



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:42 AM UTC

PDB ID : 8SEY / pdb_00008sey
EMDB ID : EMD-40433
Title : Cryo-EM Structure of RyR1 + Adenosine (Local Refinement of TMD)
Authors : Cholak, S.; Saville, J.W.; Zhu, X.; Berezuk, A.M.; Tuttle, K.S.; Haji-Ghassemi, O.; Van Petegem, F.; Subramaniam, S.
Deposited on : 2023-04-10
Resolution : 2.99 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:

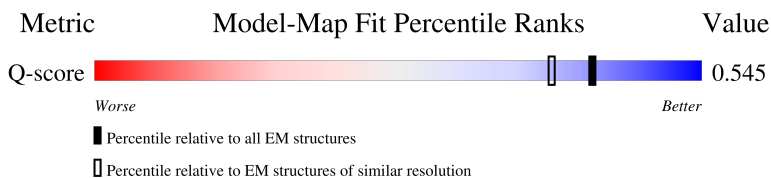
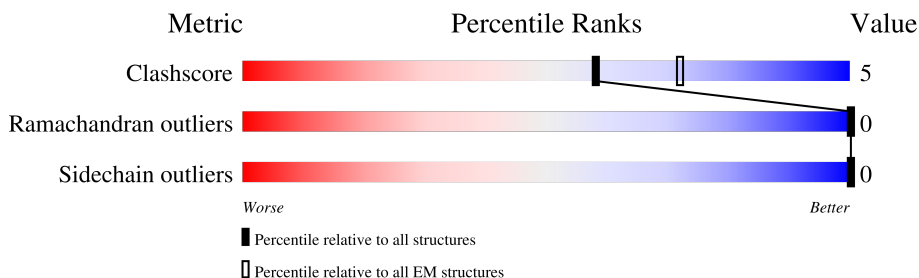
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.99 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	13287 (2.49 - 3.49)

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	 11% . 88%
1	B	5037	 11% . 88%
1	C	5037	 11% . 88%
1	D	5037	 11% . 88%

2 Entry composition [i](#)

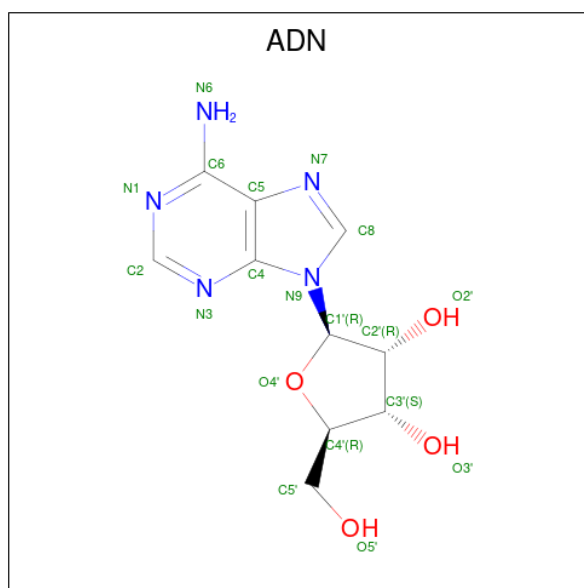
There are 3 unique types of molecules in this entry. The entry contains 20568 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	626	Total	C	N	O	S	0	0
			5122	3330	815	937	40		
1	B	626	Total	C	N	O	S	0	0
			5122	3330	815	937	40		
1	C	626	Total	C	N	O	S	0	0
			5122	3330	815	937	40		
1	D	626	Total	C	N	O	S	0	0
			5122	3330	815	937	40		

- Molecule 2 is ADENOSINE (CCD ID: ADN) (formula: $C_{10}H_{13}N_5O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			19	10	5	4	
2	B	1	Total	C	N	O	0
			19	10	5	4	

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Mol	Chain	Residues	Atoms				AltConf
2	C	1	Total	C	N	O	0
			19	10	5	4	
2	D	1	Total	C	N	O	0
			19	10	5	4	

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

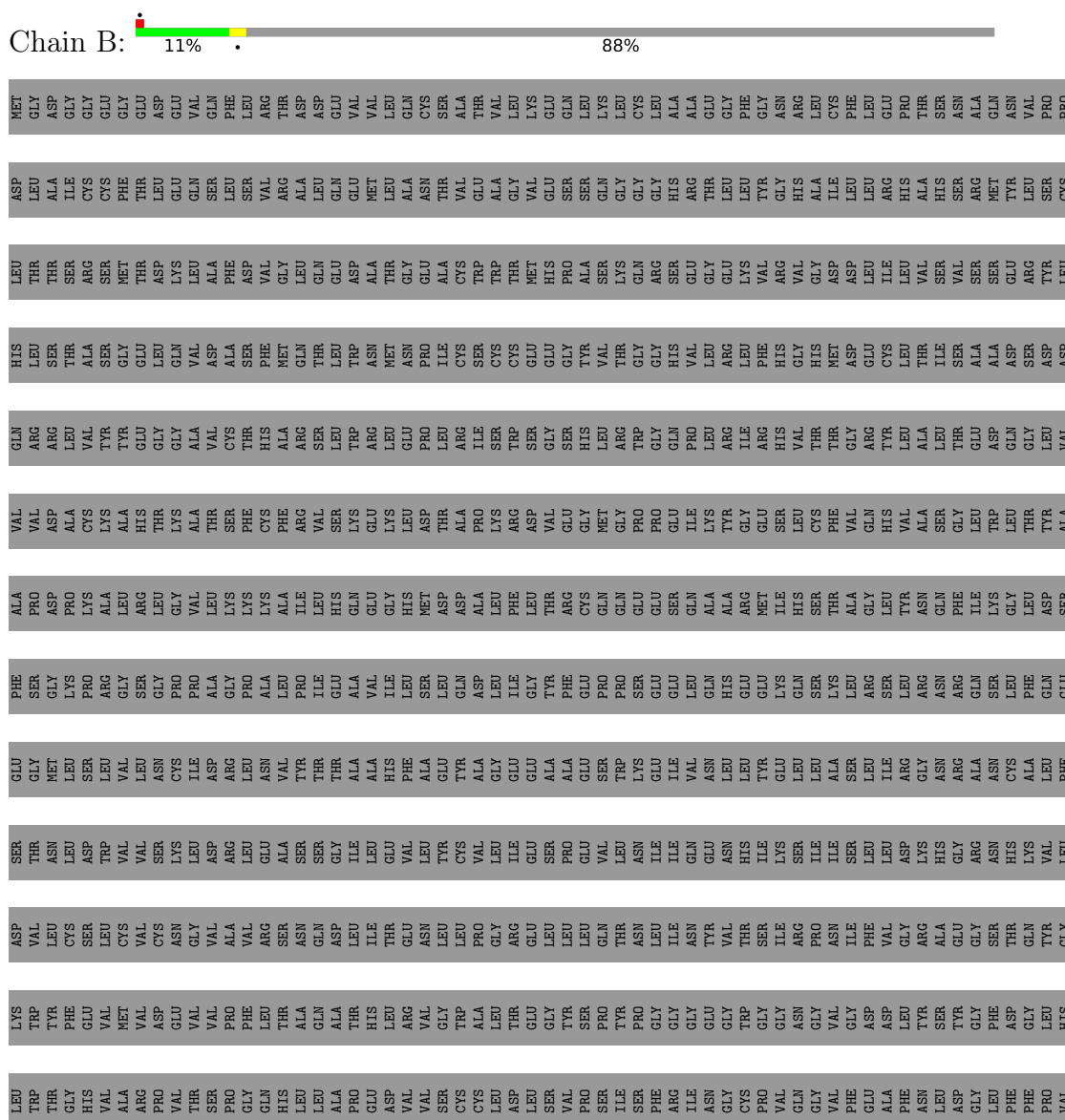
Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	B	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	







