



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:46 AM UTC

PDB ID : 8VDP / pdb_00008vdp
EMDB ID : EMD-43154
Title : Cryogenic electron microscopy model of full-length talin without FABD
Authors : Izard, T.; Rangarajan, E.S.
Deposited on : 2023-12-17
Resolution : 3.40 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

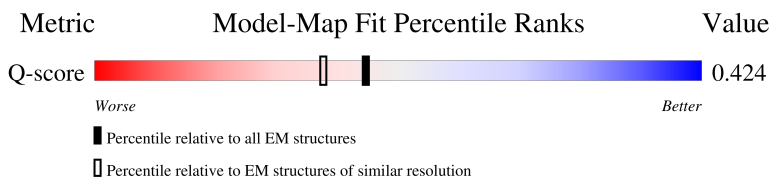
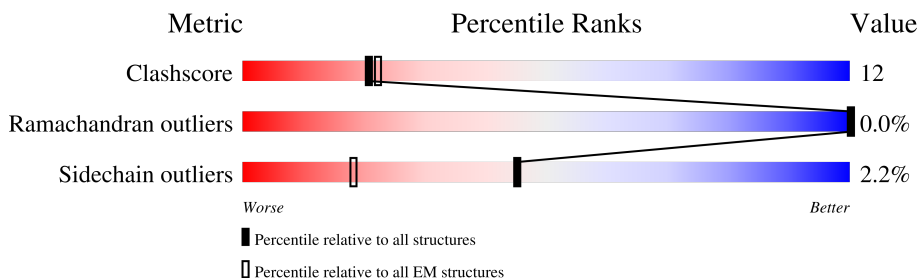
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	2804	8% 53% 19% 28%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14732 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	2005	Total	C	N	O	S	0	0
			14732	9077	2631	2950	74		

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-262	MET	-	expression tag	UNP P42212
A	-261	HIS	-	expression tag	UNP P42212
A	-260	HIS	-	expression tag	UNP P42212
A	-259	HIS	-	expression tag	UNP P42212
A	-258	HIS	-	expression tag	UNP P42212
A	-257	HIS	-	expression tag	UNP P42212
A	-256	HIS	-	expression tag	UNP P42212
A	-255	HIS	-	expression tag	UNP P42212
A	-254	HIS	-	expression tag	UNP P42212
A	-253	HIS	-	expression tag	UNP P42212
A	-252	HIS	-	expression tag	UNP P42212
A	-251	MET	-	expression tag	UNP P42212
A	-250	VAL	-	expression tag	UNP P42212
A	-187	LEU	PHE	conflict	UNP P42212
A	-186	THR	SER	conflict	UNP P42212
A	-20	LEU	HIS	conflict	UNP P42212
A	-12	GLY	-	linker	UNP P42212
A	-11	SER	-	linker	UNP P42212
A	-10	LEU	-	linker	UNP P42212
A	-9	GLU	-	linker	UNP P42212
A	-8	VAL	-	linker	UNP P42212
A	-7	LEU	-	linker	UNP P42212
A	-6	PHE	-	linker	UNP P42212
A	-5	GLN	-	linker	UNP P42212
A	-4	GLY	-	linker	UNP P42212
A	-3	PRO	-	linker	UNP P42212
A	-2	ALA	-	linker	UNP P42212
A	-1	ALA	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	linker	UNP P42212
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



GLU	LEU	GLU	GLU	GLU	ALA	ARG	LEU	GLN	ALA	ARG	LYS	ILE	GLU	ASP	K2274	R2209	R2144
GLU	GLU	GLU	GLU	GLU	ALA	ARG	LEU	GLN	ALA	ASP	LEU	GLN	GLU	ASP	R2210	R2145	A2145
ALA	ALA	ALA	ALA	ALA	ARG	LEU	GLN	ALA	ARG	SER	LEU	GLN	GLU	SER	D2214	E2147	E2148
ARG	ARG	ALA	ALA	ALA	MET	ALA	LEU	MET	ALA	LEU	LEU	LEU	LEU	LEU	M2215	A2149	A2148
LYS	LYS	GLN	LYS	ASN	VAL	VAL	ASN	VAL	ASN	ASN	ASN	VAL	ASN	ASN	L2216	T2150	T2149
LYS	LYS	ASN	ASN	ALA	PHE	ALA	PHE	ALA	PHE	PHE	PHE	ALA	PHE	PHE	R2217	T2150	T2149
LEU	LEU	ALA	ALA	ALA	ALA	ALA	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	A2218	E2151	E2152
ALA	ALA	VAL	ALA	ALA	ALA	VAL	ALA	ALA	ALA	GLU	GLN	GLN	GLN	GLN	E2221	I2153	I2152
GLN	GLN	LYS	LYS	THR	THR	ASN	THR	ASN	THR	ILE	ILE	ILE	ILE	ILE	E2222	R2154	I2153
ILE	ILE	ARG	ARG	ASN	ASN	ASN	ASN	ASN	ASN	LEU	LEU	LEU	LEU	LEU	A2222	Q2155	I2153
ARG	ARG	ALA	ALA	ASN	ASN	ALA	ASN	ASN	ASN	GLU	GLU	GLU	GLU	GLU	A2223	E2156	I2153
GLN	GLN	SER	SER	LEU	LEU	SER	LEU	SER	LEU	GLU	GLU	GLU	GLU	GLU	F2224	L2157	L2157
GLN	GLN	ASP	ASP	GLN	CYS	ALA	ASP	ALA	ALA	ALA	VAL	VAL	VAL	VAL	H2225	P2163	P2163
TYR	TYR	ASN	ASN	GLU	GLU	ALA	ASN	ALA	ALA	VAL	VAL	VAL	VAL	VAL	P2226	P2165	P2165
GLN	GLN	LEU	LEU	ALA	ALA	ALA	LEU	ALA	ALA	LYS	LYS	LYS	LYS	LYS	V2228	P2166	P2166
LYS	LYS	VAL	VAL	ALA	ALA	ALA	SER	ALA	SER	LYS	LYS	LYS	LYS	LYS	E2227	A2167	A2167
PHE	PHE	LYS	LYS	ASN	ASN	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	E2227	K2168	K2168
LEU	LEU	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	V2229	T2169	T2169
PRO	PRO	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	A2229	C2161	C2161
SER	SER	GLN	GLN	VAL	VAL	VAL	VAL	VAL	VAL	GLY	GLY	THR	THR	GLY	P2230	S2162	S2162
LEU	LEU	LYS	LYS	GLN	GLN	THR	THR	THR	THR	K2291	K2291	GLY	GLY	GLY	D2231	P2163	P2163
LEU	LEU	ALA	ALA	THR	THR	THR	THR	THR	THR	ALA	ALA	THR	THR	ALA	P2230	E2164	E2164
LEU	LEU	ALA	ALA	GLY	GLY	GLY	GLY	GLY	GLY	ALA	ALA	ALA	ALA	ALA	D2231	P2165	P2165
ARG	ARG	ALA	ALA	HIS	HIS	ALA	ALA	ALA	ALA	GLU	GLU	GLU	GLU	GLU	V2232	A2167	A2167
ASP	ASP	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	LEU	LEU	LEU	LEU	LEU	R2232	K2168	K2168
GLU	GLU	ALA	ALA	SER	SER	PHE	SER	SER	SER	VAL	VAL	VAL	VAL	VAL	R2233	T2169	T2169
GLU	GLU	ALA	ALA	GLN	GLN	GLN	GLN	GLN	GLN	ASP	ASP	ASP	ASP	ASP	L2234		
HIS		ASP	ASP	GLU	GLU	GLU	GLU	GLU	GLU	LYS	LYS	LYS	LYS	LYS	L2234		
		GLU	GLU	ALA	ALA	ALA	ALA	ALA	ALA	PRO	PRO	PRO	PRO	PRO	R2235		
		GLN	GLN	LYS	LYS	LYS	LYS	LYS	LYS	ALA	ALA	ALA	ALA	ALA	A2236		
		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ALA	ALA	ALA	ALA	ALA	R2237		
		GLU	GLU	LEU	LEU	LEU	LEU	LEU	LEU	ASP	ASP	ASP	ASP	ASP	L2237		
		LYS	LYS	ASN	ASN	ILE	ILE	ILE	ILE	ALA	ALA	ALA	ALA	ALA	H2238		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68494	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	1.137	Depositor
Minimum map value	-0.676	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.15	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	0.25	0/14902	0.46	3/20195 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	1384	ILE	N-CA-C	-6.15	106.51	112.29
1	A	2261	PRO	N-CA-C	-5.97	105.22	113.53
1	A	2262	ASN	CA-C-O	-5.54	116.65	120.47

