



wwPDB EM Validation Summary Report ⓘ

Mar 13, 2026 – 09:16 AM UTC

PDB ID : 8XS4 / pdb_00008xs4
EMDB ID : EMD-38614
Title : Cryo-EM structure of OSCA1.2-DOPC-1:20-contracted1 state
Authors : Zhang, Y.; Han, Y.
Deposited on : 2024-01-08
Resolution : 3.23 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

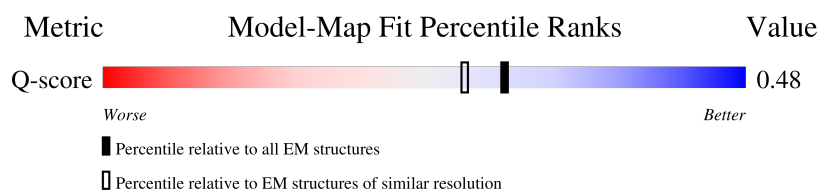
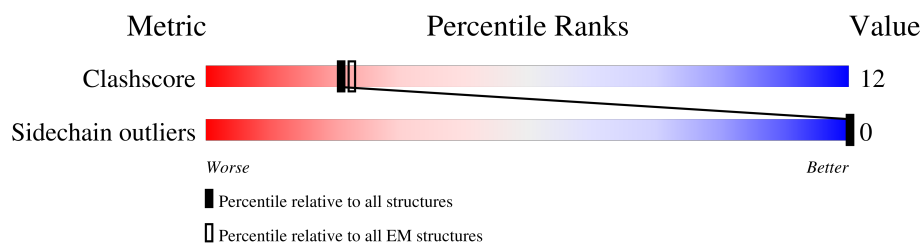
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.23 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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14612 (2.73 - 3.73)

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	777	
1	B	777	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 11132 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 Calcium permeable stress-gated cation channel 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	696	Total	C	N	O	S	0	0
			5566	3683	907	951	25		
1	B	696	Total	C	N	O	S	0	0
			5566	3683	907	951	25		

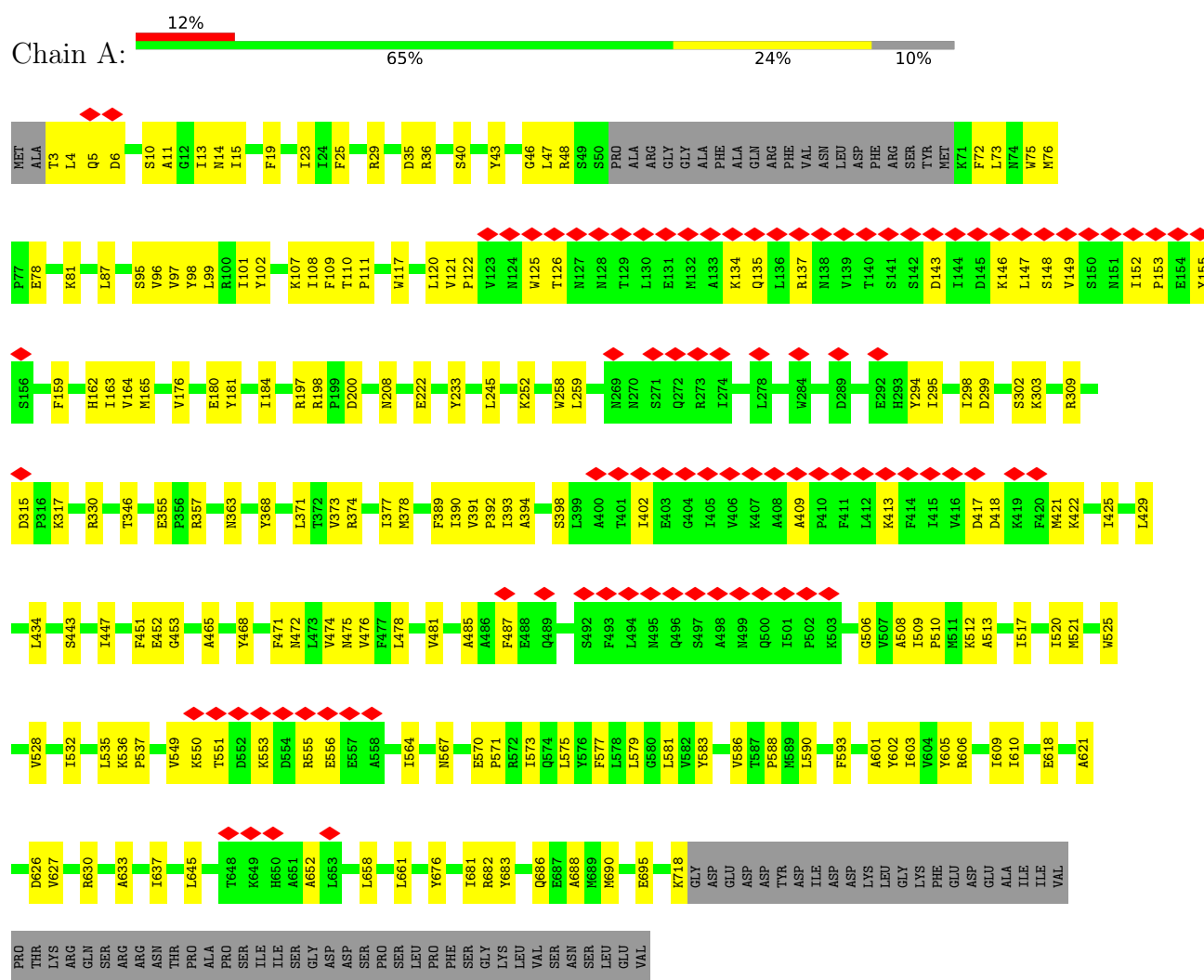
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	772	SER	-	expression tag	UNP Q5XEZ5
A	773	ASN	-	expression tag	UNP Q5XEZ5
A	774	SER	-	expression tag	UNP Q5XEZ5
A	775	LEU	-	expression tag	UNP Q5XEZ5
A	776	GLU	-	expression tag	UNP Q5XEZ5
A	777	VAL	-	expression tag	UNP Q5XEZ5
B	772	SER	-	expression tag	UNP Q5XEZ5
B	773	ASN	-	expression tag	UNP Q5XEZ5
B	774	SER	-	expression tag	UNP Q5XEZ5
B	775	LEU	-	expression tag	UNP Q5XEZ5
B	776	GLU	-	expression tag	UNP Q5XEZ5
B	777	VAL	-	expression tag	UNP Q5XEZ5

