



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 09:37 AM UTC

PDB ID : 8TKD / pdb_00008tkd
EMDB ID : EMD-41347
Title : Human Type 3 IP3 Receptor - Preactivated State (+IP3/ATP)
Authors : Paknejad, N.; Sapuru, V.; Hite, R.K.
Deposited on : 2023-07-25
Resolution : 3.70 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

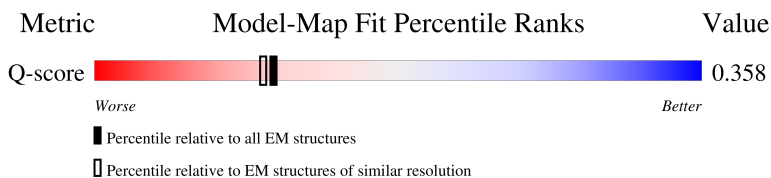
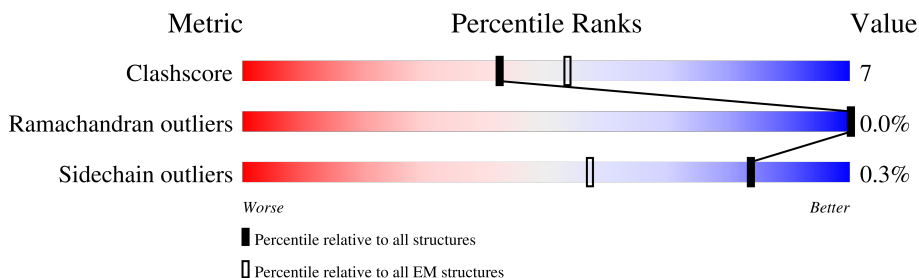
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	<div> <div>10%</div> <div>72%</div> <div>12%</div> <div>16%</div> </div>
1	B	2671	<div> <div>11%</div> <div>72%</div> <div>12%</div> <div>16%</div> </div>
1	C	2671	<div> <div>10%</div> <div>72%</div> <div>12%</div> <div>16%</div> </div>
1	D	2671	<div> <div>10%</div> <div>71%</div> <div>13%</div> <div>16%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 144452 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.

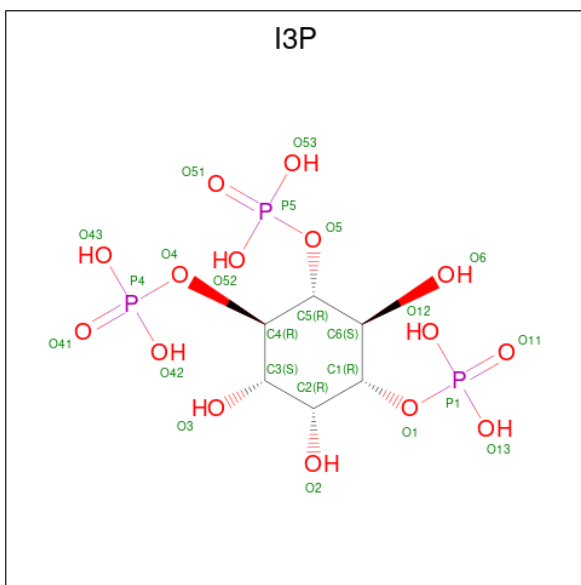
- Molecule 1 is a protein called Inositol 1,4,5-trisphosphate receptor type 3.

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) (labeled as "Ligand of Interest" by depositor).

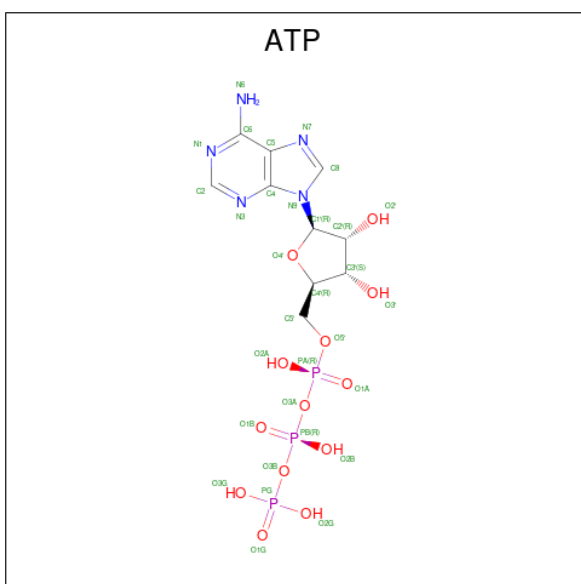
Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Zn	0
			1	1	
2	B	1	Total	Zn	0
			1	1	
2	C	1	Total	Zn	0
			1	1	
2	D	1	Total	Zn	0
			1	1	

- Molecule 3 is D-MYO-INOSITOL-1,4,5-TRIPHOSPHATE (CCD ID: I3P) (formula: C₆H₁₅O₁₅P₃).



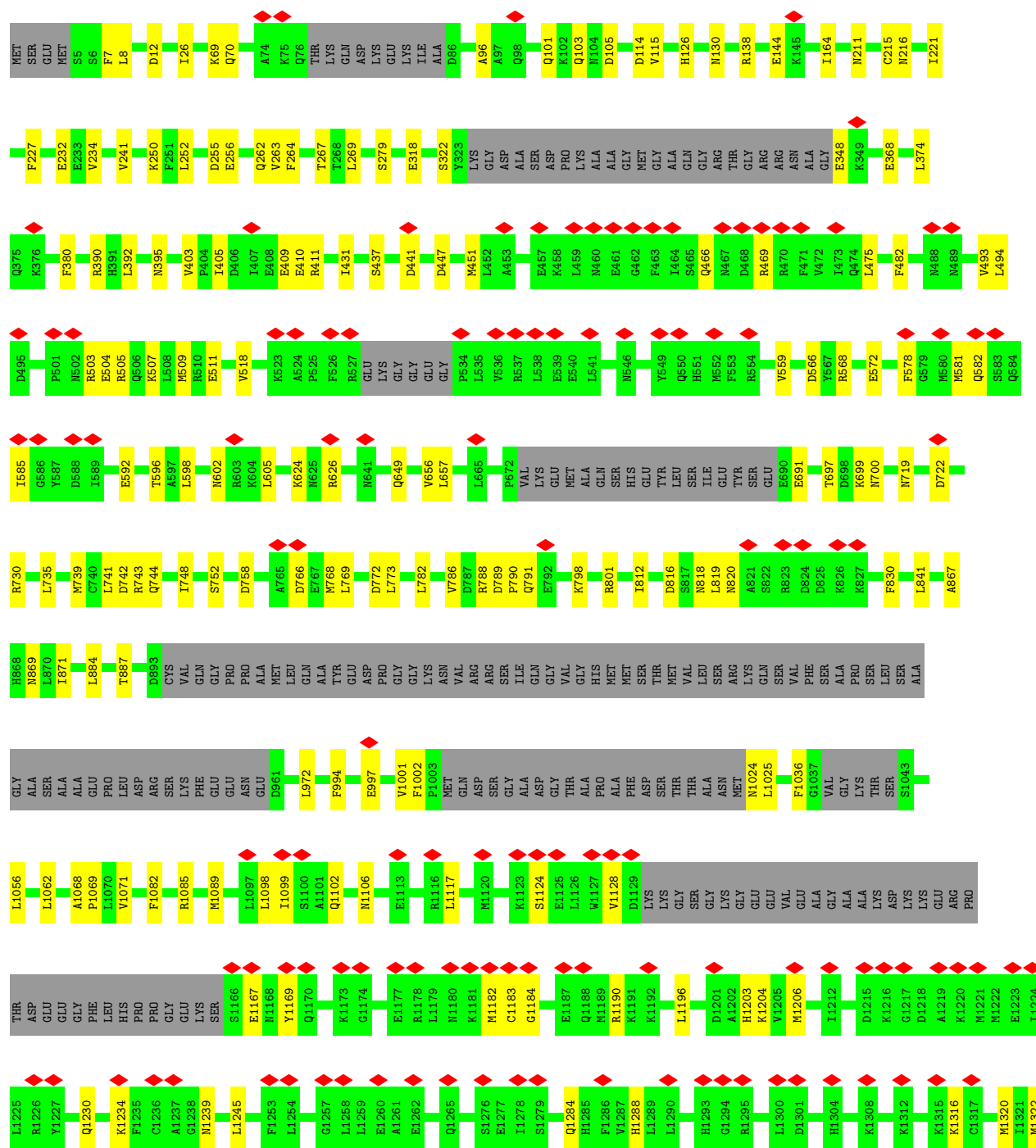
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	B	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	C	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	D	1	Total	C	H	O	P	0
			33	6	9	15	3	

