



Full wwPDB EM Validation Report ⓘ

Sep 8, 2026 – 08:42 PM JST

PDB ID : 9M7G / pdb_00009m7g
EMDB ID : EMD-63682
Title : Cryo-EM structure of the human glucagon receptor (GCGR) in ligand free state resolved via the fusion/crosslinking strategy
Authors : Han, S.C.; Li, M.H.
Deposited on : 2025-03-10
Resolution : 3.38 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

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.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
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) : 2.50

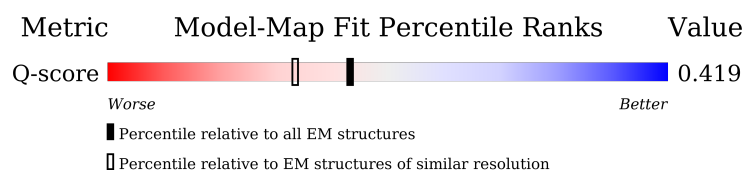
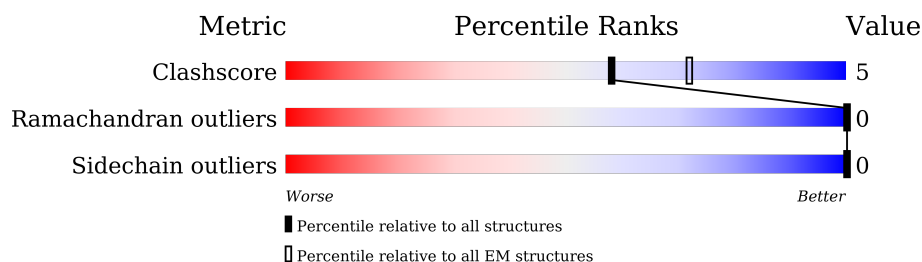
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.38 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	14261 (2.88 - 3.88)

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	476	
2	B	196	
3	C	294	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5972 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 Glucagon receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	282	Total	C	N	O	S	0	0
			2247	1489	371	374	13		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	257	CYS	THR	conflict	UNP P47871
A	1001	ARG	-	linker	UNP P47871
A	1002	ARG	-	linker	UNP P47871
A	1003	GLN	-	linker	UNP P47871
A	1004	LEU	-	linker	UNP P47871
A	1005	GLY	-	linker	UNP P47871
A	1006	HIS	-	linker	UNP P47871
A	1007	TYR	-	linker	UNP P47871
A	1008	LEU	-	linker	UNP P47871
A	1009	SER	-	linker	UNP P47871
A	1010	THR	-	linker	UNP P47871
A	1011	GLN	-	linker	UNP P47871
A	1012	THR	-	linker	UNP P47871
A	1013	SER	-	linker	UNP P47871
A	1014	LEU	-	linker	UNP P47871
A	1015	SER	-	linker	UNP P47871
A	1016	LYS	-	linker	UNP P47871
A	1017	ASP	-	linker	UNP P47871
A	1018	LEU	-	linker	UNP P47871
A	1019	ASN	-	linker	UNP P47871
A	1020	GLU	-	linker	UNP P47871
A	1021	LYS	-	linker	UNP P47871
A	1022	ARG	-	linker	UNP P47871
A	1023	ASP	-	linker	UNP P47871
A	1024	HIS	-	linker	UNP P47871
A	1025	MET	-	linker	UNP P47871
A	1026	VAL	-	linker	UNP P47871
A	1027	LEU	-	linker	UNP P47871

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1028	LEU	-	linker	UNP P47871
A	1029	GLU	-	linker	UNP P47871
A	1030	PHE	-	linker	UNP P47871
A	1031	VAL	-	linker	UNP P47871
A	1032	THR	-	linker	UNP P47871
A	1033	ALA	-	linker	UNP P47871
A	1034	ALA	-	linker	UNP P47871
A	1035	GLY	-	linker	UNP P47871
A	1036	LEU	-	linker	UNP P47871
A	1037	GLN	-	linker	UNP P47871
A	1038	LYS	-	linker	UNP P47871
A	1039	GLU	-	linker	UNP P47871

- Molecule 2 is a protein called Green fluorescent protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	194	Total	C	N	O	S	0	0
			1565	997	268	295	5		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP A0A059PIQ0
B	1	GLY	-	expression tag	UNP A0A059PIQ0
B	2	THR	-	expression tag	UNP A0A059PIQ0
B	17	ILE	VAL	conflict	UNP A0A059PIQ0
B	31	ARG	SER	conflict	UNP A0A059PIQ0
B	40	TYR	ASN	conflict	UNP A0A059PIQ0
B	67	CRO	THR	conflict	UNP A0A059PIQ0
B	?	-	TYR	deletion	UNP A0A059PIQ0
B	?	-	GLY	deletion	UNP A0A059PIQ0
B	73	SER	ALA	conflict	UNP A0A059PIQ0
B	81	ARG	GLN	conflict	UNP A0A059PIQ0
B	100	TYR	SER	conflict	UNP A0A059PIQ0
B	154	MET	THR	conflict	UNP A0A059PIQ0
B	159	ASN	LYS	conflict	UNP A0A059PIQ0

- Molecule 3 is a protein called GFP-clamp E186C.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	287	Total	C	N	O	S	0	0
			2160	1367	370	421	2		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	107457	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.653	Depositor
Minimum map value	-4.213	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.093	Depositor
Recommended contour level	0.2	Depositor
Map size ($\text{\AA}$)	281.6, 281.6, 281.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CRO

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	0.13	0/2299	0.45	4/3115 (0.1%)
2	B	0.10	0/1578	0.29	0/2130
3	C	0.12	0/2199	0.35	0/2996
All	All	0.12	0/6076	0.37	4/8241 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	167	SER	N-CA-C	-9.73	95.14	108.86
1	A	166	LEU	N-CA-C	7.87	127.57	110.80
1	A	167	SER	N-CA-CB	5.30	120.16	111.31
1	A	166	LEU	CB-CA-C	-5.01	100.45	110.42

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	2247	0	2312	18	0
2	B	1565	0	1525	10	0
3	C	2160	0	2113	29	0
All	All	5972	0	5950	56	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 5.

