



wwPDB EM Validation Summary Report ⓘ

Nov 12, 2024 – 05:48 AM EST

PDB ID : 7RJ5
EMDB ID : EMD-24481
Title : The structure of BAM in complex with EspP at 7 Angstrom resolution
Authors : Wu, R.R.; Noinaj, N.
Deposited on : 2021-07-20
Resolution : 7.00 Å(reported)

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 ⓘ 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

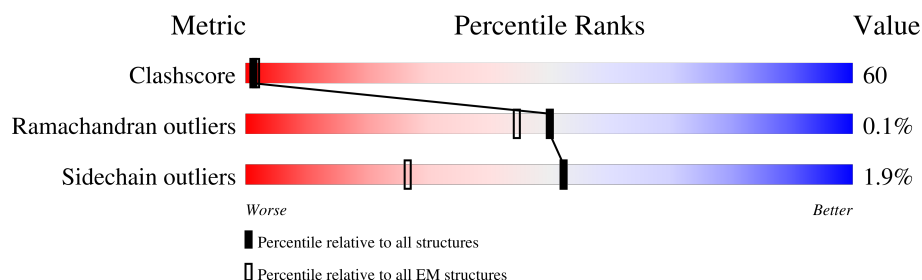
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.00 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	G	723	
2	A	810	
3	B	373	
4	C	344	
5	D	245	
6	E	123	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12639 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 Maltodextrin-binding protein, Autotransporter outer membrane beta-barrel domain-containing protein chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	G	87	Total	C	N	O	S	0	0
			614	385	111	116	2		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	578	MET	-	expression tag	UNP A0A4Z0THX4
G	579	GLY	-	expression tag	UNP A0A4Z0THX4
G	892	VAL	ALA	conflict	UNP A0A4Z0THX4
G	947	GLY	-	linker	UNP A0A4Z0THX4
G	948	SER	-	linker	UNP A0A4Z0THX4

- Molecule 2 is a protein called Outer membrane protein assembly factor BamA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	787	Total	C	N	O	S	0	0
			6228	3930	1049	1233	16		

- Molecule 3 is a protein called Outer membrane protein assembly factor BamB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	373	Total	C	N	O	S	0	0
			2807	1760	480	560	7		

- Molecule 4 is a protein called Outer membrane protein assembly factor BamC.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	66	Total	C	N	O	S	0	0
			474	296	82	94	2		

- Molecule 5 is a protein called Outer membrane protein assembly factor BamD.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	224	Total	C	N	O	S	0	0
			1801	1131	316	346	8		

- Molecule 6 is a protein called Outer membrane protein assembly factor BamE.


Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	91	Total	C	N	O	S	0	0
			712	448	123	138	3		

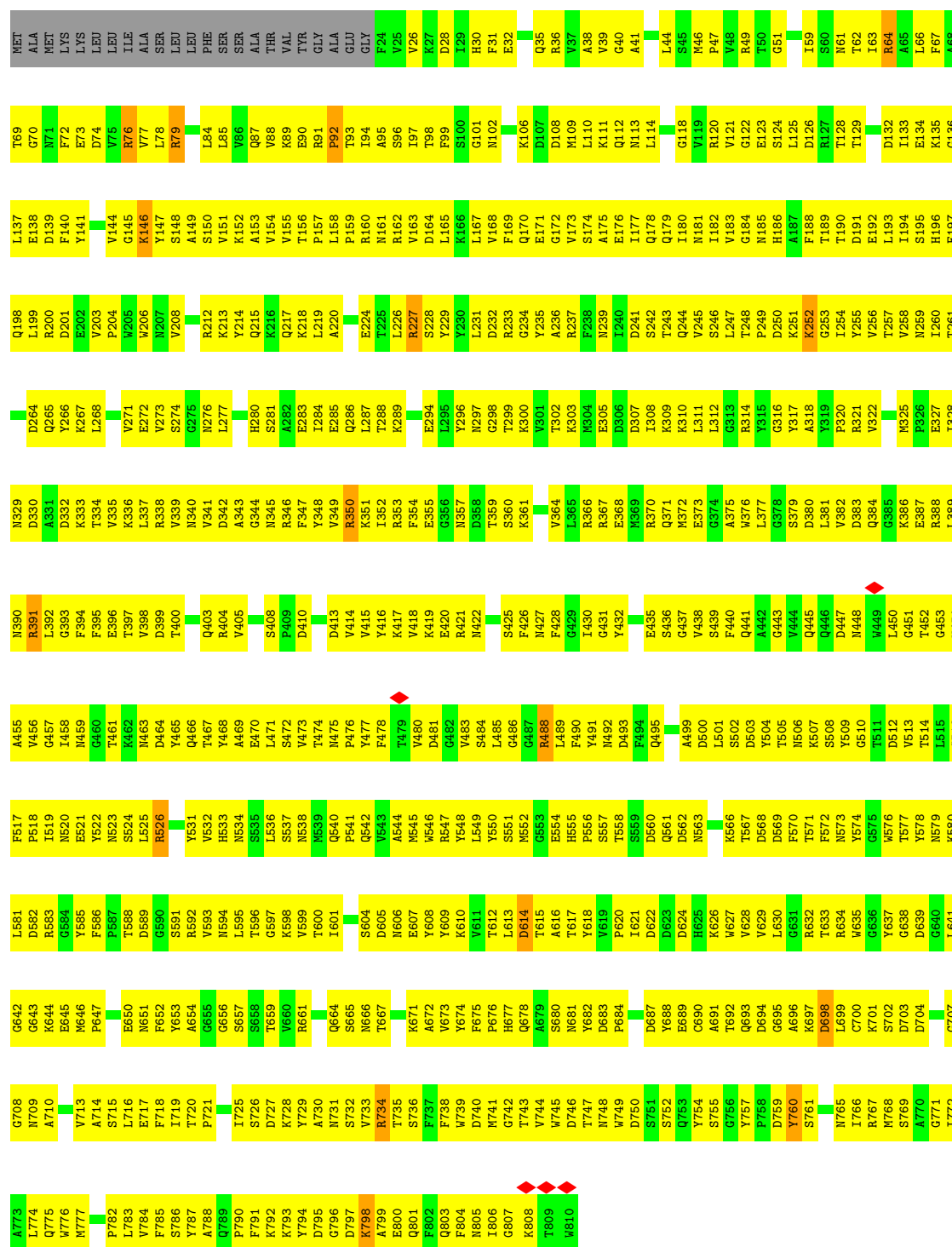
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	114	GLY	-	expression tag	UNP A0A3L5AP29
E	115	GLY	-	expression tag	UNP A0A3L5AP29
E	116	HIS	-	expression tag	UNP A0A3L5AP29
E	117	HIS	-	expression tag	UNP A0A3L5AP29
E	118	HIS	-	expression tag	UNP A0A3L5AP29
E	119	HIS	-	expression tag	UNP A0A3L5AP29
E	120	HIS	-	expression tag	UNP A0A3L5AP29
E	121	HIS	-	expression tag	UNP A0A3L5AP29
E	122	HIS	-	expression tag	UNP A0A3L5AP29
E	123	HIS	-	expression tag	UNP A0A3L5AP29


