



wwPDB EM Validation Summary Report ⓘ

Aug 27, 2026 – 05:22 am BST

PDB ID : 9SFW / pdb_00009sfw
EMDB ID : EMD-54867
Title : Structure of Pex8 in complex with peroxisomal receptor Pex5
Authors : Ekal, L.; Mullapudi, E.; Chojnowski, G.; Wilmanns, M.
Deposited on : 2025-08-21
Resolution : 4.50 Å(reported)
Based on initial model : .

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.dev133
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) : 2.50

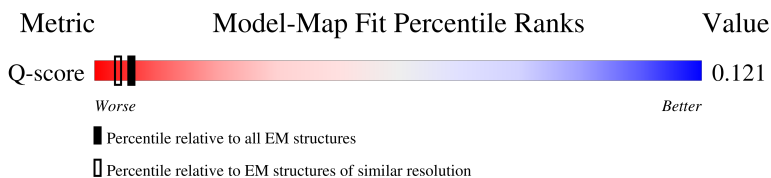
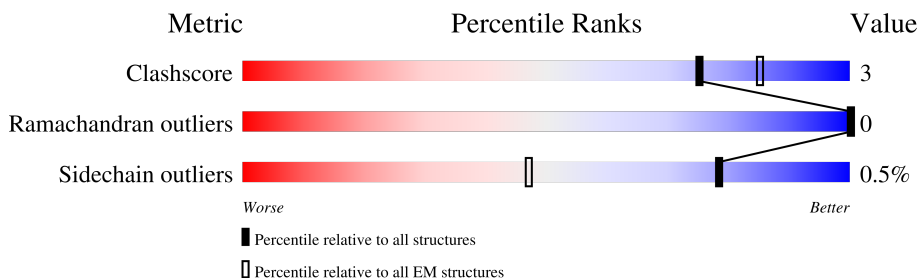
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 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	2937 (4.00 - 5.00)

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	713	
2	B	576	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7698 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 Peroxisomal biogenesis factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	635	Total	C	N	O	S	0	0
			5123	3313	825	966	19		

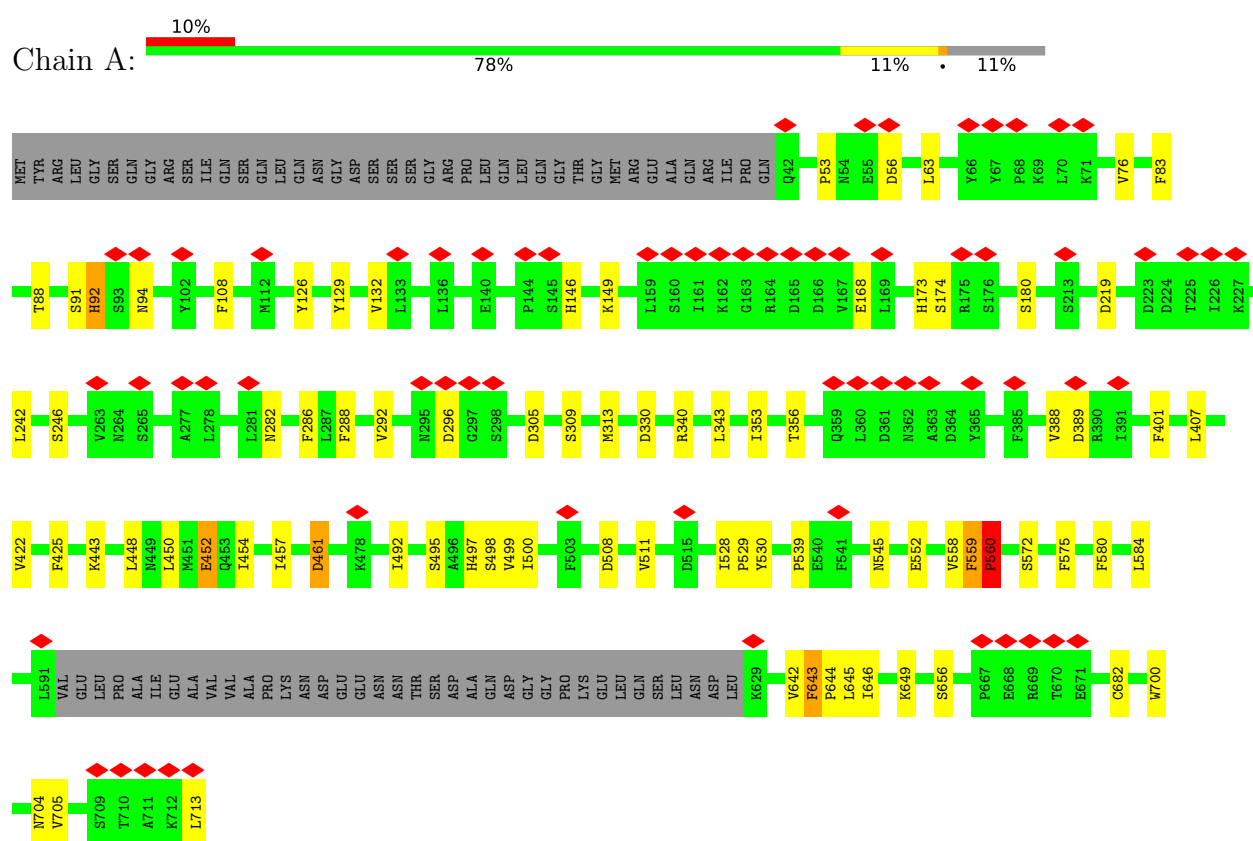
- Molecule 2 is a protein called Peroxisomal targeting signal receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	326	Total	C	N	O	S	0	0
			2575	1610	440	509	16		

