



wwPDB NMR Structure Validation Summary Report ⓘ

Jun 17, 2020 – 12:42 am BST

PDB ID : 2MZH
Title : NMR Solution Structure of the PRO Form of Human Matrilysin (proMMP-7)
in Complex with Zwitterionic Membrane
Authors : Prior, S.H.; Van Doren, S.R.
Deposited on : 2015-02-12

This is a wwPDB NMR Structure 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/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

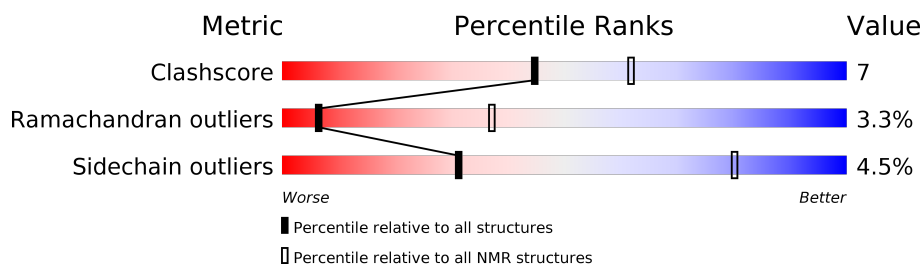
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 44%.

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)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	248	

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 11 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:11-A:239 (229)	0.66	11

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 17, 19
2	9, 18
3	3, 15
Single-model clusters	16; 20

3 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9696 atoms, of which 1898 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Matrilysin.

Mol	Chain	Residues	Atoms						Trace
1	A	248	Total	C	H	N	O	S	0
			3850	1240	1898	339	364	9	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	195	ALA	GLU	ENGINEERED MUTATION	UNP P09237

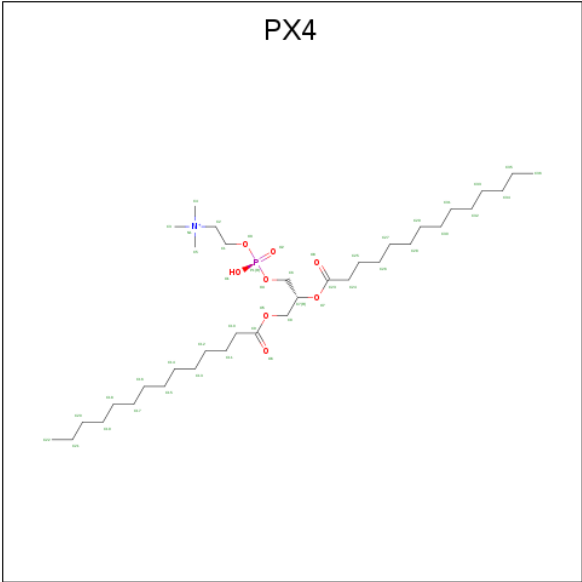
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	
2	A	2	Total	Ca
			2	2

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
3	A	2	Total	Zn
			2	2

- Molecule 4 is 1,2-DIMYRISTOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PX4) (formula: C₃₆H₇₃NO₈P).



Mol	Chain	Residues	Atoms				
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1

Continued on next page...

Continued from previous page...

[illegible]

Continued on next page...

[illegible]

[illegible]

[illegible]

Continued from previous page...

[illegible]

Continued on next page...

Continued from previous page...

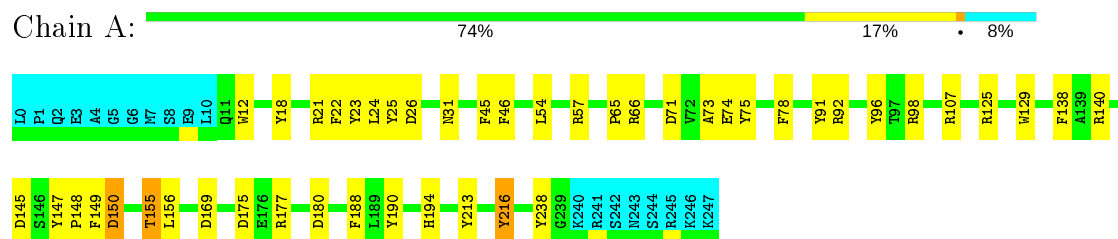
Mol	Chain	Residues	Atoms				
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1
4	A	1	Total	C	N	O	P
			46	36	1	8	1

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

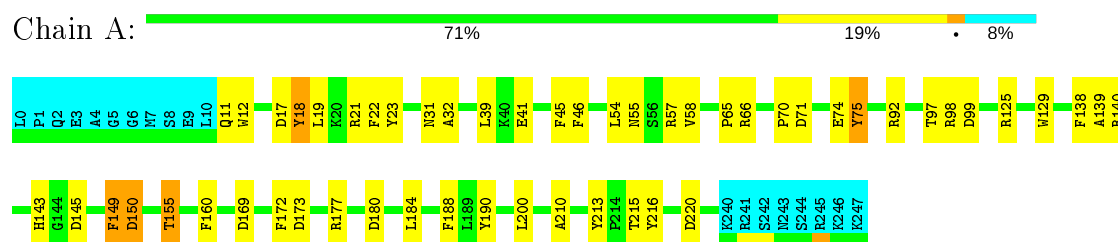
- Molecule 1: Matrilysin



4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 11. Colouring as in section 4.1 above.

- Molecule 1: Matrilysin



5 Refinement protocol and experimental data overview

The models were refined using the following method: *molecular dynamics*.

Of the 10000 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
HADDOCK	structure solution	2.1
GROMOS	refinement	4.5.7

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1503
Number of shifts mapped to atoms	1503
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	44%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, CA, PX4

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 (average) 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	0.52±0.00	0±0/1858 (0.0± 0.0%)	2.04±0.04	58±6/2520 (2.3± 0.2%)
All	All	0.52	0/37160 (0.0%)	2.04	1156/50400 (2.3%)

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	Planarity
1	A	0.0±0.0	6.8±2.3
All	All	0	135

There are no bond-length outliers.

5 of 435 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	140	ARG	NE-CZ-NH2	-20.93	109.84	120.30	5	9
1	A	75	TYR	CB-CG-CD2	-17.54	110.47	121.00	4	5
1	A	177	ARG	NE-CZ-NH2	-17.42	111.59	120.30	13	9
1	A	18	TYR	CB-CG-CD2	-17.28	110.63	121.00	7	9
1	A	98	ARG	NE-CZ-NH2	-16.76	111.92	120.30	18	8

There are no chirality outliers.

5 of 58 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	23	TYR	Sidechain,Peptide	9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group	Models (Total)
1	A	238	TYR	Sidechain	6
1	A	147	TYR	Sidechain	6
1	A	216	TYR	Sidechain	6
1	A	96	TYR	Sidechain,Mainchain	6

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1805	1741	1741	2±2
4	A	5842	0	9144	125±14
All	All	153020	34820	217699	2534

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

5 of 2457 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
4:A:320:PX4:H17	4:A:353:PX4:H16	0.96	1.32	10	1
4:A:373:PX4:H41	4:A:421:PX4:H66	0.96	1.37	1	1
4:A:389:PX4:H50	4:A:398:PX4:H22	0.95	1.37	2	1
4:A:313:PX4:H25	4:A:348:PX4:H64	0.95	1.39	6	1
4:A:313:PX4:H26	4:A:354:PX4:H50	0.94	1.35	5	1

6.3 Torsion angles [i](#)

6.3.1 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 NMR 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	229/248 (92%)	202±3 (88±1%)	20±3 (9±1%)	8±2 (3±1%)	6	37

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	4580/4960 (92%)	4036 (88%)	391 (9%)	153 (3%)	6	37

5 of 32 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	155	THR	20
1	A	65	PRO	17
1	A	31	ASN	15
1	A	150	ASP	13
1	A	74	GLU	11

6.3.2 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 NMR 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	190/206 (92%)	182±3 (96±2%)	9±3 (4±2%)	31	80
All	All	3800/4120 (92%)	3630 (96%)	170 (4%)	31	80

5 of 60 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	155	THR	13
1	A	150	ASP	13
1	A	156	LEU	11
1	A	216	TYR	11
1	A	180	ASP	9

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

Of 131 ligands modelled in this entry, 4 are monoatomic - leaving 127 for Mogul analysis.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
4	PX4	A	392	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	340	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	407	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	405	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	403	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	317	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	310	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	333	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	337	-	45,45,45	0.63±0.01	0±0 (0±0%)
4	PX4	A	376	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	323	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	429	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	359	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	410	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	307	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	380	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	399	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	328	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	319	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	327	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	424	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	316	-	45,45,45	0.63±0.01	0±0 (0±0%)
4	PX4	A	330	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	391	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	430	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	355	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	326	-	45,45,45	0.63±0.00	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
4	PX4	A	320	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	358	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	374	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	384	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	413	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	381	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	387	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	419	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	365	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	347	-	45,45,45	0.63±0.01	0±0 (0±0%)
4	PX4	A	357	-	45,45,45	0.63±0.01	0±0 (0±0%)
4	PX4	A	428	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	362	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	397	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	425	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	409	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	324	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	408	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	344	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	411	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	343	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	389	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	366	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	394	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	311	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	417	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	334	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	351	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	415	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	412	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	346	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	426	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	309	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	364	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	431	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	361	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	341	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	321	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	390	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	427	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	313	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	402	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	370	-	45,45,45	0.63±0.00	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
4	PX4	A	414	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	375	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	385	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	422	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	418	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	393	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	372	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	404	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	354	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	382	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	367	-	45,45,45	0.63±0.01	0±0 (0±0%)
4	PX4	A	349	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	312	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	378	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	338	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	373	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	332	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	383	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	379	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	377	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	369	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	314	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	306	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	406	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	325	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	305	-	45,45,45	0.63±0.01	0±0 (0±0%)
4	PX4	A	421	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	329	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	315	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	371	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	420	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	322	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	352	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	350	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	318	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	308	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	335	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	363	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	348	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	368	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	345	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	423	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	353	-	45,45,45	0.63±0.00	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
4	PX4	A	416	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	356	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	388	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	360	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	401	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	395	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	398	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	386	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	331	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	336	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	400	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	396	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	339	-	45,45,45	0.63±0.00	0±0 (0±0%)
4	PX4	A	342	-	45,45,45	0.63±0.01	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
4	PX4	A	392	-	51,53,53	1.53±0.14	0±1 (0±1%)
4	PX4	A	340	-	51,53,53	1.44±0.13	0±0 (0±0%)
4	PX4	A	407	-	51,53,53	1.51±0.16	0±1 (0±1%)
4	PX4	A	405	-	51,53,53	1.50±0.15	0±0 (0±0%)
4	PX4	A	403	-	51,53,53	1.52±0.13	0±0 (0±0%)
4	PX4	A	317	-	51,53,53	1.47±0.16	0±0 (0±0%)
4	PX4	A	310	-	51,53,53	1.50±0.10	0±1 (0±0%)
4	PX4	A	333	-	51,53,53	1.49±0.12	0±0 (0±0%)
4	PX4	A	337	-	51,53,53	1.55±0.17	0±1 (0±1%)
4	PX4	A	376	-	51,53,53	1.54±0.19	0±0 (0±0%)
4	PX4	A	323	-	51,53,53	1.44±0.12	0±0 (0±0%)
4	PX4	A	429	-	51,53,53	1.45±0.18	0±0 (0±0%)
4	PX4	A	359	-	51,53,53	1.48±0.13	0±0 (0±0%)
4	PX4	A	410	-	51,53,53	1.51±0.17	0±0 (0±0%)
4	PX4	A	307	-	51,53,53	1.50±0.17	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
4	PX4	A	380	-	51,53,53	1.50±0.15	0±0 (0±0%)
4	PX4	A	399	-	51,53,53	1.44±0.17	0±0 (0±0%)
4	PX4	A	328	-	51,53,53	1.47±0.14	0±0 (0±0%)
4	PX4	A	319	-	51,53,53	1.55±0.15	0±0 (0±0%)
4	PX4	A	327	-	51,53,53	1.45±0.15	0±0 (0±0%)
4	PX4	A	424	-	51,53,53	1.43±0.14	0±0 (0±0%)
4	PX4	A	316	-	51,53,53	1.53±0.10	0±0 (0±0%)
4	PX4	A	330	-	51,53,53	1.49±0.17	0±0 (0±0%)
4	PX4	A	391	-	51,53,53	1.50±0.14	0±0 (0±0%)
4	PX4	A	430	-	51,53,53	1.48±0.17	0±1 (0±0%)
4	PX4	A	355	-	51,53,53	1.54±0.12	0±1 (0±0%)
4	PX4	A	326	-	51,53,53	1.55±0.13	0±0 (0±0%)
4	PX4	A	320	-	51,53,53	1.47±0.15	0±0 (0±0%)
4	PX4	A	358	-	51,53,53	1.48±0.11	0±0 (0±0%)
4	PX4	A	374	-	51,53,53	1.53±0.10	0±0 (0±0%)
4	PX4	A	384	-	51,53,53	1.55±0.18	0±0 (0±0%)
4	PX4	A	413	-	51,53,53	1.46±0.14	0±0 (0±0%)
4	PX4	A	381	-	51,53,53	1.51±0.15	0±0 (0±0%)
4	PX4	A	387	-	51,53,53	1.42±0.11	0±0 (0±0%)
4	PX4	A	419	-	51,53,53	1.51±0.15	0±0 (0±0%)
4	PX4	A	365	-	51,53,53	1.45±0.16	0±0 (0±0%)
4	PX4	A	347	-	51,53,53	1.45±0.11	0±0 (0±0%)
4	PX4	A	357	-	51,53,53	1.48±0.14	0±0 (0±0%)
4	PX4	A	428	-	51,53,53	1.52±0.16	0±0 (0±0%)
4	PX4	A	362	-	51,53,53	1.44±0.14	0±0 (0±0%)
4	PX4	A	397	-	51,53,53	1.48±0.07	0±0 (0±0%)
4	PX4	A	425	-	51,53,53	1.50±0.14	0±0 (0±0%)
4	PX4	A	409	-	51,53,53	1.49±0.13	0±0 (0±0%)
4	PX4	A	324	-	51,53,53	1.50±0.14	0±0 (0±0%)
4	PX4	A	408	-	51,53,53	1.49±0.12	0±0 (0±0%)
4	PX4	A	344	-	51,53,53	1.48±0.08	0±0 (0±0%)
4	PX4	A	411	-	51,53,53	1.55±0.12	0±0 (0±0%)
4	PX4	A	343	-	51,53,53	1.49±0.13	0±0 (0±0%)
4	PX4	A	389	-	51,53,53	1.47±0.14	0±0 (0±0%)
4	PX4	A	366	-	51,53,53	1.45±0.13	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
4	PX4	A	394	-	51,53,53	1.43±0.14	0±0 (0±0%)
4	PX4	A	311	-	51,53,53	1.56±0.13	0±0 (0±0%)
4	PX4	A	417	-	51,53,53	1.45±0.15	0±0 (0±0%)
4	PX4	A	334	-	51,53,53	1.48±0.11	0±0 (0±0%)
4	PX4	A	351	-	51,53,53	1.52±0.15	0±0 (0±0%)
4	PX4	A	415	-	51,53,53	1.53±0.12	0±0 (0±0%)
4	PX4	A	412	-	51,53,53	1.51±0.17	0±0 (0±0%)
4	PX4	A	346	-	51,53,53	1.48±0.15	0±0 (0±0%)
4	PX4	A	426	-	51,53,53	1.45±0.17	0±0 (0±0%)
4	PX4	A	309	-	51,53,53	1.46±0.11	0±0 (0±0%)
4	PX4	A	364	-	51,53,53	1.45±0.12	0±0 (0±0%)
4	PX4	A	431	-	51,53,53	1.53±0.13	0±0 (0±0%)
4	PX4	A	361	-	51,53,53	1.51±0.11	0±0 (0±0%)
4	PX4	A	341	-	51,53,53	1.47±0.09	0±0 (0±0%)
4	PX4	A	321	-	51,53,53	1.51±0.18	0±0 (0±0%)
4	PX4	A	390	-	51,53,53	1.53±0.17	0±1 (0±1%)
4	PX4	A	427	-	51,53,53	1.47±0.13	0±0 (0±0%)
4	PX4	A	313	-	51,53,53	1.50±0.14	0±0 (0±0%)
4	PX4	A	402	-	51,53,53	1.49±0.13	0±0 (0±0%)
4	PX4	A	370	-	51,53,53	1.53±0.14	0±0 (0±0%)
4	PX4	A	414	-	51,53,53	1.54±0.13	0±1 (0±1%)
4	PX4	A	375	-	51,53,53	1.45±0.17	0±0 (0±0%)
4	PX4	A	385	-	51,53,53	1.53±0.17	0±0 (0±0%)
4	PX4	A	422	-	51,53,53	1.49±0.14	0±0 (0±0%)
4	PX4	A	418	-	51,53,53	1.52±0.08	0±0 (0±0%)
4	PX4	A	393	-	51,53,53	1.49±0.12	0±0 (0±0%)
4	PX4	A	372	-	51,53,53	1.55±0.16	0±0 (0±0%)
4	PX4	A	404	-	51,53,53	1.43±0.12	0±0 (0±0%)
4	PX4	A	354	-	51,53,53	1.50±0.17	0±0 (0±0%)
4	PX4	A	382	-	51,53,53	1.49±0.12	0±0 (0±0%)
4	PX4	A	367	-	51,53,53	1.51±0.18	0±0 (0±0%)
4	PX4	A	349	-	51,53,53	1.54±0.13	0±0 (0±0%)
4	PX4	A	312	-	51,53,53	1.55±0.17	0±0 (0±0%)
4	PX4	A	378	-	51,53,53	1.49±0.14	0±0 (0±0%)
4	PX4	A	338	-	51,53,53	1.46±0.08	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
4	PX4	A	373	-	51,53,53	1.55±0.18	0±0 (0±0%)
4	PX4	A	332	-	51,53,53	1.51±0.15	0±0 (0±0%)
4	PX4	A	383	-	51,53,53	1.48±0.14	0±0 (0±0%)
4	PX4	A	379	-	51,53,53	1.47±0.21	0±0 (0±0%)
4	PX4	A	377	-	51,53,53	1.49±0.14	0±0 (0±0%)
4	PX4	A	369	-	51,53,53	1.52±0.19	0±1 (0±1%)
4	PX4	A	314	-	51,53,53	1.52±0.11	0±0 (0±0%)
4	PX4	A	306	-	51,53,53	1.53±0.16	0±0 (0±0%)
4	PX4	A	406	-	51,53,53	1.52±0.14	0±0 (0±0%)
4	PX4	A	325	-	51,53,53	1.49±0.16	0±1 (0±1%)
4	PX4	A	305	-	51,53,53	1.48±0.15	0±1 (0±1%)
4	PX4	A	421	-	51,53,53	1.53±0.15	0±0 (0±0%)
4	PX4	A	329	-	51,53,53	1.46±0.13	0±0 (0±0%)
4	PX4	A	315	-	51,53,53	1.50±0.15	0±0 (0±0%)
4	PX4	A	371	-	51,53,53	1.46±0.12	0±0 (0±0%)
4	PX4	A	420	-	51,53,53	1.51±0.14	0±0 (0±0%)
4	PX4	A	322	-	51,53,53	1.47±0.13	0±0 (0±0%)
4	PX4	A	352	-	51,53,53	1.49±0.19	0±0 (0±0%)
4	PX4	A	350	-	51,53,53	1.43±0.18	0±0 (0±0%)
4	PX4	A	318	-	51,53,53	1.53±0.13	0±0 (0±0%)
4	PX4	A	308	-	51,53,53	1.44±0.11	0±0 (0±0%)
4	PX4	A	335	-	51,53,53	1.50±0.11	0±0 (0±0%)
4	PX4	A	363	-	51,53,53	1.54±0.13	0±0 (0±0%)
4	PX4	A	348	-	51,53,53	1.51±0.13	0±0 (0±0%)
4	PX4	A	368	-	51,53,53	1.52±0.13	0±0 (0±0%)
4	PX4	A	345	-	51,53,53	1.49±0.10	0±0 (0±0%)
4	PX4	A	423	-	51,53,53	1.52±0.17	0±0 (0±0%)
4	PX4	A	353	-	51,53,53	1.55±0.16	0±0 (0±0%)
4	PX4	A	416	-	51,53,53	1.43±0.10	0±0 (0±0%)
4	PX4	A	356	-	51,53,53	1.49±0.13	0±0 (0±0%)
4	PX4	A	388	-	51,53,53	1.53±0.17	0±1 (0±0%)
4	PX4	A	360	-	51,53,53	1.48±0.13	0±0 (0±0%)
4	PX4	A	401	-	51,53,53	1.51±0.17	0±0 (0±0%)
4	PX4	A	395	-	51,53,53	1.54±0.12	0±0 (0±0%)
4	PX4	A	398	-	51,53,53	1.47±0.15	0±0 (0±0%)
4	PX4	A	386	-	51,53,53	1.52±0.14	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
4	PX4	A	331	-	51,53,53	1.50±0.18	0±0 (0±0%)
4	PX4	A	336	-	51,53,53	1.48±0.17	0±0 (0±0%)
4	PX4	A	400	-	51,53,53	1.45±0.17	0±0 (0±0%)
4	PX4	A	396	-	51,53,53	1.46±0.12	0±0 (0±0%)
4	PX4	A	339	-	51,53,53	1.46±0.14	0±0 (0±0%)
4	PX4	A	342	-	51,53,53	1.48±0.12	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PX4	A	425	-	-	0±0,49,49,49	-
4	PX4	A	326	-	-	0±0,49,49,49	-
4	PX4	A	402	-	-	0±0,49,49,49	-
4	PX4	A	404	-	-	0±0,49,49,49	-
4	PX4	A	332	-	-	0±0,49,49,49	-
4	PX4	A	340	-	-	0±0,49,49,49	-
4	PX4	A	355	-	-	0±0,49,49,49	-
4	PX4	A	377	-	-	0±0,49,49,49	-
4	PX4	A	306	-	-	0±0,49,49,49	-
4	PX4	A	367	-	-	0±0,49,49,49	-
4	PX4	A	353	-	-	0±0,49,49,49	-
4	PX4	A	308	-	-	0±0,49,49,49	-
4	PX4	A	390	-	-	0±0,49,49,49	-
4	PX4	A	379	-	-	0±0,49,49,49	-
4	PX4	A	398	-	-	0±0,49,49,49	-
4	PX4	A	319	-	-	0±0,49,49,49	-
4	PX4	A	352	-	-	0±0,49,49,49	-
4	PX4	A	401	-	-	0±0,49,49,49	-
4	PX4	A	389	-	-	0±0,49,49,49	-
4	PX4	A	349	-	-	0±0,49,49,49	-
4	PX4	A	324	-	-	0±0,49,49,49	-
4	PX4	A	382	-	-	0±0,49,49,49	-
4	PX4	A	375	-	-	0±0,49,49,49	-
4	PX4	A	369	-	-	0±0,49,49,49	-
4	PX4	A	328	-	-	0±0,49,49,49	-
4	PX4	A	341	-	-	0±0,49,49,49	-
4	PX4	A	396	-	-	0±0,49,49,49	-
4	PX4	A	374	-	-	0±0,49,49,49	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PX4	A	385	-	-	0±0,49,49,49	-
4	PX4	A	331	-	-	0±0,49,49,49	-
4	PX4	A	411	-	-	0±0,49,49,49	-
4	PX4	A	305	-	-	0±0,49,49,49	-
4	PX4	A	358	-	-	0±0,49,49,49	-
4	PX4	A	405	-	-	0±0,49,49,49	-
4	PX4	A	424	-	-	0±0,49,49,49	-
4	PX4	A	417	-	-	0±0,49,49,49	-
4	PX4	A	431	-	-	0±0,49,49,49	-
4	PX4	A	384	-	-	0±0,49,49,49	-
4	PX4	A	336	-	-	0±0,49,49,49	-
4	PX4	A	307	-	-	0±0,49,49,49	-
4	PX4	A	388	-	-	0±0,49,49,49	-
4	PX4	A	392	-	-	0±0,49,49,49	-
4	PX4	A	345	-	-	0±0,49,49,49	-
4	PX4	A	415	-	-	0±0,49,49,49	-
4	PX4	A	372	-	-	0±0,49,49,49	-
4	PX4	A	311	-	-	0±0,49,49,49	-
4	PX4	A	403	-	-	0±0,49,49,49	-
4	PX4	A	412	-	-	0±0,49,49,49	-
4	PX4	A	343	-	-	0±0,49,49,49	-
4	PX4	A	360	-	-	0±0,49,49,49	-
4	PX4	A	399	-	-	0±0,49,49,49	-
4	PX4	A	387	-	-	0±0,49,49,49	-
4	PX4	A	430	-	-	0±0,49,49,49	-
4	PX4	A	426	-	-	0±0,49,49,49	-
4	PX4	A	322	-	-	0±0,49,49,49	-
4	PX4	A	321	-	-	0±0,49,49,49	-
4	PX4	A	383	-	-	0±0,49,49,49	-
4	PX4	A	351	-	-	0±0,49,49,49	-
4	PX4	A	363	-	-	0±0,49,49,49	-
4	PX4	A	397	-	-	0±0,49,49,49	-
4	PX4	A	409	-	-	0±0,49,49,49	-
4	PX4	A	423	-	-	0±0,49,49,49	-
4	PX4	A	391	-	-	0±0,49,49,49	-
4	PX4	A	347	-	-	0±0,49,49,49	-
4	PX4	A	418	-	-	0±0,49,49,49	-
4	PX4	A	393	-	-	0±0,49,49,49	-
4	PX4	A	344	-	-	0±0,49,49,49	-
4	PX4	A	414	-	-	1±0,49,49,49	-
4	PX4	A	312	-	-	0±0,49,49,49	-
4	PX4	A	373	-	-	0±0,49,49,49	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PX4	A	370	-	-	0±0,49,49,49	-
4	PX4	A	422	-	-	0±0,49,49,49	-
4	PX4	A	316	-	-	0±0,49,49,49	-
4	PX4	A	421	-	-	0±0,49,49,49	-
4	PX4	A	342	-	-	0±0,49,49,49	-
4	PX4	A	356	-	-	0±0,49,49,49	-
4	PX4	A	357	-	-	0±0,49,49,49	-
4	PX4	A	408	-	-	0±0,49,49,49	-
4	PX4	A	394	-	-	0±0,49,49,49	-
4	PX4	A	413	-	-	0±0,49,49,49	-
4	PX4	A	406	-	-	0±0,49,49,49	-
4	PX4	A	329	-	-	0±0,49,49,49	-
4	PX4	A	362	-	-	0±0,49,49,49	-
4	PX4	A	410	-	-	0±0,49,49,49	-
4	PX4	A	346	-	-	0±0,49,49,49	-
4	PX4	A	427	-	-	0±0,49,49,49	-
4	PX4	A	325	-	-	0±0,49,49,49	-
4	PX4	A	429	-	-	0±0,49,49,49	-
4	PX4	A	335	-	-	0±0,49,49,49	-
4	PX4	A	339	-	-	0±0,49,49,49	-
4	PX4	A	315	-	-	0±0,49,49,49	-
4	PX4	A	371	-	-	0±0,49,49,49	-
4	PX4	A	309	-	-	0±0,49,49,49	-
4	PX4	A	365	-	-	0±0,49,49,49	-
4	PX4	A	380	-	-	0±0,49,49,49	-
4	PX4	A	359	-	-	0±0,49,49,49	-
4	PX4	A	366	-	-	0±0,49,49,49	-
4	PX4	A	378	-	-	0±0,49,49,49	-
4	PX4	A	350	-	-	0±0,49,49,49	-
4	PX4	A	333	-	-	0±0,49,49,49	-
4	PX4	A	419	-	-	0±0,49,49,49	-
4	PX4	A	416	-	-	0±0,49,49,49	-
4	PX4	A	310	-	-	0±0,49,49,49	-
4	PX4	A	330	-	-	0±0,49,49,49	-
4	PX4	A	428	-	-	0±0,49,49,49	-
4	PX4	A	314	-	-	0±0,49,49,49	-
4	PX4	A	381	-	-	0±0,49,49,49	-
4	PX4	A	337	-	-	0±0,49,49,49	-
4	PX4	A	320	-	-	0±0,49,49,49	-
4	PX4	A	327	-	-	0±0,49,49,49	-
4	PX4	A	334	-	-	0±0,49,49,49	-
4	PX4	A	354	-	-	0±0,49,49,49	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PX4	A	407	-	-	0±0,49,49,49	-
4	PX4	A	361	-	-	0±0,49,49,49	-
4	PX4	A	395	-	-	0±0,49,49,49	-
4	PX4	A	317	-	-	0±0,49,49,49	-
4	PX4	A	368	-	-	0±0,49,49,49	-
4	PX4	A	420	-	-	0±0,49,49,49	-
4	PX4	A	348	-	-	0±0,49,49,49	-
4	PX4	A	386	-	-	0±0,49,49,49	-
4	PX4	A	364	-	-	0±0,49,49,49	-
4	PX4	A	323	-	-	0±0,49,49,49	-
4	PX4	A	338	-	-	0±0,49,49,49	-
4	PX4	A	313	-	-	0±0,49,49,49	-
4	PX4	A	376	-	-	0±0,49,49,49	-
4	PX4	A	400	-	-	0±0,49,49,49	-
4	PX4	A	318	-	-	0±0,49,49,49	-

There are no bond-length outliers.

5 of 267 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
4	A	343	PX4	C8-C7-C6	7.96	92.97	111.79	16	1
4	A	392	PX4	C7-O7-C23	7.71	136.78	117.79	11	1
4	A	384	PX4	C5-N1-C4	7.66	89.28	108.97	6	1
4	A	369	PX4	C8-C7-C6	7.48	94.09	111.79	12	6
4	A	356	PX4	C8-C7-C6	7.31	94.49	111.79	5	3

There are no chirality outliers.

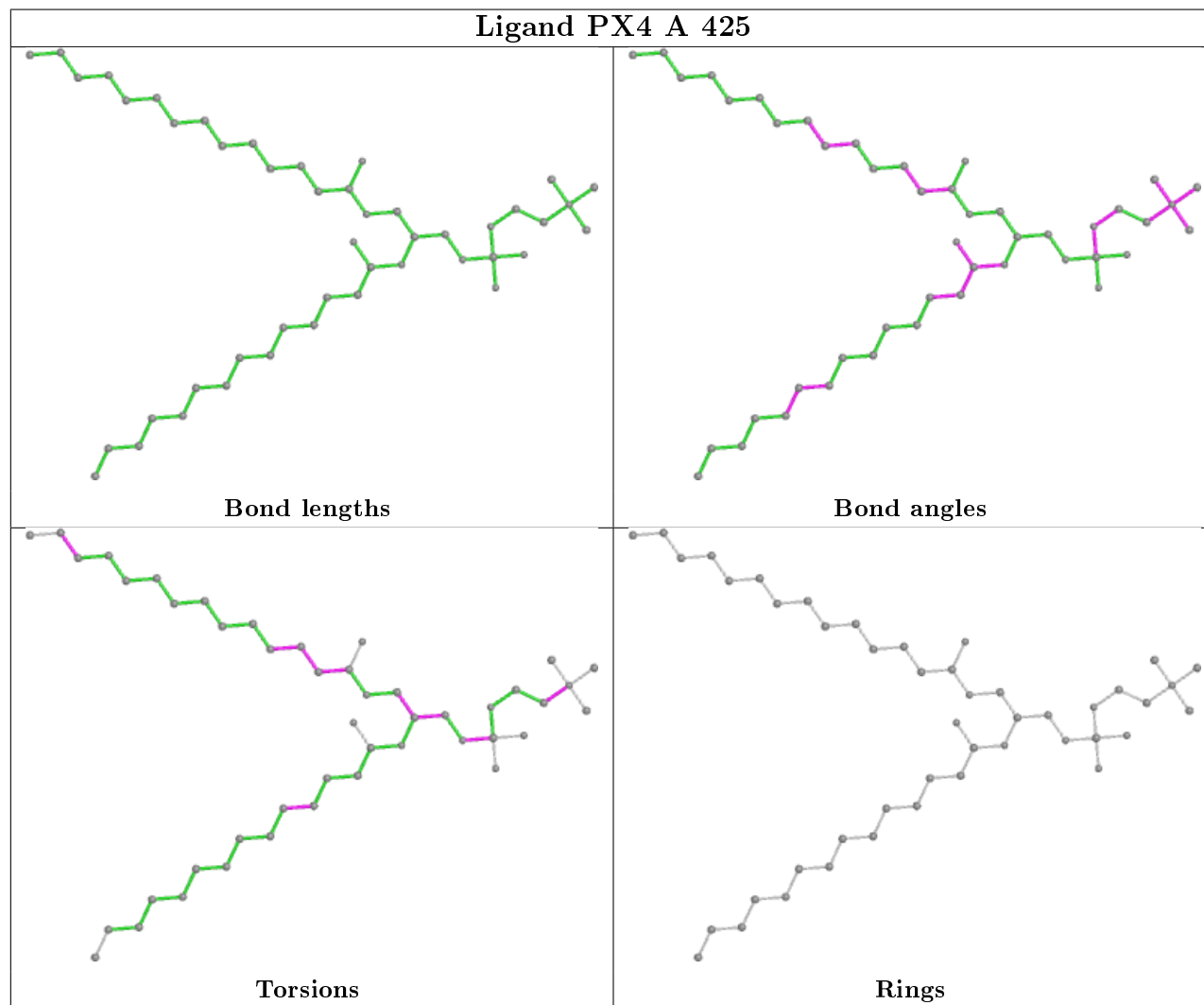
All unique torsion outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

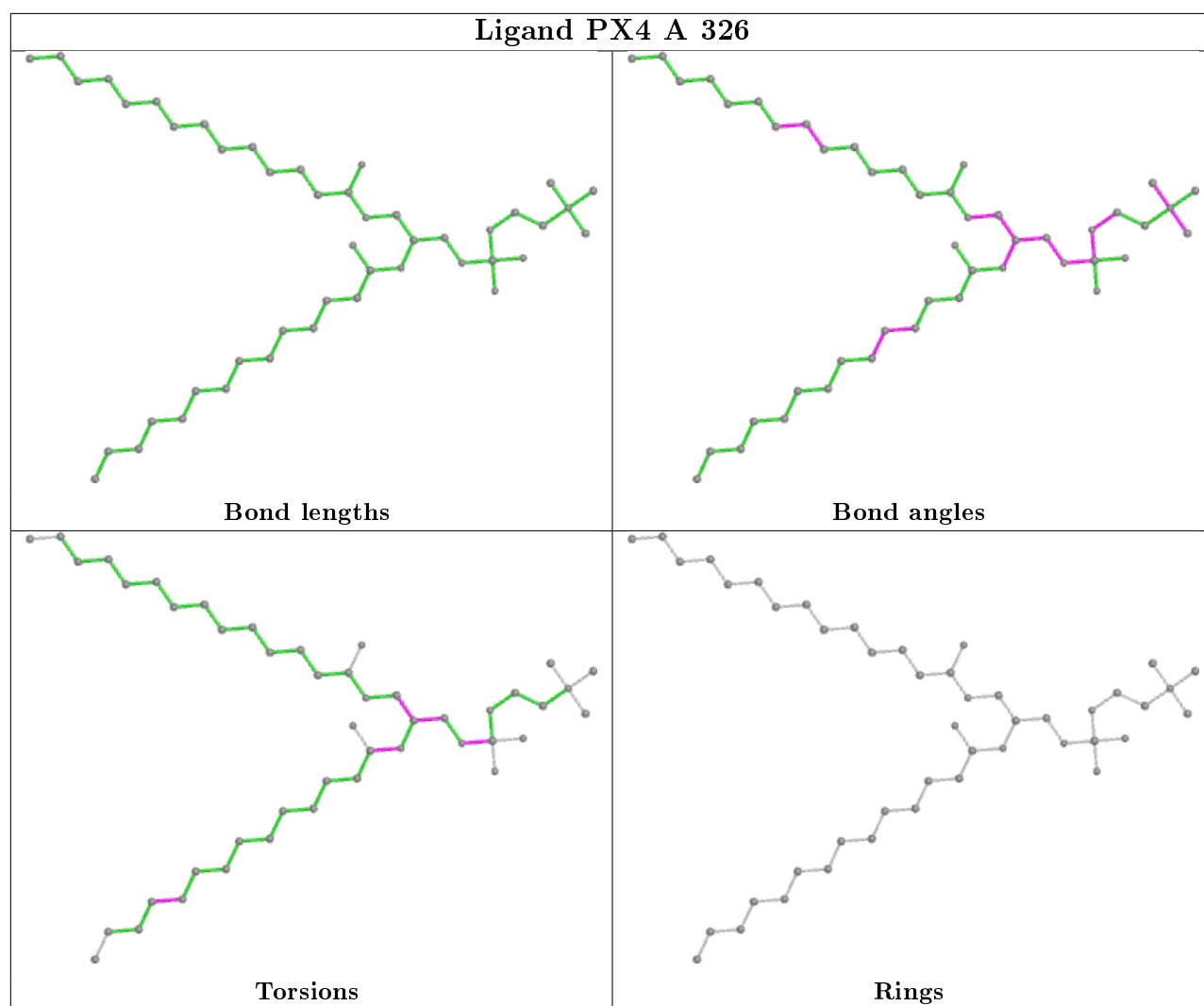
Mol	Chain	Res	Type	Atoms	Models (Total)
4	A	414	PX4	O8-C23-O7-C7	4
4	A	331	PX4	O8-C23-O7-C7	2
4	A	323	PX4	O8-C23-O7-C7	1
4	A	321	PX4	O8-C23-O7-C7	1

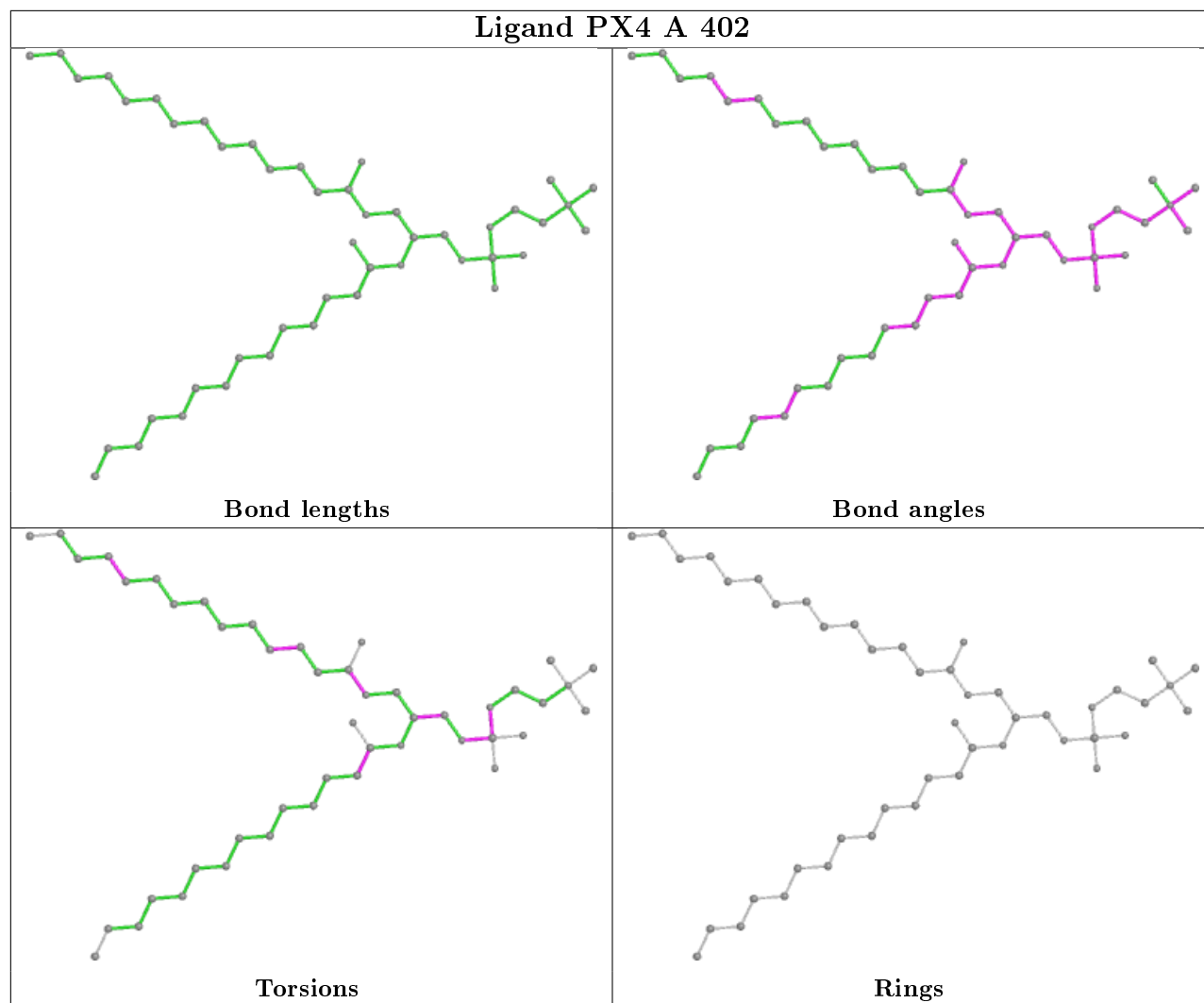
There are no ring outliers.

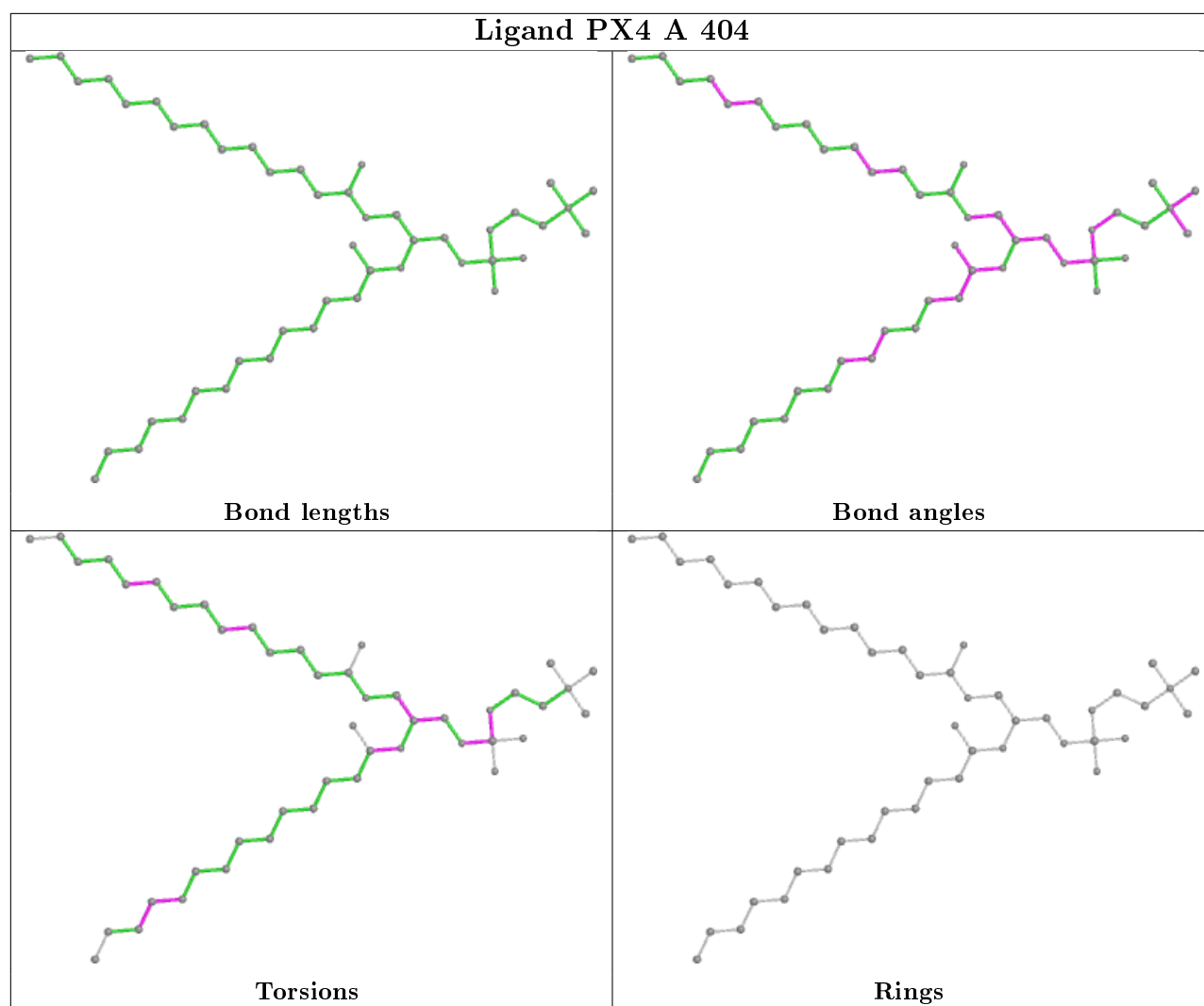
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

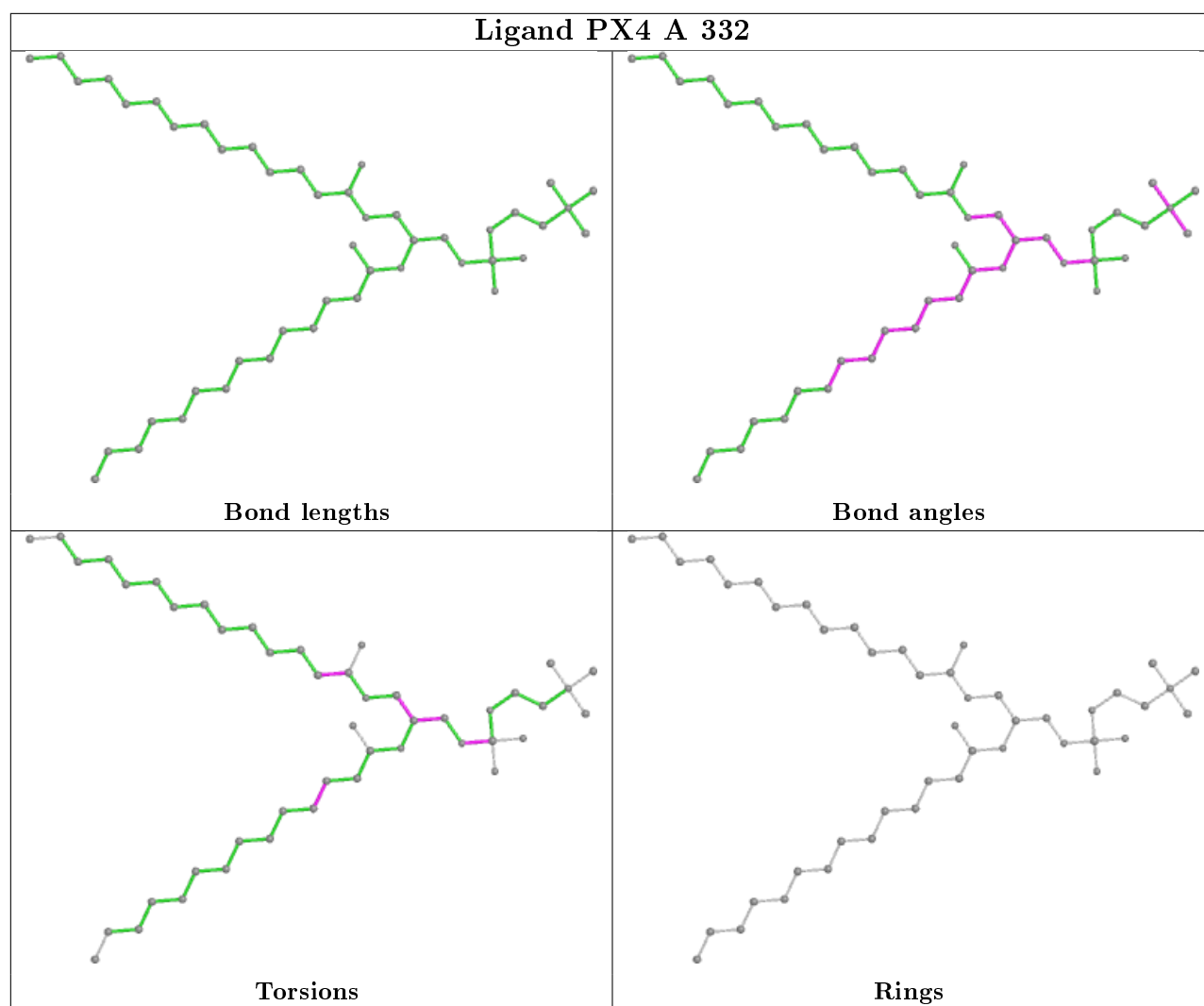
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. 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.

