



wwPDB EM Validation Summary Report ⓘ

Jul 20, 2025 – 12:31 AM JST

PDB ID : 9M8M / pdb_00009m8m
EMDB ID : EMD-63714
Title : Structure of photosynthetic LH1-RC complex the Halophilic Nonsulfur Purple Bacterium, Rhodothalassium salexigens
Authors : Tani, K.; Kanno, R.; Inami, M.; Ooya, T.; Matsushita, R.; Minamino, A.; Takenaka, S.; Takaichi, S.; Purba, E.R.; Hall, M.; Mochizuki, T.; Yu, L.-J.; Mizoguchi, A.; Humbel, B.M.; Madigan, M.T.; Kimura, Y.; Wang-Otomo, Z.-Y.
Deposited on : 2025-03-12
Resolution : 2.30 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.dev118
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

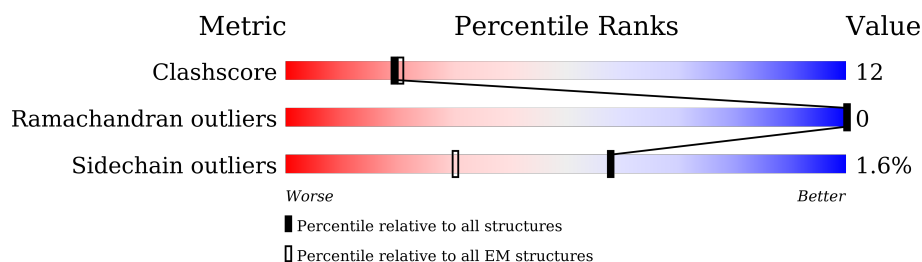
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.30 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	C	385	71% 18% 11%
2	L	275	76% 23%
3	M	323	72% 25% ..
4	H	324	65% 17% . 17%
5	1	59	61% 15% . 20%
5	3	59	54% 22% . 22%
5	5	59	59% 20% 20%





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Mol	Chain	Length	Quality of chain
5	7	59	
5	9	59	
5	A	59	
5	D	59	
5	F	59	
5	I	59	
5	K	59	
5	O	59	
5	Q	59	
5	S	59	
5	U	59	
5	W	59	
5	Y	59	
6	0	67	
6	2	67	
6	4	67	
6	6	67	
6	8	67	
6	B	67	
6	E	67	
6	G	67	
6	J	67	
6	N	67	
6	P	67	
6	R	67	

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Mol	Chain	Length	Quality of chain
6	T	67	 54% 13% 33%
6	V	67	 54% 12% 34%
6	X	67	 54% 15% 31%
6	Z	67	 54% 13% 33%

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 27731 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 Photosynthetic reaction center cytochrome c subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	344	Total	C	N	O	S	0	0
			2675	1663	465	523	24		

- Molecule 2 is a protein called Reaction center protein L chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	274	Total	C	N	O	S	0	0
			2175	1469	347	351	8		

- Molecule 3 is a protein called Reaction center protein M chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	318	Total	C	N	O	S	0	0
			2518	1679	412	418	9		

- Molecule 4 is a protein called Photosynthetic reaction center subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	268	Total	C	N	O	S	0	0
			2109	1350	351	402	6		

- Molecule 5 is a protein called Light-harvesting complex 1 alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	47	Total	C	N	O	S	0	0
			414	283	66	62	3		
5	D	47	Total	C	N	O	S	0	0
			414	283	66	62	3		
5	F	47	Total	C	N	O	S	0	0
			414	283	66	62	3		
5	I	47	Total	C	N	O	S	0	0
			414	283	66	62	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	47	Total 414	C 283	N 66	O 62	S 3	0	0
5	O	47	Total 414	C 283	N 66	O 62	S 3	0	0
5	Q	47	Total 414	C 283	N 66	O 62	S 3	0	0
5	S	47	Total 414	C 283	N 66	O 62	S 3	0	0
5	U	47	Total 414	C 283	N 66	O 62	S 3	0	0
5	W	47	Total 414	C 283	N 66	O 62	S 3	0	0
5	Y	46	Total 405	C 278	N 65	O 59	S 3	0	0
5	1	47	Total 414	C 283	N 66	O 62	S 3	0	0
5	3	46	Total 405	C 278	N 65	O 59	S 3	0	0
5	5	47	Total 414	C 283	N 66	O 62	S 3	0	0
5	7	47	Total 414	C 283	N 66	O 62	S 3	0	0
5	9	47	Total 414	C 283	N 66	O 62	S 3	0	0

- Molecule 6 is a protein called Light-harvesting complex 1 beta chain.

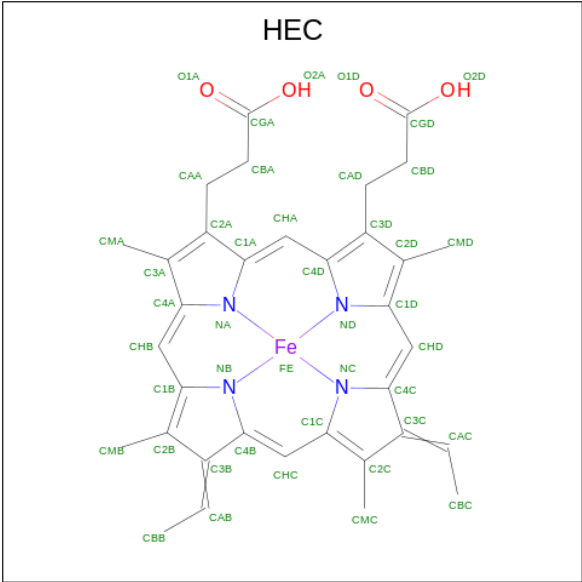
Mol	Chain	Residues	Atoms				AltConf	Trace
6	B	46	Total 374	C 252	N 59	O 63	0	0
6	E	47	Total 382	C 258	N 60	O 64	0	0
6	G	46	Total 374	C 252	N 59	O 63	0	0
6	J	45	Total 367	C 248	N 58	O 61	0	0
6	N	44	Total 363	C 246	N 57	O 60	0	0
6	P	45	Total 368	C 249	N 58	O 61	0	0
6	R	45	Total 367	C 248	N 58	O 61	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	T	45	Total 367	C 248	N 58	O 61	0	0
6	V	44	Total 363	C 246	N 57	O 60	0	0
6	X	46	Total 374	C 252	N 59	O 63	0	0
6	Z	45	Total 368	C 249	N 58	O 61	0	0
6	2	46	Total 374	C 252	N 59	O 63	0	0
6	4	45	Total 367	C 248	N 58	O 61	0	0
6	6	44	Total 363	C 246	N 57	O 60	0	0
6	8	44	Total 363	C 246	N 57	O 60	0	0
6	0	48	Total 386	C 260	N 61	O 65	0	0

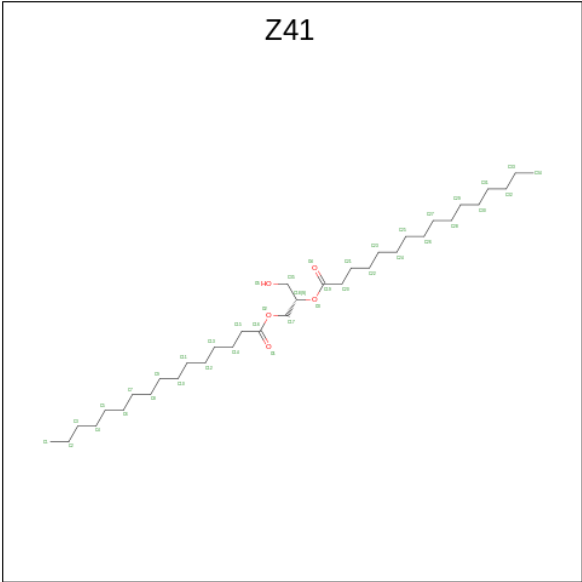
- # HEM

- Molecule 8 is HEME C (CCD ID: HEC) (formula: $\text{C}_{34}\text{H}_{34}\text{FeN}_4\text{O}_4$).



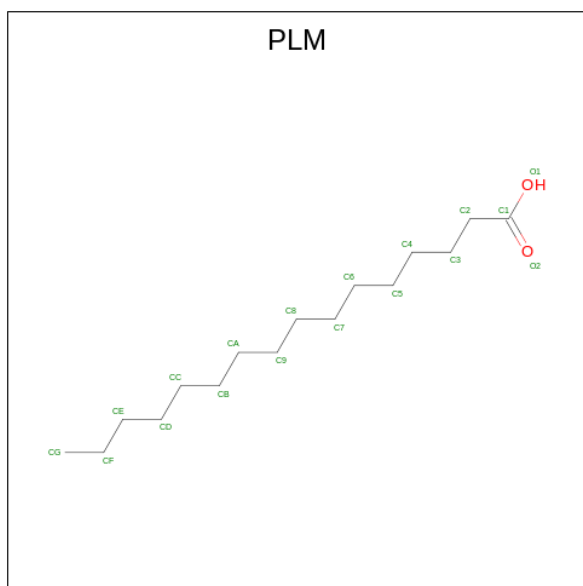
Mol	Chain	Residues	Atoms					AltConf
8	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
8	C	1	Total 43	C 34	Fe 1	N 4	O 4	0
8	C	1	Total 43	C 34	Fe 1	N 4	O 4	0

- Molecule 9 is (2S)-3-hydroxypropane-1,2-diyl dihexadecanoate (CCD ID: Z41) (formula: C₃₅H₆₈O₅).



Mol	Chain	Residues	Atoms			AltConf
9	C	1	Total	C	O	0
			26	22	4	

- Molecule 10 is PALMITIC ACID (CCD ID: PLM) (formula: $C_{16}H_{32}O_2$).



Mol	Chain	Residues	Atoms			AltConf
10	C	1	Total	C	O	0
			12	11	1	

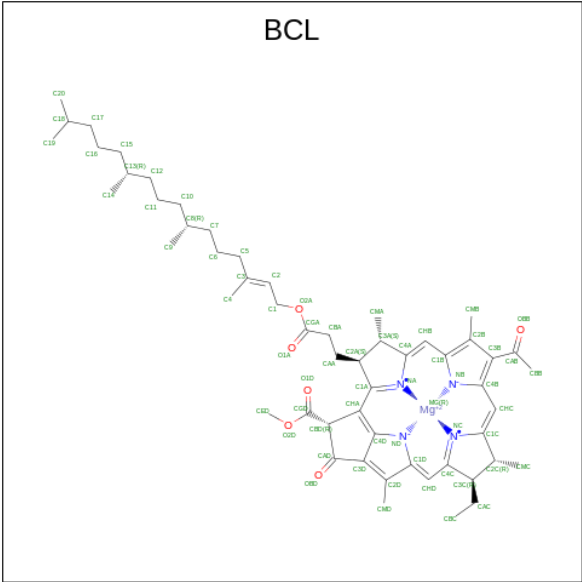
- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
11	C	2	Total	Mg	0
			2	2	

- Molecule 12 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
12	L	1	Total	Ca	0
			1	1	

- Molecule 13 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: $C_{55}H_{74}MgN_4O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
13	L	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	L	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	L	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	M	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	A	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	B	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	D	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	E	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	F	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	G	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	I	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	J	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	K	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	N	1	Total 66	C 55	Mg 1	N 4	O 6	0

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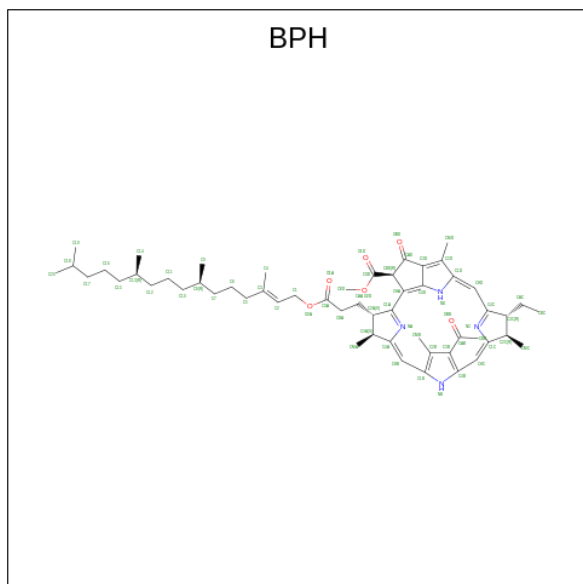
Mol	Chain	Residues	Atoms					AltConf
13	O	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	P	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	Q	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	R	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	S	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	T	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	U	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	V	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	W	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	X	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	Y	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	Z	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	1	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	2	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	4	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	5	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	6	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	7	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	8	1	Total 66	C 55	Mg 1	N 4	O 6	0
13	9	1	Total 66	C 55	Mg 1	N 4	O 6	0

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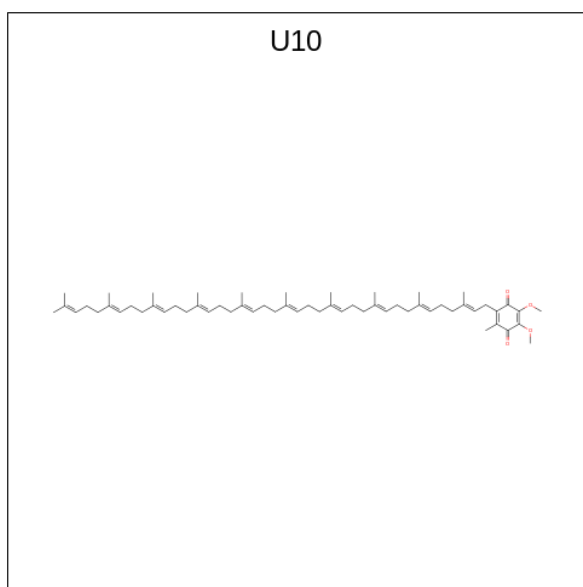
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	0	1	66	55	1	4	6	0

- Molecule 14 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$).



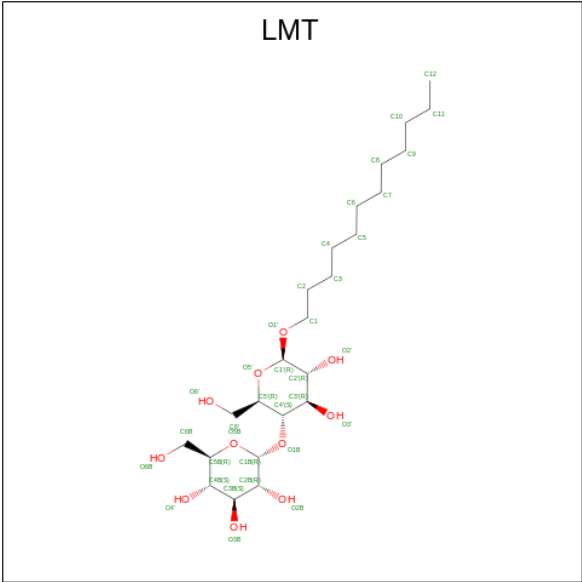
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
14	L	1	65	55	4	6	0
14	M	1	65	55	4	6	0

- Molecule 15 is UBIQUINONE-10 (CCD ID: U10) (formula: $C_{59}H_{90}O_4$).



