



Full wwPDB EM Validation Report ⓘ

Jun 22, 2026 – 12:39 PM EDT

PDB ID : 9YNO / pdb_00009yno
EMDB ID : EMD-73219
Title : Human type 2 IP3 receptor dimer (IP3/ATP/Ca2+)
Authors : Liu, C.; Lan, Y.; Tang, Q.; Karakas, E.
Deposited on : 2025-10-11
Resolution : 4.06 Å(reported)

This is a Full wwPDB EM Validation 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

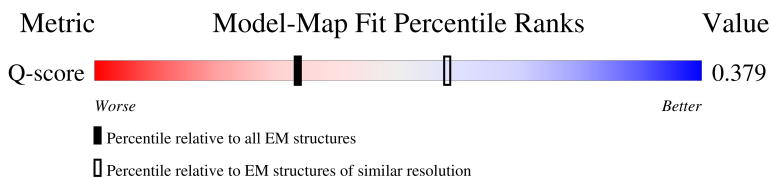
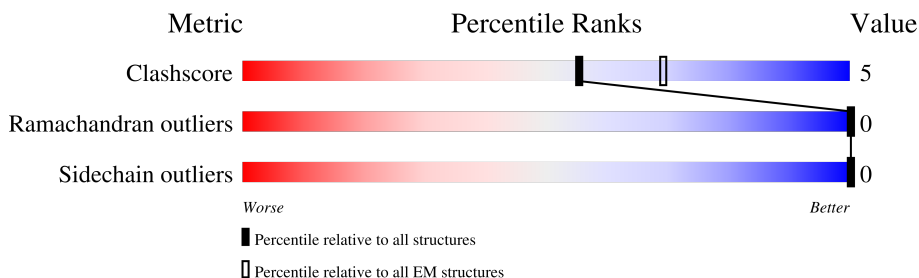
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.06 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	6515 (3.56 - 4.56)

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	2745	 64% 12% 23%
1	B	2745	 6% 57% 43%
1	C	2745	 15% 85%
1	D	2745	 15% 85%

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Mol	Chain	Length	Quality of chain
1	E	2745	 A horizontal bar chart showing the quality of chain E. The bar is divided into three segments: a red segment at the beginning, a green segment labeled '25%', a yellow segment labeled '5%', and a grey segment labeled '70%'. The red segment is very small, followed by the green segment, then the yellow segment, and finally the large grey segment.

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 34590 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 Inositol 1,4,5-trisphosphate-gated calcium channel ITPR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2102	Total	C	N	O	S	0	0
			15856	10005	2797	2965	89		
1	B	1572	Total	C	N	O		0	0
			7801	4657	1572	1572			
1	C	420	Total	C	N	O		0	0
			2080	1240	420	420			
1	D	411	Total	C	N	O		0	0
			2035	1213	411	411			
1	E	821	Total	C	N	O	S	0	0
			6640	4225	1150	1230	35		

There are 220 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2702	ALA	-	expression tag	UNP Q14571
A	2703	SER	-	expression tag	UNP Q14571
A	2704	ALA	-	expression tag	UNP Q14571
A	2705	SER	-	expression tag	UNP Q14571
A	2706	ASN	-	expression tag	UNP Q14571
A	2707	GLY	-	expression tag	UNP Q14571
A	2708	LEU	-	expression tag	UNP Q14571
A	2709	VAL	-	expression tag	UNP Q14571
A	2710	PRO	-	expression tag	UNP Q14571
A	2711	ARG	-	expression tag	UNP Q14571
A	2712	GLY	-	expression tag	UNP Q14571
A	2713	SER	-	expression tag	UNP Q14571
A	2714	ALA	-	expression tag	UNP Q14571
A	2715	ALA	-	expression tag	UNP Q14571
A	2716	ALA	-	expression tag	UNP Q14571
A	2717	GLY	-	expression tag	UNP Q14571
A	2718	TRP	-	expression tag	UNP Q14571
A	2719	SER	-	expression tag	UNP Q14571
A	2720	HIS	-	expression tag	UNP Q14571
A	2721	PRO	-	expression tag	UNP Q14571

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2722	GLN	-	expression tag	UNP Q14571
A	2723	PHE	-	expression tag	UNP Q14571
A	2724	GLU	-	expression tag	UNP Q14571
A	2725	LYS	-	expression tag	UNP Q14571
A	2726	GLY	-	expression tag	UNP Q14571
A	2727	GLY	-	expression tag	UNP Q14571
A	2728	GLY	-	expression tag	UNP Q14571
A	2729	SER	-	expression tag	UNP Q14571
A	2730	GLY	-	expression tag	UNP Q14571
A	2731	GLY	-	expression tag	UNP Q14571
A	2732	GLY	-	expression tag	UNP Q14571
A	2733	SER	-	expression tag	UNP Q14571
A	2734	GLY	-	expression tag	UNP Q14571
A	2735	GLY	-	expression tag	UNP Q14571
A	2736	SER	-	expression tag	UNP Q14571
A	2737	ALA	-	expression tag	UNP Q14571
A	2738	TRP	-	expression tag	UNP Q14571
A	2739	SER	-	expression tag	UNP Q14571
A	2740	HIS	-	expression tag	UNP Q14571
A	2741	PRO	-	expression tag	UNP Q14571
A	2742	GLN	-	expression tag	UNP Q14571
A	2743	PHE	-	expression tag	UNP Q14571
A	2744	GLU	-	expression tag	UNP Q14571
A	2745	LYS	-	expression tag	UNP Q14571
B	2702	ALA	-	expression tag	UNP Q14571
B	2703	SER	-	expression tag	UNP Q14571
B	2704	ALA	-	expression tag	UNP Q14571
B	2705	SER	-	expression tag	UNP Q14571
B	2706	ASN	-	expression tag	UNP Q14571
B	2707	GLY	-	expression tag	UNP Q14571
B	2708	LEU	-	expression tag	UNP Q14571
B	2709	VAL	-	expression tag	UNP Q14571
B	2710	PRO	-	expression tag	UNP Q14571
B	2711	ARG	-	expression tag	UNP Q14571
B	2712	GLY	-	expression tag	UNP Q14571
B	2713	SER	-	expression tag	UNP Q14571
B	2714	ALA	-	expression tag	UNP Q14571
B	2715	ALA	-	expression tag	UNP Q14571
B	2716	ALA	-	expression tag	UNP Q14571
B	2717	GLY	-	expression tag	UNP Q14571
B	2718	TRP	-	expression tag	UNP Q14571
B	2719	SER	-	expression tag	UNP Q14571

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2720	HIS	-	expression tag	UNP Q14571
B	2721	PRO	-	expression tag	UNP Q14571
B	2722	GLN	-	expression tag	UNP Q14571
B	2723	PHE	-	expression tag	UNP Q14571
B	2724	GLU	-	expression tag	UNP Q14571
B	2725	LYS	-	expression tag	UNP Q14571
B	2726	GLY	-	expression tag	UNP Q14571
B	2727	GLY	-	expression tag	UNP Q14571
B	2728	GLY	-	expression tag	UNP Q14571
B	2729	SER	-	expression tag	UNP Q14571
B	2730	GLY	-	expression tag	UNP Q14571
B	2731	GLY	-	expression tag	UNP Q14571
B	2732	GLY	-	expression tag	UNP Q14571
B	2733	SER	-	expression tag	UNP Q14571
B	2734	GLY	-	expression tag	UNP Q14571
B	2735	GLY	-	expression tag	UNP Q14571
B	2736	SER	-	expression tag	UNP Q14571
B	2737	ALA	-	expression tag	UNP Q14571
B	2738	TRP	-	expression tag	UNP Q14571
B	2739	SER	-	expression tag	UNP Q14571
B	2740	HIS	-	expression tag	UNP Q14571
B	2741	PRO	-	expression tag	UNP Q14571
B	2742	GLN	-	expression tag	UNP Q14571
B	2743	PHE	-	expression tag	UNP Q14571
B	2744	GLU	-	expression tag	UNP Q14571
B	2745	LYS	-	expression tag	UNP Q14571
C	2702	ALA	-	expression tag	UNP Q14571
C	2703	SER	-	expression tag	UNP Q14571
C	2704	ALA	-	expression tag	UNP Q14571
C	2705	SER	-	expression tag	UNP Q14571
C	2706	ASN	-	expression tag	UNP Q14571
C	2707	GLY	-	expression tag	UNP Q14571
C	2708	LEU	-	expression tag	UNP Q14571
C	2709	VAL	-	expression tag	UNP Q14571
C	2710	PRO	-	expression tag	UNP Q14571
C	2711	ARG	-	expression tag	UNP Q14571
C	2712	GLY	-	expression tag	UNP Q14571
C	2713	SER	-	expression tag	UNP Q14571
C	2714	ALA	-	expression tag	UNP Q14571
C	2715	ALA	-	expression tag	UNP Q14571
C	2716	ALA	-	expression tag	UNP Q14571
C	2717	GLY	-	expression tag	UNP Q14571

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Chain	Residue	Modelled	Actual	Comment	Reference
C	2718	TRP	-	expression tag	UNP Q14571
C	2719	SER	-	expression tag	UNP Q14571
C	2720	HIS	-	expression tag	UNP Q14571
C	2721	PRO	-	expression tag	UNP Q14571
C	2722	GLN	-	expression tag	UNP Q14571
C	2723	PHE	-	expression tag	UNP Q14571
C	2724	GLU	-	expression tag	UNP Q14571
C	2725	LYS	-	expression tag	UNP Q14571
C	2726	GLY	-	expression tag	UNP Q14571
C	2727	GLY	-	expression tag	UNP Q14571
C	2728	GLY	-	expression tag	UNP Q14571
C	2729	SER	-	expression tag	UNP Q14571
C	2730	GLY	-	expression tag	UNP Q14571
C	2731	GLY	-	expression tag	UNP Q14571
C	2732	GLY	-	expression tag	UNP Q14571
C	2733	SER	-	expression tag	UNP Q14571
C	2734	GLY	-	expression tag	UNP Q14571
C	2735	GLY	-	expression tag	UNP Q14571
C	2736	SER	-	expression tag	UNP Q14571
C	2737	ALA	-	expression tag	UNP Q14571
C	2738	TRP	-	expression tag	UNP Q14571
C	2739	SER	-	expression tag	UNP Q14571
C	2740	HIS	-	expression tag	UNP Q14571
C	2741	PRO	-	expression tag	UNP Q14571
C	2742	GLN	-	expression tag	UNP Q14571
C	2743	PHE	-	expression tag	UNP Q14571
C	2744	GLU	-	expression tag	UNP Q14571
C	2745	LYS	-	expression tag	UNP Q14571
D	2702	ALA	-	expression tag	UNP Q14571
D	2703	SER	-	expression tag	UNP Q14571
D	2704	ALA	-	expression tag	UNP Q14571
D	2705	SER	-	expression tag	UNP Q14571
D	2706	ASN	-	expression tag	UNP Q14571
D	2707	GLY	-	expression tag	UNP Q14571
D	2708	LEU	-	expression tag	UNP Q14571
D	2709	VAL	-	expression tag	UNP Q14571
D	2710	PRO	-	expression tag	UNP Q14571
D	2711	ARG	-	expression tag	UNP Q14571
D	2712	GLY	-	expression tag	UNP Q14571
D	2713	SER	-	expression tag	UNP Q14571
D	2714	ALA	-	expression tag	UNP Q14571
D	2715	ALA	-	expression tag	UNP Q14571

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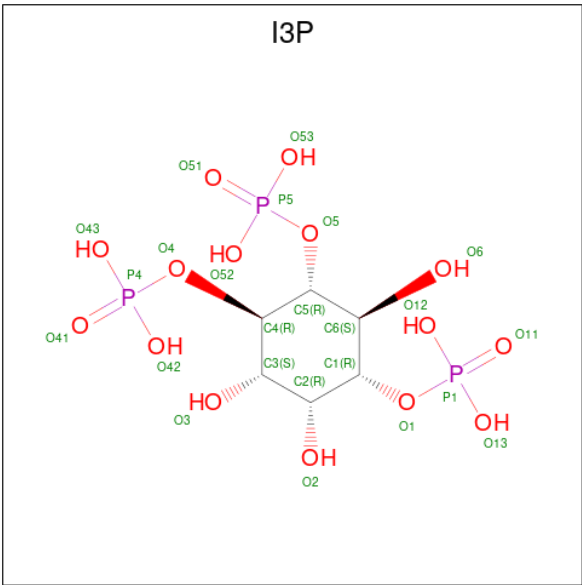
Chain	Residue	Modelled	Actual	Comment	Reference
D	2716	ALA	-	expression tag	UNP Q14571
D	2717	GLY	-	expression tag	UNP Q14571
D	2718	TRP	-	expression tag	UNP Q14571
D	2719	SER	-	expression tag	UNP Q14571
D	2720	HIS	-	expression tag	UNP Q14571
D	2721	PRO	-	expression tag	UNP Q14571
D	2722	GLN	-	expression tag	UNP Q14571
D	2723	PHE	-	expression tag	UNP Q14571
D	2724	GLU	-	expression tag	UNP Q14571
D	2725	LYS	-	expression tag	UNP Q14571
D	2726	GLY	-	expression tag	UNP Q14571
D	2727	GLY	-	expression tag	UNP Q14571
D	2728	GLY	-	expression tag	UNP Q14571
D	2729	SER	-	expression tag	UNP Q14571
D	2730	GLY	-	expression tag	UNP Q14571
D	2731	GLY	-	expression tag	UNP Q14571
D	2732	GLY	-	expression tag	UNP Q14571
D	2733	SER	-	expression tag	UNP Q14571
D	2734	GLY	-	expression tag	UNP Q14571
D	2735	GLY	-	expression tag	UNP Q14571
D	2736	SER	-	expression tag	UNP Q14571
D	2737	ALA	-	expression tag	UNP Q14571
D	2738	TRP	-	expression tag	UNP Q14571
D	2739	SER	-	expression tag	UNP Q14571
D	2740	HIS	-	expression tag	UNP Q14571
D	2741	PRO	-	expression tag	UNP Q14571
D	2742	GLN	-	expression tag	UNP Q14571
D	2743	PHE	-	expression tag	UNP Q14571
D	2744	GLU	-	expression tag	UNP Q14571
D	2745	LYS	-	expression tag	UNP Q14571
E	2702	ALA	-	expression tag	UNP Q14571
E	2703	SER	-	expression tag	UNP Q14571
E	2704	ALA	-	expression tag	UNP Q14571
E	2705	SER	-	expression tag	UNP Q14571
E	2706	ASN	-	expression tag	UNP Q14571
E	2707	GLY	-	expression tag	UNP Q14571
E	2708	LEU	-	expression tag	UNP Q14571
E	2709	VAL	-	expression tag	UNP Q14571
E	2710	PRO	-	expression tag	UNP Q14571
E	2711	ARG	-	expression tag	UNP Q14571
E	2712	GLY	-	expression tag	UNP Q14571
E	2713	SER	-	expression tag	UNP Q14571

