



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 10:09 AM UTC

PDB ID : 8TKE / pdb_00008tke
EMDB ID : EMD-41348
Title : Human Type 3 IP3 Receptor - Preactivated+Ca²⁺ State (+IP3/ATP/JD Ca²⁺)
Authors : Paknejad, N.; Sapuru, V.; Hite, R.K.
Deposited on : 2023-07-25
Resolution : 3.60 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

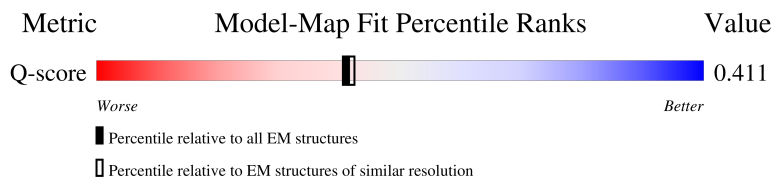
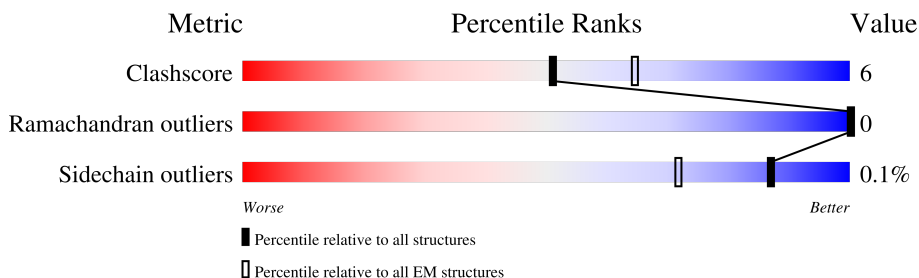
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

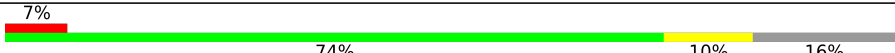
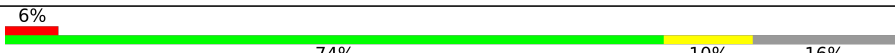
The reported resolution of this entry is 3.60 Å.

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	12797 (3.10 - 4.10)

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	2671	
1	B	2671	
1	C	2671	
1	D	2671	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 144456 atoms, of which 72136 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.

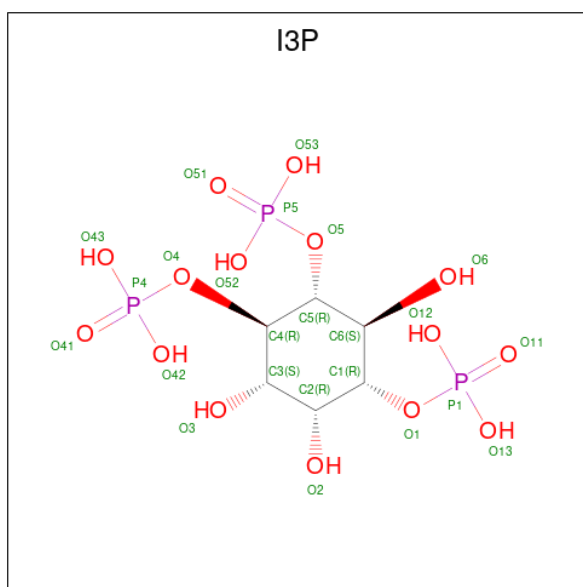
- Molecule 1 is a protein called Inositol 1,4,5-trisphosphate receptor type 3.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2249	Total	C	H	N	O	S	0	0
			36036	11497	18013	3089	3326	111		
1	B	2249	Total	C	H	N	O	S	0	0
			36036	11497	18013	3089	3326	111		
1	C	2249	Total	C	H	N	O	S	0	0
			36036	11497	18013	3089	3326	111		
1	D	2249	Total	C	H	N	O	S	0	0
			36036	11497	18013	3089	3326	111		

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is D-MYO-INOSITOL-1,4,5-TRIPHOSPHATE (CCD ID: I3P) (formula: C₆H₁₅O₁₅P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	B	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	C	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	D	1	Total	C	H	O	P	0
			33	6	9	15	3	

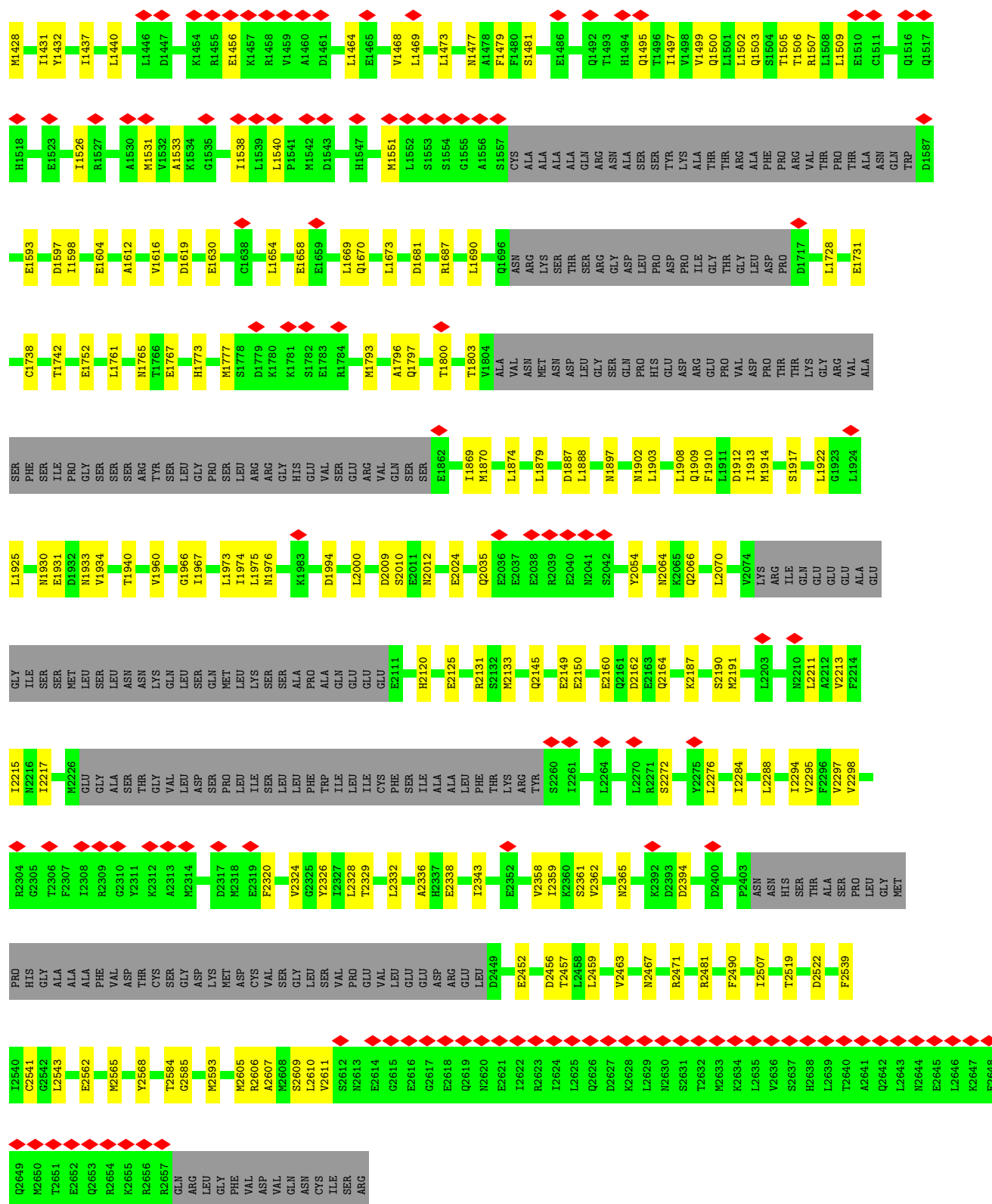
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

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

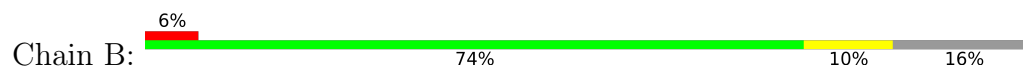
- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



