



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:01 PM UTC

PDB ID : 7ZH5 / pdb_00007zh5
EMDB ID : EMD-14724
Title : SARS CoV Spike protein, Open conformation
Authors : Toelzer, C.; Gupta, K.; Yadav, S.K.N.; Buzas, D.; Borucu, U.; Schaffitzel, C.;
Berger, I.
Deposited on : 2022-04-05
Resolution : 3.30 Å(reported)
Based on initial model : 6ACD

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.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

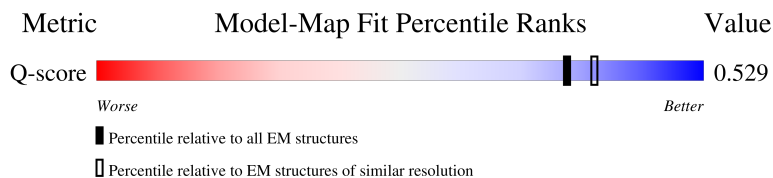
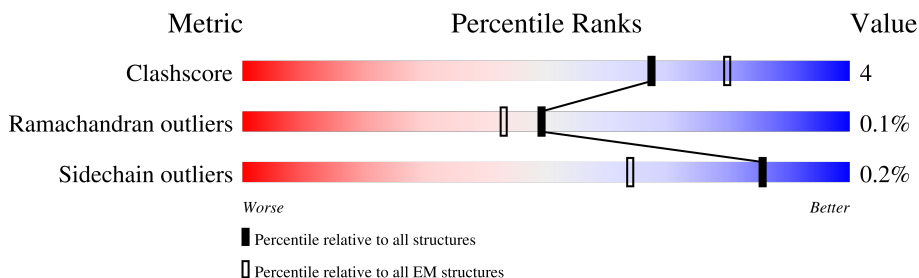
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1227	
1	B	1227	
1	C	1227	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 21592 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 protein called Spike glycoprotein,Fibritin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	904	Total	C	N	O	S	0	0
			6920	4430	1161	1290	39		
1	B	926	Total	C	N	O	S	0	0
			7018	4495	1169	1315	39		
1	C	962	Total	C	N	O	S	0	0
			7332	4687	1233	1376	36		

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	ASP	GLY	conflict	UNP P59594
A	244	THR	ILE	conflict	UNP P59594
A	1194	PRO	-	linker	UNP P59594
A	1195	SER	-	linker	UNP P59594
A	1196	GLY	-	linker	UNP P59594
A	1197	ARG	-	linker	UNP P59594
A	1198	LEU	-	linker	UNP P59594
A	1199	VAL	-	linker	UNP P59594
A	1200	PRO	-	linker	UNP P59594
A	1201	ARG	-	linker	UNP P59594
A	1202	GLY	-	linker	UNP P59594
A	1203	SER	-	linker	UNP P59594
A	1204	PRO	-	linker	UNP P59594
A	1205	GLY	-	linker	UNP P59594
A	1206	SER	-	linker	UNP P59594
A	1228	LEU	PHE	conflict	UNP P10104
A	1234	GLY	-	expression tag	UNP P10104
A	1235	HIS	-	expression tag	UNP P10104
A	1236	HIS	-	expression tag	UNP P10104
A	1237	HIS	-	expression tag	UNP P10104
A	1238	HIS	-	expression tag	UNP P10104
A	1239	HIS	-	expression tag	UNP P10104
A	1240	HIS	-	expression tag	UNP P10104
B	77	ASP	GLY	conflict	UNP P59594

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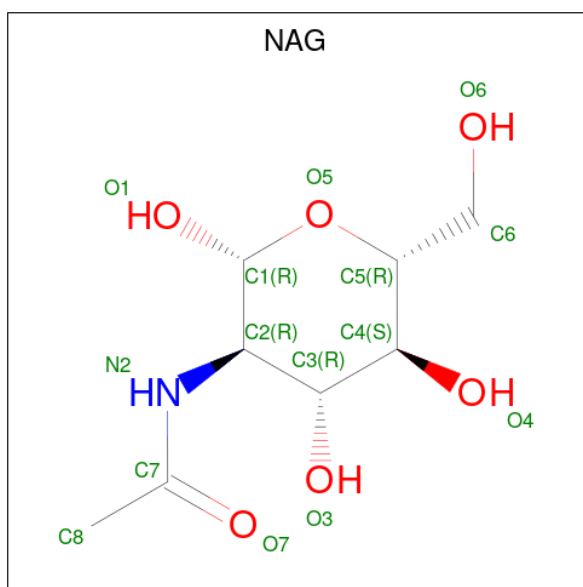
Chain	Residue	Modelled	Actual	Comment	Reference
B	244	THR	ILE	conflict	UNP P59594
B	1194	PRO	-	linker	UNP P59594
B	1195	SER	-	linker	UNP P59594
B	1196	GLY	-	linker	UNP P59594
B	1197	ARG	-	linker	UNP P59594
B	1198	LEU	-	linker	UNP P59594
B	1199	VAL	-	linker	UNP P59594
B	1200	PRO	-	linker	UNP P59594
B	1201	ARG	-	linker	UNP P59594
B	1202	GLY	-	linker	UNP P59594
B	1203	SER	-	linker	UNP P59594
B	1204	PRO	-	linker	UNP P59594
B	1205	GLY	-	linker	UNP P59594
B	1206	SER	-	linker	UNP P59594
B	1228	LEU	PHE	conflict	UNP P10104
B	1234	GLY	-	expression tag	UNP P10104
B	1235	HIS	-	expression tag	UNP P10104
B	1236	HIS	-	expression tag	UNP P10104
B	1237	HIS	-	expression tag	UNP P10104
B	1238	HIS	-	expression tag	UNP P10104
B	1239	HIS	-	expression tag	UNP P10104
B	1240	HIS	-	expression tag	UNP P10104
C	77	ASP	GLY	conflict	UNP P59594
C	244	THR	ILE	conflict	UNP P59594
C	1194	PRO	-	linker	UNP P59594
C	1195	SER	-	linker	UNP P59594
C	1196	GLY	-	linker	UNP P59594
C	1197	ARG	-	linker	UNP P59594
C	1198	LEU	-	linker	UNP P59594
C	1199	VAL	-	linker	UNP P59594
C	1200	PRO	-	linker	UNP P59594
C	1201	ARG	-	linker	UNP P59594
C	1202	GLY	-	linker	UNP P59594
C	1203	SER	-	linker	UNP P59594
C	1204	PRO	-	linker	UNP P59594
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C	1228	LEU	PHE	conflict	UNP P10104
C	1234	GLY	-	expression tag	UNP P10104
C	1235	HIS	-	expression tag	UNP P10104
C	1236	HIS	-	expression tag	UNP P10104
C	1237	HIS	-	expression tag	UNP P10104

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1238	HIS	-	expression tag	UNP P10104
C	1239	HIS	-	expression tag	UNP P10104
C	1240	HIS	-	expression tag	UNP P10104

