



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 10:51 PM UTC

PDB ID : 8QP5 / pdb_00008qp5
EMDB ID : EMD-18543
Title : Release Complex: BAM bound EspP (SurA released)
Authors : Fenn, K.L.; Ranson, N.A.
Deposited on : 2023-09-29
Resolution : 4.40 Å(reported)
Based on initial model : 8PZ1

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:

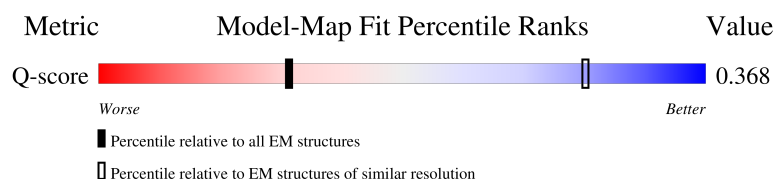
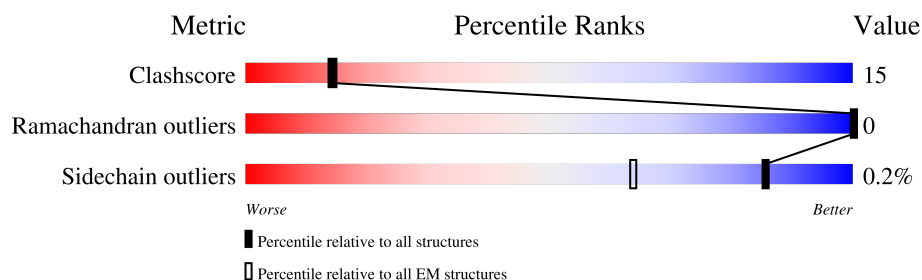
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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	3132 (3.91 - 4.90)

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	790	13% 51% 26% 22%
2	B	373	82% 61% 35% .
3	C	320	32% 40% 14% 47%
4	D	226	8% 62% 34% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	E	104	
6	P	814	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12554 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 Outer membrane protein assembly factor BamA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	614	Total	C	N	O	S	0	0
			4886	3090	820	962	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	425	CYS	SER	engineered mutation	UNP P0A940

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	357	Total	C	N	O	S	0	0
			2674	1677	460	531	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	171	Total	C	N	O	S	0	0
			1036	634	190	209	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	216	Total	C	N	O	S	0	0
			1744	1099	307	331	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	89	Total	C	N	O	S	0	0
			693	436	122	133	2		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	114	GLY	-	expression tag	UNP P0A937
E	115	GLY	-	expression tag	UNP P0A937
E	116	HIS	-	expression tag	UNP P0A937
E	117	HIS	-	expression tag	UNP P0A937
E	118	HIS	-	expression tag	UNP P0A937
E	119	HIS	-	expression tag	UNP P0A937
E	120	HIS	-	expression tag	UNP P0A937
E	121	HIS	-	expression tag	UNP P0A937
E	122	HIS	-	expression tag	UNP P0A937
E	123	HIS	-	expression tag	UNP P0A937

- Molecule 6 is a protein called Chaperone SurA, Serine protease EspP.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	P	299	Total	C	N	O	S	1	0
			1521	900	310	310	1		

There are 55 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	487	GLY	-	expression tag	UNP P0ABZ6
P	488	SER	-	expression tag	UNP P0ABZ6
P	489	SER	-	expression tag	UNP P0ABZ6
P	490	ALA	-	expression tag	UNP P0ABZ6
P	491	TRP	-	expression tag	UNP P0ABZ6
P	492	SER	-	expression tag	UNP P0ABZ6
P	493	HIS	-	expression tag	UNP P0ABZ6
P	494	PRO	-	expression tag	UNP P0ABZ6
P	495	GLN	-	expression tag	UNP P0ABZ6
P	496	PHE	-	expression tag	UNP P0ABZ6
P	497	GLU	-	expression tag	UNP P0ABZ6
P	498	LYS	-	expression tag	UNP P0ABZ6
P	499	GLY	-	expression tag	UNP P0ABZ6
P	500	GLY	-	expression tag	UNP P0ABZ6
P	501	GLY	-	expression tag	UNP P0ABZ6
P	502	SER	-	expression tag	UNP P0ABZ6
P	503	GLY	-	expression tag	UNP P0ABZ6
P	504	GLY	-	expression tag	UNP P0ABZ6
P	505	GLY	-	expression tag	UNP P0ABZ6
P	506	SER	-	expression tag	UNP P0ABZ6
P	507	GLY	-	expression tag	UNP P0ABZ6
P	508	GLY	-	expression tag	UNP P0ABZ6
P	509	SER	-	expression tag	UNP P0ABZ6

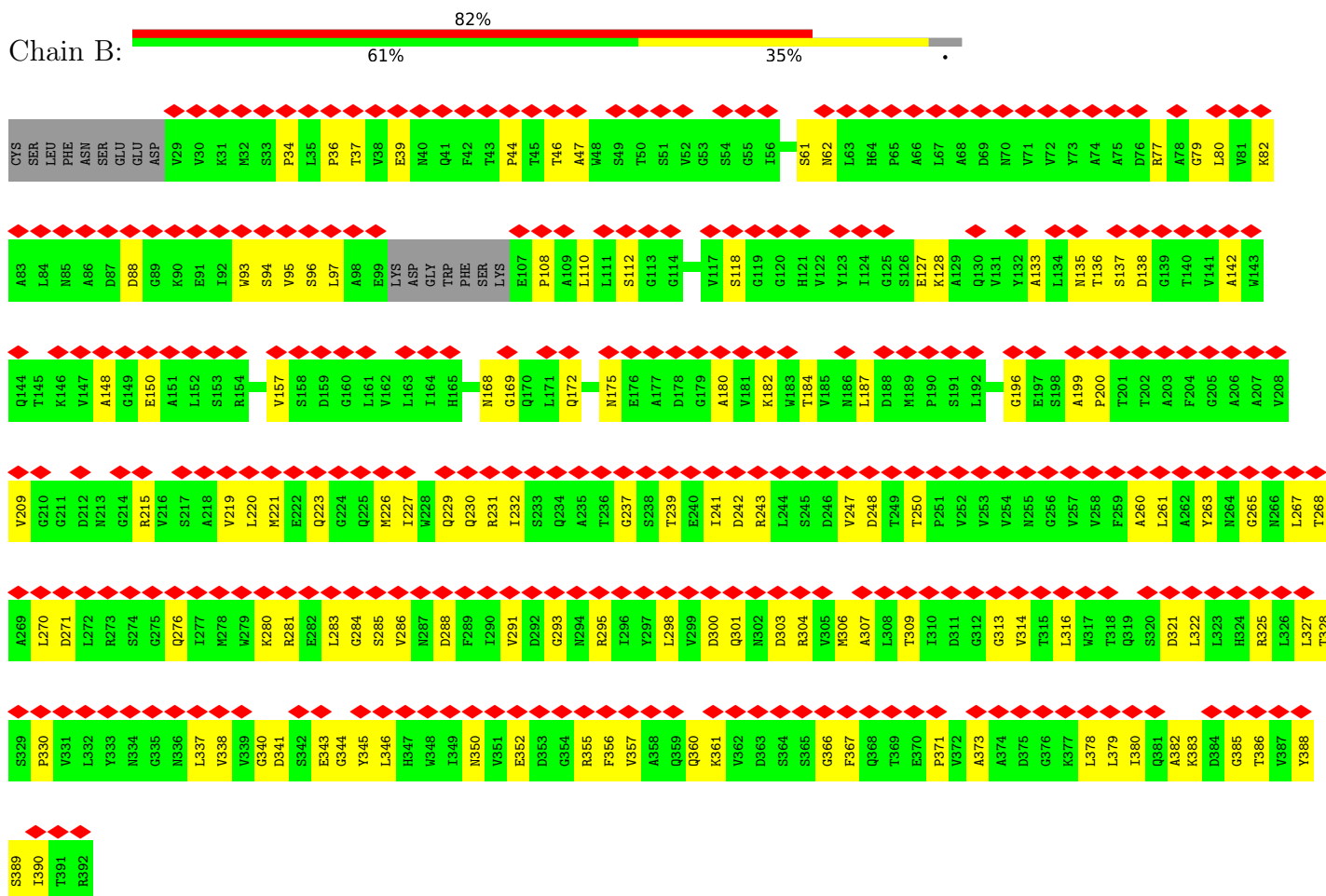
Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
P	510	ALA	-	expression tag	UNP P0ABZ6
P	511	TRP	-	expression tag	UNP P0ABZ6
P	512	SER	-	expression tag	UNP P0ABZ6
P	513	HIS	-	expression tag	UNP P0ABZ6
P	514	PRO	-	expression tag	UNP P0ABZ6
P	515	GLN	-	expression tag	UNP P0ABZ6
P	516	PHE	-	expression tag	UNP P0ABZ6
P	517	GLU	-	expression tag	UNP P0ABZ6
P	518	LYS	-	expression tag	UNP P0ABZ6
P	519	SER	-	expression tag	UNP P0ABZ6
P	520	SER	-	expression tag	UNP P0ABZ6
P	521	GLY	-	expression tag	UNP P0ABZ6
P	522	GLU	-	expression tag	UNP P0ABZ6
P	523	ASN	-	expression tag	UNP P0ABZ6
P	524	LEU	-	expression tag	UNP P0ABZ6
P	525	TYR	-	expression tag	UNP P0ABZ6
P	526	PHE	-	expression tag	UNP P0ABZ6
P	527	GLN	-	expression tag	UNP P0ABZ6
P	528	GLY	-	expression tag	UNP P0ABZ6
P	535	CYS	LYS	conflict	UNP P0ABZ6
P	937	GLY	-	linker	UNP P0ABZ6
P	938	GLY	-	linker	UNP P0ABZ6
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	SER	engineered mutation	UNP Q7BSW5