All (56) 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:168:LYS:HZ3	1:A:407:VAL:HA	1.51	0.75
3:C:77:THR:HB	3:C:107:LEU:HD23	1.78	0.63
2:B:63:THR:O	2:B:97:ARG:NH1	2.31	0.63
2:B:37:ASP:HB3	2:B:42:LYS:HB2	1.82	0.61
2:B:156:ASP:H	2:B:162:ILE:HA	1.66	0.60
3:C:218:LEU:HD12	3:C:219:GLU:N	2.16	0.59
1:A:163:LEU:HD11	1:A:174:ASN:HB3	1.85	0.59
1:A:140:SER:HA	1:A:143:VAL:HG12	1.86	0.57
3:C:88:LEU:HA	3:C:92:ALA:HB3	1.86	0.56
3:C:21:LEU:HB2	3:C:26:ALA:HB3	1.90	0.53
1:A:167:SER:HB3	1:A:168:LYS:HD2	1.90	0.53
3:C:276:ASP:HA	3:C:279:ILE:HG22	1.91	0.53
3:C:65:ASP:OD1	3:C:65:ASP:N	2.44	0.51
2:B:170:HIS:HB2	2:B:178:GLN:HB3	1.91	0.51
1:A:163:LEU:HD23	1:A:164:GLY:N	2.25	0.51
2:B:67:CRO:N2	2:B:67:CRO:HD2	2.26	0.50
1:A:168:LYS:HB3	1:A:174:ASN:CG	2.37	0.49
3:C:81:LEU:HA	3:C:116:ILE:HD11	1.95	0.49
2:B:67:CRO:C2	2:B:97:ARG:HH22	2.24	0.49
1:A:1022:ARG:O	1:A:1024:HIS:ND1	2.46	0.49
3:C:45:ARG:HD2	3:C:47:HIS:CD2	2.48	0.49
1:A:1036:LEU:HD12	2:B:79:MET:HG2	1.96	0.48
3:C:98:ASP:OD1	3:C:102:HIS:N	2.47	0.47
1:A:167:SER:C	1:A:168:LYS:HD2	2.39	0.47
2:B:151:VAL:HA	2:B:166:PHE:HB3	1.97	0.46
1:A:228:ALA:O	1:A:232:GLN:HG2	2.15	0.46
1:A:194:ILE:HB	1:A:227:ALA:HB1	1.98	0.46
3:C:103:THR:OG1	3:C:106:HIS:ND1	2.25	0.45
3:C:53:VAL:HG22	3:C:57:TYR:CZ	2.52	0.45
1:A:295:TRP:CD1	1:A:295:TRP:N	2.82	0.45
2:B:99:ILE:HB	2:B:107:TYR:HB2	1.98	0.45
3:C:177:LEU:HD22	3:C:188:VAL:HG23	1.98	0.45
1:A:173:ARG:HG2	1:A:177:HIS:CE1	2.52	0.45
3:C:51:VAL:HG21	3:C:83:ILE:HD11	1.98	0.45
3:C:218:LEU:HD12	3:C:218:LEU:C	2.42	0.44
3:C:286:ILE:O	3:C:290:LEU:HD12	2.17	0.44
3:C:22:MET:HE1	3:C:57:TYR:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:VAL:HB	1:A:275:PRO:HB3	2.00	0.44
3:C:1:ASP:O	3:C:5:LYS:HG3	2.18	0.44
3:C:275:PHE:C	3:C:275:PHE:CD2	2.96	0.43
1:A:140:SER:O	1:A:143:VAL:HG12	2.19	0.43
1:A:376:THR:OG1	1:A:377:LEU:N	2.47	0.42
3:C:2:LEU:HD23	3:C:2:LEU:H	1.85	0.42
1:A:354:LEU:HD23	1:A:354:LEU:HA	1.90	0.42
3:C:175:THR:HG22	3:C:177:LEU:H	1.85	0.42
3:C:40:HIS:HD2	3:C:71:PRO:HG3	1.83	0.41
3:C:65:ASP:C	3:C:67:TRP:H	2.29	0.41
1:A:258:LEU:HB2	1:A:259:PRO:HD2	2.02	0.41
3:C:263:ASP:OD1	3:C:263:ASP:C	2.63	0.41
3:C:73:HIS:NE2	3:C:104:PRO:HD3	2.36	0.41
3:C:243:HIS:O	3:C:247:ILE:HG13	2.20	0.41
3:C:2:LEU:HD12	3:C:26:ALA:HA	2.03	0.41
3:C:201:ALA:HB1	3:C:205:GLY:HA2	2.03	0.41
3:C:70:THR:H	3:C:73:HIS:HD1	1.68	0.41
2:B:131:PHE:CE2	2:B:137:ILE:HG21	2.57	0.40
3:C:254:VAL:O	3:C:258:LEU:HD13	2.22	0.40

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	276/476 (58%)	257 (93%)	19 (7%)	0	100	100
2	B	189/196 (96%)	180 (95%)	9 (5%)	0	100	100
3	C	283/294 (96%)	271 (96%)	12 (4%)	0	100	100
All	All	748/966 (77%)	708 (95%)	40 (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	242/409 (59%)	242 (100%)	0	100	100
2	B	168/169 (99%)	168 (100%)	0	100	100
3	C	217/218 (100%)	217 (100%)	0	100	100
All	All	627/796 (79%)	627 (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
1	A	177	HIS
1	A	1011	GLN
2	B	147	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CRO	B	67	2	23,23,24	2.71	7 (30%)	30,32,34	2.83	8 (26%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CRO	B	67	2	-	5/12/31/32	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	67	CRO	C1-N2	7.17	1.42	1.32
2	B	67	CRO	CA2-C2	6.17	1.54	1.48
2	B	67	CRO	C1-N3	5.26	1.46	1.37
2	B	67	CRO	C2-N3	3.75	1.48	1.39
2	B	67	CRO	CG2-CB2	3.72	1.54	1.46
2	B	67	CRO	CB2-CA2	-2.42	1.33	1.35
2	B	67	CRO	CA2-N2	2.28	1.43	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	67	CRO	CA2-C2-N3	8.64	107.45	103.37
2	B	67	CRO	O2-C2-CA2	-8.20	126.36	130.96
2	B	67	CRO	C2-N3-C1	-5.41	105.23	107.97
2	B	67	CRO	CA2-N2-C1	4.92	109.40	105.77
2	B	67	CRO	C2-CA2-N2	-4.02	106.12	108.93
2	B	67	CRO	CG2-CB2-CA2	-3.42	125.76	129.94
2	B	67	CRO	CB2-CA2-C2	2.13	124.82	122.28
2	B	67	CRO	O3-C3-CA3	-2.05	120.21	126.39

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	67	CRO	C3-CA3-N3-C2
2	B	67	CRO	C1-CA1-CB1-OG1
2	B	67	CRO	C1-CA1-CB1-CG1
2	B	67	CRO	N1-CA1-CB1-CG1
2	B	67	CRO	C3-CA3-N3-C1

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	67	CRO	2	0

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.

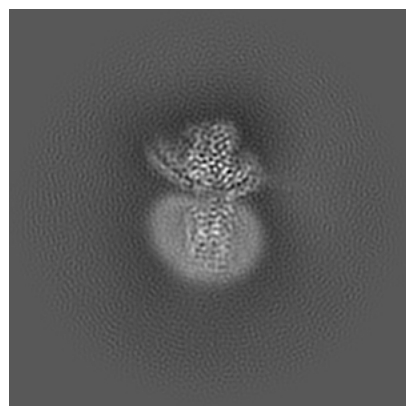
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63682. These allow visual inspection of the internal detail of the map and identification of artifacts.

