



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:11 PM UTC

PDB ID : 7F63 / pdb_00007f63
EMDB ID : EMD-31471
Title : Cryo-EM structure of SARS-CoV-2 spike in complex with a neutralizing antibody chAb-45 (Focused refinement of S-RBD and chAb-45 region)
Authors : Yang, T.J.; Yu, P.Y.; Wu, H.C.; Hsu, S.T.D.
Deposited on : 2021-06-24
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

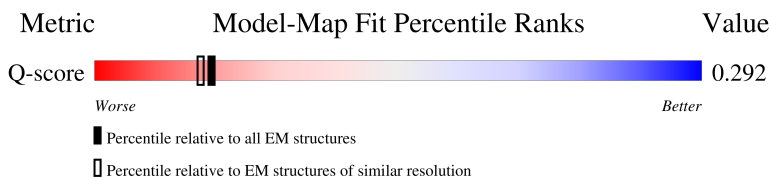
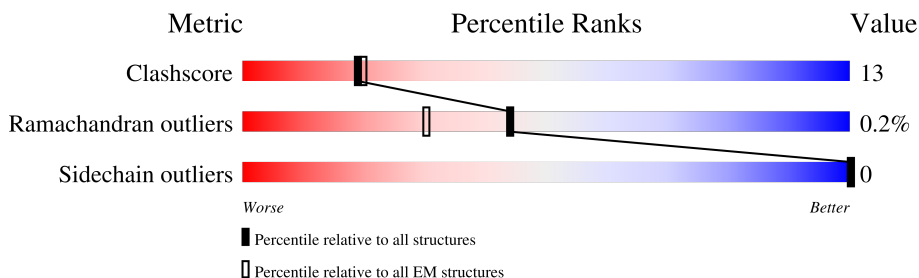
1 Overall quality at a glance

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	1283	
2	H	449	
3	L	214	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3375 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	199	Total	C	N	O	S	0	0
			1578	1012	264	294	8		

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	682	GLY	ARG	conflict	UNP P0DTC2
A	683	SER	ARG	conflict	UNP P0DTC2
A	685	SER	ARG	conflict	UNP P0DTC2
A	986	PRO	LYS	conflict	UNP P0DTC2
A	987	PRO	VAL	conflict	UNP P0DTC2
A	1209	GLU	-	expression tag	UNP P0DTC2
A	1210	PHE	-	expression tag	UNP P0DTC2
A	1211	GLY	-	expression tag	UNP P0DTC2
A	1212	SER	-	expression tag	UNP P0DTC2
A	1213	GLY	-	expression tag	UNP P0DTC2
A	1214	GLY	-	expression tag	UNP P0DTC2
A	1215	TYR	-	expression tag	UNP P0DTC2
A	1216	ILE	-	expression tag	UNP P0DTC2
A	1217	PRO	-	expression tag	UNP P0DTC2
A	1218	GLU	-	expression tag	UNP P0DTC2
A	1219	ALA	-	expression tag	UNP P0DTC2
A	1220	PRO	-	expression tag	UNP P0DTC2
A	1221	ARG	-	expression tag	UNP P0DTC2
A	1222	ASP	-	expression tag	UNP P0DTC2
A	1223	GLY	-	expression tag	UNP P0DTC2
A	1224	GLN	-	expression tag	UNP P0DTC2
A	1225	ALA	-	expression tag	UNP P0DTC2
A	1226	TYR	-	expression tag	UNP P0DTC2
A	1227	VAL	-	expression tag	UNP P0DTC2
A	1228	ARG	-	expression tag	UNP P0DTC2
A	1229	LYS	-	expression tag	UNP P0DTC2
A	1230	ASP	-	expression tag	UNP P0DTC2
A	1231	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1232	GLU	-	expression tag	UNP P0DTC2
A	1233	TRP	-	expression tag	UNP P0DTC2
A	1234	VAL	-	expression tag	UNP P0DTC2
A	1235	LEU	-	expression tag	UNP P0DTC2
A	1236	LEU	-	expression tag	UNP P0DTC2
A	1237	SER	-	expression tag	UNP P0DTC2
A	1238	THR	-	expression tag	UNP P0DTC2
A	1239	PHE	-	expression tag	UNP P0DTC2
A	1240	LEU	-	expression tag	UNP P0DTC2
A	1241	LYS	-	expression tag	UNP P0DTC2
A	1242	GLY	-	expression tag	UNP P0DTC2
A	1243	GLN	-	expression tag	UNP P0DTC2
A	1244	ASP	-	expression tag	UNP P0DTC2
A	1245	ASN	-	expression tag	UNP P0DTC2
A	1246	SER	-	expression tag	UNP P0DTC2
A	1247	ALA	-	expression tag	UNP P0DTC2
A	1248	ASP	-	expression tag	UNP P0DTC2
A	1249	ILE	-	expression tag	UNP P0DTC2
A	1250	GLN	-	expression tag	UNP P0DTC2
A	1251	HIS	-	expression tag	UNP P0DTC2
A	1252	SER	-	expression tag	UNP P0DTC2
A	1253	GLY	-	expression tag	UNP P0DTC2
A	1254	ARG	-	expression tag	UNP P0DTC2
A	1255	PRO	-	expression tag	UNP P0DTC2
A	1256	LEU	-	expression tag	UNP P0DTC2
A	1257	GLU	-	expression tag	UNP P0DTC2
A	1258	SER	-	expression tag	UNP P0DTC2
A	1259	ARG	-	expression tag	UNP P0DTC2
A	1260	GLY	-	expression tag	UNP P0DTC2
A	1261	PRO	-	expression tag	UNP P0DTC2
A	1262	PHE	-	expression tag	UNP P0DTC2
A	1263	GLU	-	expression tag	UNP P0DTC2
A	1264	GLN	-	expression tag	UNP P0DTC2
A	1265	LYS	-	expression tag	UNP P0DTC2
A	1266	LEU	-	expression tag	UNP P0DTC2
A	1267	ILE	-	expression tag	UNP P0DTC2
A	1268	SER	-	expression tag	UNP P0DTC2
A	1269	GLU	-	expression tag	UNP P0DTC2
A	1270	GLU	-	expression tag	UNP P0DTC2
A	1271	ASP	-	expression tag	UNP P0DTC2
A	1272	LEU	-	expression tag	UNP P0DTC2
A	1273	ASN	-	expression tag	UNP P0DTC2

