



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:37 PM UTC

PDB ID : 8TK8 / pdb_00008tk8
EMDB ID : EMD-41323
Title : Human Type 3 IP3 Receptor - Resting State (+IP3/ATP)
Authors : Paknejad, N.; Sapuru, V.; Hite, R.K.
Deposited on : 2023-07-25
Resolution : 2.70 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:

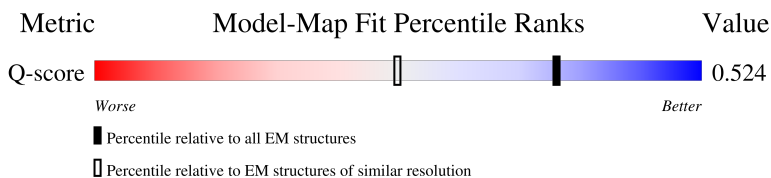
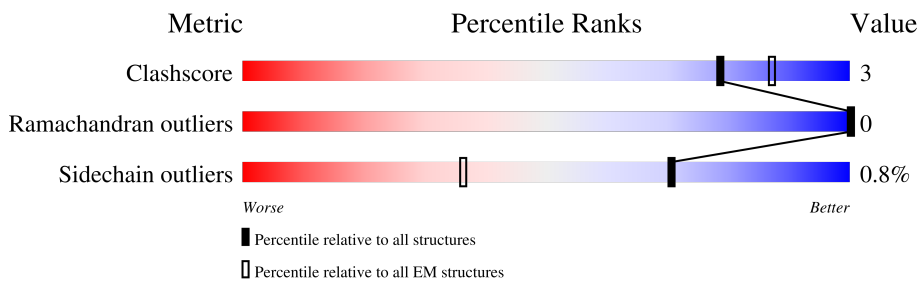
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 2.70 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	10327 (2.20 - 3.20)

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	 78% 6% 15%
1	B	2671	 78% 6% 15%
1	C	2671	 78% 6% 15%
1	D	2671	 79% 6% 15%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 148540 atoms, of which 74460 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.

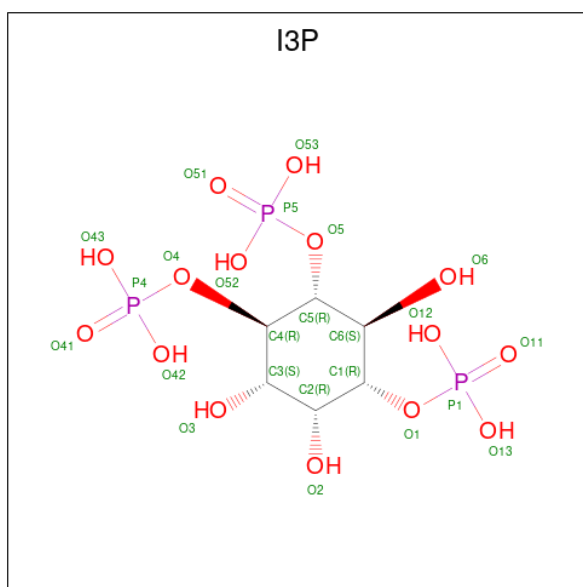
- Molecule 1 is a protein called Inositol 1,4,5-trisphosphate receptor type 3.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	2268	36394	11601	18207	3116	3355	115	0	0
1	B	2268	36395	11601	18208	3116	3355	115	0	0
1	C	2268	36394	11601	18207	3116	3355	115	0	0
1	D	2268	36395	11601	18208	3116	3355	115	0	0

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

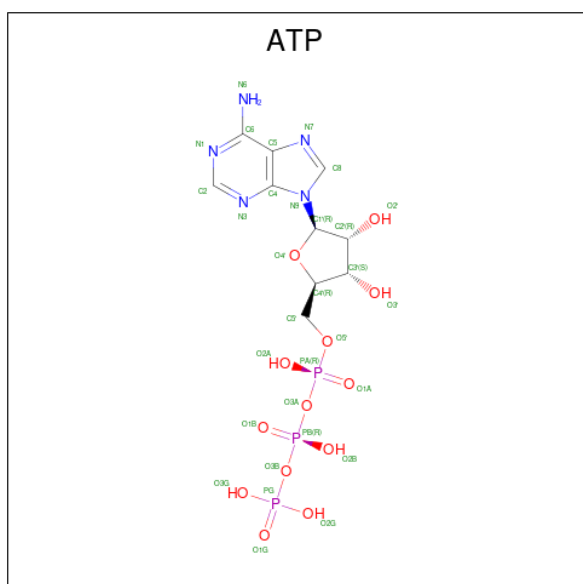
Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total 1	Zn 1	0
2	B	1	Total 1	Zn 1	0
2	C	1	Total 1	Zn 1	0
2	D	1	Total 1	Zn 1	0

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



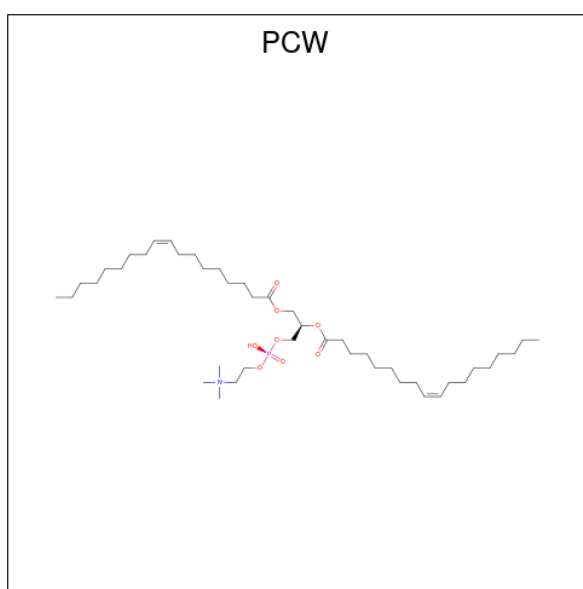
Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	O	P	
3	A	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	B	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	C	1	Total	C	H	O	P	0
			33	6	9	15	3	
3	D	1	Total	C	H	O	P	0
			33	6	9	15	3	

- 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	
			Total	C	H	N	O		P
4	A	1	43	10	12	5	13	3	0
4	B	1	43	10	12	5	13	3	0
4	C	1	43	10	12	5	13	3	0
4	D	1	43	10	12	5	13	3	0

- Molecule 5 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW) (formula: C₄₄H₈₅NO₈P).

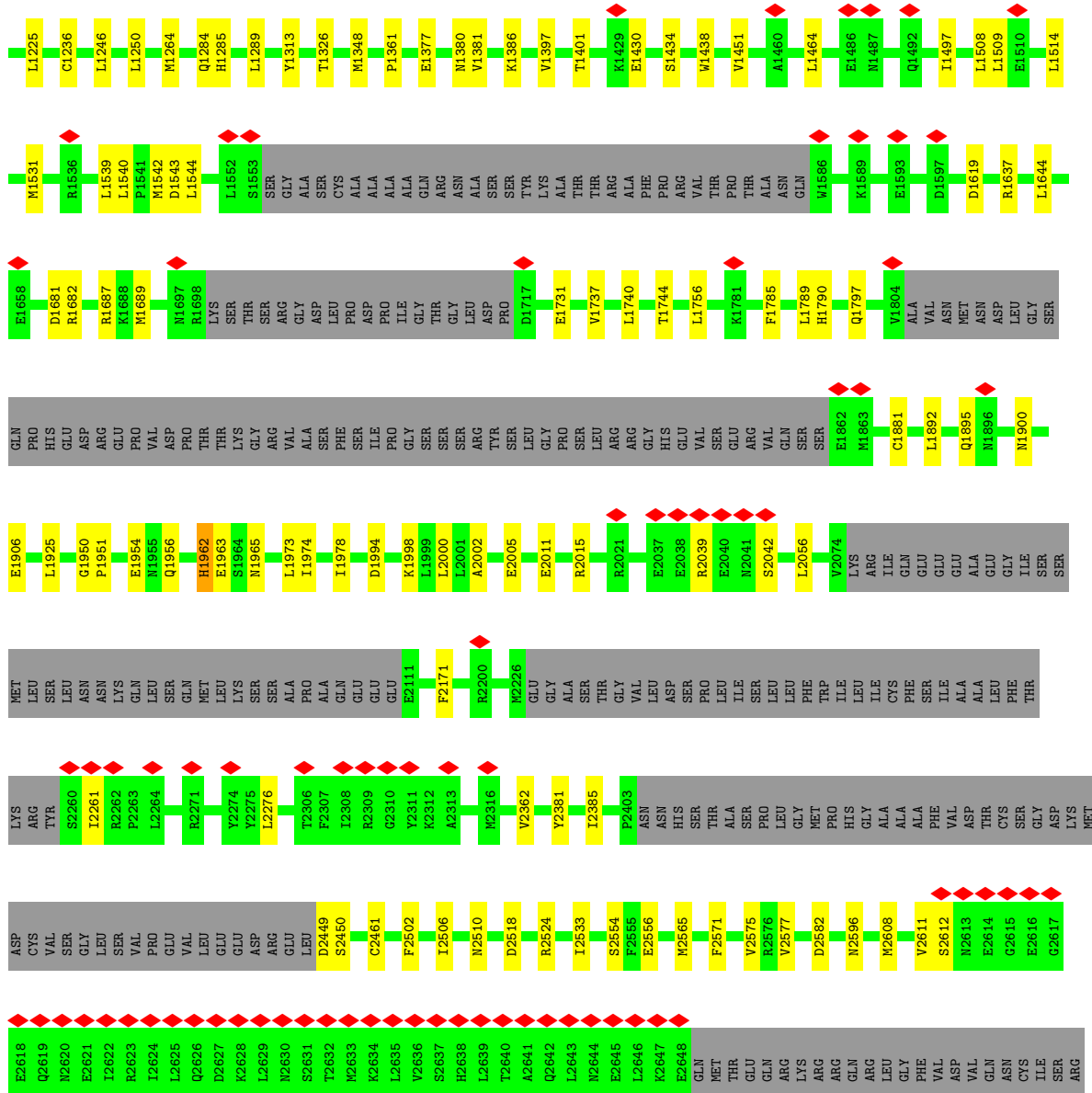


Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
5	A	1	101	33	58	1	8	1	0
5	A	1	117	38	69	1	8	1	0
5	A	1	98	31	57	1	8	1	0
5	A	1	108	36	62	1	8	1	0
5	A	1	112	38	64	1	8	1	0
5	A	1	108	36	62	1	8	1	0
5	A	1	126	41	75	1	8	1	0

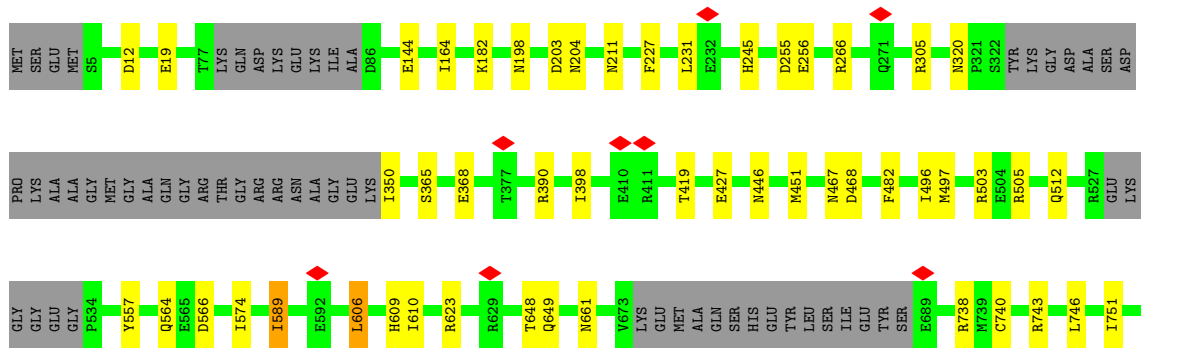
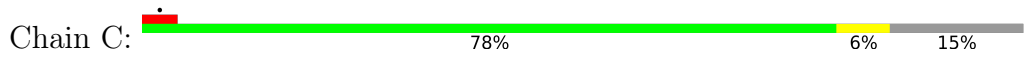
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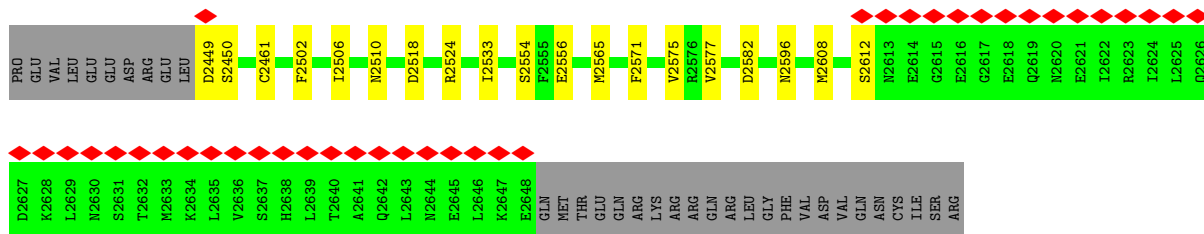
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Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
5	B	1	Total 126	C 41	H 75	N 1	O 8	P 1	0
5	B	1	Total 101	C 33	H 58	N 1	O 8	P 1	0
5	B	1	Total 117	C 38	H 69	N 1	O 8	P 1	0
5	B	1	Total 98	C 31	H 57	N 1	O 8	P 1	0
5	B	1	Total 112	C 38	H 64	N 1	O 8	P 1	0
5	C	1	Total 126	C 41	H 75	N 1	O 8	P 1	0
5	C	1	Total 101	C 33	H 58	N 1	O 8	P 1	0
5	C	1	Total 117	C 38	H 69	N 1	O 8	P 1	0
5	C	1	Total 98	C 31	H 57	N 1	O 8	P 1	0
5	C	1	Total 108	C 36	H 62	N 1	O 8	P 1	0
5	C	1	Total 113	C 38	H 65	N 1	O 8	P 1	0
5	C	1	Total 108	C 36	H 62	N 1	O 8	P 1	0
5	D	1	Total 117	C 38	H 69	N 1	O 8	P 1	0
5	D	1	Total 126	C 41	H 75	N 1	O 8	P 1	0
5	D	1	Total 101	C 33	H 58	N 1	O 8	P 1	0
5	D	1	Total 117	C 38	H 69	N 1	O 8	P 1	0
5	D	1	Total 98	C 31	H 57	N 1	O 8	P 1	0



- 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, C4	Depositor
Number of particles used	767556	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	139.562	Depositor
Minimum map value	-52.157	Depositor
Average map value	0.159	Depositor
Map value standard deviation	1.900	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: PCW, ATP, I3P, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.11	2/18521 (0.0%)	0.23	0/25031
1	B	0.11	2/18521 (0.0%)	0.23	0/25031
1	C	0.11	2/18521 (0.0%)	0.23	0/25031
1	D	0.11	2/18521 (0.0%)	0.23	0/25031
All	All	0.11	8/74084 (0.0%)	0.23	0/100124

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1962	HIS	CE1-NE2	-5.64	1.26	1.32
1	B	1962	HIS	CE1-NE2	-5.63	1.26	1.32
1	C	1962	HIS	CE1-NE2	-5.63	1.26	1.32
1	D	1962	HIS	CE1-NE2	-5.63	1.26	1.32
1	C	1962	HIS	CG-ND1	-5.54	1.32	1.38

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1962	HIS	Sidechain
1	B	1962	HIS	Sidechain
1	C	1962	HIS	Sidechain
1	D	1962	HIS	Sidechain

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	18187	18207	18211	104	0
1	B	18187	18208	18211	105	0
1	C	18187	18207	18211	103	0
1	D	18187	18208	18211	102	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	0	0
3	B	24	9	9	0	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
5	A	323	447	449	5	0
5	B	231	323	325	5	0
5	C	323	448	449	7	0
5	D	231	328	325	7	0
All	All	74080	74460	74476	417	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 3.

The worst 5 of 417 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:2608:MET:O	1:B:2612:SER:OG	1.98	0.82
1:A:2608:MET:O	1:A:2612:SER:OG	1.98	0.82
1:B:1430:GLU:O	1:B:1434:SER:OG	1.98	0.81
1:D:1430:GLU:O	1:D:1434:SER:OG	1.98	0.81
1:C:2608:MET:O	1:C:2612:SER:OG	1.98	0.80

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	4/2671 (0%)	4 (100%)	0	0	100	100
1	B	230/2671 (9%)	227 (99%)	3 (1%)	0	100	100
1	D	1362/2671 (51%)	1333 (98%)	29 (2%)	0	100	100
All	All	1596/8013 (20%)	1564 (98%)	32 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	21/2385 (1%)	21 (100%)	0	100	100
1	B	192/2385 (8%)	188 (98%)	4 (2%)	47	75
1	C	2021/2385 (85%)	2007 (99%)	14 (1%)	76	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	2021/2385 (85%)	2007 (99%)	14 (1%)	76	90
All	All	4255/9540 (45%)	4223 (99%)	32 (1%)	70	88

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	2461	CYS
1	D	2533	ILE
1	C	1531	MET
1	C	1515	GLN
1	D	2582	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	70	GLN
1	D	474	GLN
1	D	1518	HIS
1	D	222	ASN
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 36 ligands modelled in this entry, 4 are monoatomic - leaving 32 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PCW	A	3005	-	47,47,53	0.52	0	53,55,61	0.52	1 (1%)
5	PCW	A	3009	-	45,45,53	0.53	0	51,53,61	0.49	0
5	PCW	B	2705	-	42,42,53	0.53	0	48,50,61	0.49	0
5	PCW	D	2708	-	40,40,53	0.56	0	46,48,61	0.57	0
3	I3P	C	2703	-	24,24,24	2.18	3 (12%)	39,39,39	0.91	1 (2%)
5	PCW	A	3006	-	40,40,53	0.56	0	46,48,61	0.57	0
5	PCW	D	2701	-	47,47,53	0.53	0	53,55,61	0.50	0
5	PCW	C	2705	-	42,42,53	0.54	0	48,50,61	0.49	0
4	ATP	D	2705	-	32,33,33	0.26	0	48,52,52	0.67	0
5	PCW	C	2708	-	45,45,53	0.53	0	51,53,61	0.49	0
5	PCW	B	2708	-	47,47,53	0.53	0	53,55,61	0.50	0
5	PCW	D	2706	-	42,42,53	0.54	0	48,50,61	0.49	0
5	PCW	C	2707	-	40,40,53	0.55	0	46,48,61	0.57	0
5	PCW	C	2709	-	47,47,53	0.53	0	53,55,61	0.50	0
5	PCW	B	2701	-	50,50,53	0.50	0	56,58,61	0.52	0
3	I3P	A	3002	-	24,24,24	2.18	3 (12%)	39,39,39	0.91	1 (2%)
5	PCW	C	2701	-	50,50,53	0.50	0	56,58,61	0.52	0
5	PCW	D	2702	-	50,50,53	0.50	0	56,58,61	0.52	0
5	PCW	C	2710	-	45,45,53	0.53	0	51,53,61	0.49	0
5	PCW	A	3008	-	47,47,53	0.53	0	53,55,61	0.51	0
5	PCW	A	3007	-	45,45,53	0.53	0	51,53,61	0.49	0
4	ATP	C	2704	-	32,33,33	0.26	0	48,52,52	0.67	0
3	I3P	B	2703	-	24,24,24	2.18	3 (12%)	39,39,39	0.92	1 (2%)
5	PCW	C	2706	-	47,47,53	0.52	0	53,55,61	0.52	1 (1%)
4	ATP	B	2704	-	32,33,33	0.26	0	48,52,52	0.67	0
5	PCW	B	2706	-	47,47,53	0.52	0	53,55,61	0.52	1 (1%)
5	PCW	A	3010	-	50,50,53	0.50	0	56,58,61	0.52	0
5	PCW	B	2707	-	40,40,53	0.56	0	46,48,61	0.57	0
5	PCW	A	3004	-	42,42,53	0.54	0	48,50,61	0.49	0
3	I3P	D	2704	-	24,24,24	2.18	3 (12%)	39,39,39	0.92	1 (2%)
5	PCW	D	2707	-	47,47,53	0.52	0	53,55,61	0.52	1 (1%)
4	ATP	A	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
5	PCW	A	3005	-	-	18/51/51/57	-
5	PCW	A	3009	-	-	15/49/49/57	-
5	PCW	B	2705	-	-	8/46/46/57	-
5	PCW	D	2708	-	-	16/44/44/57	-
3	I3P	C	2703	-	-	1/15/39/39	0/1/1/1
5	PCW	A	3006	-	-	16/44/44/57	-
5	PCW	D	2701	-	-	13/51/51/57	-
5	PCW	C	2705	-	-	8/46/46/57	-
4	ATP	D	2705	-	-	10/22/38/38	0/3/3/3
5	PCW	C	2708	-	-	15/49/49/57	-
5	PCW	B	2708	-	-	13/51/51/57	-
5	PCW	D	2706	-	-	8/46/46/57	-
5	PCW	C	2707	-	-	16/44/44/57	-
5	PCW	C	2709	-	-	13/51/51/57	-
5	PCW	B	2701	-	-	18/54/54/57	-
3	I3P	A	3002	-	-	1/15/39/39	0/1/1/1
5	PCW	C	2701	-	-	18/54/54/57	-
5	PCW	D	2702	-	-	18/54/54/57	-
5	PCW	C	2710	-	-	15/49/49/57	-
5	PCW	A	3008	-	-	13/51/51/57	-
5	PCW	A	3007	-	-	15/49/49/57	-
4	ATP	C	2704	-	-	10/22/38/38	0/3/3/3
3	I3P	B	2703	-	-	1/15/39/39	0/1/1/1
5	PCW	C	2706	-	-	18/51/51/57	-
4	ATP	B	2704	-	-	10/22/38/38	0/3/3/3
5	PCW	B	2706	-	-	18/51/51/57	-
5	PCW	A	3010	-	-	18/54/54/57	-
5	PCW	B	2707	-	-	16/44/44/57	-
5	PCW	A	3004	-	-	8/46/46/57	-
3	I3P	D	2704	-	-	1/15/39/39	0/1/1/1
5	PCW	D	2707	-	-	18/51/51/57	-
4	ATP	A	3003	-	-	10/22/38/38	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	D	2704	I3P	P4-O4	6.08	1.70	1.59
3	B	2703	I3P	P4-O4	6.08	1.70	1.59
3	C	2703	I3P	P4-O4	6.08	1.70	1.59
3	A	3002	I3P	P4-O4	6.08	1.70	1.59
3	B	2703	I3P	P5-O5	5.92	1.69	1.59

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2703	I3P	O5-P5-O51	-2.04	102.08	109.33
5	B	2706	PCW	C3-C2-C1	2.04	116.53	111.78
5	C	2706	PCW	C3-C2-C1	2.04	116.53	111.78
3	A	3002	I3P	O5-P5-O51	-2.03	102.08	109.33
3	B	2703	I3P	O5-P5-O51	-2.03	102.08	109.33

There are no chirality outliers.

