



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 07:03 PM UTC

PDB ID : 3IY9 / pdb_00003iy9
EMDB ID : EMD-5113
Title : Leishmania Tarentolae Mitochondrial Large Ribosomal Subunit Model
Authors : Sharma, M.R.; Booth, T.M.; Simpson, L.; Maslov, D.A.; Agrawal, R.K.
Deposited on : 2009-04-20
Resolution : 14.10 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

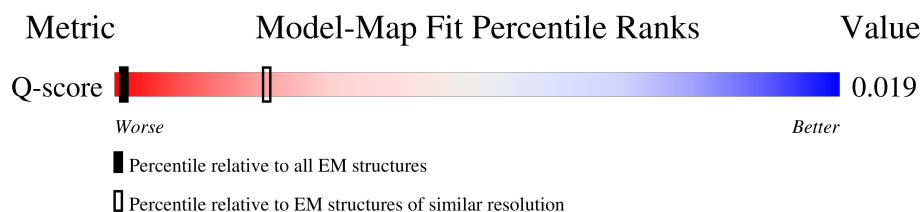
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 14.10 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	53 (13.60 - 14.50)

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

2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 3158 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 Leishmania Tarentolae Mitochondrial Large Ribosomal Subunit.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	A	1027	Total	P	0	1027
			1027	1027		

- Molecule 2 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
2	B	136	Total	C	0	136
			136	136		

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	C	209	Total	C	0	209
			209	209		

- Molecule 4 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	D	175	Total	C	0	175
			175	175		

- Molecule 5 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms		AltConf	Trace
5	H	60	Total	C	0	60
			60	60		

- Molecule 6 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
6	G	145	Total	C	0	145
			145	145		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms		AltConf	Trace
7	J	140	Total	C	0	140
			140	140		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms		AltConf	Trace
8	K	121	Total	C	0	121
			121	121		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms		AltConf	Trace
9	L	144	Total	C	0	144
			144	144		

- Molecule 10 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
10	I	118	Total	C	0	118
			118	118		

- Molecule 11 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
11	S	116	Total	C	0	116
			116	116		

- Molecule 12 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms		AltConf	Trace
12	Q	117	Total	C	0	117
			117	117		

- Molecule 13 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms		AltConf	Trace
13	R	103	Total	C	0	103
			103	103		

- Molecule 14 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
14	M	110	Total	C	0	110
			110	110		

- Molecule 15 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms		AltConf	Trace
15	T	99	Total	C	0	99
			99	99		

- Molecule 16 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
16	N	96	Total	C	0	96
			96	96		

- Molecule 17 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
17	O	69	Total	C	0	69
			69	69		

- Molecule 18 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms		AltConf	Trace
18	X	63	Total	C	0	63
			63	63		

- Molecule 19 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms		AltConf	Trace
19	Y	58	Total	C	0	58
			58	58		

- Molecule 20 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
20	P	52	Total	C	0	52
			52	52		

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	53475	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Each Micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	50760	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.004	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.00055	Depositor
Map size ($\text{\AA}$)	358.8, 358.8, 358.8	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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 ⓘ

There are no chain breaks in this entry.

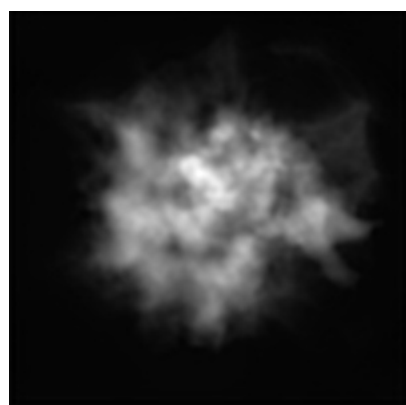
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5113. These allow visual inspection of the internal detail of the map and identification of artifacts.