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	

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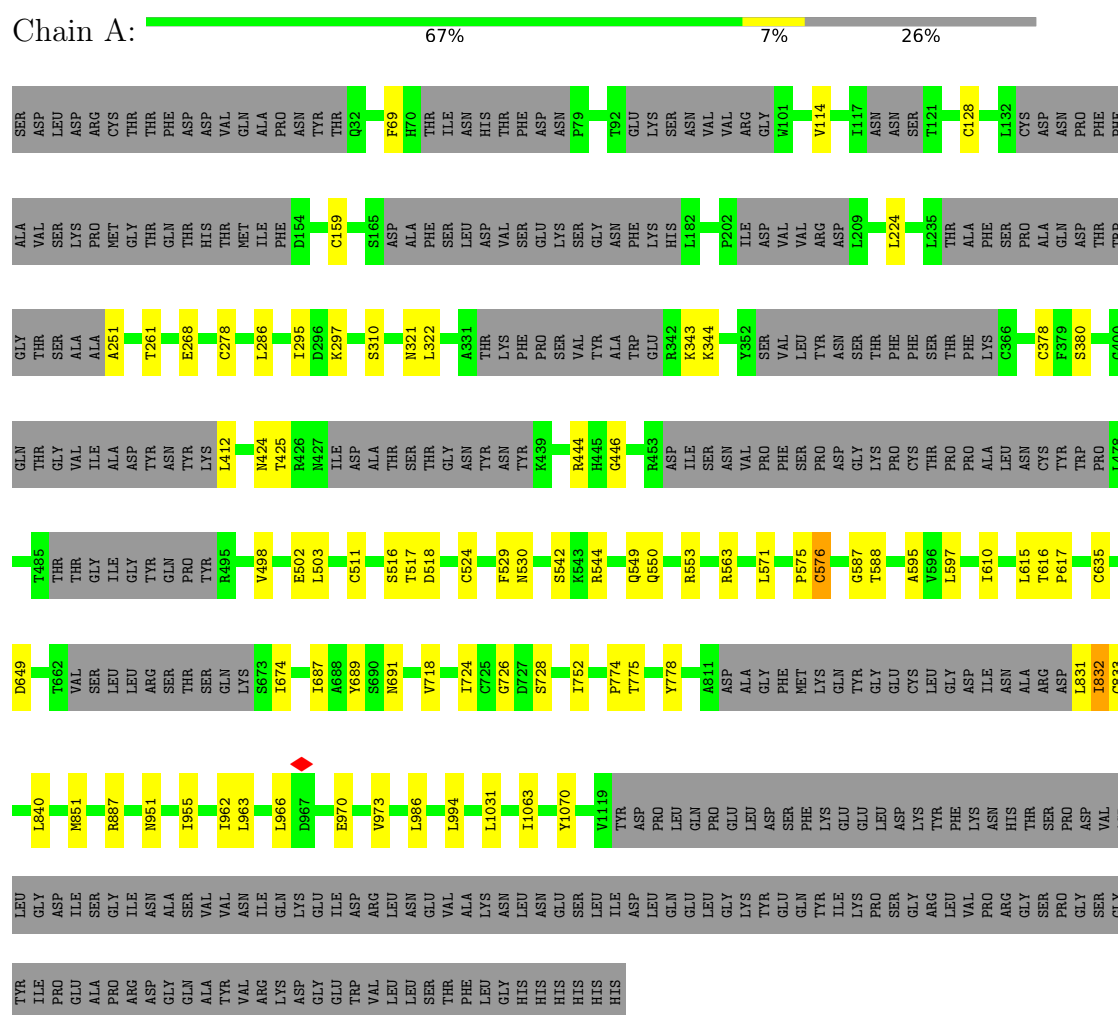
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Mol	Chain	Residues	Atoms				AltConf
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	

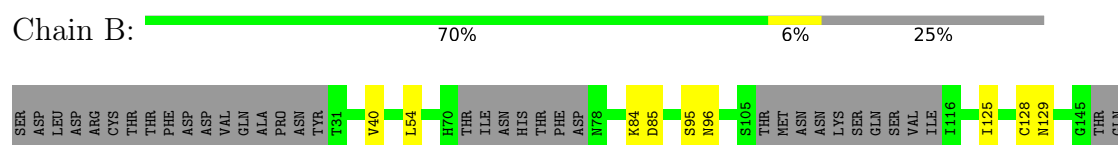
3 Residue-property plots

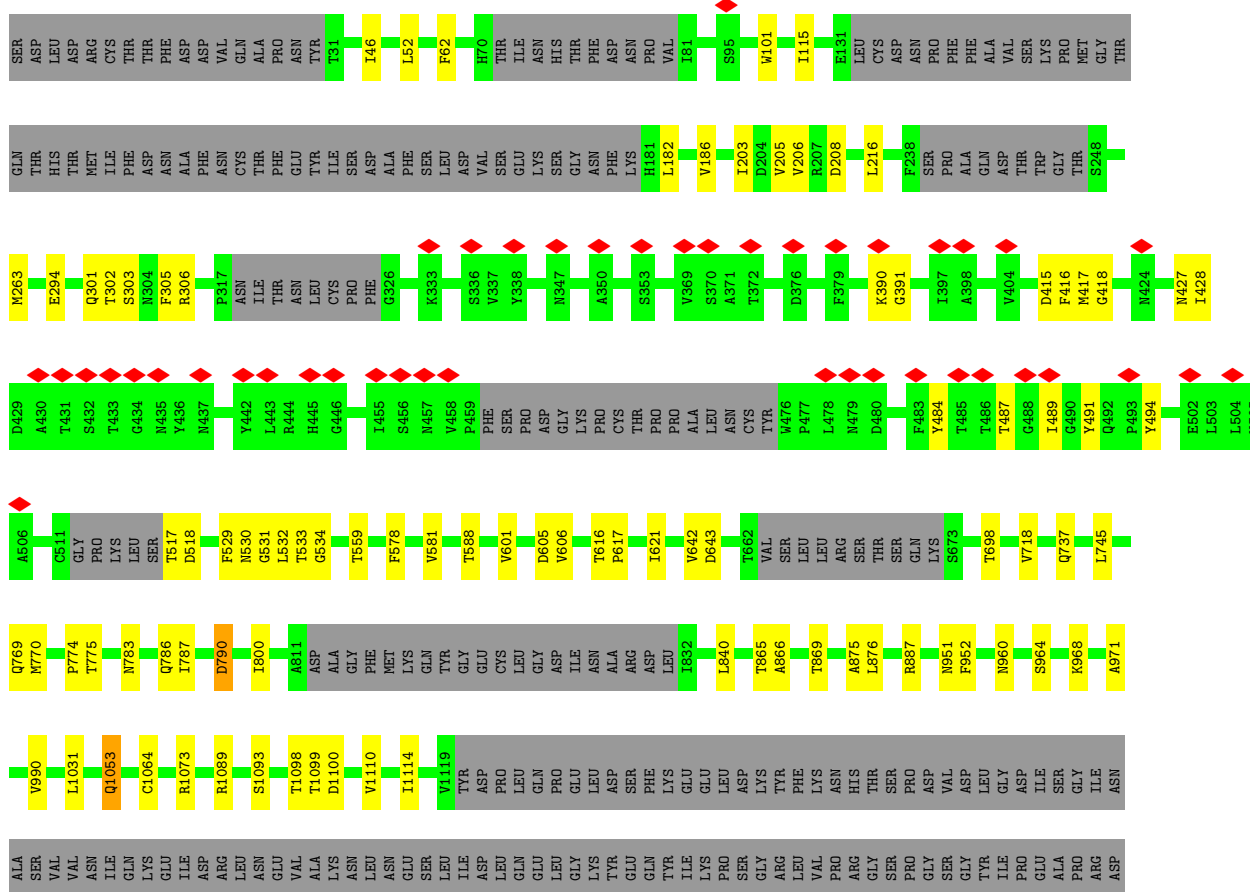
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Spike glycoprotein,Fibritin



- Molecule 1: Spike glycoprotein,Fibritin





GLY	GLN	ALA	TYR	VAL	ARG	LYS	ASP	GLY	GLU	TRP	VAL	LEU	LEU	SER	THR	PHE	LEU	GLY	HIS	HIS	HIS	HIS	HIS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81242	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS TALOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	62.65	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.254	Depositor
Minimum map value	-0.168	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	230.99998, 230.99998, 230.99998	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	A	0.14	0/7060	0.31	0/9585
1	B	0.15	0/7172	0.31	0/9763
1	C	0.22	0/7490	0.40	4/10194 (0.0%)
All	All	0.18	0/21722	0.35	4/29542 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	62	PHE	CA-C-O	-10.51	109.63	121.19
1	C	62	PHE	O-C-N	5.32	129.41	122.87
1	C	786	GLN	N-CA-CB	5.25	119.37	110.49
1	C	1110	VAL	N-CA-C	5.01	111.57	106.21

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	A	6920	0	6714	53	0
1	B	7018	0	6761	45	0
1	C	7332	0	7037	60	0
2	A	126	0	117	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	98	0	91	4	0
2	C	98	0	91	7	0
All	All	21592	0	20811	161	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 4.

