



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:50 PM UTC

PDB ID : 7OTI / pdb_00007oti
EMDB ID : EMD-13060
Title : Structure of ABCB1/P-glycoprotein in apo state
Authors : Ford, R.C.; Barbieri, A.; Thonghin, N.; Shafi, T.; Prince, S.M.; Collins, R.F.
Deposited on : 2021-06-10
Resolution : 4.20 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

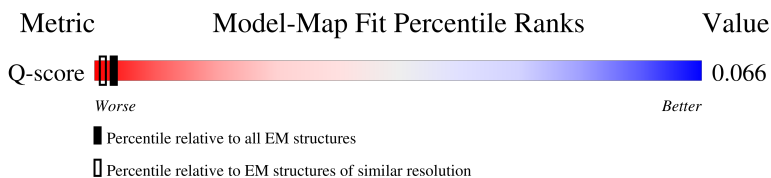
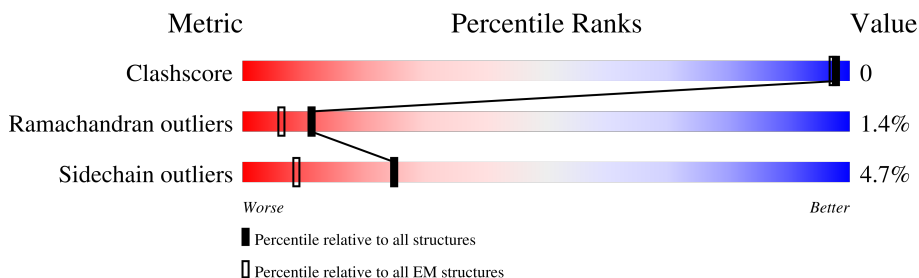
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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	5410 (3.70 - 4.70)

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 $\leq 5\%$. 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	1284	44% 83% 8% 8%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9171 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 Multidrug resistance protein 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1182	Total	C	N	O	S	0	0
			9171	5895	1552	1686	38		

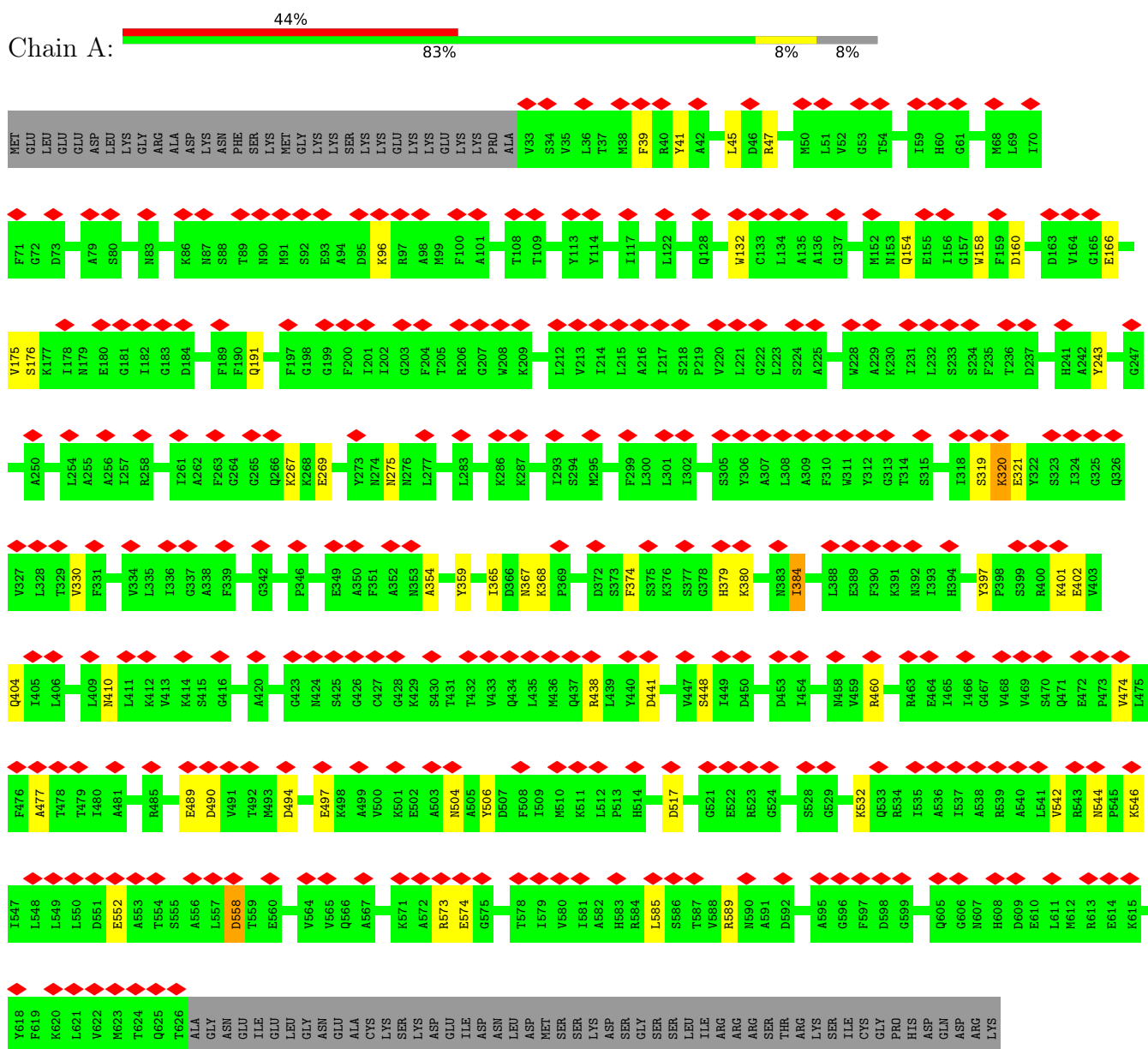
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1277	LEU	-	expression tag	UNP P21447
A	1278	GLU	-	expression tag	UNP P21447
A	1279	HIS	-	expression tag	UNP P21447
A	1280	HIS	-	expression tag	UNP P21447
A	1281	HIS	-	expression tag	UNP P21447
A	1282	HIS	-	expression tag	UNP P21447
A	1283	HIS	-	expression tag	UNP P21447
A	1284	HIS	-	expression tag	UNP P21447

