



wwPDB EM Validation Summary Report ⓘ

Jan 9, 2025 – 04:50 PM EST

PDB ID : 8VYB
EMDB ID : EMD-43655
Title : Cryo-EM structure of human core Rab3GAP1/2 complex
Authors : Nguyen, K.M.; Yip, C.K.
Deposited on : 2024-02-07
Resolution : 3.37 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.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) : 2.40

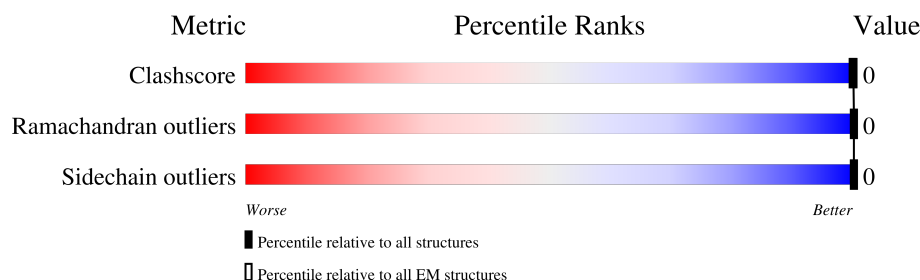
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.37 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	1038	<div> <div>8%</div> <div>45%</div> <div>55%</div> </div>
2	B	585	<div> <div>8%</div> <div>78%</div> <div>22%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7249 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Isoform 2 of Rab3 GTPase-activating protein catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	464	Total	C	N	O	S	0	0
			3700	2372	629	684	15		

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-49	MET	-	initiating methionine	UNP Q15042
A	-48	TRP	-	expression tag	UNP Q15042
A	-47	SER	-	expression tag	UNP Q15042
A	-46	HIS	-	expression tag	UNP Q15042
A	-45	PRO	-	expression tag	UNP Q15042
A	-44	GLN	-	expression tag	UNP Q15042
A	-43	PHE	-	expression tag	UNP Q15042
A	-42	GLU	-	expression tag	UNP Q15042
A	-41	LYS	-	expression tag	UNP Q15042
A	-40	GLY	-	expression tag	UNP Q15042
A	-39	GLY	-	expression tag	UNP Q15042
A	-38	GLY	-	expression tag	UNP Q15042
A	-37	SER	-	expression tag	UNP Q15042
A	-36	GLY	-	expression tag	UNP Q15042
A	-35	GLY	-	expression tag	UNP Q15042
A	-34	GLY	-	expression tag	UNP Q15042
A	-33	SER	-	expression tag	UNP Q15042
A	-32	GLY	-	expression tag	UNP Q15042
A	-31	GLY	-	expression tag	UNP Q15042
A	-30	GLY	-	expression tag	UNP Q15042
A	-29	SER	-	expression tag	UNP Q15042
A	-28	TRP	-	expression tag	UNP Q15042
A	-27	SER	-	expression tag	UNP Q15042
A	-26	HIS	-	expression tag	UNP Q15042
A	-25	PRO	-	expression tag	UNP Q15042
A	-24	GLN	-	expression tag	UNP Q15042
A	-23	PHE	-	expression tag	UNP Q15042
A	-22	GLU	-	expression tag	UNP Q15042

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	LYS	-	expression tag	UNP Q15042
A	-20	LEU	-	expression tag	UNP Q15042
A	-19	GLU	-	expression tag	UNP Q15042
A	-18	VAL	-	expression tag	UNP Q15042
A	-17	LEU	-	expression tag	UNP Q15042
A	-16	PHE	-	expression tag	UNP Q15042
A	-15	GLN	-	expression tag	UNP Q15042
A	-14	GLY	-	expression tag	UNP Q15042
A	-13	PRO	-	expression tag	UNP Q15042
A	-12	ARG	-	expression tag	UNP Q15042
A	-11	SER	-	expression tag	UNP Q15042
A	-10	GLU	-	expression tag	UNP Q15042
A	-9	ALA	-	expression tag	UNP Q15042
A	-8	ARG	-	expression tag	UNP Q15042
A	-7	GLY	-	expression tag	UNP Q15042
A	-6	ILE	-	expression tag	UNP Q15042
A	-5	GLN	-	expression tag	UNP Q15042
A	-4	ARG	-	expression tag	UNP Q15042
A	-3	PRO	-	expression tag	UNP Q15042
A	-2	THR	-	expression tag	UNP Q15042
A	-1	SER	-	expression tag	UNP Q15042
A	0	THR	-	expression tag	UNP Q15042
A	975	SER	-	expression tag	UNP Q15042
A	976	SER	-	expression tag	UNP Q15042
A	977	ASP	-	expression tag	UNP Q15042
A	978	THR	-	expression tag	UNP Q15042
A	979	SER	-	expression tag	UNP Q15042
A	980	PHE	-	expression tag	UNP Q15042
A	981	PHE	-	expression tag	UNP Q15042

- Molecule 2 is a protein called Rab3 GTPase-activating protein non-catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	456	Total	C	N	O	S	0	0
			3549	2265	609	655	20		

There are 38 discrepancies between the modelled and reference sequences:

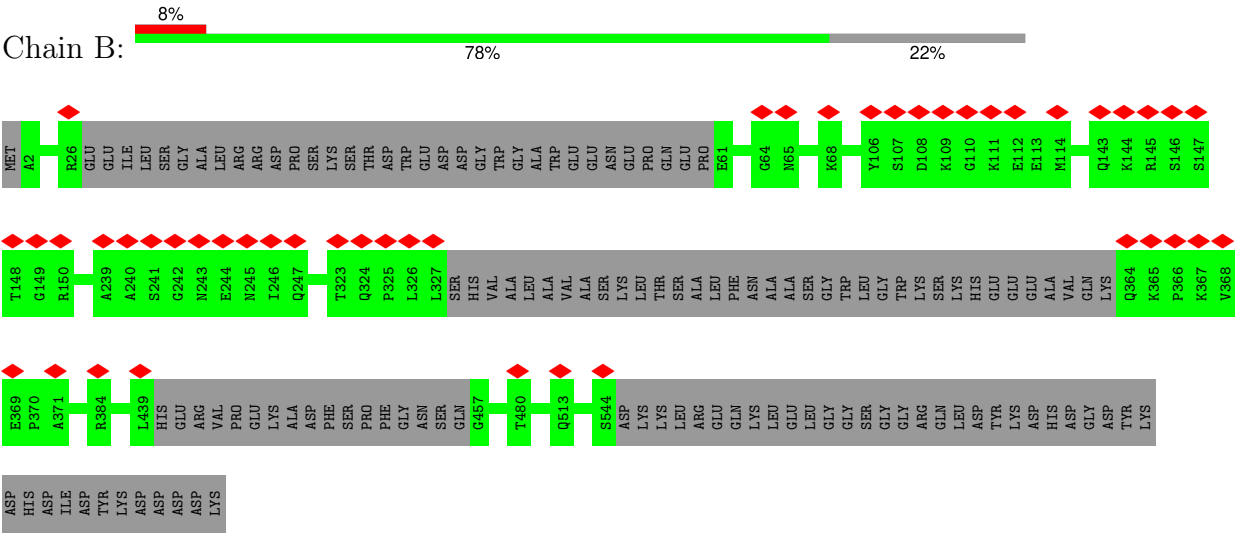
Chain	Residue	Modelled	Actual	Comment	Reference
B	548	LEU	-	expression tag	UNP Q9H2M9
B	549	ARG	-	expression tag	UNP Q9H2M9
B	550	GLU	-	expression tag	UNP Q9H2M9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	551	GLN	-	expression tag	UNP Q9H2M9
B	552	LYS	-	expression tag	UNP Q9H2M9
B	553	LEU	-	expression tag	UNP Q9H2M9
B	554	GLU	-	expression tag	UNP Q9H2M9
B	555	LEU	-	expression tag	UNP Q9H2M9
B	556	GLY	-	expression tag	UNP Q9H2M9
B	557	GLY	-	expression tag	UNP Q9H2M9
B	558	SER	-	expression tag	UNP Q9H2M9
B	559	GLY	-	expression tag	UNP Q9H2M9
B	560	GLY	-	expression tag	UNP Q9H2M9
B	561	ARG	-	expression tag	UNP Q9H2M9
B	562	GLN	-	expression tag	UNP Q9H2M9
B	563	LEU	-	expression tag	UNP Q9H2M9
B	564	ASP	-	expression tag	UNP Q9H2M9
B	565	TYR	-	expression tag	UNP Q9H2M9
B	566	LYS	-	expression tag	UNP Q9H2M9
B	567	ASP	-	expression tag	UNP Q9H2M9
B	568	HIS	-	expression tag	UNP Q9H2M9
B	569	ASP	-	expression tag	UNP Q9H2M9
B	570	GLY	-	expression tag	UNP Q9H2M9
B	571	ASP	-	expression tag	UNP Q9H2M9
B	572	TYR	-	expression tag	UNP Q9H2M9
B	573	LYS	-	expression tag	UNP Q9H2M9
B	574	ASP	-	expression tag	UNP Q9H2M9
B	575	HIS	-	expression tag	UNP Q9H2M9
B	576	ASP	-	expression tag	UNP Q9H2M9
B	577	ILE	-	expression tag	UNP Q9H2M9
B	578	ASP	-	expression tag	UNP Q9H2M9
B	579	TYR	-	expression tag	UNP Q9H2M9
B	580	LYS	-	expression tag	UNP Q9H2M9
B	581	ASP	-	expression tag	UNP Q9H2M9
B	582	ASP	-	expression tag	UNP Q9H2M9
B	583	ASP	-	expression tag	UNP Q9H2M9
B	584	ASP	-	expression tag	UNP Q9H2M9
B	585	LYS	-	expression tag	UNP Q9H2M9

● Molecule 2: Rab3 GTPase-activating protein non-catalytic subunit



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	170636	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	215000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.543	Depositor
Minimum map value	-1.198	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	377.59998, 377.59998, 377.59998	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.59, 0.59, 0.59	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	0.44	0/3792	0.55	0/5138
2	B	0.46	0/3632	0.55	0/4938
All	All	0.45	0/7424	0.55	0/10076

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

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	3700	0	3674	0	0
2	B	3549	0	3535	0	0
All	All	7249	0	7209	0	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 0.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	456/1038 (44%)	431 (94%)	25 (6%)	0	100	100
2	B	448/585 (77%)	424 (95%)	24 (5%)	0	100	100
All	All	904/1623 (56%)	855 (95%)	49 (5%)	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	412/904 (46%)	412 (100%)	0	100	100
2	B	389/497 (78%)	389 (100%)	0	100	100
All	All	801/1401 (57%)	801 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

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.

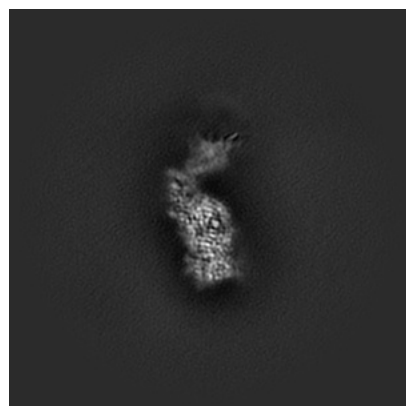
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43655. These allow visual inspection of the internal detail of the map and identification of artifacts.

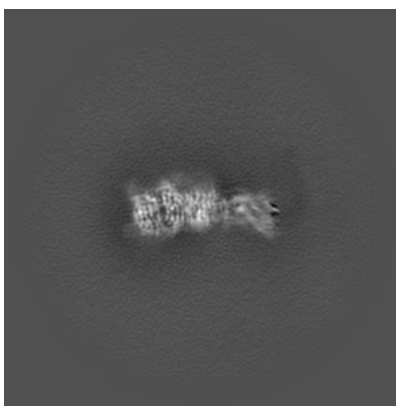
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

