



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 01:56 AM UTC

PDB ID : 8VDO / pdb_00008vdo
EMDB ID : EMD-43152
Title : Cryogenic electron microscopy model of full-length talin lacking F2, R12 and FABD.
Authors : Izard, T.; Rangarajan, E.S.
Deposited on : 2023-12-16
Resolution : 2.70 Å(reported)
Based on initial model : 6r9t

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

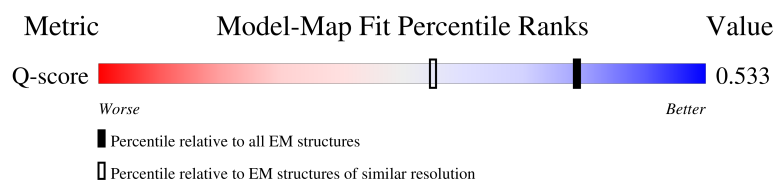
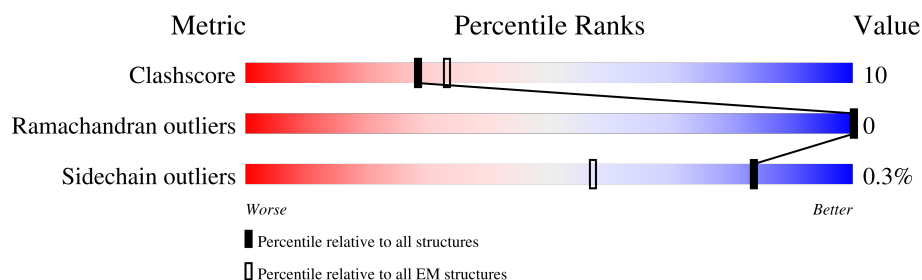
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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	10327 (2.20 - 3.20)

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	2804	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12691 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 Green fluorescent protein, Talin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1740	Total	C	N	O	S	3	0
			12691	7794	2267	2568	62		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-262	MET	-	expression tag	UNP A0A9X4KGN5
A	-261	HIS	-	expression tag	UNP A0A9X4KGN5
A	-260	HIS	-	expression tag	UNP A0A9X4KGN5
A	-259	HIS	-	expression tag	UNP A0A9X4KGN5
A	-258	HIS	-	expression tag	UNP A0A9X4KGN5
A	-257	HIS	-	expression tag	UNP A0A9X4KGN5
A	-256	HIS	-	expression tag	UNP A0A9X4KGN5
A	-255	HIS	-	expression tag	UNP A0A9X4KGN5
A	-254	HIS	-	expression tag	UNP A0A9X4KGN5
A	-253	HIS	-	expression tag	UNP A0A9X4KGN5
A	-252	HIS	-	expression tag	UNP A0A9X4KGN5
A	-12	GLY	-	linker	UNP A0A9X4KGN5
A	-11	SER	-	linker	UNP A0A9X4KGN5
A	-10	LEU	-	linker	UNP A0A9X4KGN5
A	-9	GLU	-	linker	UNP A0A9X4KGN5
A	-8	VAL	-	linker	UNP A0A9X4KGN5
A	-7	LEU	-	linker	UNP A0A9X4KGN5
A	-6	PHE	-	linker	UNP A0A9X4KGN5
A	-5	GLN	-	linker	UNP A0A9X4KGN5
A	-4	GLY	-	linker	UNP A0A9X4KGN5
A	-3	PRO	-	linker	UNP A0A9X4KGN5
A	-2	ALA	-	linker	UNP A0A9X4KGN5
A	-1	ALA	-	linker	UNP A0A9X4KGN5
A	0	ALA	-	linker	UNP A0A9X4KGN5
A	639	LEU	GLN	conflict	UNP P26039
A	673	ASN	LYS	conflict	UNP P26039
A	1227	LEU	SER	conflict	UNP P26039
A	2349	VAL	ALA	conflict	UNP P26039

V2111	R1919	K2021	L1607	Q1442	R1298	M1211	K1068	E892	L778	M669	P487
V2112	V1920	K2024	A1610	A1443	A1299	R1214	A1069	A893	L781	Q670	L488
T2126	Q1921	V2025	A1760	A1444	Q1300	A1215	L1079	A904	H784	L671	Q492
L2129	S1928	L2026	L1613	Y1445	V1301	V1216	E1082	1909	V875	V675	S502
K2133	V1944	V2027	I1614	V1447	L1335	D1218	T1083	P942	A878	A679	V606
A2134	Y1945	E2028	R1618	Q1472	R1340	K1221	M1084	K943	H785	A679	Q507
V2135	T1946	D2029	A1621	M1476	T1343	R1222	S1094	A944	A787	L682	A508
GLU	K1947	T2030	R1624	E1481	M1347	L1223	T1095	S945	A789	V683	A509
ASP	K1948	V2032	R1625	G1482	T1351	L1224	V1098	A946	T790	L698	Q510
ALA	L1950	L2033	P1628	E1483	T1354	S1225	G947	P948	A792	V702	A511
THR	L1951	L2034	R1632	P1484	Q1355	D1226	K1104	Q954	G793	A705	T812
LYS	E1952	A2045	P1635	G1485	Q1356	L1227	L1105	K957	P794	E517	E517
GLY	R1955	A2048	G1635	T1487	Q1357	L1228	E1108	A958	A795	S528	S528
THR	V1961	Q2049	R1638	Q1488	A1357	L1229	I1109	V970	G796	K529	K529
ARG	A1967	V2052	G1639	Q1489	P1358	P1230	A1120	E961	R797	K533	K533
ALA	L1968	L2055	V1640	V1491	K1361	T1231	V1124	S973	T804	V547	V547
LEU	G1971	L2055	R1638	Q1490	E1362	T1232	R1129	Q974	L806	I550	I550
ALA	L1971	L2055	T1639	V1491	C1363	G1233	R1129	S973	T804	V547	V547
THR	T1975	K2059	V1640	L1492	D1364	T1234	A1132	Q974	R797	I550	I550
THR	V1985	D2060	S1643	C1509	N1365	F1235	A1132	S973	T804	V547	V547
GLU	H1985	K2063	I1644	T1520	A1366	Q1236	P800	Q974	E821	V547	V547
GLU	L1986	L2064	M1651	R1523	R1367	E1237	R1136	P800	E821	V547	V547
ARG	I1988	G2065	M1651	R1523	R1367	E1237	R1136	P800	E821	V547	V547
GLN	D1991	A2067	L1668	S1528	R1367	E1237	R1136	P800	E821	V547	V547
LEU	L1992	L2067	D1676	S1528	R1367	E1237	R1136	P800	E821	V547	V547
ALA	D1993	S2068	D1676	S1528	R1367	E1237	R1136	P800	E821	V547	V547
VAL	I1996	K2069	A1682	L1546	Q1382	A1245	L1152	S990	D843	V577	V577
PHE	M1997	G2070	I1693	D1547	P1383	A1245	D1153	S990	A844	I580	I580
CYS	F1998	A2071	T1693	G1548	P1383	M1250	T1154	L994	E945	V743	V743
PRO	A1999	D2072	M1702	D1549	I1384	N1250	V1158	G997	G846	A744	A744
GLU	T2000	L2073	S1710	F1550	N1385	L1256	E1168	V1001	E947	V747	V747
PRO	G2002	P2074	L1716	T1551	D1394	Q1265	H1175	A1004	D849	C750	C750
ALA	G2002	E2075	L1716	E1552	S1395	Q1265	P1176	A1004	L850	V751	V751
THR	T2003	T2076	L1727	E1553	V1396	A1268	G1177	V1008	E951	Q755	Q755
THR	L2004	Q2077	G1729	R1554	M1397	R1269	D1178	V1008	N852	E759	E759
PRO	N2005	L2081	H1729	A1556	E1398	R1273	P1179	I1011	S853	D760	D760
GLU	R2006	V2084	K1730	Q1557	E1398	Q1276	E1180	Q1012	R854	L763	L763
ASP	E2007	K2085	S1732	R1559	Q1412	D1277	Q1183	R1035	R855	L764	L764
PHE	G2008	D2086	Q1733	A1560	K1415	F1278	R1184	L1054	L856	R765	R765
ILE	A2009	L2091	Q1736	A1561	N1418	F1281	V1188	L1054	A859	L764	L764
ARG	E2010	K2099	G1747	T1562	L1419	V1286	V1192	Q1058	L863	A769	A769
THR	T2011	L2099	E1421	A1563	P1420	G1285	V1192	M1059	T867	A770	A770
LYS	P2012	V2104	D1424	P1564	E1421	V1286	V1192	L1060	M870	A771	A771
ILE	A2013	V2105	S1750	E1567	D1424	G1290	Q1183	D1063	H880	T772	T772
THR	D2014	G2106	K1751	L1572	F1436	Q1291	R1184	L1064	H880	Q776	Q776
GLY	H1911	D2107	H1755	L1572	T1437	A1292	V1192	L1064	H880	A777	A777
THR	H1915	L2108	H1755	L1572	T1437	A1292	V1192	L1064	H880	Q776	Q776
ALA	H1915	G2109	H1755	L1572	T1437	A1292	V1192	L1064	H880	A777	A777

