



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:19 PM UTC

PDB ID : 8IO4 / pdb_00008io4
EMDB ID : EMD-35607
Title : Herg1a-herg1b open state
Authors : Zhang, M.F.
Deposited on : 2023-03-10
Resolution : 3.50 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

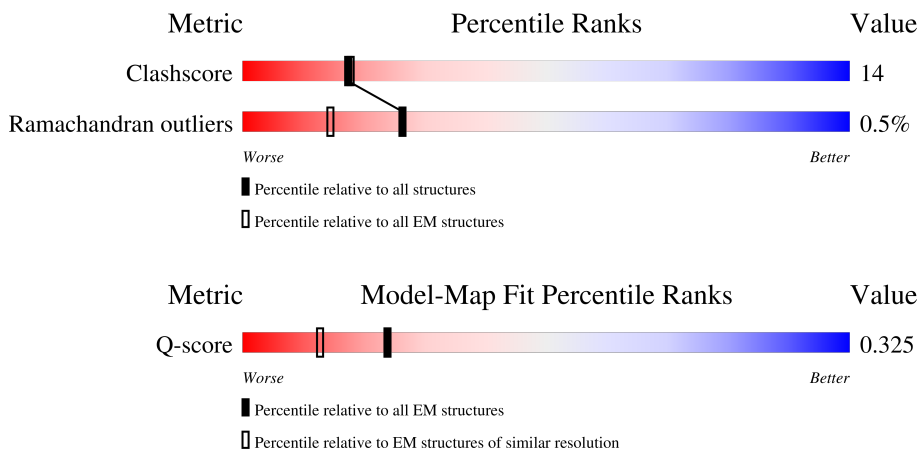
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	1159	
1	B	1159	
1	C	1159	
1	D	1159	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13736 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 Potassium voltage-gated channel subfamily H member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	431	Total	C	N	O	S	0	0
			3434	2252	581	584	17		
1	C	431	Total	C	N	O	S	0	0
			3434	2252	581	584	17		
1	D	431	Total	C	N	O	S	0	0
			3434	2252	581	584	17		
1	B	431	Total	C	N	O	S	0	0
			3434	2252	581	584	17		



PRO	PRO	CYS	LEU	THR	R836	L775	A715	I655	G546	P486	T421	PRO	ARG	PRO	ARG	PRO	ALA	ARG	GLN
ALA	ALA	PRO	VAL	ASP	D836	L776	V716	F656	A547	G487	A422	LYS	ARG	LYS	ARG	ILE	VAL	ILE	ARG
THR	THR	THR	PHE	ASP	D837	I777	L717	G657	A548	R488	V423	GLY	GLY	GLY	GLY	THR	PHE	THR	CYS
ALA	ALA	PRO	SER	THR	L838	A778	K718	N658	V549	I489	F424	GLU	ALA	ALA	ALA	ILE	GLY	THR	CYS
VAL	VAL	SER	SER	GLU	L839	L779	G719	V659	L550	A490	T425	THR	GLY	GLY	GLY	ILE	GLY	ASP	GLY
THR	THR	LEU	ARG	GLN	E840	F780	F720	S660	F551	V491	L432	HIS	LEU	LEU	ALA	ASN	PHE	ASP	PHE
GLY	GLY	PRO	GLY	GLY	V841	F781	E722	A661	L552	H492	LEU	ASN	PRO	PRO	HIS	GLY	PHE	LEU	LEU
PRO	PRO	ILE	VAL	VAL	L842	I782	E722	I662	L553	Y493	GLI	LYS	ASN	VAL	VAL	GLY	PHE	GLY	HIS
GLY	GLY	PRO	SER	SER	D843	S783	C723	I663	M554	Y494	THR	THR	ARG	GLY	ARG	ALA	VAL	VAL	PRO
PRO	PRO	LEU	PRO	ALA	Y844	R784	L724	Q664	F557	K495	GLU	LYS	SER	VAL	THR	ALA	THR	ARG	ARG
SER	SER	SER	PRO	LEU	Y845	G785	Q725	R665	+	G496	VAL	VAL	HIS	VAL	VAL	ALA	THR	THR	THR
THR	THR	SER	GLY	GLY	P846	S786	A726	L666	W563	H497	GLY	THR	LEU	THR	VAL	VAL	VAL	VAL	GLN
THR	THR	GLY	GLY	GLY	E847	I787	D727	Y667	L564	F498	PRO	VAL	ASN	VAL	VAL	VAL	VAL	ASP	ARG
ARG	ARG	ARG	GLY	ARG	P848	E788	I728	S668	+	L499	ALA	THR	SER	THR	THR	GLY	GLY	GLY	THR
PRO	PRO	ARG	ALA	ALA	S849	I789	C729	Q669	I567	I500	THR	SER	ASP	ASP	ASP	ALA	ALA	ALA	ALA
LEU	LEU	PRO	MET	GLY	D850	L790	L730	T670	W568	D501	GLU	CYS	SER	LEU	LEU	SER	THR	THR	THR
ALA	ALA	GLY	ASP	GLY	H851	R791	H731	A671	Y569	M502	GLY	GLY	GLY	ALA	ALA	ALA	ALA	ALA	ALA
VAL	VAL	ASP	PRO	PRO	H852	G792	L732	R672	+	A504	ALA	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
SER	SER	VAL	GLY	SER	W853	D793	N733	Y673	M574	A505	+	LEU	SER	SER	SER	THR	THR	THR	THR
LEU	LEU	SER	SER	ARG	S854	V794	R734	H674	E575	I506	Q450	TYR	ARG	ARG	ARG	TYR	TYR	TYR	TYR
ARG	ARG	ARG	GLY	GLY	S855	V796	S735	T675	Q576	+	P451	GLY	ALA	ALA	ALA	ALA	ALA	ALA	ALA
THR	THR	LEU	ASP	THR	L856	L736	L736	Q676	P577	F508	L452	THR	ARG	ARG	ARG	GLY	GLY	GLY	GLY
GLY	GLY	ASP	GLY	GLY	E857	A797	L737	M677	HIS	D509	+	LEU	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	ALA	CYS	CYS	L858	I798	Q738	L678	ASP	+	V454	GLN	ARG	ALA	ALA	ALA	ALA	ALA	ALA
GLN	GLN	LEU	ASN	GLY	T859	L799	H739	R679	MET	LEU	+	ALA	SER	LEU	LEU	LEU	LEU	LEU	LEU
ASP	ASP	LEU	PRO	PRO	F860	G800	C740	V680	ARG	+	V455	PRO	ARG	PRO	PRO	PRO	PRO	PRO	PRO
SER	SER	LEU	GLY	GLY	R861	X801	K741	R681	I583	ILE	D456	ARG	ILE	ILE	ILE	ILE	ILE	ILE	ILE
GLN	GLN	LEU	SER	SER	L862	N802	P742	E682	+	GLY	L457	GLN	SER	GLY	GLY	GLY	GLY	GLY	GLY
VAL	VAL	ARG	PHE	PRO	R863	D803	F743	F683	NS88	SER	I458	THR	THR	THR	THR	THR	THR	THR	THR
SER	SER	LEU	SER	SER	+	+	R744	I684	+	GLY	V459	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
GLU	GLU	THR	GLY	GLY	ASP	T804	G745	R685	D591	SER	D460	ASN	VAL	VAL	VAL	VAL	VAL	VAL	VAL
THR	THR	THR	ASN	GLY	P805	F805	G745	R685	Q592	GLY	I461	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
LEU	LEU	LEU	LEU	LEU	G806	G806	A746	F686	T593	GLU	+	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
ALA	ALA	LEU	ASN	SER	E807	E807	T747	H687	+	THR	M462	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
ALA	ALA	SER	ILE	SER	PRO	P808	K748	Q688	Y597	ILE	F463	LEU	SER	SER	SER	SER	SER	SER	SER
GLU	GLU	PRO	PHE	PRO	GLY	L809	G749	I689	ASN	S220	+	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ASP	ASP	SER	SER	GLU	+	+	+	+	SER	G522	I464	THR	ALA	ALA	ALA	ALA	ALA	ALA	ALA
LEU	LEU	LEU	PHE	GLY	THR	N810	C750	P690	SER	L523	I465	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
GLY	GLY	PRO	PHE	SER	GLY	L811	G751	N691	GLY	L524	D466	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
VAL	VAL	THR	GLY	SER	THR	Y812	R752	H695	LEU	K525	I467	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
GLN	GLN	ASP	ASP	ASP	THR	A813	A753	L693	G603	+	L468	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
LEU	LEU	GLU	GLY	GLY	GLU	L814	L754	R694	K608	T526	I469	SER	SER	SER	SER	SER	SER	SER	SER
PRO	PRO	GLY	GLY	GLY	LEU	H814	L754	R694	D609	A527	V409	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
GLY	GLY	LEU	LEU	LEU	GLY	P815	A755	Q695	L610	R528	N470	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
GLN	GLN	GLY	GLY	GLY	GLY	G816	T756	R696	K610	L529	F471	THR	THR	THR	THR	THR	THR	THR	THR
THR	THR	GLY	THR	SER	GLY	K817	K757	L697	F619	L530	R472	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
SER	SER	GLY	SER	SER	PHE	S818	K758	E698	+	R531	T473	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
SER	SER	ARG	SER	SER	ARG	N819	F758	E699	V644	+	T474	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
PRO	PRO	GLN	PRO	PRO	GLN	G820	T760	Y700	M645	L532	+	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	LEU	LEU	ARG	L825	T761	F701	L646	V533	+	THR	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	LEU	LEU	LEU	ARG	T826	T762	Q702	I647	V535	N477	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
ARG	ARG	ARG	ARG	ARG	ARG	Y827	H763	H703	M651	A536	A478	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
ARG	ARG	ARG	ARG	ARG	ARG	C828	A763	A704	Y652	R537	V418	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
ARG	ARG	ARG	ARG	ARG	ARG	D829	L769	T708	A653	K538	E480	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ARG	ARG	ARG	ARG	ARG	ARG	L830	L769	T708	S654	+	V482	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
ARG	ARG	ARG	ARG	ARG	ARG	T832	L769	T708	+	+	V483	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
ARG	ARG	ARG	ARG	ARG	ARG	D833	L769	T708	+	+	S484	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
ARG	ARG	ARG	ARG	ARG	ARG	H834	D774	N714	+	+	H485	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO