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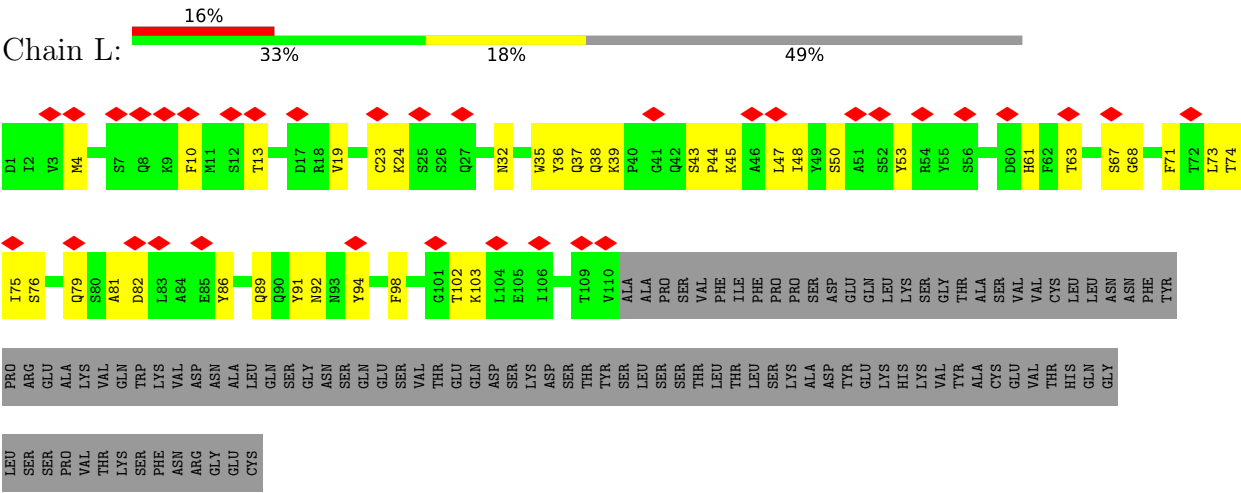
Chain	Residue	Modelled	Actual	Comment	Reference
A	1274	MET	-	expression tag	UNP P0DTC2
A	1275	HIS	-	expression tag	UNP P0DTC2
A	1276	THR	-	expression tag	UNP P0DTC2
A	1277	GLY	-	expression tag	UNP P0DTC2
A	1278	HIS	-	expression tag	UNP P0DTC2
A	1279	HIS	-	expression tag	UNP P0DTC2
A	1280	HIS	-	expression tag	UNP P0DTC2
A	1281	HIS	-	expression tag	UNP P0DTC2
A	1282	HIS	-	expression tag	UNP P0DTC2
A	1283	HIS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called RBD-chAb45, Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	120	Total	C	N	O	S	0	0
			945	602	148	192	3		

- Molecule 3 is a protein called RBD-chAb45, Light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	110	Total	C	N	O	S	0	0
			852	535	143	170	4		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	200245	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.557	Depositor
Minimum map value	-0.924	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.42	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	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	0.11	0/1622	0.29	0/2205
2	H	0.11	0/969	0.36	0/1316
3	L	0.11	0/872	0.32	0/1183
All	All	0.11	0/3463	0.32	0/4704

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	1578	0	1500	29	0
2	H	945	0	899	30	0
3	L	852	0	813	30	0
All	All	3375	0	3212	84	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 13.