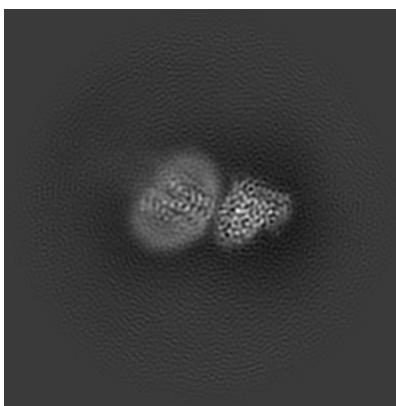
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

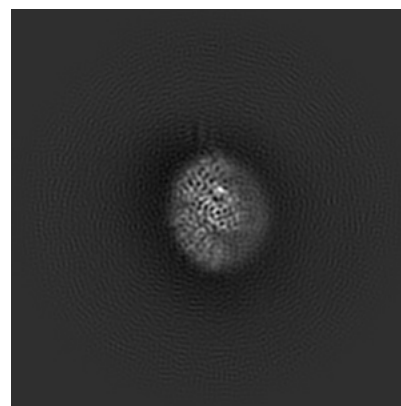
6.1.1 Primary map



X

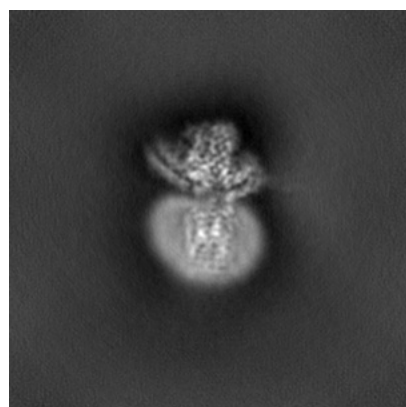


Y

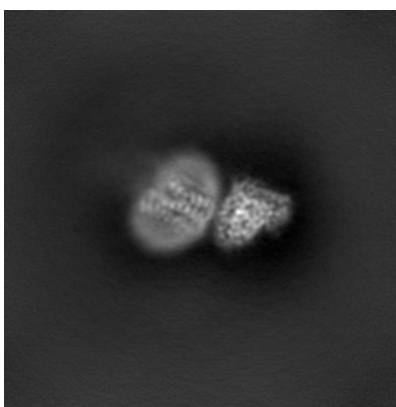


Z

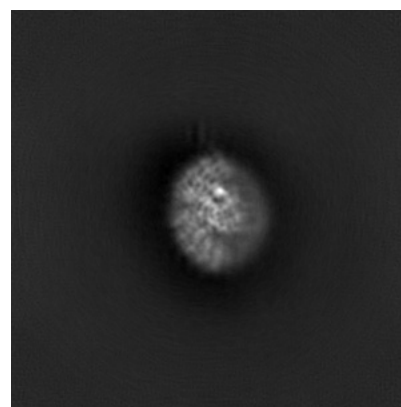
6.1.2 Raw map



X



Y

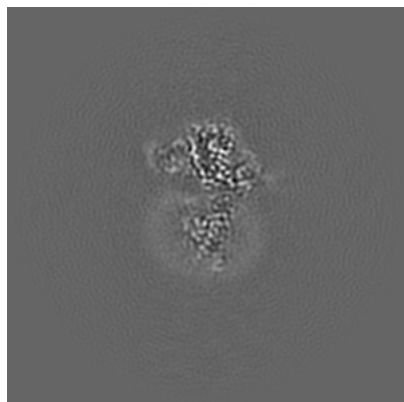


Z

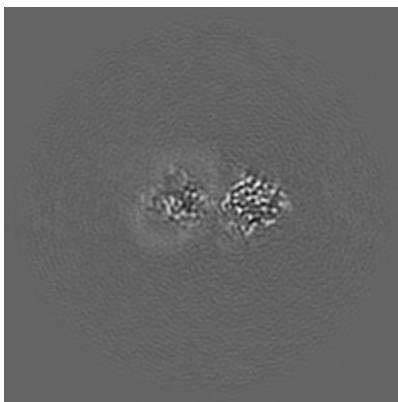
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

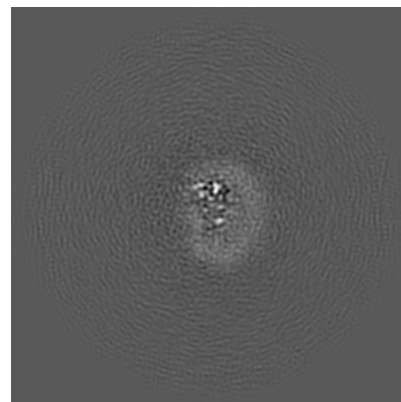
6.2.1 Primary map



X Index: 128

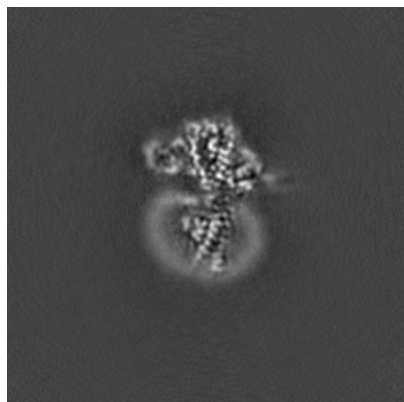


Y Index: 128

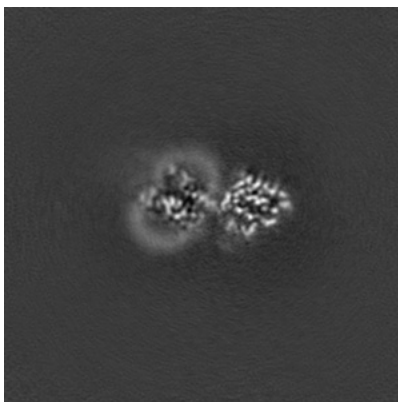


Z Index: 128

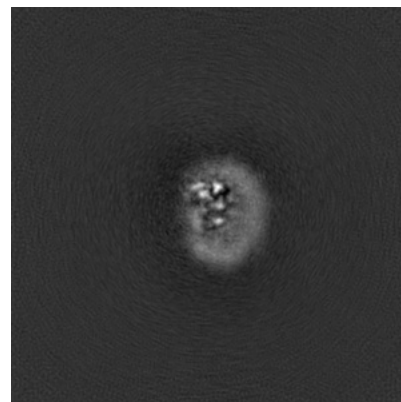
6.2.2 Raw map



X Index: 128



Y Index: 128

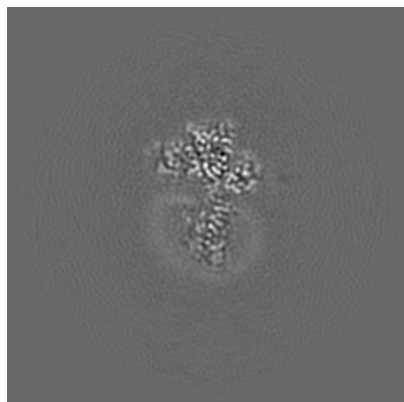


Z Index: 128

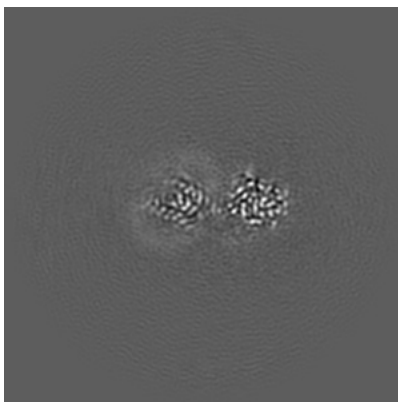
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