ARG
LEU
SER
LEU
PRO
GLY
GLN
LEU
GLY
ALA
LEU
THR
SER
GLN
PRO
LEU
HIS
ARG
HIS
GLY
SER
ASP
PRO
GLY
SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.943	Depositor
Minimum map value	-0.562	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.22	Depositor
Map size ($\text{\AA}$)	339.59998, 339.59998, 339.59998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.8489999, 0.8489999, 0.8489999	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	0.17	0/3524	0.44	0/4788
1	B	0.16	0/3524	0.43	0/4788
1	C	0.17	0/3524	0.44	0/4788
1	D	0.16	0/3524	0.44	0/4788
All	All	0.16	0/14096	0.44	0/19152

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	3434	0	3453	97	0
1	B	3434	0	3453	105	0
1	C	3434	0	3453	94	0
1	D	3434	0	3453	102	0
All	All	13736	0	13812	375	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 14.

The worst 5 of 375 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:D:417:LEU:HD11	1:D:459:VAL:HG22	1.58	0.85
1:A:417:LEU:HD11	1:A:459:VAL:HG22	1.58	0.84
1:B:720:PHE:HB3	1:B:724:LEU:HB3	1.61	0.83
1:D:720:PHE:HB3	1:D:724:LEU:HB3	1.61	0.83
1:C:417:LEU:HD11	1:C:459:VAL:HG22	1.58	0.83

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	59/1159 (5%)	56 (95%)	2 (3%)	1 (2%)	7	35
1	B	421/1159 (36%)	396 (94%)	24 (6%)	1 (0%)	43	74
1	C	350/1159 (30%)	328 (94%)	20 (6%)	2 (1%)	21	54
1	D	421/1159 (36%)	396 (94%)	23 (6%)	2 (0%)	24	57
All	All	1251/4636 (27%)	1176 (94%)	69 (6%)	6 (0%)	26	57

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	688	GLN
1	C	688	GLN
1	D	688	GLN
1	B	688	GLN
1	C	450	GLN

5.3.2 Protein sidechains [i](#)

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

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.

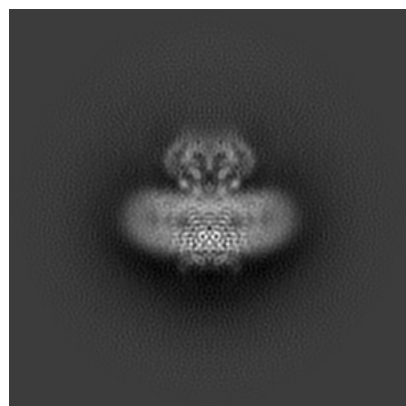
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35607. These allow visual inspection of the internal detail of the map and identification of artifacts.

