



## Full wwPDB EM Validation Report ⓘ

May 19, 2026 – 05:34 PM JST

PDB ID : 9UXS / pdb\_00009uxs  
EMDB ID : EMD-64597  
Title : The local refine of 3D reconstruction of the complex formed by SARS-CoV2 BA.1 spike glycoprotein and a single-domain antibody  
Authors : Wu, B.; Rao, G.; Cao, S.; Gong, R.  
Deposited on : 2025-05-14  
Resolution : 3.40 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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

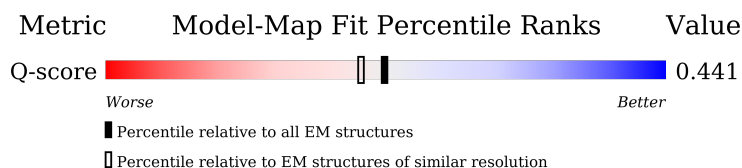
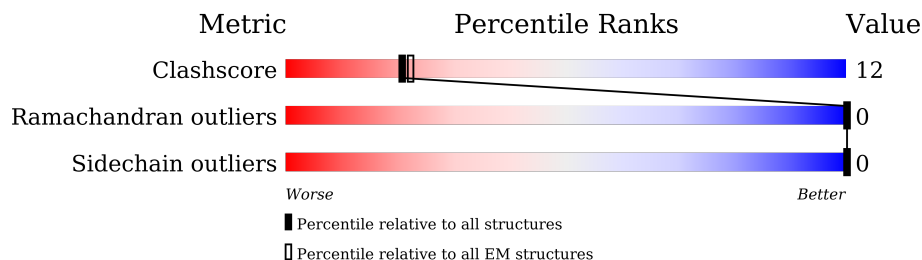
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.40 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	14717 ( 2.90 - 3.90 )

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  $\geq 3$ , 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	137	
2	B	1245	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2559 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 single-domain antibody.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	116	Total	C	N	O	S	0	0
			951	609	158	179	5		

- Molecule 2 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	200	Total	C	N	O	S	0	0
			1608	1039	271	290	8		

There are 105 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	70	VAL	ALA	variant	UNP P0DTC2
B	?	-	HIS	deletion	UNP P0DTC2
B	?	-	VAL	deletion	UNP P0DTC2
B	96	ILE	THR	variant	UNP P0DTC2
B	143	ASP	GLY	variant	UNP P0DTC2
B	?	-	VAL	deletion	UNP P0DTC2
B	?	-	TYR	deletion	UNP P0DTC2
B	?	-	TYR	deletion	UNP P0DTC2
B	?	-	ASN	deletion	UNP P0DTC2
B	209	ILE	LEU	conflict	UNP P0DTC2
B	212	GLU	-	insertion	UNP P0DTC2
B	213	PRO	-	insertion	UNP P0DTC2
B	214	GLU	-	insertion	UNP P0DTC2
B	339	ASP	GLY	variant	UNP P0DTC2
B	371	LEU	SER	variant	UNP P0DTC2
B	373	PRO	SER	variant	UNP P0DTC2
B	375	PHE	SER	variant	UNP P0DTC2
B	417	ASN	LYS	variant	UNP P0DTC2
B	440	LYS	ASN	variant	UNP P0DTC2
B	446	SER	GLY	variant	UNP P0DTC2
B	477	ASN	SER	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	478	LYS	THR	variant	UNP P0DTC2
B	484	ALA	GLU	variant	UNP P0DTC2
B	493	ARG	GLN	variant	UNP P0DTC2
B	496	SER	GLY	variant	UNP P0DTC2
B	498	ARG	GLN	variant	UNP P0DTC2
B	501	TYR	ASN	variant	UNP P0DTC2
B	505	HIS	TYR	variant	UNP P0DTC2
B	547	LYS	THR	variant	UNP P0DTC2
B	614	GLY	ASP	variant	UNP P0DTC2
B	655	TYR	HIS	variant	UNP P0DTC2
B	?	-	ASN	deletion	UNP P0DTC2
B	?	-	SER	deletion	UNP P0DTC2
B	?	-	PRO	deletion	UNP P0DTC2
B	?	-	ARG	deletion	UNP P0DTC2
B	679	LYS	ARG	conflict	UNP P0DTC2
B	680	SER	ALA	conflict	UNP P0DTC2
B	760	LYS	ASN	variant	UNP P0DTC2
B	792	TYR	ASP	variant	UNP P0DTC2
B	813	PRO	PHE	conflict	UNP P0DTC2
B	852	LYS	ASN	variant	UNP P0DTC2
B	888	PRO	ALA	conflict	UNP P0DTC2
B	895	PRO	ALA	conflict	UNP P0DTC2
B	938	PRO	ALA	conflict	UNP P0DTC2
B	950	HIS	GLN	variant	UNP P0DTC2
B	965	LYS	ASN	variant	UNP P0DTC2
B	982	PRO	LYS	conflict	UNP P0DTC2
B	983	PRO	VAL	conflict	UNP P0DTC2
B	1205	GLY	-	expression tag	UNP P0DTC2
B	1206	SER	-	expression tag	UNP P0DTC2
B	1207	GLY	-	expression tag	UNP P0DTC2
B	1208	TYR	-	expression tag	UNP P0DTC2
B	1209	ILE	-	expression tag	UNP P0DTC2
B	1210	PRO	-	expression tag	UNP P0DTC2
B	1211	GLU	-	expression tag	UNP P0DTC2
B	1212	ALA	-	expression tag	UNP P0DTC2
B	1213	PRO	-	expression tag	UNP P0DTC2
B	1214	ARG	-	expression tag	UNP P0DTC2
B	1215	ASP	-	expression tag	UNP P0DTC2
B	1216	GLY	-	expression tag	UNP P0DTC2
B	1217	GLN	-	expression tag	UNP P0DTC2
B	1218	ALA	-	expression tag	UNP P0DTC2
B	1219	TYR	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1220	VAL	-	expression tag	UNP P0DTC2
B	1221	ARG	-	expression tag	UNP P0DTC2
B	1222	LYS	-	expression tag	UNP P0DTC2
B	1223	ASP	-	expression tag	UNP P0DTC2
B	1224	GLY	-	expression tag	UNP P0DTC2
B	1225	GLU	-	expression tag	UNP P0DTC2
B	1226	TRP	-	expression tag	UNP P0DTC2
B	1227	VAL	-	expression tag	UNP P0DTC2
B	1228	LEU	-	expression tag	UNP P0DTC2
B	1229	LEU	-	expression tag	UNP P0DTC2
B	1230	SER	-	expression tag	UNP P0DTC2
B	1231	THR	-	expression tag	UNP P0DTC2
B	1232	PHE	-	expression tag	UNP P0DTC2
B	1233	LEU	-	expression tag	UNP P0DTC2
B	1234	GLY	-	expression tag	UNP P0DTC2
B	1235	ARG	-	expression tag	UNP P0DTC2
B	1236	SER	-	expression tag	UNP P0DTC2
B	1237	LEU	-	expression tag	UNP P0DTC2
B	1238	GLU	-	expression tag	UNP P0DTC2
B	1239	VAL	-	expression tag	UNP P0DTC2
B	1240	LEU	-	expression tag	UNP P0DTC2
B	1241	PHE	-	expression tag	UNP P0DTC2
B	1242	GLN	-	expression tag	UNP P0DTC2
B	1243	GLY	-	expression tag	UNP P0DTC2
B	1244	PRO	-	expression tag	UNP P0DTC2
B	1245	GLY	-	expression tag	UNP P0DTC2
B	1246	GLY	-	expression tag	UNP P0DTC2
B	1247	GLY	-	expression tag	UNP P0DTC2
B	1248	GLY	-	expression tag	UNP P0DTC2
B	1249	GLY	-	expression tag	UNP P0DTC2
B	1250	SER	-	expression tag	UNP P0DTC2
B	1251	GLY	-	expression tag	UNP P0DTC2
B	1252	GLY	-	expression tag	UNP P0DTC2
B	1253	GLY	-	expression tag	UNP P0DTC2
B	1254	GLY	-	expression tag	UNP P0DTC2
B	1255	SER	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	HIS	-	expression tag	UNP P0DTC2
B	1259	HIS	-	expression tag	UNP P0DTC2
B	1260	HIS	-	expression tag	UNP P0DTC2
B	1261	HIS	-	expression tag	UNP P0DTC2



