



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 10:44 AM UTC

PDB ID : 3IZZ / pdb_00003izz
EMDB ID : EMD-1854
Title : Models for ribosome components that are nearest neighbors to the bovine mitochondrial initiation factor2 bound to the E. Coli ribosome
Authors : Yassin, A.S.; Haque, E.; Datta, P.P.; Elmore, K.; Banavali, N.K.; Spremulli, L.L.; Agrawal, R.K.
Deposited on : 2011-01-20
Resolution : 10.80 Å(reported)

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 10.80 Å.

There are no overall percentile quality scores available for this entry.

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

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9118 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 Helix 5, 14, 15 (Small Subunit).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	59	1262	563	231	409	59	0	0

- Molecule 2 is a RNA chain called Helix 18 (Small Subunit).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	D	60	1289	575	241	414	59	0	0

- Molecule 3 is a RNA chain called Helix 44 (Small Subunit).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	E	100	2148	956	401	692	99	0	0

- Molecule 4 is a protein called Protein S12 (Small Subunit).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	F	124	970	611	195	163	1	0	0

- Molecule 5 is a RNA chain called Helix 69, 71, 89, 92, 95 (Large Subunit).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	B	118	2519	1123	448	830	118	0	0

- Molecule 6 is a protein called Protein L14 (Large Subunit).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	121	930	582	179	164	5	0	0

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, C1	Depositor
Number of particles used	121742	Depositor
Resolution determination method	Not provided	
CTF correction method	Every micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	50760	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	262.889	Depositor
Minimum map value	-90.403	Depositor
Average map value	6.195	Depositor
Map value standard deviation	29.837	Depositor
Recommended contour level	60	Depositor
Map size (\AA)	358.8, 358.8, 358.8	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	2.76, 2.76, 2.76	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](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	B	4
1	A	3
3	E	2

The worst 5 of 9 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	1960:A	O3'	2456:C	P	61.59
1	B	2495:G	O3'	2547:A	P	42.07
1	B	1924:C	O3'	1946:U	P	41.90
1	A	58:C	O3'	339:C	P	33.11
1	B	2561:U	O3'	2646:C	P	28.71

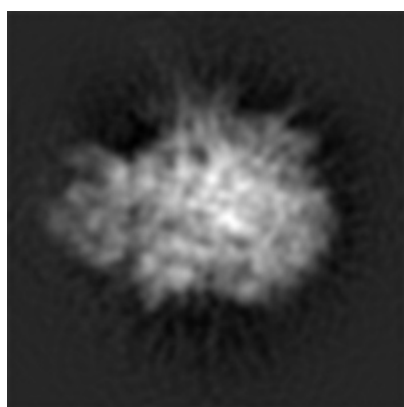
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1854. These allow visual inspection of the internal detail of the map and identification of artifacts.

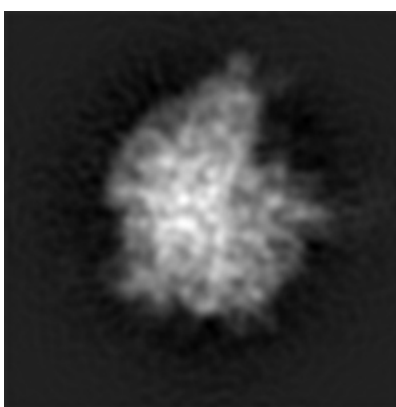
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