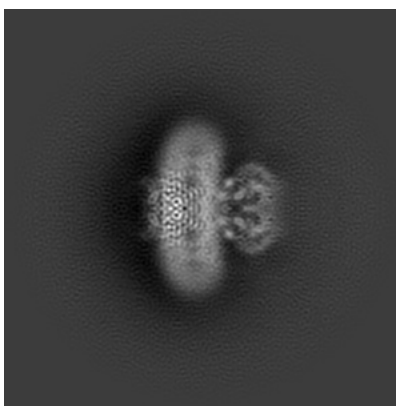
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

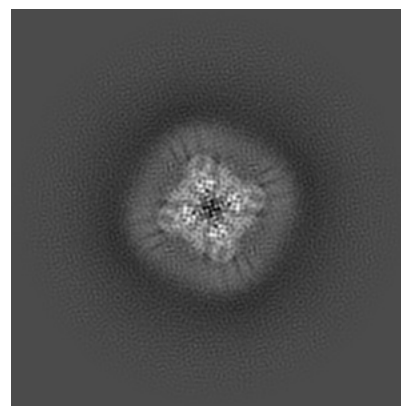
6.1.1 Primary map



X

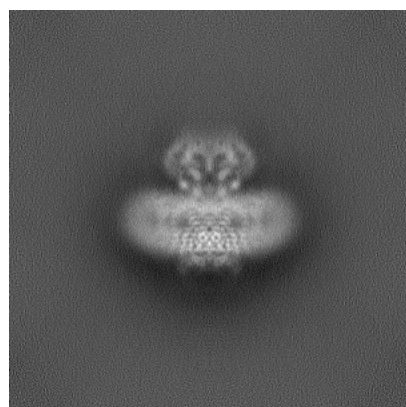


Y

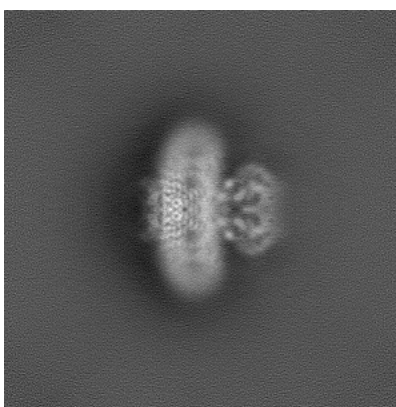


Z

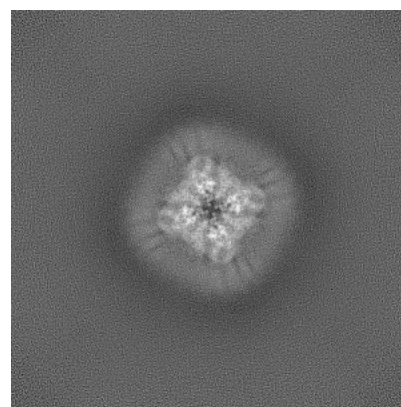
6.1.2 Raw map



X



Y

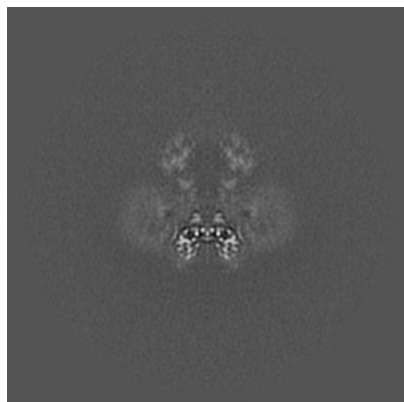


Z

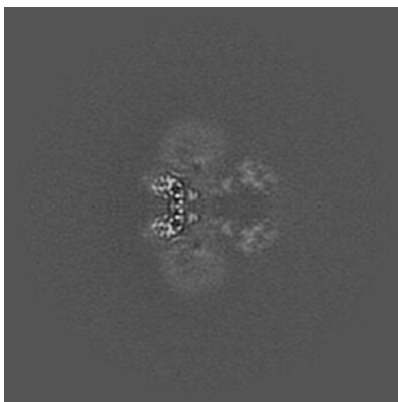
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