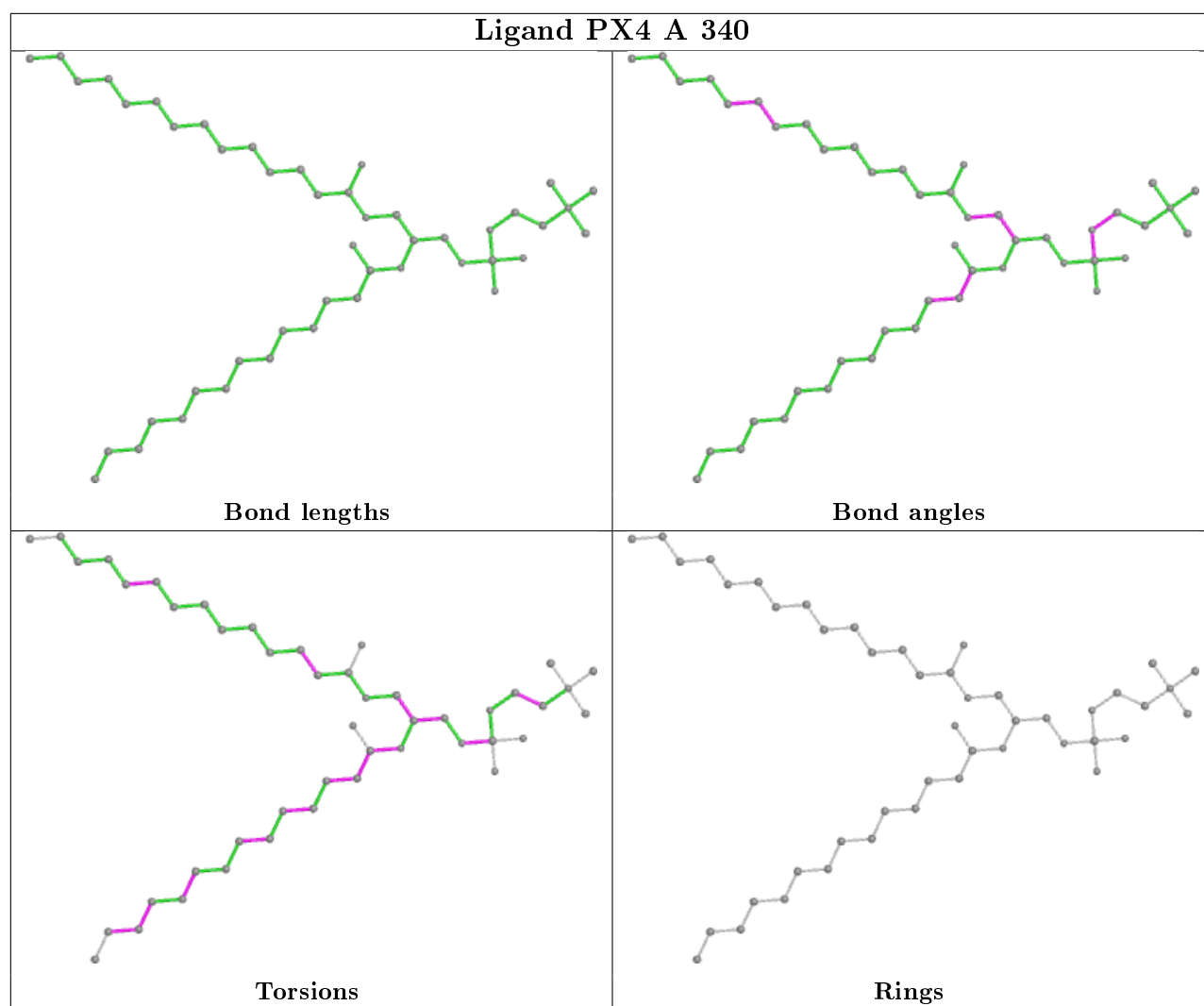


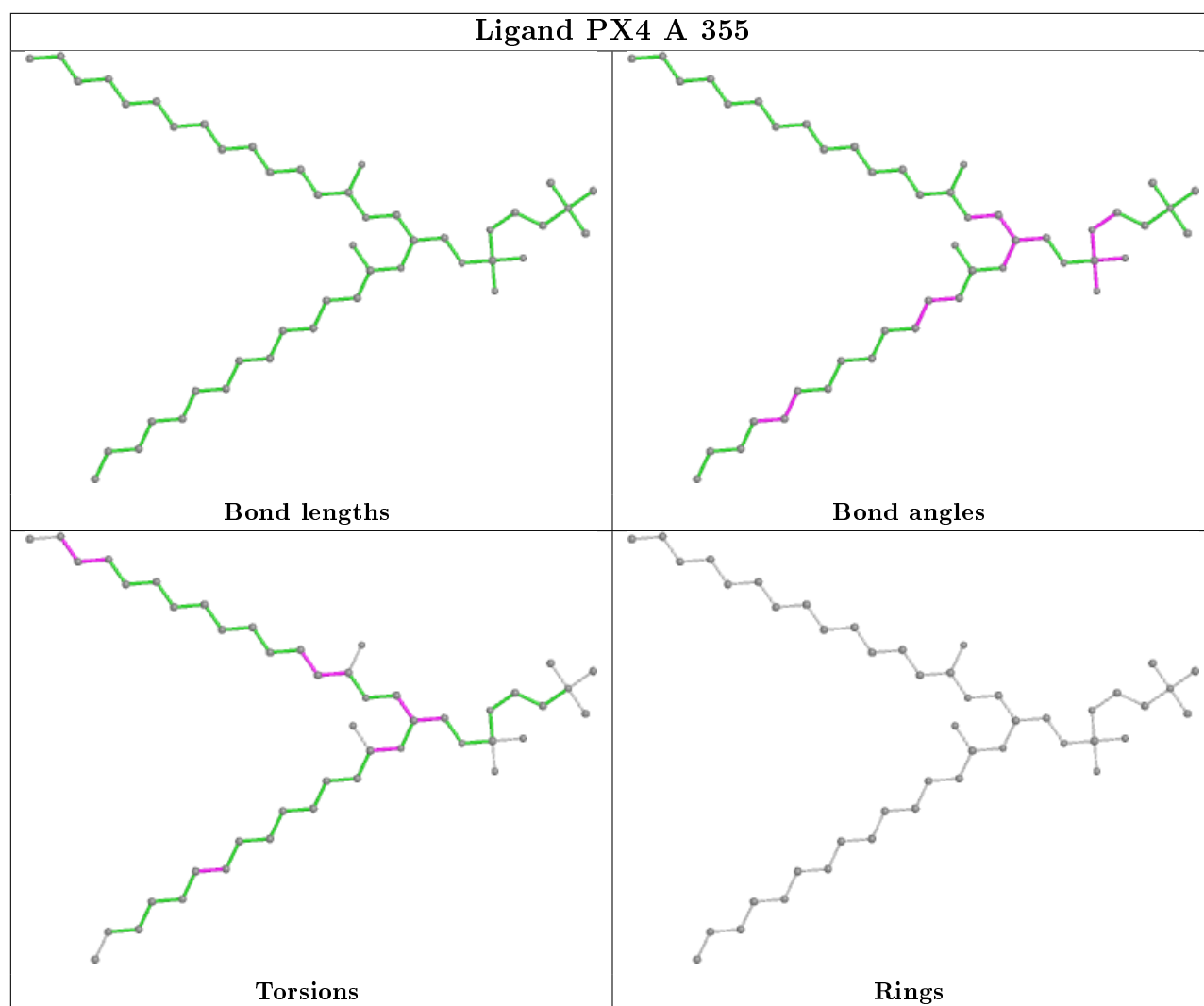




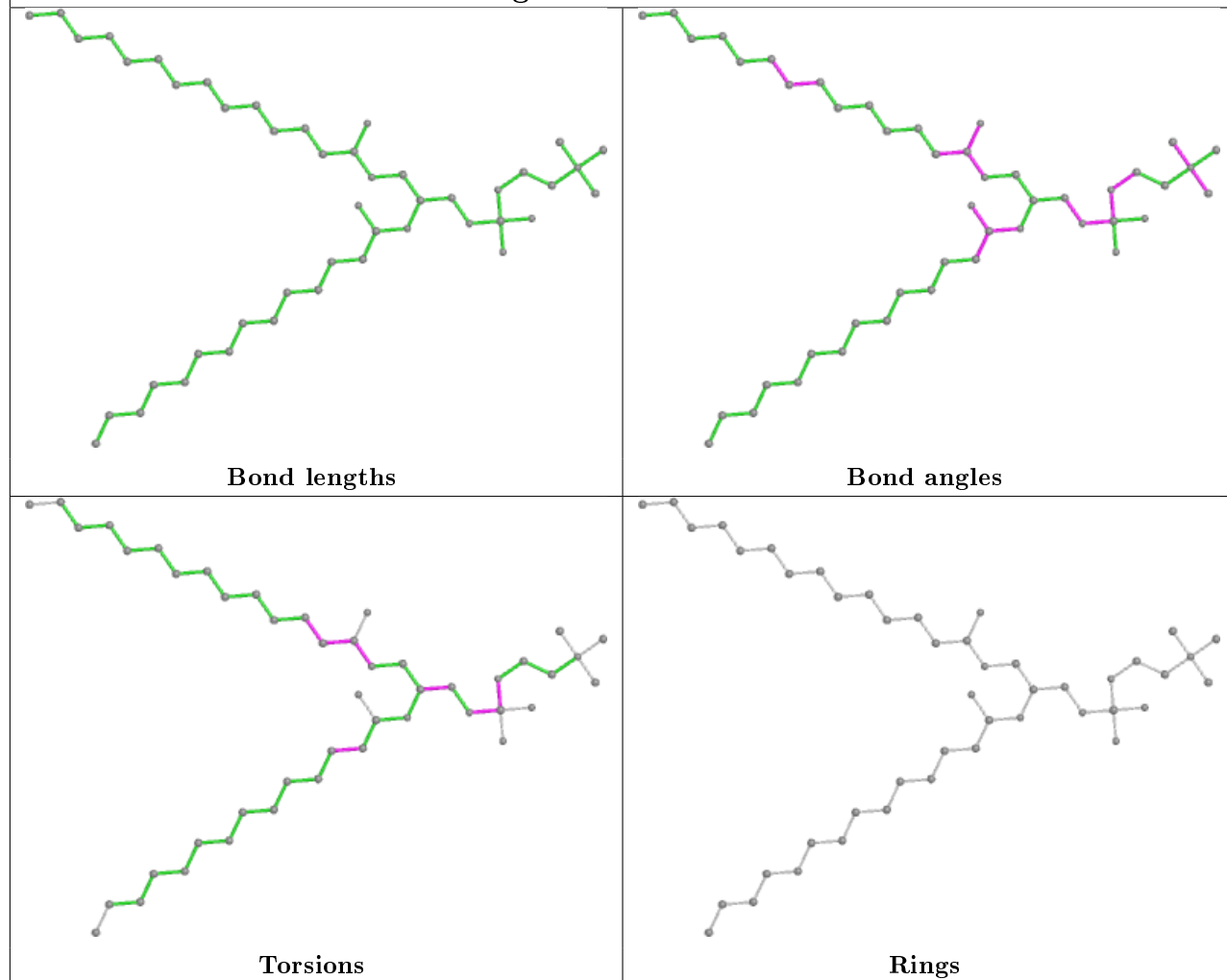


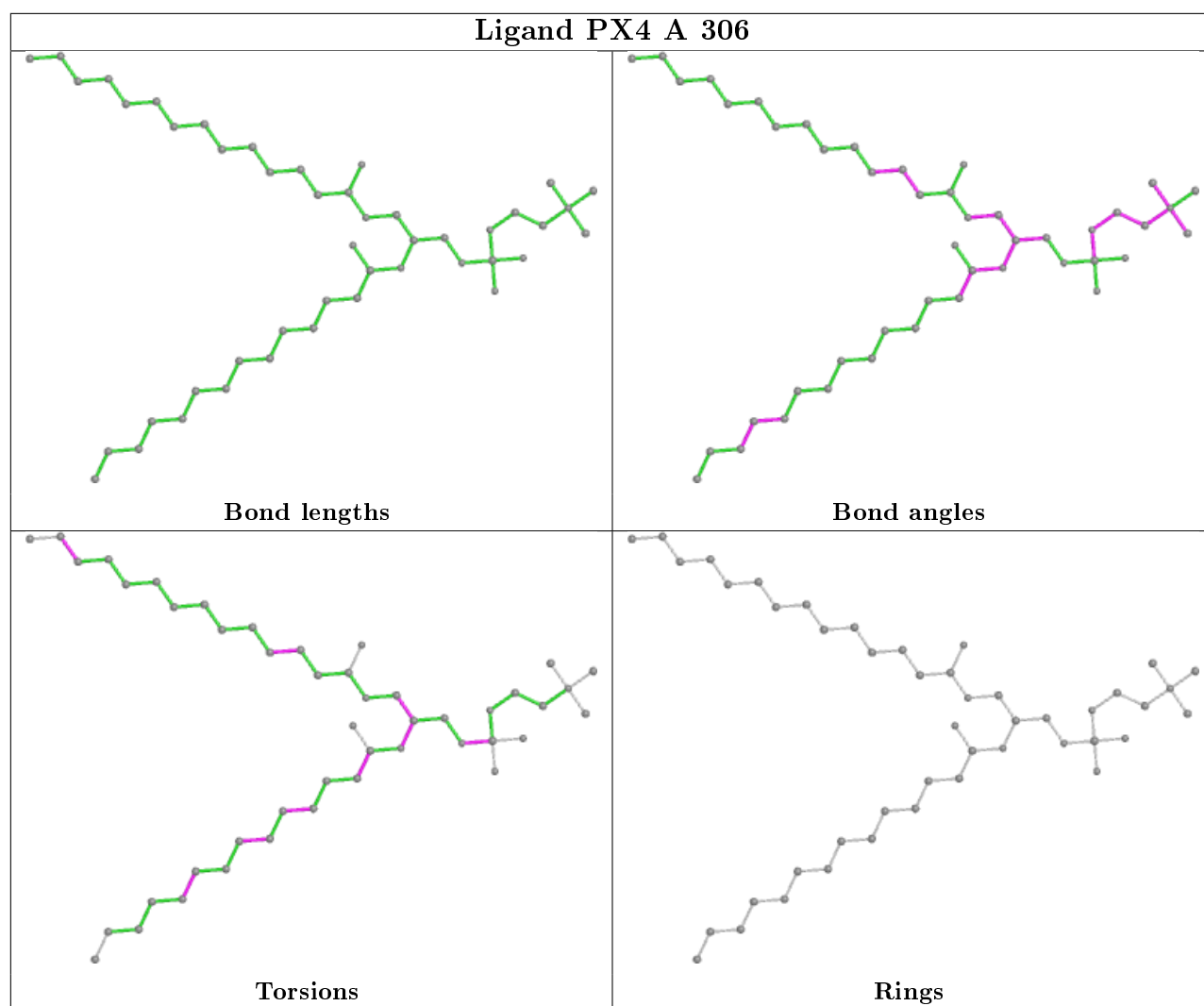




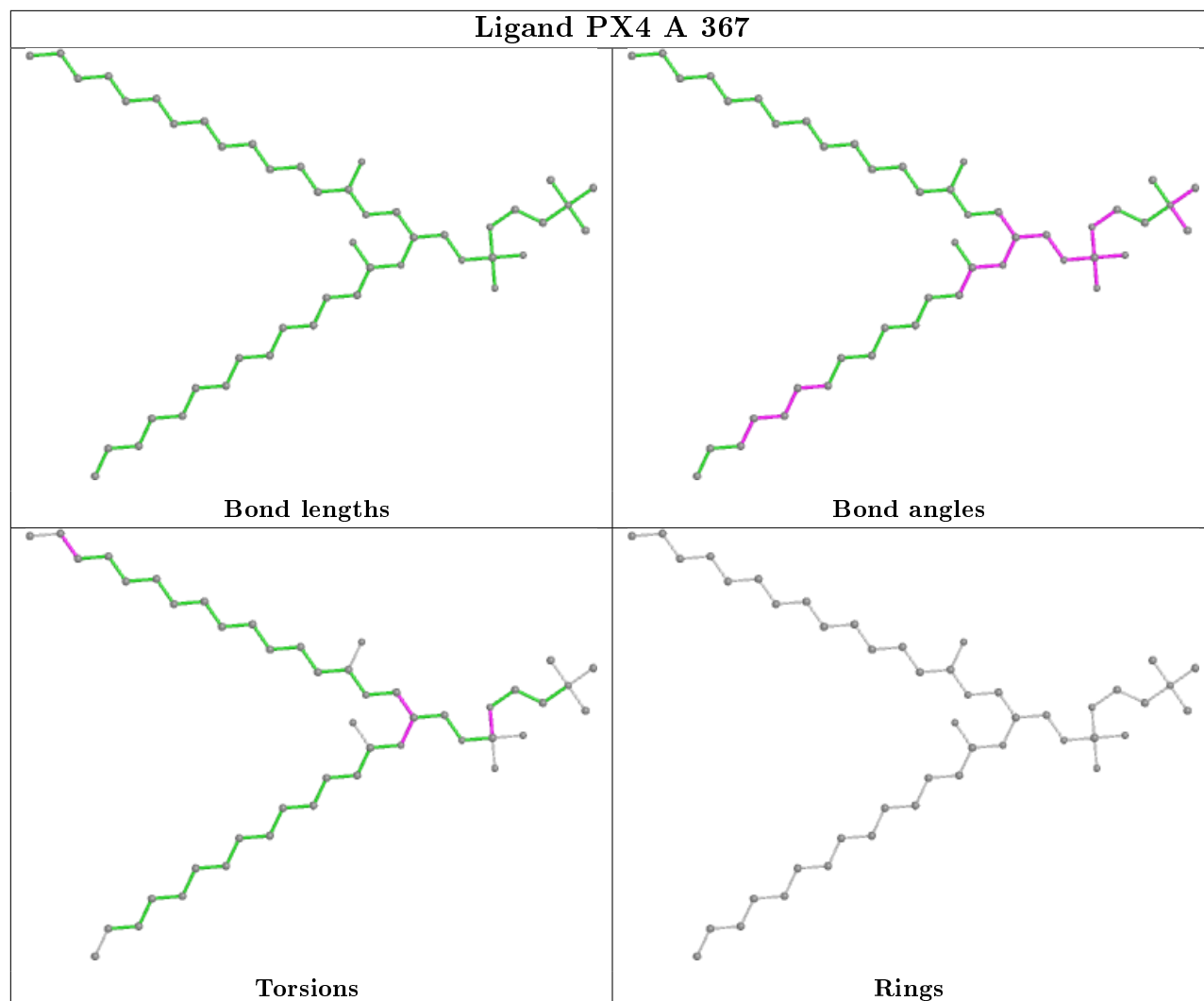


Ligand PX4 A 377

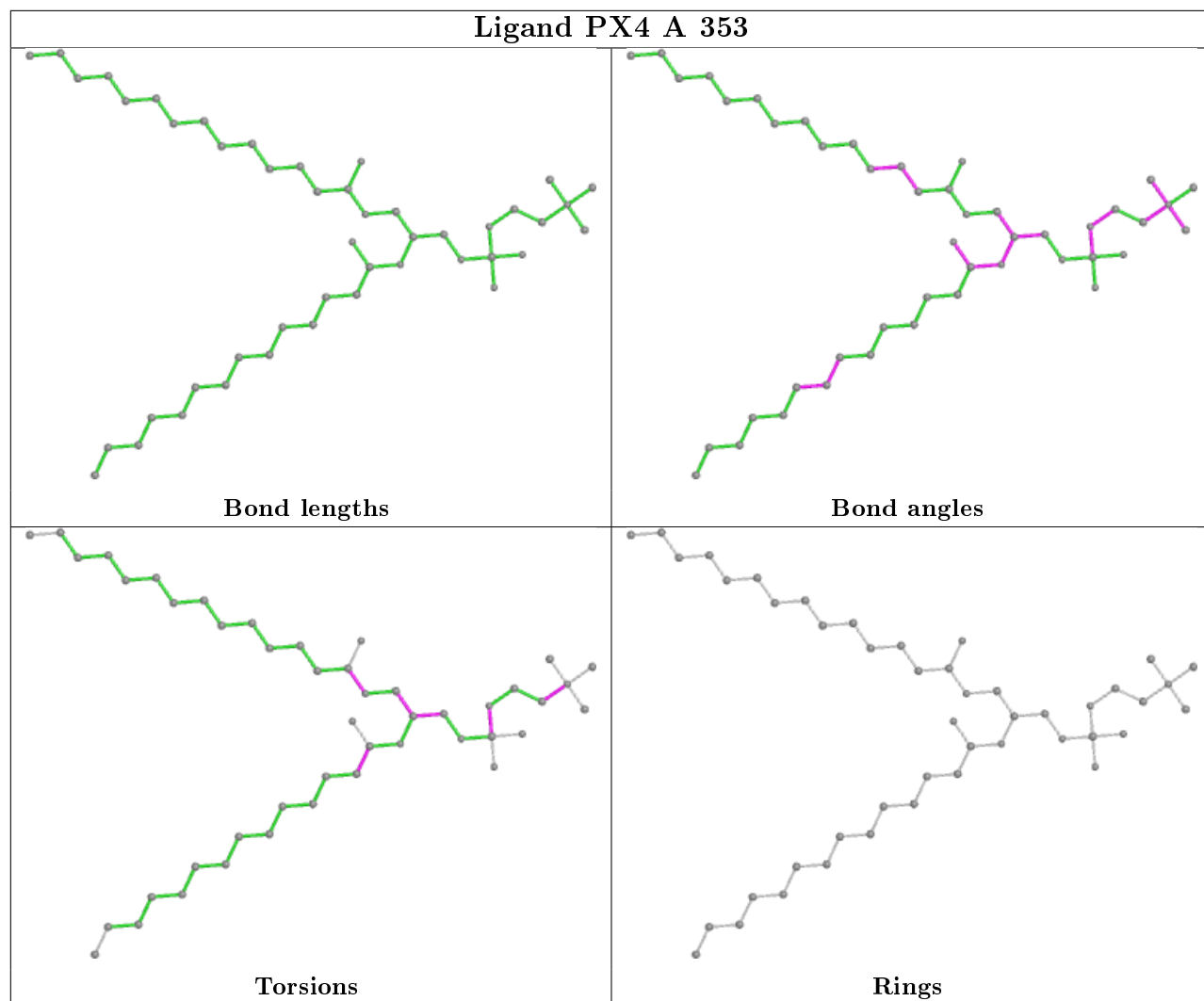


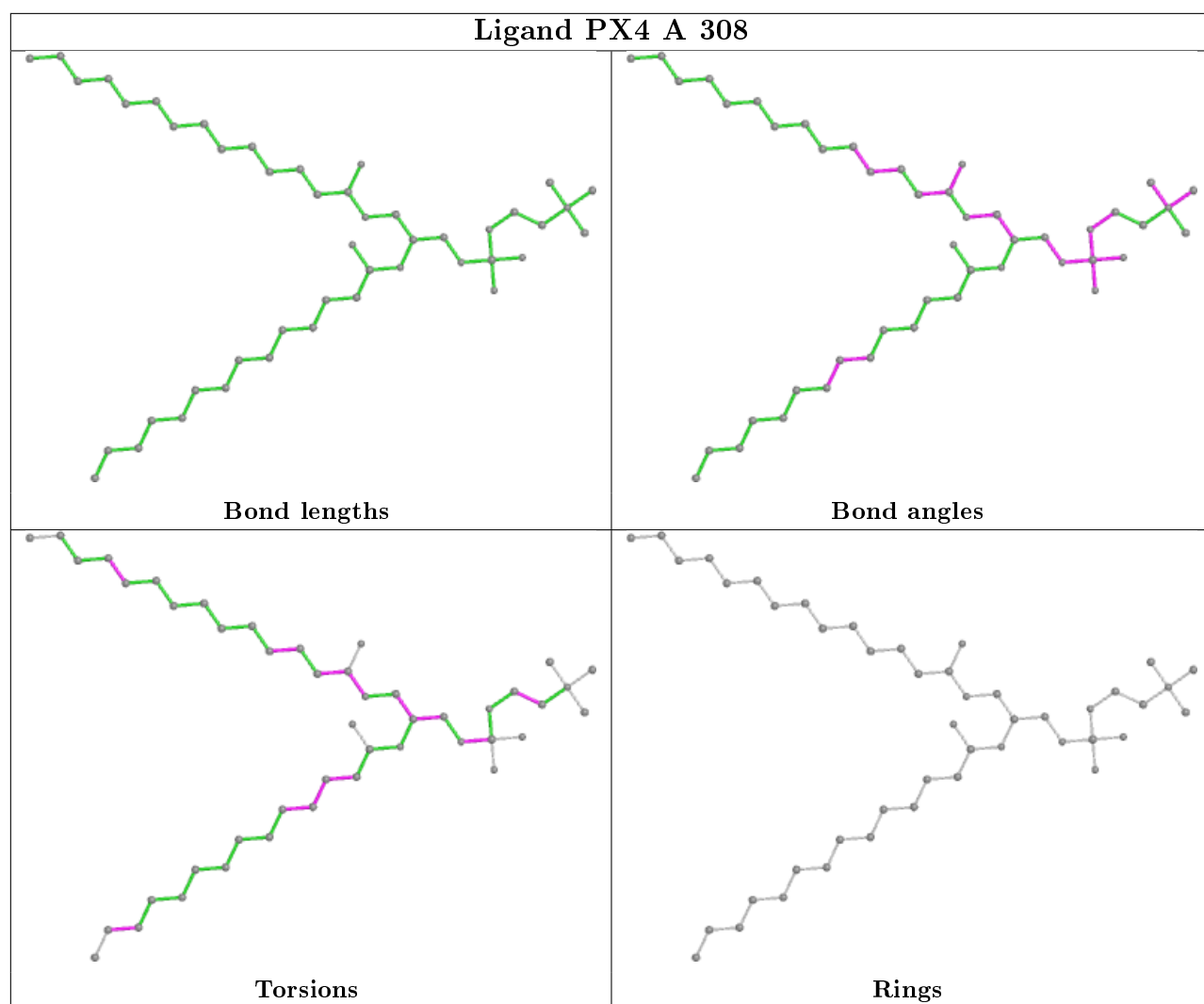


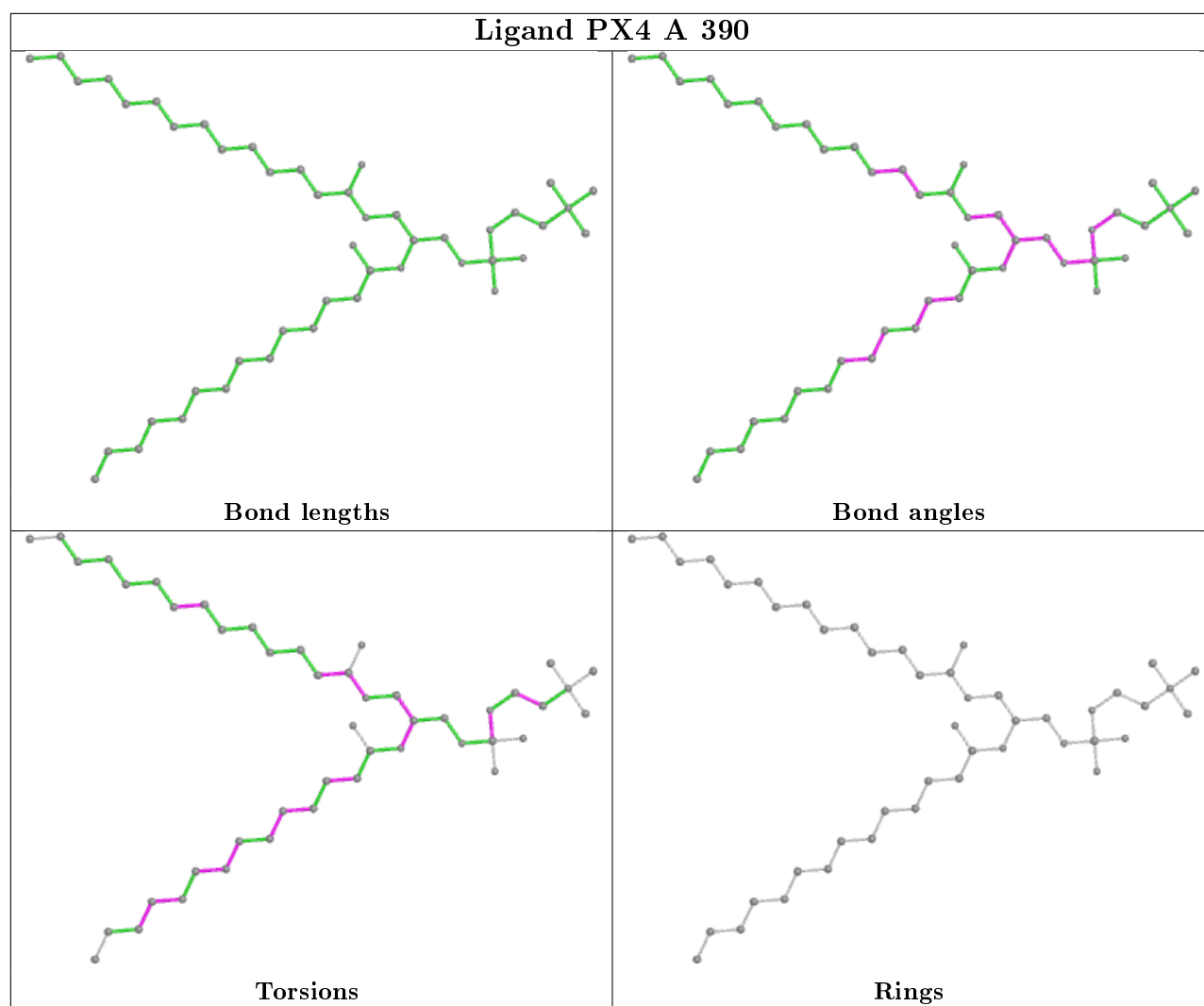
Ligand PX4 A 367



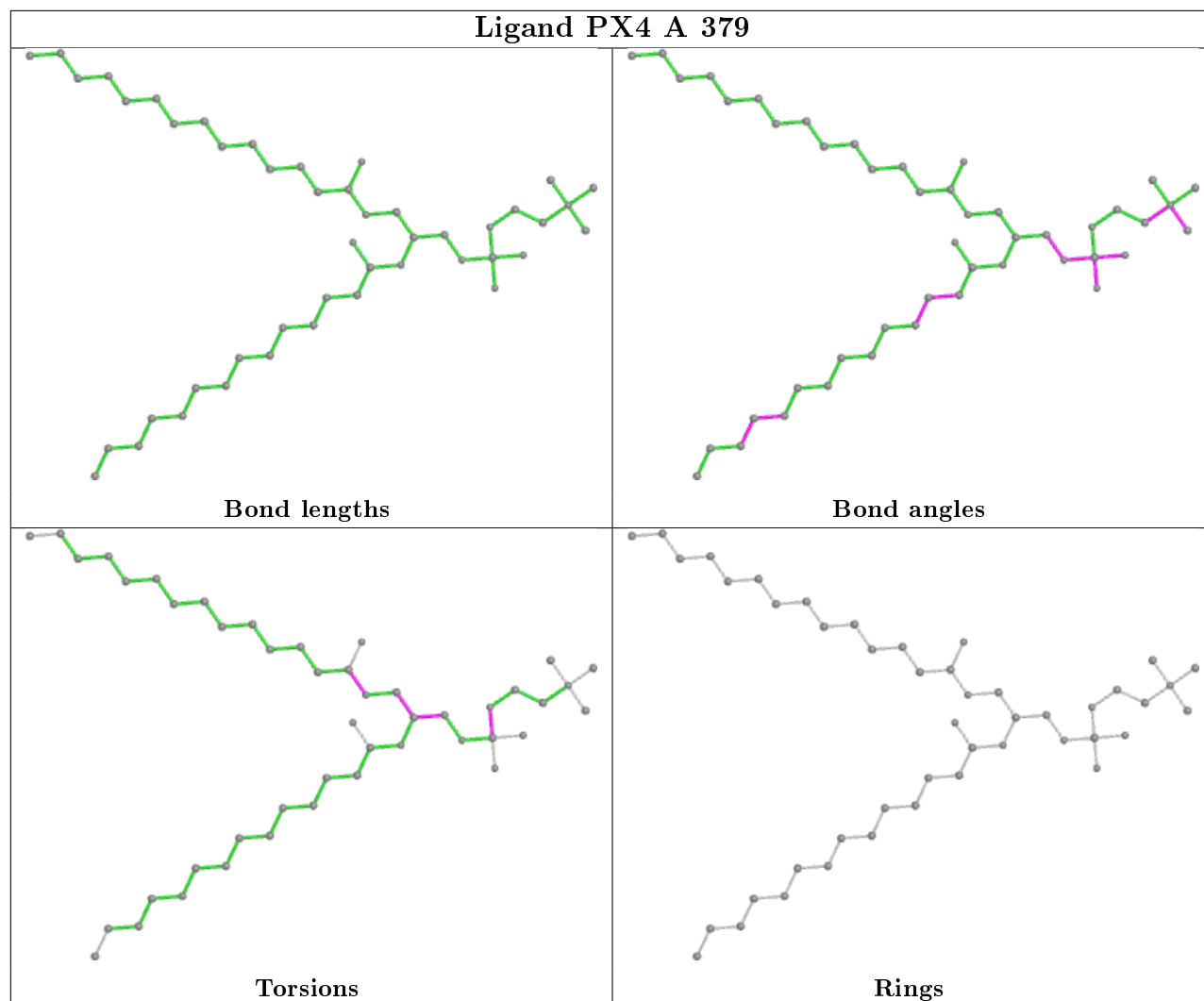
Ligand PX4 A 353

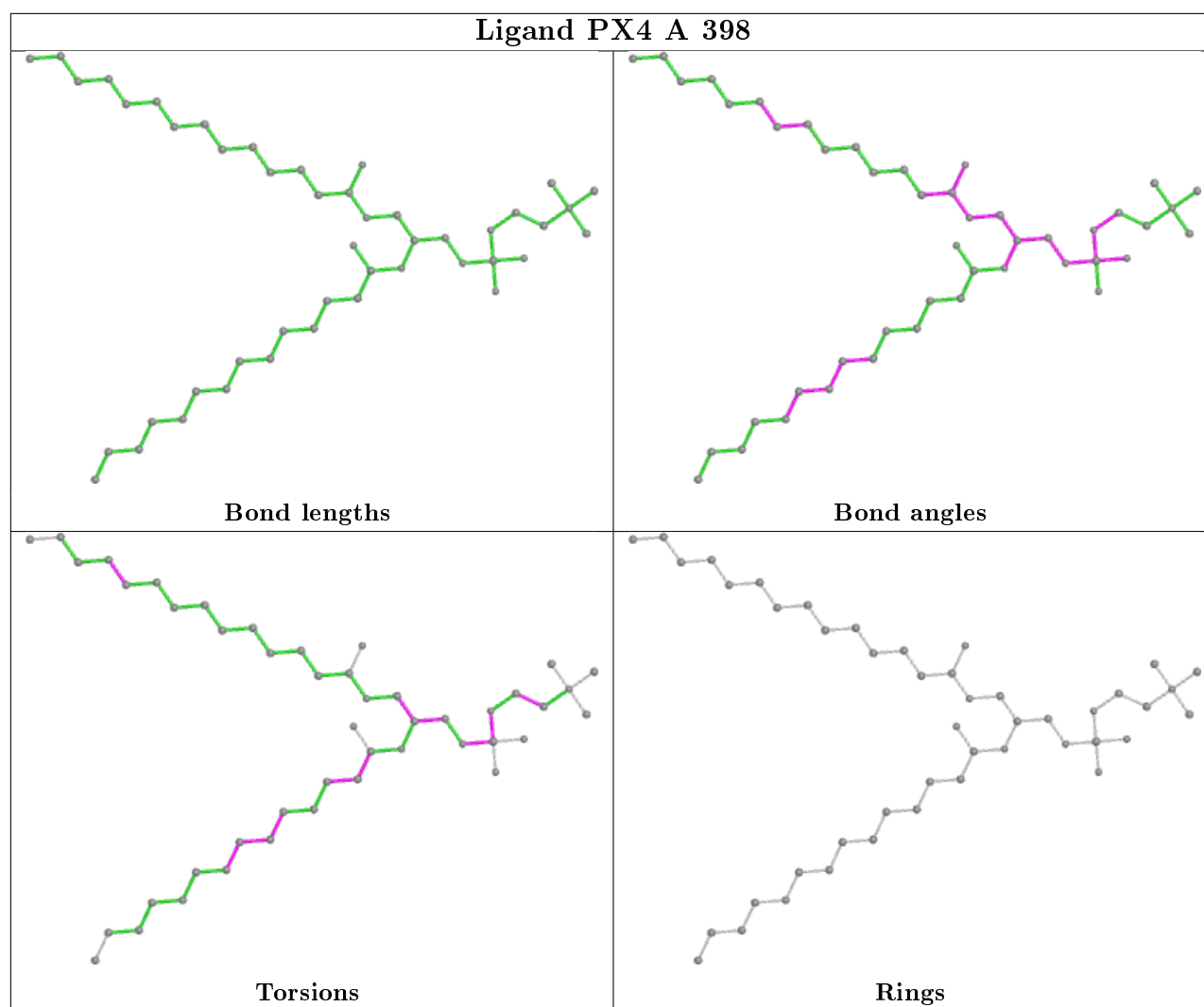


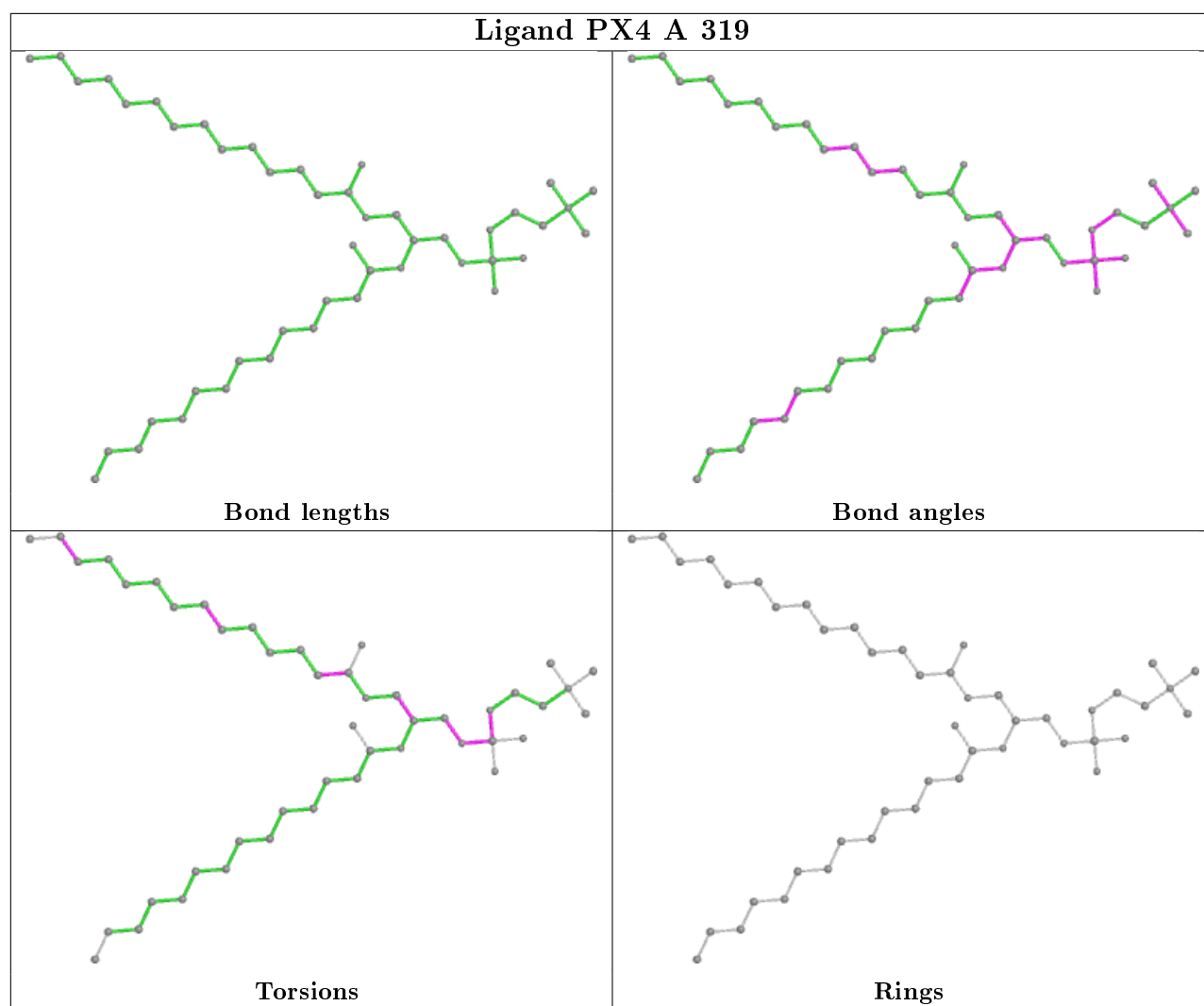


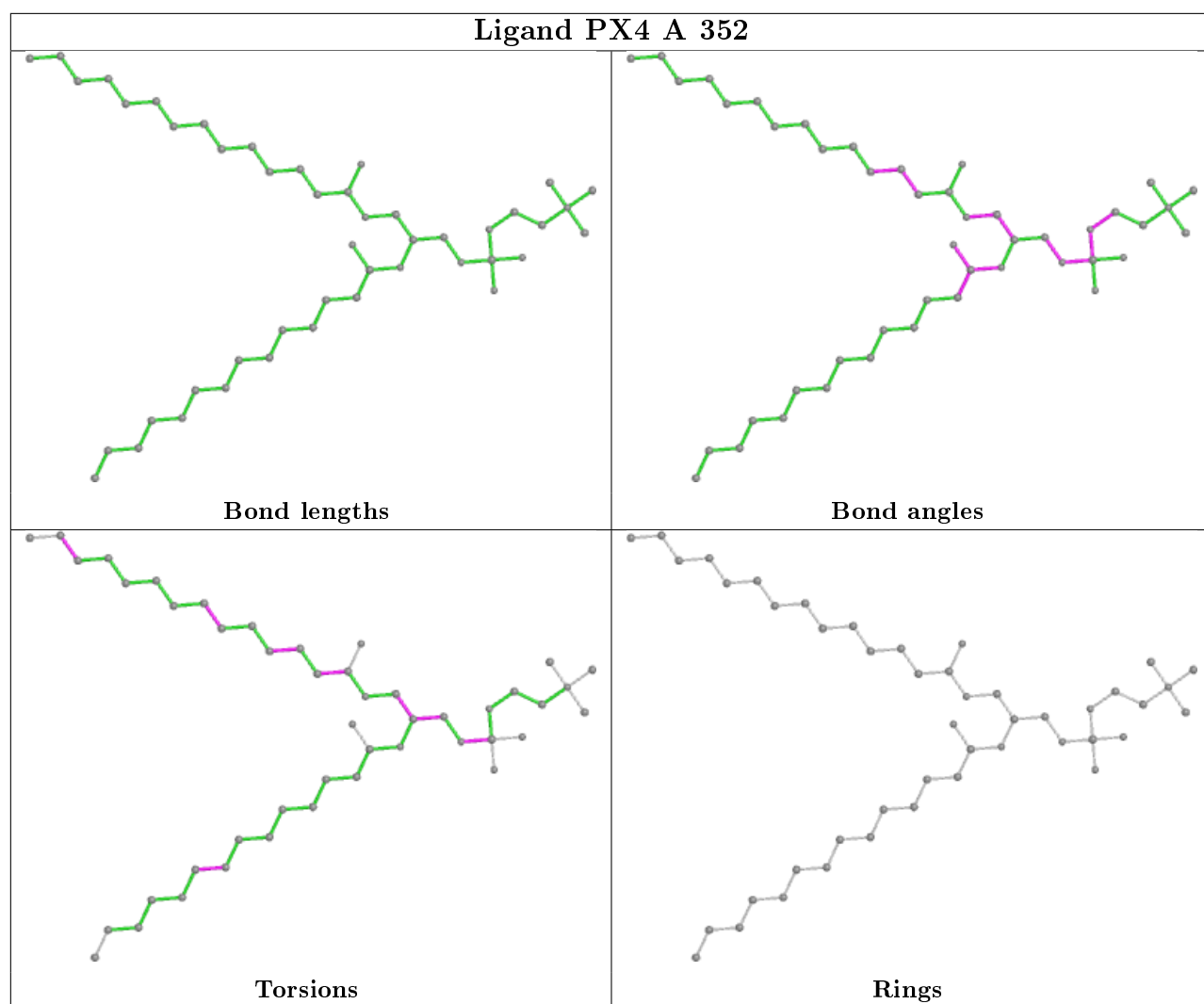


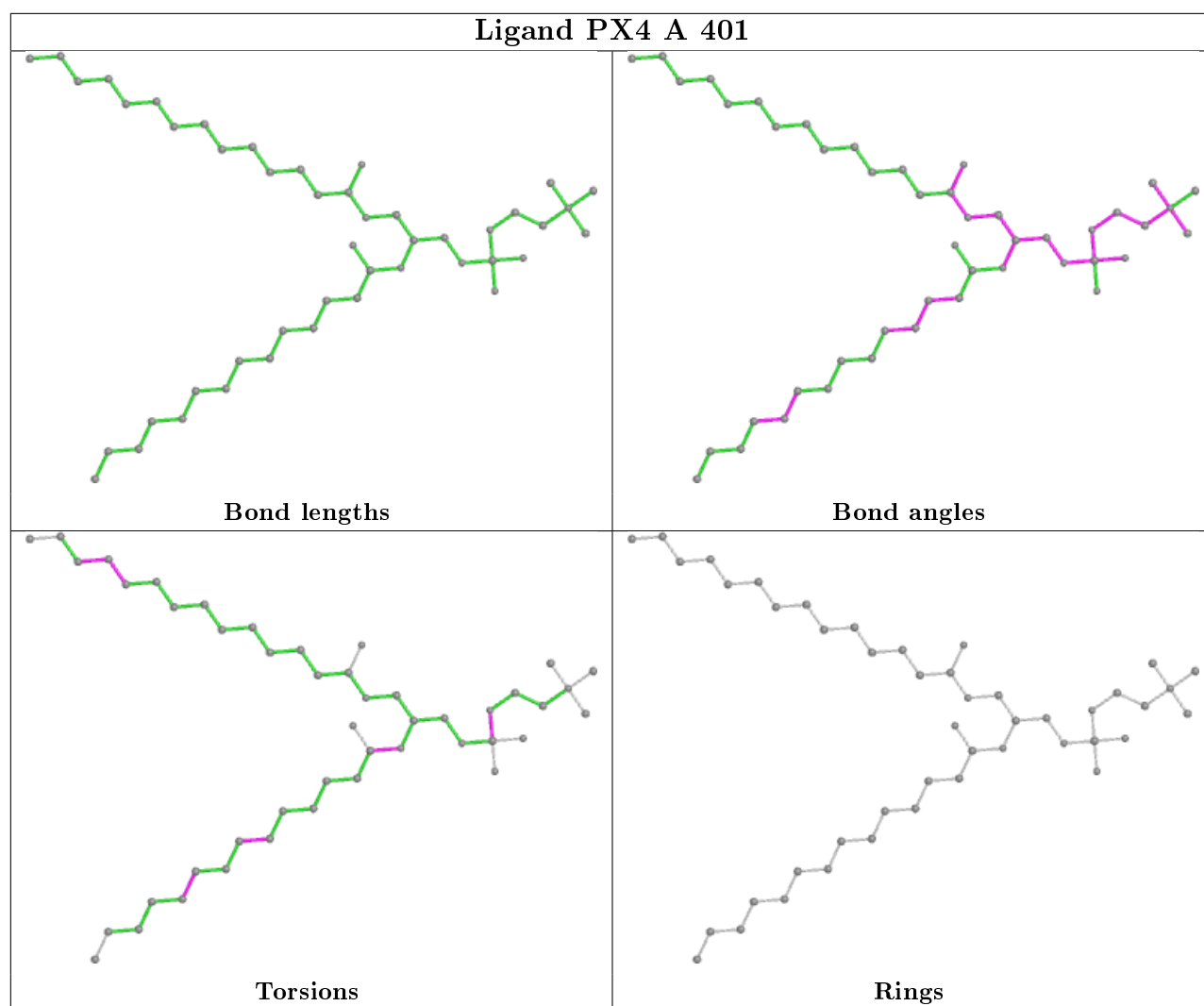
Ligand PX4 A 379

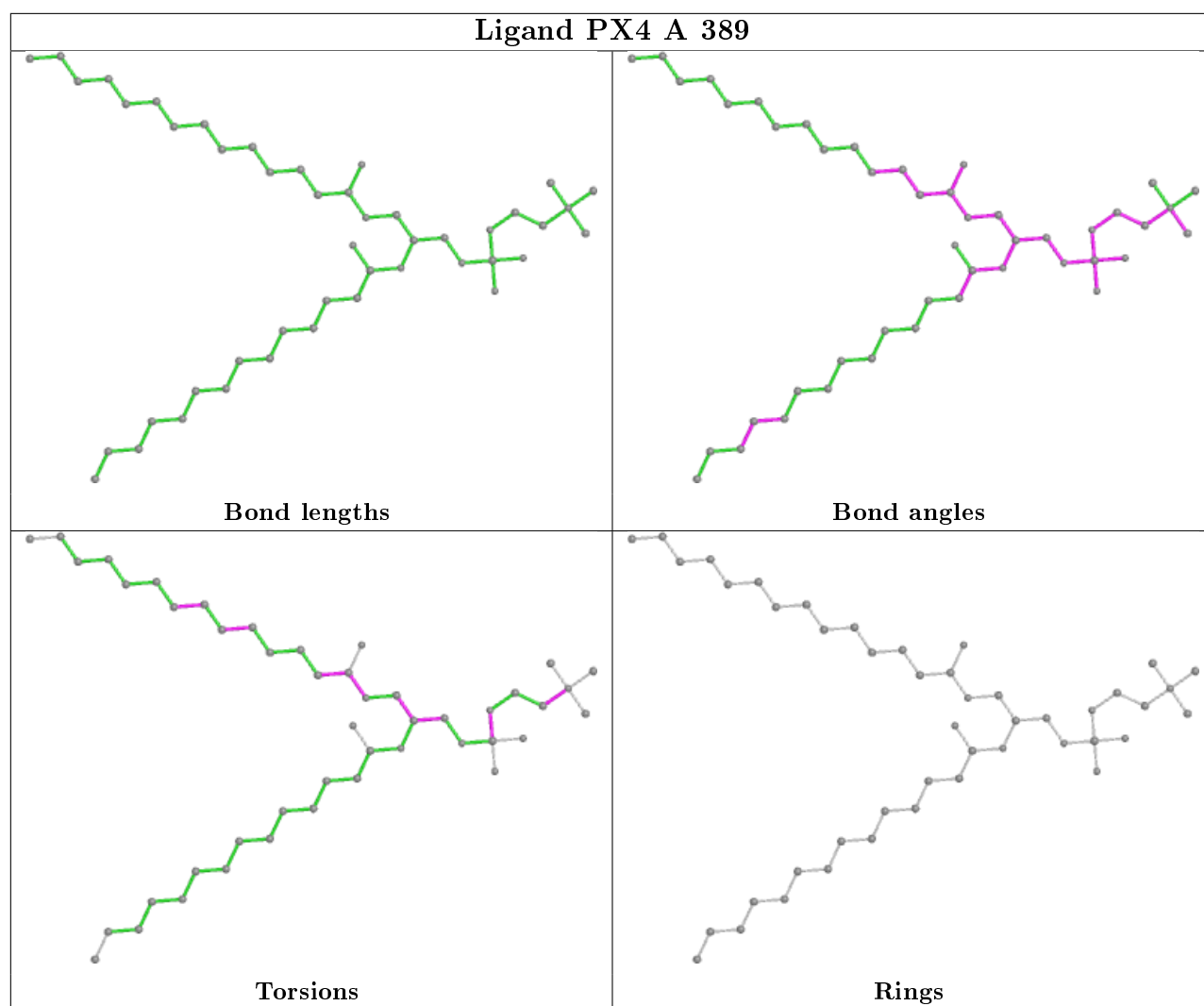


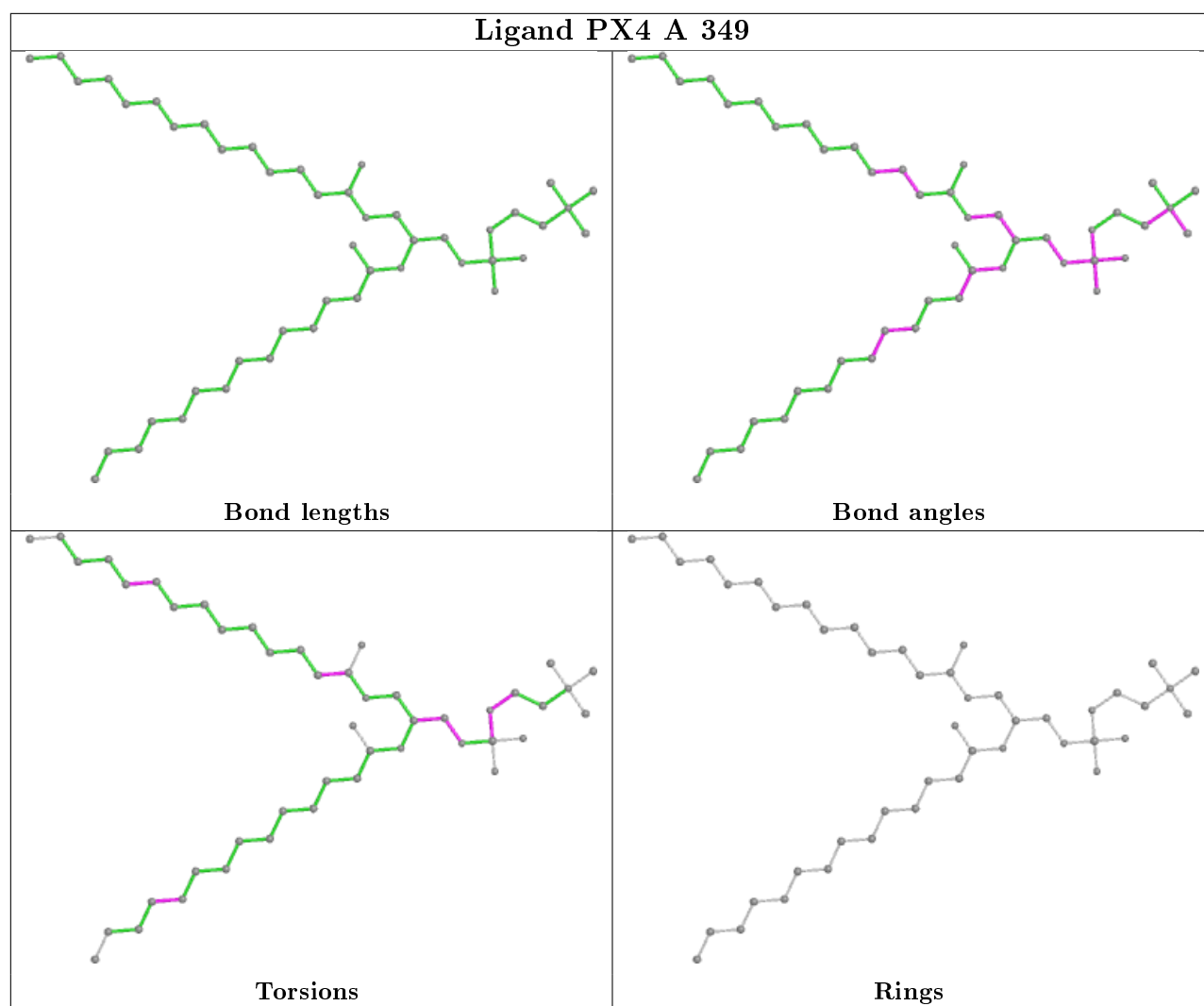


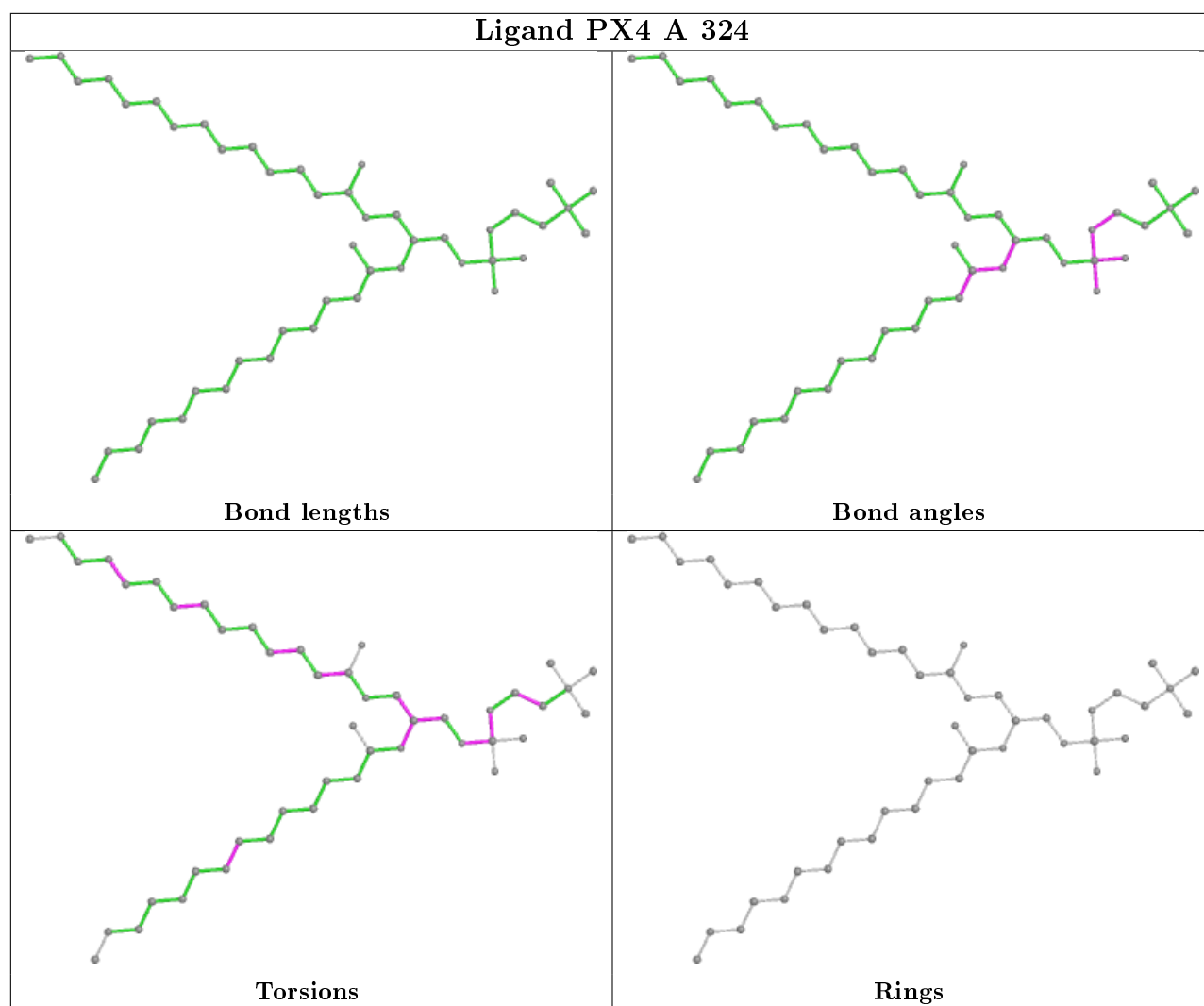


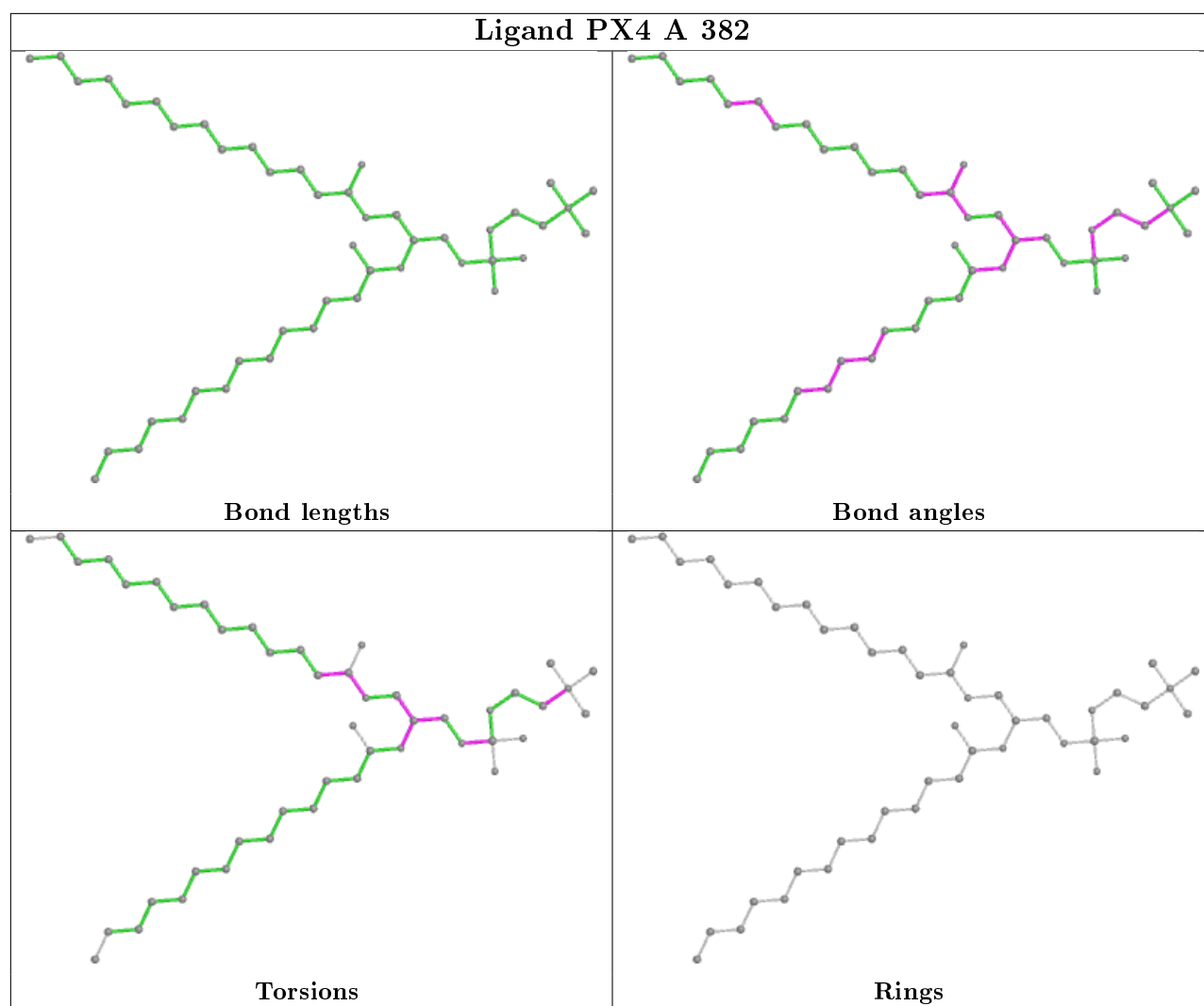


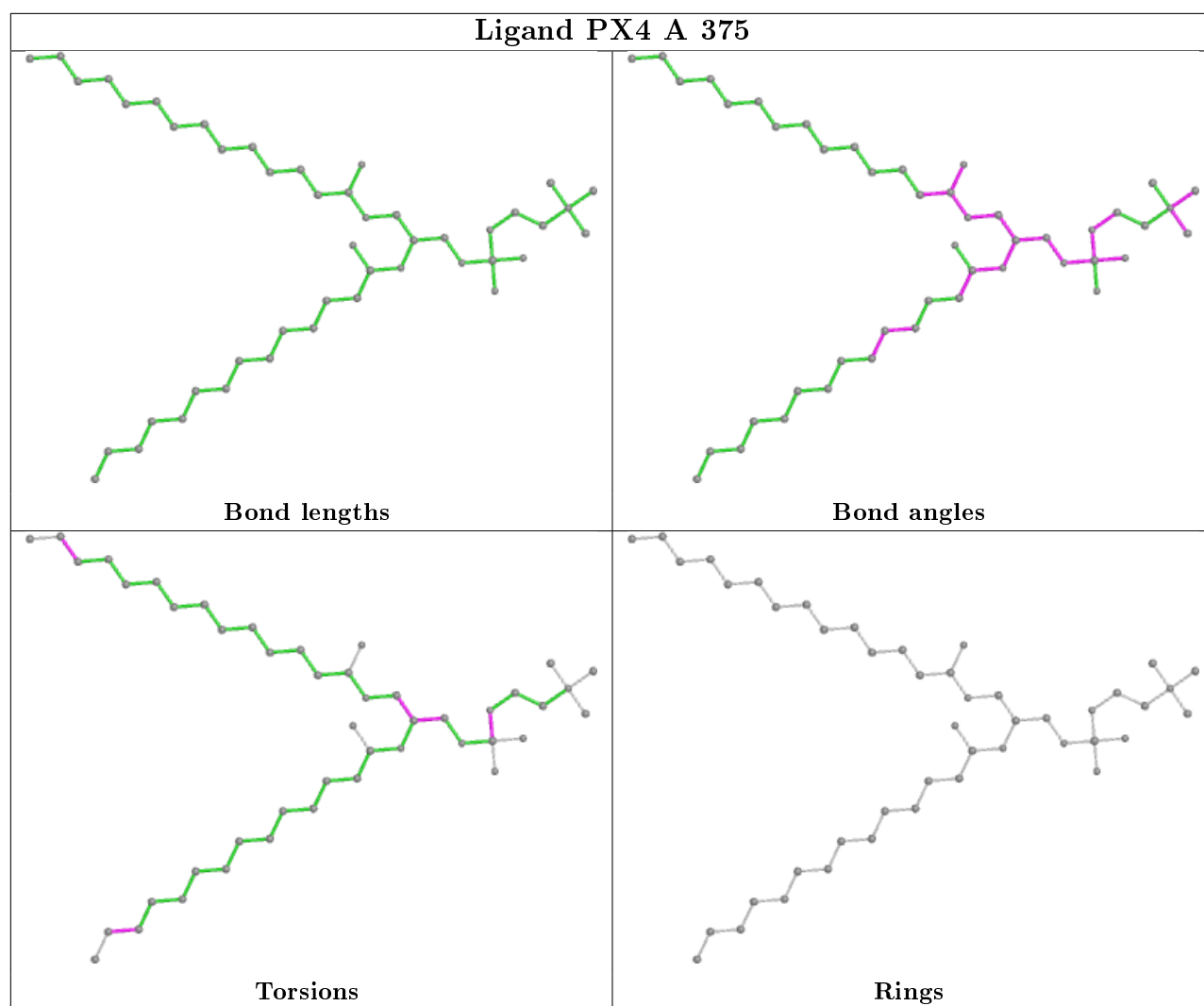


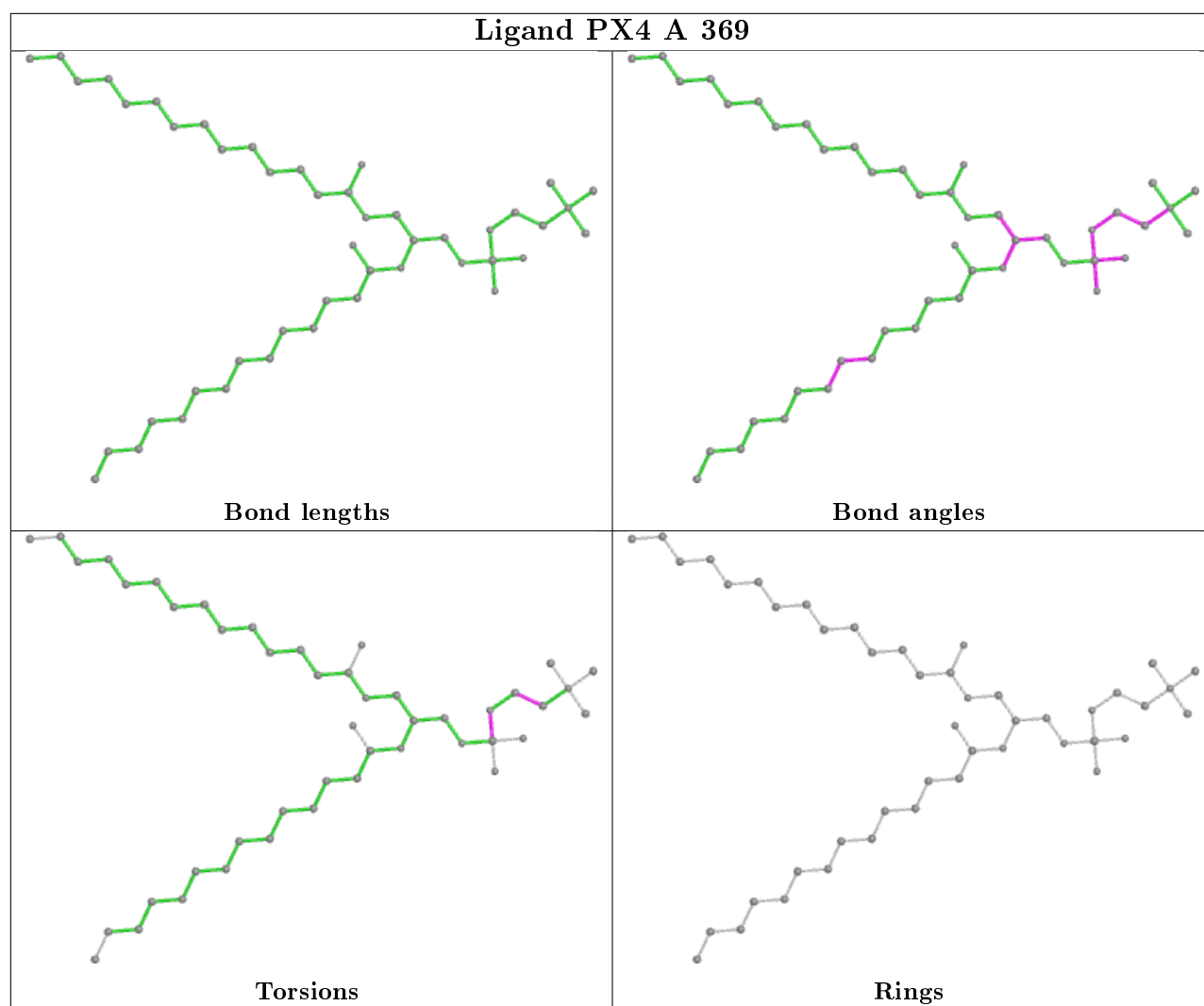


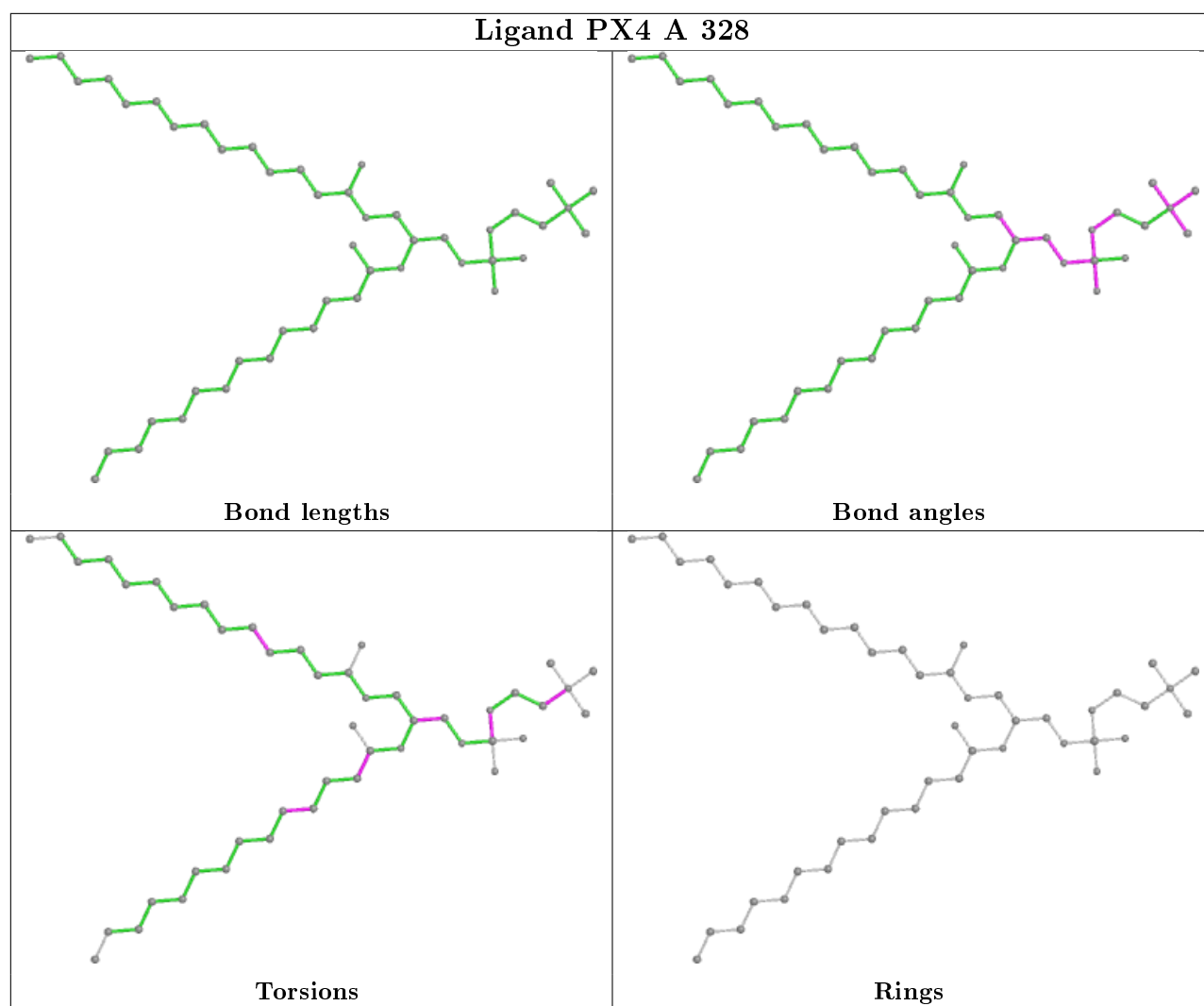


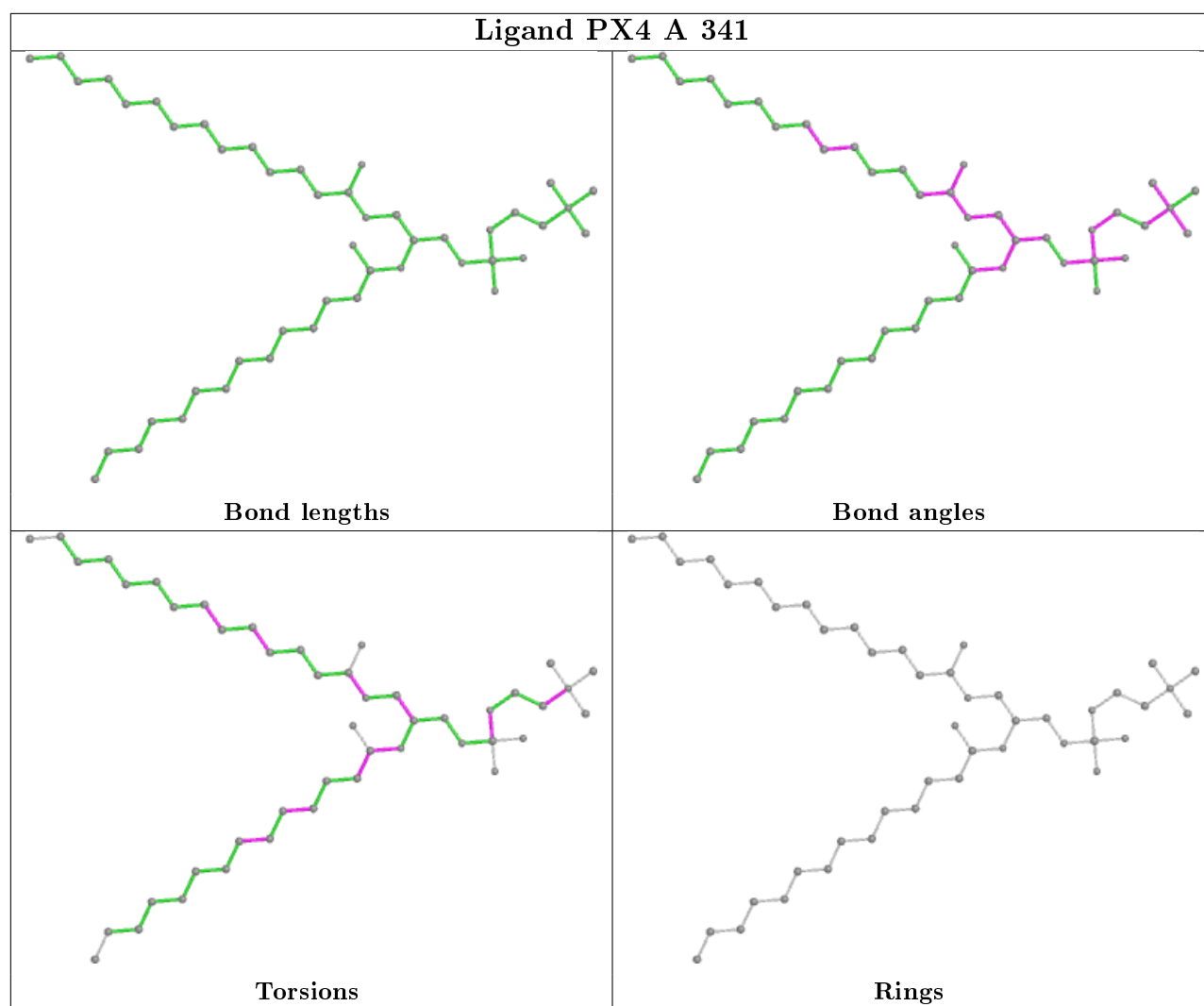


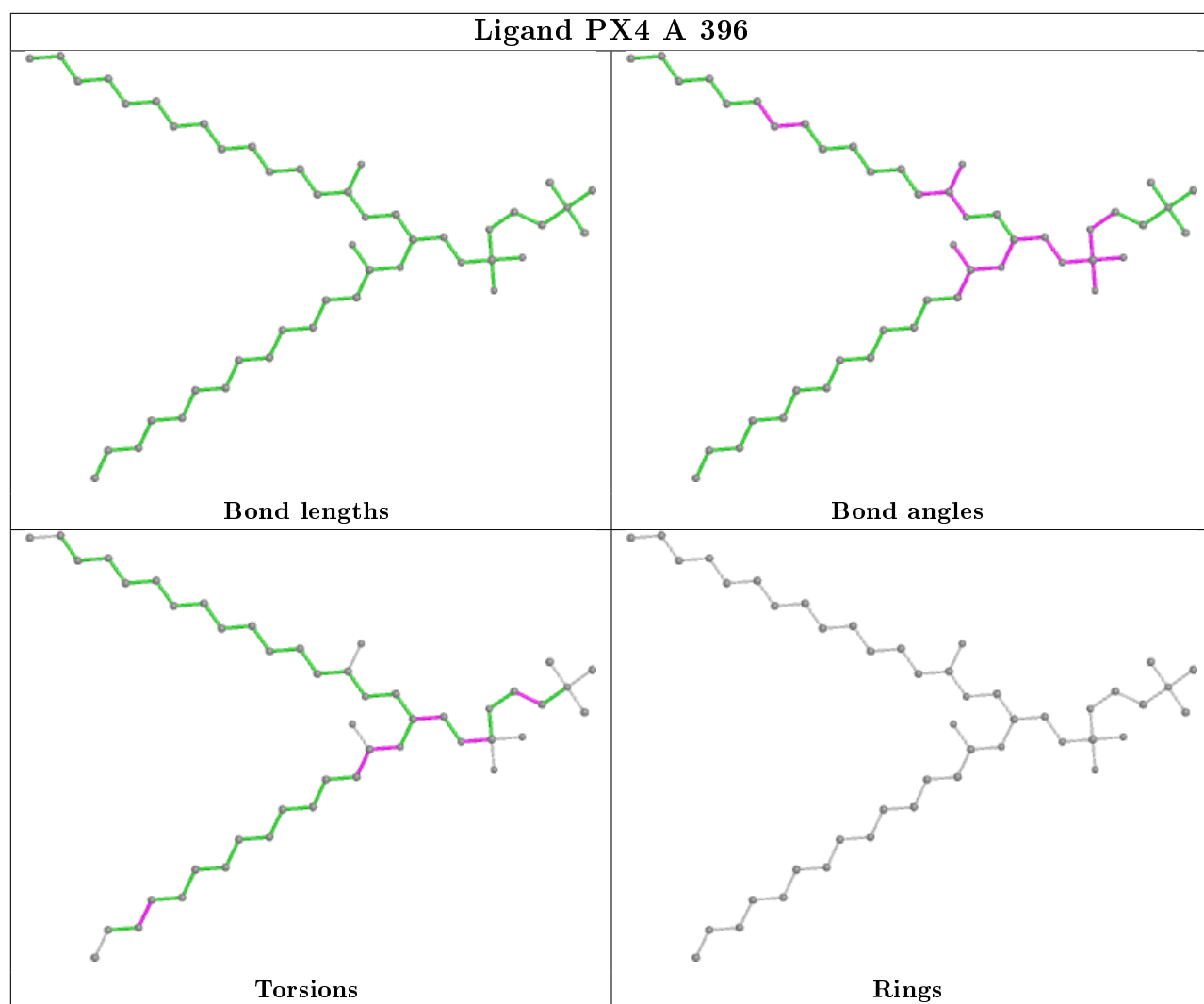


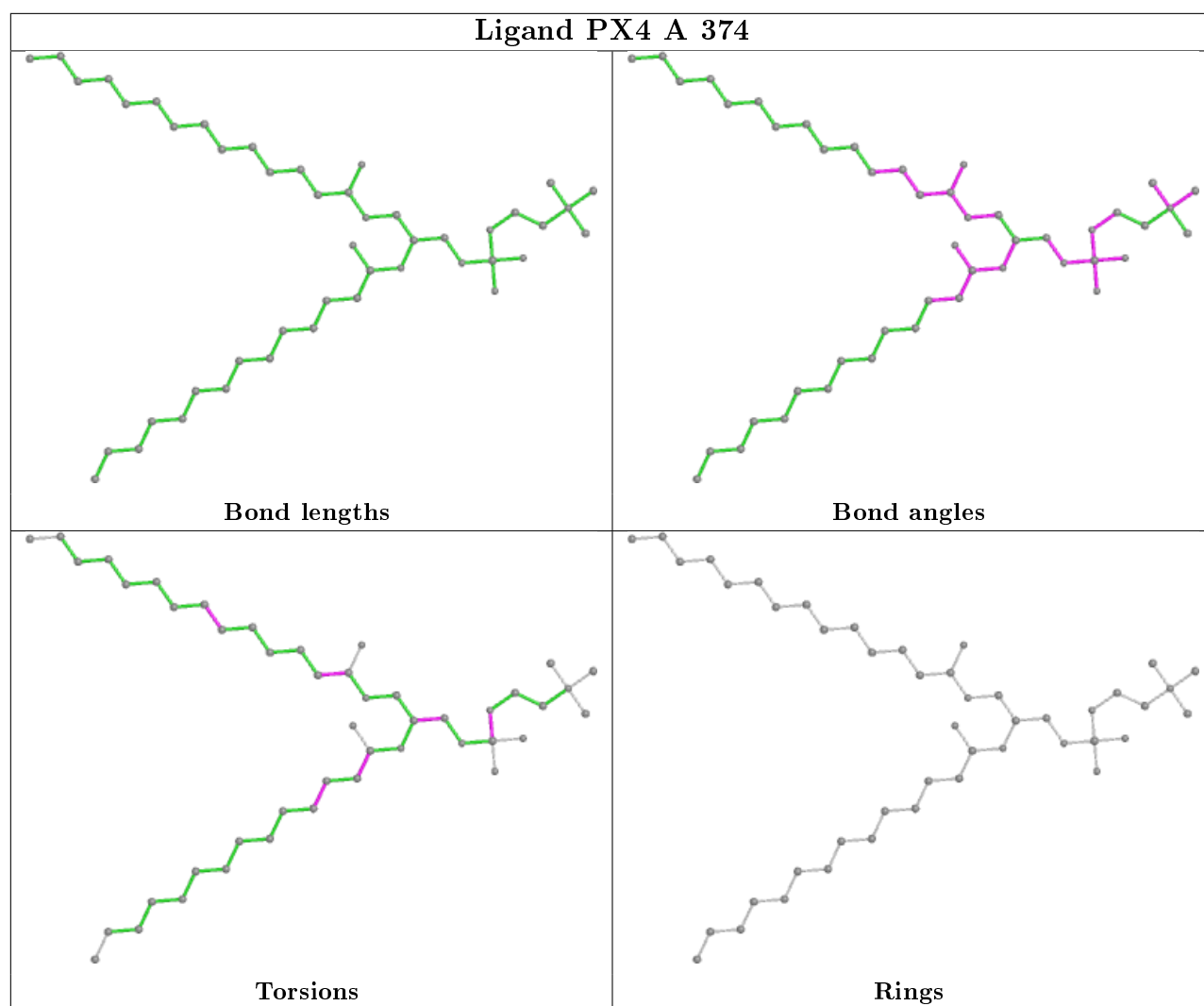




