



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 10:32 AM UTC

PDB ID : 1LU3 / pdb_00001lu3
EMDB ID : EMD-1045
Title : Separate Fitting of the Anticodon Loop Region of tRNA (nucleotide 26-42) in the Low Resolution Cryo-EM Map of an EF-Tu Ternary Complex (GDP and Kirromycin) Bound to E. coli 70S Ribosome
Authors : Valle, M.; Sengupta, J.; Swami, N.K.; Grassucci, R.A.; Burkhardt, N.; Nierhaus, K.H.; Agrawal, R.K.; Frank, J.
Deposited on : 2002-05-21
Resolution : 16.80 Å(reported)
Based on initial model : 1TTT

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
Mogul : 2022.3.0, CSD as543be (2022)
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

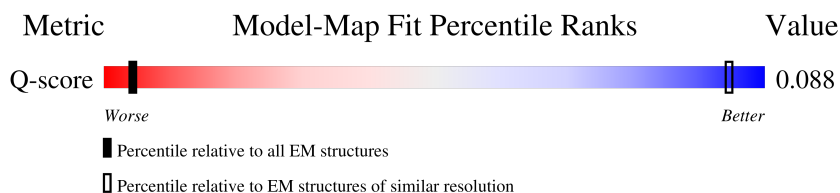
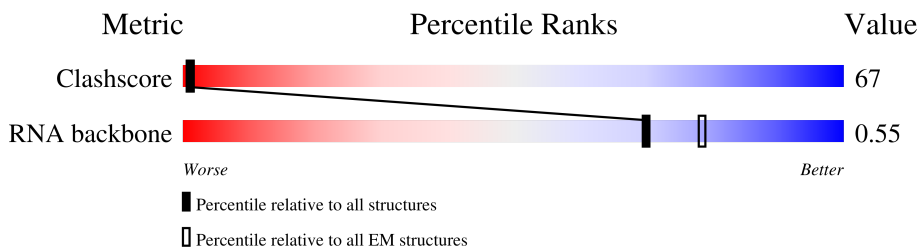
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 16.80 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	36 (16.30 - 17.30)

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	17	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 365 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.

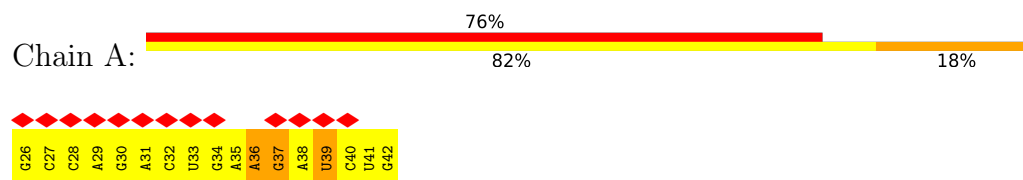
- Molecule 1 is a RNA chain called PHENYLALANINE TRANSFER RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	17	Total	C	N	O	P	0	0
			365	163	68	117	17		

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: PHENYLALANINE TRANSFER RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	7985	Depositor
Resolution determination method	Not provided	
CTF correction method	CTF correction of 3D-maps	Depositor
Microscope	FEI/PHILIPS EM420	Depositor
Voltage (kV)	100	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	52000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	184.764	Depositor
Minimum map value	-82.175	Depositor
Average map value	4.364	Depositor
Map value standard deviation	20.064	Depositor
Recommended contour level	48.3	Depositor
Map size ($\text{\AA}$)	365.84, 365.84, 365.84	wwPDB
Map dimensions	136, 136, 136	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	2.69, 2.69, 2.69	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: PSU

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	1.61	0/386	1.65	1/600 (0.2%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	36	A	O3'-P-O5'	5.08	111.61	104.00

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	365	0	185	37	0
All	All	365	0	185	37	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 67.