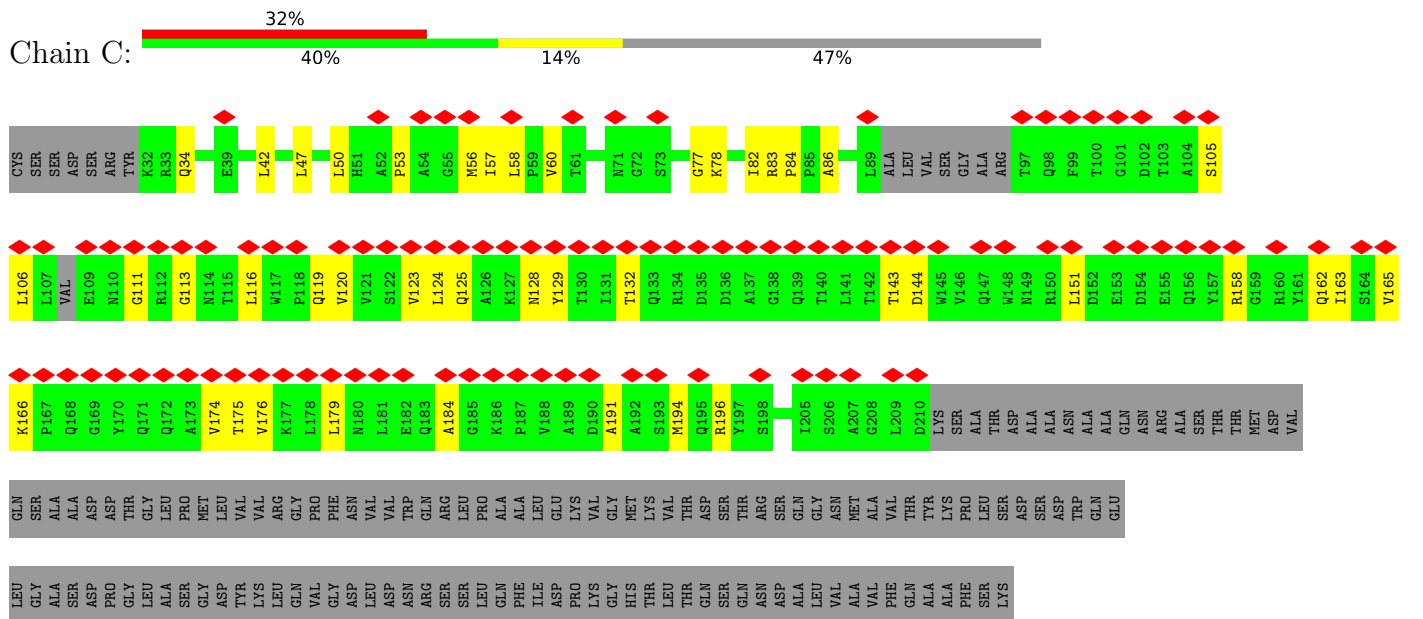
- Molecule 2: Outer membrane protein assembly factor BamB

Chain B:

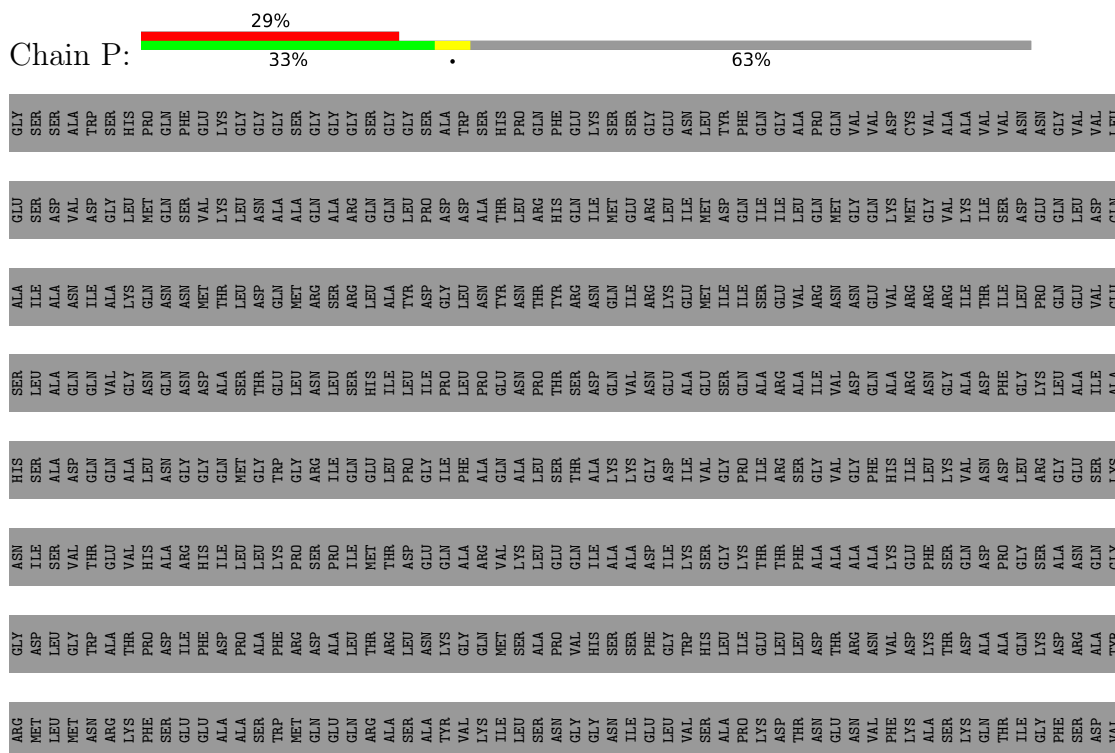


- Molecule 3: Outer membrane protein assembly factor BamC

Chain C:



- Molecule 4: Outer membrane protein assembly factor BamD



F1283	V1221	A1151	A1091	K1027	THR
G1284	T1222	G1152	S1092	R1028	PRO
K1285	A1223	G1153	A1093	M1029	VAL
Y1286	E1224	E1154	D1094	G1030	ILE
N1287	A1225	A1155	V1095	D1031	THR
V1288	G1226	G1156	F1096	L1032	ARG
D1289	L1227	Y1157	S1097	R1033	THR
M1290	G1228	H1160	G1098	D1034	GLY
A1291	Y1229	V1161	K1099	I1035	GLU
V1292	Q1230	T1162	T1100	N1036	ASN
M1293	F1231	E1163	K1101	G1037	LEU
	D1232	D1164	S1102	E1038	TYR
	L1233	A1165	V1103	A1039	PHE
F1296	L1234	A1166	G1104	A1041	GLN
	A1235	W1166	A1105	G1040	GLY
C1299	N1236		G1106	A1042	ASP
F1300	G1237		L1107	A1043	LYS
	E1238	L1173	A1108	R1044	THR
	T1239	V1174	A1109	I1045	TRP
	V1240	G1176	S1110	M1046	SER
	L1241	S1177	A1111	S1047	LEU
	R1242	V1178	M1112	G1048	GLY
	D1243	S1179	F1113	T1049	TVR
	A1244	G1180	D1114	G1050	ASN
	S1245	K1181	S1115	S1051	THR
	G1246	Q1182	G1116	A1052	VAL
	E1247	F1183	A1117	S1053	ALA
	K1248	A1184	V1118	G1054	ASN
	R1249	W1185	T1119	G1055	LYS
I1250	R1249	K1186	D1120	F1056	A1002
K1251	G1251	D1187	L1121	S1057	A1003
G1252	E1252	Q1188	I1122	D1058	T1004
E1253	G1253	G1189	G1123		R1005
K1254	K1254	M1190	K1124	V1063	M1006
D1255	S1255	H1191	V1125	Q1064	A1007
S1256	R1257	L1192	V1126	V1065	A1008
		S1193	H1127	G1066	A1009
		M1194	H1128	V1067	L1010
		K1195	D1129	D1068	S1011
		D1196	M1130	K1069	A1012
		K1197	E1131	K1070	D1014
S1261	S1261	K1197	V1132	H1071	V1015
V1262	V1262	D1198	T1133	E1072	K1016
G1263	G1263	Y1199	A1134	L1073	A1017
L1264	M1260	M1200	T1135	D1074	F1018
N1265	A1266	I1203	F1136	G1075	L1019
A1267	E1267		A1137	L1076	M1020
I1268	I1268	T1206	G1138	D1077	E1021
		G1207	L1139	L1078	V1022
		V1208	G1140	F1079	N1023
		D1209	T1141	T1080	M1024
N1271	V1272	V1210	R1142	G1081	L1025
L1273	F1273	G1211	D1143		N1026
		K1212	Y1144	F1082	
		S1213	S1145	T1083	
E1277	F1277	F1214	T1146	V1084	
F1278	E1278	S1215	H1147	T1085	
E1279	K1280	W1219	S1148	H1086	
S1281	A1282	K1220	V1149	S1089	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	67655	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	37.4	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	165000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.570	Depositor
Minimum map value	-0.373	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.125	Depositor
Map size ($\text{\AA}$)	222.0, 222.0, 222.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.74, 0.74, 0.74	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	0.16	0/5009	0.37	0/6795
2	B	0.13	0/2720	0.34	0/3711
3	C	0.37	0/1047	0.48	0/1440
4	D	0.16	0/1784	0.36	0/2423
5	E	0.13	0/708	0.31	0/965
6	P	0.12	0/1524	0.32	0/2101
All	All	0.17	0/12792	0.37	0/17435

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	4886	0	4615	153	0
2	B	2674	0	2633	86	0
3	C	1036	0	811	34	0
4	D	1744	0	1685	62	0
5	E	693	0	674	32	0
6	P	1521	0	804	18	0
All	All	12554	0	11222	365	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 15.

The worst 5 of 365 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:580:LYS:O	1:A:590:GLY:HA3	1.83	0.78
4:D:192:VAL:H	5:E:34:GLN:HE21	1.31	0.78
2:B:215:ARG:HH21	2:B:229:GLN:HG2	1.48	0.76
1:A:600:THR:HG21	1:A:607:GLU:HA	1.65	0.76
6:P:1238:GLU:HA	6:P:1250:ILE:O	1.87	0.75

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	610/790 (77%)	570 (93%)	40 (7%)	0	100	100
2	B	353/373 (95%)	313 (89%)	40 (11%)	0	100	100
3	C	165/320 (52%)	141 (86%)	24 (14%)	0	100	100
4	D	214/226 (95%)	201 (94%)	13 (6%)	0	100	100
5	E	87/104 (84%)	81 (93%)	6 (7%)	0	100	100
6	P	298/814 (37%)	283 (95%)	15 (5%)	0	100	100
All	All	1727/2627 (66%)	1589 (92%)	138 (8%)	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	524/672 (78%)	523 (100%)	1 (0%)	87	85
2	B	289/304 (95%)	289 (100%)	0	100	100
3	C	67/258 (26%)	67 (100%)	0	100	100
4	D	181/190 (95%)	181 (100%)	0	100	100
5	E	77/90 (86%)	76 (99%)	1 (1%)	61	72
6	P	16/656 (2%)	16 (100%)	0	100	100
All	All	1154/2170 (53%)	1152 (100%)	2 (0%)	85	85

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

Mol	Chain	Res	Type
1	A	709	ASN
5	E	110	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	230	GLN
2	B	266	ASN
5	E	34	GLN
4	D	47	ASN
4	D	230	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

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.

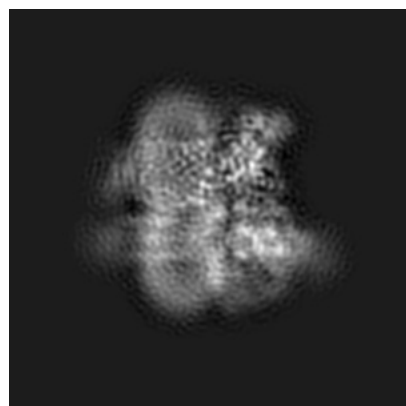
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18543. These allow visual inspection of the internal detail of the map and identification of artifacts.

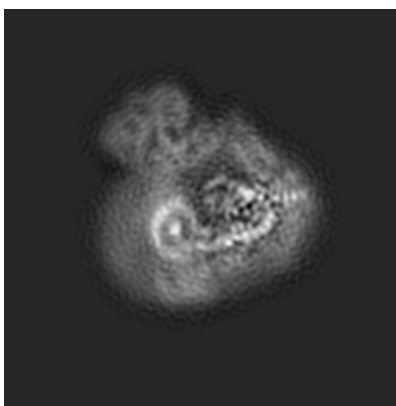
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