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Multidrug resistance protein 1A





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	104000	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 ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.732	Depositor
Minimum map value	-2.225	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.210	Depositor
Recommended contour level	1.05	Depositor
Map size (Å)	229.45999, 229.45999, 229.45999	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.043, 1.043, 1.043	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	0.85	0/9339	1.44	29/12626 (0.2%)

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	13

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	689	PRO	N-CA-C	9.61	122.42	110.70
1	A	979	PHE	CA-CB-CG	8.20	122.00	113.80
1	A	740	PRO	N-CA-C	7.61	119.98	110.70
1	A	558	ASP	CA-CB-CG	7.17	119.77	112.60
1	A	39	PHE	CA-CB-CG	6.03	119.83	113.80
1	A	275	ASN	CA-CB-CG	6.00	118.60	112.60
1	A	544	ASN	CB-CA-C	5.88	116.24	110.71
1	A	45	LEU	CA-C-N	5.88	128.48	120.54
1	A	45	LEU	C-N-CA	5.88	128.48	120.54
1	A	374	PHE	CA-CB-CG	5.81	119.61	113.80
1	A	934	PHE	CA-CB-CG	5.60	119.40	113.80
1	A	833	PHE	CA-CB-CG	5.60	119.40	113.80
1	A	154	GLN	OE1-CD-NE2	-5.50	117.11	122.60
1	A	191	GLN	OE1-CD-NE2	-5.45	117.16	122.60
1	A	354	ALA	CA-C-N	5.39	127.82	120.54
1	A	354	ALA	C-N-CA	5.39	127.82	120.54
1	A	448	SER	CA-C-N	5.34	129.92	122.23
1	A	448	SER	C-N-CA	5.34	129.92	122.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1091	PHE	CA-CB-CG	5.23	119.03	113.80
1	A	573	ARG	CA-C-N	5.22	131.51	121.54
1	A	573	ARG	C-N-CA	5.22	131.51	121.54
1	A	379	HIS	CB-CG-CD2	-5.19	124.45	131.20
1	A	850	GLY	CA-C-N	5.18	131.43	121.54
1	A	850	GLY	C-N-CA	5.18	131.43	121.54
1	A	942	GLN	OE1-CD-NE2	-5.16	117.44	122.60
1	A	460	ARG	CD-NE-CZ	5.12	131.57	124.40
1	A	489	GLU	CA-C-N	5.06	131.20	121.54
1	A	489	GLU	C-N-CA	5.06	131.20	121.54
1	A	517	ASP	CB-CA-C	5.04	119.25	111.13

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1017	TYR	Sidechain
1	A	1083	TYR	Sidechain
1	A	1092	LEU	Peptide
1	A	1118	LEU	Peptide
1	A	1263	TYR	Peptide
1	A	243	TYR	Sidechain
1	A	359	TYR	Sidechain
1	A	384	ILE	Peptide
1	A	41	TYR	Peptide
1	A	474	VAL	Peptide
1	A	506	TYR	Sidechain
1	A	589	ARG	Sidechain
1	A	688	VAL	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9171	0	9344	9	0
All	All	9171	0	9344	9	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 0.

