



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:06 PM UTC

PDB ID : 9MY8 / pdb_00009my8
EMDB ID : EMD-48730
Title : D7 Herpes Virus Simplex Neutralizing Nanobody Bound to HSV Glycoprotein gD
Authors : Viadiu, H.; Abernathy, E.; Lee, C.V.; Hung, M.; Yu, Y.; Xing, W.; Yu, X.
Deposited on : 2025-01-21
Resolution : 2.30 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

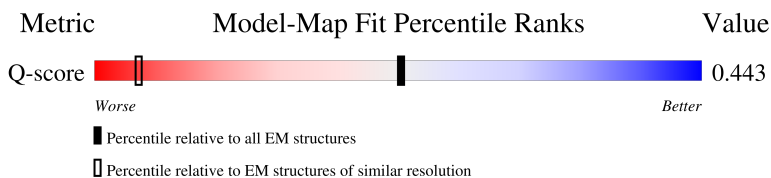
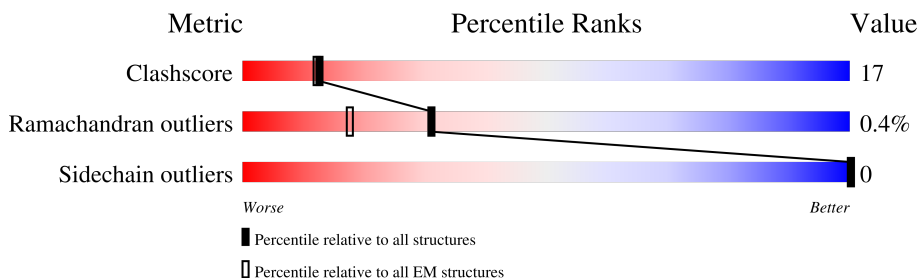
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.30 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	4254 (1.80 - 2.80)

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	H	244	20% 62% 30% 7%
2	L	214	25% 64% 33% .
3	A	125	6% 68% 26% . 5%
4	B	327	10% 46% 20% 34%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7403 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 Anti-Nb Fab Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	227	Total	C	N	O	S	0	0
			1716	1092	284	335	5		

- Molecule 2 is a protein called Ig-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	208	Total	C	N	O	S	0	0
			1582	987	267	323	5		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	18	ARG	THR	conflict	UNP Q7Z3Y4
L	28	SER	ASP	conflict	UNP Q7Z3Y4
L	29	VAL	ILE	conflict	UNP Q7Z3Y4
L	31	SER	ASN	conflict	UNP Q7Z3Y4
L	32	ALA	TYR	conflict	UNP Q7Z3Y4
L	33	VAL	LEU	conflict	UNP Q7Z3Y4
L	36	TYR	PHE	conflict	UNP Q7Z3Y4
L	46	LEU	SER	conflict	UNP Q7Z3Y4
L	50	SER	GLY	conflict	UNP Q7Z3Y4
L	55	TYR	GLN	conflict	UNP Q7Z3Y4
L	59	PRO	GLN	conflict	UNP Q7Z3Y4
L	61	ARG	LYS	conflict	UNP Q7Z3Y4
L	66	ARG	GLY	conflict	UNP Q7Z3Y4
L	91	SER	TYR	conflict	UNP Q7Z3Y4
L	92	SER	LYS	conflict	UNP Q7Z3Y4
L	94	SER	TYR	conflict	UNP Q7Z3Y4
L	95	LEU	PRO	conflict	UNP Q7Z3Y4
L	96	ILE	VAL	conflict	UNP Q7Z3Y4
L	104	VAL	LEU	conflict	UNP Q7Z3Y4
L	123	SER	GLU	conflict	UNP Q7Z3Y4

- Molecule 3 is a protein called D7 Neutralizing Nanobody against HSV Glycoprotein D.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	119	Total	C	N	O	S	0	0
			896	564	153	175	4		

- Molecule 4 is a protein called Glycoprotein D.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	217	Total	C	N	O	S	0	0
			1720	1103	294	313	10		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	306	GLY	-	expression tag	UNP Q5ICU7
B	307	GLY	-	expression tag	UNP Q5ICU7
B	308	GLY	-	expression tag	UNP Q5ICU7
B	309	SER	-	expression tag	UNP Q5ICU7
B	310	HIS	-	expression tag	UNP Q5ICU7
B	311	HIS	-	expression tag	UNP Q5ICU7
B	312	HIS	-	expression tag	UNP Q5ICU7
B	313	HIS	-	expression tag	UNP Q5ICU7
B	314	HIS	-	expression tag	UNP Q5ICU7
B	315	HIS	-	expression tag	UNP Q5ICU7
B	316	HIS	-	expression tag	UNP Q5ICU7
B	317	HIS	-	expression tag	UNP Q5ICU7
B	318	GLY	-	expression tag	UNP Q5ICU7
B	319	SER	-	expression tag	UNP Q5ICU7
B	320	ASP	-	expression tag	UNP Q5ICU7
B	321	TYR	-	expression tag	UNP Q5ICU7
B	322	LYS	-	expression tag	UNP Q5ICU7
B	323	ASP	-	expression tag	UNP Q5ICU7
B	324	ASP	-	expression tag	UNP Q5ICU7
B	325	ASP	-	expression tag	UNP Q5ICU7
B	326	ASP	-	expression tag	UNP Q5ICU7
B	327	LYS	-	expression tag	UNP Q5ICU7

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		AltConf
5	H	385	Total	O	0
			385	385	