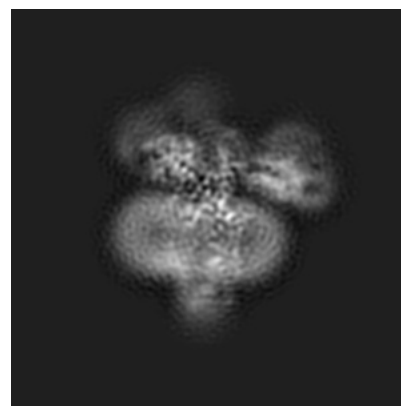
6.1.1 Primary map



X

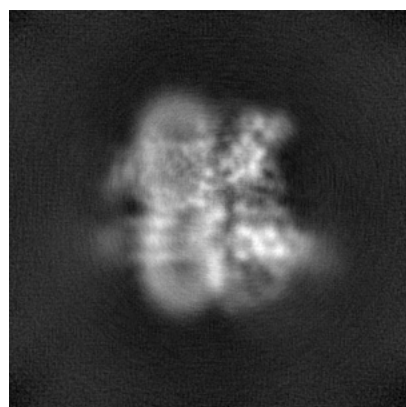


Y

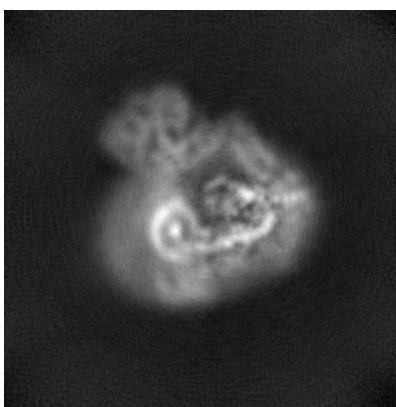


Z

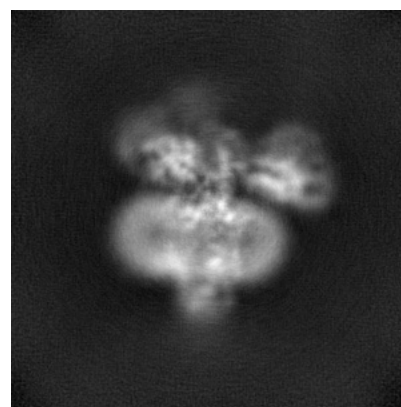
6.1.2 Raw map



X



Y

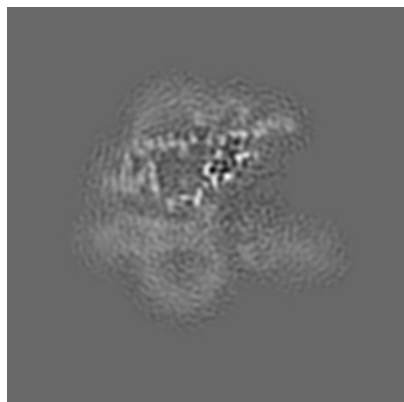


Z

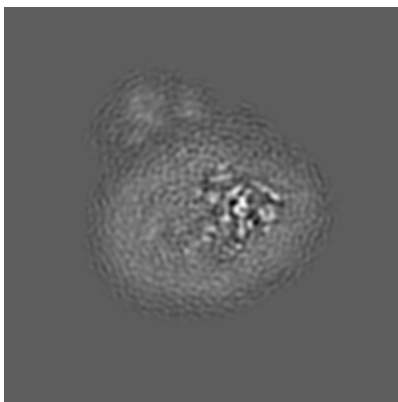
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

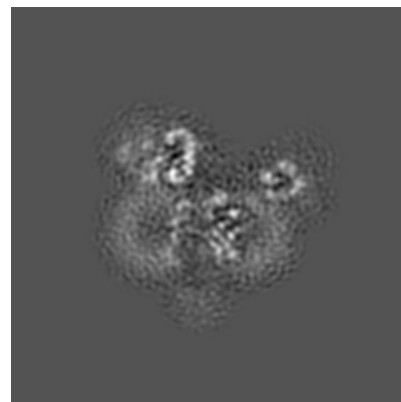
6.2.1 Primary map



X Index: 150

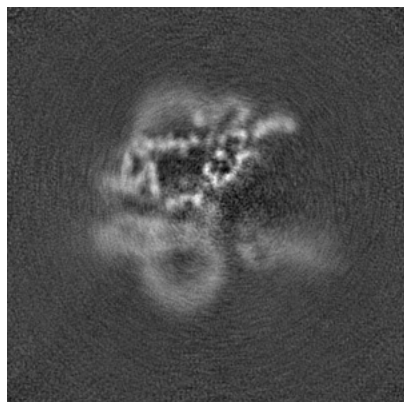


Y Index: 150

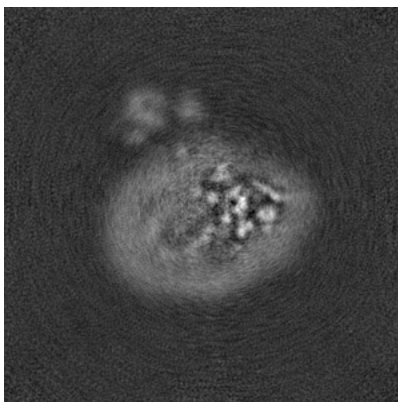


Z Index: 150

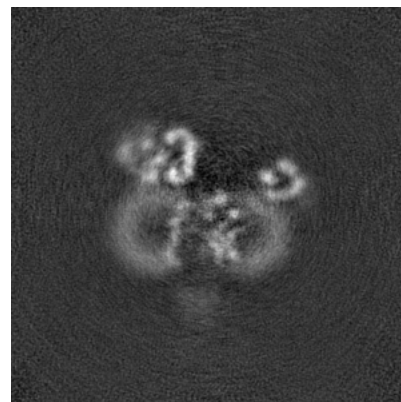
6.2.2 Raw map



X Index: 150



Y Index: 150

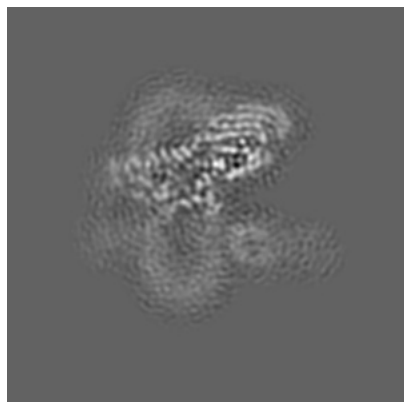


Z Index: 150

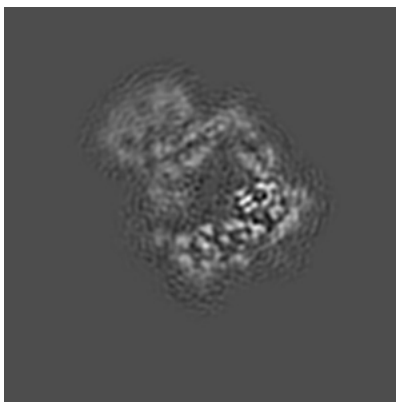
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

