



Full wwPDB EM Validation Report ⓘ

Nov 20, 2022 – 01:14 AM EST

PDB ID : 7TT7
EMDB ID : EMD-26113
Title : BamABCDE bound to substrate EspP in the barrelized EspP/continuous open BamA state
Authors : Doyle, M.T.; Jimah, J.R.; Dowdy, T.; Ohlemacher, S.I.; Larion, M.; Hinshaw, J.E.; Bernstein, H.D.
Deposited on : 2022-01-31
Resolution : 4.80 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

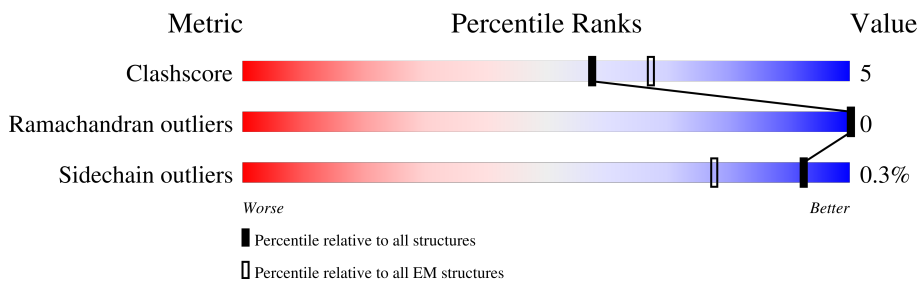
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.80 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	800	
2	C	320	
3	E	94	
4	D	226	
5	P	764	

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 13296 atoms, of which 6468 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 Outer membrane protein assembly factor BamA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	496	7625	2488	3688	659	775	15	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	ALA	-	expression tag	UNP C3TPJ2
A	12	HIS	-	expression tag	UNP C3TPJ2
A	13	HIS	-	expression tag	UNP C3TPJ2
A	14	HIS	-	expression tag	UNP C3TPJ2
A	15	HIS	-	expression tag	UNP C3TPJ2
A	16	HIS	-	expression tag	UNP C3TPJ2
A	17	HIS	-	expression tag	UNP C3TPJ2
A	18	HIS	-	expression tag	UNP C3TPJ2
A	19	HIS	-	expression tag	UNP C3TPJ2
A	20	GLY	-	expression tag	UNP C3TPJ2
A	21	GLY	-	expression tag	UNP C3TPJ2
A	425	CYS	SER	conflict	UNP C3TPJ2

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
2	C	28	396	132	192	30	42	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
3	E	89	1381	441	682	121	135	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
4	D	102	1599	507	787	148	153	4	0	0

- Molecule 5 is a protein called Maltose/maltodextrin-binding periplasmic protein, Serine protease EspP chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
5	P	152	2295	755	1119	200	216	5	0	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	537	ALA	-	expression tag	UNP P0AEX9
P	538	TRP	-	expression tag	UNP P0AEX9
P	539	SER	-	expression tag	UNP P0AEX9
P	540	HIS	-	expression tag	UNP P0AEX9
P	541	PRO	-	expression tag	UNP P0AEX9
P	542	GLN	-	expression tag	UNP P0AEX9
P	543	PHE	-	expression tag	UNP P0AEX9
P	544	GLU	-	expression tag	UNP P0AEX9
P	545	LYS	-	expression tag	UNP P0AEX9
P	546	GLY	-	expression tag	UNP P0AEX9
P	547	GLY	-	expression tag	UNP P0AEX9
P	548	GLY	-	expression tag	UNP P0AEX9
P	549	SER	-	expression tag	UNP P0AEX9
P	550	GLY	-	expression tag	UNP P0AEX9
P	551	GLY	-	expression tag	UNP P0AEX9
P	552	GLY	-	expression tag	UNP P0AEX9
P	553	SER	-	expression tag	UNP P0AEX9
P	554	GLY	-	expression tag	UNP P0AEX9
P	555	GLY	-	expression tag	UNP P0AEX9
P	556	SER	-	expression tag	UNP P0AEX9
P	557	ALA	-	expression tag	UNP P0AEX9
P	558	TRP	-	expression tag	UNP P0AEX9
P	559	SER	-	expression tag	UNP P0AEX9
P	560	HIS	-	expression tag	UNP P0AEX9
P	561	PRO	-	expression tag	UNP P0AEX9
P	562	GLN	-	expression tag	UNP P0AEX9
P	563	PHE	-	expression tag	UNP P0AEX9
P	564	GLU	-	expression tag	UNP P0AEX9
P	565	LYS	-	expression tag	UNP P0AEX9
P	566	GLY	-	expression tag	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
P	567	GLY	-	expression tag	UNP P0AEX9
P	935	ASN	-	linker	UNP P0AEX9
P	936	SER	-	linker	UNP P0AEX9
P	937	GLY	-	linker	UNP P0AEX9
P	938	SER	-	linker	UNP P0AEX9
P	976	GLY	-	insertion	UNP Q7BSW5
P	977	GLU	-	insertion	UNP Q7BSW5
P	978	ASN	-	insertion	UNP Q7BSW5
P	979	LEU	-	insertion	UNP Q7BSW5
P	980	TYR	-	insertion	UNP Q7BSW5
P	981	PHE	-	insertion	UNP Q7BSW5
P	982	GLN	-	insertion	UNP Q7BSW5
P	983	GLY	-	insertion	UNP Q7BSW5
P	984	GLY	-	insertion	UNP Q7BSW5
P	1299	CYS	-	expression tag	UNP Q7BSW5
P	1300	PHE	-	expression tag	UNP Q7BSW5

