



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 09:35 PM UTC

PDB ID : 8XFP / pdb_00008xfp
EMDB ID : EMD-38307
Title : the pentamerA complex of LGR4-RSPO2-ZNRF3(delta RING)
Authors : Geng, Y.; Wang, L.
Deposited on : 2023-12-14
Resolution : 3.21 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:

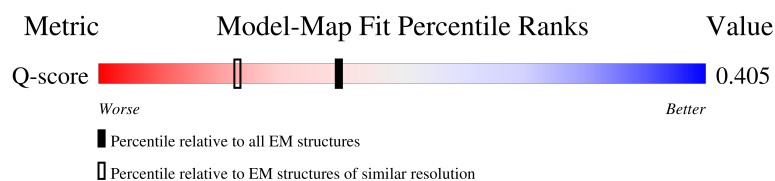
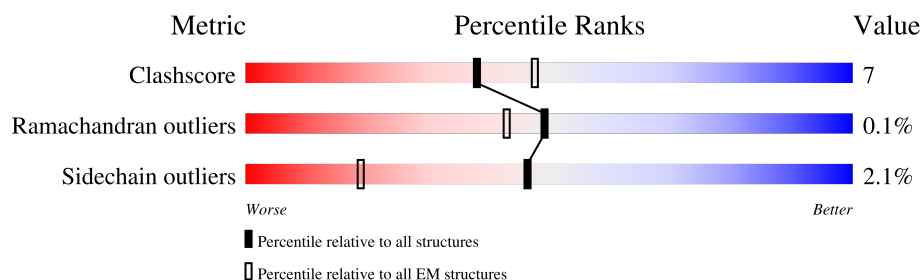
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.21 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	14613 (2.71 - 3.71)

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	951	
2	E	560	
3	C	936	
3	H	936	

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Mol	Chain	Length	Quality of chain
4	G	101	77% 22% .
4	J	101	75% 23% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10742 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 Leucine-rich repeat-containing G-protein coupled receptor 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	734	Total	C	N	O	S	0	0
			5733	3725	943	1037	28		

- Molecule 2 is a protein called nanobody Nb52.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	114	Total	C	N	O	S	0	0
			876	550	149	170	7		

- Molecule 3 is a protein called E3 ubiquitin-protein ligase ZNRF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	181	Total	C	N	O	S	0	0
			1400	896	232	266	6		
3	H	152	Total	C	N	O	S	0	0
			1171	736	202	229	4		

- Molecule 4 is a protein called R-spondin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	100	Total	C	N	O	S	0	0
			781	479	144	140	18		
4	J	100	Total	C	N	O	S	0	0
			781	479	144	140	18		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	130	ALA	ASP	conflict	UNP Q8BFU0
J	130	ALA	ASP	conflict	UNP Q8BFU0



- Molecule 3: E3 ubiquitin-protein ligase ZNRF3

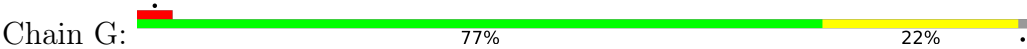


PRO	ASP	HIS	GLY	GLY	ARG	CYS	SER	SER	GLY	ASN	ASP	LEU	F66
GLY	HIS	GLY	GLU	GLU	THR	SER	GLY	GLN	GLU	PRO	THR	ALA	E67
LEU	PRO	GLU	TRP	ARG	THR	ARG	SER	THR	SER	ALA	SER	PHE	S68
PRO	ARG	PRO	PRO	SER	SER	SER	SER	MET	TYR	CYS	SER	VAL	S69
THR	SER	GLY	GLY	SER	SER	SER	PHE	TYR	SER	VAL	SER	VAL	G72
ASP	CYS	ALA	ALA	SER	PRO	LEU	GLN	GLN	PRO	GLU	THR	SER	D73
VAL	CYS	SER	SER	SER	TYR	SER	CYS	HIS	THR	THR	SER	VAL	Y74
PRO	VAL	PRO	VAL	SER	TYR	VAL	CYS	TYR	THR	SER	ASP	VAL	T75
ALA	ALA	TYR	SER	TYR	GLY	GLY	HIS	PHE	PRO	ASN	CYS	CYS	T76
THR	CYS	SER	SER	TYR	ARG	SER	HIS	GLN	ALA	LEU	ALA	LEU	R84
GLY	GLU	GLY	GLY	ASP	GLY	ASP	GLN	GLN	TYR	SER	ILE	ILE	F85
GLY	GLN	GLN	GLN	PHE	ARG	PHE	GLY	GLY	ILE	ARG	CYS	LEU	T91
PRO	PRO	PRO	VAL	ILE	VAL	CYS	VAL	SER	ARG	GLY	GLU	VAL	L92
CYS	SER	SER	SER	TYR	TYR	TYR	TYR	TYR	GLN	GLN	LYS	LYS	G96
CYS	PHE	ALA	THR	ARG	SER	SER	GLY	GLU	PRO	ARG	ILE	ILE	E97
THR	GLY	SER	SER	SER	CYS	SER	GLY	GLN	ARG	VAL	ASP	LEU	Y98
GLU	GLU	LEU	GLU	SER	PRO	GLU	GLY	GLY	THR	VAL	GLY	LYS	D111
LYS	ALA	GLY	MET	CYS	MET	CYS	ASP	GLN	PRO	GLU	GLU	GLN	E112
VAL	VAL	GLY	ASN	ARG	ALA	ALA	PRO	HIS	VAL	LEU	LEU	ARG	E113
ALA	ALA	ALA	THR	ARG	THR	ALA	PRO	HIS	ASN	HIS	ARG	SER	D114
GLY	ALA	GLY	ALA	SER	SER	GLY	PRO	PRO	TYR	VAL	VAL	GLN	G119
ALA	GLY	SER	SER	ALA	ASP	ALA	GLY	SER	PRO	PRO	PRO	ASN	K125
THR	THR	SER	GLY	GLY	SER	GLY	SER	PRO	ARG	VAL	THR	ASN	T152
GLY	PHE	GLY	GLU	GLY	SER	GLY	SER	ARG	HIS	HIS	ARG	ARG	D187
GLY	GLY	SER	ARG	SER	SER	SER	SER	ALA	GLU	ASN	HIS	VAL	M192
PRO	PRO	CYS	GLY	GLY	GLY	GLY	SER	ARG	HIS	ALA	ARG	GLN	Q198
THR	HIS	GLY	ARG	ARG	ARG	GLY	GLY	ALA	ILE	ILE	LYS	ALA	K199
THR	ASN	GLY	ASN	GLY	GLY	GLY	PHE	PHE	PRO	PRO	CYS	LEU	V200
GLU	TYR	SER	SER	PRO	PRO	CYS	PRO	PRO	ALA	ALA	VAL	GLU	LEU
ASP	GLU	ALA	SER	HIS	ALA	ALA	HIS	PRO	TYR	TYR	ASP	LYS	LEU
TYR	GLY	THR	LEU	CYS	LEU	CYS	SER	SER	PRO	PRO	PRO	MET	LEU
SER	SER	SER	SER	CYS	SER	CYS	GLY	GLY	THR	THR	TRP	GLU	R202
VAL	GLY	PHE	GLU	GLY	GLY	GLY	SER	SER	ARG	LEU	LEU	THR	GLY
SER	PRO	GLY	VAL	GLY	GLY	GLY	GLY	GLY	THR	THR	ARG	ARG	LEU
VAL	VAL	GLY	GLY	GLY	GLY	GLY	ASP	SER	SER	THR	GLN	LYS	I205
GLN	TYR	GLY	GLY	PRO	SER	PRO	VAL	LEU	MET	HIS	HIS	PHE	Q206
THR	GLU	GLY	ALA	PRO	VAL	VAL	PHE	LEU	ARG	ASP	ASN	ASN	H207
THR	GLN	SER	SER	PRO	ASP	CYS	PRO	PRO	LYS	SER	THR	SER	ARG
LEU	GLN	GLY	ALA	PRO	SER	GLY	PRO	THR	GLY	CYS	LYS	PRO	ALA
THR	GLY	GLY	ALA	GLY	GLY	GLY	THR	THR	GLY	PRO	GLN	GLY	ALA
PRO	PRO	SER	PRO	ALA	ALA	ALA	VAL	HIS	THR	HIS	ARG	THR	ALA
PRO	GLN	SER	ASP	VAL	VAL	VAL	ASN	ALA	LEU	LEU	ASN	GLU	ALA
GLY	GLY	LEU	LEU	HIS	THR	THR	GLN	PRO	PHE	THR	LYS	TYR	ARG
CYS	TYR	ARG	ARG	SER	SER	SER	GLY	PRO	THR	ILE			

