



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 02:59 AM UTC

PDB ID : 8X4D / pdb_00008x4d
EMDB ID : EMD-38047
Title : Cryo-EM structure of Ryanodine receptor 1 (TM helix S0,20 uM Ca²⁺, 2 mM ATP)
Authors : Chen, Q.; Hu, H.
Deposited on : 2023-11-15
Resolution : 3.90 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

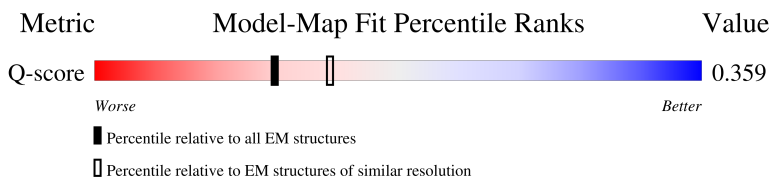
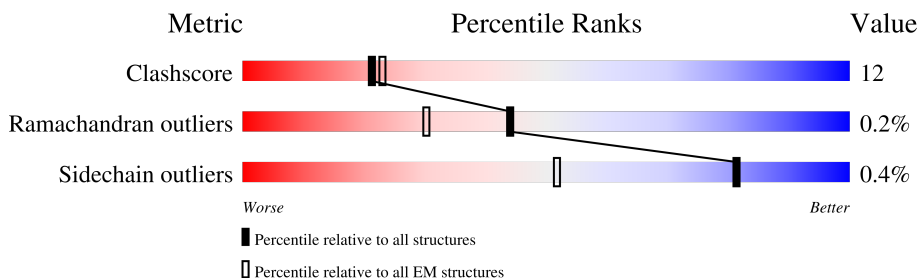
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	 5% 60% 19% 21%
1	B	5037	 5% 60% 19% 21%
1	C	5037	 5% 60% 19% 21%
1	D	5037	 5% 60% 19% 21%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 118144 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.

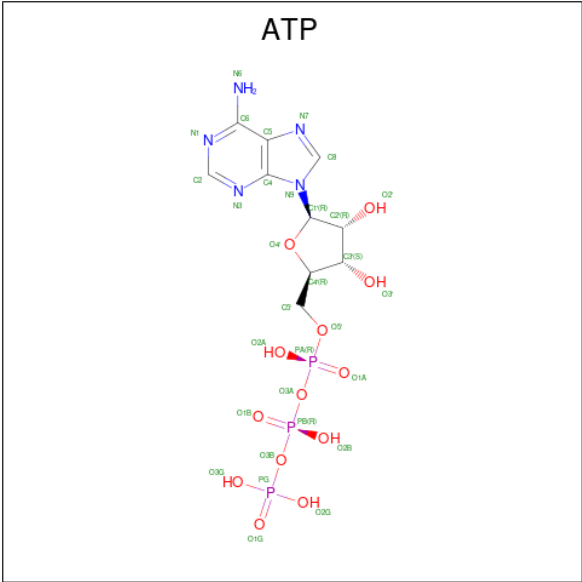
- Molecule 1 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3979	Total	C	N	O	S	0	0
			29504	18775	5121	5420	188		
1	B	3979	Total	C	N	O	S	0	0
			29504	18775	5121	5420	188		
1	C	3979	Total	C	N	O	S	0	0
			29504	18775	5121	5420	188		
1	D	3979	Total	C	N	O	S	0	0
			29504	18775	5121	5420	188		

- 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	Ca	0
			1	1	
2	B	1	Total	Ca	0
			1	1	
2	C	1	Total	Ca	0
			1	1	
2	D	1	Total	Ca	0
			1	1	

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

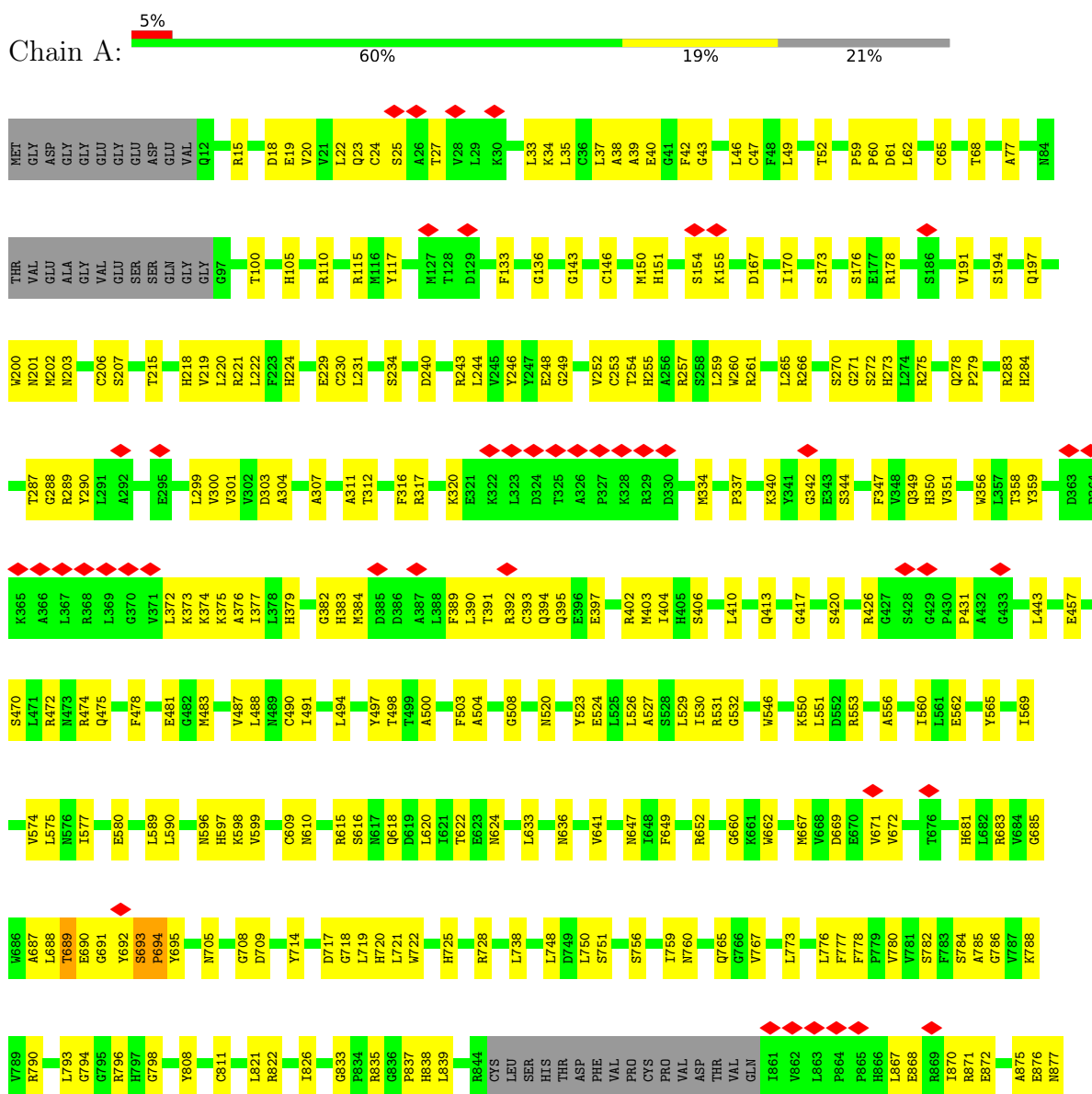


Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	D	1	Total	C	N	O	P	0
			31	10	5	13	3	

