



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 08:02 PM UTC

PDB ID : 7Y89 / pdb_00007y89
EMDB ID : EMD-33682
Title : Structure of the GPR17-Gi complex
Authors : Ye, F.; Chen, G.
Deposited on : 2022-06-23
Resolution : 3.02 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

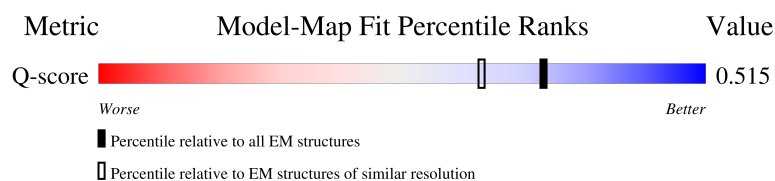
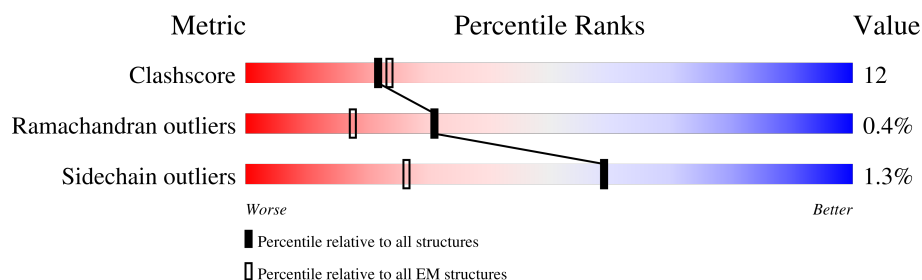
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.02 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	13913 (2.52 - 3.52)

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	C	351	 50% 8% 41%
2	B	337	 77% 21%
3	G	56	 73% 20% 5%
4	S	248	 77% 17% 6%

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Mol	Chain	Length	Quality of chain
5	A	293	63% 31% ...

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8641 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 Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	206	Total	C	N	O	S	0	0
			1639	1044	279	305	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	203	ALA	GLY	conflict	UNP P63096
C	326	SER	ALA	conflict	UNP P63096

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	331	Total	C	N	O	S	0	0
			2530	1563	452	494	21		

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	53	Total	C	N	O	S	0	0
			412	258	73	78	3		

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S	233	Total	C	N	O	S	0	0
			1772	1128	296	338	10		

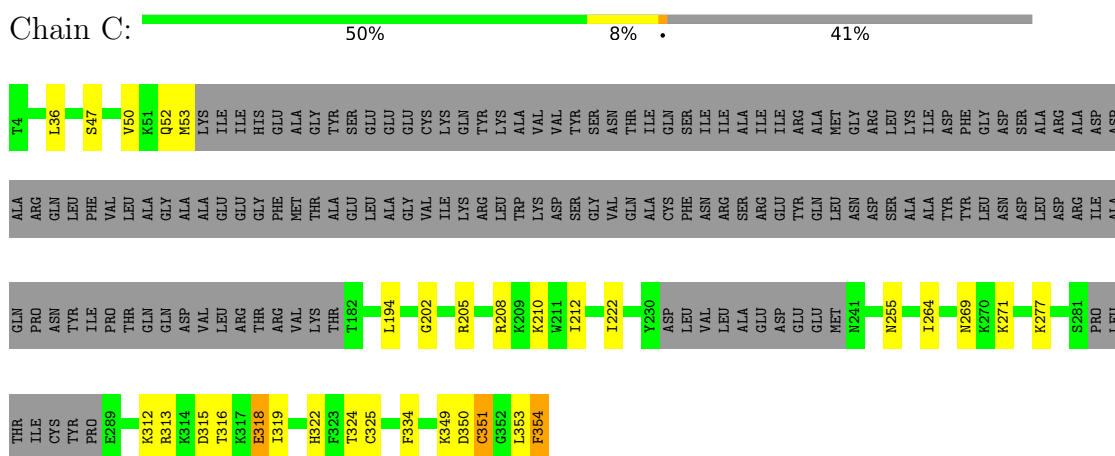
- Molecule 5 is a protein called Uracil nucleotide/cysteinyl leukotriene receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	287	Total	C	N	O	S	0	0
			2288	1513	390	369	16		

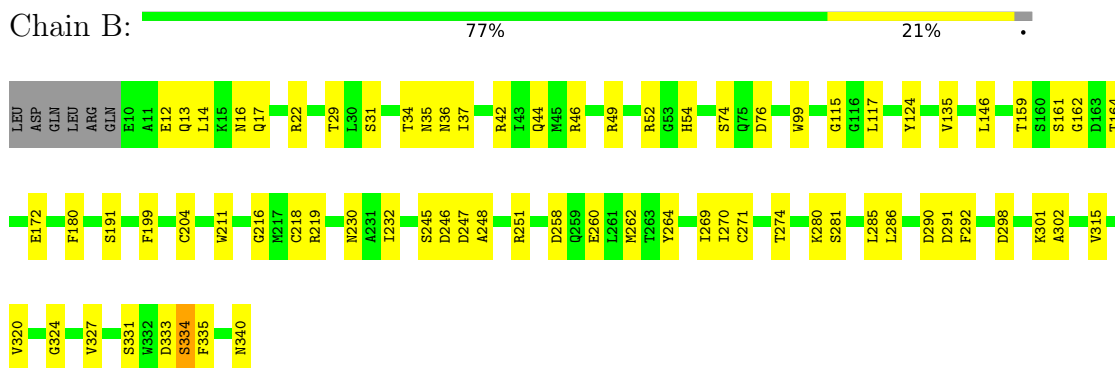
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

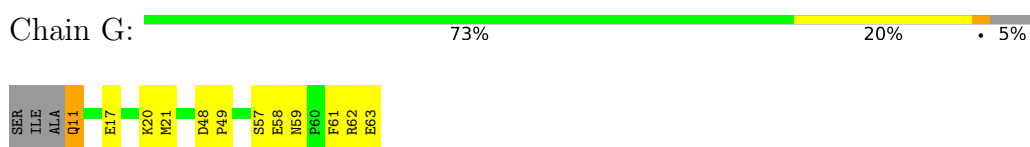
- Molecule 1: Guanine nucleotide-binding protein G(i) subunit alpha-1



- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



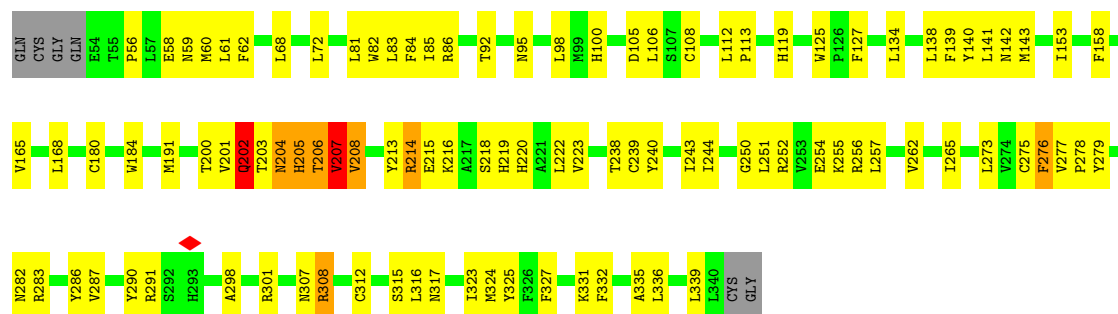
- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



- Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

GLY	L11	GLY	L15	GLY	L18	GLY	L24	GLY	L30	GLY	L35	GLY	L40	GLY	L45	GLY	L50	GLY	L59	GLY	L61	GLY	L62	GLY	L63	GLY	L64	GLY	L69	GLY	L74	GLY	L77	GLY	L82	GLY	L85	GLY	L91	GLY	L92	GLY	L93	GLY	L94	GLY	L95	GLY	L96	GLY	L97	GLY	L98	GLY	L99	GLY	L107	GLY	L111	GLY	L119	GLY	L120	GLY	L121	GLY	L123	GLY	L124	GLY	L125	GLY	L126	GLY	L127	GLY	L128	GLY	L129	GLY	L130	GLY	L131	GLY	L132	GLY	L133	GLY	L134	GLY	L135	GLY	L136	GLY	L137	GLY	L138	GLY	L139	GLY	L140	GLY	L141	GLY	L142	GLY	L143	GLY	L144	GLY	L145	GLY	L146	GLY	L147	GLY	L148	GLY	L149	GLY	L150	GLY	L151	GLY	L152	GLY	L153	GLY	L154	GLY	L155	GLY	L156	GLY	L157	GLY	L158	GLY	L159	GLY	L160	GLY	L161	GLY	L162	GLY	L163	GLY	L164	GLY	L165	GLY	L166	GLY	L167	GLY	L168	GLY	L169	GLY	L170	GLY	L171	GLY	L172	GLY	L173	GLY	L174	GLY	L175	GLY	L176	GLY	L177	GLY	L178	GLY	L179	GLY	L180	GLY	L181	GLY	L182	GLY	L183	GLY	L184	GLY	L185	GLY	L186	GLY	L187	GLY	L188	GLY	L189	GLY	L190	GLY	L191	GLY	L192	GLY	L193	GLY	L194	GLY	L195	GLY	L196	GLY	L197	GLY	L198	GLY	L199	GLY	L200	GLY	L201	GLY	L202	GLY	L203	GLY	L204	GLY	L205	GLY	L206	GLY	L207	GLY	L208	GLY	L209	GLY	L210	GLY	L211	GLY	L212	GLY	L213	GLY	L214	GLY	L215	GLY	L216	GLY	L217	GLY	L218	GLY	L219	GLY	L220	GLY	L221	GLY	L222	GLY	L223	GLY	L224	GLY	L225	GLY	L226	GLY	L227	GLY	L228	GLY	L229	GLY	L230	GLY	L231	GLY	L232	GLY	L233	GLY	L234	GLY	L235	GLY	L236	GLY	L237	GLY	L238	GLY	L239	GLY	L240	GLY	L241	GLY	L242	GLY	L243	GLY	L244	GLY	L245	GLY	L246	GLY	L247	GLY	L248	GLY	L249	GLY	L250	GLY	L251	GLY	L252	GLY	L253	GLY	L254	GLY	L255	GLY	L256	GLY	L257	GLY	L258	GLY	L259	GLY	L260	GLY	L261	GLY	L262	GLY	L263	GLY	L264	GLY	L265	GLY	L266	GLY	L267	GLY	L268	GLY	L269	GLY	L270	GLY	L271	GLY	L272	GLY	L273	GLY	L274	GLY	L275	GLY	L276	GLY	L277	GLY	L278	GLY	L279	GLY	L280	GLY	L281	GLY	L282	GLY	L283	GLY	L284	GLY	L285	GLY	L286	GLY	L287	GLY	L288	GLY	L289	GLY	L290	GLY	L291	GLY	L292	GLY	L293	GLY	L294	GLY	L295	GLY	L296	GLY	L297	GLY	L298	GLY	L299	GLY	L300	GLY	L301	GLY	L302	GLY	L303	GLY	L304	GLY	L305	GLY	L306	GLY	L307	GLY	L308	GLY	L309	GLY	L310	GLY	L311	GLY	L312	GLY	L313	GLY	L314	GLY	L315	GLY	L316	GLY	L317	GLY	L318	GLY	L319	GLY	L320	GLY	L321	GLY	L322	GLY	L323	GLY	L324	GLY	L325	GLY	L326	GLY	L327	GLY	L328	GLY	L329	GLY	L330	GLY	L331	GLY	L332	GLY	L333	GLY	L334	GLY	L335	GLY	L336	GLY	L337	GLY	L338	GLY	L339	GLY	L340	GLY	L341	GLY	L342	GLY	L343	GLY	L344	GLY	L345	GLY	L346	GLY	L347	GLY	L348	GLY	L349	GLY	L350	GLY	L351	GLY	L352	GLY	L353	GLY	L354	GLY	L355	GLY	L356	GLY	L357	GLY	L358	GLY	L359	GLY	L360	GLY	L361	GLY	L362	GLY	L363	GLY	L3
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Chain A: 63% 31% ...



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	314674	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 ($e^-/\text{\AA}^2$)	57	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.848	Depositor
Minimum map value	-0.511	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	272.0, 272.0, 272.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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	C	0.31	0/1664	0.46	1/2227 (0.0%)
2	B	0.35	0/2577	0.42	0/3495
3	G	0.22	0/418	0.41	0/563
4	S	0.30	0/1816	0.47	0/2465
5	A	0.29	0/2349	0.51	1/3202 (0.0%)
All	All	0.31	0/8824	0.46	2/11952 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	A	207	VAL	CA-C-O	-6.20	113.77	119.91
1	C	351	CYS	N-CA-C	-5.39	105.93	112.88

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	C	1639	0	1620	29	0
2	B	2530	0	2431	54	0
3	G	412	0	420	9	0
4	S	1772	0	1698	27	0
5	A	2288	0	2375	92	0
All	All	8641	0	8544	199	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.