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: Calcium permeable stress-gated cation channel 1



- Molecule 1: Calcium permeable stress-gated cation channel 1



LYS	ARG	GLN	SER	ARG	ARG	ASN	THR	PRO	ALA	PRO	SER	ILE	SER	GLY	ASP	ASP	SER	PRO	SER	LEU	PRO	PHE	SER	GLY	LYS	VAL	VAL	SER	ASN	SER	LEU	GLU	VAL																		
R630	V631	I632	A633	I637	L645	T648	K649	H650	A651	A652	L653	L658	L661	Y676	I681	R682	Y683	Q686	E687	A688	W689	M690	E695	K718	GLY	ASP	GLU	ASP	ASP	TYR	ASP	ILE	ASP	ASP	LYS	LEU	GLY	LYS	PHE	LYS	PHE	GLU	ASP	GLU	ASP	ALA	ILE	ILE	VAL	PRO	THR
I532	K536	P537	V549	K550	T551	D552	K553	D554	R555	E556	E557	A558	W559	D560	I564	N567	E570	P571	R572	Q574	L575	Y576	F577	L578	L579	L581	Y582	Y583	V586	T587	P588	W589	L590	F593	Y602	Y605	R606	I609	I610	E618	A621	D626	V627								
S443	I447	F451	E452	G453	A465	Y468	F471	N472	L473	V474	N475	V476	F477	L478	V481	A485	A486	F487	E488	Q489	L490	N491	S492	F493	L494	N495	Q496	S497	A498	N499	Q500	I501	P502	K503	G506	V507	A508	I509	P510	W511	K512	A513	T514	I517	T520	W521	W525				
K317	R330	T346	E355	P356	R357	N363	Y368	L371	T372	V373	R374	I377	M378	F389	I390	V391	P392	I393	A394	S398	L399	A400	T401	I402	E403	G404	I405	V406	K407	A408	A409	P410	F411	L412	K413	F414	I415	V416	D417	D418	K419	F420	M421	K422	I425	L429	L434				
H162	I163	V164	M165	V176	L177	E180	Y181	I184	R197	I198	P199	D200	N208	E222	Y233	L245	K252	W258	L259	S271	Q272	R273	I274	L278	G282	L283	W284	D289	E292	H293	Y294	I295	T298	D299	S302	K303	R309	D315	P316												
K81	L87	S95	V96	V97	Y98	R100	I101	Y102	K107	I108	F109	T110	P111	W117	L120	V121	P122	V123	N124	W125	T126	N127	N128	T129	L130	E131	M132	A133	K134	Q135	L136	R137	N138	V139	T140	S141	S142	D143	I144	D145	K146	L147	S148	V149	S150	N151	I152	P153	E154	Y155	F159
MET	ALA	T3	L4	Q5	D6	A11	N14	I15	F19	I23	I24	F25	R29	D35	R36	S40	Y43	G46	L47	R48	S49	S50	PRO	ALA	ARG	GLY	GLY	ALA	PHE	ALA	GLN	ARG	PHE	VAL	ASN	LEU	ASP	PHE	ARG	SER	TYR	MET	K71	F72	L73	W74	W75	M76	F77	E78	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	246302	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 ($e^-/\text{\AA}^2$)	49.41	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.830	Depositor
Minimum map value	-3.236	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.093	Depositor
Recommended contour level	0.406	Depositor
Map size (Å)	253.19998, 253.19998, 253.19998	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.055, 1.055, 1.055	Depositor

5 Model quality

5.1 Standard geometry

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	0.18	0/5722	0.44	0/7788
1	B	0.18	0/5722	0.44	0/7788
All	All	0.18	0/11444	0.44	0/15576

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

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	5566	0	5602	135	0
1	B	5566	0	5602	131	0
All	All	11132	0	11204	266	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 266 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:481:VAL:HA	1:A:512:LYS:HG3	1.59	0.84
1:B:481:VAL:HA	1:B:512:LYS:HG3	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:374:ARG:NH1	1:B:451:PHE:O	2.21	0.73
1:A:374:ARG:NH1	1:A:451:PHE:O	2.21	0.73
1:A:506:GLY:HA2	1:A:645:LEU:HG	1.69	0.72

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	586/672 (87%)	586 (100%)	0	100	100
1	B	586/672 (87%)	586 (100%)	0	100	100
All	All	1172/1344 (87%)	1172 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	241	ASN
1	B	338	GLN
1	B	615	GLN
1	A	338	GLN
1	A	241	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-38614. These allow visual inspection of the internal detail of the map and identification of artifacts.

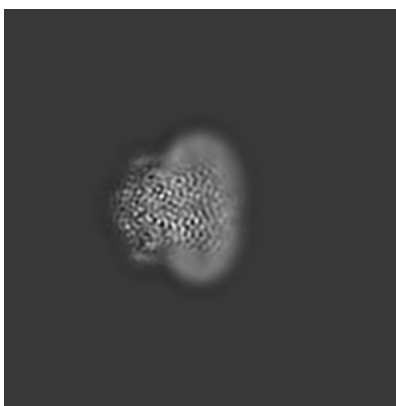
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

