



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 10:30 AM UTC

PDB ID : 2W6D / pdb_00002w6d
EMDB ID : EMD-1589
Title : BACTERIAL DYNAMIN-LIKE PROTEIN LIPID TUBE BOUND
Authors : Low, H.H.; Sachse, C.; Amos, L.A.; Lowe, J.
Deposited on : 2008-12-18
Resolution : 9.00 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

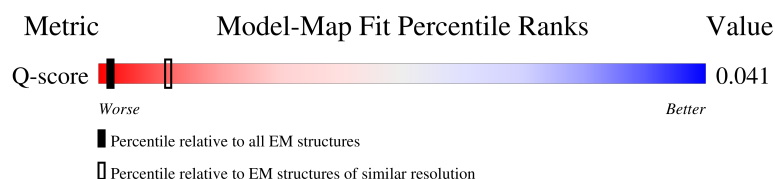
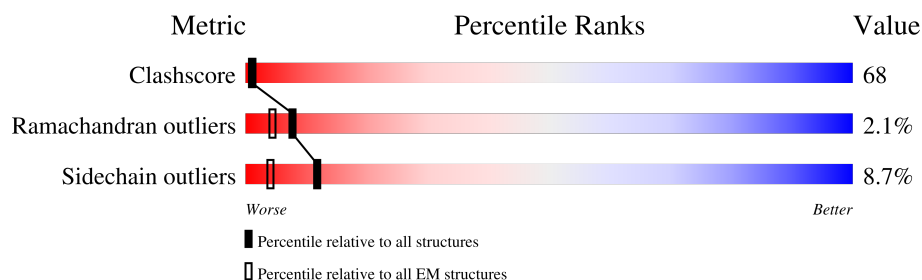
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 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	257 (8.50 - 9.50)

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	695	41% 44% 45% 8% .
1	B	695	41% 45% 45% 8% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CPL	A	1697	-	-	X	-
2	CPL	A	1700	-	-	X	-
2	CPL	A	1701	-	-	X	-
2	CPL	A	1702	-	-	X	-
2	CPL	A	1703	-	-	X	-
2	CPL	A	1705	-	-	X	-
2	CPL	A	1707	-	-	X	-
2	CPL	A	1708	-	-	X	-
2	CPL	A	1709	-	-	X	-
2	CPL	A	1710	-	-	X	-
2	CPL	A	1718	-	-	X	-
2	CPL	A	3097	-	-	X	-
2	CPL	B	1696	-	-	X	-
2	CPL	B	1697	-	-	X	-
2	CPL	B	1700	-	-	X	-
2	CPL	B	1701	-	-	X	-
2	CPL	B	1703	-	-	X	-
2	CPL	B	1704	-	-	X	-
2	CPL	B	1705	-	-	X	-
2	CPL	B	1710	-	-	X	-
3	GDP	A	1696	-	-	X	-
3	GDP	B	1706	-	-	X	-

2 Entry composition [i](#)

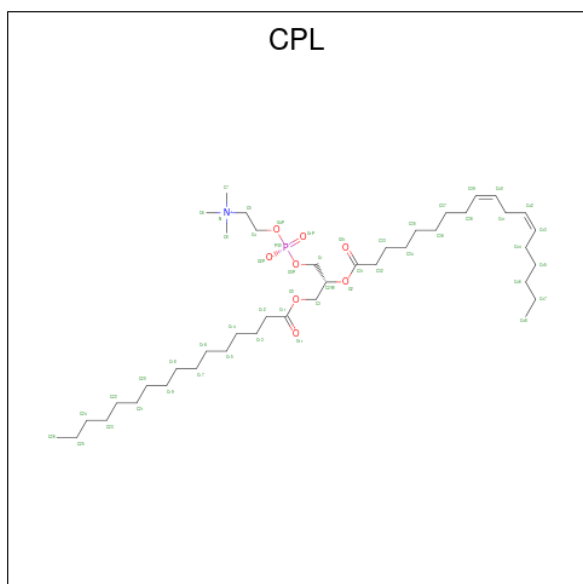
There are 3 unique types of molecules in this entry. The entry contains 13202 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DYNAMIN FAMILY PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	680	Total	C	N	O	S	0	0
			5429	3423	952	1043	11		
1	B	680	Total	C	N	O	S	0	0
			5429	3423	952	1043	11		

- Molecule 2 is 1-PALMITOYL-2-LINOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: CPL) (formula: $C_{42}H_{80}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	

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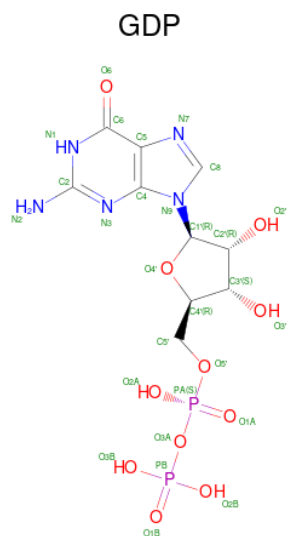
Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

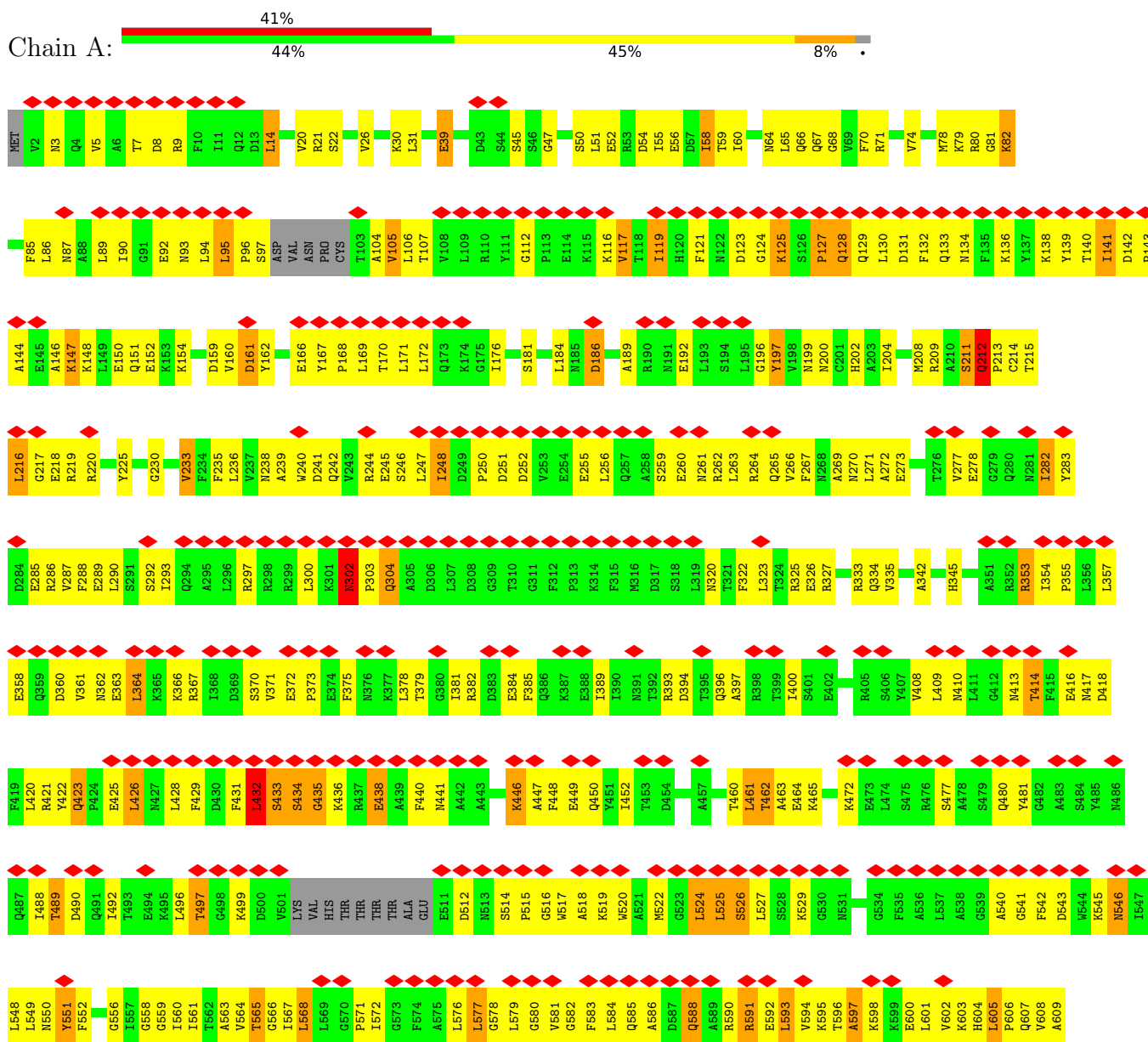


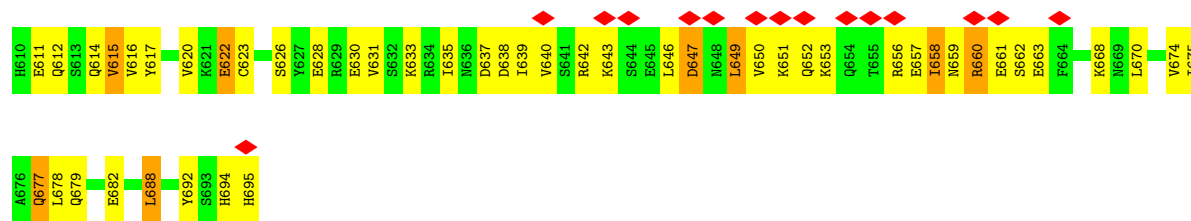
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total 28	C 10	N 5	O 11	P 2	0
3	B	1	Total 28	C 10	N 5	O 11	P 2	0

3 Residue-property plots

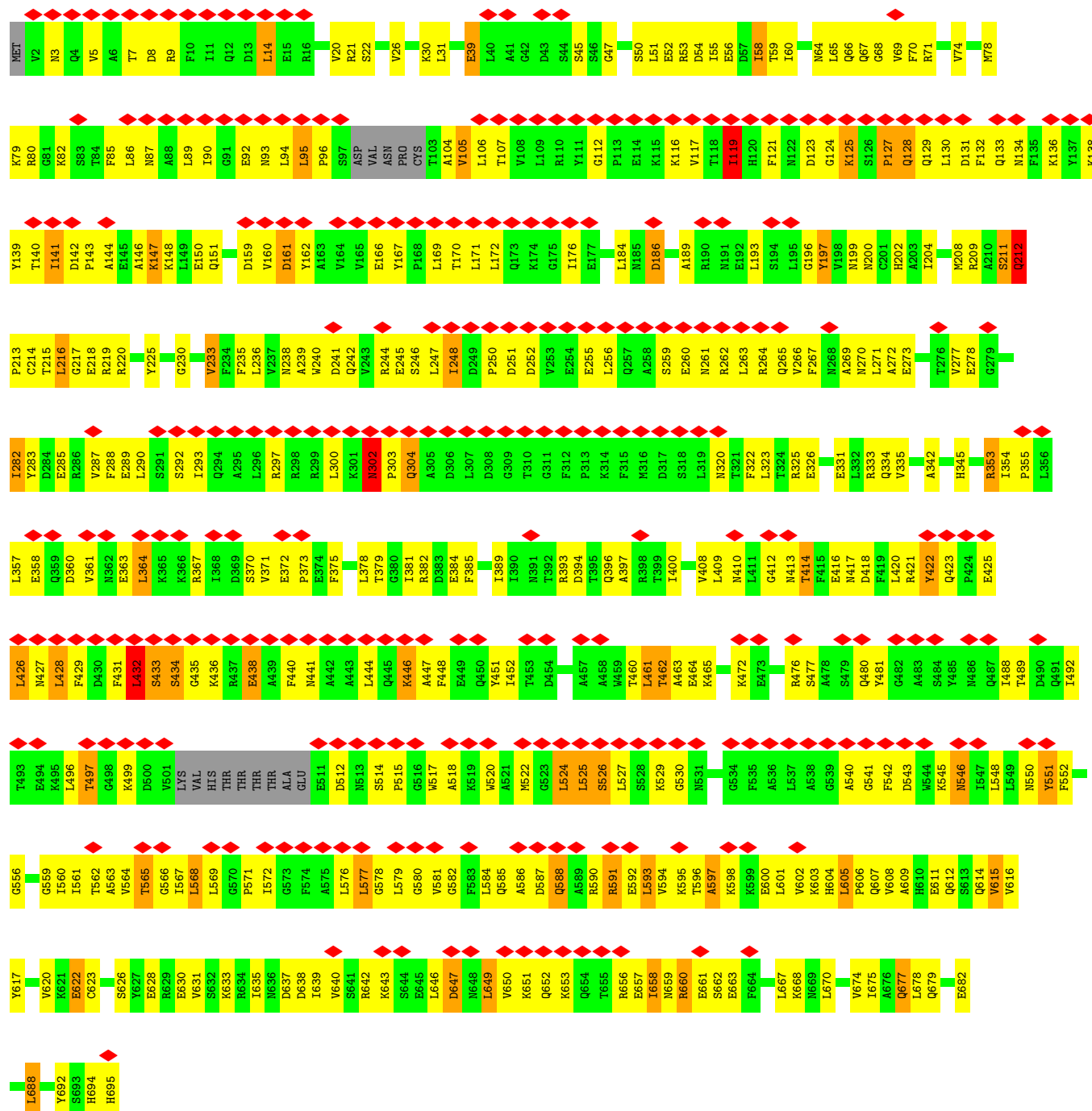
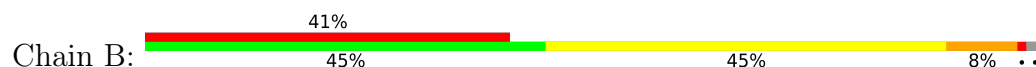
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DYNAMIN FAMILY PROTEIN





• Molecule 1: DYNAMIN FAMILY PROTEIN



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	59000	Depositor
Image detector	GENERIC FILM	Depositor
Maximum map value	4.644	Depositor
Minimum map value	-3.495	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.001	Depositor
Recommended contour level	1.47	Depositor
Map size (Å)	671.213, 671.213, 671.213	wwPDB
Map dimensions	330, 330, 81	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	2.03398, 2.03398, 2.03398	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: CPL, GDP

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	0.49	0/5509	0.96	26/7428 (0.4%)
1	B	0.49	0/5509	0.96	27/7428 (0.4%)
All	All	0.49	0/11018	0.96	53/14856 (0.4%)

There are no bond length outliers.

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	216	LEU	N-CA-C	-7.87	102.78	111.36
1	B	216	LEU	N-CA-C	-7.81	102.84	111.36
1	A	546	ASN	N-CA-C	-7.10	104.43	113.23
1	B	546	ASN	N-CA-C	-7.08	104.46	113.23
1	B	615	VAL	N-CA-C	-7.05	104.11	111.58

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	5429	0	5411	998	0
1	B	5429	0	5407	986	0
2	A	1352	0	2047	454	0
2	B	936	0	1408	368	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	28	0	9	10	0
3	B	28	0	9	11	0
All	All	13202	0	14291	1863	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 68.

The worst 5 of 1863 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:A:446:LYS:CD	2:A:1708:CPL:HC72	1.26	1.65
1:B:585:GLN:CG	2:B:1696:CPL:H261	1.14	1.61
1:A:432:LEU:CB	2:A:1709:CPL:H322	1.14	1.61
1:B:581:VAL:CA	2:B:1699:CPL:H461	1.16	1.61
1:A:579:LEU:CD2	2:A:1705:CPL:H462	1.26	1.60

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	666/695 (96%)	571 (86%)	81 (12%)	14 (2%)	5	30
1	B	666/695 (96%)	570 (86%)	82 (12%)	14 (2%)	5	30
All	All	1332/1390 (96%)	1141 (86%)	163 (12%)	28 (2%)	8	30

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	128	GLN
1	A	197	TYR

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Mol	Chain	Res	Type
1	B	128	GLN
1	B	197	TYR
1	A	125	LYS

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	587/601 (98%)	536 (91%)	51 (9%)	9	29
1	B	587/601 (98%)	536 (91%)	51 (9%)	9	29
All	All	1174/1202 (98%)	1072 (91%)	102 (9%)	12	29

5 of 102 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	89	LEU
1	B	364	LEU
1	B	670	LEU
1	B	127	PRO
1	B	211	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	671	GLN
1	B	618	ASN
1	B	151	GLN
1	B	607	GLN
1	B	441	ASN

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](#)

46 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	$\# Z > 2$
2	CPL	A	3077	-	51,51,51	0.84	2 (3%)	57,59,59	0.89	3 (5%)
2	CPL	A	1707	-	51,51,51	0.86	4 (7%)	57,59,59	0.85	2 (3%)
2	CPL	B	1713	-	51,51,51	0.90	3 (5%)	57,59,59	0.92	2 (3%)
2	CPL	B	1711	-	51,51,51	0.86	3 (5%)	57,59,59	0.78	1 (1%)
2	CPL	B	1712	-	51,51,51	0.85	3 (5%)	57,59,59	0.99	2 (3%)
2	CPL	A	1715	-	51,51,51	0.86	3 (5%)	57,59,59	0.75	1 (1%)
2	CPL	A	1718	-	51,51,51	0.86	3 (5%)	57,59,59	0.78	1 (1%)
2	CPL	A	3097	-	51,51,51	0.84	3 (5%)	57,59,59	0.89	3 (5%)
2	CPL	B	1699	-	51,51,51	0.90	3 (5%)	57,59,59	0.90	2 (3%)
2	CPL	A	1703	-	51,51,51	0.86	3 (5%)	57,59,59	0.99	2 (3%)
2	CPL	B	1701	-	51,51,51	0.86	3 (5%)	57,59,59	0.98	2 (3%)
2	CPL	B	1708	-	51,51,51	0.90	3 (5%)	57,59,59	0.89	2 (3%)
3	GDP	B	1706	-	29,30,30	1.00	1 (3%)	45,47,47	1.79	12 (26%)
2	CPL	A	1701	-	51,51,51	0.88	3 (5%)	57,59,59	1.01	2 (3%)
2	CPL	A	1709	-	51,51,51	0.87	3 (5%)	57,59,59	1.03	2 (3%)
2	CPL	A	3181	-	51,51,51	0.88	4 (7%)	57,59,59	1.02	2 (3%)
2	CPL	A	1698	-	51,51,51	0.86	3 (5%)	57,59,59	0.85	2 (3%)
2	CPL	B	1700	-	51,51,51	0.90	3 (5%)	57,59,59	0.90	2 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CPL	B	1698	-	51,51,51	0.86	3 (5%)	57,59,59	0.99	2 (3%)
2	CPL	B	1703	-	51,51,51	0.88	4 (7%)	57,59,59	1.01	2 (3%)
2	CPL	B	1707	-	51,51,51	0.88	3 (5%)	57,59,59	1.01	2 (3%)
2	CPL	A	1706	-	51,51,51	0.90	3 (5%)	57,59,59	0.90	2 (3%)
2	CPL	A	1697	-	51,51,51	0.86	3 (5%)	57,59,59	0.78	1 (1%)
2	CPL	B	1709	-	51,51,51	0.87	3 (5%)	57,59,59	1.03	2 (3%)
2	CPL	B	1702	-	51,51,51	0.86	3 (5%)	57,59,59	0.78	1 (1%)
2	CPL	A	1702	-	51,51,51	0.86	3 (5%)	57,59,59	0.99	2 (3%)
2	CPL	A	1716	-	51,51,51	0.88	4 (7%)	57,59,59	1.02	2 (3%)
2	CPL	A	1711	-	51,51,51	0.86	3 (5%)	57,59,59	0.78	1 (1%)
2	CPL	A	1712	-	51,51,51	0.90	3 (5%)	57,59,59	0.89	2 (3%)
2	CPL	A	1704	-	51,51,51	0.88	3 (5%)	57,59,59	1.01	2 (3%)
2	CPL	B	1697	-	51,51,51	0.90	3 (5%)	57,59,59	0.90	2 (3%)
2	CPL	A	1705	-	51,51,51	0.88	3 (5%)	57,59,59	1.01	2 (3%)
2	CPL	A	1699	-	51,51,51	0.85	3 (5%)	57,59,59	0.84	2 (3%)
2	CPL	A	1710	-	51,51,51	0.86	3 (5%)	57,59,59	0.99	2 (3%)
2	CPL	A	1708	-	51,51,51	0.86	3 (5%)	57,59,59	0.99	2 (3%)
2	CPL	A	1700	-	51,51,51	0.90	3 (5%)	57,59,59	0.91	2 (3%)
2	CPL	B	1705	-	51,51,51	0.86	3 (5%)	57,59,59	0.86	2 (3%)
2	CPL	B	1714	-	51,51,51	0.86	3 (5%)	57,59,59	0.77	1 (1%)
2	CPL	A	1713	-	51,51,51	0.90	3 (5%)	57,59,59	0.92	2 (3%)
2	CPL	A	1714	-	51,51,51	0.86	3 (5%)	57,59,59	0.85	1 (1%)
2	CPL	B	1704	-	51,51,51	0.89	4 (7%)	57,59,59	0.90	2 (3%)
2	CPL	B	1696	-	51,51,51	0.85	3 (5%)	57,59,59	0.98	2 (3%)
2	CPL	B	1710	-	51,51,51	0.85	3 (5%)	57,59,59	0.99	2 (3%)
3	GDP	A	1696	-	29,30,30	1.00	1 (3%)	45,47,47	1.78	12 (26%)
2	CPL	A	3094	-	51,51,51	0.90	3 (5%)	57,59,59	0.91	2 (3%)
2	CPL	A	1717	-	51,51,51	0.86	3 (5%)	57,59,59	0.99	2 (3%)

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
2	CPL	A	3077	-	-	13/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CPL	A	1707	-	-	11/55/55/55	-
2	CPL	B	1713	-	-	14/55/55/55	-
2	CPL	B	1711	-	-	11/55/55/55	-
2	CPL	B	1712	-	-	14/55/55/55	-
2	CPL	A	1715	-	-	11/55/55/55	-
2	CPL	A	1718	-	-	11/55/55/55	-
2	CPL	A	3097	-	-	12/55/55/55	-
2	CPL	B	1699	-	-	14/55/55/55	-
2	CPL	A	1703	-	-	14/55/55/55	-
2	CPL	B	1701	-	-	14/55/55/55	-
2	CPL	B	1708	-	-	15/55/55/55	-
3	GDP	B	1706	-	-	0/16/32/32	0/3/3/3
2	CPL	A	1701	-	-	11/55/55/55	-
2	CPL	A	1709	-	-	12/55/55/55	-
2	CPL	A	3181	-	-	12/55/55/55	-
2	CPL	A	1698	-	-	12/55/55/55	-
2	CPL	B	1700	-	-	15/55/55/55	-
2	CPL	B	1698	-	-	14/55/55/55	-
2	CPL	B	1703	-	-	11/55/55/55	-
2	CPL	B	1707	-	-	11/55/55/55	-
2	CPL	A	1706	-	-	15/55/55/55	-
2	CPL	A	1697	-	-	10/55/55/55	-
2	CPL	B	1709	-	-	12/55/55/55	-
2	CPL	B	1702	-	-	11/55/55/55	-
2	CPL	A	1702	-	-	14/55/55/55	-
2	CPL	A	1716	-	-	12/55/55/55	-
2	CPL	A	1711	-	-	11/55/55/55	-
2	CPL	A	1712	-	-	15/55/55/55	-
2	CPL	A	1704	-	-	11/55/55/55	-
2	CPL	B	1697	-	-	15/55/55/55	-
2	CPL	A	1705	-	-	11/55/55/55	-
2	CPL	A	1699	-	-	11/55/55/55	-
2	CPL	A	1710	-	-	14/55/55/55	-
2	CPL	A	1708	-	-	14/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CPL	A	1700	-	-	15/55/55/55	-
2	CPL	B	1705	-	-	11/55/55/55	-
2	CPL	B	1714	-	-	11/55/55/55	-
2	CPL	A	1713	-	-	14/55/55/55	-
2	CPL	A	1714	-	-	11/55/55/55	-
2	CPL	B	1704	-	-	14/55/55/55	-
2	CPL	B	1696	-	-	14/55/55/55	-
2	CPL	B	1710	-	-	14/55/55/55	-
3	GDP	A	1696	-	-	0/16/32/32	0/3/3/3
2	CPL	A	3094	-	-	15/55/55/55	-
2	CPL	A	1717	-	-	14/55/55/55	-

The worst 5 of 138 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1708	CPL	C43-C42	3.50	1.51	1.31
2	A	1715	CPL	C43-C42	3.48	1.51	1.31
2	A	3077	CPL	C43-C42	3.47	1.51	1.31
2	A	1712	CPL	C43-C42	3.47	1.51	1.31
2	A	3097	CPL	C43-C42	3.45	1.51	1.31

The worst 5 of 106 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1706	GDP	C2-N3-C4	5.45	121.69	112.30
3	A	1696	GDP	C2-N3-C4	5.41	121.63	112.30
3	B	1706	GDP	C5-C4-N3	-4.85	120.67	128.39
3	A	1696	GDP	C5-C4-N3	-4.82	120.72	128.39
2	A	1709	CPL	C2-O2-C31	4.26	127.99	117.80

There are no chirality outliers.

5 of 561 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	3077	CPL	C12-C11-O3-C3
2	A	3077	CPL	O11-C11-O3-C3
2	A	3077	CPL	C1-O3P-P-O1P
2	A	3077	CPL	C1-O3P-P-O2P
2	A	3077	CPL	C1-O3P-P-O4P

There are no ring outliers.

