



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 08:28 PM EDT

PDB ID : 8DTM
EMDB ID : EMD-27705
Title : Cryo-EM structure of insulin receptor (IR) bound with S597 component 2
Authors : Park, J.; Li, J.; Mayer, J.P.; Ball, K.A.; Wu, J.Y.; Hall, C.; Accili, D.; Stowell, M.H.B.; Bai, X.C.; Choi, E.
Deposited on : 2022-07-26
Resolution : 3.50 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

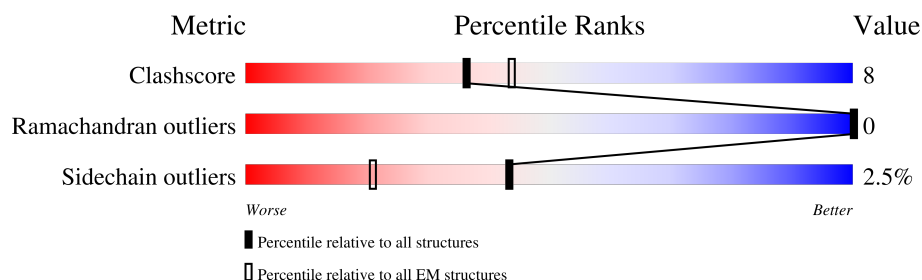
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1345	
1	B	1345	
2	C	20	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6498 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 Insulin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	444	Total	C	N	O	S	0	0
			3560	2250	615	656	39		
1	B	340	Total	C	N	O	S	0	0
			2793	1790	475	518	10		

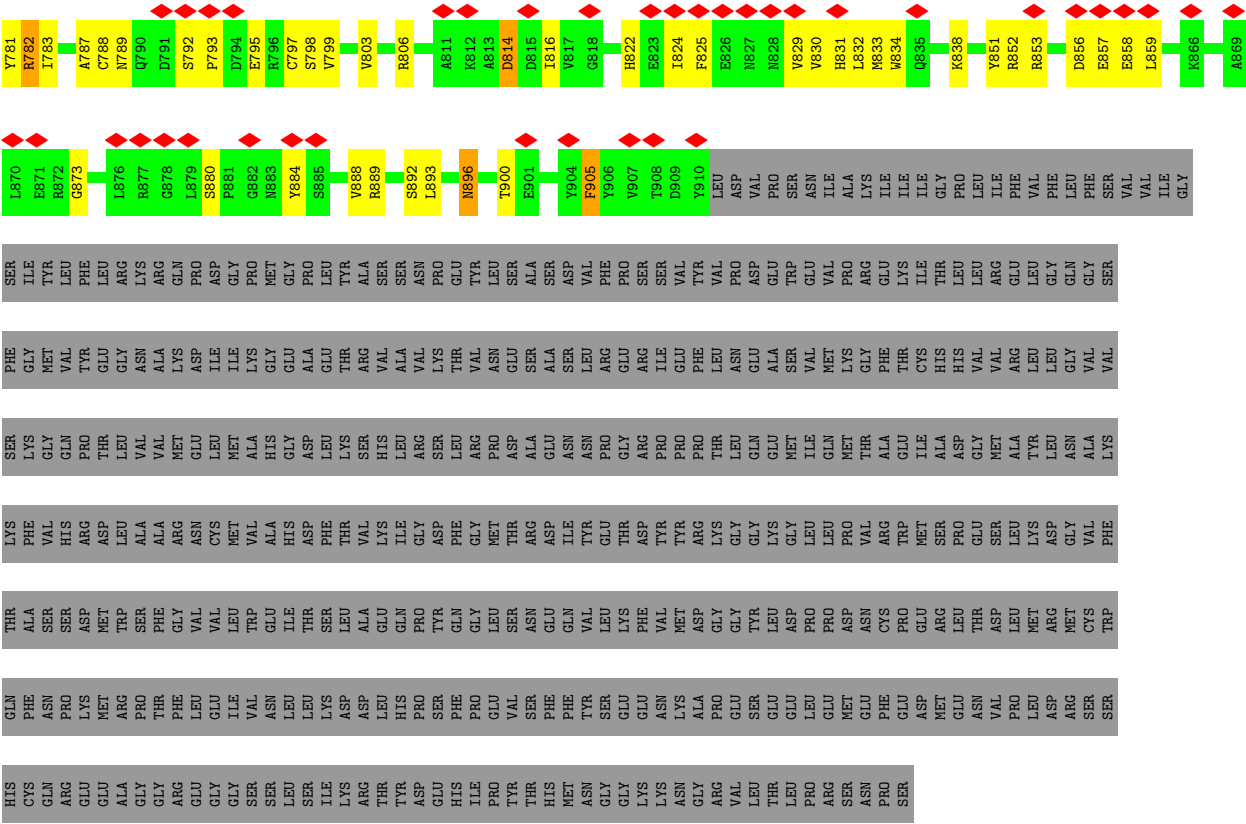
- Molecule 2 is a protein called Insulin mimetic peptide S597 component 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	18	Total	C	N	O	S	0	0
			145	89	23	31	2		