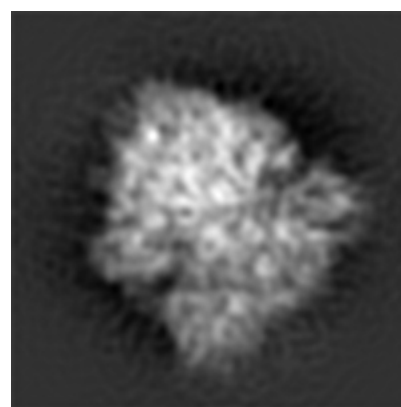
5.1.1 Primary map



X



Y

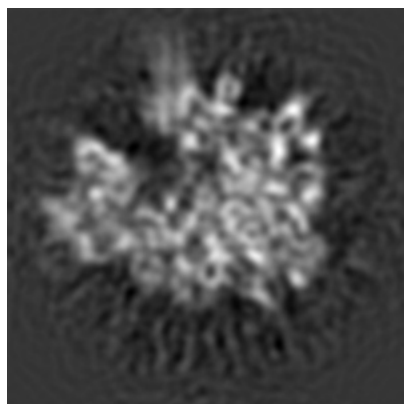


Z

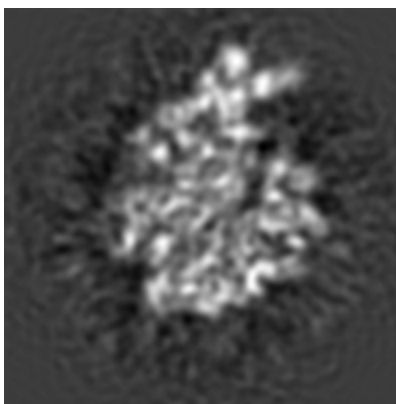
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

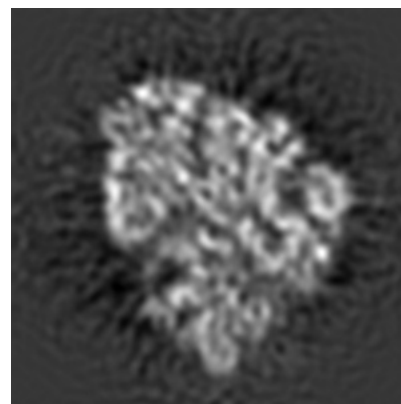
5.2.1 Primary map



X Index: 65



Y Index: 65

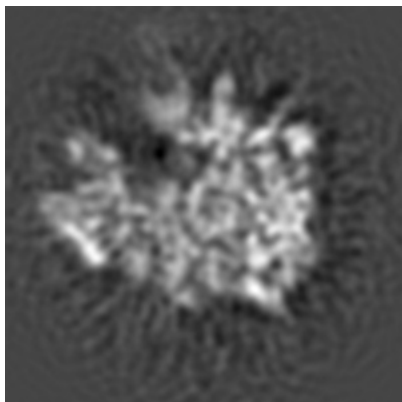


Z Index: 65

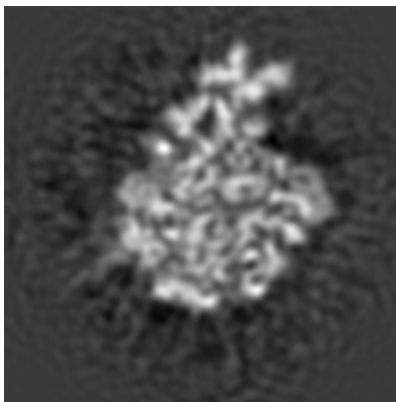
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [\(i\)](#)

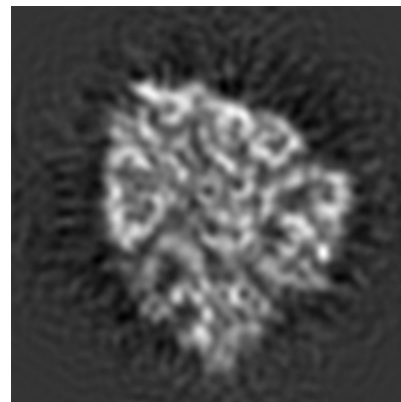
5.3.1 Primary map



X Index: 68



Y Index: 68

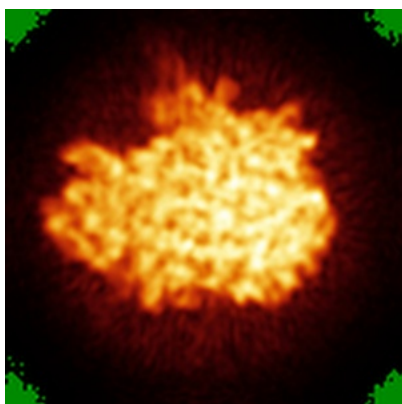


Z Index: 67

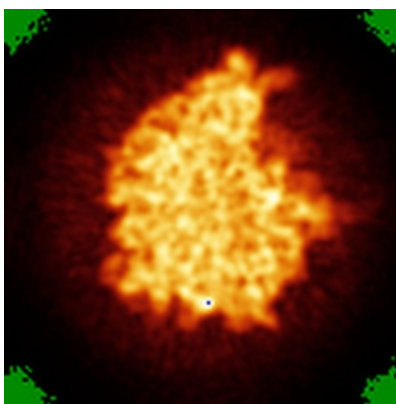
The images above show the largest variance slices of the map in three orthogonal directions.

