



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 01:46 PM UTC

PDB ID : 7M68 / pdb_00007m68
EMDB ID : EMD-23690
Title : E1435Q Ycf1 mutant in inward-facing narrow conformation
Authors : Khandelwal, N.K.; Millan, C.R.; Thaker, T.M.; Tomasiak, T.M.
Deposited on : 2021-03-25
Resolution : 4.04 Å(reported)
Based on initial model : 6JB1

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
Mogul : 2022.3.0, CSD as543be (2022)
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

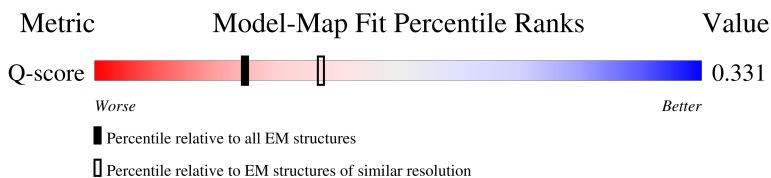
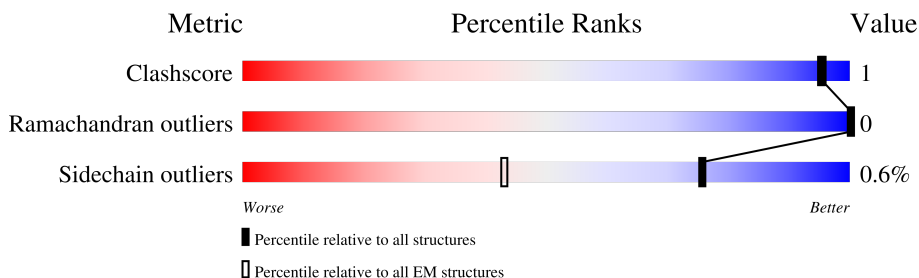
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.04 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	6625 (3.54 - 4.54)

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	1559	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 21820 atoms, of which 10933 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 Metal resistance protein YCF1.

Mol	Chain	Residues	Atoms								AltConf	Trace
1	A	1390	Total	C	H	N	O	P	S		0	0
			21820	7024	10933	1833	1981	3	46			

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	ALA	-	expression tag	UNP P39109
A	-21	SER	-	expression tag	UNP P39109
A	-20	ASP	-	expression tag	UNP P39109
A	-19	TYR	-	expression tag	UNP P39109
A	-18	LYS	-	expression tag	UNP P39109
A	-17	ASP	-	expression tag	UNP P39109
A	-16	ASP	-	expression tag	UNP P39109
A	-15	ASP	-	expression tag	UNP P39109
A	-14	ASP	-	expression tag	UNP P39109
A	-13	LYS	-	expression tag	UNP P39109
A	-12	GLY	-	expression tag	UNP P39109
A	-11	ALA	-	expression tag	UNP P39109
A	-10	LEU	-	expression tag	UNP P39109
A	-9	GLU	-	expression tag	UNP P39109
A	-8	VAL	-	expression tag	UNP P39109
A	-7	LEU	-	expression tag	UNP P39109
A	-6	PHE	-	expression tag	UNP P39109
A	-5	GLN	-	expression tag	UNP P39109
A	-4	GLY	-	expression tag	UNP P39109
A	-3	PRO	-	expression tag	UNP P39109
A	-2	SER	-	expression tag	UNP P39109
A	-1	SER	-	expression tag	UNP P39109
A	0	PRO	-	expression tag	UNP P39109
A	1435	GLN	GLU	engineered mutation	UNP P39109
A	1516	GLY	-	expression tag	UNP P39109
A	1517	LEU	-	expression tag	UNP P39109
A	1518	VAL	-	expression tag	UNP P39109
A	1519	PRO	-	expression tag	UNP P39109

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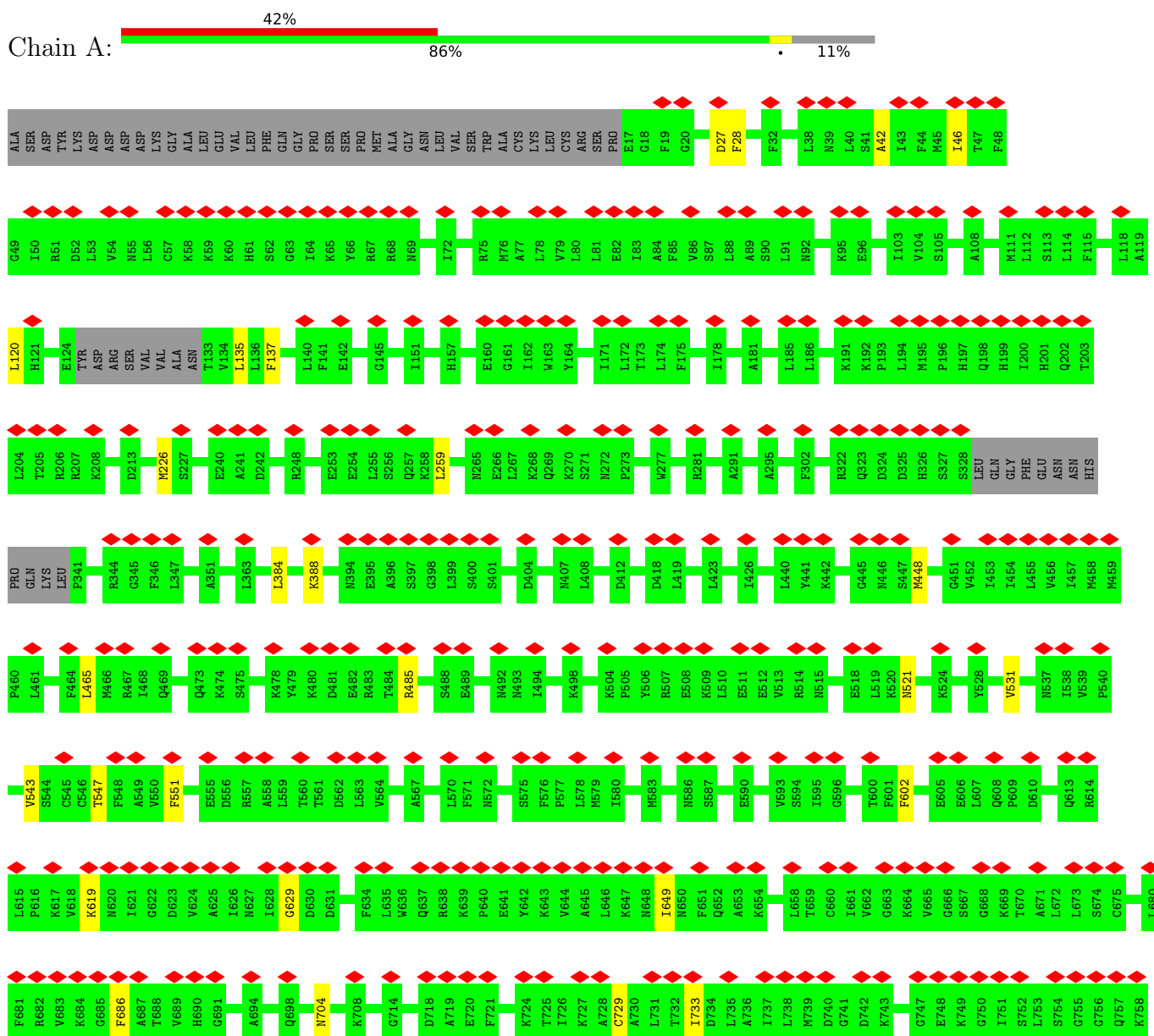
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Chain	Residue	Modelled	Actual	Comment	Reference
A	1520	ARG	-	expression tag	UNP P39109
A	1521	GLY	-	expression tag	UNP P39109
A	1522	SER	-	expression tag	UNP P39109
A	1523	SER	-	expression tag	UNP P39109
A	1524	ALA	-	expression tag	UNP P39109
A	1525	HIS	-	expression tag	UNP P39109
A	1526	HIS	-	expression tag	UNP P39109
A	1527	HIS	-	expression tag	UNP P39109
A	1528	HIS	-	expression tag	UNP P39109
A	1529	HIS	-	expression tag	UNP P39109
A	1530	HIS	-	expression tag	UNP P39109
A	1531	HIS	-	expression tag	UNP P39109
A	1532	HIS	-	expression tag	UNP P39109
A	1533	HIS	-	expression tag	UNP P39109
A	1534	HIS	-	expression tag	UNP P39109
A	1535	GLY	-	expression tag	UNP P39109
A	1536	ALA	-	expression tag	UNP P39109