WORLDWIDE  
**PDB**  
PROTEIN DATA BANK

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	204934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.654	Depositor
Minimum map value	-2.541	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.5	Depositor
Map size ( $\text{\AA}$ )	486.4, 486.4, 486.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.95, 0.95, 0.95	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	0/980	0.46	0/1334
2	B	0.17	0/1657	0.38	0/2256
All	All	0.21	0/2637	0.42	0/3590

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	951	0	915	19	0
2	B	1608	0	1540	44	0
All	All	2559	0	2455	60	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 12.

All (60) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:TYR:HB3	2:B:377:PHE:HB3	1.74	0.70
1:A:82:LYS:HG2	1:A:112:THR:HG23	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:416:GLY:O	2:B:420:ASP:N	2.26	0.67
2:B:353:TRP:HZ3	2:B:355:ARG:HD3	1.63	0.64
2:B:355:ARG:HD2	2:B:398:ASP:OD1	1.97	0.64
2:B:379:CYS:HB3	2:B:384:PRO:HD3	1.84	0.59
2:B:350:VAL:HG22	2:B:422:ASN:HB3	1.88	0.56
1:A:71:LEU:HB2	1:A:74:ASP:HB2	1.91	0.52
2:B:425:LEU:HD21	2:B:429:PHE:CD2	2.45	0.52
1:A:93:TYR:HB3	1:A:97:GLY:O	2.11	0.51
1:A:32:HIS:O	2:B:386:LYS:NZ	2.39	0.51
2:B:350:VAL:HG21	2:B:418:ILE:HG23	1.92	0.51
1:A:32:HIS:CG	2:B:386:LYS:NZ	2.80	0.50
1:A:13:THR:HG22	1:A:20:PRO:HB3	1.94	0.50
2:B:398:ASP:O	2:B:511:VAL:HA	2.12	0.49
2:B:474:GLN:HB2	2:B:480:CYS:HB2	1.93	0.49
2:B:395:VAL:HG23	2:B:524:VAL:HG21	1.93	0.49
2:B:375:PHE:CD2	2:B:376:THR:HG23	2.48	0.49
1:A:26:VAL:HG11	1:A:85:VAL:HG11	1.95	0.48
1:A:42:ASP:HA	1:A:80:GLU:HB3	1.93	0.48
2:B:379:CYS:HA	2:B:432:CYS:HA	1.96	0.48
2:B:457:ARG:NH1	2:B:467:ASP:OD2	2.45	0.48
1:A:52:LYS:HG2	1:A:98:TYR:CE1	2.49	0.47
2:B:417:ASN:HD21	2:B:455:LEU:HD12	1.80	0.47
2:B:355:ARG:HE	2:B:396:TYR:HB3	1.80	0.46
2:B:498:ARG:HB2	2:B:501:TYR:CD2	2.51	0.46
1:A:6:LEU:HB2	1:A:23:THR:OG1	2.15	0.46
1:A:83:CYS:SG	1:A:111:CYS:HB3	2.56	0.46
2:B:332:ILE:HG23	2:B:362:VAL:HG21	1.98	0.45
2:B:421:TYR:HD1	2:B:457:ARG:HB3	1.81	0.45
2:B:353:TRP:CE2	2:B:423:TYR:HD2	2.34	0.45
1:A:13:THR:HB	1:A:76:LEU:HD21	1.99	0.45
2:B:359:SER:OG	2:B:523:THR:OG1	2.25	0.44
1:A:25:VAL:HB	1:A:65:VAL:HG23	1.98	0.44
2:B:384:PRO:HA	2:B:387:LEU:HG	1.98	0.44
2:B:436:TRP:CE3	2:B:509:ARG:HB2	2.53	0.44
2:B:355:ARG:HD2	2:B:355:ARG:HA	1.83	0.44
1:A:85:VAL:O	1:A:86:SER:OG	2.35	0.43
1:A:23:THR:HG22	1:A:67:LYS:HG3	2.00	0.43
2:B:497:PHE:CZ	2:B:507:PRO:HB3	2.53	0.43
2:B:518:LEU:O	2:B:520:ALA:N	2.50	0.42
1:A:34:ILE:C	1:A:87:ALA:HB3	2.44	0.42
2:B:402:ILE:HD11	2:B:407:VAL:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:394:ASN:HB3	2:B:396:TYR:CE1	2.55	0.42
2:B:490:PHE:O	2:B:492:LEU:N	2.51	0.42
1:A:3:VAL:HG22	1:A:4:LEU:N	2.34	0.42
1:A:26:VAL:HG22	1:A:64:VAL:HG12	2.00	0.42
2:B:351:TYR:CE1	2:B:492:LEU:HD21	2.55	0.42
2:B:448:ASN:HD22	2:B:497:PHE:HD2	1.68	0.42
2:B:353:TRP:CZ3	2:B:355:ARG:HD3	2.50	0.42
2:B:442:ASP:OD2	2:B:451:TYR:OH	2.25	0.41
2:B:501:TYR:HB3	2:B:505:HIS:HB2	2.02	0.41
2:B:394:ASN:HB3	2:B:396:TYR:HE1	1.85	0.41
2:B:414:GLN:OE1	2:B:414:GLN:HA	2.20	0.41
2:B:384:PRO:O	2:B:387:LEU:HG	2.20	0.41
2:B:415:THR:O	2:B:415:THR:HG23	2.20	0.41
2:B:435:ALA:HA	2:B:509:ARG:O	2.21	0.41
2:B:455:LEU:HG	2:B:456:PHE:CE1	2.56	0.41
2:B:386:LYS:O	2:B:390:LEU:HD23	2.21	0.40
2:B:338:PHE:CE2	2:B:363:ALA:HB1	2.57	0.40

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	114/137 (83%)	105 (92%)	9 (8%)	0	100	100
2	B	198/1245 (16%)	184 (93%)	14 (7%)	0	100	100
All	All	312/1382 (23%)	289 (93%)	23 (7%)	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	106/122 (87%)	106 (100%)	0	100	100
2	B	175/1081 (16%)	175 (100%)	0	100	100
All	All	281/1203 (23%)	281 (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. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	343	ASN
2	B	417	ASN
2	B	506	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.