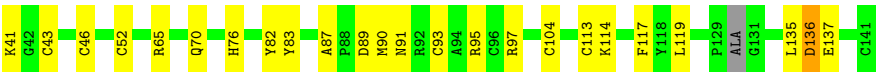
ARG
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● Molecule 4: R-spondin-2



● Molecule 4: R-spondin-2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73170	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.944	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.393	Depositor
Minimum map value	-0.228	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	385.56, 385.56, 385.56	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.071, 1.071, 1.071	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	0.10	0/5869	0.27	0/7981
2	E	0.10	0/894	0.26	0/1212
3	C	0.10	0/1425	0.26	0/1934
3	H	0.10	0/1191	0.24	0/1615
4	G	0.08	0/798	0.25	0/1062
4	J	0.10	0/798	0.27	0/1062
All	All	0.10	0/10975	0.27	0/14866

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	5733	0	5787	79	0
2	E	876	0	841	18	0
3	C	1400	0	1405	24	0
3	H	1171	0	1167	18	0
4	G	781	0	711	14	0
4	J	781	0	710	17	0
All	All	10742	0	10621	158	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 158 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)
2:E:518:TYR:O	2:E:543:GLY:HA2	1.87	0.74
2:E:515:THR:HA	2:E:546:VAL:O	1.87	0.73
1:A:329:THR:OG1	1:A:353:ASN:OD1	2.10	0.69
1:A:161:ASP:OD1	1:A:162:ASP:N	2.25	0.69
4:G:43:CYS:SG	4:G:44:LEU:N	2.65	0.68

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	726/951 (76%)	679 (94%)	47 (6%)	0	100	100
2	E	110/560 (20%)	105 (96%)	5 (4%)	0	100	100
3	C	177/936 (19%)	170 (96%)	6 (3%)	1 (1%)	21	55
3	H	150/936 (16%)	146 (97%)	4 (3%)	0	100	100
4	G	96/101 (95%)	89 (93%)	7 (7%)	0	100	100
4	J	96/101 (95%)	87 (91%)	9 (9%)	0	100	100
All	All	1355/3585 (38%)	1276 (94%)	78 (6%)	1 (0%)	49	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	75	THR

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	646/827 (78%)	633 (98%)	13 (2%)	48	70
2	E	93/452 (21%)	93 (100%)	0	100	100
3	C	153/773 (20%)	150 (98%)	3 (2%)	48	70
3	H	127/773 (16%)	120 (94%)	7 (6%)	19	50
4	G	85/88 (97%)	84 (99%)	1 (1%)	63	77
4	J	85/88 (97%)	84 (99%)	1 (1%)	63	77
All	All	1189/3001 (40%)	1164 (98%)	25 (2%)	46	69

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	98	ILE
3	H	65	LEU
4	J	136	ASP
4	G	119	LEU
3	H	85	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
3	H	100	GLN
3	H	207	HIS
4	J	91	ASN
3	H	196	ASN
1	A	354	ASN

5.3.3 RNA ⓘ

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.

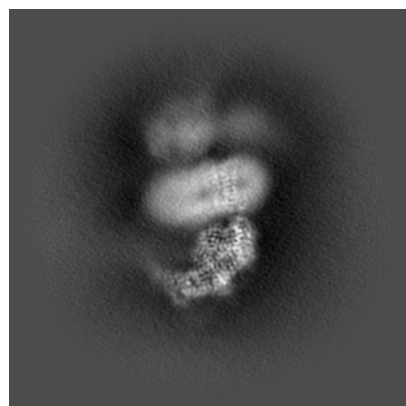
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38307. These allow visual inspection of the internal detail of the map and identification of artifacts.

