



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:04 AM UTC

PDB ID : 8PBY / pdb_00008pby
EMDB ID : EMD-17588
Title : Single particle cryo-EM of the P140-P110 heterodimer with an alternative conformation in the P140 stalk of Mycoplasma genitalium at a resolution of 3.7 Angstrom.
Authors : Sprankel, L.; Scheffer, M.P.; Frangakis, A.S.
Deposited on : 2023-06-09
Resolution : 3.70 Å(reported)
Based on initial models : 6R3T, 6RUT

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.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

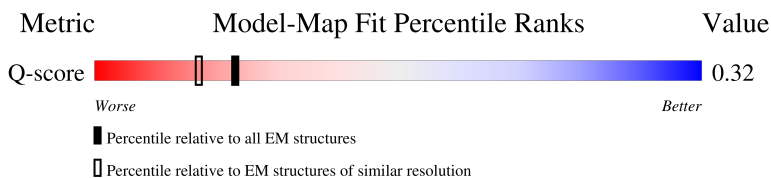
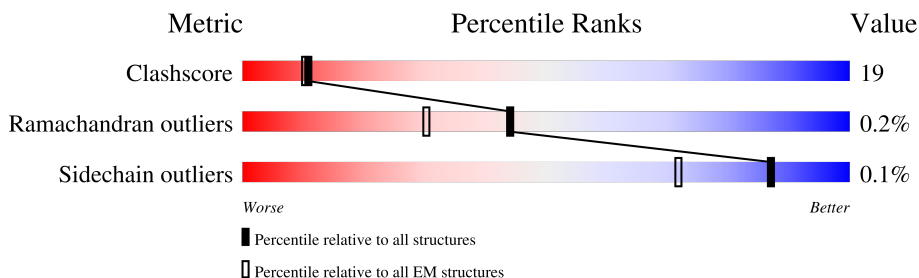
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	1059	14% 58% 27% 15%
2	B	1444	16% 54% 35% 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 33480 atoms, of which 16474 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 Mgp-operon protein 3.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	902	Total	C	H	N	O	S	2	0
			13658	4350	6714	1165	1423	6		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1053	HIS	-	expression tag	UNP P22747
A	1054	HIS	-	expression tag	UNP P22747
A	1055	HIS	-	expression tag	UNP P22747
A	1056	HIS	-	expression tag	UNP P22747
A	1057	HIS	-	expression tag	UNP P22747
A	1058	HIS	-	expression tag	UNP P22747

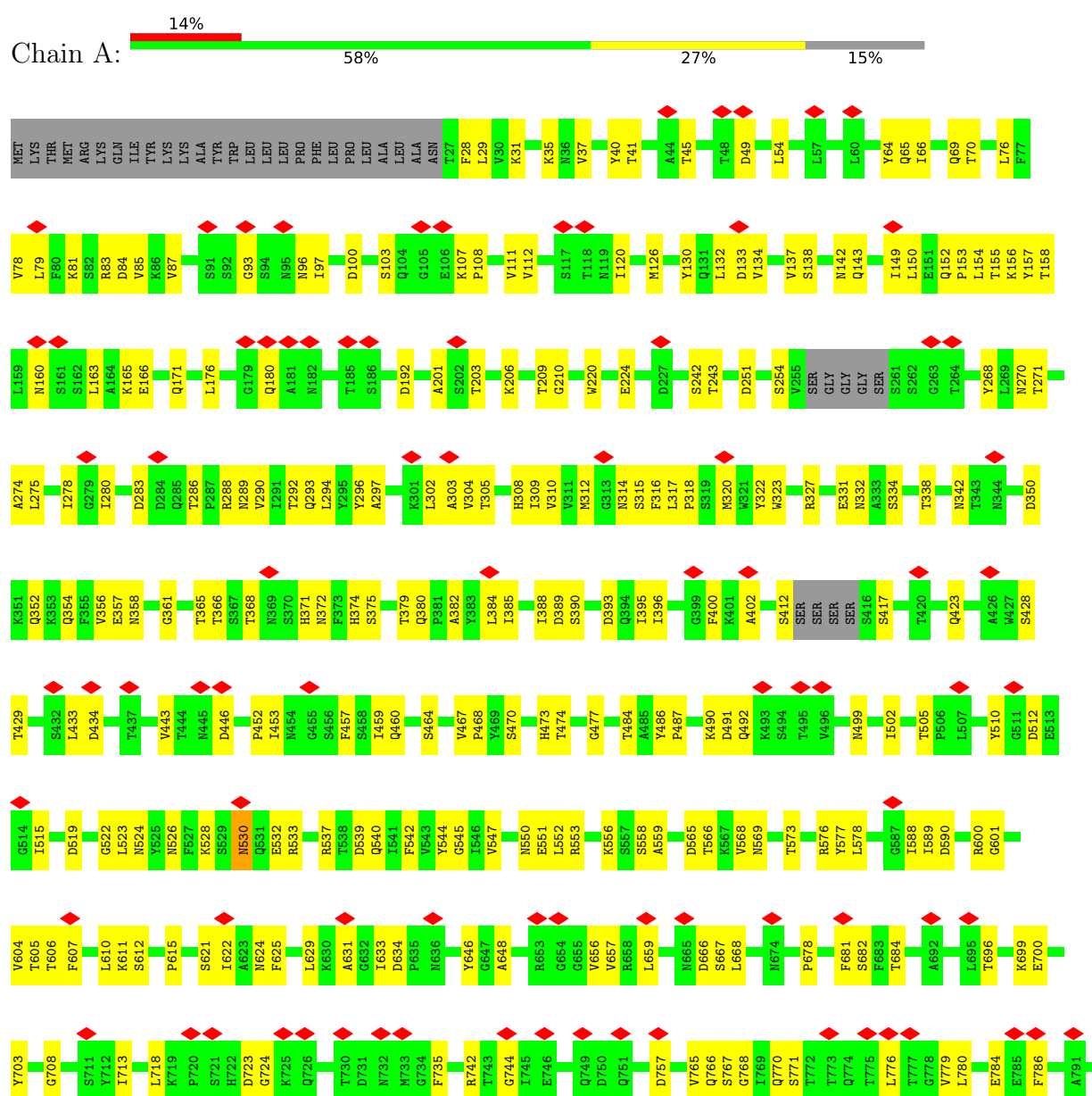
- Molecule 2 is a protein called Adhesin P1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	1285	Total	C	H	N	O	S	0	0
			19822	6373	9760	1701	1974	14		