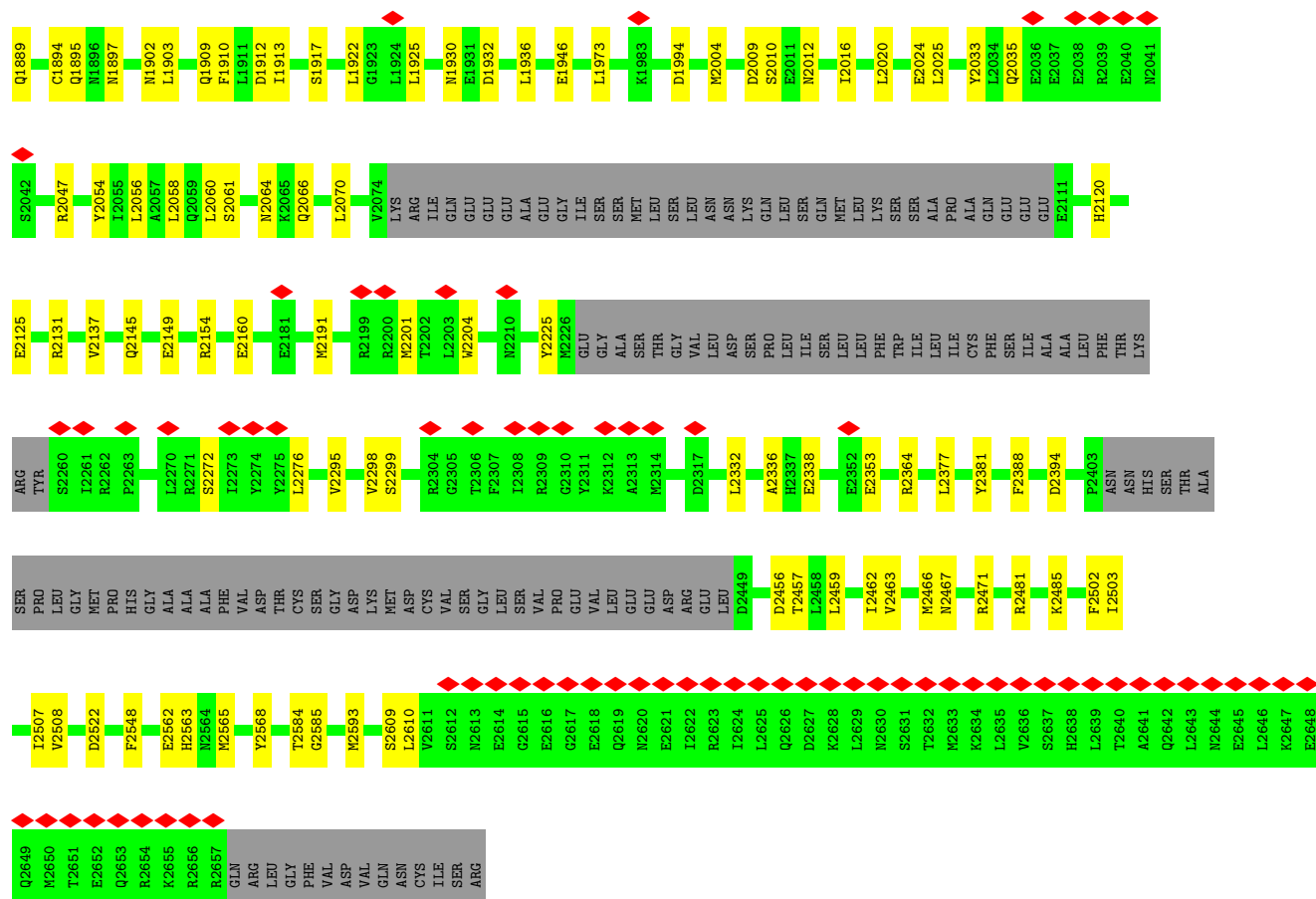
Mol	Chain	Residues	Atoms						AltConf
5	A	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
5	B	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
5	C	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
5	D	1	Total 43	C 10	H 12	N 5	O 13	P 3	0



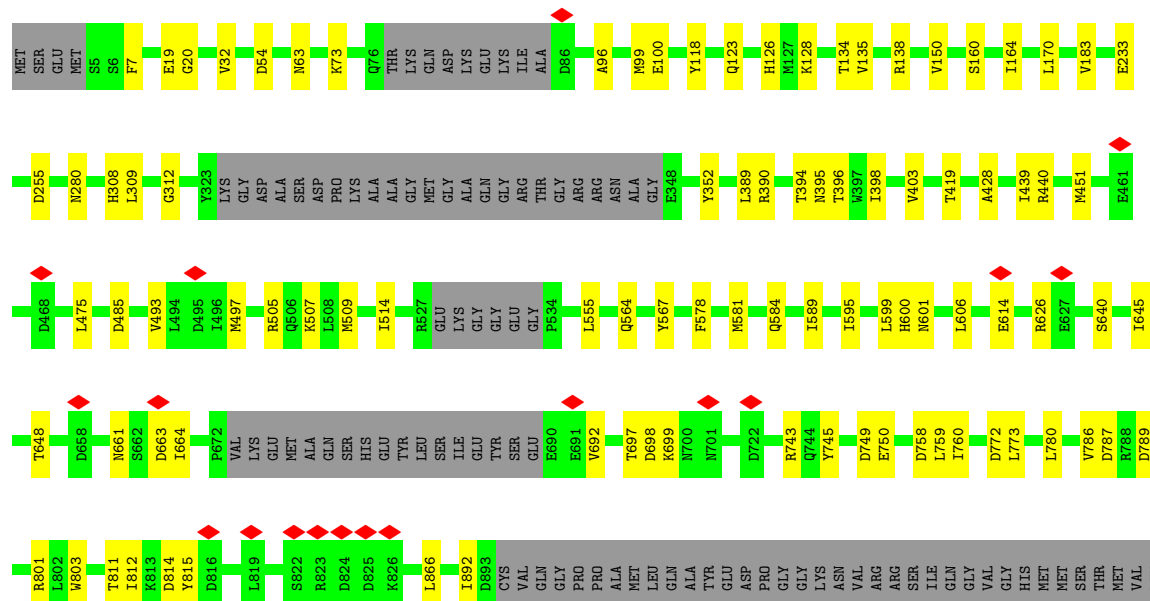
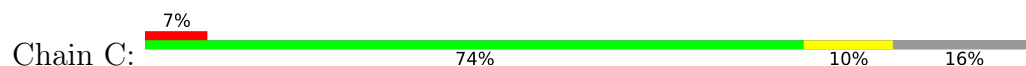
- Molecule 1: Inositol 1,4,5-trisphosphate receptor type 3







• Molecule 1: Inositol 1,4,5-trisphosphate receptor type 3



P2403	ASN	GLU	ILE	P2403	L1647	L1539	E1427	L1245	GLY	SER	SER
ASN	E2111	GLU	ALA	L1647	L1539	L1540	M1428	L1246	ALA	ARG	ARG
ASN	H2120	LEU	ALA	L1654	L1540	P1541	M1428	H1247	ALA	LYS	LYS
HIS	H2120	LEU	ALA	M1654	P1541	M1542	Y1432	H1248	LYS	GLN	GLN
THR	E2125	THR	PHE	E1658	M1542	D1543	H1436	H1249	ASP	ASN	ASN
ALA	R2131	LYS	THR	E1659	D1543	D1544	I1437	L1250	LYS	VAL	VAL
SER	R2131	LYS	THR	E1659	D1544	D1545	I1437	H1251	LYS	PHE	PHE
ARG	Q1145	LEU	THR	L1669	D1545	A1546	D1447	L1252	GLU	SER	SER
TYR	E2149	GLY	LEU	D1681	H1547	H1547	M1448	L1264	PRO	ALA	ALA
S2260	E2149	SER	GLN	Q1698	M1551	M1551	A1449	C1275	ASP	LEU	LEU
I2261	E2160	PRO	HIS	Q1698	M1551	L1552	R1455	I1278	GLU	SER	SER
R2262	K2167	GLY	ASP	Q1698	L1552	S1553	R1456	I1278	VAL	ALA	ALA
P2263	K2167	GLY	ASP	Q1698	L1552	S1553	E1456	I1278	GLY	GLY	GLY
L2270	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	LYS	ALA	ALA
R2271	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	THR	THR	THR
S2272	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	LEU	LEU	LEU
I2273	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	SER	ALA	ALA
P2274	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	PRO	ALA	ALA
V2275	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	PRO	GLU	GLU
L2276	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLY	PRO	PRO
G2277	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	LYS	LEU	LEU
T2281	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	LYS	ASP	ASP
R2304	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	SER	ARG	ARG
G2305	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	SER	ARG	ARG
T2306	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	LYS	LYS	LYS
F2307	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	PHE	PHE	PHE
I2308	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
R2309	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	ASN	ASN	ASN
V2310	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
Y2311	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
K2312	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
A2313	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
M2314	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
D2317	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
Y2326	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
E2338	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
E2352	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
E2353	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
V2358	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
S2361	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
N2365	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
Y2381	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
I2385	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
F2388	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU
D2394	K2167	ALA	ASP	Q1698	L1552	S1553	E1456	I1278	GLU	GLU	GLU





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	123416	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	66	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	4300	Depositor
Magnification	29000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	132.507	Depositor
Minimum map value	-38.790	Depositor
Average map value	0.152	Depositor
Map value standard deviation	1.648	Depositor
Recommended contour level	6	Depositor
Map size (Å)	422.68802, 422.68802, 422.68802	wwPDB
Map dimensions	672, 672, 672	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.629, 0.629, 0.629	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, ZN, CA, 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	0.09	0/18354	0.24	0/24804
1	B	0.09	0/18354	0.24	0/24804
1	C	0.09	0/18354	0.23	0/24804
1	D	0.09	0/18354	0.24	0/24804
All	All	0.09	0/73416	0.24	0/99216

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	18023	18013	18013	220	0
1	B	18023	18013	18013	192	0
1	C	18023	18013	18013	196	0
1	D	18023	18013	18013	209	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	24	9	9	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	24	9	9	2	0
3	C	24	9	9	2	0
3	D	24	9	9	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	31	12	12	0	0
5	B	31	12	12	3	0
5	C	31	12	12	0	0
5	D	31	12	12	1	0
All	All	72320	72136	72136	795	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 6.