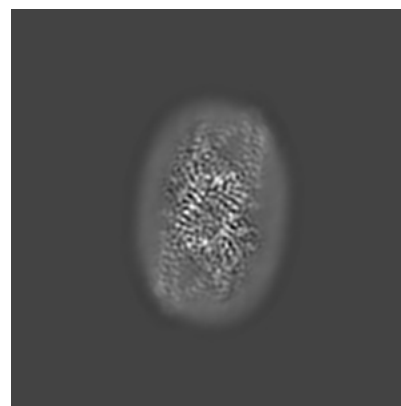
6.1.1 Primary map



X

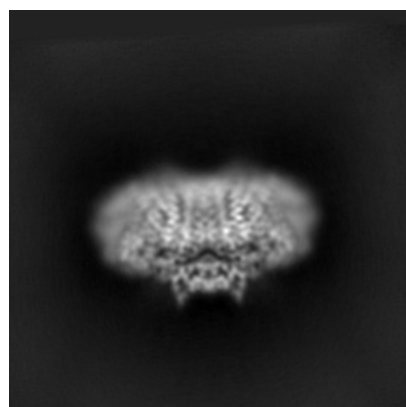


Y

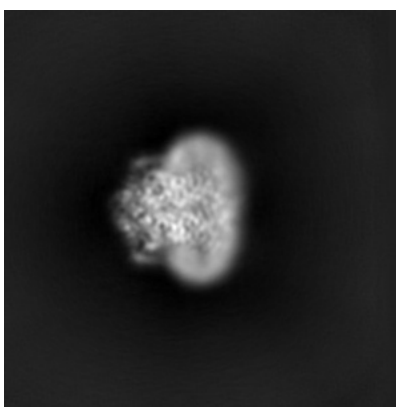


Z

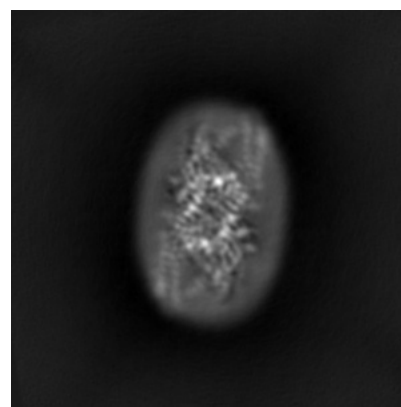
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

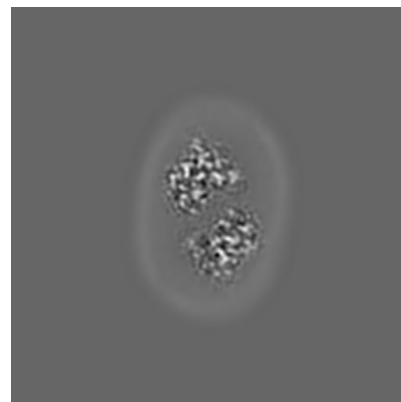
6.2.1 Primary map



X Index: 120

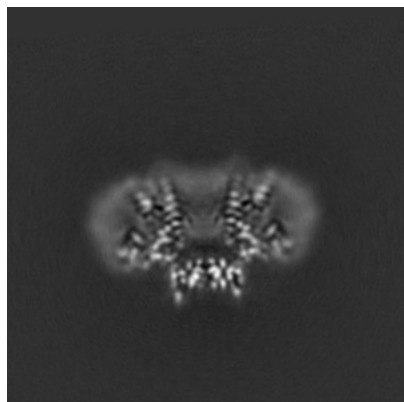


Y Index: 120

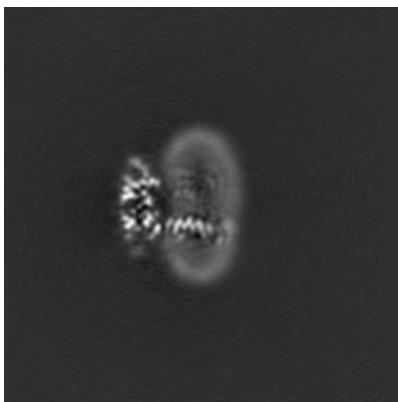


Z Index: 120

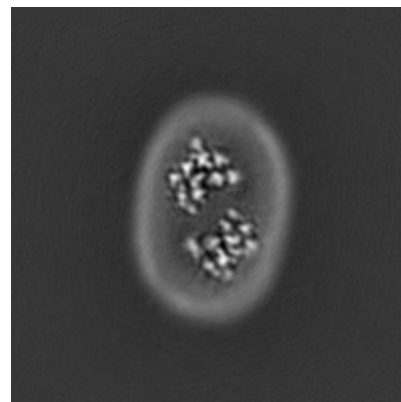
6.2.2 Raw map



X Index: 120



Y Index: 120



Z Index: 120

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

6.3 Largest variance slices [i](#)

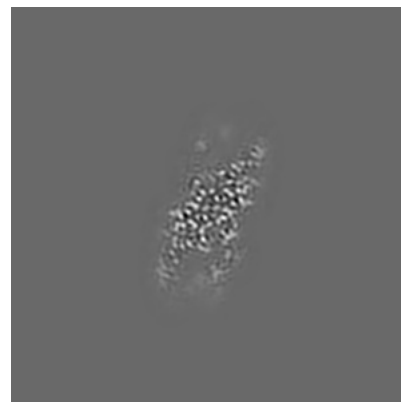
6.3.1 Primary map



X Index: 112

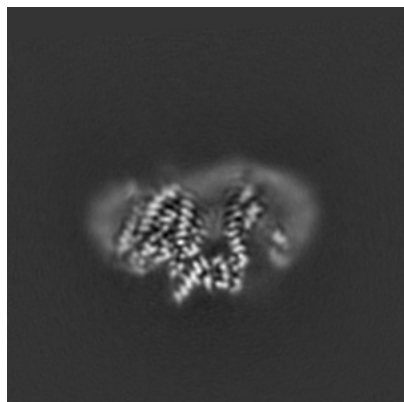


Y Index: 130

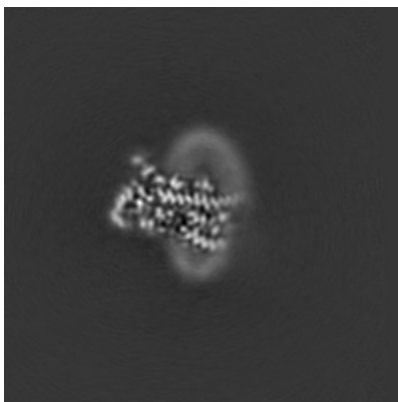


Z Index: 85

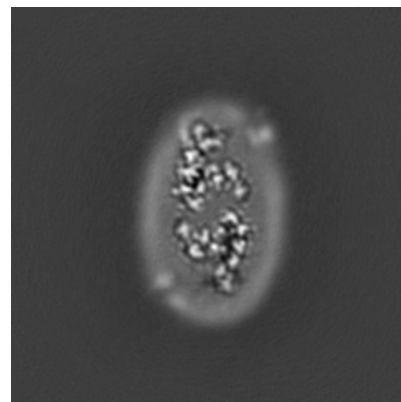
6.3.2 Raw map



X Index: 127



Y Index: 137



Z Index: 106

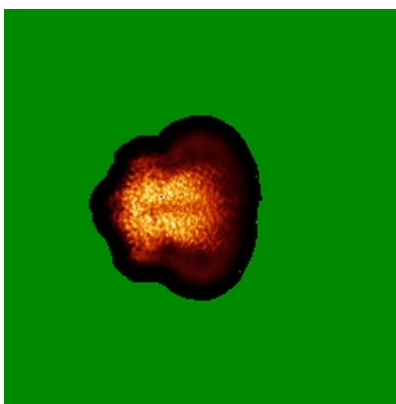
The images above show the largest variance slices of the map in three orthogonal directions.