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: Mgp-operon protein 3





LYS	LYS	TLE	D1296	D1222	D1129	S1047	L960	T890	SER
LYS	LEU	VAL	Q1297	K1224	A1134	S1048	Y961	S891	ALA
LYS	GLN	ILE	S1299		L1143	L1049	N962	D892	SER
ALA	LEU	ILE	I1300	V1228	L1150	Q1050	L965	H893	
THR	SER	VAL	R1301	T1231	K1153	D1051	L966	T894	
PRO	THR	THR	L1302	P1232	L1153	Q1052	H967	T896	
LYS	LEU	THR	K1303	L1233	L1153	T1053	Y968	N895	
GLY	LEU	THR	V1304	V1234	G1156	I1054	Y969	S797	
THR	LEU	THR	V1234		T1059	I1055	G973	N798	
LYS	THR	THR	G1241		T1062			G802	
PRO	THR	THR	A1242		K1065			I807	
LYS	THR	THR	T1243		Y1068			L811	
PRO	PRO	THR	S1244		T1074			T816	
LYS	PRO	THR	D1245		P1075			F820	
PRO	PRO	THR	S1246		L1078			N823	
PRO	VAL	ARG	D1247		W1079			F824	
LYS	LYS	ARG	T1248		D1080			I828	
LYS	ALA	LYS	E1249		P1081			G833	
GLN	GLN	GLN	K1250		L1084			Y834	
ALA	ALA	GLY	I1251		K1085			R835	
ALA	ALA	PHE	S1252		S1086			V836	
GLY	GLY	ASP	F1253		L1087			Q837	
THR	THR	LEU	K1254		P1088			I845	
LEU	SER	SER	P1255		N1089			F846	
ASN	ASN	ASN	G1256		S1089			F847	
LYS	LYS	LYS	I1259		S1090			V850	
VAL	VAL	VAL	L1267		T1091			K851	
VAL	VAL	THR	P1268		T1092			N855	
LEU	LEU	THR	V1269		T1093			S856	
LYS	LYS	LYS	T1270		Y1094			T857	
ALA	ALA	ALA	E1271		D1095			P858	
VAL	VAL	VAL	L1272		T1096			F859	
GLY	GLY	SER	F1273		N1097			D860	
VAL	VAL	PHE	D1274		L1100			D864	
LYS	LYS	LYS	P1275		Q1105			D865	
GLU	GLU	THR	N1276		L1106			N866	
ILE	ILE	THR	T1277		Y1107			G872	
ILE	ILE	THR	T1278		Q1108			G873	
ASN	ASN	THR	F1279		P1109			T878	
THR	THR	THR	V1280		N1110			Y880	
GLY	GLY	GLY	V1281		K1111			P884	
ALA	ALA	THR	Y1282		V1112			N885	
ASP	ASP	THR	D1283		Q1116			S886	
TYR	TYR	THR	Q1283		N1119			I887	
VAL	VAL	ALA	K1204		T1120				
LEU	LEU	ALA	Y1284		Y1121				
PRO	PRO	PRO	V1285		L1124				
LEU	LEU	LEU	P1286		I1125				
ILE	ILE	THR	L1287						
THR	THR	THR	L1288						
VAL	VAL	VAL	V1289						
VAL	VAL	VAL	N1290						
PRO	PRO	PRO	L1291						
			P1292						
			S1293						
			G1294						
			F1295						

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	67091	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.945	Depositor
Minimum map value	-1.485	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.062	Depositor
Recommended contour level	0.34	Depositor
Map size (Å)	315.0, 315.0, 315.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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	0.12	0/7076	0.29	0/9624
2	B	0.12	0/10316	0.32	0/14045
All	All	0.12	0/17392	0.31	0/23669

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	589	LEU	Peptide

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	6944	6714	6705	230	0
2	B	10062	9760	9759	397	0
All	All	17006	16474	16464	620	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 19.

The worst 5 of 620 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:530:ASN:O	1:A:530:ASN:ND2	2.03	0.91
1:A:165:LYS:NZ	1:A:206:LYS:O	2.05	0.90
2:B:387:TYR:OH	2:B:418:ASN:OD1	1.89	0.89
2:B:273:ARG:NH2	2:B:878:THR:OG1	2.07	0.88
2:B:391:ASN:OD1	2:B:418:ASN:ND2	2.08	0.87

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	896/1059 (85%)	839 (94%)	56 (6%)	1 (0%)	48	78
2	B	1281/1444 (89%)	1151 (90%)	126 (10%)	4 (0%)	36	65
All	All	2177/2503 (87%)	1990 (91%)	182 (8%)	5 (0%)	44	72

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	233	SER
2	B	234	PHE
2	B	1300	ILE
1	A	120	ILE
2	B	143	ILE

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	786/920 (85%)	785 (100%)	1 (0%)	88	88
2	B	1127/1267 (89%)	1127 (100%)	0	100	100
All	All	1913/2187 (88%)	1912 (100%)	1 (0%)	87	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	530	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	111	ASN
2	B	360	HIS
2	B	1023	GLN
2	B	631	ASN
2	B	975	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.

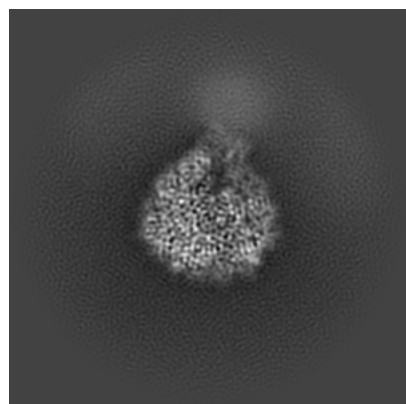
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17588. These allow visual inspection of the internal detail of the map and identification of artifacts.

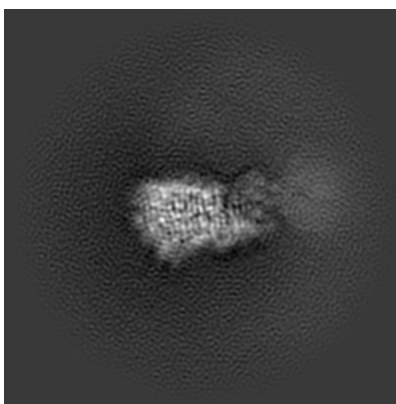
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