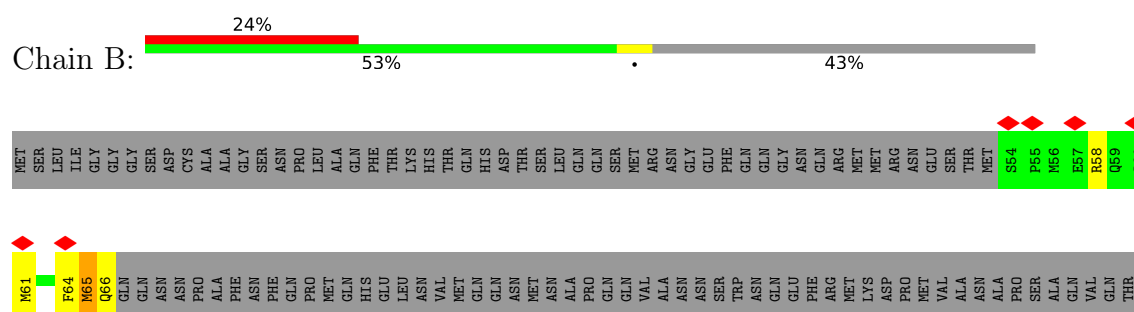
3 Residue-property plots

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: Peroxisomal biogenesis factor 8



• Molecule 2: Peroxisomal targeting signal receptor



PRO	ASN	VAL	GLN	SER	THR	ASN	THR	ALA	GLN	SER	PHE	GLN	ALA	GLY	PRO	GLU	VAL	GLN	GLY	ASP	ARG	LEU	ASN	HIS	ILE	GLN	GLN	HIS	THR	LEU	GLN	PRO	PRO	GLY	GLY	ARG	GLN	GLY	ILE	TYR	ASN	GLY	THR	PHE	GLY	ARG	LEU	MET	GLY	TRP	ASP	GLY	SER	SER	MET	MET	GLN	VAL	ASN	ARG	SER	TYR	ALA	ALA	GLN	ASP	VAL	GLU	GLN	THR
ASN	PRO	ALA	GLN	GLN	ALA	GLN	ALA	GLN	THR	THR	SER	GLN	GLN	ASP	GLY	ASP	GLY	ARG	LEU	ASN	HIS	ILE	GLN	GLN	THR	GLN	GLY	PRO	PRO	PRO	LYS	THR	VAL	ARG	GLN	GLY	ILE	TYR	ASN	GLY	THR	PHE	GLY	ARG	LEU	VAL	TRP	ASP	GLY	SER	MET	ILE	GLN	VAL	ASN	ARG	SER	TYR	ALA	ALA	GLN	ASP	VAL	GLU	LEU	GLN	THR			
ASP	GLN	PHE	GLN	GLN	ALA	ALA	GLN	THR	TRP	GLY	ASP	PHE	ALA	GLN	TYR	ALA	GLY	GLY	ARG	LEU	ASN	ASN	TYR	G264	E265	Y268	E269	E270	K271	N272	Q273	F274	R275	N276	D277	P278	D279	E282	R286	A303	A304	V305	Q306	Q307	D308	P309	K310	H311	V312	D313	E326	K327	E328	L341	D342															
P343	T344	N345	L346	A347	M350	T351	L352	A353	I354	S355	N358	D359	D362	Y366	R371	E374	T375	P378	D379	I380	A381	S382	R383	A384	R385	S386	S387	N388	P389	D390	L391	D392	G393	G394	D395	R396	I397	E398	Q399	N400	F407	Q412	L413	S414	P415	D416	V417	A418	S419	M420																				
G427	V430	S434	M435	E436	E437	A447	A448	I449	E450	V451	L457	N458	W459	N460	R461	A464	N470	V476	Y479	S480	R481	R491	Y494	N495	F500	I501	N502	M503	G504	R505	Y506	K507	L513	E523	G524	V525	D526	A527	S528	E529	M530	S531	N538	N539																										
A540	L541	V542	E543	T544	L545	K546	R547	A548	F549	G551	M552	N553	R554	R555	K560	V561	Y562	P563	G564	M565	G566	L567	A568	Q569	F570	R571	K572	M573	F576																																									

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	85869	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 ($e^-/\text{\AA}^2$)	64.5	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.252	Depositor
Minimum map value	-0.417	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.2	Depositor
Map size ($\text{\AA}$)	329.12, 329.12, 329.12	wwPDB
Map dimensions	242, 242, 242	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.36, 1.36, 1.36	Depositor

5 Model quality

5.1 Standard geometry

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	0.76	1/5233 (0.0%)	1.43	32/7111 (0.5%)
2	B	0.60	0/2619	1.15	4/3530 (0.1%)
All	All	0.71	1/7852 (0.0%)	1.34	36/10641 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	645	LEU	C-N	5.22	1.39	1.33

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	559	PHE	CA-CB-CG	-13.82	99.98	113.80
2	B	65	MET	CG-SD-CE	9.52	121.84	100.90
1	A	389	ASP	CA-CB-CG	8.46	121.06	112.60
1	A	330	ASP	CA-CB-CG	8.18	120.78	112.60
1	A	219	ASP	CA-CB-CG	7.75	120.35	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	704	ASN	Peptide
2	B	58	ARG	Sidechain

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	5123	0	5136	37	0
2	B	2575	0	2492	14	0
All	All	7698	0	7628	47	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 3.

The worst 5 of 47 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:282:ASN:HB2	2:B:64:PHE:CE2	2.19	0.78
1:A:559:PHE:HB3	1:A:560:PRO:HD2	1.73	0.69
1:A:452:GLU:HB2	1:A:499:VAL:HG22	1.80	0.63
1:A:559:PHE:HB3	1:A:560:PRO:CD	2.31	0.60
1:A:282:ASN:ND2	2:B:64:PHE:CD1	2.71	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	631/713 (88%)	618 (98%)	13 (2%)	0	100	100
2	B	322/576 (56%)	319 (99%)	3 (1%)	0	100	100
All	All	953/1289 (74%)	937 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	588/653 (90%)	585 (100%)	3 (0%)	81	81
2	B	270/484 (56%)	269 (100%)	1 (0%)	84	82
All	All	858/1137 (76%)	854 (100%)	4 (0%)	78	81

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	461	ASP
1	A	539	PRO
1	A	560	PRO
2	B	539	ASN

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	695	ASN
2	B	363	ASN
2	B	569	GLN
2	B	520	HIS
2	B	538	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-54867. These allow visual inspection of the internal detail of the map and identification of artifacts.