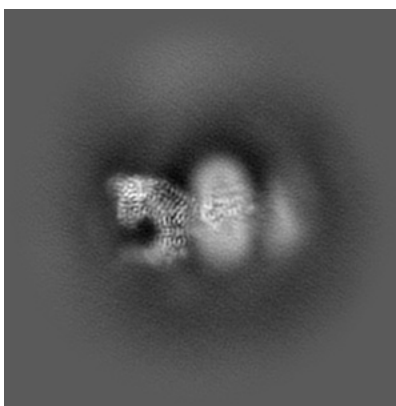
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

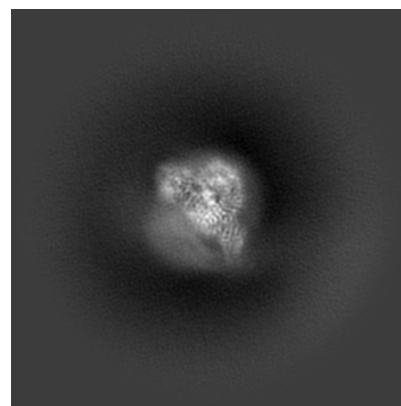
6.1.1 Primary map



X

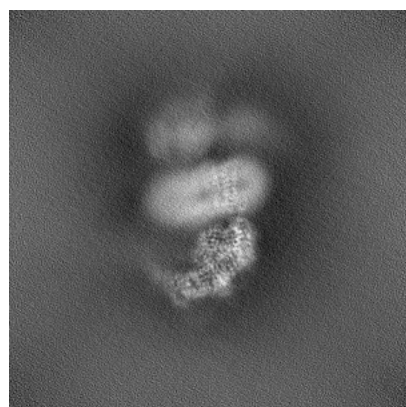


Y

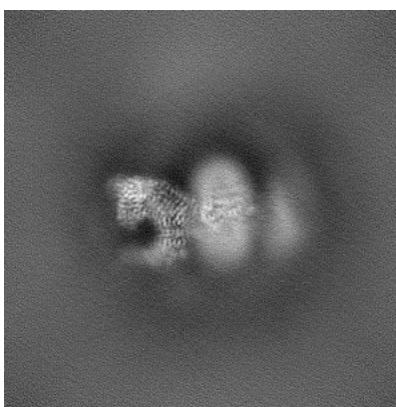


Z

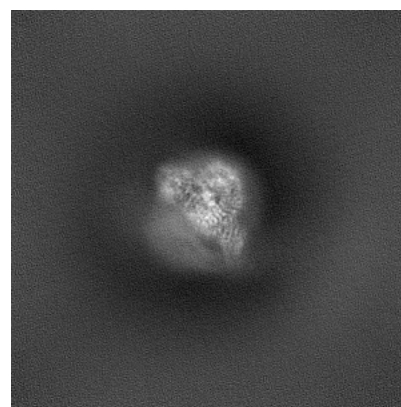
6.1.2 Raw map



X



Y

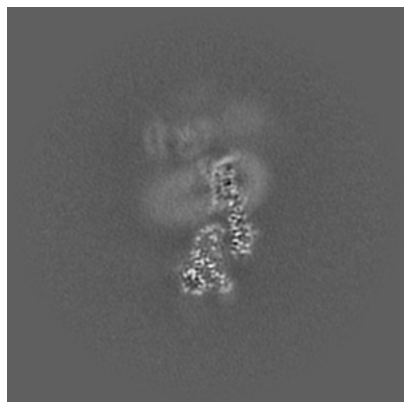


Z

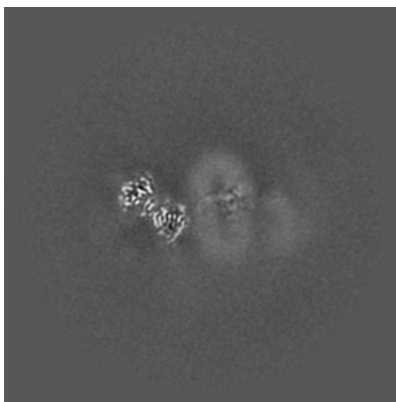
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

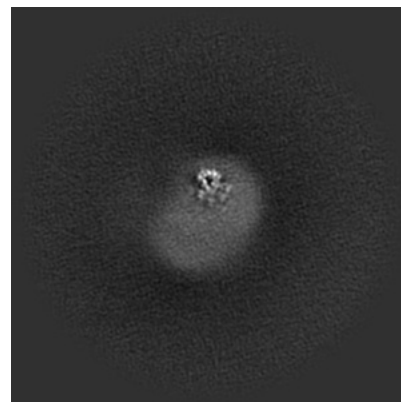
6.2.1 Primary map



X Index: 180

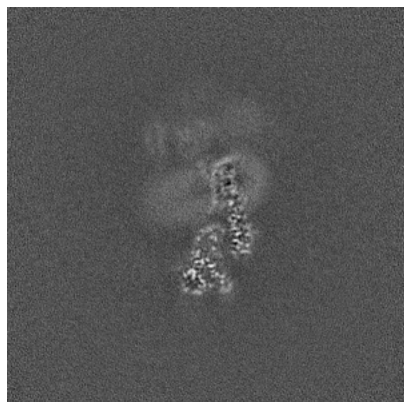


Y Index: 180



Z Index: 180

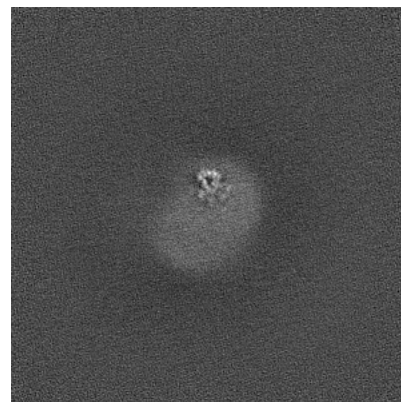
6.2.2 Raw map



X Index: 180



Y Index: 180



Z Index: 180

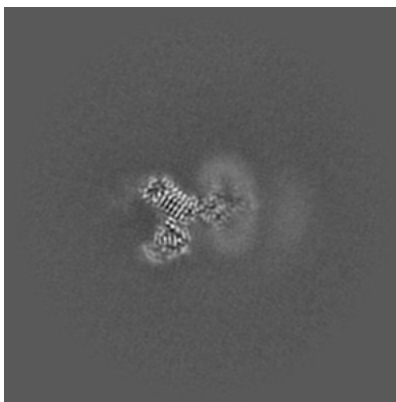
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