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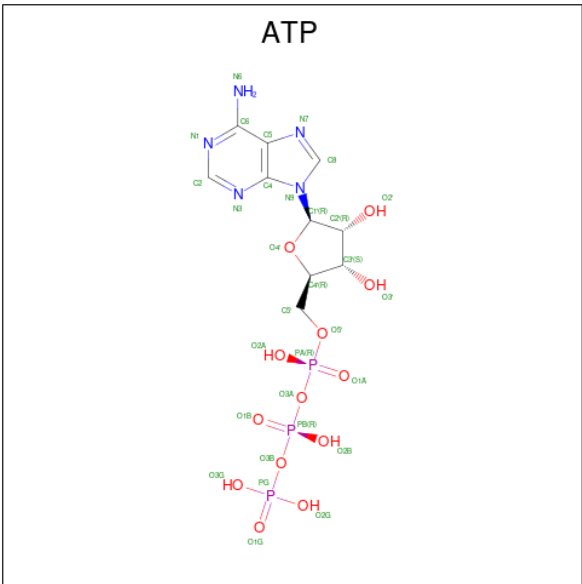
Chain	Residue	Modelled	Actual	Comment	Reference
E	2714	ALA	-	expression tag	UNP Q14571
E	2715	ALA	-	expression tag	UNP Q14571
E	2716	ALA	-	expression tag	UNP Q14571
E	2717	GLY	-	expression tag	UNP Q14571
E	2718	TRP	-	expression tag	UNP Q14571
E	2719	SER	-	expression tag	UNP Q14571
E	2720	HIS	-	expression tag	UNP Q14571
E	2721	PRO	-	expression tag	UNP Q14571
E	2722	GLN	-	expression tag	UNP Q14571
E	2723	PHE	-	expression tag	UNP Q14571
E	2724	GLU	-	expression tag	UNP Q14571
E	2725	LYS	-	expression tag	UNP Q14571
E	2726	GLY	-	expression tag	UNP Q14571
E	2727	GLY	-	expression tag	UNP Q14571
E	2728	GLY	-	expression tag	UNP Q14571
E	2729	SER	-	expression tag	UNP Q14571
E	2730	GLY	-	expression tag	UNP Q14571
E	2731	GLY	-	expression tag	UNP Q14571
E	2732	GLY	-	expression tag	UNP Q14571
E	2733	SER	-	expression tag	UNP Q14571
E	2734	GLY	-	expression tag	UNP Q14571
E	2735	GLY	-	expression tag	UNP Q14571
E	2736	SER	-	expression tag	UNP Q14571
E	2737	ALA	-	expression tag	UNP Q14571
E	2738	TRP	-	expression tag	UNP Q14571
E	2739	SER	-	expression tag	UNP Q14571
E	2740	HIS	-	expression tag	UNP Q14571
E	2741	PRO	-	expression tag	UNP Q14571
E	2742	GLN	-	expression tag	UNP Q14571
E	2743	PHE	-	expression tag	UNP Q14571
E	2744	GLU	-	expression tag	UNP Q14571
E	2745	LYS	-	expression tag	UNP Q14571

- Molecule 2 is D-MYO-INOSITOL-1,4,5-TRIPHOSPHATE (CCD ID: I3P) (formula: $C_6H_{15}O_{15}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	O	P	0
			24	6	15	3	
2	E	1	Total	C	O	P	0
			24	6	15	3	

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (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	

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Mol	Chain	Residues	Atoms					AltConf
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	

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

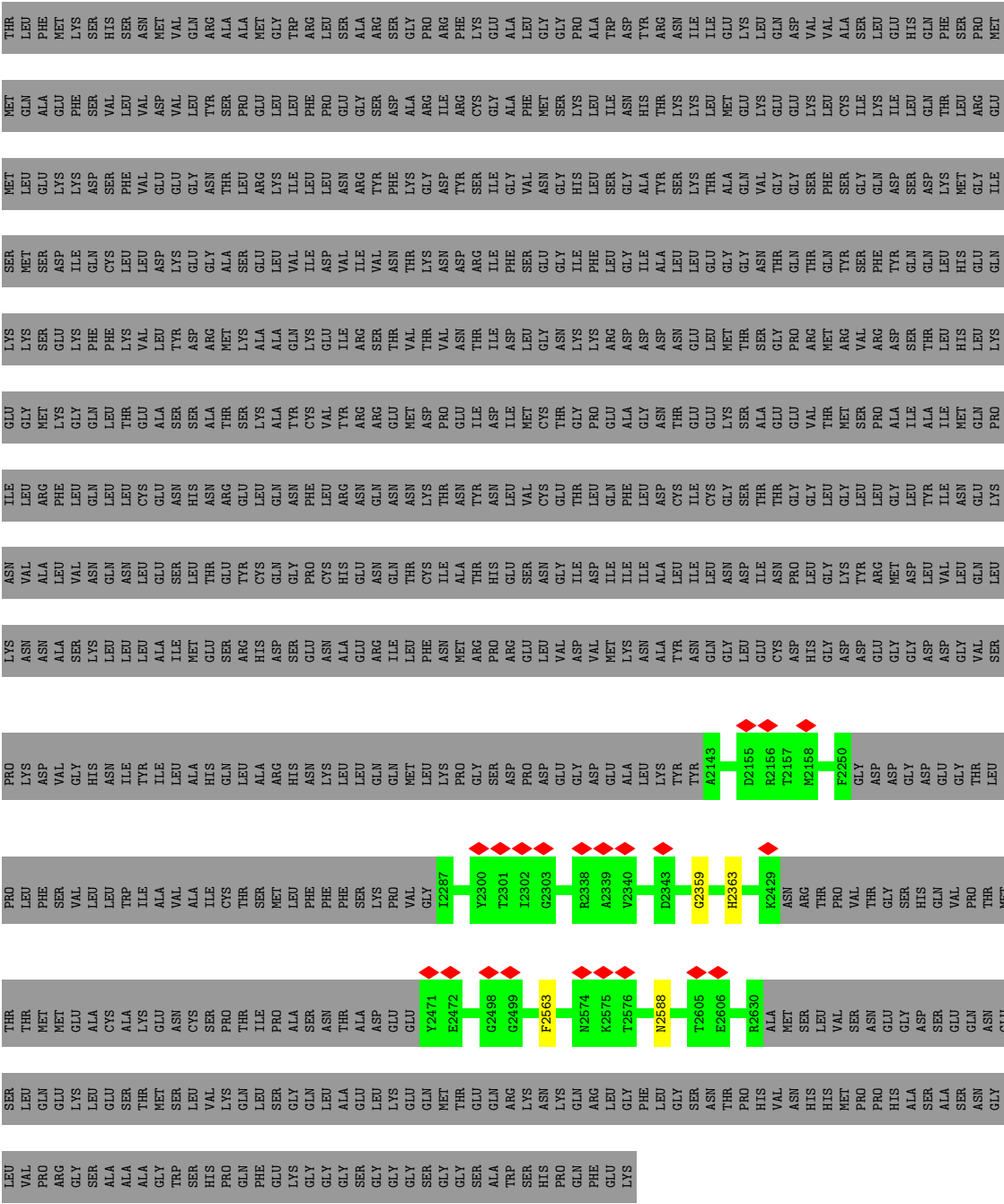
Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Ca	0
			1	1	
5	B	1	Total	Ca	0
			1	1	



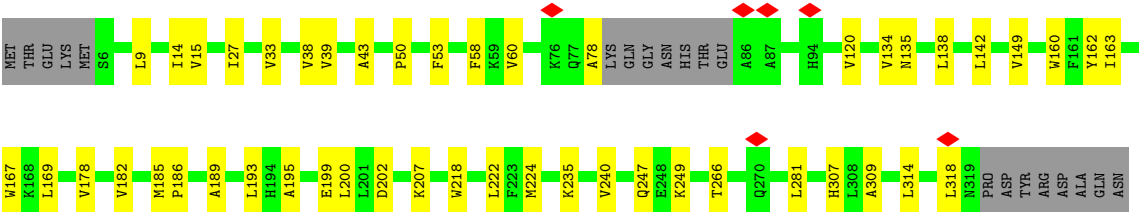








● Molecule 1: Inositol 1,4,5-trisphosphate-gated calcium channel ITPR2







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	144037	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 ($e^-/\text{\AA}^2$)	54.7	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.563	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	420.864, 420.864, 420.864	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.822, 0.822, 0.822	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: ATP, I3P, 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	0.15	0/16100	0.31	0/21793
1	B	0.08	0/7786	0.24	0/10841
1	C	0.08	0/2077	0.24	0/2891
1	D	0.08	0/2032	0.23	0/2828
1	E	0.11	0/6760	0.28	0/9132
All	All	0.12	0/34755	0.28	0/47485

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	15856	0	14876	214	0
1	B	7801	0	3367	2	0
1	C	2080	0	900	1	0
1	D	2035	0	879	3	0
1	E	6640	0	6697	90	0
2	A	24	0	9	1	0
2	E	24	0	9	0	0
3	A	31	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	31	0	12	0	0
3	C	31	0	12	0	0
3	D	31	0	12	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
All	All	34590	0	26785	305	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.