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	14732	0	14899	354	0
All	All	14732	0	14899	354	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 12.

The worst 5 of 354 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:1223:LEU:HD13	1:A:1286:VAL:HG12	1.58	0.85
1:A:233:ASP:OD1	1:A:234:LYS:N	2.10	0.84
1:A:1088:THR:HG22	1:A:1203:LEU:HD11	1.60	0.83
1:A:1901:LYS:HG3	1:A:1902:PRO:HD3	1.59	0.82
1:A:2262:ASN:HB3	1:A:2265:LEU:HB2	1.64	0.78

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	2001/2804 (71%)	1948 (97%)	52 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2259	GLN

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	369/2215 (17%)	361 (98%)	8 (2%)	45	63

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2269	LEU
1	A	2267	GLN
1	A	2260	LYS
1	A	2258	LEU
1	A	2264	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2262	ASN
1	A	2259	GLN
1	A	390	GLN
1	A	349	GLN
1	A	534	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

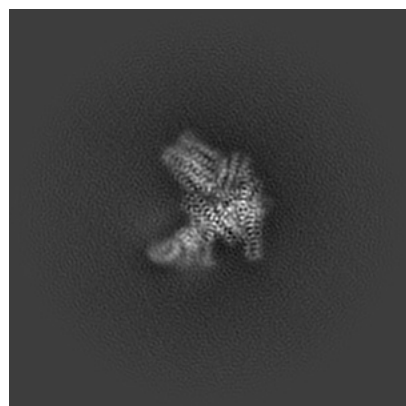
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43154. These allow visual inspection of the internal detail of the map and identification of artifacts.

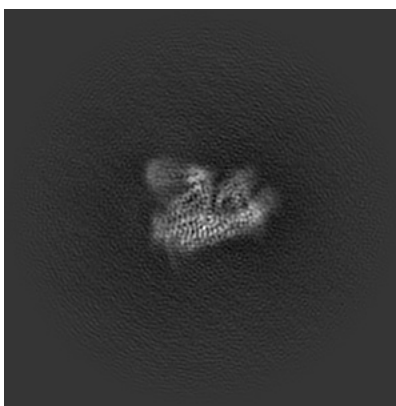
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