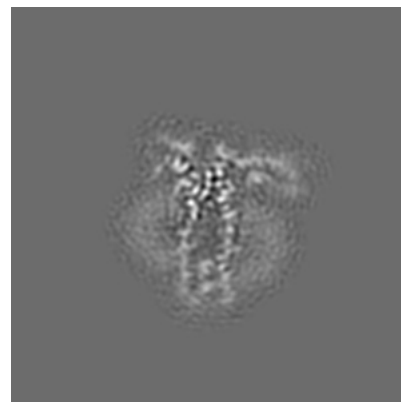
6.3.1 Primary map



X Index: 159

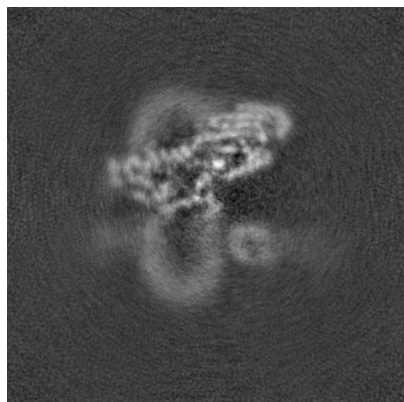


Y Index: 175

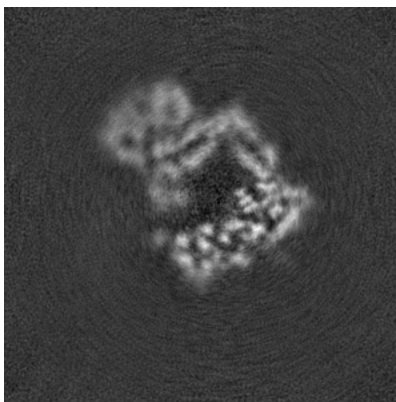


Z Index: 183

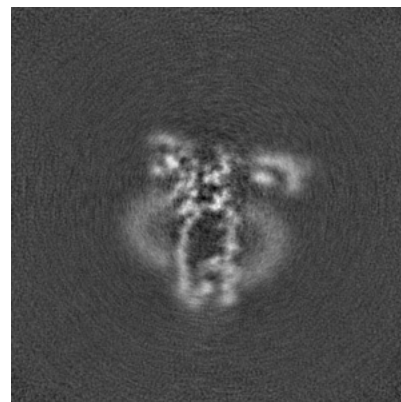
6.3.2 Raw map



X Index: 159



Y Index: 175

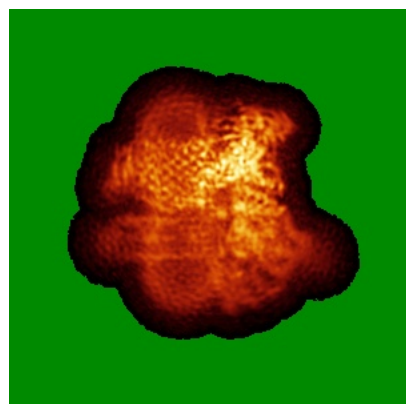


Z Index: 179

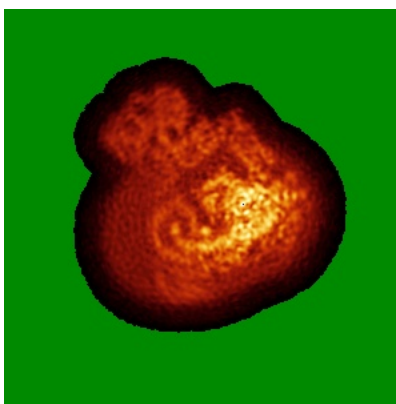
The images above show the largest variance slices of the map in three orthogonal directions.

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

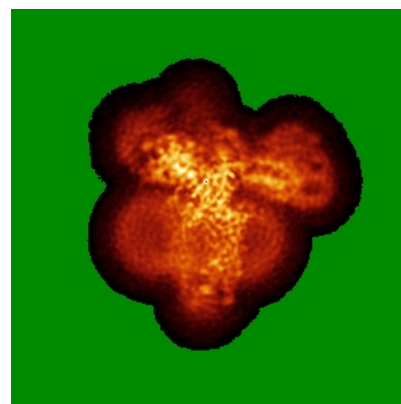
6.4.1 Primary map



X

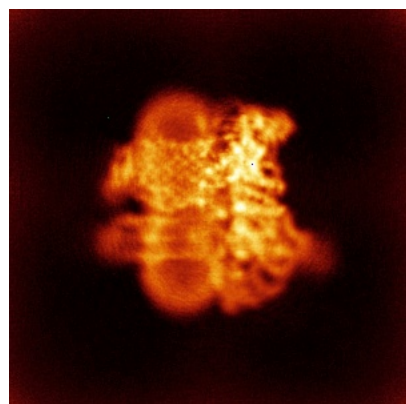


Y

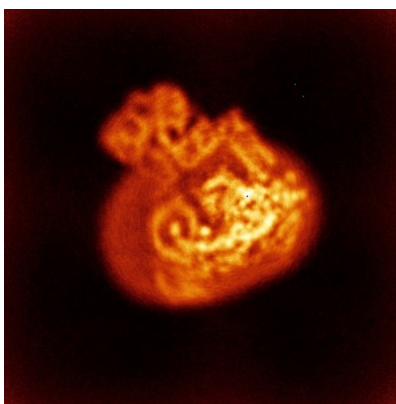


Z

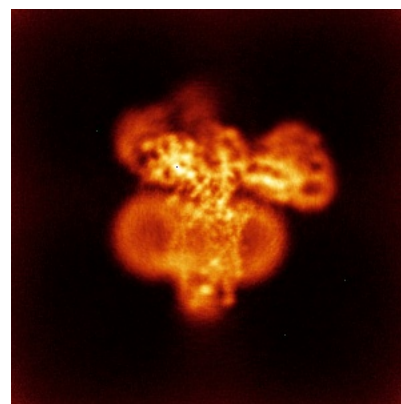
6.4.2 Raw map



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.

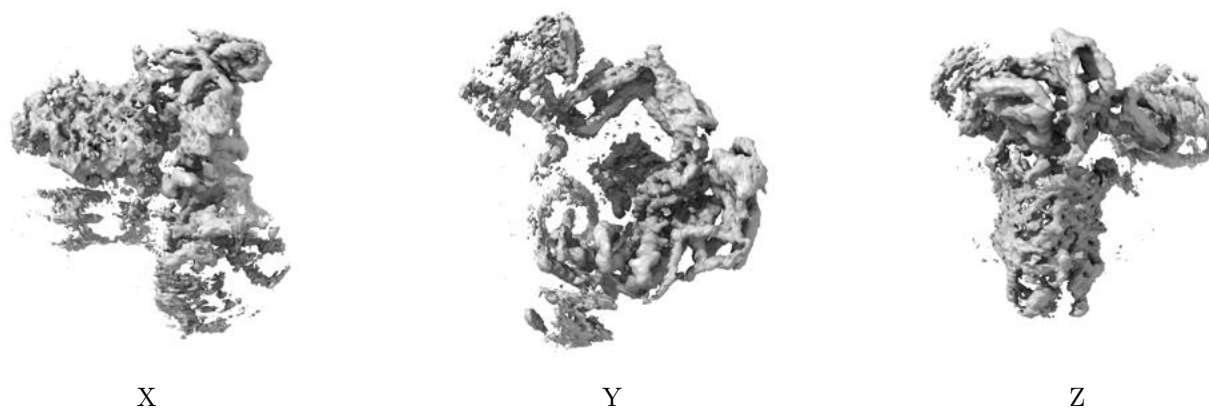
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.125. 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



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.