The worst 5 of 795 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:1925:LEU:HD21	1:B:1973:LEU:HD23	1.58	0.85
1:D:465:SER:OG	1:D:468:ASP:OD1	1.95	0.84
1:A:465:SER:OG	1:A:468:ASP:OD1	1.95	0.83
1:B:465:SER:OG	1:B:468:ASP:OD1	1.96	0.83
1:C:1925:LEU:HD21	1:C:1973:LEU:HD23	1.62	0.82

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	2219/2671 (83%)	2179 (98%)	40 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	2219/2671 (83%)	2191 (99%)	28 (1%)	0	100	100
1	C	2219/2671 (83%)	2192 (99%)	27 (1%)	0	100	100
1	D	2219/2671 (83%)	2190 (99%)	29 (1%)	0	100	100
All	All	8876/10684 (83%)	8752 (99%)	124 (1%)	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	1995/2385 (84%)	1993 (100%)	2 (0%)	88	87
1	B	1995/2385 (84%)	1995 (100%)	0	100	100
1	C	1995/2385 (84%)	1993 (100%)	2 (0%)	88	87
1	D	1995/2385 (84%)	1988 (100%)	7 (0%)	84	81
All	All	7980/9540 (84%)	7969 (100%)	11 (0%)	87	87

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	1210	LEU
1	D	1363	MET
1	D	2510	ASN
1	D	1367	SER
1	D	374	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	192	GLN
1	C	1344	HIS
1	D	1965	ASN

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Mol	Chain	Res	Type
1	C	551	HIS
1	C	1084	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	$\# Z > 2$
5	ATP	B	3004	-	32,33,33	0.26	0	48,52,52	0.67	0
5	ATP	C	3004	-	32,33,33	0.26	0	48,52,52	0.67	0
3	I3P	A	3002	-	24,24,24	2.17	3 (12%)	39,39,39	0.86	0
3	I3P	D	3002	-	24,24,24	2.17	3 (12%)	39,39,39	0.86	0
3	I3P	B	3002	-	24,24,24	2.17	3 (12%)	39,39,39	0.86	0
3	I3P	C	3002	-	24,24,24	2.17	3 (12%)	39,39,39	0.86	0
5	ATP	D	3004	-	32,33,33	0.26	0	48,52,52	0.67	0
5	ATP	A	3004	-	32,33,33	0.26	0	48,52,52	0.67	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
5	ATP	B	3004	-	-	9/22/38/38	0/3/3/3
5	ATP	C	3004	-	-	10/22/38/38	0/3/3/3
3	I3P	A	3002	-	-	2/15/39/39	0/1/1/1
3	I3P	D	3002	-	-	1/15/39/39	0/1/1/1
3	I3P	B	3002	-	-	2/15/39/39	0/1/1/1
3	I3P	C	3002	-	-	1/15/39/39	0/1/1/1
5	ATP	D	3004	-	-	9/22/38/38	0/3/3/3
5	ATP	A	3004	-	-	9/22/38/38	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	3002	I3P	P4-O4	6.02	1.70	1.59
3	A	3002	I3P	P4-O4	6.02	1.70	1.59
3	C	3002	I3P	P4-O4	6.02	1.70	1.59
3	D	3002	I3P	P4-O4	6.02	1.70	1.59
3	C	3002	I3P	P5-O5	5.84	1.69	1.59

There are no bond angle outliers.

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	3004	ATP	PB-O3B-PG-O3G
5	A	3004	ATP	C5'-O5'-PA-O2A
5	B	3004	ATP	PB-O3B-PG-O3G
5	B	3004	ATP	C5'-O5'-PA-O1A
5	B	3004	ATP	C5'-O5'-PA-O2A

There are no ring outliers.

6 monomers are involved in 12 short contacts:

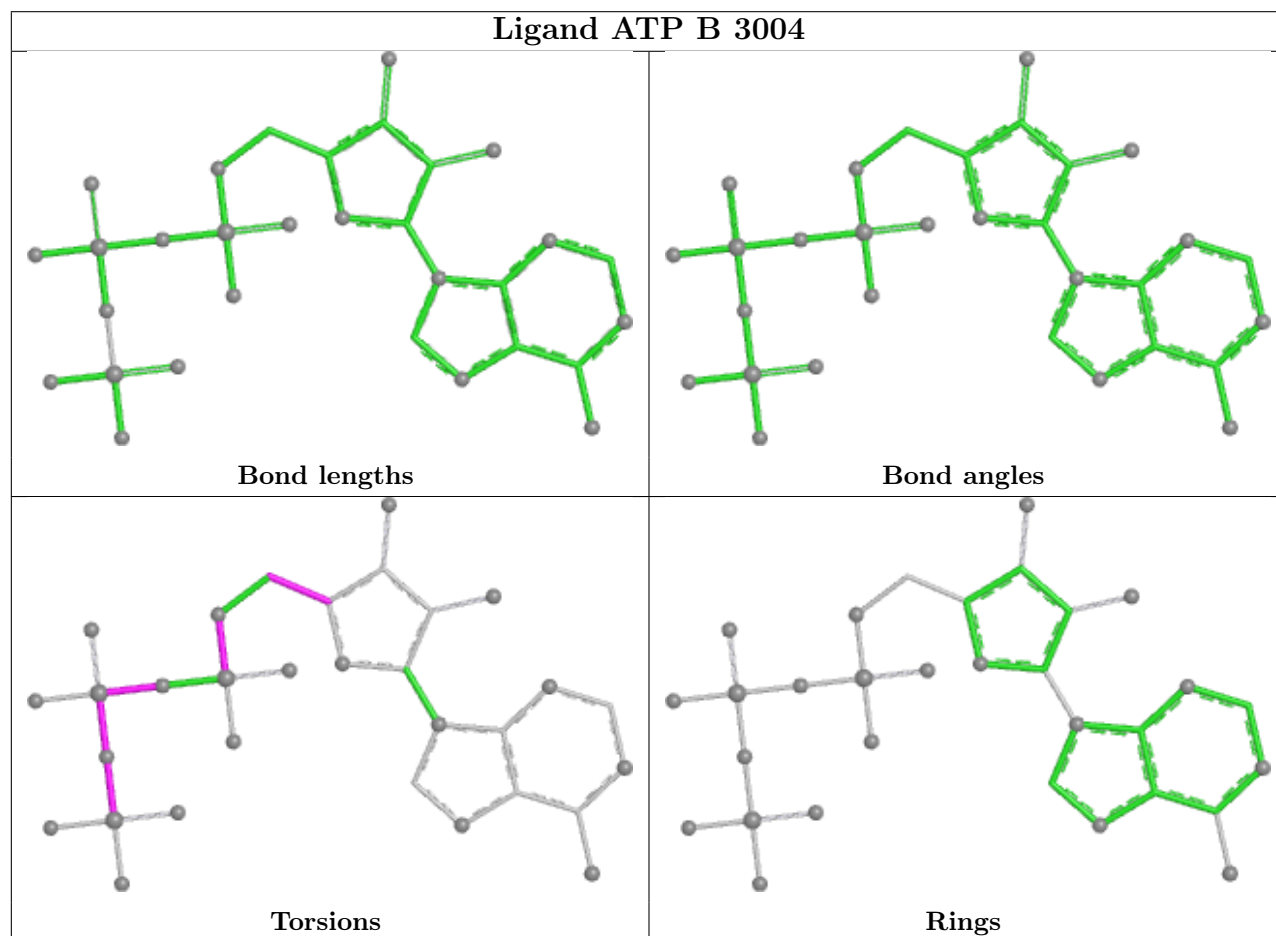
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	3004	ATP	3	0
3	A	3002	I3P	2	0
3	D	3002	I3P	2	0
3	B	3002	I3P	2	0
3	C	3002	I3P	2	0

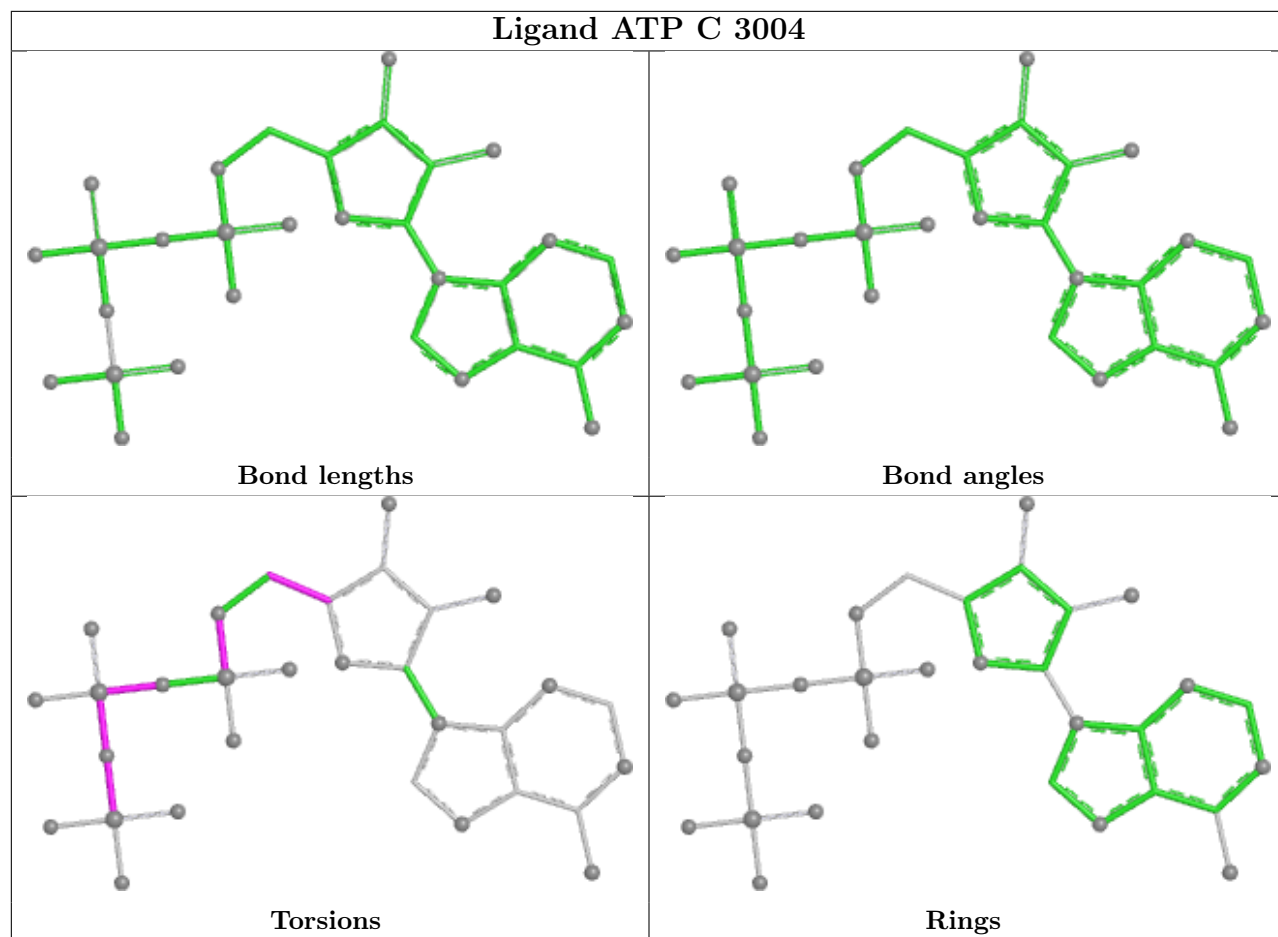
Continued on next page...

