wwPDB EM Validation Summary Report (i)

Mar 8, 2026 – 06:47 AM UTC

PDB ID	:	7X96 / pdb_00007x96
EMDB ID	:	EMD-33068
Title	:	The SARS-CoV-2 receptor binding domain bound with the Fab fragment of a human neutralizing antibody Ab847
Authors	:	Kamada, K.; Shirouzu, M.
Deposited on	:	2022-03-15
Resolution	:	3.40 Å(reported)
Based on initial model	:	5CCK

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 (i) 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 (i)) were used in the production of this report:

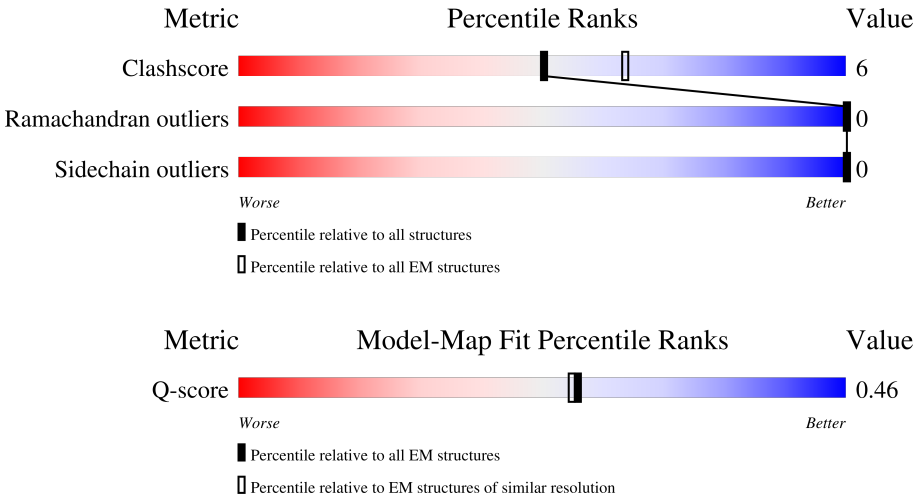
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 3.40 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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 <=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	G	1278	14% 85%
2	H	262	39% 6% 54%
3	L	242	38% 7% 55%
4	A	6	50% 50% 50%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6647 atoms, of which 3245 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	G	198	3065	1007	1496	262	292	8	0	0

There are 79 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	682	GLY	ARG	engineered mutation	UNP P0DTC2
G	683	SER	ARG	engineered mutation	UNP P0DTC2
G	685	SER	ARG	engineered mutation	UNP P0DTC2
G	817	PRO	PHE	engineered mutation	UNP P0DTC2
G	892	PRO	ALA	engineered mutation	UNP P0DTC2
G	899	PRO	ALA	engineered mutation	UNP P0DTC2
G	942	PRO	ALA	engineered mutation	UNP P0DTC2
G	986	PRO	LYS	engineered mutation	UNP P0DTC2
G	987	PRO	VAL	engineered mutation	UNP P0DTC2
G	1209	ALA	-	expression tag	UNP P0DTC2
G	1210	ALA	-	expression tag	UNP P0DTC2
G	1211	ALA	-	expression tag	UNP P0DTC2
G	1212	GLY	-	expression tag	UNP P0DTC2
G	1213	SER	-	expression tag	UNP P0DTC2
G	1214	GLY	-	expression tag	UNP P0DTC2
G	1215	TYR	-	expression tag	UNP P0DTC2
G	1216	ILE	-	expression tag	UNP P0DTC2
G	1217	PRO	-	expression tag	UNP P0DTC2
G	1218	GLU	-	expression tag	UNP P0DTC2
G	1219	ALA	-	expression tag	UNP P0DTC2
G	1220	PRO	-	expression tag	UNP P0DTC2
G	1221	ARG	-	expression tag	UNP P0DTC2
G	1222	ASP	-	expression tag	UNP P0DTC2
G	1223	GLY	-	expression tag	UNP P0DTC2
G	1224	GLN	-	expression tag	UNP P0DTC2
G	1225	ALA	-	expression tag	UNP P0DTC2
G	1226	TYR	-	expression tag	UNP P0DTC2
G	1227	VAL	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1228	ARG	-	expression tag	UNP P0DTC2
G	1229	LYS	-	expression tag	UNP P0DTC2
G	1230	ASP	-	expression tag	UNP P0DTC2
G	1231	GLY	-	expression tag	UNP P0DTC2
G	1232	GLU	-	expression tag	UNP P0DTC2
G	1233	TRP	-	expression tag	UNP P0DTC2
G	1234	VAL	-	expression tag	UNP P0DTC2
G	1235	LEU	-	expression tag	UNP P0DTC2
G	1236	LEU	-	expression tag	UNP P0DTC2
G	1237	SER	-	expression tag	UNP P0DTC2
G	1238	THR	-	expression tag	UNP P0DTC2
G	1239	PHE	-	expression tag	UNP P0DTC2
G	1240	LEU	-	expression tag	UNP P0DTC2
G	1241	GLY	-	expression tag	UNP P0DTC2
G	1242	SER	-	expression tag	UNP P0DTC2
G	1243	SER	-	expression tag	UNP P0DTC2
G	1244	GLY	-	expression tag	UNP P0DTC2
G	1245	ARG	-	expression tag	UNP P0DTC2
G	1246	GLU	-	expression tag	UNP P0DTC2
G	1247	ASN	-	expression tag	UNP P0DTC2
G	1248	LEU	-	expression tag	UNP P0DTC2
G	1249	TYR	-	expression tag	UNP P0DTC2
G	1250	PHE	-	expression tag	UNP P0DTC2
G	1251	GLN	-	expression tag	UNP P0DTC2
G	1252	GLY	-	expression tag	UNP P0DTC2
G	1253	GLY	-	expression tag	UNP P0DTC2
G	1254	GLY	-	expression tag	UNP P0DTC2
G	1255	GLY	-	expression tag	UNP P0DTC2
G	1256	SER	-	expression tag	UNP P0DTC2
G	1257	GLY	-	expression tag	UNP P0DTC2
G	1258	LEU	-	expression tag	UNP P0DTC2
G	1259	ASN	-	expression tag	UNP P0DTC2
G	1260	ASP	-	expression tag	UNP P0DTC2
G	1261	ILE	-	expression tag	UNP P0DTC2
G	1262	PHE	-	expression tag	UNP P0DTC2
G	1263	GLU	-	expression tag	UNP P0DTC2
G	1264	ALA	-	expression tag	UNP P0DTC2
G	1265	GLN	-	expression tag	UNP P0DTC2
G	1266	LYS	-	expression tag	UNP P0DTC2
G	1267	ILE	-	expression tag	UNP P0DTC2
G	1268	GLU	-	expression tag	UNP P0DTC2
G	1269	TRP	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1270	HIS	-	expression tag	UNP P0DTC2
G	1271	GLU	-	expression tag	UNP P0DTC2
G	1272	GLY	-	expression tag	UNP P0DTC2
G	1273	HIS	-	expression tag	UNP P0DTC2
G	1274	HIS	-	expression tag	UNP P0DTC2
G	1275	HIS	-	expression tag	UNP P0DTC2
G	1276	HIS	-	expression tag	UNP P0DTC2
G	1277	HIS	-	expression tag	UNP P0DTC2
G	1278	HIS	-	expression tag	UNP P0DTC2

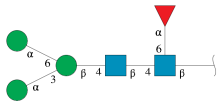
- Molecule 2 is a protein called Ab847 heavy chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	H	120	Total	C	H	N	O	S	0	0
			1826	589	896	154	182	5		

- Molecule 3 is a protein called Ab847 light chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	L	109	Total	C	H	N	O	S	0	0
			1624	523	792	138	167	4		

