



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 10:37 PM UTC

PDB ID : 8EDN / pdb_00008edn
EMDB ID : EMD-28037
Title : Cryo-EM structure of the full-length human NF1 dimer
Authors : Darling, J.E.; Merk, A.; Grishammer, R.; Ognjenovic, J.
Deposited on : 2022-09-05
Resolution : 3.80 Å(reported)

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

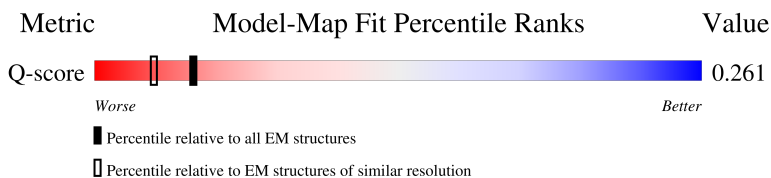
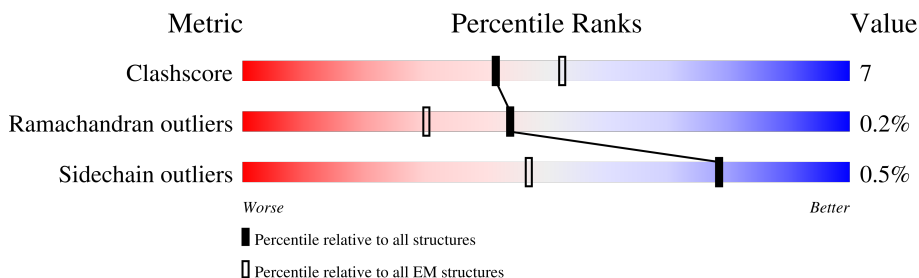
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	2818	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3683 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 Isoform I of Neurofibromin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	579	Total	C	N	O	S	0	0
			3683	2360	662	648	13		



Lys	Lys	Leu	Gly	Val	Val	Val	Lys	Tyr	Leu	Pro	Ile	Phe	Ile	Leu
Lys	Lys	Asn	Pro	Val	Val	Val	Leu	Pro	Thr	Glu	Ala	Ala	Ala	Leu
Ile	Ile	Leu	Phe	His	Val	Val	Leu	Ile	Thr	Val	Phe	Phe	Phe	Leu
Val	Val	Ser	Ser	Asn	Ser	Ser	Gly	His	Val	Val	Thr	Gln	Arg	Leu
		Asn	Lys	Leu	Glu	Glu	Thr	Lys	Val	Phe	Tyr	Ser	Ser	Ala
		Ser	Gln	Leu	Ser	Ser	Arg	Gly	Asn	Met	Asn	Pro	Asn	Ser
		Met	Thr	Asp	Asn	Val	Lys	Asp	Cys	Ala	Gln	Pro	Tyr	Thr
		Ser	Gln	Val	Val	Val	Ser	Pro	His	Ile	Pro	Ser	Arg	His
		Thr	Ile	Lys	Leu	Leu	Phe	Tyr	Arg	Arg	Leu	Asp	Asp	Lys
		Leu	Pro	Ile	Leu	Leu	Asp	Tyr	Asn	Asn	Leu	Gln	Glu	Leu
		Ala	Asp	Asn	Asp	Asp	His	Arg	Cys	Pro	Asn	Pro	Val	Leu
		Thr	Tyr	Thr	Glu	Glu	Leu	Thr	Asp	Leu	Lys	Arg	Phe	Ile
		Ser	Ala	Leu	Glu	Glu	Ile	Leu	Lys	Glu	Asp	Ala	Ser	Asn
		Gln	Glu	Val	Val	Val	Ser	Lys	Phe	Trp	Pro	Leu	Gly	Ile
		Leu	Leu	Ser	Leu	Leu	Asp	Glu	Thr	His	Val	Val	Val	Thr
		Ser	Ile	Leu	Thr	Thr	Thr	Gln	Asn	Cys	Thr	Tyr	Ser	Ser
		Leu	Ile	Cys	Cys	Cys	Lys	Gln	Asn	Lys	His	Gly	Gly	Leu
		Gly	Lys	Gln	Gln	Gln	Pro	Trp	Gln	Met	Ala	Cys	Arg	Cys
		Ile	Phe	Asp	Asp	Ile	Lys	Ser	Gln	Met	Ala	Gly	Arg	Thr
		Asp	Leu	Pro	Ile	Val	Leu	Val	Leu	Leu	Val	Val	Val	His
		Thr	Thr	Thr	Thr	Thr	Thr	Gly	Ala	Gly	Val	Val	Val	Gln
		Leu	Thr	His	Val	Val	Gly	Glu	Ala	Phe	Ala	His	Ser	Val
		Ser	Tyr	His	Thr	Thr	Gly	Tyr	Leu	Phe	Gly	Leu	Ser	Leu
		Pro	Leu	Leu	Leu	Leu	Ile	Tyr	Thr	Asn	Gln	Gln	Glu	Glu
		Thr	Pro	Ile	Ile	Ala	Thr	Leu	Thr	Ser	Ile	Thr	Thr	Thr
		Thr	Gly	Val	Val	Thr	Thr	Ala	Val	Val	Lys	Val	Lys	Lys
		Gly	Ile	Gln	Leu	Leu	Thr	Ala	Ser	Asn	Leu	Leu	Leu	Leu
		His	Asp	Ser	Val	Val	Pro	Ala	Glu	Phe	Gln	Arg	Val	Val
		Cys	Glu	Ser	Val	Val	Glu	Glu	Glu	Ala	Ile	Ala	Ala	Val
		Asn	Glu	Val	Val	Val	Met	Tyr	Val	Ala	Ala	Ala	Ala	Val
		Ser	Thr	Thr	Thr	Thr	Arg	Thr	Arg	Leu	Leu	Ile	Arg	Arg
		Gly	Ser	His	His	Thr	Arg	Val	Ser	Val	Leu	Glu	Ser	Leu
		Arg	Glu	Glu	Asp	Asp	Val	Gly	Arg	Gly	Leu	Met	Met	Leu
		Thr	Thr	Glu	Glu	Glu	Ala	Gln	Cys	His	Ala	Lys	Cys	Phe
		Ser	Ser	Ser	Phe	Phe	Glu	Thr	Ser	Leu	Gly	Lys	Met	Thr
		His	Leu	Pro	Pro	Thr	Thr	Ser	Leu	Leu	Ala	Pro	Trp	Thr
		Ser	Leu	Thr	Thr	Thr	Gln	Met	Leu	Ala	Thr	Lys	Lys	Leu
		Leu	Pro	Leu	Leu	Ala	Arg	Ser	His	Leu	Asp	Asp	Val	Val
		Ala	Pro	Tyr	Thr	Ile	Tyr	Arg	Arg	Tyr	Leu	Arg	Val	Val
		Ser	Pro	Gln	Gln	Gln	Met	Ala	Arg	Leu	Cys	Met	Ser	Ser
		Ala	Thr	Gln	Gln	Leu	Glu	Ala	Arg	Leu	Arg	Leu	Leu	Leu
		Ser	Thr	Thr	Thr	Thr	Glu	Lys	Lys	Lys	Ala	Glu	Glu	Leu
		Gln	Ser	Ser	Ser	Ser	Thr	Lys	His	His	Lys	Ser	Trp	Phe
		Val	Pro	Val	Val	Val	Thr	Pro	Ser	Pro	Pro	Asp	Val	Thr
		Ser	Gln	Gln	Gln	Gln	Gln	Met	Ser	Ser	Thr	Asp	Gln	Lys
		Leu	Pro	Gln	Ala	Ala	Ile	Leu	Leu	Ala	Thr	Thr	Trp	Lys
		Arg	Ala	Ser	Glu	Glu	Ser	Asp	Thr	Val	Tyr	Thr	Thr	Leu
		Ser	Leu	Phe	Ala	Ala	Ser	Ile	Ile	Val	Asn	Gly	Gln	Val
		Ala	Gly	Gly	Val	Val	Gln	Gln	Met	Arg	Val	Ser	Val	Val
		Ser	Gln	Ser	Asn	Val	Gln	Pro	Glu	Thr	Arg	Gln	Val	Val
		Phe	Leu	Gly	Gly	Gly	His	Arg	His	Thr	Val	Val	Val	Val
		Thr	Leu	Ser	Leu	Thr	Thr	Ser	Leu	Val	Ile	Leu	Val	Val
		Arg	Ser	Ser	Thr	Thr	Pro	Thr	Val	Arg	Thr	Thr	Thr	Val
		Ser	Leu	Thr	Thr	Thr	Thr	Val	Val	Leu	Val	Val	Val	Val
		Leu	Thr	Thr	Thr	Thr	Thr	Val	Val	Val	Val	Val	Val	Val