All (305) 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:2562:CYS:HB3	1:A:2565:CYS:SG	2.21	0.81
1:E:38:VAL:HG11	1:E:200:LEU:HD11	1.68	0.75
1:E:178:VAL:HG11	1:E:222:LEU:HB2	1.68	0.74
1:A:142:LEU:HB3	1:A:198:ILE:HD12	1.69	0.74
1:A:178:VAL:HG11	1:A:222:LEU:HB2	1.69	0.74
1:A:1982:VAL:HG21	1:A:2036:LEU:HB3	1.68	0.73
1:A:2042:ASN:HB2	1:A:2104:VAL:HG22	1.70	0.72
1:A:251:LEU:HG	1:A:262:ILE:HD11	1.72	0.71
1:A:1275:ARG:HH11	1:A:1315:THR:HG21	1.56	0.71
1:E:787:VAL:HG21	1:E:867:LEU:HD11	1.74	0.70
1:A:1974:GLY:HA2	1:A:2026:ILE:HG23	1.75	0.69
1:A:1100:LEU:HD11	1:A:1206:LEU:HD13	1.75	0.69
1:A:63:MET:HE1	1:A:122:GLN:HG3	1.74	0.68
1:A:308:LEU:HD21	1:A:439:VAL:HG23	1.76	0.68
1:A:1814:MET:HA	1:A:1918:MET:HE1	1.75	0.67
1:A:1973:LEU:HD21	1:A:2021:LEU:HD23	1.77	0.67
1:A:2124:GLN:HA	1:A:2127:LYS:HG2	1.77	0.66
1:E:363:ILE:HD12	1:E:366:LEU:HD12	1.78	0.66
1:E:281:LEU:HD12	1:E:442:LEU:HD13	1.79	0.65
1:E:249:LYS:HE3	1:E:266:THR:HG22	1.77	0.65
1:A:802:ARG:HH22	1:A:990:SER:HB2	1.61	0.65
1:A:2070:PRO:HB3	1:A:2122:LEU:HD13	1.79	0.64
1:A:835:MET:HE2	1:A:876:PHE:HB3	1.79	0.64
1:A:2562:CYS:CB	1:A:2565:CYS:SG	2.84	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:ARG:NH2	1:E:673:MET:HA	2.12	0.63
1:A:2048:LEU:HD23	1:A:2051:ILE:HD12	1.80	0.63
1:A:134:VAL:HG22	1:A:149:VAL:HG22	1.80	0.63
1:A:1355:LEU:HG	1:A:1359:MET:HE2	1.80	0.62
1:A:1926:GLN:HG3	1:A:1994:GLU:HG3	1.82	0.62
1:E:134:VAL:HG22	1:E:149:VAL:HG22	1.82	0.61
1:A:657:LEU:HD11	1:A:752:ILE:HD11	1.83	0.61
1:A:469:ARG:HA	1:A:472:VAL:HG12	1.84	0.60
1:E:558:ARG:HH11	1:E:561:ARG:HD3	1.66	0.60
1:A:640:SER:HB3	1:A:645:ILE:HD11	1.84	0.60
1:A:1939:PHE:O	1:A:1943:GLN:HG3	2.02	0.60
1:A:709:ILE:HG12	1:A:770:LEU:HD21	1.82	0.59
1:A:734:LEU:HD22	1:A:781:LEU:HD22	1.85	0.59
1:D:2563:PHE:H	3:D:2801:ATP:HN62	1.48	0.59
1:E:186:PRO:HG2	1:E:189:ALA:HB3	1.84	0.59
1:A:761:ILE:HG21	1:A:782:MET:HB2	1.84	0.59
1:A:1196:ASN:HD21	1:A:1198:LYS:HE3	1.65	0.59
1:A:623:ARG:HG2	1:A:664:ILE:HG21	1.85	0.59
1:E:193:LEU:HB2	1:E:218:TRP:HE1	1.68	0.58
1:A:1053:GLY:HA3	1:A:1702:ARG:HD2	1.84	0.58
1:A:2603:ASP:HB3	1:A:2606:GLU:HB2	1.84	0.58
1:A:298:GLN:HB3	1:A:301:SER:HB3	1.84	0.58
1:E:162:TYR:HB2	1:E:185:MET:O	2.04	0.57
1:A:14:ILE:HD13	1:A:224:MET:HB3	1.86	0.57
1:E:368:GLU:HB2	1:E:392:LEU:HD11	1.86	0.57
1:A:117:TYR:HE2	1:A:170:ARG:HB3	1.70	0.57
1:A:139:PRO:HG2	1:E:704:PRO:HB2	1.86	0.57
1:A:1078:GLN:HG2	1:A:1670:LEU:HD11	1.87	0.56
1:A:398:VAL:HG22	1:A:419:THR:HG22	1.86	0.56
1:E:789:ARG:HG3	1:E:791:PRO:HD2	1.88	0.56
1:A:234:LEU:HB3	1:A:381:VAL:HG23	1.87	0.56
1:A:831:PHE:HD2	1:A:876:PHE:HE2	1.53	0.56
1:E:564:GLN:HB3	1:E:574:ILE:HD12	1.86	0.56
1:A:1818:GLN:OE1	1:A:1958:PHE:HA	2.05	0.56
1:E:167:TRP:NE1	1:E:169:LEU:HB3	2.20	0.56
1:E:745:GLN:HG3	1:E:747:LEU:H	1.70	0.56
1:A:137:ARG:HG2	1:E:671:VAL:HG11	1.89	0.55
1:A:1982:VAL:HG11	1:A:2036:LEU:HD13	1.87	0.55
1:A:1217:LEU:HD22	1:A:1262:LEU:HD12	1.87	0.55
1:A:14:ILE:HG22	1:A:57:LEU:HD12	1.89	0.55
1:A:1346:TYR:HB2	1:A:1355:LEU:HD22	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2177:LYS:HG2	1:A:2590:TRP:CE2	2.42	0.55
1:A:59:LYS:HD3	1:A:124:LEU:HD23	1.90	0.54
1:A:1246:CYS:SG	1:A:1256:LEU:HD12	2.47	0.54
1:A:761:ILE:O	1:A:765:VAL:HG23	2.06	0.54
1:A:783:LEU:HD13	1:A:867:LEU:HA	1.90	0.54
1:E:247:GLN:HB3	1:E:249:LYS:HD2	1.88	0.54
1:A:2120:LYS:O	1:A:2123:GLN:HG2	2.07	0.54
1:A:230:ARG:HB3	1:A:233:VAL:HG12	1.90	0.54
1:A:1297:VAL:HG13	1:A:1342:VAL:HG21	1.90	0.54
1:A:871:LEU:HD22	1:A:876:PHE:CD2	2.43	0.53
1:A:984:ARG:HH22	1:A:1086:GLN:HE21	1.55	0.53
1:E:581:MET:HB3	1:E:595:ILE:HD11	1.89	0.53
1:A:541:LEU:HD22	1:A:550:LYS:HB2	1.91	0.53
1:A:1682:LEU:HD23	1:A:1745:ILE:HG22	1.91	0.53
1:A:1093:ALA:O	1:A:1097:VAL:HG13	2.09	0.52
1:E:666:ILE:H	1:E:733:GLN:HE22	1.55	0.52
1:A:564:GLN:HB3	1:A:574:ILE:HD12	1.92	0.52
1:A:19:ALA:O	1:A:24:ASN:HA	2.10	0.52
1:A:137:ARG:HH21	1:E:673:MET:HA	1.74	0.52
1:A:2065:LEU:HG	1:A:2115:LEU:HD22	1.90	0.52
1:E:307:HIS:CE1	1:E:309:ALA:HB3	2.45	0.52
1:A:585:ILE:HD11	1:A:592:GLU:HG3	1.90	0.52
1:E:538:LEU:HD21	1:E:584:GLN:HG2	1.91	0.52
1:A:569:LYS:HZ2	2:A:2801:I3P:H6	1.75	0.52
1:A:765:VAL:HG22	1:A:778:PHE:HB3	1.91	0.52
1:A:1100:LEU:HB3	1:A:1105:ASP:HB3	1.91	0.52
1:A:803:LEU:HD11	1:A:1106:VAL:HG22	1.92	0.52
1:B:639:VAL:HA	1:B:644:ALA:HA	1.92	0.52
1:A:1094:PHE:O	1:A:1097:VAL:HG22	2.09	0.51
1:A:1996:CYS:SG	1:A:2007:ILE:HD12	2.50	0.51
1:A:2116:ALA:HB1	1:A:2123:GLN:HB3	1.92	0.51
1:E:448:ALA:HA	1:E:475:LEU:HD11	1.92	0.51
1:A:369:LEU:HD22	1:A:387:VAL:HG21	1.92	0.51
1:A:1629:VAL:HG13	1:A:1681:MET:HG2	1.92	0.51
1:A:9:LEU:HB3	1:A:176:ILE:HG23	1.93	0.51
1:E:14:ILE:HB	1:E:224:MET:HB2	1.92	0.51
1:E:314:LEU:HD11	1:E:354:LEU:HD13	1.92	0.51
1:A:263:PHE:CG	1:A:414:MET:HB2	2.46	0.51
1:A:523:LYS:HG2	1:A:580:VAL:HG21	1.93	0.50
1:A:666:ILE:HG21	1:A:695:LEU:HD23	1.94	0.50
1:A:308:LEU:HD23	1:A:442:LEU:HD23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:786:HIS:HB3	1:E:831:PHE:HE1	1.76	0.50
1:A:1077:LEU:HD13	1:A:1674:ILE:HD11	1.94	0.50
1:A:2023:LEU:HD21	1:A:2073:LEU:HD12	1.92	0.50
1:E:163:ILE:HD11	1:E:182:VAL:HG11	1.92	0.50
1:A:988:ARG:HG2	1:A:1037:MET:HG2	1.94	0.49
1:A:2026:ILE:HG22	1:A:2029:LEU:HB3	1.93	0.49
1:A:162:TYR:HB2	1:A:185:MET:O	2.12	0.49
1:A:298:GLN:HB3	1:A:301:SER:CB	2.42	0.49
1:A:1633:TYR:HE1	1:A:1748:LEU:HD22	1.78	0.49
1:A:1606:LEU:HA	1:A:1609:VAL:HG22	1.94	0.49
1:A:518:VAL:O	1:A:521:ILE:HG22	2.13	0.49
1:A:581:MET:HB3	1:A:595:ILE:HD11	1.95	0.49
1:E:653:CYS:SG	1:E:740:MET:HG2	2.53	0.49
1:E:877:TYR:HD1	1:E:881:GLU:HB3	1.76	0.49
1:A:596:THR:O	1:A:600:HIS:HB2	2.13	0.48
1:A:606:LEU:HD22	1:A:645:ILE:HD13	1.95	0.48
1:A:1999:PRO:HD3	1:A:2609:GLY:HA3	1.95	0.48
1:A:1952:VAL:HG22	1:A:1995:TYR:CD2	2.48	0.48
1:E:672:SER:HA	1:E:691:GLU:HA	1.95	0.48
1:A:2023:LEU:HA	1:A:2076:VAL:HG21	1.96	0.48
1:E:644:ALA:HB2	1:E:742:LEU:HB3	1.95	0.48
1:A:259:LYS:HE2	1:A:261:HIS:CE1	2.49	0.48
1:A:98:LEU:O	1:A:101:LYS:HG3	2.13	0.48
1:A:1822:ARG:HD2	1:A:1961:CYS:SG	2.54	0.48
1:E:541:LEU:HD22	1:E:550:LYS:HB2	1.95	0.48
1:D:2359:GLY:HA2	1:D:2363:HIS:O	2.14	0.48
1:A:71:GLN:HE22	1:A:92:LEU:HD22	1.79	0.47
1:A:1324:VAL:HG12	1:A:1327:CYS:H	1.79	0.47
1:E:761:ILE:O	1:E:765:VAL:HG23	2.15	0.47
1:A:1122:THR:HA	1:A:1171:ILE:HD11	1.95	0.47
1:A:251:LEU:HD11	1:A:417:ILE:HG21	1.97	0.47
1:A:287:VAL:CG1	1:A:302:LEU:HB2	2.44	0.47
1:A:1219:LEU:O	1:A:1222:ILE:HG12	2.14	0.47
1:A:716:ALA:HB1	1:A:724:LEU:HD13	1.97	0.47
1:A:522:LEU:HD23	1:A:553:LEU:HD22	1.96	0.47
1:A:1918:MET:HG2	1:A:1958:PHE:CZ	2.49	0.47
1:A:879:PHE:HE1	1:A:983:VAL:HG23	1.79	0.47
1:E:469:ARG:HA	1:E:472:VAL:HG12	1.96	0.47
1:A:758:VAL:HA	1:A:782:MET:HE1	1.96	0.46
1:A:2079:ASN:HA	1:A:2082:ASN:ND2	2.30	0.46
1:E:635:SER:HB2	1:E:739:ARG:HG3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:ILE:HD12	1:A:366:LEU:HD12	1.96	0.46
1:A:1808:LYS:HB2	1:A:1949:TYR:HE2	1.80	0.46
1:A:87:ALA:O	1:A:90:LYS:HG3	2.15	0.46
1:A:984:ARG:NH2	1:A:1086:GLN:HE21	2.13	0.46
1:A:703:GLU:O	1:A:703:GLU:HG2	2.14	0.46
1:A:2572:PHE:HA	1:A:2575:LYS:HD2	1.96	0.46
1:E:841:TYR:HD2	1:E:864:VAL:HG11	1.80	0.46
1:E:970:LYS:HA	1:E:973:ILE:HD12	1.96	0.46
1:A:744:ARG:HB3	1:A:746:TYR:CZ	2.50	0.46
1:A:410:GLU:HG3	1:A:411:ARG:H	1.81	0.46
1:E:843:LYS:NZ	1:E:888:THR:HG21	2.30	0.46
1:E:886:THR:HG23	1:E:977:LEU:HD21	1.97	0.46
1:A:1239:HIS:O	1:A:1243:GLN:HG3	2.15	0.46
1:A:68:ALA:O	1:A:71:GLN:HG3	2.15	0.46
1:E:626:ARG:HA	1:E:626:ARG:HD3	1.68	0.46
1:A:882:LEU:HB3	1:A:980:ILE:HD12	1.98	0.45
1:E:142:LEU:HD11	1:E:200:LEU:HA	1.98	0.45
1:A:707:LYS:HE2	1:A:711:HIS:CE1	2.51	0.45
1:A:1255:LEU:HD23	1:A:1255:LEU:HA	1.79	0.45
1:A:2577:VAL:HG21	1:A:2633:SER:HB2	1.99	0.45
1:D:2588:ASN:HA	3:D:2801:ATP:N7	2.31	0.45
1:A:1330:MET:O	1:A:1334:GLU:HG2	2.16	0.45
1:A:2523:LEU:O	1:A:2527:ILE:CB	2.65	0.45
1:E:364:ALA:O	1:E:391:HIS:HE1	2.00	0.45
1:A:672:SER:HA	1:A:691:GLU:HG2	1.98	0.45
1:A:672:SER:HB2	1:A:674:GLN:HG2	1.99	0.45
1:A:1207:LEU:HD23	1:A:1207:LEU:HA	1.85	0.45
1:A:1672:ILE:HG23	1:A:1773:GLU:HG3	1.97	0.45
1:A:1808:LYS:HB2	1:A:1949:TYR:CE2	2.52	0.45
1:A:352:TYR:HB2	1:A:419:THR:OG1	2.17	0.45
1:E:405:ILE:HD11	1:E:416:LYS:HG3	1.98	0.45
1:E:33:VAL:HG11	1:E:478:ASP:OD1	2.16	0.45
1:E:518:VAL:O	1:E:521:ILE:HG22	2.17	0.45
1:A:1629:VAL:HG21	1:A:1680:GLU:HG3	1.99	0.45
1:A:2074:VAL:HG21	1:A:2125:MET:HG3	1.99	0.45
1:E:373:THR:HG23	1:E:376:ARG:HH12	1.81	0.45
1:E:509:MET:HA	1:E:514:ILE:HD12	1.98	0.45
1:A:573:TYR:HA	1:A:576:LYS:HD3	1.98	0.45
1:A:978:GLN:HG3	1:A:1079:LEU:HD21	1.99	0.45
1:A:2194:ASN:O	1:A:2198:GLN:HG2	2.17	0.45
1:A:314:LEU:HD23	1:A:367:PHE:HE2	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2359:GLY:HA2	1:C:2363:HIS:O	2.16	0.44
1:A:2065:LEU:HD13	1:A:2119:ASN:HB2	1.98	0.44
1:A:714:GLN:HG3	1:E:78:ALA:HA	2.00	0.44
1:A:2015:ILE:HD12	1:A:2015:ILE:H	1.81	0.44
1:E:623:ARG:NH2	1:E:661:ASN:HA	2.32	0.44
1:E:578:PHE:CE1	1:E:595:ILE:HD12	2.52	0.44
1:E:657:LEU:HD11	1:E:752:ILE:HD11	2.00	0.44
1:E:666:ILE:N	1:E:733:GLN:HE22	2.14	0.44
1:A:1064:LEU:HG	1:A:1072:LEU:HD21	2.00	0.44
1:E:39:VAL:HG21	1:E:195:ALA:HB1	2.00	0.44
1:E:837:PHE:O	1:E:840:GLU:HG3	2.18	0.44
1:A:1964:GLY:HA3	1:A:1968:GLY:HA3	1.99	0.44
1:E:9:LEU:HD11	1:E:60:VAL:HG21	2.00	0.44
1:A:2597:VAL:O	1:A:2601:VAL:HG22	2.18	0.44
1:E:199:GLU:HG3	1:E:207:LYS:HE3	2.00	0.43
1:A:302:LEU:HD23	1:A:366:LEU:HD22	1.99	0.43
1:A:558:ARG:HA	1:A:558:ARG:HD3	1.78	0.43
1:A:1119:LEU:HD11	1:A:1182:VAL:HG13	2.00	0.43
1:A:1196:ASN:ND2	1:A:1198:LYS:HB3	2.33	0.43
1:A:1218:ASP:O	1:A:1222:ILE:HG23	2.18	0.43
1:E:744:ARG:HB3	1:E:746:TYR:CE2	2.54	0.43
1:A:17:LEU:HD12	1:A:27:ILE:HD11	2.00	0.43
1:A:162:TYR:CE2	1:A:187:VAL:HG22	2.54	0.43
1:A:2180:VAL:HB	1:A:2590:TRP:HH2	1.83	0.43
1:E:645:ILE:O	1:E:649:GLN:HB2	2.19	0.43
1:A:831:PHE:CD2	1:A:876:PHE:HE2	2.35	0.43
1:A:2169:CYS:HA	1:A:2207:MET:SD	2.59	0.43
1:E:536:LEU:HD21	1:E:541:LEU:HG	2.00	0.43
1:A:815:GLU:O	1:A:819:ILE:HG12	2.19	0.43
1:A:889:LEU:HD22	1:A:973:ILE:HG12	2.01	0.43
1:E:50:PRO:HD2	1:E:53:PHE:HD1	1.84	0.43
1:A:854:ASP:C	1:A:856:GLU:H	2.27	0.43
1:A:50:PRO:HD2	1:A:53:PHE:CD1	2.53	0.43
1:A:827:MET:HE3	1:A:827:MET:HB3	1.79	0.43
1:A:2196:PHE:O	1:A:2200:THR:HG23	2.18	0.43
1:A:225:LYS:HE2	1:A:225:LYS:HB3	1.83	0.43
1:A:744:ARG:HB3	1:A:746:TYR:CE2	2.54	0.43
1:A:1036:THR:HB	1:A:1044:LYS:HB2	2.01	0.43
1:A:388:ARG:HE	1:A:423:LYS:HE2	1.84	0.42
1:A:619:VAL:O	1:A:623:ARG:HG3	2.19	0.42
1:B:2359:GLY:HA2	1:B:2363:HIS:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:202:ASP:HB3	1:E:471:PHE:CE1	2.53	0.42
1:E:399:THR:HG22	1:E:427:GLU:HG3	2.00	0.42
1:A:51:LYS:HD2	1:A:51:LYS:HA	1.90	0.42
1:A:230:ARG:HG2	1:A:232:ASP:H	1.84	0.42
1:A:304:ARG:HG2	1:A:365:SER:O	2.20	0.42
1:A:1068:ASP:OD1	1:A:1655:LYS:HD2	2.19	0.42
1:A:2158:MET:HG3	1:A:2630:ARG:NH2	2.34	0.42
1:A:2197:PHE:HA	1:A:2200:THR:HG23	2.00	0.42
1:E:445:ALA:HB1	1:E:514:ILE:HD11	2.00	0.42
1:E:711:HIS:O	1:E:714:GLN:HG2	2.19	0.42
1:A:349:LYS:HD2	1:A:401:THR:HG22	2.00	0.42
1:A:1917:ILE:C	1:A:1920:PRO:HD2	2.43	0.42
1:A:989:ILE:HD11	1:A:1093:ALA:HB1	2.01	0.42
1:E:617:THR:O	1:E:621:LEU:HG	2.20	0.42
1:A:63:MET:HE3	1:A:120:VAL:HG12	2.01	0.42
1:A:132:LEU:HA	1:A:151:LEU:HD23	2.00	0.42
1:A:1116:LEU:HD23	1:A:1116:LEU:HA	1.77	0.42
1:E:390:ARG:HB2	1:E:397:TRP:CZ3	2.55	0.42
1:A:699:ASP:HB2	1:A:703:GLU:HG2	2.02	0.42
1:A:792:GLN:HE21	1:A:876:PHE:HZ	1.65	0.42
1:A:835:MET:HG2	1:A:877:TYR:CE1	2.55	0.42
1:A:2203:LEU:HD13	1:A:2593:LEU:HD22	2.01	0.42
1:A:741:CYS:HB3	1:A:749:ILE:HG12	2.01	0.41
1:A:1919:GLN:HB3	1:A:1920:PRO:HD3	2.02	0.41
1:A:2038:LEU:HD13	1:A:2101:PRO:HG3	2.01	0.41
1:A:1204:GLN:OE1	1:A:1249:ASN:ND2	2.53	0.41
1:A:992:MET:O	1:A:995:ILE:HG22	2.20	0.41
1:A:1197:LYS:HG3	1:A:1200:ARG:NH2	2.35	0.41
1:E:135:ASN:ND2	1:E:138:LEU:HD23	2.35	0.41
1:E:235:LYS:HE2	1:E:235:LYS:HB2	1.93	0.41
1:A:1762:ILE:HD13	1:A:1806:PHE:HE1	1.86	0.41
1:A:287:VAL:HG11	1:A:302:LEU:HB2	2.02	0.41
1:A:727:LEU:HD23	1:A:727:LEU:HA	1.85	0.41
1:A:502:ASN:ND2	1:A:505:ARG:HG3	2.35	0.41
1:E:558:ARG:NH1	1:E:561:ARG:HD3	2.33	0.41
1:A:1081:PHE:HE1	1:A:1628:LEU:HD21	1.86	0.41
1:A:1818:GLN:O	1:A:1822:ARG:HD3	2.21	0.41
1:E:576:LYS:HA	1:E:576:LYS:HD2	1.91	0.41
1:E:973:ILE:HA	1:E:976:ILE:HD12	2.01	0.41
1:A:186:PRO:HG2	1:A:189:ALA:HB3	2.02	0.41
1:A:2106:HIS:CD2	1:A:2164:PRO:HB3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:MET:HB3	1:A:65:ARG:HH21	1.86	0.41
1:A:143:GLU:HB2	1:A:198:ILE:HD13	2.03	0.41
1:A:873:TYR:CE1	1:A:979:PHE:HB2	2.55	0.41
1:A:1657:ILE:HG23	1:A:1757:LEU:HD22	2.03	0.41
1:A:2203:LEU:O	1:A:2207:MET:HG3	2.21	0.41
1:A:2564:ILE:HD13	1:A:2564:ILE:HA	1.90	0.41
1:A:2610:PRO:O	1:A:2614:VAL:HG23	2.20	0.41
1:E:15:VAL:HG12	1:E:222:LEU:HA	2.02	0.41
1:E:240:VAL:HA	1:E:434:VAL:HG23	2.03	0.41
1:E:795:VAL:HG11	1:E:875:GLY:HA3	2.03	0.41
1:A:15:VAL:HB	1:A:220:ILE:HG23	2.02	0.41
1:E:120:VAL:HG13	1:E:160:TRP:HB3	2.02	0.41
1:A:602:ASN:HB3	1:A:605:LEU:HB2	2.02	0.40
1:A:1061:LEU:HA	1:A:1061:LEU:HD23	1.89	0.40
1:E:843:LYS:HZ2	1:E:888:THR:HG21	1.85	0.40
1:A:448:ALA:HA	1:A:475:LEU:HD11	2.02	0.40
1:A:2079:ASN:HA	1:A:2082:ASN:HD21	1.84	0.40
1:E:43:ALA:HB1	1:E:50:PRO:HB3	2.03	0.40
1:E:585:ILE:HG21	1:E:617:THR:HG21	2.02	0.40
1:A:1056:THR:O	1:A:1060:VAL:HG13	2.21	0.40
1:A:1356:LEU:HA	1:A:1359:MET:HE3	2.03	0.40
1:A:1927:LEU:HD23	1:A:1927:LEU:HA	1.90	0.40
1:E:27:ILE:HG23	1:E:58:PHE:HE2	1.87	0.40
1:E:602:ASN:HD22	1:E:602:ASN:HA	1.80	0.40
1:E:618:PHE:HE2	1:E:633:TYR:HB3	1.85	0.40
1:A:509:MET:O	1:A:514:ILE:HB	2.20	0.40
1:E:50:PRO:HD2	1:E:53:PHE:CD1	2.56	0.40
1:E:522:LEU:HD23	1:E:522:LEU:HA	1.91	0.40
1:E:789:ARG:HE	1:E:789:ARG:HB2	1.63	0.40
1:A:749:ILE:O	1:A:753:SER:HB3	2.22	0.40
1:A:1085:SER:O	1:A:1089:GLU:HG2	2.21	0.40
1:A:1312:PHE:O	1:A:1316:ILE:HG23	2.21	0.40
1:E:33:VAL:HG21	1:E:478:ASP:OD2	2.21	0.40
1:E:318:LEU:HA	1:E:352:TYR:CD1	2.56	0.40
1:E:824:ARG:O	1:E:828:LYS:HB2	2.22	0.40

