



wwPDB EM Validation Summary Report ⓘ

Jan 1, 2025 – 01:45 PM EST

PDB ID : 8VDO
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.

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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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

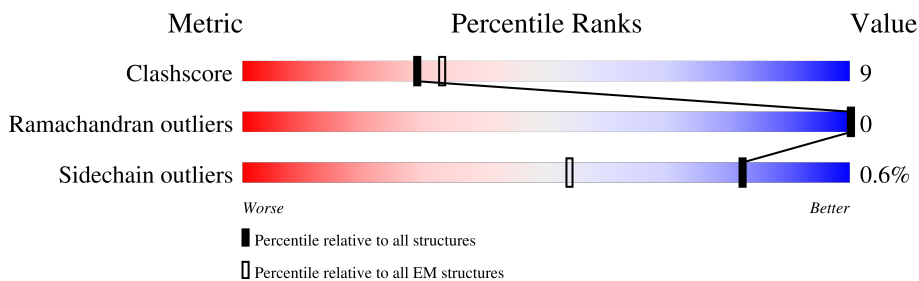
1 Overall quality at a glance

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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	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
			Total	C	N	O	S		
1	A	1740	12691	7794	2267	2568	62	3	0

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

ARG	A2059	THR	A1967	THR	V1807	THR	A1621	THR	V1447	THR	R1340	THR	D1218	THR	L1079	THR	A904	THR	L781	THR	Q670	THR	P487
ARG	D2060	THR	G1971	THR	V1828	THR	F1624	THR	L481	THR	T1343	THR	K1221	THR	E1082	THR	I909	THR	H784	THR	L671	THR	L488
ALA	K2063	THR	T1975	THR	T1832	THR	R1625	THR	G1482	THR	M1347	THR	R1222	THR	S1094	THR	P942	THR	K786	THR	V675	THR	Q492
ASP	L2064	THR	V1985	THR	T1835	THR	P1628	THR	F1483	THR	T1351	THR	L1223	THR	T1095	THR	K943	THR	H787	THR	A678	THR	S502
MET	G2065	THR	I1988	THR	M1836	THR	L1633	THR	G1485	THR	T1354	THR	L1224	THR	V1098	THR	A944	THR	H788	THR	A679	THR	V606
LEU	A2067	THR	L1838	THR	M1837	THR	G1634	THR	C1486	THR	Q1355	THR	S1225	THR	K1104	THR	A946	THR	A789	THR	V682	THR	Q507
ALA	S2068	THR	D1839	THR	L1839	THR	G1635	THR	C1487	THR	Q1356	THR	D1226	THR	L1105	THR	G947	THR	T790	THR	V683	THR	A508
GLY	G2070	THR	G1841	THR	L1839	THR	R1638	THR	Q1488	THR	Q1357	THR	L1227	THR	E1108	THR	P948	THR	A792	THR	L698	THR	A509
ALA	A2071	THR	P1842	THR	M1840	THR	V1640	THR	A1489	THR	P1358	THR	L1228	THR	P794	THR	P948	THR	A793	THR	V702	THR	Q510
HIS	E2072	THR	M1843	THR	G1841	THR	G1635	THR	Q1490	THR	K1361	THR	P1229	THR	I1109	THR	Q954	THR	A795	THR	A705	THR	E517
PRO	D2073	THR	M1844	THR	S1643	THR	S1643	THR	C1509	THR	E1362	THR	T1232	THR	A1120	THR	K957	THR	R797	THR	T713	THR	S528
PRO	P2074	THR	G1844	THR	I1644	THR	I1644	THR	T1520	THR	C1363	THR	G1233	THR	V1124	THR	A958	THR	R797	THR	S714	THR	K529
ALA	E2075	THR	D1845	THR	L1668	THR	L1668	THR	T1520	THR	D1364	THR	T1234	THR	R1129	THR	E961	THR	T804	THR	Q715	THR	K533
VAL	T2076	THR	P1846	THR	L1676	THR	D1676	THR	R1523	THR	M1365	THR	F1235	THR	A1132	THR	V970	THR	I805	THR	L716	THR	V547
ALA	Q2077	THR	E1847	THR	I1693	THR	I1693	THR	S1528	THR	R1367	THR	Q1236	THR	A1132	THR	S973	THR	V808	THR	V717	THR	V547
PRO	I2081	THR	F1850	THR	S1710	THR	S1710	THR	L1546	THR	Q1368	THR	A1238	THR	R1136	THR	Q974	THR	V808	THR	C719	THR	I550
VAL	K2084	THR	Y1853	THR	L1716	THR	L1716	THR	D1547	THR	L1370	THR	Q1239	THR	D1144	THR	Q974	THR	E821	THR	V722	THR	V558
LEU	V2085	THR	M1857	THR	G1728	THR	G1728	THR	G1548	THR	E1371	THR	S1240	THR	D1152	THR	P980	THR	M822	THR	V723	THR	V558
ARG	D2086	THR	A1865	THR	H1729	THR	H1729	THR	F1550	THR	P1383	THR	Q1241	THR	L1152	THR	A882	THR	V823	THR	I727	THR	D569
LEU	L2091	THR	D1892	THR	K1730	THR	K1730	THR	F1551	THR	M1385	THR	L1242	THR	T1154	THR	Q983	THR	R824	THR	C732	THR	V573
ASP	K2099	THR	R1895	THR	V1731	THR	V1731	THR	E1552	THR	M1385	THR	L1242	THR	V1158	THR	L984	THR	R827	THR	G674	THR	G674
ARG	K2104	THR	K1901	THR	S1732	THR	S1732	THR	E1553	THR	D1394	THR	L1266	THR	E1168	THR	L984	THR	D843	THR	L736	THR	V577
GLY	G2106	THR	P1902	THR	Q1733	THR	Q1733	THR	M1554	THR	S1395	THR	Q1265	THR	H1175	THR	G997	THR	A844	THR	V743	THR	V577
GLY	D2107	THR	A1903	THR	Q1736	THR	Q1736	THR	R1555	THR	V1396	THR	A1268	THR	P1176	THR	V1001	THR	E945	THR	A744	THR	I580
LEU	A2110	THR	E1911	THR	G1747	THR	G1747	THR	Q1557	THR	M1397	THR	R1269	THR	G1177	THR	A1004	THR	S848	THR	V747	THR	E586
LEU	A2111	THR	H1915	THR	S1750	THR	S1750	THR	R1558	THR	E1398	THR	R1273	THR	D1178	THR	A1004	THR	D949	THR	C750	THR	R589
ASP	V2112	THR	R1919	THR	K1751	THR	K1751	THR	A1561	THR	Q1412	THR	R1276	THR	P1179	THR	V1008	THR	L850	THR	V751	THR	K592
VAL	T2126	THR	V1920	THR	H1755	THR	H1755	THR	T1562	THR	K1415	THR	Q1276	THR	E1180	THR	V1008	THR	E851	THR	Q755	THR	D600
LEU	L2129	THR	Q1921	THR	Q1758	THR	Q1758	THR	P1564	THR	M1418	THR	D1277	THR	Q1183	THR	I1011	THR	S853	THR	E759	THR	E801
THR	K2133	THR	S1928	THR	K1766	THR	K1766	THR	E1567	THR	L1419	THR	F1278	THR	R1184	THR	Q1012	THR	K855	THR	D760	THR	D661
LEU	A2134	THR	V1944	THR	M1785	THR	M1785	THR	L1572	THR	P1420	THR	F1281	THR	V1188	THR	R1035	THR	A859	THR	L763	THR	R624
GLN	V2135	THR	Y1945	THR	M1785	THR	M1785	THR	L1572	THR	E1421	THR	G1285	THR	V1192	THR	L1054	THR	L863	THR	L764	THR	R634
PRO	GLU	THR	T1946	THR	Q1788	THR	Q1788	THR	G1592	THR	D1424	THR	V1286	THR	L1196	THR	Q1058	THR	T867	THR	R765	THR	S648
ASN	ASP	THR	K1947	THR	H1791	THR	H1791	THR	M1596	THR	F1436	THR	Q1290	THR	D1208	THR	M1059	THR	M870	THR	A769	THR	A770
ASP	GLU	THR	L1949	THR	H1791	THR	H1791	THR	L1607	THR	T1437	THR	A1292	THR	D1208	THR	L1060	THR	M870	THR	A771	THR	A771
LEU	ALA	THR	L1950	THR	E1794	THR	E1794	THR	L1610	THR	E1438	THR	Q1295	THR	M1211	THR	D1063	THR	H880	THR	T772	THR	T772
LEU	ALA	THR	I1951	THR	A1610	THR	A1610	THR	L1613	THR	Q1442	THR	E1296	THR	R1214	THR	L1064	THR	H880	THR	Q776	THR	F664
LEU	LYS	THR	E1952	THR	L1613	THR	L1613	THR	I1614	THR	A1443	THR	D1297	THR	A1215	THR	L1064	THR	H880	THR	A777	THR	A777
LEU	LYS	THR	R1955	THR	I1614	THR	I1614	THR	R1618	THR	Y1445	THR	R1298	THR	V1216	THR	D1067	THR	H880	THR	L778	THR	L778
GLN	ARG	THR	V1961	THR	M1802	THR	M1802	THR	R1618	THR	L1446	THR	A1299	THR	K1068	THR	I1067	THR	Q886	THR	A891	THR	A891
ALA	ALA	THR	A2048	THR	M1802	THR	M1802	THR	R1618	THR	L1446	THR	Q1300	THR	K1068	THR	I1067	THR	Q886	THR	A891	THR	A891
LEU	GLU	THR	V2052	THR	M1802	THR	M1802	THR	R1618	THR	L1446	THR	Q1300	THR	K1068	THR	I1067	THR	Q886	THR	A891	THR	A891
ALA	ALA	THR	I2065	THR	M1802	THR	M1802	THR	R1618	THR	L1446	THR	Q1300	THR	K1068	THR	I1067	THR	Q886	THR	A891	THR	A891