- Molecule 7 is water.

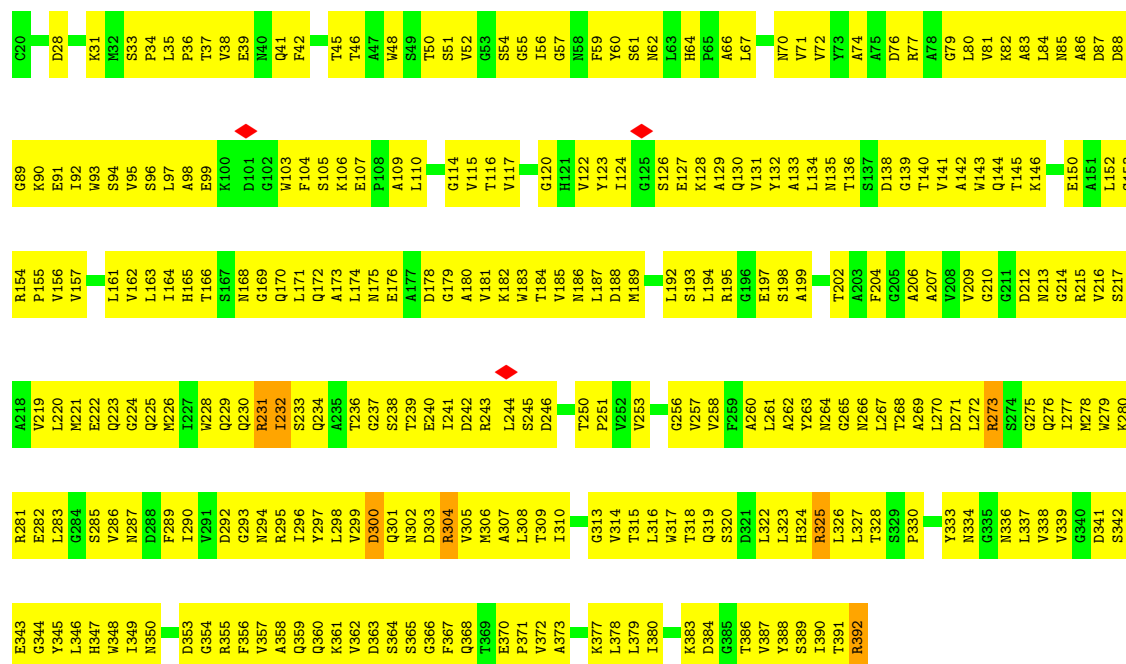
Mol	Chain	Residues	Atoms		AltConf
7	A	3	Total	O	0
			3	3	

Chain A: 