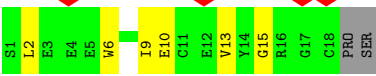
GLU	GLY	GLU	LEU	VAL	ASN	GLU	ASP
GLY	GLY	ILE	ILE	VAL	CYS	MET	ILE
SER	SER	VAL	VAL	TRP	VAL	ALA	LYS
SER	SER	ASN	ASN	GLU	ALA	HIS	GLY
LEU	LEU	LEU	ILE	ILE	HIS	ASP	GLU
SER	SER	LEU	THR	THR	ASP	ASP	ALA
ILE	ILE	LYS	SER	SER	PHE	LEU	GLU
ARG	ARG	ASP	THR	THR	THR	LYS	THR
THR	THR	LEU	ALA	VAL	VAL	HIS	VAL
TYR	TYR	GLU	GLU	GLN	ILE	LEU	ALA
ASP	ASP	PRO	PRO	PRO	GLY	ARG	VAL
HIS	HIS	SER	SER	TYR	ASP	SER	LYS
GLU	GLU	PHE	PHE	GLU	ASP	GLU	THR
ILE	ILE	PRO	ILE	GLY	GLY	ARG	VAL
PRO	PRO	VAL	VAL	VAL	TYR	ASN	ASN
TYR	TYR	VAL	SER	ASN	THR	GLY	ARG
HIS	HIS	SER	VAL	LYS	THR	GLY	GLU
THR	THR	GLU	PHE	PHE	ASP	ARG	ARG
ASN	ASN	ASN	VAL	VAL	TYR	PRO	ILE
GLY	GLY	GLY	GLY	GLY	LYS	THR	PHE
LYS	LYS	GLU	GLU	TYR	GLY	LEU	ASN
ASN	ASN	SER	SER	TYR	GLY	GLN	GLU
GLY	GLY	LEU	LEU	ASP	LEU	ILE	ALA
ARG	ARG	PRO	PRO	PRO	LEU	MET	VAL
VAL	VAL	GLU	GLY	GLY	PRO	GLN	LYS
LEU	LEU	GLU	TYR	TYR	PRO	THR	GLY
THR	THR	GLU	LEU	ASN	VAL	THR	GLY
THR	THR	PHE	THR	ASN	VAL	ASP	HIS
SER	SER	GLU	ASP	PRO	PRO	ASP	VAL
ASN	ASN	GLU	ASN	GLU	GLY	GLY	VAL
SER	SER	PHE	PHE	CYS	ARG	ALA	ARG
		THR	THR	PRO	TRP	GLU	LEU
		ASP	ASP	GLU	MET	ILE	LEU
		MET	MET	ARG	ASP	LEU	GLY
		GLU	GLU	LEU	PRO	ASN	VAL
		ASN	ASN	THR	GLY	ALA	VAL
		VAL	VAL	ASP	SER	VAL	VAL
		PRO	PRO	LEU	LYS	LYS	VAL
		ASP	ASP	MET	PHE	PHE	GLY
		SER	SER	CYS	ALA	VAL	LYS
		HIS	HIS	ASN	SER	HIS	GLN
		ARG	ARG	PRO	SER	ASP	GLN
		GLU	GLU	LYS	ASP	ARG	PRO
		THR	THR	GLN	THR	THR	THR
		ILE	ILE	PHE	PHE	THR	THR
		ASN	ASN	THR	THR	GLY	THR
		VAL	VAL	ASN	ASN	PHE	THR
		GLY	GLY	GLY	GLY	GLY	GLY
		ASP	ASP	THR	THR	ASP	ASP

- Molecule 1: Insulin receptor

[illegible]



● Molecule 2: Insulin mimetic peptide S597 component 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	135709	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.175	Depositor
Minimum map value	-0.104	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	324.0, 324.0, 324.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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	0.26	0/3636	0.50	0/4915
1	B	0.27	0/2871	0.52	0/3897
2	C	0.31	0/147	0.47	0/197
All	All	0.26	0/6654	0.51	0/9009

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	3560	0	3467	41	0
1	B	2793	0	2700	55	0
2	C	145	0	127	7	0
All	All	6498	0	6294	96	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 8.

The worst 5 of 96 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:612:GLN:HA	1:B:772:ILE:O	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:ARG:NH2	1:B:533:ASP:OD1	2.23	0.70
1:B:634:TRP:HE1	1:B:760:PRO:HB2	1.56	0.70
1:B:884:TYR:HB2	1:B:905:PHE:HE1	1.59	0.67
1:B:816:ILE:HD11	1:B:834:TRP:HB2	1.77	0.66

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	434/1345 (32%)	409 (94%)	25 (6%)	0	100	100
1	B	330/1345 (24%)	310 (94%)	20 (6%)	0	100	100
2	C	16/20 (80%)	16 (100%)	0	0	100	100
All	All	780/2710 (29%)	735 (94%)	45 (6%)	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	406/1211 (34%)	400 (98%)	6 (2%)	60	77
1	B	309/1211 (26%)	297 (96%)	12 (4%)	27	56
2	C	15/17 (88%)	15 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	730/2439 (30%)	712 (98%)	18 (2%)	43 67

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

Mol	Chain	Res	Type
1	B	822	HIS
1	B	905	PHE
1	B	896	ASN
1	B	634	TRP
1	B	814	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	337	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

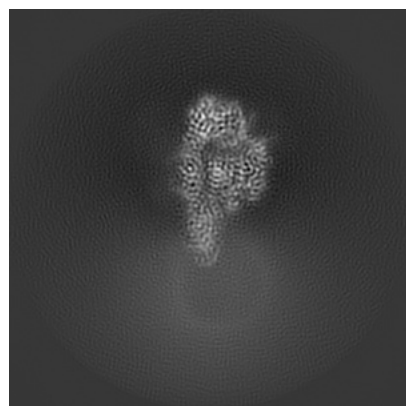
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27705. These allow visual inspection of the internal detail of the map and identification of artifacts.

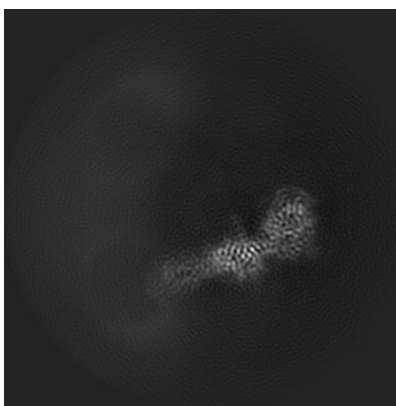
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