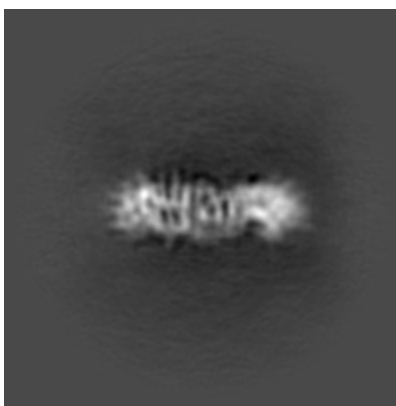
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

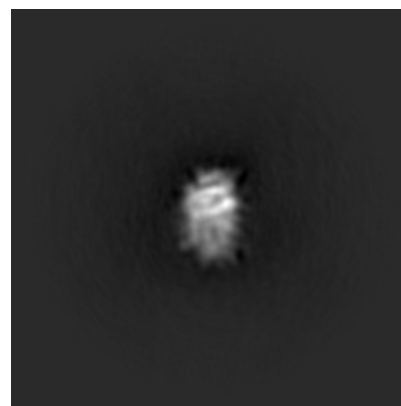
6.1.1 Primary map



X

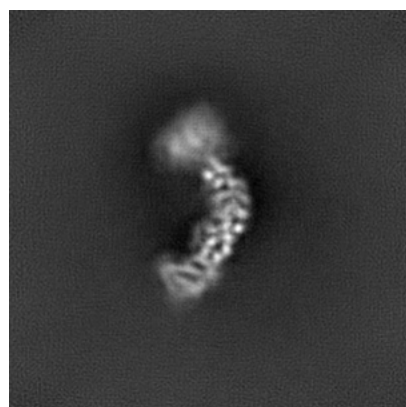


Y

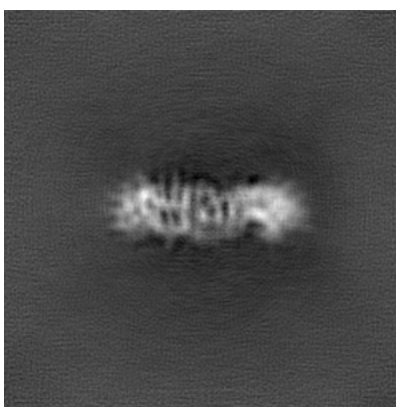


Z

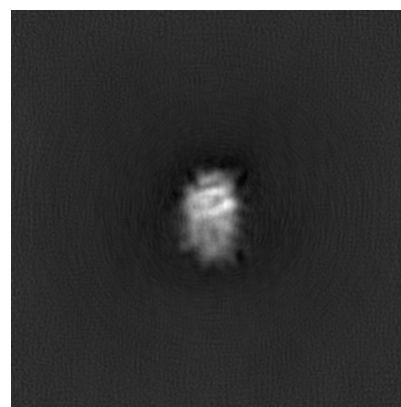
6.1.2 Raw map



X



Y



Z

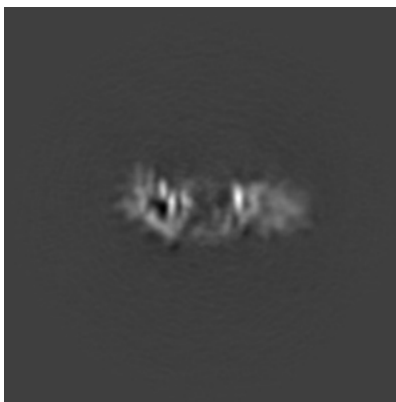
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

