



## wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 08:23 AM EST

PDB ID : 1ZN0  
EMDB ID : EMD-1127  
Title : Coordinates of RRF and EF-G fitted into Cryo-EM map of the 50S subunit bound with both EF-G (GDPNP) and RRF  
Authors : Gao, N.; Zavialov, A.V.; Li, W.; Sengupta, J.; Valle, M.; Gursky, R.P.; Ehrenberg, M.; Frank, J.  
Deposited on : 2005-05-11  
Resolution : 15.50 Å (reported)  
Based on initial models : 1PN6, 1EK8, 1P6G

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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

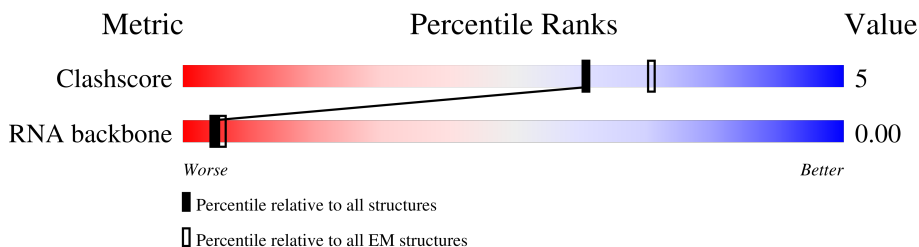
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

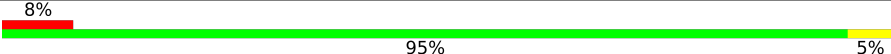
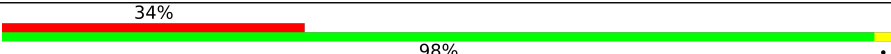
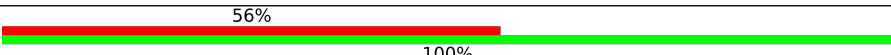
The reported resolution of this entry is 15.50 Å.

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  $\geq 3$ , 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	C	40	
2	A	185	
3	B	655	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 880 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 16S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	C	40	Total	P	0	40
			40	40		

- Molecule 2 is a protein called Ribosome recycling factor.

Mol	Chain	Residues	Atoms		AltConf	Trace
2	A	185	Total	C	0	185
			185	185		

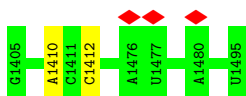
- Molecule 3 is a protein called ELONGATION FACTOR G.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	B	655	Total	C	0	655
			655	655		

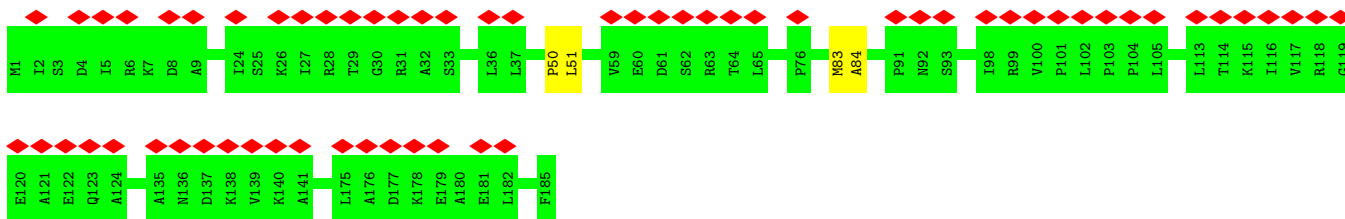
### 3 Residue-property plots [i](#)

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.