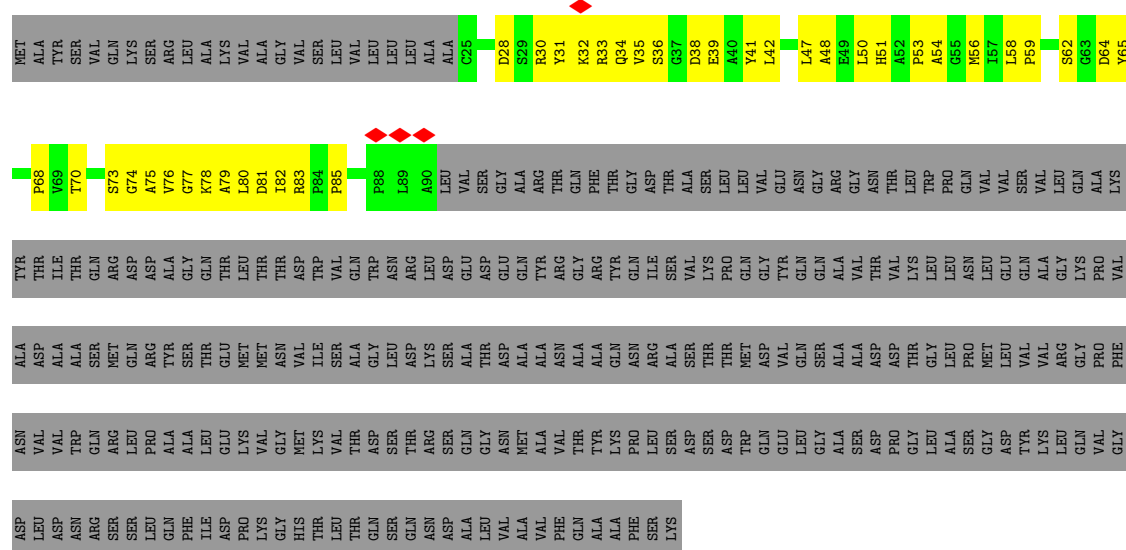


• Molecule 3: Outer membrane protein assembly factor BamB

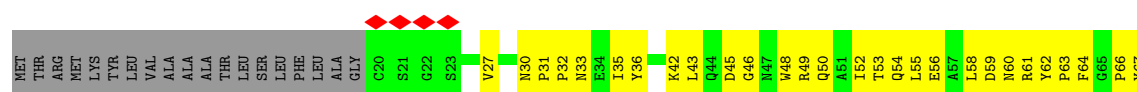
Chain B: 

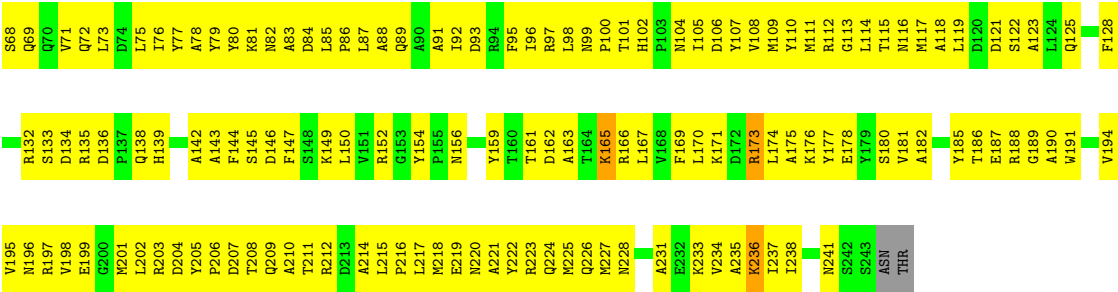


• Molecule 4: Outer membrane protein assembly factor BamC

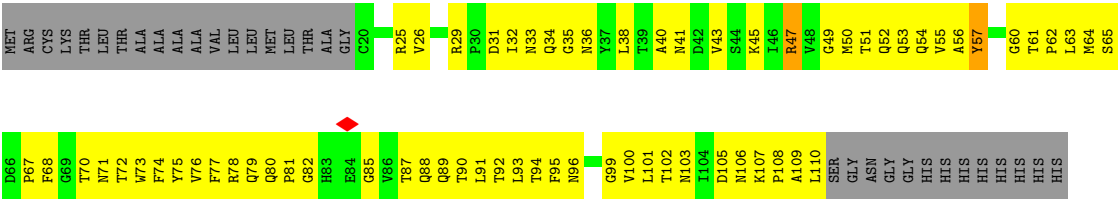
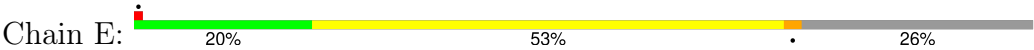


• Molecule 5: Outer membrane protein assembly factor BamD





● Molecule 6: Outer membrane protein assembly factor BamE



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	70031	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 ($e^-/\text{\AA}^2$)	51.14	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	0.027	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0025	Depositor
Map size (\AA)	251.99998, 251.99998, 251.99998	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

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	G	0.28	0/623	0.54	0/840
2	A	0.35	0/6373	0.54	0/8647
3	B	0.33	0/2858	0.58	0/3897
4	C	0.32	0/484	0.50	0/661
5	D	0.34	0/1841	0.49	0/2499
6	E	0.33	0/727	0.56	0/992
All	All	0.34	0/12906	0.54	0/17536

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
2	A	0	4
3	B	0	1
All	All	0	5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	123	GLU	Peptide
2	A	146	LYS	Peptide
2	A	698	ASP	Peptide
2	A	760	TYR	Peptide
3	B	300	ASP	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	G	614	0	506	63	0
2	A	6228	0	5938	744	0
3	B	2807	0	2748	384	0
4	C	474	0	469	55	0
5	D	1801	0	1736	232	0
6	E	712	0	694	84	0
7	A	3	0	0	0	0
All	All	12639	0	12091	1474	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 60.

