



Full wwPDB EM Validation Report ⓘ

Oct 14, 2024 – 07:14 PM JST

PDB ID : 7WEE
EMDB ID : EMD-32448
Title : SARS-CoV-2 Omicron variant spike RBD in complex with Fab XGv265
Authors : Wang, X.; Wang, L.
Deposited on : 2021-12-23
Resolution : 4.00 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

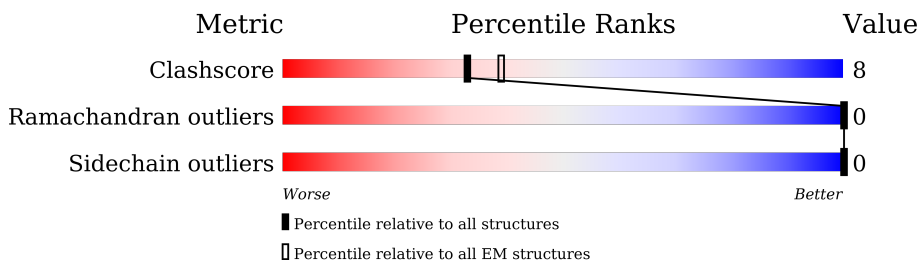
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	E	1270	 14% 55% 84%
2	H	119	 19% 81% 19%
3	L	109	 28% 72% 28%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3350 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	E	201	Total	C	N	O	S	0	0
			1612	1039	273	292	8		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	70	VAL	ALA	variant	UNP P0DTC2
E	?	-	HIS	deletion	UNP P0DTC2
E	?	-	VAL	deletion	UNP P0DTC2
E	96	ILE	THR	variant	UNP P0DTC2
E	139	ASP	GLY	variant	UNP P0DTC2
E	?	-	VAL	deletion	UNP P0DTC2
E	?	-	TYR	deletion	UNP P0DTC2
E	?	-	TYR	deletion	UNP P0DTC2
E	?	-	ASN	deletion	UNP P0DTC2
E	212	GLU	-	insertion	UNP P0DTC2
E	213	PRO	-	insertion	UNP P0DTC2
E	214	GLU	-	insertion	UNP P0DTC2
E	339	ASP	GLY	variant	UNP P0DTC2
E	371	LEU	SER	variant	UNP P0DTC2
E	373	PRO	SER	variant	UNP P0DTC2
E	375	PHE	SER	variant	UNP P0DTC2
E	417	ASN	LYS	variant	UNP P0DTC2
E	440	LYS	ASN	variant	UNP P0DTC2
E	446	SER	GLY	variant	UNP P0DTC2
E	477	ASN	SER	variant	UNP P0DTC2
E	478	LYS	THR	variant	UNP P0DTC2
E	484	ALA	GLU	variant	UNP P0DTC2
E	493	ARG	GLN	variant	UNP P0DTC2
E	496	SER	GLY	variant	UNP P0DTC2
E	498	ARG	GLN	variant	UNP P0DTC2
E	501	TYR	ASN	variant	UNP P0DTC2
E	505	HIS	TYR	variant	UNP P0DTC2
E	547	LYS	THR	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	614	GLY	ASP	variant	UNP P0DTC2
E	655	TYR	HIS	variant	UNP P0DTC2
E	679	LYS	ASN	variant	UNP P0DTC2
E	681	HIS	PRO	variant	UNP P0DTC2
E	764	LYS	ASN	variant	UNP P0DTC2
E	796	TYR	ASP	variant	UNP P0DTC2
E	856	LYS	ASN	variant	UNP P0DTC2
E	954	HIS	GLN	variant	UNP P0DTC2
E	969	LYS	ASN	variant	UNP P0DTC2
E	981	PHE	LEU	variant	UNP P0DTC2

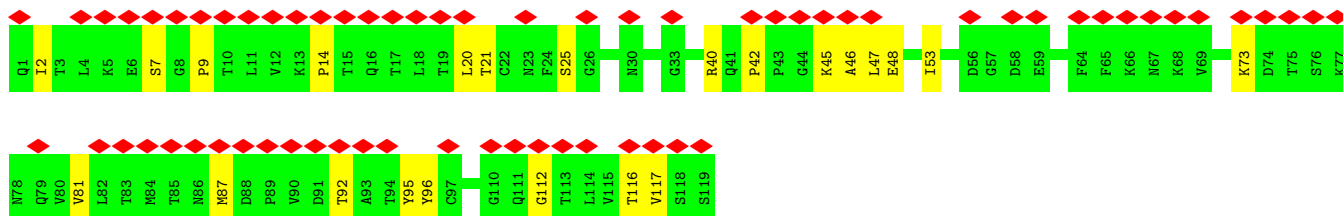
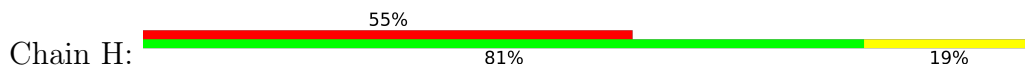
- Molecule 2 is a protein called The heavy chain of Fab XGv265.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	119	Total	C	N	O	S	0	0
			938	608	151	175	4		