45 monomers are involved in 838 short contacts:

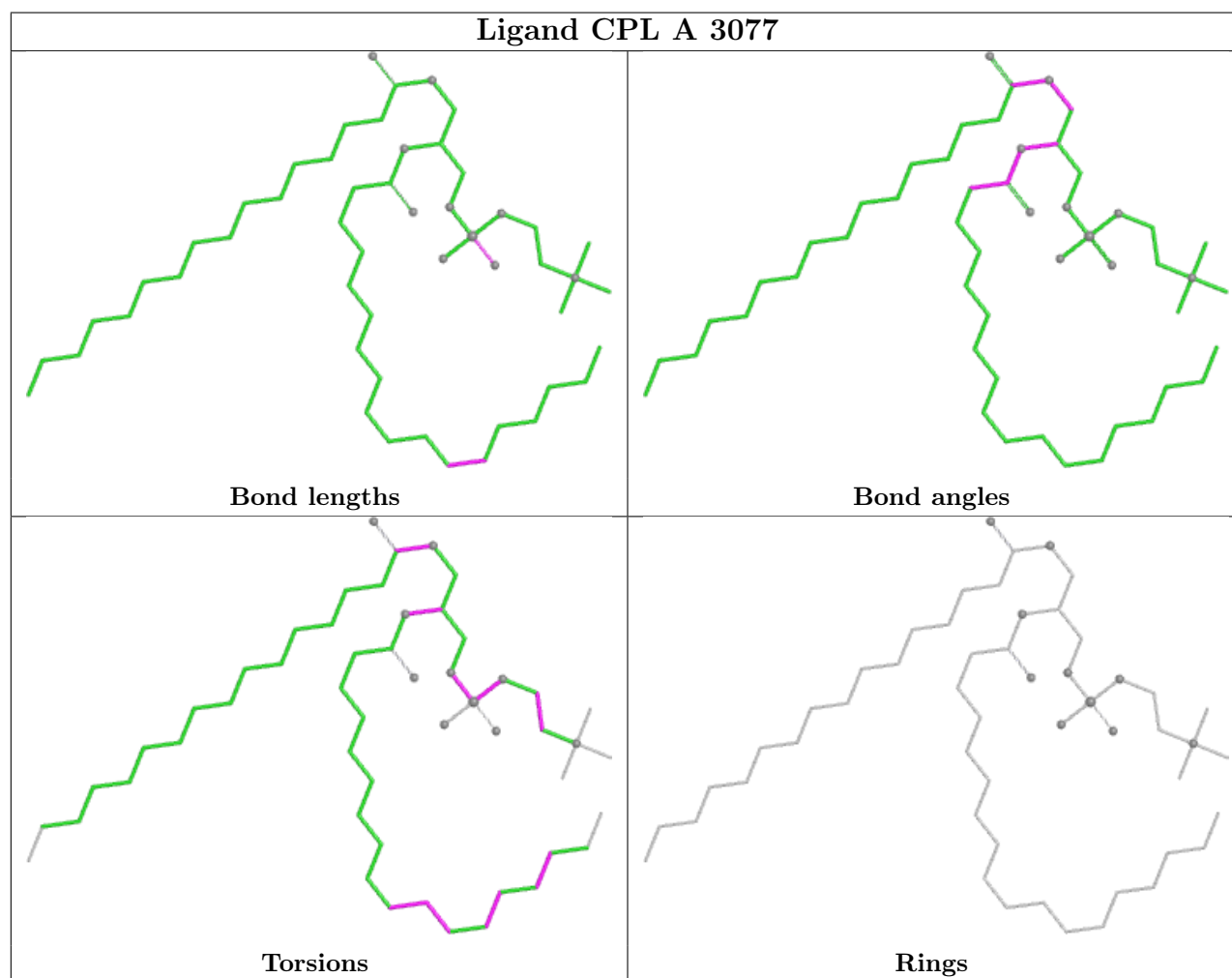
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3077	CPL	6	0
2	A	1707	CPL	48	0
2	B	1711	CPL	9	0
2	B	1712	CPL	18	0
2	A	1715	CPL	14	0
2	A	1718	CPL	24	0
2	A	3097	CPL	24	0
2	B	1699	CPL	18	0
2	A	1703	CPL	32	0
2	B	1701	CPL	36	0
2	B	1708	CPL	2	0
3	B	1706	GDP	11	0
2	A	1701	CPL	53	0
2	A	1709	CPL	53	0
2	A	3181	CPL	7	0
2	A	1698	CPL	15	0
2	B	1700	CPL	33	0
2	B	1698	CPL	7	0
2	B	1703	CPL	74	0
2	B	1707	CPL	7	0
2	A	1706	CPL	6	0
2	A	1697	CPL	37	0
2	B	1709	CPL	6	0
2	B	1702	CPL	7	0
2	A	1702	CPL	27	0
2	A	1716	CPL	7	0
2	A	1711	CPL	10	0
2	A	1712	CPL	4	0
2	A	1704	CPL	17	0
2	B	1697	CPL	84	0
2	A	1705	CPL	53	0
2	A	1699	CPL	14	0
2	A	1710	CPL	21	0
2	A	1708	CPL	60	0
2	A	1700	CPL	41	0
2	B	1705	CPL	42	0
2	B	1714	CPL	16	0
2	A	1713	CPL	4	0
2	A	1714	CPL	14	0
2	B	1704	CPL	27	0

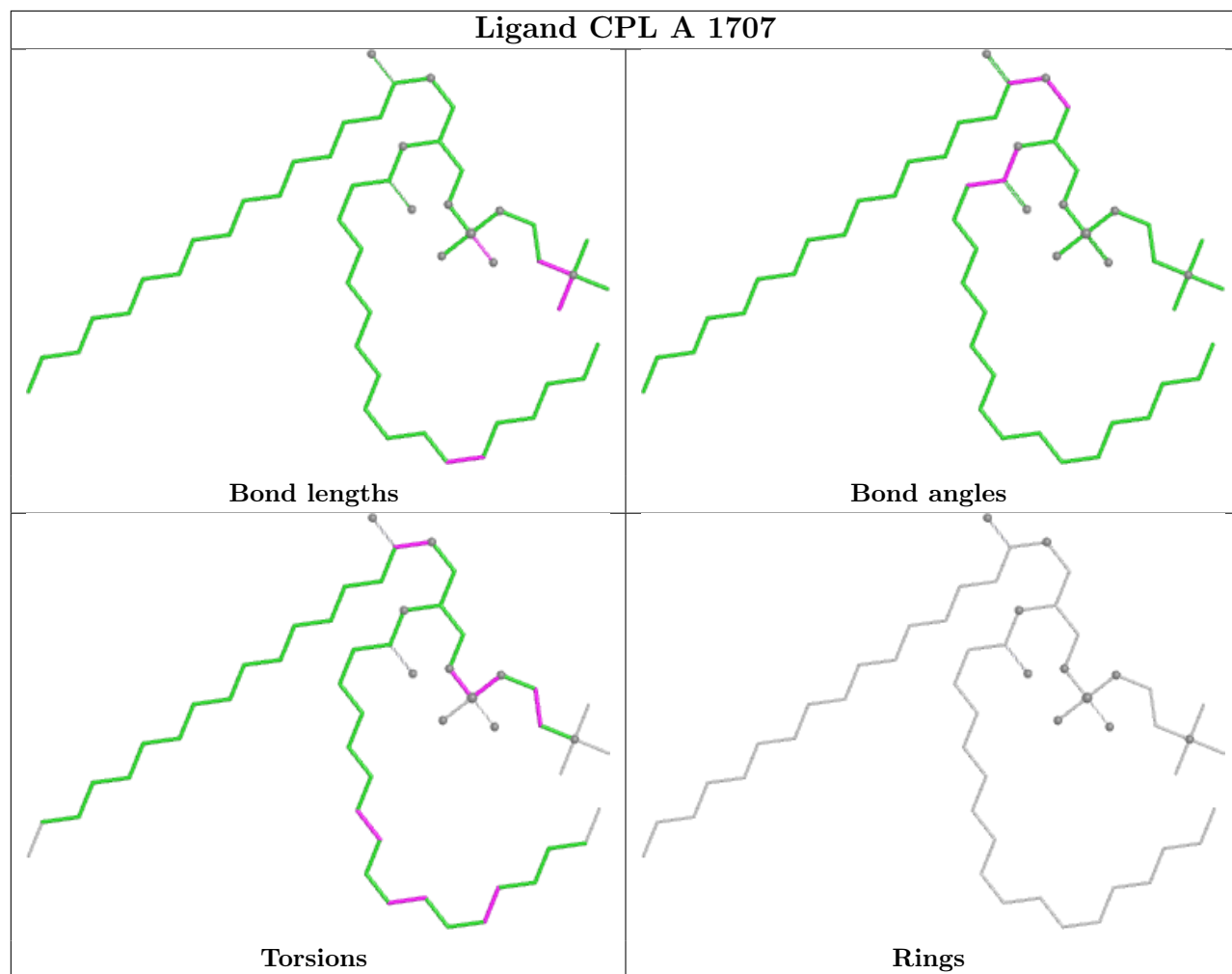
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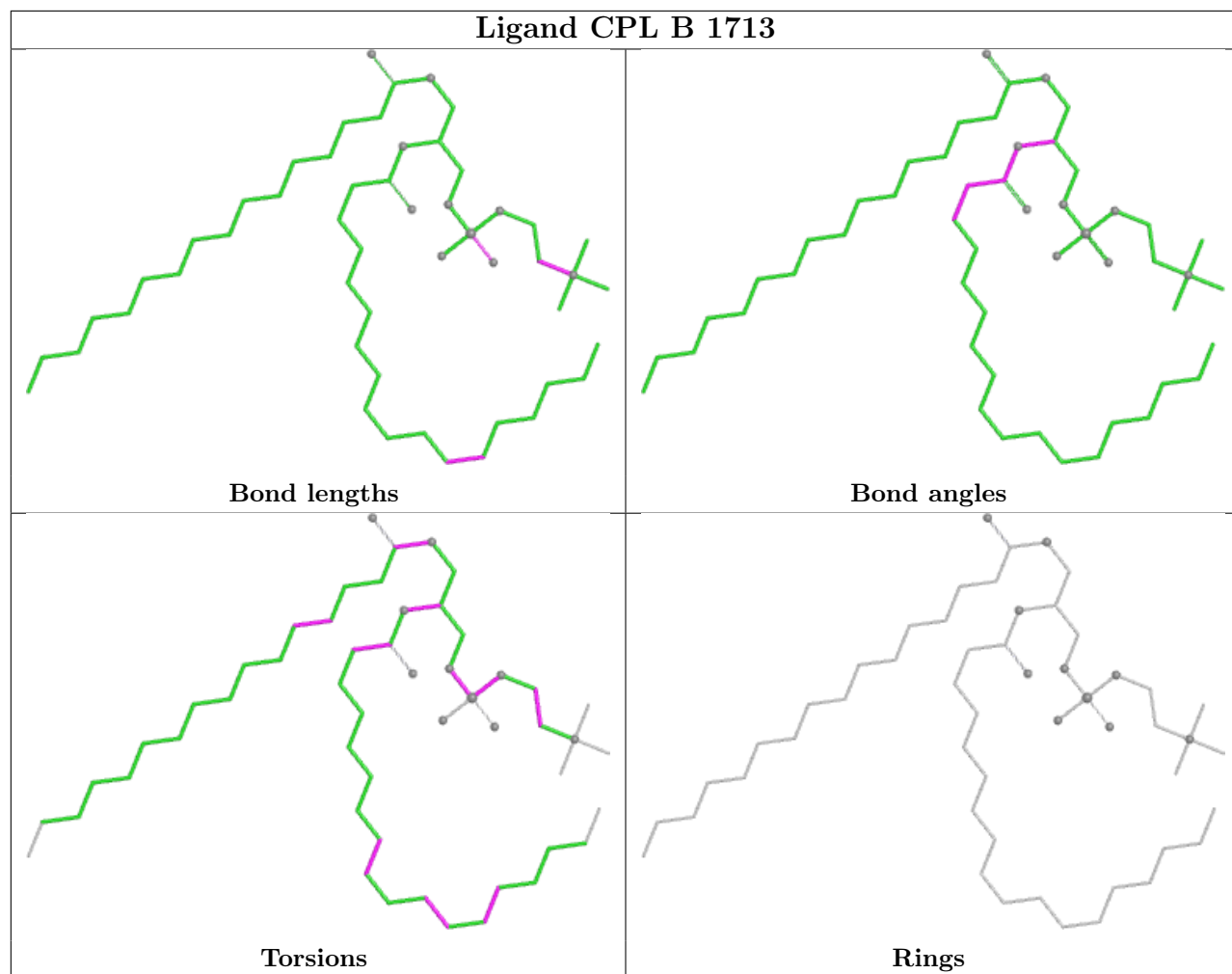
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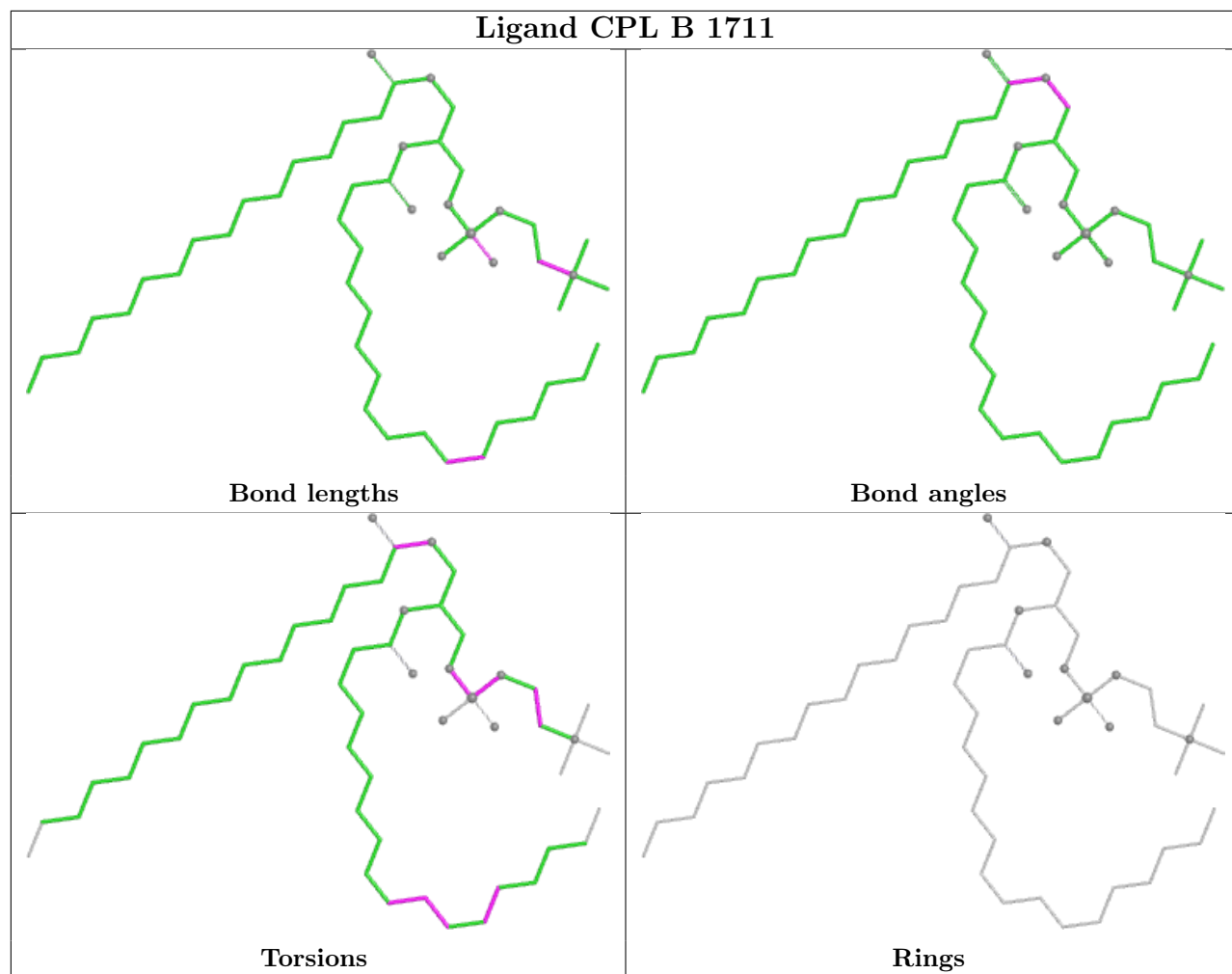
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1696	CPL	26	0
2	B	1710	CPL	26	0
3	A	1696	GDP	10	0
2	A	3094	CPL	7	0
2	A	1717	CPL	4	0

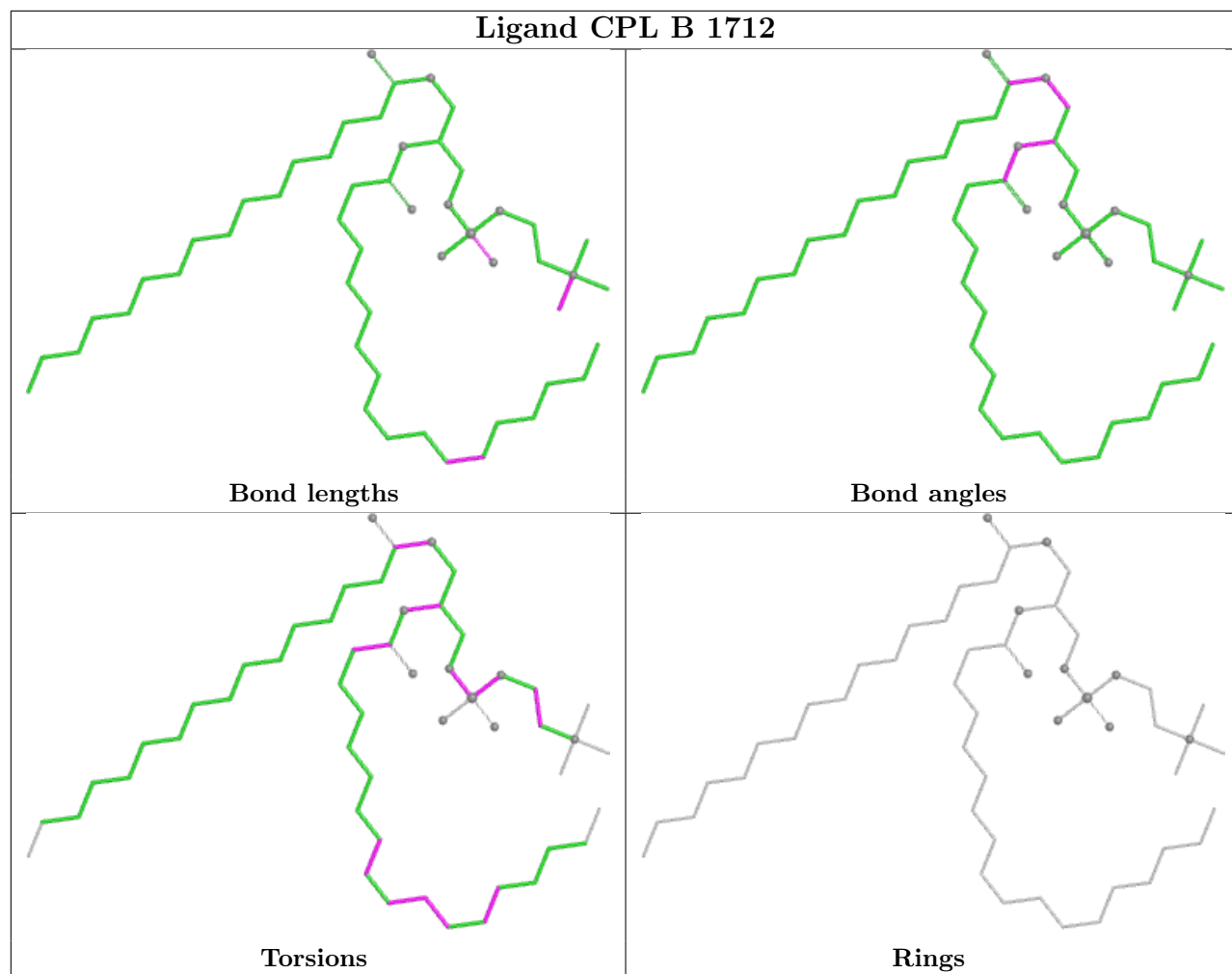
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