The worst 5 of 1474 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)
5:D:237:ILE:O	5:D:241:ASN:HB2	1.53	1.07
2:A:355:GLU:HG2	2:A:417:LYS:HD3	1.40	1.03
3:B:371:PRO:HB3	3:B:380:ILE:HA	1.45	0.97
2:A:182:ILE:HA	2:A:258:VAL:HB	1.46	0.97
3:B:123:TYR:HH	3:B:143:TRP:HE1	1.12	0.96

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	G	83/723 (12%)	71 (86%)	12 (14%)	0	100	100
2	A	785/810 (97%)	612 (78%)	171 (22%)	2 (0%)	37	73
3	B	371/373 (100%)	280 (76%)	91 (24%)	0	100	100
4	C	64/344 (19%)	53 (83%)	11 (17%)	0	100	100
5	D	222/245 (91%)	188 (85%)	34 (15%)	0	100	100
6	E	89/123 (72%)	72 (81%)	17 (19%)	0	100	100
All	All	1614/2618 (62%)	1276 (79%)	336 (21%)	2 (0%)	50	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	92	PRO
2	A	796	GLY

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	G	47/578 (8%)	46 (98%)	1 (2%)	48	66
2	A	671/688 (98%)	659 (98%)	12 (2%)	54	71
3	B	304/304 (100%)	298 (98%)	6 (2%)	50	68
4	C	49/276 (18%)	49 (100%)	0	100	100
5	D	188/204 (92%)	184 (98%)	4 (2%)	48	66
6	E	80/103 (78%)	78 (98%)	2 (2%)	42	61
All	All	1339/2153 (62%)	1314 (98%)	25 (2%)	52	69

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	232	ILE
3	B	325	ARG
6	E	57	TYR

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Continued from previous page...

Mol	Chain	Res	Type
3	B	304	ARG
3	B	392	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
5	D	125	GLN
6	E	88	GLN
6	E	79	GLN
3	B	276	GLN
5	D	116	ASN

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-24481. These allow visual inspection of the internal detail of the map and identification of artifacts.

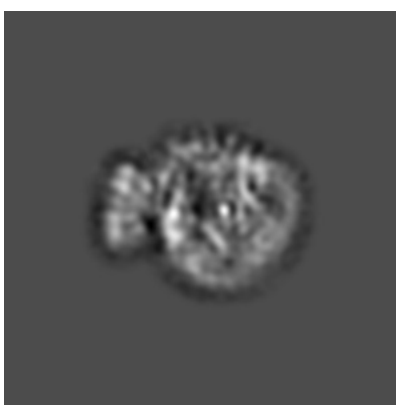
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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: 120



Y Index: 120



Z Index: 120

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: 113



Y Index: 113



Z Index: 142

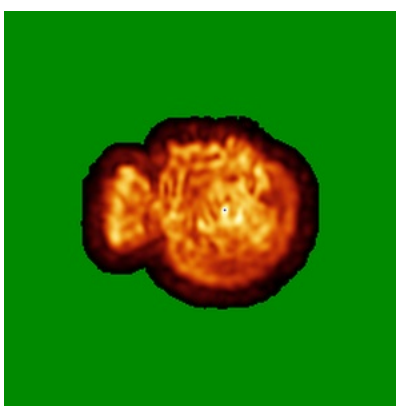
The images above show the largest variance slices of the map in three orthogonal directions.

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 0.0025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