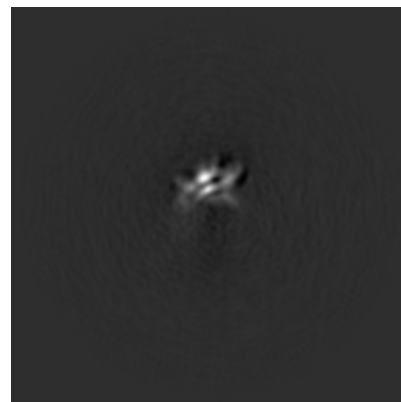
6.2.1 Primary map



X Index: 121

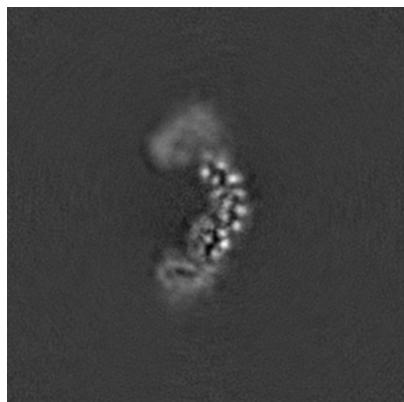


Y Index: 121

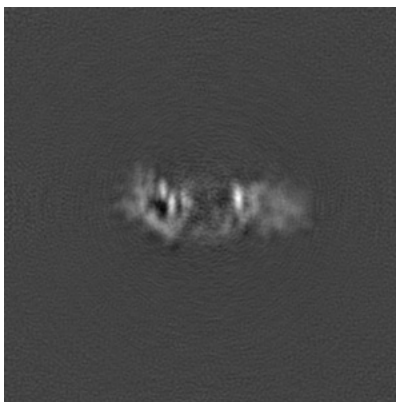


Z Index: 121

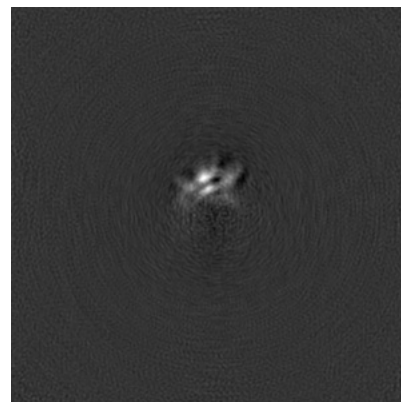
6.2.2 Raw map



X Index: 121



Y Index: 121

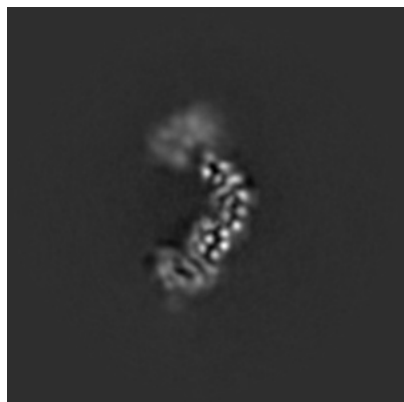


Z Index: 121

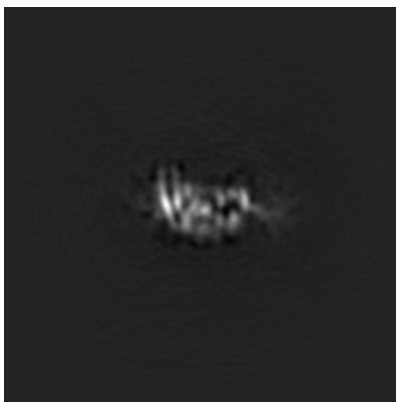
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

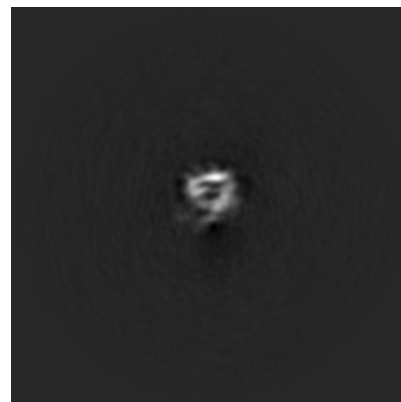
6.3.1 Primary map



X Index: 124

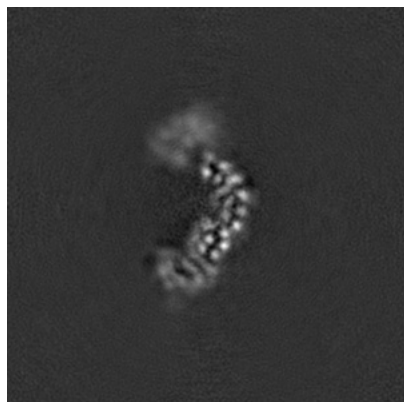


Y Index: 131

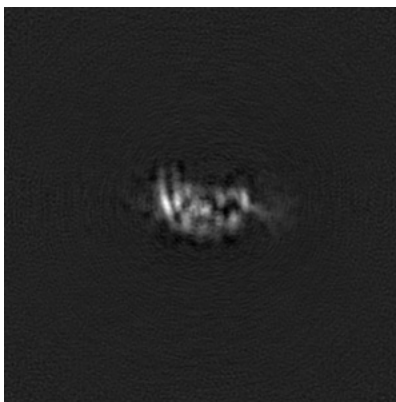


Z Index: 109

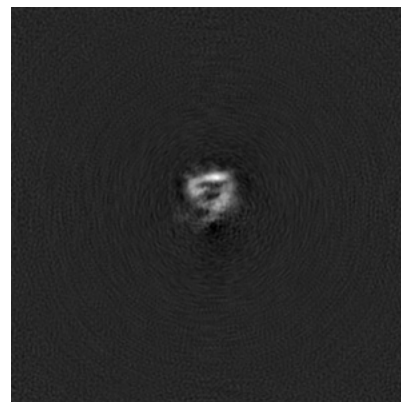
6.3.2 Raw map



X Index: 124



Y Index: 131



Z Index: 109

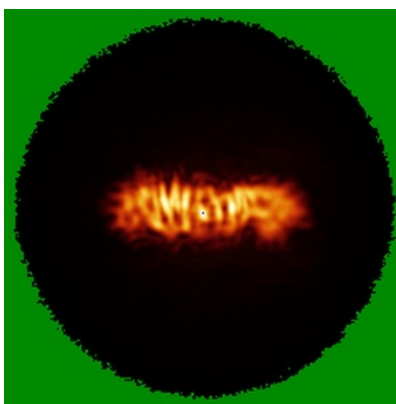
The images above show the largest variance slices of the map in three orthogonal directions.

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

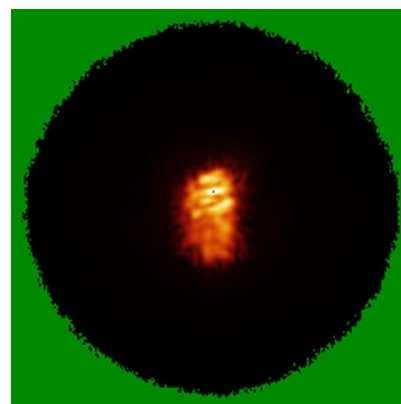
6.4.1 Primary map



X



Y

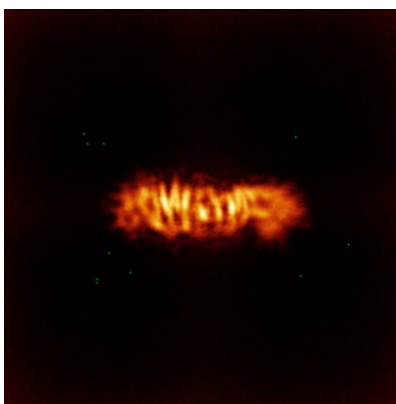


Z

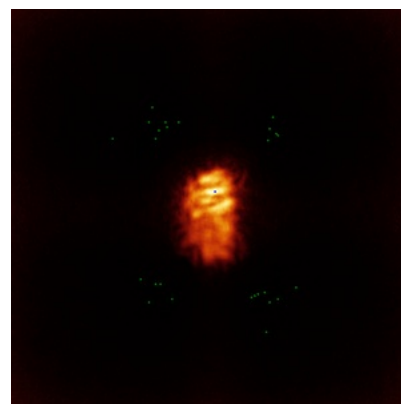
6.4.2 Raw map



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 0.2. 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.