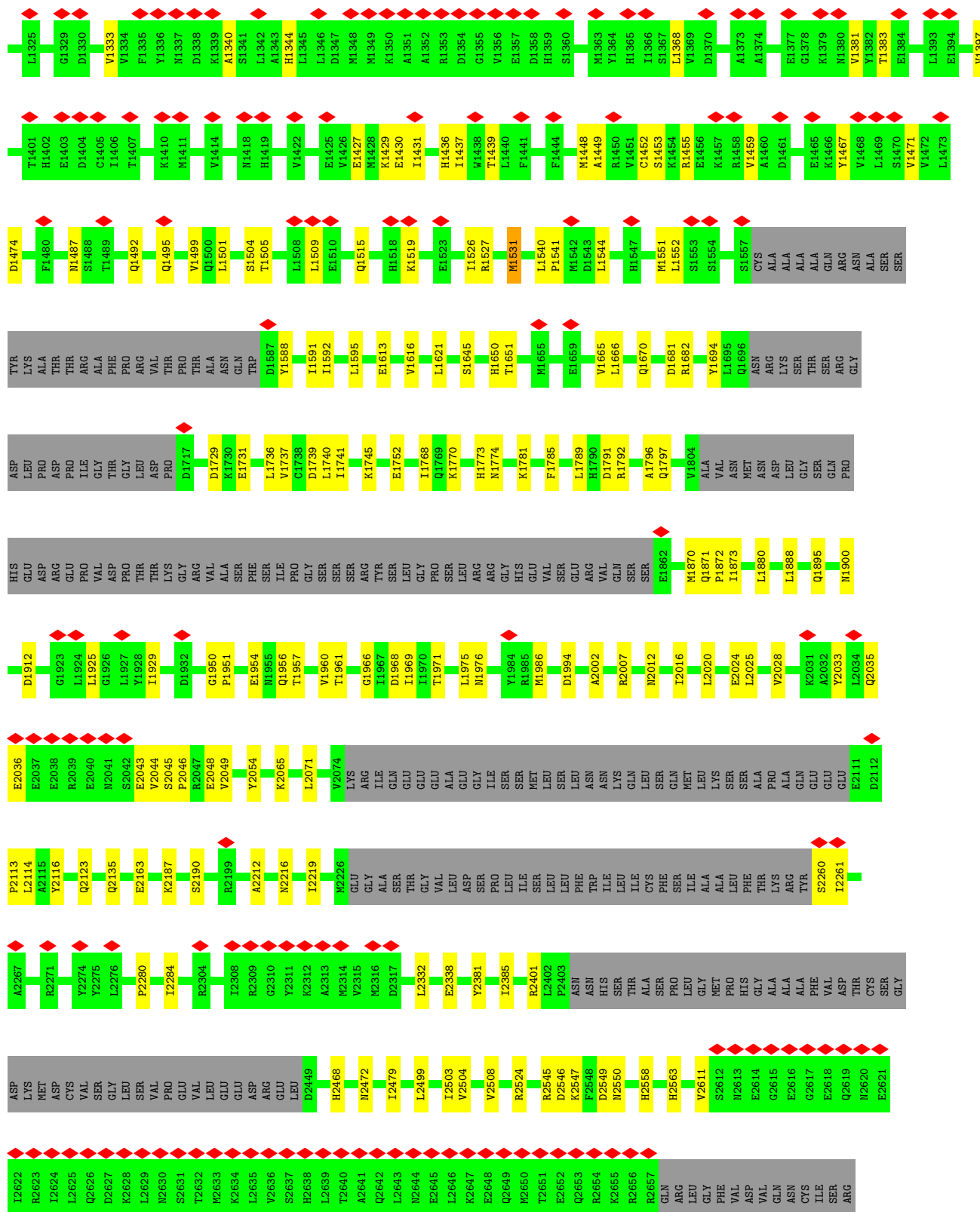
- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
4	A	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
4	B	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
4	C	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
4	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







THR	GLY	LEU	ASP	PRO	D1717	L1736	V1737	C1738	D1739	L1740	I1741	T1744	K1745	E1752	K1770	H1773	H1774	K1780	K1781	S1782	F1785	L1789	H1790	D1791	R1792	A1796	Q1797	V1804	ALA	VAL	ASN	MET	ASN	ASP	LEU	GLY	SER	GLN	PRO	HIS	GLU	ASP	ARG	PRO	VAL	ASP	PRO	THR				
THR	LYS	GLY	ARG	VAL	ALA	SER	PHE	ILE	PRO	GLY	SER	SER	ARG	TYR	SER	LEU	GLY	ARG	GLY	HIS	GLU	VAL	SER	GLU	ARG	SER	E1862	M1863	M1870	Q1871	P1872	I1873	L1880	L1888	Q1895	M1900	D1912	G1921	L1924	L1925	G1926	L1927										
Y1928	I1929	D1932	G1950	P1951	E1954	N1955	Q1956	T1957	V1960	T1961	N1965	G1966	I1967	D1968	I1969	I1970	T1971	L1975	M1976	Y1984	R1985	M1986	D1994	A2002	R2007	N2012	T2016	L2020	E2024	Y2033	L2034	Q2035	E2036	E2037	E2038	R2039	E2040	N2041	S2042	E2043	V2044	S2045	P2046	R2047								
E2048	V2049	Y2054	K2065	L2071	V2074	LYS	ARG	ILE	GLN	GLU	GLU	ALA	GLU	GLY	ILE	SER	MET	LEU	SER	ASN	LYS	GLN	LEU	SER	GLN	MET	LEU	LYS	SER	SER	ALA	ALA	PRO	ALA	GLN	GLU	GLU	E2111	D2112	P2113	L2114	A2115	Y2116	Q2123	Q2135	E2163	K2187					
L2188	R2189	S2190	R2199	A2212	N2216	I2219	M2226	GLU	GLY	ALA	SER	THR	GLY	VAL	LEU	ASP	SER	PRO	ILE	SER	LEU	PHE	TRP	ILE	LEU	ILE	CYS	PHE	ILE	ALA	ALA	LEU	PHE	THR	LYS	ARG	TYR	S2260	I2261	L2264	R2271	S2272	I2273	Y2274	Y2275	L2276	P2280					
I2284	R2304	G2305	T2306	F2307	T2308	R2309	G2310	Y2311	K2312	A2313	M2314	V2315	M2316	D2317	L2332	E2338	L2371	Y2381	T2385	R2401	L2402	F2403	ASN	ASN	HIS	SER	THR	ALA	ALA	SER	PRO	LEU	GLY	MET	PRO	HIS	GLY	ALA	ALA	PHE	VAL	ASP	THR	CYS	SER	GLY	ASP	LYS	MET	ASP	CYS	VAL
SER	GLY	LEU	SER	VAL	PRO	GLU	VAL	LEU	GLU	GLU	ASP	ARG	GLU	D2449	H2468	N2472	I2479	L2499	I2503	I2507	V2508	D2518	R2524	K2527	E2531	R2545	D2546	K2547	F2548	D2549	N2550	H2558	H2563	V2611	S2612	N2613	E2614	G2615	E2616	C2617	E2618	Q2619	N2620	E2621								
I2622	R2623	I2624	L2625	Q2626	D2627	K2628	L2629	N2630	S2631	T2632	M2633	K2634	L2635	V2636	S2637	H2638	L2639	T2640	A2641	Q2642	L2643	N2644	E2645	L2646	K2647	E2648	Q2649	M2650	T2651	E2652	Q2653	R2654	K2655	R2656	R2657	GLN	ARG	LEU	GLY	PHE	VAL	ASP	VAL	GLN	ASN	CYS	ILE	SER	ARG			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	186210	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	143.445	Depositor
Minimum map value	-70.325	Depositor
Average map value	0.159	Depositor
Map value standard deviation	1.690	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: I3P, ZN, ATP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.09	0/18354	0.24	0/24804
1	B	0.09	0/18354	0.24	0/24804
1	C	0.09	0/18354	0.24	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	246	0
1	B	18023	18013	18013	241	0
1	C	18023	18013	18013	242	0
1	D	18023	18013	18013	251	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	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	24	9	9	1	0
3	C	24	9	9	1	0
3	D	24	9	9	2	0
4	A	31	12	12	0	0
4	B	31	12	12	0	0
4	C	31	12	12	0	0
4	D	31	12	12	0	0
All	All	72316	72136	72136	961	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 7.

The worst 5 of 961 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:D:772:ASP:OD1	1:D:773:LEU:N	2.10	0.85
1:B:772:ASP:OD1	1:B:773:LEU:N	2.10	0.85
1:A:772:ASP:OD1	1:A:773:LEU:N	2.10	0.84
1:C:772:ASP:OD1	1:C:773:LEU:N	2.10	0.84
1:A:503:ARG:NH2	1:A:566:ASP:OD1	2.17	0.78

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%)	39 (2%)	1 (0%)	100	100
1	B	2219/2671 (83%)	2180 (98%)	39 (2%)	0	100	100
1	C	2219/2671 (83%)	2179 (98%)	39 (2%)	1 (0%)	100	100
1	D	2219/2671 (83%)	2179 (98%)	39 (2%)	1 (0%)	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	8876/10684 (83%)	8717 (98%)	156 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1782	SER
1	C	1782	SER
1	D	1782	SER

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	1995/2385 (84%)	1989 (100%)	6 (0%)	86	83
1	B	1995/2385 (84%)	1991 (100%)	4 (0%)	87	86
1	C	1995/2385 (84%)	1990 (100%)	5 (0%)	86	83
1	D	1995/2385 (84%)	1989 (100%)	6 (0%)	86	83
All	All	7980/9540 (84%)	7959 (100%)	21 (0%)	84	83

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1797	GLN
1	D	758	ASP
1	D	1797	GLN
1	D	792	GLU
1	D	511	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1265	GLN
1	D	94	GLN

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Mol	Chain	Res	Type
1	C	1270	ASN
1	C	1884	HIS
1	D	512	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 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	$\# Z > 2$
3	I3P	C	3002	-	24,24,24	2.18	3 (12%)	39,39,39	0.93	1 (2%)
3	I3P	D	3002	-	24,24,24	2.18	3 (12%)	39,39,39	0.93	1 (2%)
4	ATP	A	3003	-	32,33,33	0.26	0	48,52,52	0.67	0
4	ATP	B	3003	-	32,33,33	0.26	0	48,52,52	0.67	0
3	I3P	A	3002	-	24,24,24	2.18	3 (12%)	39,39,39	0.93	1 (2%)
3	I3P	B	3002	-	24,24,24	2.18	3 (12%)	39,39,39	0.93	1 (2%)
4	ATP	C	3003	-	32,33,33	0.26	0	48,52,52	0.67	0
4	ATP	D	3003	-	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
3	I3P	C	3002	-	-	2/15/39/39	0/1/1/1
3	I3P	D	3002	-	-	2/15/39/39	0/1/1/1
4	ATP	A	3003	-	-	8/22/38/38	0/3/3/3
4	ATP	B	3003	-	-	8/22/38/38	0/3/3/3
3	I3P	A	3002	-	-	2/15/39/39	0/1/1/1
3	I3P	B	3002	-	-	2/15/39/39	0/1/1/1
4	ATP	C	3003	-	-	8/22/38/38	0/3/3/3
4	ATP	D	3003	-	-	8/22/38/38	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	C	3002	I3P	P4-O4	6.09	1.70	1.59
3	A	3002	I3P	P4-O4	6.09	1.70	1.59
3	B	3002	I3P	P4-O4	6.09	1.70	1.59
3	D	3002	I3P	P4-O4	6.09	1.70	1.59
3	B	3002	I3P	P5-O5	5.88	1.69	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	3002	I3P	O1-P1-O11	-2.11	101.80	109.33
3	A	3002	I3P	O1-P1-O11	-2.11	101.80	109.33
3	D	3002	I3P	O1-P1-O11	-2.11	101.80	109.33
3	C	3002	I3P	O1-P1-O11	-2.11	101.80	109.33