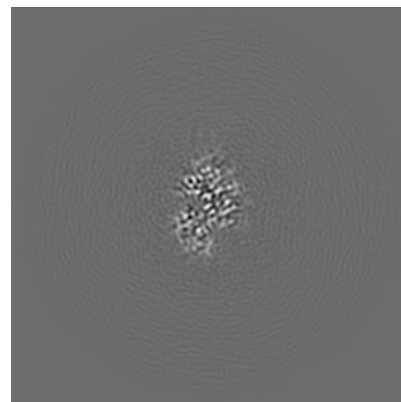
6.3.1 Primary map



X Index: 126

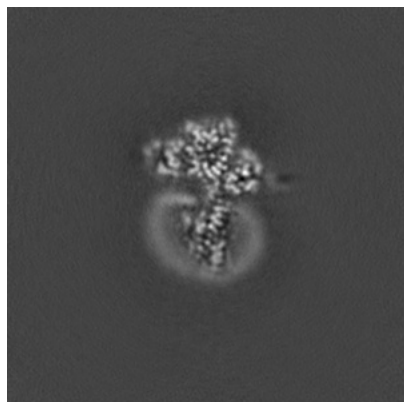


Y Index: 131

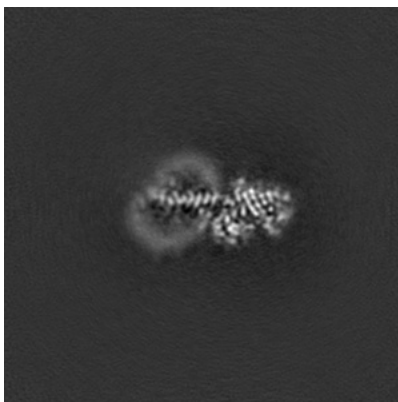


Z Index: 150

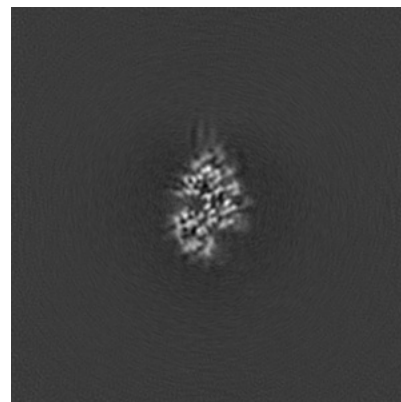
6.3.2 Raw map



X Index: 126



Y Index: 139

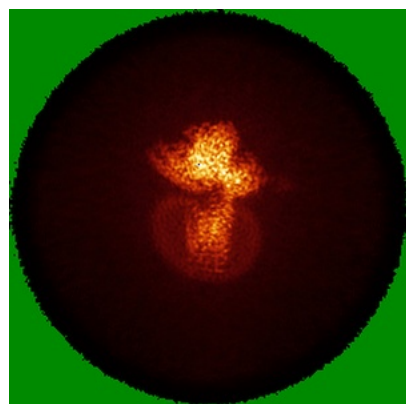


Z Index: 150

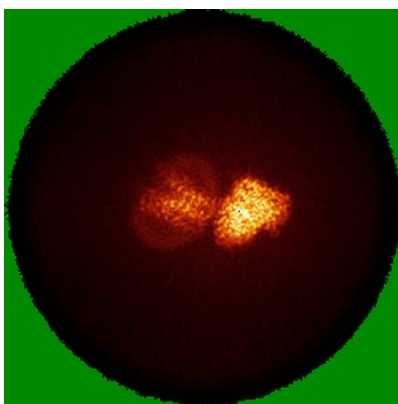
The images above show the largest variance slices of the map in three orthogonal directions.