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	2062/2745 (75%)	1988 (96%)	74 (4%)	0	100	100
1	B	1542/2745 (56%)	1501 (97%)	41 (3%)	0	100	100
1	C	414/2745 (15%)	409 (99%)	5 (1%)	0	100	100
1	D	405/2745 (15%)	398 (98%)	7 (2%)	0	100	100
1	E	805/2745 (29%)	785 (98%)	20 (2%)	0	100	100
All	All	5228/13725 (38%)	5081 (97%)	147 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	1561/2448 (64%)	1561 (100%)	0	100	100
1	E	739/2448 (30%)	739 (100%)	0	100	100
All	All	2300/4896 (47%)	2300 (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. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	384	ASN
1	A	714	GLN

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Mol	Chain	Res	Type
1	A	784	HIS
1	A	792	GLN
1	A	1086	GLN
1	A	1111	GLN
1	A	1118	GLN
1	A	1195	GLN
1	A	1221	GLN
1	A	1236	ASN
1	A	1249	ASN
1	A	1607	GLN
1	A	1764	ASN
1	A	1790	GLN
1	A	2106	HIS
1	A	2616	GLN
1	E	502	ASN
1	E	667	GLN
1	E	733	GLN
1	E	745	GLN
1	E	755	GLN
1	E	870	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	2801	-	32,33,33	0.28	0	48,52,52	0.39	0
3	ATP	C	2801	-	32,33,33	0.28	0	48,52,52	0.38	0
3	ATP	D	2801	-	32,33,33	0.28	0	48,52,52	0.38	0
3	ATP	A	2802	-	32,33,33	0.30	0	48,52,52	0.37	0
2	I3P	E	2801	-	24,24,24	2.17	3 (12%)	39,39,39	0.87	0
2	I3P	A	2801	-	24,24,24	2.17	3 (12%)	39,39,39	1.06	2 (5%)

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	2801	-	-	2/22/38/38	0/3/3/3
3	ATP	C	2801	-	-	5/22/38/38	0/3/3/3
3	ATP	D	2801	-	-	5/22/38/38	0/3/3/3
3	ATP	A	2802	-	-	7/22/38/38	0/3/3/3
2	I3P	E	2801	-	-	1/15/39/39	0/1/1/1
2	I3P	A	2801	-	-	6/15/39/39	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2801	I3P	P5-O5	5.98	1.70	1.59
2	E	2801	I3P	P5-O5	5.97	1.70	1.59
2	E	2801	I3P	P4-O4	5.90	1.69	1.59
2	A	2801	I3P	P4-O4	5.86	1.69	1.59
2	A	2801	I3P	P1-O1	5.66	1.69	1.59
2	E	2801	I3P	P1-O1	5.63	1.69	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2801	I3P	C5-C6-C1	3.66	116.52	109.11
2	A	2801	I3P	O43-P4-O42	2.00	115.31	107.80