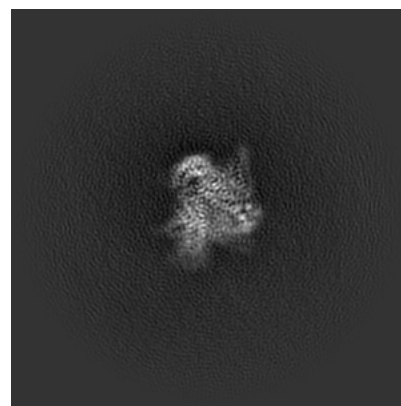
6.1.1 Primary map



X

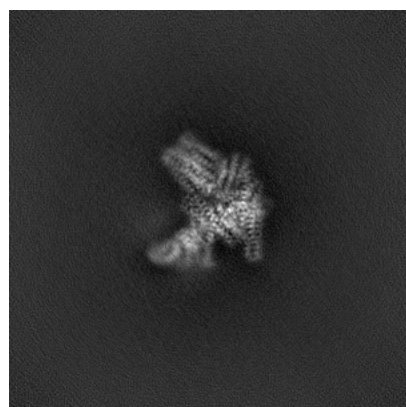


Y

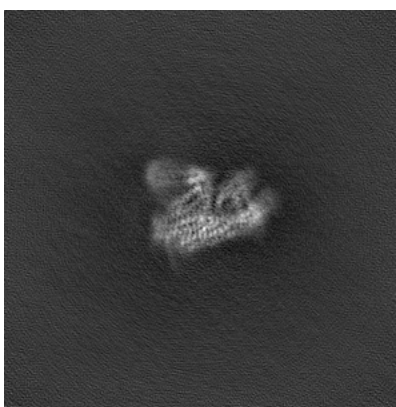


Z

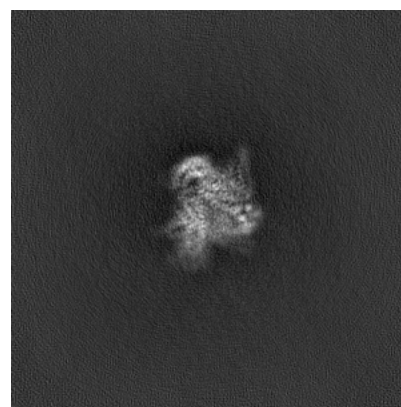
6.1.2 Raw map



X



Y

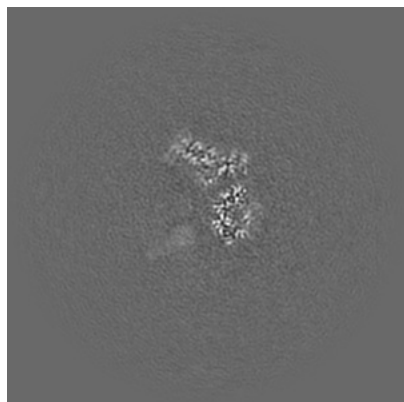


Z

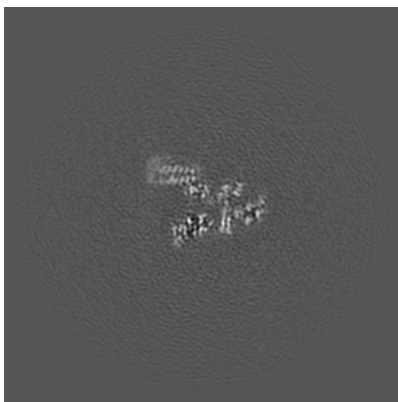
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

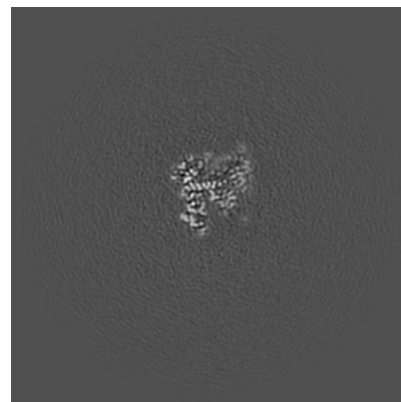
6.2.1 Primary map



X Index: 160

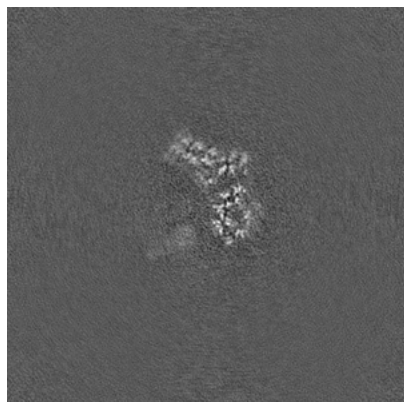


Y Index: 160

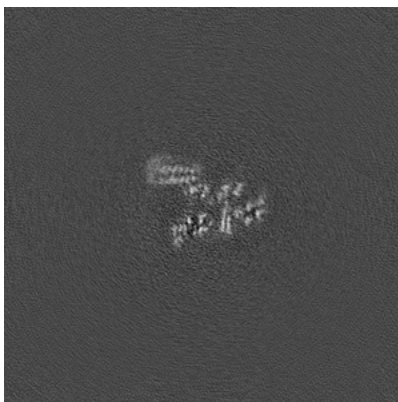


Z Index: 160

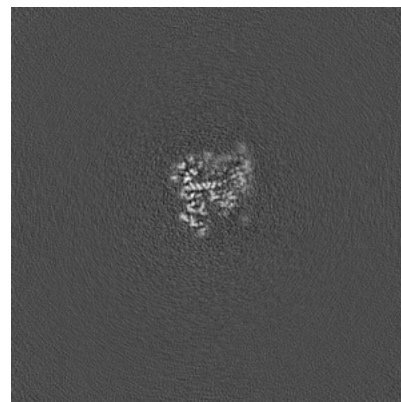
6.2.2 Raw map



X Index: 160



Y Index: 160

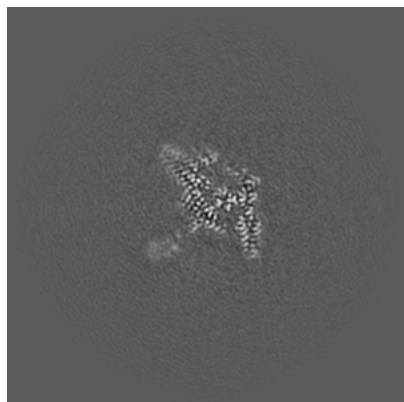


Z Index: 160

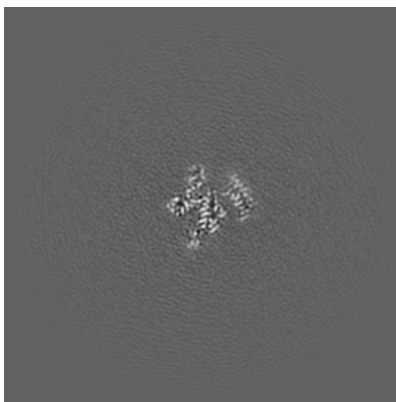
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