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

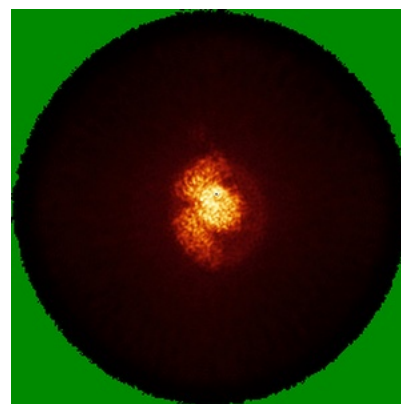
6.4.1 Primary map



X

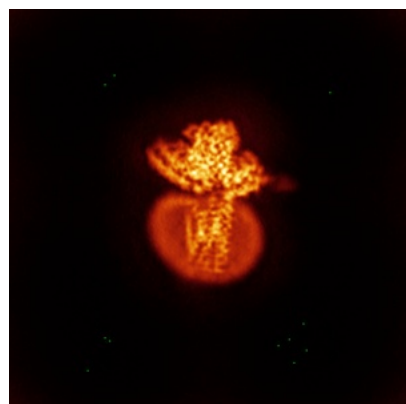


Y

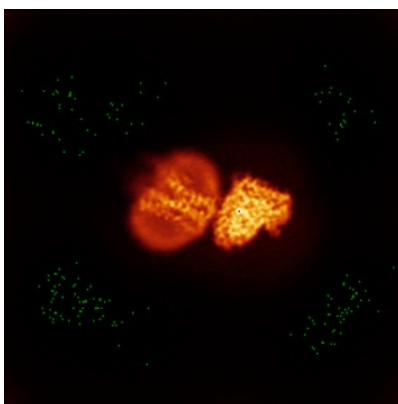


Z

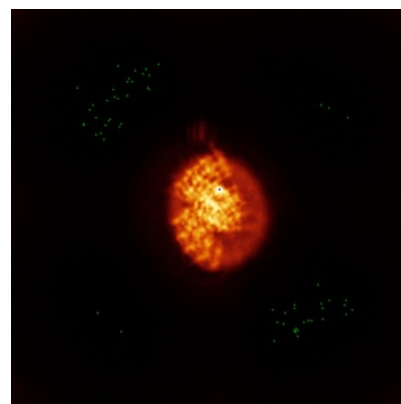
6.4.2 Raw map



X



Y

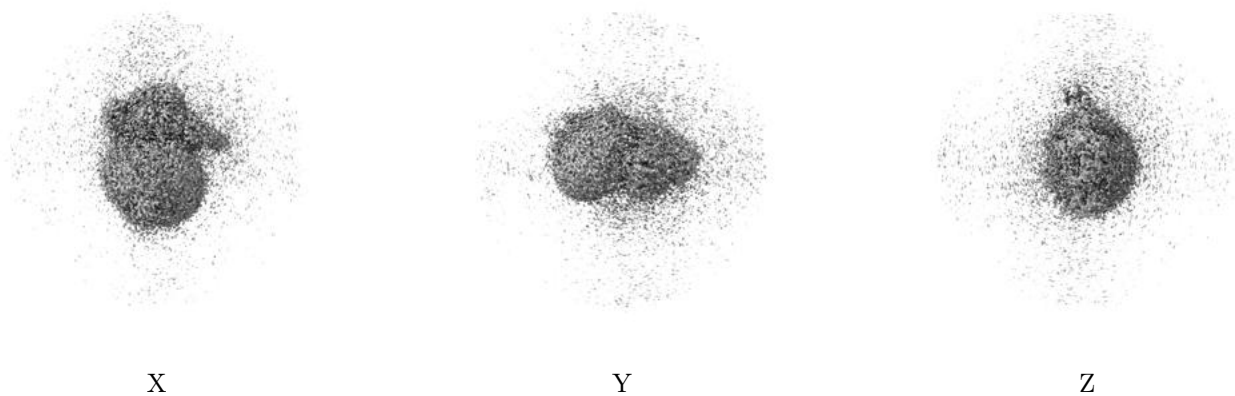


Z

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.

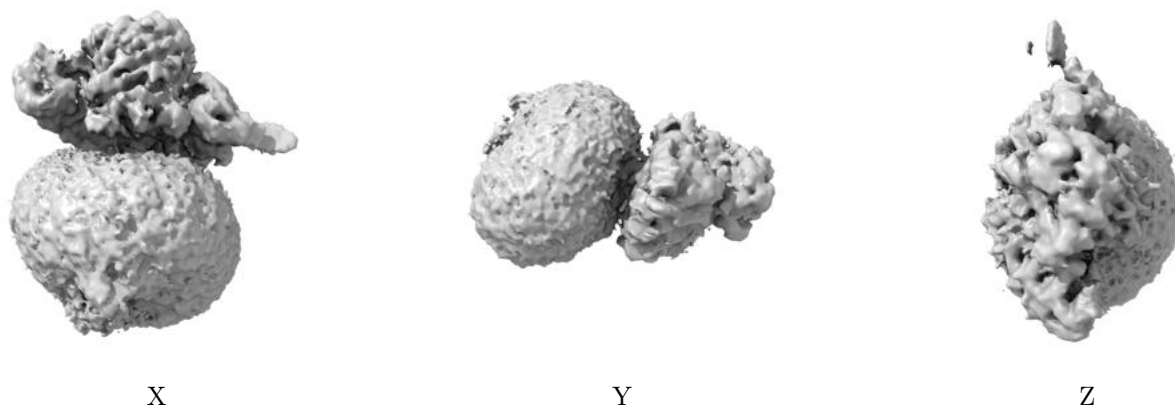
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. 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.

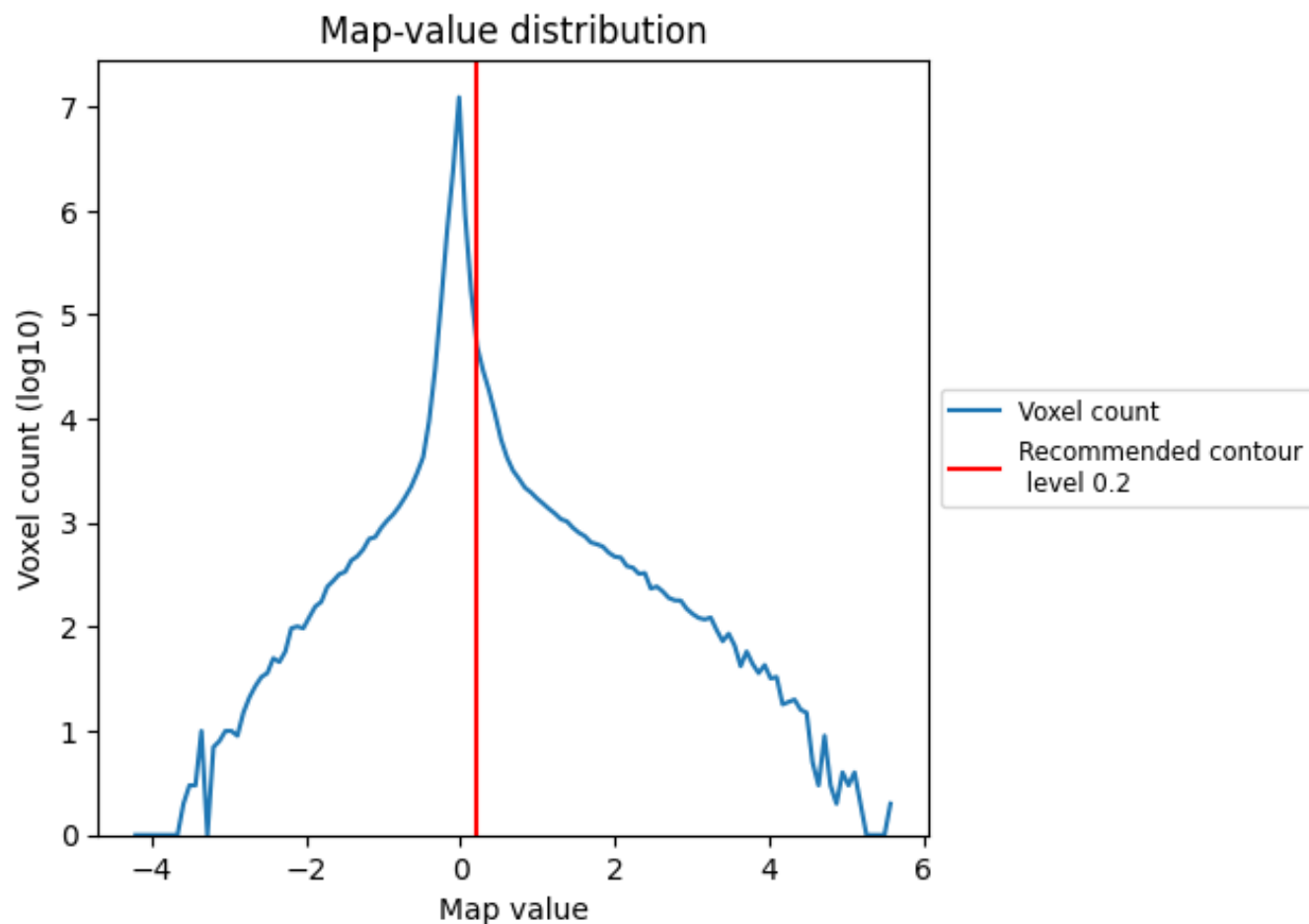
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