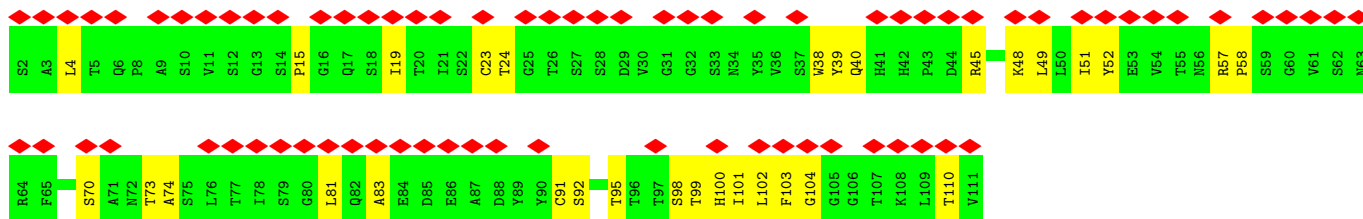
- Molecule 3 is a protein called The light chain of Fab XGv265.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	109	Total	C	N	O	S	0	0
			800	492	136	170	2		

- Molecule 2: The heavy chain of Fab XGv265



- Molecule 3: The light chain of Fab XGv265



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	138359	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.164	Depositor
Minimum map value	-0.089	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0246	Depositor
Map size (\AA)	385.2, 385.2, 385.2	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	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	E	0.26	0/1660	0.48	0/2258
2	H	0.33	0/964	0.66	2/1318 (0.2%)
3	L	0.24	0/817	0.50	0/1114
All	All	0.27	0/3441	0.54	2/4690 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	9	PRO	CA-N-CD	-11.16	95.88	111.50
2	H	9	PRO	N-CD-CG	-8.09	91.07	103.20

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	E	1612	0	1550	10	0
2	H	938	0	930	18	0
3	L	800	0	758	31	0
All	All	3350	0	3238	54	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 8.

All (54) 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:21:THR:HG22	2:H:81:VAL:HG12	1.75	0.68
3:L:15:PRO:HA	3:L:81:LEU:HB2	1.76	0.68
2:H:2:ILE:HA	2:H:25:SER:O	1.94	0.67
3:L:95:THR:OG1	3:L:98:SER:O	2.12	0.67
2:H:14:PRO:HA	2:H:87:MET:HB2	1.77	0.66
3:L:57:ARG:HG2	3:L:58:PRO:HD2	1.78	0.66
3:L:91:CYS:HB3	3:L:103:PHE:HD2	1.65	0.61
2:H:46:ALA:HB2	3:L:104:GLY:HA2	1.83	0.61
3:L:101:ILE:HG13	3:L:102:LEU:H	1.65	0.61
1:E:454:ARG:NH2	1:E:469:SER:O	2.34	0.60
3:L:38:TRP:HB2	3:L:51:ILE:HB	1.82	0.60
3:L:91:CYS:HB3	3:L:103:PHE:CD2	2.38	0.57
2:H:48:GLU:HG3	3:L:102:LEU:HD11	1.86	0.57
1:E:445:VAL:HG22	3:L:99:THR:HG21	1.87	0.56
3:L:4:LEU:HB3	3:L:103:PHE:CE1	2.40	0.56
3:L:24:THR:HA	3:L:73:THR:HG22	1.88	0.55
3:L:39:TYR:HD1	3:L:49:LEU:HA	1.71	0.55
2:H:47:LEU:HD11	3:L:101:ILE:HD11	1.89	0.55
3:L:40:GLN:HE21	3:L:48:LYS:HE2	1.72	0.54
2:H:40:ARG:O	2:H:48:GLU:N	2.42	0.53
1:E:349:SER:OG	1:E:452:LEU:O	2.27	0.52
3:L:23:CYS:HB2	3:L:103:PHE:CE2	2.45	0.52
3:L:101:ILE:HG13	3:L:102:LEU:N	2.25	0.51
3:L:100:HIS:HB2	3:L:102:LEU:HD23	1.92	0.51
2:H:95:TYR:O	2:H:112:GLY:CA	2.59	0.51
2:H:92:THR:HG22	2:H:116:THR:HA	1.92	0.51
3:L:19:ILE:HG22	3:L:81:LEU:HD21	1.93	0.49
2:H:92:THR:HG22	2:H:117:VAL:H	1.77	0.49
3:L:70:SER:OG	3:L:73:THR:OG1	2.28	0.49
2:H:42:PRO:HG2	2:H:45:LYS:HD3	1.96	0.48
3:L:39:TYR:CD1	3:L:49:LEU:HA	2.48	0.48
1:E:402:ILE:HD11	1:E:407:VAL:HA	1.94	0.48
1:E:358:ILE:HB	1:E:395:VAL:HB	1.96	0.48
3:L:23:CYS:SG	3:L:74:ALA:HB3	2.54	0.47
3:L:4:LEU:HD11	3:L:95:THR:HG21	1.97	0.46
2:H:95:TYR:O	2:H:112:GLY:HA3	2.16	0.46
1:E:359:SER:HB2	1:E:523:THR:HG21	1.99	0.45
3:L:23:CYS:HB2	3:L:103:PHE:HE2	1.81	0.45
3:L:45:ARG:HB2	3:L:45:ARG:NH1	2.32	0.45
3:L:49:LEU:HD21	3:L:52:TYR:HB3	1.99	0.44
2:H:7:SER:O	2:H:20:LEU:HD12	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:4:LEU:HD13	3:L:103:PHE:HE1	1.84	0.43
1:E:371:LEU:HG	1:E:373:PRO:HD2	2.01	0.43
2:H:7:SER:OG	2:H:21:THR:OG1	2.28	0.43
1:E:523:THR:HG23	1:E:524:VAL:HG23	2.02	0.41
1:E:382:VAL:HG21	1:E:387:LEU:HD21	2.03	0.41
2:H:47:LEU:O	3:L:102:LEU:HD13	2.20	0.41
2:H:53:ILE:HD13	2:H:73:LYS:HB3	2.03	0.41
2:H:96:TYR:CD2	2:H:112:GLY:HA3	2.56	0.41
3:L:83:ALA:HA	3:L:110:THR:HG21	2.02	0.41
2:H:45:LYS:NZ	2:H:46:ALA:O	2.54	0.40
1:E:378:LYS:HD3	1:E:380:TYR:HE1	1.86	0.40
3:L:52:TYR:HD2	3:L:58:PRO:HD3	1.86	0.40
3:L:92:SER:OG	3:L:101:ILE:HG21	2.21	0.40

