



Full wwPDB EM Validation Report ⓘ

May 13, 2025 – 02:55 AM EDT

PDB ID : 7TT0 / pdb_00007tt0
EMDB ID : EMD-26106
Title : BamABCDE bound to substrate EspP class 2
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 : 4.30 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.43.1

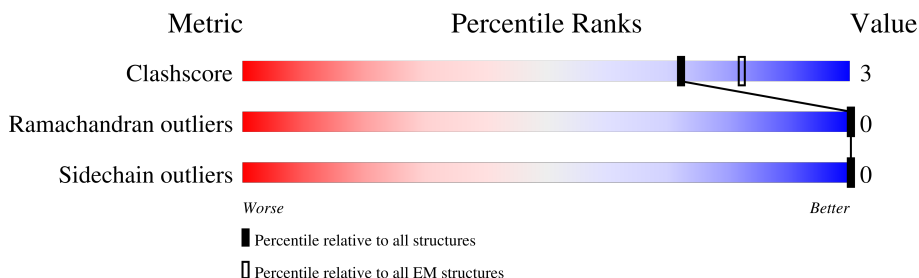
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 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	A	800	
2	E	94	
3	D	226	
4	C	320	
5	P	764	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14884 atoms, of which 7253 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
1	A	588	Total	C	H	N	O	S	0	0
			9052	2951	4381	781	924	15		

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 BamE.

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
3	D	213	Total	C	H	N	O	S	0	0
			3390	1086	1668	303	326	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	C	48	Total	C	H	N	O	S	0	0
			675	216	336	55	67	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	P	24	Total	C	H	N	O	S	0	0
			386	126	186	37	36	1		

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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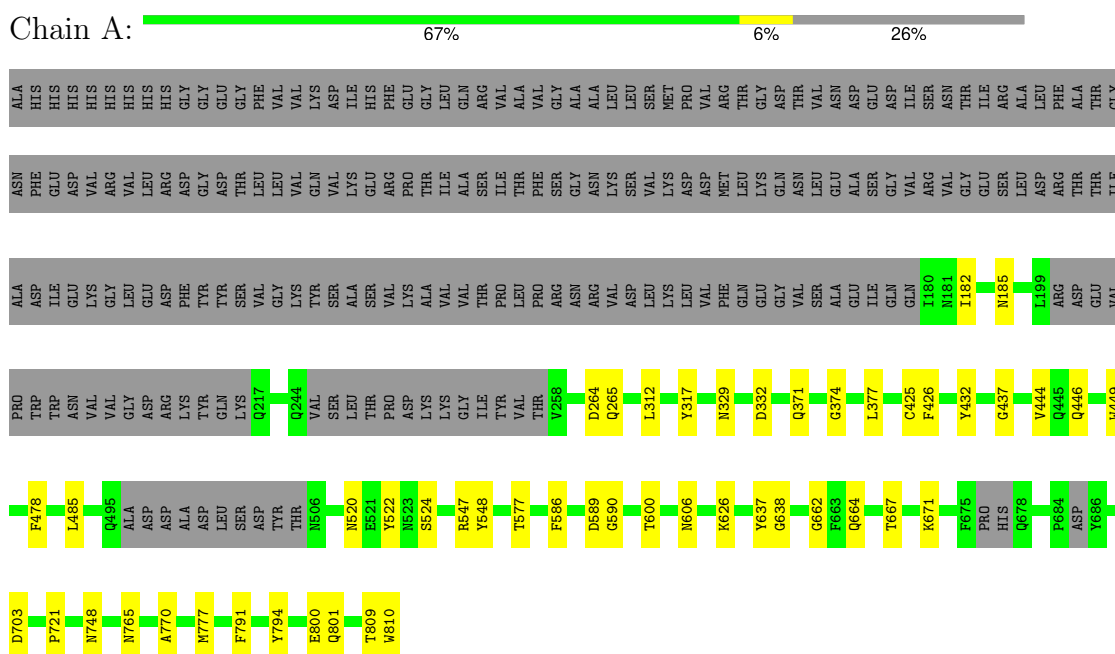
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Chain	Residue	Modelled	Actual	Comment	Reference
P	567	GLY	-	expression tag	UNP P0AEX9
P	935	ASN	-	linker	UNP P0AEX9
P	936	SER	-	linker	UNP P0AEX9
P	937	GLY	-	linker	UNP P0AEX9
P	938	SER	-	linker	UNP P0AEX9
P	976	GLY	-	insertion	UNP Q7BSW5
P	977	GLU	-	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

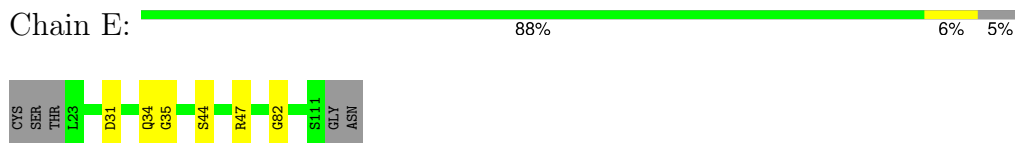
3 Residue-property plots [i](#)

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.