The worst 5 of 199 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:G:11:GLN:HE21	3:G:11:GLN:N	1.55	1.04
5:A:213:TYR:CZ	5:A:308:ARG:HD3	2.12	0.85
5:A:214:ARG:HB2	5:A:214:ARG:HH11	1.46	0.79
4:S:130:GLN:NE2	4:S:217:CYS:SG	2.56	0.78
1:C:255:ASN:HD21	1:C:312:LYS:HG2	1.56	0.71

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	C	198/351 (56%)	184 (93%)	14 (7%)	0	100	100
2	B	329/337 (98%)	310 (94%)	18 (6%)	1 (0%)	36	68
3	G	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
4	S	229/248 (92%)	200 (87%)	29 (13%)	0	100	100
5	A	285/293 (97%)	256 (90%)	26 (9%)	3 (1%)	11	41
All	All	1092/1285 (85%)	999 (92%)	89 (8%)	4 (0%)	31	63

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	A	208	VAL
5	A	276	PHE
2	B	334	SER
5	A	202	GLN

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	C	176/304 (58%)	174 (99%)	2 (1%)	65	82
2	B	272/280 (97%)	272 (100%)	0	100	100
3	G	44/46 (96%)	42 (96%)	2 (4%)	24	57
4	S	190/201 (94%)	190 (100%)	0	100	100
5	A	249/253 (98%)	241 (97%)	8 (3%)	34	66
All	All	931/1084 (86%)	919 (99%)	12 (1%)	59	80

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	A	206	THR
5	A	207	VAL
5	A	331	LYS
5	A	214	ARG
3	G	63	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
5	A	142	ASN
5	A	163	HIS
1	C	333	GLN
2	B	62	HIS
4	S	77	ASN

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.

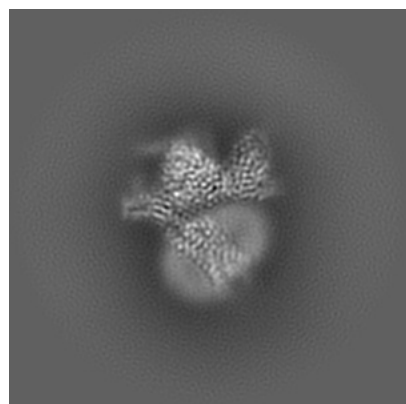
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33682. These allow visual inspection of the internal detail of the map and identification of artifacts.

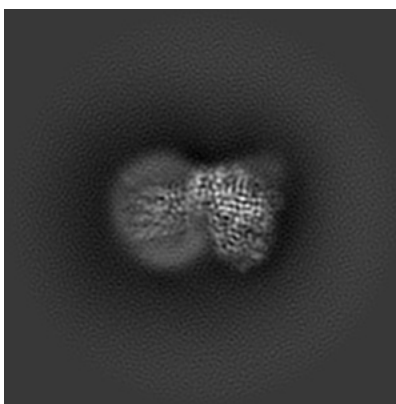
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

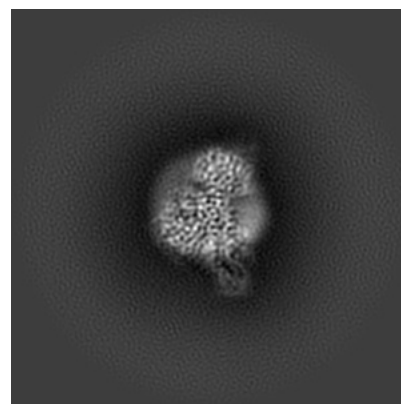
6.1.1 Primary map



X

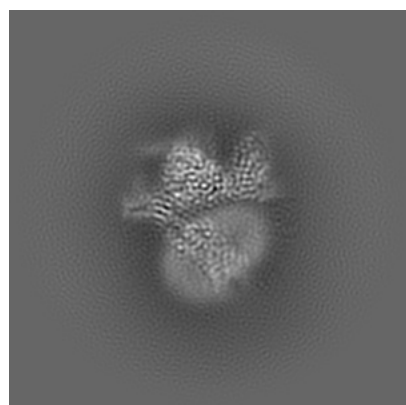


Y

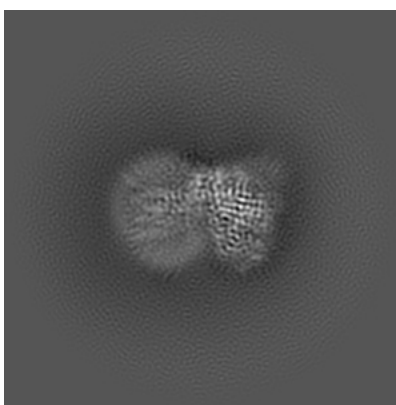


Z

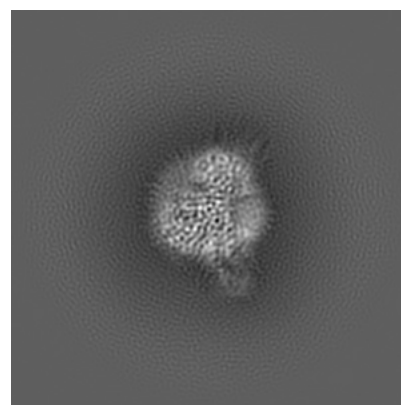
6.1.2 Raw map



X



Y

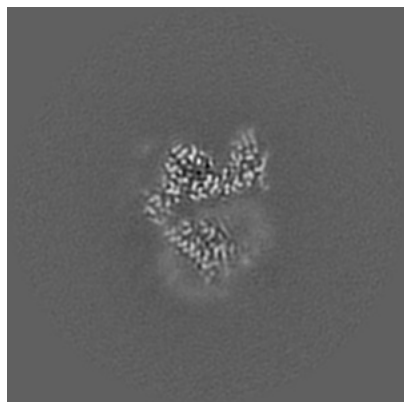


Z

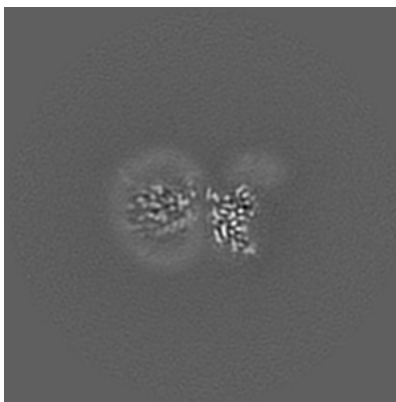
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