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	E	199/1270 (16%)	192 (96%)	7 (4%)	0	100	100
2	H	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
3	L	107/109 (98%)	101 (94%)	6 (6%)	0	100	100
All	All	423/1498 (28%)	404 (96%)	19 (4%)	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	E	176/1112 (16%)	176 (100%)	0	100	100
2	H	104/104 (100%)	104 (100%)	0	100	100
3	L	91/91 (100%)	91 (100%)	0	100	100
All	All	371/1307 (28%)	371 (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 (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	L	40	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

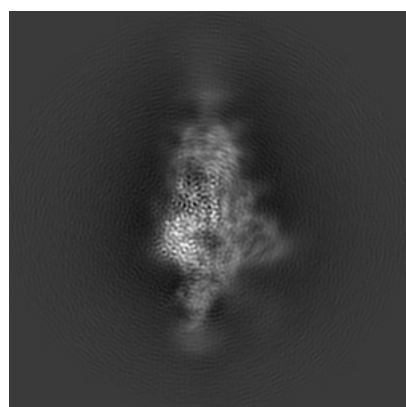
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32448. These allow visual inspection of the internal detail of the map and identification of artifacts.

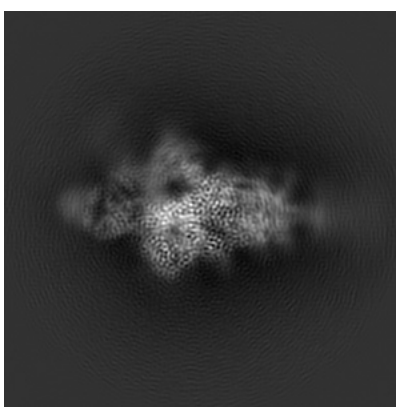
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

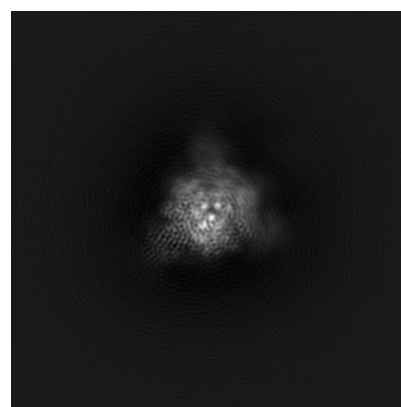
6.1.1 Primary map



X



Y

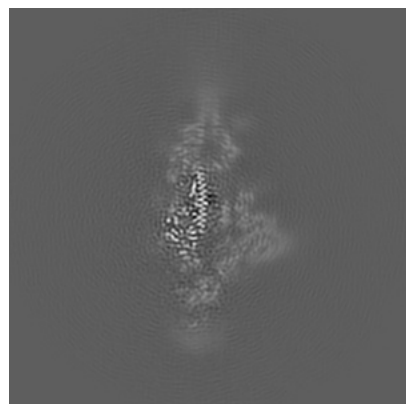


Z

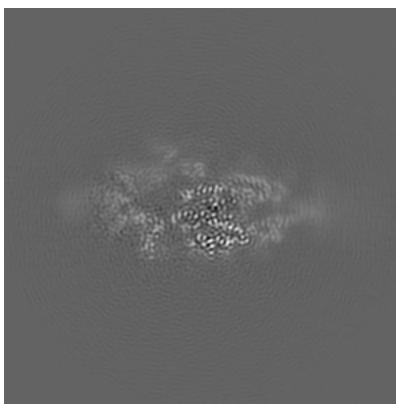
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