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2802	ATP	PB-O3B-PG-O2G
3	A	2802	ATP	C5'-O5'-PA-O3A
3	A	2802	ATP	O4'-C4'-C5'-O5'
3	D	2801	ATP	PB-O3B-PG-O2G
3	A	2802	ATP	C3'-C4'-C5'-O5'
3	C	2801	ATP	C3'-C4'-C5'-O5'
3	A	2802	ATP	PB-O3B-PG-O1G
3	C	2801	ATP	O4'-C4'-C5'-O5'
3	A	2802	ATP	C5'-O5'-PA-O1A
3	C	2801	ATP	C5'-O5'-PA-O1A
3	D	2801	ATP	C5'-O5'-PA-O1A
3	D	2801	ATP	C5'-O5'-PA-O2A
3	D	2801	ATP	C5'-O5'-PA-O3A
2	A	2801	I3P	C1-O1-P1-O13
2	A	2801	I3P	C5-O5-P5-O52
3	B	2801	ATP	PG-O3B-PB-O3A
3	D	2801	ATP	PB-O3B-PG-O1G
2	A	2801	I3P	C1-O1-P1-O11
3	C	2801	ATP	PG-O3B-PB-O3A
3	B	2801	ATP	PG-O3B-PB-O1B
3	C	2801	ATP	PG-O3B-PB-O1B
2	A	2801	I3P	C1-O1-P1-O12
2	A	2801	I3P	C5-O5-P5-O53
2	E	2801	I3P	C4-O4-P4-O42
3	A	2802	ATP	C4'-C5'-O5'-PA
2	A	2801	I3P	C5-O5-P5-O51

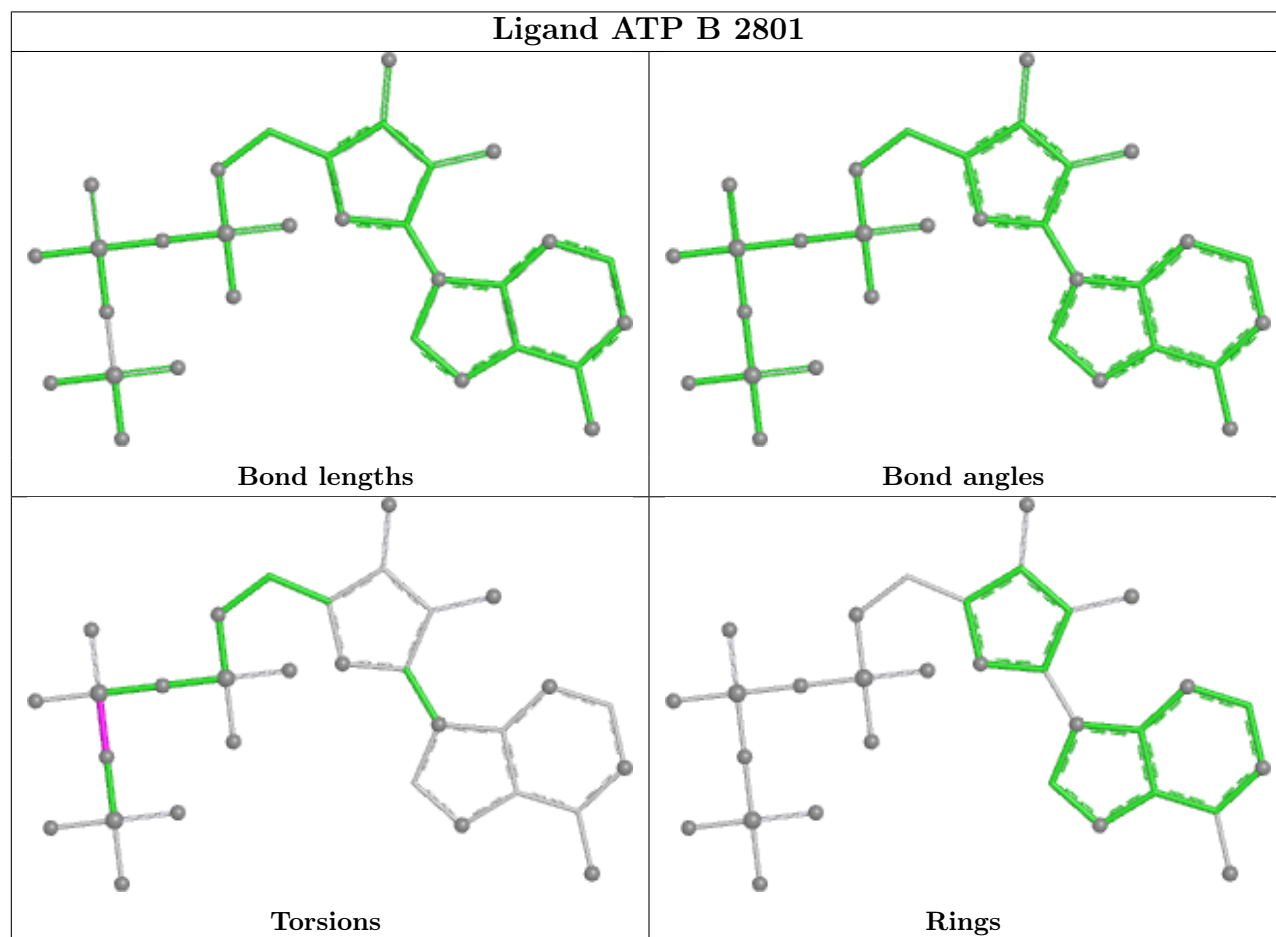
There are no ring outliers.

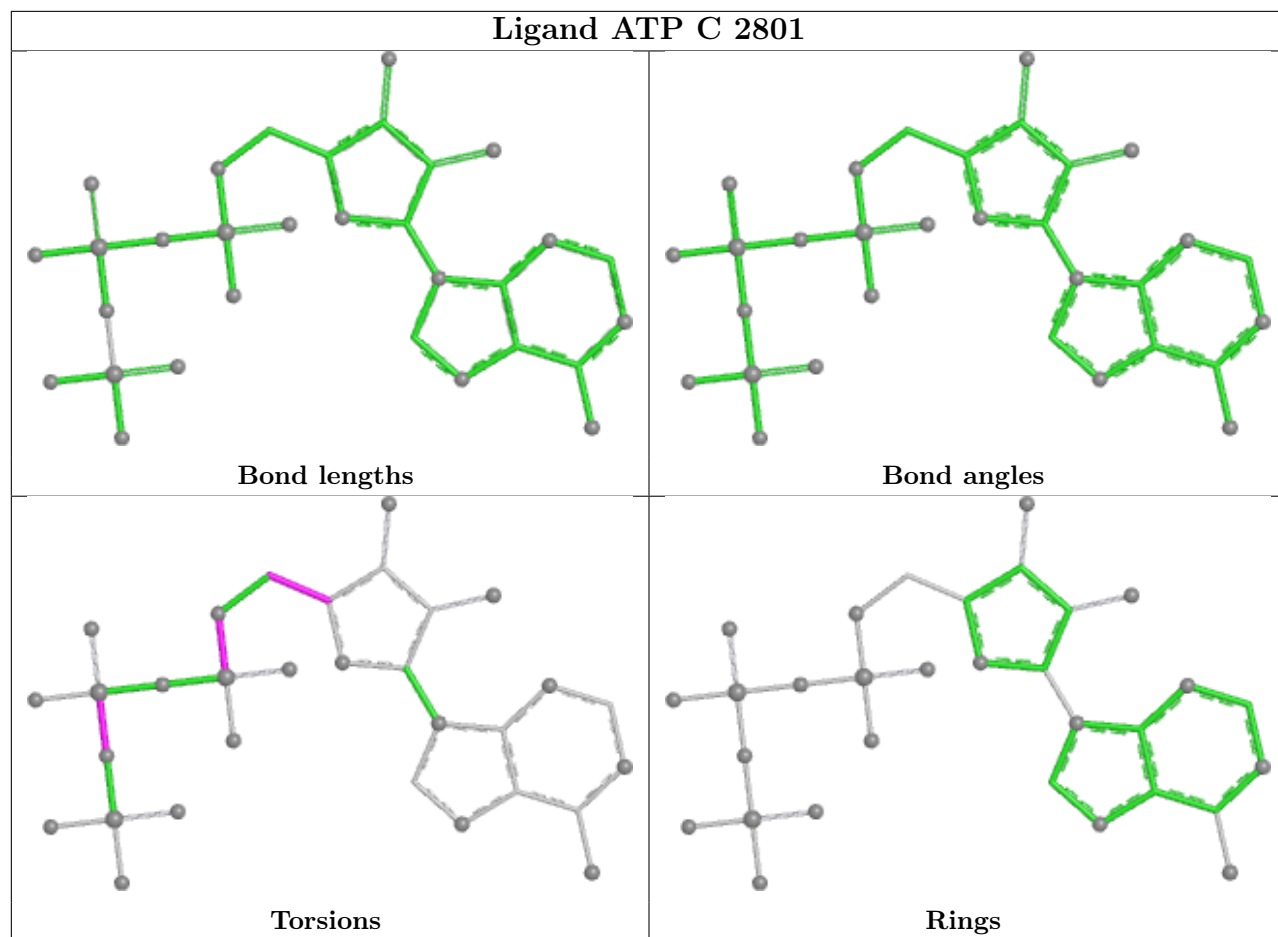
2 monomers are involved in 3 short contacts:

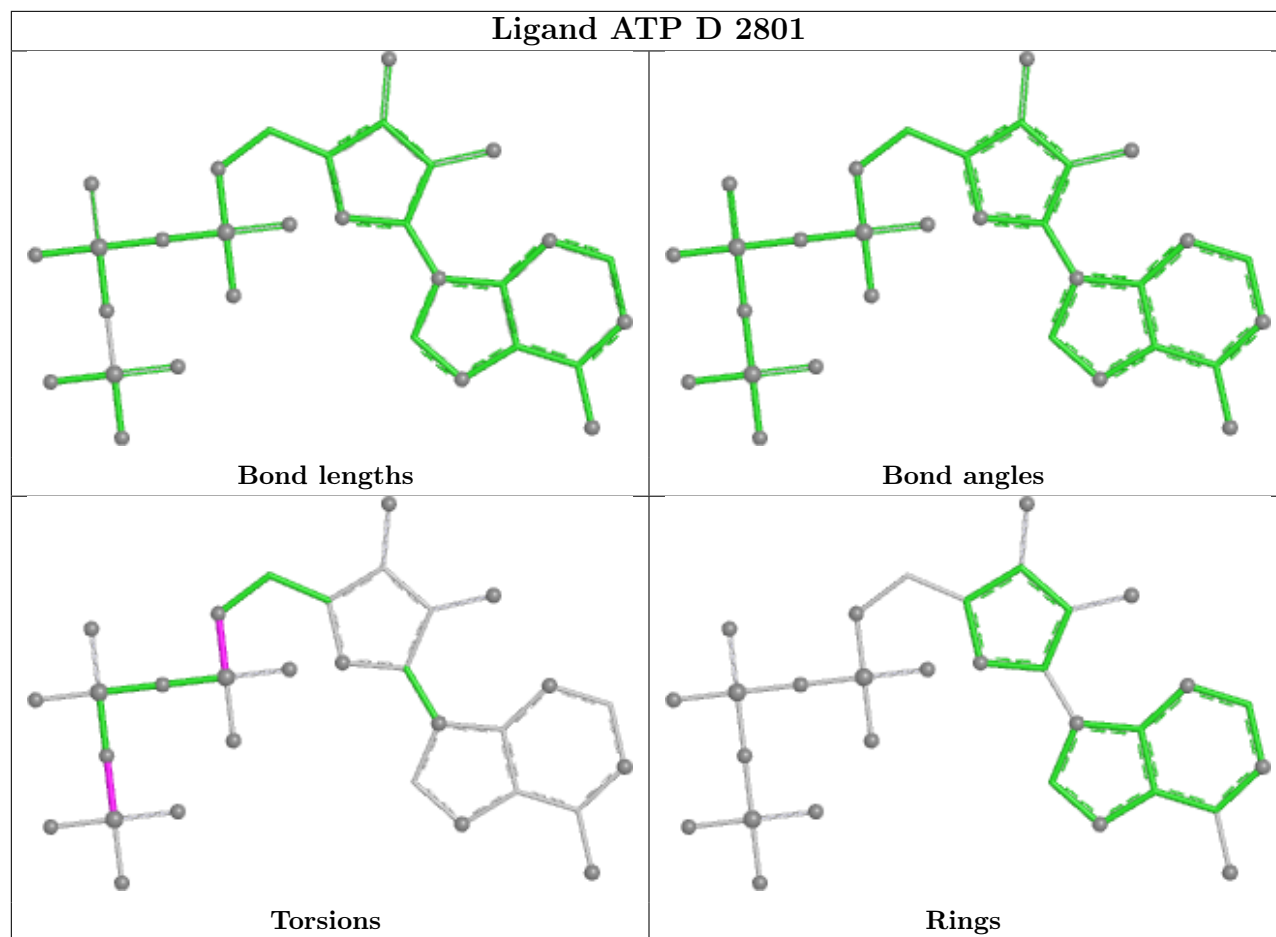
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	2801	ATP	2	0
2	A	2801	I3P	1	0