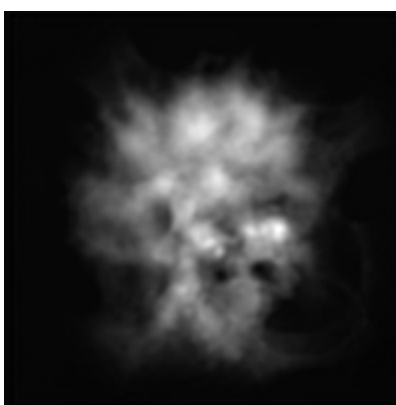
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

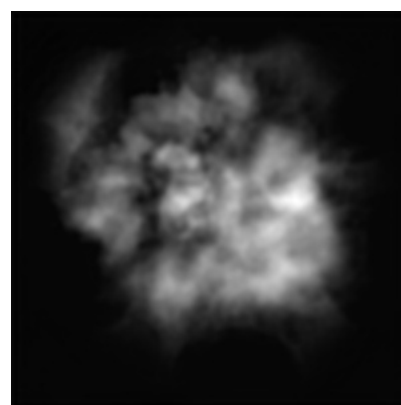
5.1.1 Primary map



X



Y

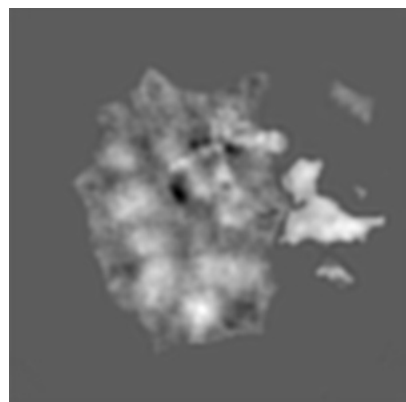


Z

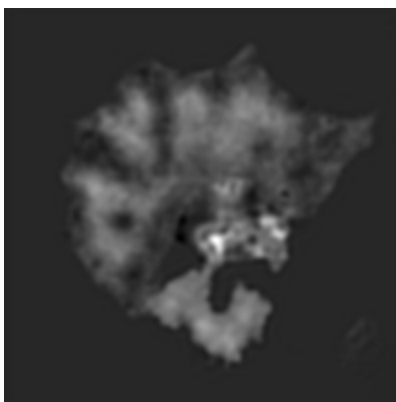
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

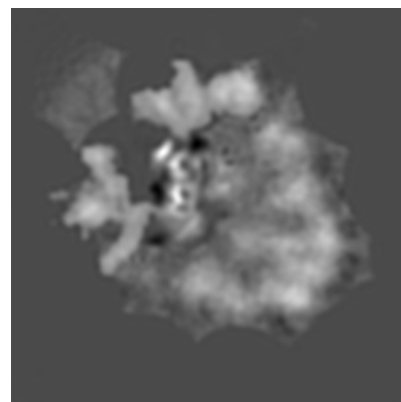
5.2.1 Primary map



X Index: 65



Y Index: 65

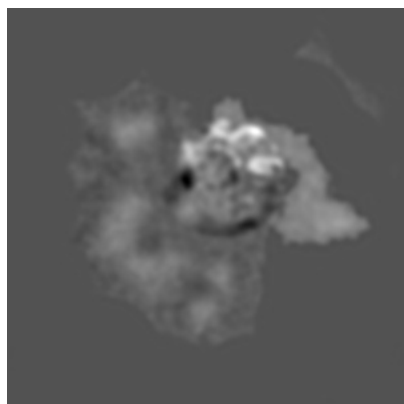


Z Index: 65

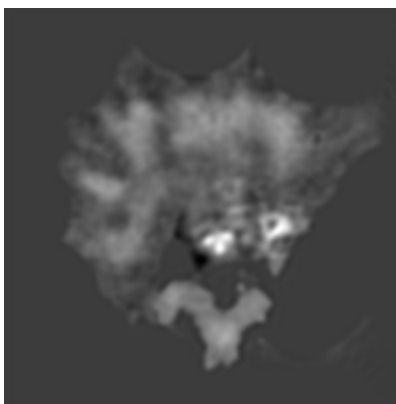
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