THR	GLY	THR	ALA	ASN	GLU
ALA	TYR	GLN	GLN	ASN	GLU
LYS	LEU	LYS	LEU	LEU	GLU
ALA	GLU	LYS	LEU	LEU	GLU
VAL	LEU	GLN	LEU	GLY	VAL
ALA	LEU	LYS	VAL	ALA	ALA
ASP	ASP	GLY	GLN	ALA	GLY
GLY	HIS	ASN	GLN	GLN	GLY
VAL	VAL	ASN	VAL	ASN	VAL
SER	LEU	LYS	LYS	ALA	SER
CYS	LEU	LYS	VAL	ILE	GLY
ARG	THR	GLY	GLY	GLY	GLY
GLN	LEU	GLN	ALA	ALA	GLN
GLU	GLN	LYS	ALA	ALA	GLU
ASP	PRO	ASP	LYS	PRO	ASP
ILE	ASN	ASN	LYS	ASN	ILE
THR	PRO	GLU	LEU	LEU	THR
ALA	ASP	ALA	GLN	GLN	ALA
ALA	LEU	LYS	LEU	LEU	ALA
ILE	HIS	PRO	GLY	LYS	ILE
ASP	LYS	LYS	ILE	LYS	ASP
MET	ARG	SER	ALA	ASP	MET
LEU	VAL	GLU	ALA	GLU	LEU
ARG	ALA	GLN	ALA	ALA	ARG
ALA	GLY	GLY	ALA	ALA	ALA
ILE	GLN	GLY	GLY	GLY	ILE
ALA	GLN	ASN	THR	THR	ALA
PRO	ALA	ALA	ASN	LEU	PRO
GLU	ALA	GLU	LEU	GLU	GLU
VAL	GLU	ALA	CYS	ASP	VAL
ALA	VAL	LYS	ALA	ASN	ALA
PRO	MET	LYS	ALA	LEU	PRO
ASP	LYS	SER	ASN	VAL	ASP
VAL	GLY	ILE	ASN	ALA	VAL
THR	THR	ALA	ALA	ALA	THR
ARG	TRP	ALA	VAL	VAL	ARG
ALA	VAL	GLN	GLN	GLN	ALA
LEU	ASP	GLY	GLY	GLY	LEU
HIS	TYR	ALA	HIS	ALA	HIS
GLU	GLU	LEU	ALA	ALA	GLU
CYS	VAL	GLN	ALA	ALA	CYS
ILE	ILE	LEU	SER	GLU	ILE
ALA	ALA	SER	GLN	GLU	ALA
ASN	ASN	ILE	ASN	LYS	ASN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	439156	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.117	Depositor
Minimum map value	-2.423	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.218	Depositor
Map size (Å)	368.63998, 368.63998, 368.63998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.152, 1.152, 1.152	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	0.23	0/12823	0.44	0/17391

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	12691	0	12828	243	0
All	All	12691	0	12828	243	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 10.

The worst 5 of 243 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:2055:ILE:HG13	1:A:2091:LEU:HD22	1.46	0.97
1:A:377:TYR:HE2	1:A:379:SER:HB3	1.52	0.75
1:A:1223:LEU:HB3	1:A:1286:VAL:HG11	1.68	0.74
1:A:1211:ASN:OD1	1:A:1214:ARG:NH1	2.20	0.74
1:A:1250:ASN:ND2	1:A:1371:GLU:OE1	2.20	0.74

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	1739/2804 (62%)	1723 (99%)	16 (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	1328/2215 (60%)	1322 (100%)	6 (0%)	81	92

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1035	ARG
1	A	1136[A]	ARG
1	A	1136[B]	ARG
1	A	891[A]	ARG
1	A	772	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1385	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2113	GLN
1	A	1677	GLN
1	A	1888	GLN
1	A	1658	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 [i](#)

There are no chain breaks in this entry.

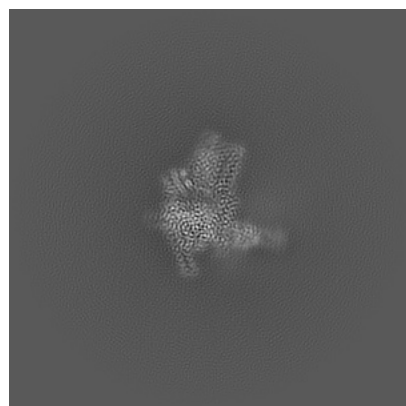
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43152. These allow visual inspection of the internal detail of the map and identification of artifacts.

