



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 04:18 PM EST

PDB ID : 1EG0
EMDB ID : EMD-1003
Title : FITTING OF COMPONENTS WITH KNOWN STRUCTURE INTO AN
11.5 Å CRYO-EM MAP OF THE E.COLI 70S RIBOSOME
Authors : Gabashvili, I.S.; Agrawal, R.K.; Spahn, C.M.T.; Grassucci, R.A.; Svergun,
D.I.; Frank, J.; Penczek, P.
Deposited on : 2000-02-11
Resolution : 11.50 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.dev43
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) : 2.31.3

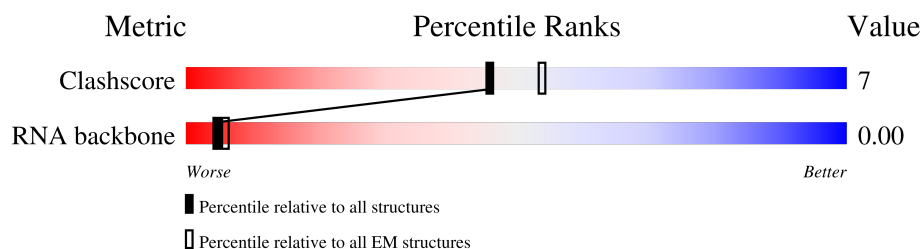
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

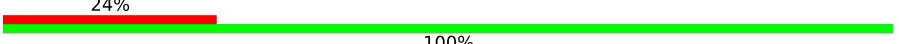
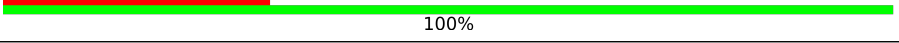
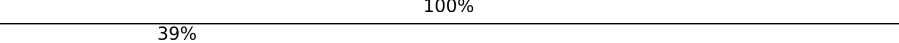

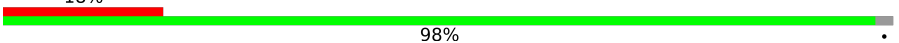
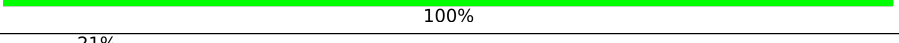
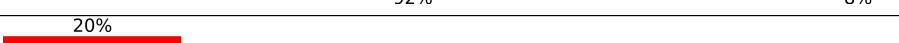


The reported resolution of this entry is 11.50 Å.

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)
Clashscore	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	I	33	 24% 100%
2	L	57	 30% 100%
3	M	26	 100%
4	O	76	 39% 100%
5	A	159	 23% 100%
6	B	148	 18% 98% .
7	C	97	 21% 100%
8	D	146	 21% 92% 8%
9	E	138	 20% 98% ..

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Mol	Chain	Length	Quality of chain
10	F	89	
11	G	93	
12	H	100	
13	N	229	
14	J	171	
15	K	140	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 1658 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 FRAGMENT OF 16S RRNA HELIX 23.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	I	33	Total	P	0	33
			33	33		

- Molecule 2 is a RNA chain called FRAGMENT OF 23S RRNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
2	L	57	Total	P	0	57
			57	57		

- Molecule 3 is a RNA chain called HELIX 95 OF 23S RRNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	M	26	Total	P	0	26
			26	26		

- Molecule 4 is a RNA chain called FORMYL-METHIONYL-TRNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	O	76	Total	P	0	76
			76	76		

- Molecule 5 is a protein called PROTEIN (S4 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
5	A	159	Total	C	0	159
			159	159		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	ARG	EXPRESSION TAG	UNP P81288

- Molecule 6 is a protein called PROTEIN (S5 RIBOSOMAL PROTEIN).

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

- Molecule 7 is a protein called PROTEIN (S6 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
7	C	97	Total 97	C 97	0	97

- Molecule 8 is a protein called PROTEIN (S7 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
8	D	135	Total 135	C 135	0	135

- Molecule 9 is a protein called PROTEIN (S8 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
9	E	136	Total 136	C 136	0	136

- Molecule 10 is a protein called PROTEIN (S15 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
10	F	88	Total 88	C 88	0	88

- Molecule 11 is a protein called PROTEIN (S17 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
11	G	89	Total 89	C 89	0	89

- Molecule 12 is a protein called PROTEIN (S20 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
12	H	100	Total 100	C 100	0	100

- Molecule 13 is a protein called PROTEIN (RIBOSOMAL PROTEIN L1).

Mol	Chain	Residues	Atoms		AltConf	Trace
13	N	220	Total 220	C 220	0	220

- Molecule 14 is a protein called PROTEIN (RIBOSOMAL PROTEIN L6).

Mol	Chain	Residues	Atoms		AltConf	Trace
14	J	164	Total 164	C 164	0	164

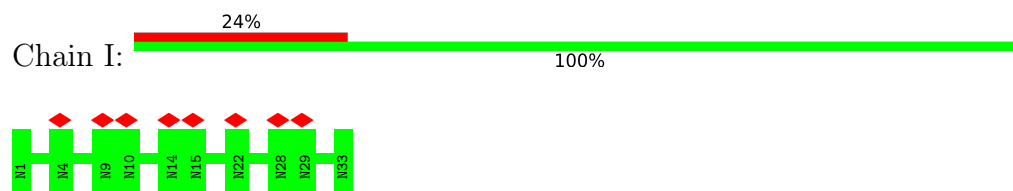
- Molecule 15 is a protein called PROTEIN (RIBOSOMAL PROTEIN L11).