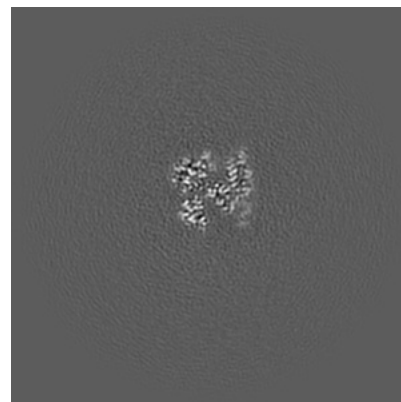
6.3.1 Primary map



X Index: 149

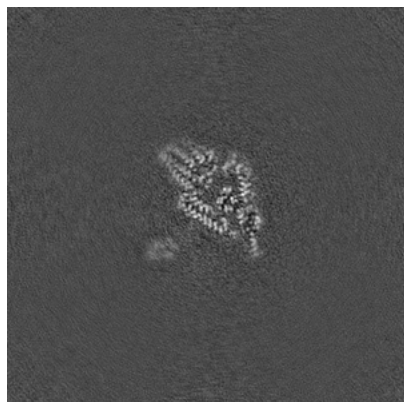


Y Index: 177

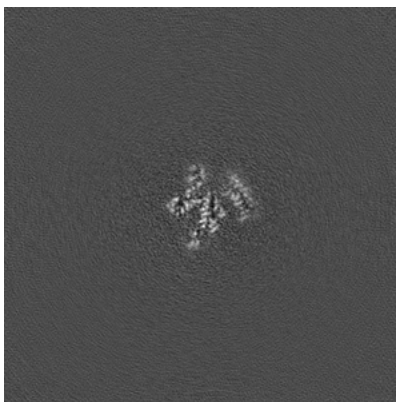


Z Index: 156

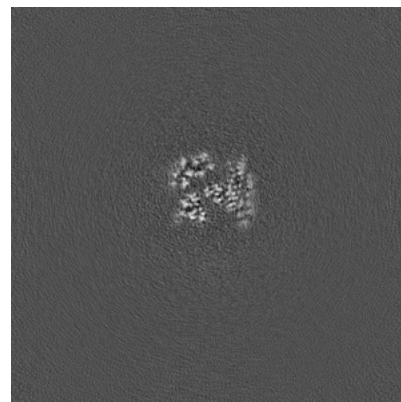
6.3.2 Raw map



X Index: 152



Y Index: 177

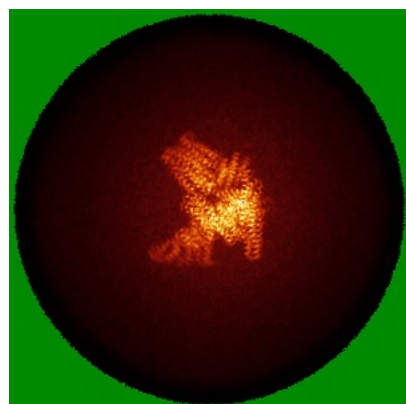


Z Index: 152

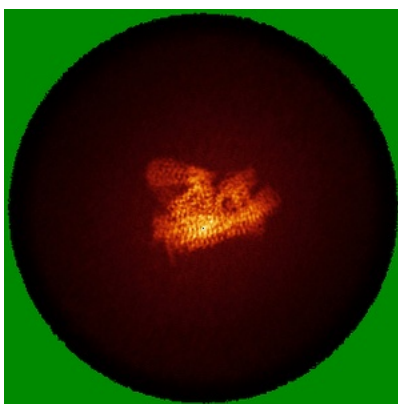
The images above show the largest variance slices of the map in three orthogonal directions.

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

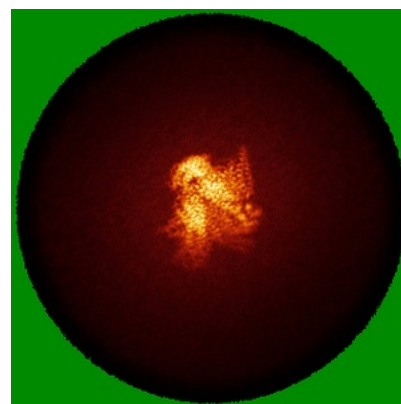
6.4.1 Primary map



X

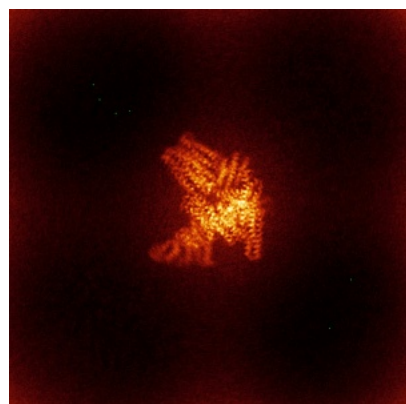


Y



Z

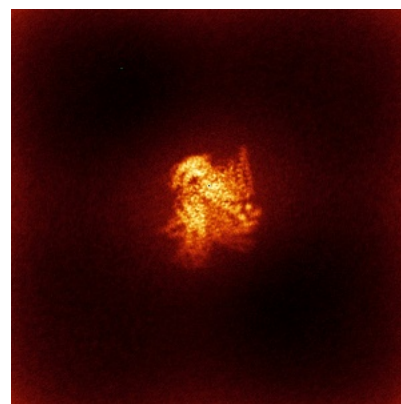
6.4.2 Raw map



X



Y

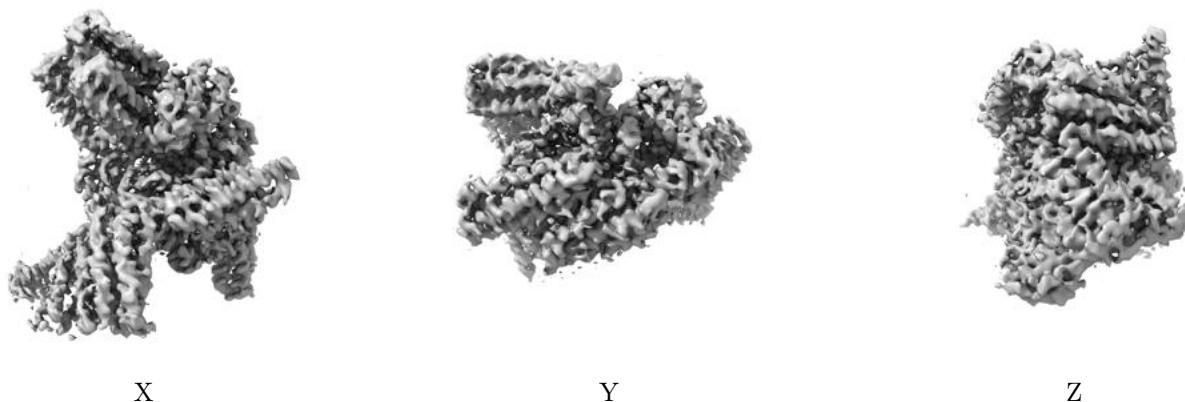


Z

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.

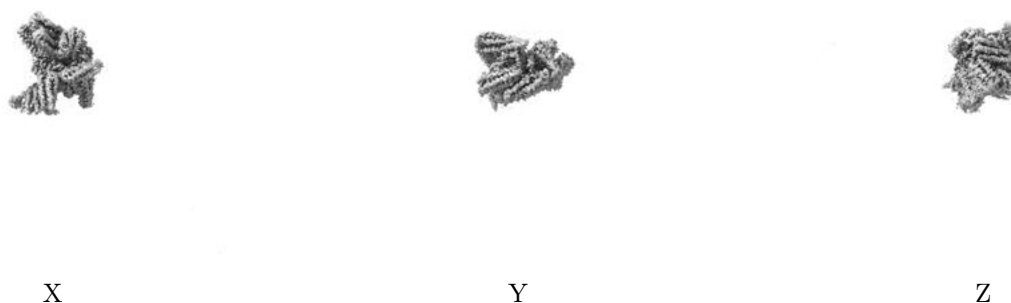
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

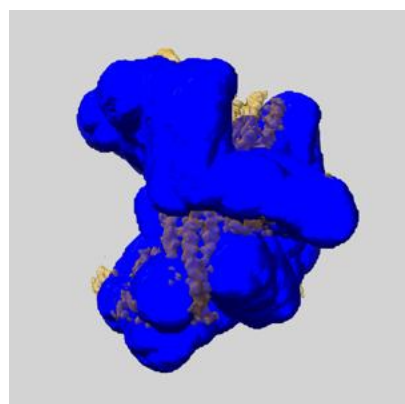
6.6 Mask visualisation [i](#)