All (84) 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:444:LYS:HB2	1:A:447:GLY:HA2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:35:TRP:HB2	3:L:48:ILE:HG22	1.70	0.72
3:L:61:HIS:O	3:L:76:SER:OG	2.14	0.66
2:H:106:ALA:O	3:L:36:TYR:OH	2.14	0.66
2:H:70:LEU:HD22	2:H:81:MET:HE1	1.78	0.65
3:L:63:THR:HB	3:L:74:THR:HB	1.78	0.64
2:H:28:THR:OG1	2:H:31:GLU:OE2	2.17	0.63
1:A:405:ASP:O	1:A:408:ARG:NH1	2.35	0.59
1:A:474:GLN:NE2	1:A:478:THR:O	2.35	0.59
2:H:94:TYR:O	2:H:113:GLY:HA2	2.02	0.59
1:A:457:ARG:NH1	1:A:467:ASP:OD2	2.36	0.59
3:L:32:ASN:ND2	3:L:91:TYR:O	2.36	0.58
3:L:86:TYR:HB2	3:L:102:THR:HB	1.85	0.58
3:L:32:ASN:OD1	3:L:92:ASN:ND2	2.39	0.56
1:A:485:GLY:H	1:A:488:CYS:HB2	1.71	0.55
1:A:444:LYS:HB3	1:A:499:PRO:HG3	1.89	0.54
1:A:358:ILE:HG13	1:A:395:VAL:HB	1.90	0.53
2:H:83:LEU:HD23	2:H:86:LEU:HD11	1.90	0.53
1:A:486:PHE:HE1	2:H:52:ASN:HB2	1.74	0.53
2:H:32:TYR:HD2	2:H:98:ARG:HE	1.57	0.52
1:A:520:ALA:HB3	1:A:521:PRO:HD3	1.91	0.52
1:A:406:GLU:HG2	1:A:418:ILE:HD13	1.93	0.51
2:H:6:GLN:H	2:H:112:GLN:HE22	1.59	0.49
1:A:364:ASP:OD1	1:A:388:ASN:ND2	2.44	0.49
2:H:67:LYS:HD3	2:H:83:LEU:HG	1.93	0.49
3:L:37:GLN:HG2	3:L:47:LEU:HB2	1.95	0.49
1:A:486:PHE:HB3	3:L:94:TYR:CE1	2.48	0.49
2:H:51:ASN:ND2	2:H:70:LEU:HD12	2.28	0.49
2:H:12:VAL:HG12	2:H:18:VAL:HG11	1.94	0.49
2:H:81:MET:HE2	2:H:81:MET:HA	1.96	0.48
1:A:353:TRP:H	1:A:353:TRP:CD1	2.32	0.48
1:A:501:ASN:HB3	1:A:505:TYR:HB2	1.96	0.47
2:H:23:LYS:HD3	2:H:78:THR:HB	1.96	0.47
2:H:64:PHE:O	2:H:64:PHE:CD2	2.68	0.47
3:L:37:GLN:N	3:L:45:LYS:O	2.37	0.47
3:L:19:VAL:HG23	3:L:75:ILE:HB	1.95	0.47
2:H:73:ASP:N	2:H:73:ASP:OD1	2.48	0.47
3:L:89:GLN:HG3	3:L:98:PHE:CZ	2.51	0.46
1:A:433:VAL:HG22	1:A:512:VAL:HG22	1.97	0.46
2:H:20:ILE:HD13	2:H:83:LEU:HD13	1.97	0.46
2:H:4:LEU:HB2	2:H:109:PHE:HE2	1.81	0.46
3:L:86:TYR:N	3:L:102:THR:O	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:29:PHE:HD2	2:H:98:ARG:HH12	1.63	0.46
1:A:336:CYS:HB3	1:A:361:CYS:HB2	1.71	0.45
1:A:429:PHE:CZ	1:A:431:GLY:HA3	2.51	0.45
1:A:426:PRO:HD3	1:A:463:PRO:HB3	1.98	0.45
2:H:38:LYS:HD2	2:H:94:TYR:CZ	2.52	0.45
2:H:91:SER:HA	2:H:116:VAL:O	2.16	0.45
3:L:24:LYS:HE3	3:L:24:LYS:HB3	1.88	0.44
3:L:50:SER:HB2	3:L:53:TYR:CD2	2.53	0.44
2:H:71:THR:CG2	2:H:80:TYR:HB2	2.48	0.44
3:L:13:THR:HG21	3:L:19:VAL:HG12	1.99	0.44
2:H:60:TYR:HE1	2:H:70:LEU:HD23	1.83	0.43
3:L:73:LEU:HD12	3:L:74:THR:N	2.33	0.43
2:H:34:ILE:HD11	2:H:98:ARG:HH11	1.83	0.43
1:A:347:PHE:CD2	1:A:509:ARG:HD2	2.54	0.43
1:A:451:TYR:O	1:A:494:SER:HA	2.19	0.43
1:A:366:SER:HA	1:A:369:TYR:CE2	2.53	0.43
2:H:38:LYS:HG3	2:H:48:ILE:HG13	2.01	0.42
3:L:50:SER:HB2	3:L:53:TYR:HD2	1.84	0.42
3:L:39:LYS:NZ	3:L:81:ALA:O	2.53	0.42
1:A:418:ILE:HA	1:A:422:ASN:HD22	1.83	0.42
1:A:347:PHE:HD2	1:A:509:ARG:HD2	1.85	0.42
2:H:31:GLU:HG2	2:H:32:TYR:H	1.84	0.42
2:H:48:ILE:HD13	2:H:48:ILE:HA	1.92	0.42
3:L:38:GLN:OE1	3:L:44:PRO:HG3	2.20	0.42
2:H:48:ILE:HG23	2:H:64:PHE:CZ	2.55	0.42
2:H:95:TYR:HE2	3:L:43:SER:HA	1.85	0.42
1:A:361:CYS:H	1:A:524:VAL:HG12	1.85	0.42
1:A:453:TYR:CE1	1:A:493:GLN:HB2	2.55	0.42
3:L:35:TRP:HZ3	3:L:86:TYR:HB3	1.85	0.41
3:L:37:GLN:OE1	3:L:47:LEU:HD22	2.19	0.41
1:A:418:ILE:HG23	1:A:422:ASN:HB2	2.03	0.41
1:A:374:PHE:HB3	1:A:434:ILE:HD11	2.02	0.41
3:L:23:CYS:HB3	3:L:71:PHE:HB2	2.03	0.41
1:A:378:LYS:HD3	1:A:378:LYS:HA	1.88	0.41
3:L:35:TRP:CZ3	3:L:86:TYR:HB3	2.55	0.41
3:L:10:PHE:HB2	3:L:103:LYS:HB3	2.02	0.41
3:L:4:MET:HE2	3:L:4:MET:HB2	1.97	0.41
3:L:79:GLN:N	3:L:82:ASP:OD2	2.45	0.41
2:H:31:GLU:HG2	2:H:32:TYR:N	2.36	0.40
2:H:69:THR:HG21	2:H:82:GLU:HB3	2.02	0.40
3:L:67:SER:OG	3:L:68:GLY:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:PHE:O	3:L:94:TYR:OH	2.35	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	A	195/1283 (15%)	185 (95%)	9 (5%)	1 (0%)	24	59
2	H	118/449 (26%)	107 (91%)	11 (9%)	0	100	100
3	L	108/214 (50%)	93 (86%)	15 (14%)	0	100	100
All	All	421/1946 (22%)	385 (91%)	35 (8%)	1 (0%)	44	74

