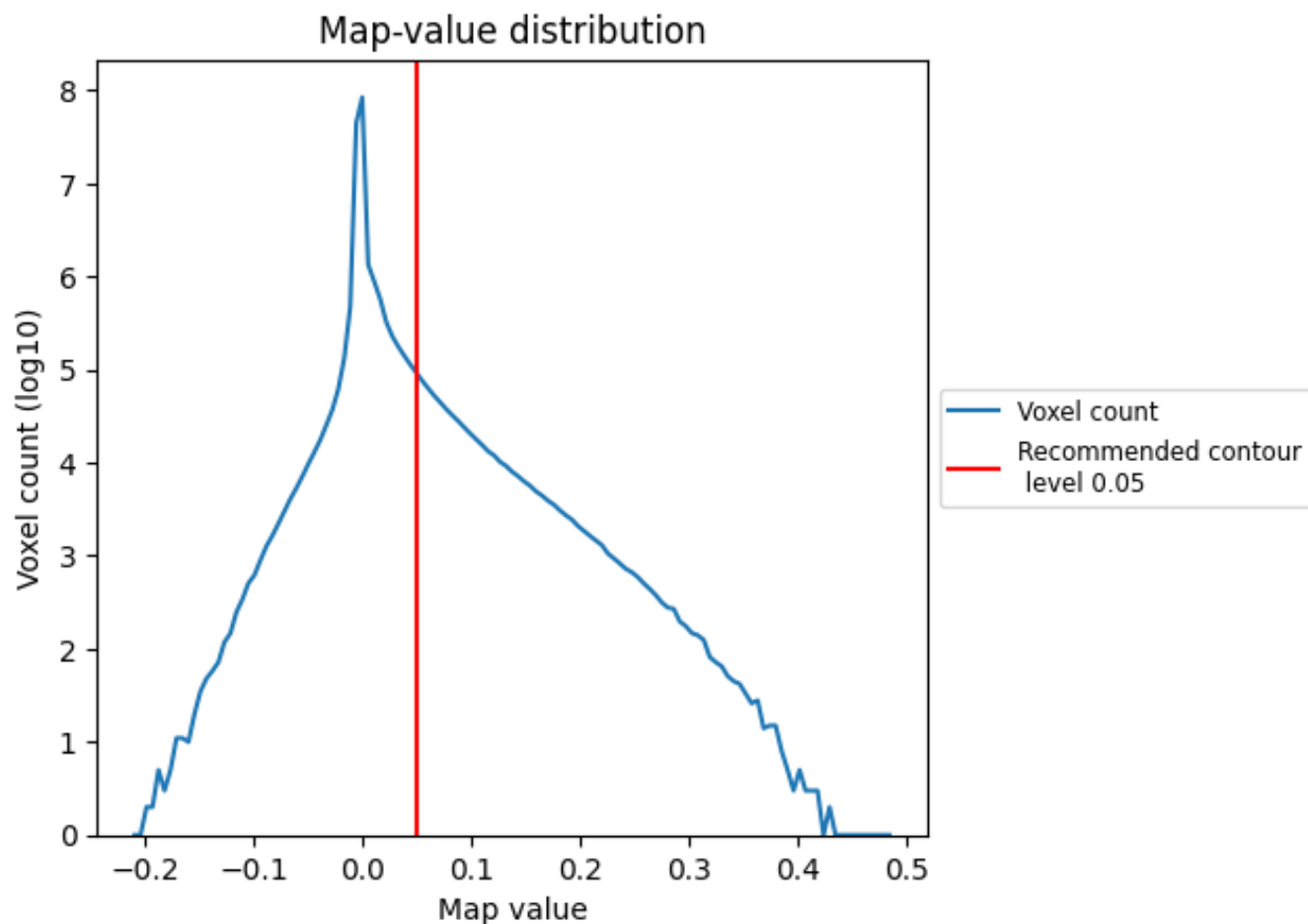
5.6 Mask visualisation

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

6 Map analysis [i](#)

