



wwPDB EM Validation Summary Report ⓘ

Aug 8, 2026 – 02:16 PM EDT

PDB ID : 9YMZ / pdb_00009ymz
EMDB ID : EMD-73129
Title : Human type 2 IP3 receptor in the inactive-like state (IP3/ATP)
Authors : Liu, C.; Lan, Y.; Tang, Q.; Karakas, E.
Deposited on : 2025-10-10
Resolution : 3.14 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.dev133
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) : 2.50

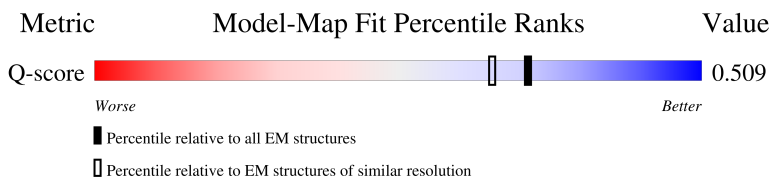
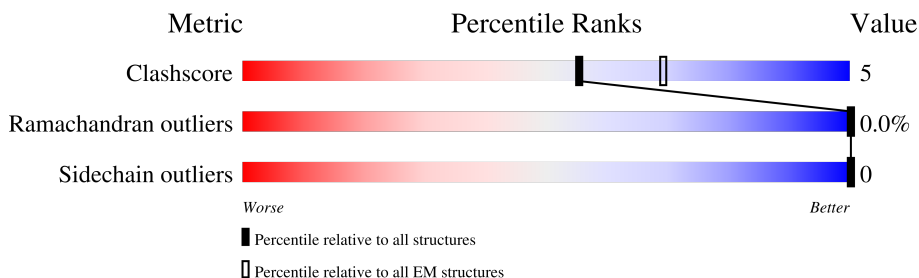
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.14 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	14483 (2.64 - 3.64)

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	 66% 11% 23%
1	B	2745	 48% 8% 44%
1	C	2745	 21% 77%
1	D	2745	 13% 85%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 38034 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	2112	Total	C	N	O	S	0	0
			16945	10843	2904	3096	102		
1	B	1547	Total	C	N	O	S	0	0
			12417	7973	2107	2256	81		
1	C	625	Total	C	N	O	S	0	0
			5107	3311	859	903	34		
1	D	416	Total	C	N	O	S	0	0
			3413	2239	561	594	19		

There are 176 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
A	2722	GLN	-	expression tag	UNP Q14571
A	2723	PHE	-	expression tag	UNP Q14571

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Chain	Residue	Modelled	Actual	Comment	Reference
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
B	2720	HIS	-	expression tag	UNP Q14571
B	2721	PRO	-	expression tag	UNP Q14571

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Chain	Residue	Modelled	Actual	Comment	Reference
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
C	2718	TRP	-	expression tag	UNP Q14571
C	2719	SER	-	expression tag	UNP Q14571

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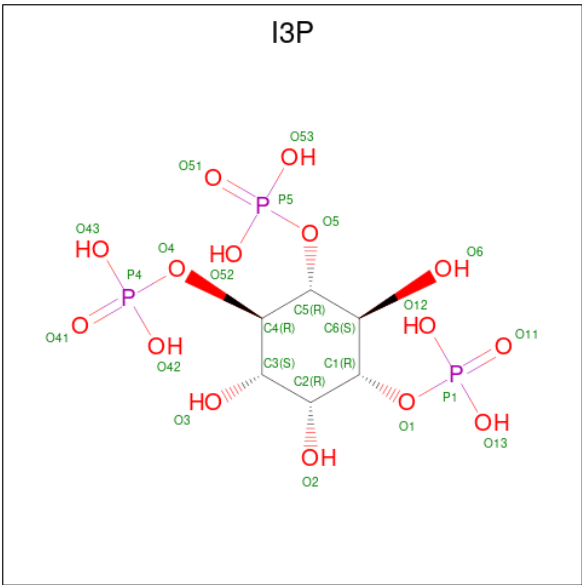
Chain	Residue	Modelled	Actual	Comment	Reference
C	2720	HIS	-	expression tag	UNP Q14571
C	2721	PRO	-	expression tag	UNP Q14571
C	2722	GLN	-	expression tag	UNP Q14571
C	2723	PHE	-	expression tag	UNP Q14571
C	2724	GLU	-	expression tag	UNP Q14571
C	2725	LYS	-	expression tag	UNP Q14571
C	2726	GLY	-	expression 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
D	2716	ALA	-	expression tag	UNP Q14571
D	2717	GLY	-	expression tag	UNP Q14571

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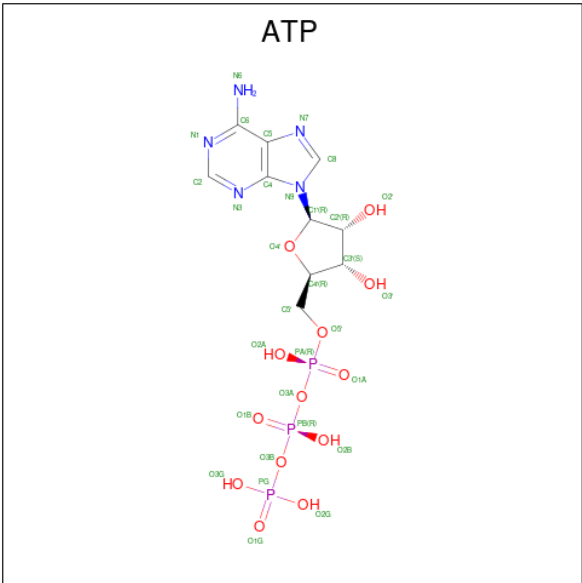
Chain	Residue	Modelled	Actual	Comment	Reference
D	2718	TRP	-	expression tag	UNP Q14571
D	2719	SER	-	expression tag	UNP Q14571
D	2720	HIS	-	expression tag	UNP Q14571
D	2721	PRO	-	expression tag	UNP Q14571
D	2722	GLN	-	expression tag	UNP Q14571
D	2723	PHE	-	expression tag	UNP Q14571
D	2724	GLU	-	expression 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

- 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
			Total	C	O	P	
2	A	1	24	6	15	3	0

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



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

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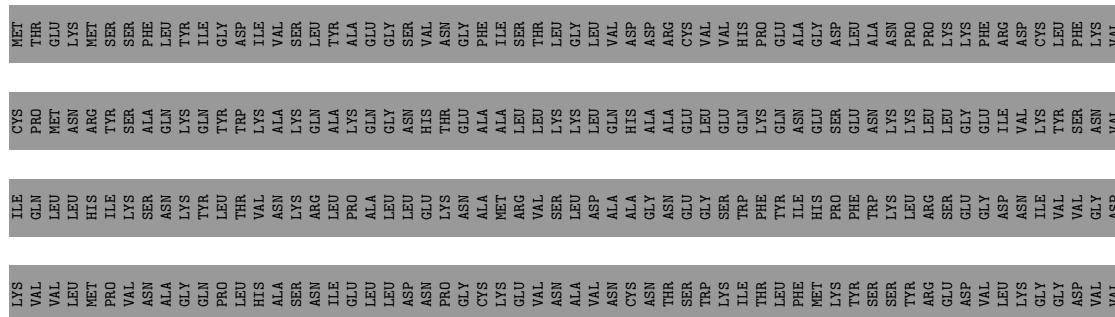
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Mol	Chain	Residues	Atoms					AltConf
3	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	D	1	Total	C	N	O	P	0
			31	10	5	13	3	

