



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 09:12 PM UTC

PDB ID : 7CWO / pdb_00007cwo
EMDB ID : EMD-30485
Title : SARS-CoV-2 spike protein RBD and P17 fab complex
Authors : Wang, X.; Wang, N.
Deposited on : 2020-08-29
Resolution : 3.90 Å(reported)

This is a Full wwPDB EM Validation 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
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

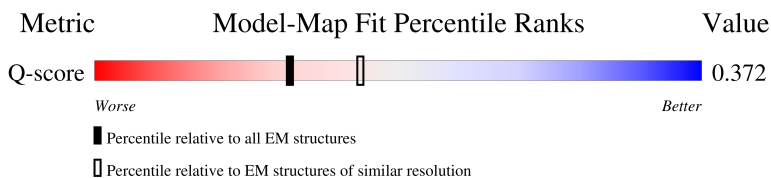
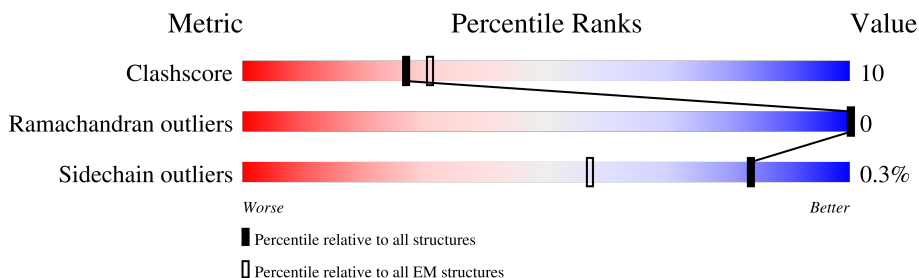
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	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	8855 (3.40 - 4.40)

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	1273	
2	H	120	
3	L	108	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3254 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	194	Total	C	N	O	S	0	0
			1519	978	256	277	8		

- Molecule 2 is a protein called heavy chain of P17 Fab.

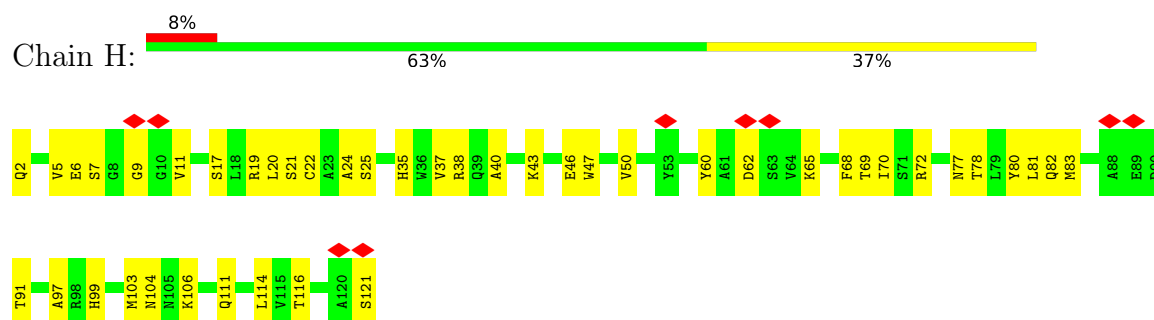
Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	120	Total	C	N	O	S	0	0
			918	574	165	175	4		

- Molecule 3 is a protein called light chain of P17 Fab.

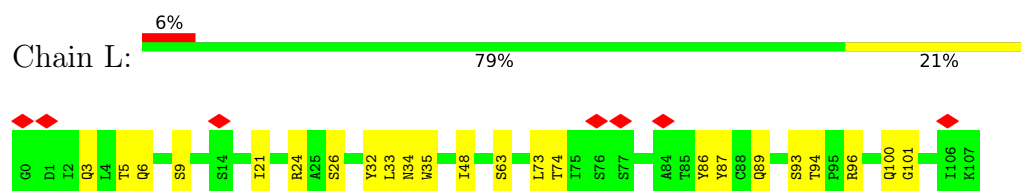
Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	108	Total	C	N	O	S	0	0
			817	511	137	167	2		