Mol	Chain	Residues	Atoms			AltConf
15	L	1	Total	C	O	0
			33	29	4	
15	L	1	Total	C	O	0
			18	14	4	
15	L	1	Total	C	O	0
			30	26	4	
15	D	1	Total	C	O	0
			46	42	4	
15	U	1	Total	C	O	0
			18	14	4	
15	Y	1	Total	C	O	0
			20	16	4	
15	1	1	Total	C	O	0
			45	41	4	
15	7	1	Total	C	O	0
			53	49	4	

- Molecule 16 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula: C₂₄H₄₆O₁₁).



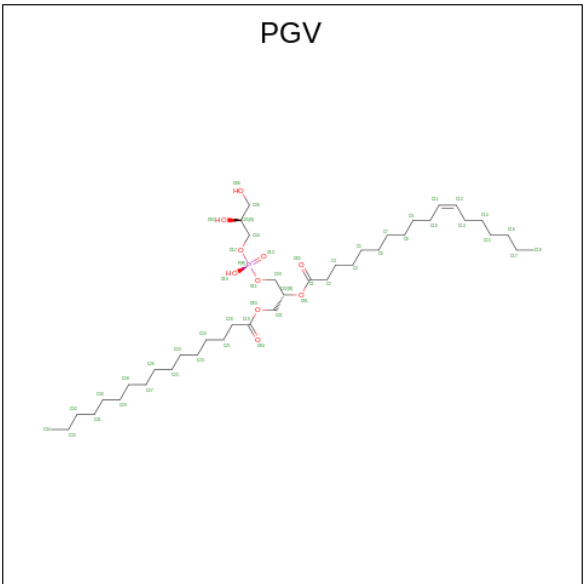
Mol	Chain	Residues	Atoms			AltConf
16	L	1	Total	C	O	0
			32	21	11	
16	M	1	Total	C	O	0
			31	20	11	
16	H	1	Total	C	O	0
			26	15	11	
16	B	1	Total	C	O	0
			34	23	11	
16	D	1	Total	C	O	0
			31	20	11	
16	E	1	Total	C	O	0
			35	24	11	
16	F	1	Total	C	O	0
			32	21	11	
16	J	1	Total	C	O	0
			30	19	11	
16	K	1	Total	C	O	0
			35	24	11	
16	O	1	Total	C	O	0
			35	24	11	
16	P	1	Total	C	O	0
			35	24	11	
16	T	1	Total	C	O	0
			35	24	11	
16	V	1	Total	C	O	0
			35	24	11	
16	X	1	Total	C	O	0
			34	23	11	

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Mol	Chain	Residues	Atoms			AltConf
16	Z	1	Total	C	O	0
			35	24	11	
16	Z	1	Total	C	O	0
			35	24	11	
16	4	1	Total	C	O	0
			35	24	11	
16	4	1	Total	C	O	0
			32	21	11	
16	5	1	Total	C	O	0
			30	19	11	
16	7	1	Total	C	O	0
			31	20	11	
16	9	1	Total	C	O	0
			25	14	11	

- Molecule 17 is (1R)-2-{{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (CCD ID: PGV) (formula: C₄₀H₇₇O₁₀P).



Mol	Chain	Residues	Atoms				AltConf
17	L	1	Total	C	O	P	0
			36	27	8	1	
17	L	1	Total	C	O	P	0
			51	40	10	1	
17	M	1	Total	C	O	P	0
			37	26	10	1	

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Mol	Chain	Residues	Atoms				AltConf
17	M	1	Total 29	C 18	O 10	P 1	0
17	M	1	Total 35	C 26	O 8	P 1	0
17	M	1	Total 20	C 9	O 10	P 1	0
17	H	1	Total 43	C 32	O 10	P 1	0
17	H	1	Total 43	C 32	O 10	P 1	0
17	H	1	Total 51	C 40	O 10	P 1	0
17	A	1	Total 17	C 8	O 8	P 1	0
17	B	1	Total 44	C 33	O 10	P 1	0
17	D	1	Total 40	C 29	O 10	P 1	0
17	E	1	Total 44	C 33	O 10	P 1	0
17	G	1	Total 44	C 33	O 10	P 1	0
17	J	1	Total 44	C 33	O 10	P 1	0
17	K	1	Total 46	C 35	O 10	P 1	0
17	N	1	Total 44	C 33	O 10	P 1	0
17	P	1	Total 44	C 33	O 10	P 1	0
17	R	1	Total 44	C 33	O 10	P 1	0
17	T	1	Total 44	C 33	O 10	P 1	0
17	V	1	Total 44	C 33	O 10	P 1	0
17	X	1	Total 44	C 33	O 10	P 1	0
17	2	1	Total 44	C 33	O 10	P 1	0
17	2	1	Total 44	C 33	O 10	P 1	0

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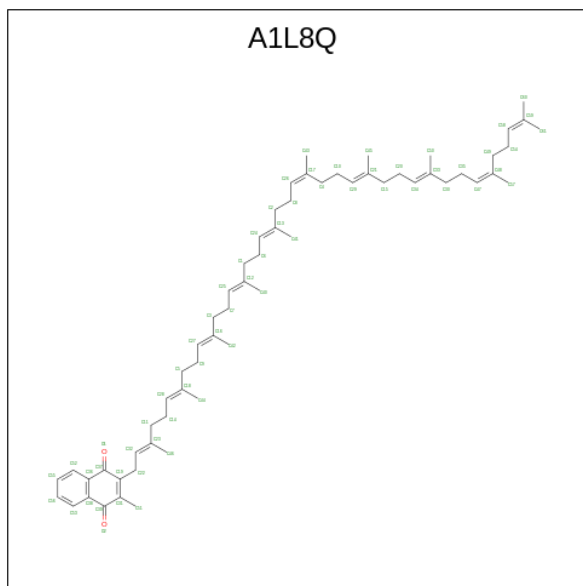
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Mol	Chain	Residues	Atoms				AltConf
17	4	1	Total	C	O	P	0
			44	33	10	1	
17	8	1	Total	C	O	P	0
			44	33	10	1	
17	8	1	Total	C	O	P	0
			44	33	10	1	
17	0	1	Total	C	O	P	0
			44	33	10	1	

- Molecule 18 is FE (III) ION (CCD ID: FE) (formula: Fe).

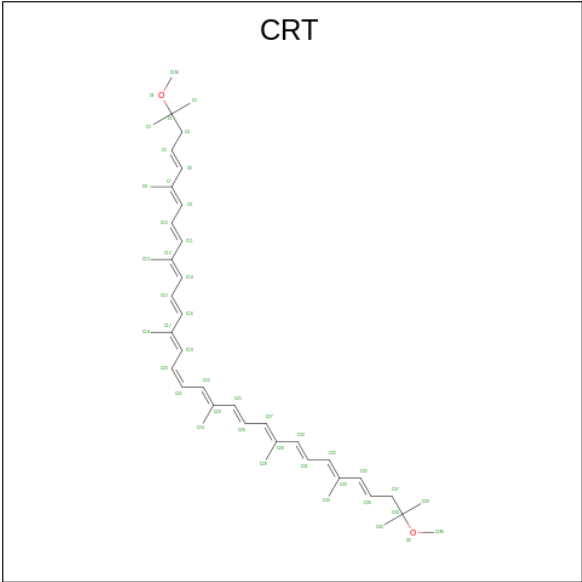
Mol	Chain	Residues	Atoms		AltConf
18	M	1	Total	Fe	0
			1	1	

- Molecule 19 is Menaquinone 10 (CCD ID: A1L8Q) (formula: C₆₁H₈₈O₂).



Mol	Chain	Residues	Atoms			AltConf
19	M	1	Total	C	O	0
			63	61	2	

- Molecule 20 is SPIRILLOXANTHIN (CCD ID: CRT) (formula: C₄₂H₆₀O₂).



Mol	Chain	Residues	Atoms			AltConf
20	M	1	Total	C	O	0
			44	42	2	
20	B	1	Total	C	O	0
			44	42	2	
20	E	1	Total	C	O	0
			44	42	2	
20	G	1	Total	C	O	0
			44	42	2	
20	J	1	Total	C	O	0
			44	42	2	
20	N	1	Total	C	O	0
			44	42	2	
20	P	1	Total	C	O	0
			44	42	2	
20	R	1	Total	C	O	0
			44	42	2	
20	T	1	Total	C	O	0
			44	42	2	
20	V	1	Total	C	O	0
			44	42	2	
20	Y	1	Total	C	O	0
			44	42	2	
20	Z	1	Total	C	O	0
			44	42	2	
20	2	1	Total	C	O	0
			44	42	2	
20	4	1	Total	C	O	0
			44	42	2	

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Mol	Chain	Residues	Atoms			AltConf
20	6	1	Total	C	O	0
			44	42	2	
20	8	1	Total	C	O	0
			44	42	2	
20	0	1	Total	C	O	0
			44	42	2	

- Molecule 21 is water.

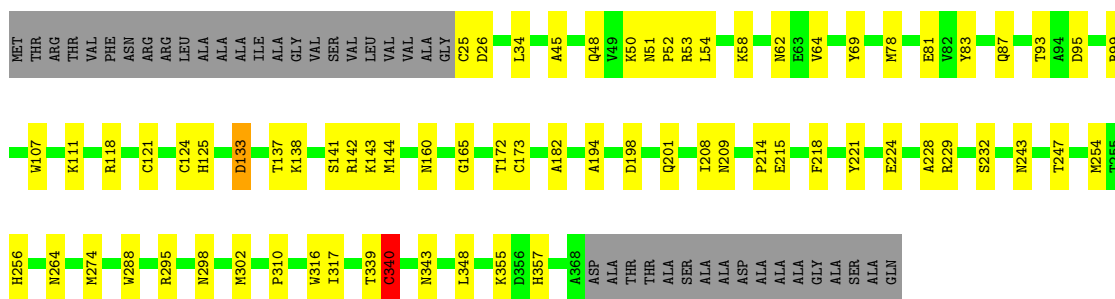
Mol	Chain	Residues	Atoms		AltConf
21	C	47	Total	O	0
			47	47	
21	L	19	Total	O	0
			19	19	
21	M	24	Total	O	0
			24	24	
21	H	5	Total	O	0
			5	5	
21	A	1	Total	O	0
			1	1	
21	D	1	Total	O	0
			1	1	
21	S	1	Total	O	0
			1	1	
21	W	1	Total	O	0
			1	1	

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.

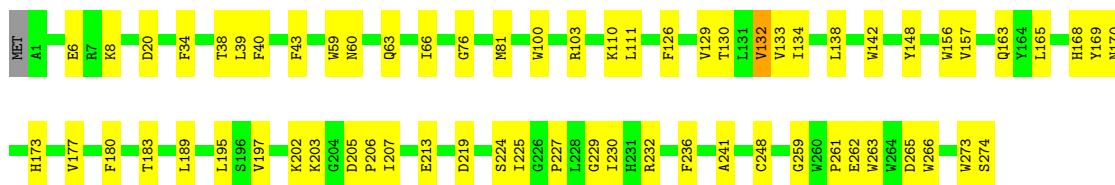
- Molecule 1: Photosynthetic reaction center cytochrome c subunit

Chain C: 



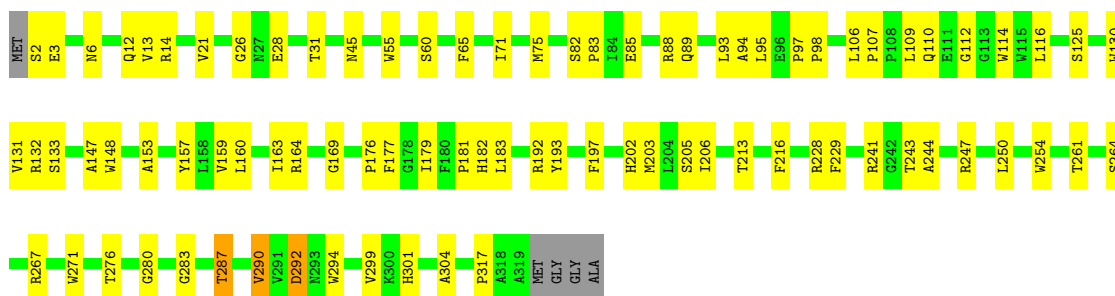
- Molecule 2: Reaction center protein L chain

Chain L: 



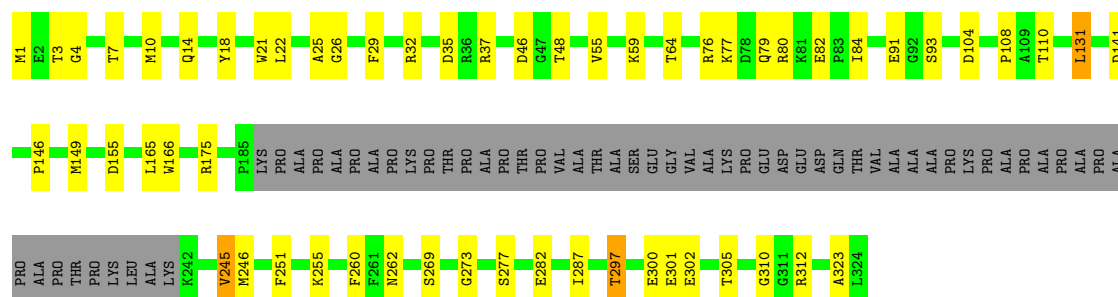
- Molecule 3: Reaction center protein M chain

Chain M: 



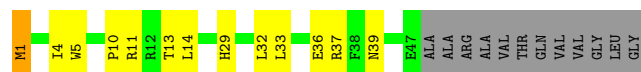
- Molecule 4: Photosynthetic reaction center subunit H

Chain H:  65% 17% 17%



- Molecule 5: Light-harvesting complex 1 alpha chain

Chain A:  58% 20% 20%



- Molecule 5: Light-harvesting complex 1 alpha chain

Chain D:  63% 15% 20%



- Molecule 5: Light-harvesting complex 1 alpha chain

Chain F:  58% 20% 20%



- Molecule 5: Light-harvesting complex 1 alpha chain

Chain I:  61% 19% 20%



- Molecule 5: Light-harvesting complex 1 alpha chain

Chain K:  56% 22% 20%

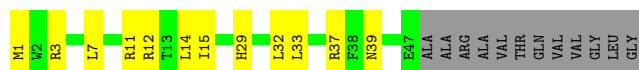


- Molecule 5: Light-harvesting complex 1 alpha chain

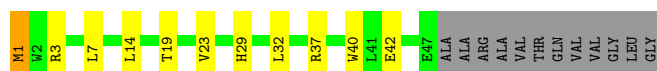
Chain O:  54% 24% 20%



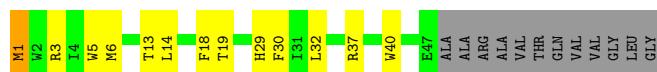
- Molecule 5: Light-harvesting complex 1 alpha chain



- Molecule 5: Light-harvesting complex 1 alpha chain



- Molecule 5: Light-harvesting complex 1 alpha chain



- Molecule 5: Light-harvesting complex 1 alpha chain



- Molecule 5: Light-harvesting complex 1 alpha chain



- Molecule 5: Light-harvesting complex 1 alpha chain



- Molecule 5: Light-harvesting complex 1 alpha chain





- Molecule 5: Light-harvesting complex 1 alpha chain



- Molecule 5: Light-harvesting complex 1 alpha chain



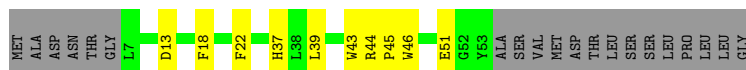
- Molecule 5: Light-harvesting complex 1 alpha chain