Mol	Chain	Residues	Atoms		AltConf	Trace
15	K	133	Total 133	C 133	0	133

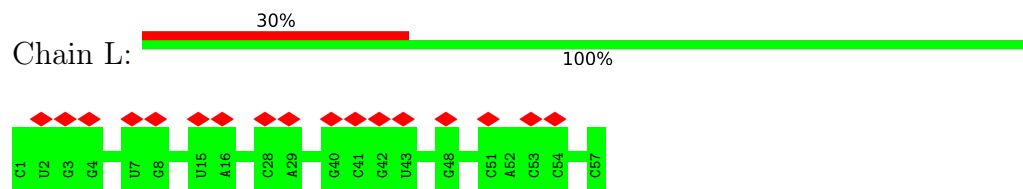
3 Residue-property plots

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.

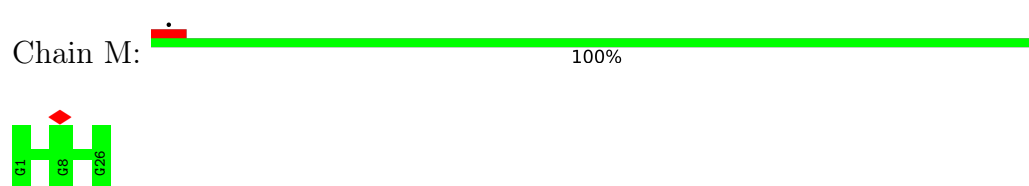
- Molecule 1: FRAGMENT OF 16S RRNA HELIX 23



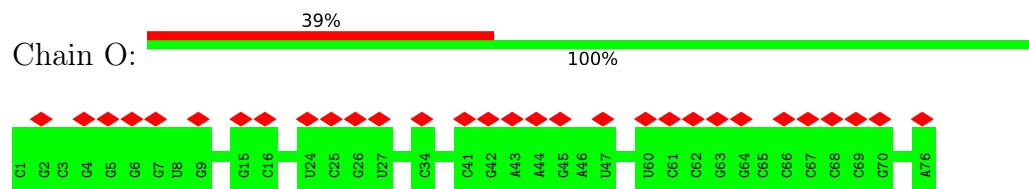
- Molecule 2: FRAGMENT OF 23S RRNA



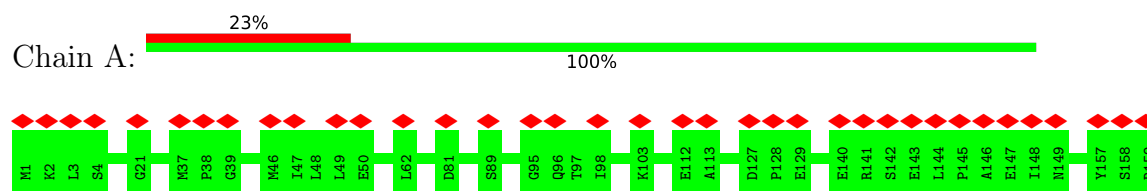
- Molecule 3: HELIX 95 OF 23S RRNA



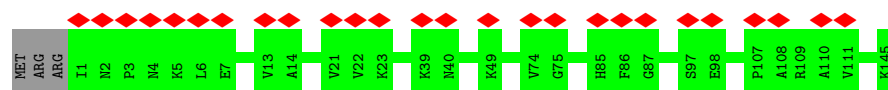
- Molecule 4: FORMYL-METHIONYL-TRNA



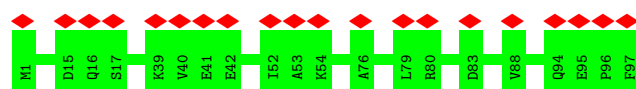
- Molecule 5: PROTEIN (S4 RIBOSOMAL PROTEIN)



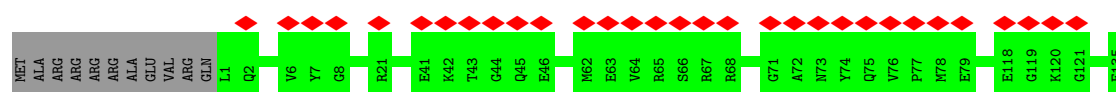
- Molecule 6: PROTEIN (S5 RIBOSOMAL PROTEIN)



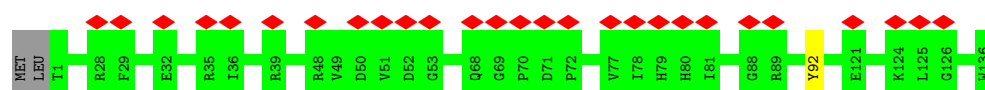
- Molecule 7: PROTEIN (S6 RIBOSOMAL PROTEIN)



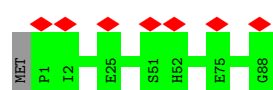
- Molecule 8: PROTEIN (S7 RIBOSOMAL PROTEIN)



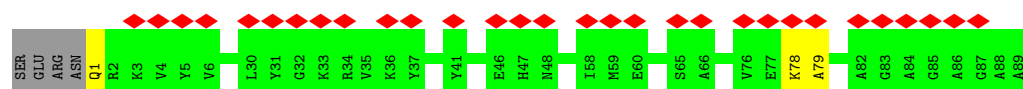
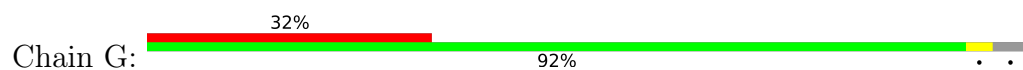
- Molecule 9: PROTEIN (S8 RIBOSOMAL PROTEIN)