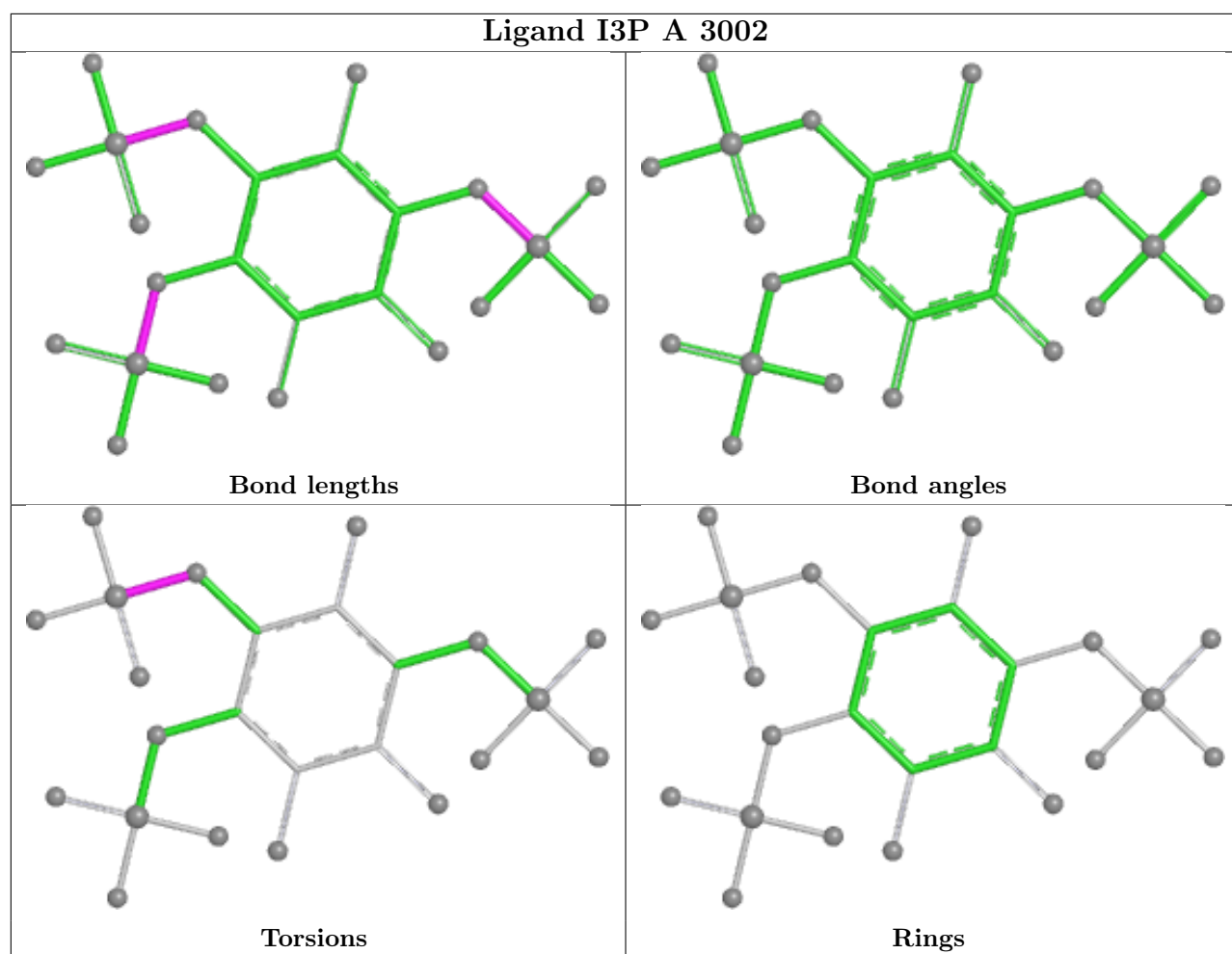
Continued from previous page...

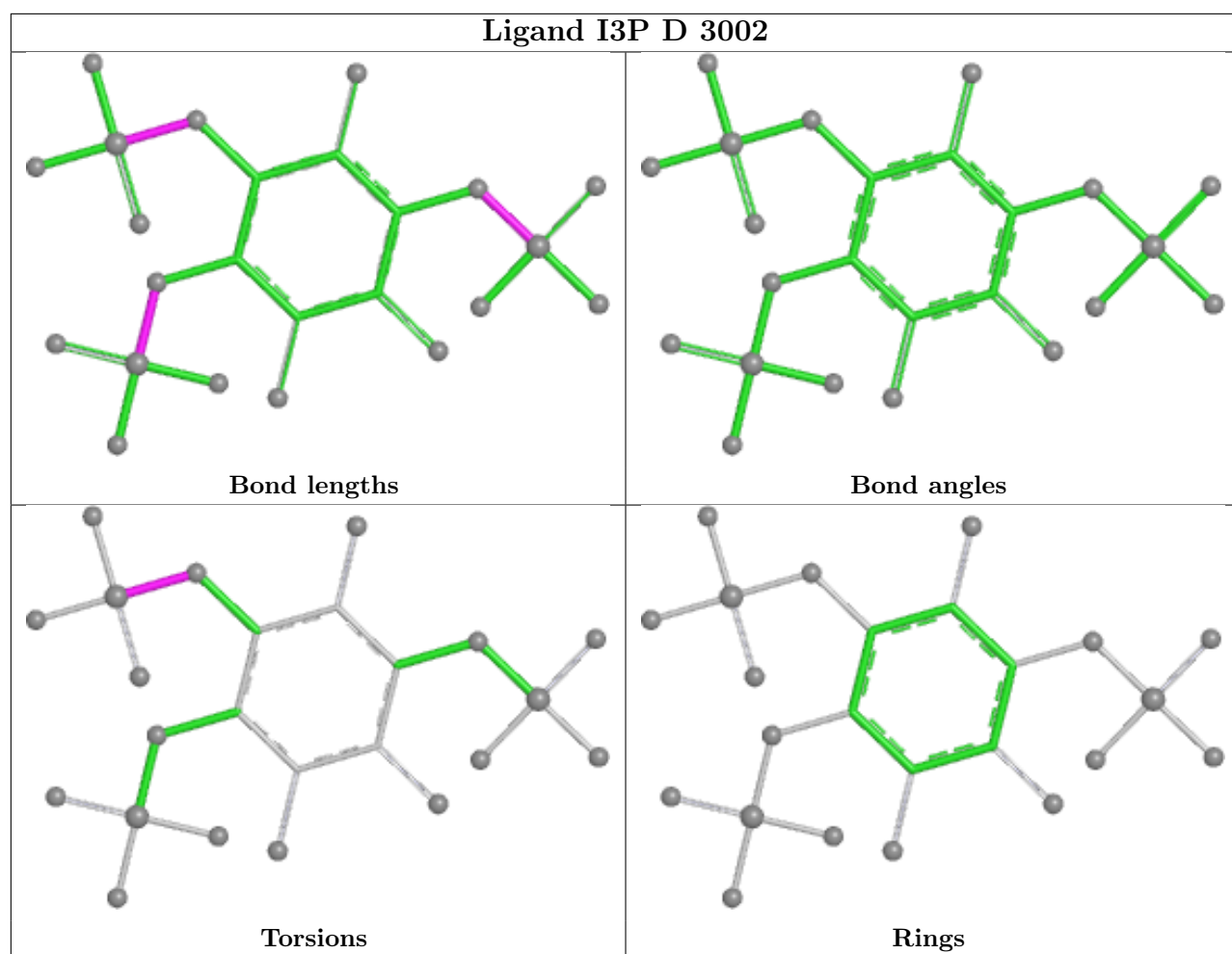
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	3004	ATP	1	0