PHE	GLU	ASP	GLU	ASP	GLN	GLU	THR	THR	ALA	ALA	ALA	TLE
ASP	GLU	ASP	GLU	GLN	GLU	GLN	THR	THR	GLU	GLN	GLN	PRO
ASP	GLU	ASP	GLU	GLN	GLU	GLN	ASP	PRO	ALA	ALA	ALA	PHE
ASP	GLU	ASP	GLU	GLN	GLU	GLN	LEU	ILE	SER	ARG	THR	GLN
GLU	GLU	GLU	GLU	GLU	GLU	GLN	GLN	CYS	ALA	ALA	LEU	MET
VAL	VAL	VAL	GLY	GLY	GLU	GLU	ASP	HIS	ASN	ASN	VAL	MET
LEU	LEU	LEU	LYS	LYS	GLY	GLY	LEU	GLY	ALA	GLN	ARG	ARG
LYS	GLY	GLY	THR	GLU	ASP	ALA	LYS	LYS	THR	ALA	LEU	PHE
LYS	VAL	VAL	GLU	GLU	SER	THR	ASP	ALA	THR	ALA	SER	ASN
LYS	THR	THR	LYS	GLU	PHE	HIS	THR	HIS	LYS	LYS	SER	GLY
LEU	LEU	LEU	ILE	ILE	GLU	PHE	GLU	PRO	MET	ASN	ILE	GLY
HIS	HIS	HIS	THR	THR	GLU	ARG	GLY	ARG	GLU	VAL	GLY	VAL
THR	THR	THR	TRP	PRO	LEU	GLY	GLY	ASN	CYS	VAL	ALA	THR
			TRP	TRP	ASP	THR	THR	THR	VAL	GLN	ILE	GLN
			LEU	LEU	ASN	HIS	GLY	GLY	LYS	LYS	ASP	ASN
			GLY	GLY	ASN	THR	THR	THR	VAL	GLY	THR	GLN
			PHE	ILE	THR	THR	THR	GLN	VAL	LYS	VAL	ASN
			ILE	VAL	SER	SER	HIS	ARG	ASP	GLY	THR	GLN
			ALA	VAL	PRO	PRO	TRP	TRP	PHE	HIS	GLU	VAL
			GLY	VAL	ASP	ASP	PHE	PHE	CYS	GLY	ARG	THR
			LEU	VAL	VAL	THR	THR	THR	GLY	LYS	LEU	ALA
			ILE	ASP	ASP	ASP	THR	GLN	LYS	GLY	GLN	ASN
			ALA	LEU	LEU	LEU	GLN	ILE	GLN	ILE	ILE	ASN
			VAL	SER	SER	SER	THR	ILE	SER	ARG	GLN	ASP
			CYS	CYS	CYS	CYS	THR	THR	ALA	LEU	LEU	ASP
			MET	MET	VAL	VAL	THR	THR	PRO	ILE	ILE	SER
			THR	THR	ASN	ASN	ASP	ASN	HIS	THR	THR	LEU
			SER	SER	ILE	ILE	ASN	GLY	GLY	GLY	GLY	SER
			CYS	CYS	GLN	GLN	THR	VAL	VAL	ARG	THR	ALA
			THR	THR	LYS	LYS	PHE	VAL	PHE	GLN	GLN	SER
			SER	SER	GLU	ILE	VAL	VAL	LEU	SER	SER	ALA
			CYS	CYS	ILE	THR	SER	SER	THR	THR	THR	SER
			LEU	LEU	ASP	ASP	GLY	GLY	HIS	VAL	GLN	LEU
			LYS	LYS	ARG	ASN	ASN	CYS	VAL	THR	THR	LEU
			CYS	CYS	LEU	THR	CYS	THR	THR	TYR	LYS	LYS
			CYS	CYS	ASN	VAL	VAL	VAL	VAL	VAL	VAL	GLN
			SER	SER	VAL	VAL	VAL	VAL	PRO	THR	THR	GLN
			CYS	CYS	ALA	ALA	ILE	ILE	ALA	GLN	GLN	ASP
			THR	THR	LYS	LYS	GLY	GLY	VAL	VAL	VAL	ASN
			SER	SER	ASN	ASN	ILE	ILE	GLU	ILE	ILE	ASN
			CYS	CYS	ASN	ASN	ASN	ASN	LYS	ARG	ARG	GLN
			LYS	LYS	THR	THR	THR	THR	PHE	ALA	ALA	ASN

- Molecule 2: heavy chain of P17 Fab



- Molecule 3: light chain of P17 Fab



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	249308	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.051	Depositor
Minimum map value	-0.032	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0115	Depositor
Map size ($\text{\AA}$)	208.0, 208.0, 208.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.32	0/1563	0.68	0/2129
2	H	0.32	0/937	0.64	0/1269
3	L	0.33	0/834	0.63	0/1131
All	All	0.32	0/3334	0.66	0/4529

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	H	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	391	CYS	Peptide
2	H	72	ARG	Peptide

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	1519	0	1439	23	0
2	H	918	0	885	27	0
3	L	817	0	800	16	0
All	All	3254	0	3124	63	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 10.

