



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:41 PM UTC

PDB ID : 6FAY / pdb_00006fay
EMDB ID : EMD-4219
Title : Teneurin3 monomer
Authors : Janssen, B.J.C.; Meijer, D.H.M.; van Bezouwen, L.S.
Deposited on : 2017-12-18
Resolution : 3.80 Å (reported)
Based on initial model : 6FB3

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:

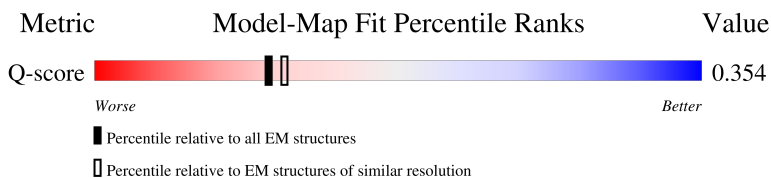
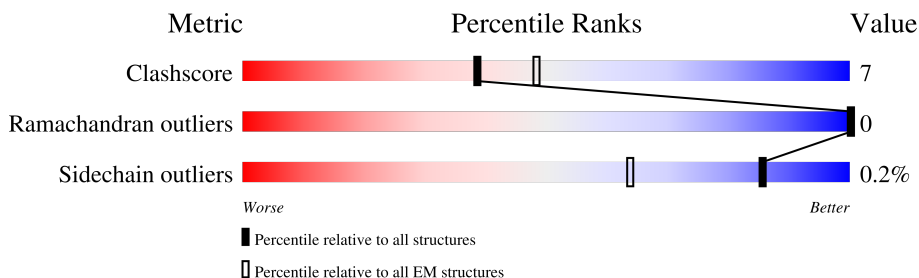
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.80 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	10198 (3.30 - 4.30)

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	1876	 64% 16% 19%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12130 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 Odz3 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1518	12060	7644	2057	2313	46	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	844	GLY	-	expression tag	UNP B7ZNJ5
A	2716	ALA	-	expression tag	UNP B7ZNJ5
A	2717	SER	-	expression tag	UNP B7ZNJ5
A	2718	ALA	-	expression tag	UNP B7ZNJ5
A	2719	ALA	-	expression tag	UNP B7ZNJ5
A	2720	ALA	-	expression tag	UNP B7ZNJ5
A	2721	HIS	-	expression tag	UNP B7ZNJ5
A	2722	HIS	-	expression tag	UNP B7ZNJ5
A	2723	HIS	-	expression tag	UNP B7ZNJ5
A	2724	HIS	-	expression tag	UNP B7ZNJ5
A	2725	HIS	-	expression tag	UNP B7ZNJ5
A	2726	HIS	-	expression tag	UNP B7ZNJ5

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

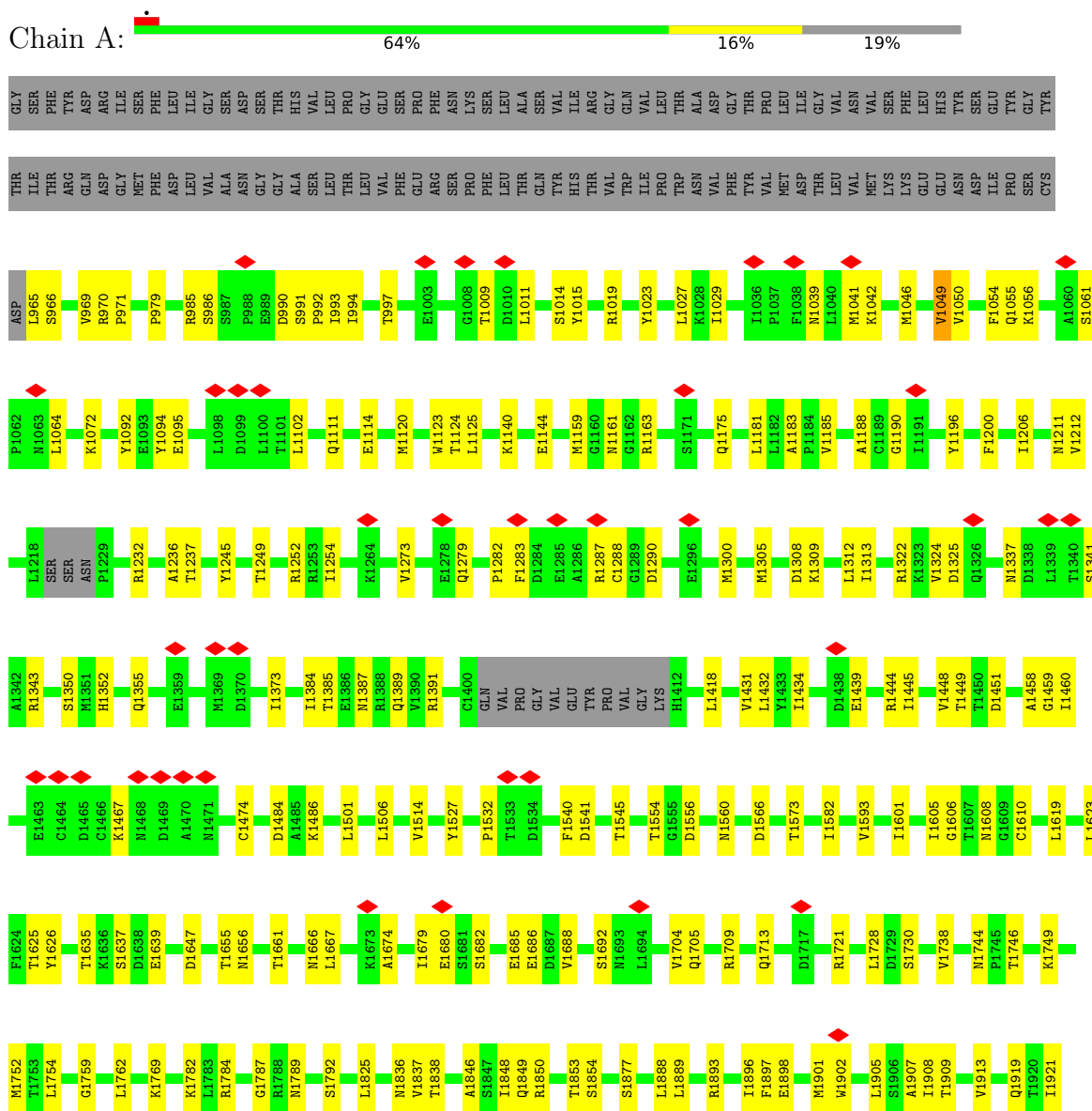


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
2	A	1	Total 14	8	1	5	0
2	A	1	Total 14	8	1	5	0
2	A	1	Total 14	8	1	5	0
2	A	1	Total 14	8	1	5	0
2	A	1	Total 14	8	1	5	0

