



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:34 AM UTC

PDB ID : 3J2E / pdb_00003j2e
EMDB ID : EMD-5507
Title : Dissecting the in vivo assembly of the 30S ribosomal subunit reveals the role of RimM
Authors : Guo, Q.; Goto, S.; Chen, Y.; Muto, A.; Himeno, H.; Deng, H.; Lei, J.; Gao, N.
Deposited on : 2012-09-28
Resolution : 15.30 Å (reported)
Based on initial model : 3OFA

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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 : 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

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 49446 atoms, of which 16554 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.

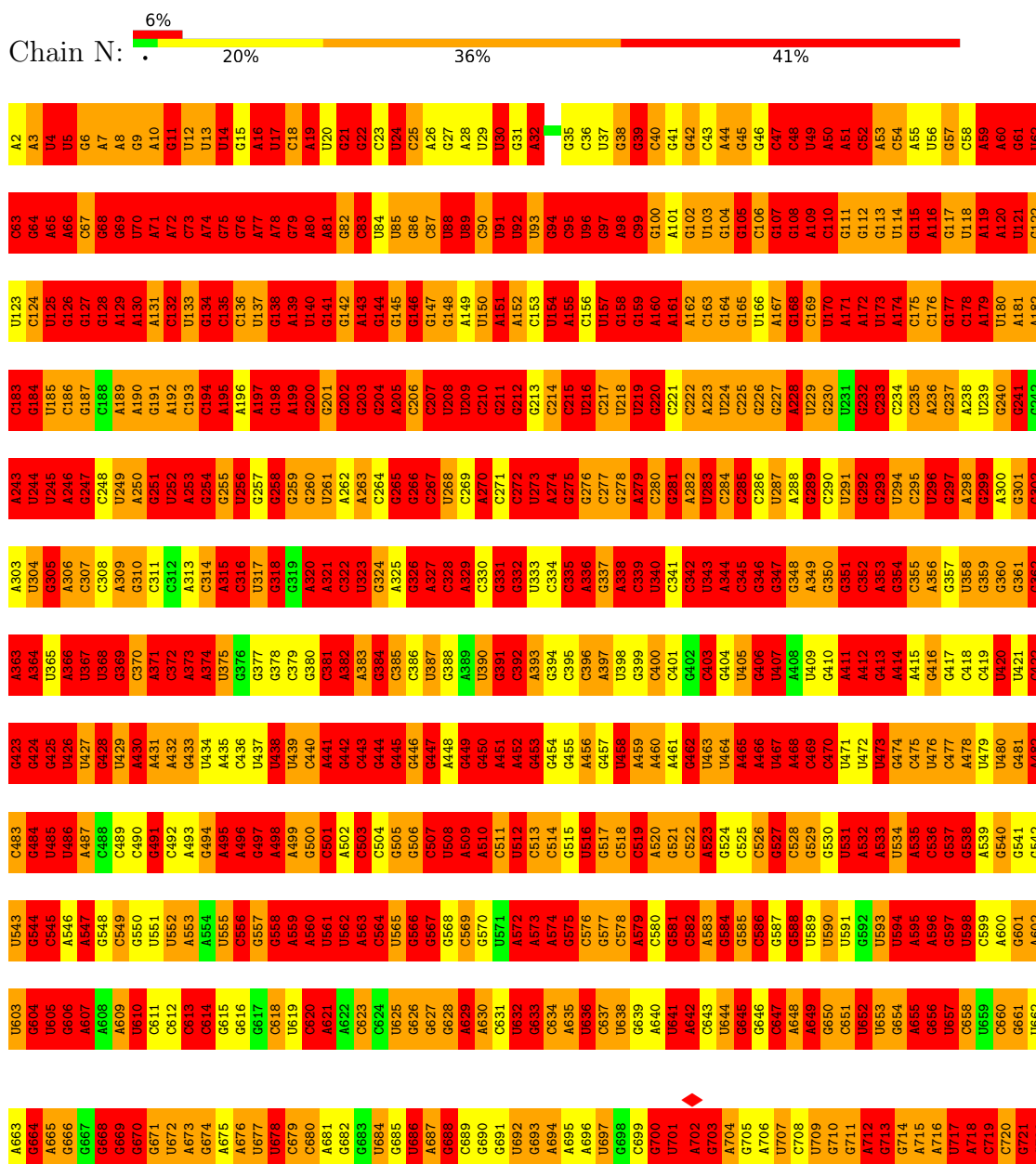
- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
1	N	1533	49446	14671	16554	6036	10653	1532	0	0