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



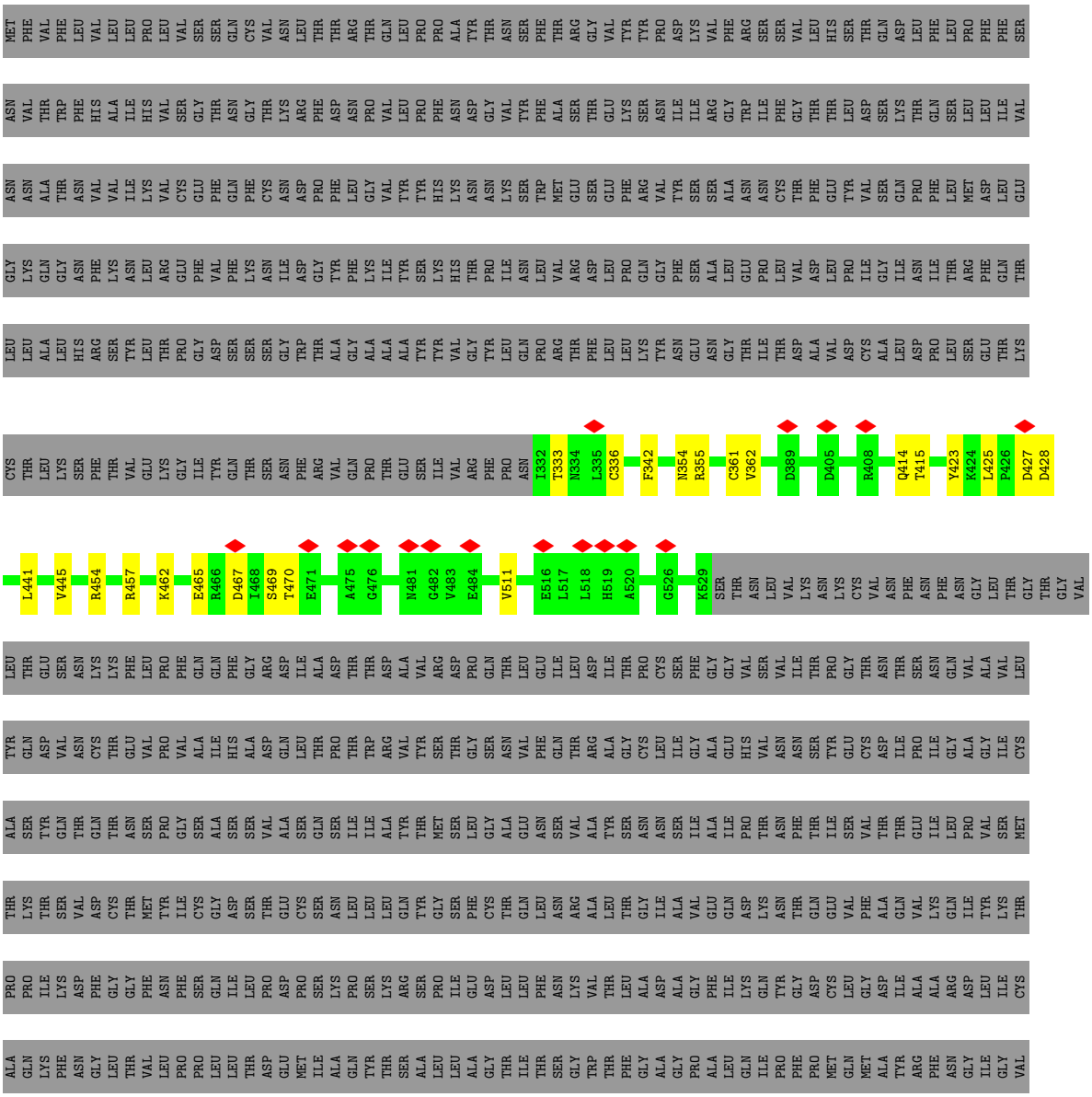
Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	6	Total	C	H	N	O	0	0
			132	40	61	2	29		

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.

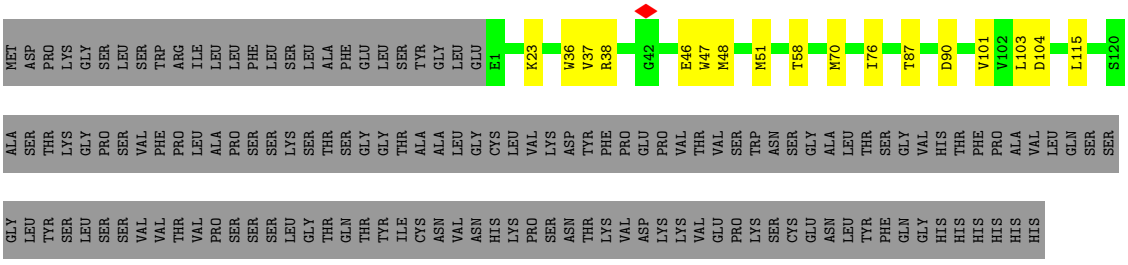
- Molecule 1: Spike glycoprotein

Chain G:



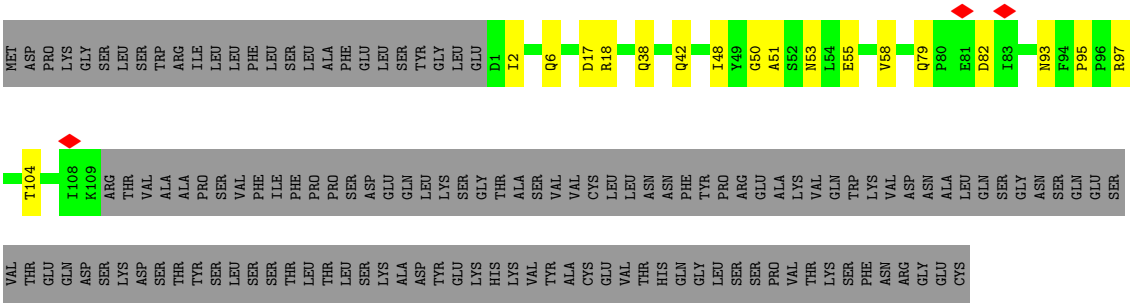
• Molecule 2: Ab847 heavy chain

Chain H:



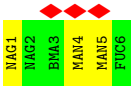
• Molecule 3: Ab847 light chain

Chain L:



• Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain A:


NAG1
NAG2
BMA3
MAN4
MAN5
FUC6

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	249414	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.034	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0114	Depositor
Map size (Å)	130.982, 130.982, 130.982	wwPDB
Map dimensions	158, 158, 158	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82899994, 0.82899994, 0.82899994	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, FUC, MAN, NAG

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	G	0.11	0/1613	0.26	0/2194
2	H	0.14	0/952	0.27	0/1298
3	L	0.14	0/852	0.34	0/1158
All	All	0.12	0/3417	0.29	0/4650

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

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	G	1569	1496	1496	15	0
2	H	930	896	898	12	0
3	L	832	792	794	12	0
4	A	71	61	61	2	0
All	All	3402	3245	3249	37	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 6.

The worst 5 of 37 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:G:454:ARG:NH2	1:G:469:SER:O	2.21	0.74
1:G:441:LEU:O	3:L:93:ASN:ND2	2.22	0.73
1:G:457:ARG:NE	1:G:467:ASP:OD2	2.23	0.70
3:L:17:ASP:OD2	3:L:18:ARG:N	2.27	0.67
4:A:1:NAG:O3	4:A:1:NAG:O7	2.14	0.66

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	196/1278 (15%)	179 (91%)	17 (9%)	0	100	100
2	H	118/262 (45%)	108 (92%)	10 (8%)	0	100	100
3	L	107/242 (44%)	97 (91%)	10 (9%)	0	100	100
All	All	421/1782 (24%)	384 (91%)	37 (9%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	171/1108 (15%)	171 (100%)	0	100	100
2	H	101/225 (45%)	101 (100%)	0	100	100
3	L	94/213 (44%)	94 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	366/1546 (24%)	366 (100%)	0	100 100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	65	GLN
3	L	93	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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)

6 monosaccharides are modelled in this entry.