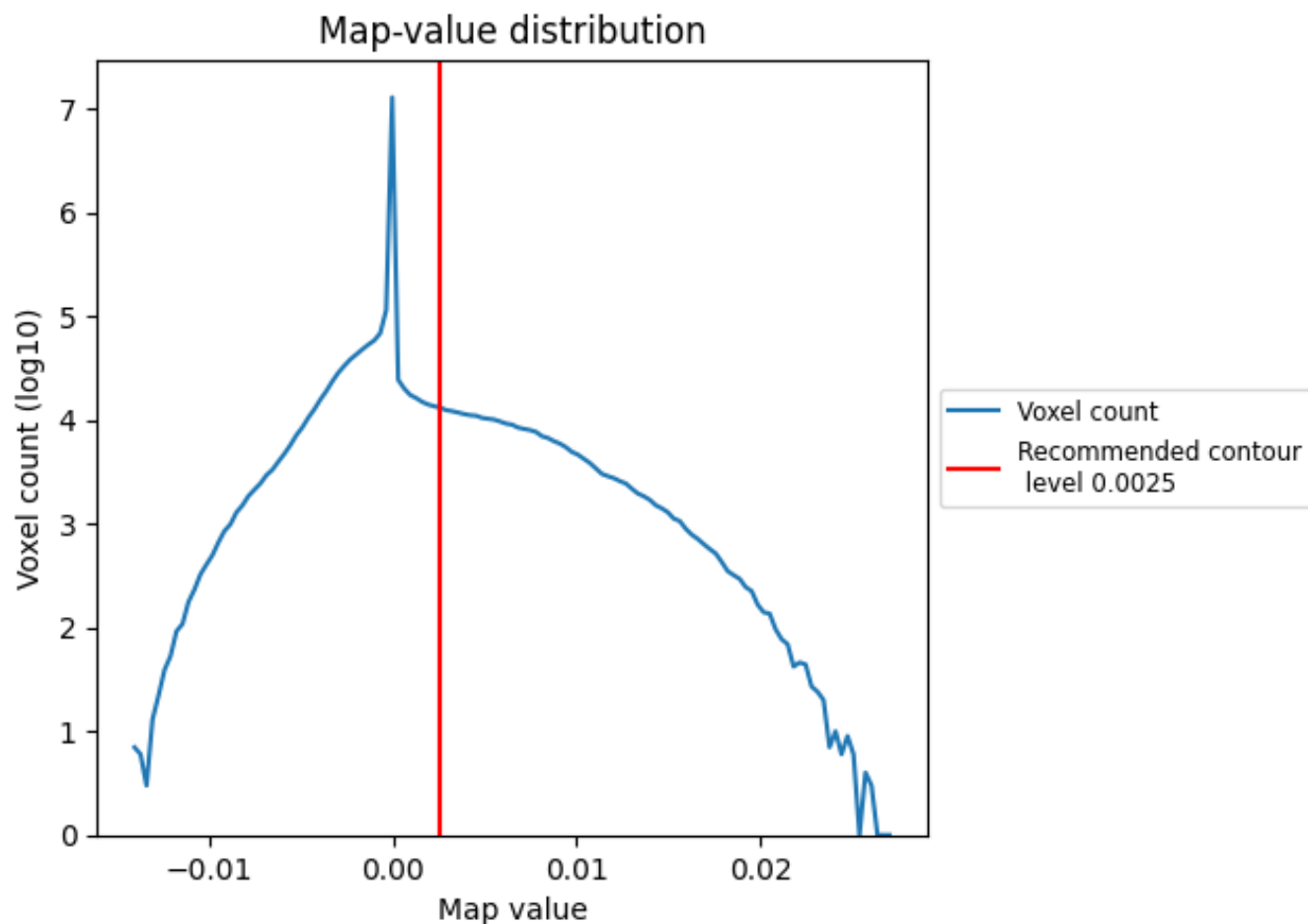
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

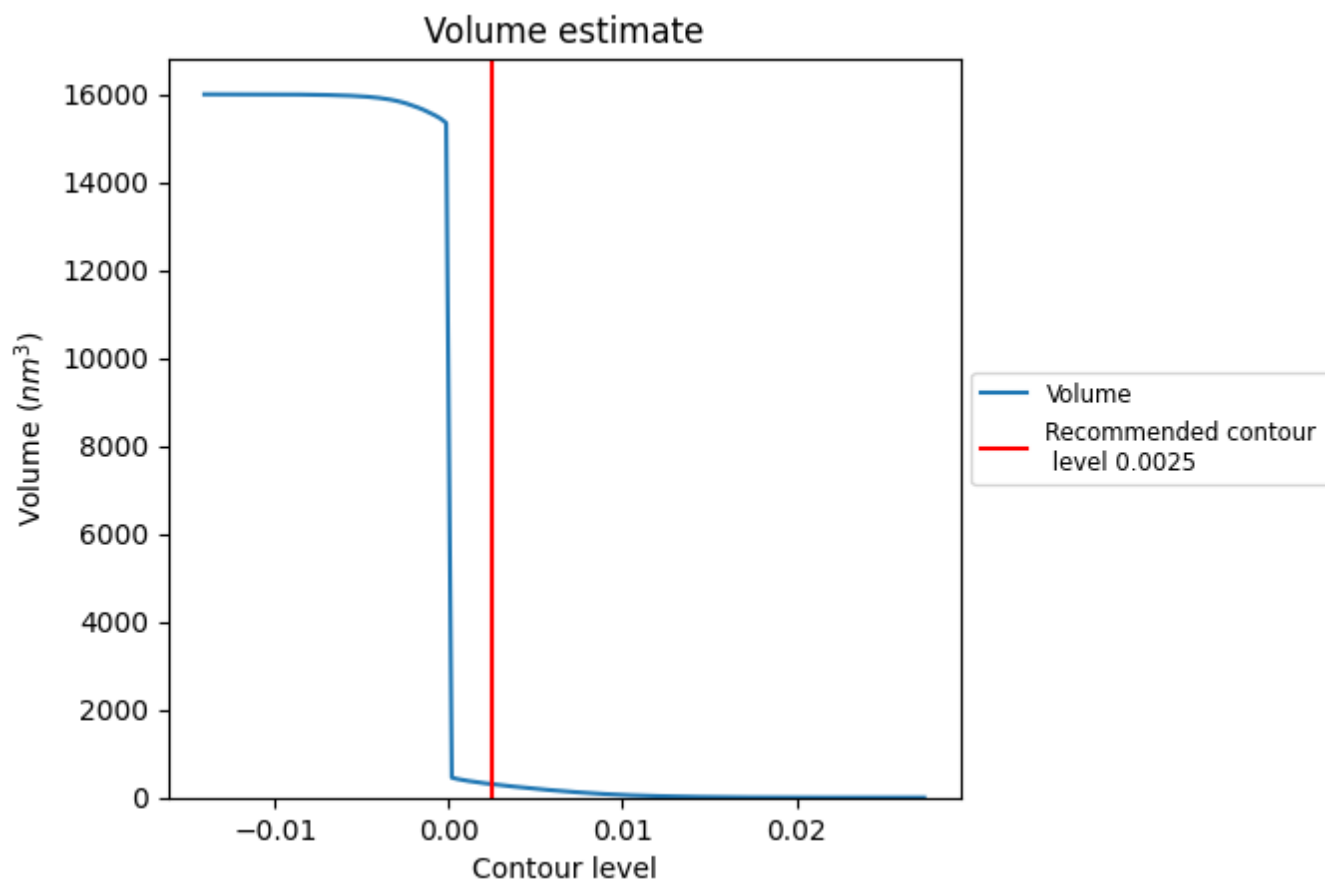
This section contains the results of statistical analysis of the map.