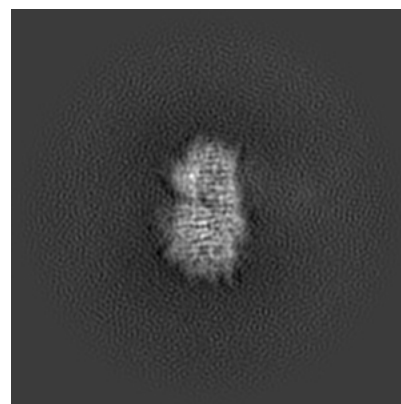
6.1.1 Primary map



X

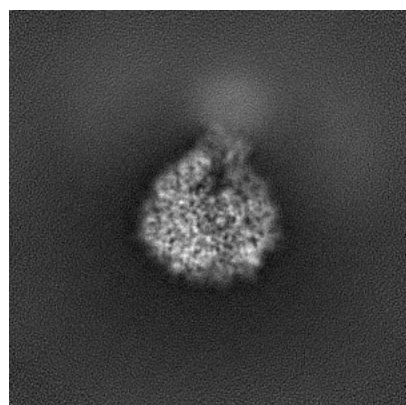


Y

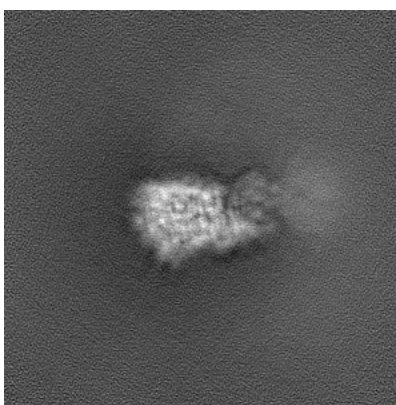


Z

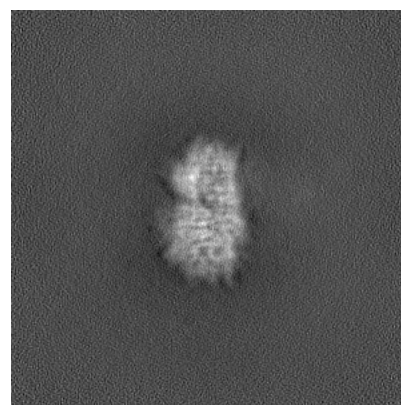
6.1.2 Raw map



X



Y

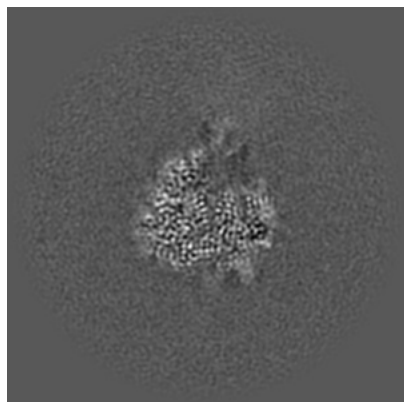


Z

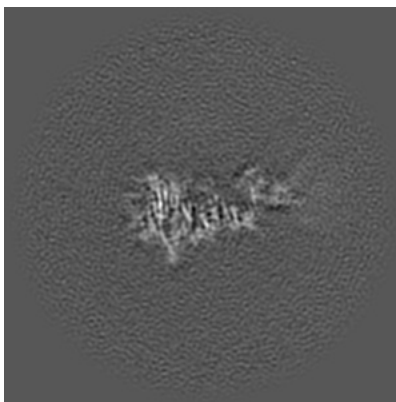
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

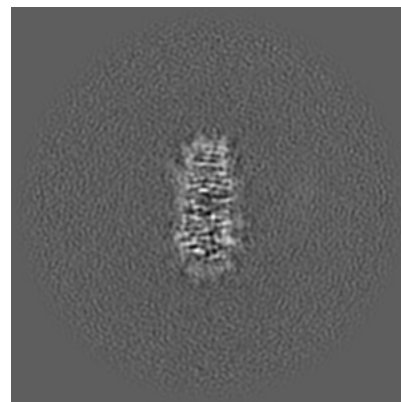
6.2.1 Primary map



X Index: 150

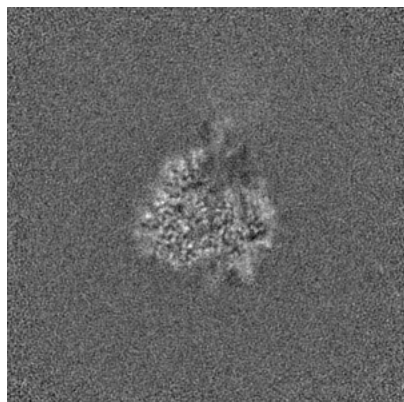


Y Index: 150

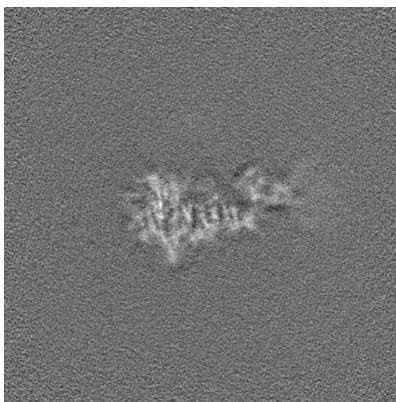


Z Index: 150

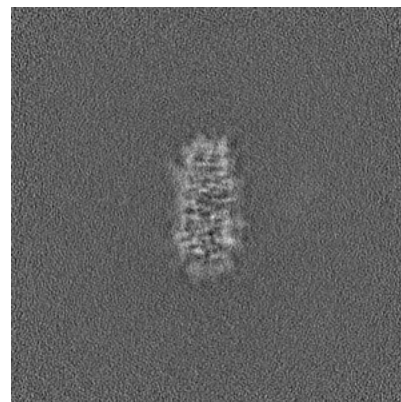
6.2.2 Raw map



X Index: 150



Y Index: 150

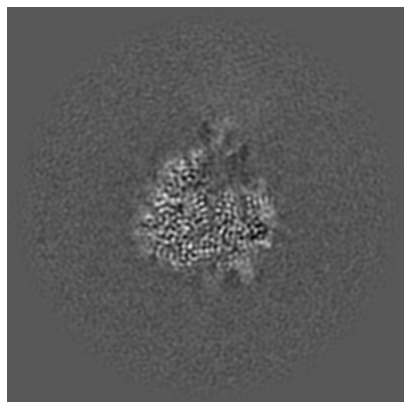


Z Index: 150

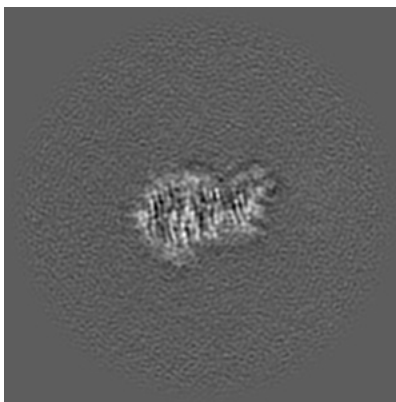
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