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	$\#\|Z\| > 2$
4	NAG	A	1	4,1	14,14,15	0.25	0	17,19,21	0.44	0
4	NAG	A	2	4	14,14,15	0.23	0	17,19,21	0.45	0
4	BMA	A	3	4	11,11,12	0.49	0	15,15,17	0.70	0
4	MAN	A	4	4	11,11,12	0.64	0	15,15,17	0.96	2 (13%)
4	MAN	A	5	4	11,11,12	0.63	0	15,15,17	0.96	2 (13%)
4	FUC	A	6	4	10,10,11	0.60	0	14,14,16	0.71	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
4	NAG	A	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	A	2	4	-	0/6/23/26	0/1/1/1
4	BMA	A	3	4	-	2/2/19/22	0/1/1/1
4	MAN	A	4	4	-	0/2/19/22	0/1/1/1
4	MAN	A	5	4	-	1/2/19/22	0/1/1/1
4	FUC	A	6	4	-	-	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	4	MAN	O2-C2-C3	-2.20	105.58	110.15
4	A	5	MAN	C1-O5-C5	2.19	115.13	112.19
4	A	5	MAN	O2-C2-C3	-2.18	105.63	110.15
4	A	4	MAN	C1-O5-C5	2.08	114.98	112.19

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	3	BMA	O5-C5-C6-O6
4	A	3	BMA	C4-C5-C6-O6
4	A	5	MAN	O5-C5-C6-O6
4	A	1	NAG	C1-C2-N2-C7
4	A	1	NAG	C3-C2-N2-C7

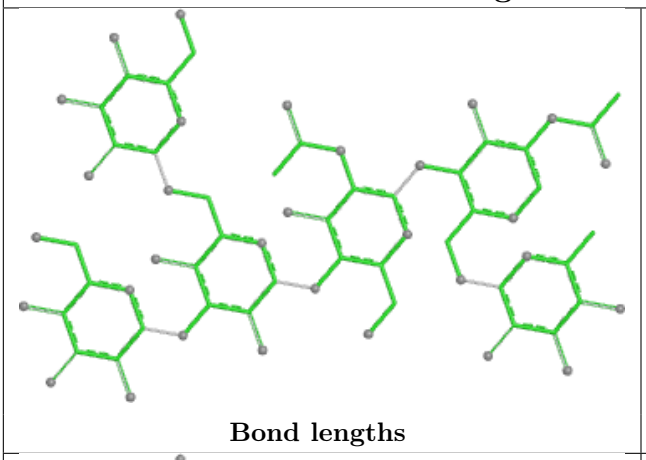
There are no ring outliers.

1 monomer is involved in 2 short contacts:

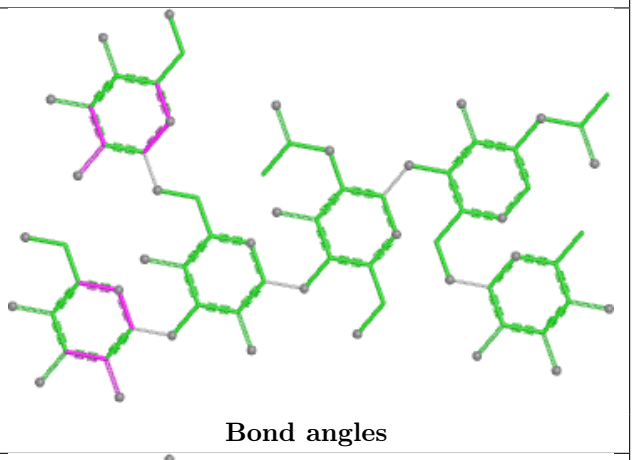
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1	NAG	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

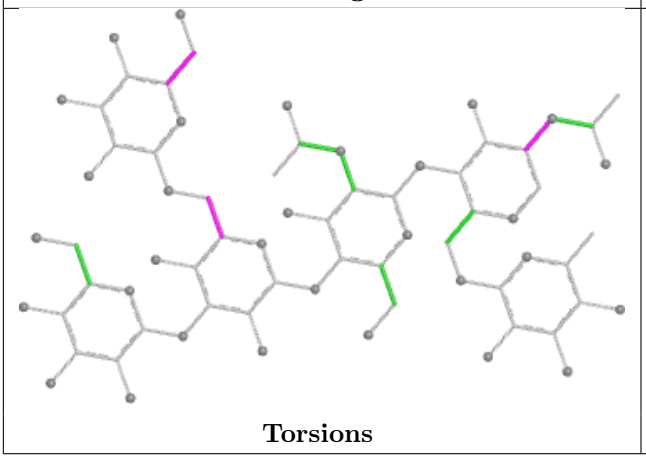
Oligosaccharide Chain A



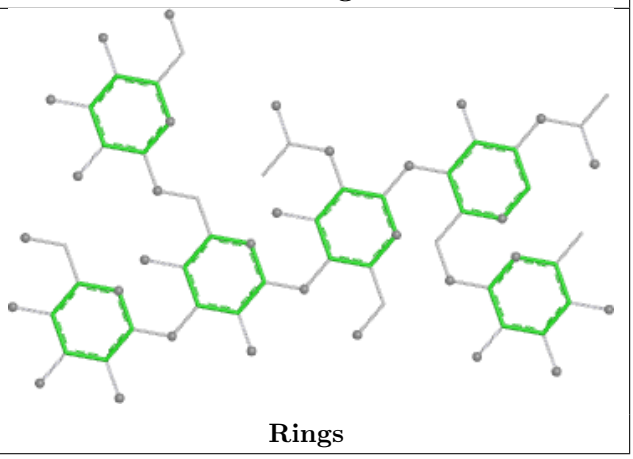
Bond lengths



Bond angles



Torsions



Rings

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.

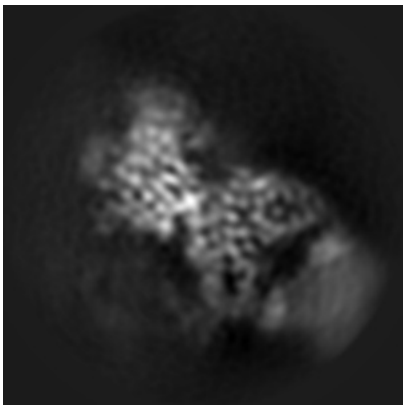
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-33068. These allow visual inspection of the internal detail of the map and identification of artifacts.