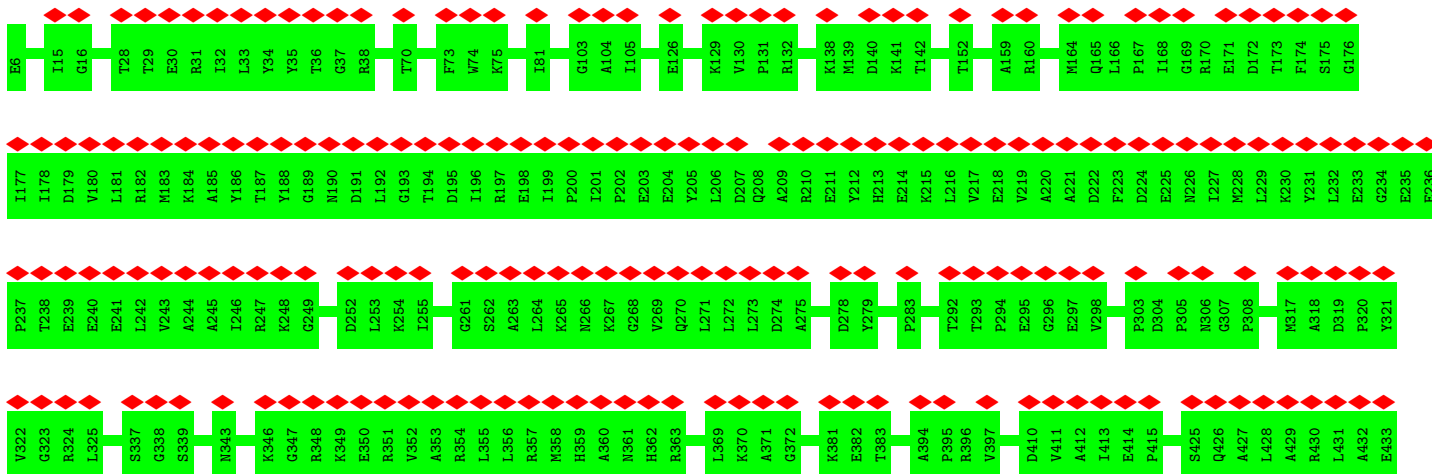
- Molecule 1: 16S RIBOSOMAL RNA



- Molecule 2: Ribosome recycling factor



- Molecule 3: ELONGATION FACTOR G



E434	F438	R439	V440	S441	T442	H443	P444	E445	T446	G447	Q448	T449	I450	I451	S452	I462	V476	G477	K478	P479	Q480	V481	A482	Y483	R484	E485	T486	I487	T488	K489	P490	V491	D492	V493	E494	G495	K496	F497	I498	R499	Q500	R504	G505	Q506	Y507	G508	H509	V510	K511	I512	K513	V514	E515	P516	L517				
P518	R519	G520	S521	G522	F523	E524	F525	V526	N527	A528	I529	V530	G531	G532	V533	I534	P535	K536	E537	Y538	I539	P540	A541	V542	Q543	K544	G545	I546	E547	E548	A549	M550	Q551	S552	G553	P554	L555	I556	G557	F558	P559	V560	V561	D562	I563	K564	V565	T566	L567	Y568	D569	G570	S571	Y572	A573	E574	V575	D576	S577
S578	E579	M580	A581	F582	K583	I584	A585	G586	S587	M588	A589	I590	K591	E592	A593	V594	Q595	K596	G597	D598	T611	T612	P613	G618	I621	G622	D623	G633	M634	E635	P636	R637	G638	N639	A640	Q641	V642	I643	T657	D658	S661	K662	T663	Q664	Y676	Q677	E678	V679	I688										

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32171	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)	-1.5	Depositor
Maximum defocus (nm)	-4.8	Depositor
Magnification	49700	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	336.361	Depositor
Minimum map value	-123.870	Depositor
Average map value	3.606	Depositor
Map value standard deviation	29.410	Depositor
Recommended contour level	55.3	Depositor
Map size ( $\text{\AA}$ )	366.6, 366.6, 366.6	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ( $^\circ$ )	90, 90, 90	wwPDB
Pixel spacing ( $\text{\AA}$ )	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	C	40	0	0	4	0
2	A	185	0	0	4	0
3	B	655	0	0	0	0
All	All	880	0	0	4	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 5.

All (4) 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:C:1410:A:P	2:A:50:PRO:CA	2.21	1.27
1:C:1412:C:P	2:A:83:MET:CA	2.36	1.14
1:C:1410:A:P	2:A:51:LEU:CA	2.51	0.98
1:C:1412:C:P	2:A:84:ALA:CA	2.83	0.66

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	C	0/40	-	-

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.



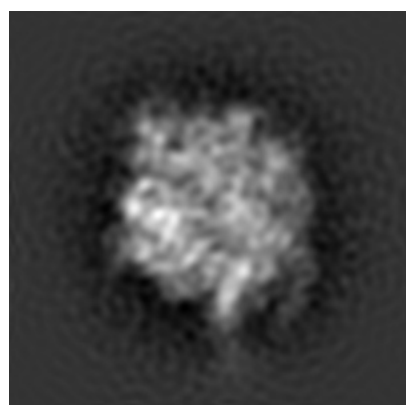
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1127. These allow visual inspection of the internal detail of the map and identification of artifacts.