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.

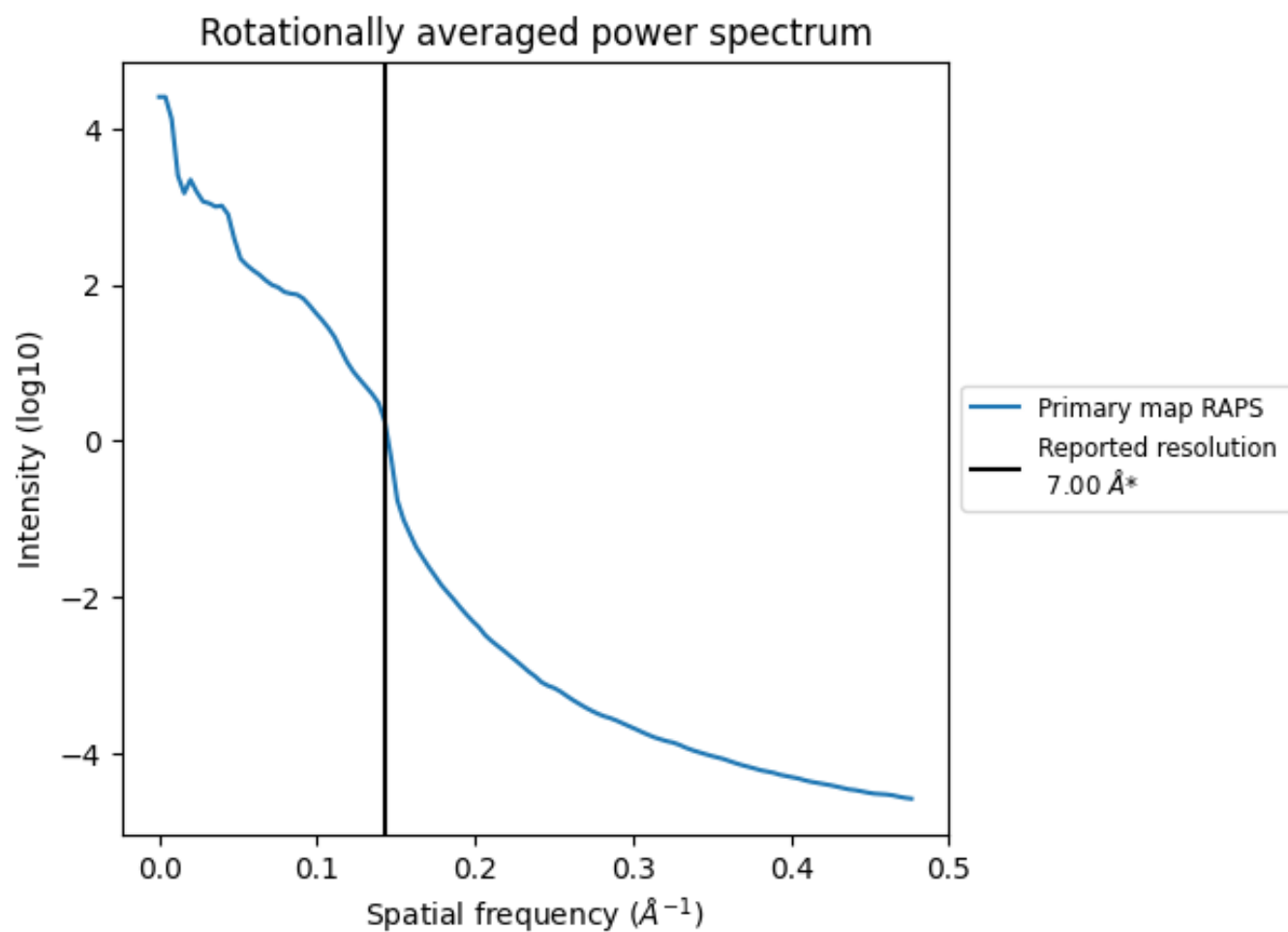
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 305 nm³; this corresponds to an approximate mass of 276 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 0.143 Å⁻¹