- 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	













SER	GLU	THR
ALA	ASP	ALA
ALA	THR	ASP
GLY	MET	GLU
TRP	SER	Y2471
SER	LEU	Y2489
HIS	VAL	Y2492
PRO	GLN	Y2496
PHE	LEU	Y2532
GLU	SER	Y2535
LYS	GLY	Y2536
GLY	GLN	Y2537
GLY	GLY	Y2557
GLY	GLN	Y2558
SER	MET	Y2559
GLY	THR	Y2560
SER	GLU	Y2561
ALA	GLN	Y2567
TRP	ARG	Y2568
SER	LYS	Y2569
HIS	ASN	Y2589
PRO	LYS	Y2590
GLN	GLN	Y2598
PHE	ARG	Y2603
GLU	LEU	Y2606
LYS	PHE	Y2625
	GLY	Y2629
	THR	Y2635
	PRO	SER
	HIS	ASN
	VAL	GLU
	ASN	THR
	GLY	GLY
	ASN	ASP
	GLY	SER
	THR	GLN
	PRO	ASN
	GLY	GLU
	VAL	ILE
	ASN	ARG
	GLY	GLY
	THR	SER
	PRO	LEU
	GLY	GLN
	VAL	GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	533134	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	0.627	Depositor
Minimum map value	-0.006	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	420.864, 420.864, 420.864	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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: ZN, ATP, I3P

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	0/17254	0.25	0/23315
1	B	0.11	0/12640	0.26	0/17077
1	C	0.10	0/5205	0.23	0/7029
1	D	0.11	0/3490	0.24	0/4723
All	All	0.11	0/38589	0.25	0/52144

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	16945	0	16919	189	0
1	B	12417	0	12367	138	0
1	C	5107	0	5183	39	0
1	D	3413	0	3464	31	0
2	A	24	0	9	0	0
3	A	31	0	12	0	0
3	B	31	0	12	0	0
3	C	31	0	12	0	0
3	D	31	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
All	All	38034	0	37990	383	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 383 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:1926:GLN:HG3	1:B:1994:GLU:HG3	1.63	0.81
1:C:2402:ALA:HB2	1:C:2532:VAL:HG11	1.66	0.77
1:A:2402:ALA:HB2	1:A:2532:VAL:HG11	1.66	0.77
1:A:1099:LEU:HD22	1:A:1606:LEU:HD22	1.69	0.75
1:B:2402:ALA:HB2	1:B:2532:VAL:HG11	1.70	0.74

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	2072/2745 (76%)	2005 (97%)	67 (3%)	0	100	100
1	B	1515/2745 (55%)	1462 (96%)	52 (3%)	1 (0%)	48	76
1	C	609/2745 (22%)	599 (98%)	10 (2%)	0	100	100
1	D	410/2745 (15%)	402 (98%)	8 (2%)	0	100	100
All	All	4606/10980 (42%)	4468 (97%)	137 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	743	ASP

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	1857/2448 (76%)	1857 (100%)	0	100	100
1	B	1357/2448 (55%)	1357 (100%)	0	100	100
1	C	568/2448 (23%)	568 (100%)	0	100	100
1	D	378/2448 (15%)	378 (100%)	0	100	100
All	All	4160/9792 (42%)	4160 (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 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	2027	ASN
1	C	2113	HIS
1	B	2118	HIS
1	B	2349	HIS
1	C	2199	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

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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	A	2802	-	32,33,33	0.28	0	48,52,52	0.31	0
3	ATP	B	2801	-	32,33,33	0.28	0	48,52,52	0.35	0
3	ATP	D	2801	-	32,33,33	0.27	0	48,52,52	0.33	0
3	ATP	C	2801	-	32,33,33	0.28	0	48,52,52	0.32	0
2	I3P	A	2801	-	24,24,24	2.17	3 (12%)	39,39,39	0.86	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	A	2802	-	-	6/22/38/38	0/3/3/3
3	ATP	B	2801	-	-	4/22/38/38	0/3/3/3
3	ATP	D	2801	-	-	4/22/38/38	0/3/3/3
3	ATP	C	2801	-	-	7/22/38/38	0/3/3/3
2	I3P	A	2801	-	-	0/15/39/39	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2801	I3P	P4-O4	6.02	1.70	1.59
2	A	2801	I3P	P5-O5	5.80	1.69	1.59
2	A	2801	I3P	P1-O1	5.70	1.69	1.59

There are no bond angle outliers.

There are no chirality outliers.

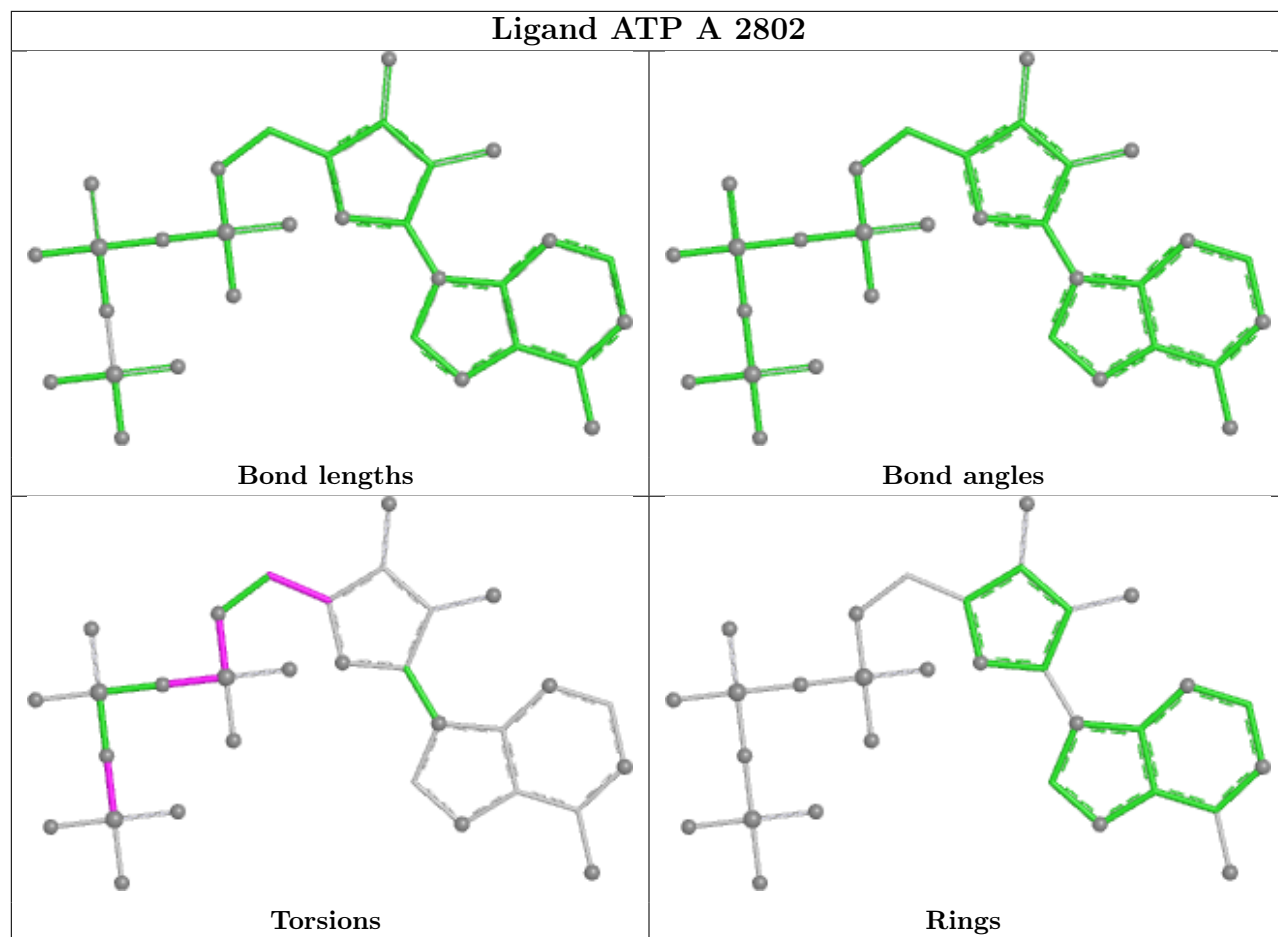
5 of 21 torsion outliers are listed below:

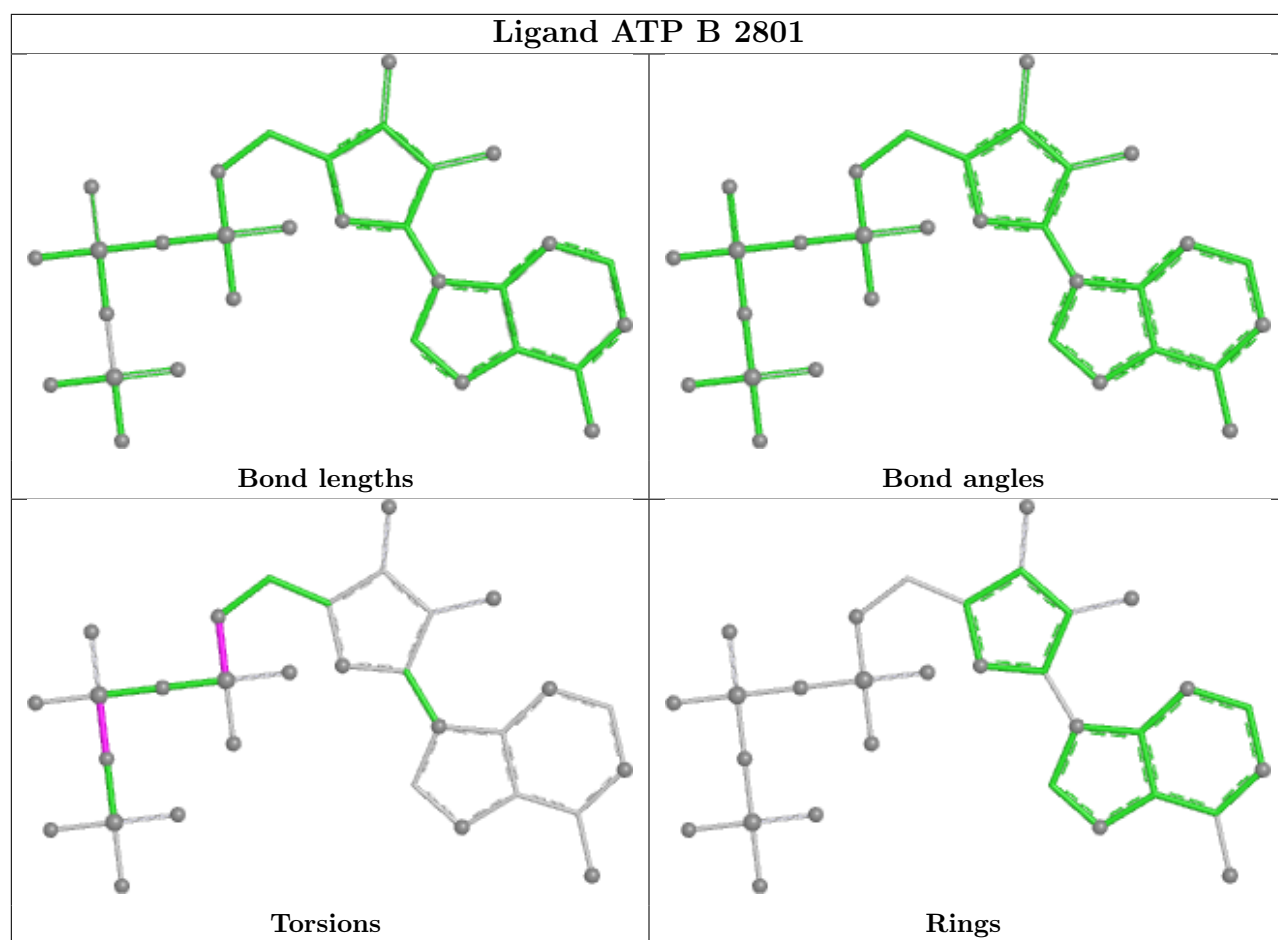
Mol	Chain	Res	Type	Atoms
3	A	2802	ATP	PB-O3B-PG-O2G
3	A	2802	ATP	C5'-O5'-PA-O1A
3	A	2802	ATP	C5'-O5'-PA-O3A
3	C	2801	ATP	PB-O3B-PG-O2G
3	C	2801	ATP	C5'-O5'-PA-O1A

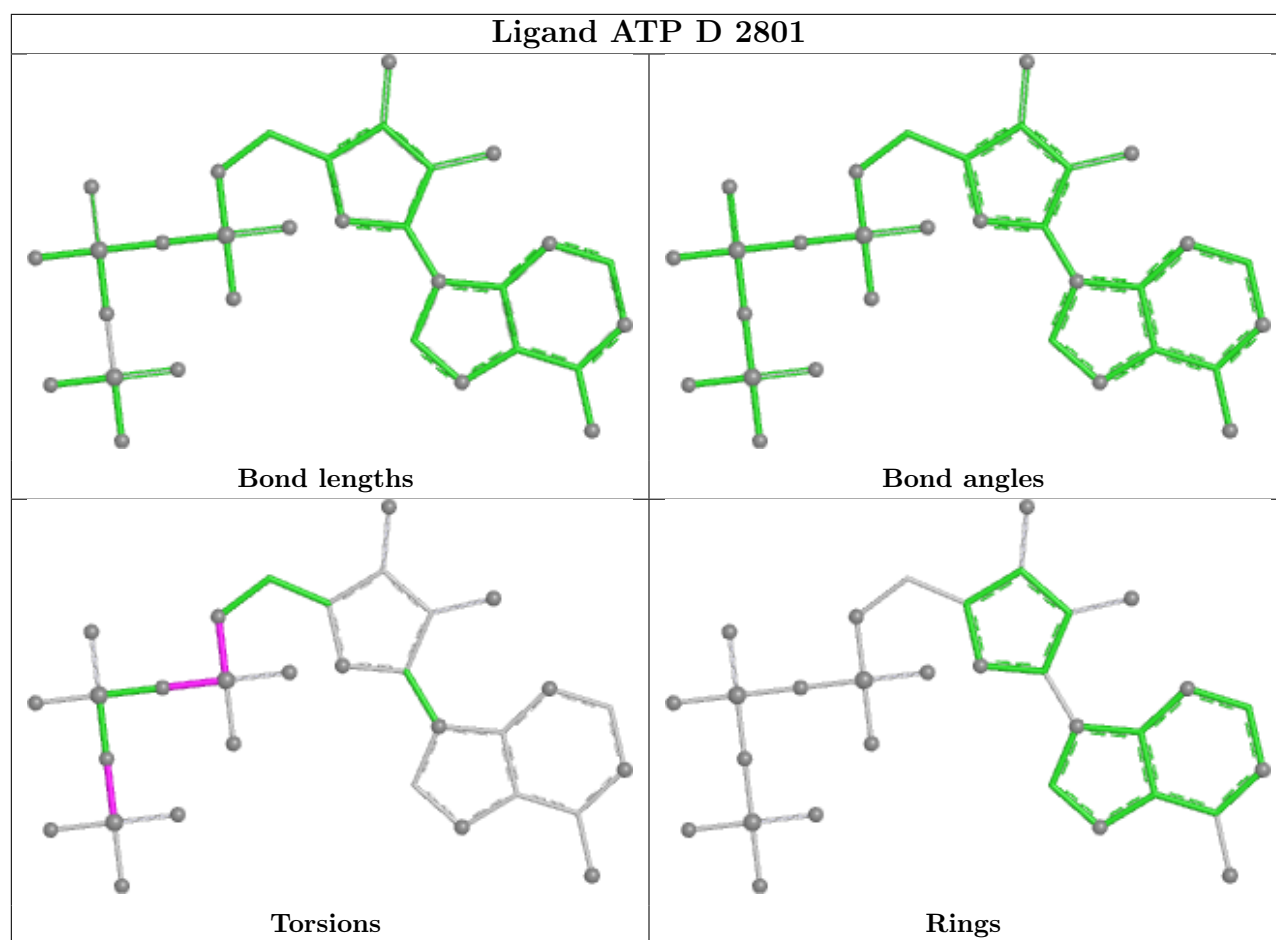
There are no ring outliers.