- Molecule 10: PROTEIN (S15 RIBOSOMAL PROTEIN)

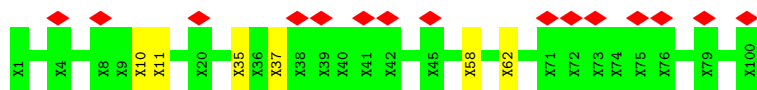


- Molecule 11: PROTEIN (S17 RIBOSOMAL PROTEIN)

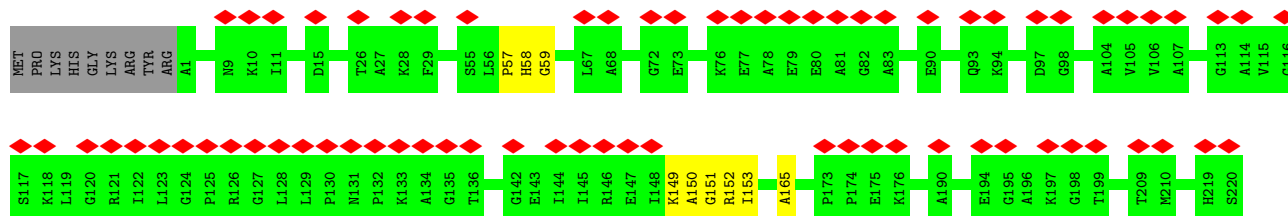


- Molecule 12: PROTEIN (S20 RIBOSOMAL PROTEIN)

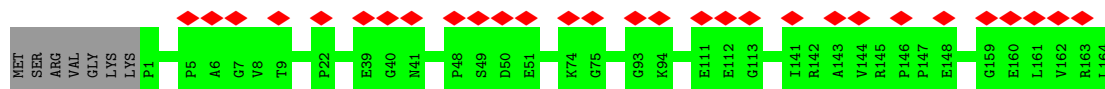




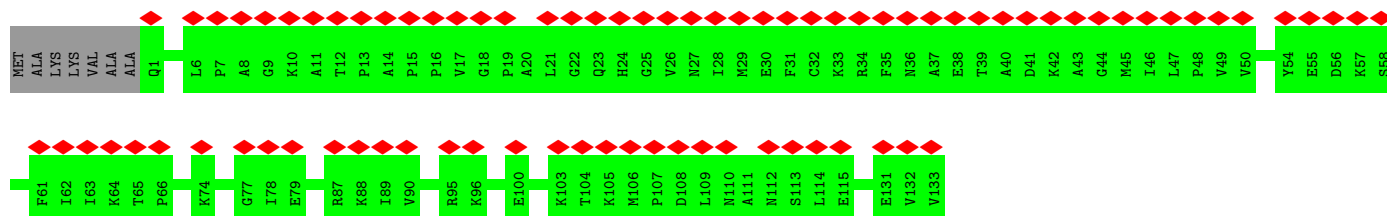
• Molecule 13: PROTEIN (RIBOSOMAL PROTEIN L1)



• Molecule 14: PROTEIN (RIBOSOMAL PROTEIN L6)



• Molecule 15: PROTEIN (RIBOSOMAL PROTEIN L11)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	73523	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI/PHILIPS CM200FEG/ST	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	730.	Depositor
Maximum defocus (nm)	4340.	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	339.987	Depositor
Minimum map value	-141.975	Depositor
Average map value	1.856	Depositor
Map value standard deviation	38.047	Depositor
Recommended contour level	82.8	Depositor
Map size (\AA)	366.25, 366.25, 366.25	wwPDB
Map dimensions	125, 125, 125	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	2.93, 2.93, 2.93	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: OMC, 4SU, PSU, H2U, 5MU

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	I	33	0	0	0	0
2	L	57	0	0	0	0
3	M	26	0	0	0	0
4	O	76	0	0	0	0
5	A	159	0	0	0	0
6	B	145	0	0	0	0
7	C	97	0	0	0	0
8	D	135	0	0	0	0
9	E	136	0	0	1	0
10	F	88	0	0	0	0
11	G	89	0	0	2	0
12	H	100	0	0	3	0
13	N	220	0	0	6	0
14	J	164	0	0	0	0
15	K	133	0	0	0	0
All	All	1658	0	0	11	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 7.

The worst 5 of 11 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)
13:N:152:ARG:CA	13:N:153:ILE:CA	1.94	1.46
13:N:150:ALA:CA	13:N:165:ALA:CA	2.46	0.92
9:E:92:TYR:CA	11:G:1:GLN:CA	2.48	0.92
11:G:78:LYS:CA	11:G:79:ALA:CA	2.50	0.89
13:N:149:LYS:CA	13:N:151:GLY:CA	2.53	0.87

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	I	0/33	-	-
2	L	0/57	-	-
3	M	0/26	-	-
4	O	0/76	-	-
All	All	0/192	-	-

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](#)

Of 5 non-standard protein/DNA/RNA residues modelled in this entry, 5 are modelled with single atom - 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.

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.

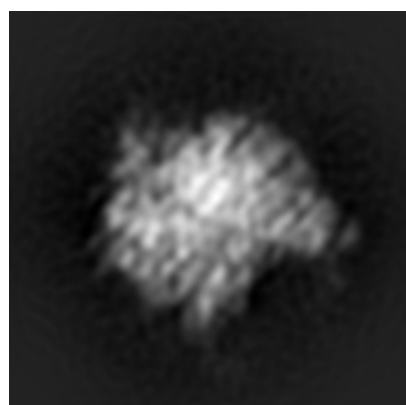
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1003. These allow visual inspection of the internal detail of the map and identification of artifacts.