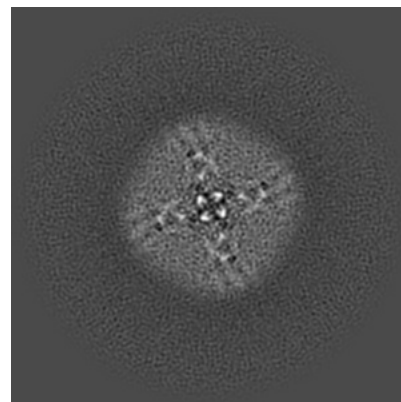
6.2.1 Primary map



X Index: 200

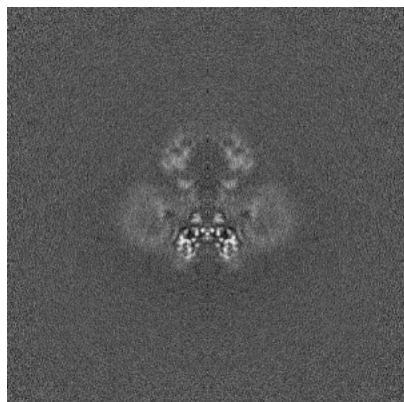


Y Index: 200

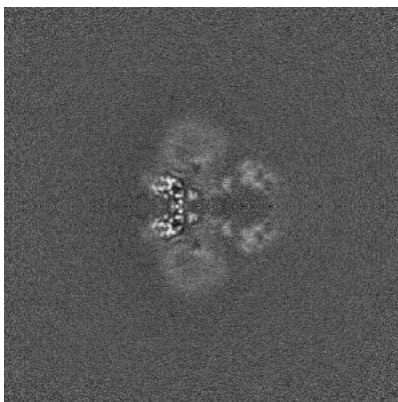


Z Index: 200

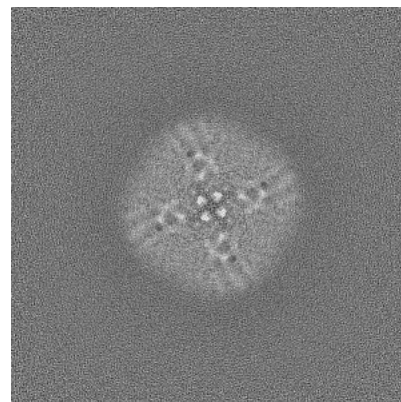
6.2.2 Raw map



X Index: 200



Y Index: 200

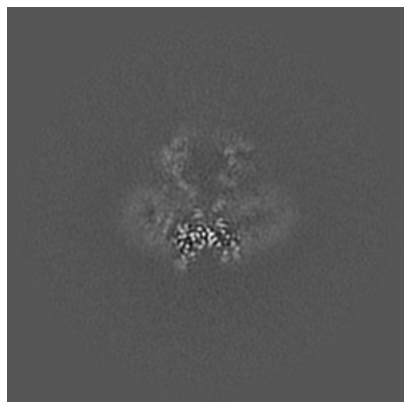


Z Index: 200

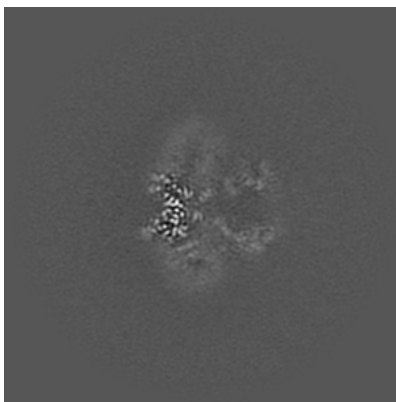
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

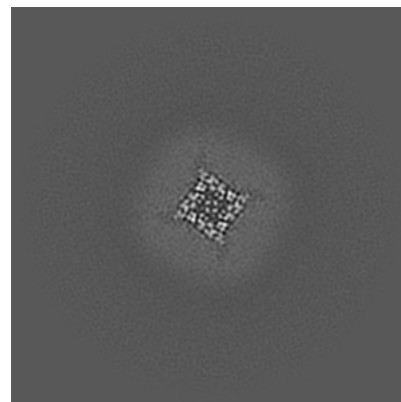
6.3.1 Primary map



X Index: 204

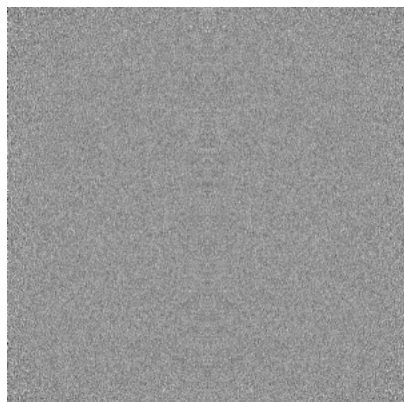


Y Index: 196

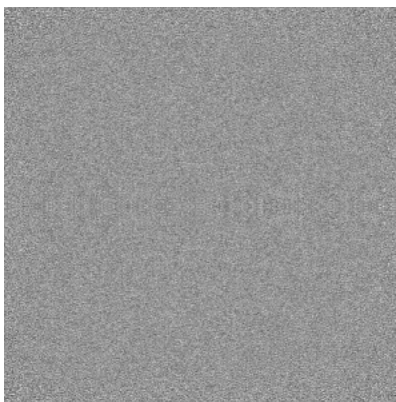


Z Index: 164

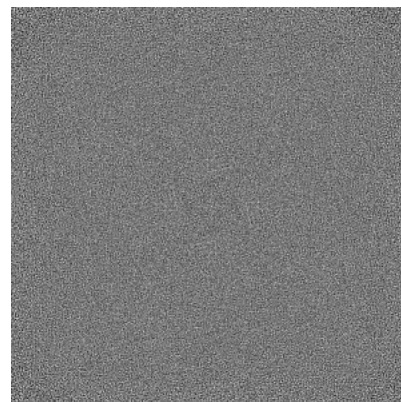
6.3.2 Raw map



X Index: 0



Y Index: 0

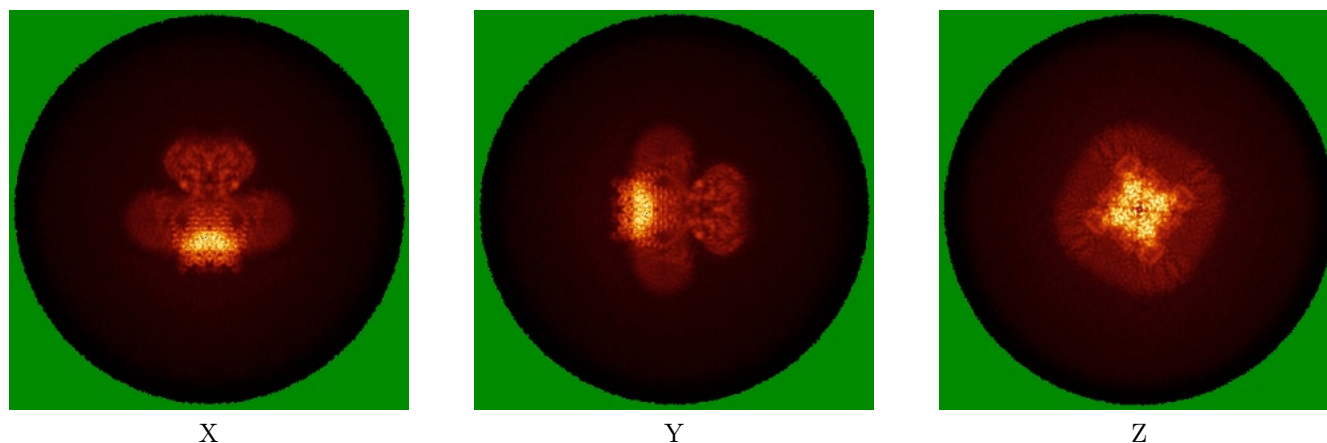


Z Index: 399

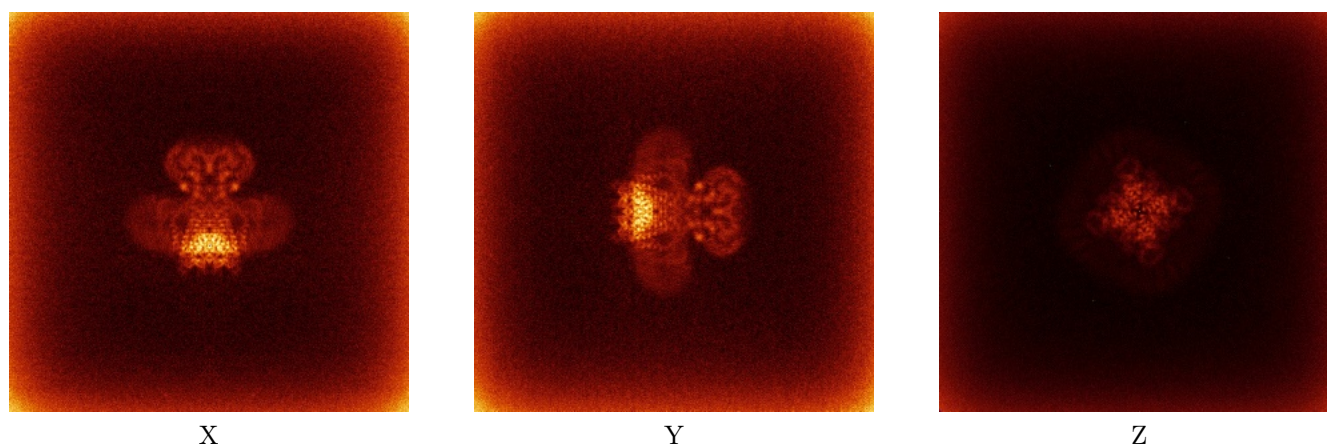
The images above show the largest variance slices of the map in three orthogonal directions.