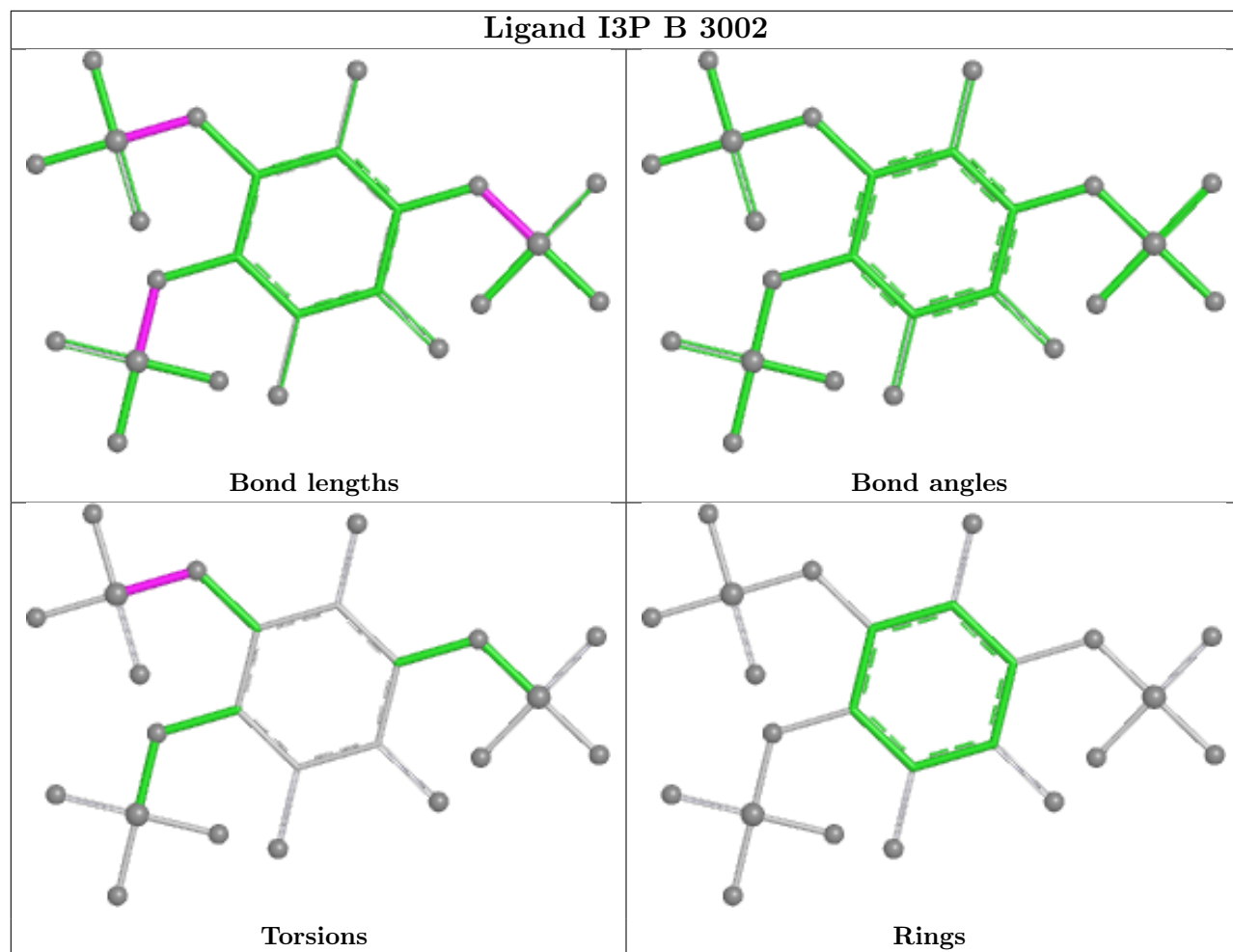
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

