wwPDB EM Validation Summary Report (i)

Oct 10, 2026 – 10:28 am BST

PDB ID	:	29RE / pdb_000029re
EMDB ID	:	EMD-57321
Title	:	SARS-CoV2 KP.3 with fab JN.1-10 local refinement
Authors	:	Duyvesteyn, H.M.E.; Ren, J.
Deposited on	:	2026-03-31
Resolution	:	3.20 Å(reported)
Based on initial models	:	., 8CIM

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

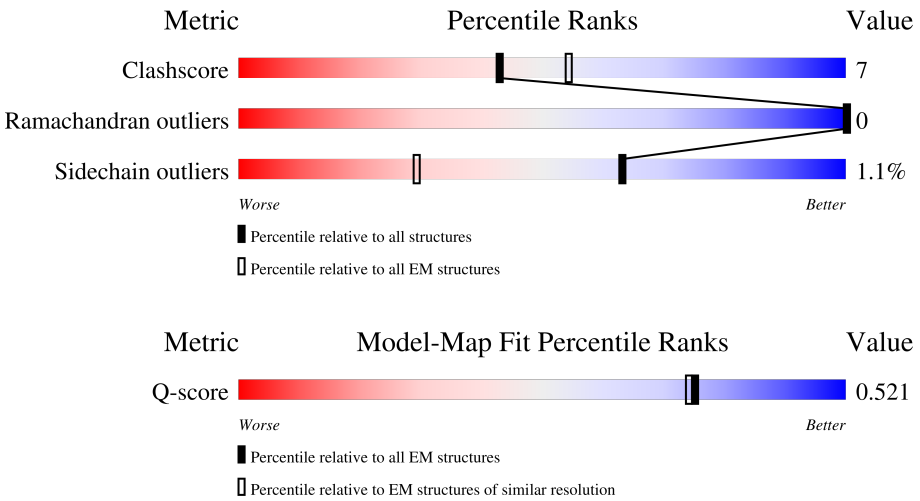
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	A	1284	13% • 84%
2	H	119	18% 75% 24% •
3	L	111	32% 86% 12% •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3346 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
			Total	C	N	O	S		
1	A	200	1607	1039	271	289	8	0	0

There are 127 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	MET	-	insertion	UNP P0DTC2
A	18	PRO	ASN	variant	UNP P0DTC2
A	20	PHE	THR	variant	UNP P0DTC2
A	21	ASN	THR	variant	UNP P0DTC2
A	22	LEU	ARG	variant	UNP P0DTC2
A	23	ILE	THR	variant	UNP P0DTC2
A	24	THR	GLN	variant	UNP P0DTC2
A	25	THR	LEU	variant	UNP P0DTC2
A	26	THR	PRO	variant	UNP P0DTC2
A	27	GLN	PRO	variant	UNP P0DTC2
A	28	SER	ALA	variant	UNP P0DTC2
A	51	LEU	SER	variant	UNP P0DTC2
A	?	-	HIS	deletion	UNP P0DTC2
A	?	-	VAL	deletion	UNP P0DTC2
A	126	PHE	VAL	variant	UNP P0DTC2
A	141	ASP	GLY	variant	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	155	SER	PHE	variant	UNP P0DTC2
A	156	GLY	ARG	variant	UNP P0DTC2
A	?	-	ASN	deletion	UNP P0DTC2
A	209	ILE	LEU	variant	UNP P0DTC2
A	210	GLY	VAL	variant	UNP P0DTC2
A	213	PHE	LEU	variant	UNP P0DTC2
A	242	ASN	HIS	variant	UNP P0DTC2
A	261	ASP	ALA	variant	UNP P0DTC2
A	329	VAL	ILE	variant	UNP P0DTC2
A	336	HIS	GLY	variant	UNP P0DTC2
A	353	THR	LYS	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	368	PHE	SER	variant	UNP P0DTC2
A	370	PRO	SER	variant	UNP P0DTC2
A	372	PHE	SER	variant	UNP P0DTC2
A	373	ALA	THR	variant	UNP P0DTC2
A	400	LYS	ARG	variant	UNP P0DTC2
A	402	ASN	ASP	variant	UNP P0DTC2
A	405	SER	ARG	variant	UNP P0DTC2
A	414	ASN	LYS	variant	UNP P0DTC2
A	437	LYS	ASN	variant	UNP P0DTC2
A	442	HIS	VAL	variant	UNP P0DTC2
A	443	SER	GLY	variant	UNP P0DTC2
A	447	ASP	ASN	variant	UNP P0DTC2
A	449	TRP	LEU	variant	UNP P0DTC2
A	452	SER	LEU	variant	UNP P0DTC2
A	453	LEU	PHE	variant	UNP P0DTC2
A	457	LYS	ASN	variant	UNP P0DTC2
A	474	ASN	SER	variant	UNP P0DTC2
A	475	LYS	THR	variant	UNP P0DTC2
A	478	LYS	ASN	variant	UNP P0DTC2
A	?	-	VAL	deletion	UNP P0DTC2
A	480	LYS	GLU	variant	UNP P0DTC2
A	482	PRO	PHE	variant	UNP P0DTC2
A	489	GLU	GLN	variant	UNP P0DTC2
A	494	ARG	GLN	variant	UNP P0DTC2
A	497	TYR	ASN	variant	UNP P0DTC2
A	501	HIS	TYR	variant	UNP P0DTC2
A	550	LYS	GLU	variant	UNP P0DTC2
A	566	VAL	ALA	variant	UNP P0DTC2
A	610	GLY	ASP	variant	UNP P0DTC2
A	617	SER	PRO	variant	UNP P0DTC2
A	651	TYR	HIS	variant	UNP P0DTC2
A	675	LYS	ASN	variant	UNP P0DTC2
A	677	ARG	PRO	variant	UNP P0DTC2
A	678	GLY	ARG	engineered mutation	UNP P0DTC2
A	679	SER	ARG	engineered mutation	UNP P0DTC2
A	681	SER	ARG	engineered mutation	UNP P0DTC2
A	760	LYS	ASN	variant	UNP P0DTC2
A	792	TYR	ASP	variant	UNP P0DTC2
A	935	PHE	SER	variant	UNP P0DTC2
A	950	HIS	GLN	variant	UNP P0DTC2
A	965	LYS	ASN	variant	UNP P0DTC2
A	982	PRO	LYS	engineered mutation	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	983	PRO	VAL	engineered mutation	UNP P0DTC2
A	1100	LEU	VAL	variant	UNP P0DTC2
A	1139	LEU	PRO	variant	UNP P0DTC2
A	1205	GLY	-	linker	UNP P0DTC2
A	1206	SER	-	linker	UNP P0DTC2
A	1228	LEU	PHE	engineered mutation	UNP P10104
A	1234	GLY	-	expression tag	UNP P10104
A	1235	ARG	-	expression tag	UNP P10104
A	1236	SER	-	expression tag	UNP P10104
A	1237	LEU	-	expression tag	UNP P10104
A	1238	GLU	-	expression tag	UNP P10104
A	1239	VAL	-	expression tag	UNP P10104
A	1240	LEU	-	expression tag	UNP P10104
A	1241	PHE	-	expression tag	UNP P10104
A	1242	GLN	-	expression tag	UNP P10104
A	1243	GLY	-	expression tag	UNP P10104
A	1244	PRO	-	expression tag	UNP P10104
A	1245	GLY	-	expression tag	UNP P10104
A	1246	HIS	-	expression tag	UNP P10104
A	1247	HIS	-	expression tag	UNP P10104
A	1248	HIS	-	expression tag	UNP P10104
A	1249	HIS	-	expression tag	UNP P10104
A	1250	HIS	-	expression tag	UNP P10104
A	1251	HIS	-	expression tag	UNP P10104
A	1252	HIS	-	expression tag	UNP P10104
A	1253	HIS	-	expression tag	UNP P10104
A	1254	GLY	-	expression tag	UNP P10104
A	1255	SER	-	expression tag	UNP P10104
A	1256	ALA	-	expression tag	UNP P10104
A	1257	TRP	-	expression tag	UNP P10104
A	1258	SER	-	expression tag	UNP P10104
A	1259	HIS	-	expression tag	UNP P10104
A	1260	PRO	-	expression tag	UNP P10104
A	1261	GLN	-	expression tag	UNP P10104
A	1262	PHE	-	expression tag	UNP P10104
A	1263	GLU	-	expression tag	UNP P10104
A	1264	LYS	-	expression tag	UNP P10104
A	1265	GLY	-	expression tag	UNP P10104
A	1266	GLY	-	expression tag	UNP P10104
A	1267	GLY	-	expression tag	UNP P10104
A	1268	SER	-	expression tag	UNP P10104
A	1269	GLY	-	expression tag	UNP P10104