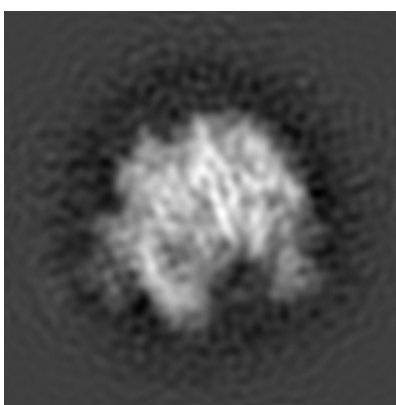
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

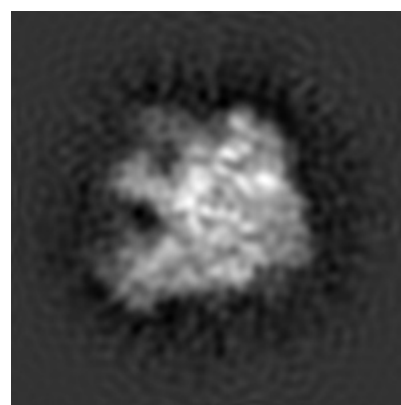
#### 6.1.1 Primary map



X



Y

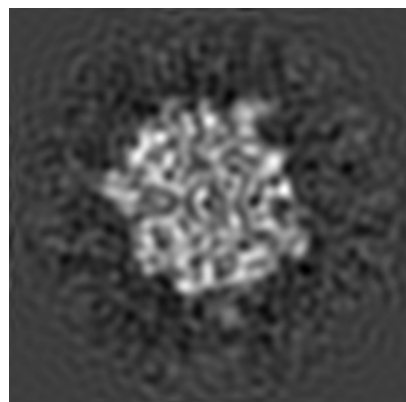


Z

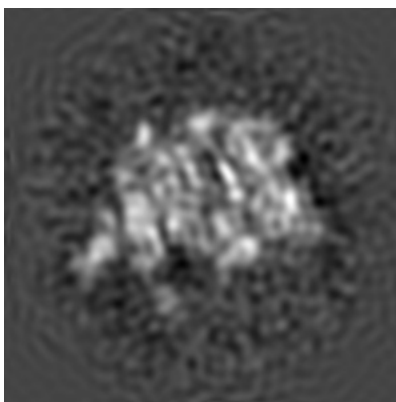
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

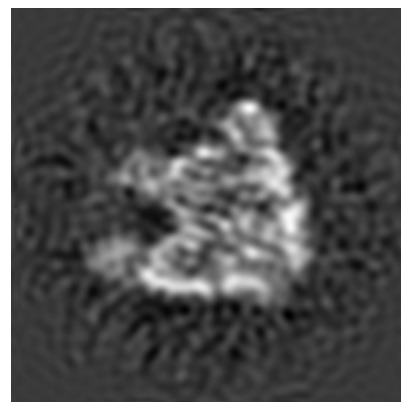
#### 6.2.1 Primary map



X Index: 65



Y Index: 65

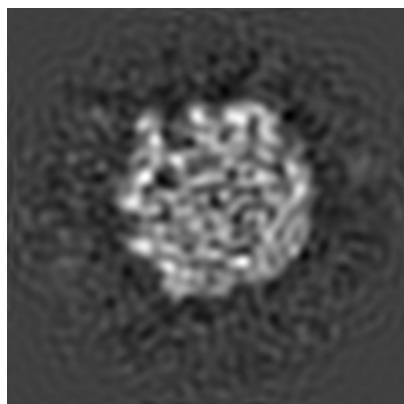


Z Index: 65

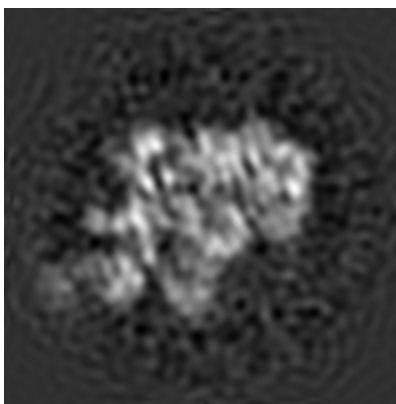
The images above show central slices of the map in three orthogonal directions.