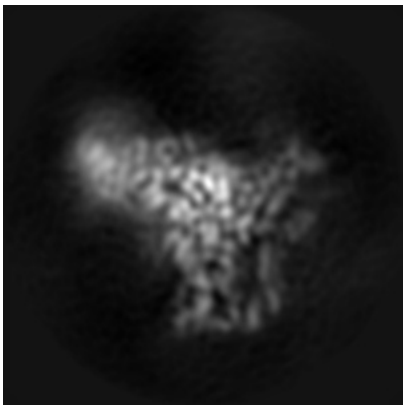
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

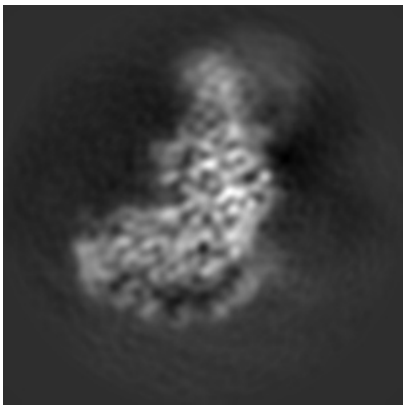
6.1.1 Primary map



X

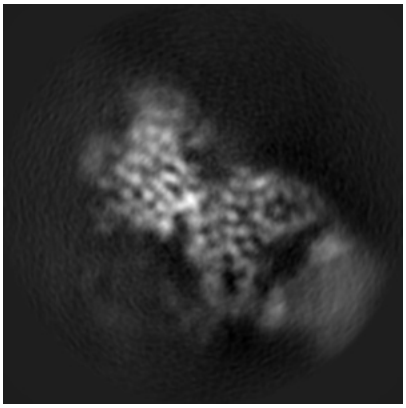


Y

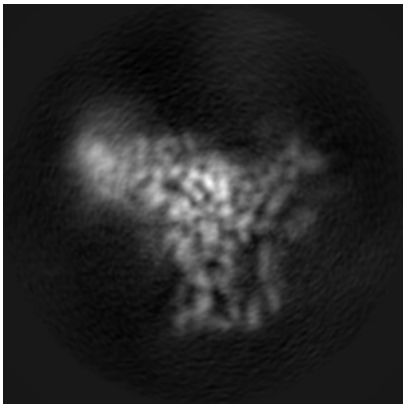


Z

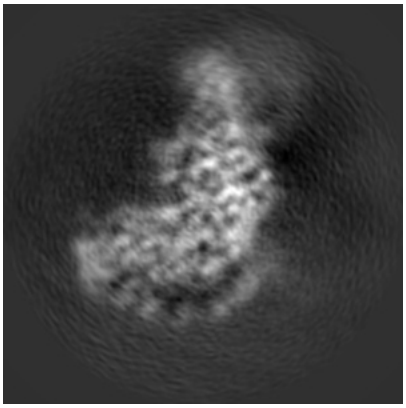
6.1.2 Raw map



X



Y

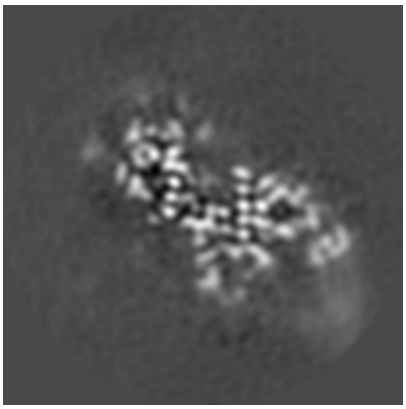


Z

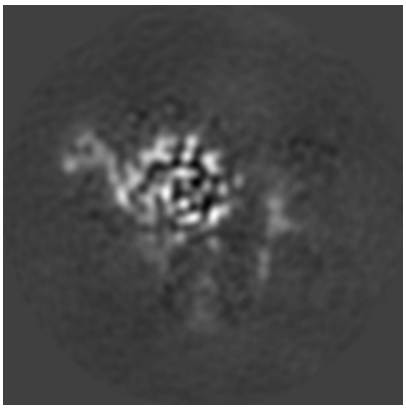
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

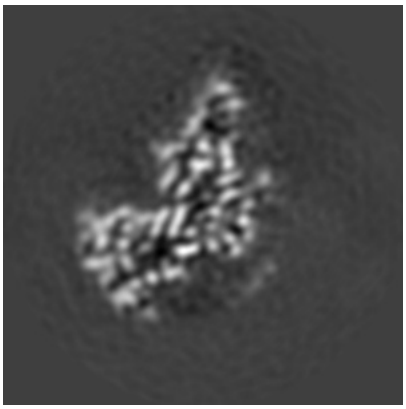
6.2.1 Primary map



X Index: 79

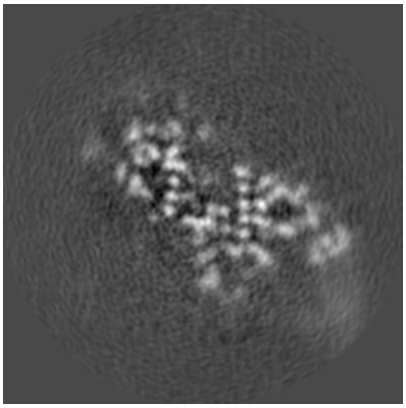


Y Index: 79

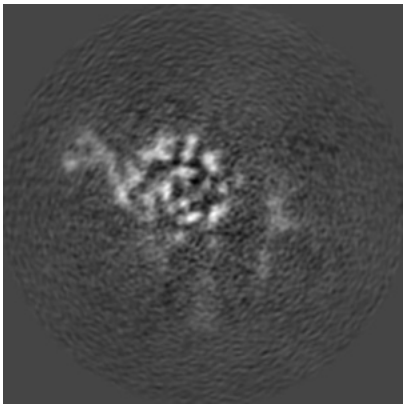


Z Index: 79

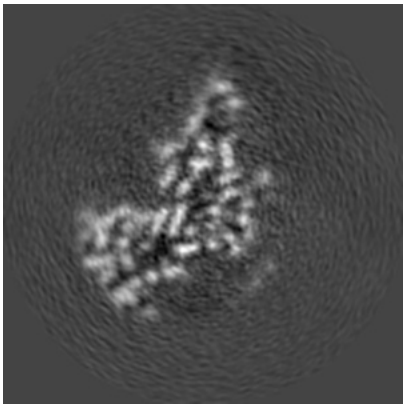
6.2.2 Raw map



X Index: 79



Y Index: 79

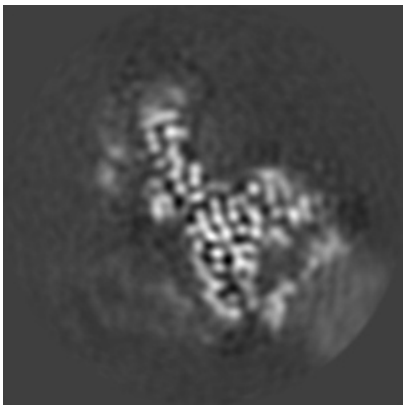


Z Index: 79

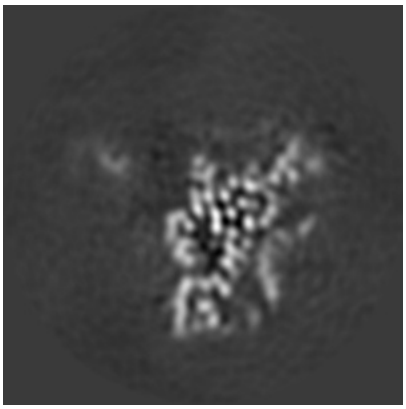
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