LEU THR
THR
GLY HIS
SER LYS
LYS LYS
ARG VAL
VAL
GLU GLU
GLY SER
SER LEU
VAL VAL
THR THR
GLU GLU

ARG ALA
ALA PRO
LYS MET
GLY LYS
ALA ASP
SER ASP
SER SER
SER LEU
ASN VAL
PHE THR
GLU GLU
GLN GLN
ILE ILE
ILE GLN
ALA LEU
GLU ILE
ALA GLU
ALA GLU
ALA ASN

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

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

LEU ARG
ARG LYS
GLY LYS
ARG ARG
GLY LYS
LEU LEU
GLU GLU
GLU GLU
ARG ARG
ALA ALA
LYS LYS
LYS LYS
LEU LEU
ALA ALA
GLN GLN
ILE ILE
ARG ARG
GLN GLN
GLN GLN
GLN GLN
TYR TYR
LYS LYS
PHE PHE
LEU LEU
PRO PRO
SER SER
GLU GLU
LEU LEU
ASP ASP
GLU GLU
HIS HIS

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	0.28	0/12823	0.45	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	234	0
All	All	12691	0	12828	234	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 9.

The worst 5 of 234 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%)	1318 (99%)	10 (1%)	79 91

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1136[B]	ARG
1	A	1554	ASN
1	A	1625	ARG
1	A	891[B]	ARG
1	A	943	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1347	ASN

Continued on next page...

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Mol	Chain	Res	Type
1	A	1369	GLN
1	A	2035	GLN
1	A	784	HIS
1	A	776	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.

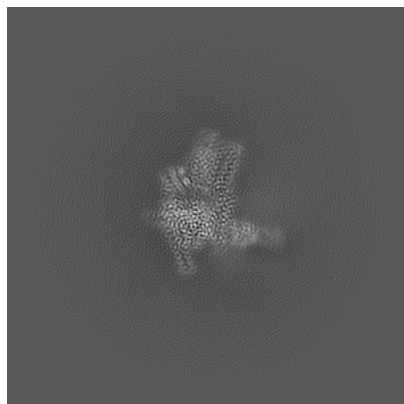
6 Map visualisation [i](#)

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.

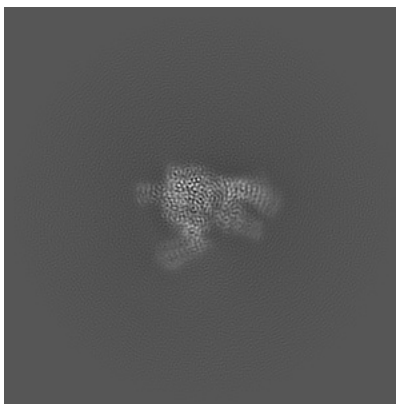
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