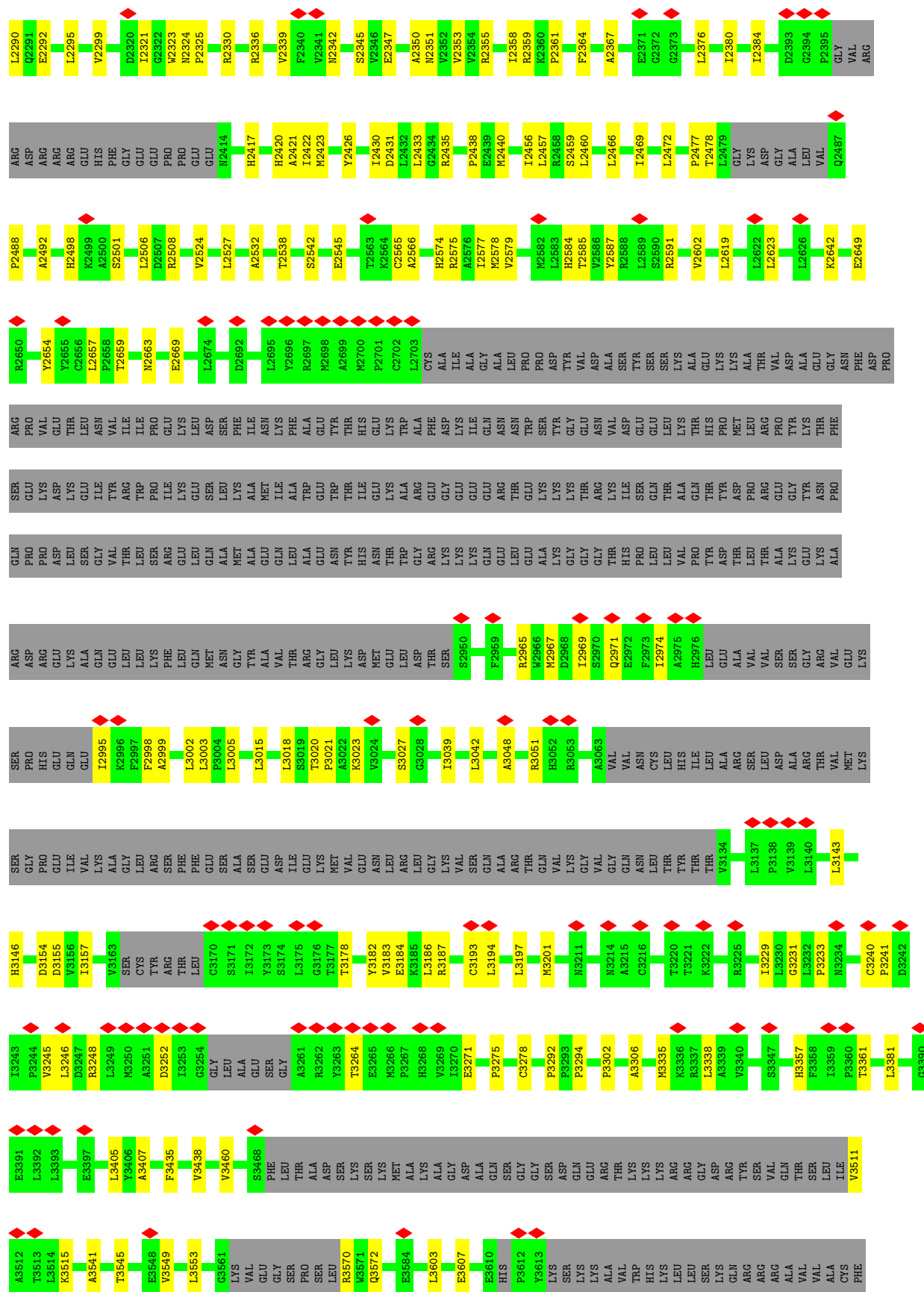
3 Residue-property plots

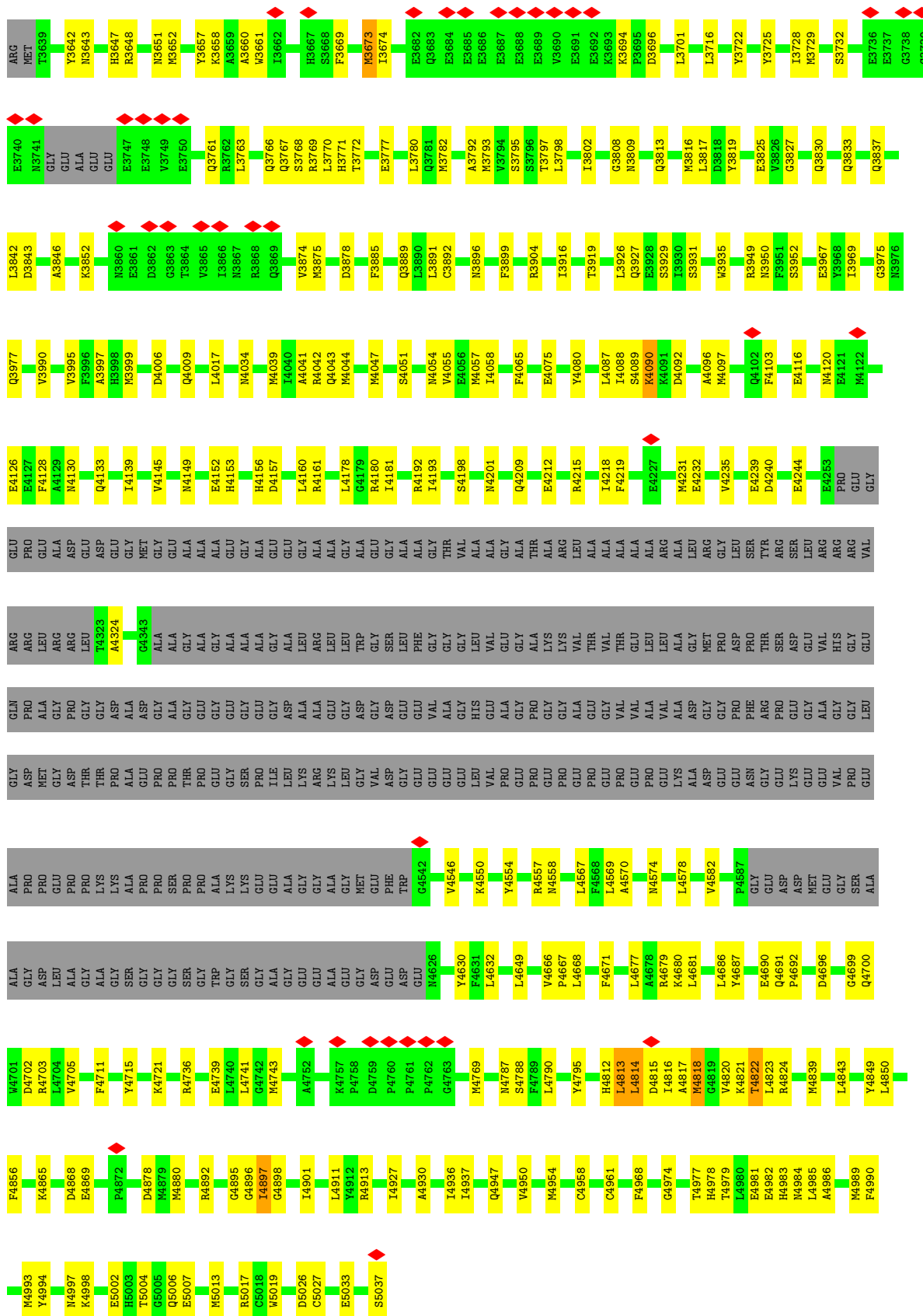
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