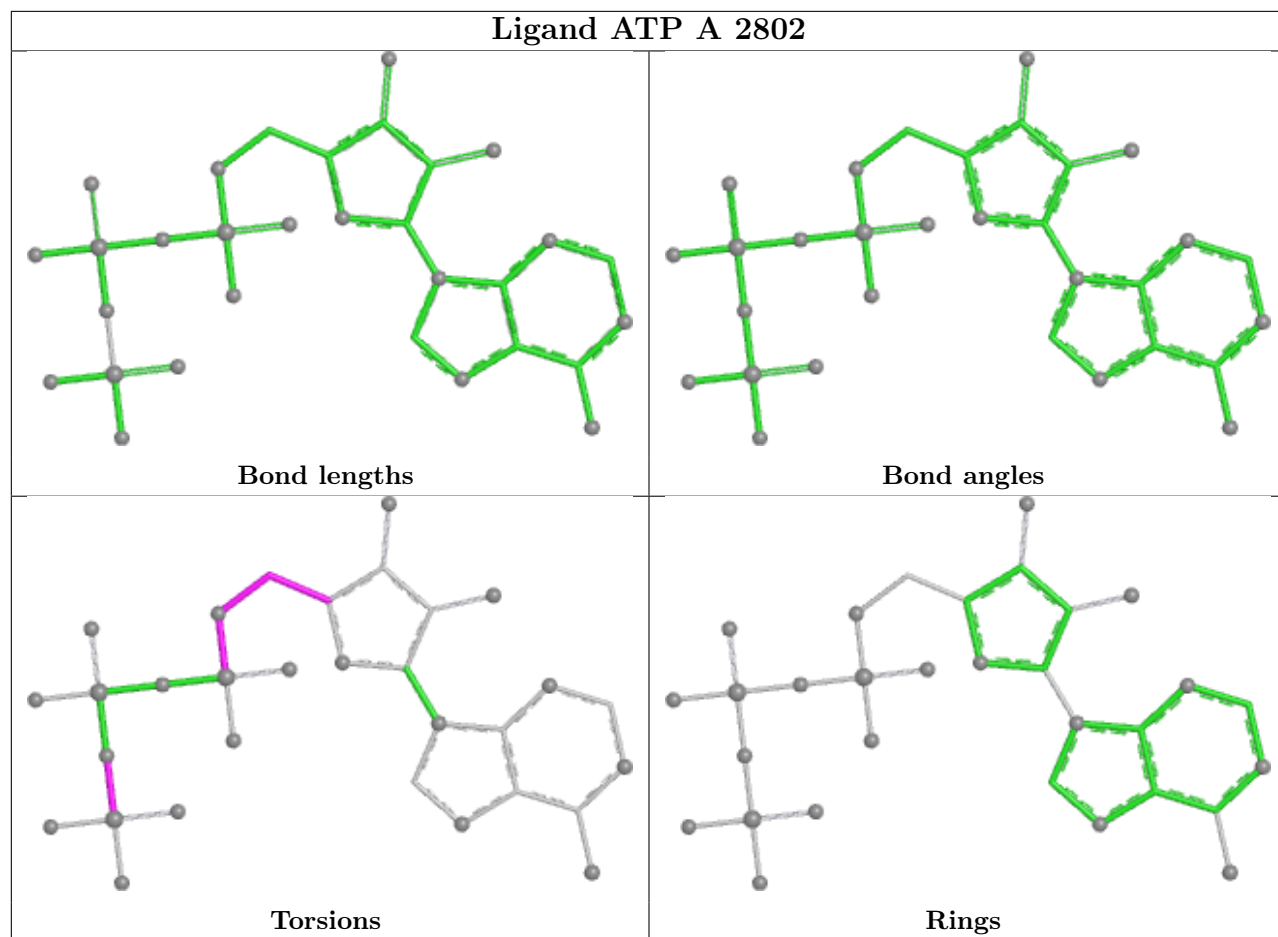
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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

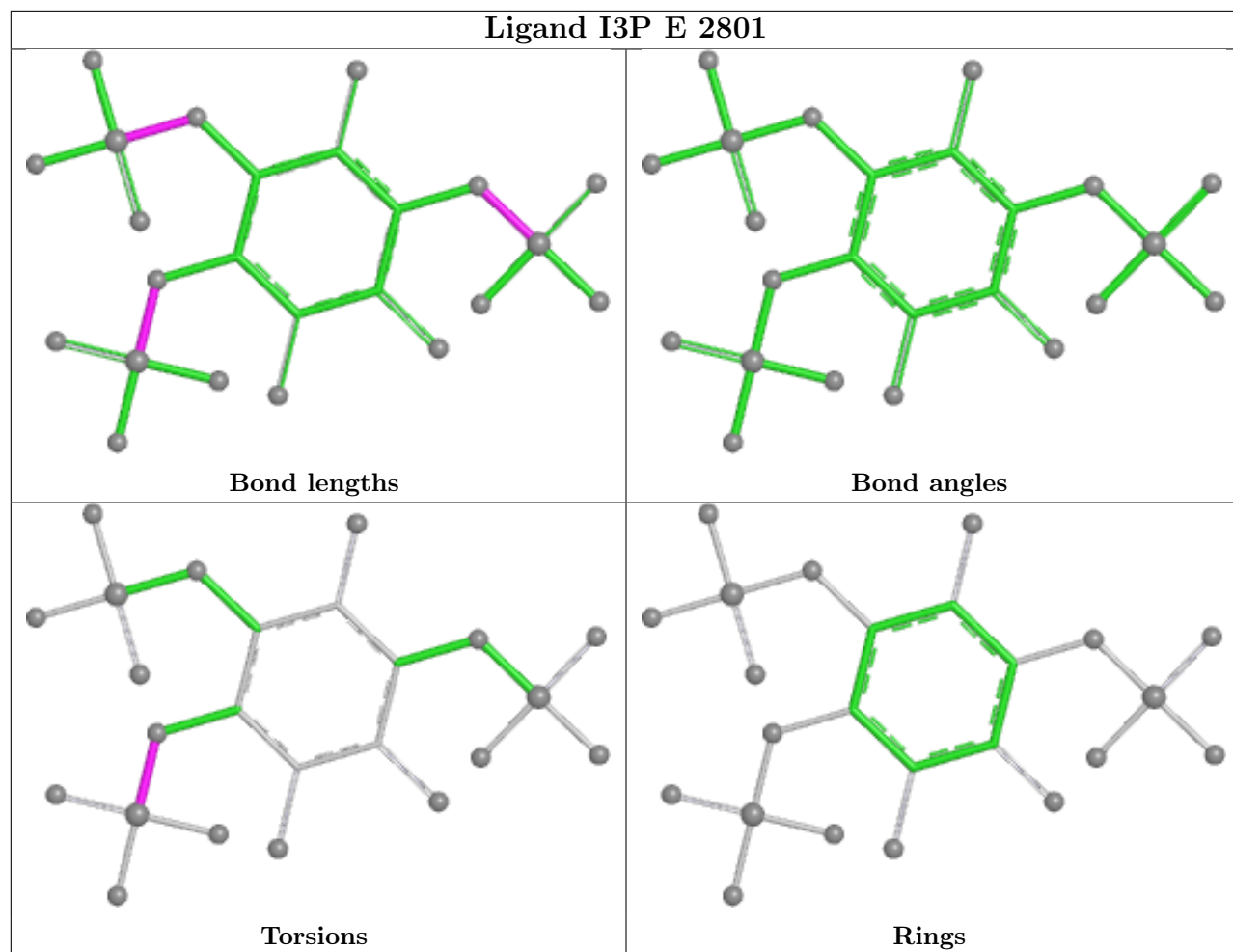
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

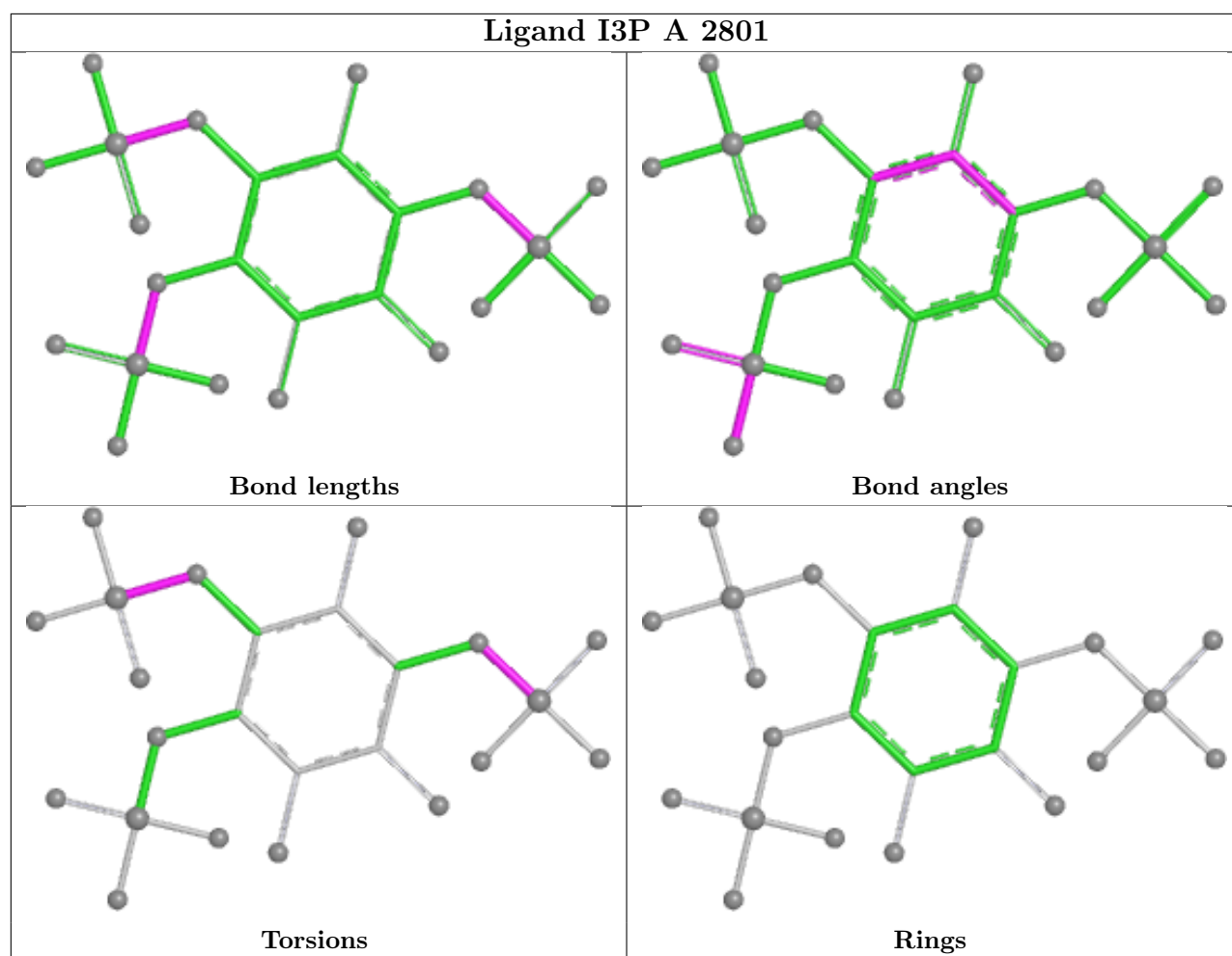












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

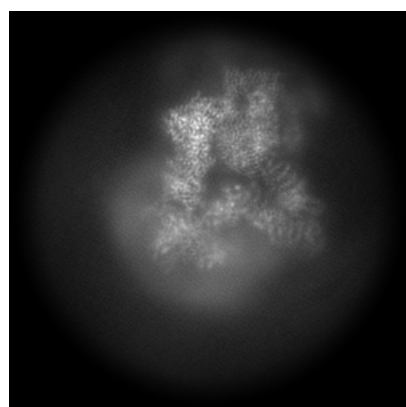
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73219. These allow visual inspection of the internal detail of the map and identification of artifacts.