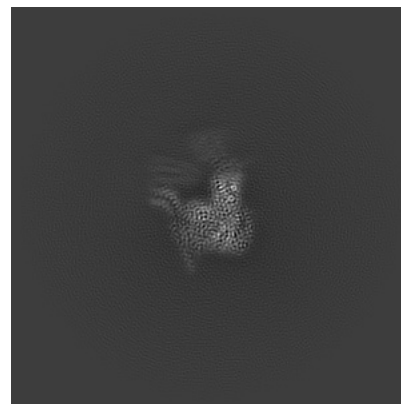
6.1.1 Primary map



X

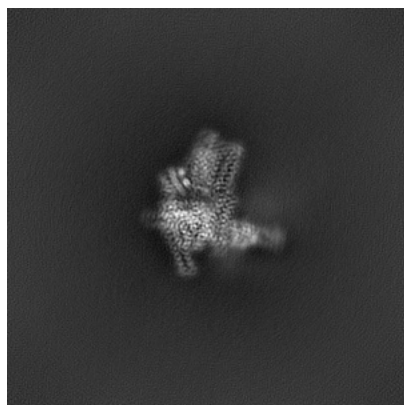


Y

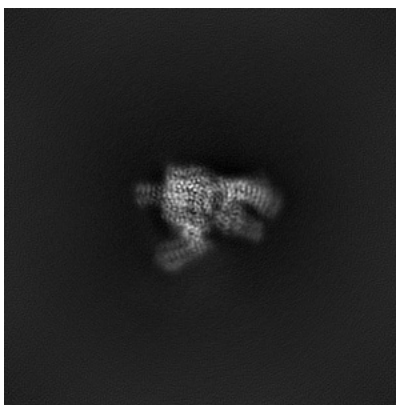


Z

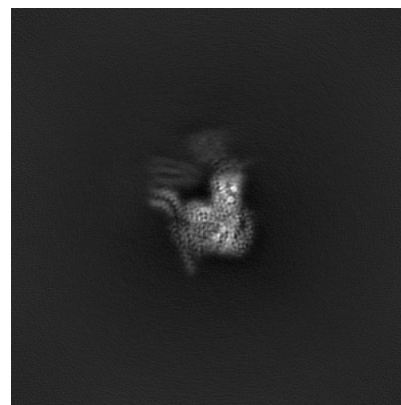
6.1.2 Raw map



X



Y

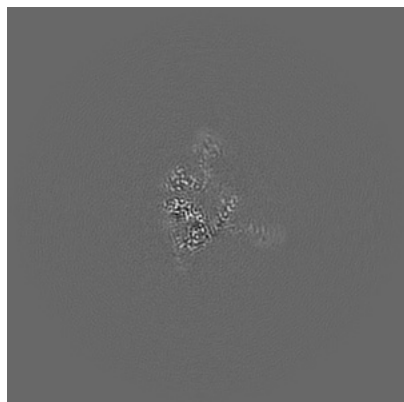


Z

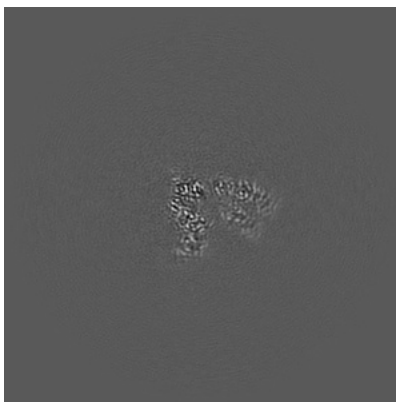
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

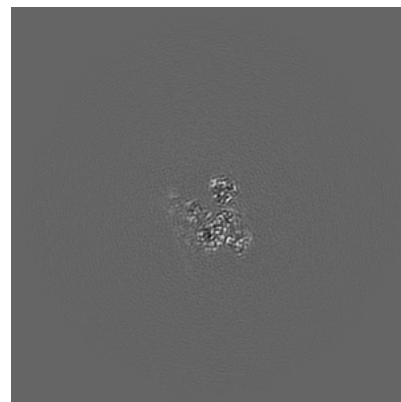
6.2.1 Primary map



X Index: 160

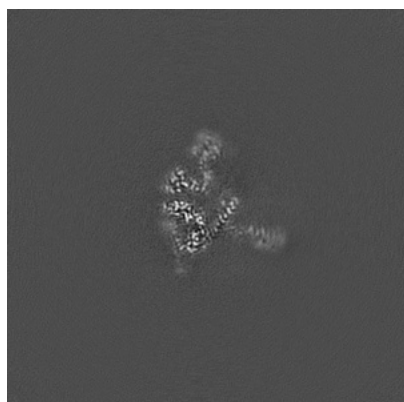


Y Index: 160



Z Index: 160

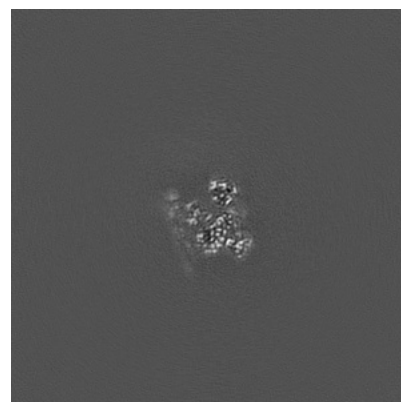
6.2.2 Raw map



X Index: 160



Y Index: 160

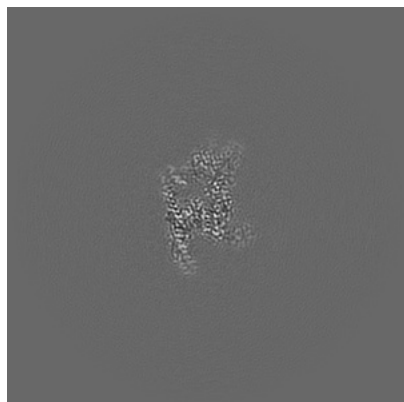


Z Index: 160

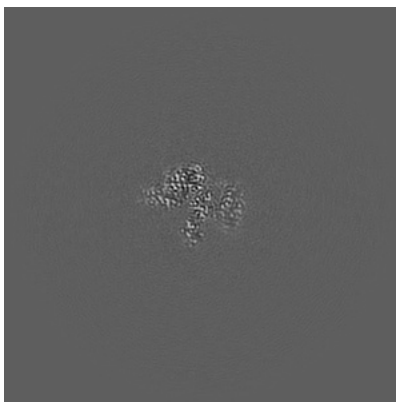
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