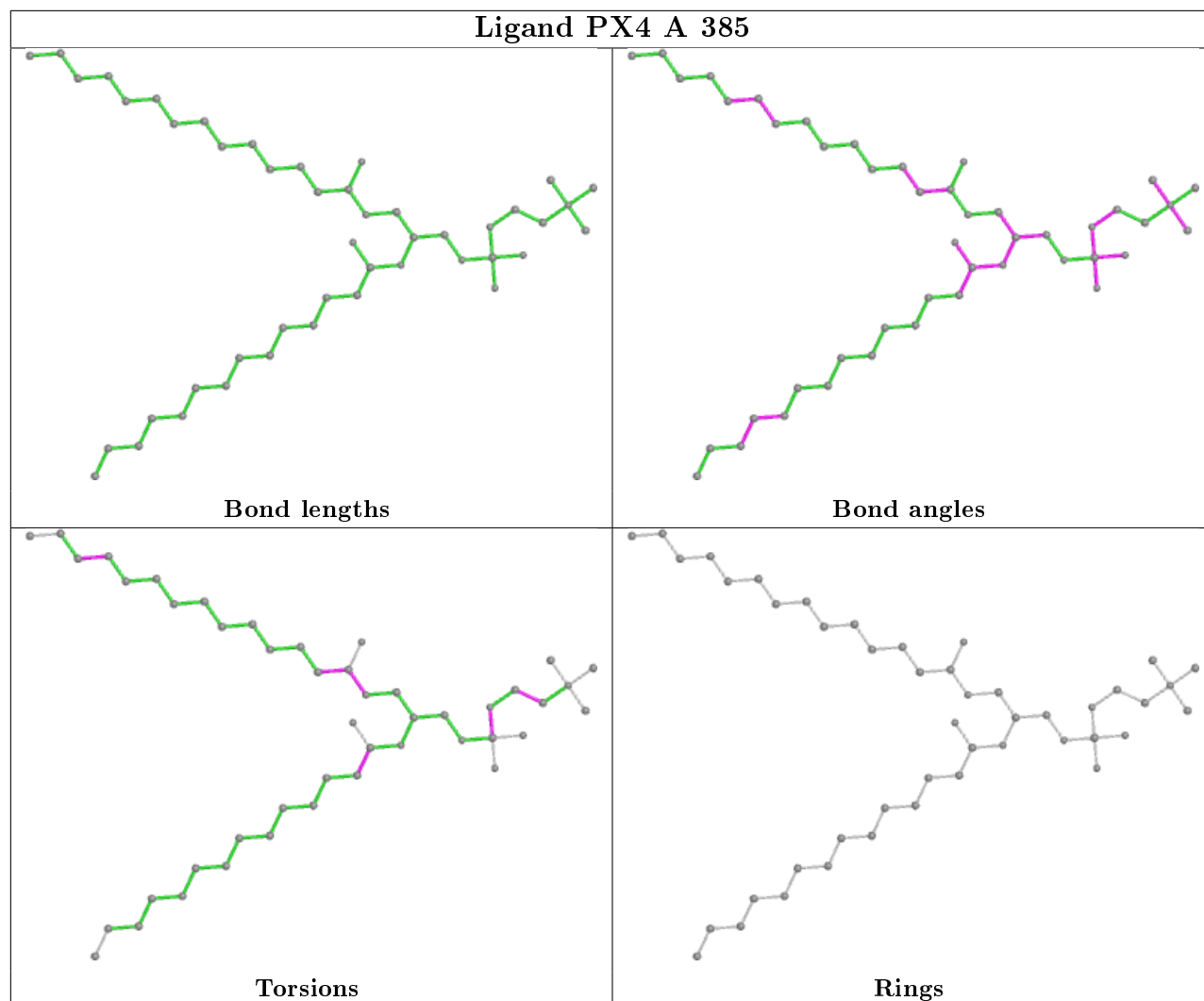


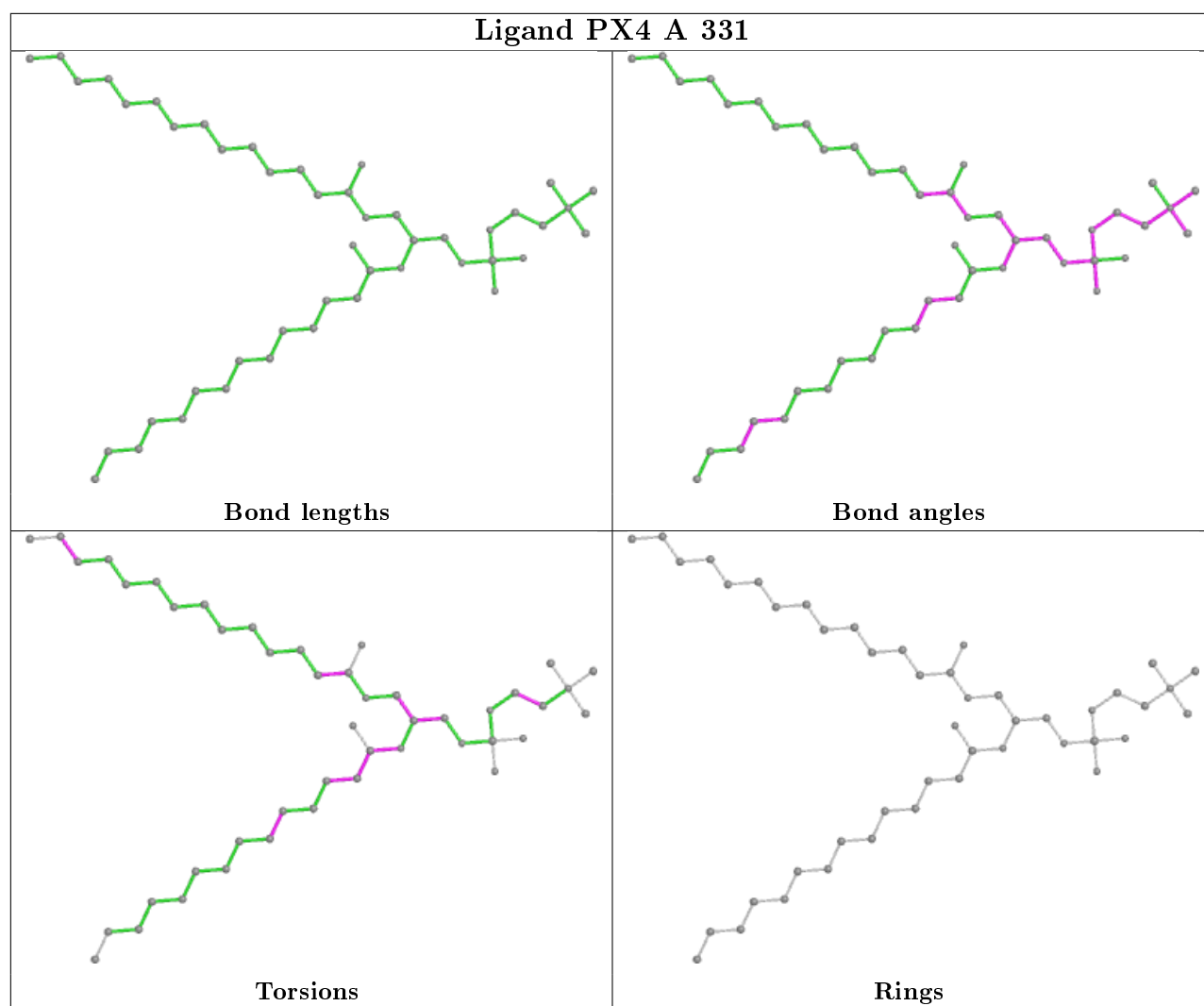


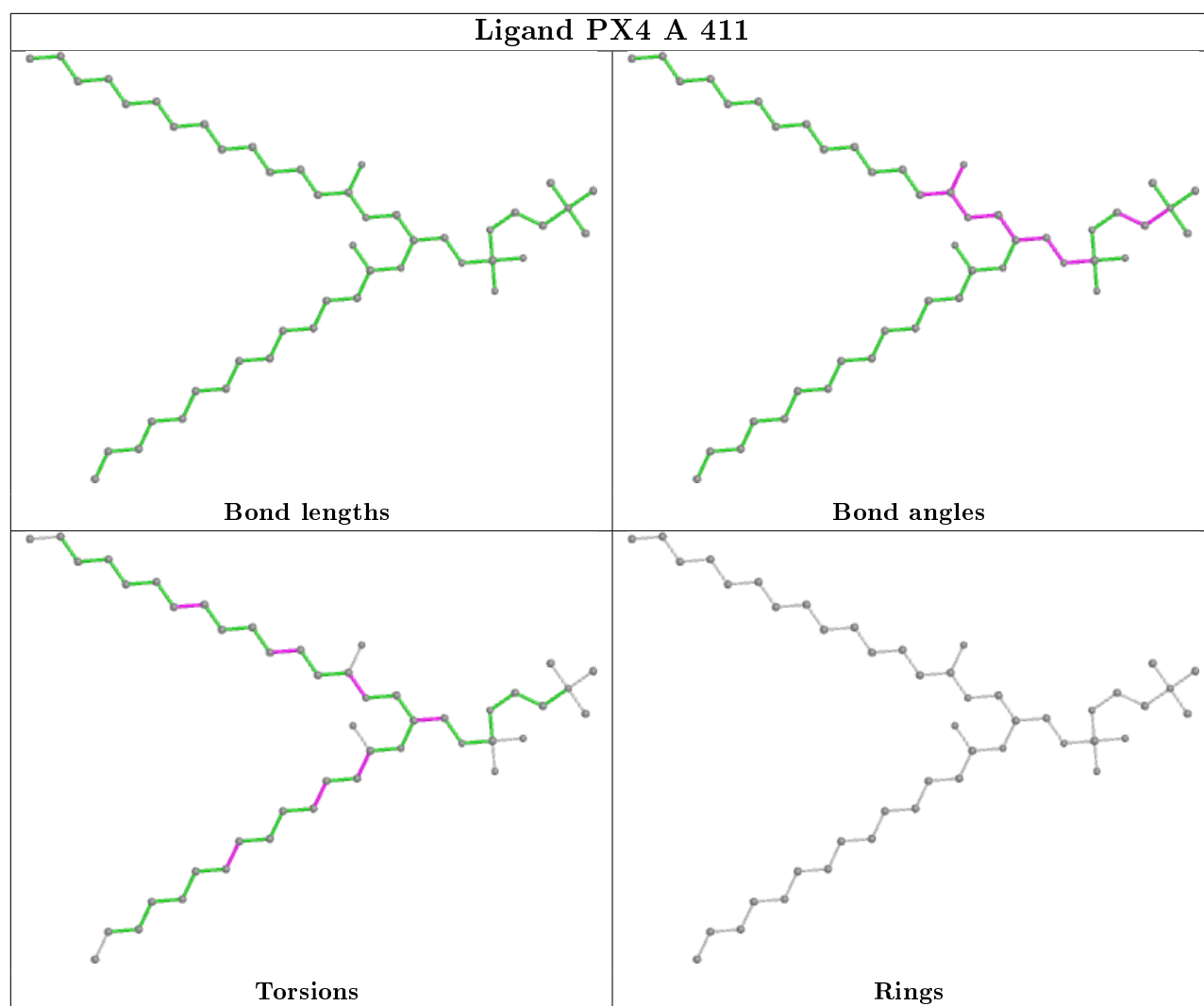


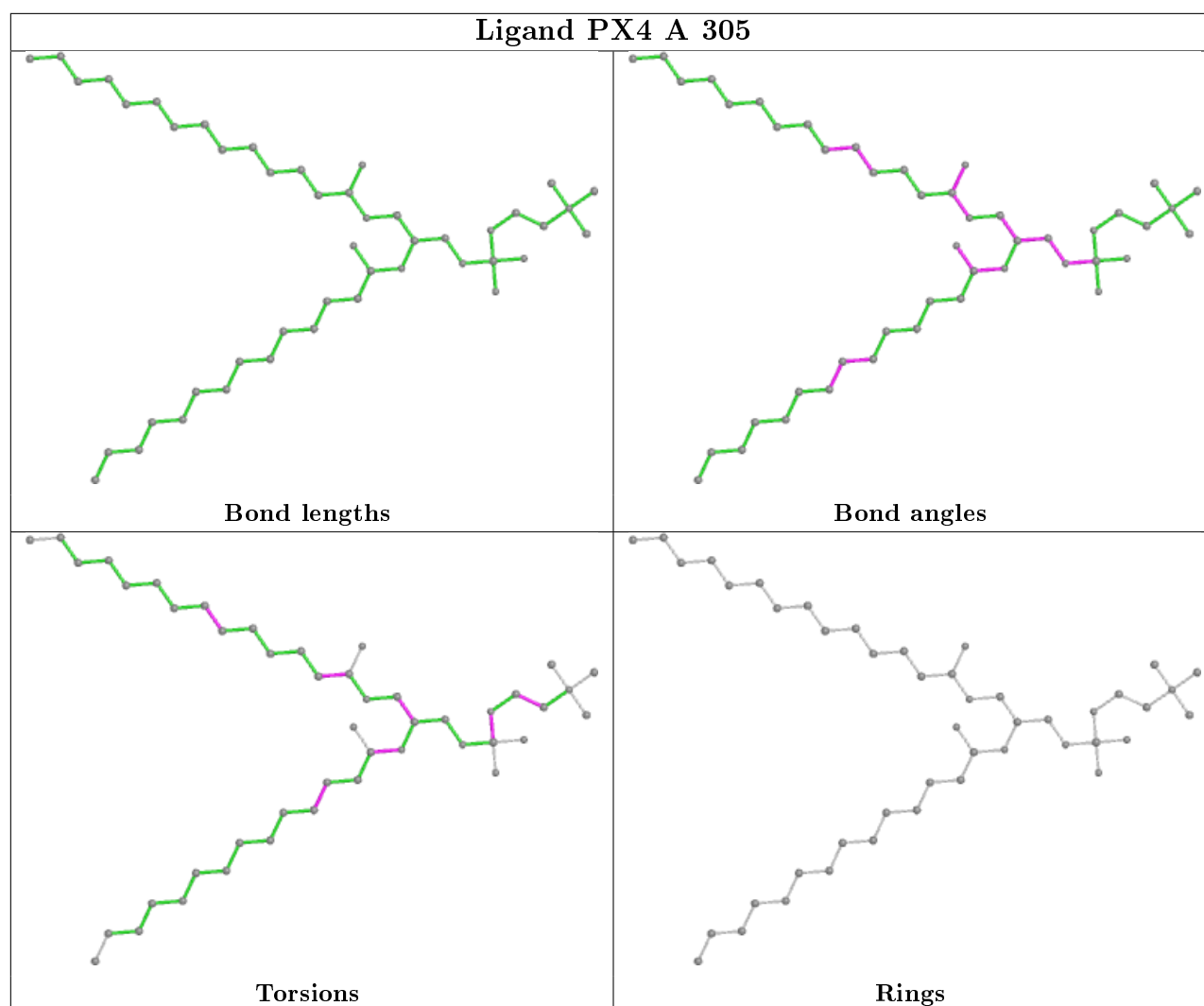


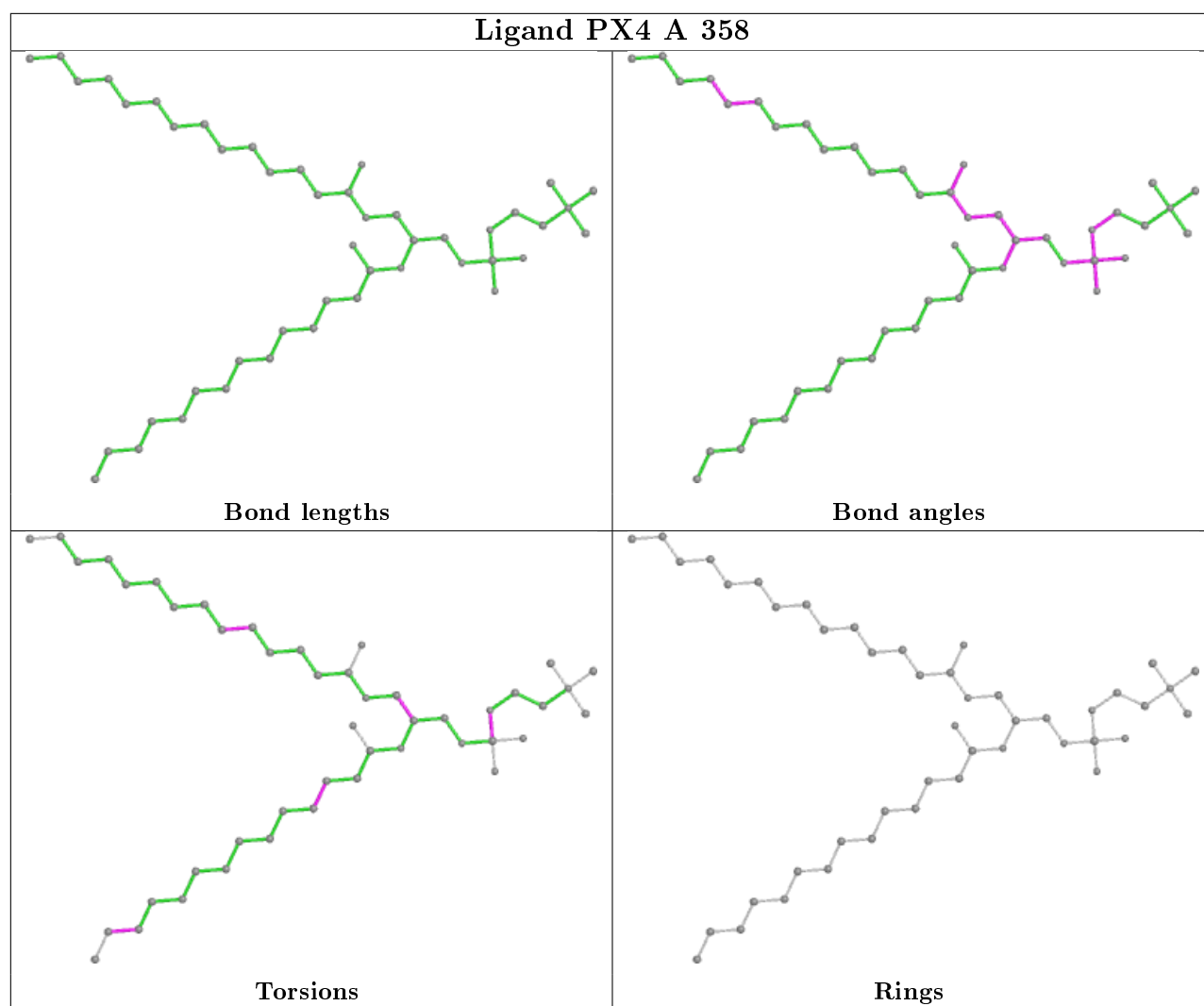
Ligand PX4 A 385

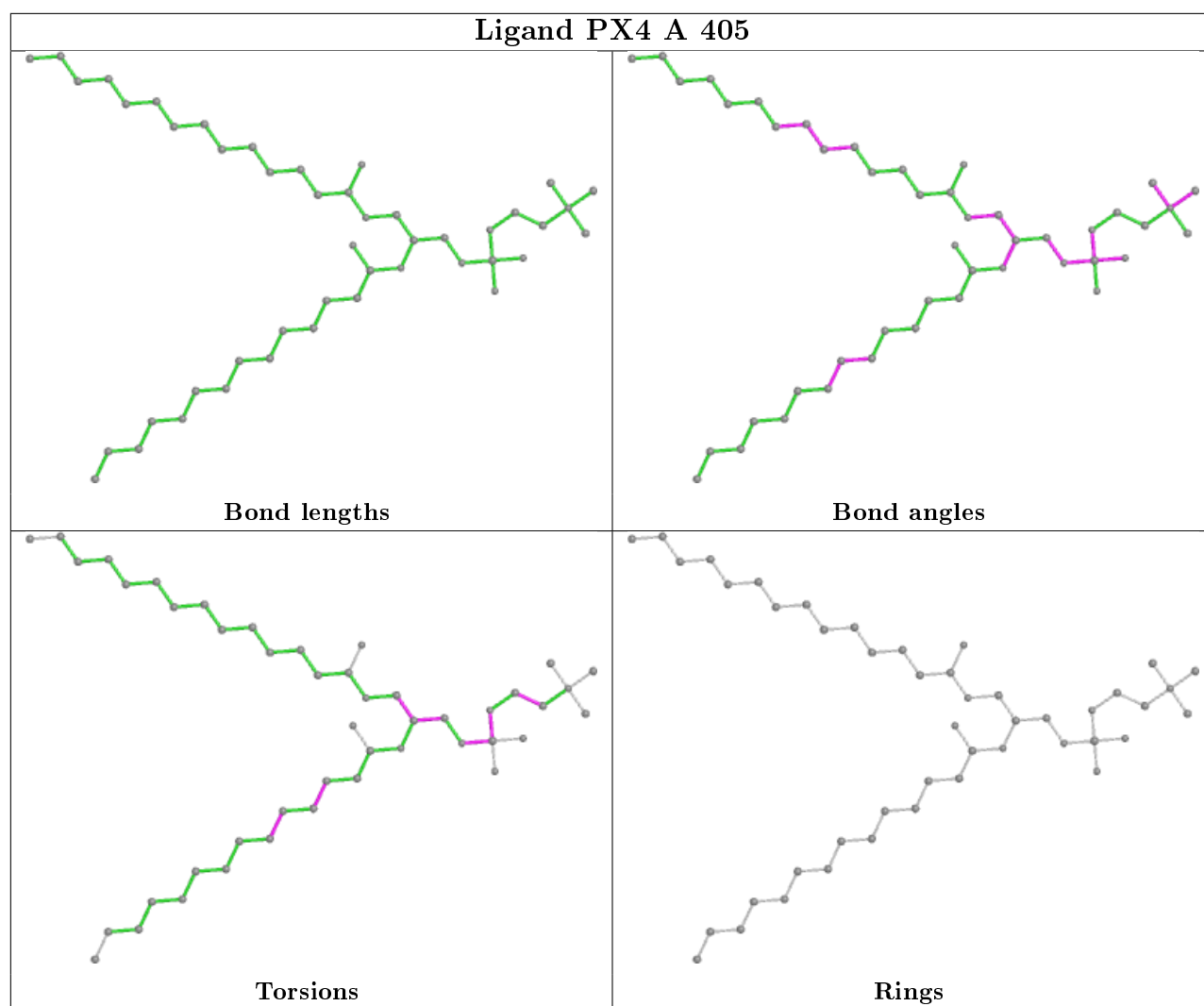


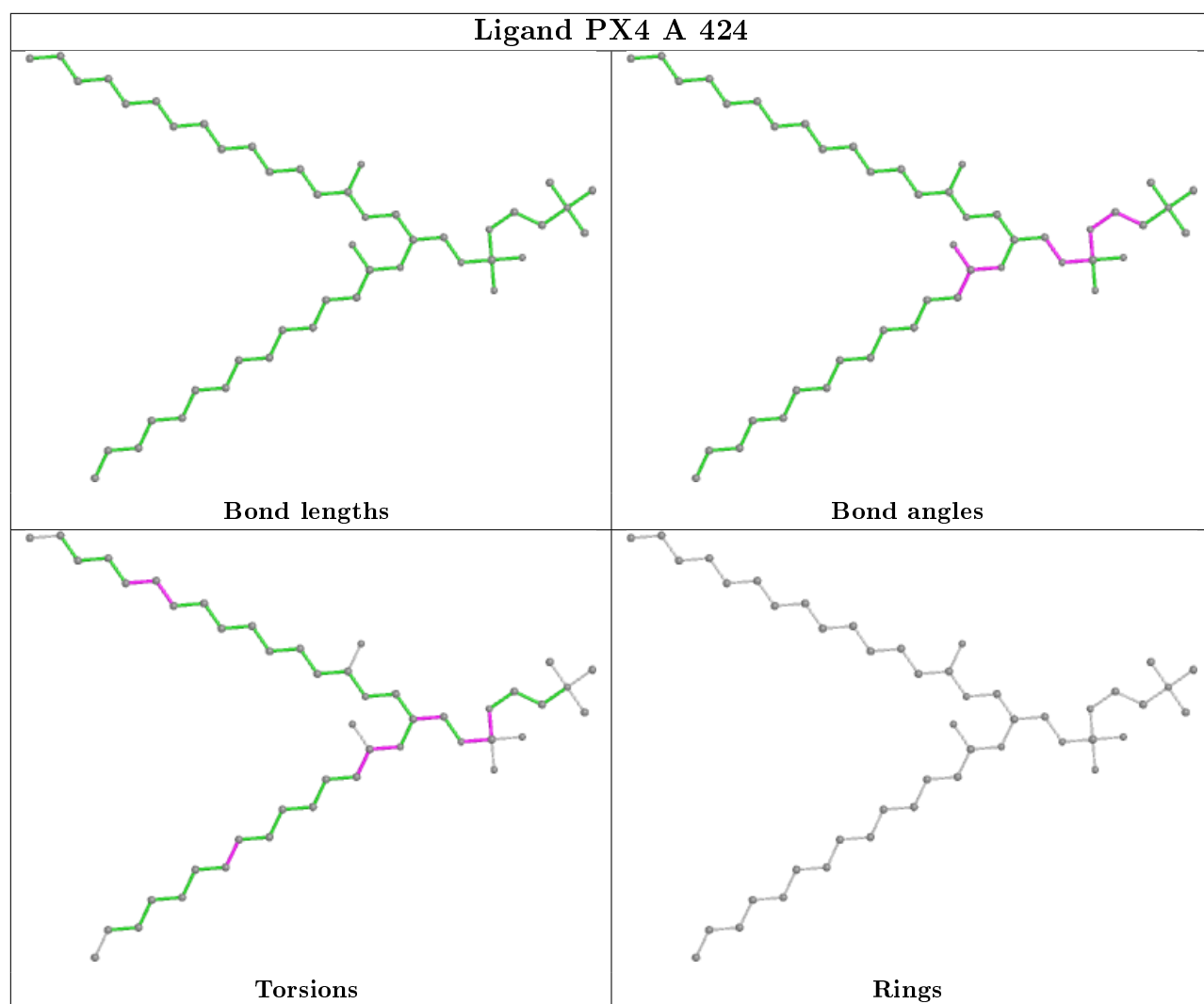


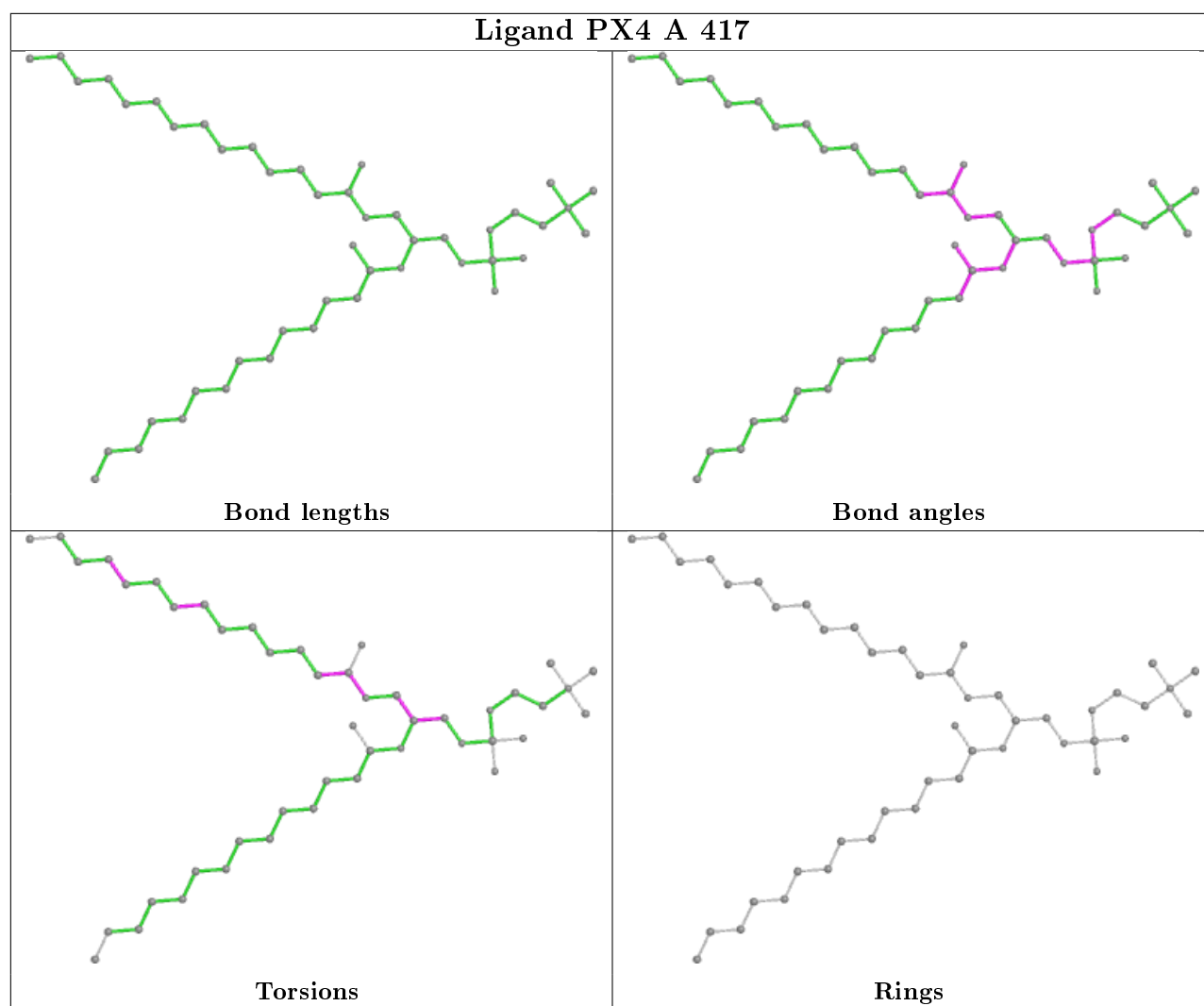


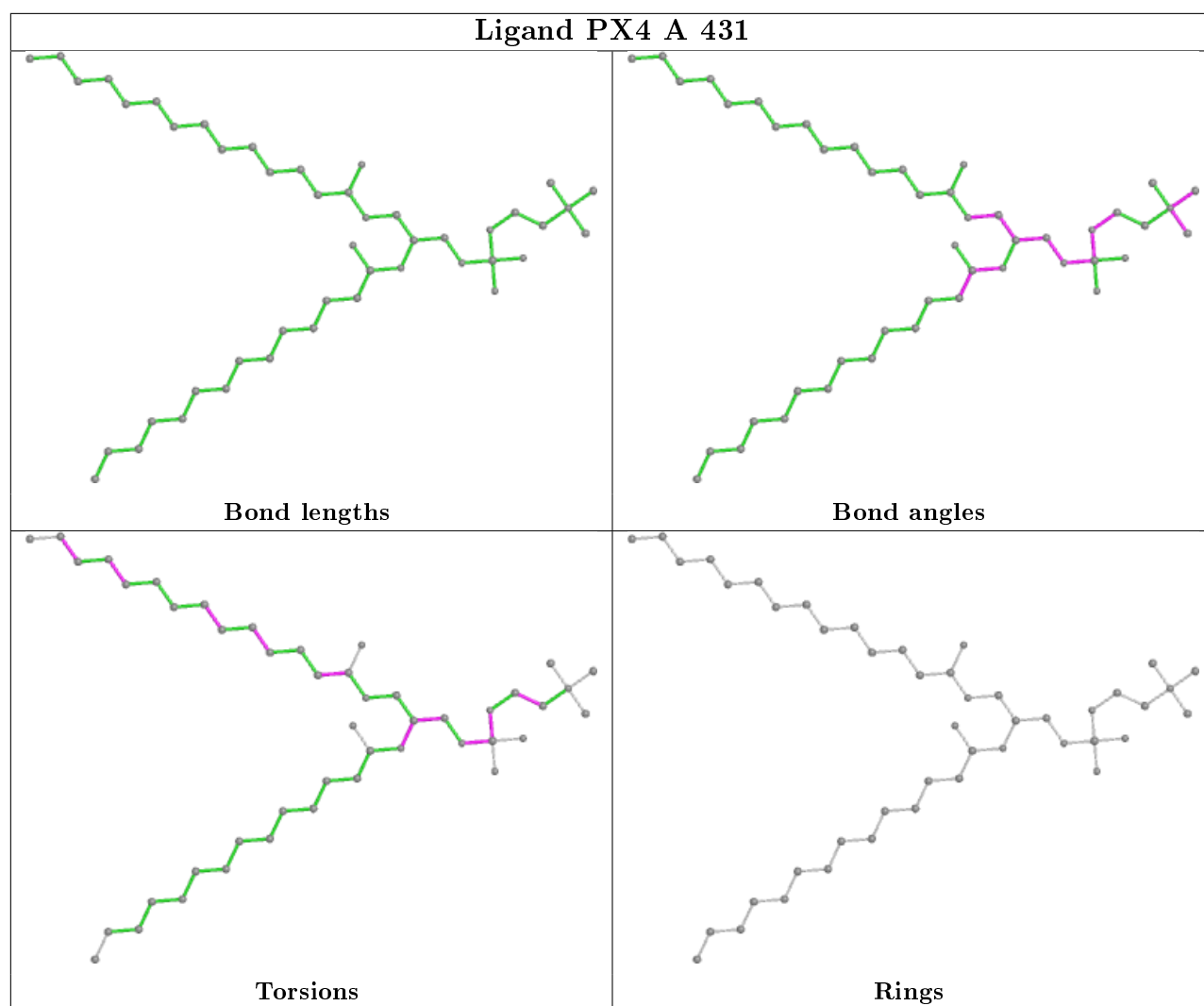


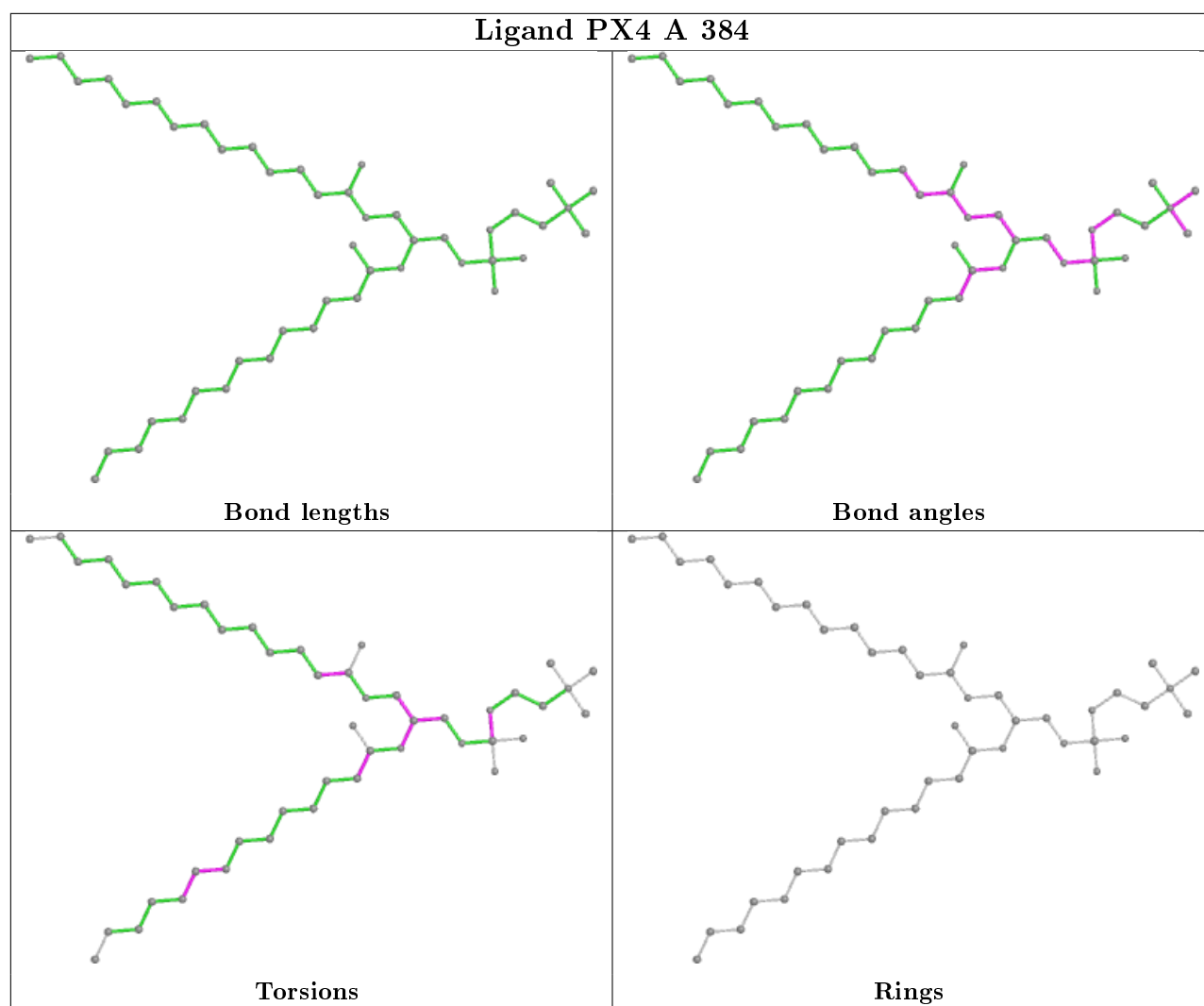




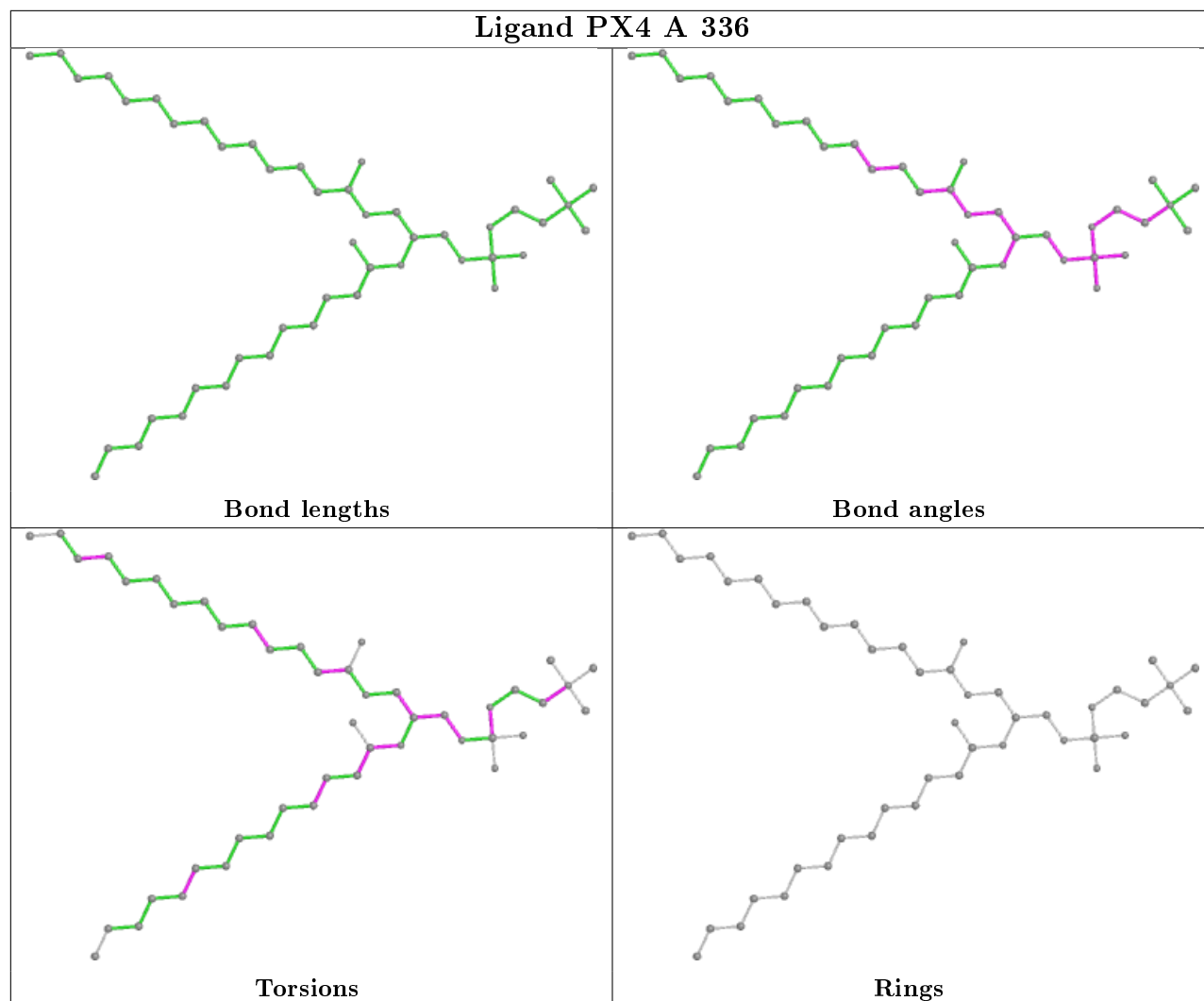


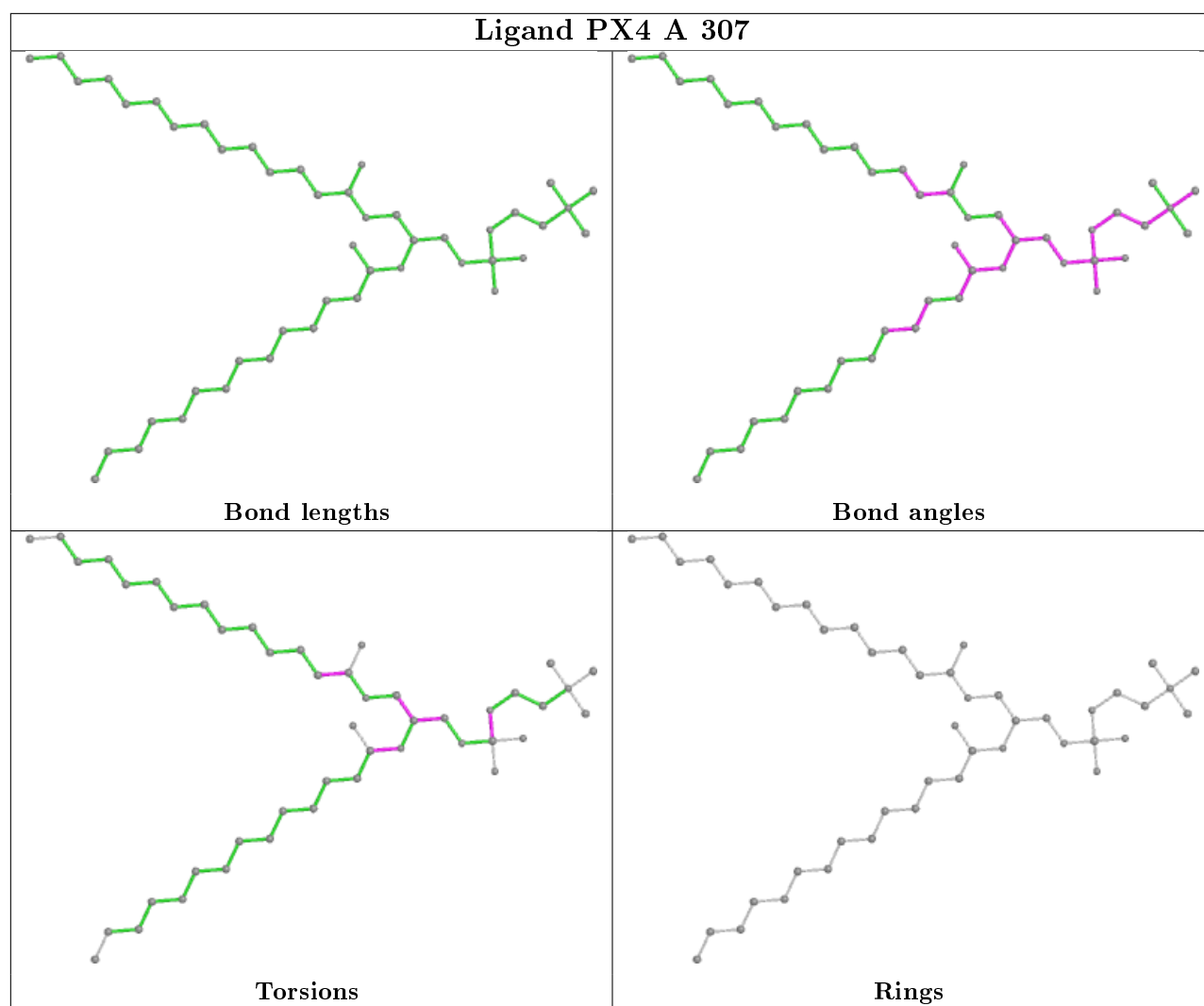


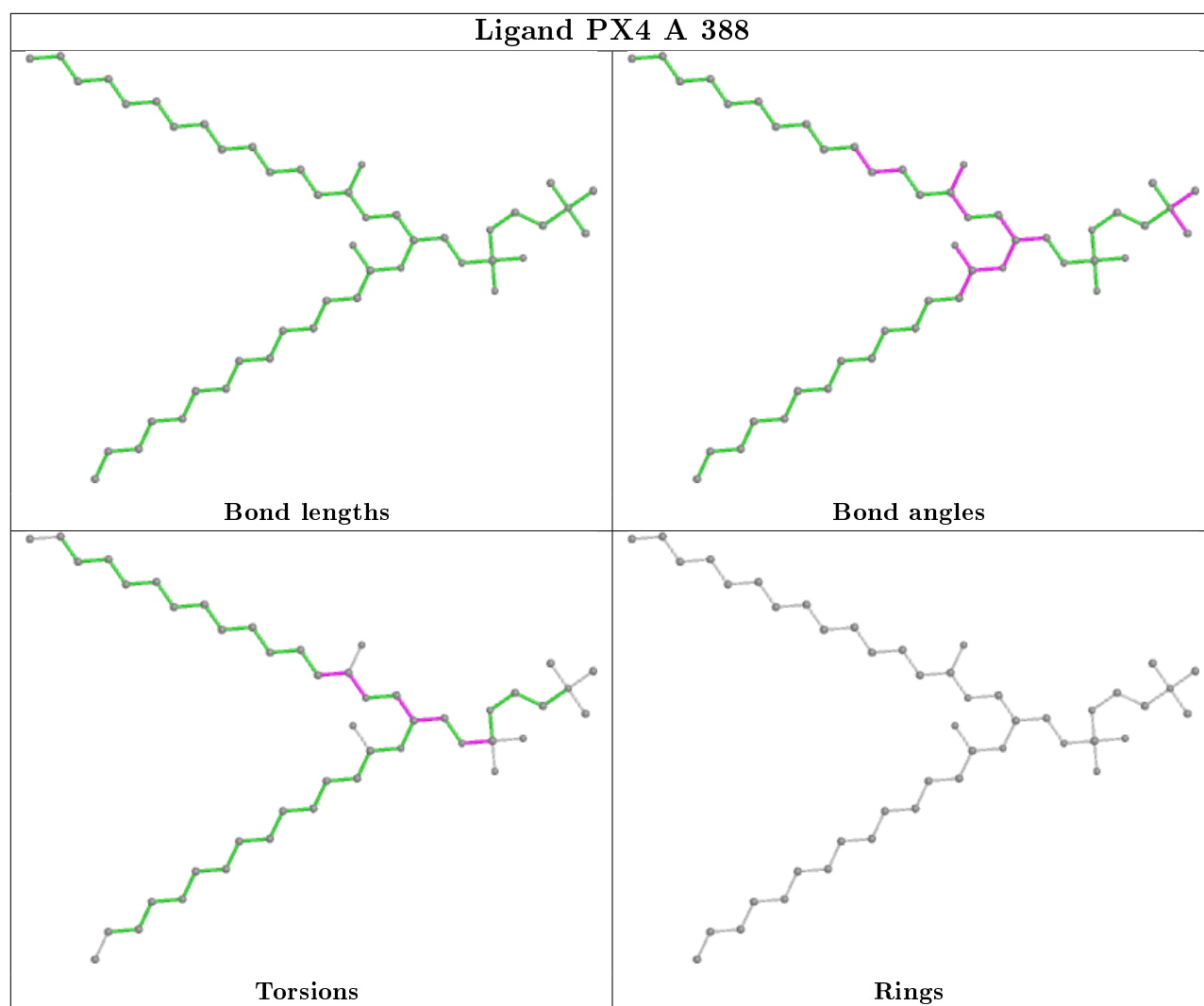


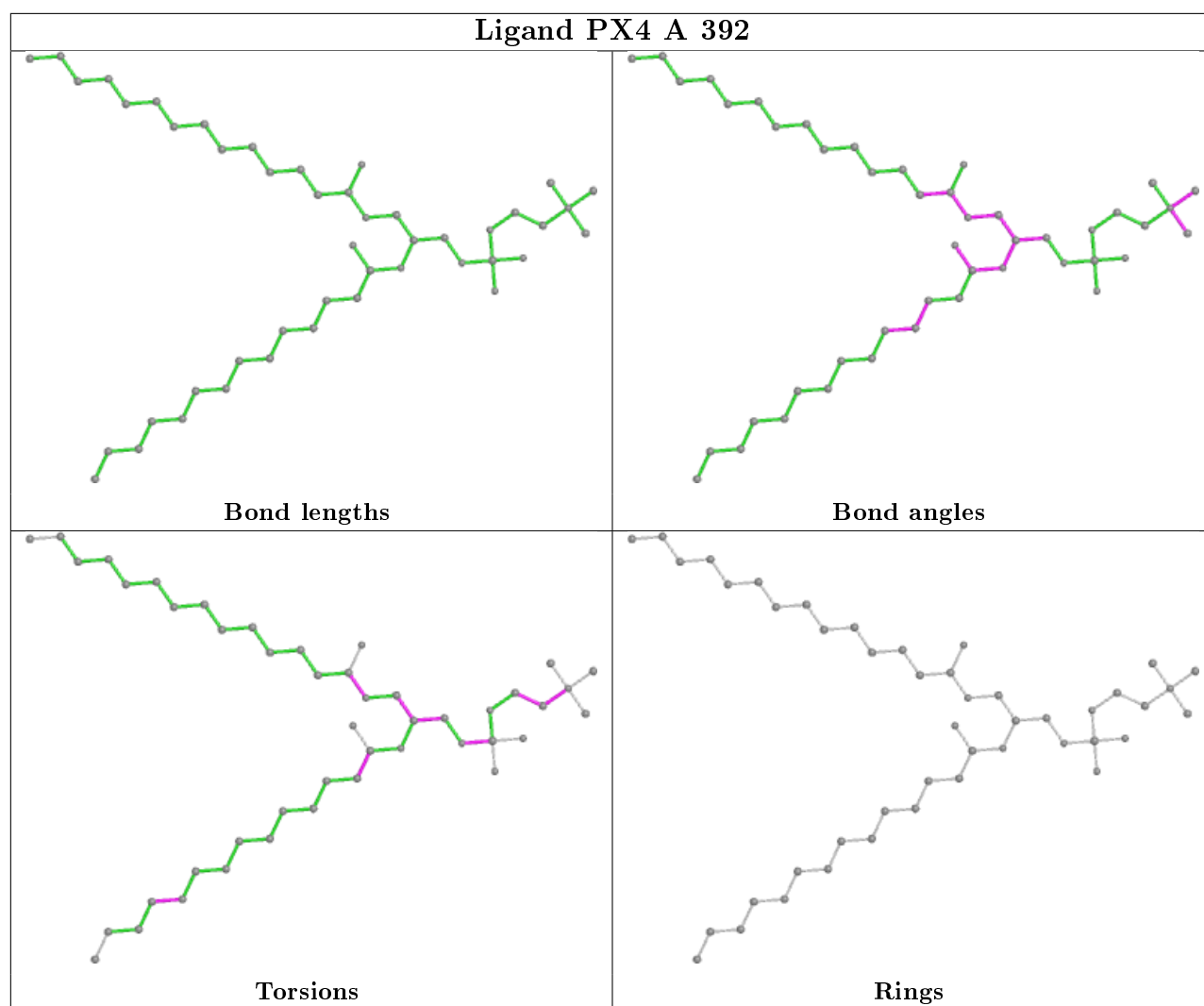


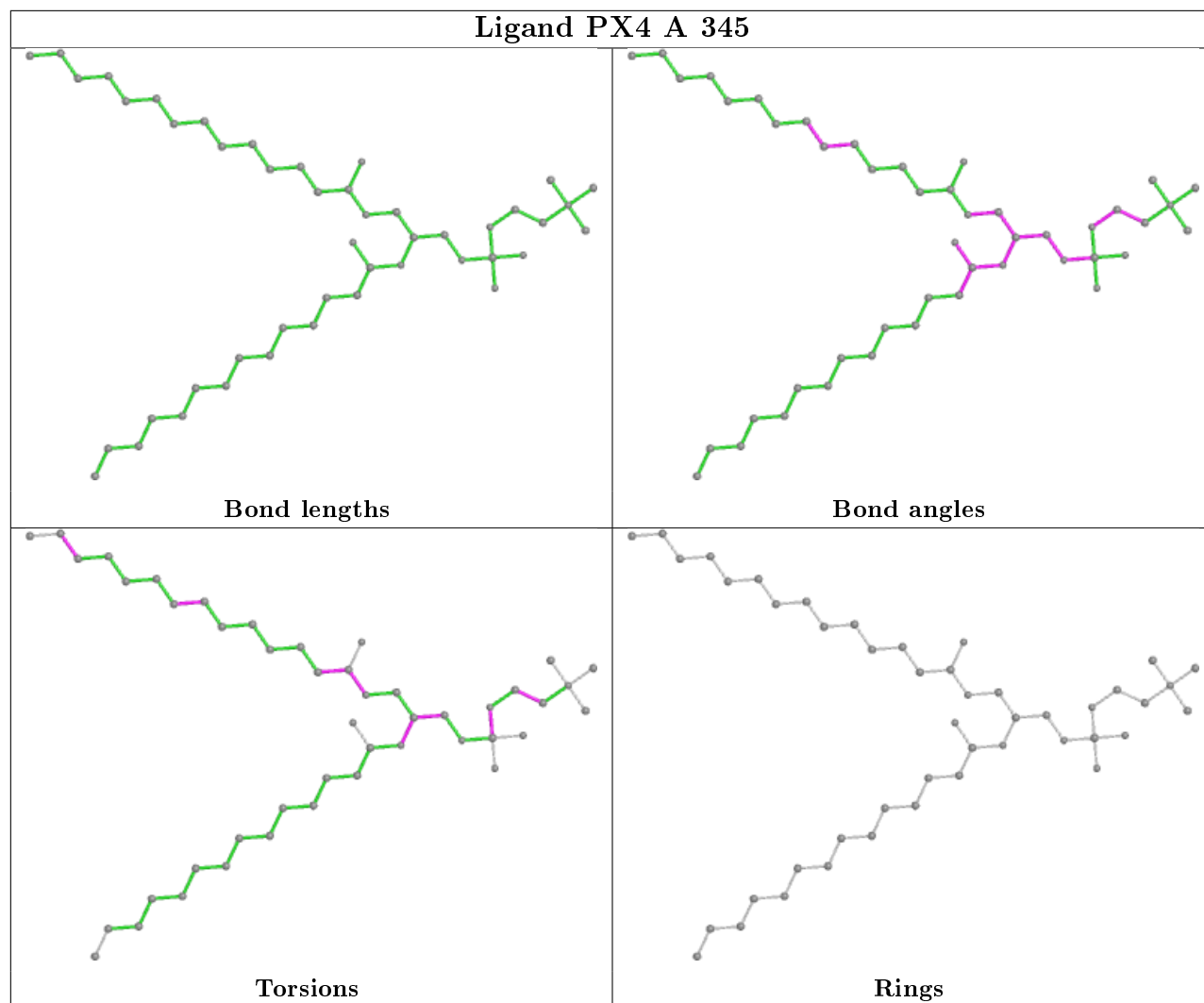
Ligand PX4 A 336

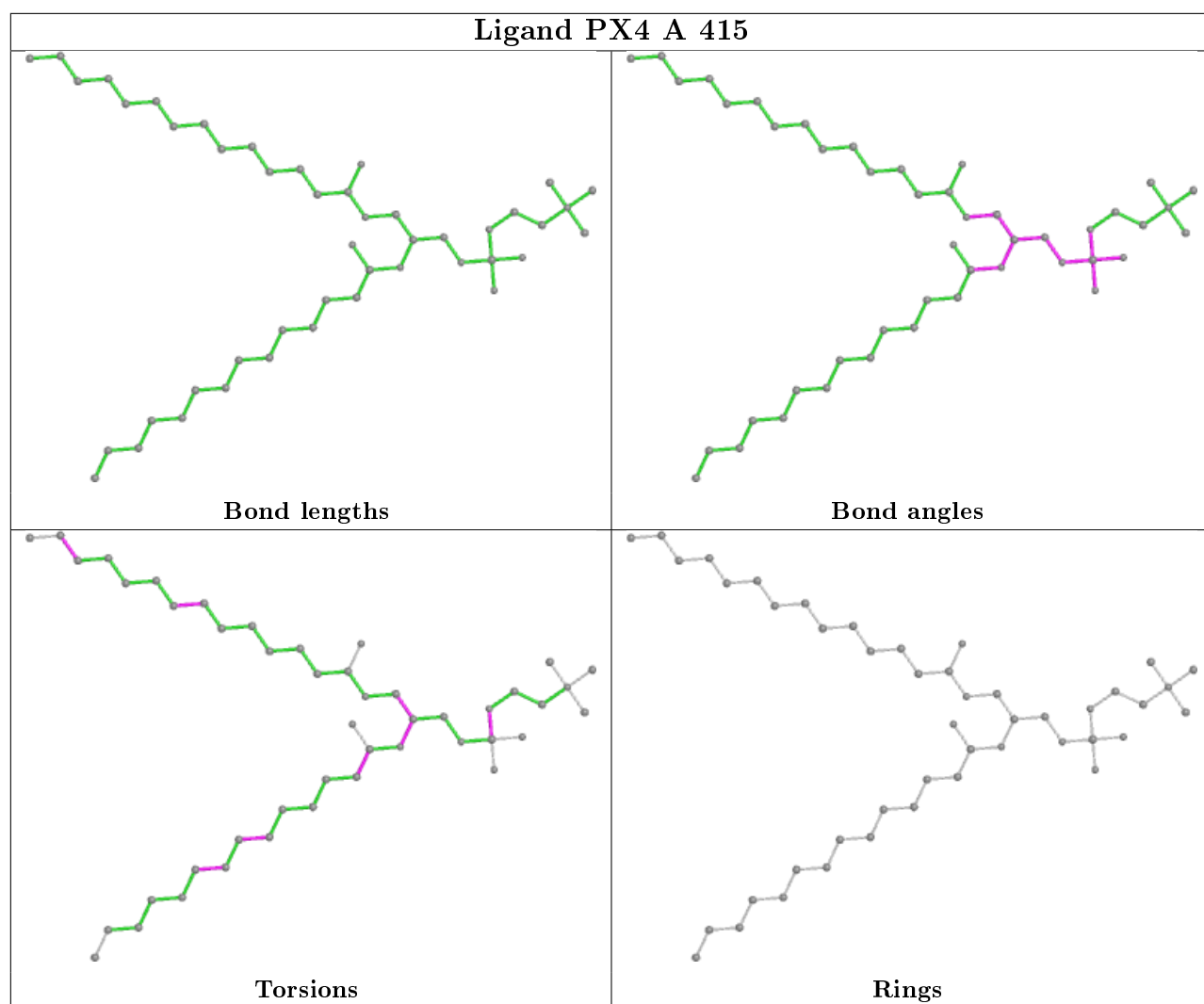




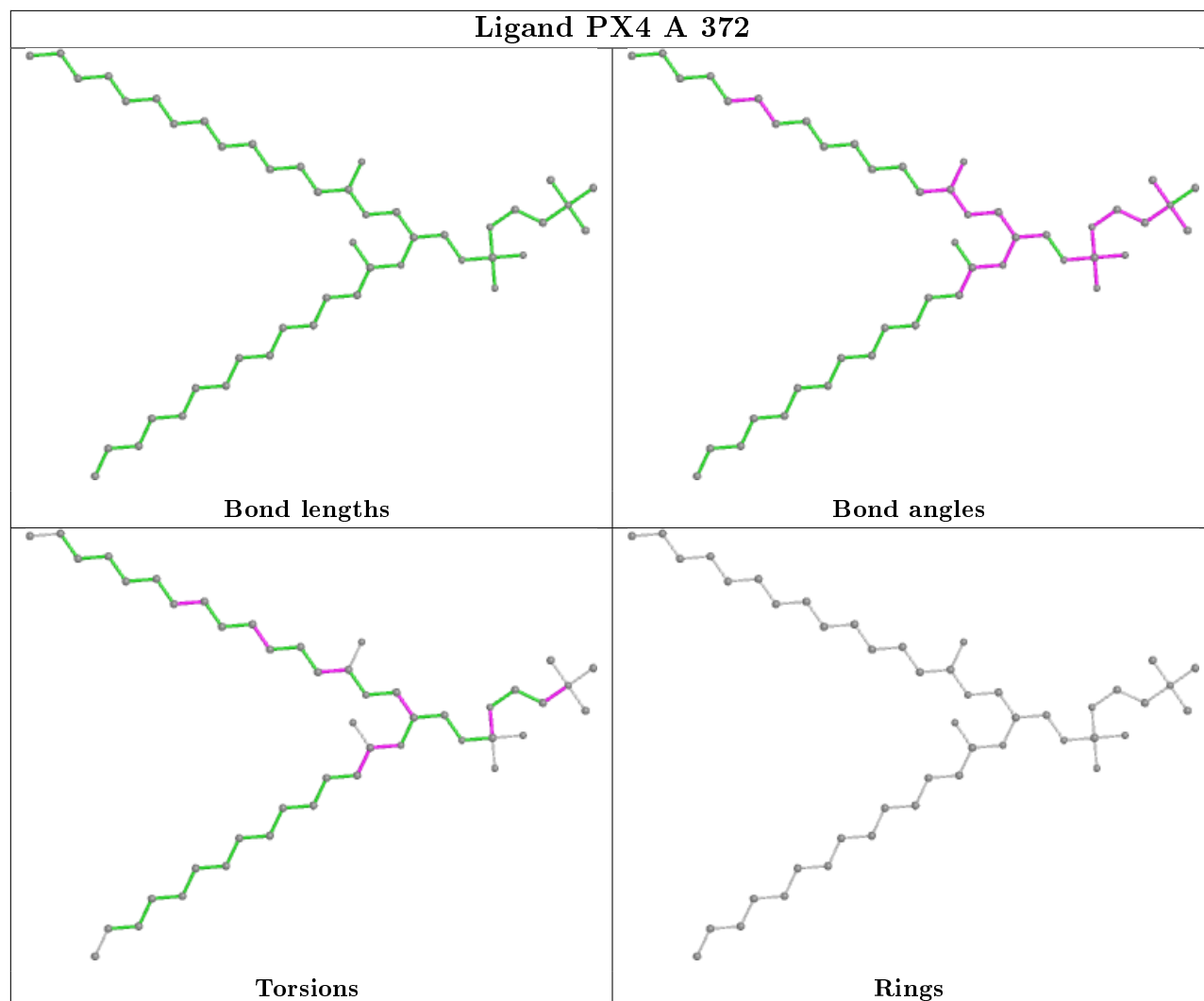


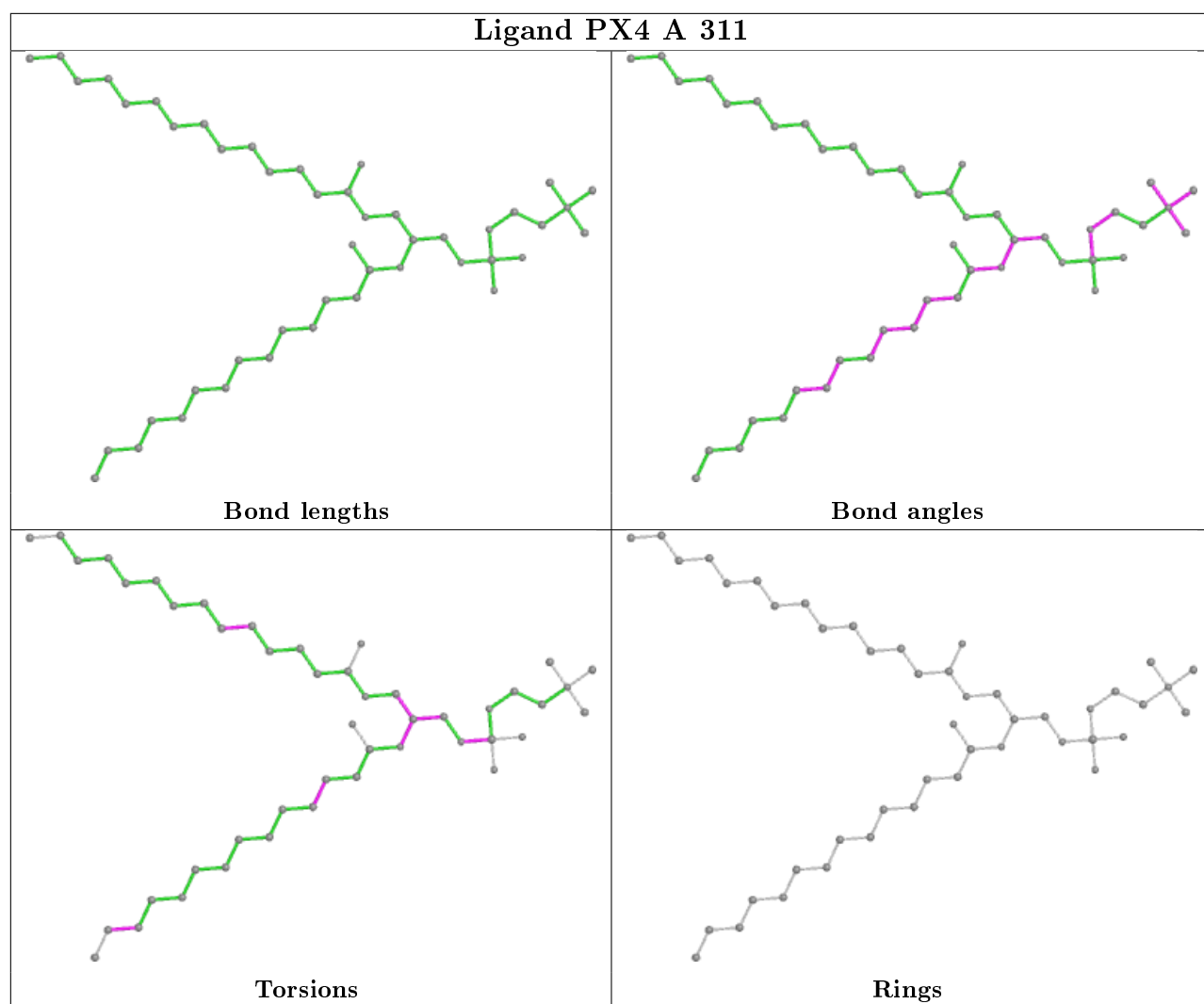


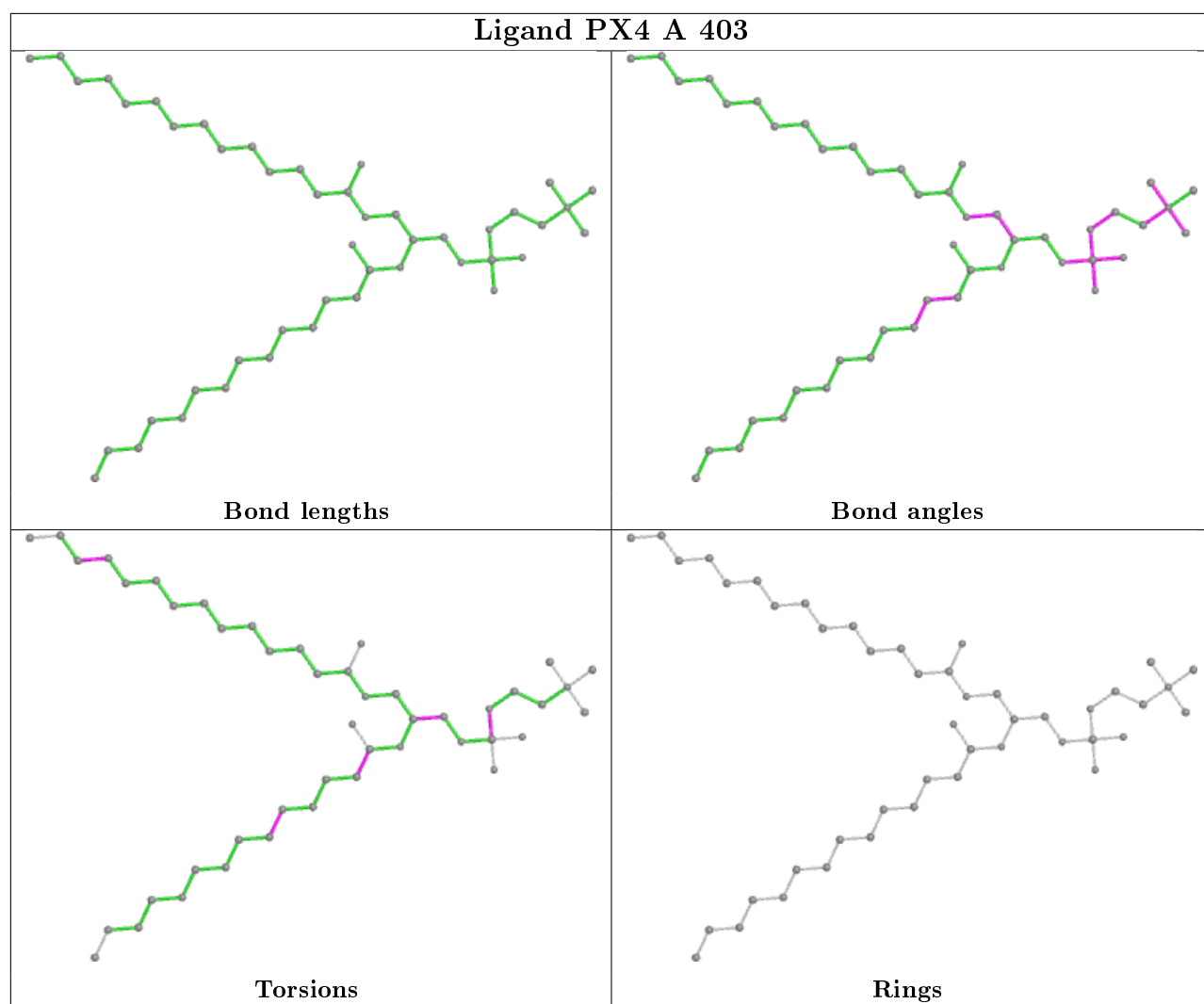


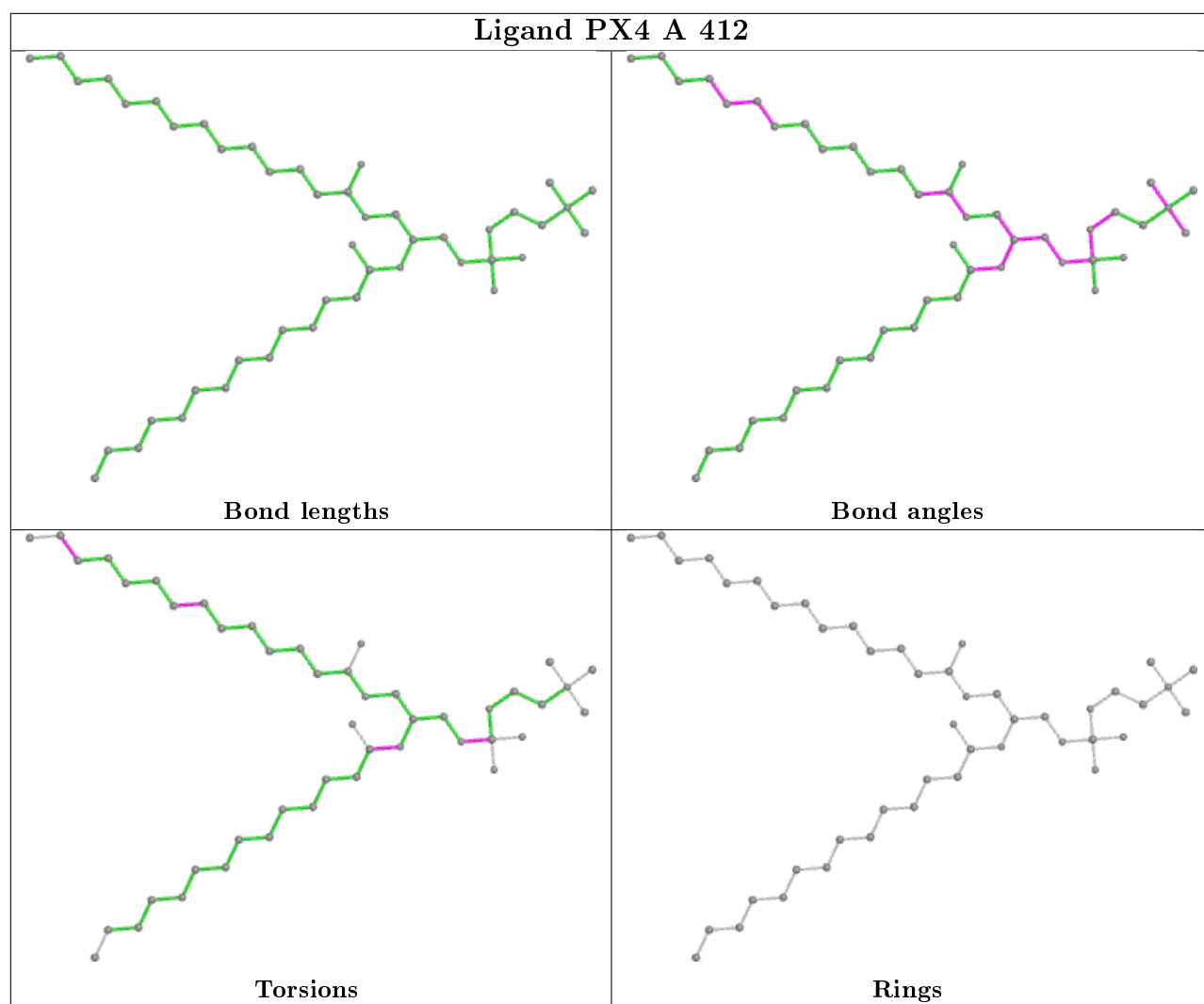


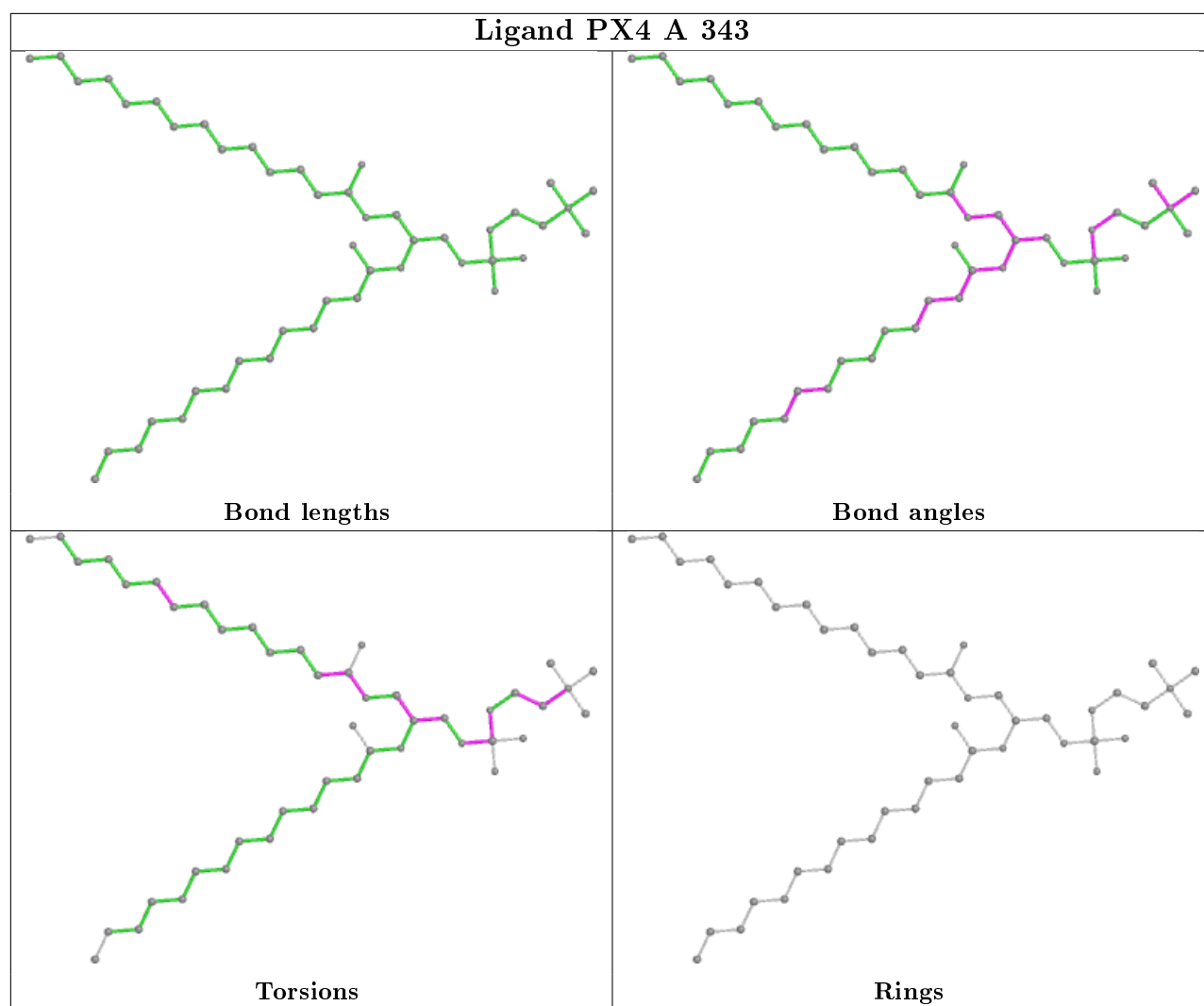
Ligand PX4 A 372

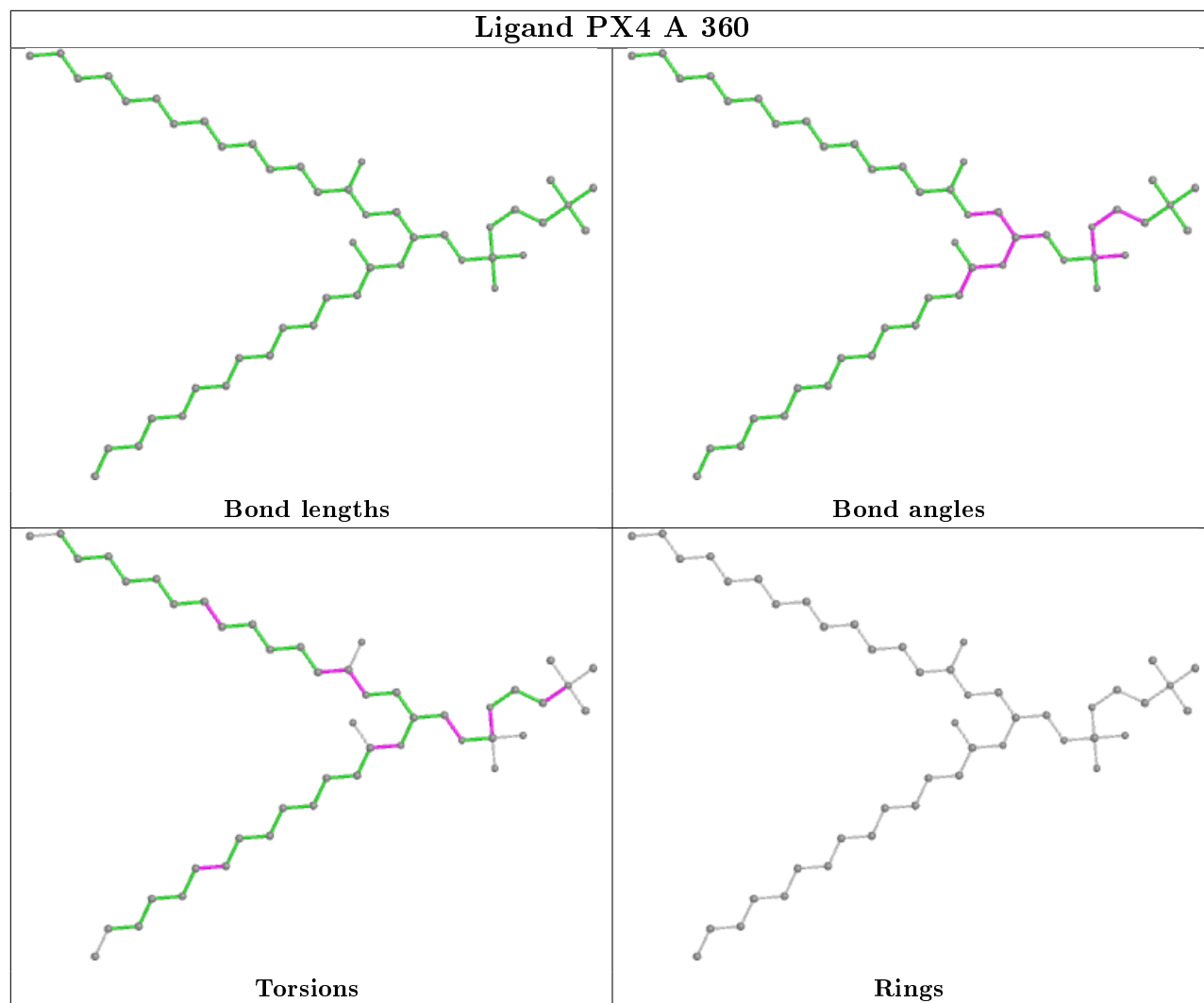


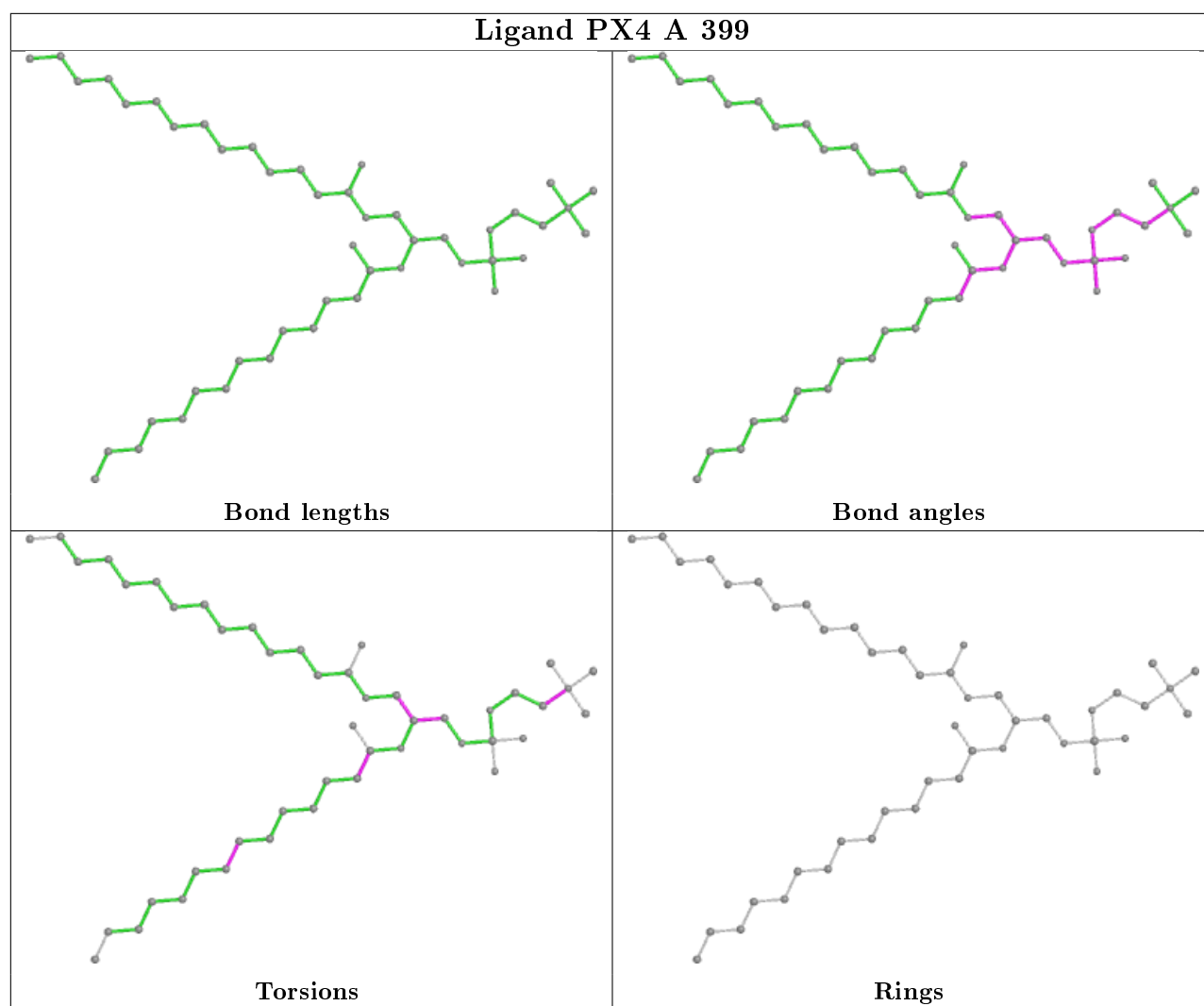