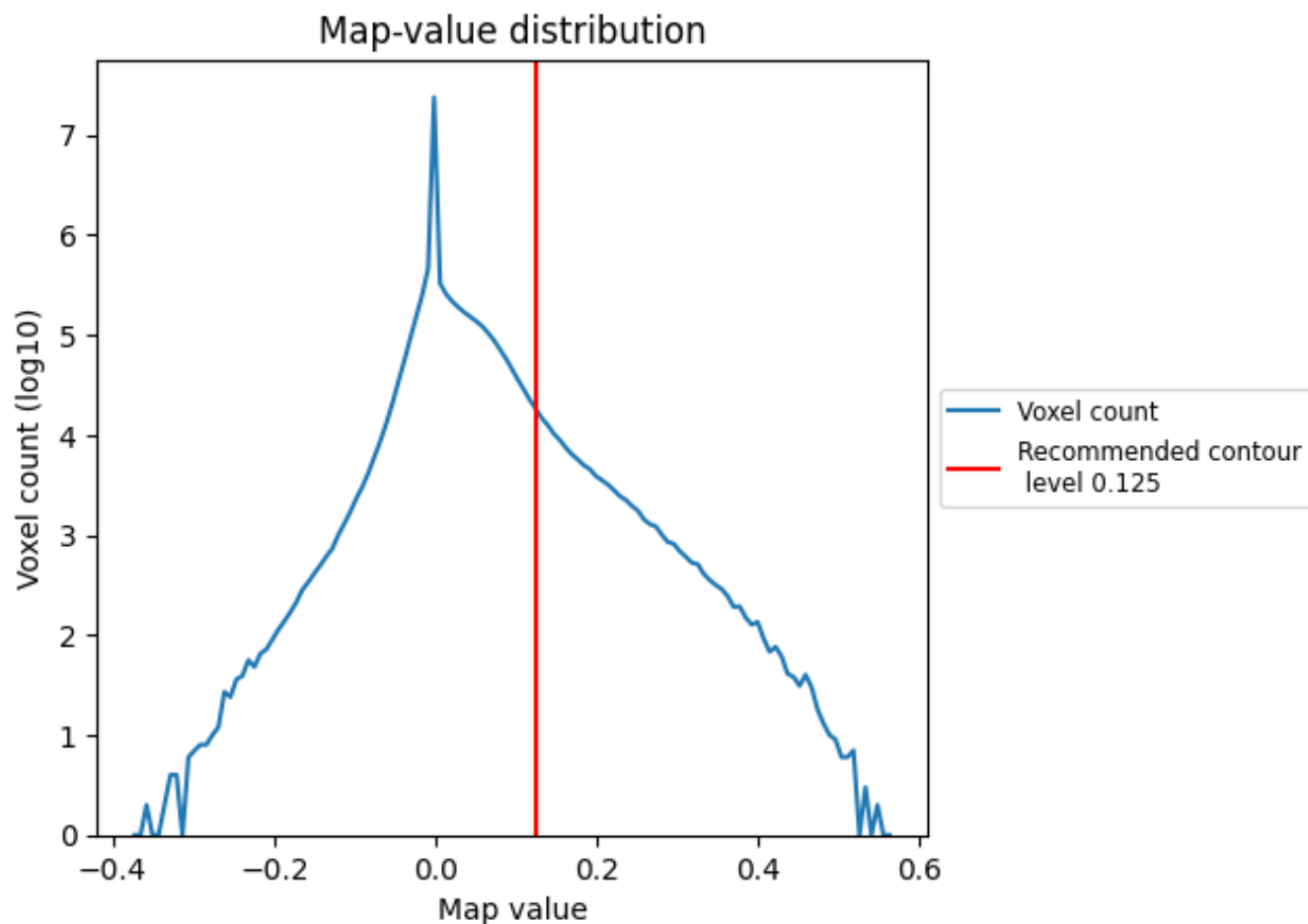
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

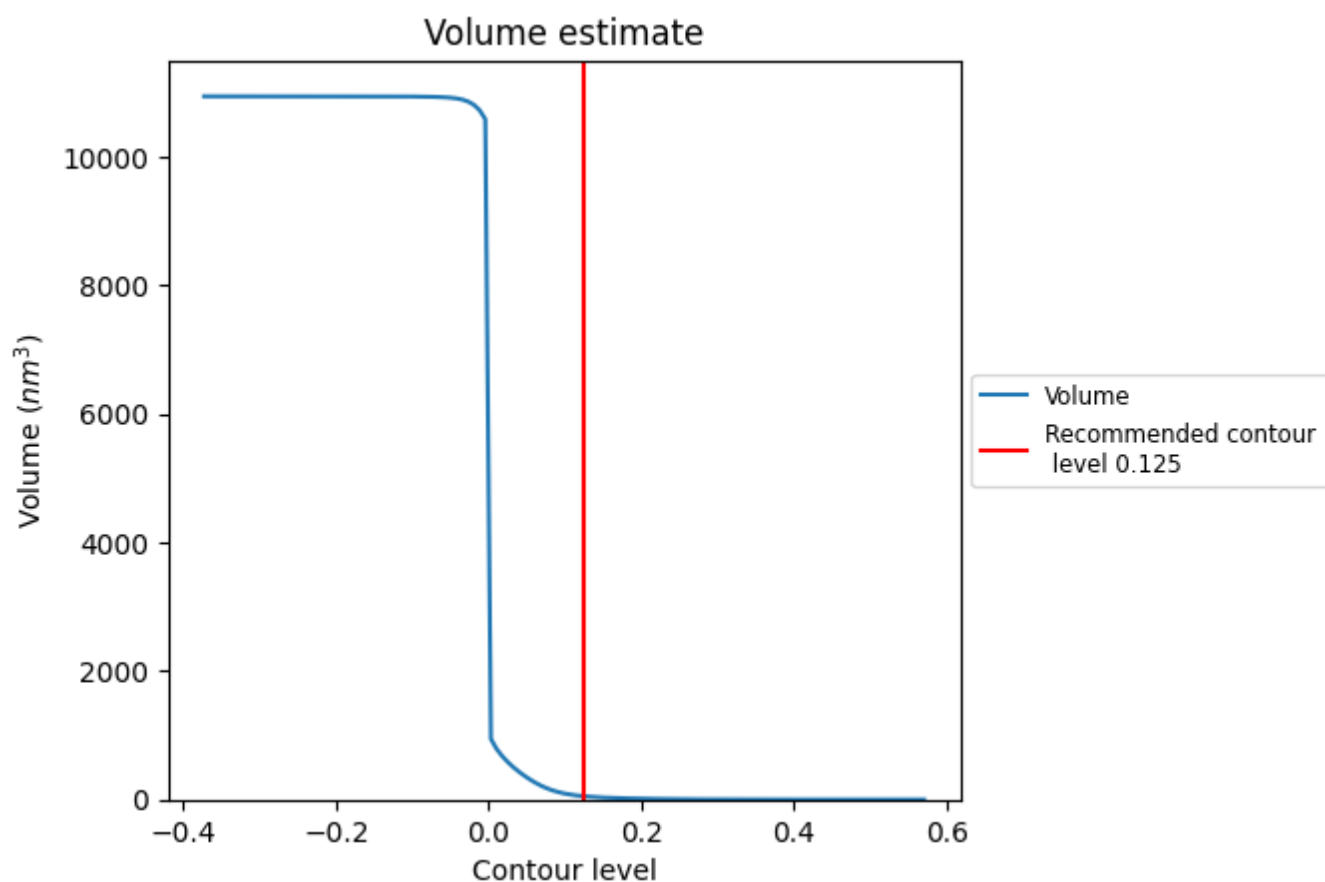
This section contains the results of statistical analysis of the map.

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.