All (37) 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)
1:A:36:A:H2'	1:A:37:G:H5''	1.15	1.12
1:A:36:A:C2'	1:A:37:G:H5''	1.98	0.94
1:A:32:C:H2'	1:A:33:U:C6	2.12	0.85
1:A:32:C:H2'	1:A:33:U:H6	1.51	0.75
1:A:28:C:H2'	1:A:29:A:H8	1.56	0.70
1:A:37:G:H2'	1:A:38:A:H8	1.58	0.68
1:A:33:U:H3	1:A:35:A:H3'	1.59	0.67
1:A:34:G:H2'	1:A:35:A:O4'	1.94	0.67
1:A:31:A:O2'	1:A:32:C:H5'	1.97	0.64
1:A:39:PSU:H2'	1:A:40:C:C6	2.35	0.61
1:A:37:G:H2'	1:A:38:A:C8	2.35	0.60
1:A:26:G:H2'	1:A:27:C:C6	2.38	0.58
1:A:33:U:N3	1:A:35:A:H3'	2.18	0.58
1:A:30:G:O2'	1:A:31:A:H5'	2.04	0.58
1:A:40:C:O2'	1:A:41:U:H5'	2.06	0.55
1:A:27:C:H2'	1:A:28:C:C6	2.43	0.54
1:A:39:PSU:H2'	1:A:40:C:H6	1.72	0.53
1:A:41:U:H2'	1:A:42:G:H8	1.72	0.53
1:A:35:A:O2'	1:A:36:A:H5'	2.09	0.53
1:A:38:A:O2'	1:A:39:PSU:H5''	2.09	0.52
1:A:29:A:O2'	1:A:30:G:H5'	2.08	0.52
1:A:36:A:H2'	1:A:37:G:C5'	2.11	0.51
1:A:38:A:H2'	1:A:39:PSU:H6	1.78	0.48
1:A:37:G:O2'	1:A:38:A:H5'	2.14	0.48
1:A:33:U:H2'	1:A:35:A:OP2	2.14	0.48
1:A:35:A:C4	1:A:36:A:C8	3.02	0.47
1:A:36:A:C2'	1:A:37:G:C5'	2.84	0.47
1:A:26:G:H2'	1:A:27:C:H6	1.80	0.46
1:A:35:A:H2'	1:A:36:A:H8	1.83	0.44
1:A:41:U:H2'	1:A:42:G:C8	2.51	0.44
1:A:33:U:C6	1:A:35:A:OP2	2.71	0.44
1:A:28:C:H2'	1:A:29:A:C8	2.46	0.43
1:A:29:A:C6	1:A:42:G:C6	3.06	0.43
1:A:30:G:C6	1:A:31:A:C5	3.07	0.43
1:A:32:C:O2'	1:A:33:U:H5'	2.20	0.42
1:A:33:U:C2	1:A:35:A:H3'	2.55	0.41
1:A:39:PSU:O2'	1:A:40:C:H5'	2.20	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	16/17 (94%)	1 (6%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	37	G

There are no RNA pucker outliers to report.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	PSU	A	39	1	18,21,22	0.79	0	21,30,33	1.57	4 (19%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A	39	1	-	0/7/25/26	0/2/2/2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	39	PSU	N1-C2-N3	3.79	119.17	115.17
1	A	39	PSU	C4-N3-C2	-3.43	121.64	126.37
1	A	39	PSU	O2-C2-N1	-2.52	120.19	122.79
1	A	39	PSU	O4'-C1'-C2'	2.17	108.15	105.15

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	39	PSU	5	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

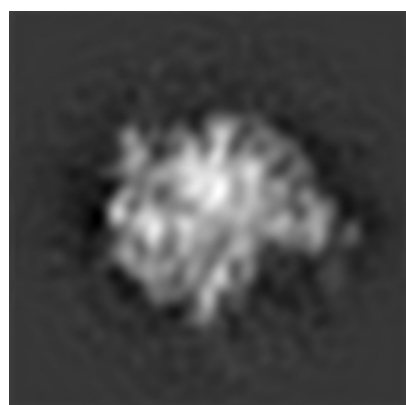
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1045. These allow visual inspection of the internal detail of the map and identification of artifacts.

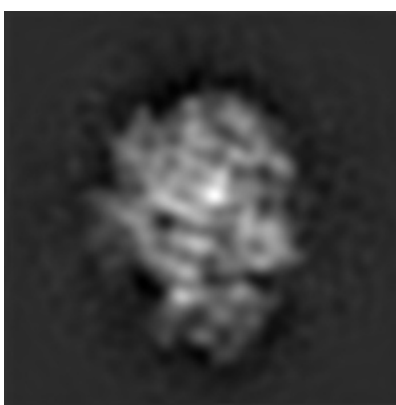
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