All (63) 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:H:17:SER:HA	2:H:83:MET:O	1.65	0.97
3:L:33:LEU:HA	3:L:89:GLN:O	1.74	0.88
3:L:63:SER:O	3:L:74:THR:HB	1.85	0.77
2:H:69:THR:O	2:H:81:LEU:HA	1.86	0.74
1:A:431:GLY:HA3	1:A:513:LEU:O	1.95	0.67
2:H:6:GLU:H	2:H:111:GLN:HE22	1.45	0.63
2:H:20:LEU:O	2:H:80:TYR:HA	1.98	0.62
1:A:455:LEU:HD23	2:H:103:MET:HE1	1.82	0.61
2:H:7:SER:HB3	2:H:21:SER:HB3	1.85	0.59
2:H:19:ARG:HA	2:H:82:GLN:HA	1.86	0.58
3:L:86:TYR:O	3:L:101:GLY:HA2	2.04	0.58
2:H:104:ASN:HB3	2:H:106:LYS:HG2	1.87	0.57
2:H:47:TRP:HZ2	2:H:50:VAL:HG13	1.71	0.56
2:H:2:GLN:N	2:H:25:SER:O	2.38	0.55
2:H:91:THR:HG23	2:H:116:THR:HA	1.88	0.55
1:A:367:VAL:HA	1:A:370:ASN:HB2	1.88	0.54
1:A:417:LYS:HE2	1:A:455:LEU:HD12	1.88	0.54
1:A:437:ASN:ND2	1:A:506:GLN:OE1	2.40	0.54
2:H:62:ASP:HA	2:H:65:LYS:HB2	1.90	0.53
1:A:334:ASN:HB2	1:A:361:CYS:HA	1.91	0.53
1:A:457:ARG:NH1	1:A:459:SER:OG	2.41	0.53
2:H:11:VAL:HA	2:H:116:THR:HB	1.91	0.52
3:L:63:SER:O	3:L:74:THR:CB	2.57	0.52
2:H:37:VAL:HG12	2:H:47:TRP:HA	1.90	0.52
2:H:70:ILE:HB	2:H:81:LEU:HD12	1.91	0.52
1:A:365:TYR:HA	1:A:368:LEU:HD13	1.90	0.52
3:L:94:THR:OG1	3:L:96:ARG:NH1	2.44	0.51
2:H:35:HIS:HB2	2:H:97:ALA:HB3	1.94	0.50
2:H:40:ALA:HB3	2:H:43:LYS:HB2	1.94	0.50
2:H:11:VAL:HG11	2:H:121:SER:HA	1.93	0.49
3:L:5:THR:HB	3:L:24:ARG:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:VAL:HG22	1:A:509:ARG:HG2	1.93	0.49
1:A:337:PRO:HB2	1:A:340:GLU:HB2	1.93	0.48
1:A:393:THR:O	1:A:523:THR:OG1	2.31	0.48
1:A:448:ASN:HB3	1:A:497:PHE:HB2	1.95	0.48
2:H:68:PHE:HB3	2:H:81:LEU:HD21	1.95	0.48
3:L:93:SER:OG	3:L:94:THR:N	2.46	0.47
1:A:418:ILE:HA	1:A:422:ASN:HB2	1.97	0.47
2:H:24:ALA:HB3	2:H:77:ASN:HB3	1.95	0.47
2:H:60:TYR:HE1	2:H:70:ILE:HG22	1.80	0.47
1:A:486:PHE:HA	3:L:32:TYR:HE2	1.80	0.46
3:L:35:TRP:HA	3:L:87:TYR:O	2.15	0.46
1:A:393:THR:HG21	1:A:518:LEU:H	1.81	0.45
3:L:34:ASN:HB2	3:L:89:GLN:HB3	1.98	0.45
2:H:5:VAL:O	2:H:22:CYS:HA	2.16	0.45
2:H:38:ARG:NH2	2:H:46:GLU:OE1	2.38	0.45
1:A:497:PHE:HA	1:A:501:ASN:HD21	1.83	0.44
1:A:356:LYS:HE3	1:A:358:ILE:HD11	1.99	0.44
3:L:35:TRP:HD1	3:L:48:ILE:HB	1.81	0.44
3:L:6:GLN:O	3:L:100:GLN:NE2	2.51	0.44
1:A:436:TRP:O	1:A:508:TYR:HA	2.18	0.43
2:H:99:HIS:CG	3:L:89:GLN:HE22	2.36	0.43
3:L:21:ILE:HD12	3:L:73:LEU:HD23	2.00	0.43
3:L:9:SER:HG	3:L:100:GLN:HE21	1.61	0.42
1:A:501:ASN:HB3	1:A:505:TYR:HB2	2.00	0.42
2:H:22:CYS:O	2:H:78:THR:HA	2.19	0.42
1:A:394:ASN:OD1	1:A:394:ASN:N	2.52	0.41
2:H:7:SER:N	2:H:21:SER:O	2.54	0.41
2:H:9:GLY:HA3	2:H:114:LEU:O	2.20	0.41
1:A:424:LYS:HB3	1:A:463:PRO:HA	2.03	0.40
1:A:498:GLN:H	1:A:501:ASN:ND2	2.19	0.40
1:A:406:GLU:O	1:A:409:GLN:HB2	2.21	0.40
3:L:3:GLN:HB2	3:L:26:SER:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	192/1273 (15%)	178 (93%)	14 (7%)	0	100	100
2	H	118/120 (98%)	106 (90%)	12 (10%)	0	100	100
3	L	106/108 (98%)	97 (92%)	9 (8%)	0	100	100
All	All	416/1501 (28%)	381 (92%)	35 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	162/1112 (15%)	161 (99%)	1 (1%)	78	80
2	H	96/98 (98%)	96 (100%)	0	100	100
3	L	93/93 (100%)	93 (100%)	0	100	100
All	All	351/1303 (27%)	350 (100%)	1 (0%)	84	85

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	524	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	501	ASN
2	H	84	ASN
3	L	38	GLN
3	L	90	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](#)

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.

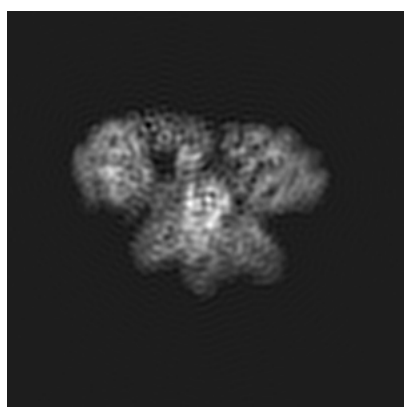
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30485. These allow visual inspection of the internal detail of the map and identification of artifacts.