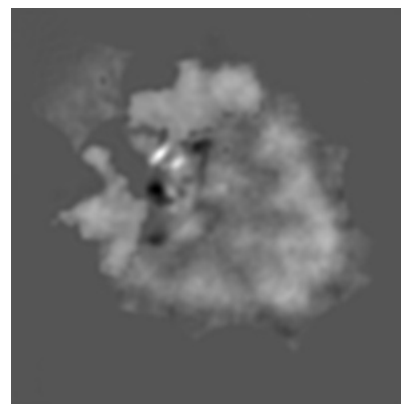
5.3.1 Primary map



X Index: 58



Y Index: 68

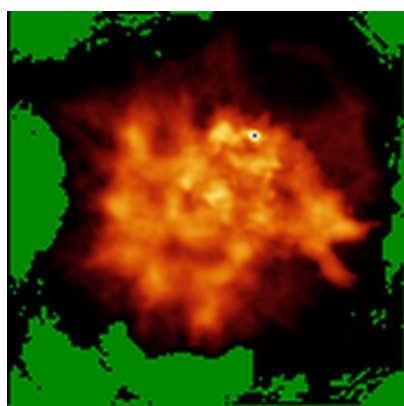


Z Index: 63

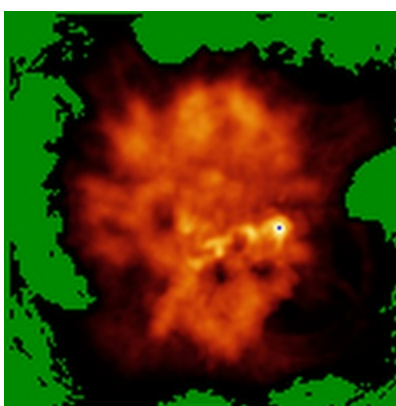
The images above show the largest variance slices of the map in three orthogonal directions.

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

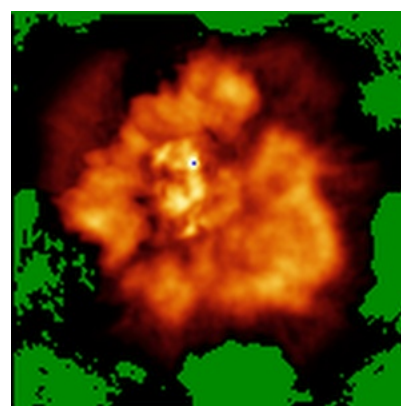
5.4.1 Primary map



X



Y

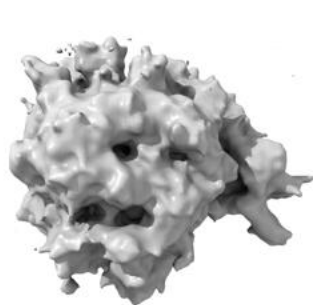


Z

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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