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

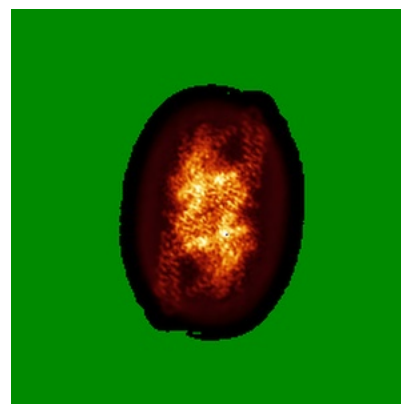
6.4.1 Primary map



X

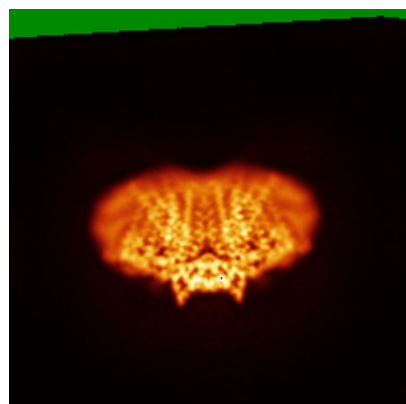


Y

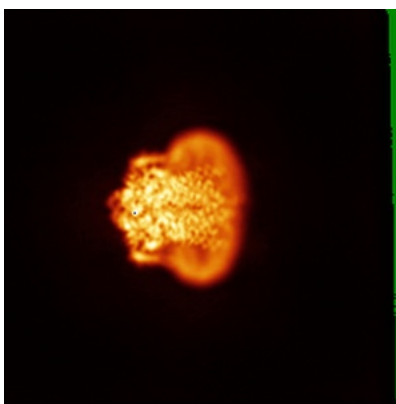


Z

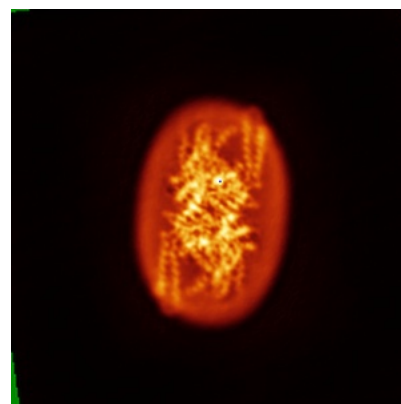
6.4.2 Raw map



X



Y

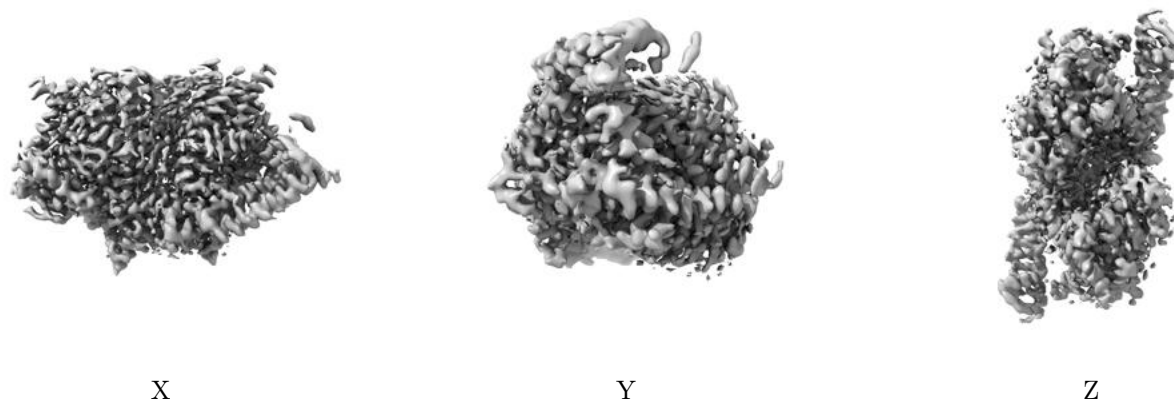


Z

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.

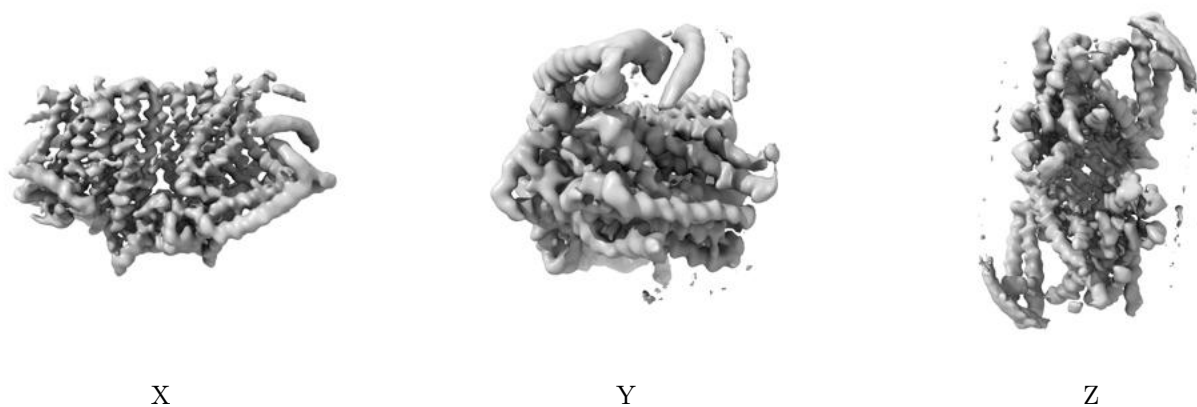
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.406. 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.

