



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 10:52 PM UTC

PDB ID : 7T3T / pdb_00007t3t
EMDB ID : EMD-25670
Title : IP3, ATP, and Ca²⁺ bound type 3 IP3 receptor in the active state
Authors : Schmitz, E.A.; Takahashi, H.; Karakas, E.
Deposited on : 2021-12-08
Resolution : 3.80 Å (reported)
Based on initial model : 6UQK

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

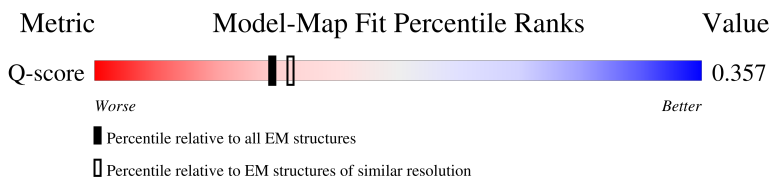
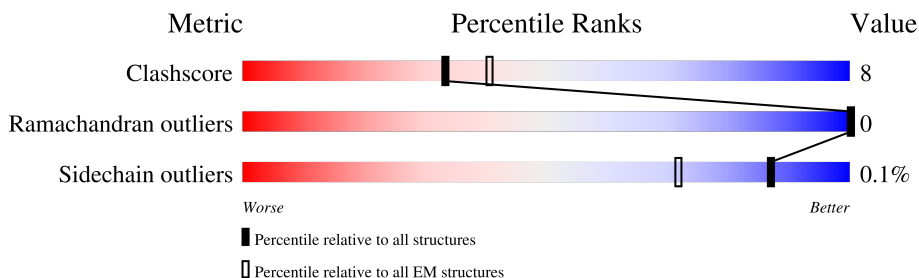
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	2633	 65% 16% 19%
1	B	2633	 65% 15% 19%
1	C	2633	 65% 16% 19%
1	D	2633	 65% 16% 19%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 68516 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.

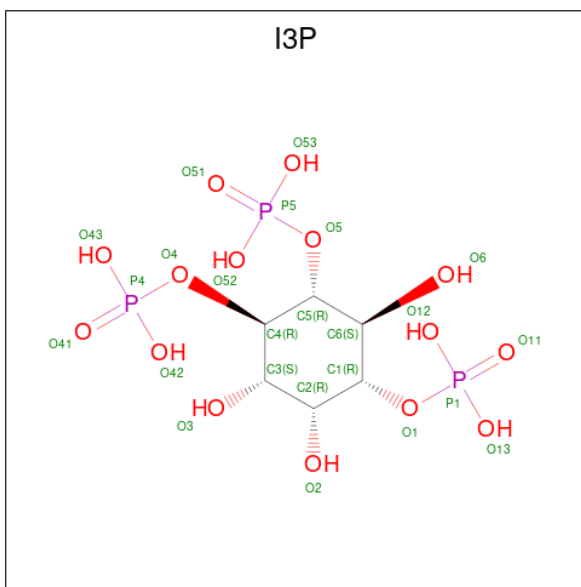
- Molecule 1 is a protein called Inositol 1,4,5-trisphosphate receptor type 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2121	Total	C	N	O	S	0	0
			17072	10908	2923	3138	103		
1	B	2121	Total	C	N	O	S	0	0
			17072	10908	2923	3138	103		
1	C	2121	Total	C	N	O	S	0	0
			17072	10908	2923	3138	103		
1	D	2121	Total	C	N	O	S	0	0
			17072	10908	2923	3138	103		

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

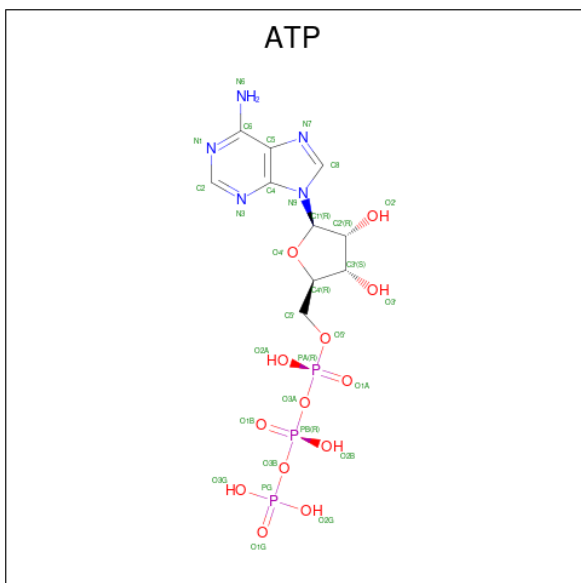
Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Zn	0
			1	1	
2	B	1	Total	Zn	0
			1	1	
2	C	1	Total	Zn	0
			1	1	
2	D	1	Total	Zn	0
			1	1	

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



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	O	P	0
			24	6	15	3	
3	B	1	Total	C	O	P	0
			24	6	15	3	
3	C	1	Total	C	O	P	0
			24	6	15	3	
3	D	1	Total	C	O	P	0
			24	6	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 31	C 10	N 5	O 13	P 3	0
4	B	1	Total 31	C 10	N 5	O 13	P 3	0
4	C	1	Total 31	C 10	N 5	O 13	P 3	0
4	D	1	Total 31	C 10	N 5	O 13	P 3	0

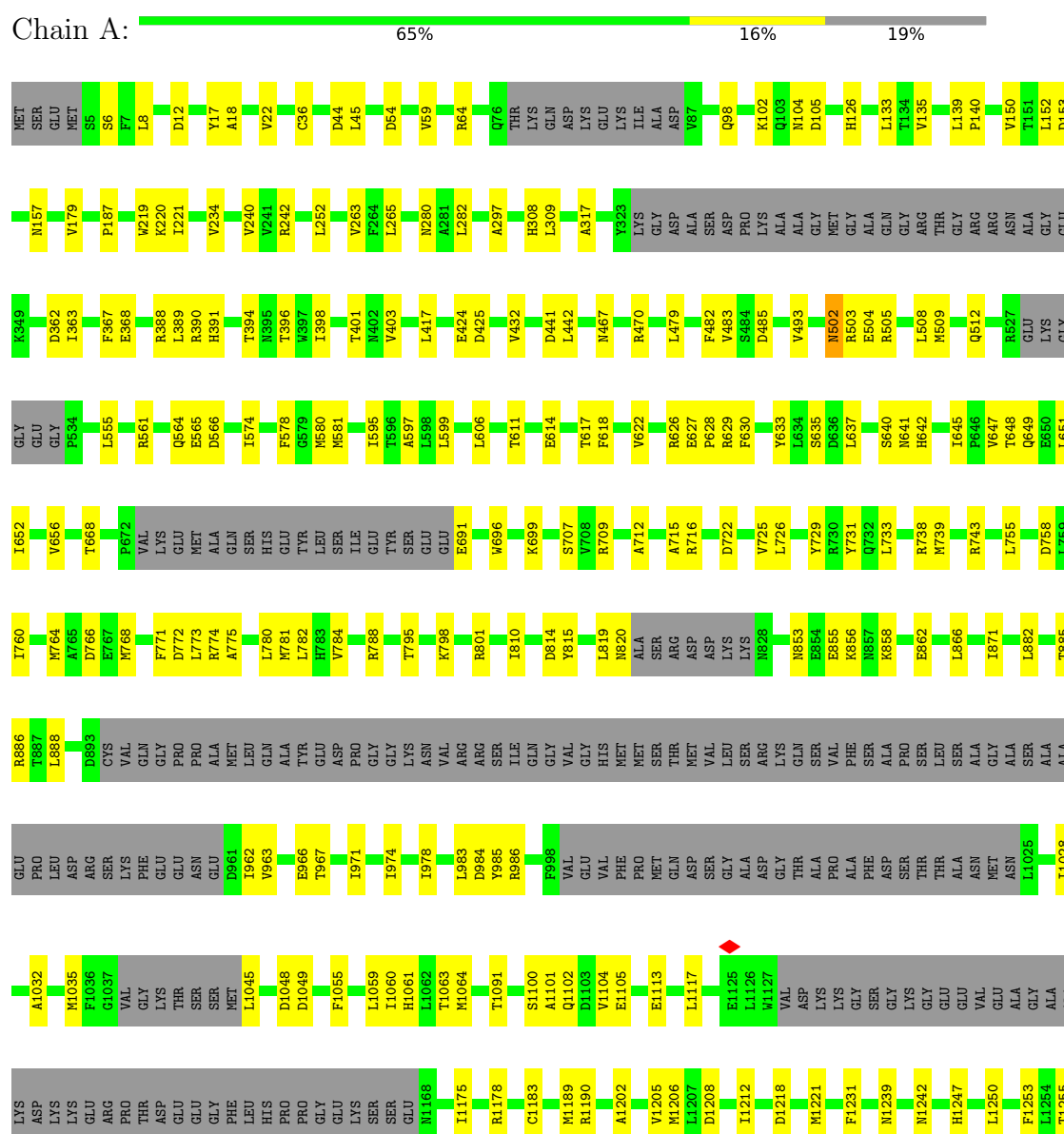
- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

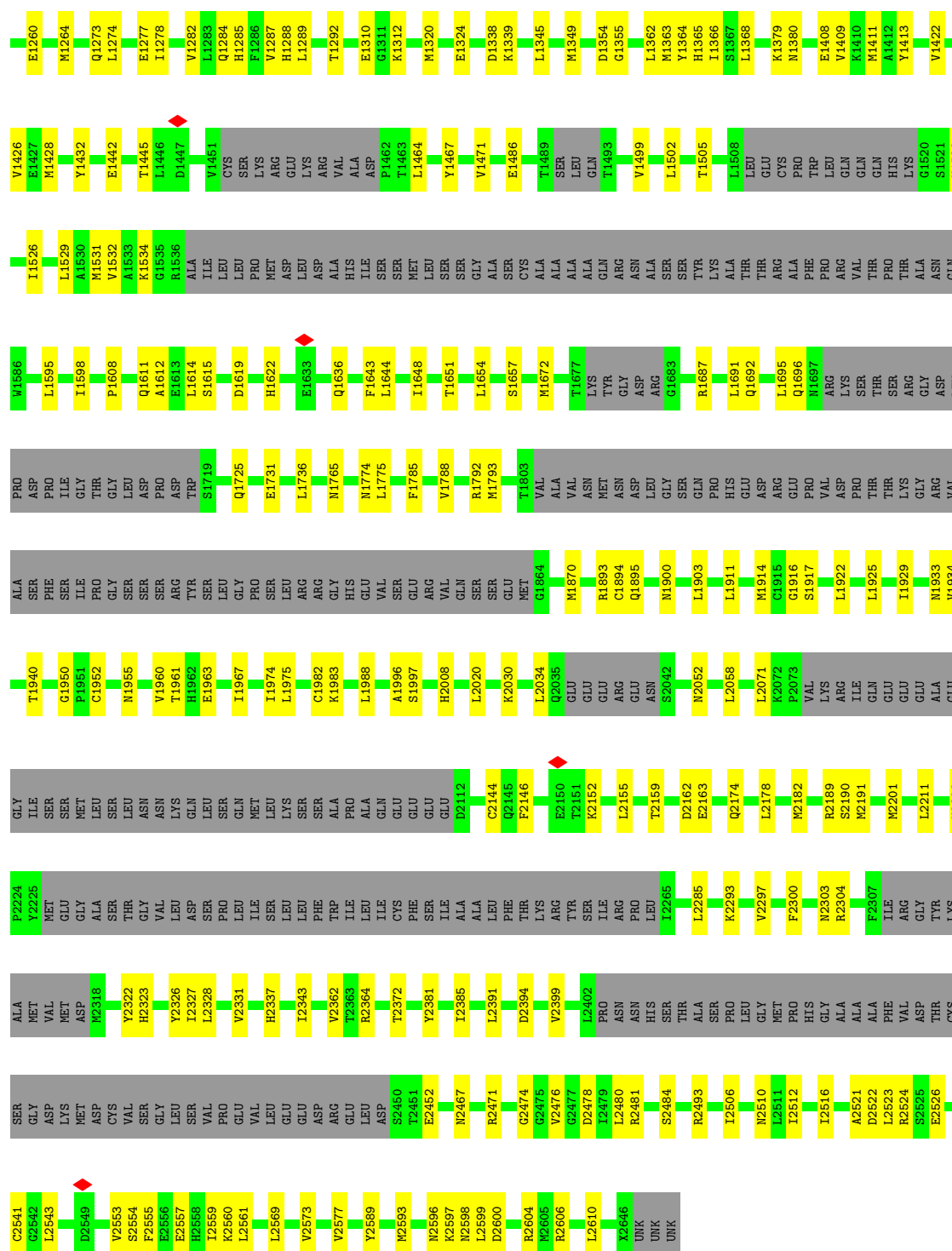
Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total 1	Ca 1	0
5	B	1	Total 1	Ca 1	0
5	C	1	Total 1	Ca 1	0
5	D	1	Total 1	Ca 1	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