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

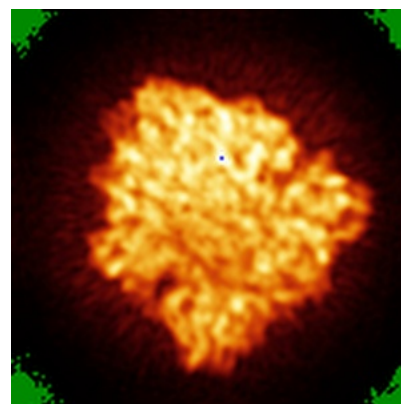
5.4.1 Primary map



X



Y

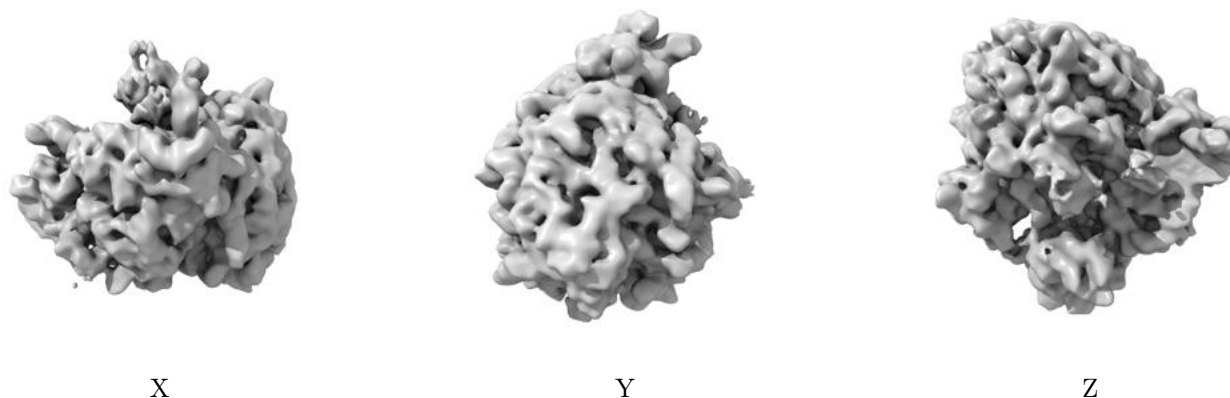


Z

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 [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 60.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

