



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 01:15 AM UTC

PDB ID : 8X49 / pdb_00008x49
EMDB ID : EMD-38043
Title : Cryo-EM structure of Ryanodine receptor 1 (100 nM Ca²⁺)
Authors : Chen, Q.; Hu, H.
Deposited on : 2023-11-15
Resolution : 3.40 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

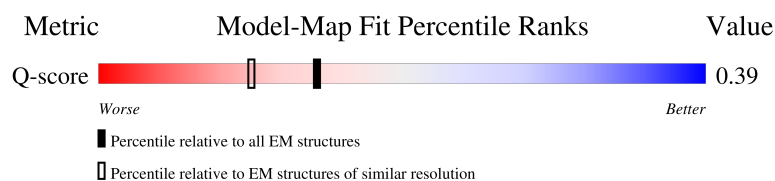
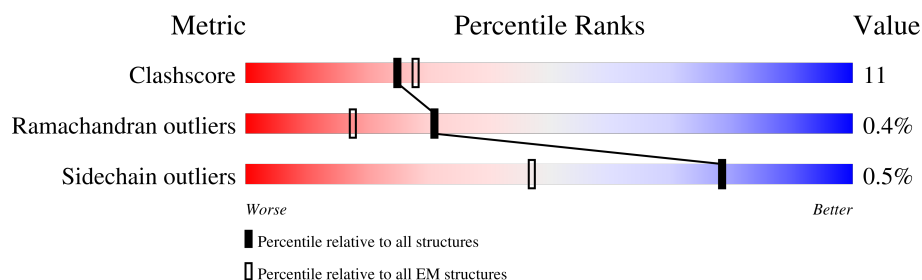
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	5037	
1	B	5037	
1	C	5037	
1	D	5037	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 117356 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 Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3952	Total 29337	C 18674	N 5081	O 5394	S 188	0	0
1	B	3952	Total 29337	C 18674	N 5081	O 5394	S 188	0	0
1	C	3952	Total 29337	C 18674	N 5081	O 5394	S 188	0	0
1	D	3952	Total 29337	C 18674	N 5081	O 5394	S 188	0	0

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

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

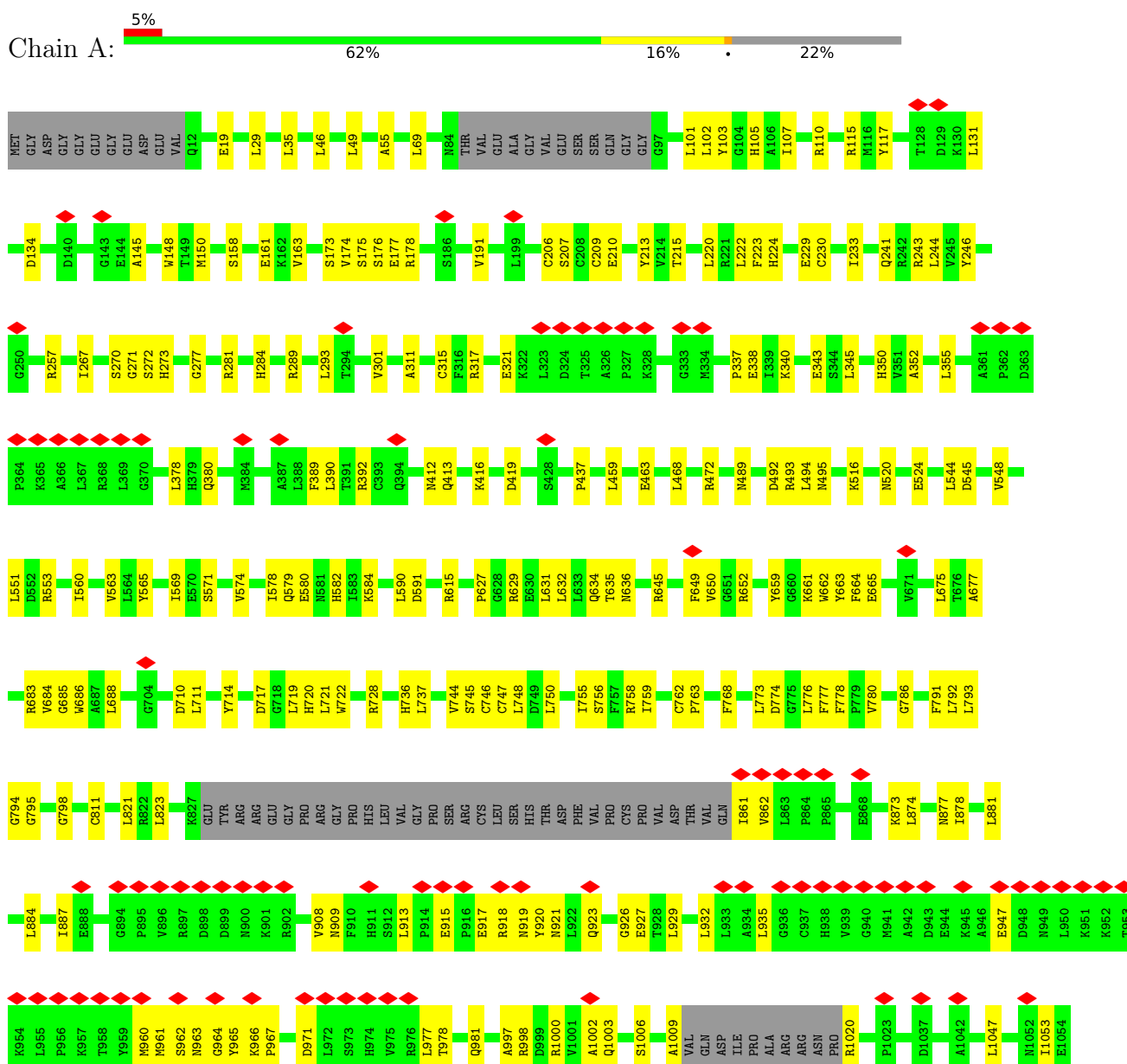
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total 1	Zn 1	0
3	B	1	Total 1	Zn 1	0
3	C	1	Total 1	Zn 1	0
3	D	1	Total 1	Zn 1	0