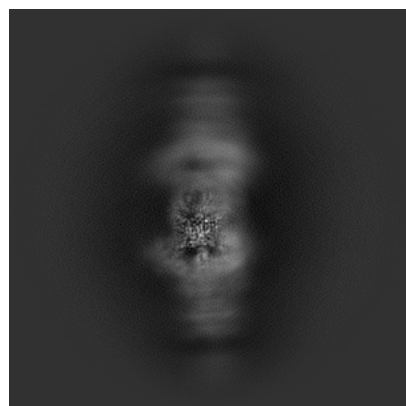
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64597. These allow visual inspection of the internal detail of the map and identification of artifacts.

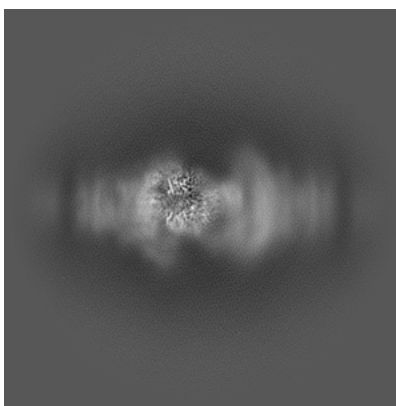
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

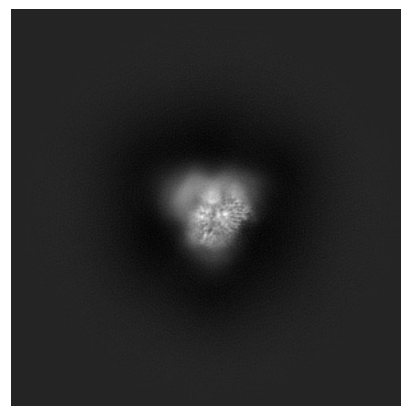
#### 6.1.1 Primary map



X

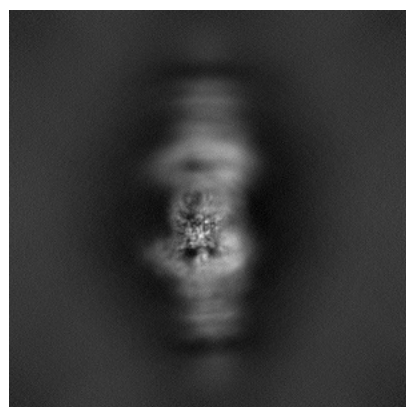


Y

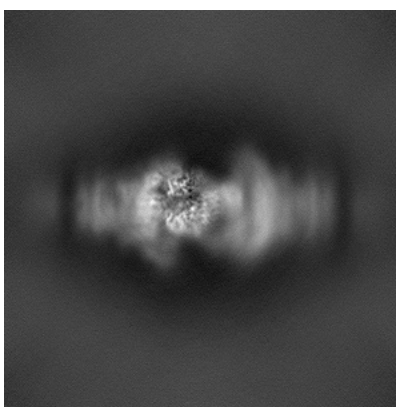


Z

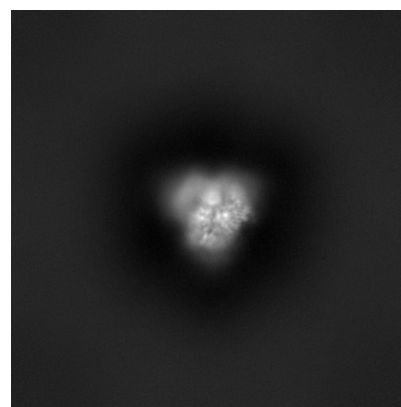
#### 6.1.2 Raw map



X



Y

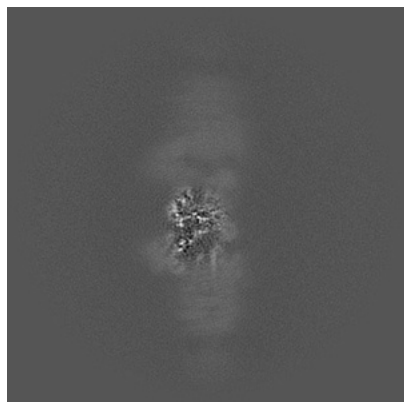


Z

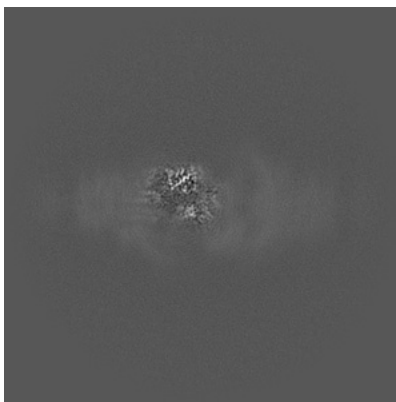
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

