



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 06:56 AM UTC

PDB ID : 7PXF / pdb_00007pxf
EMDB ID : EMD-13701
Title : Ca²⁺ free Drosophila Slo channel
Authors : Raisch, T.; Brockmann, A.; Ebbinghaus-Kintscher, U.; Freigang, J.; Gutbrod, O.; Kubicek, J.; Maertens, B.; Hofnagel, O.; Raunser, S.
Deposited on : 2021-10-08
Resolution : 2.68 Å(reported)
Based on initial model : 5TJ6

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

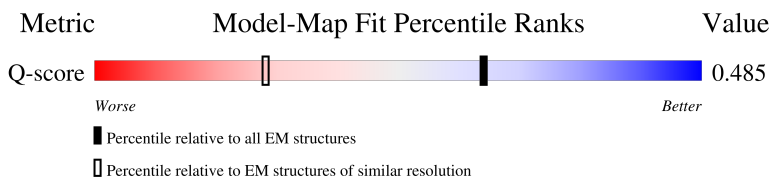
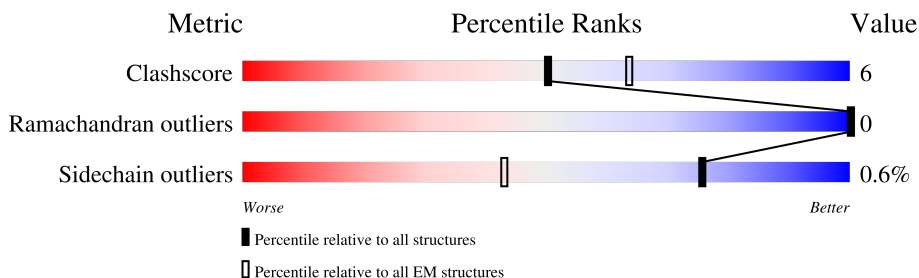
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.68 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	9255 (2.18 - 3.18)

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	1180	14% 64% 11% 25%
1	B	1180	14% 63% 12% 25%
1	C	1180	14% 63% 11% 25%
1	D	1180	14% 64% 11% 25%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 28099 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 Isoform J of Calcium-activated potassium channel slowpoke.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	885	Total	C	N	O	S	0	0
			7023	4548	1148	1279	48		
1	B	885	Total	C	N	O	S	0	0
			7023	4548	1148	1279	48		
1	C	885	Total	C	N	O	S	0	0
			7023	4548	1148	1279	48		
1	D	885	Total	C	N	O	S	0	0
			7023	4548	1148	1279	48		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	281	ASP	ASN	conflict	UNP Q03720
A	328	ILE	MET	conflict	UNP Q03720
A	332	CYS	SER	conflict	UNP Q03720
A	338	ASP	GLU	conflict	UNP Q03720
A	340	ILE	VAL	conflict	UNP Q03720
A	342	THR	SER	conflict	UNP Q03720
A	343	ARG	GLY	conflict	UNP Q03720
A	344	ALA	ASN	conflict	UNP Q03720
A	349	THR	GLU	conflict	UNP Q03720
A	352	ASN	ARG	conflict	UNP Q03720
A	354	LYS	HIS	conflict	UNP Q03720
A	356	ARG	LYS	conflict	UNP Q03720
A	974	GLY	SER	conflict	UNP Q03720
B	281	ASP	ASN	conflict	UNP Q03720
B	328	ILE	MET	conflict	UNP Q03720
B	332	CYS	SER	conflict	UNP Q03720
B	338	ASP	GLU	conflict	UNP Q03720
B	340	ILE	VAL	conflict	UNP Q03720
B	342	THR	SER	conflict	UNP Q03720
B	343	ARG	GLY	conflict	UNP Q03720
B	344	ALA	ASN	conflict	UNP Q03720
B	349	THR	GLU	conflict	UNP Q03720

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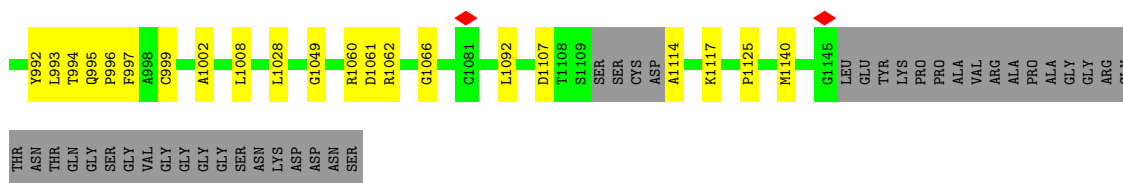
Chain	Residue	Modelled	Actual	Comment	Reference
B	352	ASN	ARG	conflict	UNP Q03720
B	354	LYS	HIS	conflict	UNP Q03720
B	356	ARG	LYS	conflict	UNP Q03720
B	974	GLY	SER	conflict	UNP Q03720
C	281	ASP	ASN	conflict	UNP Q03720
C	328	ILE	MET	conflict	UNP Q03720
C	332	CYS	SER	conflict	UNP Q03720
C	338	ASP	GLU	conflict	UNP Q03720
C	340	ILE	VAL	conflict	UNP Q03720
C	342	THR	SER	conflict	UNP Q03720
C	343	ARG	GLY	conflict	UNP Q03720
C	344	ALA	ASN	conflict	UNP Q03720
C	349	THR	GLU	conflict	UNP Q03720
C	352	ASN	ARG	conflict	UNP Q03720
C	354	LYS	HIS	conflict	UNP Q03720
C	356	ARG	LYS	conflict	UNP Q03720
C	974	GLY	SER	conflict	UNP Q03720
D	281	ASP	ASN	conflict	UNP Q03720
D	328	ILE	MET	conflict	UNP Q03720
D	332	CYS	SER	conflict	UNP Q03720
D	338	ASP	GLU	conflict	UNP Q03720
D	340	ILE	VAL	conflict	UNP Q03720
D	342	THR	SER	conflict	UNP Q03720
D	343	ARG	GLY	conflict	UNP Q03720
D	344	ALA	ASN	conflict	UNP Q03720
D	349	THR	GLU	conflict	UNP Q03720
D	352	ASN	ARG	conflict	UNP Q03720
D	354	LYS	HIS	conflict	UNP Q03720
D	356	ARG	LYS	conflict	UNP Q03720
D	974	GLY	SER	conflict	UNP Q03720