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: Ryanodine receptor 1





R3904	C3786	E3689	L3603	MET	Y3263	H3150	PRO	E2972	LYS	LYS	LYS	ALA	R2552
I3915	M3793	V3690	E3607	ALA	T3264	I3157	ILE	H2976	GLY	GLY	THR	SER	L2556
L3924	V3794	E3691	Q3608	ALA	E3265	L3158	VAL	LEU	THR	GLY	ARG	GLY	V2578
Q3927	T3797	E3692	T3609	ASP	M3266	D3159	ALA	GLU	HIS	PRO	ILE	ASP	V2579
E3928	I3802	P3697	P3612	ALA	I3272	V3163	LEU	ALA	LEU	GLU	GLN	GLU	L2583
F3933	L3805	D3717	Y3613	SER	P3292	SER	ARG	VAL	VAL	LEU	THR	LYS	H2584
F3934	L3806	Y3722	LYS	GLY	P3293	CYS	SER	VAL	VAL	LEU	ALA	LYS	T2585
Y3937	N3809	Y3725	SER	ASP	P3294	THR	PHE	SER	SER	PRO	GLN	THR	V2586
Q3946	Y3812	Y3728	LYS	GLN	D3310	LEU	SER	GLY	GLY	PRO	THR	VAL	Y2587
R3949	K3815	I3728	ALA	GLU	N3313	C3170	ALA	VAL	VAL	PRO	ASP	ASP	S2590
A3954	M3816	L3735	VAL	GLU	S3314	S3171	SER	GLU	GLU	ARG	ALA	GLU	R2591
F3962	L3817	E3736	HIS	THR	W3334	I3172	ASP	LYS	LYS	PRO	GLY	GLY	Y2613
T3966	K3821	E3737	LYS	LYS	T3359	Y3182	GLU	PRO	GLY	TYR	ASN	PHE	P2616
E3967	G3827	G3739	LEU	ARG	P3360	R3187	LYS	GLU	GLN	THR	PRO	ASP	R2625
W3986	Q3830	E3740	GLN	ASP	V3372	L3190	VAL	K2996	ASP	LYS	PRO	VAL	L2644
V3989	Q3833	N3741	ARG	TYR	E3376	A3195	LEU	F2997	GLY	LEU	ASP	THR	N2646
G3990	A3834	GLY	ARG	SER	E3391	R3196	ARG	V3024	ALA	SER	GLY	LEU	T2667
G3991	L3835	GLU	ALA	VAL	E3392	L3197	LEU	H3030	GLN	GLY	ILE	ASN	E2671
F3992	L3842	ALA	VAL	THR	L3392	A3198	GLY	A3047	VAL	GLU	THR	ILE	L2672
L3993	D3843	GLU	ALA	SER	L3393	A3199	VAL	A3048	GLN	LYS	PRO	ILE	H2673
H3994	L3844	LEU	CYS	ILE	V3394	F3205	SER	L3049	GLN	GLU	GLY	PRO	R2688
M4000	K3852	E3747	PHE	ILE	R3395	P3208	GLN	R3051	MET	SER	ALA	LEU	R2689
R4001	M3858	V3748	ARG	V3511	D3396	Y3213	VAL	H3052	GLY	LYS	ALA	LYS	R2690
K4002	V3859	E3750	Y3642	K3516	E3397	N3214	GLY	P3062	TYR	ALA	ALA	ILE	Y2691
M4023	N3860	V3751	N3643	M3517	F3398	A3215	LYS	A3063	ALA	GLU	GLN	ASN	E2694
M4026	V3865	F3753	Y3657	L3518	S3399	C3216	GLY	VAL	VAL	THR	ILE	LYS	L2695
M4039	I3866	E3754	K3657	N3523	V3400	S3217	VAL	VAL	VAL	ALA	ALA	PHE	Y2696
R4042	N3867	K3756	K3658	M3524	Y3415	Y3218	GLN	ASN	ASN	GLY	TRP	GLU	R2697
Q4042	R3868	E3757	A3659	C3525	E3426	V3219	ASN	CYS	GLY	GLU	TRP	LYS	Y2698
M4047	Q3869	K3758	W3661	A3526	P3427	I3229	LEU	LEU	LYS	TYR	THR	THR	A2699
S4051	N3870	K3760	I3662	P3527	N3430	L3232	THR	ILE	ASP	ASN	GLU	GLU	M2700
S4052	D3878	Q3761	H3667	T3528	L3434	L3233	THR	ALA	GLY	TRP	ALA	TRP	F2701
E4056	E3879	L3763	S3668	I3533	F3435	N3234	THR	ALA	ASP	GLY	ARG	ALA	C2702
M4057	R3672	Q3767	P3567	N3533	V3459	S3235	THR	ARG	THR	GLY	GLY	PHE	L2703
I4058	M3673	R3768	L3568	C3526	N3462	V3236	THR	SER	ASP	LYS	LYS	ASP	ALA
M4064	Q3889	R3769	L3569	A3527	Y3468	E3237	THR	LEU	ALA	GLN	GLN	ILE	ALA
K4069	L3770	H3771	Q3572	T3528	PHE	G3254	THR	ALA	ALA	GLY	GLY	ILE	GLY
E4075	R3772	T3772	M3573	R3577	THR	F3144	THR	THR	THR	ARG	ARG	GLN	ALA
	R3773	R3773	R3577	D3585	ALA	G3145	THR	VAL	VAL	GLY	GLY	ASN	ALA
	E3777	V3779	A3586	A3586	ASP	H3146	THR	MET	MET	LEU	THR	ASN	LEU
					LYS	I3147	GLY	LYS	LYS	GLU	GLU	TRP	PRO
					SER			SER	SER	ASP	ASP	VAL	ASP
					LYS			GLY	ALA	LYS	ALA	LYS	TYR
													VAL
													ASP