5 of 396 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-O1A
4	A	3003	ATP	C5'-O5'-PA-O2A
4	A	3003	ATP	C5'-O5'-PA-O3A
4	B	2704	ATP	PB-O3B-PG-O3G

There are no ring outliers.

14 monomers are involved in 27 short contacts:

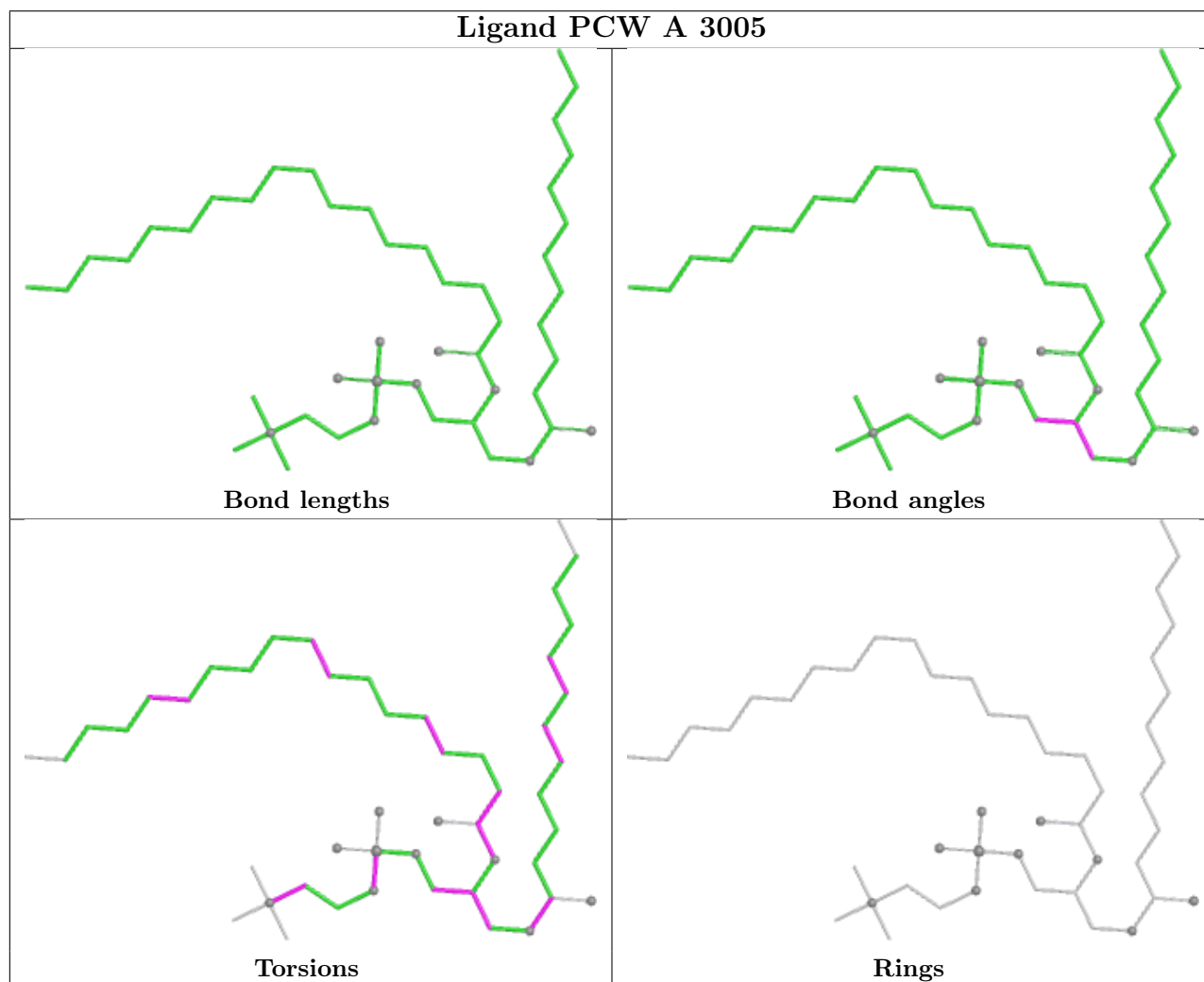
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	2708	PCW	1	0
3	C	2703	I3P	1	0
5	A	3006	PCW	1	0
5	D	2701	PCW	4	0
5	B	2708	PCW	3	0
5	C	2707	PCW	1	0
5	C	2709	PCW	5	0
5	B	2701	PCW	1	0
5	C	2701	PCW	1	0
5	D	2702	PCW	2	0
5	A	3008	PCW	2	0
5	A	3010	PCW	2	0
5	B	2707	PCW	1	0

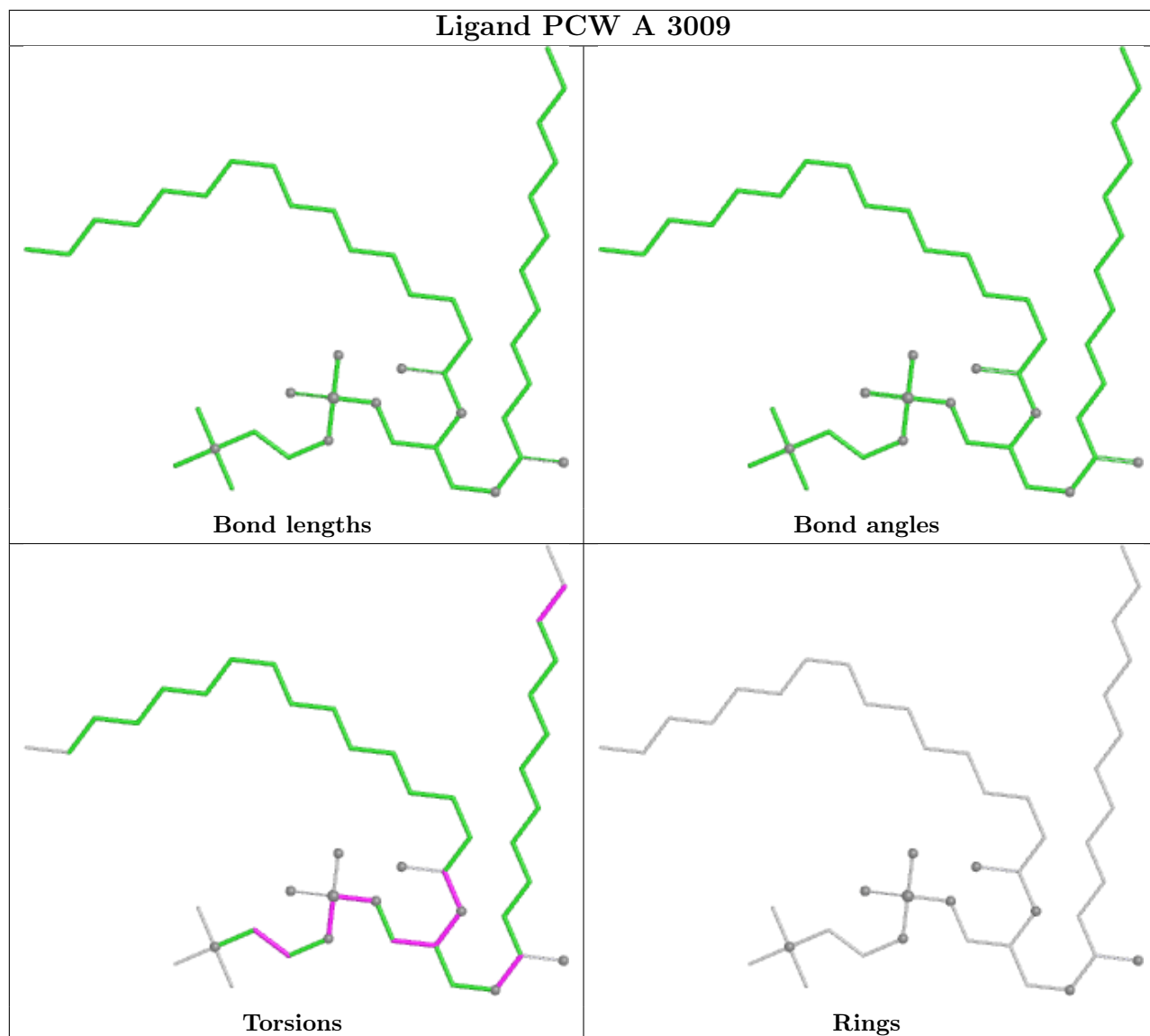
Continued on next page...

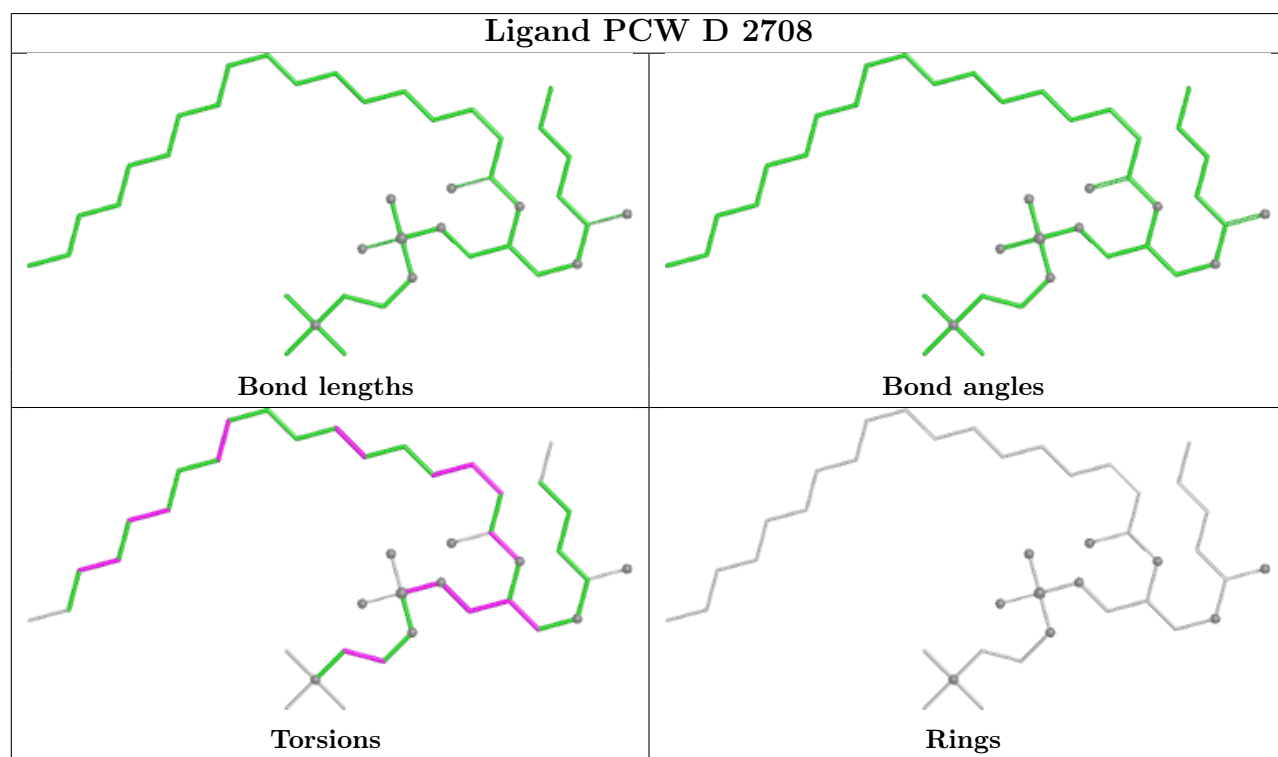
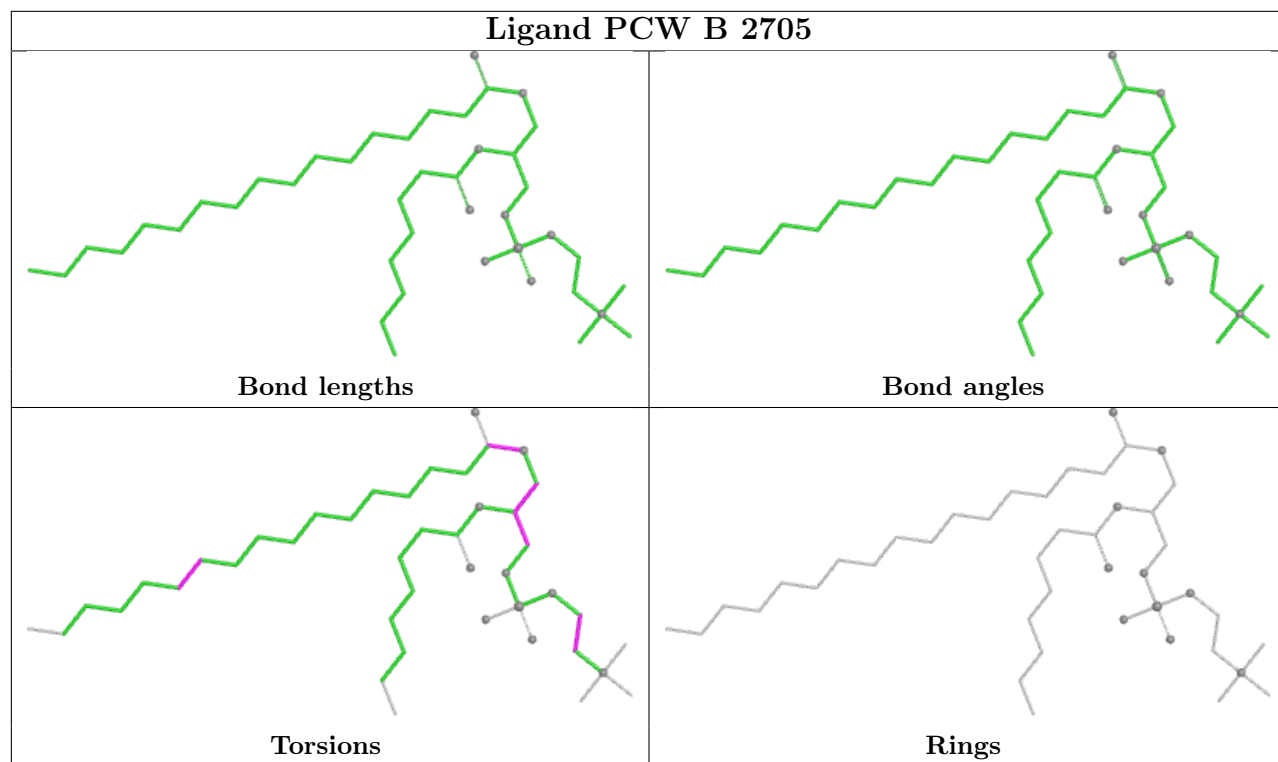
Continued from previous page...