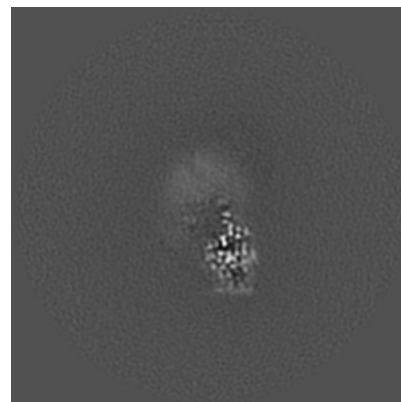
6.2.1 Primary map



X Index: 160

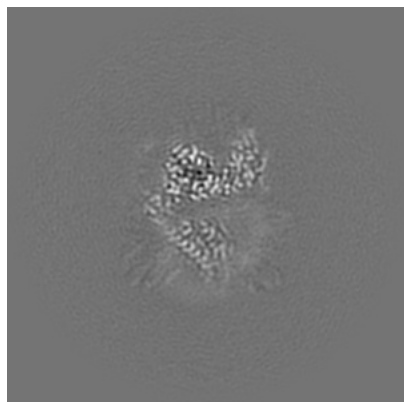


Y Index: 160

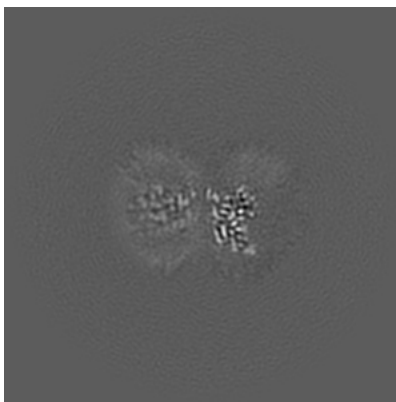


Z Index: 160

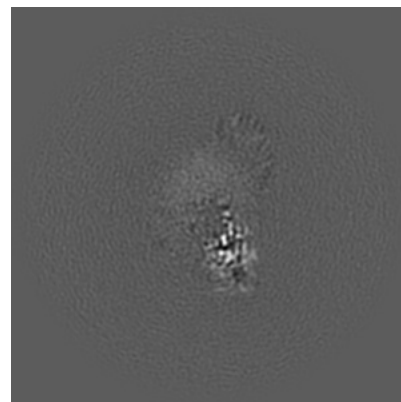
6.2.2 Raw map



X Index: 160



Y Index: 160

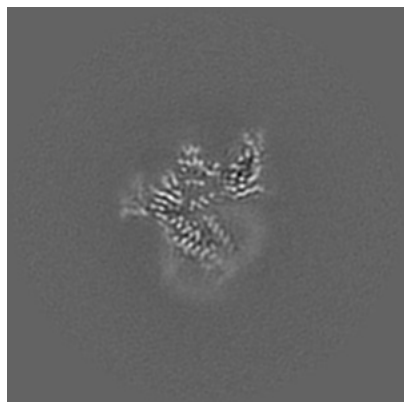


Z Index: 160

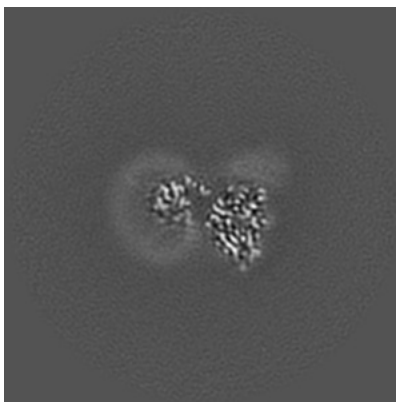
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

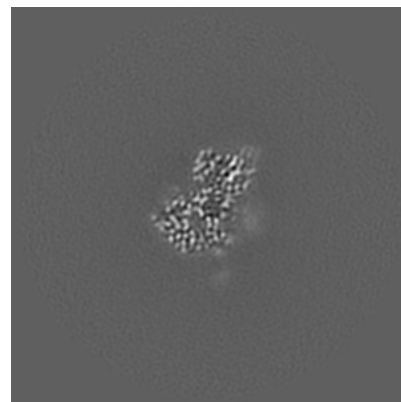
6.3.1 Primary map



X Index: 172

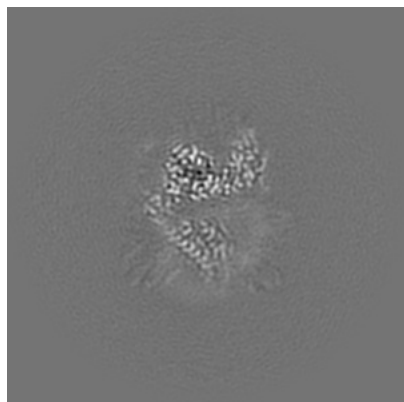


Y Index: 147

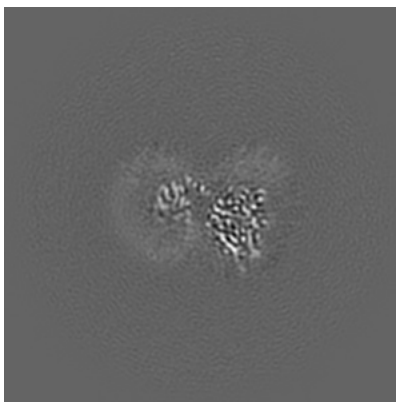


Z Index: 186

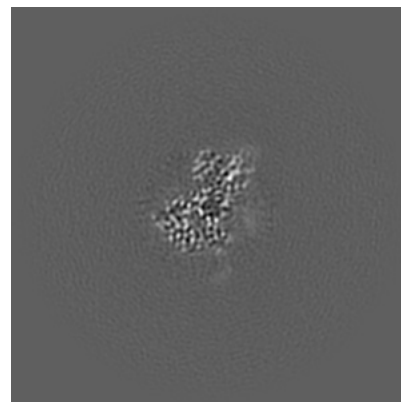
6.3.2 Raw map



X Index: 160



Y Index: 147

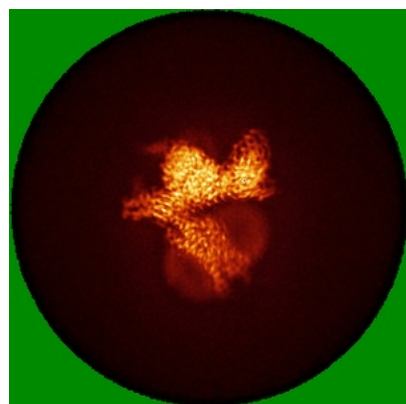


Z Index: 186

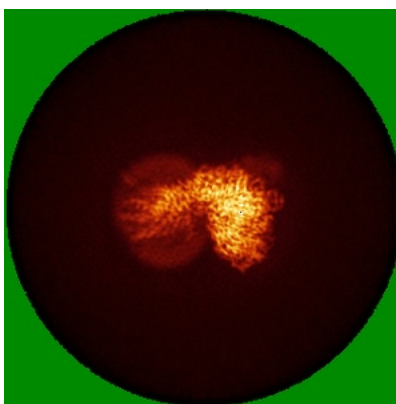
The images above show the largest variance slices of the map in three orthogonal directions.