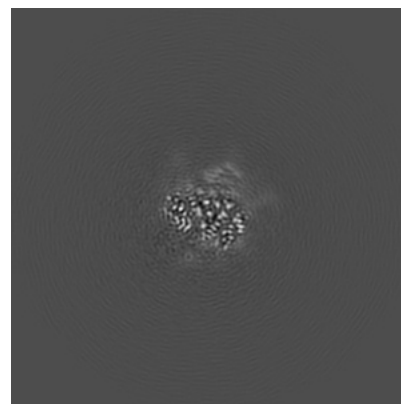
6.2.1 Primary map



X Index: 180



Y Index: 180

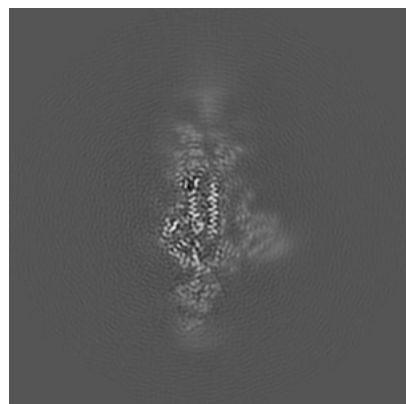


Z Index: 180

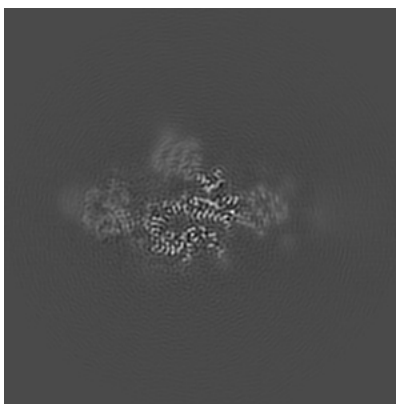
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

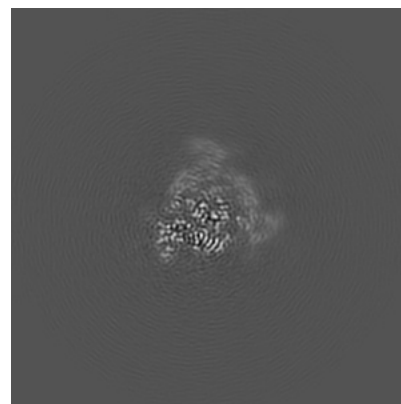
6.3.1 Primary map



X Index: 174



Y Index: 164

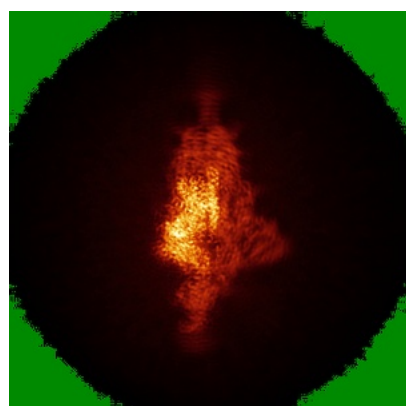


Z Index: 167

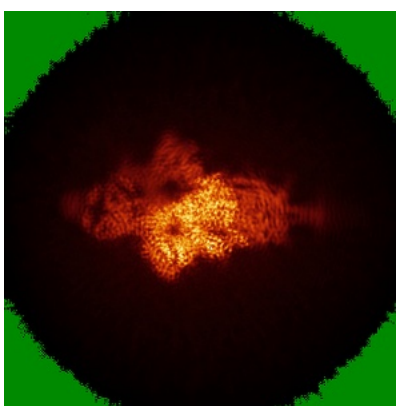
The images above show the largest variance slices of the map in three orthogonal directions.

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

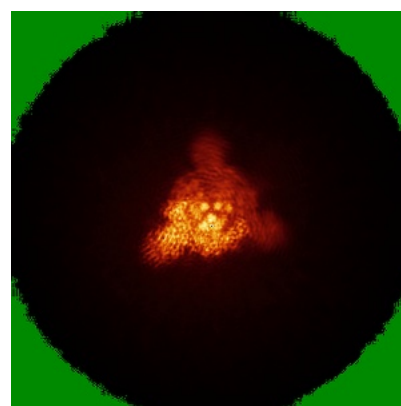
6.4.1 Primary map



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 0.0246. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

