



wwPDB EM Validation Summary Report ⓘ

Aug 24, 2026 – 06:05 pm BST

PDB ID : 9H52 / pdb_00009h52
EMDB ID : EMD-51874
Title : Assembly intermediate of human mitochondrial ribosome small subunit in complex with NOA1, ERAL1, METTL17, MCAT and TFB1M (state N1)
Authors : Singh, V.; Shiriaev, D.; Khawaja, A.; Rorbach, J.
Deposited on : 2024-10-22
Resolution : 3.90 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.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : **FAILED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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) : 2.50

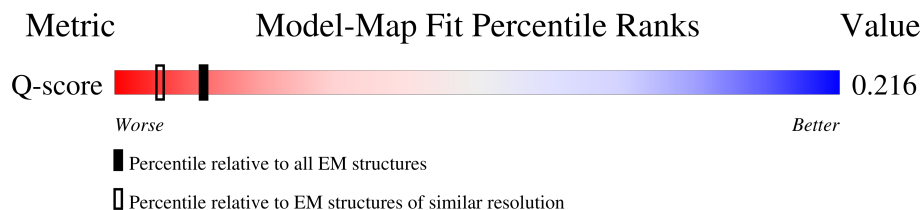
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	8855 (3.40 - 4.40)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

There are 36 unique types of molecules in this entry. The entry contains 128349 atoms, of which 60601 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 protein called GTPase Era, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	a	280	Total	C	H	N	O	S	0	0
			4513	1408	2312	375	408	10		

- Molecule 2 is a protein called Small ribosomal subunit protein mS34.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	0	211	Total	C	H	N	O	S	0	0
			3513	1108	1759	333	308	5		

- Molecule 3 is a protein called Nitric oxide-associated protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	9	446	Total	C	H	N	O	S	0	0
			7202	2271	3644	637	637	13		

- Molecule 4 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	232	Total	C	H	N	O	S	0	0
			3705	1155	1867	345	329	9		

- Molecule 5 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	105	Total	C	H	N	O	S	0	0
			1691	526	852	154	155	4		

- Molecule 6 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	J	108	Total	C	H	N	O	S	0	0
			1728	521	889	169	143	6		

- Molecule 7 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	L	124	Total	C	H	N	O	S	0	0
			2121	664	1081	182	188	6		

- Molecule 8 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	M	115	Total	C	H	N	O	S	0	0
			1862	578	949	181	148	6		

- Molecule 9 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	N	109	Total	C	H	N	O	S	0	0
			1785	557	926	155	144	3		

- Molecule 10 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	O	190	Total	C	H	N	O	S	0	0
			3112	999	1542	291	274	6		

- Molecule 11 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	P	92	Total	C	H	N	O	S	0	0
			1495	472	764	123	128	8		

- Molecule 12 is a protein called MRPS21 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	Q	3	Total	C	H	N	O	S	0	0
			35	10	15	4	5	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	1	ACE	-	acetylation	UNP A0A2J8VEN6

- Molecule 13 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	R	291	Total	C	H	N	O	S	0	0
			4794	1518	2412	409	447	8		

- Molecule 14 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	S	133	Total	C	H	N	O	S	0	0
			2204	709	1104	196	194	1		

- Molecule 15 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	T	164	Total	C	H	N	O	S	0	0
			2706	859	1362	234	240	11		

- Molecule 16 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	U	174	Total	C	H	N	O	S	0	0
			2951	905	1483	295	264	4		

- Molecule 17 is a RNA chain called 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	A	746	Total	C	H	N	O	P	0	0
			23889	7104	8042	2854	5143	746		

- Molecule 18 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	B	220	Total	C	H	N	O	S	0	0
			3581	1142	1792	324	313	10		

- Molecule 19 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	W	98	Total	C	H	N	O	S	0	0
			1569	491	794	138	142	4		

- Molecule 20 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	C	126	Total	C	H	N	O	S	0	0
			2082	679	1040	181	177	5		

- Molecule 21 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	F	208	Total	C	H	N	O	S	0	0
			3501	1104	1777	312	297	11		

- Molecule 22 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	G	292	Total	C	H	N	O	S	0	0
			4766	1522	2371	418	441	14		

- Molecule 23 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	X	352	Total	C	H	N	O	S	0	0
			5705	1822	2857	499	516	11		

- Molecule 24 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Y	108	Total	C	H	N	O	S	0	0
			1778	593	864	150	169	2		

- Molecule 25 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	1	255	Total	C	H	N	O	S	0	0
			4156	1314	2091	346	395	10		

- Molecule 26 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	4	566	Total	C	H	N	O	S	0	0
			9195	2940	4610	774	843	28		

- Molecule 27 is a protein called Malonyl-CoA-acyl carrier protein transacylase, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	8	326	Total	C	H	N	O	S	0	0
			5119	1617	2576	463	446	17		

- Molecule 28 is a protein called Isoform 2 of Ribosome assembly protein METTL17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	7	398	Total	C	H	N	O	S	0	0
			6327	2006	3182	579	544	16		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	422	ARG	-	insertion	UNP Q9H7H0
7	423	ASP	-	insertion	UNP Q9H7H0
7	424	LEU	-	insertion	UNP Q9H7H0
7	425	TYR	-	insertion	UNP Q9H7H0
7	426	ARG	-	insertion	UNP Q9H7H0
7	427	CYS	-	insertion	UNP Q9H7H0
7	428	ALA	-	insertion	UNP Q9H7H0
7	429	ARG	-	insertion	UNP Q9H7H0
7	430	VAL	-	insertion	UNP Q9H7H0

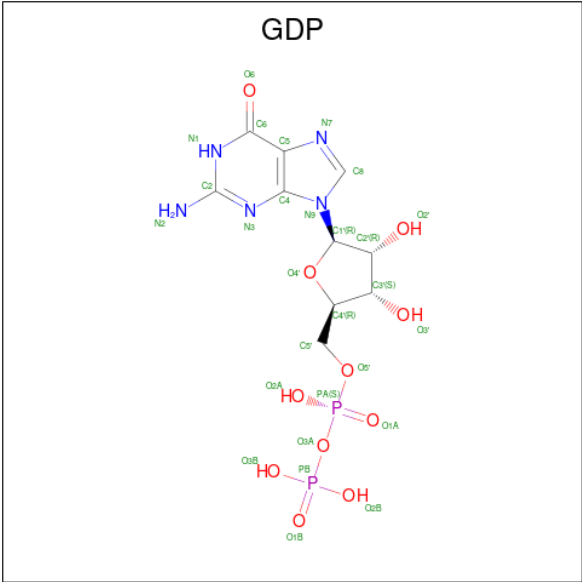
- Molecule 29 is a protein called Dimethyladenosine transferase 1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	5	319	Total	C	H	N	O	S	0	0
			5229	1648	2661	458	451	11		

- Molecule 30 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	V	359	Total	C	H	N	O	S	0	0
			5897	1891	2951	491	552	12		

- Molecule 31 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

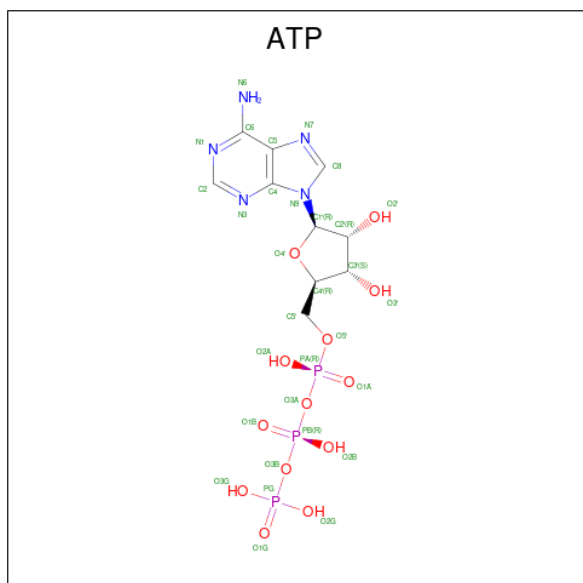


Mol	Chain	Residues	Atoms			AltConf
33	P	1	Total	Fe	S	0
			4	2	2	
33	T	1	Total	Fe	S	0
			4	2	2	