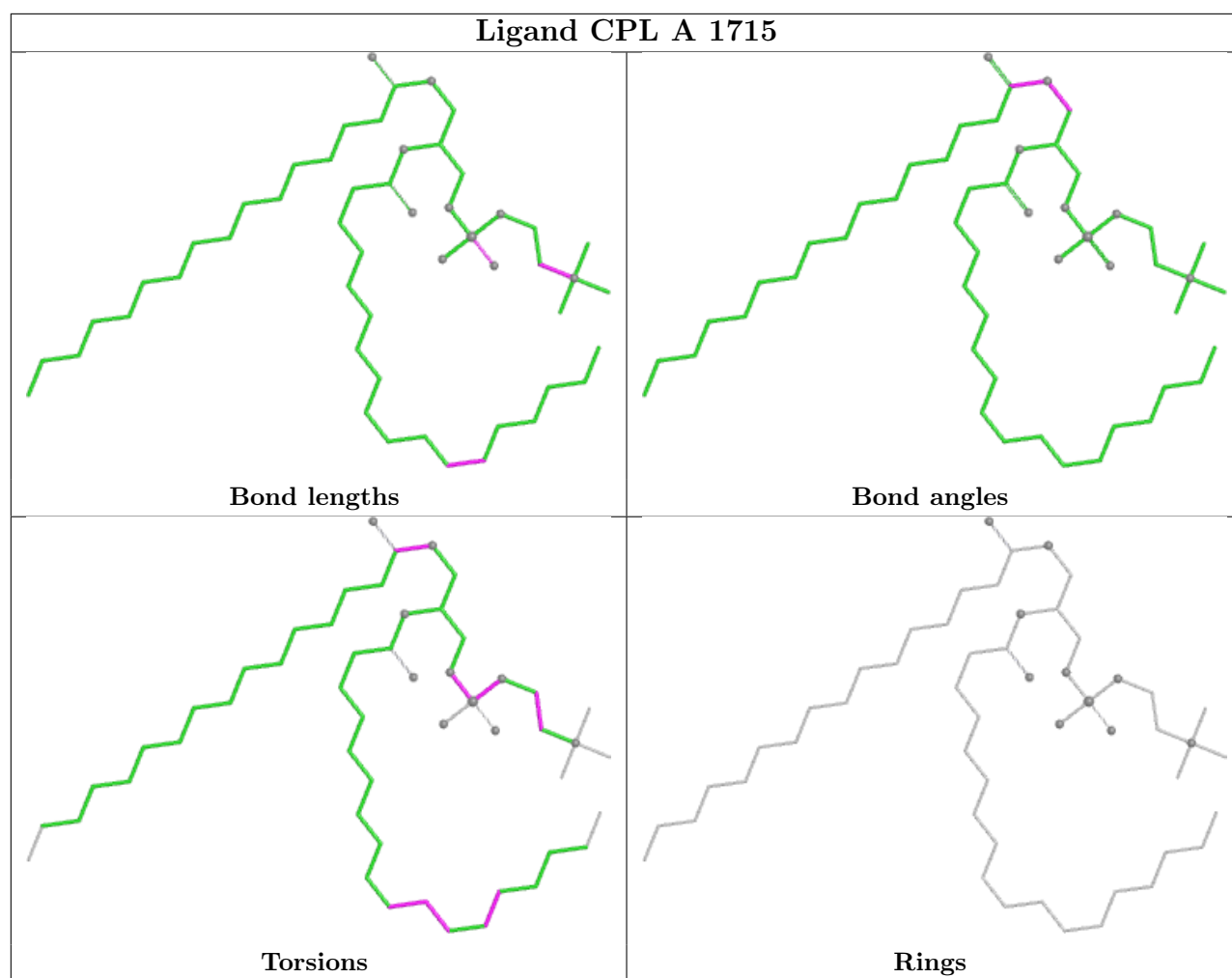


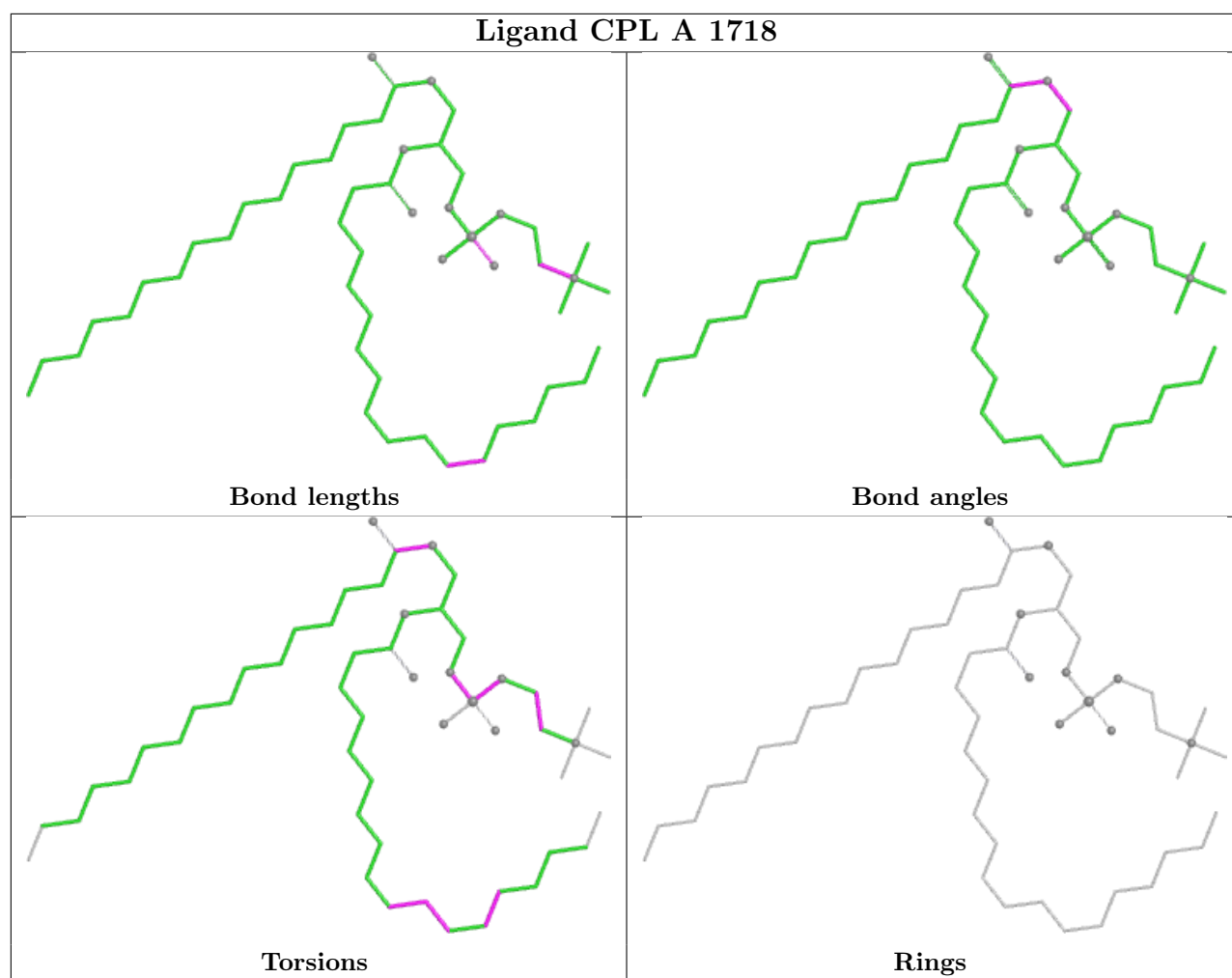


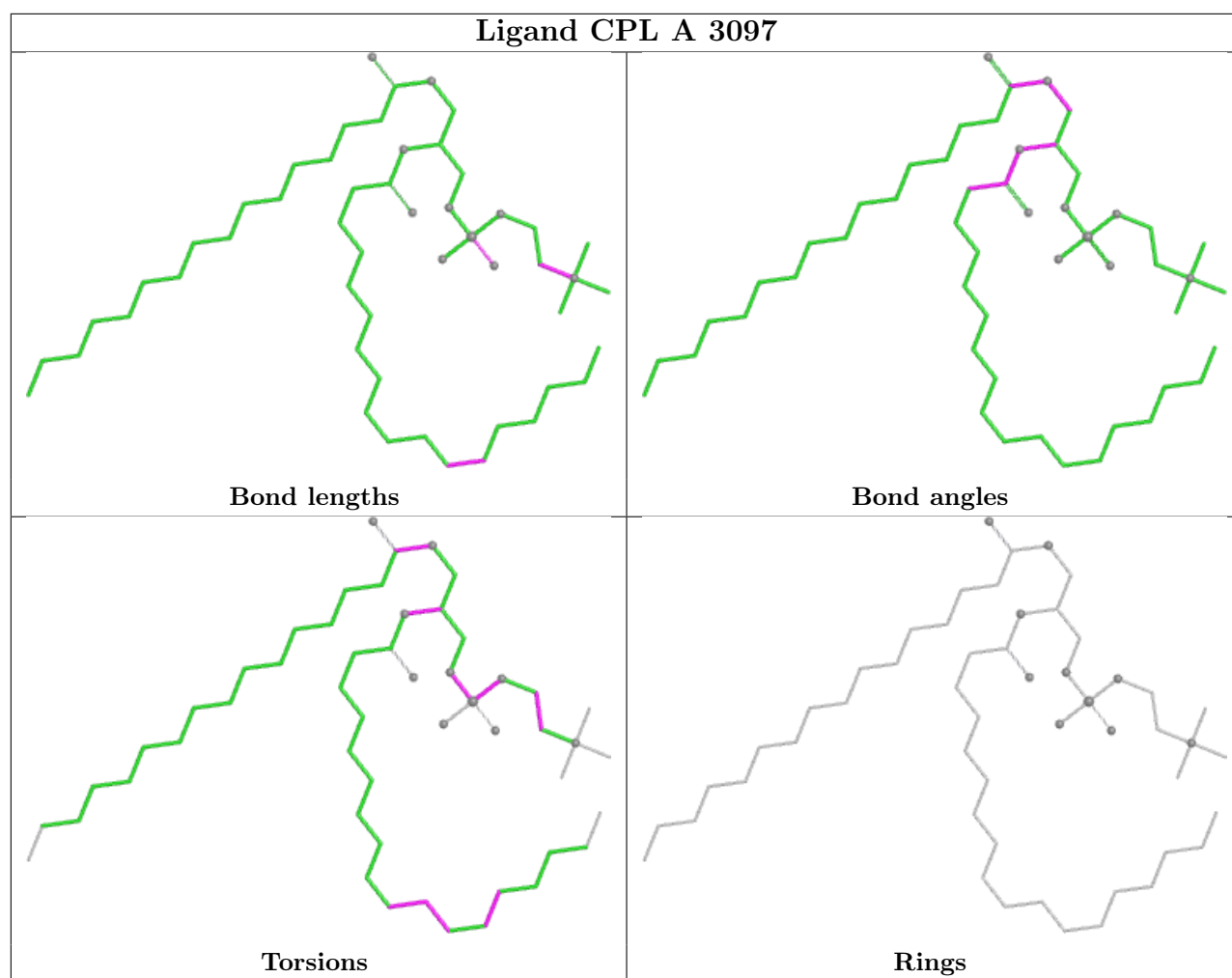


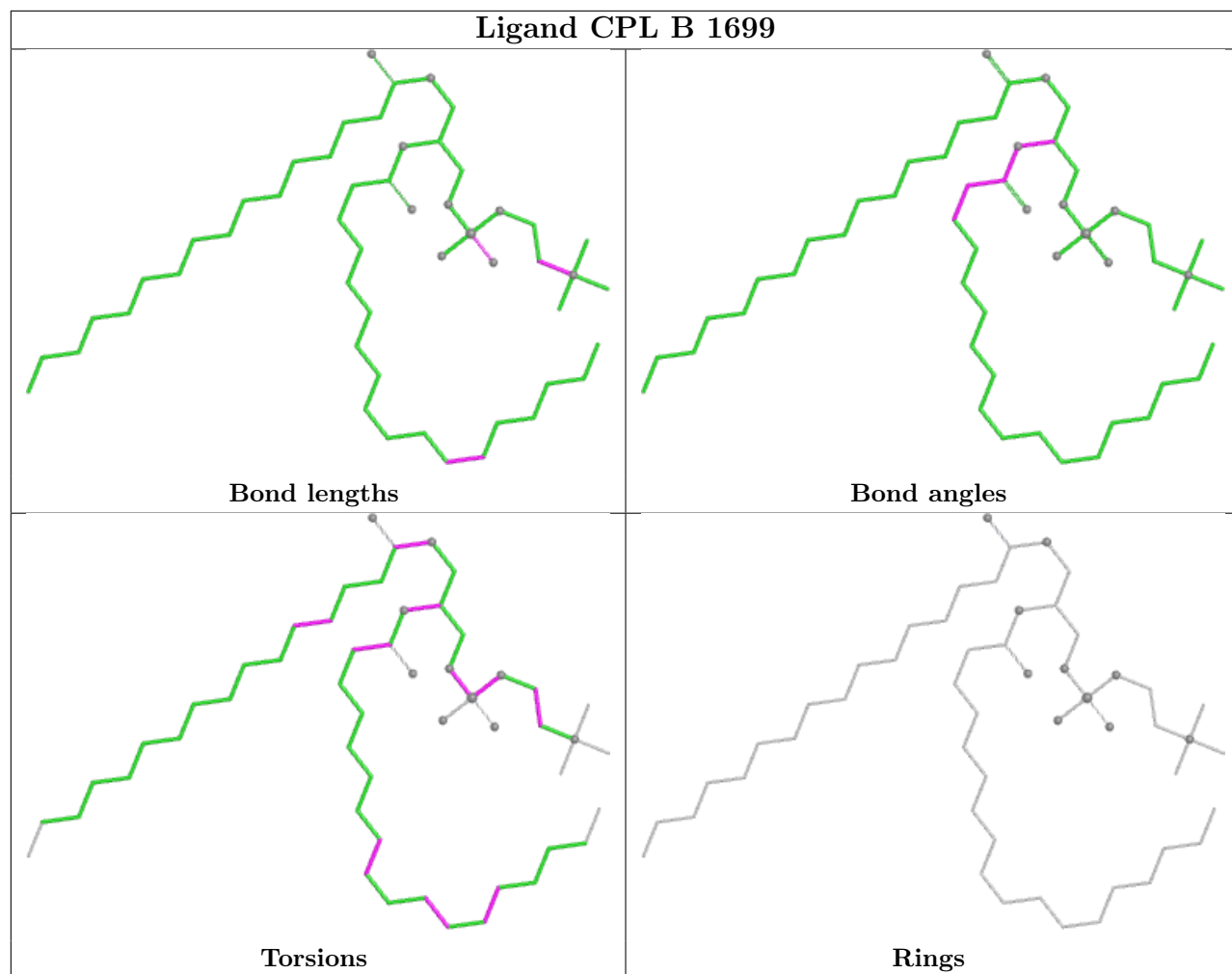


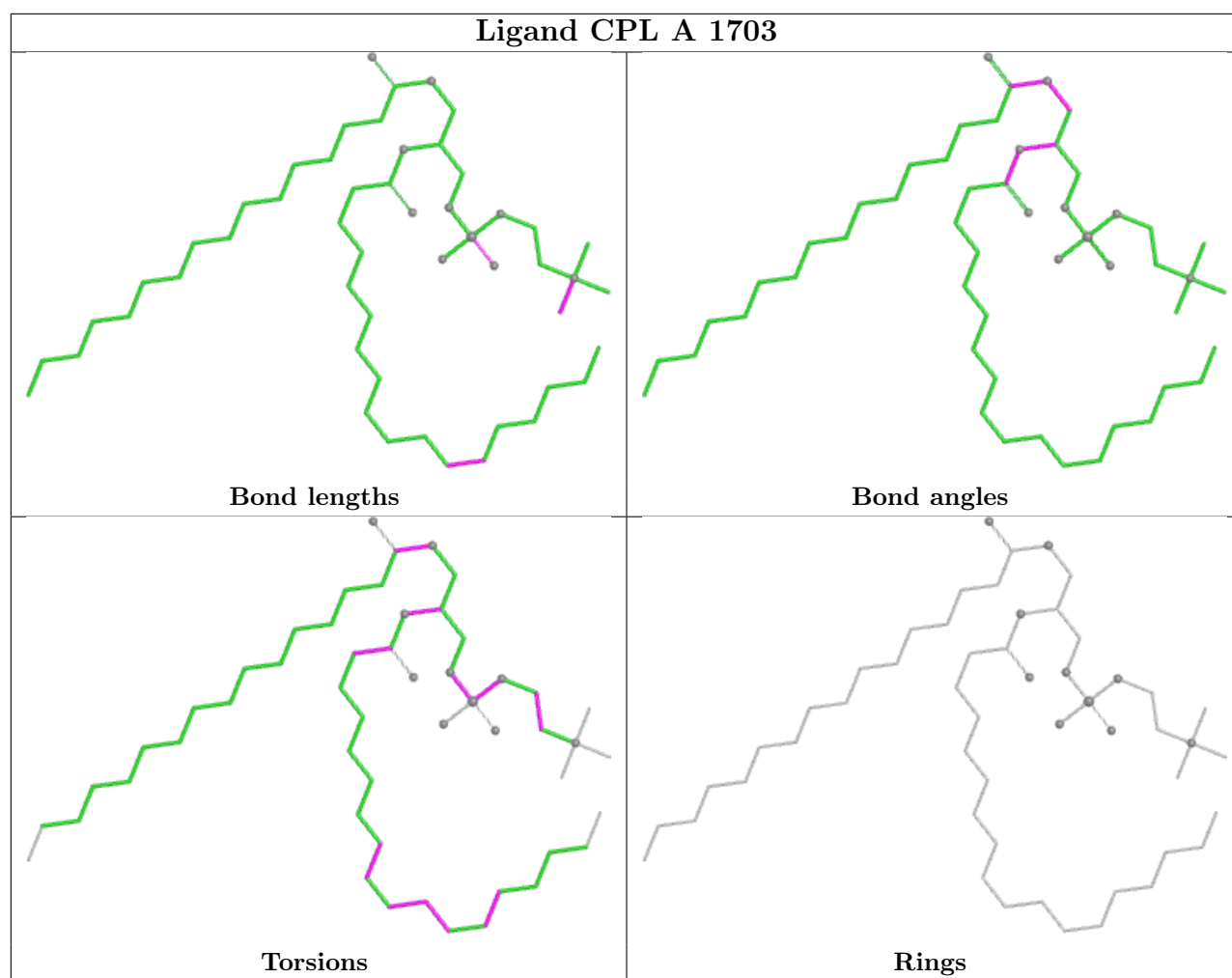


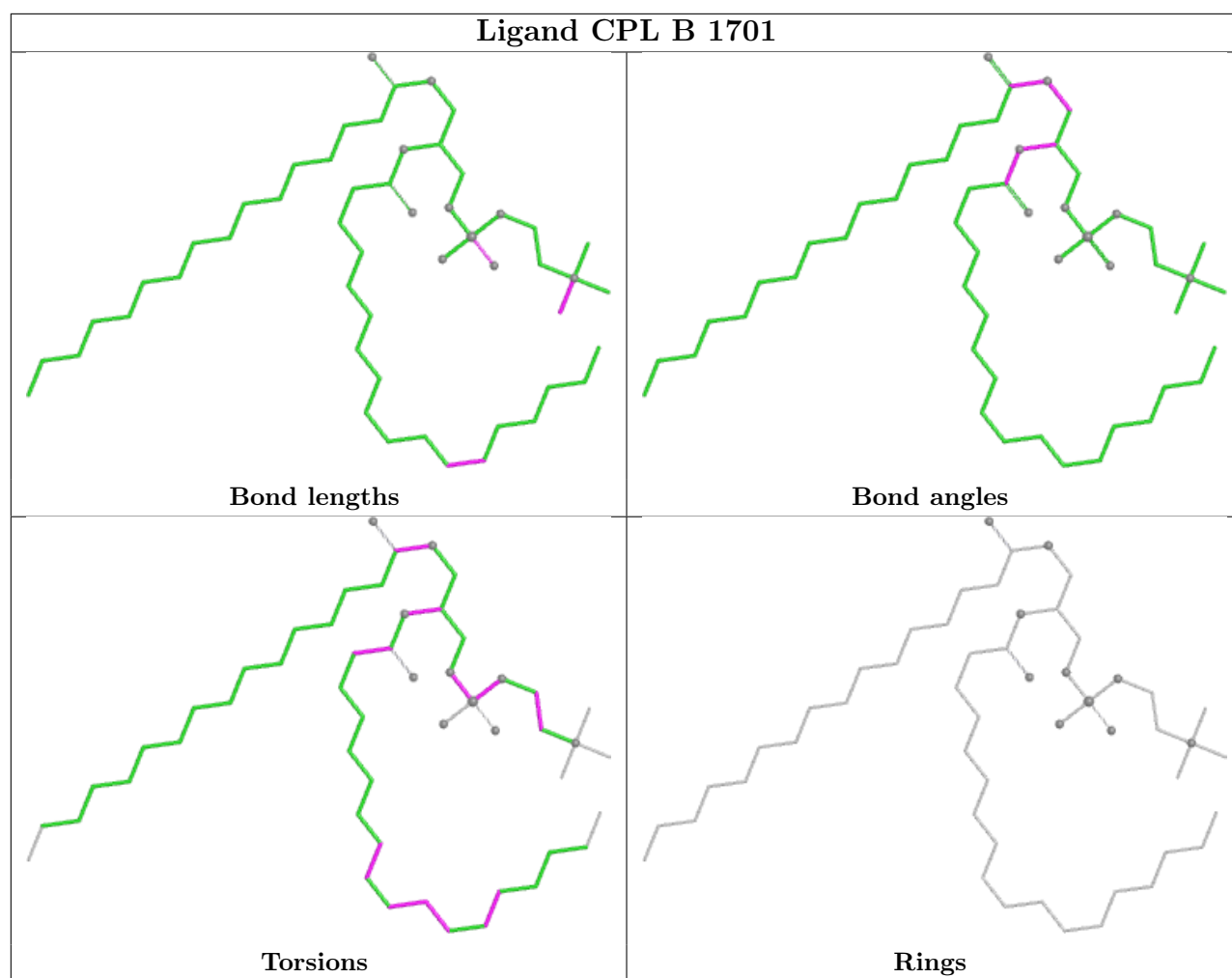


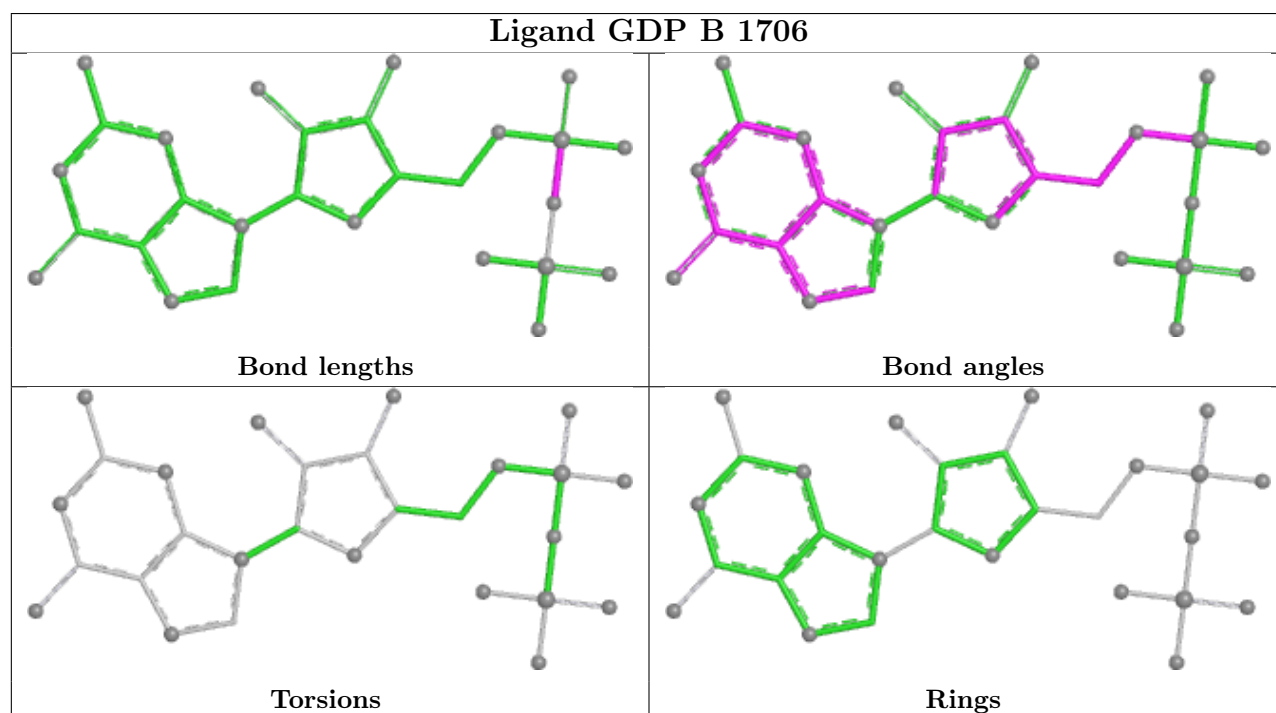
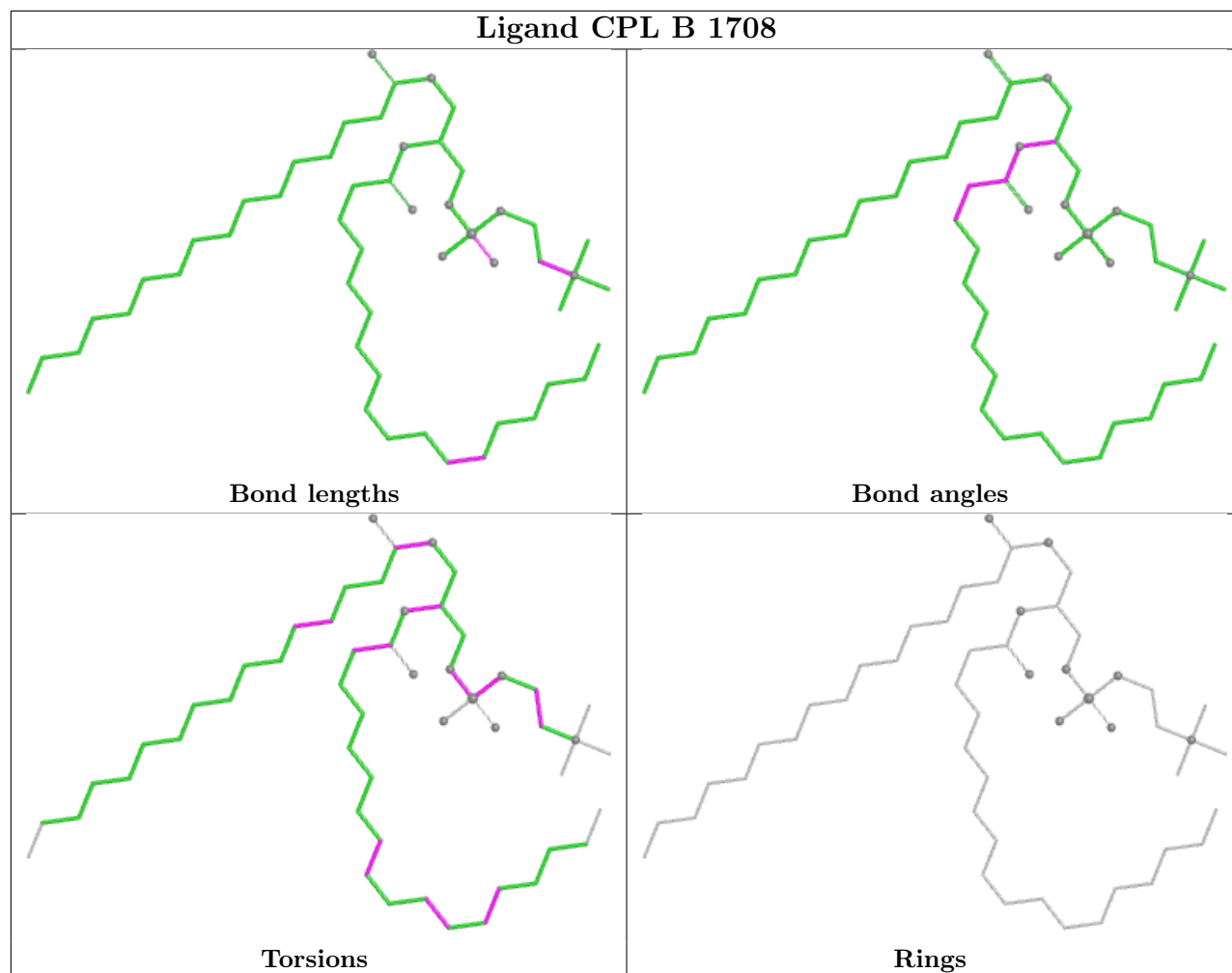