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: 16S rRNA



A1503	G724	U843	G903	G963	U1023	U1083	G1143	C1203	C1263	G1323	C1383	G1443	C1503	C1563	G1623	C1683	G1743	C1803	G1863	C1923	G1983	C2043	G2103	C2163	G2223	C2283	G2343	C2403	G2463	C2523	G2583	C2643	G2703	C2763	G2823	C2883	G2943	C3003	G3063	C3123	G3183	C3243	G3303	C3363	G3423	C3483	G3543	C3603	G3663	C3663	G3723	C3783	G3843	C3943	G3903	C4003	G4063	C4103	G4163	C4203	G4223	C4263	G4323	C4363	G4383	C4423	G4443	C4483	G4503	C4543	G4563	C4583	G4623	C4663	G4723	C4803	G4783	C4843	G4863	C4903	G4923	C4943	G4963	C4983	G5023	C5063	G5083	C5103	G5123	C5143	G5163	C5163	G5183	C5183	G5203	C5203	G5223	C5223	G5243	C5243	G5263	C5263	G5283	C5283	G5303	C5303	G5323	C5323	G5343	C5343	G5363	C5363	G5383	C5383	G5403	C5403	G5423	C5423	G5443	C5443	G5463	C5463	G5483	C5483	G5503	C5503	G5523	C5523	G5543	C5543	G5563	C5563	G5583	C5583	G5603	C5603	G5623	C5623	G5643	C5643	G5663	C5663	G5683	C5683	G5703	C5703	G5723	C5723	G5743	C5743	G5763	C5763	G5783	C5783	G5803	C5803	G5823	C5823	G5843	C5843	G5863	C5863	G5883	C5883	G5903	C5903	G5923	C5923	G5943	C5943	G5963	C5963	G5983	C5983	G6003	C6003	G6023	C6023	G6043	C6043	G6063	C6063	G6083	C6083	G6103	C6103	G6123	C6123	G6143	C6143	G6163	C6163	G6183	C6183	G6203	C6203	G6223	C6223	G6243	C6243	G6263	C6263	G6283	C6283	G6303	C6303	G6323	C6323	G6343	C6343	G6363	C6363	G6383	C6383	G6403	C6403	G6423	C6423	G6443	C6443	G6463	C6463	G6483	C6483	G6503	C6503	G6523	C6523	G6543	C6543	G6563	C6563	G6583	C6583	G6603	C6603	G6623	C6623	G6643	C6643	G6663	C6663	G6683	C6683	G6703	C6703	G6723	C6723	G6743	C6743	G6763	C6763	G6783	C6783	G6803	C6803	G6823	C6823	G6843	C6843	G6863	C6863	G6883	C6883	G6903	C6903	G6923	C6923	G6943	C6943	G6963	C6963	G6983	C6983	G7003	C7003	G7023	C7023	G7043	C7043	G7063	C7063	G7083	C7083	G7103	C7103	G7123	C7123	G7143	C7143	G7163	C7163	G7183	C7183	G7203	C7203	G7223	C7223	G7243	C7243	G7263	C7263	G7283	C7283	G7303	C7303	G7323	C7323	G7343	C7343	G7363	C7363	G7383	C7383	G7403	C7403	G7423	C7423	G7443	C7443	G7463	C7463	G7483	C7483	G7503	C7503	G7523	C7523	G7543	C7543	G7563	C7563	G7583	C7583	G7603	C7603	G7623	C7623	G7643	C7643	G7663	C7663	G7683	C7683	G7703	C7703	G7723	C7723	G7743	C7743	G7763	C7763	G7783	C7783	G7803	C7803	G7823	C7823	G7843	C7843	G7863	C7863	G7883	C7883	G7903	C7903	G7923	C7923	G7943	C7943	G7963	C7963	G7983	C7983	G8003	C8003	G8023	C8023	G8043	C8043	G8063	C8063	G8083	C8083	G8103	C8103	G8123	C8123	G8143	C8143	G8163	C8163	G8183	C8183	G8203	C8203	G8223	C8223	G8243	C8243	G8263	C8263	G8283	C8283	G8303	C8303	G8323	C8323	G8343	C8343	G8363	C8363	G8383	C8383	G8403	C8403	G8423	C8423	G8443	C8443	G8463	C8463	G8483	C8483	G8503	C8503	G8523	C8523	G8543	C8543	G8563	C8563	G8583	C8583	G8603	C8603	G8623	C8623	G8643	C8643	G8663	C8663	G8683	C8683	G8703	C8703	G8723	C8723	G8743	C8743	G8763	C8763	G8783	C8783	G8803	C8803	G8823	C8823	G8843	C8843	G8863	C8863	G8883	C8883	G8903	C8903	G8923	C8923	G8943	C8943	G8963	C8963	G8983	C8983	G9003	C9003	G9023	C9023	G9043	C9043	G9063	C9063	G9083	C9083	G9103	C9103	G9123	C9123	G9143	C9143	G9163	C9163	G9183	C9183	G9203	C9203	G9223	C9223	G9243	C9243	G9263	C9263	G9283	C9283	G9303	C9303	G9323	C9323	G9343	C9343	G9363	C9363	G9383	C9383	G9403	C9403	G9423	C9423	G9443	C9443	G9463	C9463	G9483	C9483	G9503	C9503	G9523	C9523	G9543	C9543	G9563	C9563	G9583	C9583	G9603	C9603	G9623	C9623	G9643	C9643	G9663	C9663	G9683	C9683	G9703	C9703	G9723	C9723	G9743	C9743	G9763	C9763	G9783	C9783	G9803	C9803	G9823	C9823	G9843	C9843	G9863	C9863	G9883	C9883	G9903	C9903	G9923	C9923	G9943	C9943	G9963	C9963	G9983	C9983	G10003	C10003	G10023	C10023	G10043	C10043	G10063	C10063	G10083	C10083	G10103	C10103	G10123	C10123	G10143	C10143	G10163	C10163	G10183	C10183	G10203	C10203	G10223	C10223	G10243	C10243	G10263	C10263	G10283	C10283	G10303	C10303	G10323	C10323	G10343	C10343	G10363	C10363	G10383	C10383	G10403	C10403	G10423	C10423	G10443	C10443	G10463	C10463	G10483	C10483	G10503	C10503	G10523	C10523	G10543	C10543	G10563	C10563	G10583	C10583	G10603	C10603	G10623	C10623	G10643	C10643	G10663	C10663	G10683	C10683	G10703	C10703	G10723	C10723	G10743	C10743	G10763	C10763	G10783	C10783	G10803	C10803	G10823	C10823	G10843	C10843	G10863	C10863	G10883	C10883	G10903	C10903	G10923	C10923	G10943	C10943	G10963	C10963	G10983	C10983	G11003	C11003	G11023	C11023	G11043	C11043	G11063	C11063	G11083	C11083	G11103	C11103	G11123	C11123	G11143	C11143	G11163	C11163	G11183	C11183	G11203	C11203	G11223	C11223	G11243	C11243	G11263	C11263	G11283	C11283	G11303	C11303	G11323	C11323	G11343	C11343	G11363	C11363	G11383	C11383	G11403	C11403	G11423	C11423	G11443	C11443	G11463	C11463	G11483	C11483	G11503	C11503	G11523	C11523	G11543	C11543	G11563	C11563	G11583	C11583	G11603	C11603	G11623	C11623	G11643	C11643	G11663	C11663	G11683	C11683	G11703	C11703	G11723	C11723	G11743	C11743	G11763	C11763	G11783	C11783	G11803	C11803	G11823	C11823	G11843	C11843	G11863	C11863	G11883	C11883	G11903	C11903	G11923	C11923	G11943	C11943	G11963	C11963	G11983	C11983	G12003	C12003	G12023	C12023	G12043	C12043	G12063	C12063	G12083	C12083	G12103	C12103	G12123	C12123	G12143	C12143	G12163	C12163	G12183	C12183	G12203	C12203	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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	29012	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Weiner filter	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	59000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	3.830	Depositor
Minimum map value	-6.331	Depositor
Average map value	-4.159	Depositor
Map value standard deviation	0.542	Depositor
Recommended contour level	-2.5	Depositor
Map size (\AA)	375.0, 375.0, 375.0	wwPDB
Map dimensions	125, 125, 125	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	3, 3, 3	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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	N	2.06	815/36831 (2.2%)	2.10	2078/57458 (3.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	N	0	1016