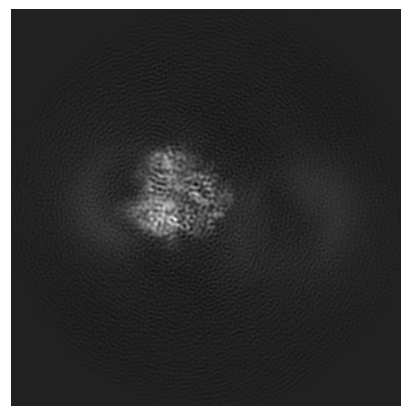
6.1.1 Primary map



X

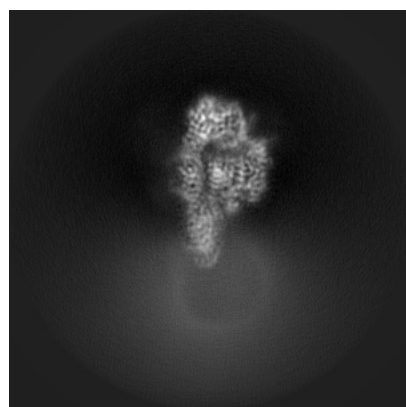


Y

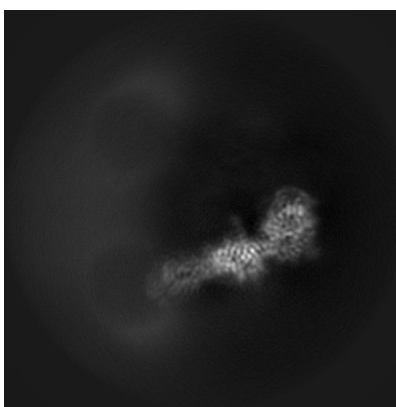


Z

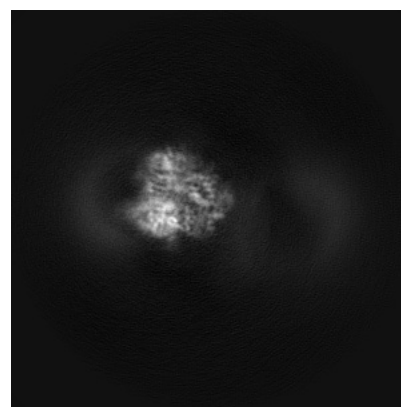
6.1.2 Raw map



X



Y

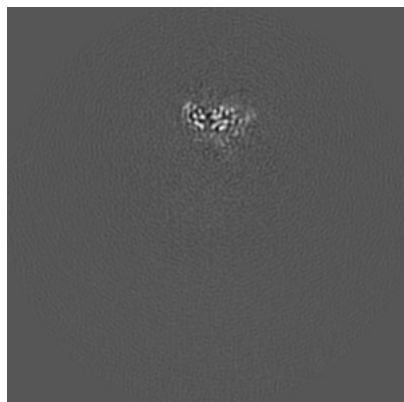


Z

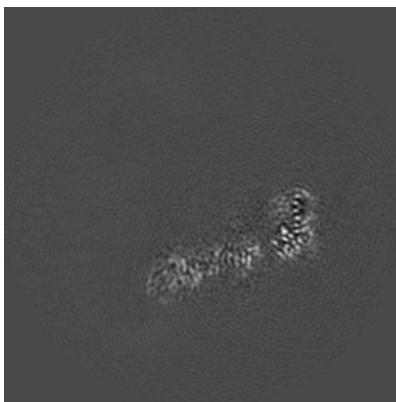
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

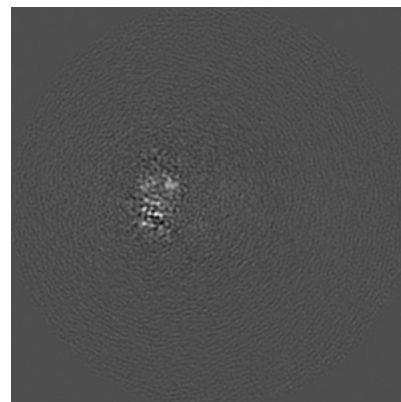
6.2.1 Primary map



X Index: 150

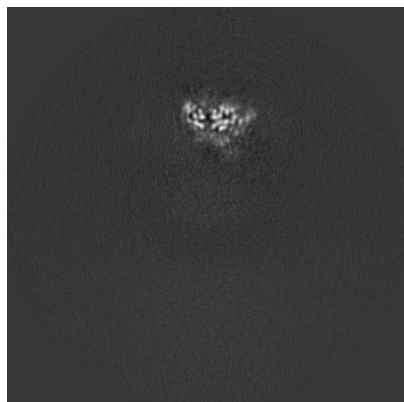


Y Index: 150

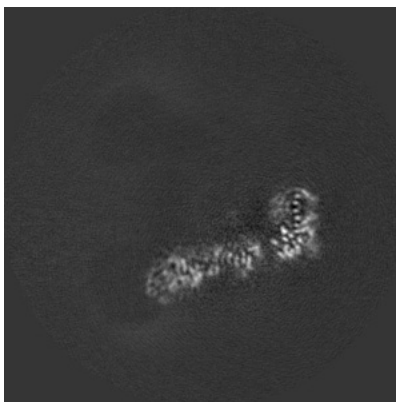


Z Index: 150

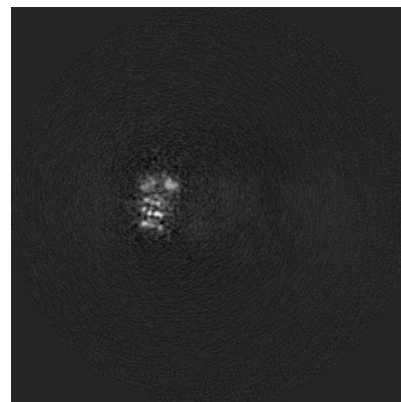
6.2.2 Raw map



X Index: 150



Y Index: 150

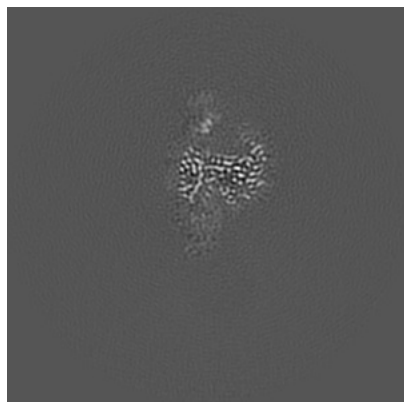


Z Index: 150

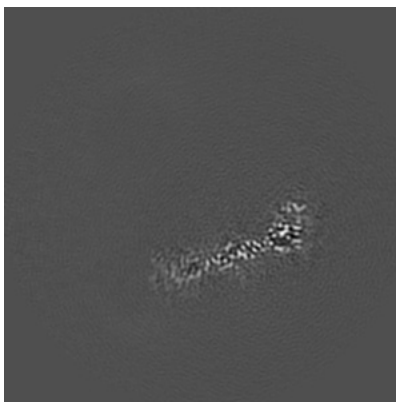
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