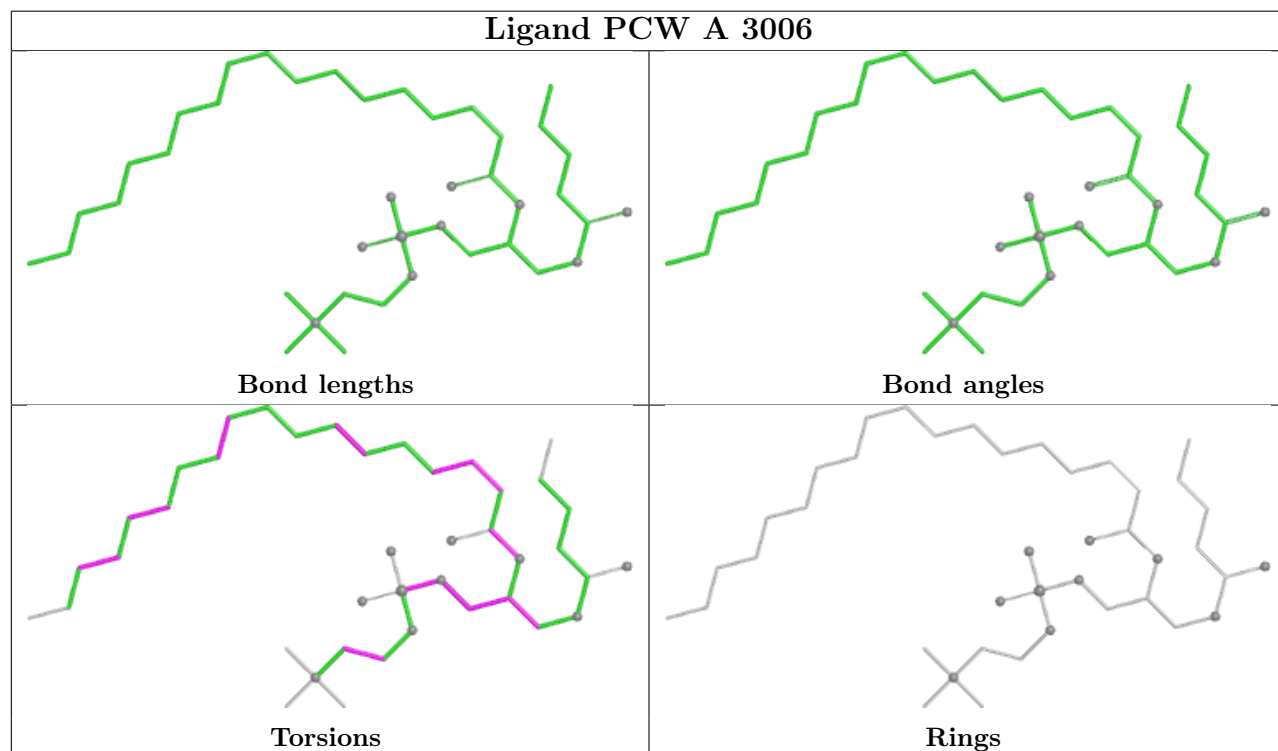
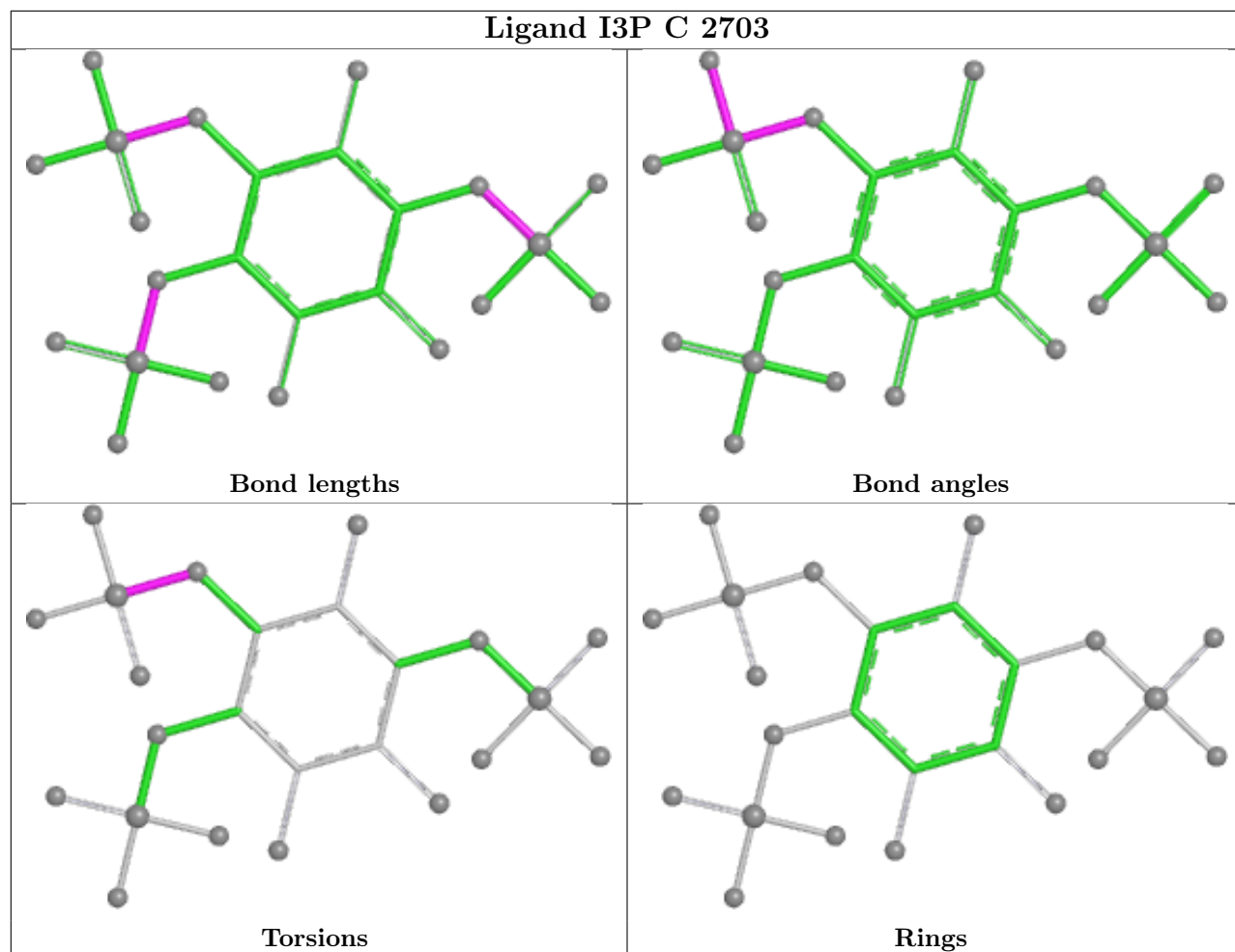
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	2704	I3P	2	0

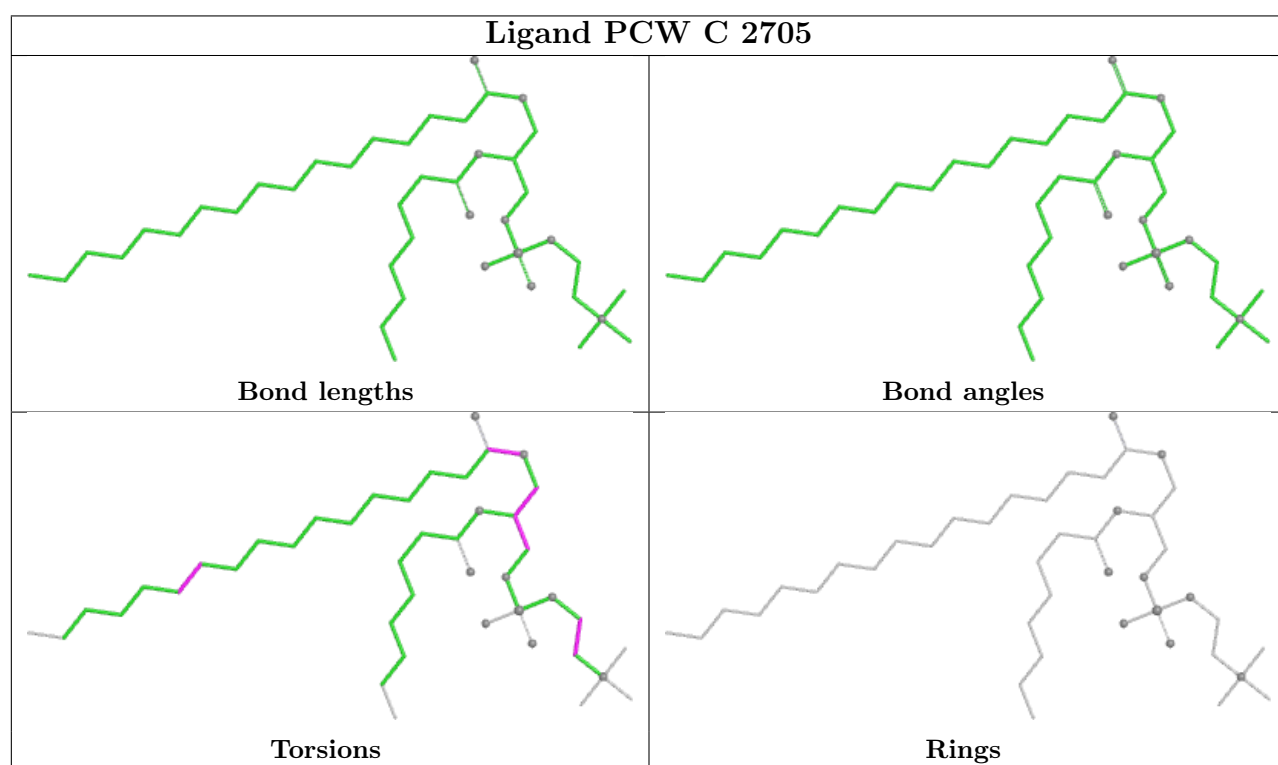
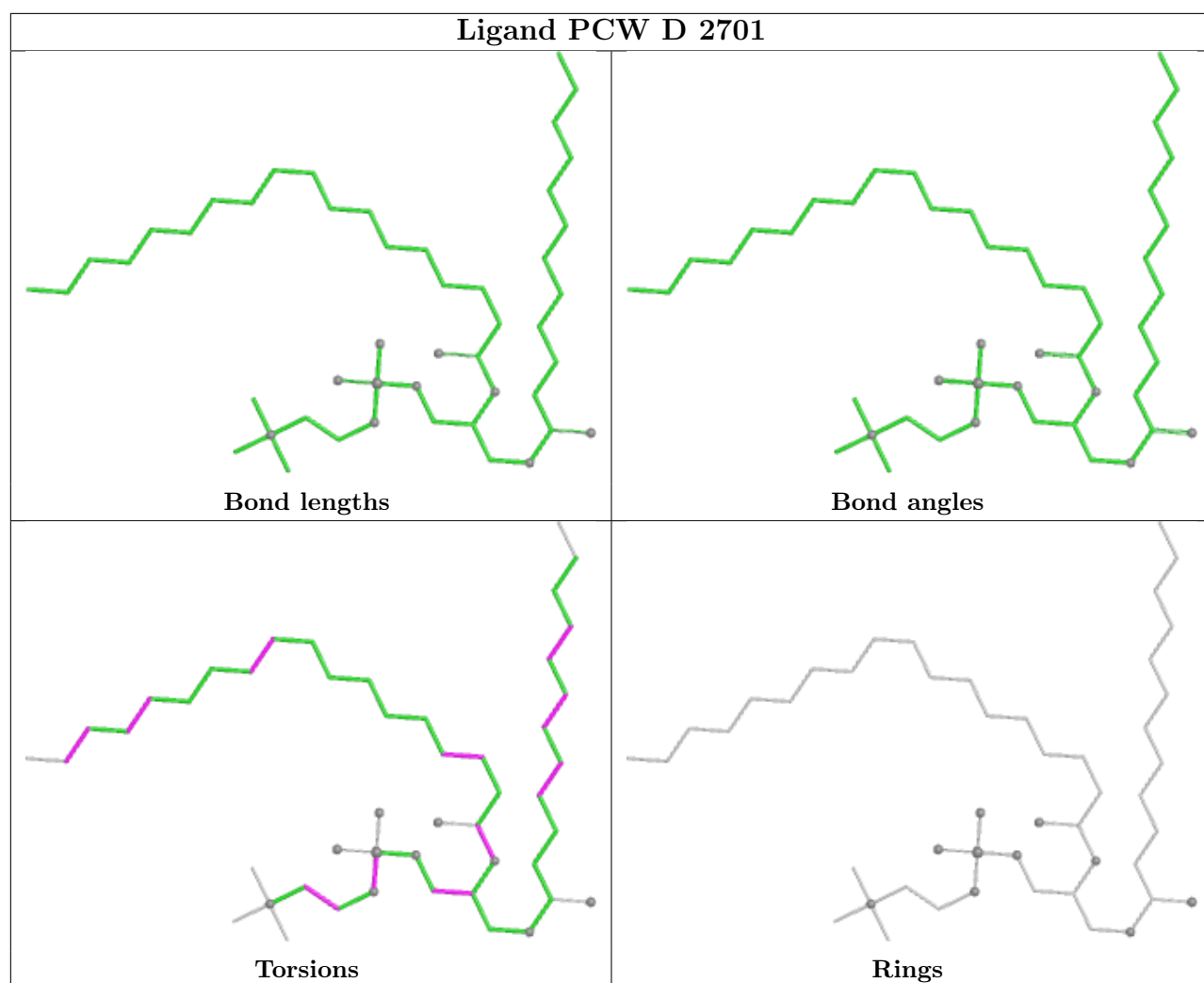
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