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: Odz3 protein



GLU	LEU	ALA	ASP	SER	ALA	ASN	ASN	ASN	ILE	GLN	LEU	ALA	ALA	LEU	GLU	ASN	GLY	ALA	ASP	SER	ARG	GLN	TRP	GLN	SER	GLY	ILE	GLN	PHE	LEU	ARG	ARG	GLN	ALA	ASP	GLY	TYR	TYR	VAL	LEU	SER	ASP	VAL	GLU	GLN	TYR	ALA	PRO																									
L2511	G2515	V2516	S2521	Q2522	ARG	VAL	THR	ASN	VAL	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN																						
R2379	D2384	I2385	W2388	K2389	R2390	I2391	P2395	N2399	M2402	T2412	HIS	ASP	VAL	LYS	ASP	TYR	ILE	LYS	THR	D2421	L2426	F2431	D2462	I2466	F2467	G2468	Q2471	S2482	L2483	G2484	K2485	MET	ALA	GLU	VAL	VAL	GLN	SER	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG																							
R2216	G2217	T2218	L2228	G2236	V2241	Y2245	R2250	S2253	T2256	H2261	L2262	Q2263	Y2266	I2275	H2281	I2286	Y2290	Y2291	D2292	L2293	Q2294	G2295	H2296	A2299	I2302	S2303	S2304	G2305	D2306	K2330	Q2331	I2332	I2352	T2363	K2364	L2365	I2366	Y2373	D2374	I2375	R2053	F2062	D2063	K2068	V2069	Q2071	G2076	M2091	K2095	D2098	R2102	Y2108	E2109	L2114	I2120	R2131	E2147	T2156	L2159	N2160	E2161	M2164	D2170	N2174	L2175	H2176	S2182	L2189	R2194	T2198	D2202	Y2205	E2209
R1928	M1929	I1930	I1940	E1946	Q1952	T1958	S1959	R1960	V1961	W1962	L1963	F1964	K1965	R1968	S1973	E1974	I1975	L1976	F1984	T1985	A1990	K1994	V1995	M1997	L1998	C2005	T2006	I2007	R2010	Q2011	I2016	D2017	R2018	D2026	V2029	R2032	F2033	D2034	R2042	I2050																																	
T2063	F2062	D2063	K2068	V2069	Q2071	G2076	M2091	K2095	D2098	R2102	Y2108	E2109	L2114	I2120	R2131	E2147	T2156	L2159	N2160	E2161	M2164	D2170	N2174	L2175	H2176	S2182	L2189	R2194	T2198	D2202	Y2205	E2209																																									

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	287402	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.191	Depositor
Minimum map value	-0.814	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.4	Depositor
Map size (\AA)	389.34, 389.34, 389.34	wwPDB
Map dimensions	378, 378, 378	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.03, 1.03, 1.03	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: NAG

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	0.19	0/12329	0.50	2/16738 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	1566	ASP	CA-C-N	5.12	131.31	121.54
1	A	1566	ASP	C-N-CA	5.12	131.31	121.54

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	12060	0	11795	176	0
2	A	70	0	65	0	0
All	All	12130	0	11860	176	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 7.

The worst 5 of 176 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:1287:ARG:HB2	1:A:1290:ASP:H	1.53	0.72
1:A:1046:MET:HG2	1:A:1055:GLN:HG2	1.76	0.66
1:A:2176:HIS:HA	1:A:2189:LEU:HB2	1.80	0.63
1:A:2426:LEU:HB3	1:A:2431:PHE:HB2	1.80	0.62
1:A:1623:LEU:HB3	1:A:1637:SER:HB2	1.82	0.62

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	1508/1876 (80%)	1369 (91%)	139 (9%)	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	1329/1632 (81%)	1327 (100%)	2 (0%)	87 87

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

Mol	Chain	Res	Type
1	A	1049	VAL
1	A	1913	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1808	HIS
1	A	1952	GLN
1	A	2434	HIS
1	A	2084	GLN
1	A	2432	HIS

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](#)

5 ligands 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	$\# Z > 2$
2	NAG	A	2801	1	14,14,15	0.59	0	17,19,21	1.03	1 (5%)
2	NAG	A	2804	1	14,14,15	0.40	0	17,19,21	0.73	1 (5%)
2	NAG	A	2805	1	14,14,15	0.37	0	17,19,21	0.58	0
2	NAG	A	2803	1	14,14,15	0.31	0	17,19,21	0.55	0
2	NAG	A	2802	1	14,14,15	0.32	0	17,19,21	0.60	1 (5%)

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
2	NAG	A	2801	1	-	4/6/23/26	0/1/1/1
2	NAG	A	2804	1	-	2/6/23/26	0/1/1/1
2	NAG	A	2805	1	-	2/6/23/26	0/1/1/1
2	NAG	A	2803	1	-	2/6/23/26	0/1/1/1
2	NAG	A	2802	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2801	NAG	C2-N2-C7	3.23	127.22	122.90
2	A	2804	NAG	C1-O5-C5	2.63	115.70	112.19
2	A	2802	NAG	C1-O5-C5	2.05	114.93	112.19

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2803	NAG	O5-C5-C6-O6
2	A	2804	NAG	O5-C5-C6-O6
2	A	2805	NAG	O5-C5-C6-O6
2	A	2801	NAG	O5-C5-C6-O6
2	A	2803	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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.

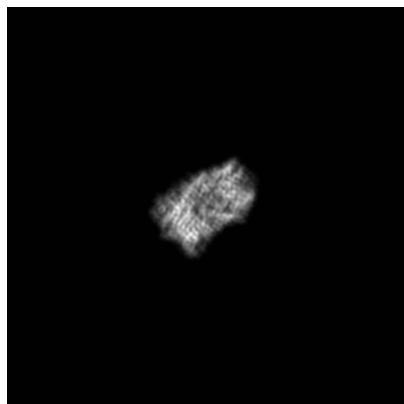
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4219. These allow visual inspection of the internal detail of the map and identification of artifacts.