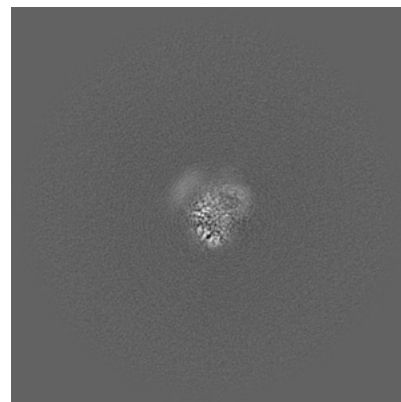
### 6.2.1 Primary map



X Index: 256

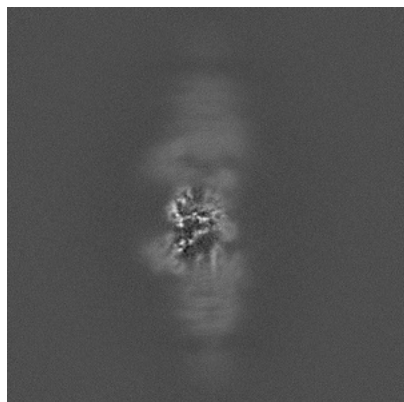


Y Index: 256

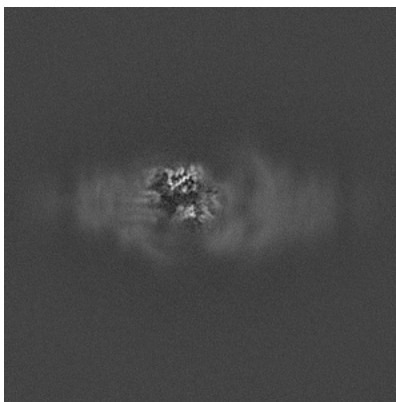


Z Index: 256

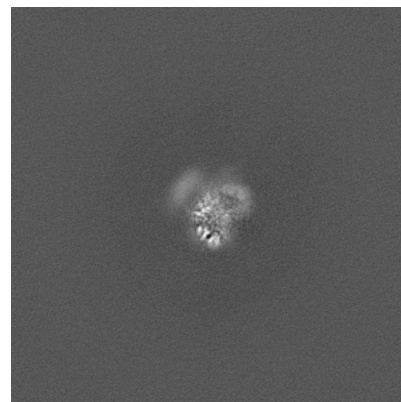
### 6.2.2 Raw map



X Index: 256



Y Index: 256

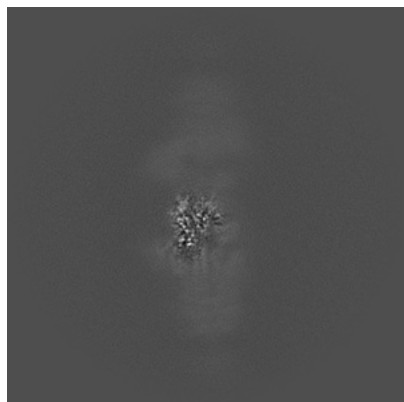


Z Index: 256

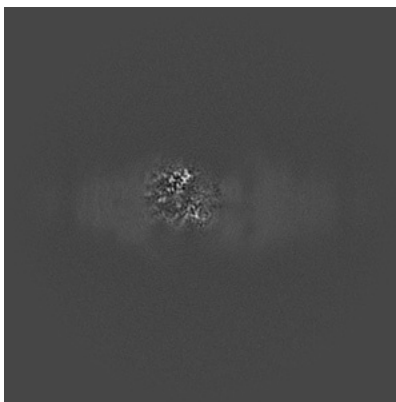
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