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

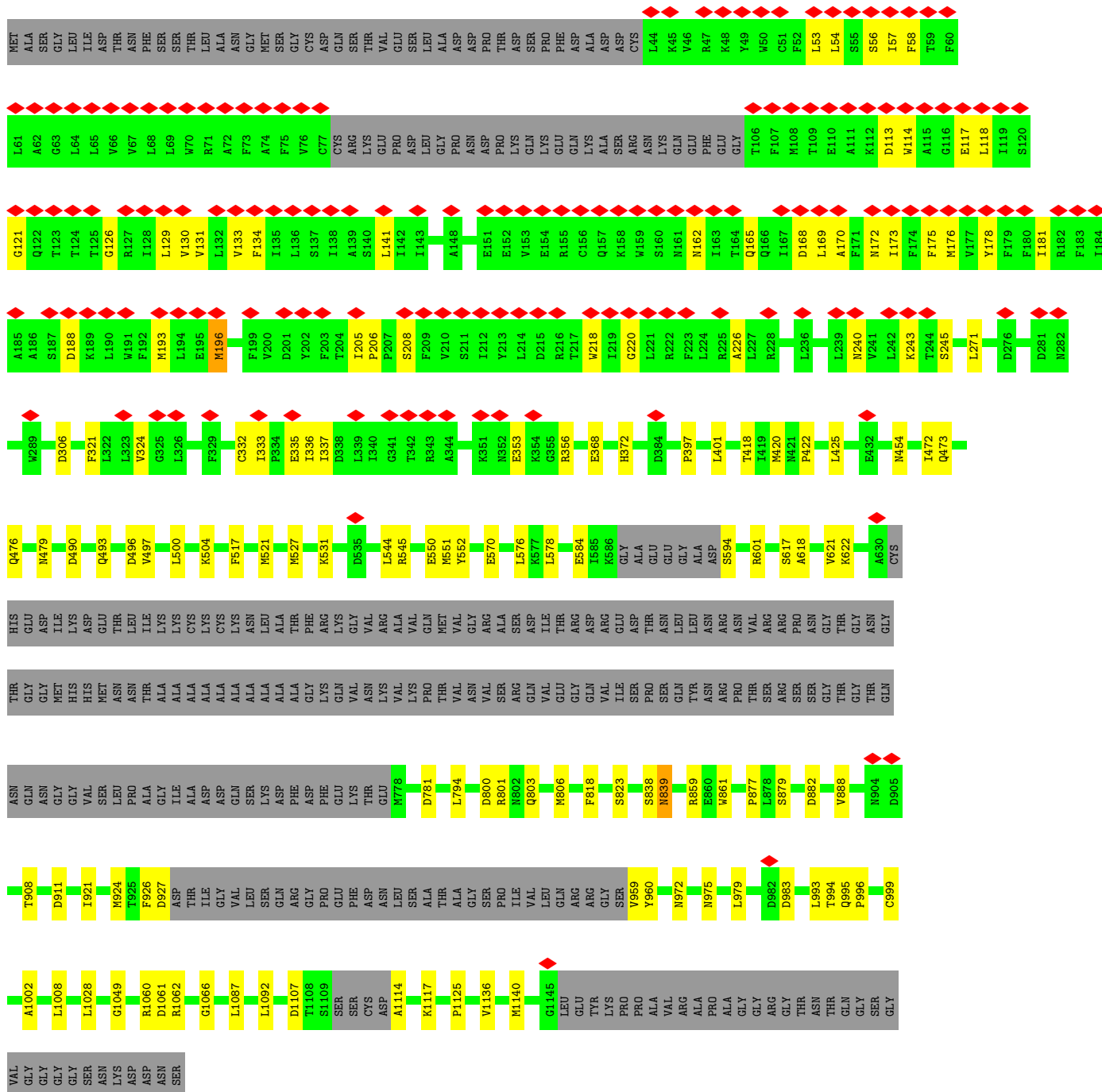
Mol	Chain	Residues	Atoms	AltConf
2	A	1	Total Mg 1 1	0
2	B	1	Total Mg 1 1	0
2	C	1	Total Mg 1 1	0
2	D	1	Total Mg 1 1	0

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

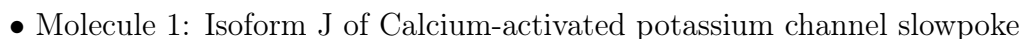
Mol	Chain	Residues	Atoms		AltConf
3	A	3	Total 3	K 3	0



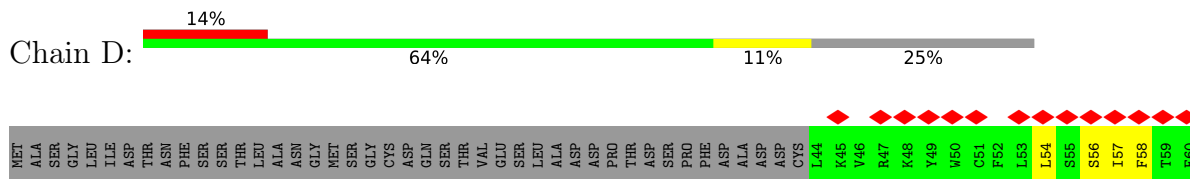
• Molecule 1: Isoform J of Calcium-activated potassium channel slowpoke



Chain C:



Chain D:



L61	A62	G63	L64	L65	V66	V67	L68	L69	W70	R71	A72	F73	A74	F75	V76	C77	CYS	ARG	LYS	GLU	GLY	PRO	GLY	ASP	LEU	GLY	PRO	ASN	ASP	PRO	LYS	GLN	LYS	GLN	LYS	ALA	ALA	SER	ARG	ASN	LYS	GLN	PHE	GLU	GLU	GLY	T106	F107	M108	T109	E110	A111	K112	D113	W114	A115	G116	E117	L118	I119	S120
G121	Q122	T123	T124	T125	G126	R127	I128	L129	V130	V131	L132	V133	F134	I135	L136	I137	I138	A139	S140	L141	I142	I143	A148	E152	V153	E154	R155	C156	Q157	K158	W159	S160	N161	N162	I163	T164	Q165	Q166	I167	D168	L169	A170	F171	N172	I173	F174	F175	M176	V177	Y178	F179	F180	I181	R182	F183	I184	A185				
A186	S187	D188	K189	L190	W191	F192	M193	L194	E195	M196	Y197	S198	F199	V200	D201	Y202	F203	T204	I205	P206	P207	S208	F209	V210	S211	I212	Y213	L214	D215	R216	G355	T217	W218	I219	G220	L221	R222	F223	L224	R225	A226	L227	R228	L236	N240	V241	L242	K243	T244	L271	D276	D281	N282	W289							
I296	D306	F321	L322	L323	V324	G325	L326	F329	A330	S331	C332	I333	E335	I336	I337	D338	L339	G341	T342	R343	A344	K351	N352	E353	K354	G355	R356	E368	H372	D384	P397	L401	T418	T419	M420	M421	P422	L425	M454	I472	Q473	D490																			
Q493	D496	V497	L500	K504	F517	M521	M527	K531	T532	D535	L544	R545	E550	M551	Y552	S557	E570	L576	V577	L578	E584	I585	K586	GLY	ALA	GLU	GLU	GLY	ALA	ASP	S594	R601	S617	A618	D619	E620	V621	K622	H623	A624	A630																				
CYS	HIS	GLU	GLY	ASP	ILE	LYS	ASP	MET	GLU	THR	ASN	LEU	ALA	THR	PHE	ARG	LYS	GLY	VAL	ARG	LYS	VAL	GLN	MET	VAL	GLY	ASN	VAL	ARG	GLU	ASP	THR	GLY	ALA	ASP	ASN	ASN	ASN	VAL	THR	ARG	ARG	ARG	PRO	ASN	GLY	THR	GLY	ASN												
GLY	THR	GLY	GLY	MET	HIS	HIS	ASP	MET	ASN	THR	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ASN	VAL	ARG	LYS	VAL	PRO	THR	VAL	ASN	VAL	VAL	SER	PRO	GLY	GLN	VAL	ILE	SER	PRO	SER	PRO	SER	GLN	TYR	ARG	PRO	THR	SER	ARG	GLY	THR	GLY	THR											
GLN	ASN	GLN	ASN	GLY	VAL	SER	VAL	SER	PRO	ALA	GLY	ILE	ALA	ALA	ASP	GLN	LYS	SER	GLN	GLY	ASP	PHE	ASP	PHE	GLU	LYS	THR	M778	D781	L794	D800	R801	N802	Q803	M806	F818	S823	S838	N839	R859	E860	W861	P877	L878	S879	D882	V888	N904													
D905	T908	D911	T921	M924	D927	ASP	THR	ILE	GLY	VAL	LEU	SER	GLN	GLY	PRO	PHE	ASP	ASN	LEU	SER	ALA	THR	ALA	GLY	SER	V959	Y960	N972	N975	L979	D982	D983	D988	L993	T994	Q995	P996																								
C999	A1002	L1008	L1028	G1049	R1060	D1061	R1062	G1066	G1081	L1087	L1092	D1107	T1108	S1109	SER	SER	CYS	ASP	A1114	K1117	P1125	V1136	M1140	G1145	LEU	GLU	TYR	LYS	PRO	PRO	ALA	VAL	ALA	ARG	ALA	PRO	ALA	GLY	GLY	ARG	GLY	THR	ASN	THR																	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	90897	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 ($e^-/\text{\AA}^2$)	79.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.007	Depositor
Minimum map value	-0.533	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	313.6, 313.6, 313.6	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.7, 0.7, 0.7	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.10	0/7181	0.25	0/9743
1	B	0.10	0/7181	0.24	0/9743
1	C	0.10	0/7181	0.25	0/9743
1	D	0.10	0/7181	0.24	0/9743
All	All	0.10	0/28724	0.25	0/38972