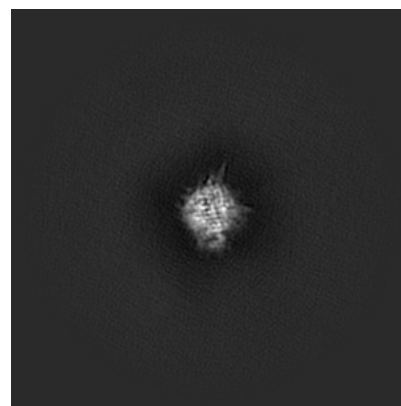
6.1.1 Primary map



X

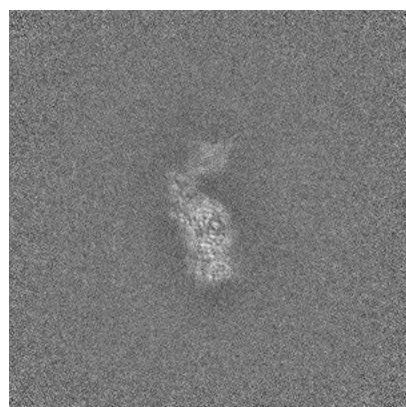


Y



Z

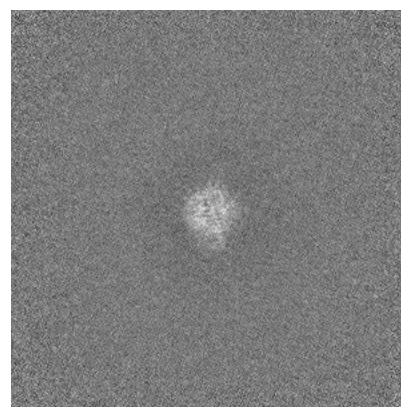
6.1.2 Raw map



X



Y

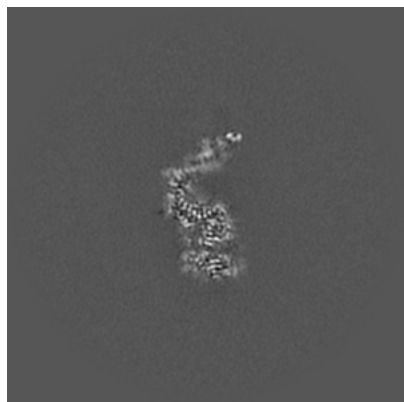


Z

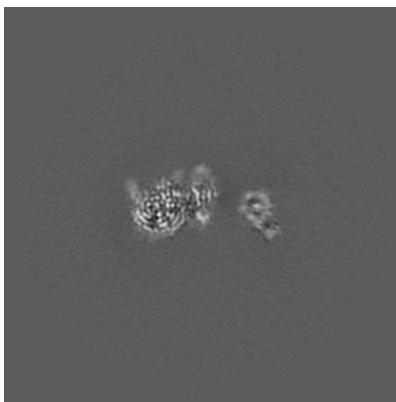
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

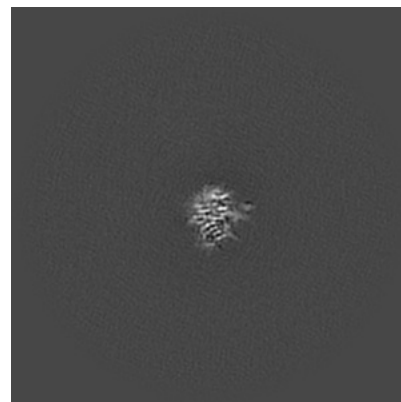
6.2.1 Primary map



X Index: 320

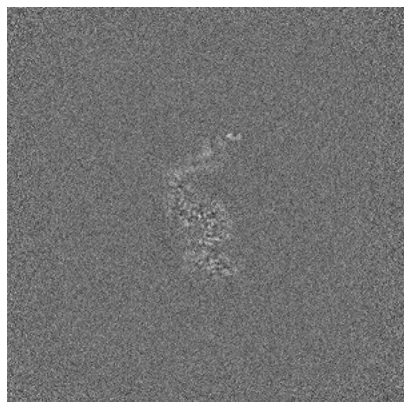


Y Index: 320

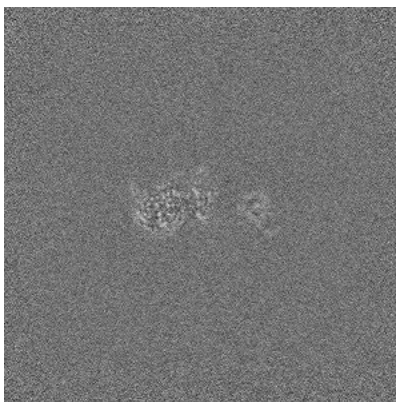


Z Index: 320

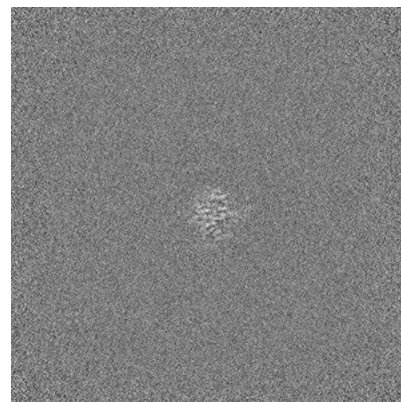
6.2.2 Raw map



X Index: 320



Y Index: 320

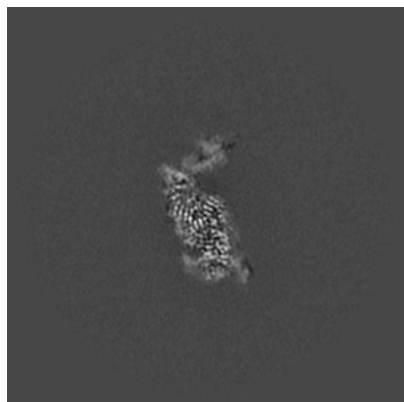


Z Index: 320

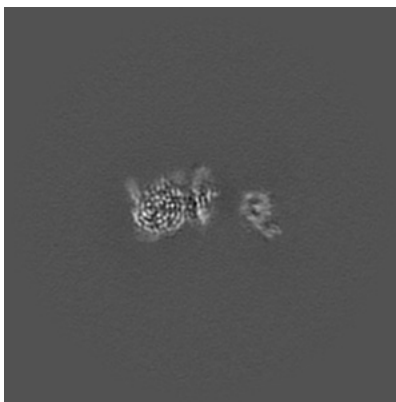
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