- Molecule 6: Light-harvesting complex 1 beta chain



- Molecule 6: Light-harvesting complex 1 beta chain



- Molecule 6: Light-harvesting complex 1 beta chain



- Molecule 6: Light-harvesting complex 1 beta chain





- Molecule 6: Light-harvesting complex 1 beta chain

Chain N: 46% 19% 34%



- Molecule 6: Light-harvesting complex 1 beta chain

Chain P: 43% 24% 33%



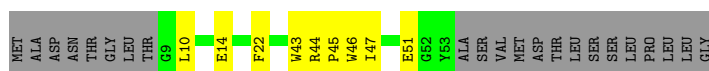
- Molecule 6: Light-harvesting complex 1 beta chain

Chain R: 49% 18% 33%



- Molecule 6: Light-harvesting complex 1 beta chain

Chain T: 54% 13% 33%



- Molecule 6: Light-harvesting complex 1 beta chain

Chain V: 54% 12% 34%



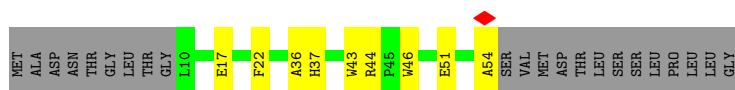
- Molecule 6: Light-harvesting complex 1 beta chain

Chain X: 54% 15% 31%



- Molecule 6: Light-harvesting complex 1 beta chain

Chain Z: 54% 13% 33%



- Molecule 6: Light-harvesting complex 1 beta chain



- Molecule 6: Light-harvesting complex 1 beta chain



- Molecule 6: Light-harvesting complex 1 beta chain



- Molecule 6: Light-harvesting complex 1 beta chain



- Molecule 6: Light-harvesting complex 1 beta chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	229234	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.250	Depositor
Minimum map value	-0.096	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.015	Depositor
Map size (\AA)	311.6, 311.6, 311.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: LMT, CRT, PGV, FE, HEC, Z41, U10, CA, MG, HEM, BCL, BPH, PLM, A1L8Q, FME

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	C	0.15	0/2750	0.37	1/3759 (0.0%)
2	L	0.11	0/2263	0.28	0/3093
3	M	0.11	0/2617	0.26	0/3592
4	H	0.10	0/2165	0.27	0/2940
5	1	0.09	0/418	0.21	0/567
5	3	0.09	0/409	0.23	0/555
5	5	0.11	0/418	0.26	0/567
5	7	0.11	0/418	0.29	0/567
5	9	0.11	0/418	0.25	0/567
5	A	0.09	0/418	0.22	0/567
5	D	0.09	0/418	0.22	0/567
5	F	0.09	0/418	0.22	0/567
5	I	0.09	0/418	0.24	0/567
5	K	0.08	0/418	0.22	0/567
5	O	0.10	0/418	0.25	0/567
5	Q	0.10	0/418	0.23	0/567
5	S	0.10	0/418	0.23	0/567
5	U	0.09	0/418	0.22	0/567
5	W	0.10	0/418	0.23	0/567
5	Y	0.10	0/409	0.24	0/555
6	0	0.11	0/401	0.29	0/547
6	2	0.10	0/389	0.23	0/531
6	4	0.08	0/382	0.22	0/521
6	6	0.10	0/378	0.29	0/516
6	8	0.10	0/378	0.25	0/516
6	B	0.10	0/389	0.25	0/531
6	E	0.09	0/397	0.23	0/542
6	G	0.10	0/389	0.24	0/531
6	J	0.10	0/382	0.22	0/521
6	N	0.11	0/378	0.27	0/516
6	P	0.10	0/383	0.26	0/523
6	R	0.11	0/382	0.32	0/521

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	T	0.11	0/382	0.27	0/521
6	V	0.08	0/378	0.24	0/516
6	X	0.08	0/389	0.21	0/531
6	Z	0.09	0/383	0.21	0/523
All	All	0.11	0/22625	0.27	1/30839 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	340	CYS	CA-CB-SG	8.35	133.60	114.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	340	CYS	Peptide

5.2 Too-close contacts ⓘ

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	C	2675	0	2496	56	0
2	L	2175	0	2131	58	0
3	M	2518	0	2464	69	0
4	H	2109	0	2052	42	0
5	1	414	0	417	11	0
5	3	405	0	411	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	5	414	0	417	12	0
5	7	414	0	417	14	0
5	9	414	0	417	16	0
5	A	414	0	417	9	0
5	D	414	0	417	12	0
5	F	414	0	417	11	0
5	I	414	0	417	9	0
5	K	414	0	417	15	0
5	O	414	0	417	18	0
5	Q	414	0	417	12	0
5	S	414	0	417	13	0
5	U	414	0	417	13	0
5	W	414	0	417	12	0
5	Y	405	0	411	17	0
6	0	386	0	374	16	0
6	2	374	0	360	9	0
6	4	367	0	353	13	0
6	6	363	0	350	12	0
6	8	363	0	350	13	0
6	B	374	0	360	14	0
6	E	382	0	371	13	0
6	G	374	0	360	9	0
6	J	367	0	353	10	0
6	N	363	0	350	17	0
6	P	368	0	355	13	0
6	R	367	0	353	11	0
6	T	367	0	353	9	0
6	V	363	0	350	11	0
6	X	374	0	360	14	0
6	Z	368	0	355	9	0
7	C	43	0	30	8	0
8	C	129	0	90	3	0
9	C	26	0	0	1	0
10	C	12	0	18	0	0
11	C	2	0	0	0	0
12	L	1	0	0	0	0
13	0	66	0	74	7	0
13	1	66	0	74	4	0
13	2	66	0	74	5	0
13	3	66	0	74	4	0
13	4	66	0	74	4	0
13	5	66	0	74	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	6	66	0	74	6	0
13	7	66	0	74	3	0
13	8	66	0	74	8	0
13	9	66	0	74	5	0
13	A	66	0	74	3	0
13	B	66	0	74	7	0
13	D	66	0	74	3	0
13	E	66	0	74	6	0
13	F	66	0	74	5	0
13	G	66	0	74	7	0
13	I	66	0	74	6	0
13	J	66	0	74	3	0
13	K	66	0	74	4	0
13	L	198	0	222	10	0
13	M	66	0	74	9	0
13	N	66	0	74	5	0
13	O	66	0	74	3	0
13	P	66	0	74	6	0
13	Q	66	0	74	3	0
13	R	66	0	74	5	0
13	S	66	0	74	3	0
13	T	66	0	74	8	0
13	U	66	0	74	5	0
13	V	66	0	74	7	0
13	W	66	0	74	7	0
13	X	66	0	74	7	0
13	Y	66	0	74	3	0
13	Z	66	0	74	5	0
14	L	65	0	76	1	0
14	M	65	0	76	5	0
15	1	45	0	59	2	0
15	7	53	0	71	7	0
15	D	46	0	60	3	0
15	L	81	0	89	16	0
15	U	18	0	15	0	0
15	Y	20	0	19	3	0
16	4	67	0	83	3	0
16	5	30	0	33	4	0
16	7	31	0	35	7	0
16	9	25	0	23	0	0
16	B	34	0	41	0	0
16	D	31	0	35	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	E	35	0	46	0	0
16	F	32	0	37	0	0
16	H	26	0	25	3	0
16	J	30	0	33	0	0
16	K	35	0	46	1	0
16	L	32	0	37	2	0
16	M	31	0	35	3	0
16	O	35	0	46	2	0
16	P	35	0	46	2	0
16	T	35	0	46	0	0
16	V	35	0	46	0	0
16	X	34	0	41	1	0
16	Z	70	0	92	1	0
17	0	44	0	56	7	0
17	2	88	0	112	8	0
17	4	44	0	56	3	0
17	8	88	0	112	10	0
17	A	17	0	12	2	0
17	B	44	0	56	6	0
17	D	40	0	50	2	0
17	E	44	0	56	4	0
17	G	44	0	56	2	0
17	H	137	0	187	11	0
17	J	44	0	56	5	0
17	K	46	0	63	4	0
17	L	87	0	122	6	0
17	M	121	0	125	6	0
17	N	44	0	56	3	0
17	P	44	0	56	3	0
17	R	44	0	56	2	0
17	T	44	0	56	5	0
17	V	44	0	56	5	0
17	X	44	0	56	5	0
18	M	1	0	0	0	0
19	M	63	0	0	0	0
20	0	44	0	60	3	0
20	2	44	0	60	3	0
20	4	44	0	60	5	0
20	6	44	0	60	12	0
20	8	44	0	60	7	0
20	B	44	0	60	4	0
20	E	44	0	60	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	G	44	0	60	4	0
20	J	44	0	60	5	0
20	M	44	0	60	5	0
20	N	44	0	60	7	0
20	P	44	0	60	4	0
20	R	44	0	60	5	0
20	T	44	0	60	7	0
20	V	44	0	60	11	0
20	Y	44	0	60	5	0
20	Z	44	0	60	4	0
21	A	1	0	0	0	0
21	C	47	0	0	2	0
21	D	1	0	0	0	0
21	H	5	0	0	0	0
21	L	19	0	0	1	0
21	M	24	0	0	0	0
21	S	1	0	0	0	0
21	W	1	0	0	0	0
All	All	27731	0	28078	690	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 12.

The worst 5 of 690 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:C:124:CYS:SG	7:C:401:HEM:HAC	1.82	1.20
1:C:124:CYS:SG	7:C:401:HEM:CAC	2.43	1.06
1:C:198:ASP:OD1	21:C:501:HOH:O	1.88	0.89
3:M:287:THR:HB	3:M:294:TRP:HE1	1.46	0.79
4:H:297:THR:HG22	4:H:300:GLU:H	1.50	0.76

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	342/385 (89%)	329 (96%)	13 (4%)	0	100	100
2	L	272/275 (99%)	265 (97%)	7 (3%)	0	100	100
3	M	316/323 (98%)	310 (98%)	6 (2%)	0	100	100
4	H	264/324 (82%)	258 (98%)	6 (2%)	0	100	100
5	1	45/59 (76%)	44 (98%)	1 (2%)	0	100	100
5	3	44/59 (75%)	43 (98%)	1 (2%)	0	100	100
5	5	45/59 (76%)	45 (100%)	0	0	100	100
5	7	45/59 (76%)	44 (98%)	1 (2%)	0	100	100
5	9	45/59 (76%)	45 (100%)	0	0	100	100
5	A	45/59 (76%)	45 (100%)	0	0	100	100
5	D	45/59 (76%)	44 (98%)	1 (2%)	0	100	100
5	F	45/59 (76%)	43 (96%)	2 (4%)	0	100	100
5	I	45/59 (76%)	45 (100%)	0	0	100	100
5	K	45/59 (76%)	44 (98%)	1 (2%)	0	100	100
5	O	45/59 (76%)	45 (100%)	0	0	100	100
5	Q	45/59 (76%)	45 (100%)	0	0	100	100
5	S	45/59 (76%)	43 (96%)	2 (4%)	0	100	100
5	U	45/59 (76%)	45 (100%)	0	0	100	100
5	W	45/59 (76%)	45 (100%)	0	0	100	100
5	Y	44/59 (75%)	44 (100%)	0	0	100	100
6	0	46/67 (69%)	44 (96%)	2 (4%)	0	100	100
6	2	44/67 (66%)	42 (96%)	2 (4%)	0	100	100
6	4	43/67 (64%)	42 (98%)	1 (2%)	0	100	100
6	6	42/67 (63%)	39 (93%)	3 (7%)	0	100	100
6	8	42/67 (63%)	39 (93%)	3 (7%)	0	100	100
6	B	44/67 (66%)	41 (93%)	3 (7%)	0	100	100
6	E	45/67 (67%)	42 (93%)	3 (7%)	0	100	100
6	G	44/67 (66%)	41 (93%)	3 (7%)	0	100	100
6	J	43/67 (64%)	41 (95%)	2 (5%)	0	100	100
6	N	42/67 (63%)	39 (93%)	3 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	P	43/67 (64%)	41 (95%)	2 (5%)	0	100	100
6	R	43/67 (64%)	40 (93%)	3 (7%)	0	100	100
6	T	43/67 (64%)	40 (93%)	3 (7%)	0	100	100
6	V	42/67 (63%)	39 (93%)	3 (7%)	0	100	100
6	X	44/67 (66%)	41 (93%)	3 (7%)	0	100	100
6	Z	43/67 (64%)	40 (93%)	3 (7%)	0	100	100
All	All	2605/3323 (78%)	2522 (97%)	83 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	289/313 (92%)	286 (99%)	3 (1%)	73	85
2	L	218/219 (100%)	213 (98%)	5 (2%)	45	63
3	M	251/253 (99%)	242 (96%)	9 (4%)	30	44
4	H	219/258 (85%)	213 (97%)	6 (3%)	40	57
5	1	42/49 (86%)	41 (98%)	1 (2%)	44	61
5	3	41/49 (84%)	41 (100%)	0	100	100
5	5	42/49 (86%)	41 (98%)	1 (2%)	44	61
5	7	42/49 (86%)	42 (100%)	0	100	100
5	9	42/49 (86%)	40 (95%)	2 (5%)	21	32
5	A	42/49 (86%)	41 (98%)	1 (2%)	44	61
5	D	42/49 (86%)	42 (100%)	0	100	100
5	F	42/49 (86%)	42 (100%)	0	100	100
5	I	42/49 (86%)	42 (100%)	0	100	100
5	K	42/49 (86%)	42 (100%)	0	100	100
5	O	42/49 (86%)	41 (98%)	1 (2%)	44	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	Q	42/49 (86%)	42 (100%)	0	100	100
5	S	42/49 (86%)	42 (100%)	0	100	100
5	U	42/49 (86%)	42 (100%)	0	100	100
5	W	42/49 (86%)	42 (100%)	0	100	100
5	Y	41/49 (84%)	41 (100%)	0	100	100
6	0	39/55 (71%)	38 (97%)	1 (3%)	41	58
6	2	38/55 (69%)	38 (100%)	0	100	100
6	4	37/55 (67%)	37 (100%)	0	100	100
6	6	37/55 (67%)	35 (95%)	2 (5%)	18	27
6	8	37/55 (67%)	35 (95%)	2 (5%)	18	27
6	B	38/55 (69%)	38 (100%)	0	100	100
6	E	39/55 (71%)	39 (100%)	0	100	100
6	G	38/55 (69%)	38 (100%)	0	100	100
6	J	37/55 (67%)	37 (100%)	0	100	100
6	N	37/55 (67%)	37 (100%)	0	100	100
6	P	37/55 (67%)	37 (100%)	0	100	100
6	R	37/55 (67%)	37 (100%)	0	100	100
6	T	37/55 (67%)	37 (100%)	0	100	100
6	V	37/55 (67%)	37 (100%)	0	100	100
6	X	38/55 (69%)	37 (97%)	1 (3%)	41	58
6	Z	37/55 (67%)	37 (100%)	0	100	100
All	All	2247/2707 (83%)	2212 (98%)	35 (2%)	58	74

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	6	17	GLU
6	6	25	SER
5	9	26	ILE
3	M	131	VAL
3	M	31	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
5	U	44	ASN
6	4	24	GLN
6	0	24	GLN
6	8	24	GLN
6	2	24	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

