



Full wwPDB EM Validation Report ⓘ

Feb 10, 2024 – 08:58 AM EST

PDB ID : 2RDO
EMDB ID : EMD-1430
Title : 50S subunit with EF-G(GDPNP) and RRF bound
Authors : Gao, N.; Zavialov, A.V.; Ehrenberg, M.; Frank, J.
Deposited on : 2007-09-24
Resolution : 9.10 Å(reported)
Based on initial models : 2AW4, 1EK8

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.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

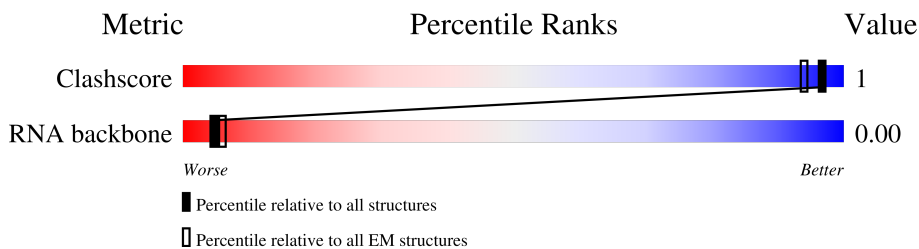
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.10 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	Whole archive (#Entries)	EM structures (#Entries)
Clashescore	158937	4297
RNA backbone	4643	859

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	120	6% (red), 98% (green), . (grey)
2	B	2904	6% (red), 98% (green), . (grey)
3	V	94	7% (red), 100% (green)
4	C	272	8% (red), 97% (green), .. (grey)
5	D	209	14% (red), 100% (green)
6	E	201	9% (red), 100% (green)
7	F	178	. (red), 100% (green)
8	G	176	9% (red), 99% (green), . (grey)
9	J	142	16% (red), 99% (green), . (grey)

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Mol	Chain	Length	Quality of chain
10	K	123	7% 98%
11	L	144	28% 100%
12	M	136	24% 100%
13	N	127	14% 100%
14	O	117	• 100%
15	P	114	6% 100%
16	Q	117	13% 100%
17	R	103	15% 98%
18	S	110	7% 100%
19	T	100	10% 99%
20	U	103	8% 99%
21	W	84	19% 100%
22	X	63	8% 100%
23	Y	58	7% 100%
24	Z	70	• 100%
25	0	56	12% 100%
26	1	54	17% 100%
27	2	46	30% 100%
28	3	64	38% 100%
29	4	38	21% 100%
30	I	141	6% 100%
31	H	149	50% 100%
32	9	233	34% 96%
33	7	704	10% 97%
34	8	185	8% 100%

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 7428 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 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	117	Total P 117 117	0	117

- Molecule 2 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	B	2841	Total P 2841 2841	0	2841

- Molecule 3 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms	AltConf	Trace
3	V	94	Total C 94 94	0	94

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms	AltConf	Trace
4	C	267	Total C 267 267	0	267

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms	AltConf	Trace
5	D	209	Total C 209 209	0	209

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms	AltConf	Trace
6	E	201	Total C 201 201	0	201

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms	AltConf	Trace
7	F	178	Total C 178 178	0	178

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms	AltConf	Trace
8	G	176	Total C 176 176	0	176

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

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

- Molecule 11 is a protein called 50S ribosomal protein L15.

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

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms	AltConf	Trace
12	M	136	Total C 136 136	0	136

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms	AltConf	Trace
13	N	127	Total C 127 127	0	127

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms	AltConf	Trace
14	O	117	Total C 117 117	0	117

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms	AltConf	Trace
15	P	114	Total C 114 114	0	114

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms	AltConf	Trace
18	S	110	Total C 110 110	0	110

- Molecule 19 is a protein called 50S ribosomal protein L23.

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

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms	AltConf	Trace
20	U	102	Total C 102 102	0	102

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms	AltConf	Trace
21	W	84	Total C 84 84	0	84

- Molecule 22 is a protein called 50S ribosomal protein L29.

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

- Molecule 23 is a protein called 50S ribosomal protein L30.

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

- Molecule 24 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms	AltConf	Trace
24	Z	70	Total C 70 70	0	70

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms	AltConf	Trace
25	0	56	Total C 56 56	0	56

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms	AltConf	Trace
26	1	54	Total C 54 54	0	54

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms	AltConf	Trace
27	2	46	Total C 46 46	0	46

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms	AltConf	Trace
28	3	64	Total C 64 64	0	64

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms	AltConf	Trace
29	4	38	Total C 38 38	0	38

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms	AltConf	Trace
30	I	141	Total C 141 141	0	141

- Molecule 31 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms	AltConf	Trace
31	H	149	Total C 149 149	0	149

- Molecule 32 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms	AltConf	Trace
32	9	223	Total C 223 223	0	223

- Molecule 33 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms	AltConf	Trace
33	7	684	Total C 684 684	0	684

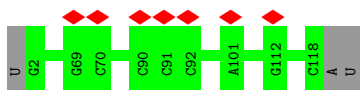
- Molecule 34 is a protein called Ribosome recycling factor.