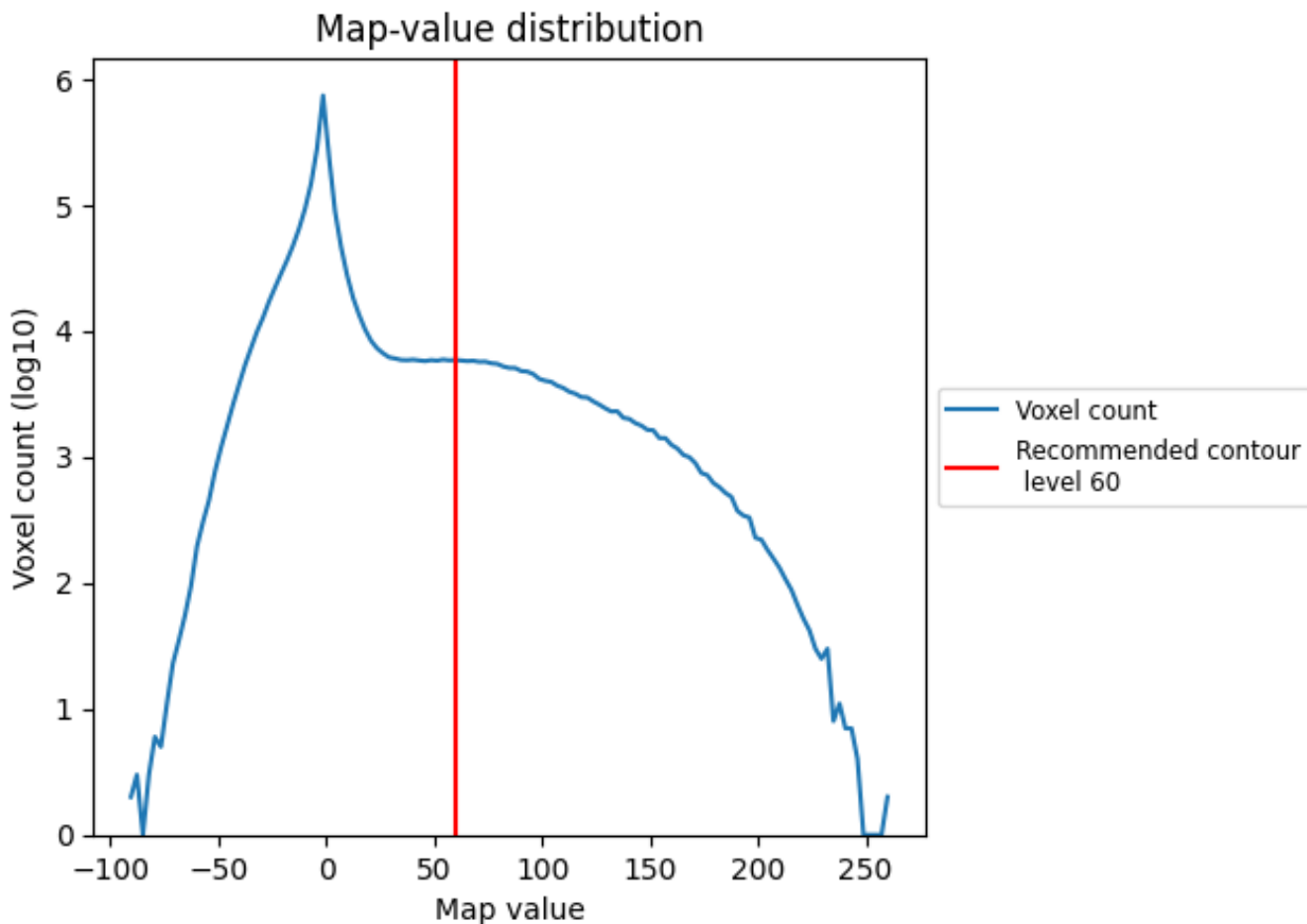
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