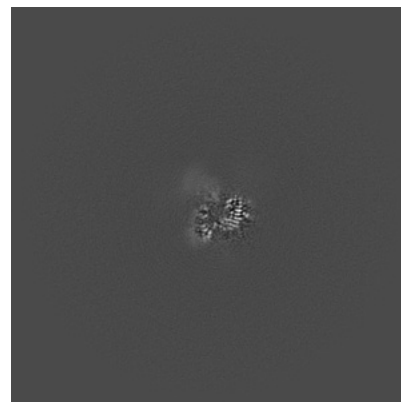
### 6.3.1 Primary map



X Index: 249

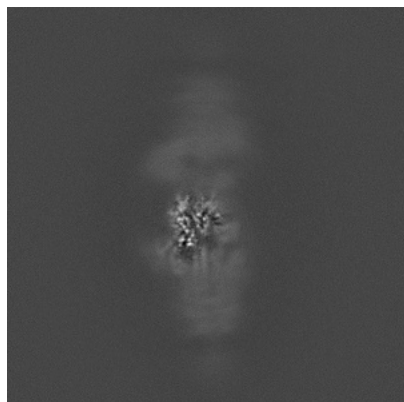


Y Index: 246

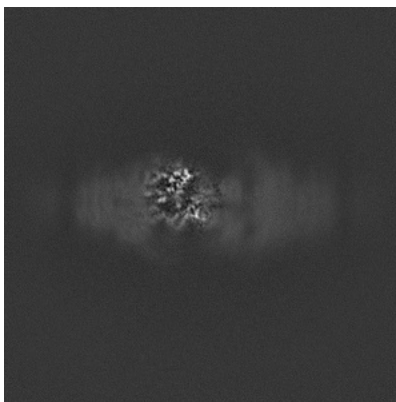


Z Index: 231

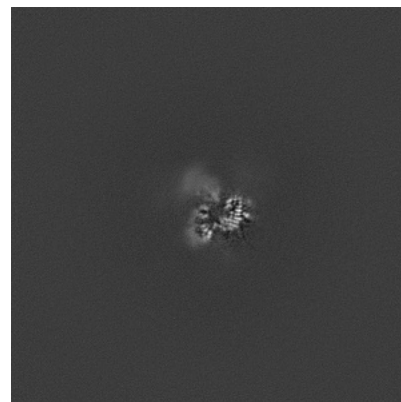
### 6.3.2 Raw map



X Index: 249



Y Index: 246



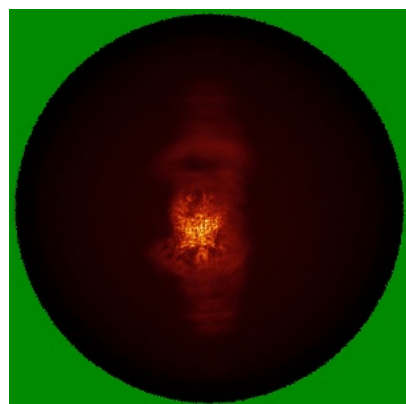
Z Index: 231

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

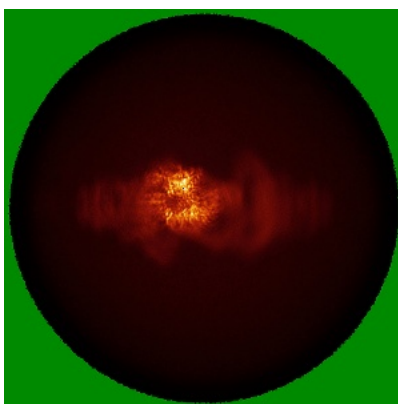


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

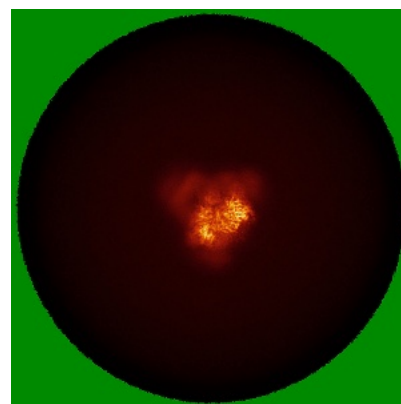
### 6.4.1 Primary map



X

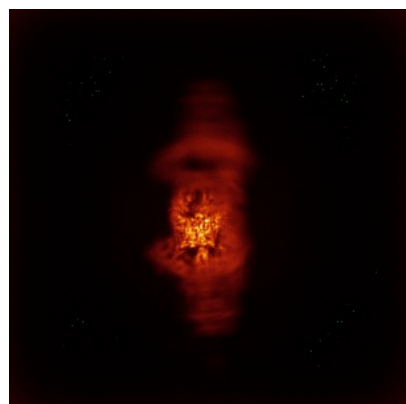


Y

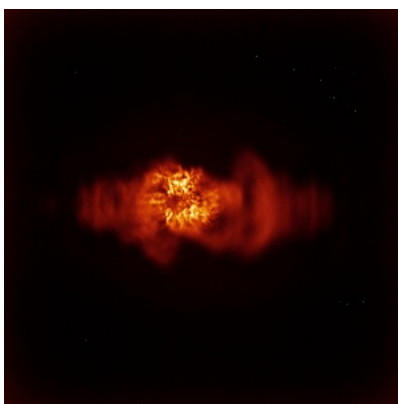


Z

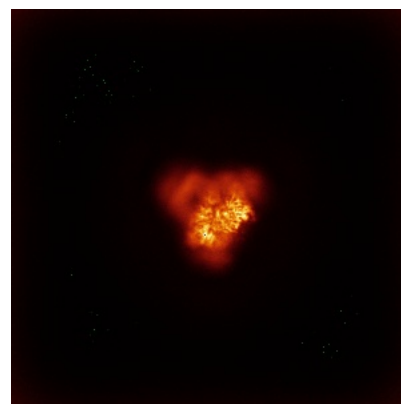
### 6.4.2 Raw map



X



Y

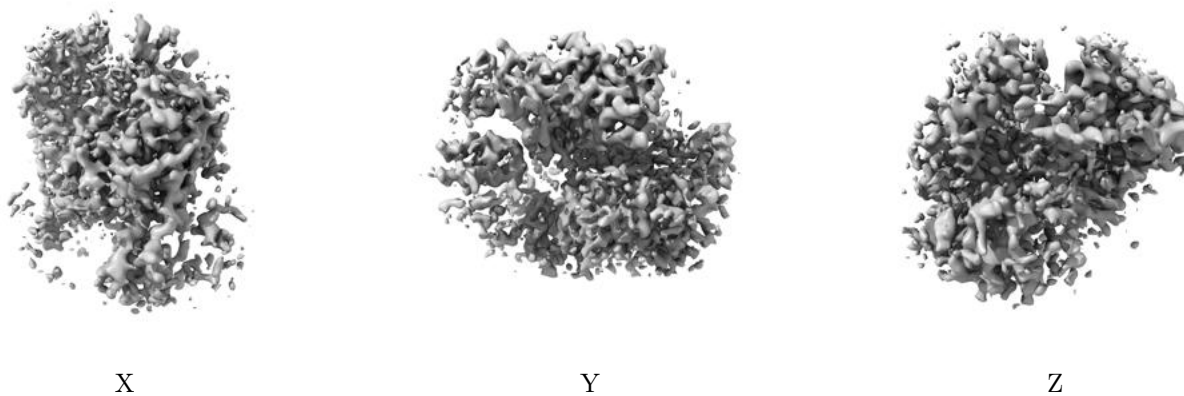


Z

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.

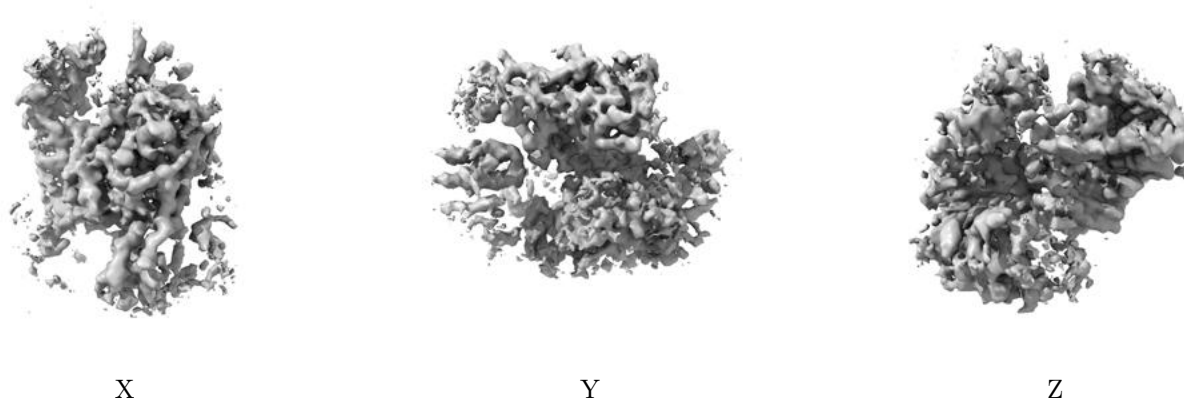
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. 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.

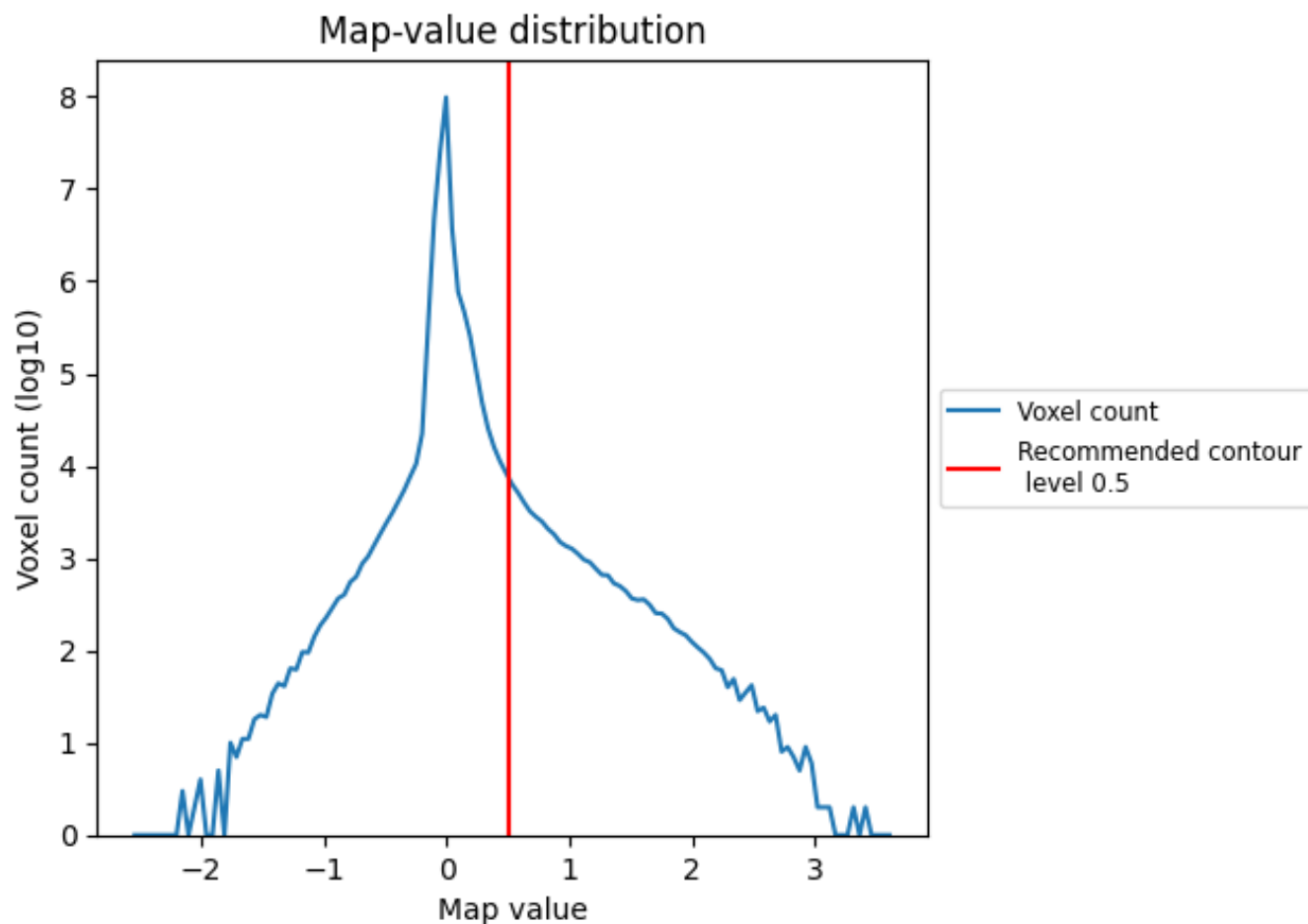
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

