



wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 10:53 PM UTC

PDB ID : 9MAN / pdb_00009man
EMDB ID : EMD-63756
Title : Structure of Norrin in complex with human Tspan12 large extracellular loop (Tspan12 LEL)
Authors : Xue, L.; Wang, Z.; Xu, W.
Deposited on : 2025-03-14
Resolution : 3.78 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

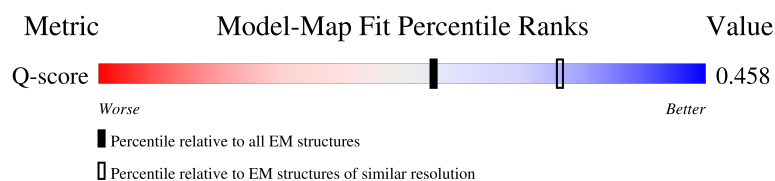
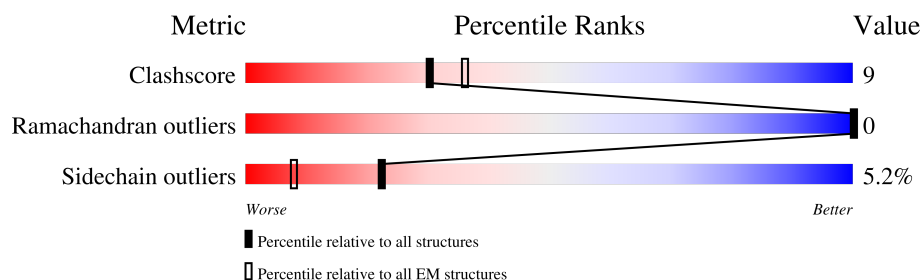
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY





The reported resolution of this entry is 3.78 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	10074 (3.28 - 4.27)

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	500	
1	B	500	
2	C	501	
2	D	501	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3066 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 Maltose/maltodextrin-binding periplasmic protein,Norrin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	99	Total	C	N	O	S	0	0
			782	477	153	138	14		
1	B	98	Total	C	N	O	S	0	0
			774	473	152	135	14		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-366	GLY	-	linker	UNP P0AEY0
A	-365	SER	-	linker	UNP P0AEY0
A	-364	HIS	-	expression tag	UNP P0AEY0
A	-363	HIS	-	expression tag	UNP P0AEY0
A	-362	HIS	-	expression tag	UNP P0AEY0
A	-361	HIS	-	expression tag	UNP P0AEY0
A	-360	HIS	-	expression tag	UNP P0AEY0
A	-359	HIS	-	expression tag	UNP P0AEY0
A	-358	HIS	-	expression tag	UNP P0AEY0
A	-357	HIS	-	expression tag	UNP P0AEY0
A	-356	MET	-	linker	UNP P0AEY0
A	12	ASN	-	linker	UNP P0AEY0
A	13	ALA	-	linker	UNP P0AEY0
A	14	ALA	-	linker	UNP P0AEY0
A	15	ALA	-	linker	UNP P0AEY0
A	16	GLU	-	linker	UNP P0AEY0
A	17	ASN	-	linker	UNP P0AEY0
A	18	LEU	-	linker	UNP P0AEY0
A	19	TYR	-	linker	UNP P0AEY0
A	20	PHE	-	linker	UNP P0AEY0
A	21	GLN	-	linker	UNP P0AEY0
A	22	GLY	-	linker	UNP P0AEY0
A	23	GLU	-	linker	UNP P0AEY0
A	24	PHE	-	linker	UNP P0AEY0
B	-366	GLY	-	linker	UNP P0AEY0
B	-365	SER	-	linker	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-364	HIS	-	expression tag	UNP P0AEY0
B	-363	HIS	-	expression tag	UNP P0AEY0
B	-362	HIS	-	expression tag	UNP P0AEY0
B	-361	HIS	-	expression tag	UNP P0AEY0
B	-360	HIS	-	expression tag	UNP P0AEY0
B	-359	HIS	-	expression tag	UNP P0AEY0
B	-358	HIS	-	expression tag	UNP P0AEY0
B	-357	HIS	-	expression tag	UNP P0AEY0
B	-356	MET	-	linker	UNP P0AEY0
B	12	ASN	-	linker	UNP P0AEY0
B	13	ALA	-	linker	UNP P0AEY0
B	14	ALA	-	linker	UNP P0AEY0
B	15	ALA	-	linker	UNP P0AEY0
B	16	GLU	-	linker	UNP P0AEY0
B	17	ASN	-	linker	UNP P0AEY0
B	18	LEU	-	linker	UNP P0AEY0
B	19	TYR	-	linker	UNP P0AEY0
B	20	PHE	-	linker	UNP P0AEY0
B	21	GLN	-	linker	UNP P0AEY0
B	22	GLY	-	linker	UNP P0AEY0
B	23	GLU	-	linker	UNP P0AEY0
B	24	PHE	-	linker	UNP P0AEY0

- Molecule 2 is a protein called Maltose/maltodextrin-binding periplasmic protein, Tetraspanin-12.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	90	Total	C	N	O	S	0	0
			755	482	127	135	11		
2	C	90	Total	C	N	O	S	0	0
			755	482	127	135	11		

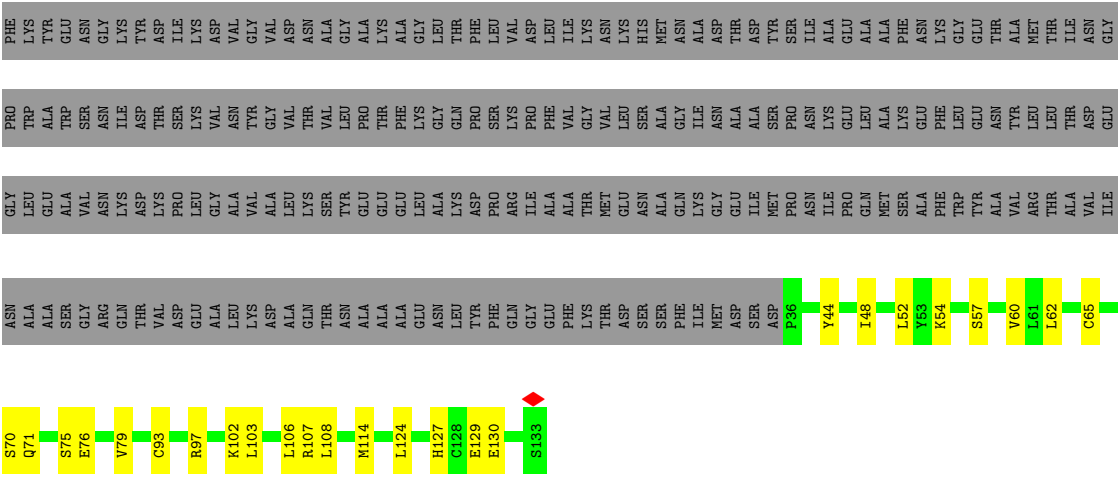
There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-276	GLY	-	linker	UNP P0AEY0
D	-275	SER	-	linker	UNP P0AEY0
D	-274	HIS	-	expression tag	UNP P0AEY0
D	-273	HIS	-	expression tag	UNP P0AEY0
D	-272	HIS	-	expression tag	UNP P0AEY0
D	-271	HIS	-	expression tag	UNP P0AEY0
D	-270	HIS	-	expression tag	UNP P0AEY0