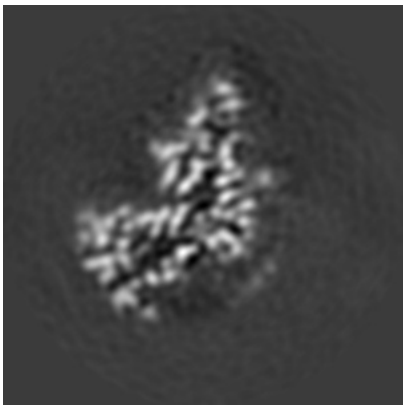
6.3.1 Primary map



X Index: 91

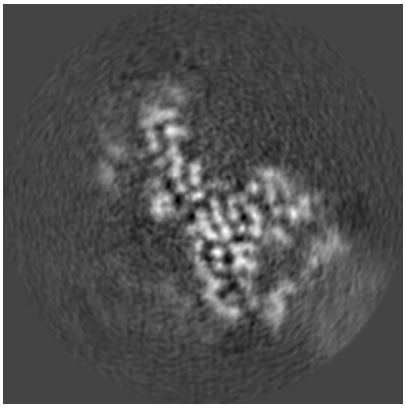


Y Index: 64

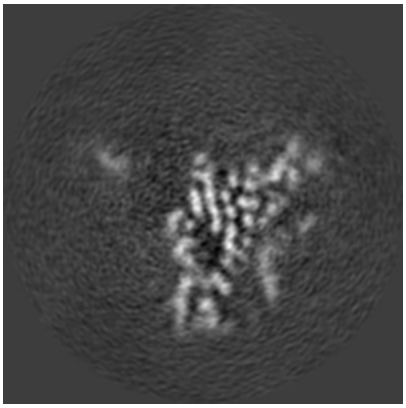


Z Index: 80

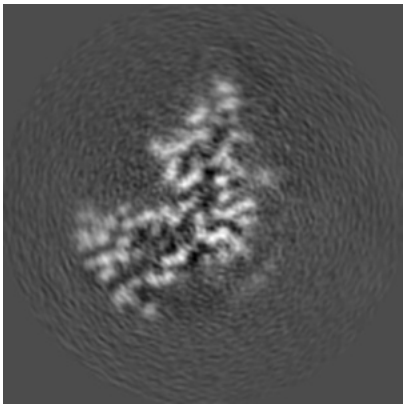
6.3.2 Raw map



X Index: 91



Y Index: 65

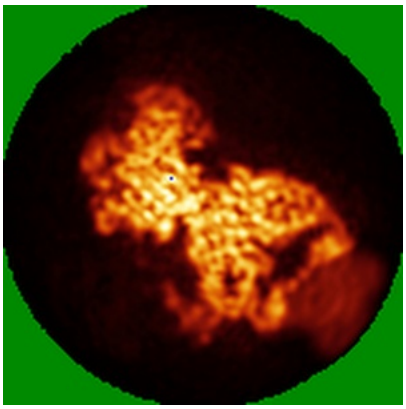


Z Index: 81

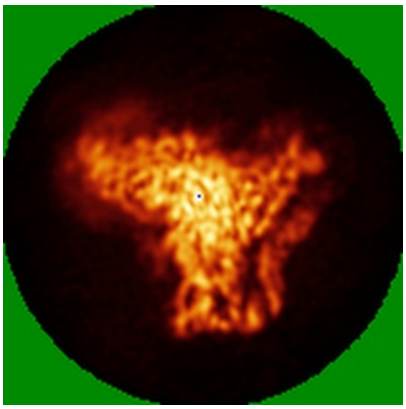
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

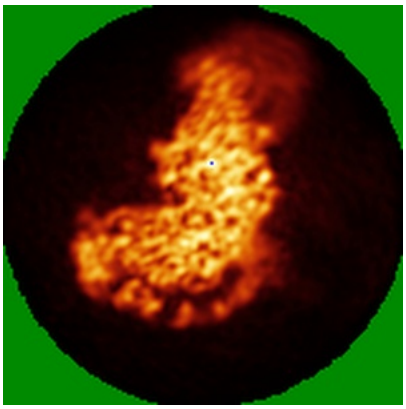
6.4.1 Primary map



X

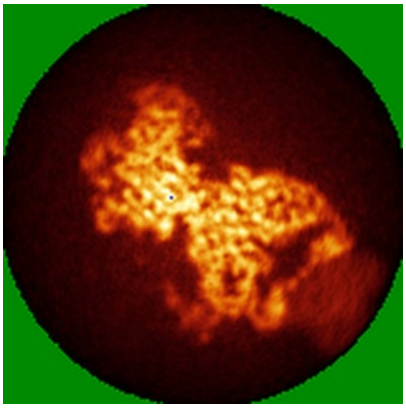


Y

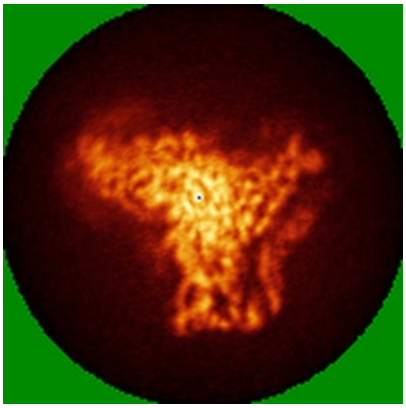


Z

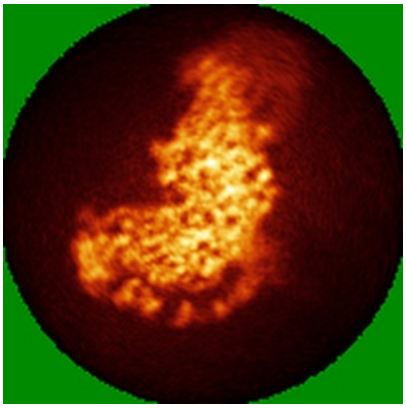
6.4.2 Raw map



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.

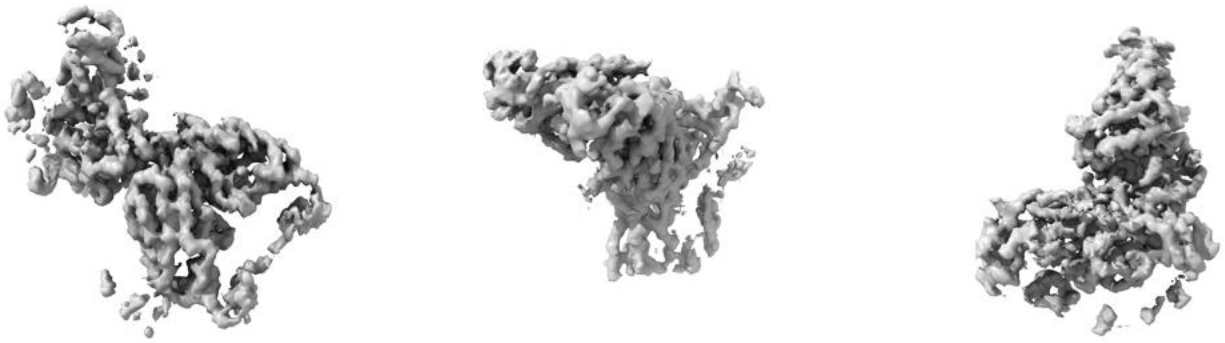
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0114. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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.