All (9) 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:830:ALA:HB1	1:A:990:PHE:CZ	2.52	0.45
1:A:1139:GLU:CD	1:A:1139:GLU:H	2.25	0.45
1:A:926:ASN:HA	1:A:929:LYS:HE3	1.99	0.44
1:A:320:LYS:HE3	1:A:321:GLU:OE1	2.18	0.43
1:A:1114:GLN:H	1:A:1114:GLN:CD	2.26	0.43
1:A:438:ARG:HE	1:A:441:ASP:CG	2.28	0.42
1:A:1003:HIS:CE1	1:A:1006:ARG:HH21	2.36	0.41
1:A:1159:ASP:CG	1:A:1163:THR:HA	2.46	0.41
1:A:160:ASP:HA	1:A:397:TYR:CZ	2.57	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	1178/1284 (92%)	1035 (88%)	127 (11%)	16 (1%)	9	39

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	384	ILE
1	A	319	SER
1	A	1203	ASP
1	A	404	GLN
1	A	797	VAL
1	A	804	LYS
1	A	851	TRP

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Mol	Chain	Res	Type
1	A	477	ALA
1	A	504	ASN
1	A	552	GLU
1	A	1121	CYS
1	A	365	ILE
1	A	96	LYS
1	A	1204	THR
1	A	1046	ILE
1	A	175	VAL

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	976/1065 (92%)	930 (95%)	46 (5%)	23	46

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	ARG
1	A	132	TRP
1	A	158	TRP
1	A	166	GLU
1	A	176	SER
1	A	267	LYS
1	A	269	GLU
1	A	320	LYS
1	A	330	VAL
1	A	367	ASN
1	A	368	LYS
1	A	380	LYS
1	A	401	LYS
1	A	402	GLU
1	A	410	ASN
1	A	490	ASP
1	A	494	ASP

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Mol	Chain	Res	Type
1	A	497	GLU
1	A	532	LYS
1	A	542	VAL
1	A	546	LYS
1	A	558	ASP
1	A	574	GLU
1	A	585	LEU
1	A	742	GLU
1	A	796	ASP
1	A	822	LYS
1	A	835	ASN
1	A	898	GLU
1	A	899	ASN
1	A	942	GLN
1	A	953	PHE
1	A	993	ASP
1	A	1009	GLU
1	A	1040	TYR
1	A	1101	ASN
1	A	1115	GLU
1	A	1129	TYR
1	A	1162	ASN
1	A	1164	ARG
1	A	1168	LYS
1	A	1188	ARG
1	A	1199	THR
1	A	1211	GLN
1	A	1216	LYS
1	A	1246	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	154	GLN
1	A	590	ASN
1	A	721	GLN
1	A	744	GLN
1	A	834	GLN
1	A	910	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.

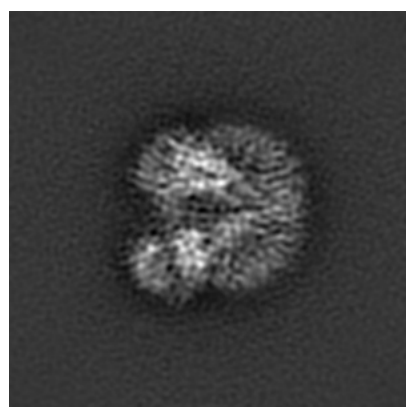
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13060. These allow visual inspection of the internal detail of the map and identification of artifacts.

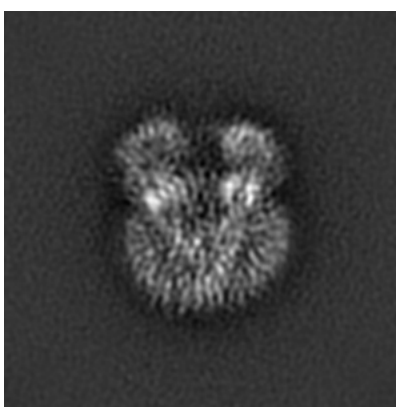
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

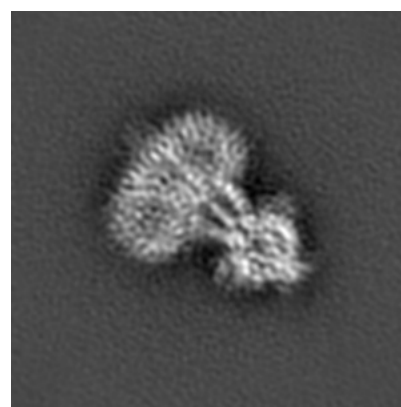
6.1.1 Primary map



X



Y

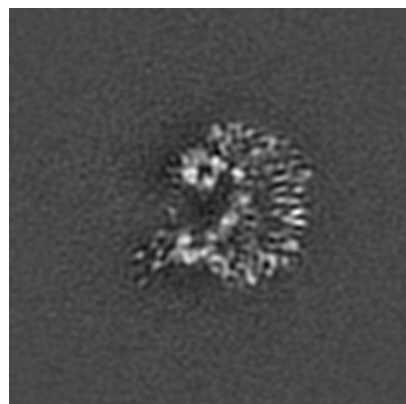


Z

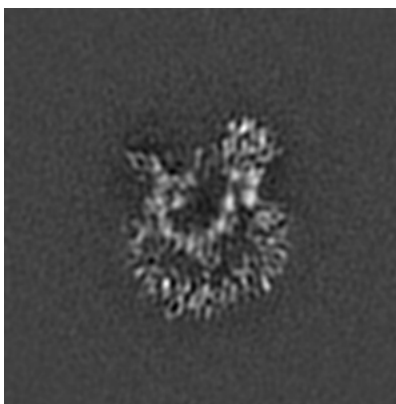
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