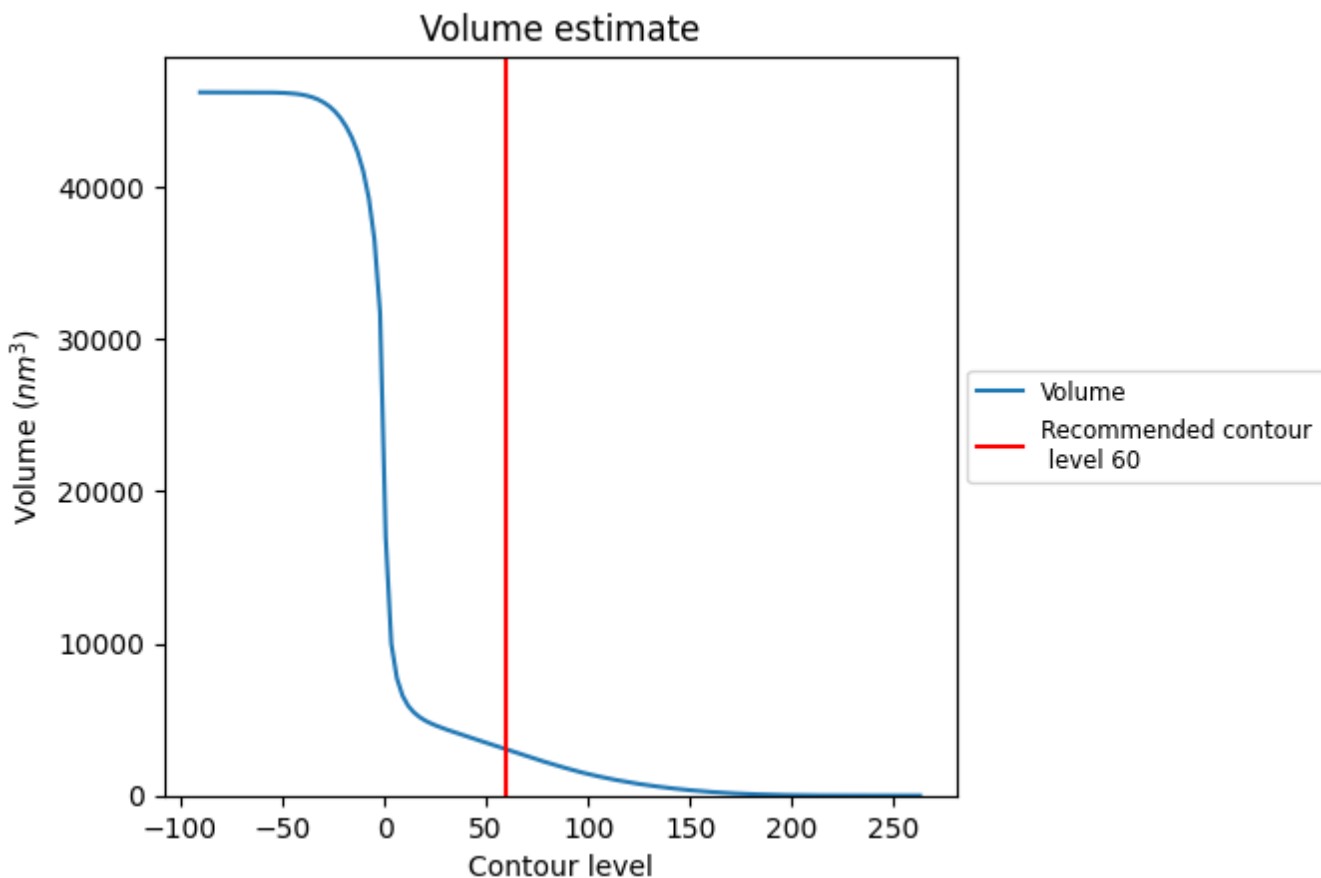
This section contains the results of statistical analysis of the map.

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.