ALA	PHE	LEU	ASN	GLU	VAL	ASN	ASN	ASN	LYS	ARG	MET	GLY	ASP	ARG	ASP	ILE	ASN	G1037	G1048	THR	GLY	SER	ALA	SER	GLY	GLY	PHE	SER	ASP	ASN	TYR	T1061	H1071	GLU	LEU	ASP	GLY	D1077	T1087	ASP	SER	SER	ALA	SER	ALA	VAL	ASP	VAL	PHE	SER	GLY	GLN	PHE	LYS	LYS	THR	ALA	LYS
SER	V1103	F1113	ASP	SER	G1116	A1117	Y1118	V1126	HIS	HIS	ASP	ASN	GLU	TYR	THR	ALA	THR	PHE	ALA	GLY	LEU	THR	ARG	ASP	TYR	HIS	THR	HIS	SER	W1149	A1153	Y1157	R1158	TYR	HIS	LYS	VAL	THR	E1163	D1164	P1169	E1172	E1172	G1176	SER	VAL	VAL	SER	VAL	GLY	LYS	GLN	PHE	LYS	ALA	TRP		
LYS	ASP	GLN	GLY	MET	HIS	LEU	SER	MET	LYS	ASP	LYS	ASP	TYR	ASN	PRO	L1202	K1212	D1218	Q1230	PHE	ASP	LEU	LEU	ALA	ALA	ASN	GLY	GLU	THR	VAL	LEU	ARG	ASP	ALA	SER	GLY	LYS	ARG	ILE	LYS	GLY	GLU	LYS	ASP	ASP	ARG	M1258	E1267	I1268	R1269	D1270	N1271	Y1272	R1273				
S1281	K1285	V1288	R1297	Y1298	C1299	F1300																																																				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	93735	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, 60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.386	Depositor
Minimum map value	-1.409	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.0962	Depositor
Map size (Å)	257.7168, 257.7168, 257.7168	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07382, 1.07382, 1.07382	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	0.28	0/4032	0.54	0/5458
2	C	0.26	0/209	0.50	0/288
3	E	0.26	0/714	0.52	0/974
4	D	0.28	0/824	0.54	0/1108
5	P	0.26	0/1197	0.53	0/1602
All	All	0.27	0/6976	0.54	0/9430

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	3937	3688	3688	38	0
2	C	204	192	191	0	0
3	E	699	682	682	7	0
4	D	812	787	787	8	0
5	P	1176	1119	1119	16	0
All	All	6828	6468	6467	66	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 5.