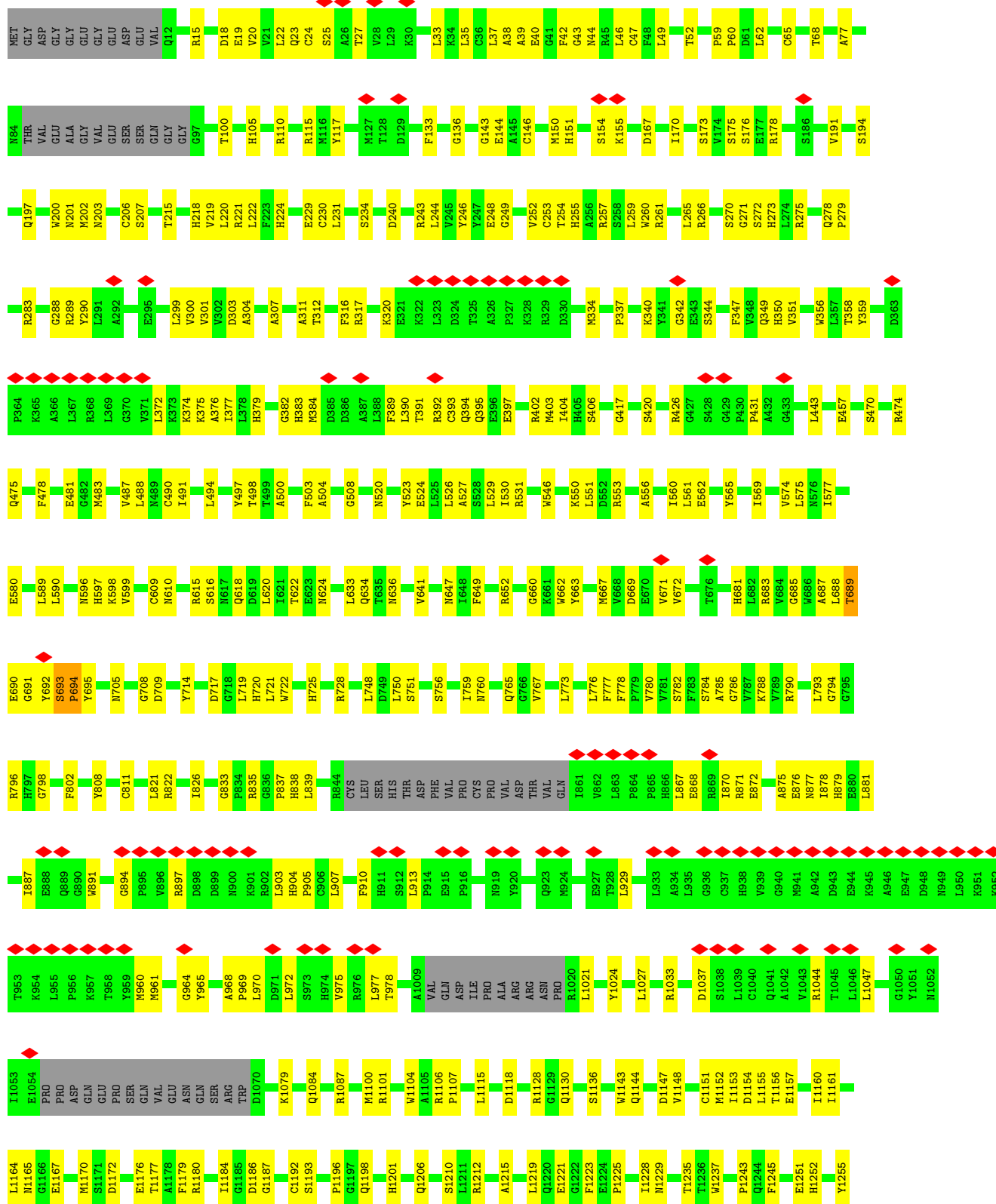






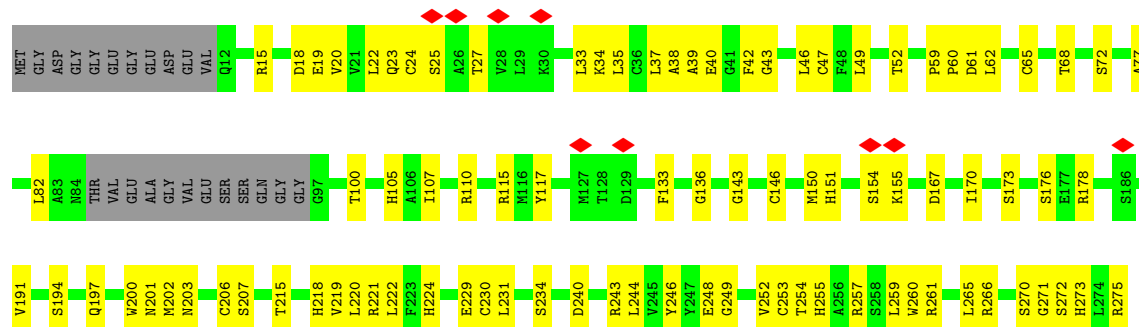


- Molecule 1: Ryanodine receptor 1





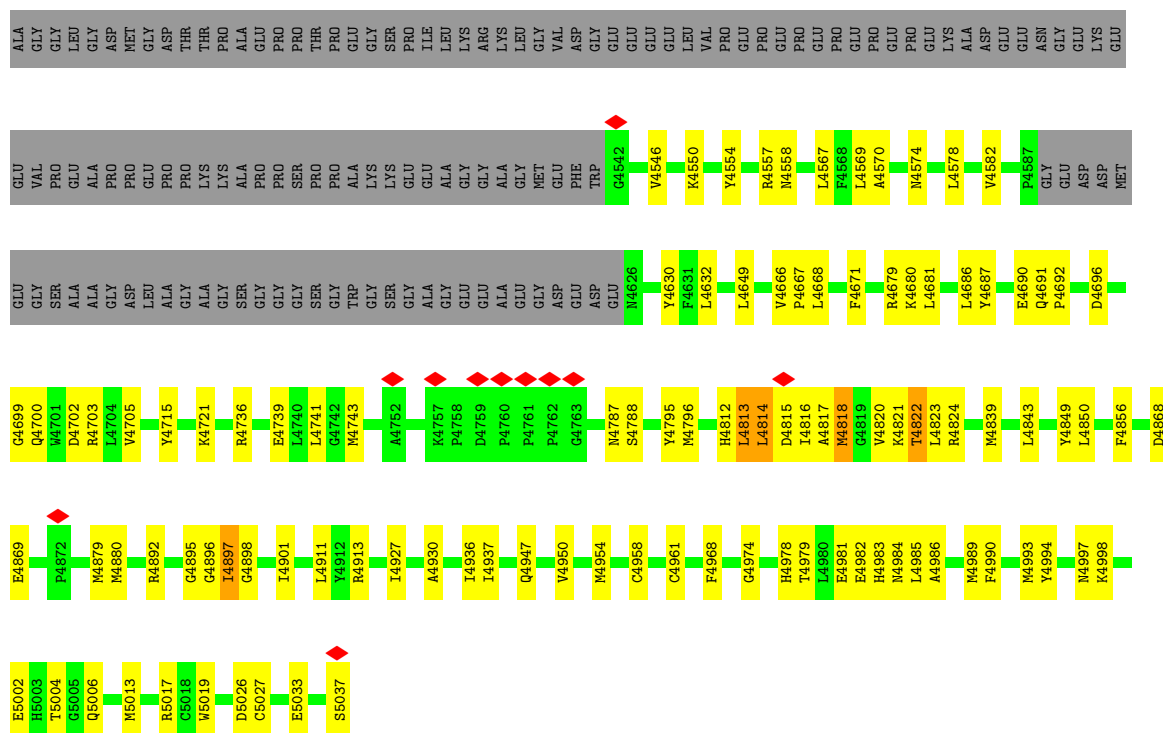




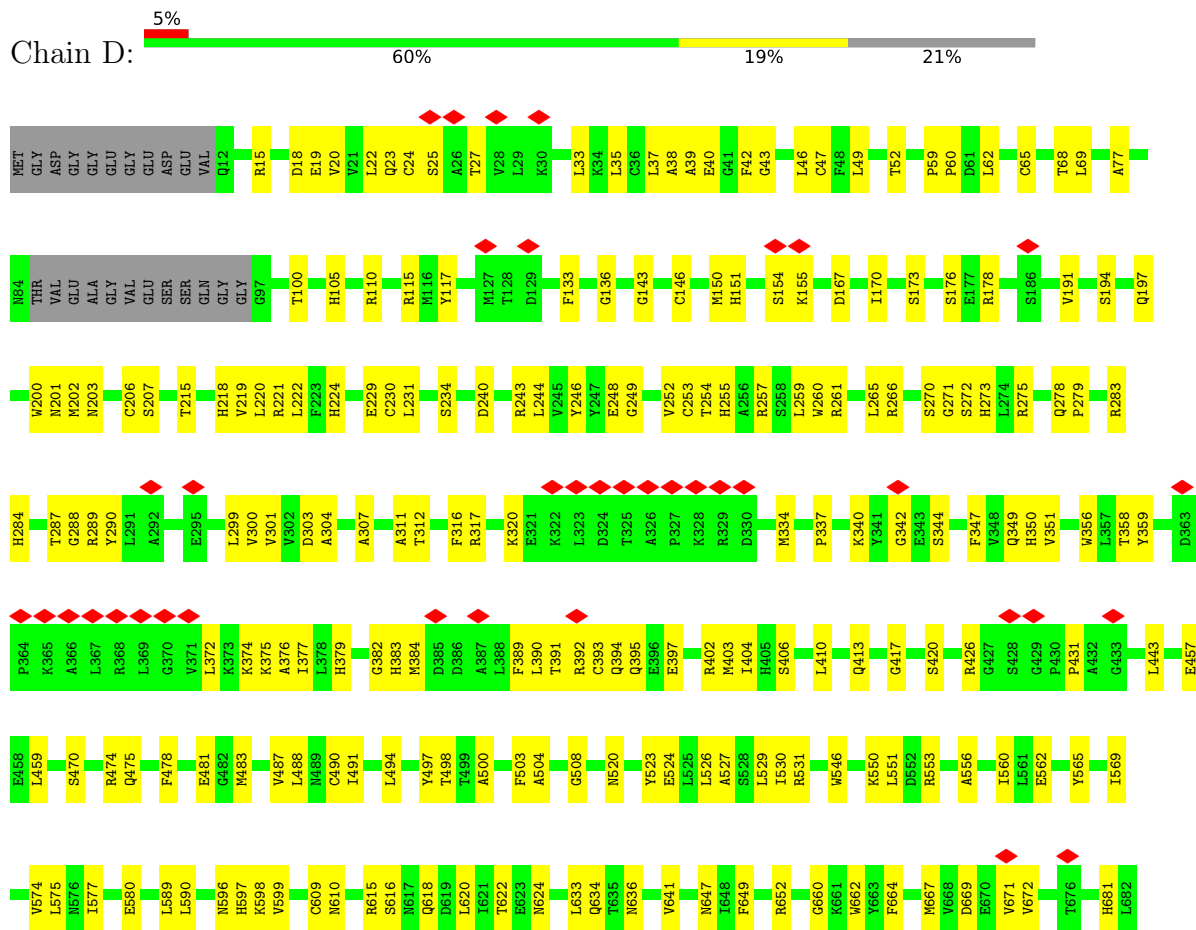








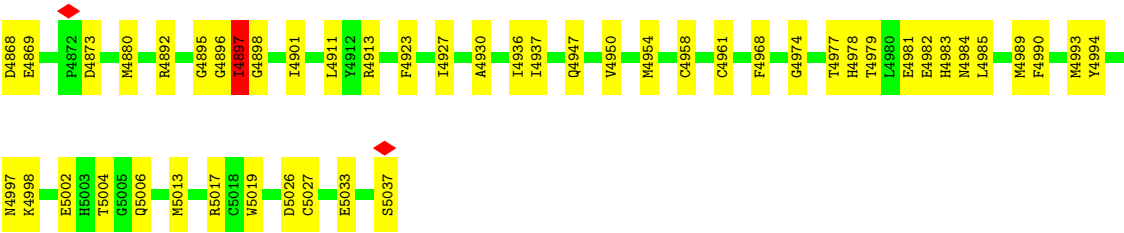
• Molecule 1: Ryanodine receptor 1







D4702	D4703	L4704	V4705	Y4715	K4721	D4730	R4736	E4739	L4740	L4741	G4742	N4743	A4752	K4757	P4758	D4759	P4760	P4761	P4762	G4763	M4769	N4787	S4788	Y4795	M4796	H4812	L4813	L4814	D4815	L4816	A4817	K4818	G4819	V4820	K4821	T4822	R4824	M4839	L4843	Y4849	L4850	F4856								
ALA	ALA	GLY	ASP	LEU	ALA	GLY	SER	GLY	GLY	TRP	SER	SER	GLY	GLY	GLY	GLY	ASP	ASP	ASP	GLY	GLY	Y4630	F4631	L4632	L4649	V4666	P4667	L4668	F4671	D4679	K4680	L4681	L4686	Y4687	E4690	Q4691	P4692	D4696	G4699	Q4700	W4701									
LEU	GLY	ASP	MET	GLY	PRO	GLY	PRO	THR	PRO	GLY	SER	LYS	LYS	PRO	PRO	ILE	LYS	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	PRO	PRO	GLY	VAL	LYS	ALA	ASP	GLY	PRO	ASN	GLY	LYS	GLY	VAL	PRO							
GLU	ALA	PRO	GLU	PRO	GLY	LYS	ALA	THR	LYS	ALA	PRO	LYS	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	SER							
VAL	ARG	ARG	LEU	ARG	ARG	T4423	A4324	G4343	ALA	ALA	ALA	ALA	GLY	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	VAL	GLY	GLY	VAL	VAL	GLY	GLY	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR						
GLY	GLY	PRO	GLU	ALA	ALA	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY							
Q3830	Q3833	Q3837	L3842	D3843	A3846	K3852	N3860	E3861	D3862	G3863	T3864	V3865	A4041	R4042	Q4043	M4044	M4047	L4048	S4051	V4055	E4056	M4057	L4058	F4065	E4075	Y4080	L4087	T4088	S4089	K4090	R4091	D4092	F4093	A4096	M4097	Q4102	F4103	E4116	R3949	N3950	F3951	S3952	E3967	Y3968						
E3736	E3737	G3738	G3739	E3740	N3741	GLY	E3747	E3748	V3749	E3750	Q3761	R3762	L3763	Q3766	Q3767	S3768	R3769	L3770	H3771	T3772	E3777	L3780	Q3781	N3782	K3787	A3792	M3793	V3794	S3795	S3796	T3797	T3802	G3808	N3809	Q3813	M3816	L3817	D3818	Y3819	Y3725	I3728	M3729	S3732							
PHE	ARG	MET	T3639	P3640	L3641	Y3642	N3643	H3647	R3648	N3651	M3652	Y3657	K3658	A3659	A3660	W3661	I3662	H3667	S3668	F3669	E3670	M3673	I3674	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	K3693	K3694	P3695	D3696	L3701	L3710	L3716	Y3722	Y3725	I3728	M3729	S3732				
V3511	A3512	T3513	L3514	K3515	A3541	T3545	E3548	V3549	L3553	G3561	LYS	VAL	GLY	VAL	PRO	SER	ALA	SER	LEU	R3570	W3571	Q3572	E3584	L3603	E3607	E3610	P3612	Y3613	LYS	SER	LYS	LYS	GLN	GLY	VAL	TRP	HIS	LYS	LEU	ARG	GLY	ASP	TYR	ARG	VAL	GLN	THR	SER	LEU	ILE



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	103688	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	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.066	Depositor
Minimum map value	-0.686	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.163	Depositor
Map size ($\text{\AA}$)	513.0, 513.0, 513.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.855, 0.855, 0.855	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: CA, ATP

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	0.14	0/30122	0.33	1/40997 (0.0%)
1	B	0.14	0/30122	0.33	1/40997 (0.0%)
1	C	0.14	0/30122	0.33	1/40997 (0.0%)
1	D	0.14	0/30122	0.33	1/40997 (0.0%)
All	All	0.14	0/120488	0.33	4/163988 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4895	GLY	N-CA-C	-5.90	104.27	112.18
1	B	4895	GLY	N-CA-C	-5.90	104.27	112.18
1	C	4895	GLY	N-CA-C	-5.90	104.27	112.18
1	D	4895	GLY	N-CA-C	-5.90	104.27	112.18

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	29504	0	27697	702	0
1	B	29504	0	27697	698	0
1	C	29504	0	27697	700	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	29504	0	27697	702	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	31	0	12	3	0
3	B	31	0	12	3	0
3	C	31	0	12	3	0
3	D	31	0	12	3	0
All	All	118144	0	110836	2706	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 2706 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:4324:ALA:CB	1:D:4880:MET:HE2	1.72	1.19
1:B:4880:MET:HE2	1:C:4324:ALA:CB	1.72	1.19
1:C:4880:MET:HE2	1:D:4324:ALA:CB	1.72	1.19
1:A:4880:MET:HE2	1:B:4324:ALA:CB	1.72	1.18
1:C:4880:MET:CE	1:D:4324:ALA:HB1	1.76	1.16

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	3927/5037 (78%)	3562 (91%)	359 (9%)	6 (0%)	43	74
1	B	3927/5037 (78%)	3562 (91%)	359 (9%)	6 (0%)	43	74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	3927/5037 (78%)	3562 (91%)	359 (9%)	6 (0%)	43	74
1	D	3927/5037 (78%)	3562 (91%)	359 (9%)	6 (0%)	43	74
All	All	15708/20148 (78%)	14248 (91%)	1436 (9%)	24 (0%)	44	74

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	693	SER
1	B	693	SER
1	C	693	SER
1	D	693	SER
1	A	1840	PRO

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	2895/4276 (68%)	2883 (100%)	12 (0%)	84	83
1	B	2895/4276 (68%)	2883 (100%)	12 (0%)	84	83
1	C	2895/4276 (68%)	2883 (100%)	12 (0%)	84	83
1	D	2895/4276 (68%)	2883 (100%)	12 (0%)	84	83
All	All	11580/17104 (68%)	11532 (100%)	48 (0%)	81	83

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3673	MET
1	C	4911	LEU
1	C	3926	LEU
1	C	4814	LEU
1	D	690	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 137 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	3162	GLN
1	D	3428	ASN
1	D	4020	GLN
1	B	2107	GLN
1	B	2003	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, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	ATP	B	6002	-	32,33,33	0.31	0	48,52,52	0.30	0
3	ATP	A	6002	-	32,33,33	0.31	0	48,52,52	0.30	0
3	ATP	D	6002	-	32,33,33	0.31	0	48,52,52	0.30	0
3	ATP	C	6002	-	32,33,33	0.31	0	48,52,52	0.30	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ATP	B	6002	-	-	7/22/38/38	0/3/3/3
3	ATP	A	6002	-	-	7/22/38/38	0/3/3/3
3	ATP	D	6002	-	-	7/22/38/38	0/3/3/3
3	ATP	C	6002	-	-	7/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