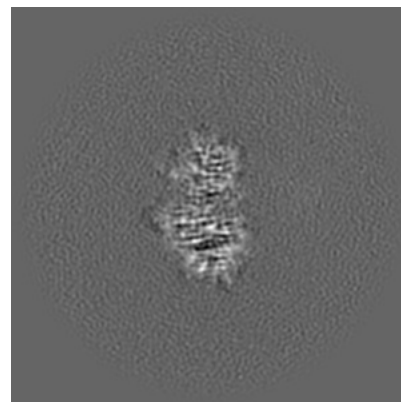
6.3.1 Primary map



X Index: 150

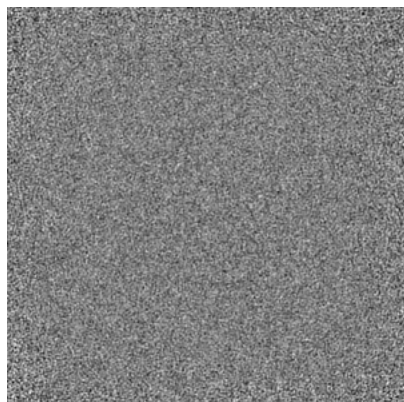


Y Index: 139

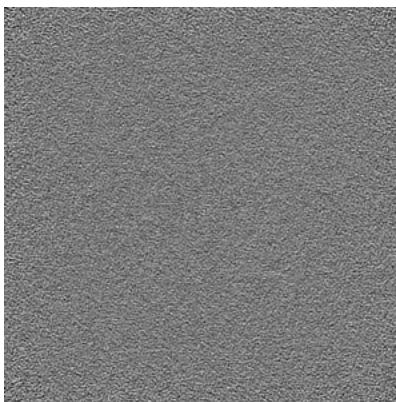


Z Index: 134

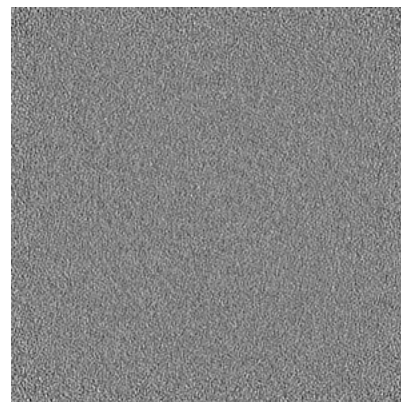
6.3.2 Raw map



X Index: 0



Y Index: 0

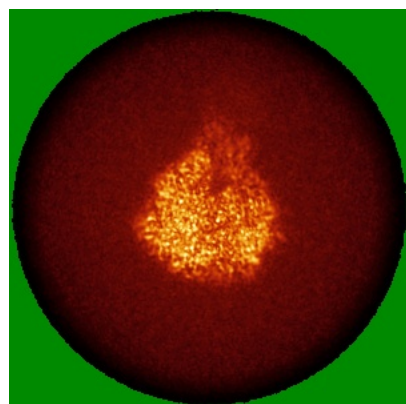


Z Index: 0

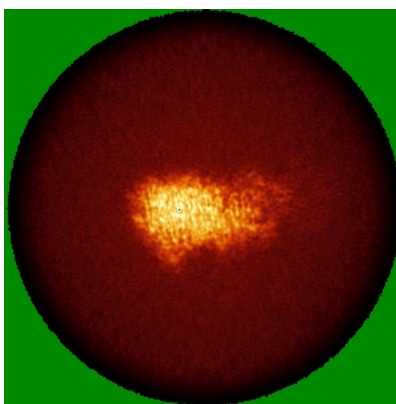
The images above show the largest variance slices of the map in three orthogonal directions.

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

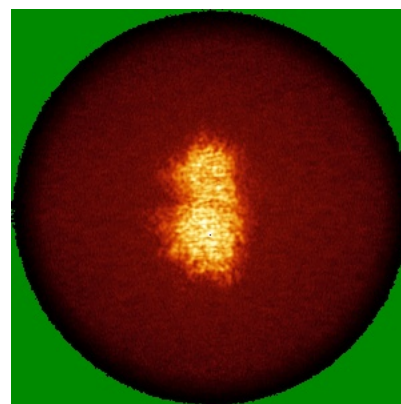
6.4.1 Primary map



X

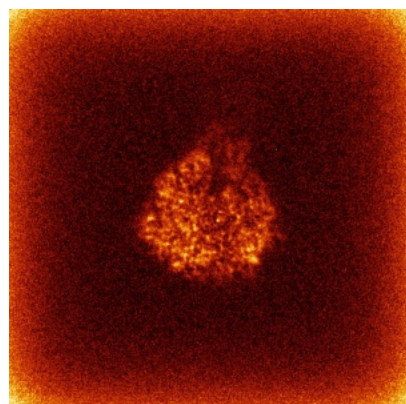


Y

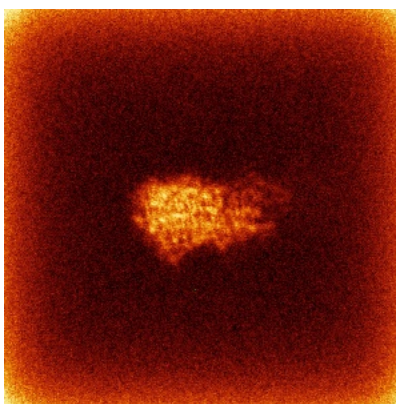


Z

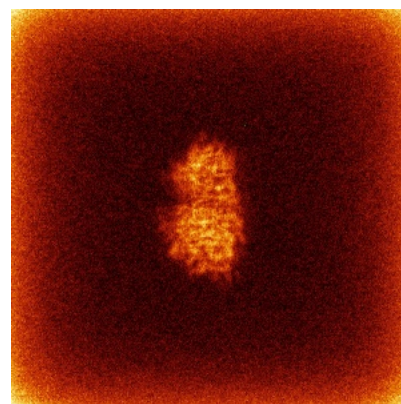
6.4.2 Raw map



X



Y

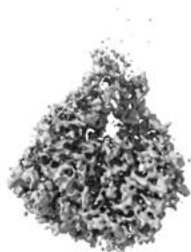


Z

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



X



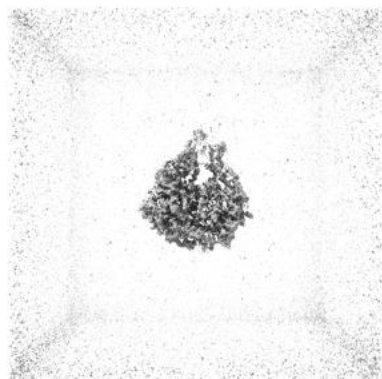
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.34. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