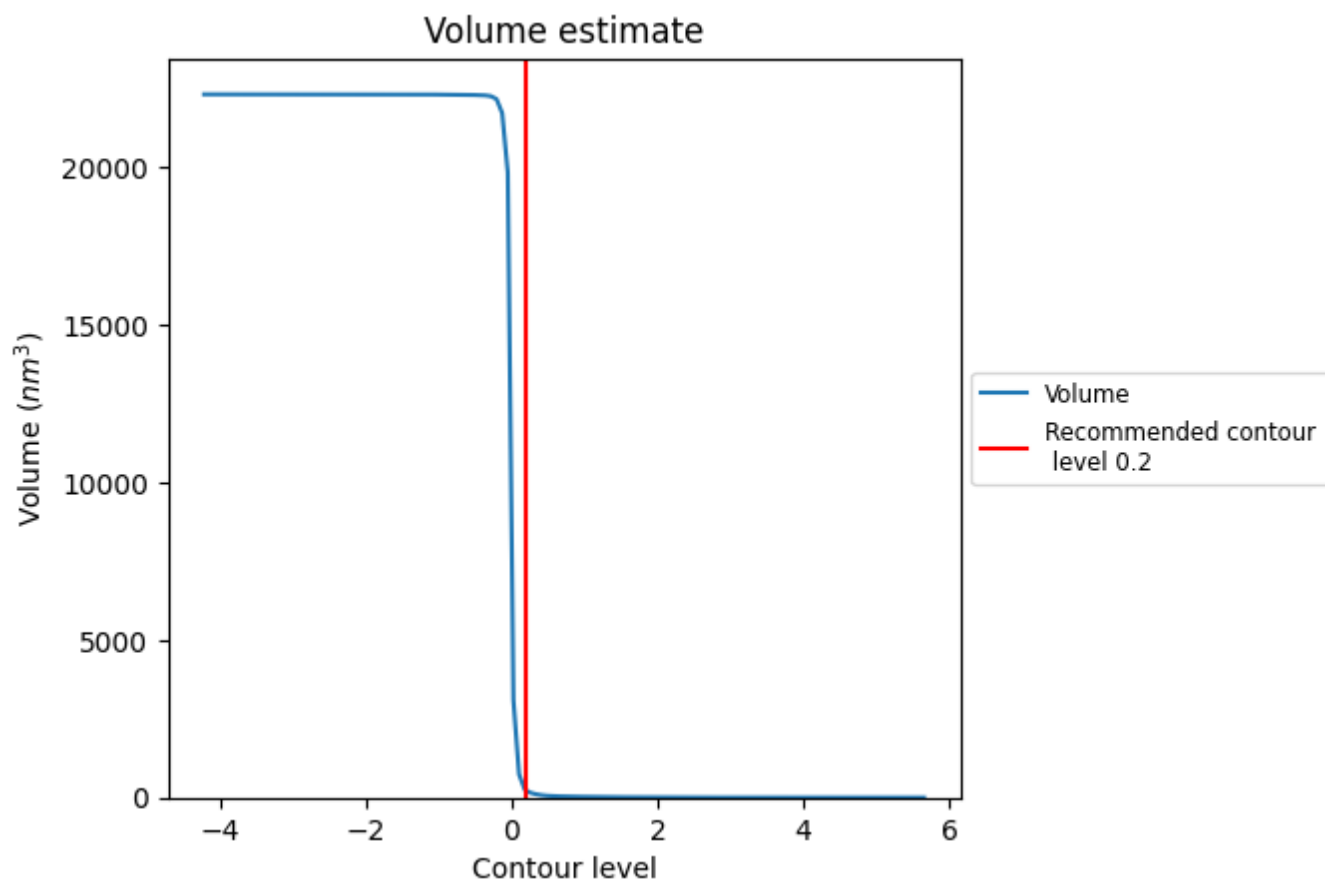
This section contains the results of statistical analysis of the map.

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.

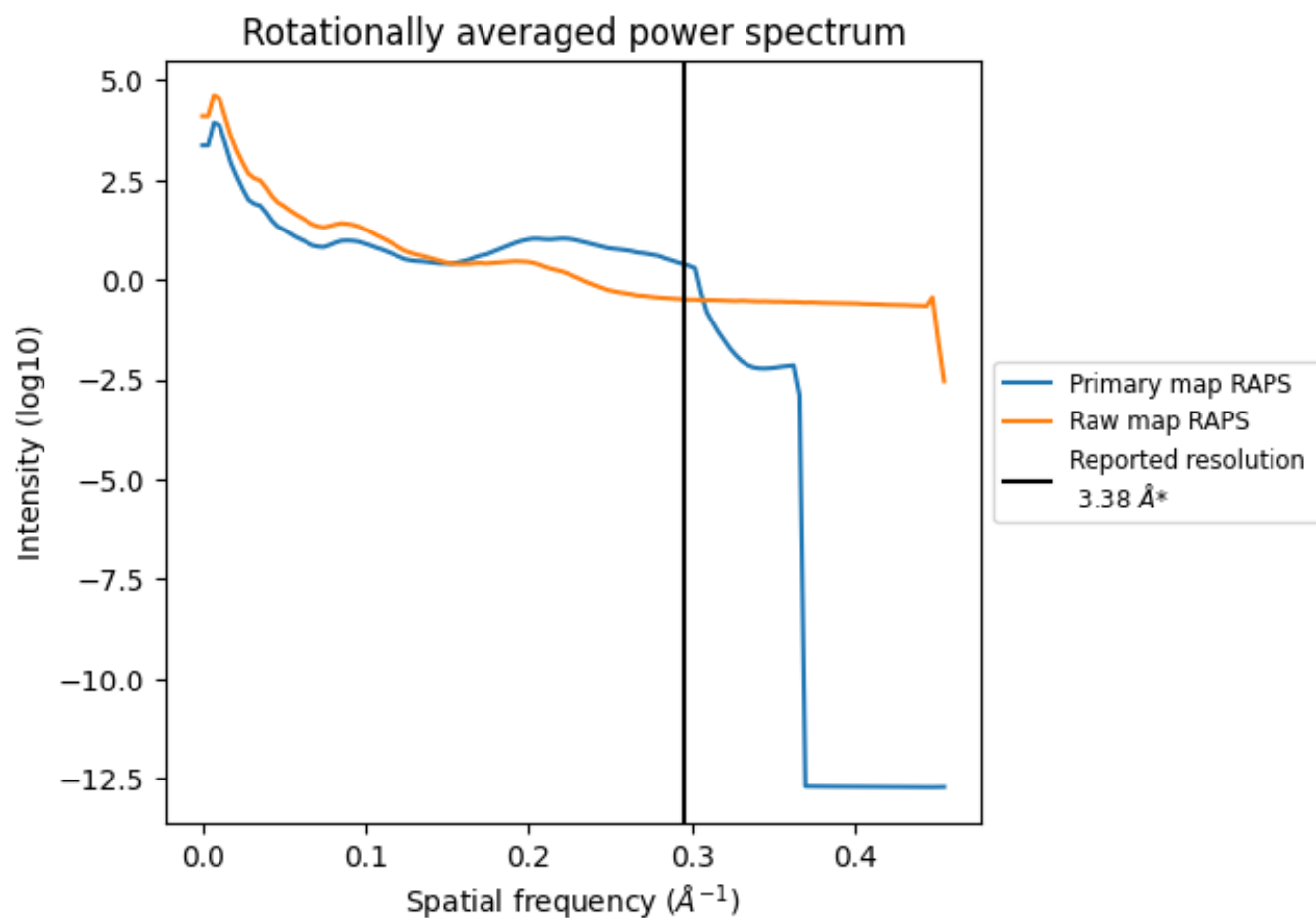
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 230 nm³; this corresponds to an approximate mass of 208 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 ⓘ