16 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
5	FME	1	1	5	8,9,10	0.51	0	7,9,11	0.95	1 (14%)
5	FME	S	1	5	8,9,10	0.50	0	7,9,11	1.12	1 (14%)
5	FME	7	1	5	8,9,10	0.52	0	7,9,11	0.98	1 (14%)
5	FME	O	1	5	8,9,10	0.51	0	7,9,11	1.02	1 (14%)
5	FME	I	1	5	8,9,10	0.50	0	7,9,11	1.11	1 (14%)
5	FME	U	1	5	8,9,10	0.52	0	7,9,11	0.96	1 (14%)
5	FME	A	1	5	8,9,10	0.49	0	7,9,11	1.13	1 (14%)
5	FME	F	1	5	8,9,10	0.51	0	7,9,11	0.98	1 (14%)
5	FME	W	1	5	8,9,10	0.49	0	7,9,11	1.10	1 (14%)
5	FME	3	1	5	8,9,10	0.51	0	7,9,11	1.01	1 (14%)
5	FME	5	1	5	8,9,10	0.50	0	7,9,11	1.02	1 (14%)
5	FME	9	1	5	8,9,10	0.52	0	7,9,11	0.89	1 (14%)
5	FME	Y	1	5	8,9,10	0.47	0	7,9,11	1.16	1 (14%)
5	FME	Q	1	5	8,9,10	0.53	0	7,9,11	0.96	1 (14%)
5	FME	D	1	5	8,9,10	0.48	0	7,9,11	1.12	1 (14%)
5	FME	K	1	5	8,9,10	0.51	0	7,9,11	1.09	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FME	1	1	5	-	2/7/9/11	-
5	FME	S	1	5	-	0/7/9/11	-
5	FME	7	1	5	-	0/7/9/11	-
5	FME	O	1	5	-	3/7/9/11	-
5	FME	I	1	5	-	0/7/9/11	-
5	FME	U	1	5	-	0/7/9/11	-
5	FME	A	1	5	-	2/7/9/11	-
5	FME	F	1	5	-	1/7/9/11	-
5	FME	W	1	5	-	1/7/9/11	-
5	FME	3	1	5	-	0/7/9/11	-
5	FME	5	1	5	-	0/7/9/11	-
5	FME	9	1	5	-	2/7/9/11	-
5	FME	Y	1	5	-	1/7/9/11	-
5	FME	Q	1	5	-	2/7/9/11	-
5	FME	D	1	5	-	2/7/9/11	-
5	FME	K	1	5	-	1/7/9/11	-

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	Y	1	FME	O-C-CA	-2.77	117.51	124.78
5	A	1	FME	O-C-CA	-2.69	117.73	124.78
5	I	1	FME	O-C-CA	-2.69	117.73	124.78
5	D	1	FME	O-C-CA	-2.69	117.74	124.78
5	S	1	FME	O-C-CA	-2.68	117.74	124.78

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	1	FME	C-CA-CB-CG
5	F	1	FME	O1-CN-N-CA
5	K	1	FME	CA-CB-CG-SD
5	O	1	FME	O1-CN-N-CA
5	O	1	FME	N-CA-CB-CG

There are no ring outliers.

10 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	1	1	FME	1	0
5	S	1	FME	1	0
5	O	1	FME	1	0
5	U	1	FME	1	0
5	A	1	FME	1	0
5	F	1	FME	1	0
5	3	1	FME	2	0
5	Y	1	FME	2	0
5	D	1	FME	3	0
5	K	1	FME	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 123 ligands modelled in this entry, 4 are monoatomic - leaving 119 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
16	LMT	E	104	-	36,36,36	0.42	0	47,47,47	0.72	1 (2%)
13	BCL	T	102	6	64,74,74	1.67	14 (21%)	78,115,115	2.22	20 (25%)
17	PGV	V	103	-	43,43,50	0.99	2 (4%)	45,49,56	1.11	3 (6%)
20	CRT	J	101	-	41,43,43	0.72	0	50,54,54	1.81	16 (32%)
20	CRT	Z	101	-	41,43,43	0.72	0	50,54,54	1.88	13 (26%)
20	CRT	P	101	-	41,43,43	0.71	0	50,54,54	1.79	15 (30%)
13	BCL	A	102	5	64,74,74	1.70	14 (21%)	78,115,115	2.35	21 (26%)
13	BCL	6	102	6	64,74,74	1.68	13 (20%)	78,115,115	2.19	20 (25%)
20	CRT	T	101	-	41,43,43	0.72	0	50,54,54	1.83	13 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
13	BCL	1	101	5	64,74,74	1.70	14 (21%)	78,115,115	2.25	20 (25%)
13	BCL	D	102	5	64,74,74	1.70	14 (21%)	78,115,115	2.26	20 (25%)
16	LMT	O	102	-	36,36,36	0.45	0	47,47,47	0.73	1 (2%)
13	BCL	R	102	6	64,74,74	1.68	14 (21%)	78,115,115	2.17	19 (24%)
13	BCL	X	101	6	64,74,74	1.67	14 (21%)	78,115,115	2.19	19 (24%)
13	BCL	S	101	5	64,74,74	1.70	14 (21%)	78,115,115	2.34	22 (28%)
8	HEC	C	402	1	32,50,50	1.54	4 (12%)	24,82,82	1.51	5 (20%)
17	PGV	H	401	-	42,42,50	0.99	2 (4%)	45,48,56	1.16	3 (6%)
17	PGV	N	103	-	43,43,50	0.99	2 (4%)	45,49,56	1.03	3 (6%)
17	PGV	4	103	-	43,43,50	0.99	2 (4%)	45,49,56	1.07	3 (6%)
13	BCL	Q	101	5	64,74,74	1.70	14 (21%)	78,115,115	2.29	18 (23%)
15	U10	D	104	-	46,46,63	0.70	2 (4%)	55,58,79	0.69	0
13	BCL	0	102	6	64,74,74	1.69	14 (21%)	78,115,115	2.23	19 (24%)
17	PGV	P	103	-	43,43,50	1.00	2 (4%)	45,49,56	1.12	4 (8%)
16	LMT	7	103	-	32,32,36	0.42	0	43,43,47	1.14	4 (9%)
13	BCL	M	402	3	64,74,74	1.71	14 (21%)	78,115,115	2.32	21 (26%)
17	PGV	G	103	-	43,43,50	0.99	2 (4%)	45,49,56	1.02	2 (4%)
17	PGV	A	101	-	16,16,50	0.54	0	17,20,56	0.74	0
13	BCL	K	101	5	64,74,74	1.70	14 (21%)	78,115,115	2.28	19 (24%)
17	PGV	B	103	-	43,43,50	0.99	2 (4%)	45,49,56	1.12	4 (8%)
16	LMT	4	105	-	33,33,36	0.43	0	44,44,47	0.65	1 (2%)
16	LMT	M	409	-	32,32,36	0.43	0	43,43,47	0.80	1 (2%)
16	LMT	5	401	-	31,31,36	0.42	0	42,42,47	0.69	1 (2%)
15	U10	Y	103	-	20,20,63	0.98	2 (10%)	24,27,79	0.91	0
20	CRT	E	101	-	41,43,43	0.72	0	50,54,54	1.76	14 (28%)
20	CRT	R	101	-	41,43,43	0.72	0	50,54,54	1.77	13 (26%)
10	PLM	C	406	1	11,11,17	0.39	0	10,10,17	0.46	0
13	BCL	F	101	5	64,74,74	1.69	14 (21%)	78,115,115	2.28	19 (24%)
16	LMT	D	103	-	32,32,36	0.42	0	43,43,47	0.78	1 (2%)
17	PGV	8	101	-	43,43,50	0.98	2 (4%)	45,49,56	1.02	2 (4%)
13	BCL	7	102	5	64,74,74	1.69	14 (21%)	78,115,115	2.26	22 (28%)
13	BCL	V	102	6	64,74,74	1.67	13 (20%)	78,115,115	2.17	19 (24%)
13	BCL	B	102	6	64,74,74	1.67	14 (21%)	78,115,115	2.20	19 (24%)
15	U10	L	308	-	18,18,63	1.07	2 (11%)	22,25,79	0.73	0
13	BCL	3	101	5	64,74,74	1.72	14 (21%)	78,115,115	2.21	20 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
14	BPH	L	303	-	51,70,70	0.53	0	52,101,101	0.61	0
20	CRT	6	101	-	41,43,43	0.71	0	50,54,54	2.09	16 (32%)
20	CRT	G	101	-	41,43,43	0.71	0	50,54,54	1.77	14 (28%)
15	U10	7	101	-	53,53,63	0.60	2 (3%)	64,67,79	0.52	0
16	LMT	F	102	-	33,33,36	0.44	0	44,44,47	0.72	1 (2%)
20	CRT	Y	101	-	41,43,43	0.72	0	50,54,54	1.77	14 (28%)
13	BCL	I	101	5	64,74,74	1.71	14 (21%)	78,115,115	2.28	20 (25%)
13	BCL	J	102	6	64,74,74	1.68	13 (20%)	78,115,115	2.17	19 (24%)
17	PGV	E	103	-	43,43,50	0.99	2 (4%)	45,49,56	1.06	3 (6%)
17	PGV	K	102	-	45,45,50	0.97	2 (4%)	48,51,56	0.99	2 (4%)
13	BCL	P	102	6	64,74,74	1.68	14 (21%)	78,115,115	2.21	20 (25%)
17	PGV	R	103	-	43,43,50	0.99	2 (4%)	45,49,56	1.01	2 (4%)
13	BCL	G	102	6	64,74,74	1.68	13 (20%)	78,115,115	2.19	19 (24%)
17	PGV	2	104	-	43,43,50	0.99	2 (4%)	45,49,56	1.11	3 (6%)
20	CRT	M	405	-	41,43,43	0.71	0	50,54,54	3.42	14 (28%)
13	BCL	4	102	6	64,74,74	1.69	14 (21%)	78,115,115	2.19	19 (24%)
16	LMT	T	104	-	36,36,36	0.38	0	47,47,47	0.69	1 (2%)
17	PGV	M	408	-	34,34,50	1.15	2 (5%)	37,39,56	1.28	4 (10%)
13	BCL	W	101	5	64,74,74	1.71	14 (21%)	78,115,115	2.29	23 (29%)
17	PGV	L	306	-	35,35,50	1.13	2 (5%)	39,40,56	1.16	3 (7%)
17	PGV	M	410	-	19,19,50	1.70	3 (15%)	20,24,56	1.36	1 (5%)
13	BCL	U	102	5	64,74,74	1.71	14 (21%)	78,115,115	2.20	21 (26%)
17	PGV	8	104	-	43,43,50	0.98	2 (4%)	45,49,56	1.08	3 (6%)
20	CRT	N	101	-	41,43,43	0.71	0	50,54,54	1.84	13 (26%)
20	CRT	B	101	-	41,43,43	0.71	0	50,54,54	1.89	15 (30%)
14	BPH	M	403	-	51,70,70	0.51	1 (1%)	52,101,101	0.65	0
16	LMT	H	402	-	27,27,36	0.46	0	37,38,47	0.81	1 (2%)
17	PGV	H	403	-	42,42,50	1.00	2 (4%)	45,48,56	1.13	3 (6%)
15	U10	L	309	-	30,30,63	0.79	1 (3%)	36,39,79	0.71	0
20	CRT	V	101	-	41,43,43	0.72	0	50,54,54	1.96	14 (28%)
15	U10	U	101	-	18,18,63	1.04	2 (11%)	22,25,79	0.85	0
16	LMT	4	104	-	36,36,36	0.41	0	47,47,47	0.82	1 (2%)
13	BCL	L	302	2	64,74,74	1.68	14 (21%)	78,115,115	2.32	22 (28%)
16	LMT	P	104	-	36,36,36	0.41	0	47,47,47	0.73	1 (2%)
17	PGV	L	307	-	50,50,50	0.91	2 (4%)	53,56,56	0.99	3 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
17	PGV	J	103	-	43,43,50	0.98	2 (4%)	45,49,56	0.98	2 (4%)
17	PGV	X	102	-	43,43,50	0.99	2 (4%)	45,49,56	0.97	2 (4%)
13	BCL	L	310	2	64,74,74	1.69	13 (20%)	78,115,115	2.25	21 (26%)
15	U10	1	102	-	45,45,63	0.67	2 (4%)	54,57,79	0.53	0
16	LMT	K	103	-	36,36,36	0.44	0	47,47,47	0.80	0
13	BCL	Z	102	6	64,74,74	1.68	13 (20%)	78,115,115	2.19	20 (25%)
16	LMT	J	104	-	31,31,36	0.45	0	42,42,47	0.75	1 (2%)
16	LMT	Z	103	-	36,36,36	0.46	0	47,47,47	1.14	3 (6%)
16	LMT	Z	104	-	36,36,36	0.40	0	47,47,47	0.79	1 (2%)
20	CRT	0	101	-	41,43,43	0.70	0	50,54,54	1.75	12 (24%)
15	U10	L	304	-	33,33,63	0.78	2 (6%)	40,43,79	0.81	0
17	PGV	M	407	-	28,28,50	1.21	2 (7%)	31,34,56	1.24	3 (9%)
17	PGV	T	103	-	43,43,50	0.99	2 (4%)	45,49,56	1.12	3 (6%)
13	BCL	2	103	6	64,74,74	1.69	13 (20%)	78,115,115	2.21	18 (23%)
20	CRT	2	102	-	41,43,43	0.72	0	50,54,54	1.87	14 (28%)
7	HEM	C	401	1	41,50,50	1.35	5 (12%)	45,82,82	1.87	11 (24%)
19	A1L8Q	M	404	-	64,64,64	0.33	1 (1%)	78,81,81	0.61	1 (1%)
17	PGV	D	101	-	39,39,50	1.03	2 (5%)	42,45,56	1.06	2 (4%)
13	BCL	Y	102	5	64,74,74	1.70	13 (20%)	78,115,115	2.28	19 (24%)
17	PGV	2	101	-	43,43,50	0.98	2 (4%)	45,49,56	1.00	2 (4%)
17	PGV	M	406	-	36,36,50	1.07	2 (5%)	39,42,56	1.12	3 (7%)
13	BCL	9	101	5	64,74,74	1.70	14 (21%)	78,115,115	2.25	20 (25%)
16	LMT	9	102	-	26,26,36	0.48	0	37,37,47	0.77	1 (2%)
17	PGV	0	103	-	43,43,50	0.99	2 (4%)	45,49,56	1.02	3 (6%)
13	BCL	O	101	5	64,74,74	1.69	14 (21%)	78,115,115	2.32	20 (25%)
13	BCL	8	103	6	64,74,74	1.69	14 (21%)	78,115,115	2.20	20 (25%)
16	LMT	L	305	-	33,33,36	0.48	0	44,44,47	0.84	2 (4%)
13	BCL	L	311	3	64,74,74	1.70	14 (21%)	78,115,115	2.25	21 (26%)
16	LMT	X	103	-	35,35,36	0.50	0	46,46,47	1.07	3 (6%)
13	BCL	N	102	6	64,74,74	1.69	14 (21%)	78,115,115	2.19	18 (23%)
9	Z41	C	405	1	25,25,39	0.32	0	27,27,41	0.29	0
8	HEC	C	403	1	32,50,50	1.57	4 (12%)	24,82,82	1.59	2 (8%)
16	LMT	V	104	-	36,36,36	0.43	0	47,47,47	0.95	3 (6%)
8	HEC	C	404	1	32,50,50	1.56	5 (15%)	24,82,82	1.30	1 (4%)
20	CRT	4	101	-	41,43,43	0.72	0	50,54,54	1.79	14 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
20	CRT	8	102	-	41,43,43	0.73	0	50,54,54	2.38	16 (32%)
13	BCL	5	402	5	64,74,74	1.72	14 (21%)	78,115,115	2.27	21 (26%)
16	LMT	B	104	-	35,35,36	0.43	0	46,46,47	0.79	0
17	PGV	H	404	-	50,50,50	0.93	2 (4%)	53,56,56	1.02	3 (5%)
13	BCL	E	102	6	64,74,74	1.69	14 (21%)	78,115,115	2.20	18 (23%)