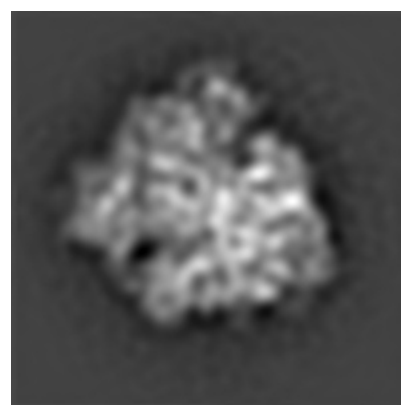
6.1.1 Primary map



X



Y

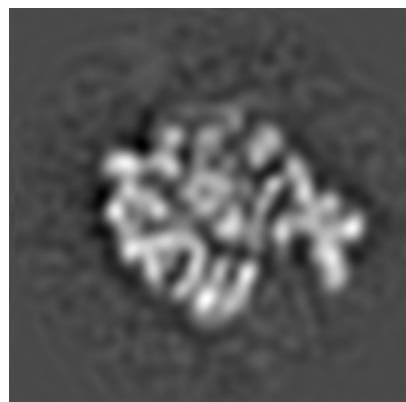


Z

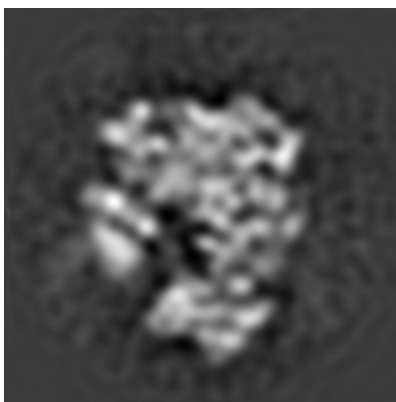
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

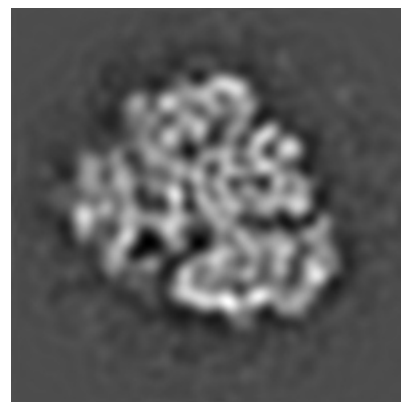
6.2.1 Primary map



X Index: 68



Y Index: 68

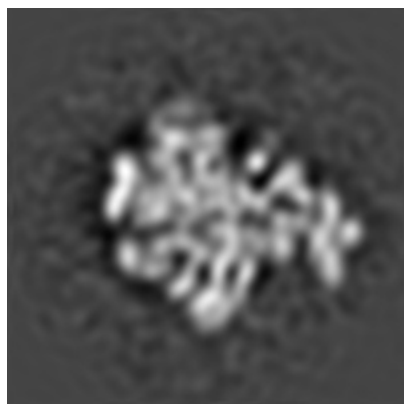


Z Index: 68

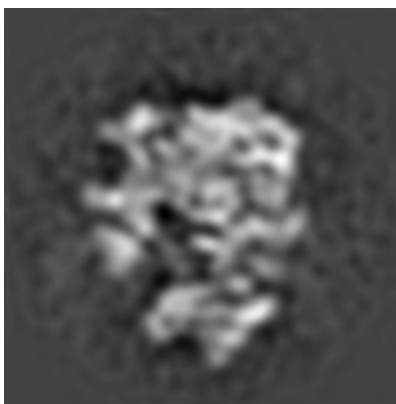
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

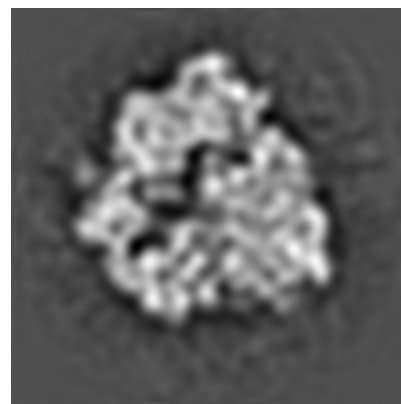
6.3.1 Primary map



X Index: 71



Y Index: 70

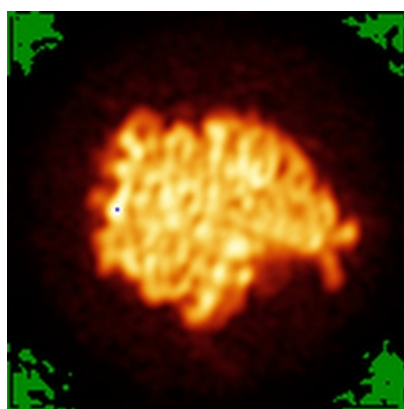


Z Index: 62

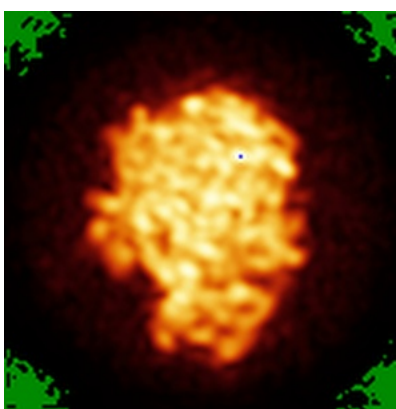
The images above show the largest variance slices of the map in three orthogonal directions.