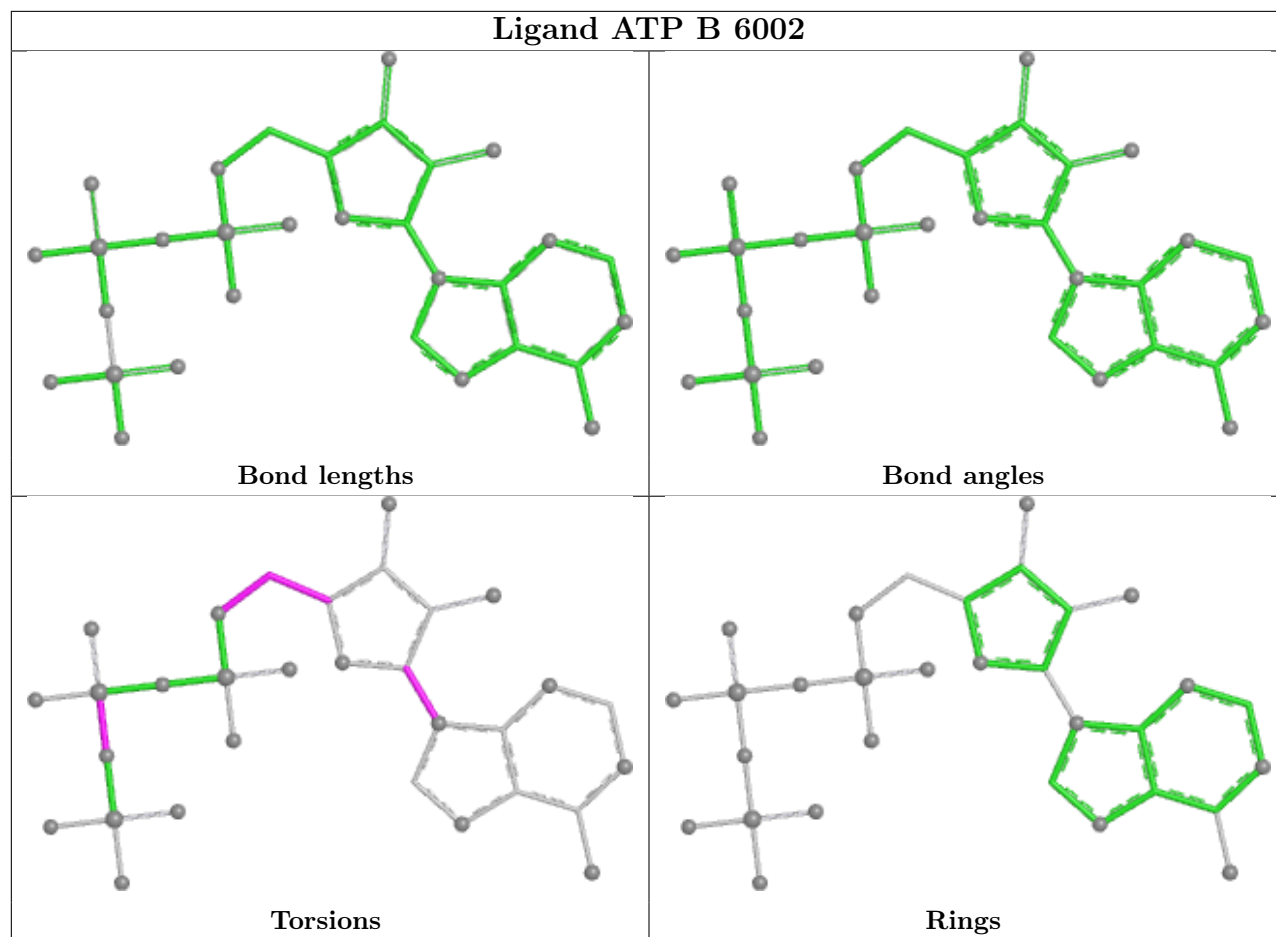
Mol	Chain	Res	Type	Atoms
3	A	6002	ATP	O4'-C4'-C5'-O5'
3	A	6002	ATP	C3'-C4'-C5'-O5'
3	B	6002	ATP	O4'-C4'-C5'-O5'
3	B	6002	ATP	C3'-C4'-C5'-O5'
3	C	6002	ATP	O4'-C4'-C5'-O5'

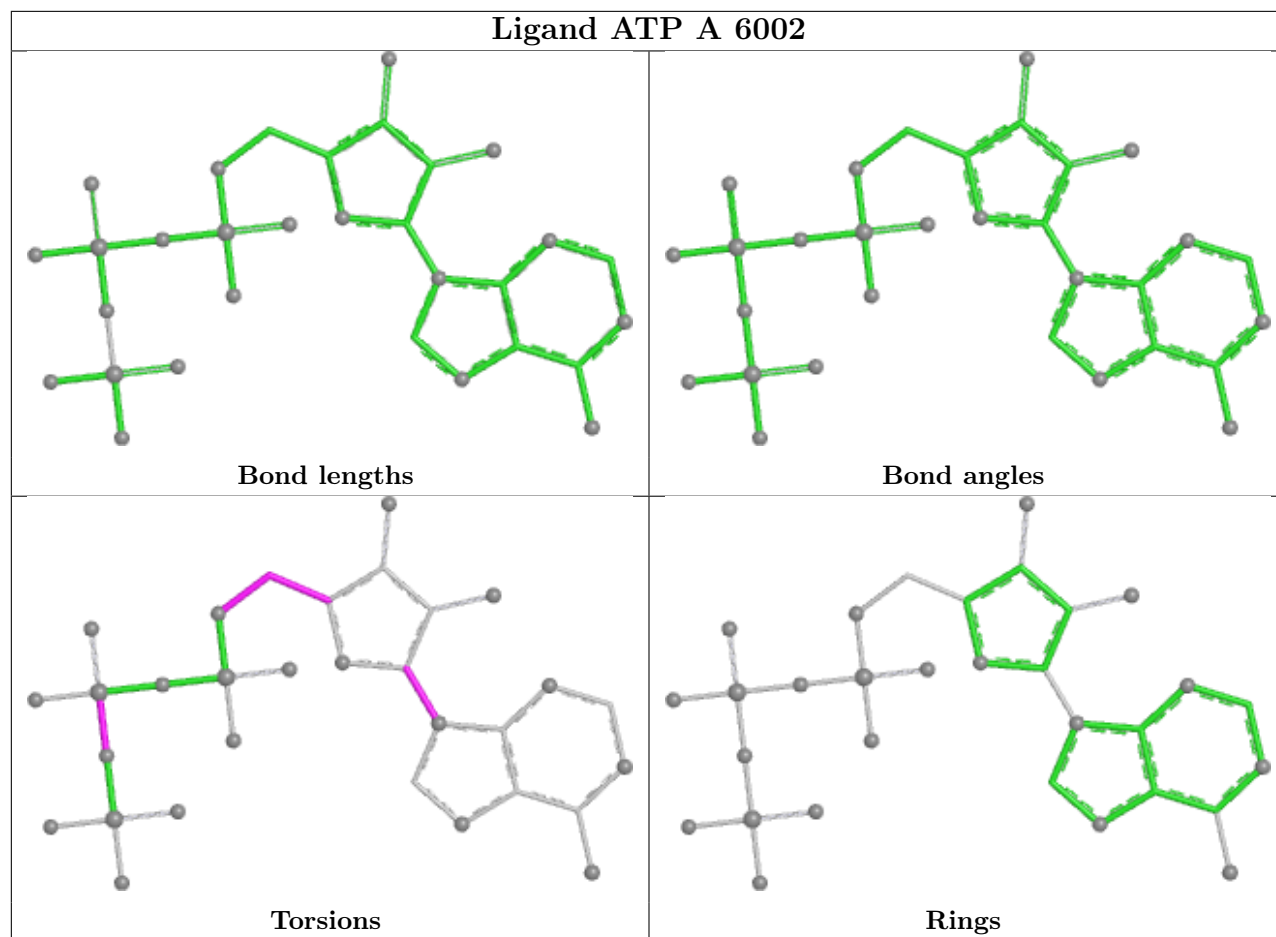
There are no ring outliers.

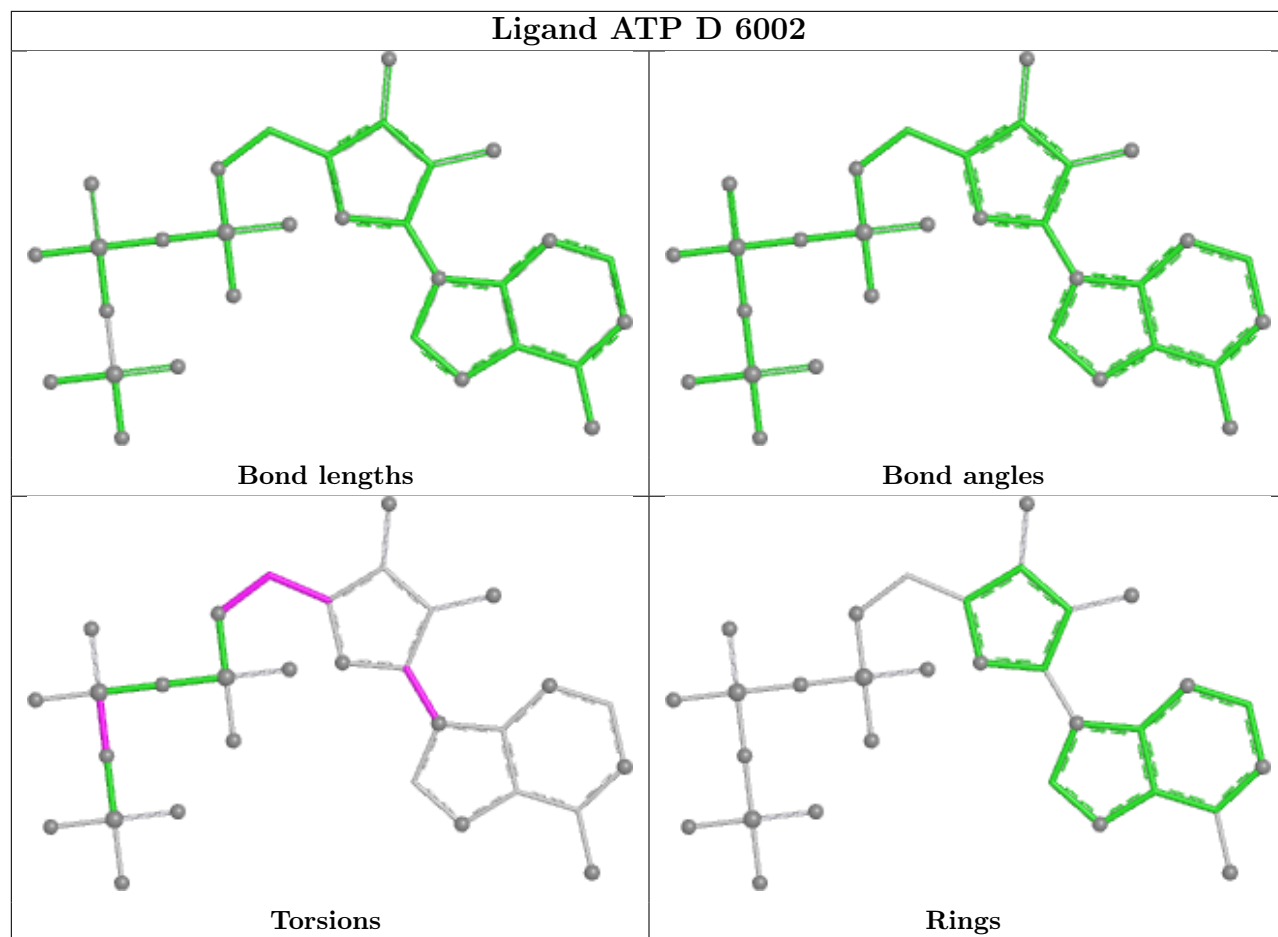
4 monomers are involved in 12 short contacts:

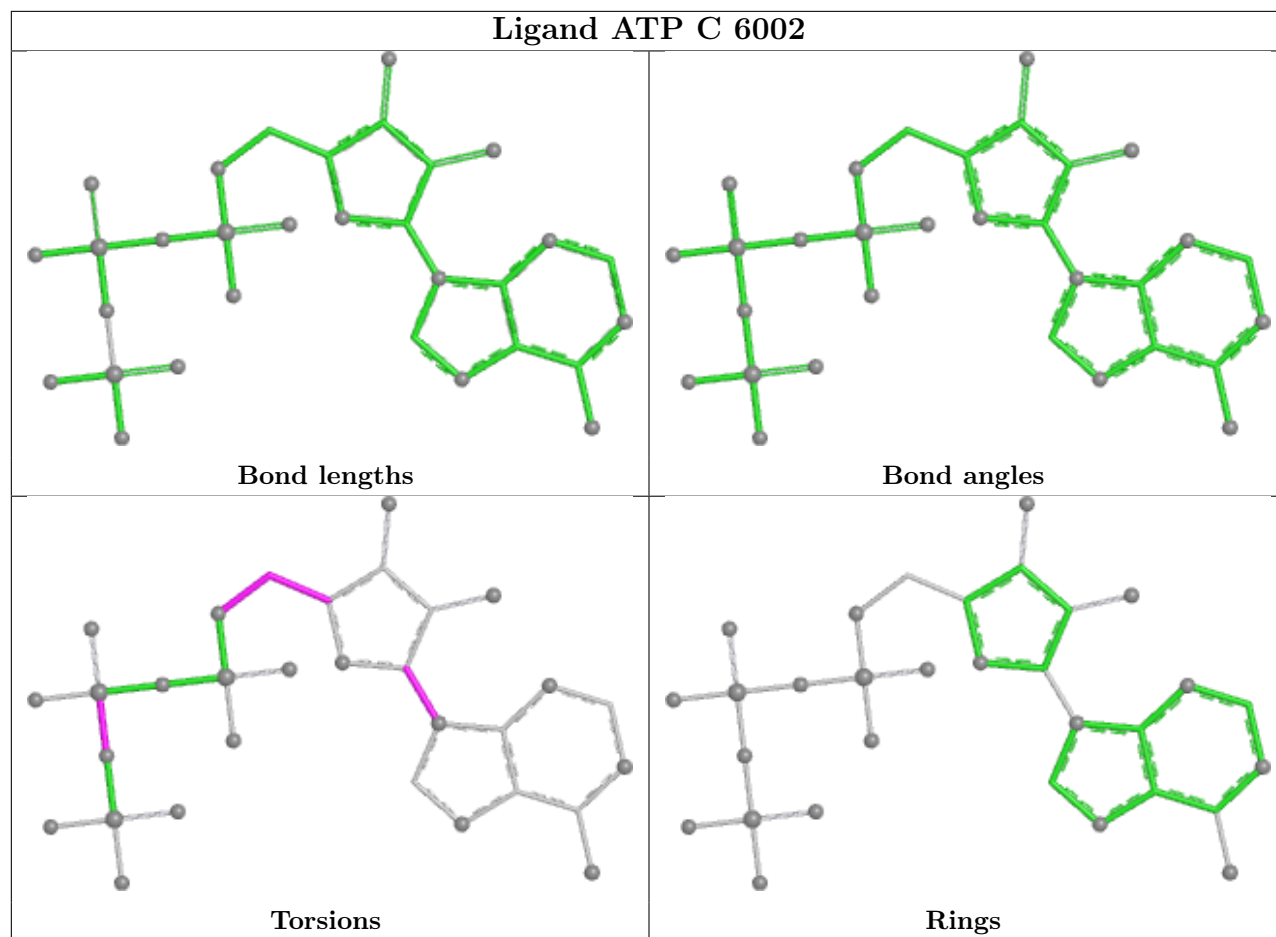
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	6002	ATP	3	0
3	A	6002	ATP	3	0
3	D	6002	ATP	3	0
3	C	6002	ATP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









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.

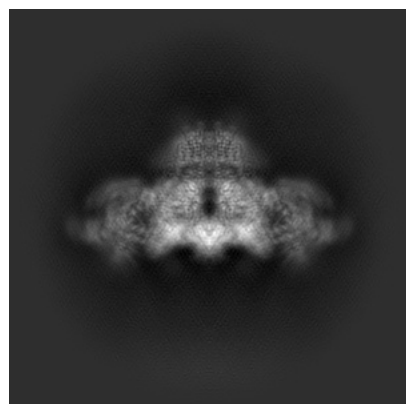
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38047. These allow visual inspection of the internal detail of the map and identification of artifacts.

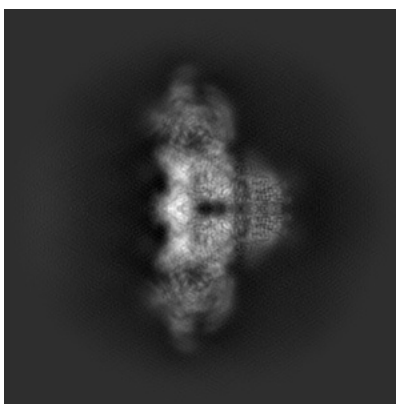
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

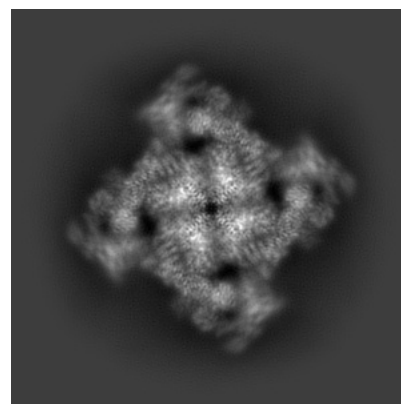
6.1.1 Primary map



X

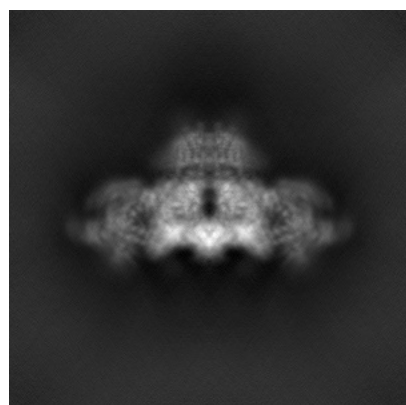


Y

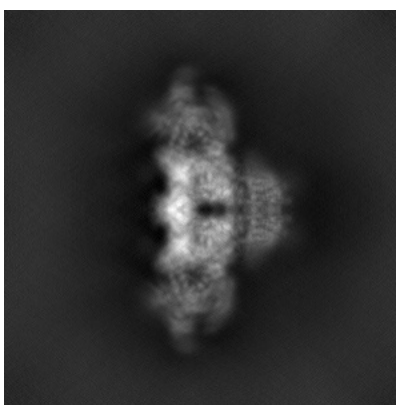


Z

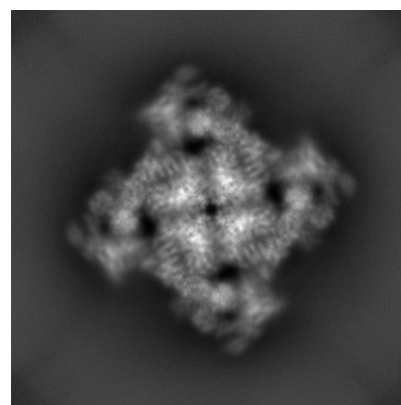
6.1.2 Raw map



X



Y

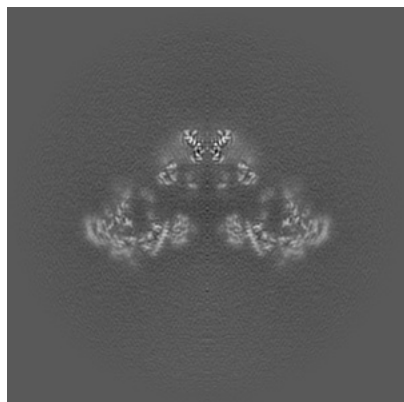


Z

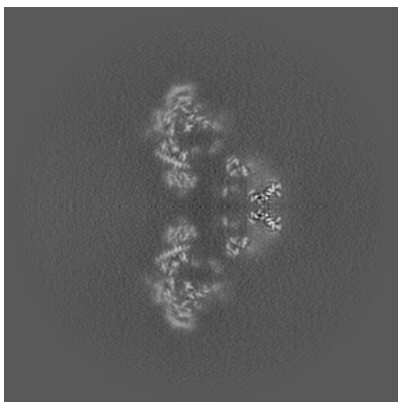
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

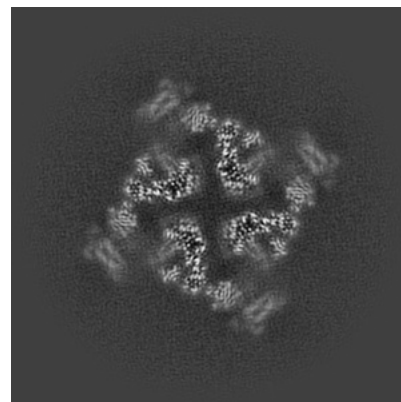
6.2.1 Primary map



X Index: 300

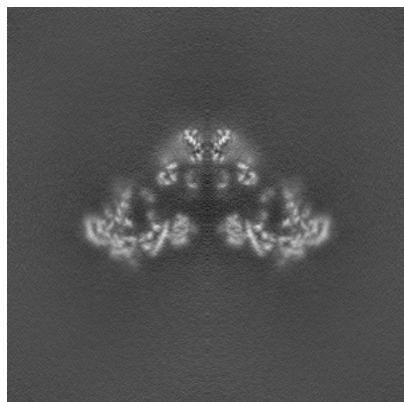


Y Index: 300

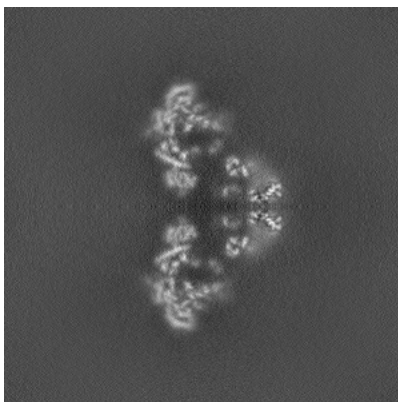


Z Index: 300

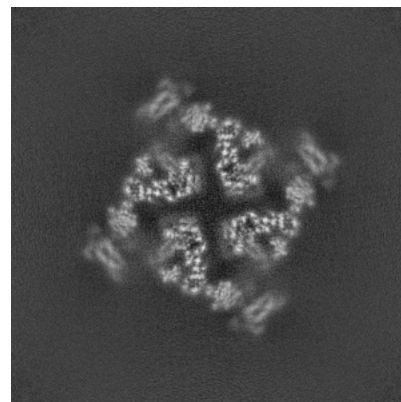
6.2.2 Raw map



X Index: 300



Y Index: 300

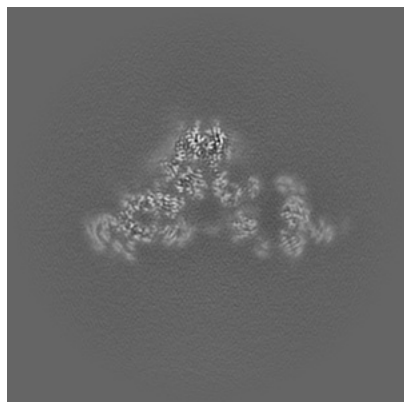


Z Index: 300

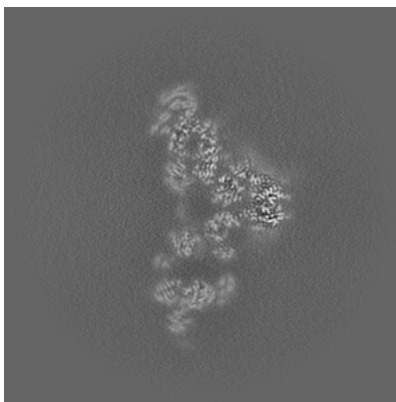
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