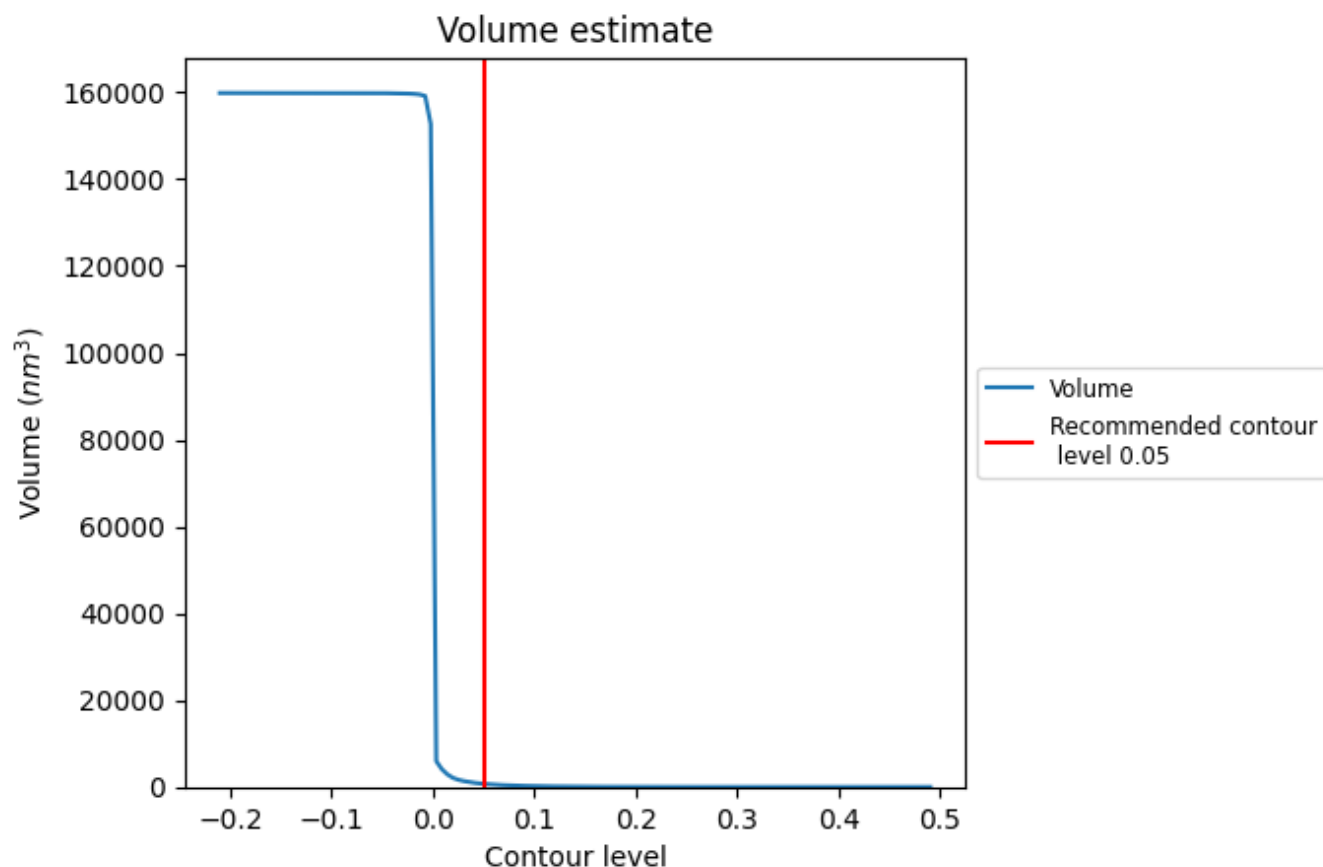
This section contains the results of statistical analysis of the map.

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.