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

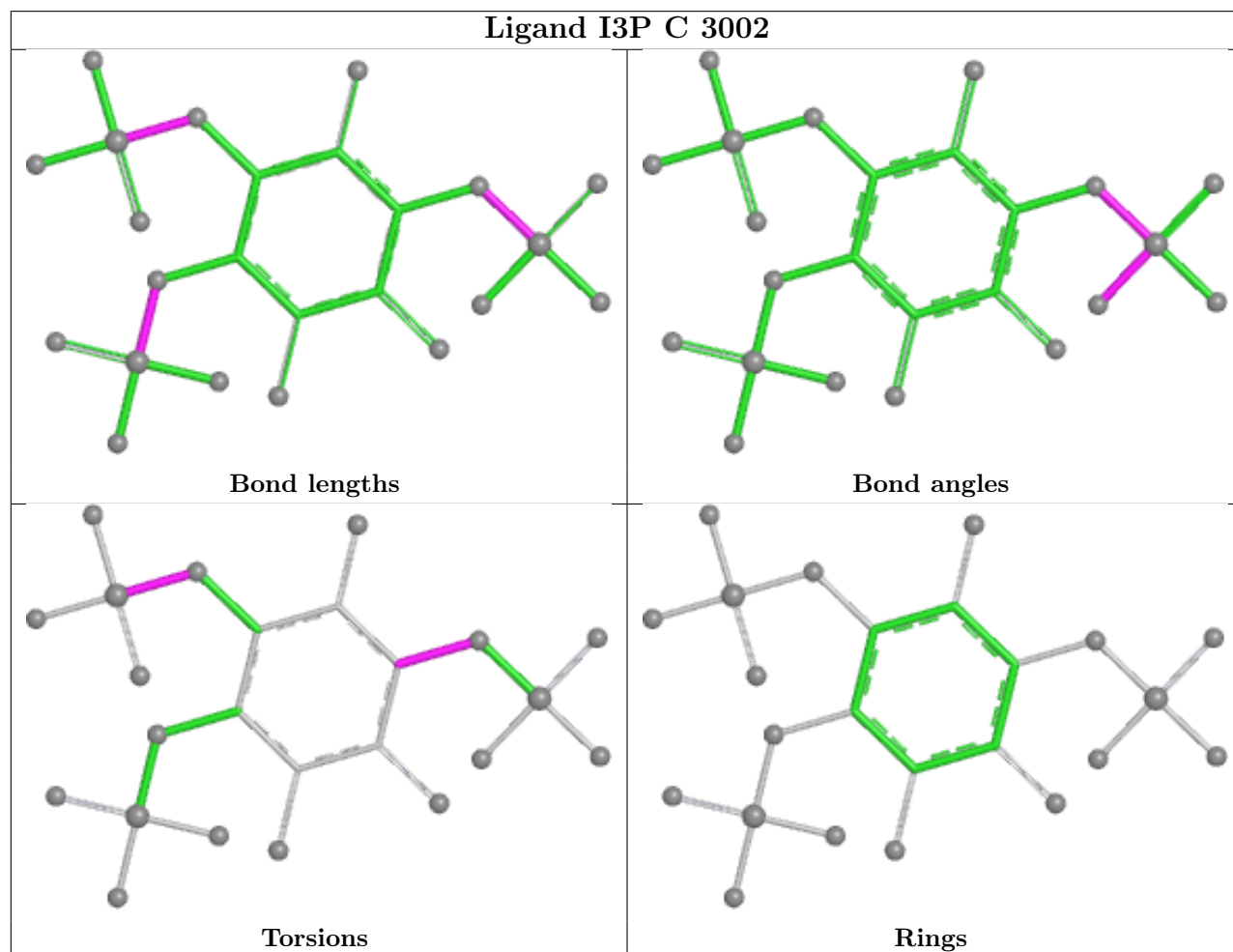
Mol	Chain	Res	Type	Atoms
4	A	3003	ATP	PB-O3B-PG-O3G
4	A	3003	ATP	C5'-O5'-PA-O2A
4	B	3003	ATP	PB-O3B-PG-O3G
4	B	3003	ATP	C5'-O5'-PA-O2A
4	C	3003	ATP	PB-O3B-PG-O3G

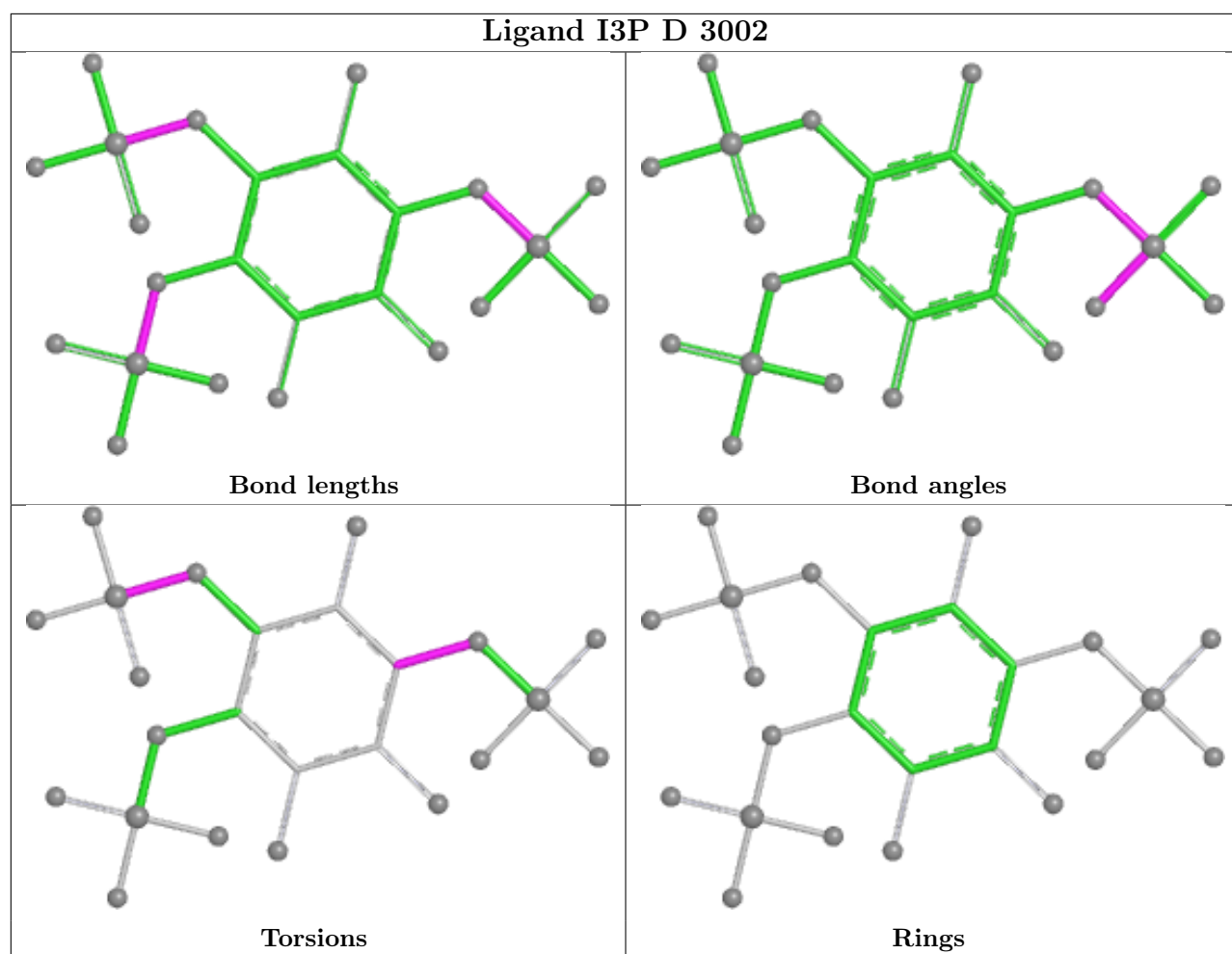
There are no ring outliers.