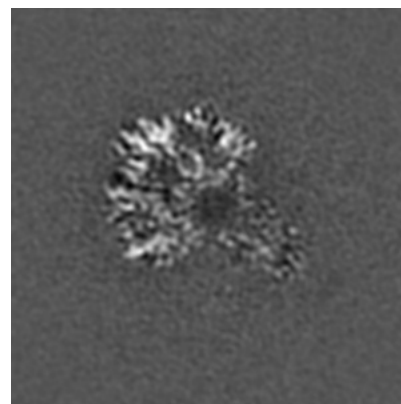
6.2.1 Primary map



X Index: 110



Y Index: 110

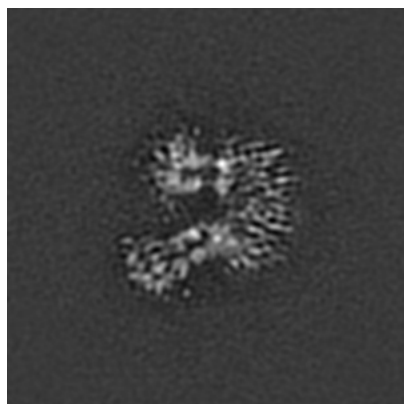


Z Index: 110

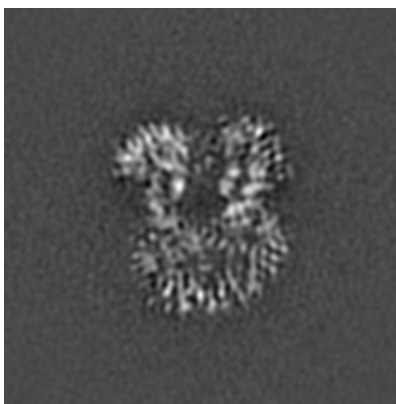
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

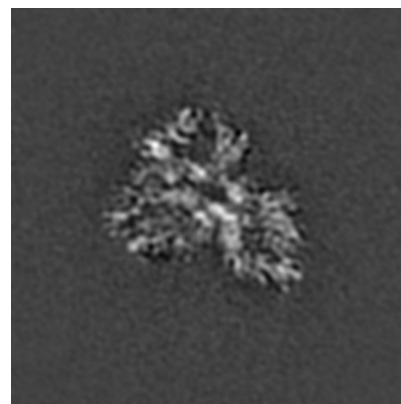
6.3.1 Primary map



X Index: 121



Y Index: 101

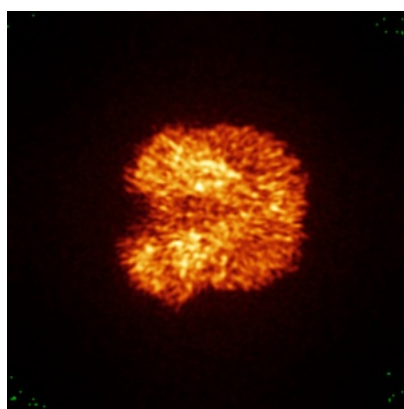


Z Index: 123

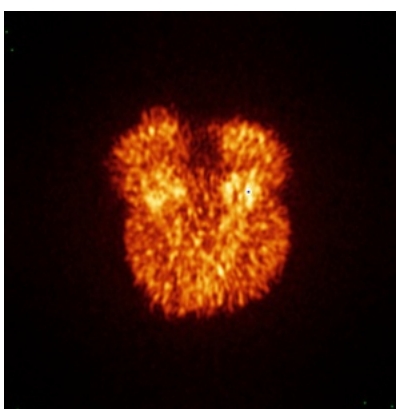
The images above show the largest variance slices of the map in three orthogonal directions.

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

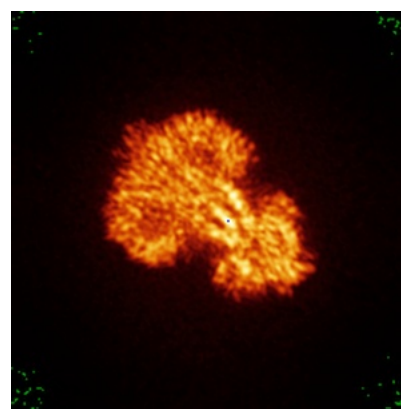
6.4.1 Primary map



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.