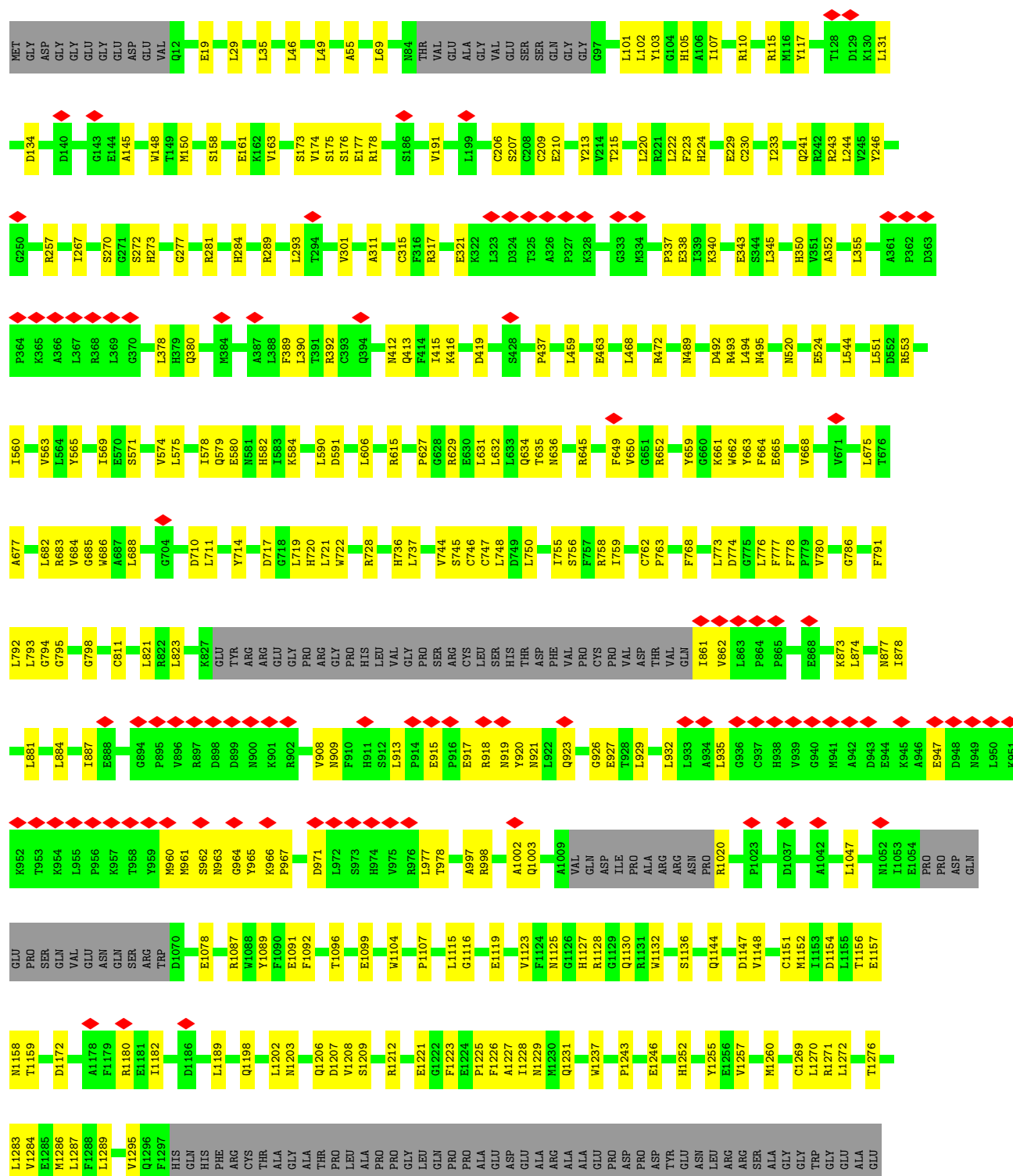






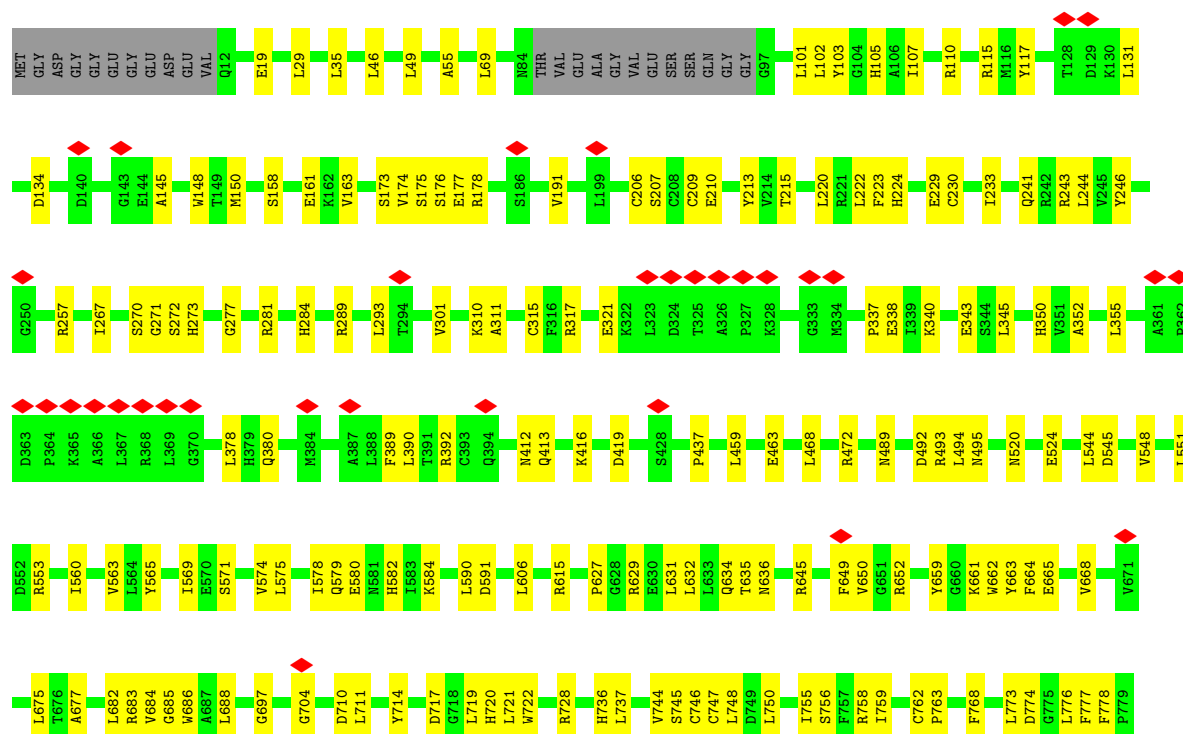


• Molecule 1: Ryanodine receptor 1















4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	183859	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	4.737	Depositor
Minimum map value	-2.523	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.130	Depositor
Recommended contour level	0.466	Depositor
Map size (Å)	516.72003, 516.72003, 516.72003	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0765, 1.0765, 1.0765	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.27	8/29956 (0.0%)	0.45	7/40772 (0.0%)
1	B	0.27	8/29956 (0.0%)	0.45	7/40772 (0.0%)
1	C	0.27	8/29956 (0.0%)	0.45	7/40772 (0.0%)
1	D	0.27	8/29956 (0.0%)	0.45	7/40772 (0.0%)
All	All	0.27	32/119824 (0.0%)	0.45	28/163088 (0.0%)

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1835	GLU	CA-C	-9.41	1.44	1.53
1	B	1835	GLU	CA-C	-9.41	1.44	1.53
1	C	1835	GLU	CA-C	-9.41	1.44	1.53
1	D	1835	GLU	CA-C	-9.41	1.44	1.53
1	A	1835	GLU	C-O	-6.72	1.18	1.23

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1844	LEU	N-CA-C	6.19	117.83	111.14
1	B	1844	LEU	N-CA-C	6.19	117.83	111.14
1	C	1844	LEU	N-CA-C	6.19	117.83	111.14
1	D	1844	LEU	N-CA-C	6.19	117.83	111.14
1	A	4810	ALA	N-CA-C	-6.07	105.53	113.12

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	29337	0	27528	618	0
1	B	29337	0	27528	624	0
1	C	29337	0	27528	610	0
1	D	29337	0	27528	616	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	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
All	All	117356	0	110112	2391	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 11.

The worst 5 of 2391 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:C:1965:TYR:CE2	1:C:1969:LEU:HD11	2.12	0.85
1:D:1965:TYR:CE2	1:D:1969:LEU:HD11	2.12	0.84
1:B:1965:TYR:CE2	1:B:1969:LEU:HD11	2.12	0.84
1:A:1965:TYR:CE2	1:A:1969:LEU:HD11	2.12	0.84
1:C:3990:VAL:HG23	1:C:4051:SER:HB3	1.61	0.82

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	3906/5037 (78%)	3513 (90%)	376 (10%)	17 (0%)	30	59
1	B	3906/5037 (78%)	3513 (90%)	376 (10%)	17 (0%)	30	59
1	C	3906/5037 (78%)	3513 (90%)	376 (10%)	17 (0%)	30	59
1	D	3906/5037 (78%)	3513 (90%)	376 (10%)	17 (0%)	30	59
All	All	15624/20148 (78%)	14052 (90%)	1504 (10%)	68 (0%)	31	59

5 of 68 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1469	VAL
1	A	1470	ARG
1	A	1472	VAL
1	A	1836	PHE
1	B	1469	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2885/4276 (68%)	2870 (100%)	15 (0%)	81	81
1	B	2885/4276 (68%)	2870 (100%)	15 (0%)	81	81
1	C	2885/4276 (68%)	2870 (100%)	15 (0%)	81	81
1	D	2885/4276 (68%)	2870 (100%)	15 (0%)	81	81
All	All	11540/17104 (68%)	11480 (100%)	60 (0%)	78	81

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	4816	ILE
1	D	4806	ASN
1	C	1841	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	1850	VAL
1	D	4818	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 113 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	44	ASN
1	D	4707	ASN
1	C	2095	GLN
1	D	3998	HIS
1	D	2095	GLN

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](#)

Of 8 ligands modelled in this entry, 8 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

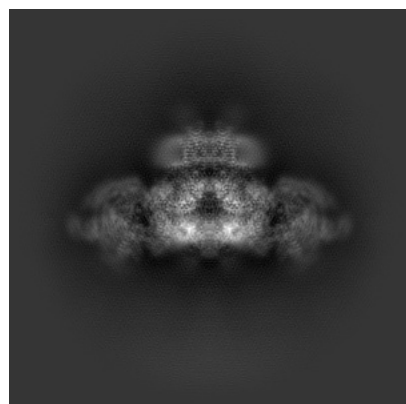
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38043. These allow visual inspection of the internal detail of the map and identification of artifacts.

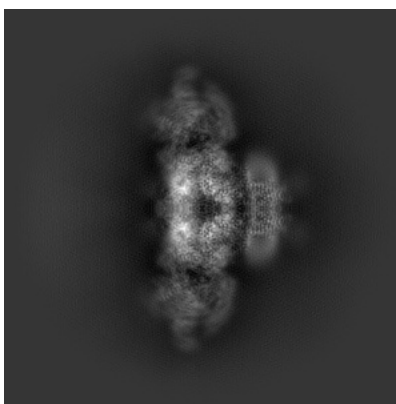
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