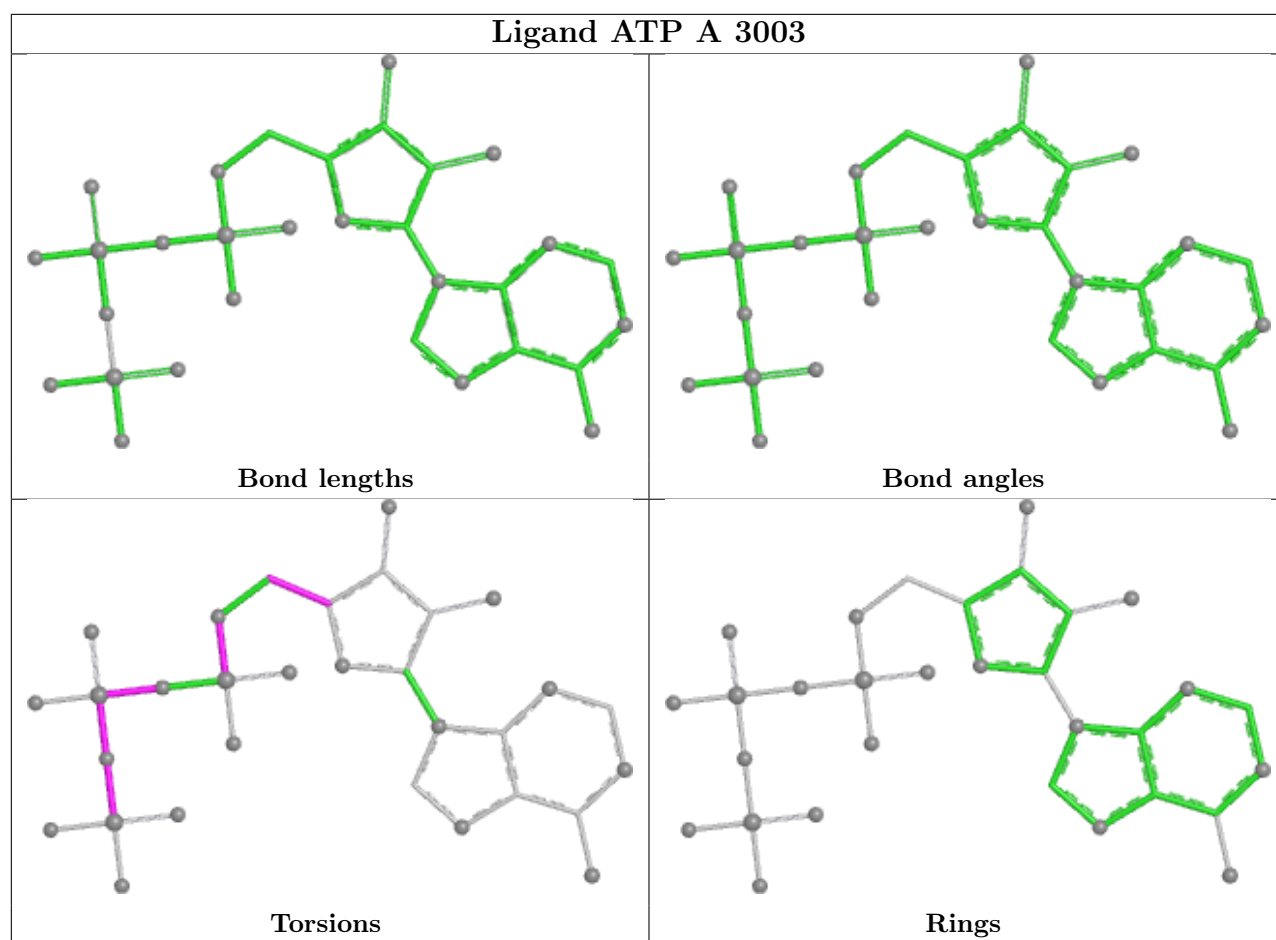
4 monomers are involved in 5 short contacts:

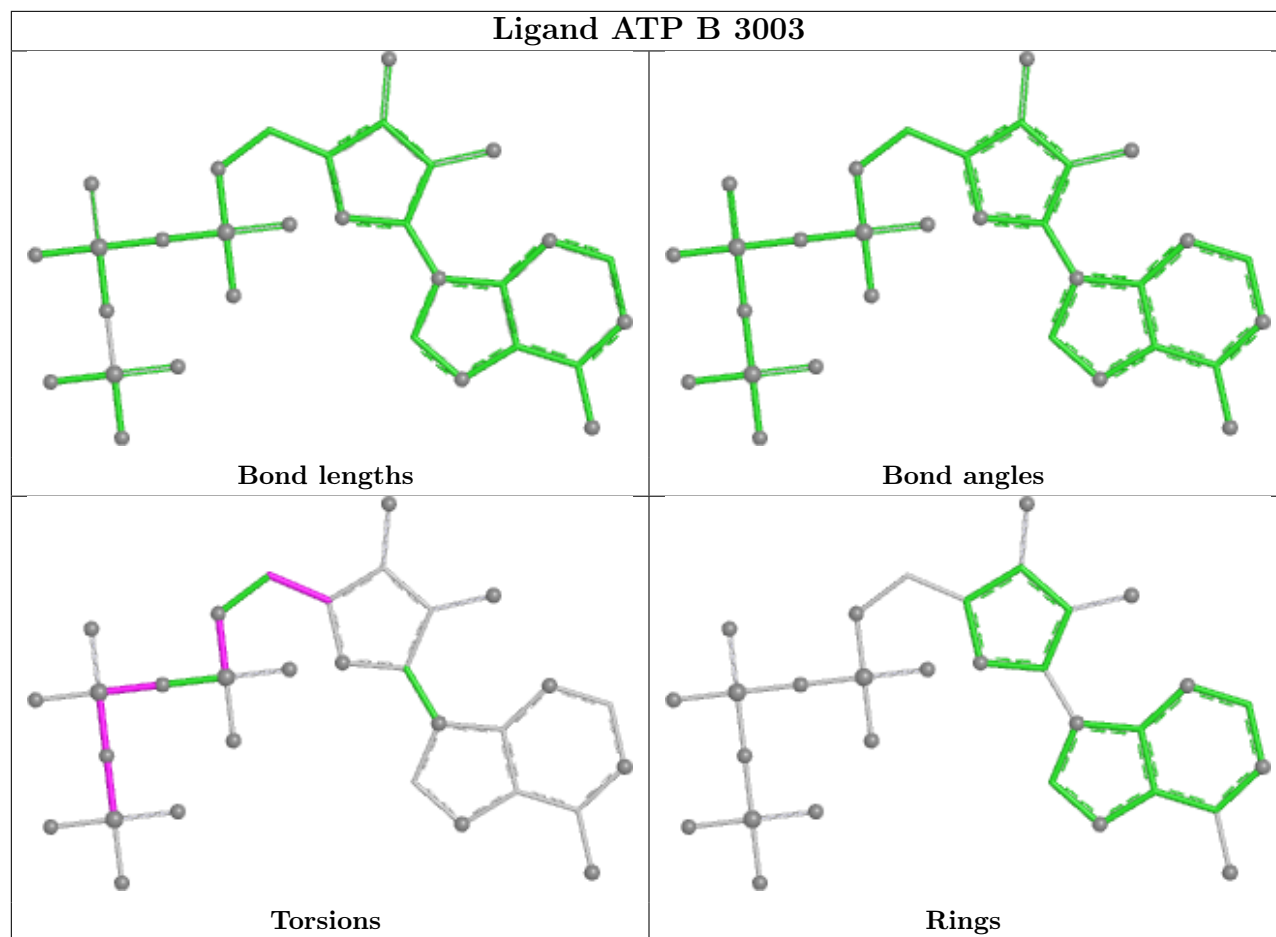
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	3002	I3P	1	0
3	D	3002	I3P	2	0
3	A	3002	I3P	1	0
3	B	3002	I3P	1	0

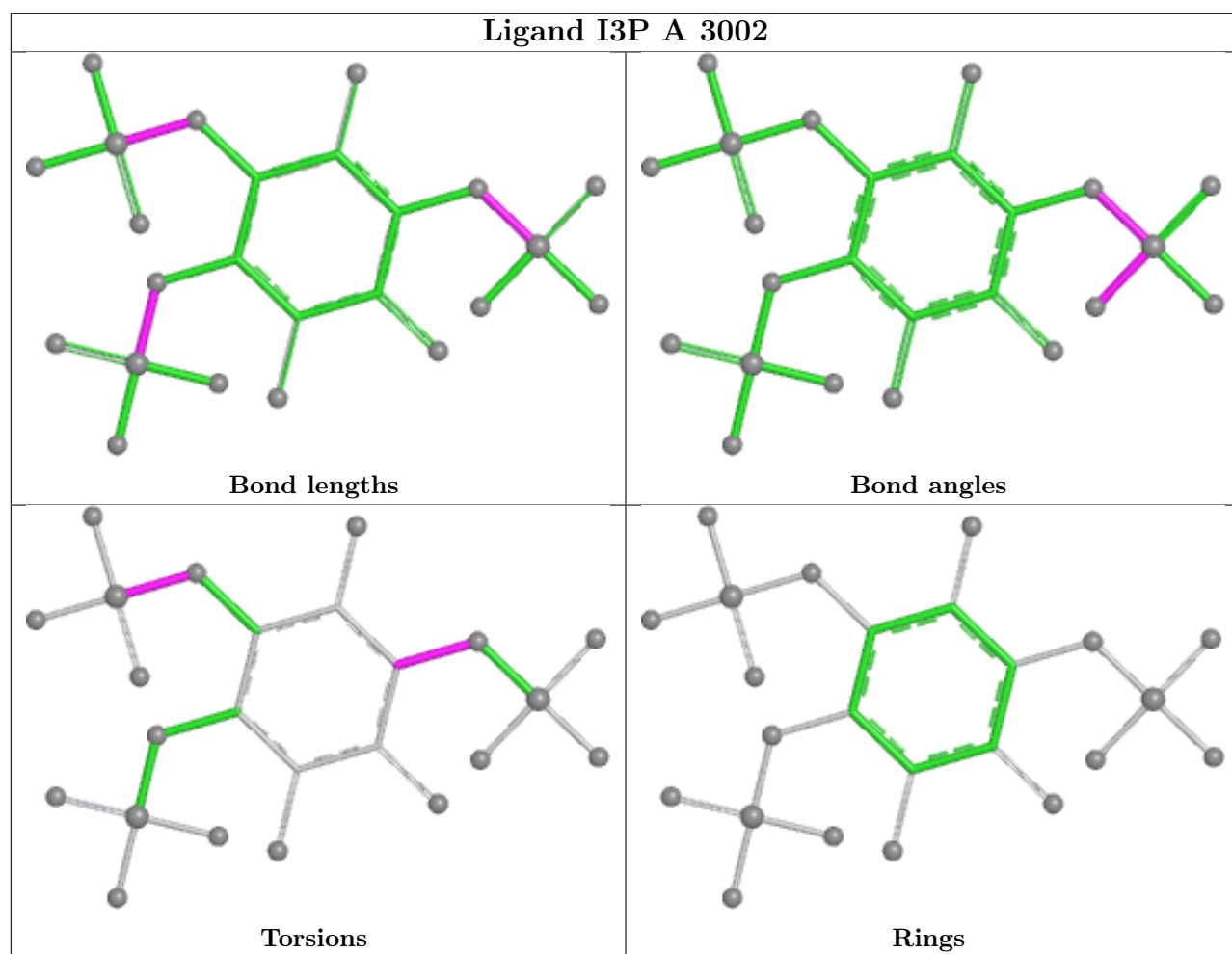
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