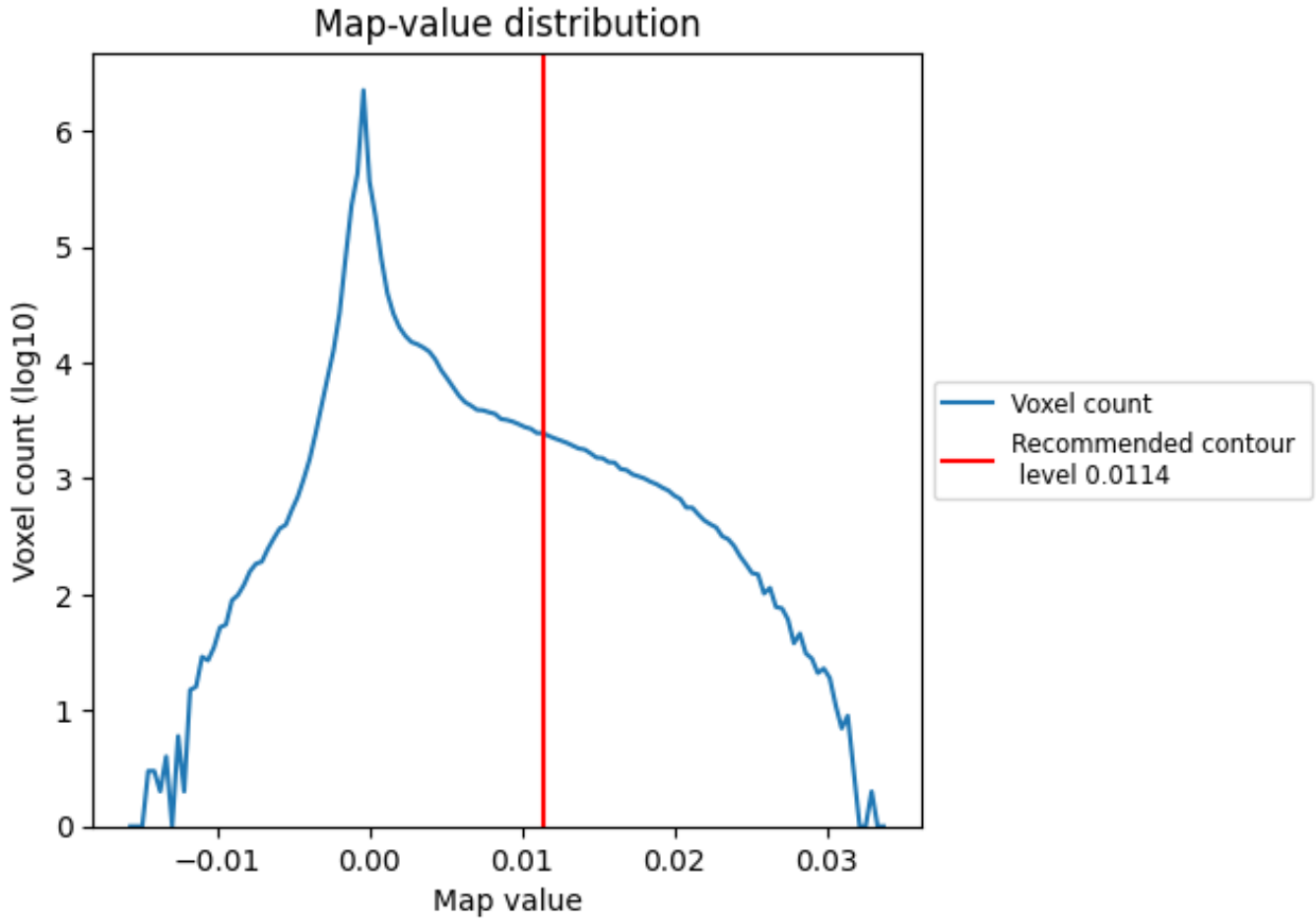
6.6 Mask visualisation (i)

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

7 Map analysis

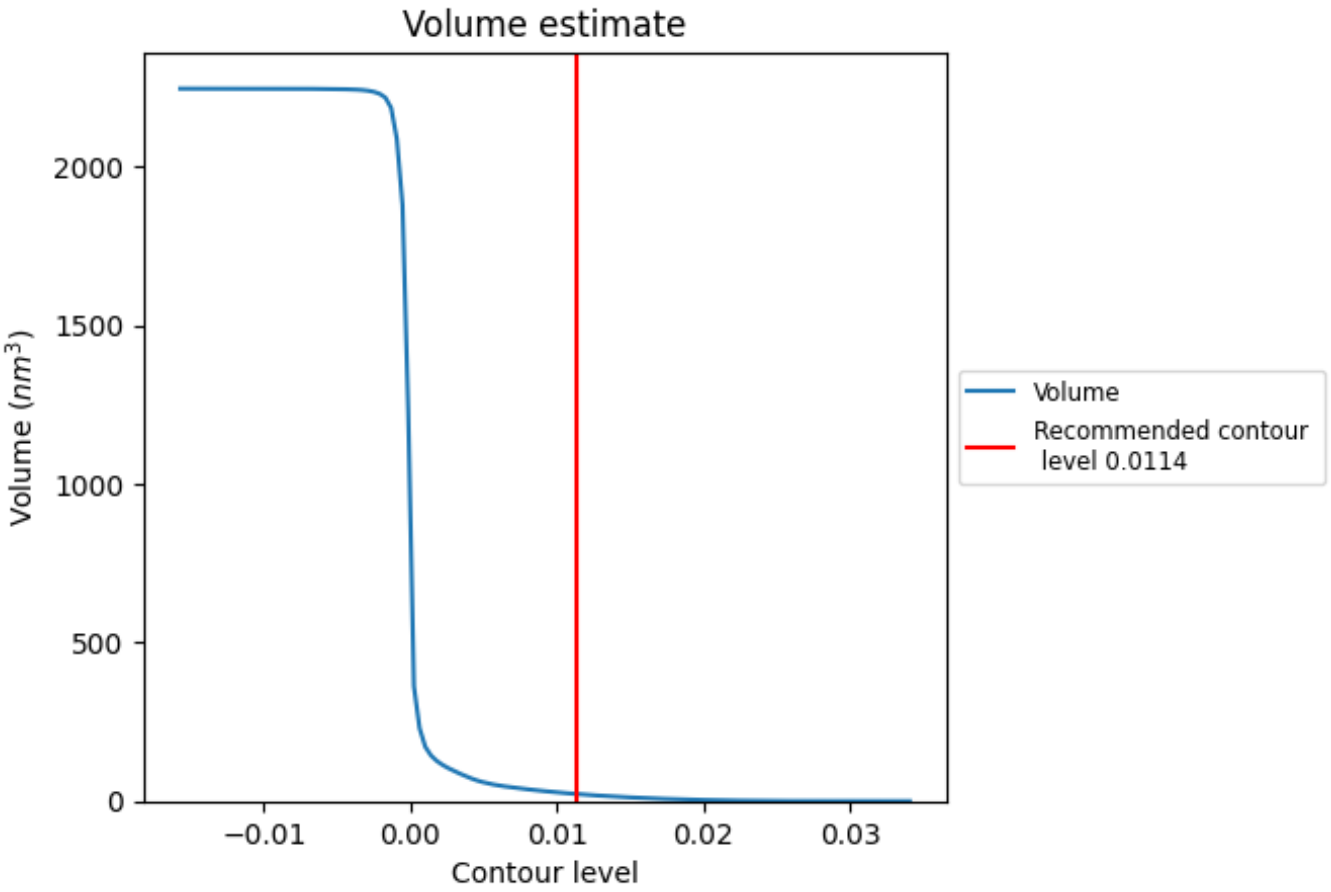
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