The worst 5 of 815 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	574	A	C4'-C3'	9.36	1.66	1.52
1	N	1269	A	C1'-N9	9.25	1.61	1.48
1	N	856	C	C2'-C1'	-9.10	1.39	1.53
1	N	804	U	C5'-C4'	9.09	1.64	1.51
1	N	166	U	P-O5'	-9.05	1.46	1.59

The worst 5 of 2078 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	1362	A	P-O3'-C3'	22.48	153.91	120.20
1	N	776	G	P-O5'-C5'	20.16	151.15	120.90
1	N	181	A	P-O3'-C3'	19.22	149.02	120.20
1	N	547	A	P-O3'-C3'	18.17	147.46	120.20
1	N	94	G	P-O3'-C3'	18.01	147.21	120.20

There are no chirality outliers.

5 of 1016 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	2	A	Sidechain
1	N	3	A	Sidechain
1	N	4	U	Sidechain
1	N	6	G	Sidechain
1	N	8	A	Sidechain

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	N	32892	16554	16522	561	0
All	All	32892	16554	16522	561	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 11.

The worst 5 of 561 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:N:594:U:C4	1:N:595:A:C6	2.75	0.74
1:N:120:A:C2	1:N:122:G:C6	2.78	0.72
1:N:67:C:H2'	1:N:68:G:C8	2.25	0.71
1:N:1343:G:C5	1:N:1344:C:C4	2.79	0.70
1:N:411:A:H61	1:N:428:G:H1'	1.56	0.70

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	N	1532/1533 (99%)	472 (30%)	155 (10%)

5 of 472 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	N	3	A
1	N	4	U
1	N	5	U
1	N	6	G
1	N	8	A

5 of 155 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	N	1167	A
1	N	1364	U
1	N	1191	A
1	N	1299	A
1	N	1498	U

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 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

There are no chain breaks in this entry.

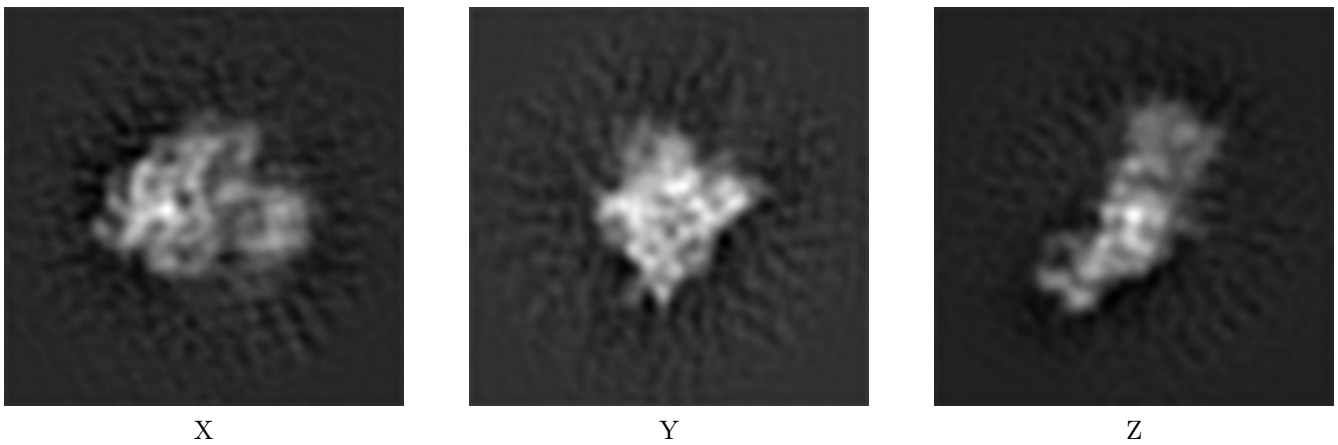
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5507. 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](#)