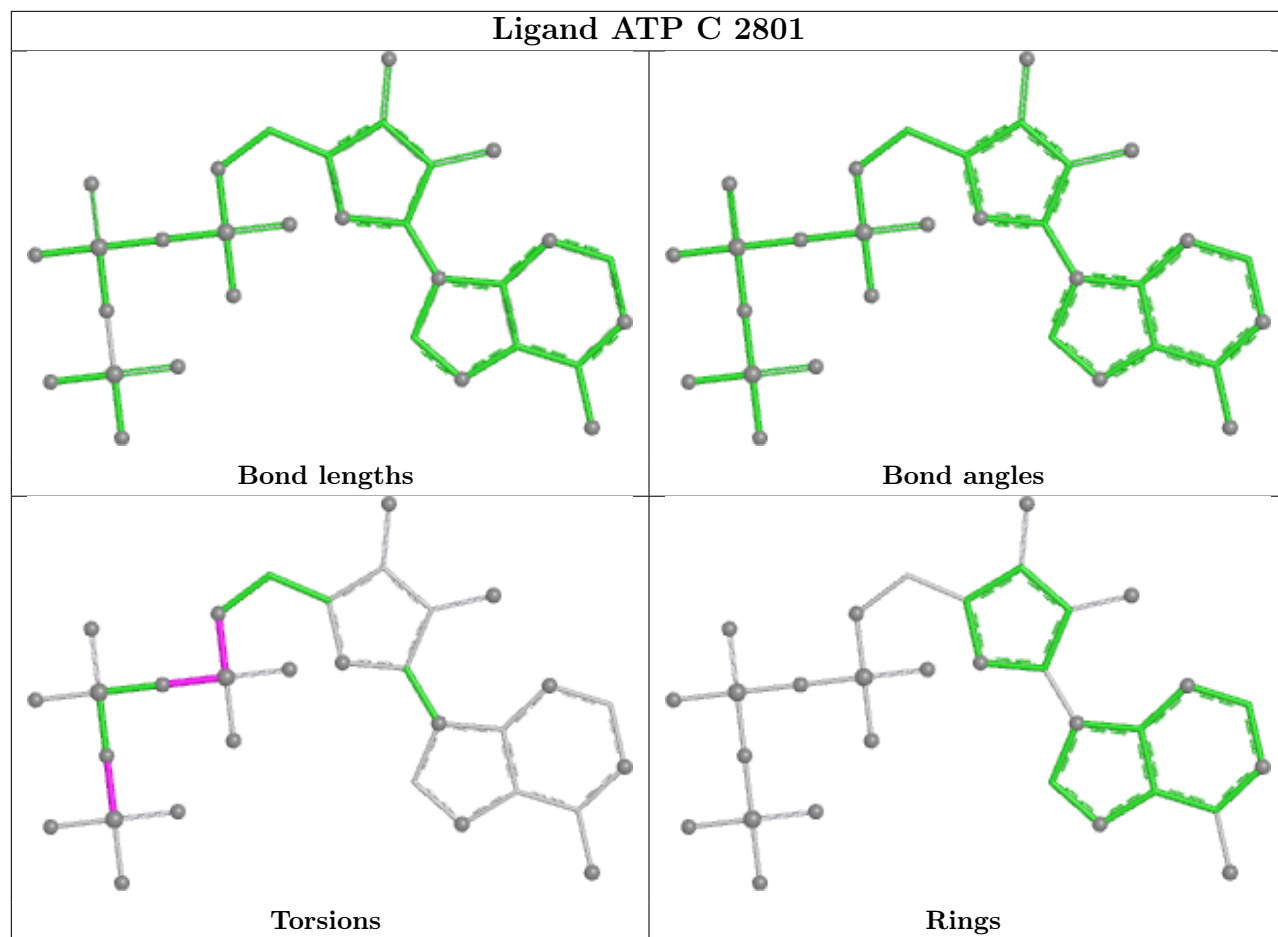
No monomer is involved in short contacts.

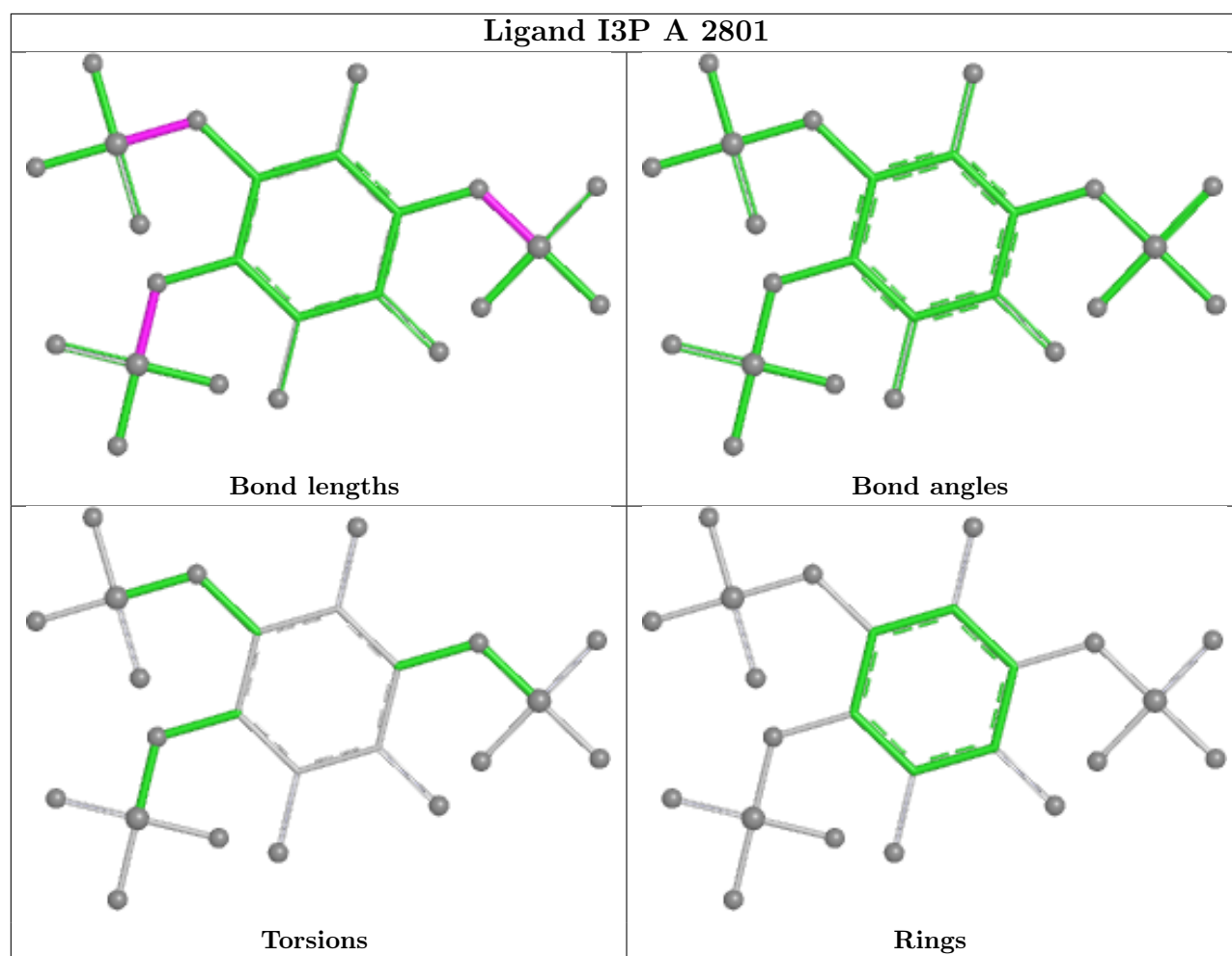
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

