



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 08:05 PM UTC

PDB ID : 7XZI / pdb_00007xzi
EMDB ID : EMD-33528
Title : Cryo-EM structure of TOC-TIC supercomplex from Chlamydomonas reinhardtii
Authors : Liu, H.; Li, A.J.; Liu, Z.F.
Deposited on : 2022-06-02
Resolution : 2.77 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:

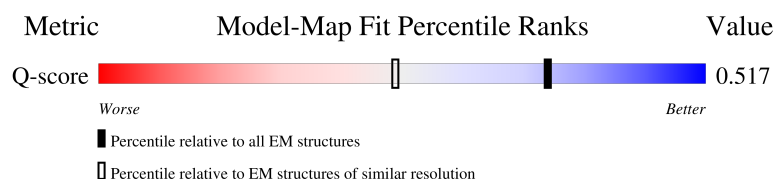
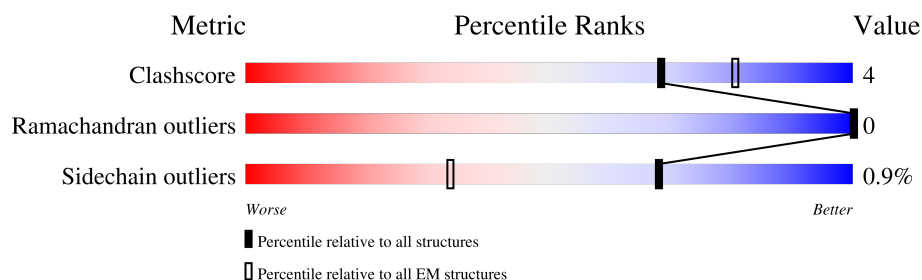
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

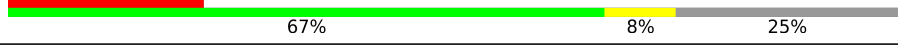
The reported resolution of this entry is 2.77 Å.

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.



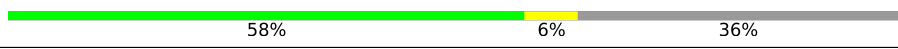
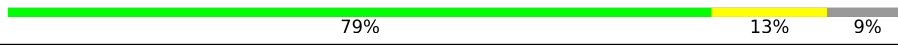
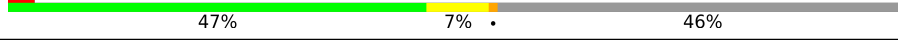
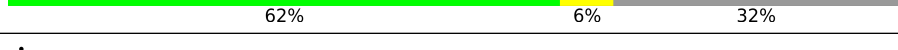
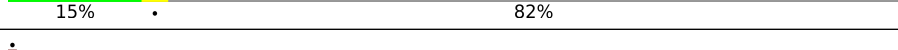
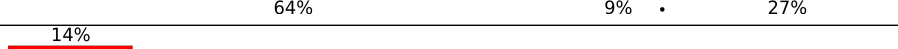
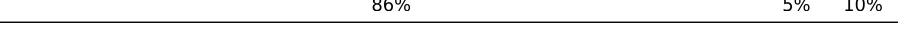
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10695 (2.27 - 3.27)

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	3	477	
2	4	363	
3	5	383	
4	7	798	

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Mol	Chain	Length	Quality of chain
5	9	967	
6	A	1995	
7	B	259	
8	C	127	
9	D	187	
10	E	955	
11	F	244	
12	G	397	
13	U	124	
14	X	21	

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 37365 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 Ctap3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	206	Total	C	N	O	S	0	0
			1528	965	271	286	6		

- Molecule 2 is a protein called Ctap4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	4	273	Total	C	N	O	S	0	0
			1734	1074	319	340	1		

- Molecule 3 is a protein called Ctap5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	196	Total	C	N	O	S	0	0
			1506	973	268	265			

- Molecule 4 is a protein called Toc75.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	7	616	Total	C	N	O	S	0	0
			4249	2674	761	800	14		

- Molecule 5 is a protein called Toc90.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	9	381	Total	C	N	O	S	0	0
			2800	1790	466	529	15		

- Molecule 6 is a protein called Tic214.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1598	Total	C	N	O	S	0	0
			12921	8361	2294	2239	27		

- Molecule 7 is a protein called Protein TIC 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	166	Total	C	N	O	S	0	0
			1409	964	206	227	12		

- Molecule 8 is a protein called Tic15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	116	Total	C	N	O	S	0	0
			947	615	170	156	6		

- Molecule 9 is a protein called Simp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	101	Total	C	N	O	S	0	0
			823	558	125	135	5		

- Molecule 10 is a protein called Tic100.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	770	Total	C	N	O	S	0	0
			6055	3784	1044	1196	31		

- Molecule 11 is a protein called Tic56.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	167	Total	C	N	O	S	0	0
			1361	877	245	230	9		

- Molecule 12 is a protein called Toc34.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	G	70	Total	C	N	O	0	0
			501	318	102	81		

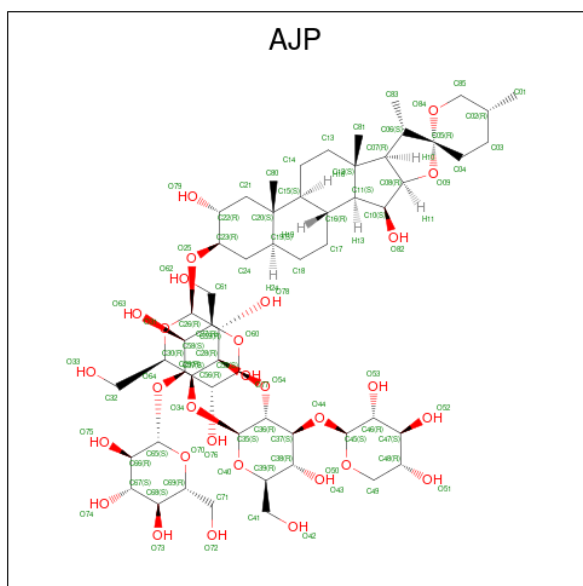
- Molecule 13 is a protein called Simp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	U	91	Total	C	N	O	S	0	0
			662	421	123	117	1		

- Molecule 14 is a protein called Unknown peptide.

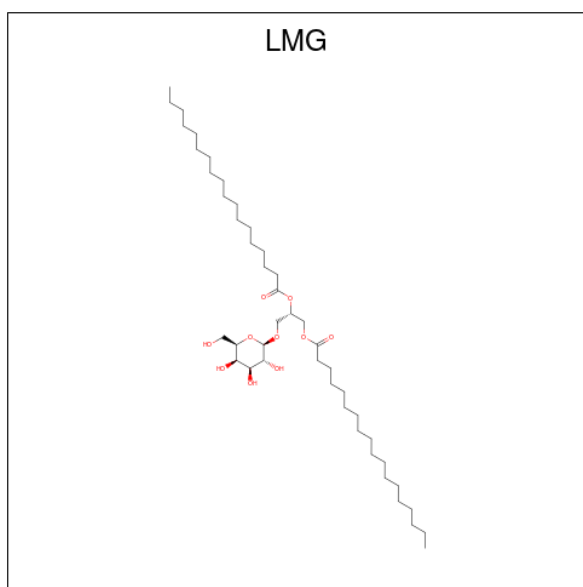
Mol	Chain	Residues	Atoms			AltConf	Trace
14	X	19	Total	C	N	O	
			93	55	19	19	
						0	0

- Molecule 15 is Digitonin (CCD ID: AJP) (formula: $C_{56}H_{92}O_{29}$).



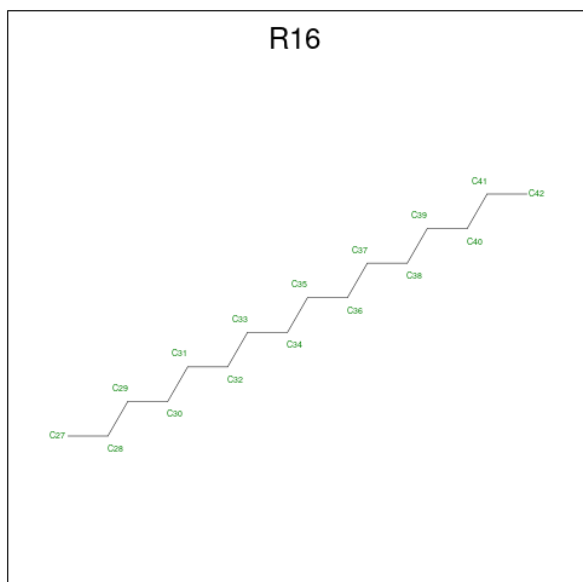
Mol	Chain	Residues	Atoms			AltConf
15	4	1	Total	C	O	
			31	27	4	0
15	5	1	Total	C	O	
			43	33	10	0
15	B	1	Total	C	O	
			42	33	9	0
15	D	1	Total	C	O	
			32	27	5	0
15	D	1	Total	C	O	
			52	39	13	0

- Molecule 16 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (CCD ID: LMG) (formula: $C_{45}H_{86}O_{10}$) (labeled as "Ligand of Interest" by depositor).



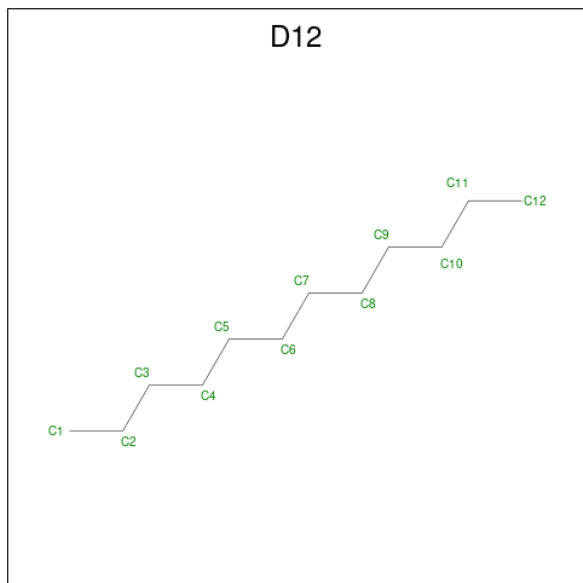
Mol	Chain	Residues	Atoms			AltConf
16	5	1	Total	C	O	0
			42	32	10	
16	A	1	Total	C	O	0
			52	42	10	
16	A	1	Total	C	O	0
			55	45	10	
16	A	1	Total	C	O	0
			39	29	10	
16	B	1	Total	C	O	0
			37	27	10	

- Molecule 17 is HEXADECANE (CCD ID: R16) (formula: $C_{16}H_{34}$).



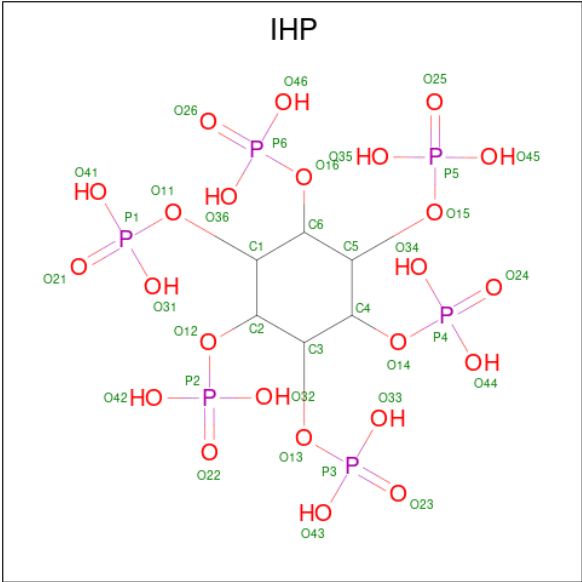
Mol	Chain	Residues	Atoms	AltConf
17	7	1	Total C 10 10	0

- Molecule 18 is DODECANE (CCD ID: D12) (formula: C₁₂H₂₆).



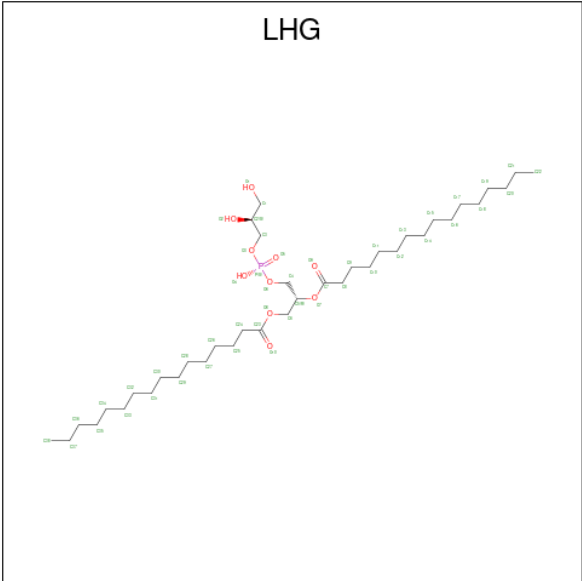
Mol	Chain	Residues	Atoms	AltConf
18	9	1	Total C 12 12	0
18	A	1	Total C 12 12	0
18	A	1	Total C 12 12	0
18	A	1	Total C 12 12	0
18	B	1	Total C 12 12	0
18	B	1	Total C 12 12	0
18	D	1	Total C 12 12	0

- Molecule 19 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
19	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 20 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: $C_{38}H_{75}O_{10}P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
20	A	1	Total	C	O	P	0
			49	38	10	1	
20	B	1	Total	C	O	P	0
			36	25	10	1	

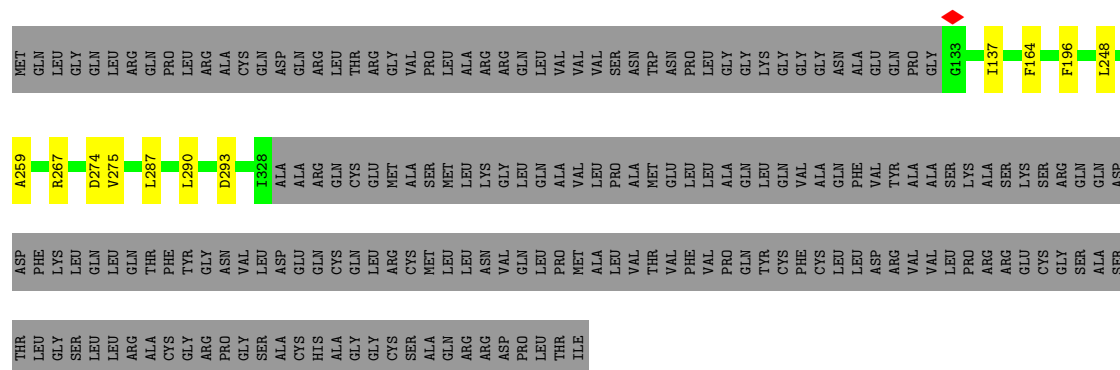
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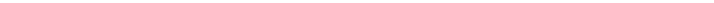
Mol	Chain	Residues	Atoms				AltConf
20	B	1	Total	C	O	P	0
			45	34	10	1	
20	C	1	Total	C	O	P	0
			47	36	10	1	
20	F	1	Total	C	O	P	0
			44	33	10	1	