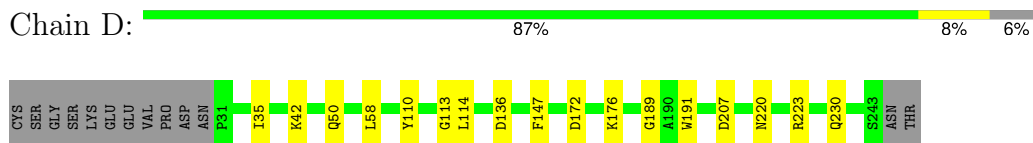
- Molecule 1: Outer membrane protein assembly factor BamA



- Molecule 2: Outer membrane protein assembly factor BamE



- Molecule 3: Outer membrane protein assembly factor BamD



- Molecule 4: Outer membrane protein assembly factor BamC

Tyr	Lys	Val	Ala	Gln	Val	Cys
	Leu	Val	Ala	Gly	Leu	Ser
	Gln	Gly	Lys	Lys	Gln	Ser
	Val	Pro	Pro	Val	Ala	Asp
	Gly	Phe	Val	Val	Asn	Ser
	Asp	Asn	Ala	Tyr	Tyr	Arg
	Leu	Val	Asp	Asp	Thr	Lys
	Asn	Val	Ala	Ala	Thr	Arg
	Asp	Trp	Trp	Ala	Thr	Gln
	Arg	Gln	Ser	Ser	Gln	Val
Ser	Leu	Met	Gln	Arg	Ser	
Ser	Leu	Gln	Met	Asp	Gly	
Leu	Pro	Arg	Arg	Asp	D38	
Gln	Leu	Ala	Tyr	Ala	E39	
Phe	Ala	Ser	Ser	Gly		
Leu	Leu	Thr	Thr	Gln	A43	
Asp	Glu	Glu	Glu	Thr		
Pro	Lys	Met	Met	Leu	A75	
Lys	Gly	Met	Met	Thr		
His	Gly	Val	Val	Asp	L80	
Thr	Thr	Lys	Ile	Trp		
Leu	Val	Val	Ser	Val	P85	
Thr	Thr	Asp	Ala	Gln	Ala	
Gln	Asp	Thr	Gly	Trp	Gln	
Ser	Ser	Ser	Leu	Trp	Pro	
Asn	Asn	Arg	Lys	Arg	Leu	
Asp	Ser	Ser	Ser	Asp	Leu	
Ala	Gln	Ala	Ala	Glu	Val	
Val	Val	Met	Ala	Gln	Ser	
Phe	Val	Ala	Ala	Tyr	Gly	
Gln	Thr	Val	Ala	Arg	Ala	
Ala	Lys	Gln	Gln	Tyr	Arg	
Phe	Pro	Asn	Asn	Gln	Thr	
Ser	Leu	Arg	Ala	Ile	Ala	
Ser	Ser	Ser	Ala	Ser	Thr	
Lys	Asp	Asp	Thr	Val	Ala	
	Ser	Ser	Ser	Lys	Ser	
	Asp	Asp	Thr	Pro	Leu	
	Trp	Met	Gln	Gln	Leu	
	Gln	Asp	Gly	Gly	Val	
	Glu	Val	Tyr	Tyr	Glu	
	Leu	Gln	Gln	Gly	Asn	
	Gly	Ser	Gln	Gly	Asn	
	Ala	Ala	Ala	Val	Arg	
	Ser	Ser	Ala	Val	Gly	
	Asp	Asp	Asp	Thr	Ala	
	Pro	Asp	Asp	Val	Asn	
	Gly	Thr	Thr	Val	Thr	
	Leu	Lys	Lys	Val	Leu	
	Leu	Gly	Gly	Leu	Trp	
	Ala	Ala	Leu	Leu	Pro	
	Ser	Ser	Pro	Asn	Gln	
	Gly	Met	Ile	Leu	Val	
	Asp	Thr	Thr	Glu	Val	
	Ser	Thr	Thr	Thr	Ser	

- Chain P:  97%

[illegible]

ARG	MET	LEU	MET	SER	VAL	GLY	Y1264	N1271	E1277	PHE	GLU	LYS	SER	ALA	PHE	GLY	LYS	TYR	ASN	VAL	ASP	ASN	A1291	Y1298	C1299	F1300
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	171948	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	2.677	Depositor
Minimum map value	-2.208	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.056	Depositor
Recommended contour level	0.112	Depositor
Map size (\AA)	257.7168, 257.7168, 257.7168	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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	0.22	0/4785	0.57	0/6482
2	E	0.20	0/714	0.52	0/974
3	D	0.26	0/1761	0.59	0/2390
4	C	0.16	0/347	0.47	0/477
5	P	0.18	0/202	0.48	0/268
All	All	0.23	0/7809	0.57	0/10591

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	4671	4381	4381	30	0
2	E	699	682	682	5	0
3	D	1722	1668	1668	11	0
4	C	339	336	336	3	0
5	P	200	186	186	4	0
All	All	7631	7253	7253	47	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 3.