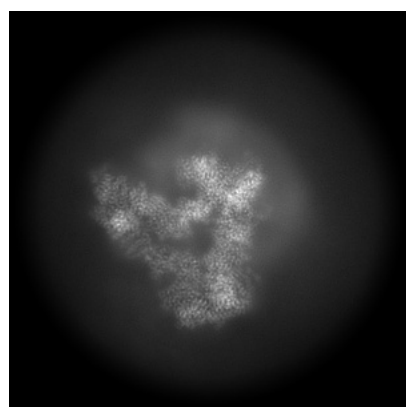
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73129. These allow visual inspection of the internal detail of the map and identification of artifacts.

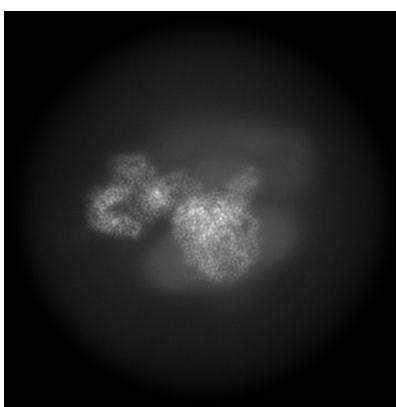
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

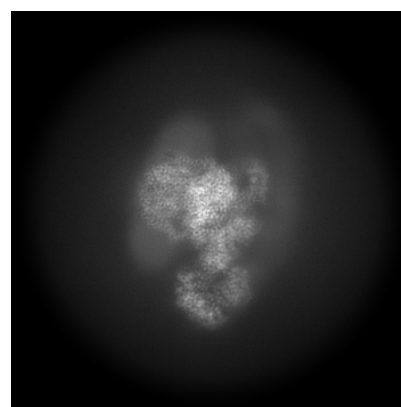
6.1.1 Primary map



X



Y

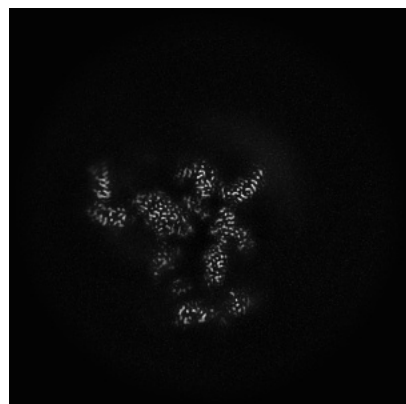


Z

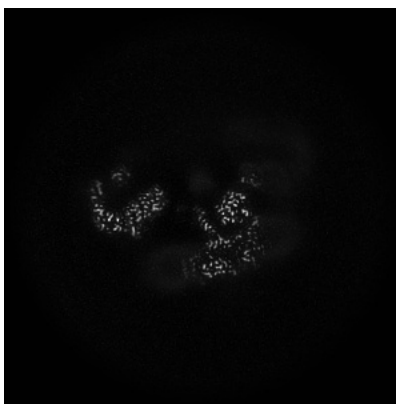
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

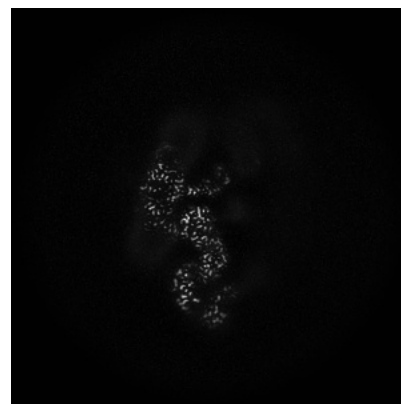
6.2.1 Primary map



X Index: 256



Y Index: 256

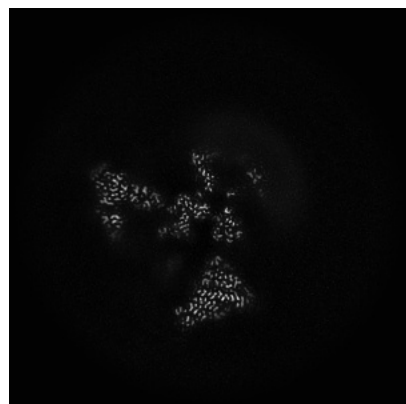


Z Index: 256

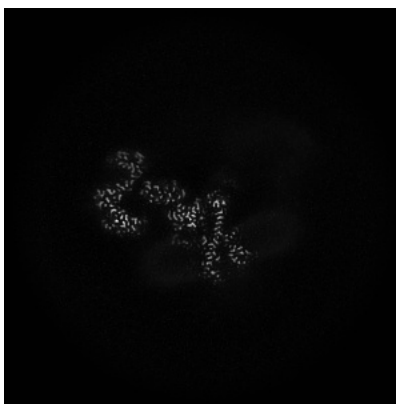
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

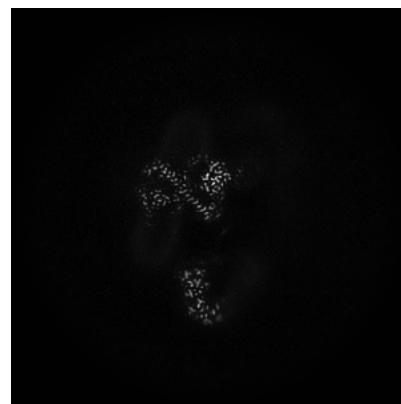
6.3.1 Primary map



X Index: 241



Y Index: 283



Z Index: 279

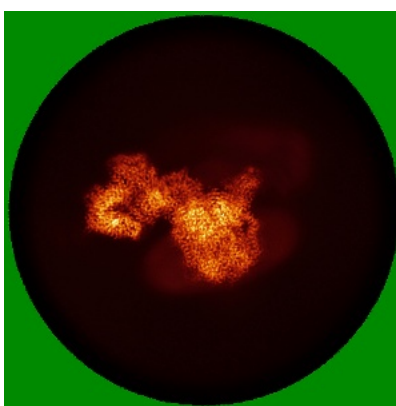
The images above show the largest variance slices of the map in three orthogonal directions.