The worst 5 of 161 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)
2:C:1302:NAG:H83	2:C:1302:NAG:H3	1.51	0.92
1:C:302:THR:HG22	1:C:303:SER:H	1.49	0.78
2:C:1306:NAG:O7	2:C:1306:NAG:O3	2.02	0.77
2:B:1307:NAG:O7	2:B:1307:NAG:O3	2.06	0.73
2:A:1307:NAG:O7	2:A:1307:NAG:O3	2.06	0.73

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	A	872/1227 (71%)	795 (91%)	75 (9%)	2 (0%)	43	71
1	B	908/1227 (74%)	821 (90%)	87 (10%)	0	100	100
1	C	944/1227 (77%)	864 (92%)	79 (8%)	1 (0%)	48	75
All	All	2724/3681 (74%)	2480 (91%)	241 (9%)	3 (0%)	49	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	530	ASN

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Mol	Chain	Res	Type
1	A	576	CYS
1	A	832	ILE

5.3.2 Protein sidechains ⓘ

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	A	744/1065 (70%)	744 (100%)	0	100	100
1	B	750/1065 (70%)	748 (100%)	2 (0%)	86	86
1	C	776/1065 (73%)	773 (100%)	3 (0%)	84	84
All	All	2270/3195 (71%)	2265 (100%)	5 (0%)	85	88

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	691	ASN
1	B	692	ASN
1	C	790	ASP
1	C	1053	GLN
1	C	1089	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1046	HIS
1	C	1046	HIS
1	C	301	GLN
1	C	1053	GLN
1	C	947	GLN

5.3.3 RNA ⓘ

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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

23 ligands 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	$\# Z > 2$
2	NAG	A	1308	1	14,14,15	0.27	0	17,19,21	0.50	0
2	NAG	B	1301	1	14,14,15	0.43	0	17,19,21	0.65	1 (5%)
2	NAG	A	1304	1	14,14,15	0.21	0	17,19,21	0.40	0
2	NAG	A	1305	1	14,14,15	0.29	0	17,19,21	0.43	0
2	NAG	A	1307	1	14,14,15	0.28	0	17,19,21	0.44	0
2	NAG	B	1303	1	14,14,15	0.28	0	17,19,21	0.36	0
2	NAG	B	1307	1	14,14,15	0.33	0	17,19,21	0.45	0
2	NAG	A	1303	1	14,14,15	0.26	0	17,19,21	0.55	0
2	NAG	A	1302	1	14,14,15	0.29	0	17,19,21	0.38	0
2	NAG	B	1305	1	14,14,15	0.23	0	17,19,21	0.46	0
2	NAG	C	1301	1	14,14,15	0.28	0	17,19,21	0.48	0
2	NAG	C	1302	1	14,14,15	0.27	0	17,19,21	0.79	1 (5%)
2	NAG	B	1302	1	14,14,15	0.21	0	17,19,21	0.48	0
2	NAG	B	1304	1	14,14,15	0.33	0	17,19,21	0.43	0
2	NAG	C	1305	1	14,14,15	0.20	0	17,19,21	0.48	0
2	NAG	A	1306	1	14,14,15	0.26	0	17,19,21	0.49	0
2	NAG	B	1306	1	14,14,15	0.23	0	17,19,21	0.49	0
2	NAG	C	1303	1	14,14,15	0.20	0	17,19,21	0.46	0
2	NAG	C	1306	1	14,14,15	0.33	0	17,19,21	0.35	0
2	NAG	A	1301	1	14,14,15	0.22	0	17,19,21	0.45	0
2	NAG	C	1304	1	14,14,15	0.17	0	17,19,21	0.42	0
2	NAG	A	1309	1	14,14,15	0.29	0	17,19,21	0.55	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	1307	1	14,14,15	0.18	0	17,19,21	0.47	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
2	NAG	A	1308	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1304	1	-	3/6/23/26	0/1/1/1
2	NAG	A	1305	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1307	1	-	1/6/23/26	0/1/1/1
2	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1307	1	-	3/6/23/26	0/1/1/1
2	NAG	A	1303	1	-	1/6/23/26	0/1/1/1
2	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1305	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1302	1	-	5/6/23/26	0/1/1/1
2	NAG	B	1302	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1304	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1305	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1306	1	-	1/6/23/26	0/1/1/1
2	NAG	B	1306	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1303	1	-	4/6/23/26	0/1/1/1
2	NAG	C	1306	1	-	3/6/23/26	0/1/1/1
2	NAG	A	1301	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1304	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1309	1	-	4/6/23/26	0/1/1/1
2	NAG	C	1307	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1301	NAG	C1-O5-C5	2.29	115.25	112.19
2	C	1302	NAG	C2-N2-C7	2.10	125.72	122.90

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1302	NAG	O5-C5-C6-O6
2	A	1308	NAG	O5-C5-C6-O6
2	B	1306	NAG	O5-C5-C6-O6
2	A	1304	NAG	O5-C5-C6-O6
2	B	1307	NAG	O5-C5-C6-O6

There are no ring outliers.

9 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1304	NAG	1	0
2	A	1305	NAG	2	0
2	A	1307	NAG	3	0
2	B	1303	NAG	1	0
2	B	1307	NAG	2	0
2	C	1301	NAG	1	0
2	C	1302	NAG	3	0
2	B	1302	NAG	1	0
2	C	1306	NAG	3	0

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.

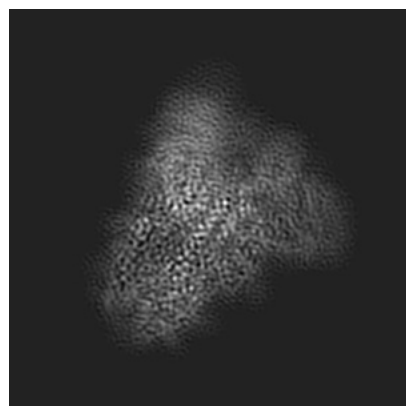
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14724. These allow visual inspection of the internal detail of the map and identification of artifacts.

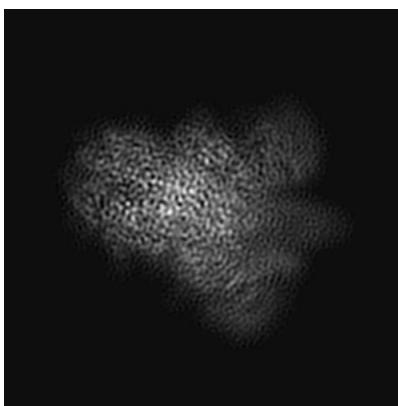
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