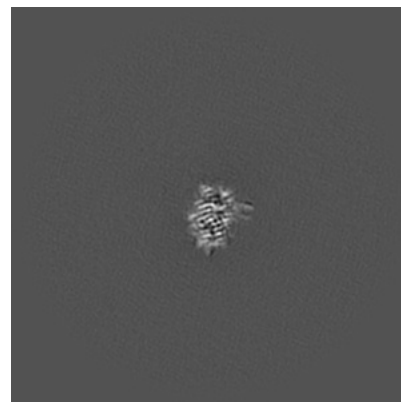
6.3.1 Primary map



X Index: 334

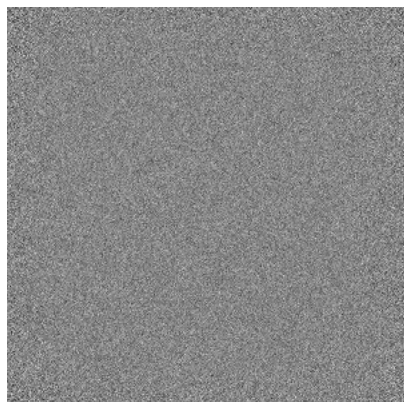


Y Index: 322

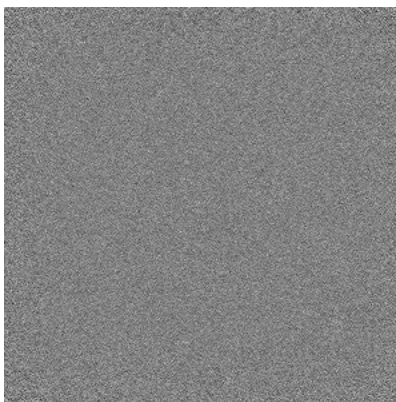


Z Index: 311

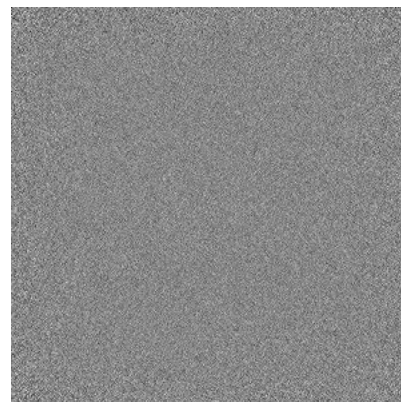
6.3.2 Raw map



X Index: 0



Y Index: 0

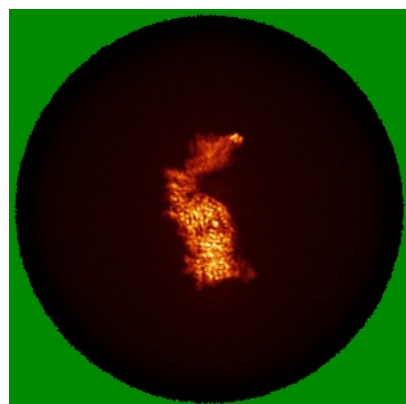


Z Index: 639

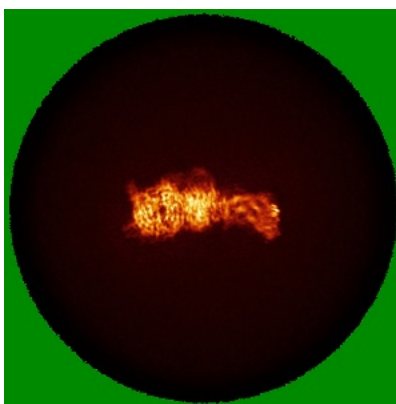
The images above show the largest variance slices of the map in three orthogonal directions.

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

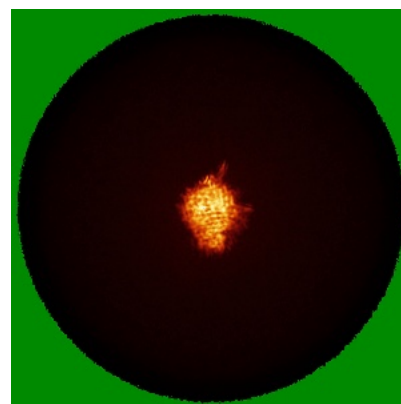
6.4.1 Primary map



X

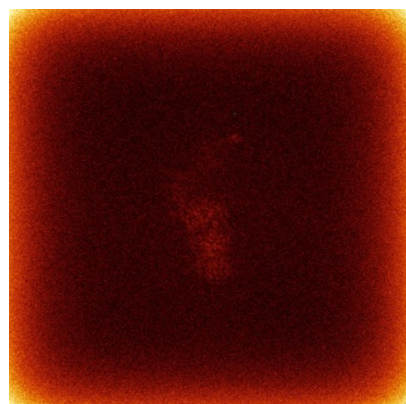


Y

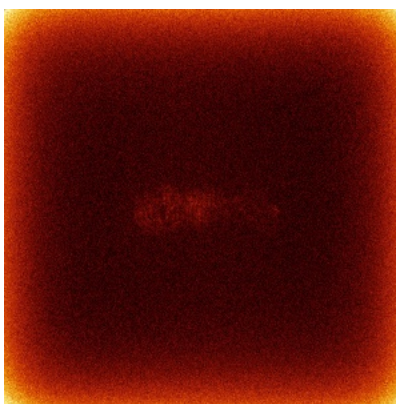


Z

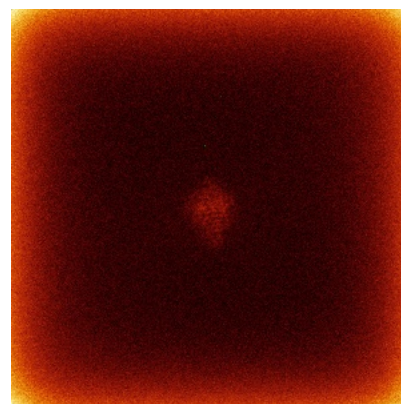
6.4.2 Raw map



X



Y

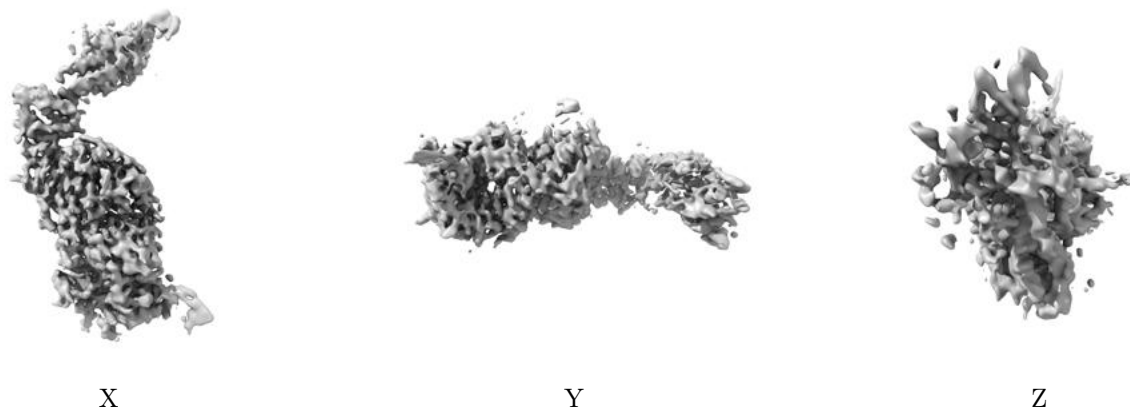


Z

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.