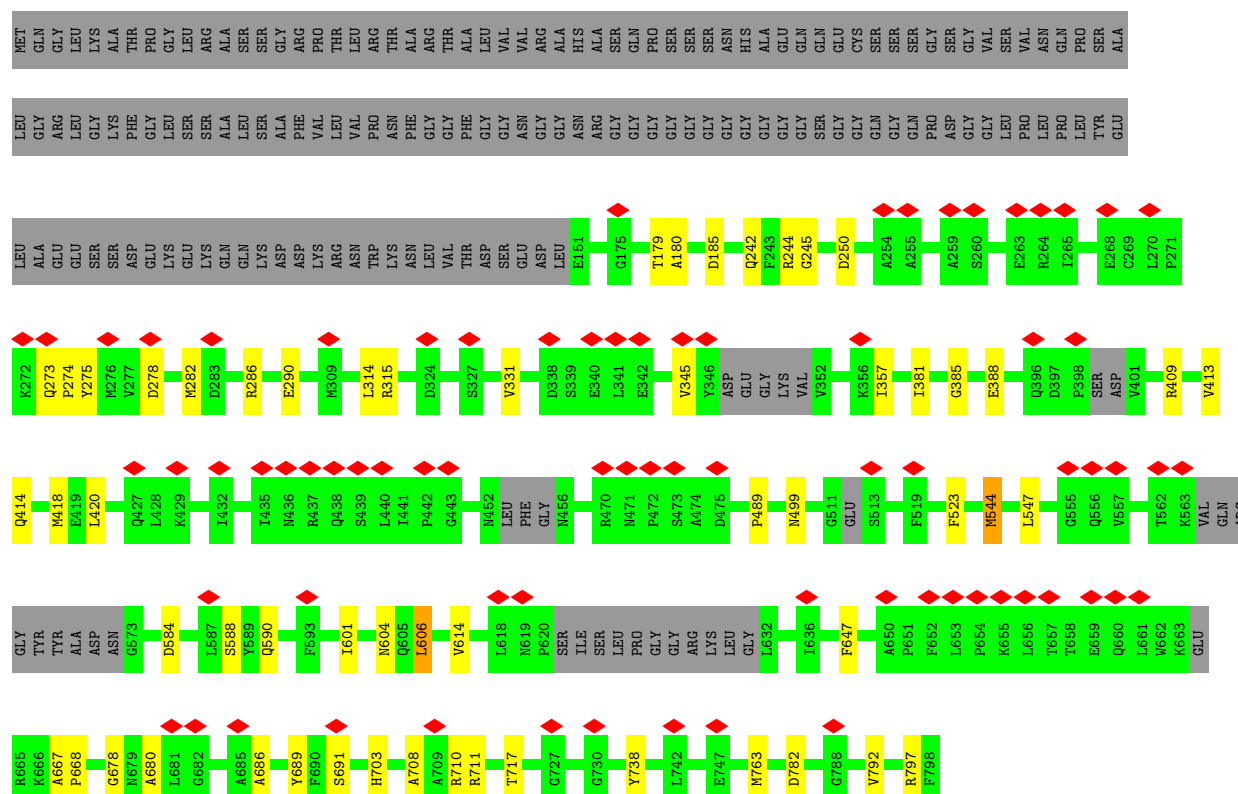
- Molecule 3: Ctap5

Chain 5: 48% . 49%



- Molecule 4: Toc75

Chain 7:  9% 70% 7% 23%





Response	Percentage
Used	58%
Not used	6%
Don't know	36%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	796731	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.956	Depositor
Minimum map value	-0.387	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	432.0, 432.0, 432.0	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.675, 0.675, 0.675	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: IHP, R16, AJP, LHG, D12, LMG

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	3	0.09	0/1561	0.22	0/2125
2	4	0.13	0/1757	0.33	0/2398
3	5	0.10	0/1543	0.24	0/2100
4	7	0.11	0/4336	0.28	0/5910
5	9	0.10	0/2882	0.27	0/3934
6	A	0.14	0/13218	0.30	1/17847 (0.0%)
7	B	0.13	0/1467	0.29	0/2007
8	C	0.11	0/984	0.28	0/1338
9	D	0.10	0/854	0.25	0/1167
10	E	0.14	0/6198	0.30	0/8393
11	F	0.11	0/1400	0.29	0/1900
12	G	0.14	0/515	0.31	0/704
13	U	0.11	0/679	0.30	0/926
14	X	0.10	0/92	0.19	0/126
All	All	0.13	0/37486	0.29	1/50875 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1943	ASN	CB-CA-C	-5.14	110.67	116.63

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	3	1528	0	1393	13	0
2	4	1734	0	1366	18	0
3	5	1506	0	1443	8	0
4	7	4249	0	3621	34	0
5	9	2800	0	2476	27	0
6	A	12921	0	12873	117	0
7	B	1409	0	1368	11	0
8	C	947	0	910	12	0
9	D	823	0	790	9	0
10	E	6055	0	5642	53	0
11	F	1361	0	1362	11	0
12	G	501	0	410	7	0
13	U	662	0	650	7	0
14	X	93	0	75	2	0
15	4	31	0	0	0	0
15	5	43	0	0	0	0
15	B	42	0	0	2	0
15	D	84	0	0	0	0
16	5	42	0	57	2	0
16	A	146	0	211	5	0
16	B	37	0	44	0	0
17	7	10	0	16	0	0
18	9	12	0	26	0	0
18	A	36	0	78	0	0
18	B	24	0	52	0	0
18	D	12	0	26	0	0
19	A	36	0	6	0	0
20	A	49	0	74	1	0
20	B	81	0	105	0	0
20	C	47	0	67	3	0
20	F	44	0	61	1	0
All	All	37365	0	35202	265	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 4.

The worst 5 of 265 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)
10:E:54:ASP:HB3	10:E:83:LEU:HD21	1.73	0.70
5:9:569:ALA:O	5:9:573:ASN:ND2	2.23	0.70
5:9:575:VAL:HG21	5:9:726:VAL:HG21	1.74	0.70
6:A:756:ILE:HD11	10:E:168:THR:HG21	1.76	0.68
1:3:406:LEU:HD13	6:A:928:LYS:HD3	1.77	0.67

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	3	204/477 (43%)	203 (100%)	1 (0%)	0	100	100
2	4	253/363 (70%)	244 (96%)	9 (4%)	0	100	100
3	5	194/383 (51%)	191 (98%)	3 (2%)	0	100	100
4	7	600/798 (75%)	587 (98%)	13 (2%)	0	100	100
5	9	375/967 (39%)	368 (98%)	7 (2%)	0	100	100
6	A	1570/1995 (79%)	1523 (97%)	47 (3%)	0	100	100
7	B	164/259 (63%)	160 (98%)	4 (2%)	0	100	100
8	C	114/127 (90%)	113 (99%)	1 (1%)	0	100	100
9	D	99/187 (53%)	96 (97%)	3 (3%)	0	100	100
10	E	762/955 (80%)	731 (96%)	31 (4%)	0	100	100
11	F	165/244 (68%)	162 (98%)	3 (2%)	0	100	100
12	G	68/397 (17%)	63 (93%)	5 (7%)	0	100	100
13	U	89/124 (72%)	87 (98%)	2 (2%)	0	100	100
14	X	17/21 (81%)	17 (100%)	0	0	100	100
All	All	4674/7297 (64%)	4545 (97%)	129 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	3	134/373 (36%)	134 (100%)	0	100	100
2	4	115/287 (40%)	115 (100%)	0	100	100
3	5	135/308 (44%)	135 (100%)	0	100	100
4	7	349/653 (53%)	341 (98%)	8 (2%)	44	75
5	9	256/713 (36%)	252 (98%)	4 (2%)	55	81
6	A	1349/1848 (73%)	1343 (100%)	6 (0%)	84	93
7	B	149/223 (67%)	149 (100%)	0	100	100
8	C	96/106 (91%)	94 (98%)	2 (2%)	47	76
9	D	84/158 (53%)	80 (95%)	4 (5%)	23	53
10	E	613/755 (81%)	610 (100%)	3 (0%)	81	92
11	F	143/213 (67%)	141 (99%)	2 (1%)	59	82
12	G	33/336 (10%)	33 (100%)	0	100	100
13	U	64/97 (66%)	63 (98%)	1 (2%)	55	81
All	All	3520/6070 (58%)	3490 (99%)	30 (1%)	68	87

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	A	1629	LEU
11	F	181	HIS
6	A	1964	LEU
13	U	42	VAL
10	E	92	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
6	A	1438	HIS
6	A	1546	ASN

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Mol	Chain	Res	Type
6	A	1439	GLN
6	A	1480	ASN
6	A	1945	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](#)

24 ligands are modelled in this entry.

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	$\# Z > 2$
18	D12	D	202	-	11,11,11	0.23	0	10,10,10	0.21	0
20	LHG	C	201	-	46,46,48	0.66	1 (2%)	49,52,54	1.29	6 (12%)
15	AJP	5	501	-	49,49,95	1.15	7 (14%)	75,80,149	1.71	15 (20%)
19	IHP	A	2001	-	36,36,36	0.86	0	60,60,60	0.52	0
17	R16	7	801	-	9,9,15	0.25	0	8,8,14	0.19	0
20	LHG	F	301	-	43,43,48	0.66	2 (4%)	46,49,54	1.24	4 (8%)
18	D12	B	302	-	11,11,11	0.24	0	10,10,10	0.19	0
15	AJP	D	203	-	59,59,95	1.05	4 (6%)	90,95,149	1.63	19 (21%)
16	LMG	A	2006	-	52,52,55	0.72	1 (1%)	60,60,63	1.38	7 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	AJP	B	305	-	48,48,95	1.06	5 (10%)	74,79,149	1.67	13 (17%)
20	LHG	A	2002	-	48,48,48	0.62	1 (2%)	51,54,54	1.29	6 (11%)
18	D12	9	1001	-	11,11,11	0.24	0	10,10,10	0.19	0
16	LMG	A	2008	-	39,39,55	0.82	1 (2%)	47,47,63	1.29	6 (12%)
15	AJP	D	201	-	37,37,95	1.20	5 (13%)	58,62,149	1.78	12 (20%)
18	D12	A	2003	-	11,11,11	0.24	0	10,10,10	0.19	0
15	AJP	4	401	-	36,36,95	1.18	4 (11%)	56,60,149	1.85	12 (21%)
18	D12	A	2004	-	11,11,11	0.24	0	10,10,10	0.19	0
16	LMG	B	301	-	37,37,55	0.84	1 (2%)	45,45,63	1.34	7 (15%)
20	LHG	B	304	-	35,35,48	0.73	1 (2%)	38,41,54	1.29	4 (10%)
16	LMG	5	502	-	42,42,55	0.80	1 (2%)	50,50,63	1.34	7 (14%)
18	D12	A	2005	-	11,11,11	0.24	0	10,10,10	0.20	0
16	LMG	A	2007	-	55,55,55	0.68	0	63,63,63	1.38	7 (11%)
20	LHG	B	306	-	44,44,48	0.66	2 (4%)	47,50,54	1.31	7 (14%)
18	D12	B	303	-	11,11,11	0.24	0	10,10,10	0.19	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
18	D12	D	202	-	-	3/9/9/9	-
20	LHG	C	201	-	-	15/51/51/53	-
15	AJP	5	501	-	-	2/6/121/220	0/7/7/11
19	IHP	A	2001	-	-	6/30/54/54	0/1/1/1
17	R16	7	801	-	-	0/7/7/13	-
20	LHG	F	301	-	-	18/48/48/53	-
18	D12	B	302	-	-	2/9/9/9	-
15	AJP	D	203	-	-	5/10/141/220	1/8/8/11
16	LMG	A	2006	-	-	24/47/67/70	0/1/1/1
15	AJP	B	305	-	-	3/4/119/220	0/7/7/11
20	LHG	A	2002	-	-	18/53/53/53	-
18	D12	9	1001	-	-	3/9/9/9	-
16	LMG	A	2008	-	-	12/34/54/70	0/1/1/1
15	AJP	D	201	-	-	-	1/6/6/11
18	D12	A	2003	-	-	0/9/9/9	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	AJP	4	401	-	-	-	0/6/6/11
18	D12	A	2004	-	-	2/9/9/9	-
16	LMG	B	301	-	-	5/32/52/70	0/1/1/1
20	LHG	B	304	-	-	13/40/40/53	-
16	LMG	5	502	-	-	20/37/57/70	0/1/1/1
18	D12	A	2005	-	-	4/9/9/9	-
16	LMG	A	2007	-	-	16/50/70/70	0/1/1/1
20	LHG	B	306	-	-	23/49/49/53	-
18	D12	B	303	-	-	3/9/9/9	-

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	D	203	AJP	C16-C11	-3.44	1.49	1.54
15	5	501	AJP	C12-C11	-2.90	1.50	1.56
15	5	501	AJP	C20-C15	-2.85	1.51	1.56
15	4	401	AJP	C16-C11	-2.84	1.50	1.54
15	4	401	AJP	C20-C15	-2.79	1.51	1.56

The worst 5 of 132 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	5	501	AJP	C12-C11-C16	-5.48	106.26	113.90
15	D	203	AJP	C12-C11-C16	-5.47	106.28	113.90
15	B	305	AJP	C12-C11-C16	-5.19	106.66	113.90
15	4	401	AJP	C12-C11-C16	-5.16	106.71	113.90
15	4	401	AJP	C20-C21-C22	-4.94	109.15	113.94

There are no chirality outliers.