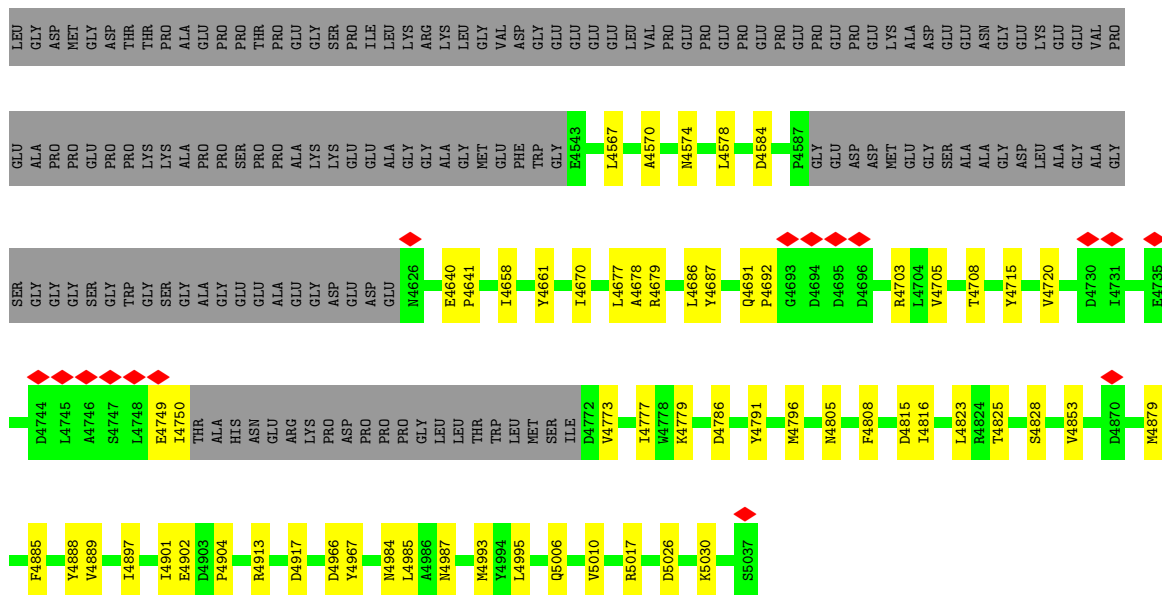
- Molecule 1: Ryanodine receptor 1



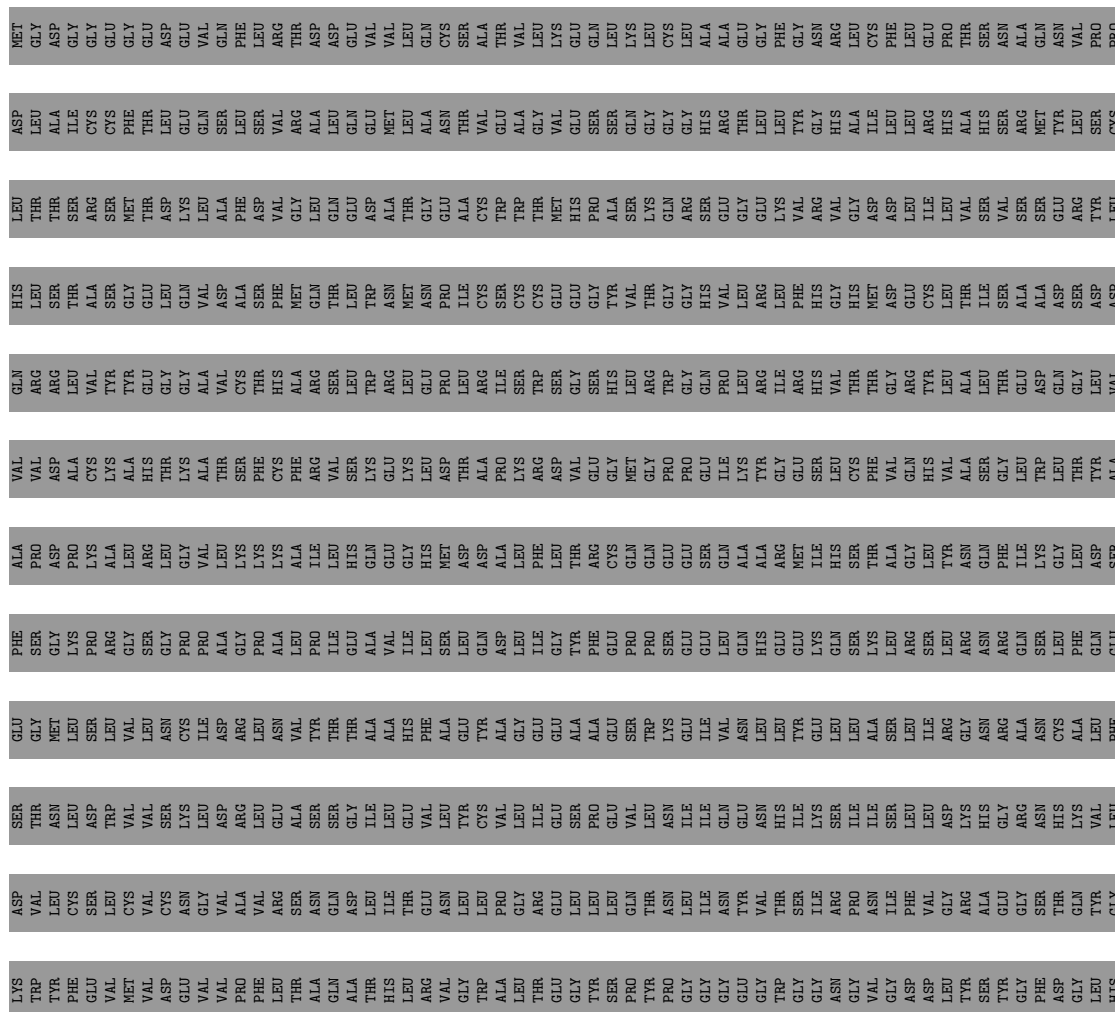








- Molecule 1: Ryanodine receptor 1















GLU	GLU	THR	L4013	ASN	VAL	GLN	LEU	THR	ALA	ALA	ALA	THR	PRO	THR	THR	THR	PRO	THR	ALA
GLY	GLY	GLY	K4014	TYR	ASP	MET	TYR	ILE	VAL	GLY	GLY	GLY	ASP	ASP	ASP	ASP	ASP	ASP	THR
ALA	ALA	PRO	E4015	LEU	ILE	ILE	LEU	THR	LEU	ASP	ASP	ASP	PRO	ILE	PRO	ILE	PRO	ILE	ALA
ALA	ALA	GLU	L4016	ARG	ASN	SER	THR	THR	TYR	ASP	ASP	GLN	THR	VAL	VAL	VAL	GLY	VAL	GLY
GLY	GLY	ILE	L4017	THR	ALA	CYS	GLN	ASP	LEU	ASP	GLU	ASP	GLY	GLY	ASP	ASP	GLY	GLN	ASN
ALA	ALA	PHE	D4018	THR	PHE	LYS	THR	HIS	GLU	ASP	GLU	ASP	GLY	VAL	ASP	ASP	GLY	GLN	CYS
GLU	GLU	LEU	M4039	GLY	ARG	GLY	THR	SER	GLN	GLU	GLU	THR	ASN	THR	ARG	ARG	PRO	ASN	LEU
GLY	GLY	LEU	Q4043	ASN	GLN	THR	MET	PHE	GLN	VAL	VAL	THR	ASN	PRO	ASP	ASP	THR	ALA	HIS
ALA	ALA	TYR	M4047	THR	ASN	GLY	THR	ASP	GLU	ARG	GLY	THR	ASP	ALA	LEU	LEU	ALA	TYR	THR
ALA	ALA	PHE	L4048	ILE	ALA	VAL	ILE	ILE	LYS	THR	GLN	THR	GLY	VAL	ASP	ASP	GLY	THR	ALA
THR	THR	ALA	E4056	ASN	GLY	THR	ASN	ASP	LYS	ASN	GLN	THR	GLY	VAL	GLY	GLY	GLY	THR	ARG
ASP	ASP	ASP	K4060	ILE	GLY	SER	ILE	ASP	THR	GLY	GLY	THR	ASP	GLY	GLY	GLY	GLY	ALA	LEU
ASN	ASN	ASN	PHE	CYS	THR	LEU	LYS	SER	ALA	HIS	HIS	ARG	VAL	ASN	GLY	GLY	GLY	ALA	ARG
THR	THR	THR	ASP	THR	VAL	LYS	VAL	ALA	TRP	GLN	GLN	ARG	GLY	ILE	ASN	ILE	ILE	THR	THR
ILE	ILE	ASN	ASP	VAL	ASN	GLY	GLY	GLY	THR	GLY	GLY	VAL	GLY	GLY	GLY	GLY	GLY	ALA	PRO
ASN	ASN	ASN	THR	THR	ASP	ILE	GLY	GLY	LYS	LYS	LYS	THR	THR	ASN	ASN	ASN	ASN	THR	THR
GLU	GLU	GLU	K4214	ARG	ILE	ASN	GLU	GLU	SER	GLY	GLY	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ALA	ALA	ASN	G4225	GLN	ASN	GLY	GLY	GLY	LYS	PRO	PRO	VAL	THR	GLN	ASN	ASN	PRO	GLY	GLY
ARG	ARG	ARG	E4226	LEU	ARG	GLY	GLY	GLY	HIS	GLY	GLY	THR	PRO	GLY	PRO	PRO	GLY	GLY	ILE
ALA	ALA	PHE	E4227	SER	GLN	ASN	VAL	GLU	ARG	LEU	LEU	LEU	GLY	VAL	GLY	GLY	VAL	ALA	ALA
LEU	LEU	GLN	E4228	ILE	ASN	ALA	GLY	VAL	ALA	TRP	GLN	VAL	ASN	GLY	ASN	ASN	GLY	GLY	GLY
ARG	ARG	GLY	A4228	SER	GLY	GLY	VAL	GLU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLY	GLY	PRO	E4232	ASP	GLY	VAL	GLN	LYS	VAL	GLN	GLN	GLN	THR	THR	THR	THR	THR	THR	THR
LEU	LEU	ALA	T4241	ALA	VAL	GLN	THR	LYS	ALA	ALA	ALA	ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY
SER	SER	ASP	I4242	THR	ALA	MET	TRP	PRO	PHE	CYS	CYS	LYS	ASP	ASP	ASP	ASP	ASP	ASP	ASP
LEU	LEU	PHE	M4245	VAL	ASP	ASP	TYR	MET	MET	ARG	ARG	ARG	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ARG	ARG	ASN	E4253	GLY	PHE	THR	GLY	HIS	THR	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
ARG	ARG	VAL	P4254	LYS	THR	LEU	LYS	THR	PRO	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
VAL	VAL	VAL	GLY	VAL	THR	GLY	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ARG	ARG	THR	GLY	ILE	PHE	LYS	ILE	THR	ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
LEU	LEU	ASN	PRO	GLN	THR	GLN	GLN	GLN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ARG	ARG	GLY	ALA	GLY	PHE	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
THR	THR	THR	ALA	LYS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ALA	ALA	THR	GLY	THR	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ALA	ALA	LEU	ALA	ASN	ALA	GLN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
ALA	ALA	ALA	ALA	THR	ALA	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY

V4889	L4745	GLY	PRO	LEU
I4897	A4746	GLY	PRO	TRP
I4901	S4747	GLY	PRO	ALA
E4902	L4748	TRP	PRO	VAL
D4903	E4749	GLY	PRO	VAL
P4904	I4750	GLY	LYS	ARG
	THR	ALA	GLU	ALA
		GLY	PRO	GLY
		GLY	PRO	ALA
		GLU	SER	ALA
		GLU	PRO	GLY
		GLU	THR	ALA
		ALA	PRO	GLY
		ARG	PRO	GLY
		LYS	ALA	GLY
		PRO	GLY	ALA
		ASP	GLY	ALA
		PRO	GLU	GLY
		PRO	GLU	GLY
		PRO	GLU	GLY
		PRO	GLY	GLY
		GLY	GLY	GLY
		GLY	GLY	GLY
		LEU	LYS	ALA
		LEU	ARG	ALA
		TRP	LYS	LEU
		LEU	GLY	LEU
		MET	GLY	LEU
		SER	GLY	LEU
		ILE	GLU	PHE
		I4772	GLY	GLY
		V4773	E4543	GLY
		I4777	L4567	GLY
		V4778	L4570	LEU
		K4779	A4574	VAL
		D4786	L4578	GLU
		Y4791	D4584	PRO
		M4796	P4587	THR
		N4805	L4587	VAL
		F4808	GLY	GLU
		D4815	ASP	GLU
		I4816	ASP	ALA
		T4825	GLY	VAL
		S4828	SER	LEU
		V4853	ALA	LEU
		D4870	GLY	LEU
		N4879	GLY	GLY
		F4885	GLY	GLY
		S5037	ALA	GLN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51504	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	5.677	Depositor
Minimum map value	-2.569	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.123	Depositor
Recommended contour level	0.585	Depositor
Map size (Å)	515.2, 515.2, 515.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.288, 1.288, 1.288	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: ADN, 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	0.11	0/5241	0.28	0/7072
1	B	0.11	0/5241	0.27	0/7072
1	C	0.11	0/5241	0.27	0/7072
1	D	0.11	0/5241	0.27	0/7072
All	All	0.11	0/20964	0.27	0/28288

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	5122	0	5019	48	0
1	B	5122	0	5019	51	0
1	C	5122	0	5019	52	0
1	D	5122	0	5019	51	0
2	A	19	0	13	0	0
2	B	19	0	13	0	0
2	C	19	0	13	0	0
2	D	19	0	13	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
All	All	20568	0	20128	193	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 5.

The worst 5 of 193 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:B:4995:LEU:HD11	1:B:5010:VAL:HG13	1.76	0.68
1:C:4995:LEU:HD11	1:C:5010:VAL:HG13	1.76	0.67
1:D:4995:LEU:HD11	1:D:5010:VAL:HG13	1.76	0.66
1:A:4995:LEU:HD11	1:A:5010:VAL:HG13	1.76	0.66
1:D:4902:GLU:O	1:D:4913:ARG:NH1	2.27	0.63

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	616/5037 (12%)	600 (97%)	16 (3%)	0	100	100
1	B	616/5037 (12%)	601 (98%)	15 (2%)	0	100	100
1	C	616/5037 (12%)	601 (98%)	15 (2%)	0	100	100
1	D	616/5037 (12%)	601 (98%)	15 (2%)	0	100	100
All	All	2464/20148 (12%)	2403 (98%)	61 (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	559/4276 (13%)	559 (100%)	0	100	100
1	B	559/4276 (13%)	559 (100%)	0	100	100
1	C	559/4276 (13%)	559 (100%)	0	100	100
1	D	559/4276 (13%)	559 (100%)	0	100	100
All	All	2236/17104 (13%)	2236 (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 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	3994	HIS
1	D	3998	HIS
1	D	4864	ASN
1	D	4558	ASN
1	C	3994	HIS

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 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	$\# Z > 2$
2	ADN	D	5101	-	21,21,21	0.17	0	31,31,31	0.31	0
2	ADN	C	5101	-	21,21,21	0.17	0	31,31,31	0.31	0
2	ADN	A	5101	-	21,21,21	0.17	0	31,31,31	0.31	0
2	ADN	B	5101	-	21,21,21	0.18	0	31,31,31	0.31	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
2	ADN	D	5101	-	-	4/6/22/22	0/3/3/3
2	ADN	C	5101	-	-	4/6/22/22	0/3/3/3
2	ADN	A	5101	-	-	4/6/22/22	0/3/3/3
2	ADN	B	5101	-	-	4/6/22/22	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

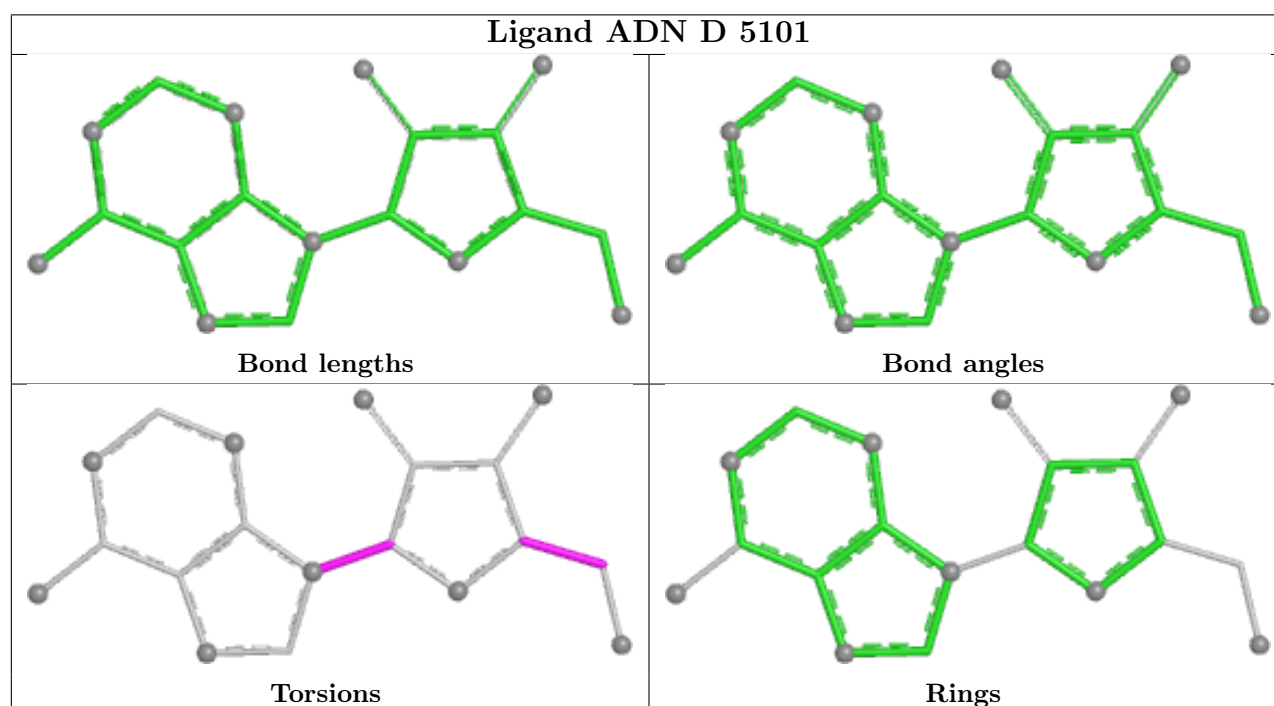
5 of 16 torsion outliers are listed below:

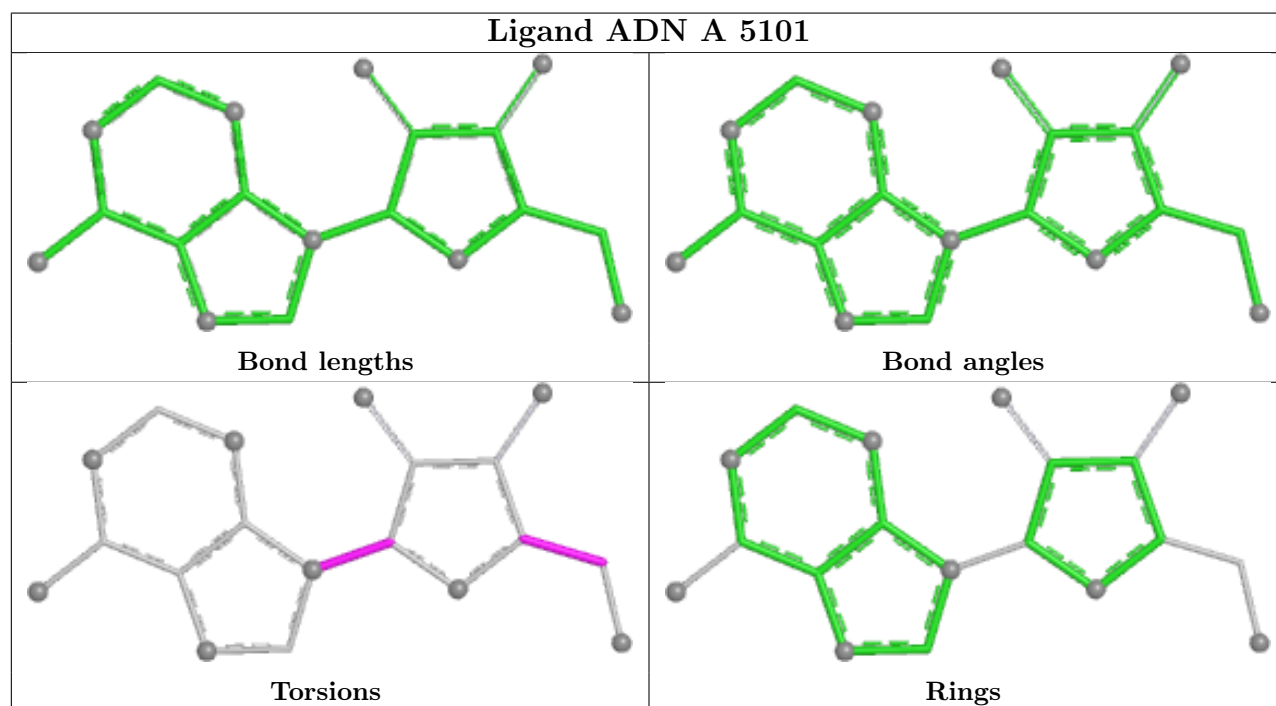
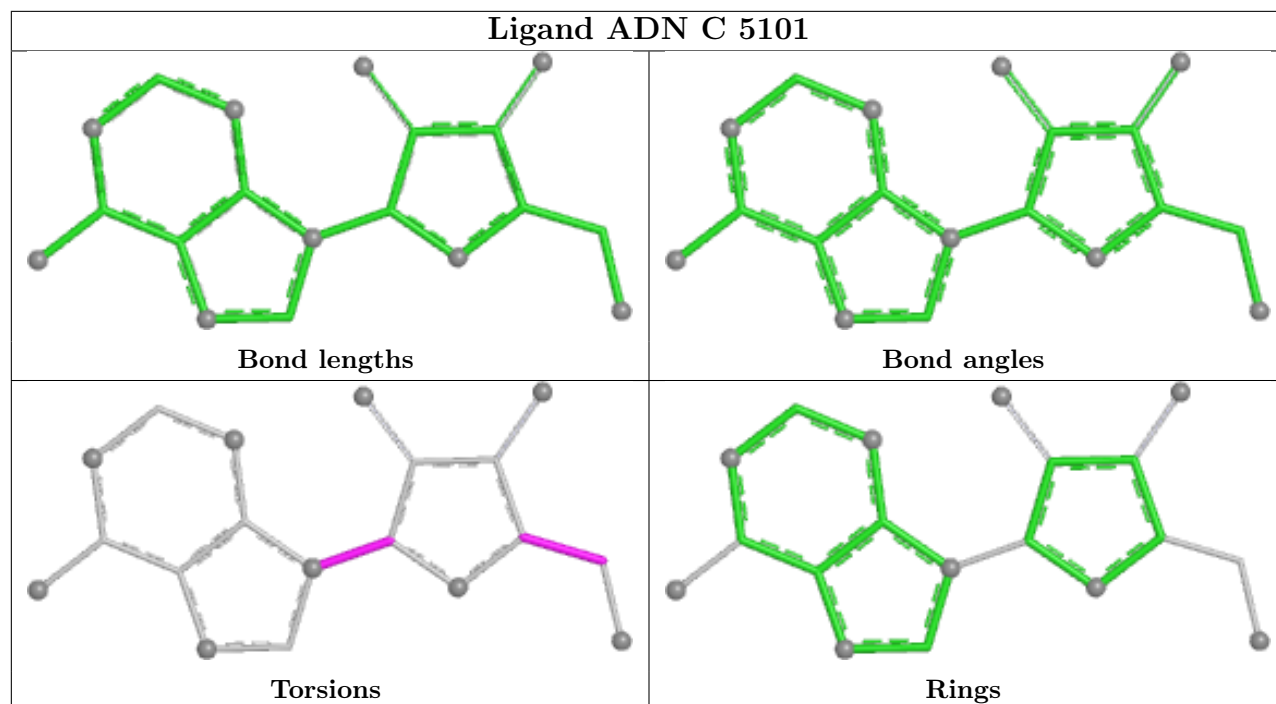
Mol	Chain	Res	Type	Atoms
2	A	5101	ADN	O4'-C4'-C5'-O5'
2	C	5101	ADN	O4'-C4'-C5'-O5'
2	D	5101	ADN	O4'-C4'-C5'-O5'
2	B	5101	ADN	O4'-C4'-C5'-O5'
2	C	5101	ADN	C3'-C4'-C5'-O5'

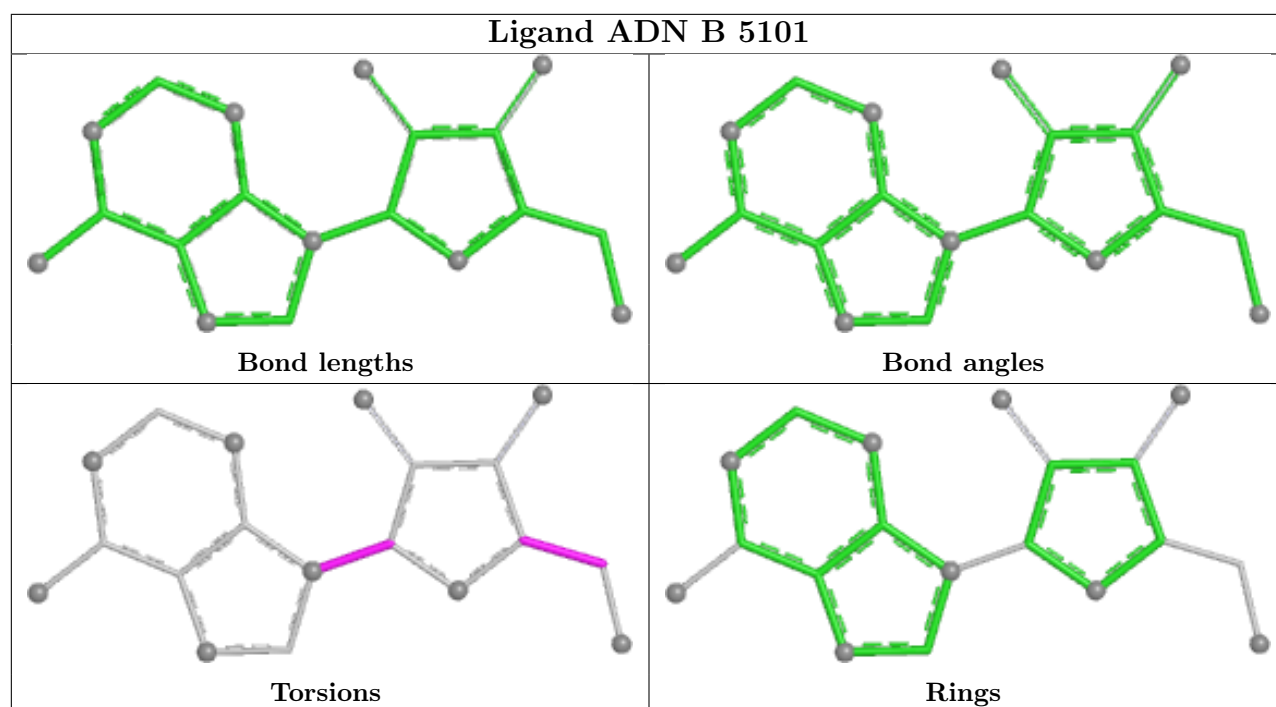
There are no ring outliers.

No monomer is involved in short contacts.

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.

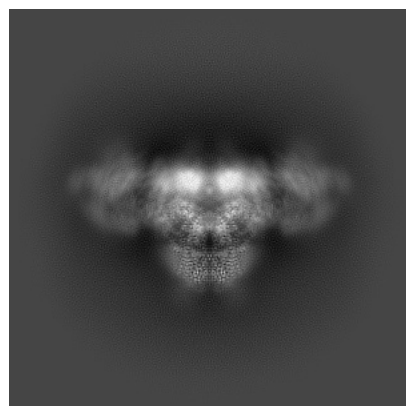
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40433. These allow visual inspection of the internal detail of the map and identification of artifacts.