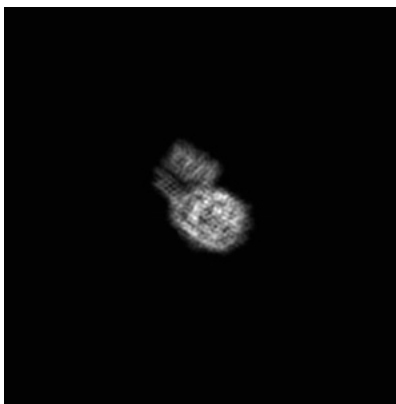
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

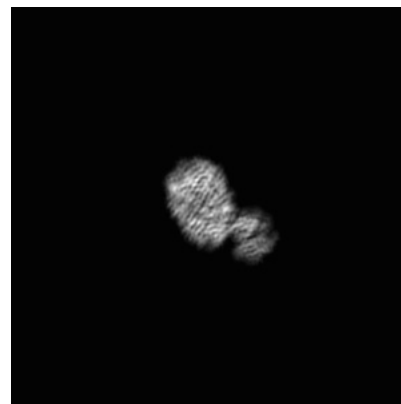
6.1.1 Primary map



X

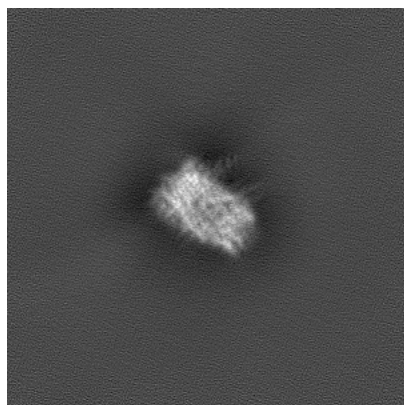


Y

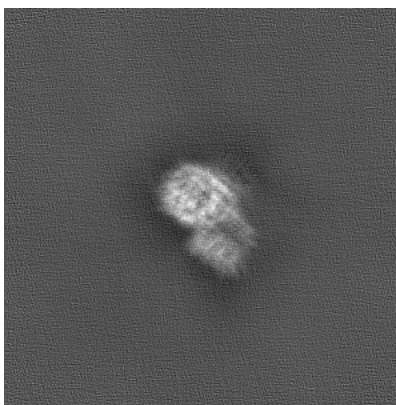


Z

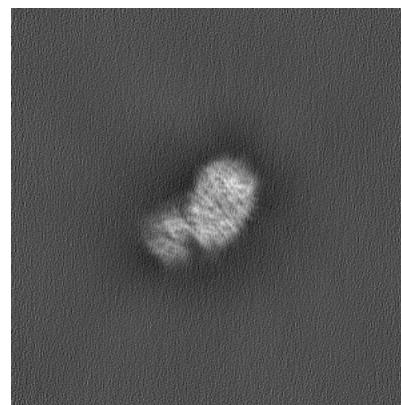
6.1.2 Raw map



X



Y

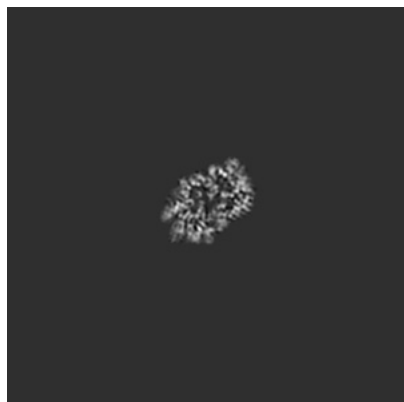


Z

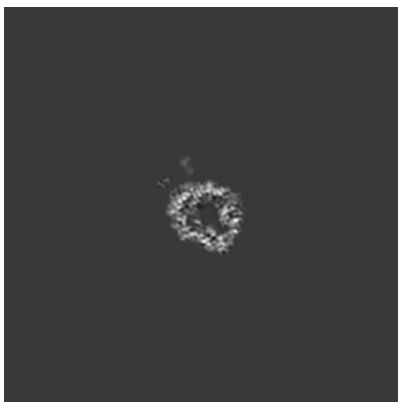
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 189

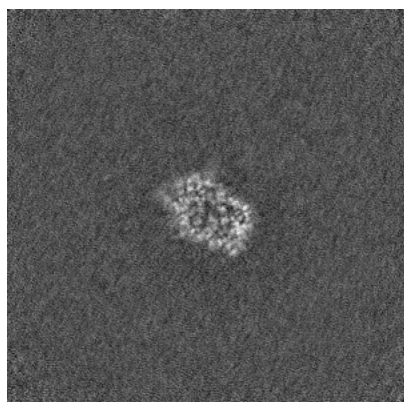


Y Index: 189

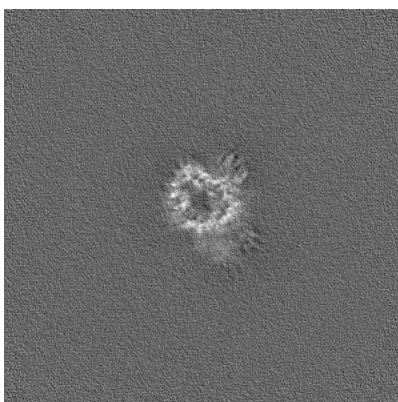


Z Index: 189

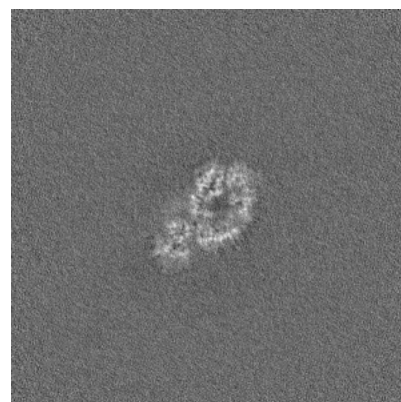
6.2.2 Raw map



X Index: 192



Y Index: 192

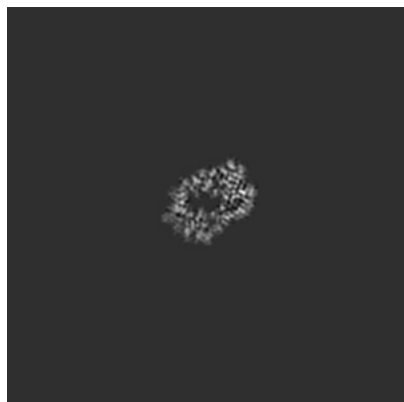


Z Index: 192

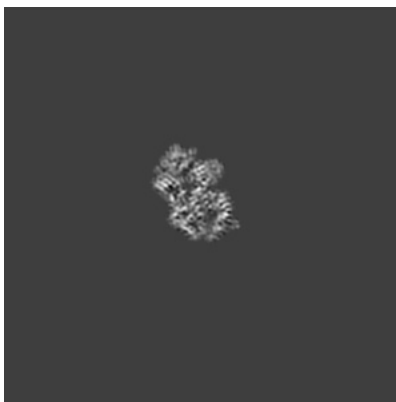
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