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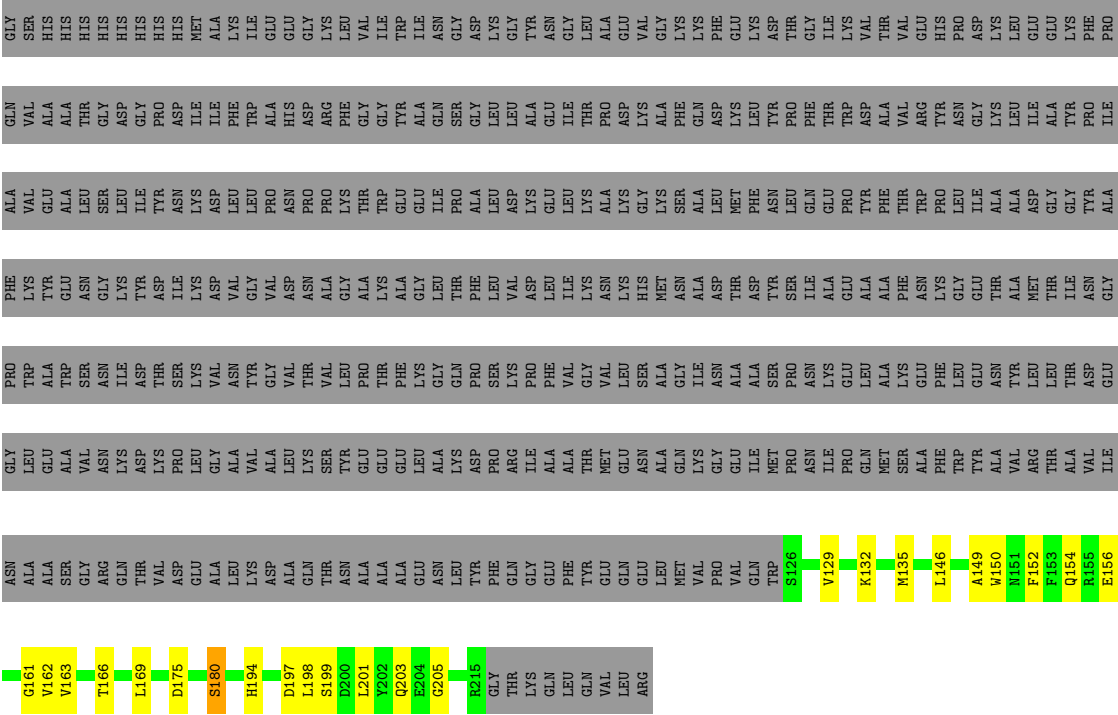
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-269	HIS	-	expression tag	UNP P0AEY0
D	-268	HIS	-	expression tag	UNP P0AEY0
D	-267	HIS	-	expression tag	UNP P0AEY0
D	-266	MET	-	linker	UNP P0AEY0
D	102	ASN	-	linker	UNP P0AEY0
D	103	ALA	-	linker	UNP P0AEY0
D	104	ALA	-	linker	UNP P0AEY0
D	105	ALA	-	linker	UNP P0AEY0
D	106	GLU	-	linker	UNP P0AEY0
D	107	ASN	-	linker	UNP P0AEY0
D	108	LEU	-	linker	UNP P0AEY0
D	109	TYR	-	linker	UNP P0AEY0
D	110	PHE	-	linker	UNP P0AEY0
D	111	GLN	-	linker	UNP P0AEY0
D	112	GLY	-	linker	UNP P0AEY0
D	113	GLU	-	linker	UNP P0AEY0
D	114	PHE	-	linker	UNP P0AEY0
C	-276	GLY	-	linker	UNP P0AEY0
C	-275	SER	-	linker	UNP P0AEY0
C	-274	HIS	-	expression tag	UNP P0AEY0
C	-273	HIS	-	expression tag	UNP P0AEY0
C	-272	HIS	-	expression tag	UNP P0AEY0
C	-271	HIS	-	expression tag	UNP P0AEY0
C	-270	HIS	-	expression tag	UNP P0AEY0
C	-269	HIS	-	expression tag	UNP P0AEY0
C	-268	HIS	-	expression tag	UNP P0AEY0
C	-267	HIS	-	expression tag	UNP P0AEY0
C	-266	MET	-	linker	UNP P0AEY0
C	102	ASN	-	linker	UNP P0AEY0
C	103	ALA	-	linker	UNP P0AEY0
C	104	ALA	-	linker	UNP P0AEY0
C	105	ALA	-	linker	UNP P0AEY0
C	106	GLU	-	linker	UNP P0AEY0
C	107	ASN	-	linker	UNP P0AEY0
C	108	LEU	-	linker	UNP P0AEY0
C	109	TYR	-	linker	UNP P0AEY0
C	110	PHE	-	linker	UNP P0AEY0
C	111	GLN	-	linker	UNP P0AEY0
C	112	GLY	-	linker	UNP P0AEY0
C	113	GLU	-	linker	UNP P0AEY0
C	114	PHE	-	linker	UNP P0AEY0



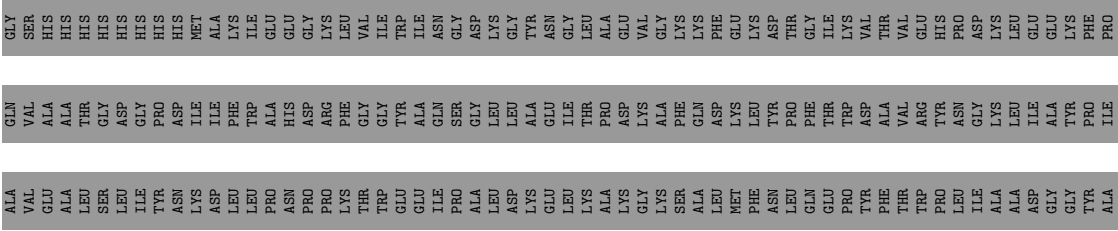
● Molecule 2: Maltose/maltodextrin-binding periplasmic protein,Tetraspanin-12

Chain D: 13% 82%



● Molecule 2: Maltose/maltodextrin-binding periplasmic protein,Tetraspanin-12

Chain C: 12% 5% 82%



T147	ASN	PHE
G161	ALA	LYS
Y164	ALA	TYR
F165	GLY	GLU
T166	SER	ASN
D167	GLY	GLY
W168	GLN	LYS
L169	THR	TYR
E170	VAL	ILE
M171	THR	ASP
T172	VAL	LYS
W176	ASP	ILE
Q192	ALA	THR
E196	GLN	LYS
D197	ASN	ASP
L198	ALA	LYS
C206	ALA	ALA
G207	ALA	GLY
W210	ASN	LEU
R215	LEU	THR
GLY	TYR	PHE
THR	PHE	LEU
LYS	GLN	LEU
GLN	GLN	VAL
LEU	GLY	ASP
GLN	ILE	PHE
VAL	ALA	VAL
LEU	ALA	GLY
ARG	THR	LYS
	MET	ASN
	VAL	ALA
	PRO	ASN
	GLN	ASP
	ILE	THR
	GLY	ASP
	MET	TYR
	TRP	SER
	S126	PRO
	D127	ASN
	M128	ILE
	V129	LYS
	T130	GLU
	L131	LEU
	K132	ALA
		ALA
		SER
		LYS
		GLY
		ASN
		PHE
		LYS
		THR
		GLY
		LEU
		GLU
		THR
		ASN
		GLY
		ASP
		ILE
		VAL
		THR
		LEU
		MET
		ALA
		THR
		ILE
		ASN
		GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	212449	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.574	Depositor
Minimum map value	-0.286	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.0641	Depositor
Map size (\AA)	465.92, 465.92, 465.92	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.832, 0.832, 0.832	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	0.12	0/798	0.27	0/1070
1	B	0.21	0/790	0.38	0/1058
2	C	0.48	0/779	0.66	0/1051
2	D	0.26	0/779	0.47	0/1051
All	All	0.30	0/3146	0.47	0/4230