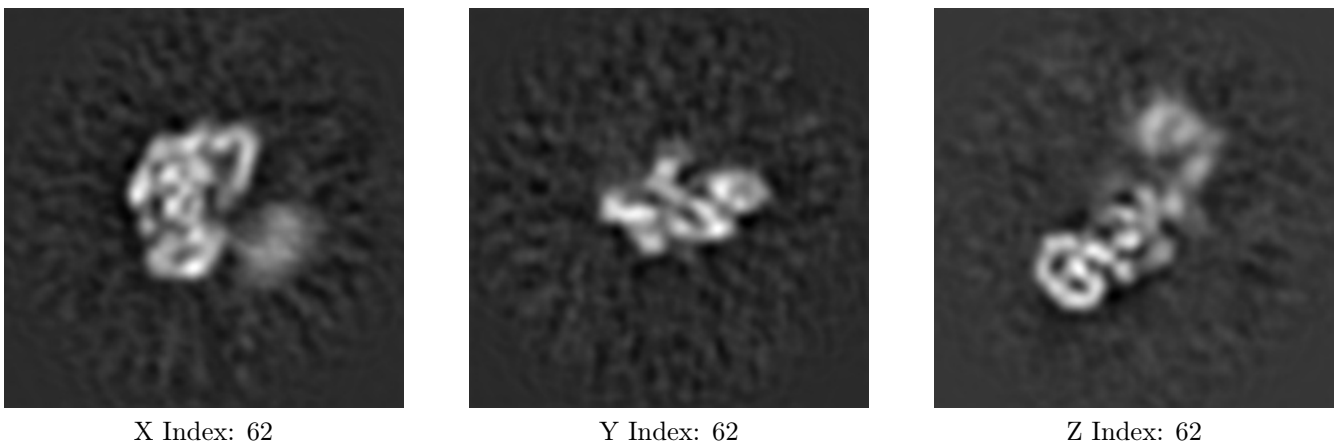
6.1.1 Primary map



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

6.2 Central slices [i](#)

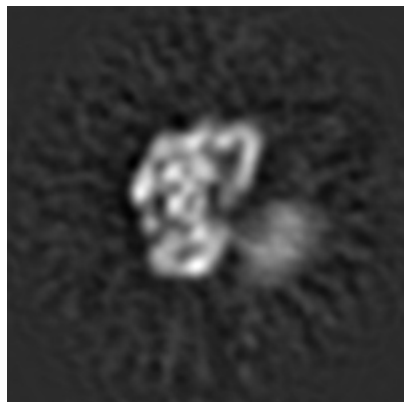
6.2.1 Primary map



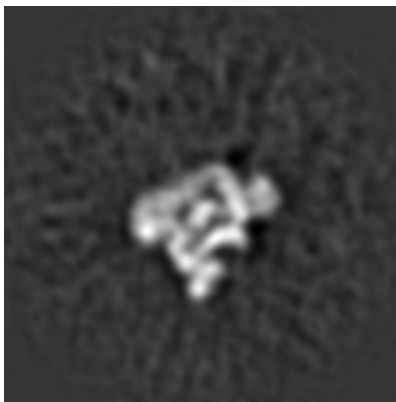
The images above show central slices of the map in three orthogonal directions.

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

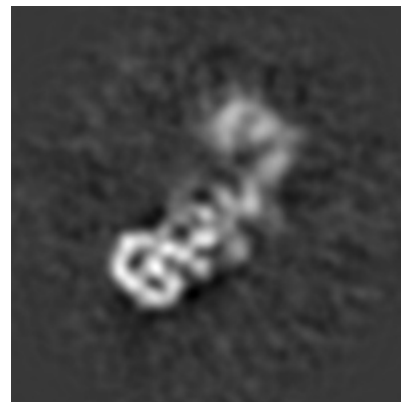
6.3.1 Primary map



X Index: 62



Y Index: 51

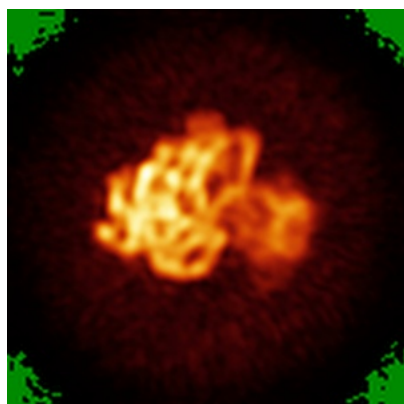


Z Index: 61

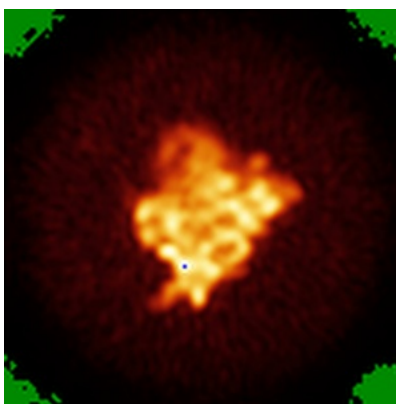
The images above show the largest variance slices of the map in three orthogonal directions.