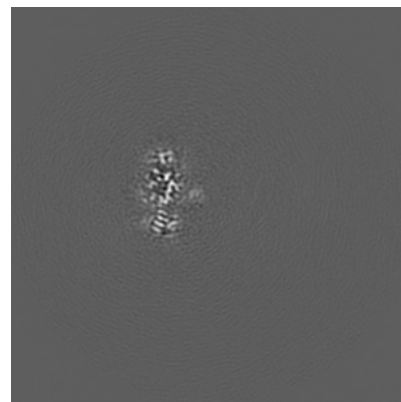
6.3.1 Primary map



X Index: 114

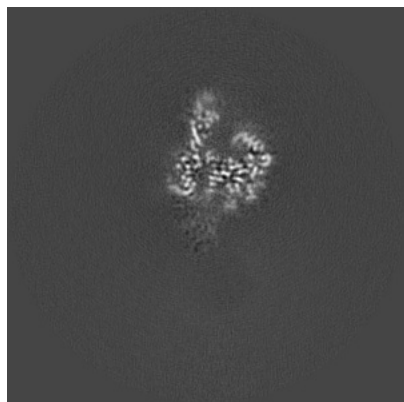


Y Index: 140

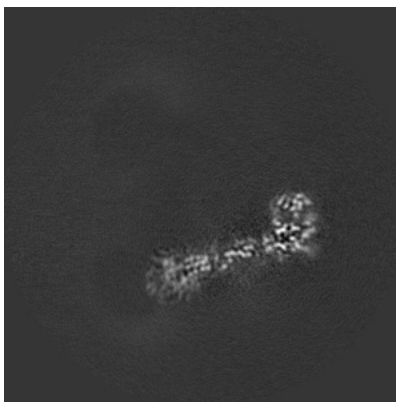


Z Index: 175

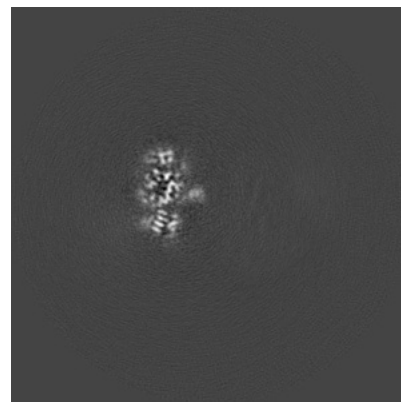
6.3.2 Raw map



X Index: 118



Y Index: 144

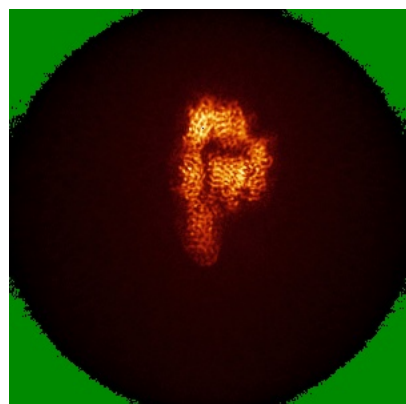


Z Index: 175

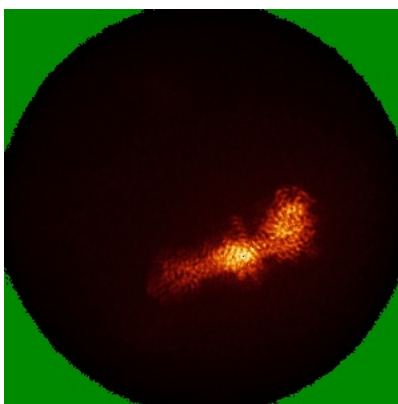
The images above show the largest variance slices of the map in three orthogonal directions.

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

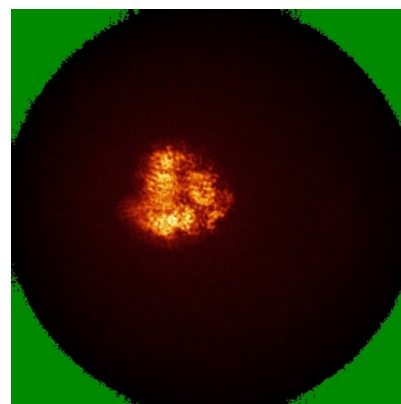
6.4.1 Primary map



X



Y

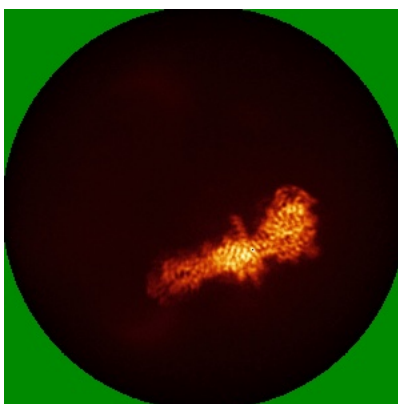


Z

6.4.2 Raw map



X



Y

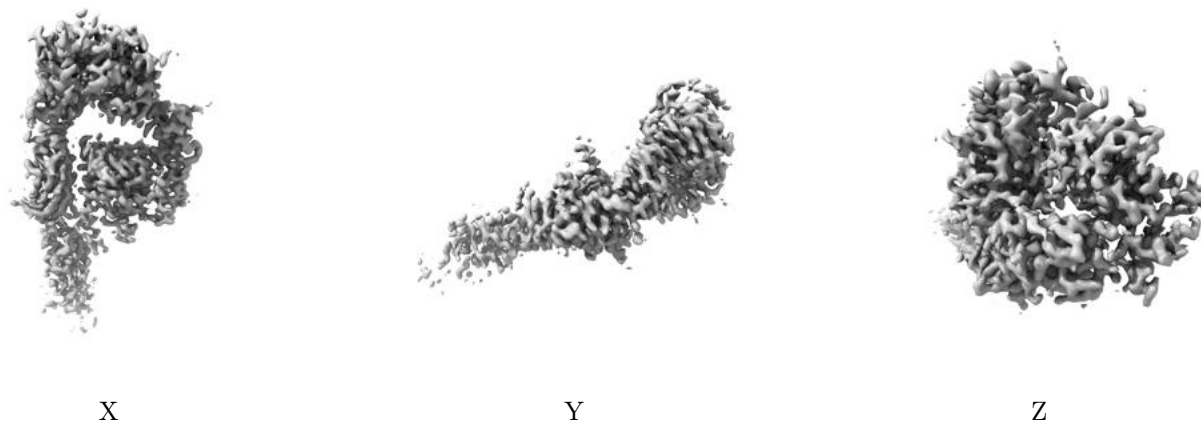


Z

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.