All (47) 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:D:220:ASN:OD1	3:D:223:ARG:NH2	2.15	0.79
1:A:547:ARG:NH1	1:A:748:ASN:O	2.15	0.79
3:D:172:ASP:OD2	3:D:176:LYS:NZ	2.18	0.76
2:E:34:GLN:NE2	3:D:189:GLY:O	2.31	0.62
1:A:548:TYR:OH	1:A:606:ASN:OD1	2.21	0.58
2:E:31:ASP:OD1	2:E:82:GLY:N	2.32	0.58
1:A:329:ASN:O	1:A:332:ASP:O	2.23	0.56
3:D:230:GLN:N	3:D:230:GLN:OE1	2.39	0.56
2:E:44:SER:O	2:E:47:ARG:NH1	2.40	0.54
1:A:182:ILE:HG22	1:A:185:ASN:OD1	2.08	0.54
2:E:34:GLN:OE1	3:D:191:TRP:N	2.43	0.51
3:D:207:ASP:OD1	4:C:48:ALA:N	2.44	0.51
4:C:38:ASP:OD1	4:C:39:GLU:N	2.36	0.49
1:A:664:GLN:HB2	1:A:667:THR:HG21	1.94	0.49
1:A:374:GLY:O	2:E:35:GLY:N	2.42	0.48
1:A:426:PHE:HB3	1:A:444:VAL:HG23	1.96	0.48
1:A:312:LEU:HB3	1:A:317:TYR:HB2	1.97	0.47
1:A:586:PHE:CZ	1:A:777:MET:HG2	2.49	0.46
1:A:765:ASN:HA	1:A:794:TYR:CZ	2.50	0.46
1:A:425:CYS:HA	5:P:1298:TYR:O	2.15	0.46
1:A:589:ASP:OD1	1:A:590:GLY:N	2.42	0.46
1:A:637:TYR:CG	1:A:638:GLY:N	2.84	0.45
1:A:520:ASN:OD1	1:A:522:TYR:N	2.46	0.45
4:C:75:ALA:O	4:C:80:LEU:HD21	2.17	0.44
3:D:136:ASP:C	3:D:136:ASP:OD1	2.60	0.44
1:A:662:GLY:HA2	1:A:800:GLU:O	2.18	0.44
1:A:770:ALA:HB3	1:A:791:PHE:HE1	1.83	0.44
1:A:478:PHE:CG	1:A:485:LEU:HD13	2.53	0.43
1:A:524:SER:OG	1:A:577:THR:OG1	2.36	0.43
1:A:426:PHE:CB	1:A:444:VAL:HA	2.49	0.42
5:P:1271:ASN:HB3	5:P:1299:CYS:SG	2.59	0.42
1:A:371:GLN:NE2	1:A:377:LEU:HA	2.34	0.42
3:D:42:LYS:NZ	3:D:50:GLN:OE1	2.42	0.42
1:A:425:CYS:HA	5:P:1299:CYS:HA	2.02	0.42
1:A:432:TYR:HA	1:A:437:GLY:O	2.19	0.42
1:A:809:THR:O	1:A:810:TRP:HB2	2.20	0.42
1:A:446:GLN:HG2	1:A:449:TRP:HA	2.02	0.41
3:D:110:TYR:CE2	3:D:114:LEU:HD11	2.55	0.41
1:A:371:GLN:HA	1:A:371:GLN:OE1	2.19	0.41
3:D:113:GLY:HA3	3:D:147:PHE:CZ	2.56	0.41
5:P:1271:ASN:HB3	5:P:1299:CYS:HB2	2.02	0.41
1:A:626:LYS:HB3	1:A:721:PRO:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:600:THR:HG21	1:A:606:ASN:O	2.21	0.40
1:A:264:ASP:OD1	1:A:265:GLN:N	2.49	0.40
3:D:35:ILE:HG21	3:D:58:LEU:HG	2.04	0.40
1:A:801:GLN:OE1	1:A:801:GLN:N	2.55	0.40
1:A:671:LYS:HG2	1:A:703:ASP:HA	2.03	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	576/800 (72%)	569 (99%)	7 (1%)	0	100	100
2	E	87/94 (93%)	87 (100%)	0	0	100	100
3	D	211/226 (93%)	209 (99%)	2 (1%)	0	100	100
4	C	46/320 (14%)	46 (100%)	0	0	100	100
5	P	20/764 (3%)	18 (90%)	2 (10%)	0	100	100
All	All	940/2204 (43%)	929 (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	498/680 (73%)	498 (100%)	0	100	100
2	E	78/82 (95%)	78 (100%)	0	100	100
3	D	178/190 (94%)	178 (100%)	0	100	100
4	C	34/258 (13%)	34 (100%)	0	100	100
5	P	20/604 (3%)	20 (100%)	0	100	100
All	All	808/1814 (44%)	808 (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 (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	411	GLN
1	A	534	ASN
1	A	561	GLN
3	D	69	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 ⓘ

There are no chain breaks in this entry.

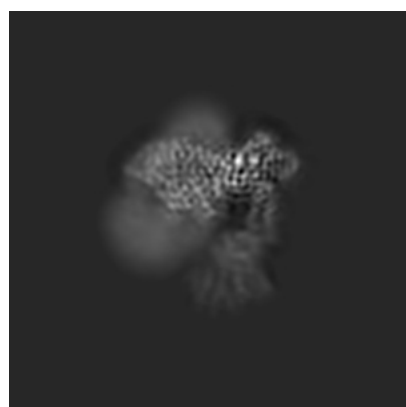
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26106. These allow visual inspection of the internal detail of the map and identification of artifacts.

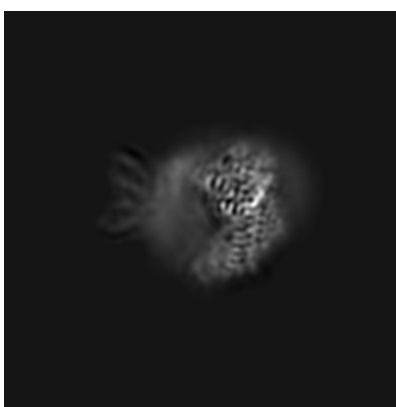
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

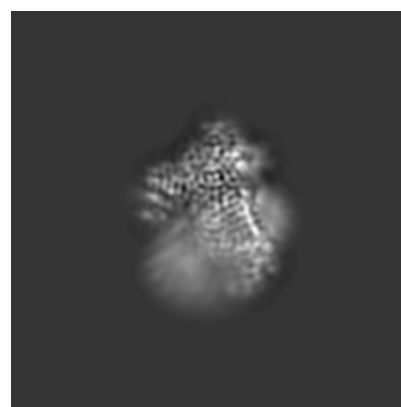
6.1.1 Primary map



X



Y



Z

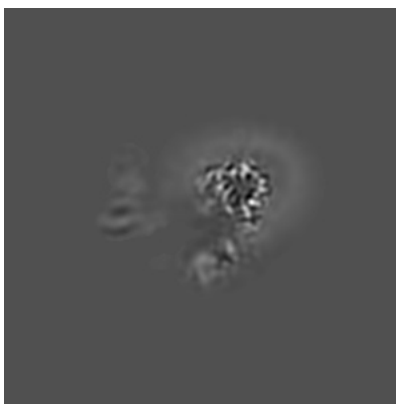
The images above show the map projected in three orthogonal directions.