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: Metal resistance protein YCF1



I1478	V1479	N1482	G1483	K1484	VAL	ALA	GLU	PHE	ASP	SER	PRO	GLY	GLN	LEU	LEU	SER	ASP	ASN	LYS	SER	LEU	PHE	TYR	LEU	CYS	MET	GLU	ALA	GLY	VAL	ASN	ASN	GLY	VAL	PRO	ARG	GLY	SER	SER	ALA	HIS	HIS	HIS	HIS	HIS	HIS	HIS	GLY	ALA										
S1411	V1412	G1413	Q1414	R1415	L1420	ALA	A1421	R1422	A1423	M1424	L1425	S1428	K1429	I1430	L1431	V1432	L1433	D1434	Q1435	A1436	T1437	A1438	A1439	V1440	D1441	V1442	E1443	T1444	D1445	K1446	E1450	T1451	I1452	R1453	T1454	A1455	F1456	K1457	D1458	R1459	T1460	I1461	L1462	T1463	L1464	A1465	H1466	R1467	L1468	N1469	T1470	I1471	M1472	D1475	R1476	I1477			
L1345	R1346	H1347	K1348	L1349	S1350	I1351	Q1354	D1355	S1356	Q1357	E1360	G1361	R1364	E1365	N1366	I1367	N1371	Q1372	Y1373	T1374	D1375	E1376	A1377	I1378	W1379	R1380	E1383	L1384	S1385	H1386	L1387	K1388	E1389	H1390	V1391	L1392	S1393	M1394	S1395	N1396	D1397	G1398	L1399	D1400	A1401	Q1402	L1403	T1404	E1405	G1406	G1407	G1408	N1409	L1410					
P1283	E1284	L1285	D1286	L1287	V1288	L1289	K1290	L1291	I1292	N1293	L1294	H1295	I1296	K1297	P1298	N1299	E1300	K1301	V1302	G1303	I1304	V1305	G1306	R1307	T1308	G1309	A1310	G1311	K1312	E1313	S1314	L1315	A1318	L1319	F1320	R1321	M1322	I1323	E1324	A1325	S1326	E1327	G1328	N1329	I1330	V1331	I1332	D1333	M1334	I1335	A1336	T1337	N1338	E1339	I1340	G1341	L1342		
F1197	K1200	Q1201	G1202	T1203	G1210	Q1221	N1224	W1225	I1226	V1227	E1234	T1235	N1236	I1237	E1241	R1242	I1243	K1244	E1245	D1248	L1249	K1250	S1251	E1252	A1253	I1256	V1257	E1258	GLY	HIS	ARG	PRO	PRO	LYS	GLU	TRP	PRO	S1268	D1271	I1272	K1273	F1274	N1275	N1276	I1277	S1278	T1279	R1280	Y1281	R1282									
T1043	I1046	G1047	N1051	R1052	F1053	S1054	K1059	V1060	D1061	R1066	F1072	V1073	N1074	I1082	I1085	C1086	I1093	F1094	I1095	I1096	I1097	P1098	L1099	Y1110	L1111	R1112	R1115	R1119	I1123	T1124	R1125	E1134	L1139	A1140	R1143	A1172	L1176	A1177	G1184	S1185																			
I955	L956	F957	L964	N967	G968	N969	W970	W971	L972	K973	R981	Y982	G983	S984	N985	P986	N987	A988	A989	R990	Y991	L992	A993	I994	Y995	F996	A997	I1000	G1001	S1002	A1003	L1004	L1007	I1008	I1011	V1012	L1013	W1014	V1015	F1016	C1017	S1022	A1023	Y1024	M1029	L1034	R1035	A1036	E1042										
ASP	PHE	GLY	ASN	SER	ASP	A901	I902	S903	L904	R905	R906	A907	S908	D909	A910	T911	L912	G913	S914	I915	D916	F917	G918	D919	D920	E921	N922	I923	A924	K925	R926	E927	H928	R929	E930	Q931	G932	K933	V934	K935	W936	N937	I938	Y939	L940	E941	Y942	A943	K944	A945	C946	N947	P948	K949	S950	V951	C952	V953	F954
G835	T836	Y837	D838	E839	I840	T841	K842	D843	A844	D845	S846	P847	L848	W849	K850	L851	LEU	ASN	ASN	TYR	GLY	LYS	LYS	ASN	ASN	ASN	GLY	LYS	SER	ASN	GLU	PHE	GLY	ASP	SER	SER	VAL	ARG	GLU	SER	SER	ILE	PRO	VAL	GLU	GLY	LEU	GLU	GLN	LEU	GLN	LYS	LEU	ASN	ASP	LEU			
A759	R760	R765	D772	T773	Y774	L775	L776	D777	D778	P779	L780	A781	A782	V783	D784	E785	H786	V787	A788	R789	E793	H794	V795	L796	N799	G800	L801	T804	K805	T806	K807	A810	T811	N812	K813	V814	S815	A816	L817	S818	S822	I823	A824	L825	L826	D827	N828	I831	T832	Q833	Q834								

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	48716	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 ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	22500	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	15.257	Depositor
Minimum map value	-12.044	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.907	Depositor
Recommended contour level	4	Depositor
Map size (Å)	309.30002, 309.30002, 309.30002	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.031, 1.031, 1.031	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, SEP

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	0.21	0/11069	0.41	0/15011

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	10887	10933	10946	22	0
All	All	10887	10933	10946	22	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 1.

The worst 5 of 22 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:1176:LEU:HD21	1:A:1227:VAL:HG11	1.85	0.59
1:A:629:GLY:N	1:A:686:PHE:O	2.36	0.58
1:A:729:CYS:SG	1:A:795:VAL:HG21	2.44	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1110:TYR:CG	1:A:1176:LEU:HD22	2.40	0.57
1:A:649:ILE:HD12	1:A:831:ILE:HG22	1.87	0.55

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	1377/1559 (88%)	1298 (94%)	79 (6%)	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	1166/1364 (86%)	1159 (99%)	7 (1%)	78	80

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	917	PHE
1	A	946	CYS
1	A	1354	GLN
1	A	1125	ARG

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Mol	Chain	Res	Type
1	A	915	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1435	GLN
1	A	1482	ASN
1	A	987	ASN
1	A	1055	ASN
1	A	1131	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	SEP	A	914	1	8,9,10	1.61	1 (12%)	7,12,14	1.47	1 (14%)
1	SEP	A	908	1	8,9,10	1.59	1 (12%)	7,12,14	1.39	1 (14%)
1	TPO	A	911	1	8,10,11	1.65	1 (12%)	10,14,16	1.92	2 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	A	914	1	-	1/6/8/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	A	908	1	-	3/6/8/10	-
1	TPO	A	911	1	-	4/9/11/13	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	911	TPO	P-O1P	3.55	1.61	1.50
1	A	914	SEP	P-O1P	3.50	1.61	1.50
1	A	908	SEP	P-O1P	3.49	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	911	TPO	P-OG1-CB	-5.20	109.18	123.33
1	A	914	SEP	OG-CB-CA	3.35	111.41	108.14
1	A	908	SEP	OG-CB-CA	3.00	111.06	108.14
1	A	911	TPO	O-C-CA	-2.13	119.30	124.77

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	908	SEP	C-CA-CB-OG
1	A	908	SEP	CA-CB-OG-P
1	A	911	TPO	N-CA-CB-OG1
1	A	911	TPO	C-CA-CB-CG2
1	A	914	SEP	N-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

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.