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	161208	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 200	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	9.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.049	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0223	Depositor
Map size ($\text{\AA}$)	266.24, 266.24, 266.24	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	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	0.16	0/3748	0.36	3/5161 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	305	LYS	CA-C-N	-5.41	112.49	120.38
1	A	305	LYS	C-N-CA	-5.41	112.49	120.38
1	A	432	VAL	N-CA-C	-5.08	108.34	113.47

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	3683	0	2778	44	0
All	All	3683	0	2778	44	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 44 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:440:ARG:NH2	1:A:509:CYS:O	2.21	0.74
1:A:598:LYS:HA	1:A:601:ARG:HD3	1.76	0.68
1:A:629:GLY:HA3	1:A:680:CYS:HB3	1.83	0.60
1:A:501:HIS:NE2	1:A:544:GLU:O	2.33	0.59
1:A:197:THR:O	1:A:201:PHE:HB2	2.04	0.58

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	561/2818 (20%)	528 (94%)	32 (6%)	1 (0%)	43 73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	341	VAL

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	217/2512 (9%)	216 (100%)	1 (0%)	81 81

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	299	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	510	ASN
1	A	562	ASN
1	A	614	ASN
1	A	682	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.

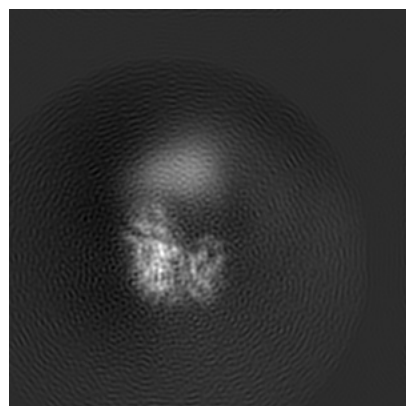
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28037. These allow visual inspection of the internal detail of the map and identification of artifacts.

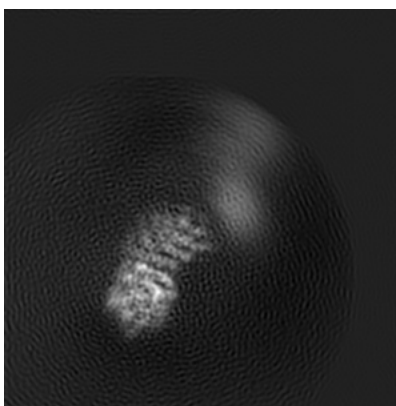
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