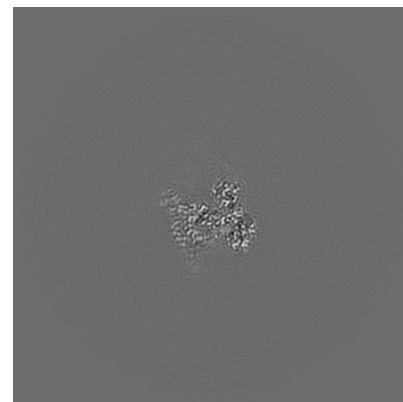
6.3.1 Primary map



X Index: 174

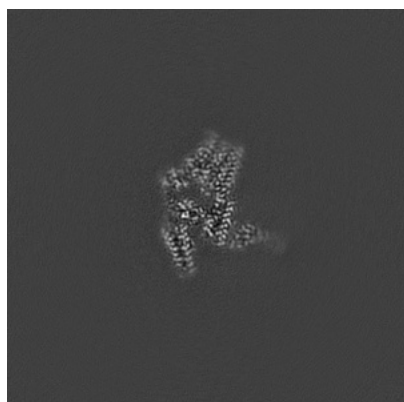


Y Index: 137

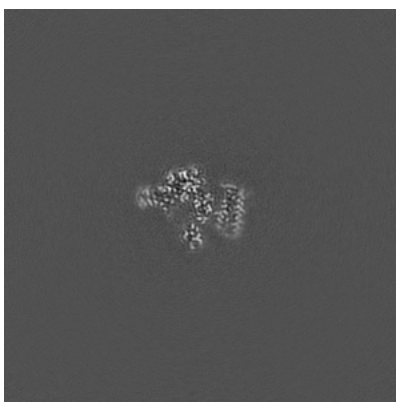


Z Index: 150

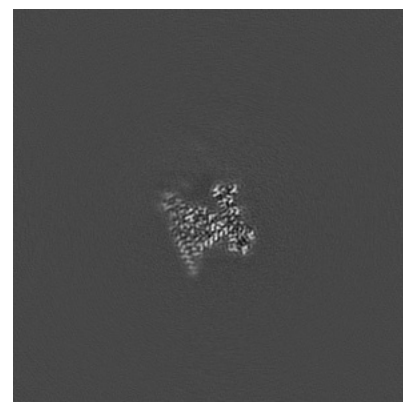
6.3.2 Raw map



X Index: 170



Y Index: 139

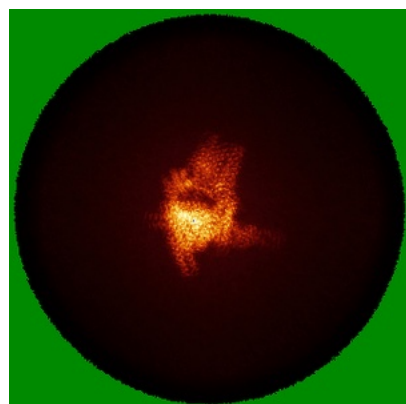


Z Index: 153

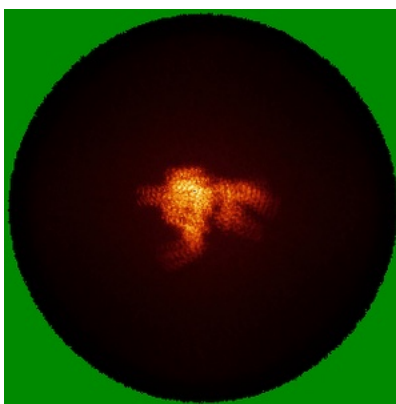
The images above show the largest variance slices of the map in three orthogonal directions.

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

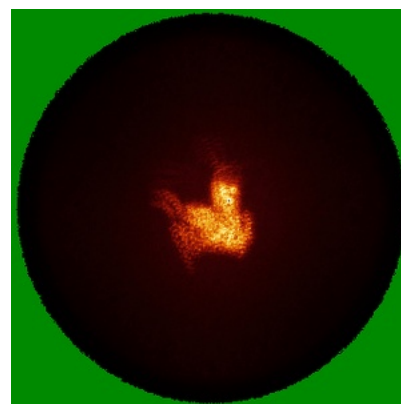
6.4.1 Primary map



X

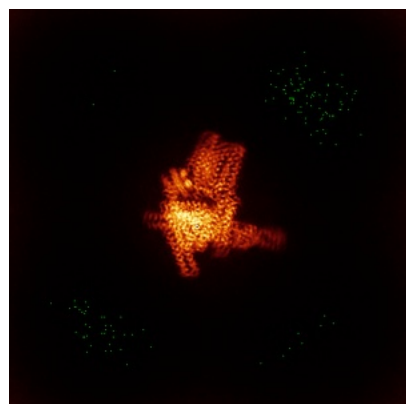


Y

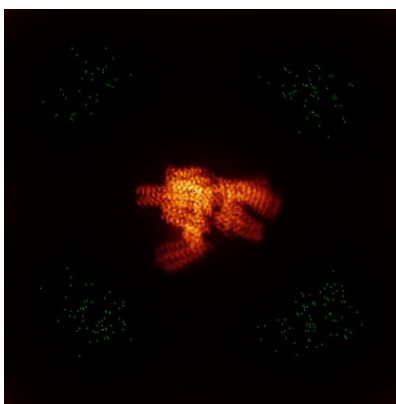


Z

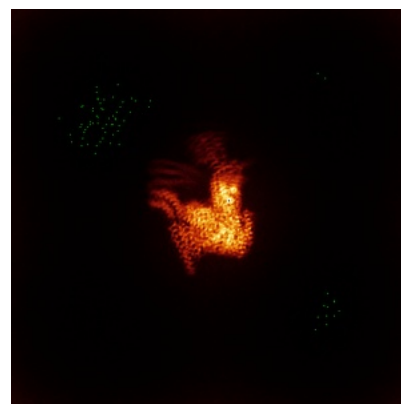
6.4.2 Raw map



X



Y

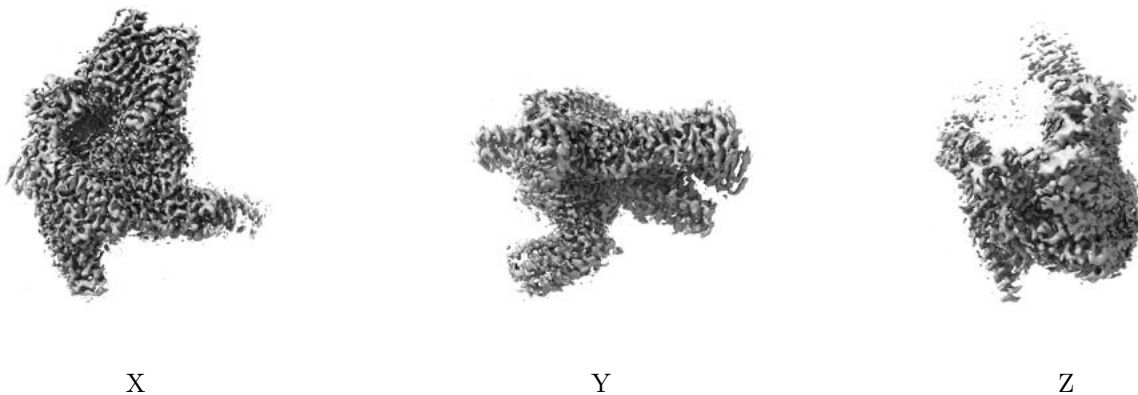


Z

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.

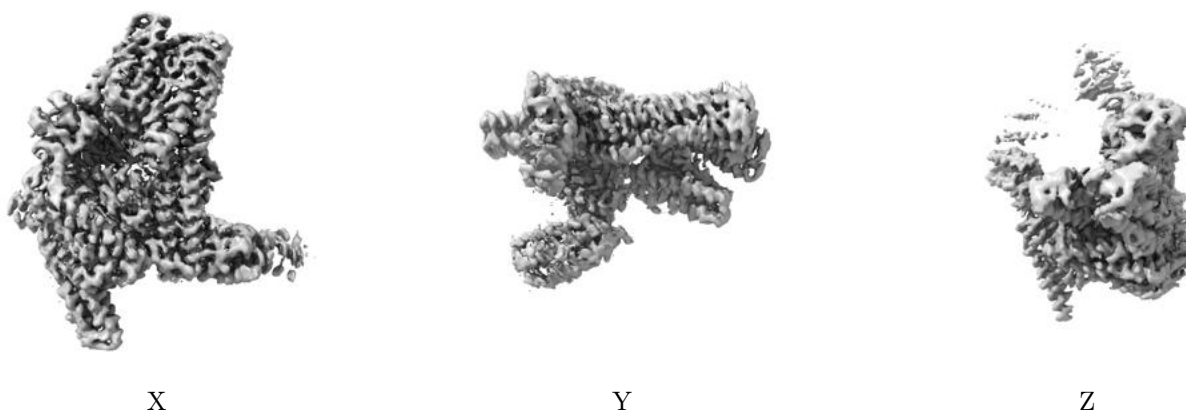
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.218. 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.