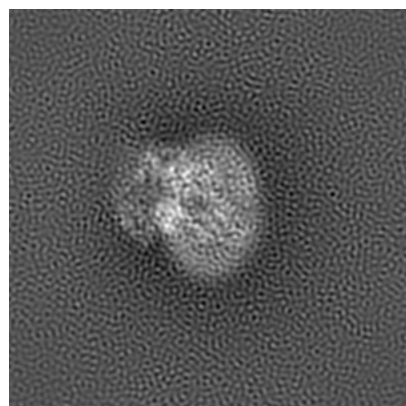
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23690. These allow visual inspection of the internal detail of the map and identification of artifacts.

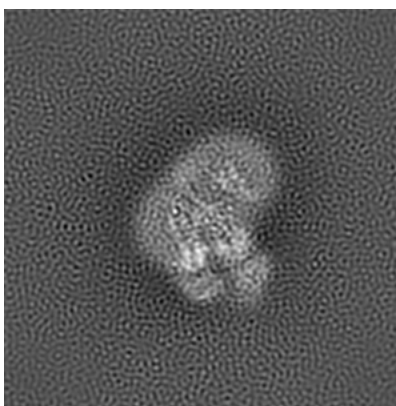
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

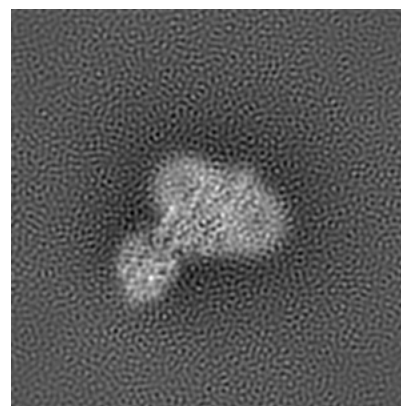
6.1.1 Primary map



X

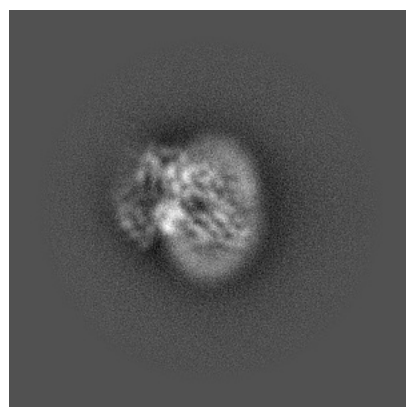


Y

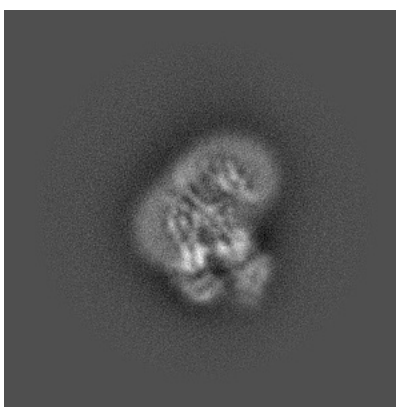


Z

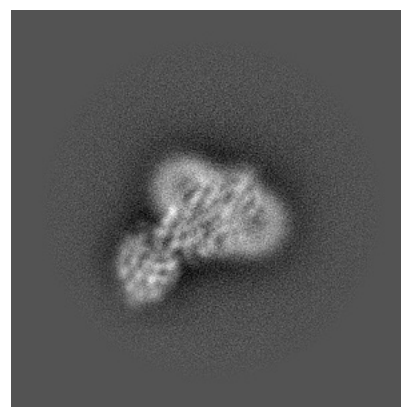
6.1.2 Raw map



X



Y

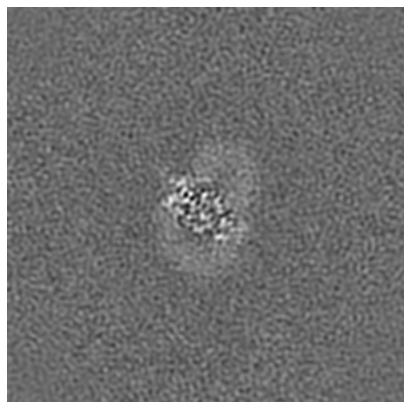


Z

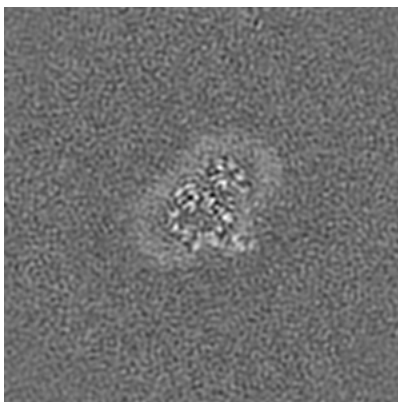
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