All (66) 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)
3:E:71:ASN:ND2	3:E:96:ASN:O	2.20	0.73
1:A:657:SER:N	1:A:803:GLN:OE1	2.21	0.73
1:A:310:LYS:NZ	1:A:380:ASP:OD1	2.24	0.66
4:D:120:ASP:O	4:D:132:ARG:NE	2.26	0.62
1:A:542:GLN:O	1:A:546:TRP:N	2.25	0.62
5:P:1230:GLN:OE1	5:P:1285:LYS:N	2.36	0.58
1:A:657:SER:O	1:A:661:ARG:NE	2.38	0.57
1:A:315:TYR:O	1:A:346:ARG:NH1	2.37	0.57
1:A:596:THR:OG1	1:A:612:THR:OG1	2.22	0.56
5:P:1113:PHE:N	5:P:1117:ALA:O	2.36	0.55
1:A:672:ALA:N	1:A:704:ASP:O	2.38	0.54
1:A:578:TYR:HB3	1:A:593:VAL:HB	1.90	0.53
5:P:1116:GLY:N	5:P:1163:GLU:OE2	2.43	0.52
1:A:396:GLU:N	1:A:419:LYS:O	2.29	0.52
1:A:533:HIS:ND1	1:A:568:ASP:OD1	2.31	0.52
1:A:727:ASP:OD1	1:A:728:LYS:N	2.42	0.51
4:D:131:ASP:OD1	4:D:132:ARG:N	2.44	0.50
1:A:593:VAL:HG13	1:A:615:THR:HG22	1.93	0.50
1:A:758:PRO:HG2	1:A:795:ASP:CG	2.32	0.49
5:P:1164:ASP:OD2	5:P:1212:LYS:NZ	2.45	0.49
1:A:512:ASP:OD1	1:A:573:ASN:ND2	2.45	0.48
1:A:356:GLY:N	4:D:136:ASP:OD2	2.42	0.48
1:A:366:ARG:NH1	4:D:185:TYR:OH	2.46	0.48
5:P:1118:TYR:H	5:P:1158:ARG:HB3	1.80	0.47
1:A:368:GLU:OE1	1:A:388:ARG:NE	2.32	0.46
5:P:1267:GLU:HG2	5:P:1273:ARG:HD2	1.98	0.46
3:E:31:ASP:OD1	3:E:82:GLY:N	2.36	0.46
5:P:1153:ALA:O	5:P:1172:GLU:HB2	2.16	0.46
3:E:88:GLN:NE2	4:D:225:MET:SD	2.88	0.46
4:D:210:ALA:HA	4:D:213:ASP:HB2	1.97	0.46
1:A:776:TRP:CD1	1:A:783:LEU:O	2.69	0.46
1:A:396:GLU:HB3	1:A:419:LYS:HG2	1.98	0.45
1:A:464:ASP:OD1	1:A:465:TYR:N	2.49	0.45
1:A:504:TYR:HB3	1:A:539:MET:HA	1.99	0.44
5:P:1268:ILE:O	5:P:1273:ARG:NH1	2.51	0.44
5:P:1157:TYR:O	5:P:1169:PRO:HD2	2.18	0.44
5:P:1270:ASP:O	5:P:1273:ARG:NH1	2.32	0.44
1:A:809:THR:O	1:A:810:TRP:HB2	2.18	0.43
4:D:137:PRO:HD3	4:D:177:TYR:CE1	2.52	0.43
1:A:663:PHE:O	1:A:803:GLN:NE2	2.52	0.43
1:A:689:GLU:O	1:A:696:ALA:O	2.36	0.43
1:A:794:TYR:N	1:A:797:ASP:OD2	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:36:ASN:N	3:E:76:VAL:O	2.49	0.43
1:A:367:ARG:HD3	1:A:477:TYR:CZ	2.53	0.43
3:E:29:ARG:O	3:E:82:GLY:HA3	2.19	0.43
1:A:548:TYR:CZ	1:A:647:PRO:HA	2.54	0.42
1:A:629:VAL:HA	1:A:717:GLU:O	2.19	0.42
1:A:309:LYS:HG2	1:A:320:PRO:HG2	2.00	0.42
1:A:722:THR:N	1:A:723:PRO:CD	2.82	0.42
5:P:1271:ASN:ND2	5:P:1299:CYS:O	2.44	0.42
3:E:52:GLN:HG3	3:E:99:GLY:O	2.19	0.42
1:A:670:PRO:HD2	1:A:707:GLY:O	2.19	0.42
5:P:1271:ASN:HB3	5:P:1299:CYS:H	1.84	0.42
1:A:477:TYR:CD2	1:A:482:GLY:HA2	2.55	0.42
5:P:1218:ASP:OD1	5:P:1269:ARG:NE	2.43	0.42
1:A:514:THR:HA	1:A:528:GLY:HA3	2.02	0.42
5:P:1230:GLN:OE1	5:P:1285:LYS:HG2	2.20	0.42
1:A:396:GLU:OE1	1:A:421:ARG:HB3	2.20	0.41
3:E:62:PRO:HG3	3:E:75:TYR:OH	2.20	0.41
4:D:191:TRP:HH2	4:D:225:MET:SD	2.44	0.41
1:A:541:PRO:HD3	1:A:561:GLN:HA	2.01	0.41
1:A:494:PHE:O	1:A:505:THR:HA	2.21	0.41
1:A:531:TYR:HB3	1:A:570:PHE:CD2	2.55	0.41
5:P:1272:VAL:HA	5:P:1297:ARG:O	2.21	0.40
1:A:545:MET:SD	1:A:648:PHE:HB2	2.60	0.40
5:P:1281:SER:OG	5:P:1288:VAL:N	2.49	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	480/800 (60%)	470 (98%)	10 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	24/320 (8%)	24 (100%)	0	0	100	100
3	E	87/94 (93%)	87 (100%)	0	0	100	100
4	D	94/226 (42%)	94 (100%)	0	0	100	100
5	P	134/764 (18%)	133 (99%)	1 (1%)	0	100	100
All	All	819/2204 (37%)	808 (99%)	11 (1%)	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	A	419/680 (62%)	418 (100%)	1 (0%)	93	96
2	C	20/258 (8%)	20 (100%)	0	100	100
3	E	78/82 (95%)	78 (100%)	0	100	100
4	D	82/190 (43%)	81 (99%)	1 (1%)	71	84
5	P	113/604 (19%)	113 (100%)	0	100	100
All	All	712/1814 (39%)	710 (100%)	2 (0%)	92	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	711	MET
4	D	173	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides 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.

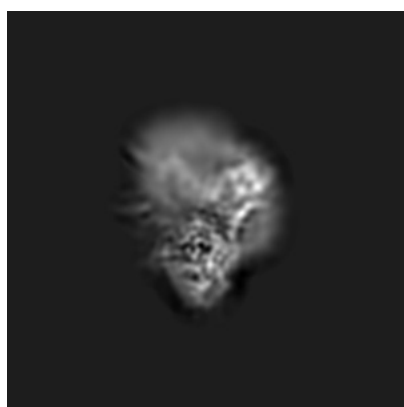
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26113. These allow visual inspection of the internal detail of the map and identification of artifacts.