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

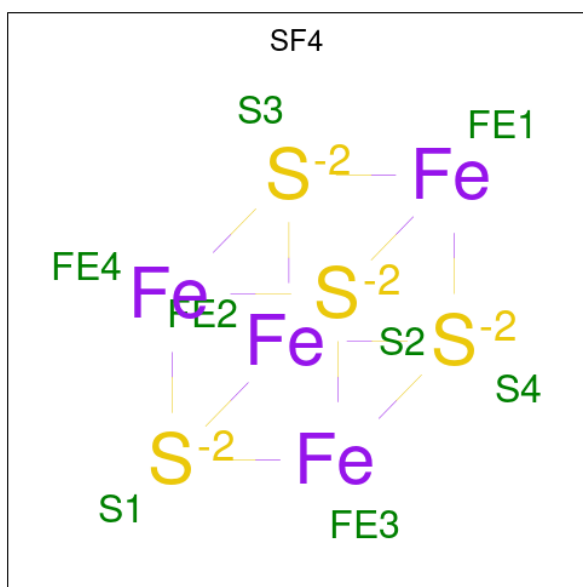
Mol	Chain	Residues	Atoms		AltConf
34	B	1	Total	Mg	0
			1	1	
34	X	1	Total	Mg	0
			1	1	

- Molecule 35 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms						AltConf
35	X	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

- Molecule 36 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
36	7	1	8	4	4	0

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11115	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.736	Depositor
Minimum map value	-1.271	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.029	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	609.12, 609.12, 609.12	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0152, 1.0152, 1.0152	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 for Mogul analysis.

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	$\# Z > 2$
35	ATP	X	501	34	29,33,33	0.48	0	44,52,52	0.52	0
36	SF4	7	501	28	0,12,12	-	-	-		
33	FES	T	201	8,15	0,4,4	-	-	-		
31	GDP	9	701	-	28,30,30	0.45	0	44,47,47	0.59	0
33	FES	P	201	11,5	0,4,4	-	-	-		
31	GDP	X	503	-	28,30,30	0.42	0	44,47,47	0.53	0

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
35	ATP	X	501	34	-	2/22/38/38	0/3/3/3
36	SF4	7	501	28	-	-	0/6/5/5
33	FES	T	201	8,15	-	-	0/1/1/1
31	GDP	9	701	-	-	3/16/32/32	0/3/3/3
33	FES	P	201	11,5	-	-	0/1/1/1
31	GDP	X	503	-	-	5/16/32/32	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

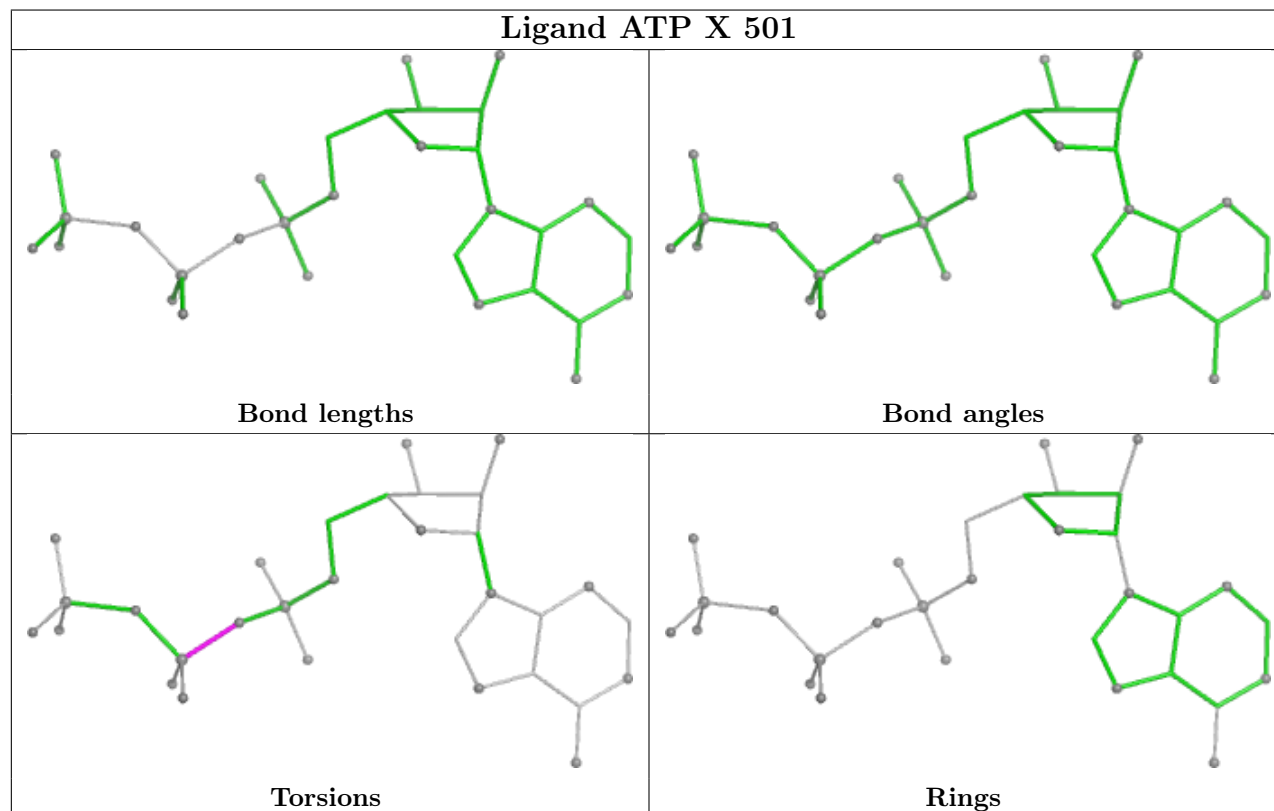
Mol	Chain	Res	Type	Atoms
31	9	701	GDP	O4'-C4'-C5'-O5'
31	9	701	GDP	C3'-C4'-C5'-O5'
31	X	503	GDP	C5'-O5'-PA-O3A
31	X	503	GDP	PB-O3A-PA-O1A
35	X	501	ATP	PA-O3A-PB-O1B