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1270	GLY	-	expression tag	UNP P10104
A	1271	GLY	-	expression tag	UNP P10104
A	1272	SER	-	expression tag	UNP P10104
A	1273	GLY	-	expression tag	UNP P10104
A	1274	GLY	-	expression tag	UNP P10104
A	1275	SER	-	expression tag	UNP P10104
A	1276	ALA	-	expression tag	UNP P10104
A	1277	TRP	-	expression tag	UNP P10104
A	1278	SER	-	expression tag	UNP P10104
A	1279	HIS	-	expression tag	UNP P10104
A	1280	PRO	-	expression tag	UNP P10104
A	1281	GLN	-	expression tag	UNP P10104
A	1282	PHE	-	expression tag	UNP P10104
A	1283	GLU	-	expression tag	UNP P10104
A	1284	LYS	-	expression tag	UNP P10104

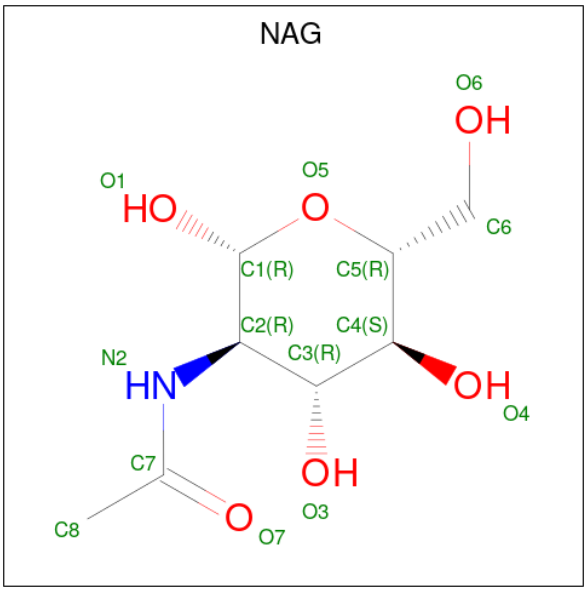
- Molecule 2 is a protein called JN1-10 fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	H	118	912	590	142	177	3	0	0

- Molecule 3 is a protein called JN1-10 fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	L	109	799	499	136	162	2	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



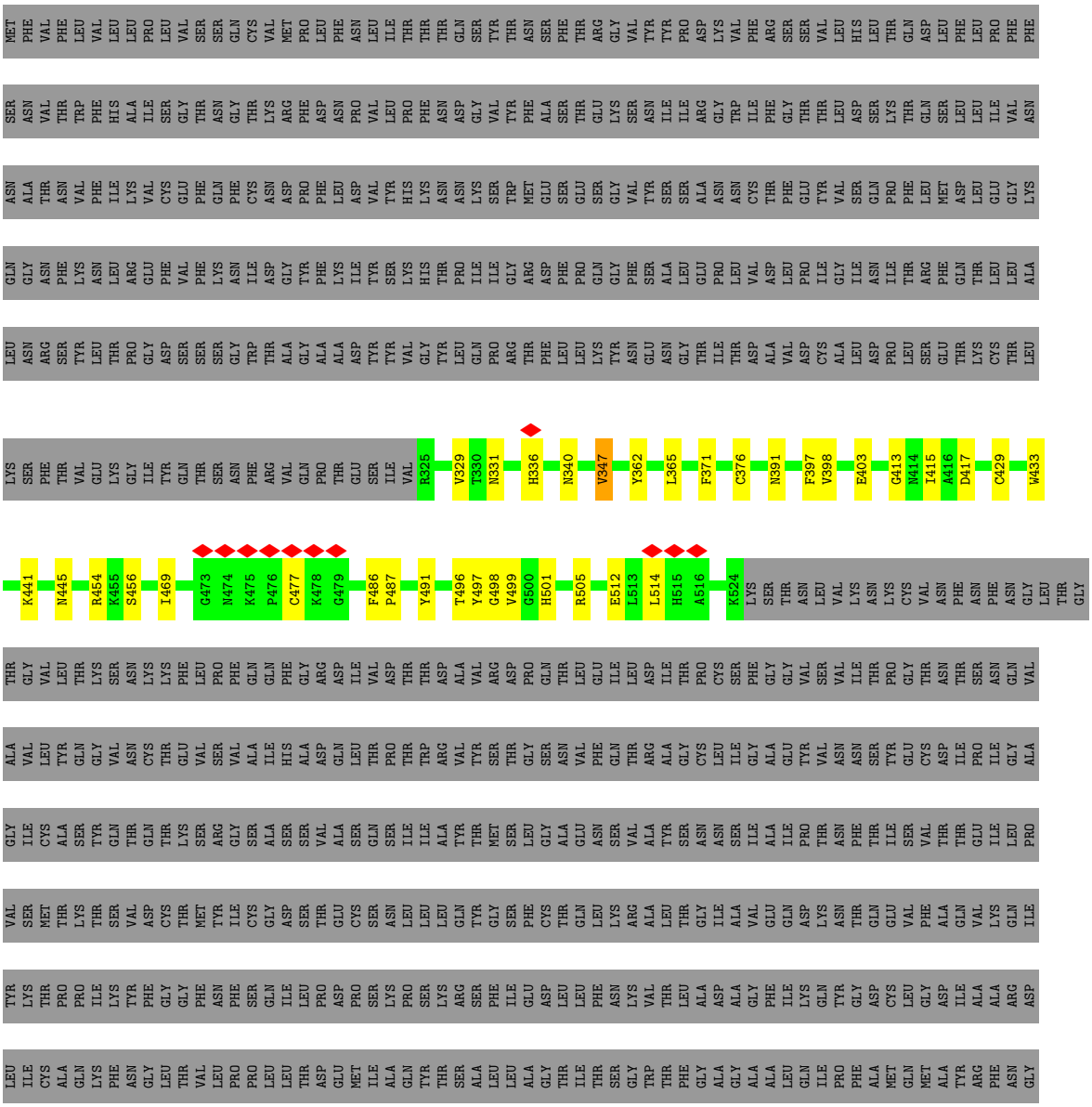
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	A	1	14	8	1	5	0
			Total	C	N	O	
4	A	1	14	8	1	5	0