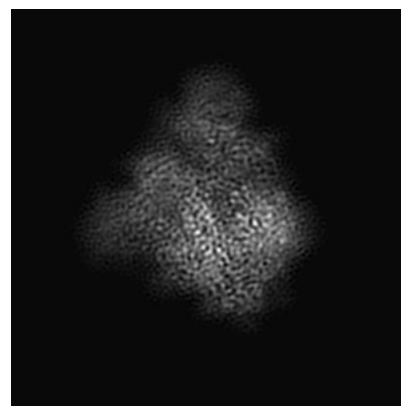
6.1.1 Primary map



X

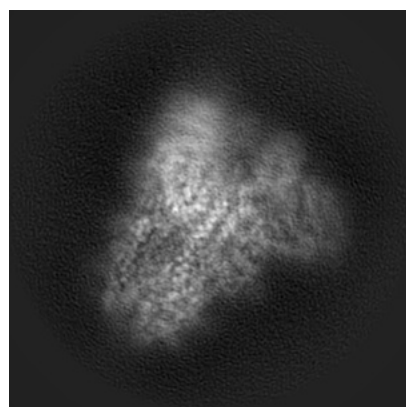


Y

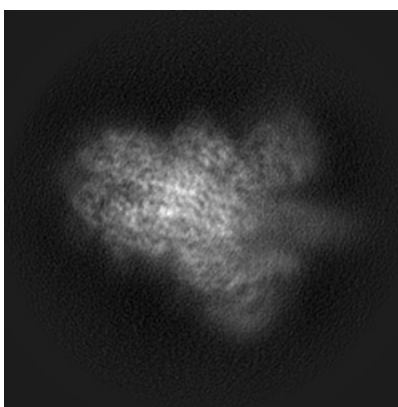


Z

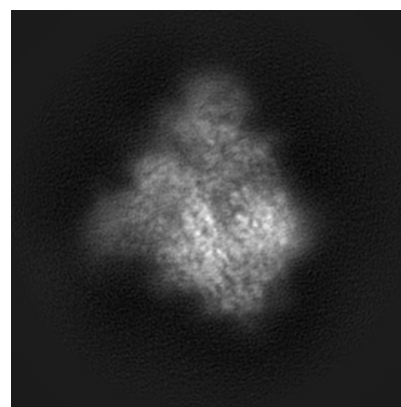
6.1.2 Raw map



X



Y

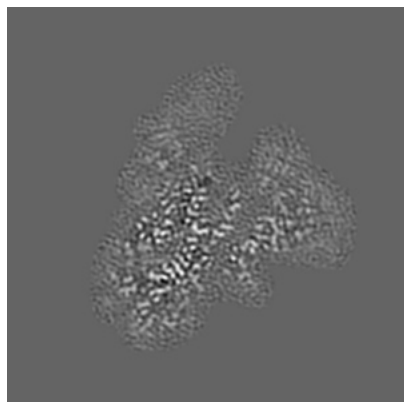


Z

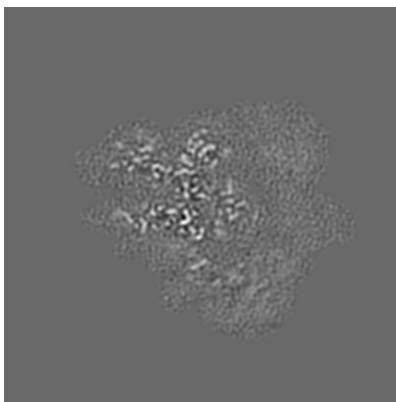
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

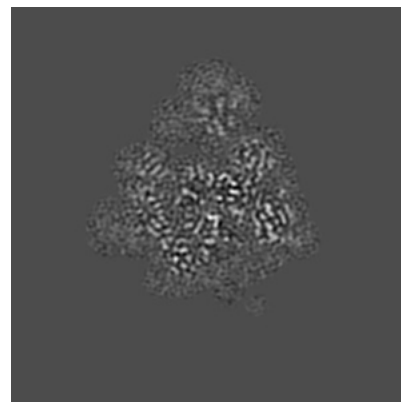
6.2.1 Primary map



X Index: 110

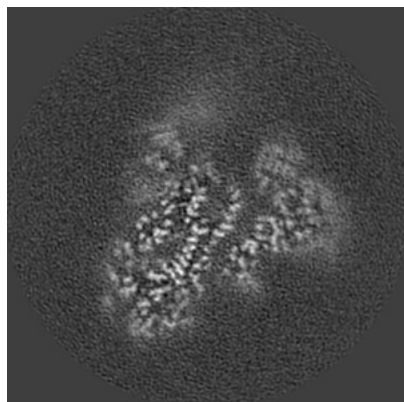


Y Index: 110

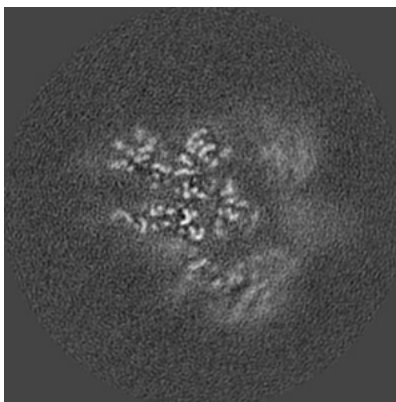


Z Index: 110

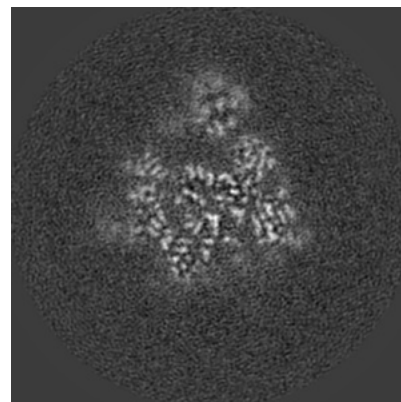
6.2.2 Raw map



X Index: 110



Y Index: 110

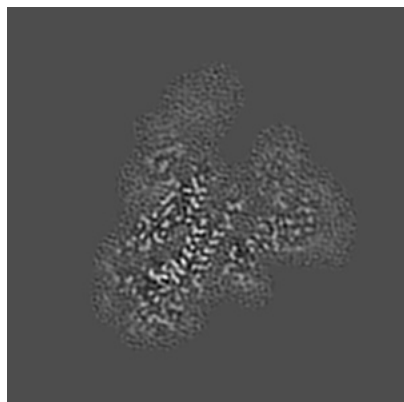


Z Index: 110

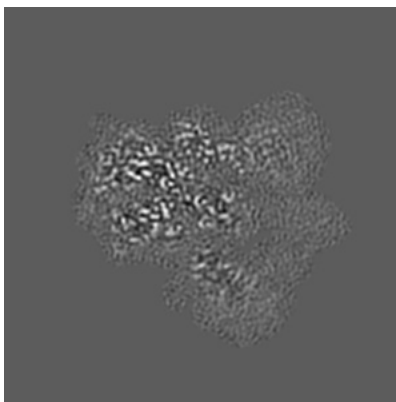
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