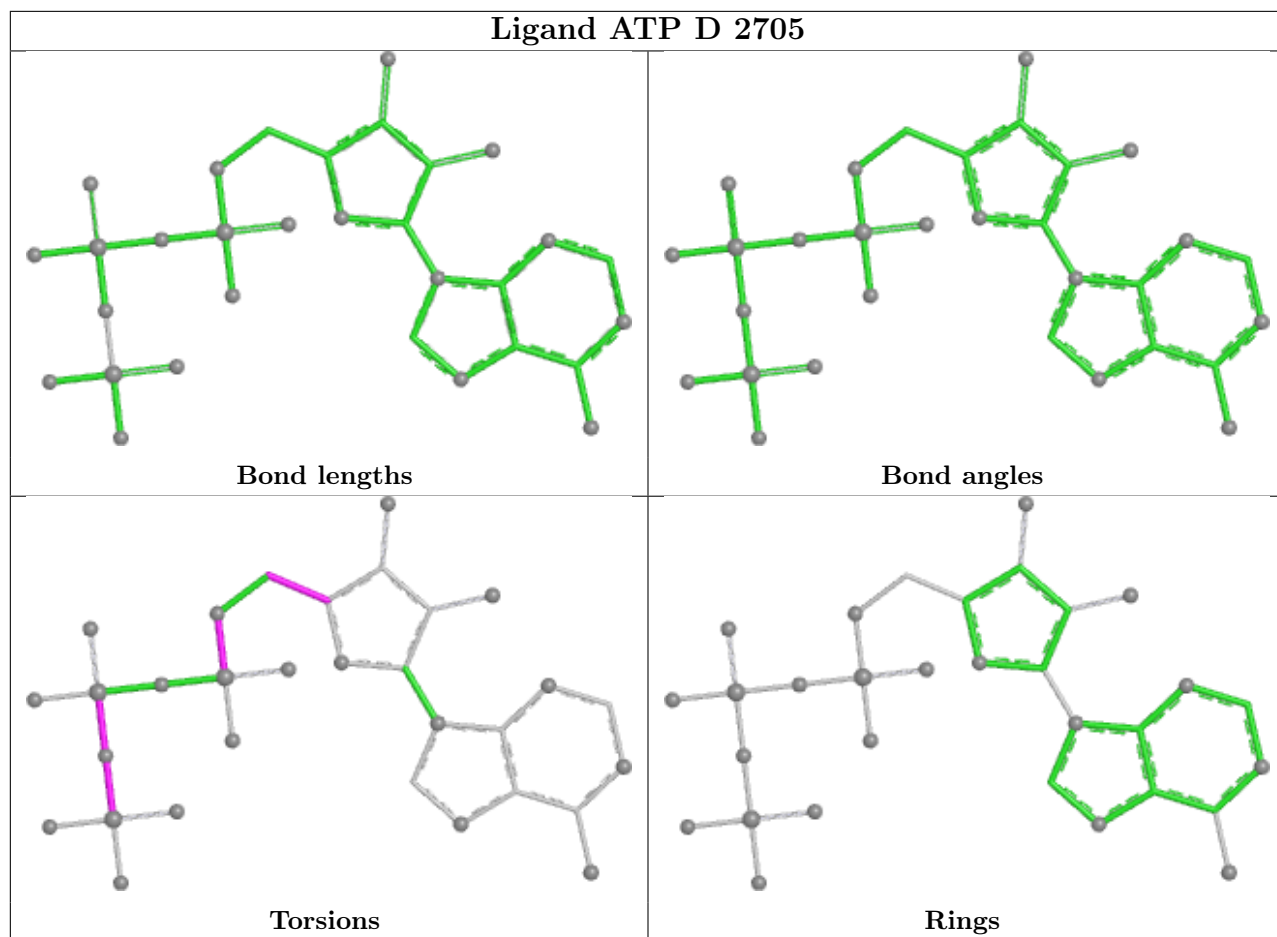


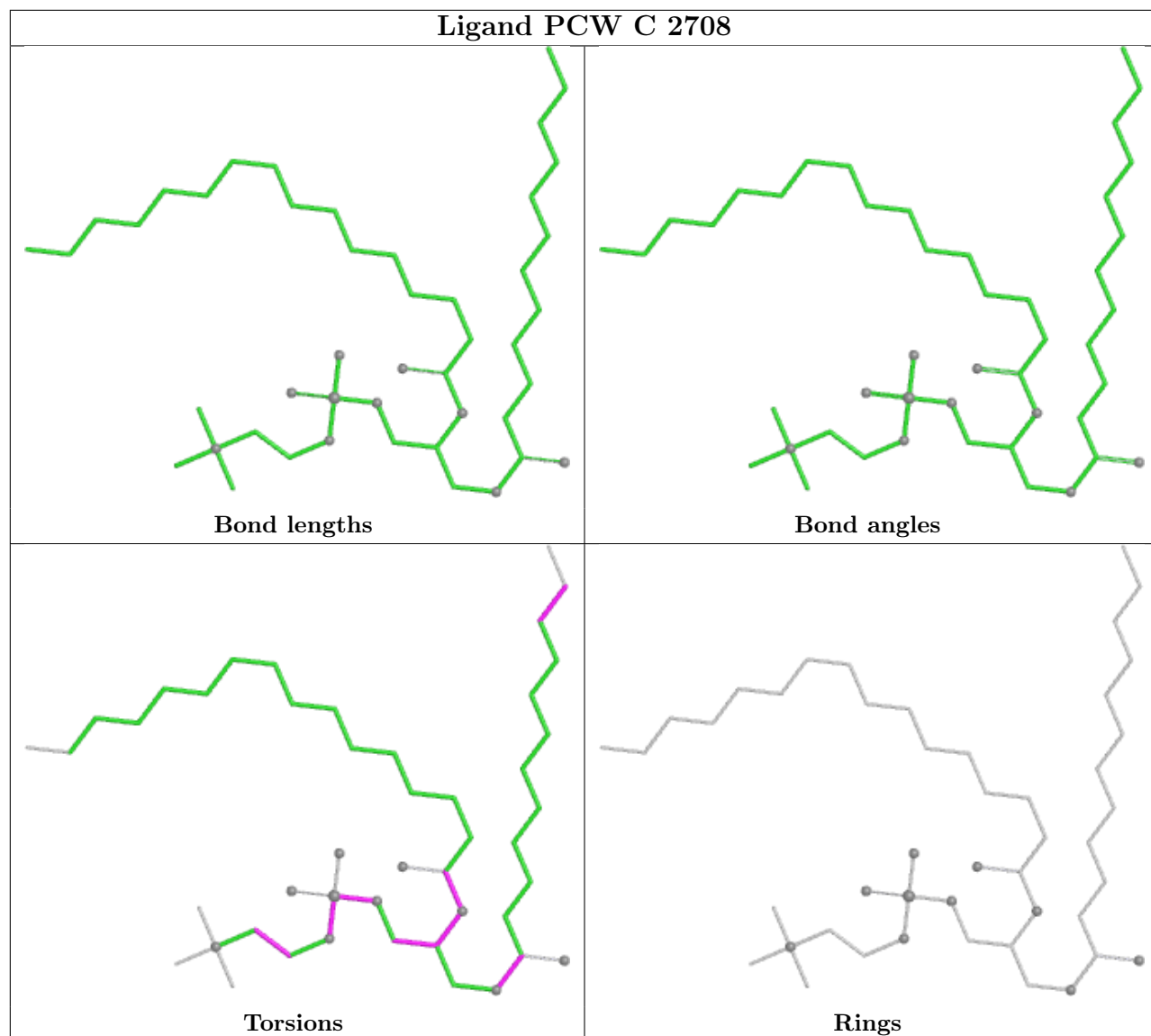


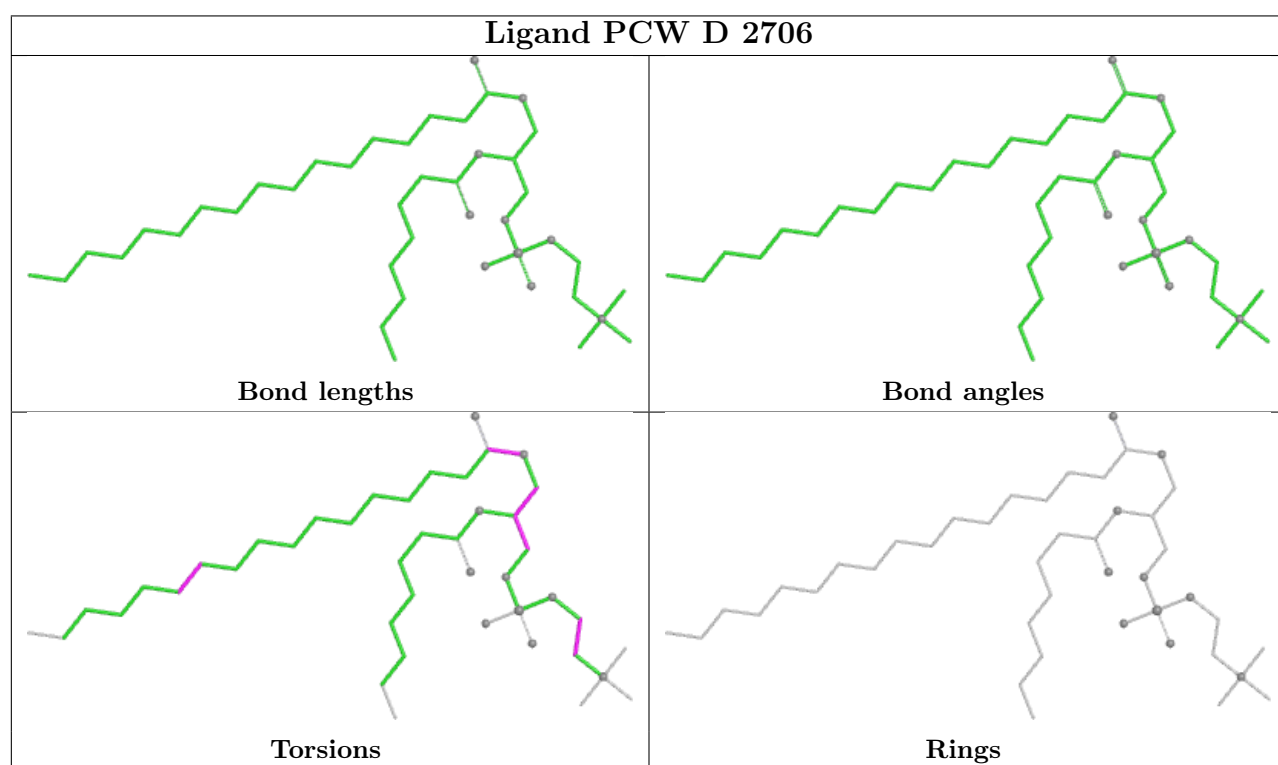
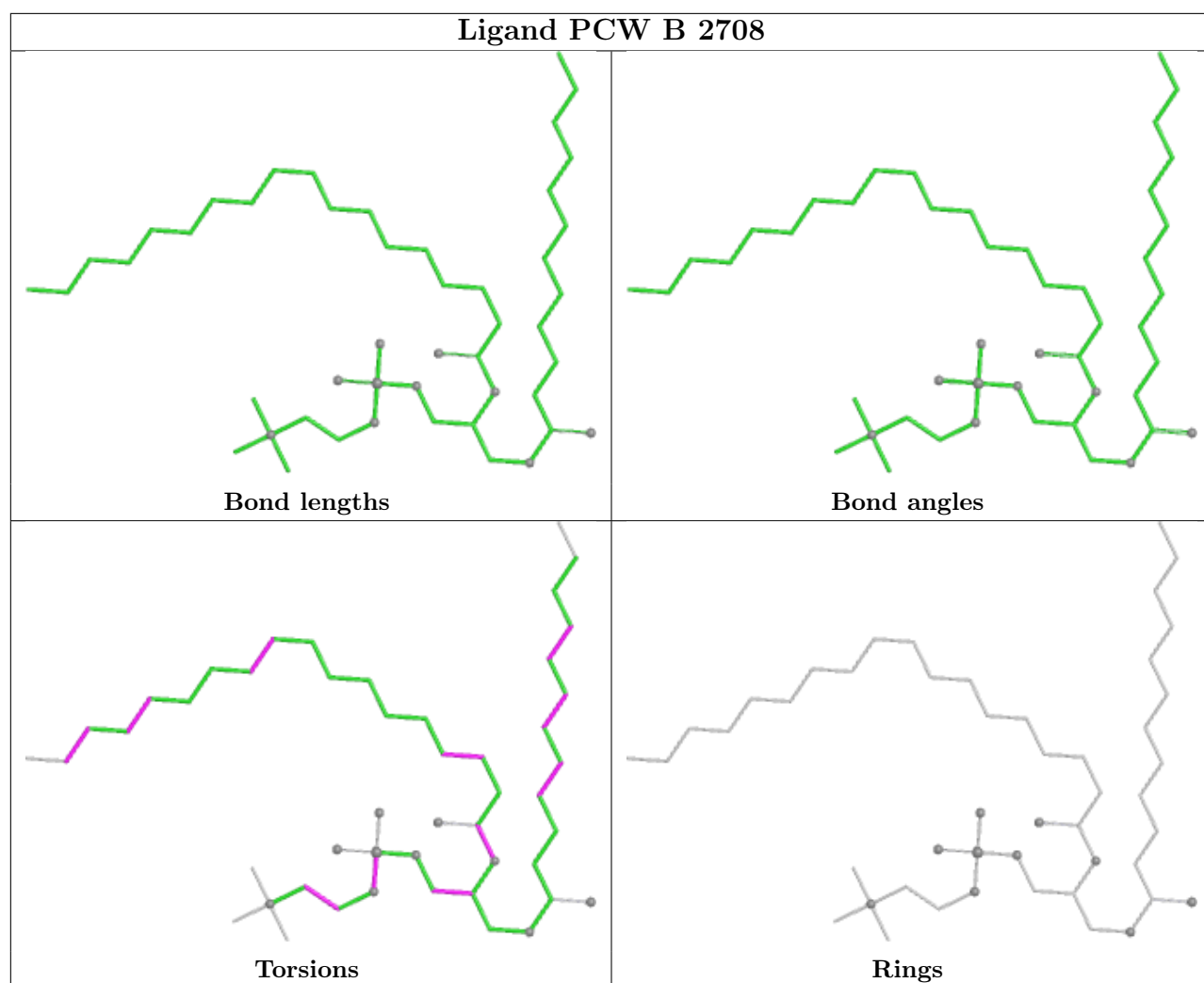


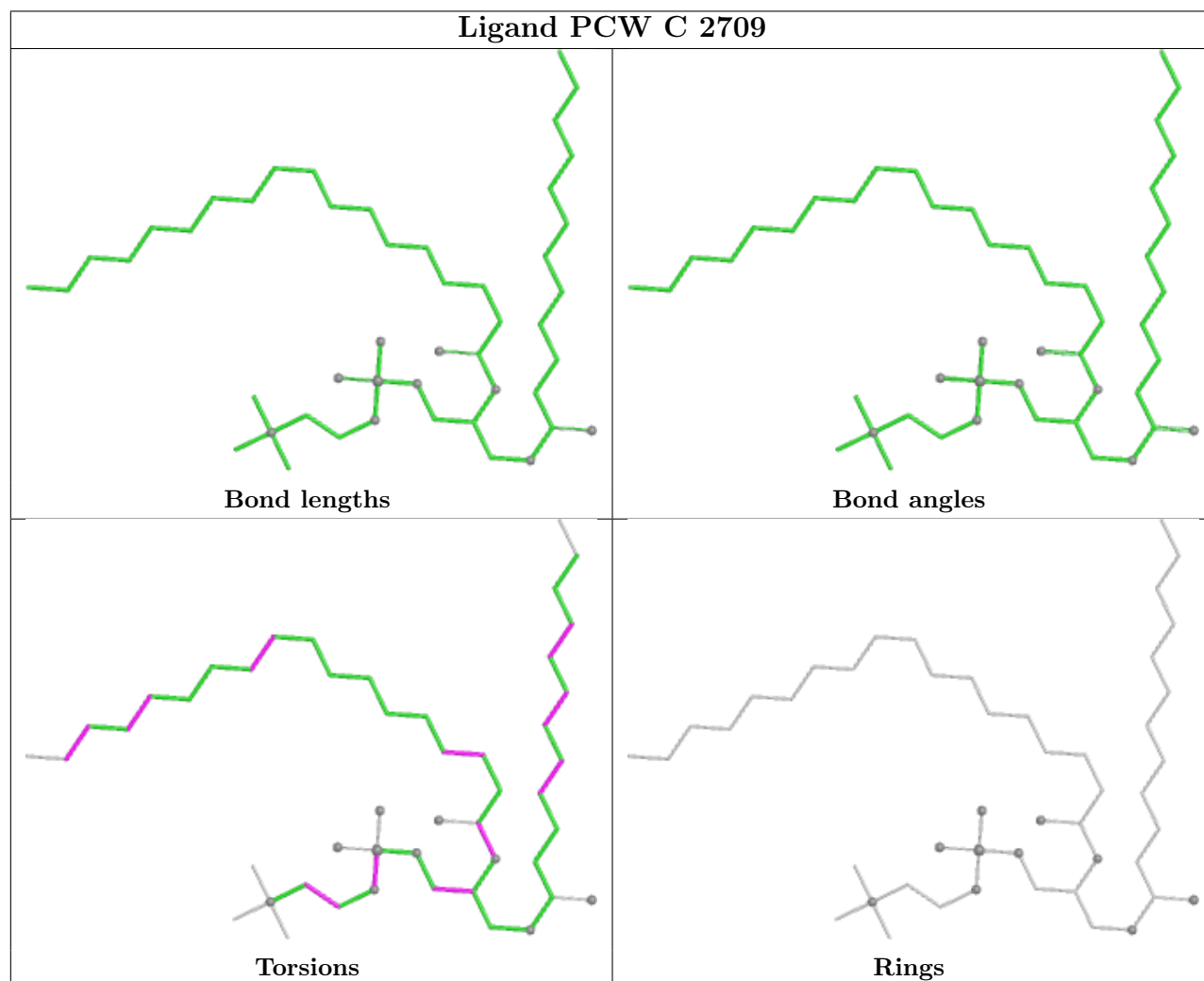
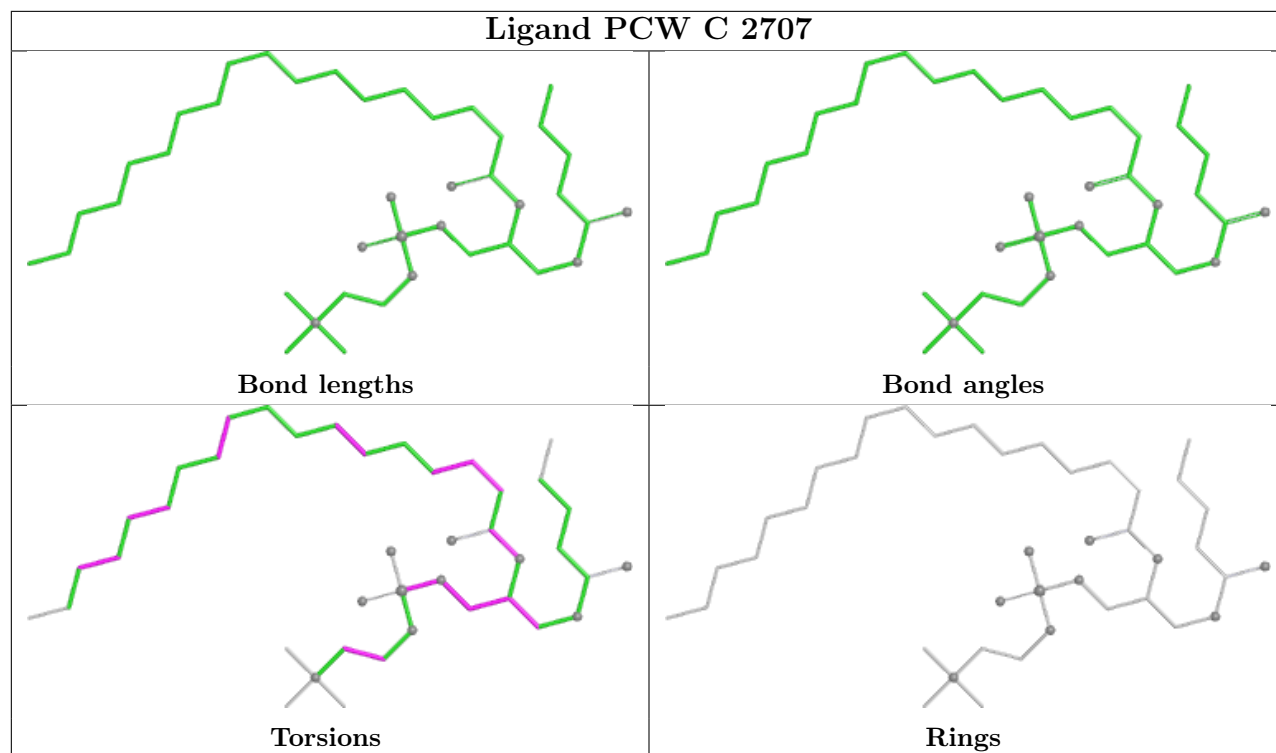