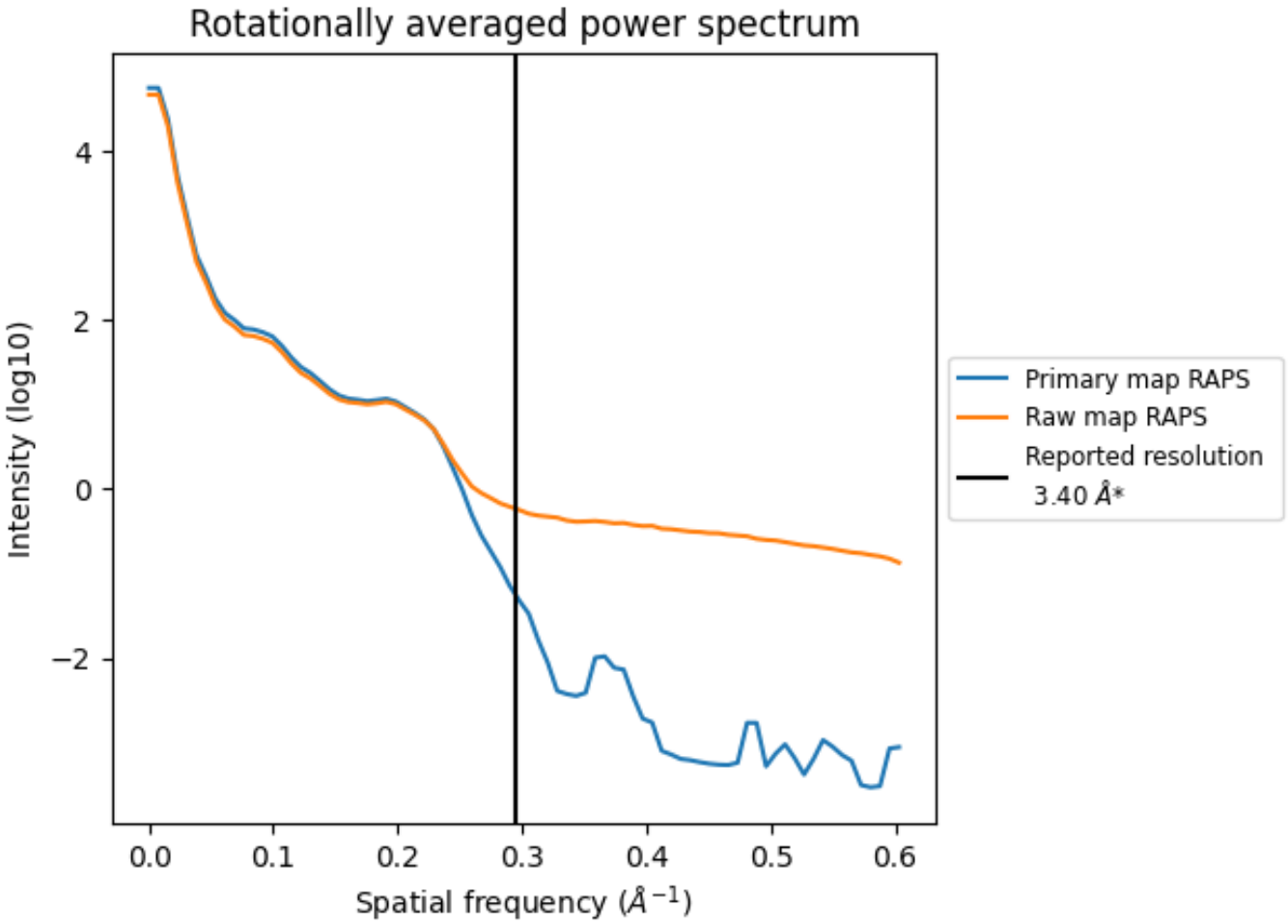
7.2 Volume estimate (i)



The volume at the recommended contour level is 22 nm^3; this corresponds to an approximate mass of 20 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)

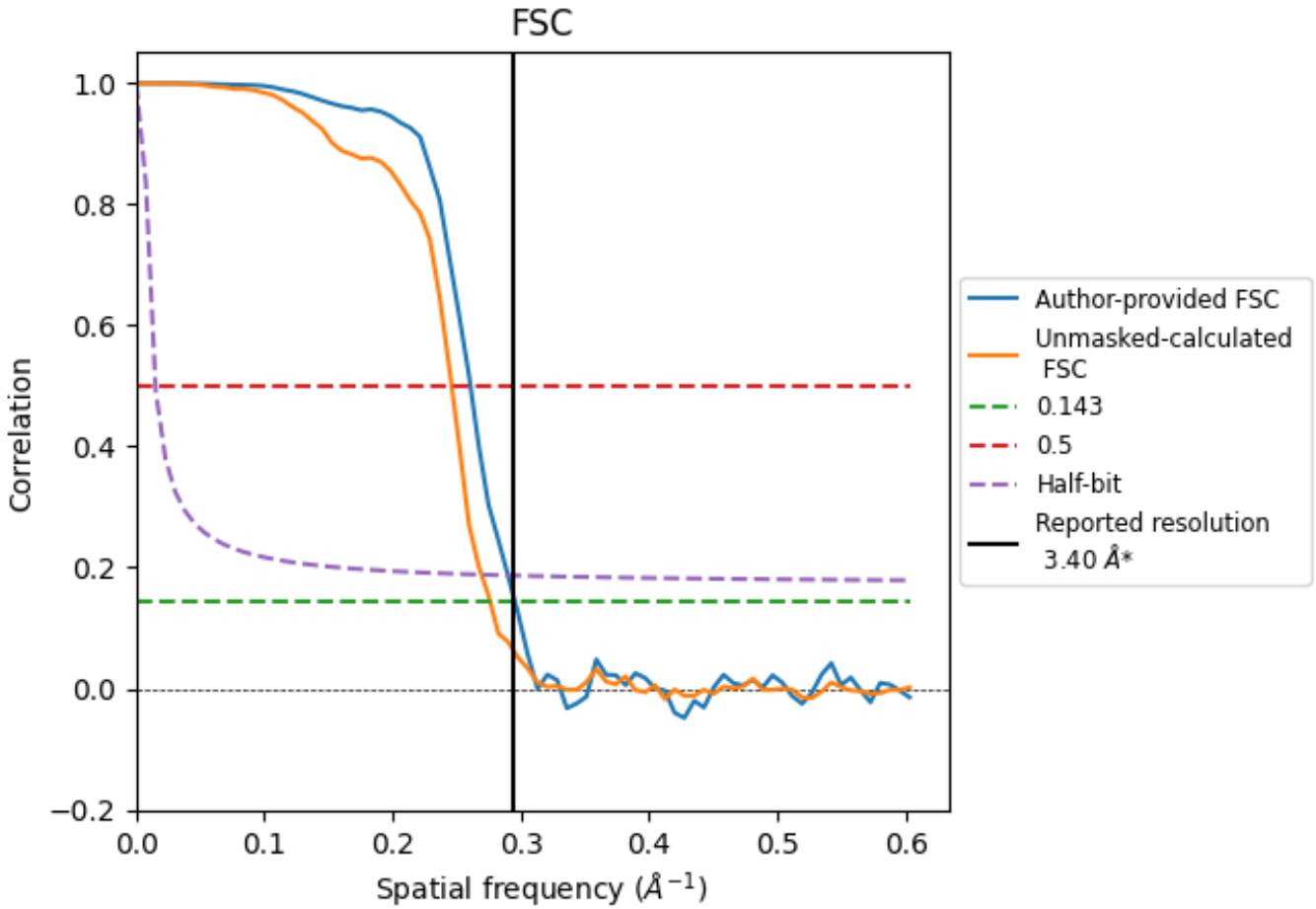


*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8 Fourier-Shell correlation

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.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8.2 Resolution estimates (i)

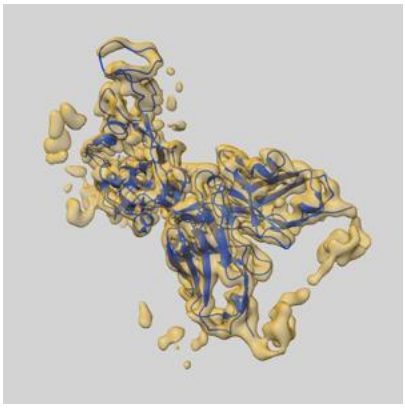
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.38	3.84	3.45
Unmasked-calculated*	3.62	4.07	3.71

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

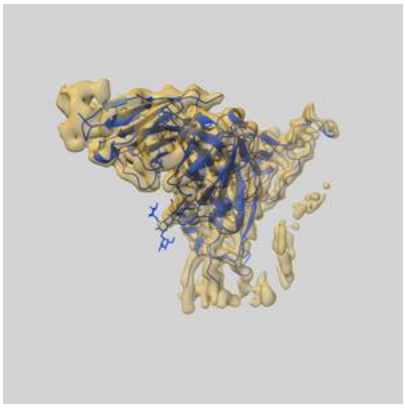
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-33068 and PDB model 7X96. Per-residue inclusion information can be found in section 3 on page 6.