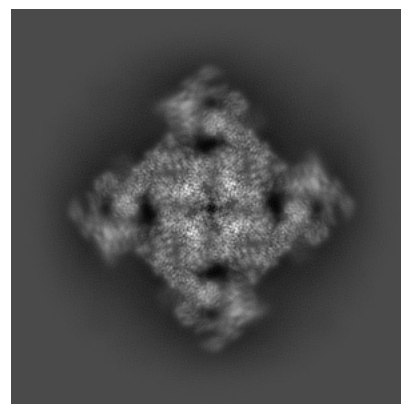
6.1.1 Primary map



X

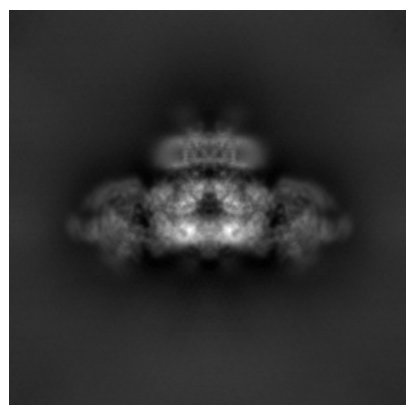


Y

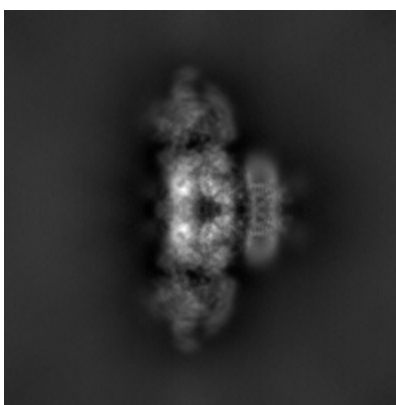


Z

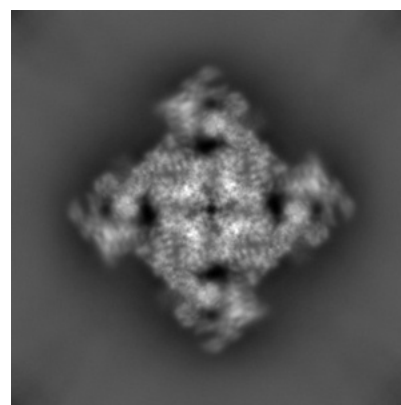
6.1.2 Raw map



X



Y

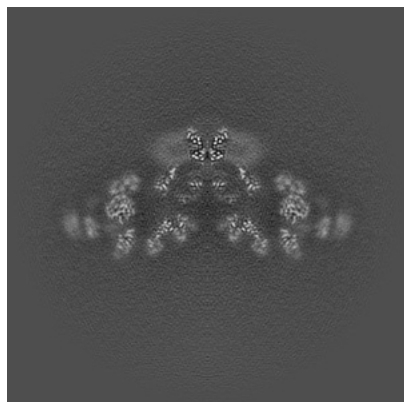


Z

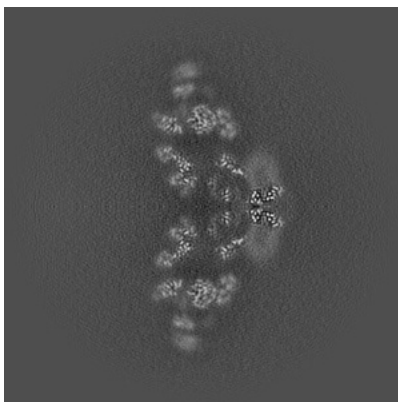
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

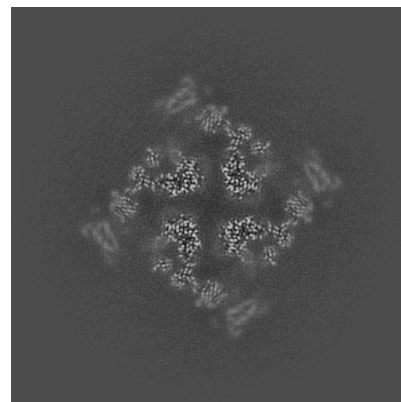
6.2.1 Primary map



X Index: 240

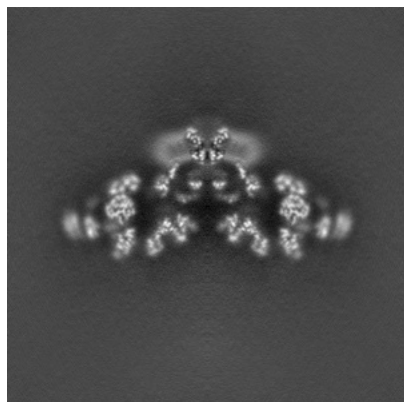


Y Index: 240

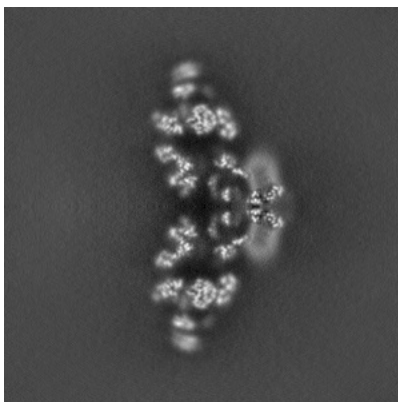


Z Index: 240

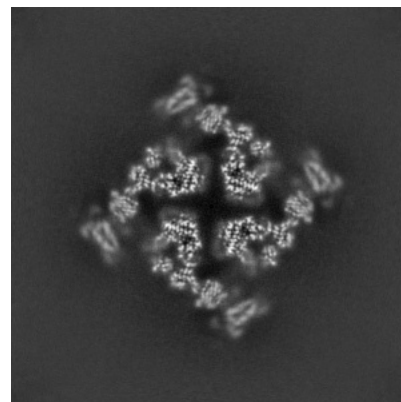
6.2.2 Raw map



X Index: 240



Y Index: 240

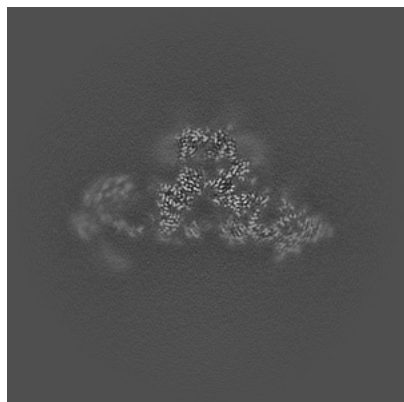


Z Index: 240

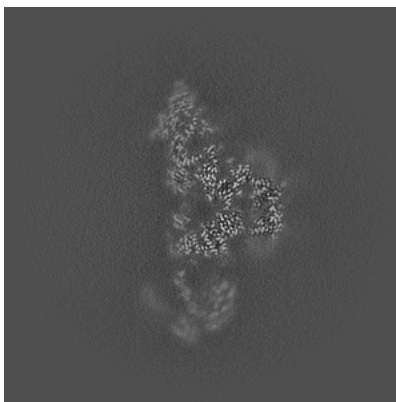
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