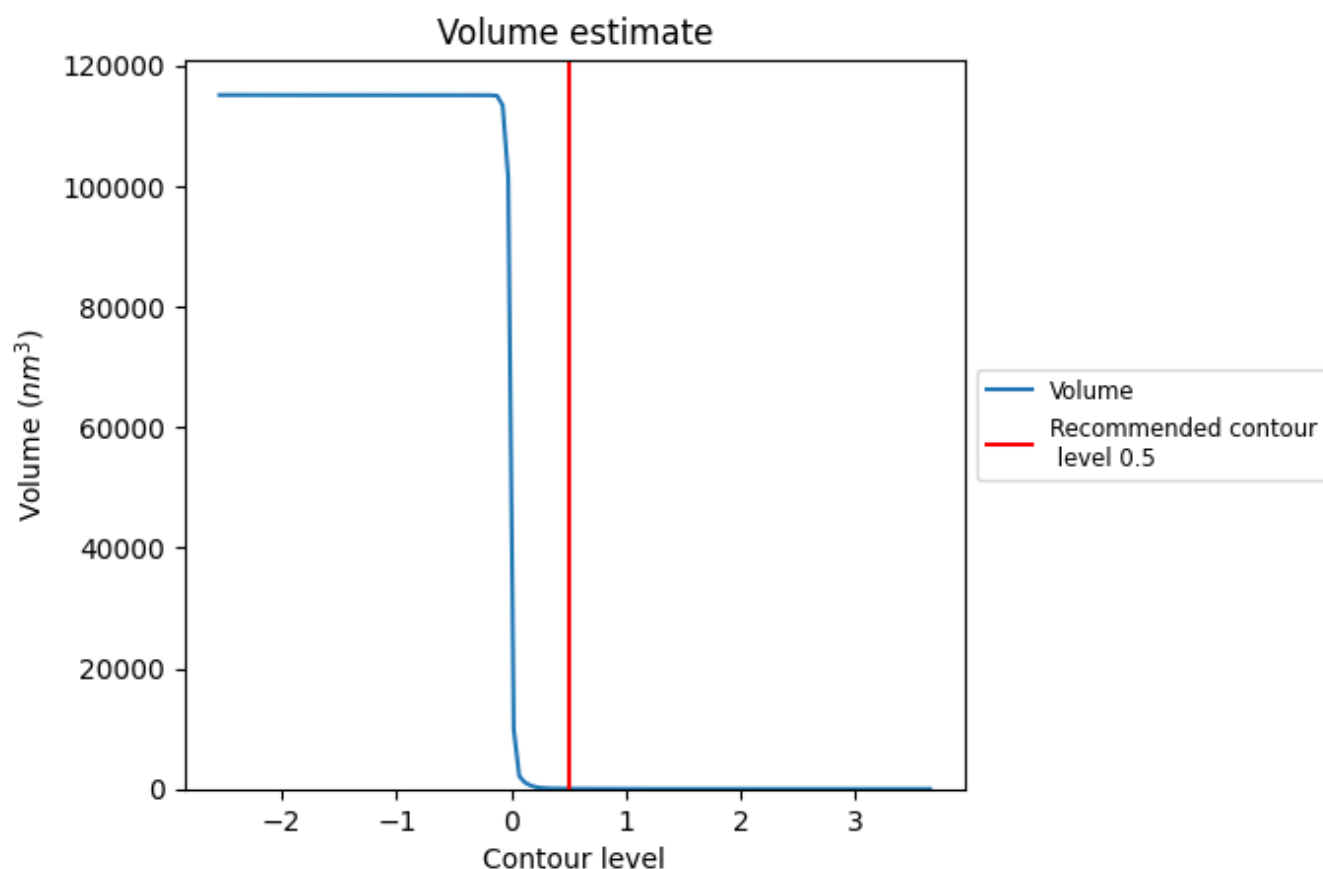
This section contains the results of statistical analysis of the map.

### 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.

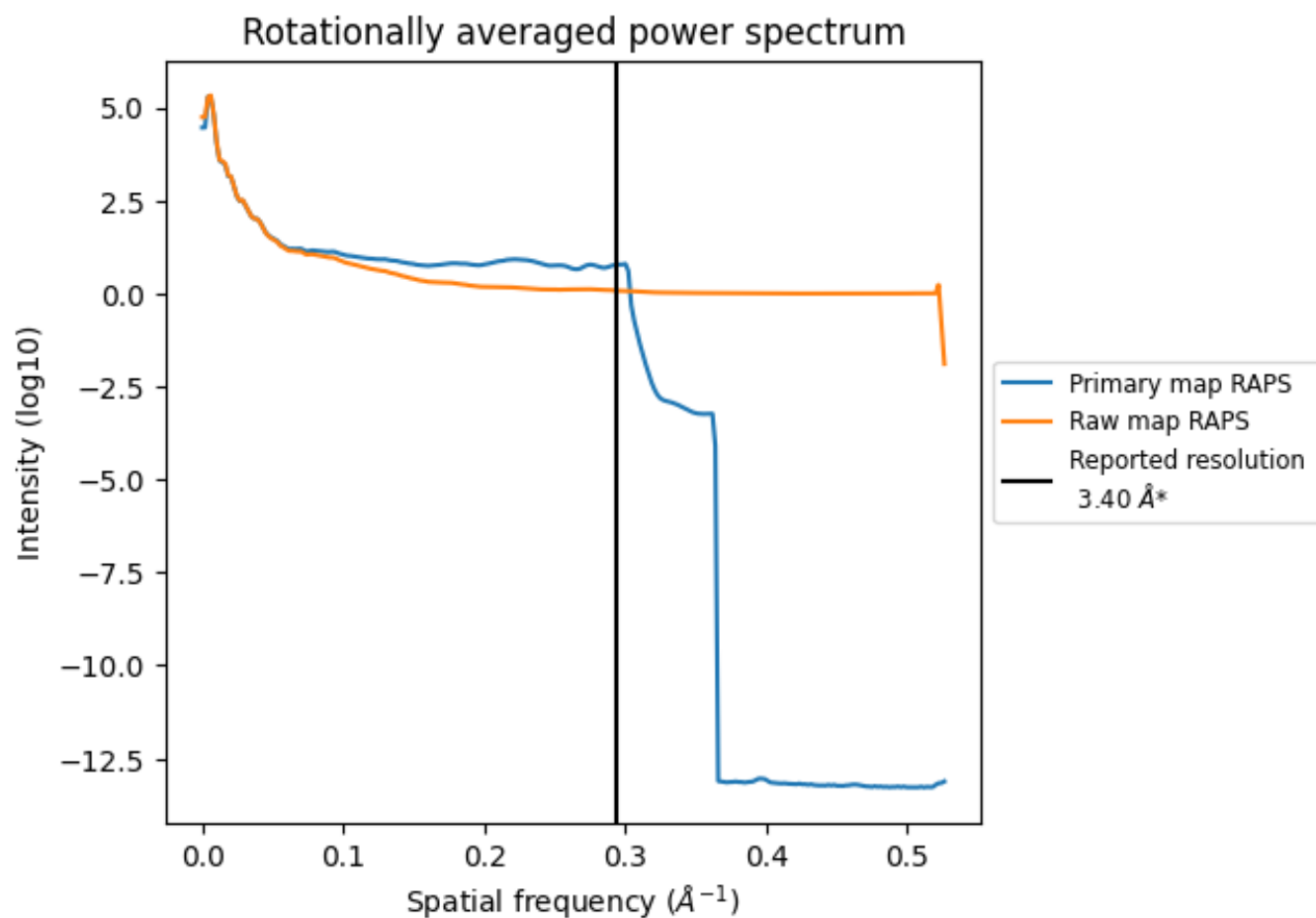
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 41 nm<sup>3</sup>; 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 ⓘ