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	520	ALA

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	172/1116 (15%)	172 (100%)	0	100	100
2	H	104/402 (26%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	L	95/188 (50%)	95 (100%)	0	100	100
All	All	371/1706 (22%)	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 (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	439	ASN
1	A	474	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.

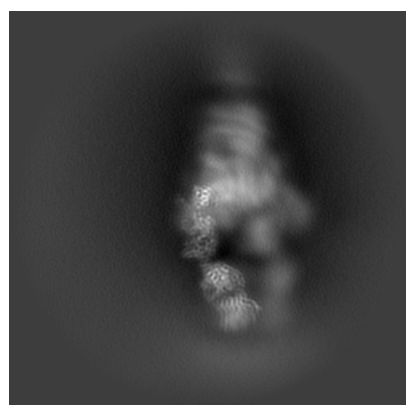
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31471. These allow visual inspection of the internal detail of the map and identification of artifacts.

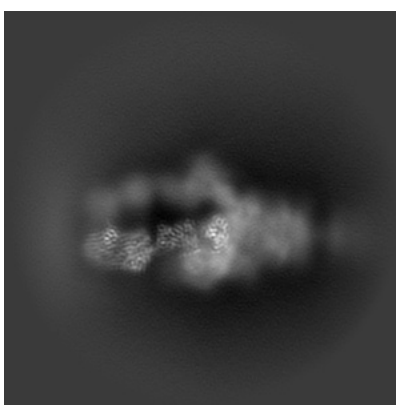
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

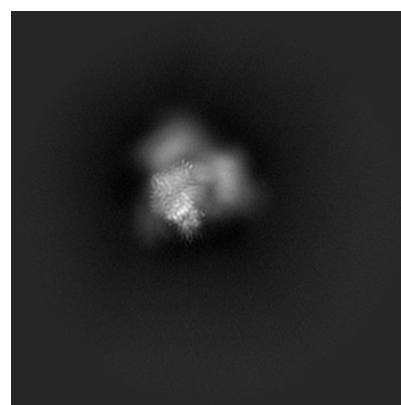
6.1.1 Primary map



X



Y

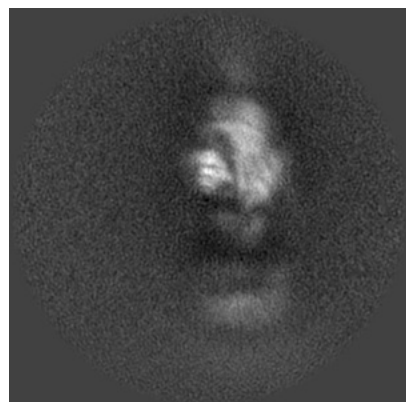


Z

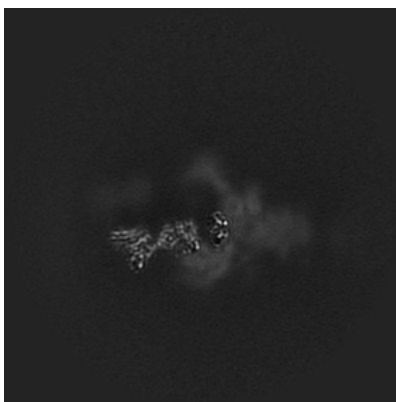
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 192