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	7023	0	7022	79	0
1	B	7023	0	7022	82	0
1	C	7023	0	7022	80	0
1	D	7023	0	7022	78	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	3	0	0	0	0
All	All	28099	0	28088	317	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 6.

The worst 5 of 317 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:994:THR:HG22	1:A:996:PRO:HD2	1.70	0.73
1:B:994:THR:HG22	1:B:996:PRO:HD2	1.70	0.73
1:C:994:THR:HG22	1:C:996:PRO:HD2	1.70	0.72
1:D:994:THR:HG22	1:D:996:PRO:HD2	1.70	0.72
1:A:823:SER:O	1:A:859:ARG:NH2	2.29	0.66

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	873/1180 (74%)	855 (98%)	18 (2%)	0	100	100
1	B	873/1180 (74%)	855 (98%)	18 (2%)	0	100	100
1	C	873/1180 (74%)	855 (98%)	18 (2%)	0	100	100
1	D	873/1180 (74%)	855 (98%)	18 (2%)	0	100	100
All	All	3492/4720 (74%)	3420 (98%)	72 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	774/1008 (77%)	769 (99%)	5 (1%)	78	90
1	B	774/1008 (77%)	769 (99%)	5 (1%)	78	90
1	C	774/1008 (77%)	769 (99%)	5 (1%)	78	90
1	D	774/1008 (77%)	769 (99%)	5 (1%)	78	90
All	All	3096/4032 (77%)	3076 (99%)	20 (1%)	76	90

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	888	VAL
1	D	271	LEU
1	D	888	VAL
1	D	839	ASN
1	B	196	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	479	ASN
1	D	608	ASN
1	D	1018	ASN
1	B	608	ASN
1	B	485	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

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

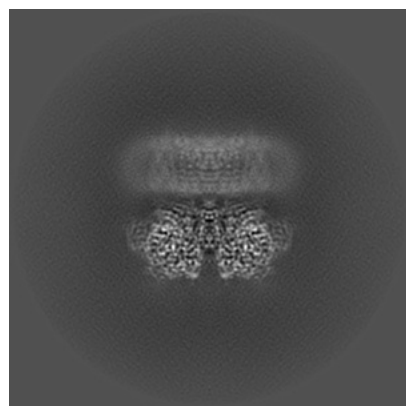
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13701. These allow visual inspection of the internal detail of the map and identification of artifacts.

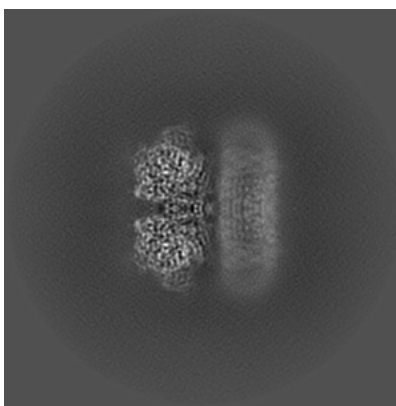
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

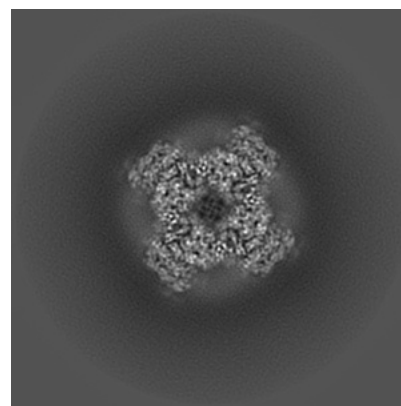
6.1.1 Primary map



X

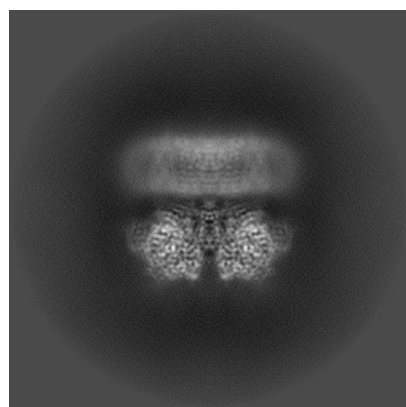


Y

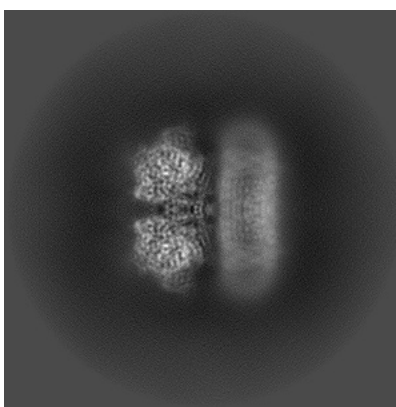


Z

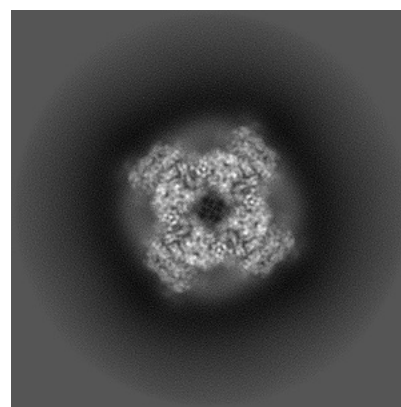
6.1.2 Raw map



X



Y

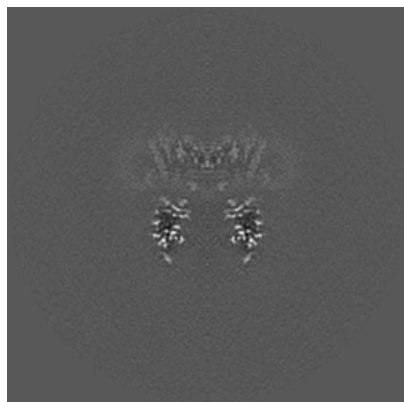


Z

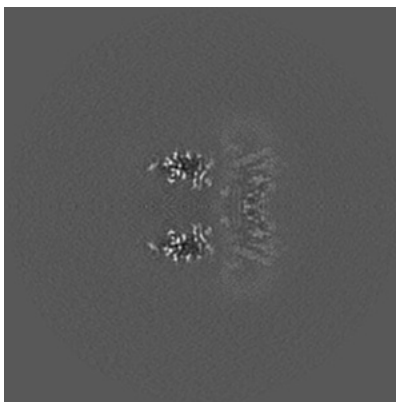
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