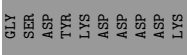
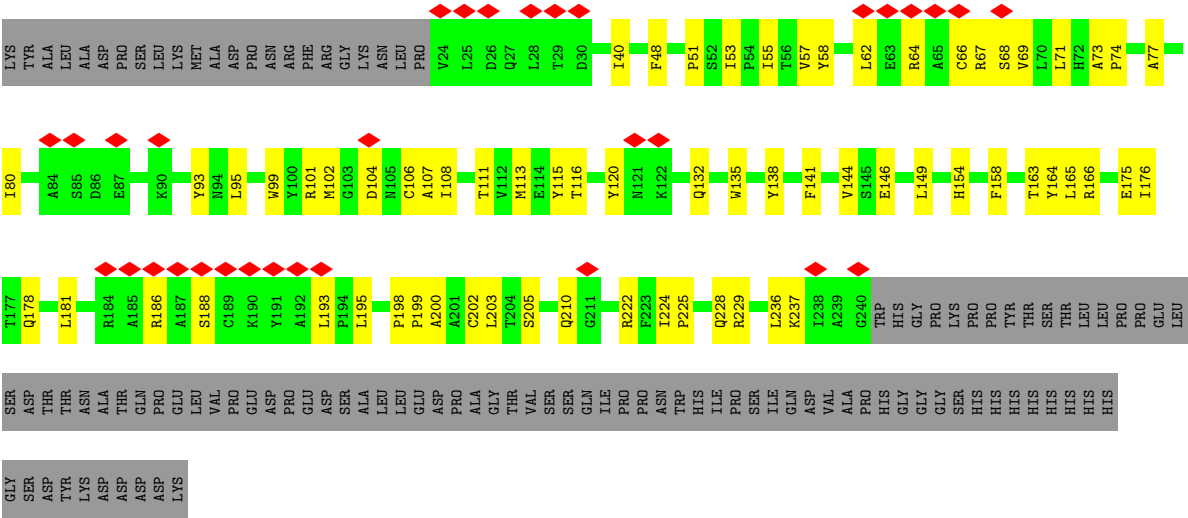
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Mol	Chain	Residues	Atoms		AltConf
5	L	400	Total 400	O 400	0
5	A	184	Total 184	O 184	0
5	B	520	Total 520	O 520	0



● Molecule 4: Glycoprotein D



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	228770	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	165000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.929	Depositor
Minimum map value	-0.723	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	233.28, 233.28, 233.28	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.729, 0.729, 0.729	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	H	0.16	0/1766	0.40	0/2413
2	L	0.14	0/1614	0.45	0/2190
3	A	0.15	0/915	0.42	0/1244
4	B	0.13	0/1768	0.42	0/2416
All	All	0.15	0/6063	0.42	0/8263

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	H	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	181	PHE	Peptide

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	H	1716	0	1638	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	1582	0	1553	58	0
3	A	896	0	881	27	0
4	B	1720	0	1710	50	0
5	A	184	0	0	0	0
5	B	520	0	0	7	0
5	H	385	0	0	4	0
5	L	400	0	0	12	0
All	All	7403	0	5782	195	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 17.

The worst 5 of 195 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)
3:A:77:THR:HG22	3:A:78:VAL:H	1.46	0.80
1:H:180:THR:HG22	2:L:166:GLN:HG2	1.64	0.77
2:L:45:LYS:NZ	5:L:301:HOH:O	2.18	0.75
1:H:91:THR:HG22	1:H:126:VAL:H	1.52	0.74
2:L:21:ILE:HD11	2:L:73:LEU:HD23	1.69	0.74

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	H	225/244 (92%)	204 (91%)	20 (9%)	1 (0%)	30	38
2	L	206/214 (96%)	184 (89%)	22 (11%)	0	100	100
3	A	117/125 (94%)	112 (96%)	3 (3%)	2 (2%)	7	7
4	B	215/327 (66%)	206 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	763/910 (84%)	706 (92%)	54 (7%)	3 (0%)	31	38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	54	SER
3	A	25	SER
3	A	32	TRP

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	H	187/204 (92%)	187 (100%)	0	100	100
2	L	184/189 (97%)	184 (100%)	0	100	100
3	A	97/103 (94%)	97 (100%)	0	100	100
4	B	188/284 (66%)	188 (100%)	0	100	100
All	All	656/780 (84%)	656 (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. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	90	GLN
2	L	160	GLN
4	B	132	GLN
4	B	27	GLN
2	L	79	GLN

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.

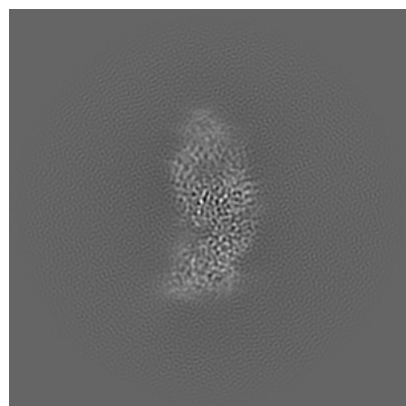
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48730. These allow visual inspection of the internal detail of the map and identification of artifacts.

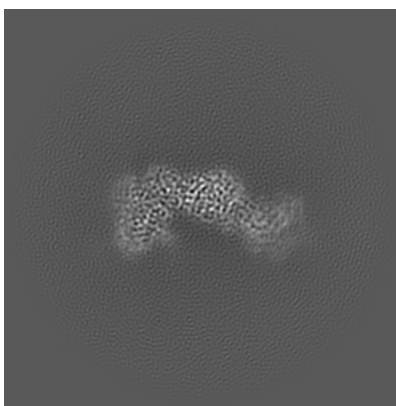
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