Y Index: 192



Z Index: 192

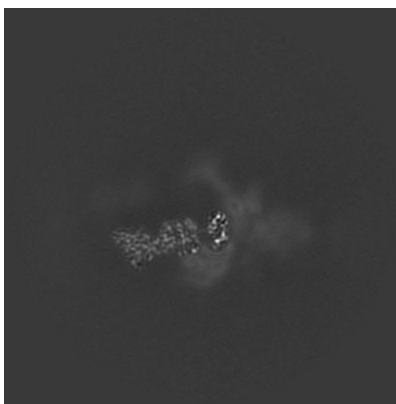
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

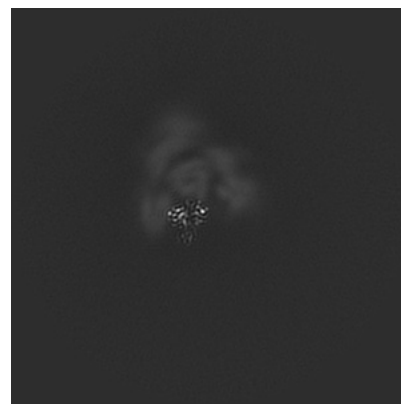
6.3.1 Primary map



X Index: 168



Y Index: 189



Z Index: 205

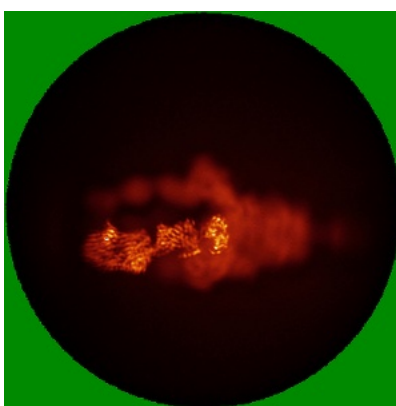
The images above show the largest variance slices of the map in three orthogonal directions.

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

This section was not generated.