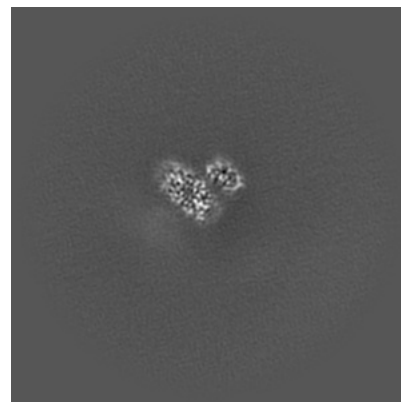
6.3.1 Primary map



X Index: 192

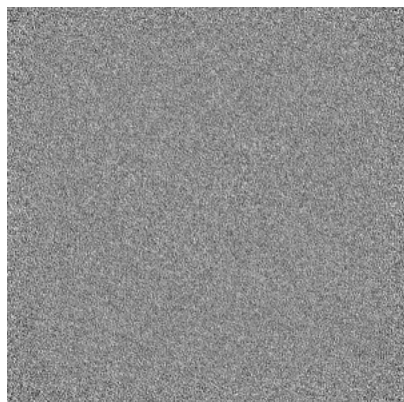


Y Index: 205

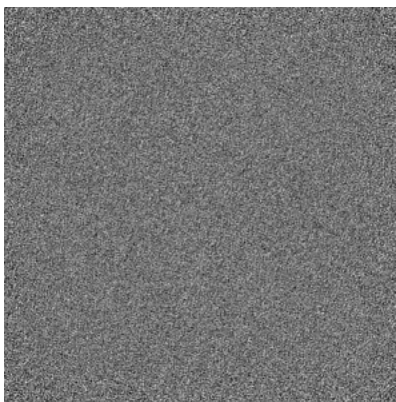


Z Index: 144

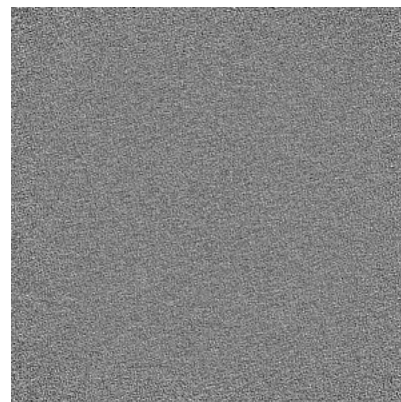
6.3.2 Raw map



X Index: 0



Y Index: 0

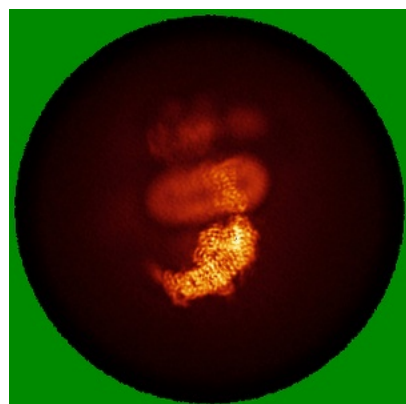


Z Index: 359

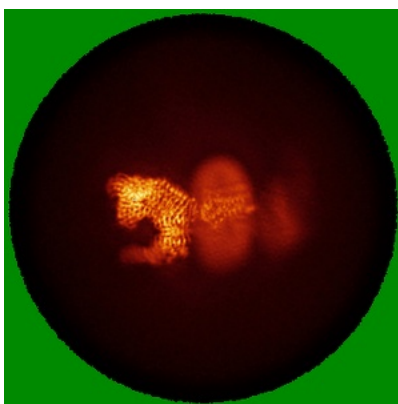
The images above show the largest variance slices of the map in three orthogonal directions.

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

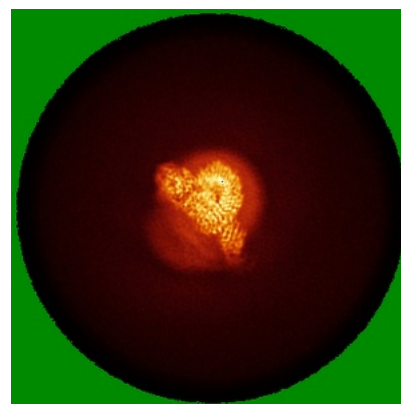
6.4.1 Primary map



X

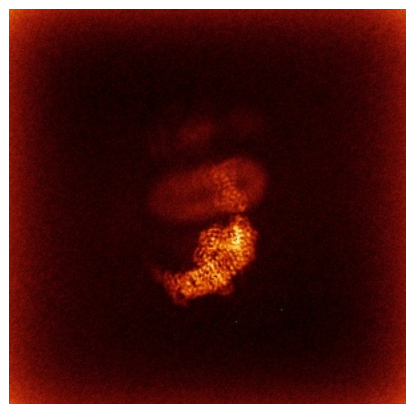


Y

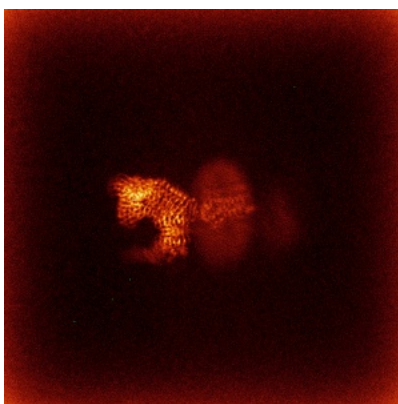


Z

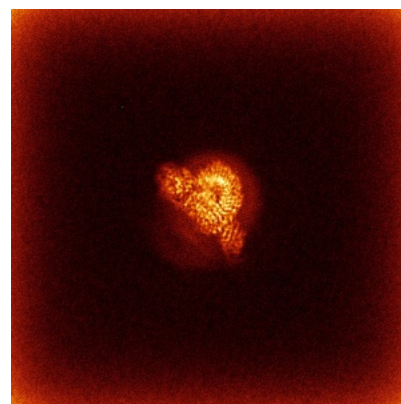
6.4.2 Raw map



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.