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

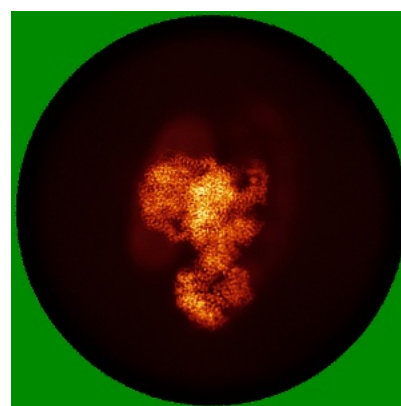
6.4.1 Primary map



X



Y

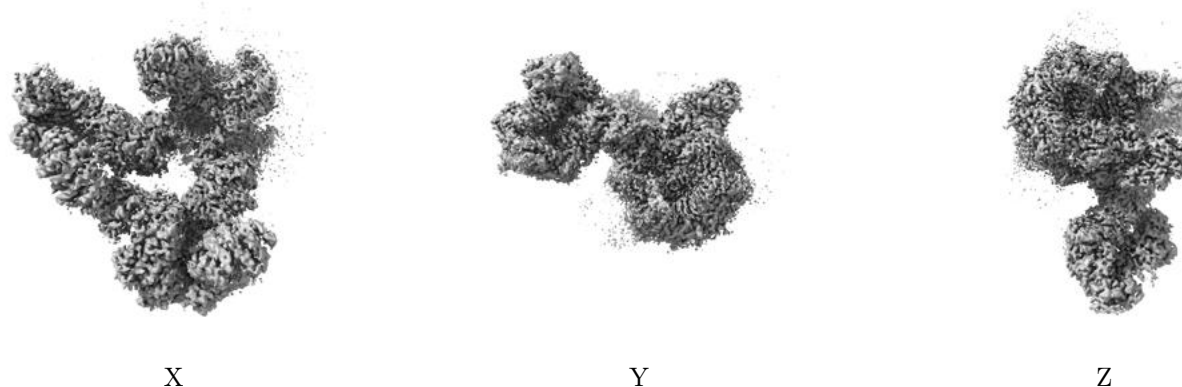


Z

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

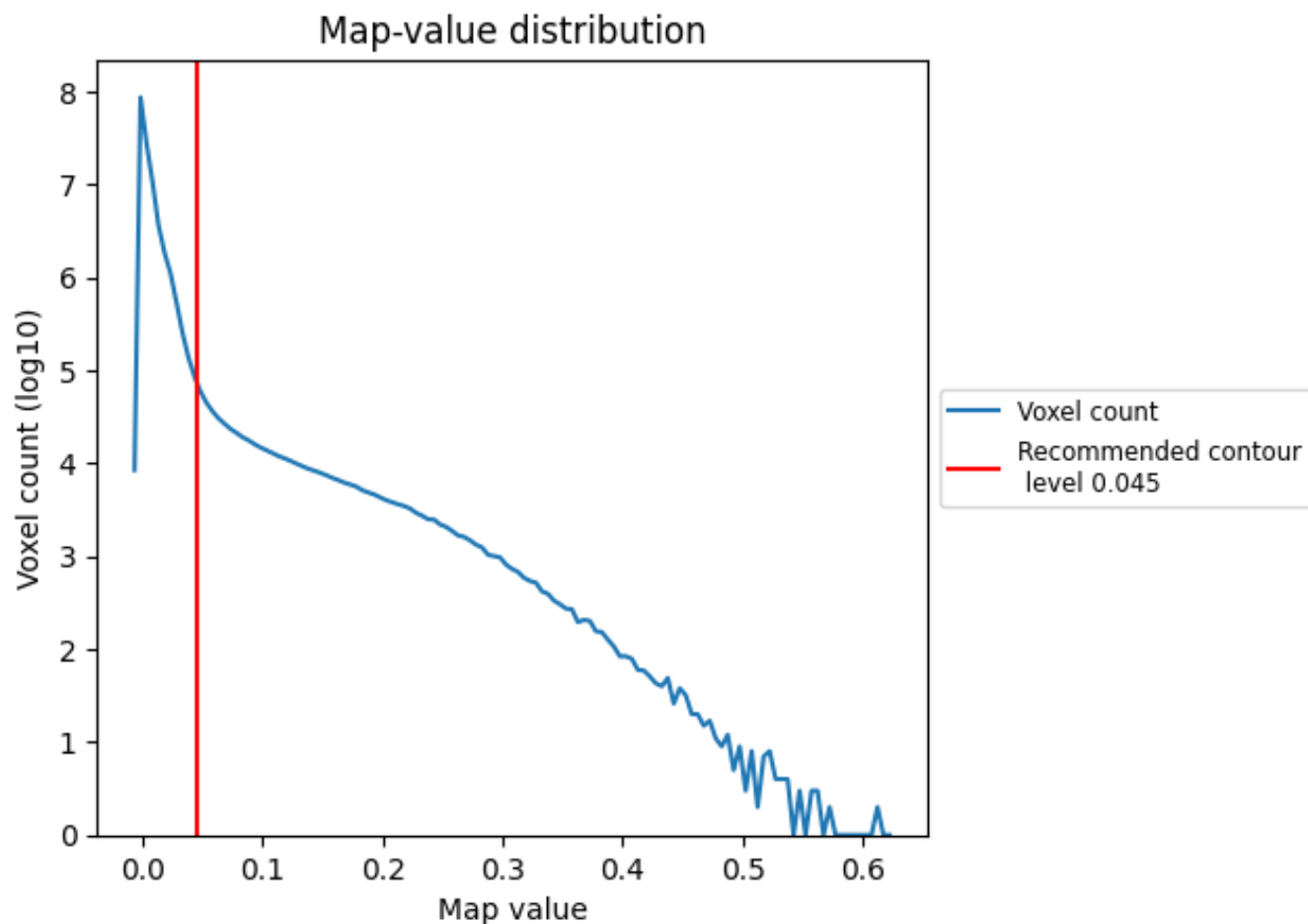
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

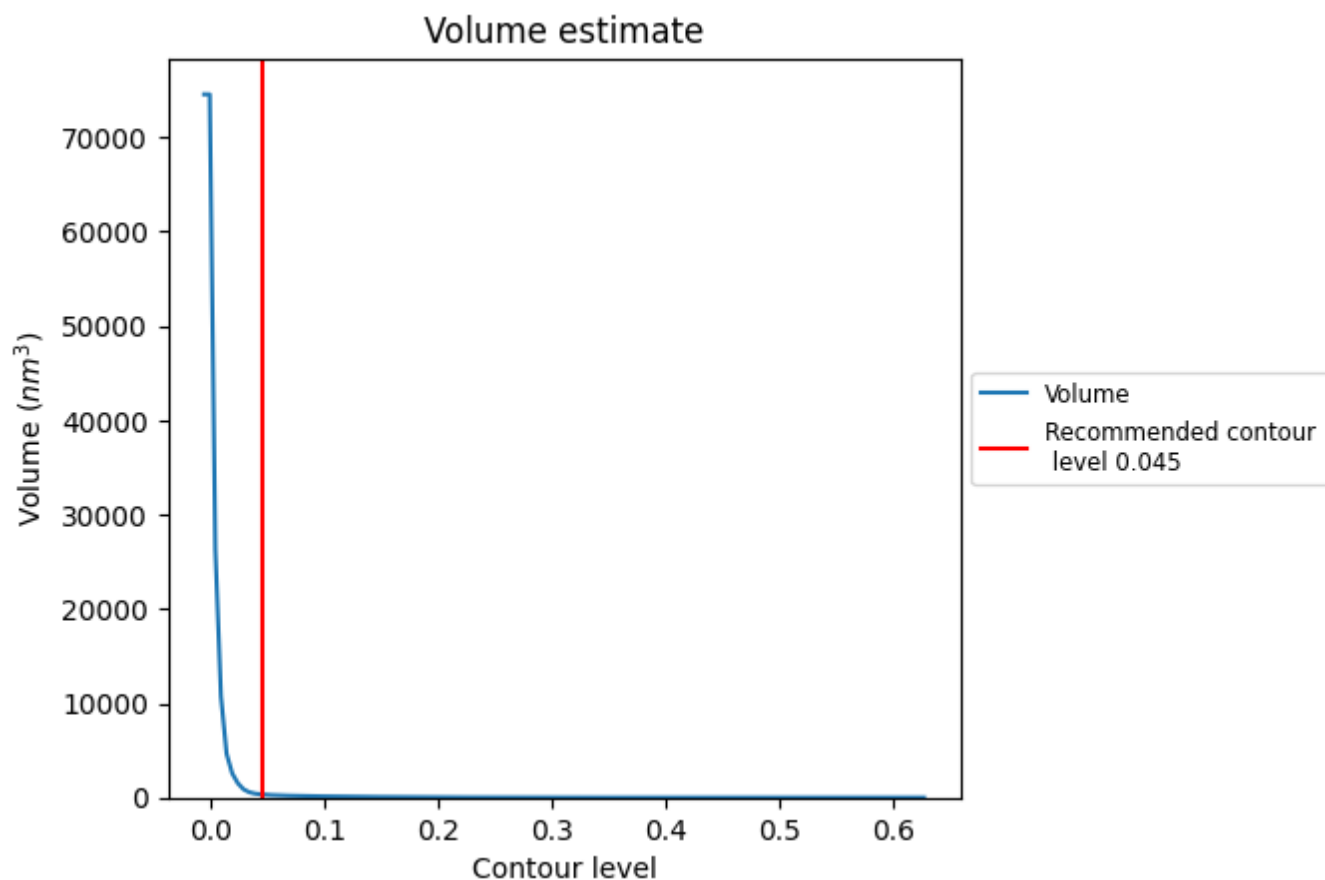
This section contains the results of statistical analysis of the map.