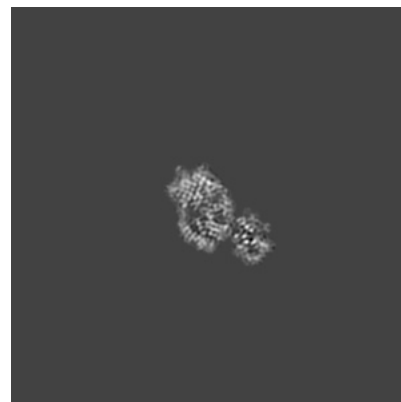
6.3.1 Primary map



X Index: 185

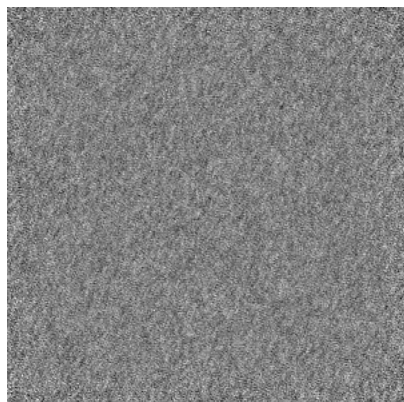


Y Index: 171

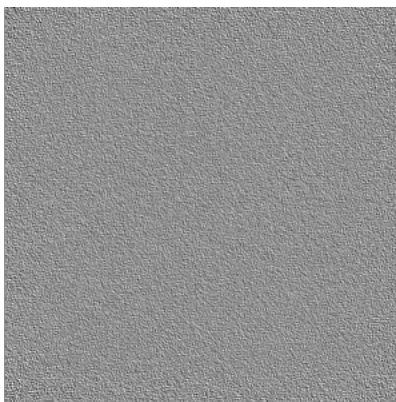


Z Index: 180

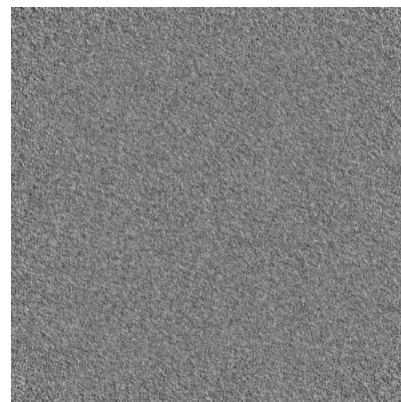
6.3.2 Raw map



X Index: 0



Y Index: 0

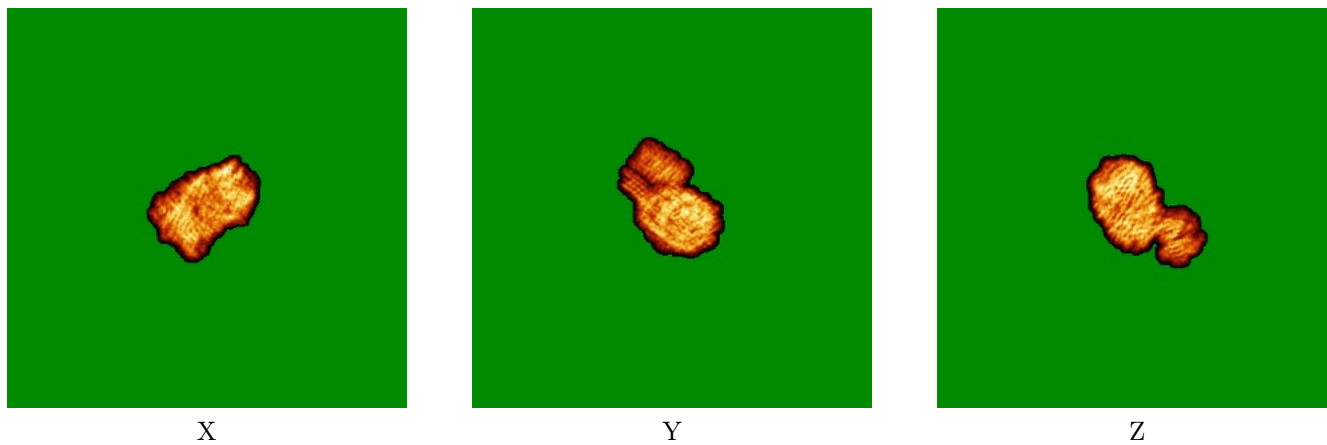


Z Index: 383

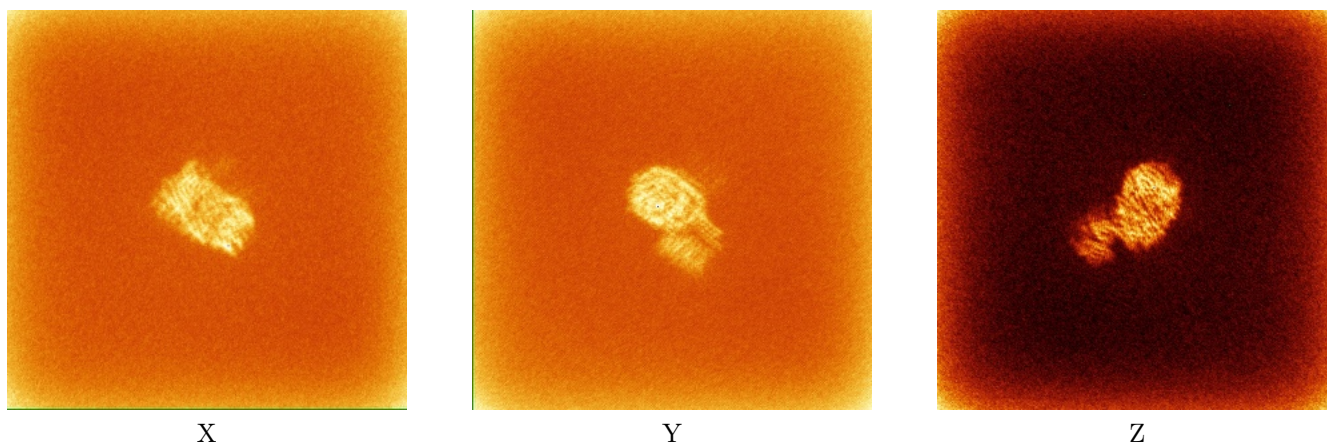
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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.