5 of 197 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	5	502	LMG	C2-C1-O1-C7
16	5	502	LMG	O6-C1-O1-C7
16	5	502	LMG	C11-C10-O7-C8
16	A	2008	LMG	O6-C1-O1-C7
20	A	2002	LHG	C3-O3-P-O5

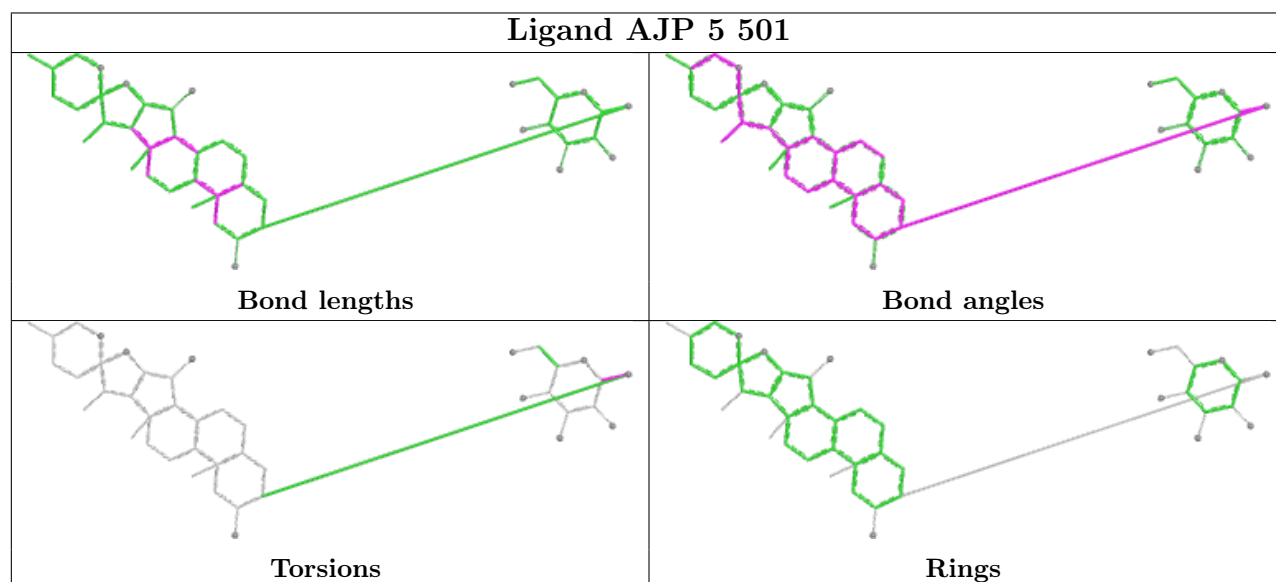
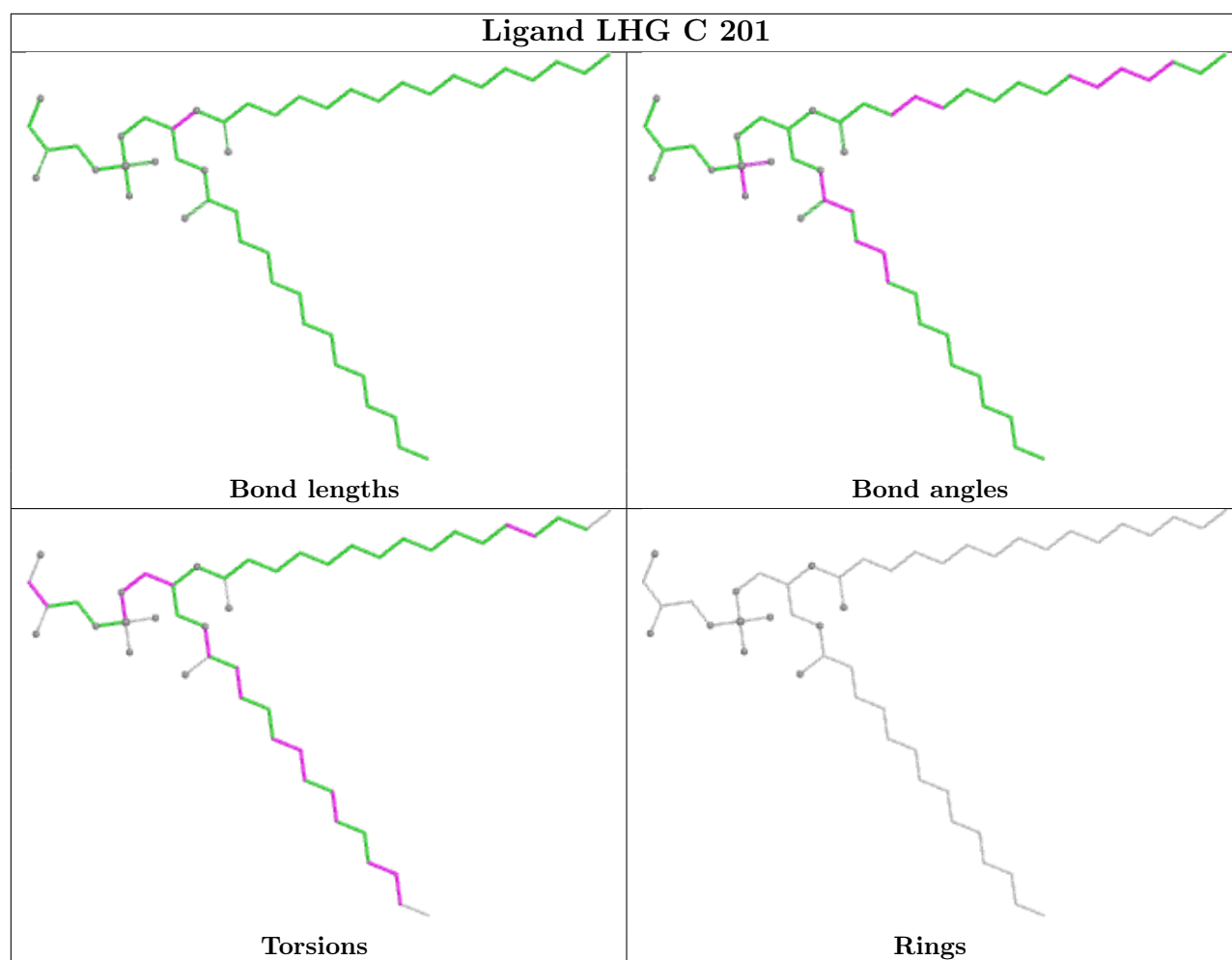
All (2) ring outliers are listed below:

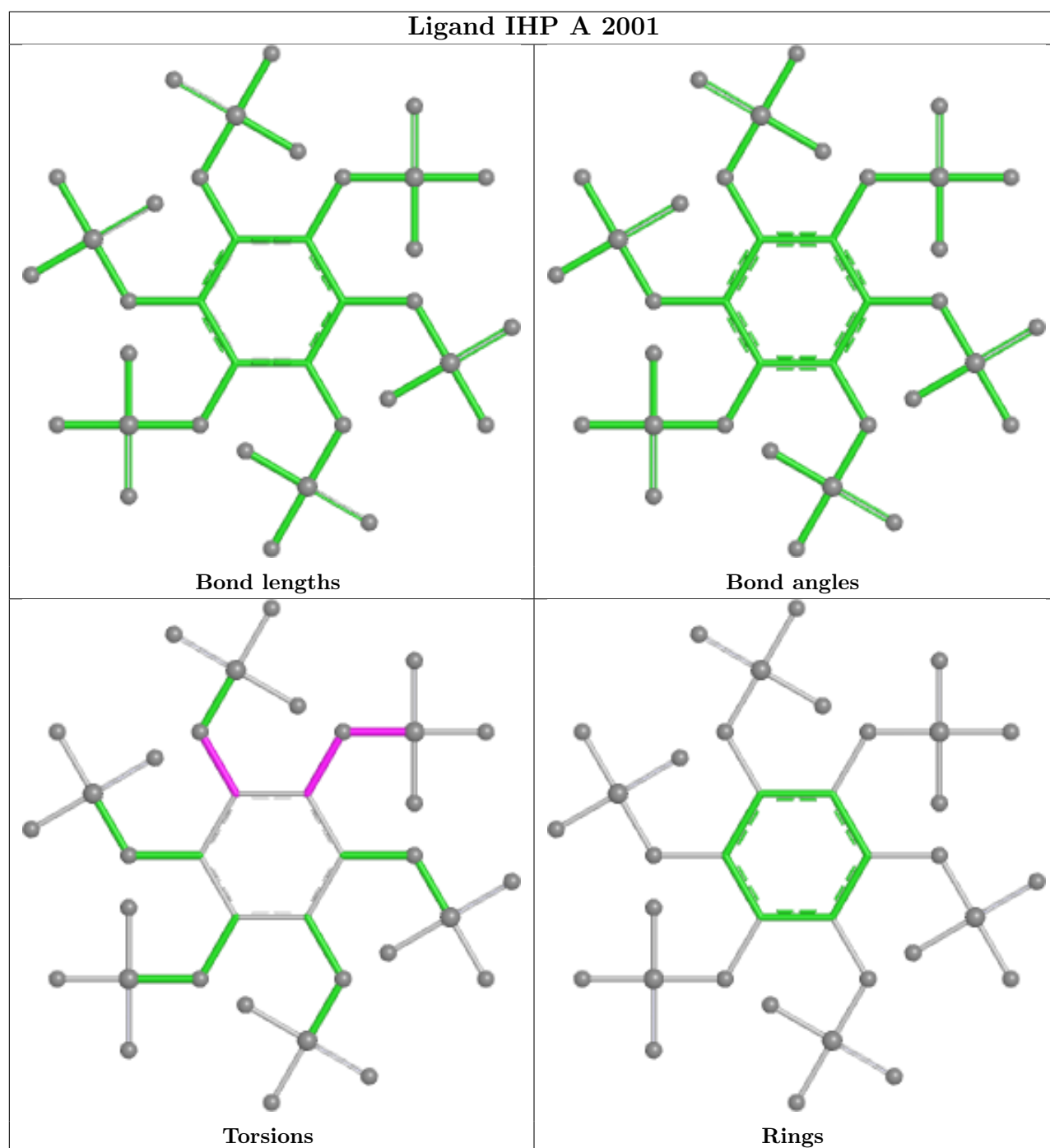
Mol	Chain	Res	Type	Atoms
15	D	201	AJP	C19-C20-C21-C22-C23-C24
15	D	203	AJP	C35-C36-C37-C38-C39-O40

8 monomers are involved in 13 short contacts:

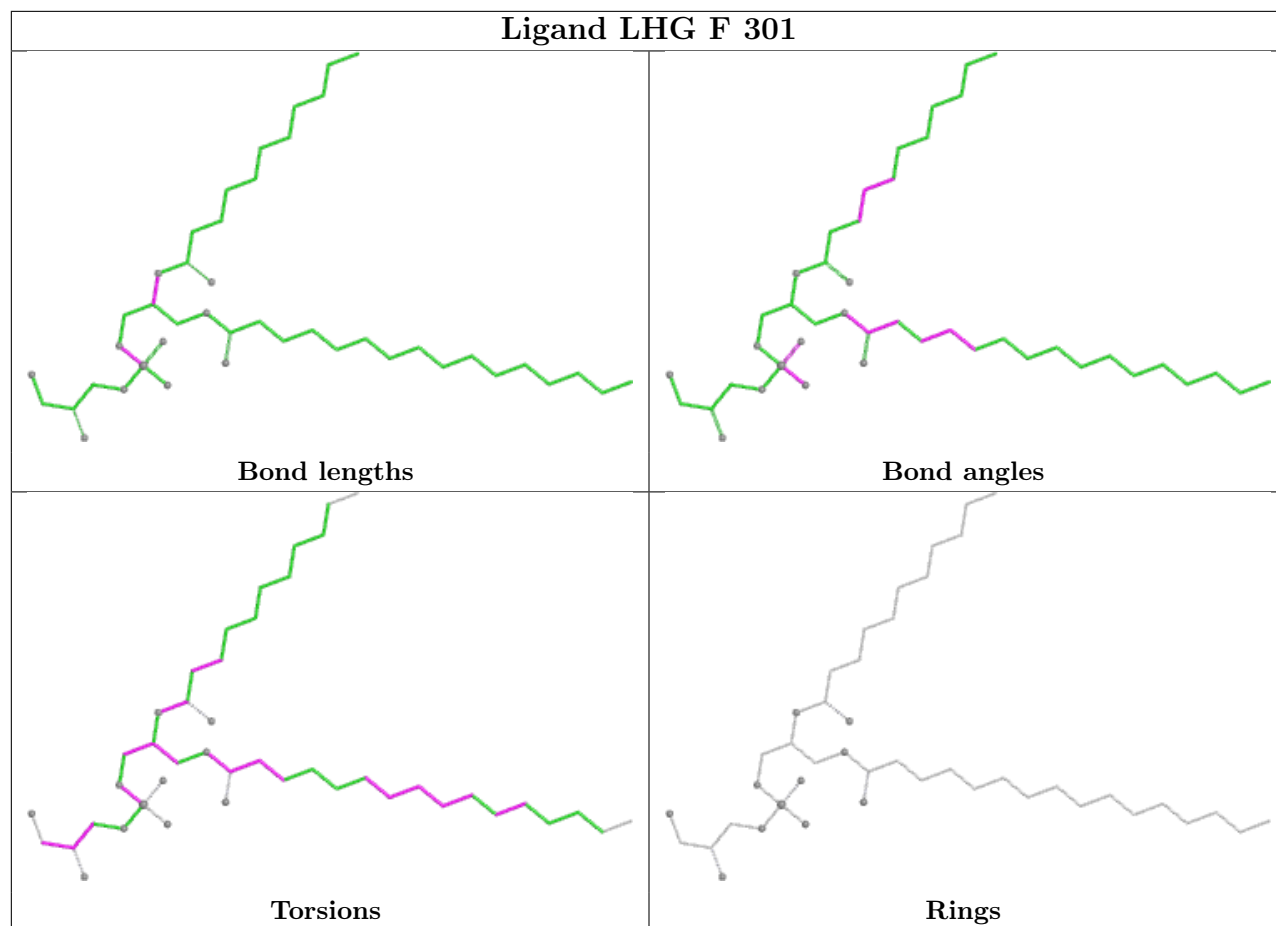
Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	C	201	LHG	3	0
20	F	301	LHG	1	0
16	A	2006	LMG	1	0
15	B	305	AJP	2	0
20	A	2002	LHG	1	0
16	A	2008	LMG	1	0
16	5	502	LMG	2	0
16	A	2007	LMG	3	0

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.