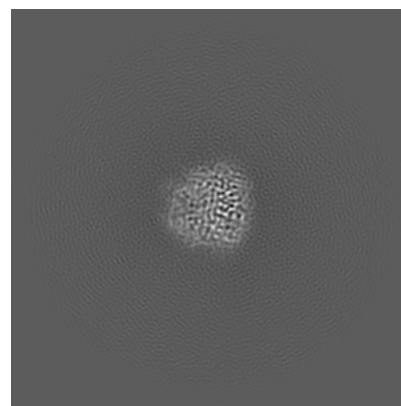
6.1.1 Primary map



X

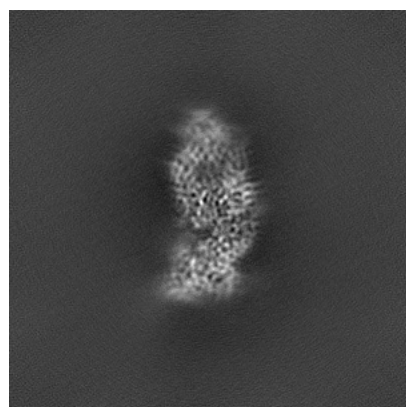


Y

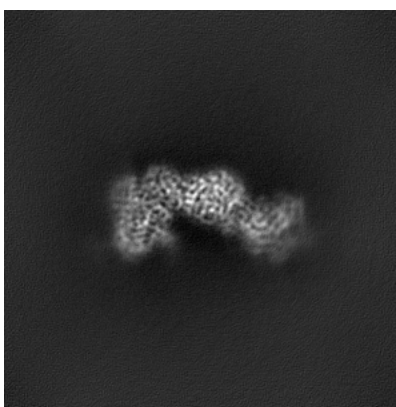


Z

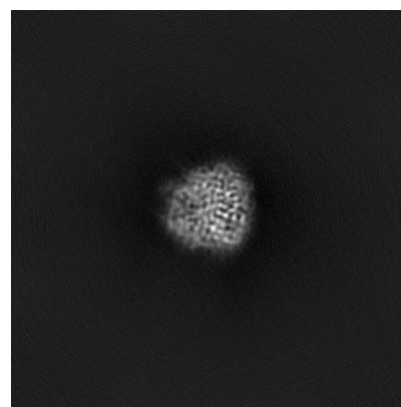
6.1.2 Raw map



X



Y

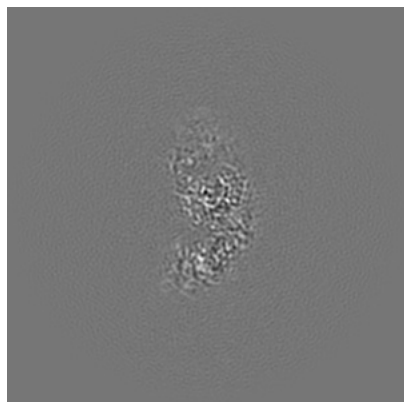


Z

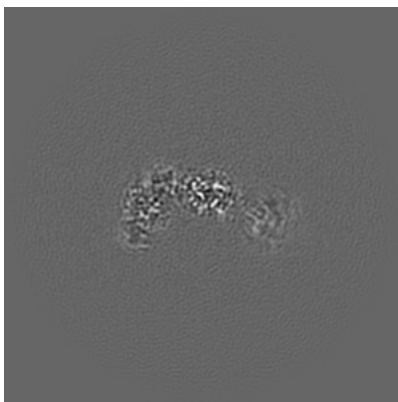
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

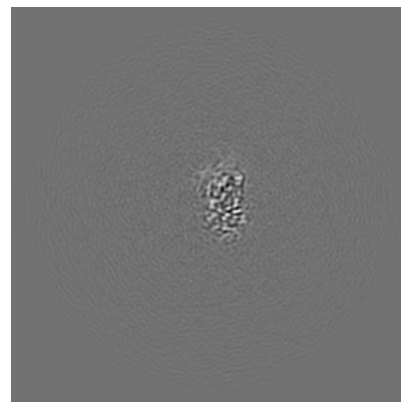
6.2.1 Primary map



X Index: 160

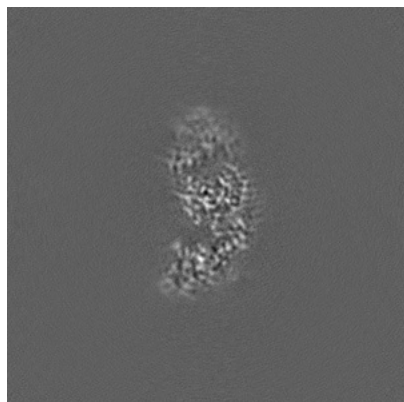


Y Index: 160

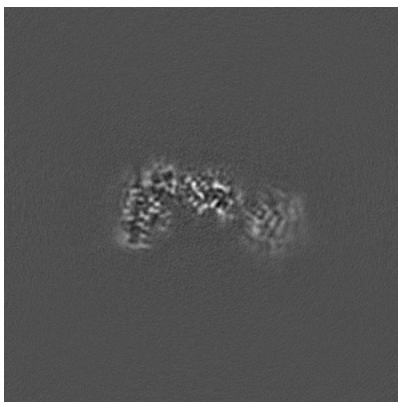


Z Index: 160

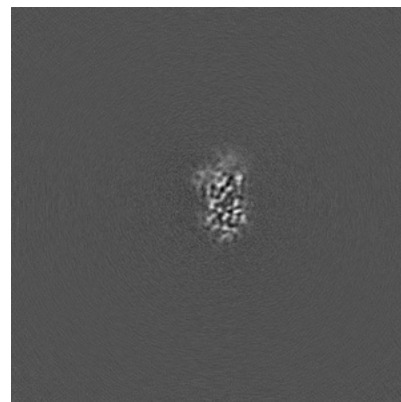
6.2.2 Raw map



X Index: 160



Y Index: 160

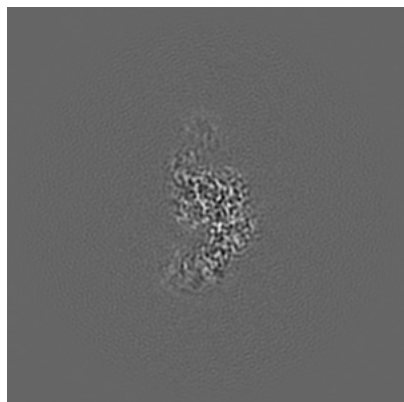


Z Index: 160

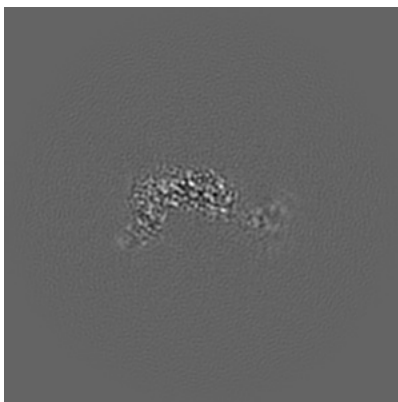
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