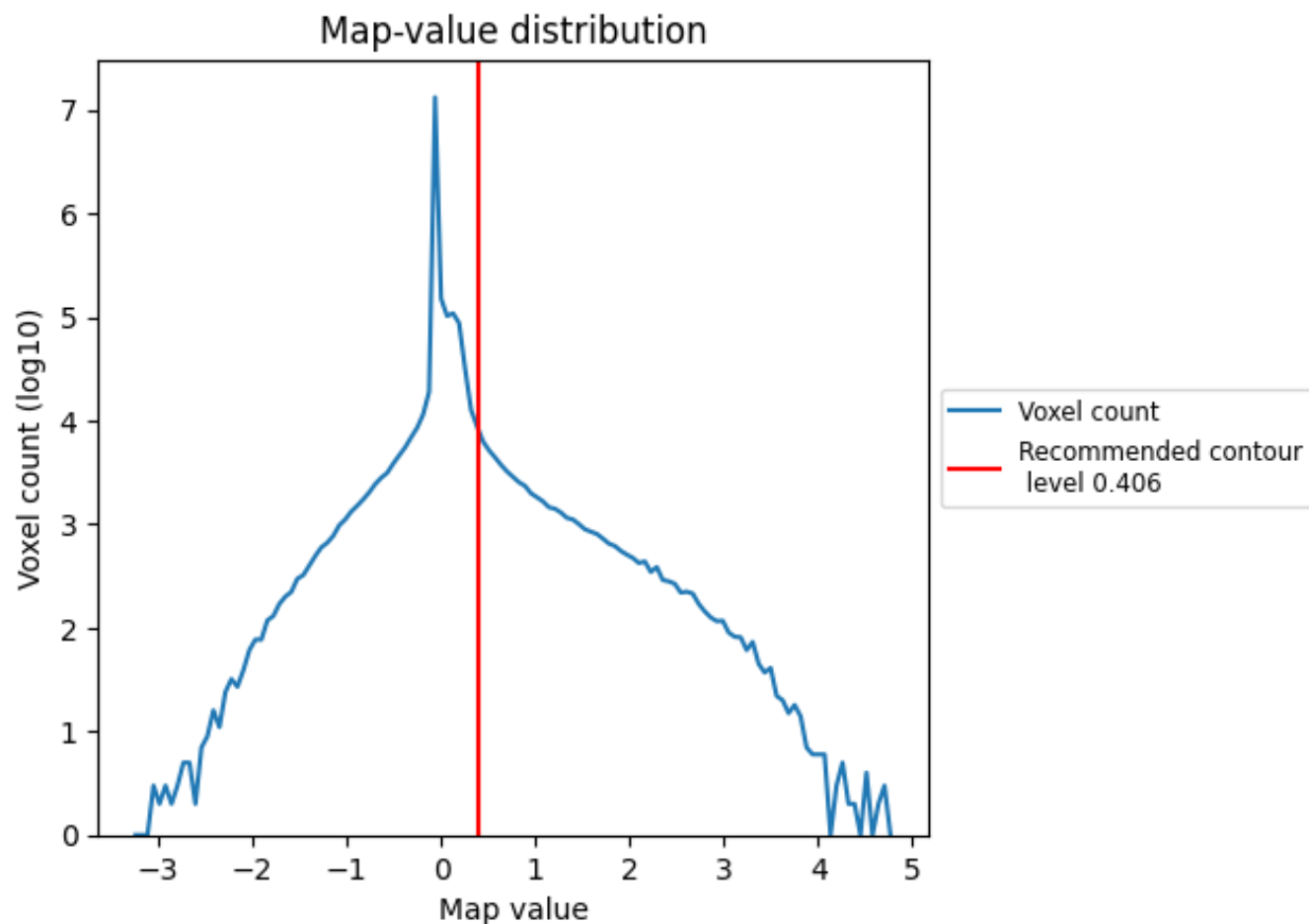
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

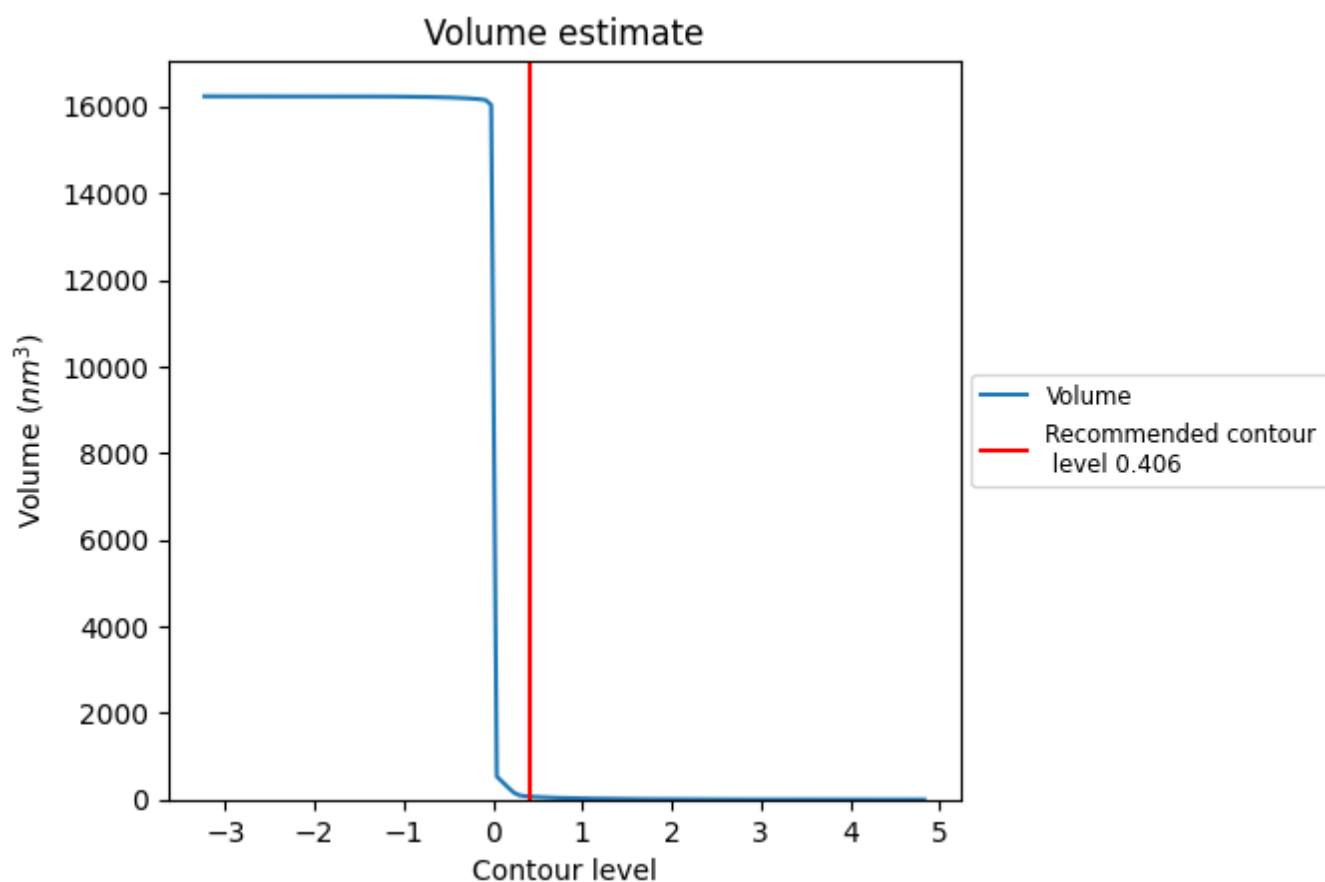
This section contains the results of statistical analysis of the map.