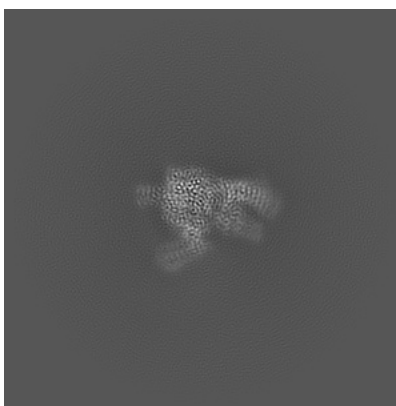
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

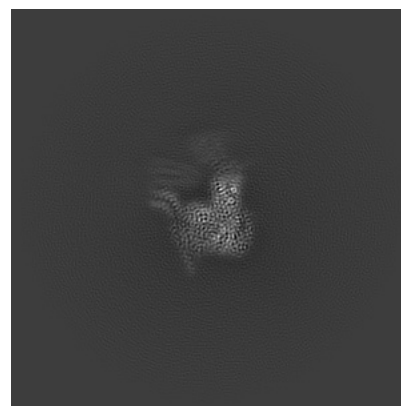
6.1.1 Primary map



X

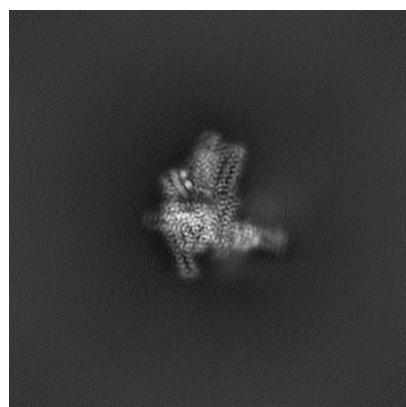


Y

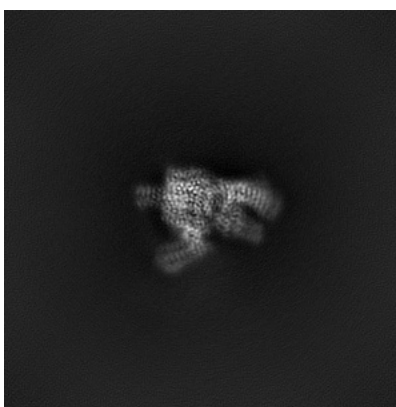


Z

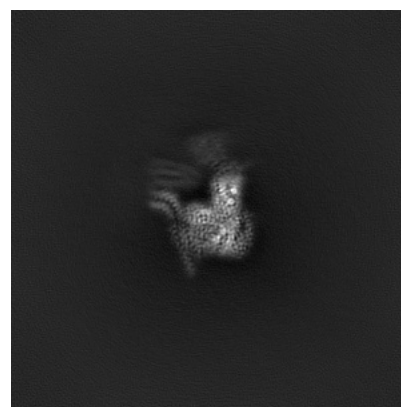
6.1.2 Raw map



X



Y

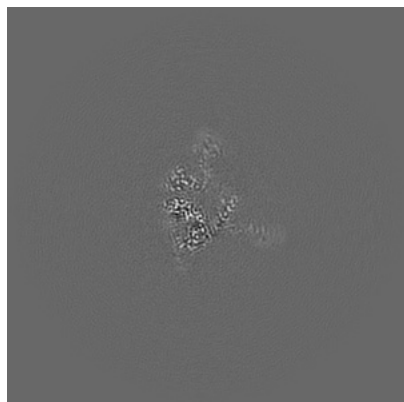


Z

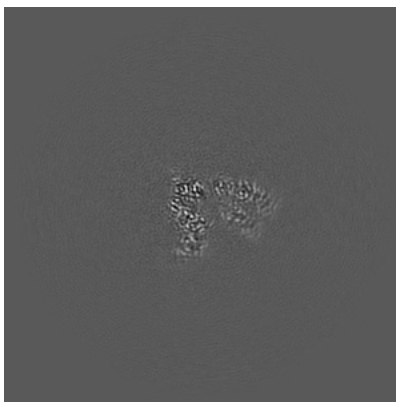
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

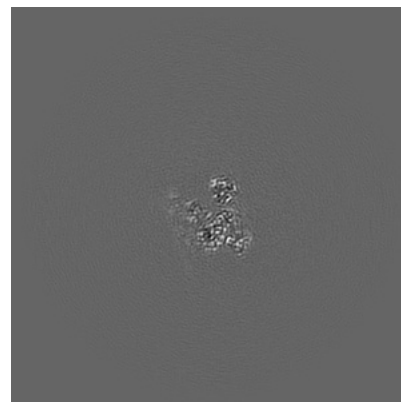
6.2.1 Primary map



X Index: 160

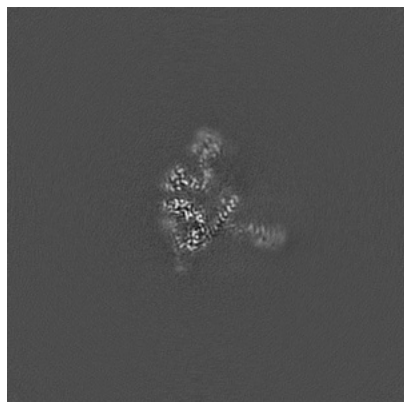


Y Index: 160



Z Index: 160

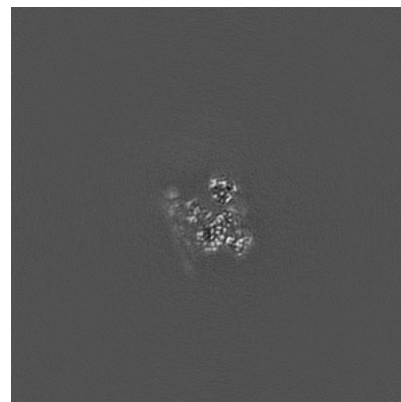
6.2.2 Raw map



X Index: 160



Y Index: 160

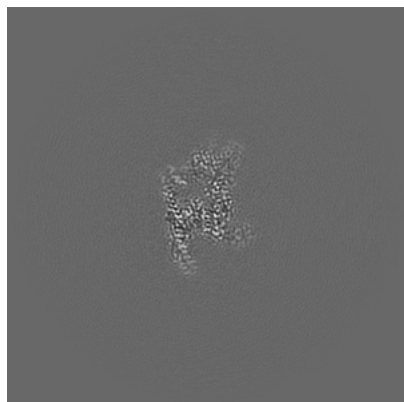


Z Index: 160

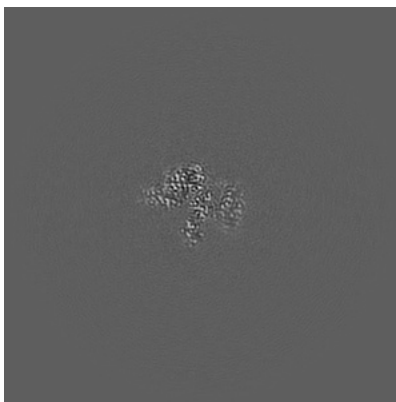
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