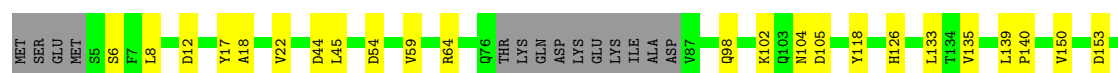
- Molecule 1: Inositol 1,4,5-trisphosphate receptor type 3





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

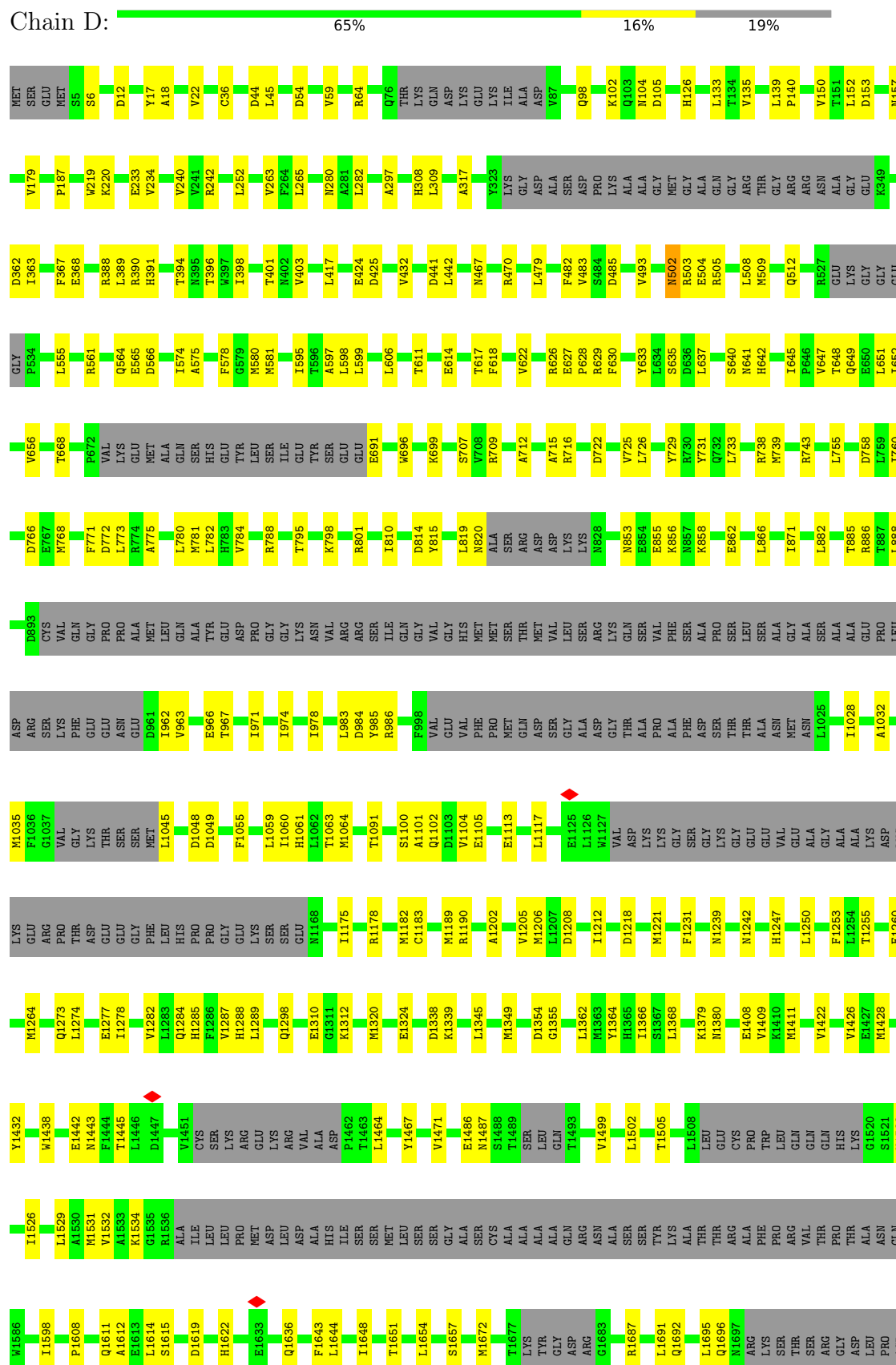
Chain B: 65% 15% 19%





L2523	R2524	S2525	E2526	C2541	G2542	L2543	D2549	V2553	S2554	F2555	E2556	E2557	H2558	I2559	K2560	L2561	L2569	V2573	V2577	Y2589	H2593	N2596	K2597	N2598	L2599	D2600	R2604	G2605	R2606	L2610	X2646	UNK	UNK	UNK															
PHE	VAL	ASP	THR	CYS	SER	GLY	ASP	VAL	SER	GLY	LEU	SER	VAL	PRO	GLU	VAL	VAL	ASP	ARG	GLU	LEU	ASP	S2450	T2451	E2452	N2467	R2471	G2474	G2475	V2476	G2477	D2478	L2479	L2480	R2481	S2484	R2493	I2506	N2510	L2511	L2512	L2516	A2521	D2522					
ILE	ARG	GLY	TYR	LYS	ALA	MET	VAL	M2318	Y2322	H2323	Y2326	I2327	L2328	V2331	H2337	I2343	V2362	T2363	R2364	T2372	Y2381	I2385	L2391	D2394	V2399	L2402	PRO	ASN	ASN	HIS	THR	ALA	SER	PRO	LEU	GLY	MET	PRO	HIS	GLY	ALA	ALA							
M2201	L2211	Y2223	P2224	Y2225	MET	GLU	GLY	ALA	THR	GLY	VAL	LEU	ASP	SER	PRO	LEU	ILE	SER	LEU	ALA	ILE	CYS	PHE	ILE	ALA	ALA	LEU	PHE	THR	LYS	ARG	TYR	SER	ILE	PRO	LEU	TLE	ARG	PRO	THR	GLY	ALA							
ILE	GLN	GLU	GLU	GLU	ALA	GLU	GLY	TLE	ILE	SER	ASN	ASN	LYS	GLN	LEU	ILE	SER	LEU	ALA	PRO	ILE	CYS	PHE	ILE	ALA	ALA	LEU	PHE	THR	LYS	ARG	TYR	SER	ILE	PRO	LEU	TLE	ARG	PRO	THR	GLY	ALA							
ARG	VAL	ALA	SER	PHE	SER	ILE	PRO	GLY	SER	ARG	TYR	SER	GLY	PRO	SER	LEU	ARG	GLN	ARG	GLY	VAL	GLN	SER	GLY	GLU	GLU	GLU	GLU	VAL	ASN	MET	ASN	ASP	LEU	GLY	SER	GLN	HIS	GLU	ASP	ARG	GLY							
LEU	PRO	ASP	PRO	ILE	GLY	THR	GLY	LEU	ASP	PRO	ASP	TRP	S1719	E1731	L1736	I1758	M1774	L1775	M1776	S1782	F1785	V1788	R1792	M1793	T1803	VAL	ALA	VAL	ASN	MET	ASN	ASN	ASP	LEU	GLY	SER	GLN	HIS	GLU	ASP	ARG	GLY							
L1595	I1598	P1608	Q1611	A1612	E1613	S1615	V1616	L1617	V1618	V1619	V1620	L1621	H1622	E1633	Q1636	F1643	L1644	I1648	T1651	L1654	S1657	M1672	T1677	L1691	Q1692	L1695	Q1696	N1697	ARG	ARG	PRO	GLU	ASP	ARG	GLU	VAL	PRO	THR	THR	GLY	ASP								
L1529	A1530	M1531	V1532	A1533	K1534	G1535	R1536	ALA	ILE	LEU	PRO	MET	ASP	LEU	ALA	HIS	ILE	SER	SER	NET	P1462	T1463	L1464	Y1467	V1471	E1486	T1489	ALA	ALA	ALA	GLN	T1493	V1499	L1502	T1505	L1508	LEU	CYS	PRO	TRP	LEU	GLN	GLN	HIS	LYS	G1520	S1521	V1522	I1526
ASP	GLU	GLY	PHE	LEU	HIS	PRO	PRO	GLY	LYS	SER	SER	SER	GLU	LYS	VAL	R1178	M1182	C1183	M1189	R1190	A1202	V1205	M1206	L1207	D1208	I1212	D1218	M1221	F1231	M1239	M1242	H1247	L1250	F1253	L1254	T1255	E1260	M1264	Q1273	L1274									
LYS	THR	SER	SER	MET	L1045	D1048	D1049	F1055	L1059	I1060	H1061	T1063	M1064	T1091	S1100	A1101	D1102	D1103	V1104	E1105	E1113	L1117	E1125	L1126	W1127	VAL	ASP	LYS	GLY	SER	GLY	LYS	GLY	GLU	GLU	VAL	ALA	GLY	ALA	ALA	LYS	ASP	LYS	LYS	GLU	ARG	PRO		

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





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20039	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.560	Depositor
Minimum map value	-0.794	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.12	Depositor
Map size ($\text{\AA}$)	397.44, 397.44, 397.44	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.828, 0.828, 0.828	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: CA, ATP, ZN, 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	0.14	0/17287	0.29	0/23345
1	B	0.14	0/17287	0.29	0/23345
1	C	0.14	0/17287	0.29	0/23345
1	D	0.14	0/17287	0.29	0/23345
All	All	0.14	0/69148	0.29	0/93380

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	17072	0	17103	290	0
1	B	17072	0	17103	283	0
1	C	17072	0	17103	293	0
1	D	17072	0	17103	290	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	0	9	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	24	0	9	0	0
3	C	24	0	9	0	0
3	D	24	0	9	0	0
4	A	31	0	12	3	0
4	B	31	0	12	3	0
4	C	31	0	12	3	0
4	D	31	0	12	2	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
All	All	68516	0	68496	1140	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 8.

The worst 5 of 1140 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:240:VAL:HG11	1:B:309:LEU:HD11	1.51	0.91
1:D:240:VAL:HG11	1:D:309:LEU:HD11	1.51	0.91
1:C:240:VAL:HG11	1:C:309:LEU:HD11	1.51	0.90
1:A:240:VAL:HG11	1:A:309:LEU:HD11	1.51	0.88
1:C:712:ALA:HB1	1:C:716:ARG:HH12	1.42	0.85

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	2058/2633 (78%)	1969 (96%)	89 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	2058/2633 (78%)	1969 (96%)	89 (4%)	0	100	100
1	C	2058/2633 (78%)	1969 (96%)	89 (4%)	0	100	100
1	D	2058/2633 (78%)	1969 (96%)	89 (4%)	0	100	100
All	All	8232/10532 (78%)	7876 (96%)	356 (4%)	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	1899/2329 (82%)	1898 (100%)	1 (0%)	88	89
1	B	1899/2329 (82%)	1898 (100%)	1 (0%)	88	89
1	C	1899/2329 (82%)	1898 (100%)	1 (0%)	88	89
1	D	1899/2329 (82%)	1898 (100%)	1 (0%)	88	89
All	All	7596/9316 (82%)	7592 (100%)	4 (0%)	87	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	502	ASN
1	B	502	ASN
1	C	502	ASN
1	D	502	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	98	GLN
1	D	1746	ASN
1	C	1084	GLN
1	D	1443	ASN

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Mol	Chain	Res	Type
1	D	1084	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 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	$\# Z > 2$
4	ATP	B	2703	-	32,33,33	0.30	0	48,52,52	0.69	0
3	I3P	B	2702	-	24,24,24	1.29	3 (12%)	39,39,39	0.81	2 (5%)
4	ATP	A	2703	-	32,33,33	0.30	0	48,52,52	0.69	0
3	I3P	A	2702	-	24,24,24	1.28	3 (12%)	39,39,39	0.81	2 (5%)
3	I3P	D	2702	-	24,24,24	1.28	3 (12%)	39,39,39	0.81	3 (7%)
4	ATP	D	2703	-	32,33,33	0.30	0	48,52,52	0.69	0
3	I3P	C	2702	-	24,24,24	1.29	3 (12%)	39,39,39	0.81	2 (5%)
4	ATP	C	2703	-	32,33,33	0.30	0	48,52,52	0.69	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
4	ATP	B	2703	-	-	5/22/38/38	0/3/3/3
3	I3P	B	2702	-	-	4/15/39/39	0/1/1/1
4	ATP	A	2703	-	-	5/22/38/38	0/3/3/3
3	I3P	A	2702	-	-	4/15/39/39	0/1/1/1
3	I3P	D	2702	-	-	4/15/39/39	0/1/1/1
4	ATP	D	2703	-	-	5/22/38/38	0/3/3/3
3	I3P	C	2702	-	-	4/15/39/39	0/1/1/1
4	ATP	C	2703	-	-	5/22/38/38	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	2702	I3P	P1-O1	3.15	1.65	1.59
3	A	2702	I3P	P1-O1	3.11	1.65	1.59
3	C	2702	I3P	P1-O1	3.11	1.65	1.59
3	D	2702	I3P	P1-O1	3.08	1.64	1.59
3	C	2702	I3P	P4-O4	3.07	1.64	1.59