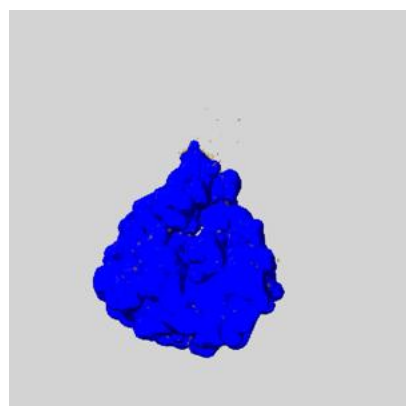
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

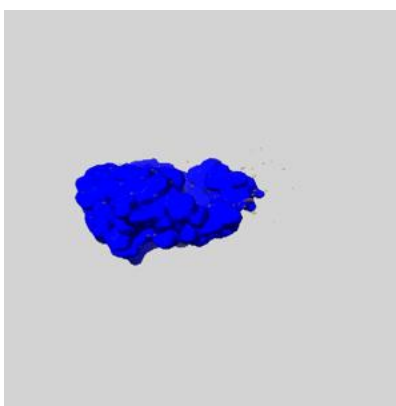
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

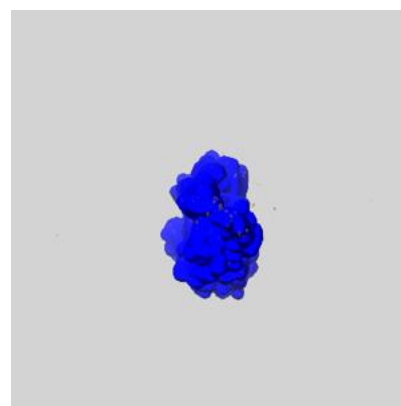
6.6.1 emd_17588_msk_1.map [i](#)