Mol	Chain	Residues	Atoms	AltConf	Trace
34	8	185	Total C 185 185	0	185

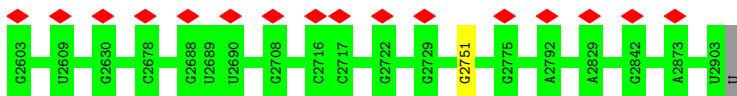
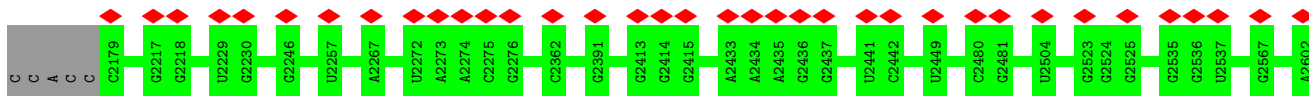
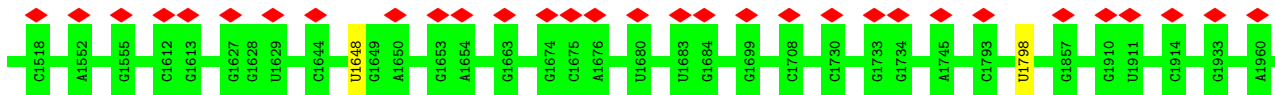
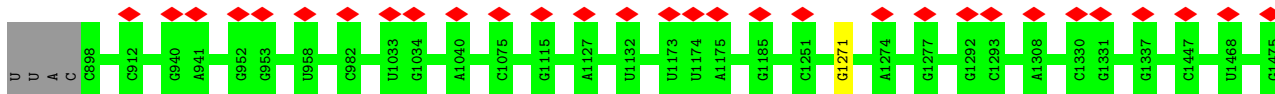
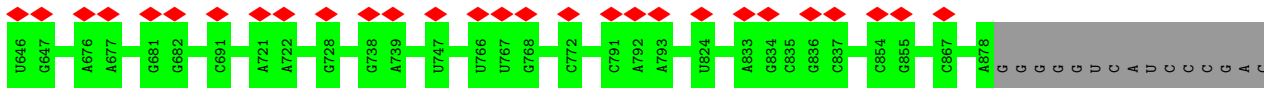
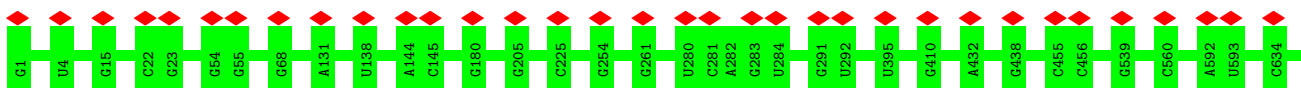
3 Residue-property plots [i](#)

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.

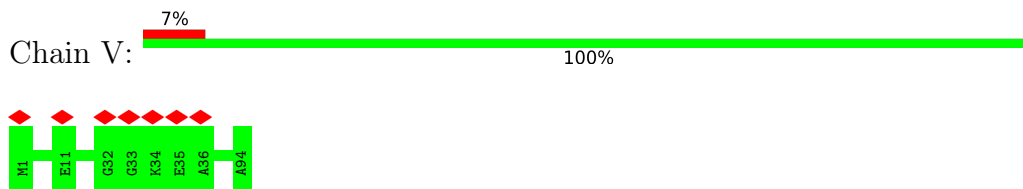
- Molecule 1: 5S RIBOSOMAL RNA



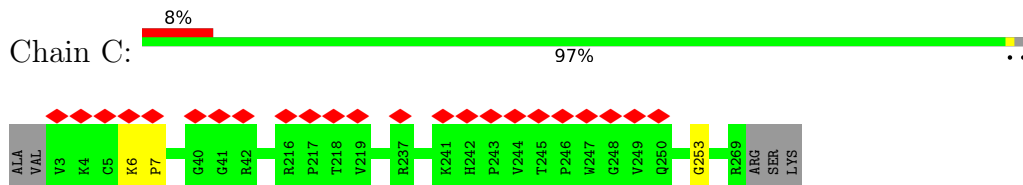
- Molecule 2: 23S RIBOSOMAL RNA



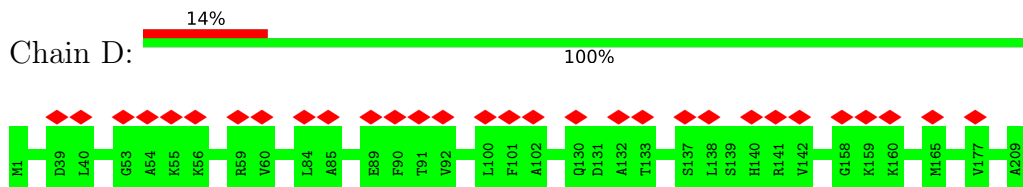
- Molecule 3: 50S ribosomal protein L25



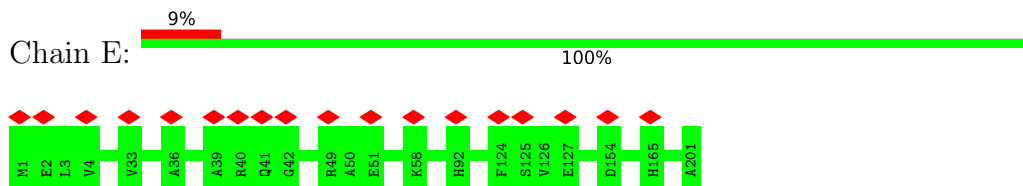
- Molecule 4: 50S ribosomal protein L2



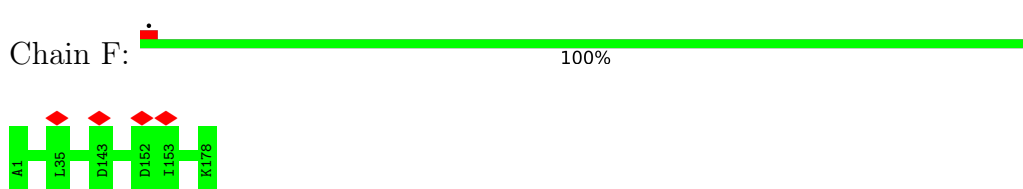
- Molecule 5: 50S ribosomal protein L3



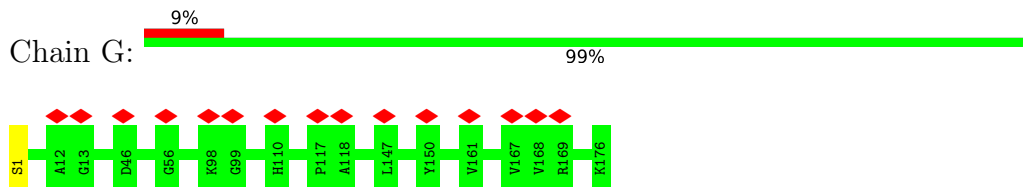
- Molecule 6: 50S ribosomal protein L4



- Molecule 7: 50S ribosomal protein L5

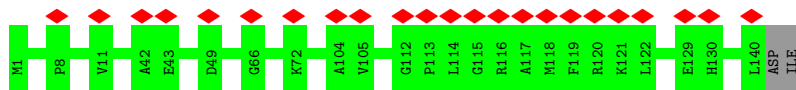


- Molecule 8: 50S ribosomal protein L6

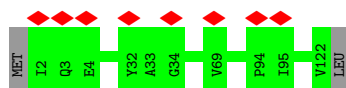


- Molecule 9: 50S ribosomal protein L13

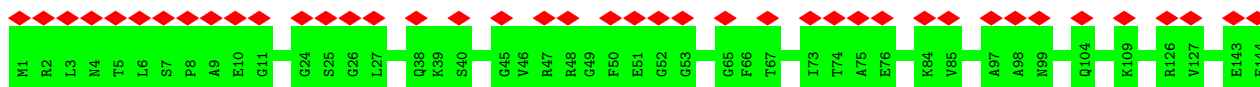




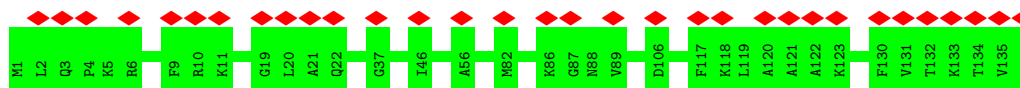
- Molecule 10: 50S ribosomal protein L14