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

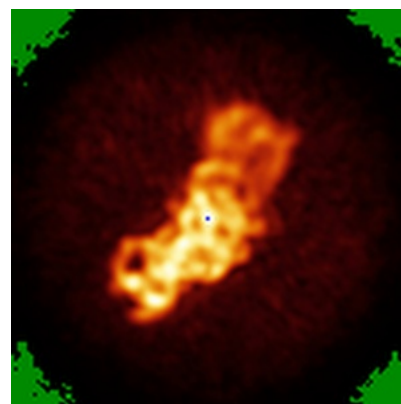
6.4.1 Primary map



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

This section was not generated.

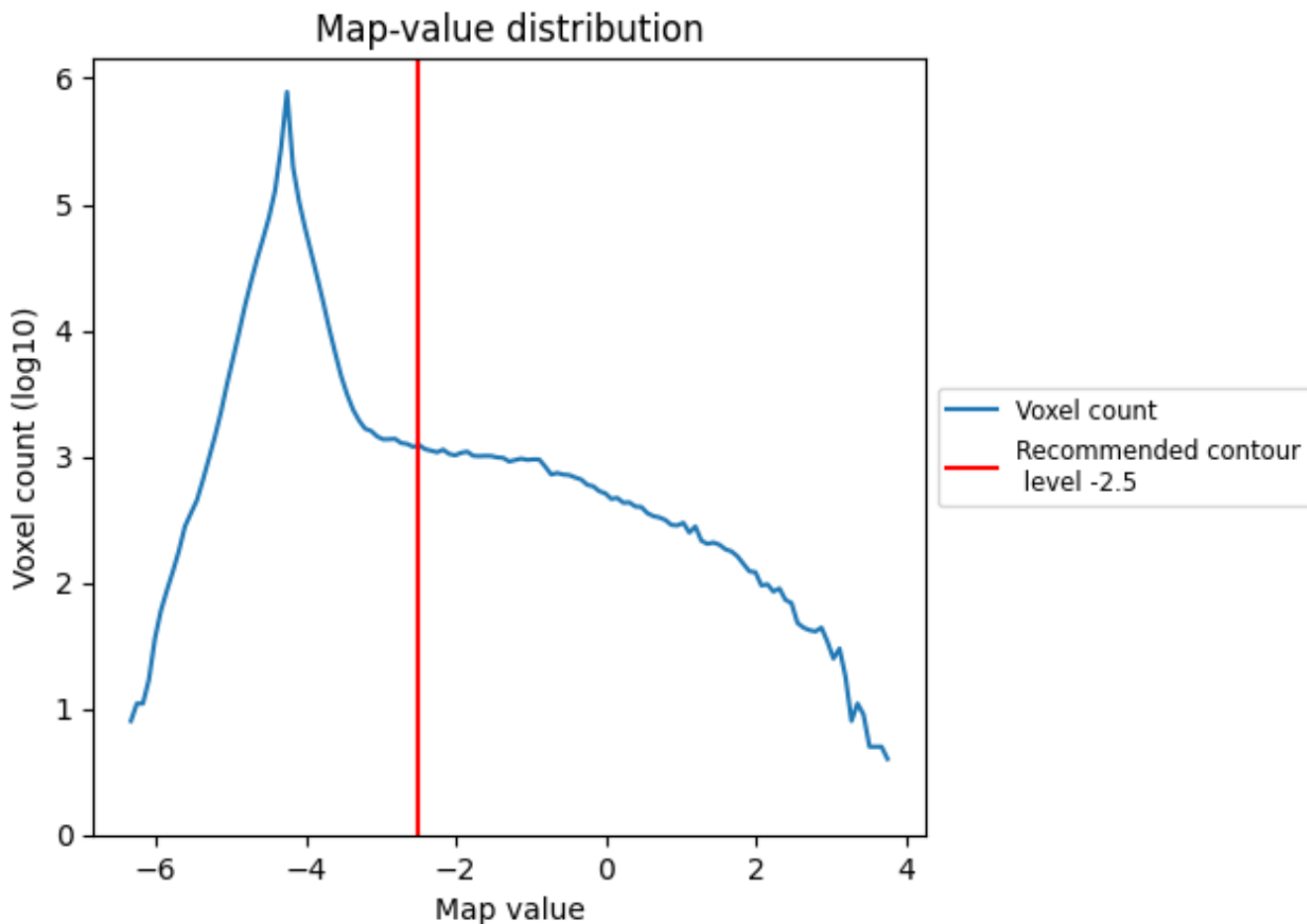
6.6 Mask visualisation

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

7 Map analysis [i](#)