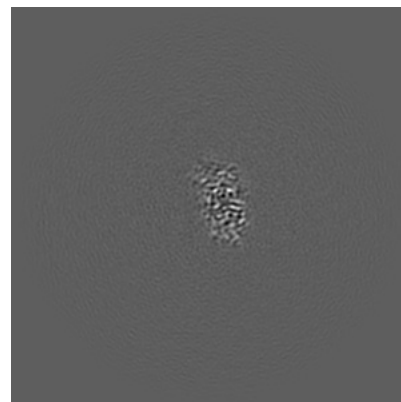
6.3.1 Primary map



X Index: 166

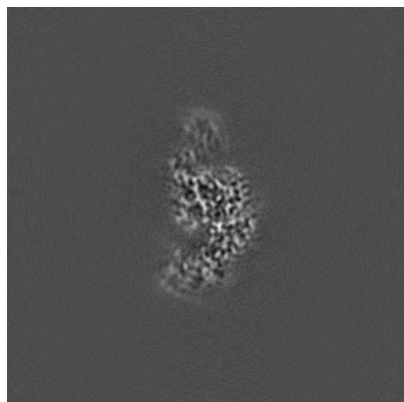


Y Index: 168

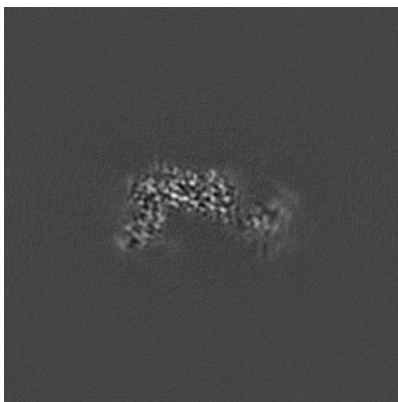


Z Index: 169

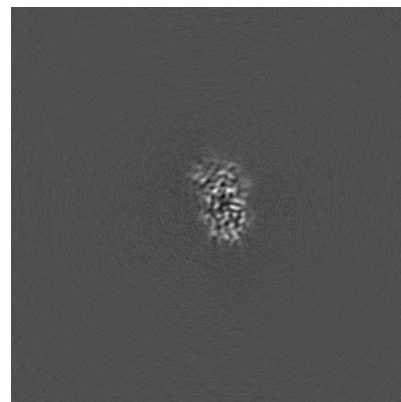
6.3.2 Raw map



X Index: 166



Y Index: 169

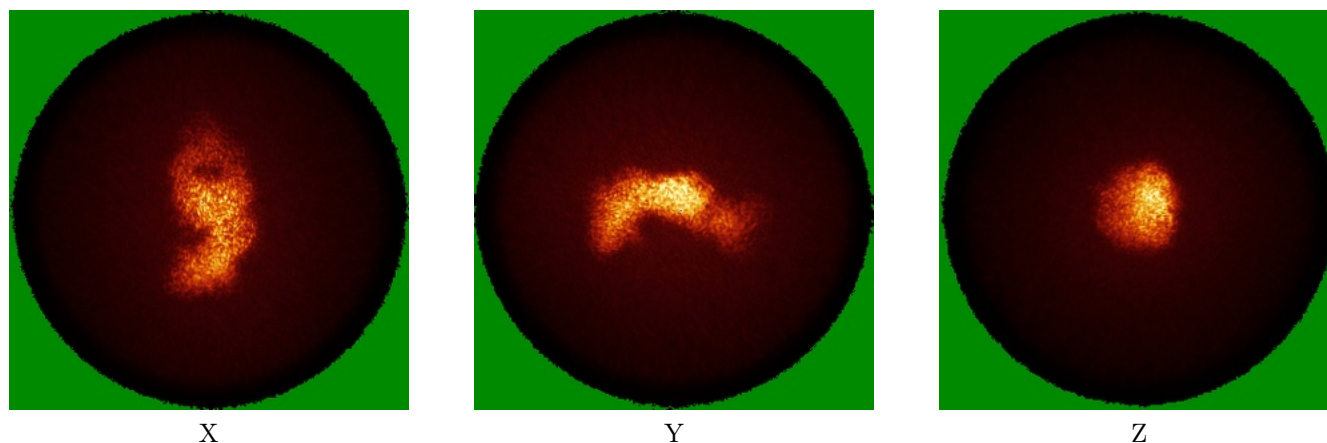


Z Index: 169

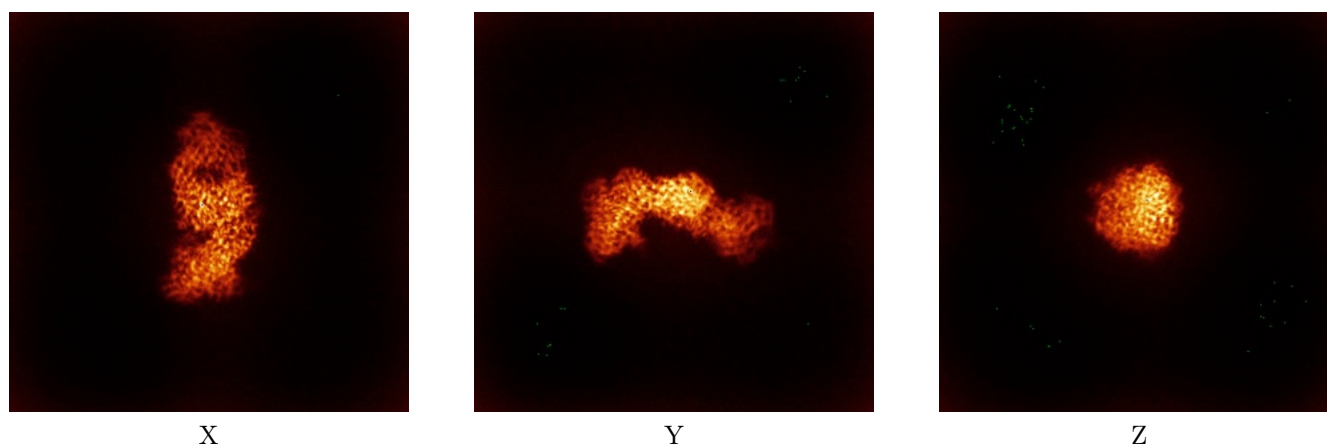
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