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

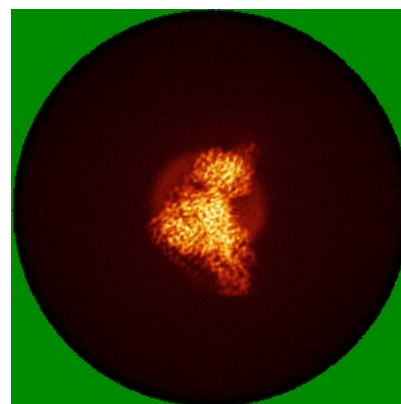
6.4.1 Primary map



X

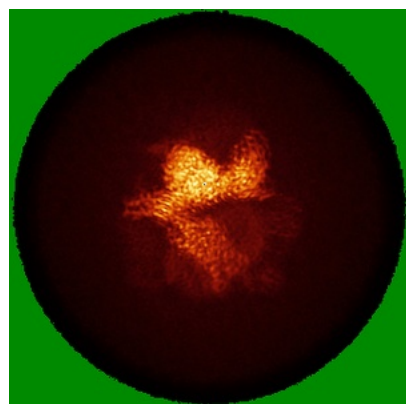


Y

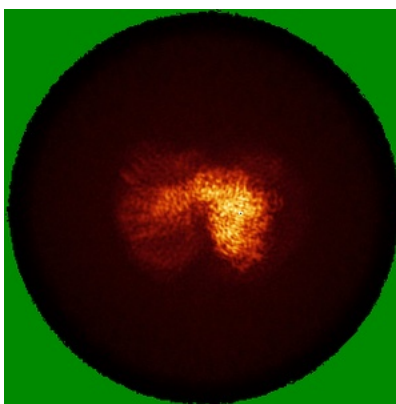


Z

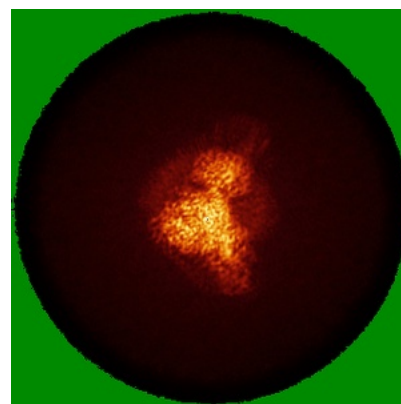
6.4.2 Raw map



X



Y

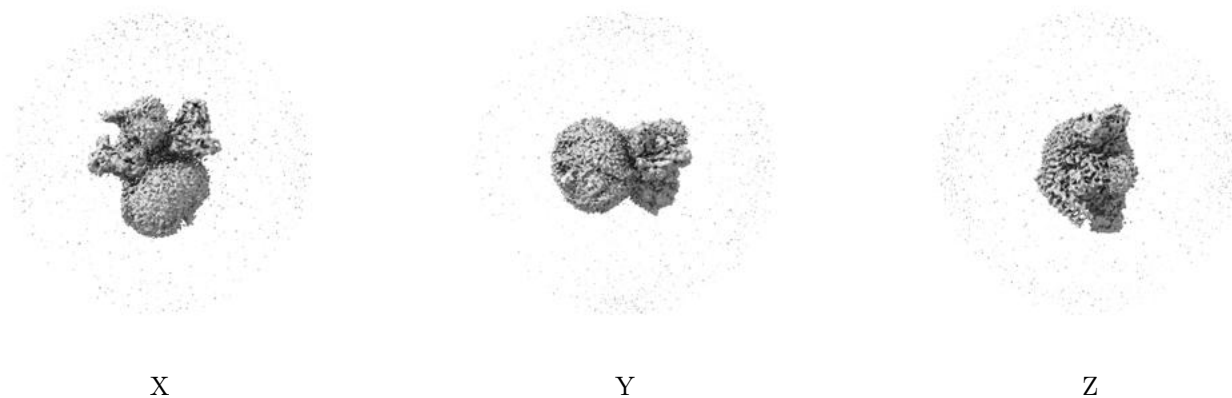


Z

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.

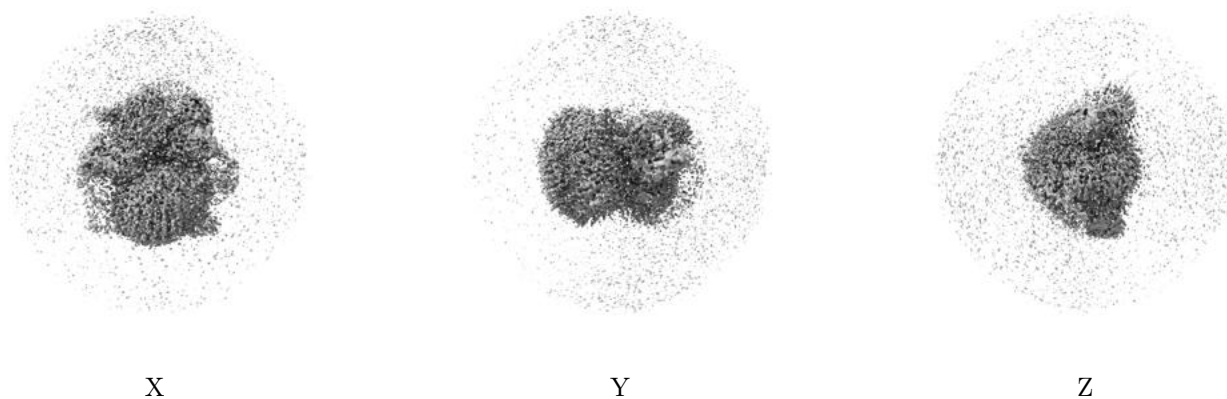
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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.

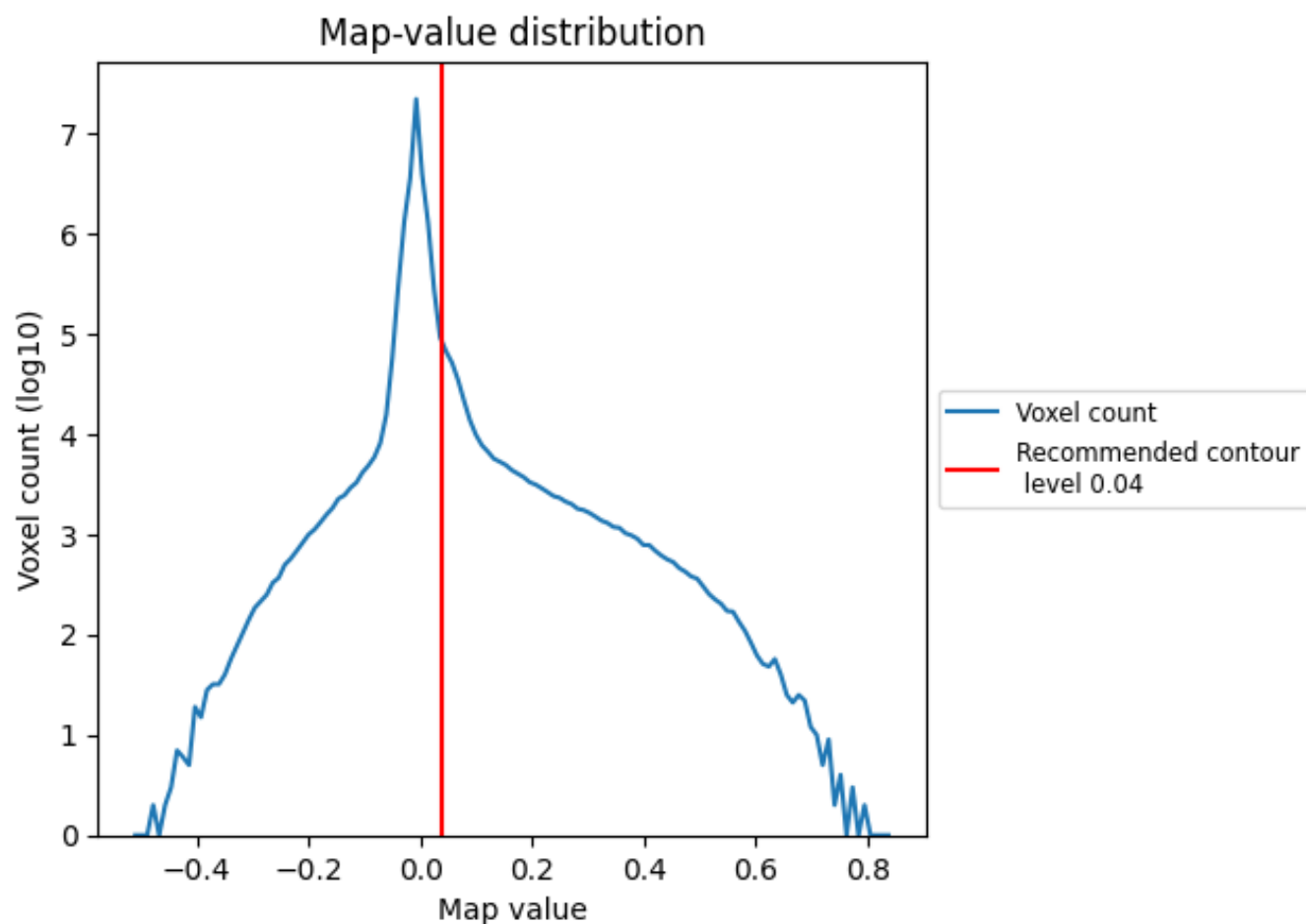
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