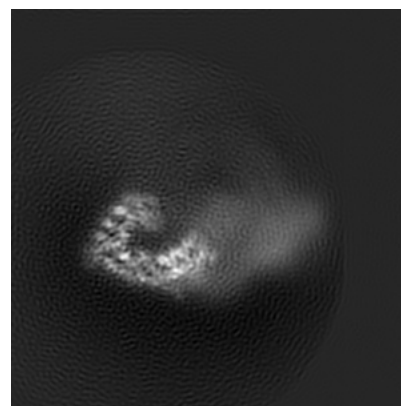
6.1.1 Primary map



X

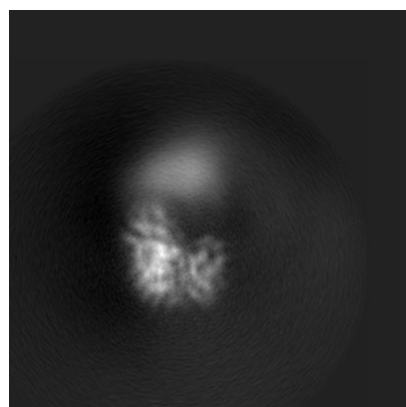


Y

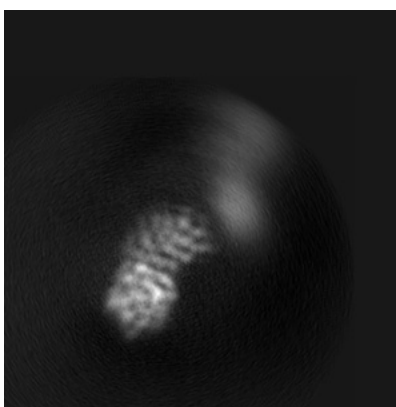


Z

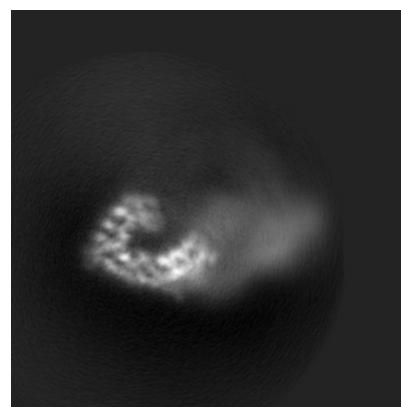
6.1.2 Raw map



X



Y

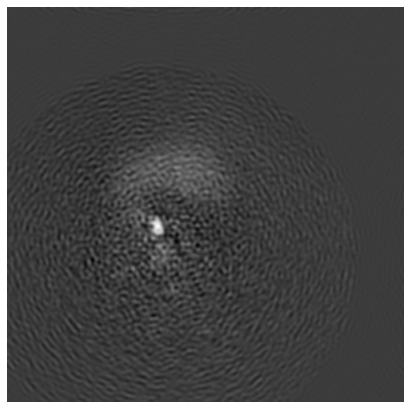


Z

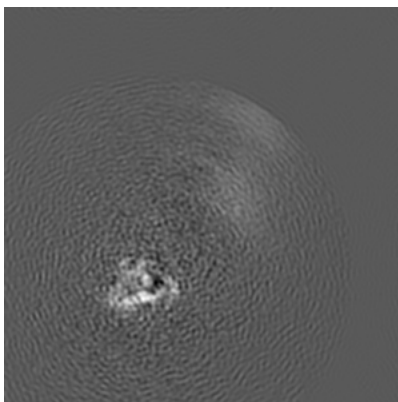
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

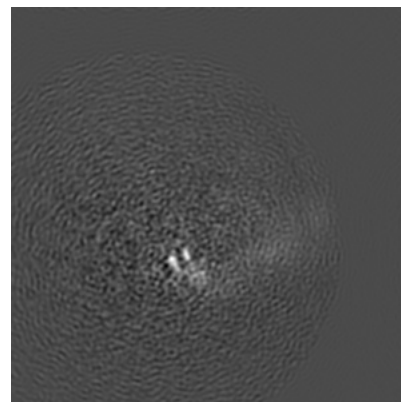
6.2.1 Primary map



X Index: 128

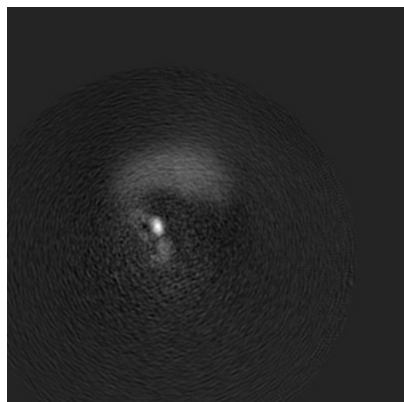


Y Index: 128

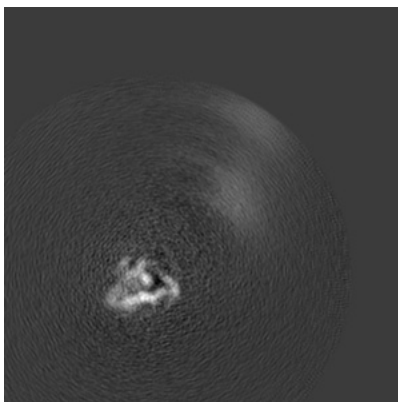


Z Index: 128

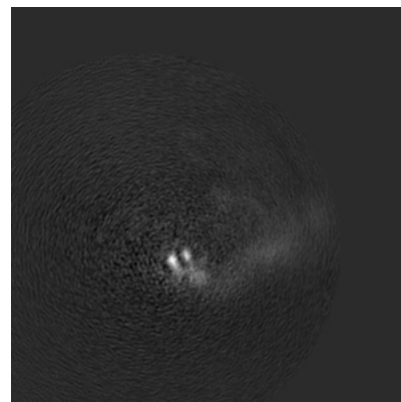
6.2.2 Raw map



X Index: 128



Y Index: 128

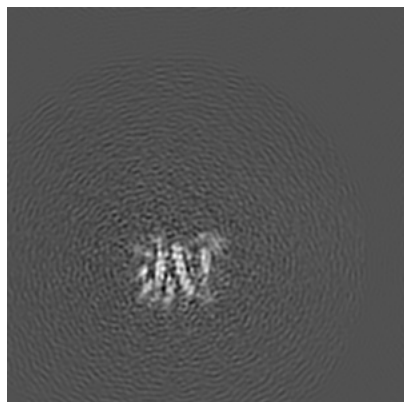


Z Index: 128

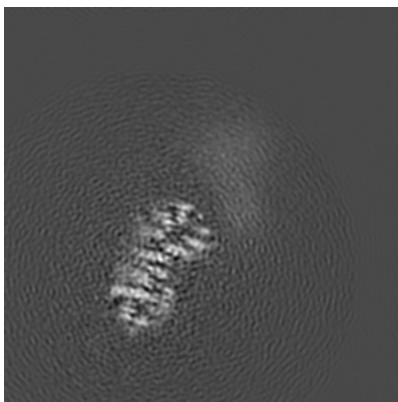
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