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	782	0	771	14	0
1	B	774	0	768	22	0
2	C	755	0	699	12	0
2	D	755	0	699	18	0
All	All	3066	0	2937	54	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 54 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:B:102:LYS:HG3	1:B:124:LEU:HD11	1.73	0.71
1:A:79:VAL:HG11	1:B:48:ILE:HG12	1.78	0.65
2:D:162:VAL:HG12	2:D:163:VAL:HG13	1.80	0.63
1:B:54:LYS:O	1:B:54:LYS:HG2	2.02	0.60
1:A:102:LYS:HD2	2:C:197:ASP:HB2	1.84	0.60

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	97/500 (19%)	94 (97%)	3 (3%)	0	100	100
1	B	96/500 (19%)	91 (95%)	5 (5%)	0	100	100
2	C	88/501 (18%)	85 (97%)	3 (3%)	0	100	100
2	D	88/501 (18%)	85 (97%)	3 (3%)	0	100	100
All	All	369/2002 (18%)	355 (96%)	14 (4%)	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	92/414 (22%)	92 (100%)	0	100	100
1	B	91/414 (22%)	89 (98%)	2 (2%)	45	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	82/413 (20%)	67 (82%)	15 (18%)	2	11
2	D	82/413 (20%)	81 (99%)	1 (1%)	63	71
All	All	347/1654 (21%)	329 (95%)	18 (5%)	22	45

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	166	THR
2	C	176	TRP
2	C	170	GLU
2	C	132	LYS
2	C	164	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no chain breaks in this entry.

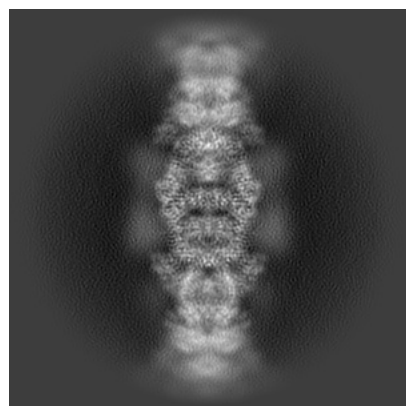
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63756. These allow visual inspection of the internal detail of the map and identification of artifacts.

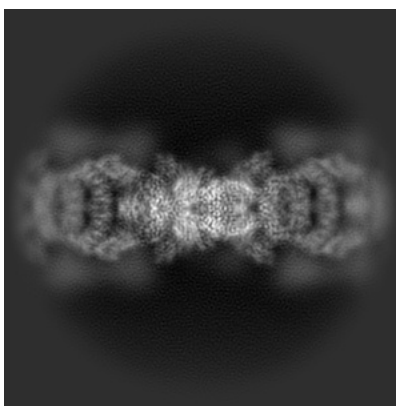
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

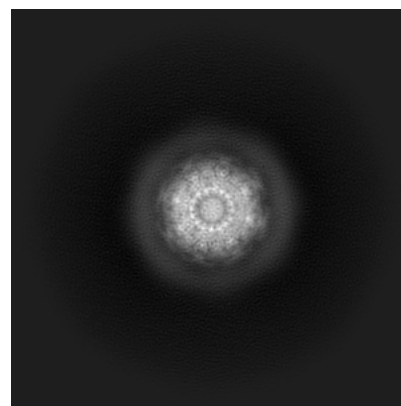
6.1.1 Primary map



X

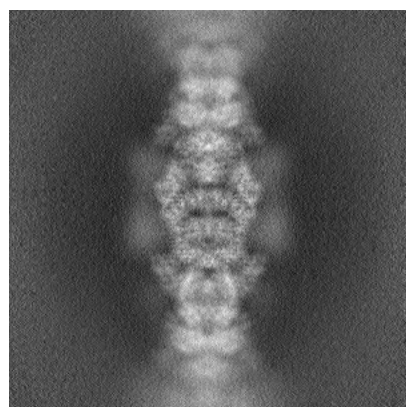


Y

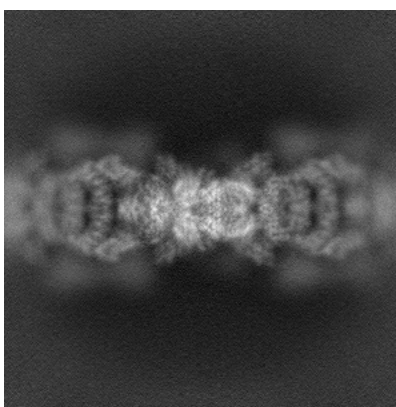


Z

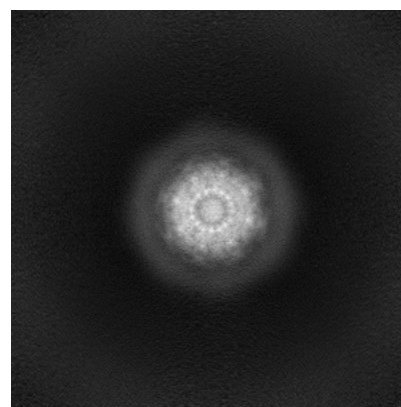
6.1.2 Raw map



X



Y

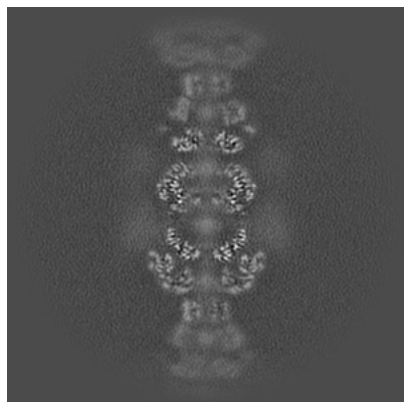


Z

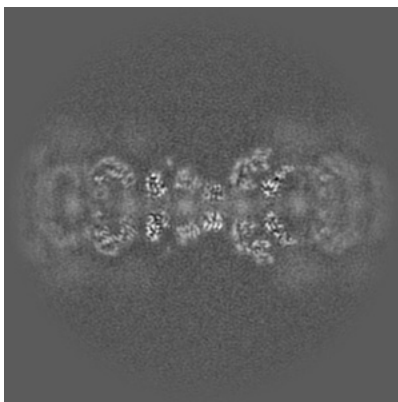
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