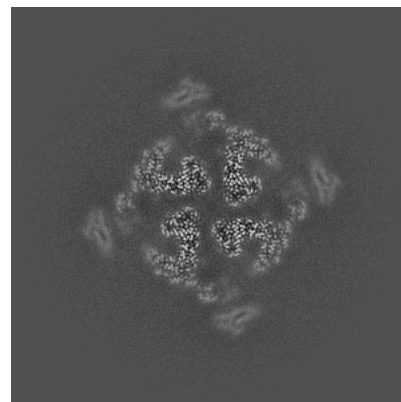
6.3.1 Primary map



X Index: 259

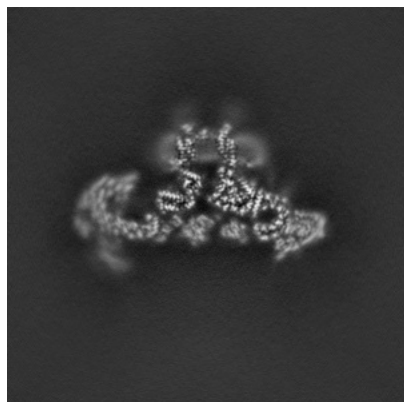


Y Index: 221

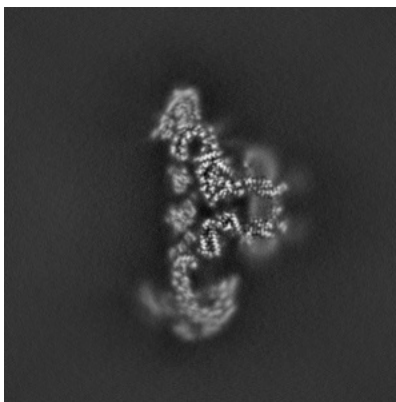


Z Index: 248

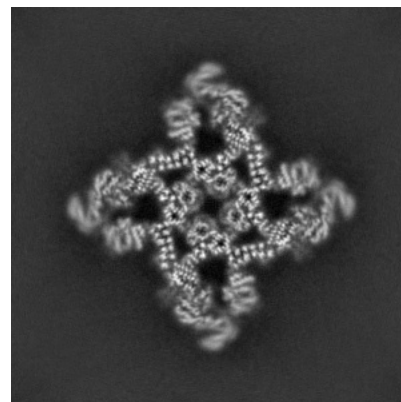
6.3.2 Raw map



X Index: 265



Y Index: 215

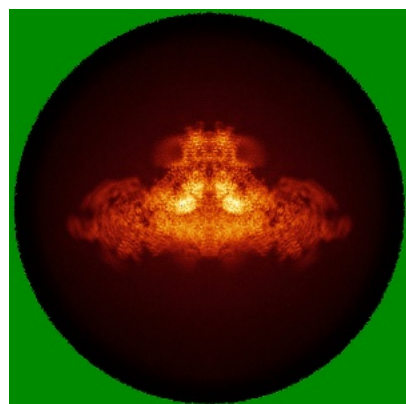


Z Index: 218

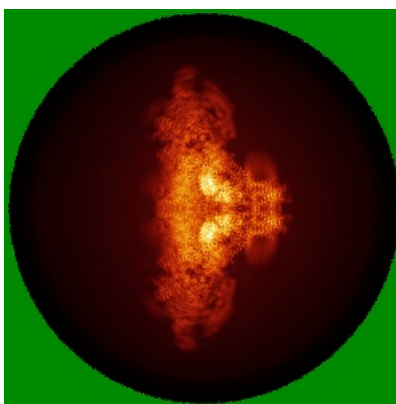
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

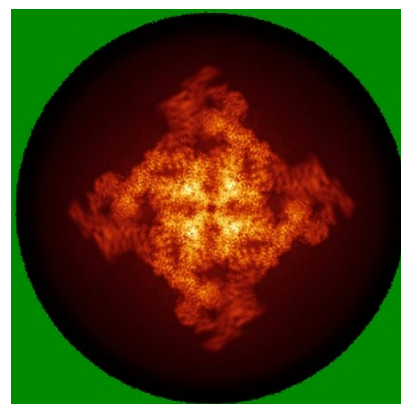
6.4.1 Primary map



X

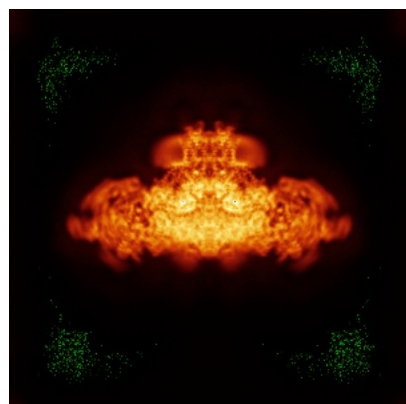


Y

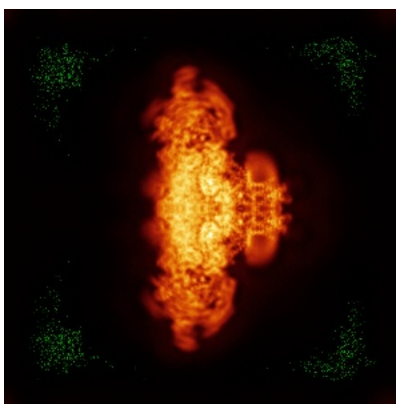


Z

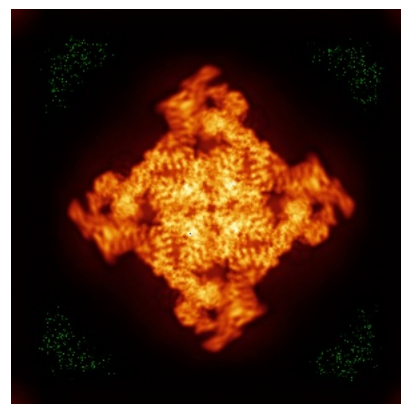
6.4.2 Raw map



X



Y

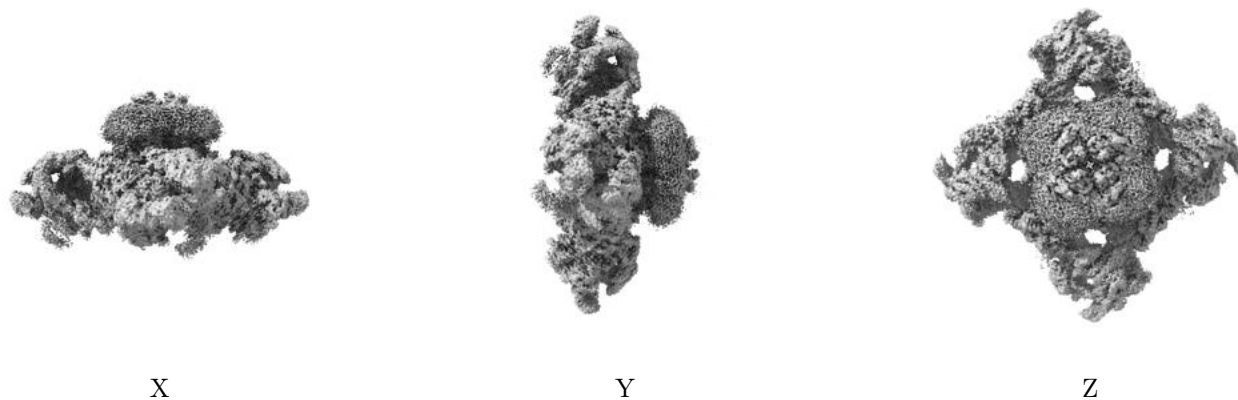


Z

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.

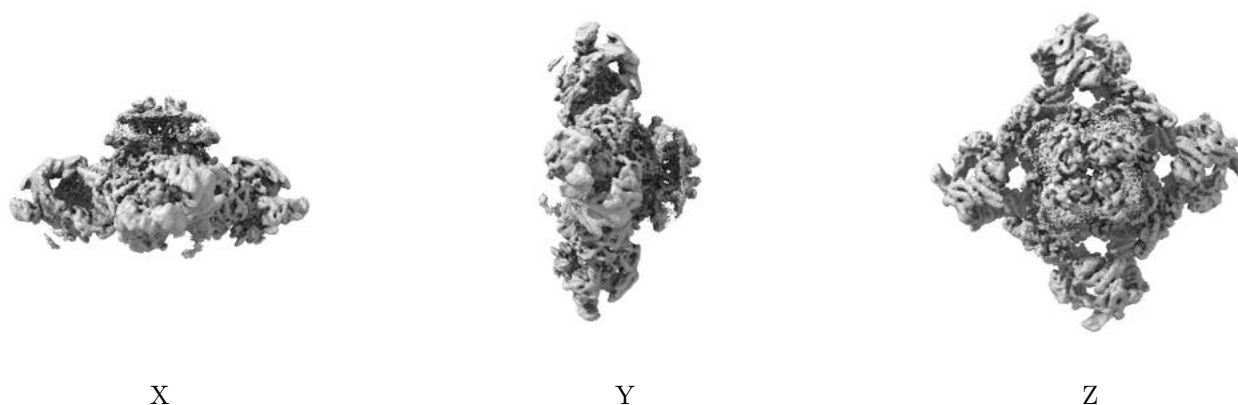
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.466. 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.