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

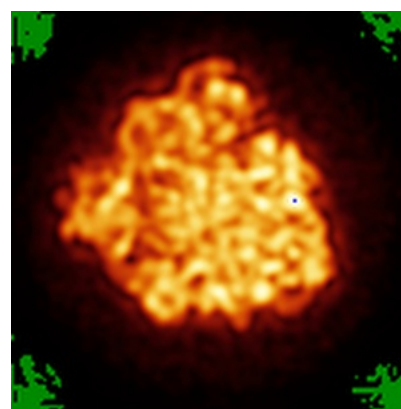
6.4.1 Primary map



X



Y

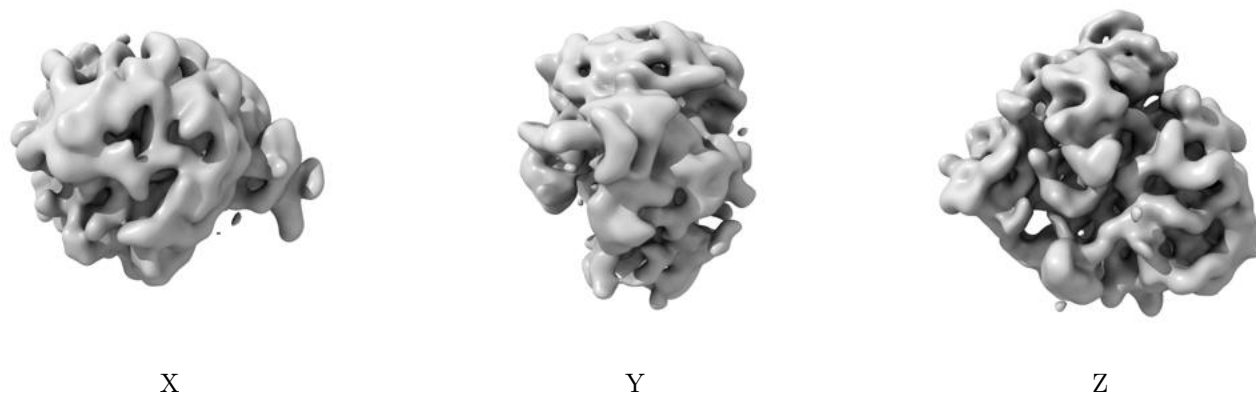


Z

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 48.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

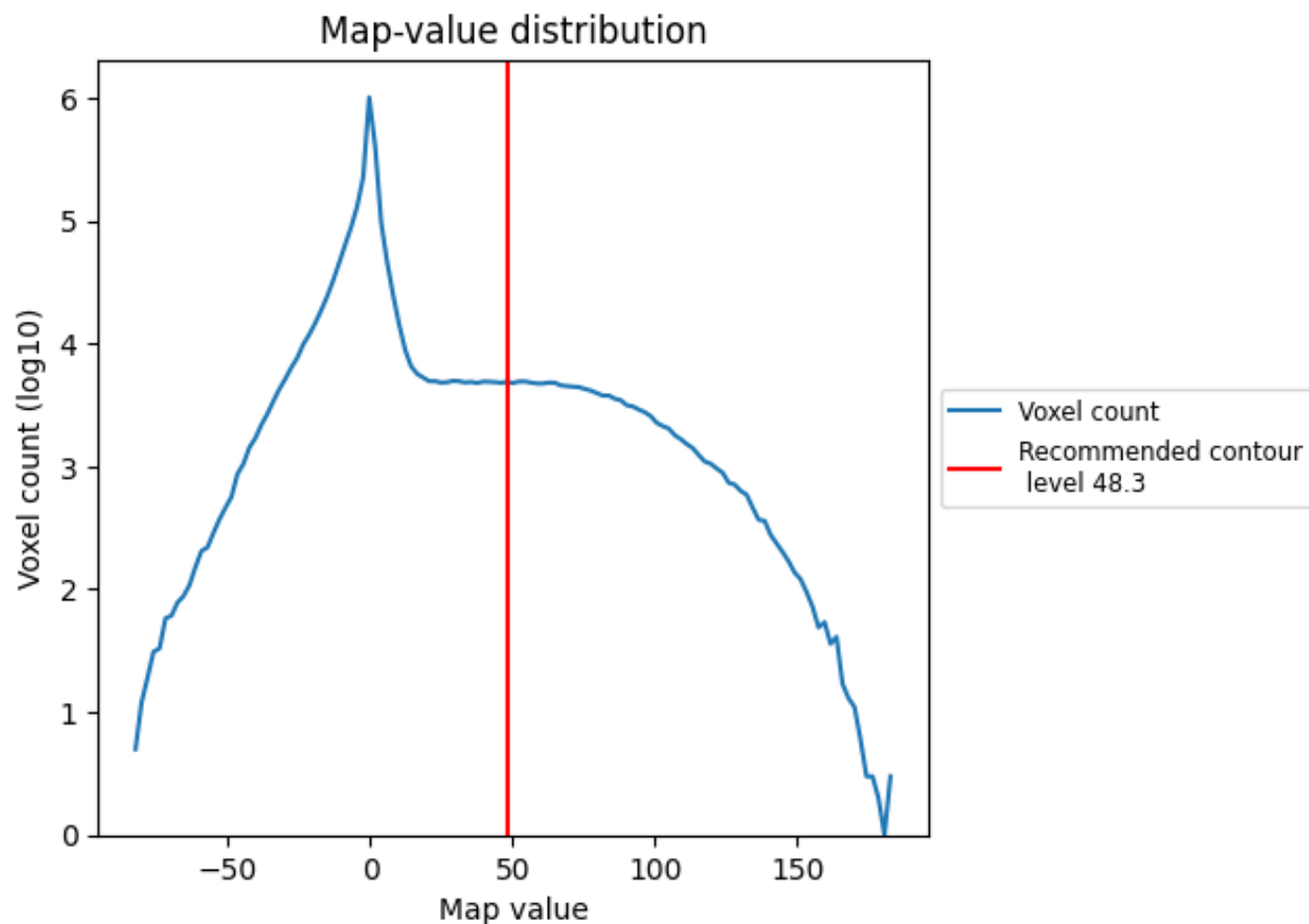
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