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](#)

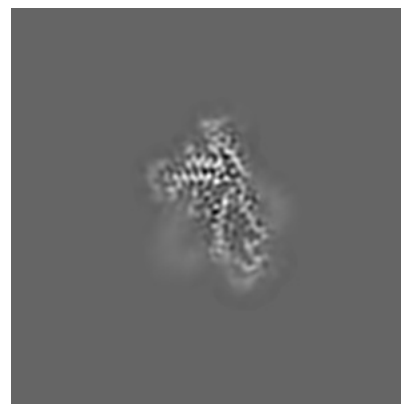
6.3.1 Primary map



X Index: 123



Y Index: 137

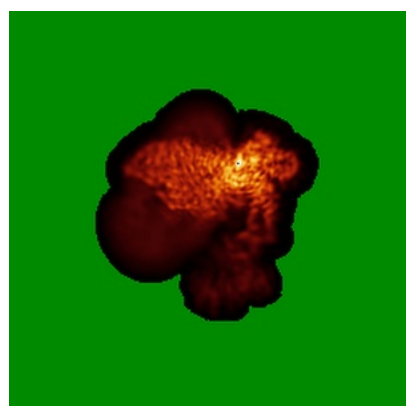


Z Index: 150

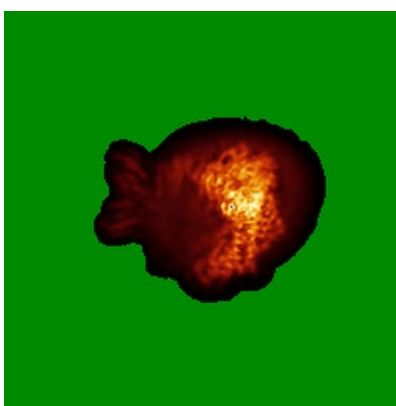
The images above show the largest variance slices of the map in three orthogonal directions.

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

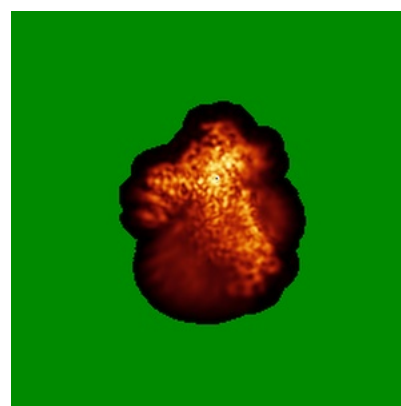
6.4.1 Primary map



X



Y

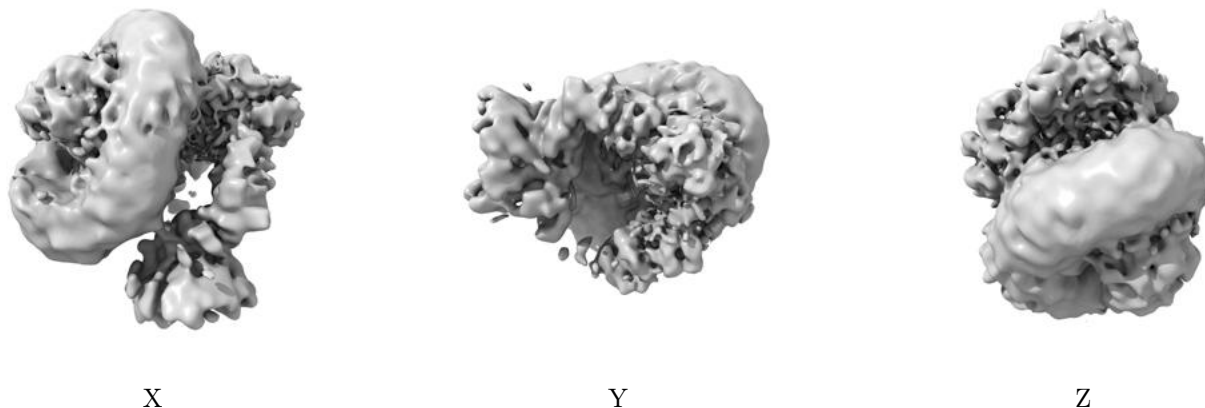


Z

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

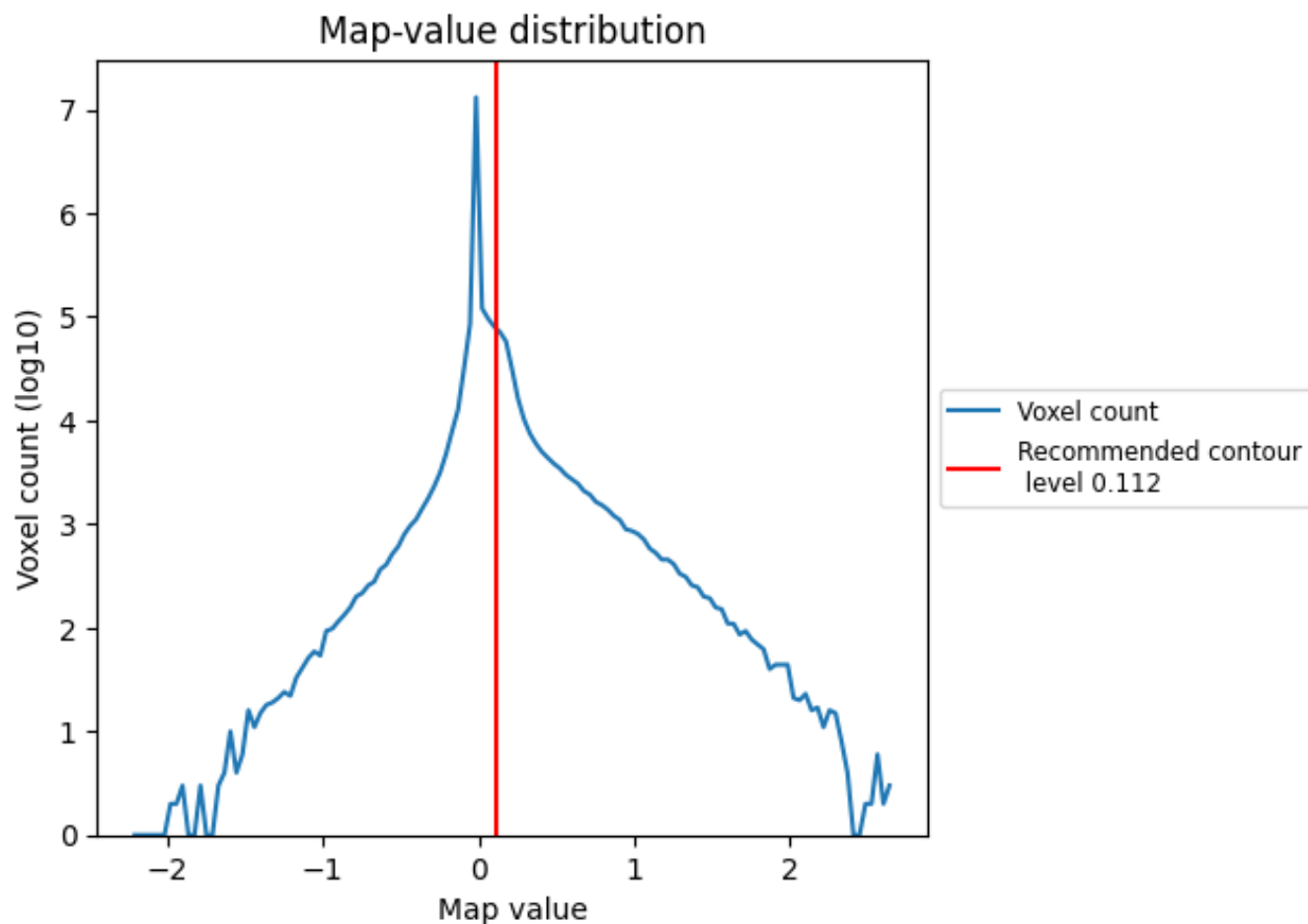
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