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

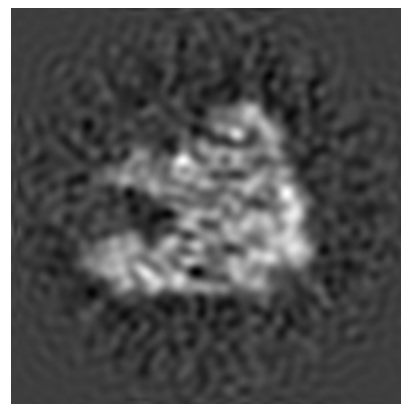
### 6.3.1 Primary map



X Index: 71



Y Index: 74

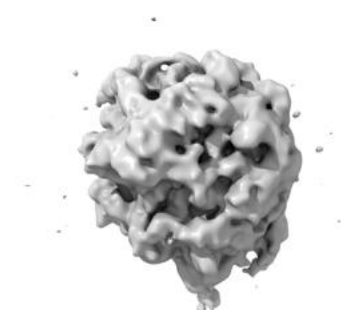


Z Index: 63

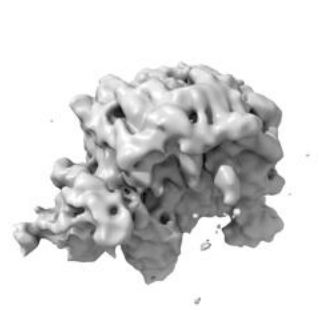
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

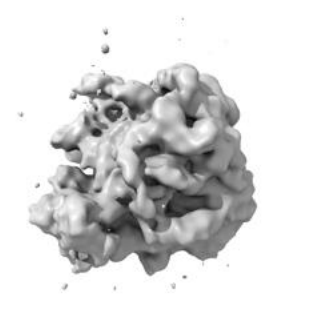
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 55.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

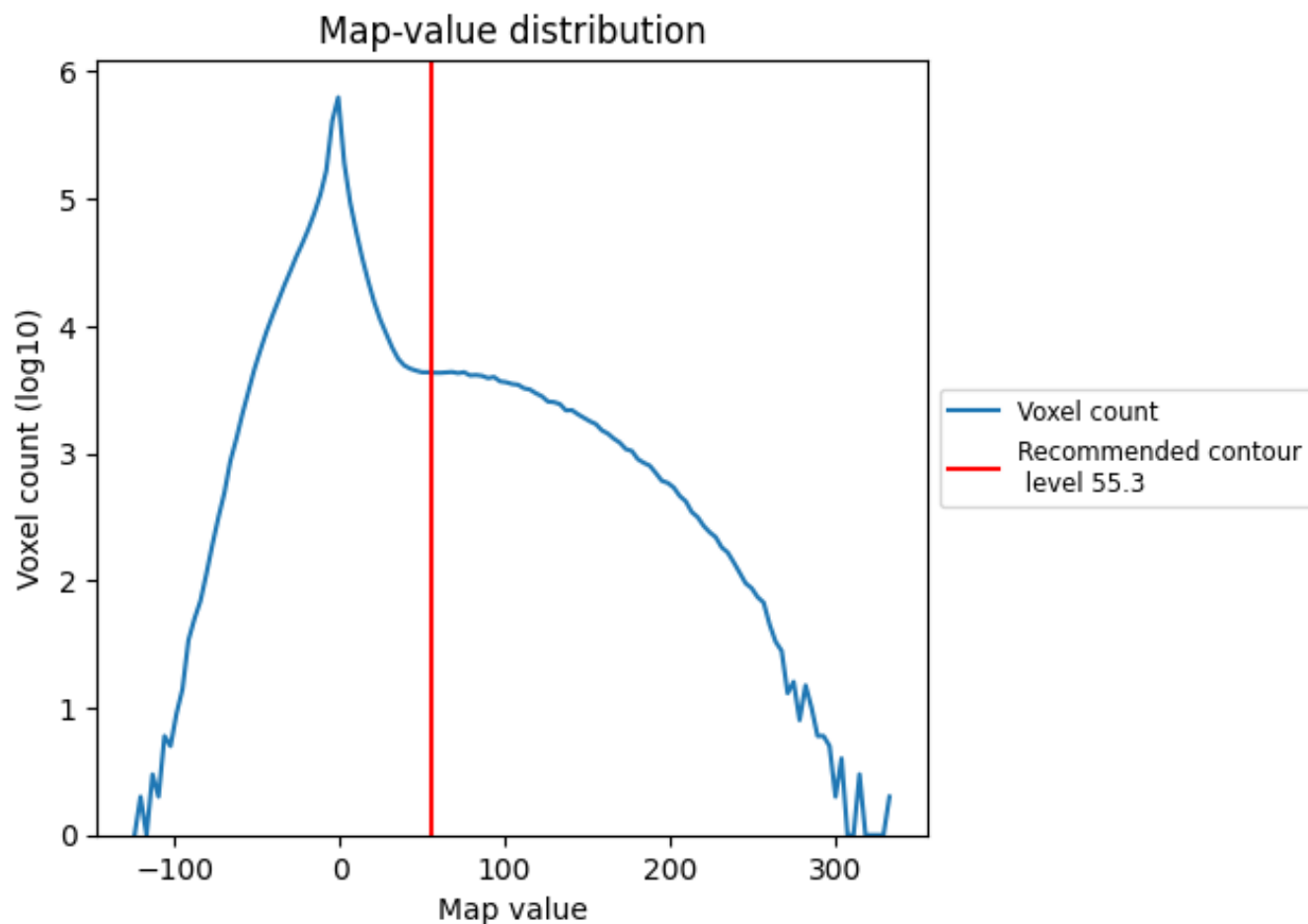
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