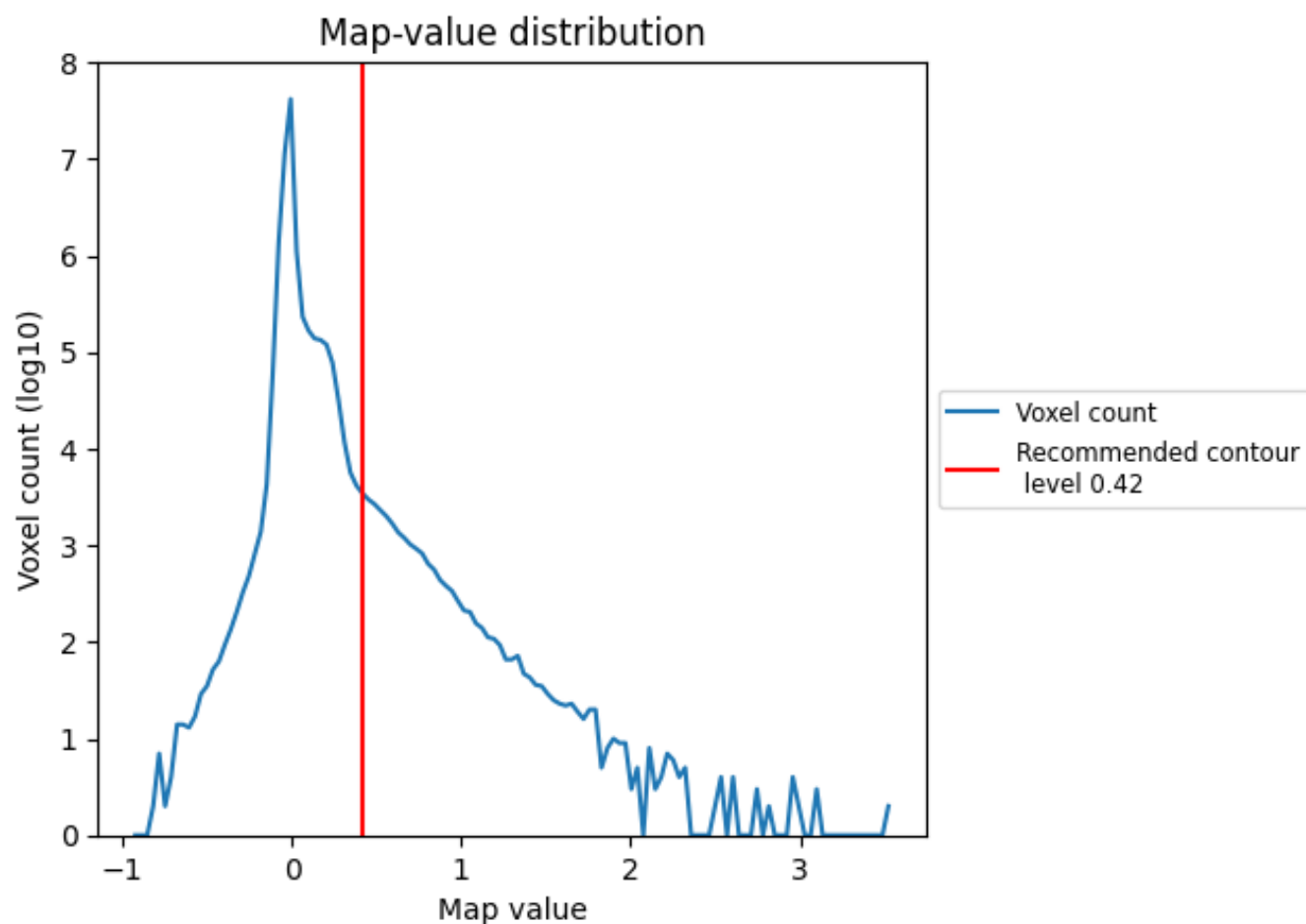
6.6 Mask visualisation

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

7 Map analysis [i](#)

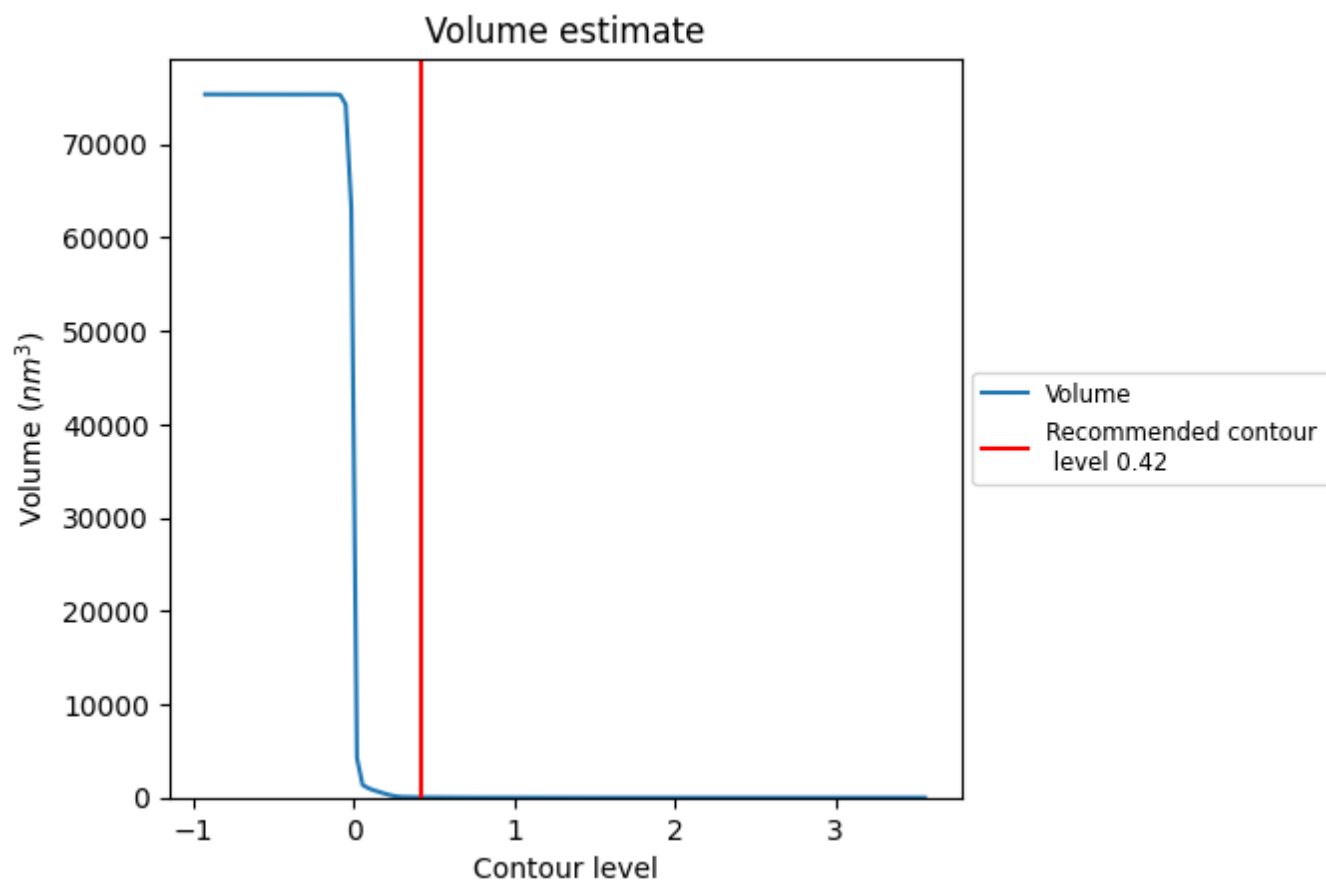
This section contains the results of statistical analysis of the map.