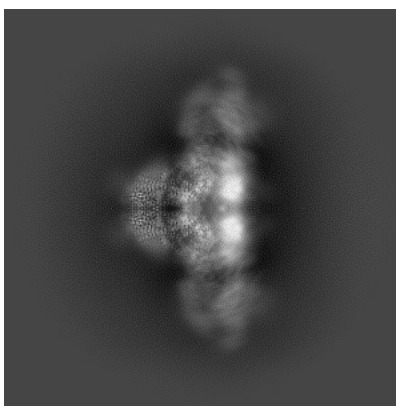
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

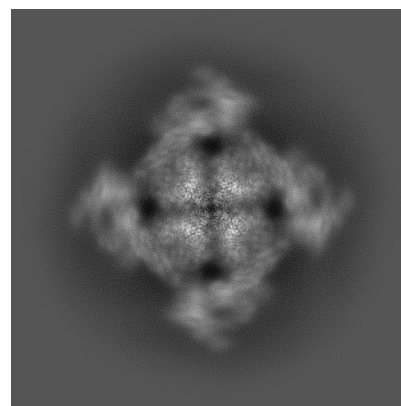
6.1.1 Primary map



X

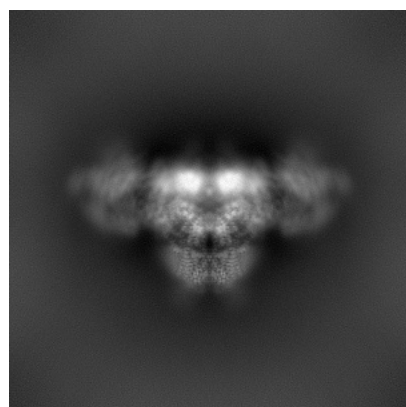


Y

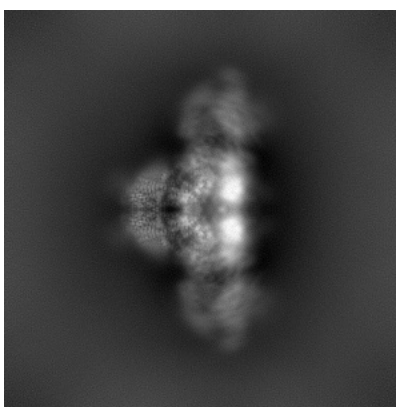


Z

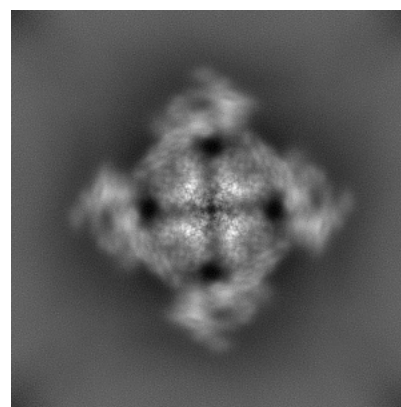
6.1.2 Raw map



X



Y



Z

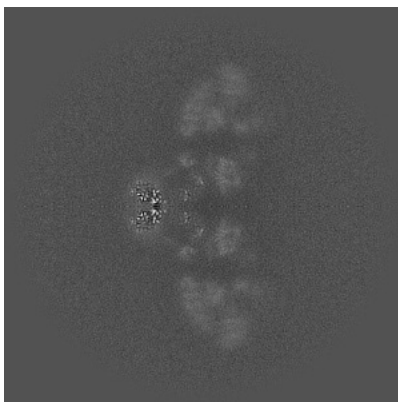
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

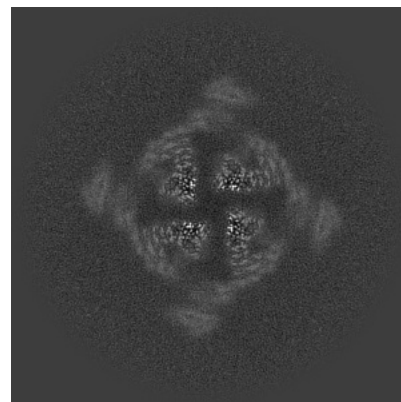
6.2.1 Primary map



X Index: 200

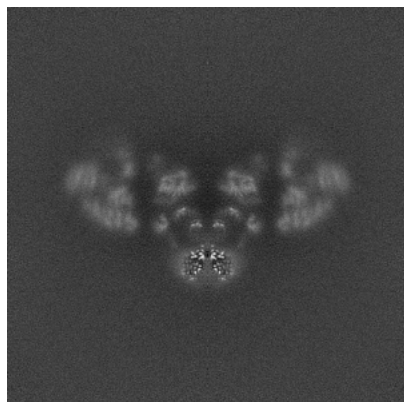


Y Index: 200

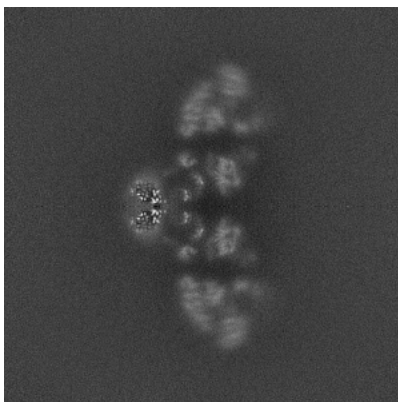


Z Index: 200

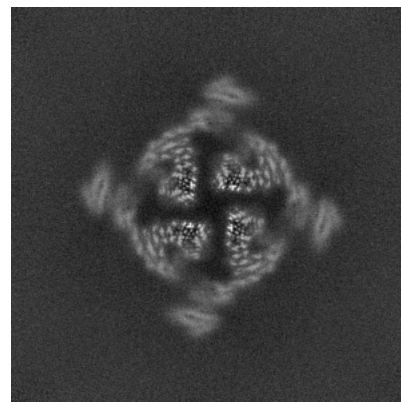
6.2.2 Raw map



X Index: 200



Y Index: 200

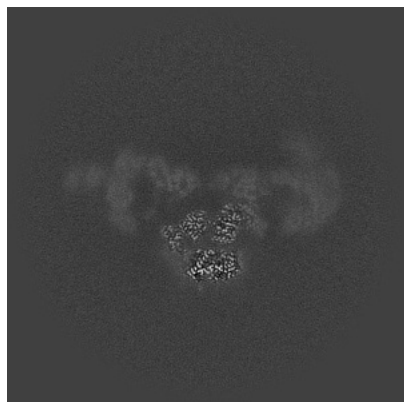


Z Index: 200

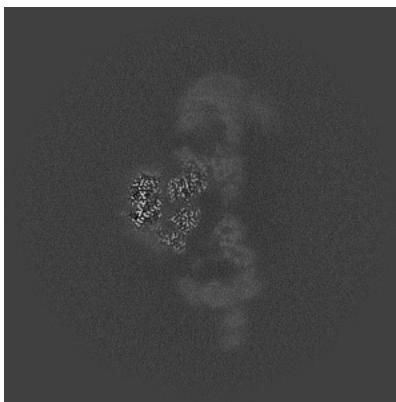
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

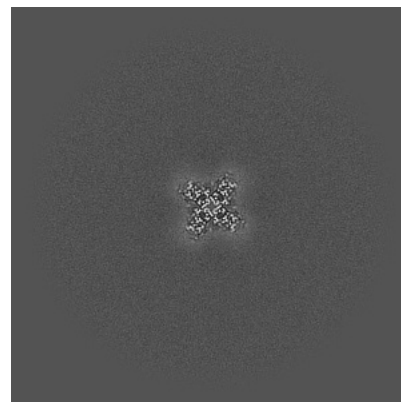
6.3.1 Primary map



X Index: 212

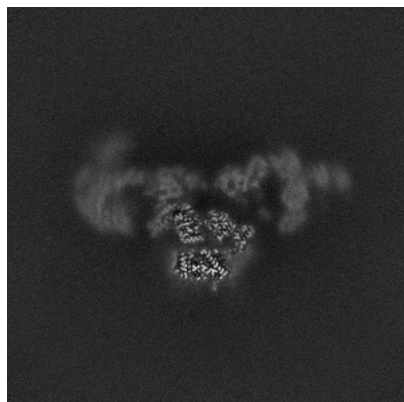


Y Index: 188

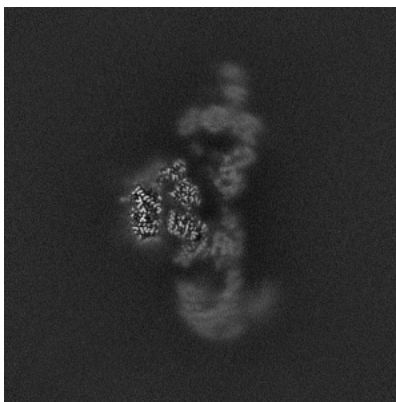


Z Index: 137

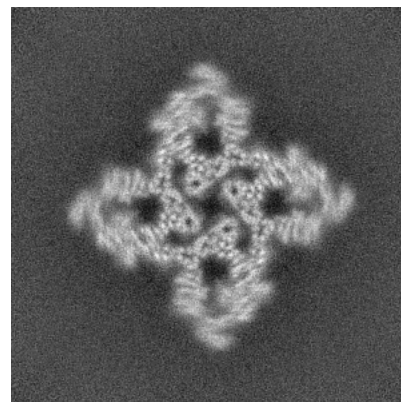
6.3.2 Raw map



X Index: 188



Y Index: 212

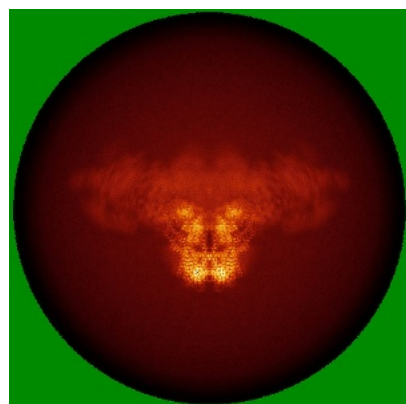


Z Index: 225

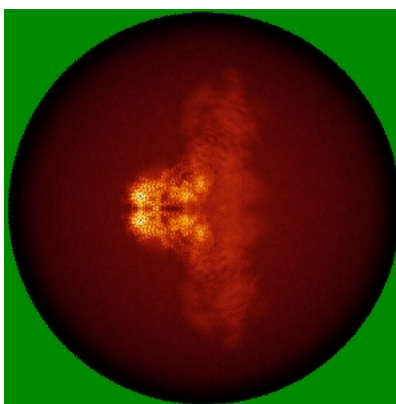
The images above show the largest variance slices of the map in three orthogonal directions.