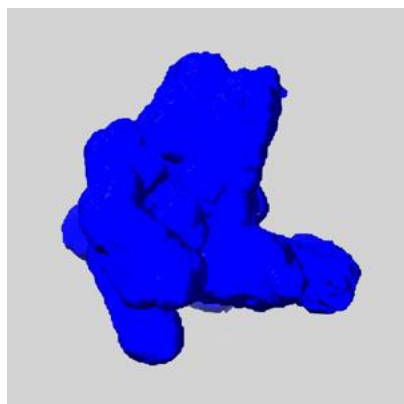
6.6 Mask visualisation [i](#)

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

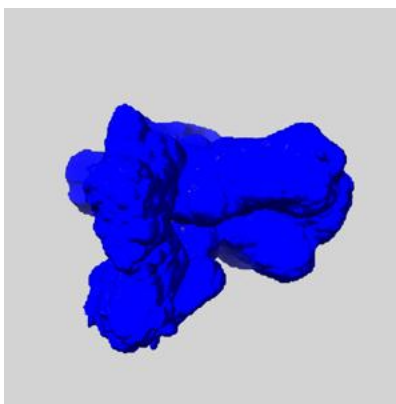
A mask typically either:

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

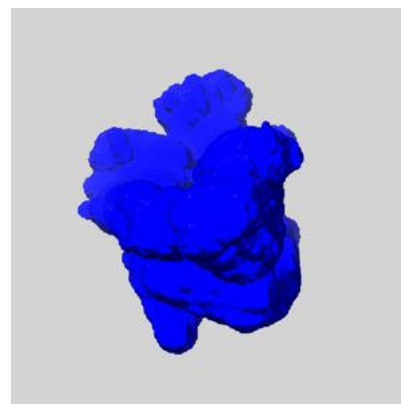
6.6.1 emd_43152_msk_1.map [i](#)