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	2702	I3P	P5-O5-C5	-2.08	117.88	123.43
3	A	2702	I3P	P5-O5-C5	-2.07	117.89	123.43
3	B	2702	I3P	P5-O5-C5	-2.07	117.89	123.43
3	C	2702	I3P	P5-O5-C5	-2.07	117.89	123.43
3	D	2702	I3P	P1-O1-C1	-2.03	118.01	123.43

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

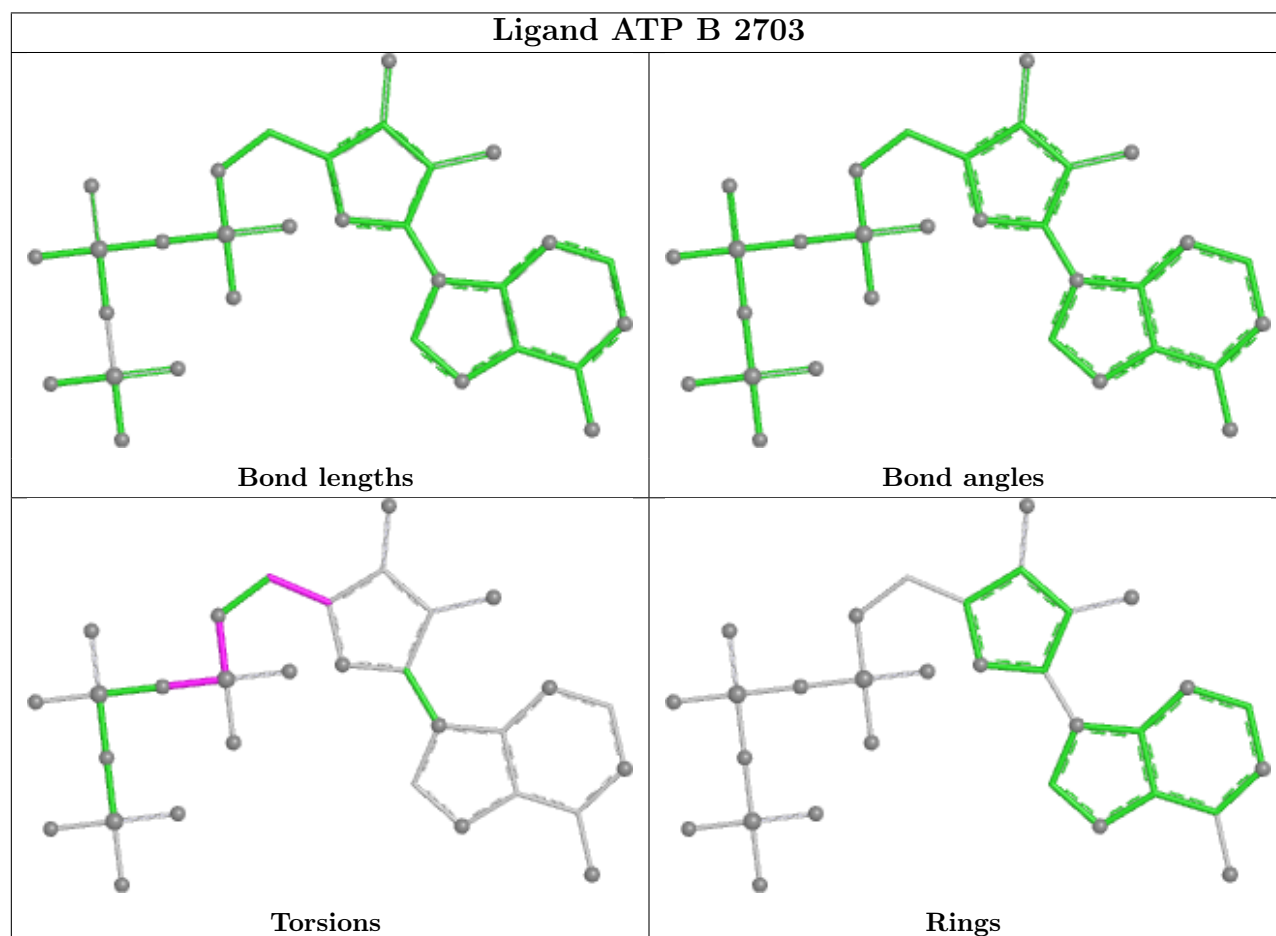
Mol	Chain	Res	Type	Atoms
4	A	2703	ATP	C5'-O5'-PA-O3A
4	B	2703	ATP	C5'-O5'-PA-O3A
4	C	2703	ATP	C5'-O5'-PA-O3A
4	D	2703	ATP	C5'-O5'-PA-O3A
4	A	2703	ATP	O4'-C4'-C5'-O5'

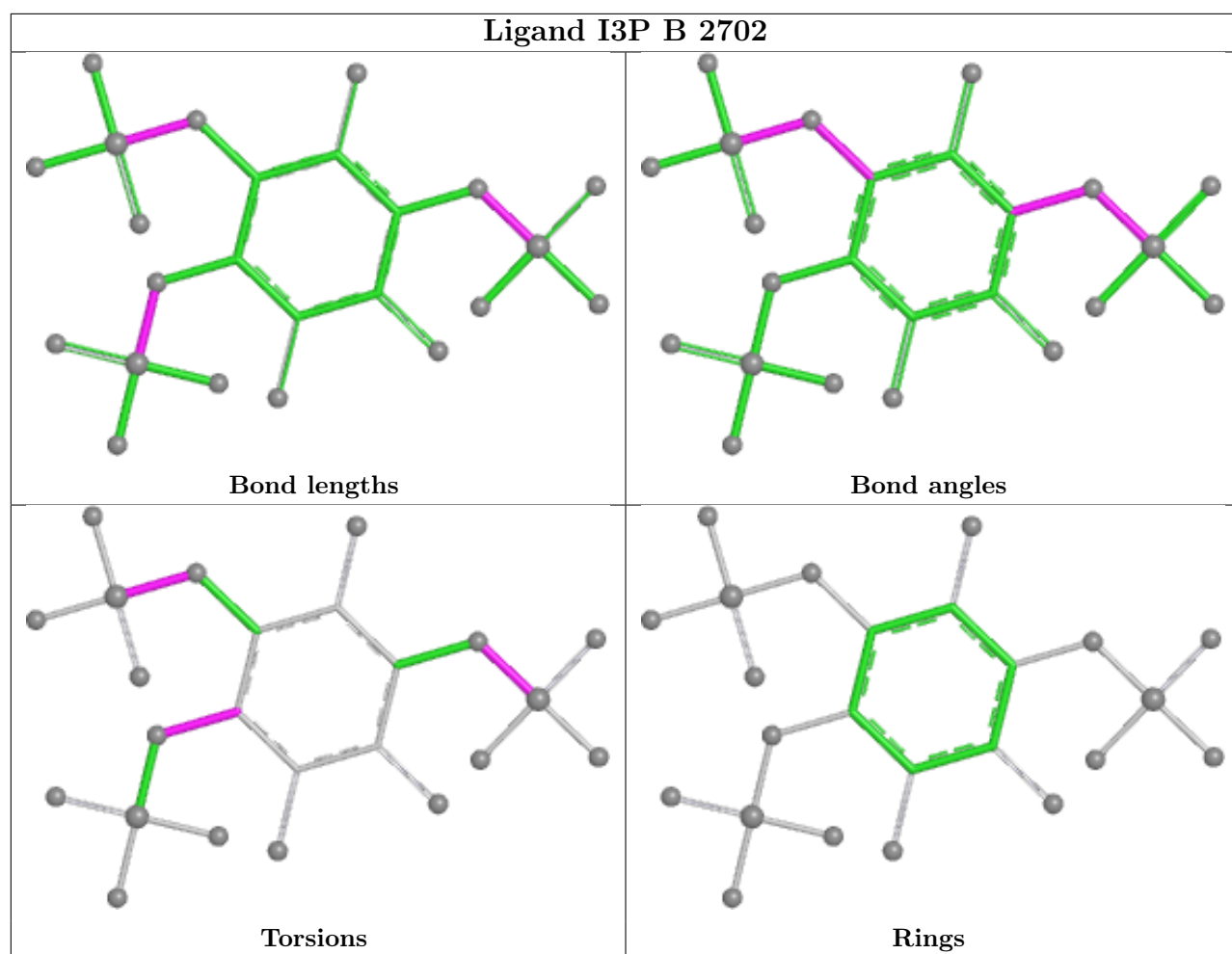
There are no ring outliers.

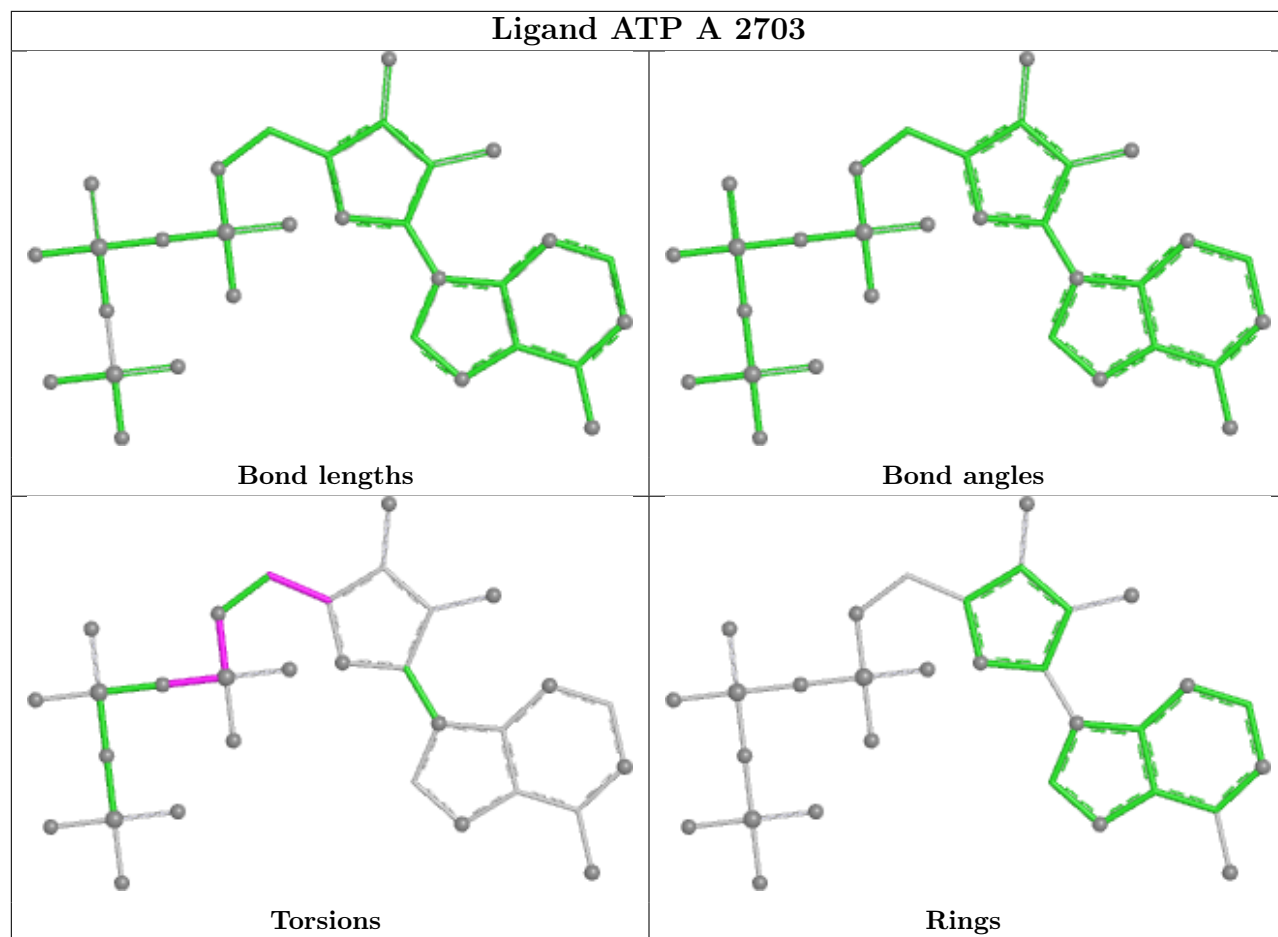
4 monomers are involved in 11 short contacts:

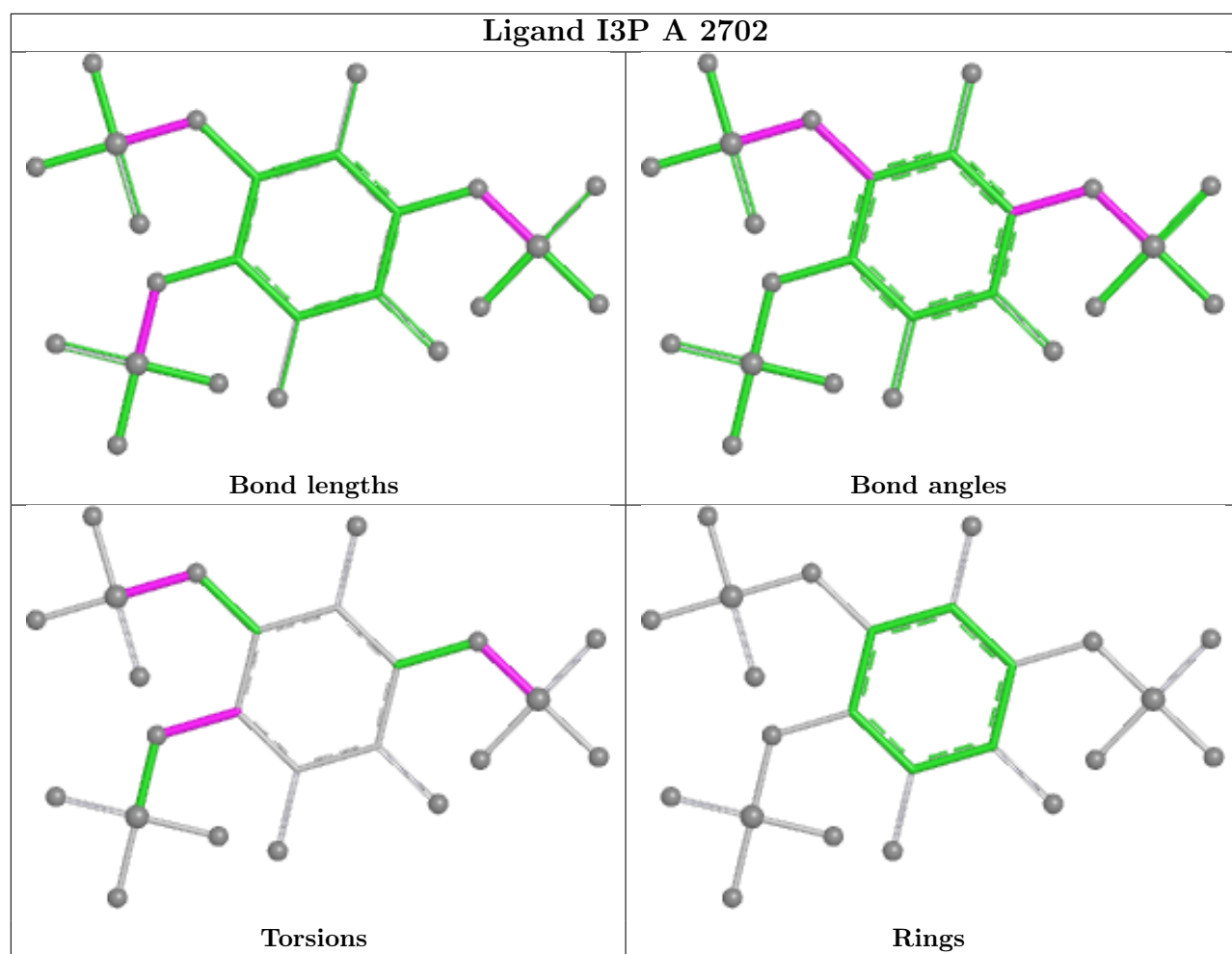
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	2703	ATP	3	0
4	A	2703	ATP	3	0
4	D	2703	ATP	2	0
4	C	2703	ATP	3	0

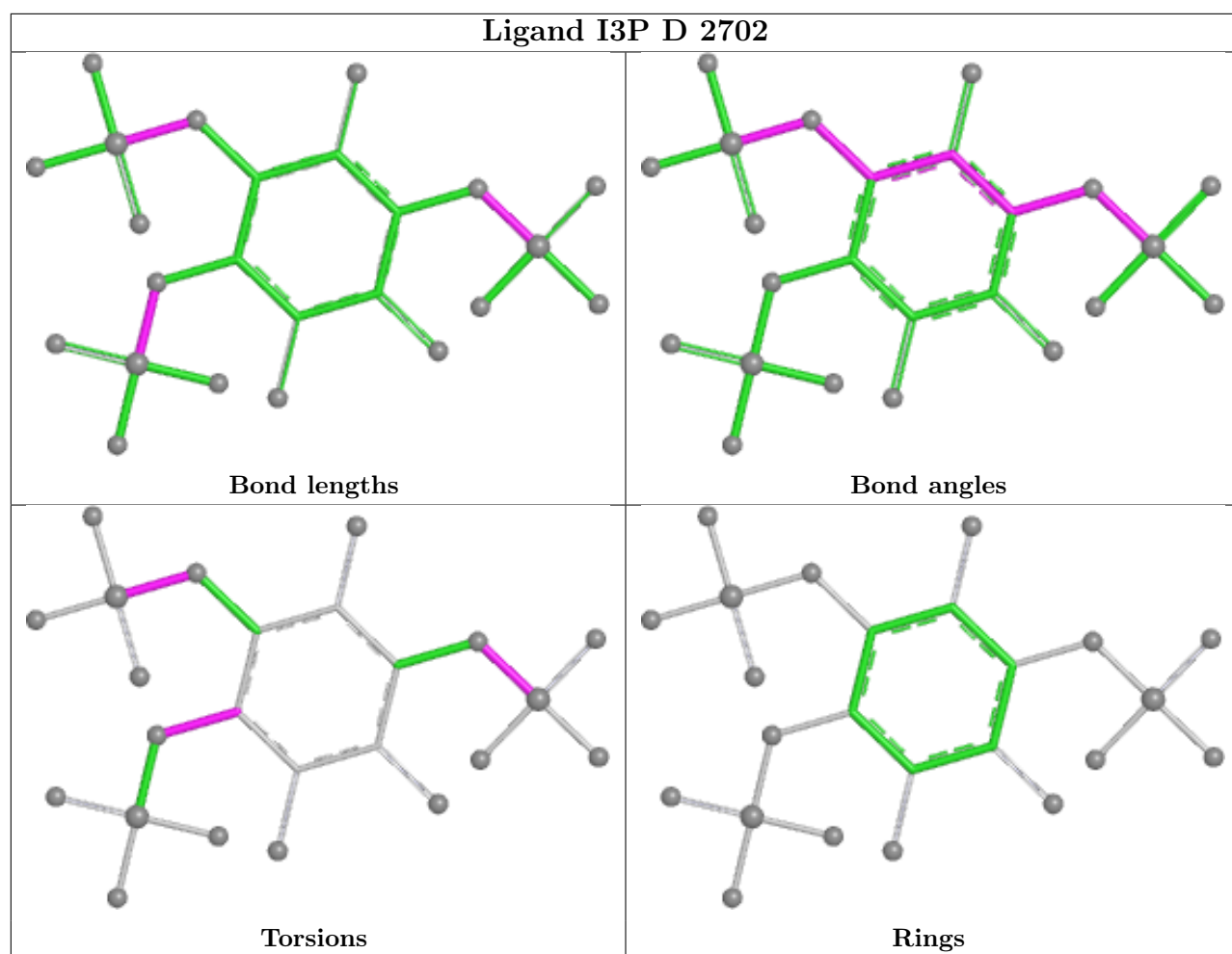
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