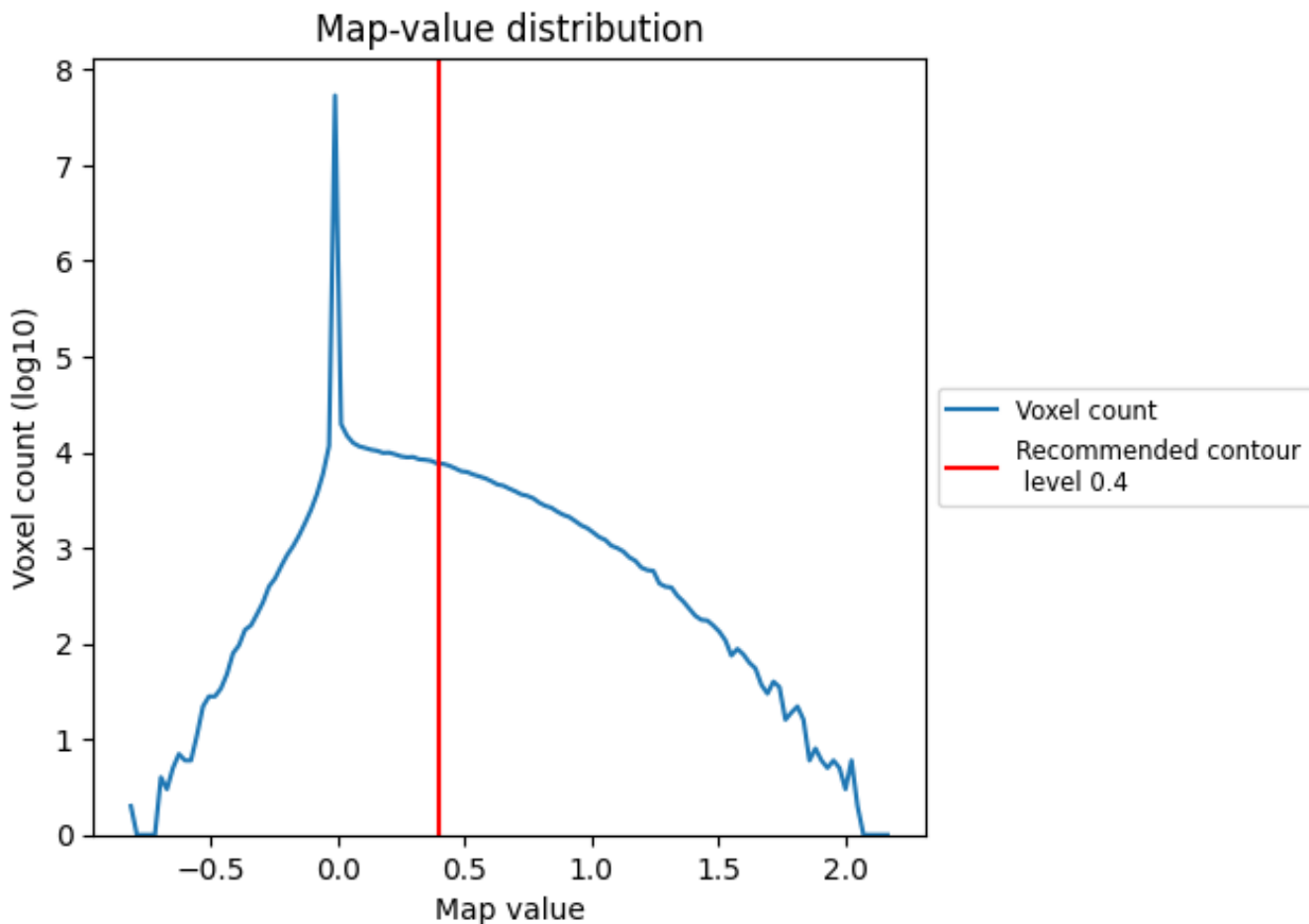
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

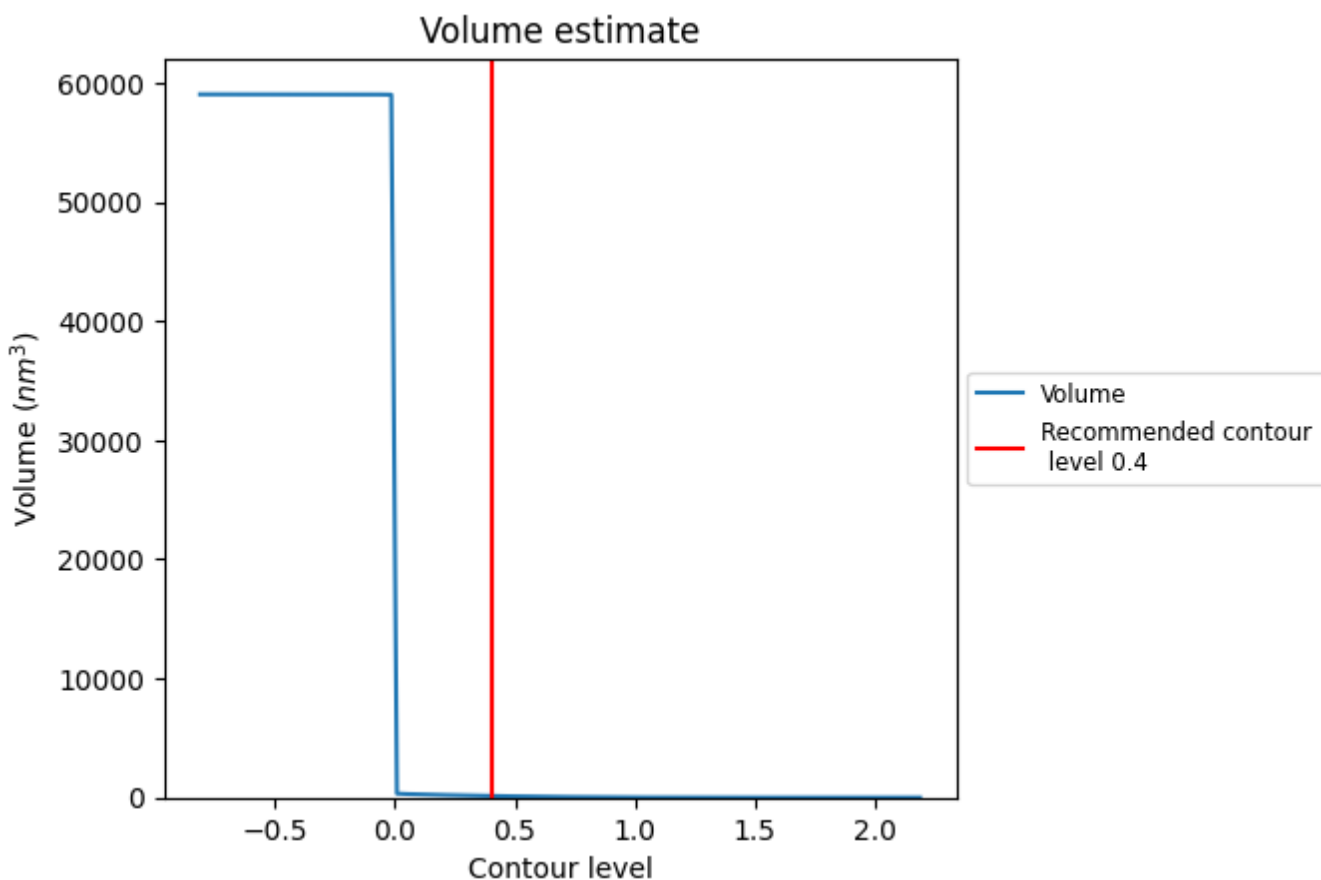
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