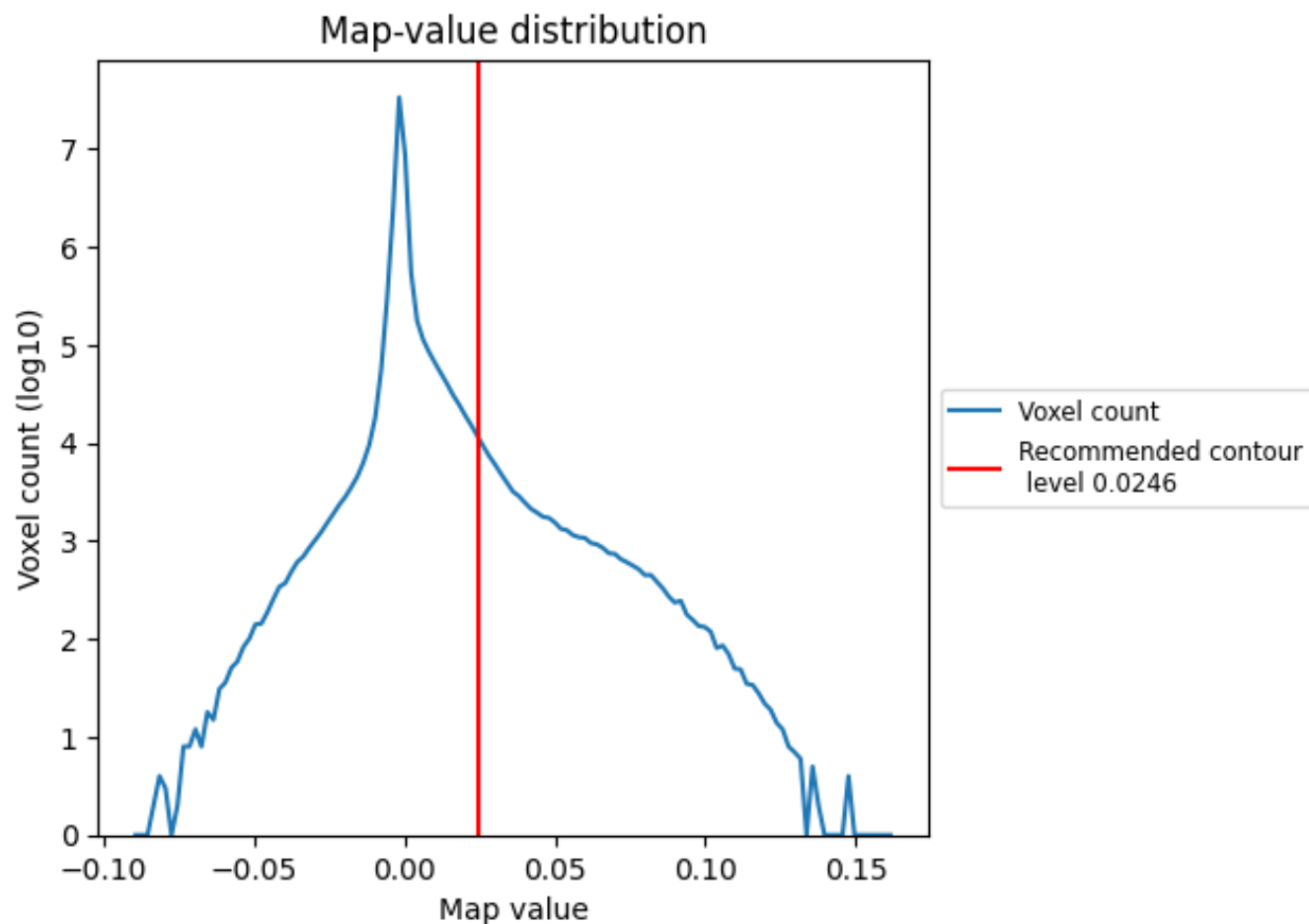
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

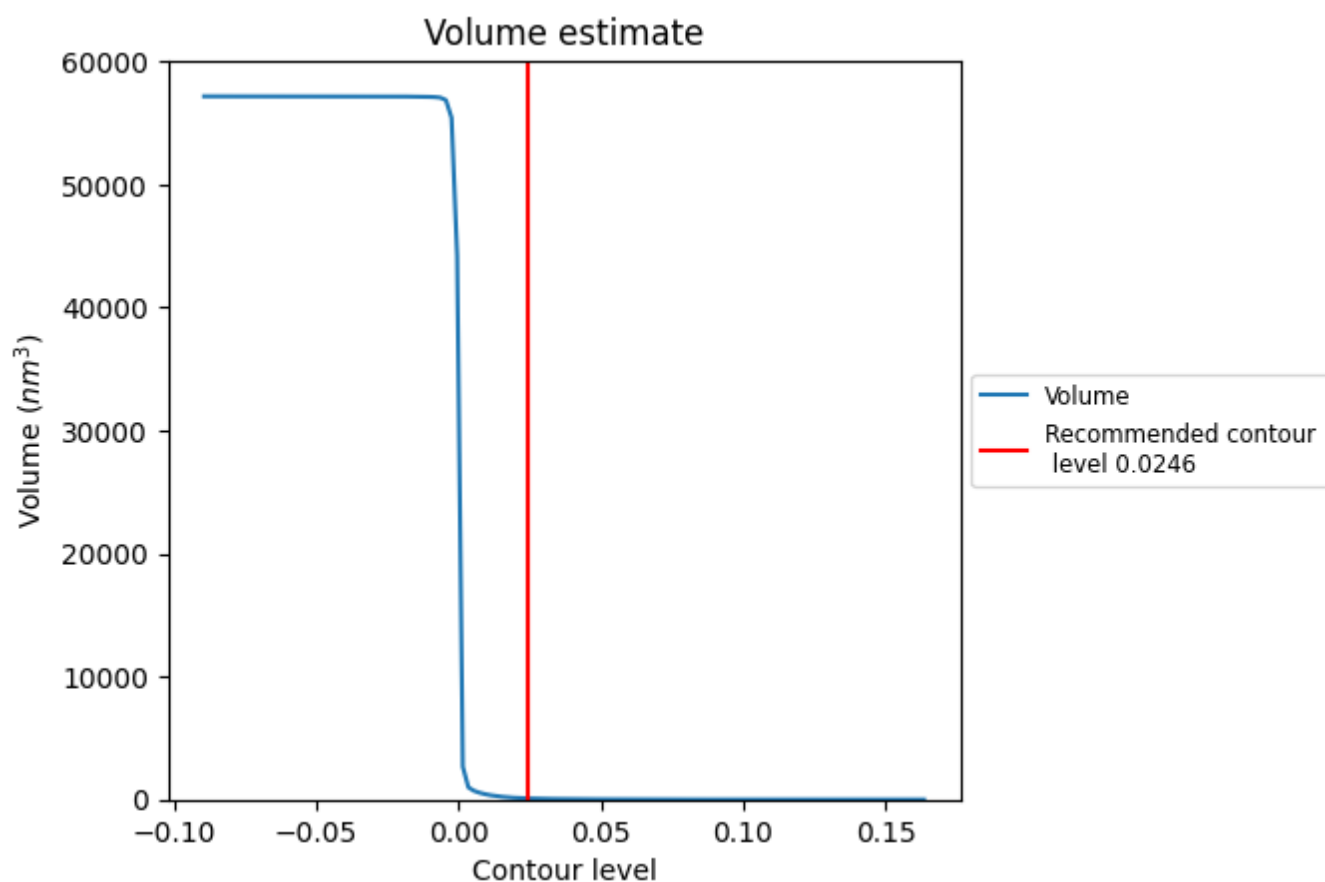
This section contains the results of statistical analysis of the map.