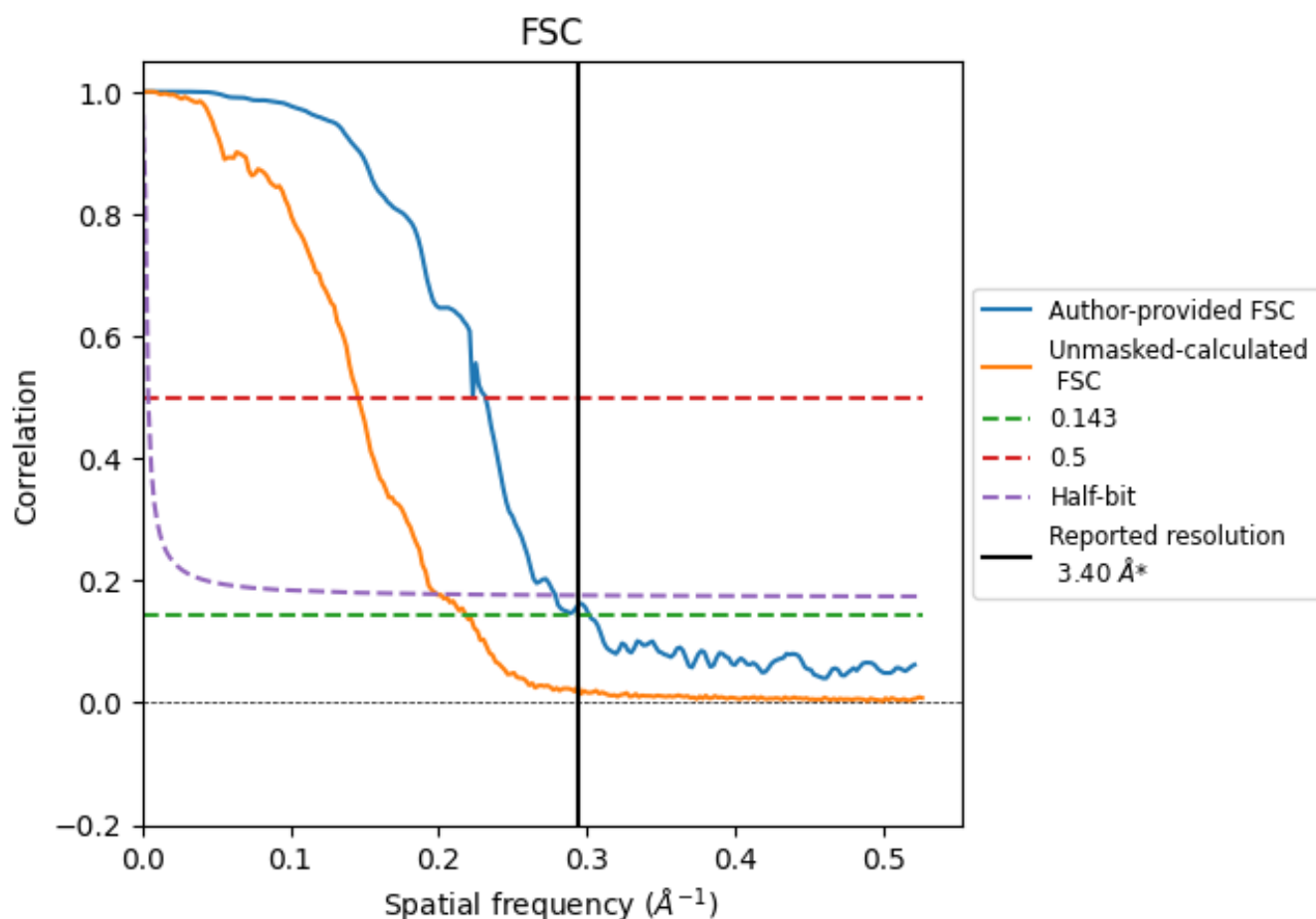


\*Reported resolution corresponds to spatial frequency of 0.294 Å<sup>-1</sup>

## 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 0.294  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

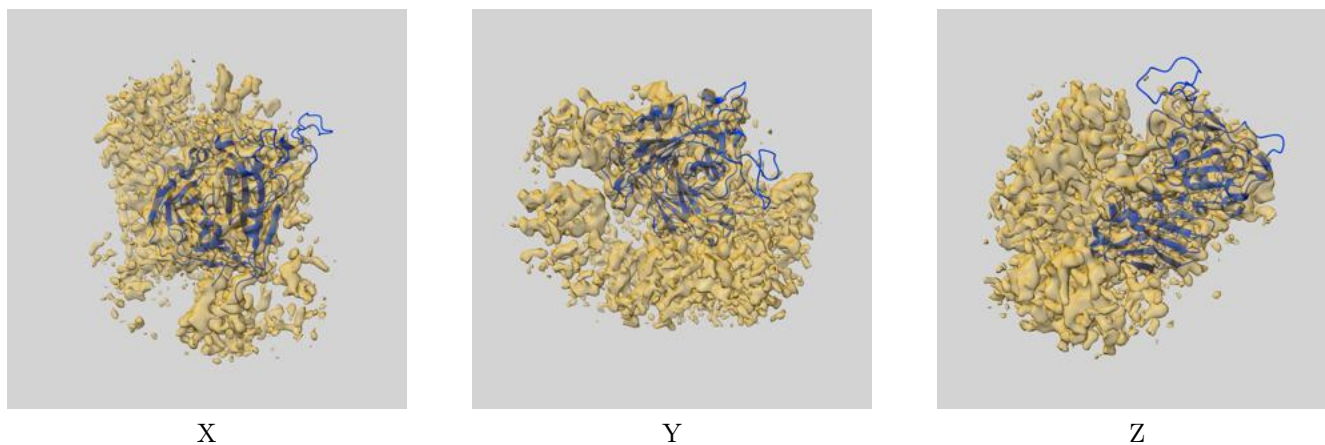
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.31	4.32	3.59
Unmasked-calculated*	4.57	6.87	5.04

\*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 4.57 differs from the reported value 3.4 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64597 and PDB model 9UXS. Per-residue inclusion information can be found in section 3 on page 6.