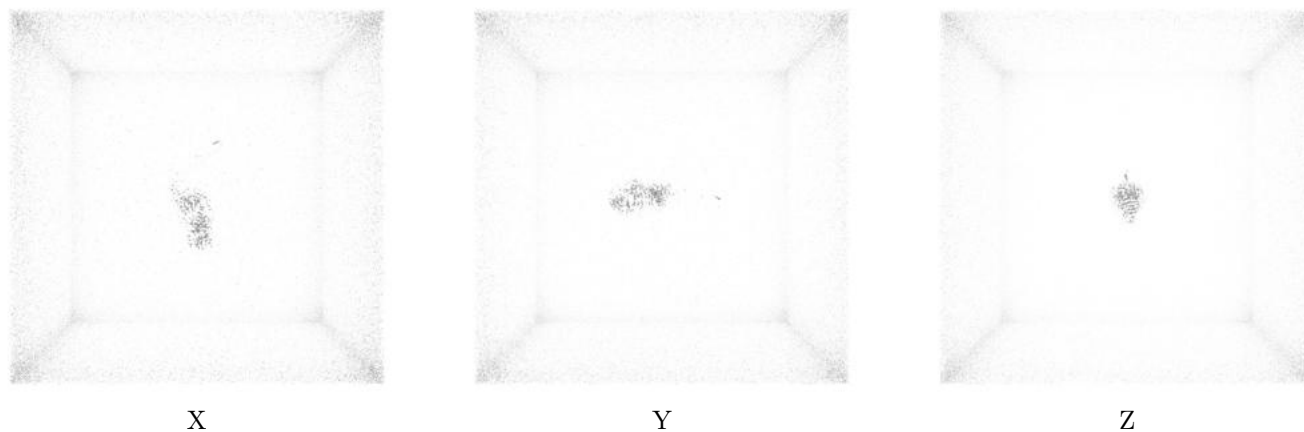
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

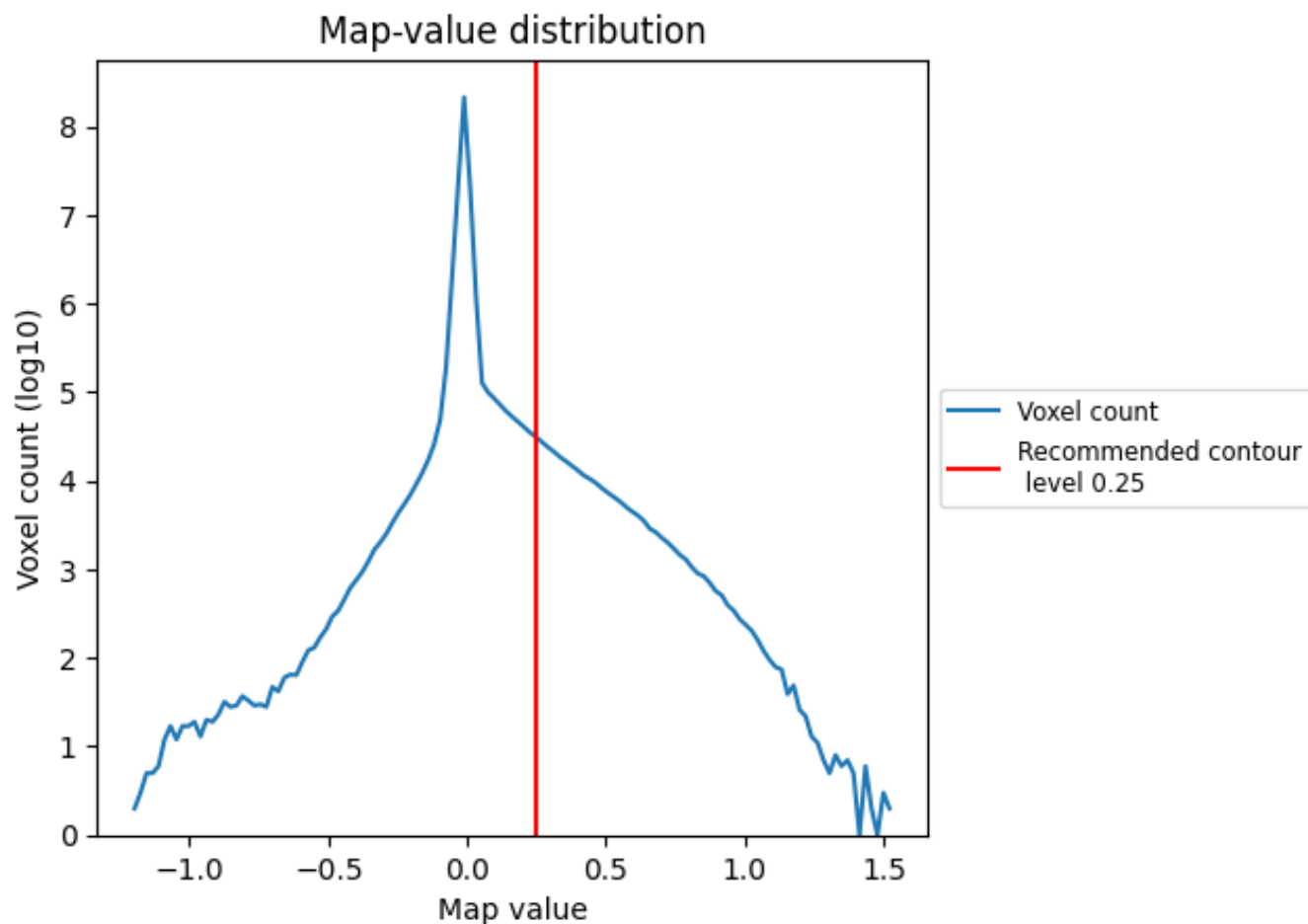
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