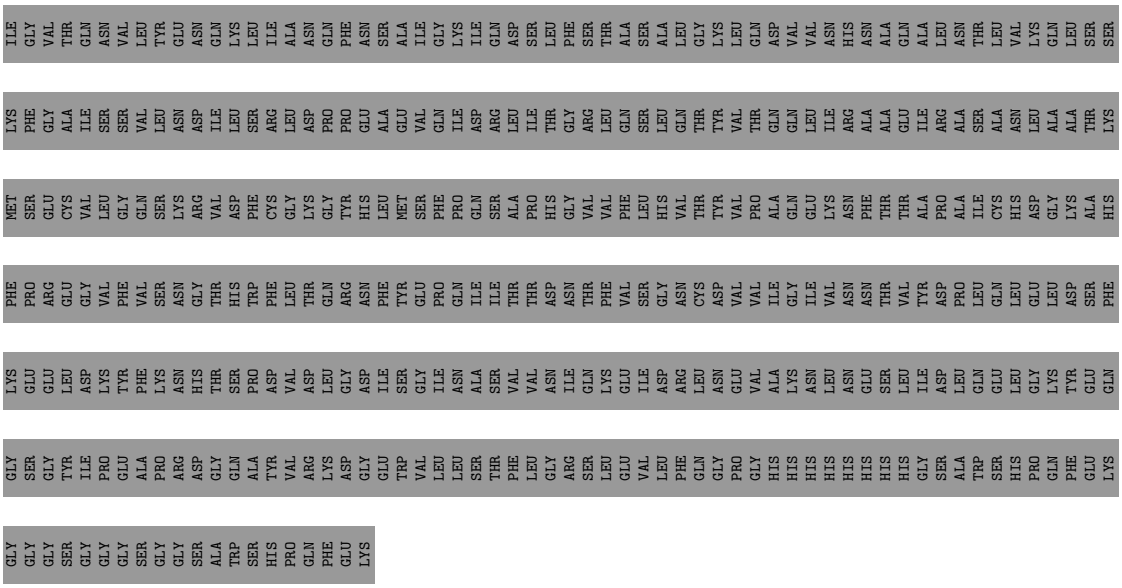
3 Residue-property plots (i)

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,Fibritin

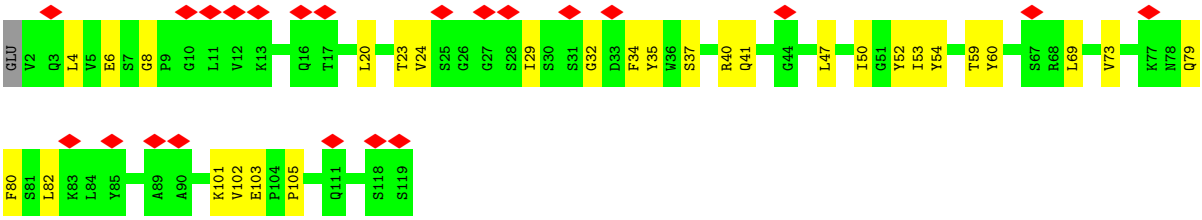
Chain A: 13% 84%





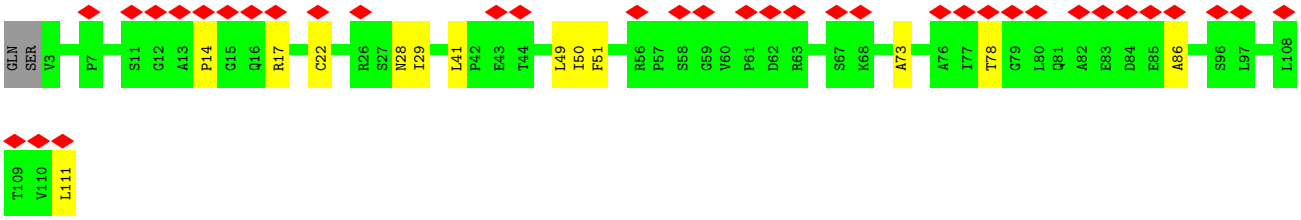
- Molecule 2: JN1-10 fab heavy chain

Chain H:



- Molecule 3: JN1-10 fab light chain

Chain L:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	163020	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Cryosparc patch CTF correction	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50.0	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	165000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.344	Depositor
Minimum map value	-0.927	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.188	Depositor
Map size (Å)	408.96802, 408.96802, 408.96802	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.7303, 0.7303, 0.7303	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	0.18	0/1660	0.27	0/2259
2	H	0.15	0/937	0.28	0/1279
3	L	0.10	0/817	0.22	0/1112
All	All	0.15	0/3414	0.26	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 (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	A	1607	0	1529	19	0
2	H	912	0	893	21	0
3	L	799	0	766	7	0
4	A	28	0	26	0	0
All	All	3346	0	3214	43	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 7.

The worst 5 of 43 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:A:391:ASN:ND2	1:A:512:GLU:OE1	2.28	0.67
3:L:14:PRO:HD3	3:L:111:LEU:HB2	1.80	0.63
1:A:501:HIS:ND1	2:H:35:TYR:OH	2.24	0.62
2:H:32:GLY:O	2:H:54:TYR:OH	2.17	0.61
2:H:53:ILE:HG13	2:H:59:THR:HG22	1.86	0.58

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	198/1284 (15%)	186 (94%)	12 (6%)	0	100	100
2	H	116/119 (98%)	109 (94%)	7 (6%)	0	100	100
3	L	107/111 (96%)	105 (98%)	2 (2%)	0	100	100
All	All	421/1514 (28%)	400 (95%)	21 (5%)	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	A	174/1111 (16%)	170 (98%)	4 (2%)	44	70
2	H	103/104 (99%)	103 (100%)	0	100	100
3	L	87/89 (98%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	364/1304 (28%)	360 (99%)	4 (1%)	63 79

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	347	VAL
1	A	477	CYS
1	A	497	TYR
1	A	514	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	402	ASN
1	A	445	ASN
2	H	16	GLN

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)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	$\#\|Z\| > 2$
4	NAG	A	1301	1	14,14,15	0.22	0	17,19,21	0.37	0
4	NAG	A	1302	1	14,14,15	0.22	0	17,19,21	0.45	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	1301	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1302	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1302	NAG	O5-C5-C6-O6
4	A	1302	NAG	C4-C5-C6-O6
4	A	1301	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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.

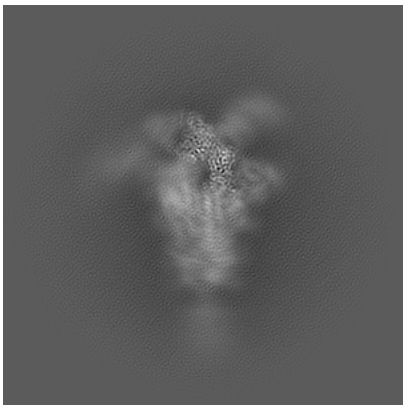
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-57321. These allow visual inspection of the internal detail of the map and identification of artifacts.