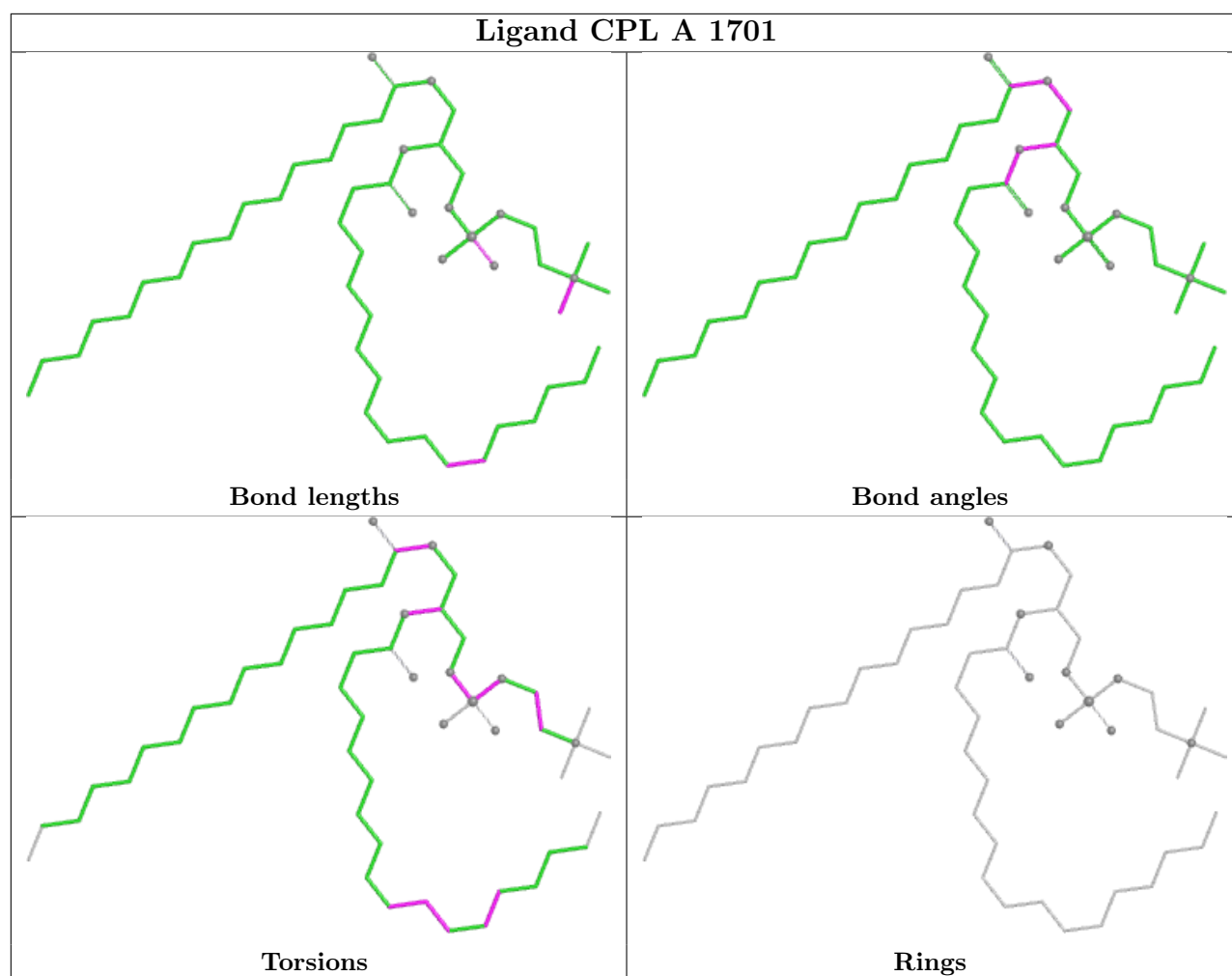


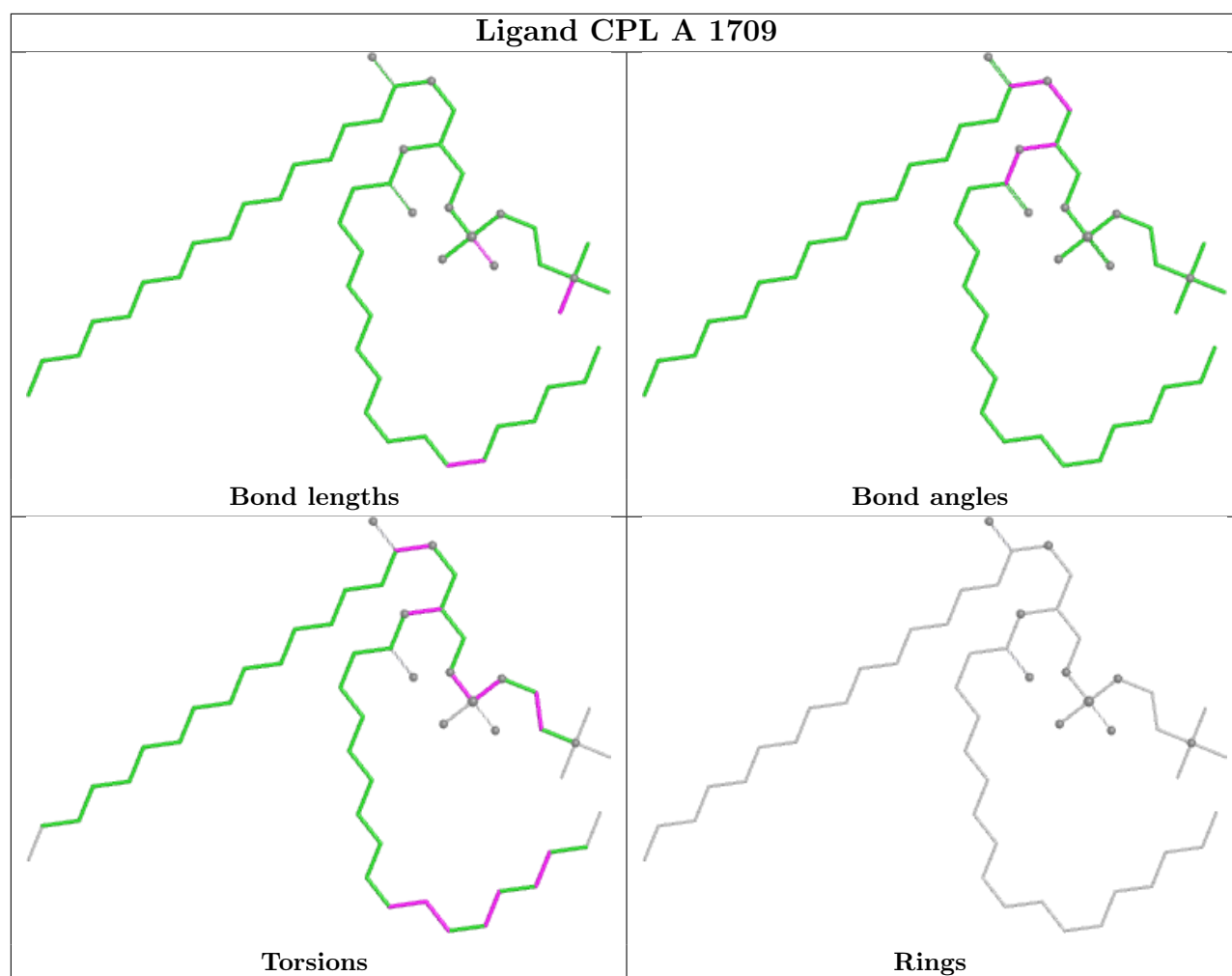


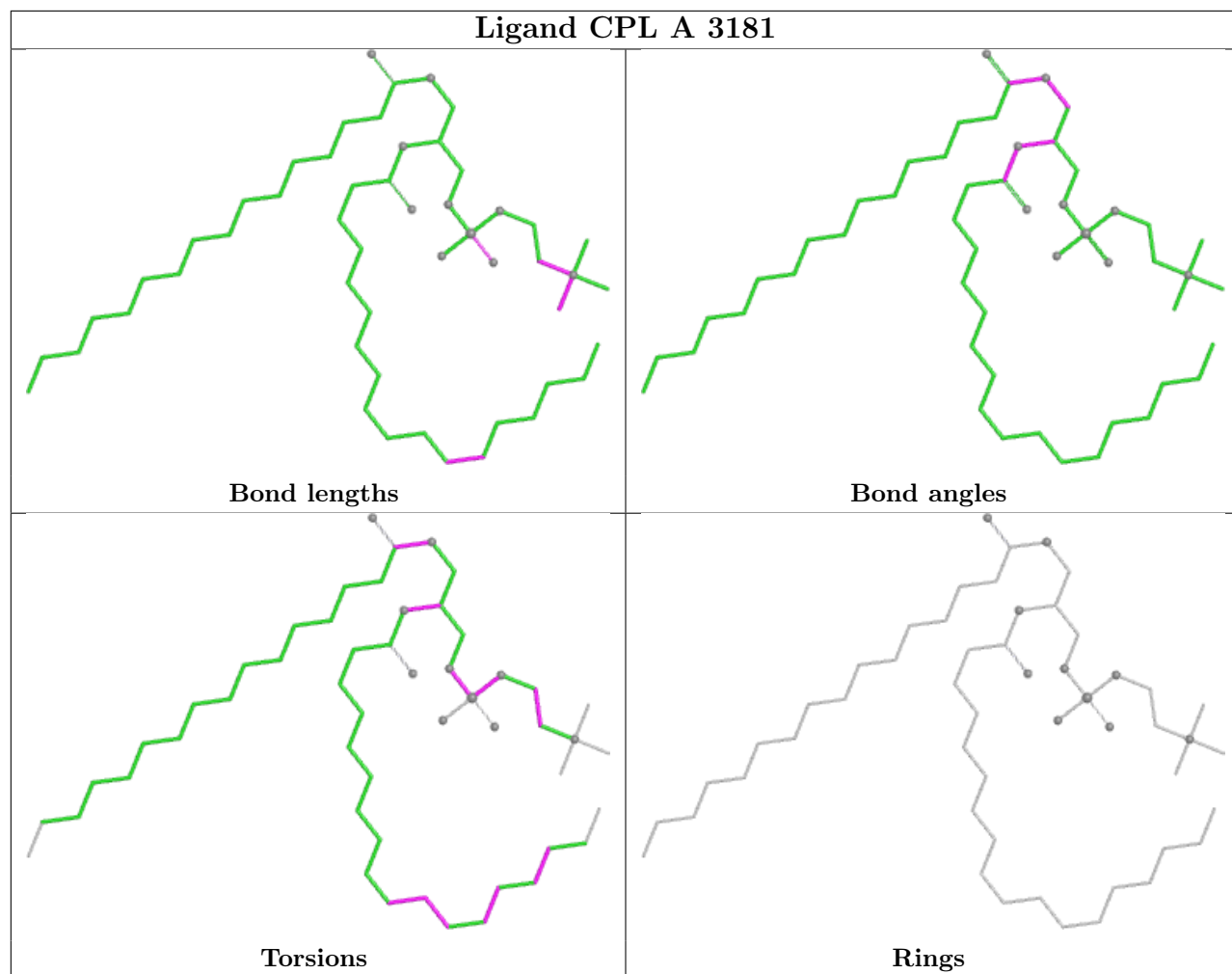


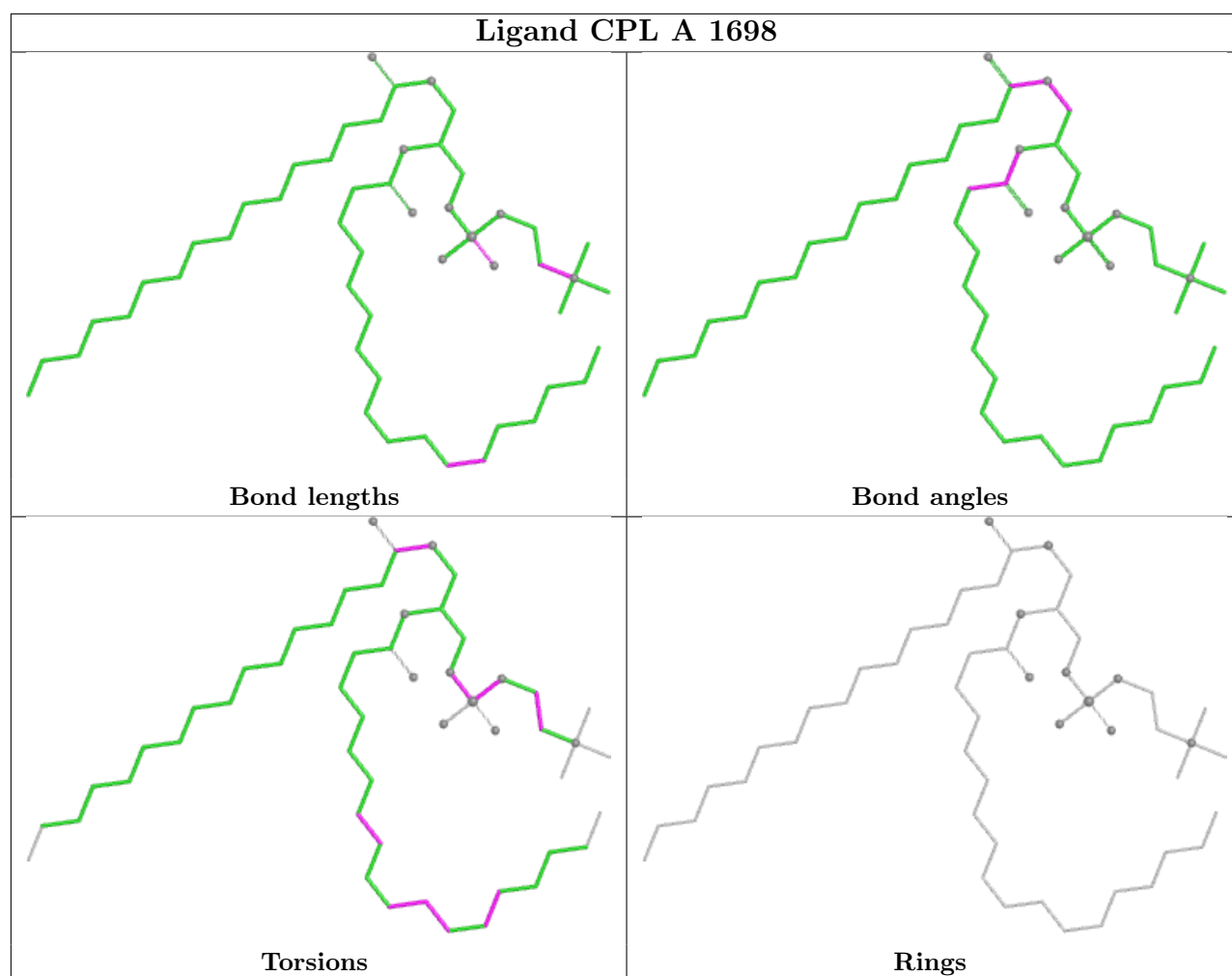


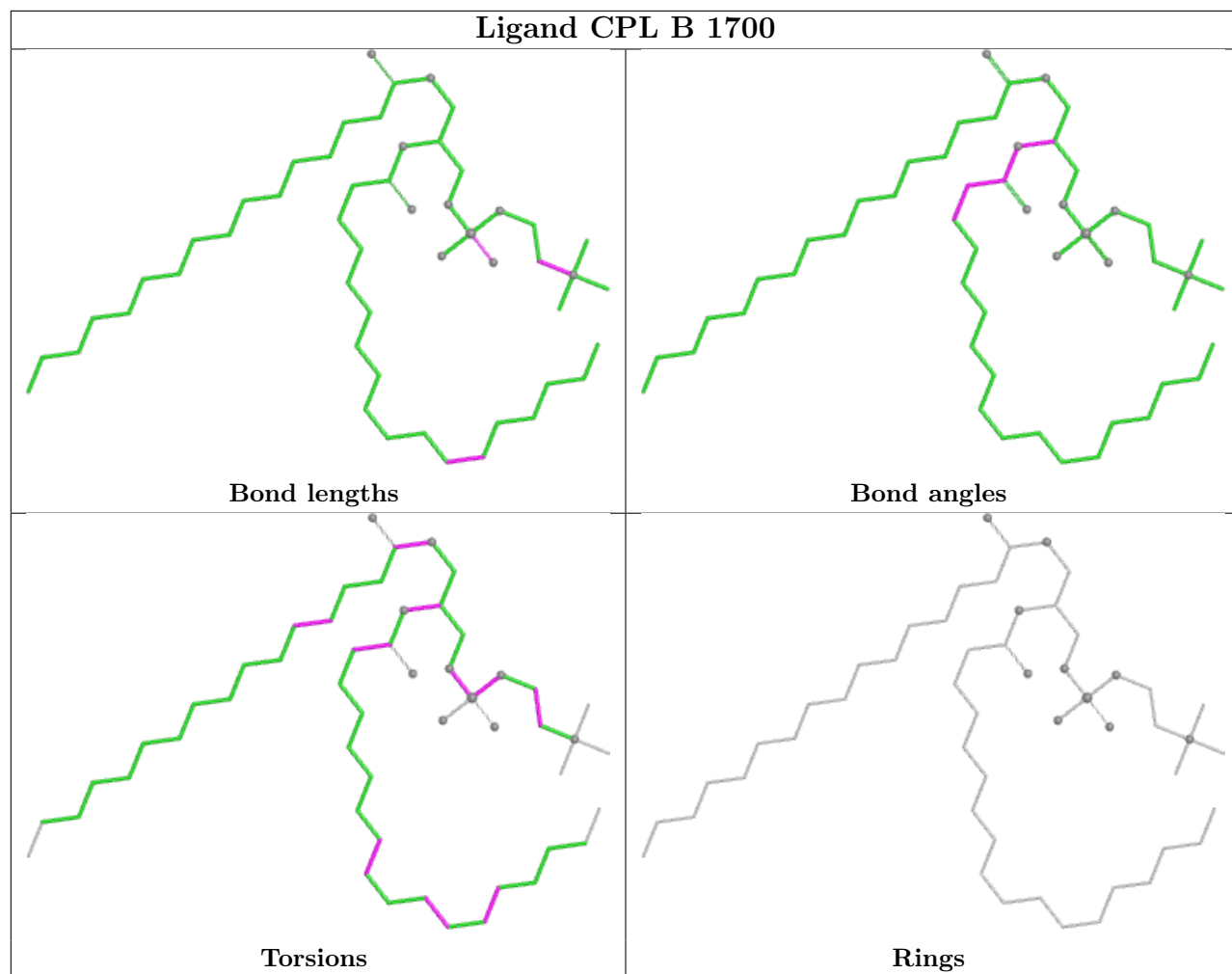


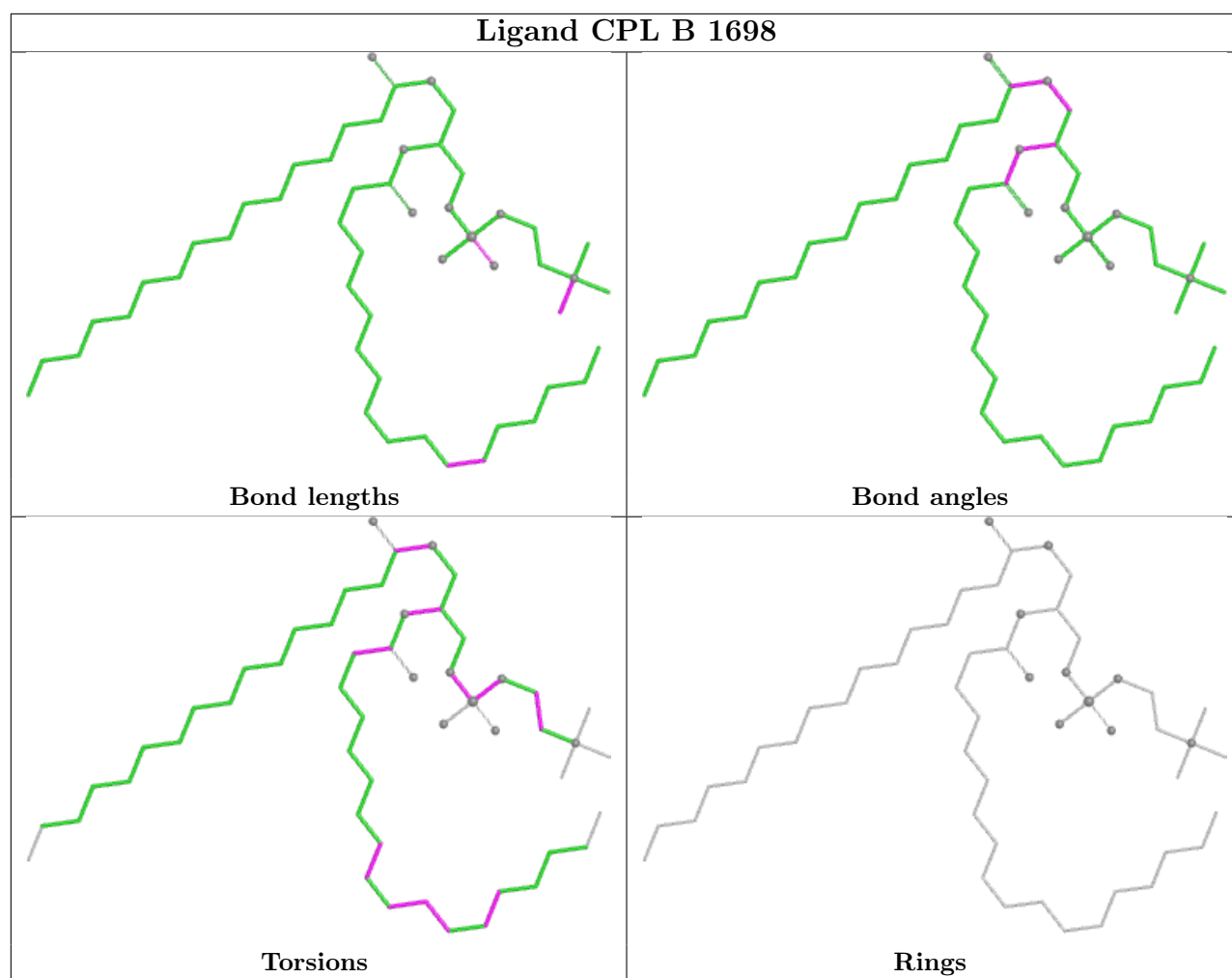


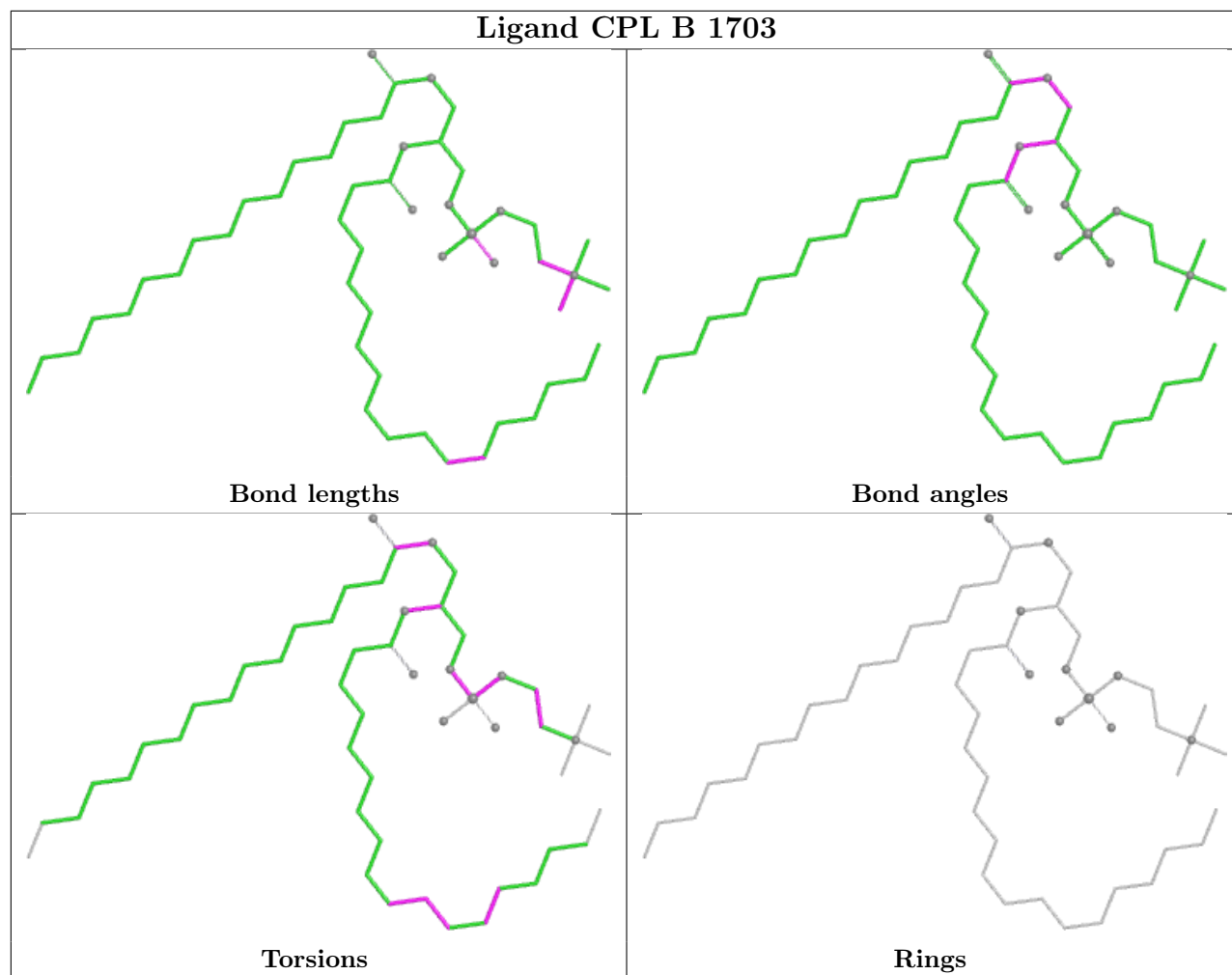


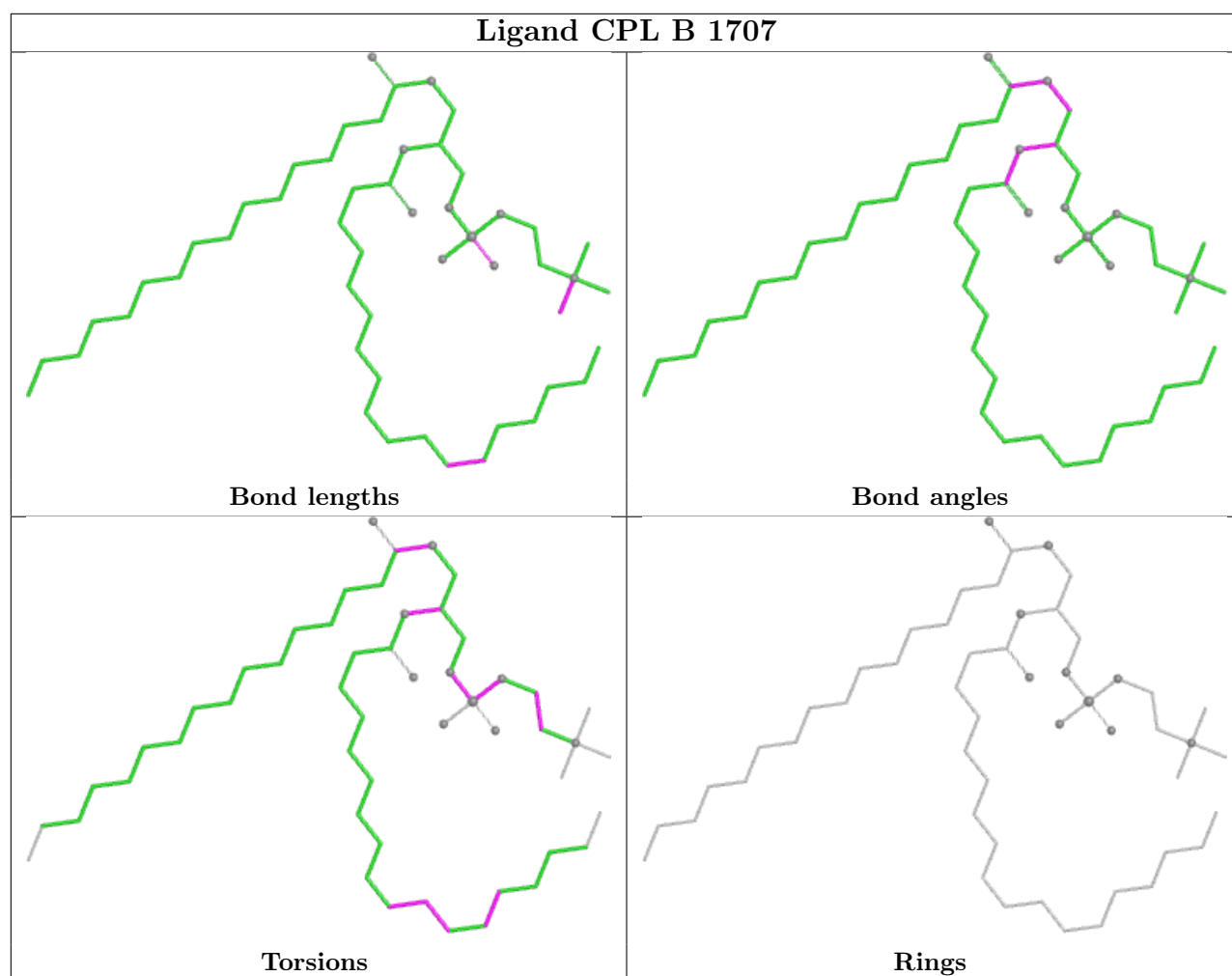