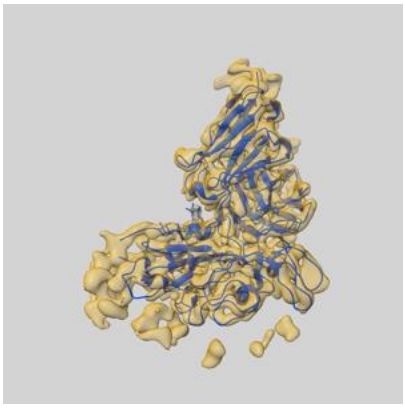
9.1 Map-model overlay



X



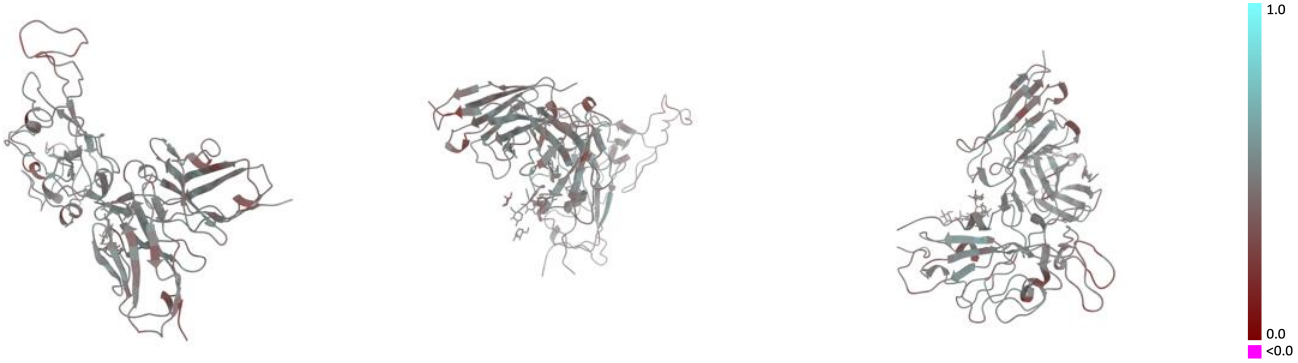
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0114 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.

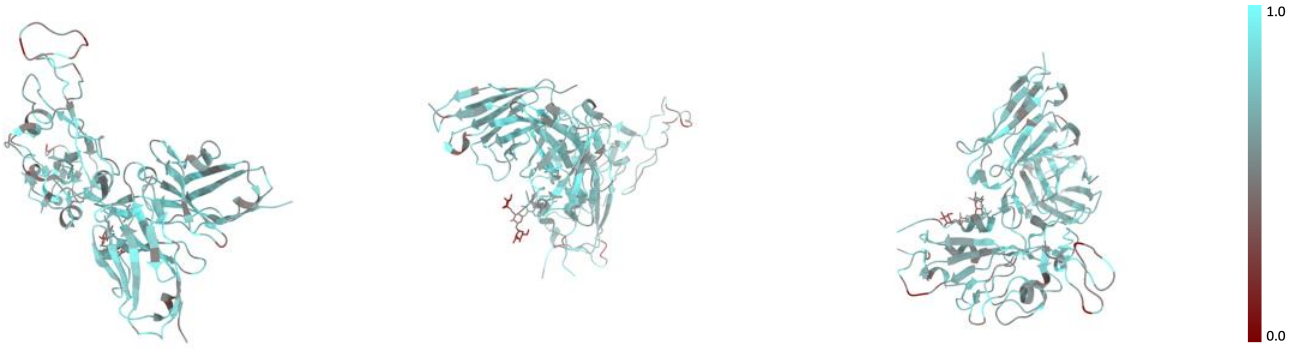
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

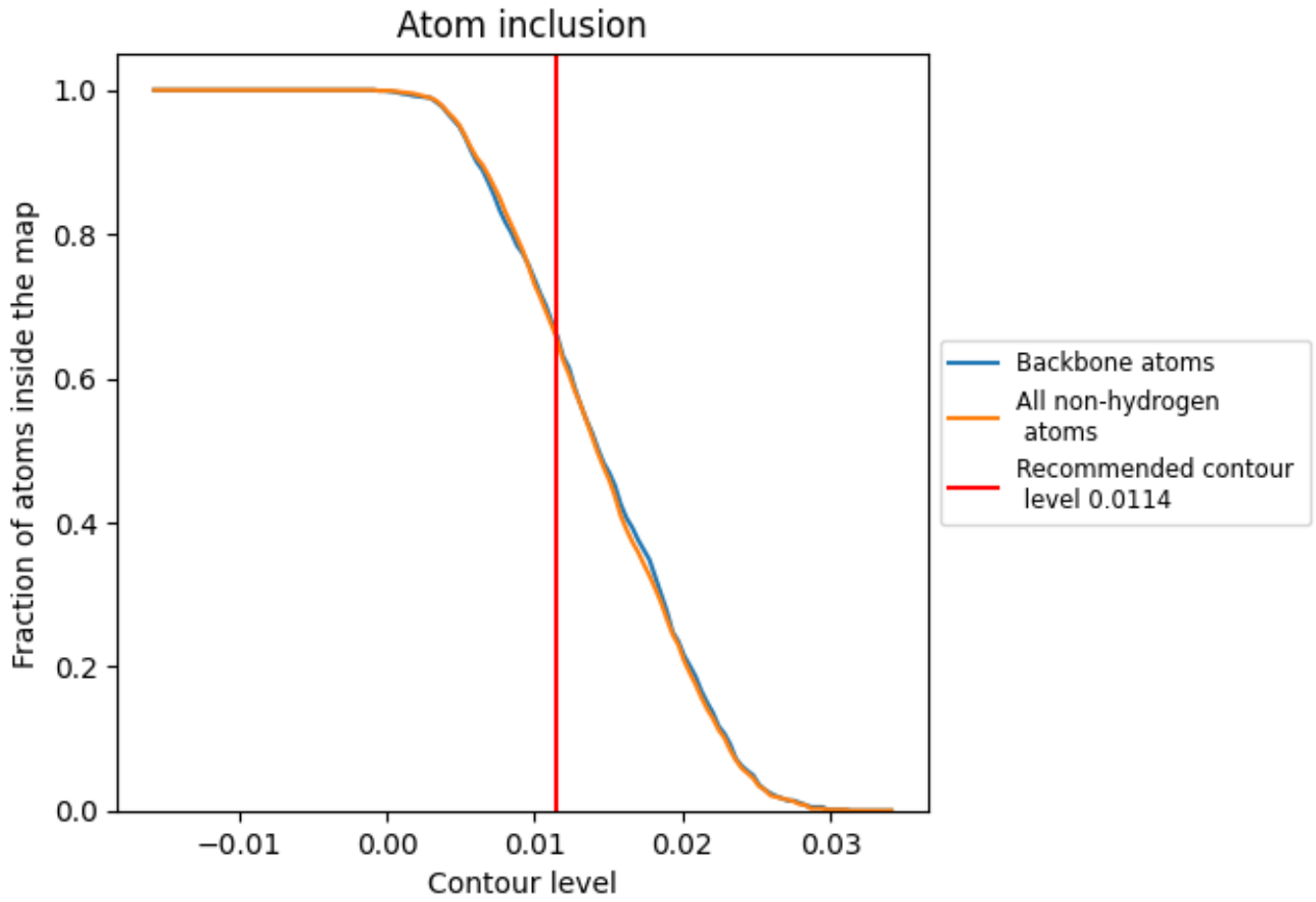
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0114).

9.4 Atom inclusion (i)



At the recommended contour level, 66% of all backbone atoms, 66% 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 (0.0114) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6610	0.4600
A	0.4080	0.4440
G	0.6450	0.4610
H	0.6990	0.4640
L	0.7040	0.4560