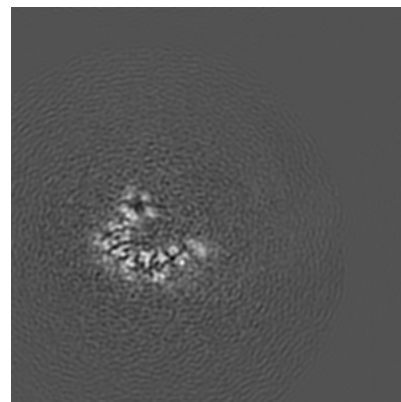
6.3.1 Primary map



X Index: 71

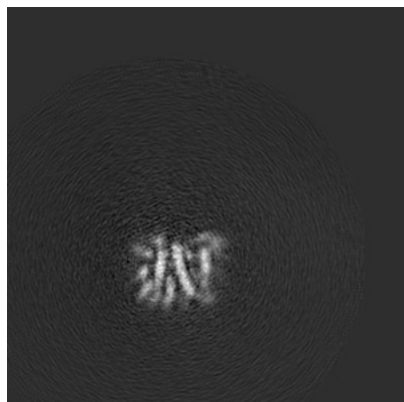


Y Index: 96

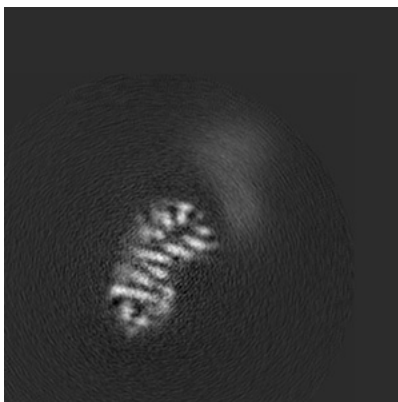


Z Index: 98

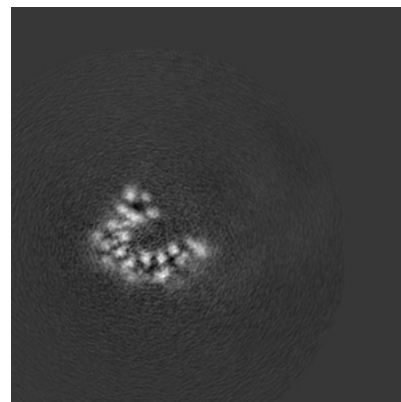
6.3.2 Raw map



X Index: 71



Y Index: 96

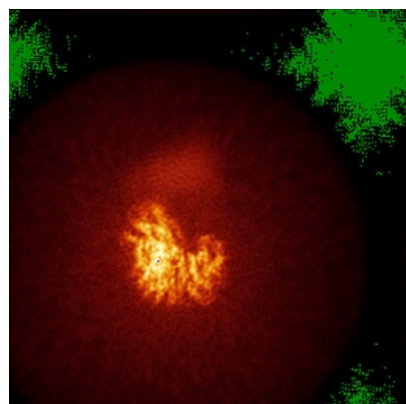


Z Index: 97

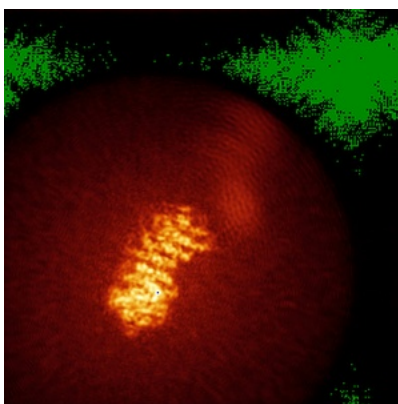
The images above show the largest variance slices of the map in three orthogonal directions.

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

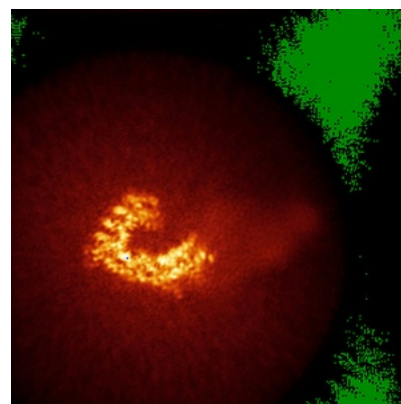
6.4.1 Primary map



X

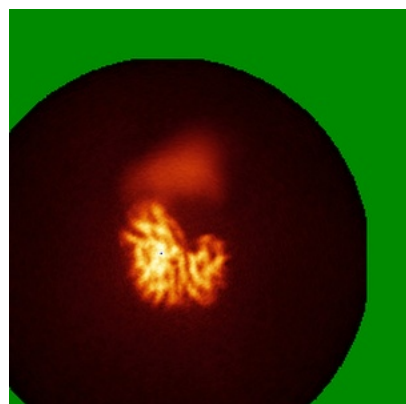


Y

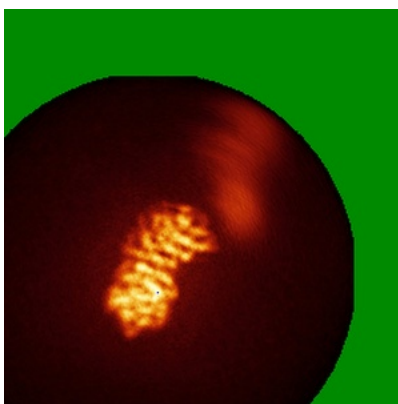


Z

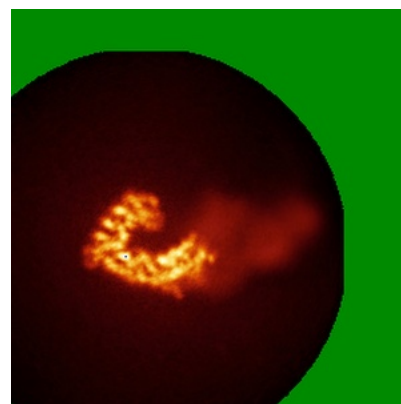
6.4.2 Raw map



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.

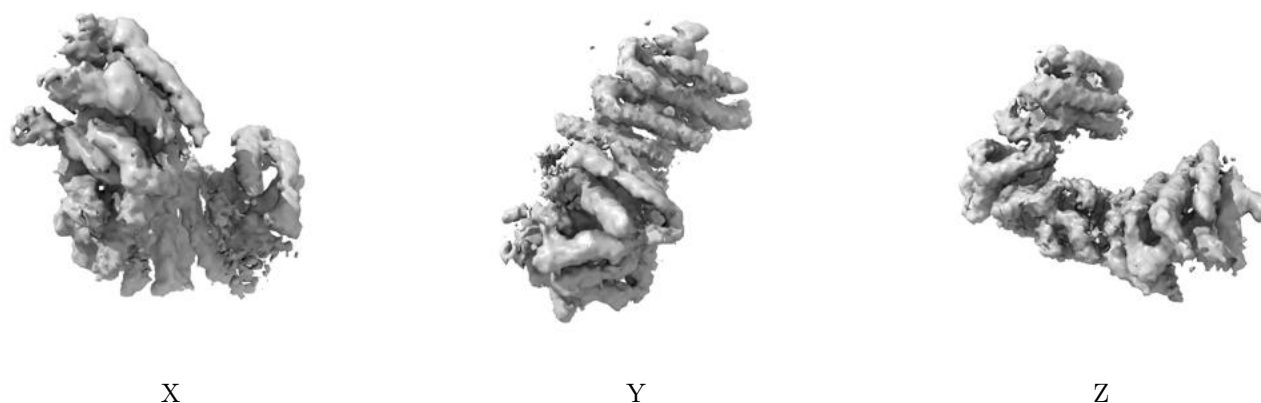
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0223. 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.