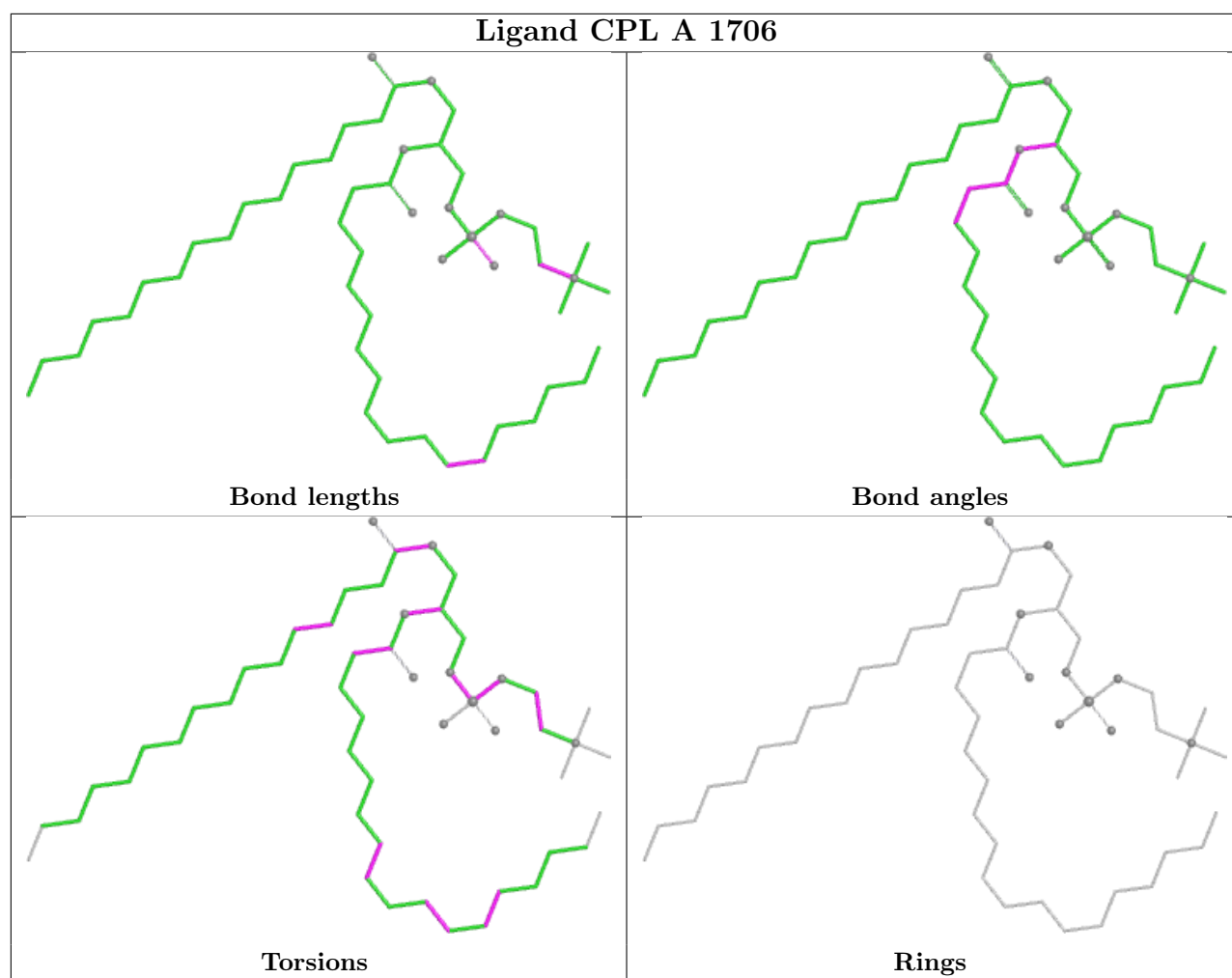


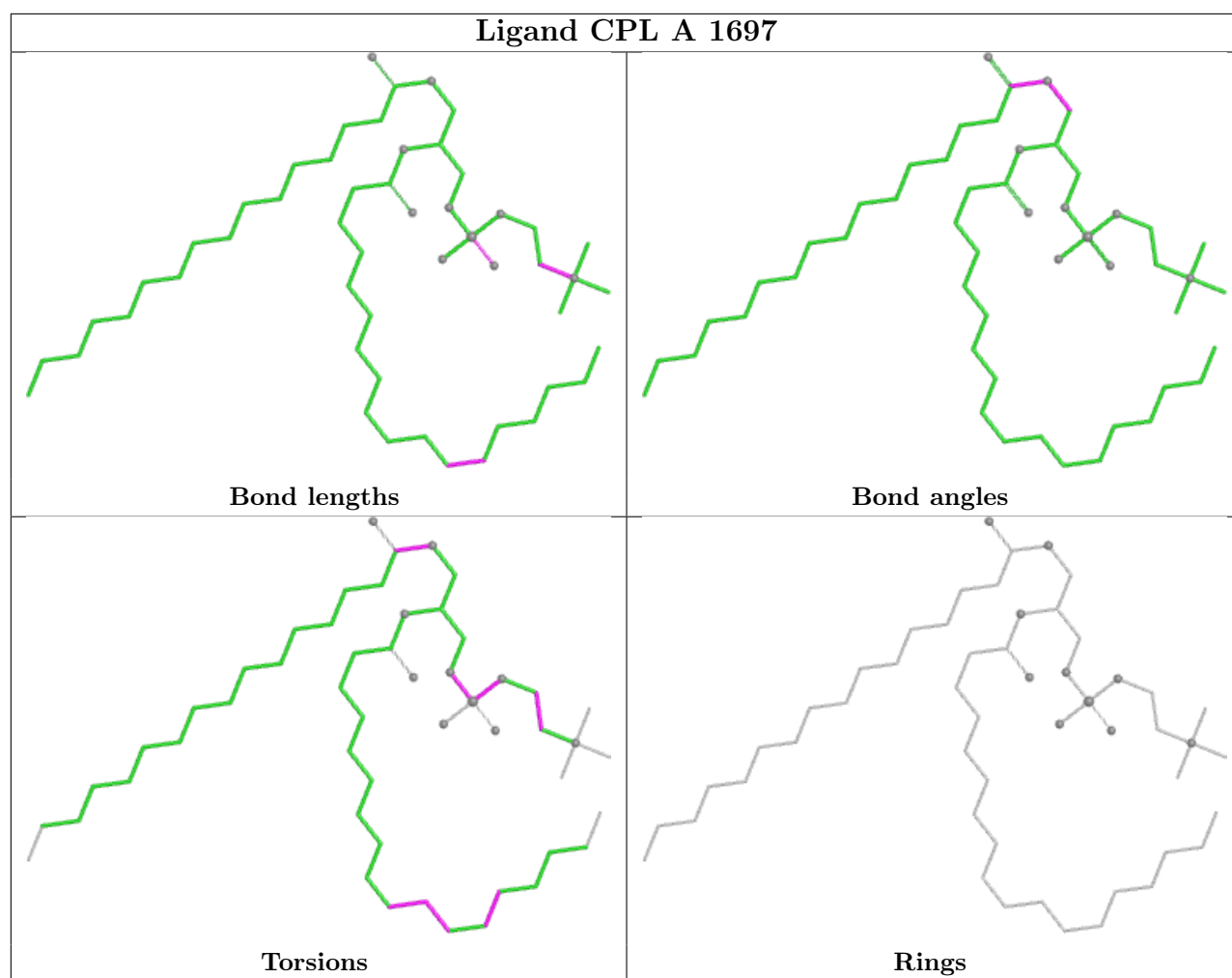


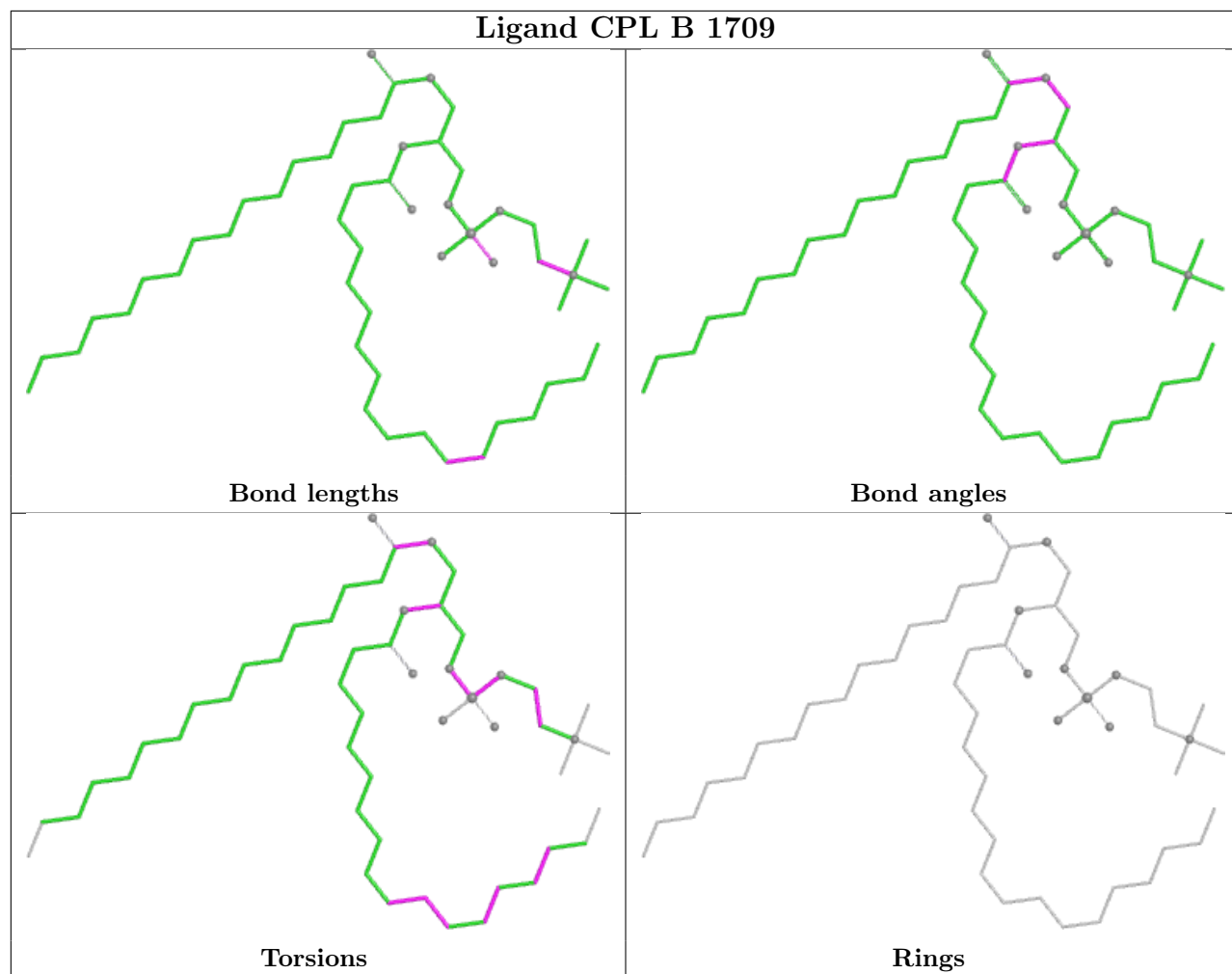


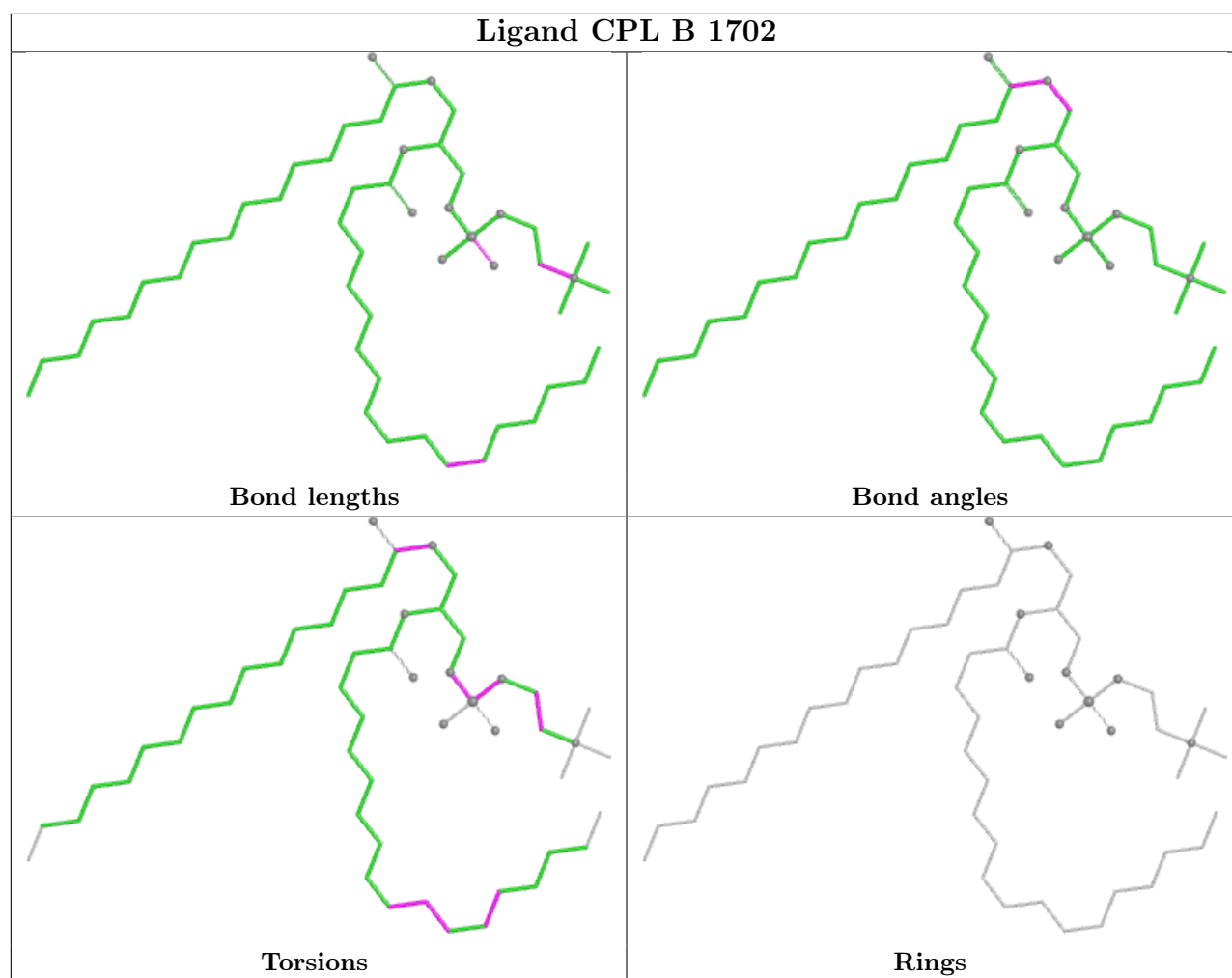


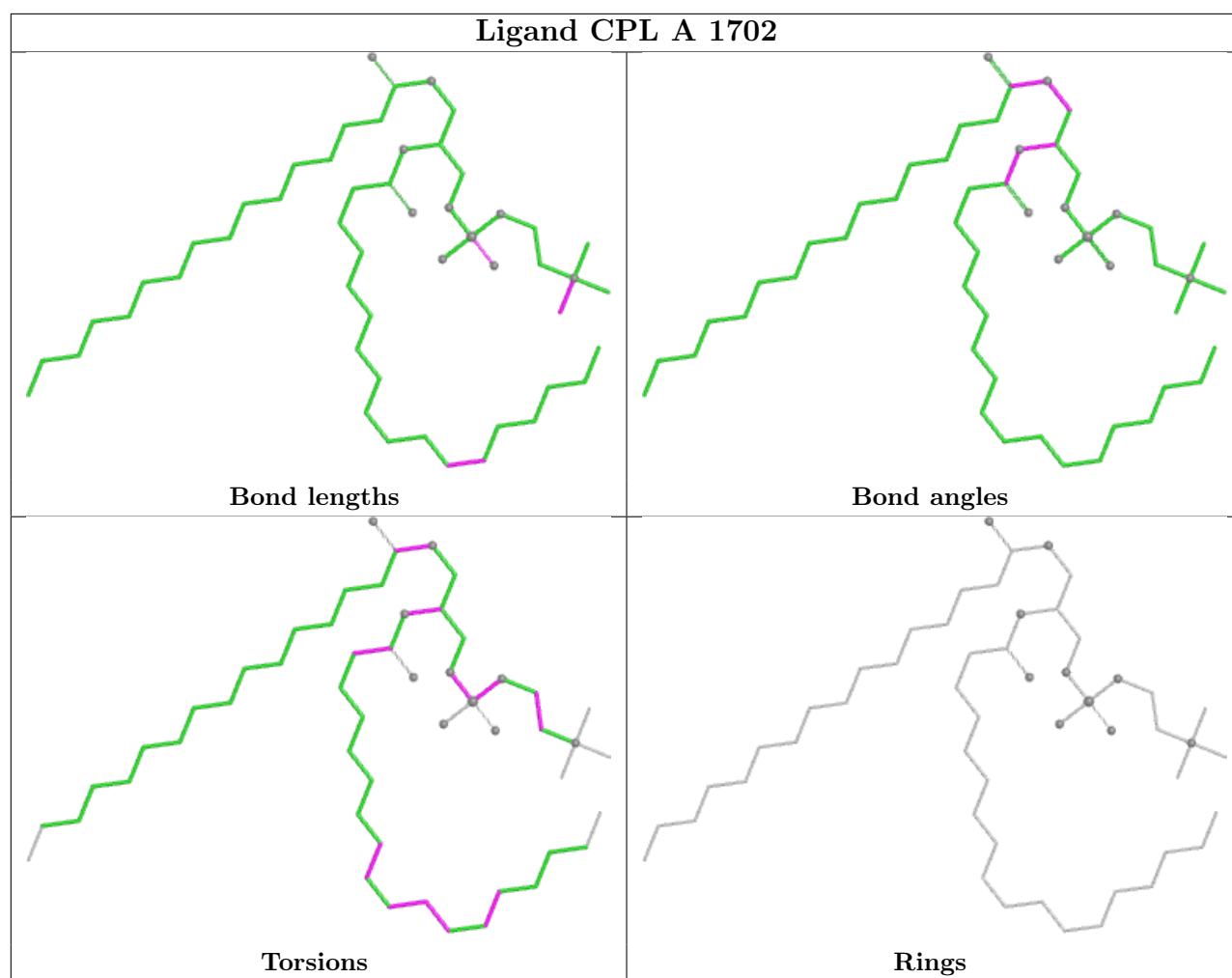


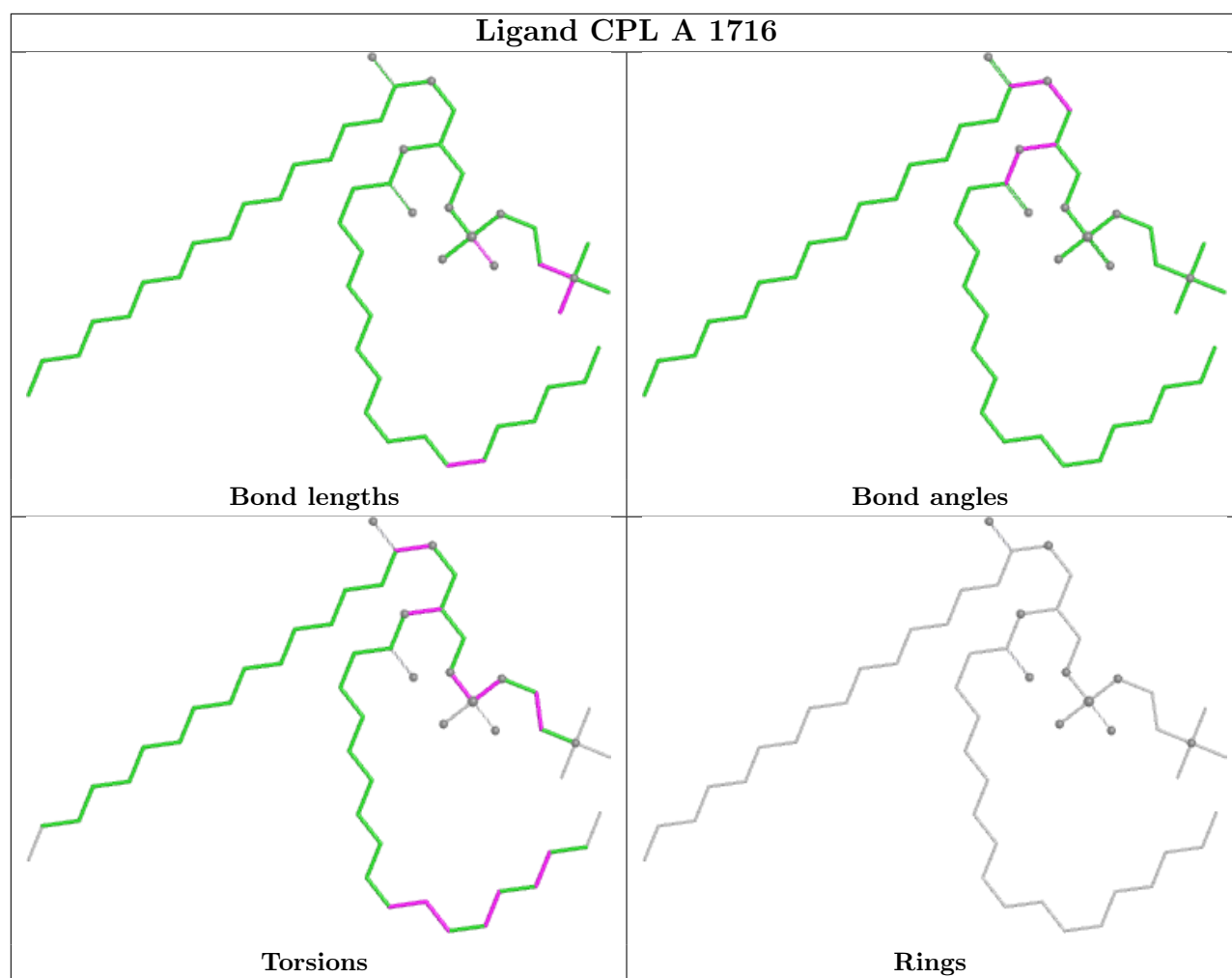


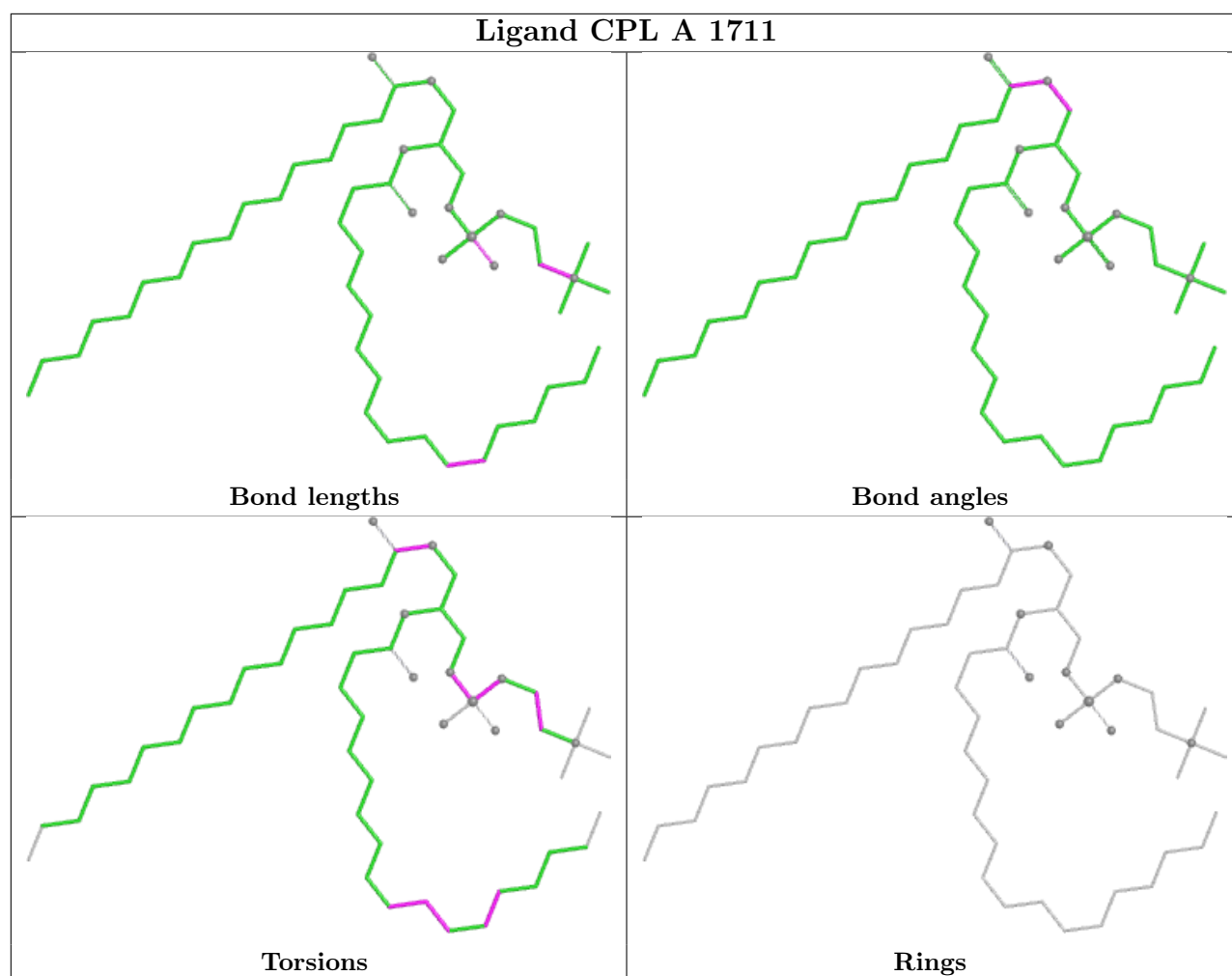