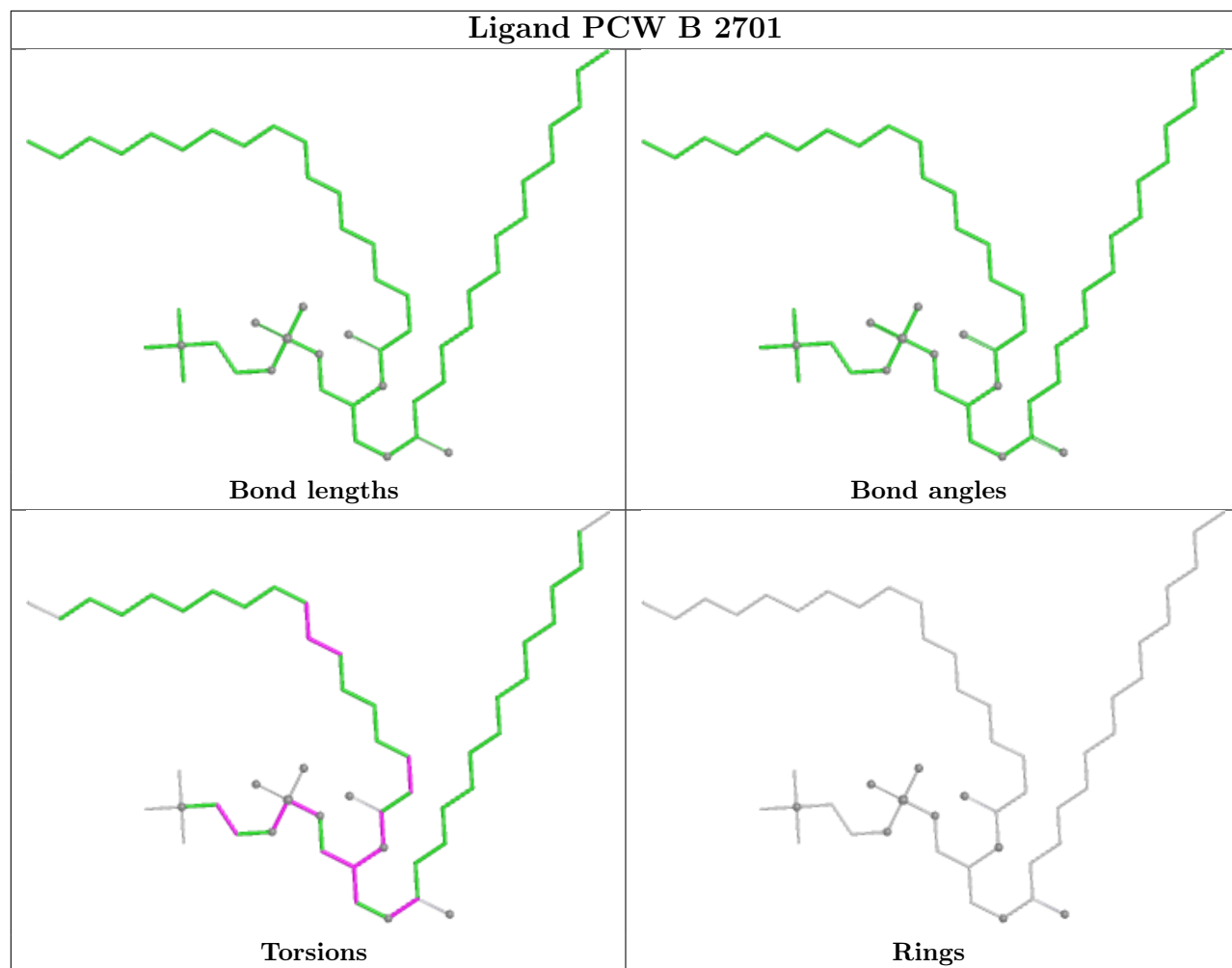


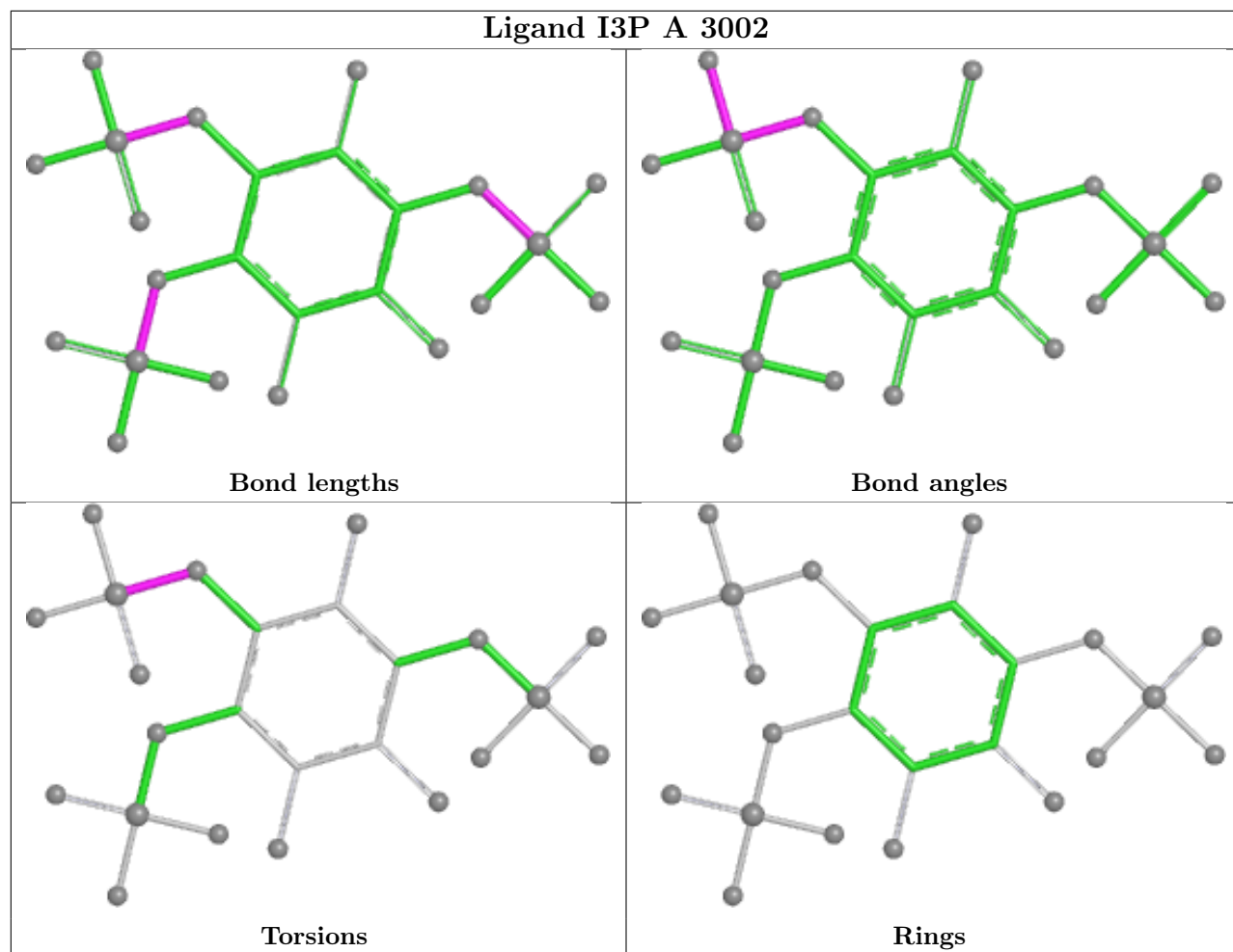


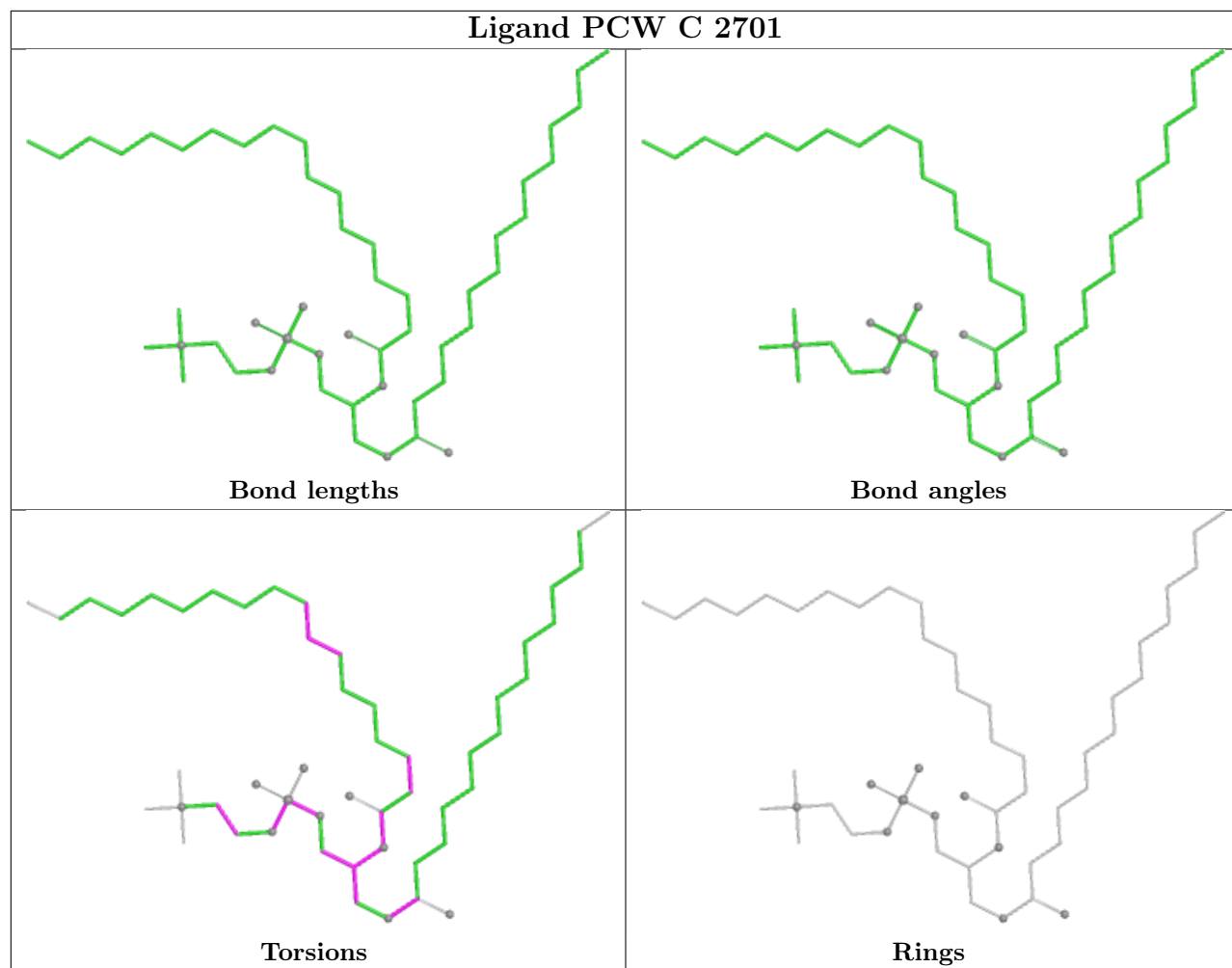


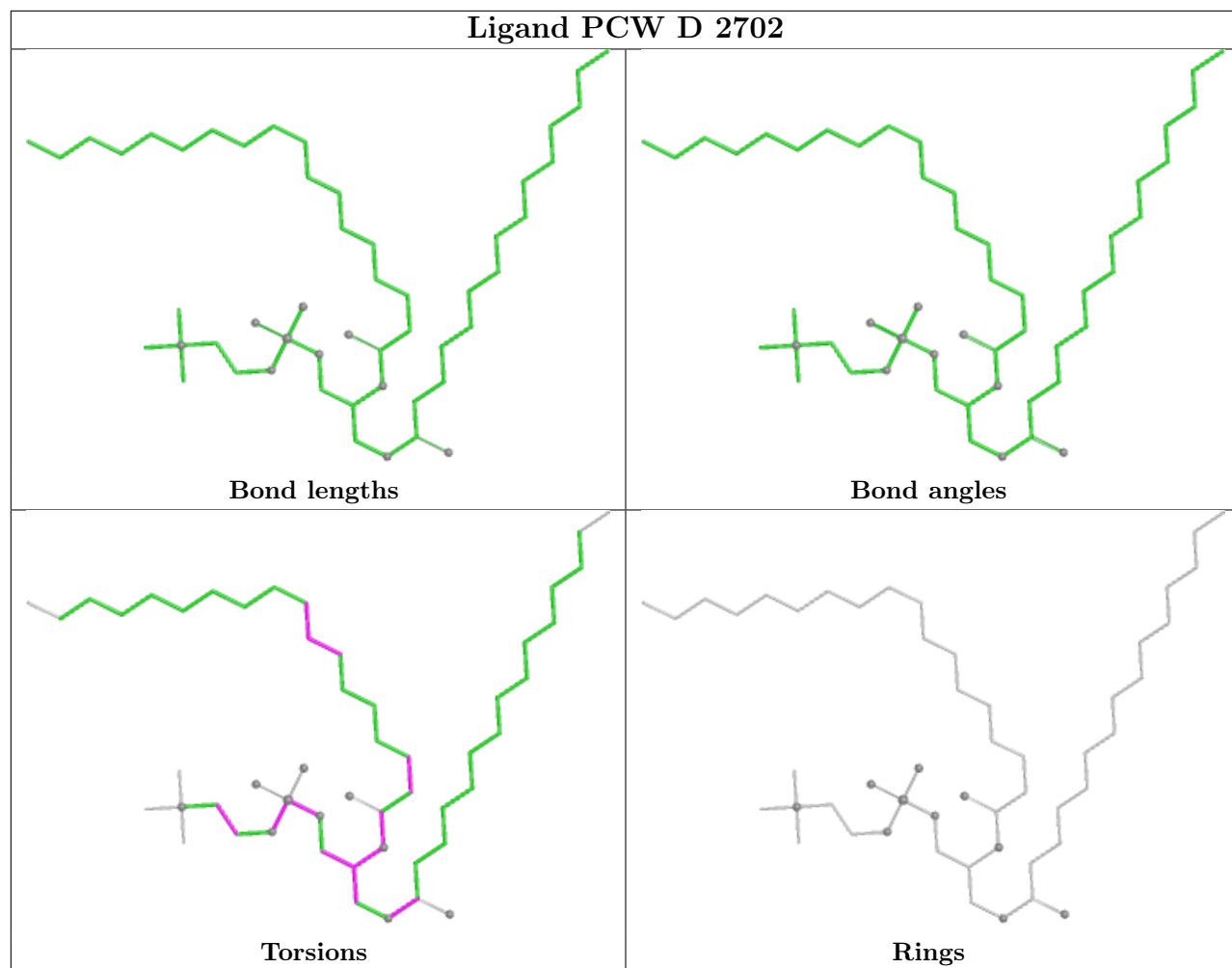


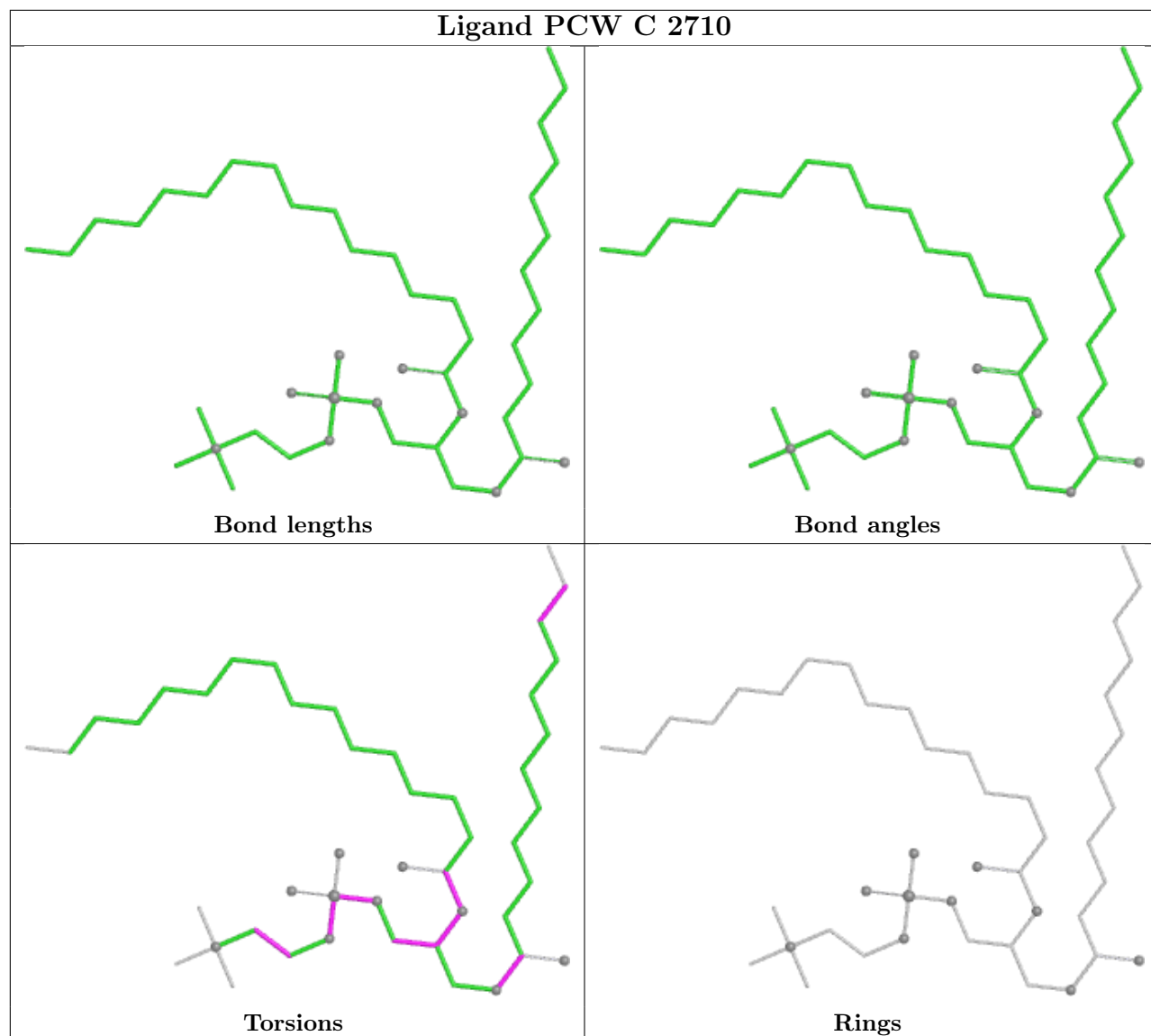


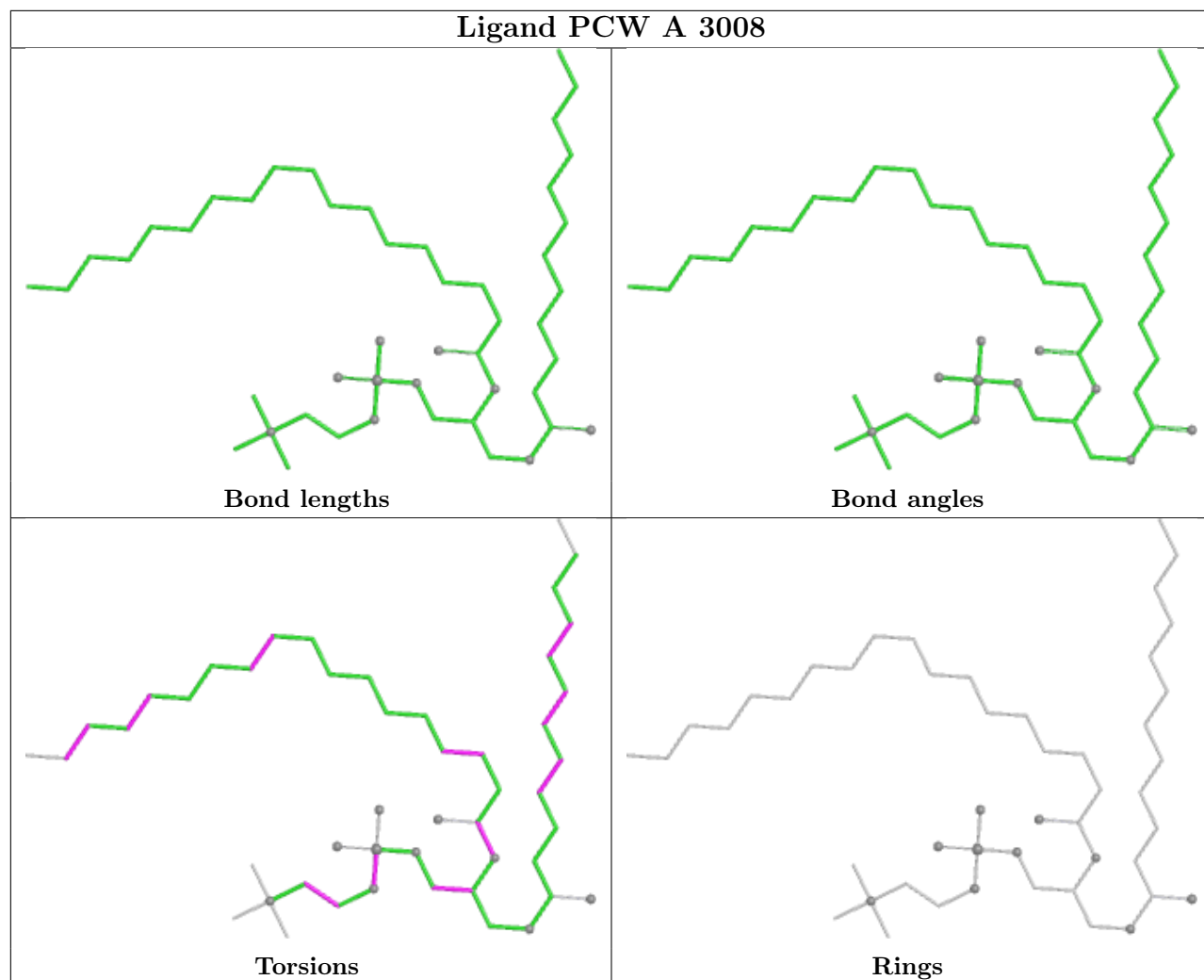


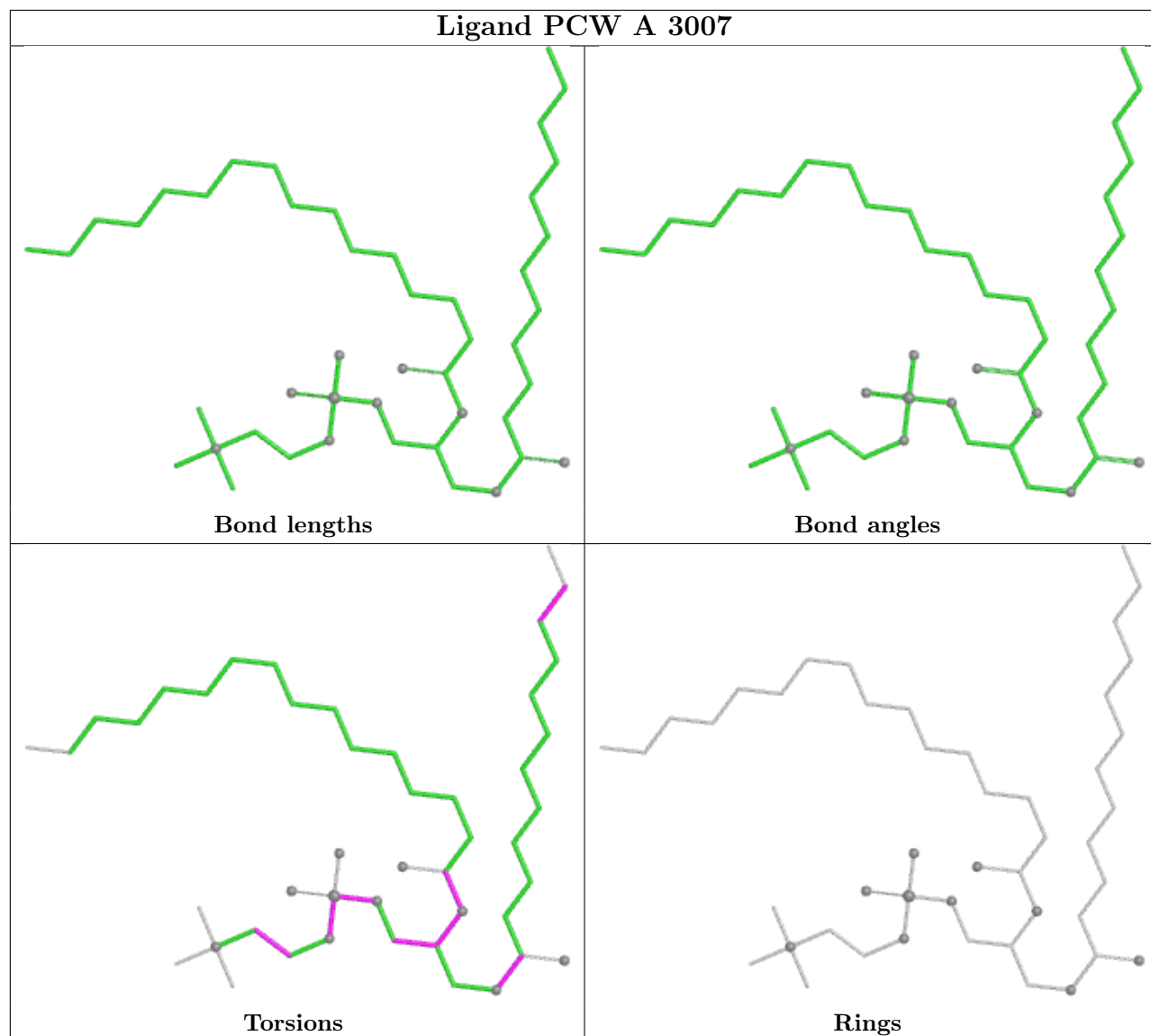


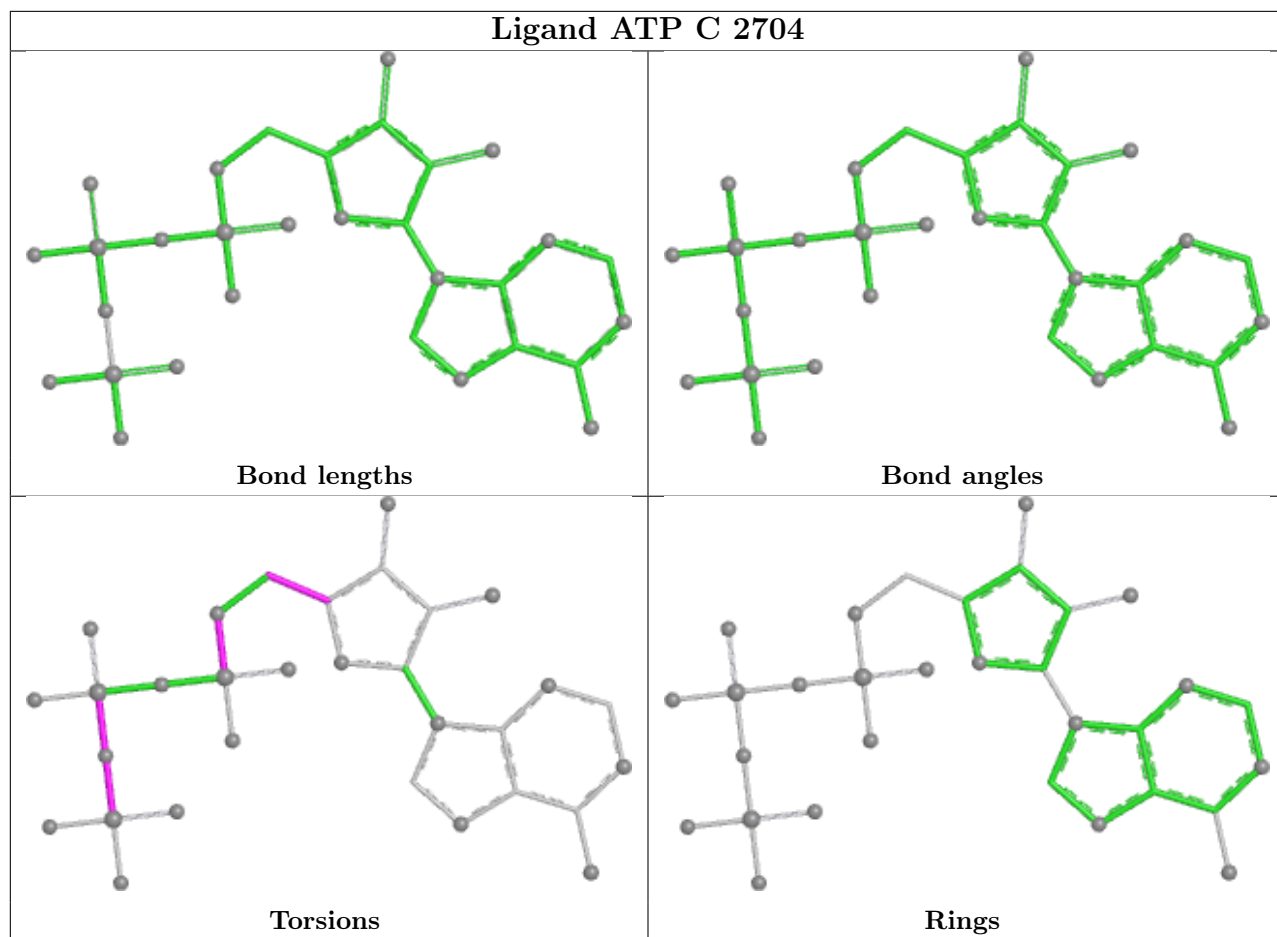


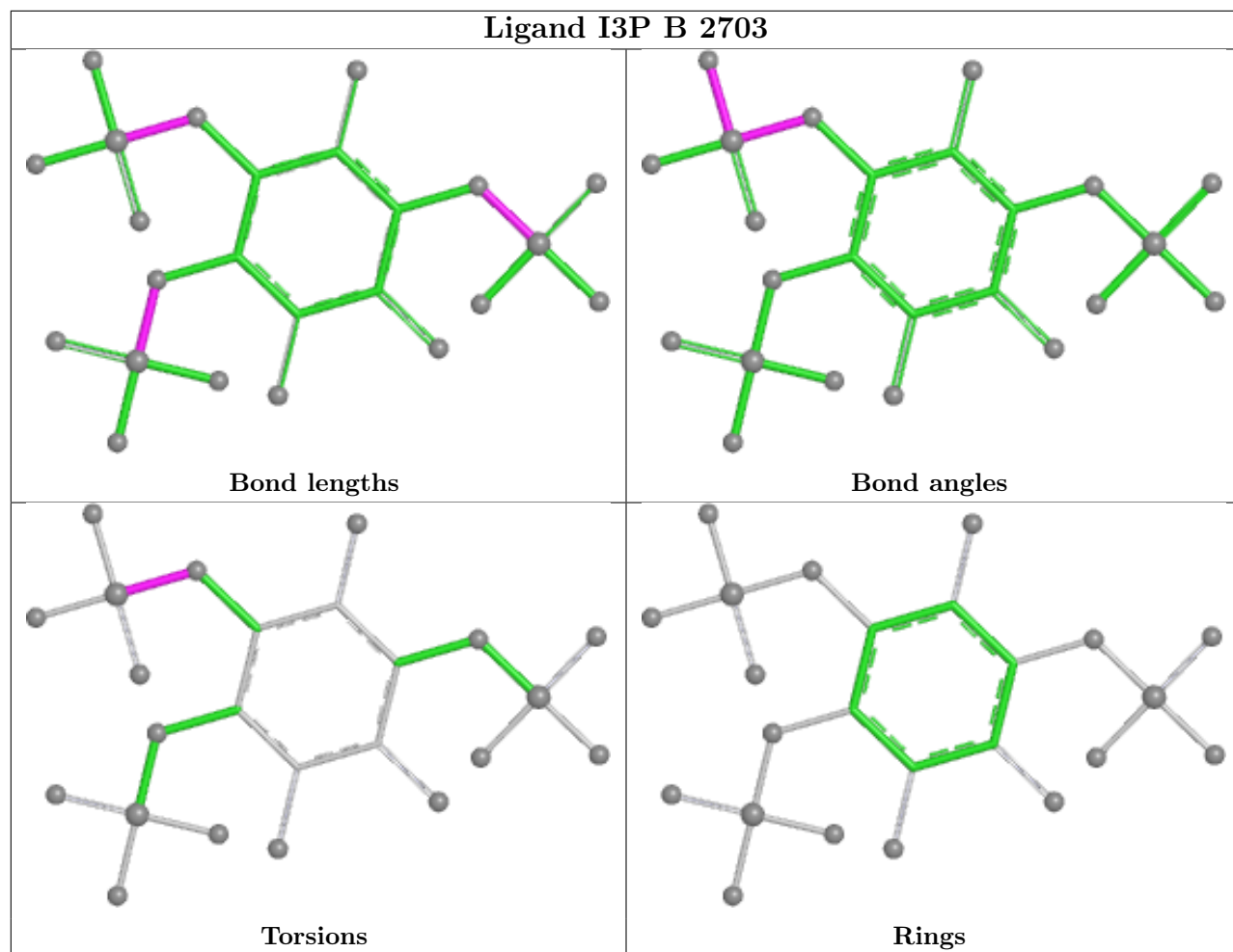


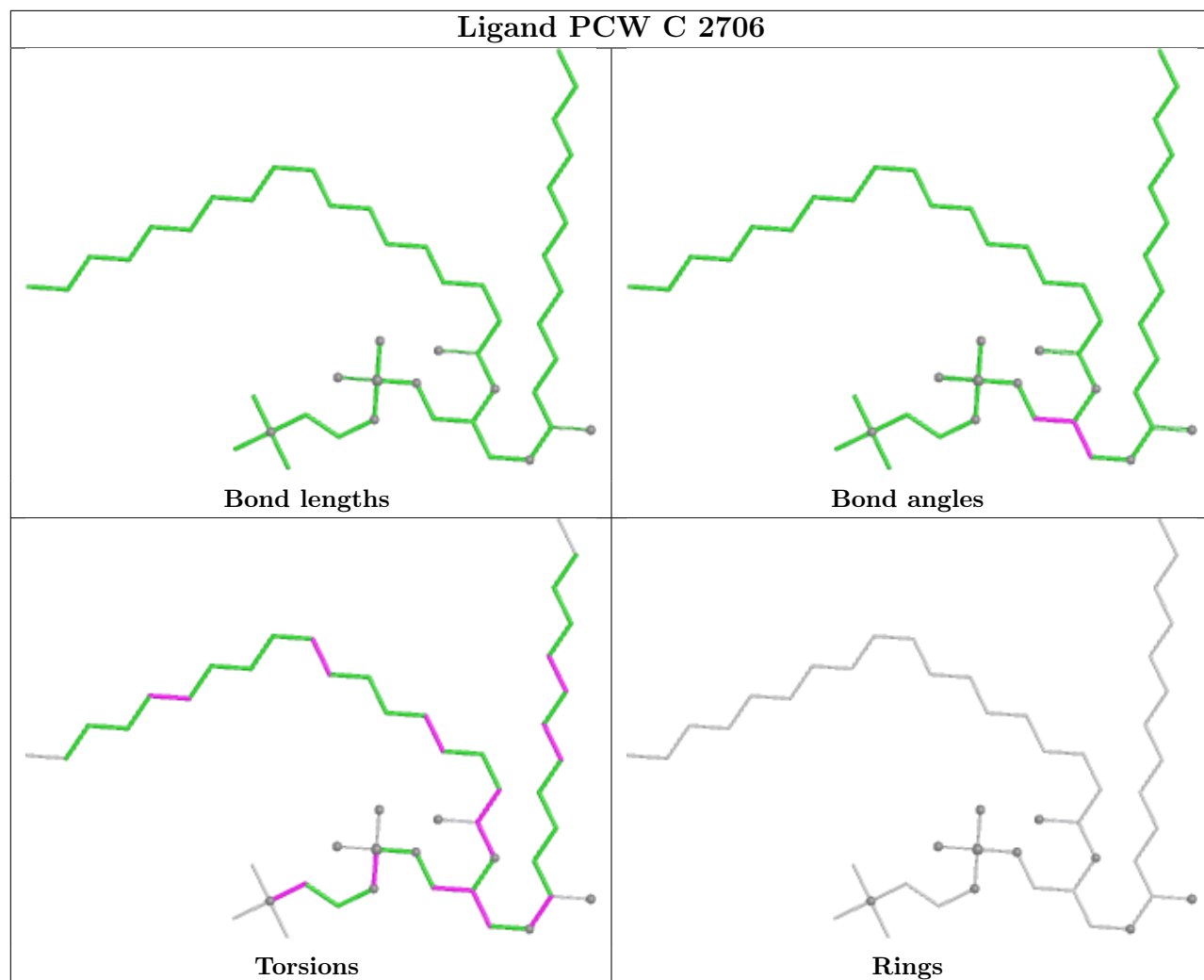


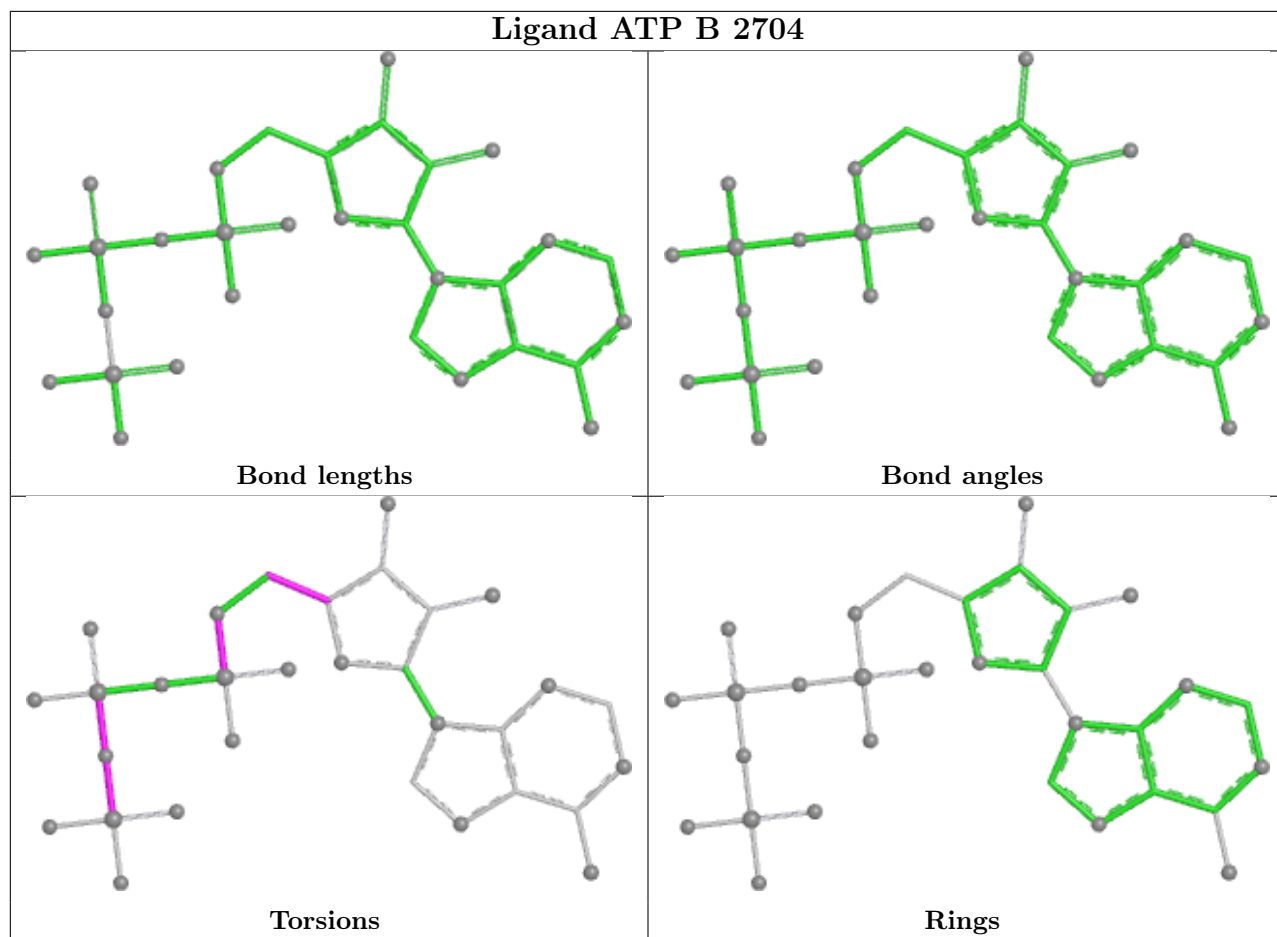