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
16	LMT	E	104	-	-	5/21/61/61	0/2/2/2
13	BCL	T	102	6	-	16/37/137/137	-
17	PGV	V	103	-	-	17/48/48/55	-
20	CRT	J	101	-	-	7/51/51/51	-
20	CRT	Z	101	-	-	4/51/51/51	-
20	CRT	P	101	-	-	0/51/51/51	-
13	BCL	A	102	5	-	7/37/137/137	-
13	BCL	6	102	6	-	10/37/137/137	-
20	CRT	T	101	-	-	3/51/51/51	-
13	BCL	1	101	5	-	14/37/137/137	-
13	BCL	D	102	5	-	10/37/137/137	-
16	LMT	O	102	-	-	4/21/61/61	0/2/2/2
13	BCL	R	102	6	-	16/37/137/137	-
13	BCL	X	101	6	-	17/37/137/137	-
13	BCL	S	101	5	-	13/37/137/137	-
8	HEC	C	402	1	-	2/10/54/54	-
17	PGV	H	401	-	-	16/47/47/55	-
17	PGV	N	103	-	-	11/48/48/55	-
17	PGV	4	103	-	-	12/48/48/55	-
13	BCL	Q	101	5	-	13/37/137/137	-
15	U10	D	104	-	-	17/43/67/87	0/1/1/1
13	BCL	0	102	6	-	14/37/137/137	-
17	PGV	P	103	-	-	10/48/48/55	-
16	LMT	7	103	-	-	5/17/57/61	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	BCL	M	402	3	-	15/37/137/137	-
17	PGV	G	103	-	-	9/48/48/55	-
17	PGV	A	101	-	-	8/19/19/55	-
13	BCL	K	101	5	-	16/37/137/137	-
17	PGV	B	103	-	-	17/48/48/55	-
16	LMT	4	105	-	-	5/18/58/61	0/2/2/2
16	LMT	M	409	-	-	2/17/57/61	0/2/2/2
16	LMT	5	401	-	-	2/16/56/61	0/2/2/2
15	U10	Y	103	-	-	2/12/36/87	0/1/1/1
20	CRT	E	101	-	-	2/51/51/51	-
20	CRT	R	101	-	-	4/51/51/51	-
10	PLM	C	406	1	-	2/8/9/15	-
13	BCL	F	101	5	-	13/37/137/137	-
16	LMT	D	103	-	-	7/17/57/61	0/2/2/2
17	PGV	8	101	-	-	14/48/48/55	-
13	BCL	7	102	5	-	14/37/137/137	-
13	BCL	V	102	6	-	18/37/137/137	-
13	BCL	B	102	6	-	17/37/137/137	-
15	U10	L	308	-	-	2/9/33/87	0/1/1/1
13	BCL	3	101	5	-	13/37/137/137	-
14	BPH	L	303	-	-	6/37/105/105	0/5/6/6
20	CRT	6	101	-	-	11/51/51/51	-
20	CRT	G	101	-	-	6/51/51/51	-
15	U10	7	101	-	-	18/51/75/87	0/1/1/1
16	LMT	F	102	-	-	4/18/58/61	0/2/2/2
20	CRT	Y	101	-	-	1/51/51/51	-
13	BCL	I	101	5	-	11/37/137/137	-
13	BCL	J	102	6	-	21/37/137/137	-
17	PGV	E	103	-	-	15/48/48/55	-
17	PGV	K	102	-	-	18/50/50/55	-
13	BCL	P	102	6	-	17/37/137/137	-
17	PGV	R	103	-	-	12/48/48/55	-
13	BCL	G	102	6	-	21/37/137/137	-
17	PGV	2	104	-	-	9/48/48/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
20	CRT	M	405	-	-	7/51/51/51	-
13	BCL	4	102	6	-	13/37/137/137	-
16	LMT	T	104	-	-	3/21/61/61	0/2/2/2
17	PGV	M	408	-	-	9/36/36/55	-
13	BCL	W	101	5	-	8/37/137/137	-
17	PGV	L	306	-	-	5/37/37/55	-
17	PGV	M	410	-	-	8/22/22/55	-
13	BCL	U	102	5	-	13/37/137/137	-
17	PGV	8	104	-	-	13/48/48/55	-
20	CRT	N	101	-	-	2/51/51/51	-
20	CRT	B	101	-	-	6/51/51/51	-
14	BPH	M	403	-	-	8/37/105/105	0/5/6/6
16	LMT	H	402	-	-	3/12/52/61	0/2/2/2
17	PGV	H	403	-	-	22/47/47/55	-
15	U10	L	309	-	-	8/24/48/87	0/1/1/1
20	CRT	V	101	-	-	7/51/51/51	-
15	U10	U	101	-	-	1/9/33/87	0/1/1/1
16	LMT	4	104	-	-	5/21/61/61	0/2/2/2
13	BCL	L	302	2	-	10/37/137/137	-
16	LMT	P	104	-	-	6/21/61/61	0/2/2/2
17	PGV	L	307	-	-	19/55/55/55	-
17	PGV	J	103	-	-	6/48/48/55	-
17	PGV	X	102	-	-	12/48/48/55	-
13	BCL	L	310	2	-	12/37/137/137	-
15	U10	1	102	-	-	7/42/66/87	0/1/1/1
16	LMT	K	103	-	-	10/21/61/61	0/2/2/2
13	BCL	Z	102	6	-	19/37/137/137	-
16	LMT	J	104	-	-	2/16/56/61	0/2/2/2
16	LMT	Z	103	-	-	7/21/61/61	0/2/2/2
16	LMT	Z	104	-	-	6/21/61/61	0/2/2/2
20	CRT	0	101	-	-	3/51/51/51	-
15	U10	L	304	-	-	6/27/51/87	0/1/1/1
17	PGV	M	407	-	-	9/33/33/55	-
17	PGV	T	103	-	-	13/48/48/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	BCL	2	103	6	-	18/37/137/137	-
20	CRT	2	102	-	-	7/51/51/51	-
7	HEM	C	401	1	-	4/12/54/54	-
19	A1L8Q	M	404	-	-	16/59/79/79	0/2/2/2
17	PGV	D	101	-	-	11/44/44/55	-
13	BCL	Y	102	5	-	17/37/137/137	-
17	PGV	2	101	-	-	8/48/48/55	-
17	PGV	M	406	-	-	13/41/41/55	-
13	BCL	9	101	5	-	15/37/137/137	-
16	LMT	9	102	-	-	1/11/51/61	0/2/2/2
17	PGV	0	103	-	-	8/48/48/55	-
13	BCL	O	101	5	-	14/37/137/137	-
13	BCL	8	103	6	-	19/37/137/137	-
16	LMT	L	305	-	-	6/18/58/61	0/2/2/2
13	BCL	L	311	3	-	12/37/137/137	-
16	LMT	X	103	-	-	10/20/60/61	0/2/2/2
13	BCL	N	102	6	-	16/37/137/137	-
9	Z41	C	405	1	-	11/26/26/41	-
8	HEC	C	403	1	-	2/10/54/54	-
16	LMT	V	104	-	-	4/21/61/61	0/2/2/2
8	HEC	C	404	1	-	2/10/54/54	-
20	CRT	4	101	-	-	5/51/51/51	-
20	CRT	8	102	-	-	7/51/51/51	-
13	BCL	5	402	5	-	13/37/137/137	-
16	LMT	B	104	-	-	8/20/60/61	0/2/2/2
17	PGV	H	404	-	-	14/55/55/55	-
13	BCL	E	102	6	-	15/37/137/137	-

The worst 5 of 586 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	M	410	PGV	O01-C1	5.62	1.45	1.33
13	M	402	BCL	O2D-CGD	5.23	1.46	1.33
13	L	302	BCL	O2D-CGD	5.15	1.45	1.33
13	W	101	BCL	O2D-CGD	5.14	1.45	1.33
13	K	101	BCL	O2D-CGD	5.14	1.45	1.33

The worst 5 of 1079 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	M	405	CRT	C2-C1-C4	-16.98	84.78	110.86
20	M	405	CRT	C3-C1-C4	-11.13	93.77	110.86
13	L	311	BCL	CHD-C1D-ND	-8.55	116.59	124.45
13	S	101	BCL	CHD-C1D-ND	-8.55	116.60	124.45
13	Q	101	BCL	CHD-C1D-ND	-8.53	116.62	124.45

There are no chirality outliers.

5 of 1159 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	C	405	Z41	C15-C16-O2-C17
9	C	405	Z41	O1-C16-O2-C17
9	C	405	Z41	O2-C17-C18-O3
9	C	405	Z41	O2-C17-C18-C35
13	L	302	BCL	CBD-CGD-O2D-CED

There are no ring outliers.

104 monomers are involved in 391 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	T	102	BCL	8	0
17	V	103	PGV	5	0
20	J	101	CRT	5	0
20	Z	101	CRT	4	0
20	P	101	CRT	4	0
13	A	102	BCL	3	0
13	6	102	BCL	6	0
20	T	101	CRT	7	0
13	1	101	BCL	4	0
13	D	102	BCL	3	0
16	O	102	LMT	2	0
13	R	102	BCL	5	0
13	X	101	BCL	7	0
13	S	101	BCL	3	0
17	H	401	PGV	8	0
17	N	103	PGV	3	0
17	4	103	PGV	3	0
13	Q	101	BCL	3	0
15	D	104	U10	3	0
13	0	102	BCL	7	0
17	P	103	PGV	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	7	103	LMT	7	0
13	M	402	BCL	9	0
17	G	103	PGV	2	0
17	A	101	PGV	2	0
13	K	101	BCL	4	0
17	B	103	PGV	6	0
16	4	105	LMT	1	0
16	M	409	LMT	3	0
16	5	401	LMT	4	0
15	Y	103	U10	3	0
20	E	101	CRT	4	0
20	R	101	CRT	5	0
13	F	101	BCL	5	0
16	D	103	LMT	4	0
17	8	101	PGV	6	0
13	7	102	BCL	3	0
13	V	102	BCL	7	0
13	B	102	BCL	7	0
15	L	308	U10	4	0
13	3	101	BCL	4	0
14	L	303	BPH	1	0
20	6	101	CRT	12	0
20	G	101	CRT	4	0
15	7	101	U10	7	0
20	Y	101	CRT	5	0
13	I	101	BCL	6	0
13	J	102	BCL	3	0
17	E	103	PGV	4	0
17	K	102	PGV	4	0
13	P	102	BCL	6	0
17	R	103	PGV	2	0
13	G	102	BCL	7	0
17	2	104	PGV	4	0
20	M	405	CRT	5	0
13	4	102	BCL	4	0
13	W	101	BCL	7	0
17	M	410	PGV	2	0
13	U	102	BCL	5	0
17	8	104	PGV	4	0
20	N	101	CRT	7	0
20	B	101	CRT	4	0
14	M	403	BPH	5	0