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.

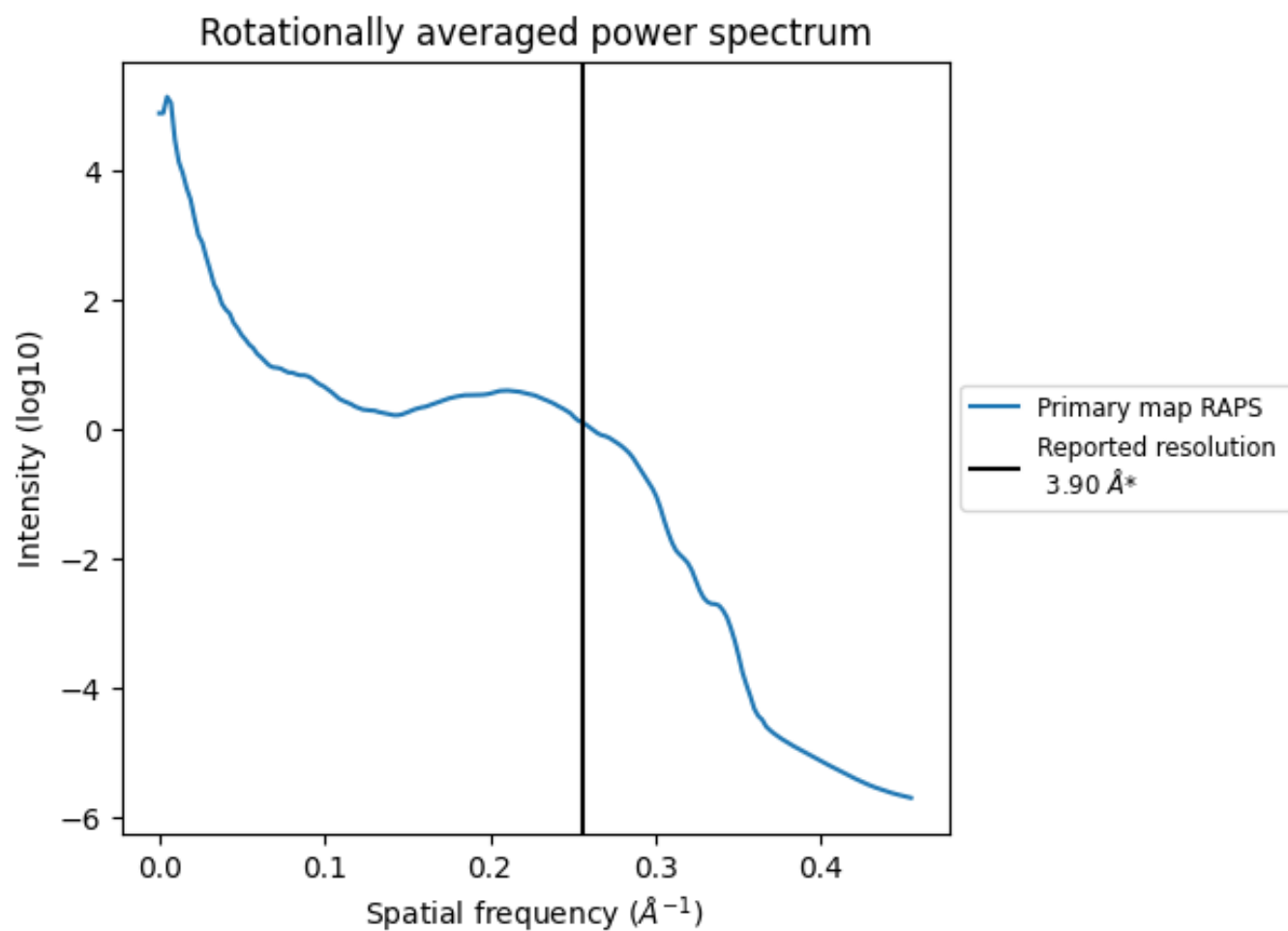
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 33 nm^3 ; this corresponds to an approximate mass of 29 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.