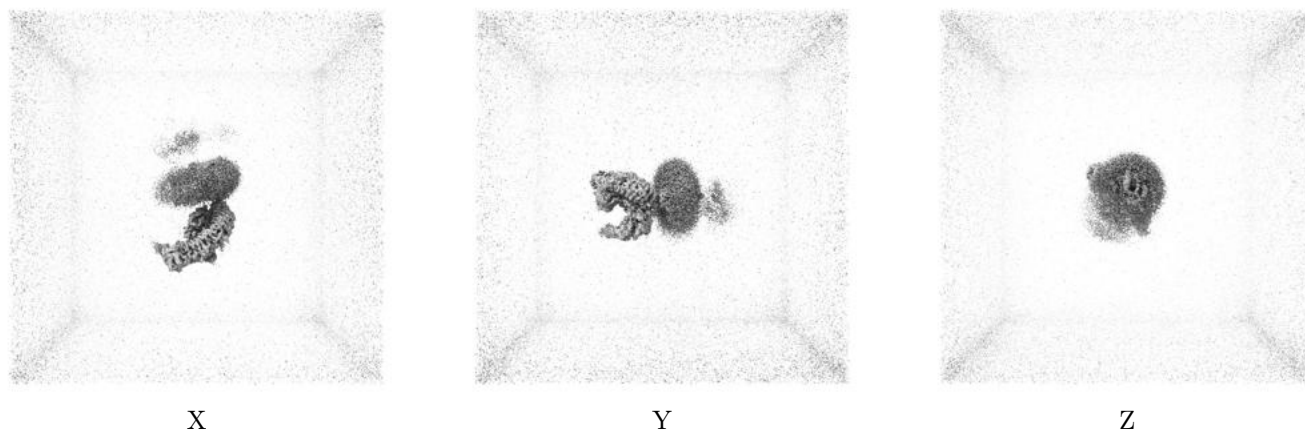
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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.

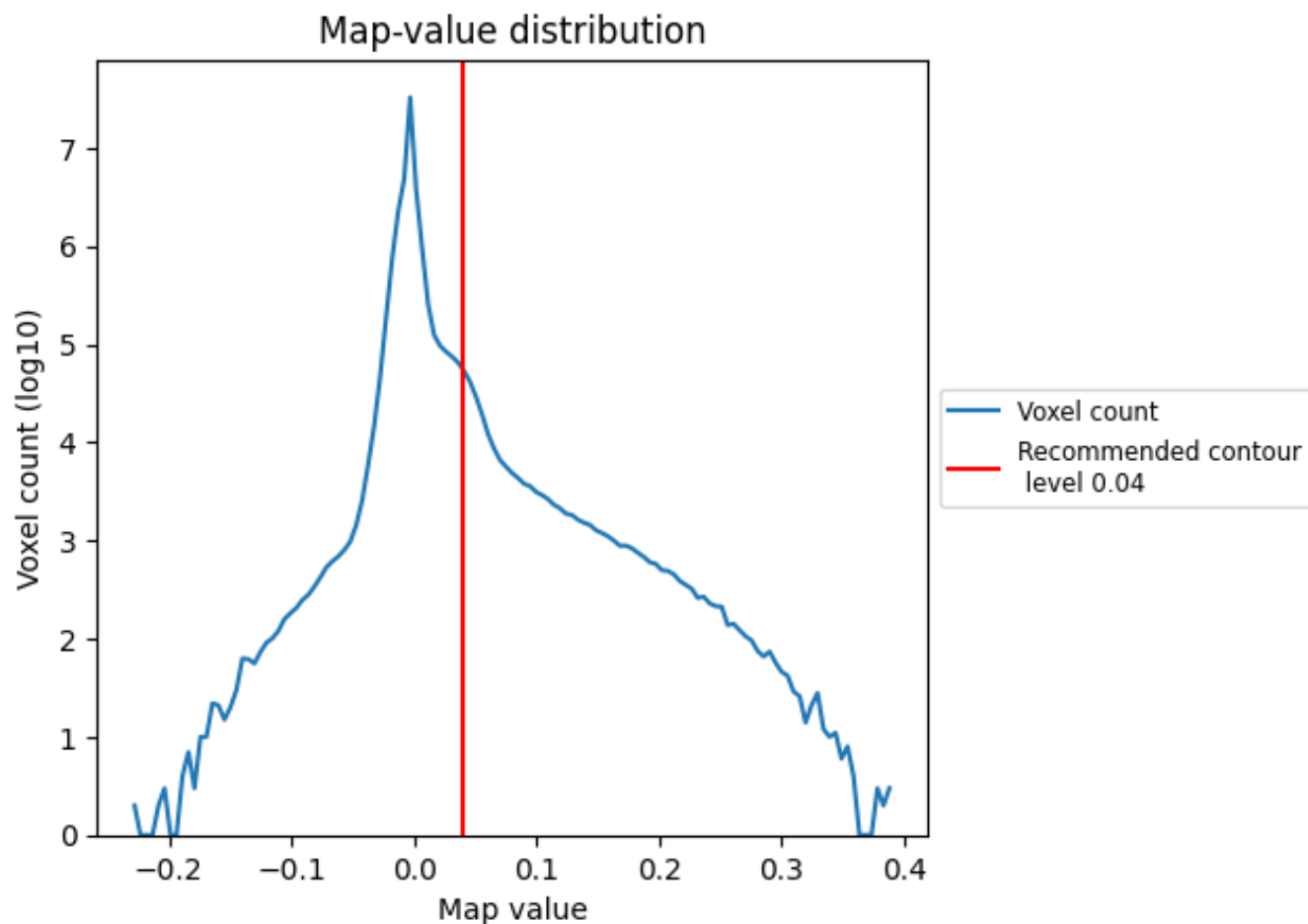
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