X



Y

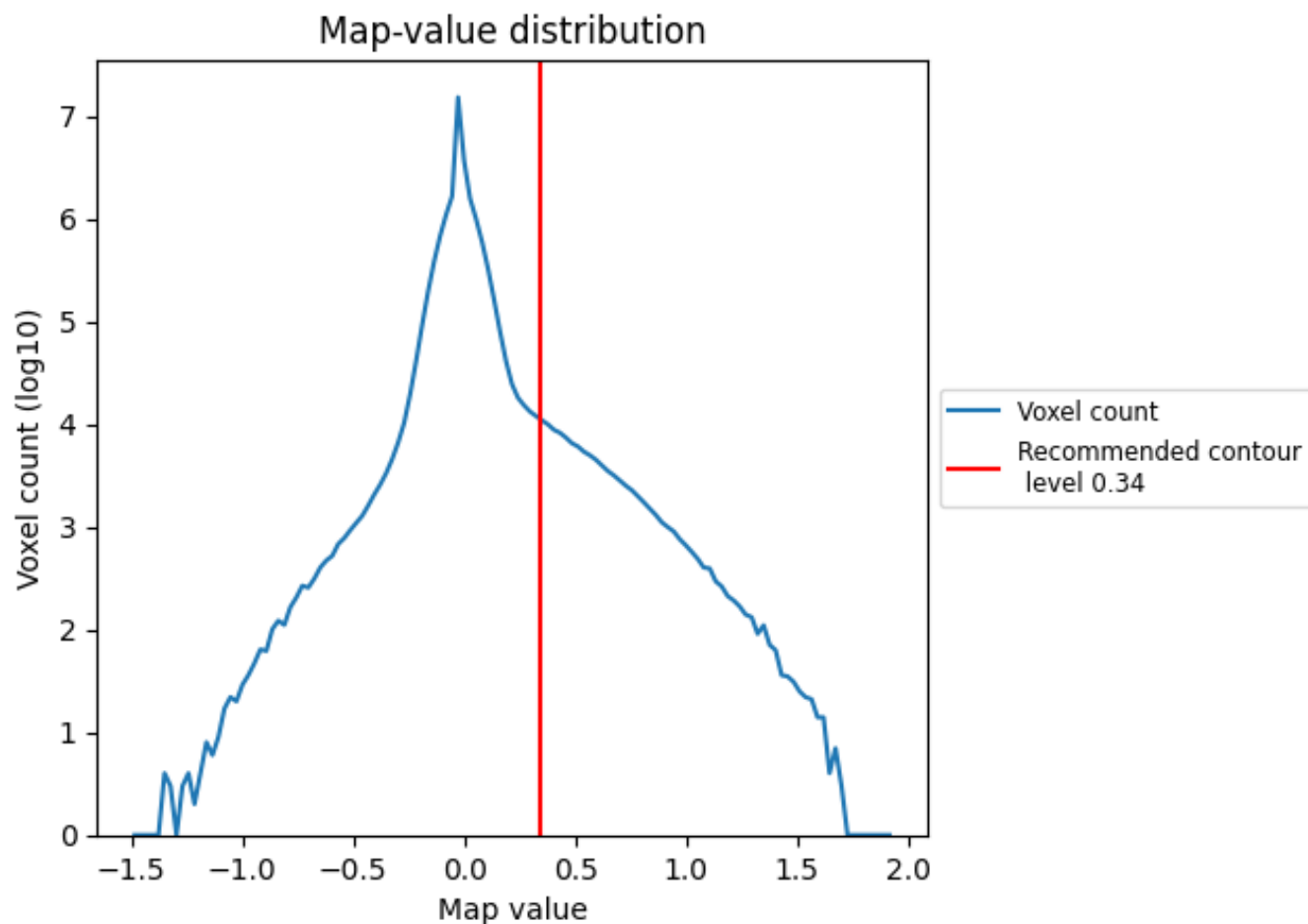


Z

7 Map analysis [i](#)

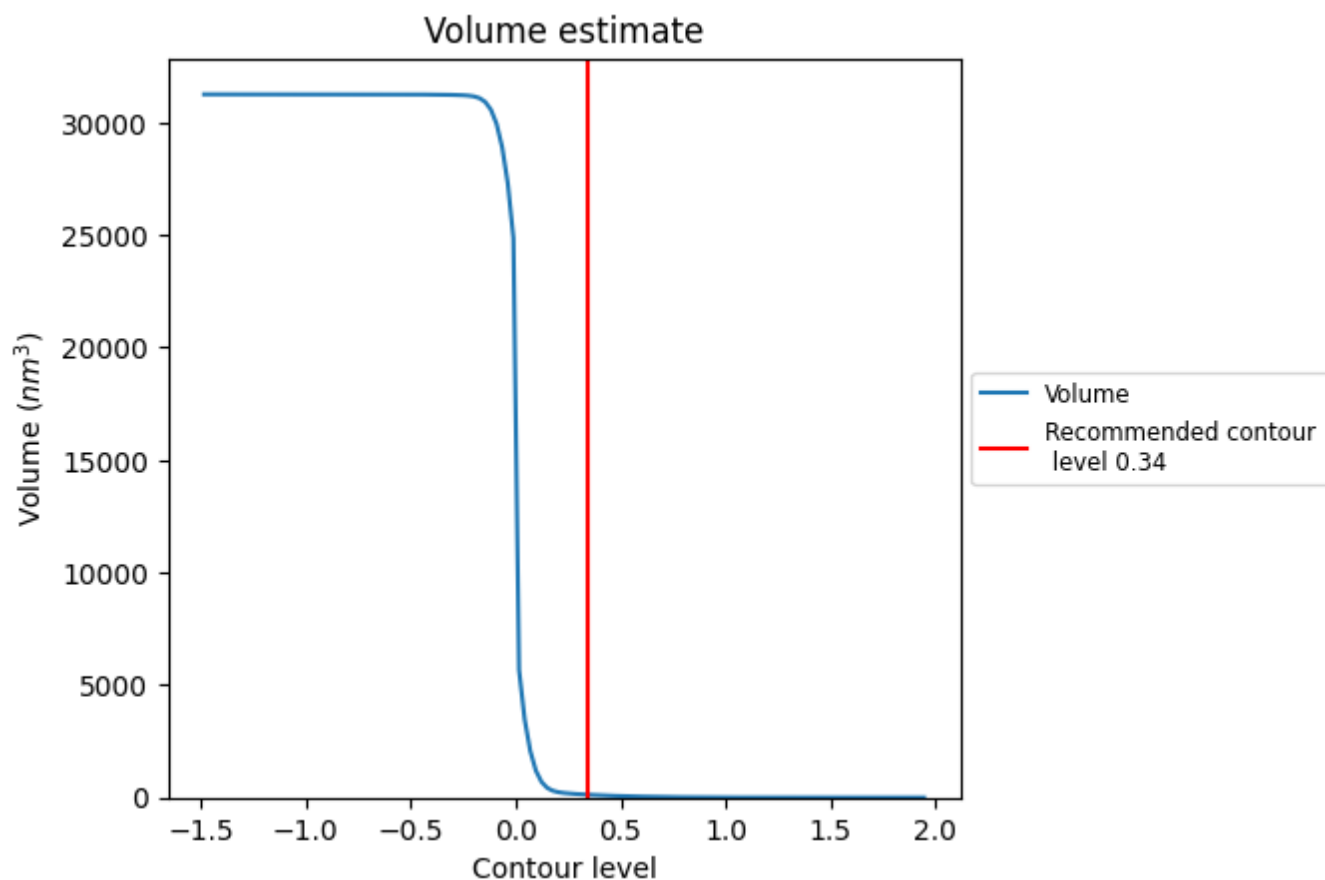
This section contains the results of statistical analysis of the map.

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.

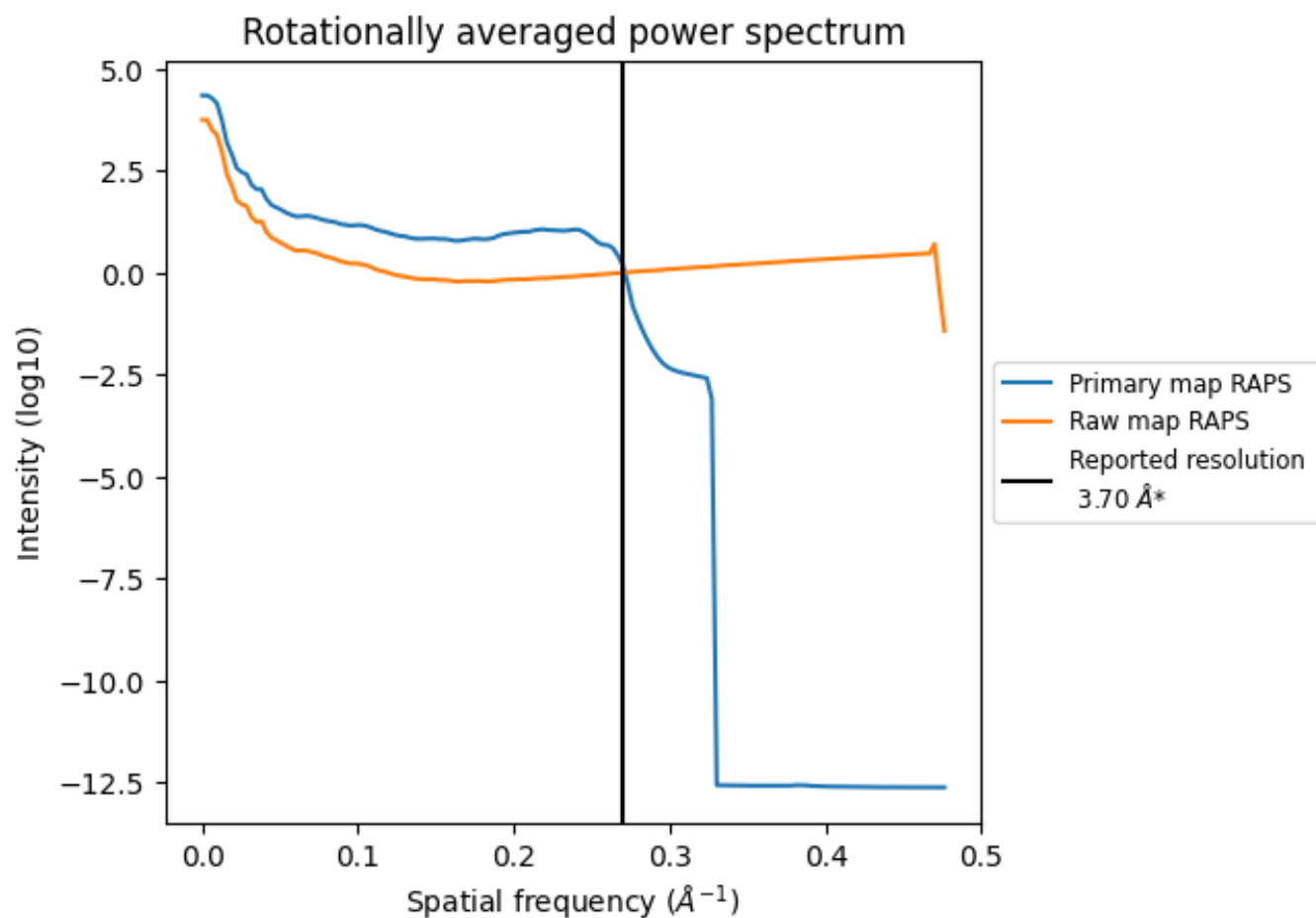
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 128 nm³; this corresponds to an approximate mass of 116 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 ⓘ