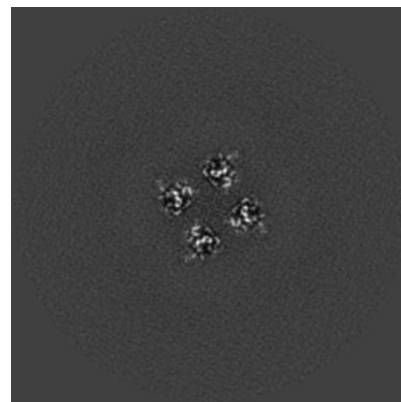
6.2.1 Primary map



X Index: 224

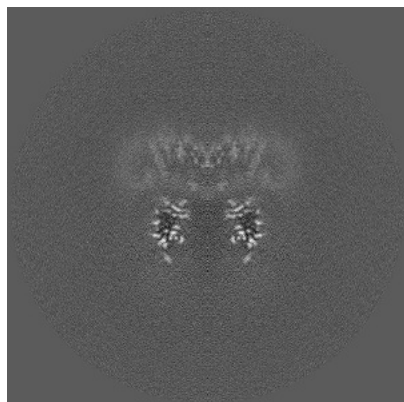


Y Index: 224

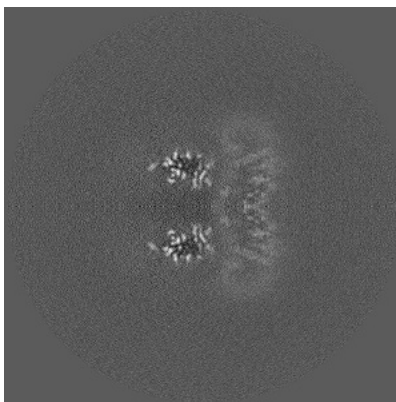


Z Index: 224

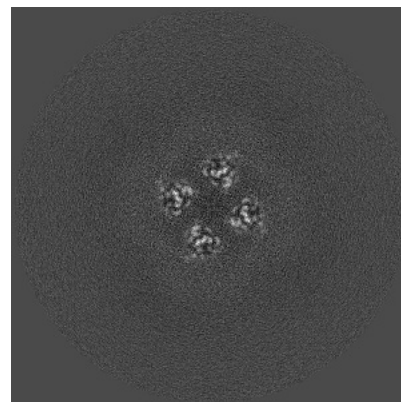
6.2.2 Raw map



X Index: 224



Y Index: 224

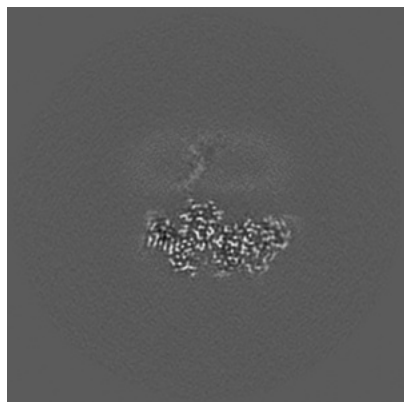


Z Index: 224

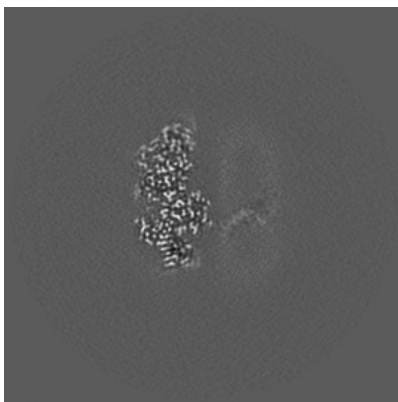
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

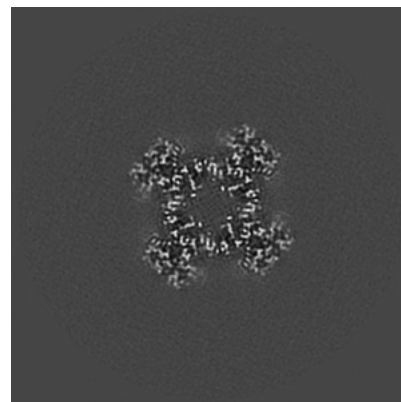
6.3.1 Primary map



X Index: 264

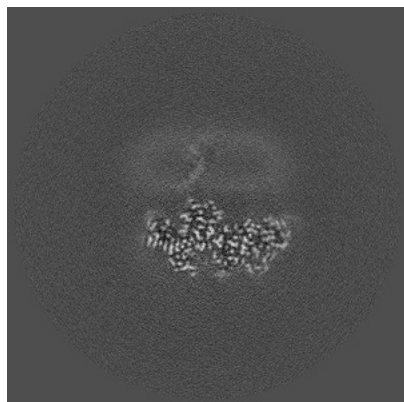


Y Index: 184

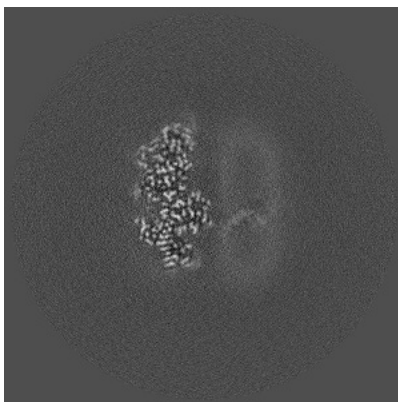


Z Index: 181

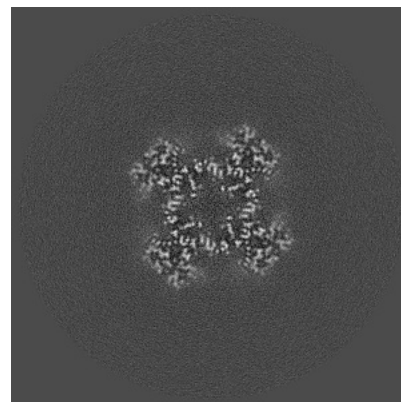
6.3.2 Raw map



X Index: 264



Y Index: 184

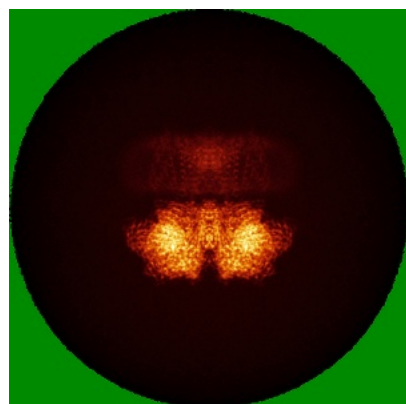


Z Index: 181

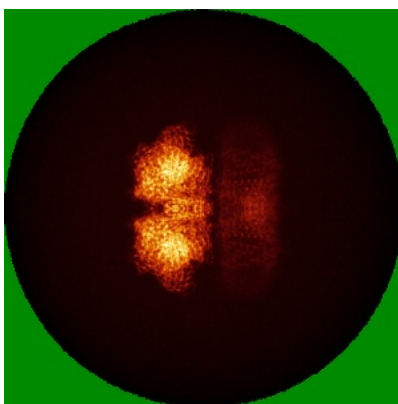
The images above show the largest variance slices of the map in three orthogonal directions.