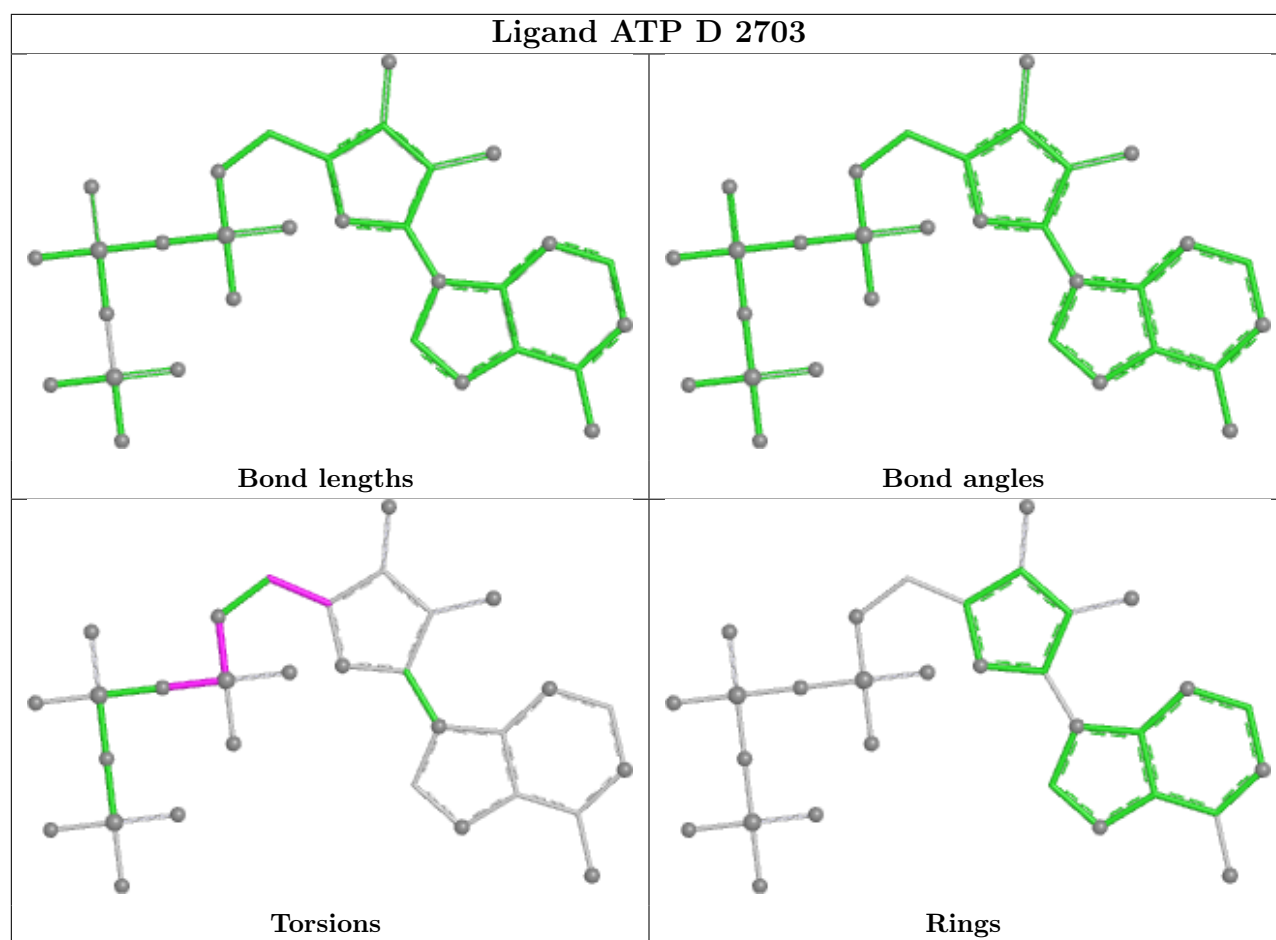


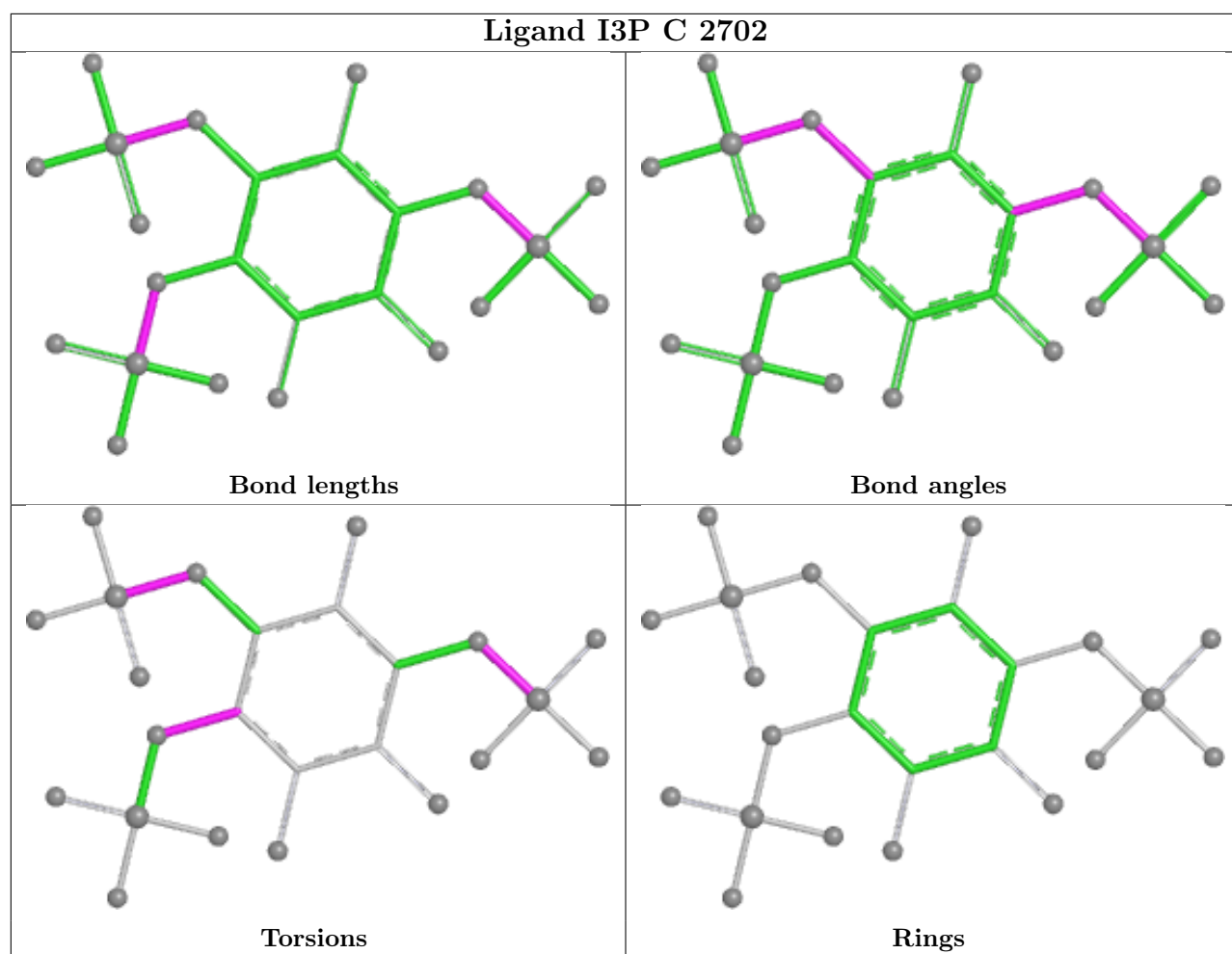


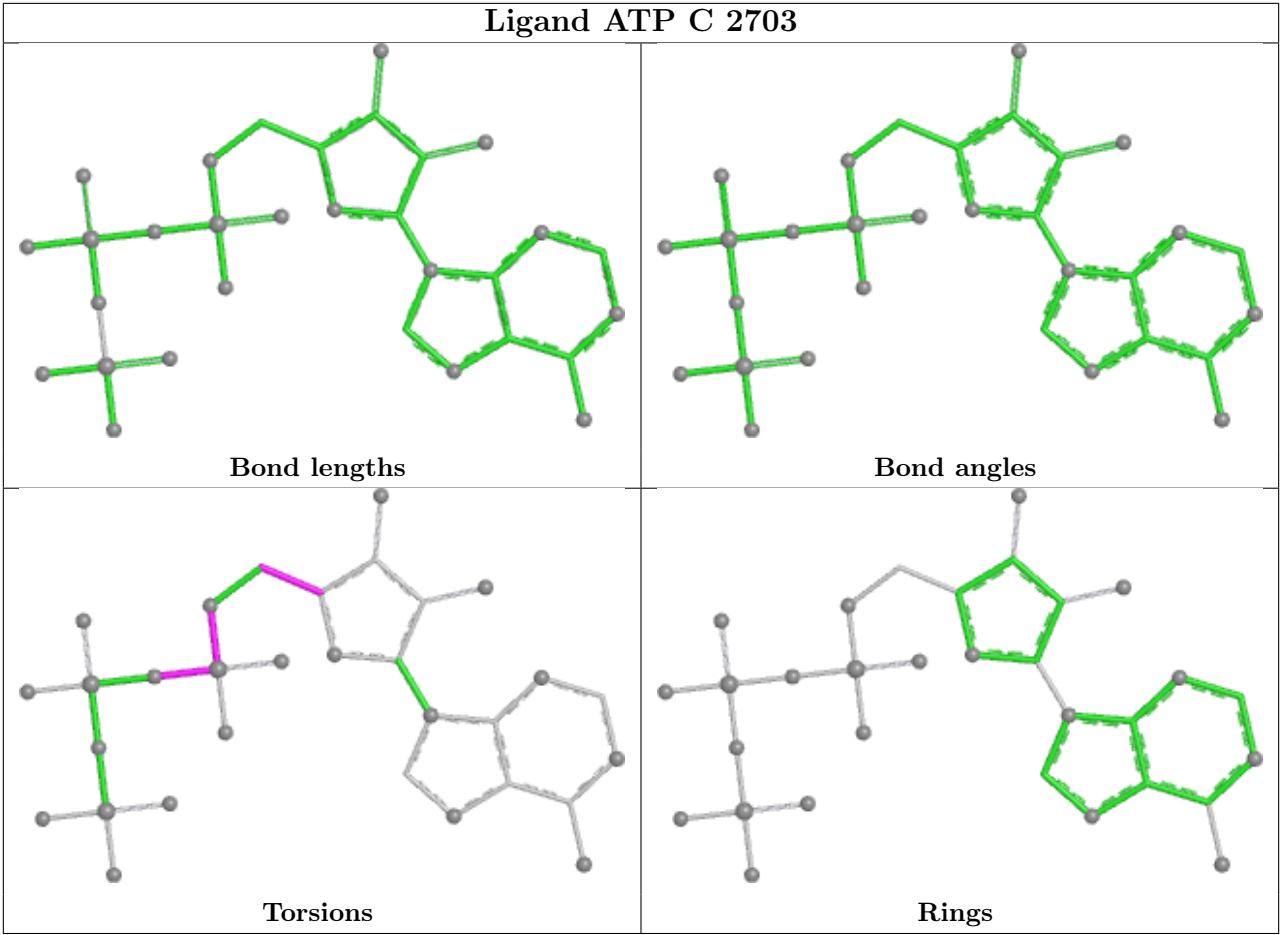












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	B	1
1	C	1
1	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2611:VAL	C	2628:UNK	N	28.89
1	B	2611:VAL	C	2628:UNK	N	28.89

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	2611:VAL	C	2628:UNK	N	28.89
1	D	2611:VAL	C	2628:UNK	N	28.89

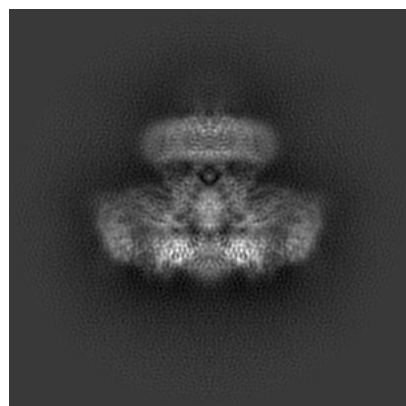
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25670. These allow visual inspection of the internal detail of the map and identification of artifacts.

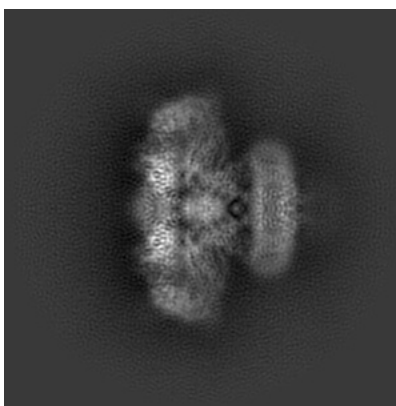
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

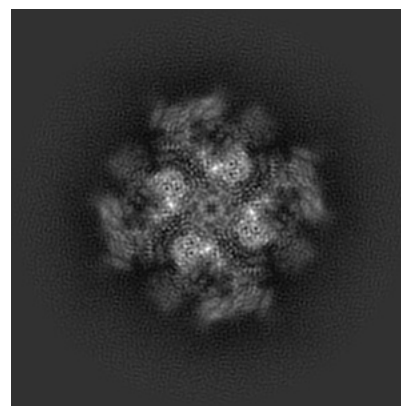
6.1.1 Primary map



X

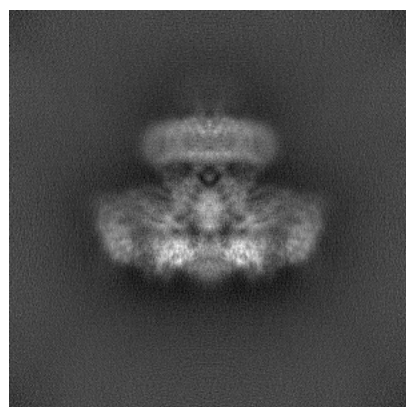


Y

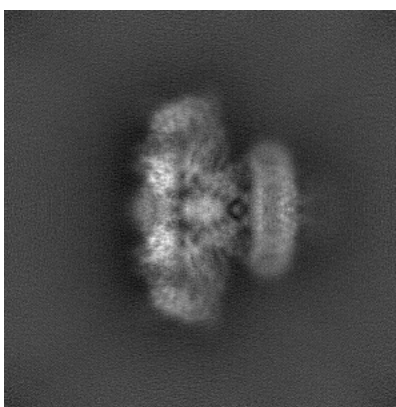


Z

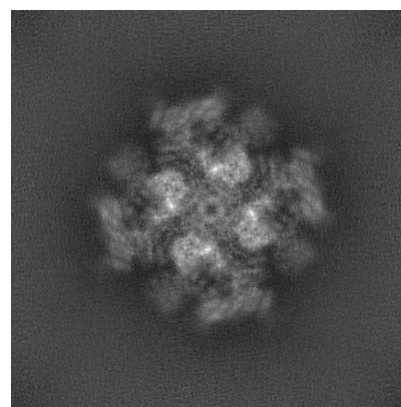
6.1.2 Raw map



X



Y

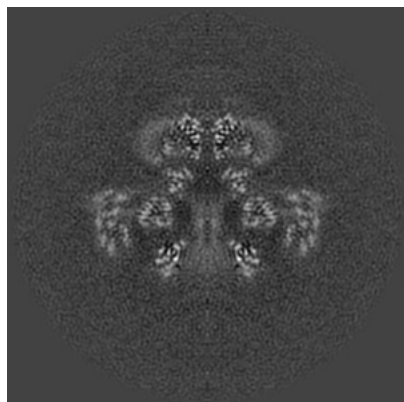


Z

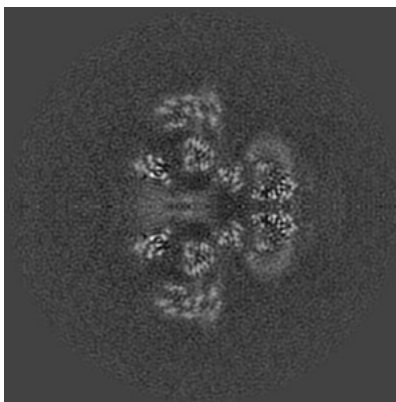
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