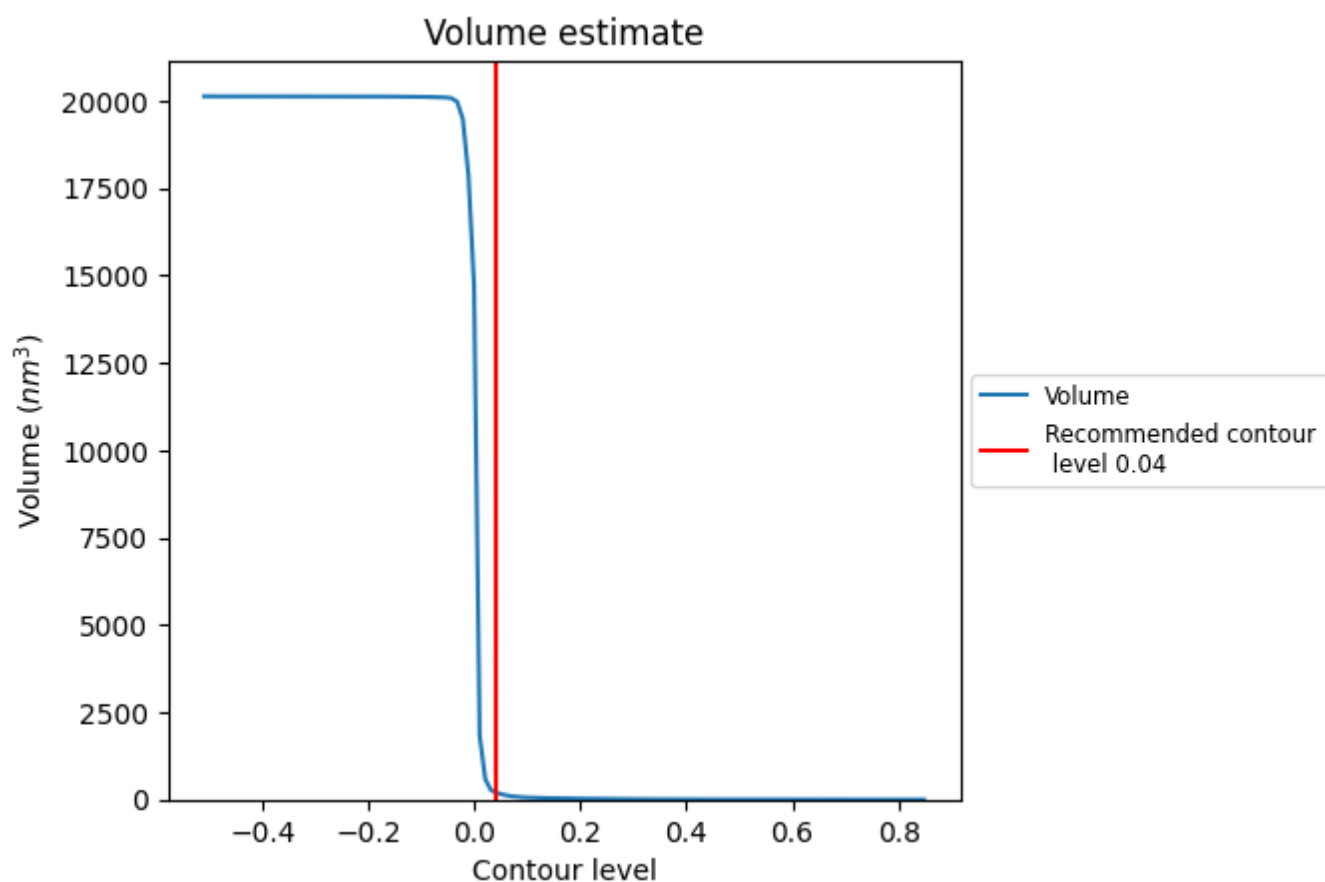
This section contains the results of statistical analysis of the map.

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.