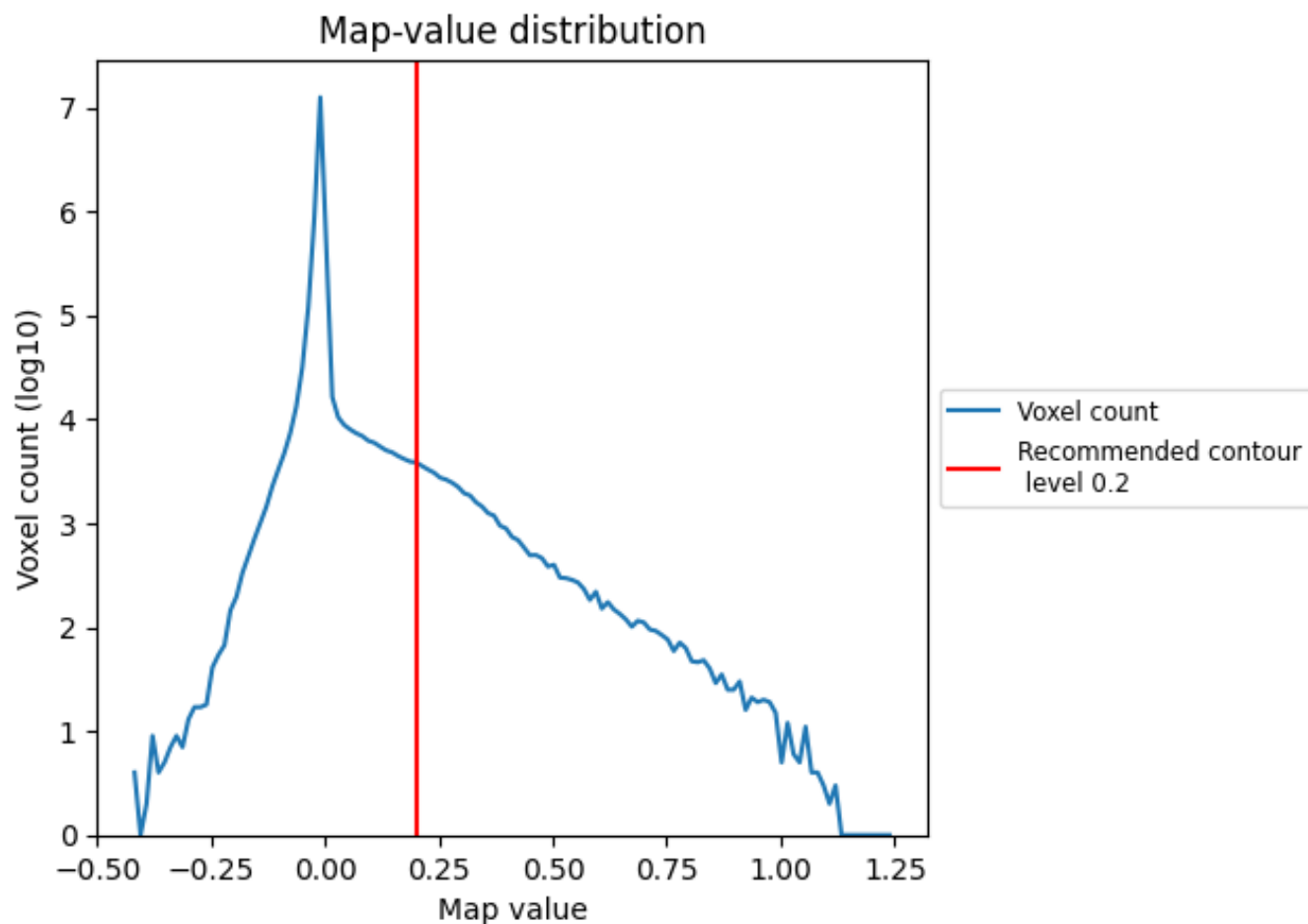
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