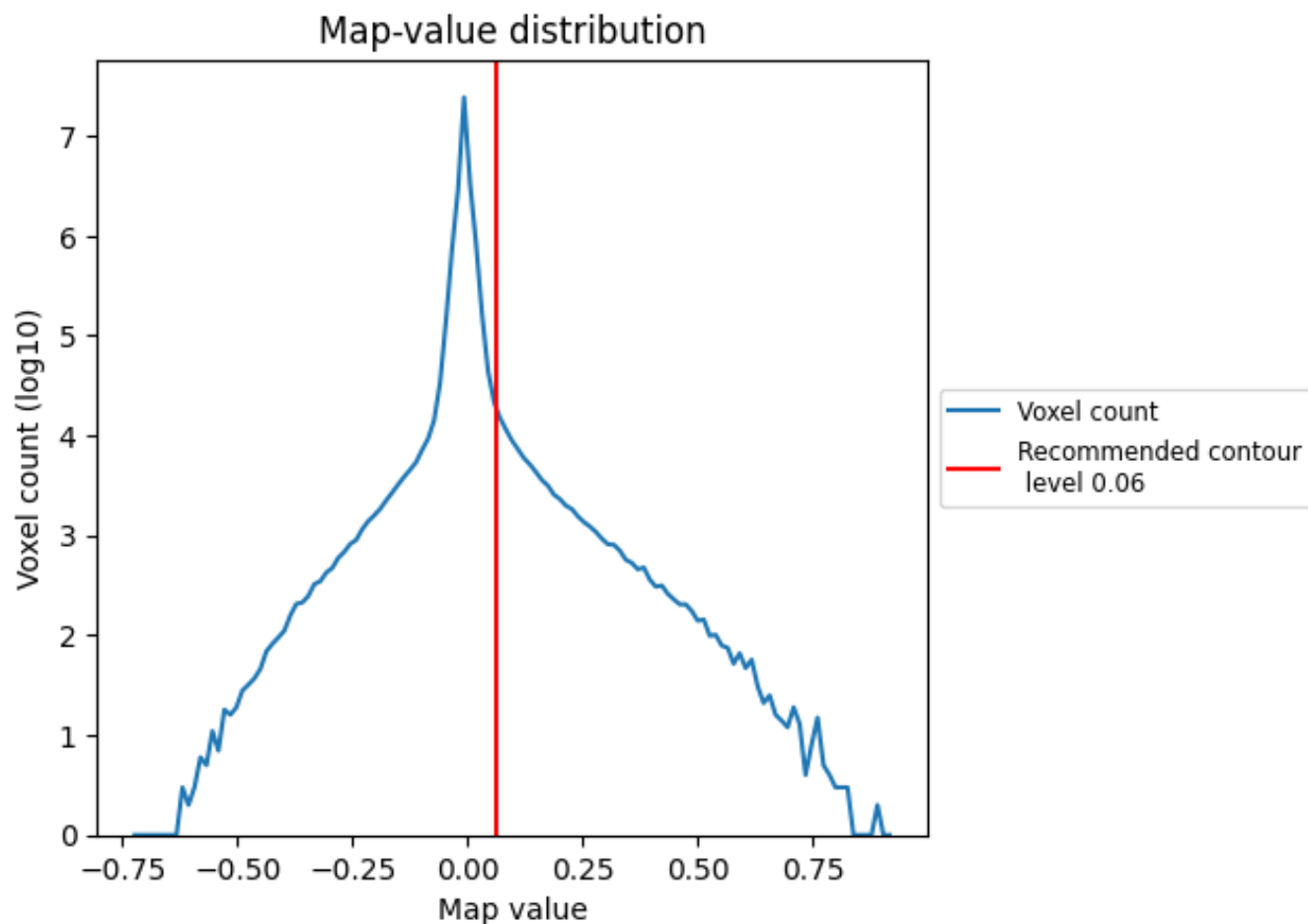
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

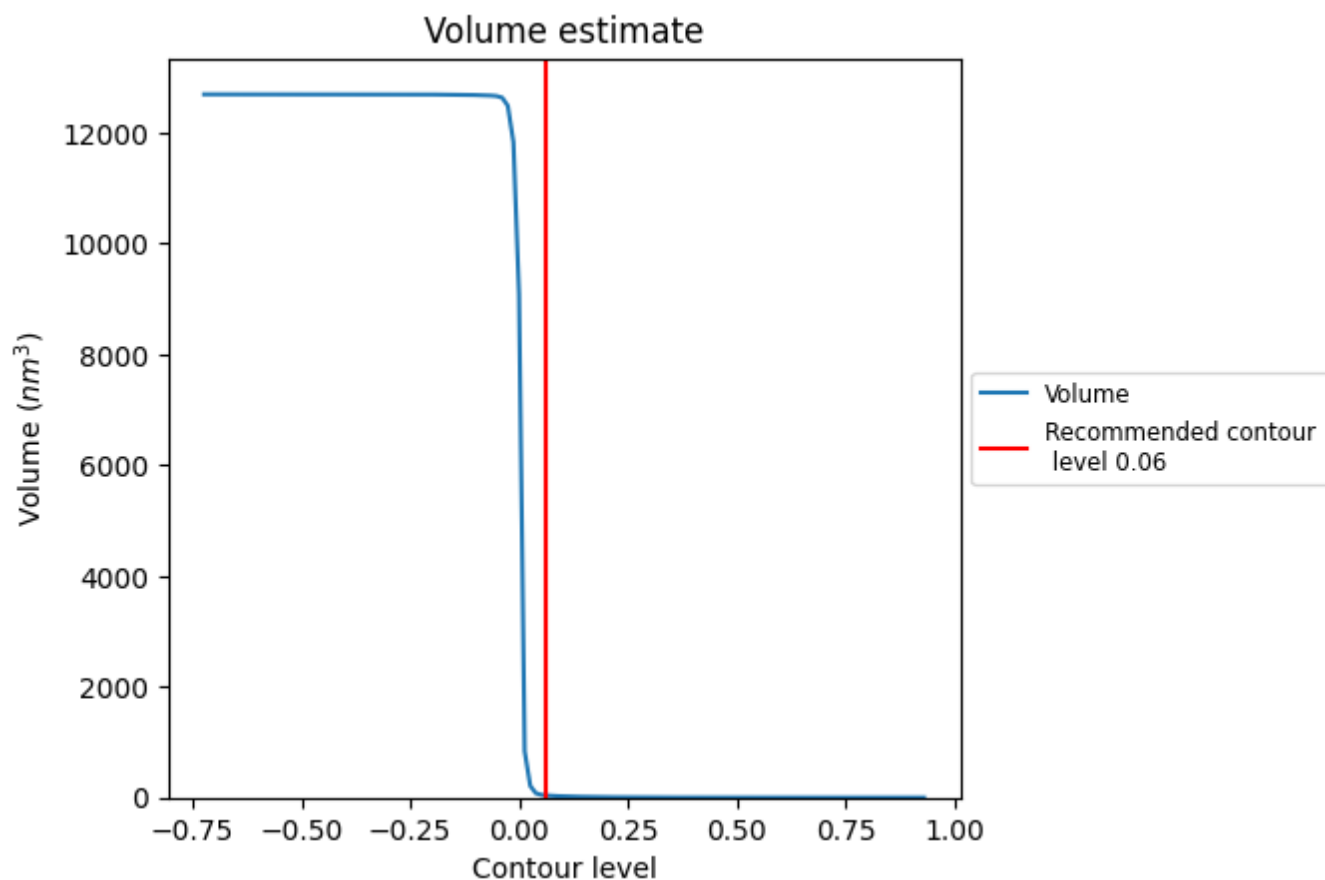
This section contains the results of statistical analysis of the map.