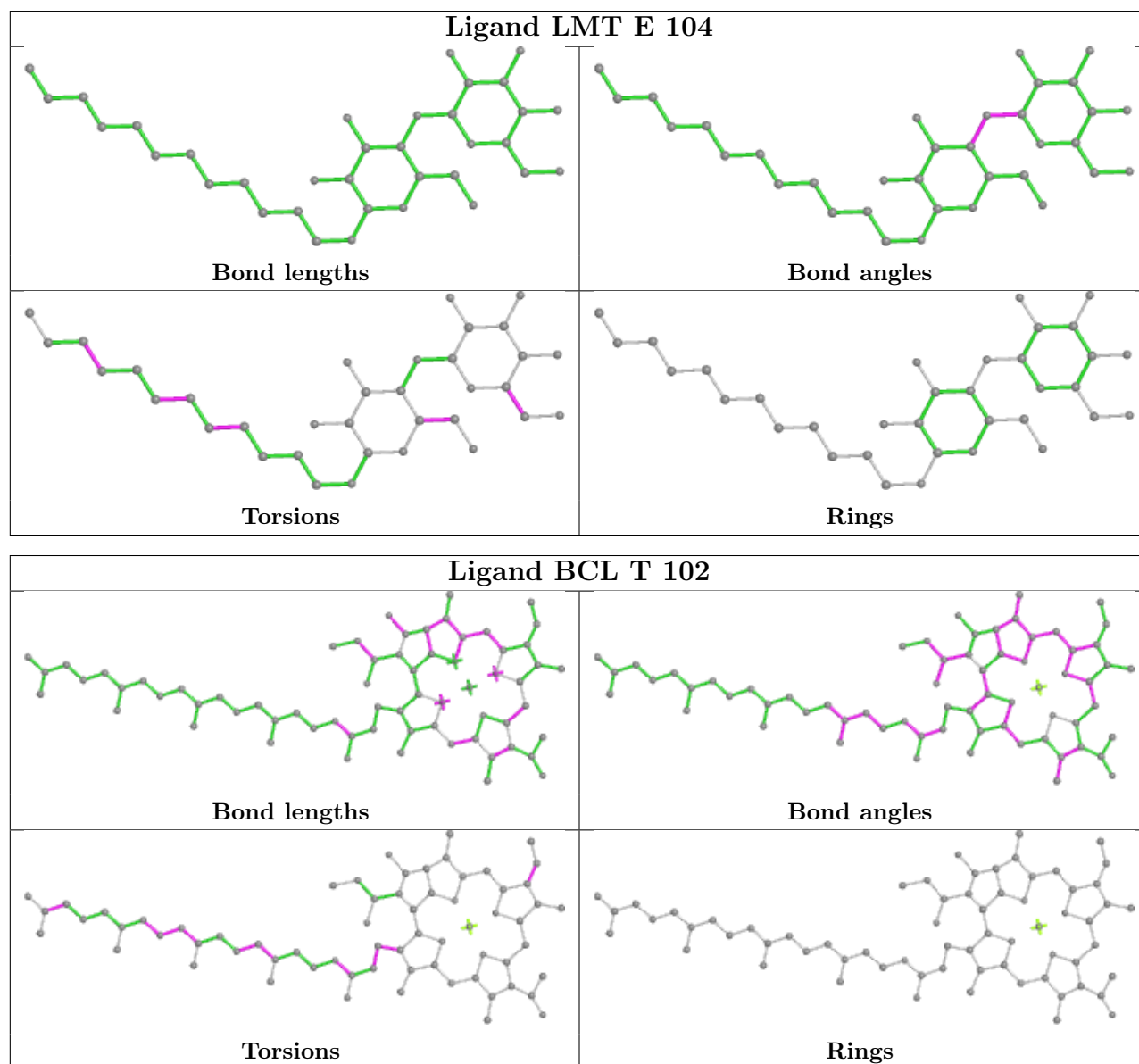
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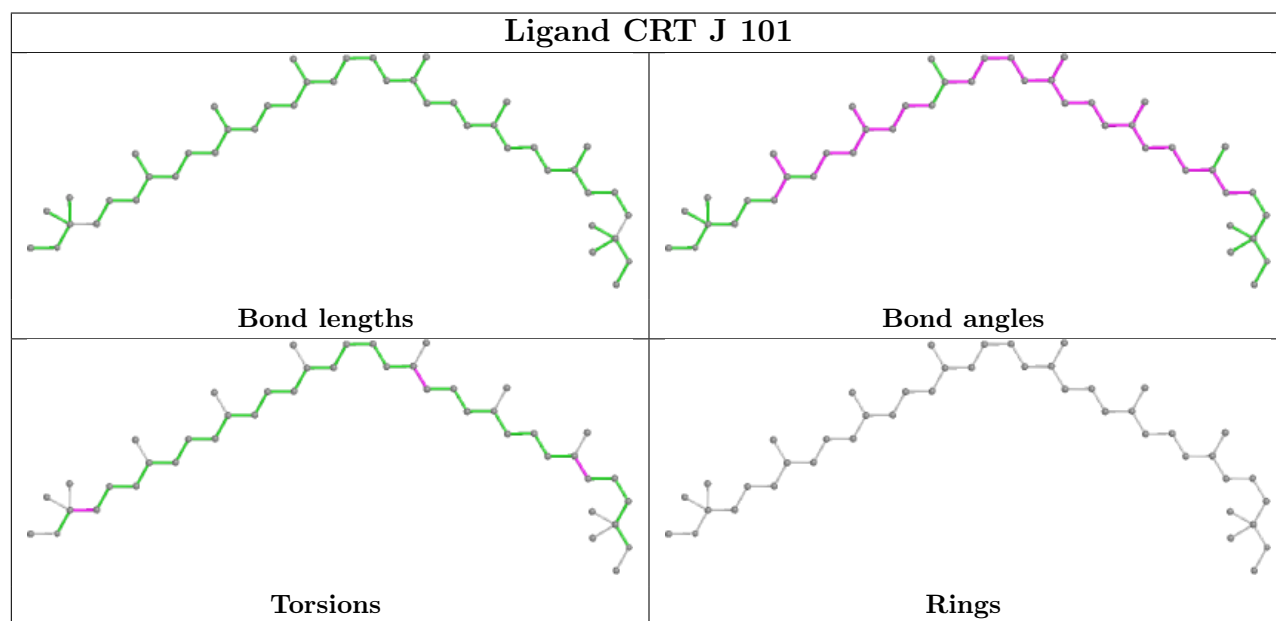
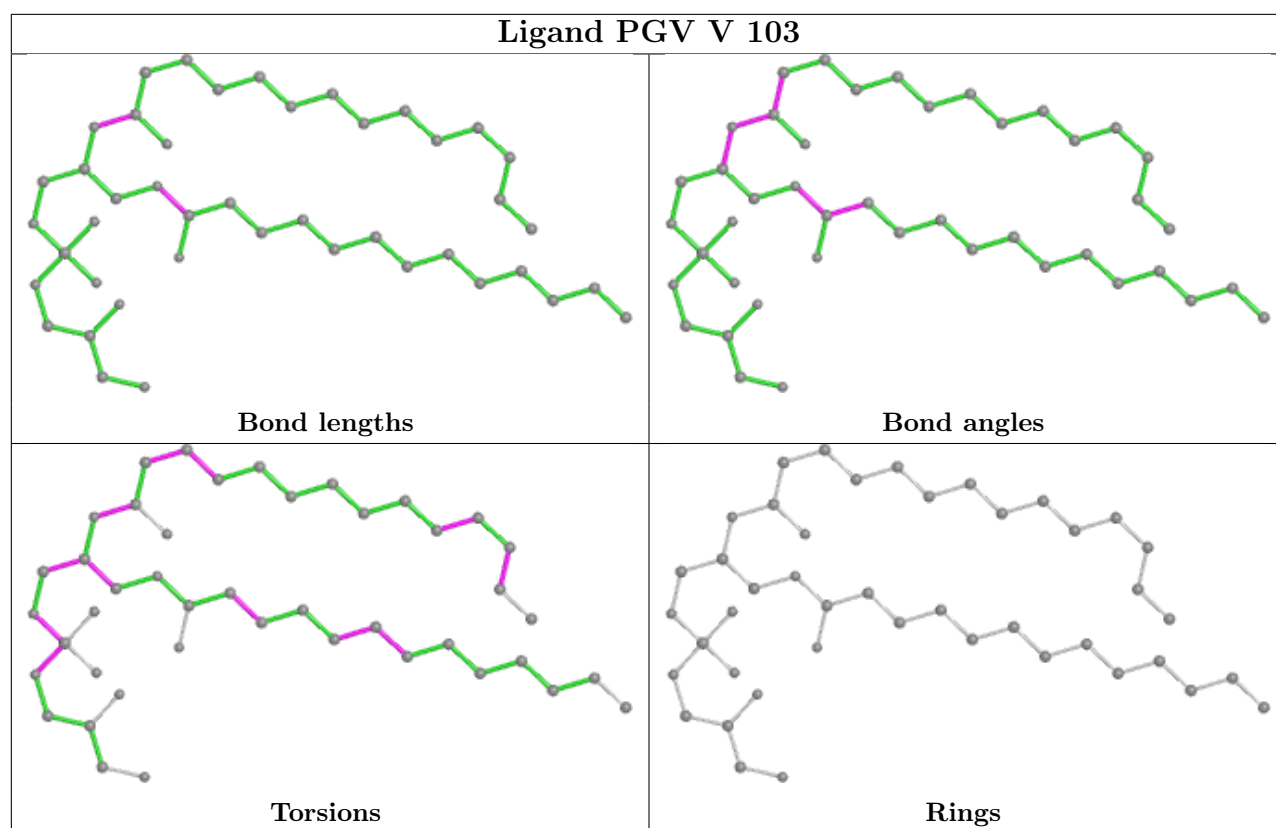
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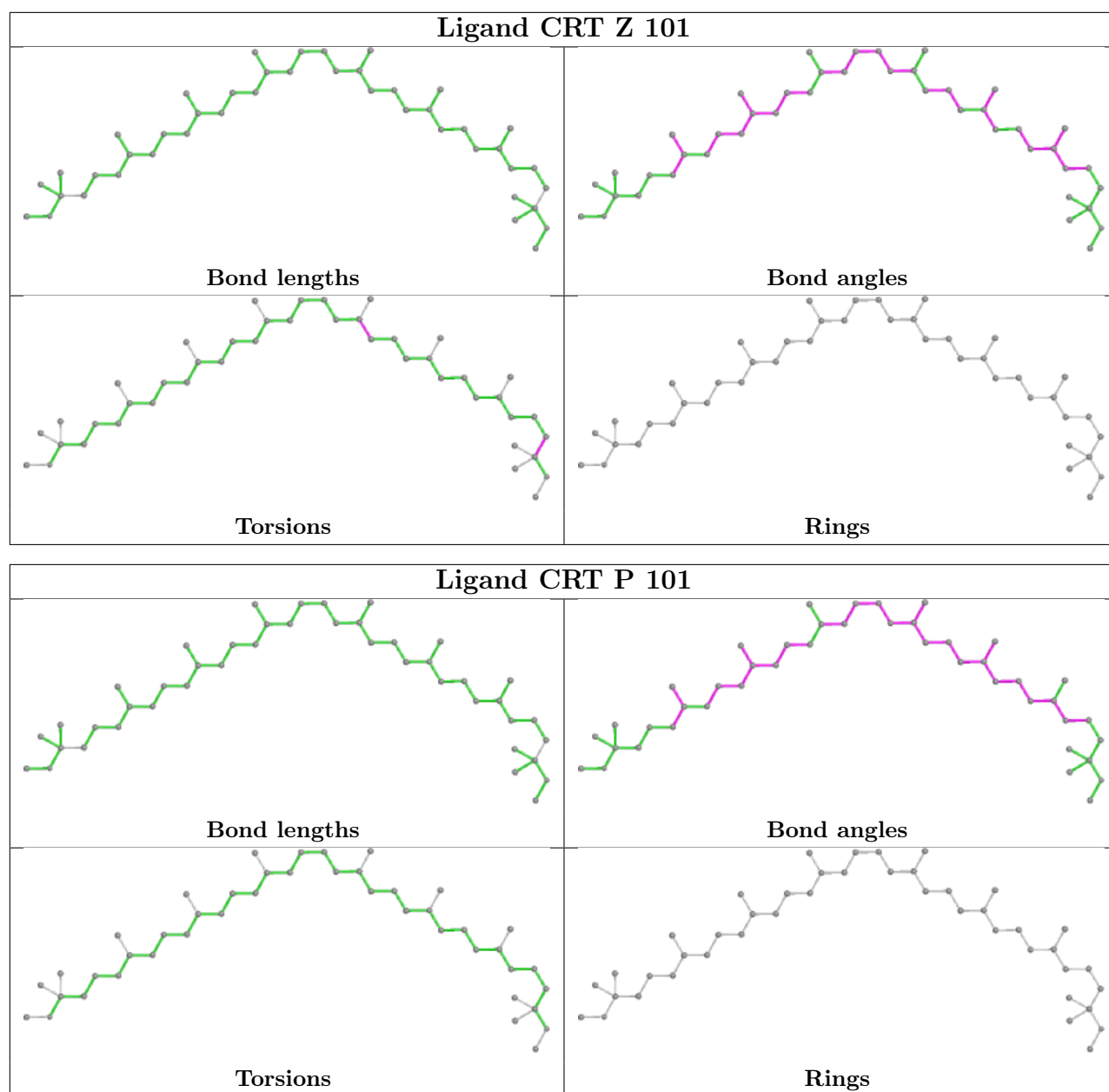
Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	H	402	LMT	3	0
17	H	403	PGV	2	0
15	L	309	U10	4	0
20	V	101	CRT	11	0
16	4	104	LMT	2	0
13	L	302	BCL	4	0
16	P	104	LMT	2	0
17	L	307	PGV	6	0
17	J	103	PGV	5	0
17	X	102	PGV	5	0
13	L	310	BCL	4	0
15	1	102	U10	2	0
16	K	103	LMT	1	0
13	Z	102	BCL	5	0
16	Z	104	LMT	1	0
20	0	101	CRT	3	0
15	L	304	U10	9	0
17	M	407	PGV	1	0
17	T	103	PGV	5	0
13	2	103	BCL	5	0
20	2	102	CRT	3	0
7	C	401	HEM	8	0
17	D	101	PGV	2	0
13	Y	102	BCL	3	0
17	2	101	PGV	4	0
17	M	406	PGV	3	0
13	9	101	BCL	5	0
17	0	103	PGV	7	0
13	O	101	BCL	3	0
13	8	103	BCL	8	0
16	L	305	LMT	2	0
13	L	311	BCL	2	0
16	X	103	LMT	1	0
13	N	102	BCL	5	0
9	C	405	Z41	1	0
8	C	403	HEC	3	0
20	4	101	CRT	5	0
20	8	102	CRT	7	0
13	5	402	BCL	4	0
17	H	404	PGV	1	0
13	E	102	BCL	6	0

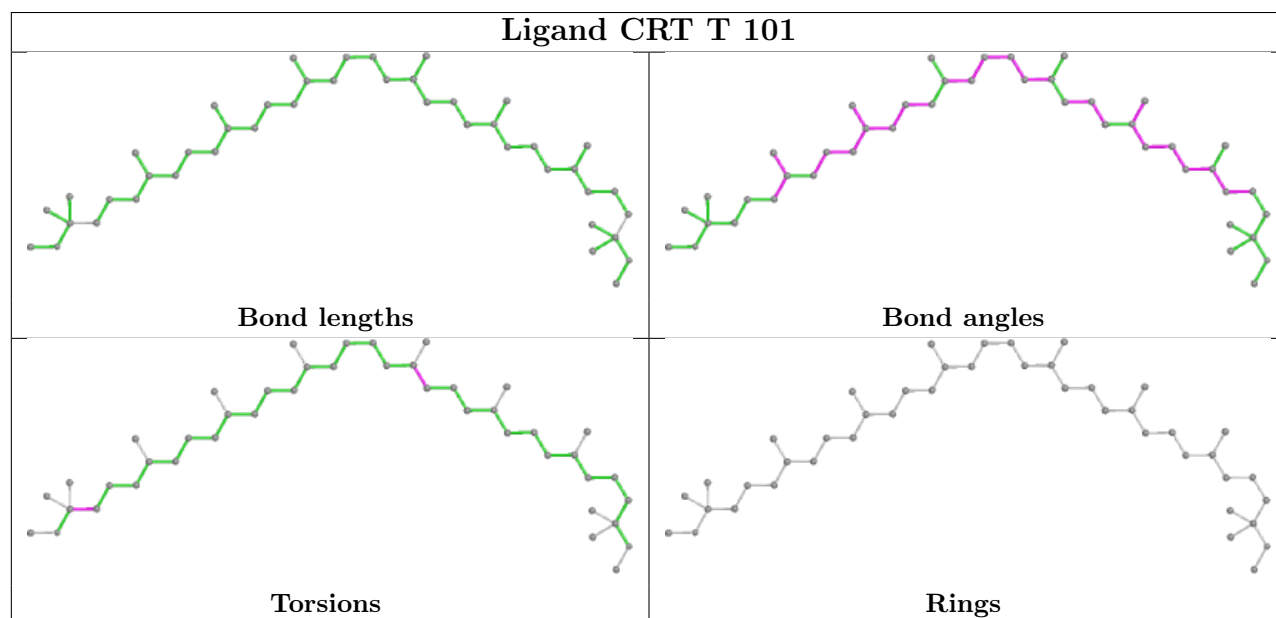
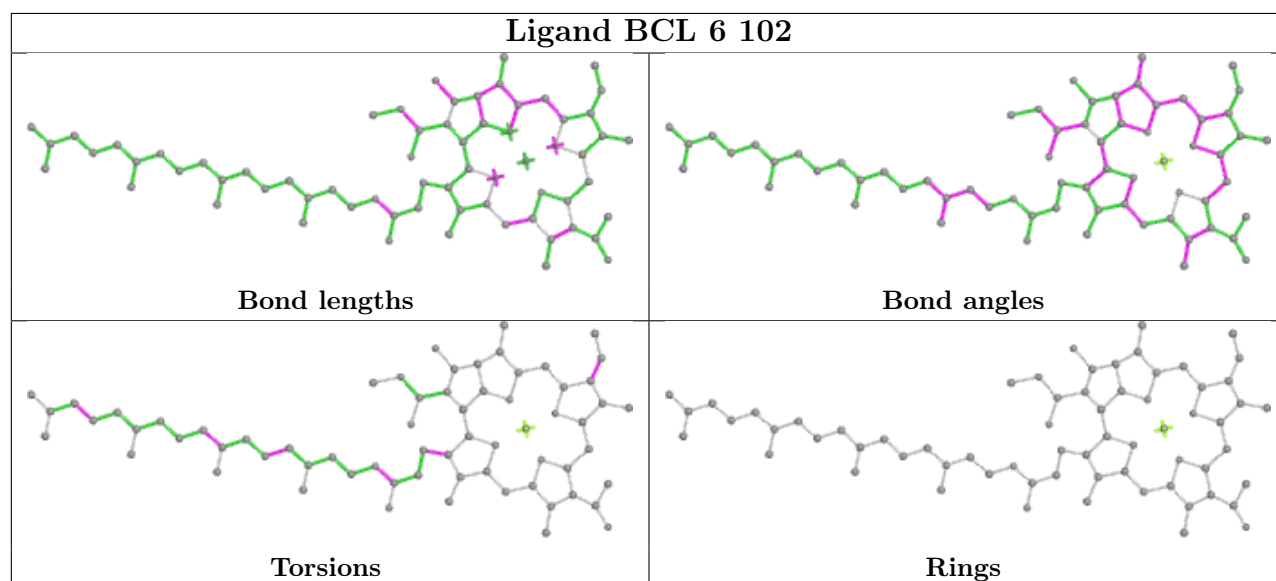
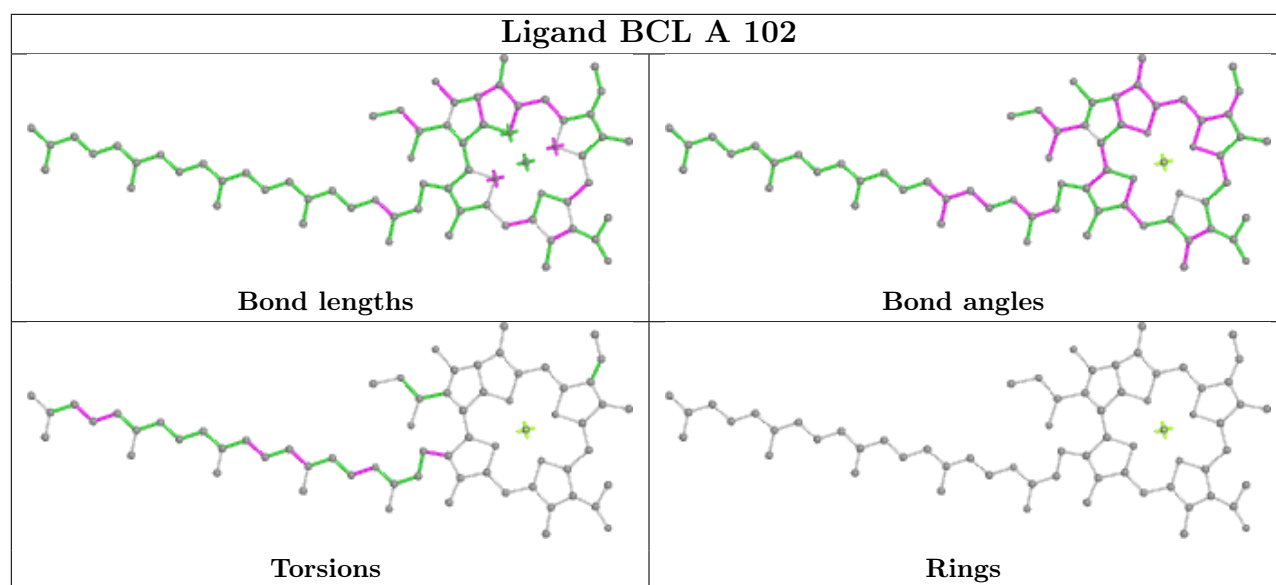
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