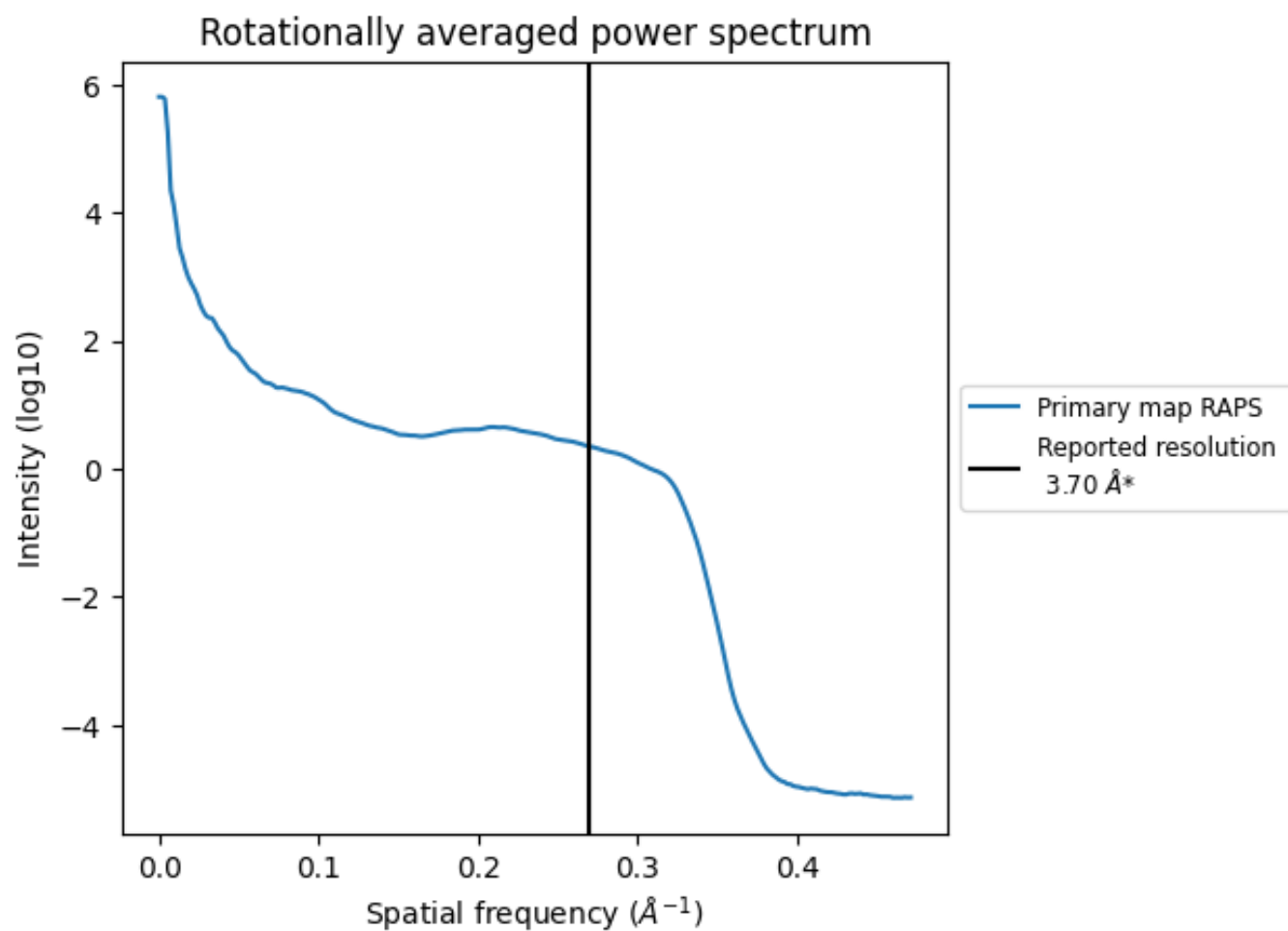
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 724 nm³; this corresponds to an approximate mass of 654 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 0.270 Å⁻¹

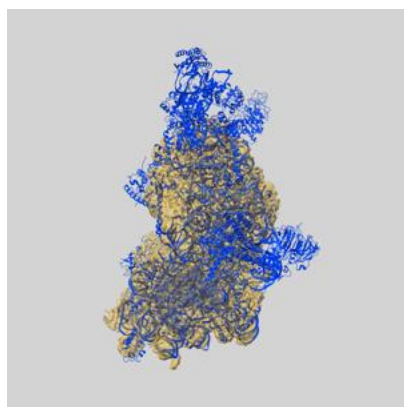
7 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

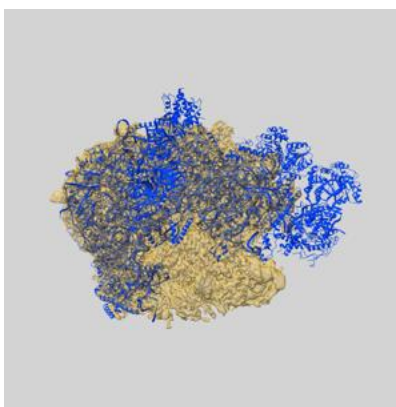
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24395 and PDB model 8ETI. Per-residue inclusion information can be found in section ?? on page ??.