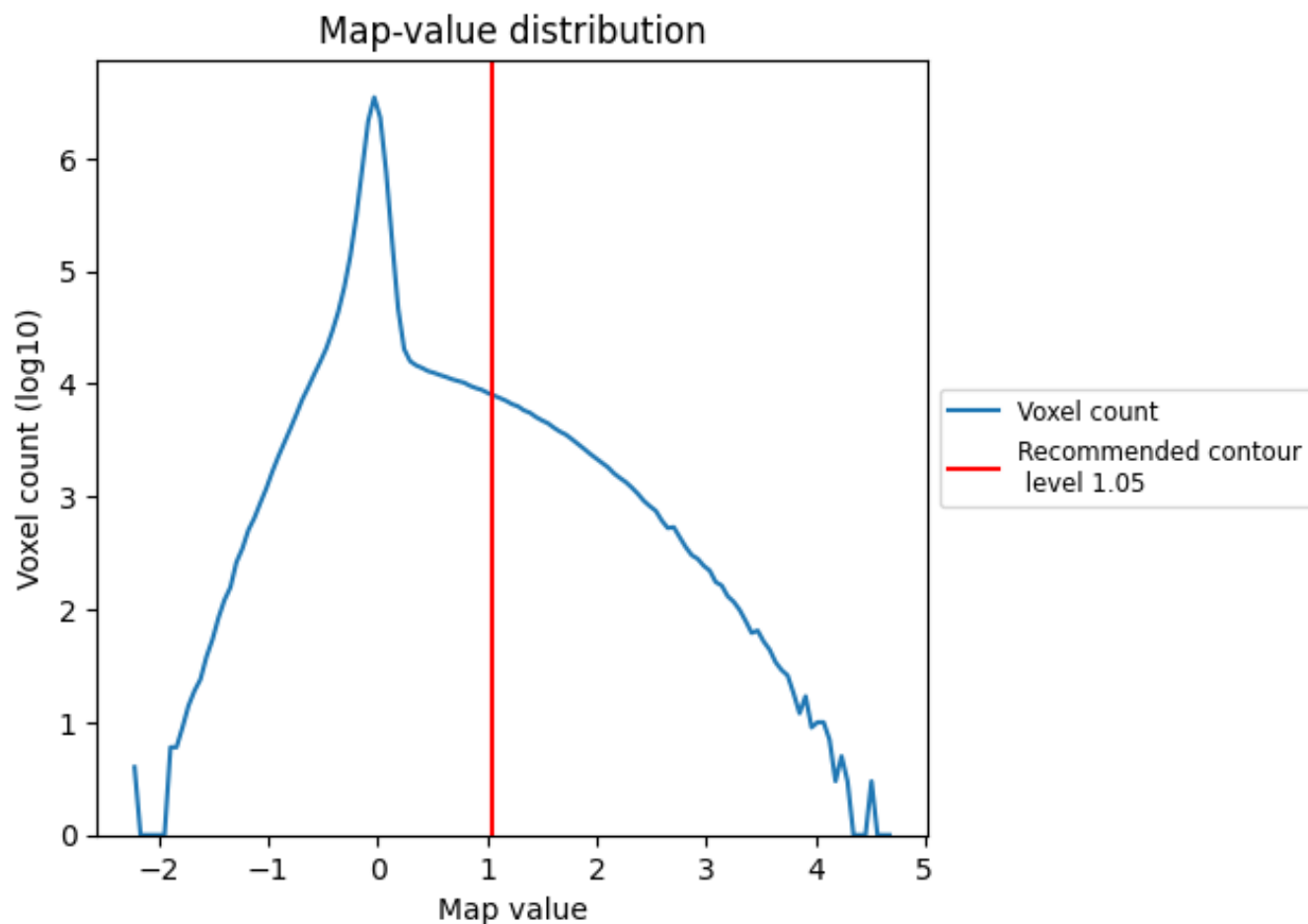
6.6 Mask visualisation

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

7 Map analysis [i](#)