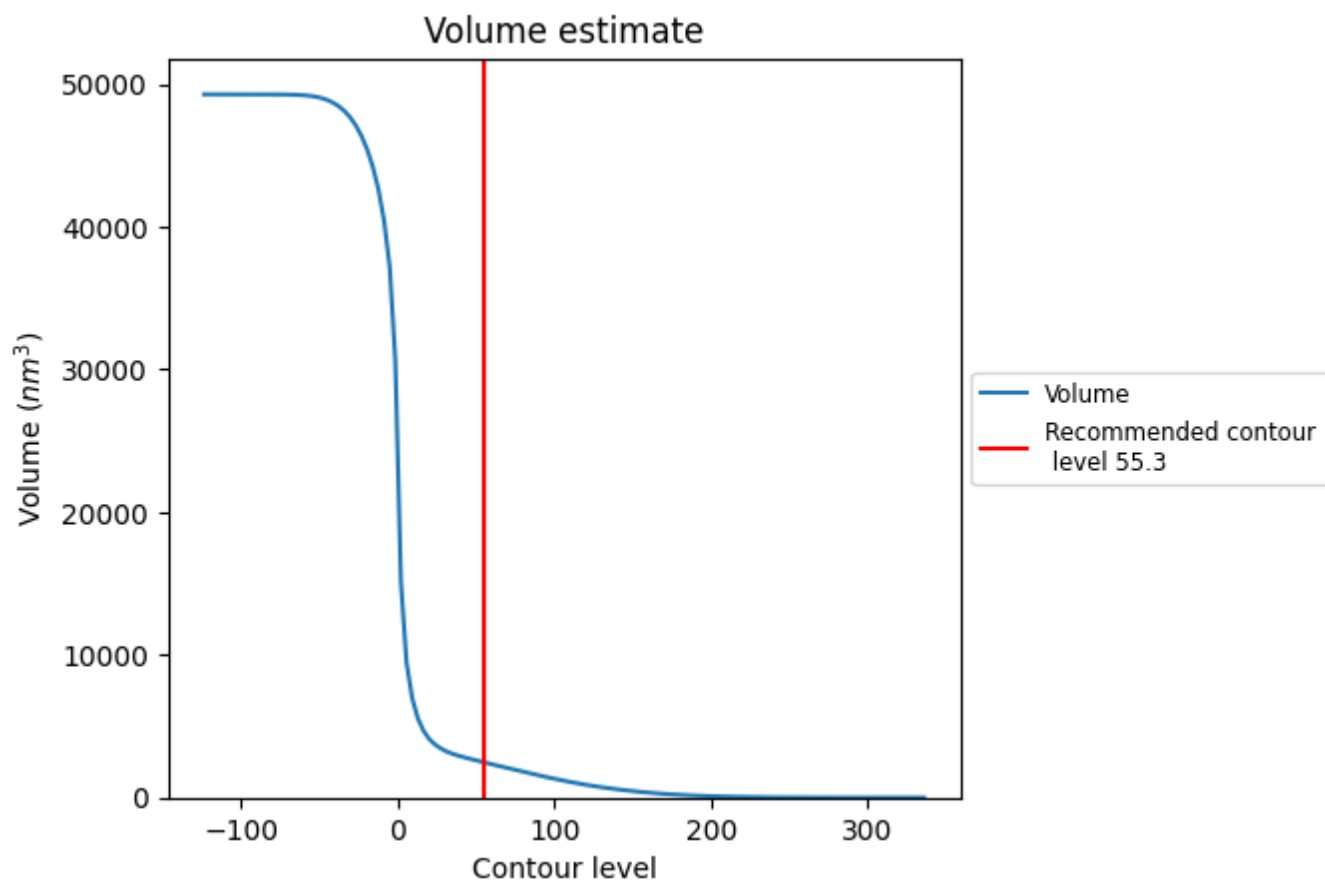
This section contains the results of statistical analysis of the map.