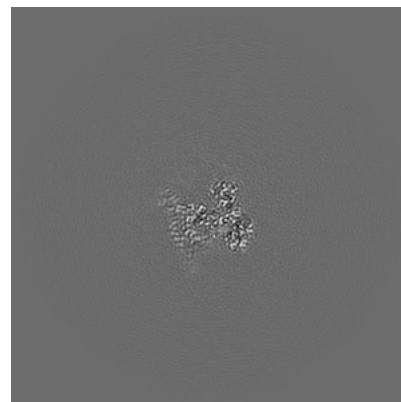
6.3.1 Primary map



X Index: 174

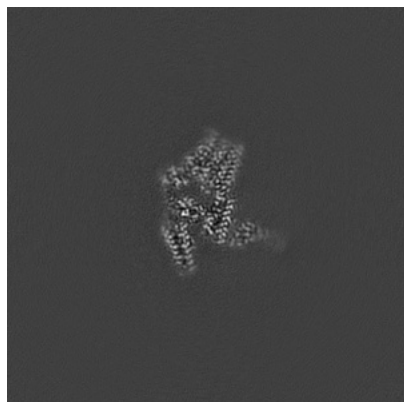


Y Index: 137

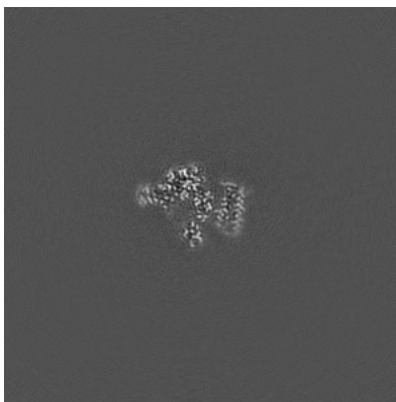


Z Index: 150

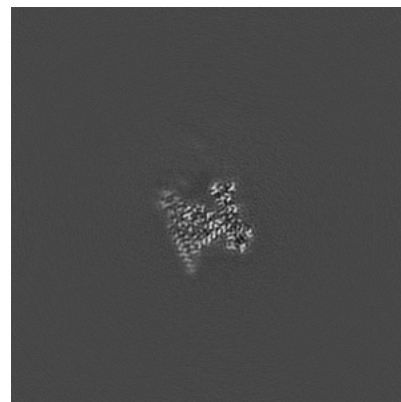
6.3.2 Raw map



X Index: 170



Y Index: 139

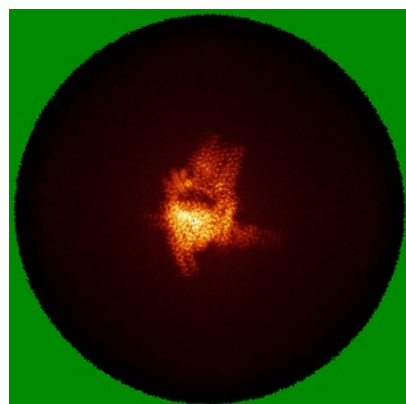


Z Index: 153

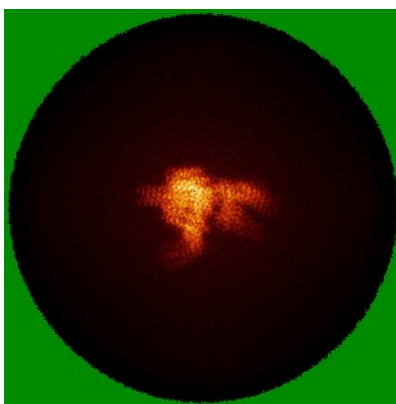
The images above show the largest variance slices of the map in three orthogonal directions.

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

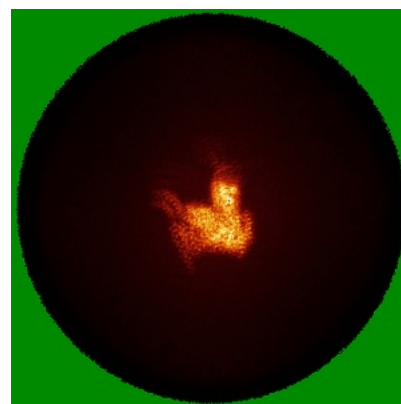
6.4.1 Primary map



X

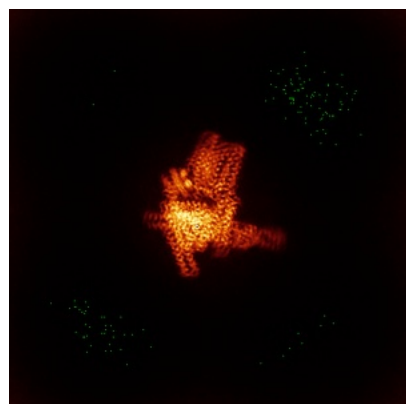


Y

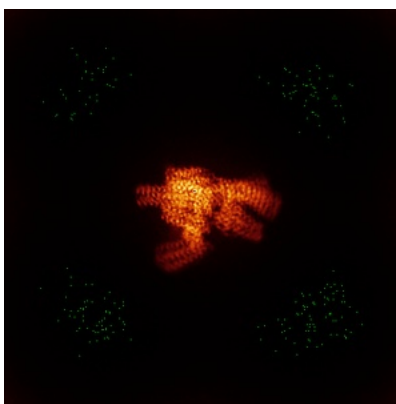


Z

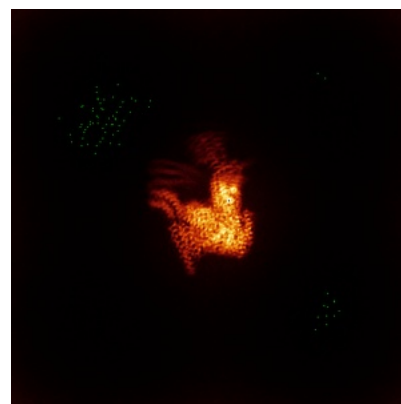
6.4.2 Raw map



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](#)

This section was not generated.