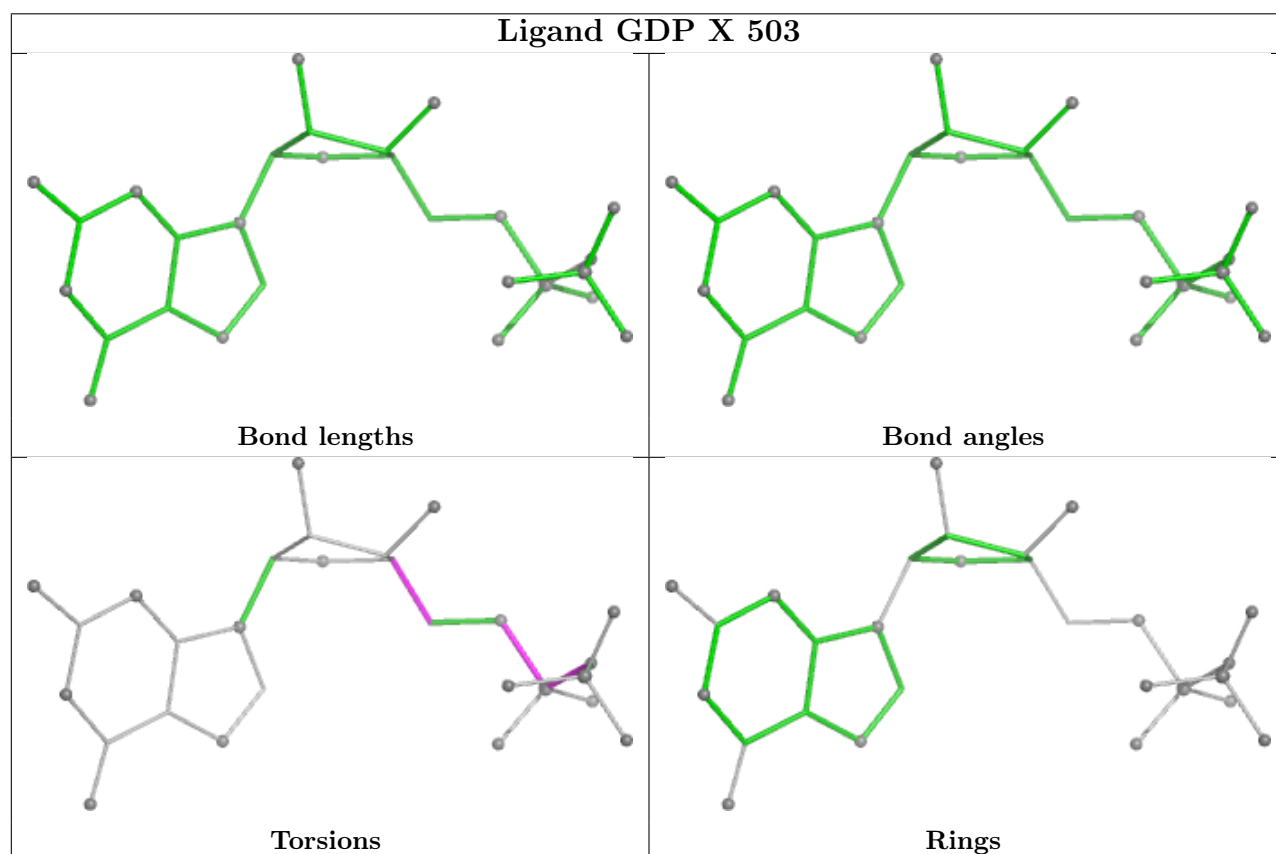
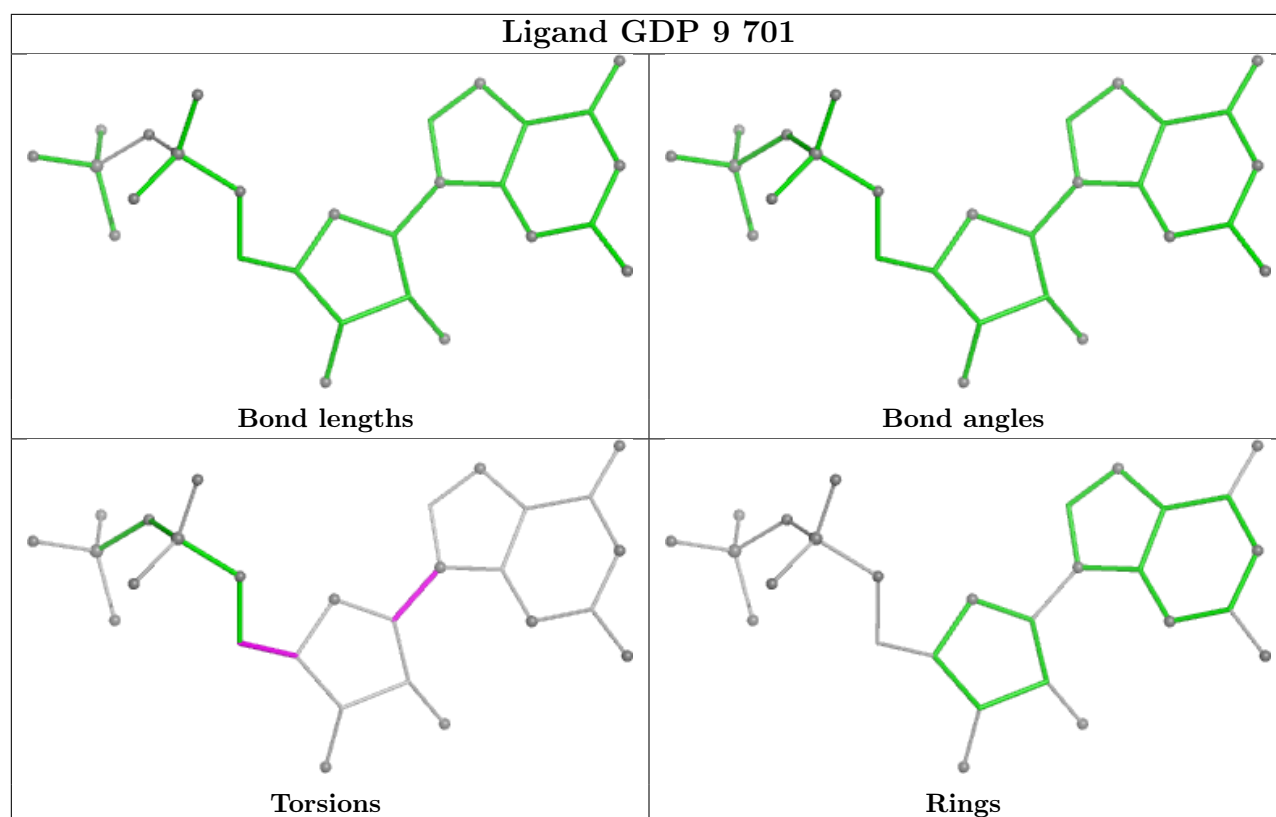
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

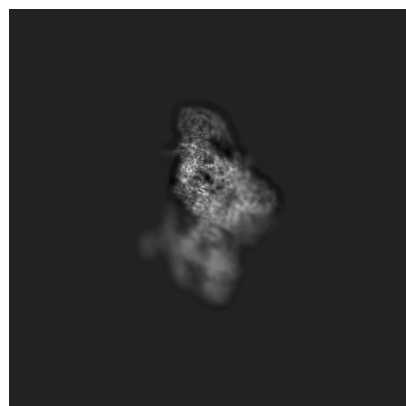
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51874. These allow visual inspection of the internal detail of the map and identification of artifacts.

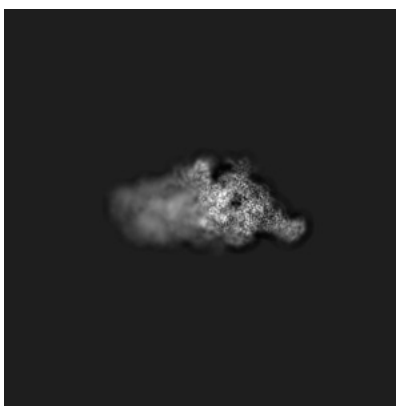
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