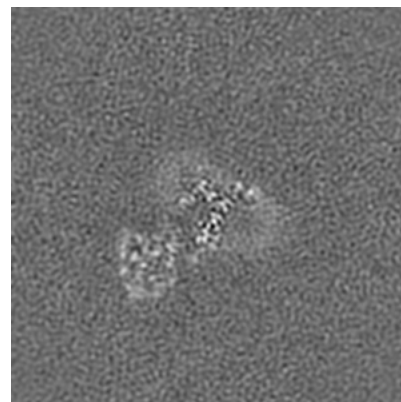
6.2.1 Primary map



X Index: 150

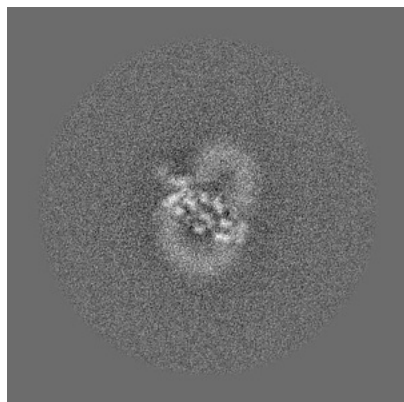


Y Index: 150

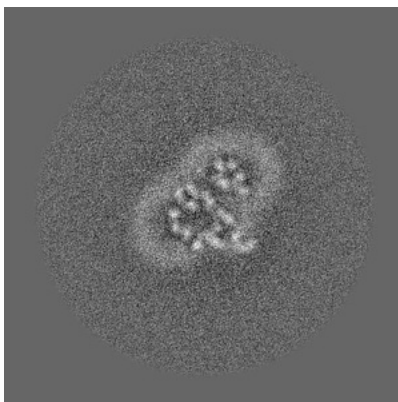


Z Index: 150

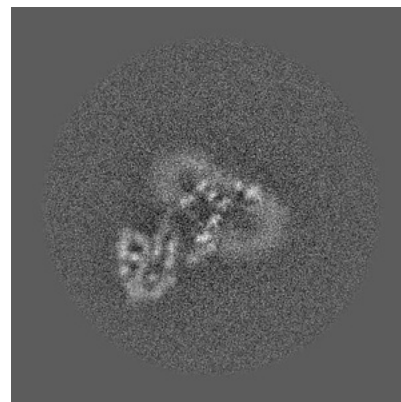
6.2.2 Raw map



X Index: 150



Y Index: 150

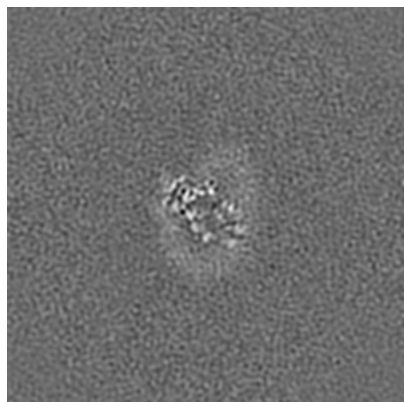


Z Index: 150

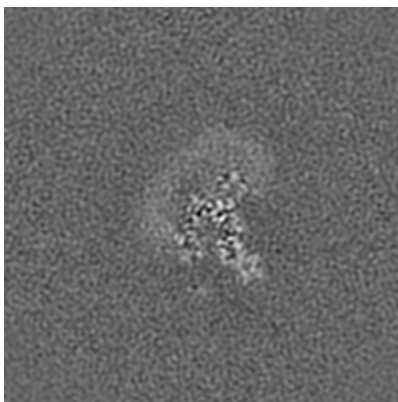
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

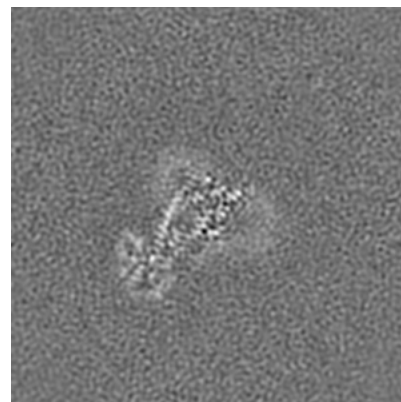
6.3.1 Primary map



X Index: 144

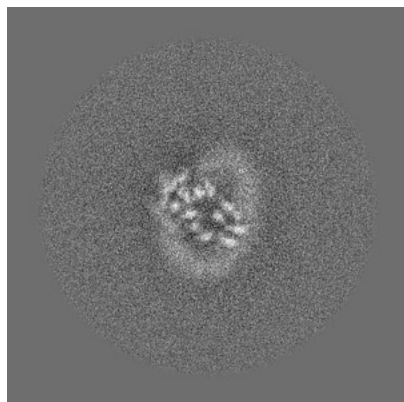


Y Index: 132

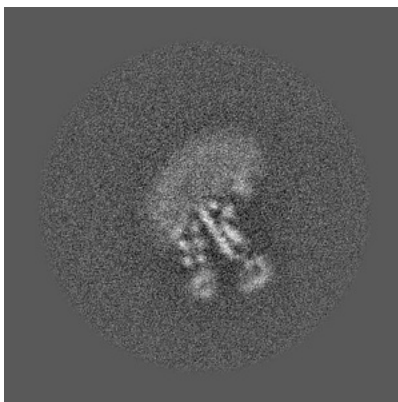


Z Index: 145

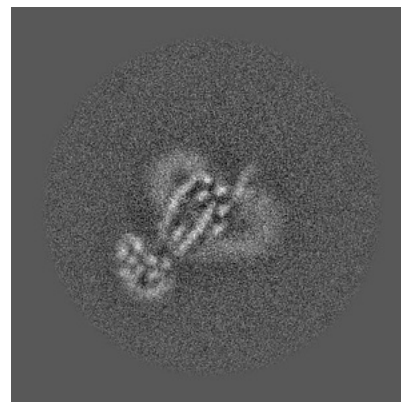
6.3.2 Raw map



X Index: 143



Y Index: 125

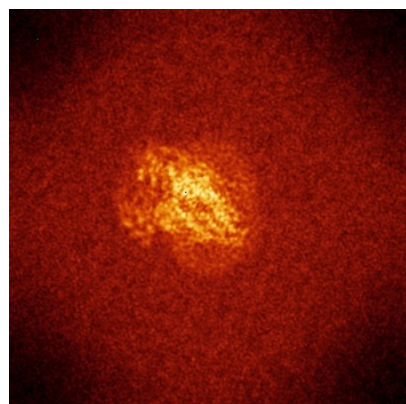


Z Index: 143

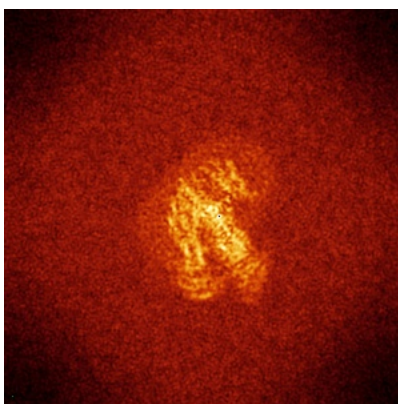
The images above show the largest variance slices of the map in three orthogonal directions.