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.

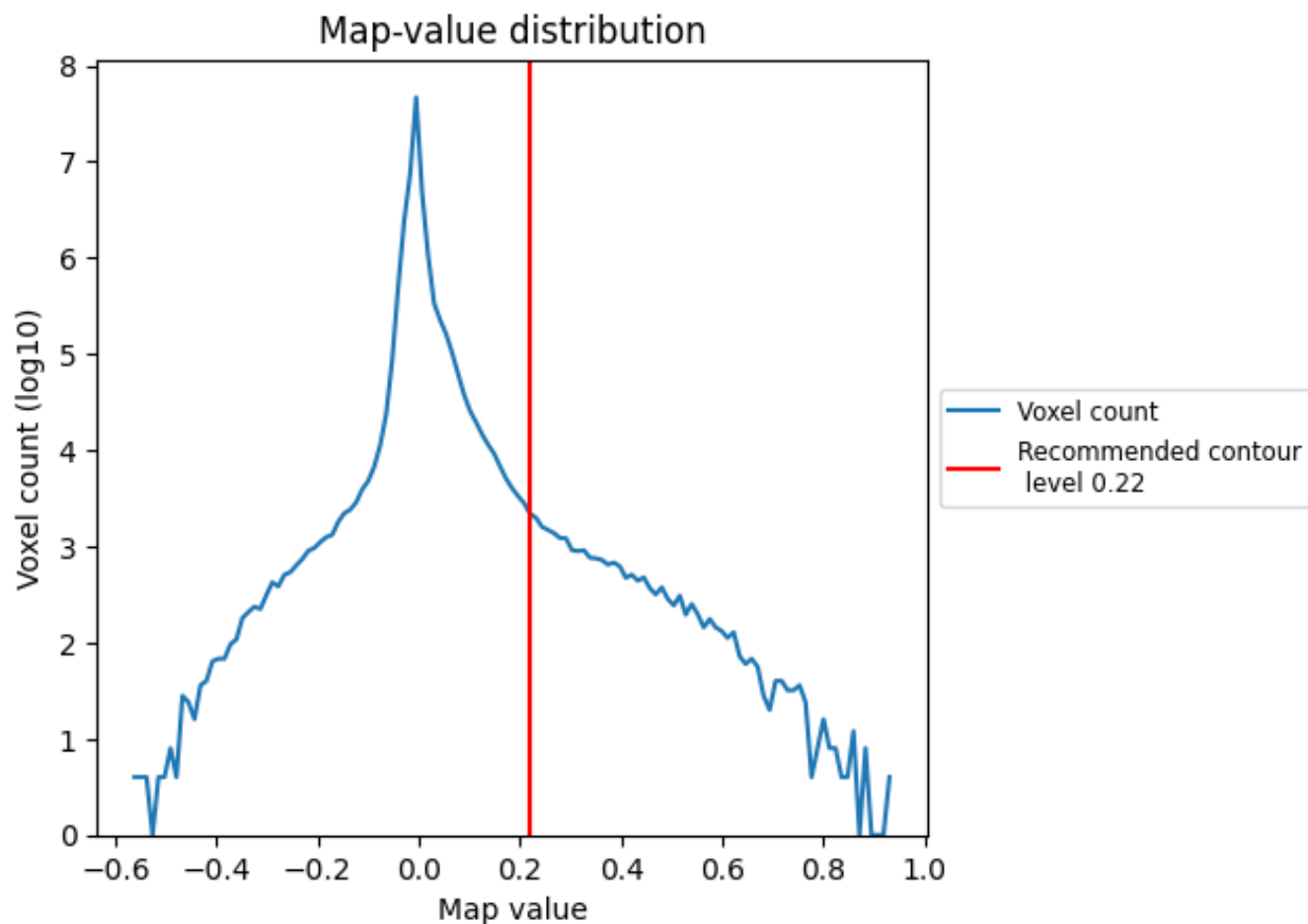
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