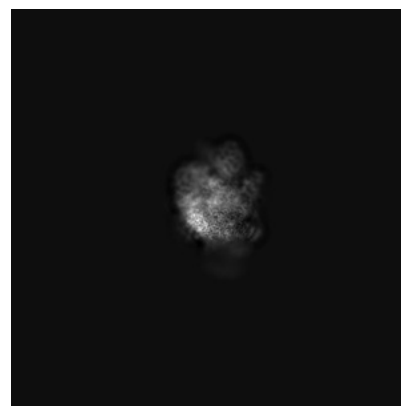
5.1.1 Primary map



X

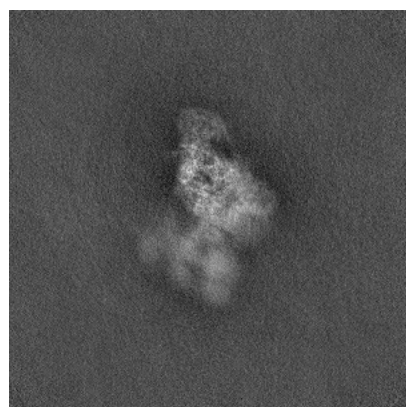


Y

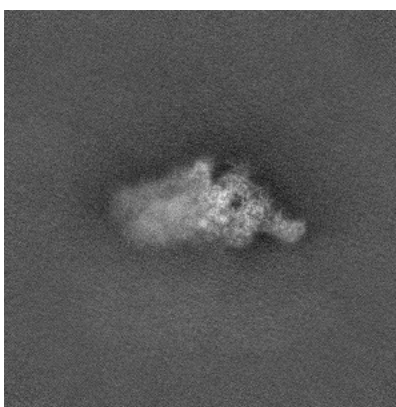


Z

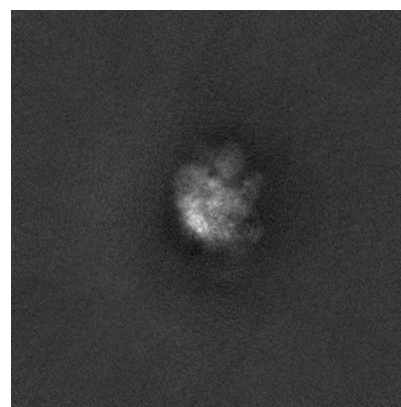
5.1.2 Raw map



X



Y

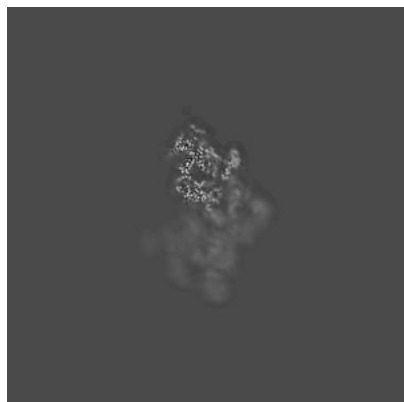


Z

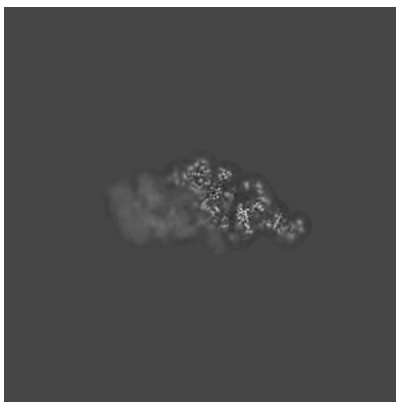
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

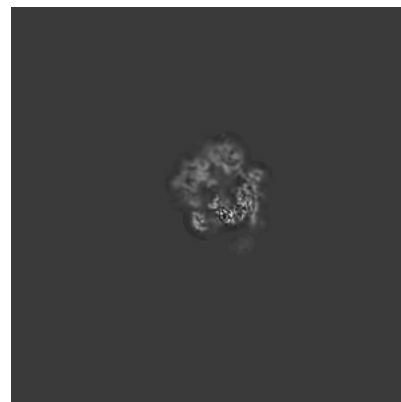
5.2.1 Primary map



X Index: 300



Y Index: 300

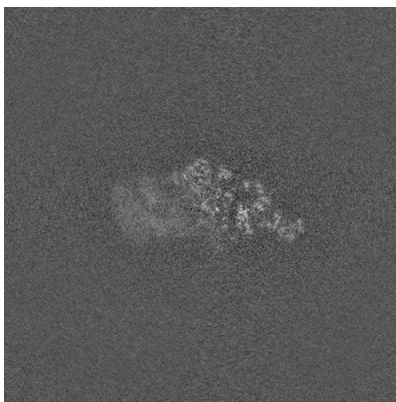


Z Index: 300

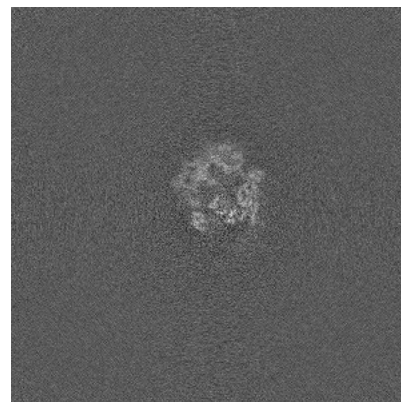
5.2.2 Raw map



X Index: 300



Y Index: 300



Z Index: 300

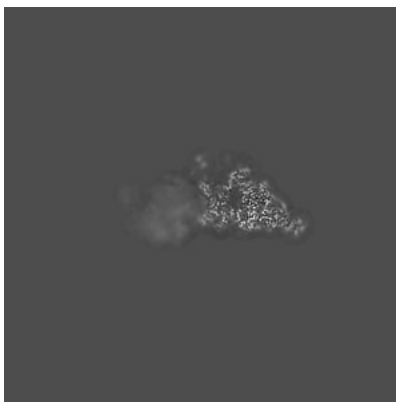
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

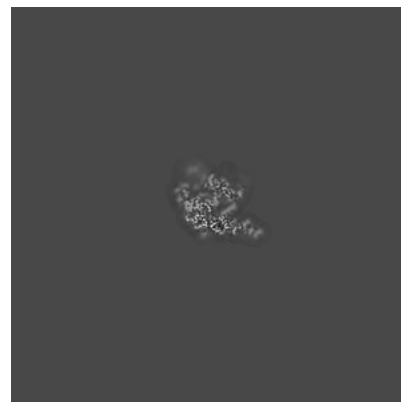
5.3.1 Primary map



X Index: 280



Y Index: 278

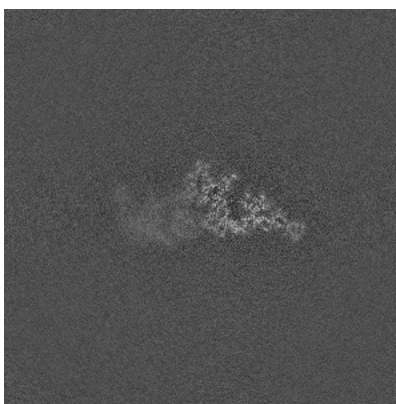


Z Index: 365

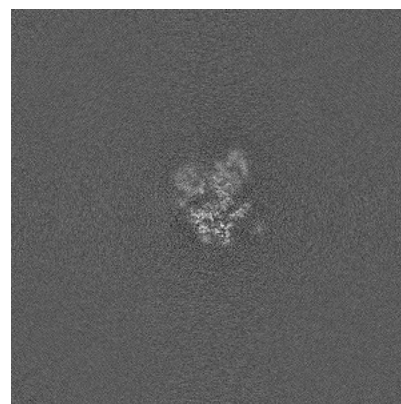
5.3.2 Raw map



X Index: 300



Y Index: 290

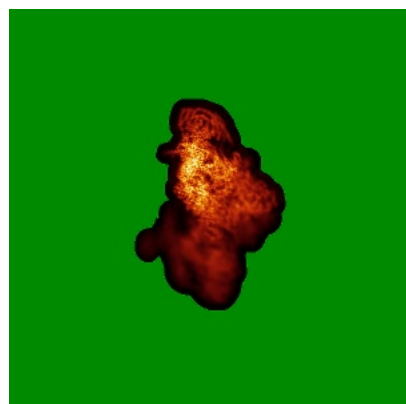


Z Index: 333

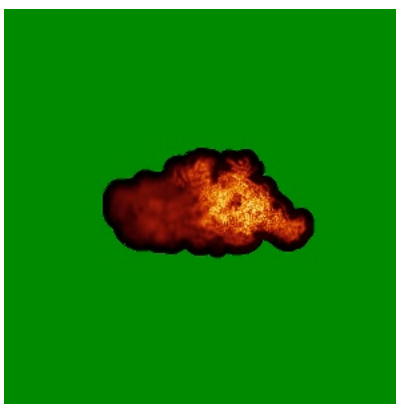
The images above show the largest variance slices of the map in three orthogonal directions.