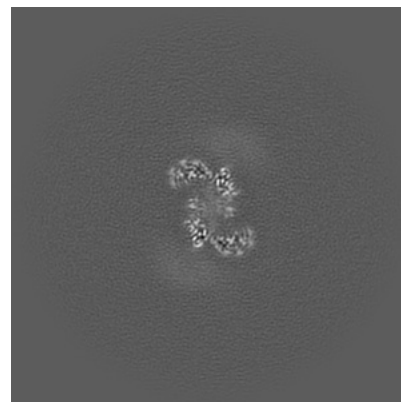
6.2.1 Primary map



X Index: 280

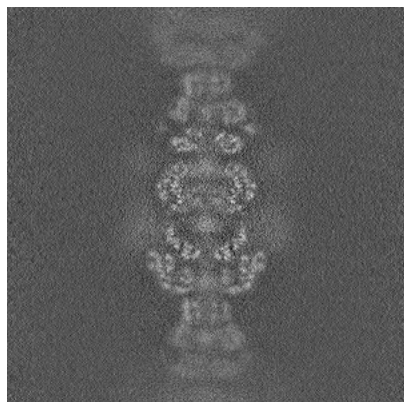


Y Index: 280

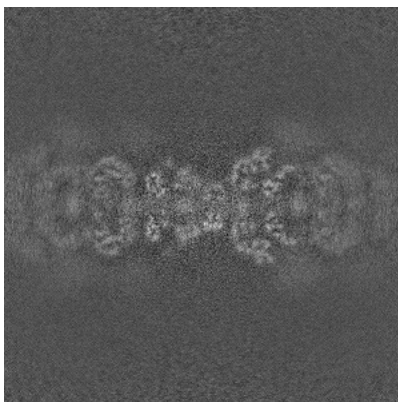


Z Index: 280

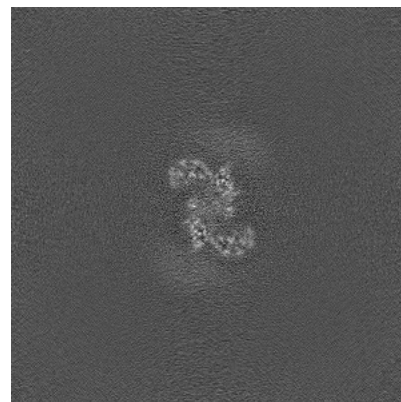
6.2.2 Raw map



X Index: 280



Y Index: 280

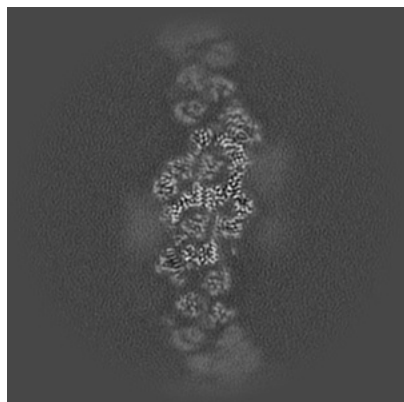


Z Index: 280

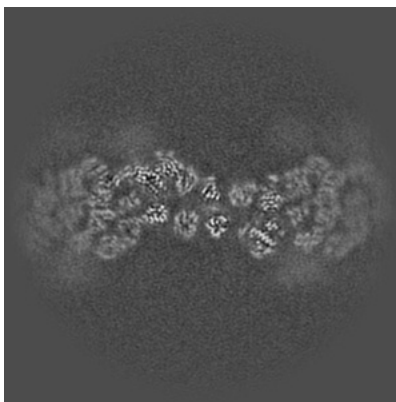
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

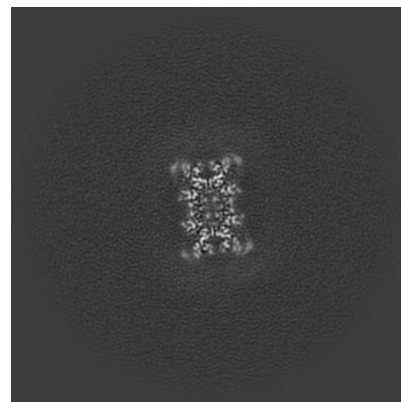
6.3.1 Primary map



X Index: 255

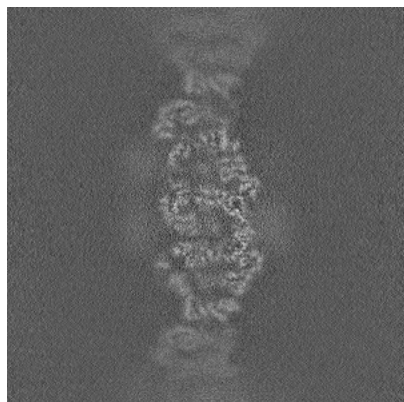


Y Index: 301

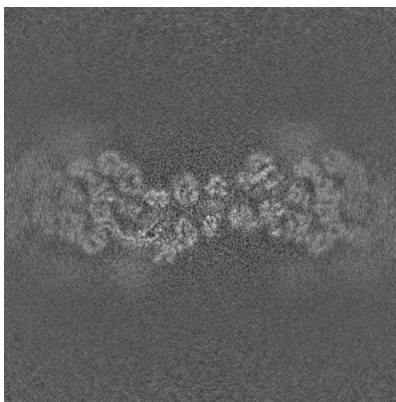


Z Index: 293

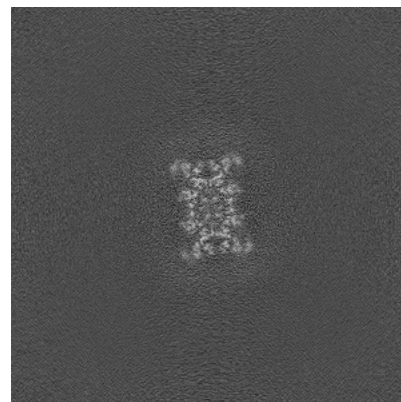
6.3.2 Raw map



X Index: 293



Y Index: 257

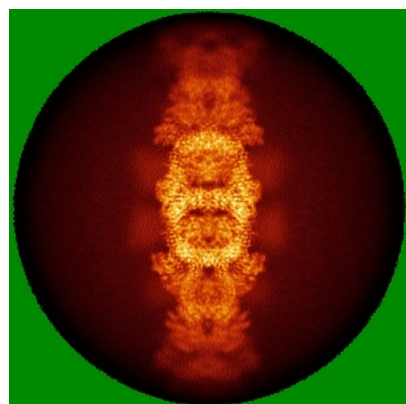


Z Index: 293

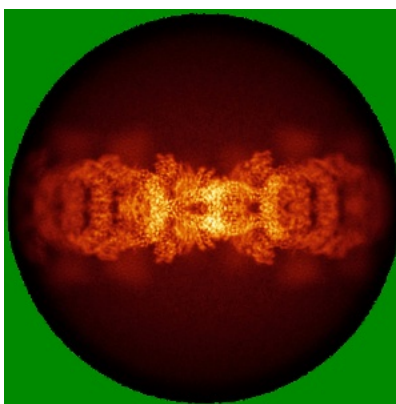
The images above show the largest variance slices of the map in three orthogonal directions.