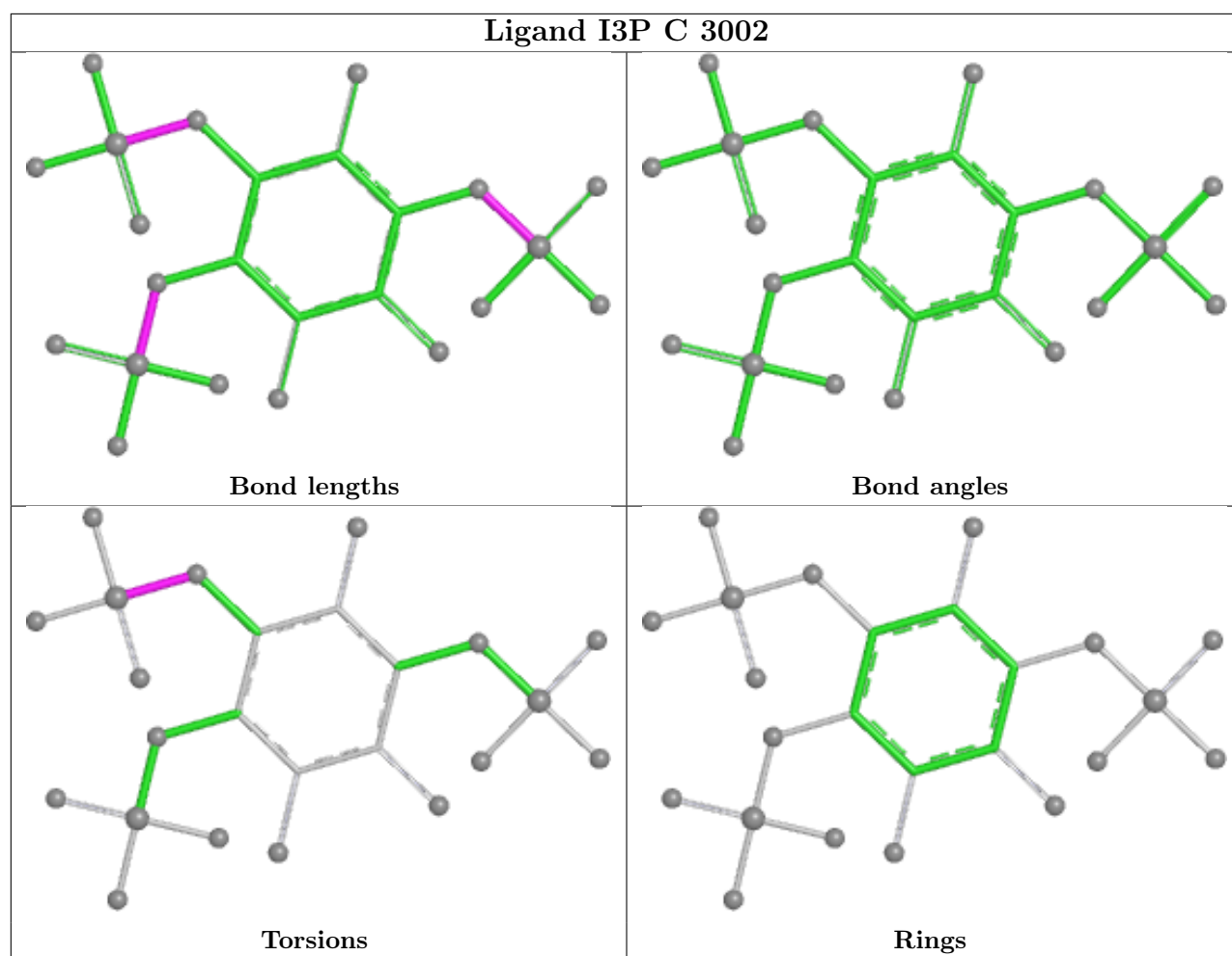


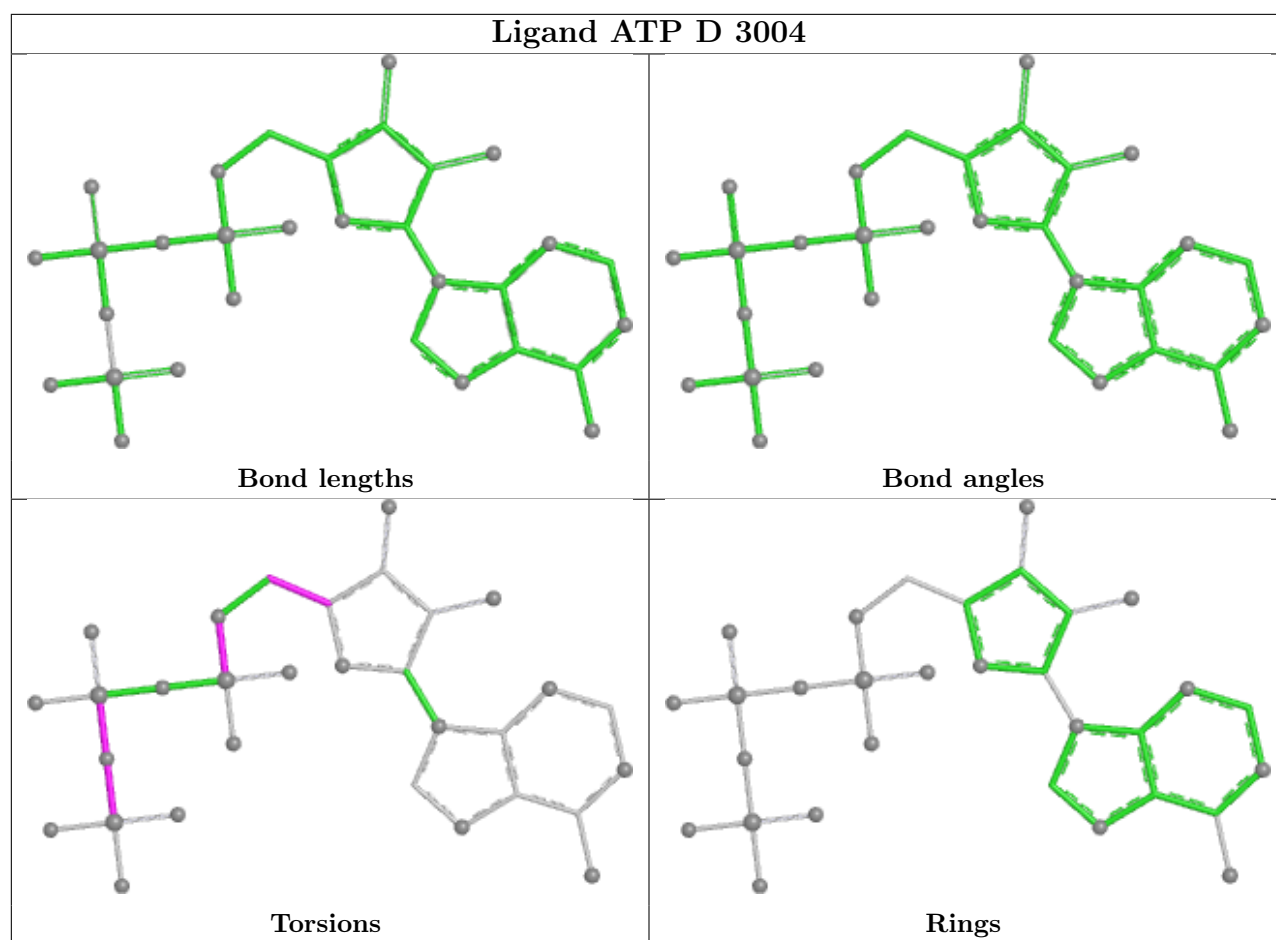


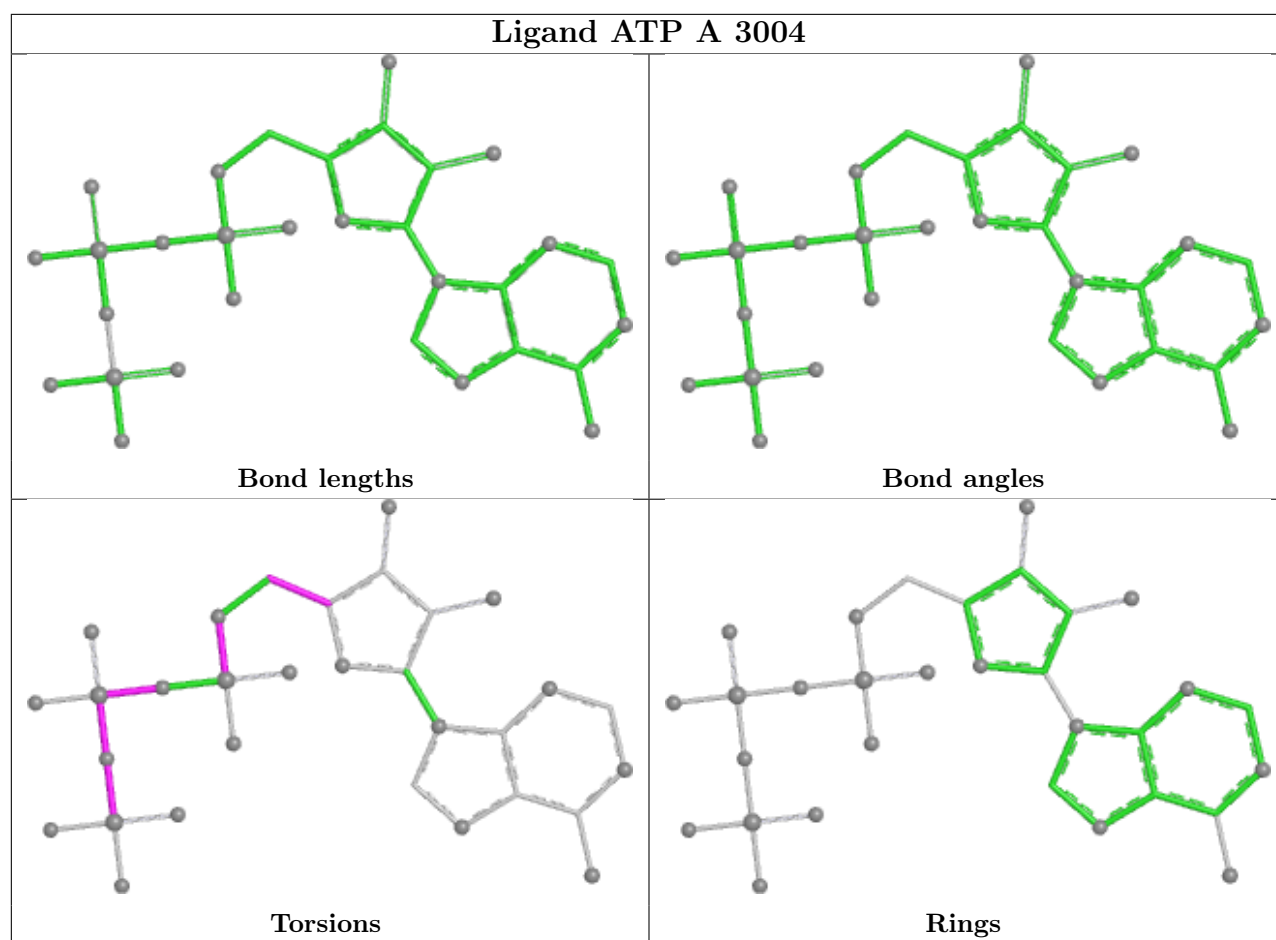












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

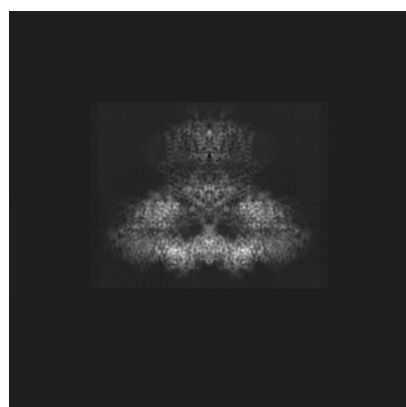
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41348. These allow visual inspection of the internal detail of the map and identification of artifacts.

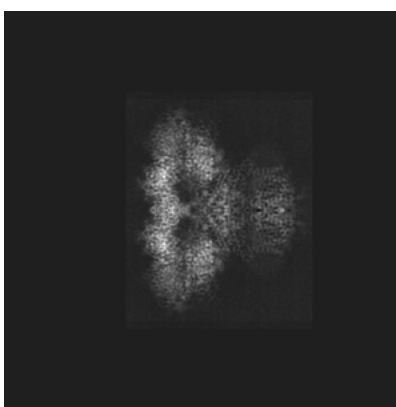
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

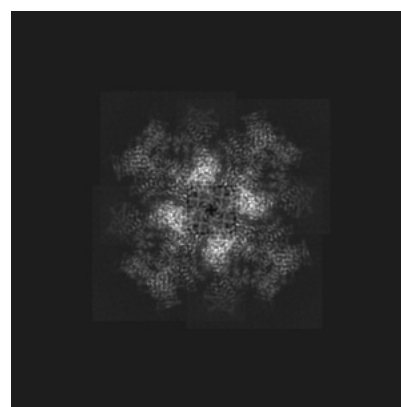
6.1.1 Primary map



X



Y

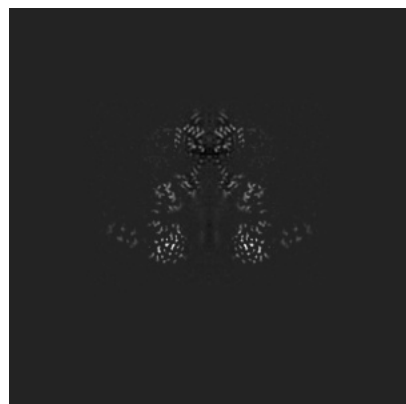


Z

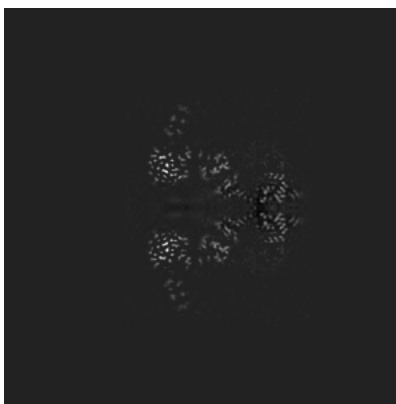
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 336



Y Index: 336

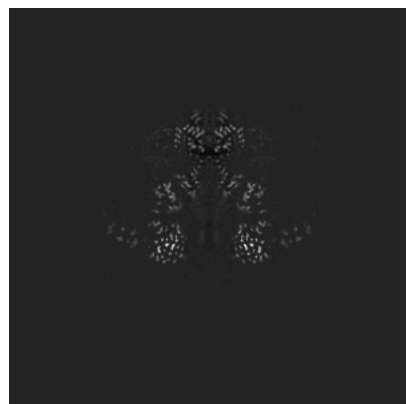


Z Index: 336

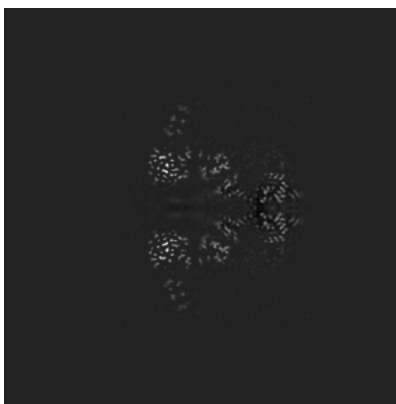
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

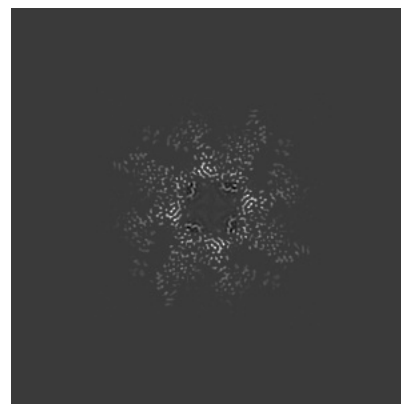
6.3.1 Primary map



X Index: 336



Y Index: 336

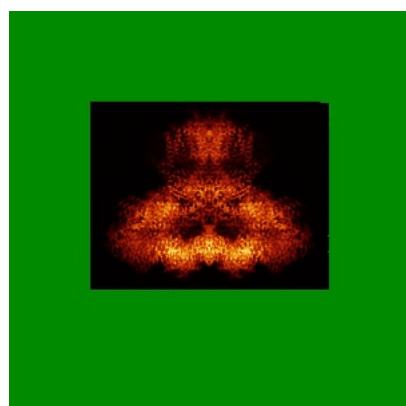


Z Index: 268

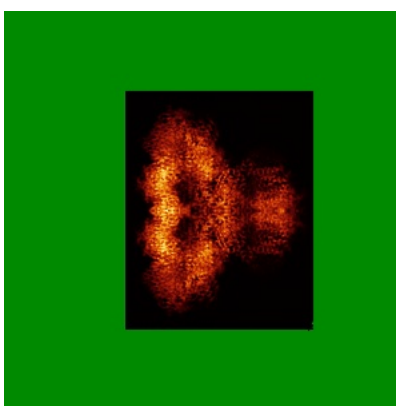
The images above show the largest variance slices of the map in three orthogonal directions.