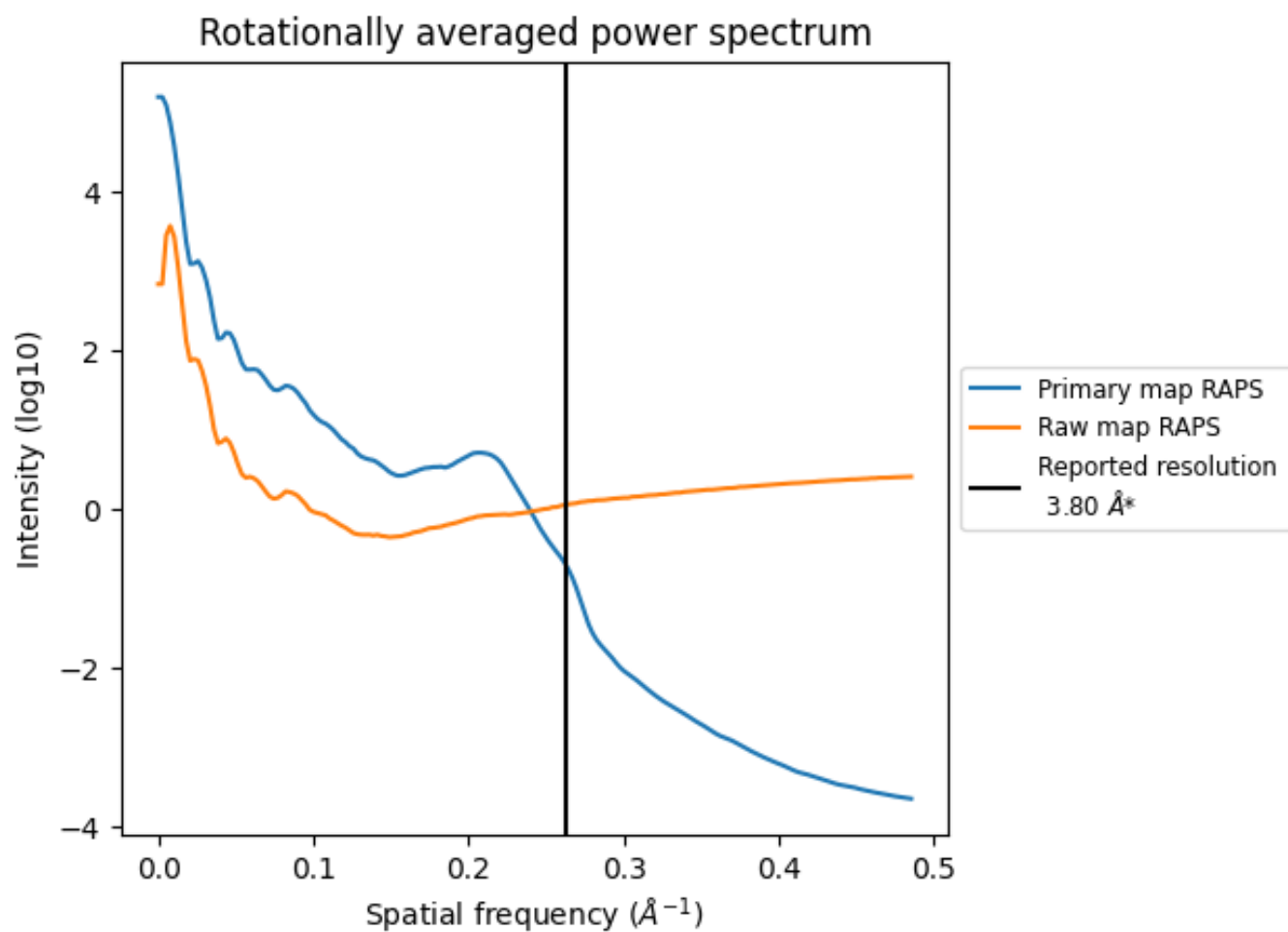
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 134 nm³; this corresponds to an approximate mass of 121 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