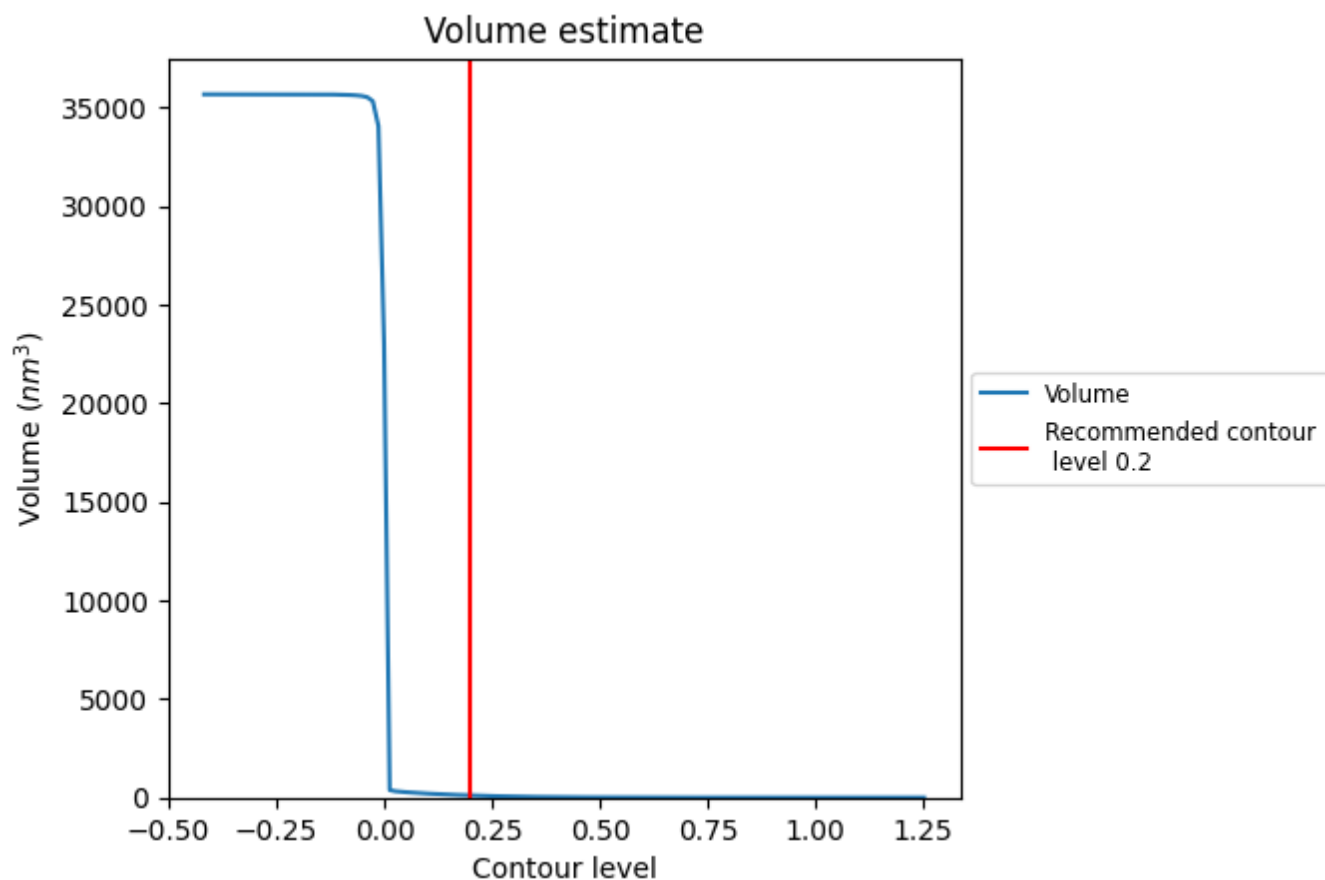
This section contains the results of statistical analysis of the map.

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.

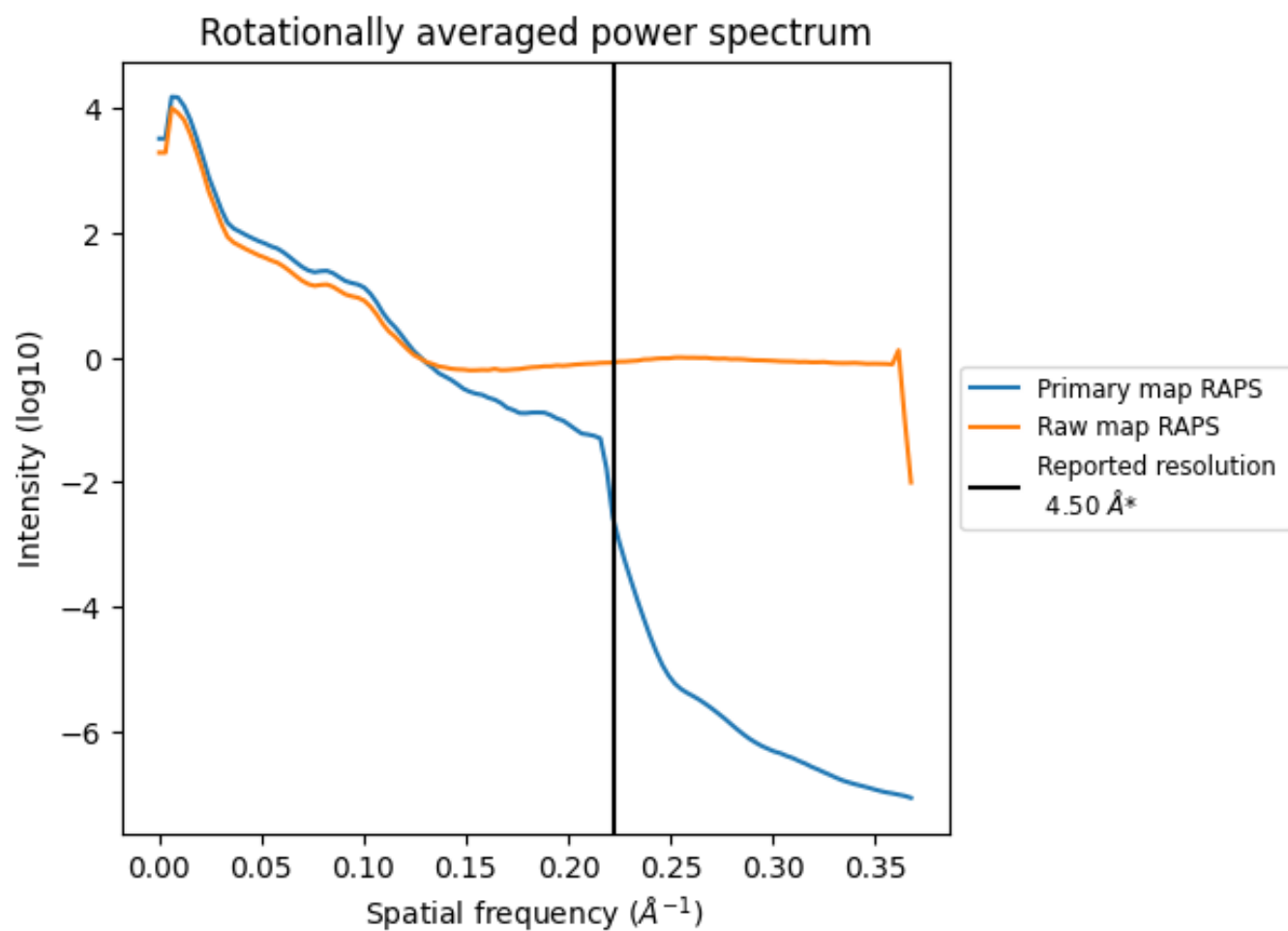
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 108 nm^3 ; this corresponds to an approximate mass of 98 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 ⓘ