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

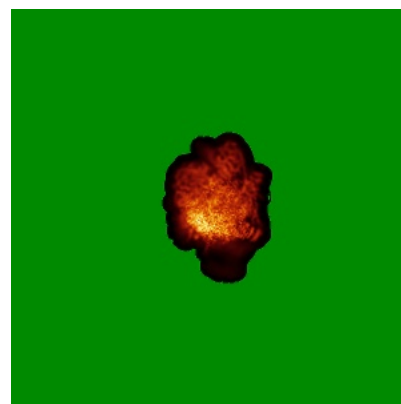
5.4.1 Primary map



X

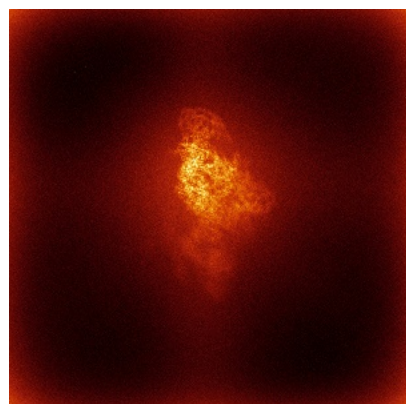


Y

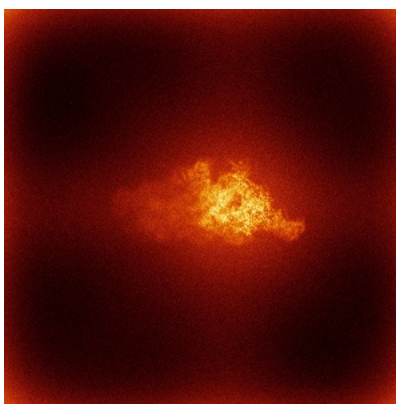


Z

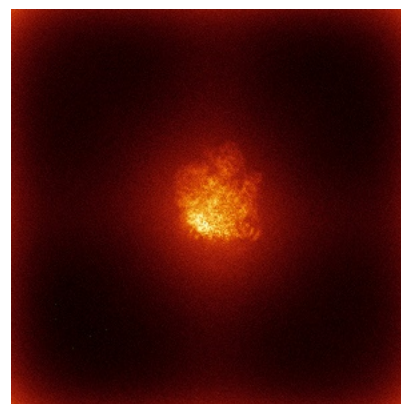
5.4.2 Raw map



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.

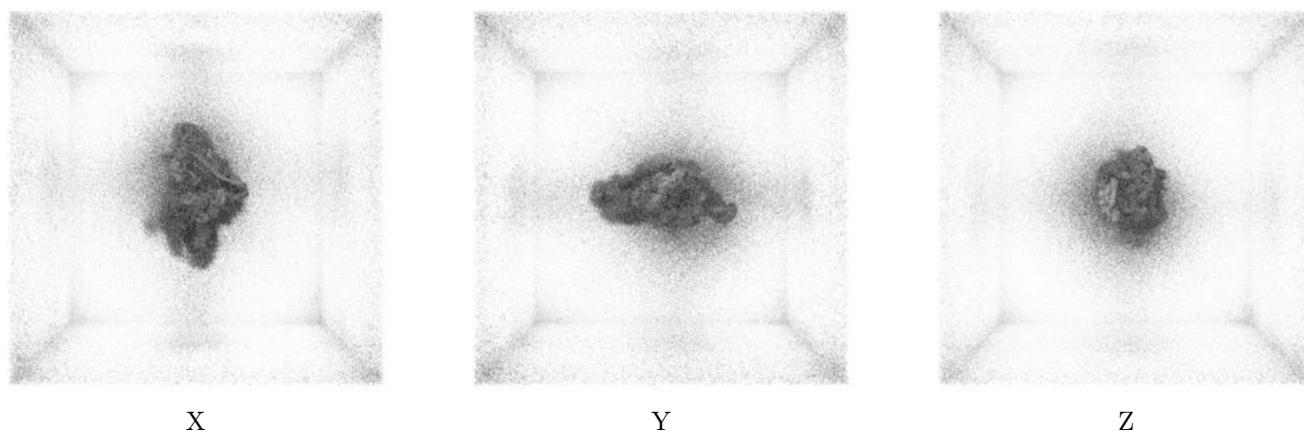
5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

5.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

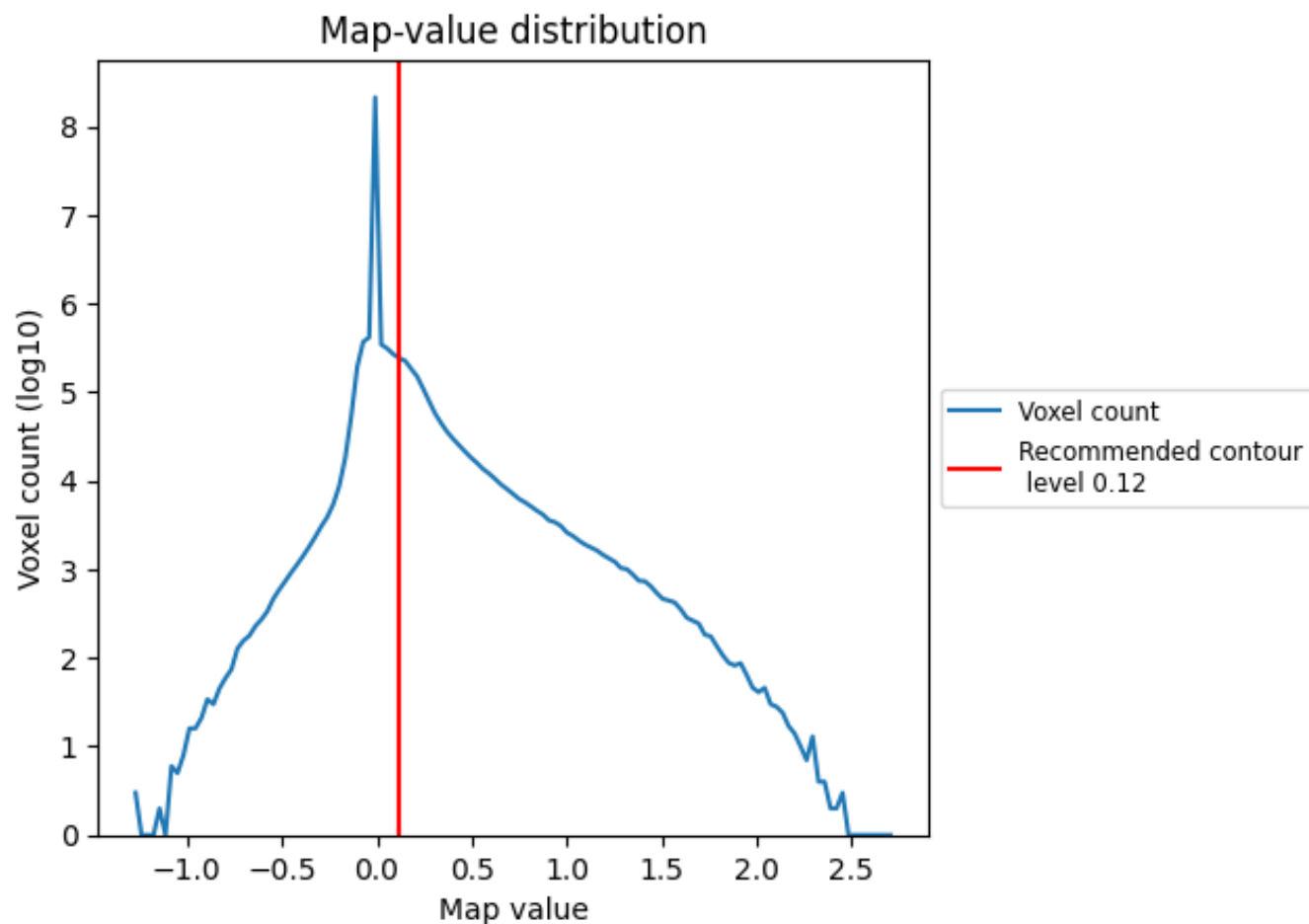
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