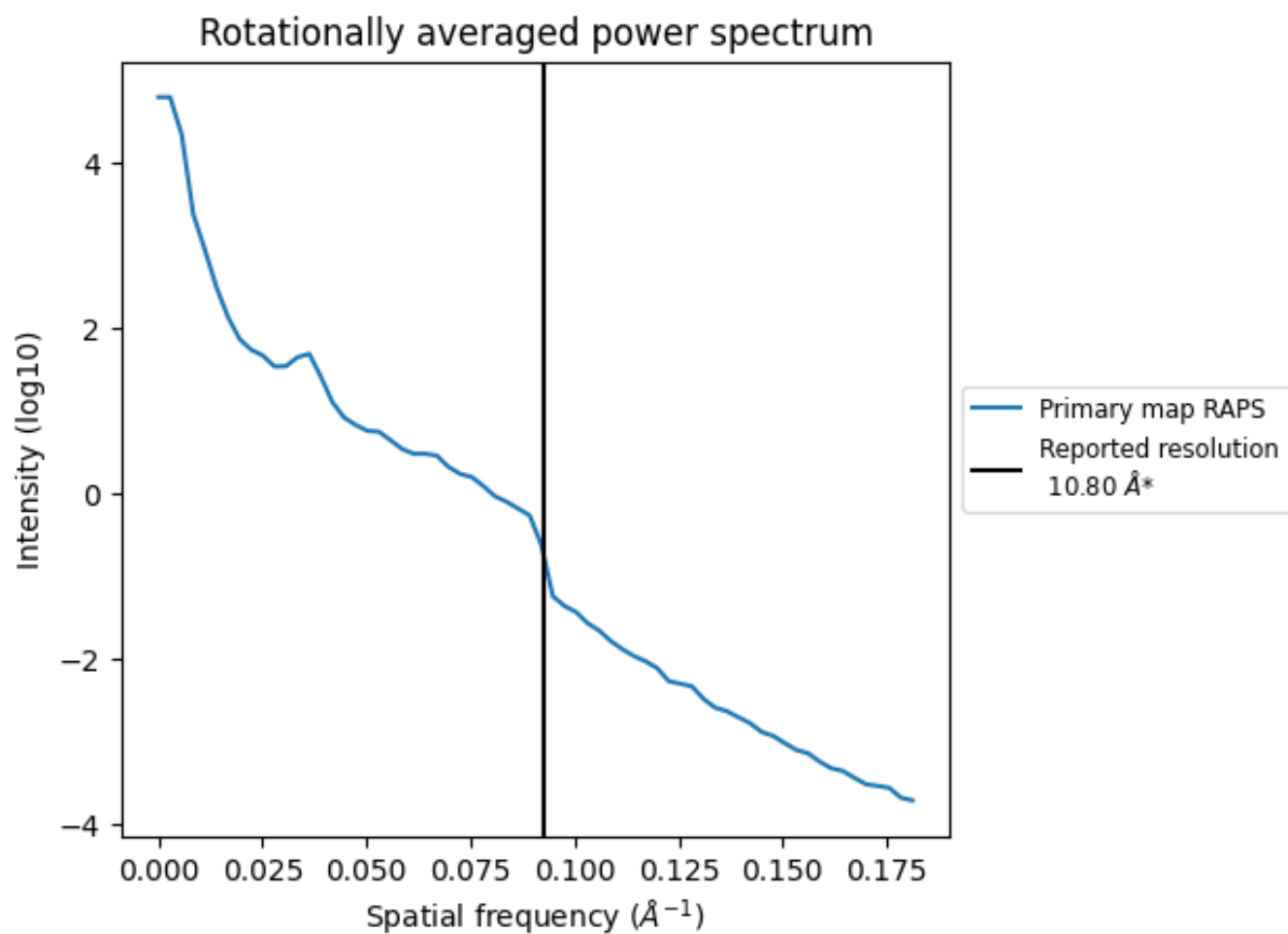
6.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 3027 nm³; this corresponds to an approximate mass of 2735 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.093 Å⁻¹