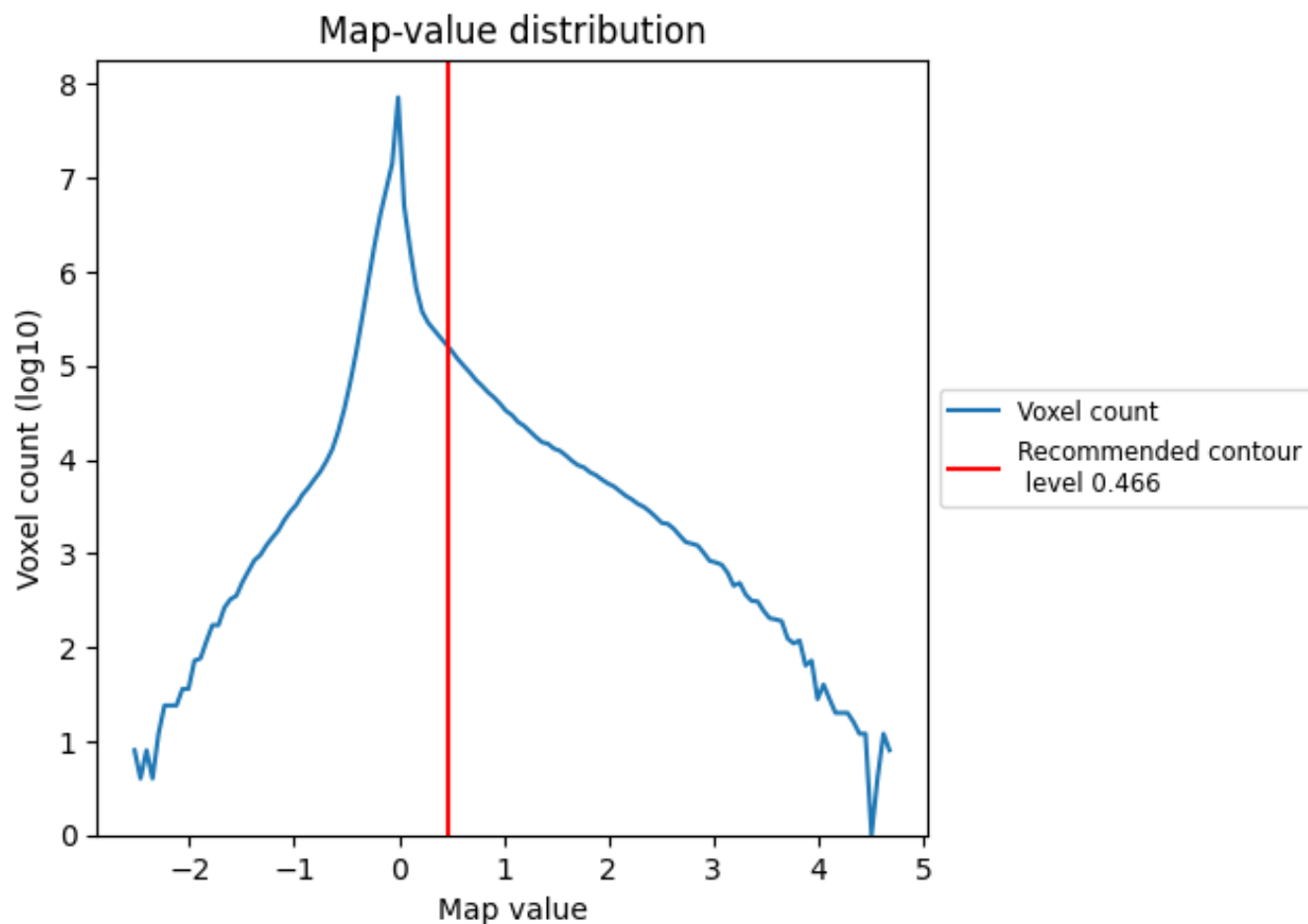
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

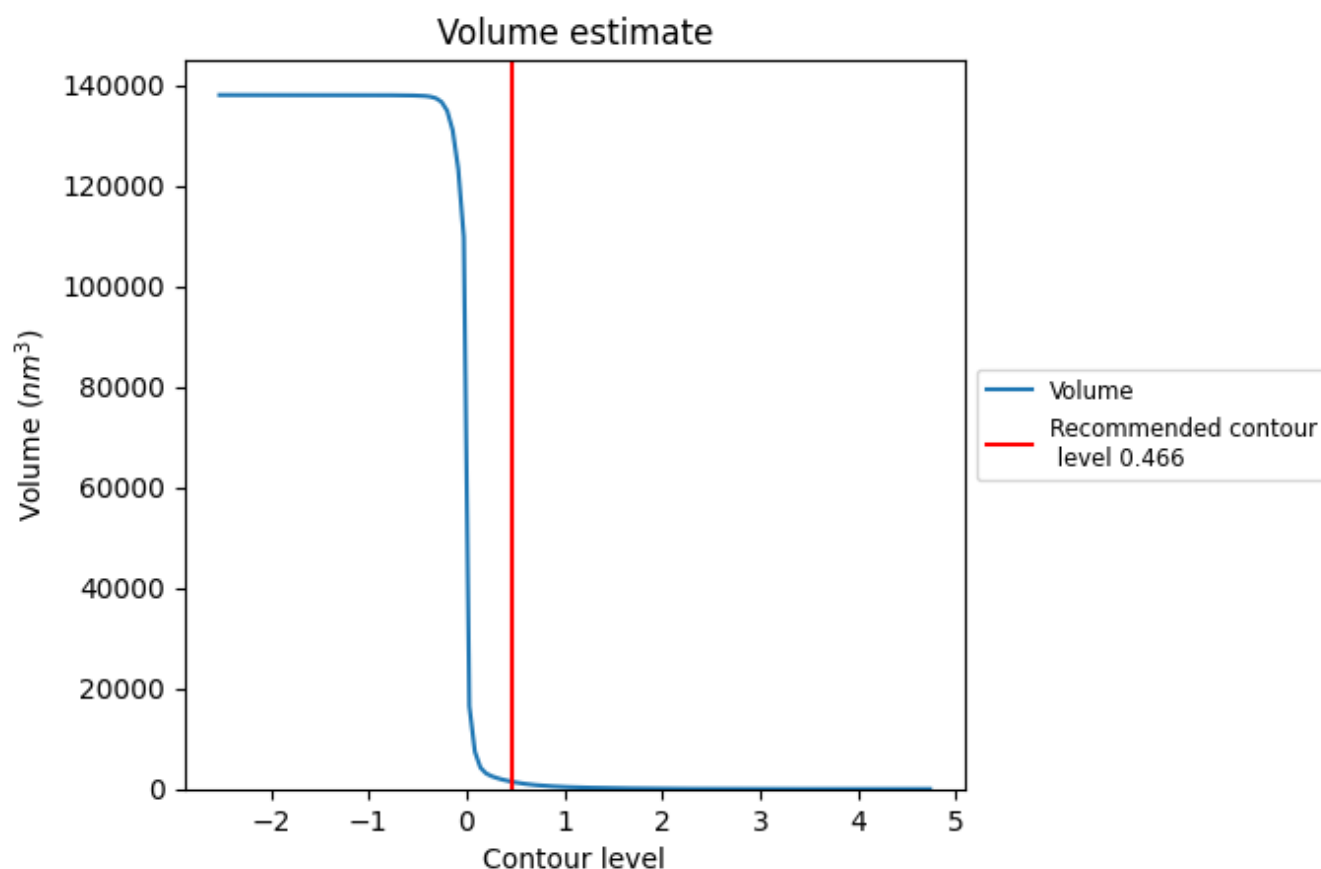
This section contains the results of statistical analysis of the map.

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.