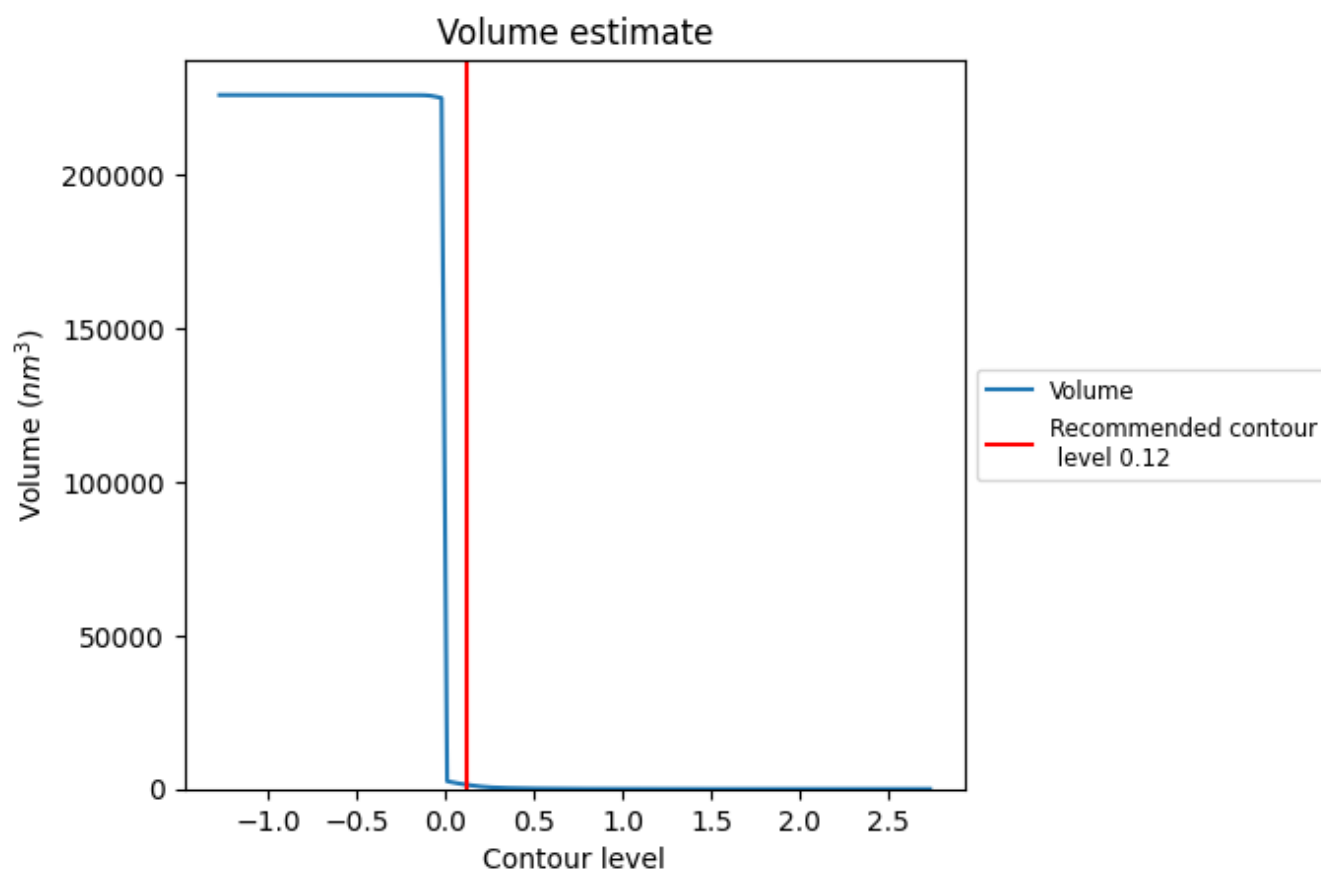
This section contains the results of statistical analysis of the map.

6.1 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.

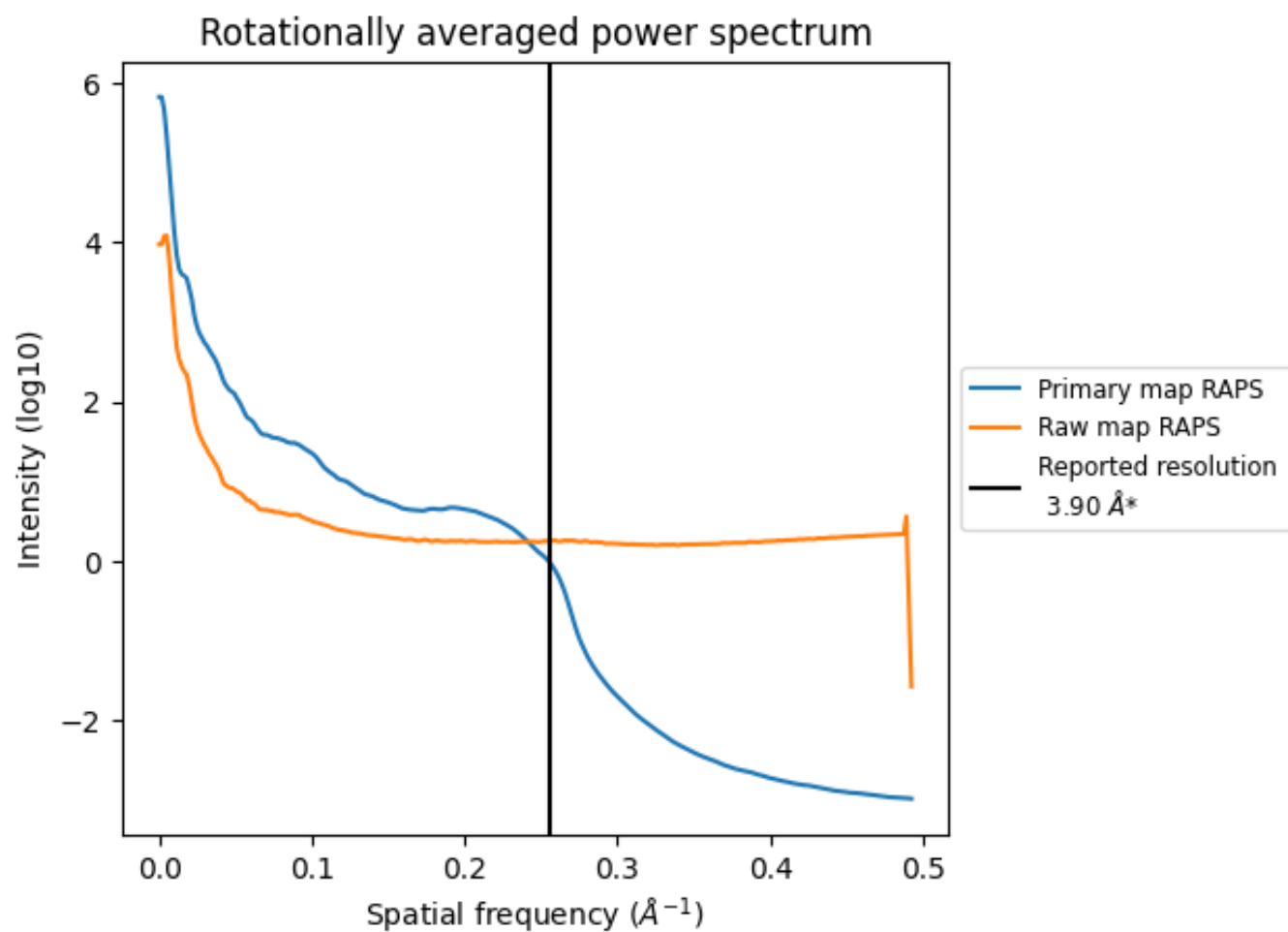
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 1403 nm^3 ; this corresponds to an approximate mass of 1267 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.