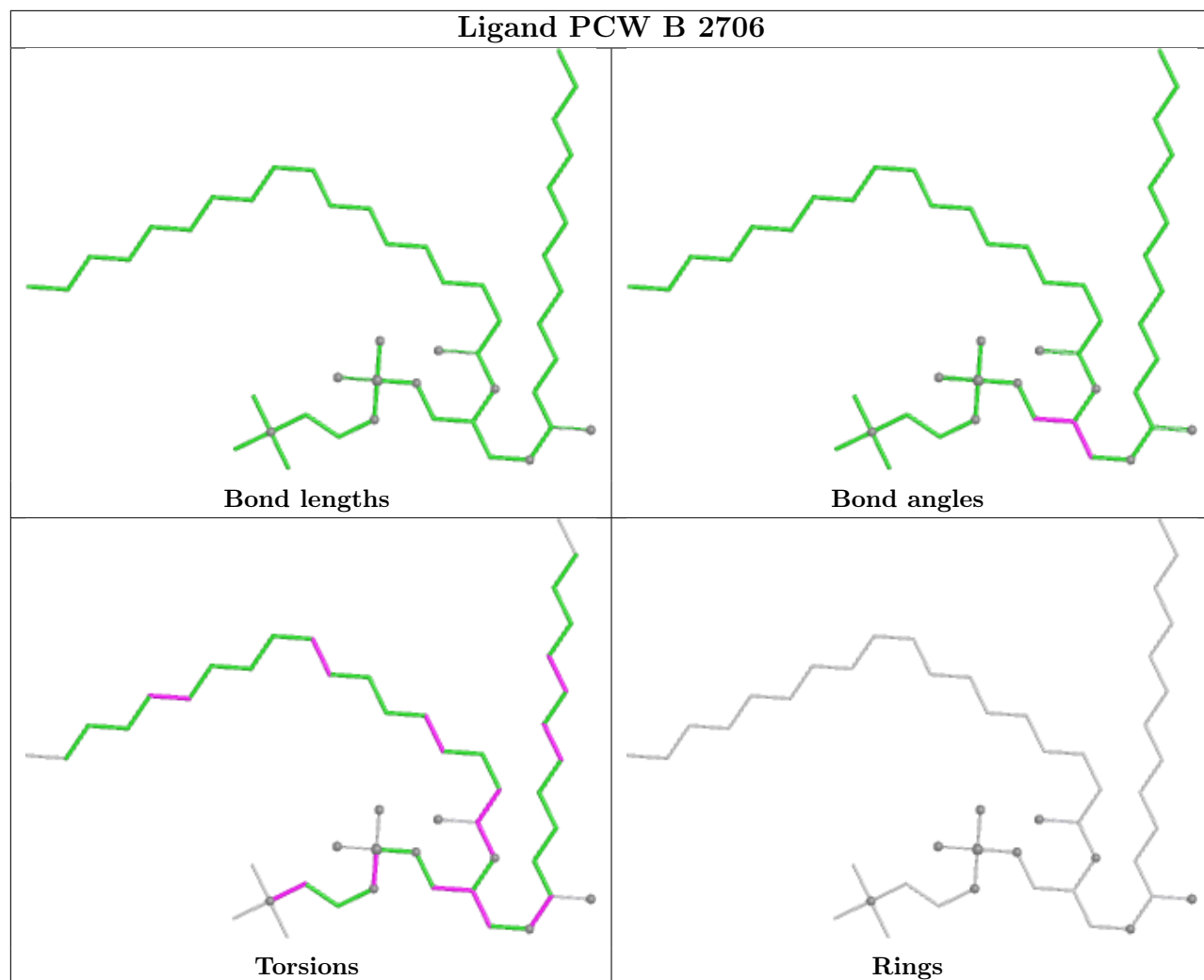


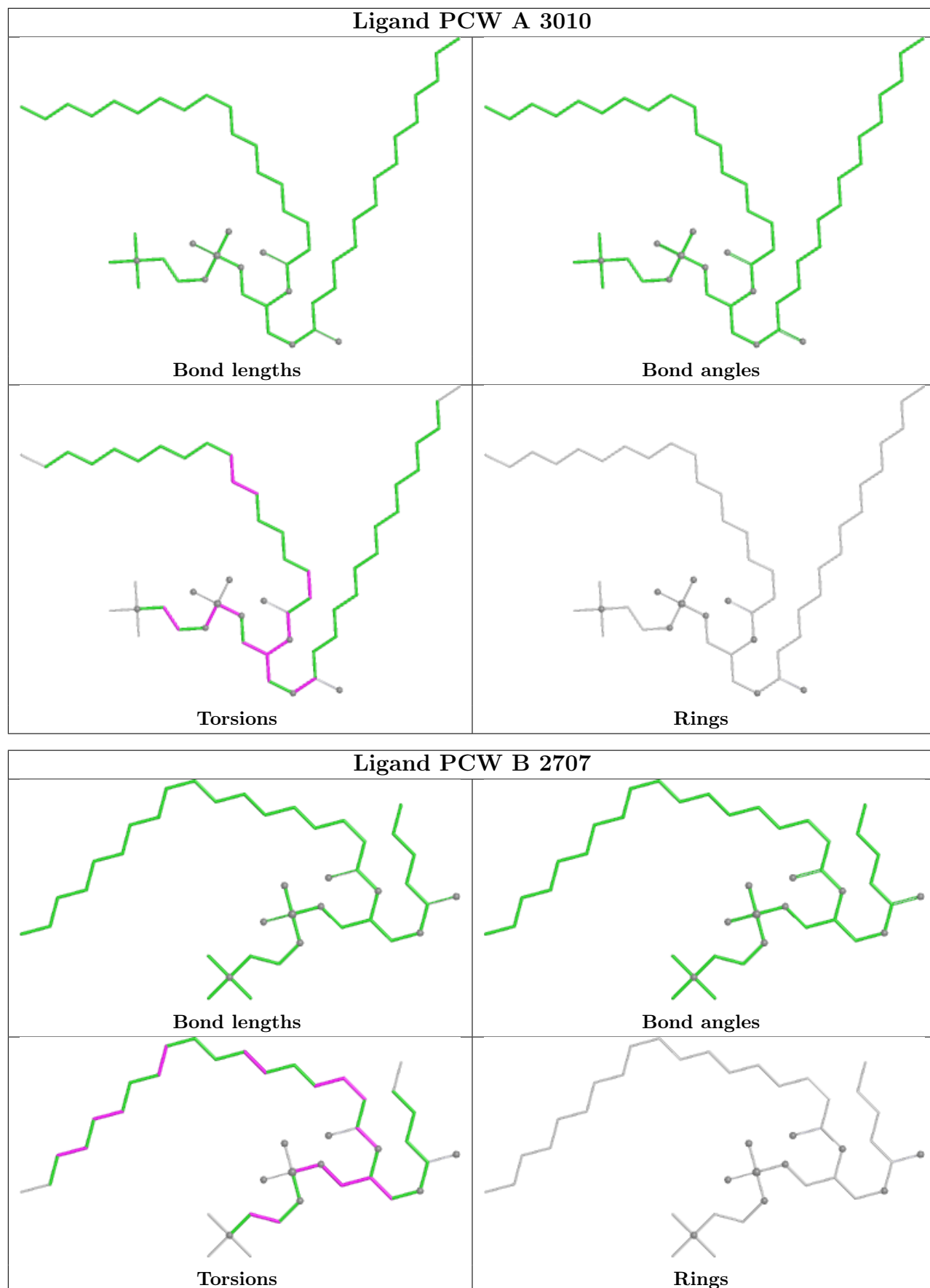


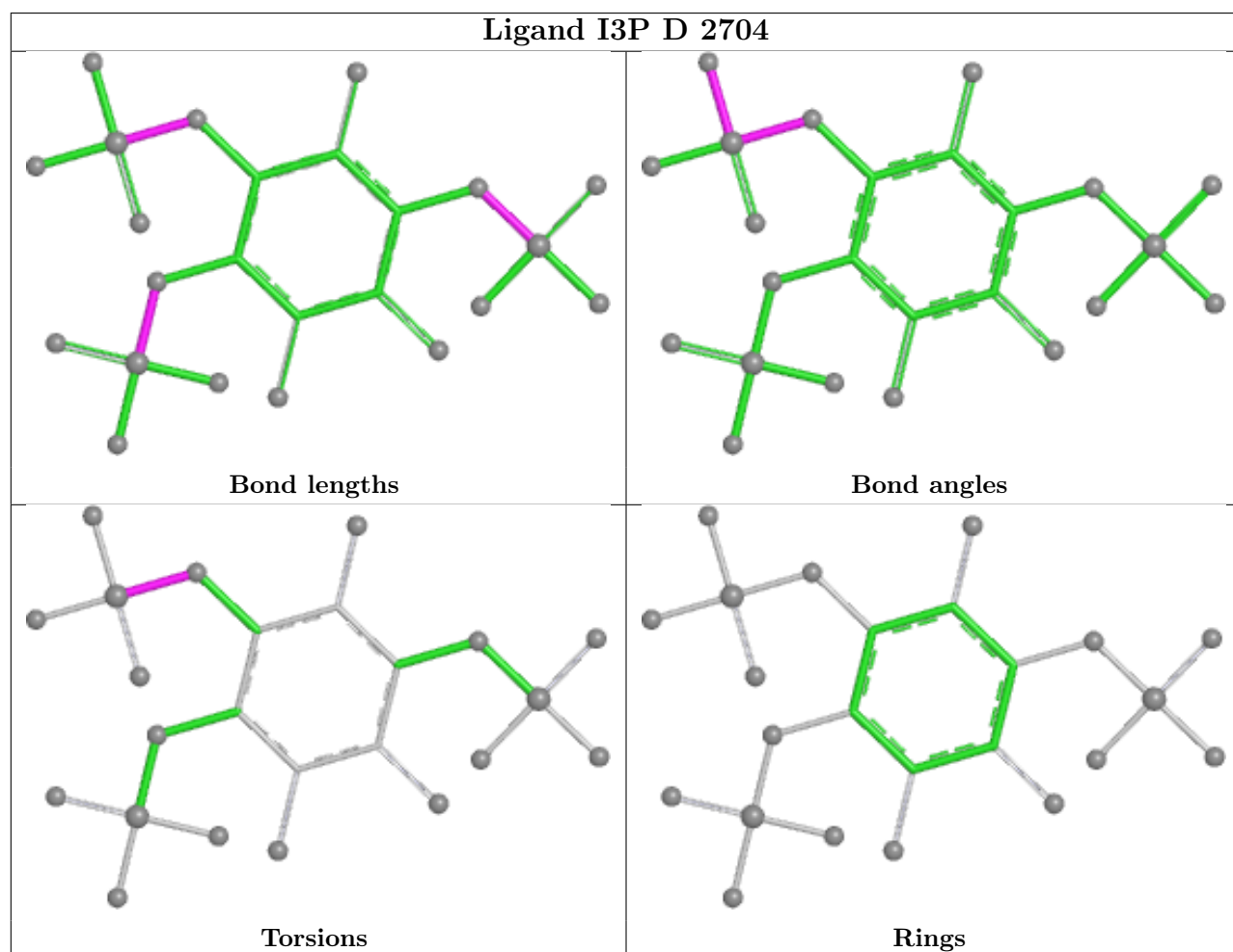
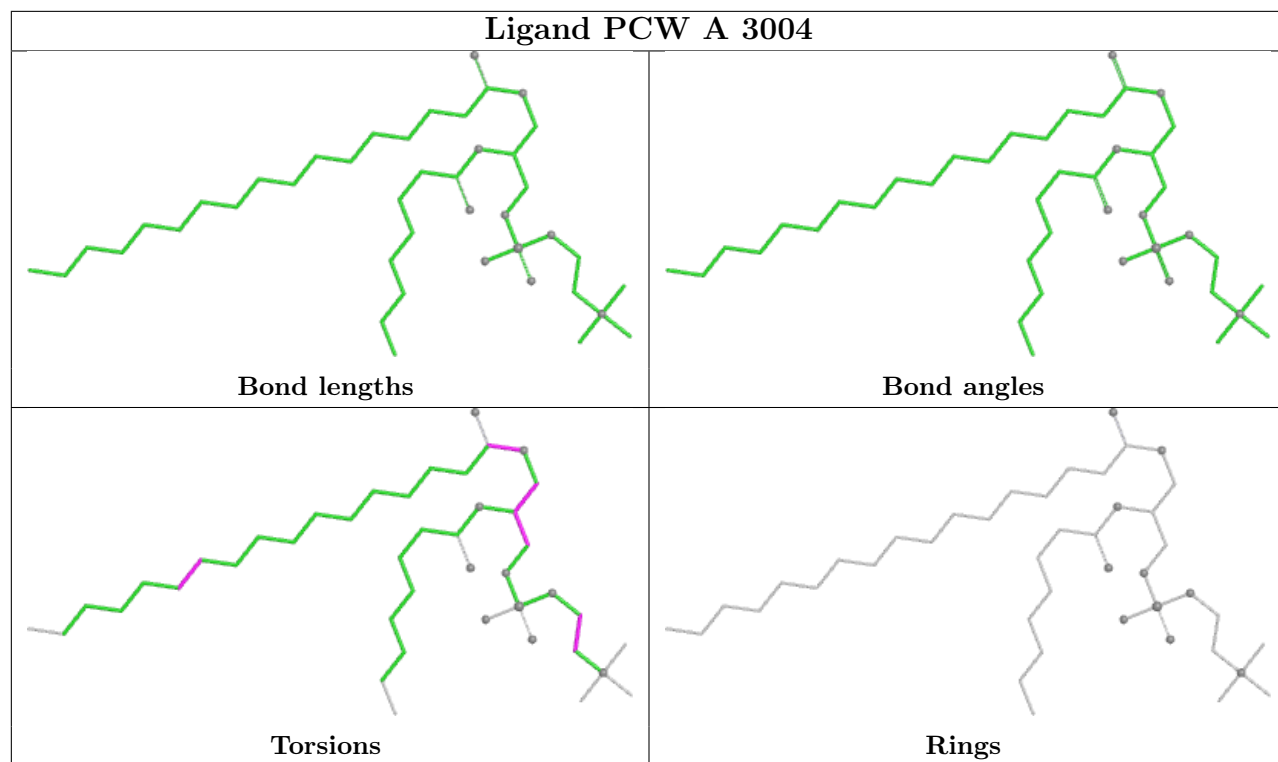


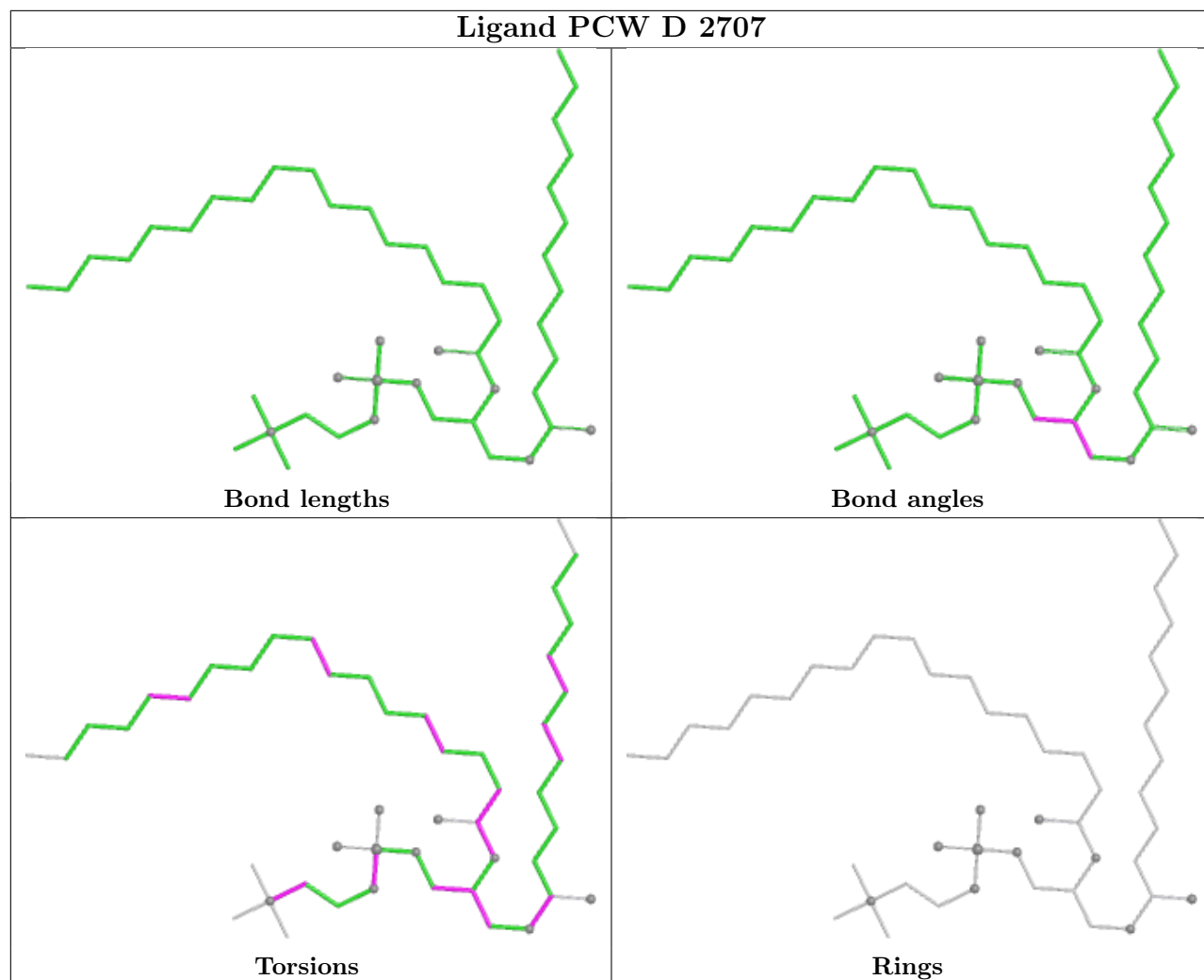


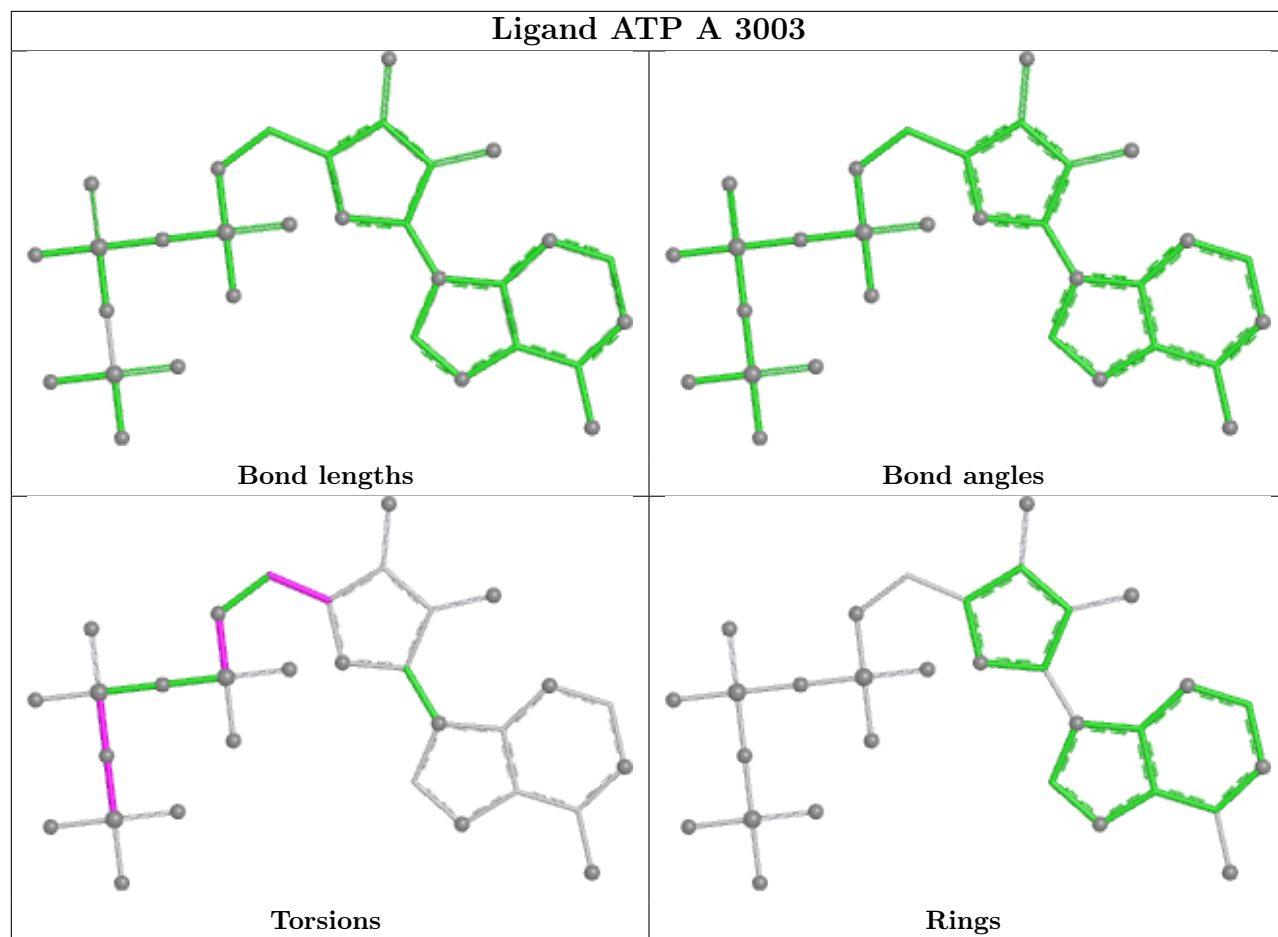












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

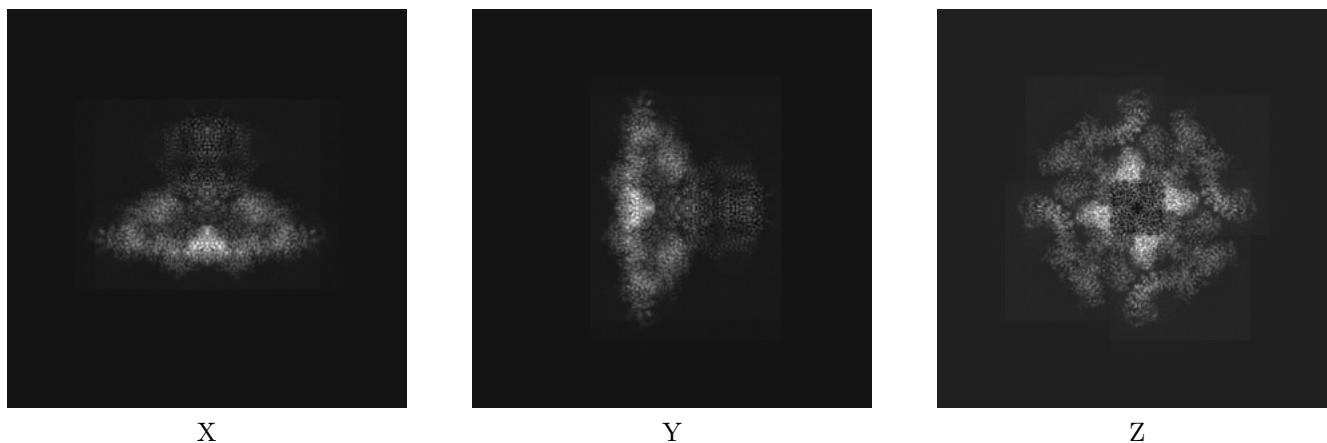
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41323. 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](#)