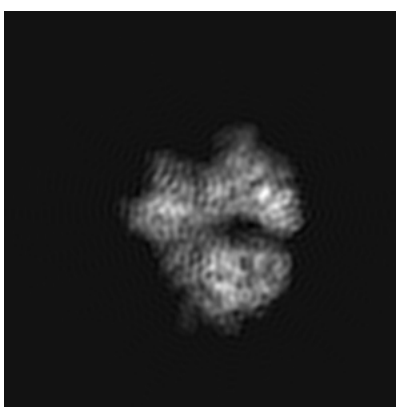
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

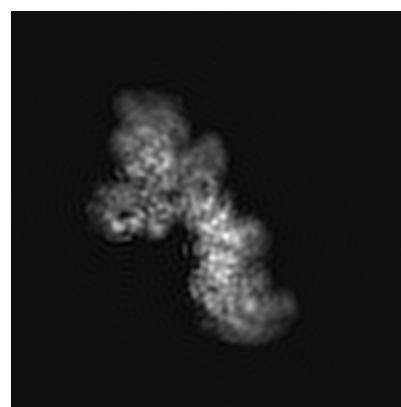
6.1.1 Primary map



X



Y

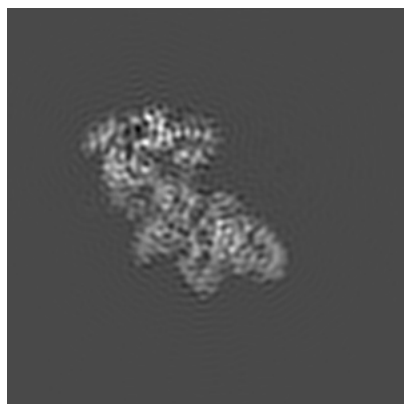


Z

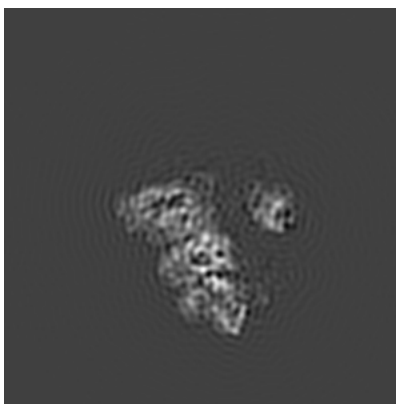
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

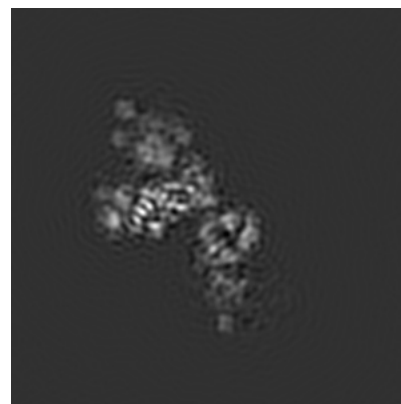
6.2.1 Primary map



X Index: 100



Y Index: 100

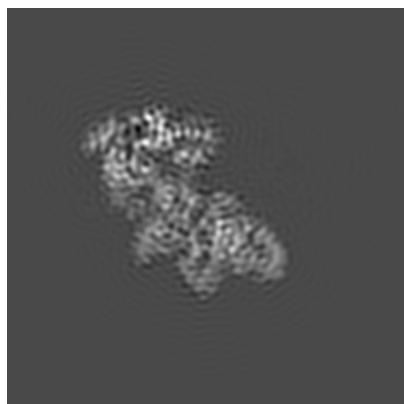


Z Index: 100

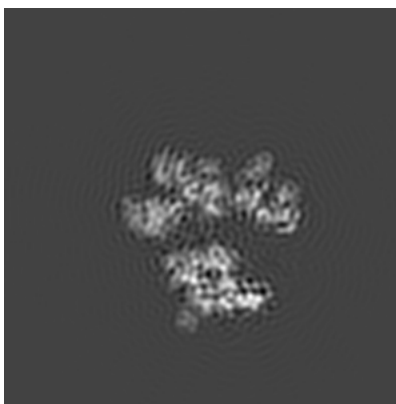
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

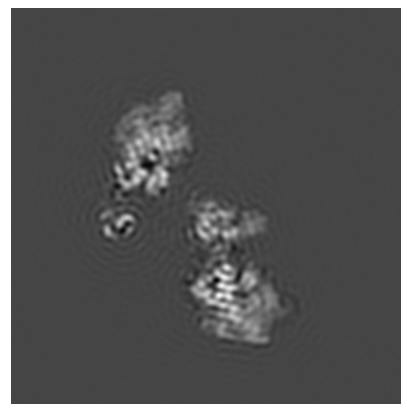
6.3.1 Primary map



X Index: 100



Y Index: 92



Z Index: 128

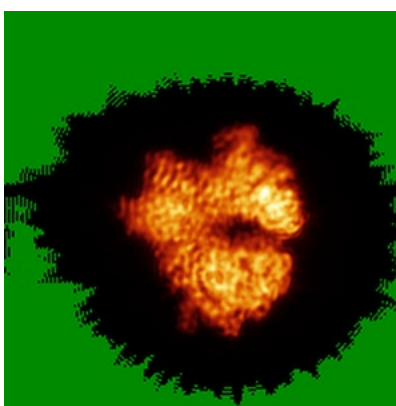
The images above show the largest variance slices of the map in three orthogonal directions.