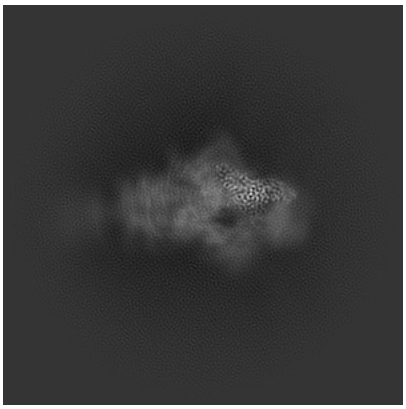
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

6.1.1 Primary map



X



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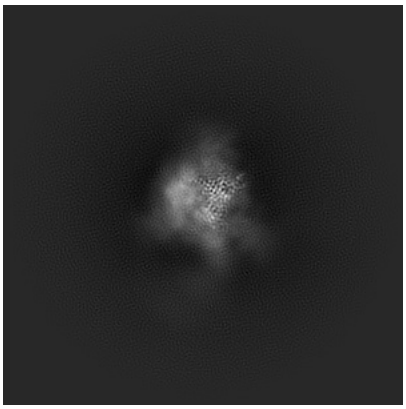
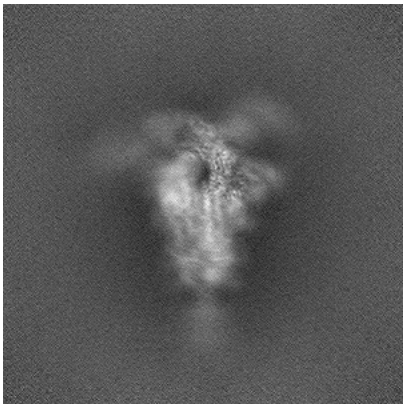
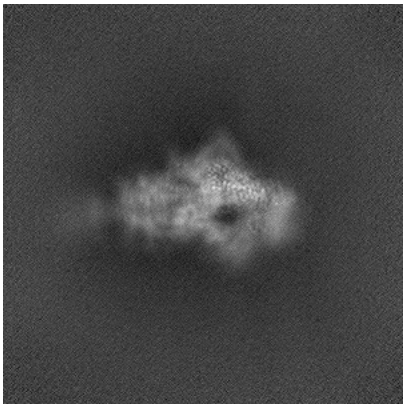


Z

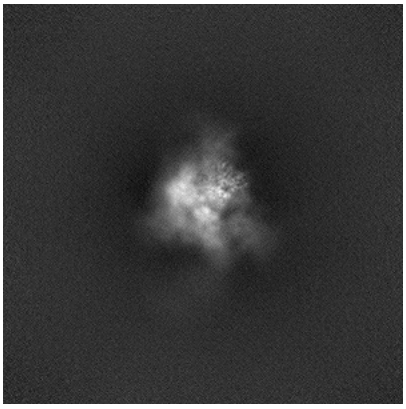
6.1.2 Raw map



X



Y

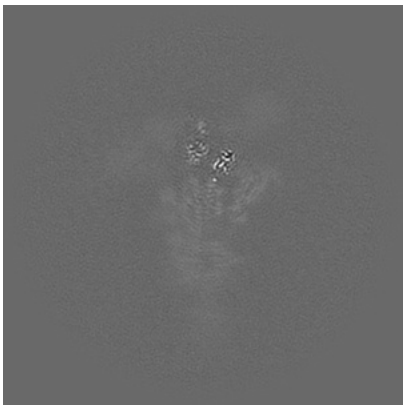


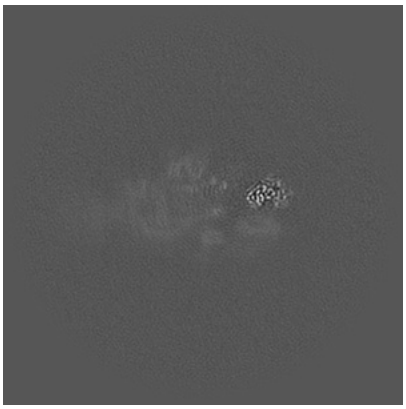
Z

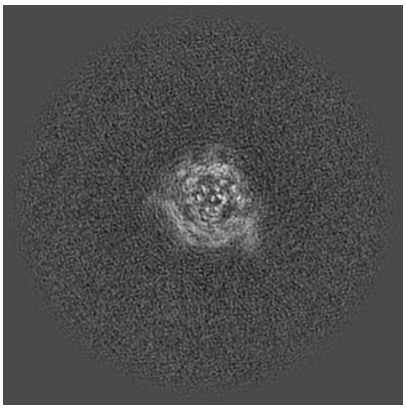
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

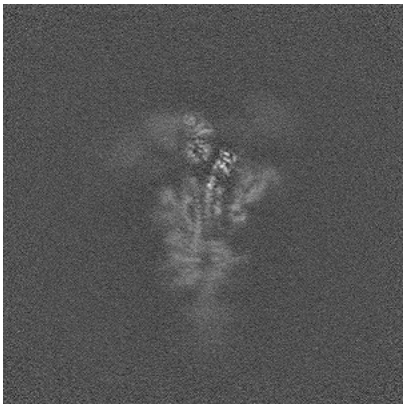
6.2.1 Primary map

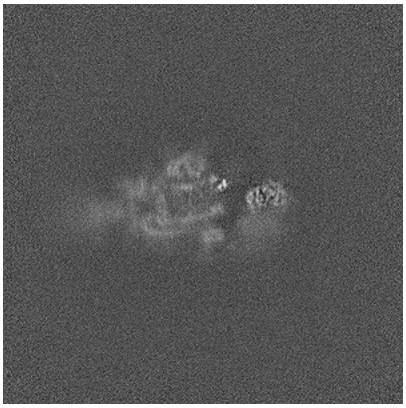

X Index: 280

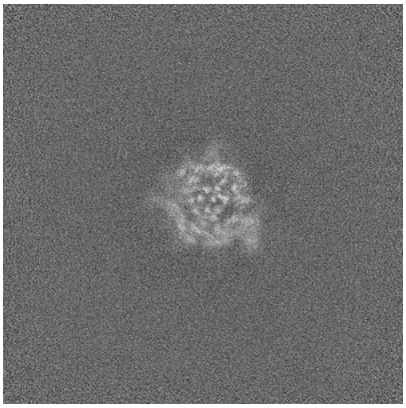

Y Index: 280


Z Index: 280

6.2.2 Raw map


X Index: 280


Y Index: 280

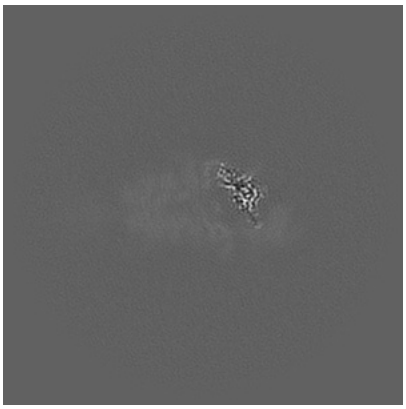

Z Index: 280

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

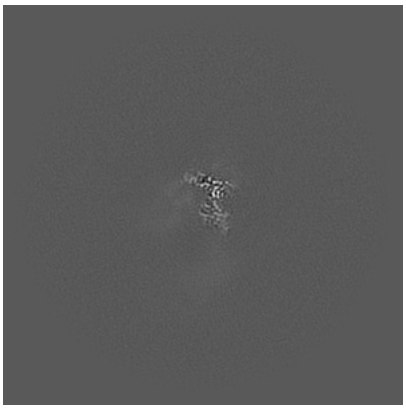
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 295