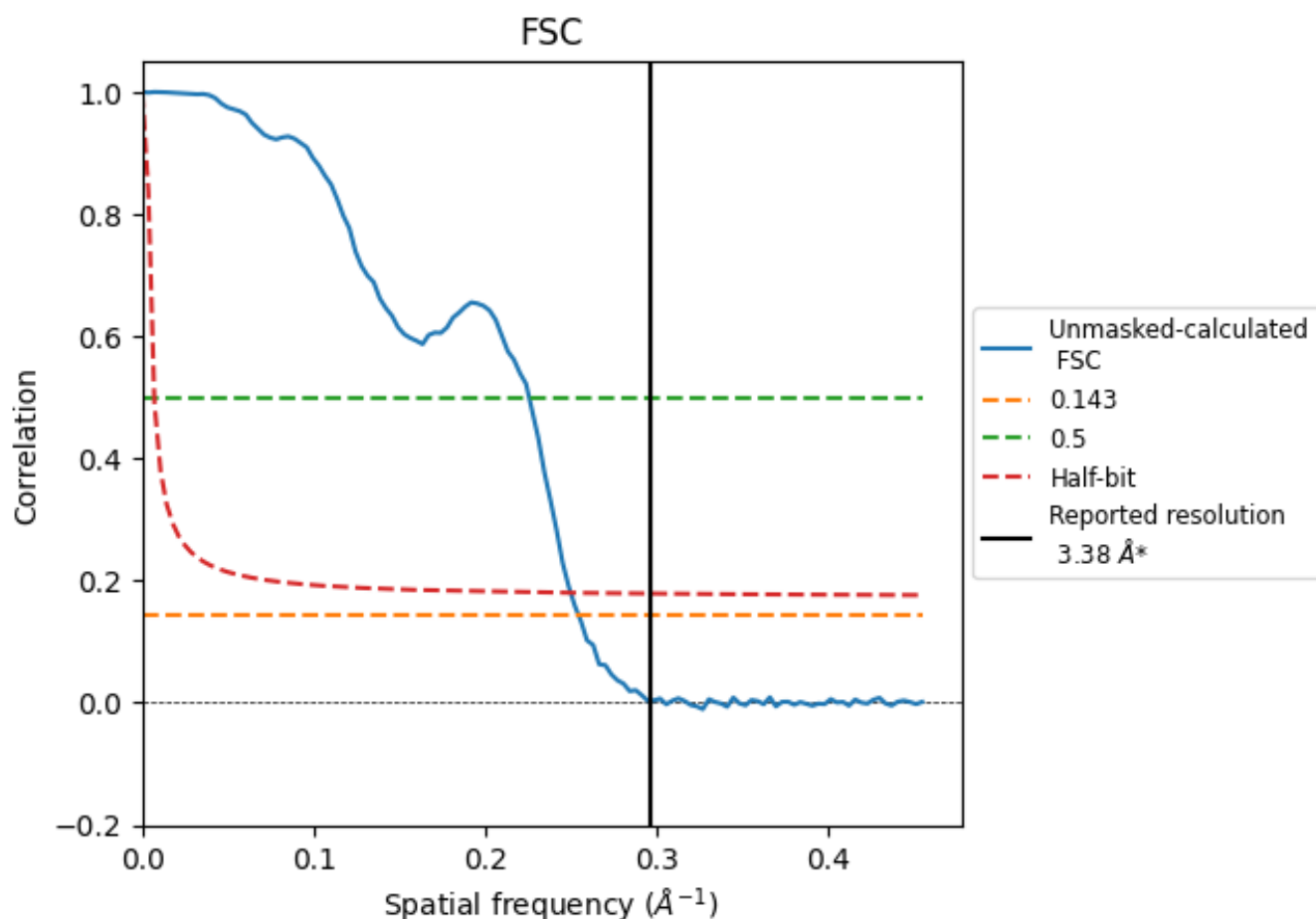


*Reported resolution corresponds to spatial frequency of 0.296 Å⁻¹

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 0.296 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

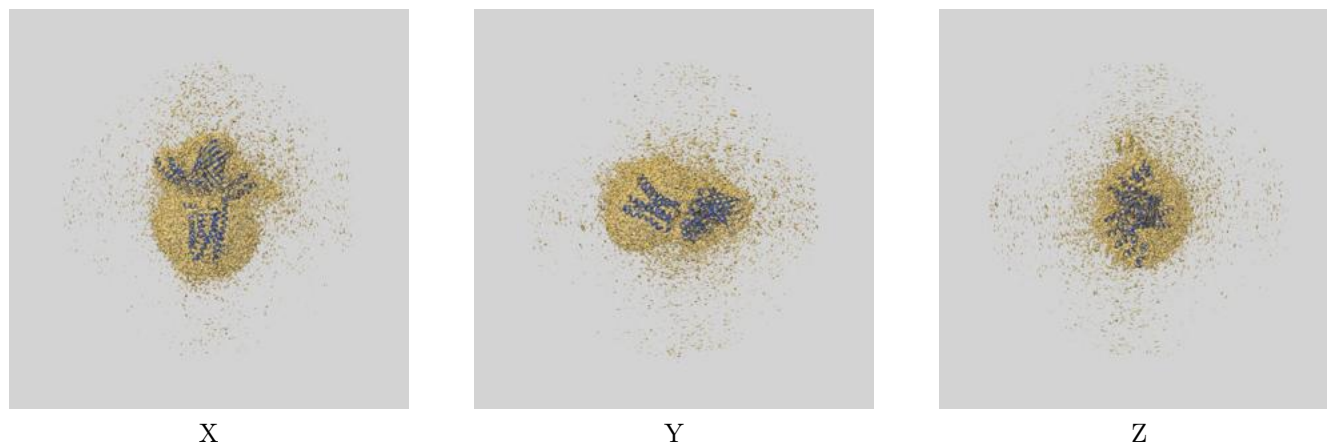
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.38	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.93	4.43	4.00

*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 3.93 differs from the reported value 3.38 by more than 10 %