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

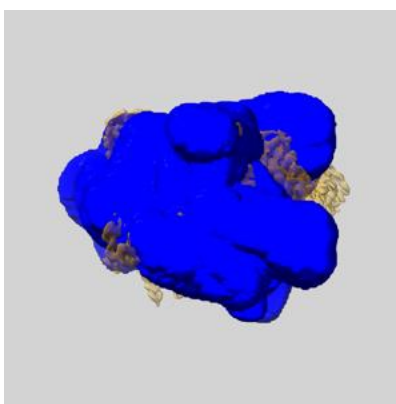
A mask typically either:

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

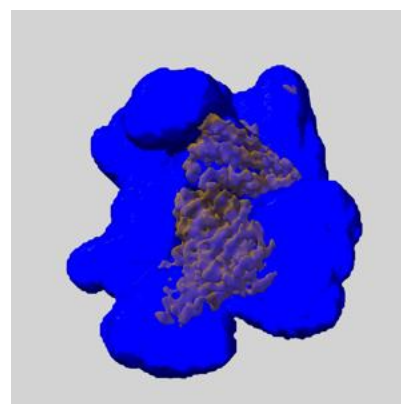
6.6.1 emd_43154_msk_1.map [i](#)



X



Y

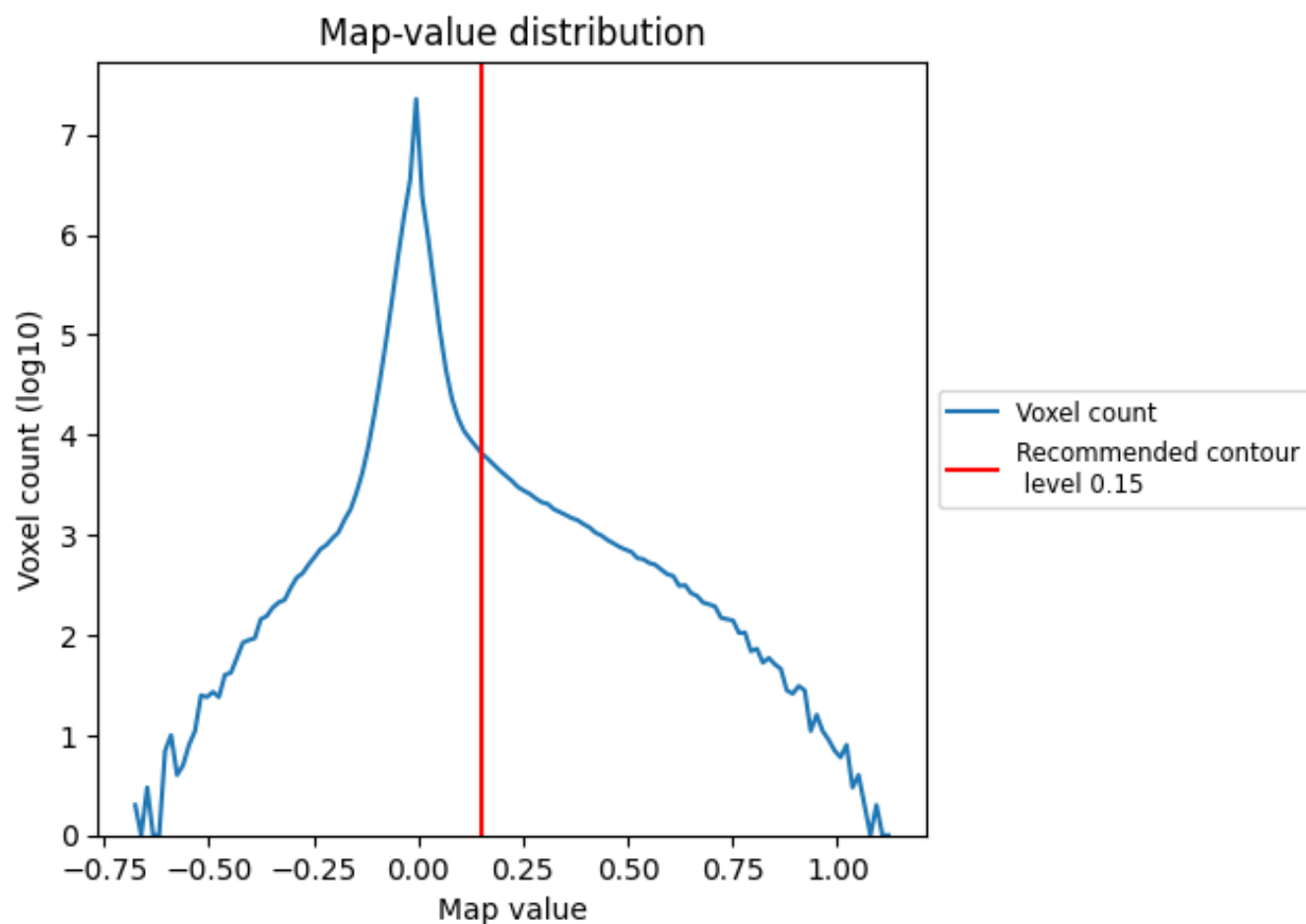


Z

7 Map analysis [i](#)

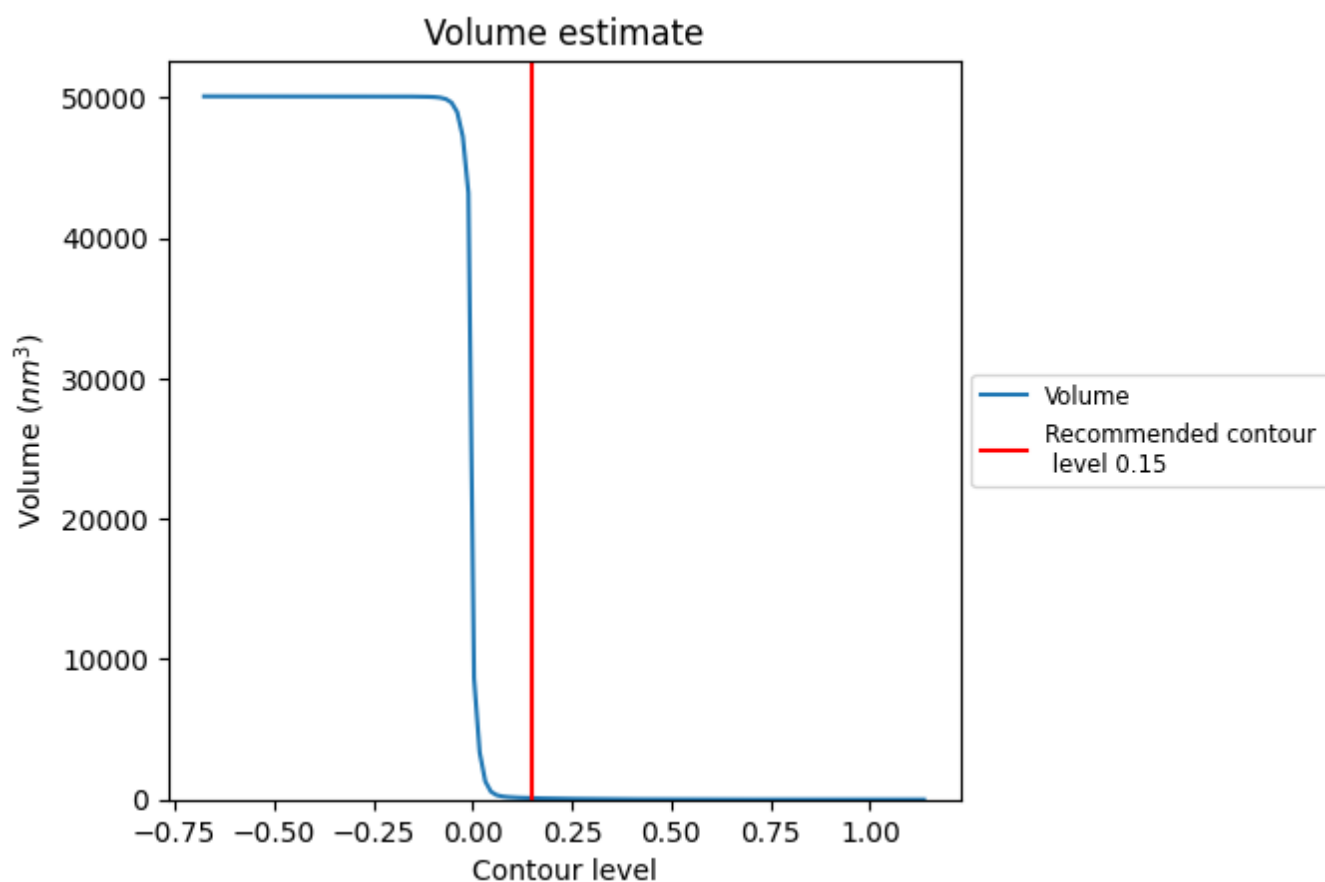