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.

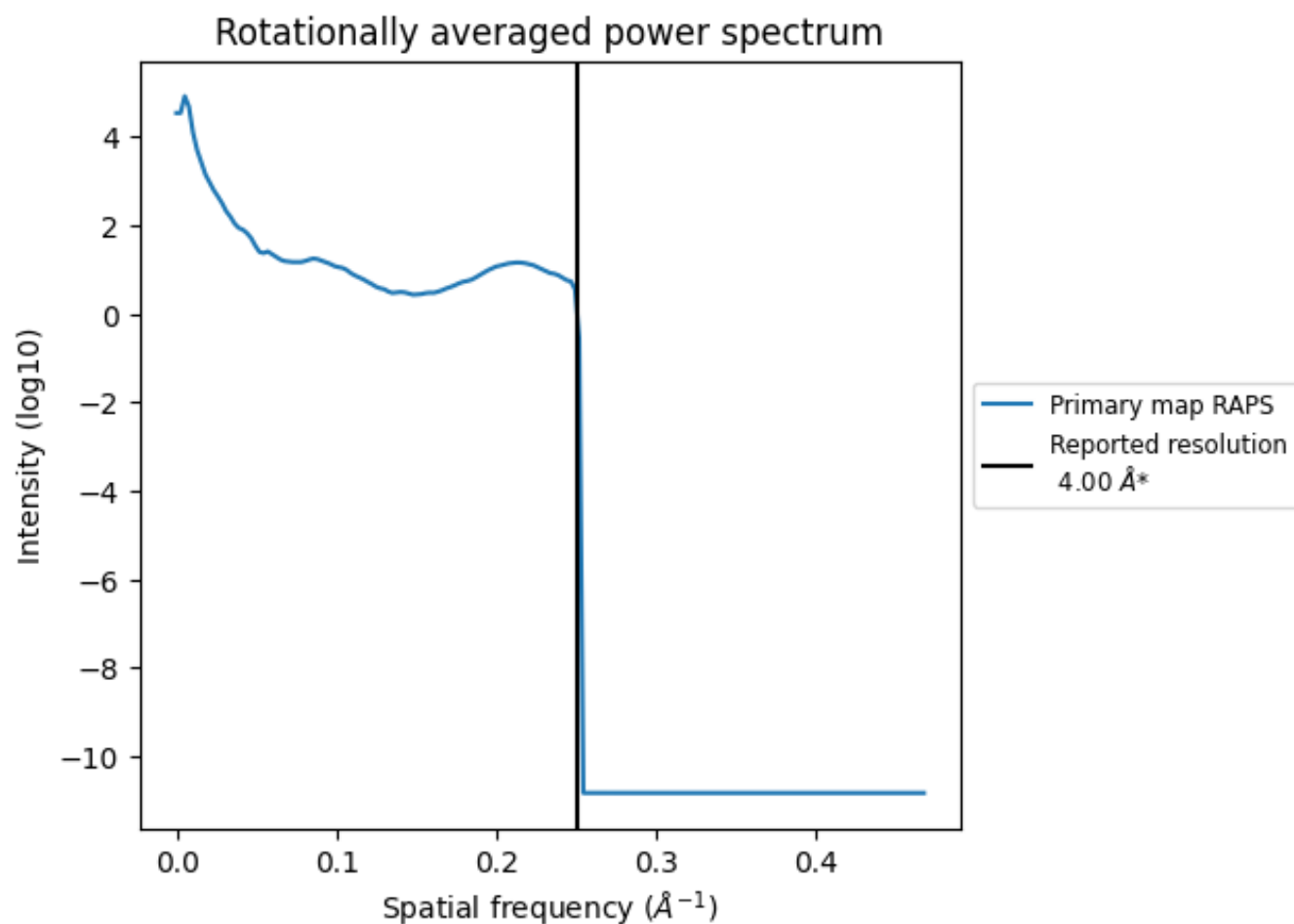
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 91 nm³; this corresponds to an approximate mass of 83 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 0.250 Å⁻¹