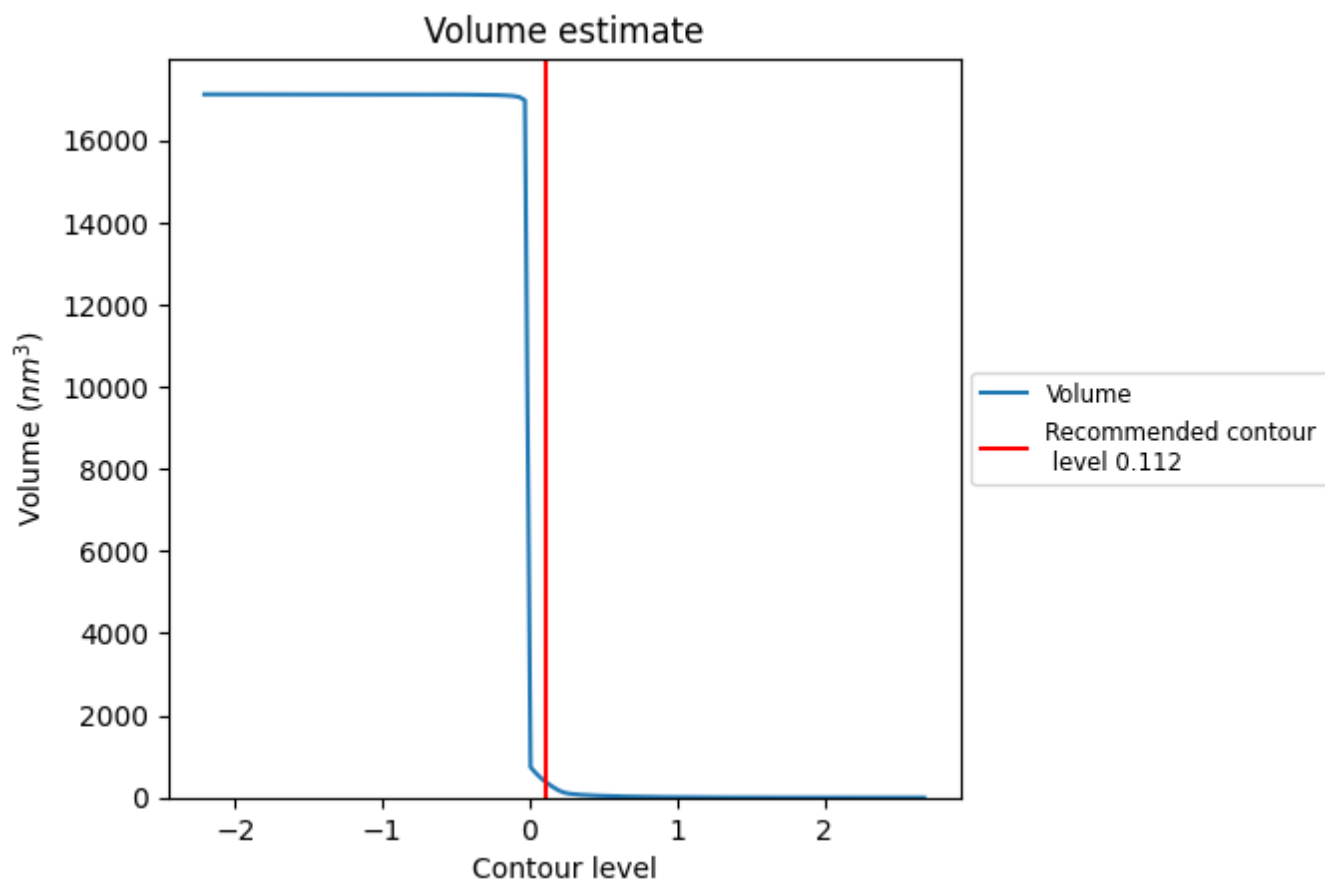
This section contains the results of statistical analysis of the map.

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.