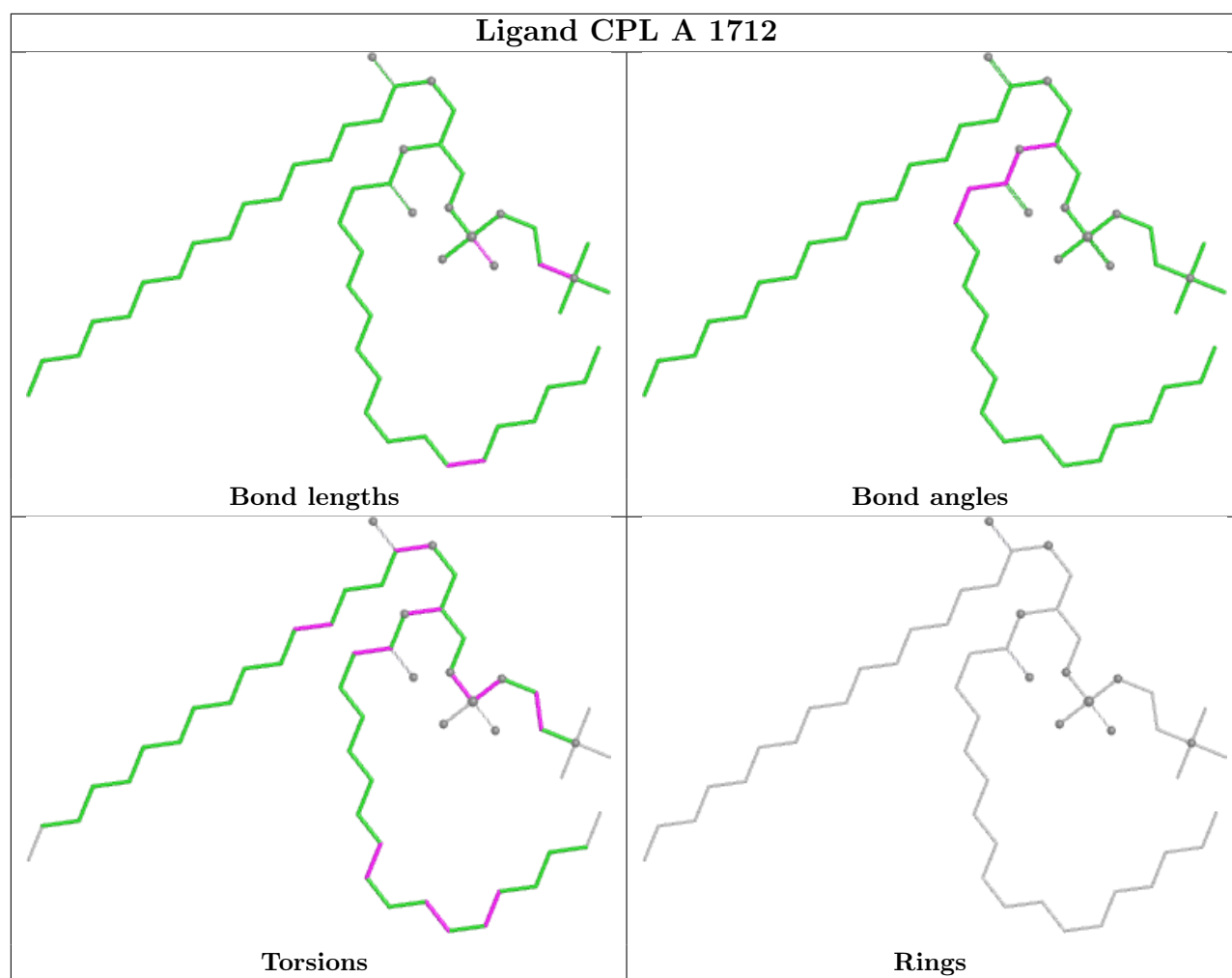


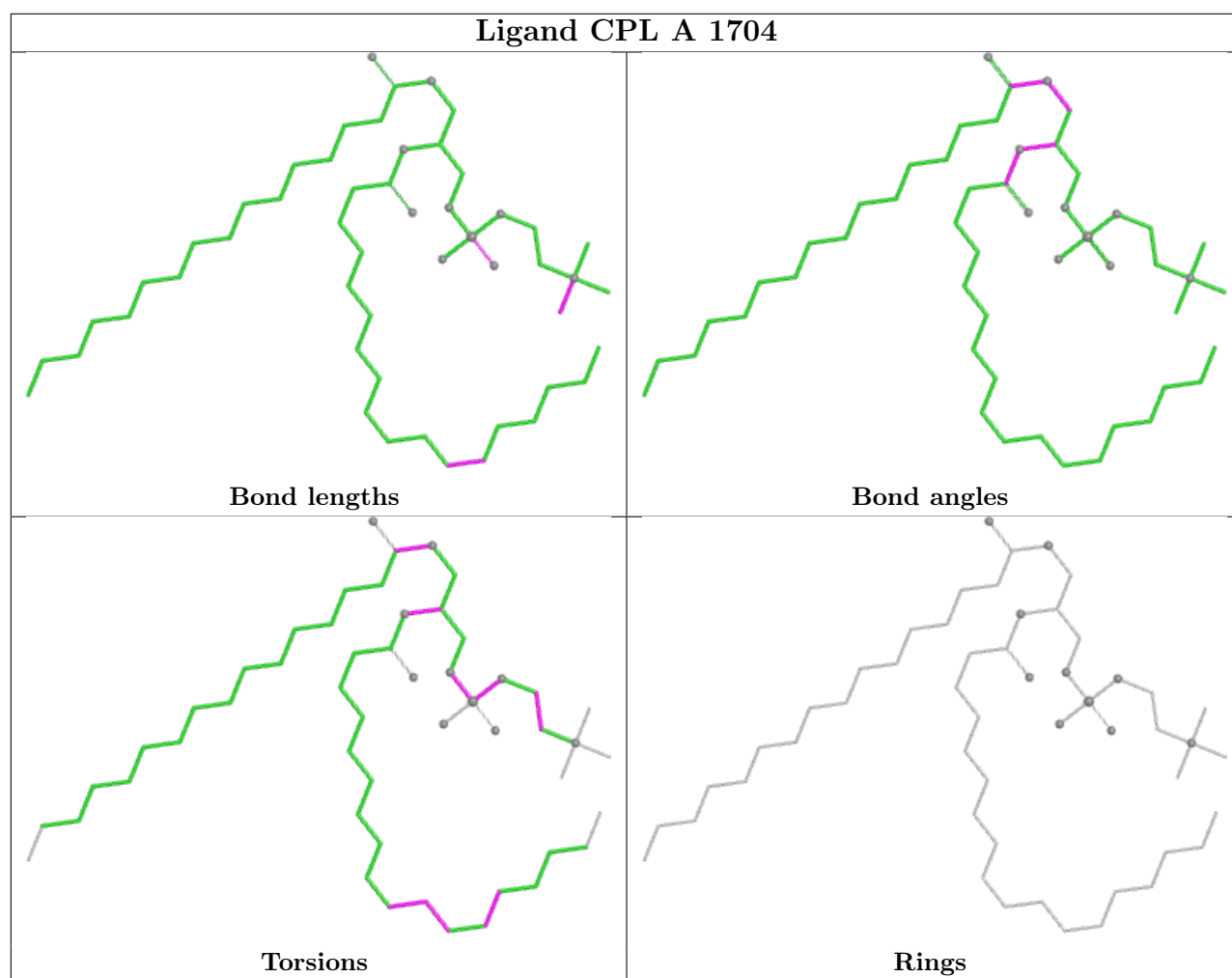


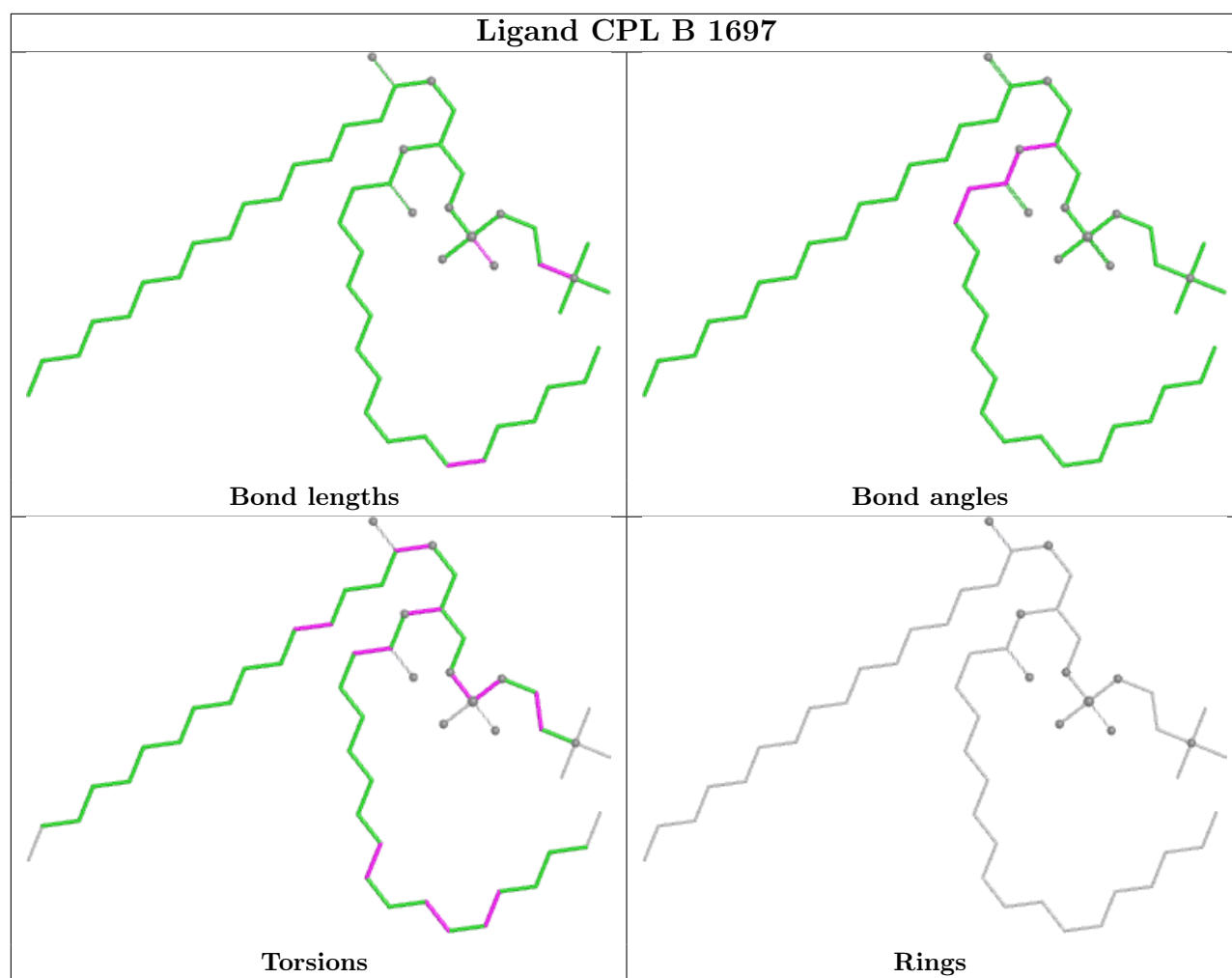


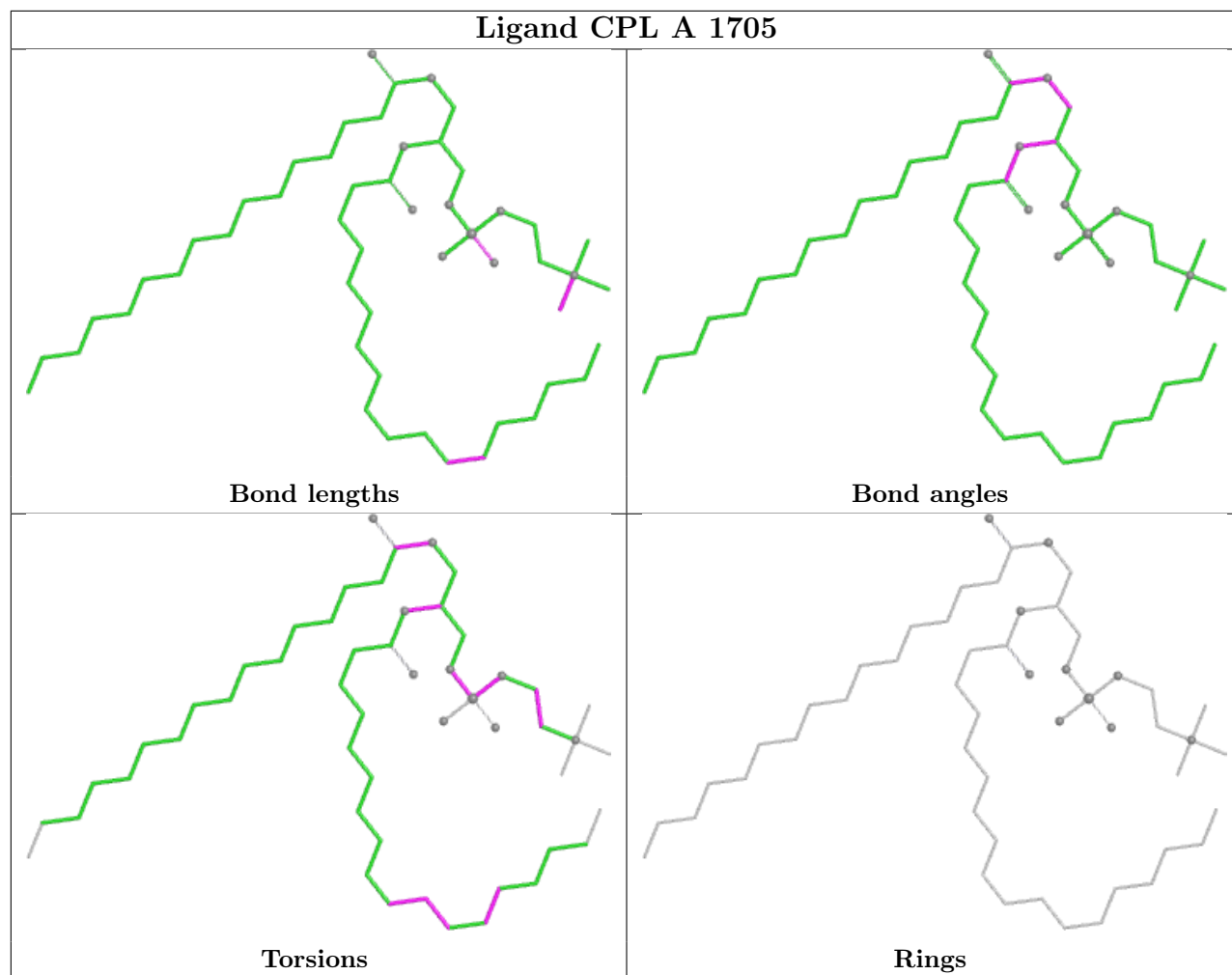


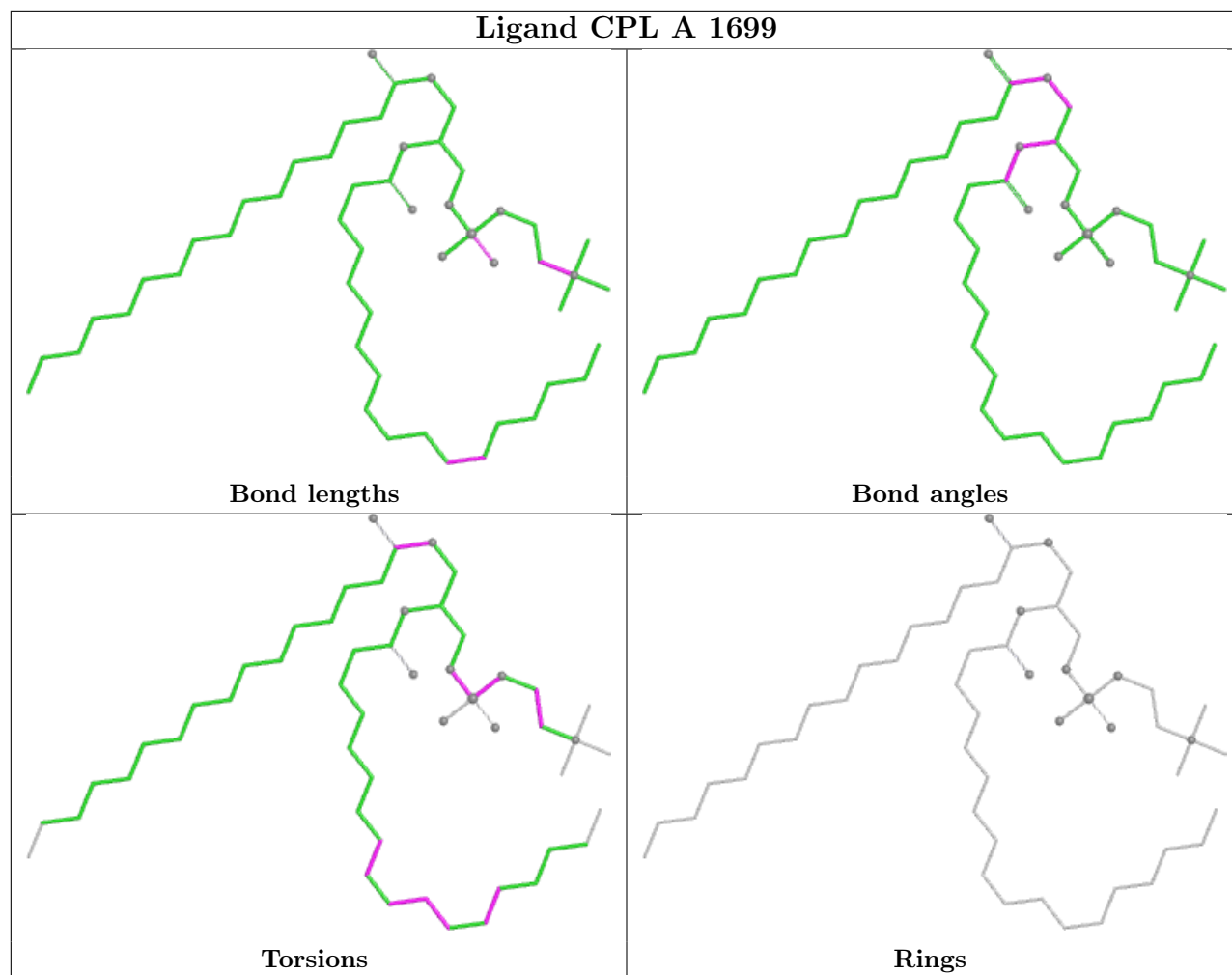


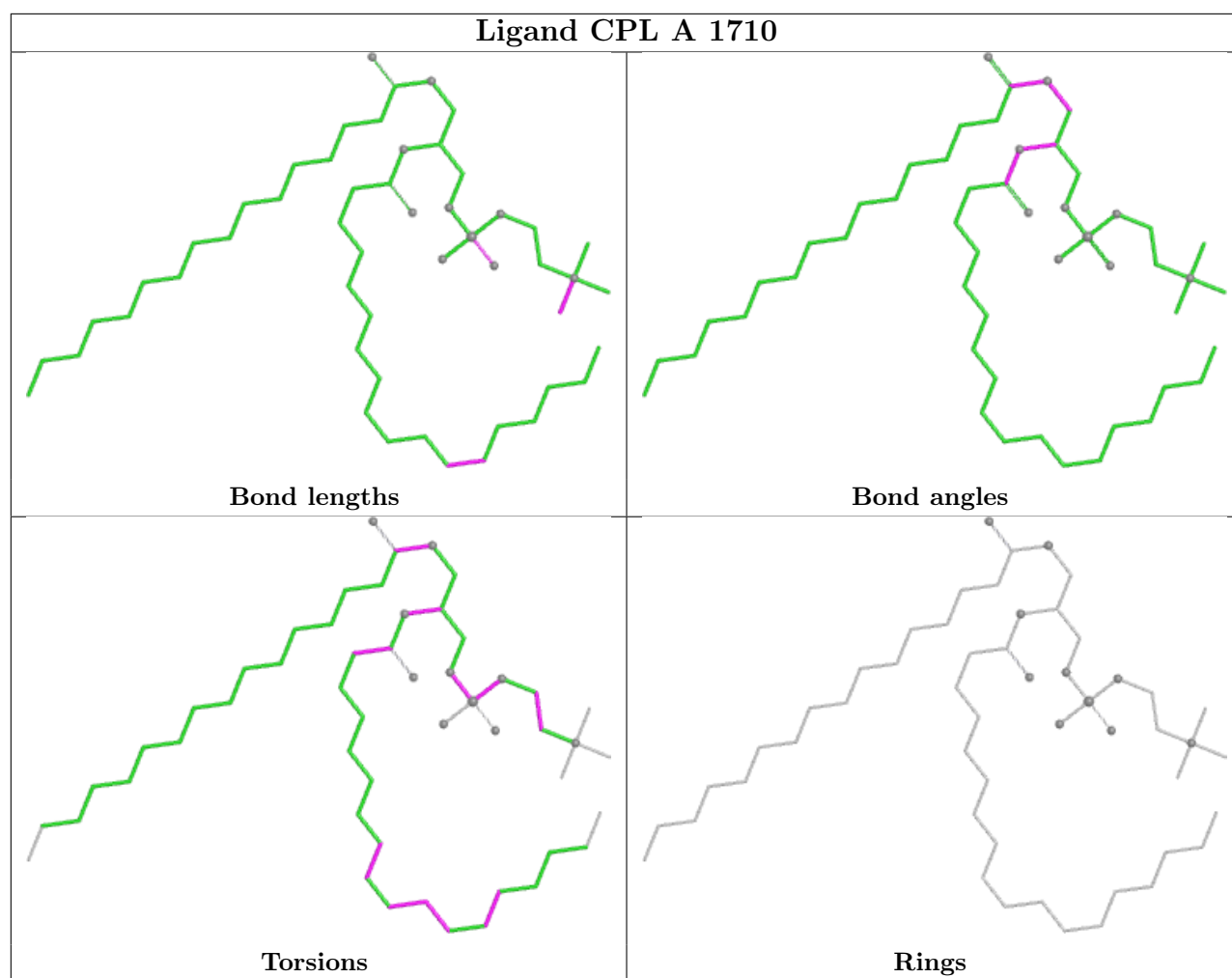


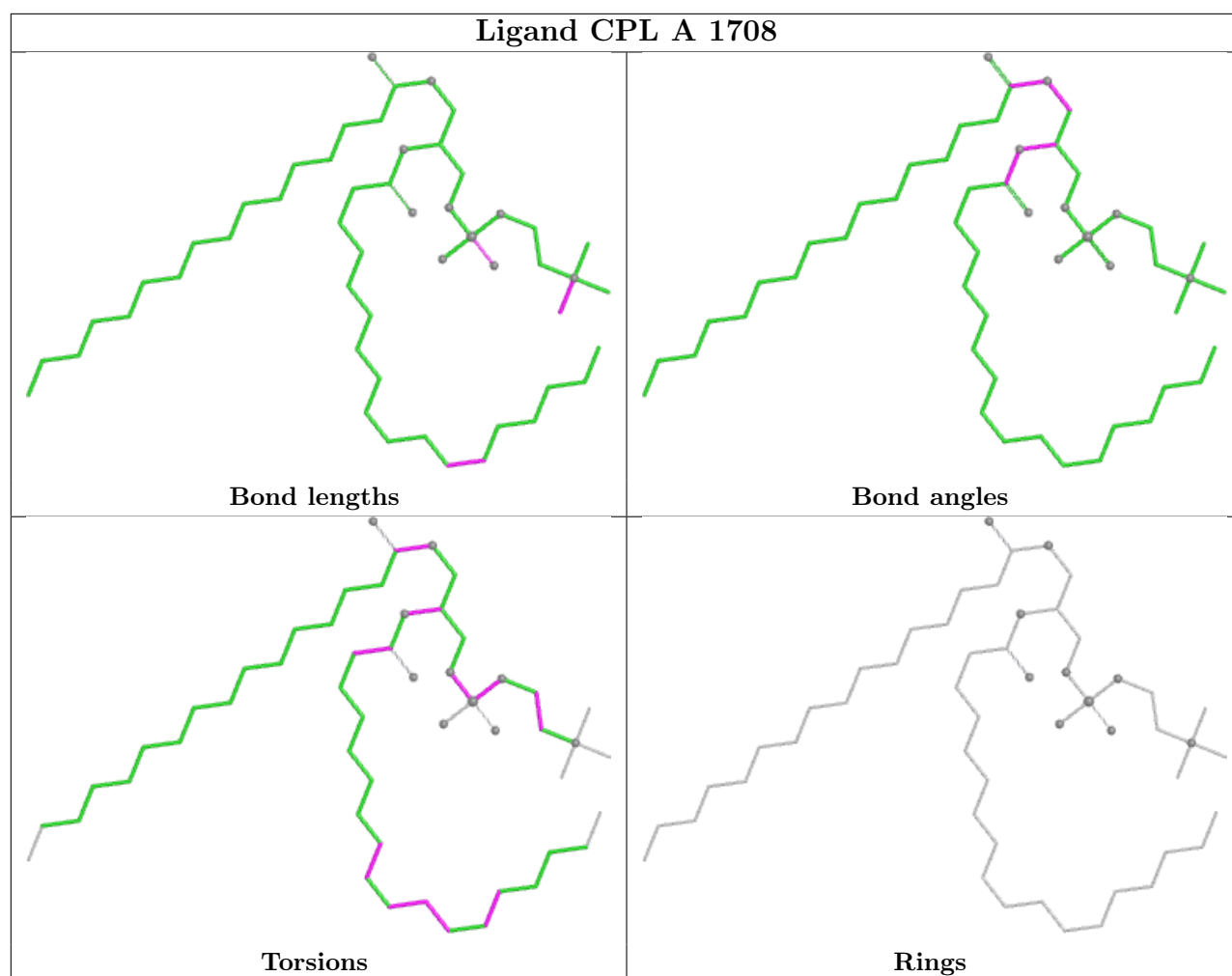


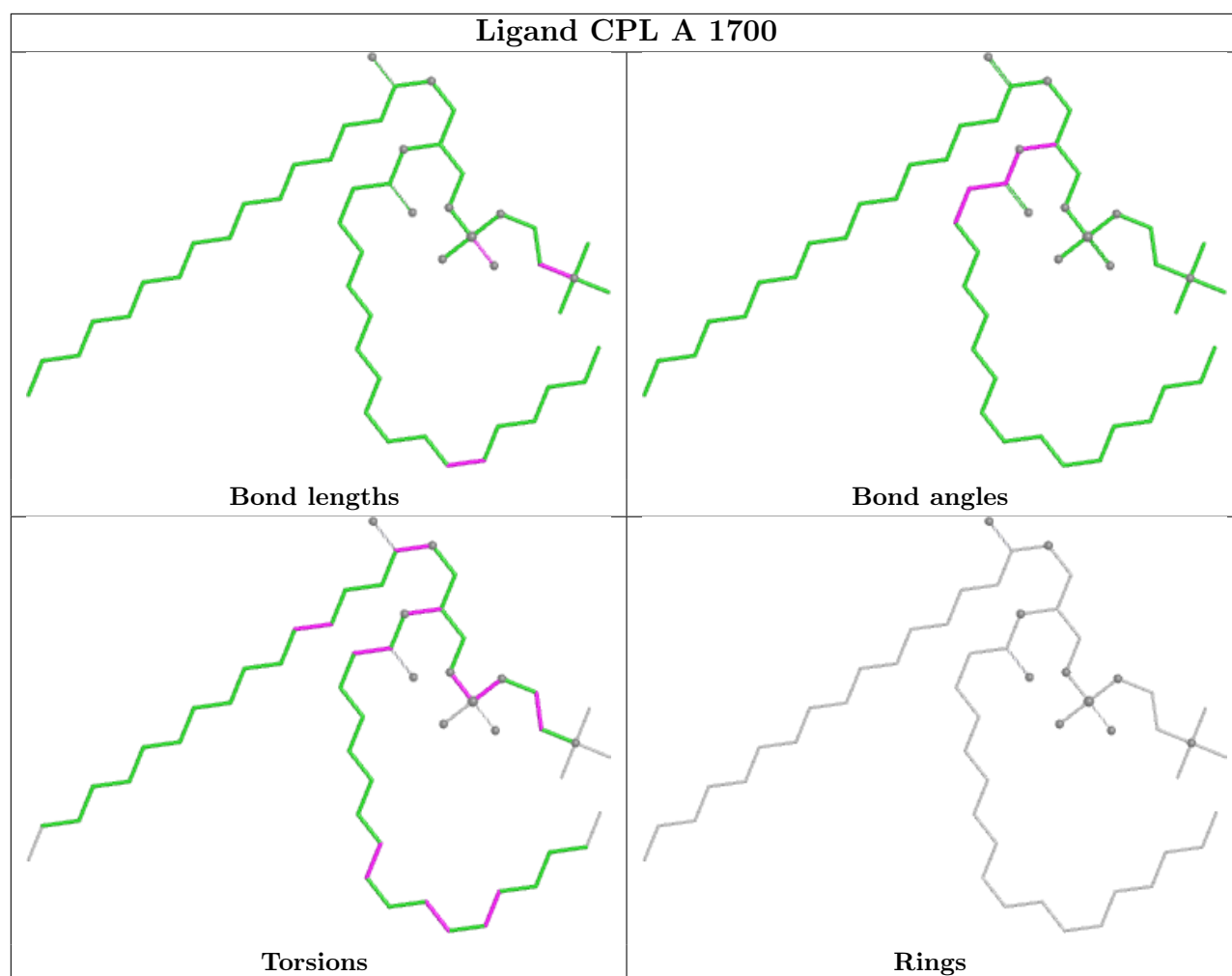