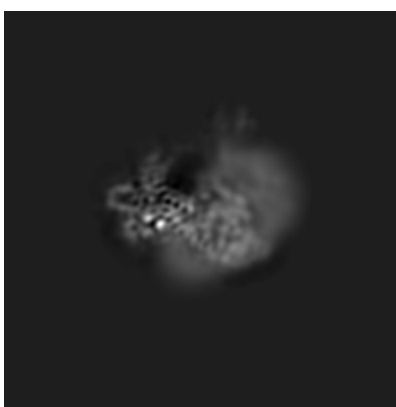
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

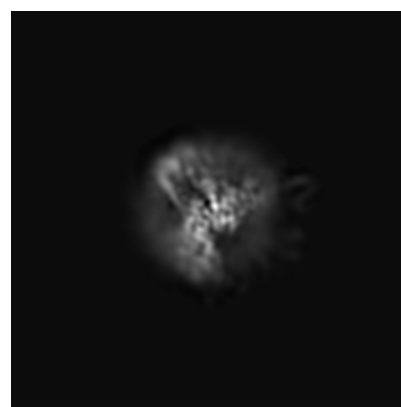
6.1.1 Primary map



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: 111



Y Index: 122

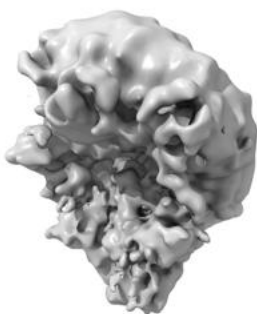


Z Index: 93

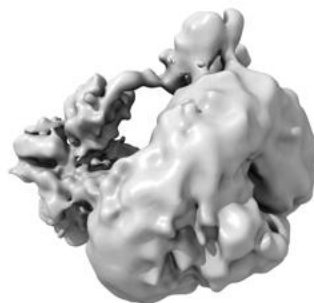
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0962. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