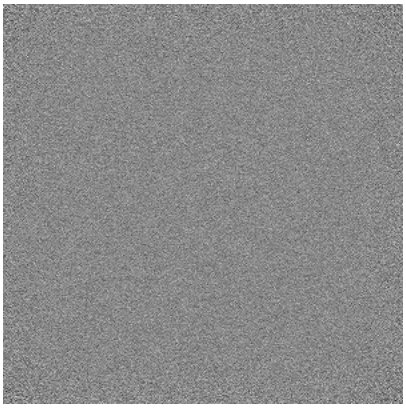


Y Index: 308

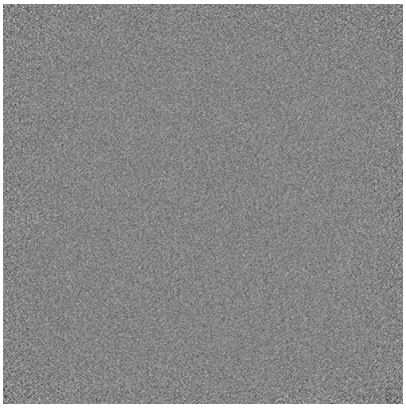


Z Index: 347

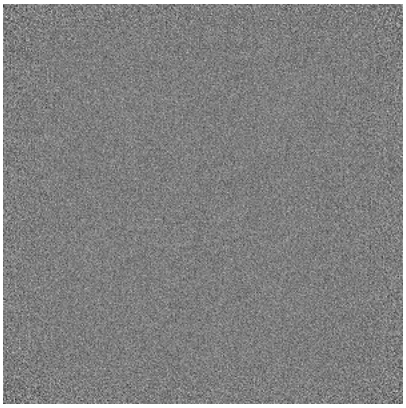
6.3.2 Raw map



X Index: 0



Y Index: 0

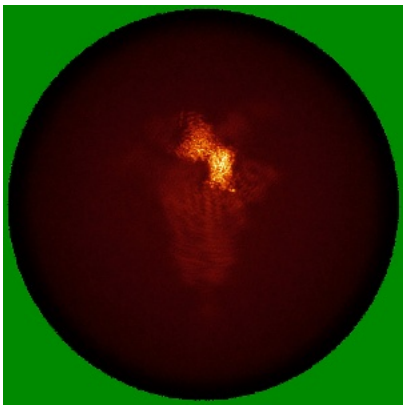


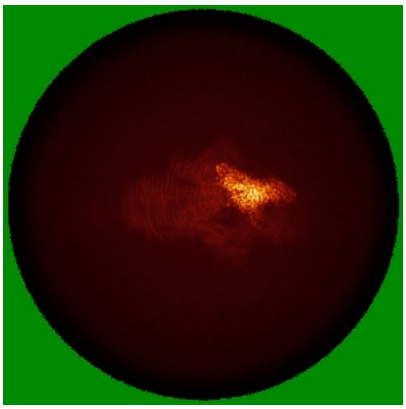
Z Index: 0

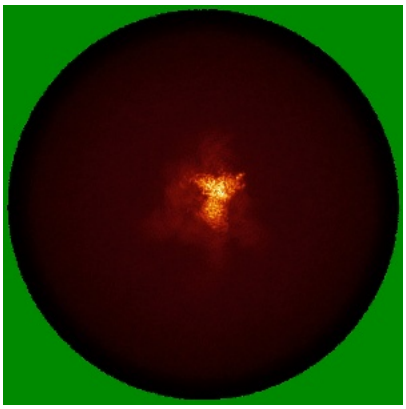
The images above show the largest variance slices of the map in three orthogonal directions.

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

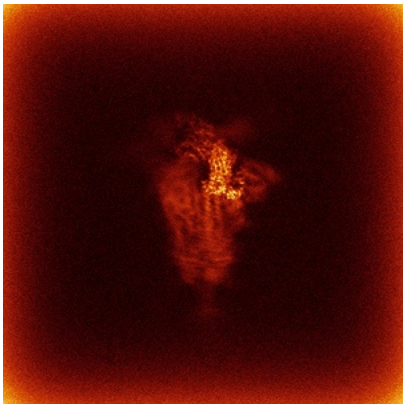
6.4.1 Primary map

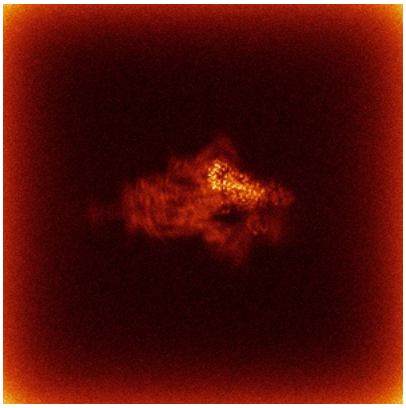

X

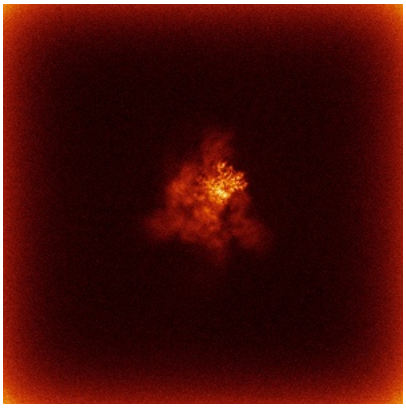

Y


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 0.188. 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.

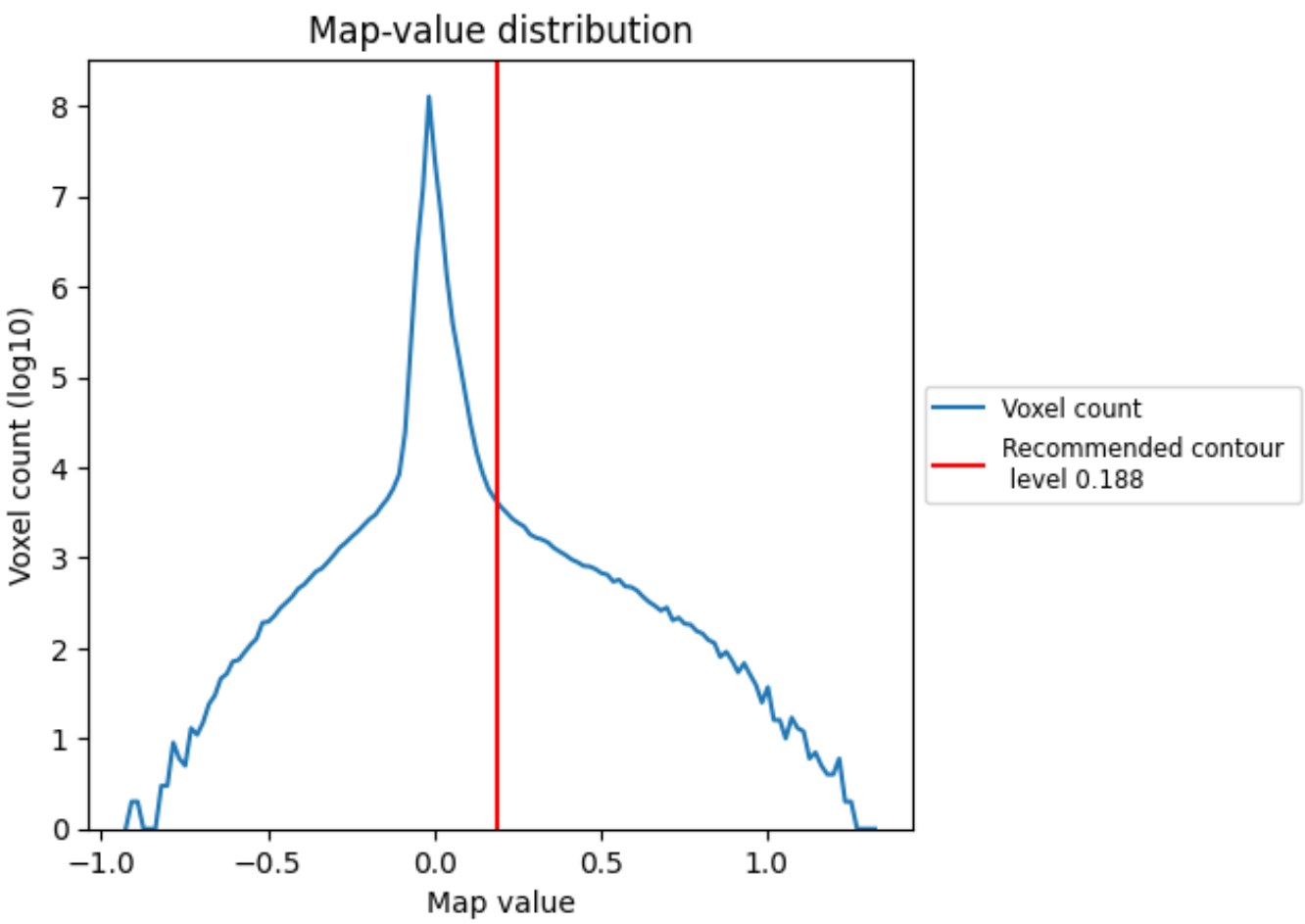
6.6 Mask visualisation (i)