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.

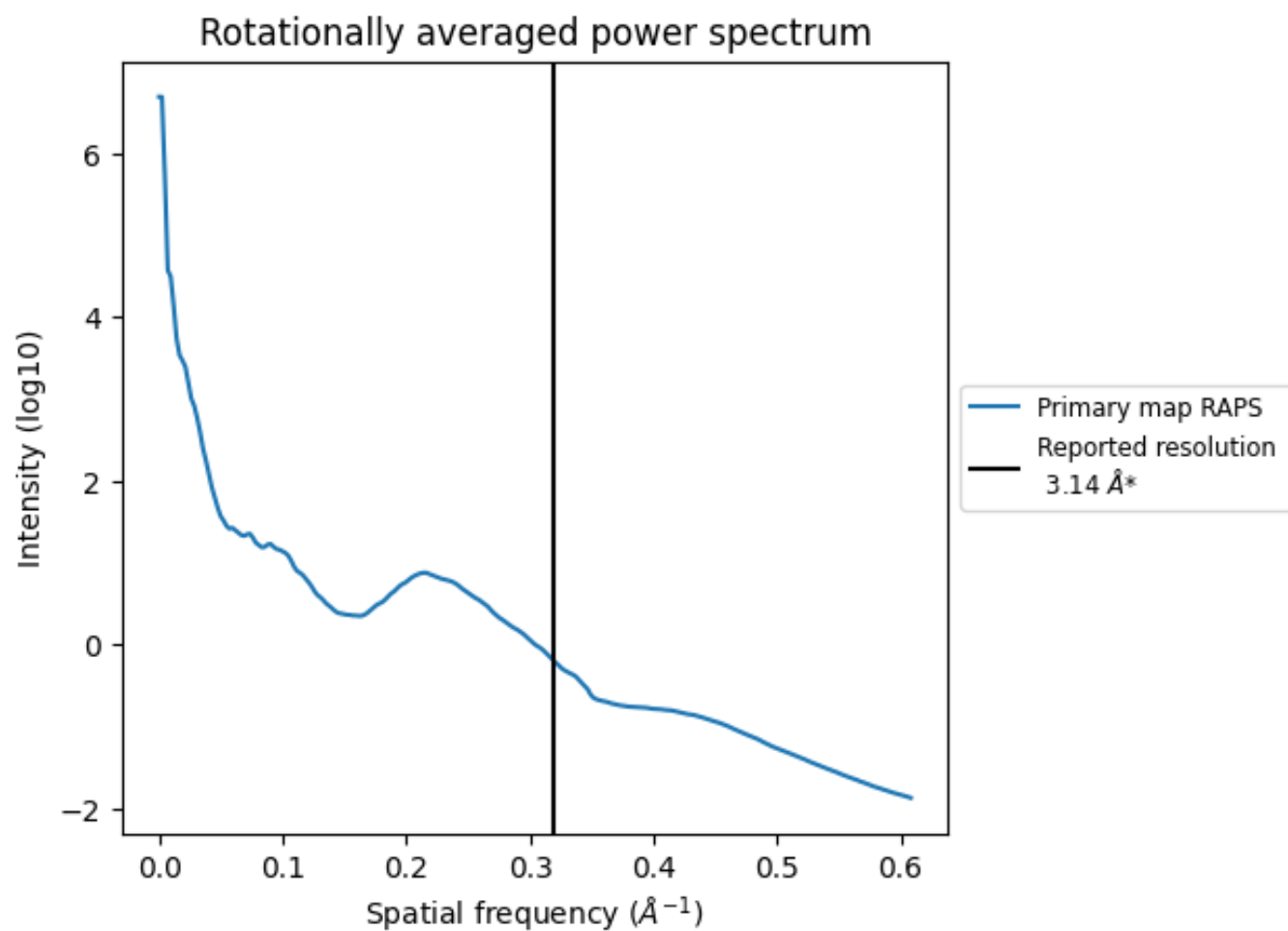
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 327 nm^3 ; this corresponds to an approximate mass of 295 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 0.318 Å⁻¹

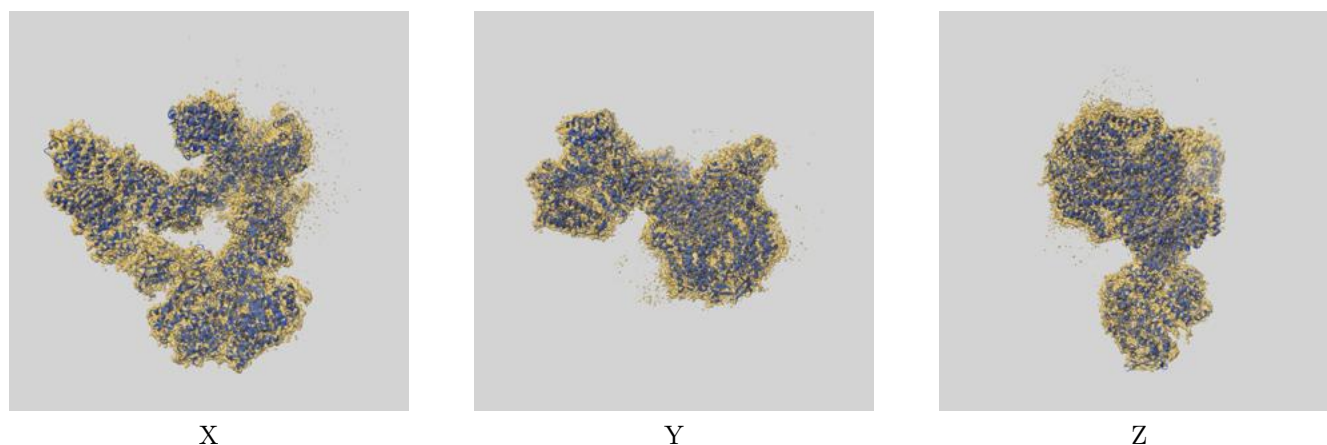
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