- Molecule 11: 50S ribosomal protein L15



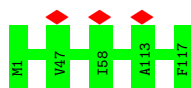
- Molecule 12: 50S ribosomal protein L16



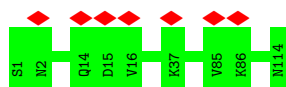
- Molecule 13: 50S ribosomal protein L17



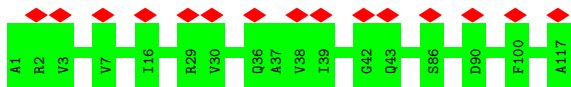
- Molecule 14: 50S ribosomal protein L18



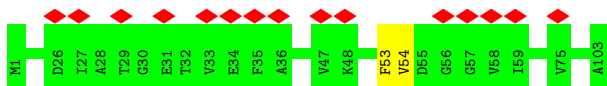
- Molecule 15: 50S ribosomal protein L19



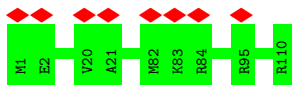
- Molecule 16: 50S ribosomal protein L20



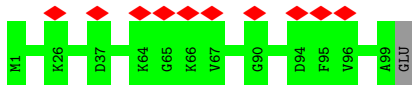
- Molecule 17: 50S ribosomal protein L21



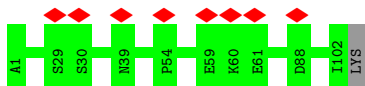
- Molecule 18: 50S ribosomal protein L22



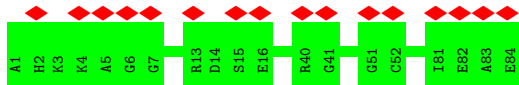
- Molecule 19: 50S ribosomal protein L23



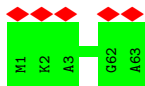
- Molecule 20: 50S ribosomal protein L24



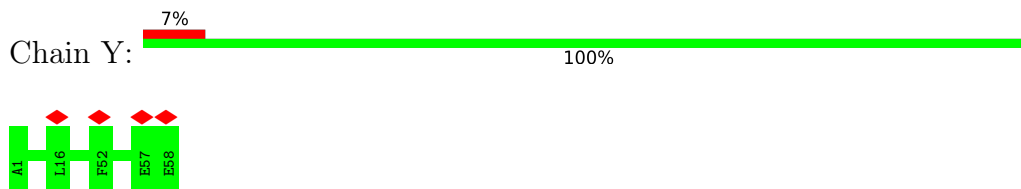
- Molecule 21: 50S ribosomal protein L27



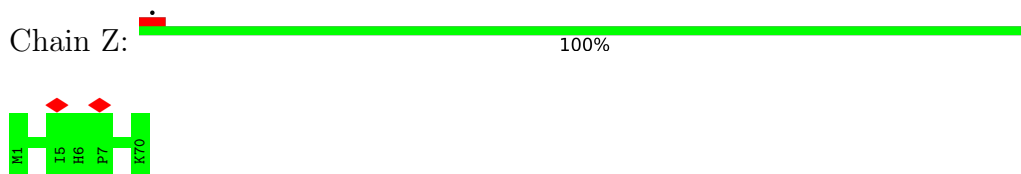
- Molecule 22: 50S ribosomal protein L29



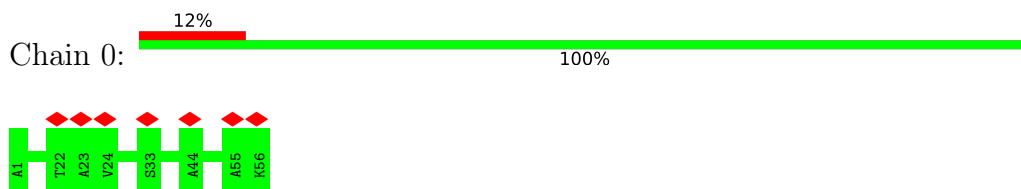
- Molecule 23: 50S ribosomal protein L30



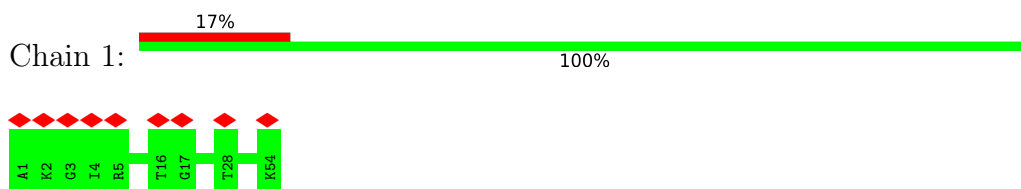
- Molecule 24: 50S ribosomal protein L31



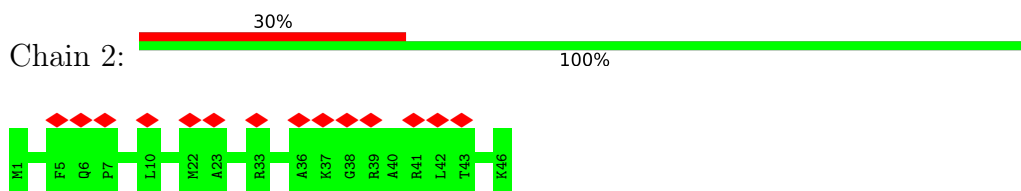
- Molecule 25: 50S ribosomal protein L32



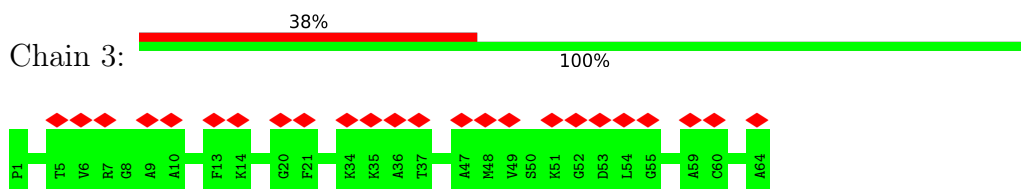
- Molecule 26: 50S ribosomal protein L33