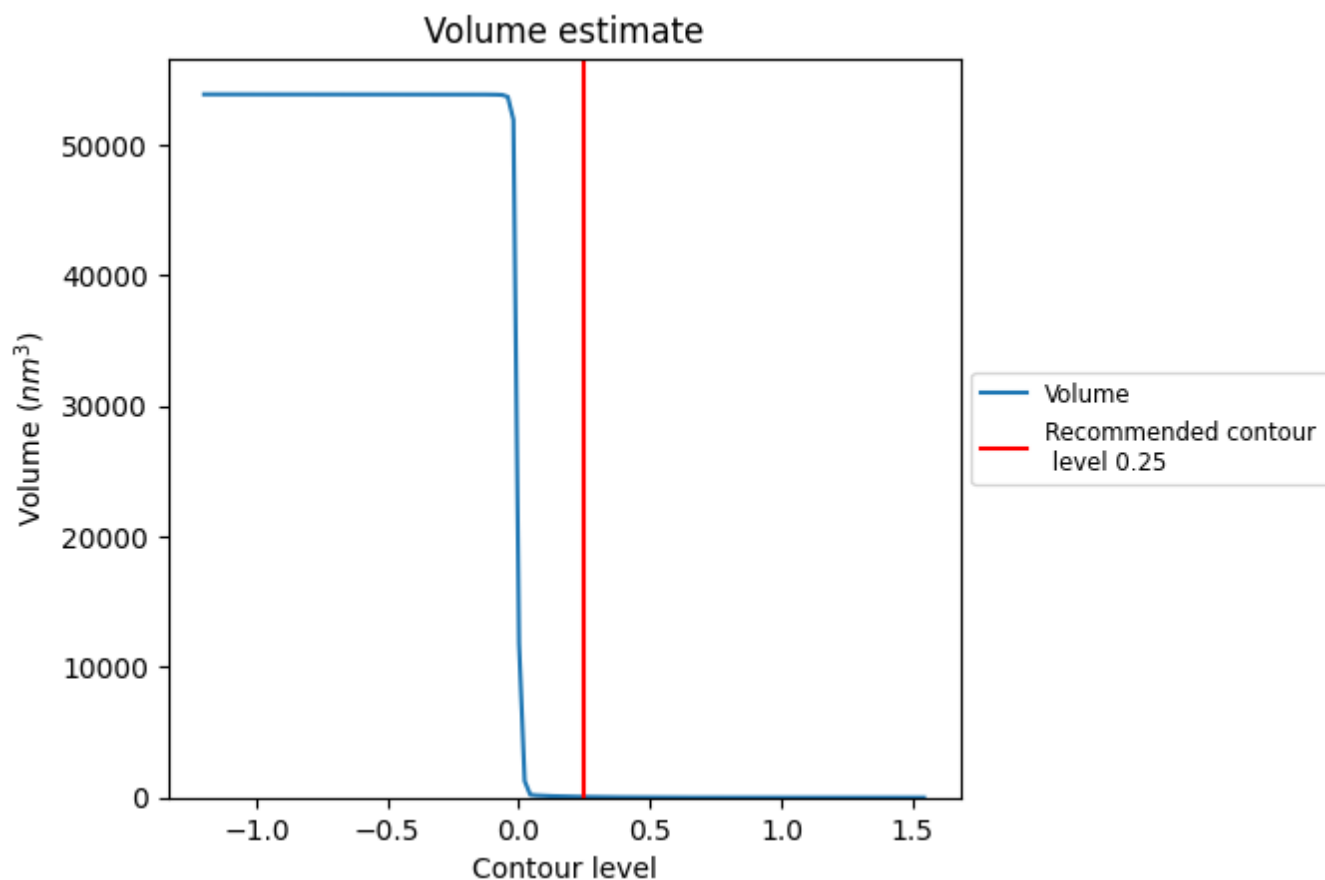
This section contains the results of statistical analysis of the map.

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.

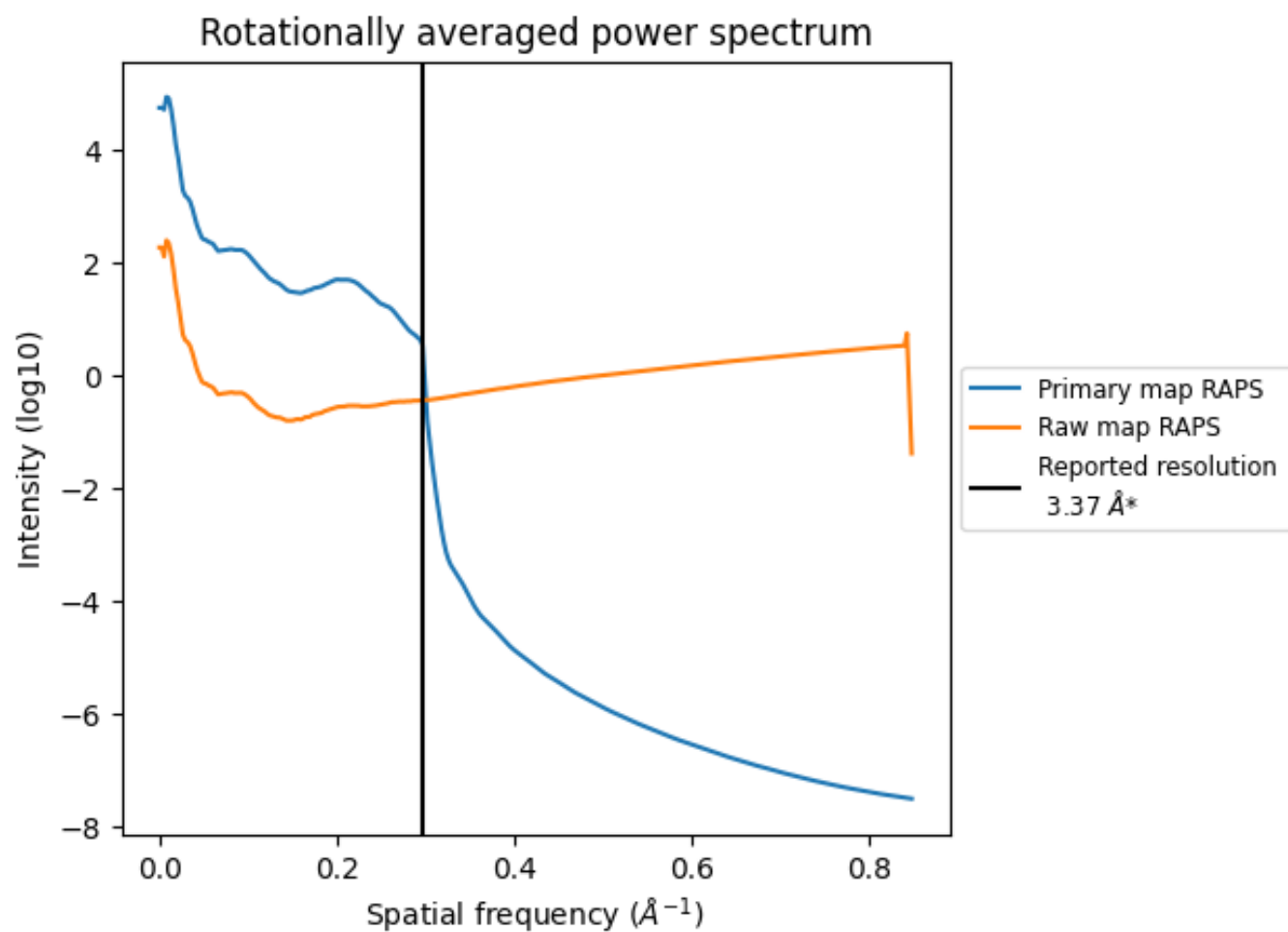
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 54 nm³; this corresponds to an approximate mass of 49 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 ⓘ