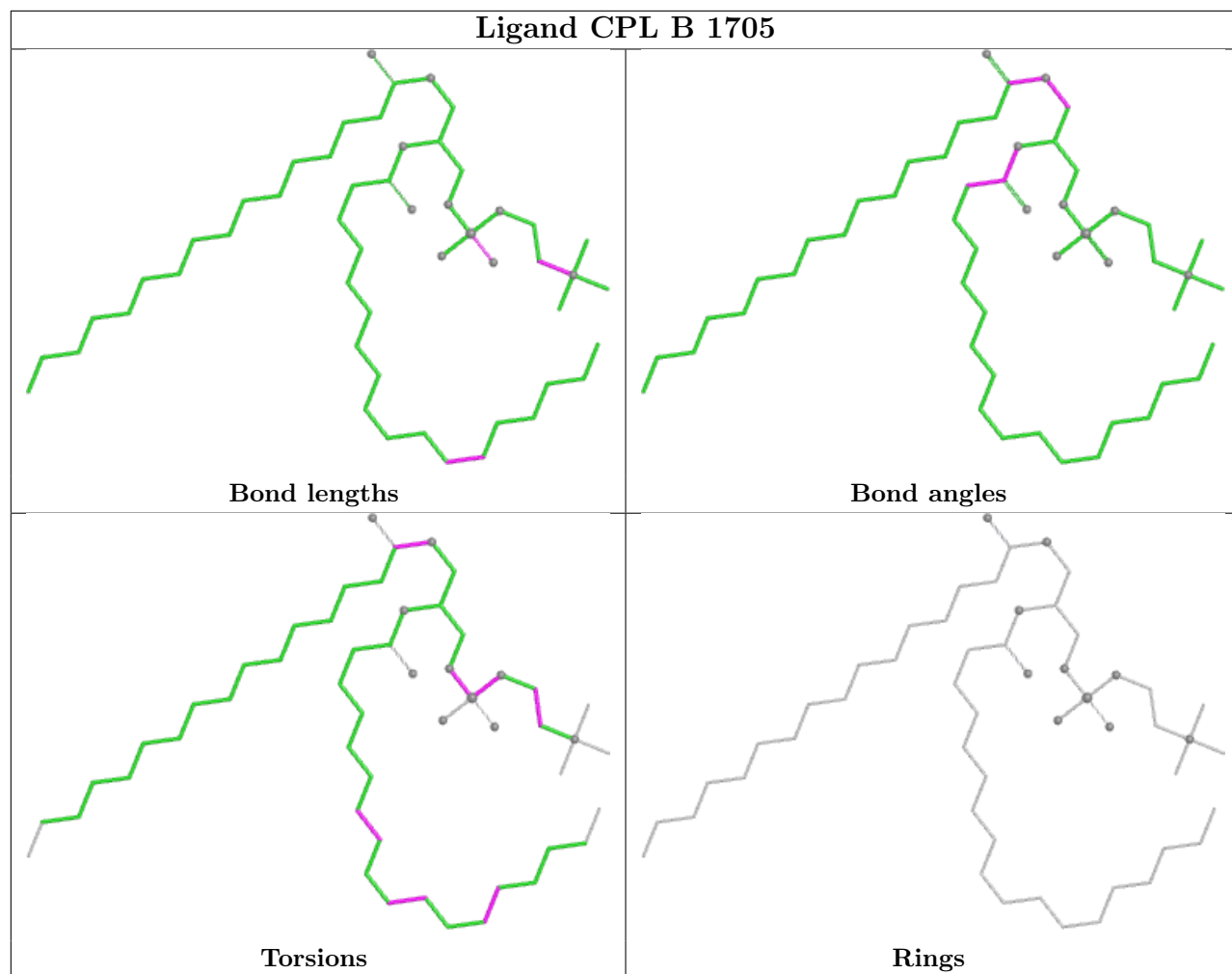


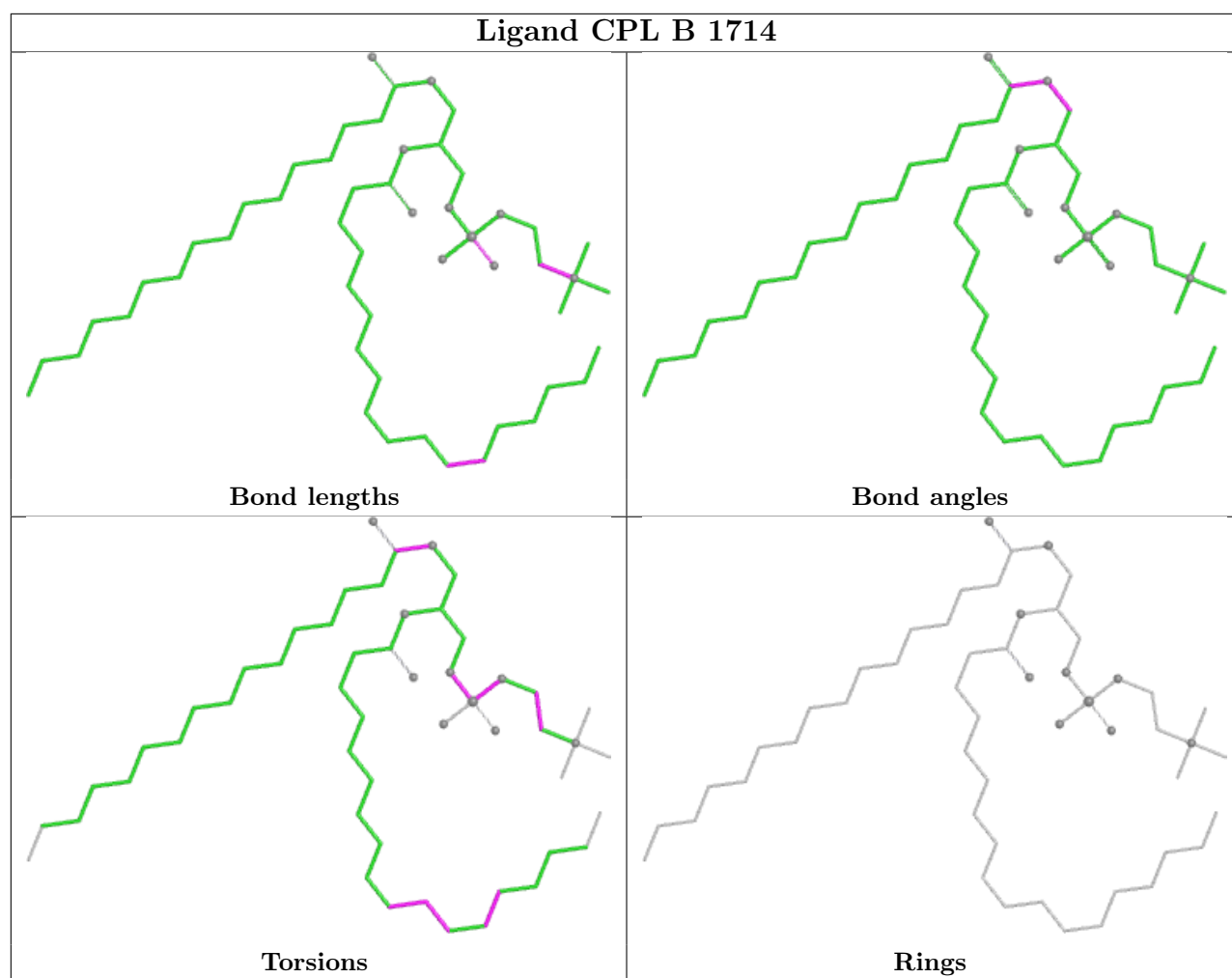


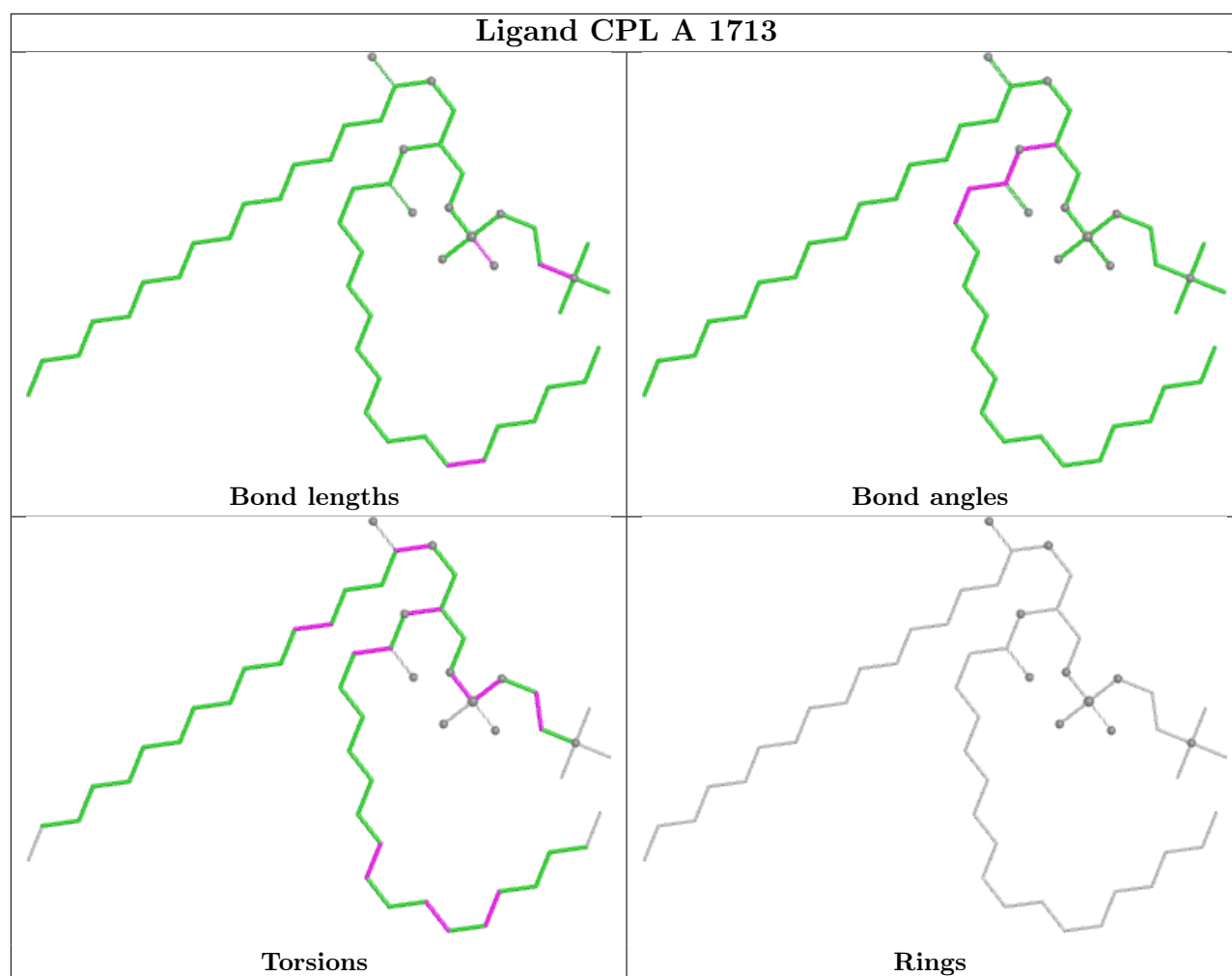


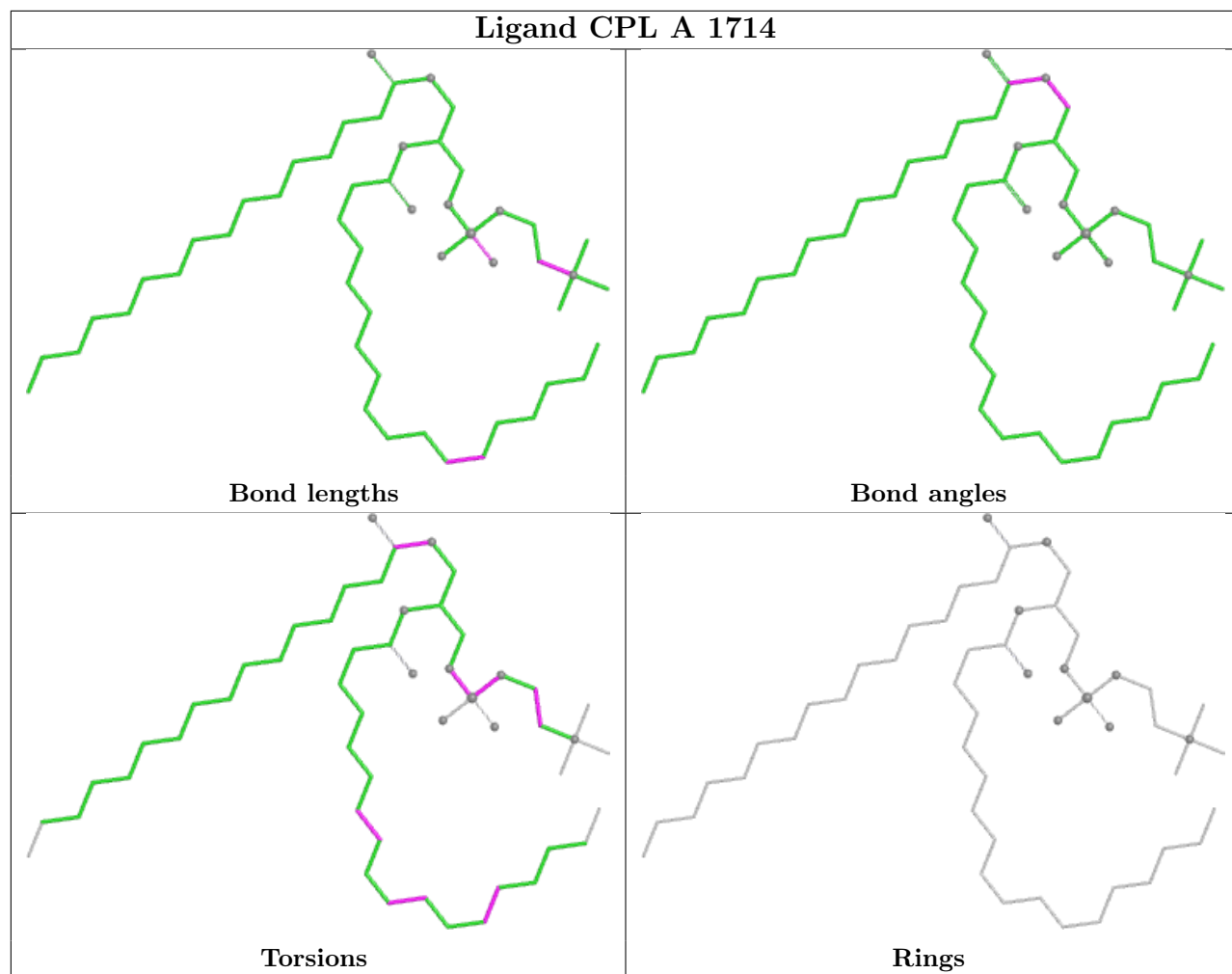


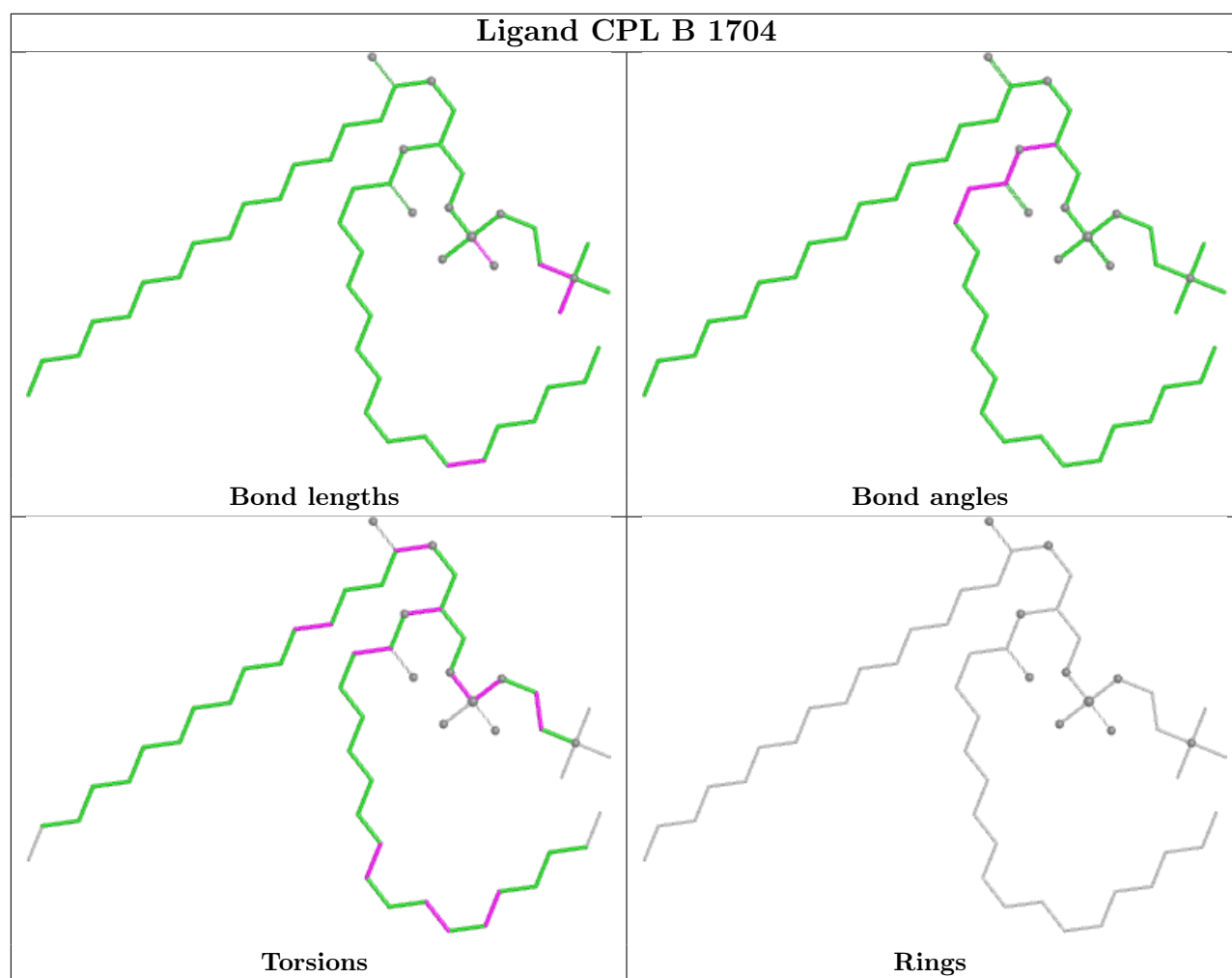


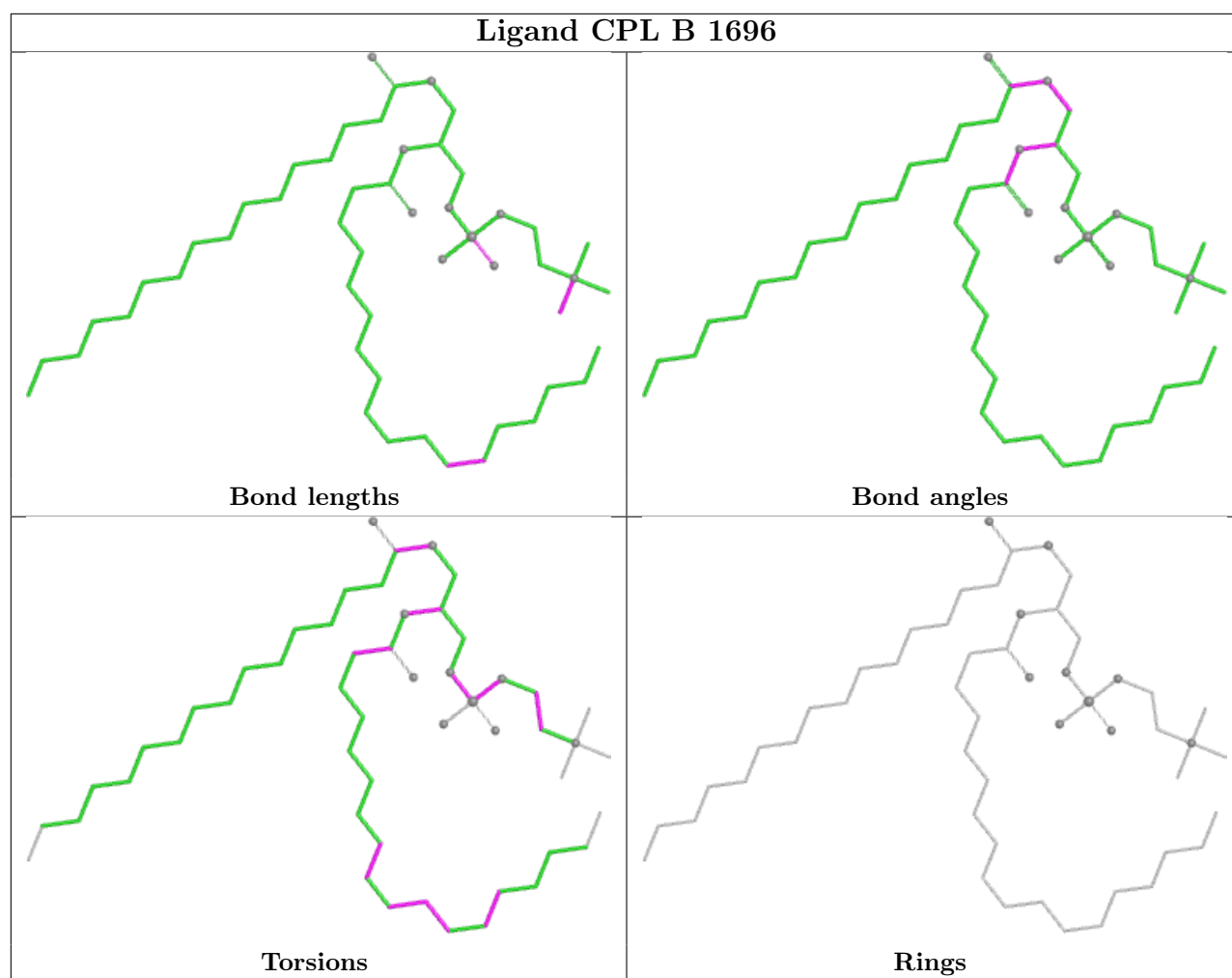


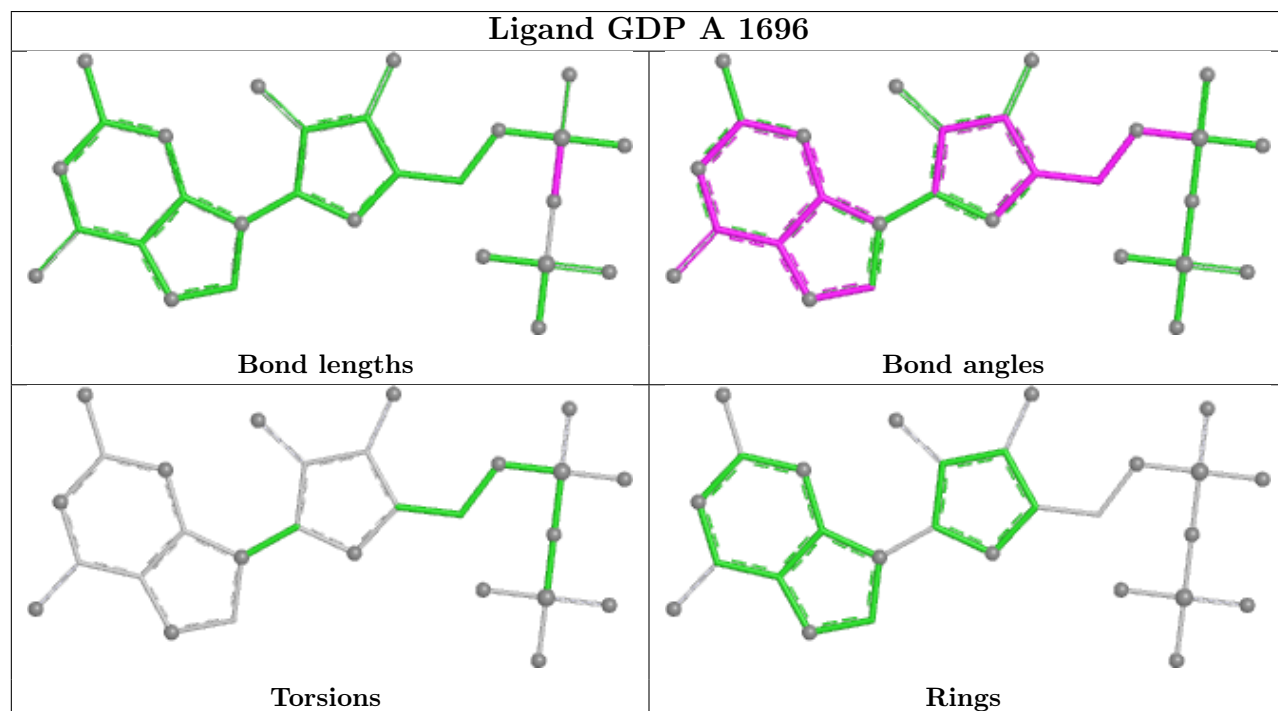
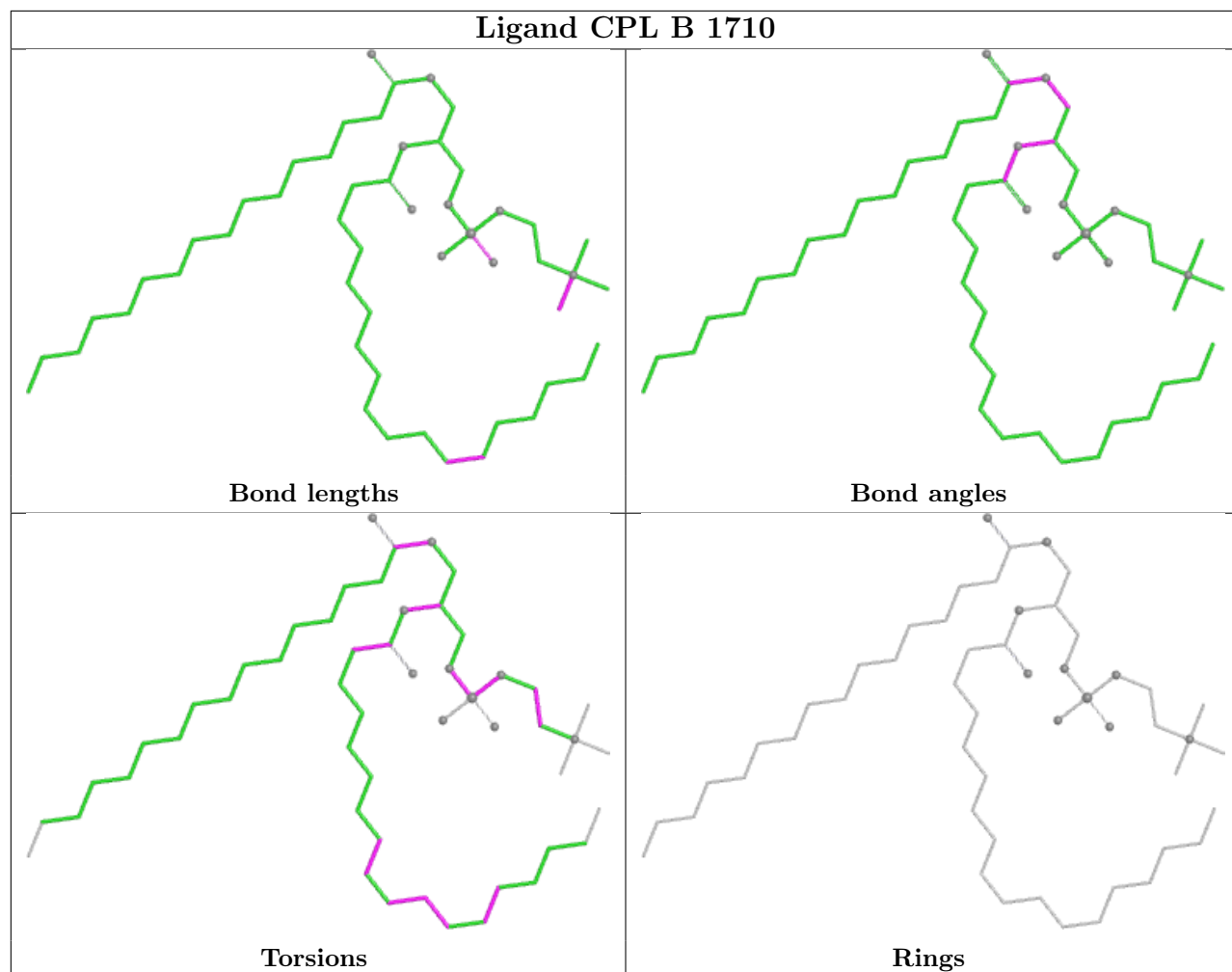