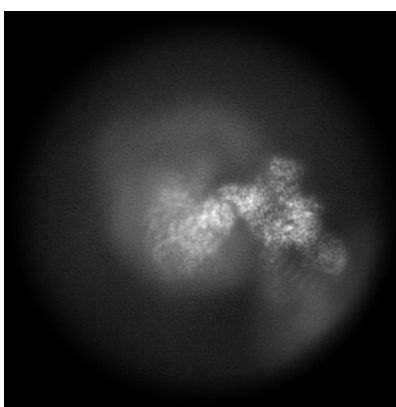
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

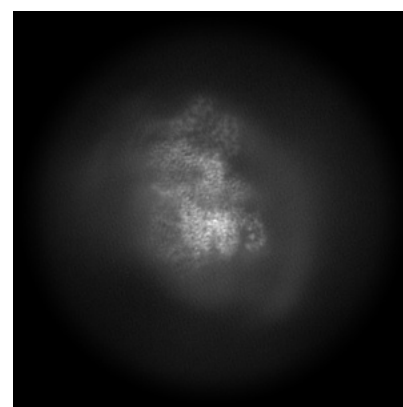
6.1.1 Primary map



X



Y

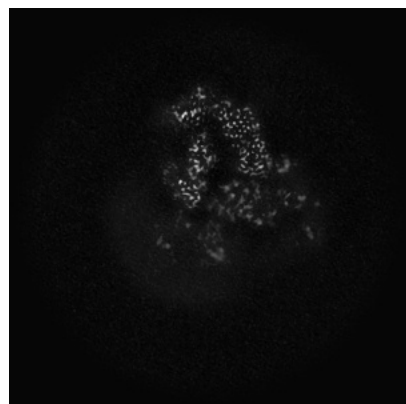


Z

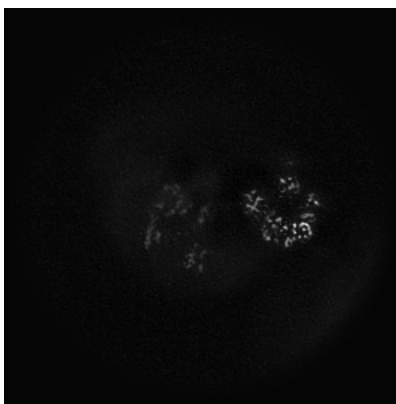
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

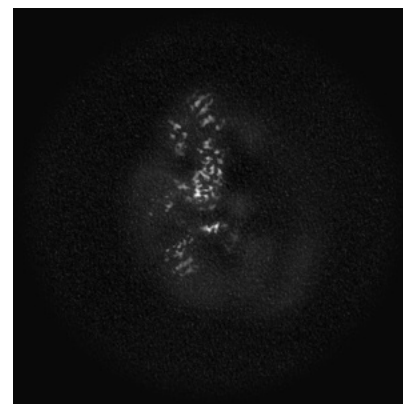
6.2.1 Primary map



X Index: 256



Y Index: 256

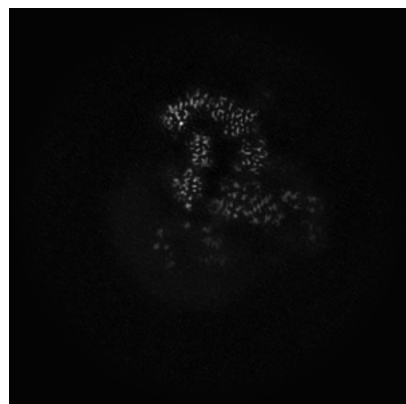


Z Index: 256

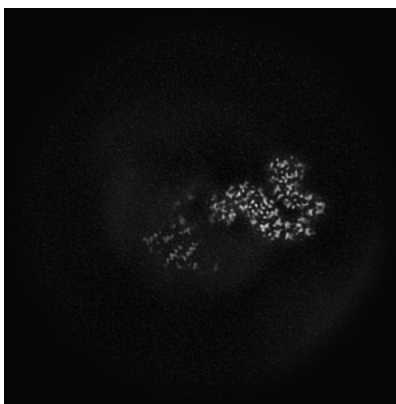
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

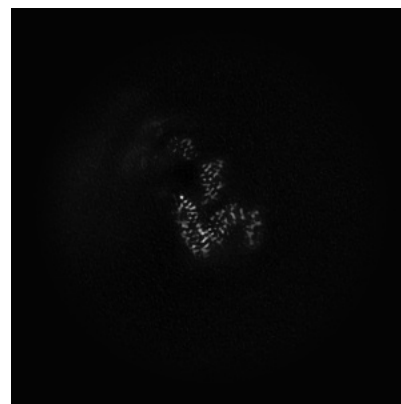
6.3.1 Primary map



X Index: 249



Y Index: 241

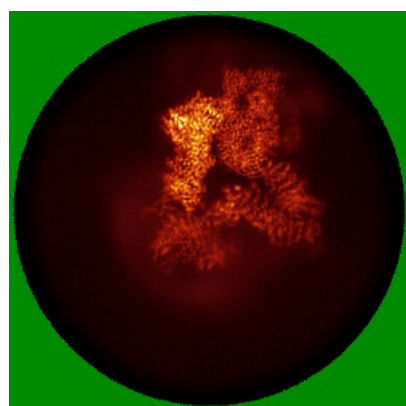


Z Index: 371

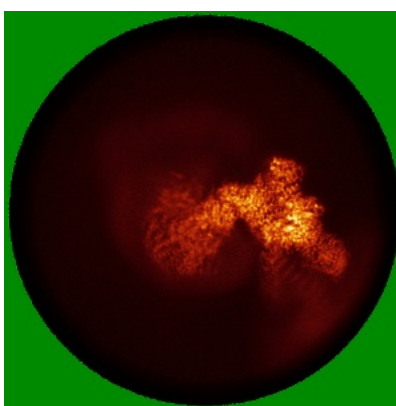
The images above show the largest variance slices of the map in three orthogonal directions.

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

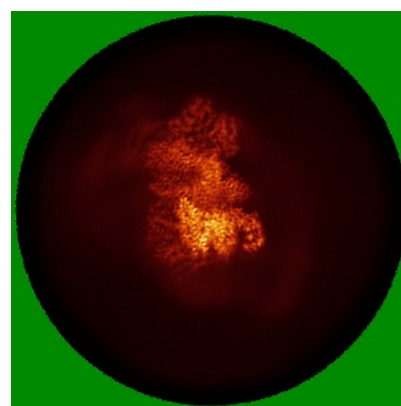
6.4.1 Primary map



X



Y



Z

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 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

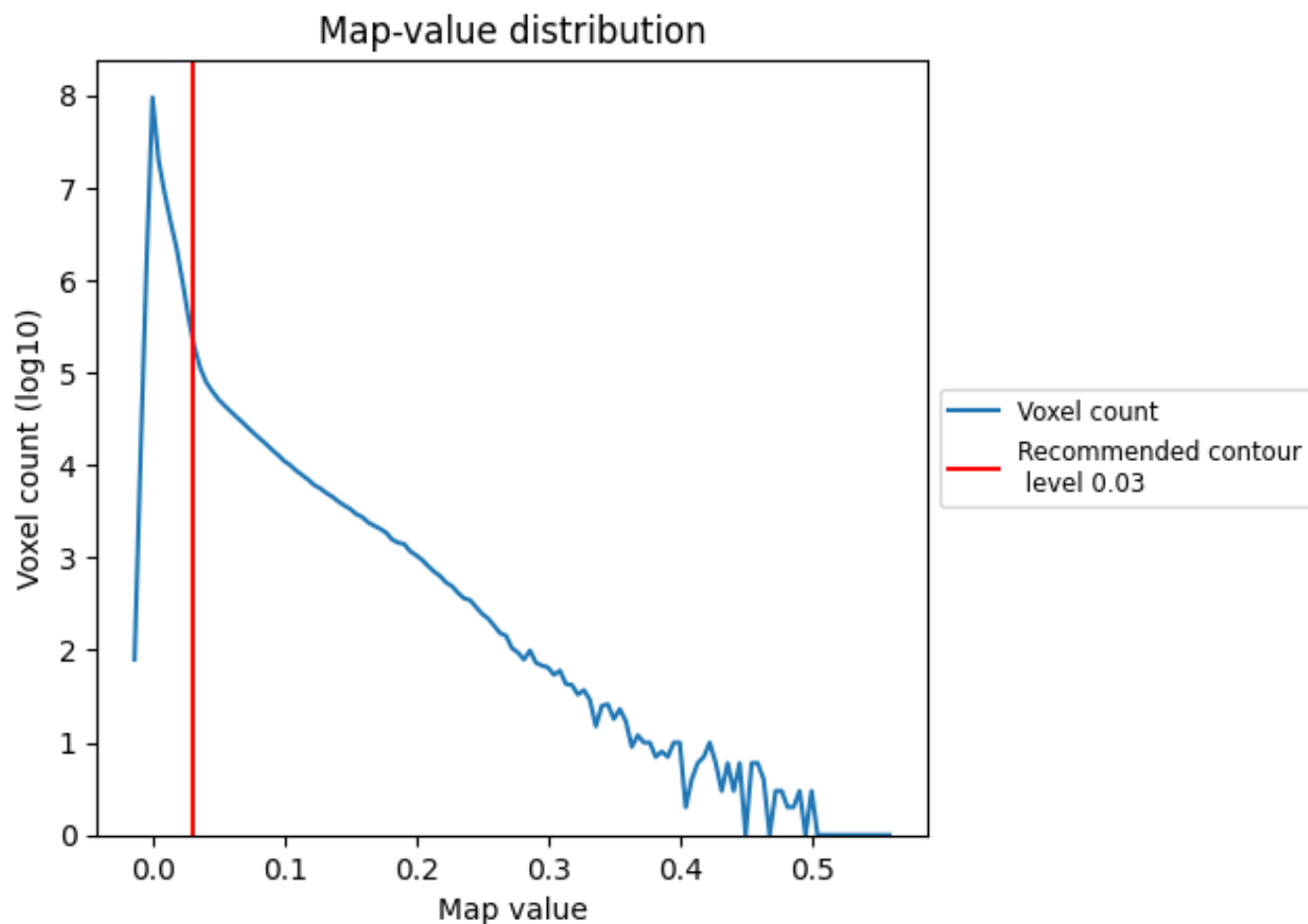
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

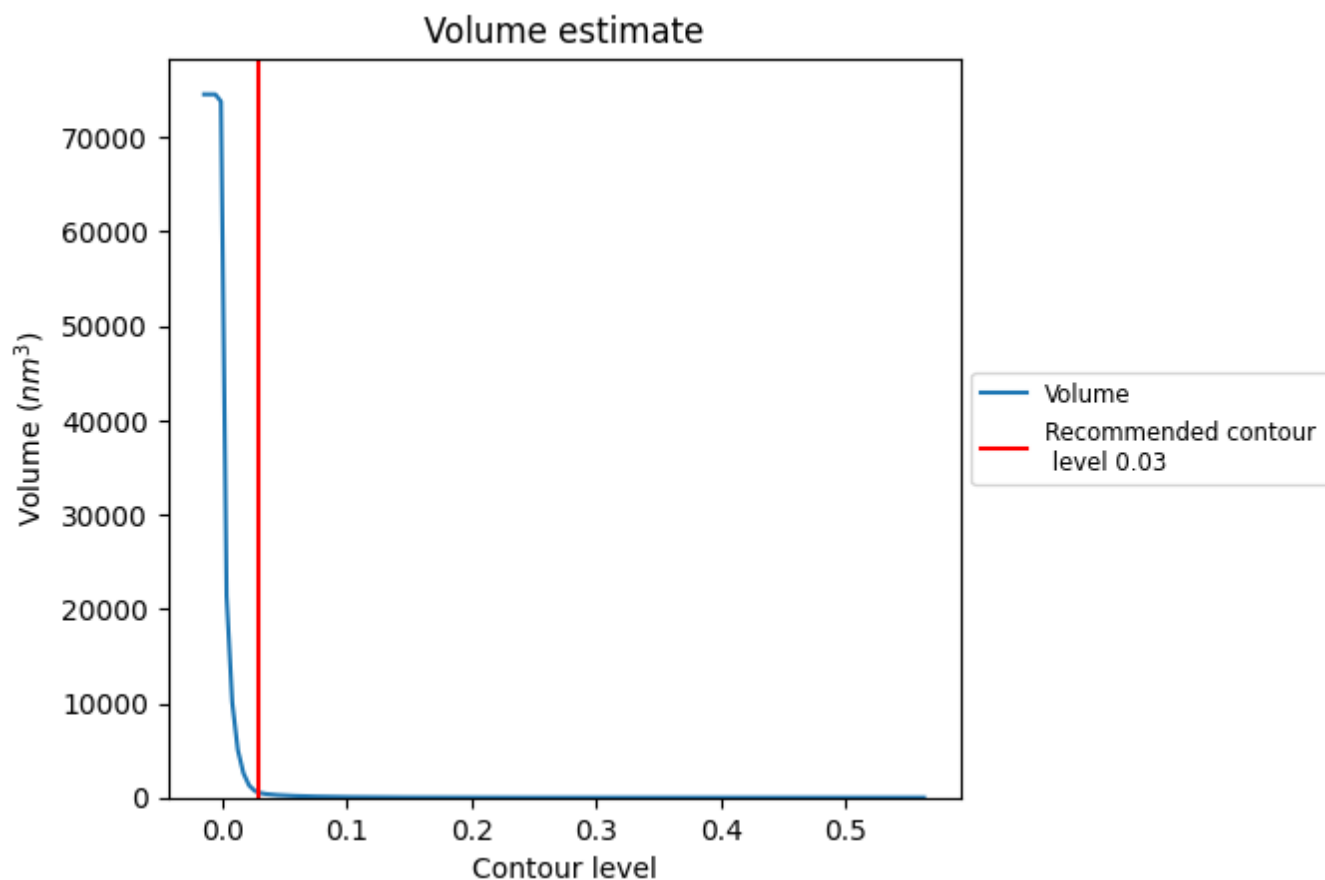
This section contains the results of statistical analysis of the map.

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.