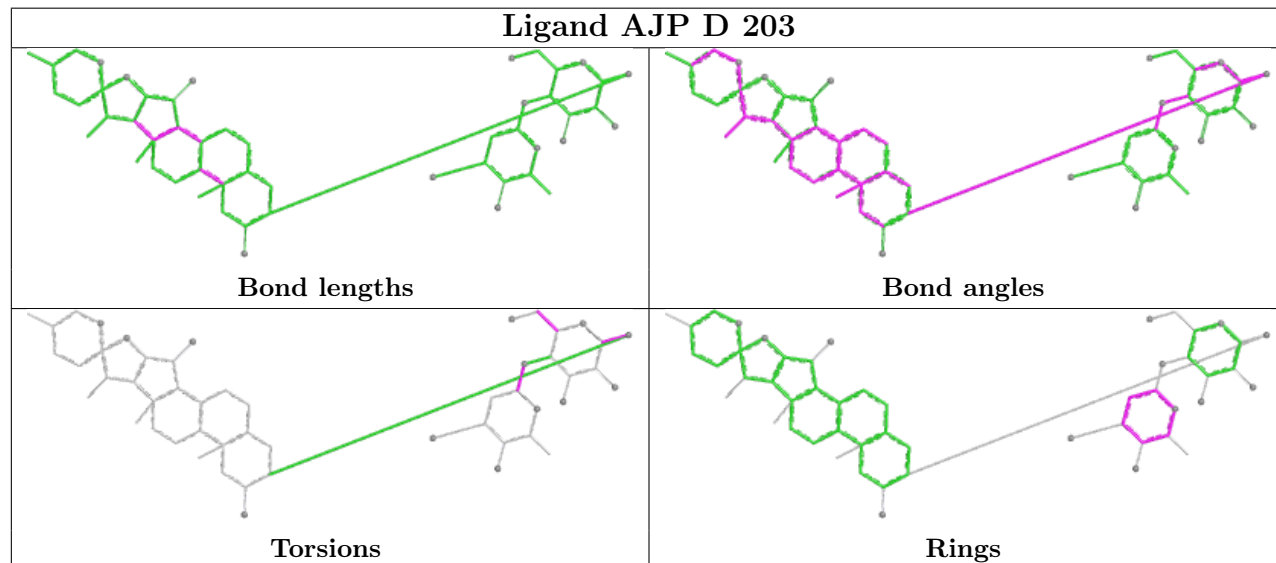


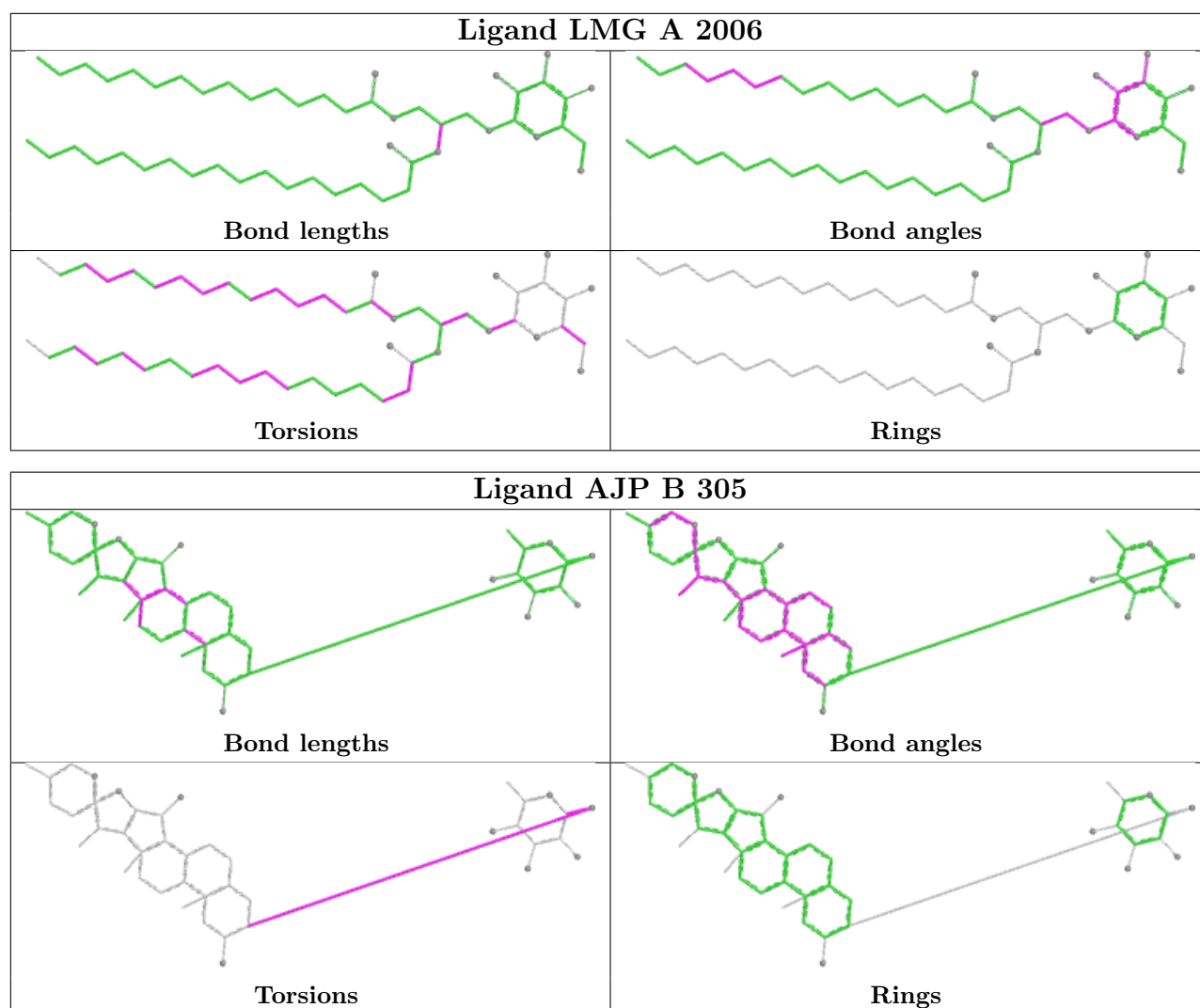


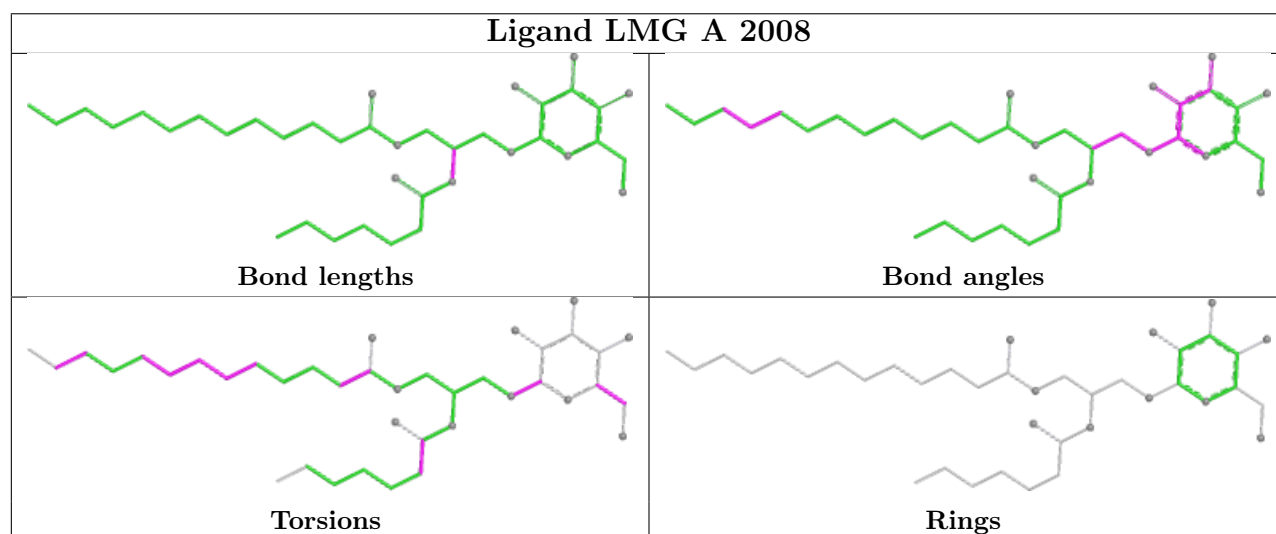
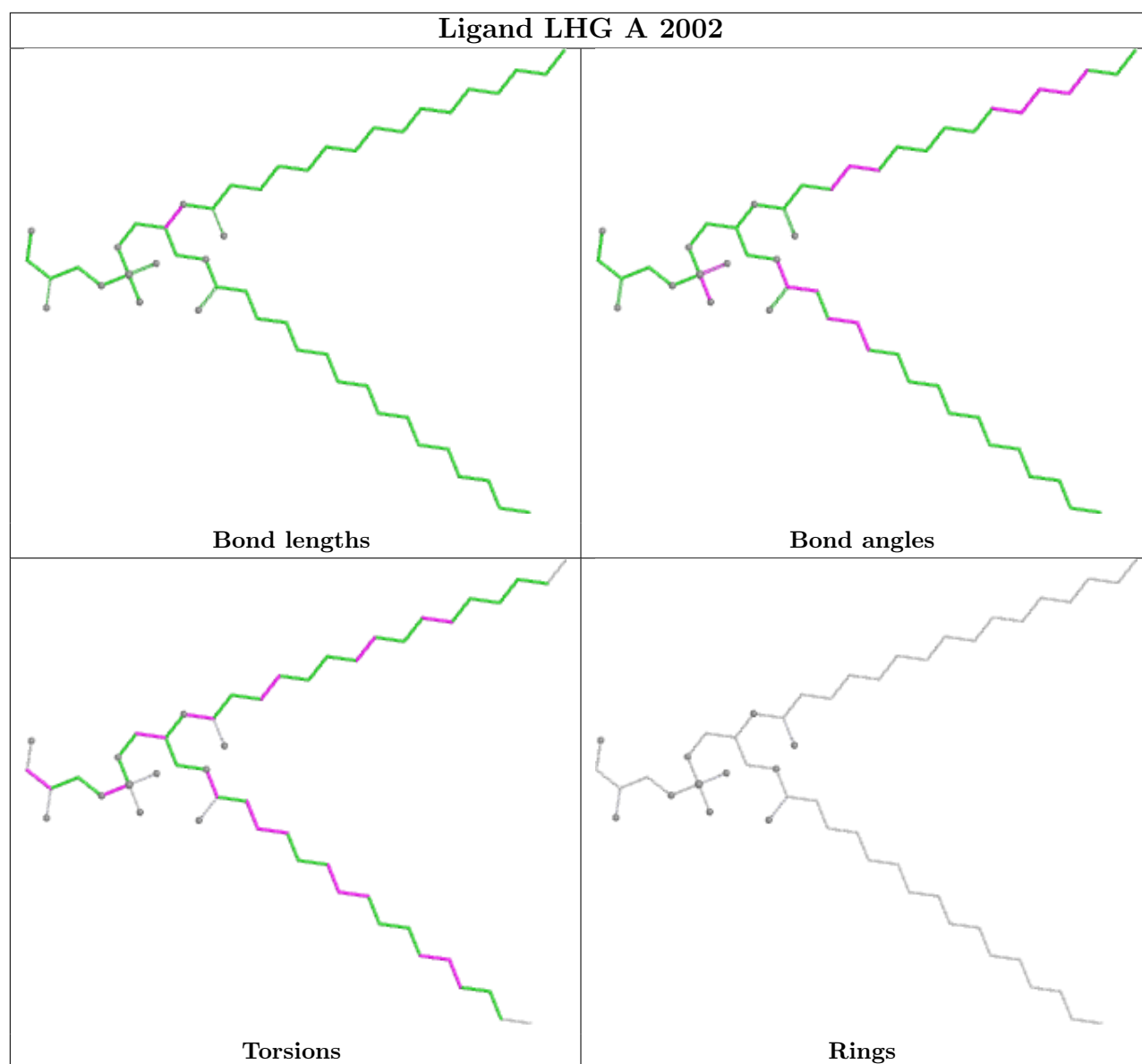
Ligand LHG F 301

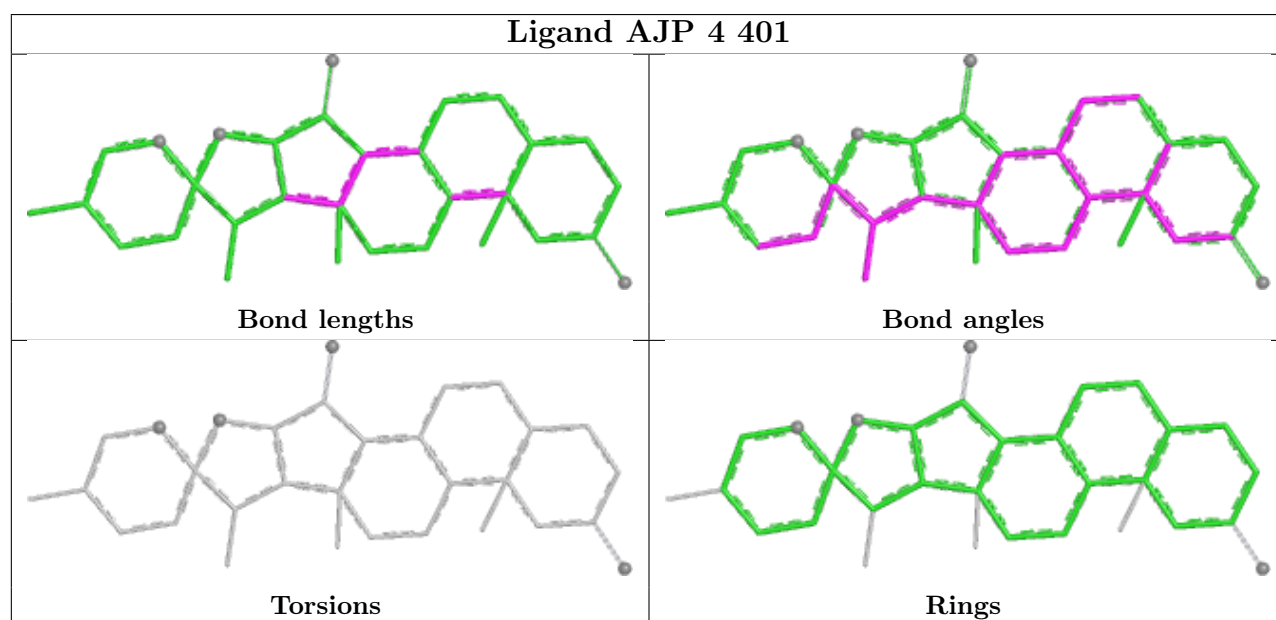
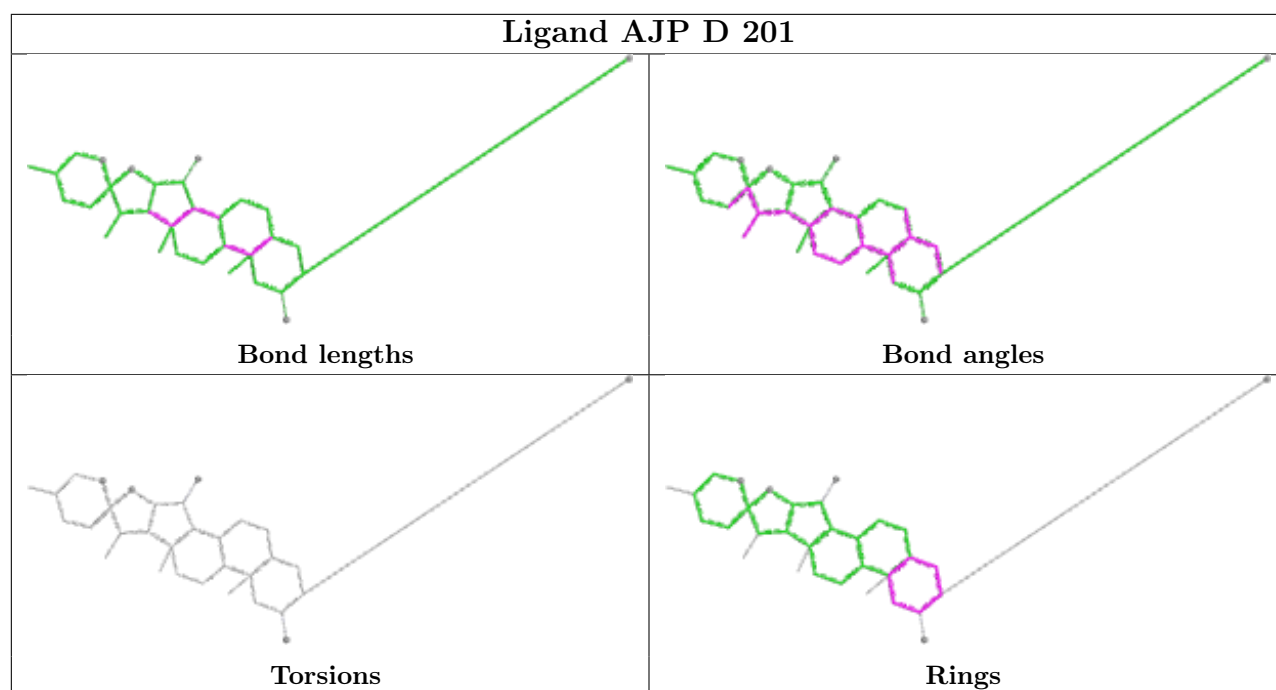