X



Y

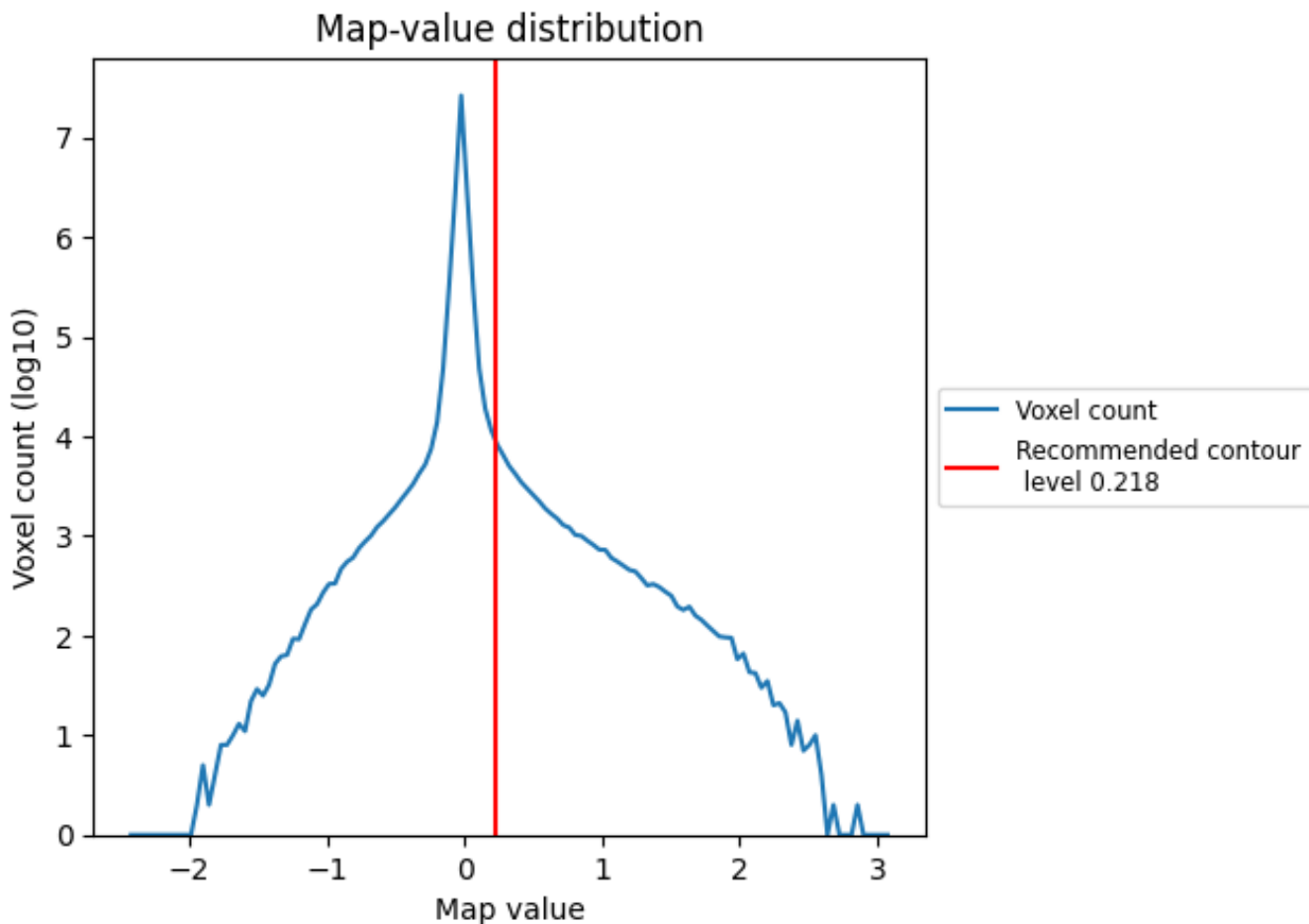


Z

7 Map analysis [i](#)

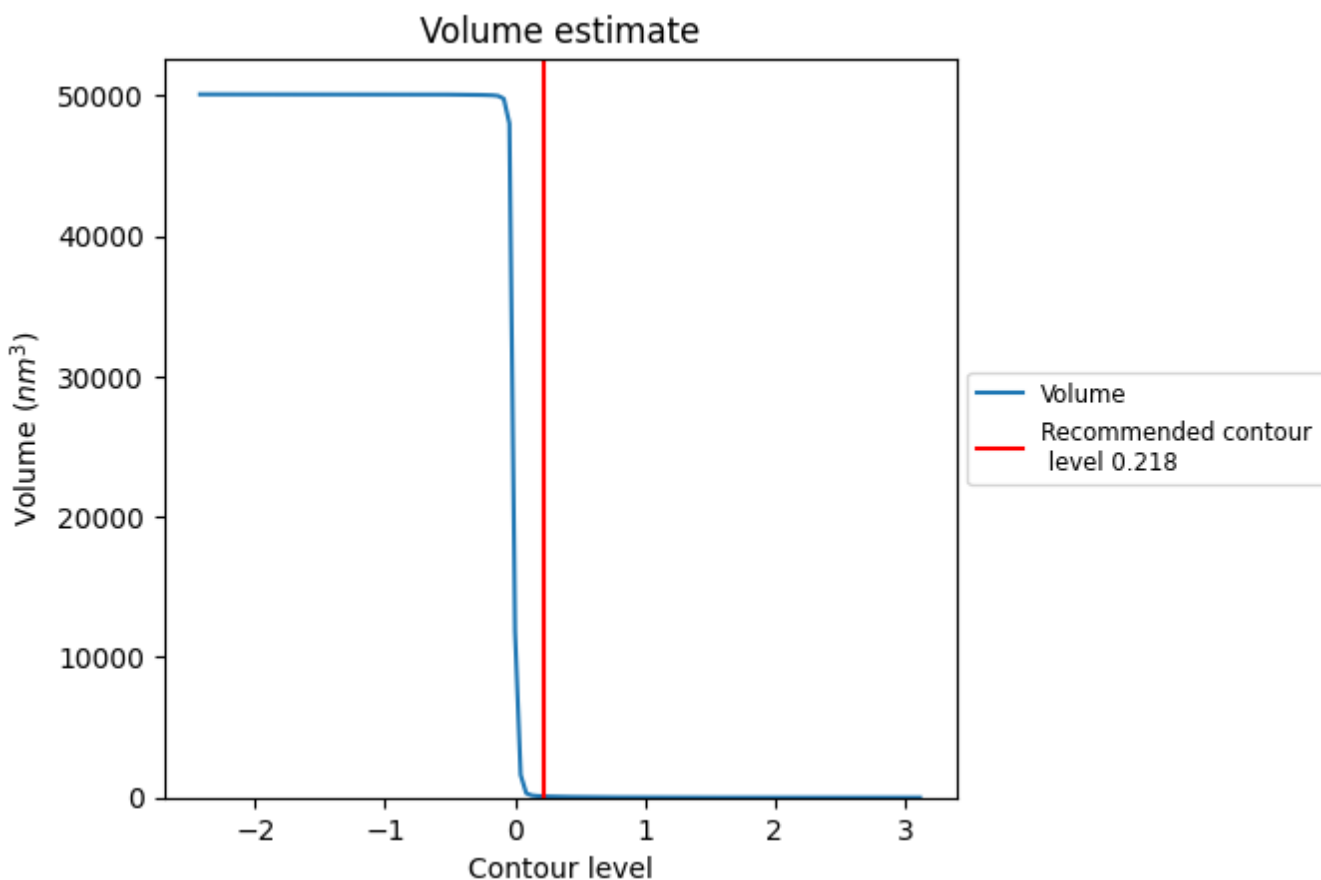
This section contains the results of statistical analysis of the map.

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.

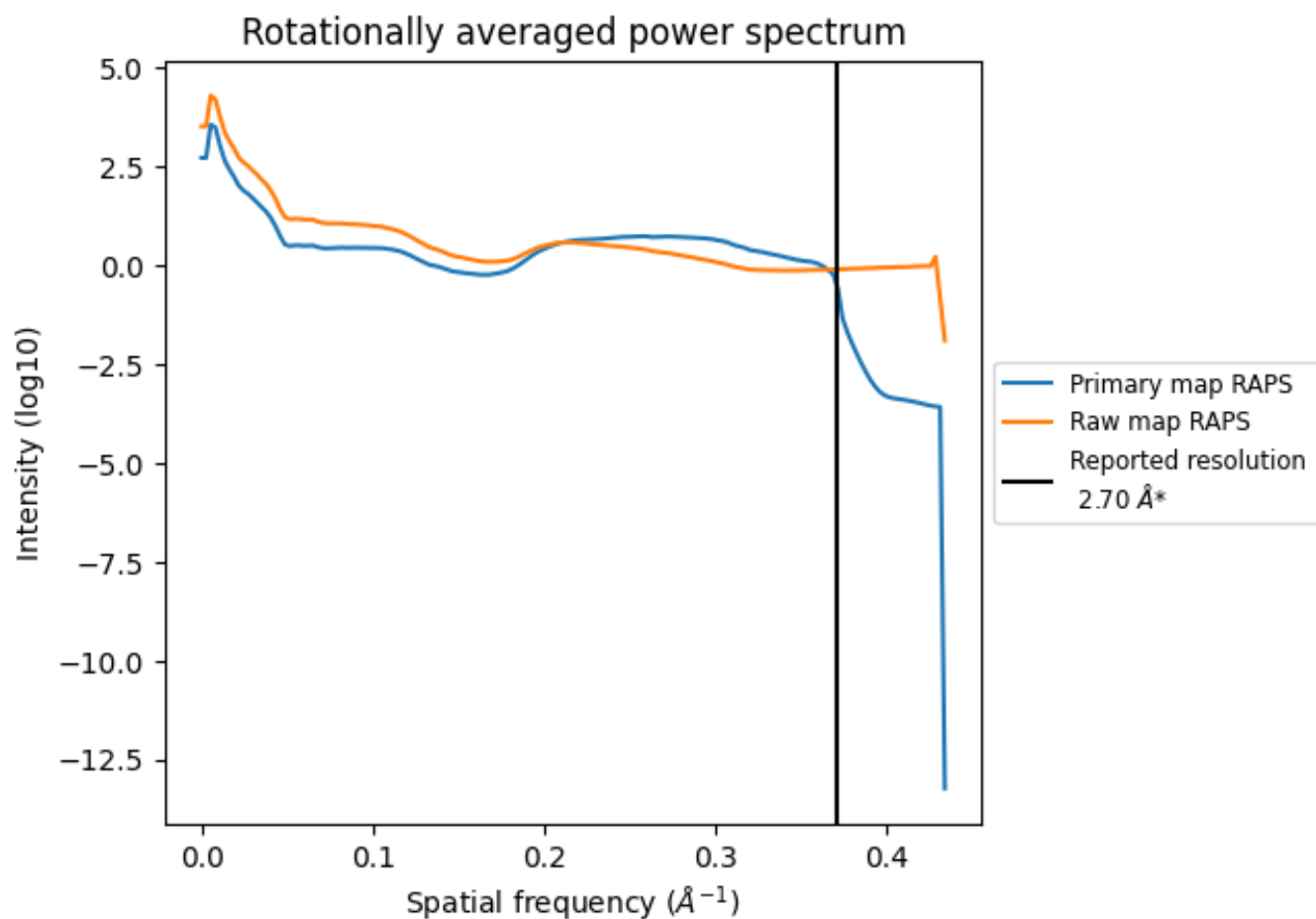
7.2 Volume estimate [i](#)