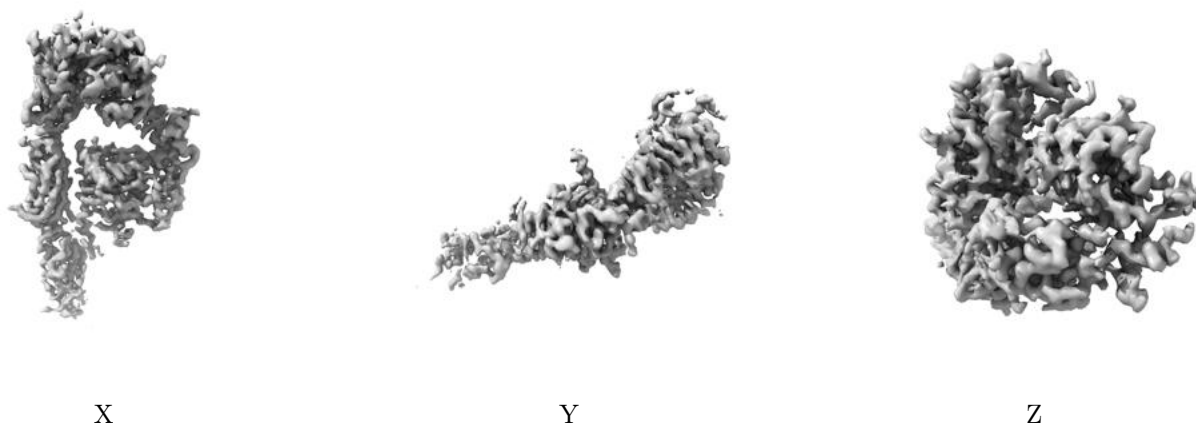
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. 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.

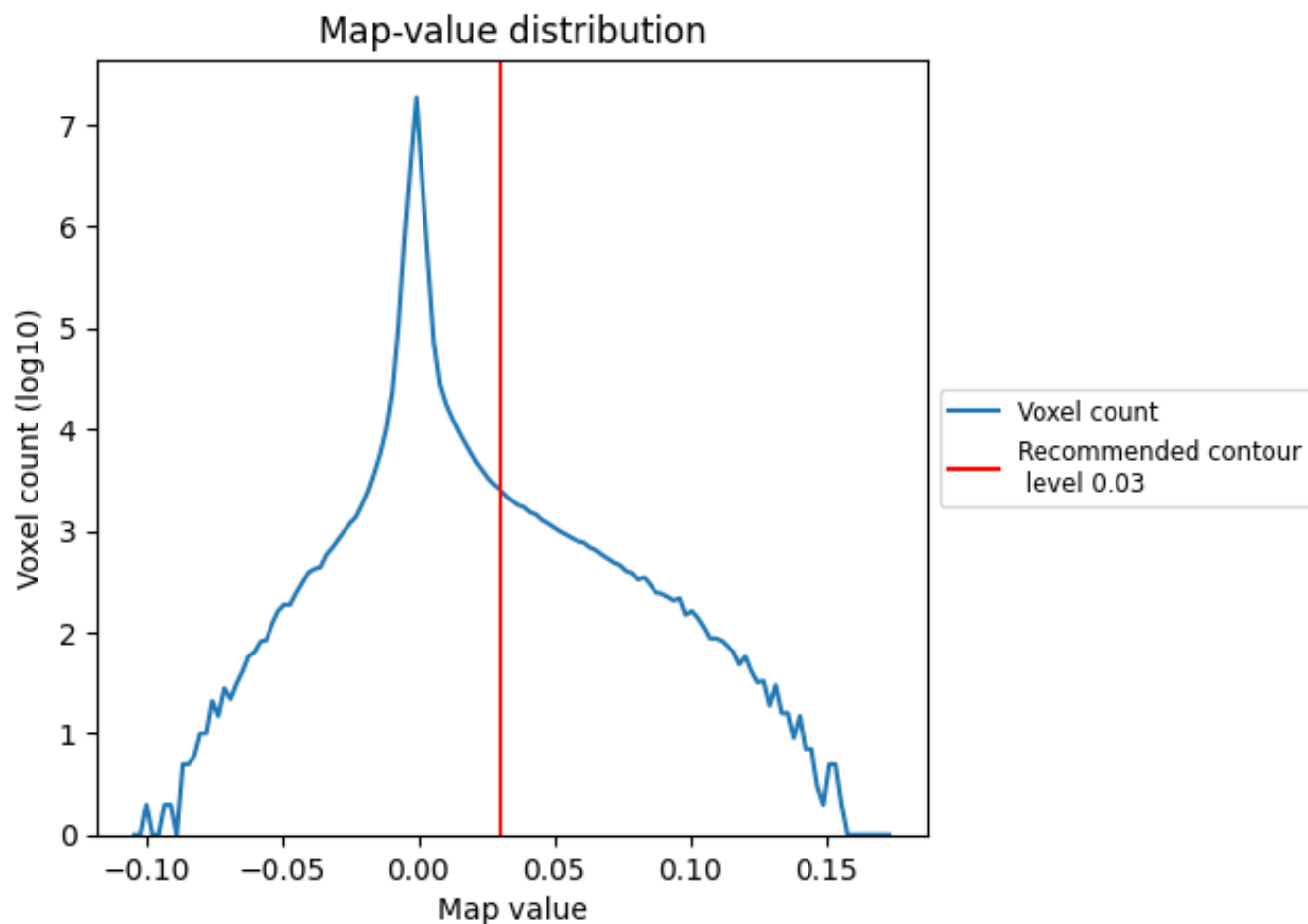
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