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

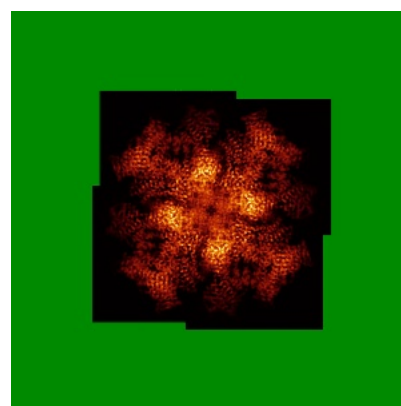
6.4.1 Primary map



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

This section was not generated.

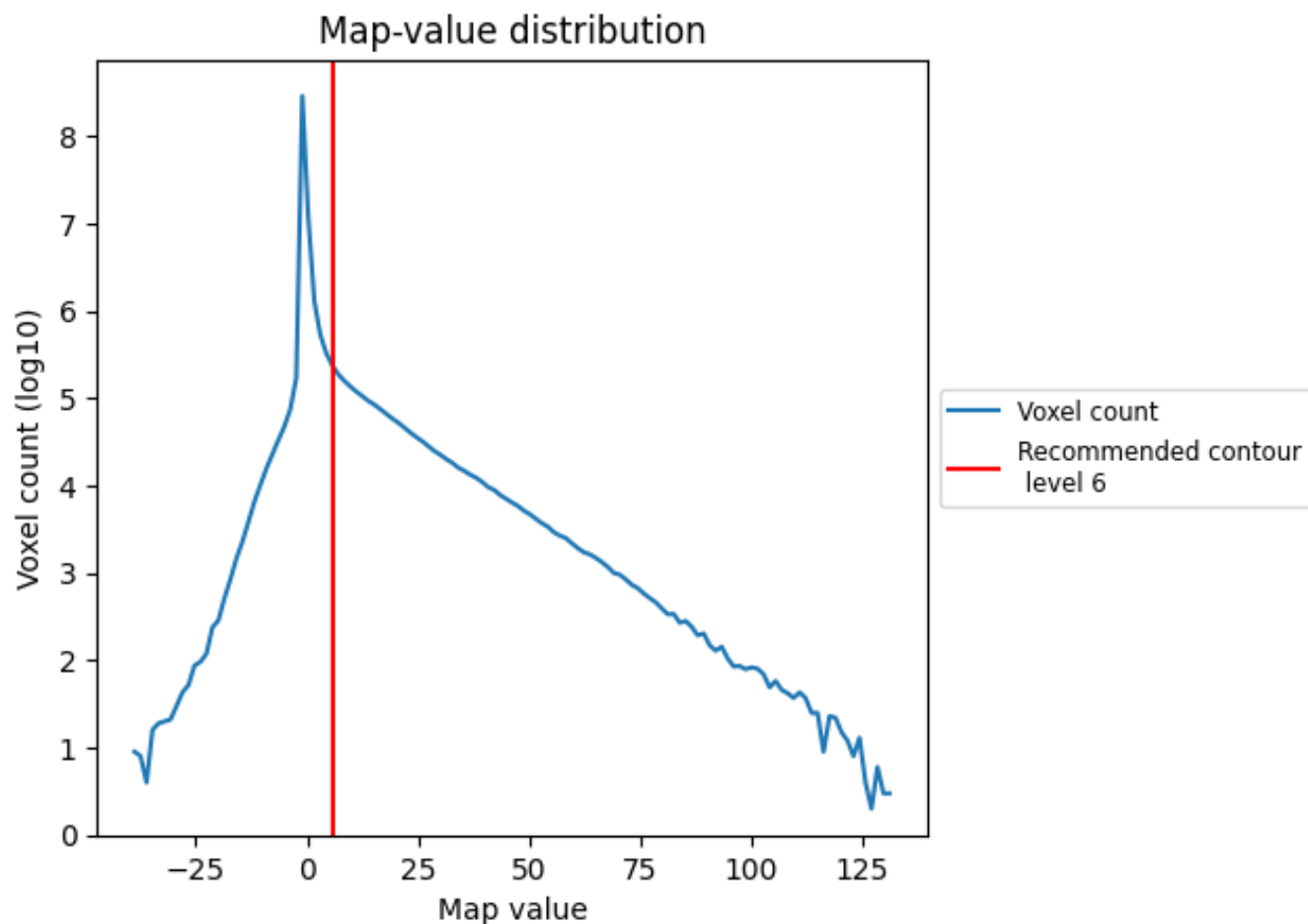
6.6 Mask visualisation

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

7 Map analysis [i](#)

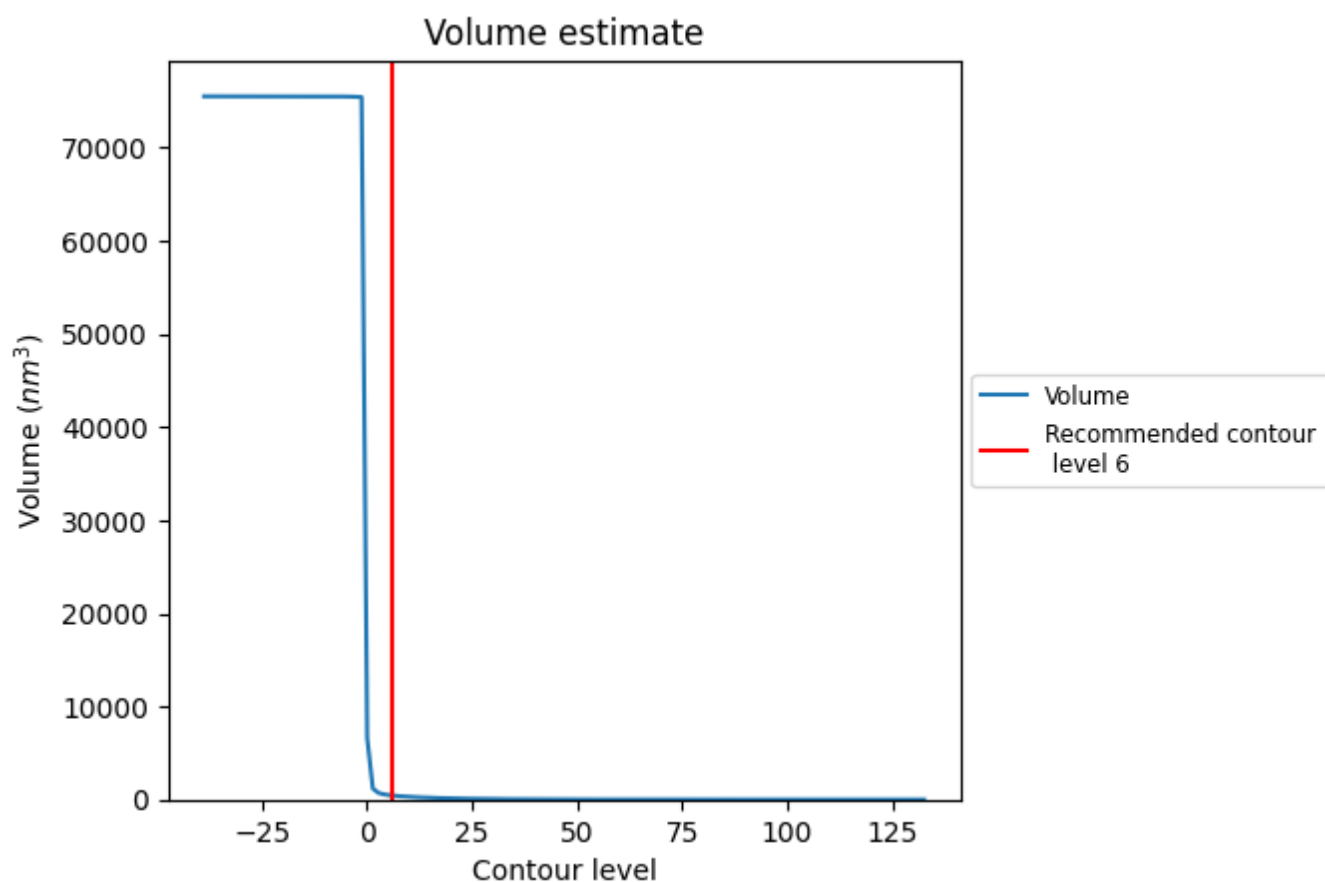
This section contains the results of statistical analysis of the map.

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.