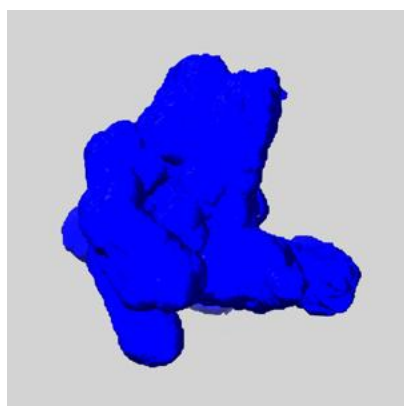
6.6 Mask visualisation [i](#)

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

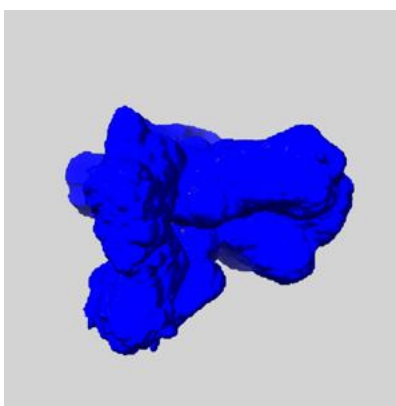
A mask typically either:

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

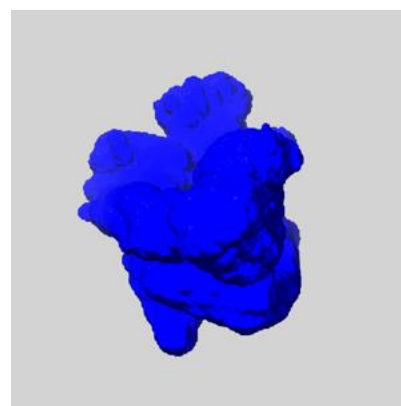
6.6.1 emd_43152_msk_1.map [i](#)