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

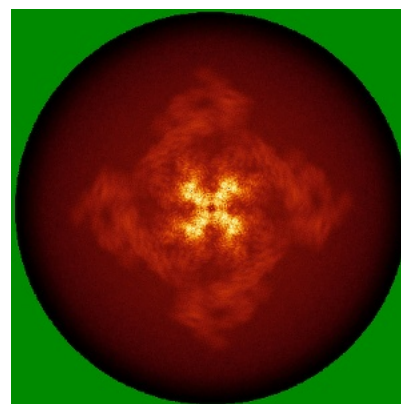
6.4.1 Primary map



X



Y

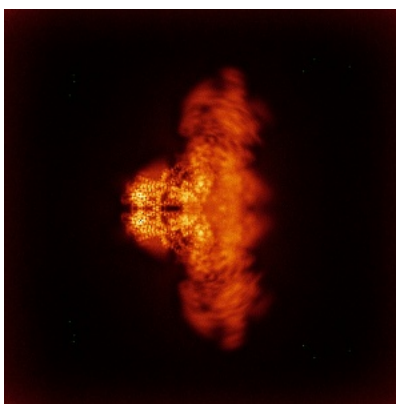


Z

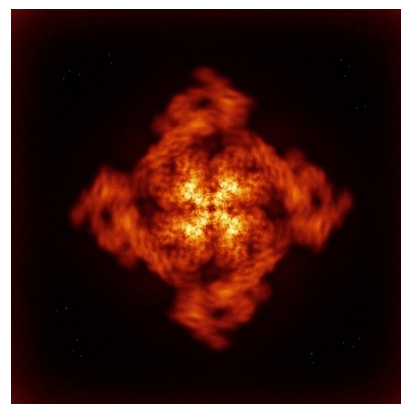
6.4.2 Raw map



X



Y

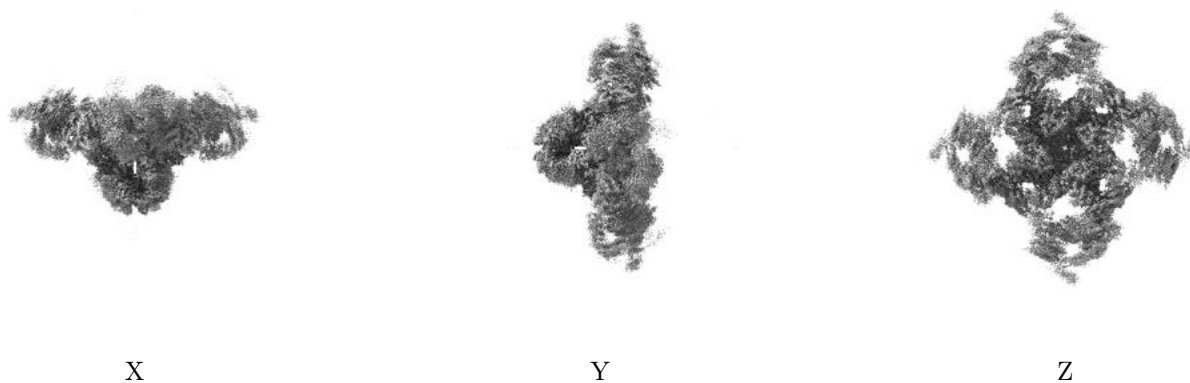


Z

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 0.585. 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.

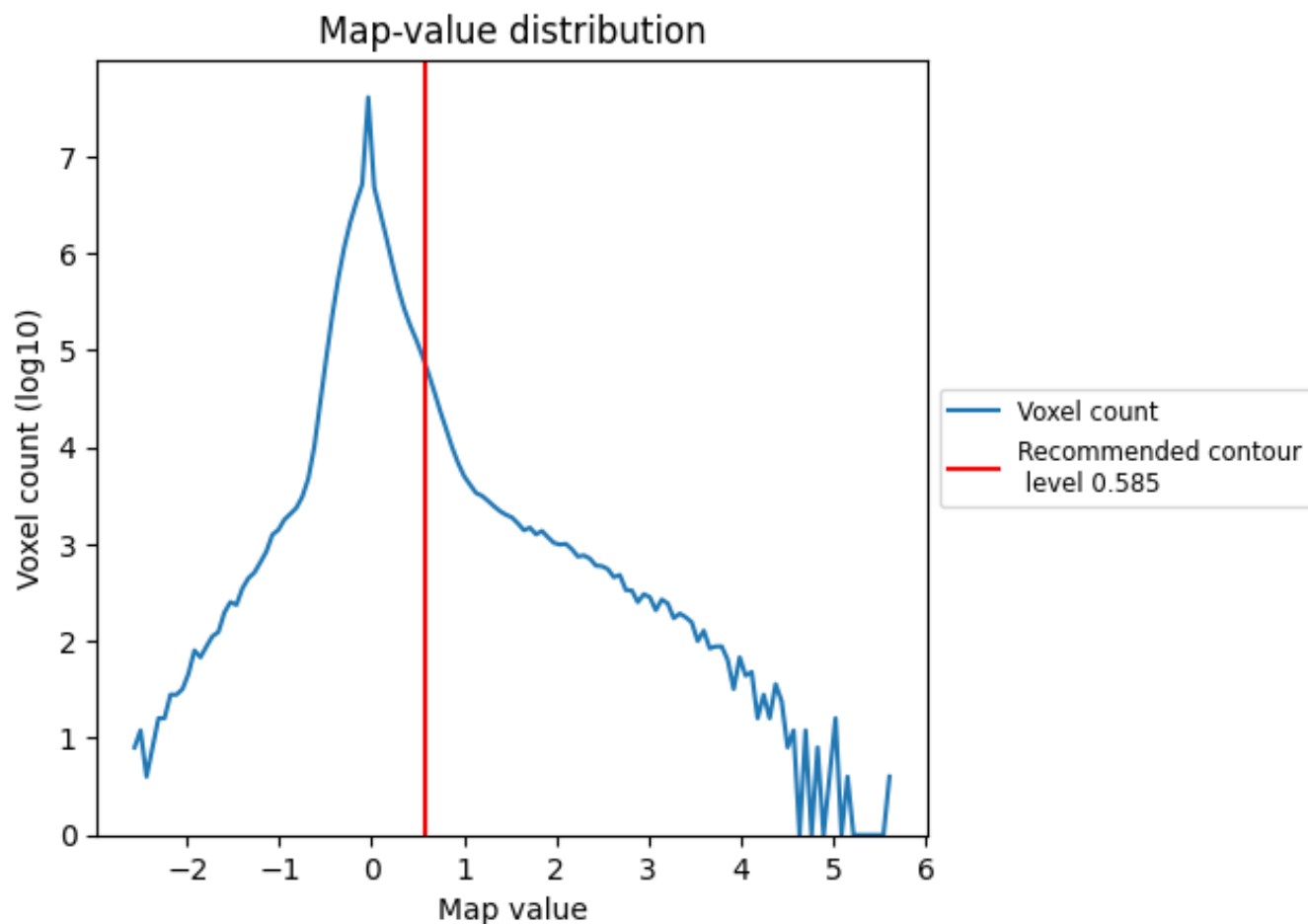
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