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

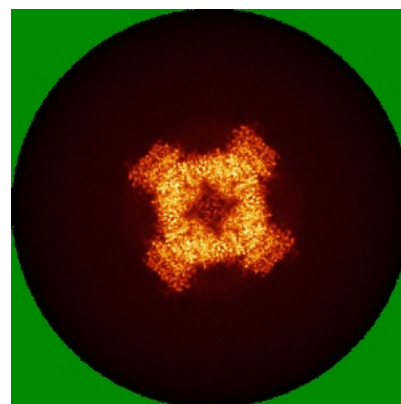
6.4.1 Primary map



X

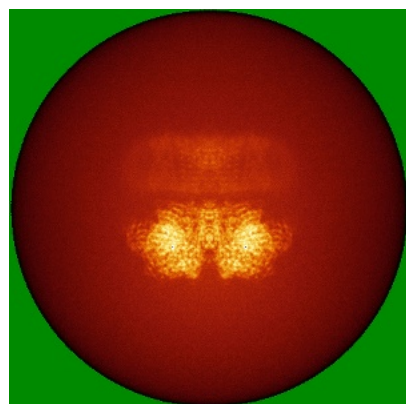


Y

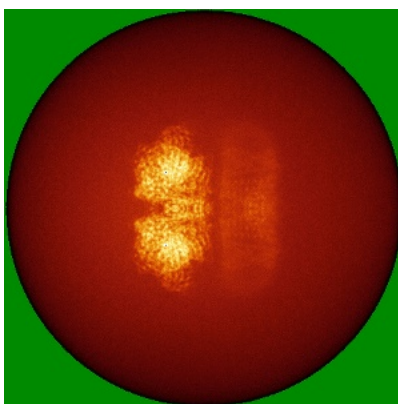


Z

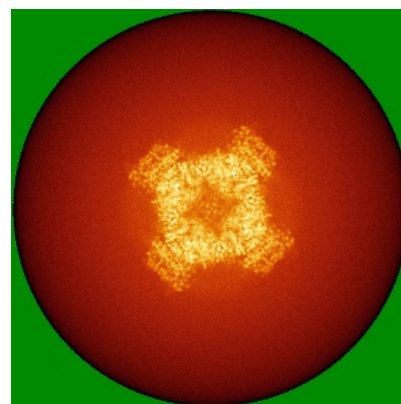
6.4.2 Raw map



X



Y

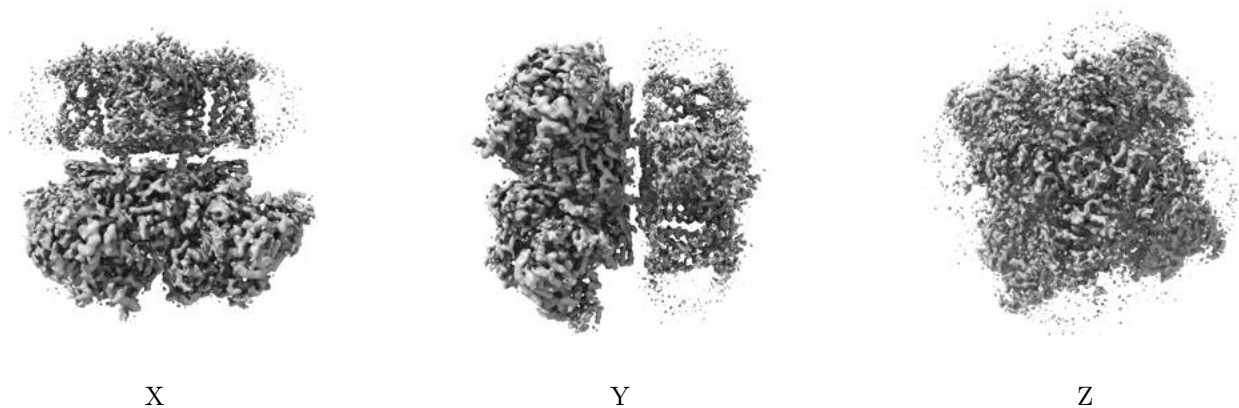


Z

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 0.09. 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.

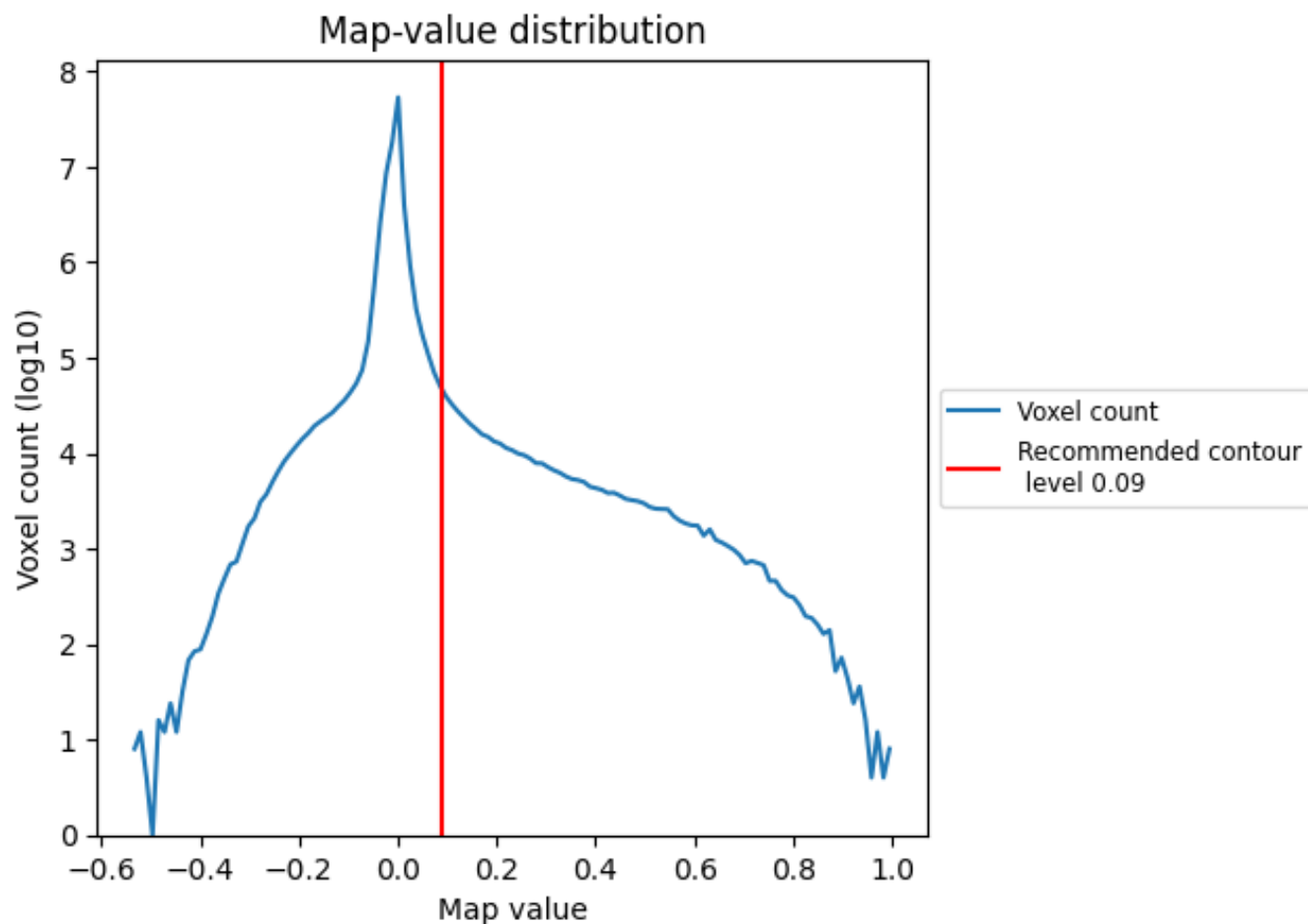
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