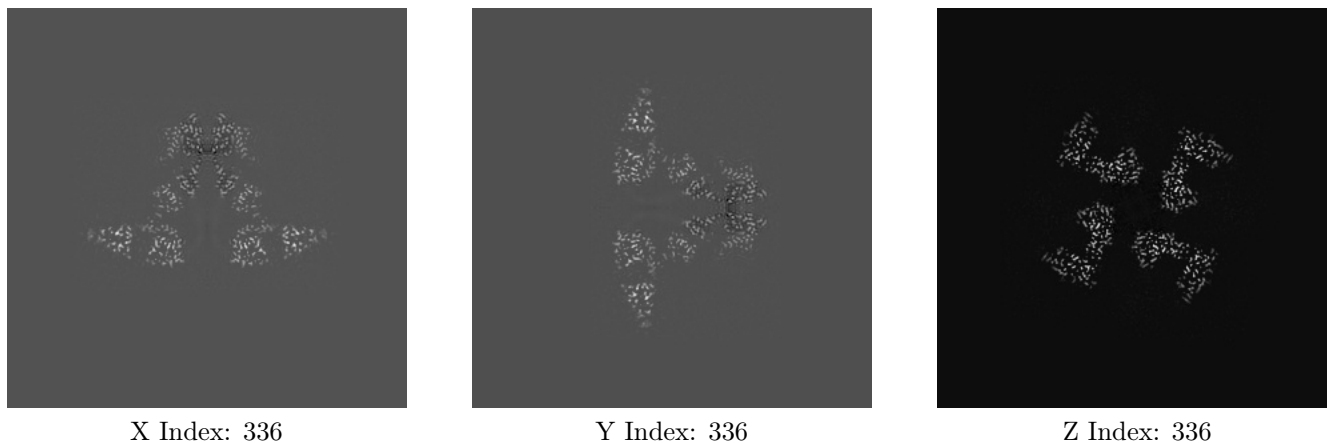
6.1.1 Primary map



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

6.2 Central slices [i](#)

6.2.1 Primary map



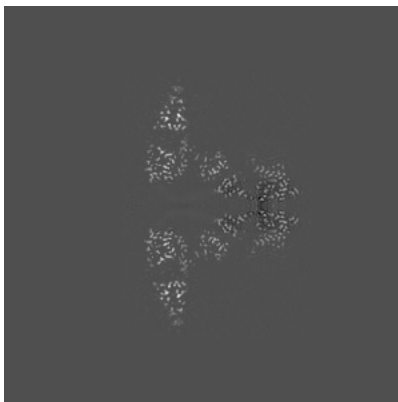
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 336



Y Index: 336

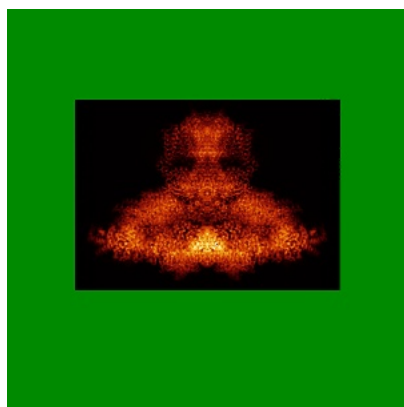


Z Index: 277

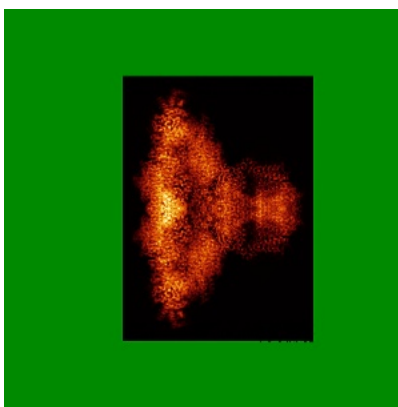
The images above show the largest variance slices of the map in three orthogonal directions.