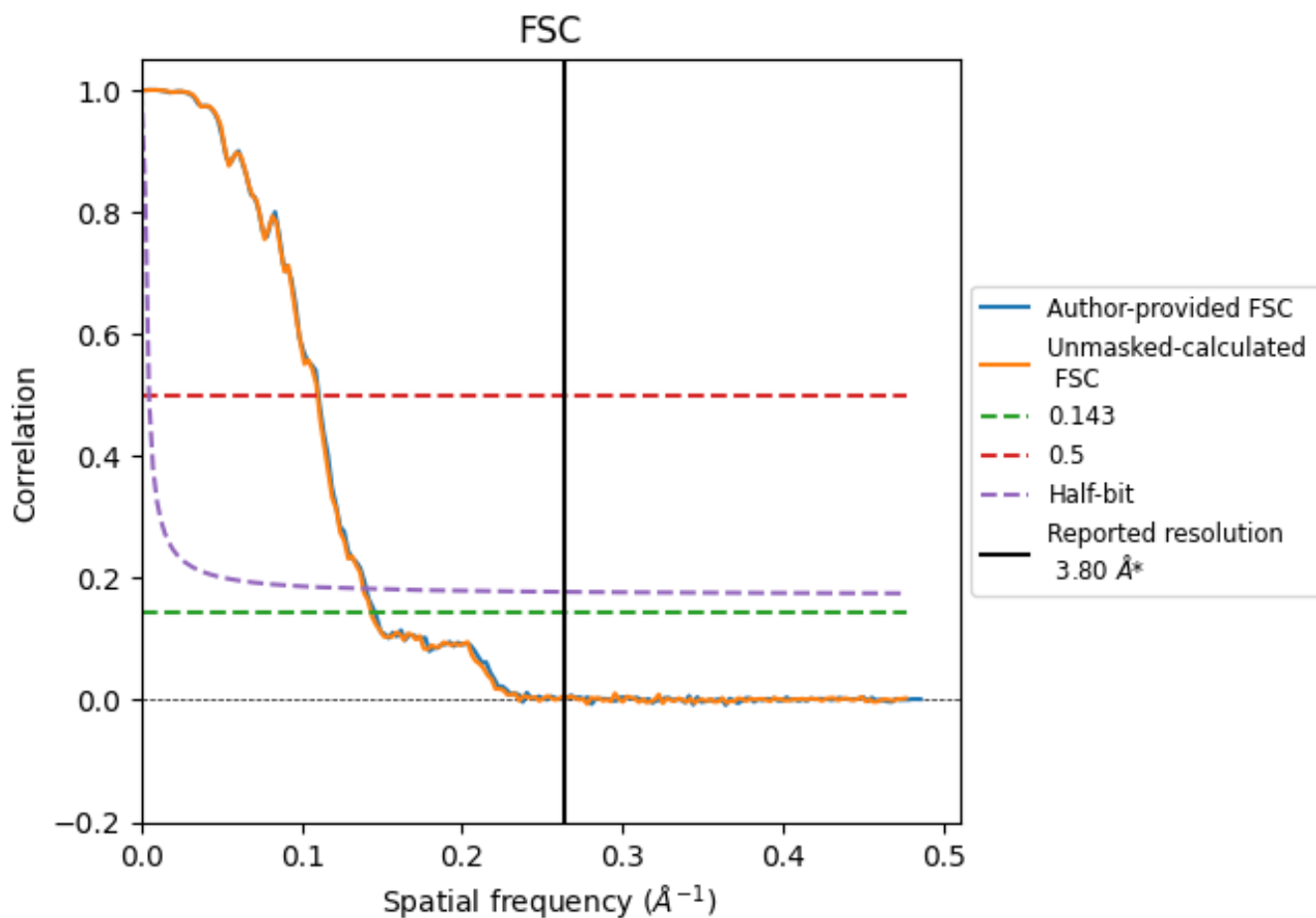


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	6.87	9.05	7.14
Unmasked-calculated*	6.98	9.10	7.23

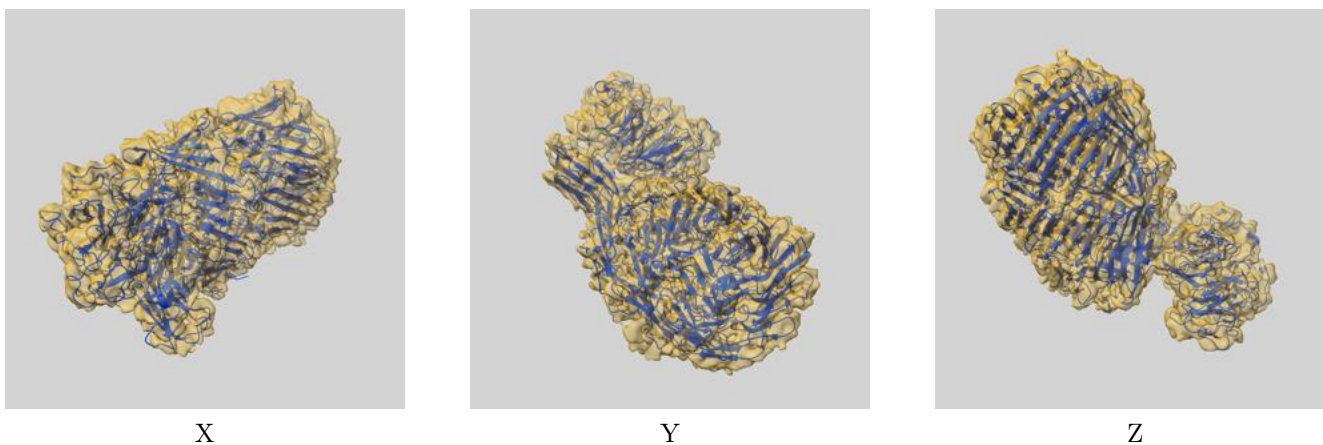
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 6.87 differs from the reported value 3.8 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.98 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

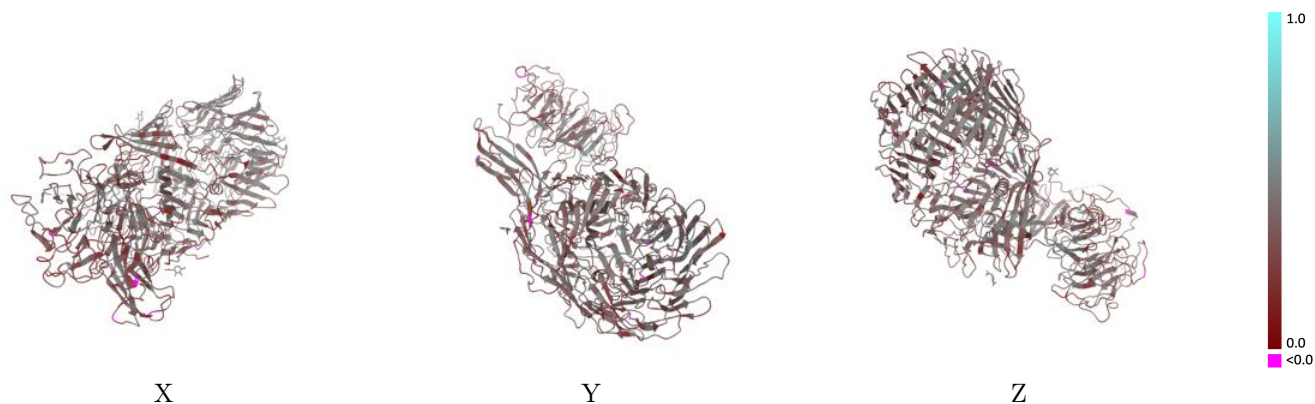
This section contains information regarding the fit between EMDB map EMD-4219 and PDB model 6FAY. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