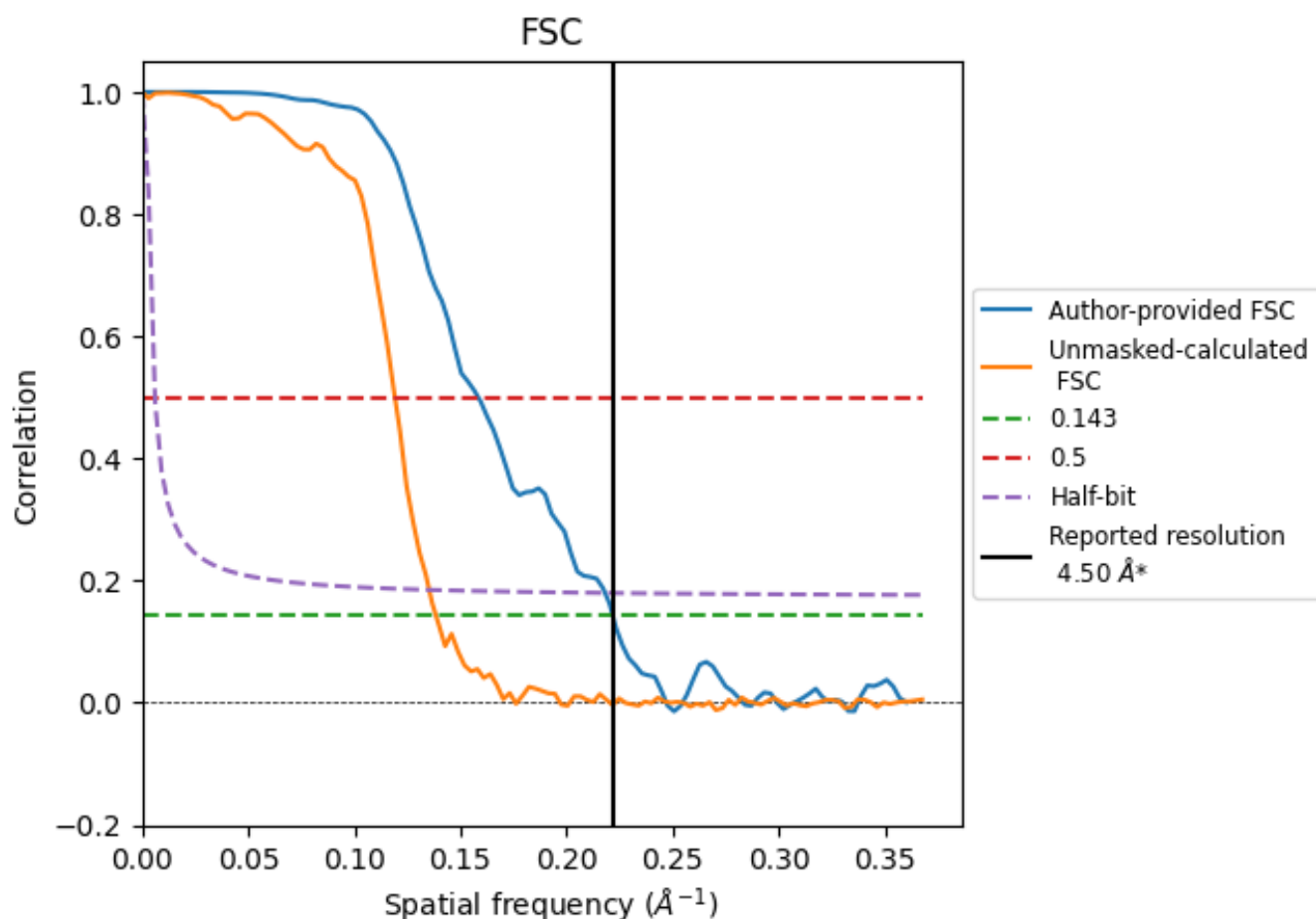


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

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 0.222 Å⁻¹

8.2 Resolution estimates [i](#)

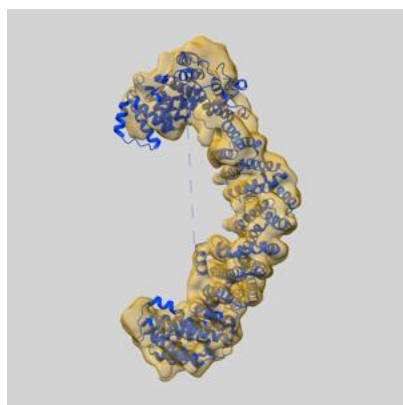
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.51	6.31	4.58
Unmasked-calculated*	7.23	8.40	7.39

*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 7.23 differs from the reported value 4.5 by more than 10 %

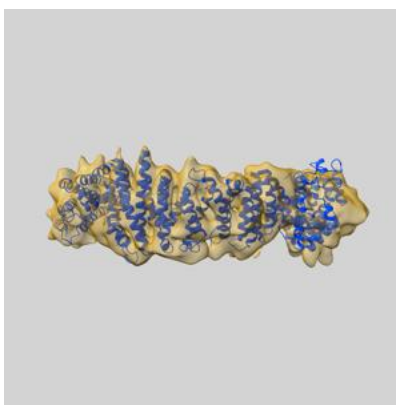
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-54867 and PDB model 9SFW. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

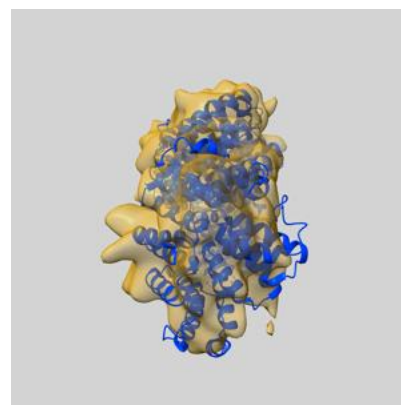
9.1 Map-model overlay [i](#)