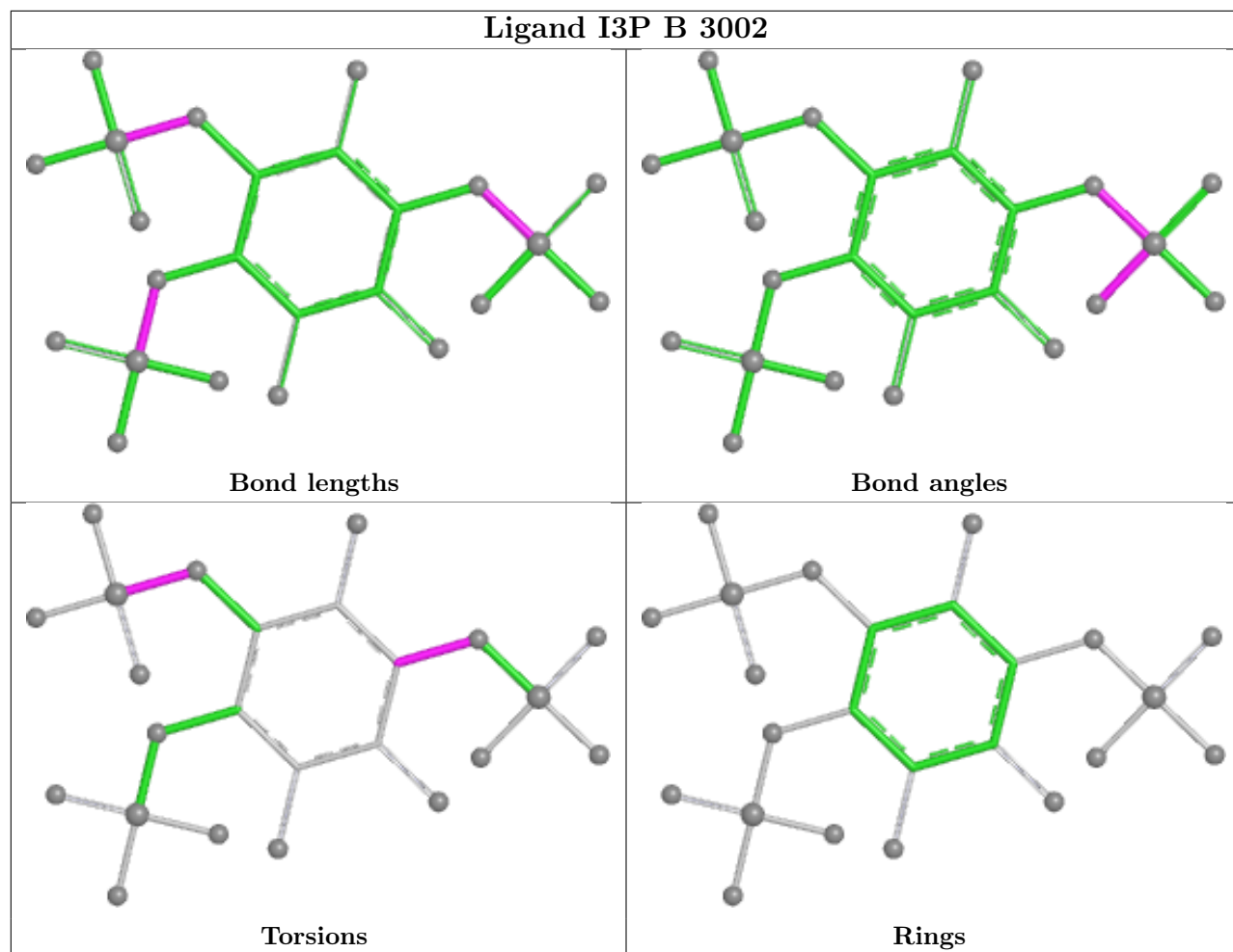


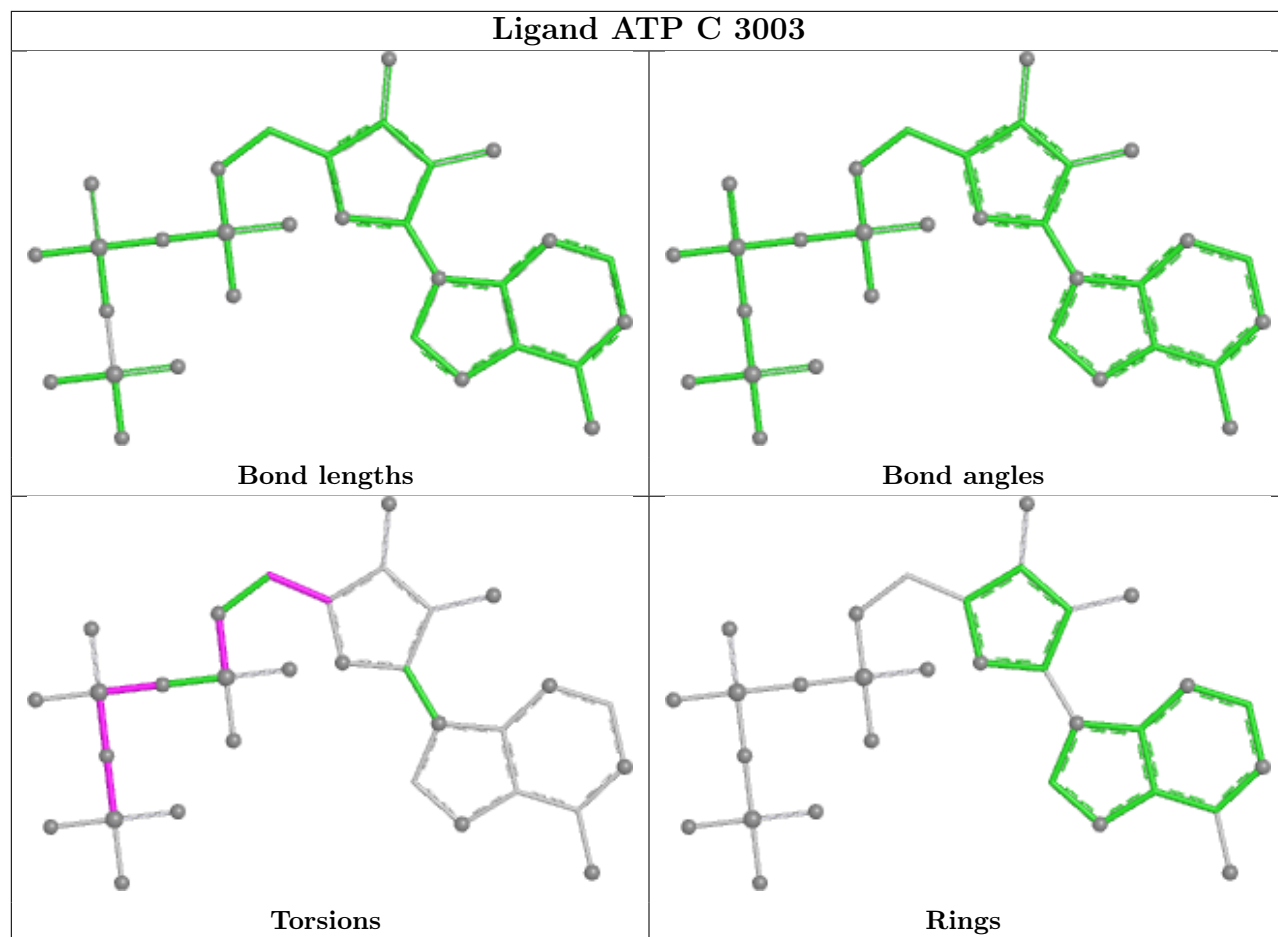


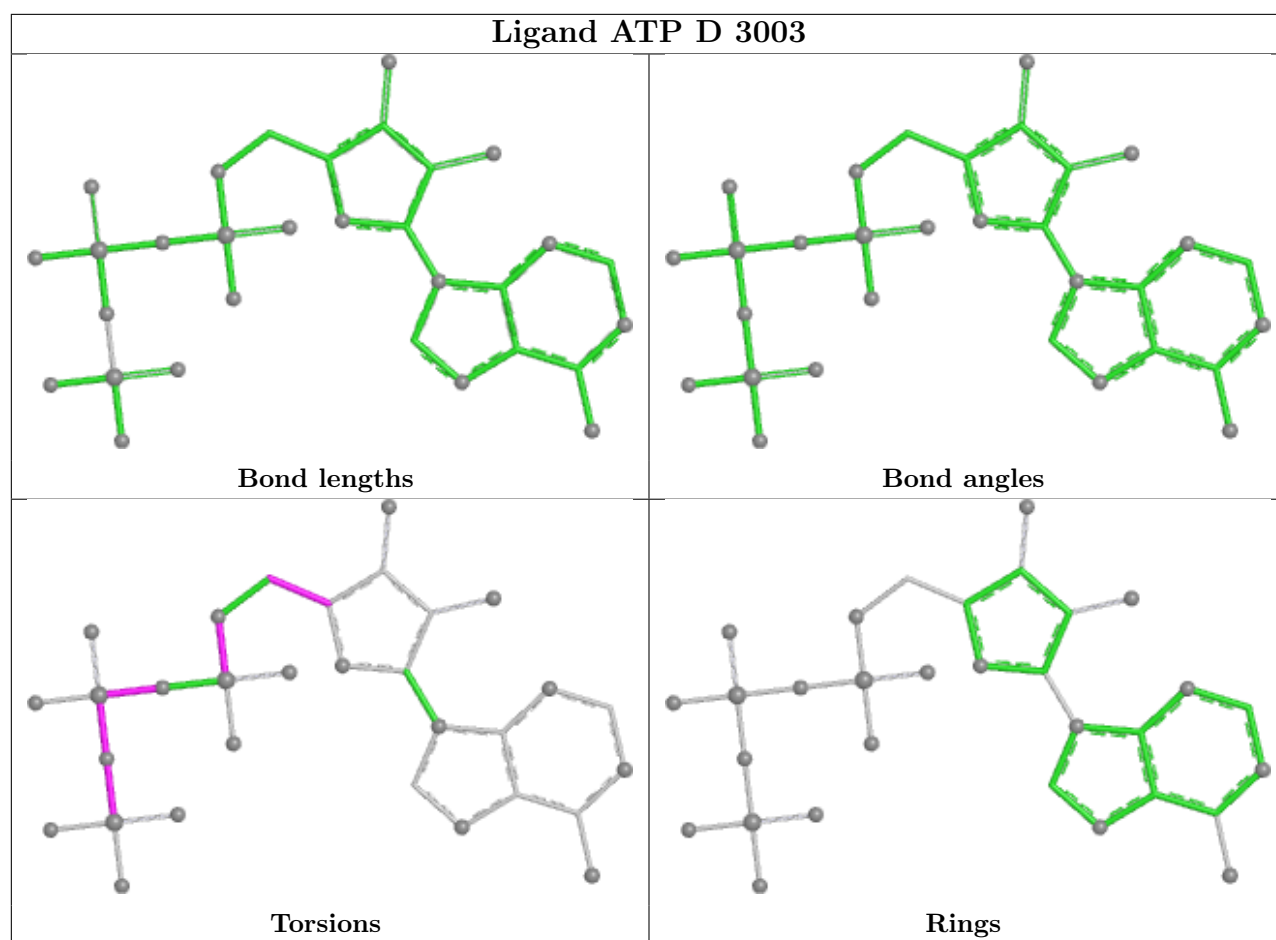












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

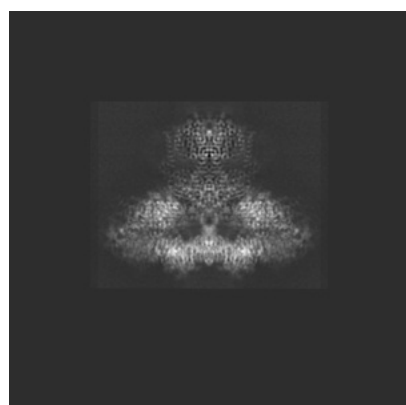
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41347. These allow visual inspection of the internal detail of the map and identification of artifacts.

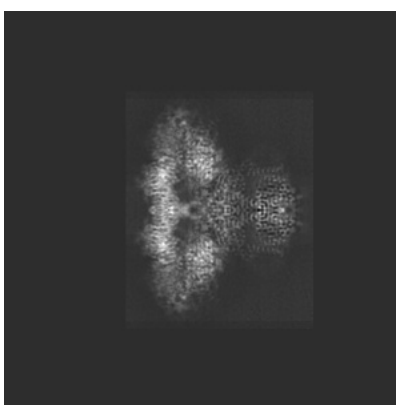
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

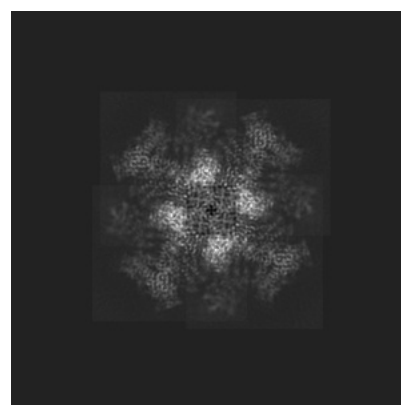
6.1.1 Primary map



X



Y

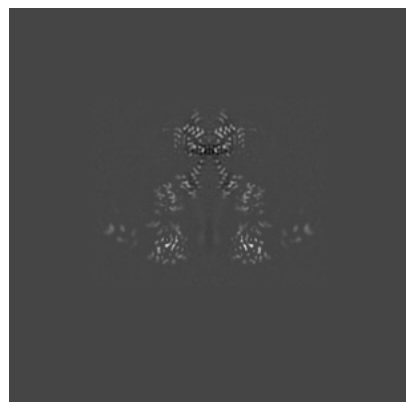


Z

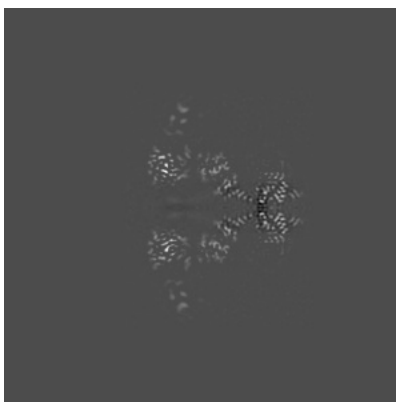
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

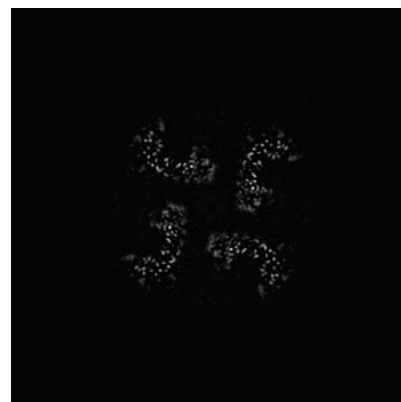