- Molecule 27: 50S ribosomal protein L34

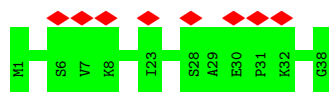


- Molecule 28: 50S ribosomal protein L35

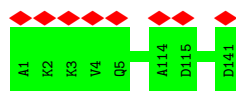


- Molecule 29: 50S ribosomal protein L36

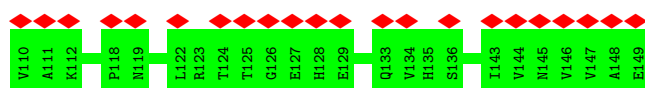
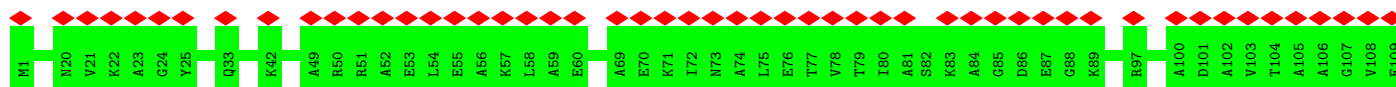




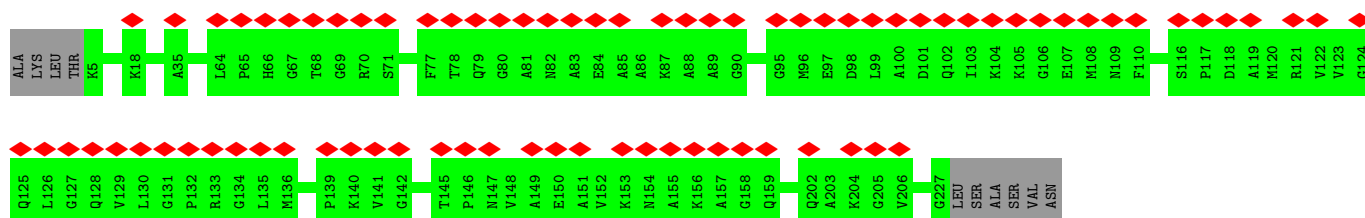
- Molecule 30: 50S ribosomal protein L11



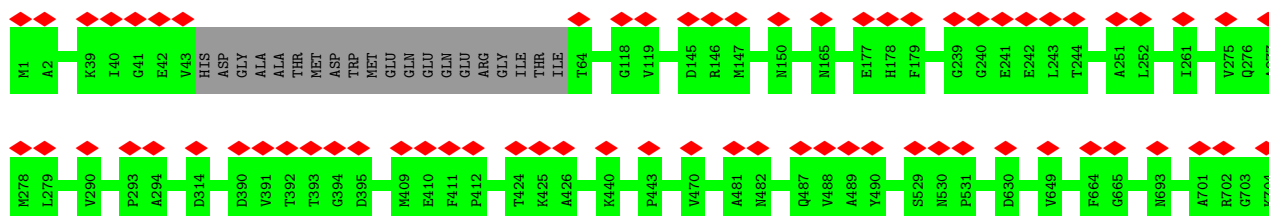
- Molecule 31: 50S ribosomal protein L9



- Molecule 32: 50S ribosomal protein L1



- Molecule 33: Elongation factor G



- Molecule 34: Ribosome recycling factor





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	113355	Depositor
Resolution determination method	Not provided	
CTF correction method	CTF correction of 3D maps by Wiener filtration	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	4900	Depositor
Magnification	49700	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	310.662	Depositor
Minimum map value	-81.829	Depositor
Average map value	5.655	Depositor
Map value standard deviation	24.204	Depositor
Recommended contour level	48.9	Depositor
Map size (\AA)	366.6, 366.6, 366.6	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	2.82, 2.82, 2.82	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

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	117	0	0	0	0
2	B	2841	0	0	3	0
3	V	94	0	0	0	0
4	C	267	0	0	2	0
5	D	209	0	0	0	0
6	E	201	0	0	0	0
7	F	178	0	0	0	0
8	G	176	0	0	1	0
9	J	140	0	0	0	0
10	K	121	0	0	0	0
11	L	144	0	0	0	0
12	M	136	0	0	0	0
13	N	127	0	0	0	0
14	O	117	0	0	0	0
15	P	114	0	0	0	0
16	Q	117	0	0	0	0
17	R	103	0	0	1	0
18	S	110	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	T	99	0	0	0	0
20	U	102	0	0	0	0
21	W	84	0	0	0	0
22	X	63	0	0	0	0
23	Y	58	0	0	0	0
24	Z	70	0	0	0	0
25	0	56	0	0	0	0
26	1	54	0	0	0	0
27	2	46	0	0	0	0
28	3	64	0	0	0	0
29	4	38	0	0	0	0
30	I	141	0	0	0	0
31	H	149	0	0	0	0
32	9	223	0	0	0	0
33	7	684	0	0	0	0
34	8	185	0	0	0	0
All	All	7428	0	0	5	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 1.

All (5) 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)
2:B:1798:U:P	4:C:253:GLY:CA	2.73	0.76
2:B:1271:G:P	2:B:1648:U:P	2.90	0.70
4:C:6:LYS:CA	4:C:7:PRO:CA	2.86	0.53
2:B:2751:G:P	8:G:1:SER:CA	3.03	0.47
17:R:53:PHE:CA	17:R:54:VAL:CA	2.96	0.43

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	0/120	-	-
2	B	0/2904	-	-
All	All	0/3024	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

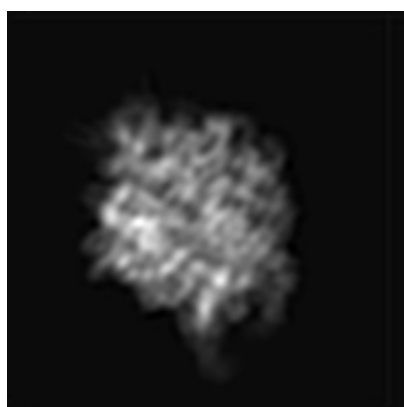
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1430. These allow visual inspection of the internal detail of the map and identification of artifacts.