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

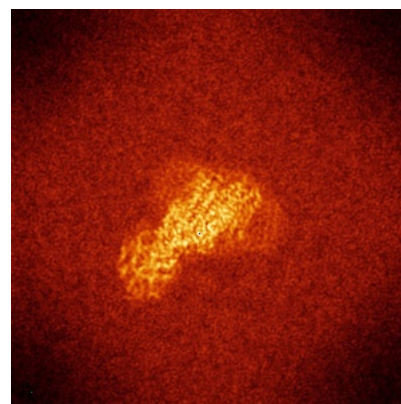
6.4.1 Primary map



X

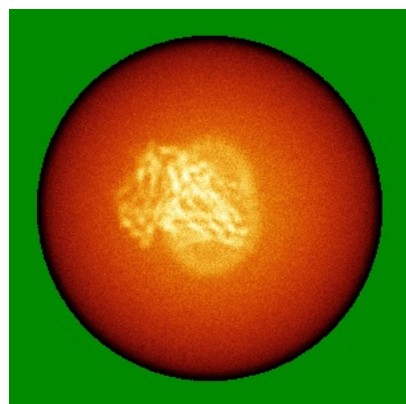


Y

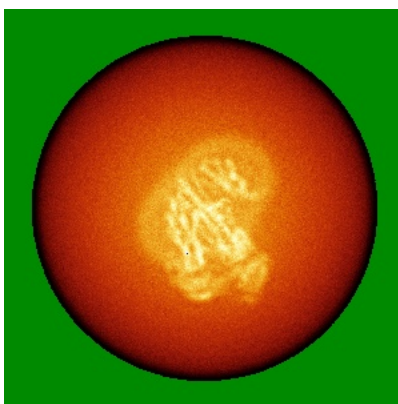


Z

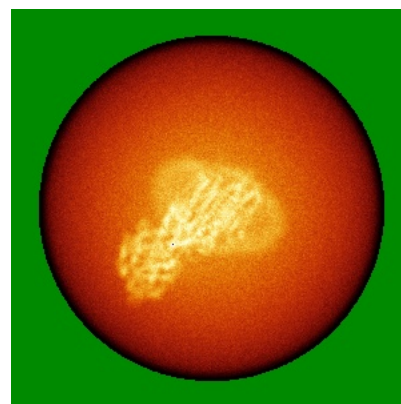
6.4.2 Raw map



X



Y

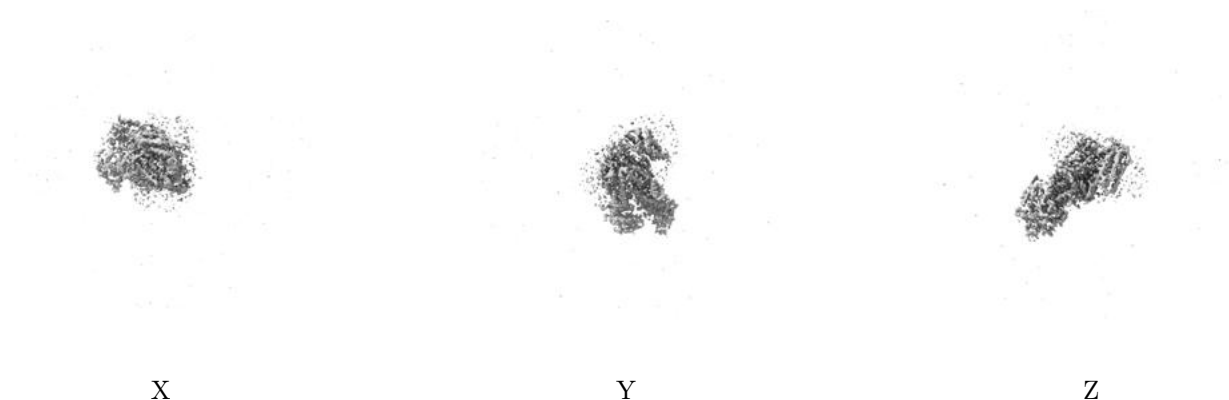


Z

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.

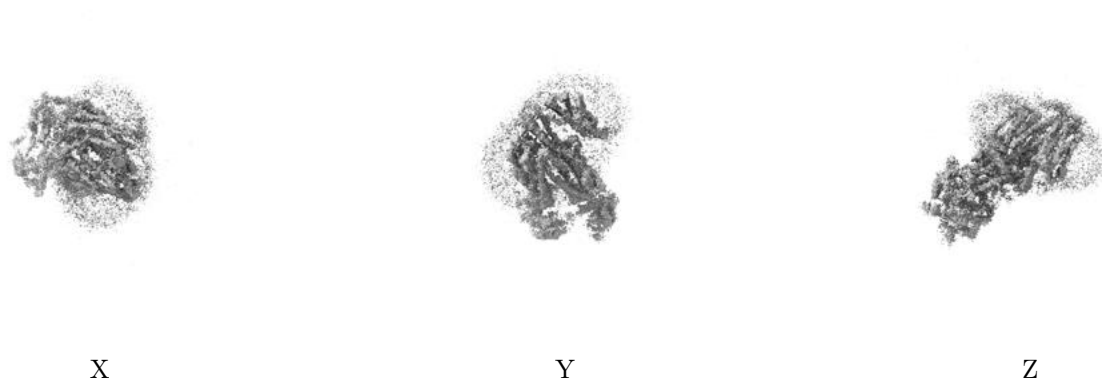
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. 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.

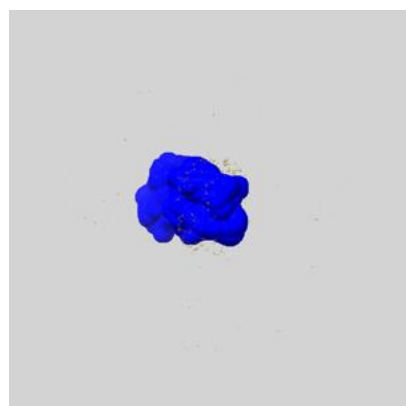
6.6 Mask visualisation [i](#)

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

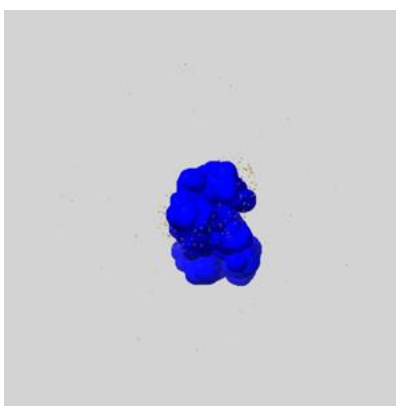
A mask typically either:

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

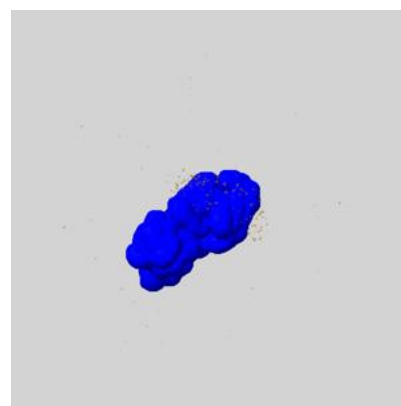
6.6.1 emd_23690_msk_1.map [i](#)