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

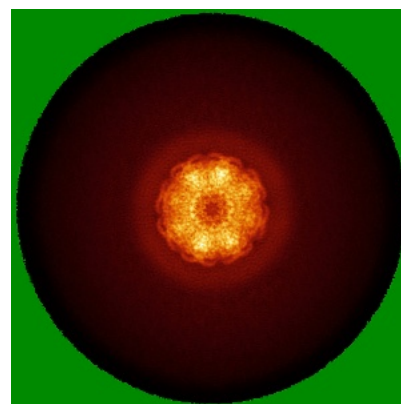
6.4.1 Primary map



X

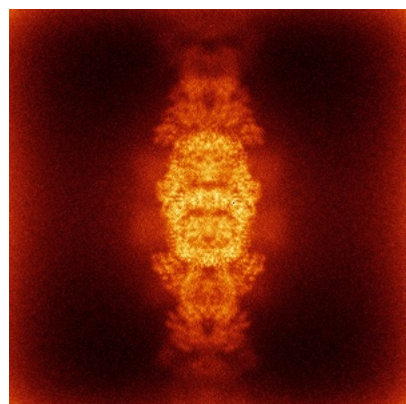


Y

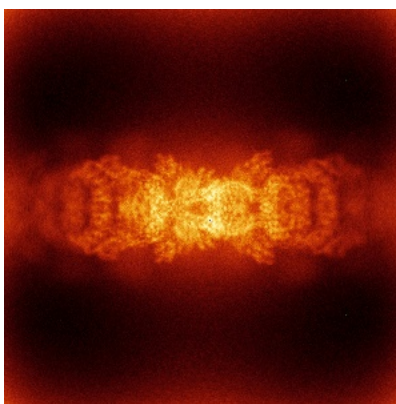


Z

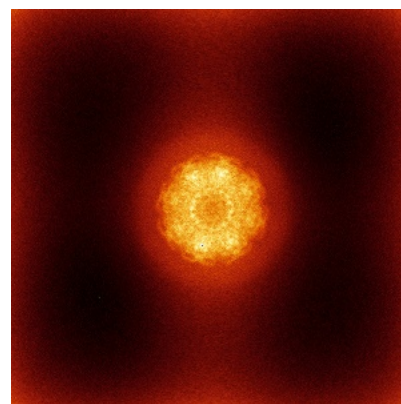
6.4.2 Raw map



X



Y

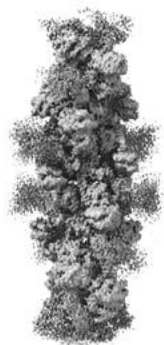


Z

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



X



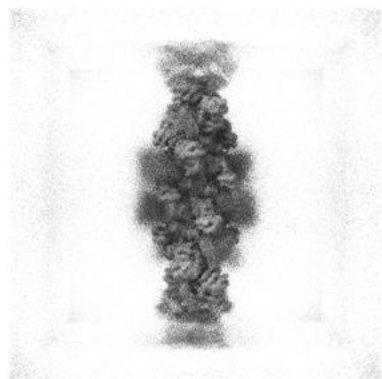
Y



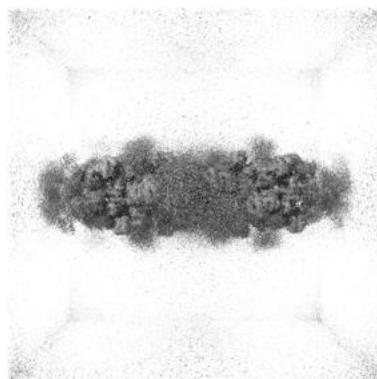
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0641. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

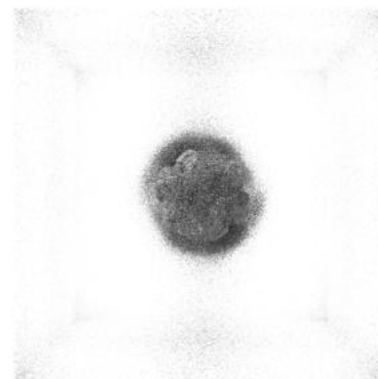
6.5.2 Raw map



X



Y



Z

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.

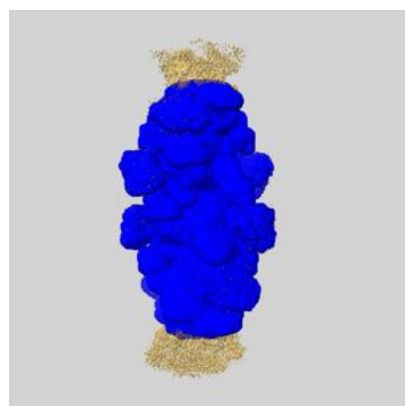
6.6 Mask visualisation [i](#)

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

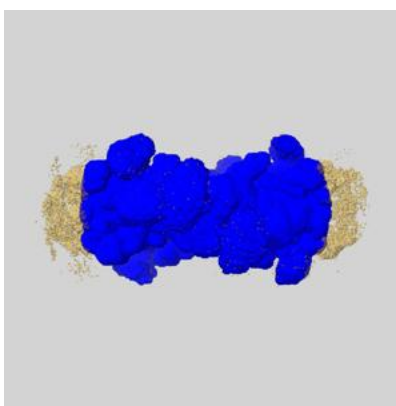
A mask typically either:

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

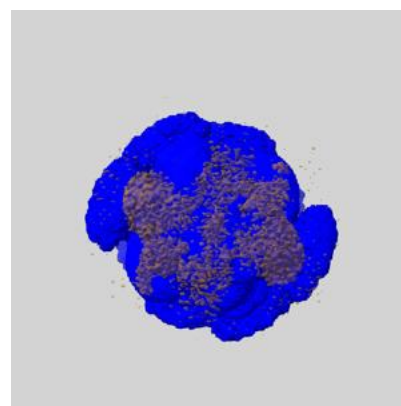
6.6.1 emd_63756_msk_1.map [i](#)