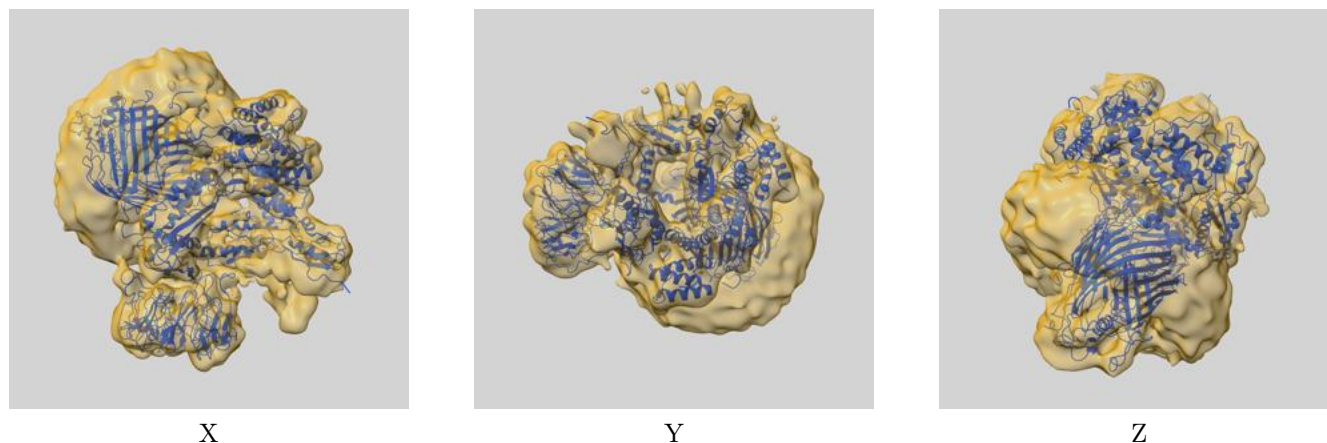
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

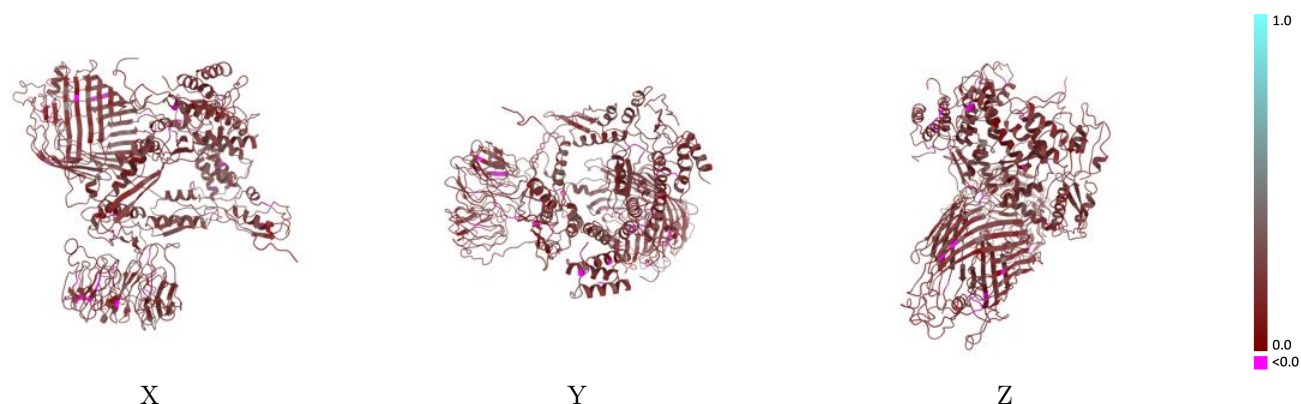
This section contains information regarding the fit between EMDB map EMD-24481 and PDB model 7RJ5. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



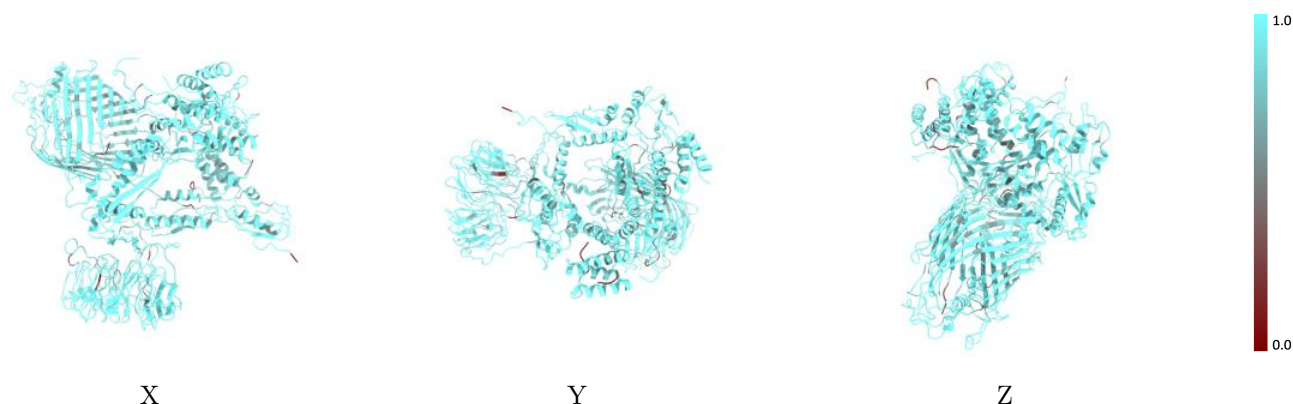
The images above show the 3D surface view of the map at the recommended contour level 0.0025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