### 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.

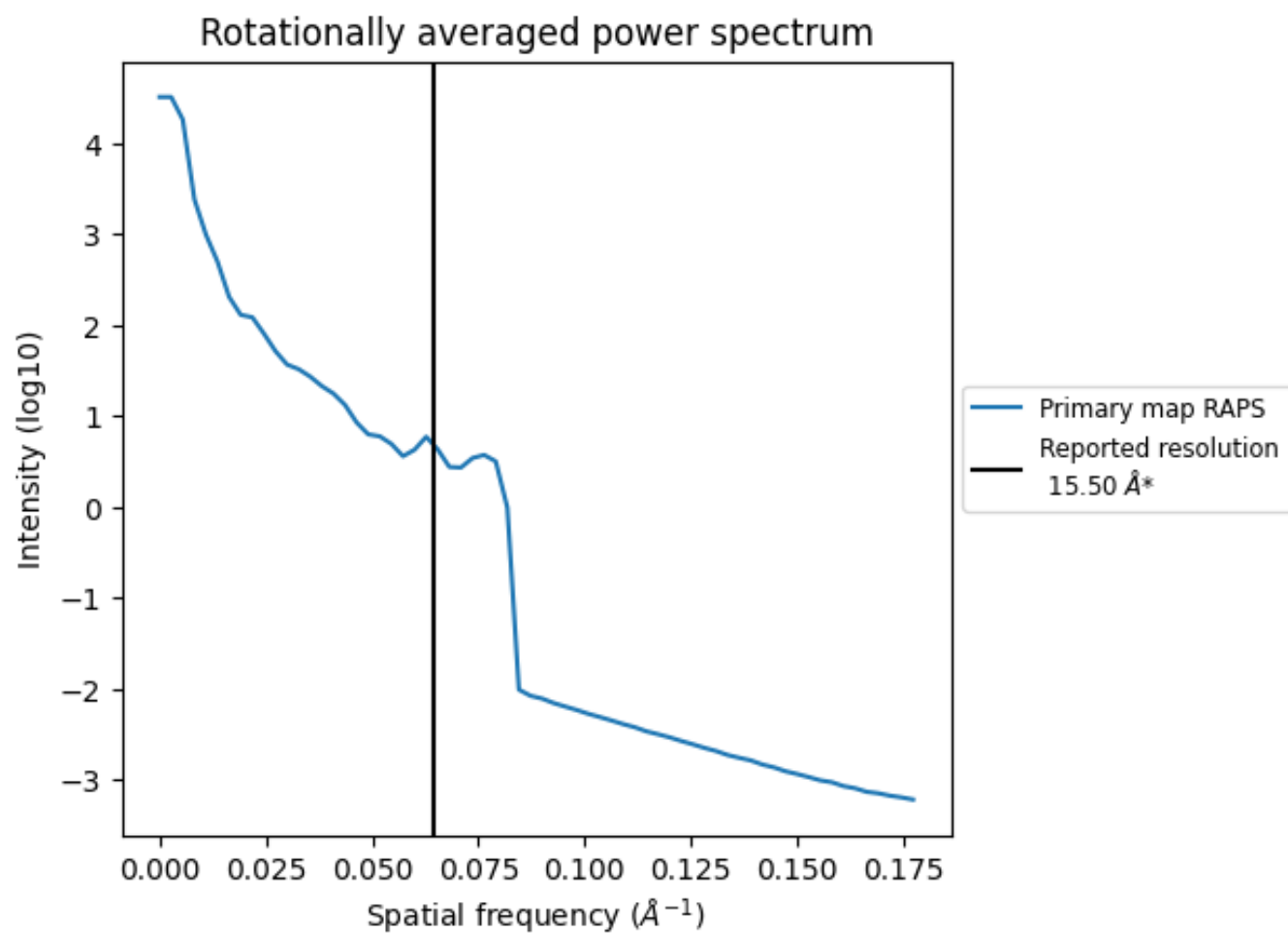
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2463 nm<sup>3</sup>; this corresponds to an approximate mass of 2225 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 0.065 Å<sup>-1</sup>

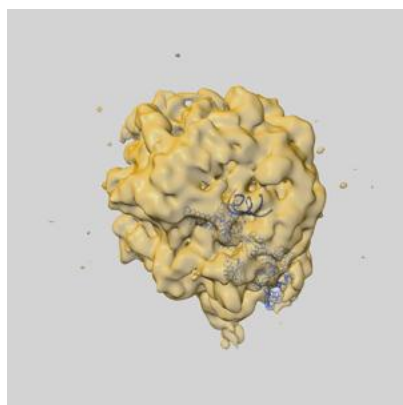
## 8 Fourier-Shell correlation ⓘ

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

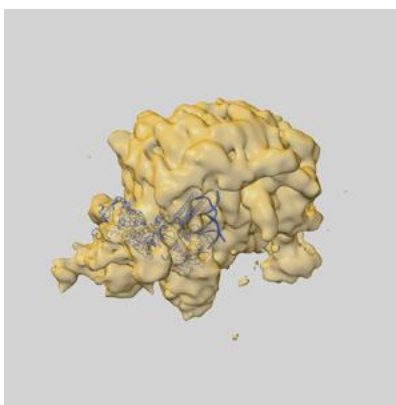
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1127 and PDB model 1ZN0. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