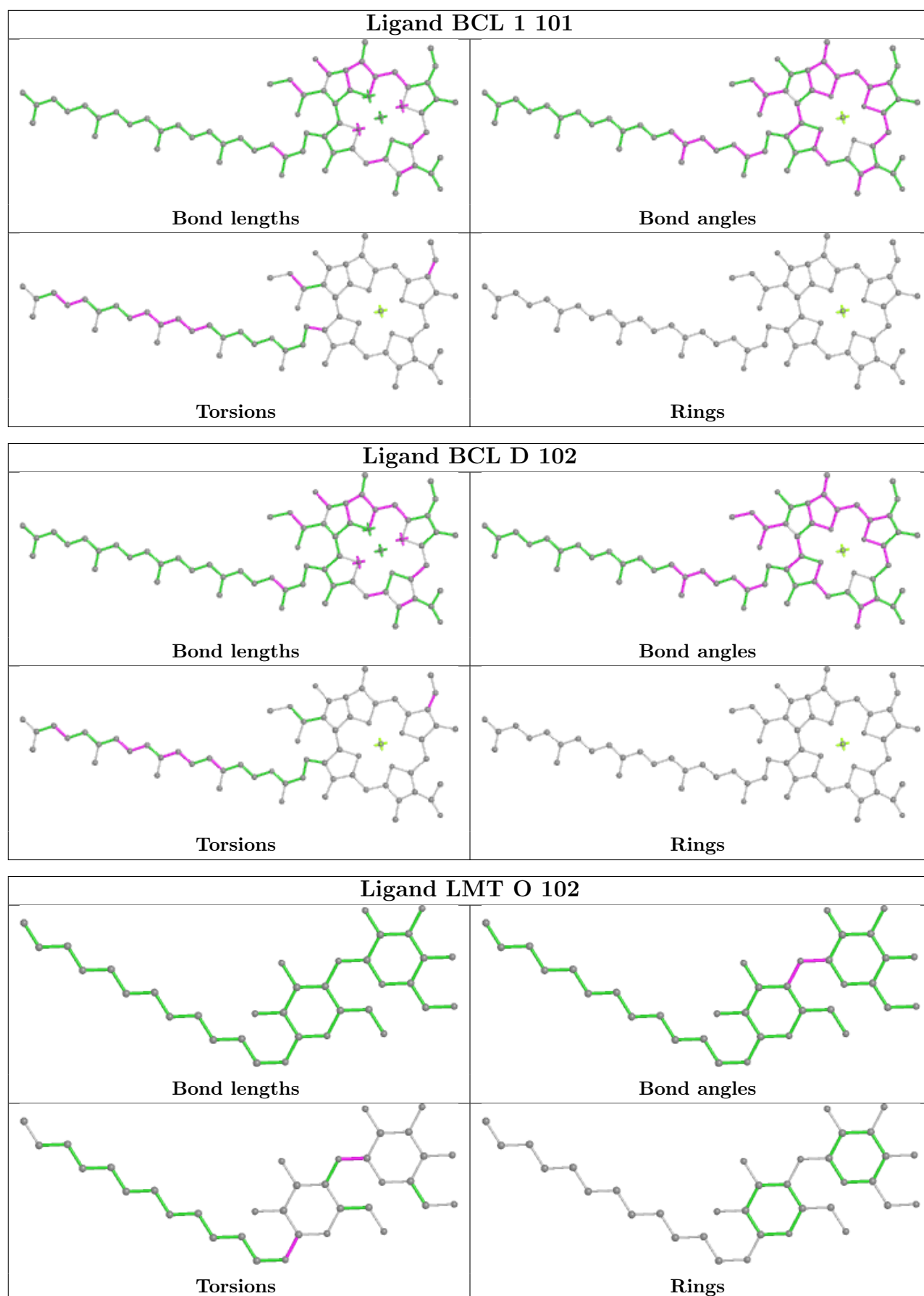
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

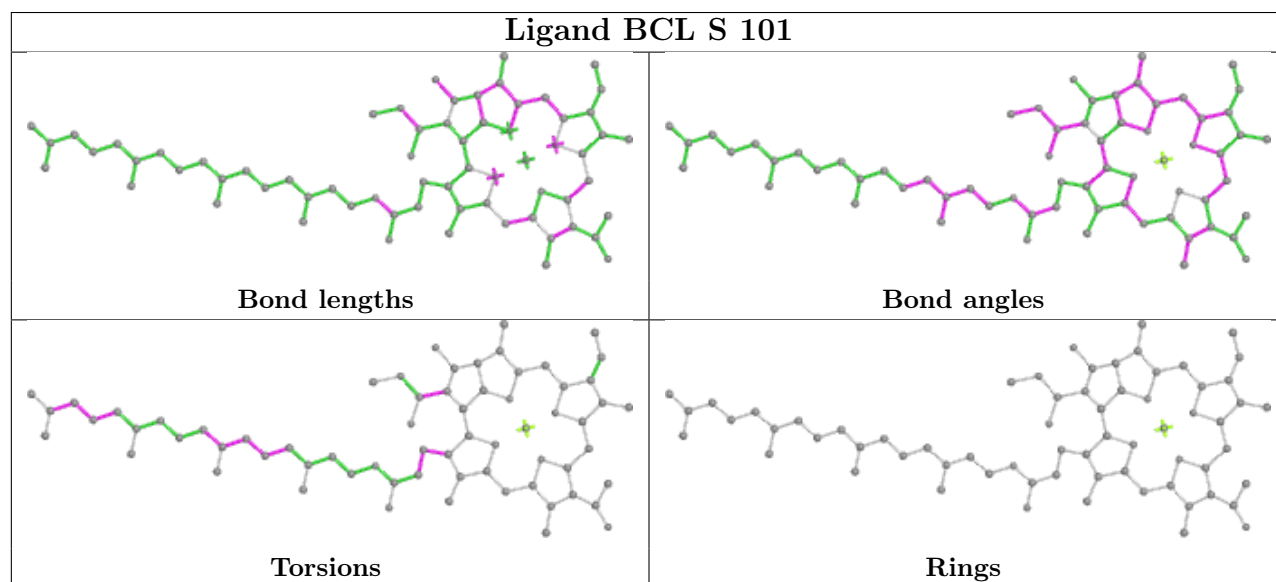
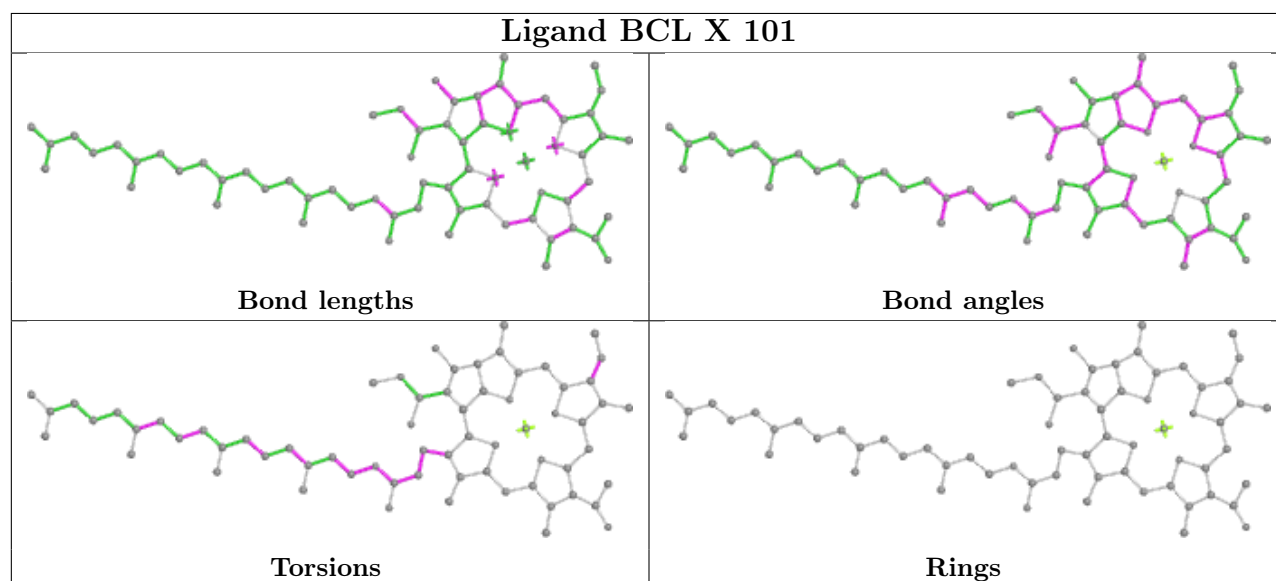
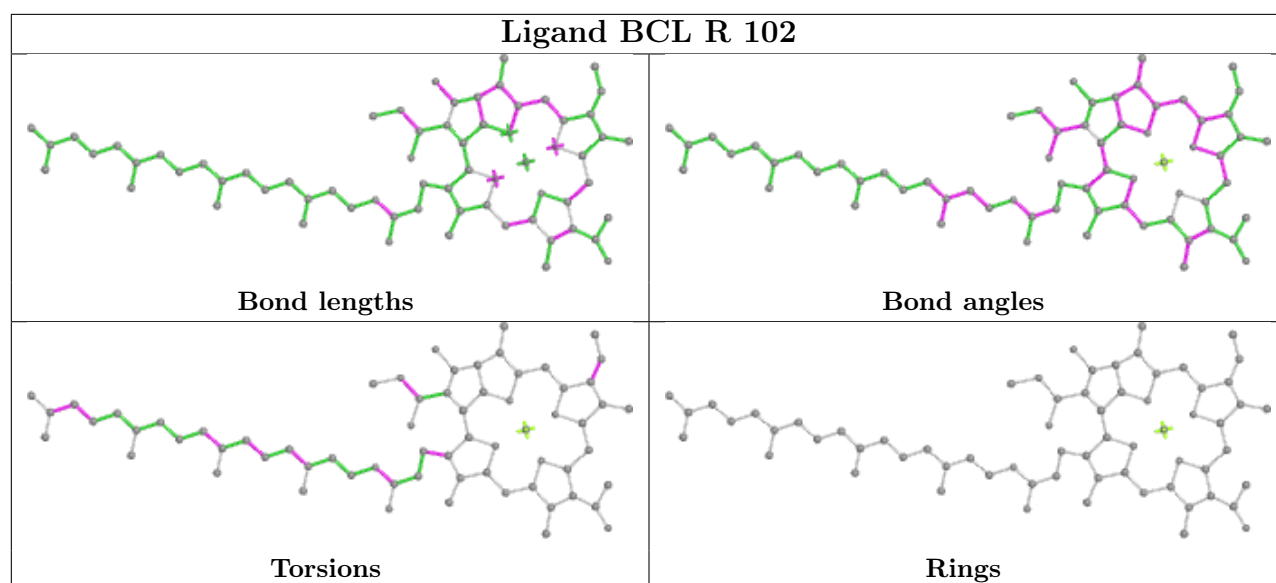