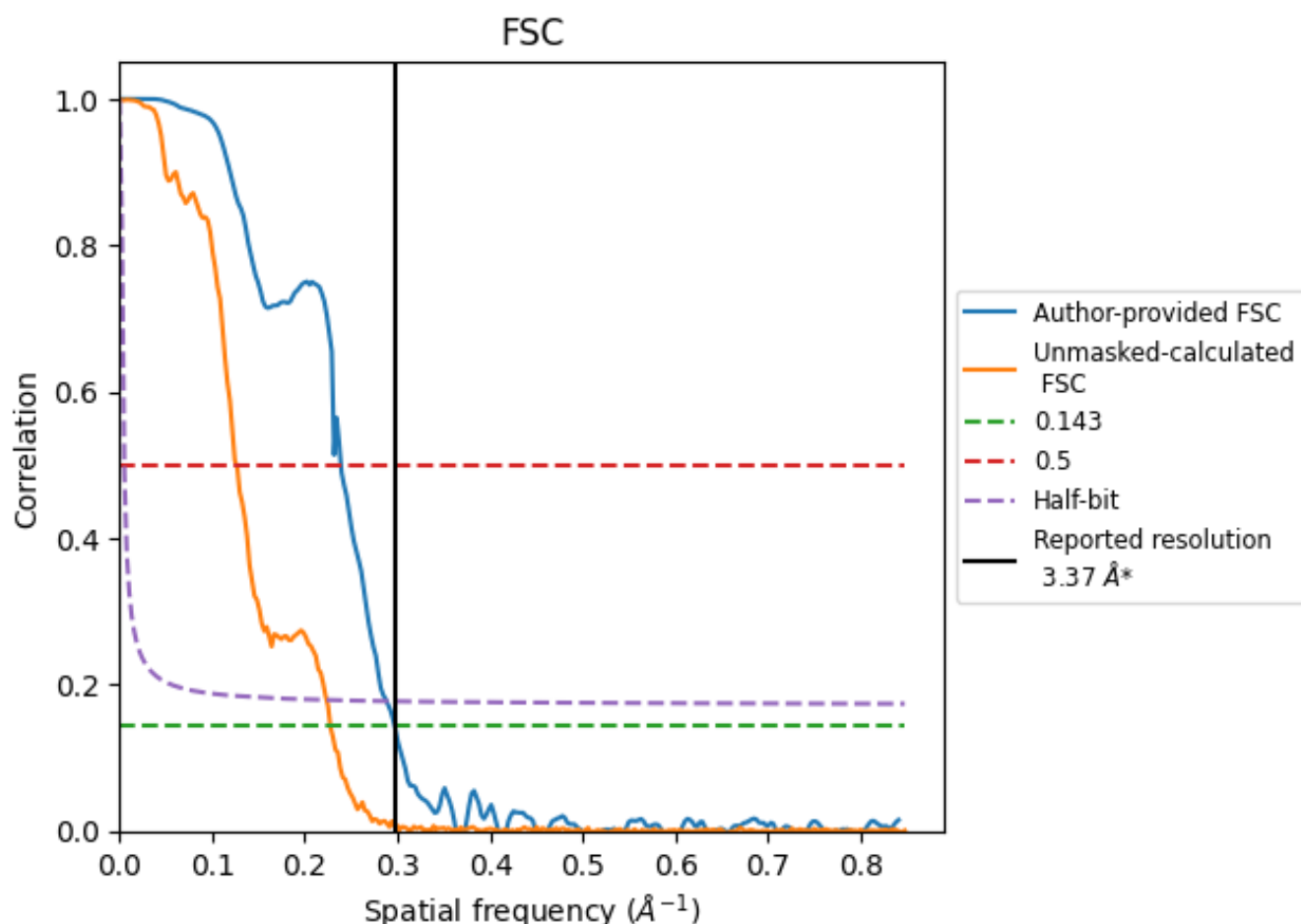


*Reported resolution corresponds to spatial frequency of 0.297 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.297 Å⁻¹

8.2 Resolution estimates [i](#)

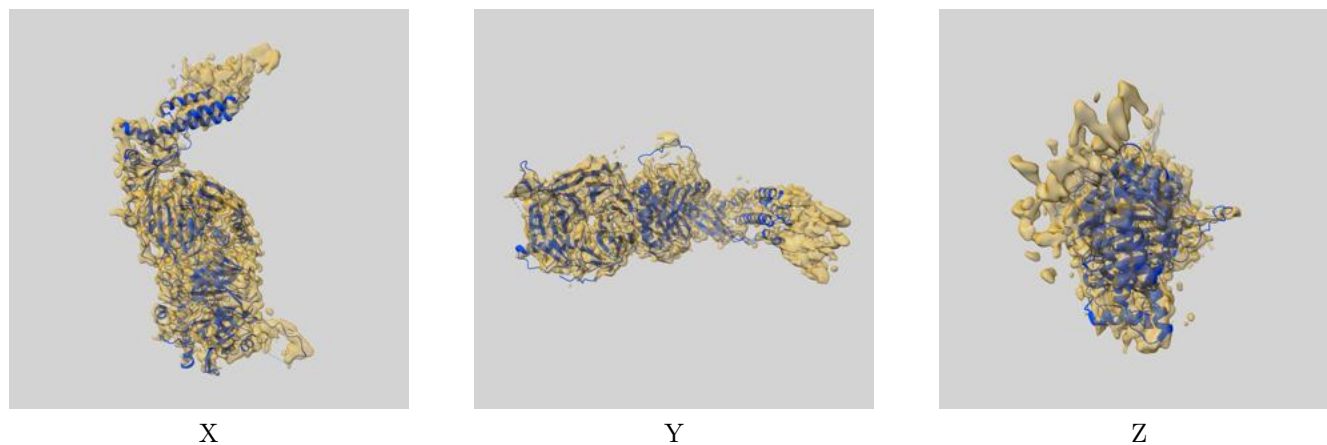
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.37	-	-
Author-provided FSC curve	3.37	4.18	3.47
Unmasked-calculated*	4.39	7.92	4.47

*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 4.39 differs from the reported value 3.37 by more than 10 %