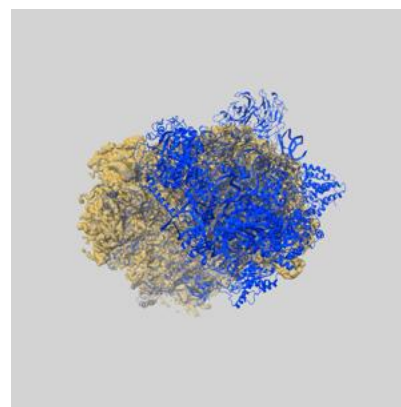
8.1 Map-model overlay [i](#)



X



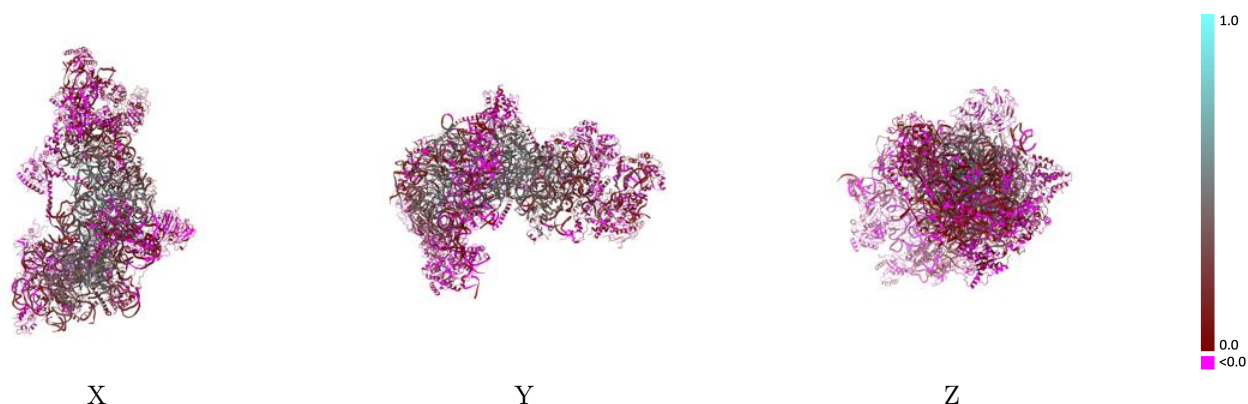
Y



Z

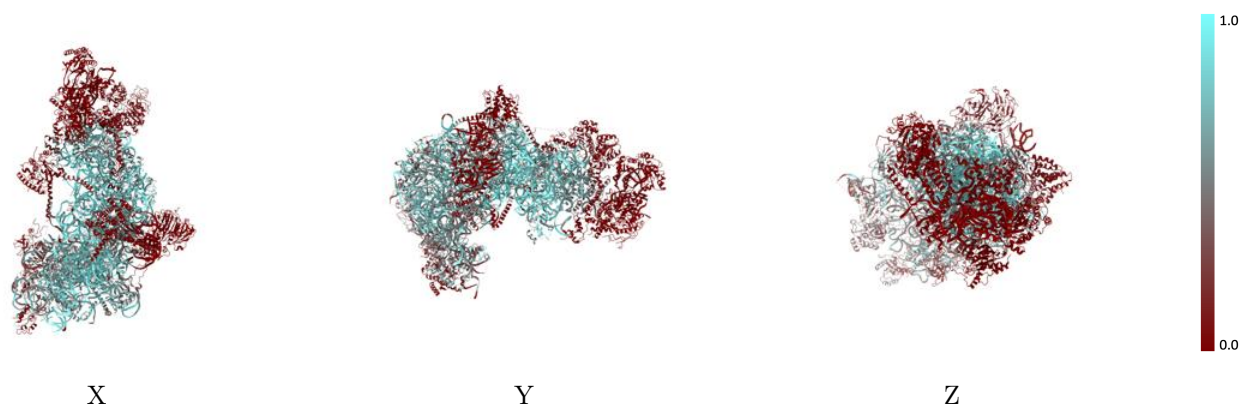
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