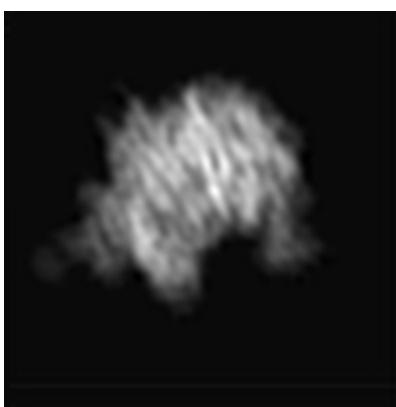
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

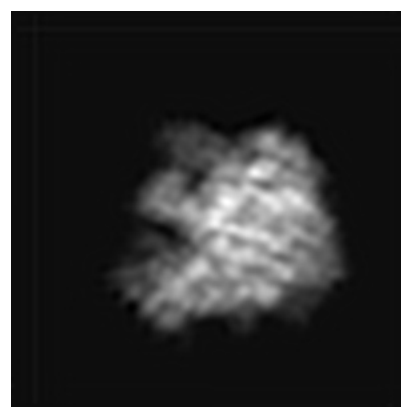
6.1.1 Primary map



X



Y

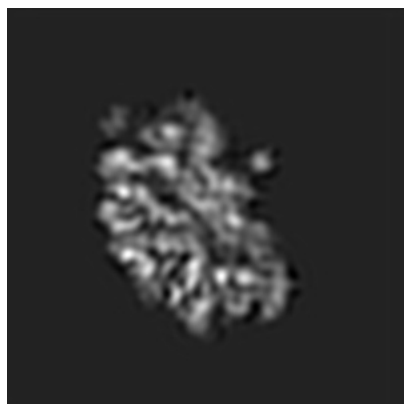


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 65



Y Index: 65



Z Index: 65

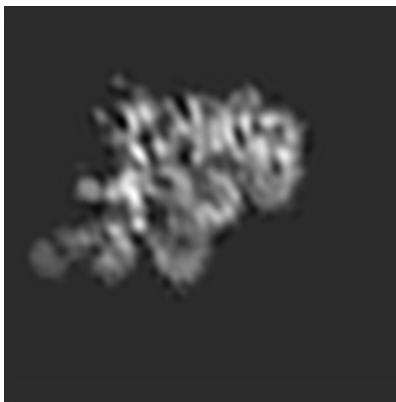
The images above show central slices of the map in three orthogonal directions.

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

6.3.1 Primary map



X Index: 82



Y Index: 68



Z Index: 61

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

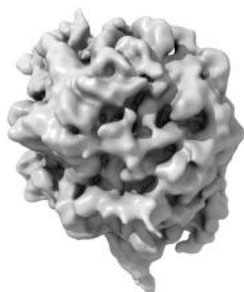


Z

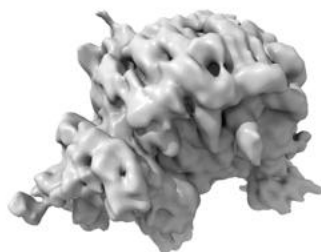
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

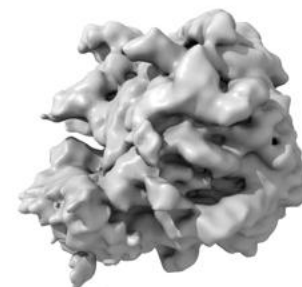
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 48.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

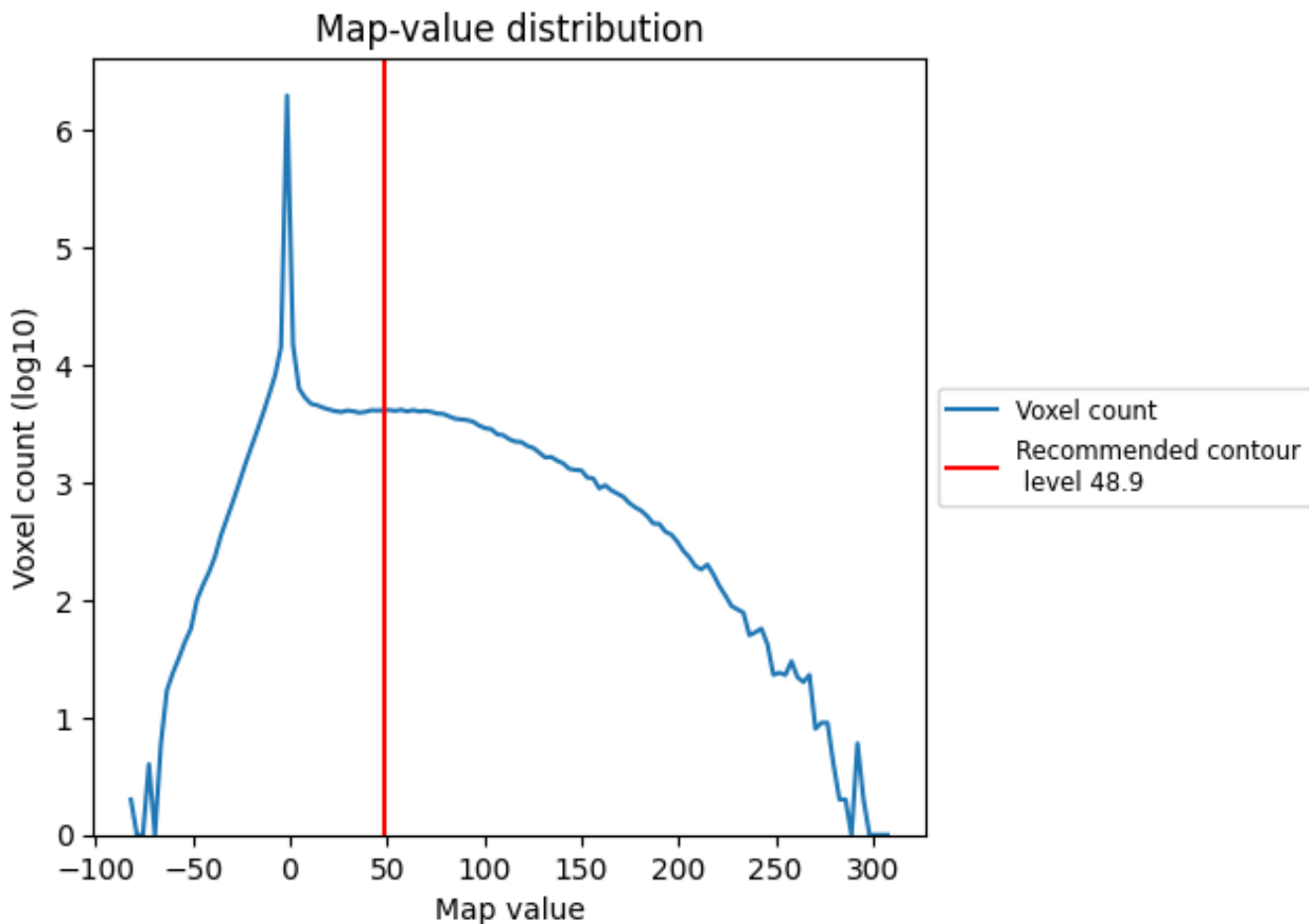
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