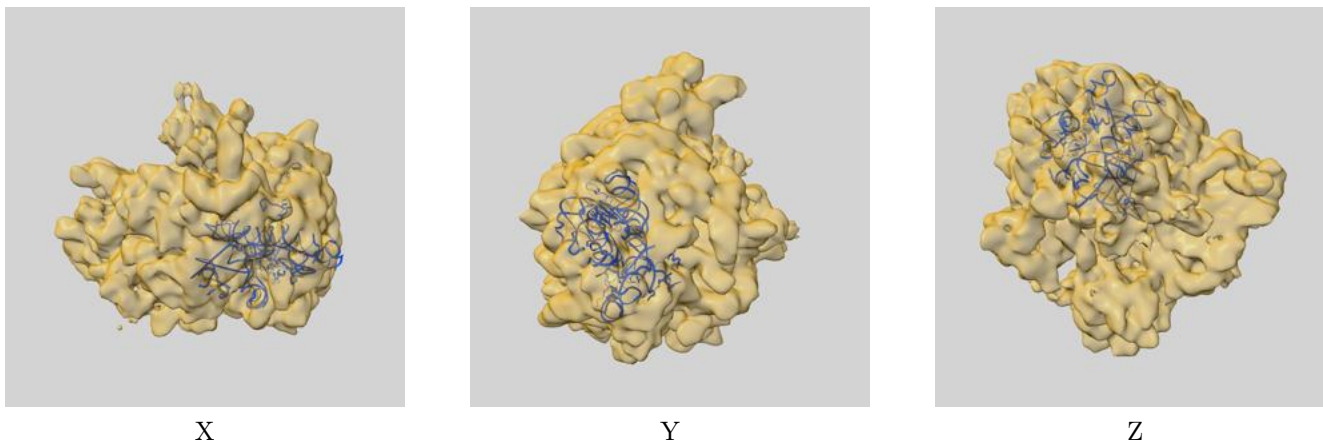
7 Fourier-Shell correlation

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

8 Map-model fit [i](#)

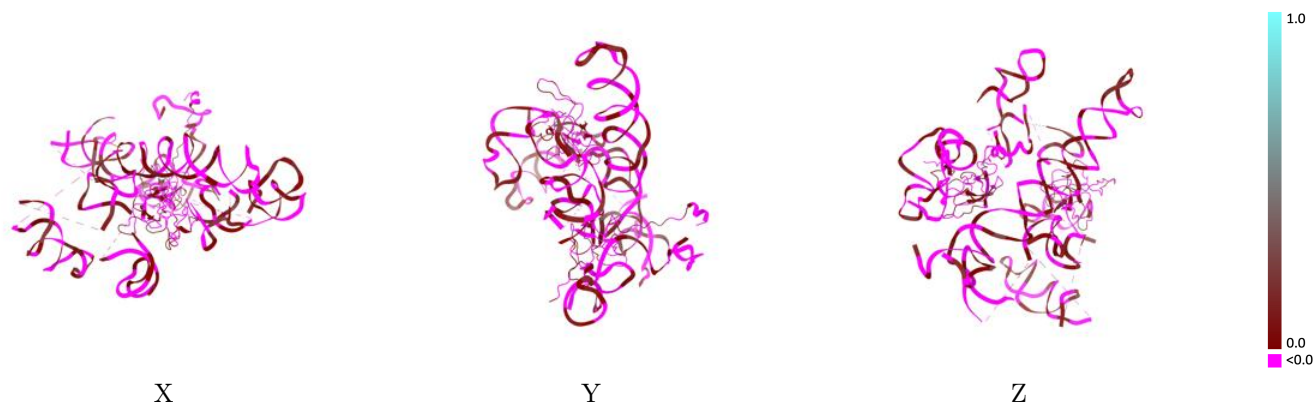
This section contains information regarding the fit between EMDB map EMD-1854 and PDB model 3IZZ. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



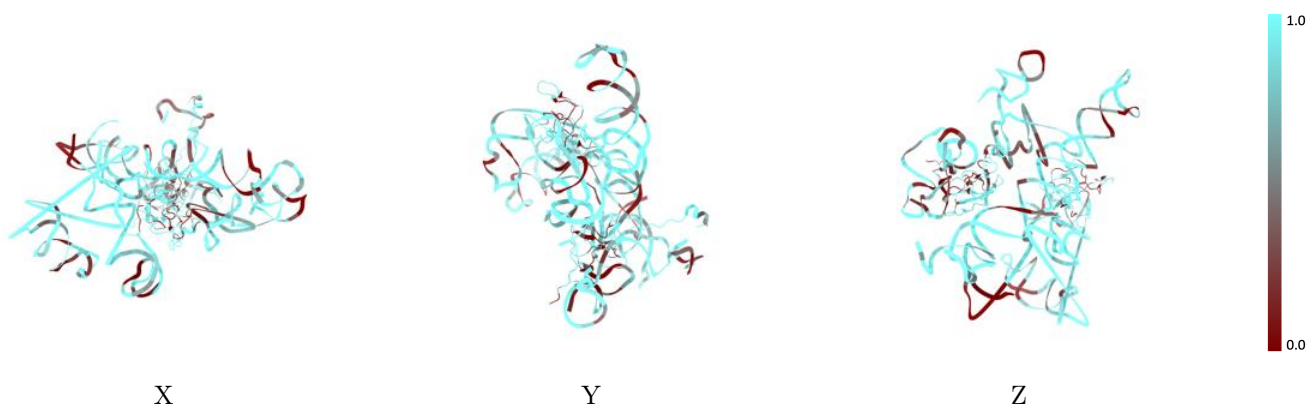
The images above show the 3D surface view of the map at the recommended contour level 60.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