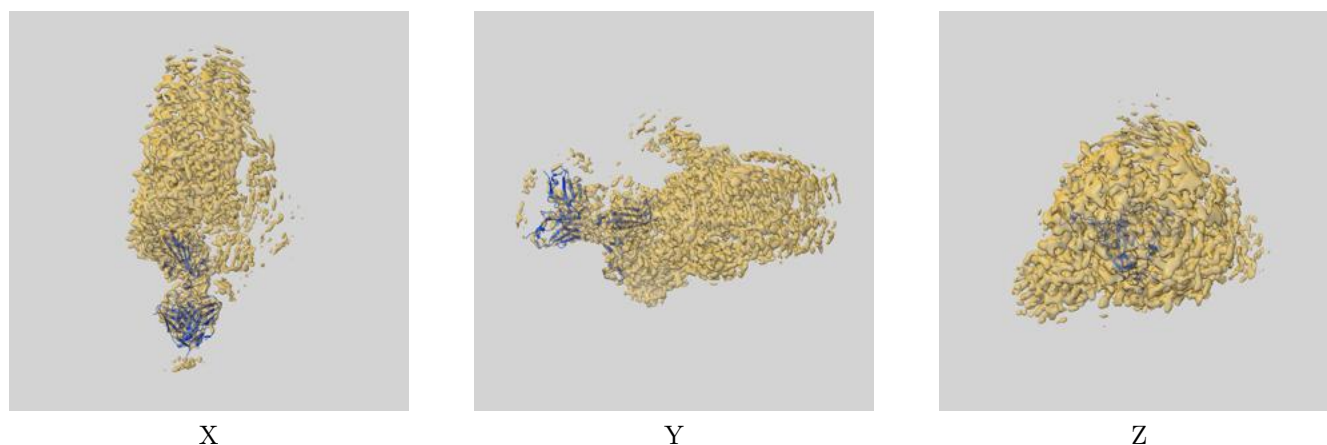
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

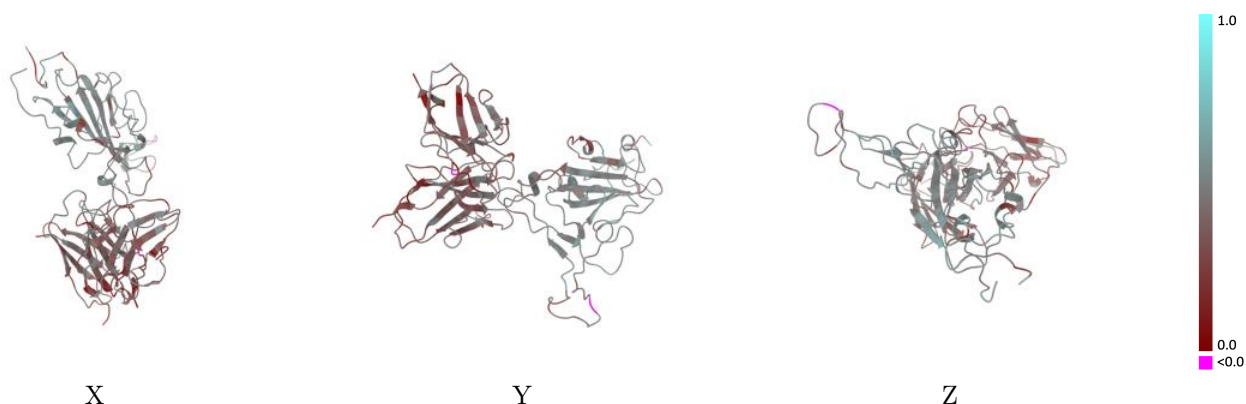
This section contains information regarding the fit between EMDB map EMD-32448 and PDB model 7WEE. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