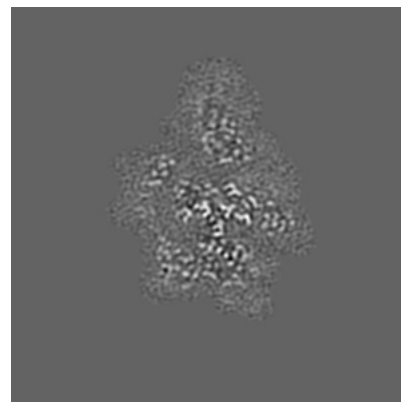
6.3.1 Primary map



X Index: 109

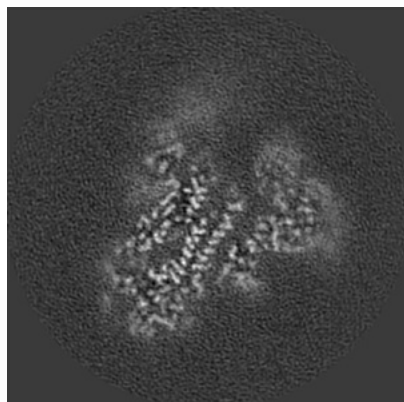


Y Index: 101

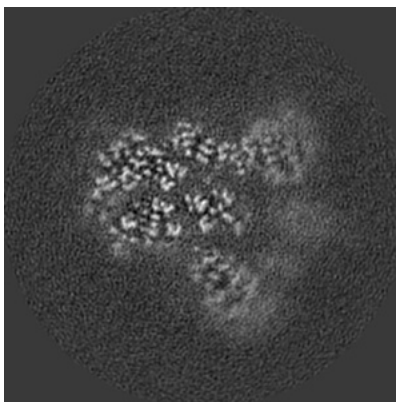


Z Index: 100

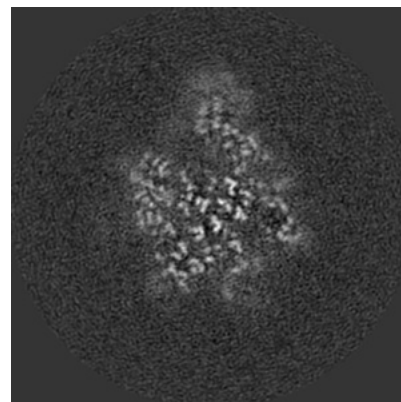
6.3.2 Raw map



X Index: 109



Y Index: 100

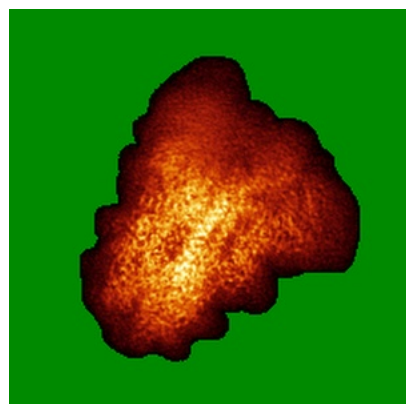


Z Index: 105

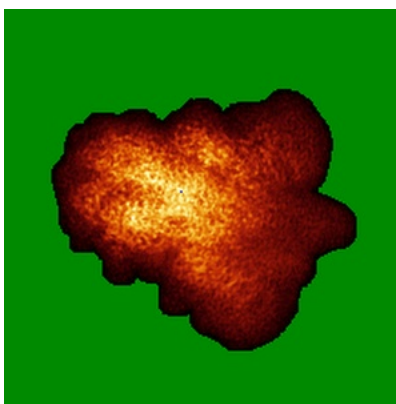
The images above show the largest variance slices of the map in three orthogonal directions.

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

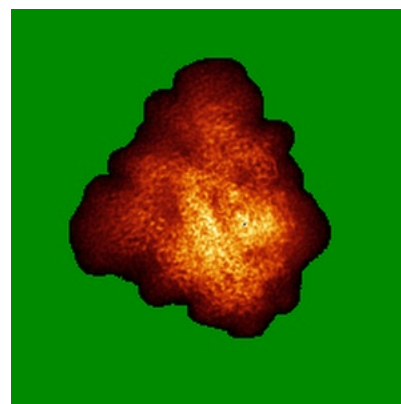
6.4.1 Primary map



X

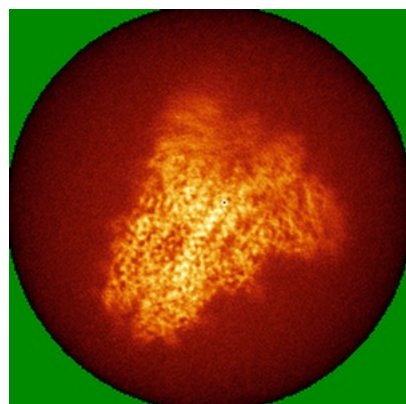


Y

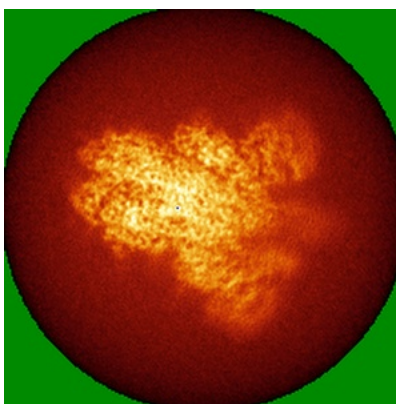


Z

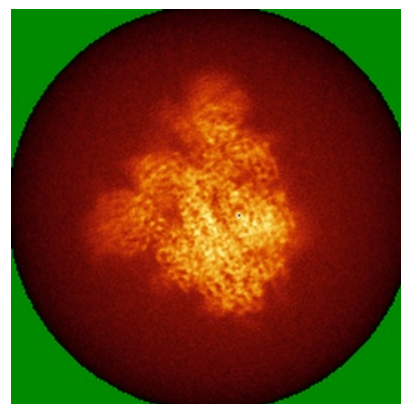
6.4.2 Raw map



X



Y

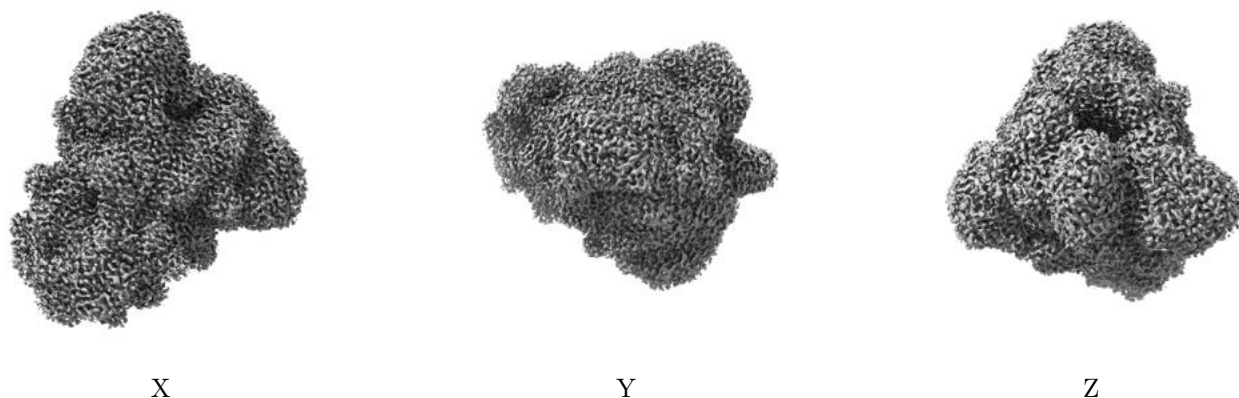


Z

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.

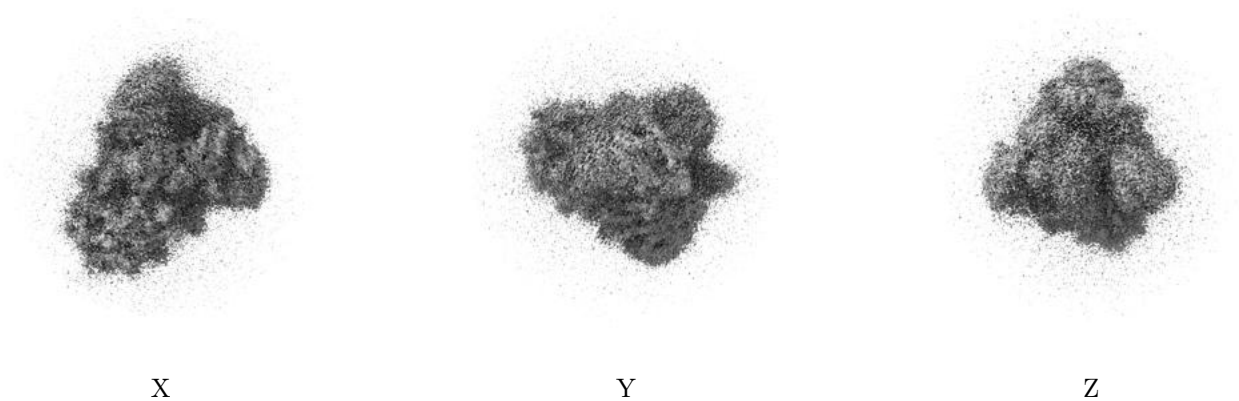
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.014. 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



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.