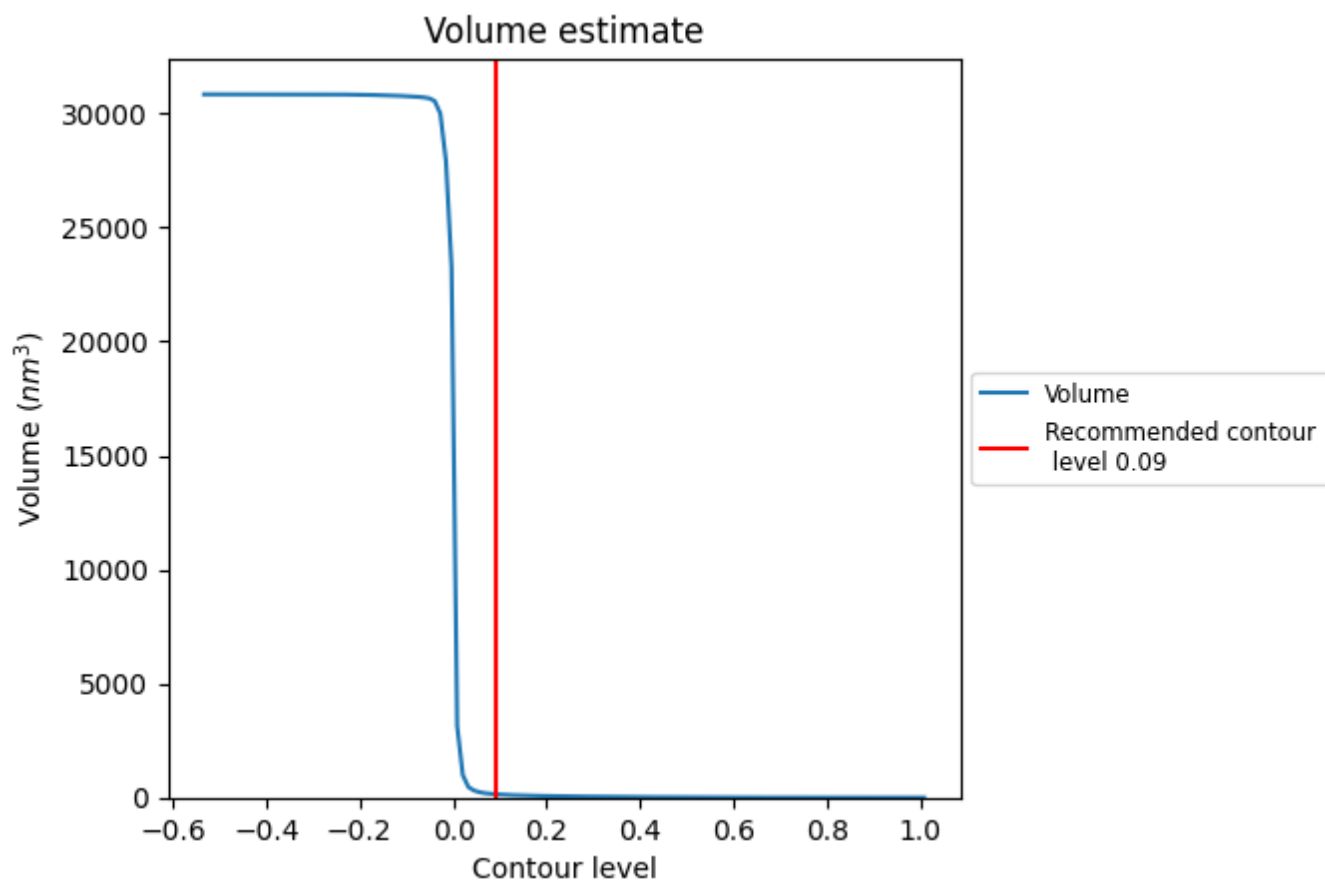
This section contains the results of statistical analysis of the map.

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.

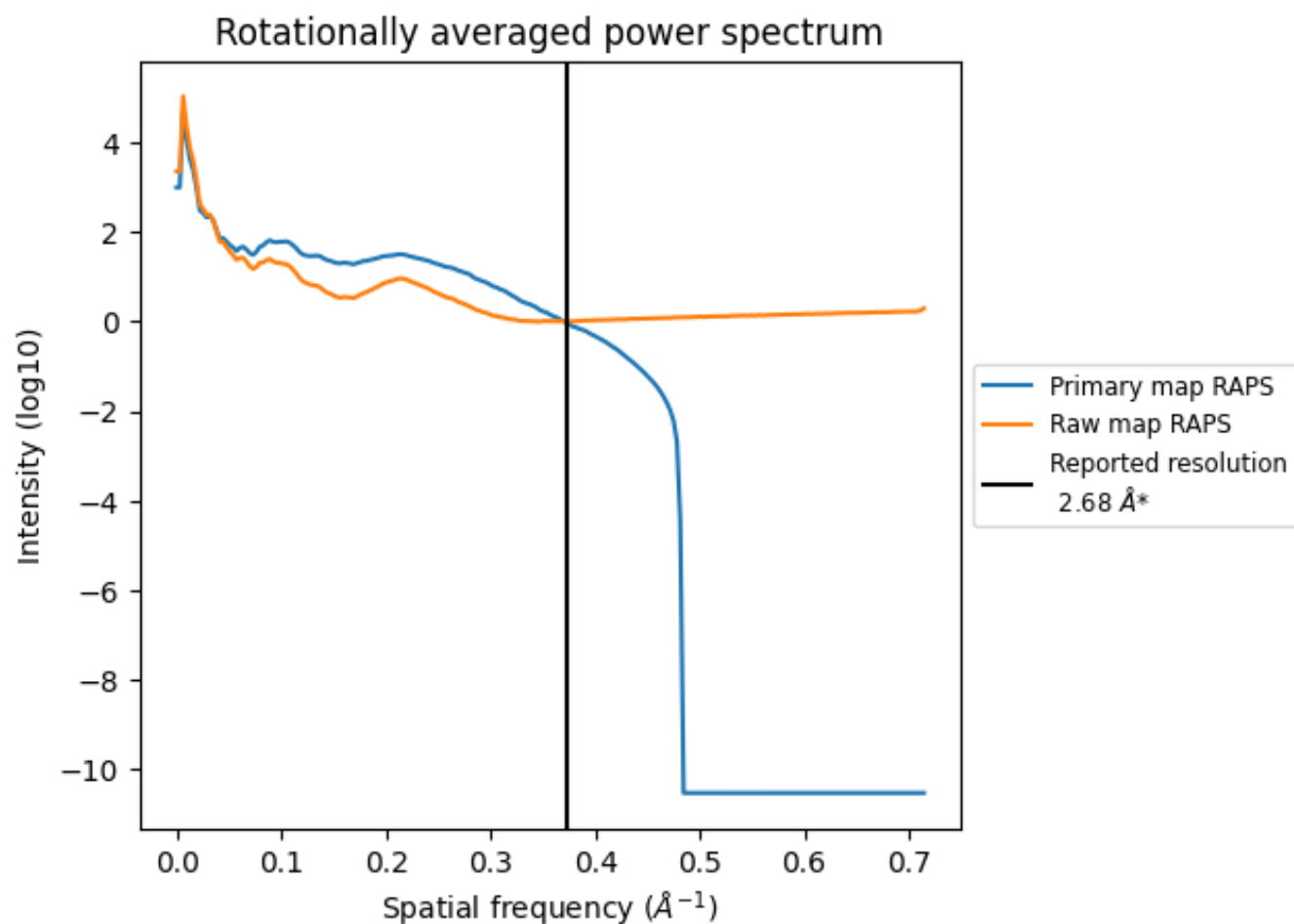
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 147 nm³; this corresponds to an approximate mass of 133 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 ⓘ