6.3 Rotationally averaged power spectrum ⓘ

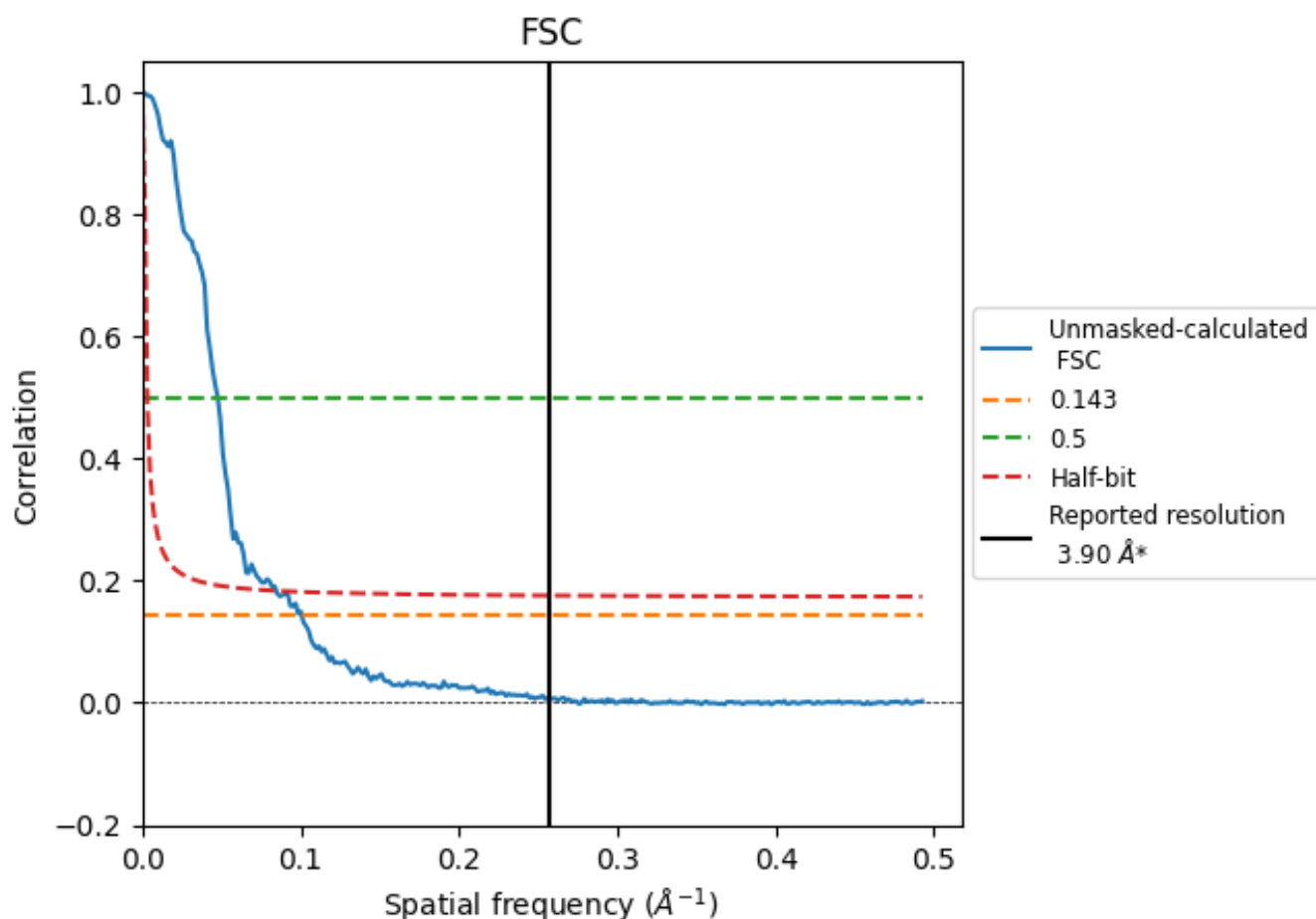


*Reported resolution corresponds to spatial frequency of 0.256 $\text{\AA}^{-1}$

7 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

7.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

7.2 Resolution estimates [i](#)

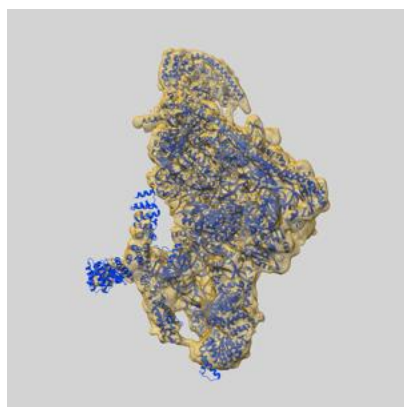
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.93	21.01	11.81

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.93 differs from the reported value 3.9 by more than 10 %

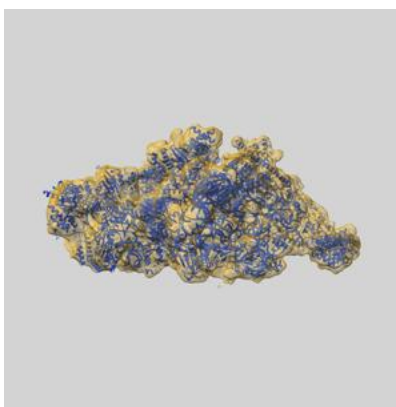
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51874 and PDB model 9H52. Per-residue inclusion information can be found in section ?? on page ??.

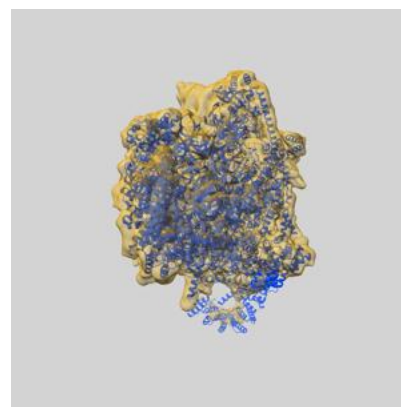
8.1 Map-model overlay [i](#)