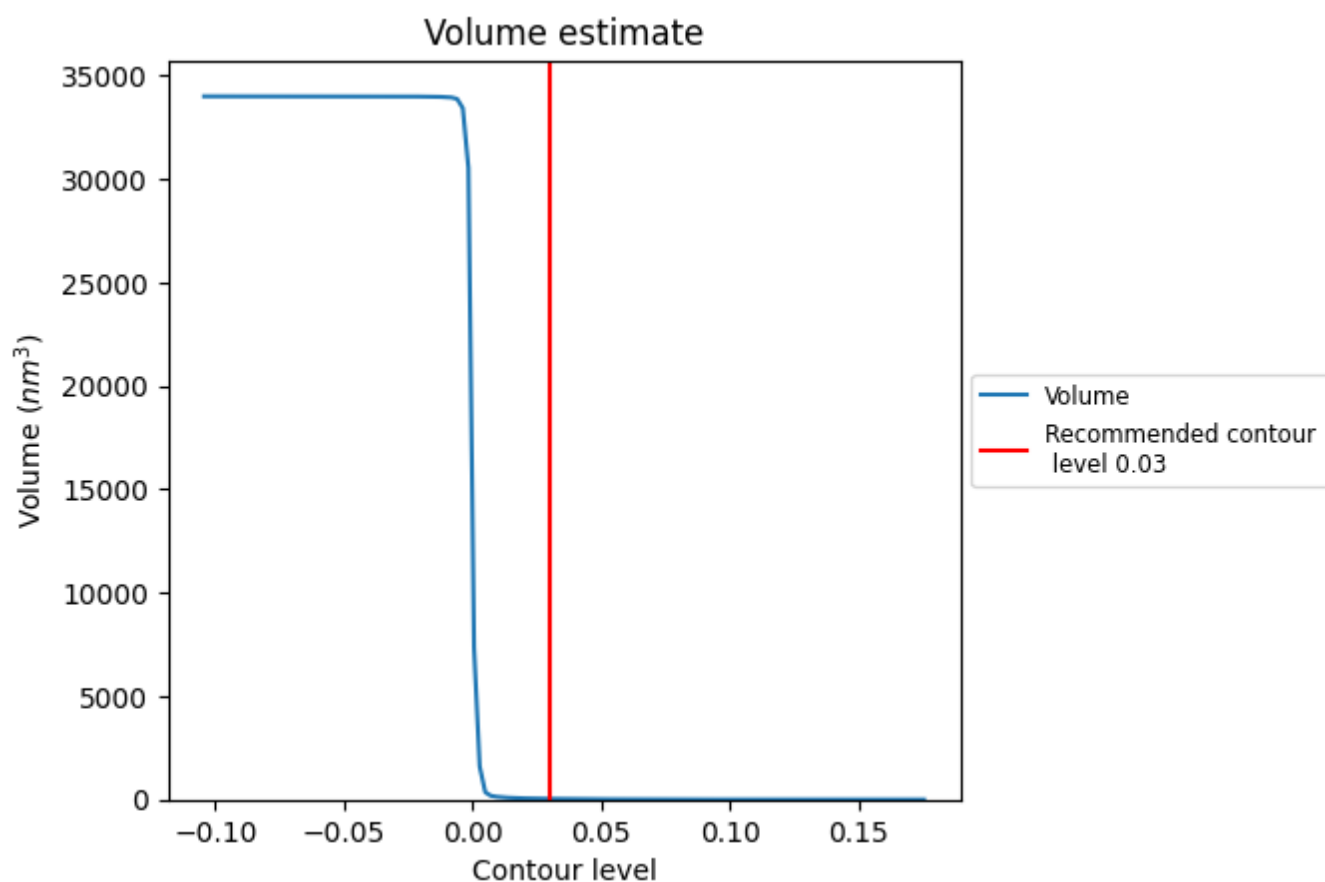
This section contains the results of statistical analysis of the map.

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.

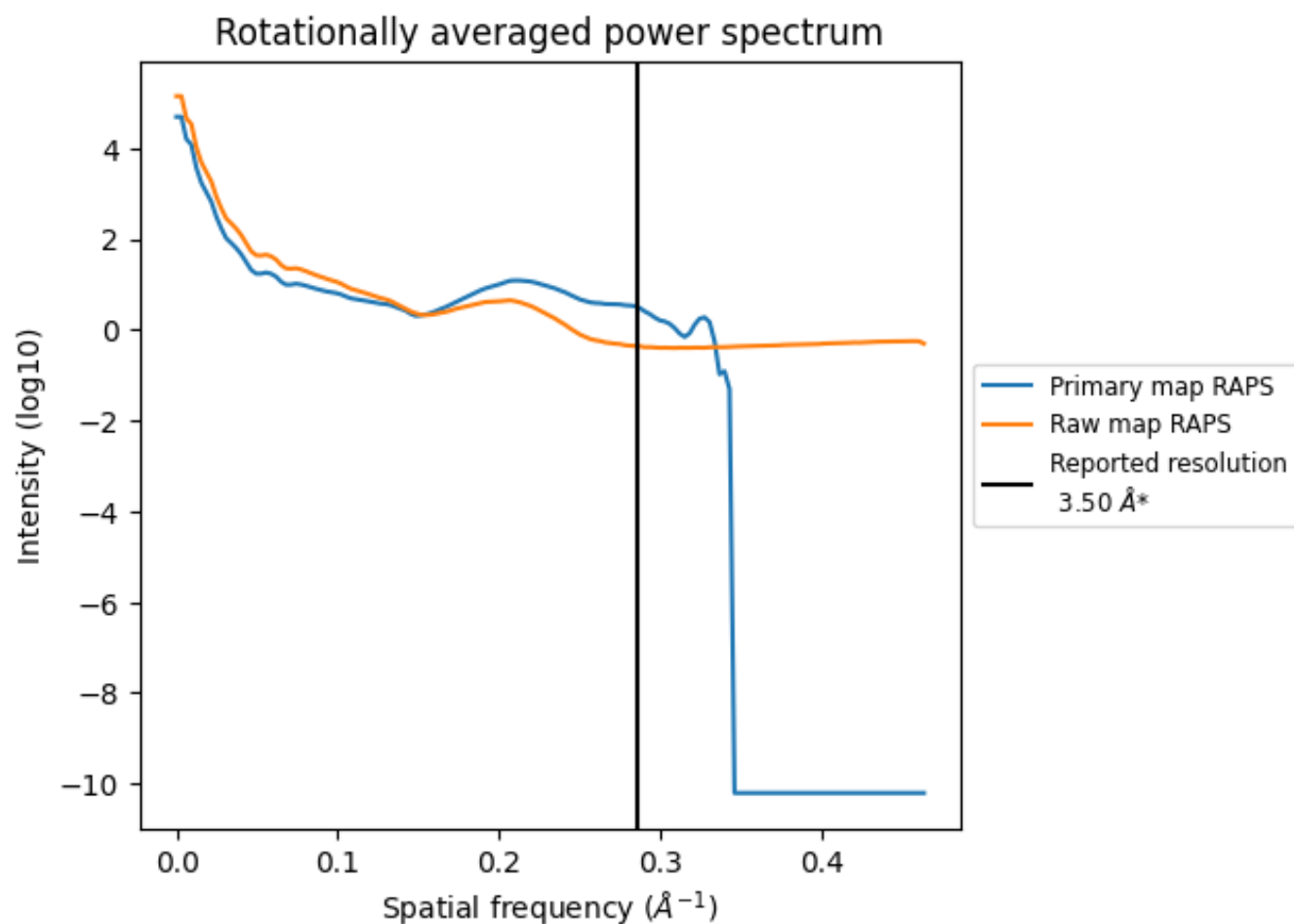
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 36 nm³; this corresponds to an approximate mass of 33 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 ⓘ