X



Y

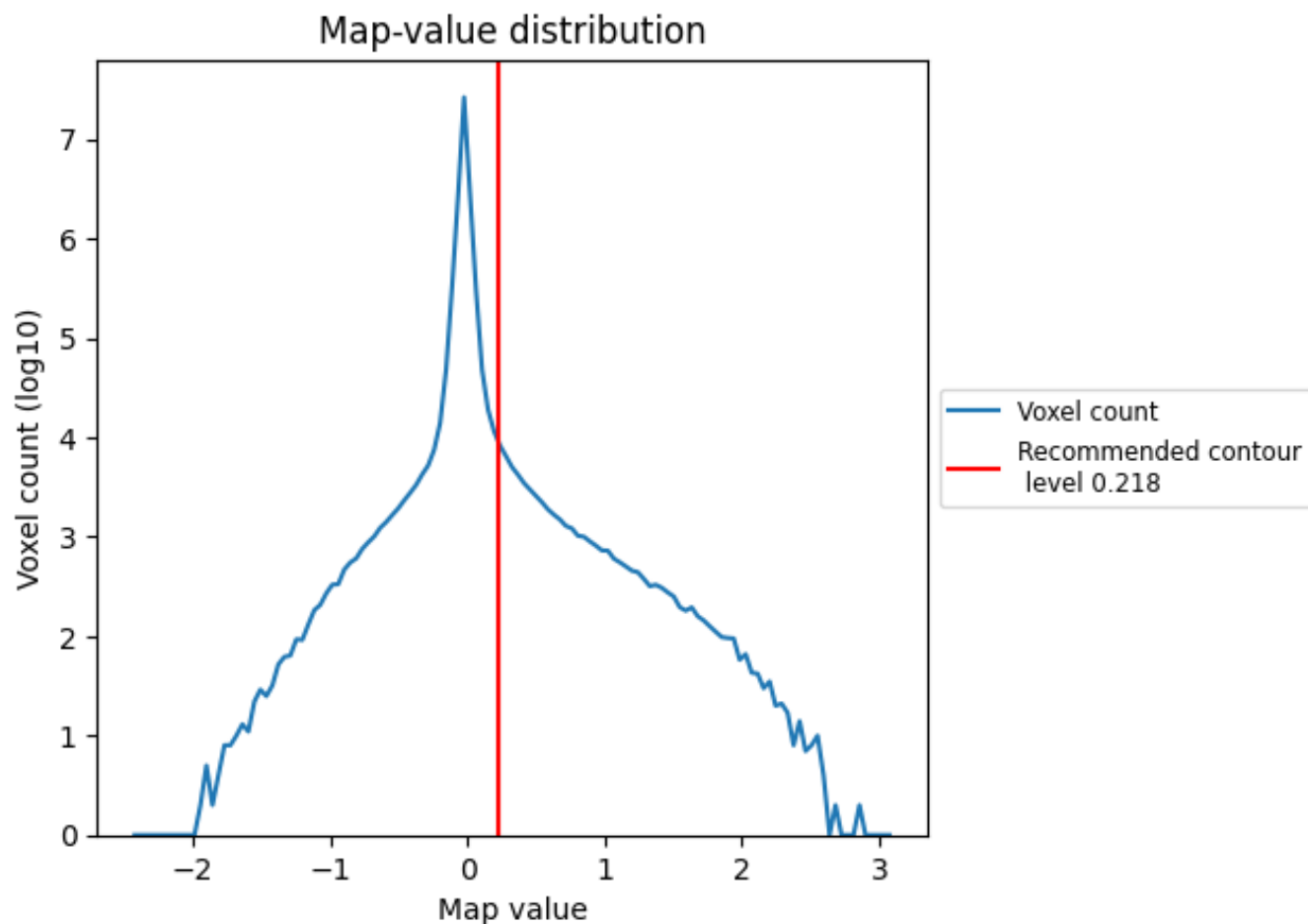


Z

7 Map analysis [i](#)

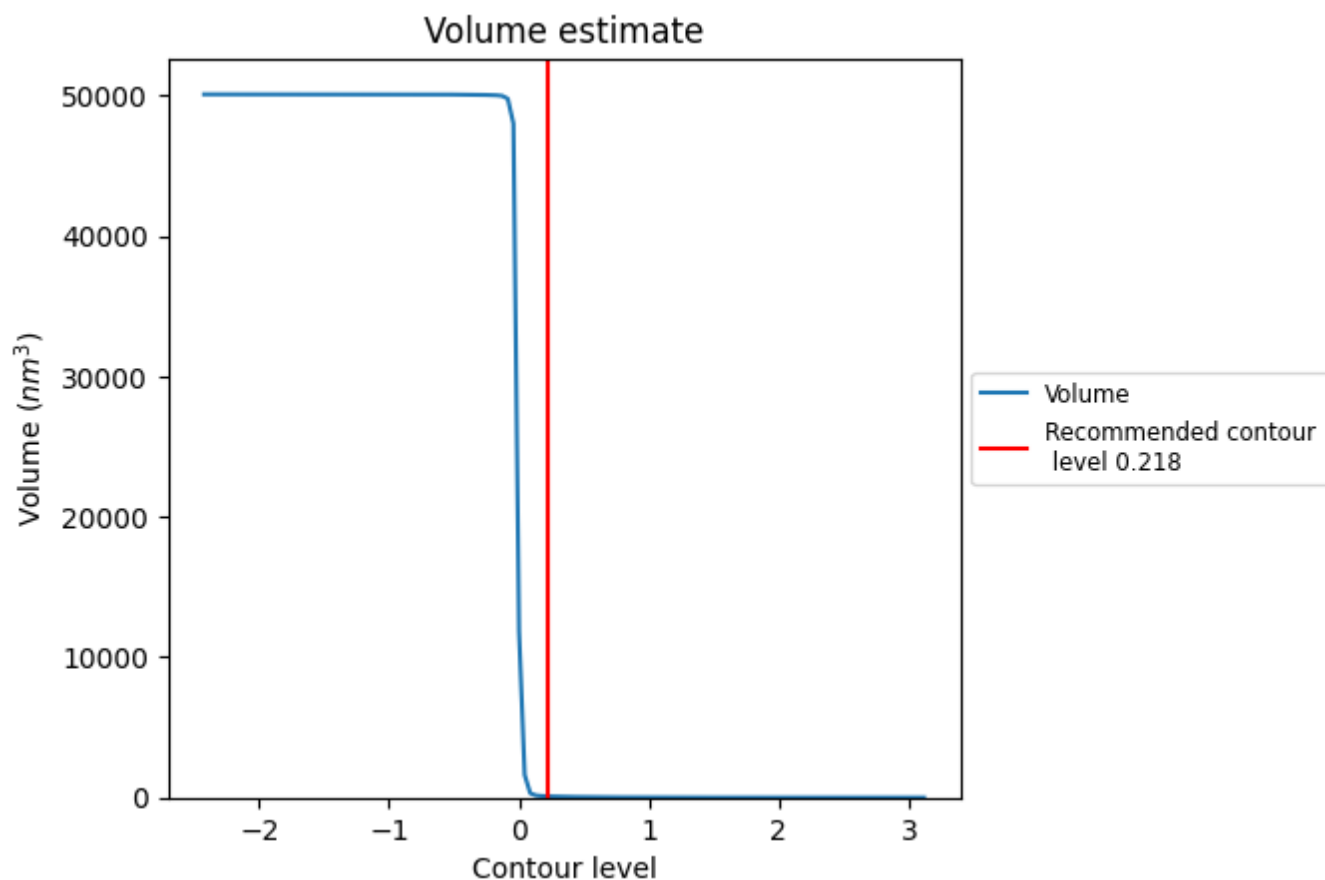
This section contains the results of statistical analysis of the map.

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.

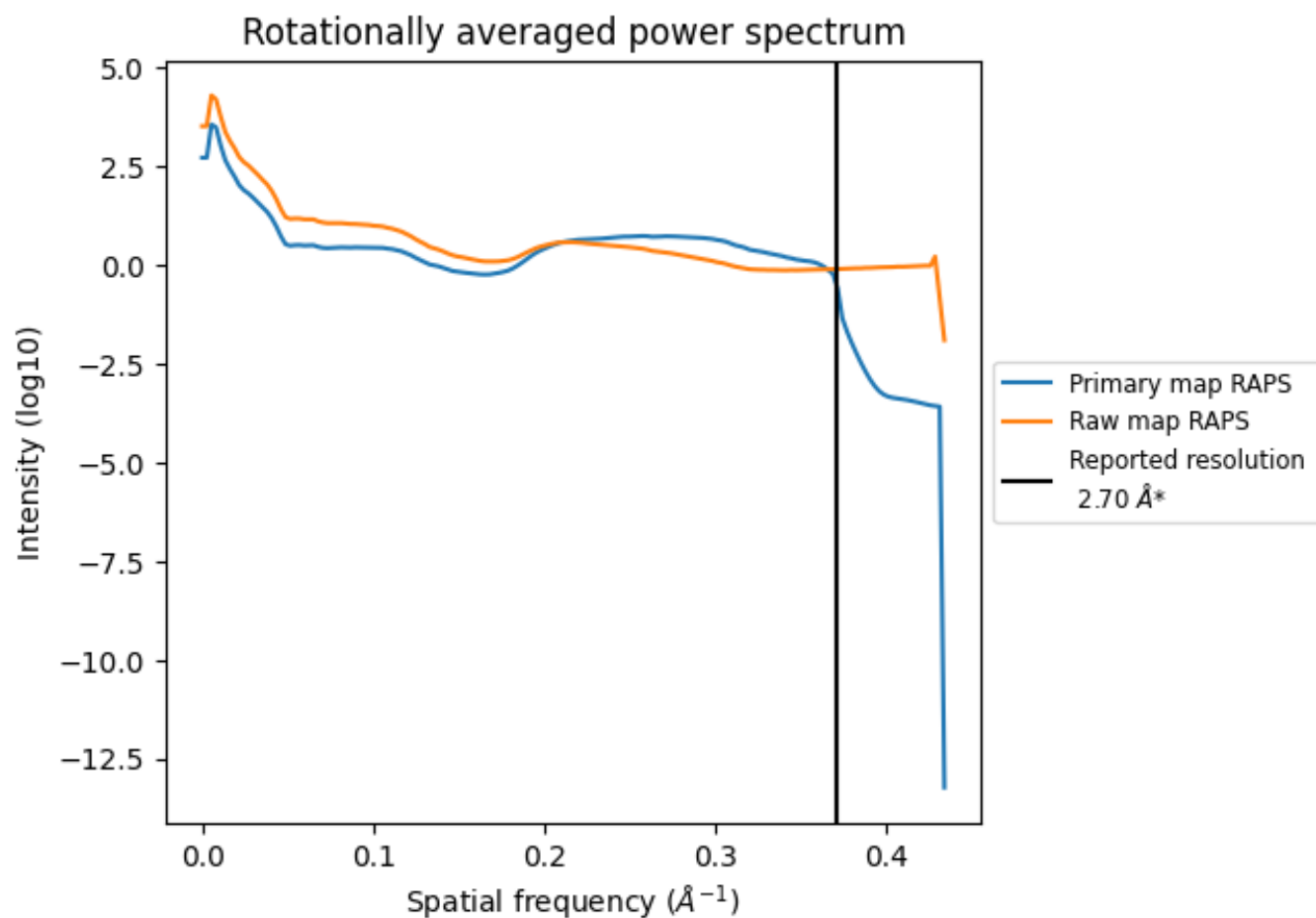
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 90 nm³; this corresponds to an approximate mass of 82 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 ⓘ