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

7 Map analysis (i)

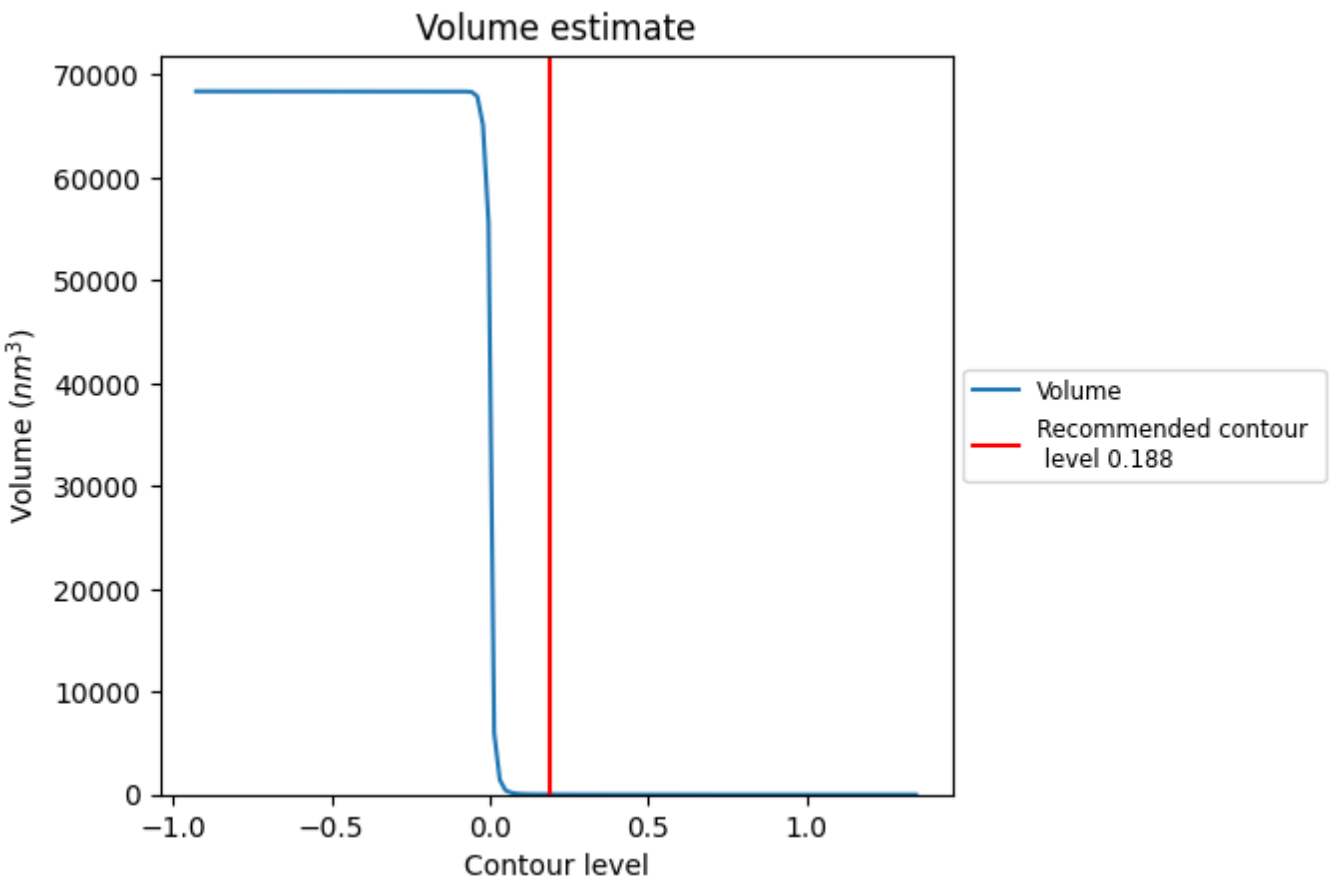
This section contains the results of statistical analysis of the map.

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.

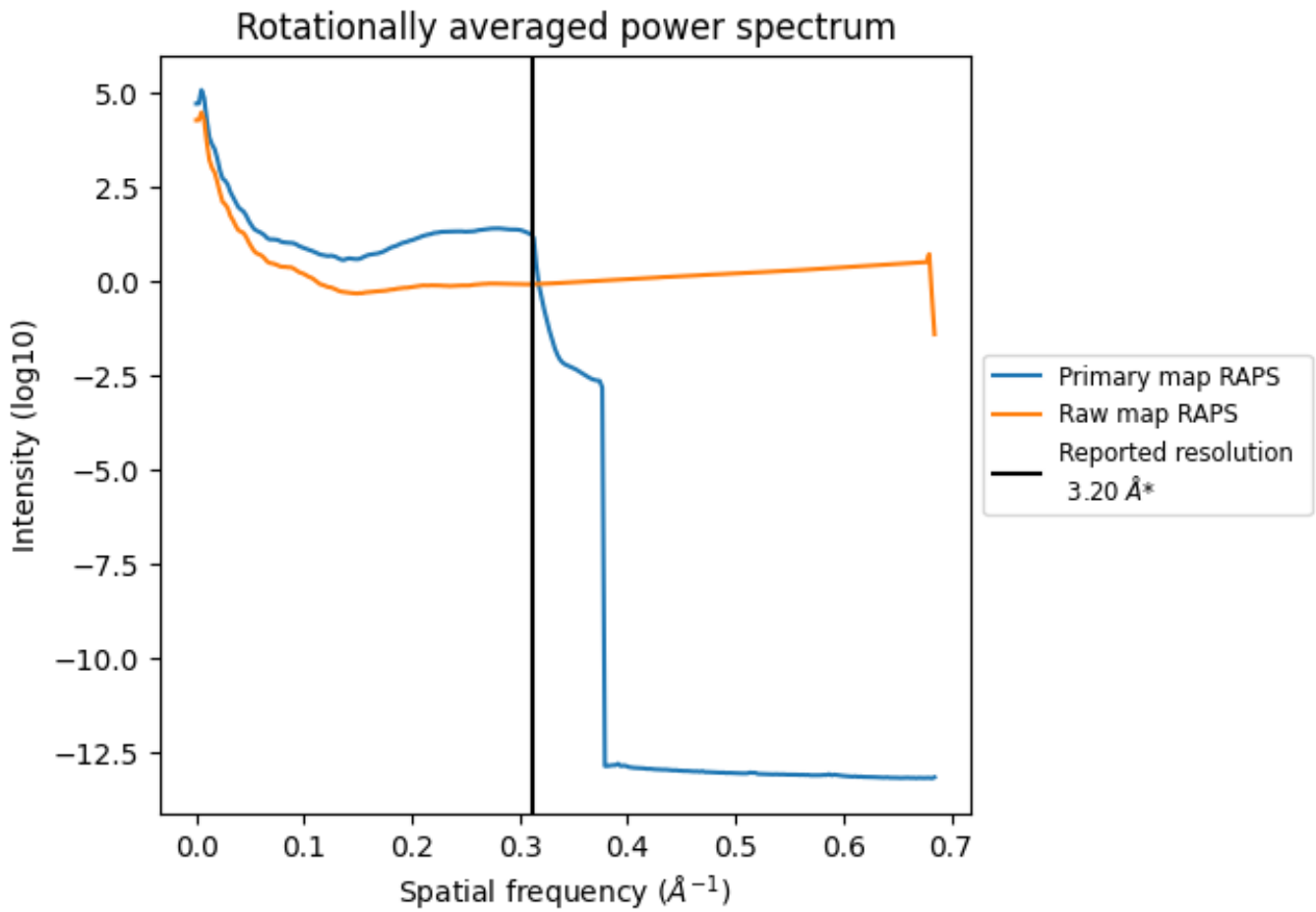
7.2 Volume estimate (i)