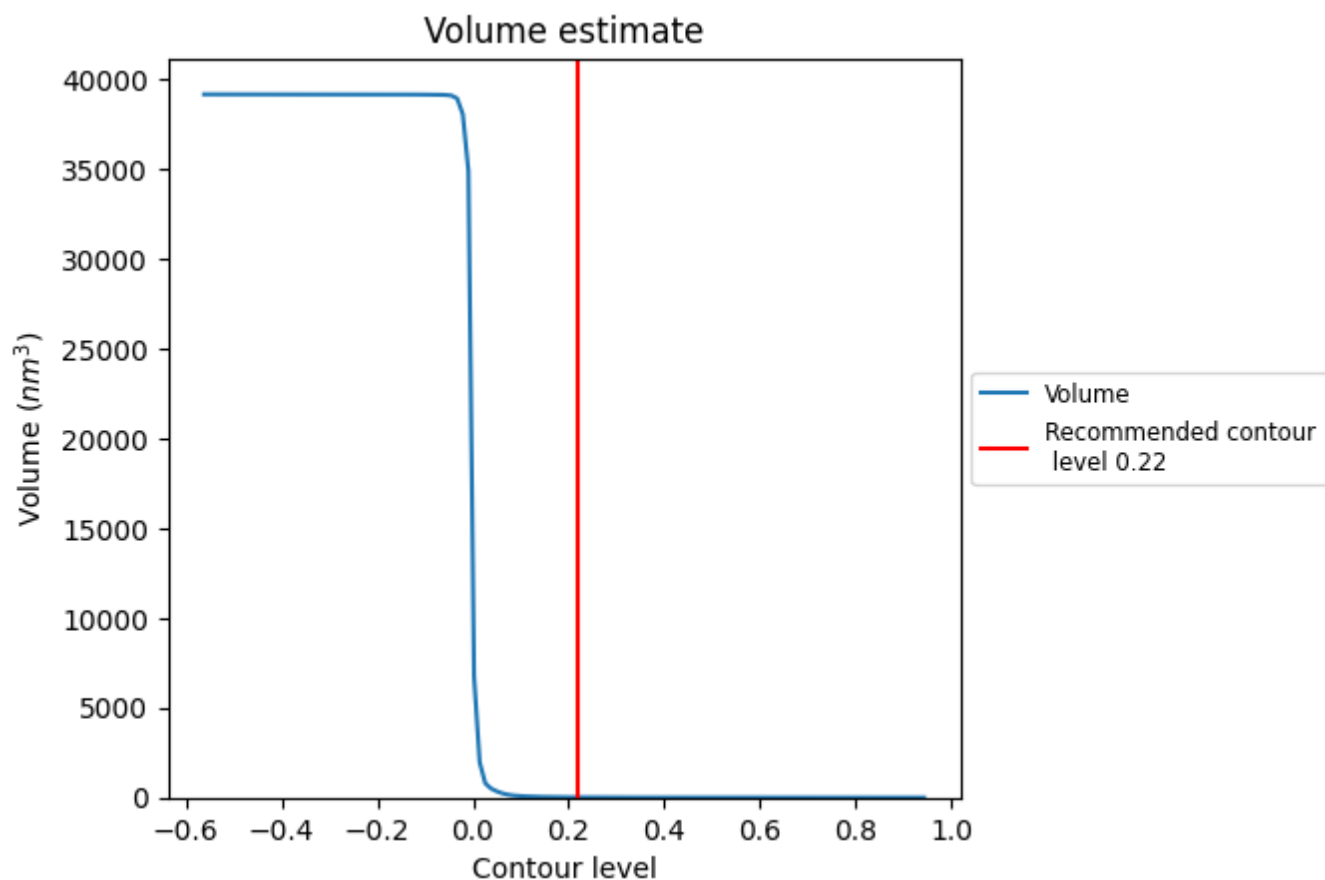
This section contains the results of statistical analysis of the map.

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.

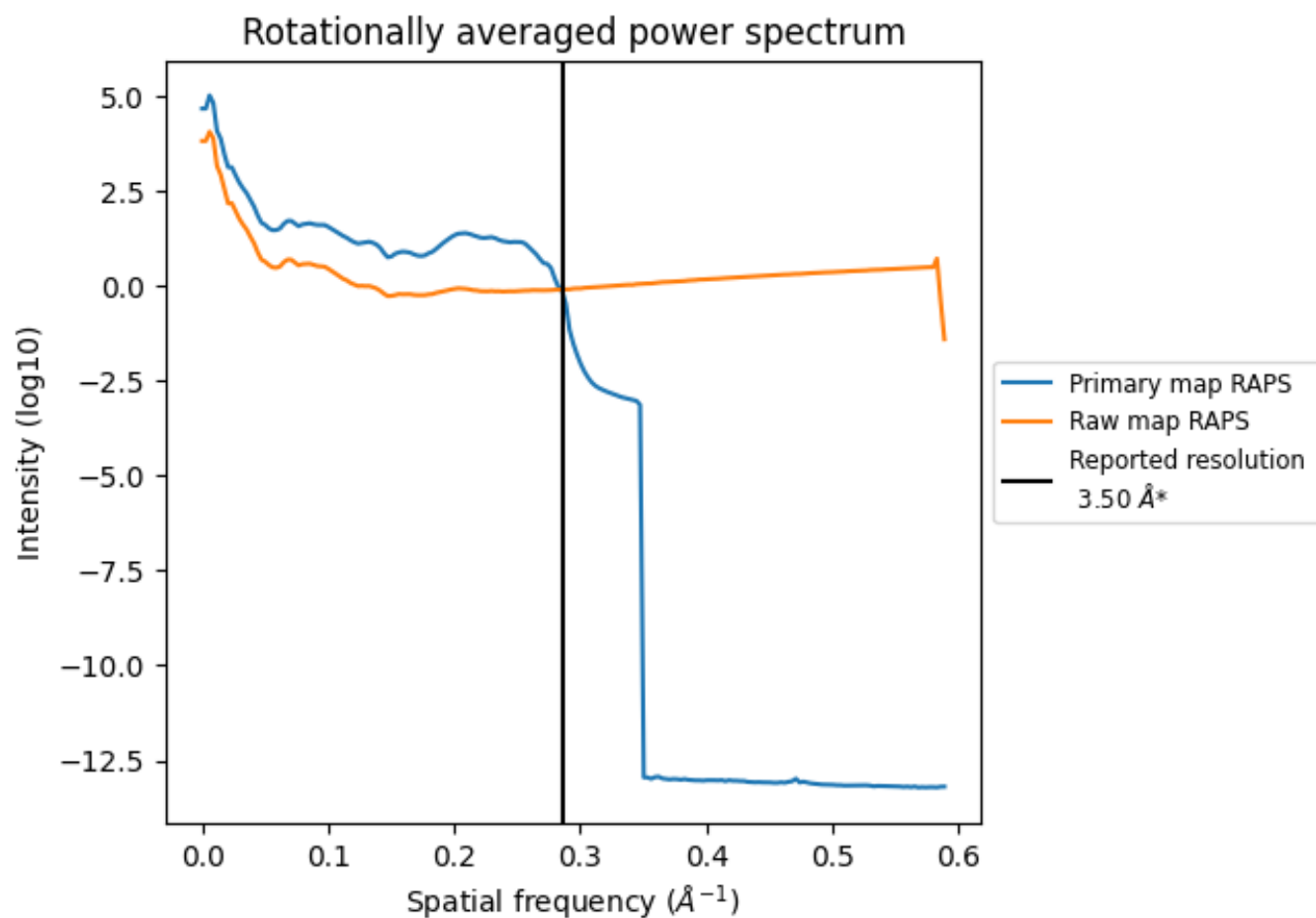
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 15 nm³; this corresponds to an approximate mass of 13 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 ⓘ