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 i

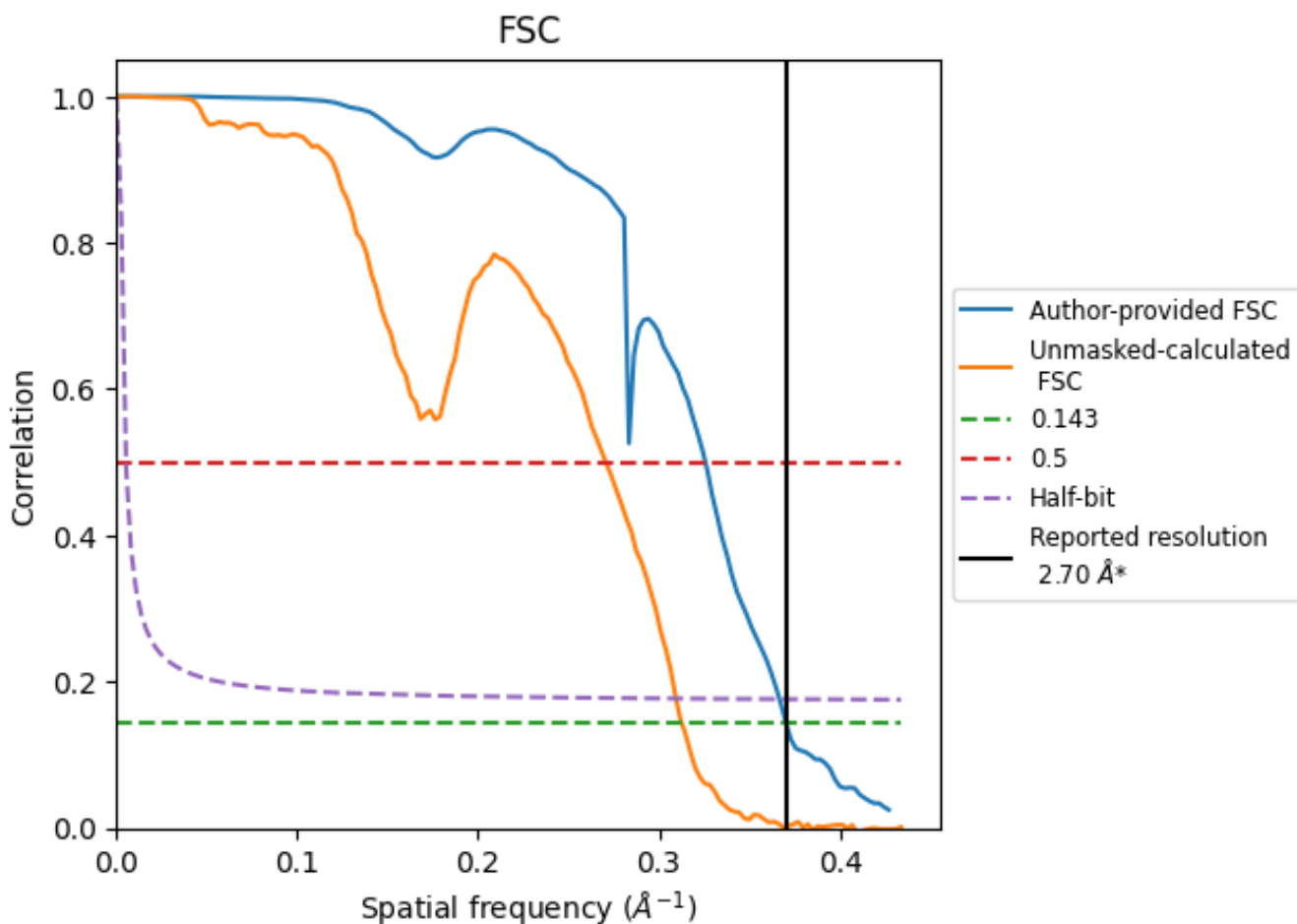


*Reported resolution corresponds to spatial frequency of 0.370 \AA^{-1}

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 0.370 Å⁻¹

8.2 Resolution estimates

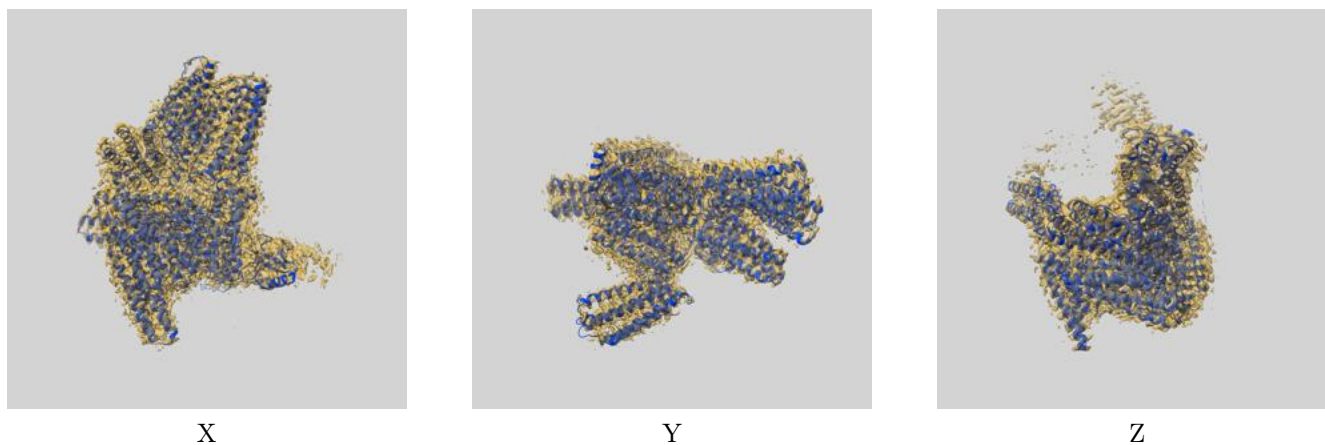
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.70	3.07	2.73
Unmasked-calculated*	3.20	3.70	3.23

*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](#)