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.

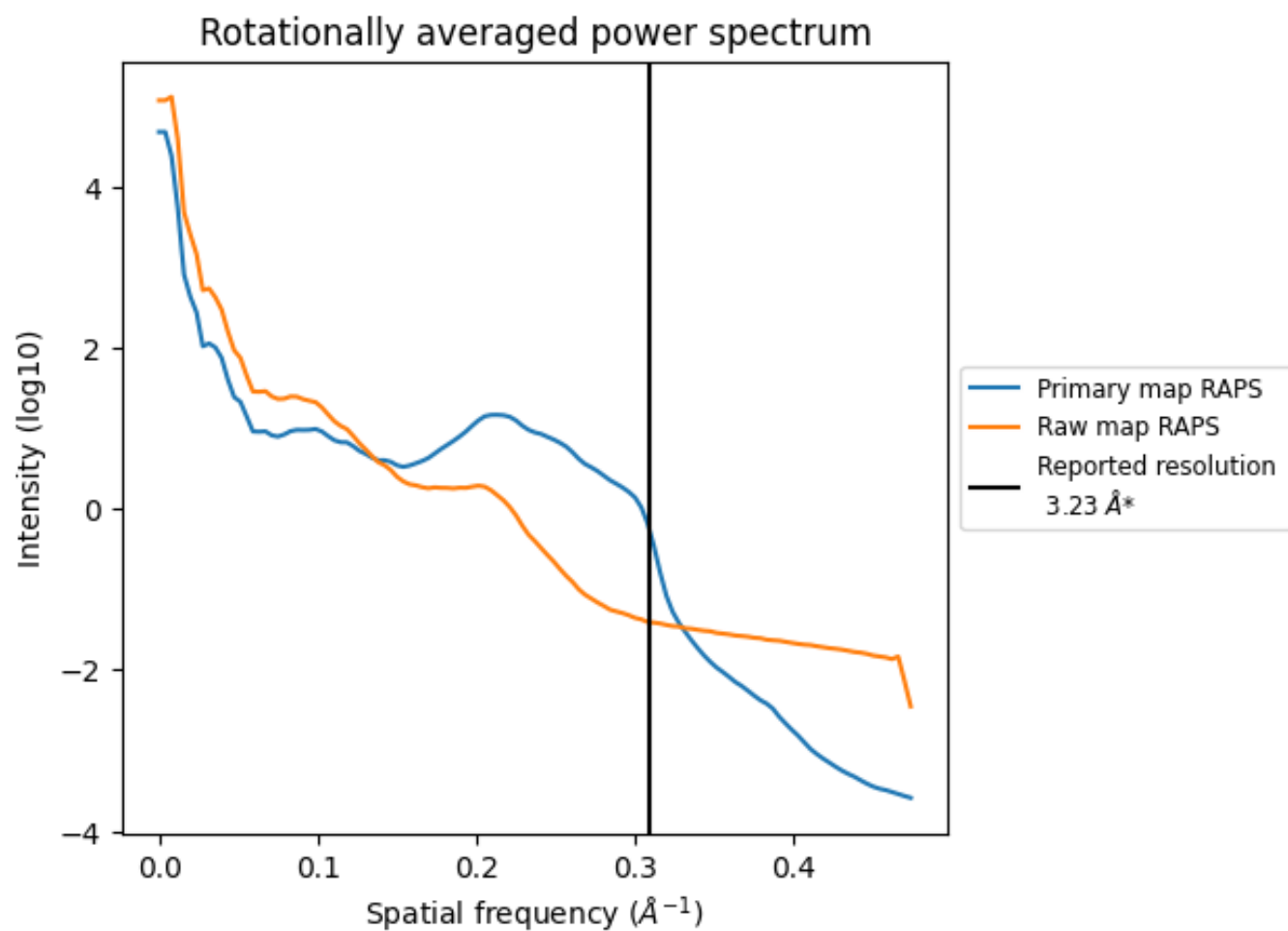
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 70 nm^3 ; this corresponds to an approximate mass of 63 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 ⓘ