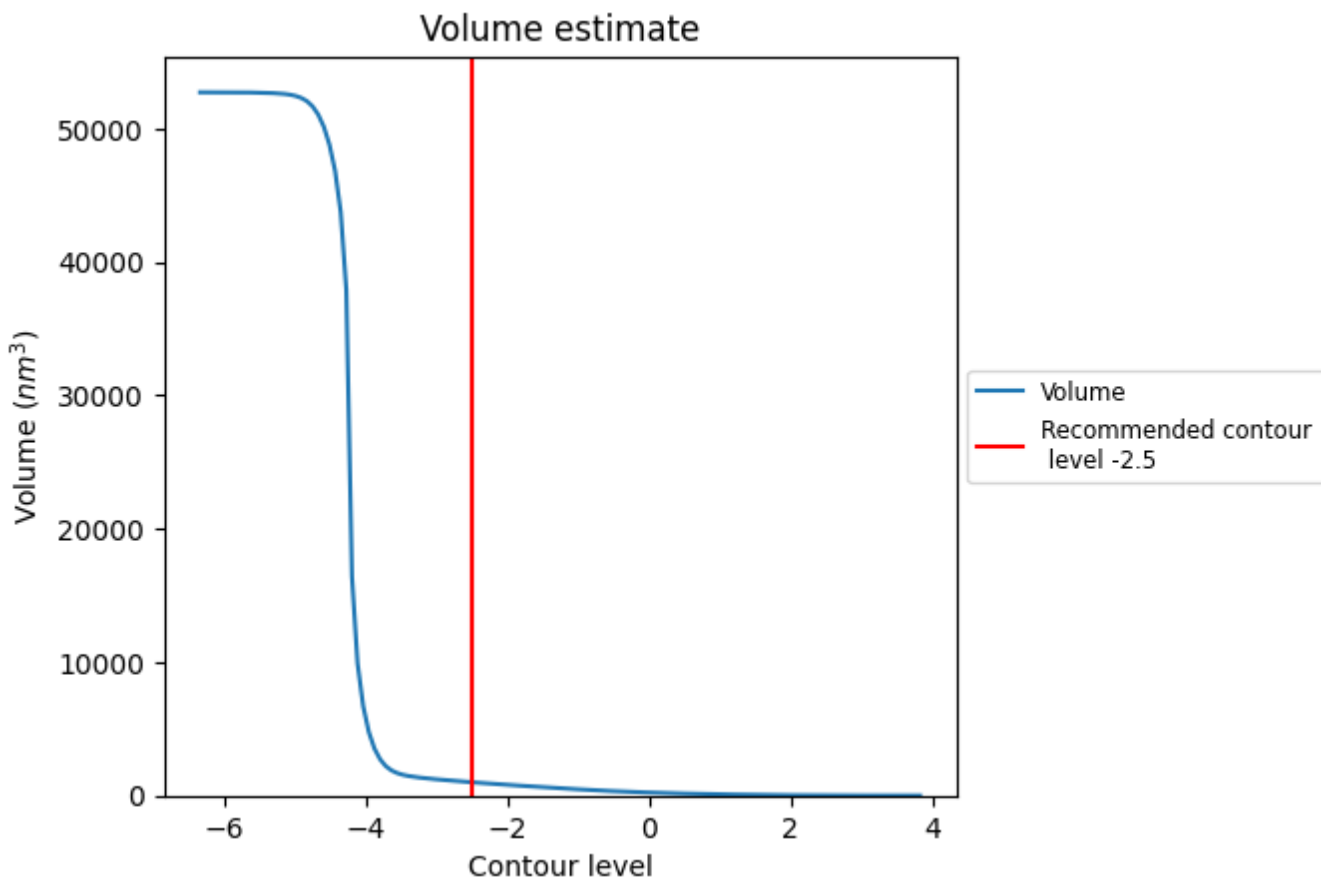
This section contains the results of statistical analysis of the map.

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.

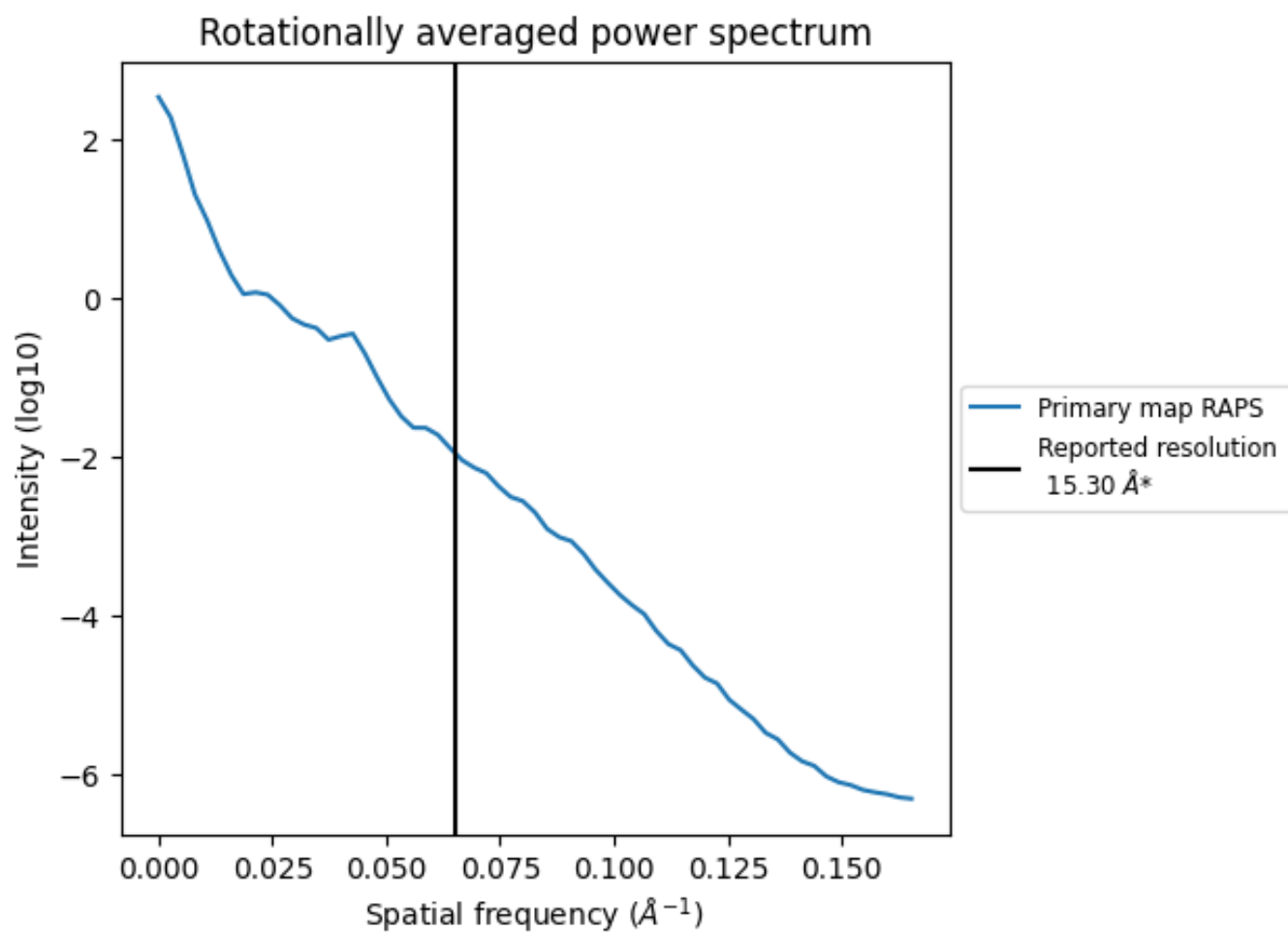
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 998 nm³; this corresponds to an approximate mass of 901 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 0.065 Å⁻¹