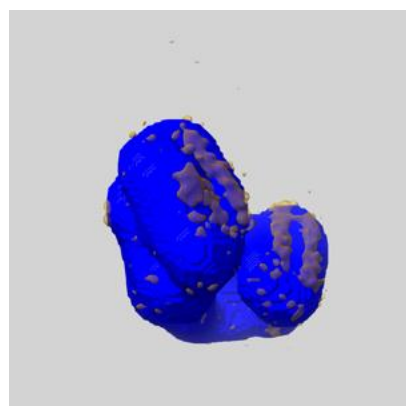
6.6 Mask visualisation [i](#)

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

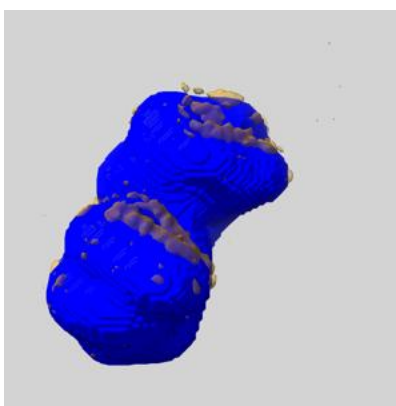
A mask typically either:

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

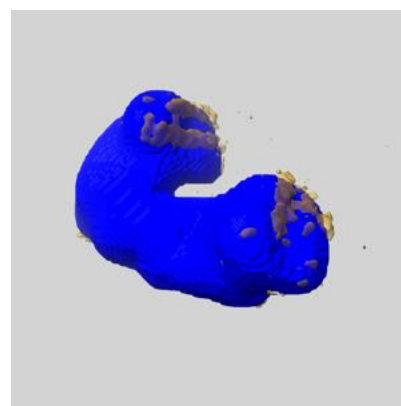
6.6.1 emd_28037_msk_1.map [i](#)