X



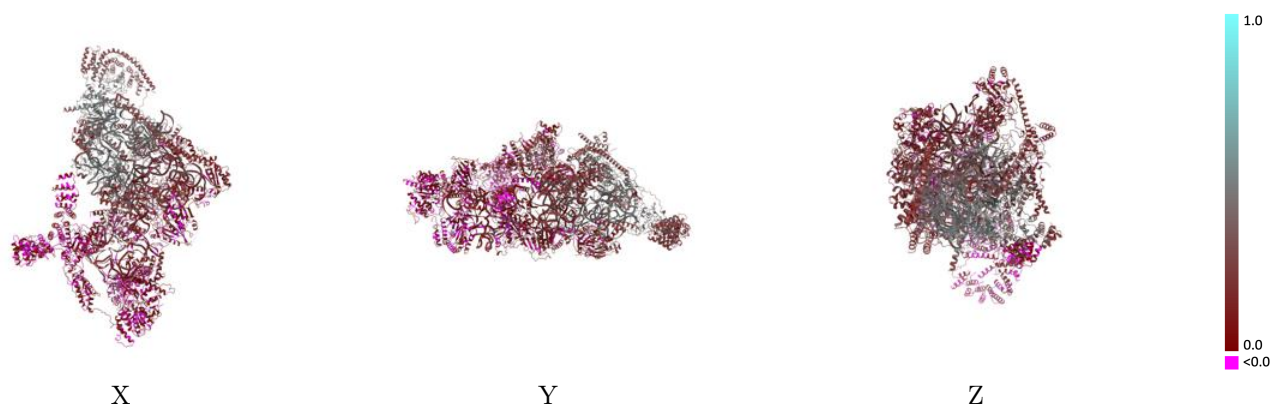
Y



Z

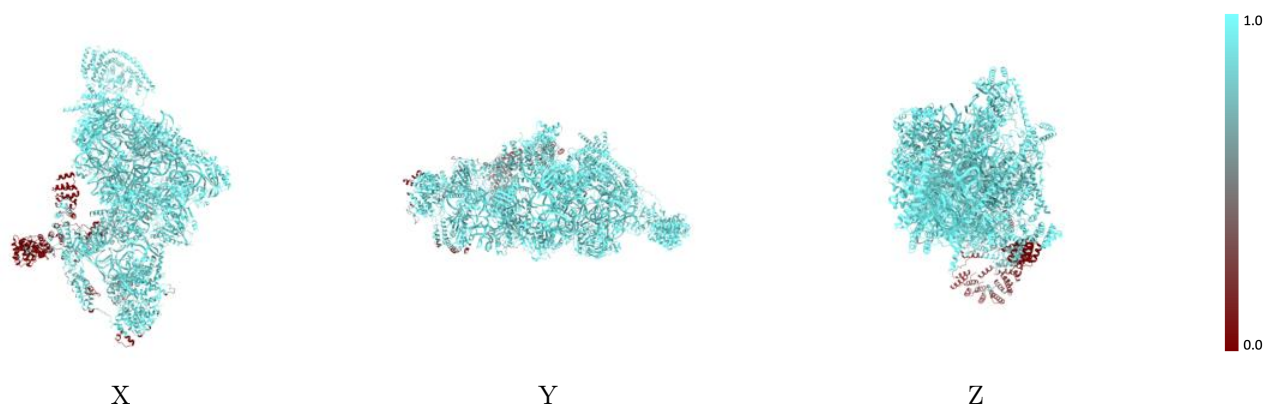
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



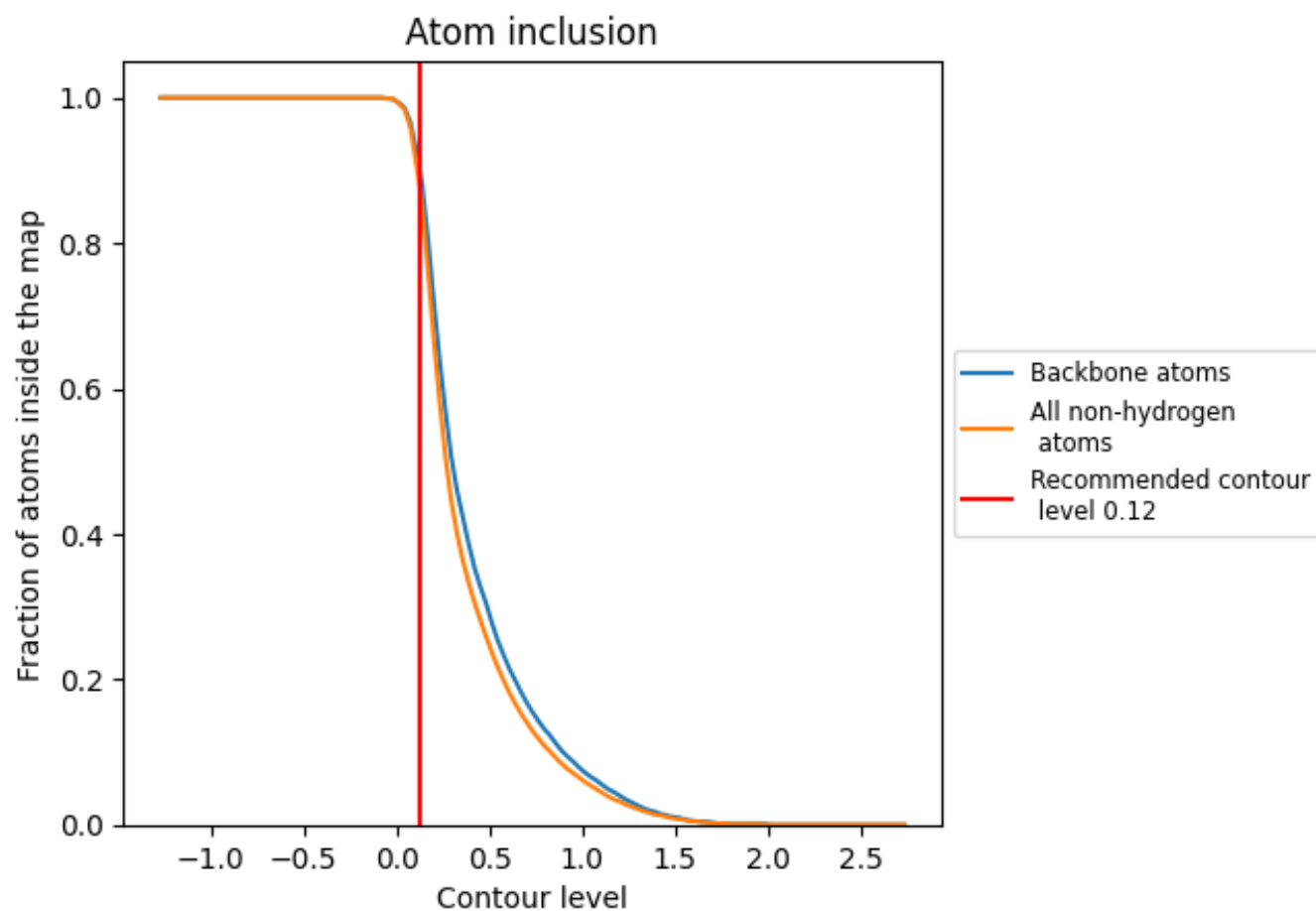
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

8.3 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 (0.12).

8.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8870	 0.2160
0	 0.9670	 0.4150
1	 0.7320	 0.0620
4	 0.3250	 0.0440
5	 0.9450	 0.1440
7	 0.9390	 0.0970
8	 0.8960	 0.0460
9	 0.9200	 0.1930
A	 0.9880	 0.2780
B	 0.9530	 0.2680
C	 0.8620	 0.0620
D	 0.9580	 0.4300
E	 0.9660	 0.1660
F	 0.9420	 0.0960
G	 0.8680	 0.1220
J	 0.9440	 0.3870
L	 0.9390	 0.1890
M	 0.9790	 0.4870
N	 0.9680	 0.4110
O	 0.9770	 0.4590
P	 0.9630	 0.1660
Q	 0.7500	 0.0090
R	 0.9700	 0.4150
S	 0.9440	 0.2480
T	 0.9560	 0.4210
U	 0.9710	 0.2970
V	 0.9550	 0.2540
W	 0.9540	 0.1820
X	 0.9390	 0.0570
Y	 0.6990	 0.0440
a	 0.9620	 0.0880