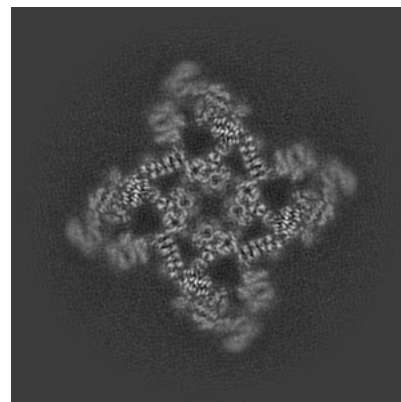
6.3.1 Primary map



X Index: 283

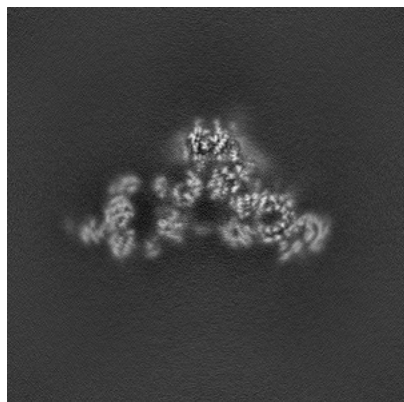


Y Index: 283

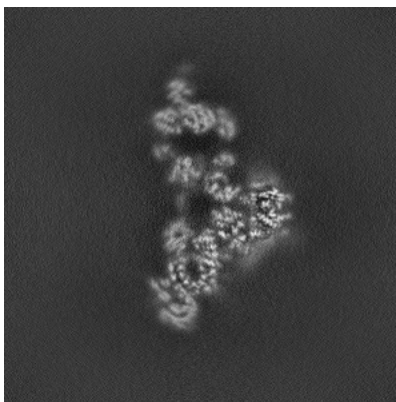


Z Index: 271

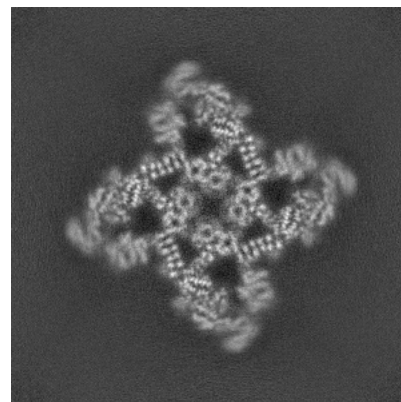
6.3.2 Raw map



X Index: 317



Y Index: 317

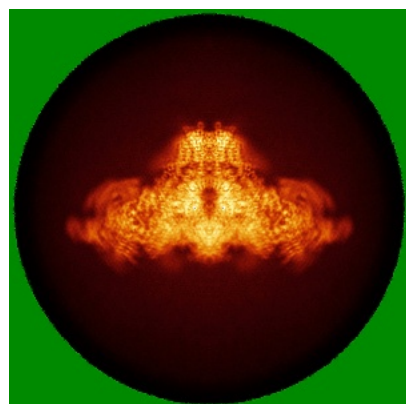


Z Index: 271

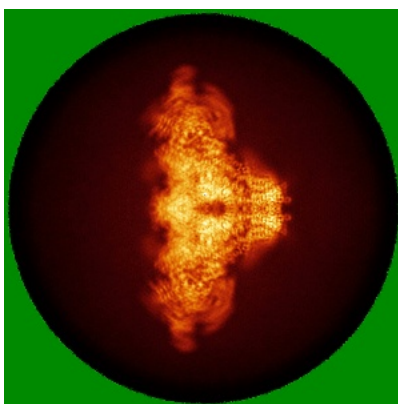
The images above show the largest variance slices of the map in three orthogonal directions.

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

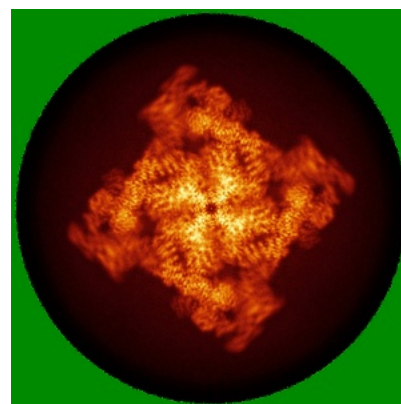
6.4.1 Primary map



X

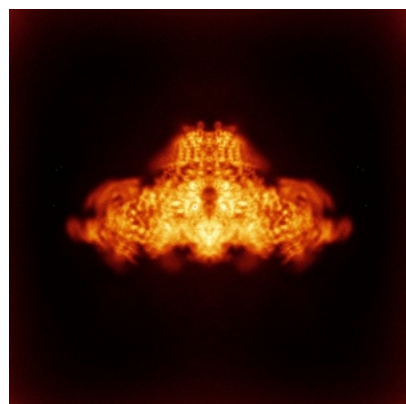


Y

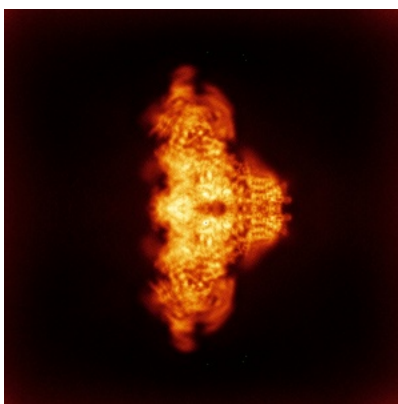


Z

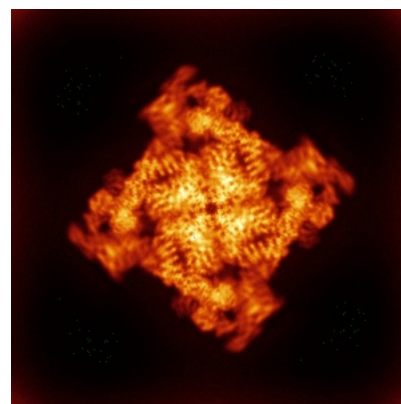
6.4.2 Raw map



X



Y

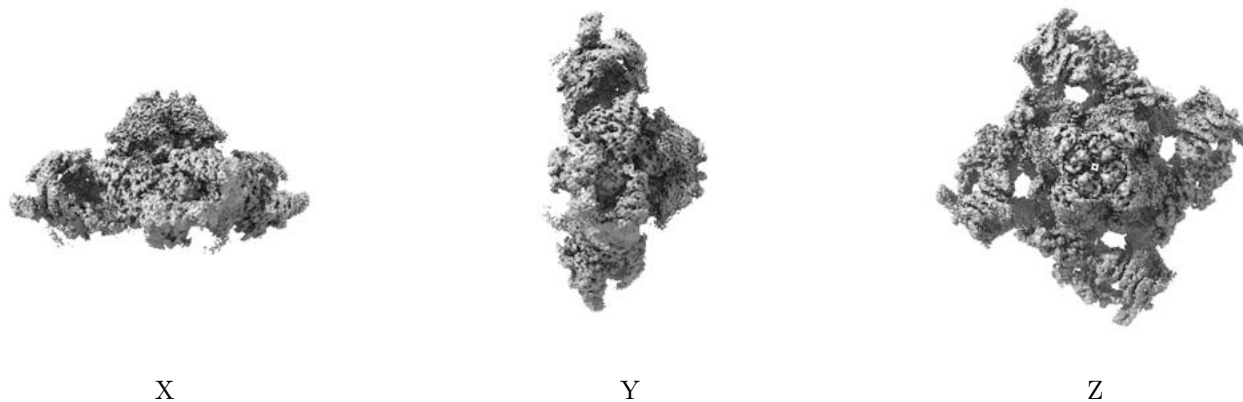


Z

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.

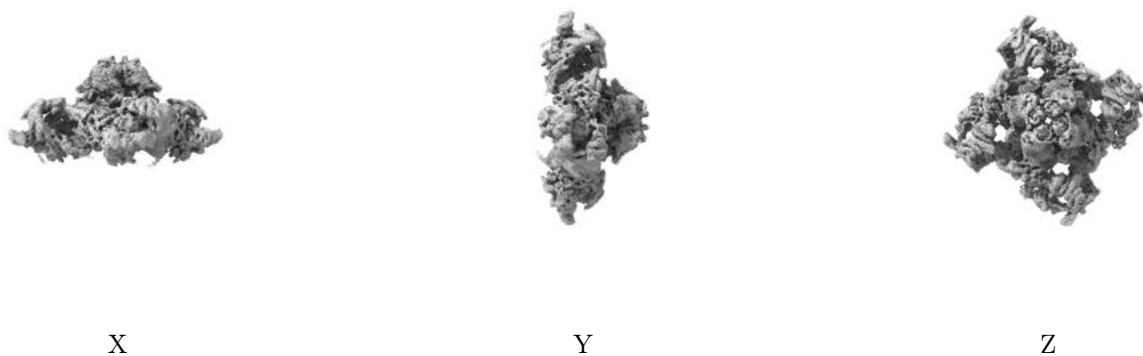
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.163. 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.