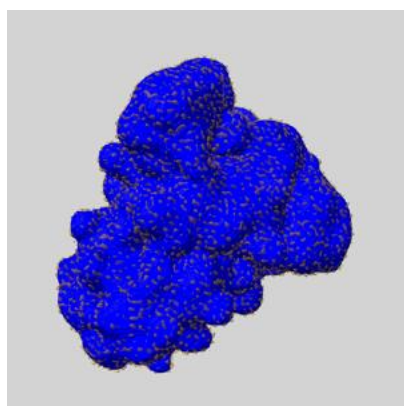
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

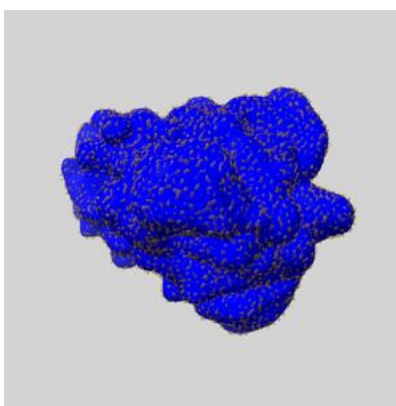
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

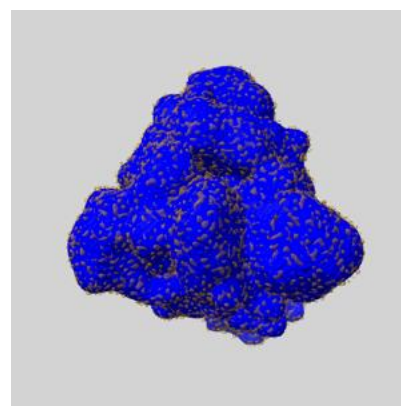
6.6.1 emd_14724_msk_1.map [i](#)



X



Y

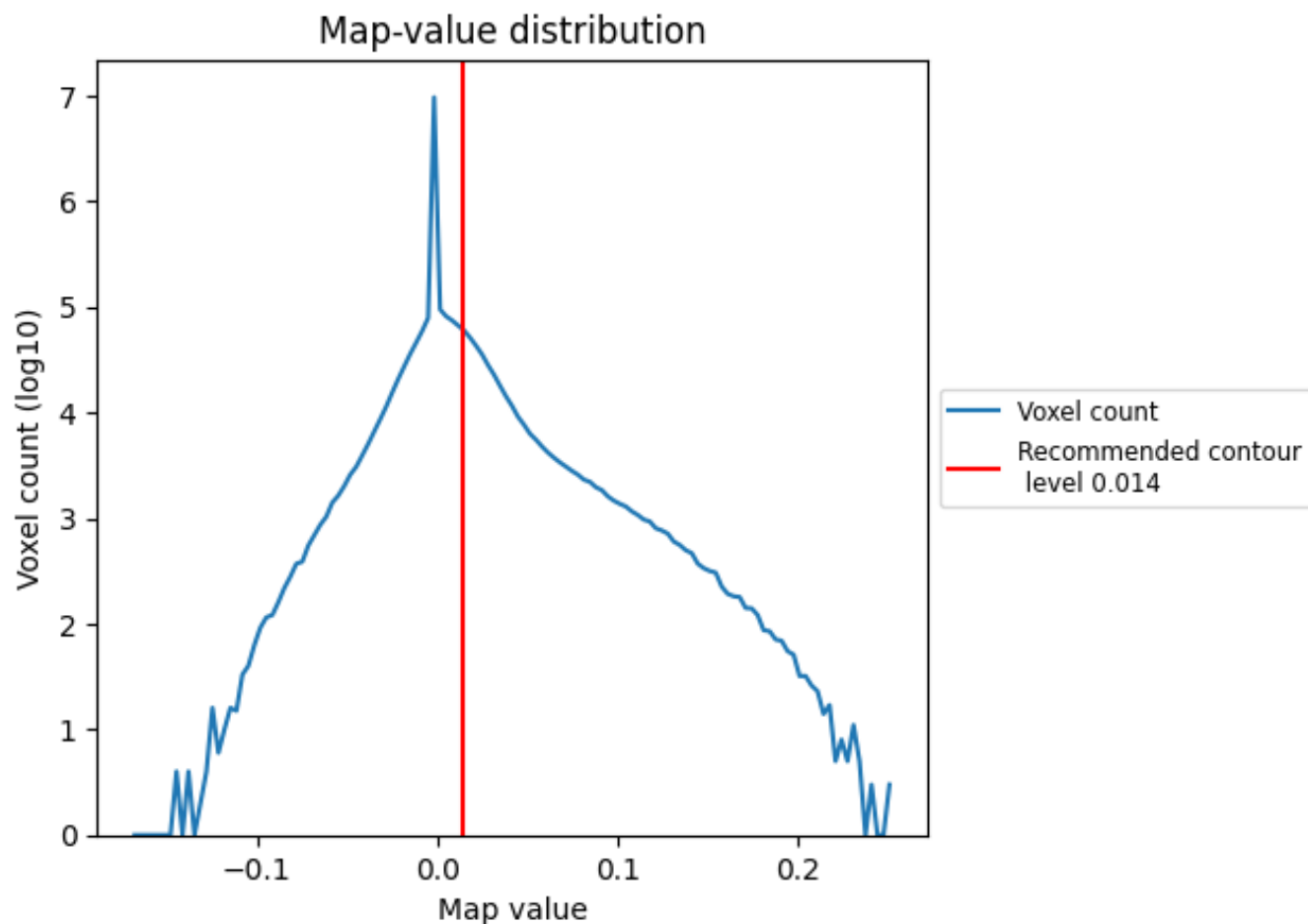


Z

7 Map analysis [i](#)

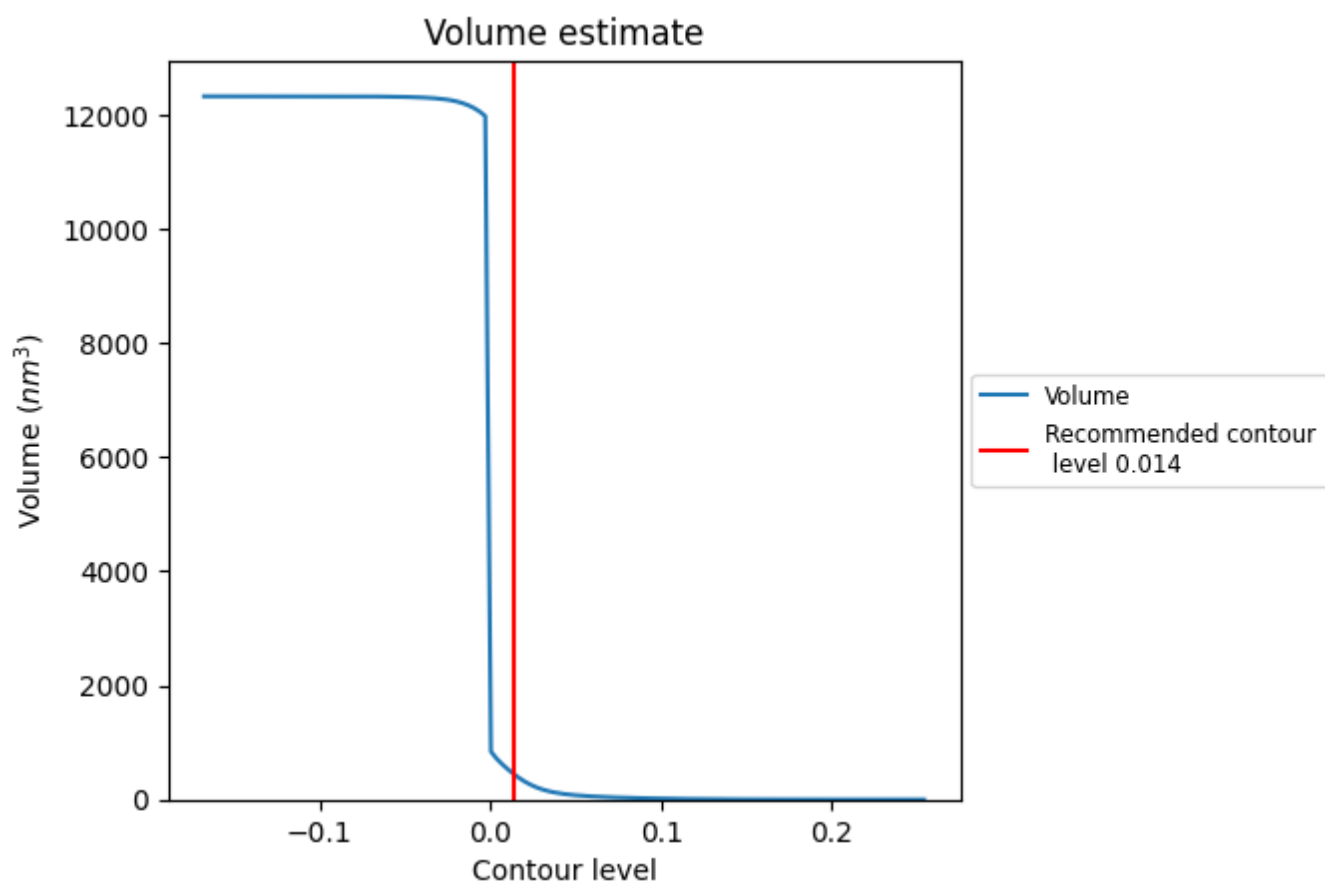
This section contains the results of statistical analysis of the map.