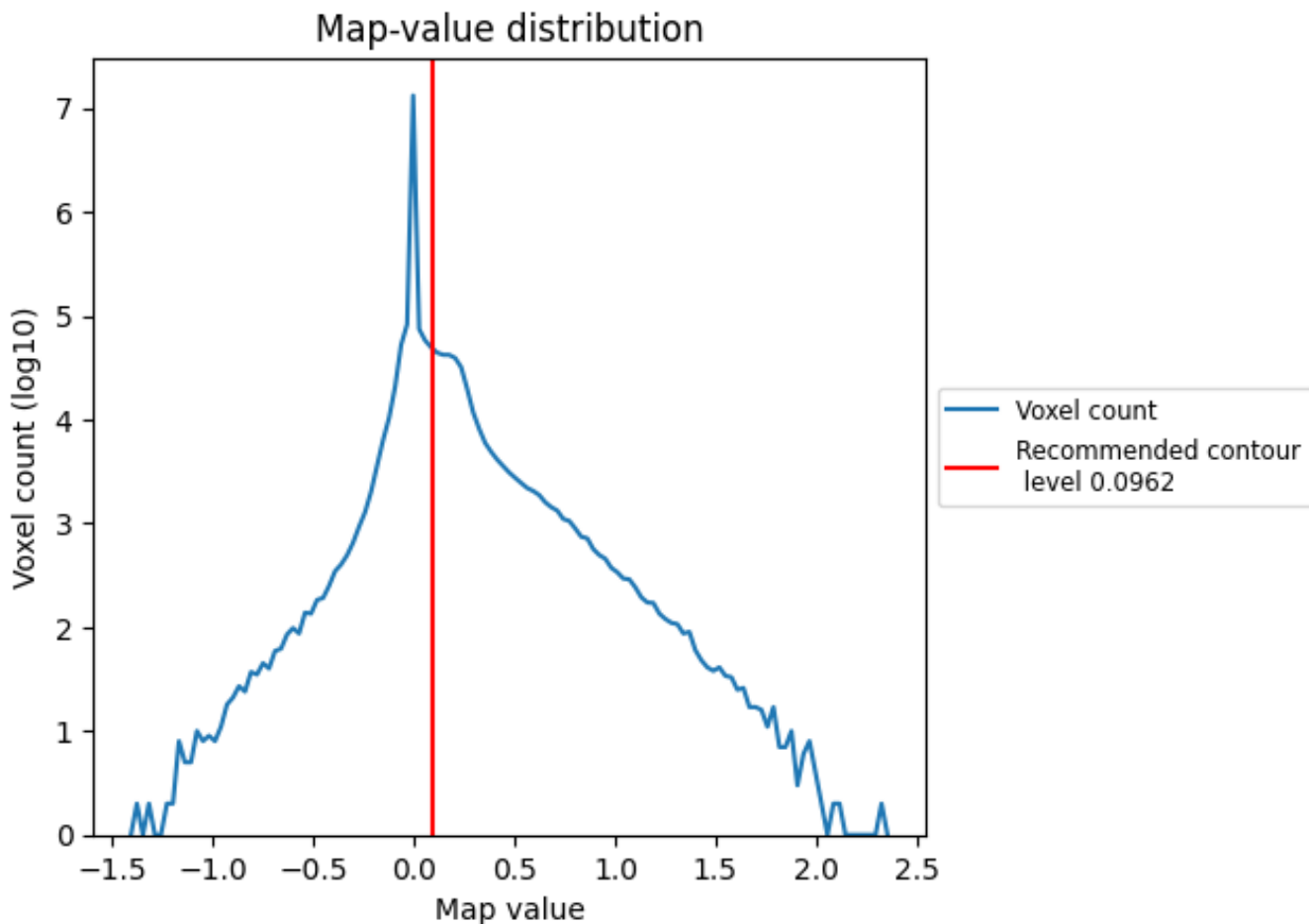
6.5 Mask visualisation

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

7 Map analysis [i](#)

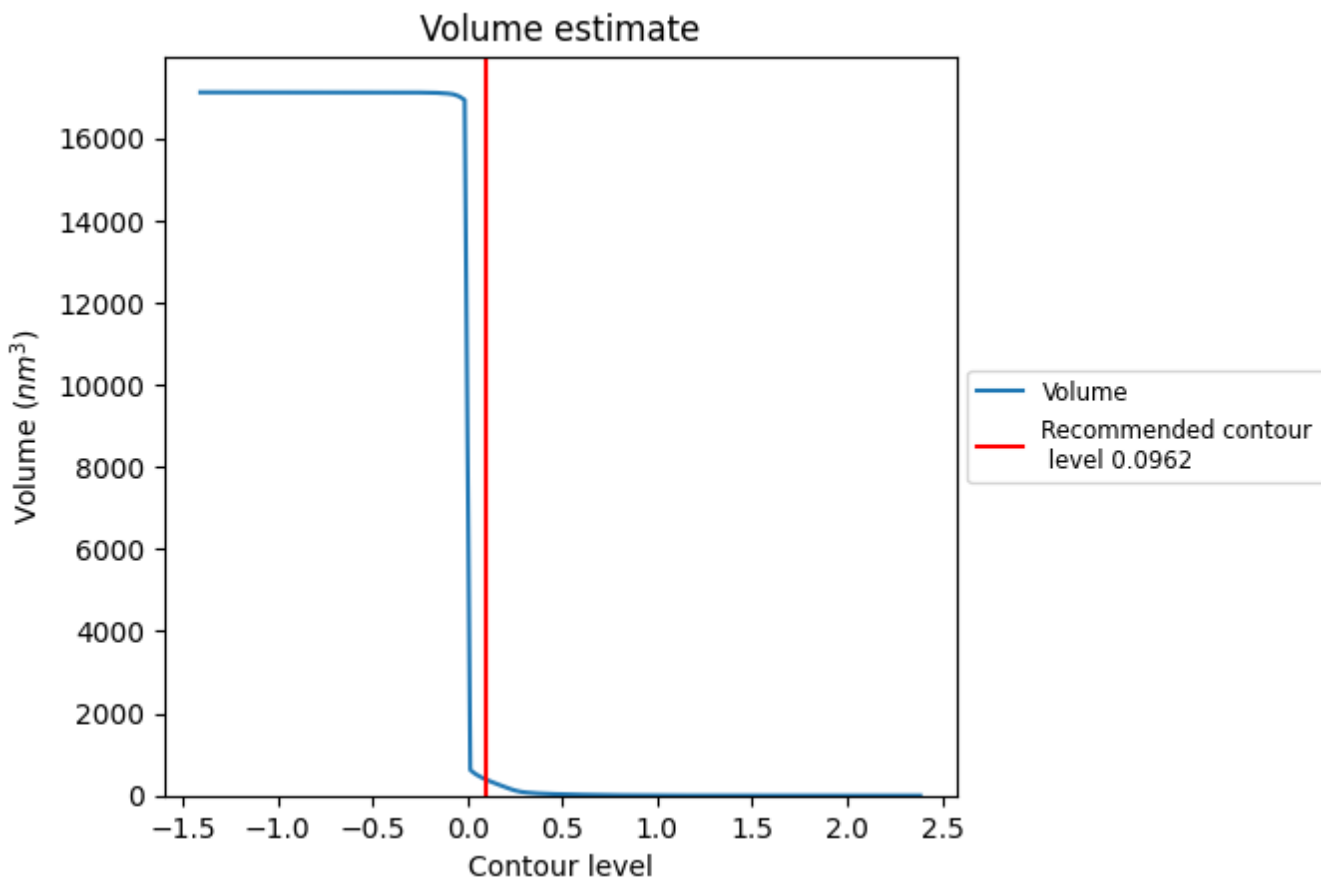
This section contains the results of statistical analysis of the map.

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.