X



Y

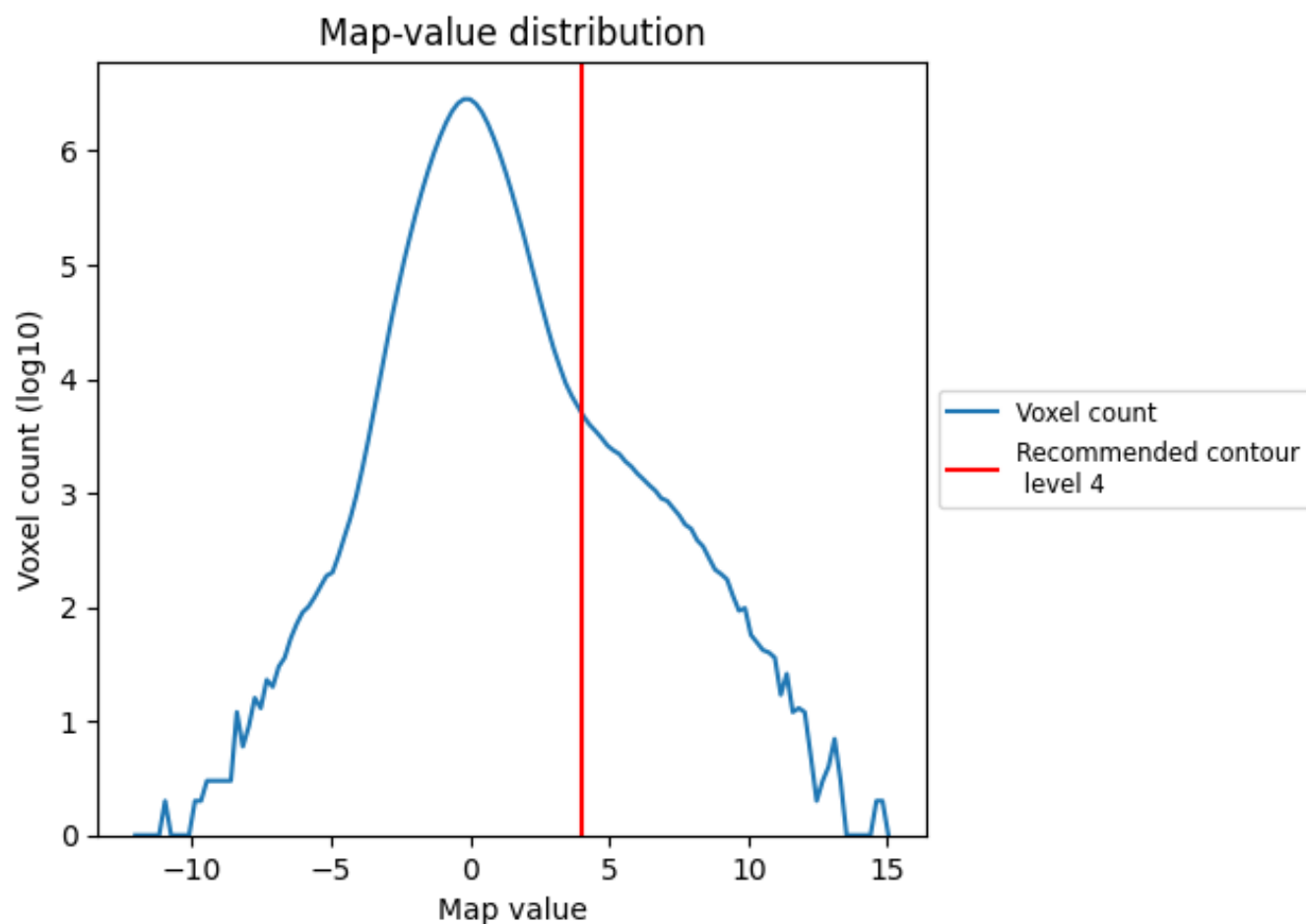


Z

7 Map analysis [i](#)

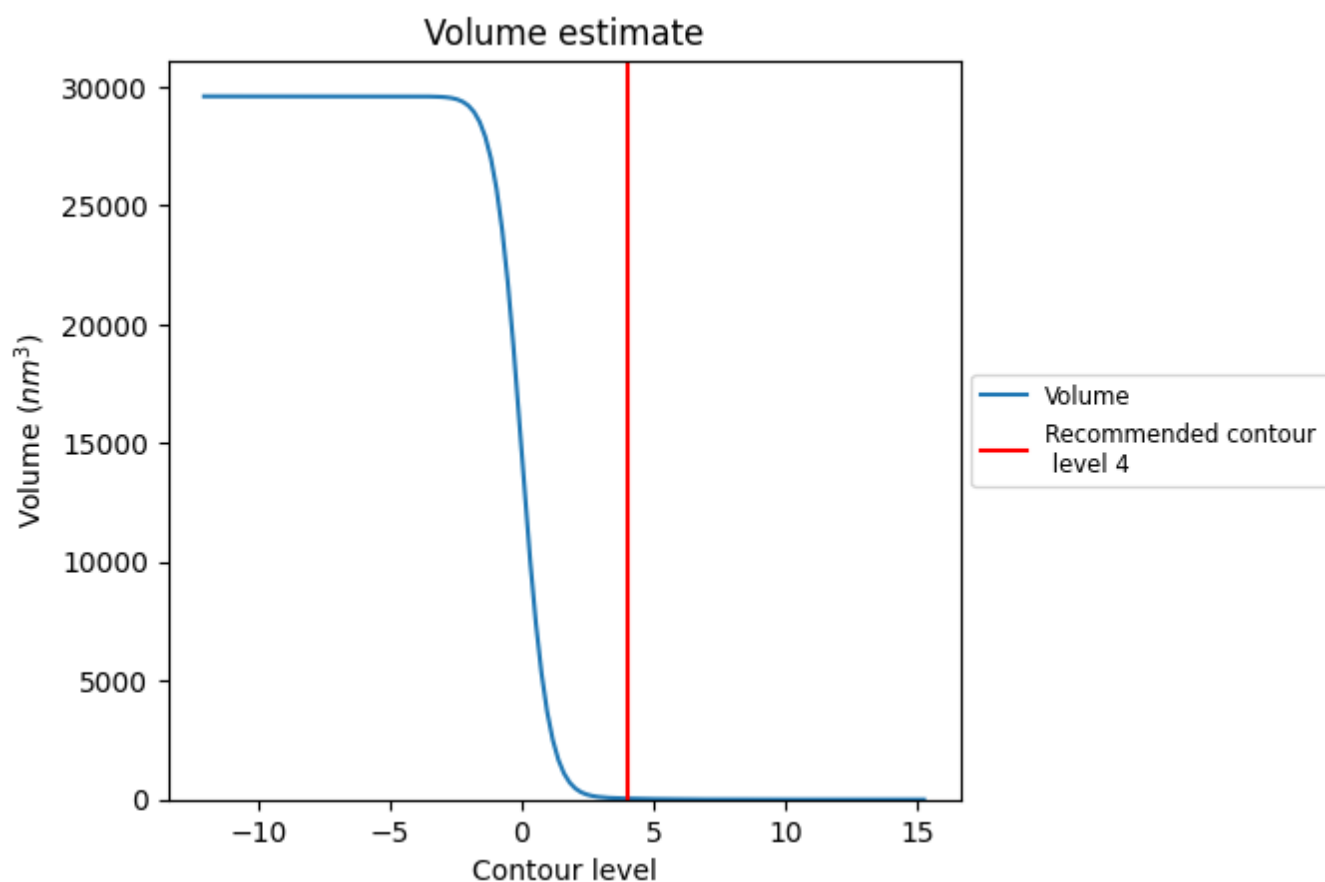
This section contains the results of statistical analysis of the map.

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.

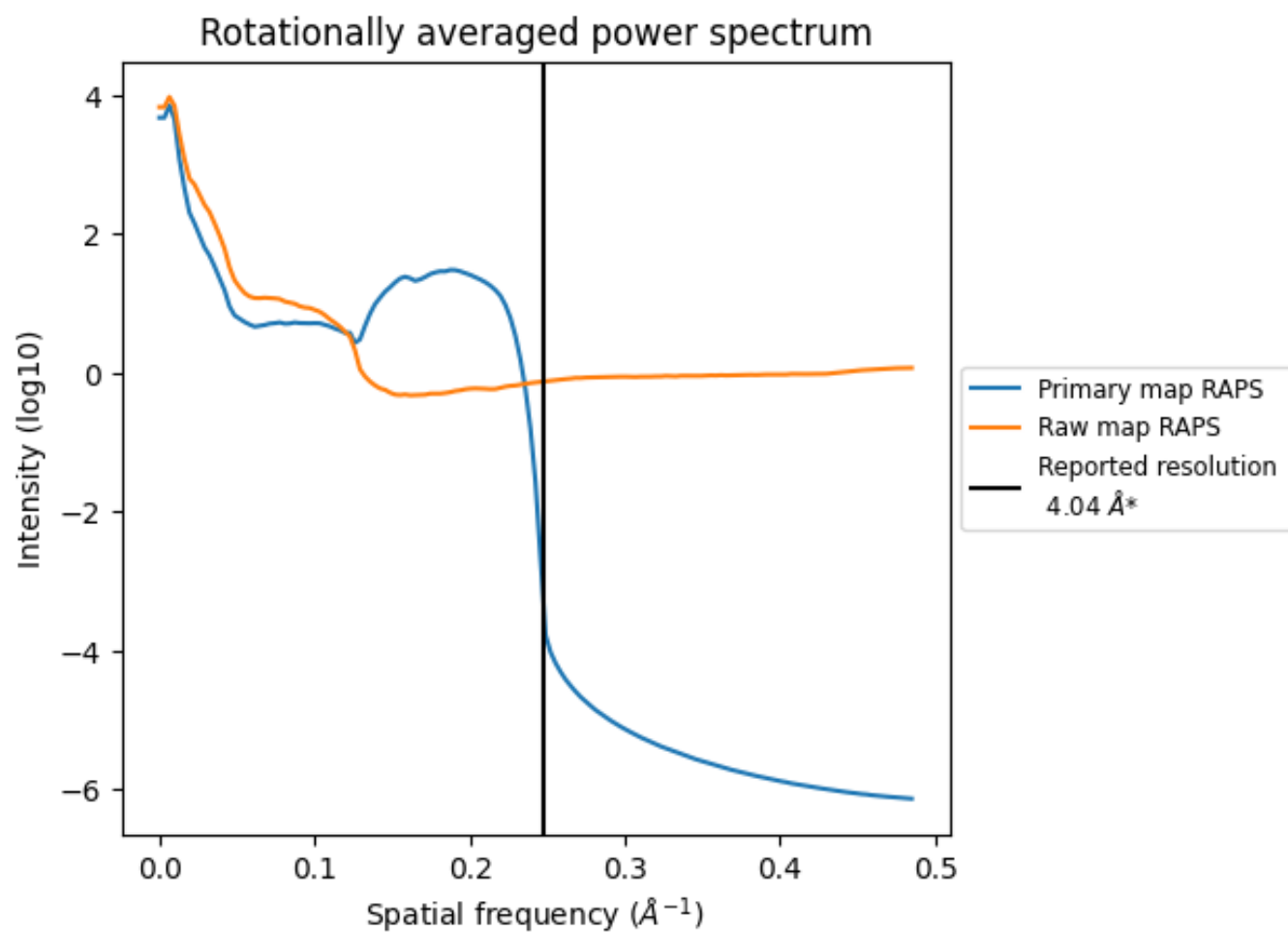
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 43 nm³; this corresponds to an approximate mass of 39 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 ⓘ