The volume at the recommended contour level is 15 nm^3; this corresponds to an approximate mass of 14 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)

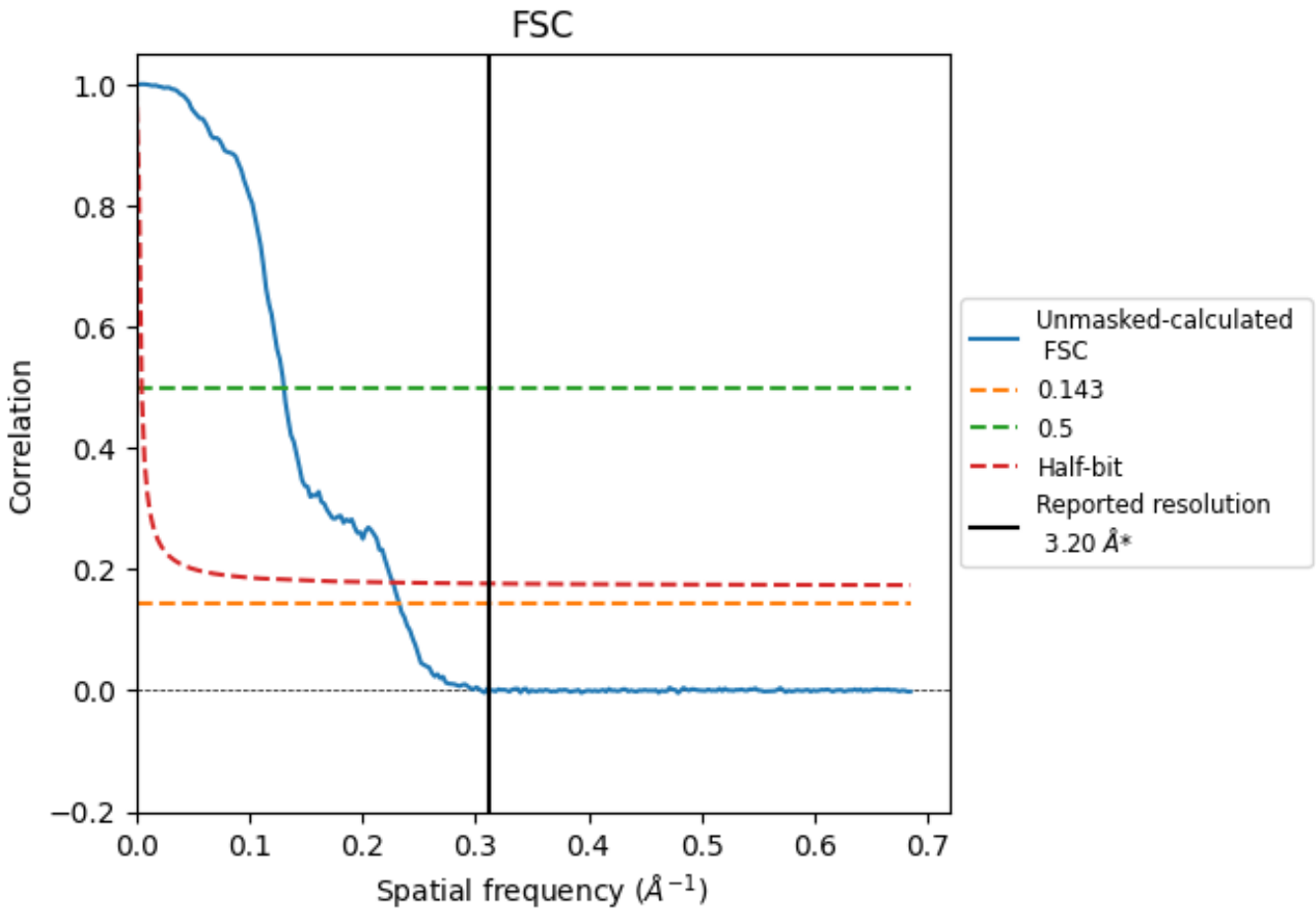


*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

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 0.312 Å^{-1}

8.2 Resolution estimates (i)

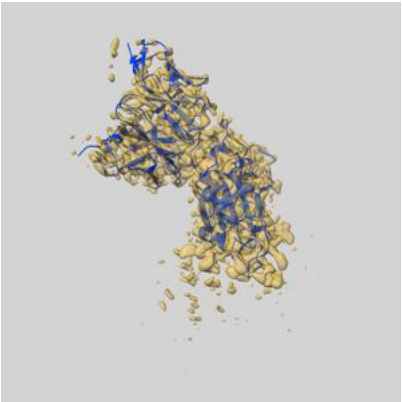
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.30	7.66	4.40

*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 4.30 differs from the reported value 3.2 by more than 10 %

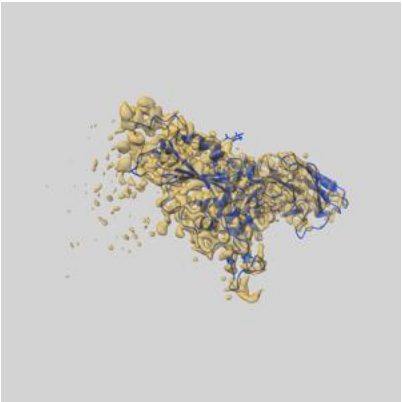
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-57321 and PDB model 29RE. Per-residue inclusion information can be found in section 3 on page 8.