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.

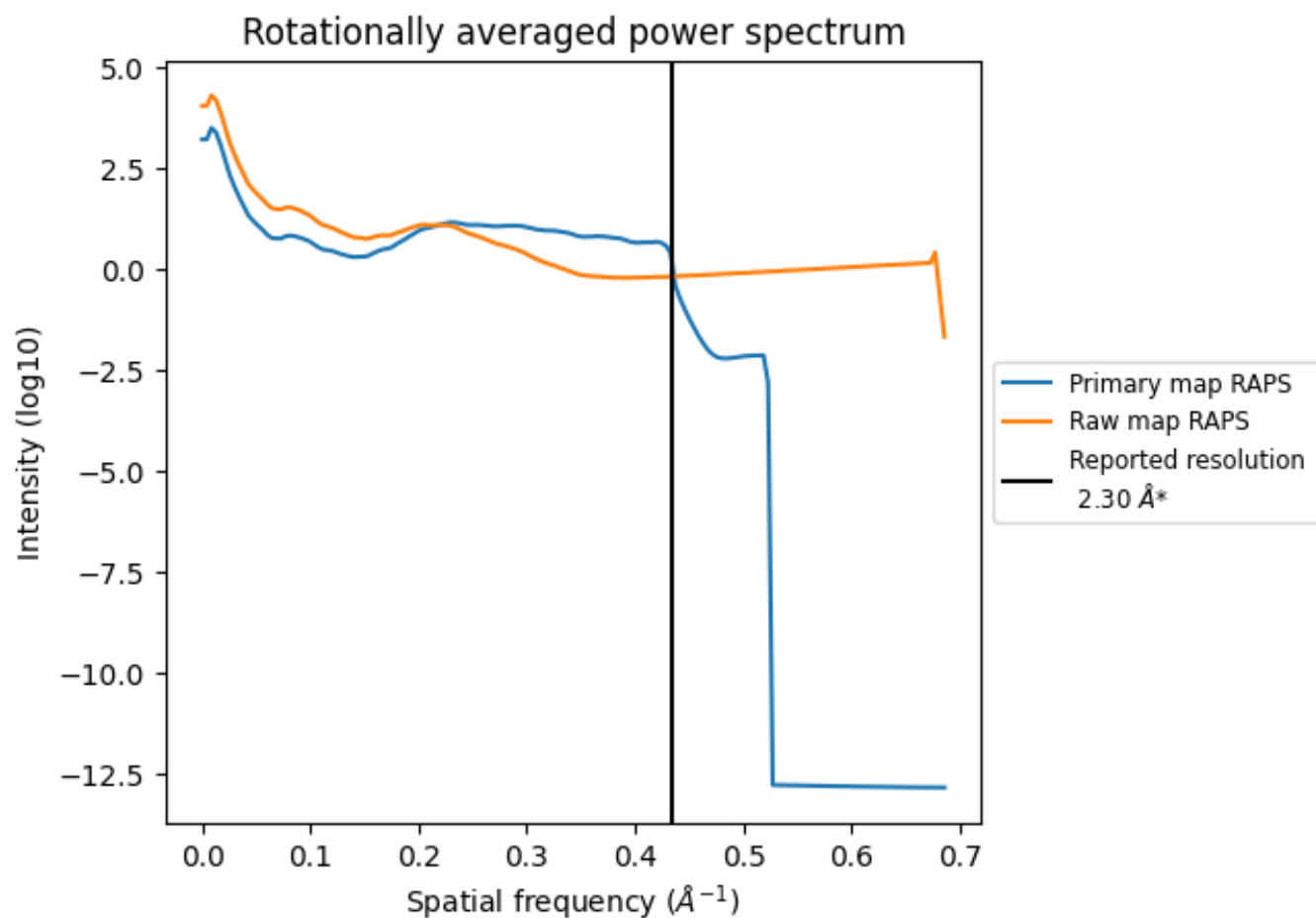
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 41 nm^3 ; this corresponds to an approximate mass of 37 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 ⓘ