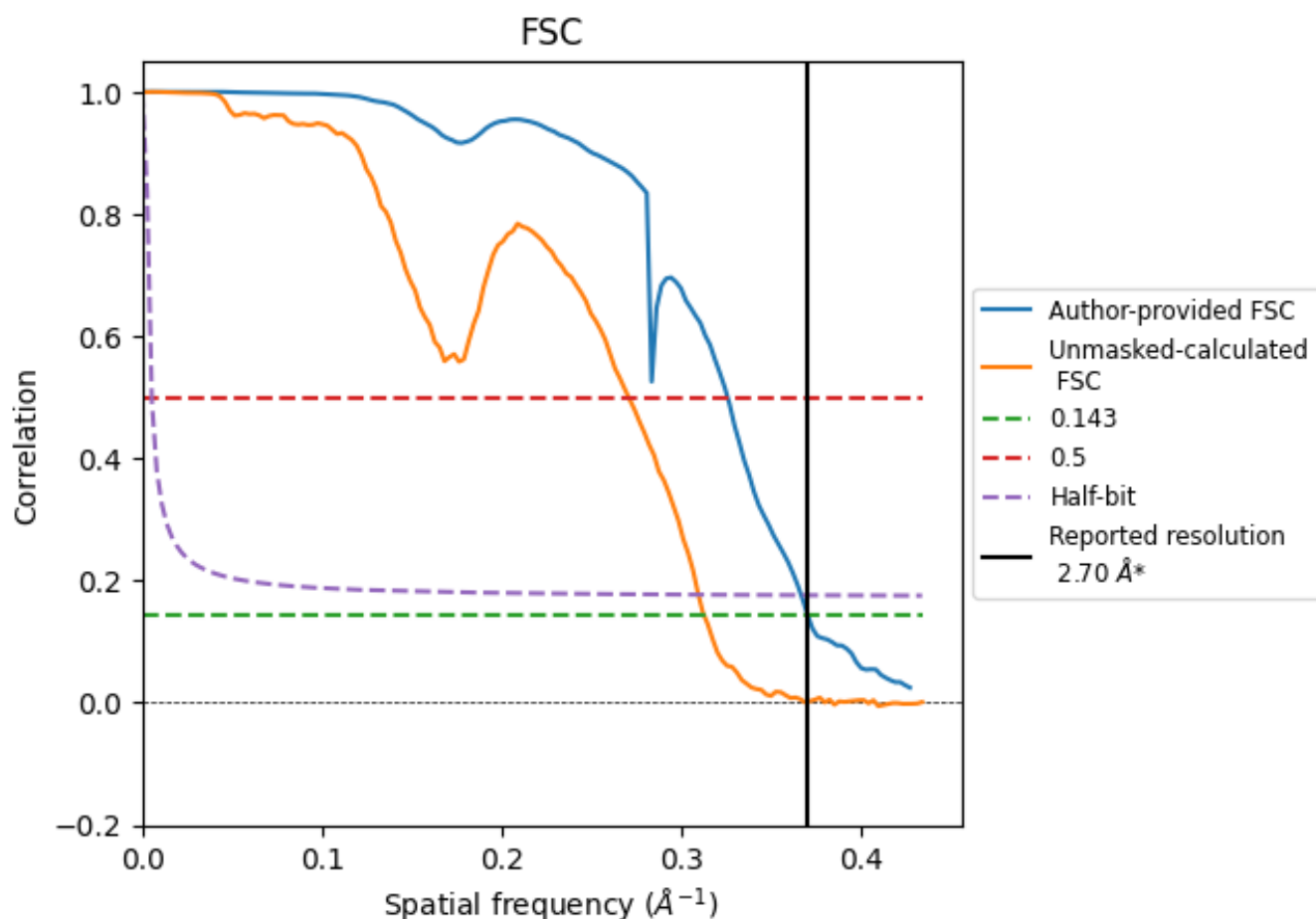


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

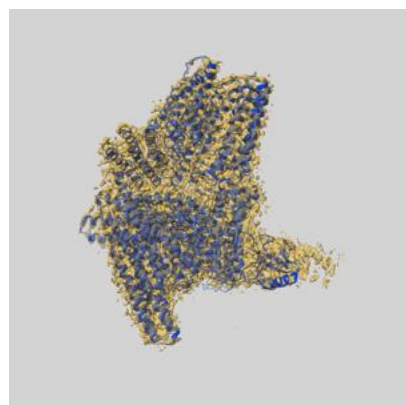
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.70	3.07	2.73
Unmasked-calculated*	3.20	3.70	3.23

*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 3.20 differs from the reported value 2.7 by more than 10 %

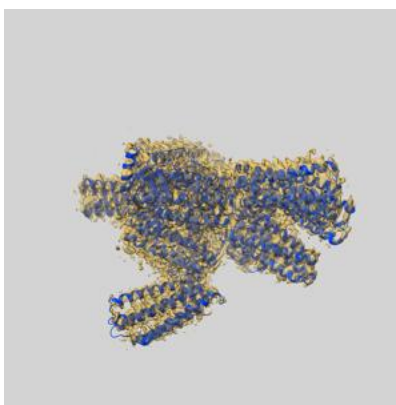
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43152 and PDB model 8VDO. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

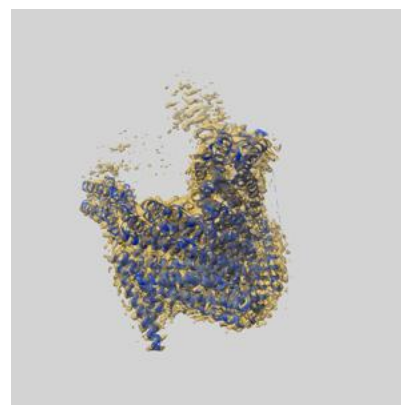
9.1 Map-model overlay [i](#)