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

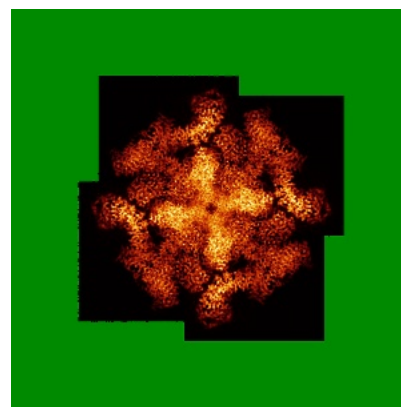
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

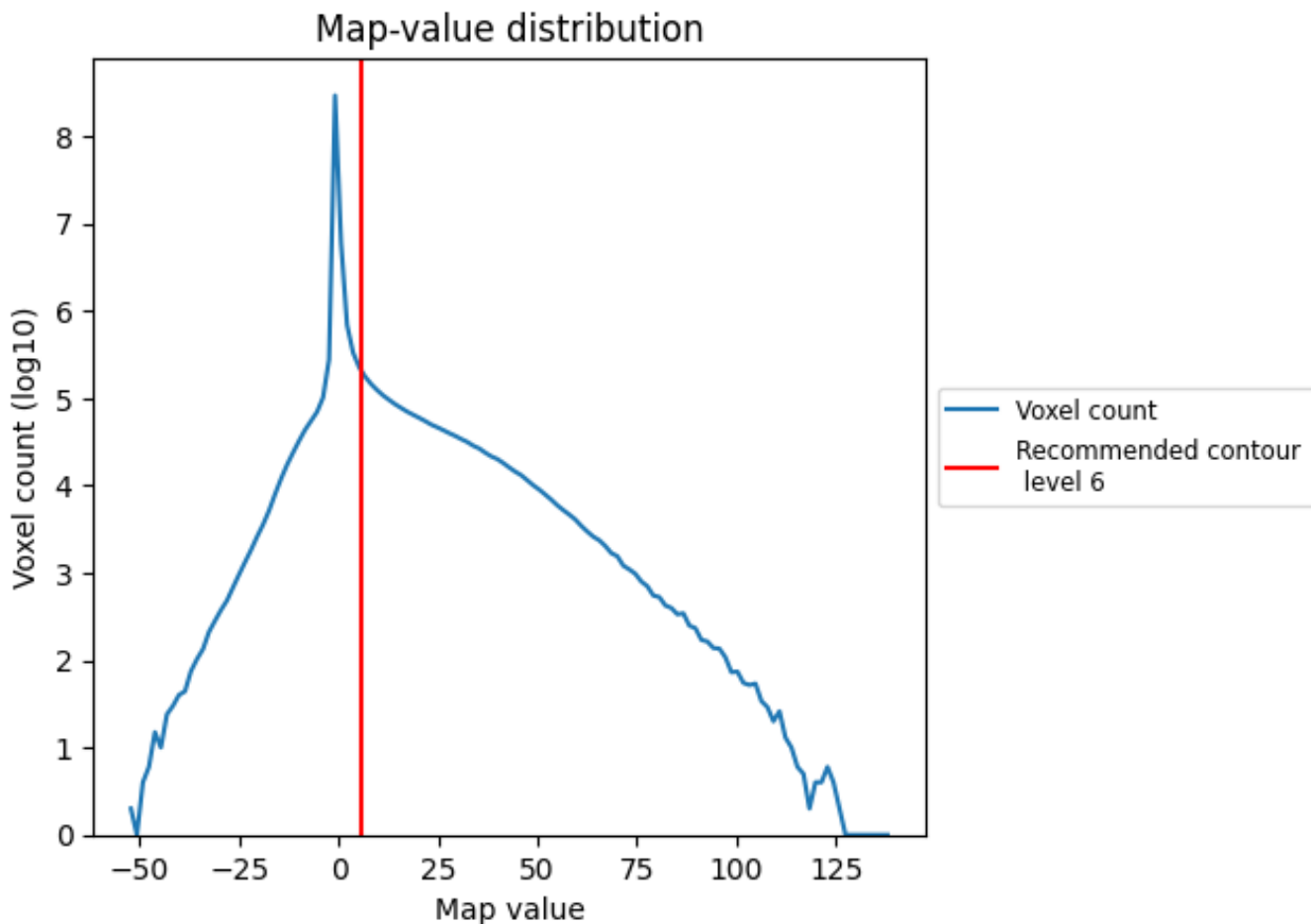
6.6 Mask visualisation

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

7 Map analysis [i](#)

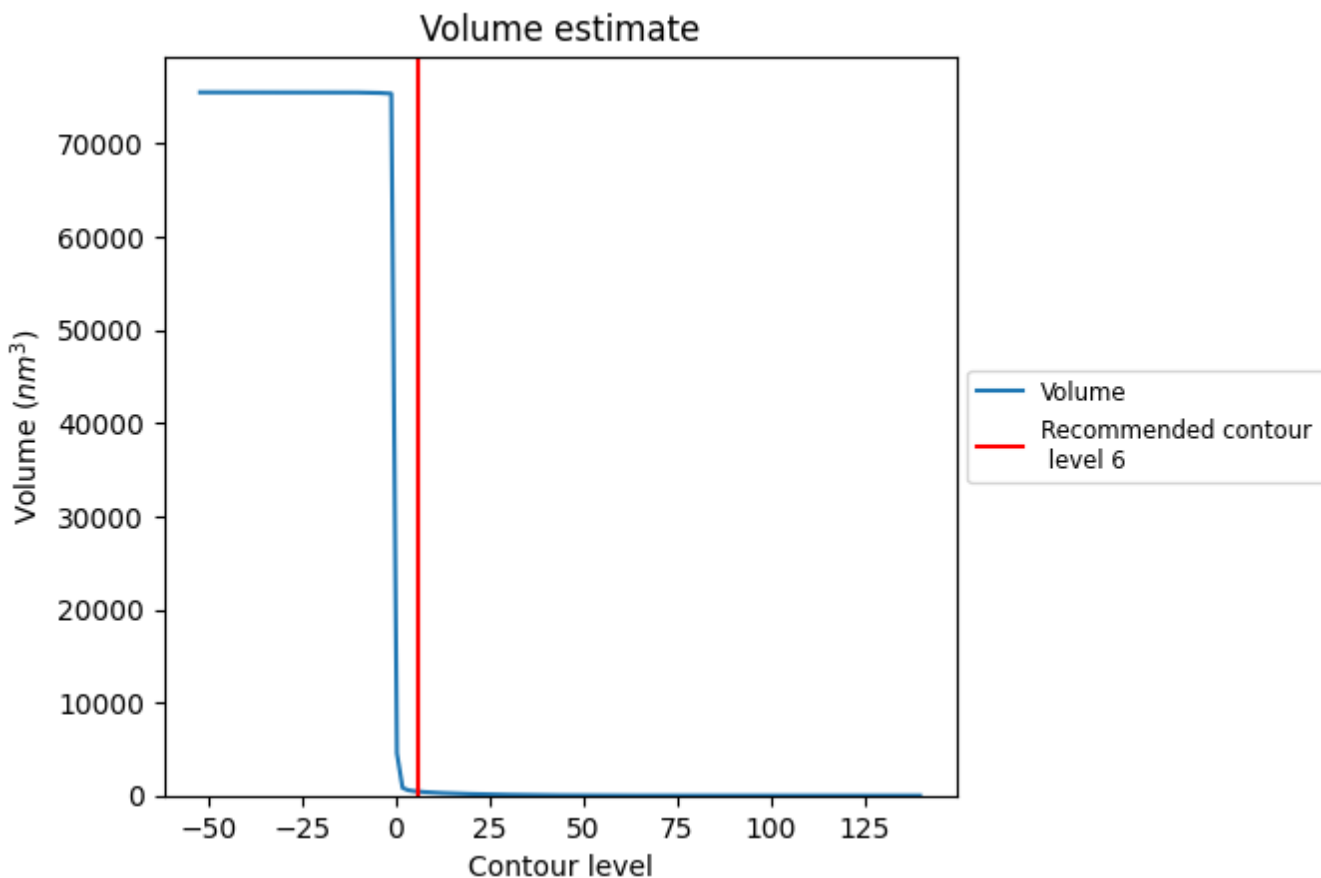
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

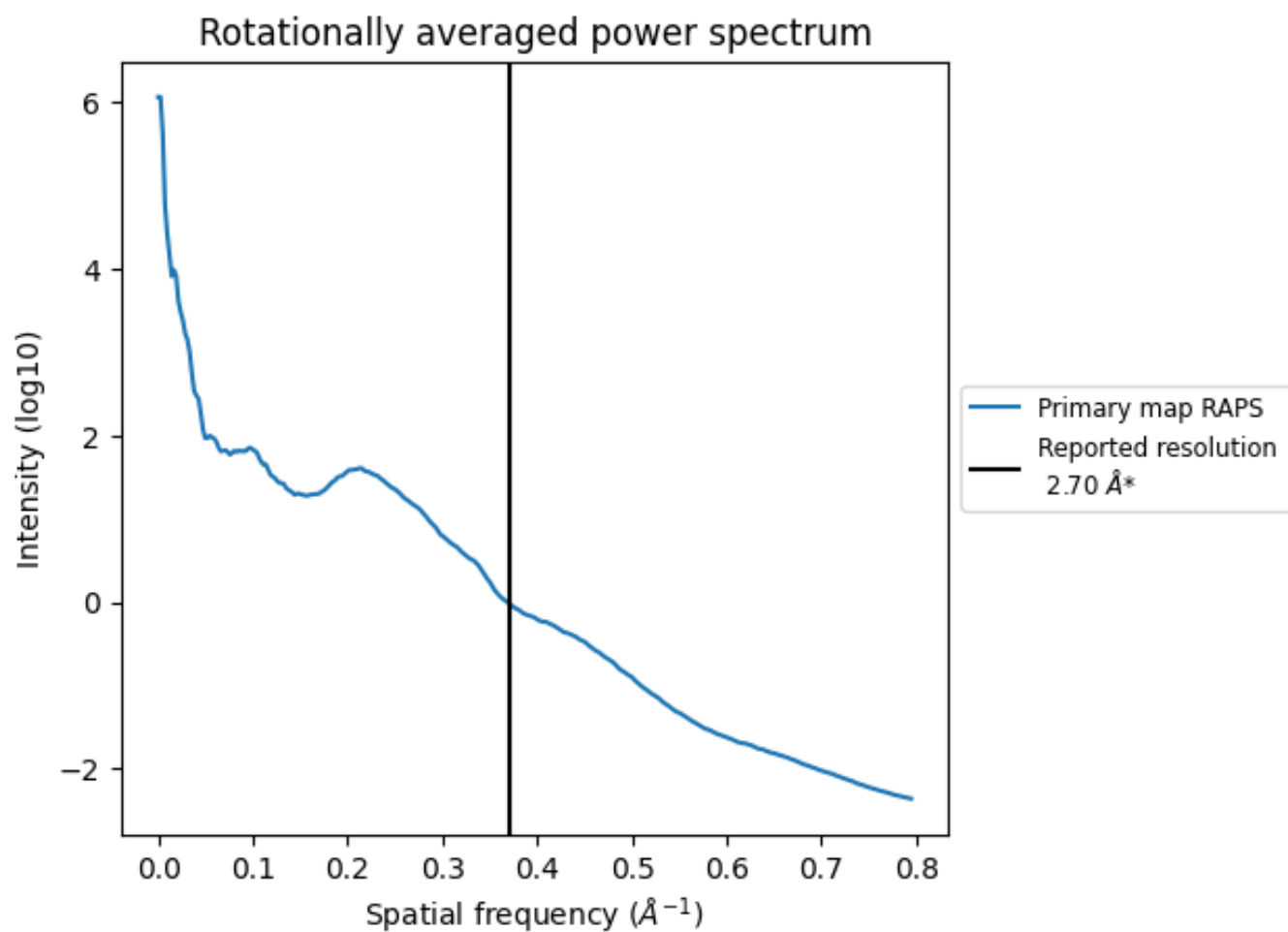
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 429 nm³; this corresponds to an approximate mass of 388 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 0.370 Å⁻¹

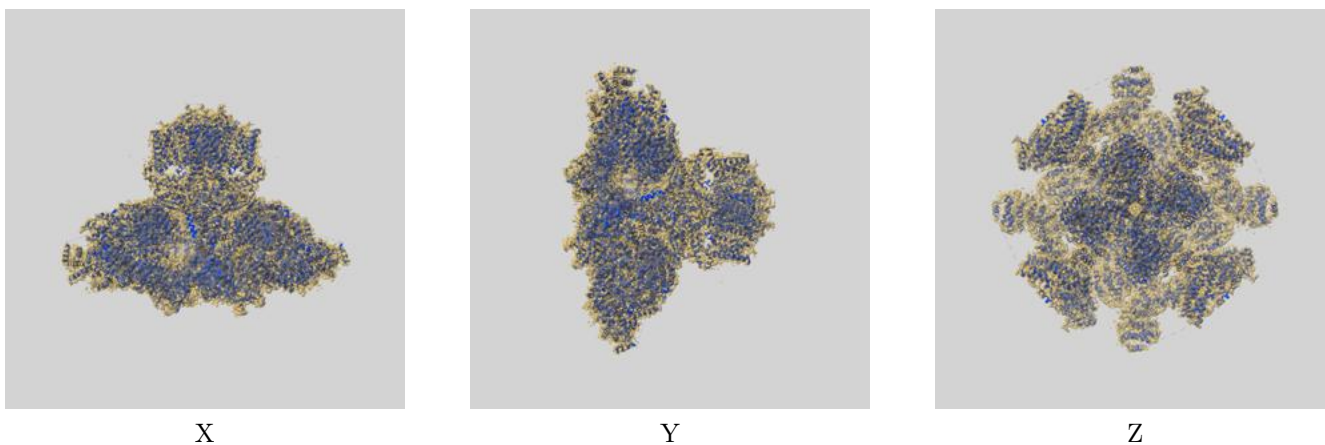
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

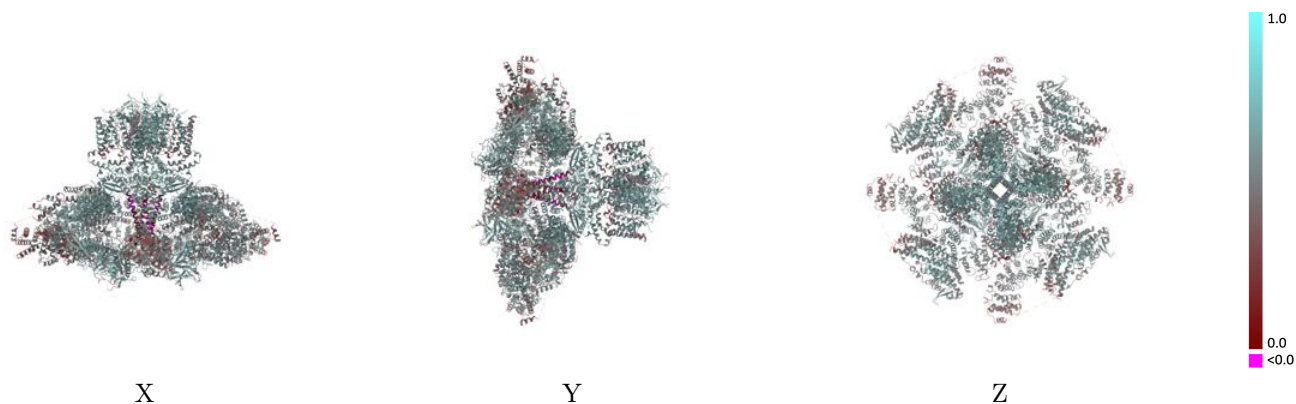
This section contains information regarding the fit between EMDB map EMD-41323 and PDB model 8TK8. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



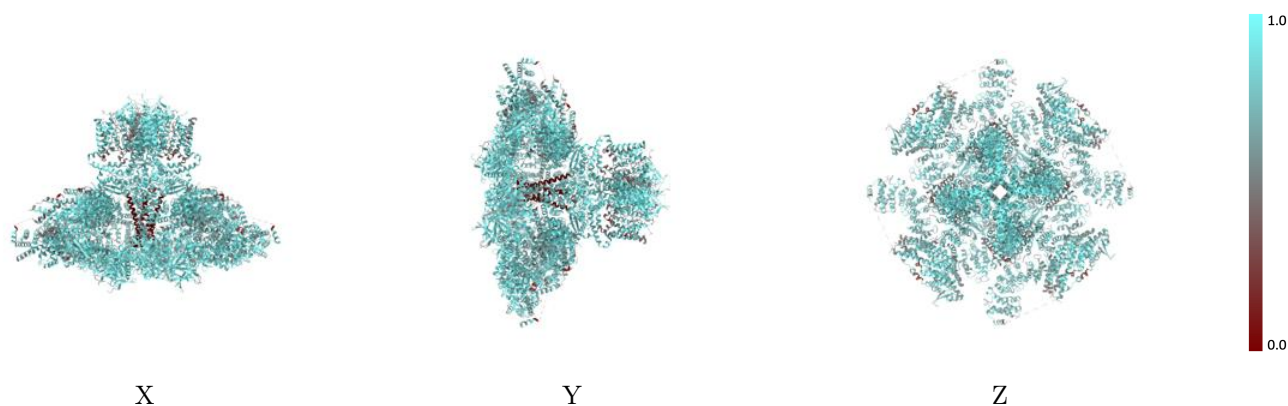
The images above show the 3D surface view of the map at the recommended contour level 6.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



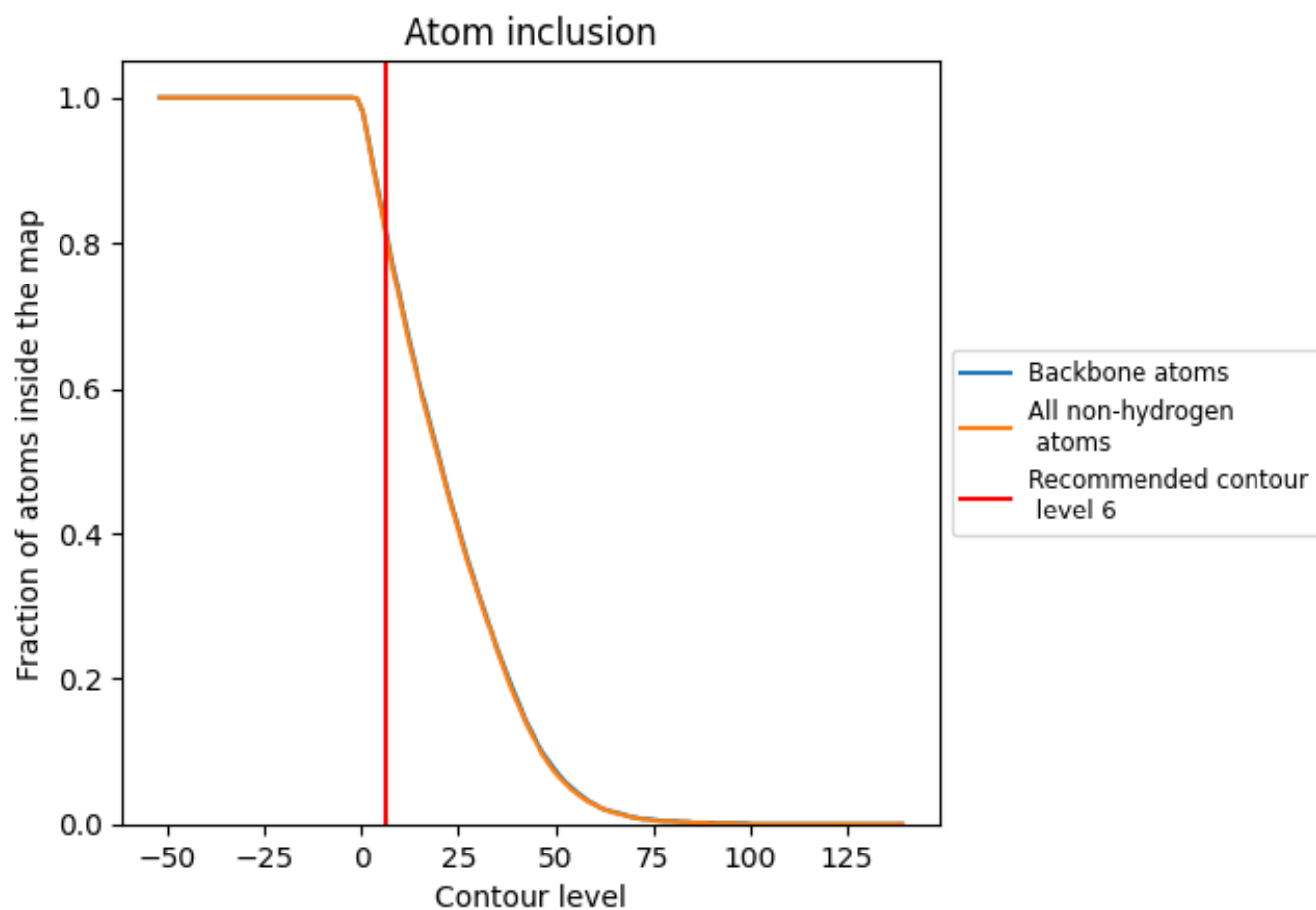
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 82% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8160	 0.5240
A	 0.8220	 0.5230
B	 0.8170	 0.5220
C	 0.8230	 0.5290
D	 0.8200	 0.5240