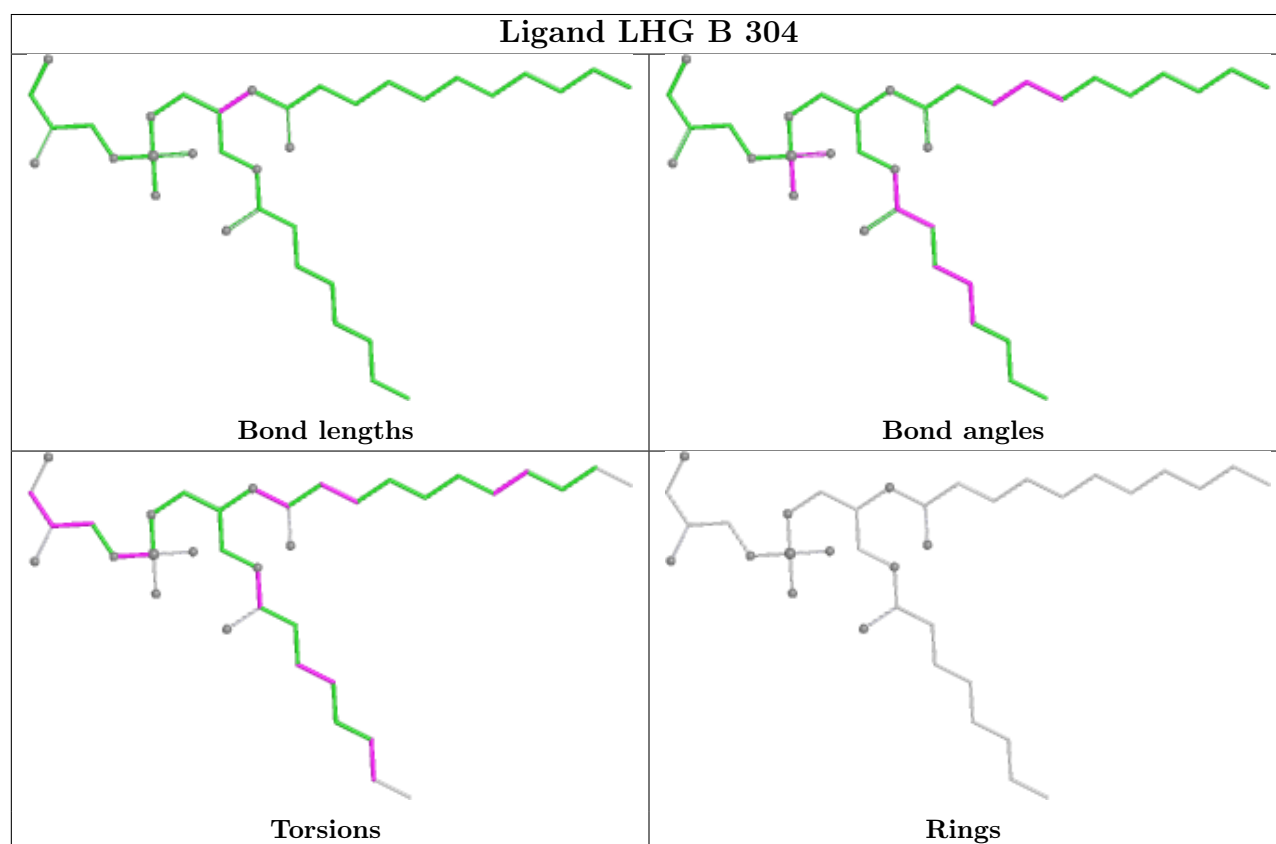
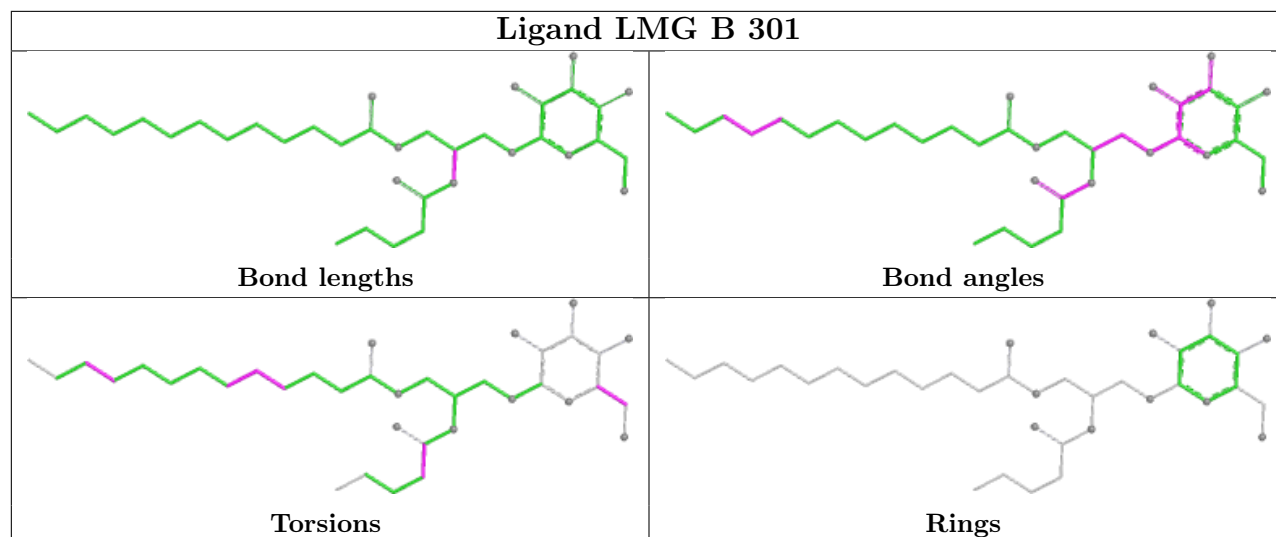
Ligand AJP D 203

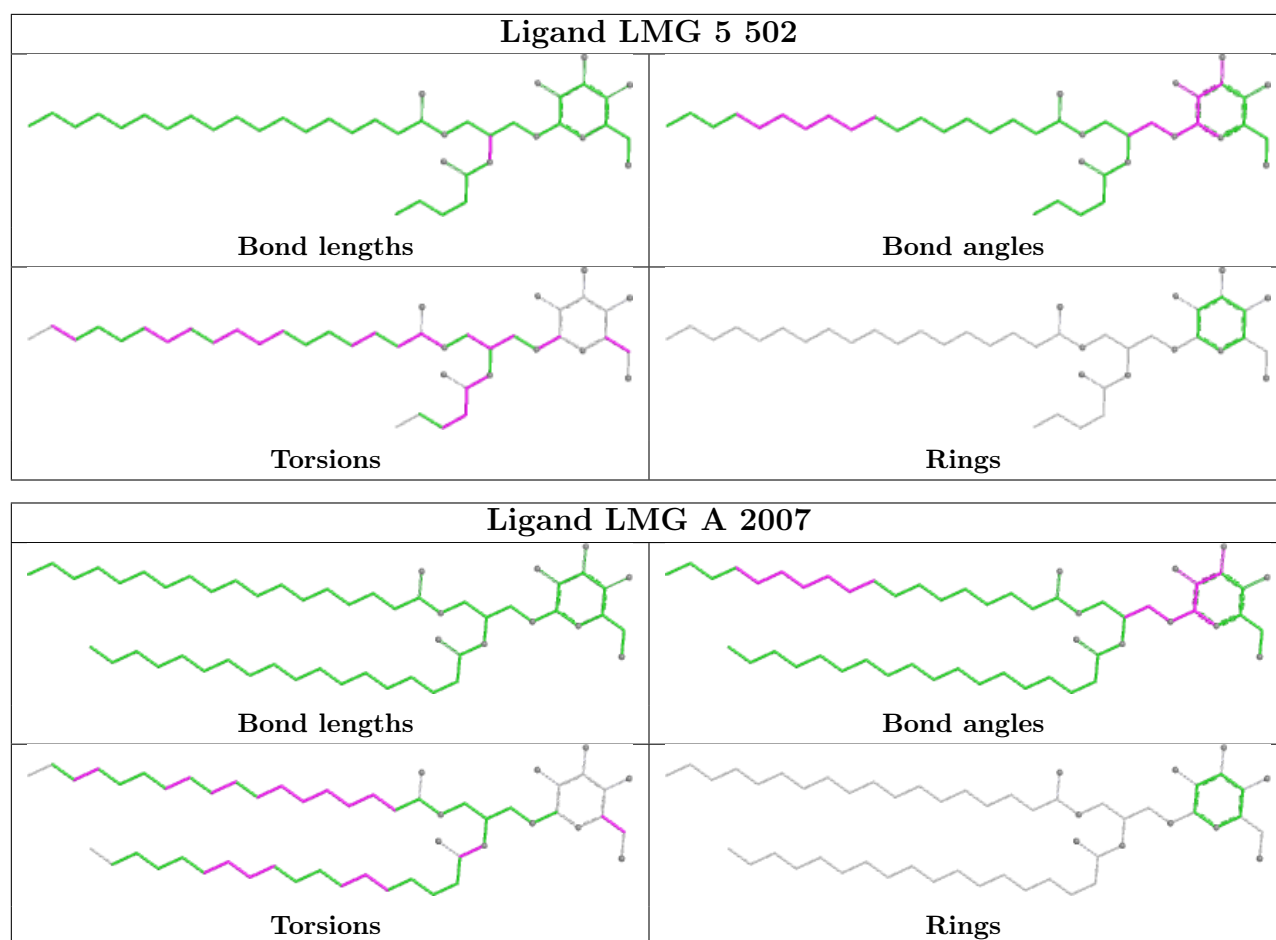


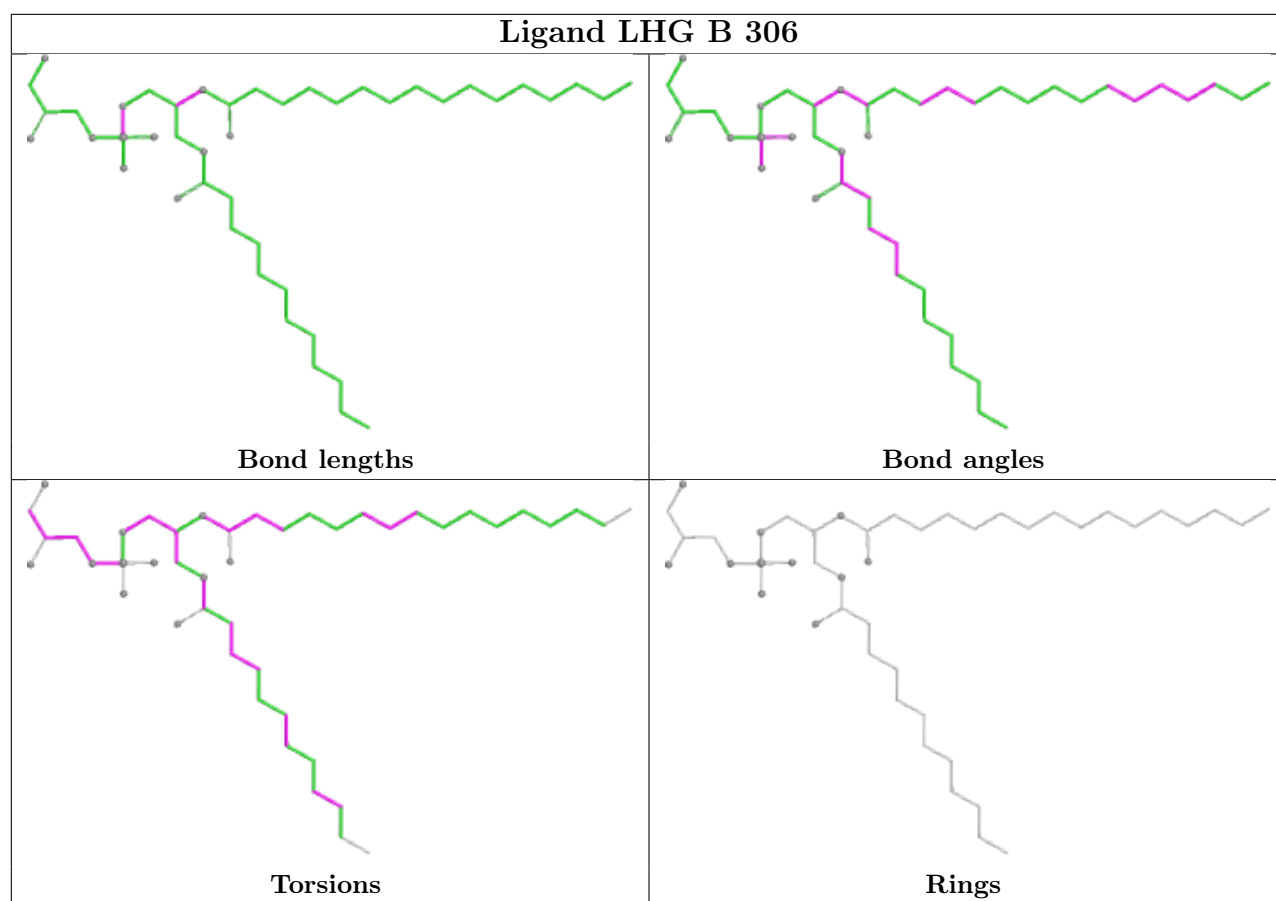












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

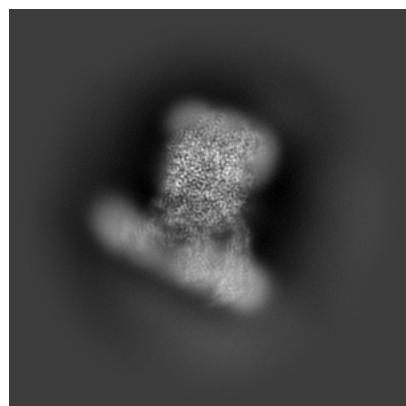
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33528. These allow visual inspection of the internal detail of the map and identification of artifacts.