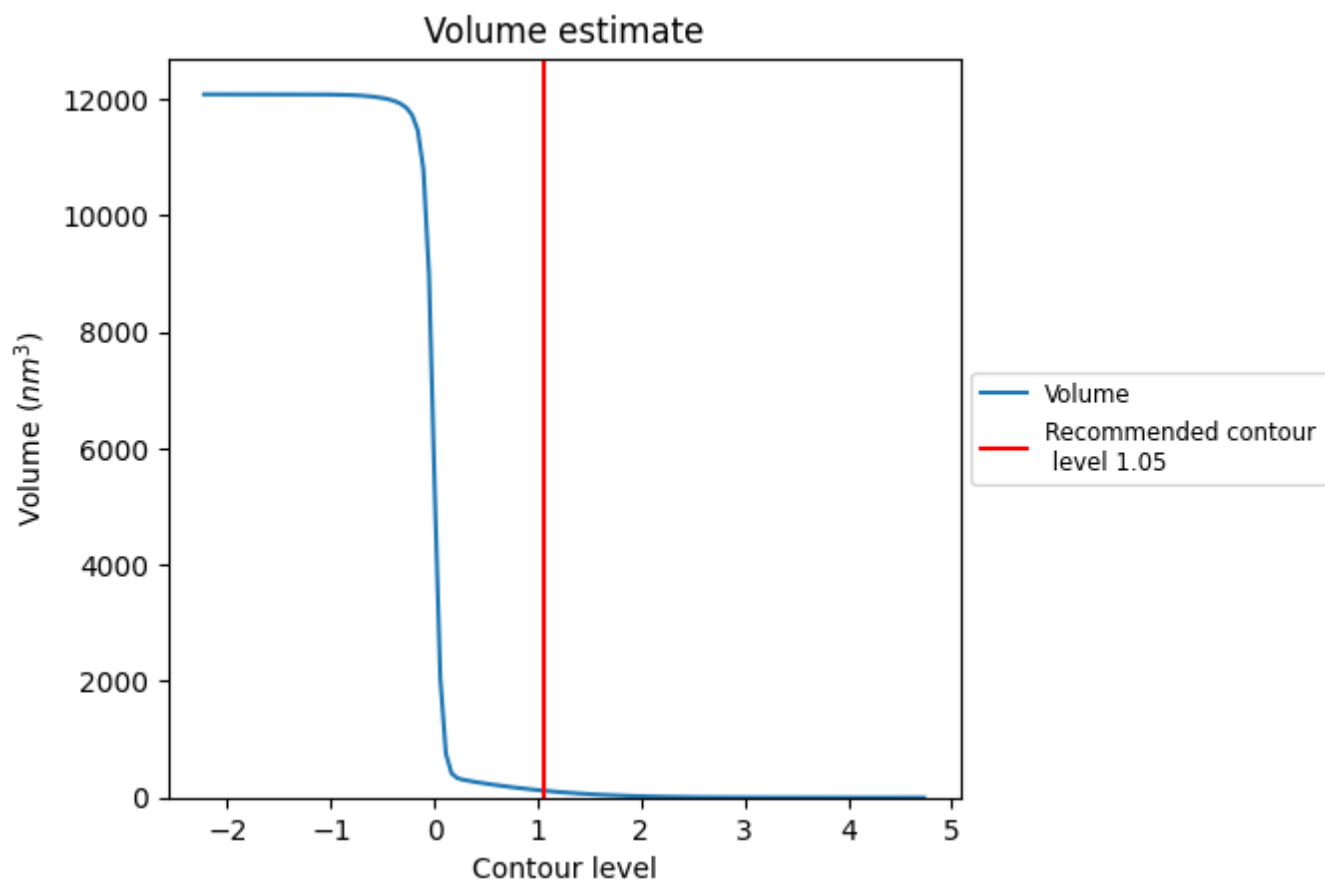
This section contains the results of statistical analysis of the map.

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.