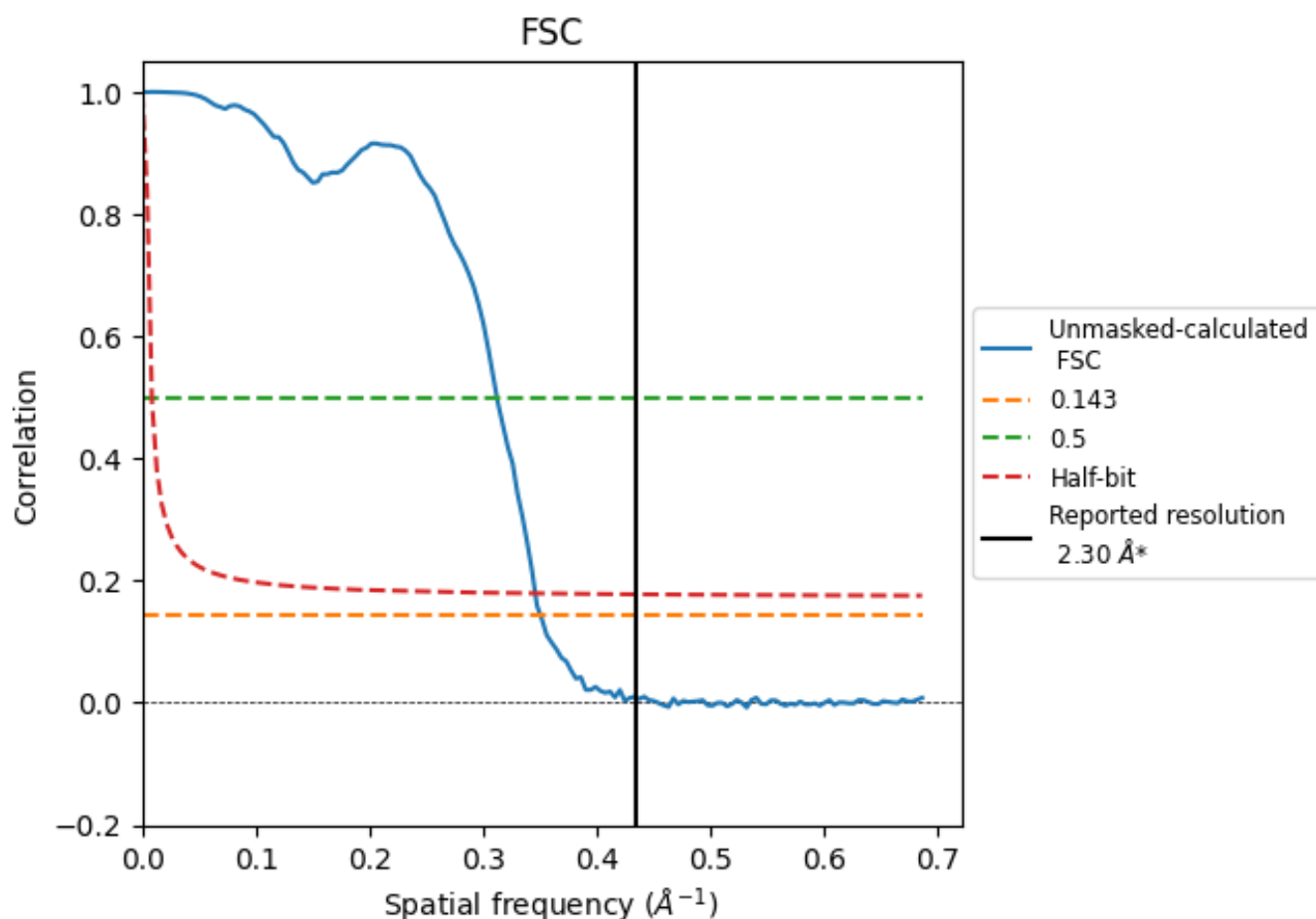


*Reported resolution corresponds to spatial frequency of 0.435 Å⁻¹

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 0.435 Å⁻¹

8.2 Resolution estimates [i](#)

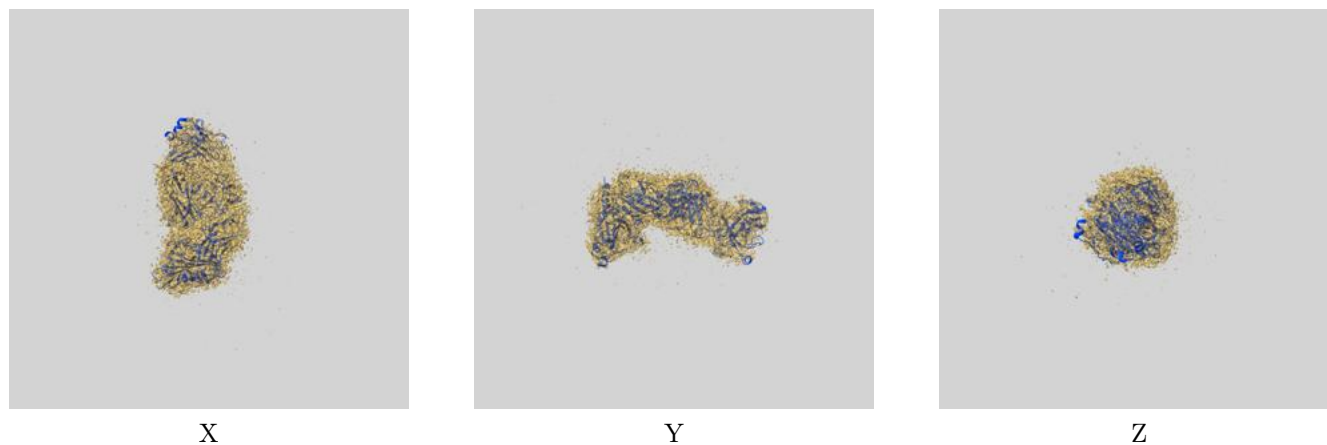
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.85	3.21	2.89

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.85 differs from the reported value 2.3 by more than 10 %

9 Map-model fit [i](#)

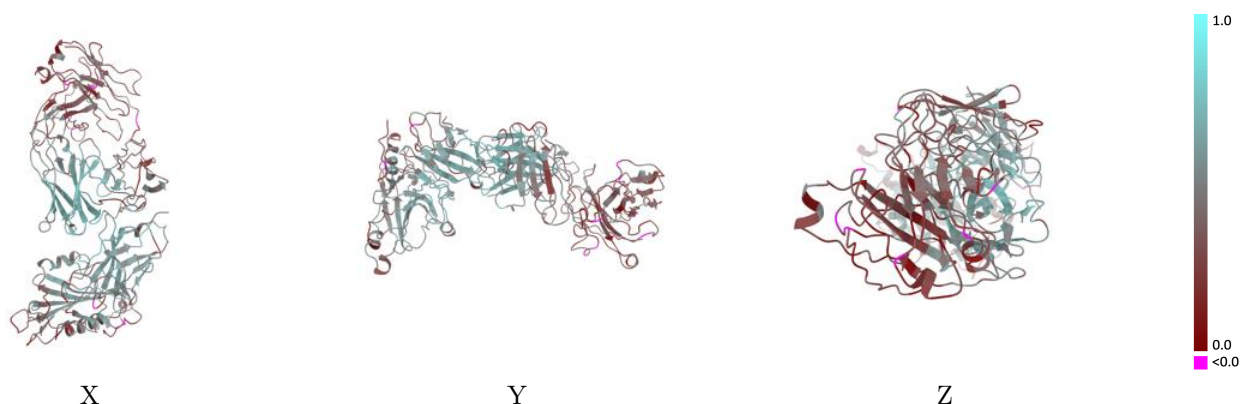
This section contains information regarding the fit between EMDB map EMD-48730 and PDB model 9MY8. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