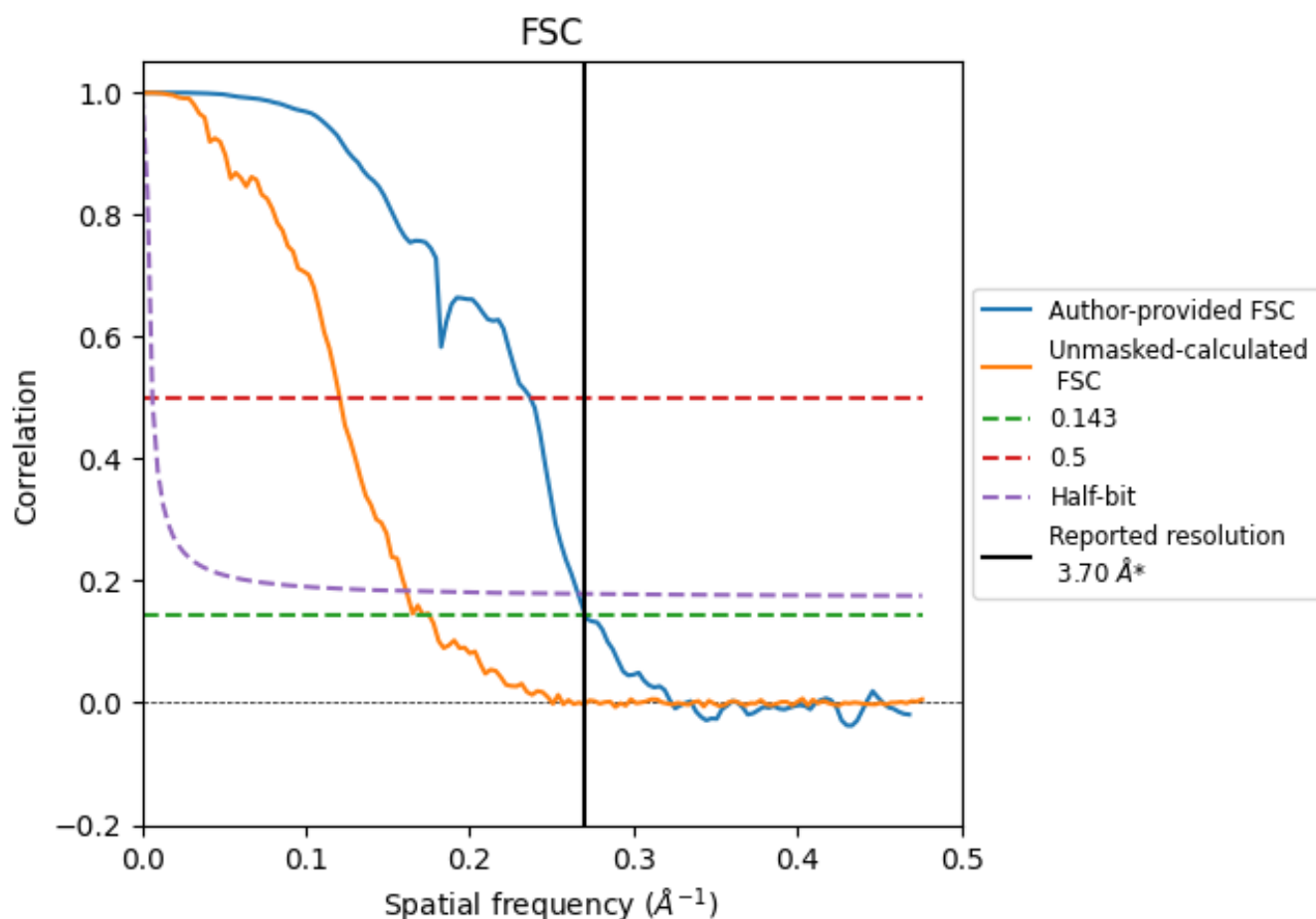


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

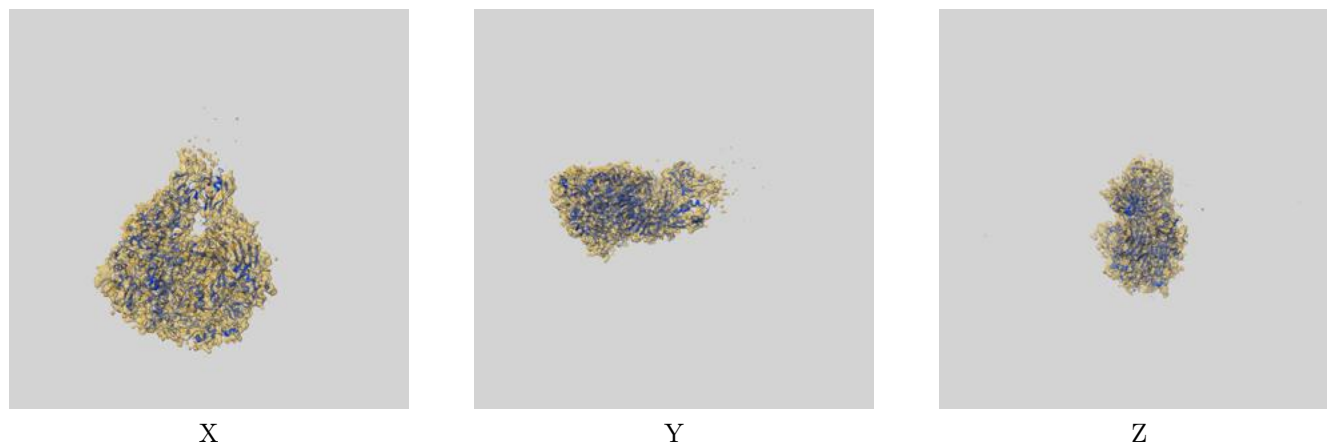
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.69	4.22	3.76
Unmasked-calculated*	5.70	8.29	6.20

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.70 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

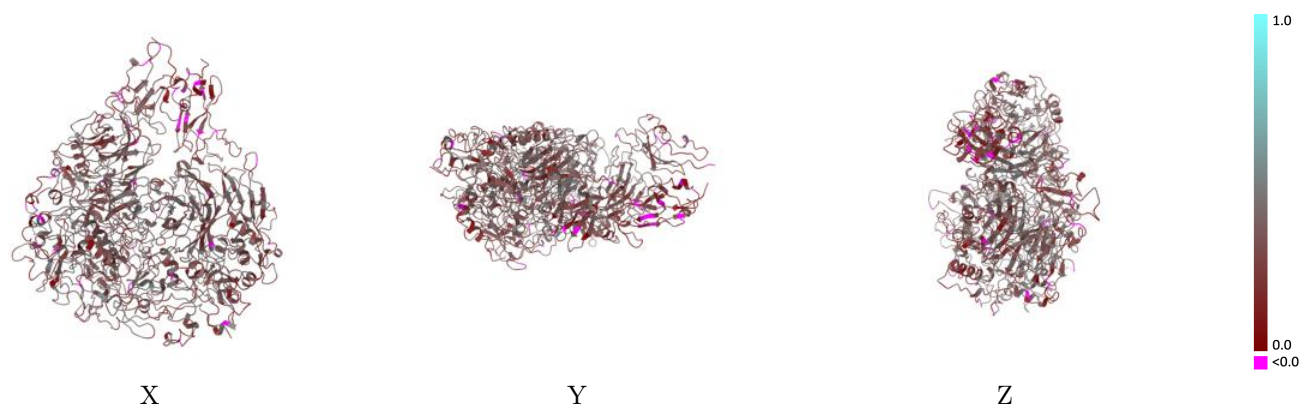
This section contains information regarding the fit between EMDB map EMD-17588 and PDB model 8PBY. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