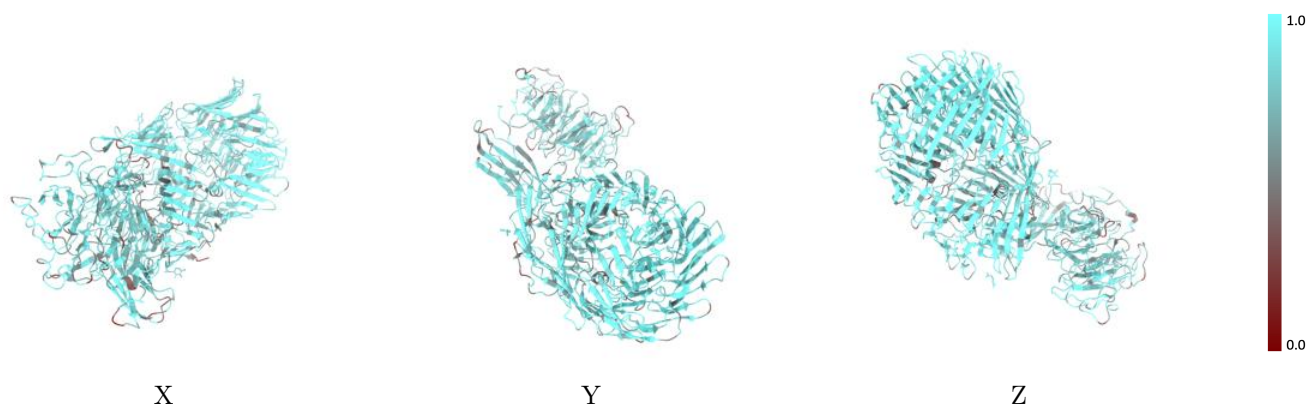
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



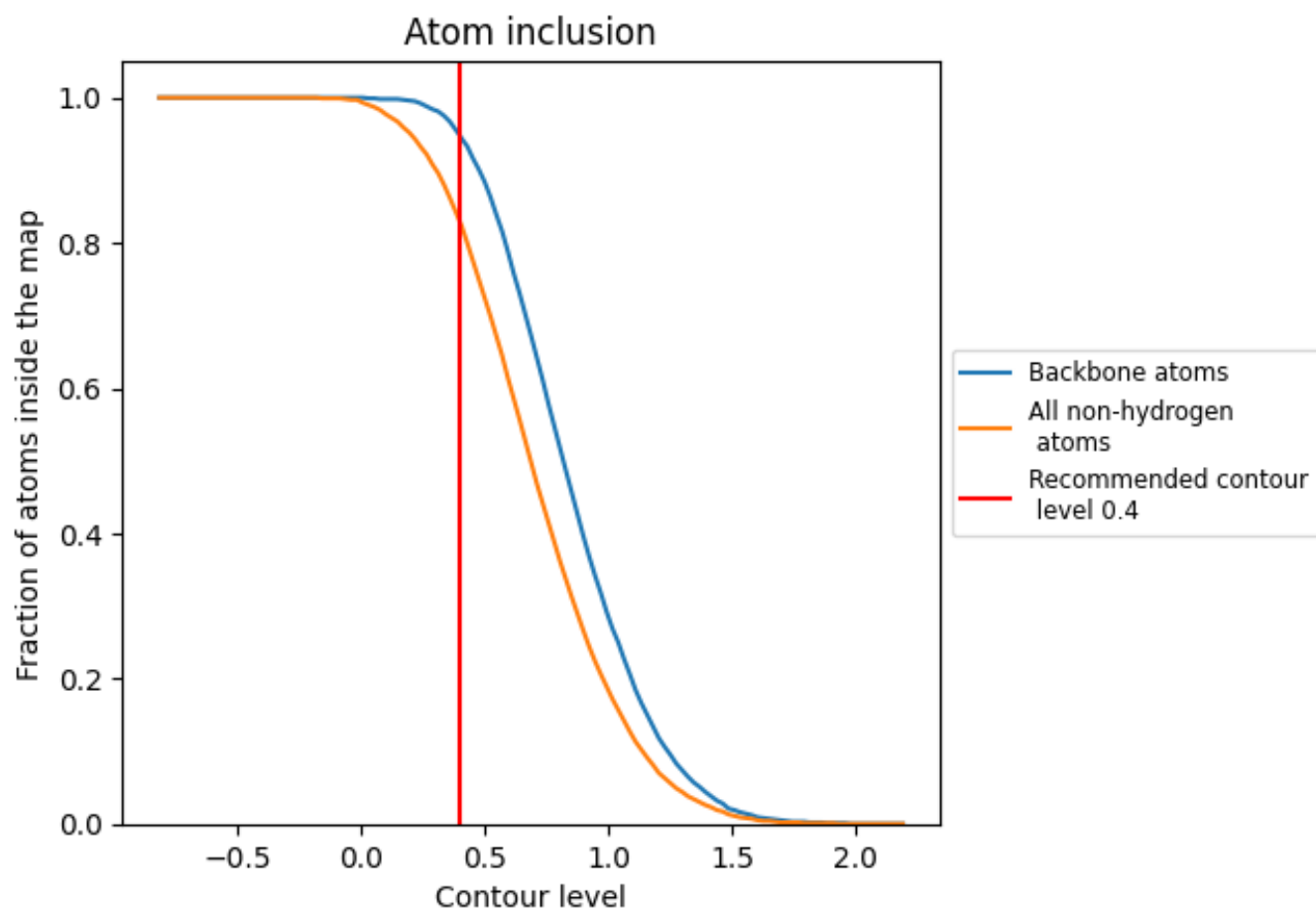
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).





9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 83% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8300	 0.3540
A	 0.8300	 0.3540