X



Y

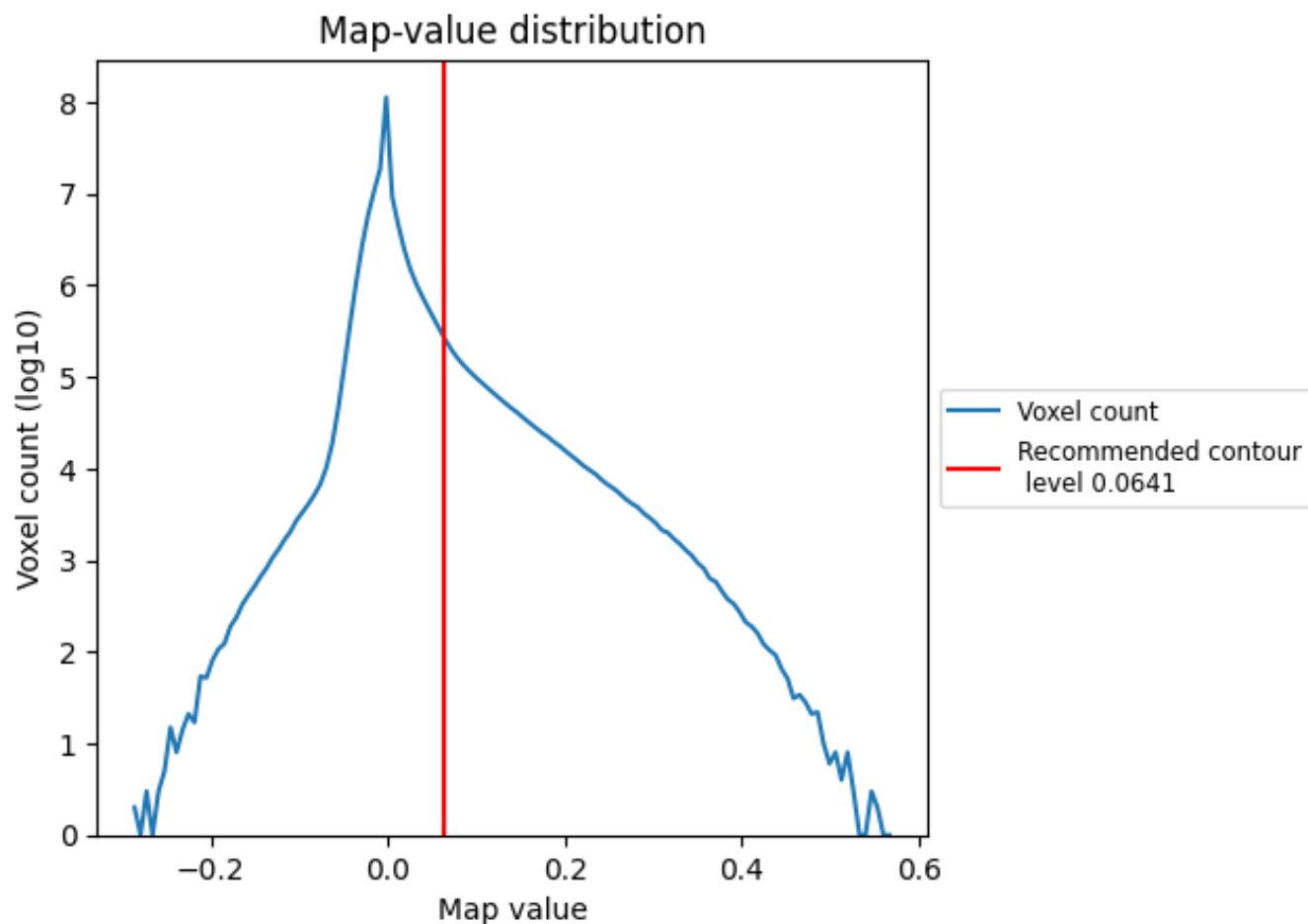


Z

7 Map analysis [i](#)

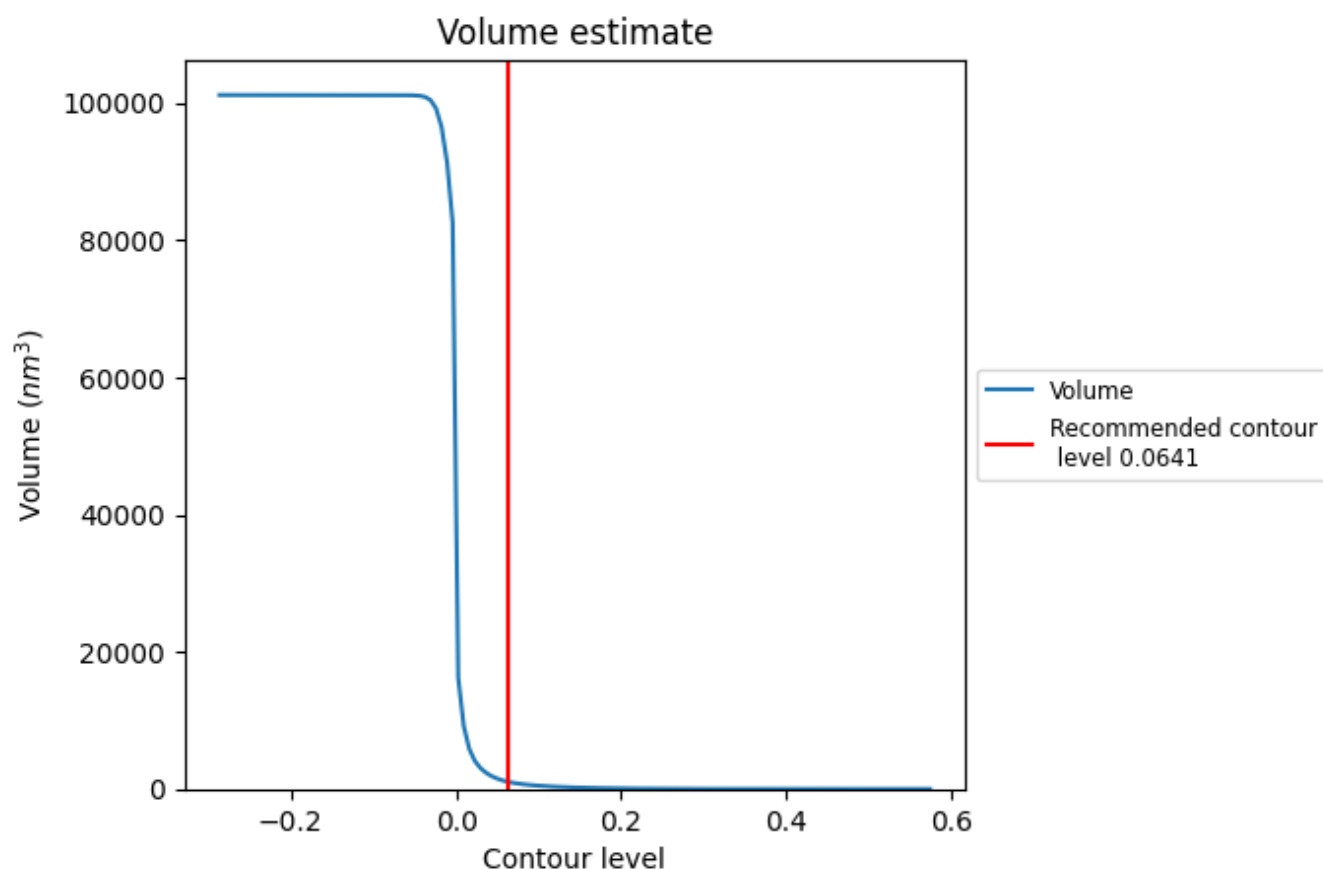
This section contains the results of statistical analysis of the map.

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.

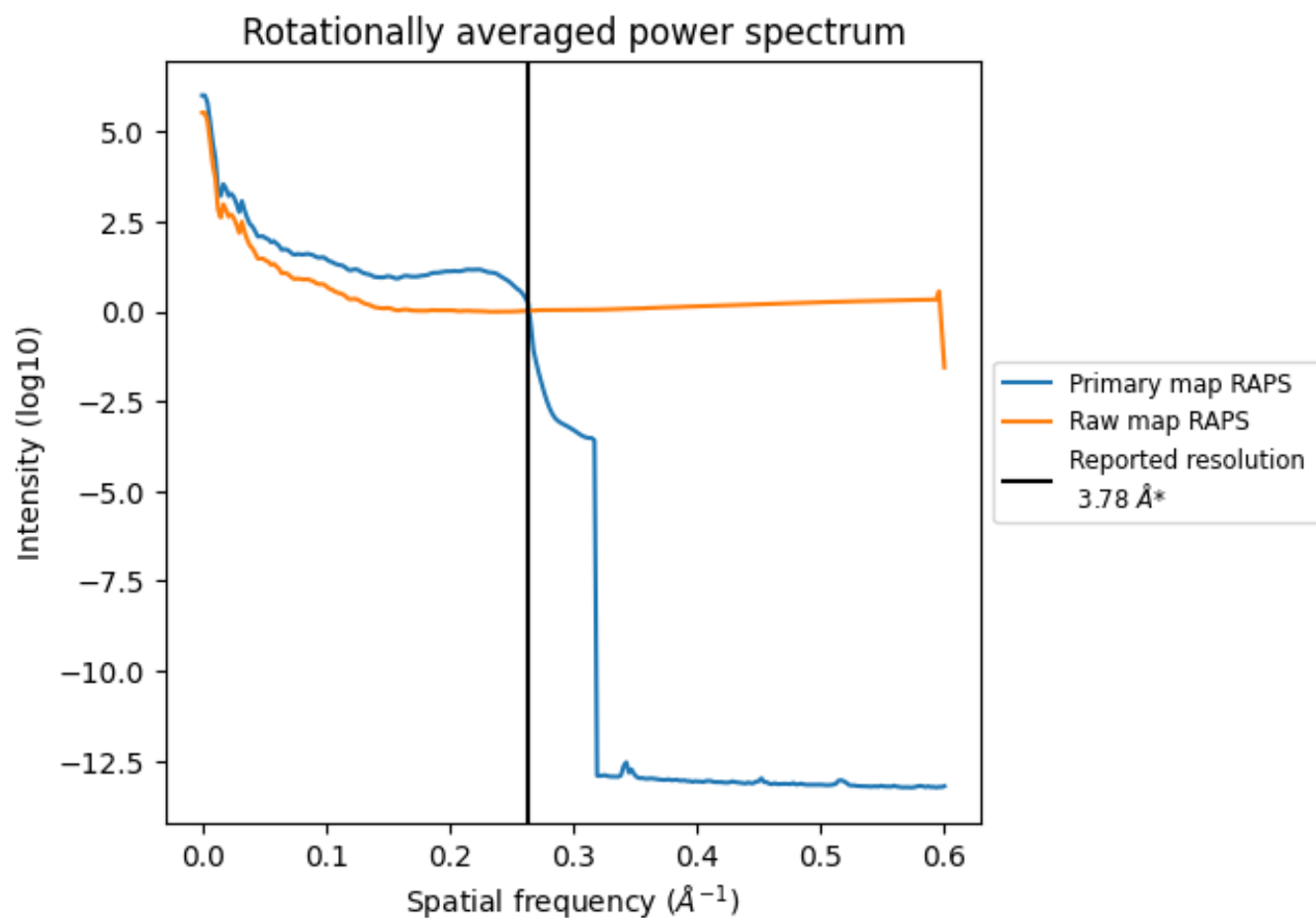
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1013 nm³; this corresponds to an approximate mass of 915 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 ⓘ