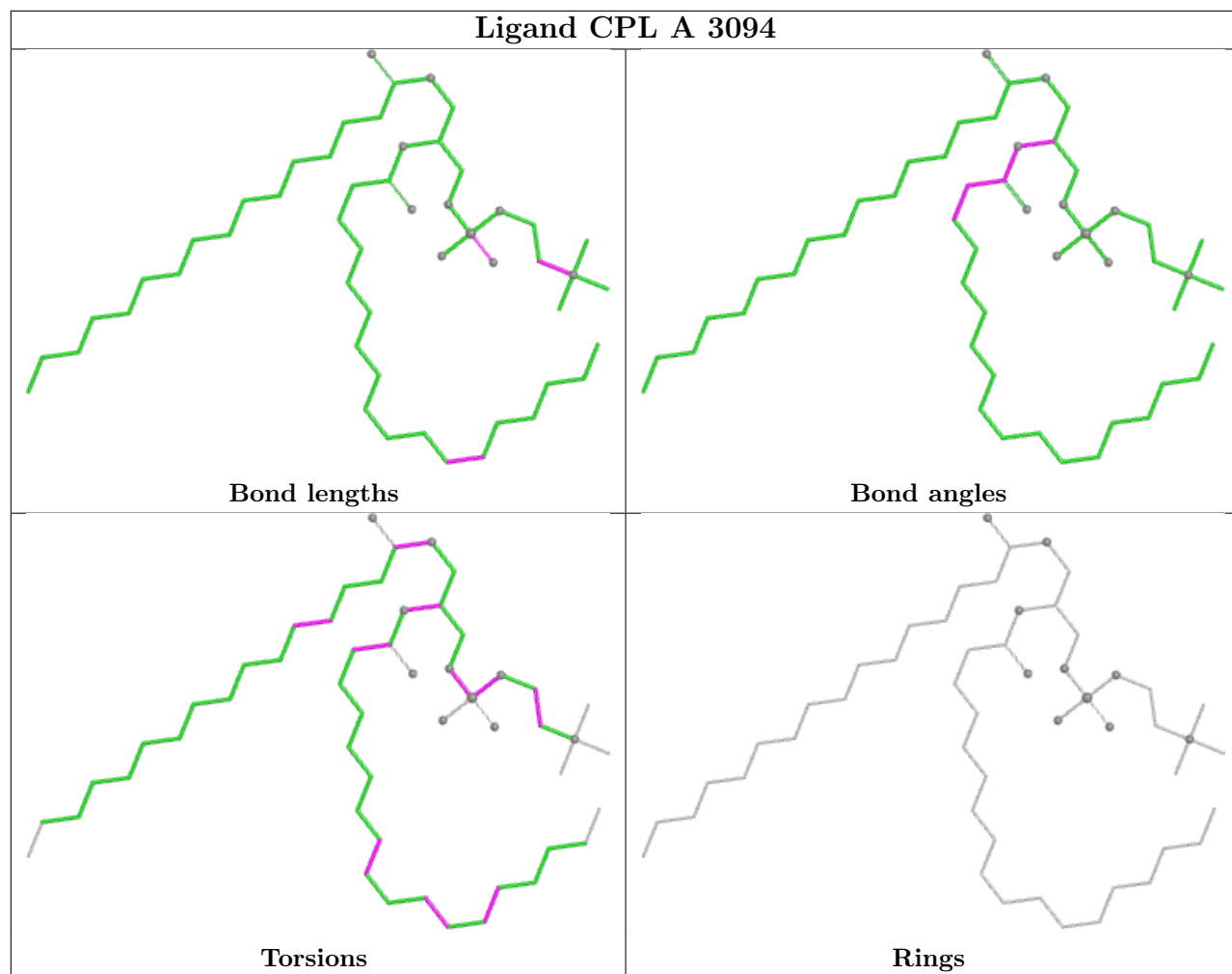


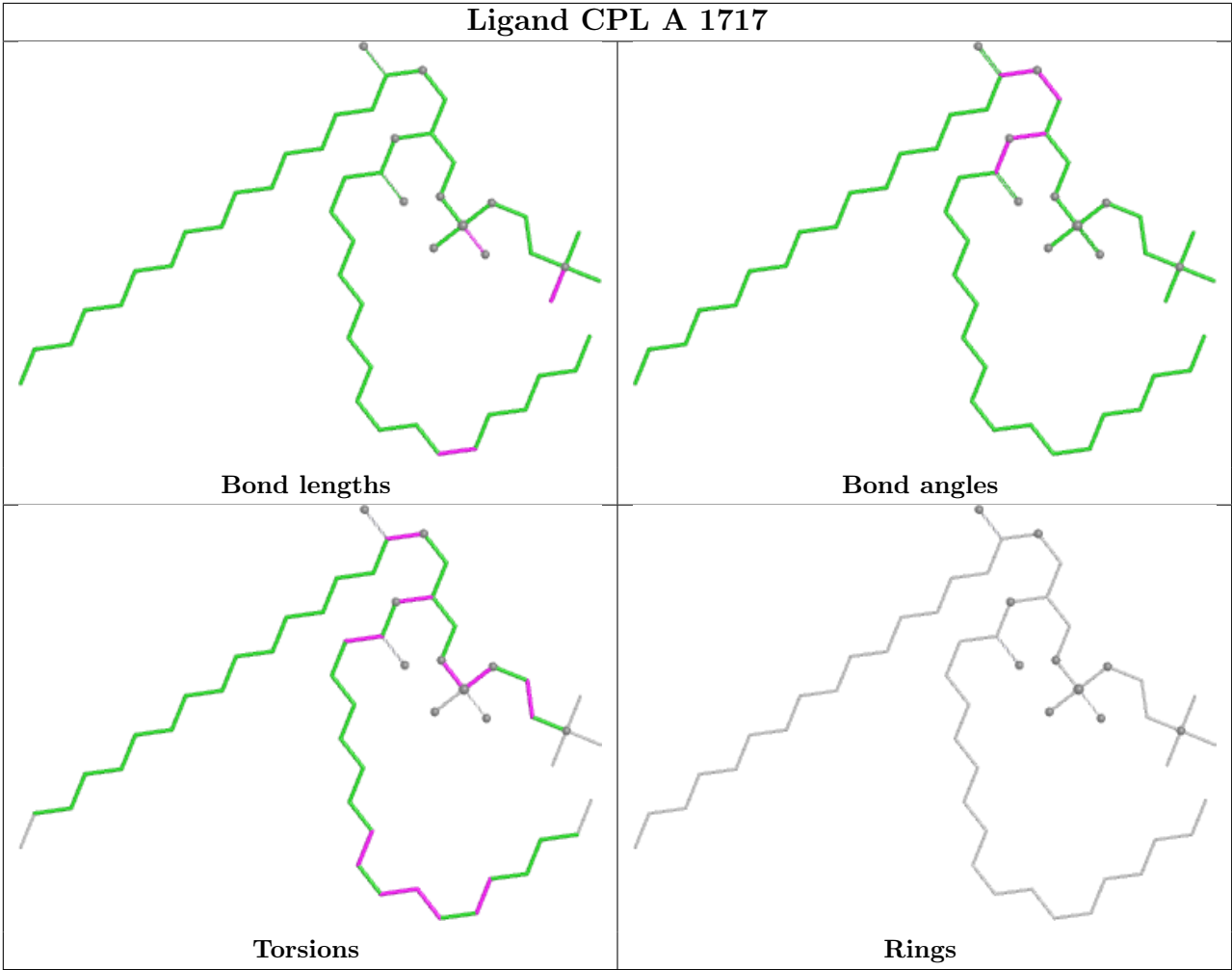












5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	4
1	A	4

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	309:GLY	C	310:THR	N	31.27
1	A	309:GLY	C	310:THR	N	30.13

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	656:ARG	C	657:GLU	N	17.03
1	A	656:ARG	C	657:GLU	N	15.14
1	B	360:ASP	C	361:VAL	N	13.73

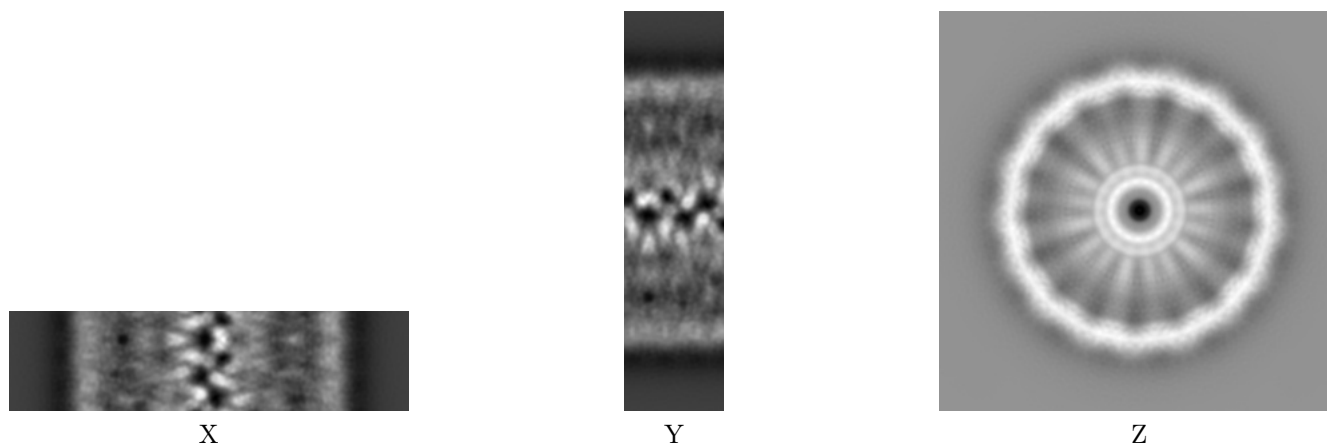
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1589. 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](#)

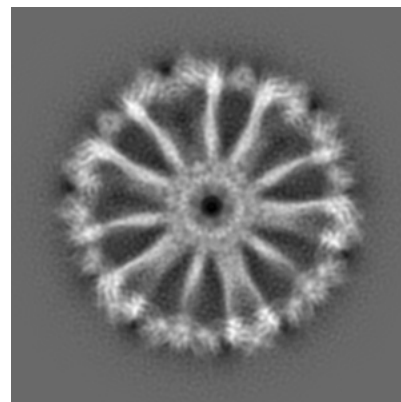
6.2.1 Primary map



X Index: 165



Y Index:
165



Z Index: 40

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

6.3 Largest variance slices [i](#)

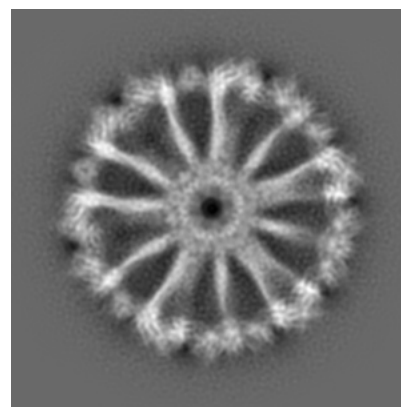
6.3.1 Primary map



X Index: 166



Y Index:
167

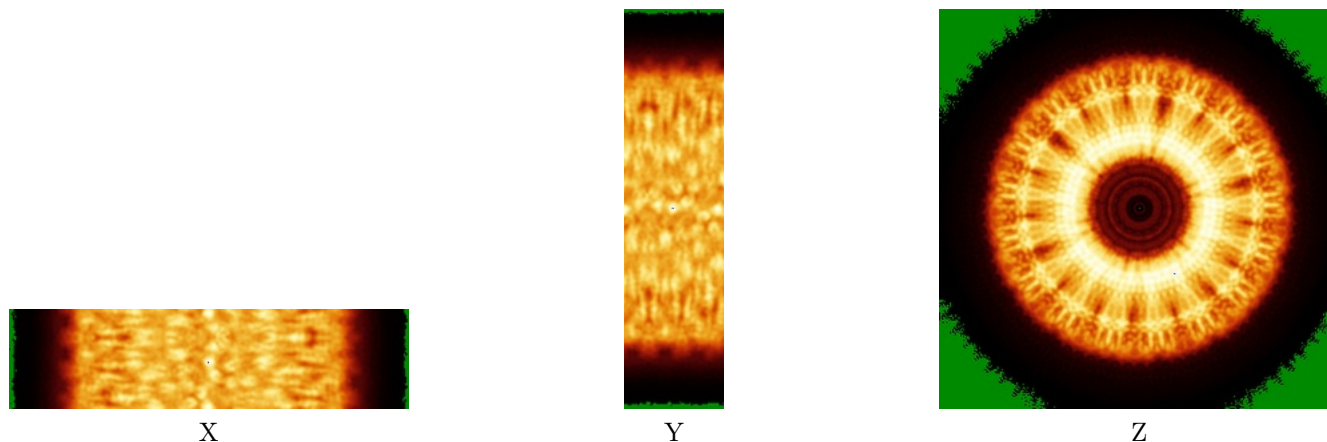


Z Index: 50

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



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](#)

This section was not generated.

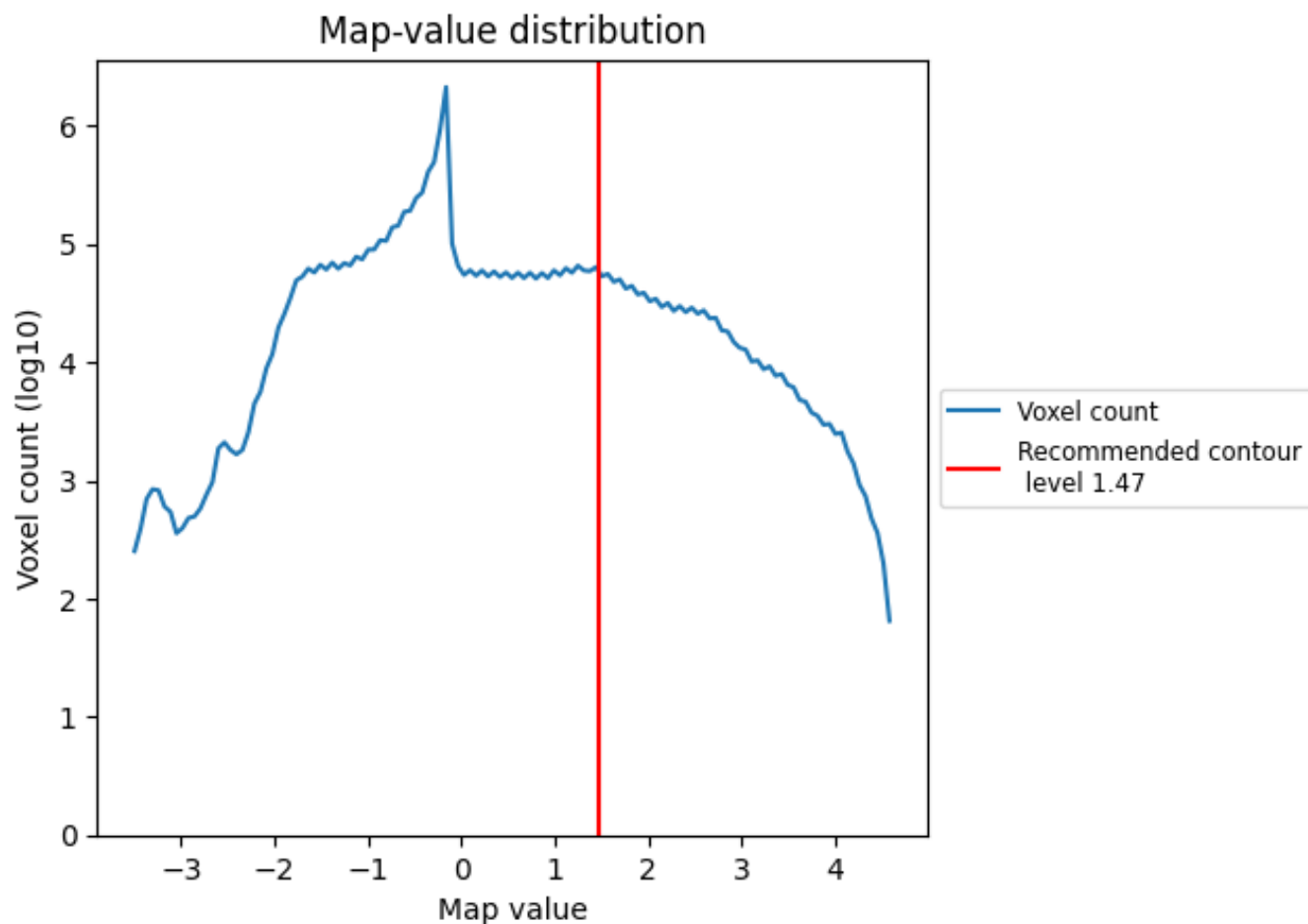
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

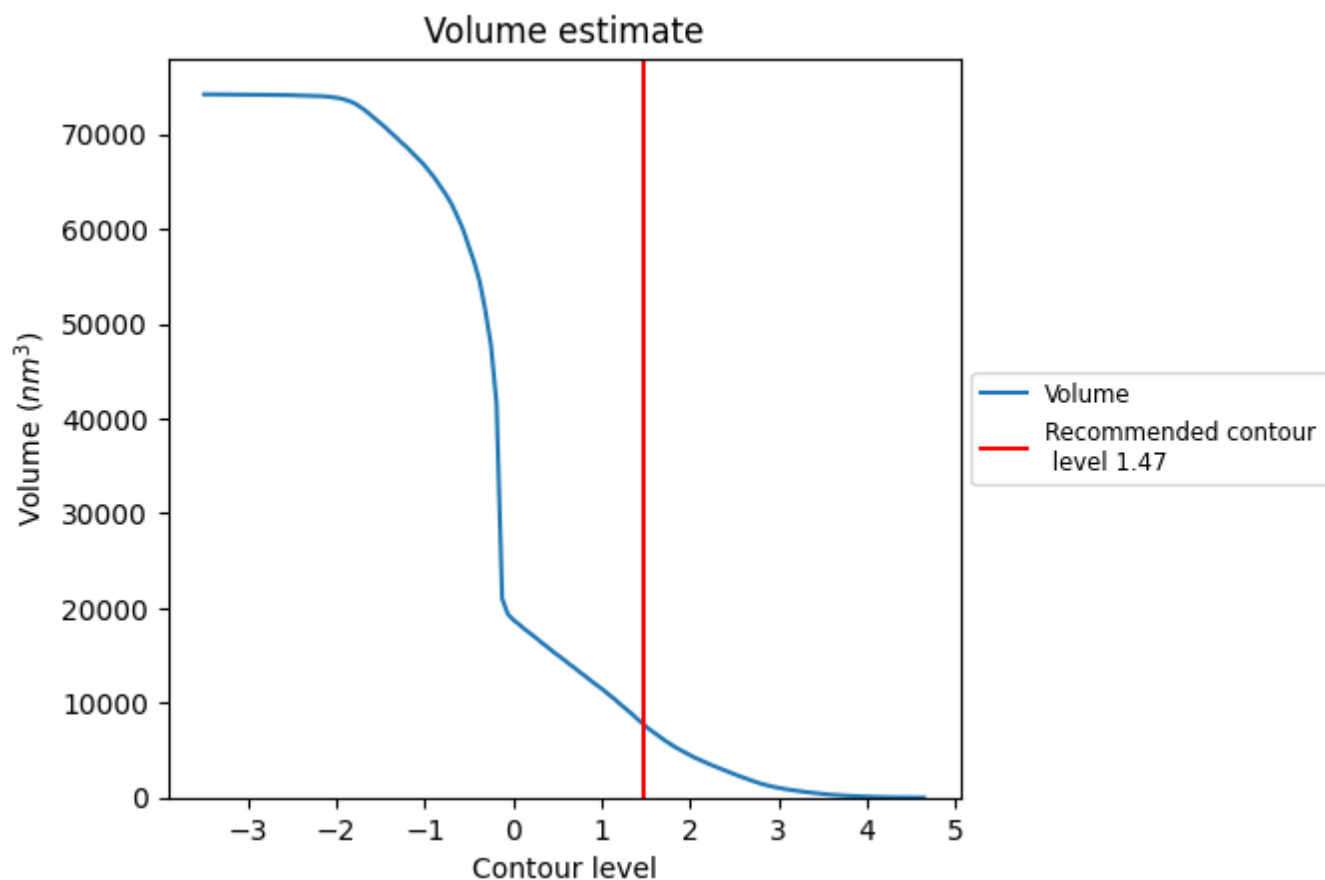
This section contains the results of statistical analysis of the map.

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 7767 nm³; this corresponds to an approximate mass of 7016 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](#)

This section was not generated. The rotationally averaged power spectrum could not be displayed.

8 Fourier-Shell correlation ⓘ

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

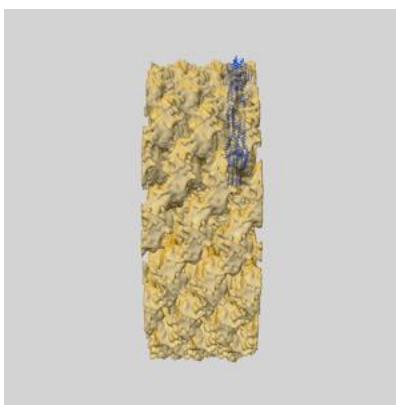
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1589 and PDB model 2W6D. Per-residue inclusion information can be found in section [3](#) on page [8](#).

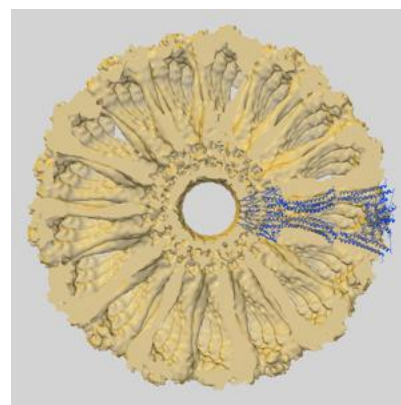
9.1 Map-model overlay [i](#)



X



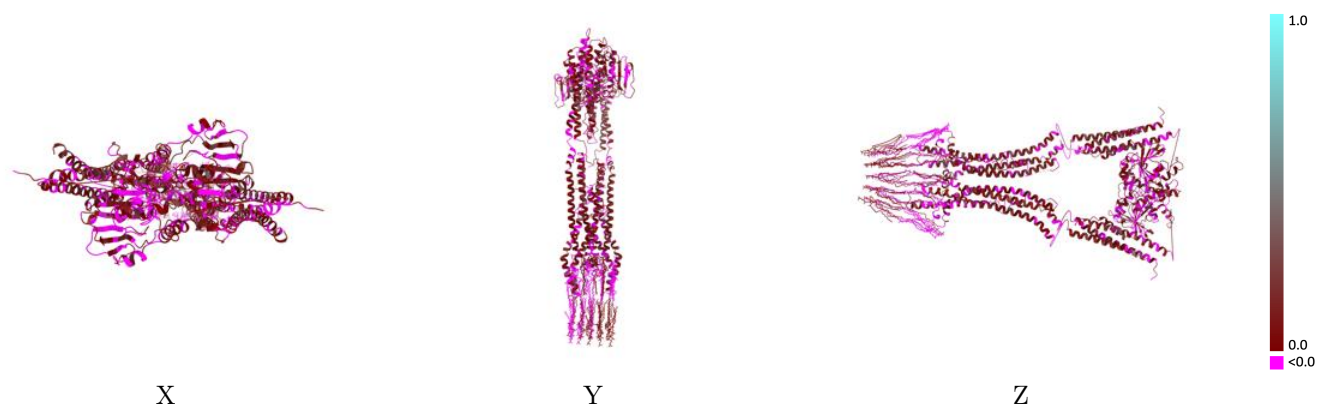
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.47 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](#)

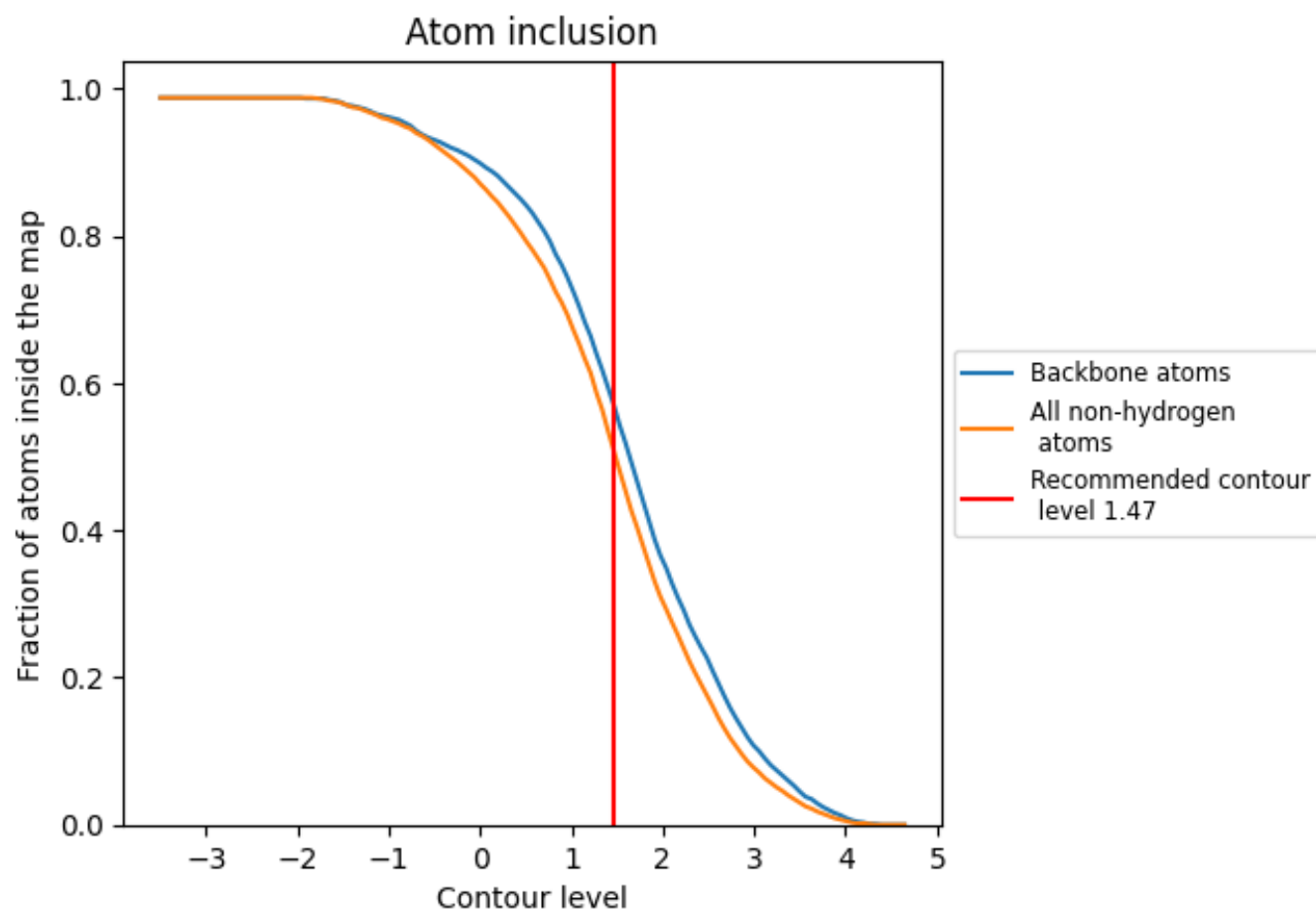


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 57% of all backbone atoms, 51% 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 (1.47) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5060	0.0410
A	0.5080	0.0390
B	0.5030	0.0430