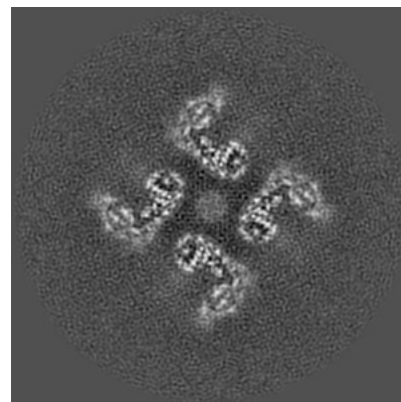
6.2.1 Primary map



X Index: 240

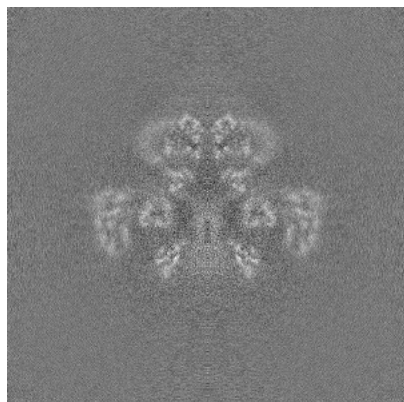


Y Index: 240

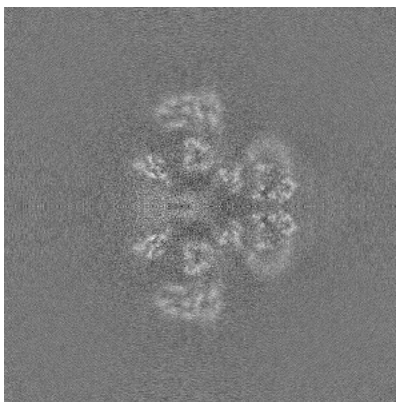


Z Index: 240

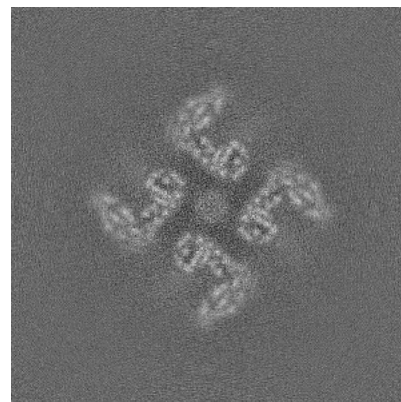
6.2.2 Raw map



X Index: 240



Y Index: 240

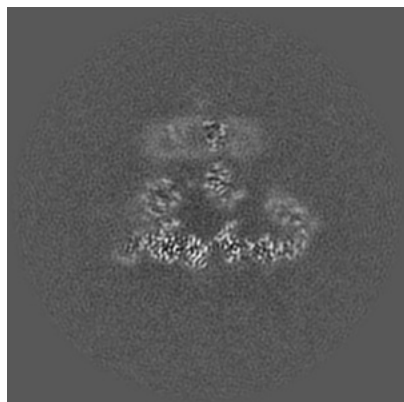


Z Index: 240

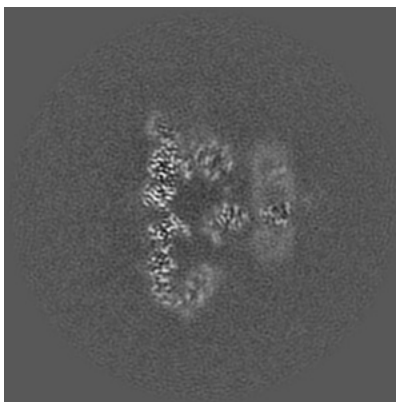
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

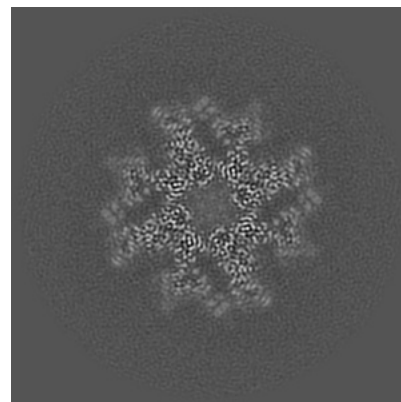
6.3.1 Primary map



X Index: 206

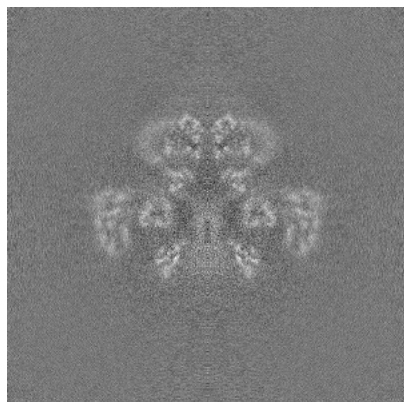


Y Index: 206

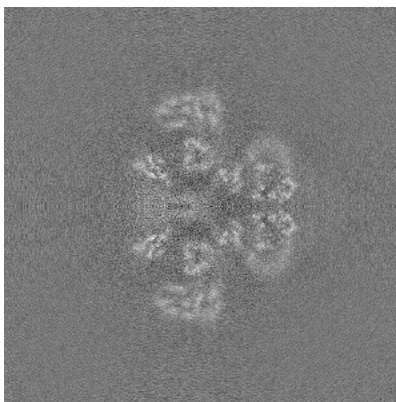


Z Index: 191

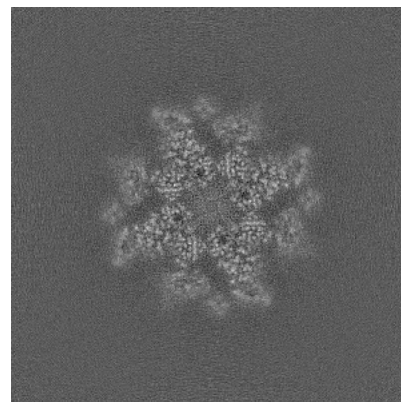
6.3.2 Raw map



X Index: 240



Y Index: 240

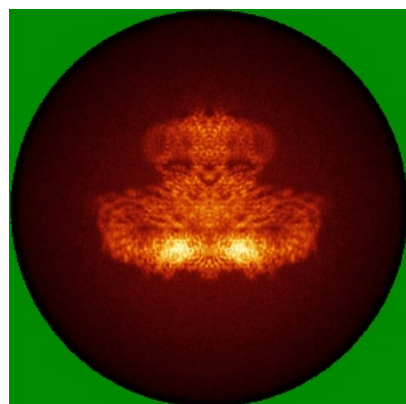


Z Index: 189

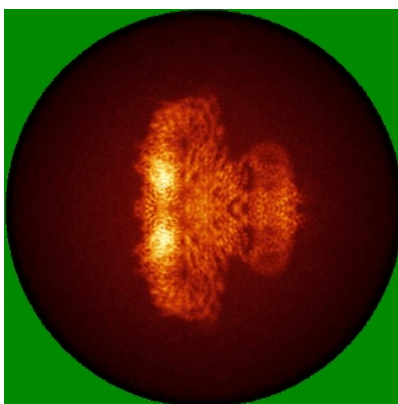
The images above show the largest variance slices of the map in three orthogonal directions.

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

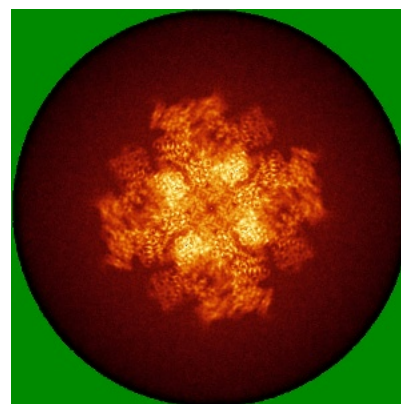
6.4.1 Primary map



X

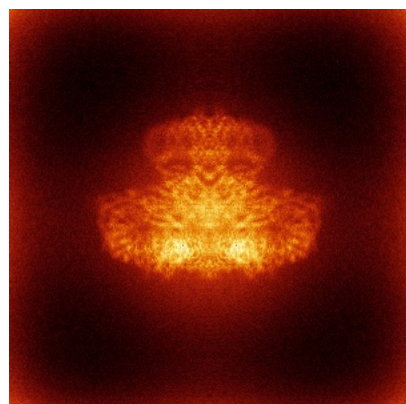


Y

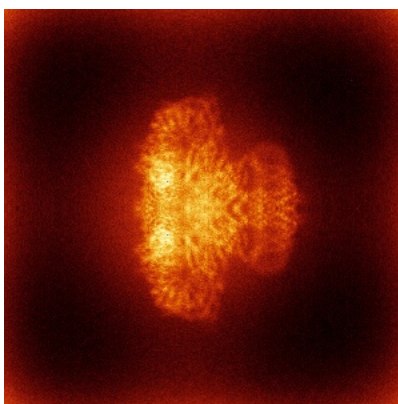


Z

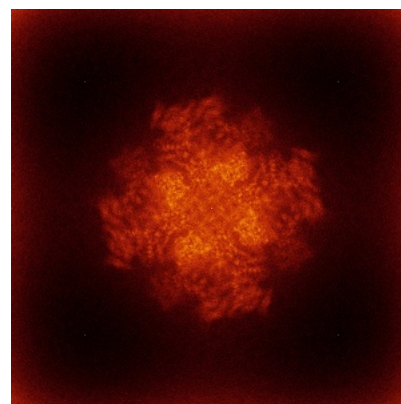
6.4.2 Raw map



X



Y

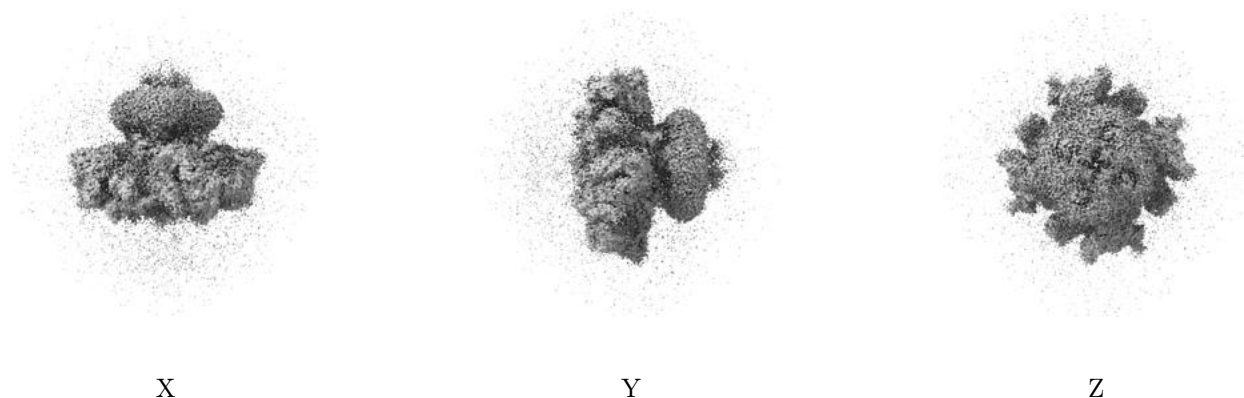


Z

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

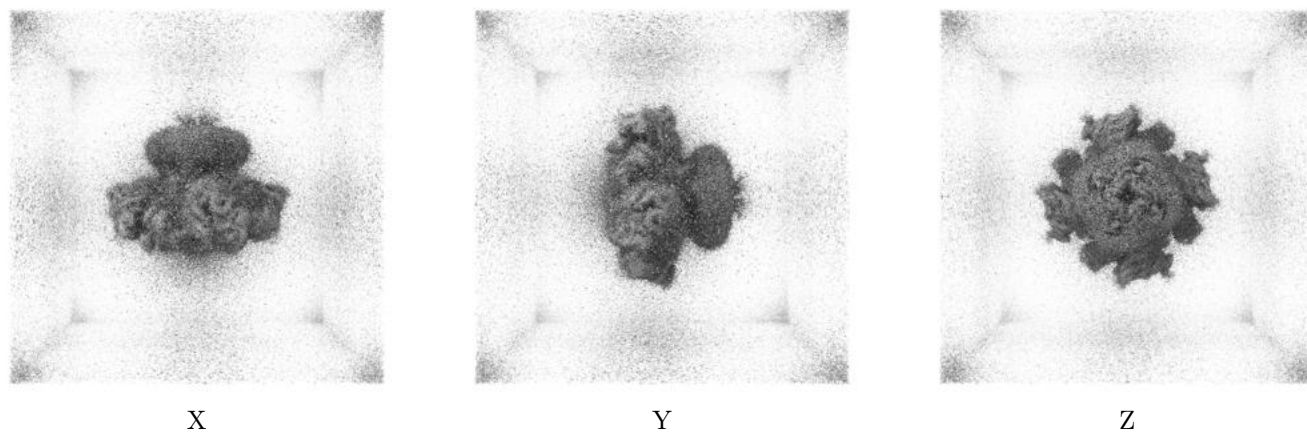
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

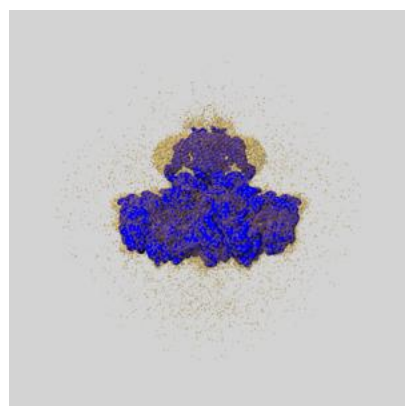
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

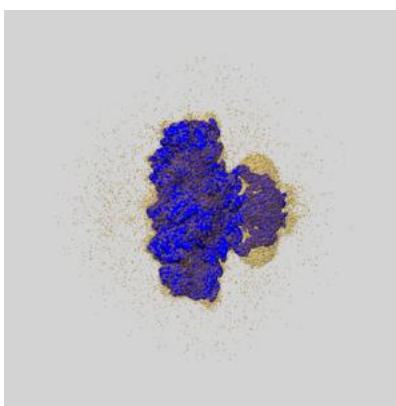
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