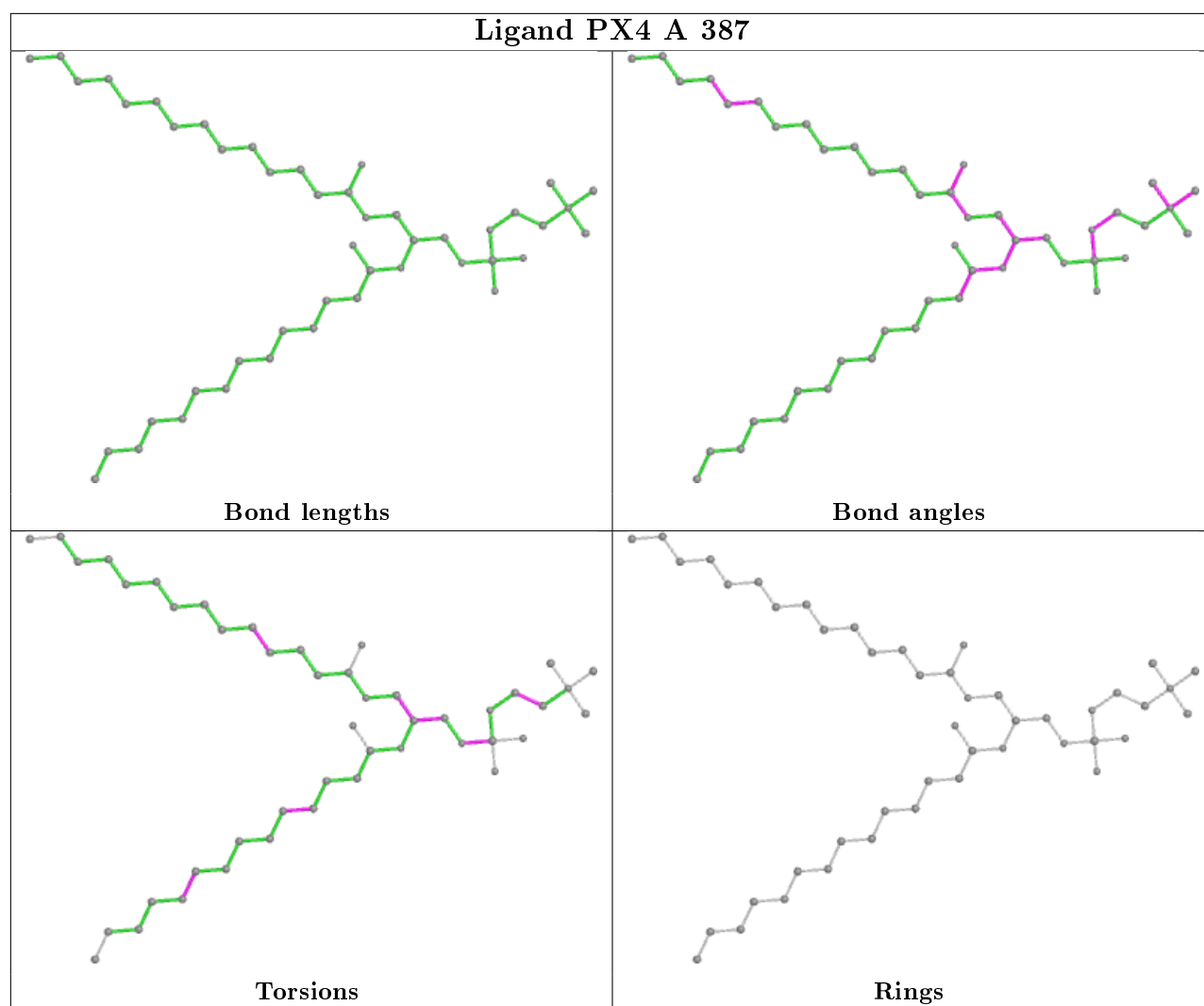


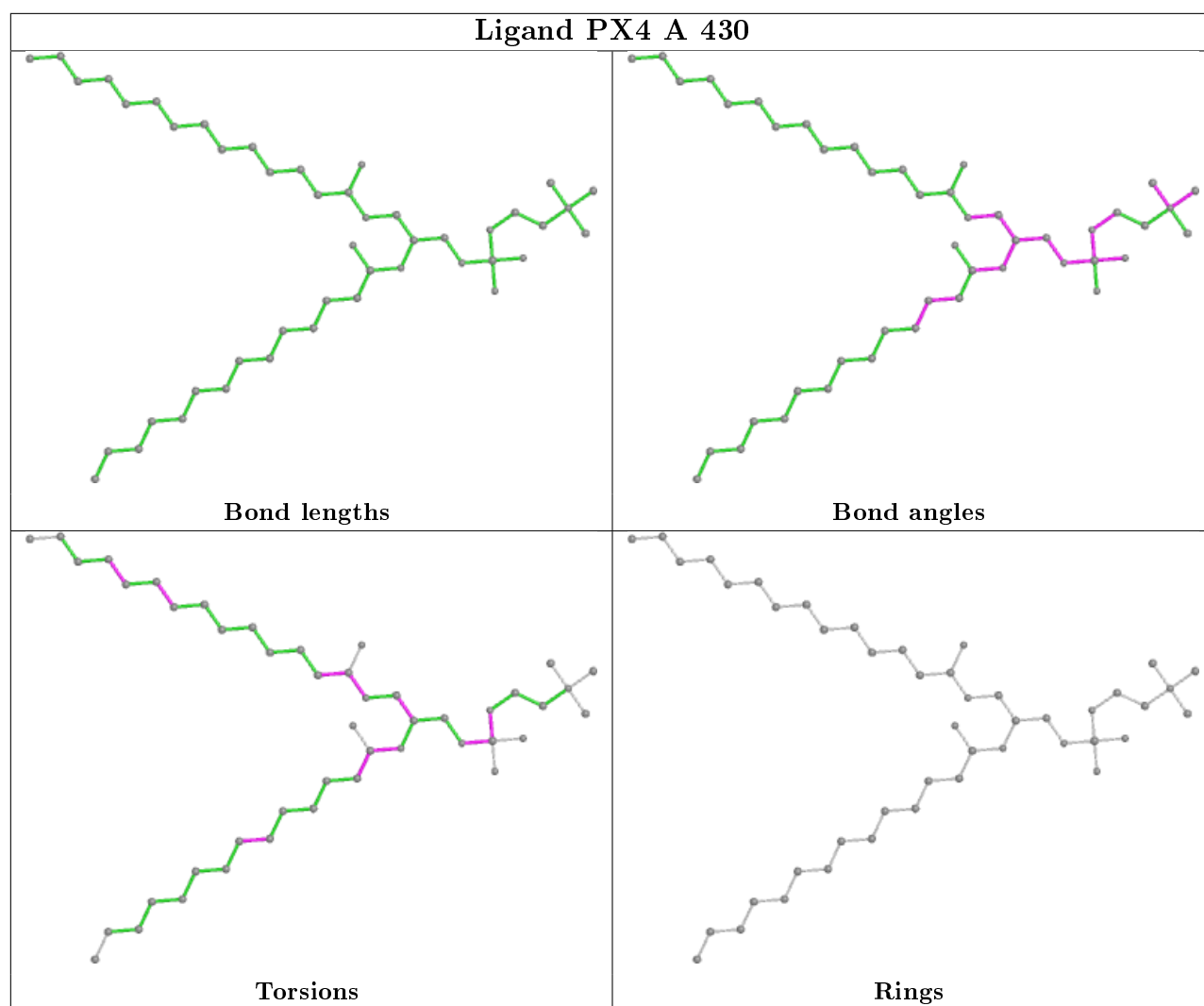


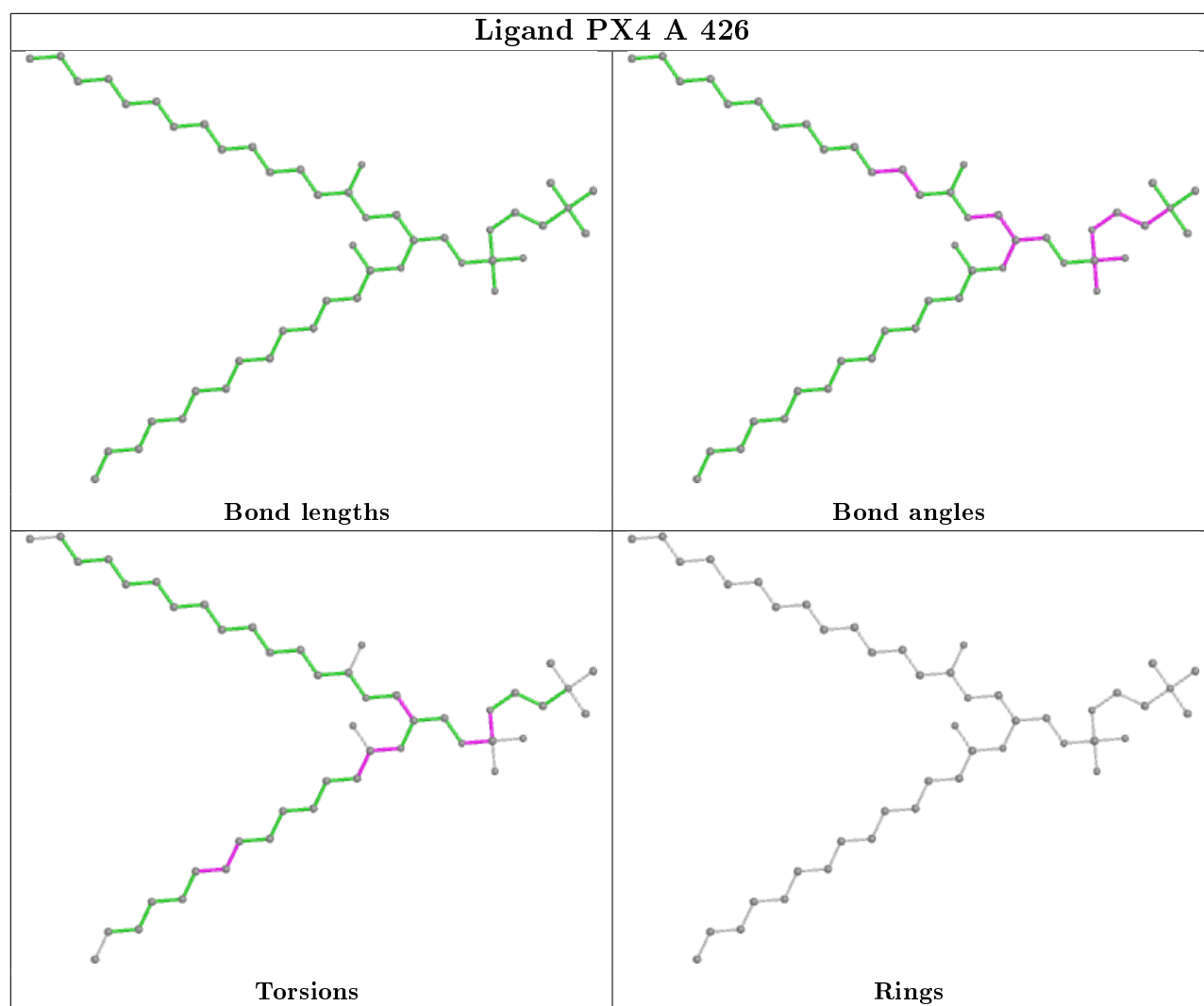


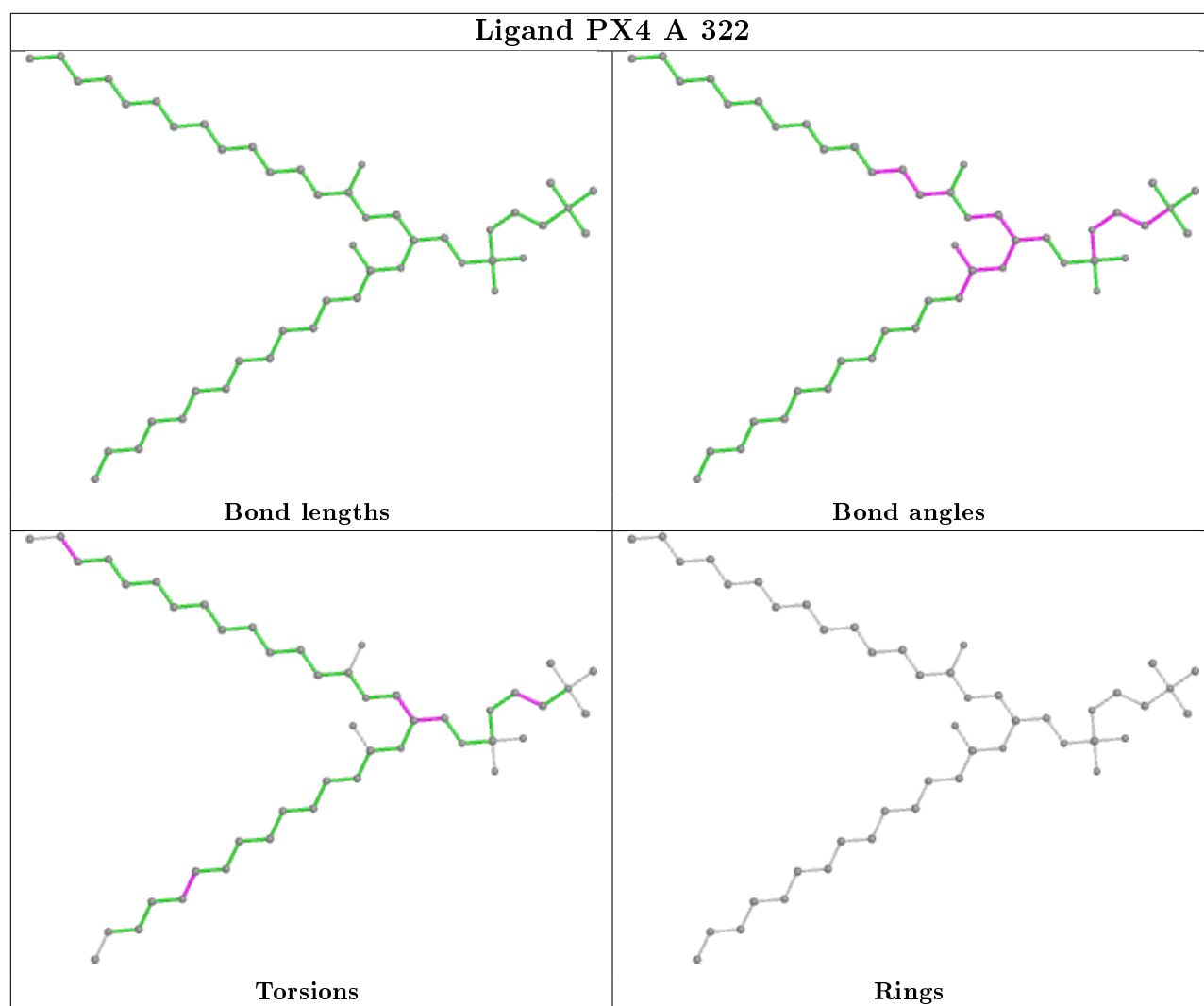


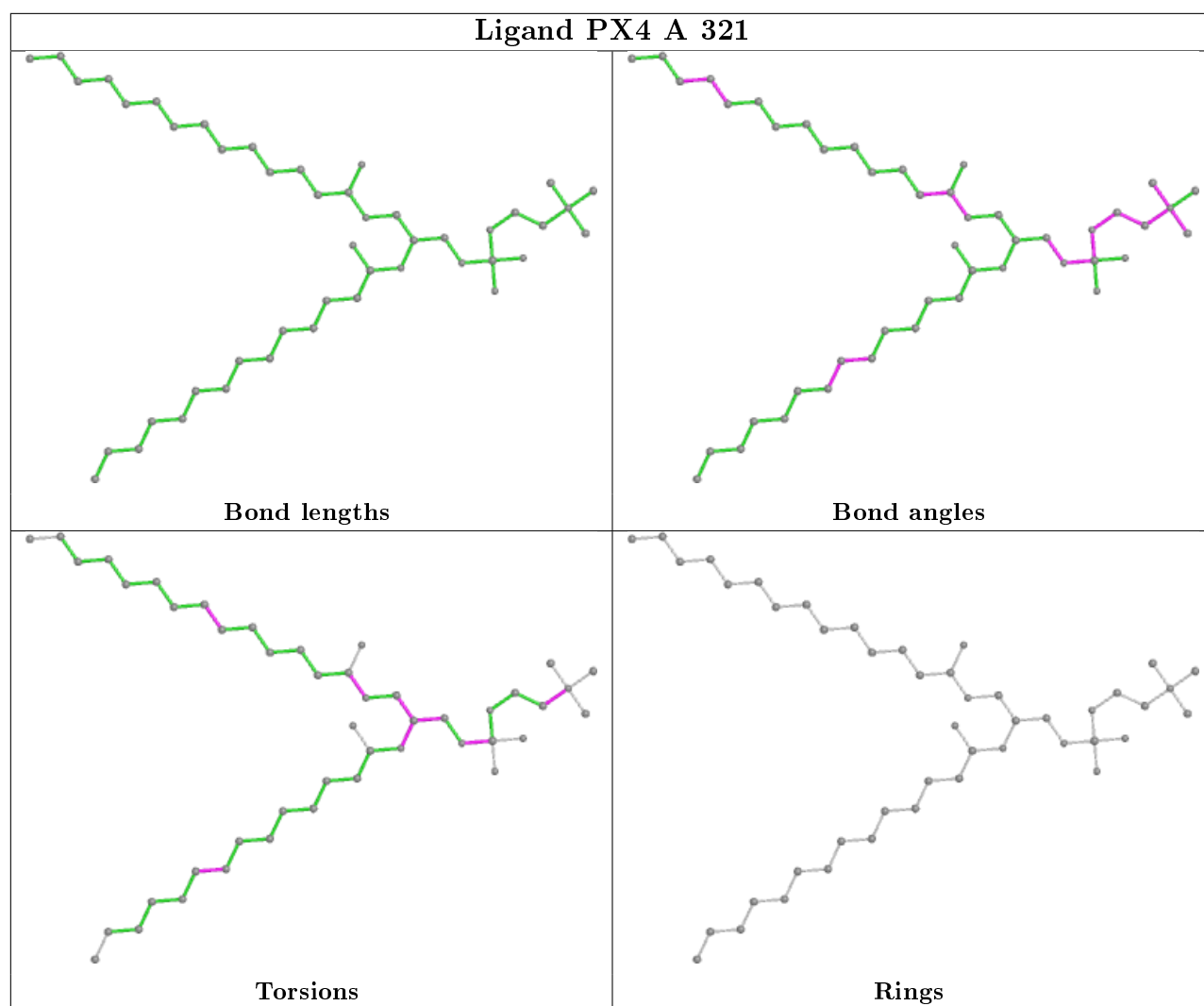




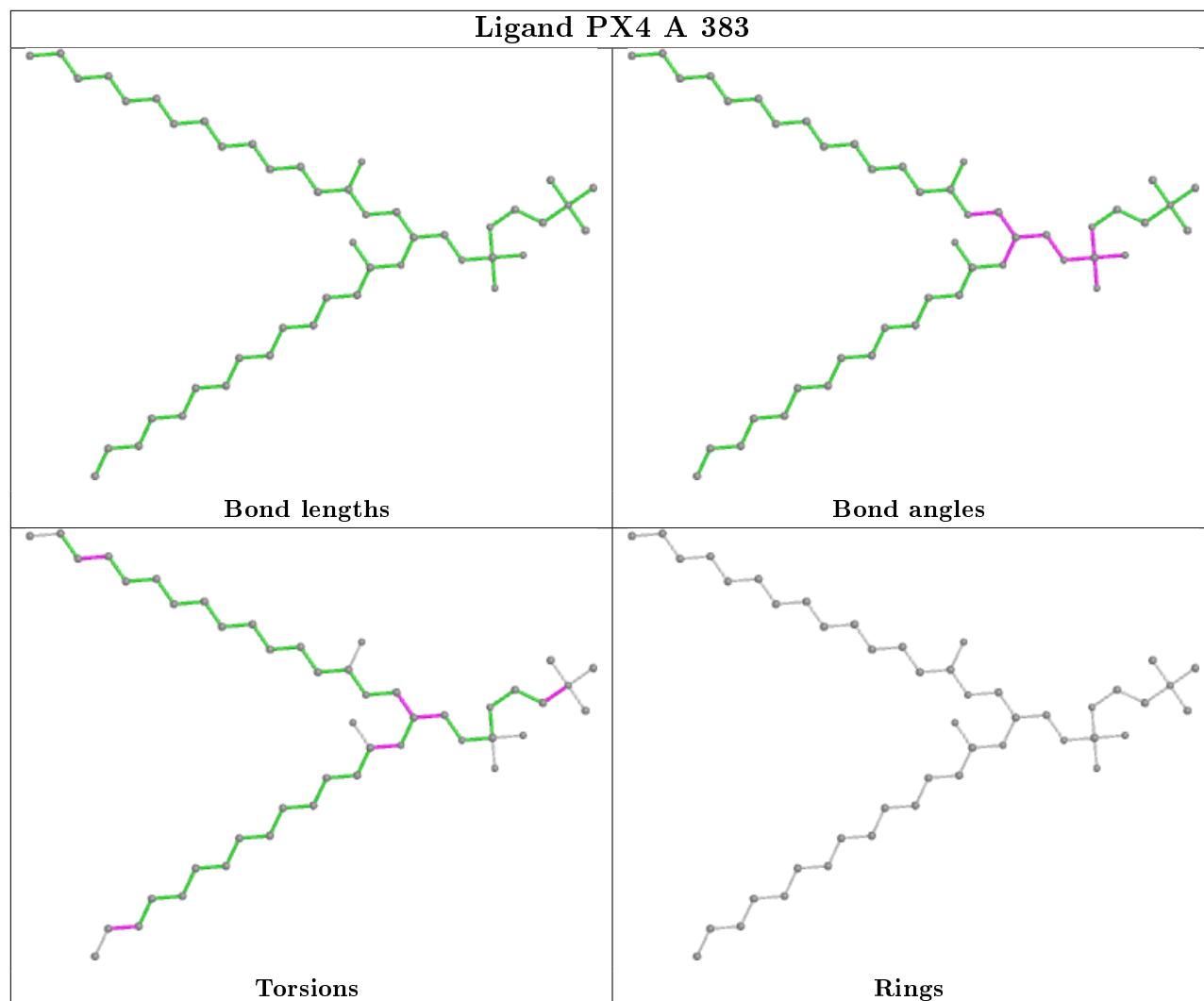




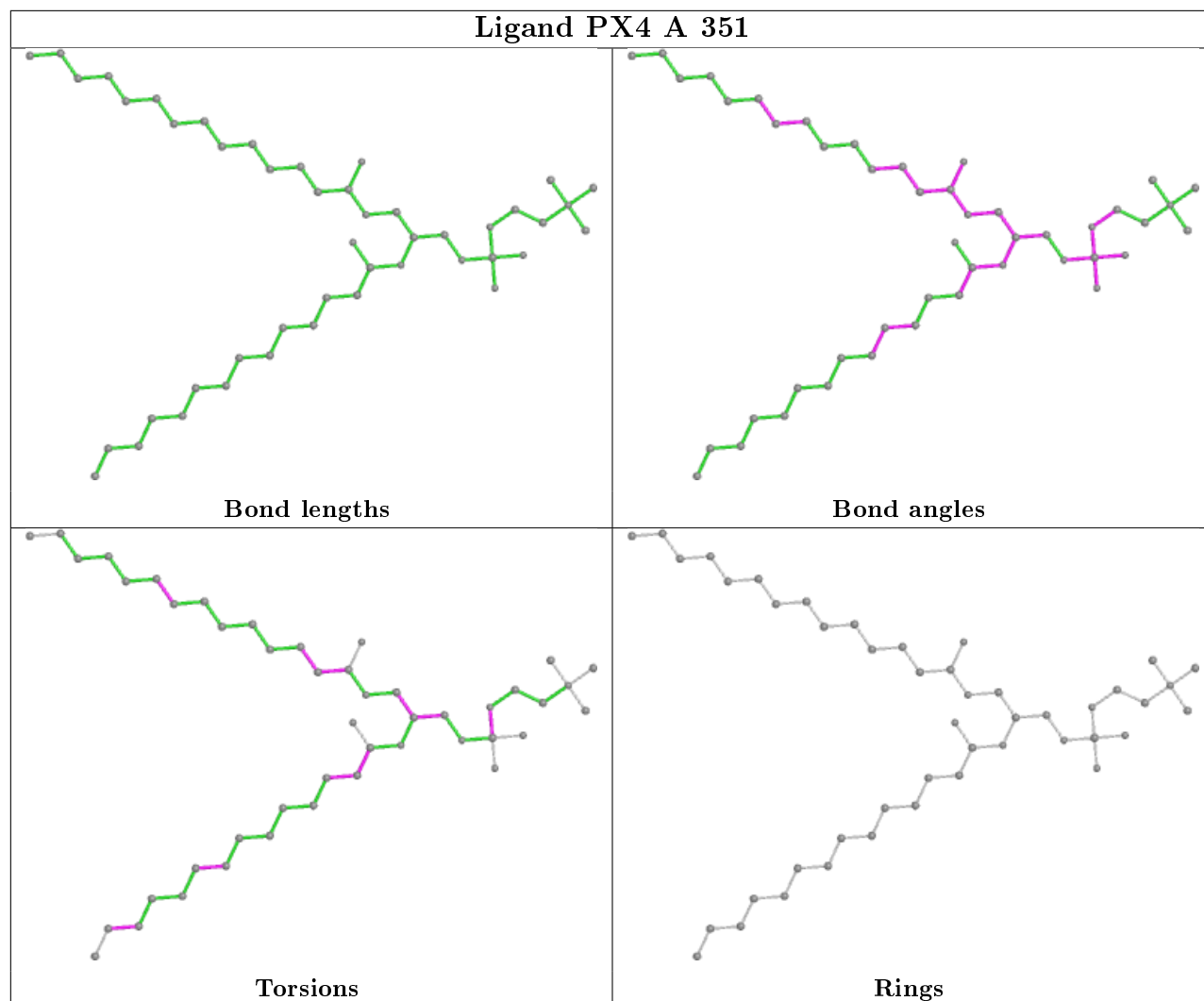


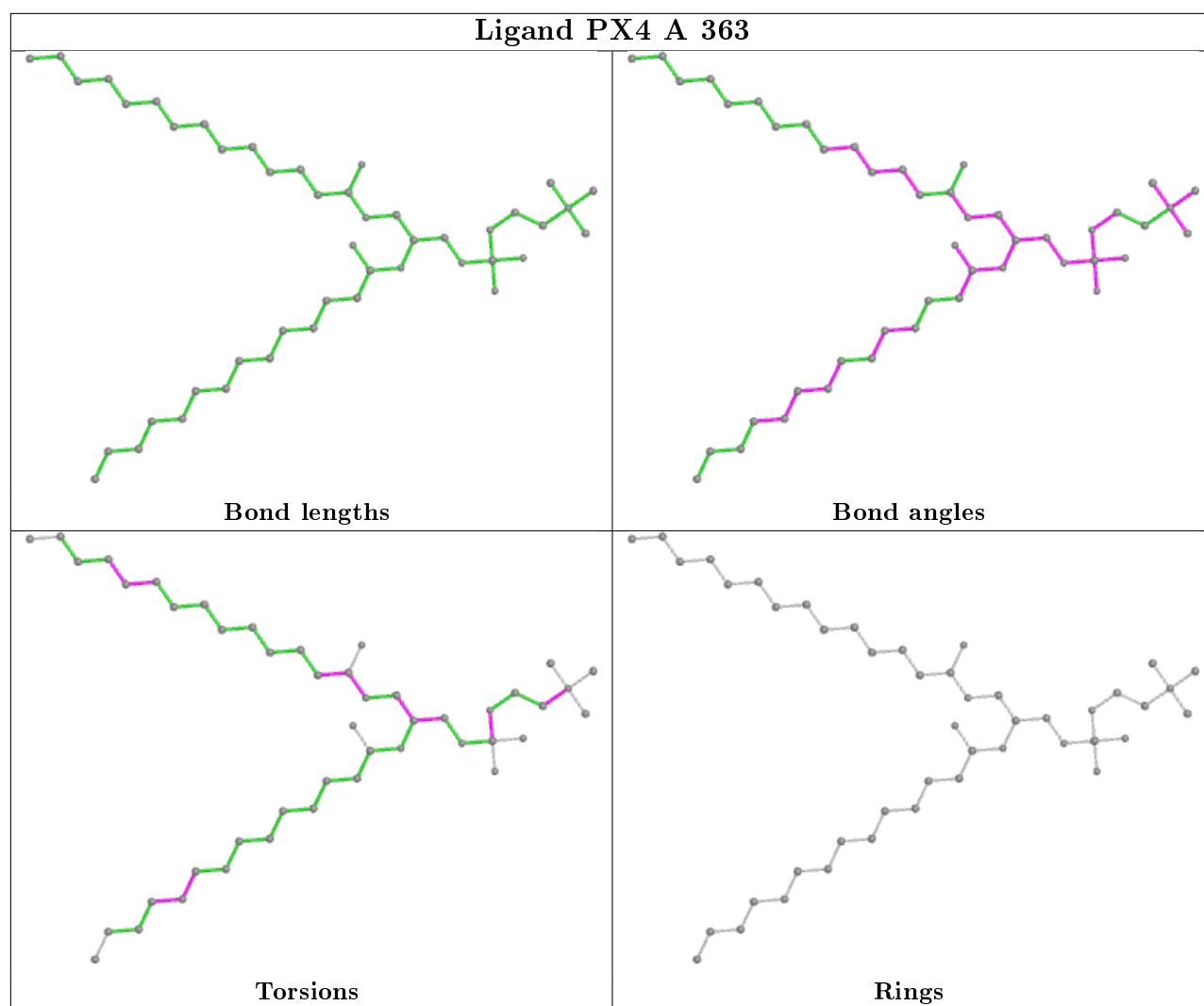


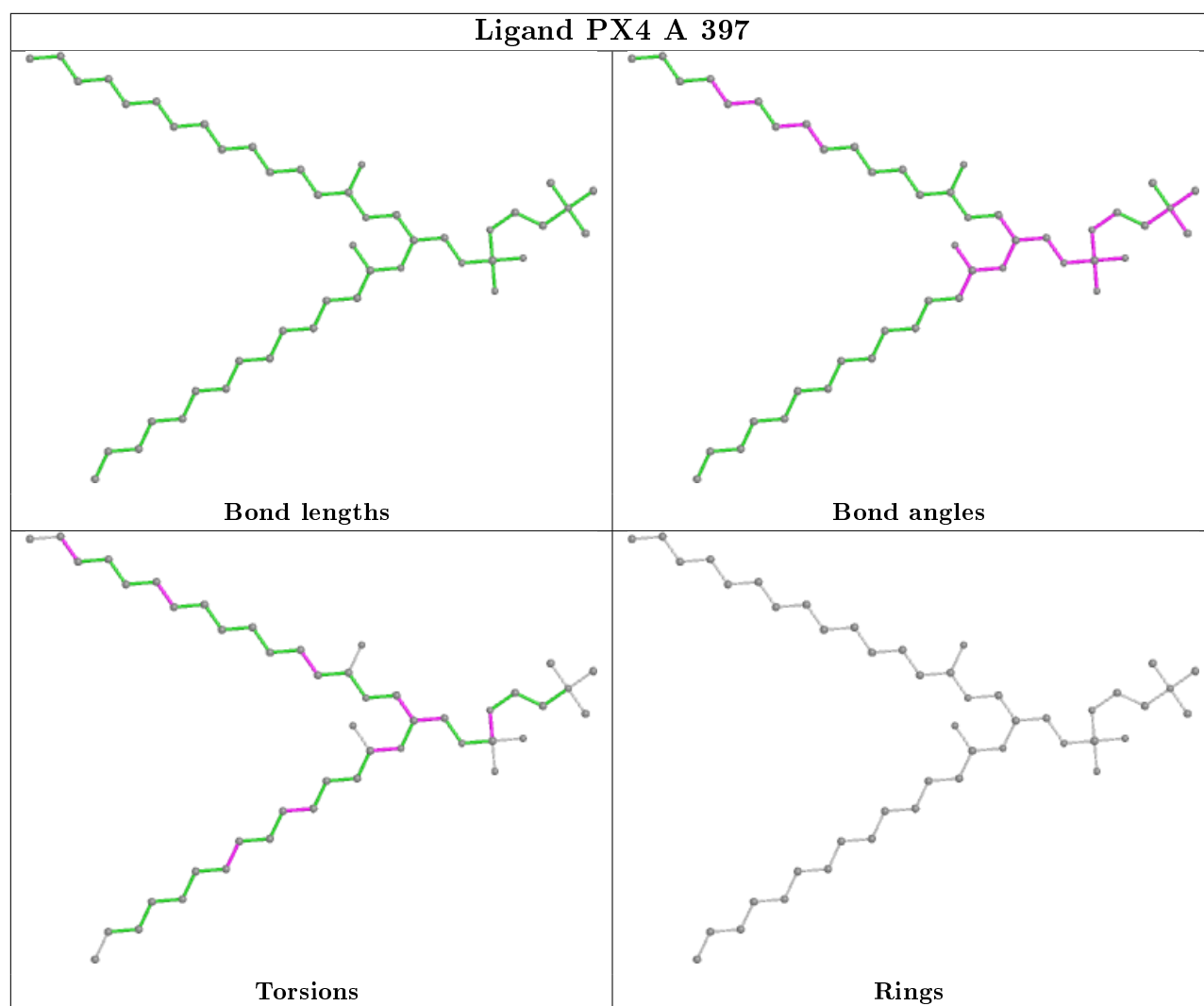
Ligand PX4 A 383

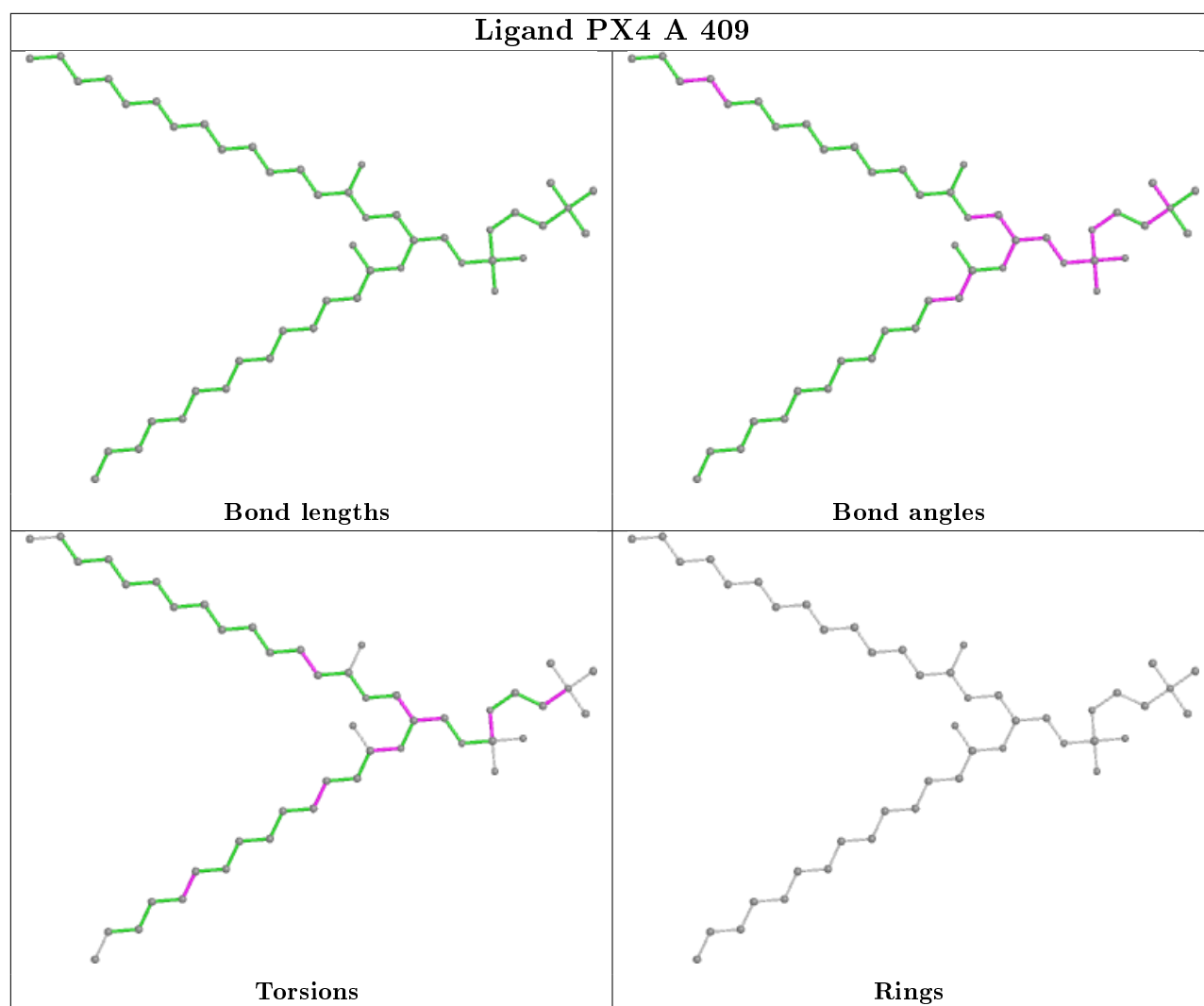


Ligand PX4 A 351

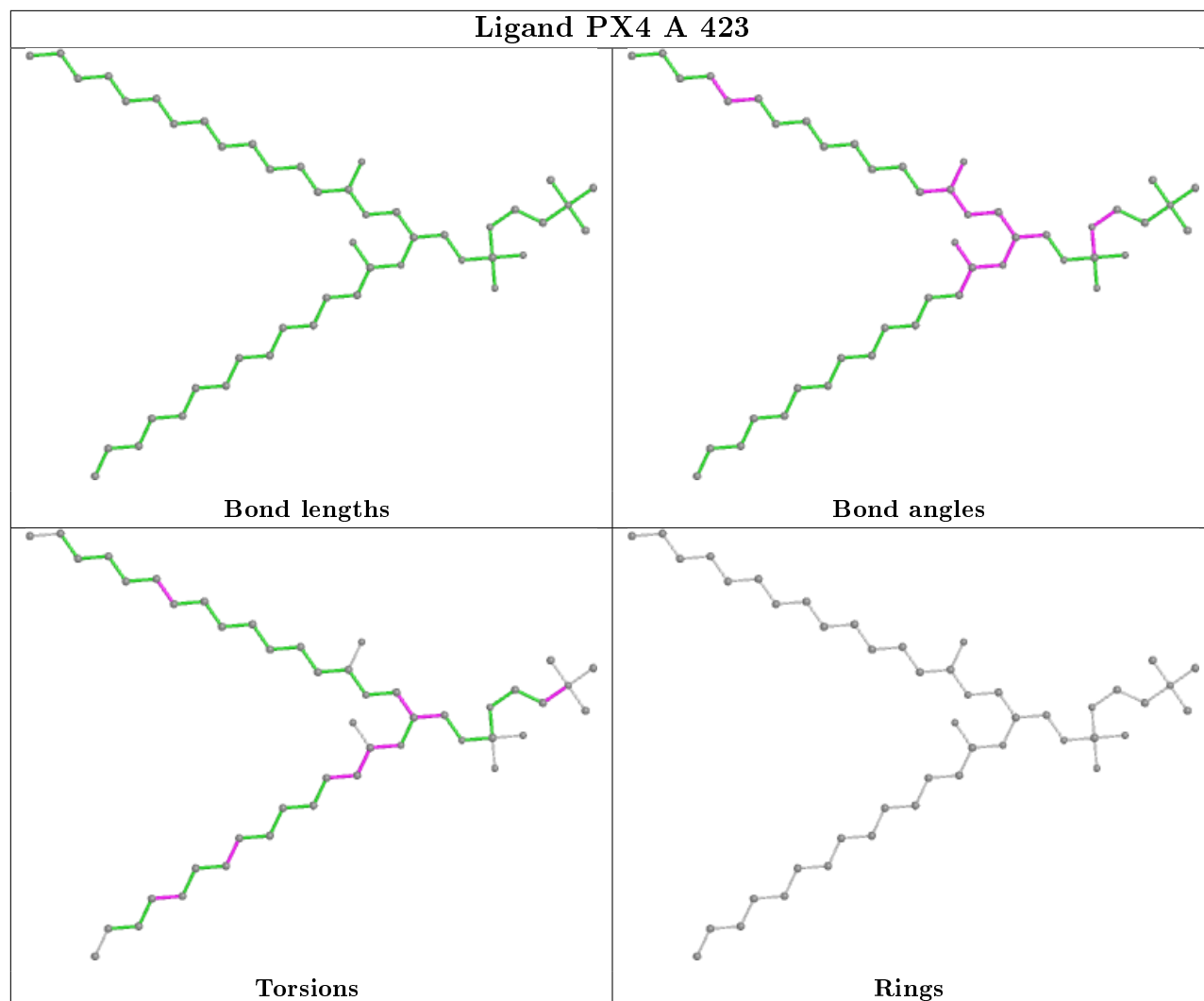


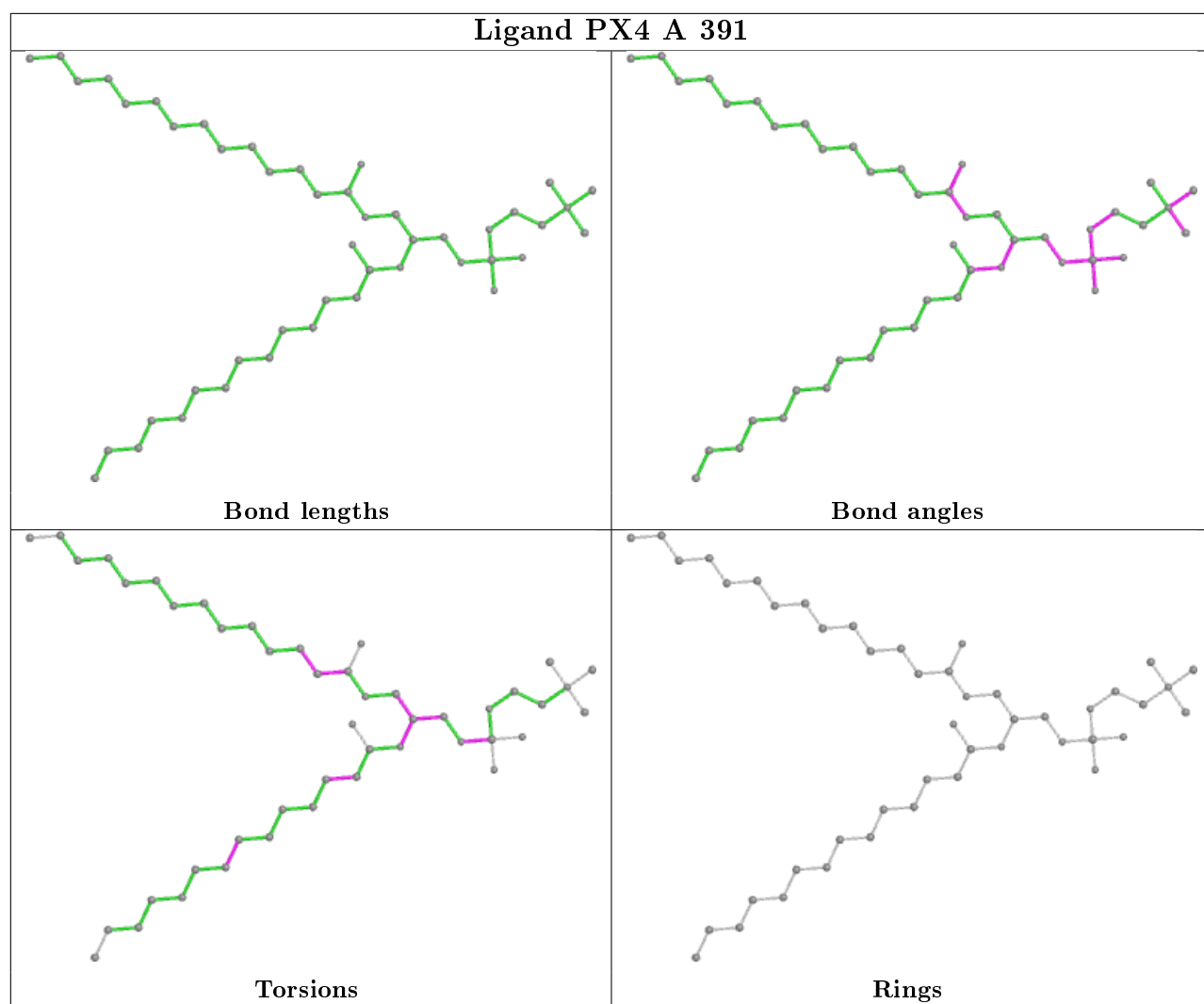




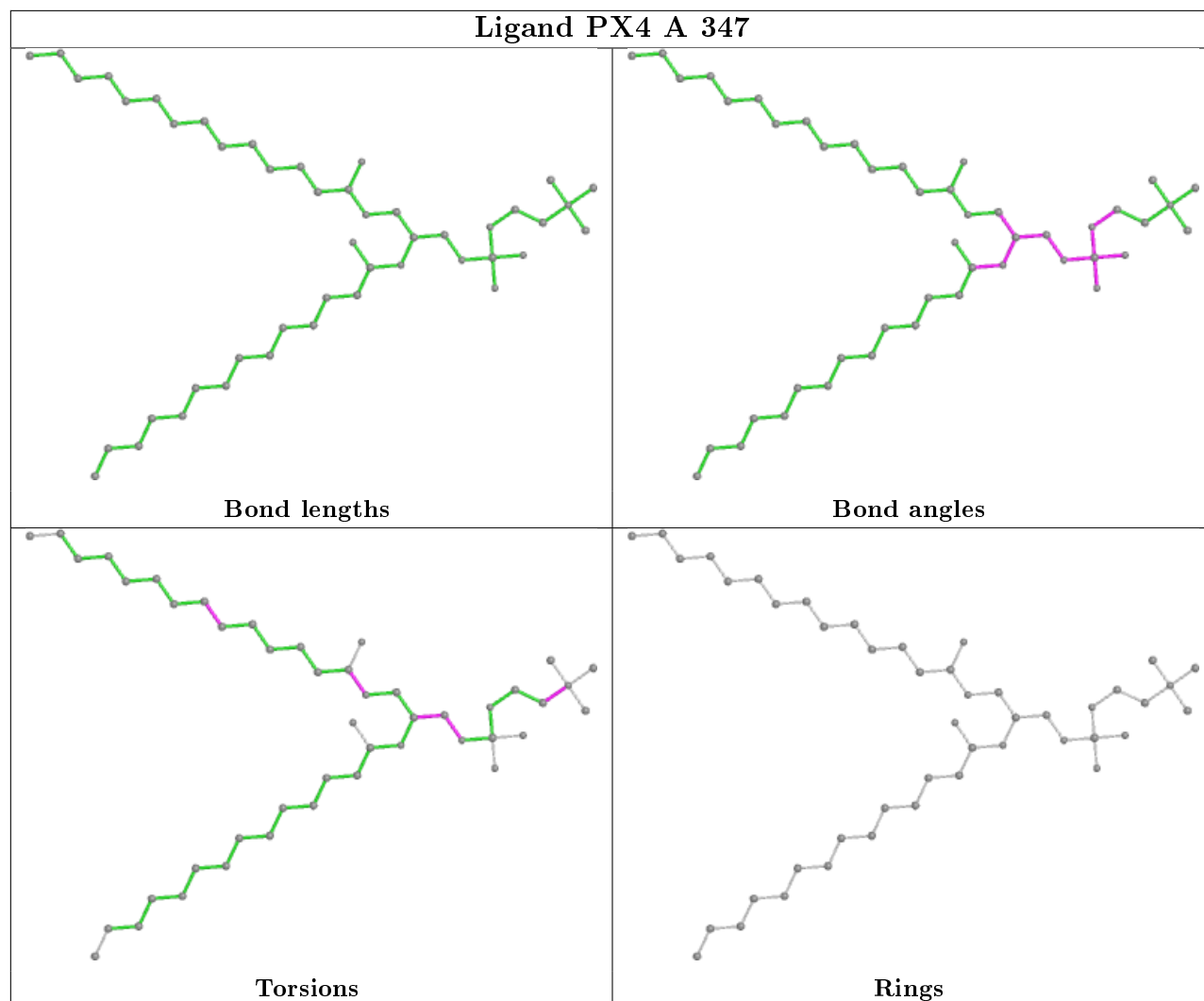


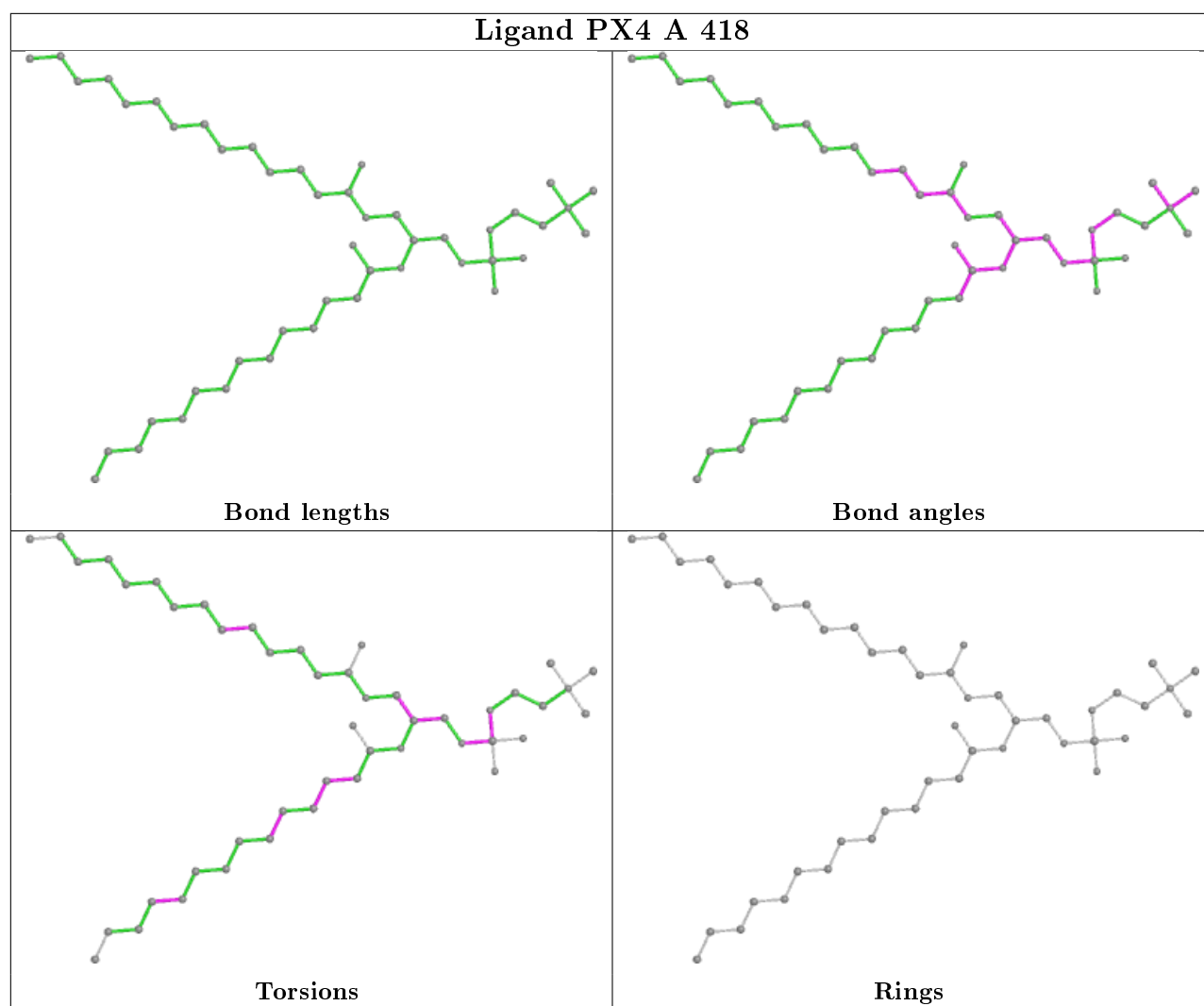
Ligand PX4 A 423

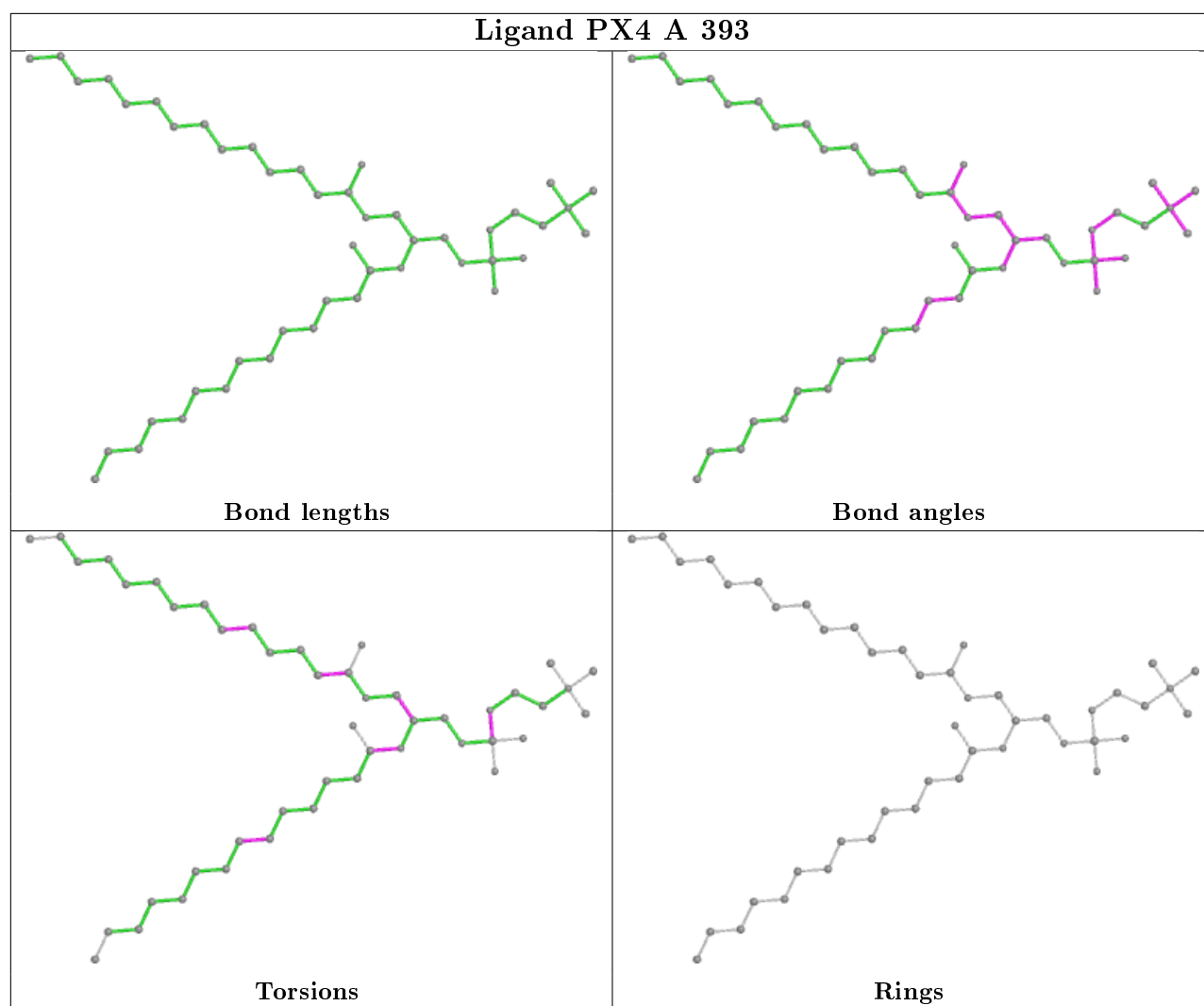


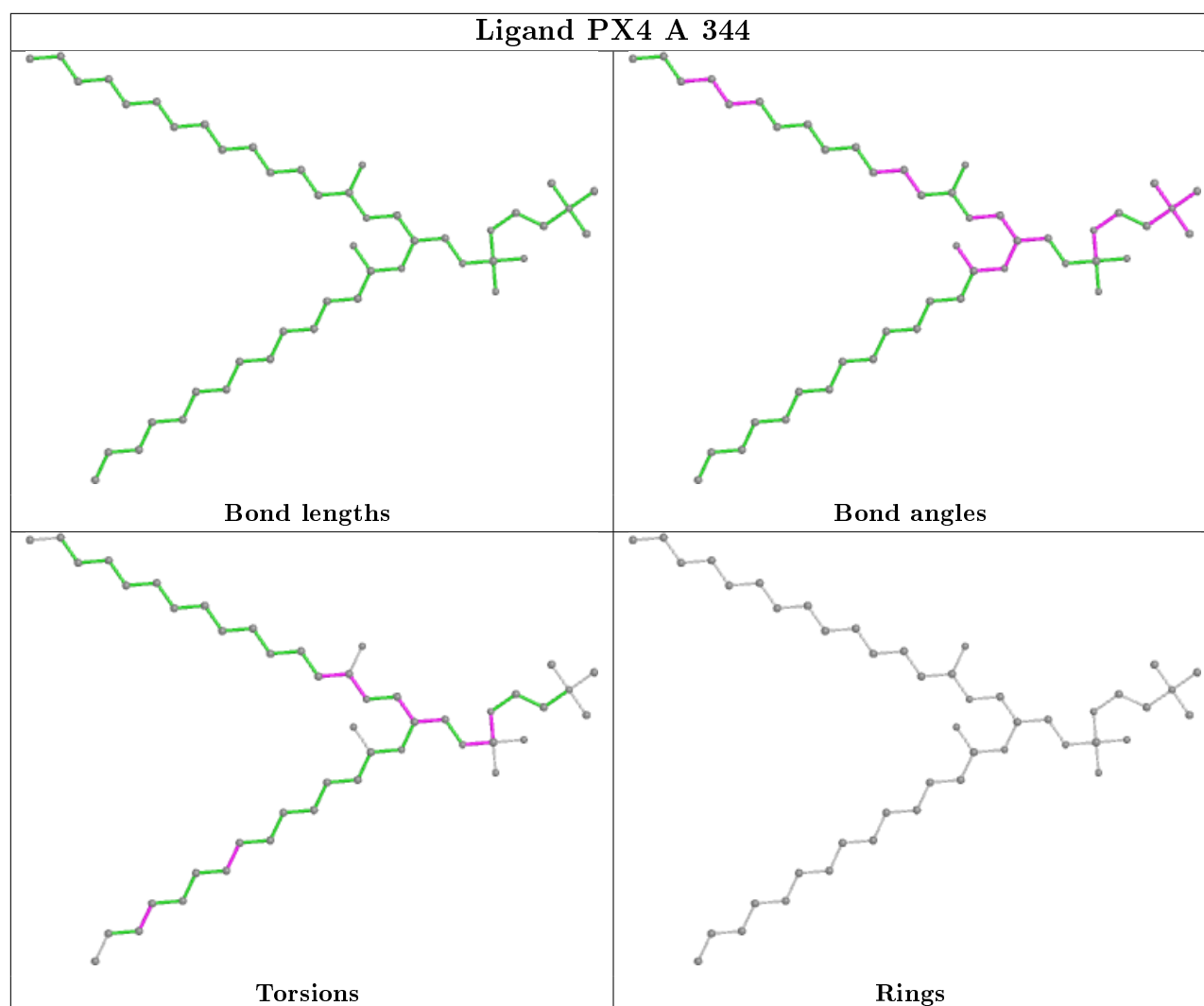


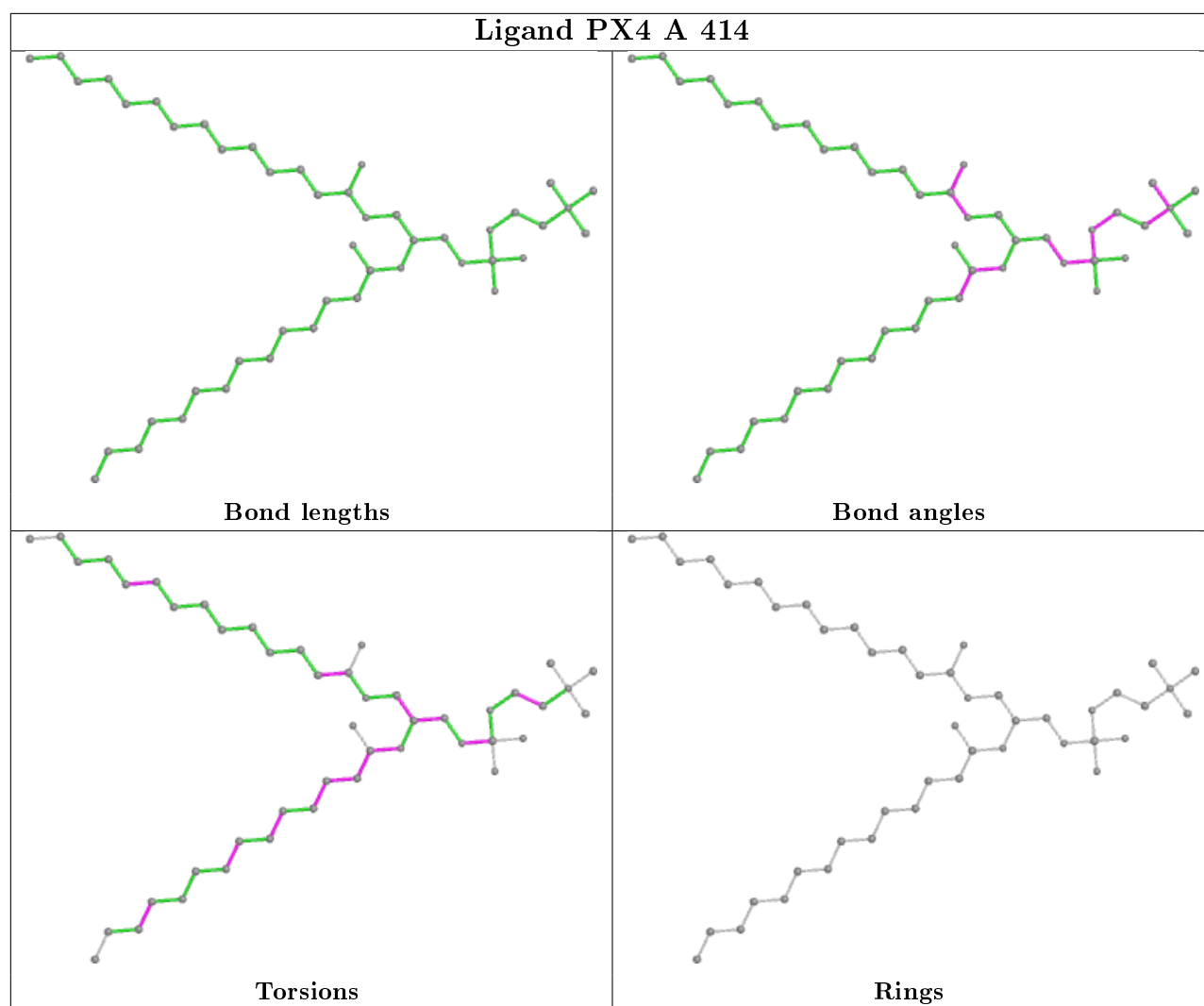
Ligand PX4 A 347



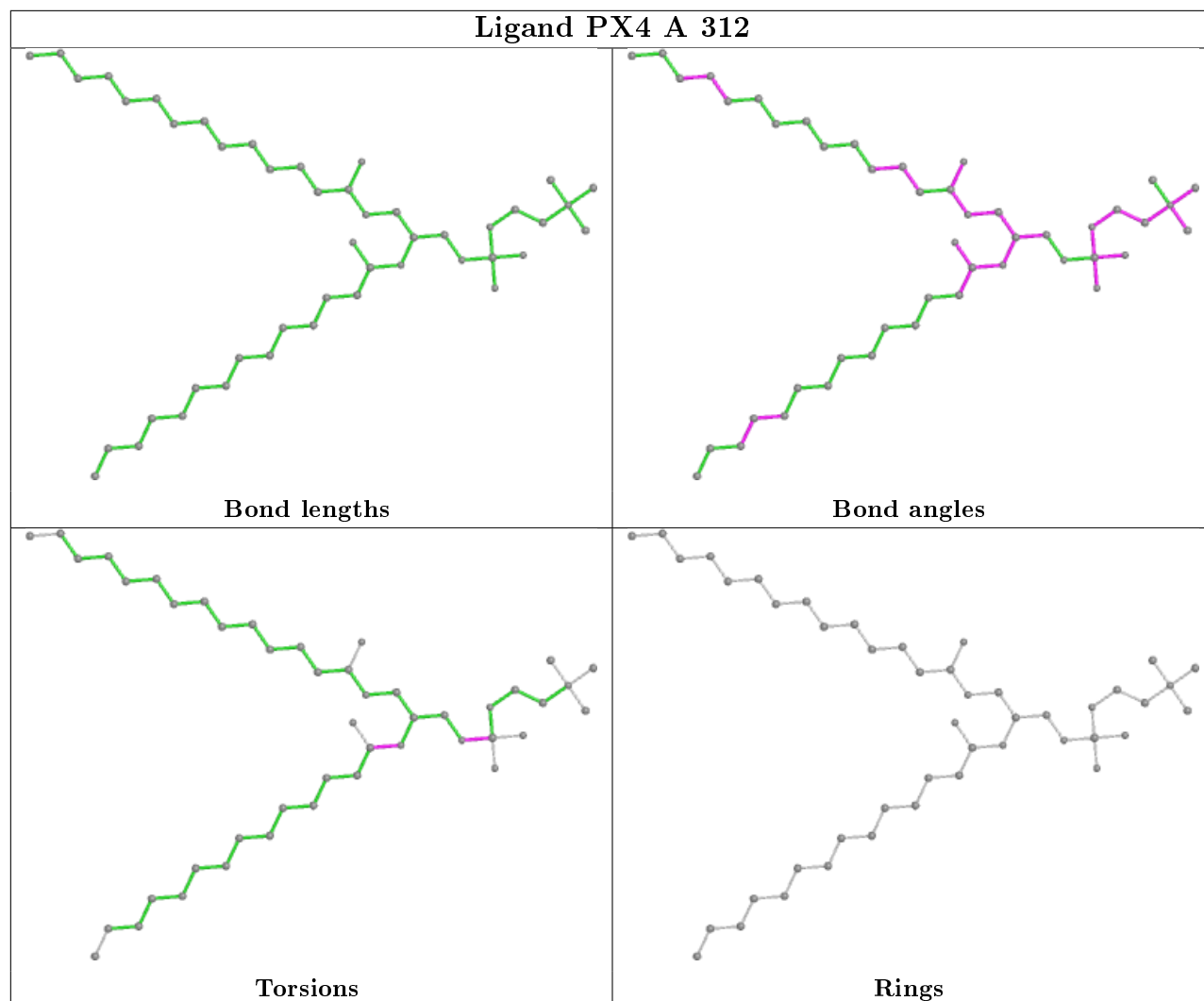




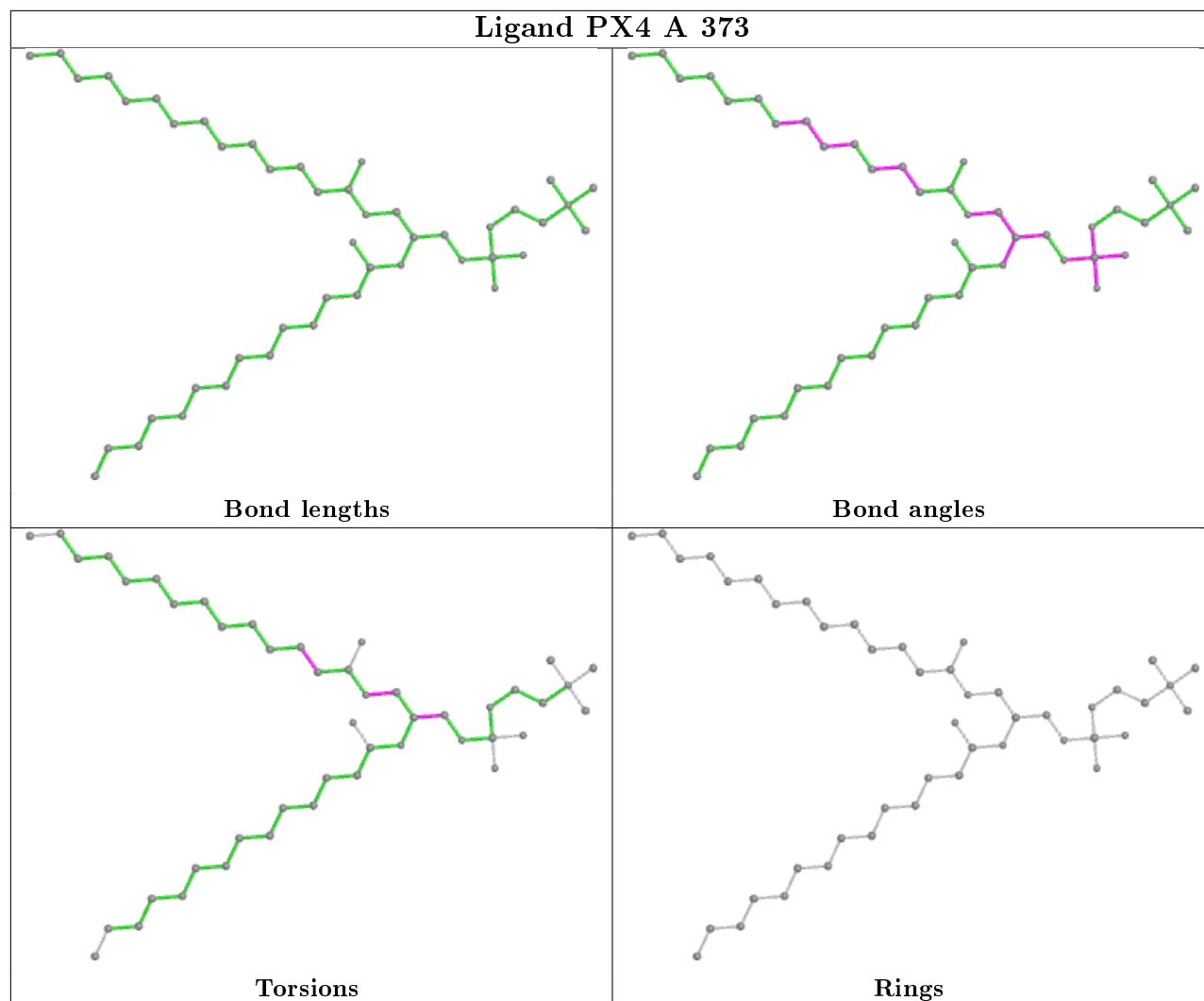




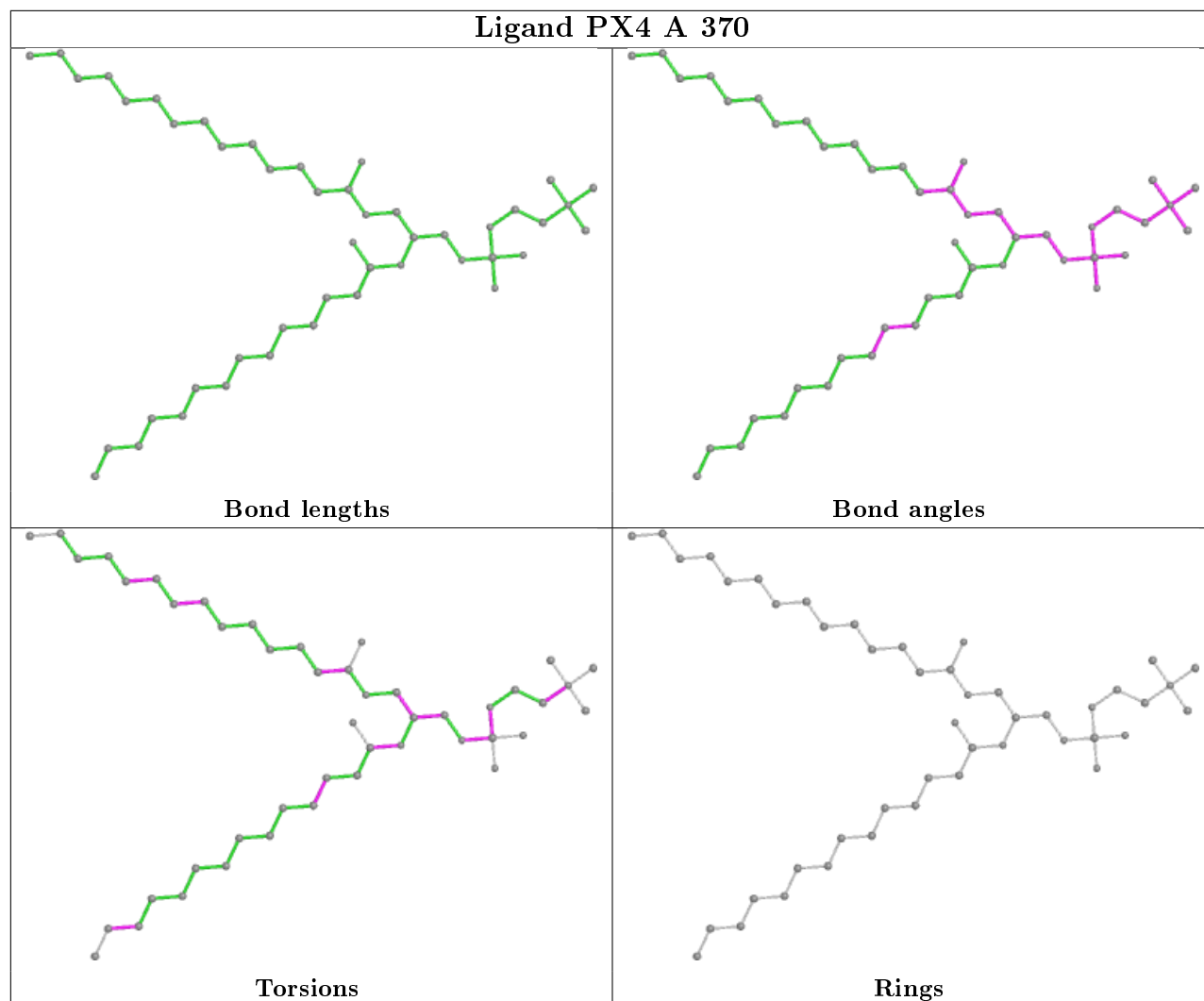
Ligand PX4 A 312



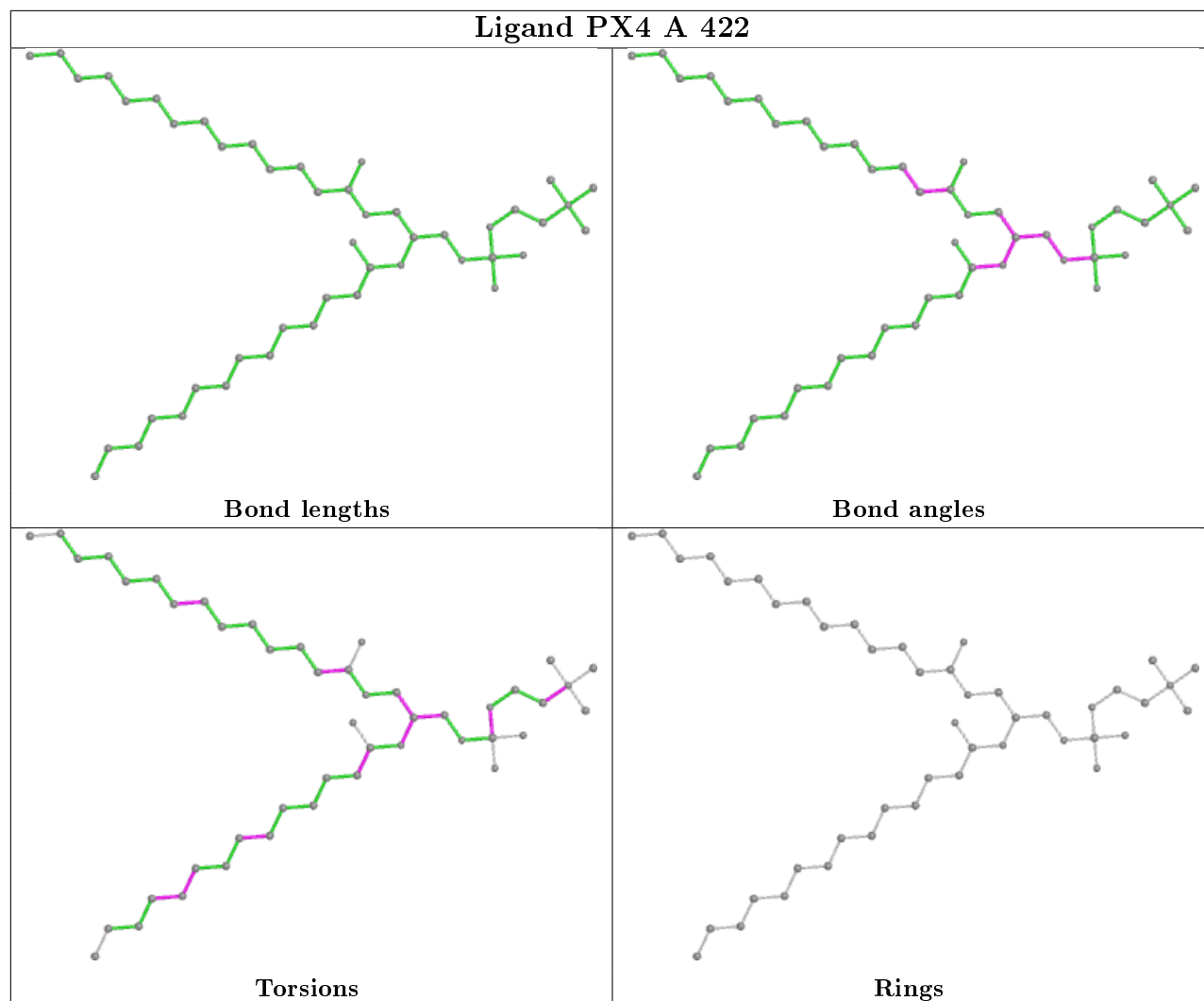
Ligand PX4 A 373



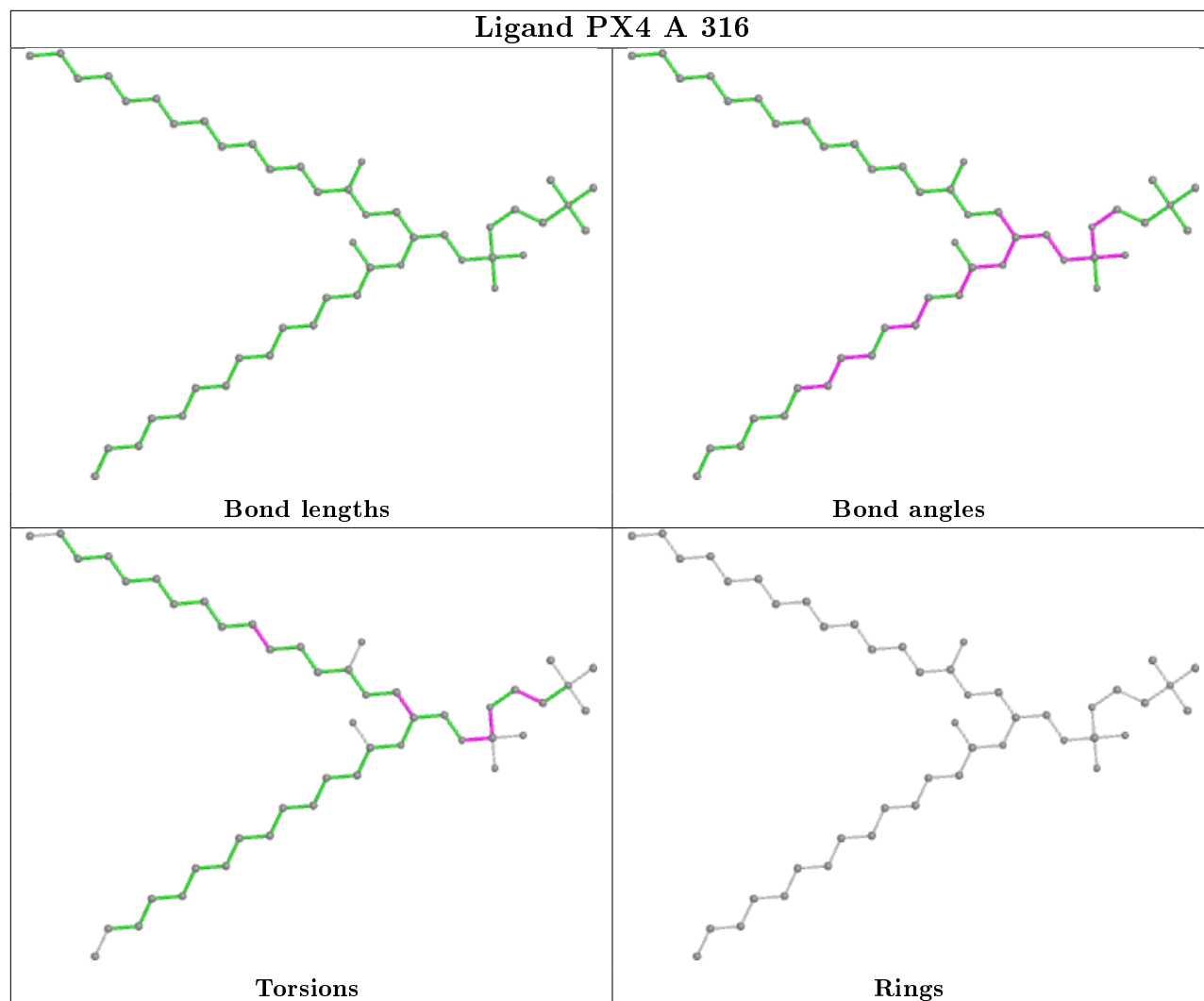