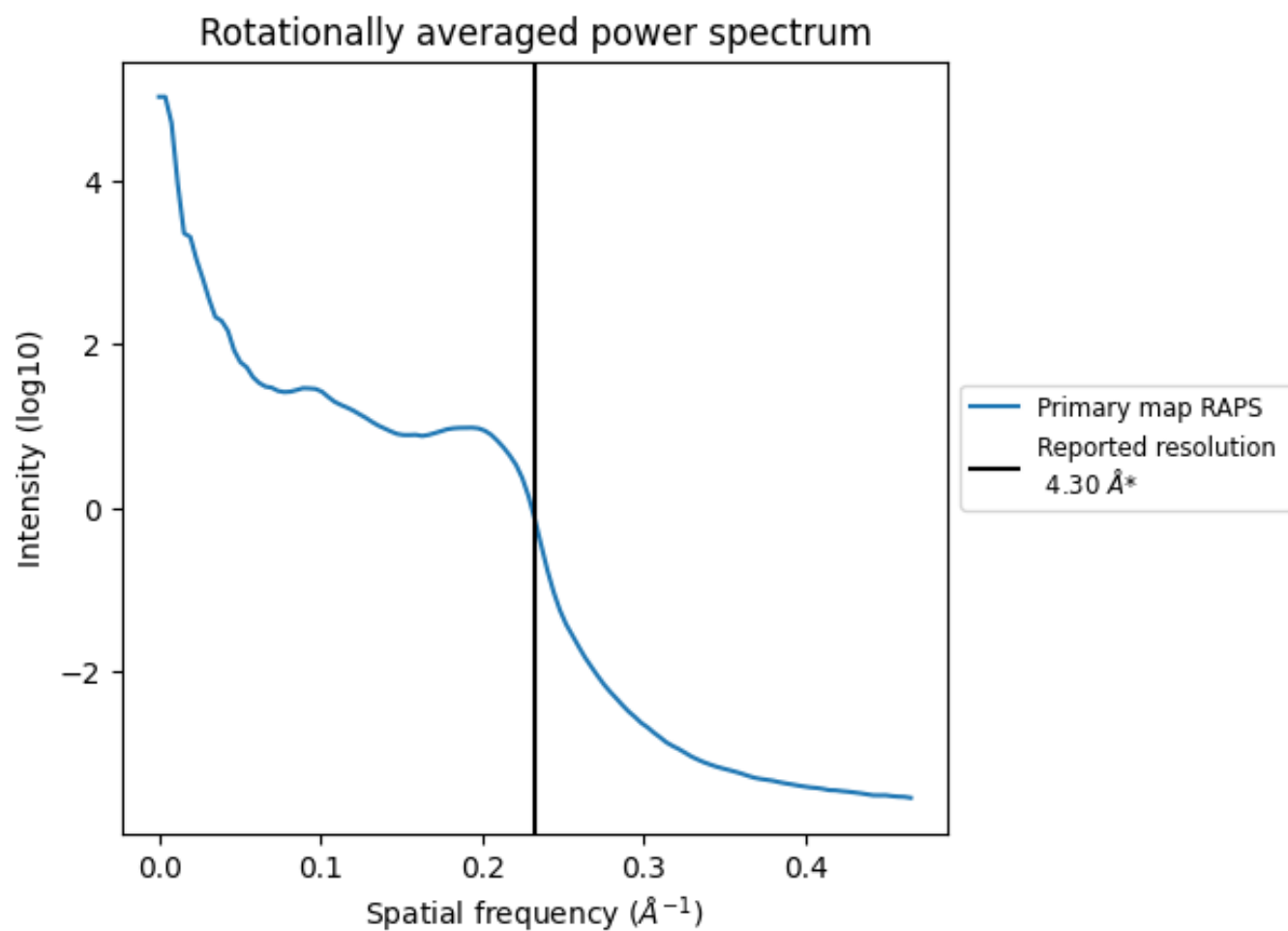
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 370 nm³; this corresponds to an approximate mass of 334 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 ⓘ