X



Y

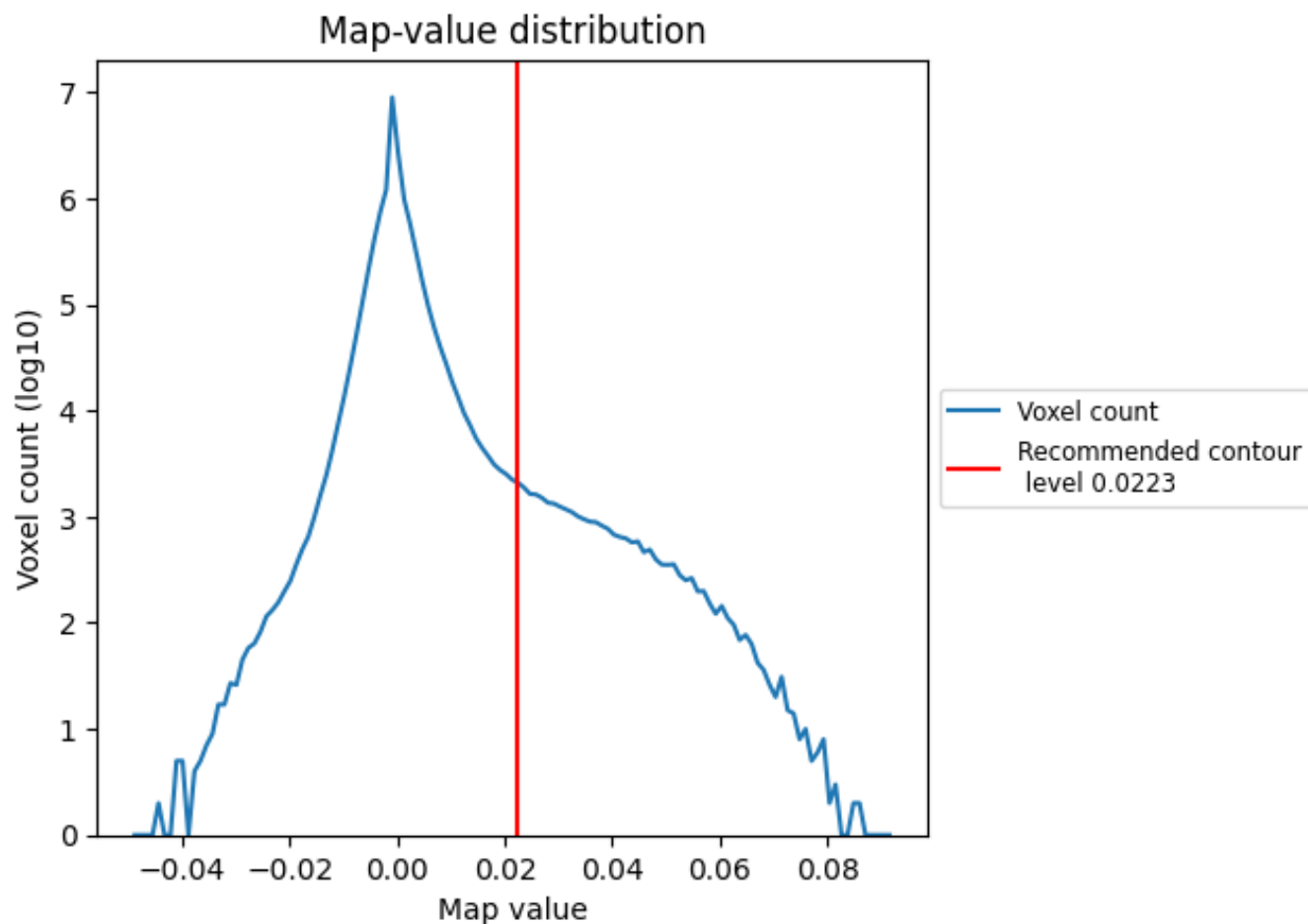


Z

7 Map analysis [i](#)

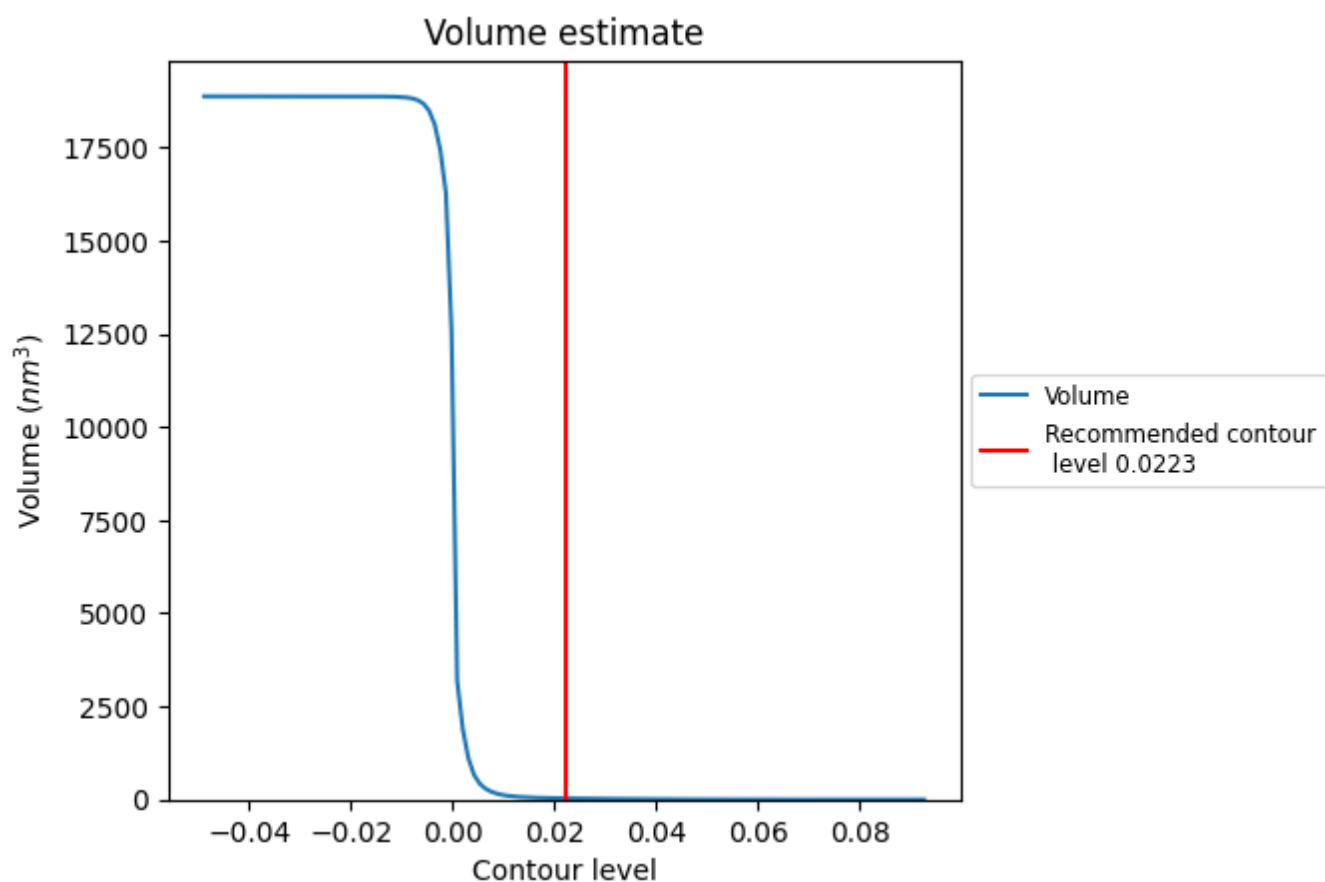
This section contains the results of statistical analysis of the map.

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.

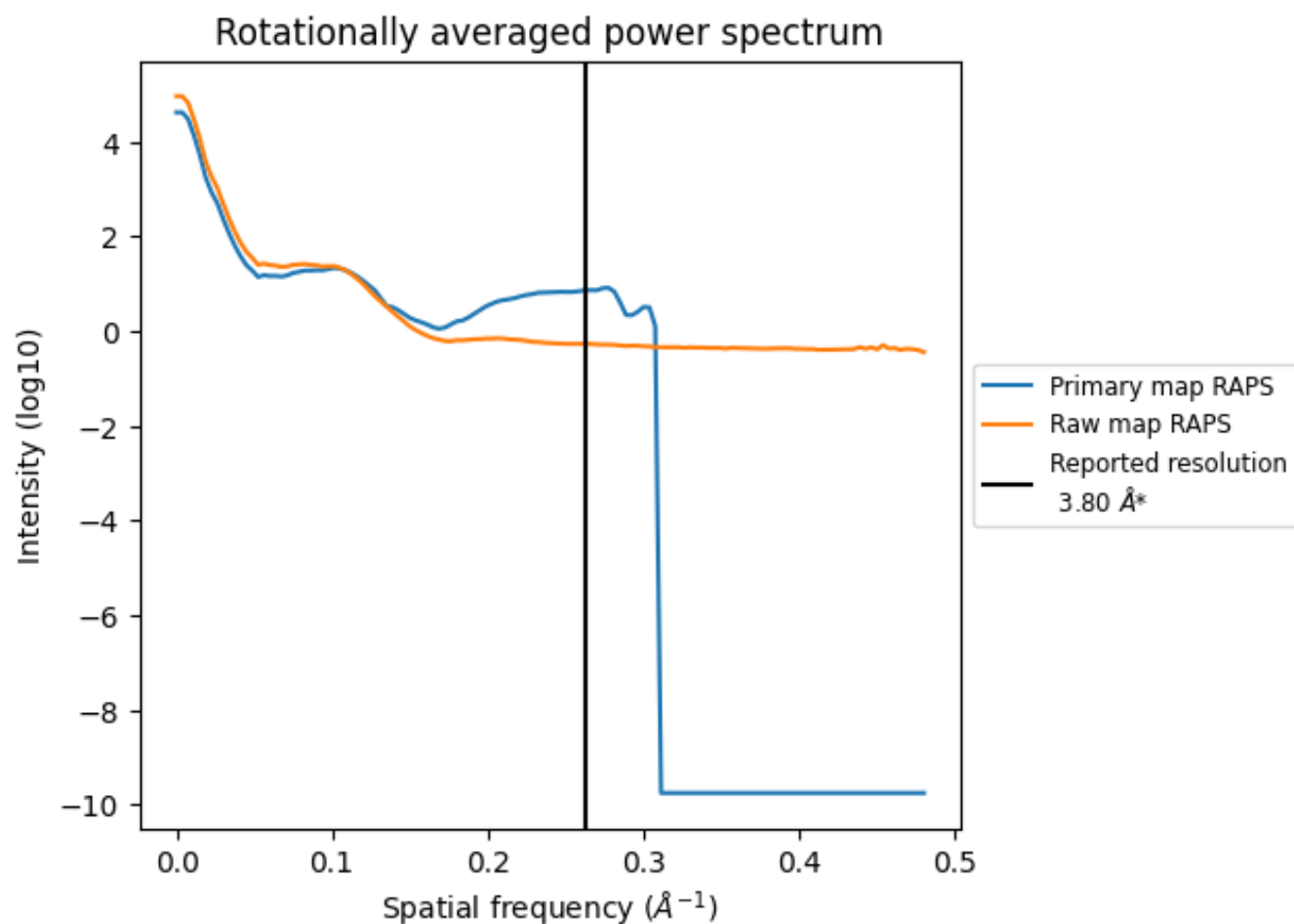
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 32 nm³; this corresponds to an approximate mass of 29 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 ⓘ