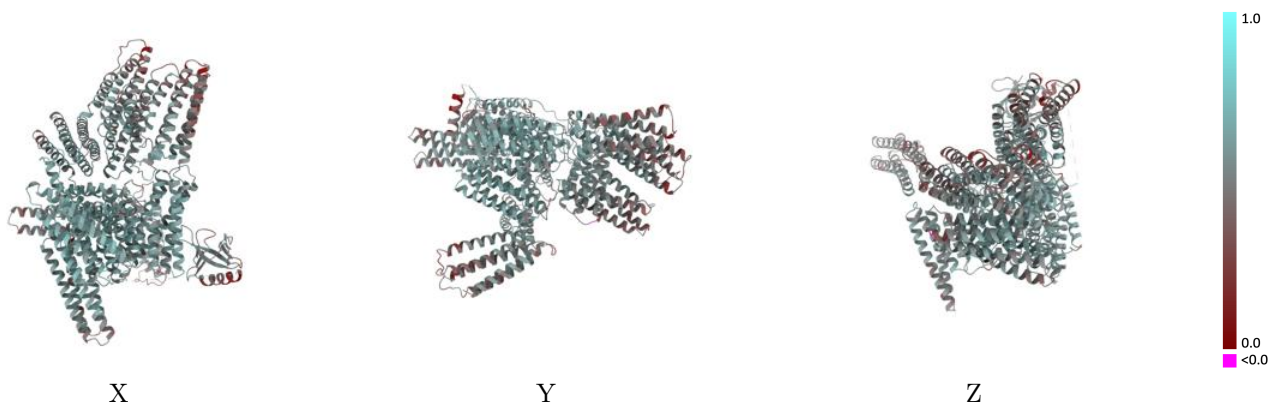
This section contains information regarding the fit between EMDB map EMD-43152 and PDB model 8VDO. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



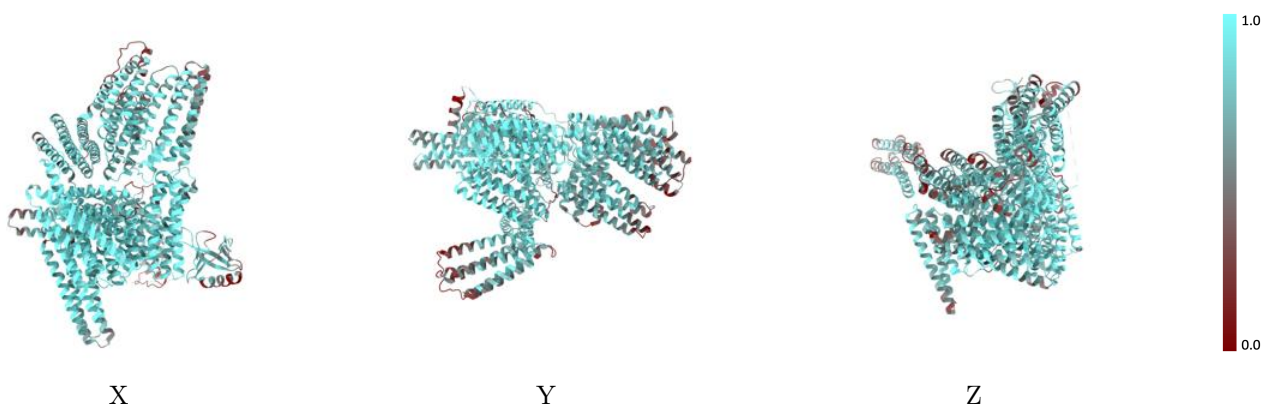
The images above show the 3D surface view of the map at the recommended contour level 0.218 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



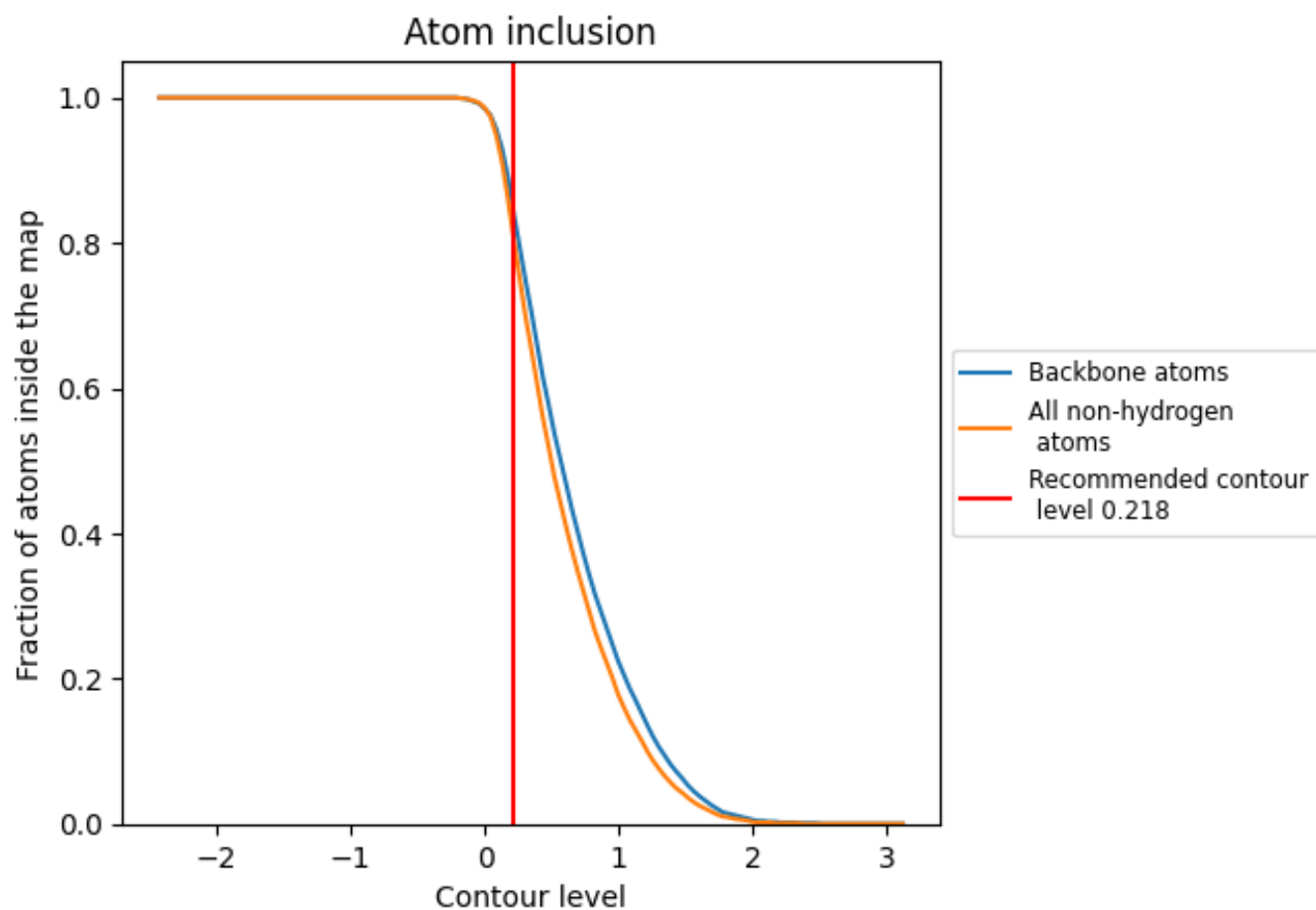
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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




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 [i](#)

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