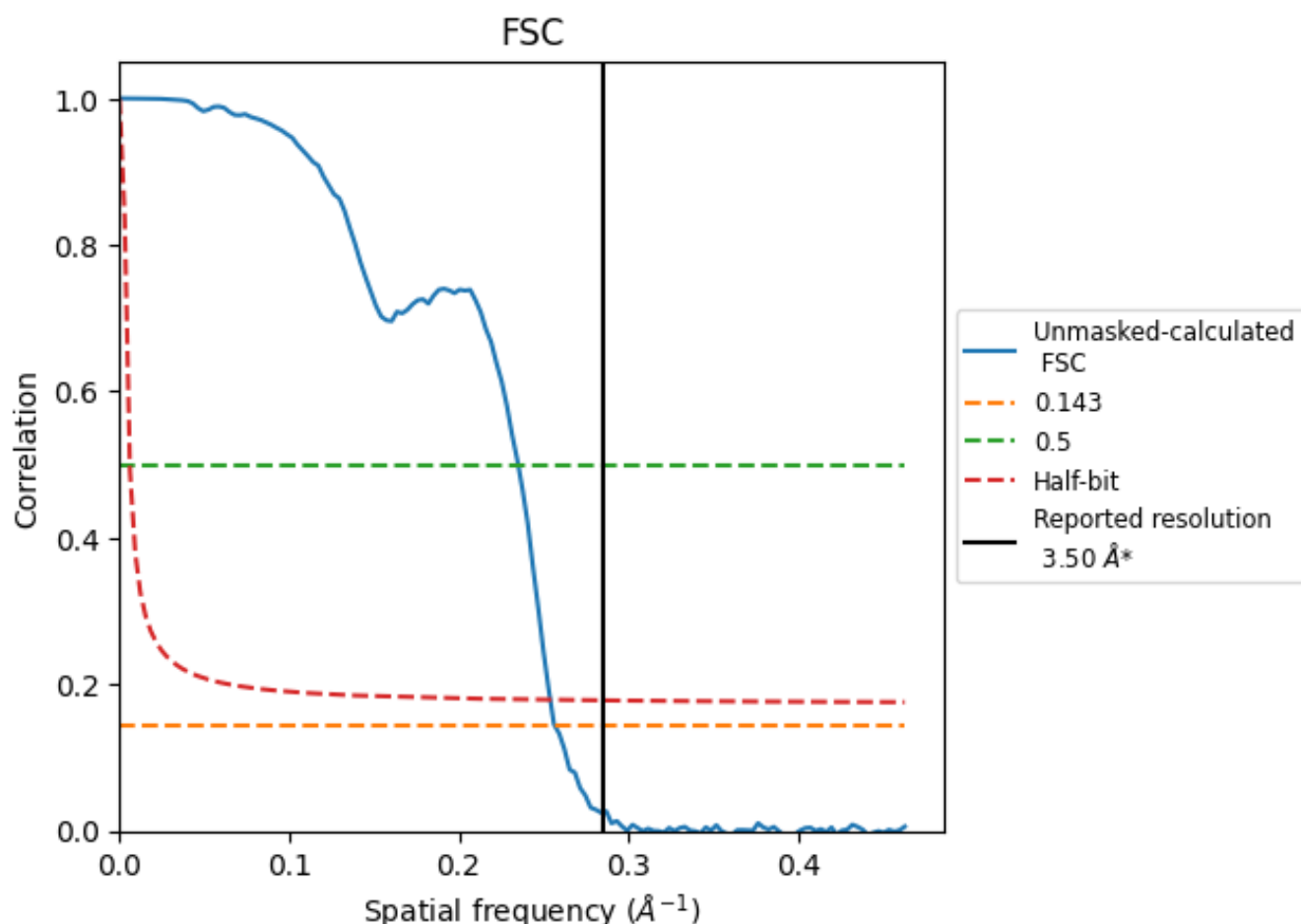


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 \AA^{-1}

8.2 Resolution estimates [i](#)

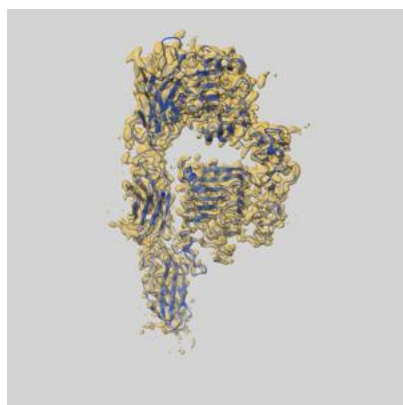
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.90	4.26	3.94

*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 3.90 differs from the reported value 3.5 by more than 10 %

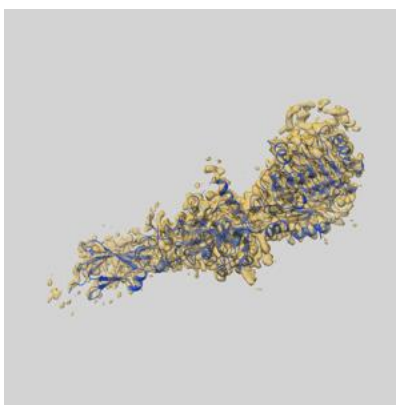
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27705 and PDB model 8DTM. Per-residue inclusion information can be found in section [3](#) on page [4](#).

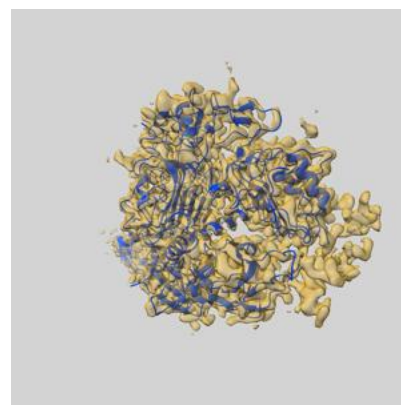
9.1 Map-model overlay [i](#)