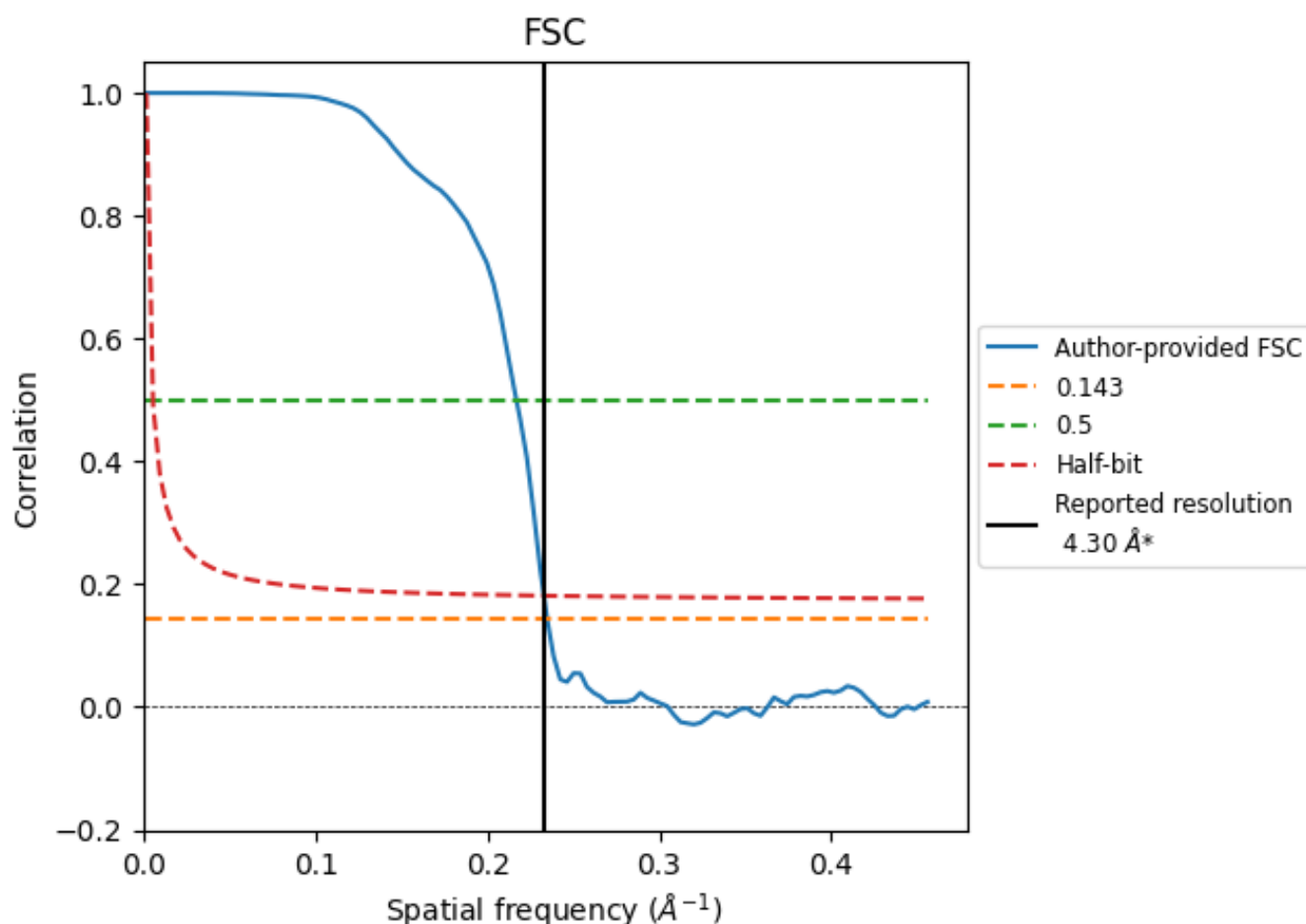


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

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 0.233 Å⁻¹

8.2 Resolution estimates [i](#)

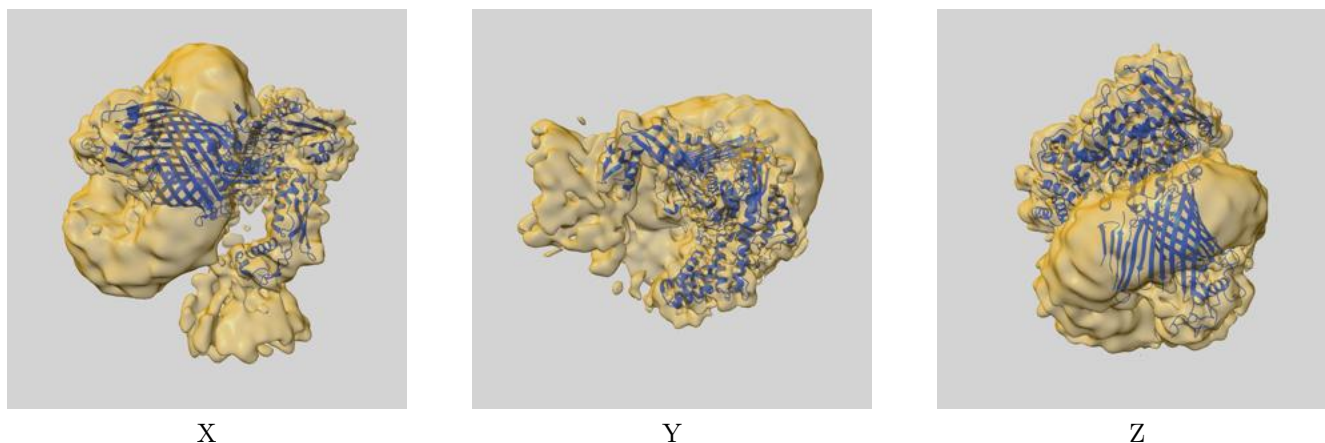
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.26	4.61	4.29
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

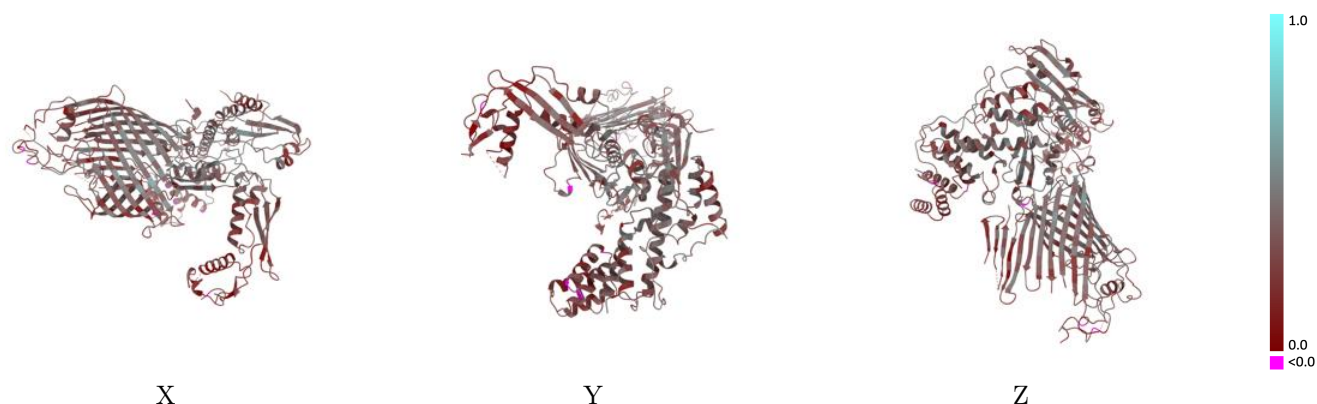
This section contains information regarding the fit between EMDB map EMD-26106 and PDB model 7TT0. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