9 Map-model fit [i](#)

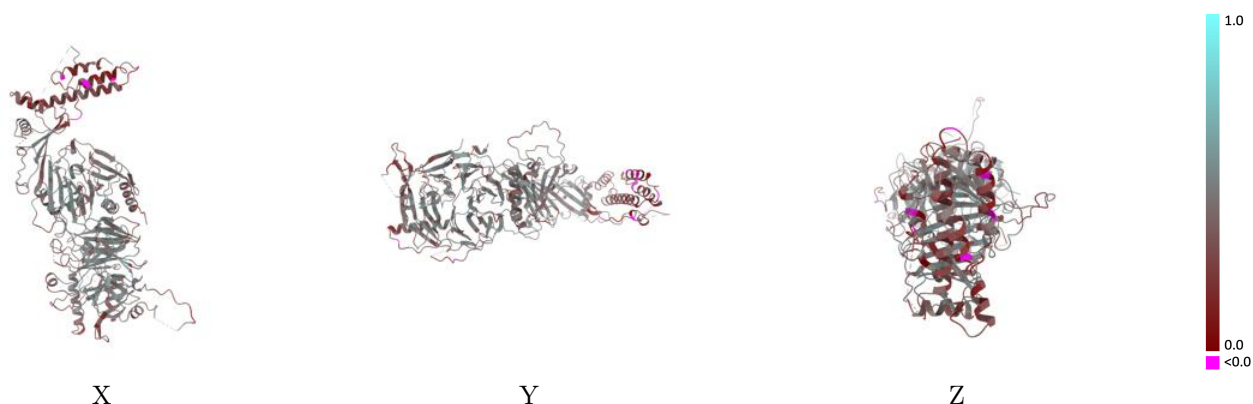
This section contains information regarding the fit between EMDB map EMD-43655 and PDB model 8VYB. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



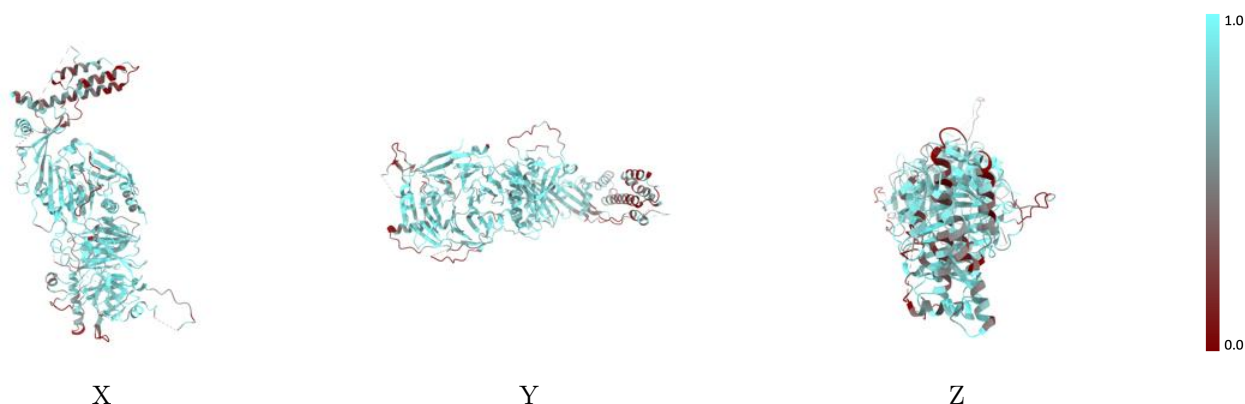
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



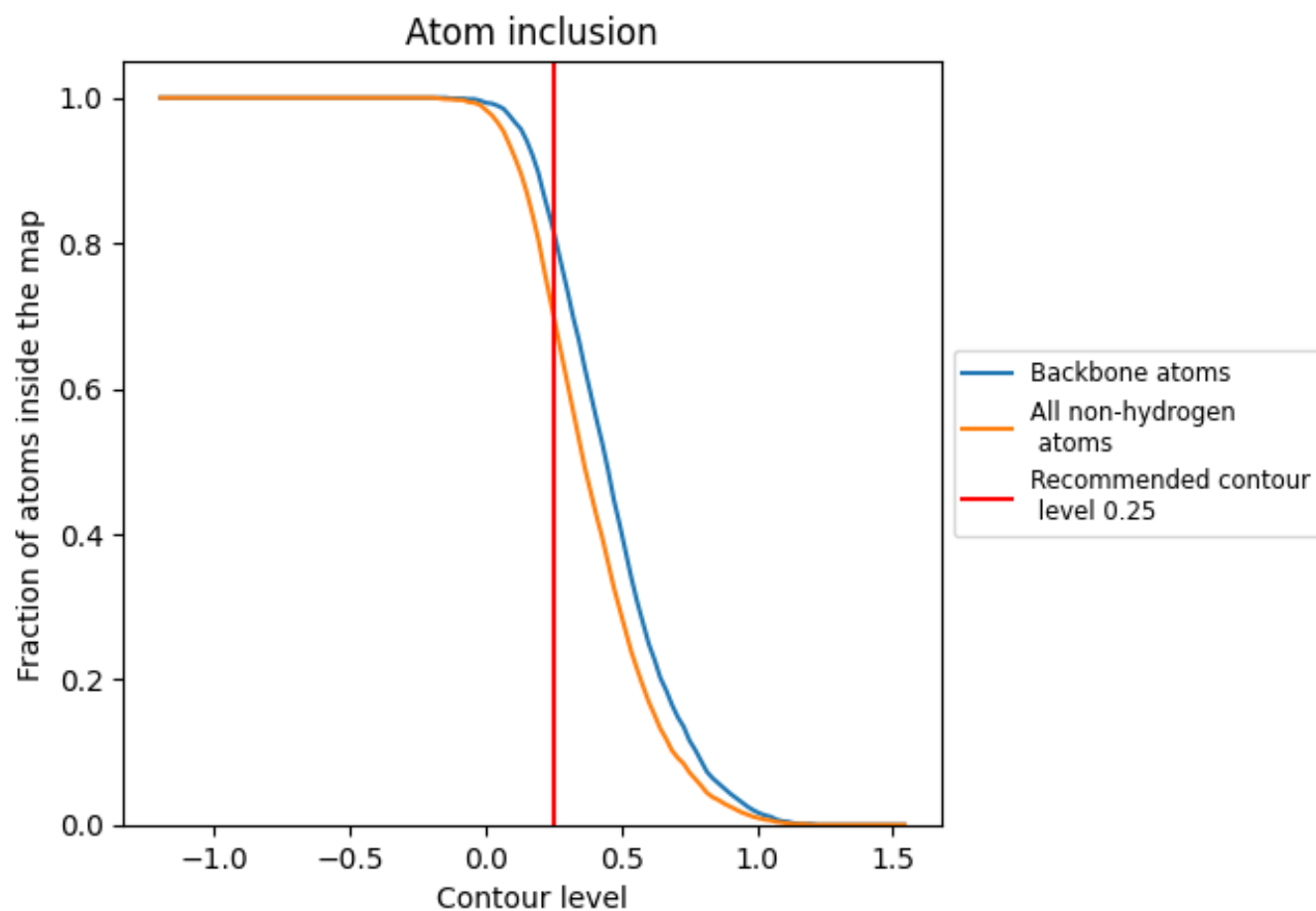
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7000	<div></div> 0.4000
A	<div></div> 0.6690	<div></div> 0.3810
B	<div></div> 0.7330	<div></div> 0.4200