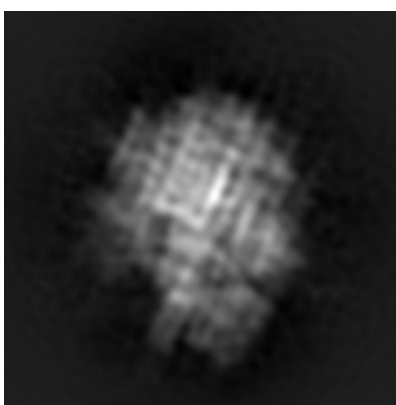
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

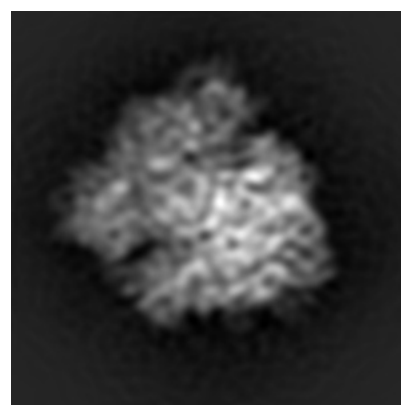
6.1.1 Primary map



X



Y

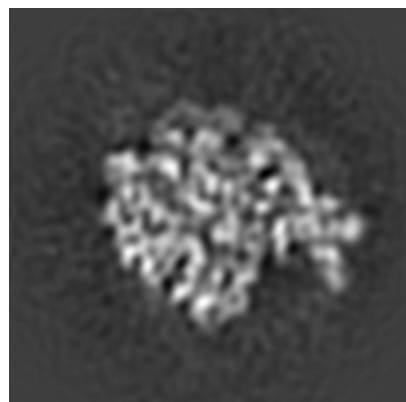


Z

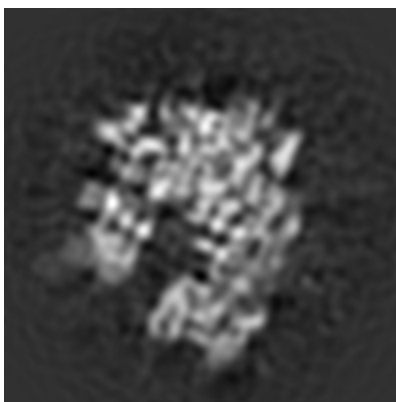
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

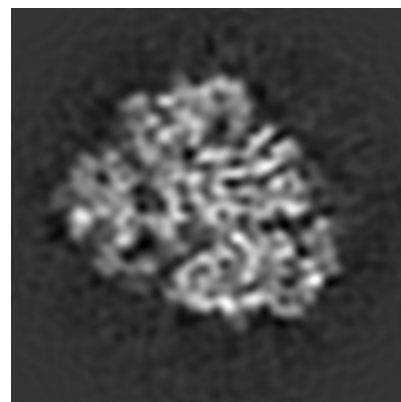
6.2.1 Primary map



X Index: 62



Y Index: 62

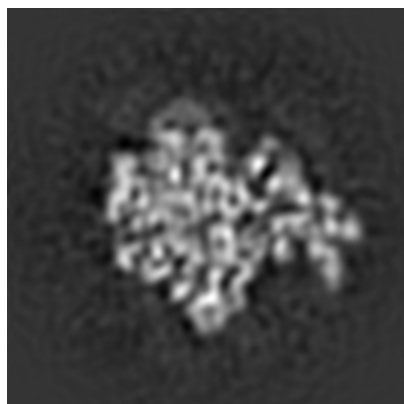


Z Index: 62

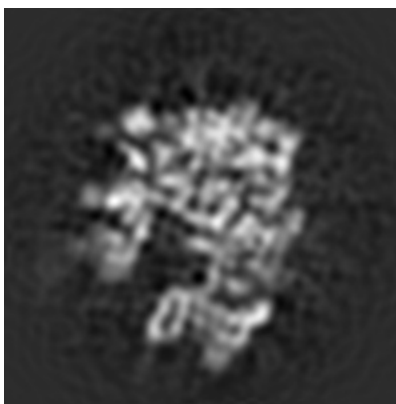
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

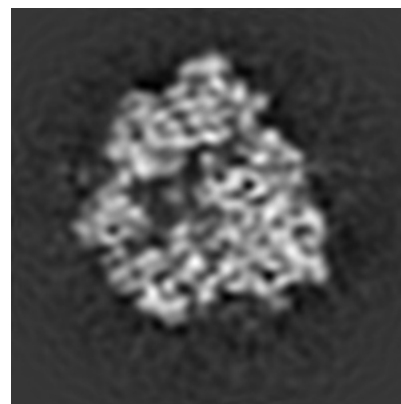
6.3.1 Primary map



X Index: 64



Y Index: 64

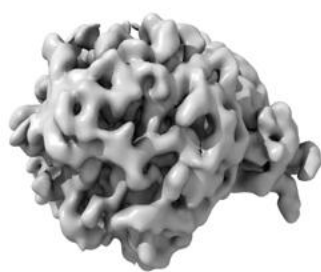


Z Index: 56

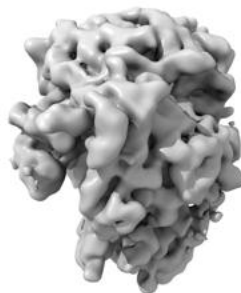
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