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.

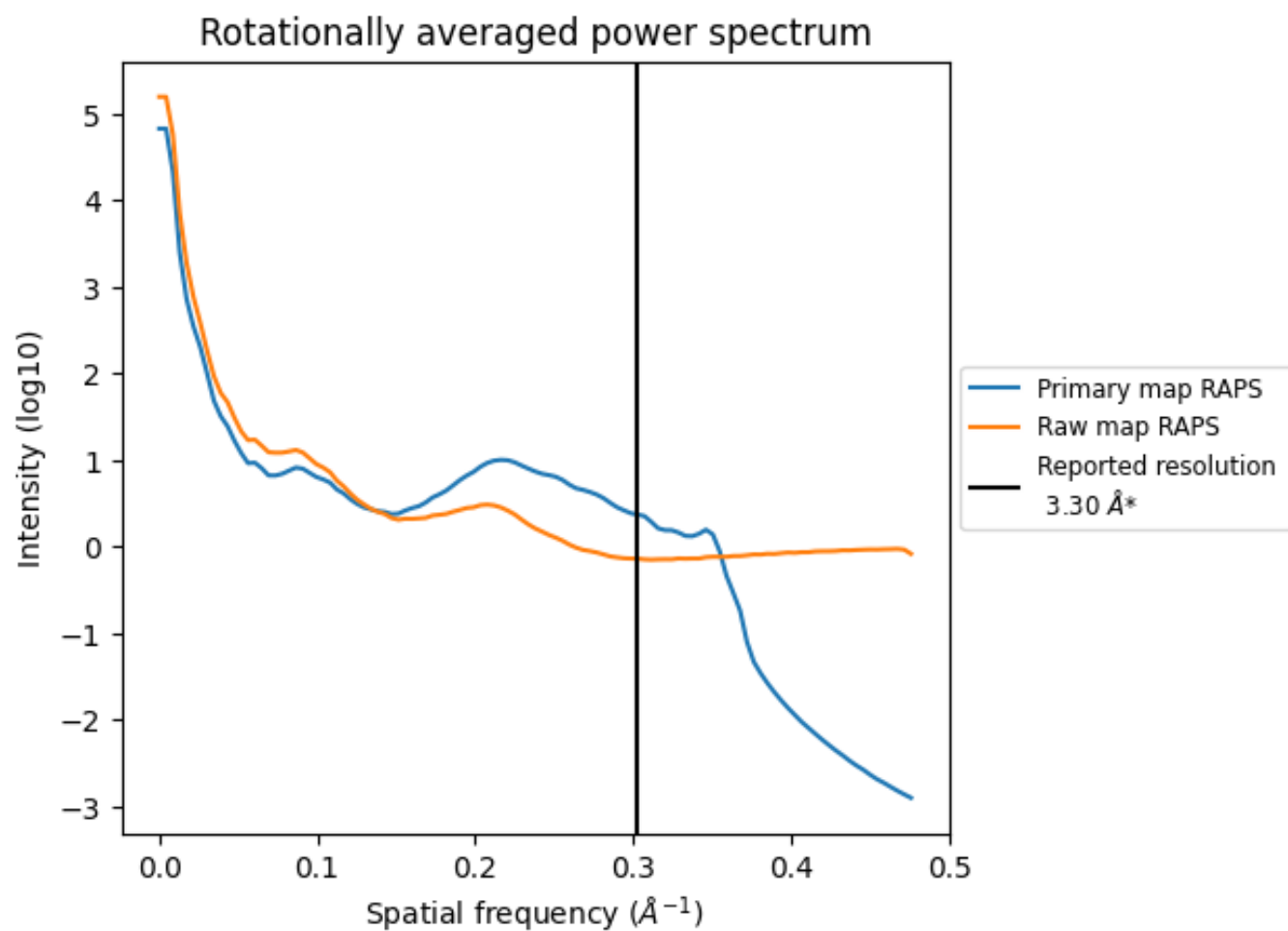
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 441 nm³; this corresponds to an approximate mass of 398 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 ⓘ