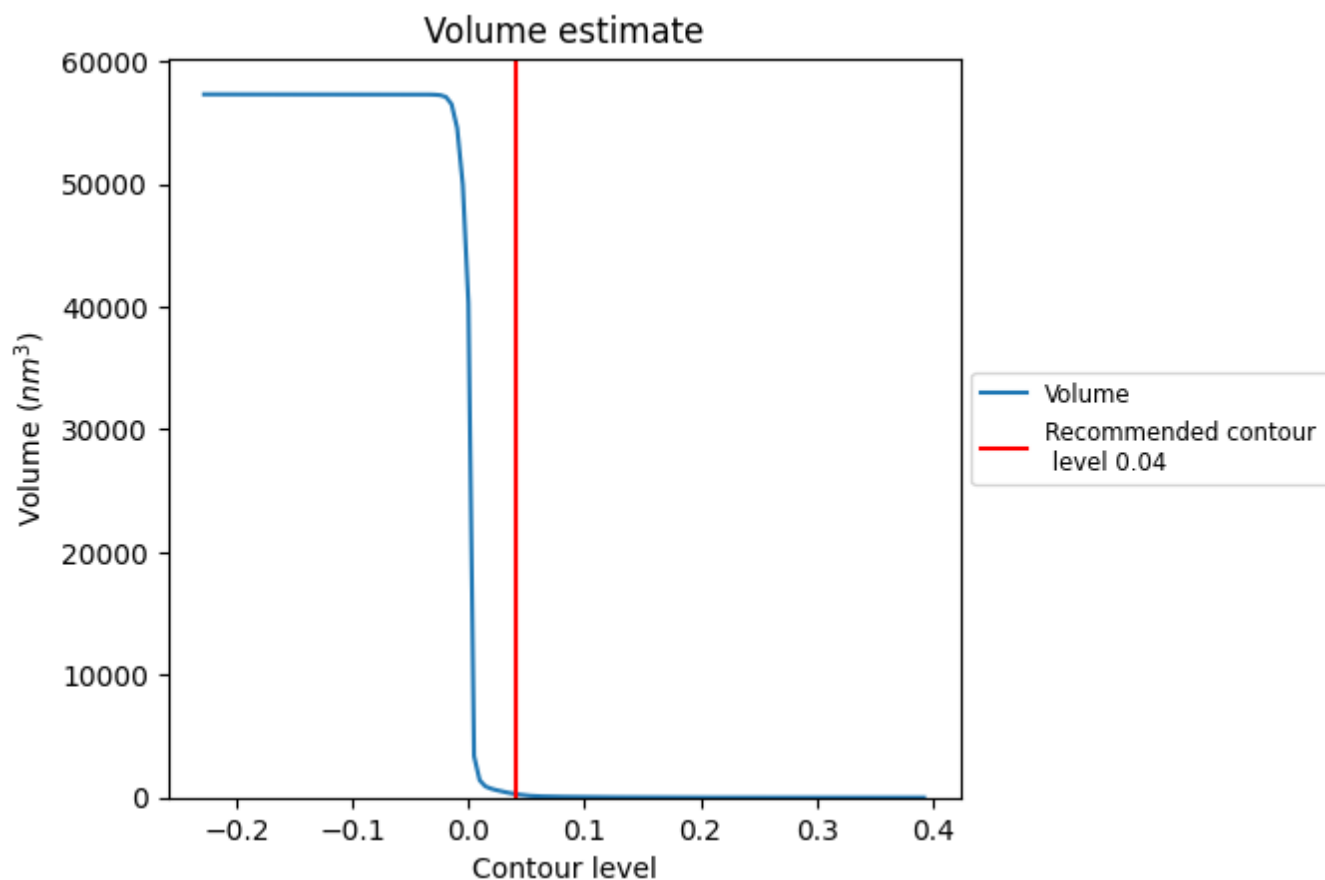
This section contains the results of statistical analysis of the map.

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.

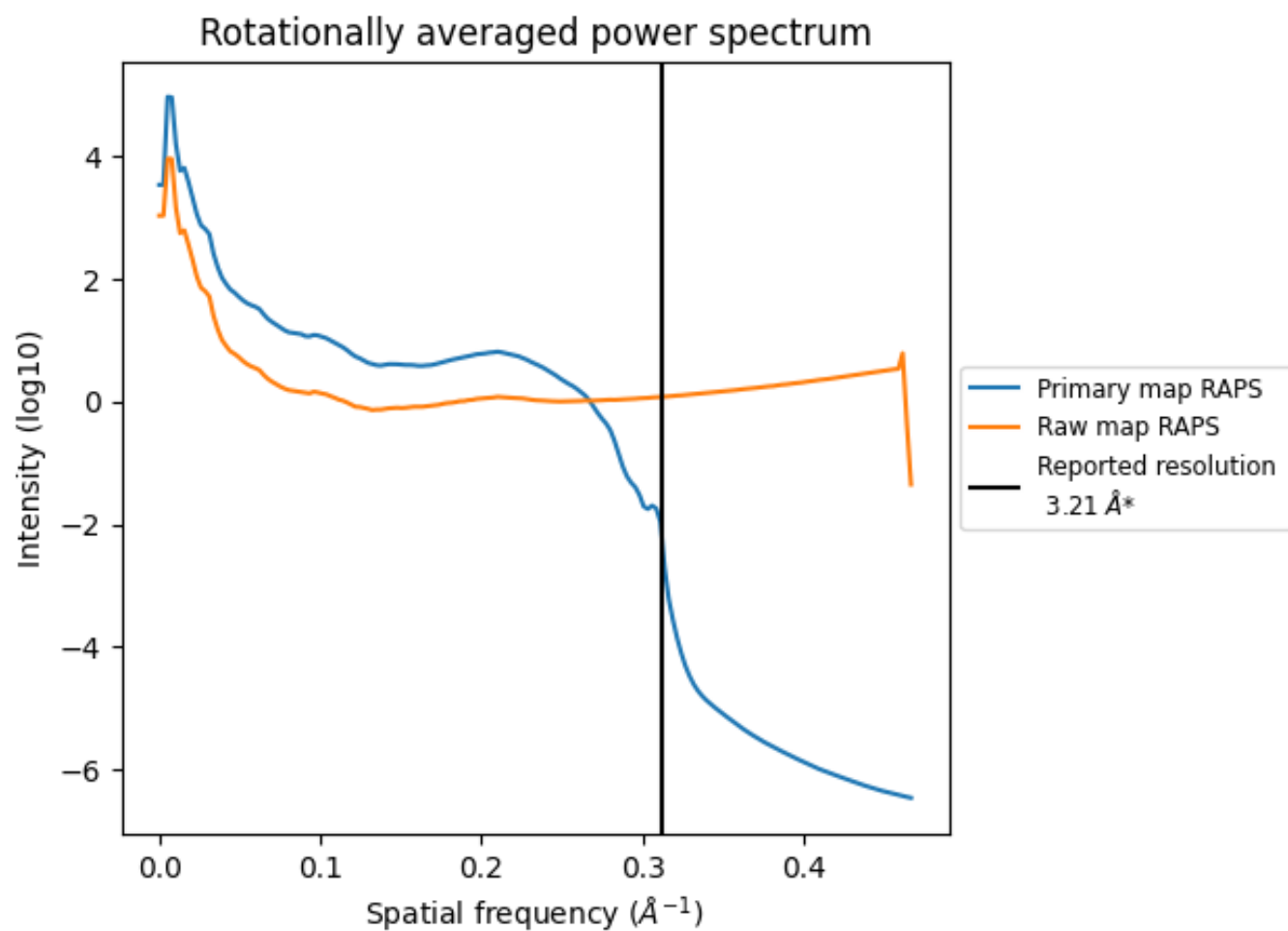
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 295 nm³; this corresponds to an approximate mass of 267 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 ⓘ