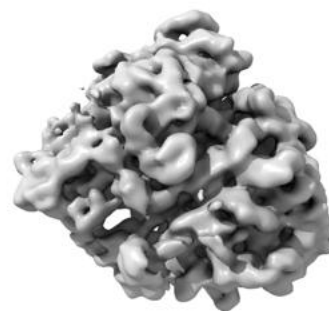
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 82.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

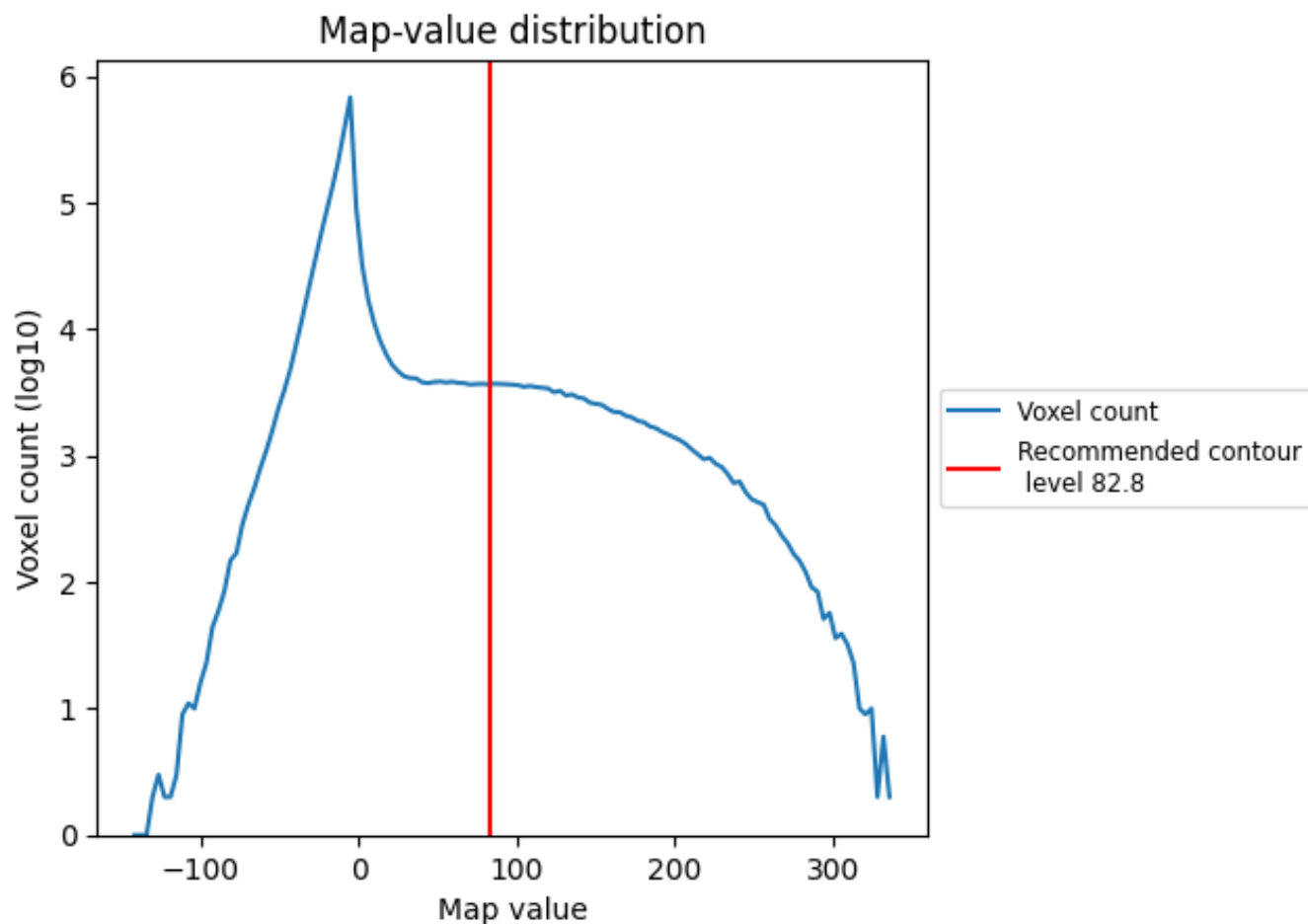
6.5 Mask visualisation

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

7 Map analysis [i](#)

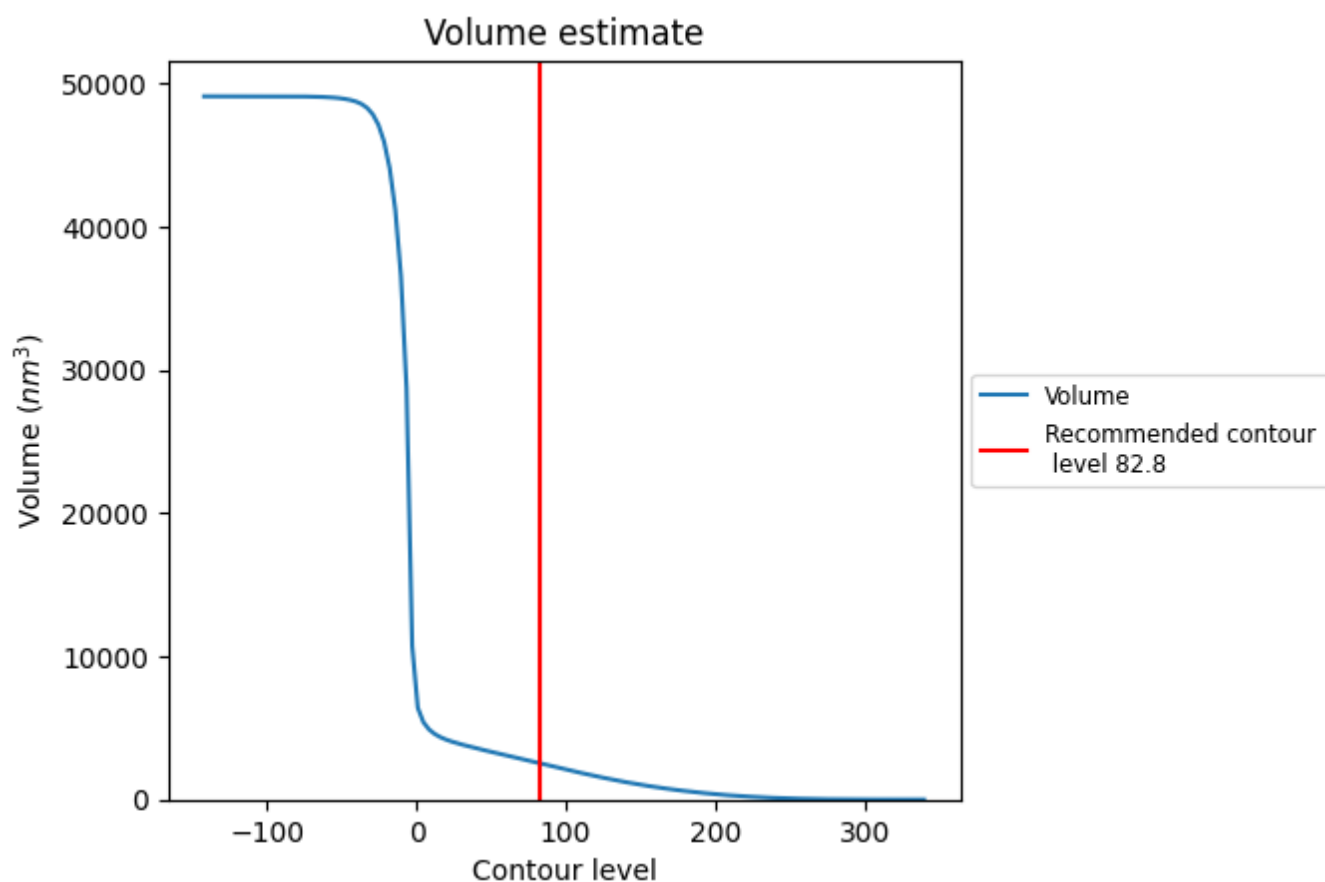