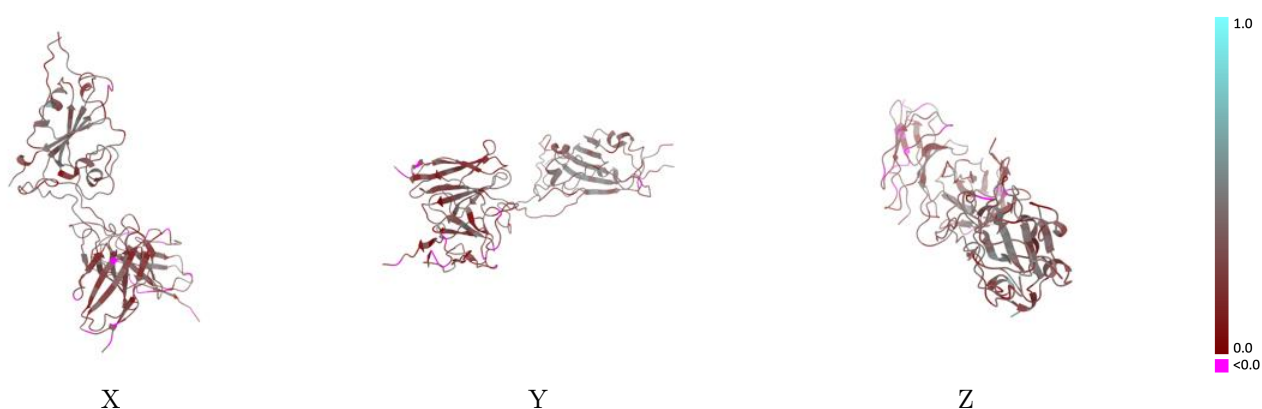
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-31471 and PDB model 7F63. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

This section was not generated.

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

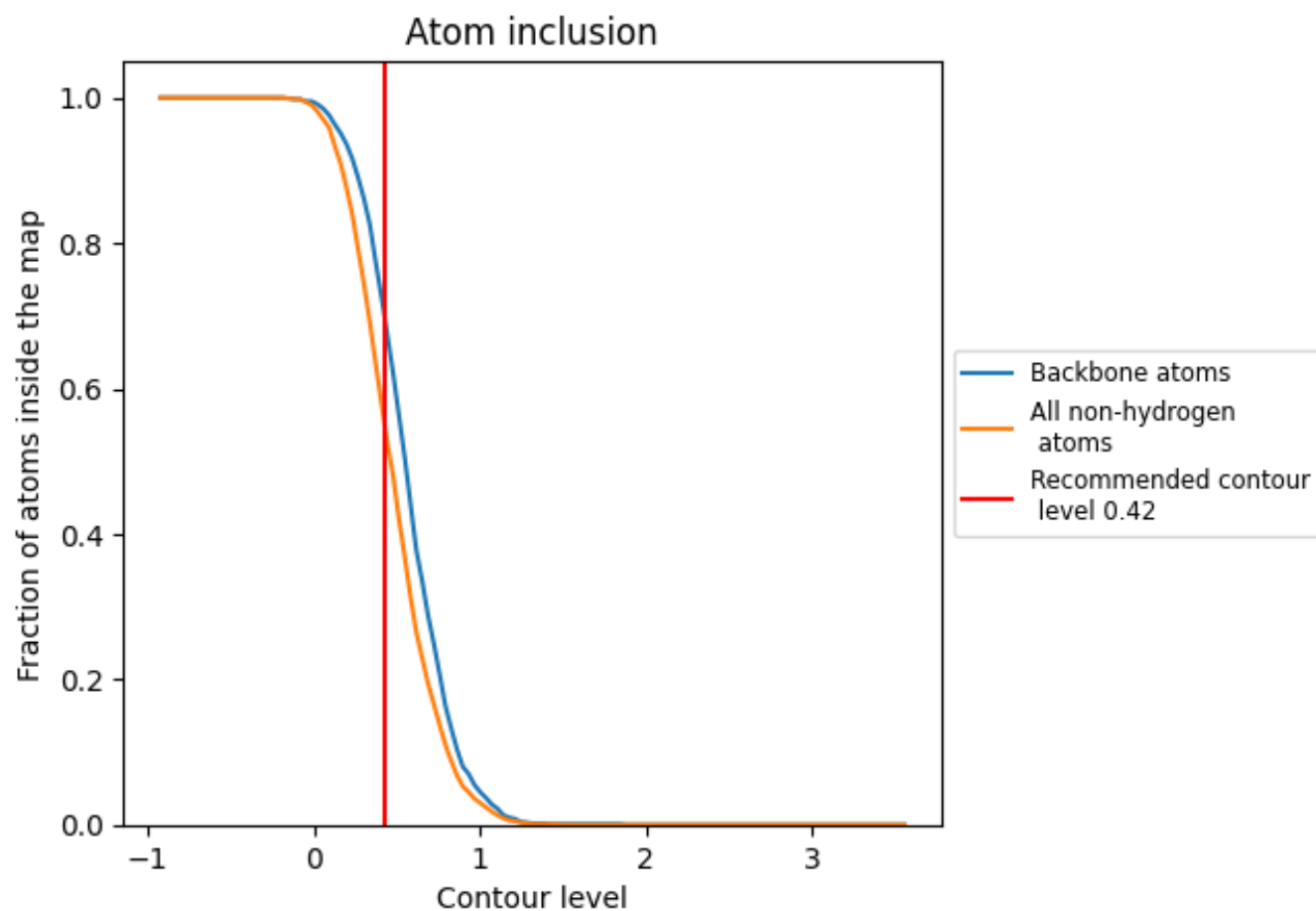


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 71% of all backbone atoms, 56% 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 (0.42) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5580	0.2920
A	0.6180	0.3440
H	0.4830	0.2650
L	0.5300	0.2260