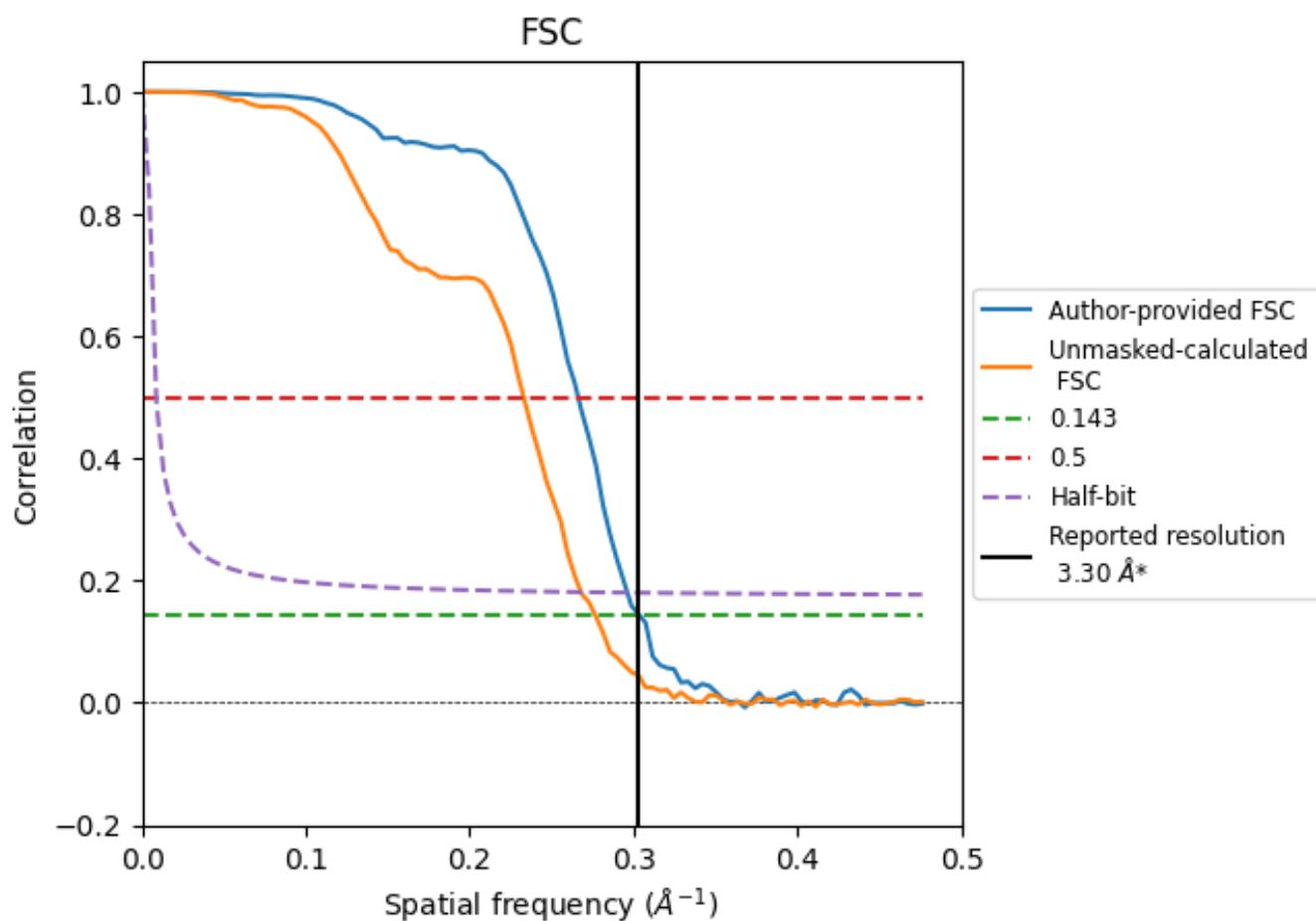


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 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.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.29	3.76	3.38
Unmasked-calculated*	3.62	4.29	3.73

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

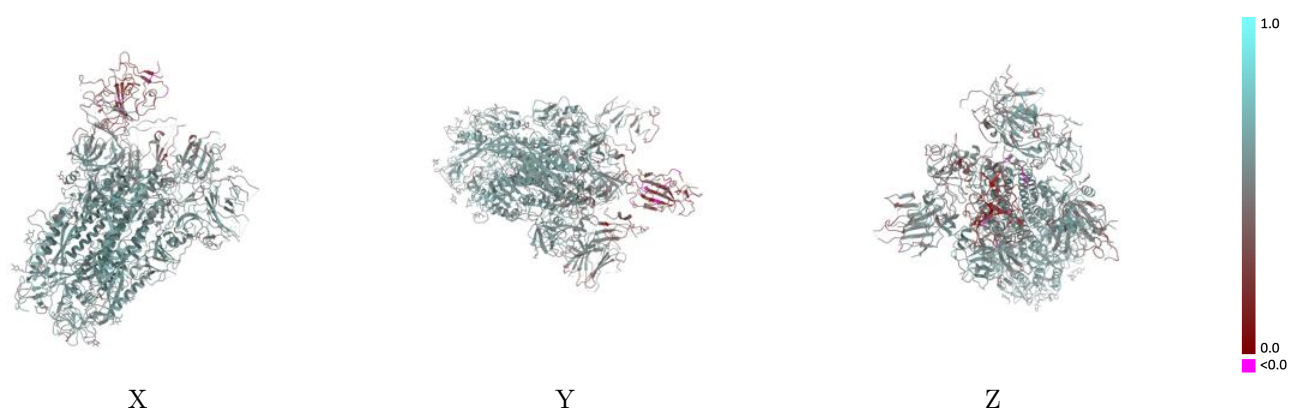
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14724 and PDB model 7ZH5. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

This section was not generated.

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

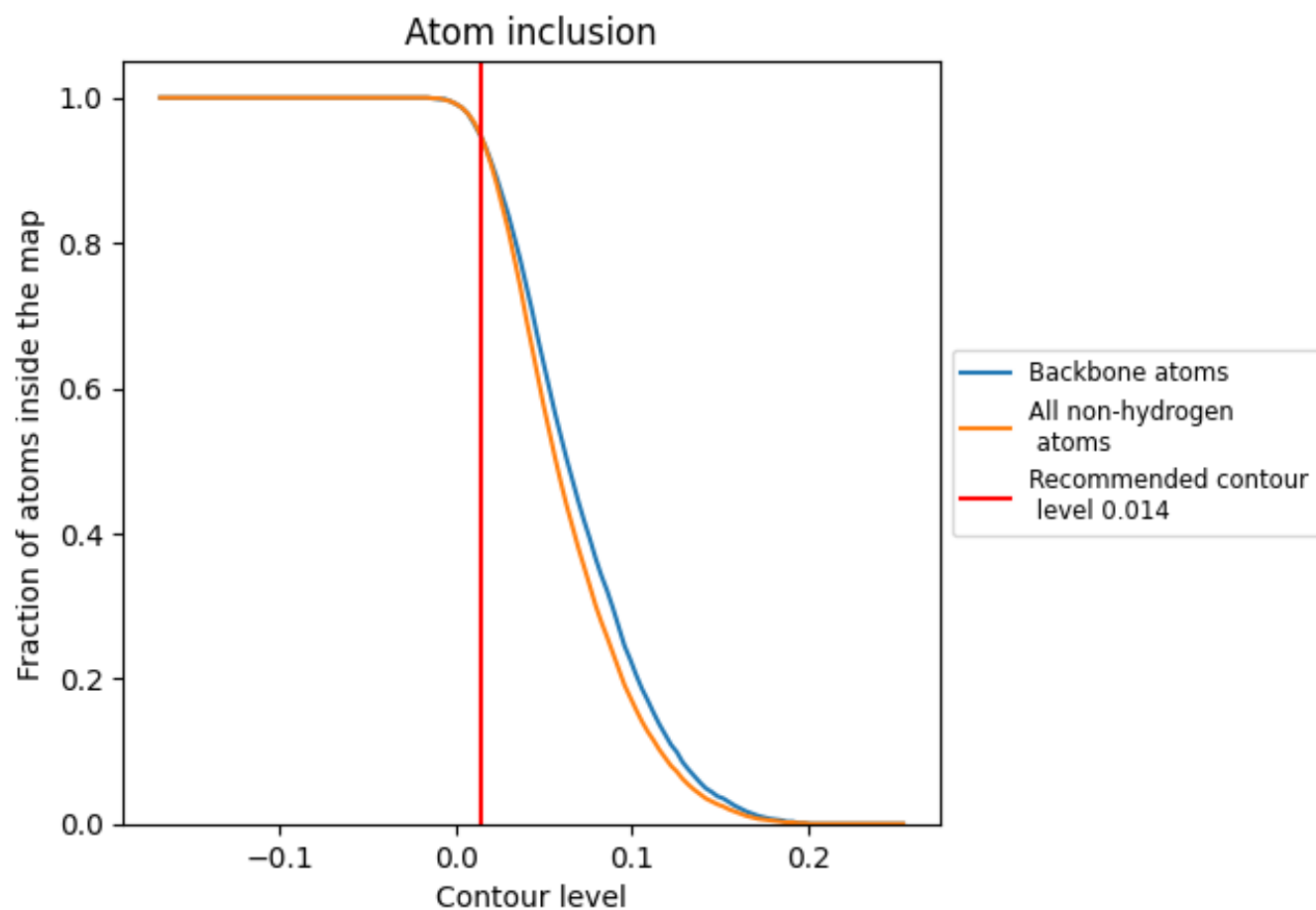


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9490	0.5290
A	0.9740	0.5490
B	0.9720	0.5420
C	0.9030	0.4990