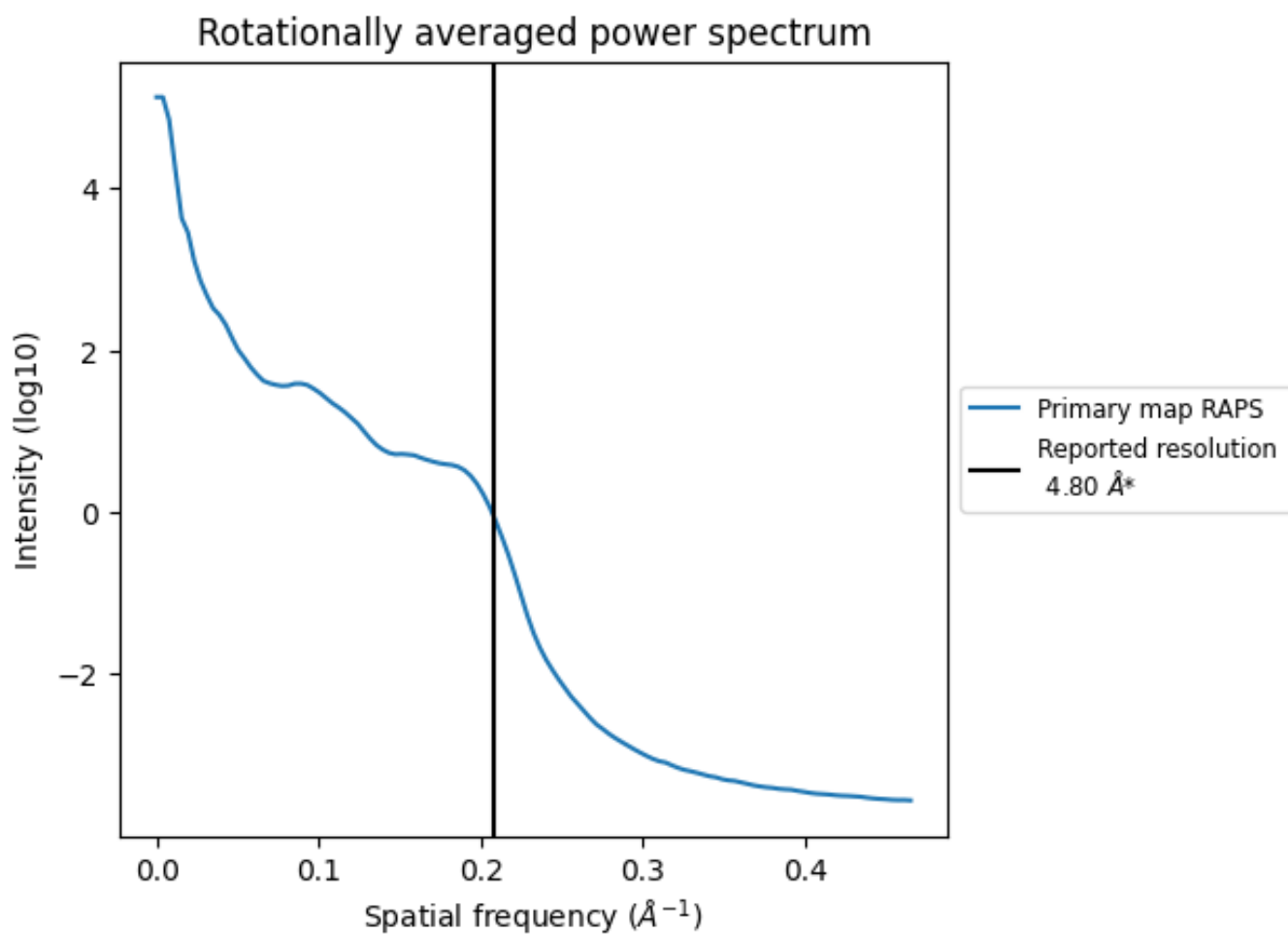
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 391 nm³; this corresponds to an approximate mass of 353 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 [i](#)