This section contains the results of statistical analysis of the map.

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.

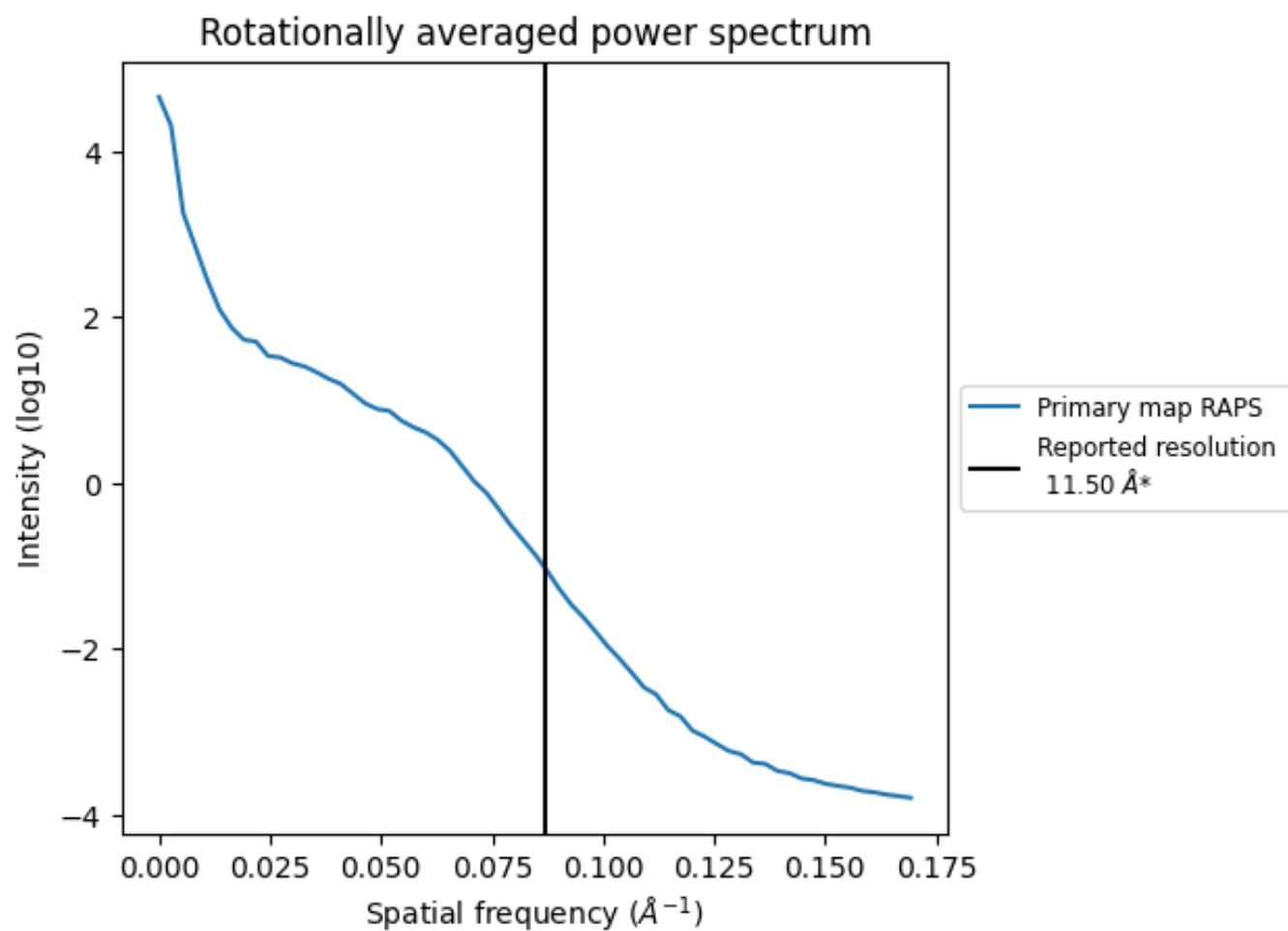
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2526 nm³; this corresponds to an approximate mass of 2282 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 0.087 Å⁻¹