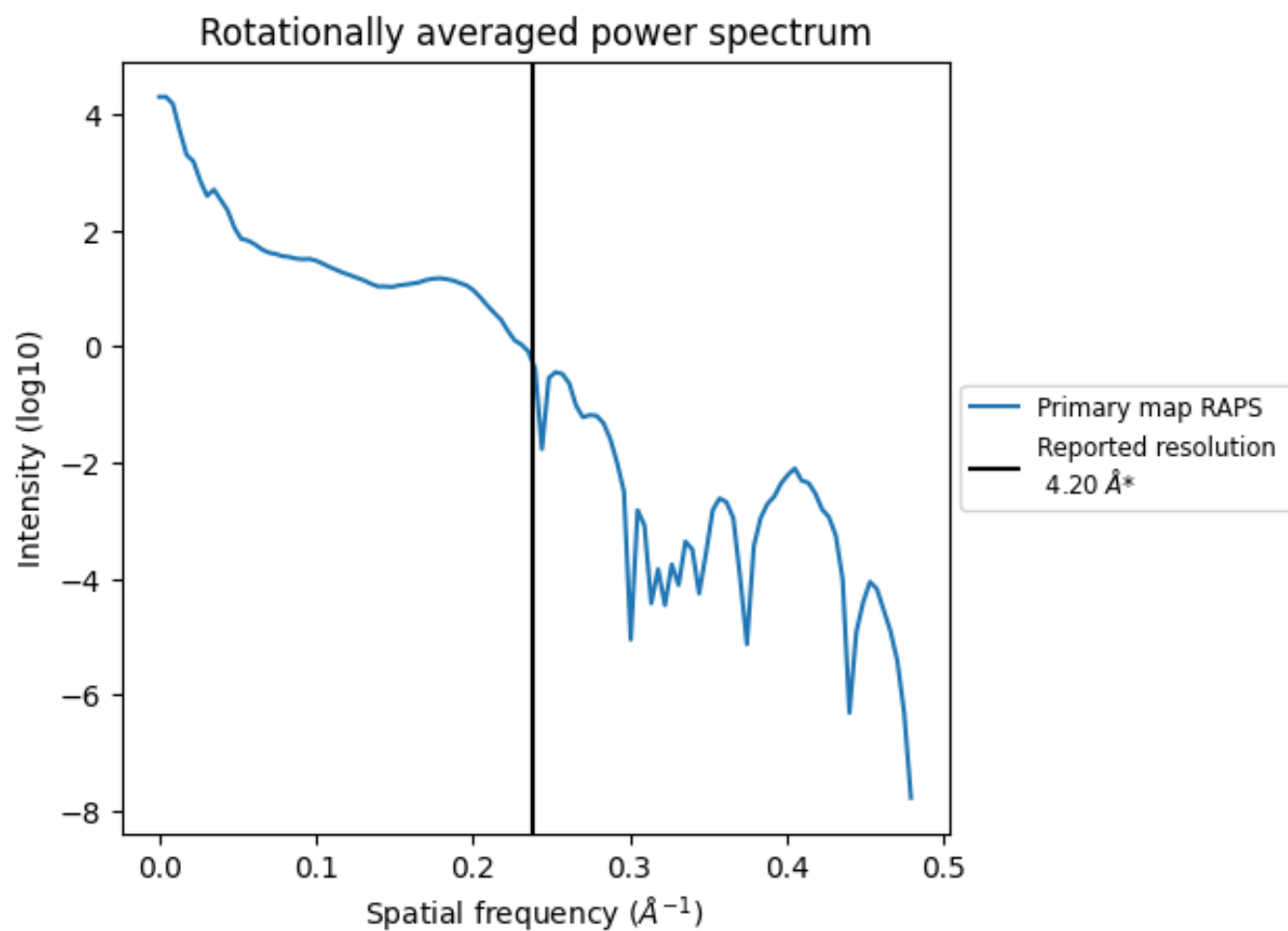
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 119 nm³; this corresponds to an approximate mass of 108 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 0.238 Å⁻¹

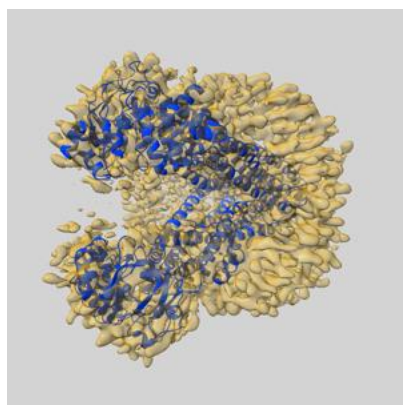
8 Fourier-Shell correlation ⓘ

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

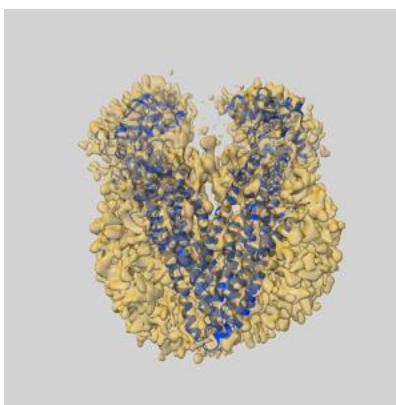
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13060 and PDB model 7OTI. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

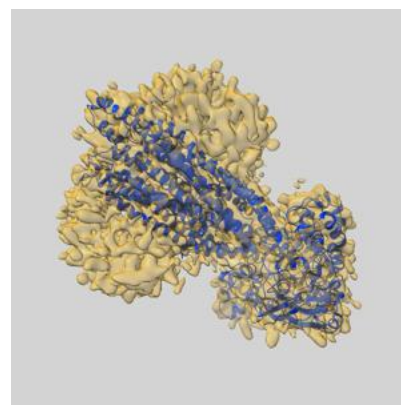
9.1 Map-model overlay [i](#)



X



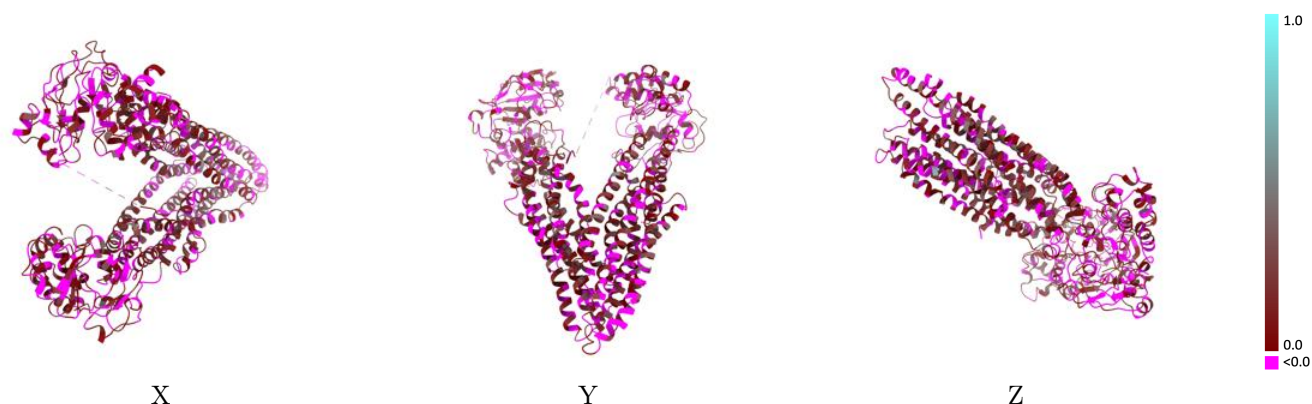
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.05 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](#)