X



Y



Z

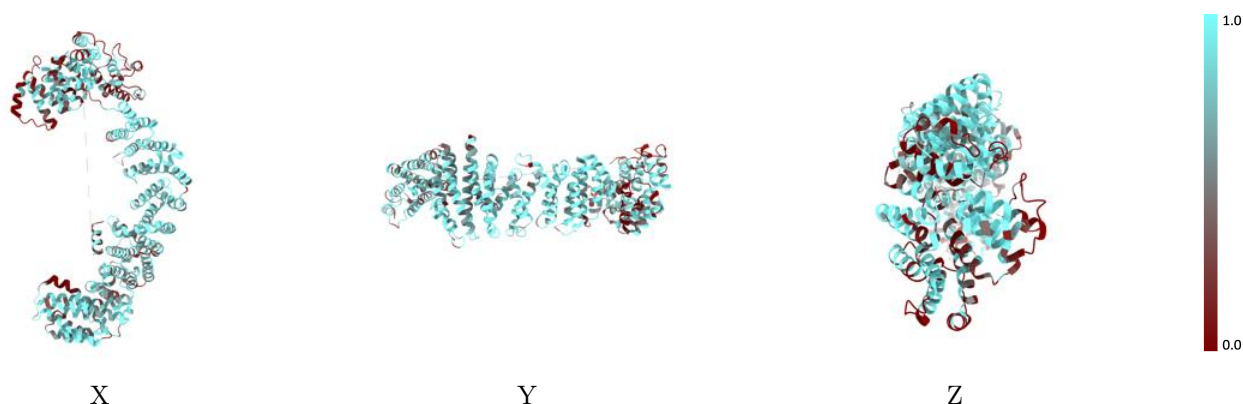
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



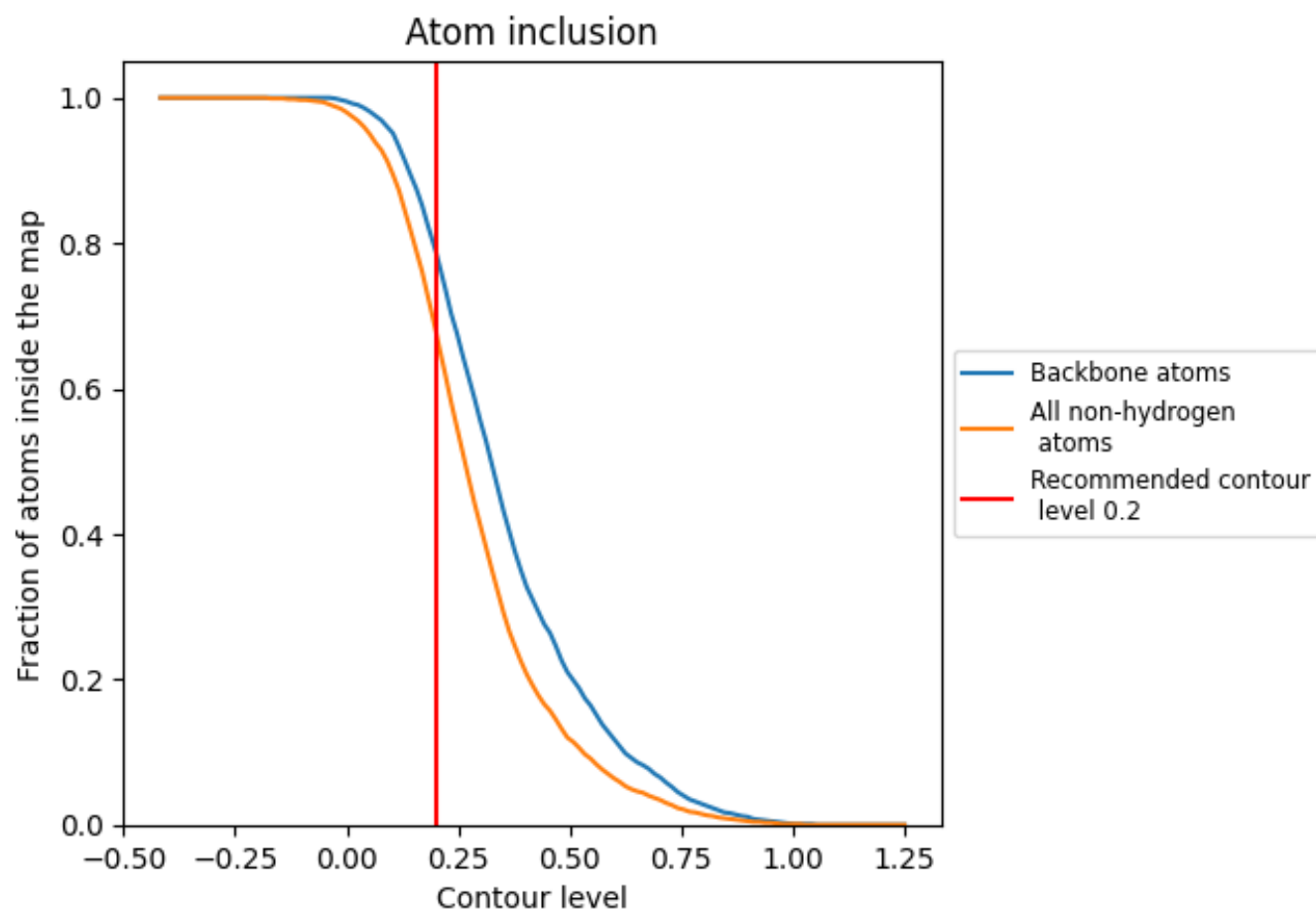
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6800	0.1210
A	0.7630	0.1580
B	0.5150	0.0470