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

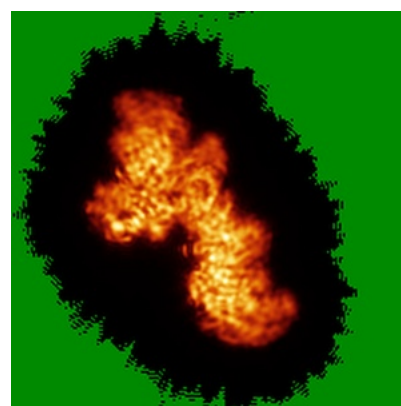
6.4.1 Primary map



X



Y

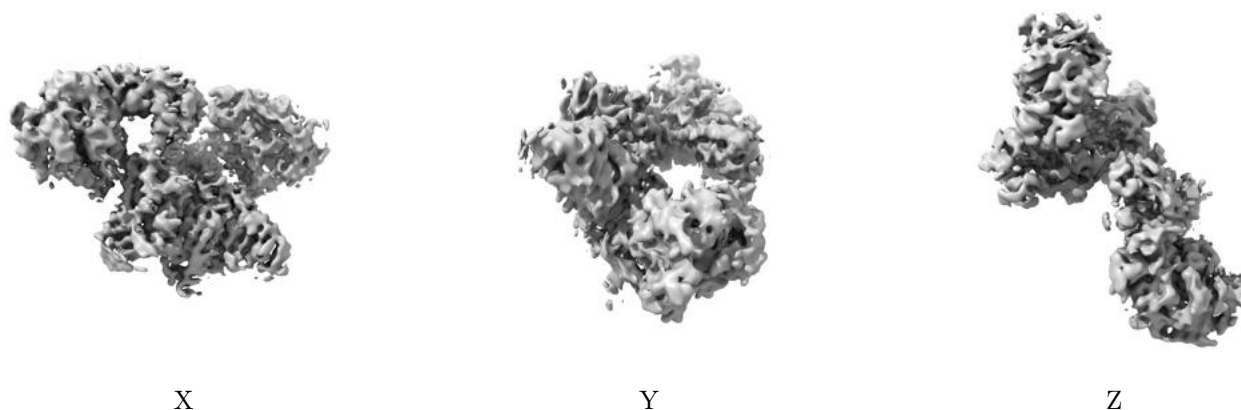


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0115. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

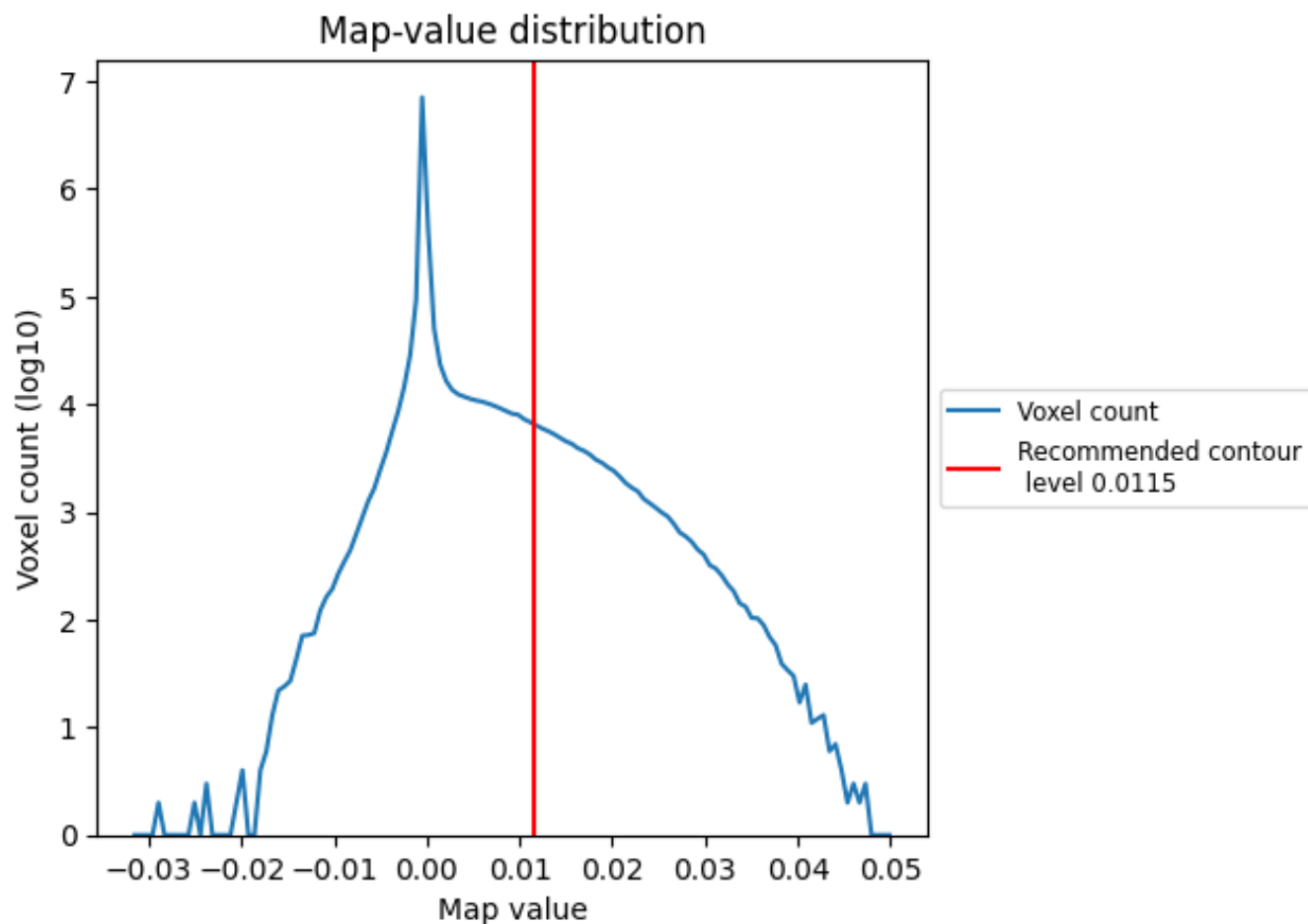
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