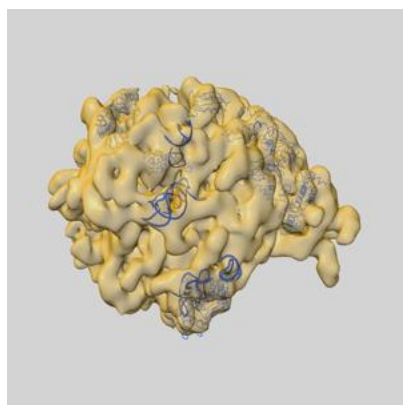
8 Fourier-Shell correlation

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

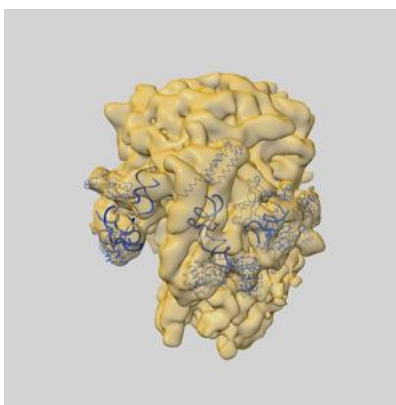
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1003 and PDB model 1EG0. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

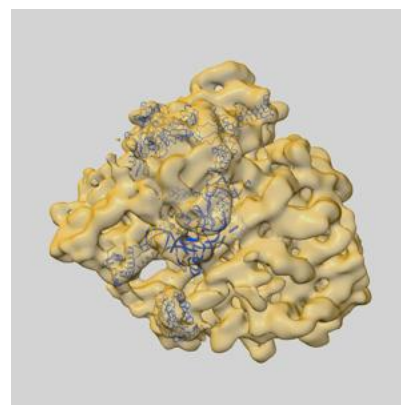
9.1 Map-model overlay [i](#)