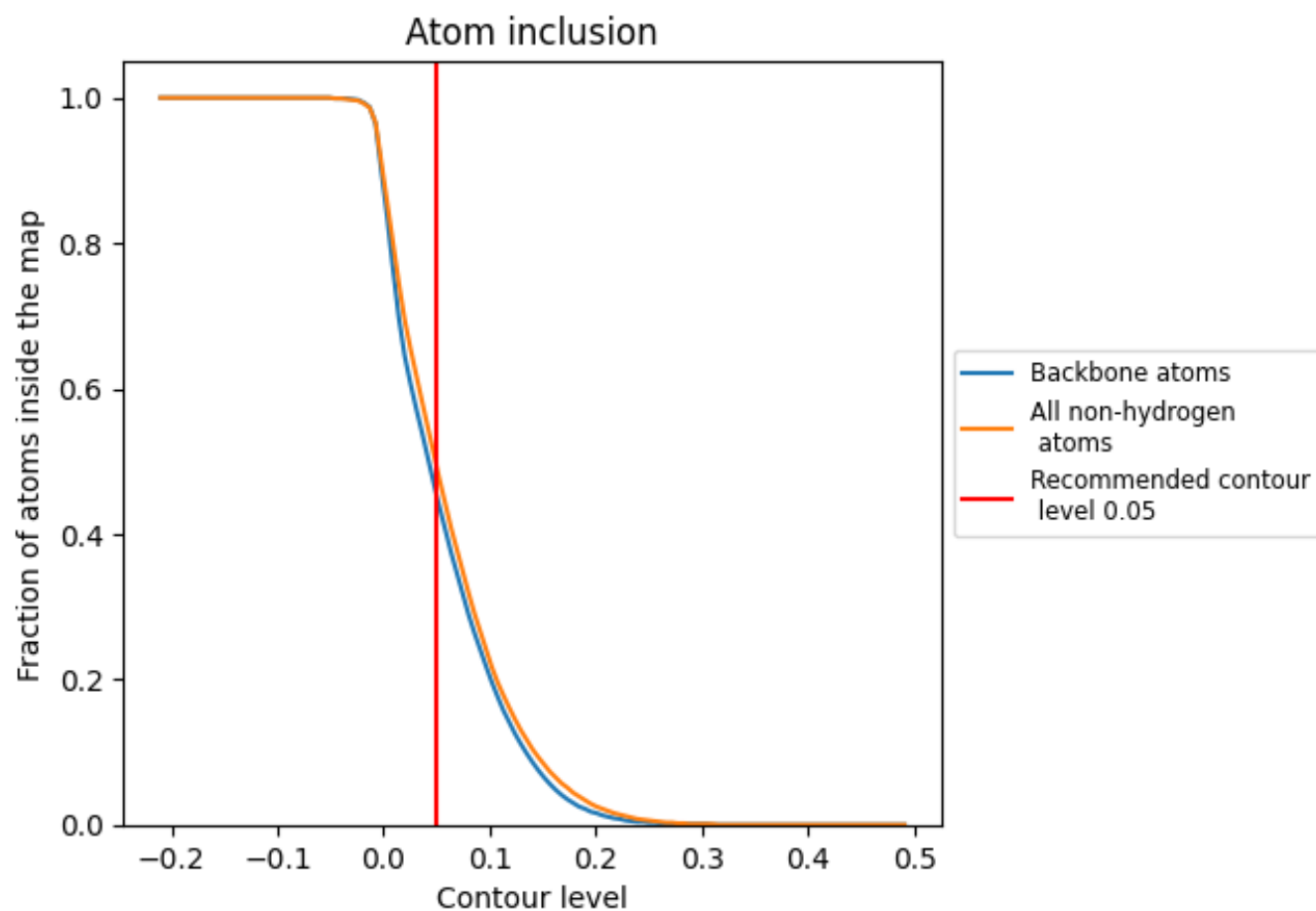
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.05).

8.4 Atom inclusion [i](#)



At the recommended contour level, 45% of all backbone atoms, 49% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4910	 0.1930
1	 0.7230	 0.2640
2	 0.7740	 0.3030
3	 0.0950	 0.0660
4	 0.0010	 0.0230
5	 0.0000	 -0.0020
6	 0.0000	 0.0910
A	 0.0270	 -0.0030
B	 0.5030	 0.1290
C	 0.7530	 0.4280
D	 0.0060	 -0.0100
E	 0.4450	 0.1270
F	 0.6640	 0.3560
G	 0.3650	 0.0980
H	 0.5180	 0.1110
J	 0.0000	 -0.0180
K	 0.0000	 0.0750
L	 0.7120	 0.3730
M	 0.6150	 0.2320
N	 0.6610	 0.2970
O	 0.6950	 0.3370
P	 0.3920	 0.0530
Q	 0.6840	 0.3500
S	 0.6120	 0.2970
T	 0.3370	 0.2730
V	 0.2520	 -0.0370
W	 0.2140	 0.0360
X	 0.4930	 0.1990
Y	 0.7460	 0.3550
b	 0.2390	 0.0380
d	 0.4680	 0.0530
e	 0.6940	 0.3750
f	 0.7710	 0.4090
h	 0.6420	 0.2830
i	 0.4360	 0.1280



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
j	 0.7590	 0.4040
m	 0.0010	 0.0230
n	 0.0030	 0.0640
o	 0.0000	 0.0840
r	 0.2390	 0.0300
t	 0.0000	 0.0550
u	 0.3210	 0.0090
v	 0.0280	 0.0140
x	 0.0080	 -0.0010
y	 0.2910	 -0.0090
z	 0.3580	 0.0840