X



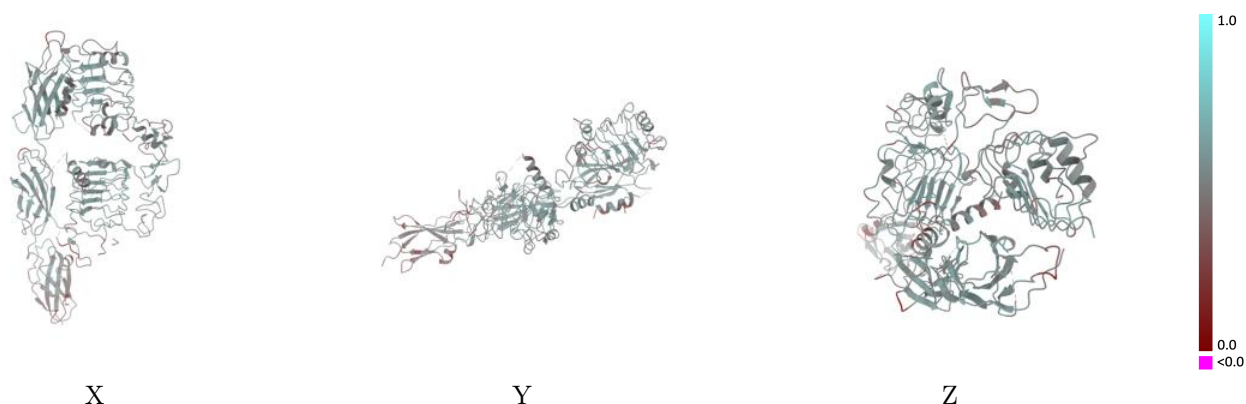
Y



Z

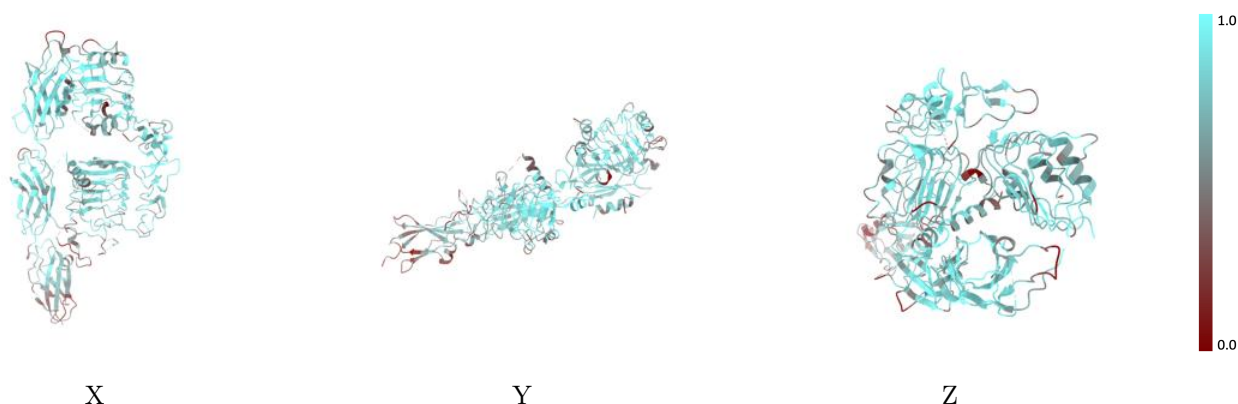
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



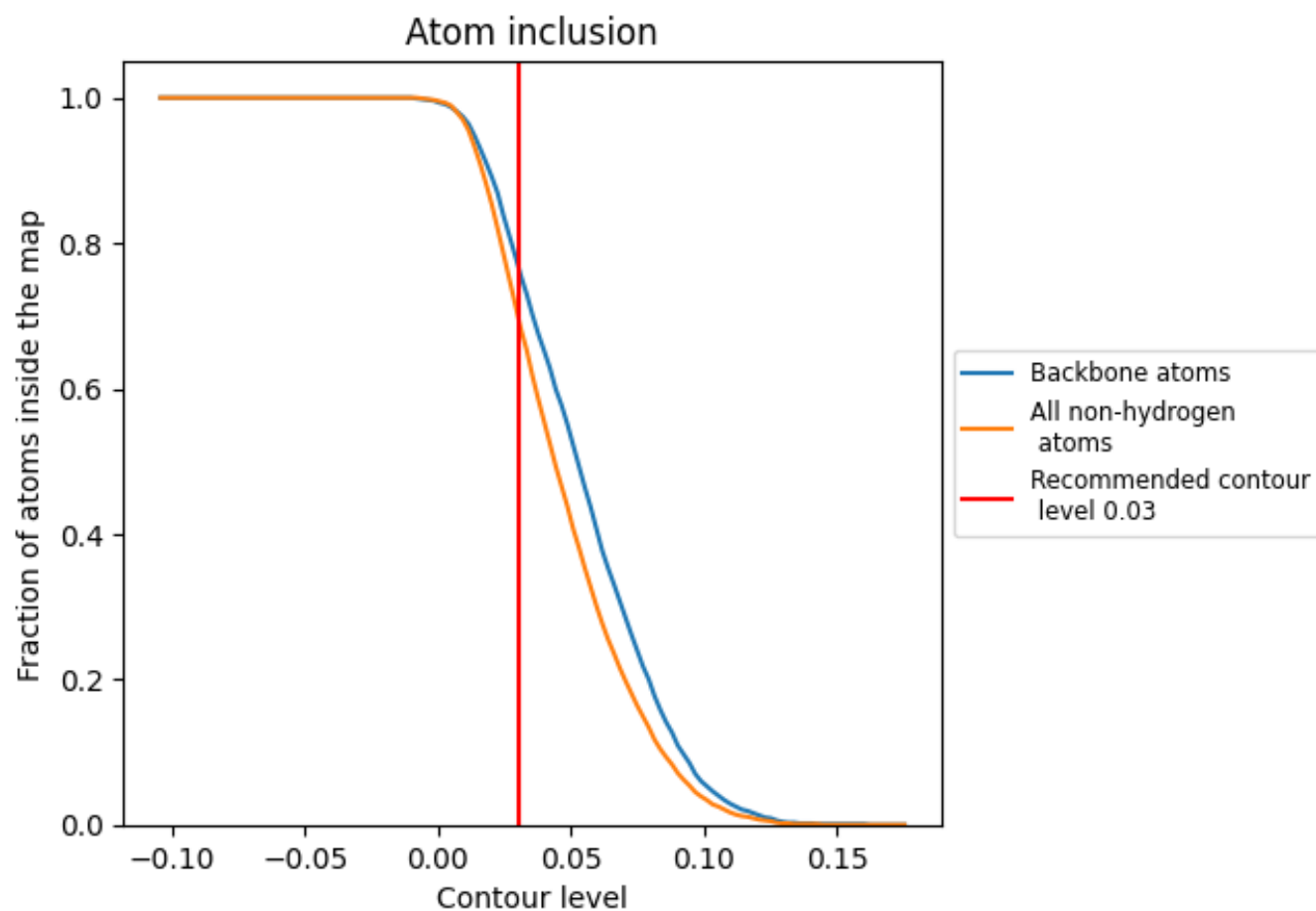
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 70% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7000	<div></div> 0.5060
A	<div></div> 0.7400	<div></div> 0.5200
B	<div></div> 0.6520	<div></div> 0.4900
C	<div></div> 0.6670	<div></div> 0.4670