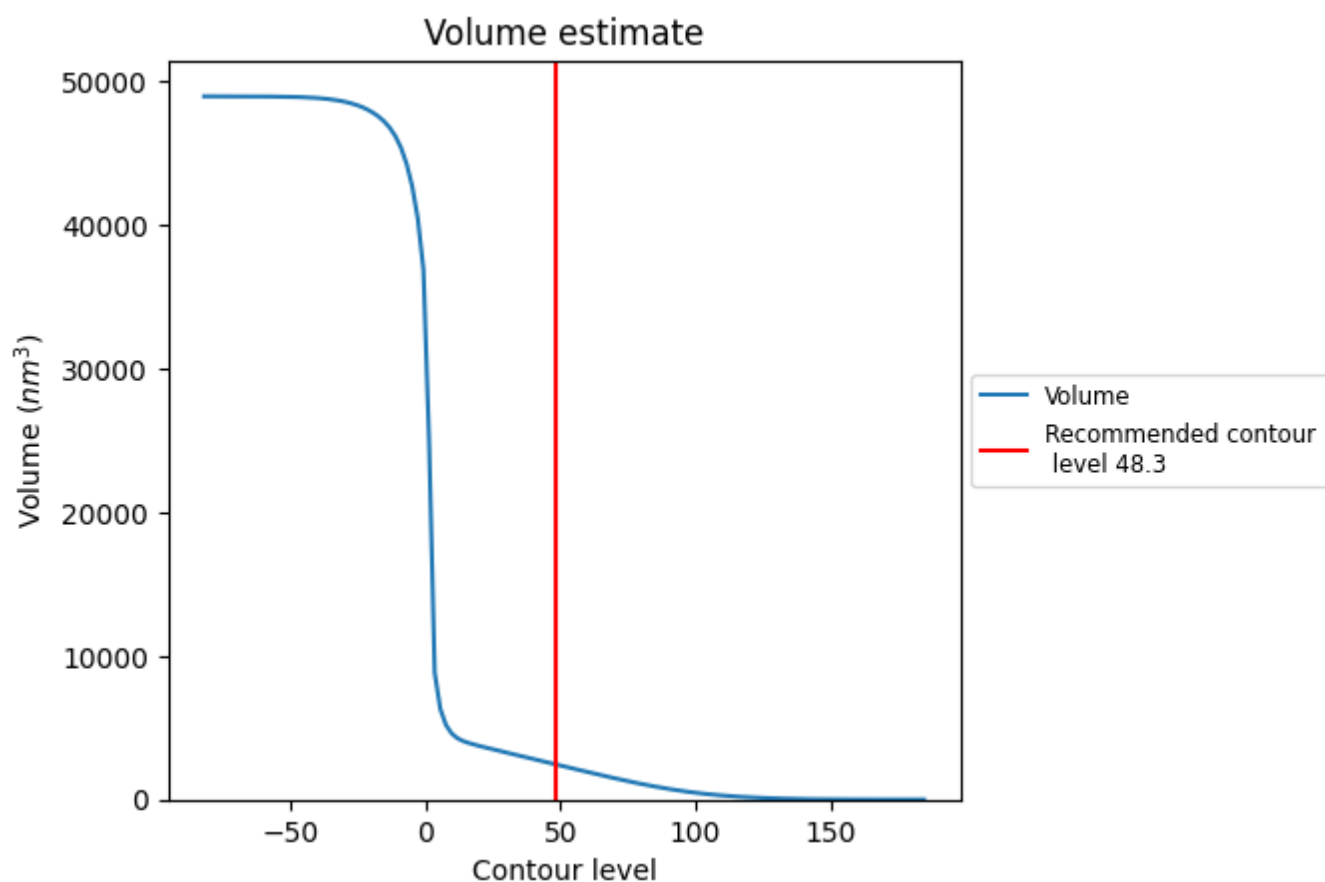
This section contains the results of statistical analysis of the map.