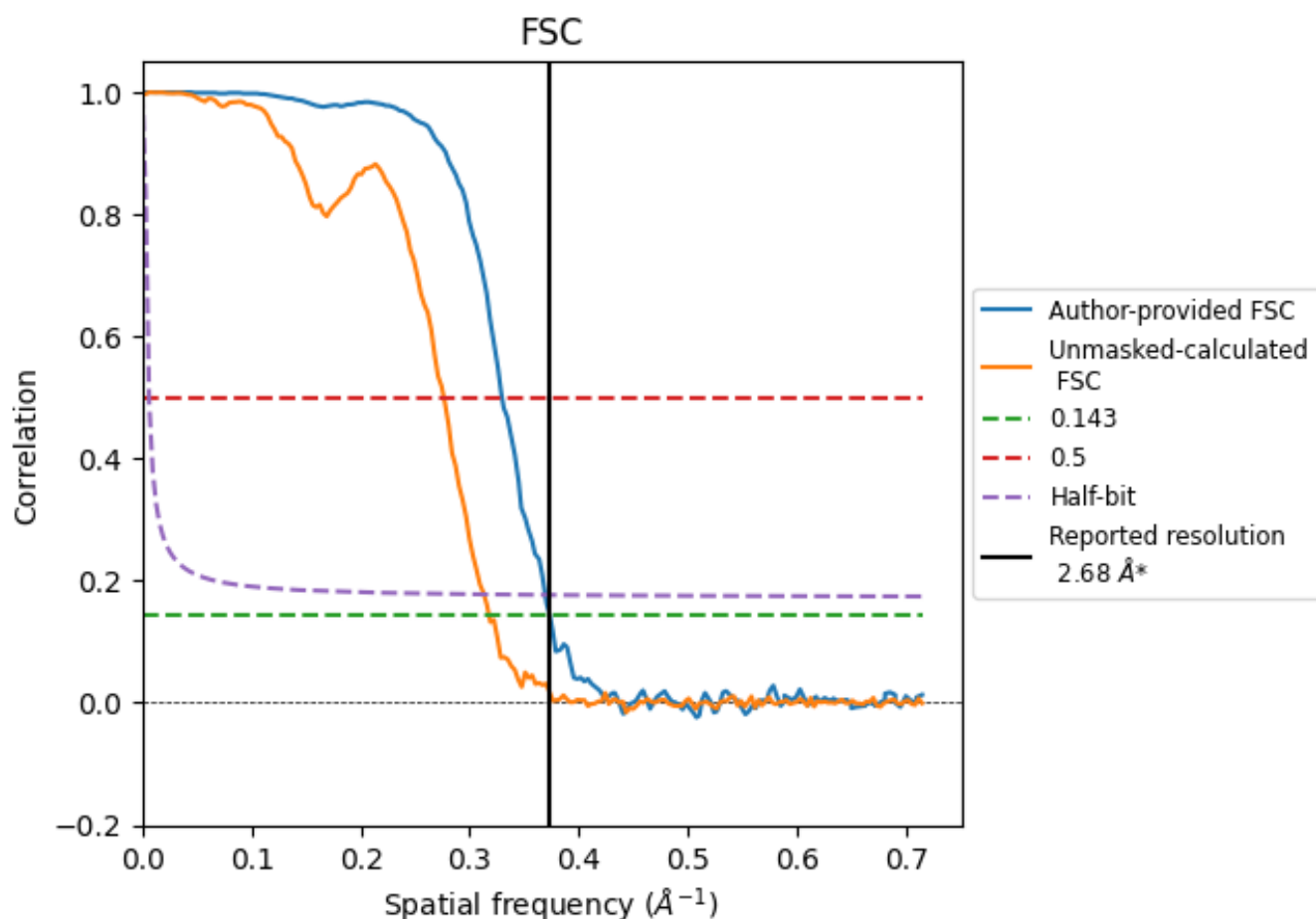


*Reported resolution corresponds to spatial frequency of 0.373 Å⁻¹

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 0.373 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

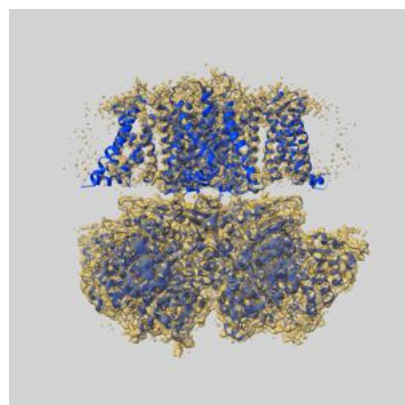
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.68	-	-
Author-provided FSC curve	2.68	3.03	2.71
Unmasked-calculated*	3.15	3.62	3.20

*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 3.15 differs from the reported value 2.68 by more than 10 %

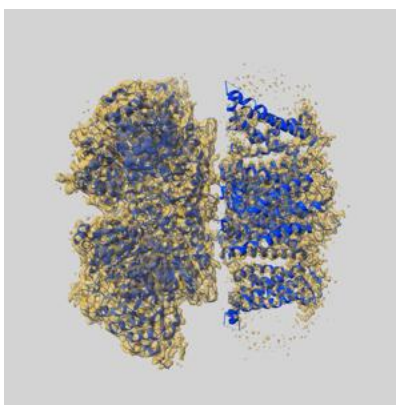
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13701 and PDB model 7PXF. Per-residue inclusion information can be found in section [3](#) on page [6](#).