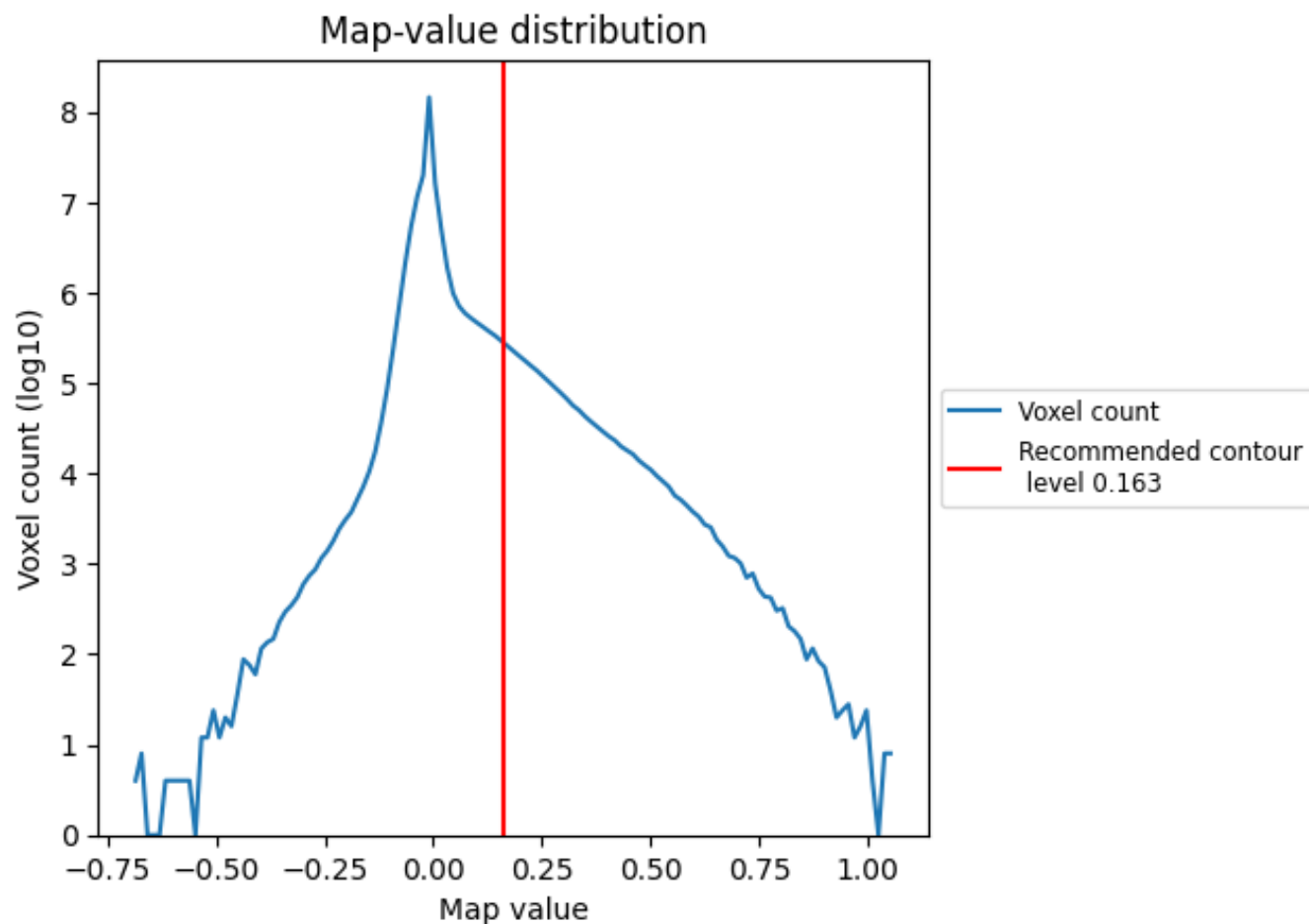
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

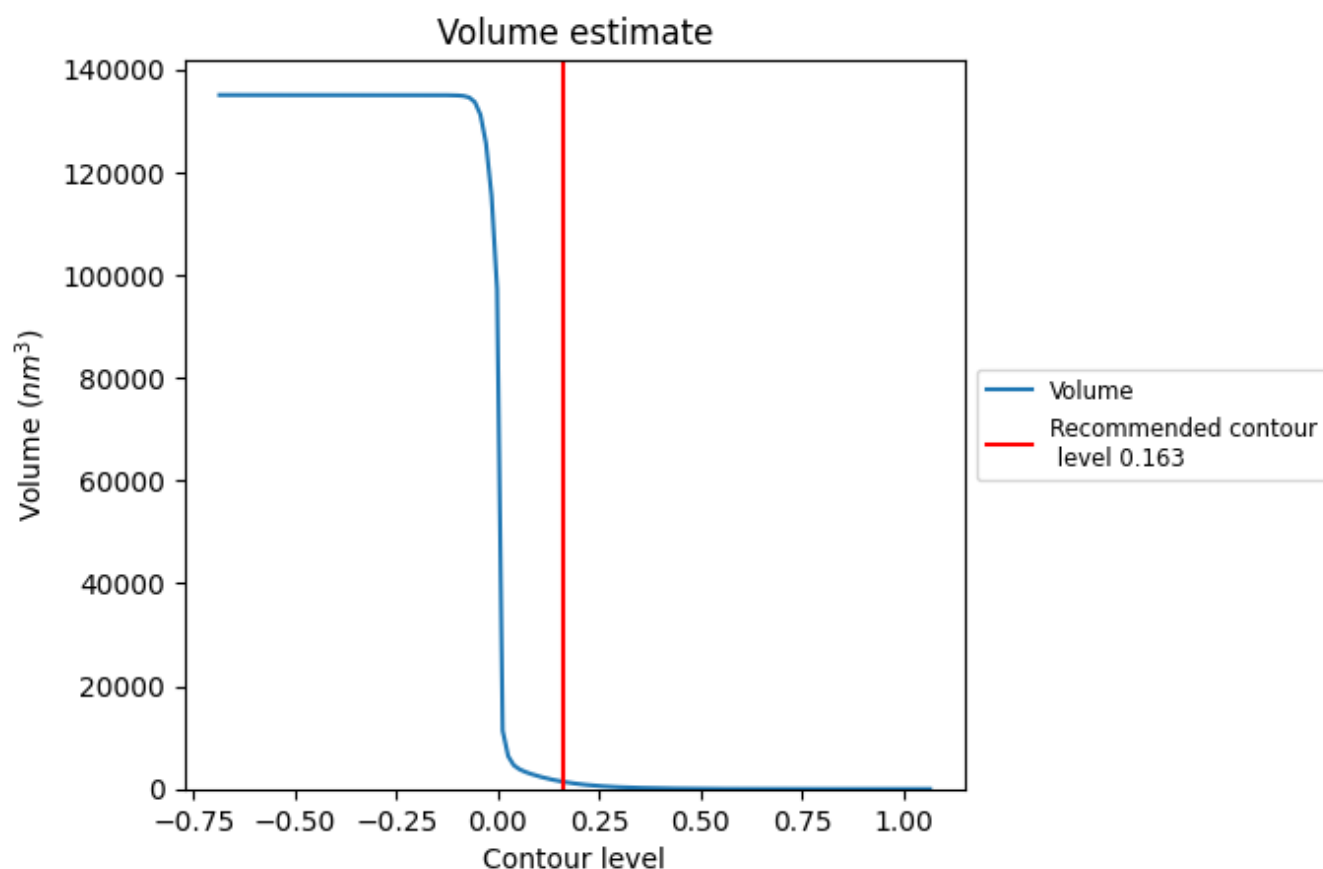
This section contains the results of statistical analysis of the map.

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.

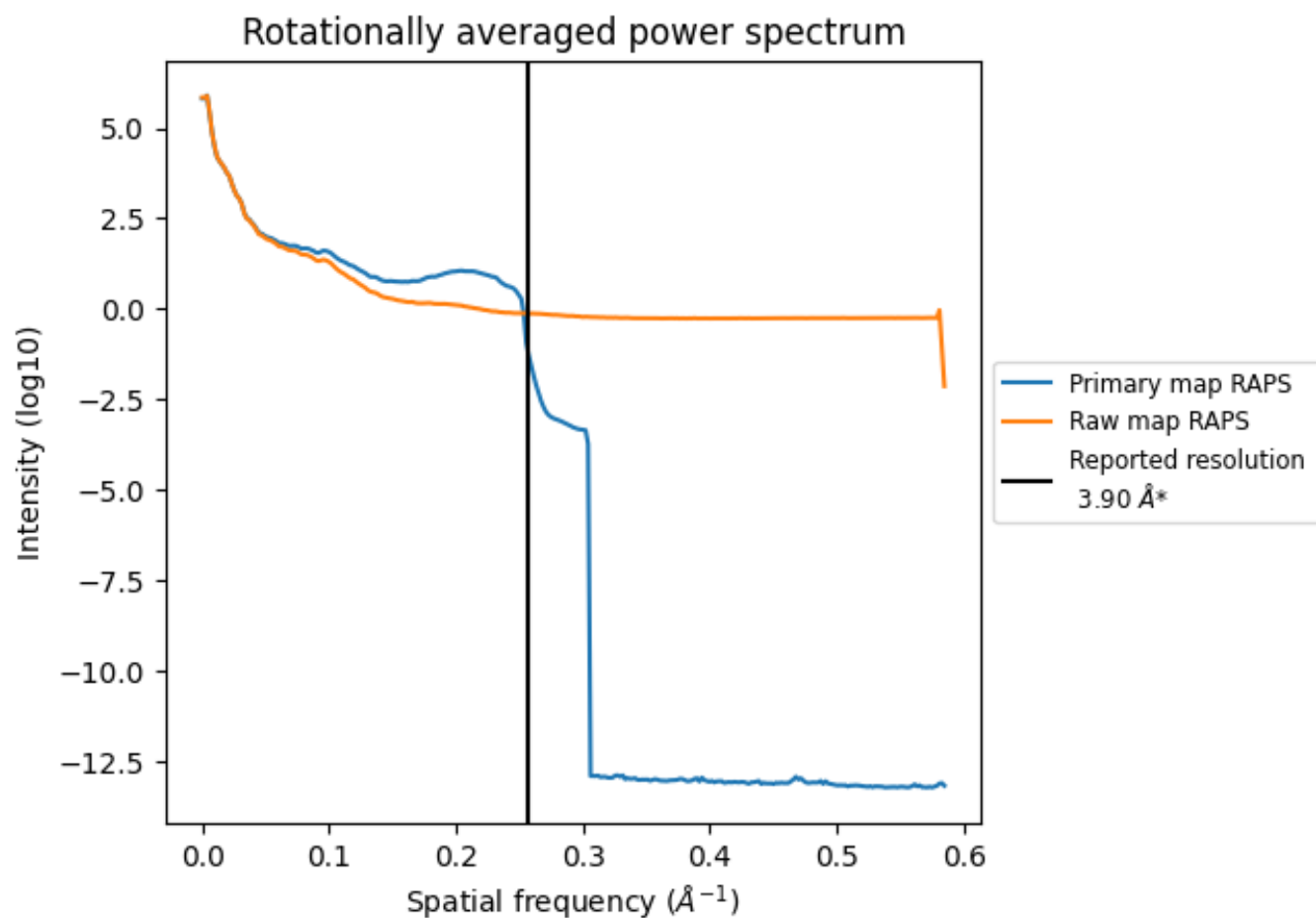
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1380 nm³; this corresponds to an approximate mass of 1247 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 ⓘ