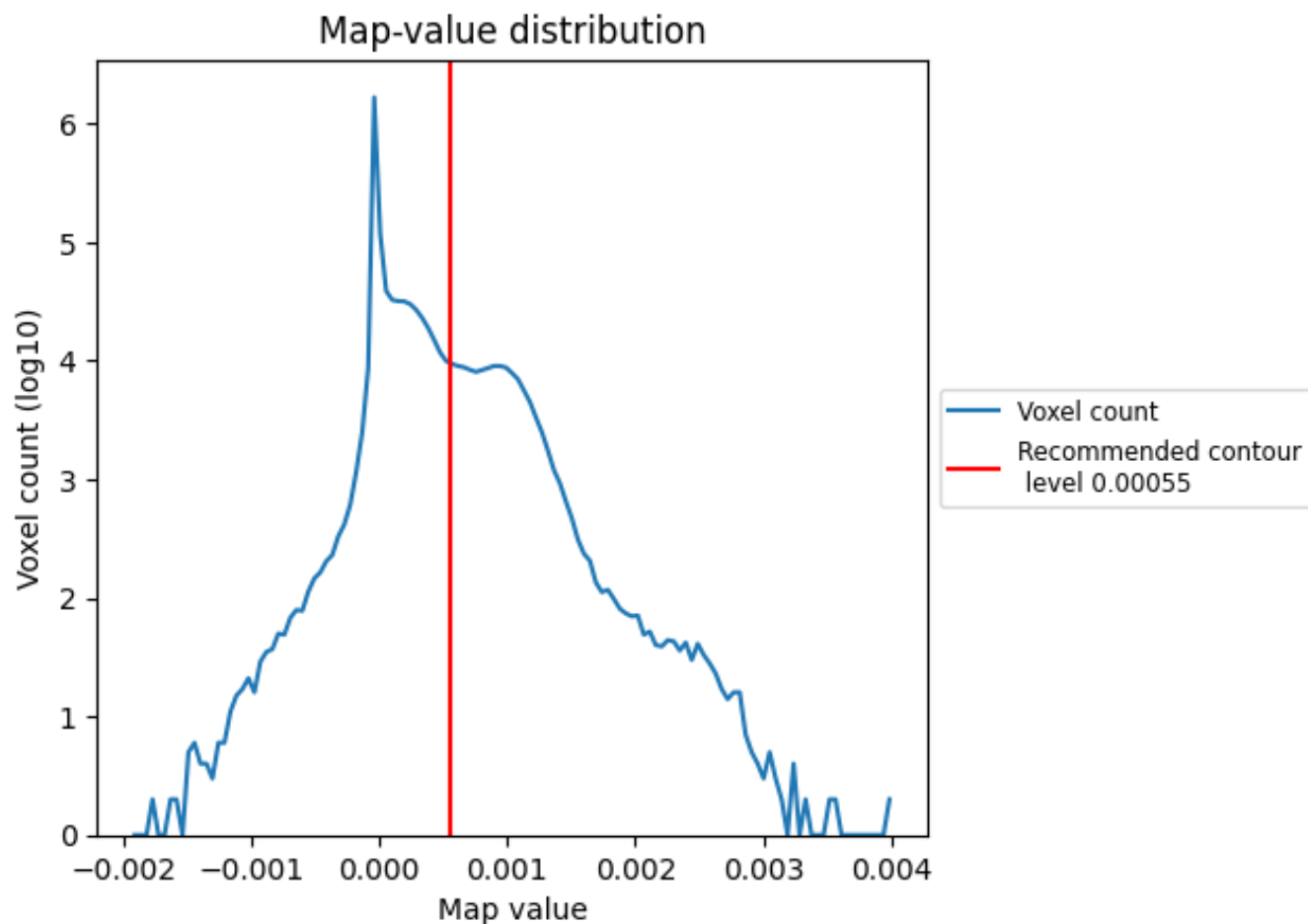
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