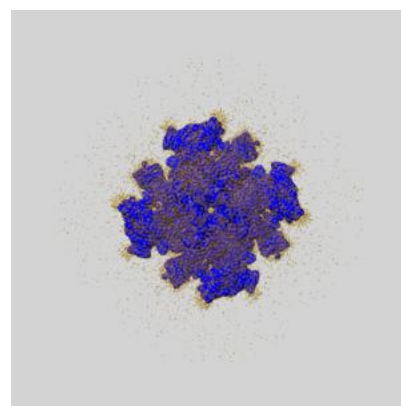
6.6.1 emd_25670_msk_1.map [i](#)



X



Y

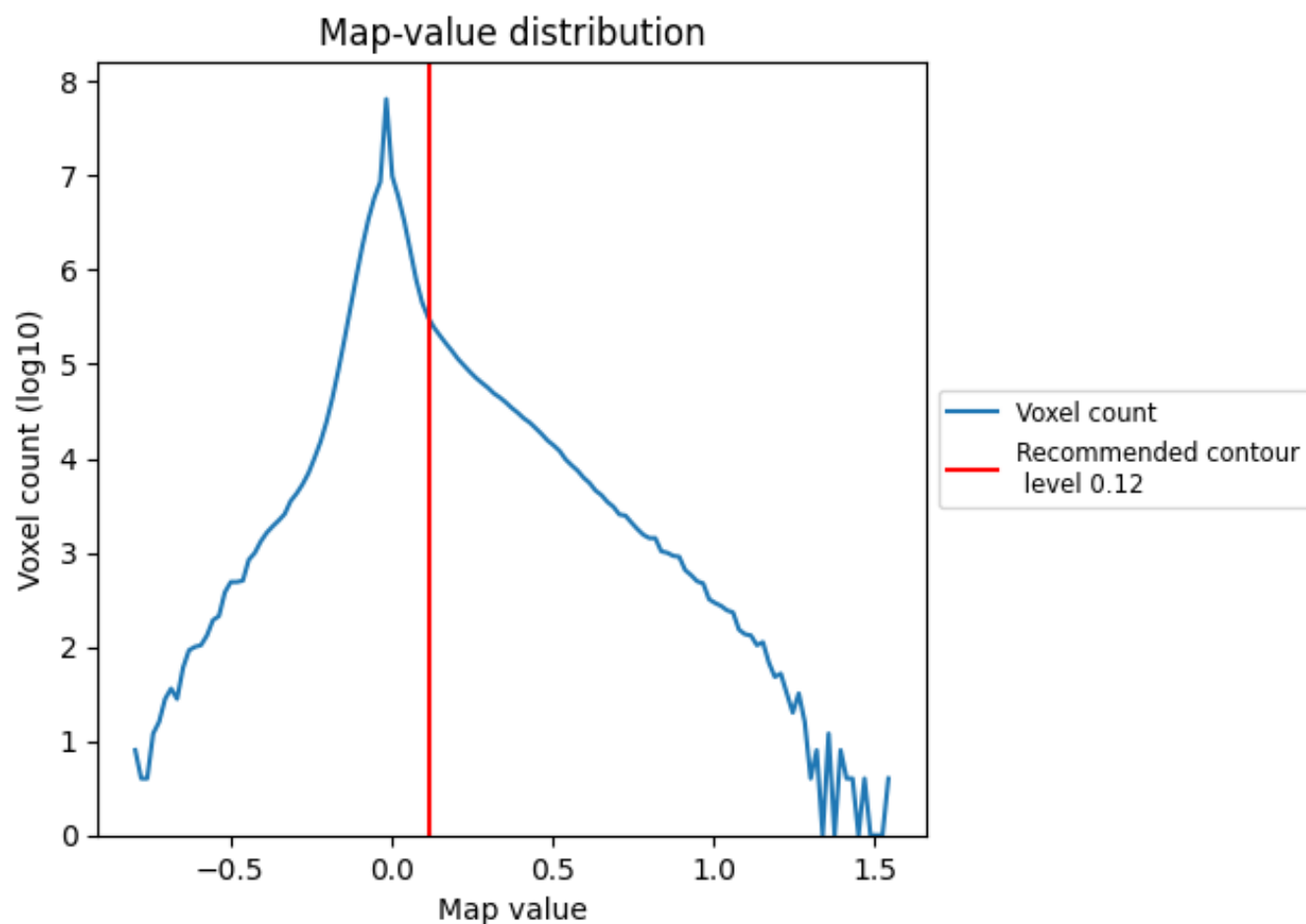


Z

7 Map analysis [i](#)

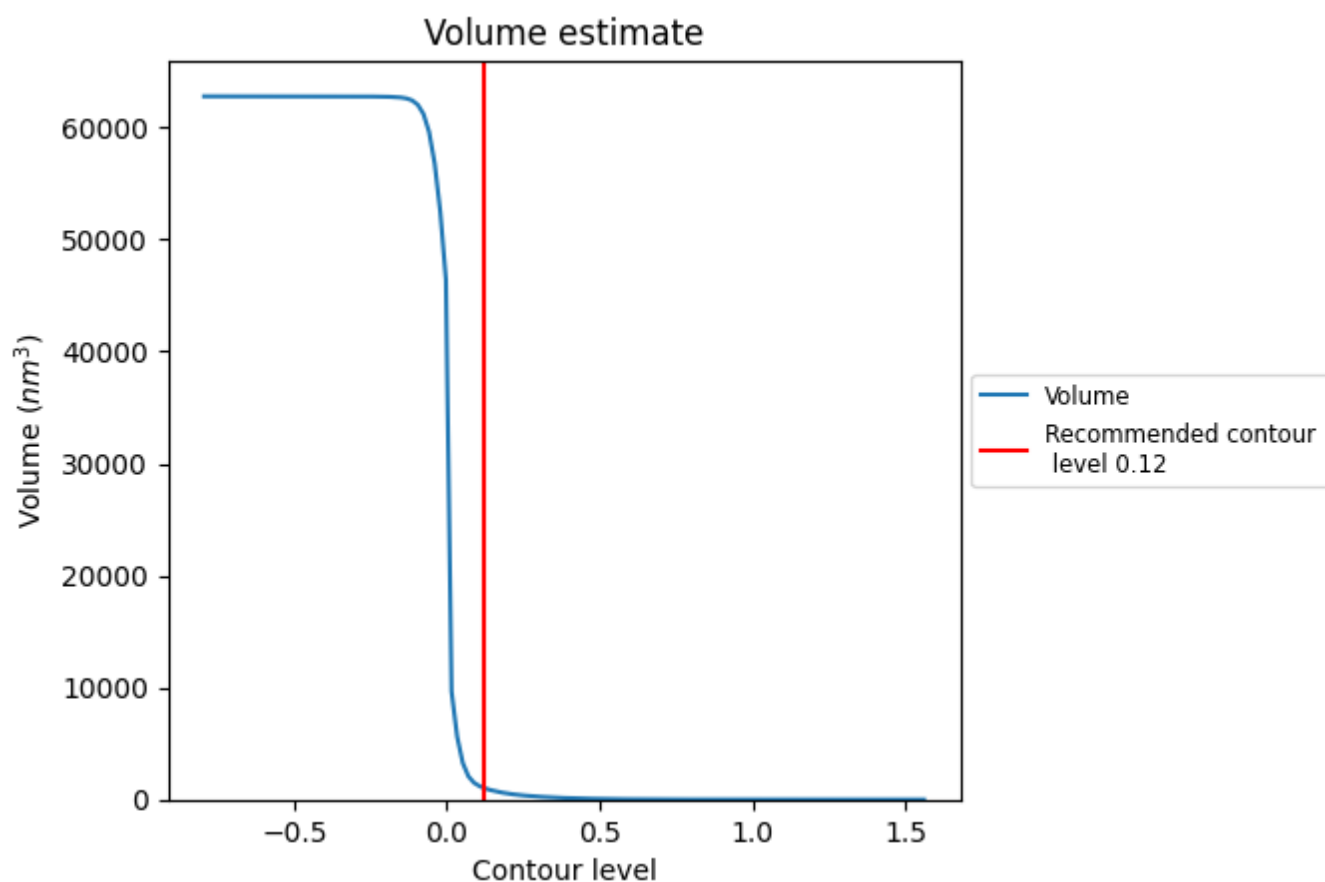
This section contains the results of statistical analysis of the map.

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.

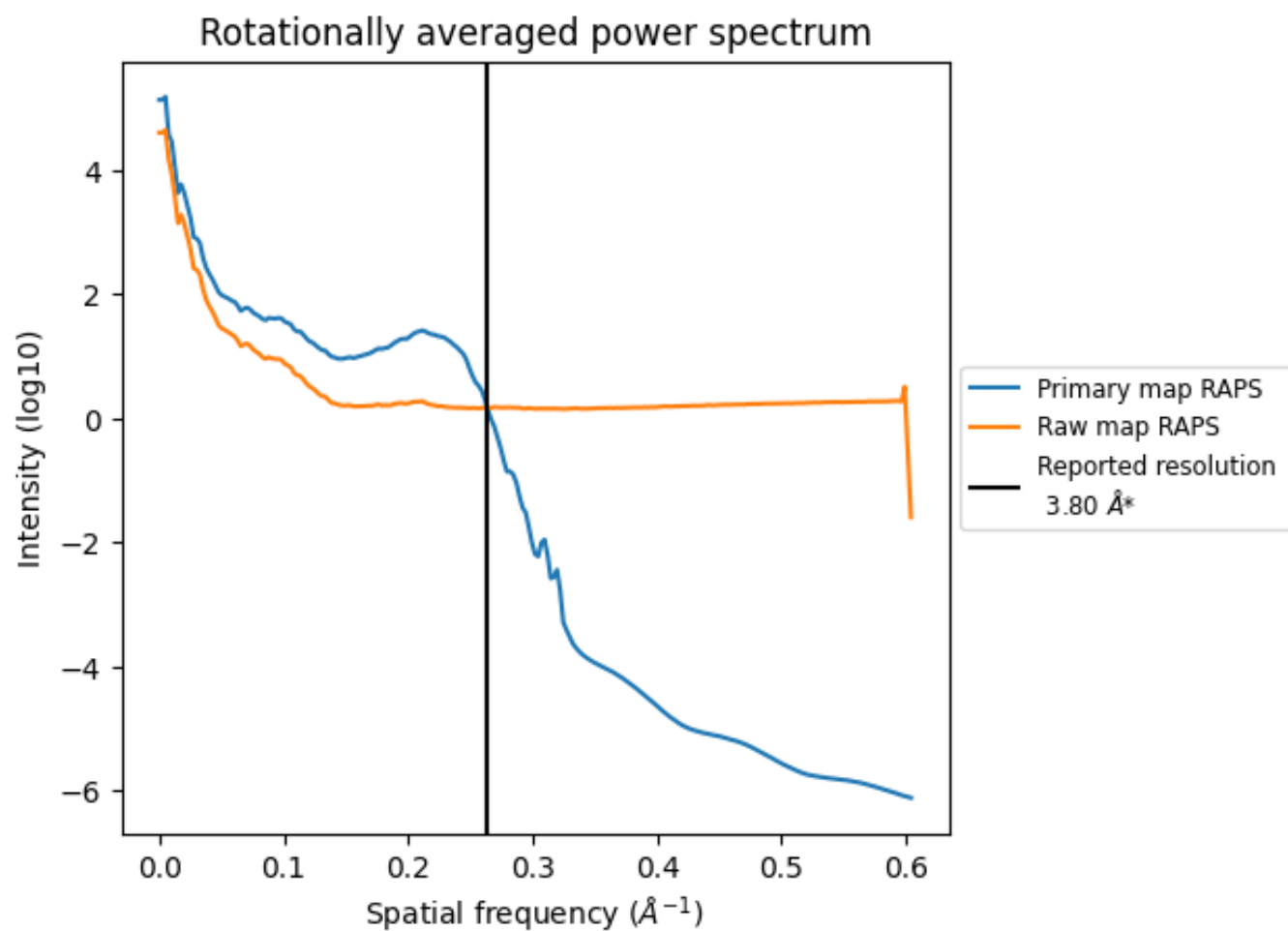
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1054 nm³; this corresponds to an approximate mass of 952 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 ⓘ