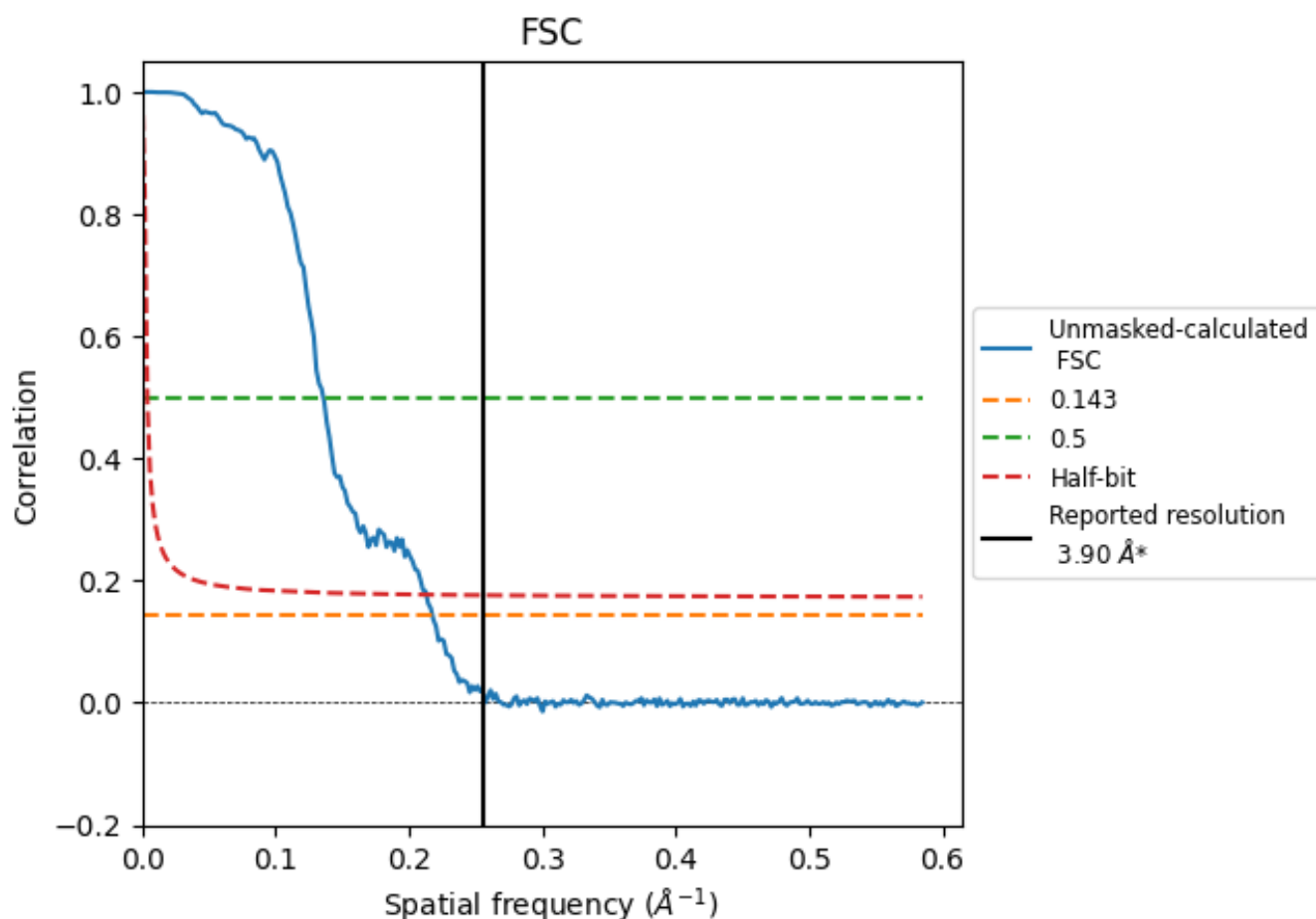


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

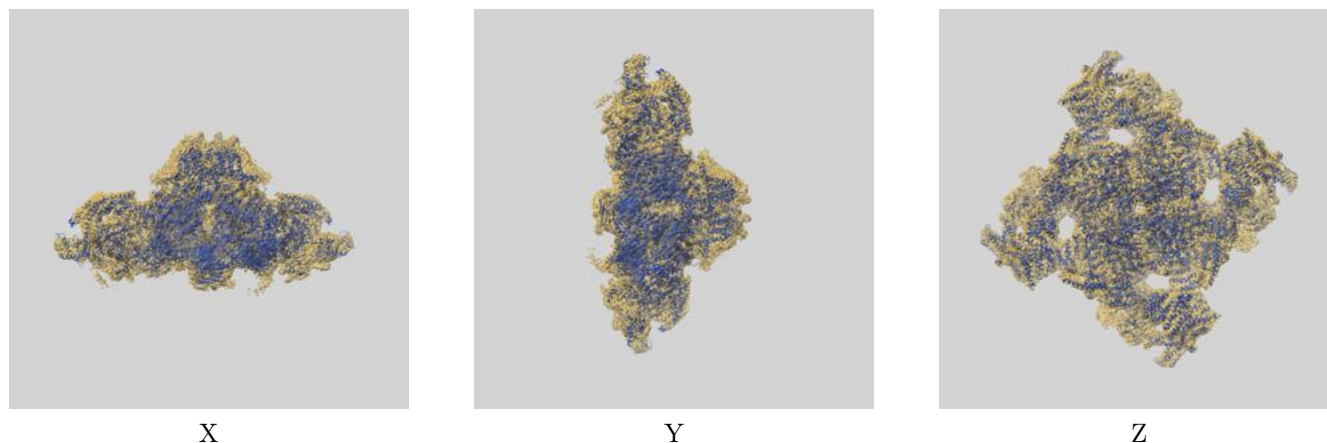
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.60	7.36	4.69

*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 4.60 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

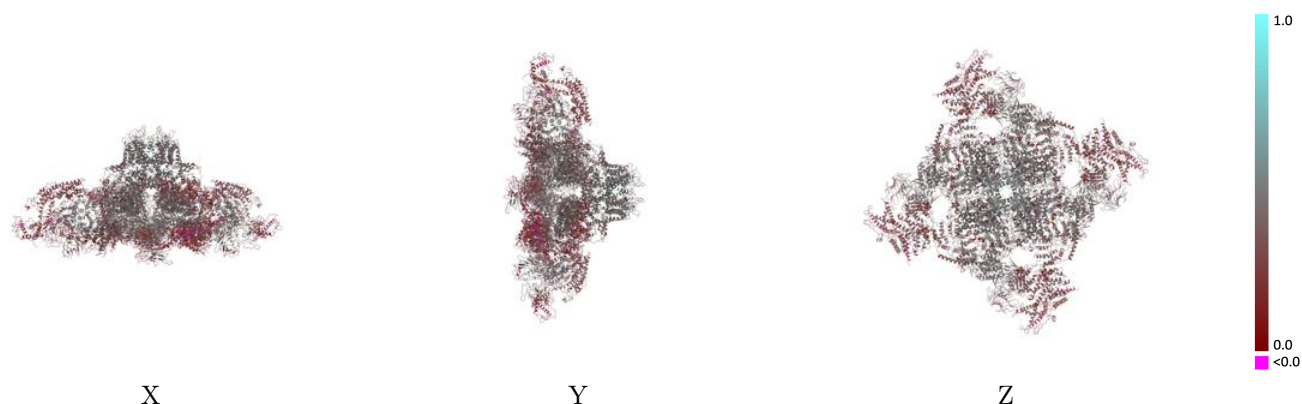
This section contains information regarding the fit between EMDB map EMD-38047 and PDB model 8X4D. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



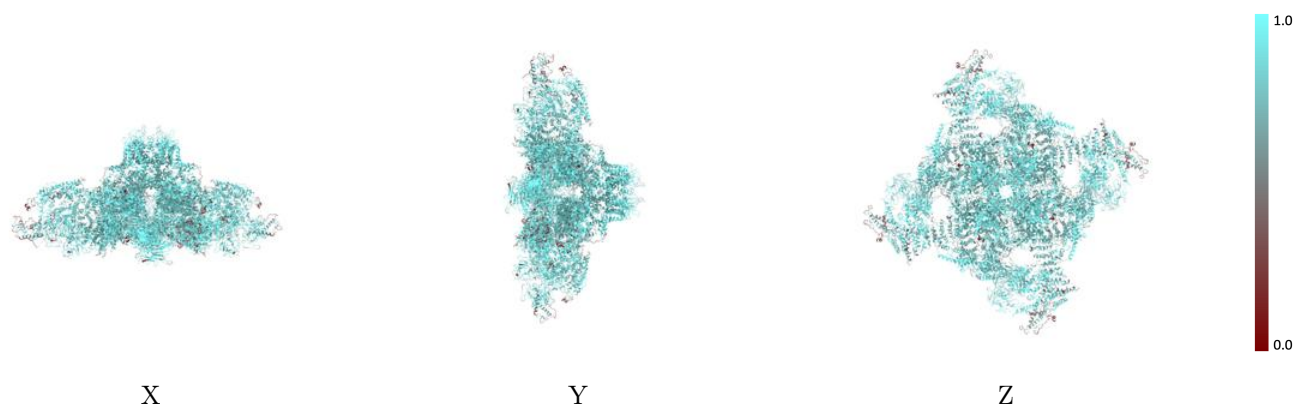
The images above show the 3D surface view of the map at the recommended contour level 0.163 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



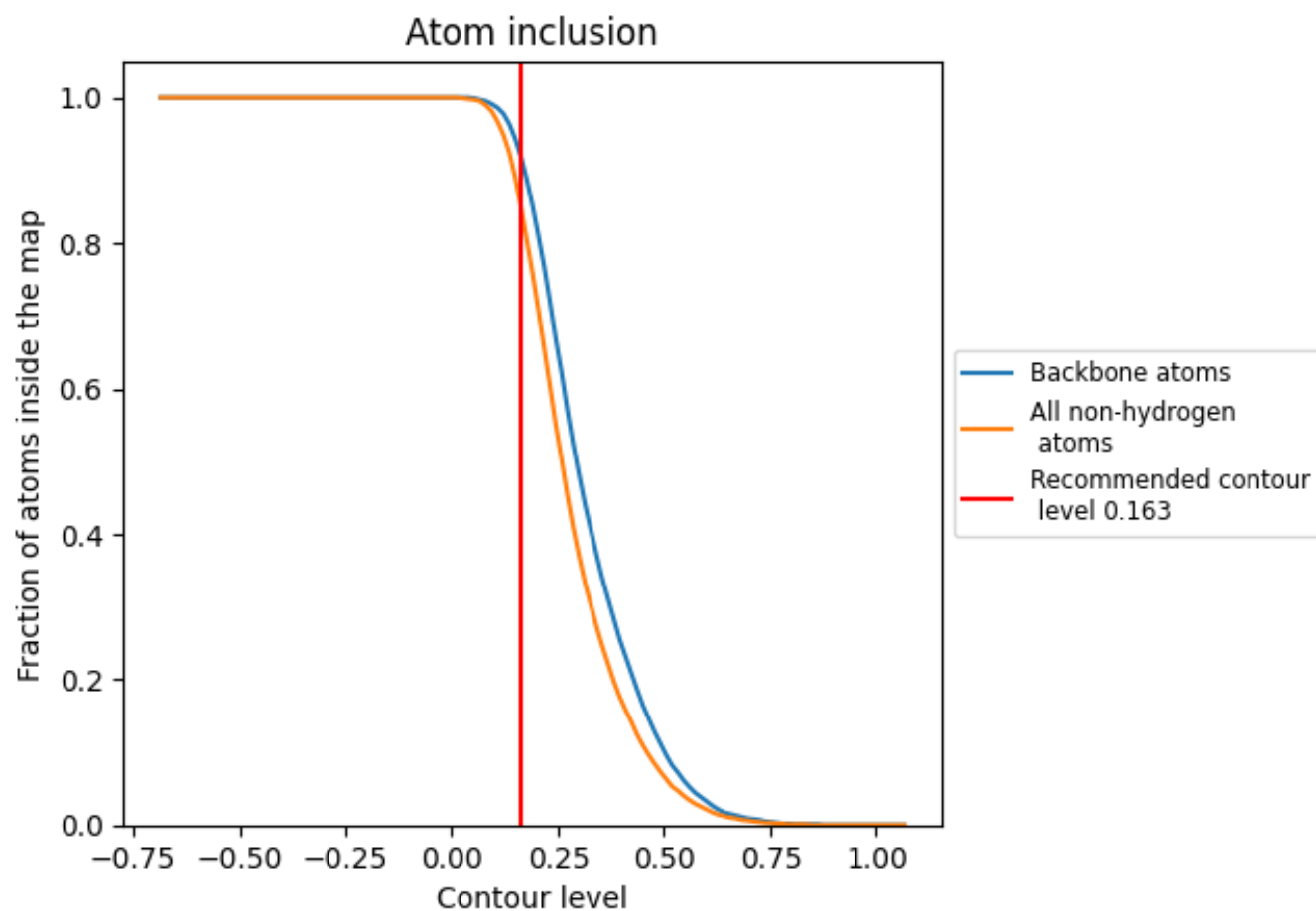
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.163).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 85% 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 (0.163) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8500	0.3590
A	0.8500	0.3590
B	0.8500	0.3590
C	0.8500	0.3590
D	0.8500	0.3590