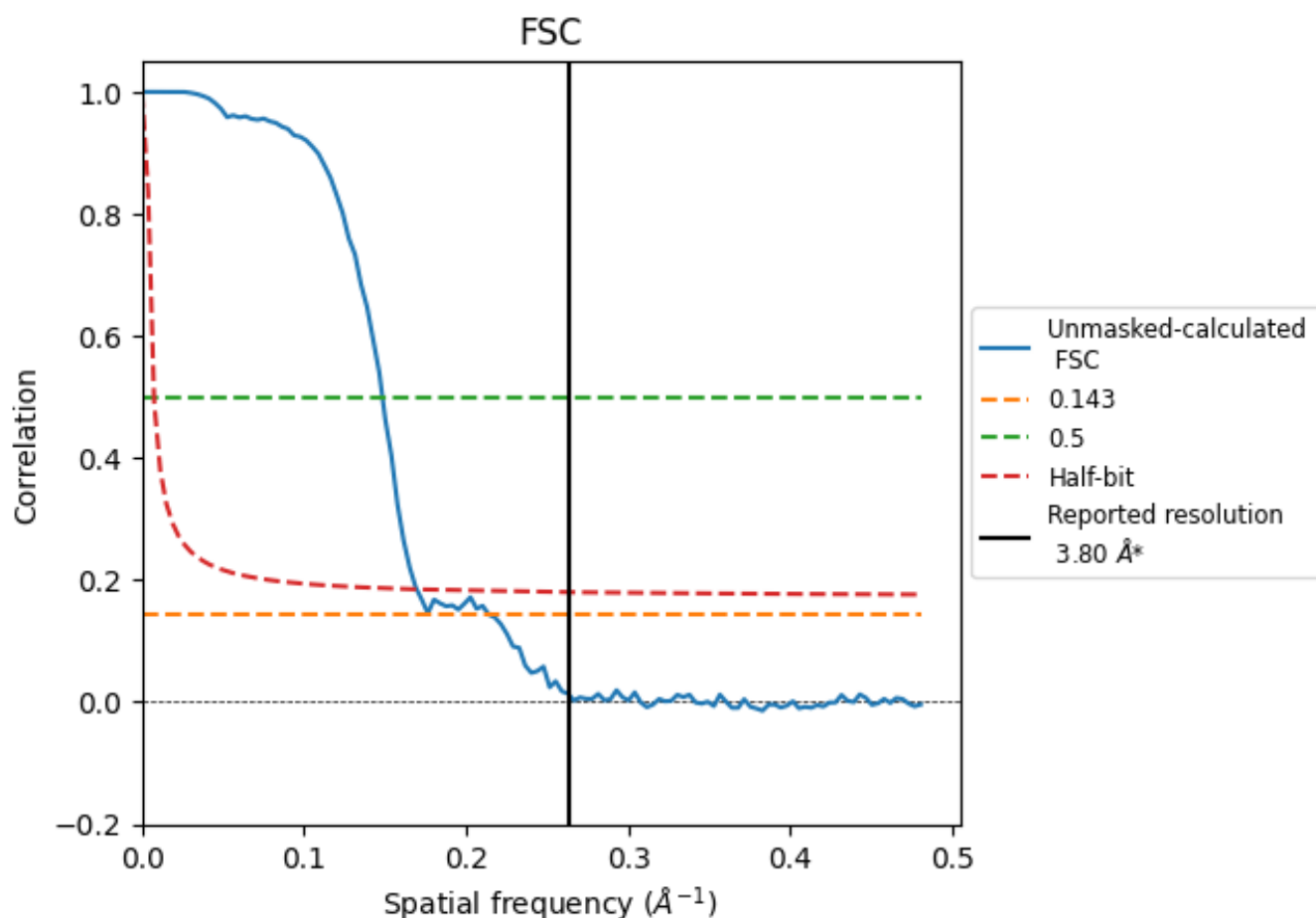


*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.263 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

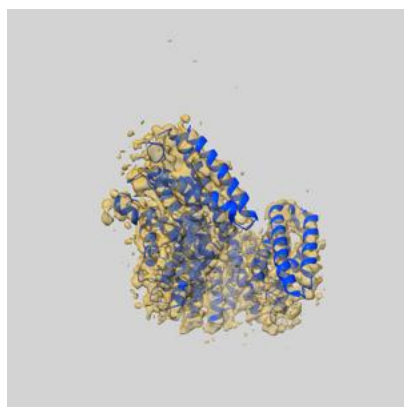
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.67	6.74	5.90

*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 4.67 differs from the reported value 3.8 by more than 10 %

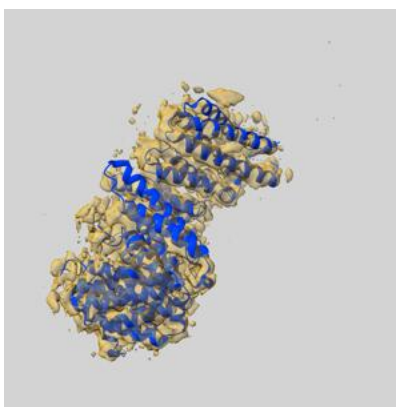
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-28037 and PDB model 8EDN. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

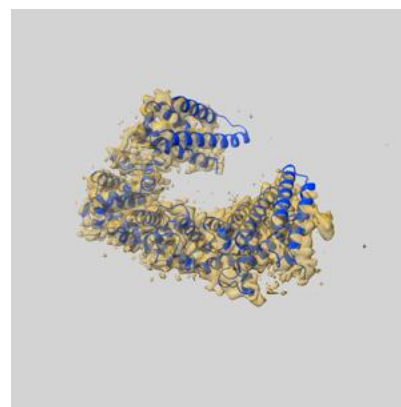
9.1 Map-model overlay [i](#)