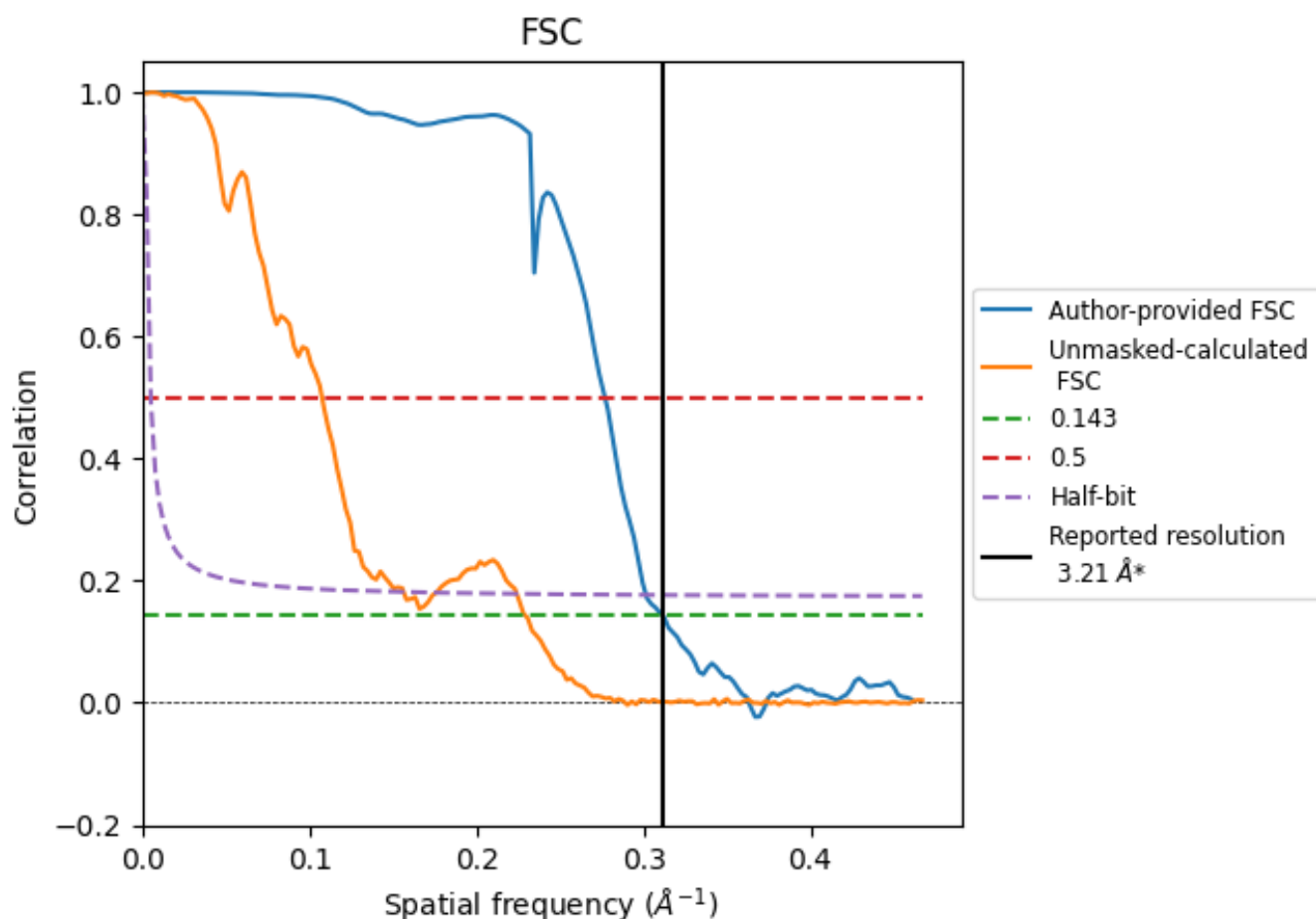


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 $0.312 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.21	-	-
Author-provided FSC curve	3.21	3.61	3.32
Unmasked-calculated*	4.36	9.29	6.39

*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 4.36 differs from the reported value 3.21 by more than 10 %

9 Map-model fit [i](#)

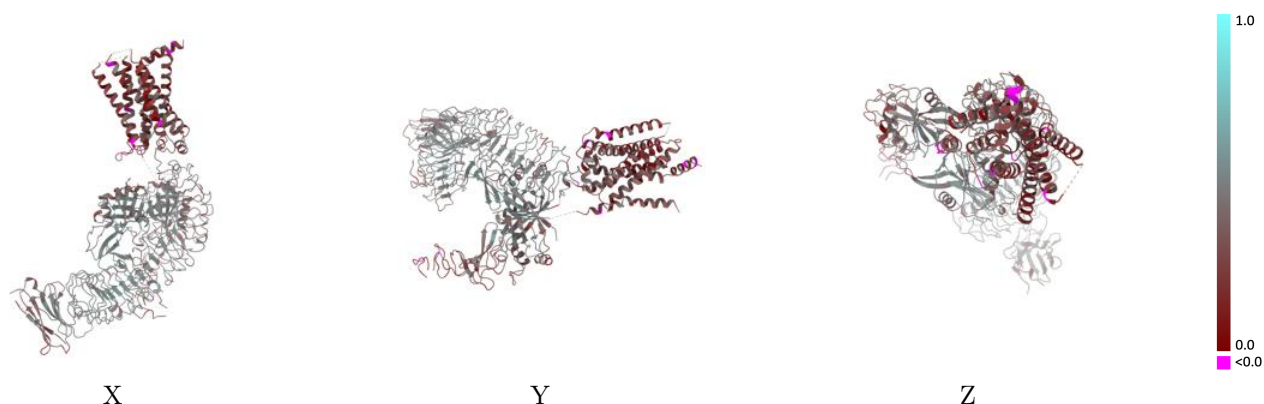
This section contains information regarding the fit between EMDB map EMD-38307 and PDB model 8XFP. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