6.2.1 Primary map



X Index: 336



Y Index: 336



Z Index: 336

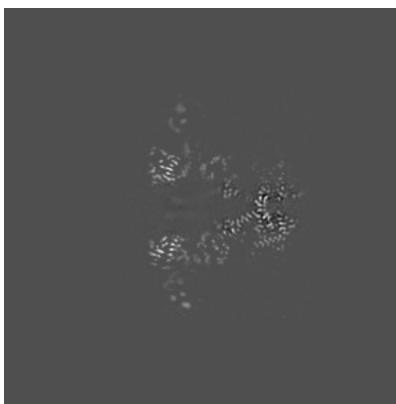
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 333



Y Index: 332

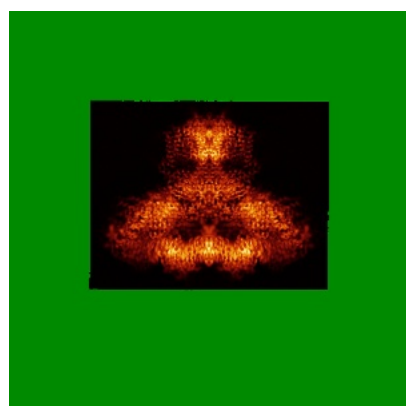


Z Index: 267

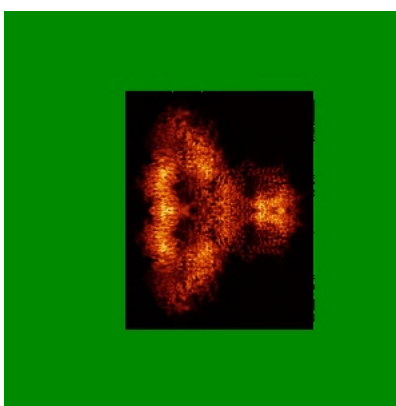
The images above show the largest variance slices of the map in three orthogonal directions.

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

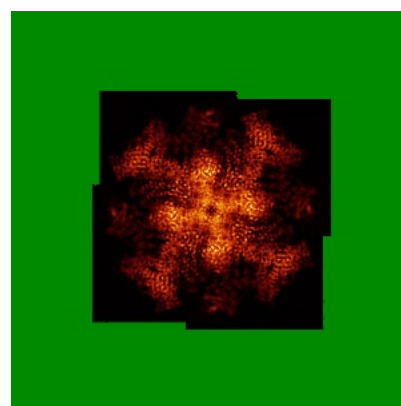
6.4.1 Primary map



X



Y



Z

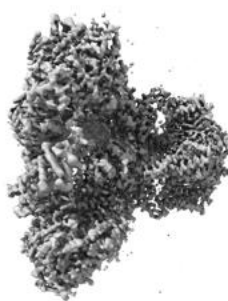
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

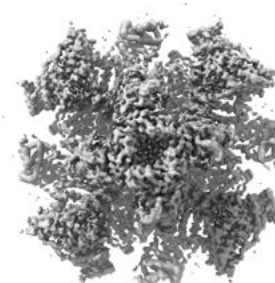
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 6.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