X



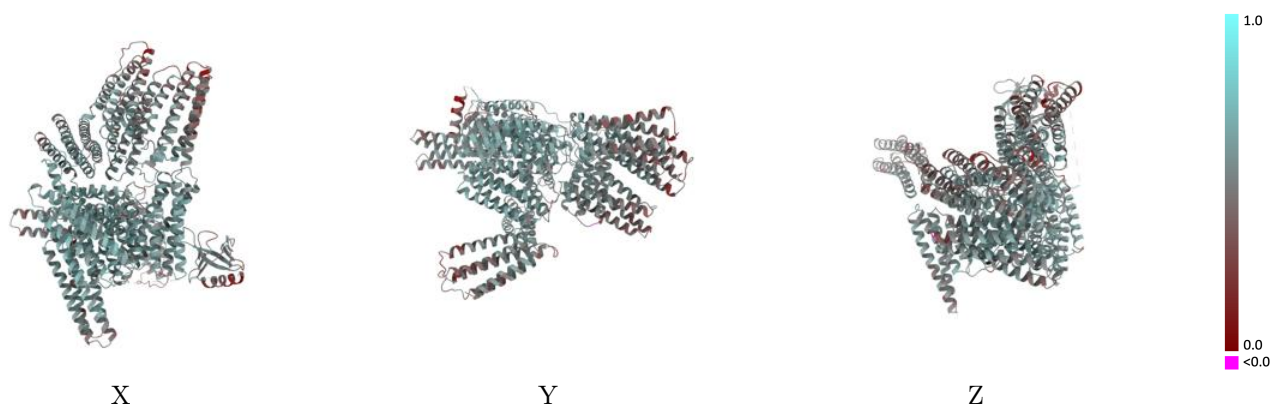
Y



Z

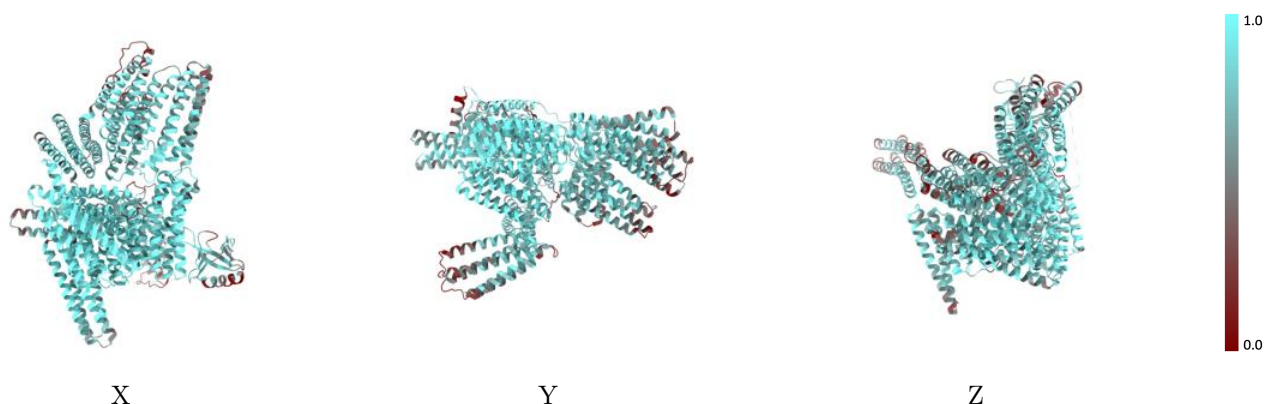
The images above show the 3D surface view of the map at the recommended contour level 0.218 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



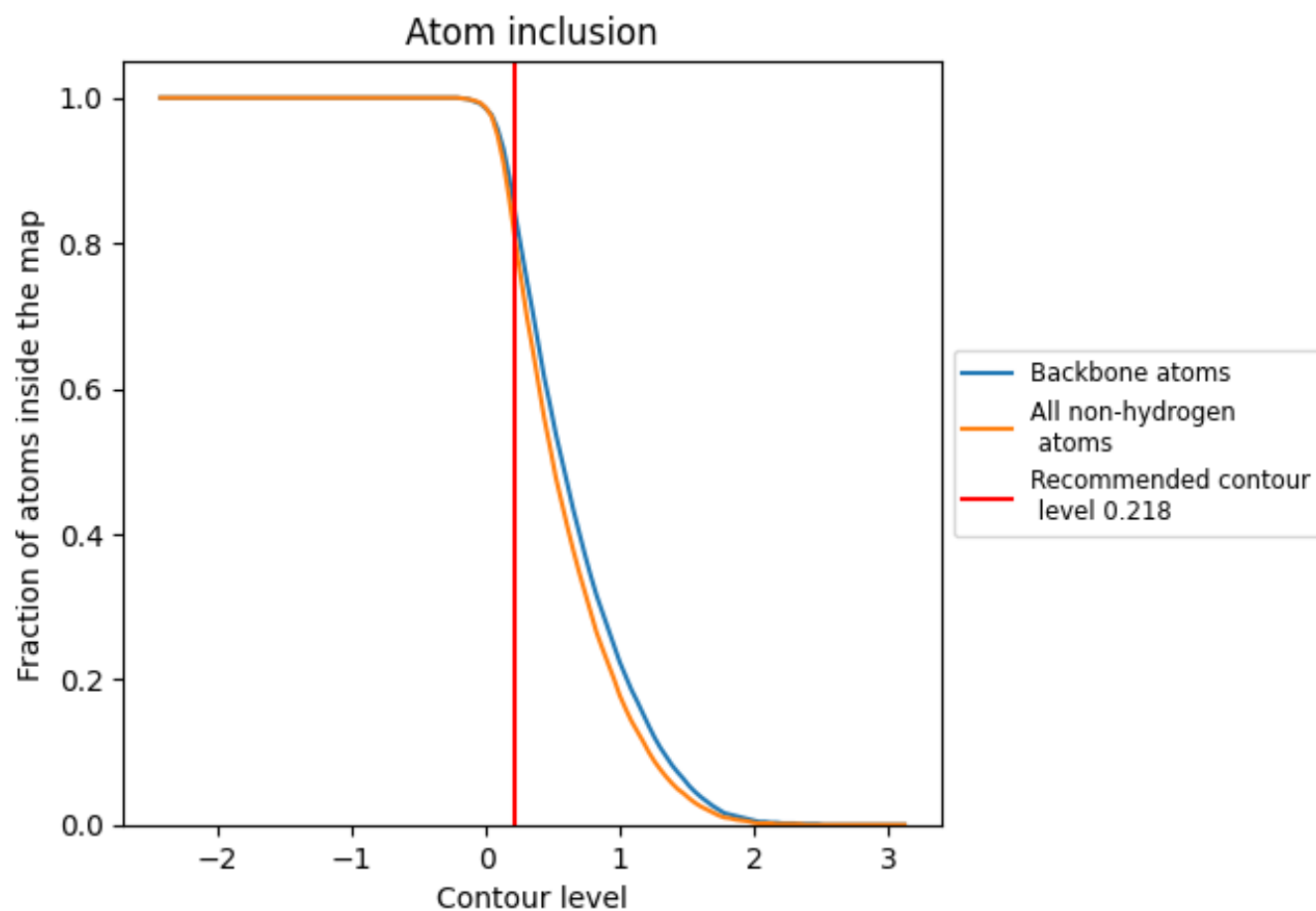
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.218).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% 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 (0.218) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8040	0.5330
A	0.8040	0.5330