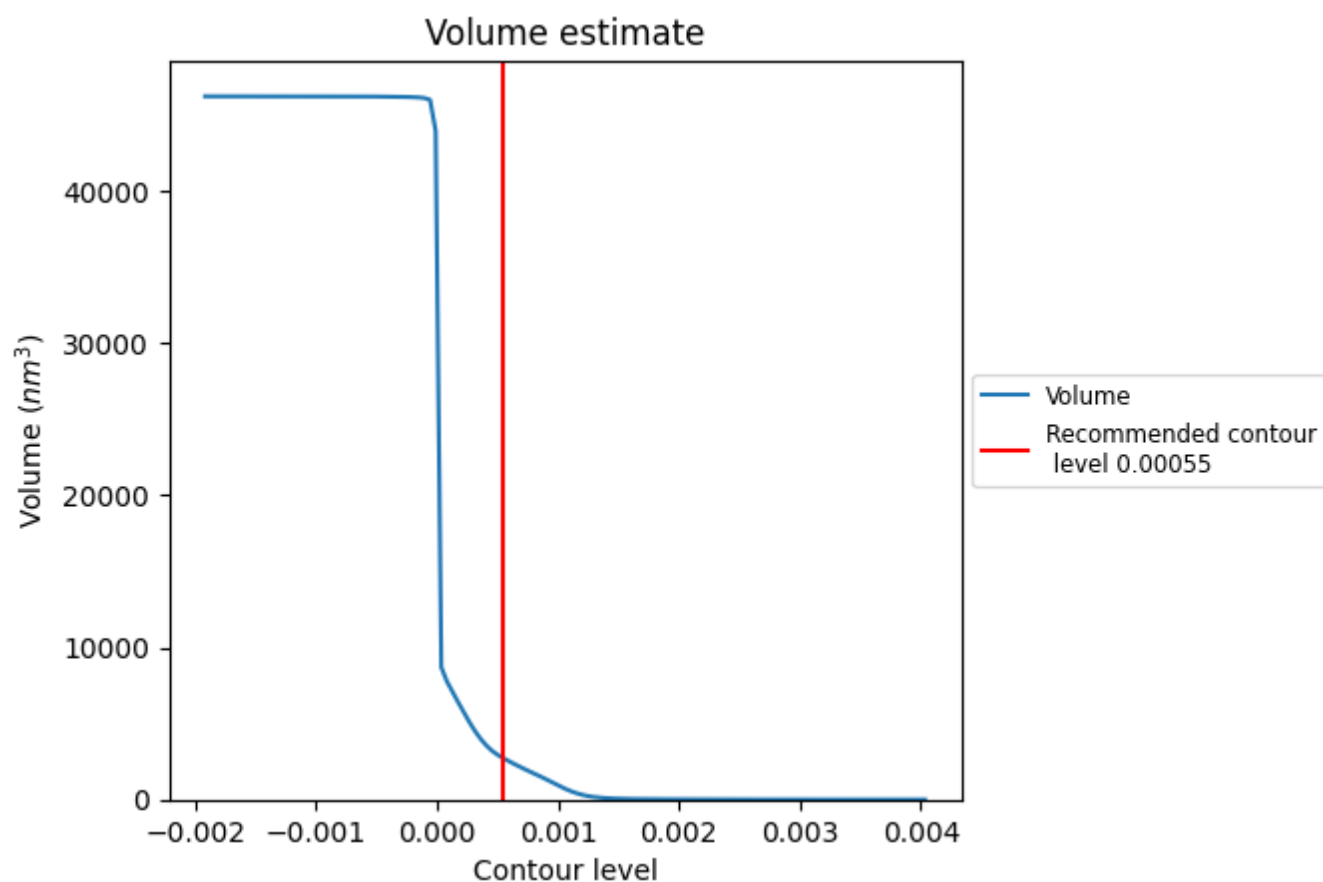
This section contains the results of statistical analysis of the map.

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.