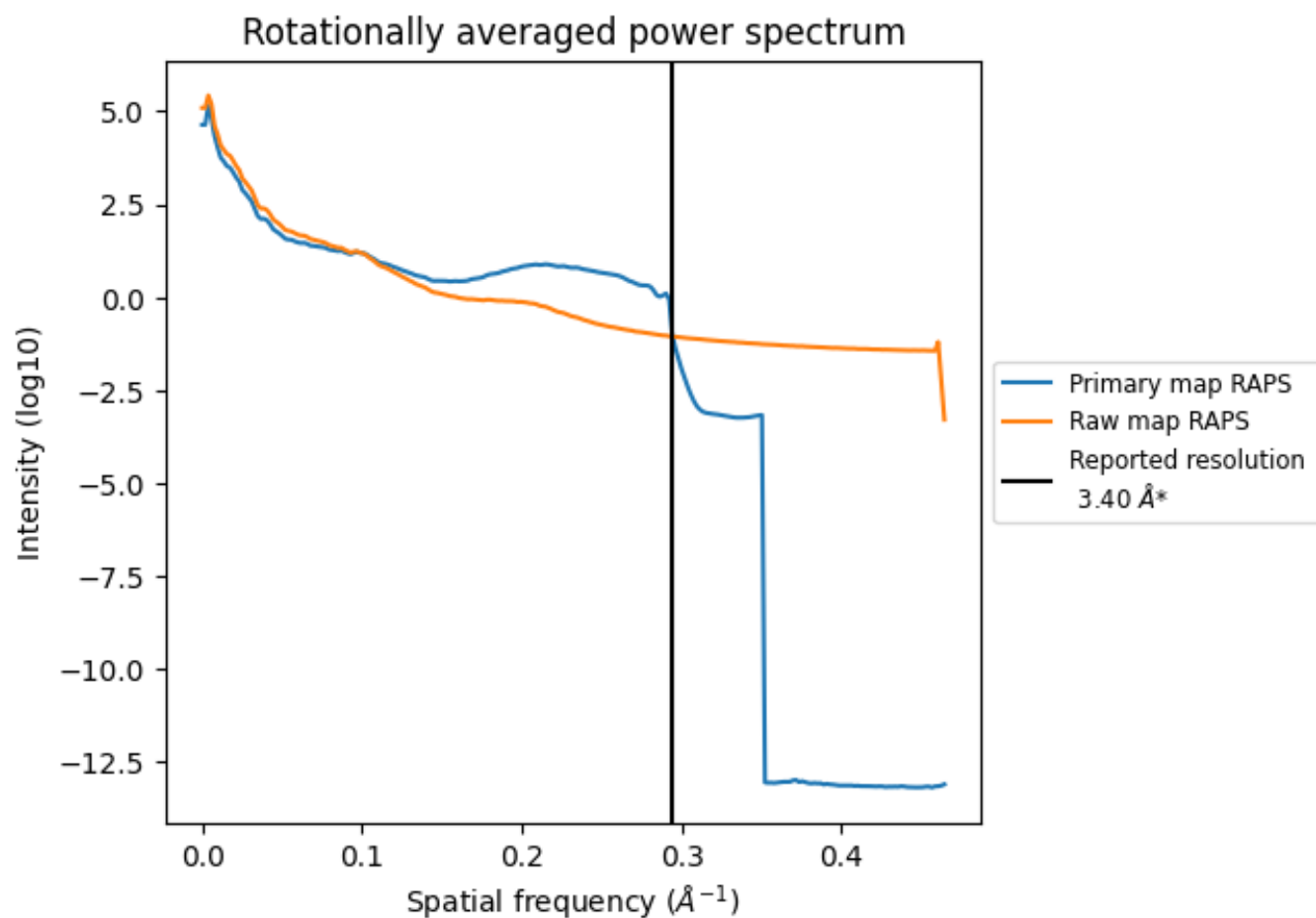
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1425 nm^3 ; this corresponds to an approximate mass of 1287 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 ⓘ

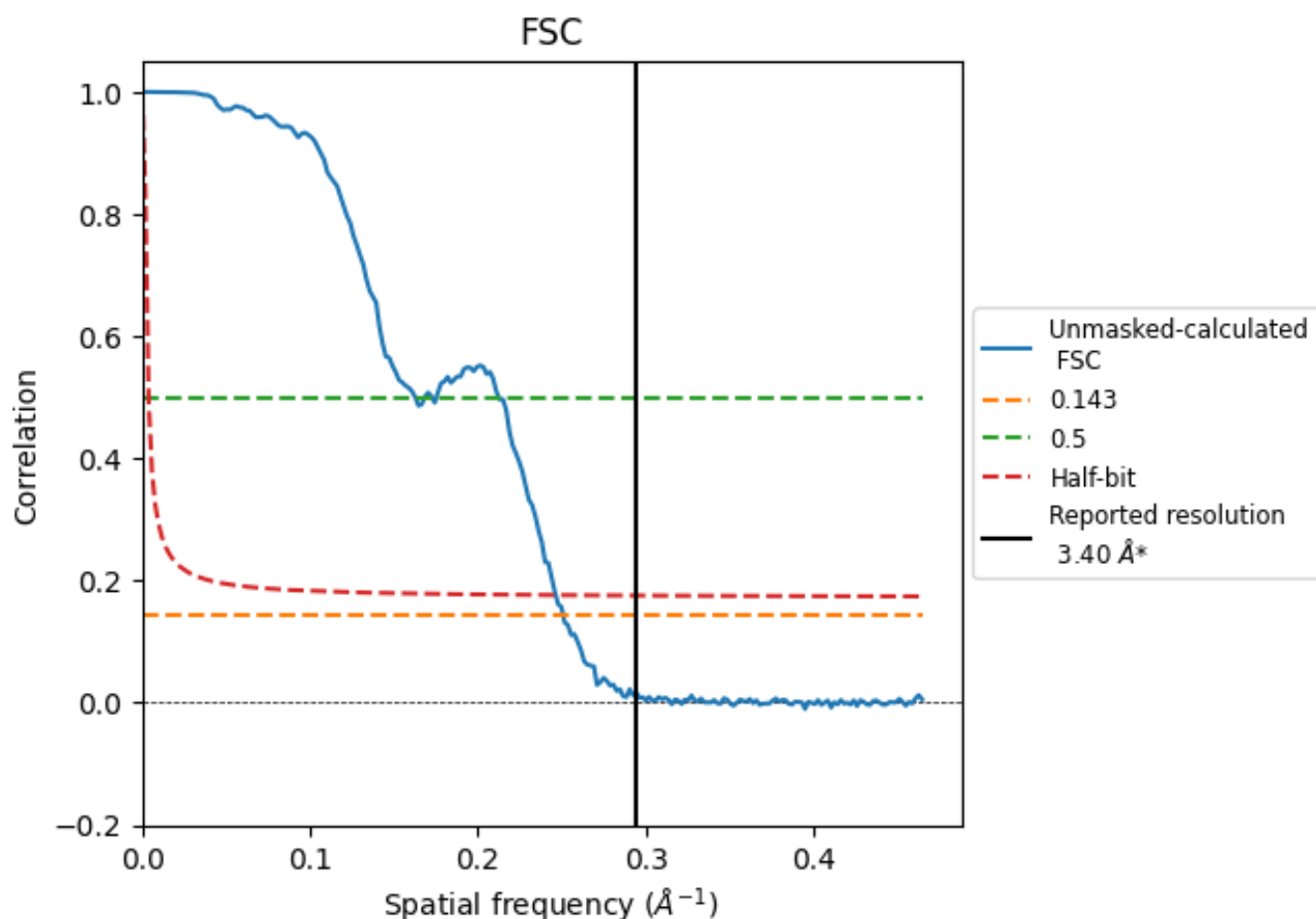


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 $0.294 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

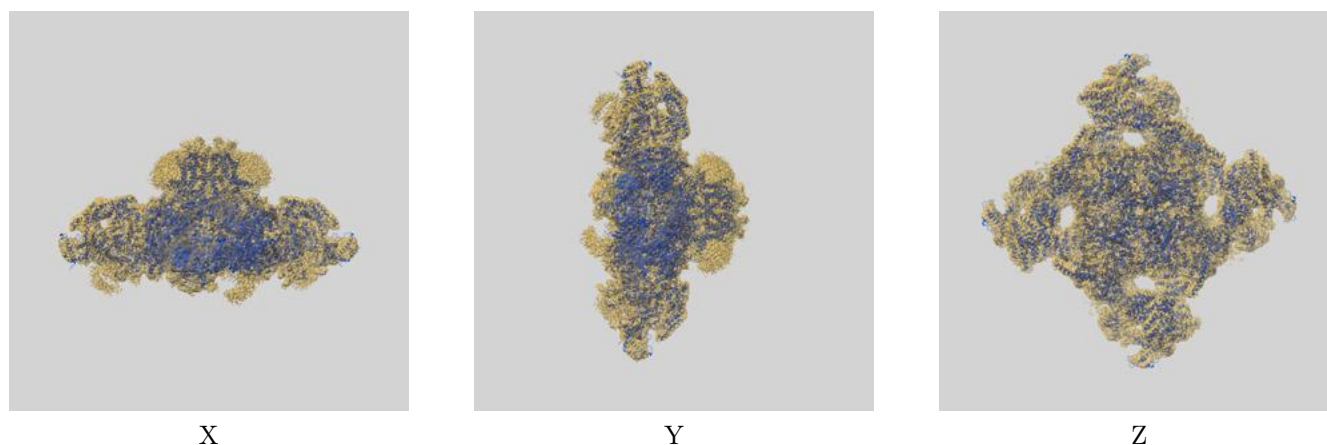
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.99	6.15	4.06