This section contains the results of statistical analysis of the map.

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.

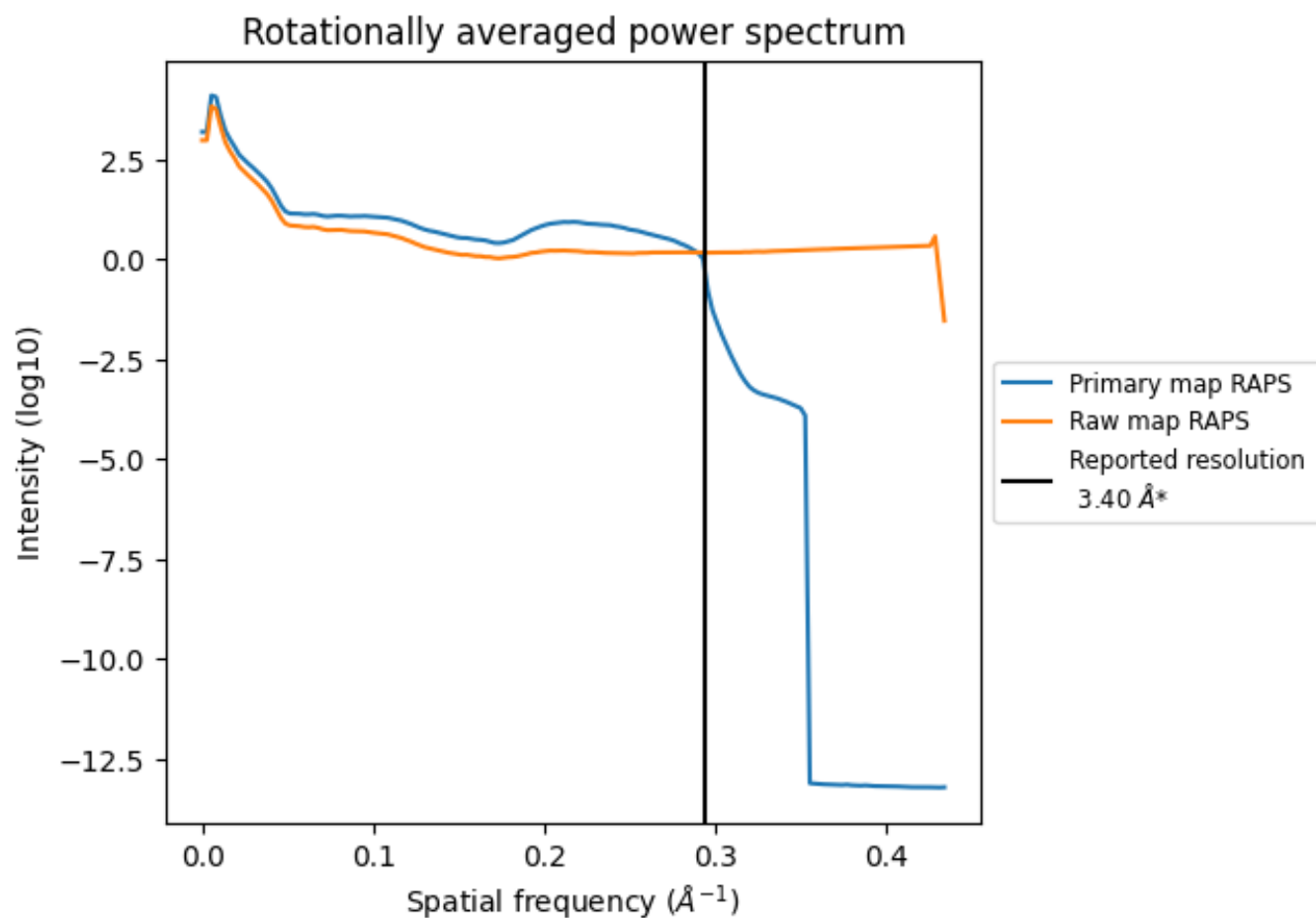
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 104 nm³; this corresponds to an approximate mass of 94 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 ⓘ