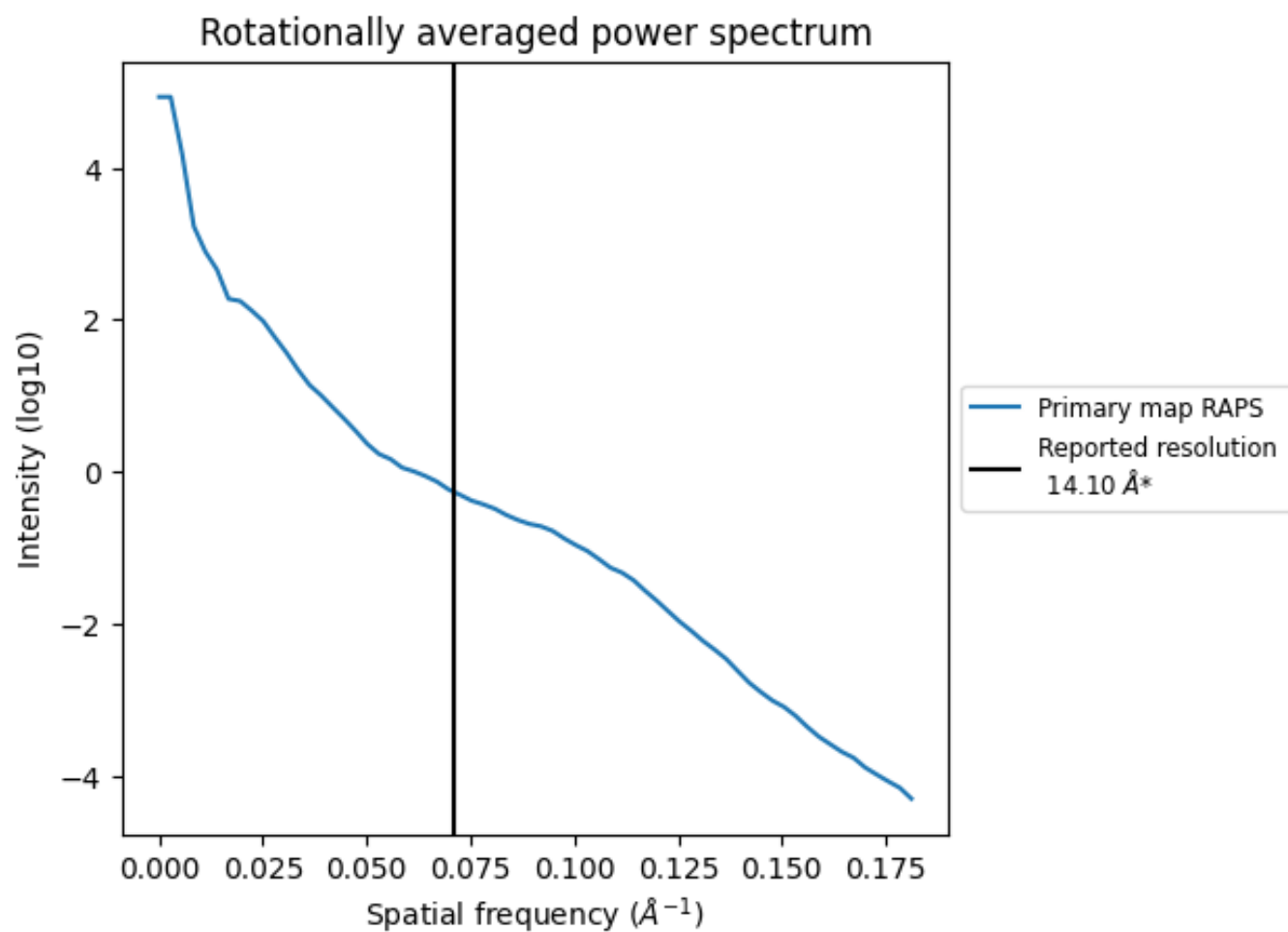
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 2711 nm³; this corresponds to an approximate mass of 2449 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 0.071 Å⁻¹