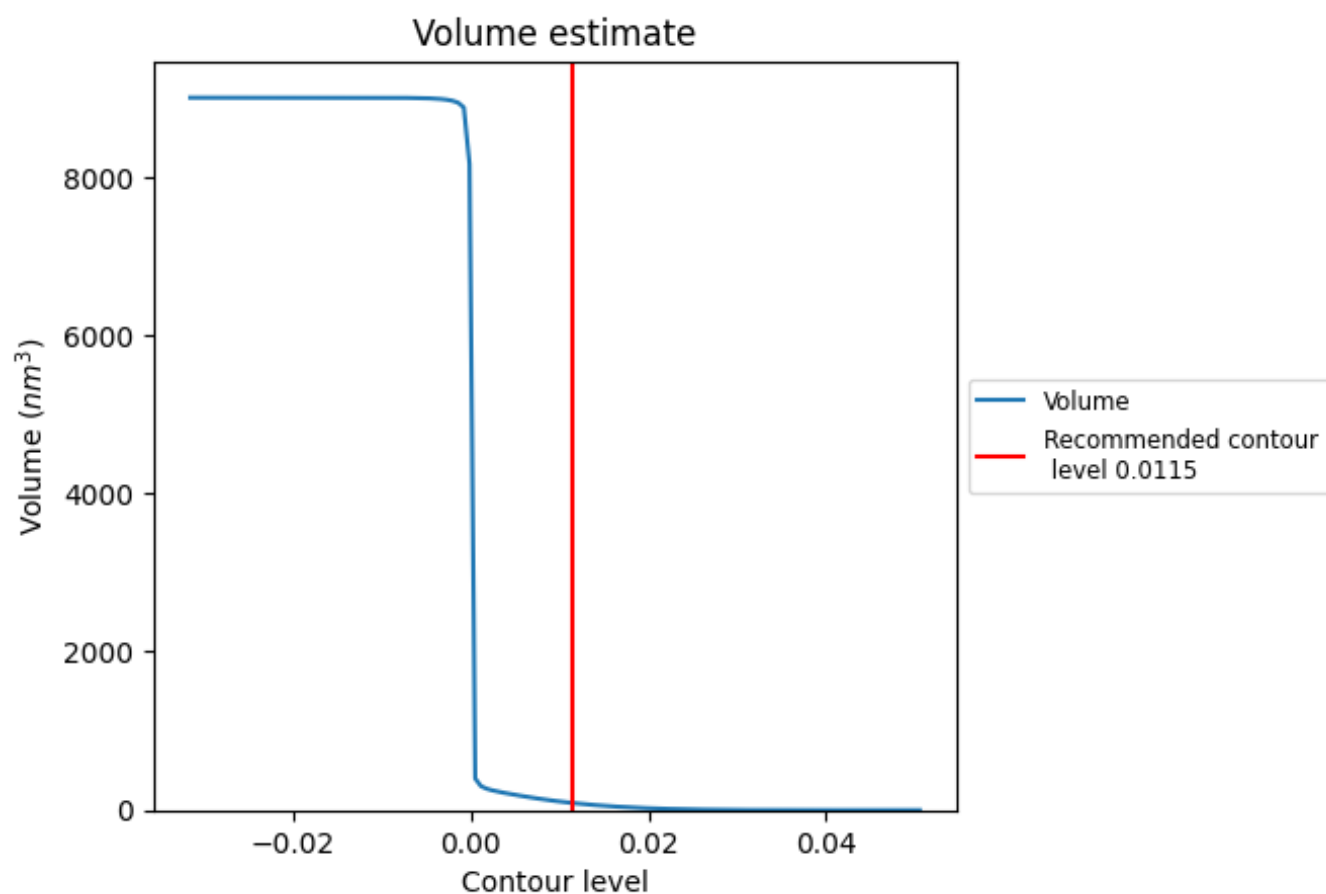
This section contains the results of statistical analysis of the map.

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.