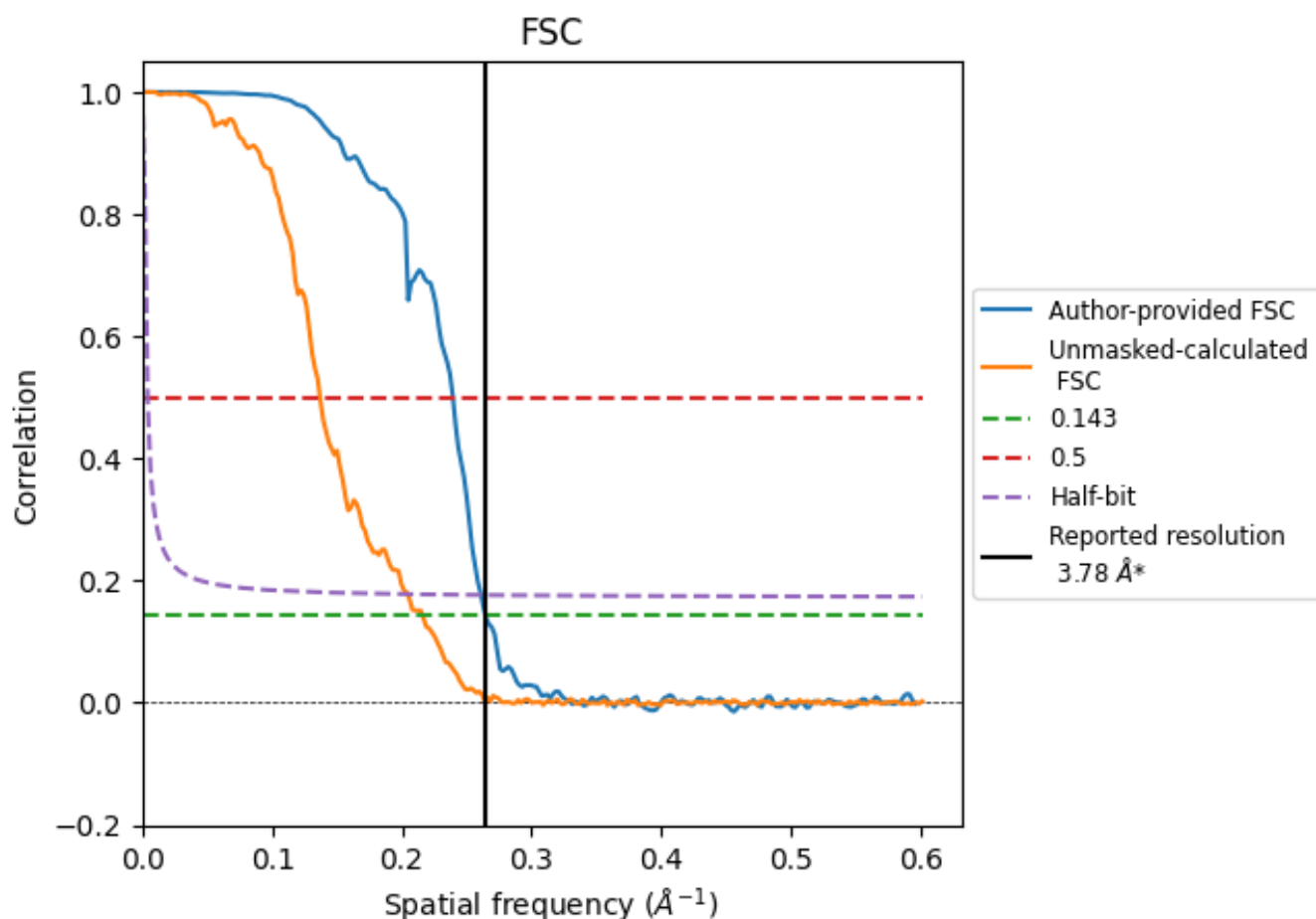


*Reported resolution corresponds to spatial frequency of 0.265 Å⁻¹

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 0.265 \AA^{-1}

8.2 Resolution estimates [i](#)

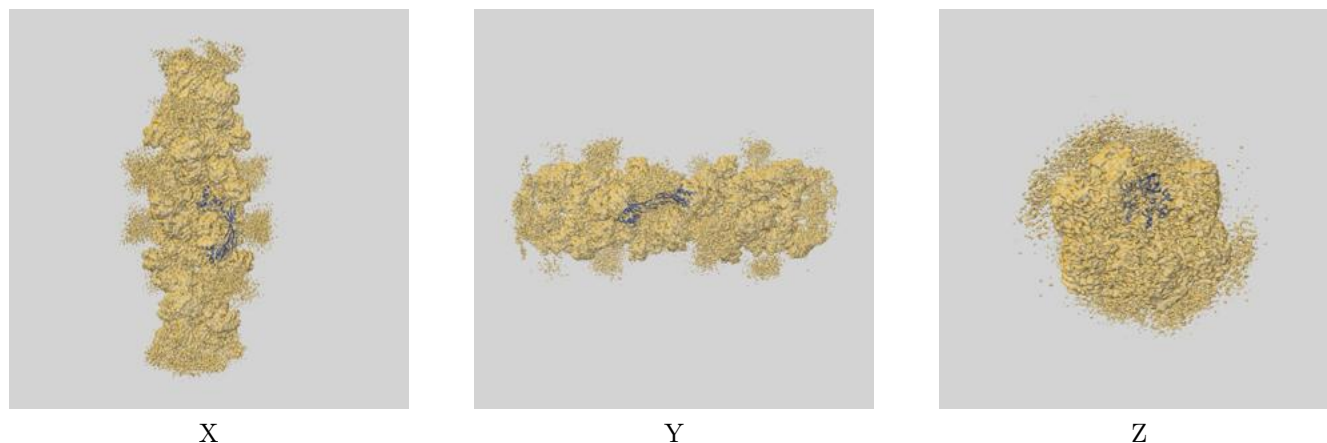
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.78	-	-
Author-provided FSC curve	3.78	4.18	3.83
Unmasked-calculated*	4.63	7.30	4.89

*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 4.63 differs from the reported value 3.78 by more than 10 %