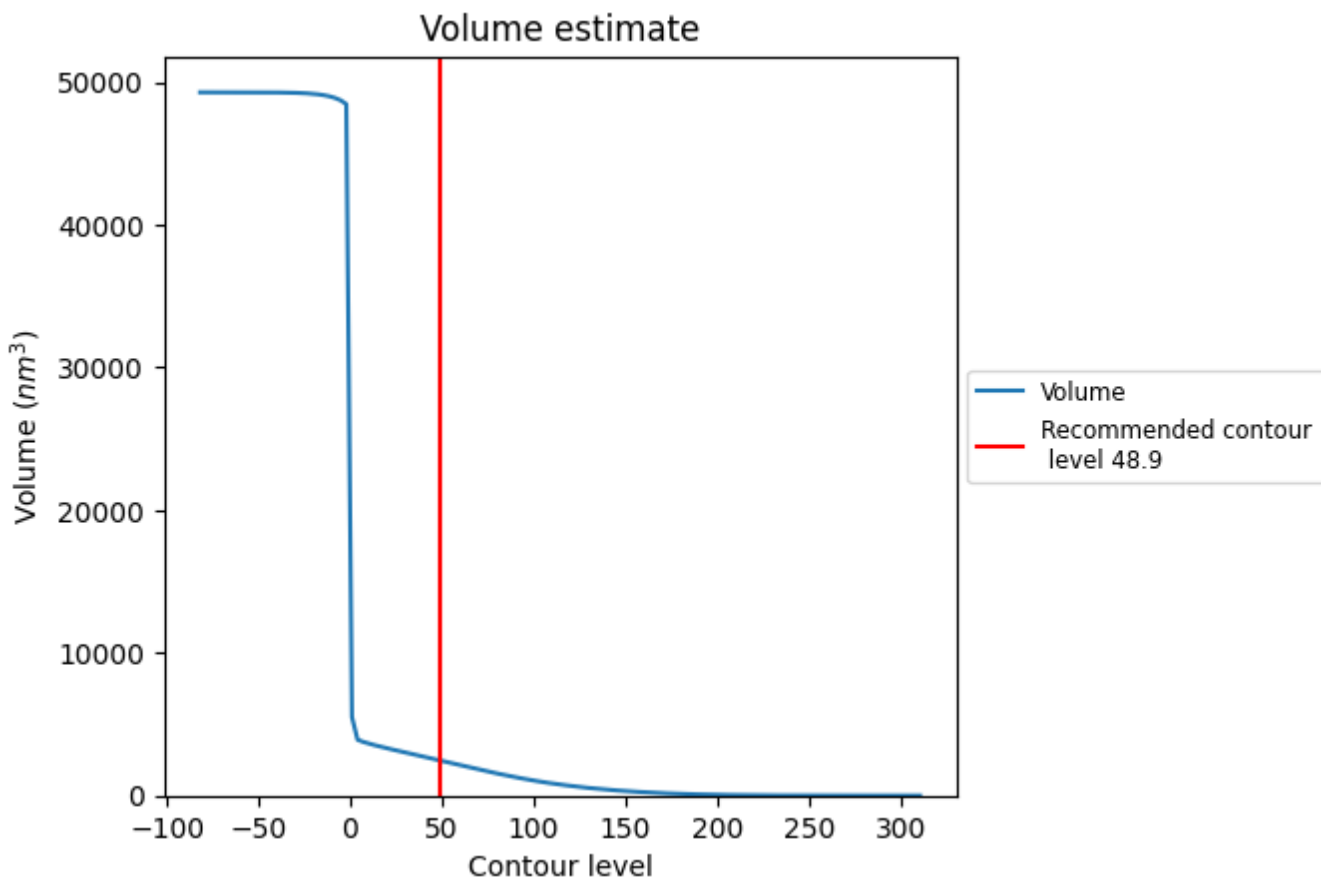
This section contains the results of statistical analysis of the map.

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.