*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 3.99 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

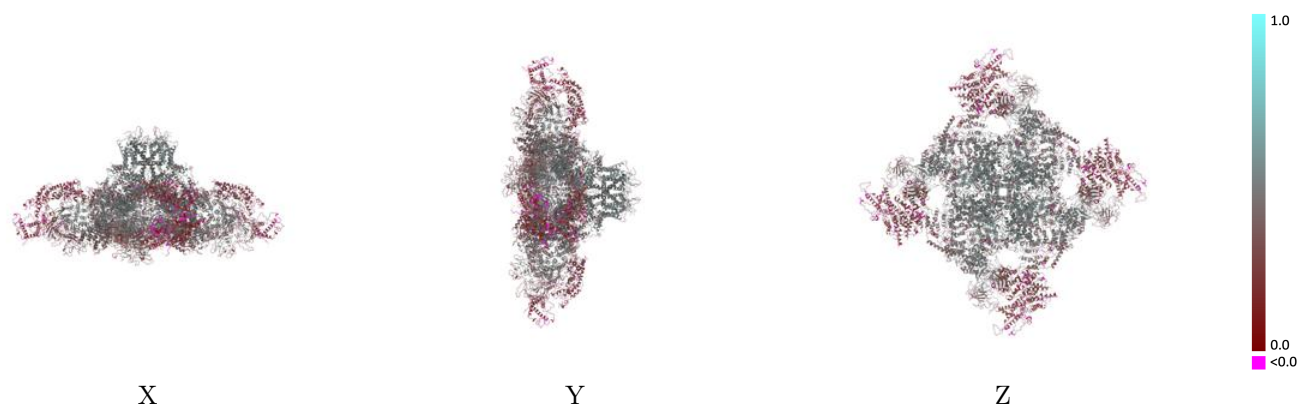
This section contains information regarding the fit between EMDB map EMD-38043 and PDB model 8X49. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



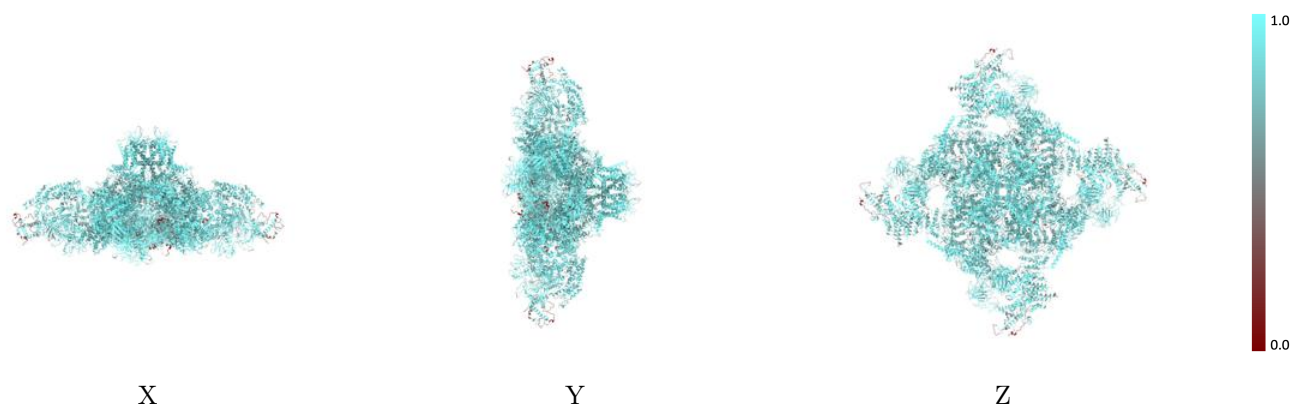
The images above show the 3D surface view of the map at the recommended contour level 0.466 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



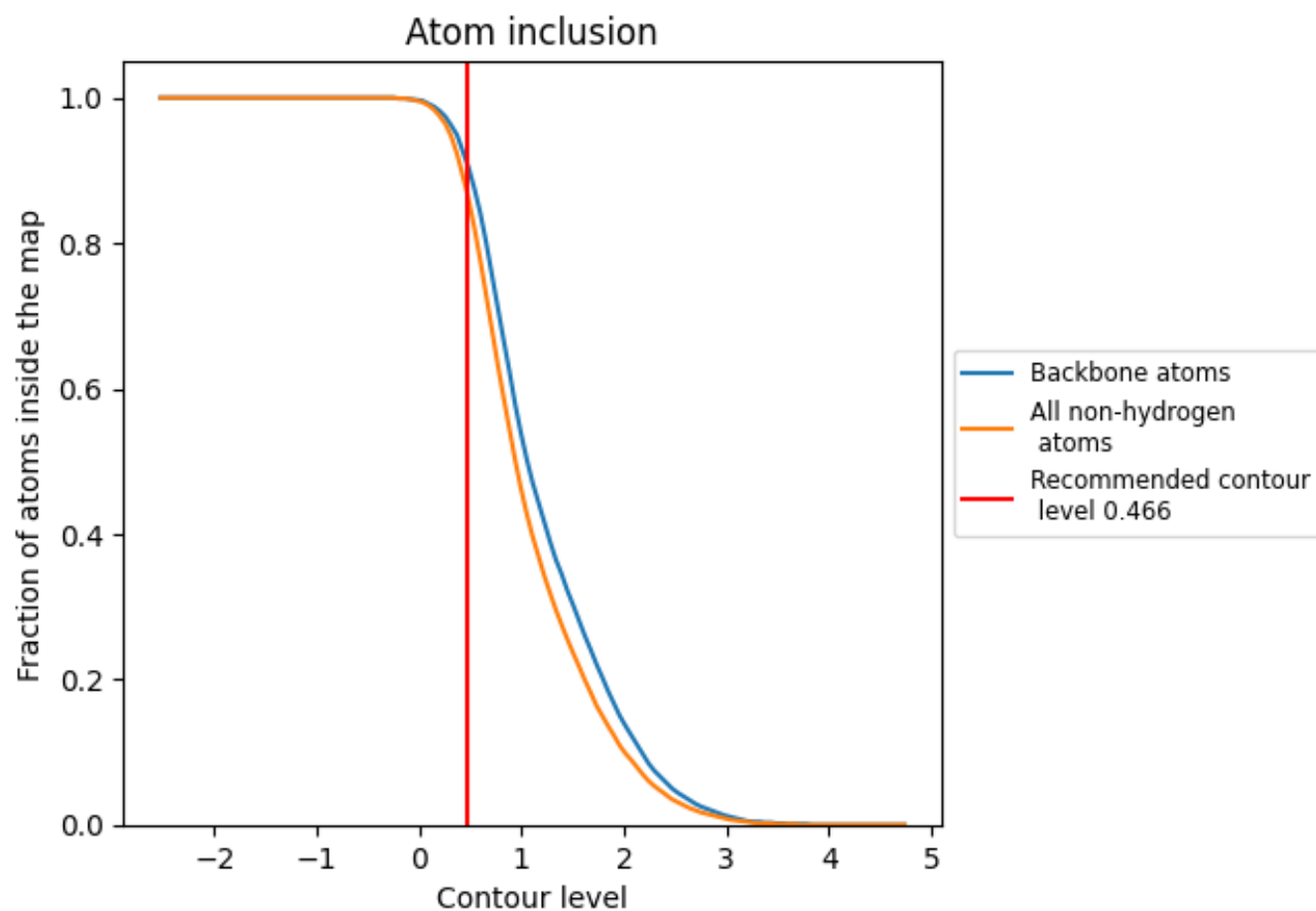
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.466).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 87% 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 (0.466) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8710	0.3900
A	0.8710	0.3900
B	0.8710	0.3900
C	0.8710	0.3900
D	0.8710	0.3900