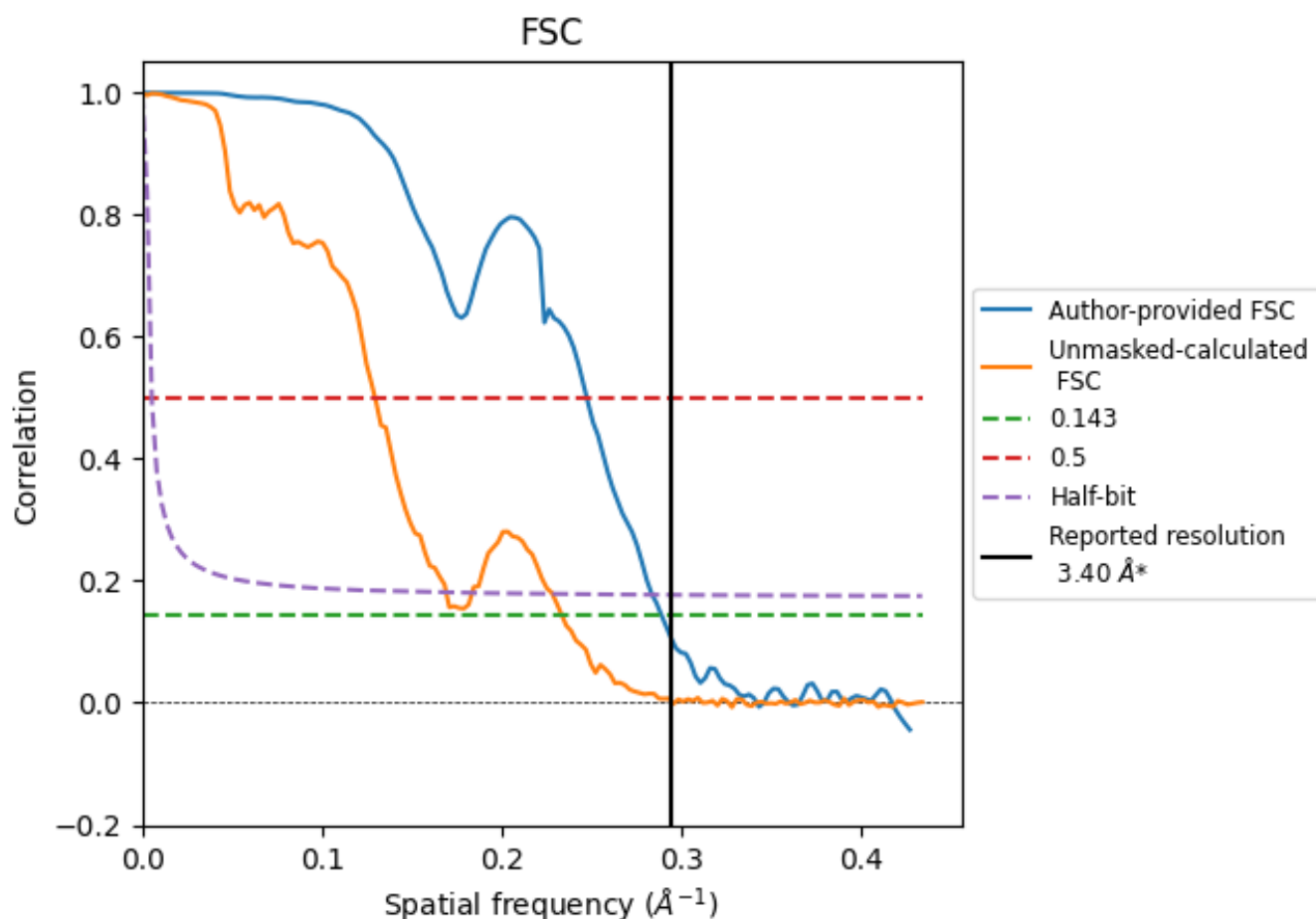


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

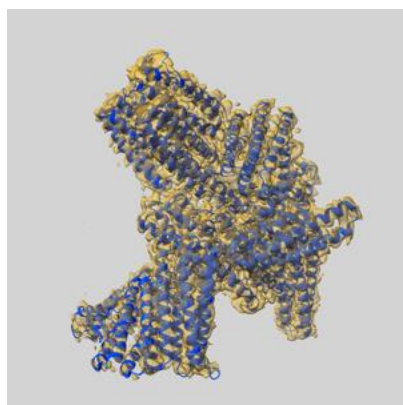
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.46	4.04	3.52
Unmasked-calculated*	4.28	7.72	5.91

*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 4.28 differs from the reported value 3.4 by more than 10 %

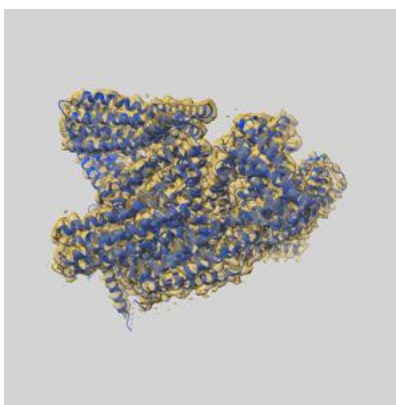
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43154 and PDB model 8VDP. Per-residue inclusion information can be found in section [3](#) on page [5](#).

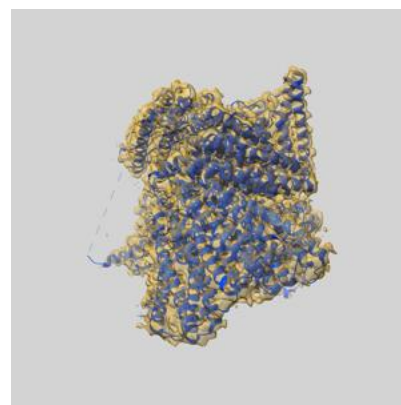
9.1 Map-model overlay [i](#)