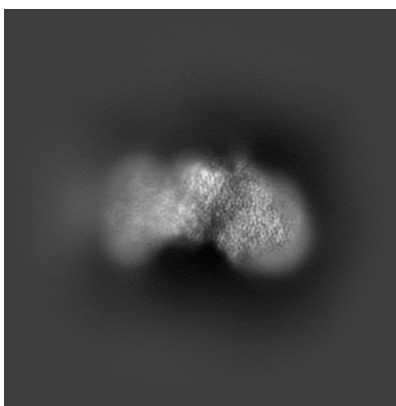
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

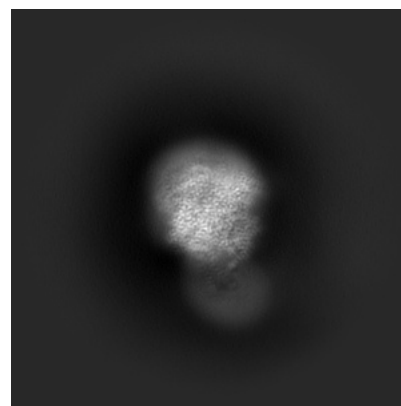
6.1.1 Primary map



X

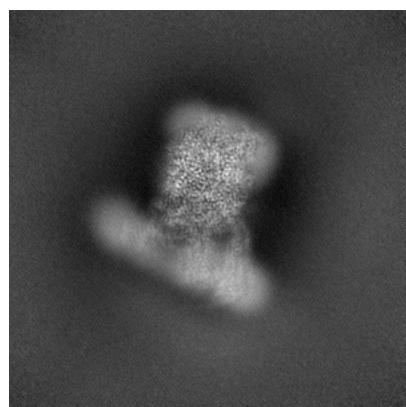


Y

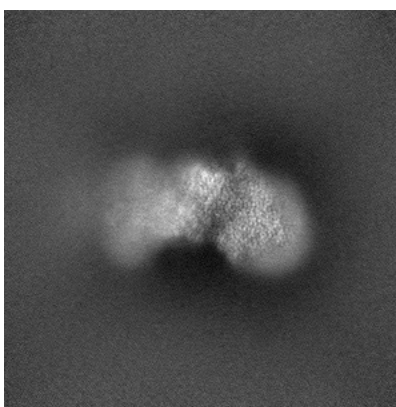


Z

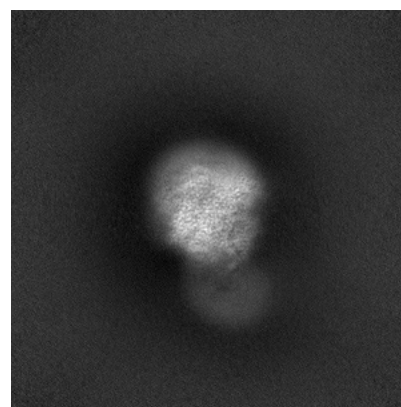
6.1.2 Raw map



X



Y

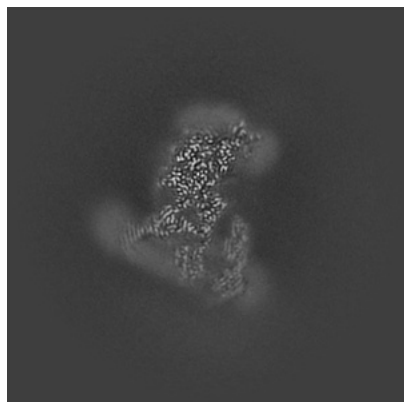


Z

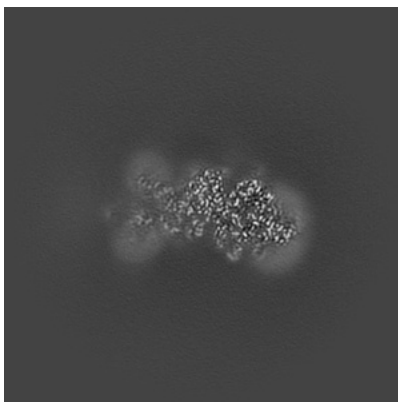
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

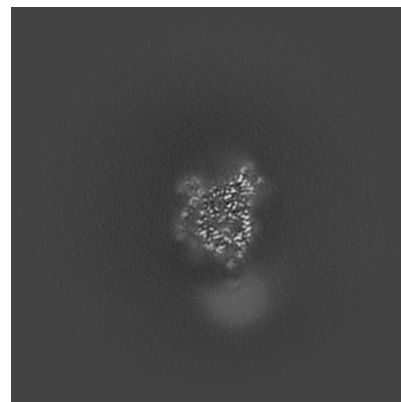
6.2.1 Primary map



X Index: 320

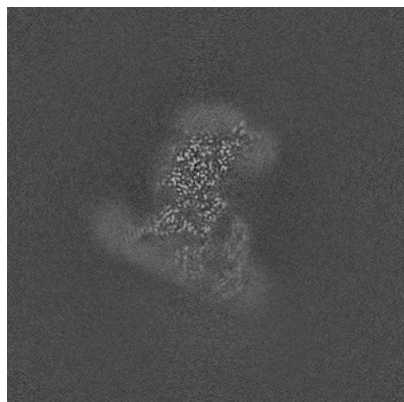


Y Index: 320

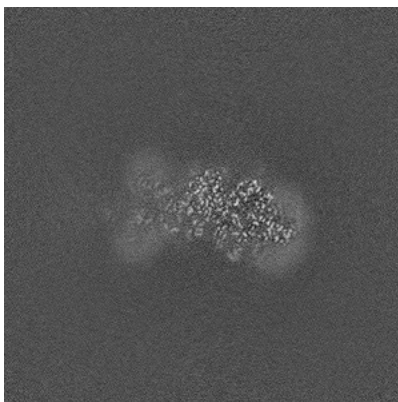


Z Index: 320

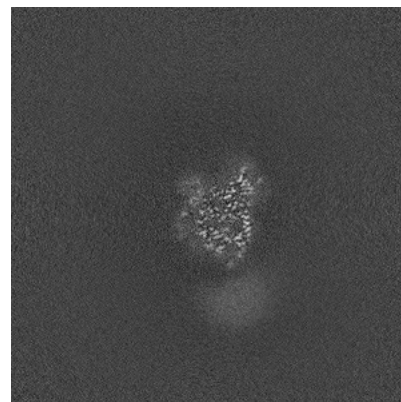
6.2.2 Raw map



X Index: 320



Y Index: 320

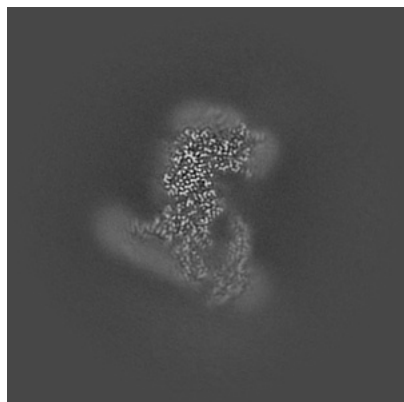


Z Index: 320

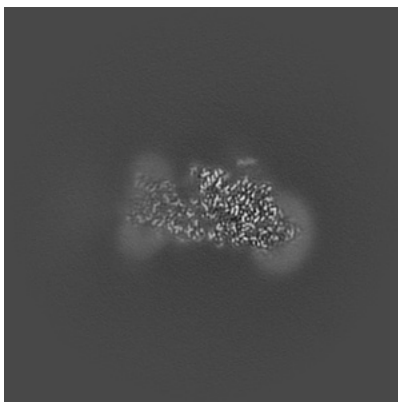
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

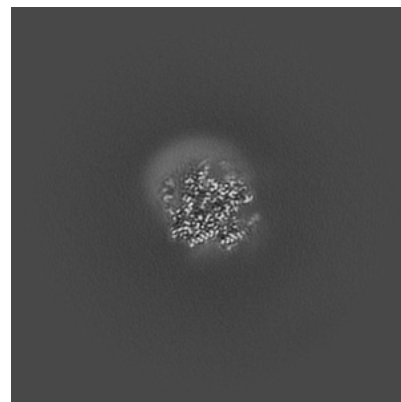
6.3.1 Primary map



X Index: 312

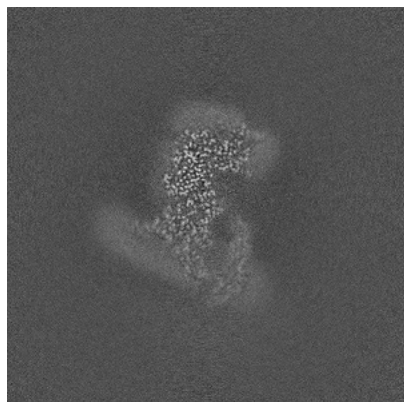


Y Index: 305

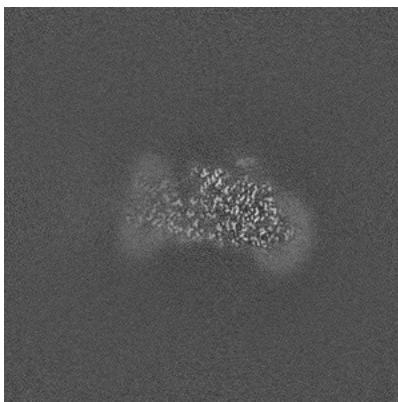


Z Index: 397

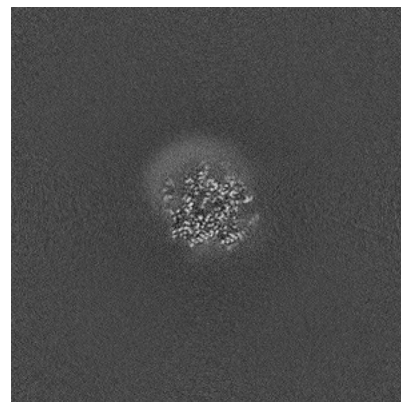
6.3.2 Raw map



X Index: 312



Y Index: 304

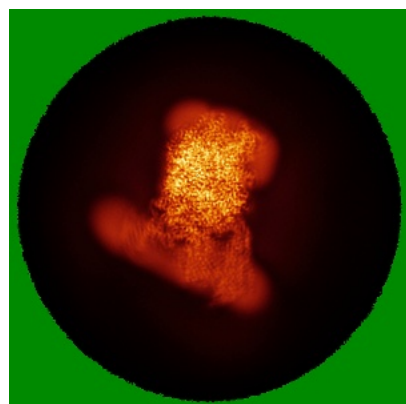


Z Index: 397

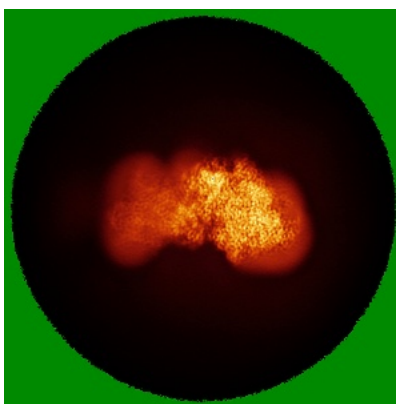
The images above show the largest variance slices of the map in three orthogonal directions.