9 Map-model fit [i](#)

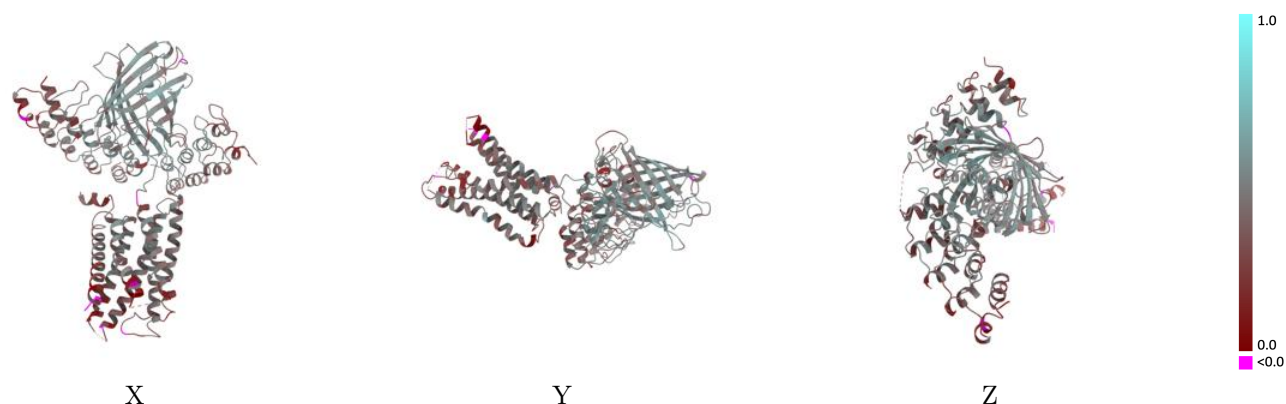
This section contains information regarding the fit between EMDB map EMD-63682 and PDB model 9M7G. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



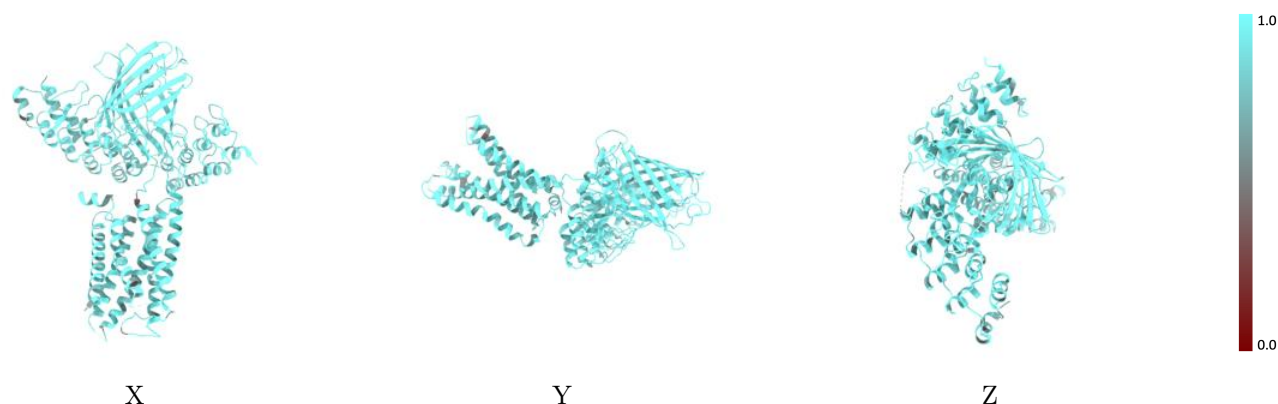
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



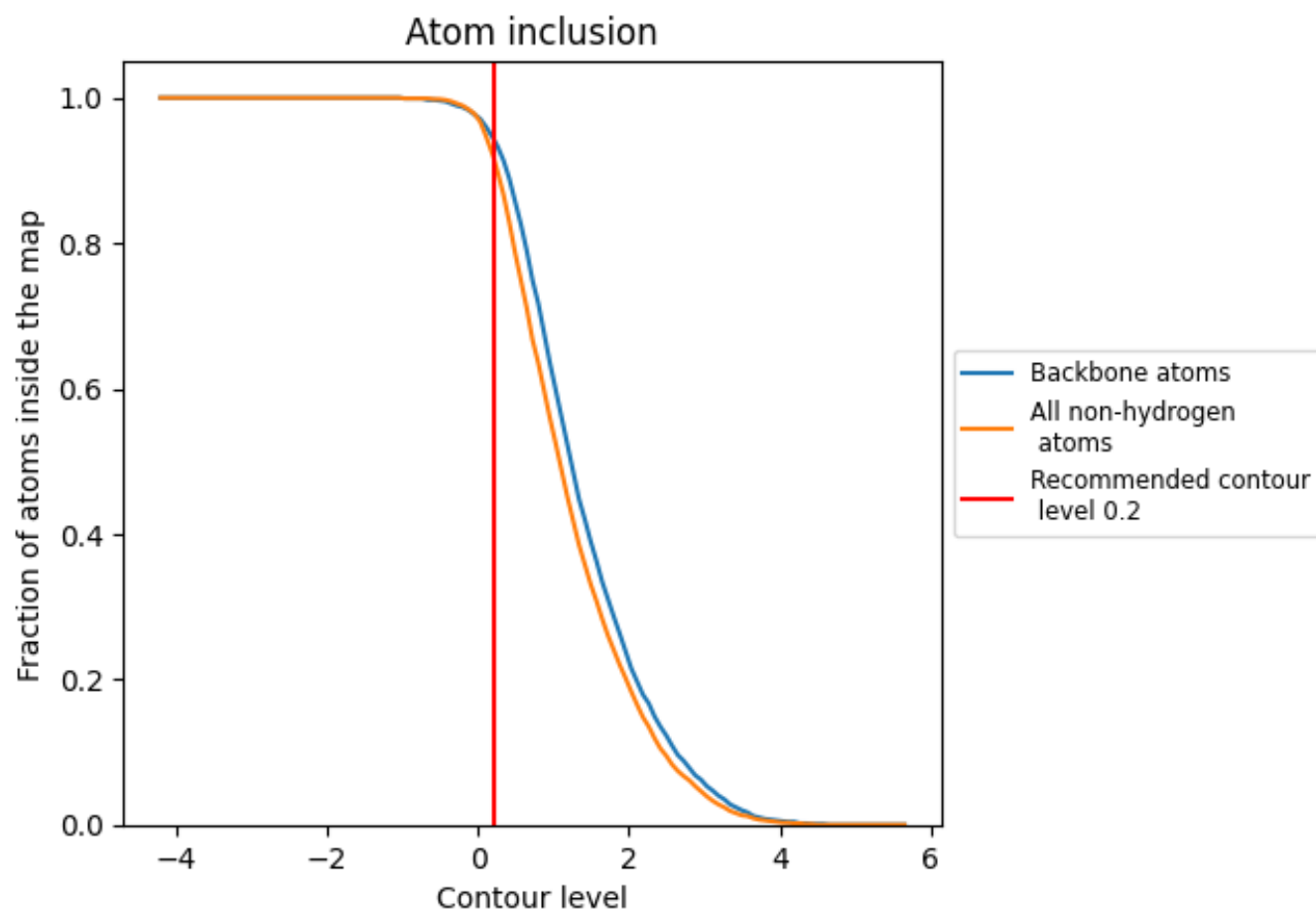
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9190	0.4190
A	0.9050	0.3770
B	0.9410	0.4930
C	0.9190	0.4080