Ligand PX4 A 370

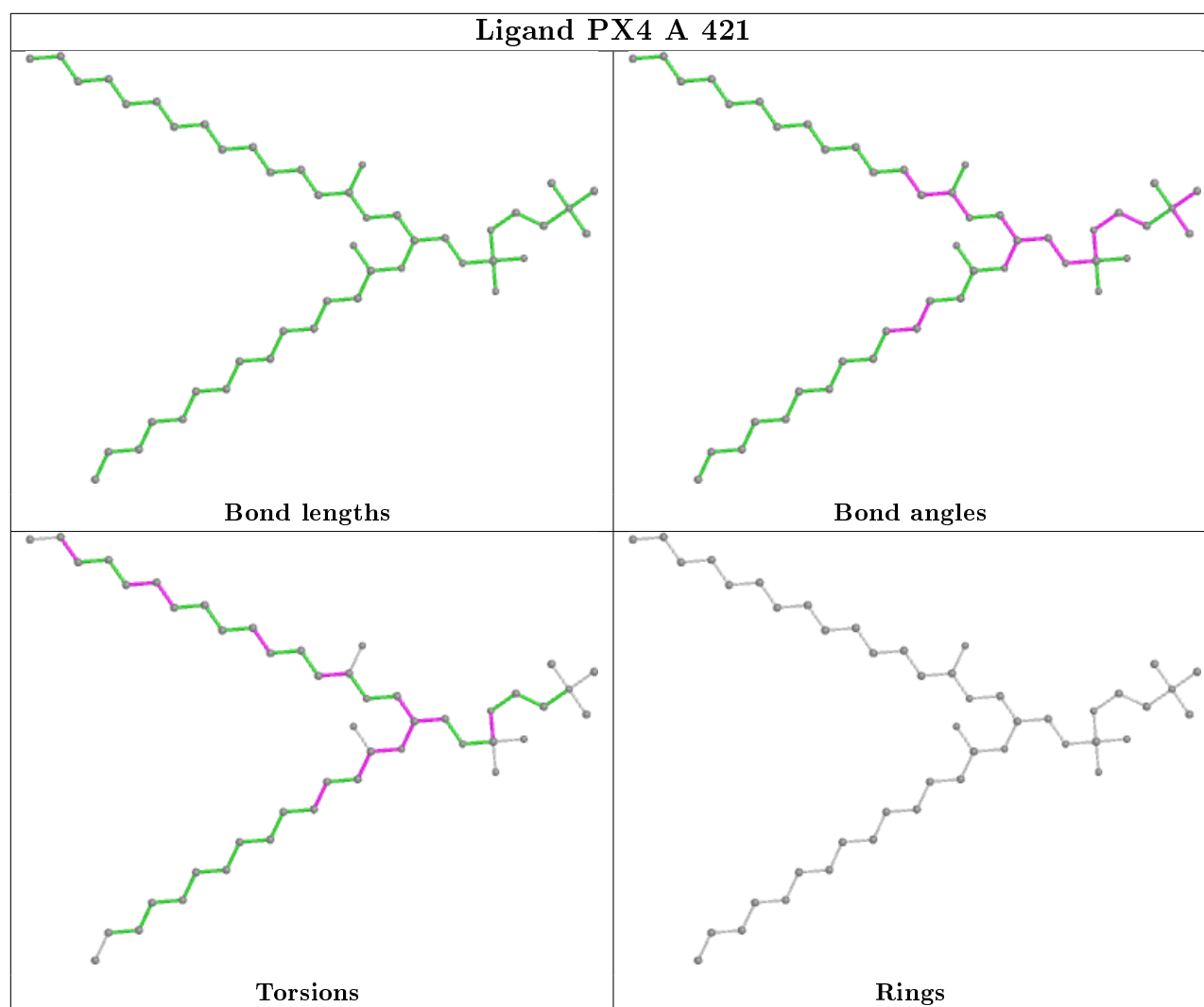


Ligand PX4 A 422

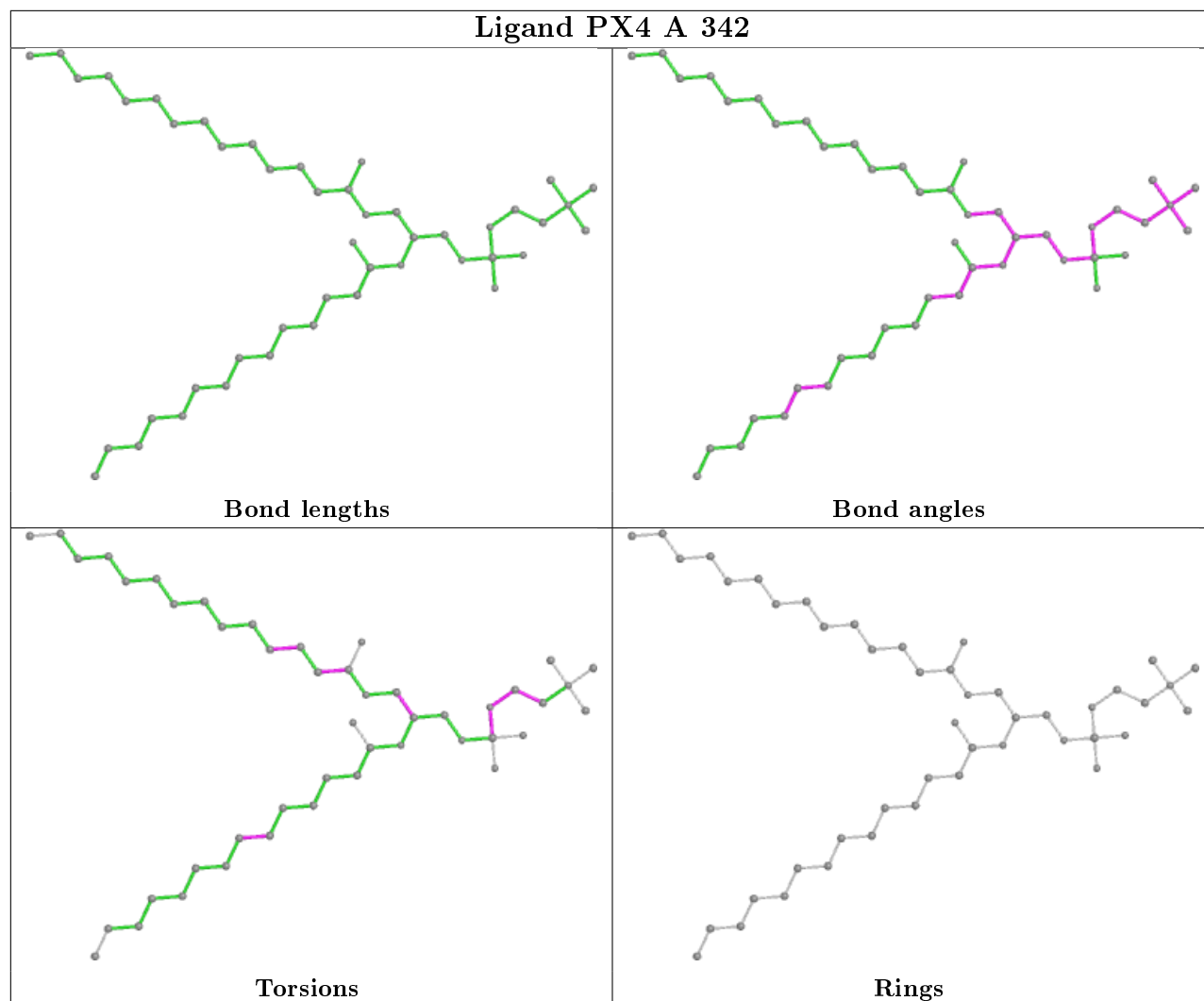


Ligand PX4 A 316

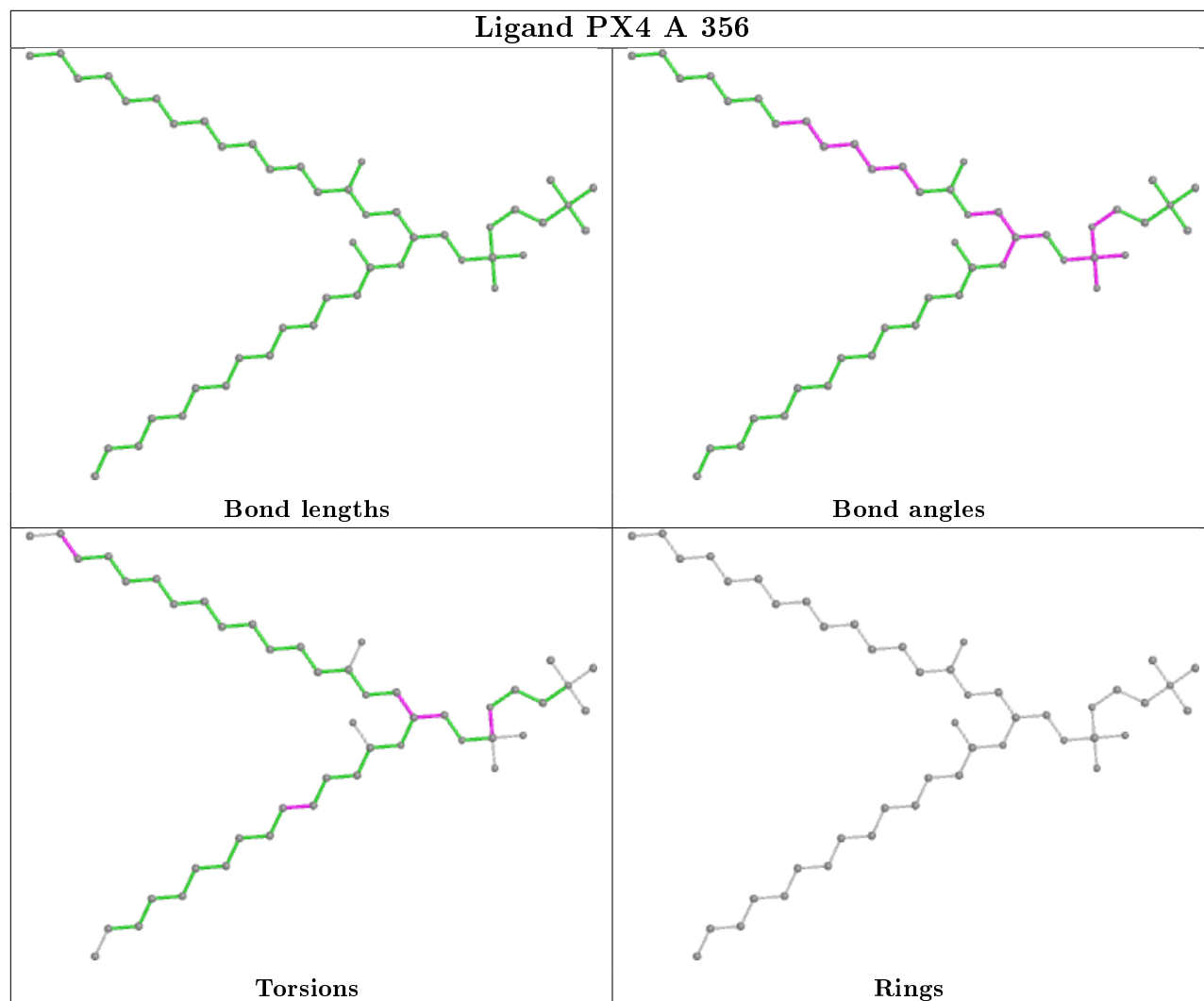




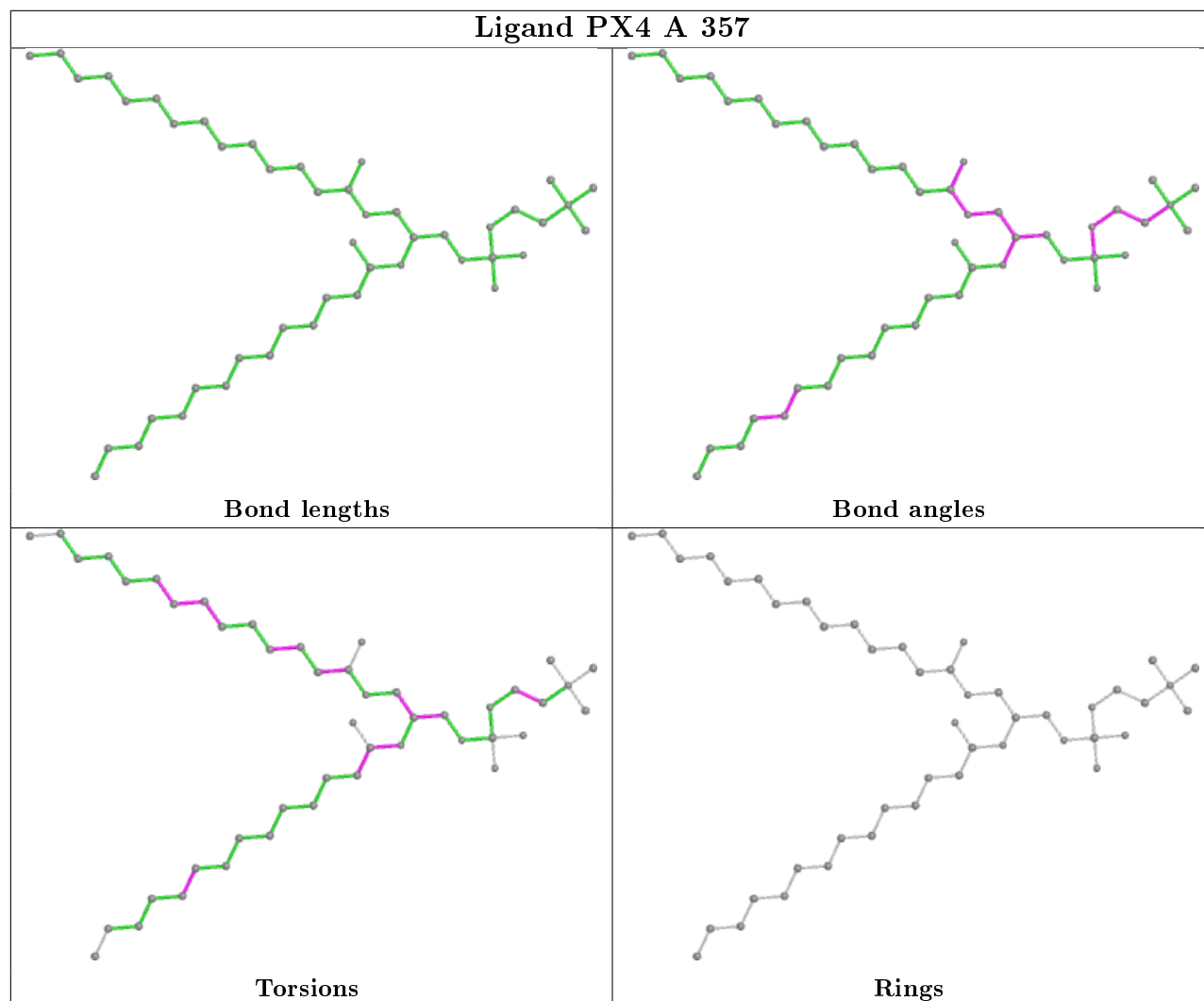
Ligand PX4 A 342



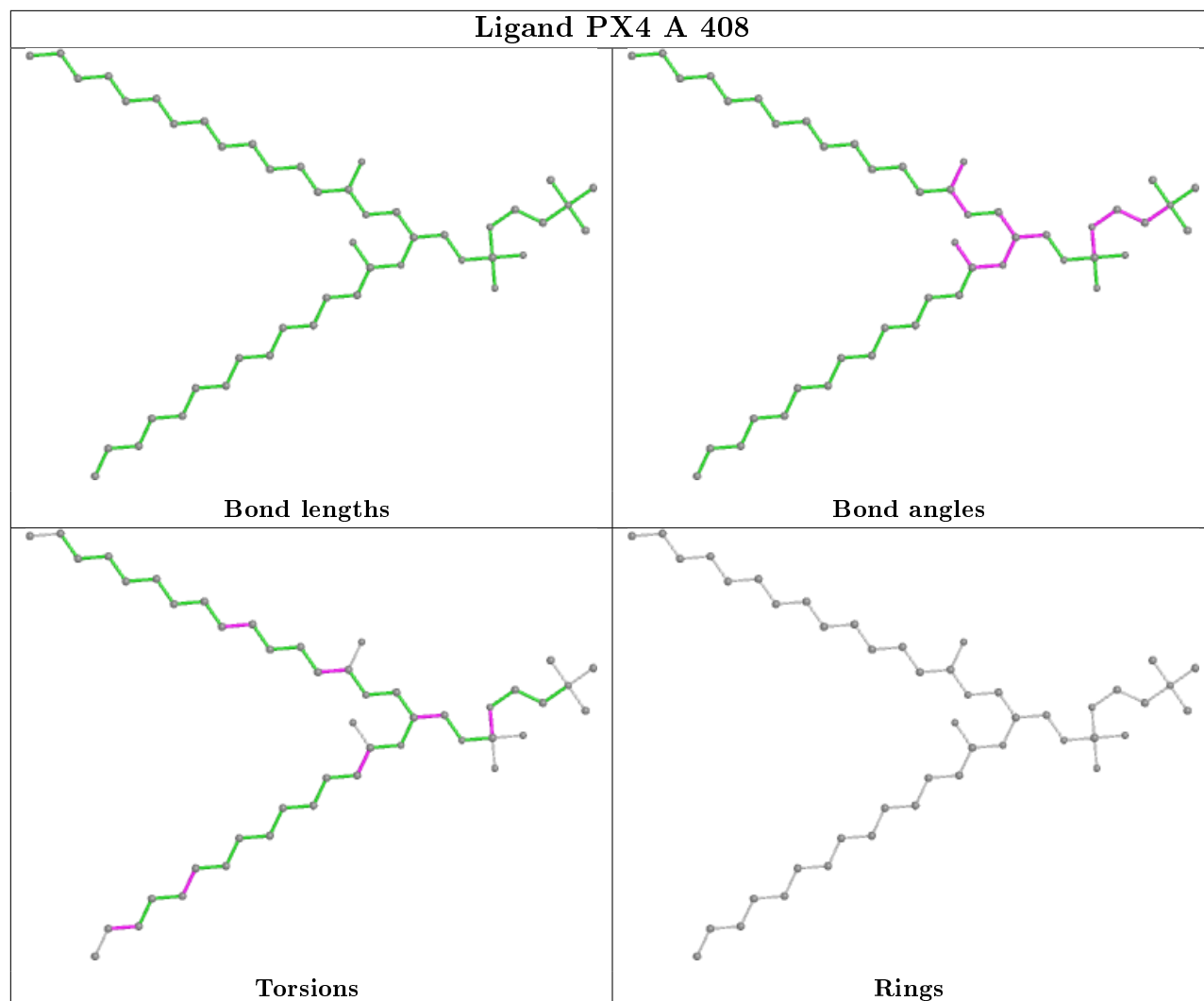
Ligand PX4 A 356



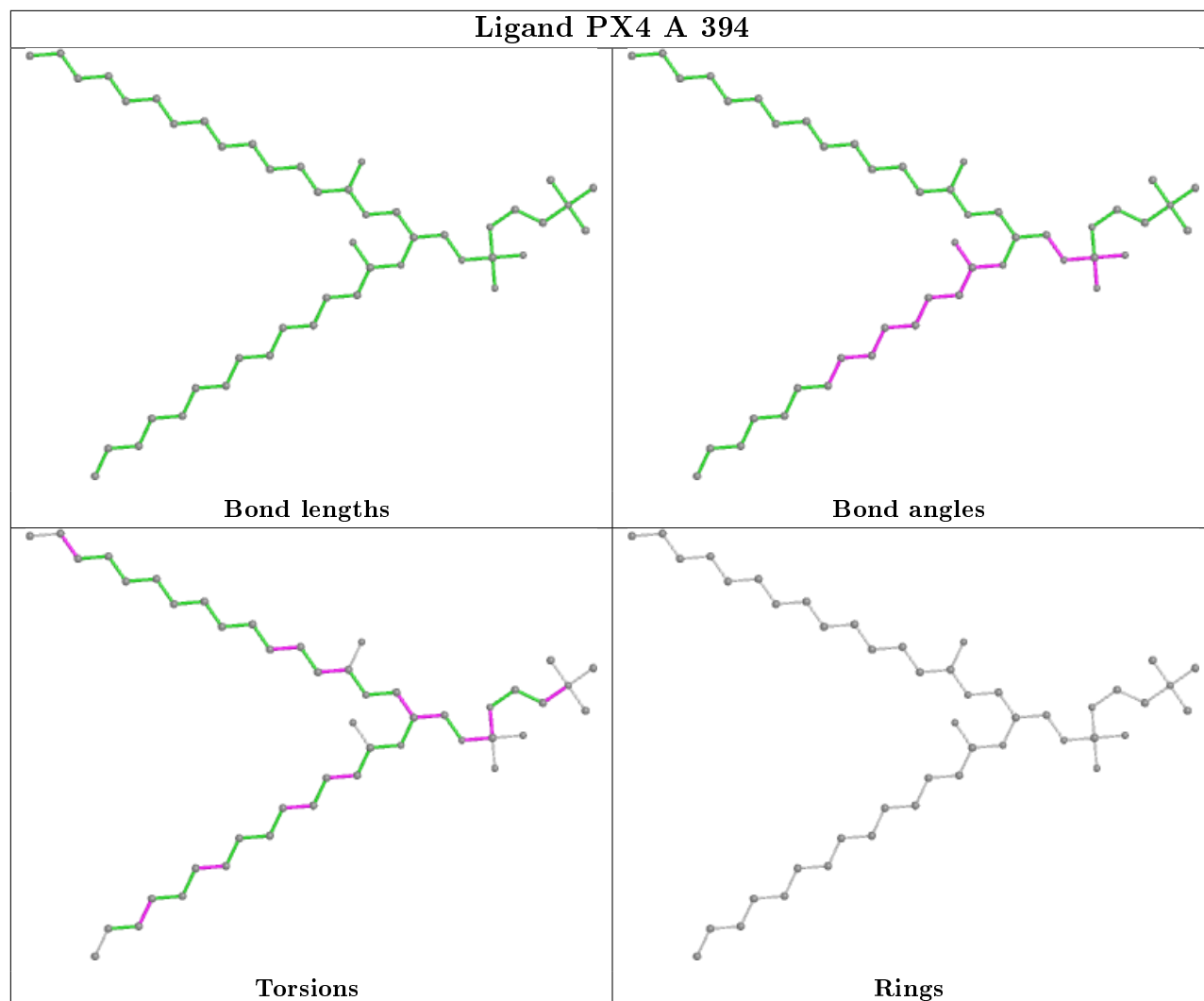
Ligand PX4 A 357



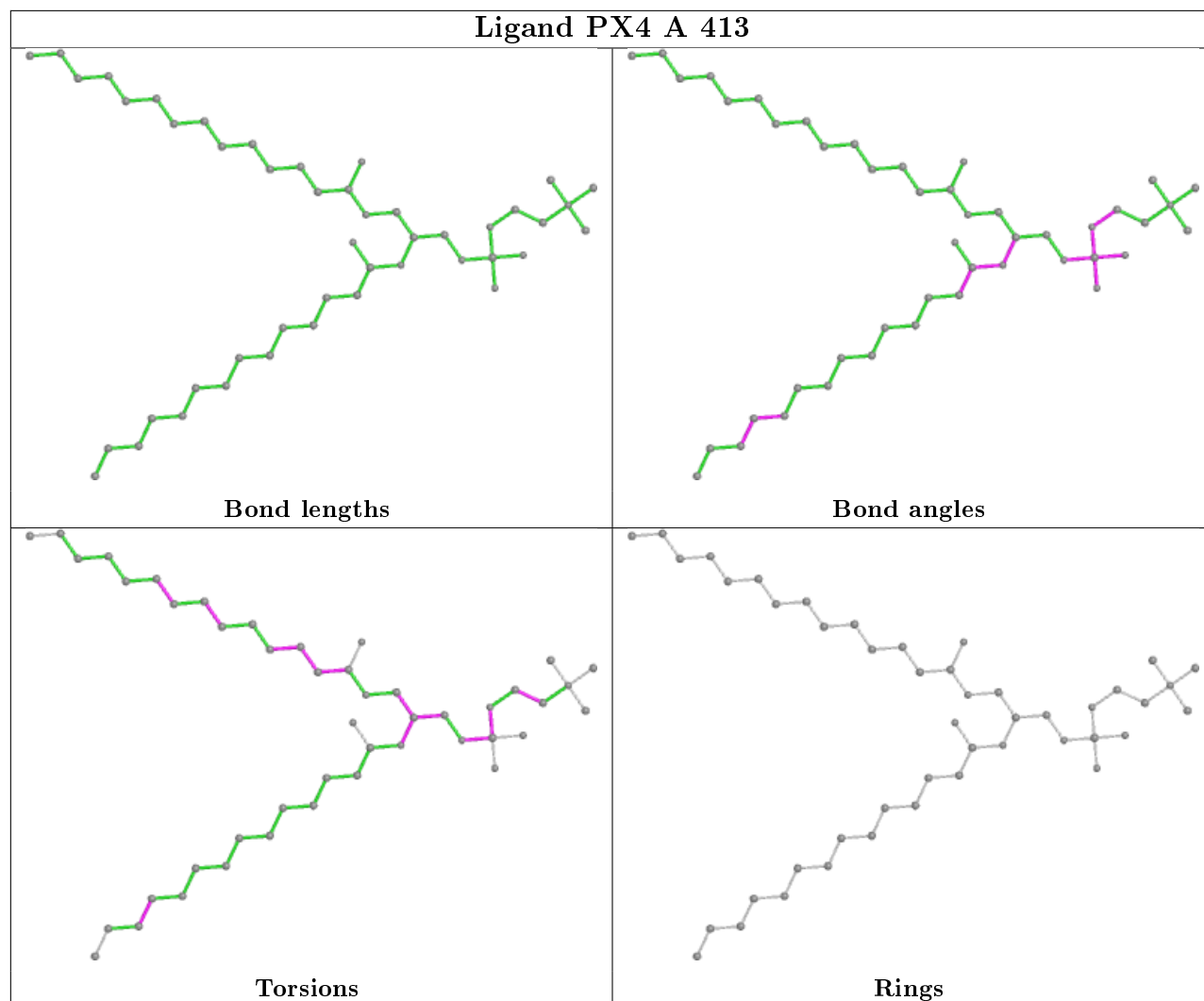
Ligand PX4 A 408



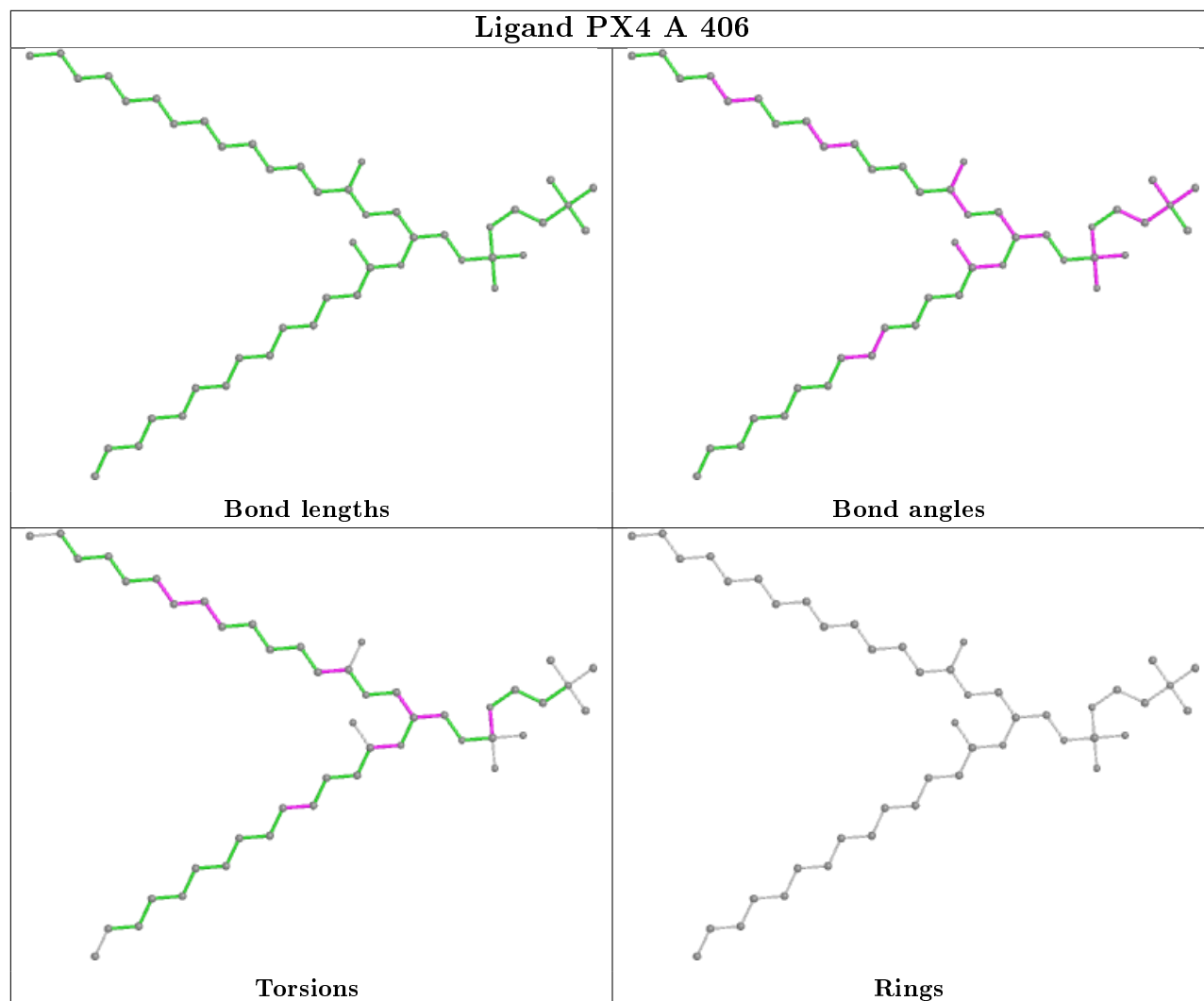
Ligand PX4 A 394



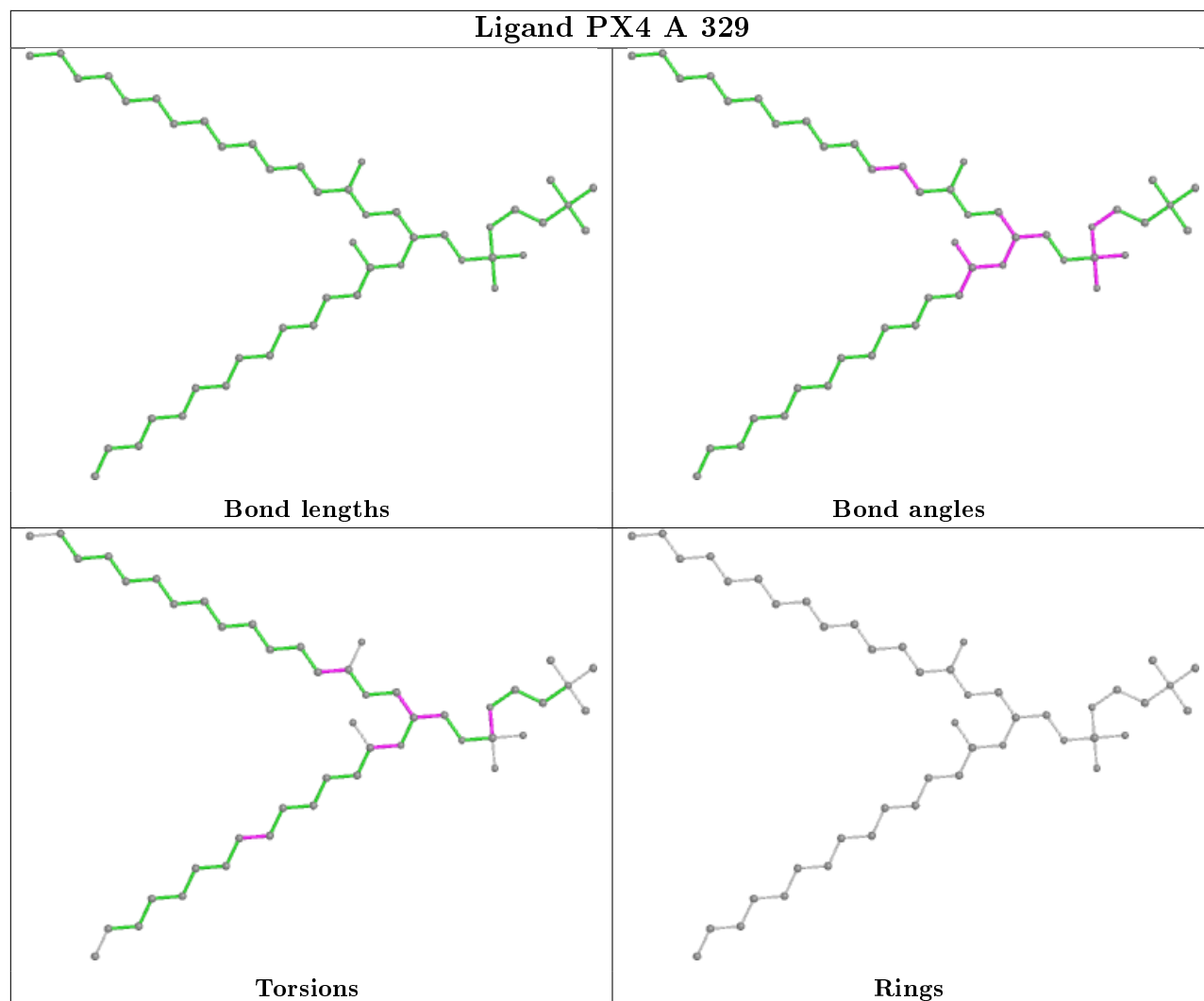
Ligand PX4 A 413

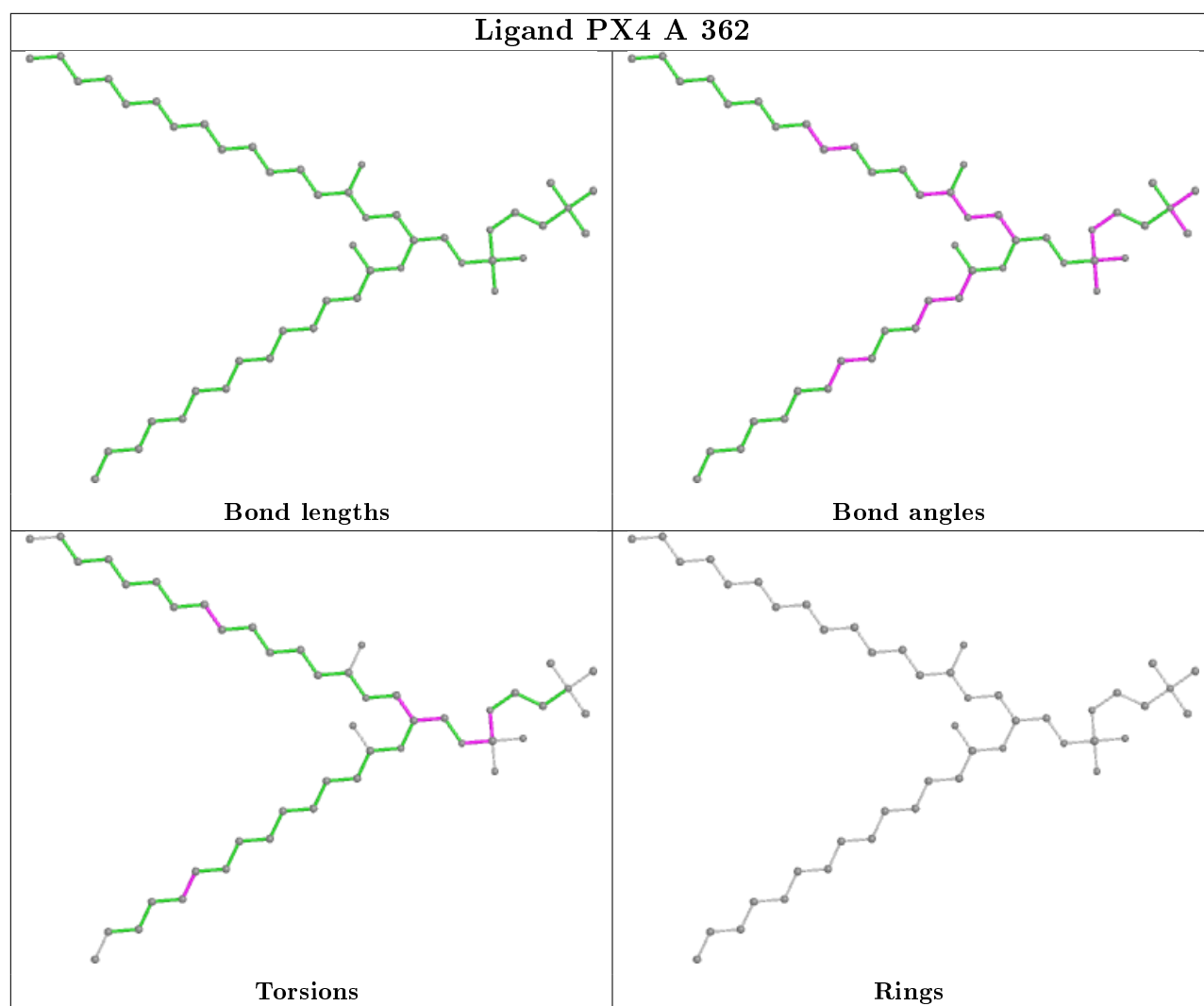


Ligand PX4 A 406

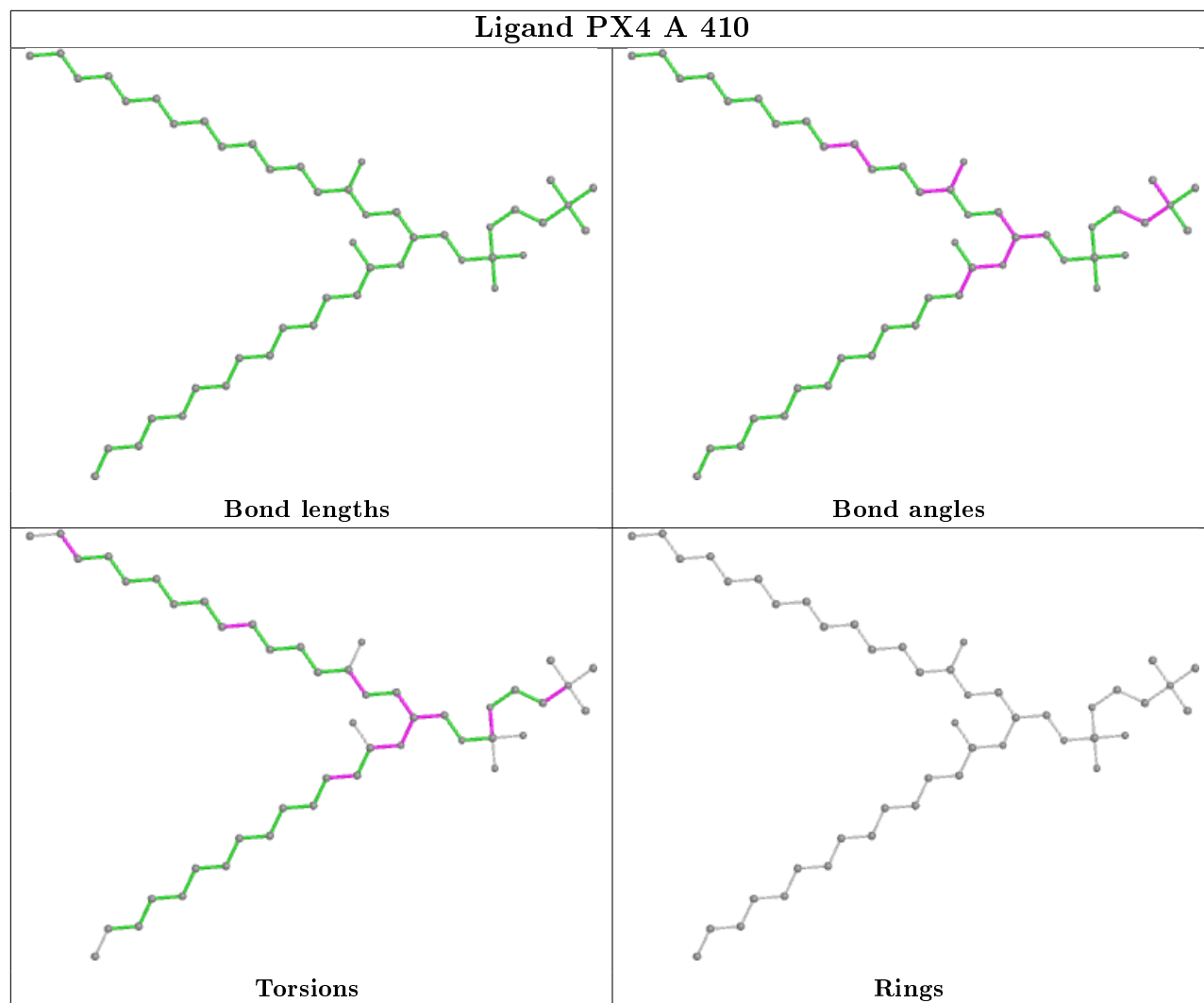


Ligand PX4 A 329

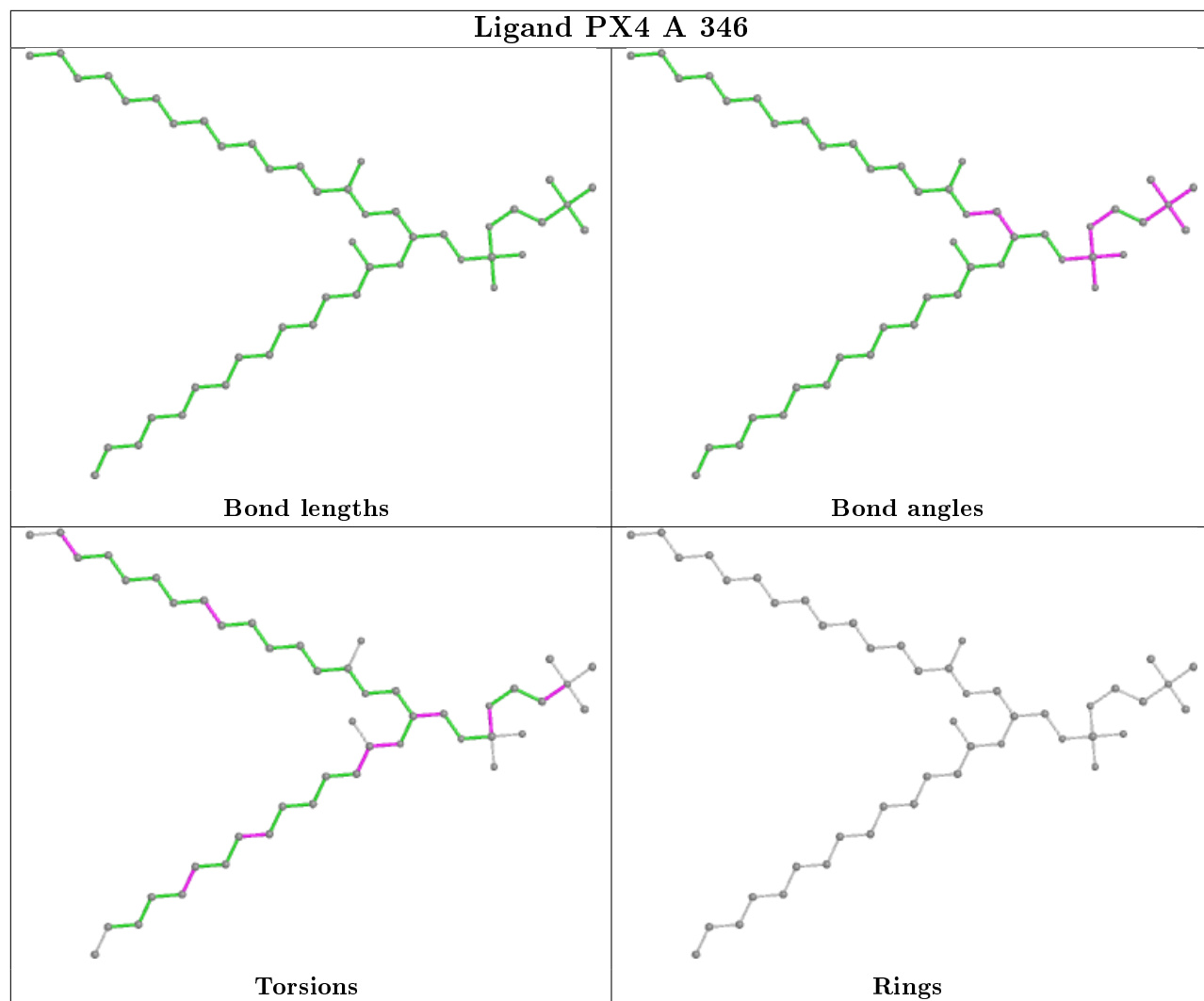


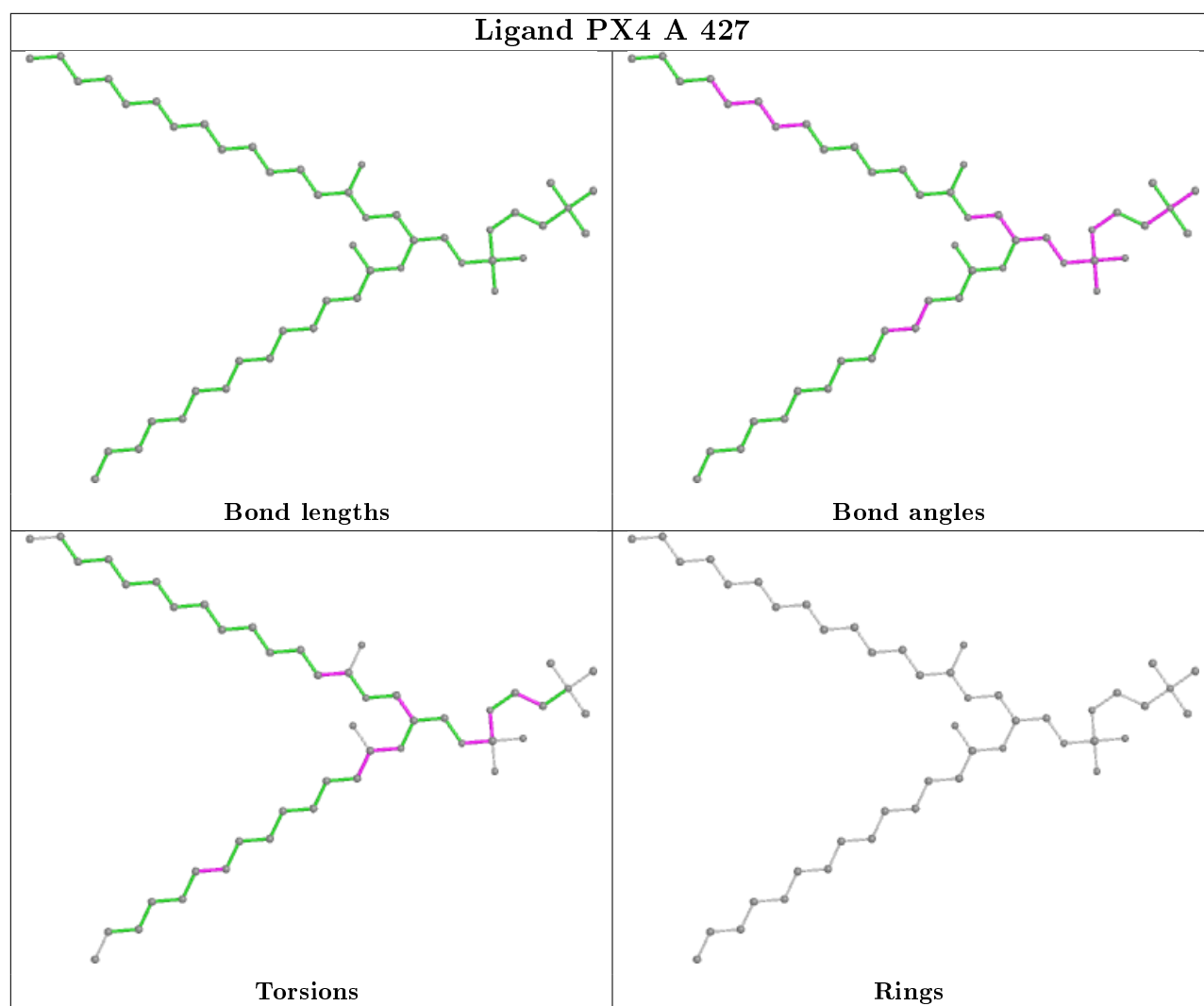


Ligand PX4 A 410

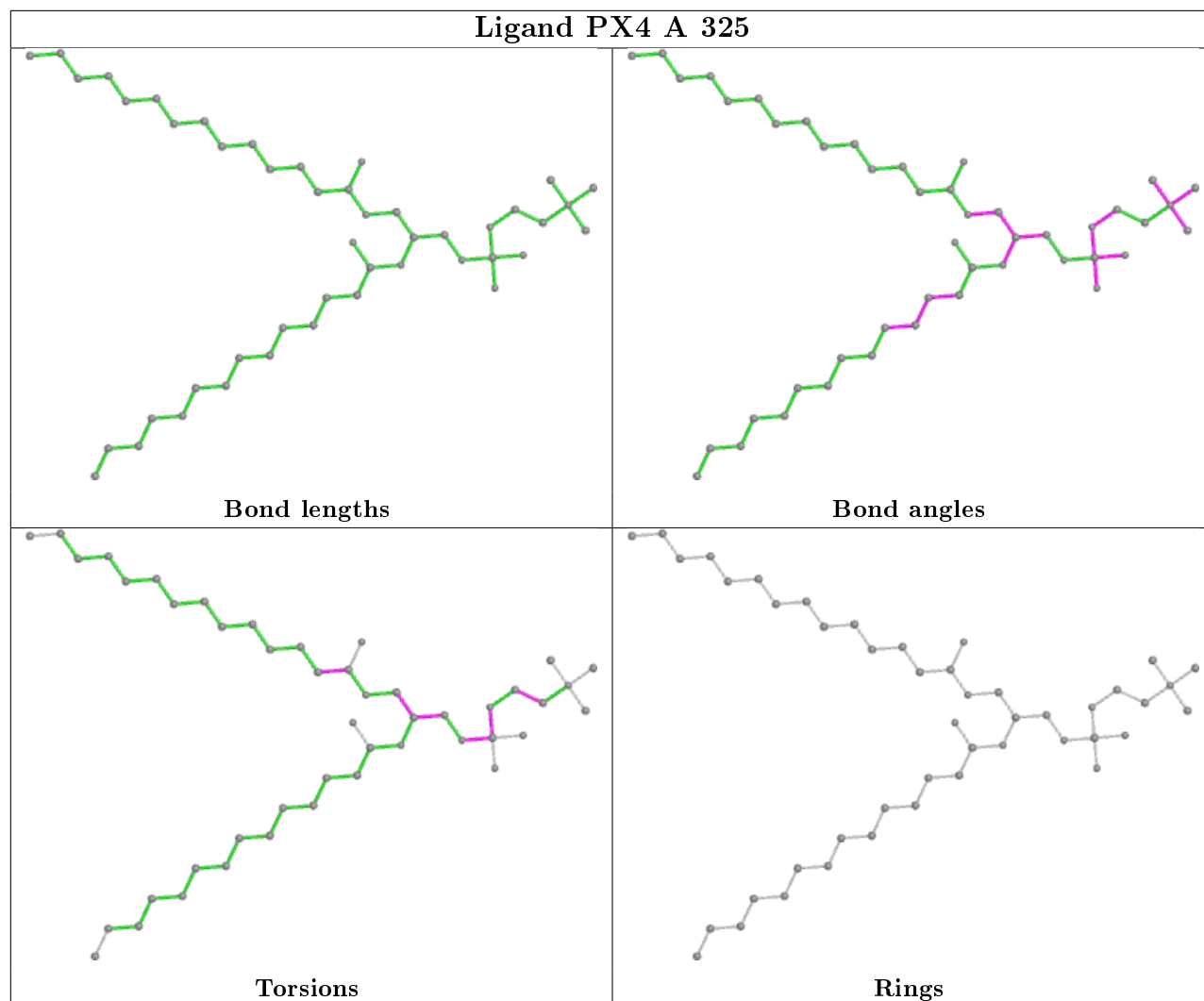


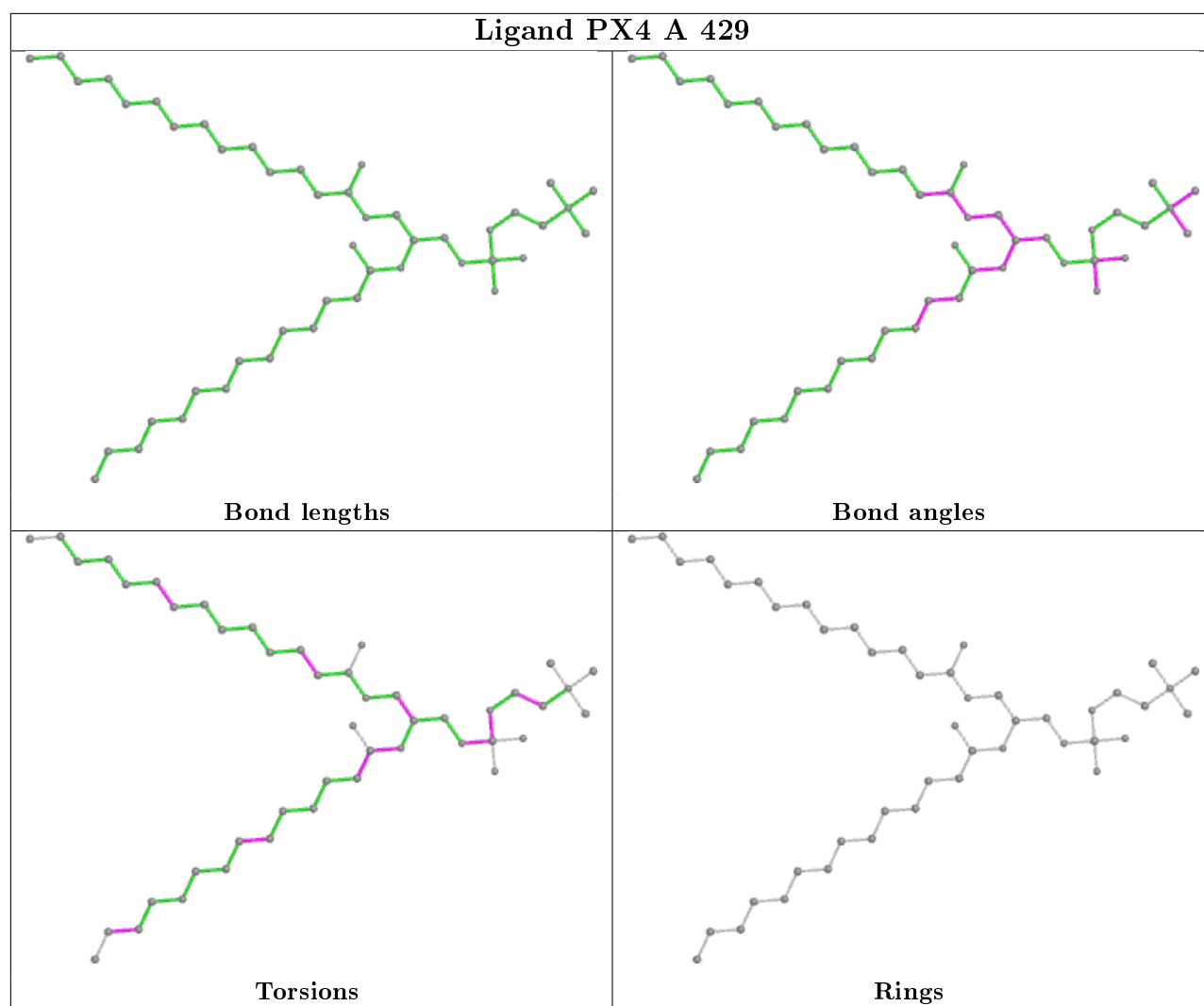
Ligand PX4 A 346



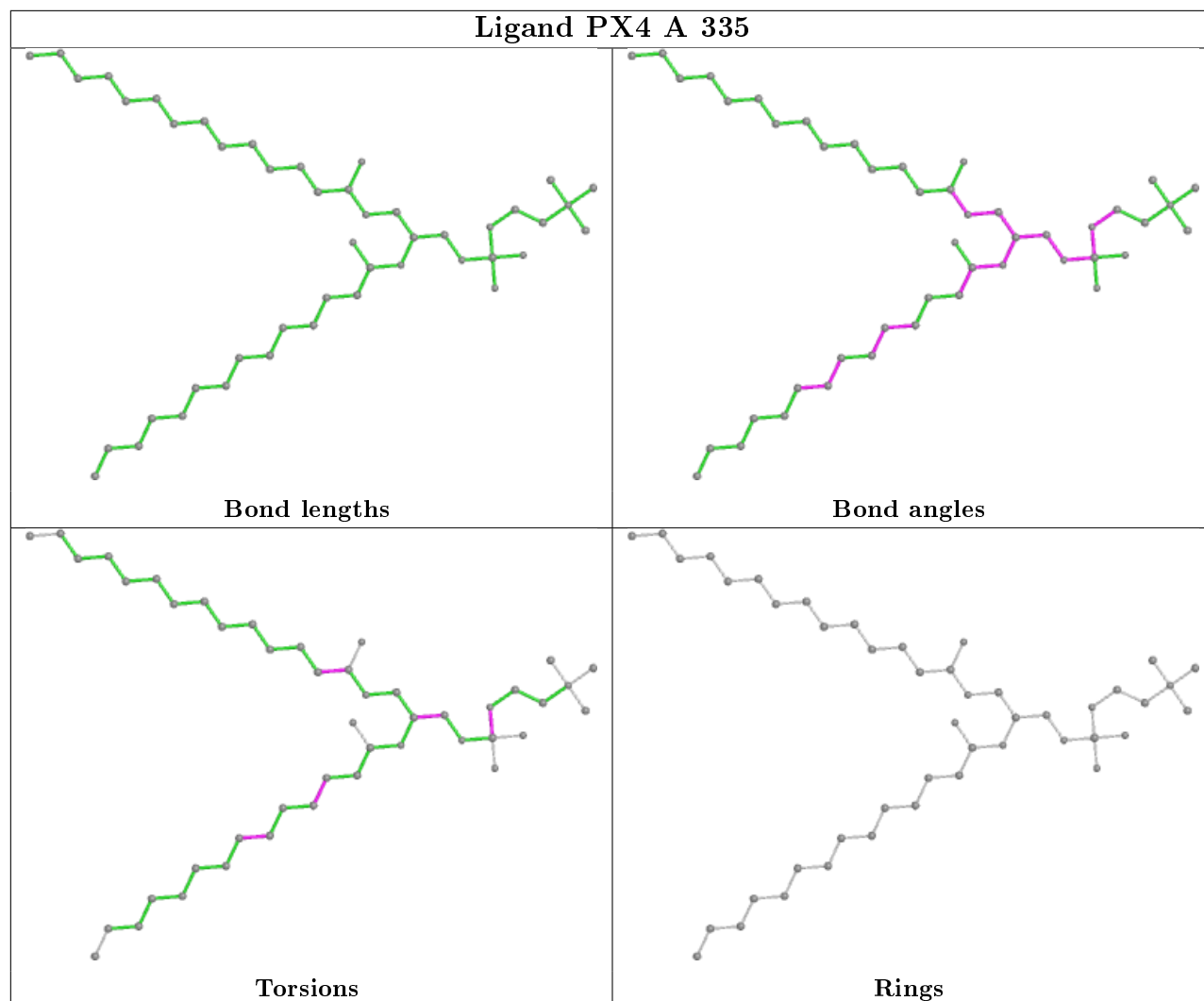


Ligand PX4 A 325

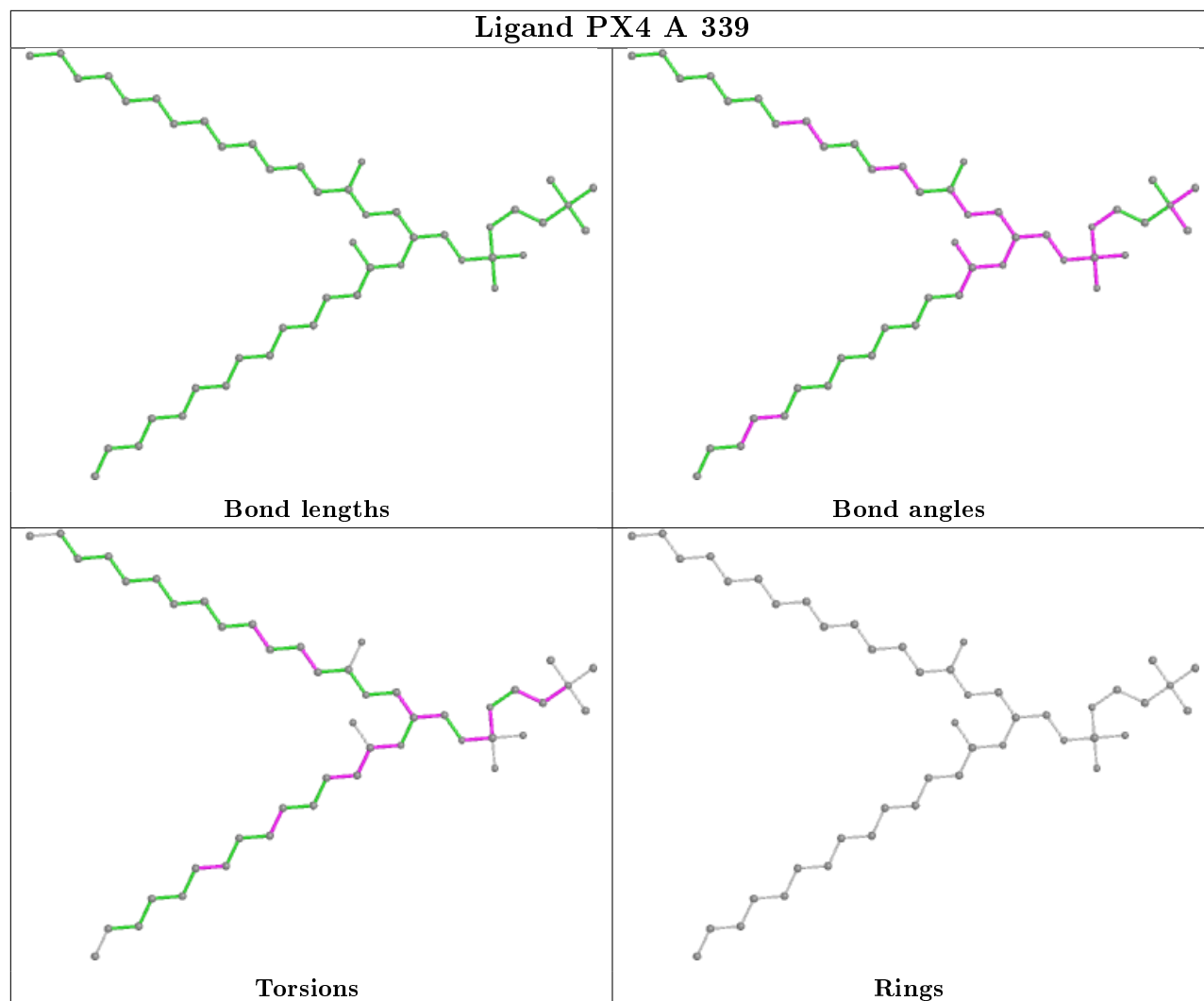




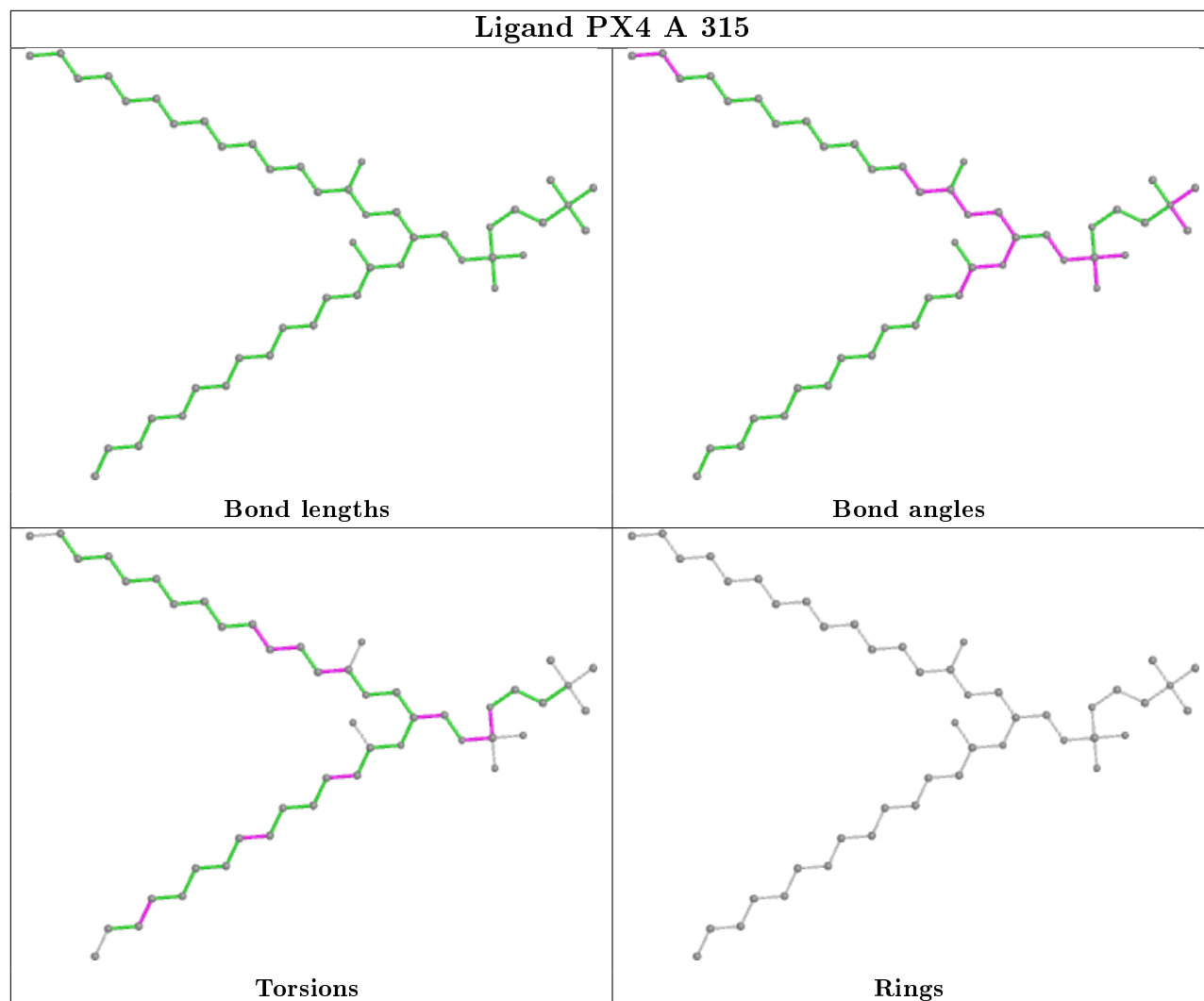
Ligand PX4 A 335