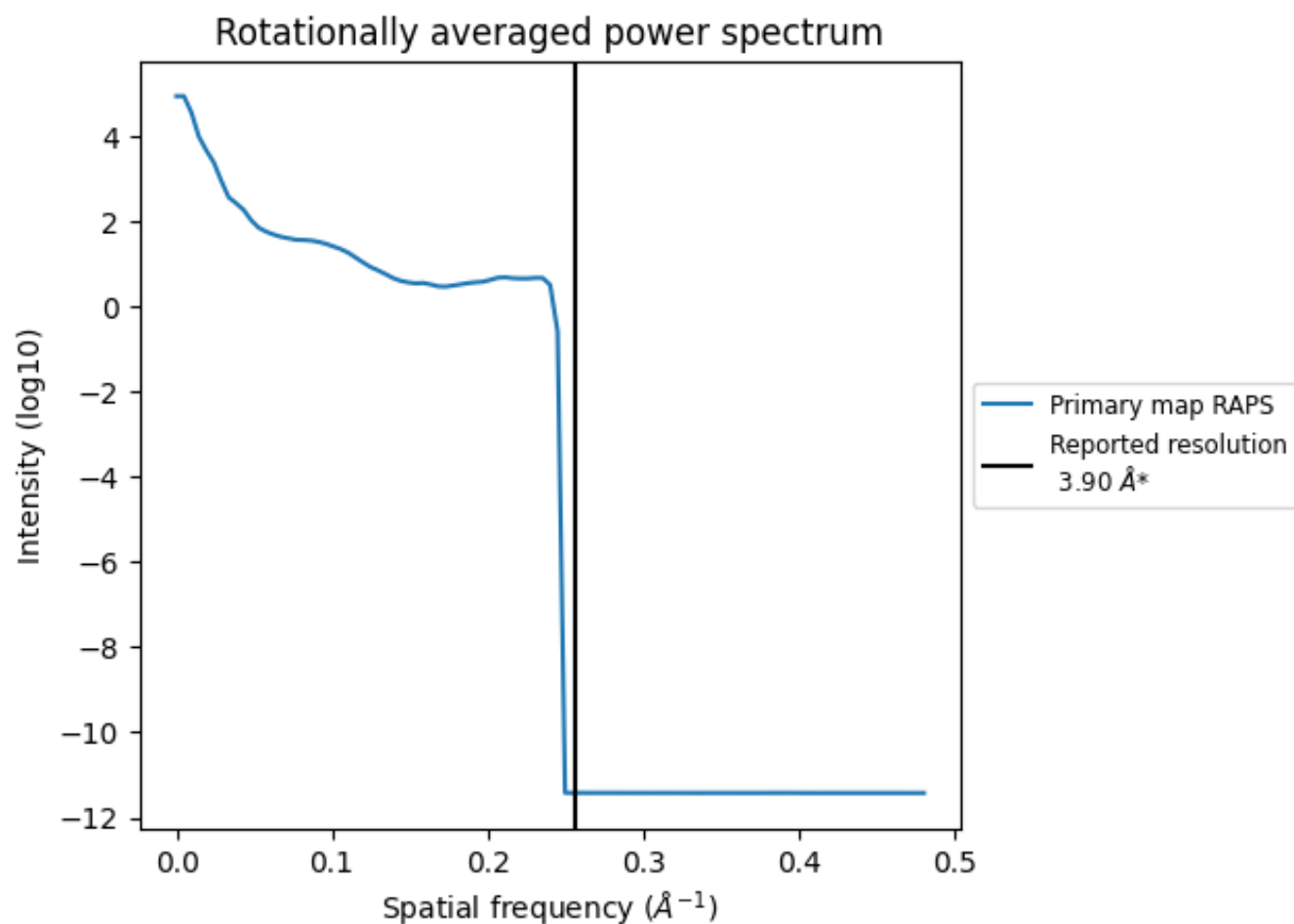
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 90 nm^3 ; this corresponds to an approximate mass of 81 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 0.256 Å⁻¹

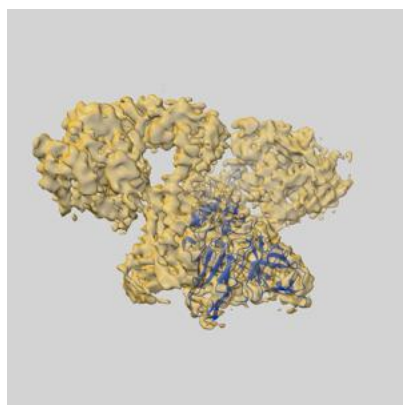
8 Fourier-Shell correlation ⓘ

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

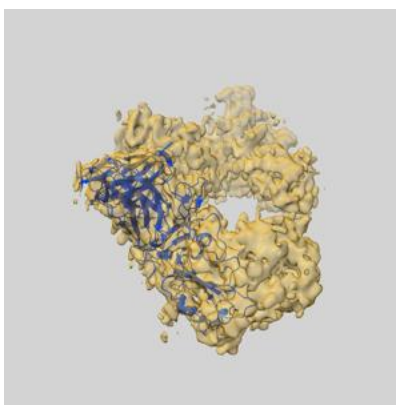
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30485 and PDB model 7CWO. Per-residue inclusion information can be found in section [3](#) on page [4](#).

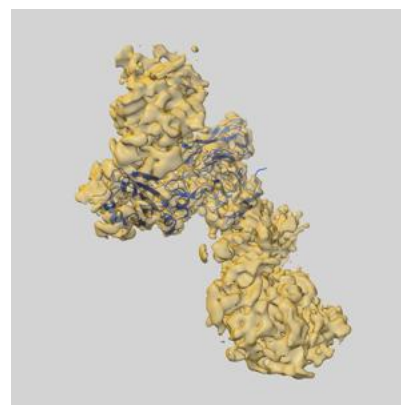
9.1 Map-model overlay [i](#)