9 Map-model fit [i](#)

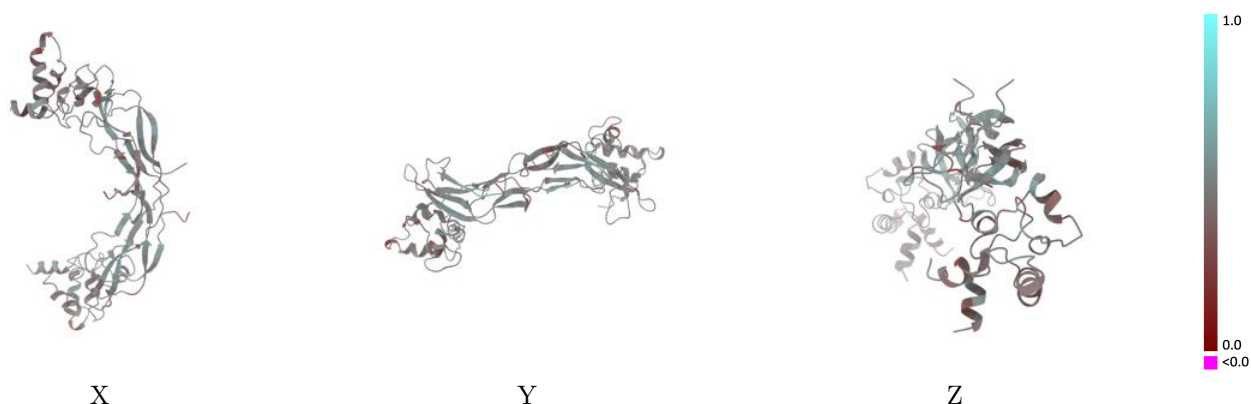
This section contains information regarding the fit between EMDB map EMD-63756 and PDB model 9MAN. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



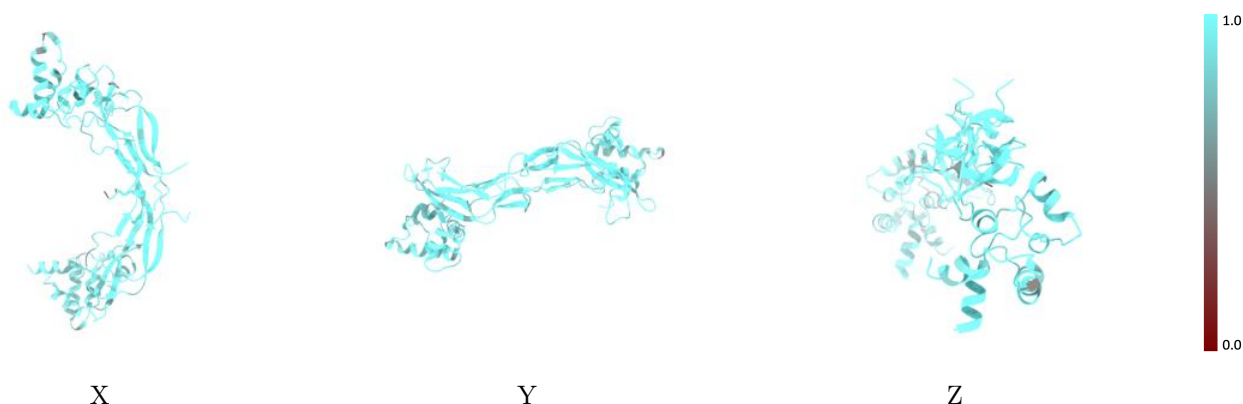
The images above show the 3D surface view of the map at the recommended contour level 0.0641 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



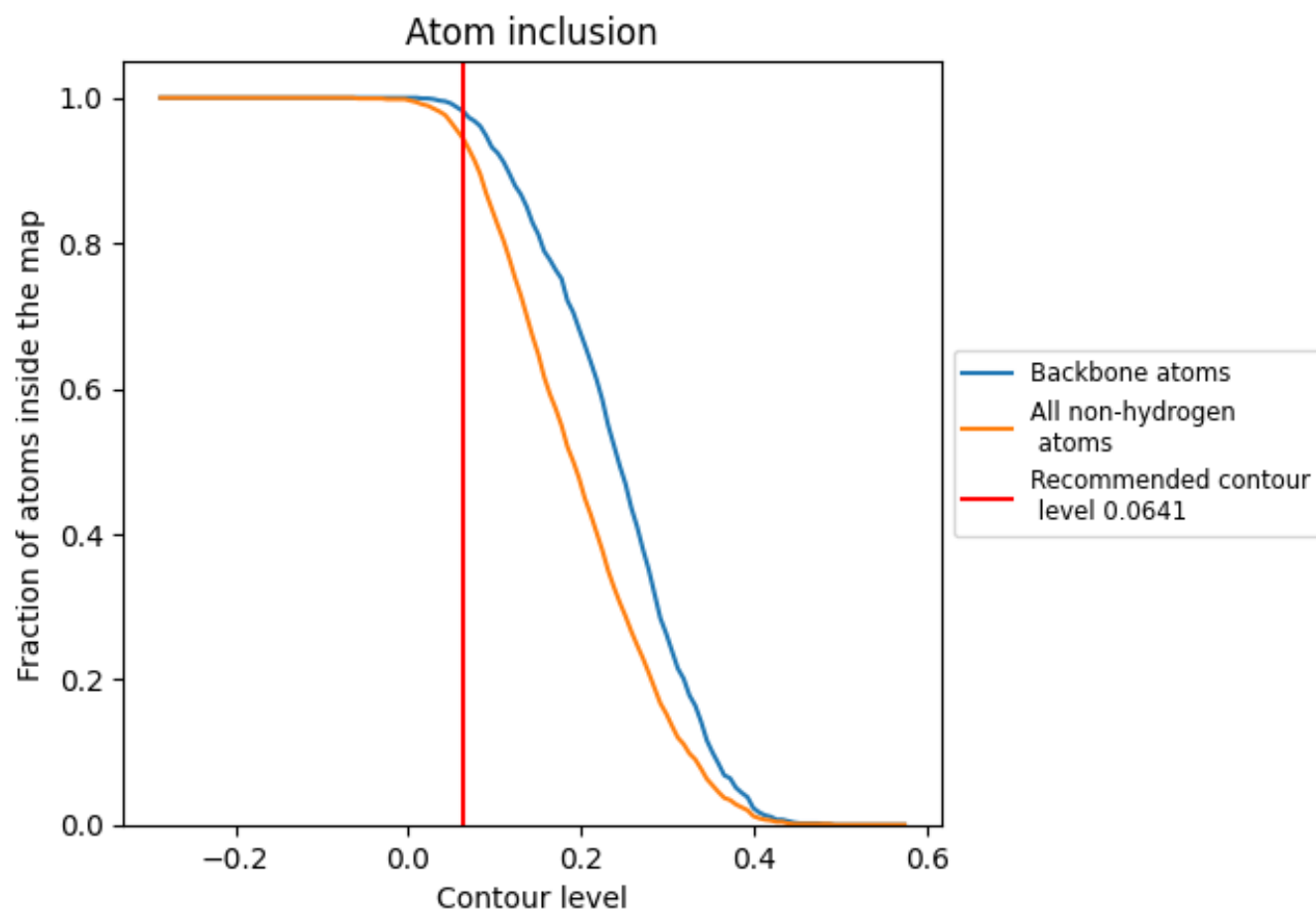
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0641).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 94% 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 (0.0641) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9430	<div></div> 0.4580
A	<div></div> 0.9390	<div></div> 0.4780
B	<div></div> 0.9520	<div></div> 0.4770
C	<div></div> 0.9300	<div></div> 0.4370
D	<div></div> 0.9510	<div></div> 0.4400