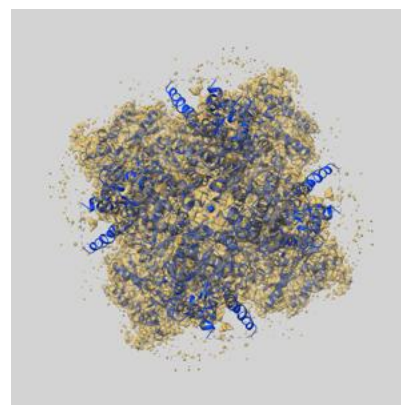
9.1 Map-model overlay [i](#)



X



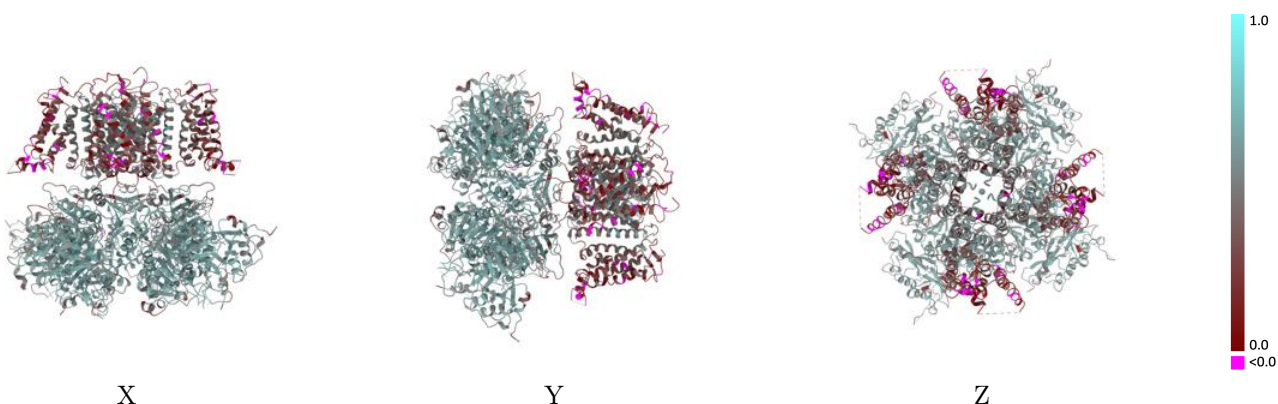
Y



Z

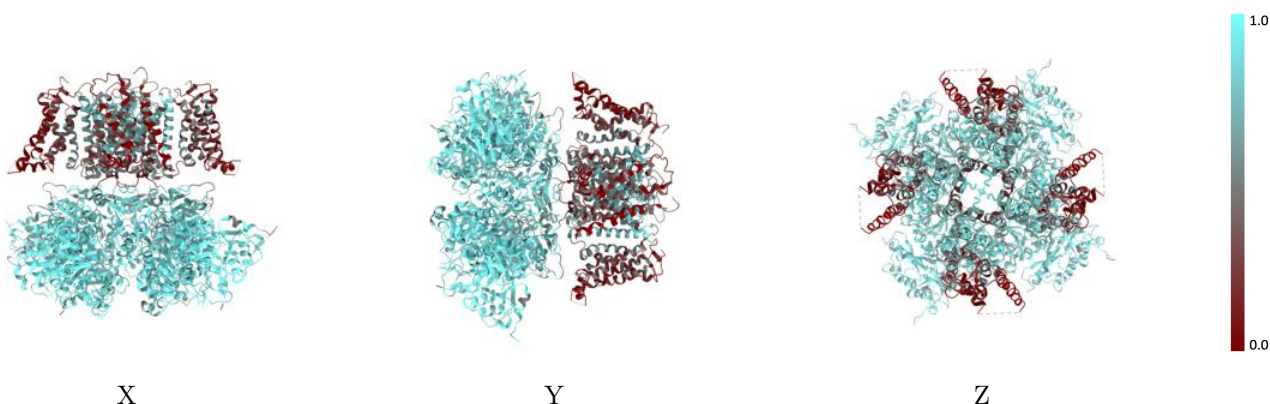
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



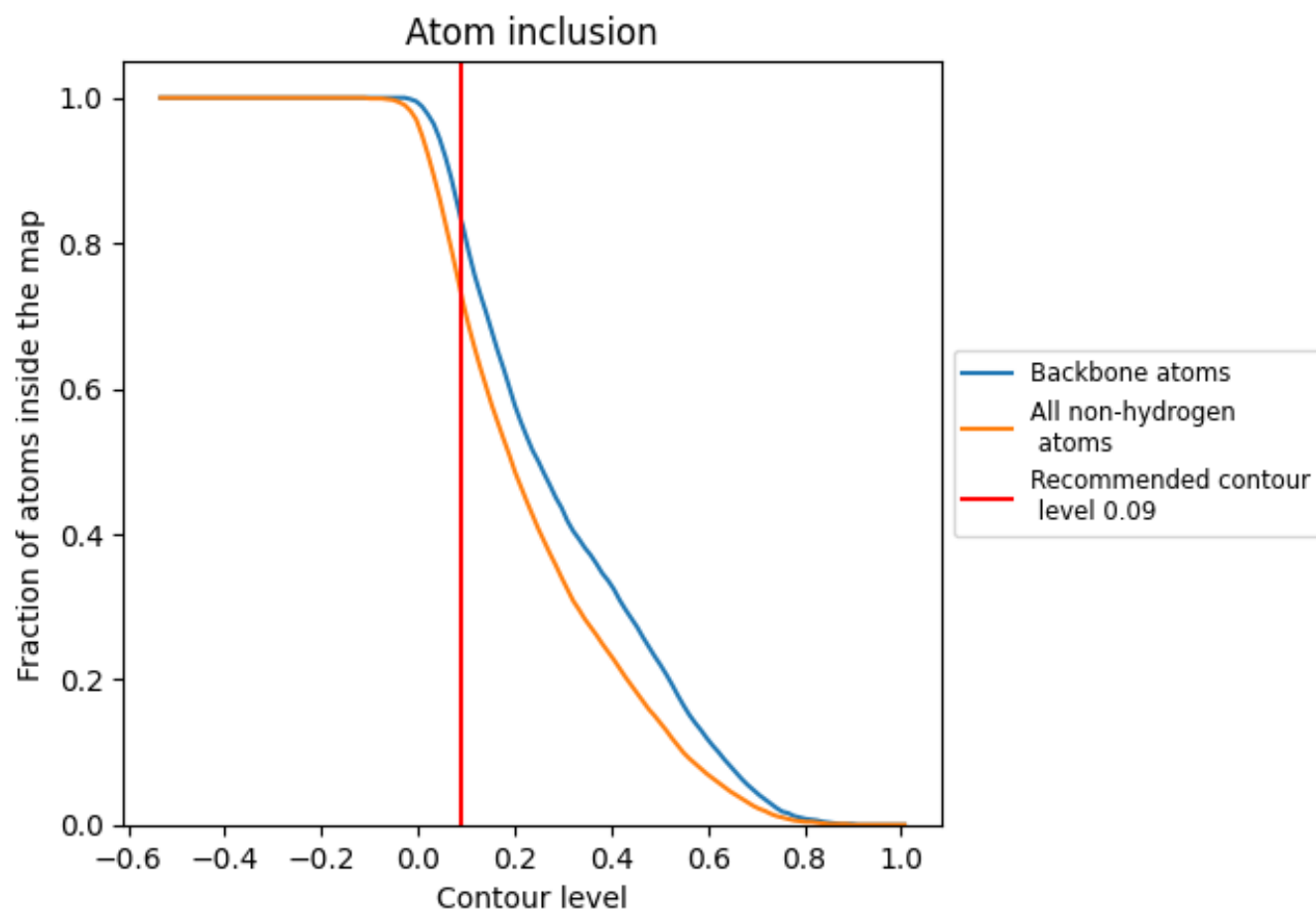
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 73% 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 (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7280	0.4850
A	0.7280	0.4860
B	0.7250	0.4830
C	0.7290	0.4850
D	0.7290	0.4860