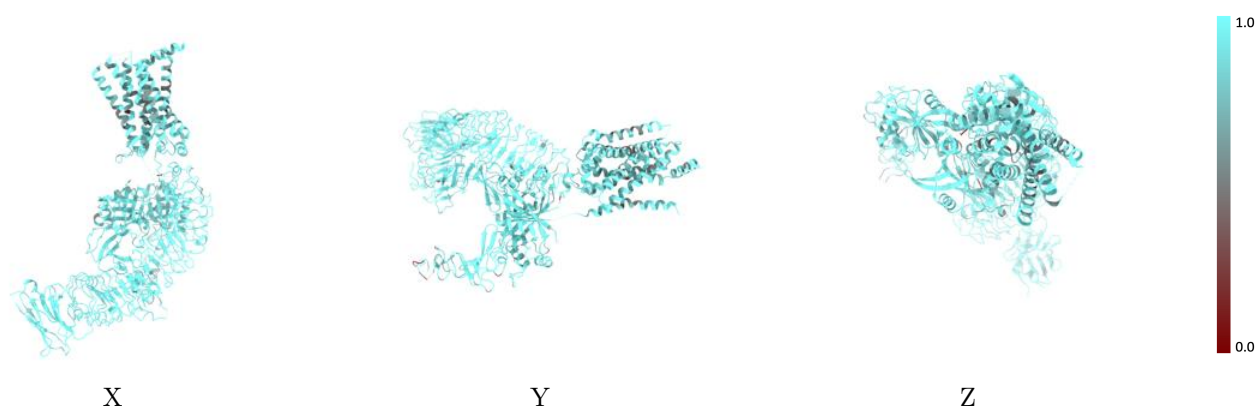
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



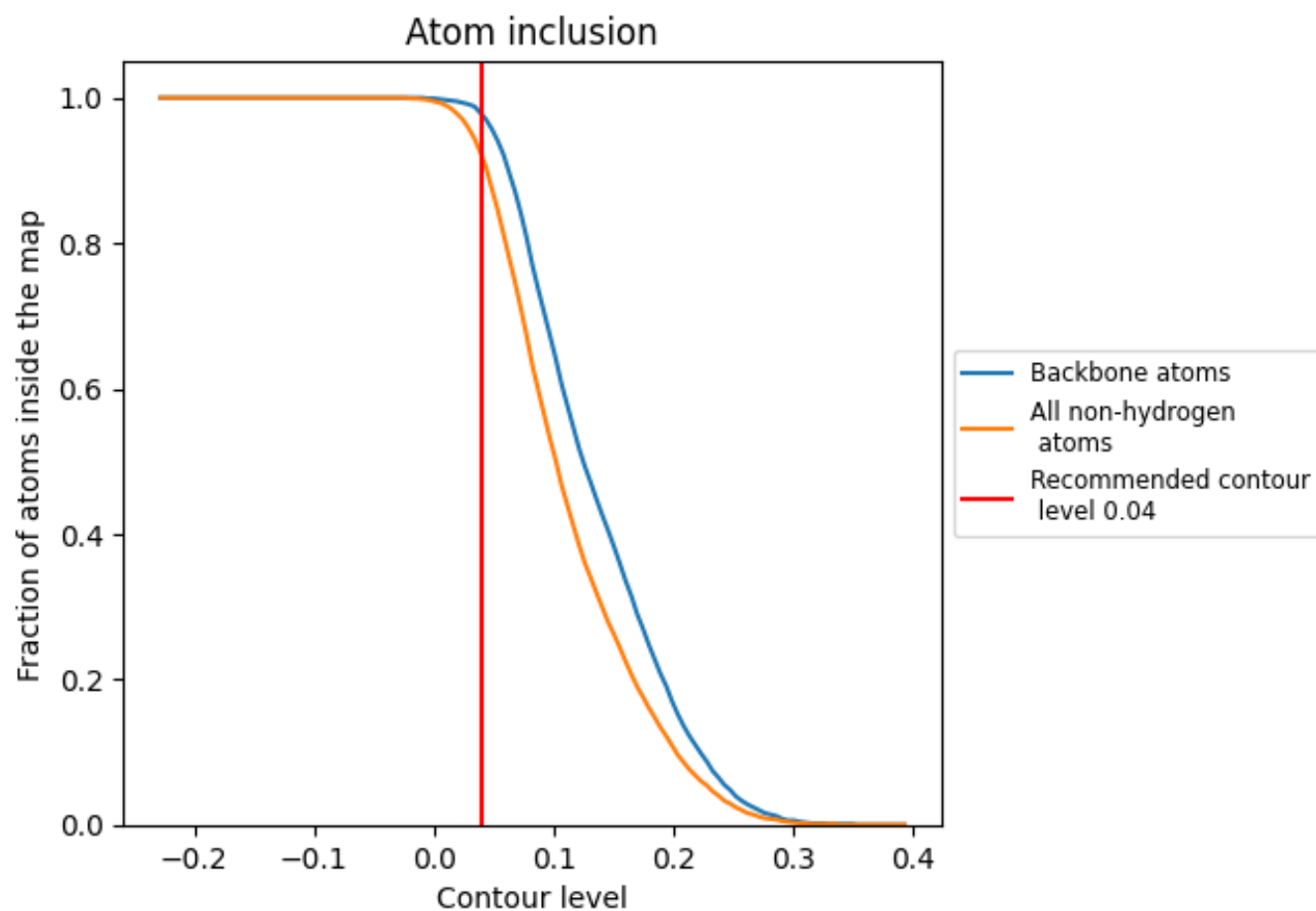
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 92% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9200	0.4050
A	0.9170	0.3980
C	0.9150	0.4040
E	0.9450	0.4180
G	0.8750	0.2880
H	0.9210	0.4650
J	0.9620	0.4740

1.0

0.0

<0.0