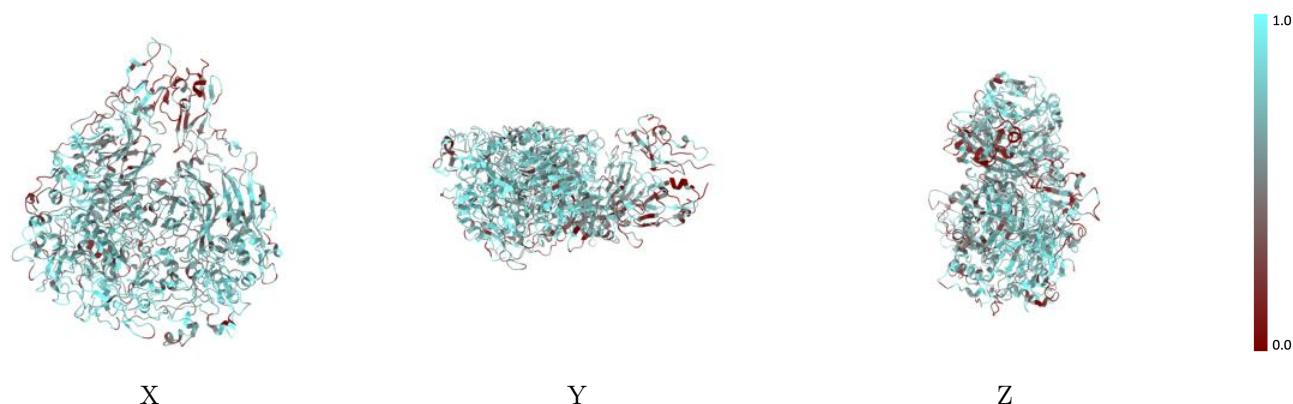
The images above show the 3D surface view of the map at the recommended contour level 0.34 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



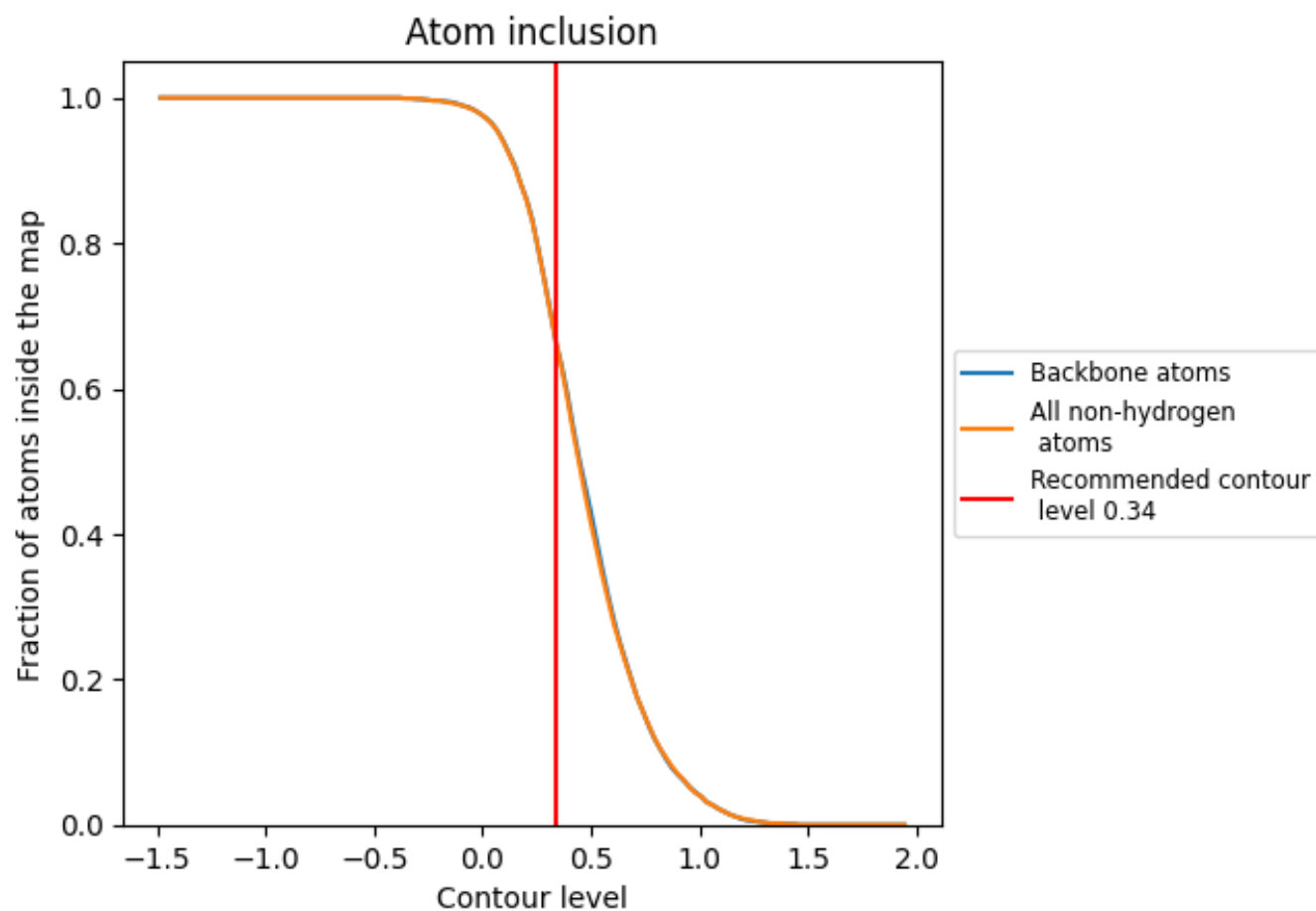
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.34).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 66% 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 (0.34) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6610	0.3200
A	0.6610	0.3130
B	0.6650	0.3240