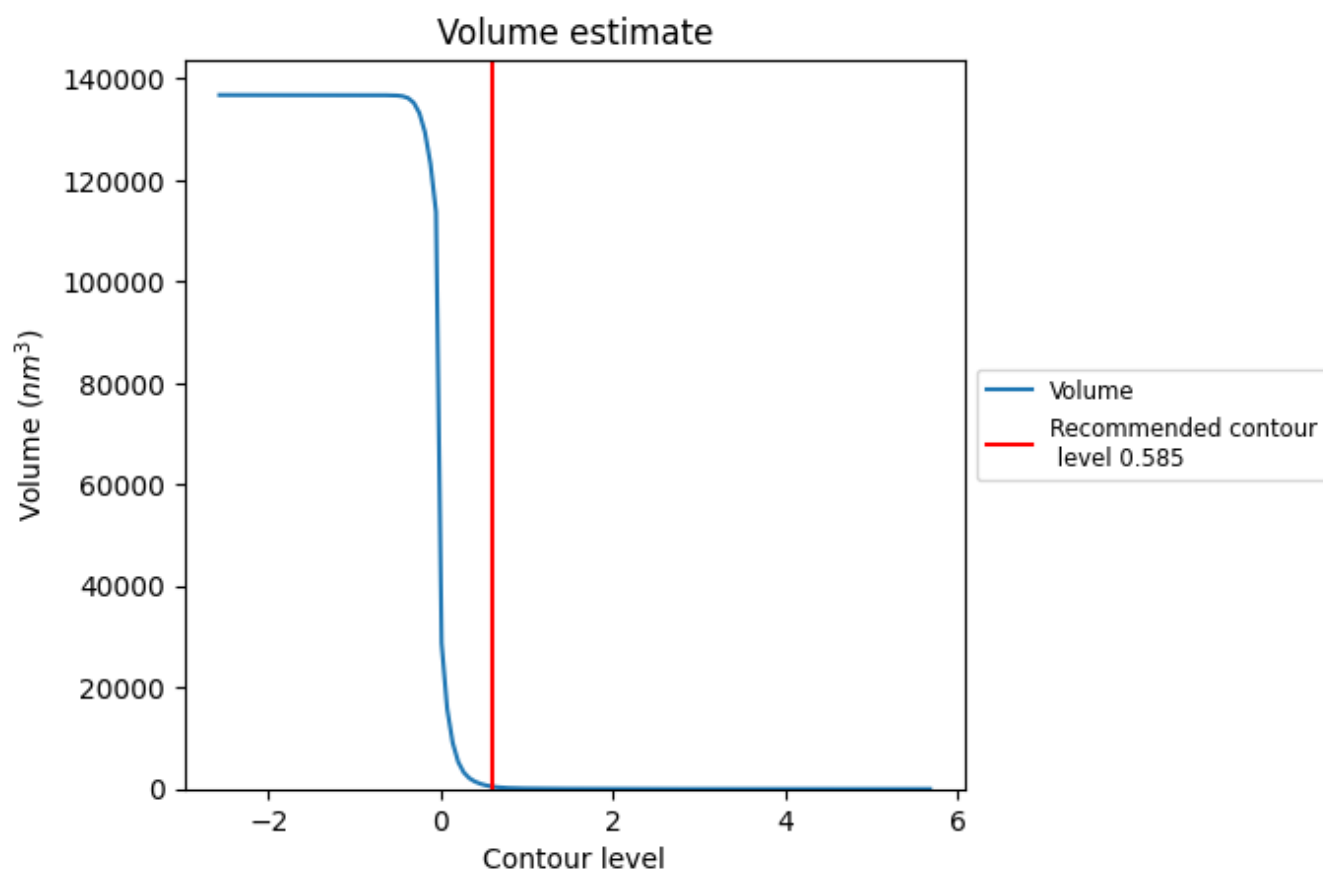
This section contains the results of statistical analysis of the map.

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.

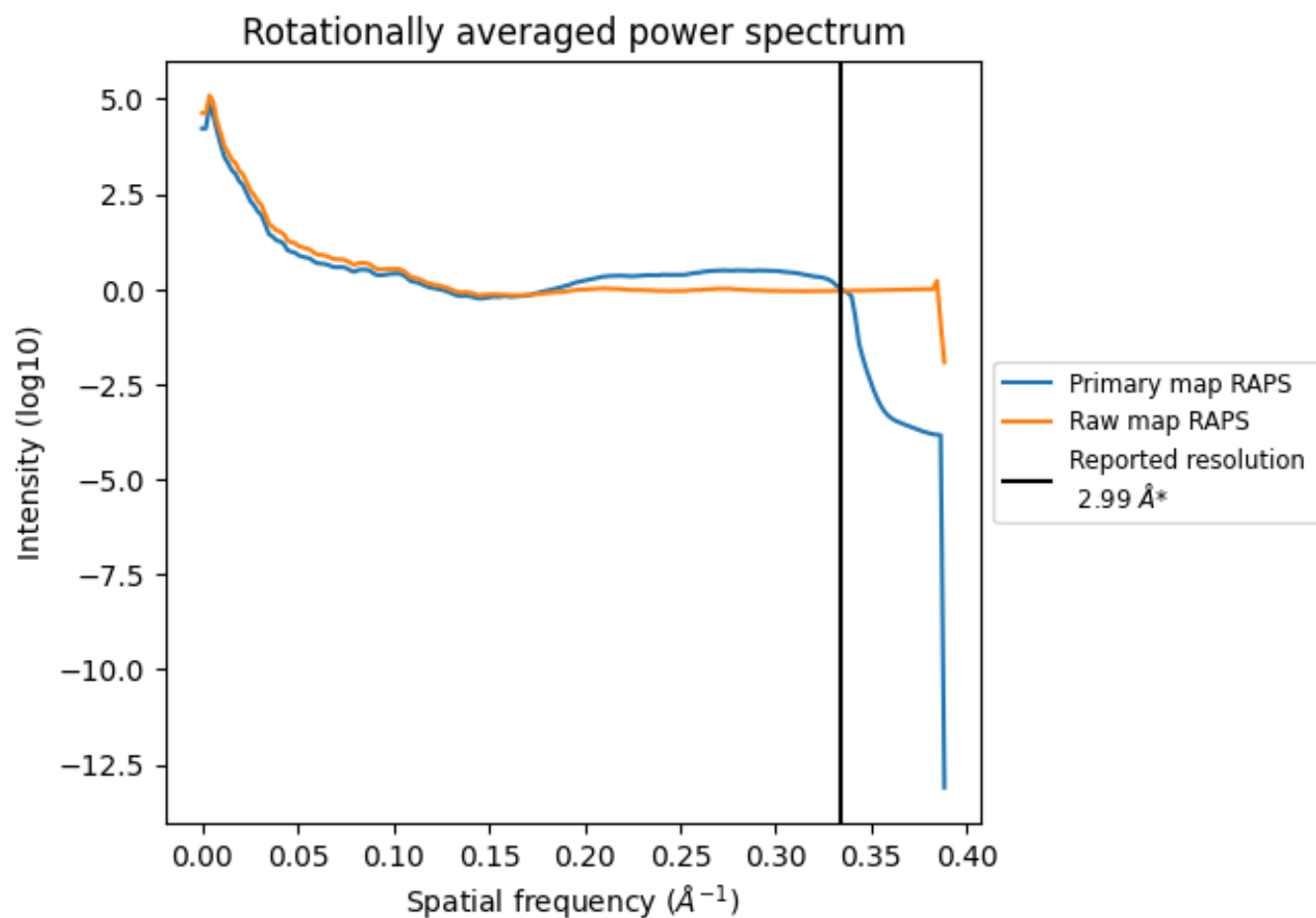
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 502 nm^3 ; this corresponds to an approximate mass of 453 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 ⓘ

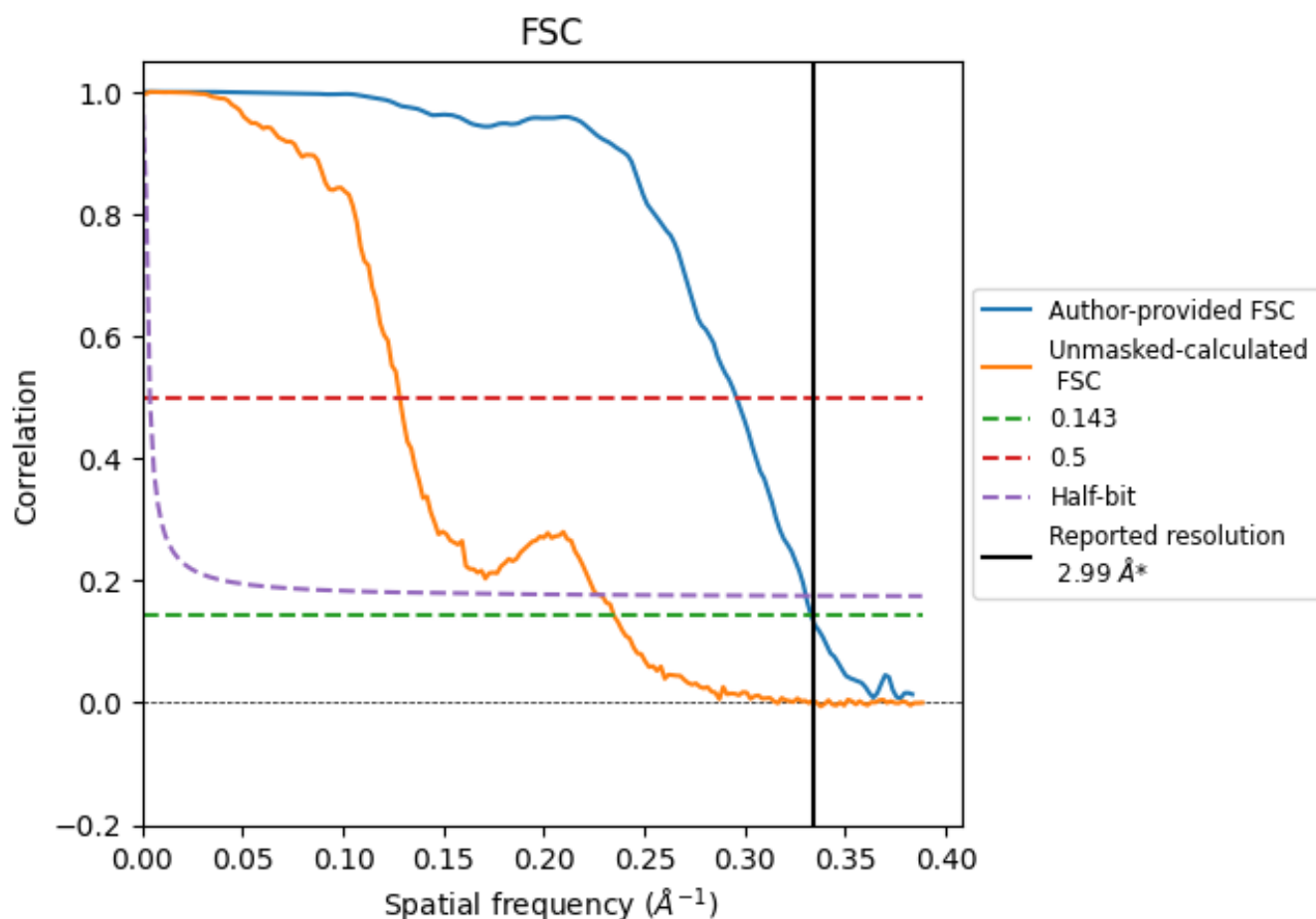


*Reported resolution corresponds to spatial frequency of 0.334 $\text{\AA}^{-1}$

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 $0.334 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