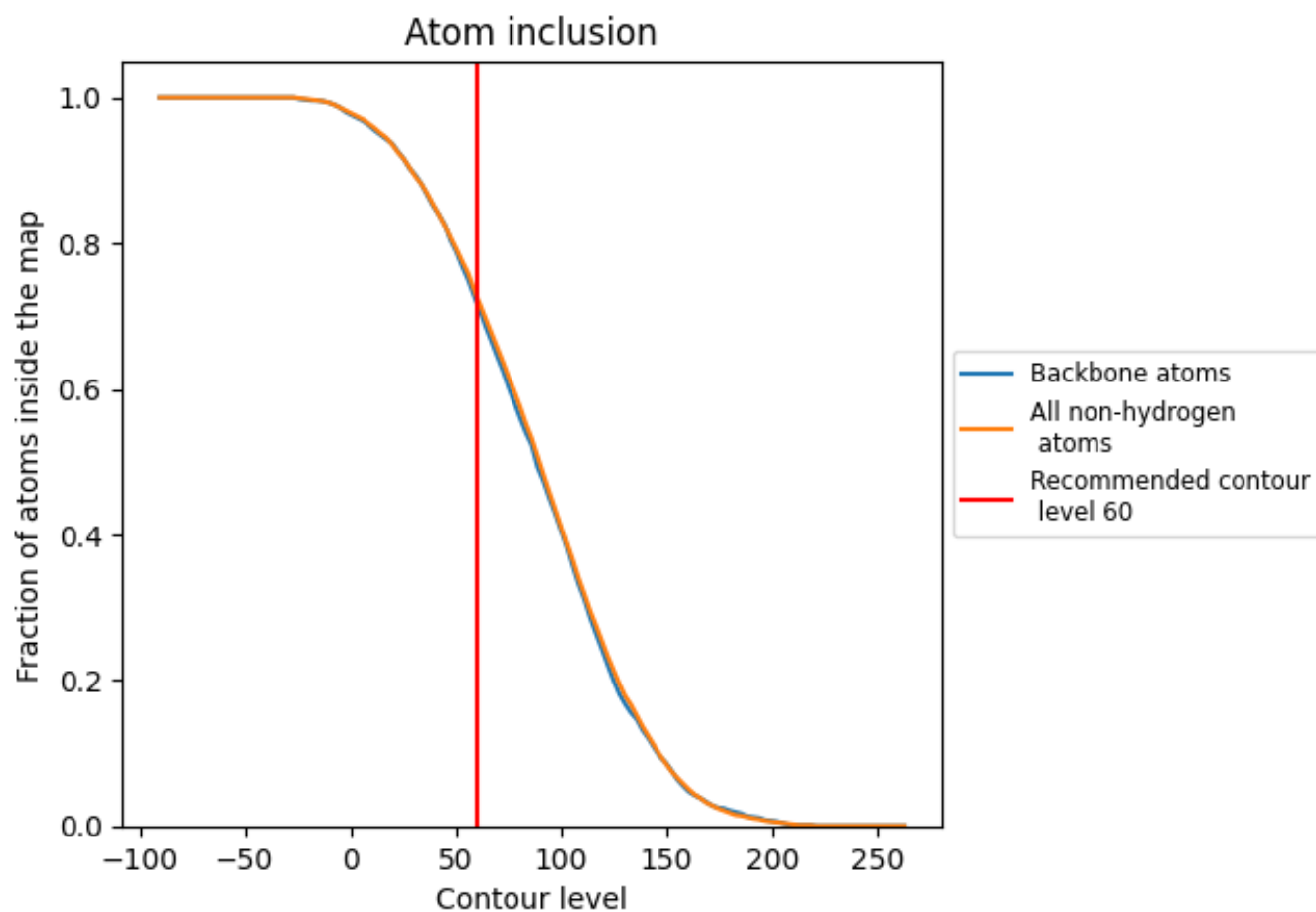
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (60).















8.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 73% 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 (60) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7260	 -0.0030
A	 0.7390	 0.0180
B	 0.7340	 0.0030
D	 0.6340	 -0.0290
E	 0.7720	 0.0010
F	 0.7230	 -0.0070
G	 0.7140	 -0.0230