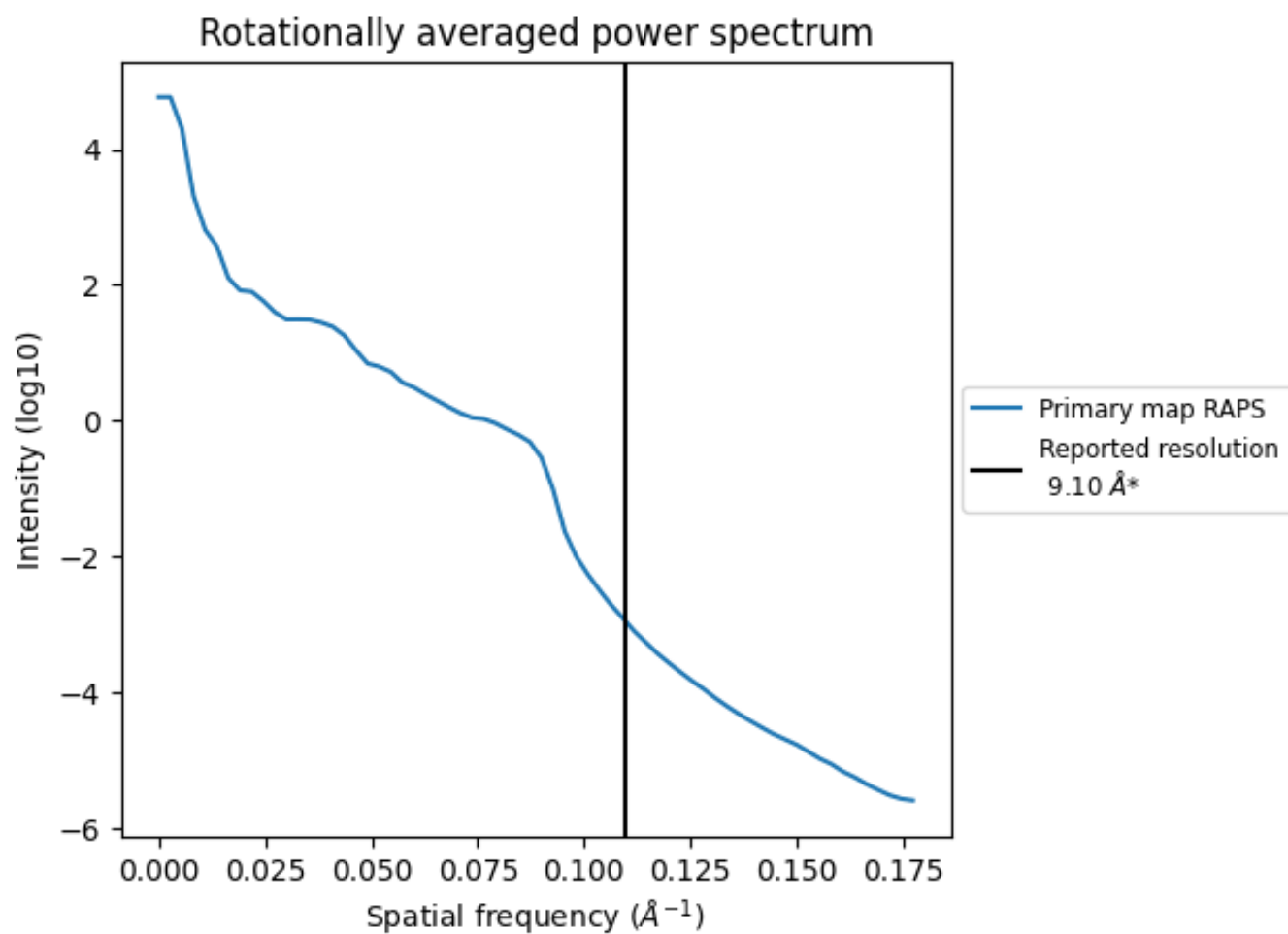
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2466 nm³; this corresponds to an approximate mass of 2227 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.110 Å⁻¹

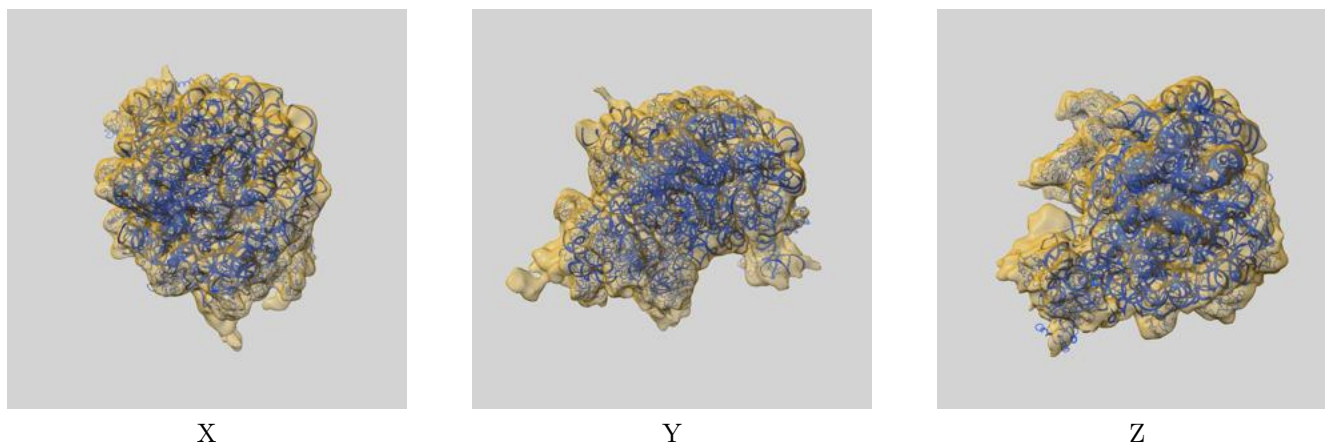
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

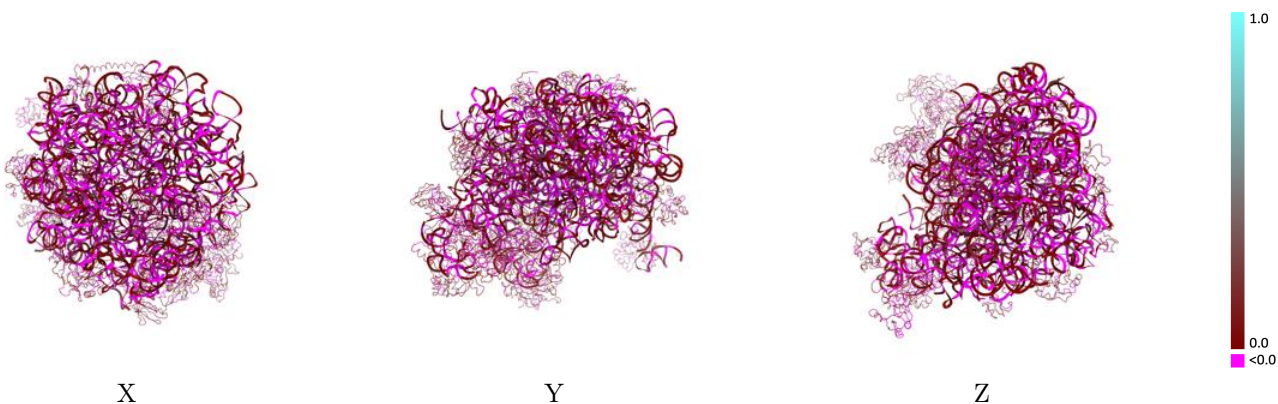
This section contains information regarding the fit between EMDB map EMD-1430 and PDB model 2RDO. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