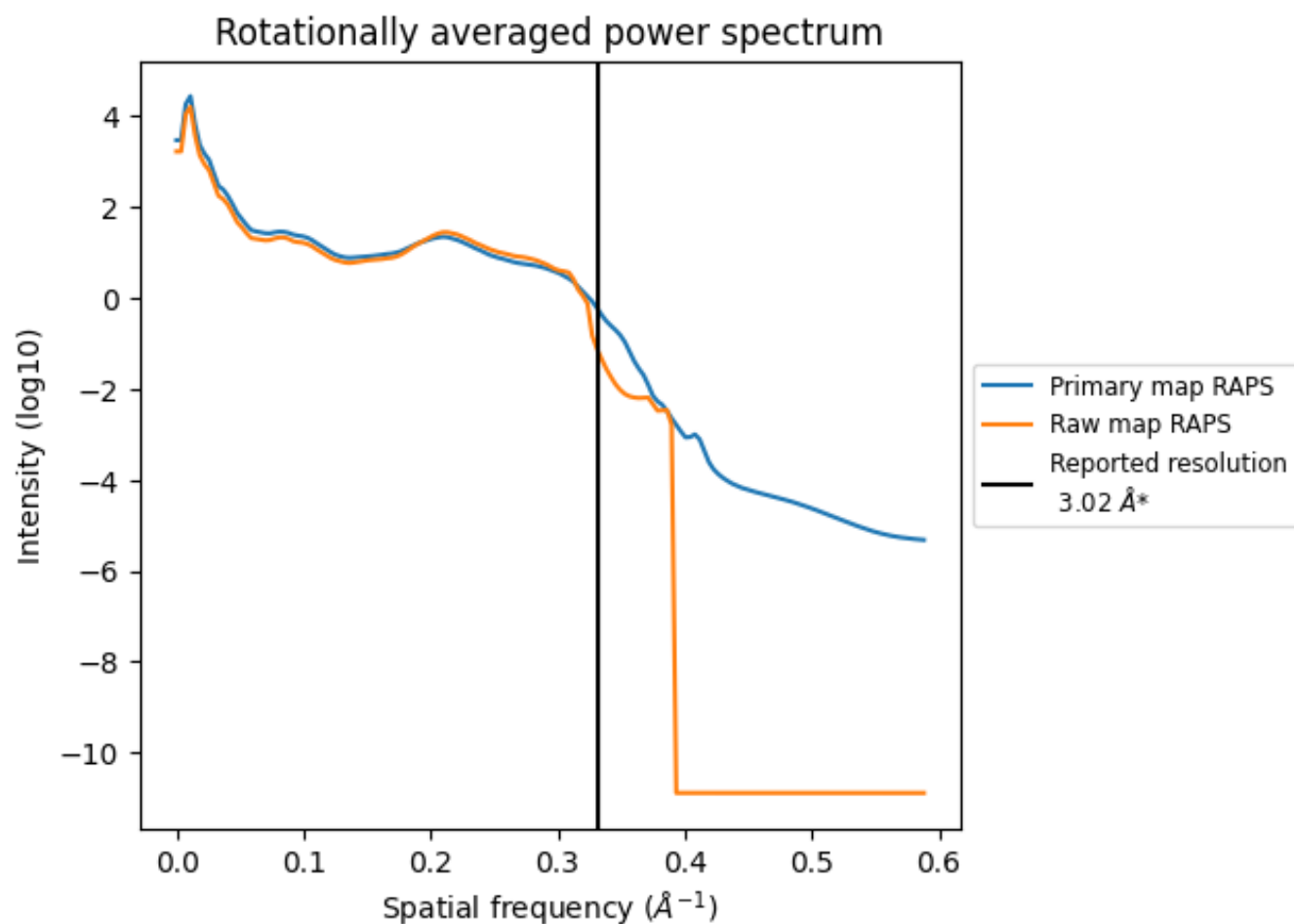
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 204 nm³; this corresponds to an approximate mass of 184 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 ⓘ

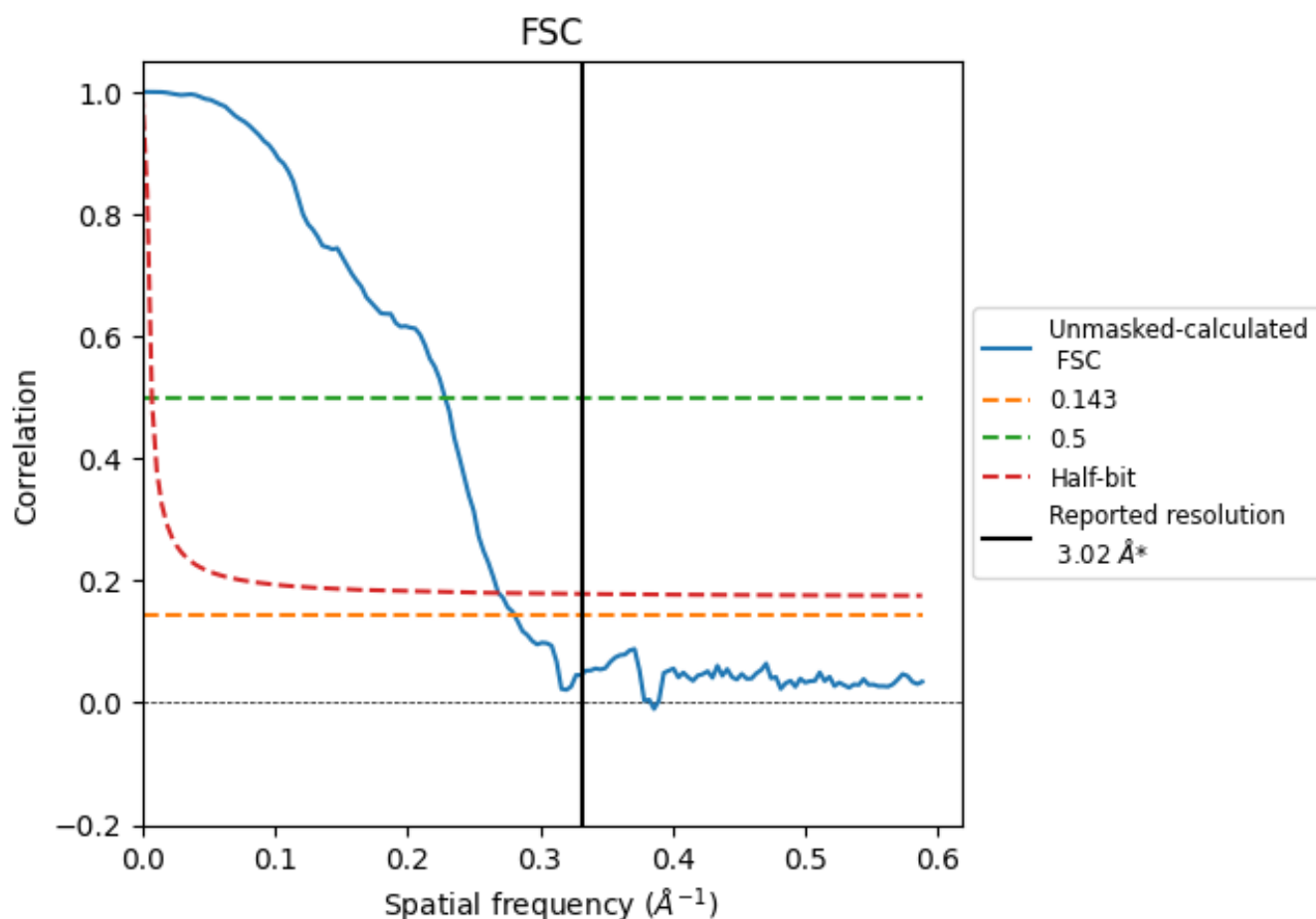


*Reported resolution corresponds to spatial frequency of 0.331 Å⁻¹

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 0.331 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