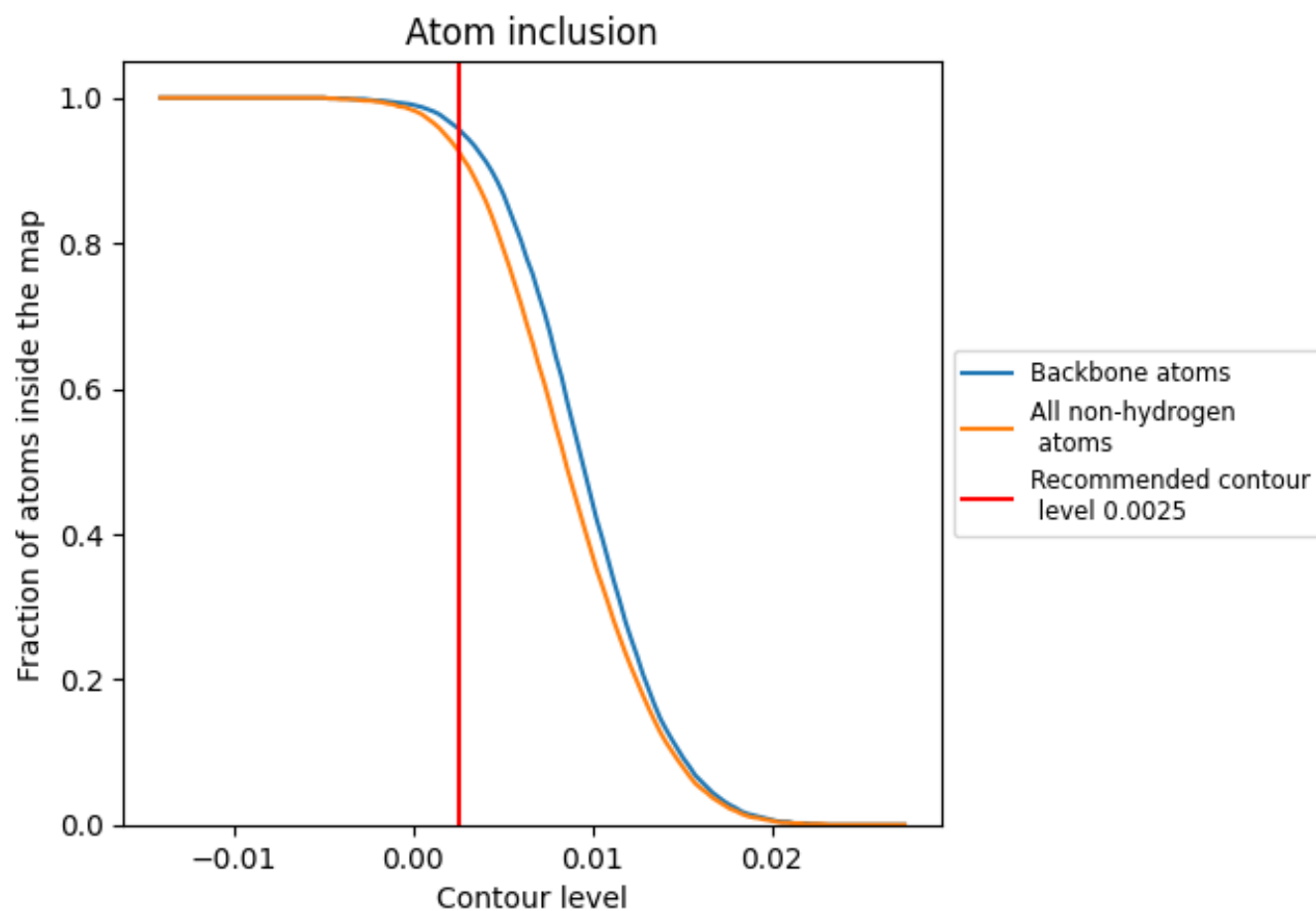
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% 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 (0.0025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.9280</div>	<div><div></div>0.2100</div>
A	<div><div></div>0.9270</div>	<div><div></div>0.2090</div>
B	<div><div></div>0.9570</div>	<div><div></div>0.2020</div>
C	<div><div></div>0.8470</div>	<div><div></div>0.2380</div>
D	<div><div></div>0.9370</div>	<div><div></div>0.2110</div>
E	<div><div></div>0.9430</div>	<div><div></div>0.2310</div>
G	<div><div></div>0.8300</div>	<div><div></div>0.2090</div>

1.0

0.0

<0.0