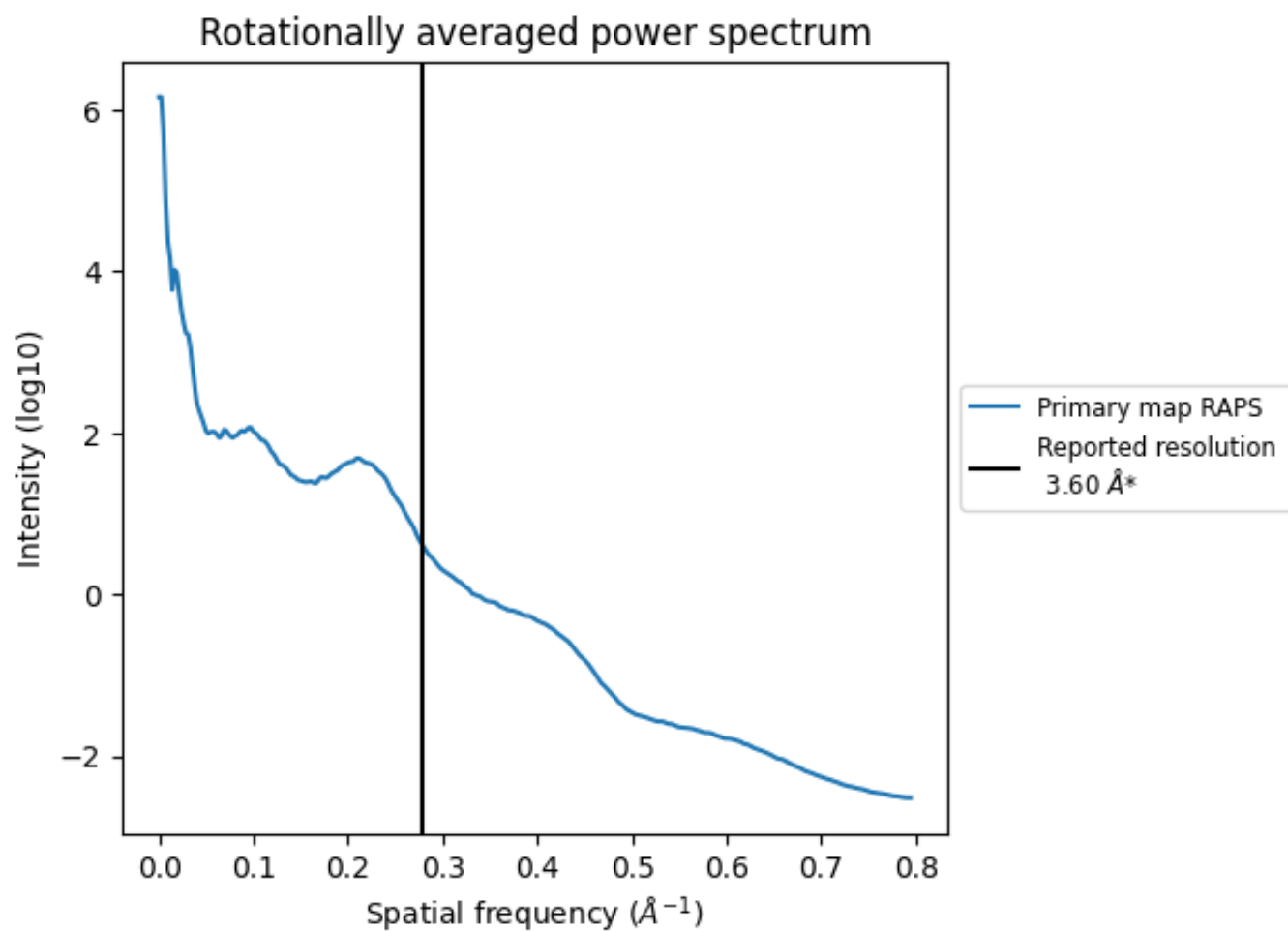
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 439 nm³; this corresponds to an approximate mass of 396 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 0.278 Å⁻¹

8 Fourier-Shell correlation

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

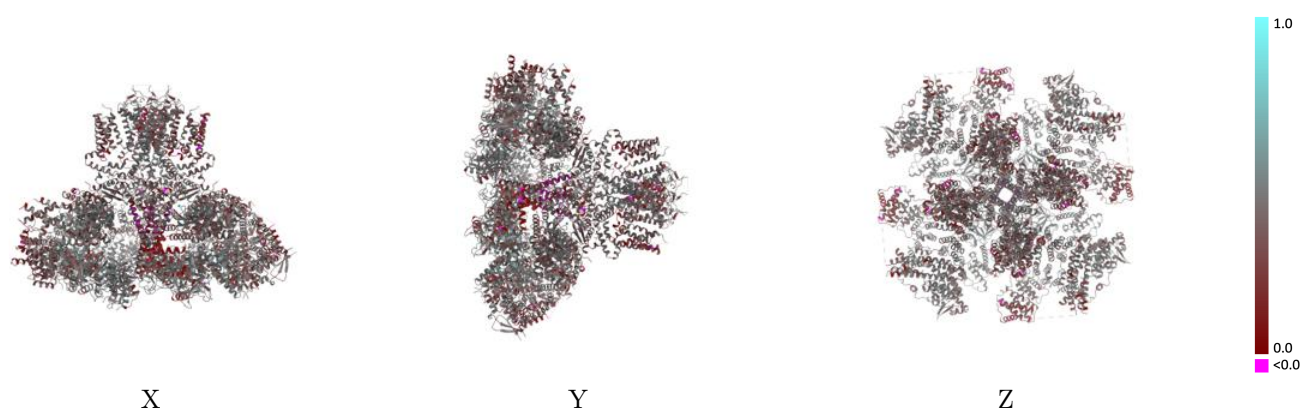
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41348 and PDB model 8TKE. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

This section was not generated.

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

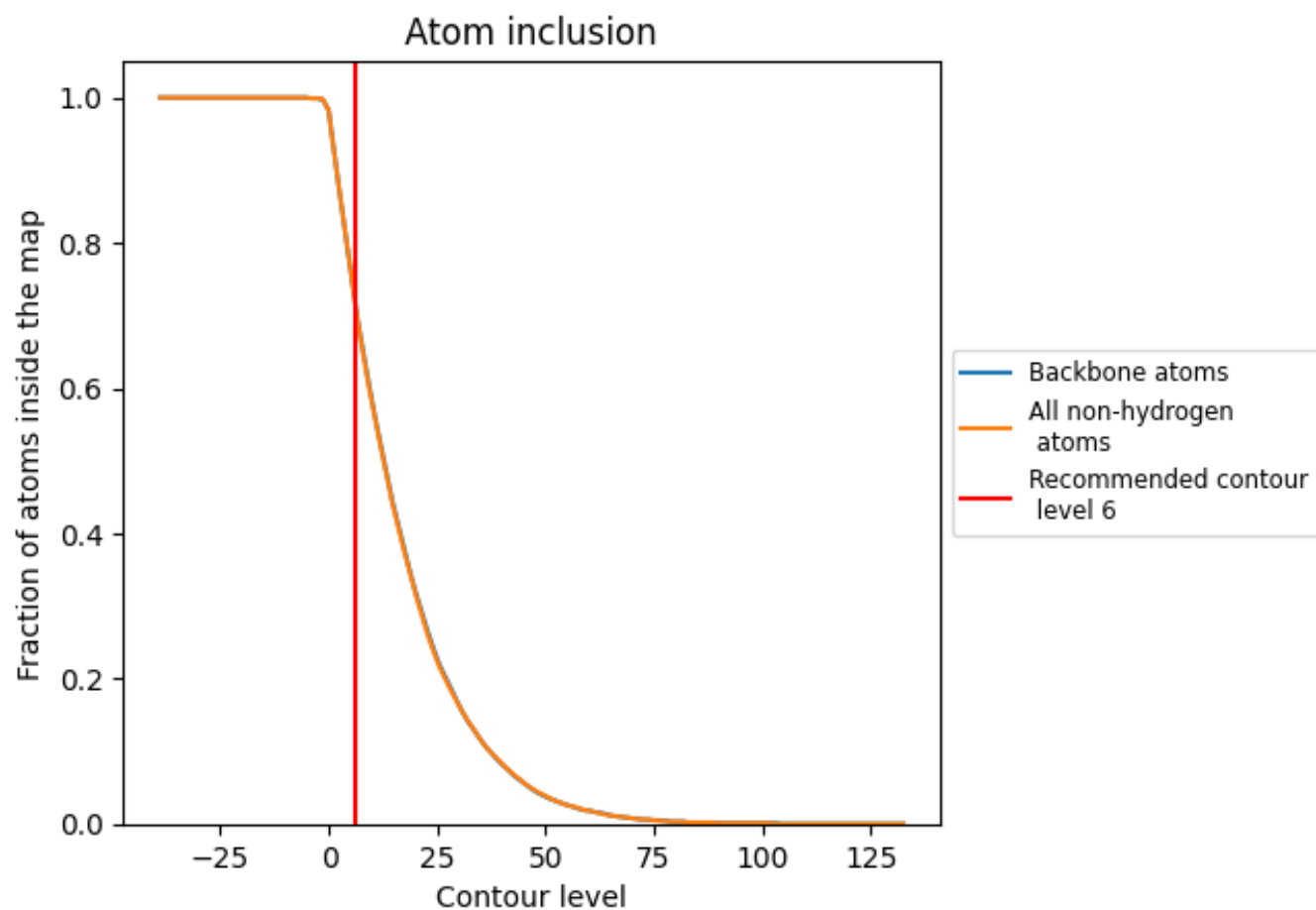


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 72% of all backbone atoms, 72% 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 (6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7220	0.4110
A	0.7290	0.4090
B	0.7290	0.4130
C	0.7270	0.4120
D	0.7290	0.4100