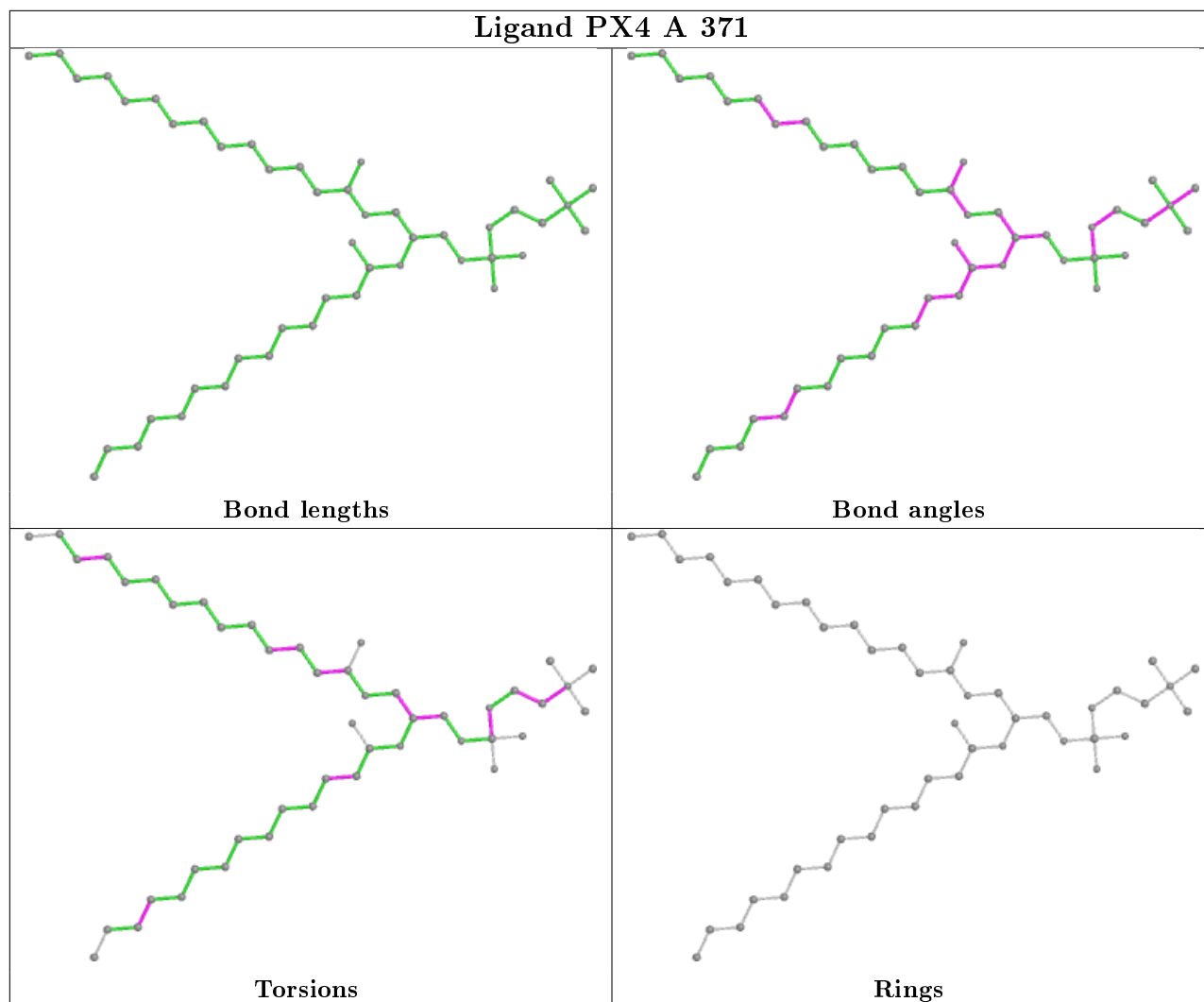
Ligand PX4 A 339



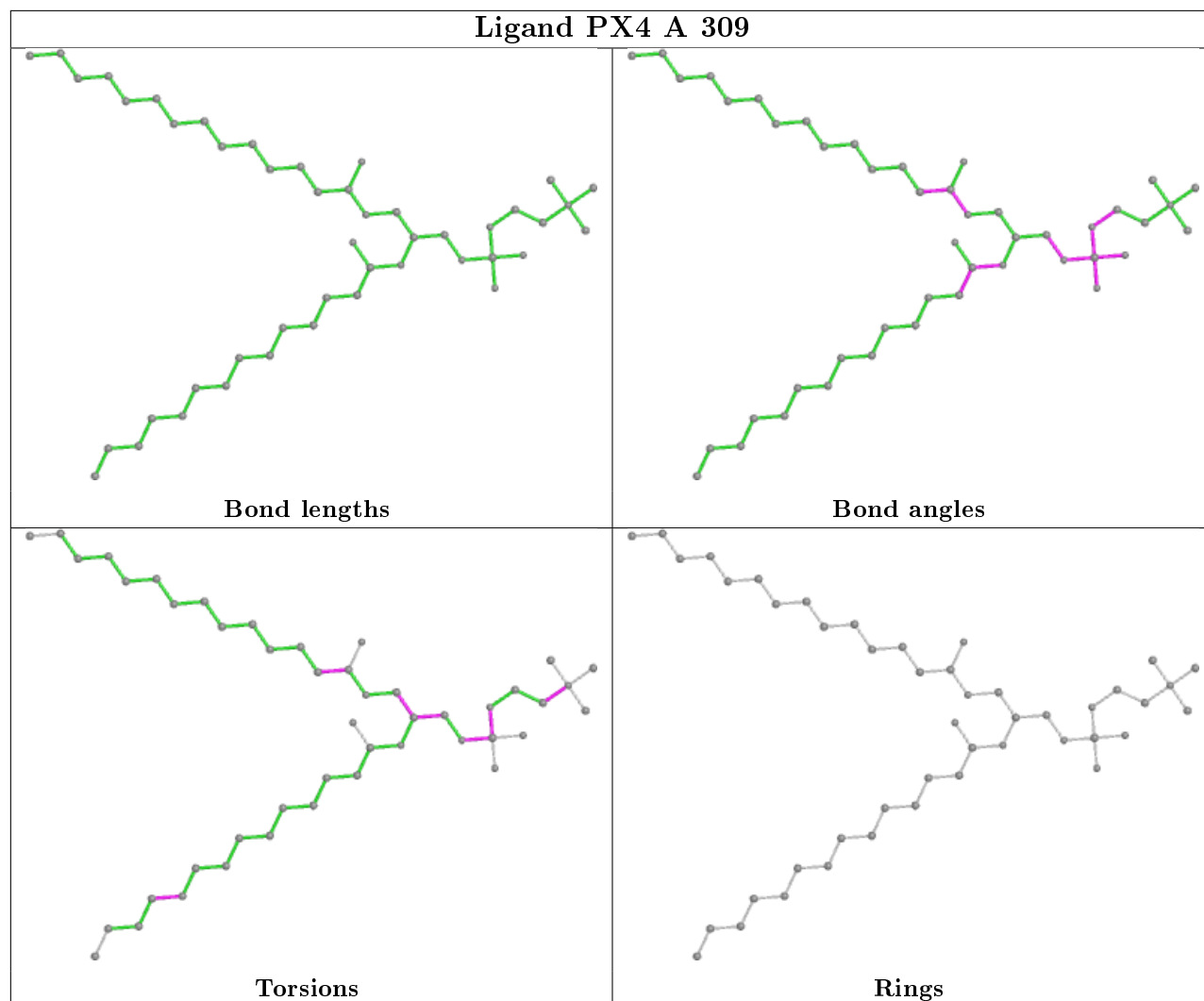
Ligand PX4 A 315



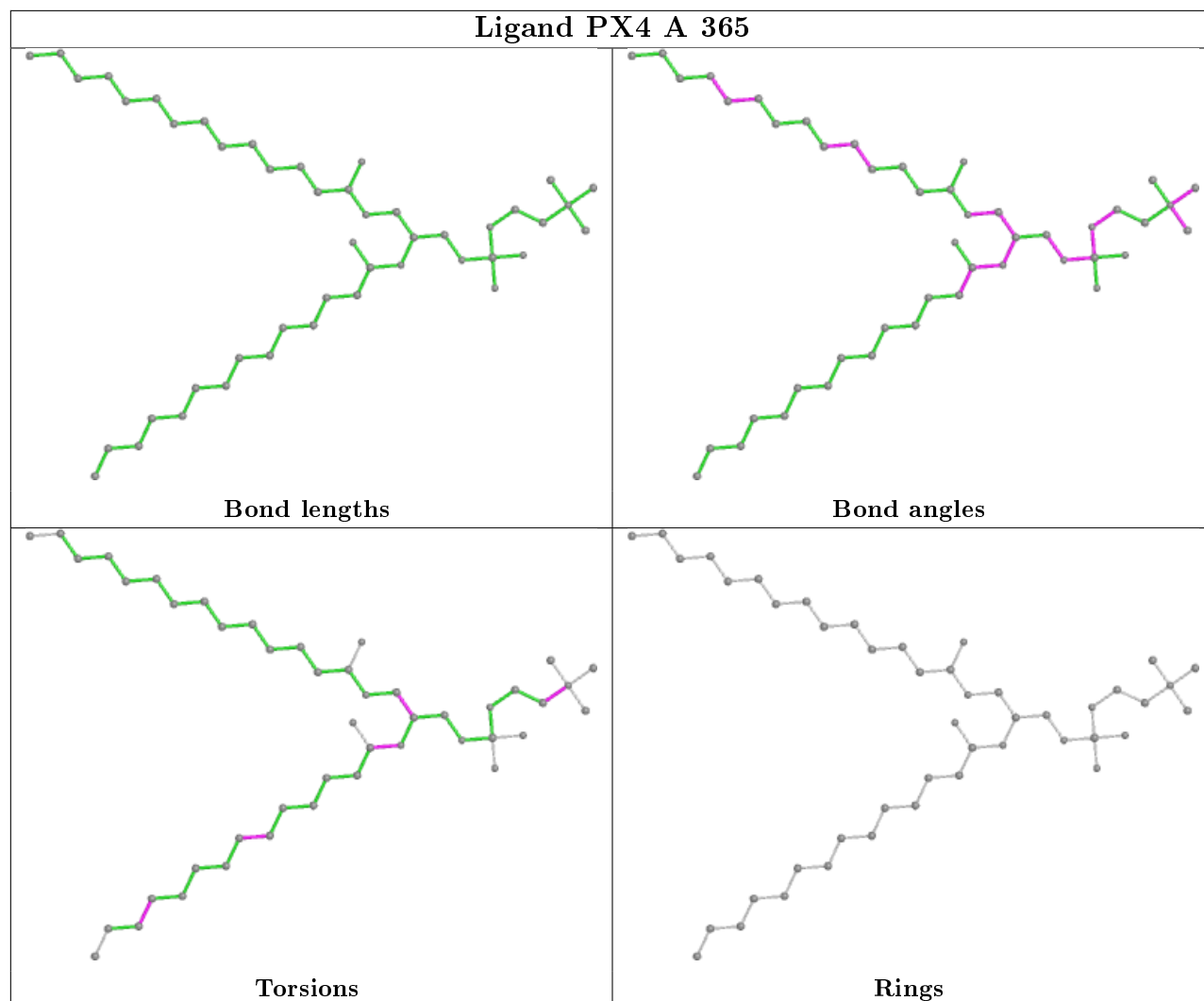
Ligand PX4 A 371



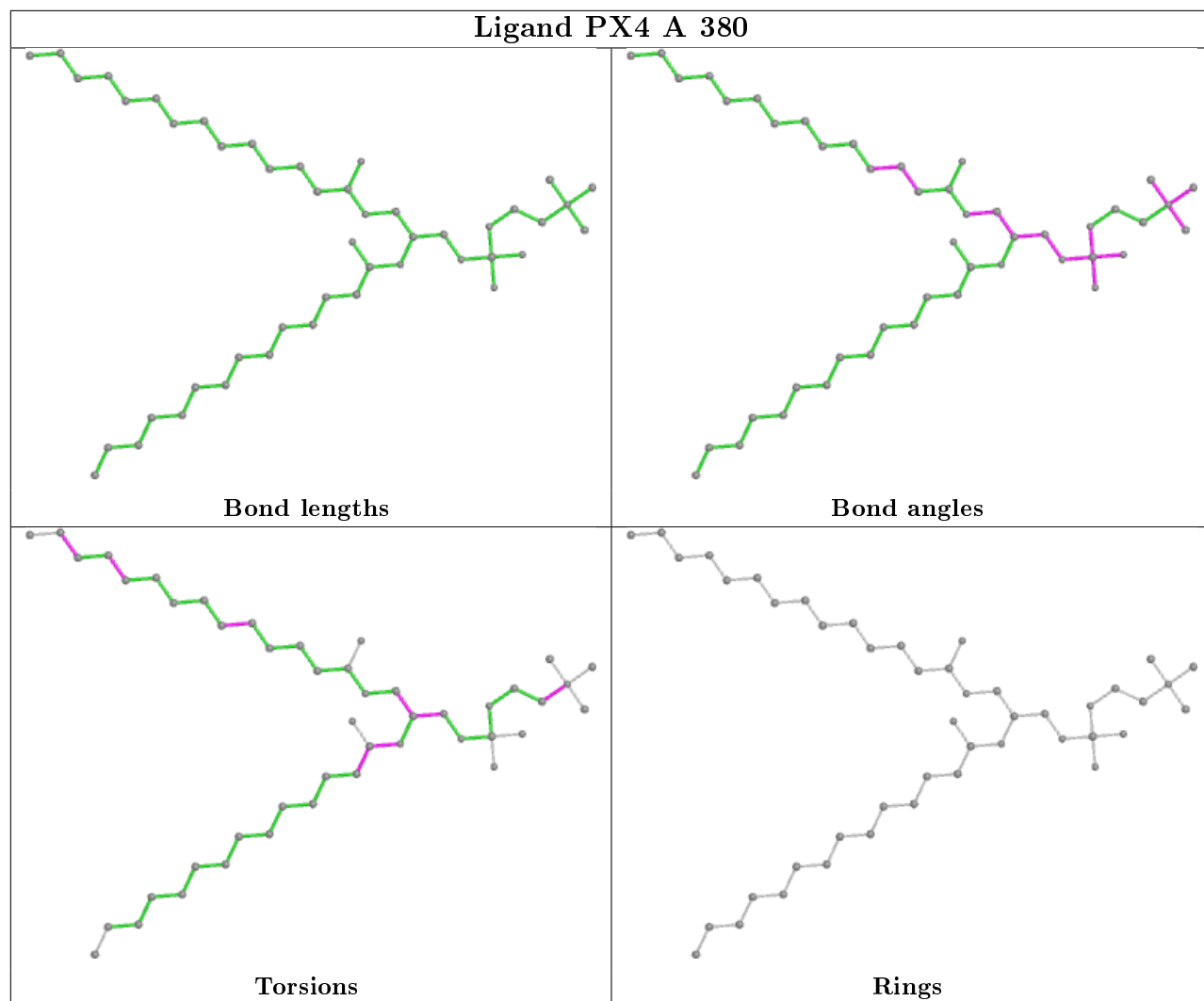
Ligand PX4 A 309



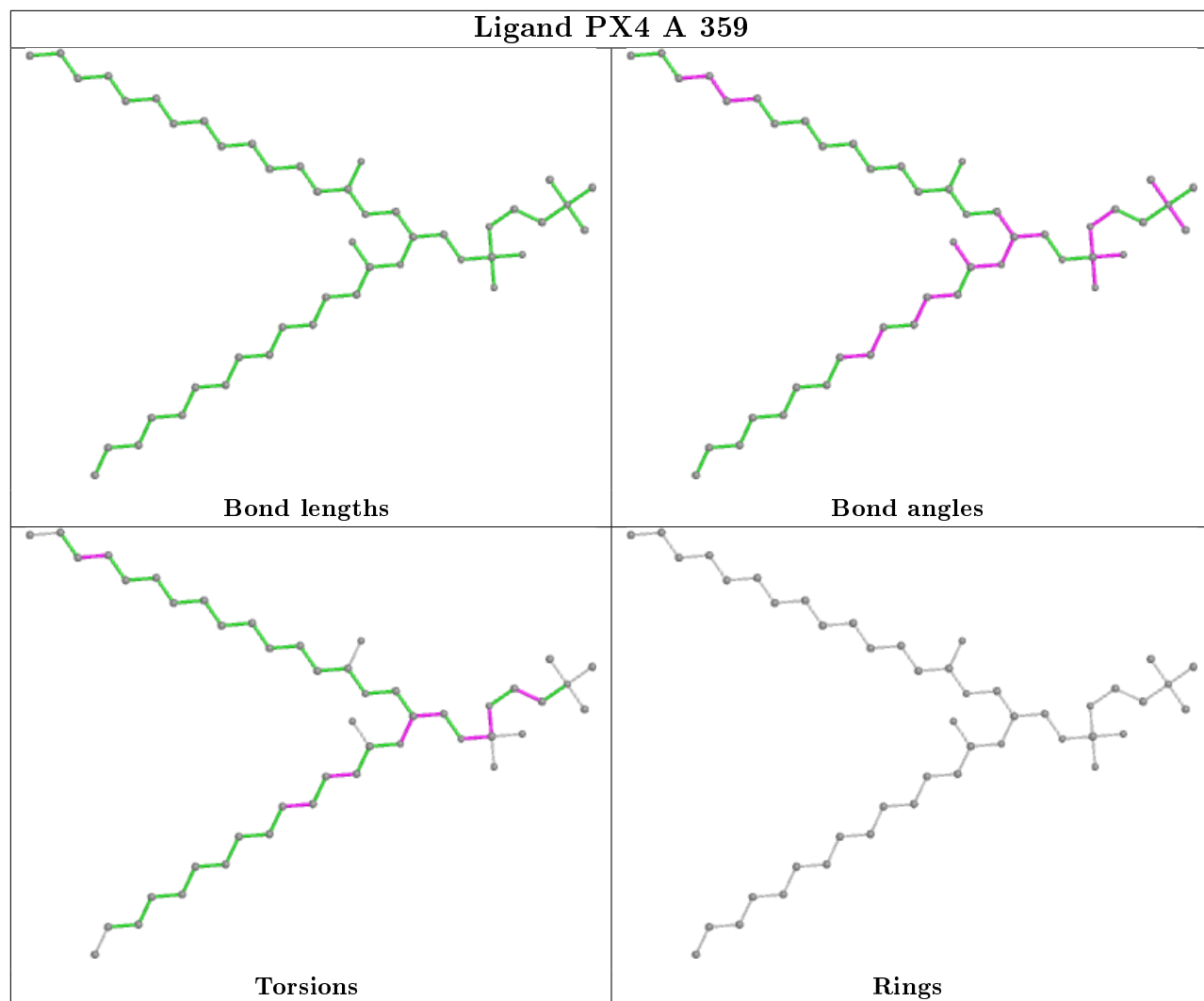
Ligand PX4 A 365



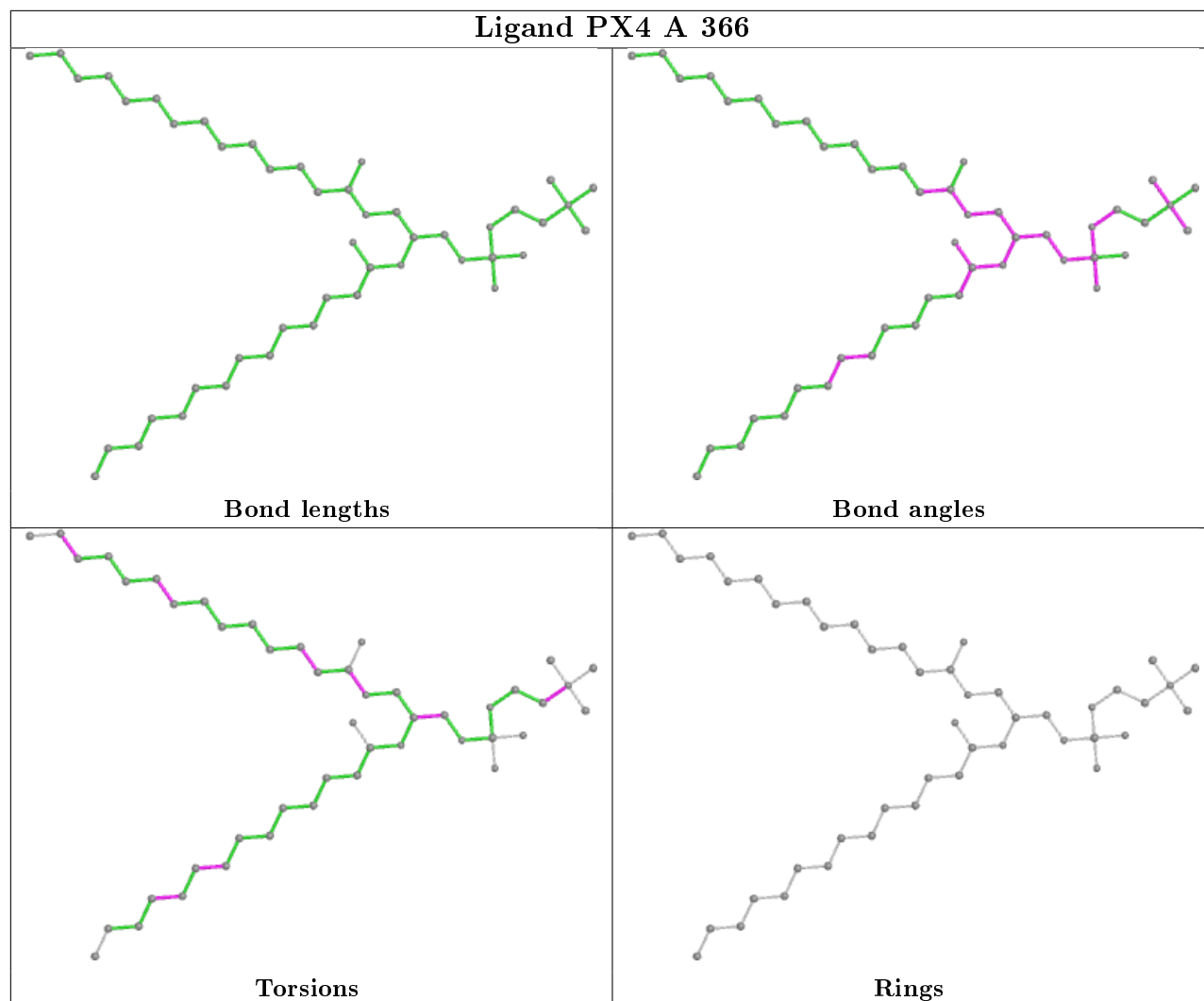
Ligand PX4 A 380



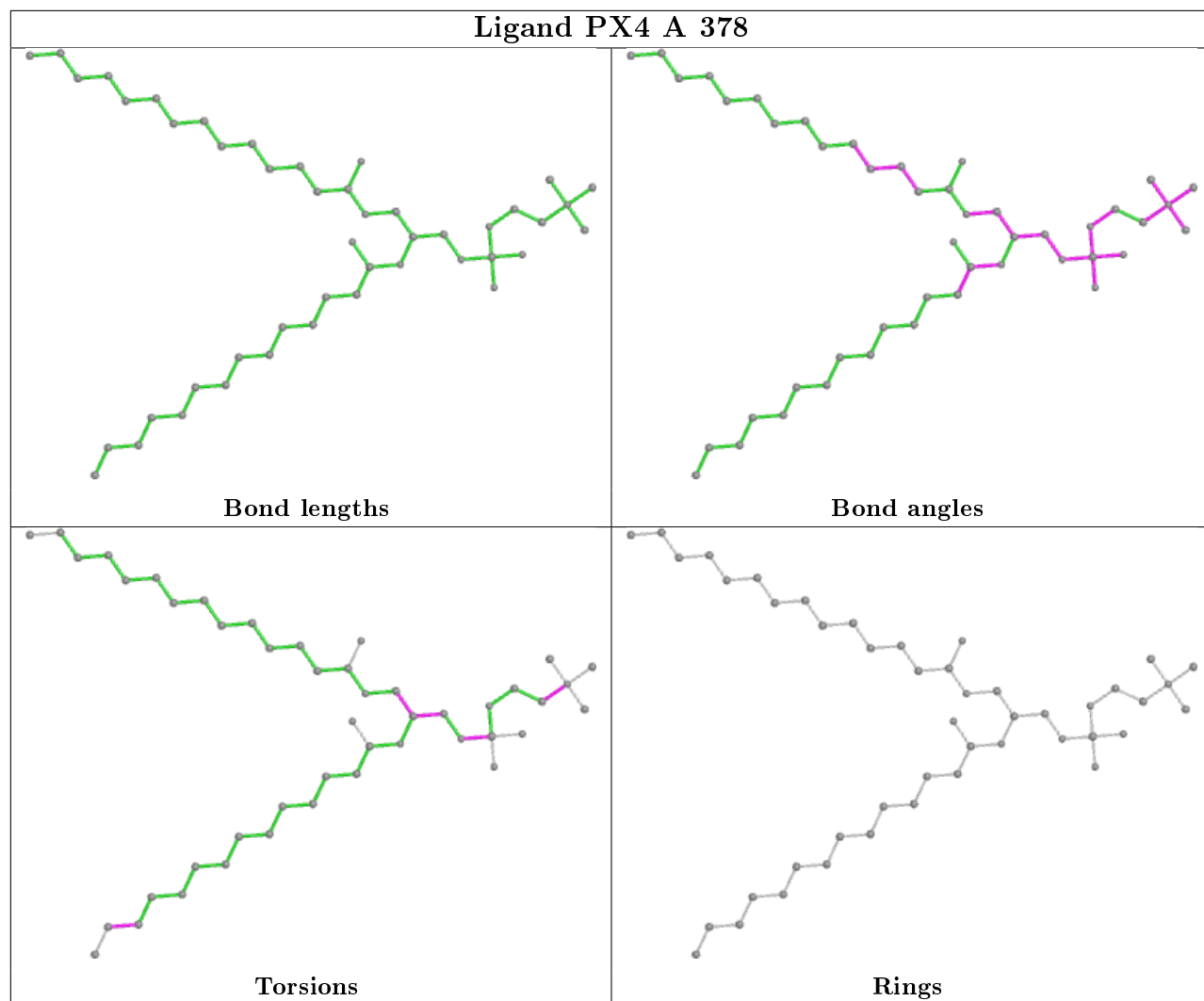
Ligand PX4 A 359



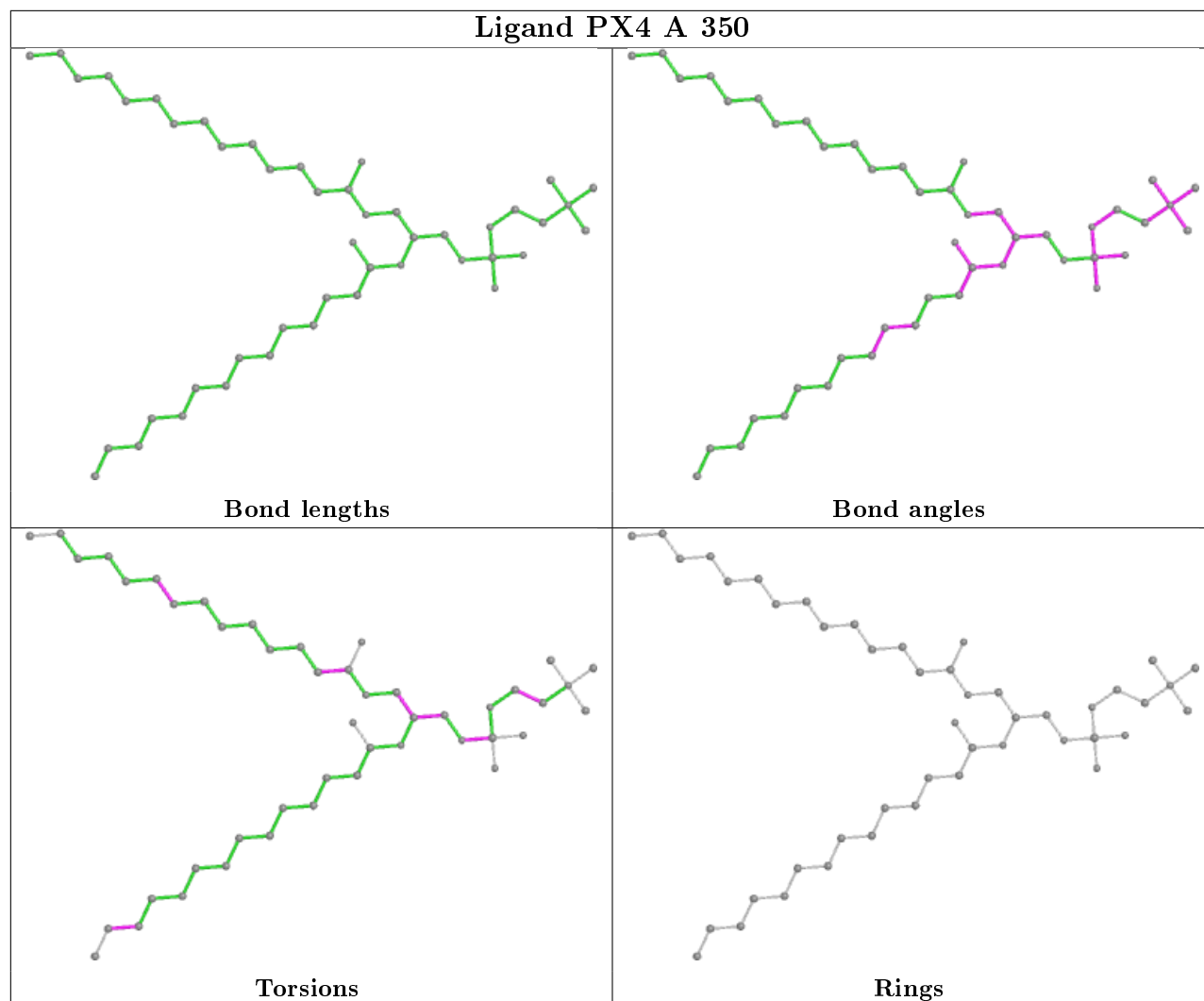
Ligand PX4 A 366



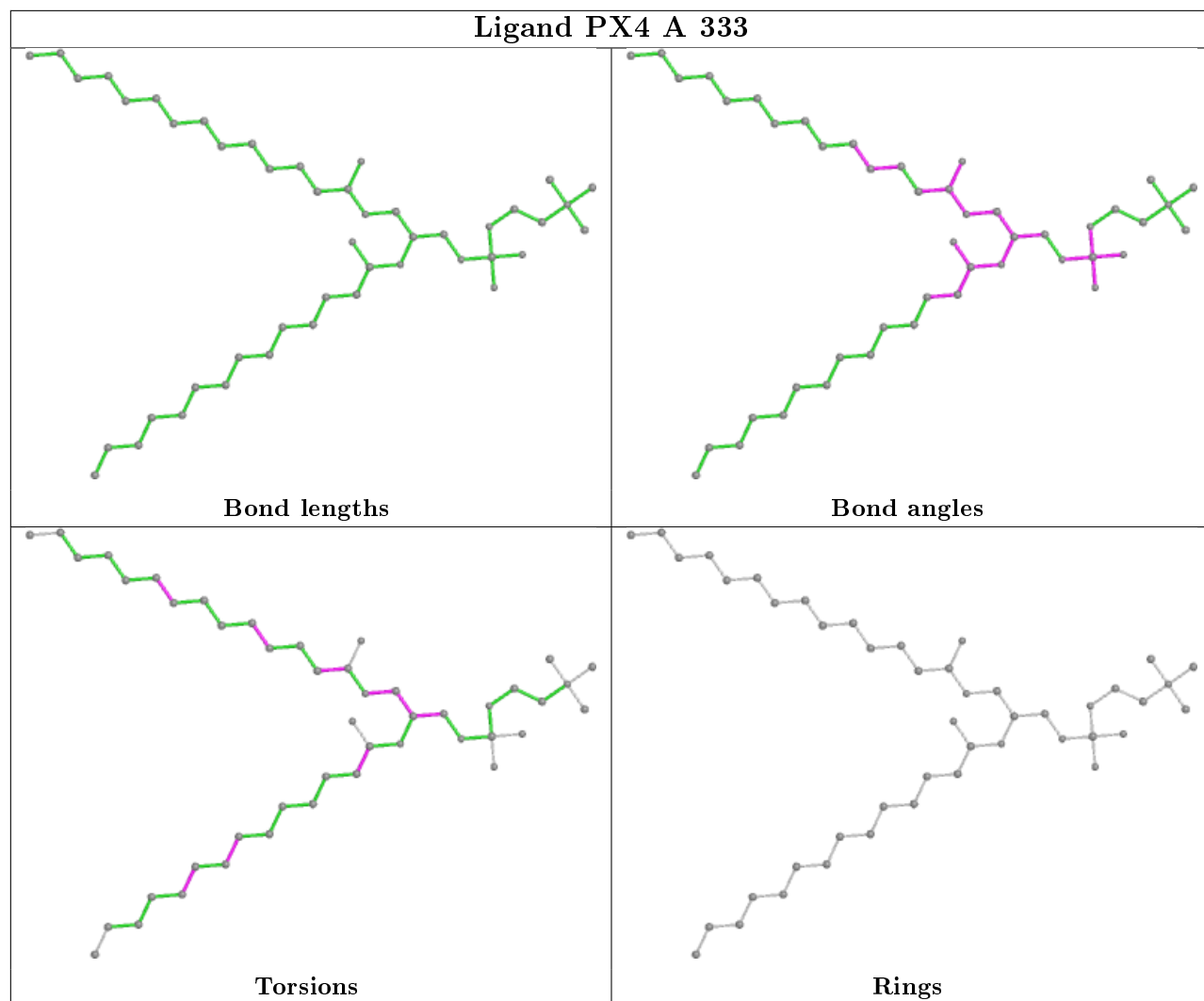
Ligand PX4 A 378



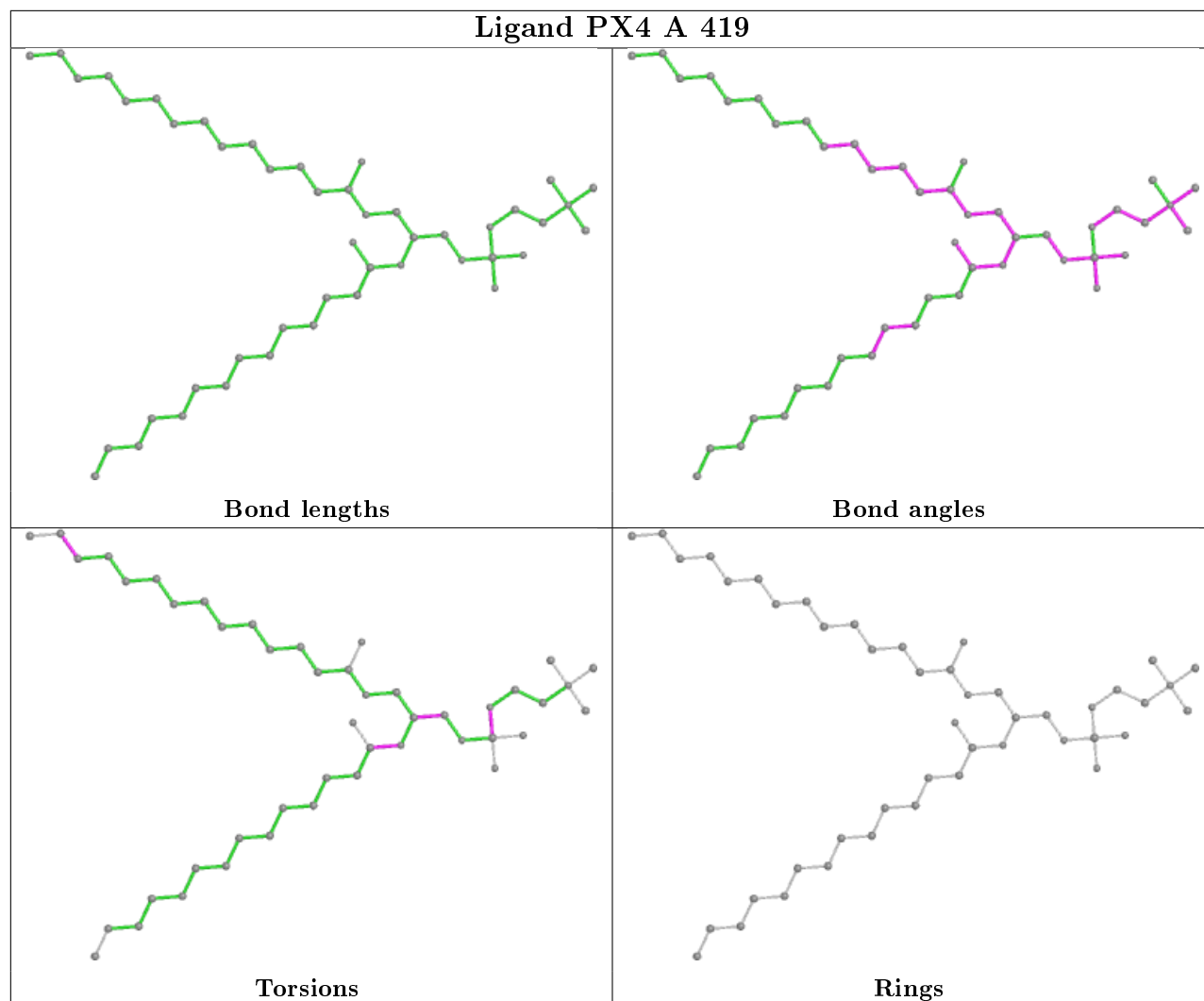
Ligand PX4 A 350



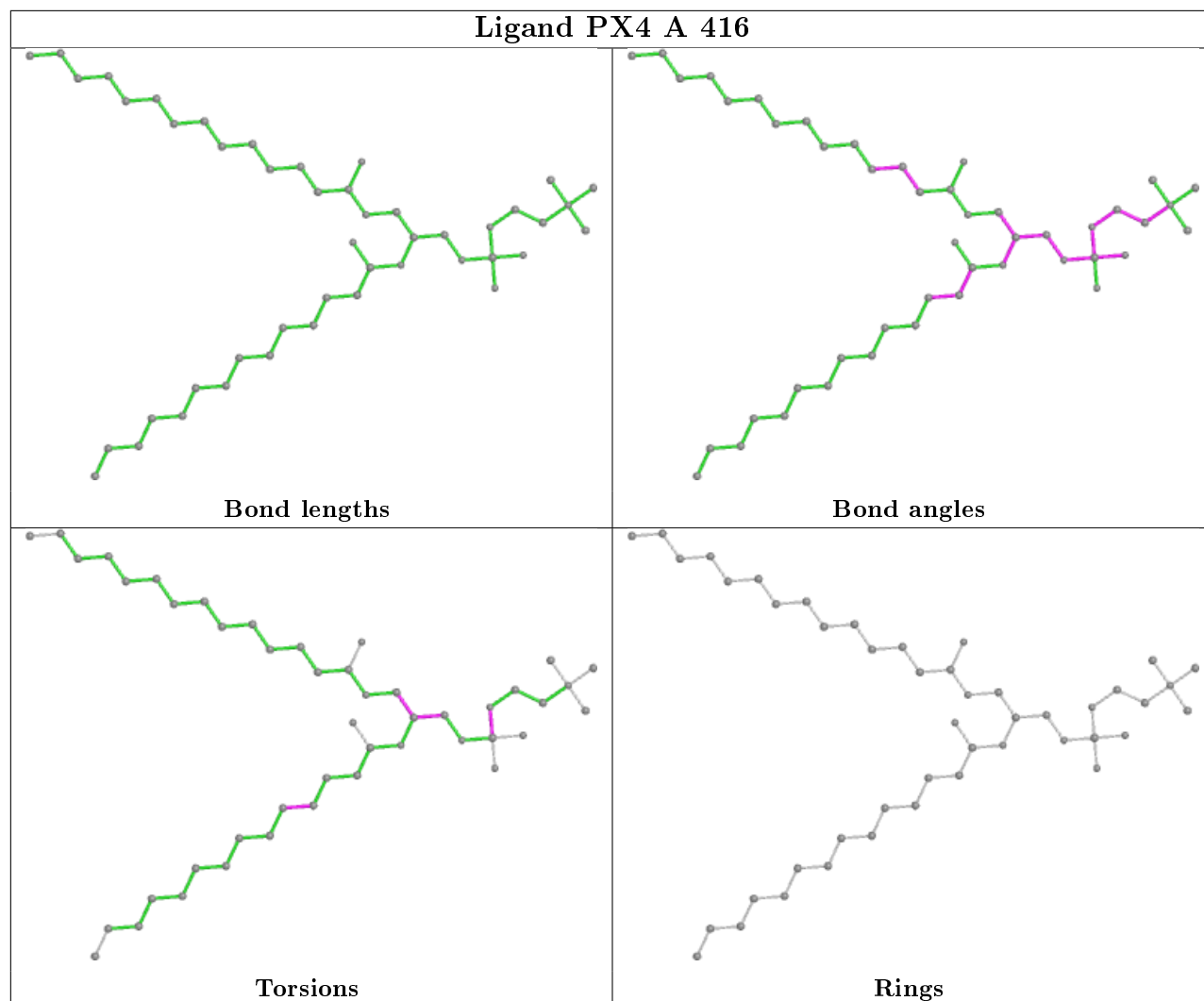
Ligand PX4 A 333



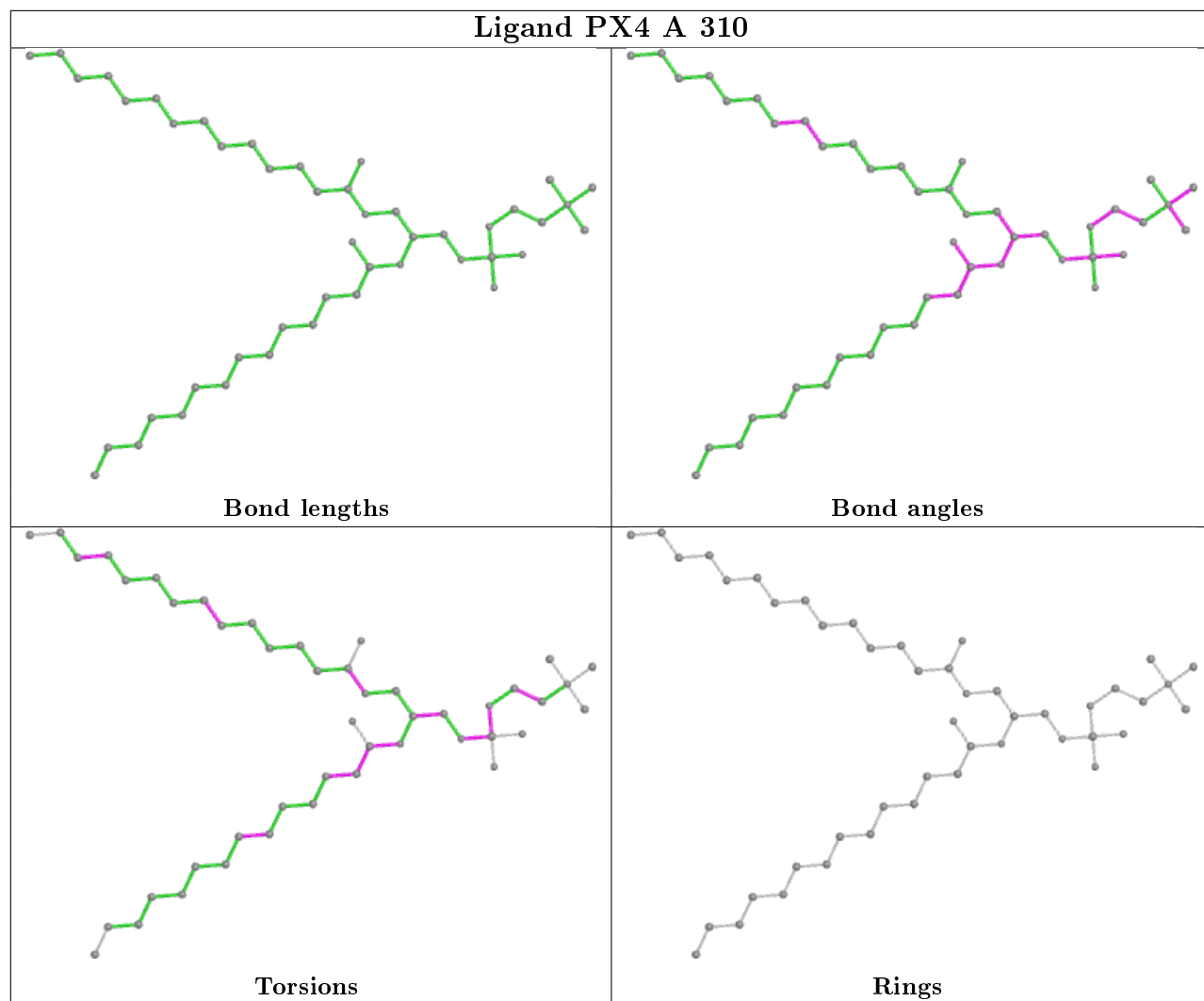
Ligand PX4 A 419

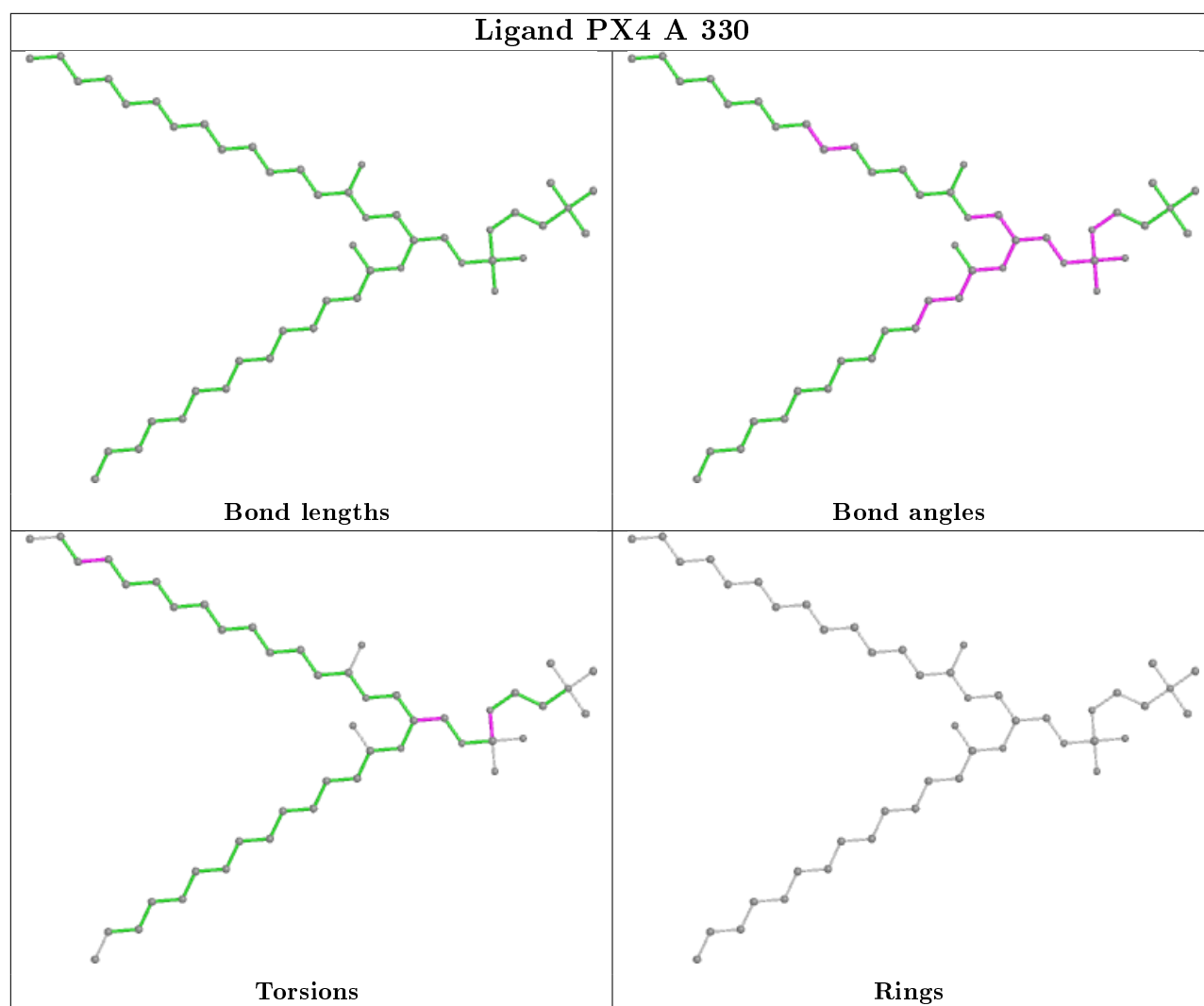


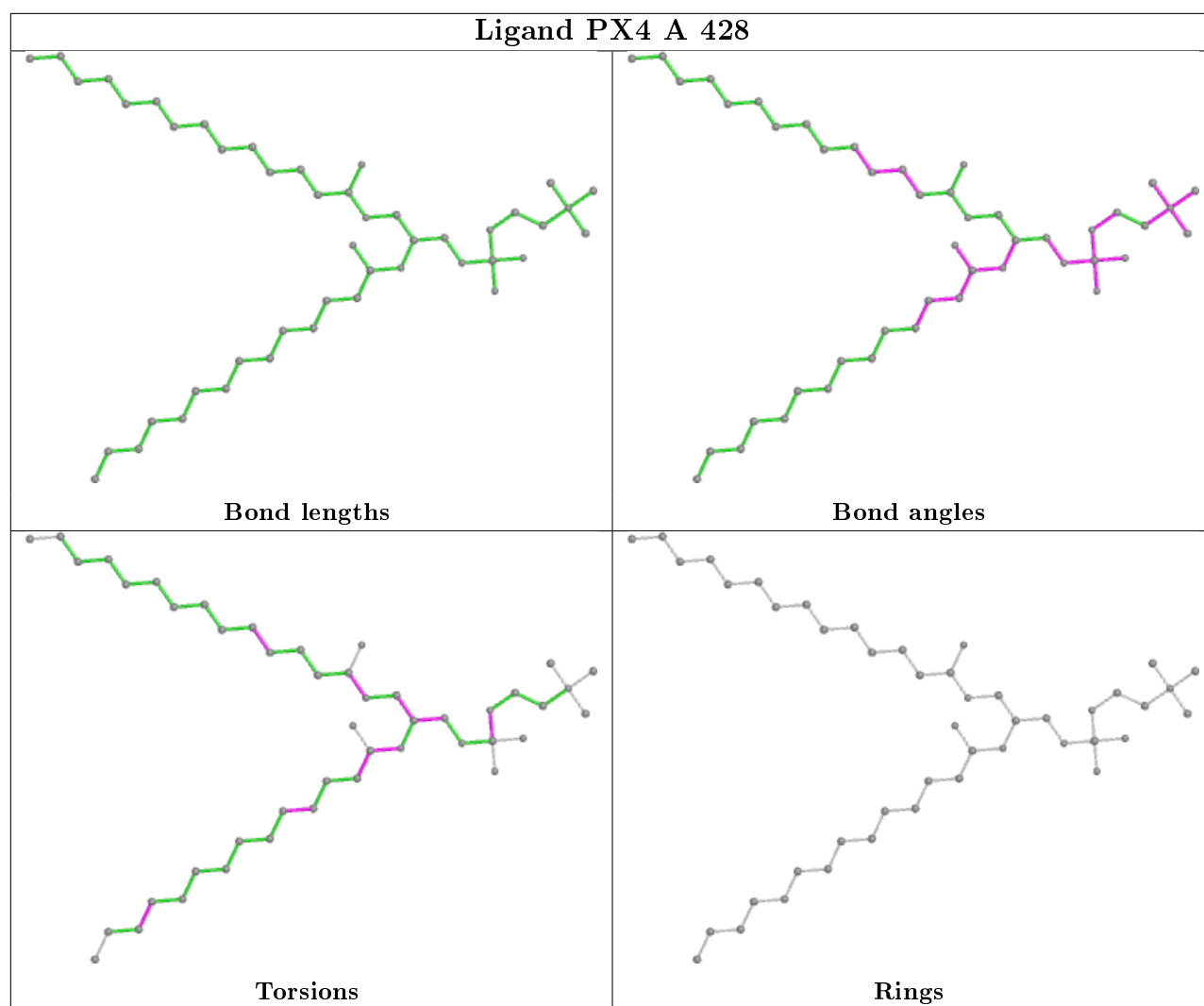
Ligand PX4 A 416



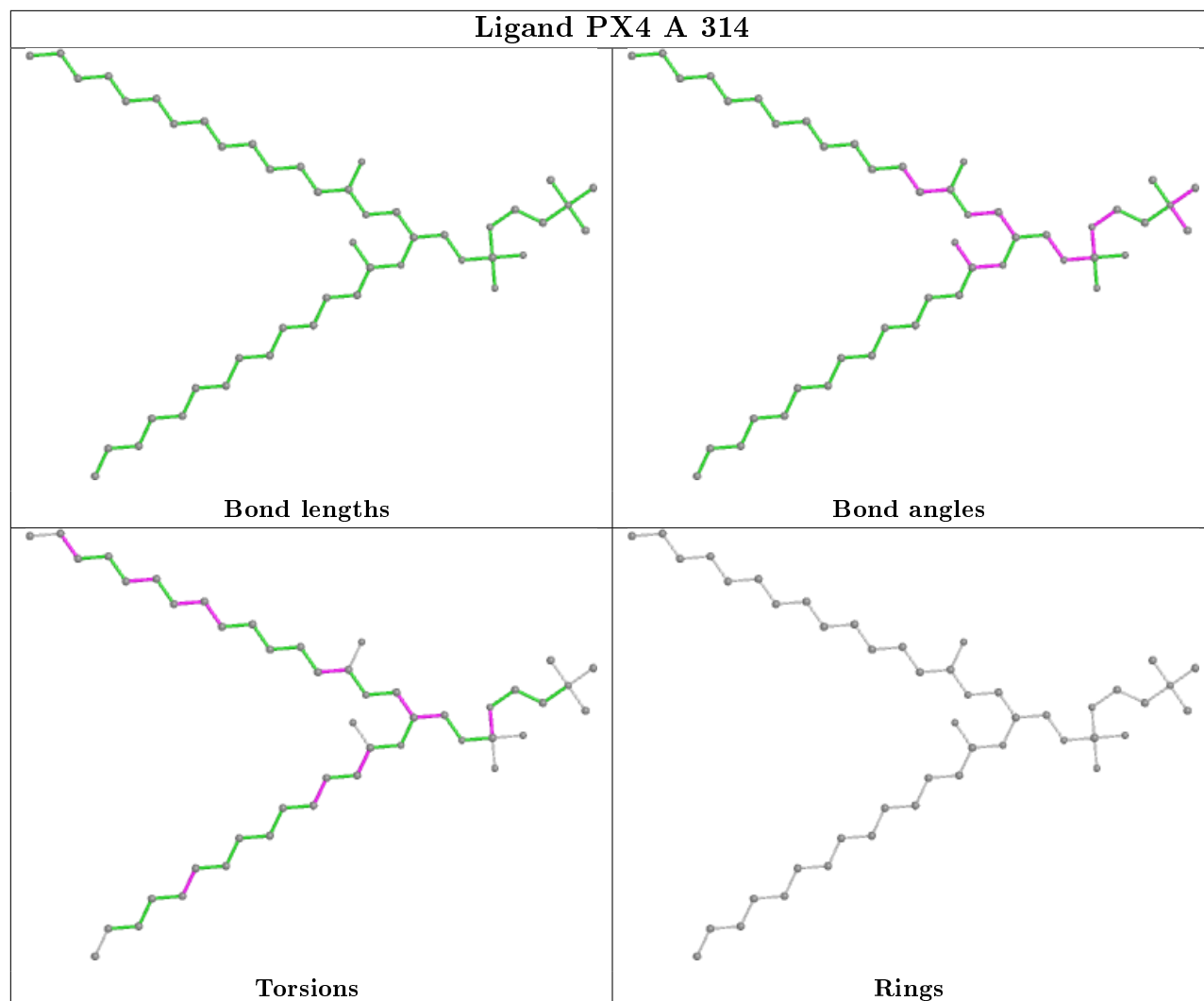
Ligand PX4 A 310

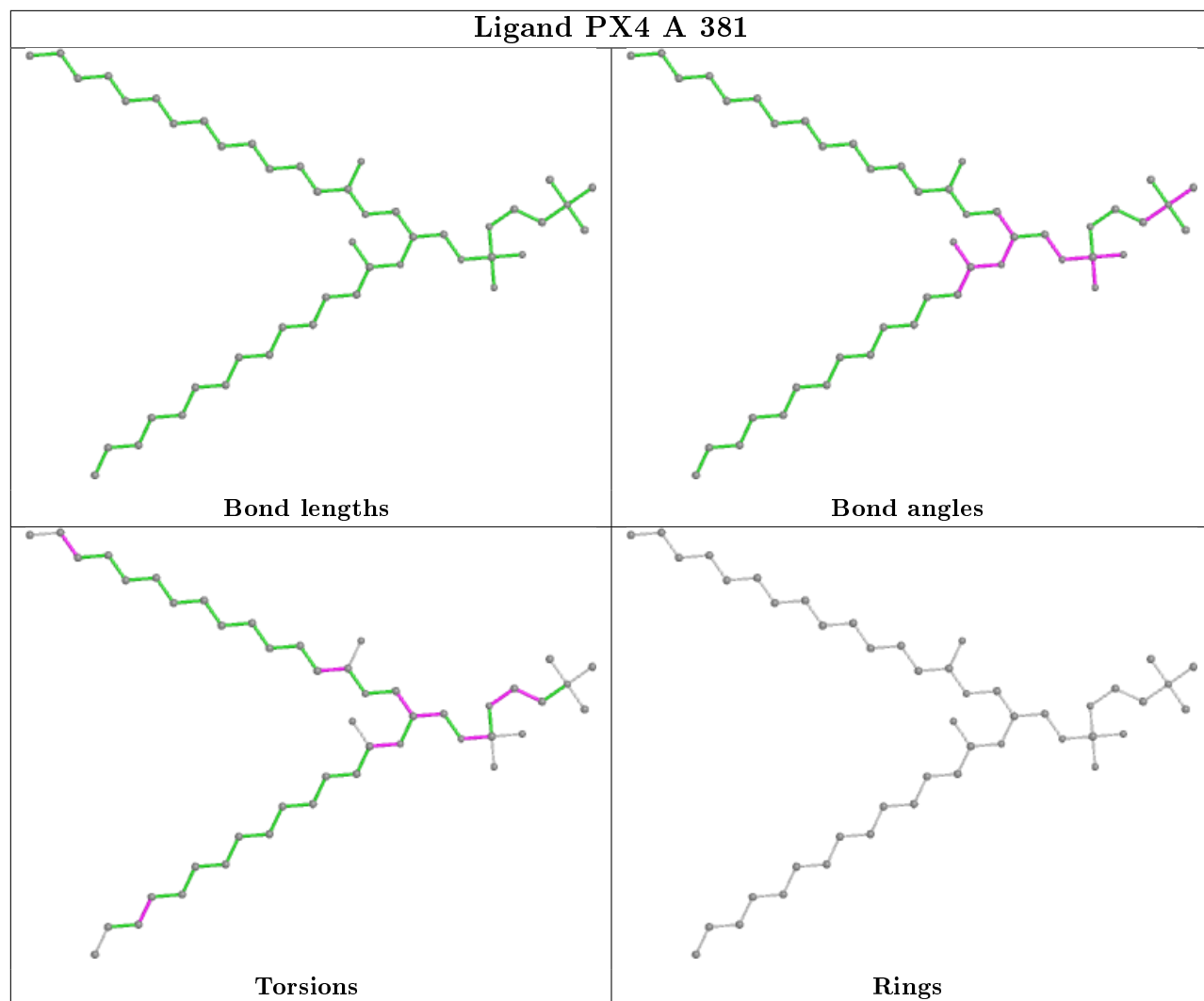




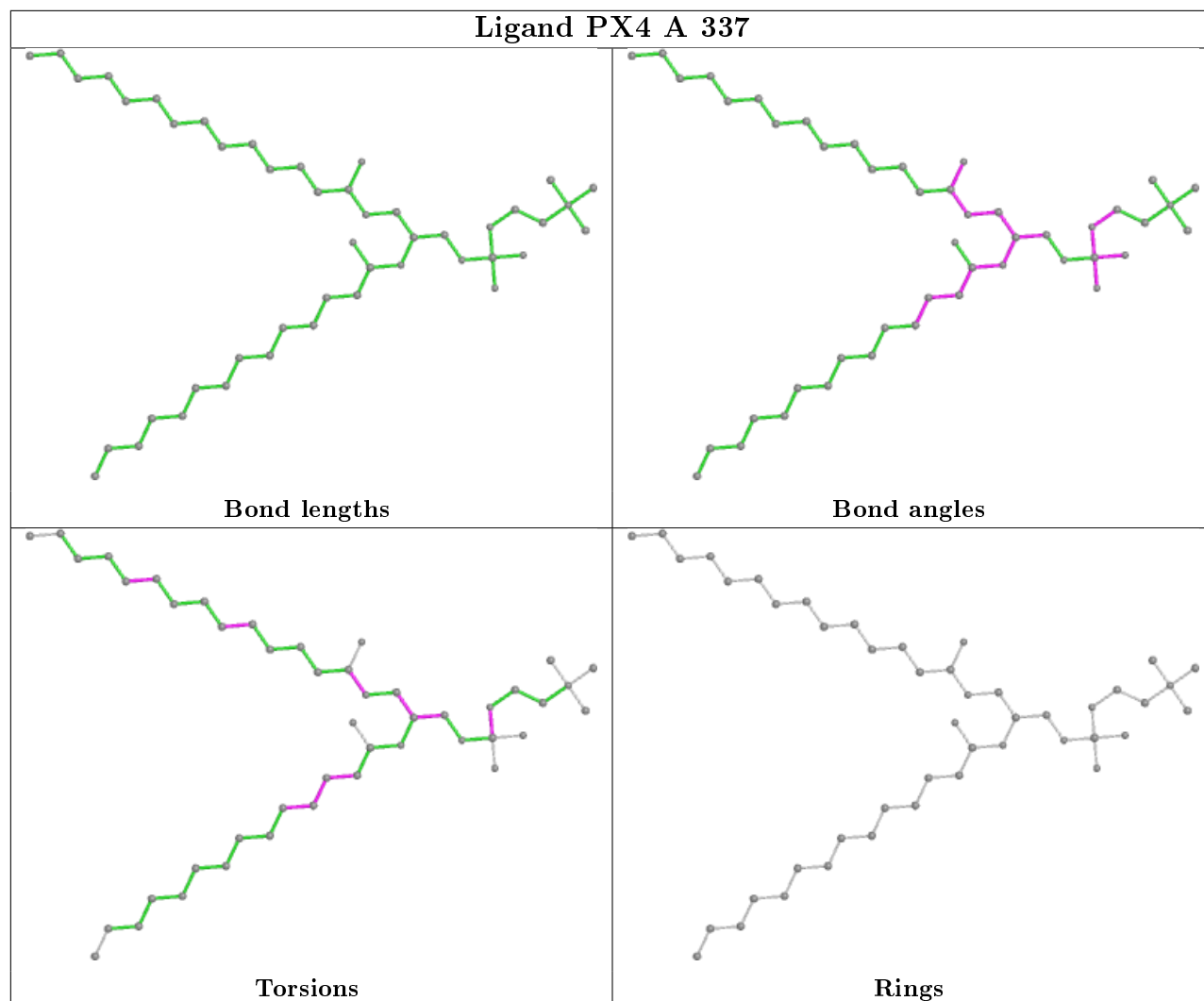


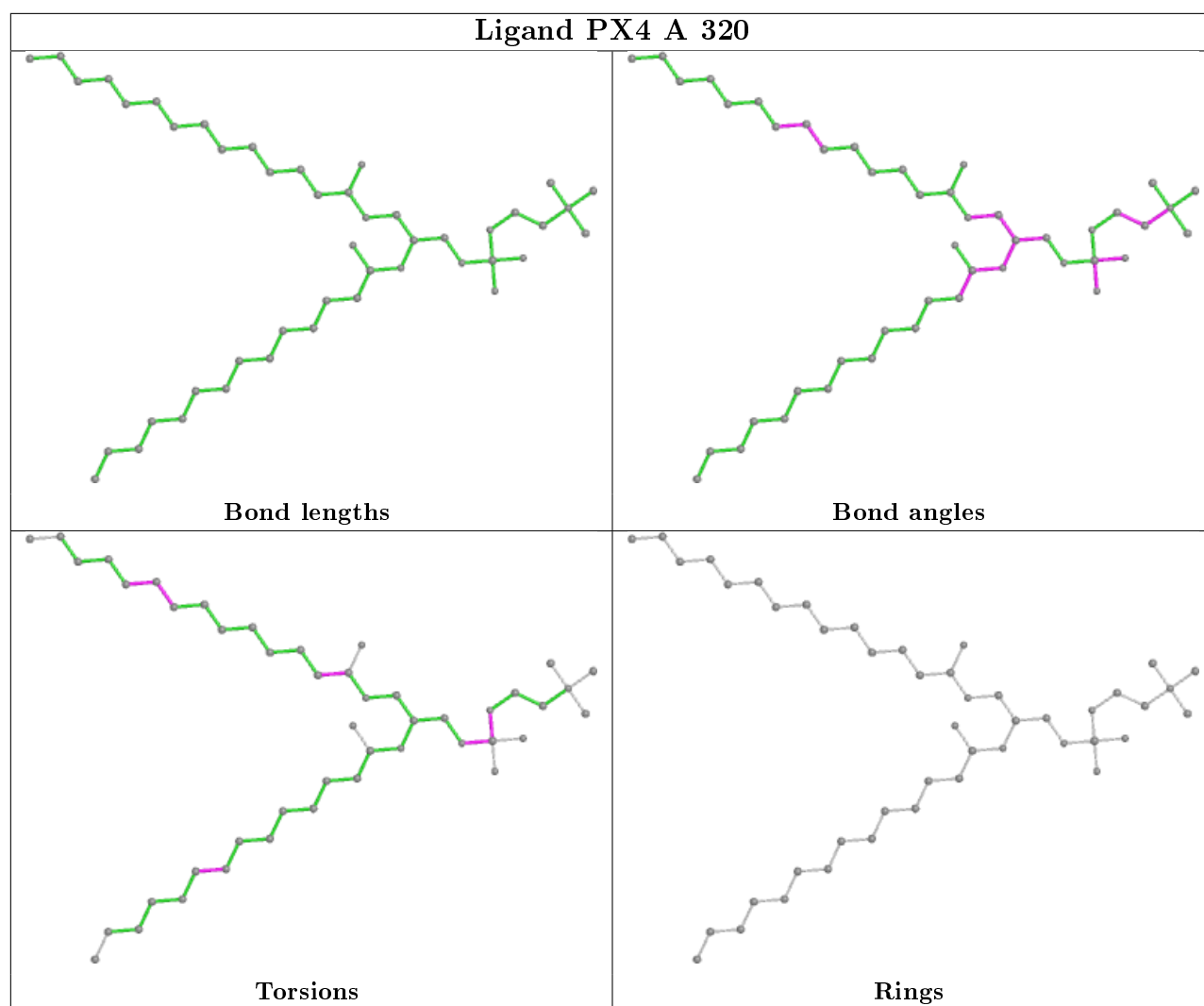
Ligand PX4 A 314