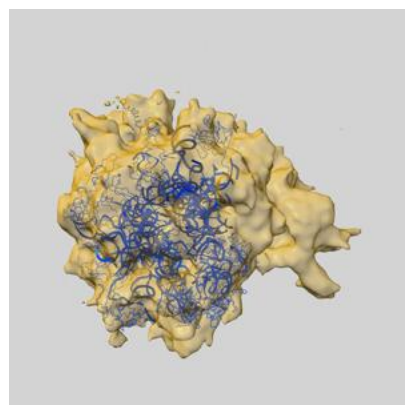
7 Fourier-Shell correlation ⓘ

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

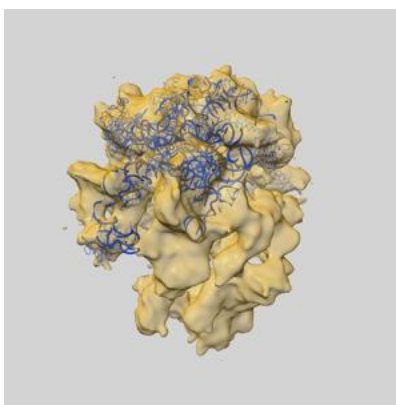
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5113 and PDB model 3IY9. Per-residue inclusion information can be found in section ?? on page ??.

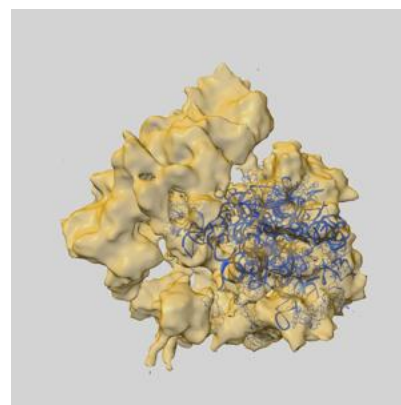
8.1 Map-model overlay [i](#)



X



Y



Z

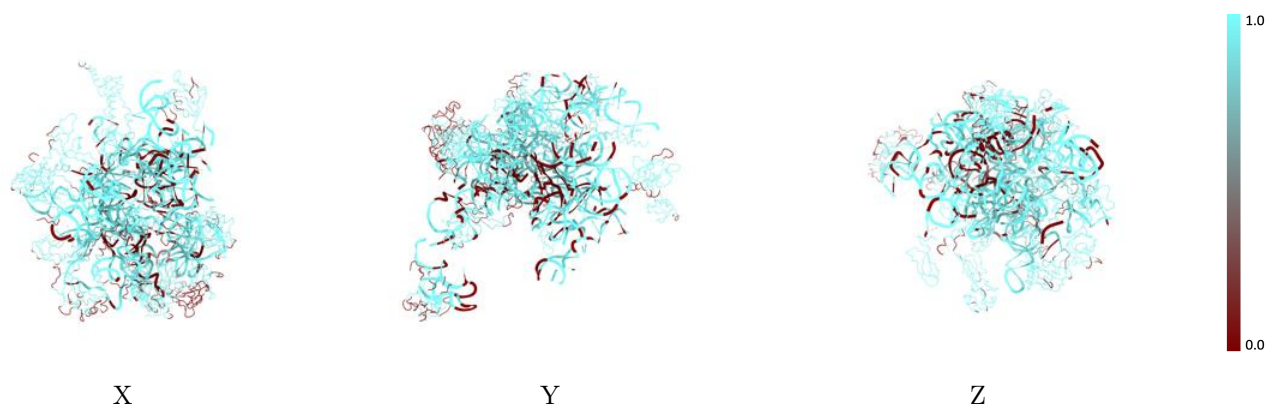
The images above show the 3D surface view of the map at the recommended contour level 0.00055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