X



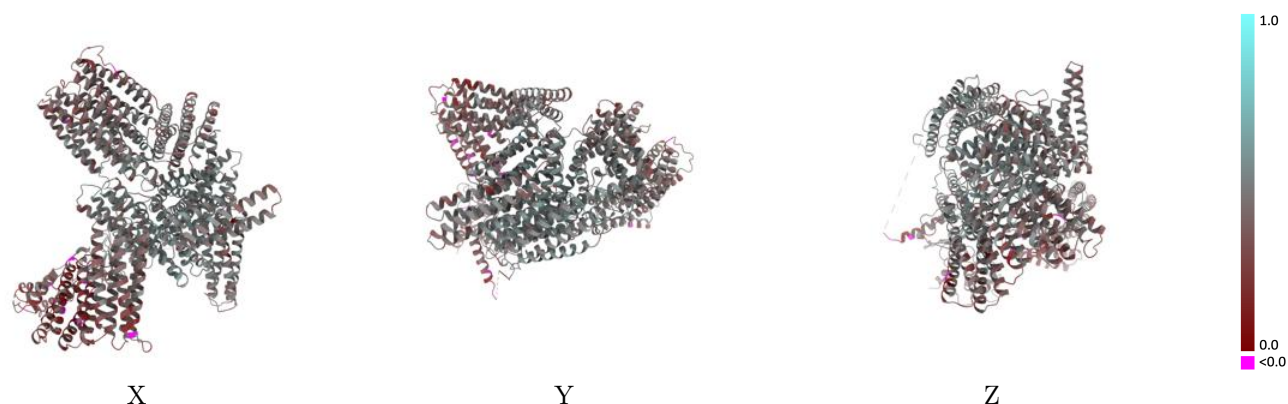
Y



Z

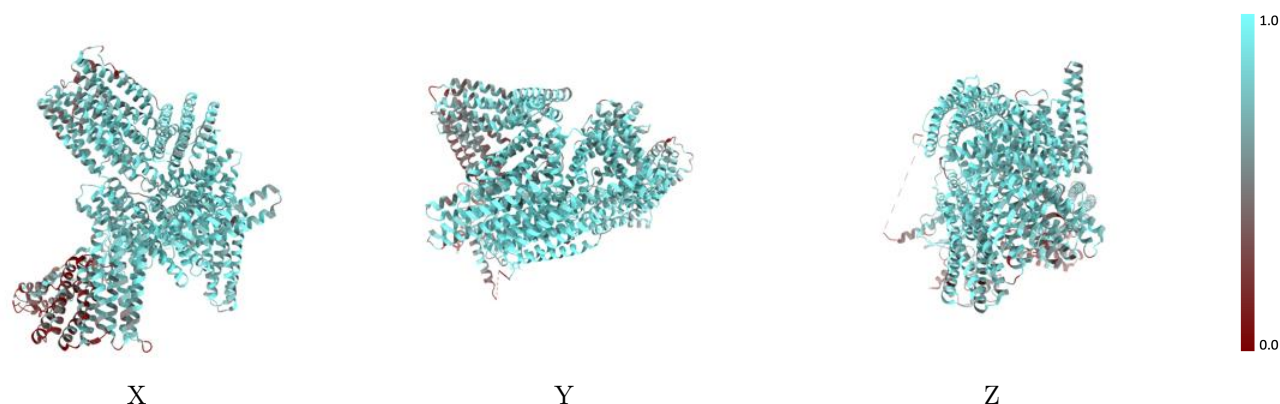
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



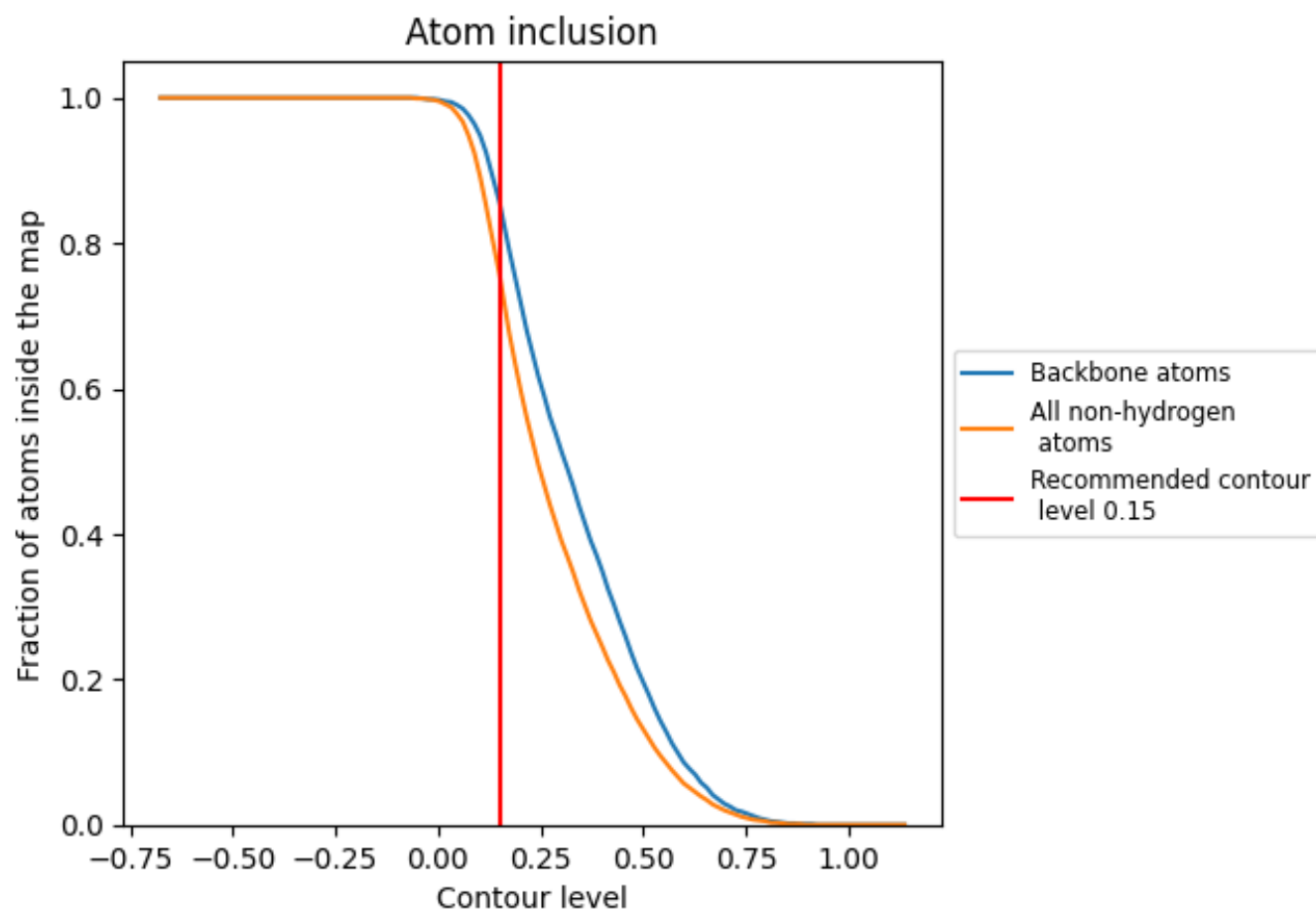
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 76% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7570	0.4240
A	0.7570	0.4240