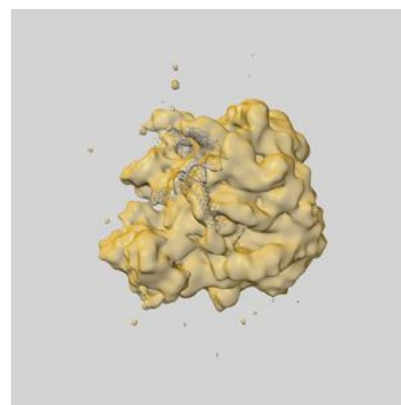
### 9.1 Map-model overlay [i](#)



X



Y

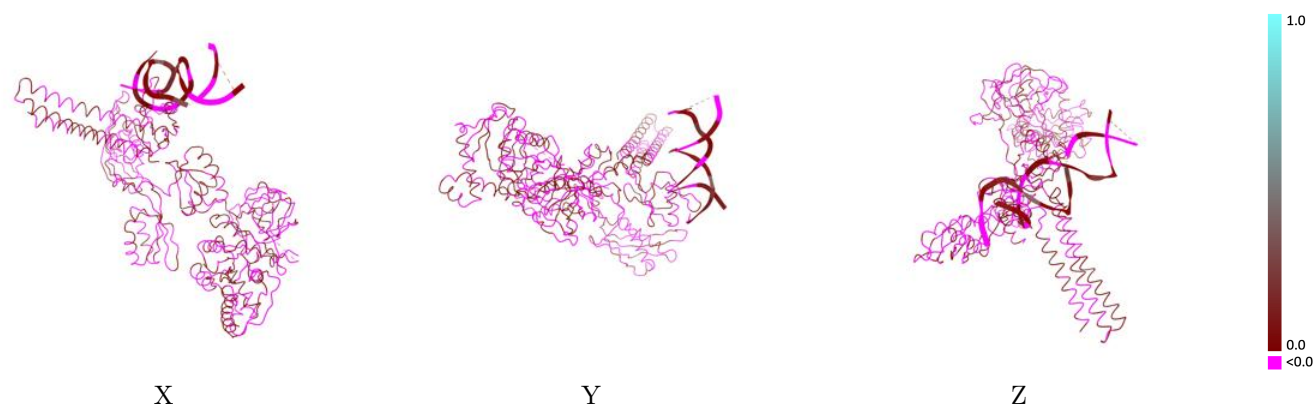


Z

The images above show the 3D surface view of the map at the recommended contour level 55.3 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.