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

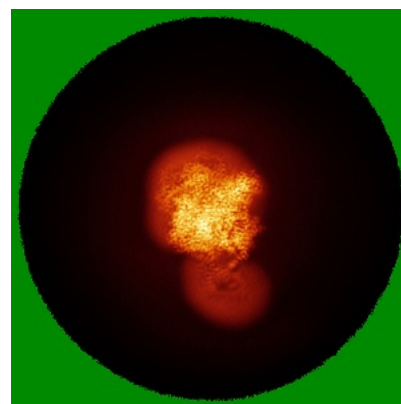
6.4.1 Primary map



X

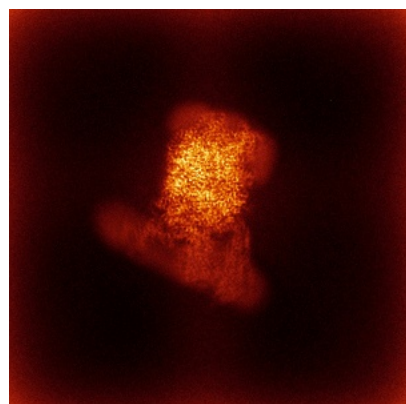


Y

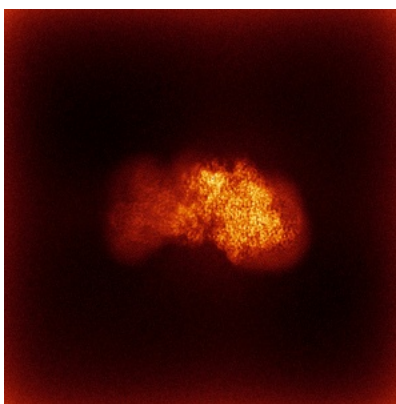


Z

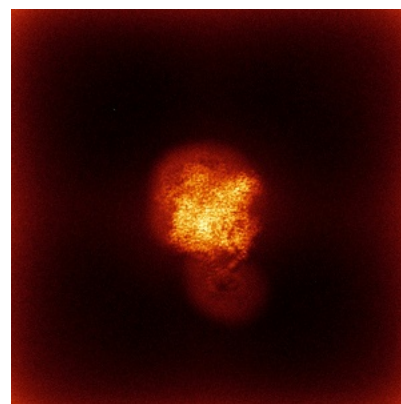
6.4.2 Raw map



X



Y

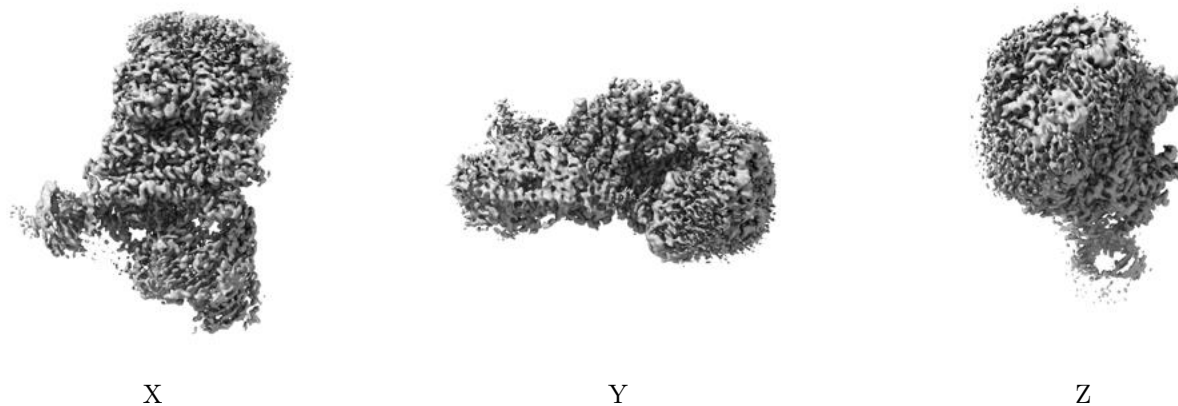


Z

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.

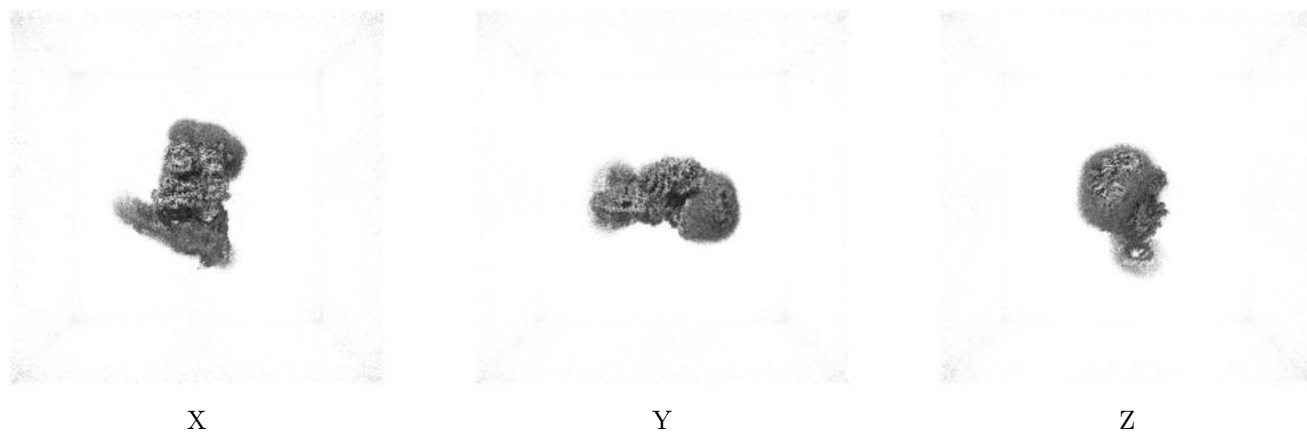
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

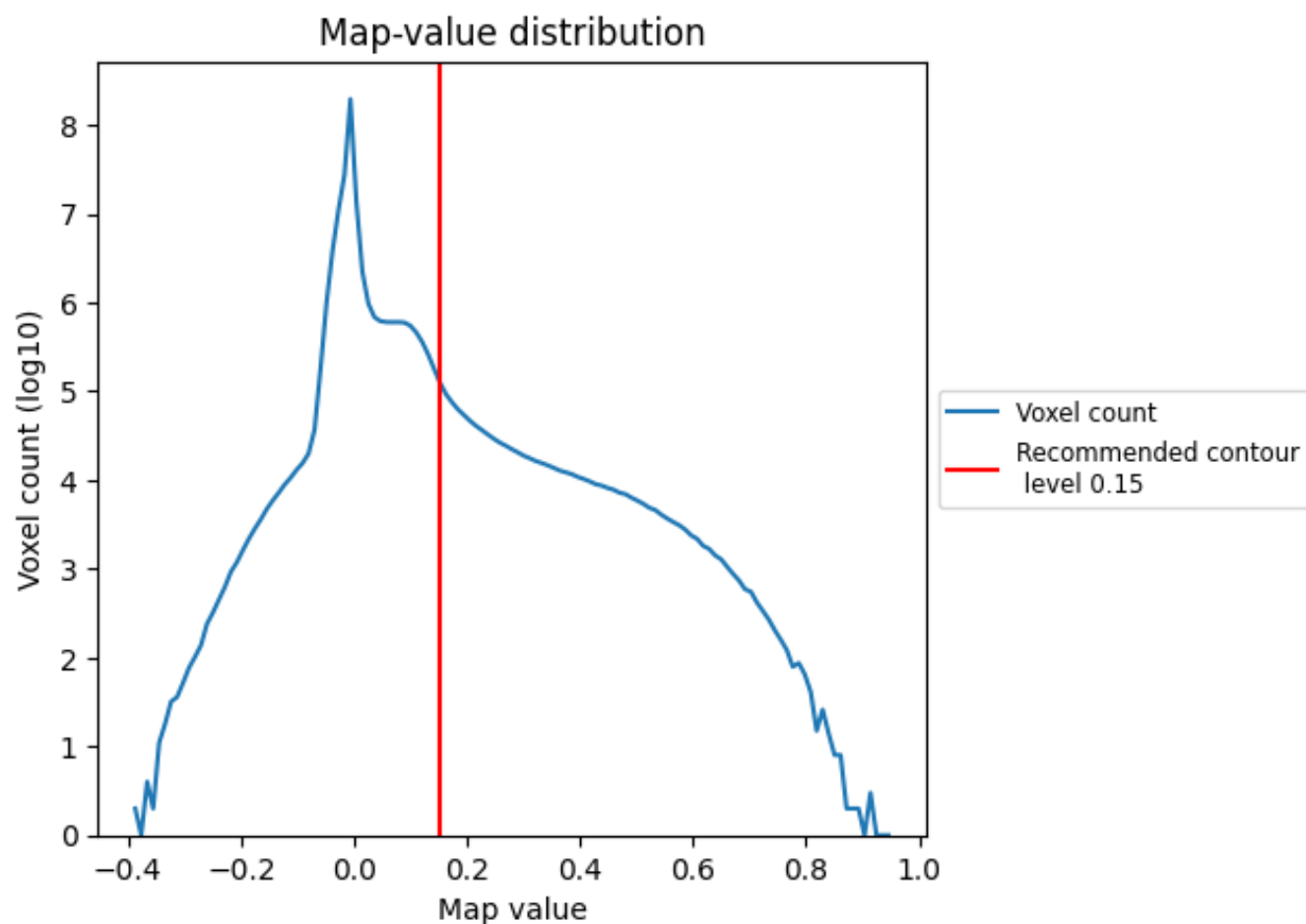
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

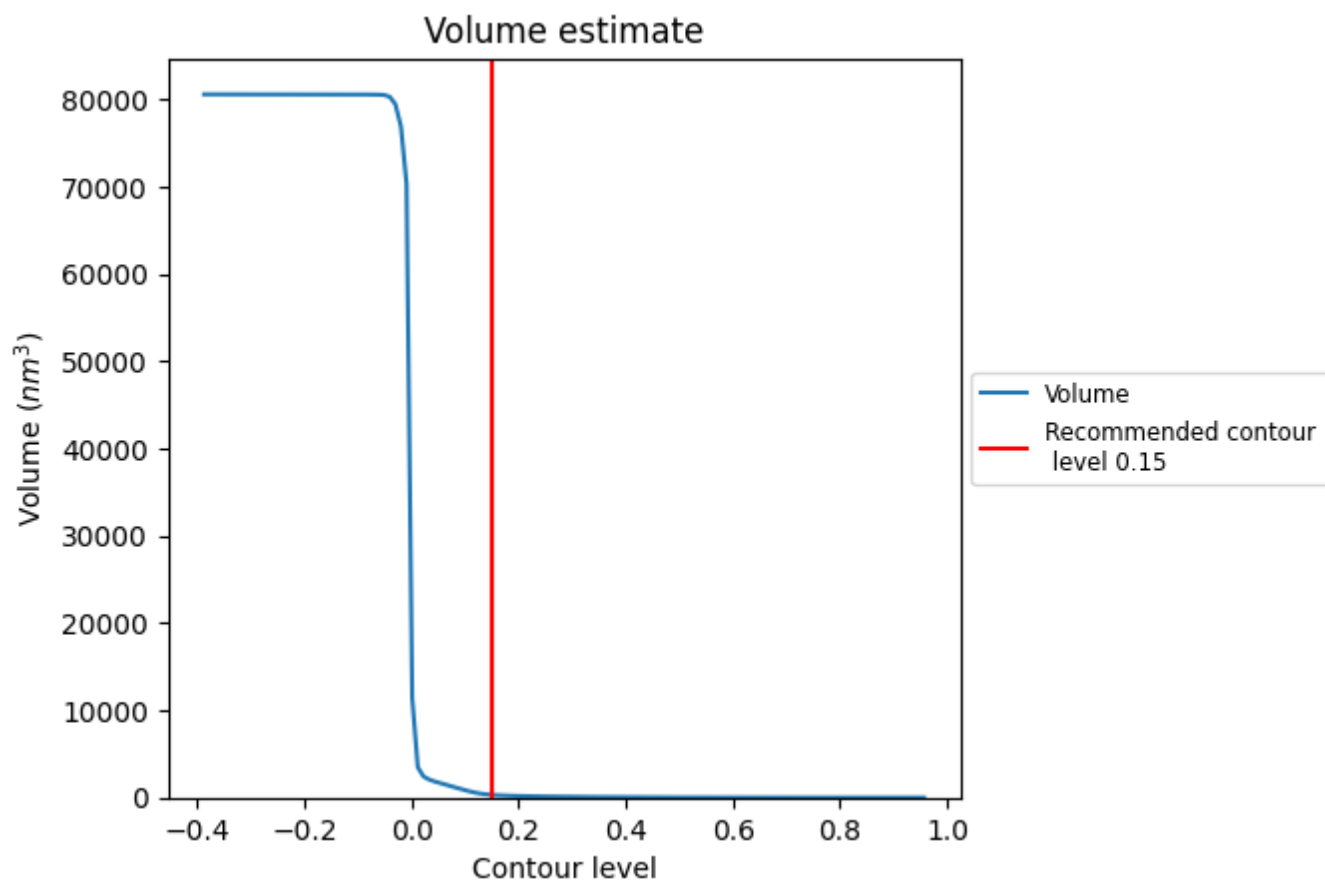
This section contains the results of statistical analysis of the map.

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.

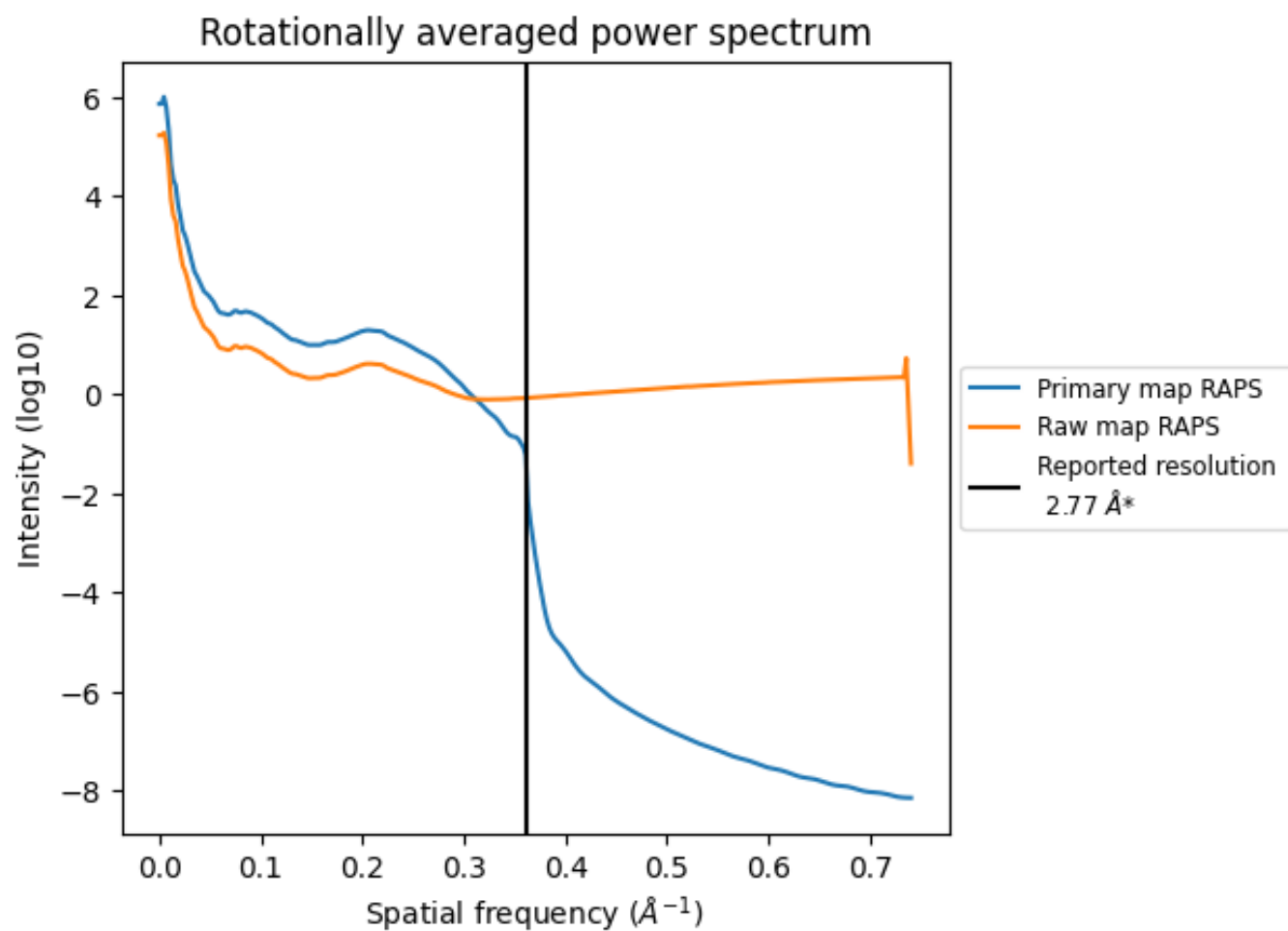
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 307 nm^3 ; this corresponds to an approximate mass of 278 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 [i](#)