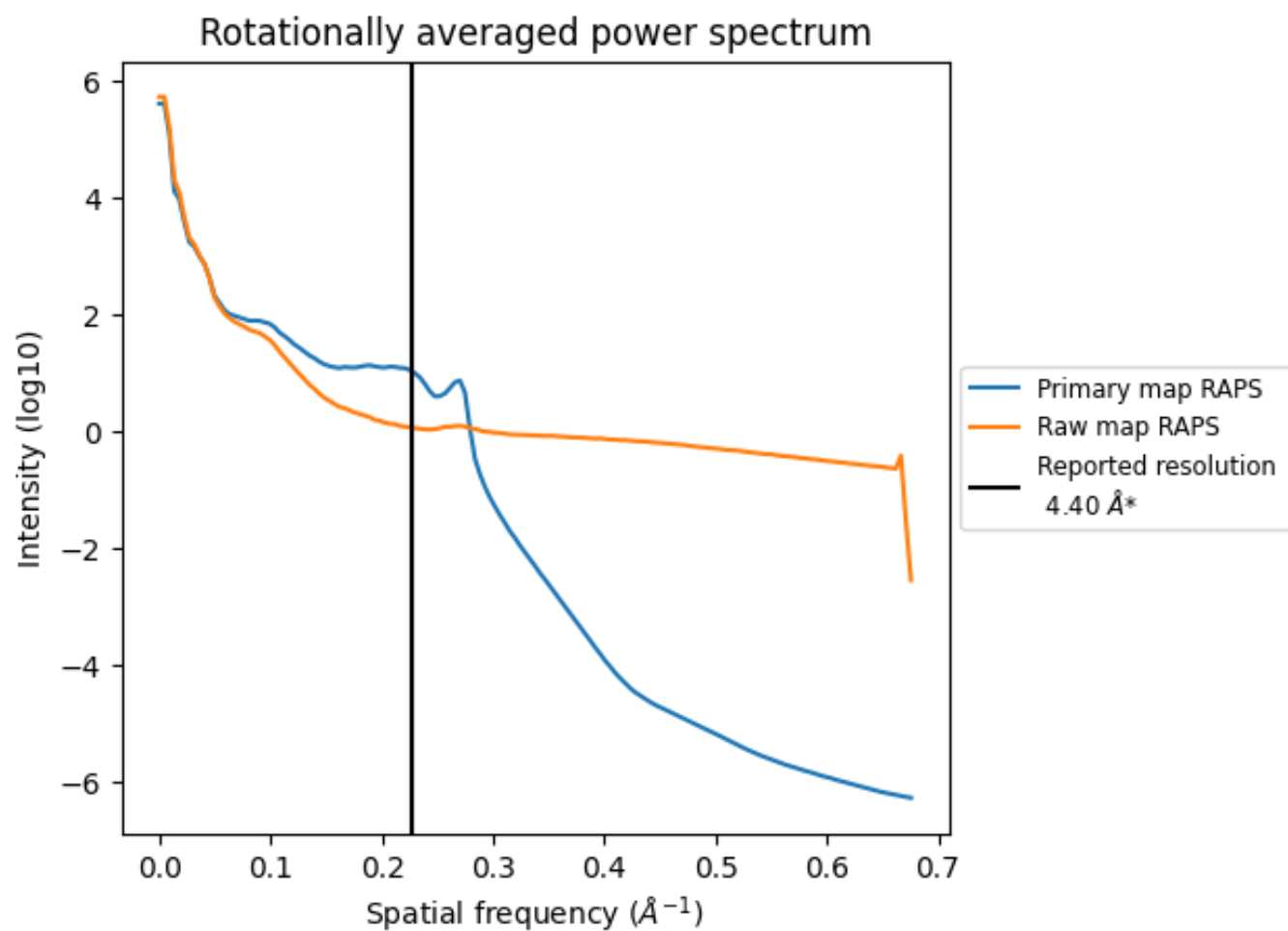
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 51 nm³; this corresponds to an approximate mass of 46 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 ⓘ

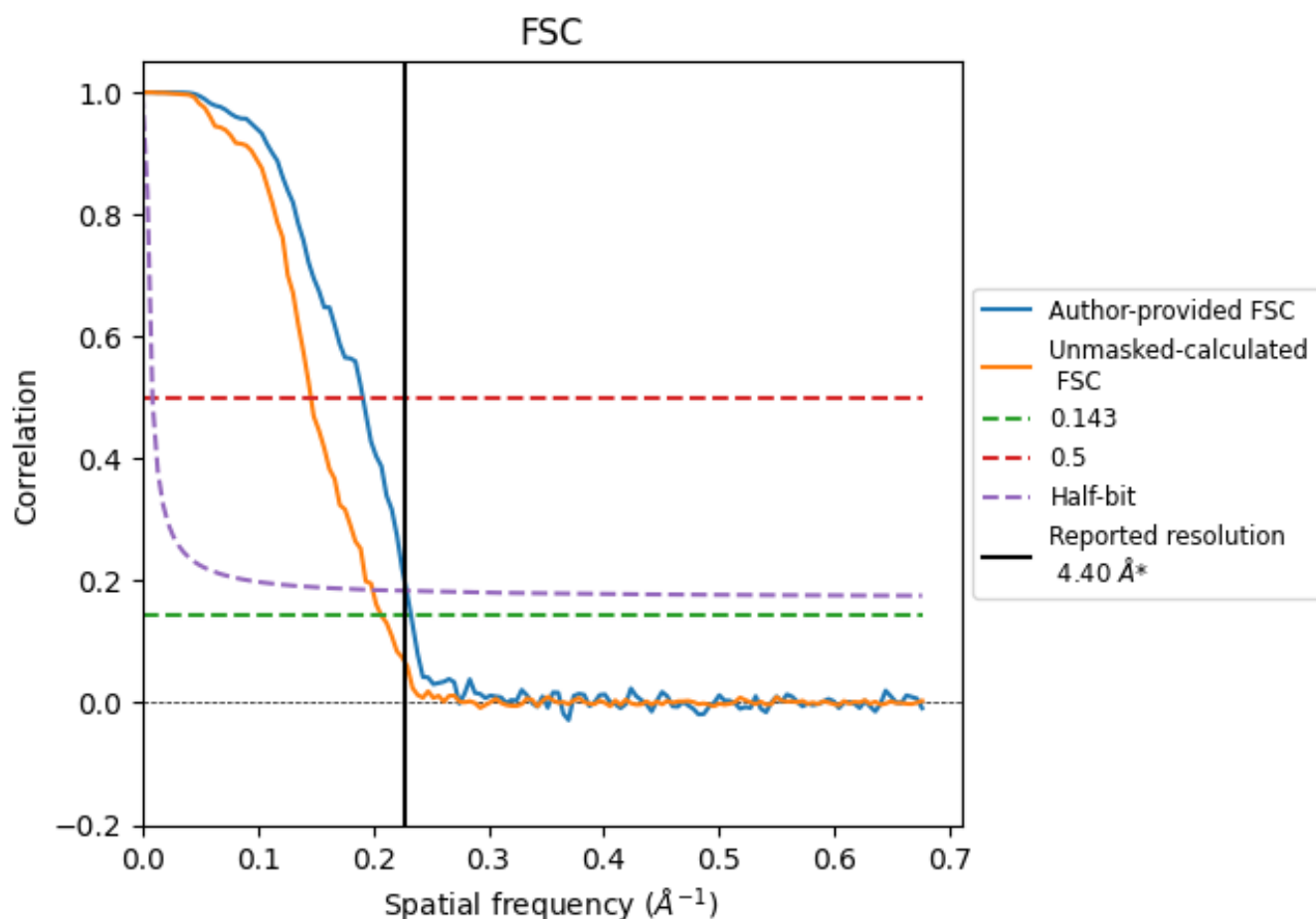


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 $0.227 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

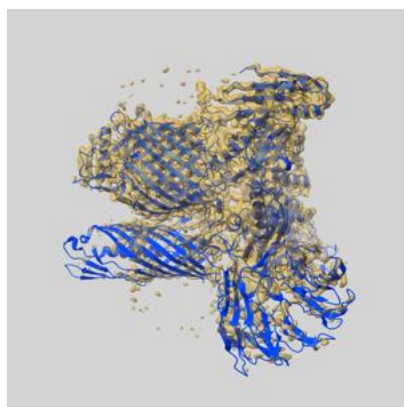
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.29	5.23	4.36
Unmasked-calculated*	4.83	6.84	5.01

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

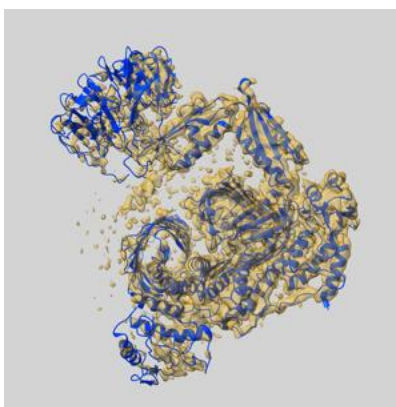
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-18543 and PDB model 8QP5. Per-residue inclusion information can be found in section [3](#) on page [7](#).