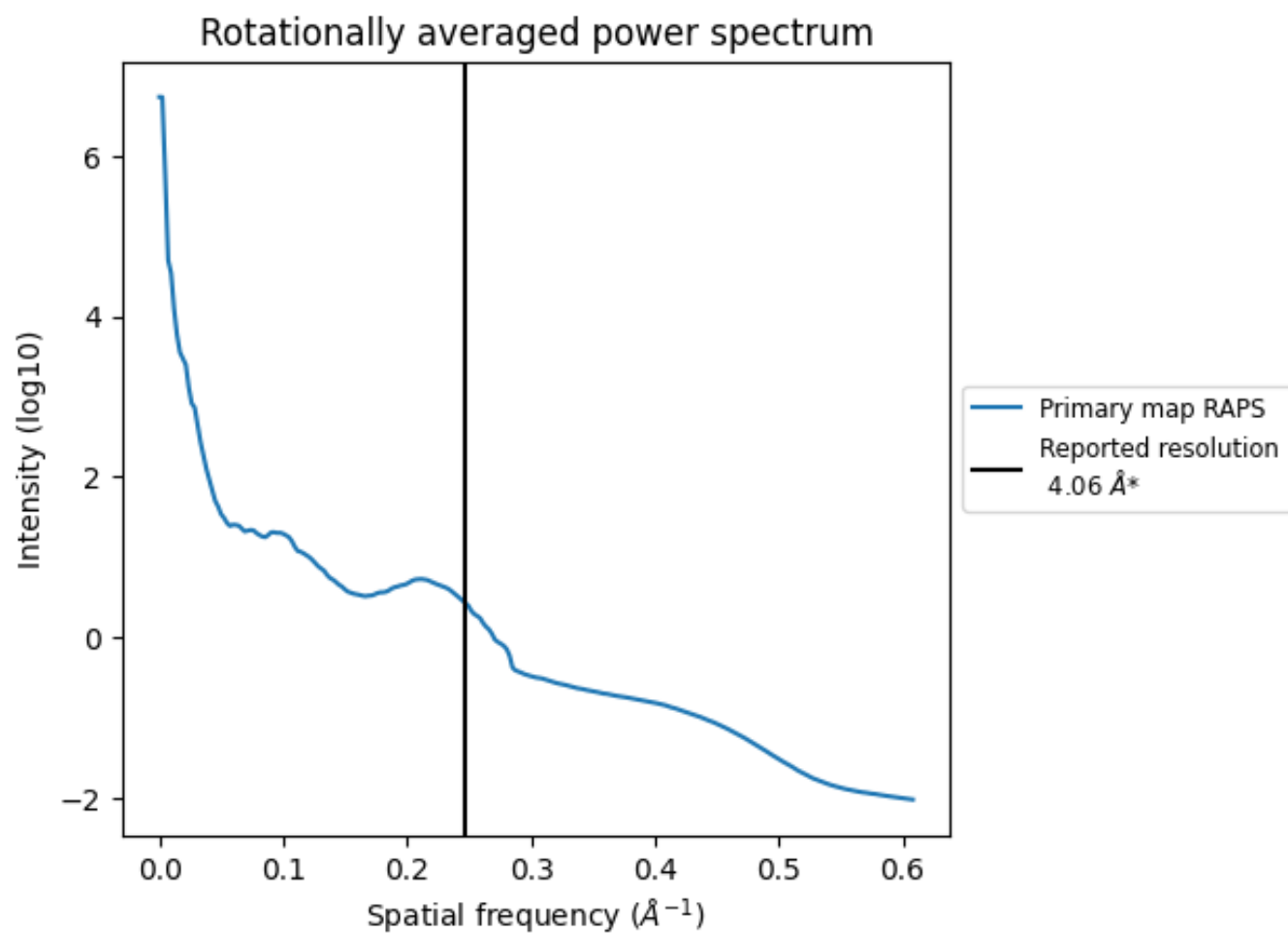
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 525 nm^3 ; this corresponds to an approximate mass of 474 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 0.246 Å⁻¹

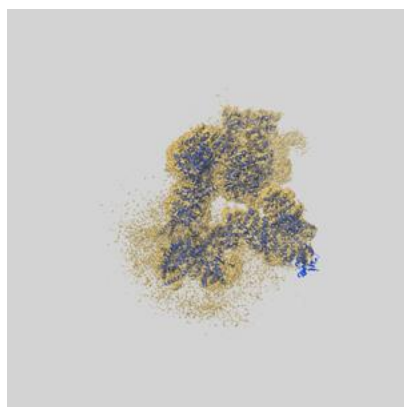
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

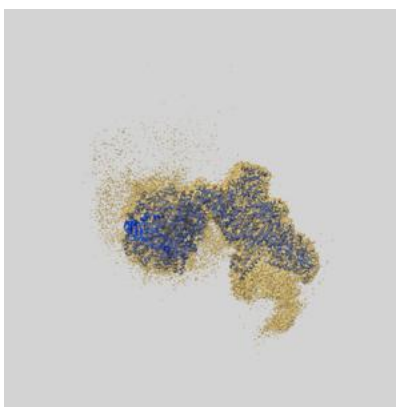
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-73219 and PDB model 9YNO. Per-residue inclusion information can be found in section [3](#) on page [12](#).

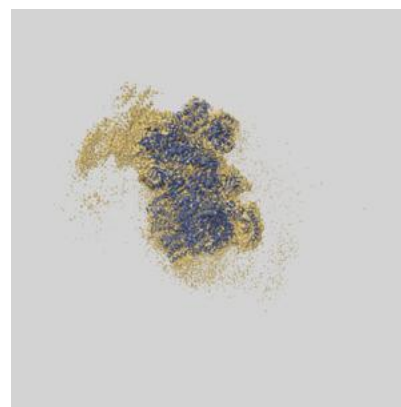
9.1 Map-model overlay [i](#)



X



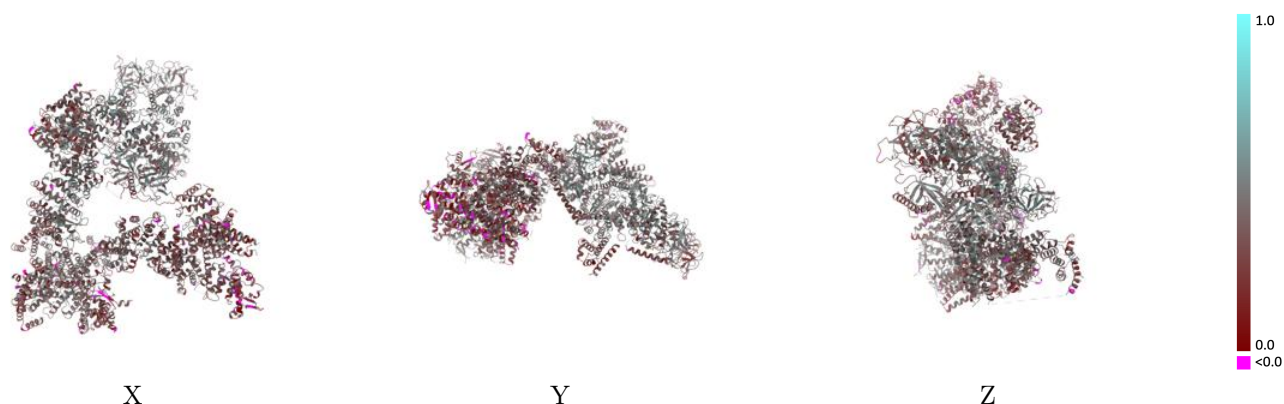
Y



Z

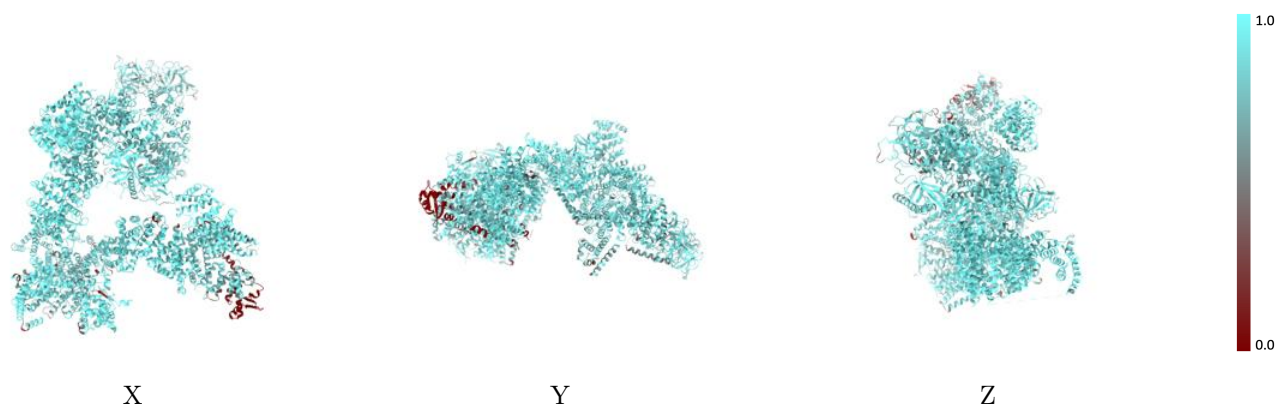
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



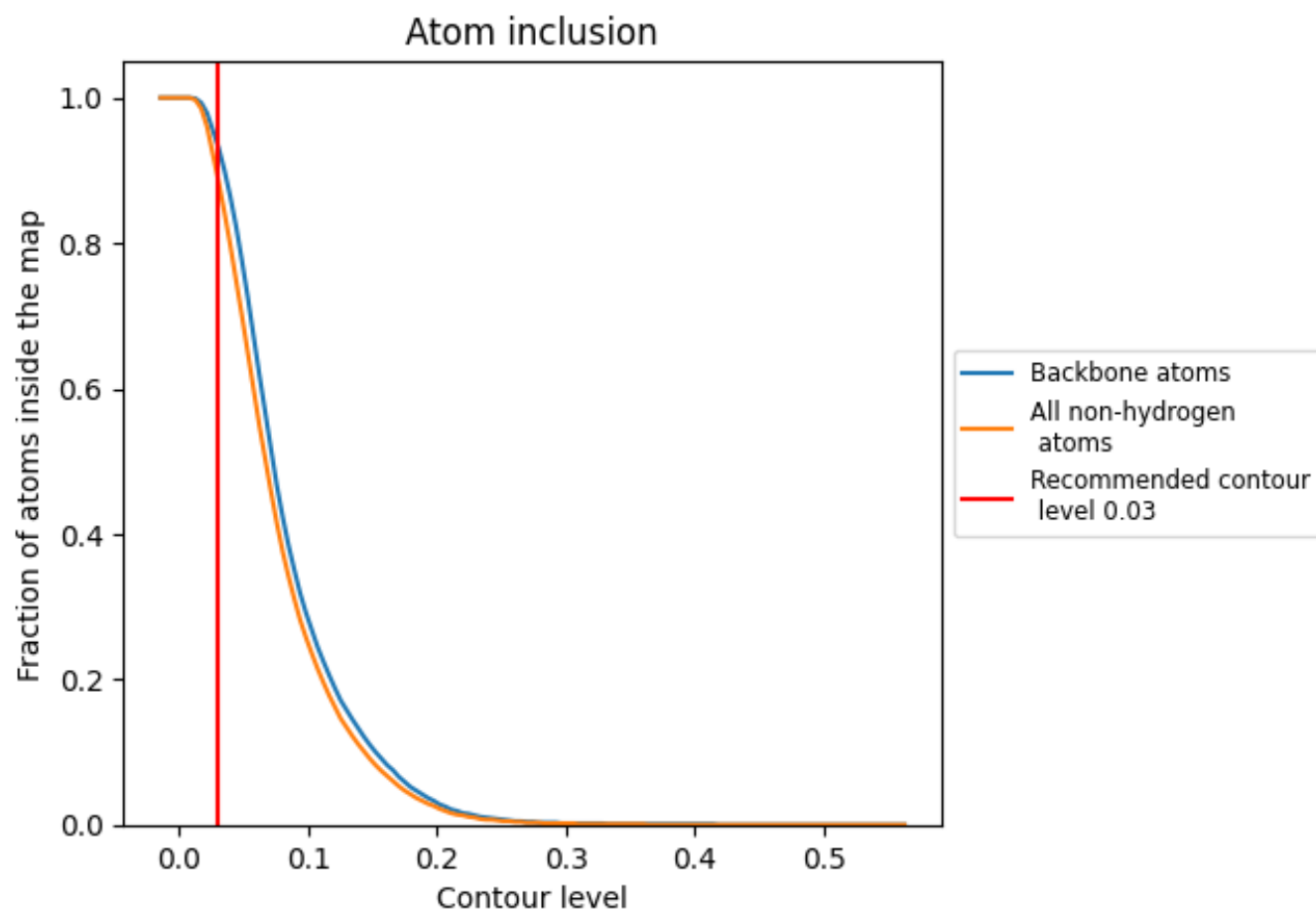
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 89% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8910	<div></div> 0.3790
A	<div></div> 0.9360	<div></div> 0.4140
B	<div></div> 0.8550	<div></div> 0.3160
C	<div></div> 0.8940	<div></div> 0.3250
D	<div></div> 0.9060	<div></div> 0.3460
E	<div></div> 0.8180	<div></div> 0.3980