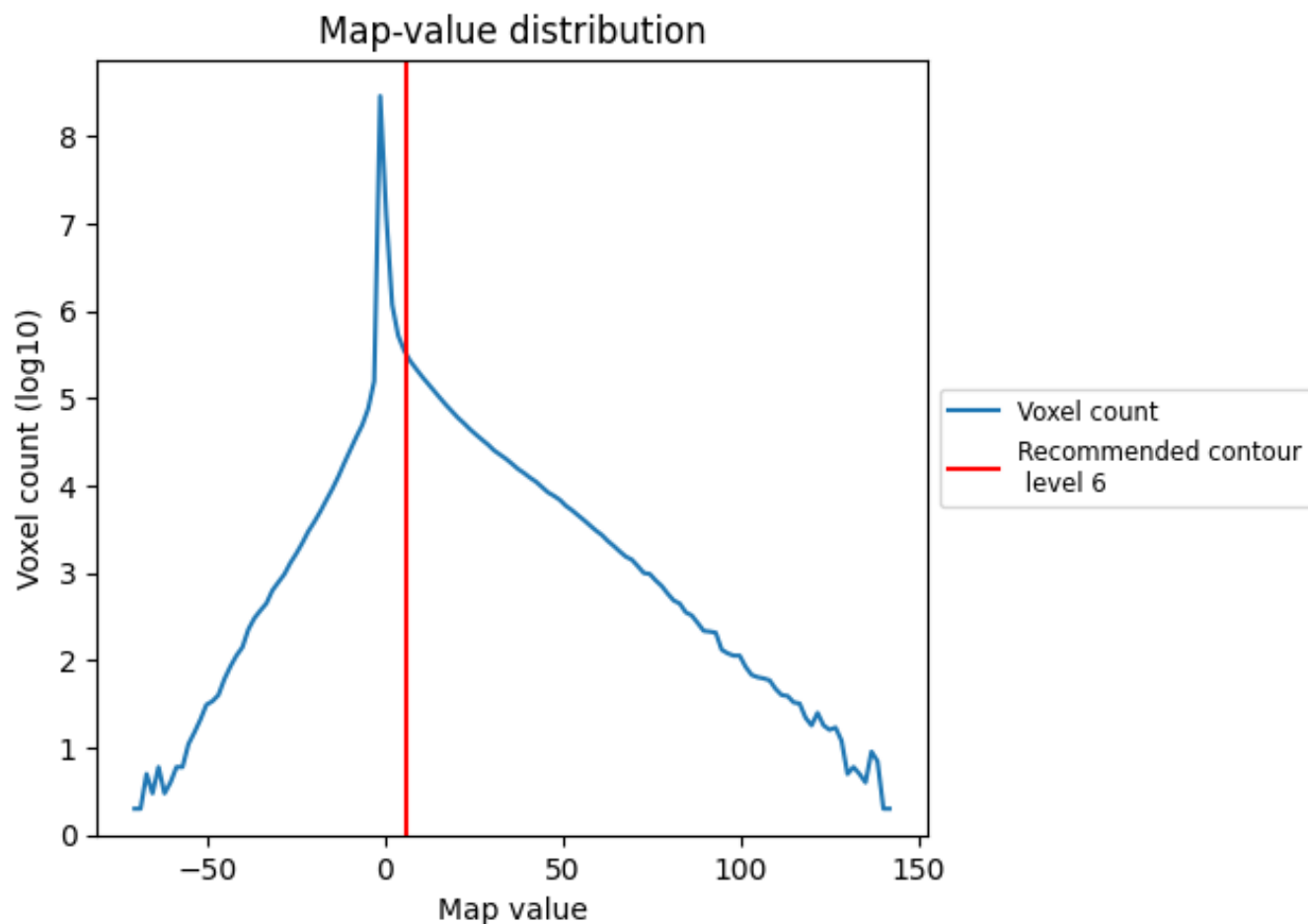
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

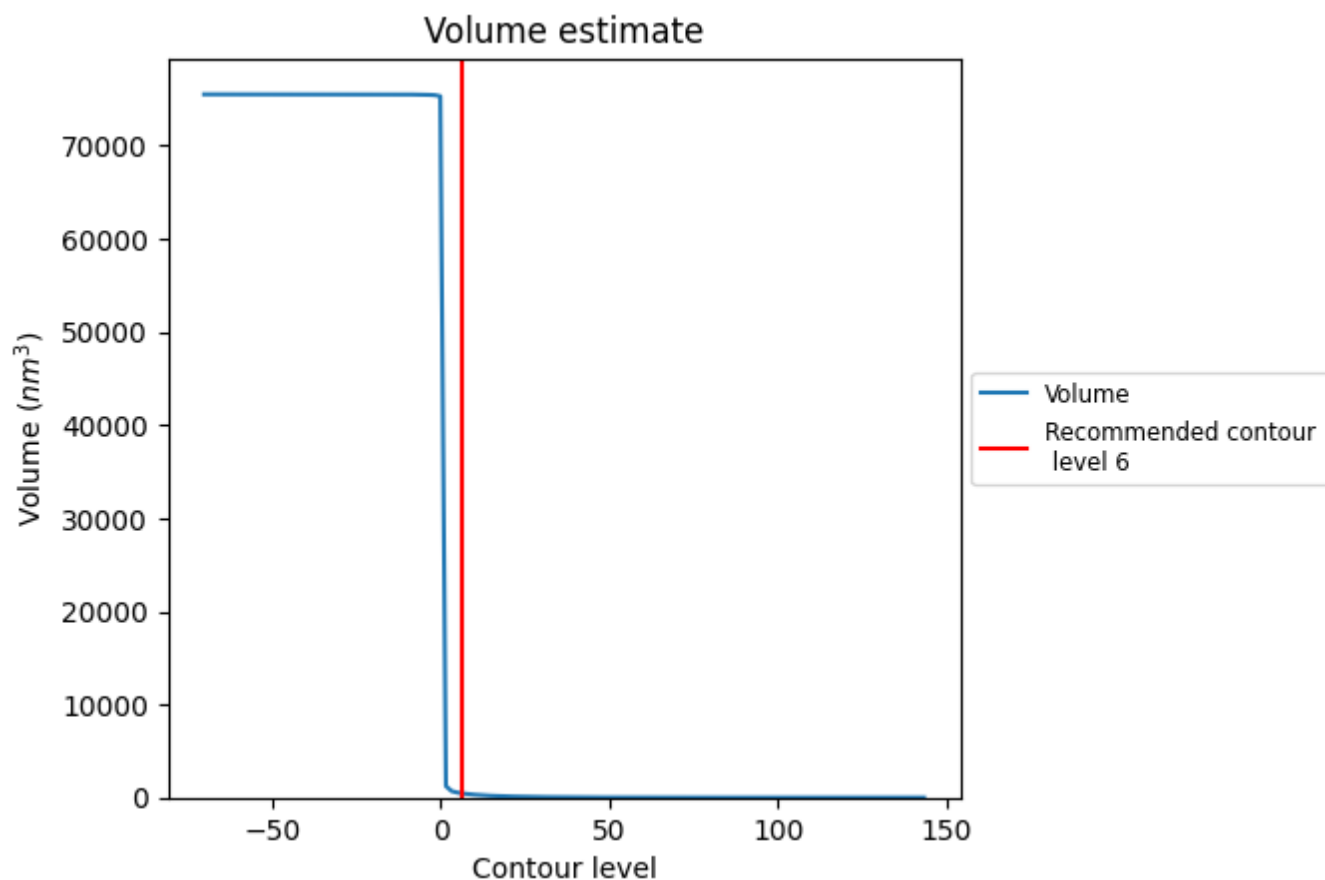
This section contains the results of statistical analysis of the map.

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.

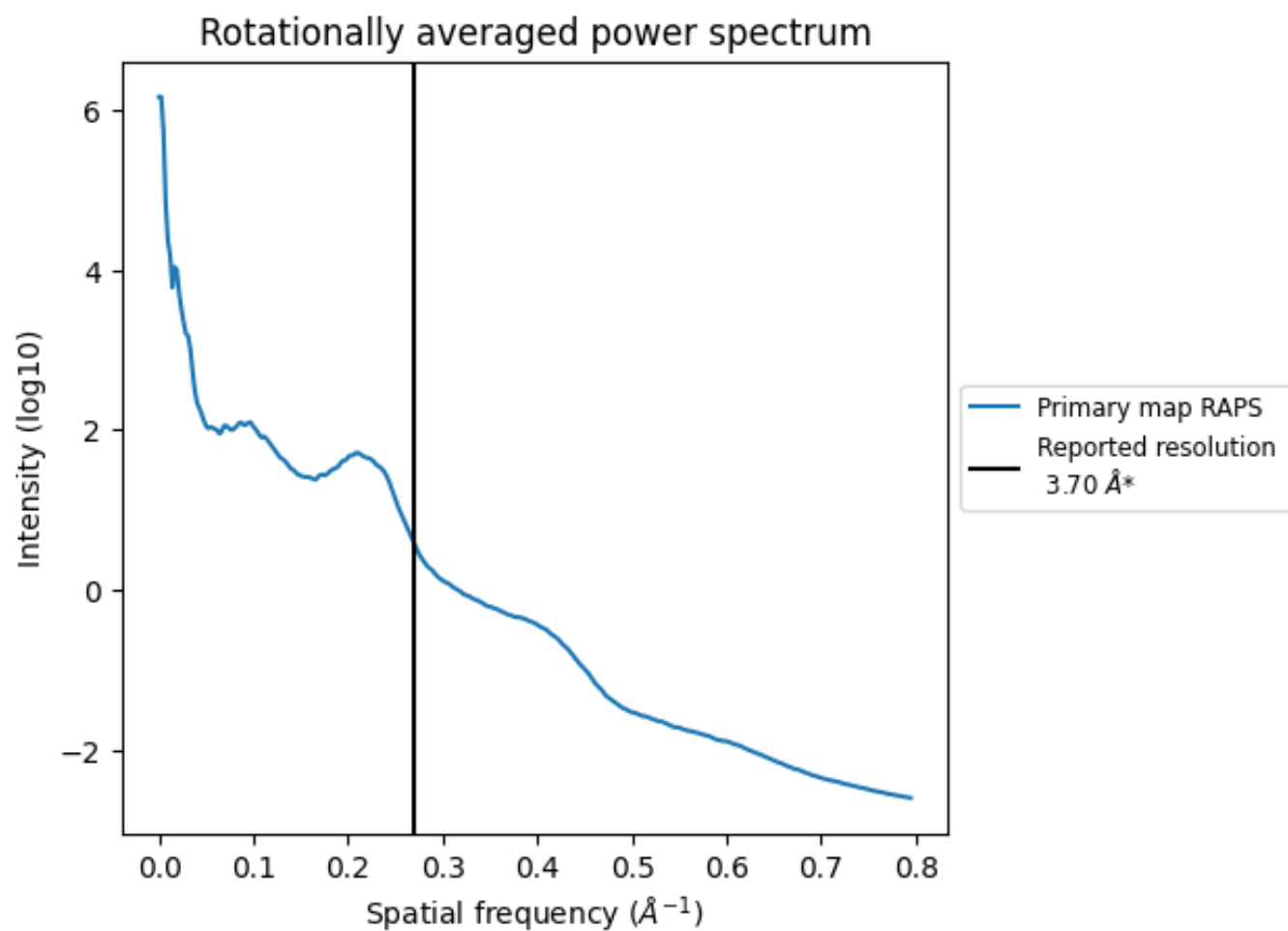
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 469 nm^3 ; this corresponds to an approximate mass of 424 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 0.270 Å⁻¹