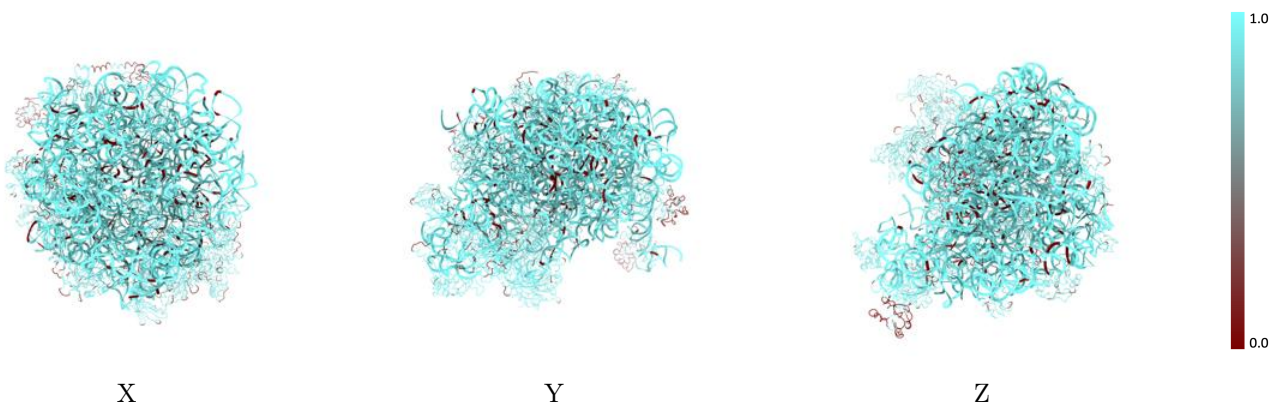
The images above show the 3D surface view of the map at the recommended contour level 48.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



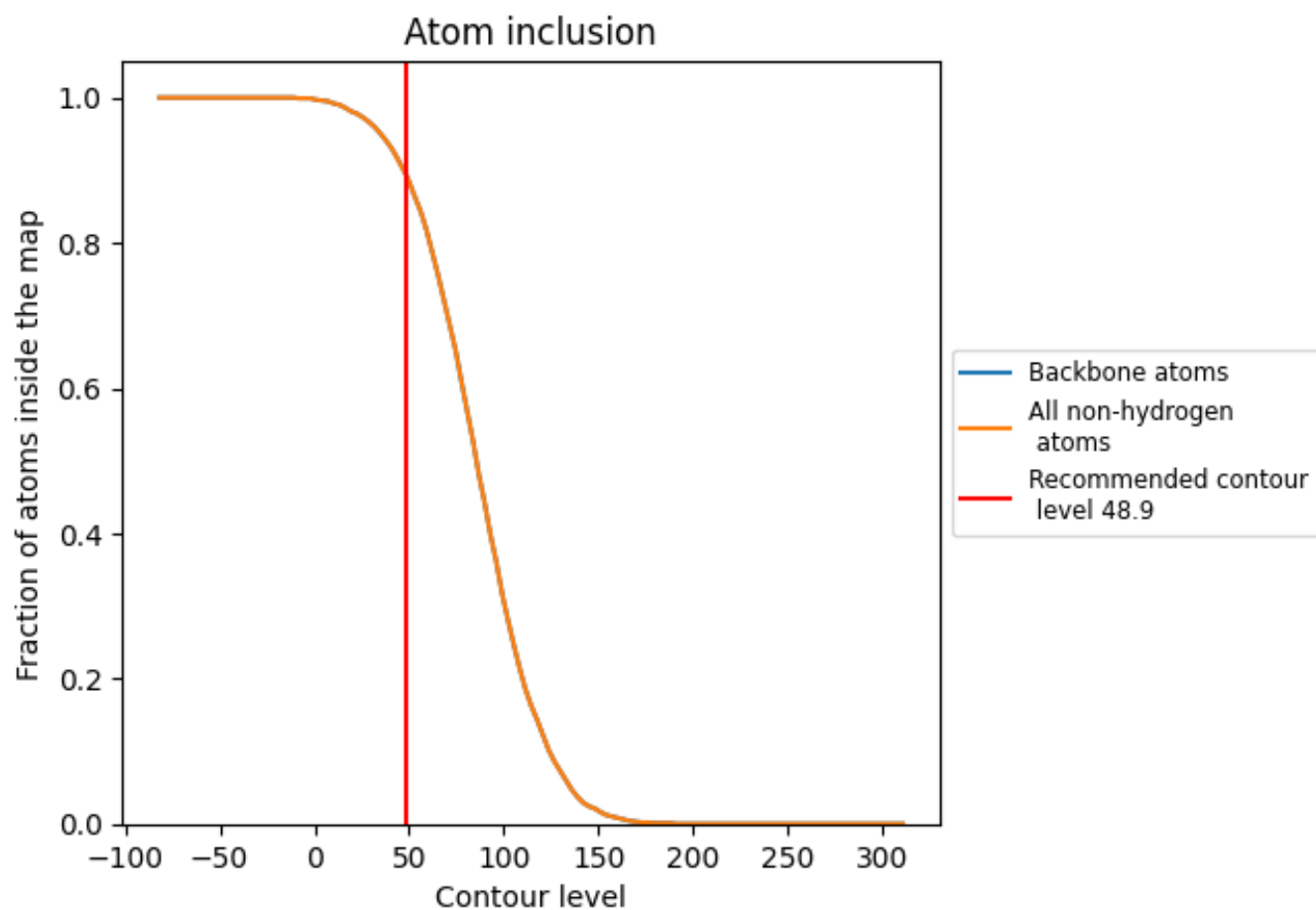
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (48.9).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 89% 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 (48.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.0390
0	 0.8750	 -0.0010
1	 0.8330	 0.0730
2	 0.6960	 0.0410
3	 0.6250	 -0.0400
4	 0.7890	 0.0610
7	 0.9010	 0.0620
8	 0.9190	 0.0690
9	 0.6460	 0.0200
A	 0.9400	 0.0110
B	 0.9340	 0.0140
C	 0.9140	 0.0510
D	 0.8570	 0.0390
E	 0.9100	 0.0360
F	 0.9780	 0.0780
G	 0.9150	 0.0730
H	 0.5030	 0.0480
I	 0.9430	 0.0830
J	 0.8360	 0.0450
K	 0.9340	 0.0810
L	 0.7150	 0.0210
M	 0.7650	 0.0410
N	 0.8580	 0.0540
O	 0.9740	 0.0750
P	 0.9390	 0.1060
Q	 0.8720	 0.0420
R	 0.8540	 0.0560
S	 0.9270	 0.0710
T	 0.8990	 0.0920
U	 0.9220	 0.0670
V	 0.9250	 0.0980
W	 0.8090	 0.0170
X	 0.9210	 0.0800
Y	 0.9310	 0.0430
Z	 0.9710	 0.0770