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.

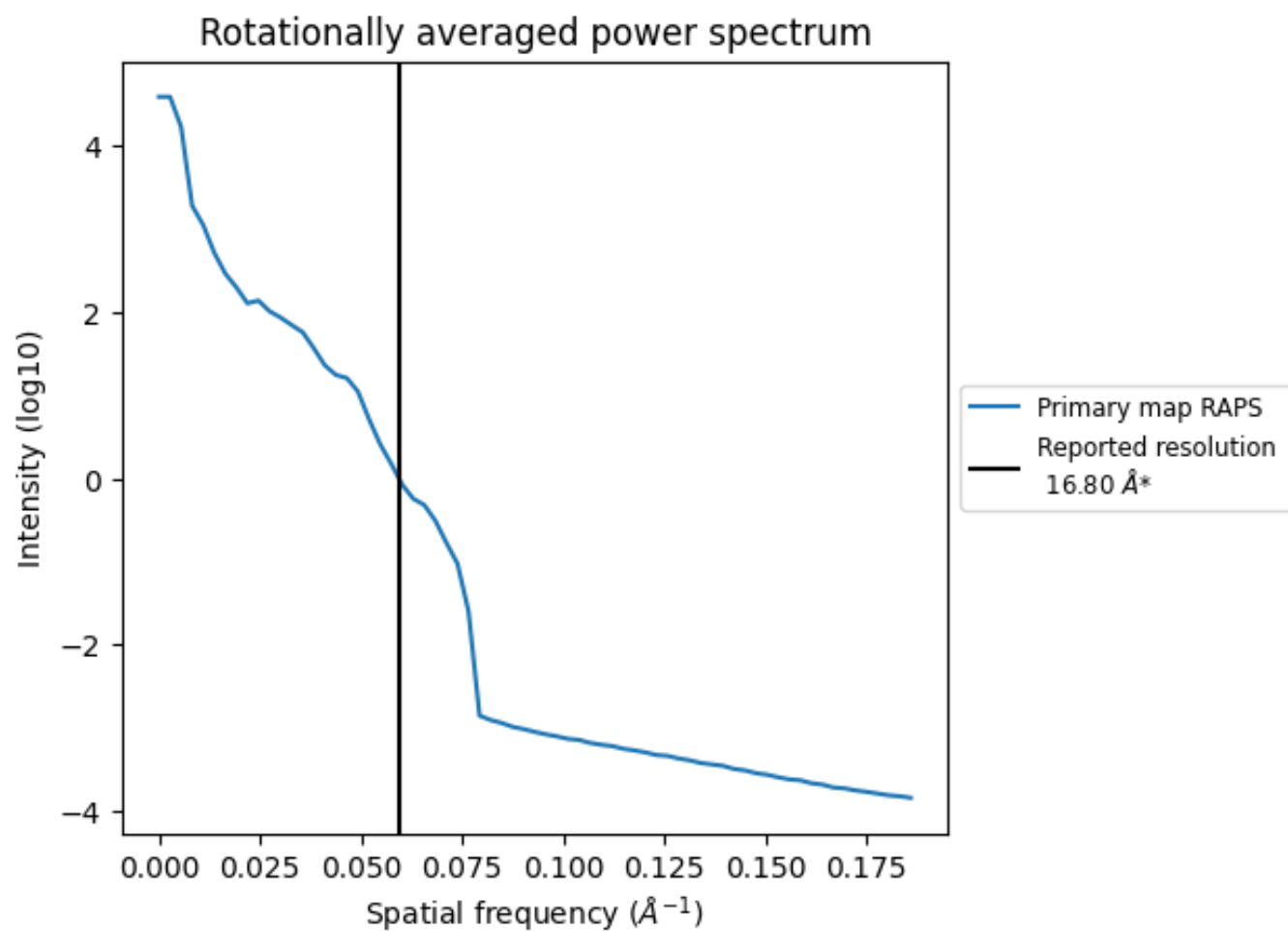
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2446 nm³; this corresponds to an approximate mass of 2210 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 0.060 Å⁻¹