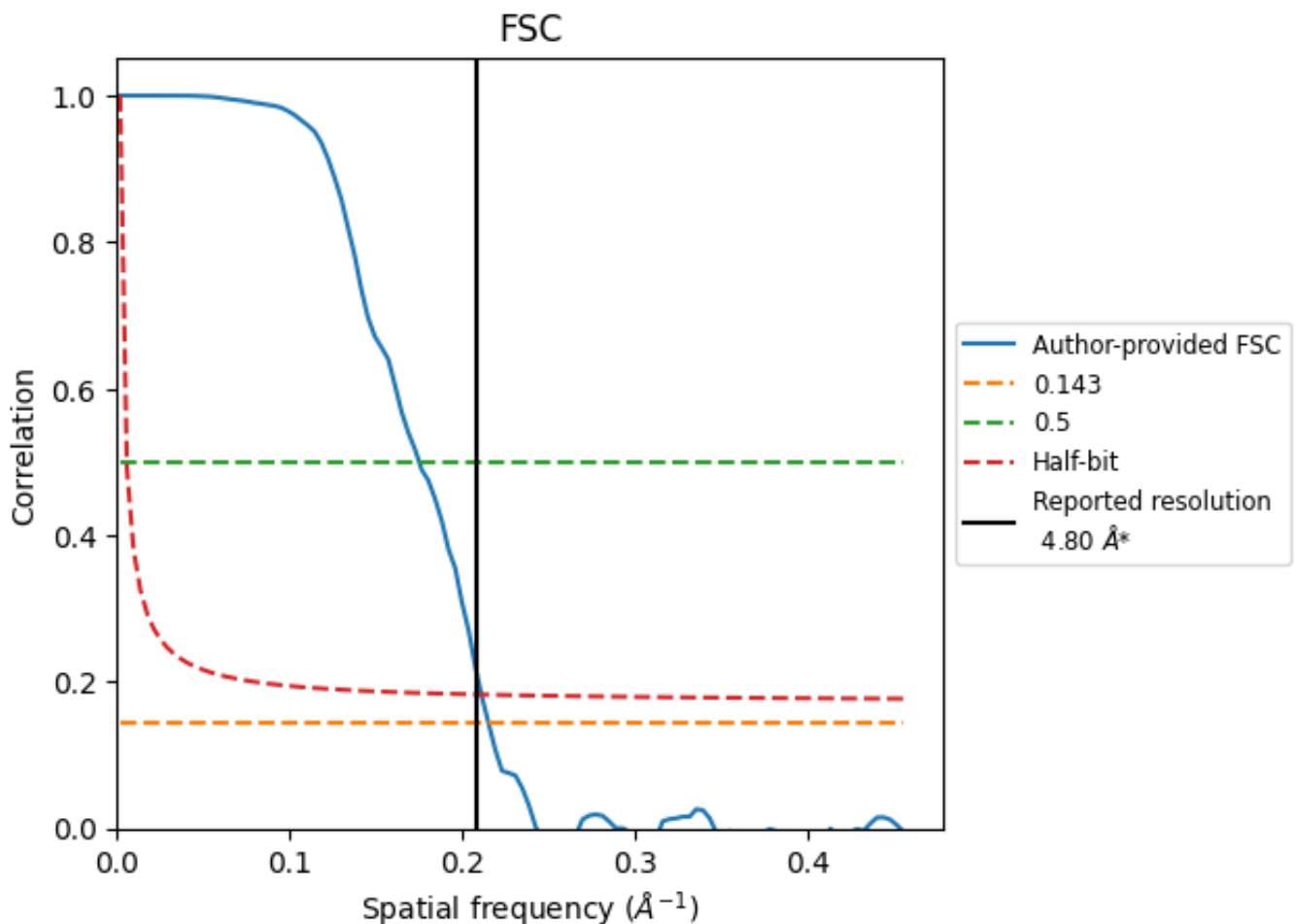


*Reported resolution corresponds to spatial frequency of 0.208\AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

8.2 Resolution estimates [i](#)

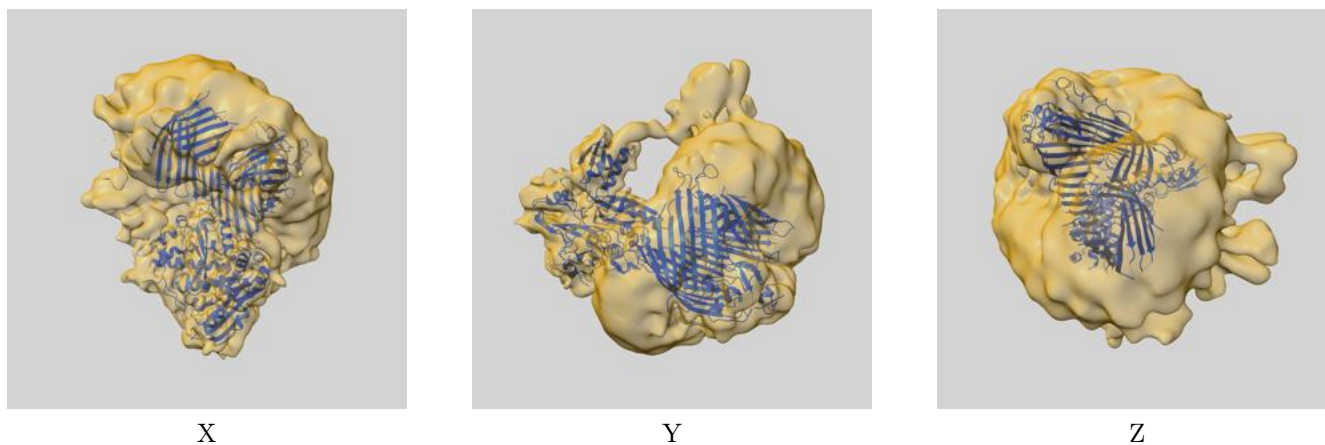
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.80	-	-
Author-provided FSC curve	4.64	5.71	4.74
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

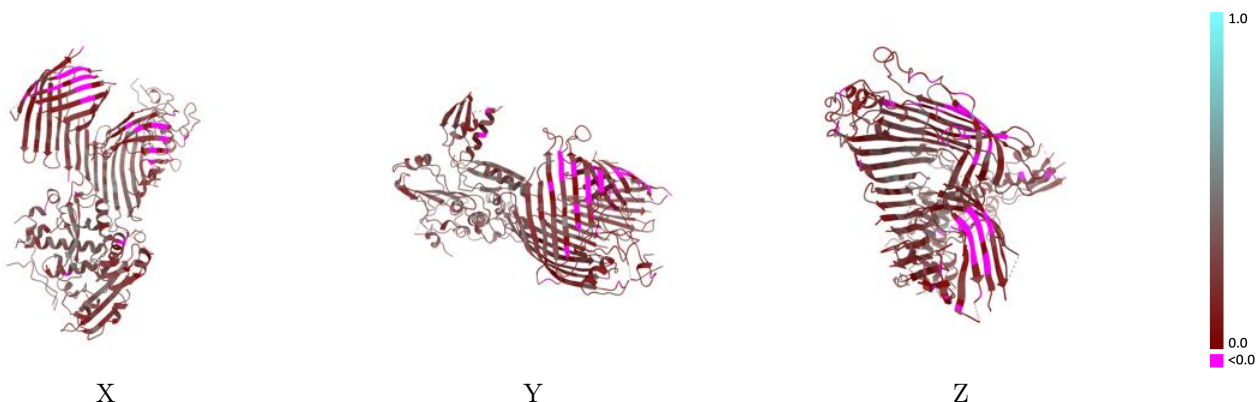
This section contains information regarding the fit between EMDB map EMD-26113 and PDB model 7TT7. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