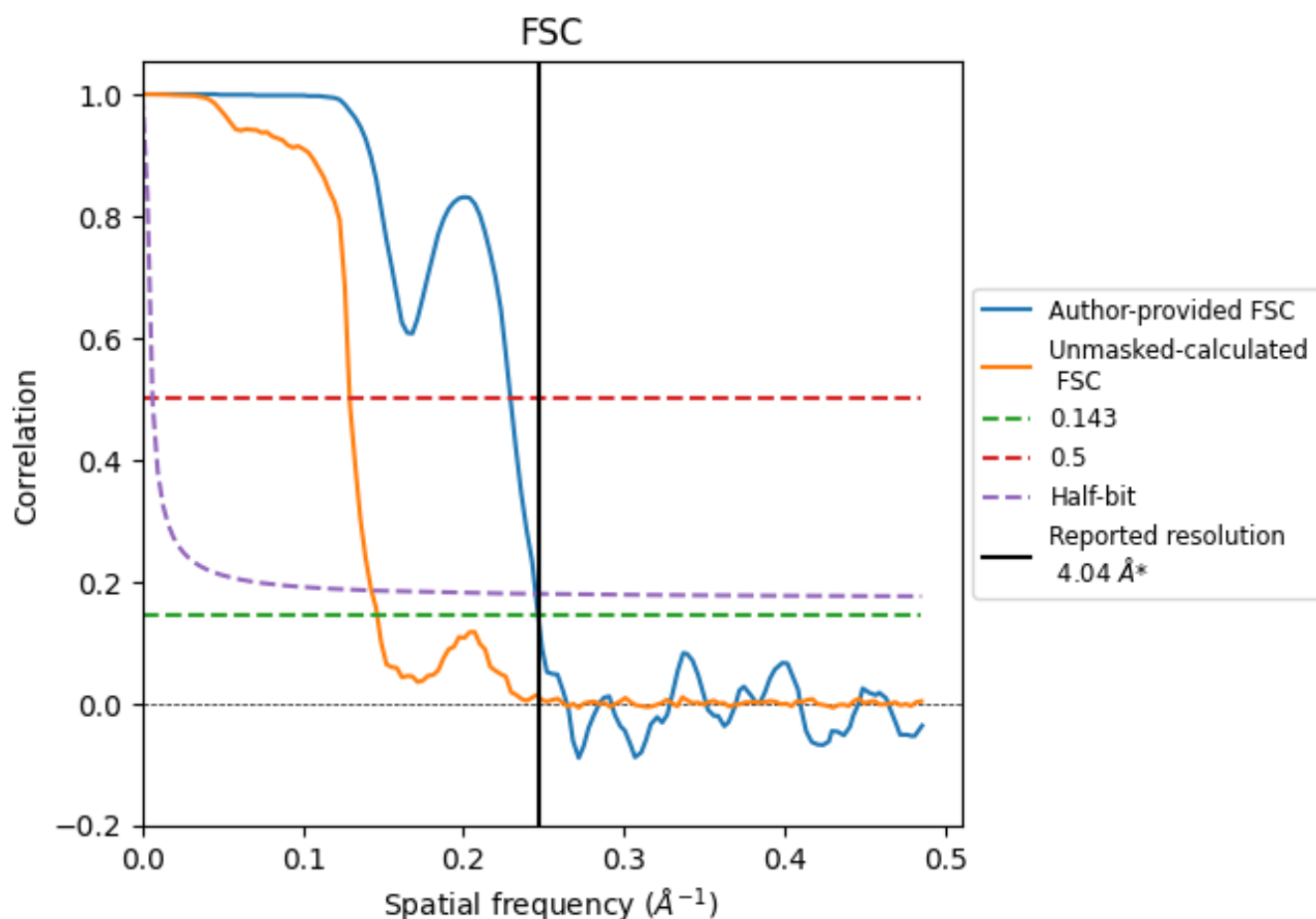


*Reported resolution corresponds to spatial frequency of 0.248 $\text{\AA}^{-1}$

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 $0.248 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

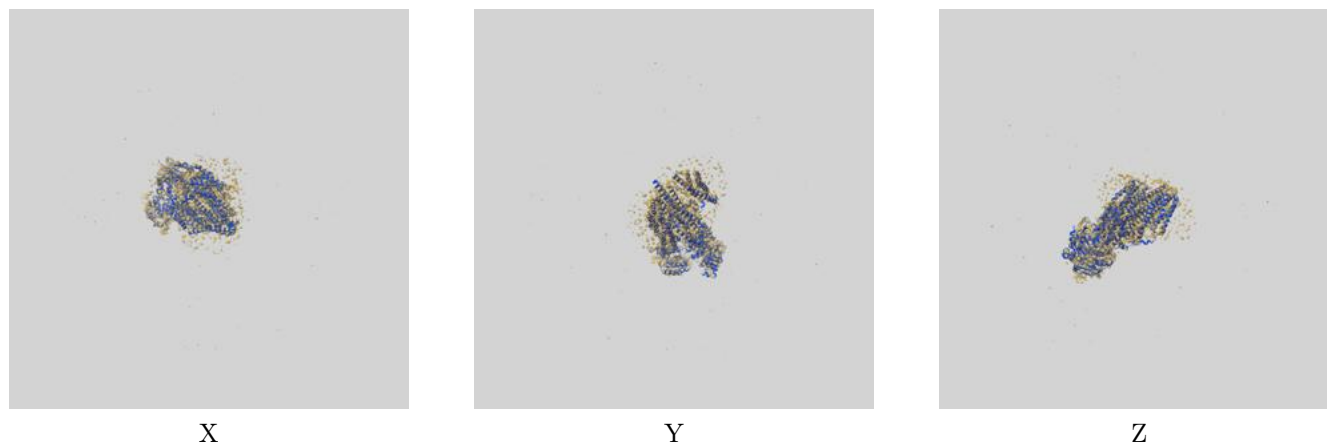
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.04	-	-
Author-provided FSC curve	4.06	4.36	4.08
Unmasked-calculated*	6.84	7.75	7.01