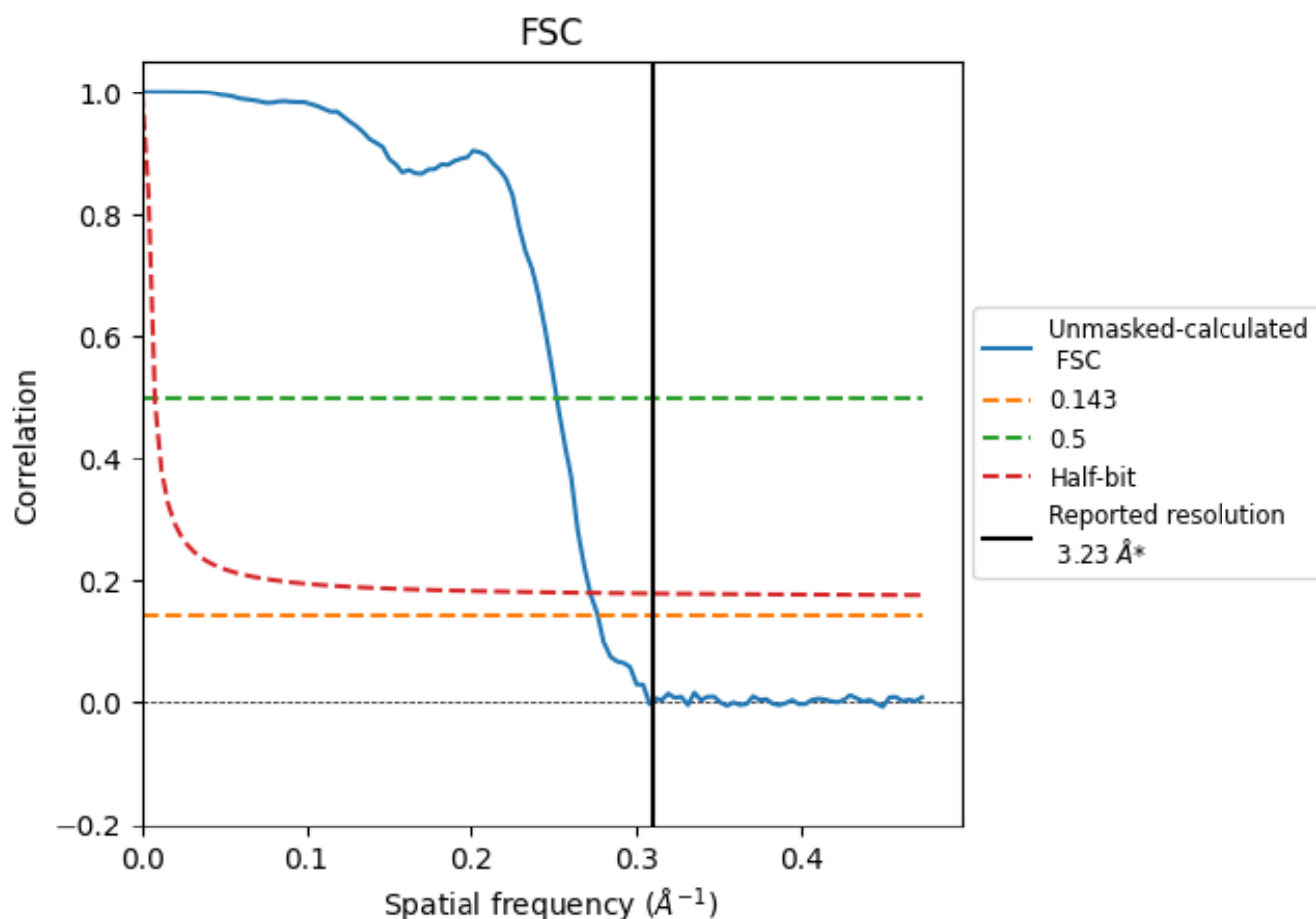


*Reported resolution corresponds to spatial frequency of $0.310 \text{ \AA}^{-1}$

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 0.310 Å⁻¹

8.2 Resolution estimates [i](#)

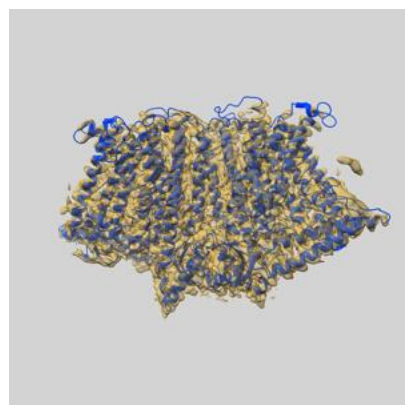
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.23	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.61	3.97	3.67

*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 3.61 differs from the reported value 3.23 by more than 10 %

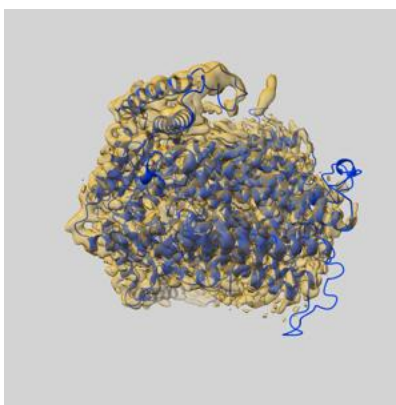
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38614 and PDB model 8XS4. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

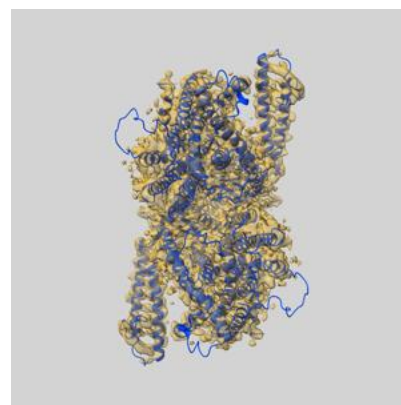
9.1 Map-model overlay [i](#)