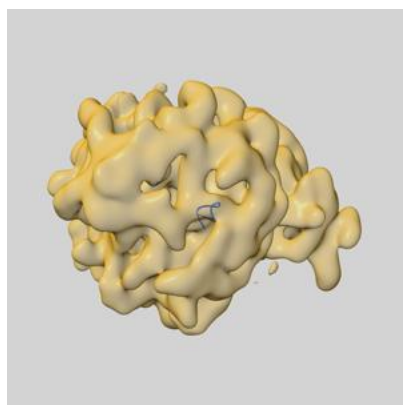
8 Fourier-Shell correlation ⓘ

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

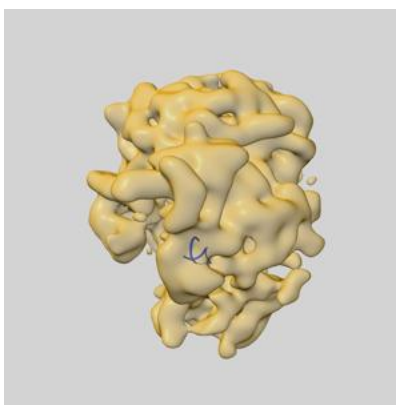
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1045 and PDB model 1LU3. Per-residue inclusion information can be found in section [3](#) on page [4](#).

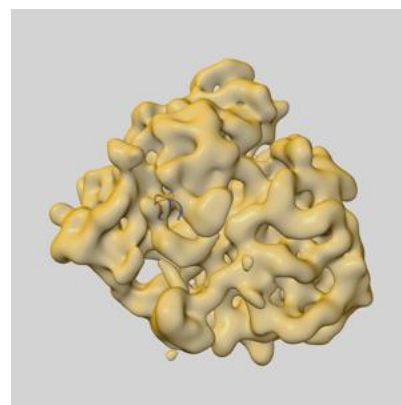
9.1 Map-model overlay [i](#)



X



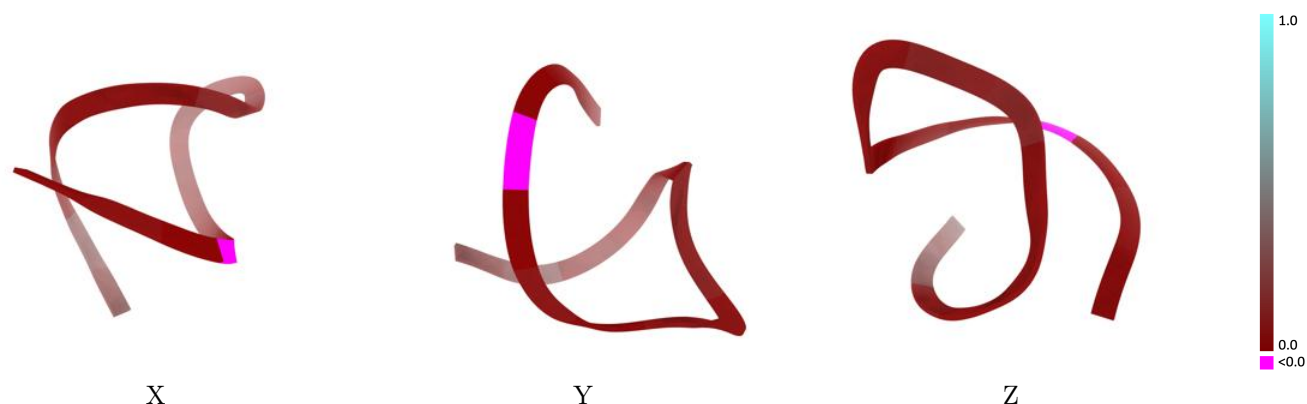
Y



Z

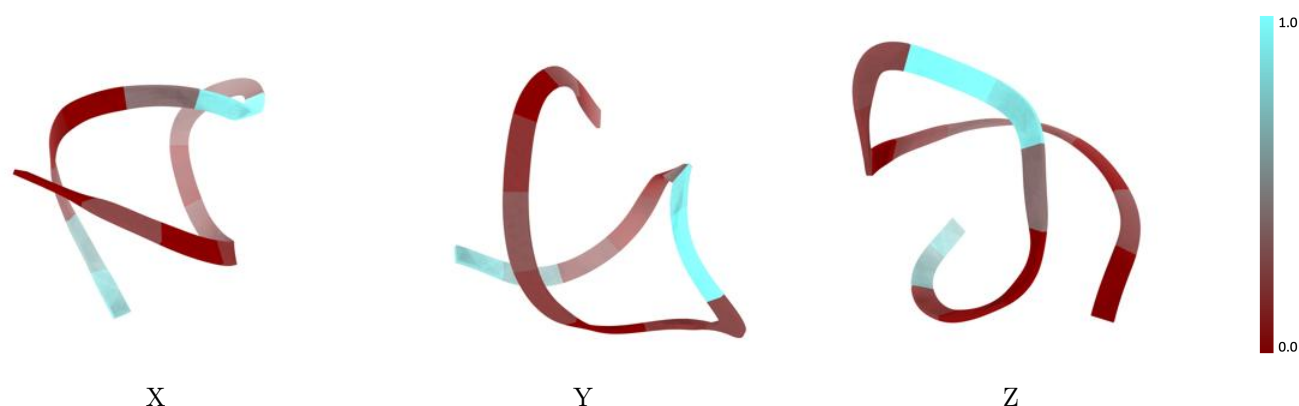
The images above show the 3D surface view of the map at the recommended contour level 48.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