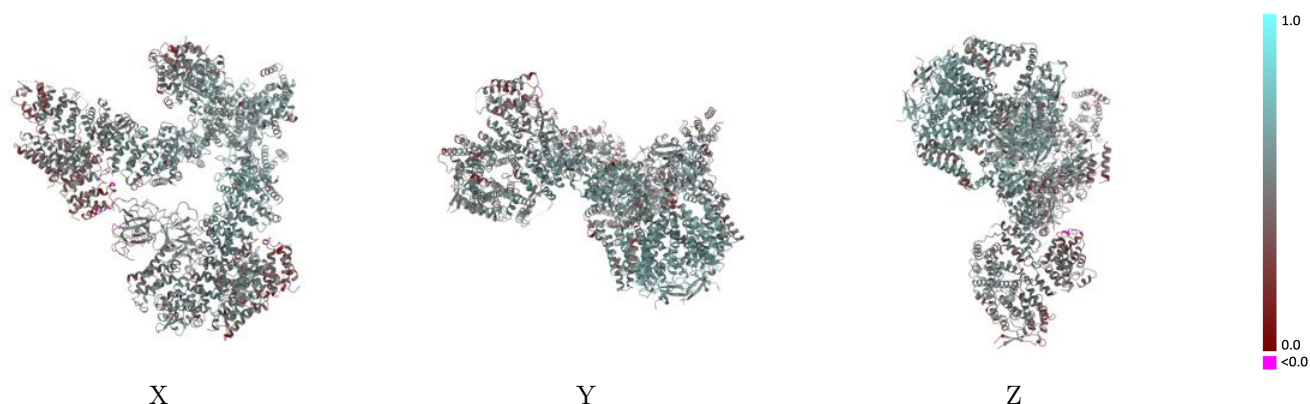
This section contains information regarding the fit between EMDB map EMD-73129 and PDB model 9YMZ. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



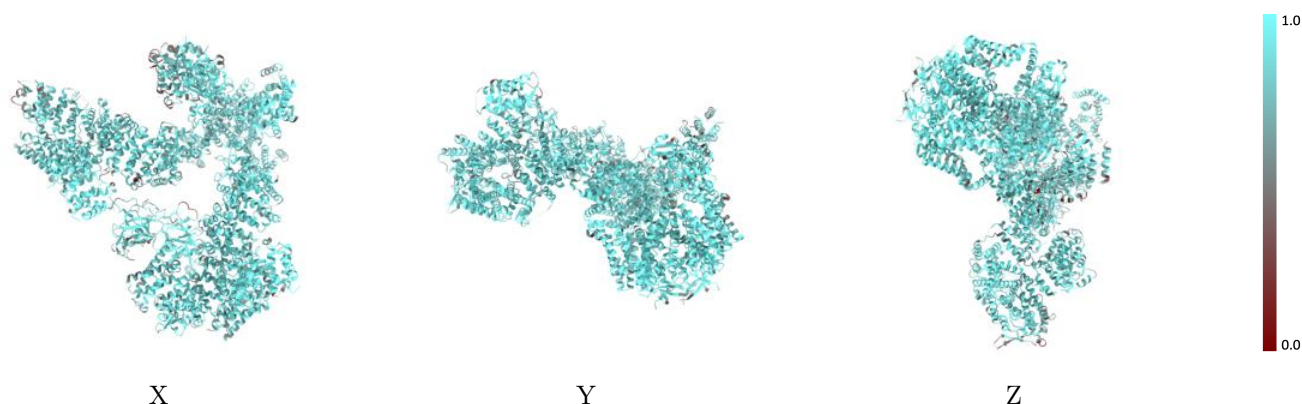
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



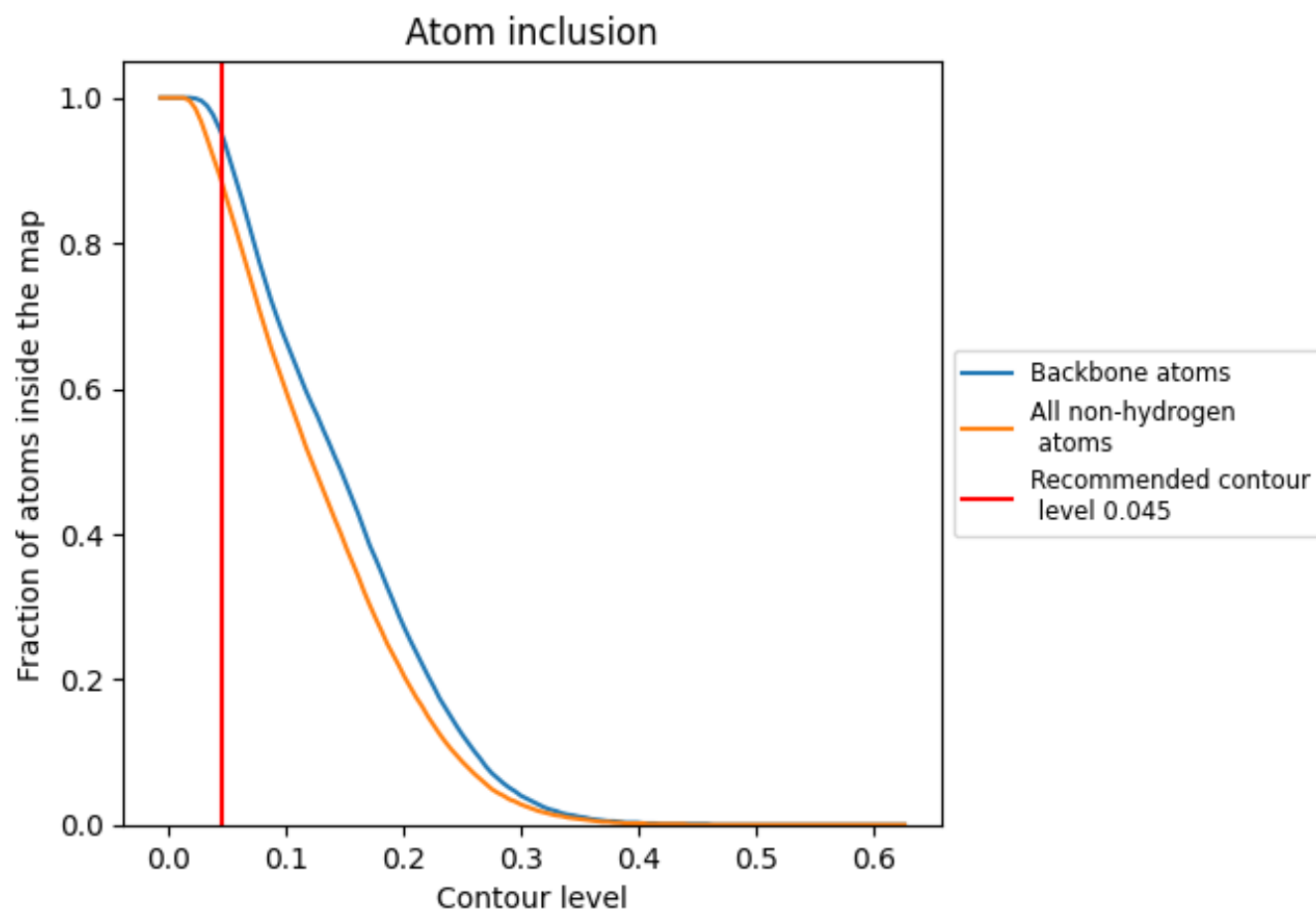
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8880	0.5090
A	0.8920	0.5100
B	0.8850	0.4940
C	0.8560	0.5150
D	0.9190	0.5480