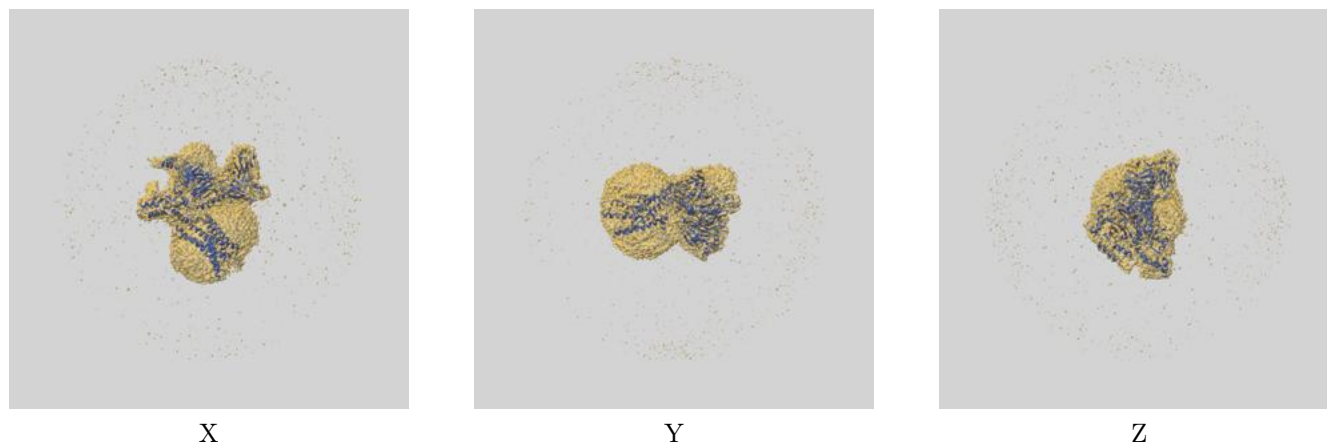
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.02	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.56	4.38	3.72

*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 3.56 differs from the reported value 3.02 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33682 and PDB model 7Y89. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



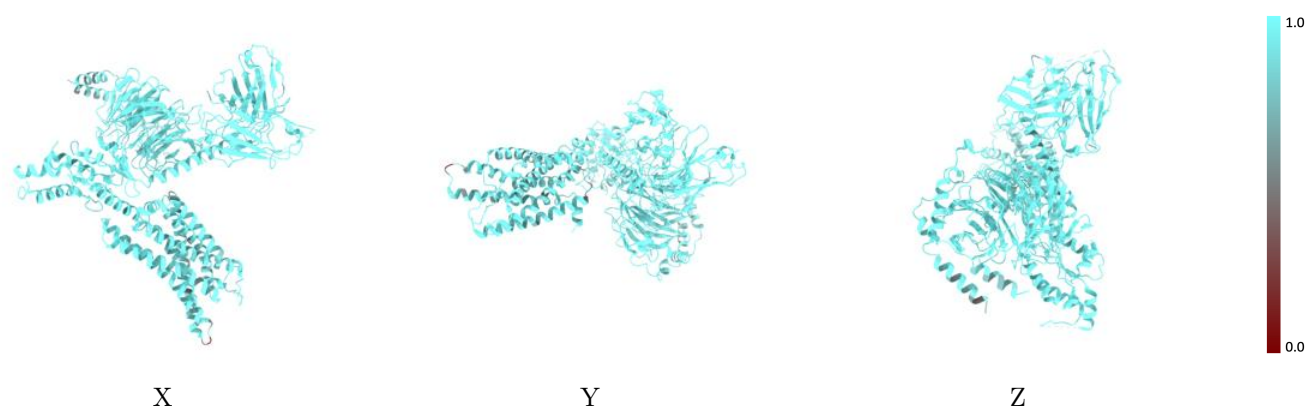
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



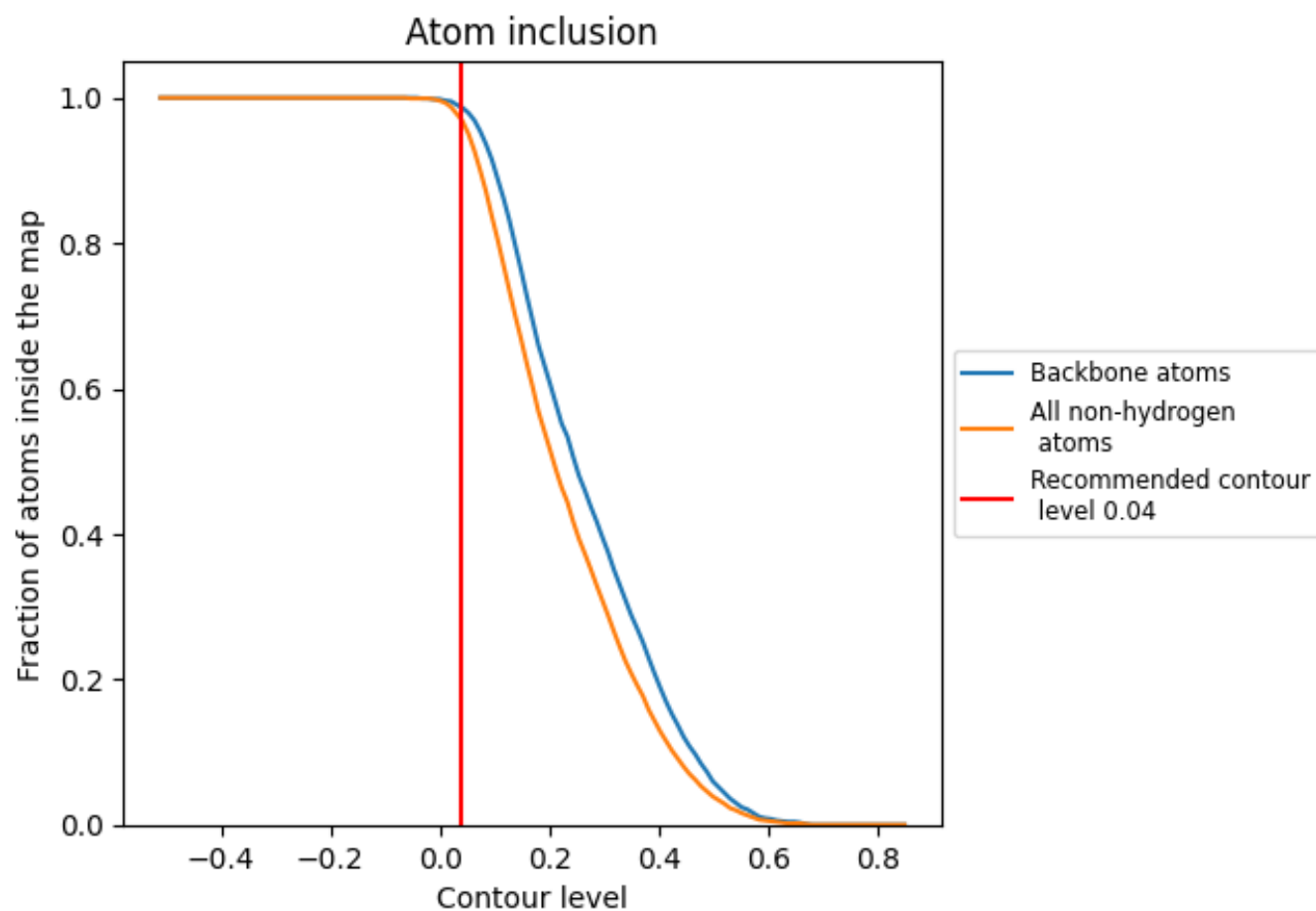
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 97% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9690	0.5150
A	0.9430	0.4380
B	0.9810	0.5640
C	0.9810	0.5240
G	0.9380	0.4790
S	0.9810	0.5460