X



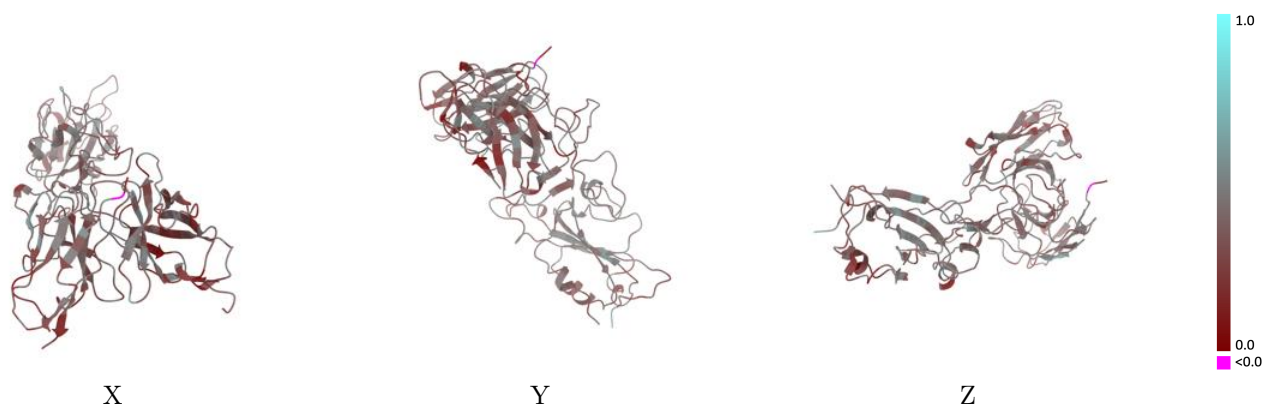
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0115 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

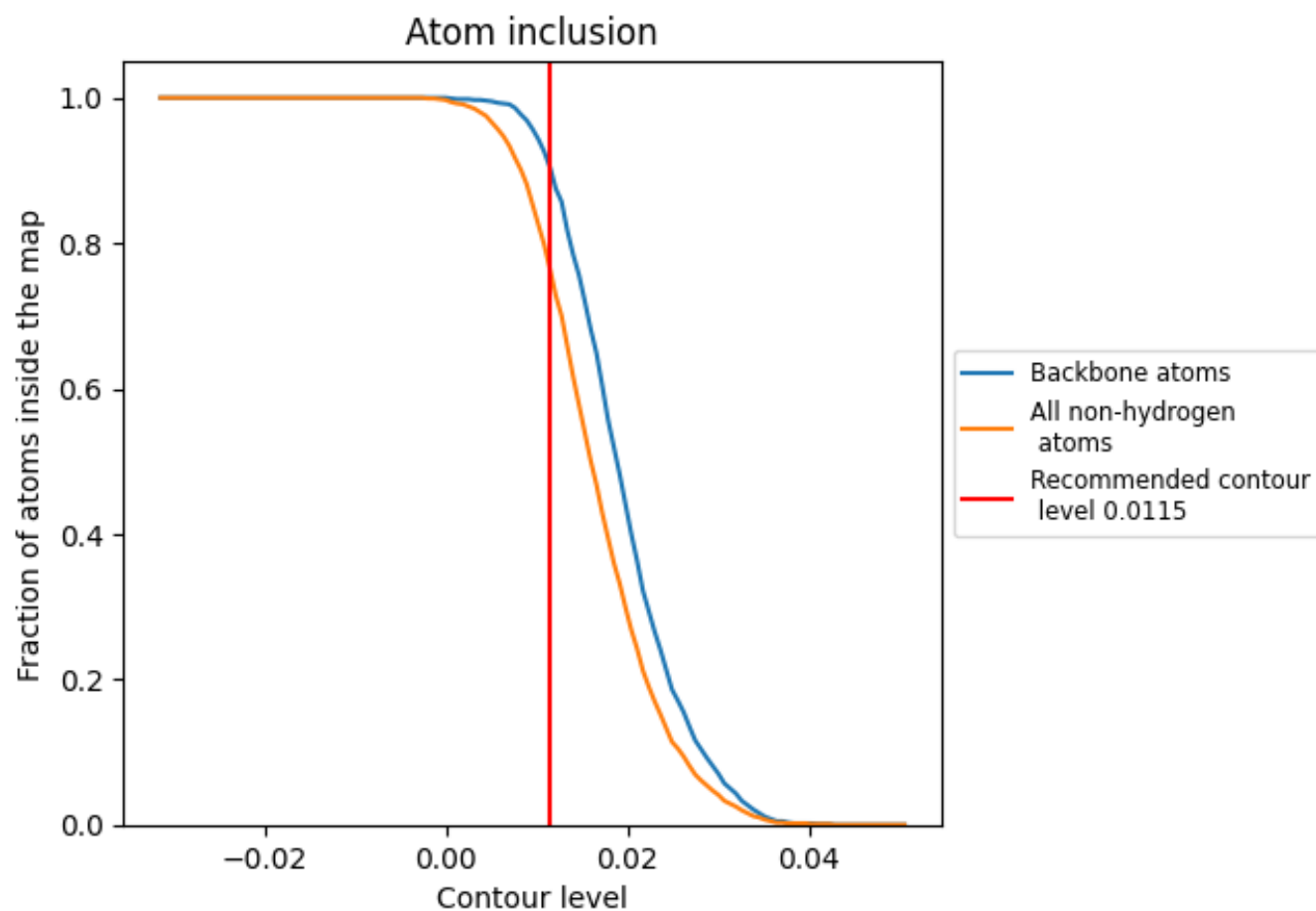


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 76% 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 (0.0115) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7610	0.3720
A	0.8110	0.3880
H	0.7510	0.3650
L	0.6810	0.3510