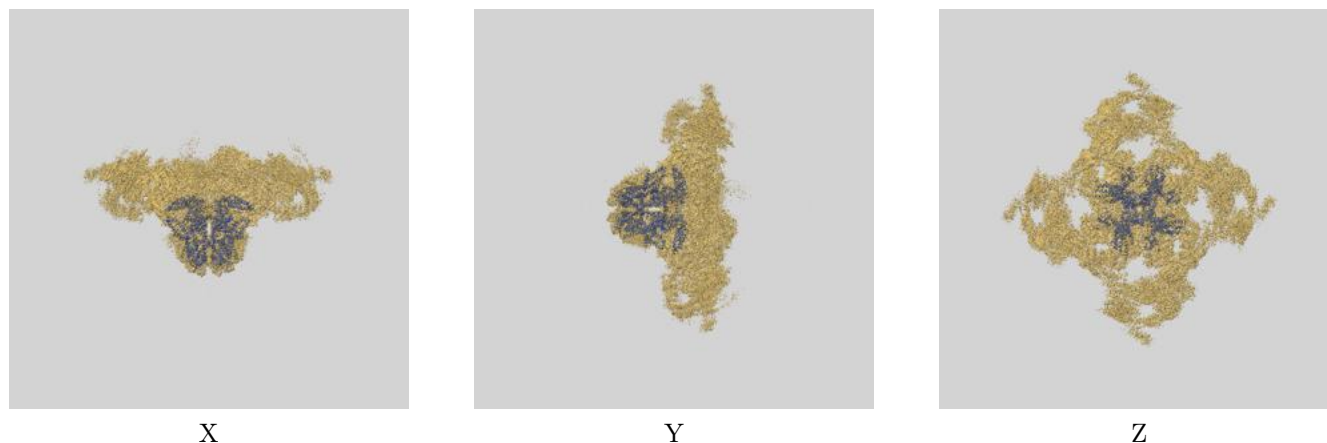
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.99	-	-
Author-provided FSC curve	3.00	3.38	3.03
Unmasked-calculated*	4.26	7.80	4.40

*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 4.26 differs from the reported value 2.99 by more than 10 %

9 Map-model fit [i](#)

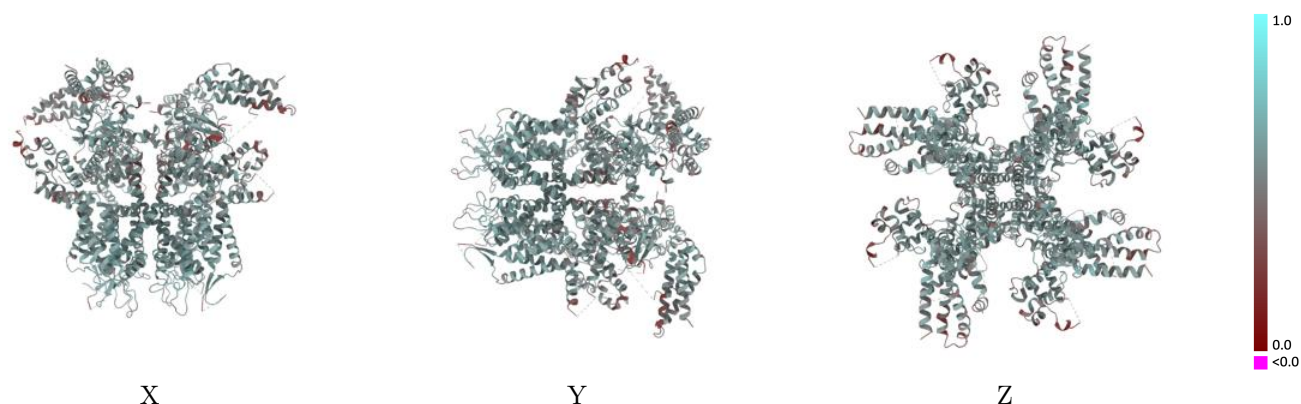
This section contains information regarding the fit between EMDB map EMD-40433 and PDB model 8SEY. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.585 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](#)

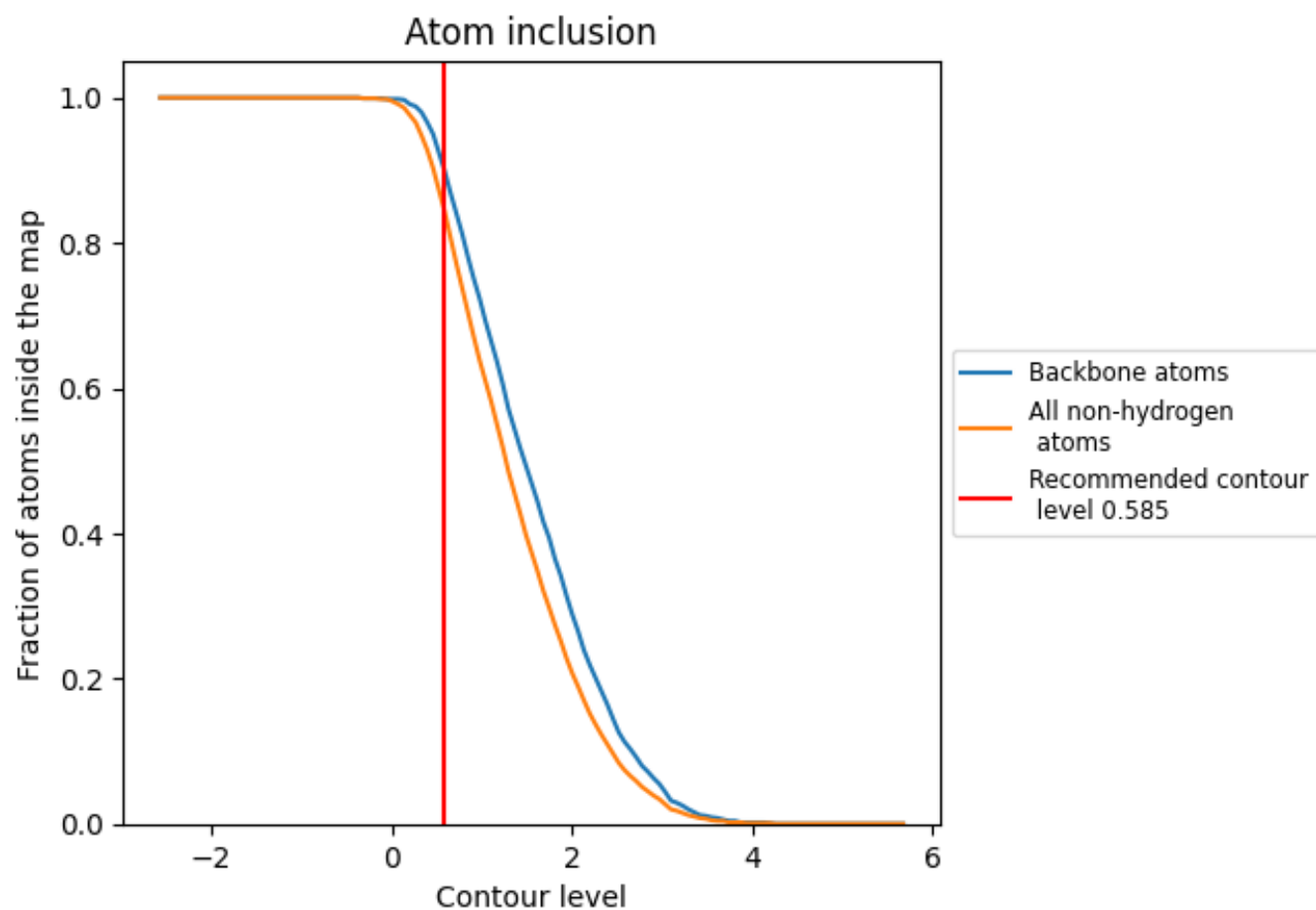


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 84% 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 (0.585) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8450	0.5450
A	0.8450	0.5450
B	0.8450	0.5440
C	0.8450	0.5450
D	0.8450	0.5450