*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 6.84 differs from the reported value 4.04 by more than 10 %

9 Map-model fit [i](#)

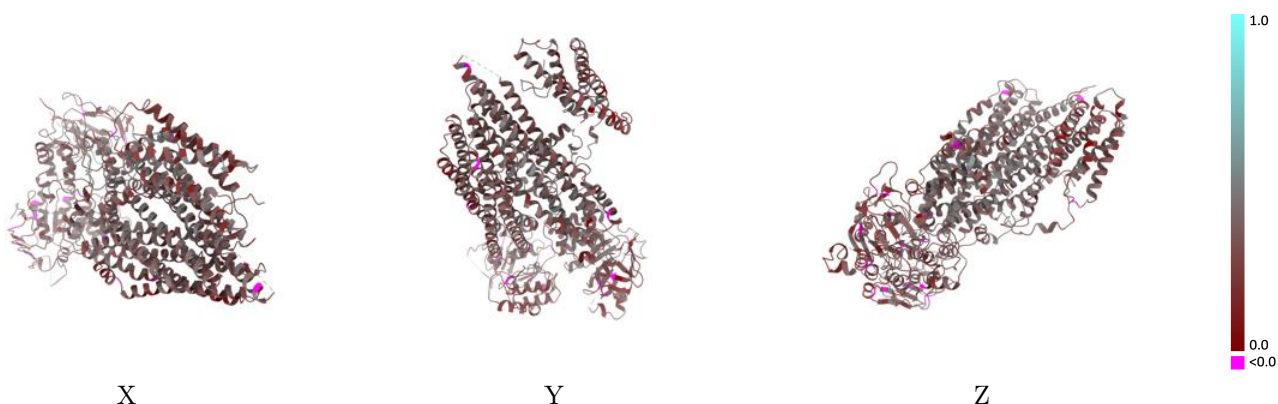
This section contains information regarding the fit between EMDB map EMD-23690 and PDB model 7M68. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



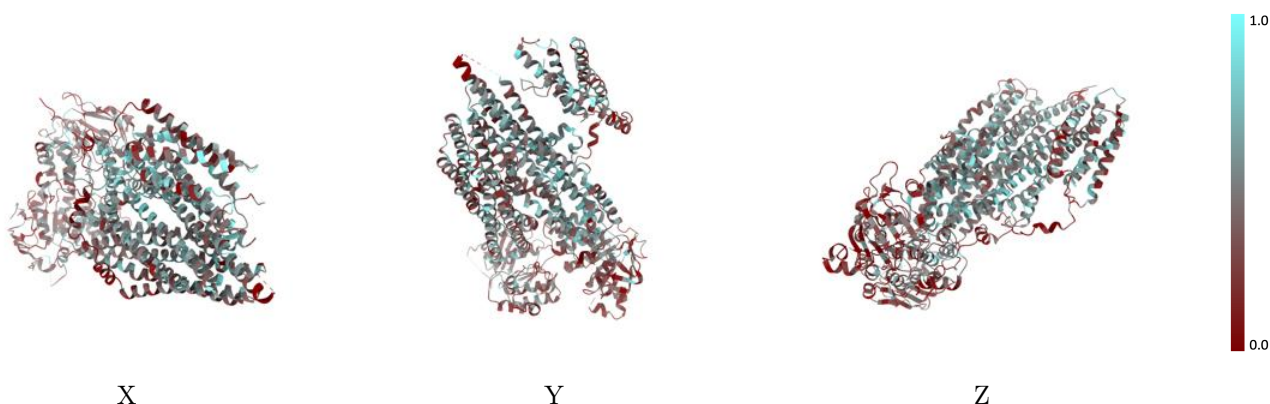
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



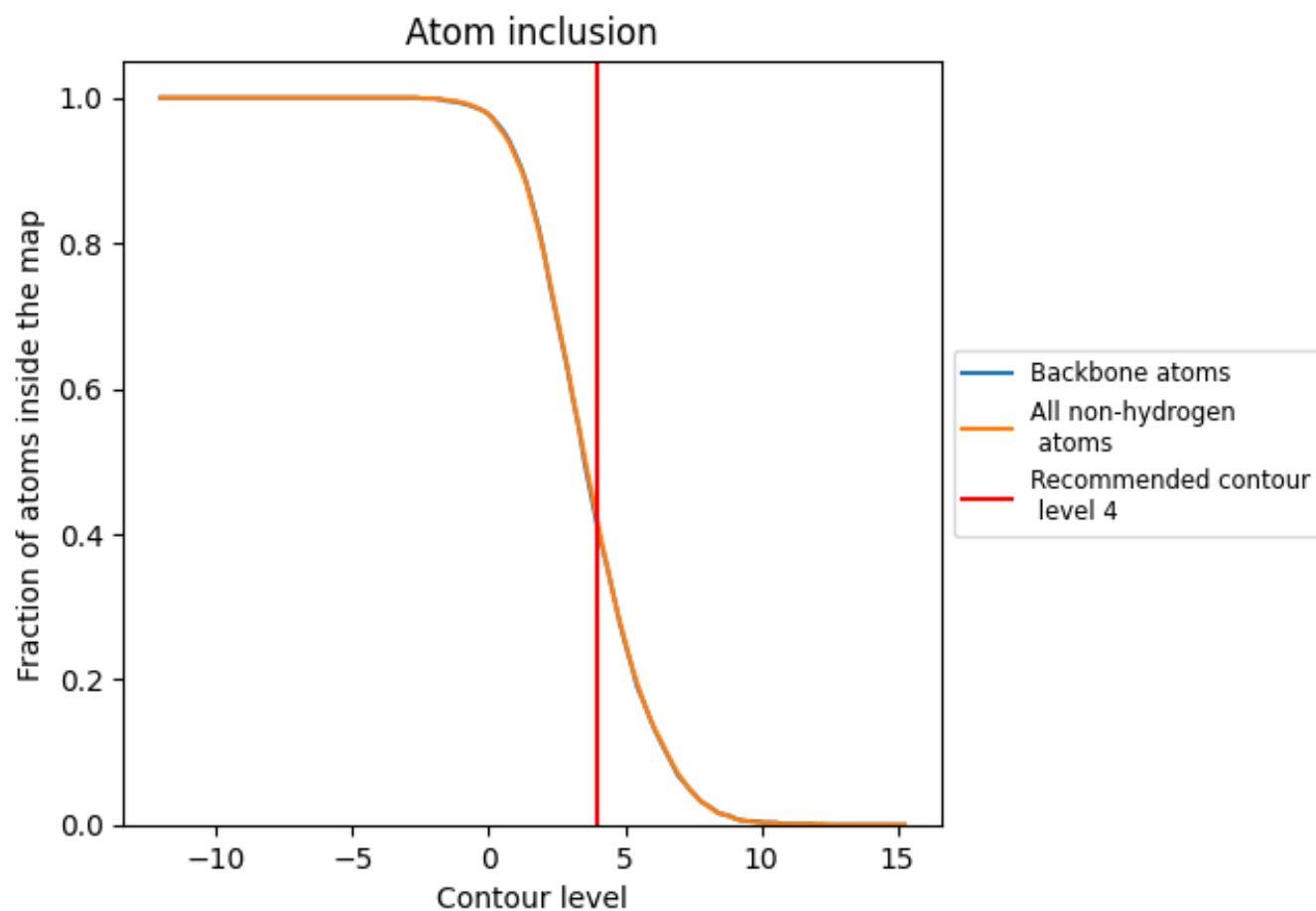
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 41% of all backbone atoms, 41% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4140	0.3310
A	0.4190	0.3310