X



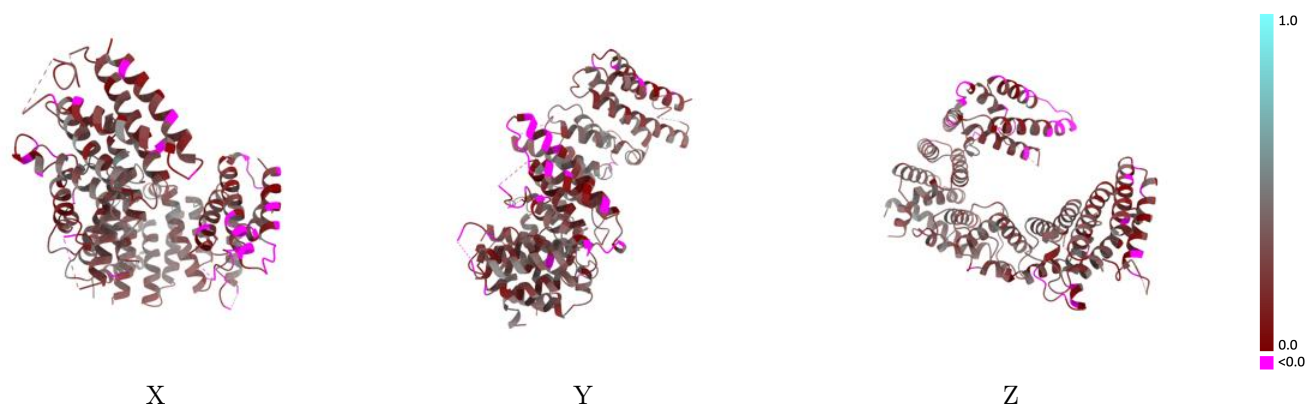
Y



Z

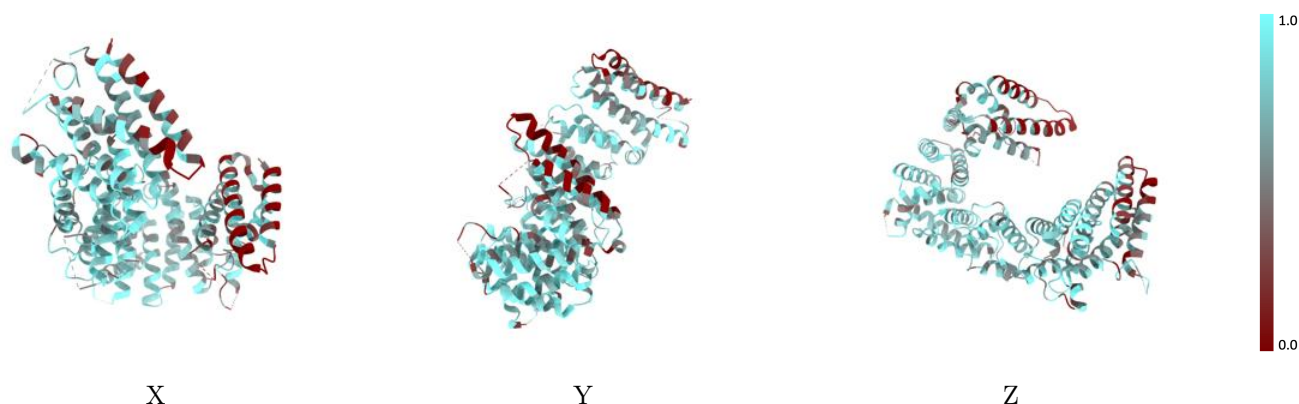
The images above show the 3D surface view of the map at the recommended contour level 0.0223 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



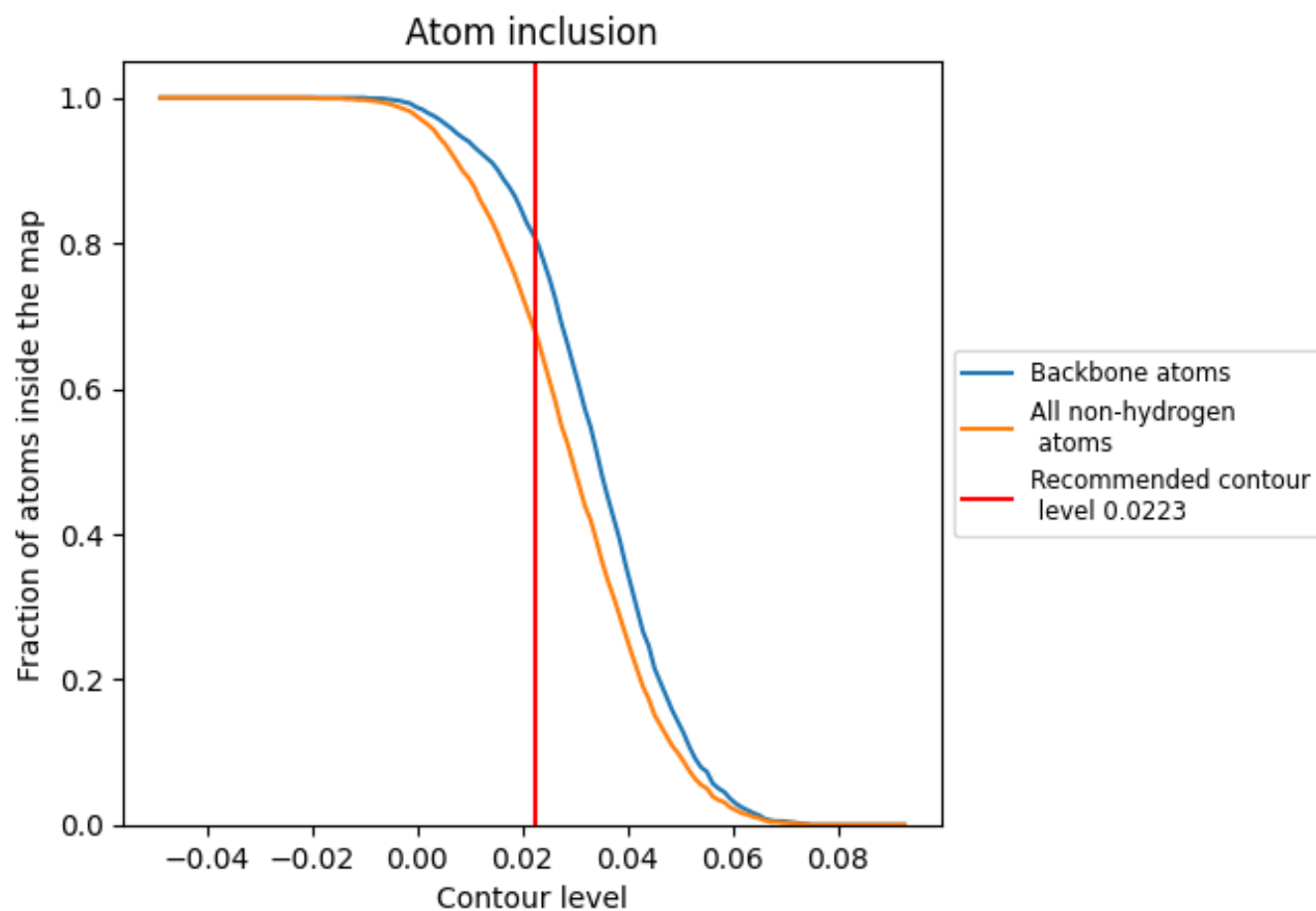
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0223).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 68% 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 (0.0223) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6810	0.2610
A	0.6810	0.2610