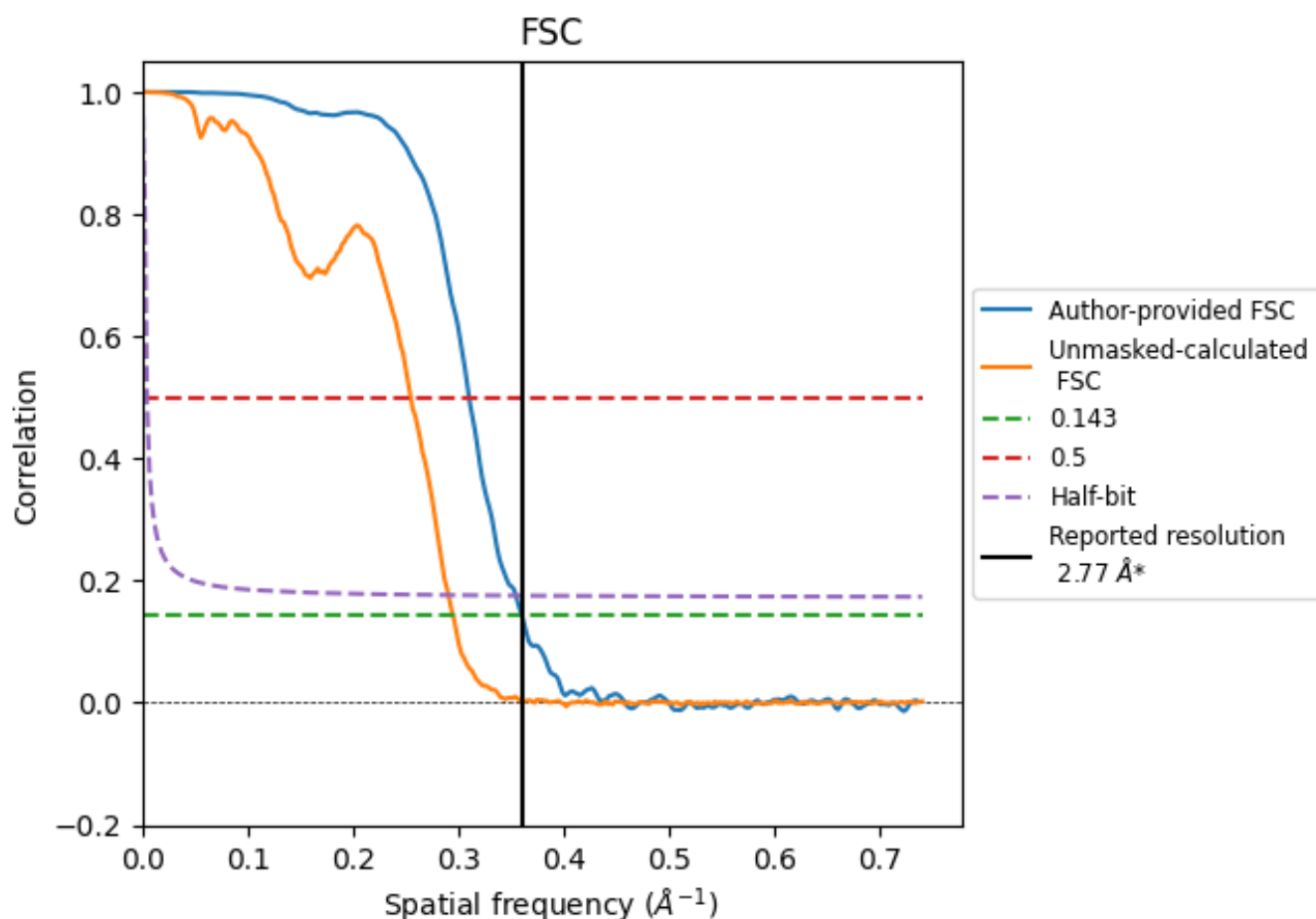


*Reported resolution corresponds to spatial frequency of 0.361 $\text{\AA}^{-1}$

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 0.361 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

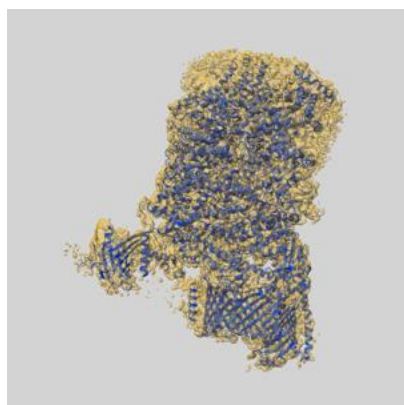
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.77	-	-
Author-provided FSC curve	2.77	3.22	2.82
Unmasked-calculated*	3.39	3.92	3.44

*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 3.39 differs from the reported value 2.77 by more than 10 %

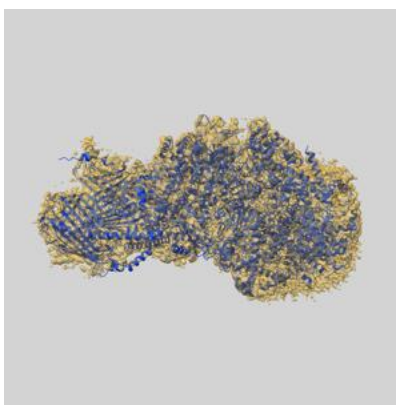
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33528 and PDB model 7XZI. Per-residue inclusion information can be found in section [3](#) on page [11](#).

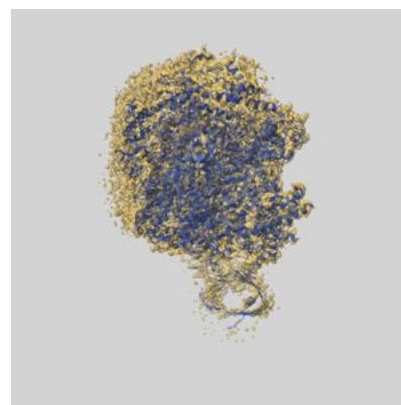
9.1 Map-model overlay [i](#)



X



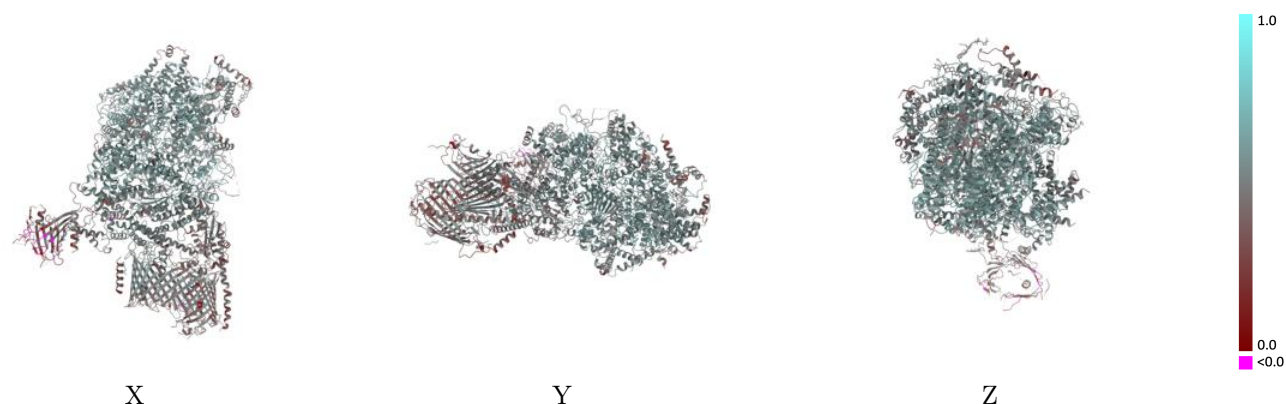
Y



Z

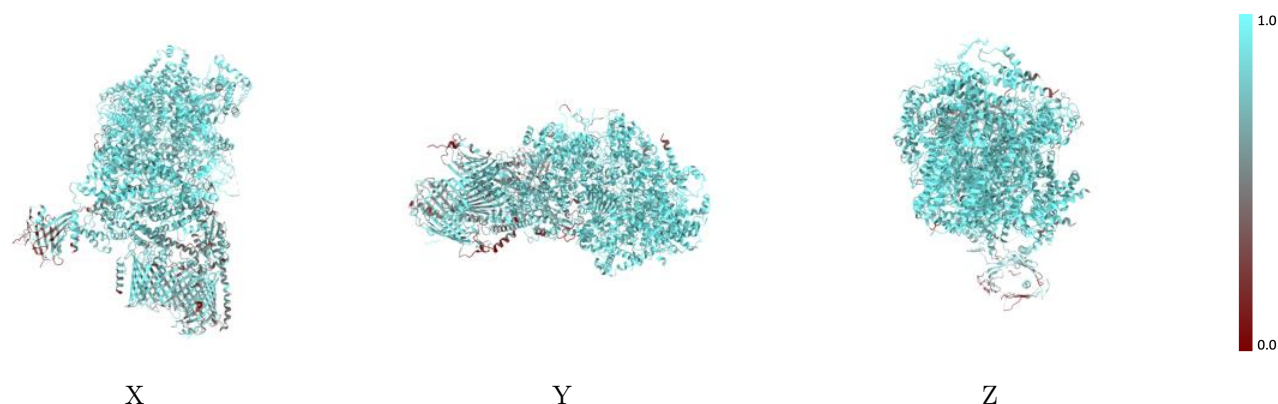
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



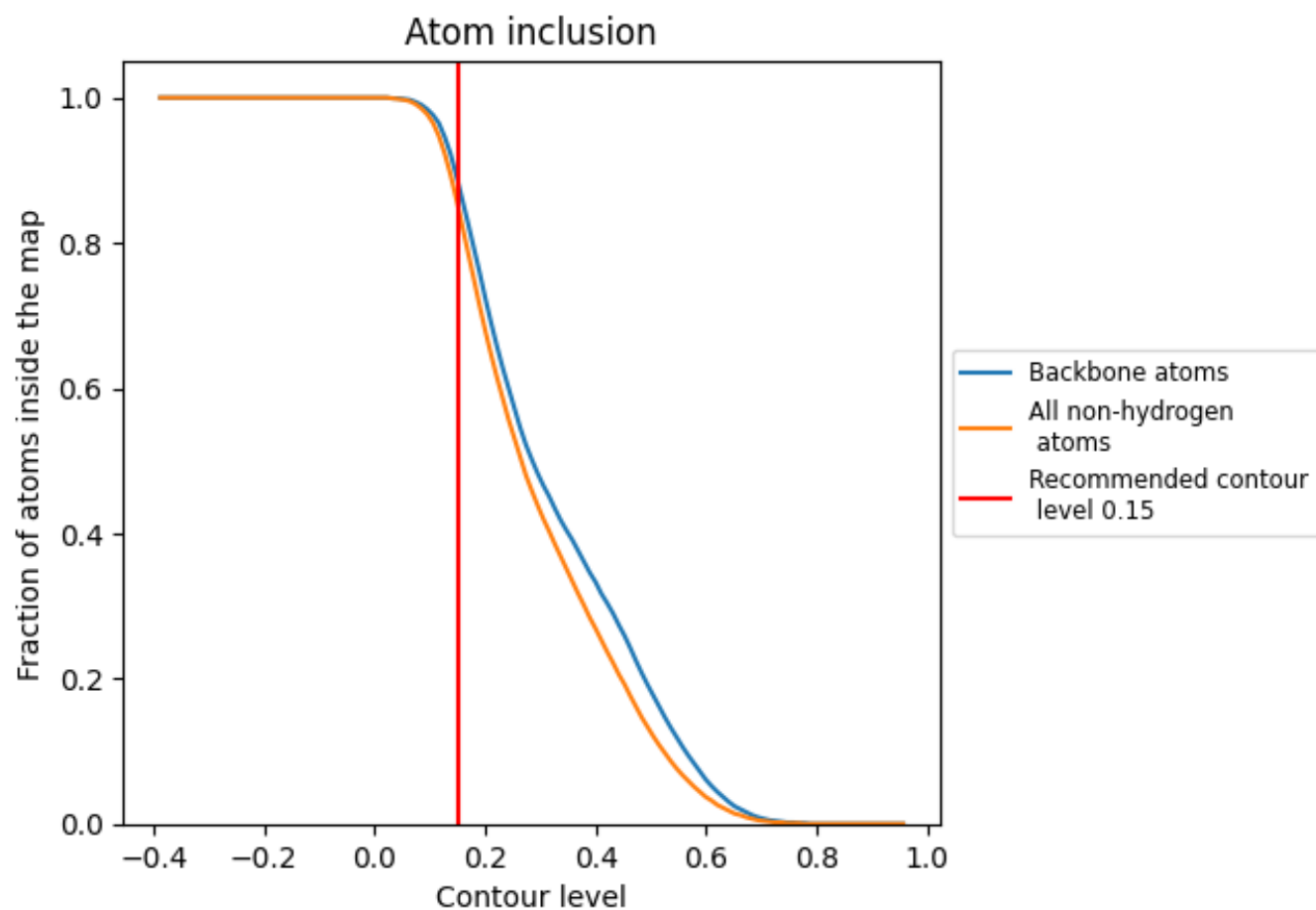
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 86% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8550	 0.5170
3	 0.8970	 0.5330
4	 0.6490	 0.3700
5	 0.9160	 0.5440
7	 0.7240	 0.4460
9	 0.7700	 0.4760
A	 0.8820	 0.5400
B	 0.9510	 0.5620
C	 0.9510	 0.5850
D	 0.8490	 0.4460
E	 0.9310	 0.5610
F	 0.9170	 0.5670
G	 0.6400	 0.3790
U	 0.8560	 0.4860
X	 0.6880	 0.3600