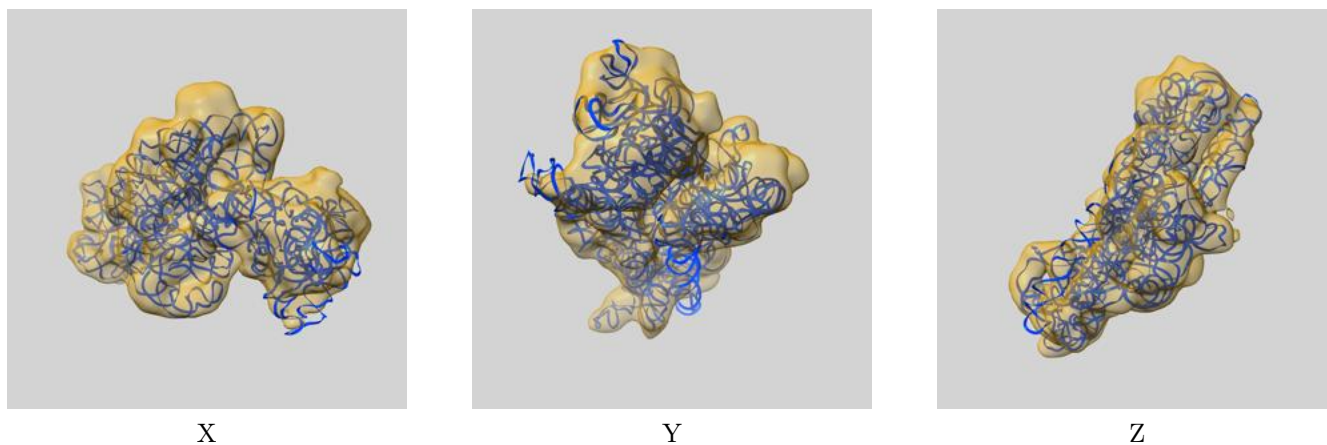
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

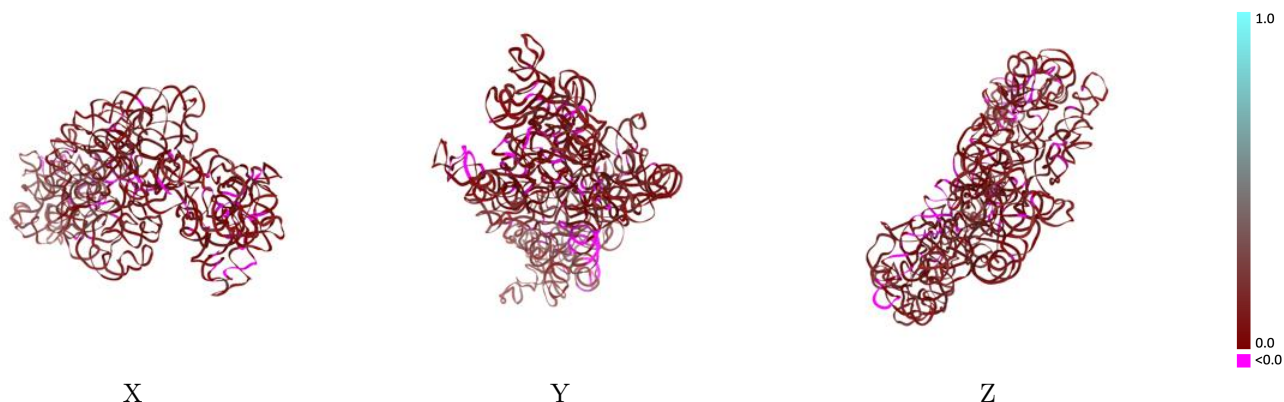
This section contains information regarding the fit between EMDB map EMD-5507 and PDB model 3J2E. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