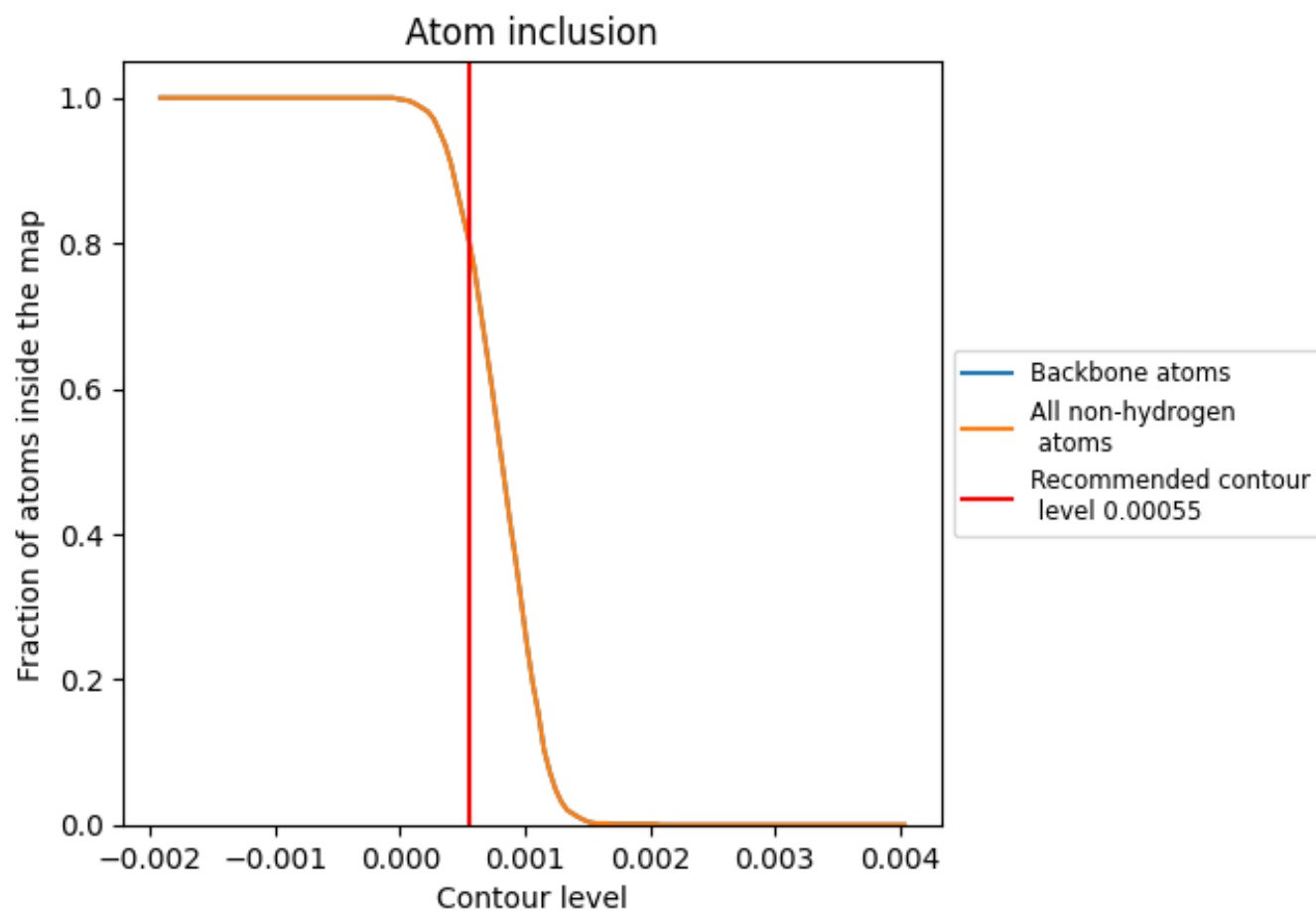
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00055).

8.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 80% 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 (0.00055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8040	 0.0190
A	 0.7860	 0.0110
B	 0.8160	 0.0220
C	 0.5600	 0.0140
D	 0.9260	 0.0130
G	 0.5860	 0.0460
H	 0.9330	 0.0920
I	 0.7460	 0.0380
J	 0.7790	 0.0250
K	 0.8100	 0.0440
L	 0.8610	 0.0170
M	 0.8460	 0.0340
N	 0.9170	 0.0180
O	 0.9570	 0.0310
P	 1.0000	 0.0440
Q	 0.7270	 -0.0120
R	 0.6890	 -0.0170
S	 0.9910	 0.0180
T	 0.9190	 0.0150
X	 1.0000	 0.0150
Y	 0.9830	 0.0160