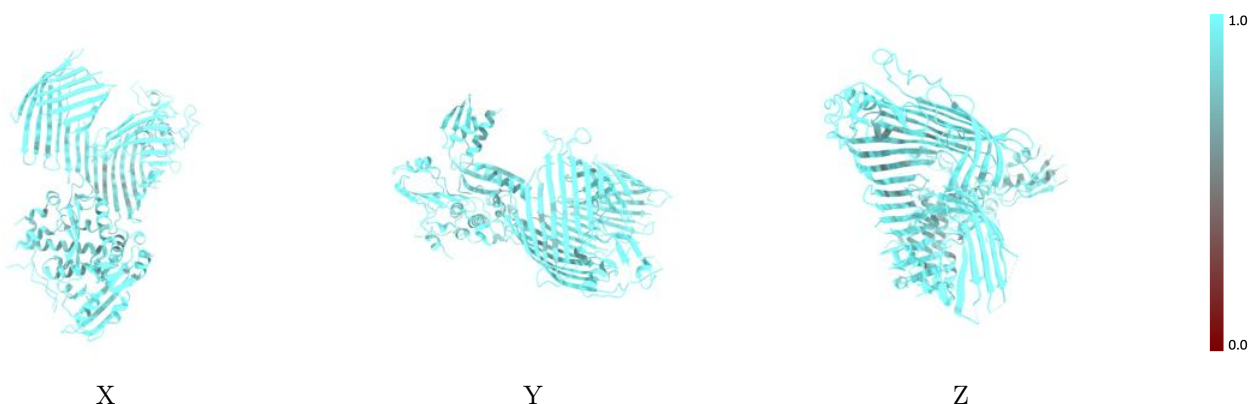
The images above show the 3D surface view of the map at the recommended contour level 0.0962 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



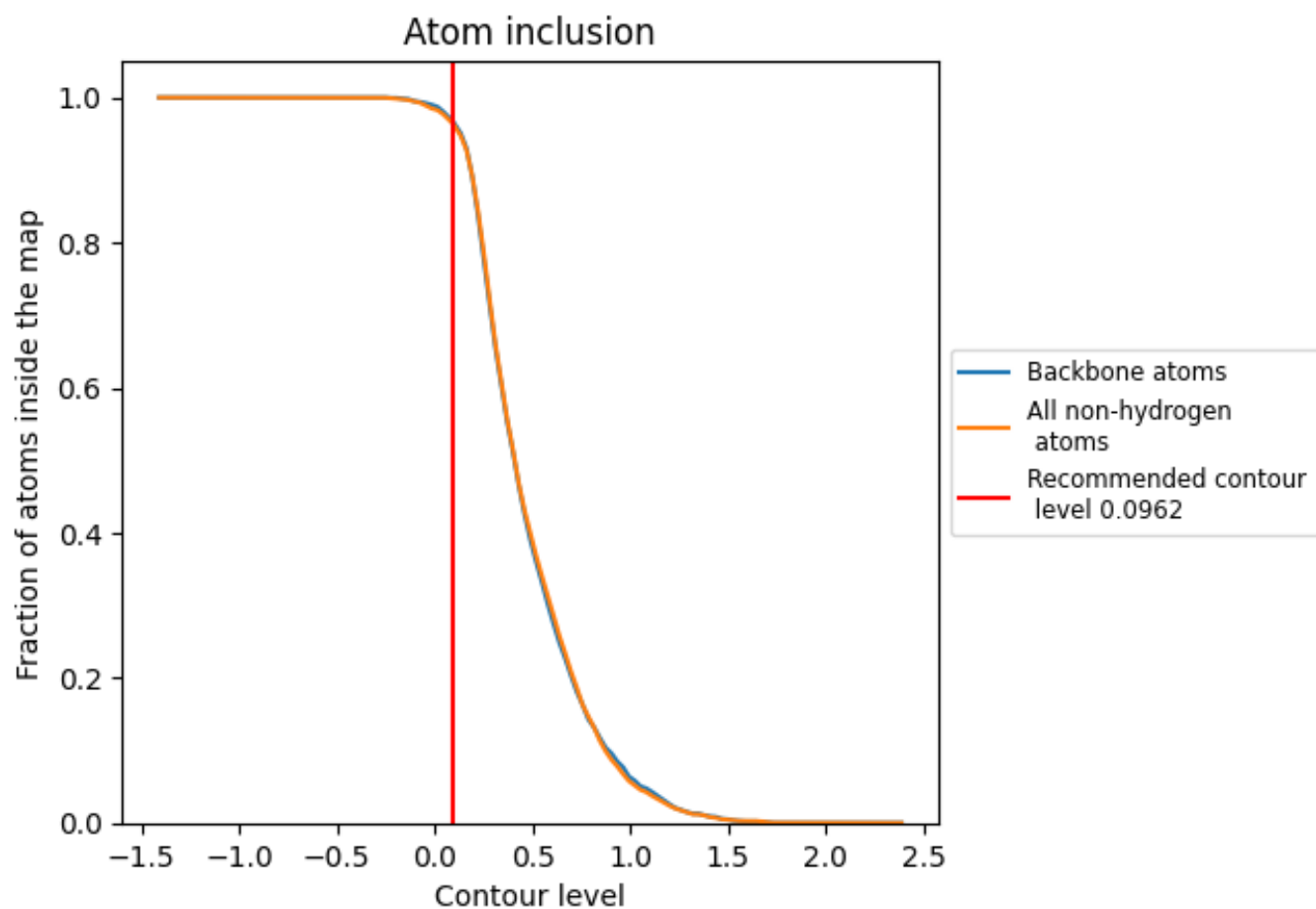
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0962).













9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% 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 (0.0962) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9629	 0.2150
A	 0.9532	 0.2200
C	 0.9653	 0.3160
D	 0.9490	 0.2570
E	 0.9679	 0.2750
P	 0.9869	 0.1200