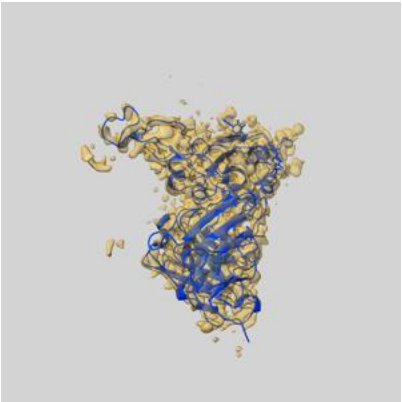
9.1 Map-model overlay (i)



X



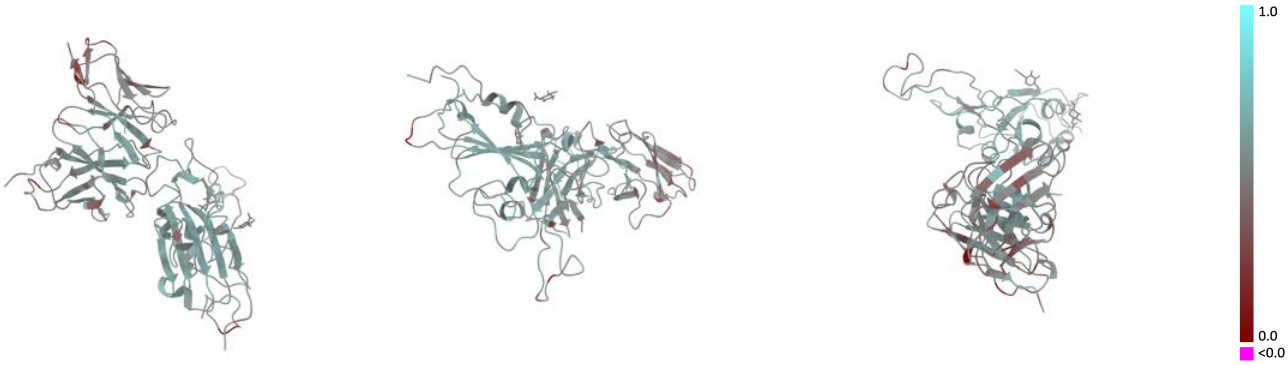
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.188 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.

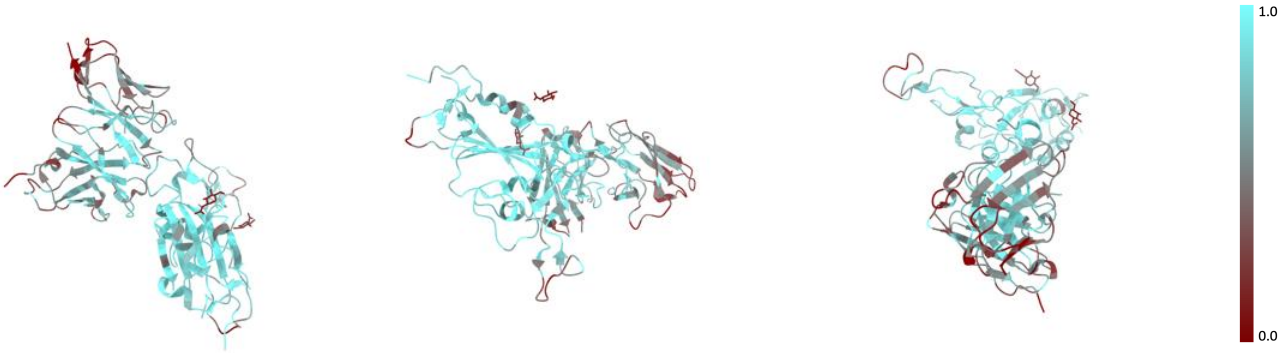
9.2 Q-score mapped to coordinate model (i)



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.

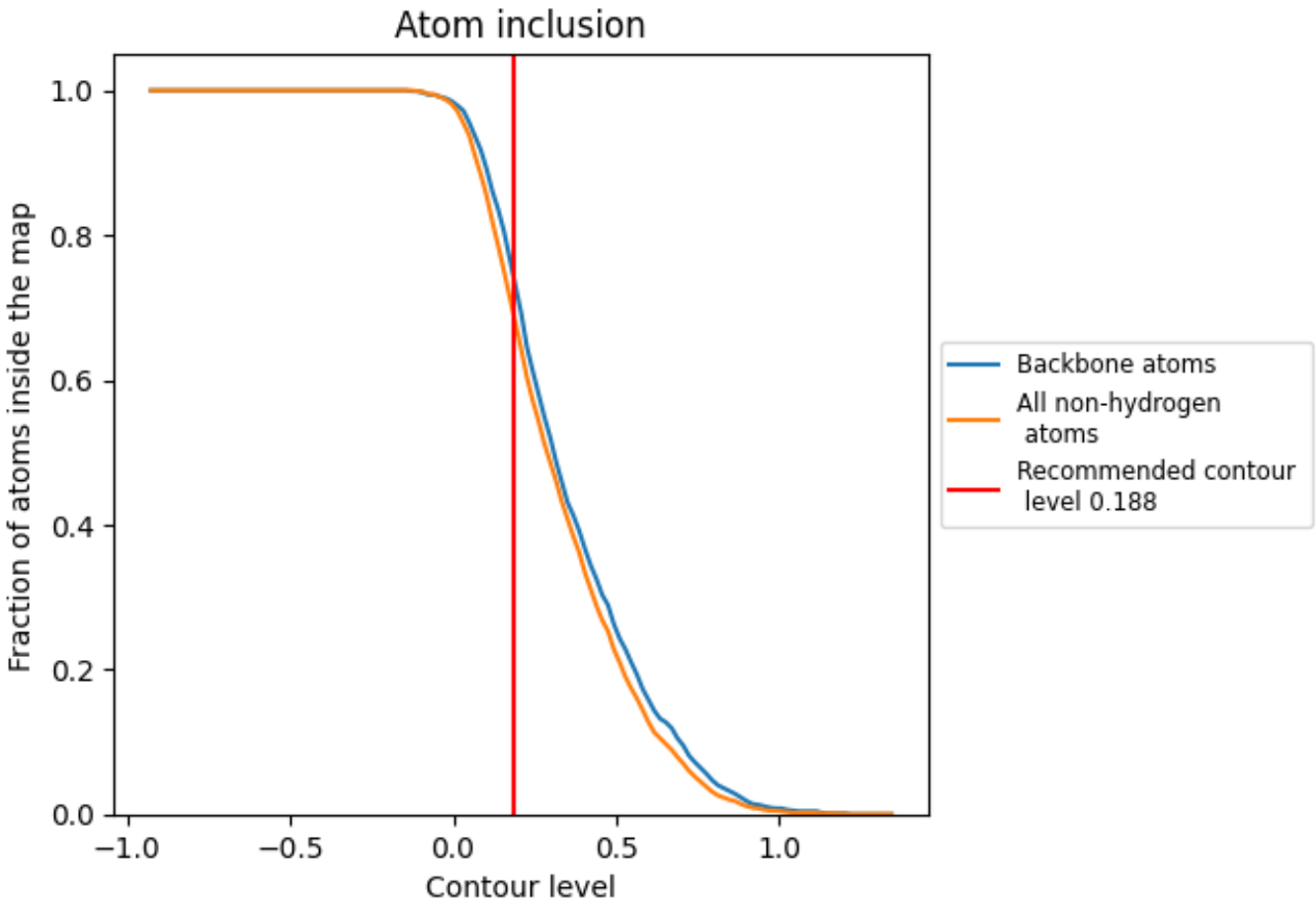
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.188).

9.4 Atom inclusion (i)



At the recommended contour level, 74% of all backbone atoms, 68% 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 (0.188) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6840	0.5210
A	0.7790	0.5520
H	0.6670	0.5140
L	0.5110	0.4640