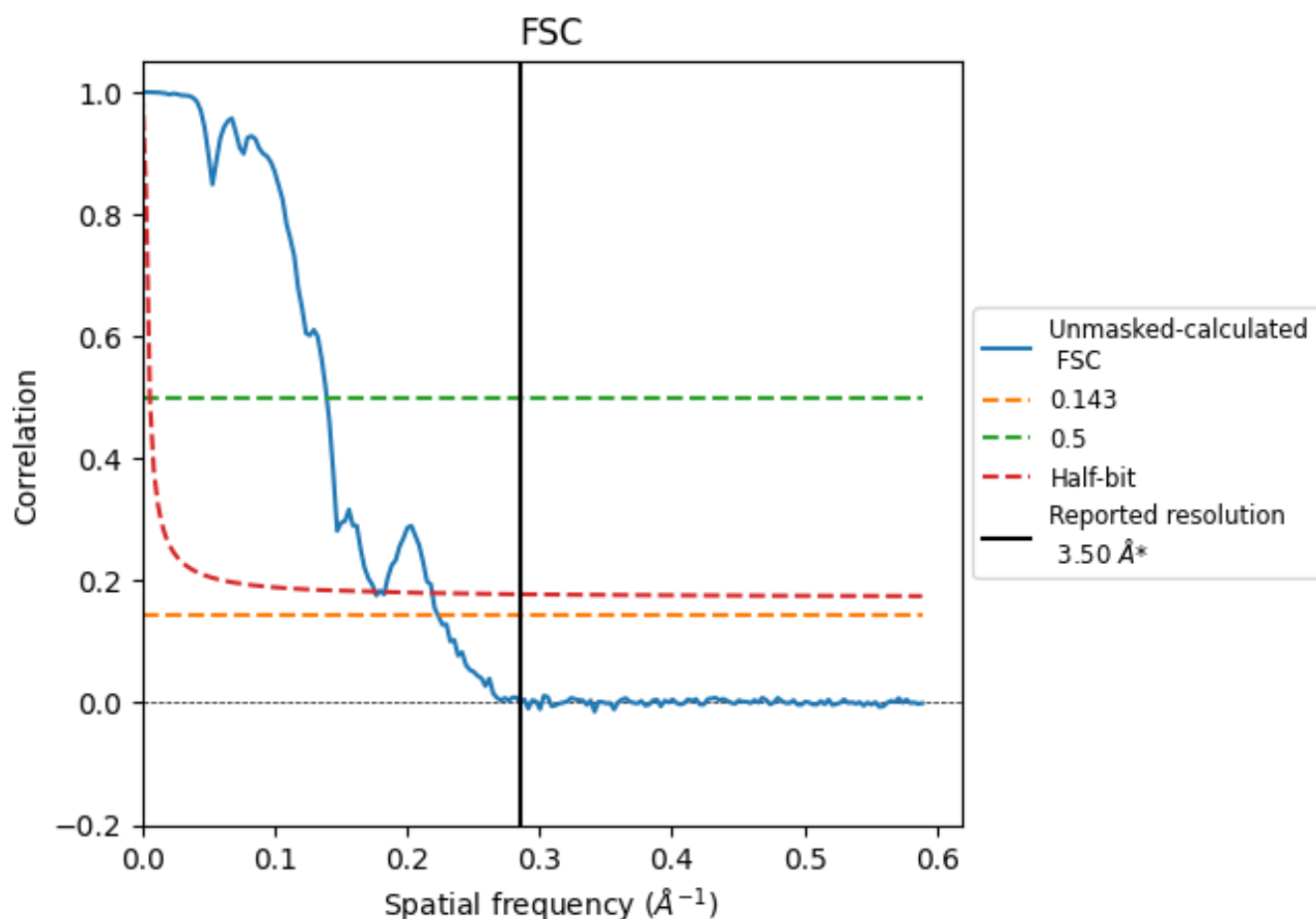


*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

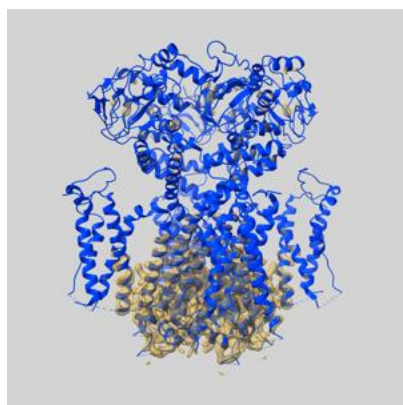
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.47	7.18	5.69

*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 4.47 differs from the reported value 3.5 by more than 10 %

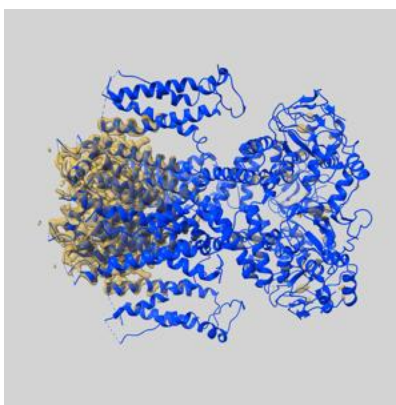
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35607 and PDB model 8IO4. Per-residue inclusion information can be found in section 3 on page 4.

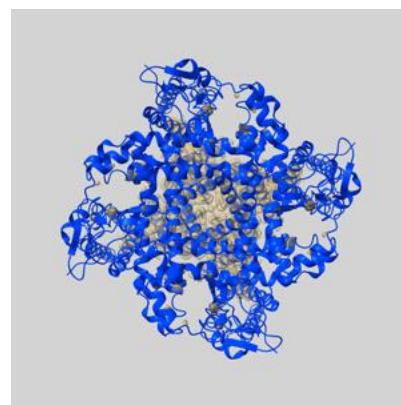
9.1 Map-model overlay [i](#)