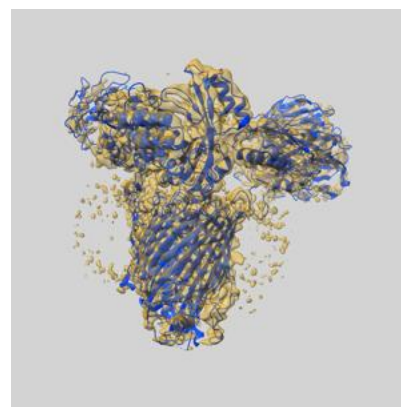
9.1 Map-model overlay [i](#)



X



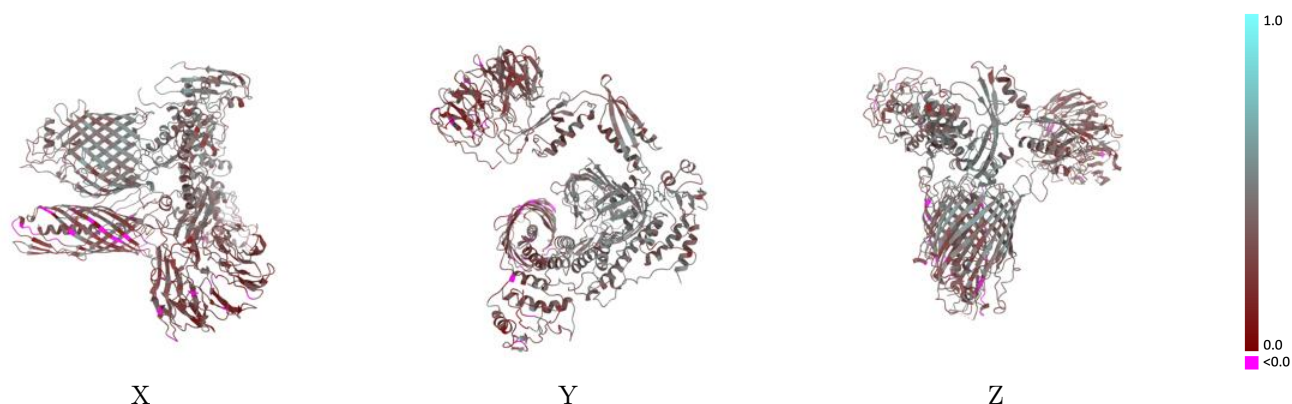
Y



Z

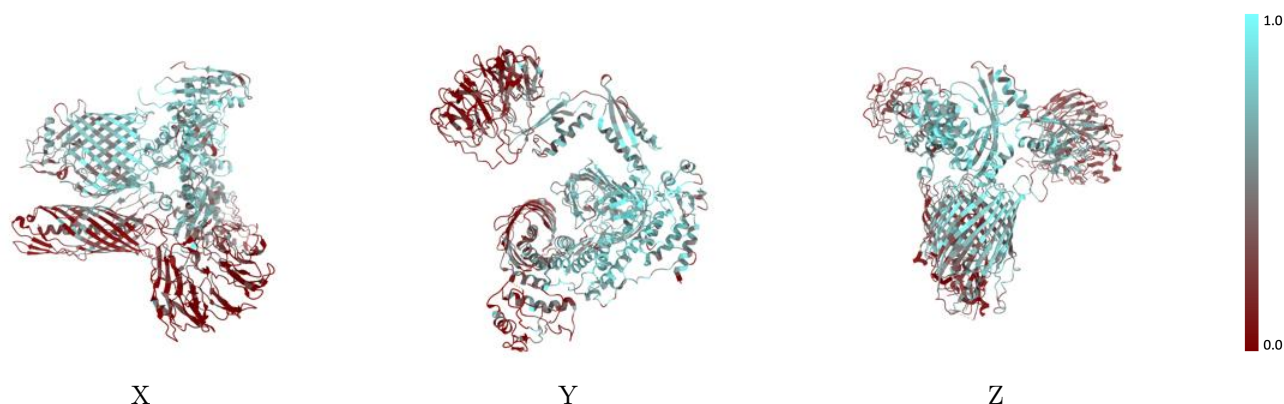
The images above show the 3D surface view of the map at the recommended contour level 0.125 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



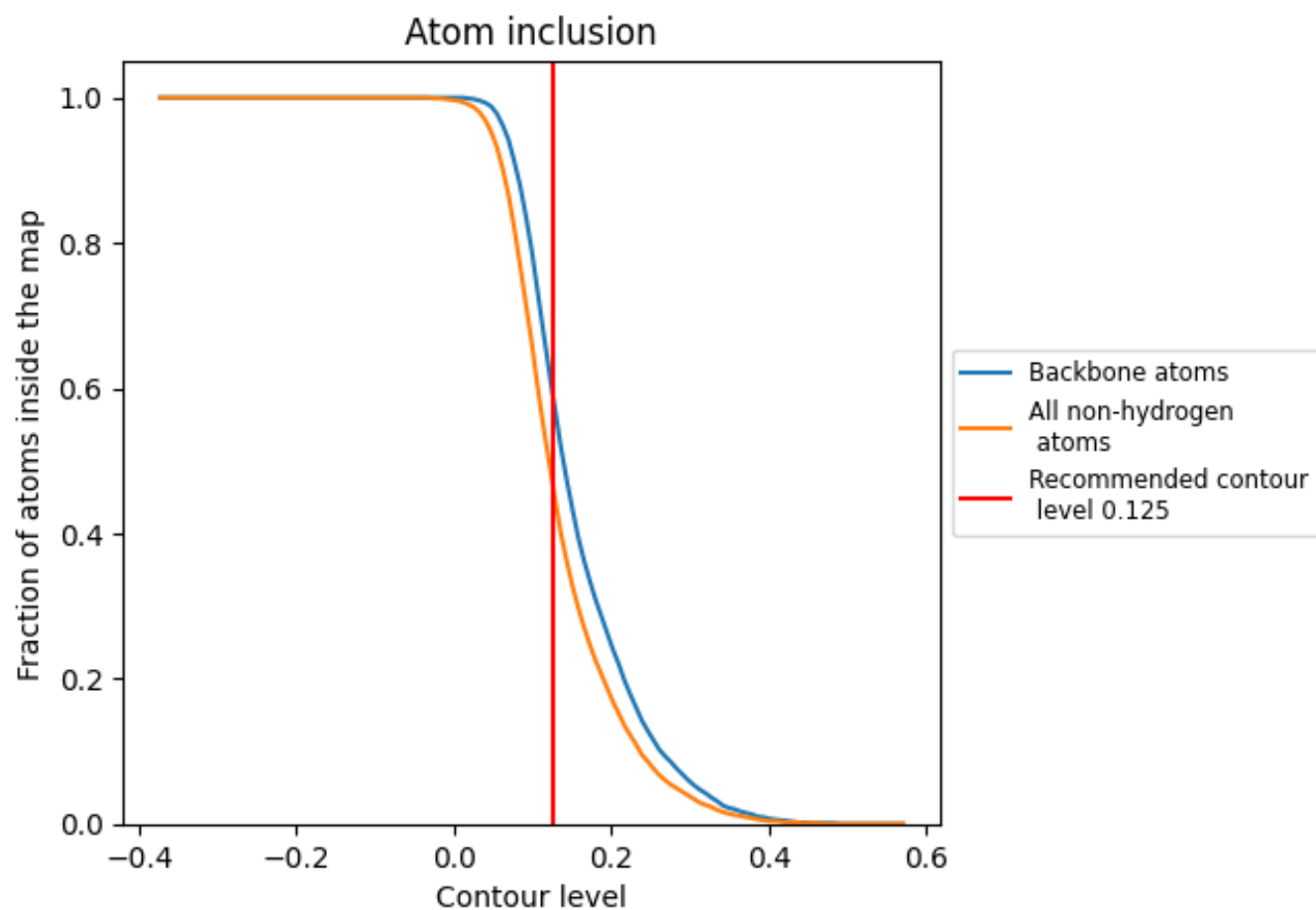
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.125).

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 47% 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 (0.125) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4680	0.3680
A	0.6110	0.4160
B	0.1850	0.2950
C	0.3820	0.3460
D	0.6820	0.4120
E	0.6600	0.4390
P	0.2420	0.2740