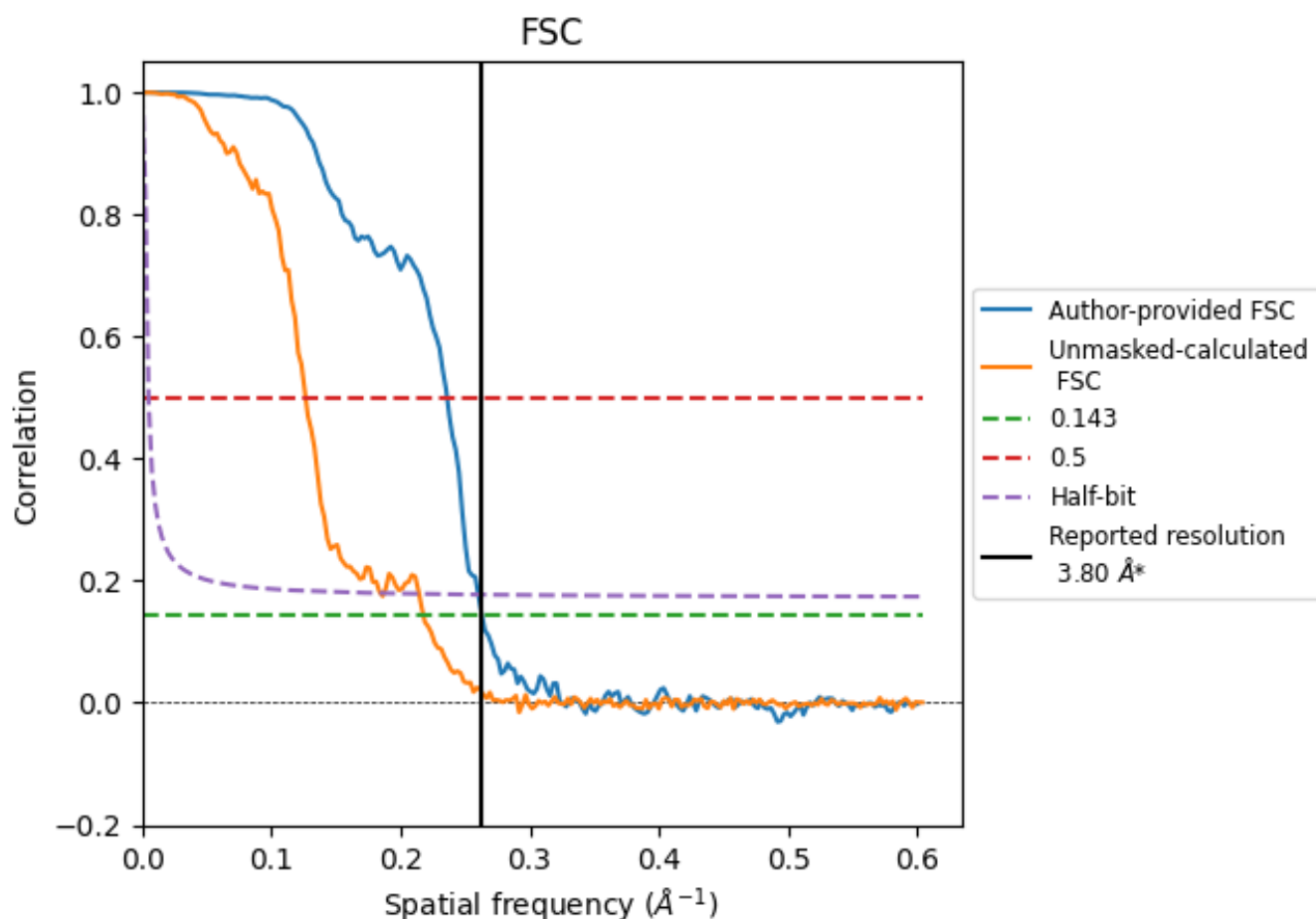


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

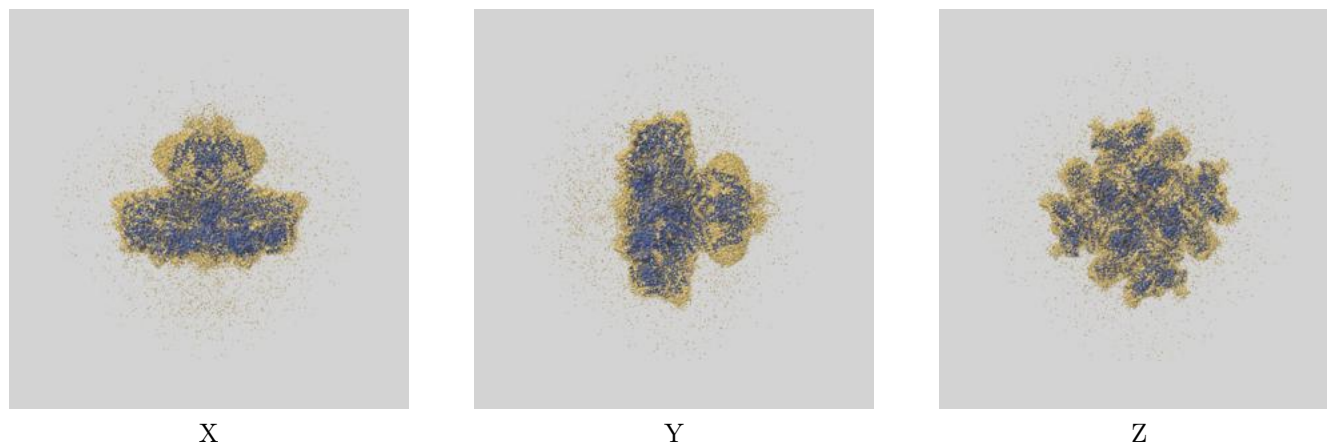
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.80	4.24	3.84
Unmasked-calculated*	4.59	7.90	5.42

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.59 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

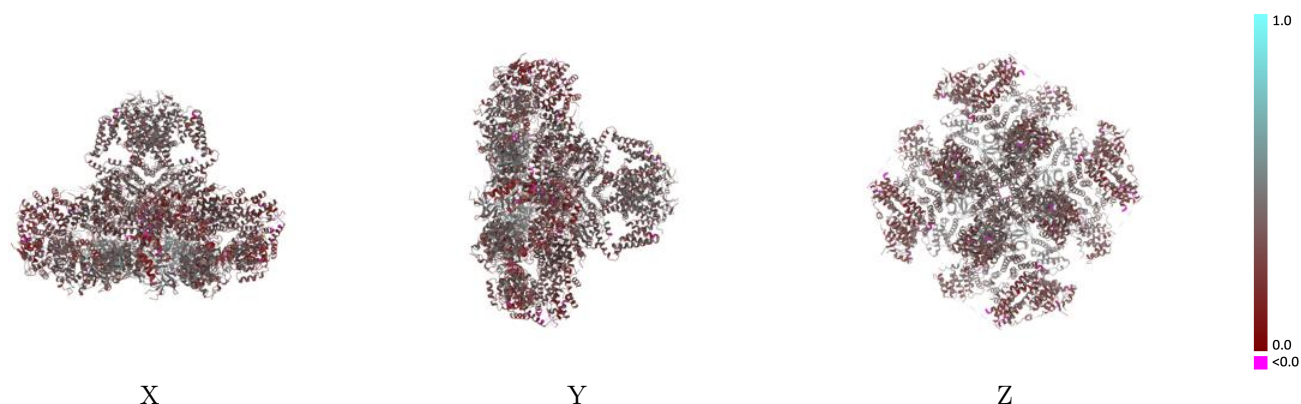
This section contains information regarding the fit between EMDB map EMD-25670 and PDB model 7T3T. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



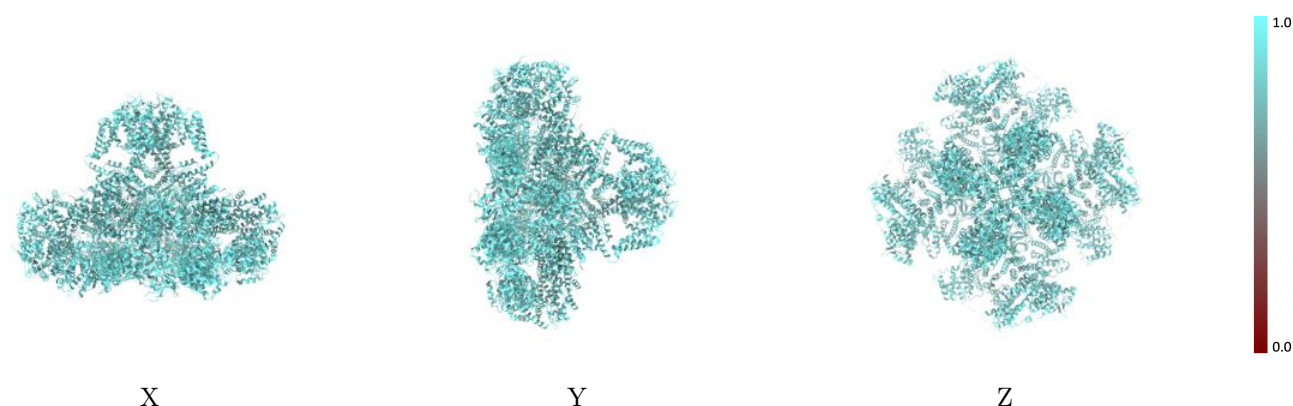
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



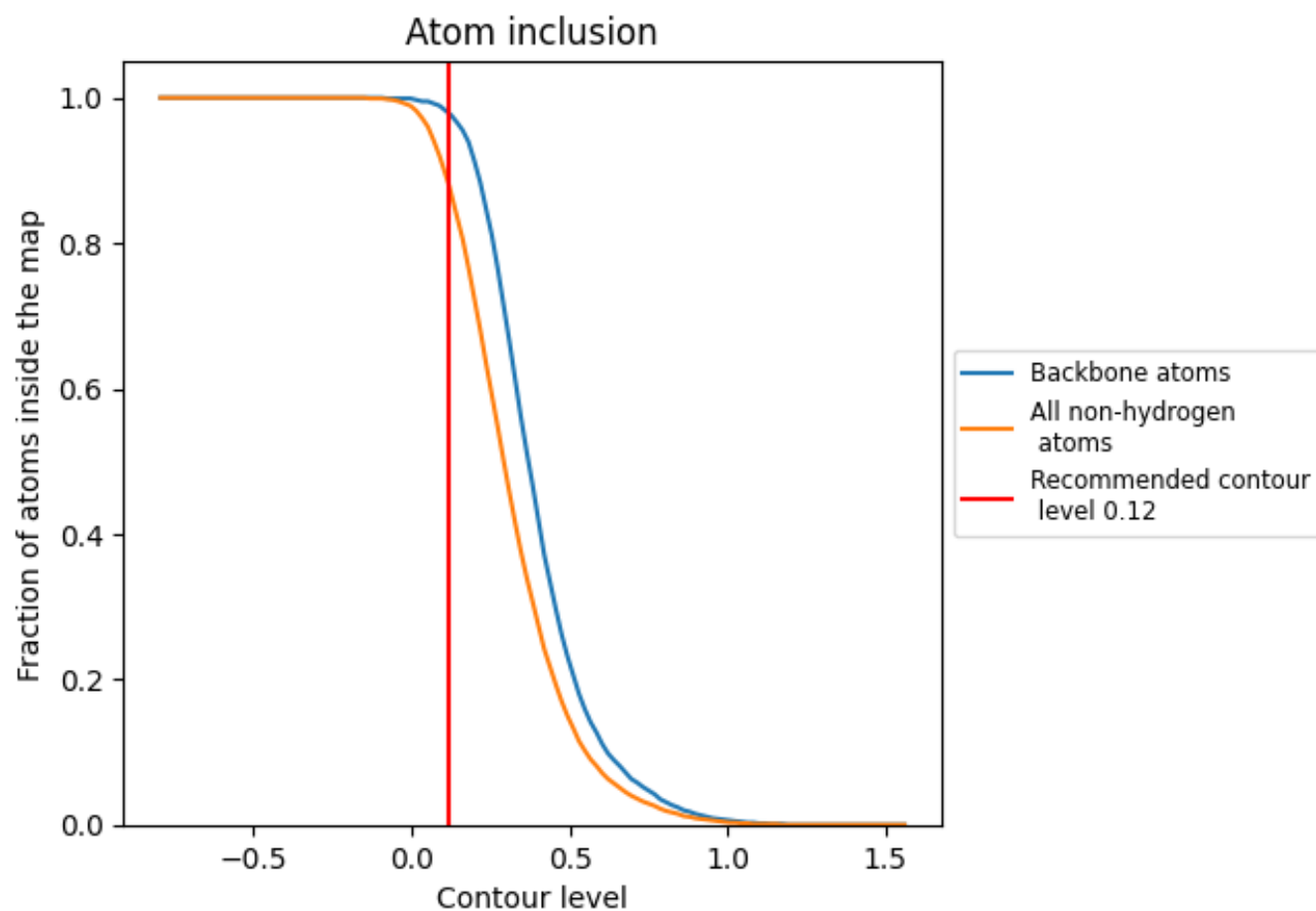
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 88% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8780	0.3570
A	0.8780	0.3570
B	0.8780	0.3570
C	0.8780	0.3570
D	0.8780	0.3570