X



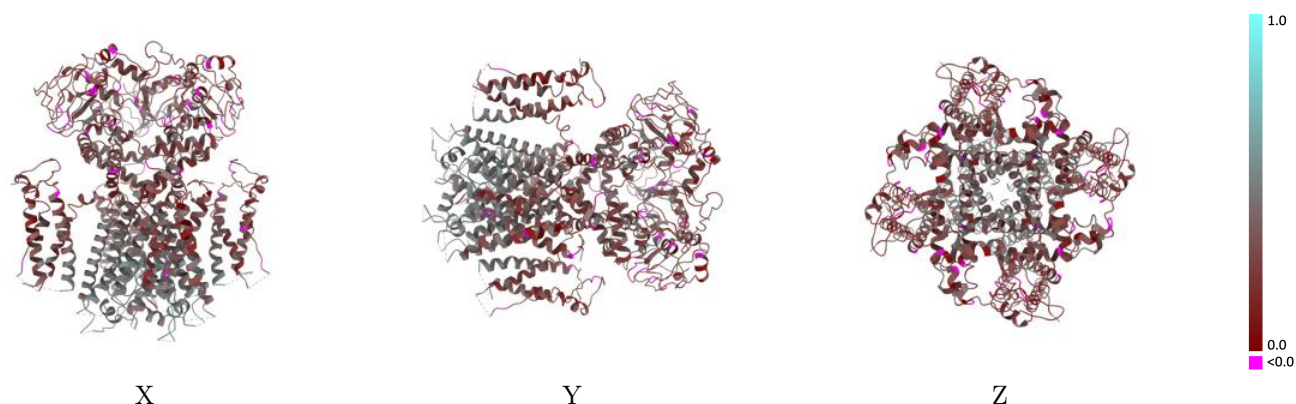
Y



Z

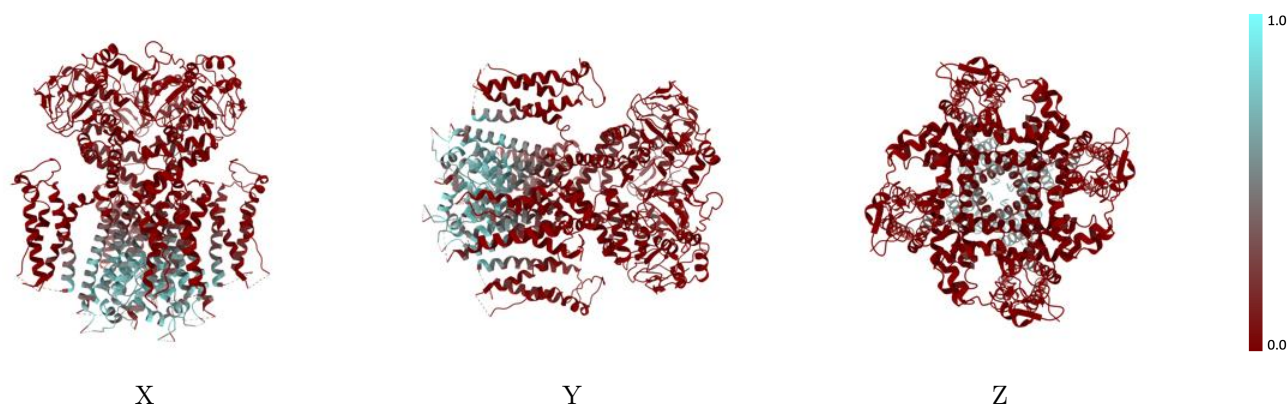
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



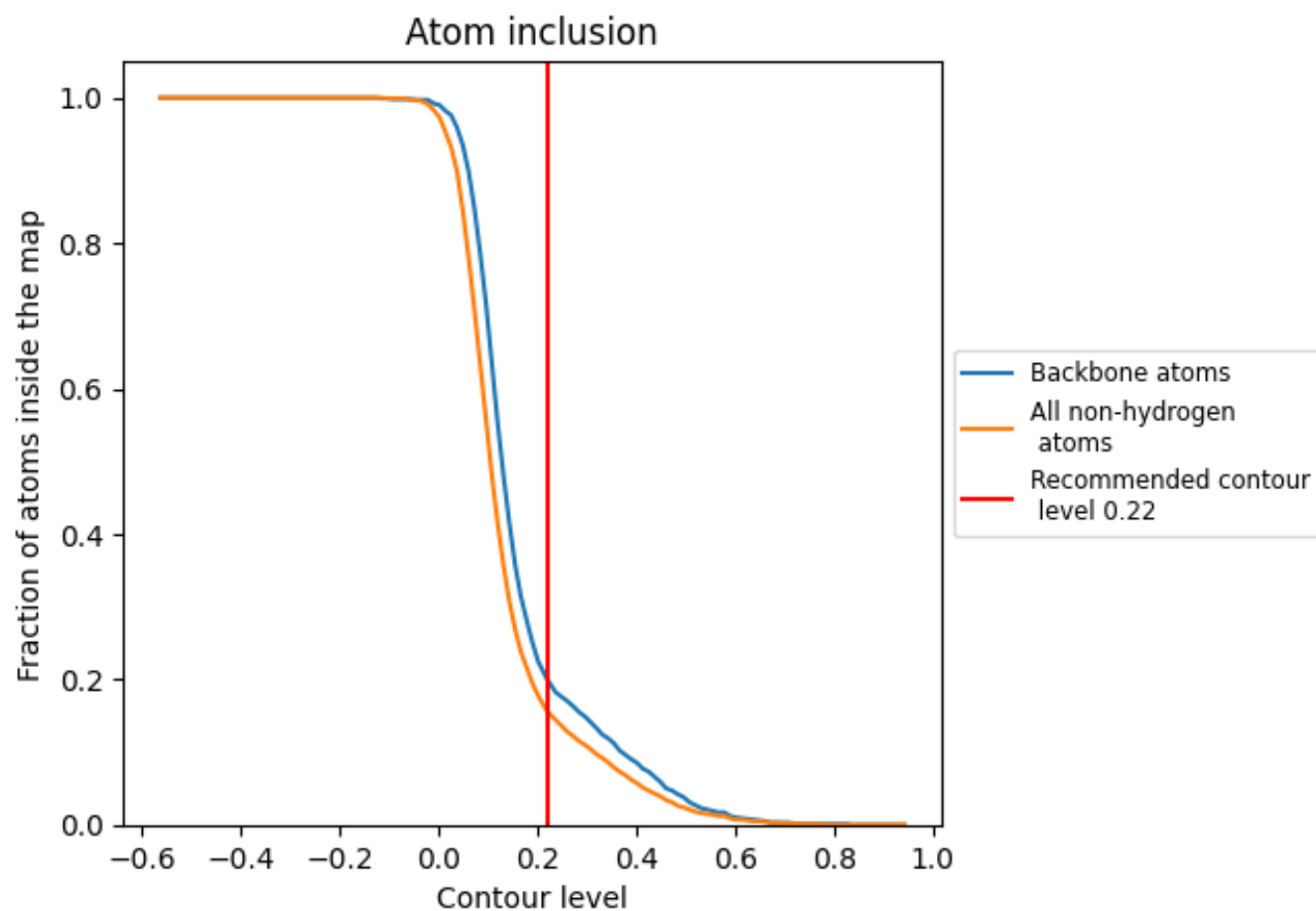
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.22).

9.4 Atom inclusion [i](#)



At the recommended contour level, 20% of all backbone atoms, 16% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.1560	0.3250
A	0.1560	0.3240
B	0.1570	0.3240
C	0.1560	0.3250
D	0.1570	0.3260