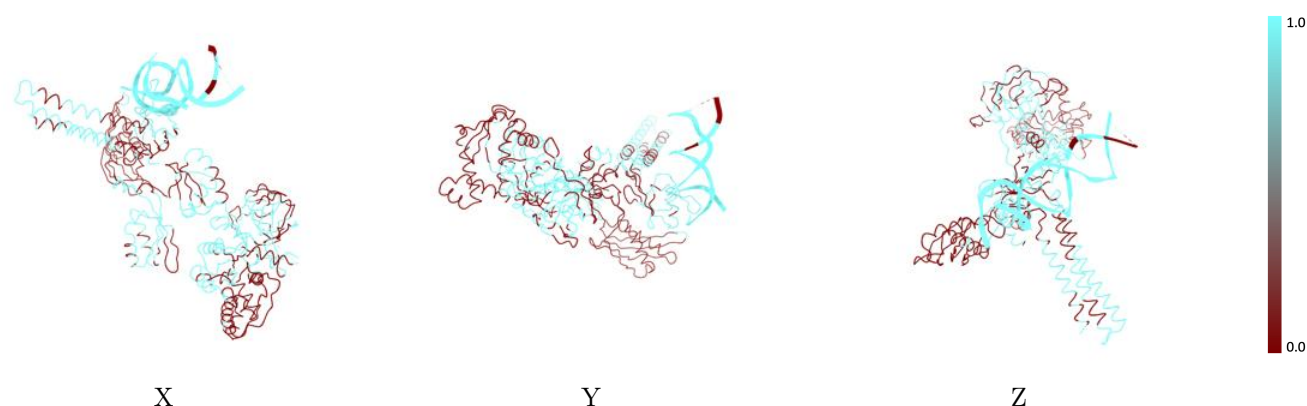


## 9.2 Q-score mapped to coordinate model [i](#)



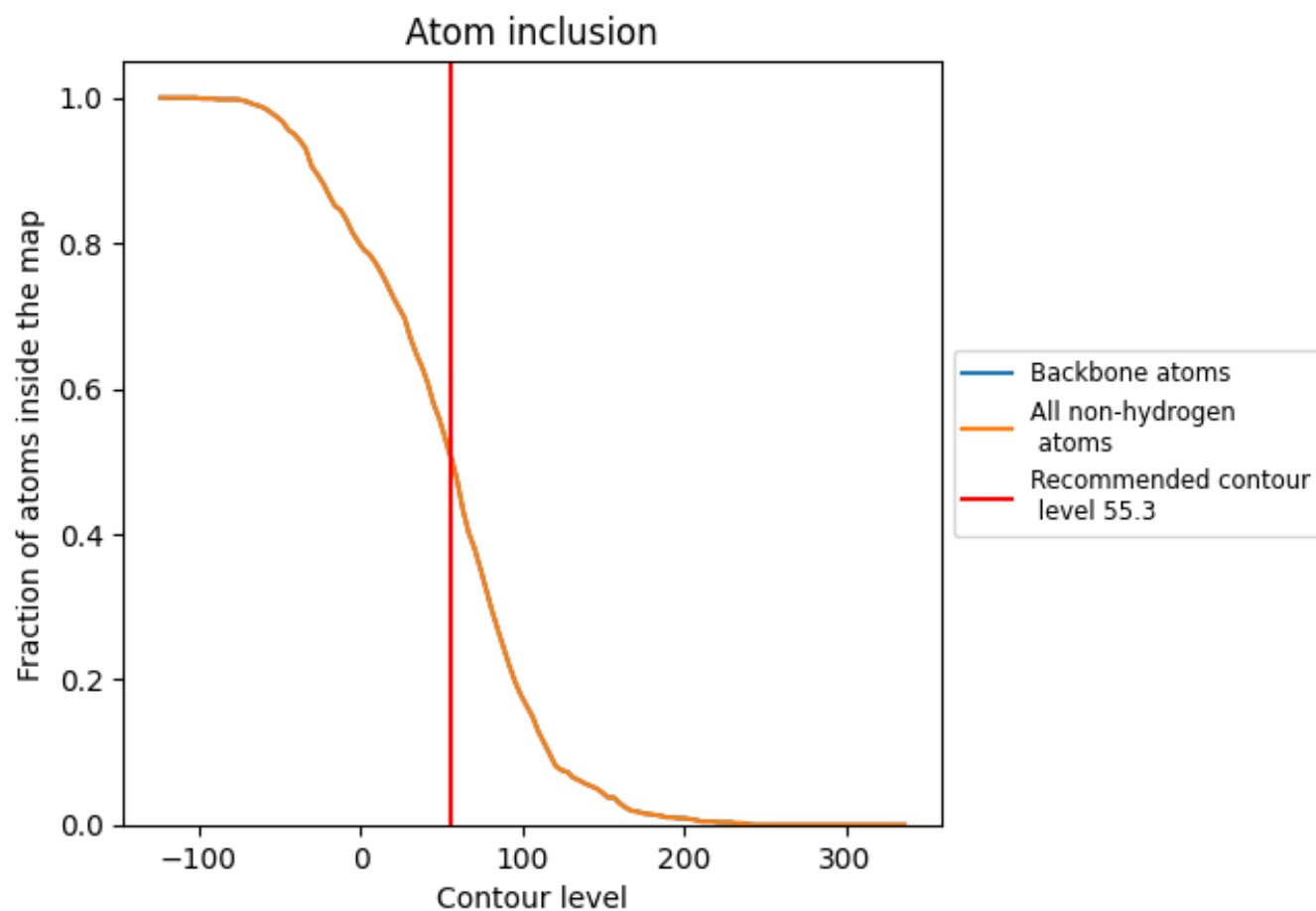
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (55.3).

## 9.4 Atom inclusion ⓘ



At the recommended contour level, 51% of all backbone atoms, 51% 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 (55.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5080	<div></div> -0.0110
A	<div></div> 0.6649	<div></div> 0.0030
B	<div></div> 0.4382	<div></div> -0.0170
C	<div></div> 0.9250	<div></div> 0.0190