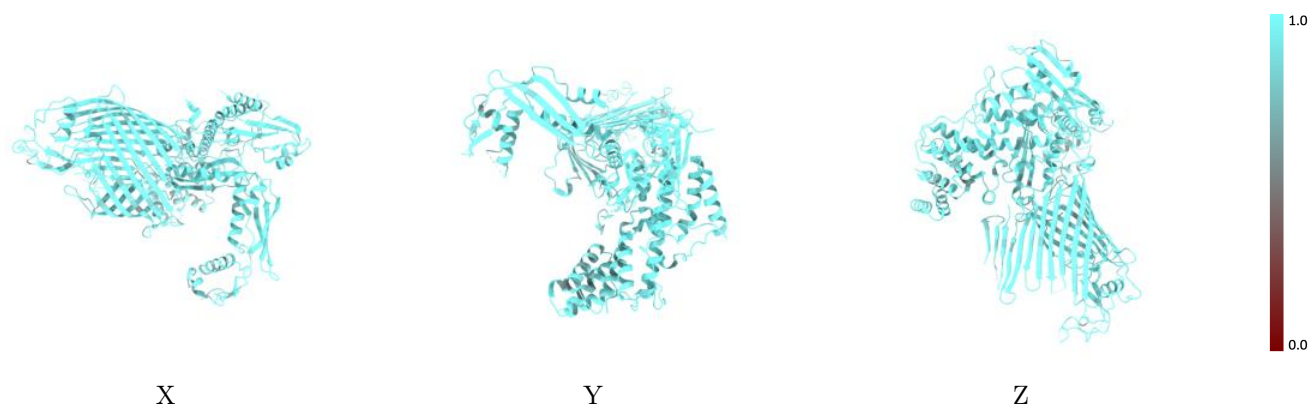
The images above show the 3D surface view of the map at the recommended contour level 0.112 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



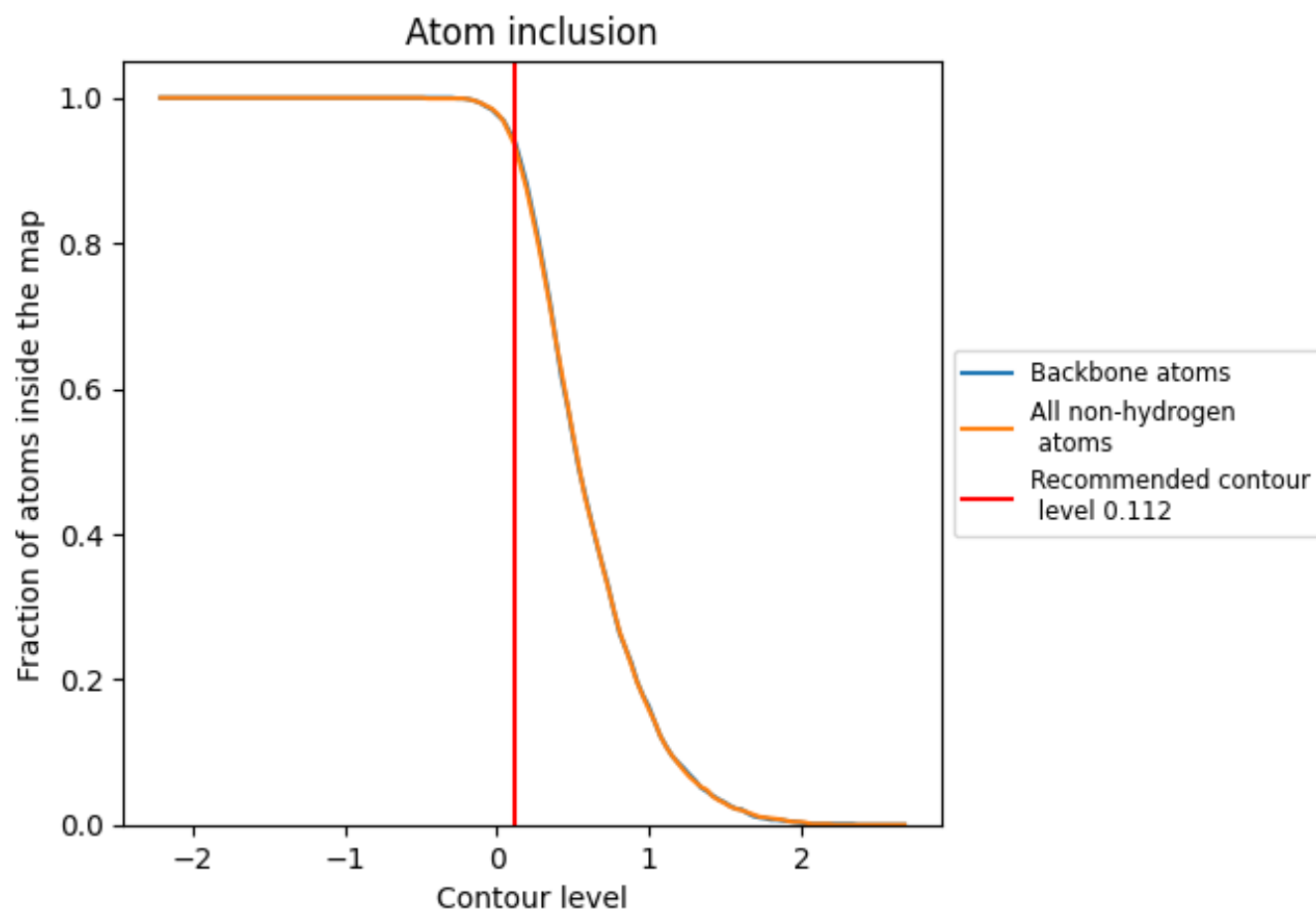
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.112).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% 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 (0.112) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9380	<div></div> 0.3310
A	<div></div> 0.9390	<div></div> 0.3320
C	<div></div> 0.9520	<div></div> 0.3660
D	<div></div> 0.9340	<div></div> 0.3140
E	<div></div> 0.9680	<div></div> 0.3680
P	<div></div> 0.9170	<div></div> 0.2570