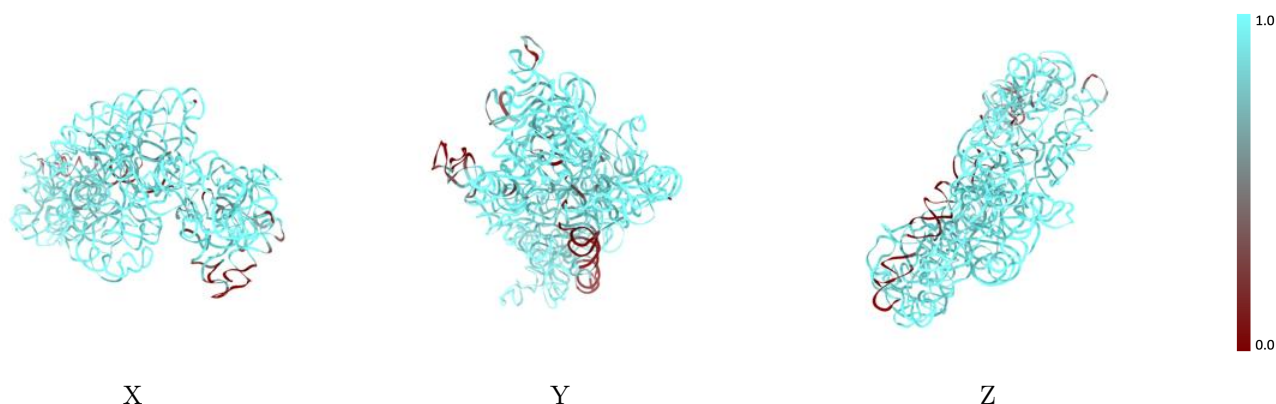
The images above show the 3D surface view of the map at the recommended contour level -2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



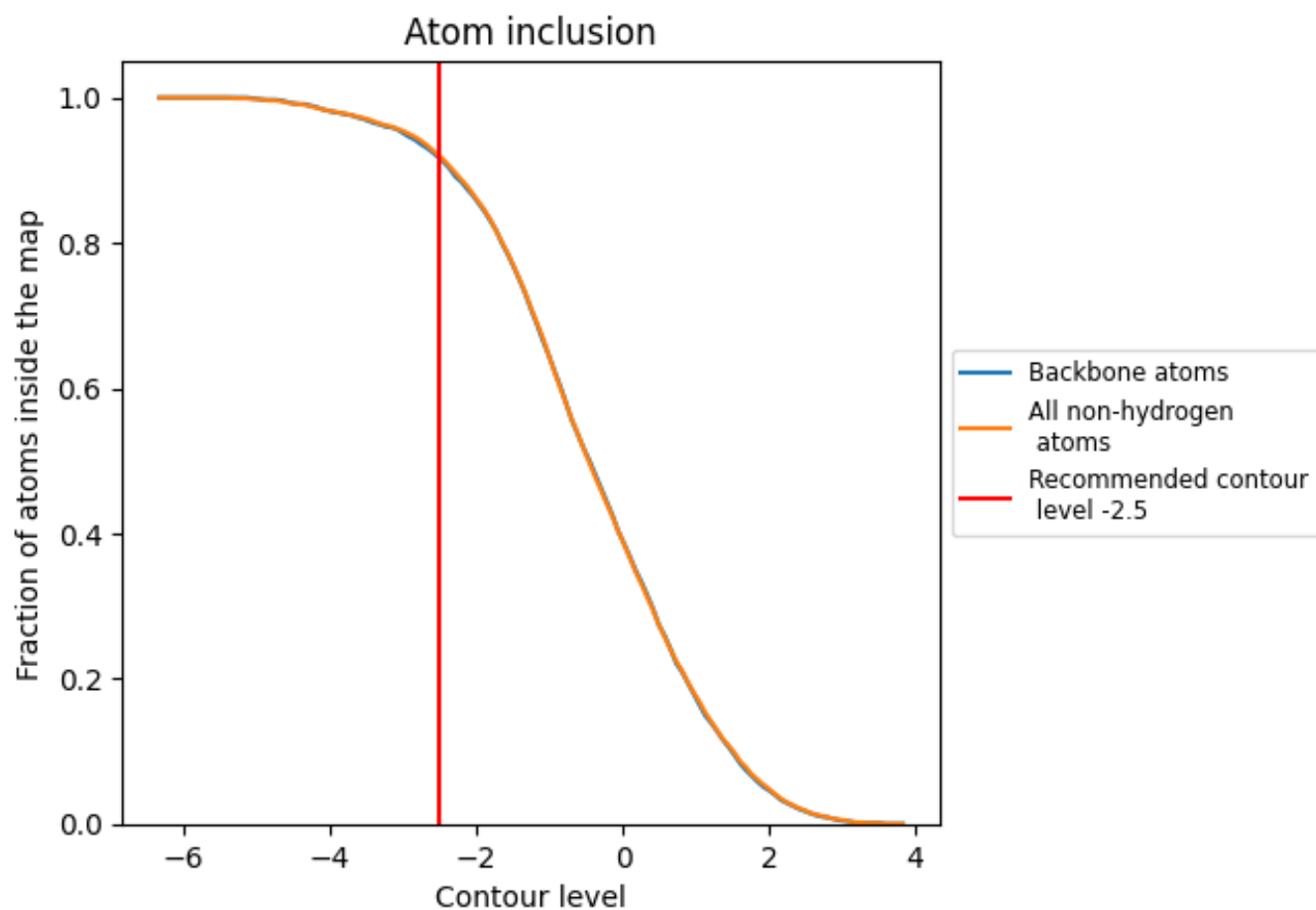
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (-2.5).





9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (-2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9190	 0.0900
N	 0.9190	 0.0900