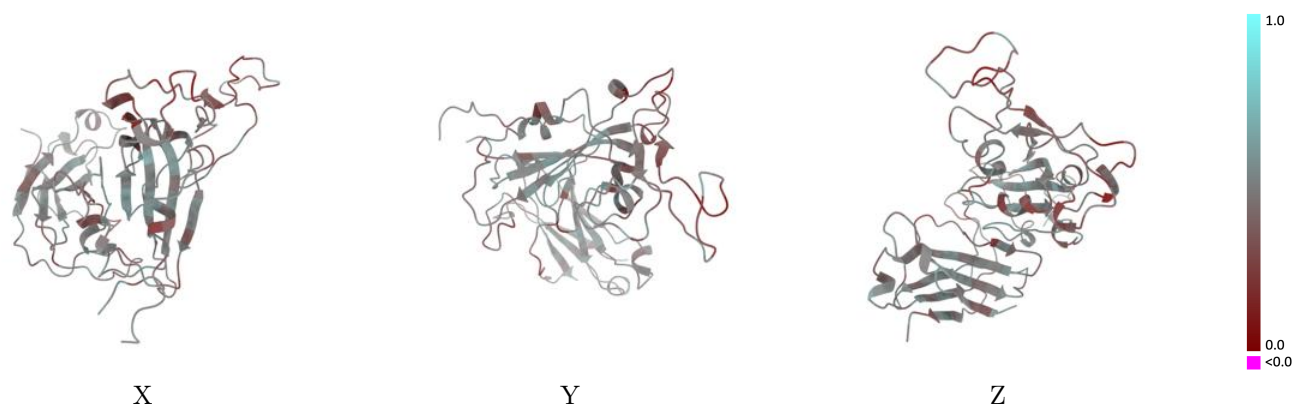
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.5 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.

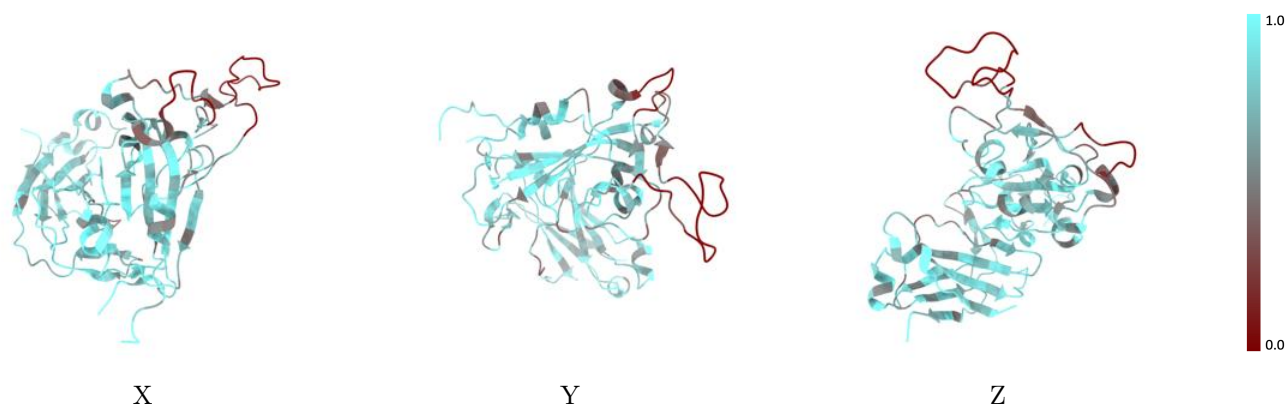


## 9.2 Q-score mapped to coordinate model [i](#)



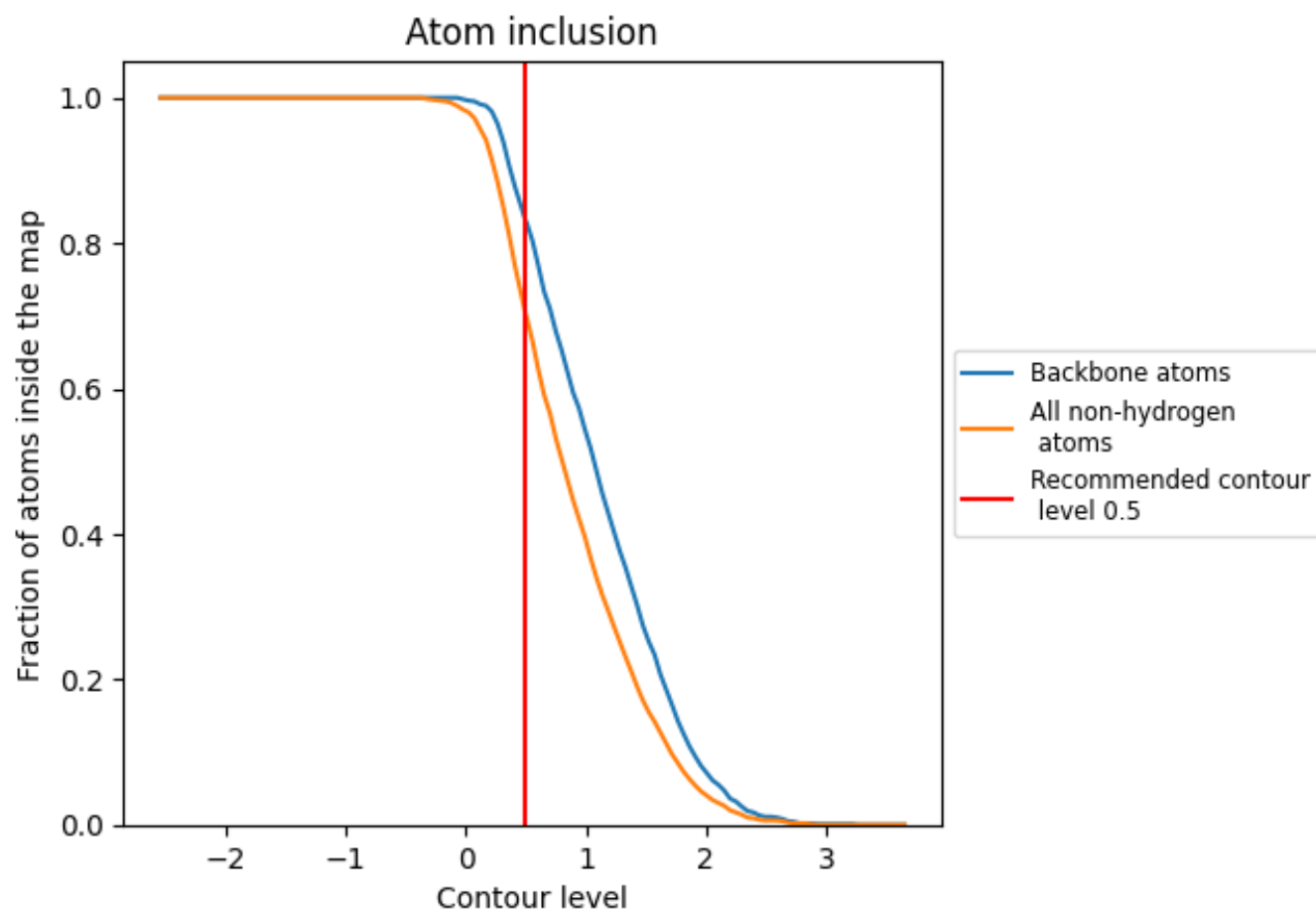
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 83% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7010	<div></div> 0.4410
A	<div></div> 0.7730	<div></div> 0.4510
B	<div></div> 0.6580	<div></div> 0.4350