X



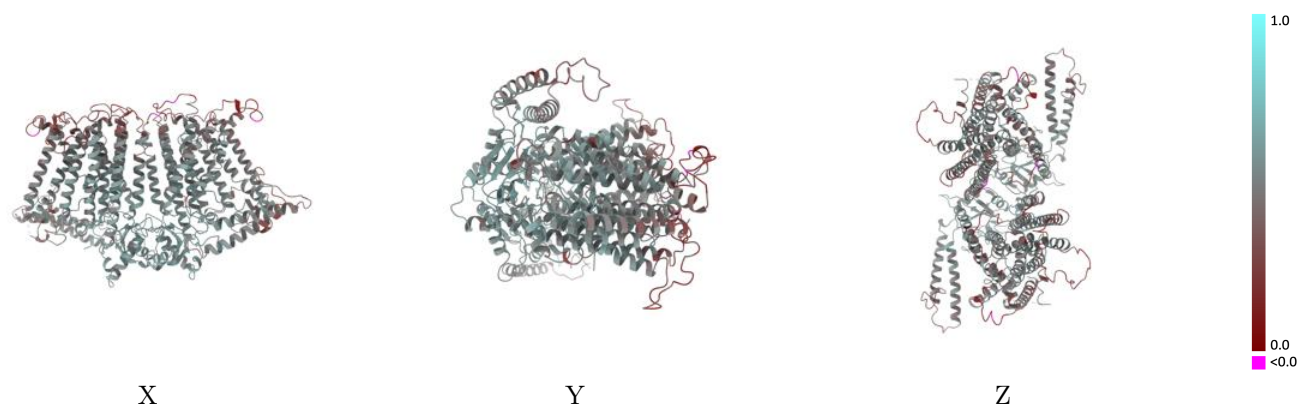
Y



Z

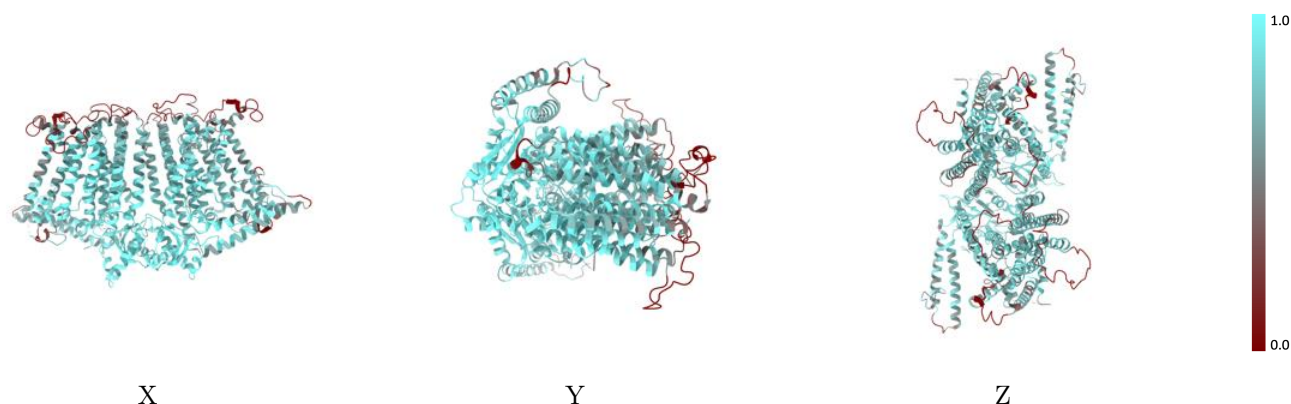
The images above show the 3D surface view of the map at the recommended contour level 0.406 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



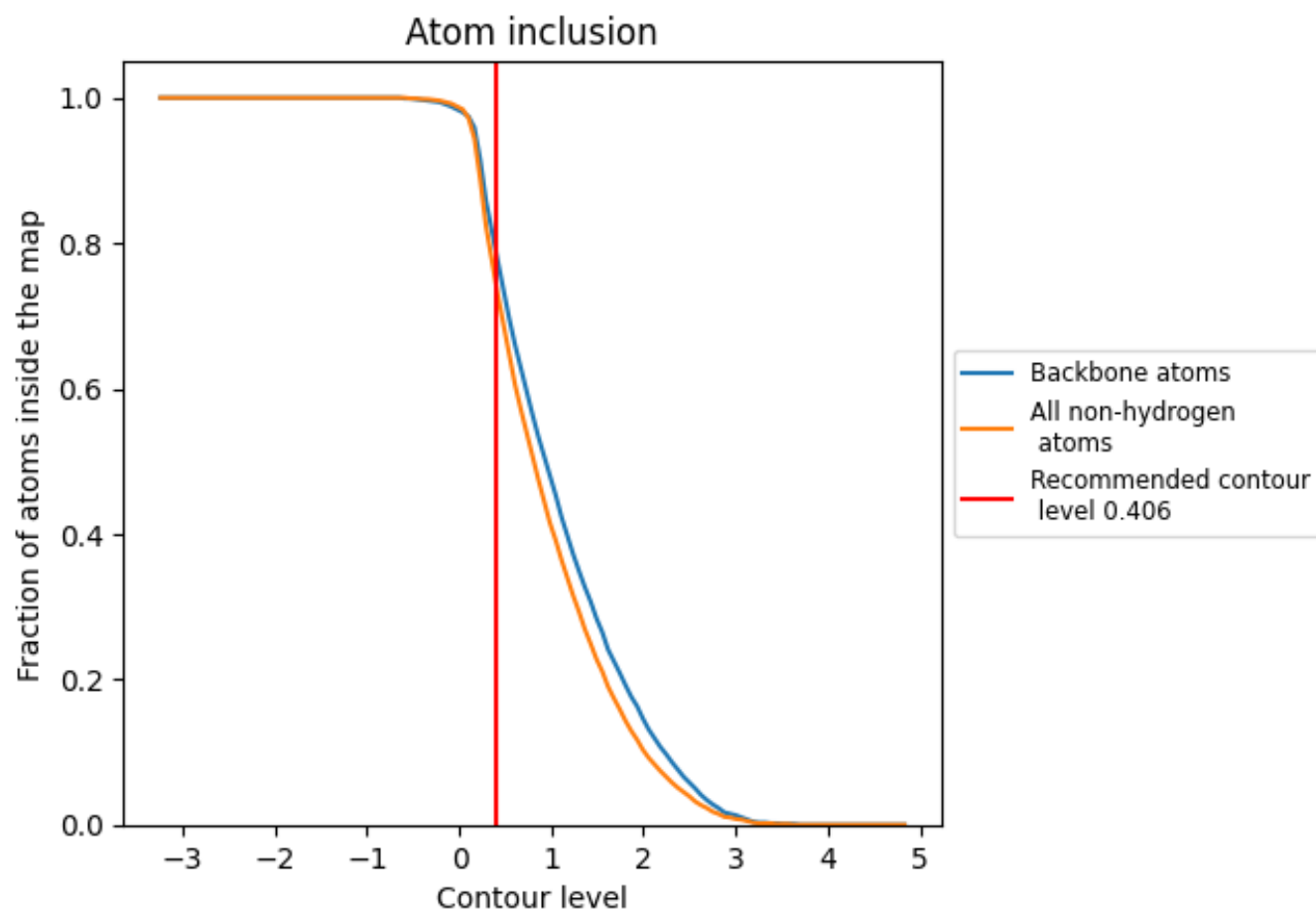
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.406).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 74% 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 (0.406) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7400	0.4800
A	0.7420	0.4790
B	0.7380	0.4800