X



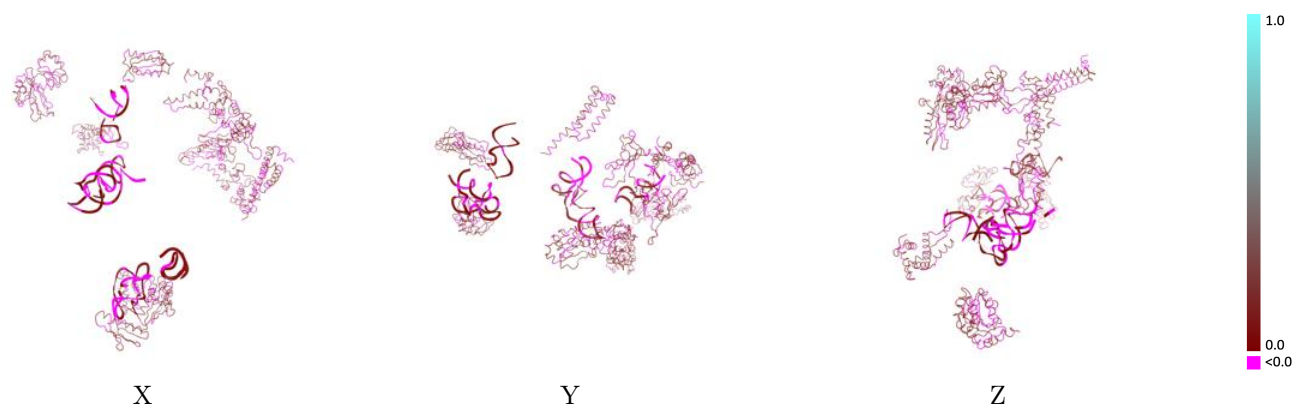
Y



Z

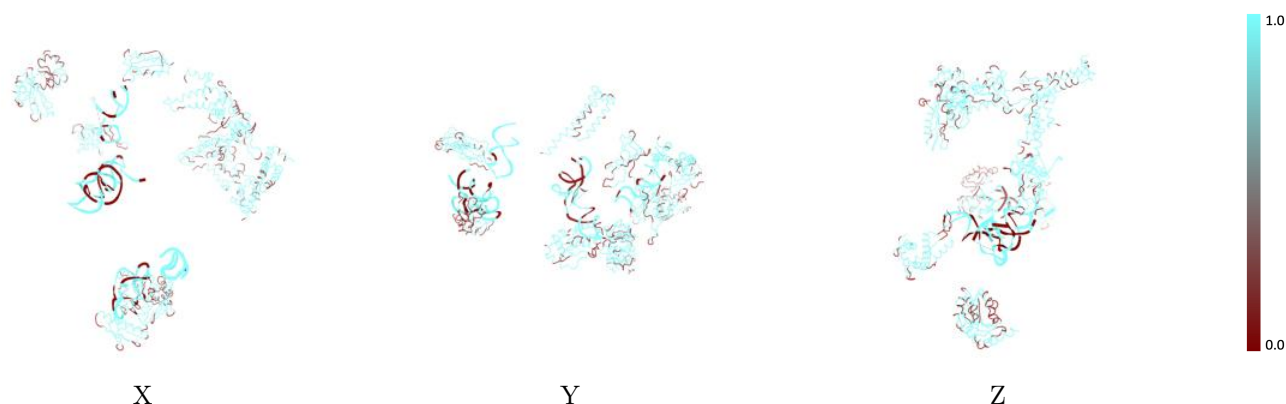
The images above show the 3D surface view of the map at the recommended contour level 82.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



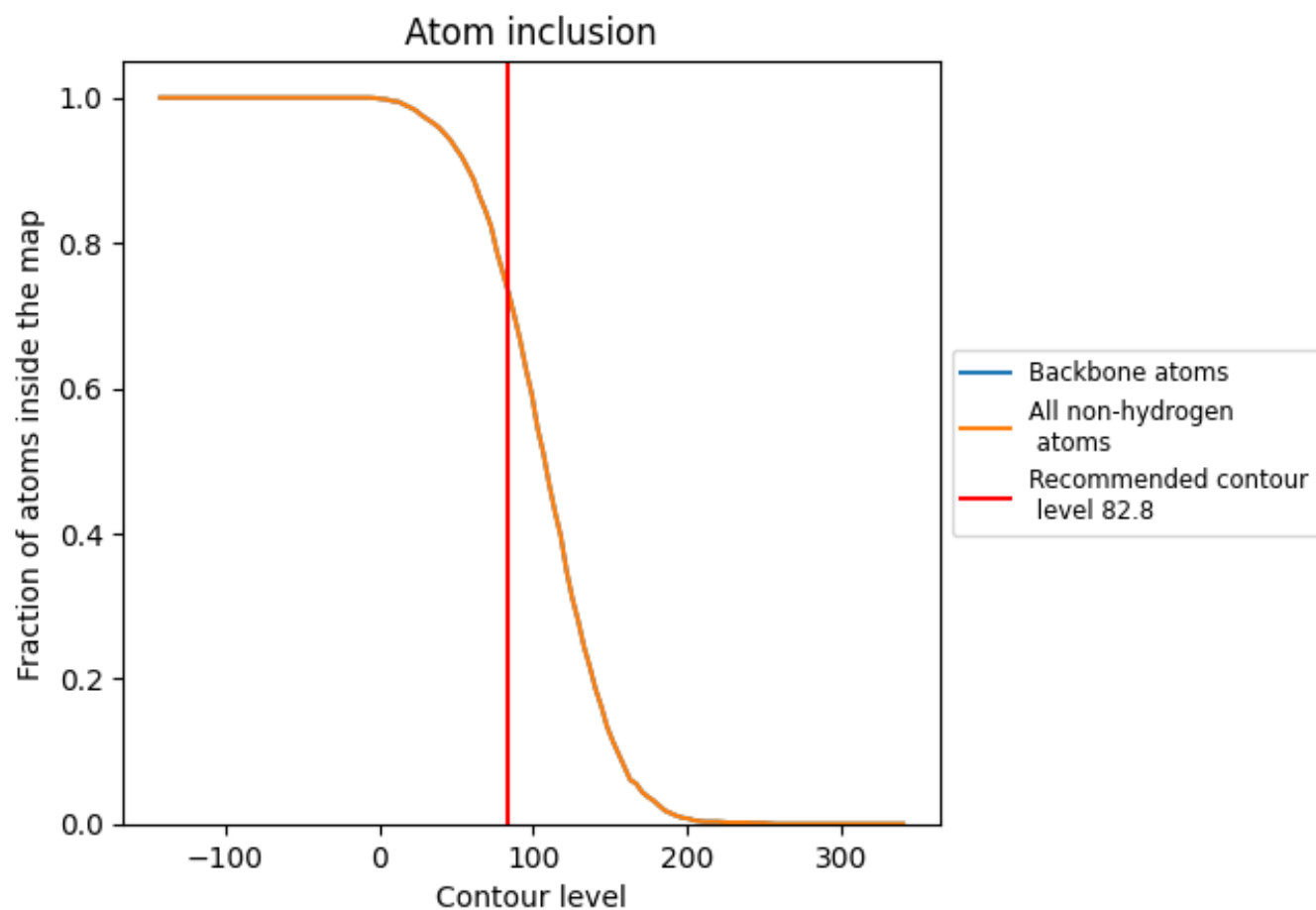
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (82.8).

































9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 74% 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 (82.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7394	 0.0510
A	 0.7673	 0.0670
B	 0.8207	 0.0610
C	 0.7938	 0.0510
D	 0.7704	 0.0590
E	 0.8015	 0.0580
F	 0.9205	 0.0700
G	 0.6629	 0.0250
H	 0.8500	 0.0350
I	 0.7576	 0.0100
J	 0.8232	 0.0810
K	 0.3835	 0.0680
L	 0.7018	 0.0090
M	 0.9615	 0.0510
N	 0.6773	 0.0390
O	 0.5921	 -0.0210