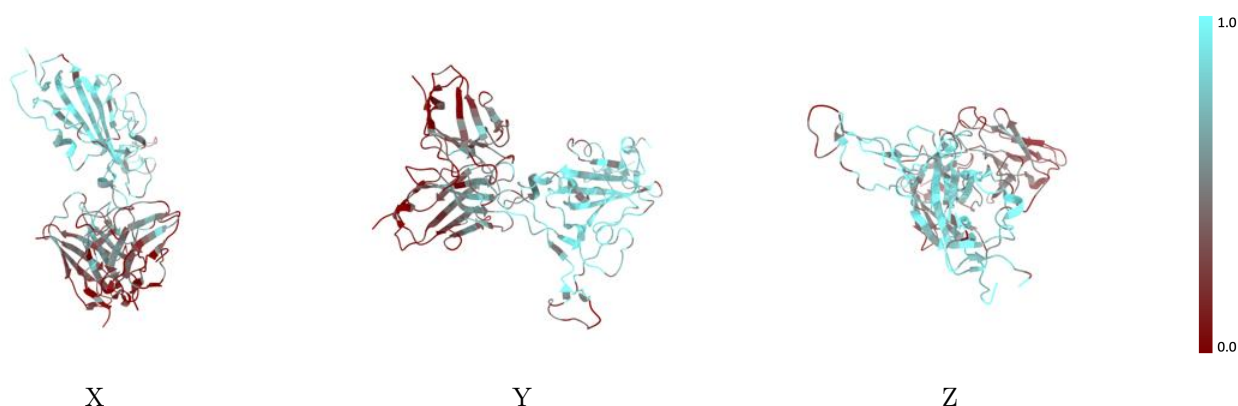
The images above show the 3D surface view of the map at the recommended contour level 0.0246 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



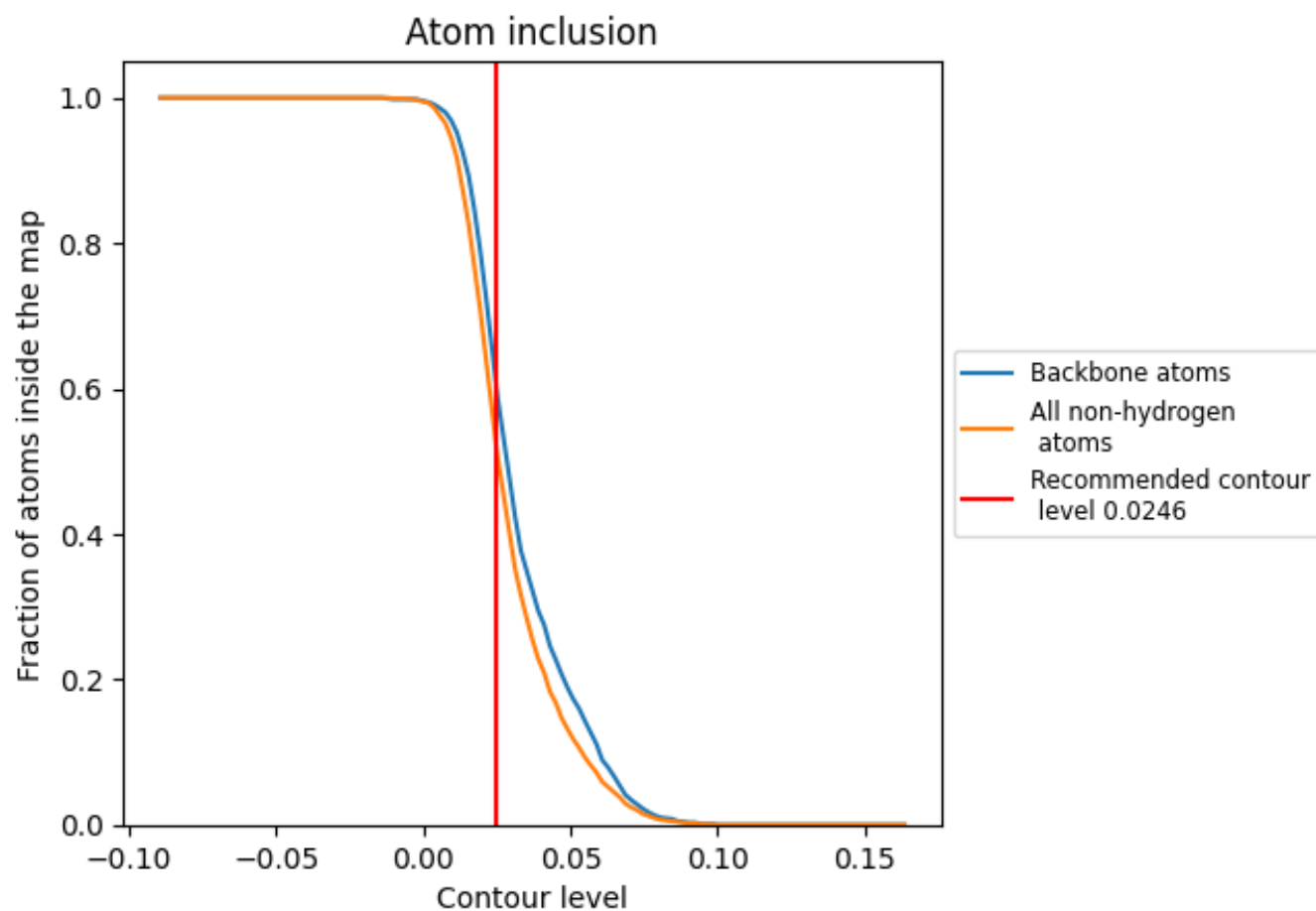
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.0246).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 52% 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 (0.0246) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5250	<div></div> 0.4150
E	<div></div> 0.7250	<div></div> 0.4760
H	<div></div> 0.3790	<div></div> 0.3780
L	<div></div> 0.2970	<div></div> 0.3330