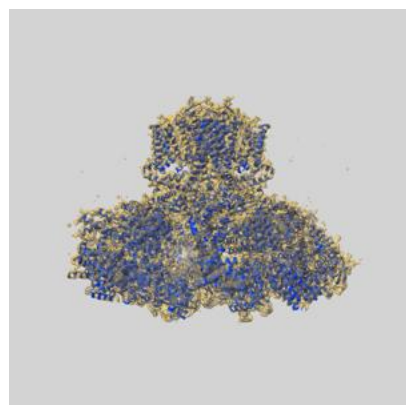
8 Fourier-Shell correlation ⓘ

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

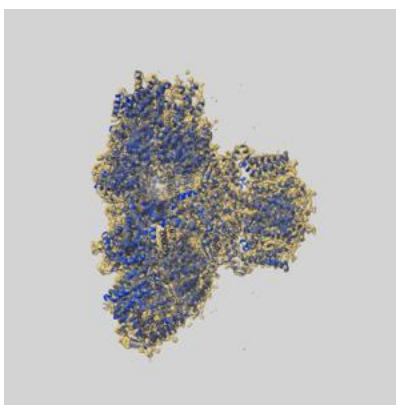
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41347 and PDB model 8TKD. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

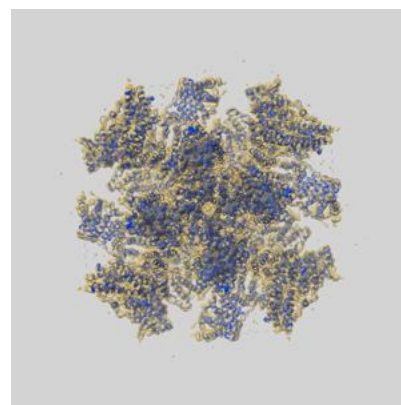
9.1 Map-model overlay [i](#)



X



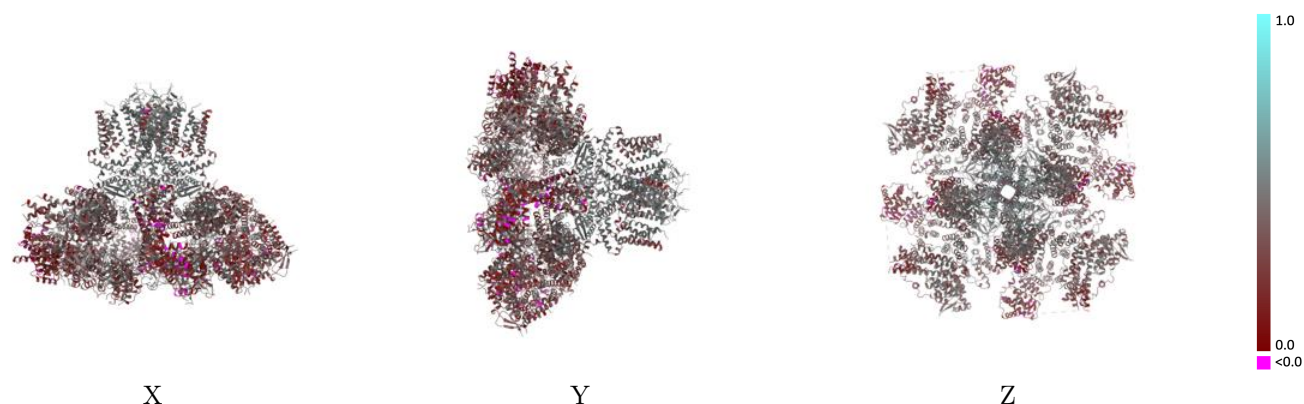
Y



Z

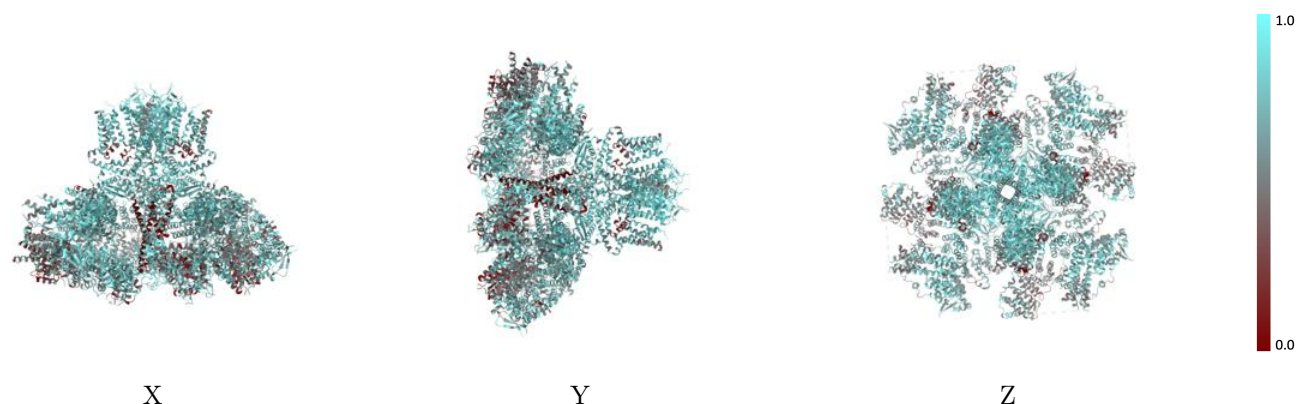
The images above show the 3D surface view of the map at the recommended contour level 6.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



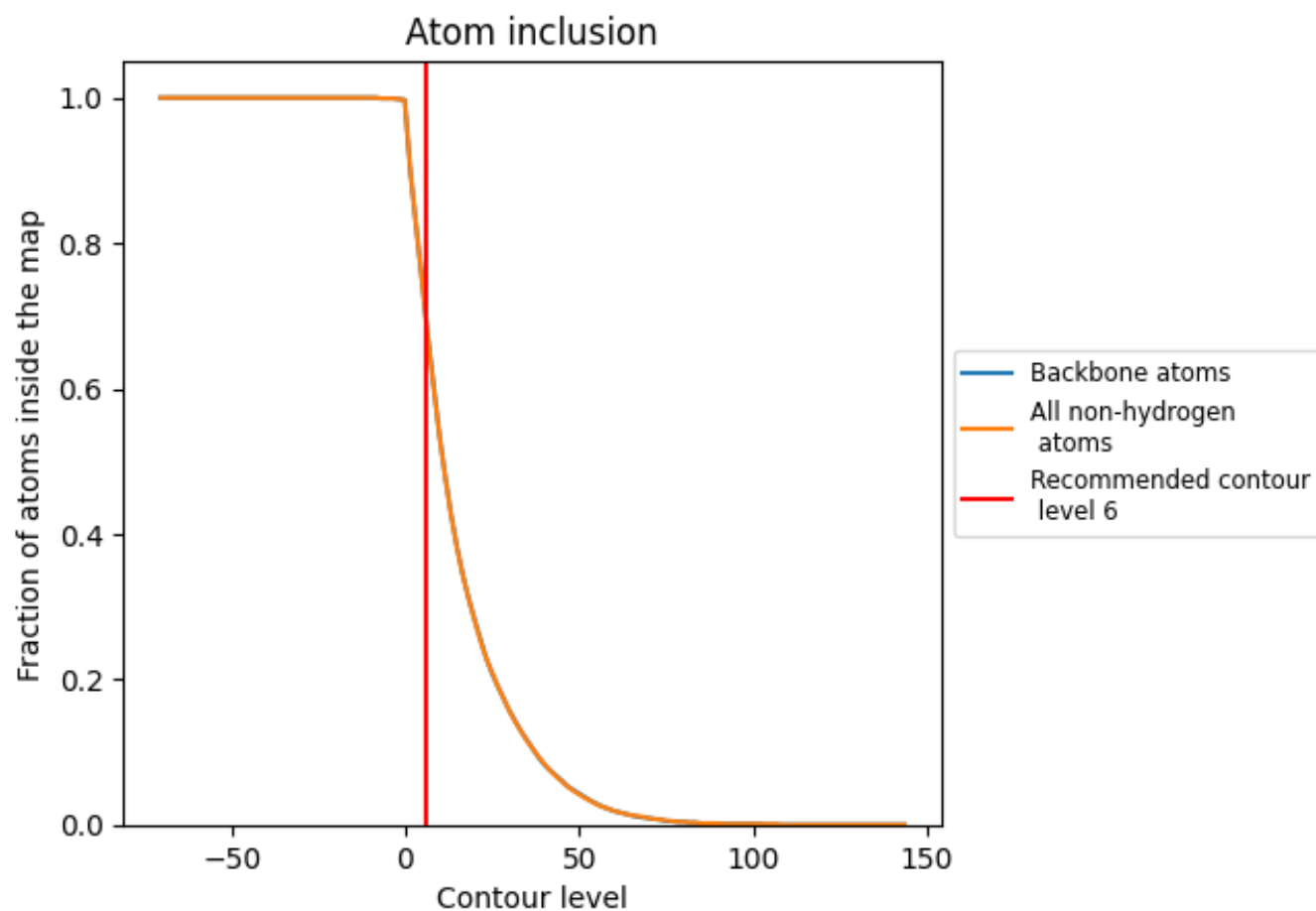
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 69% 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	<div></div> 0.6920	<div></div> 0.3580
A	<div></div> 0.7040	<div></div> 0.3590
B	<div></div> 0.6960	<div></div> 0.3520
C	<div></div> 0.7000	<div></div> 0.3600
D	<div></div> 0.7000	<div></div> 0.3600