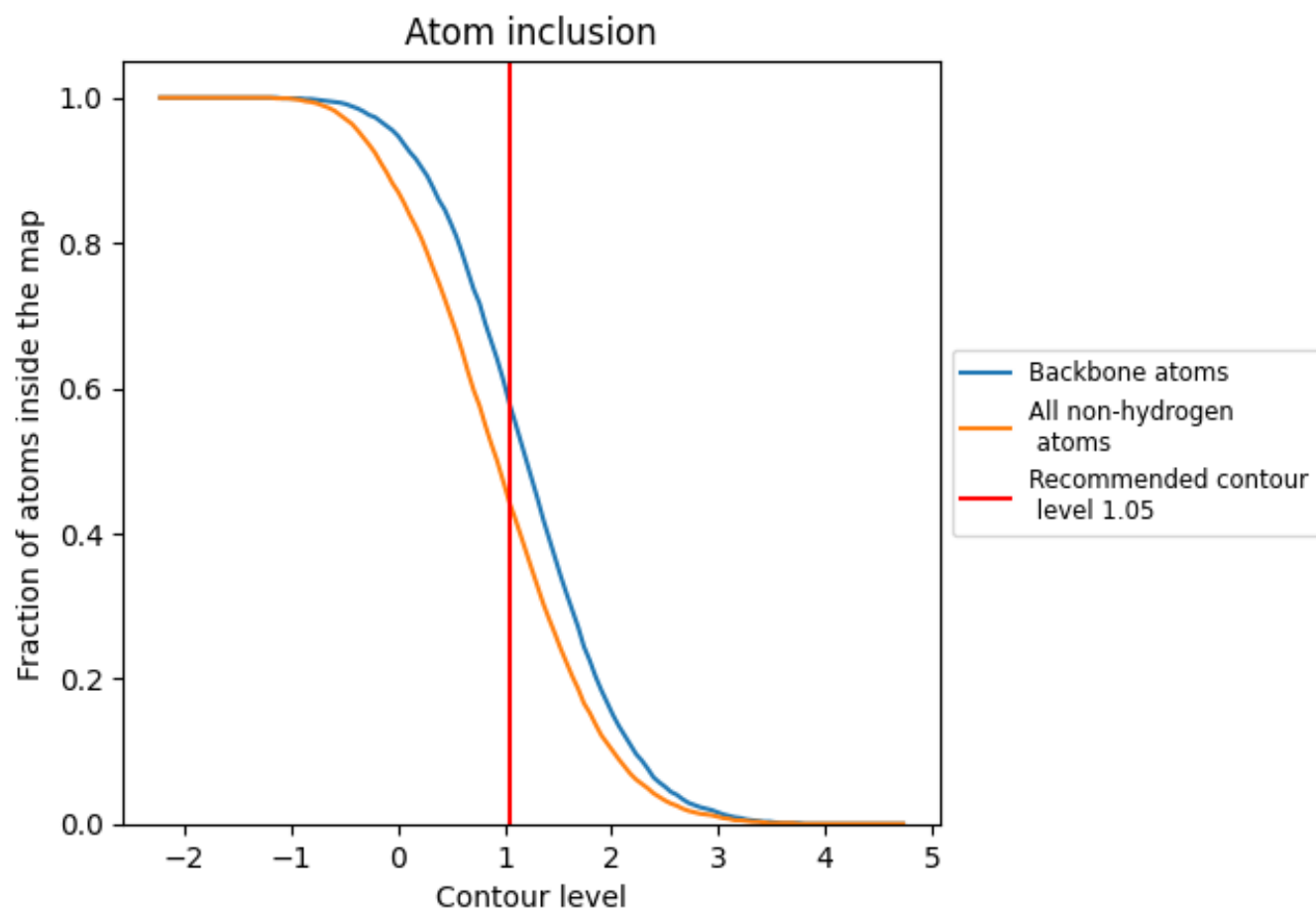


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 58% of all backbone atoms, 44% 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 (1.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4400	0.0660
A	0.4400	0.0660