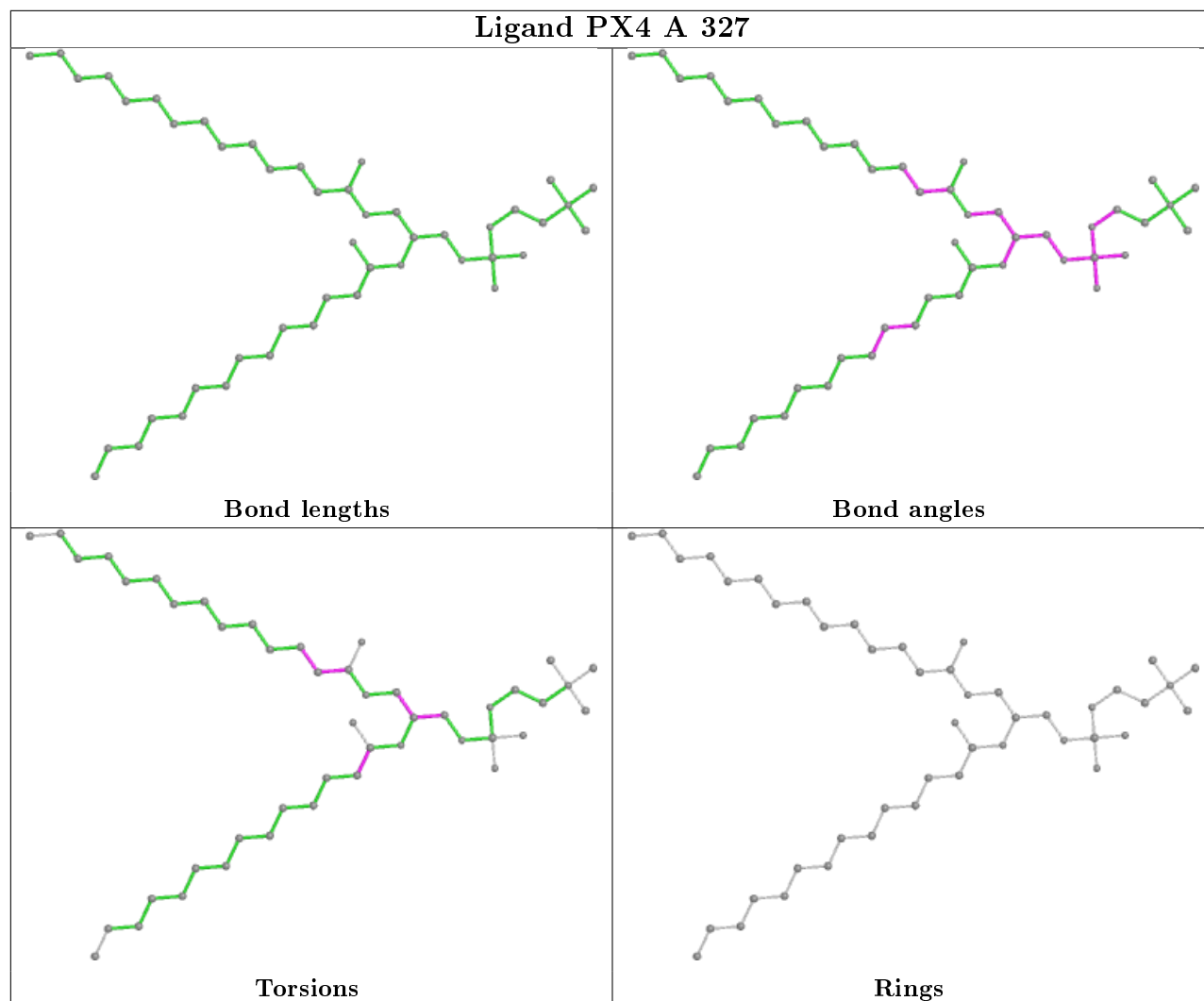


Ligand PX4 A 337

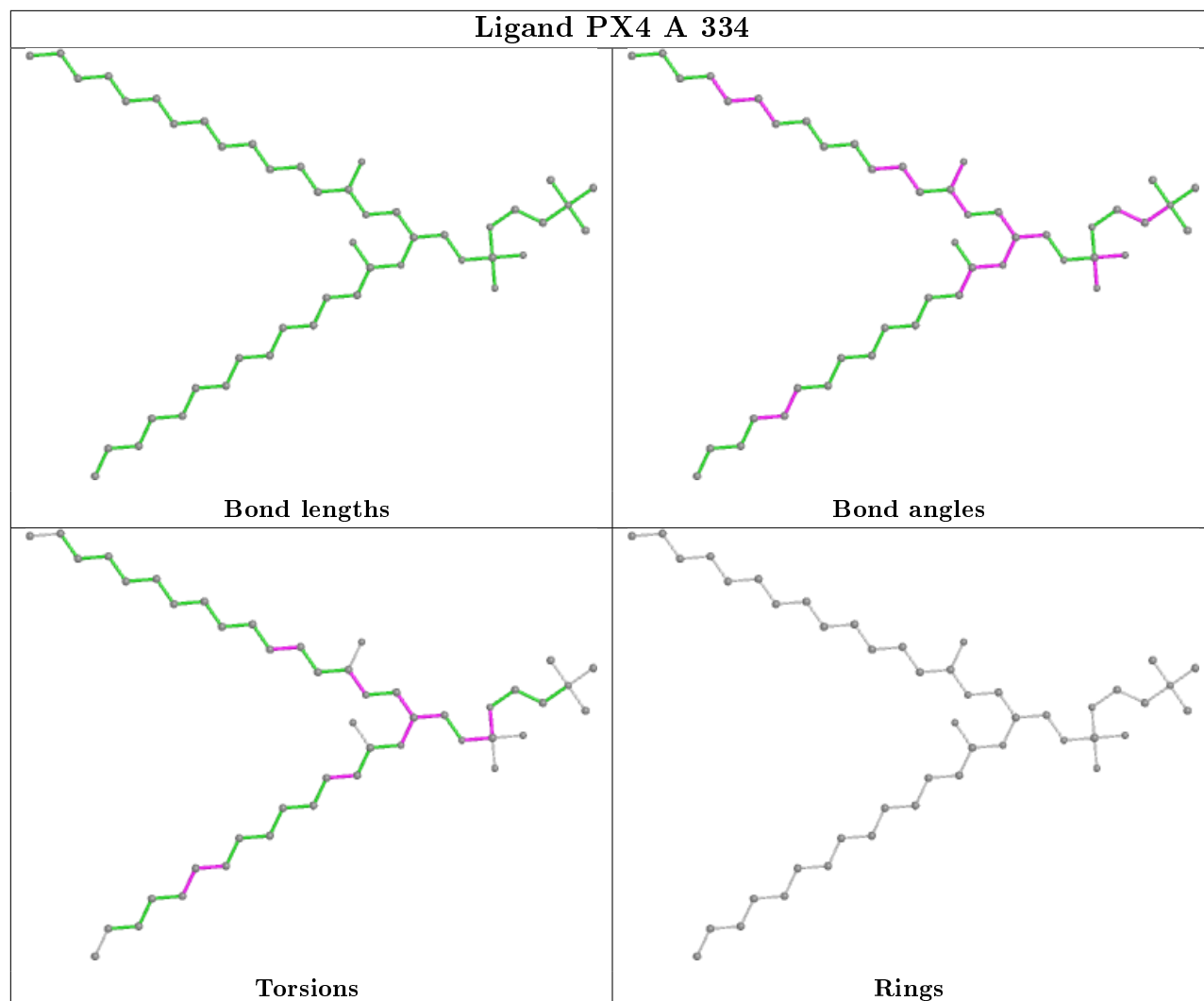




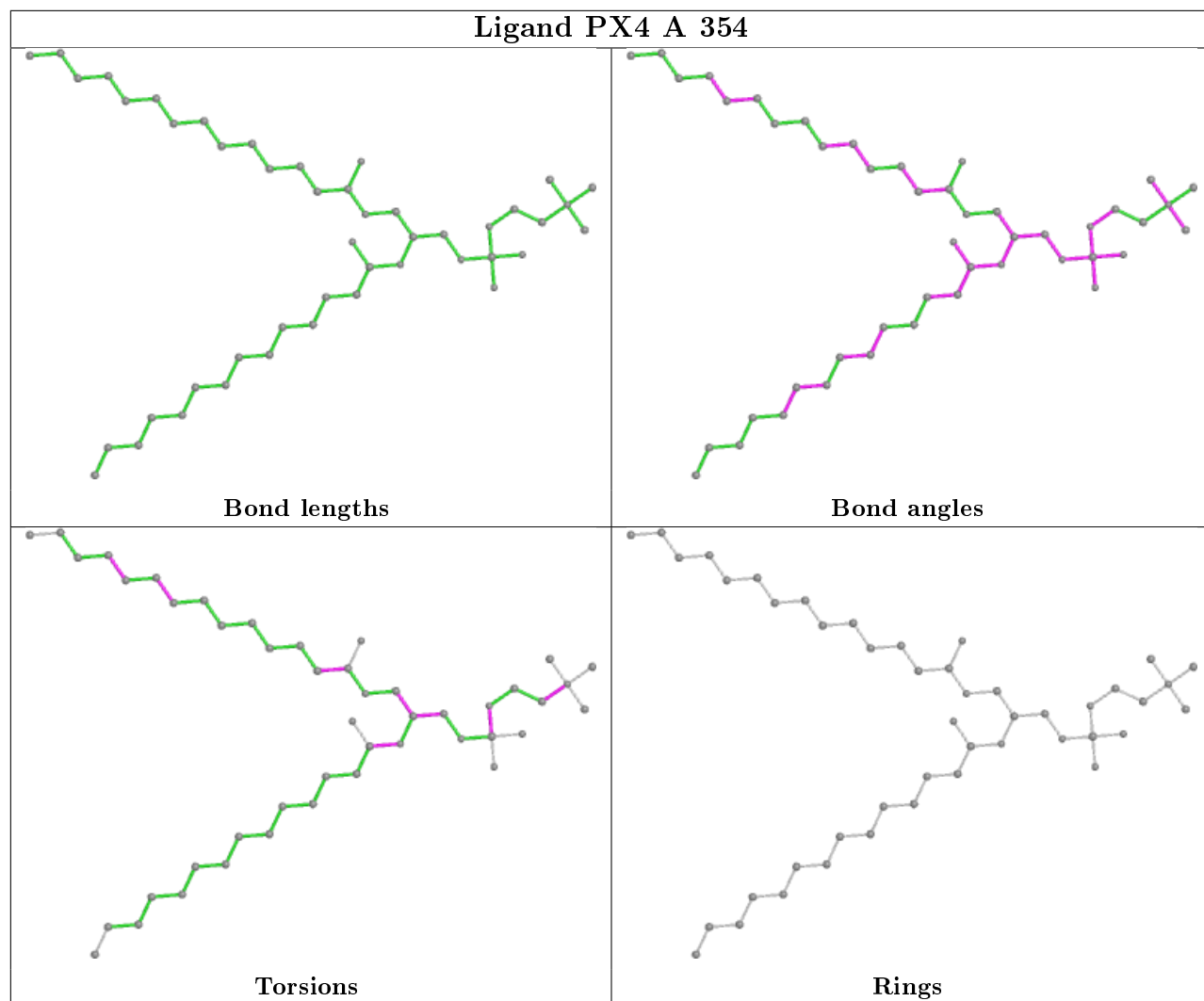
Ligand PX4 A 327

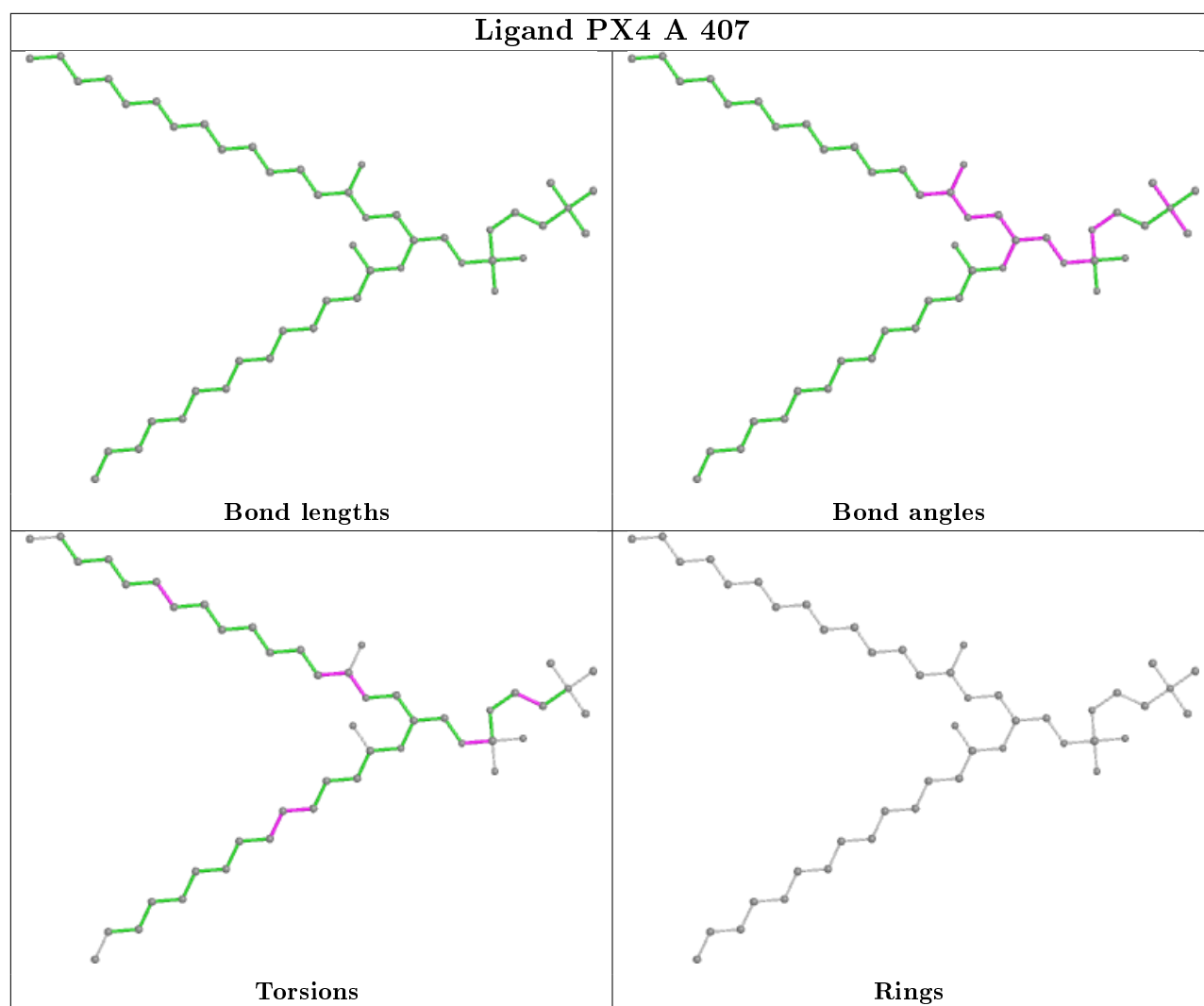


Ligand PX4 A 334

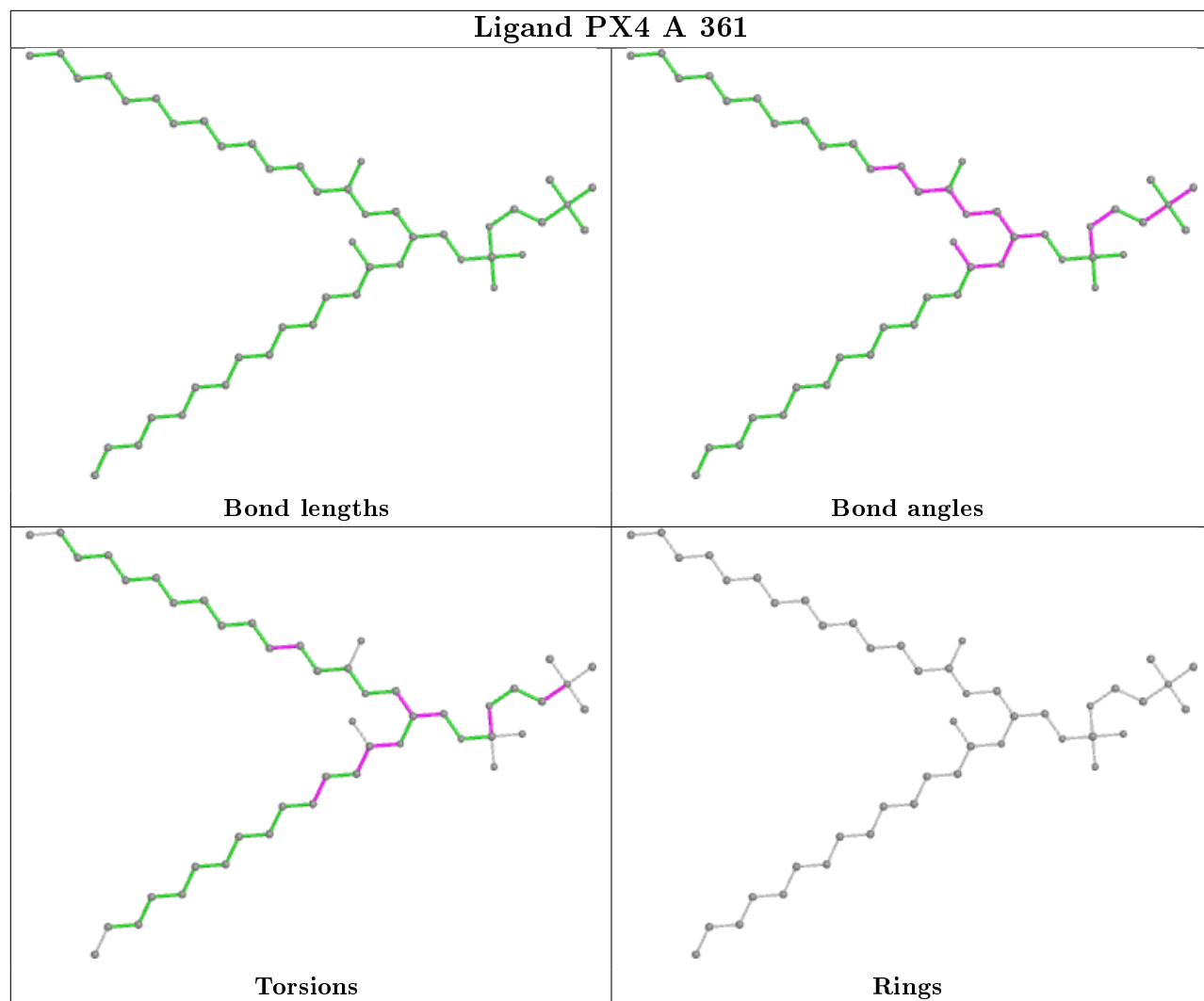


Ligand PX4 A 354

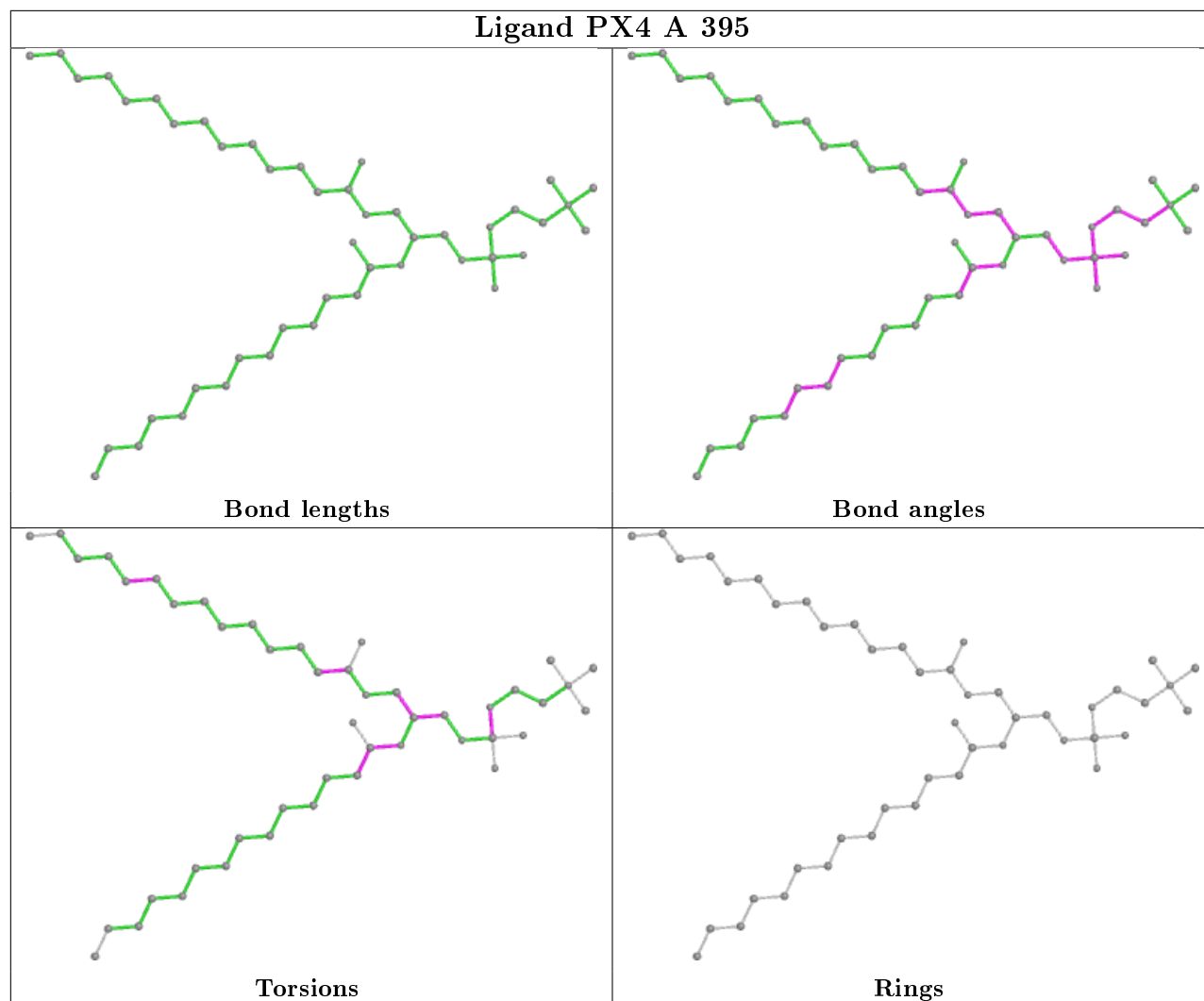




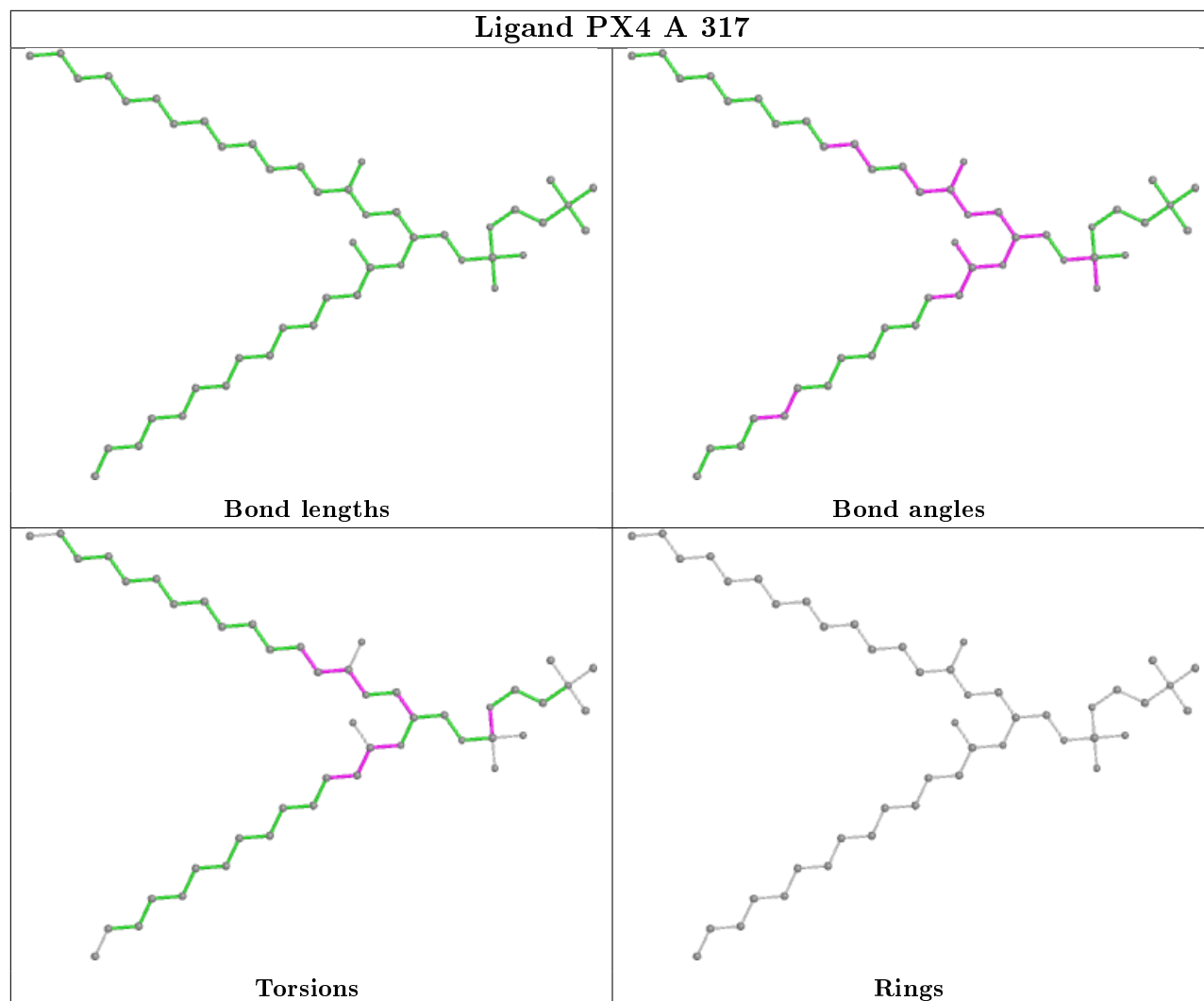
Ligand PX4 A 361



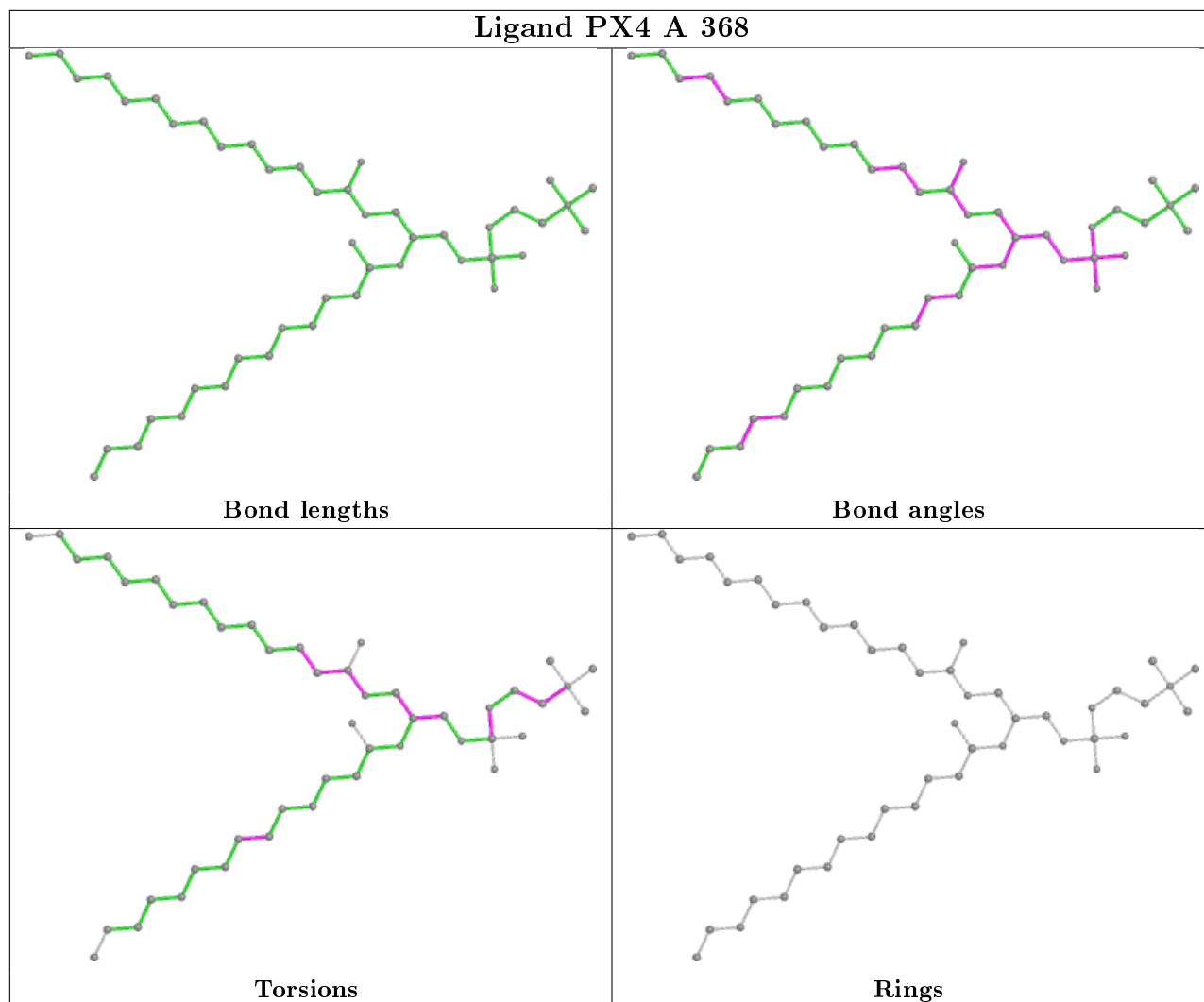
Ligand PX4 A 395

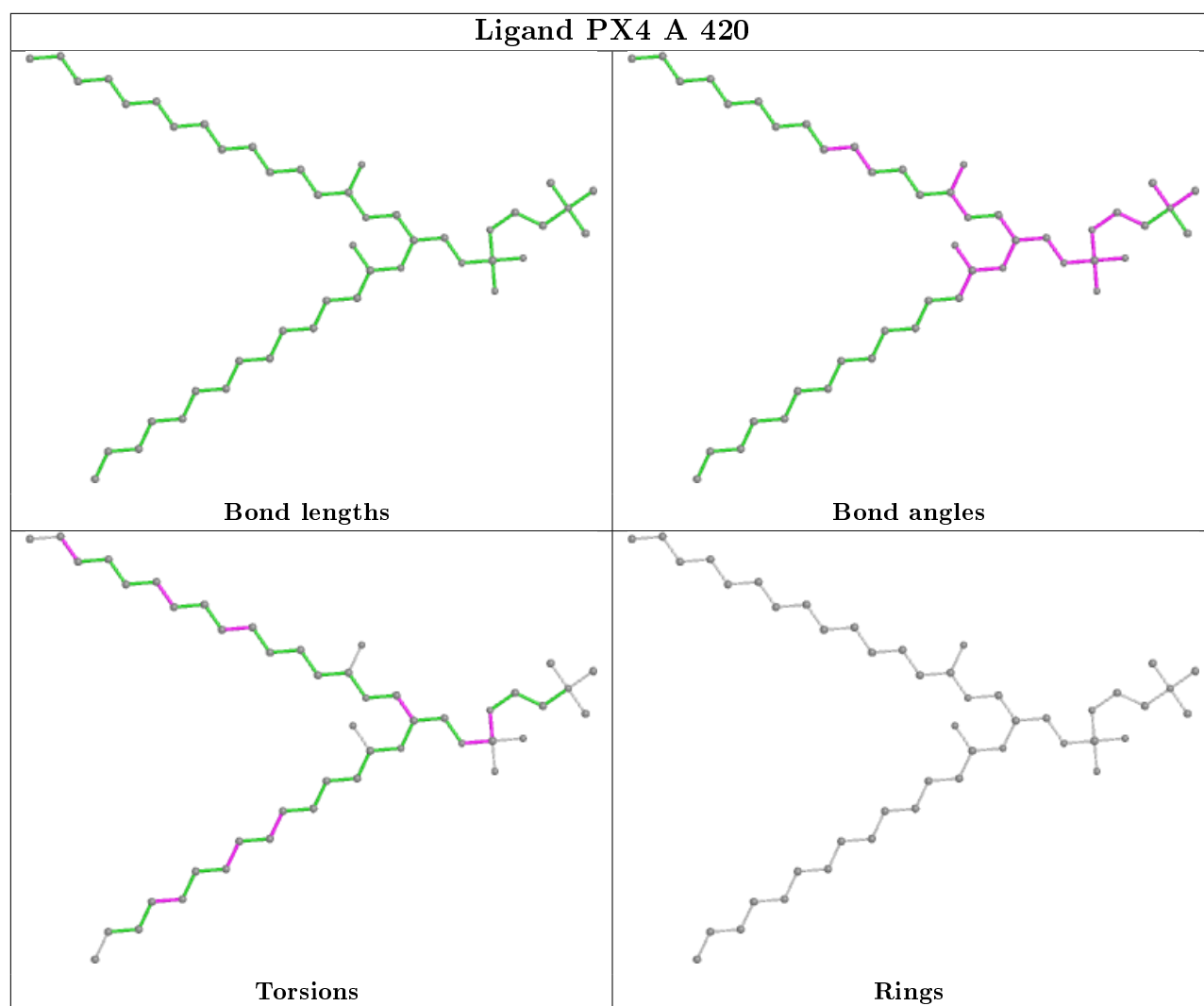


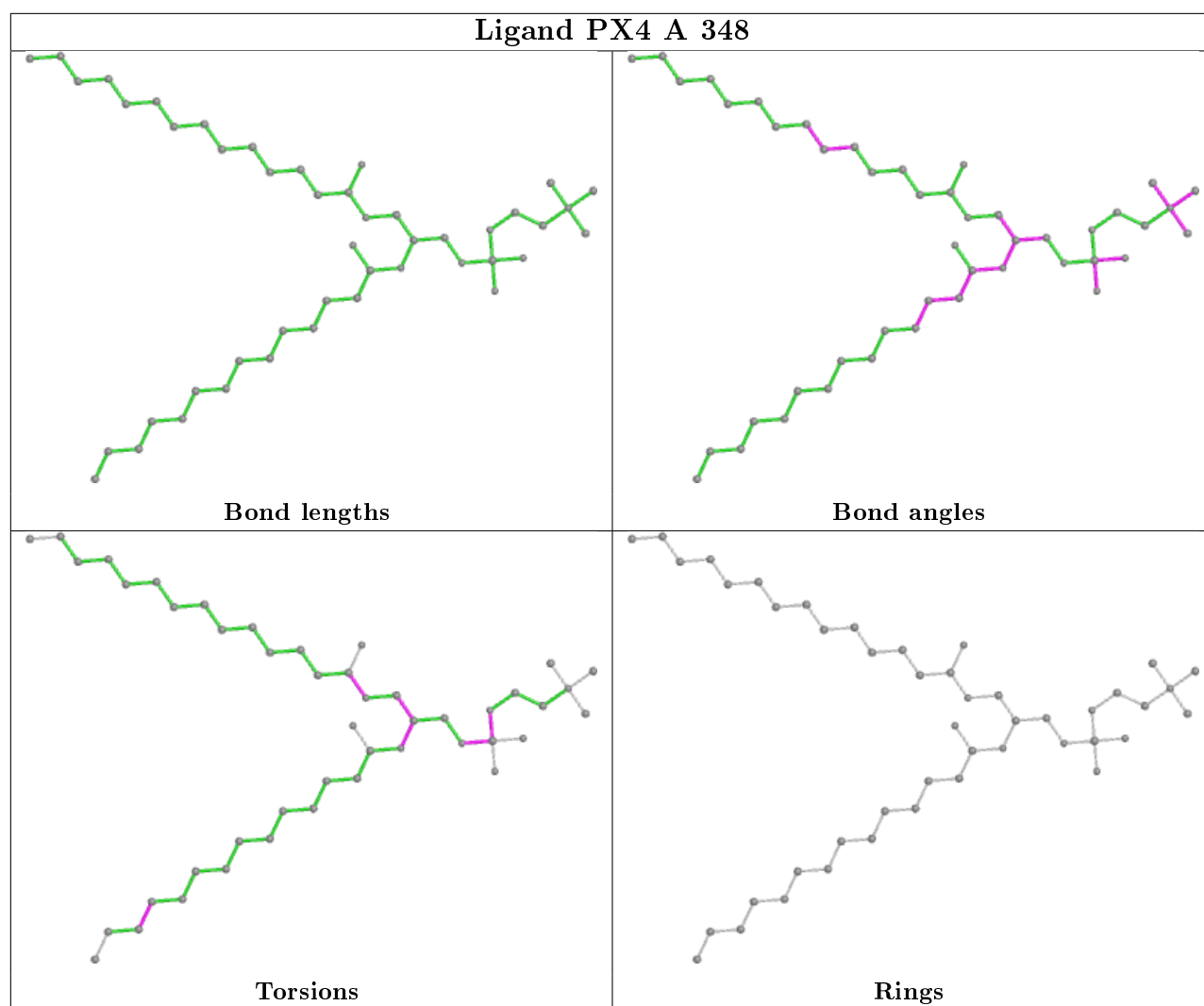
Ligand PX4 A 317



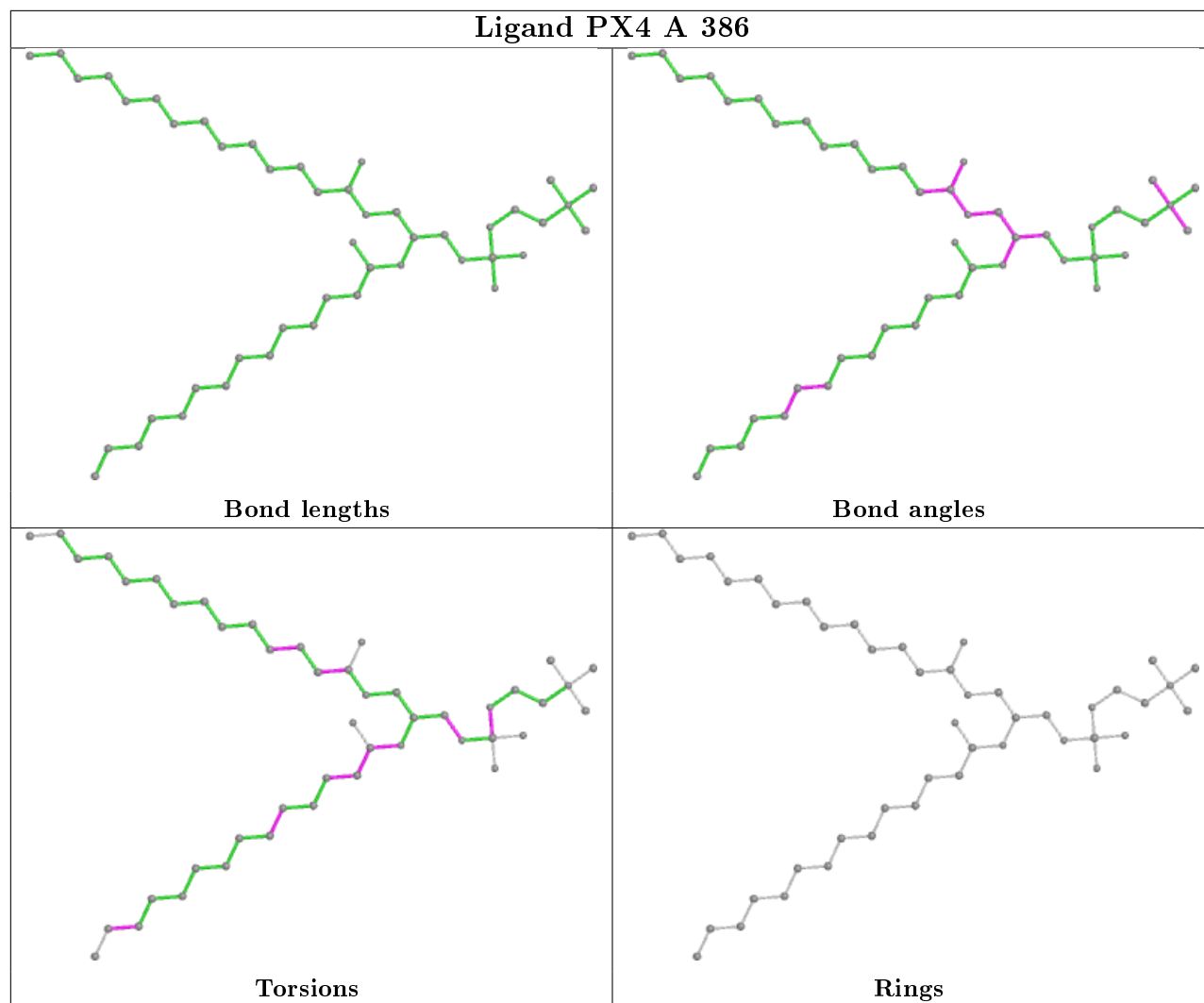
Ligand PX4 A 368



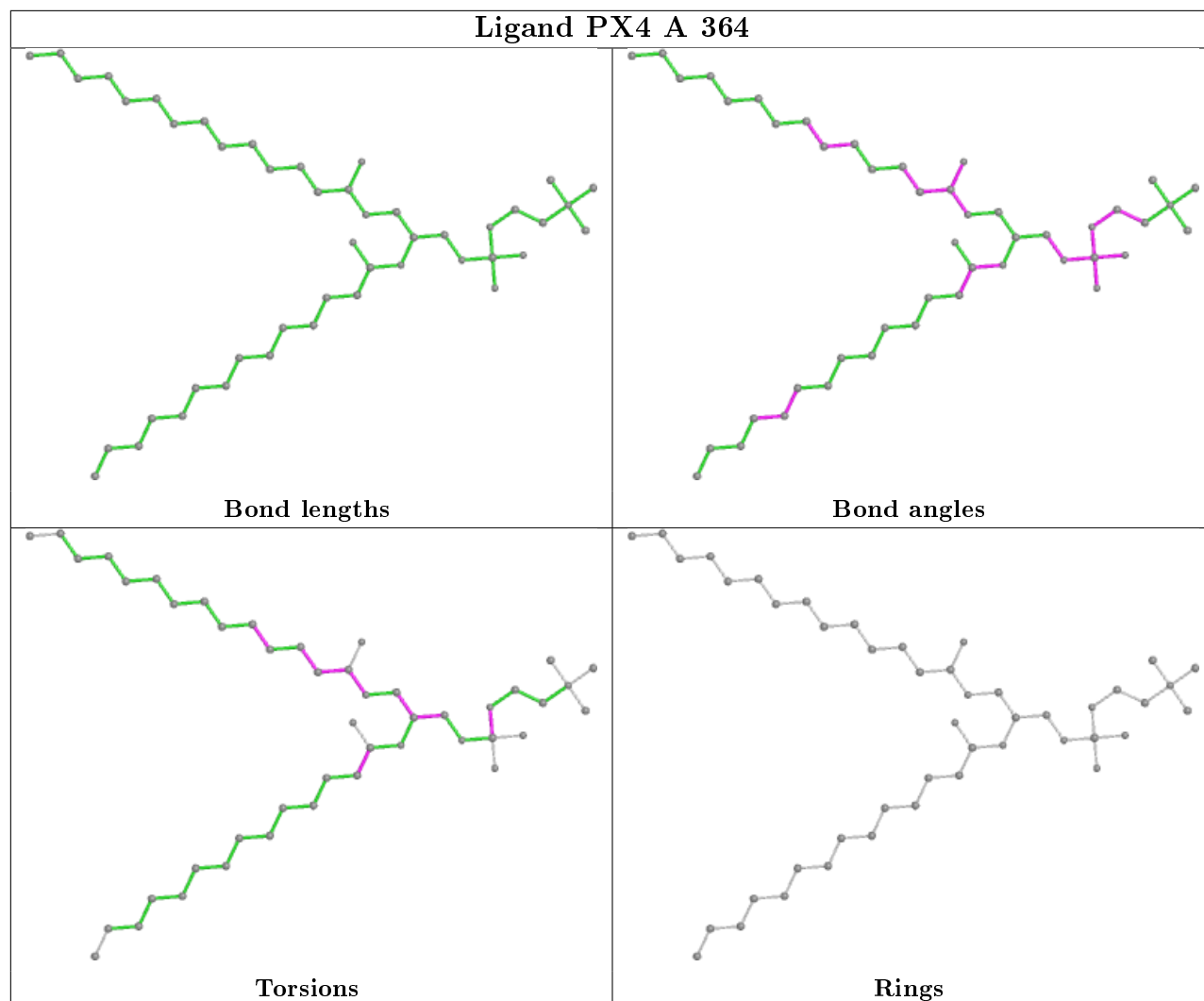




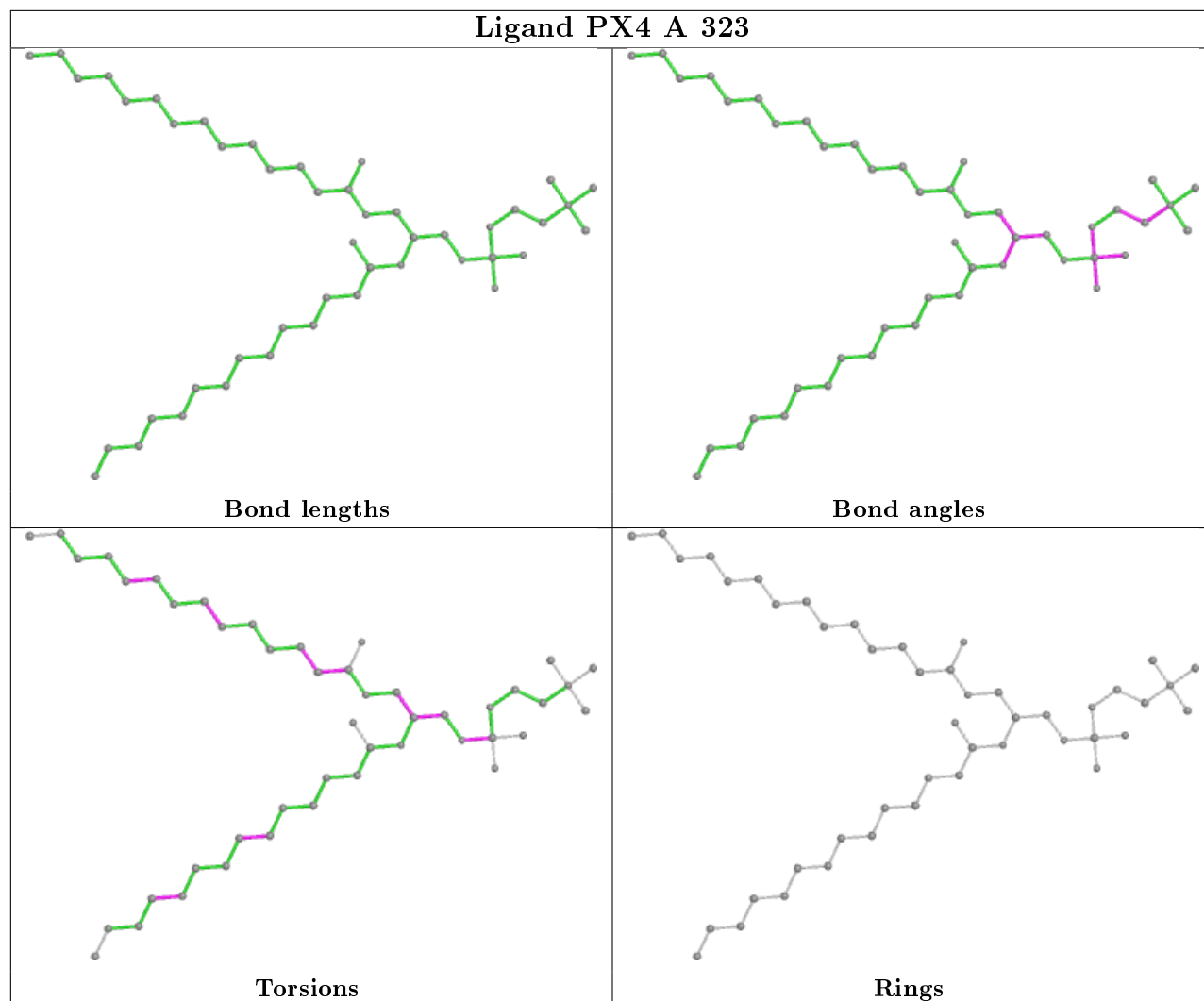
Ligand PX4 A 386



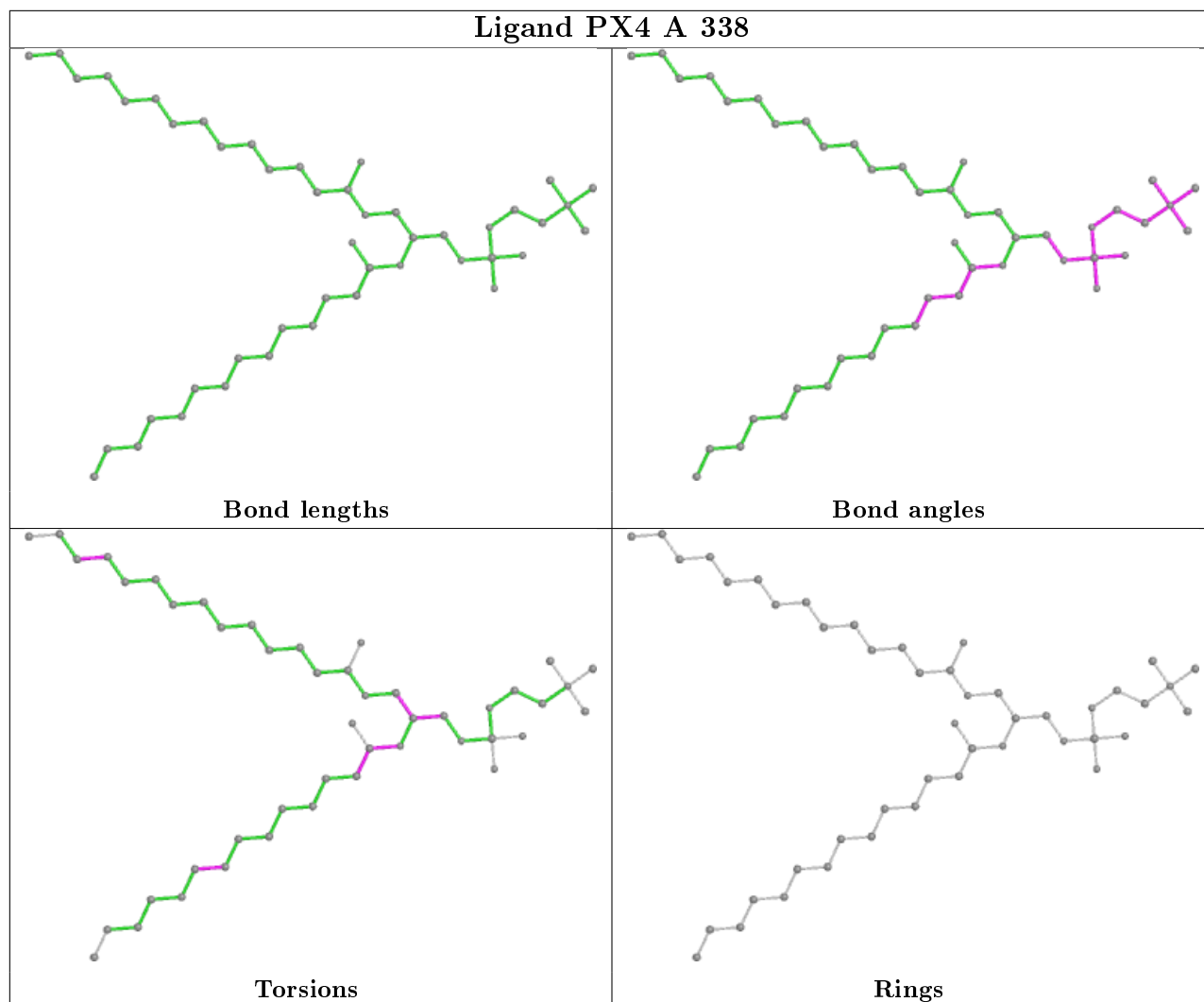
Ligand PX4 A 364



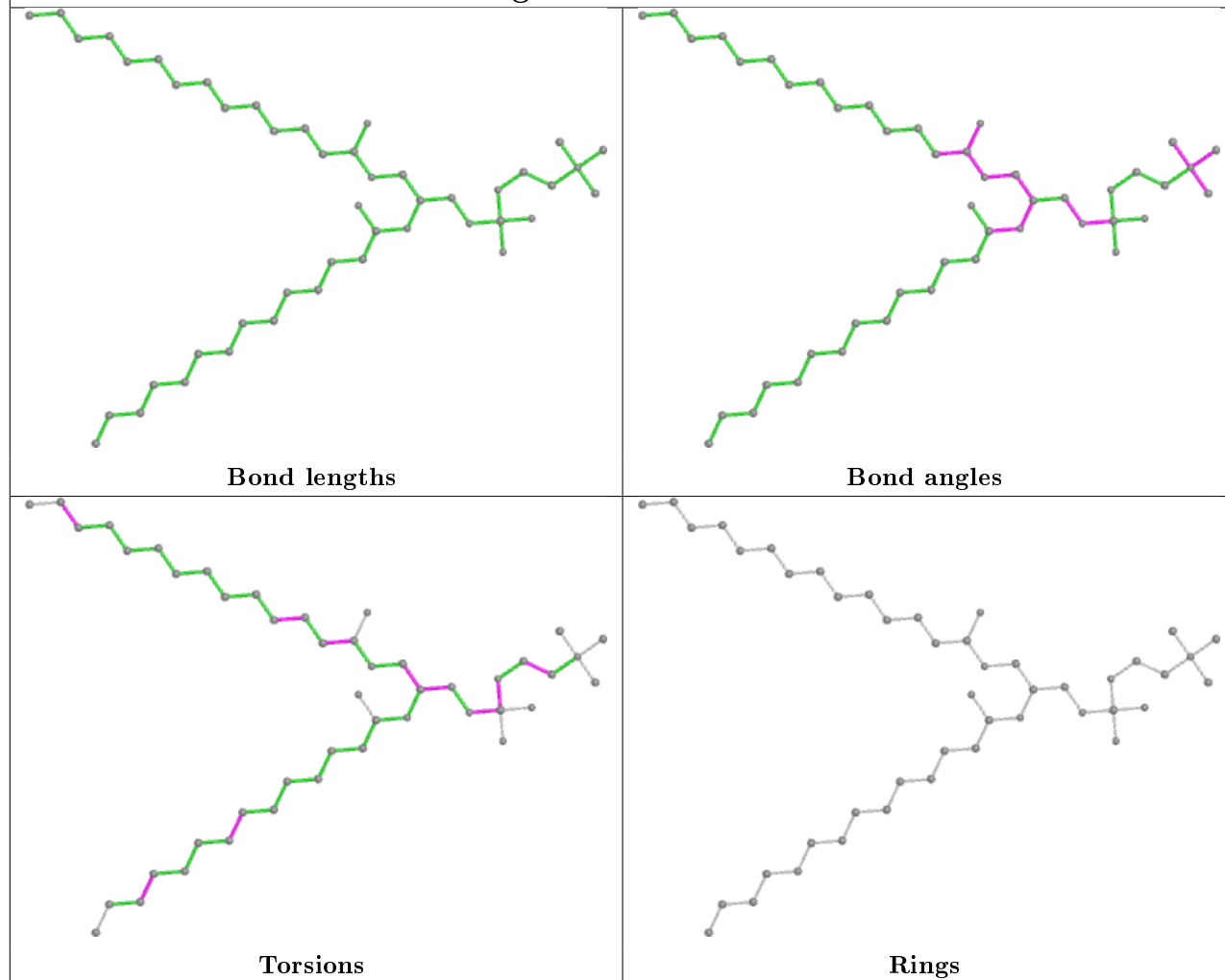
Ligand PX4 A 323



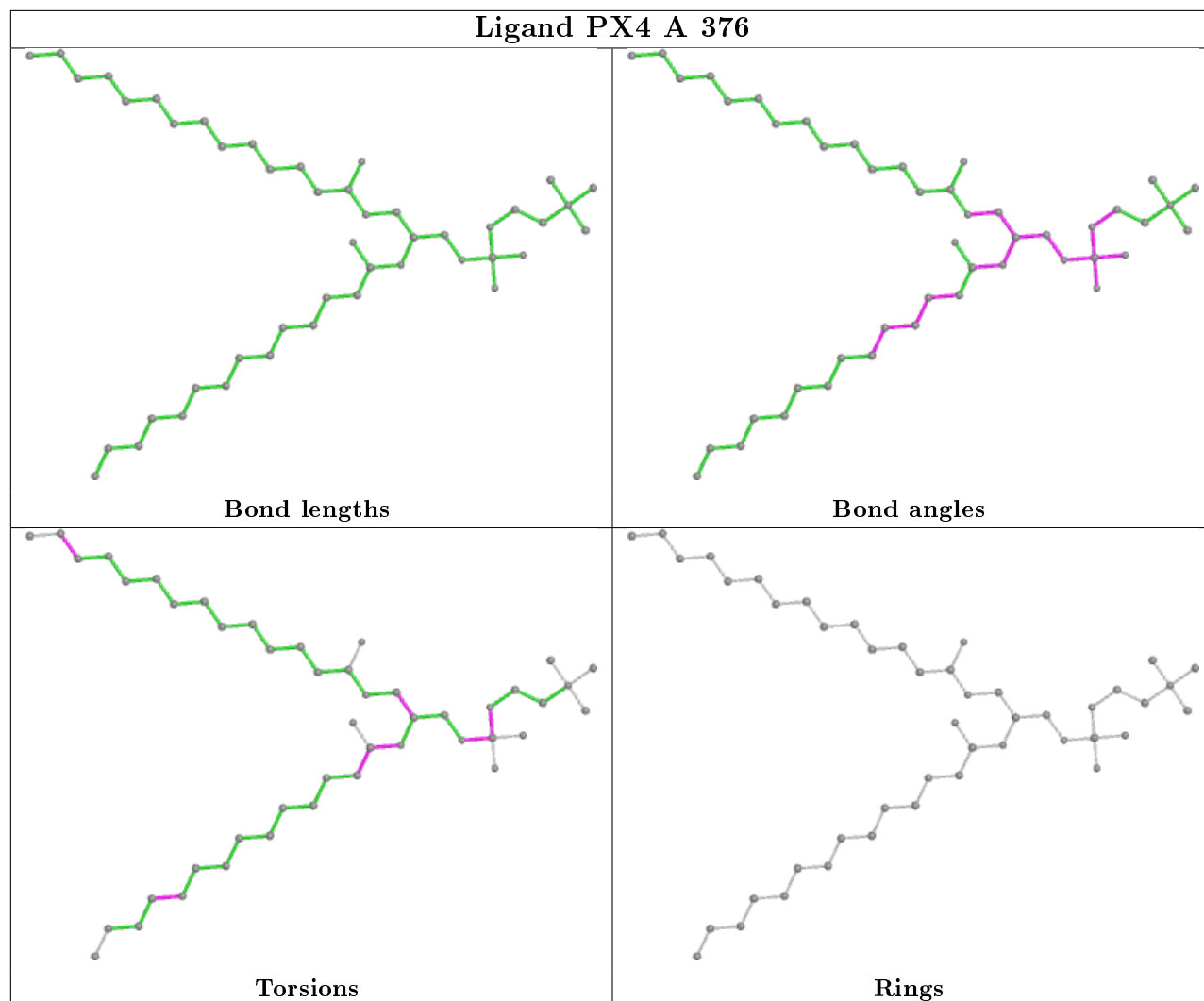
Ligand PX4 A 338



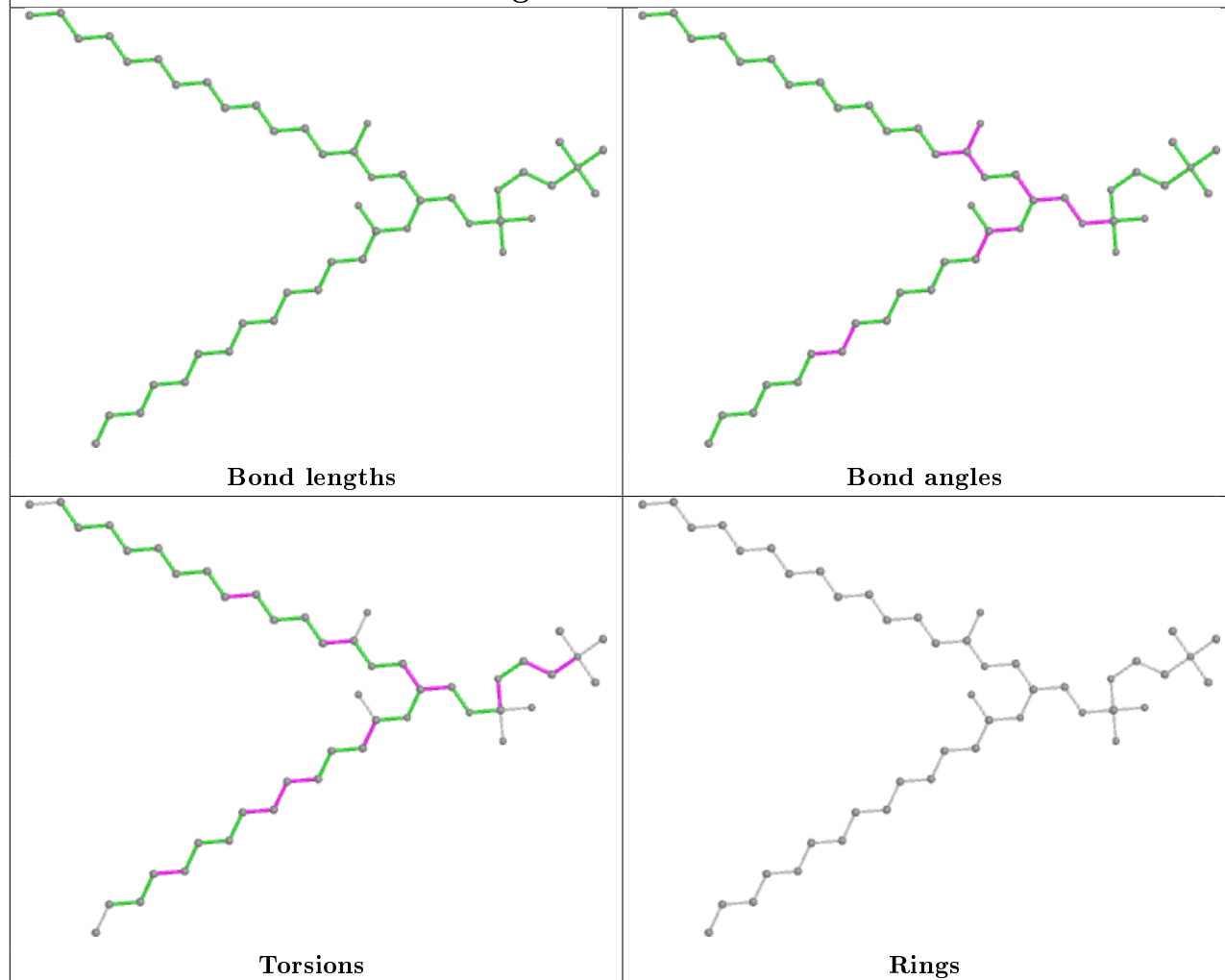
Ligand PX4 A 313

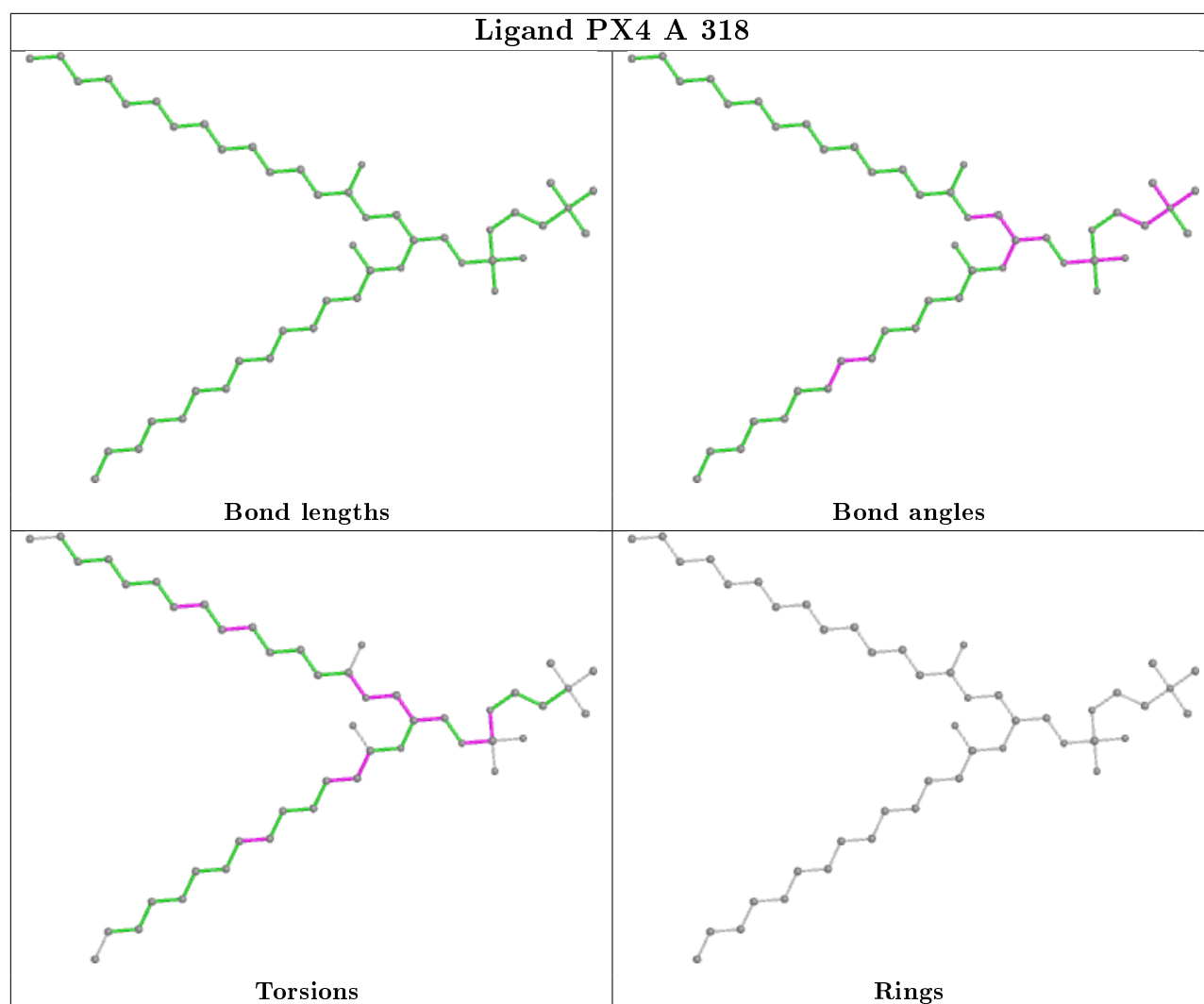


Ligand PX4 A 376



Ligand PX4 A 400





6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 44% for the well-defined parts and 41% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1503
Number of shifts mapped to atoms	1503
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	212	-0.19 ± 0.26	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 44%, i.e. 1214 atoms were assigned a chemical shift out of a possible 2785. 22 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	583/1119 (52%)	382/445 (86%)	0/458 (0%)	201/216 (93%)
Sidechain	565/1363 (41%)	497/805 (62%)	62/499 (12%)	6/59 (10%)

Continued on next page...

Continued from previous page...

	Total	^1H	^{13}C	^{15}N
Aromatic	66/303 (22%)	61/161 (38%)	0/129 (0%)	5/13 (38%)
Overall	1214/2785 (44%)	940/1411 (67%)	62/1086 (6%)	212/288 (74%)

7.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	107	ARG	NE	119.47	92.63 – 76.73	21.9
1	A	162	PRO	HB3	-0.30	3.81 – 0.21	-6.4
1	A	62	MET	HG3	0.34	4.30 – 0.50	-5.4
1	A	242	SER	N	135.65	134.24 – 98.34	5.4
1	A	97	THR	HB	2.52	5.82 – 2.52	-5.0

7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