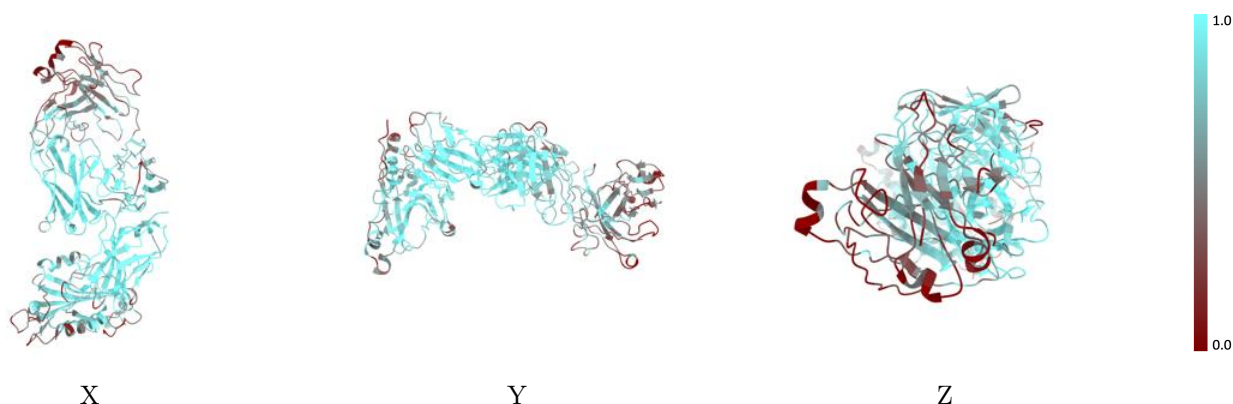
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



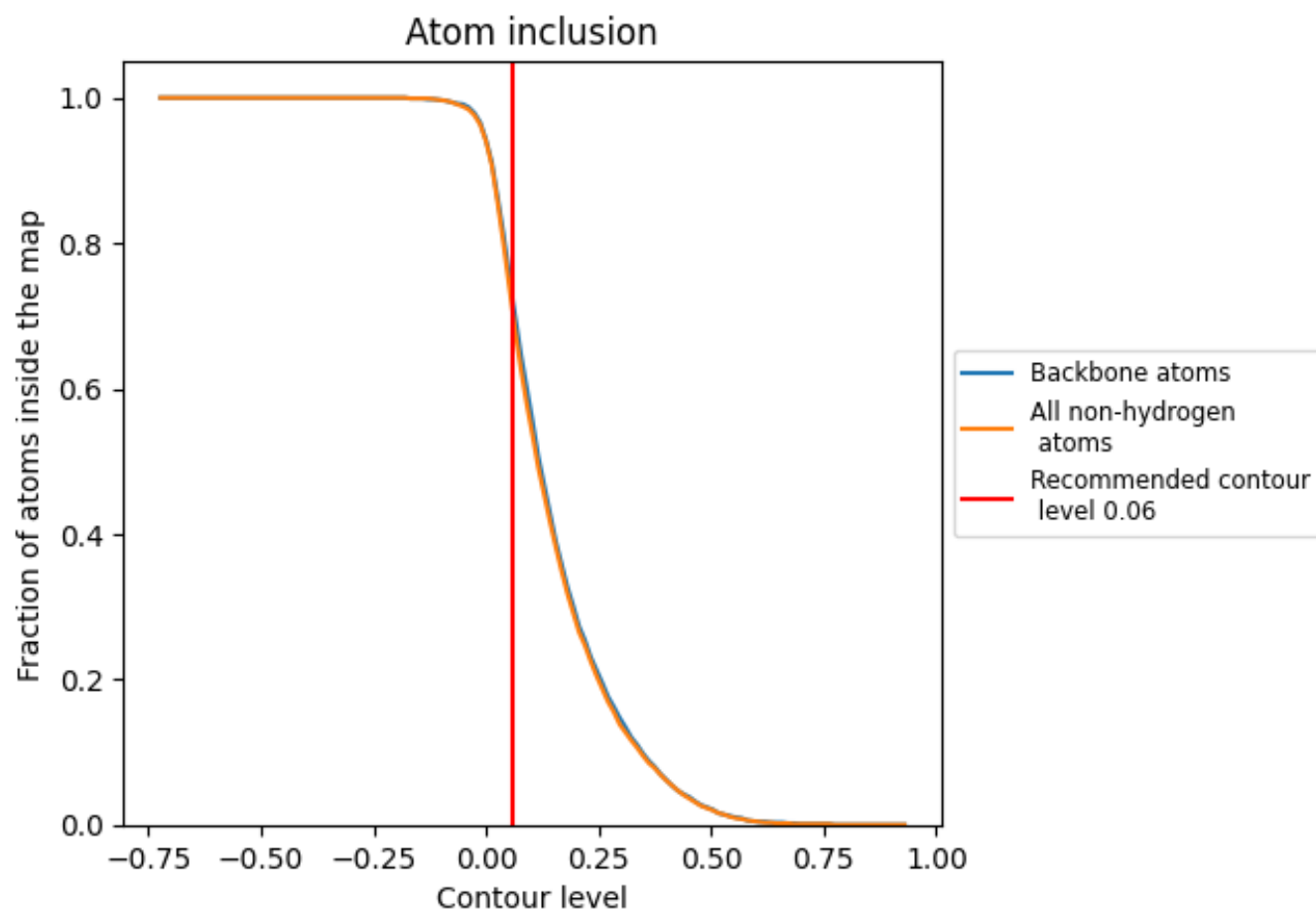
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion ⓘ



At the recommended contour level, 72% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6990	0.4430
A	0.8410	0.5120
B	0.7260	0.4700
H	0.6980	0.4500
L	0.5930	0.3680