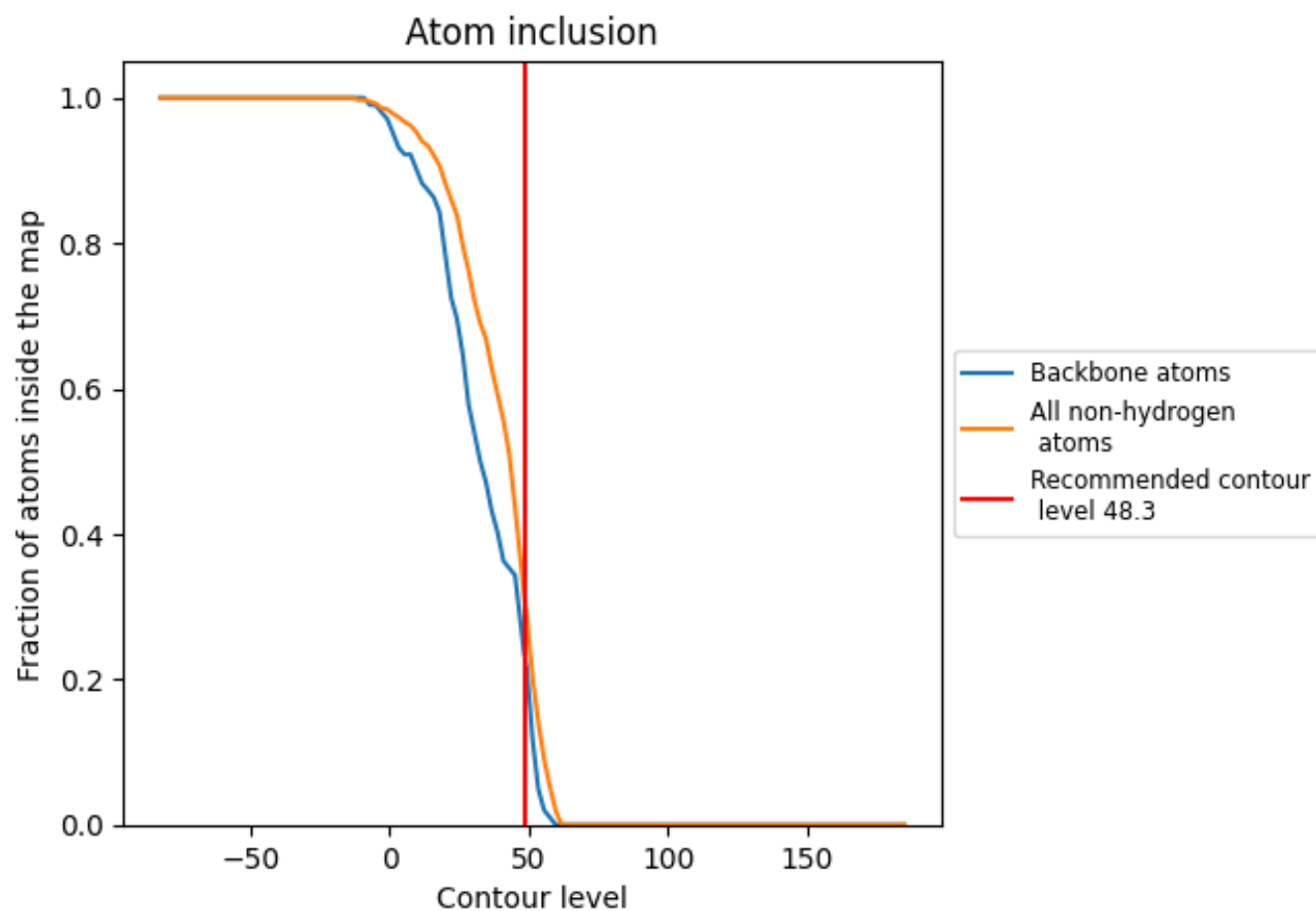
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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 (48.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 24% of all backbone atoms, 32% 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 (48.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3150	0.0880
A	0.3150	0.0880