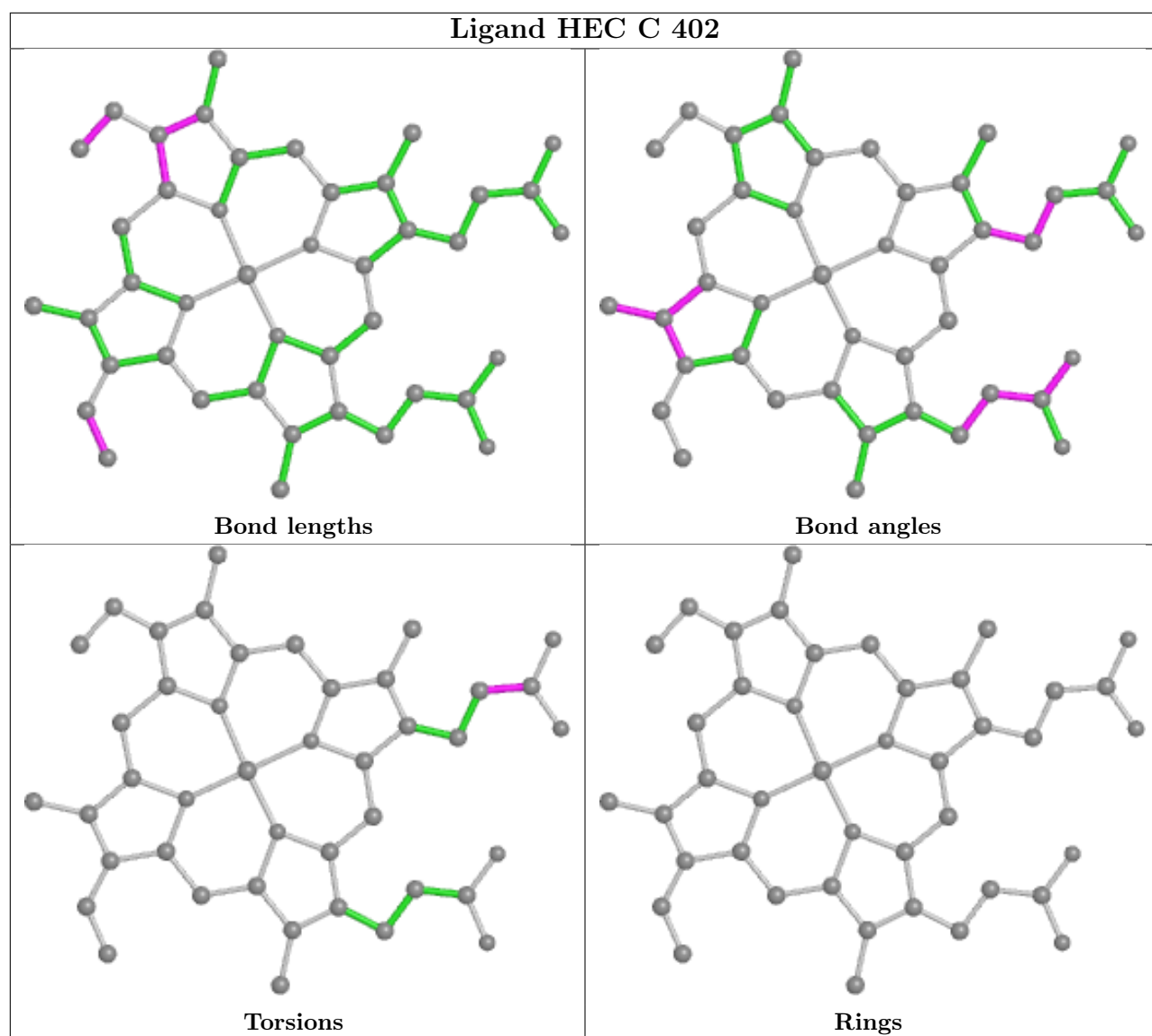


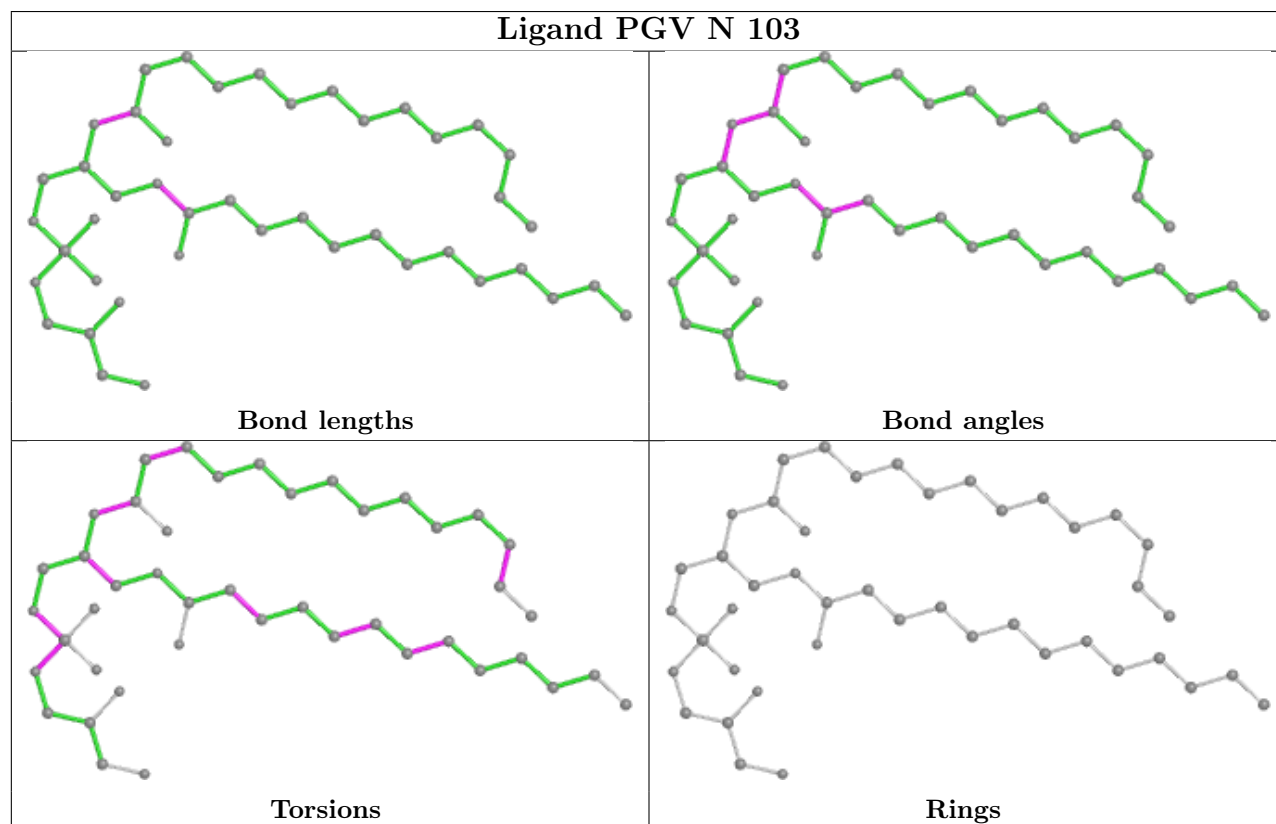
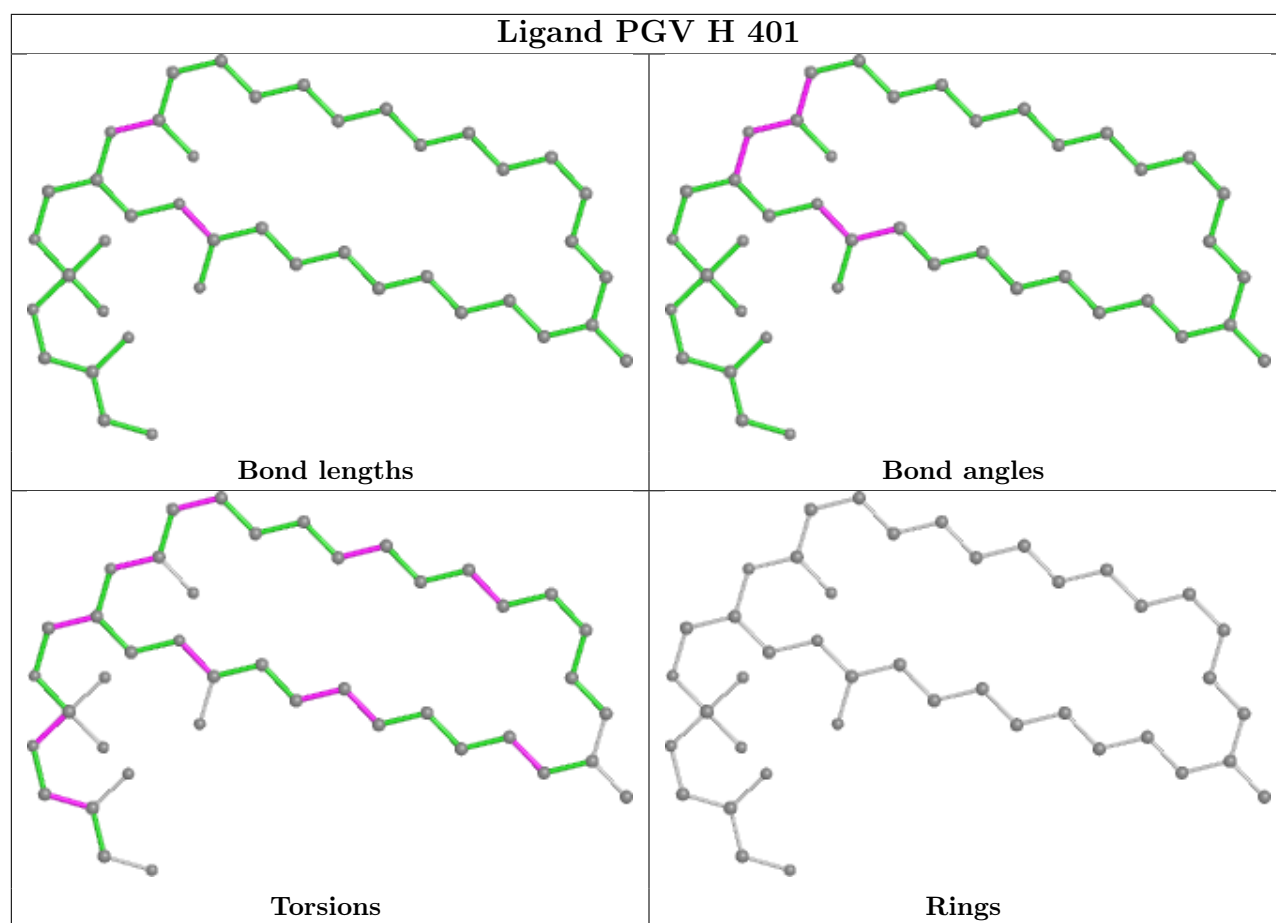


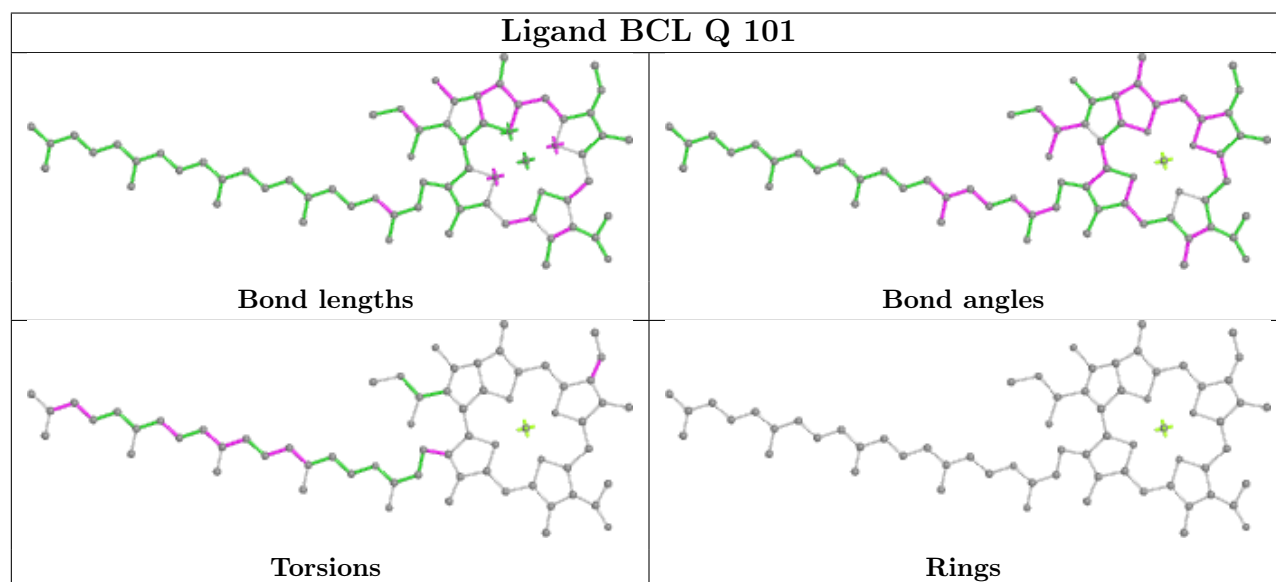
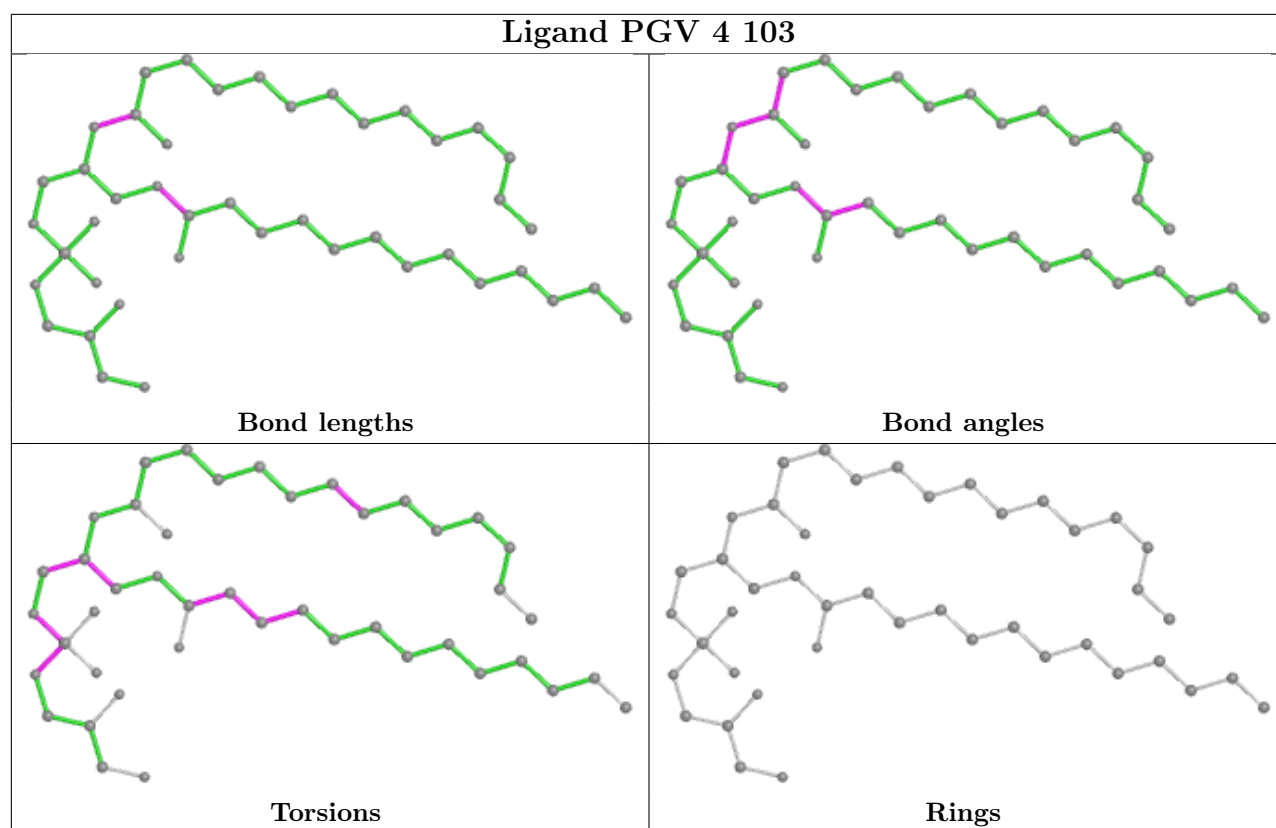


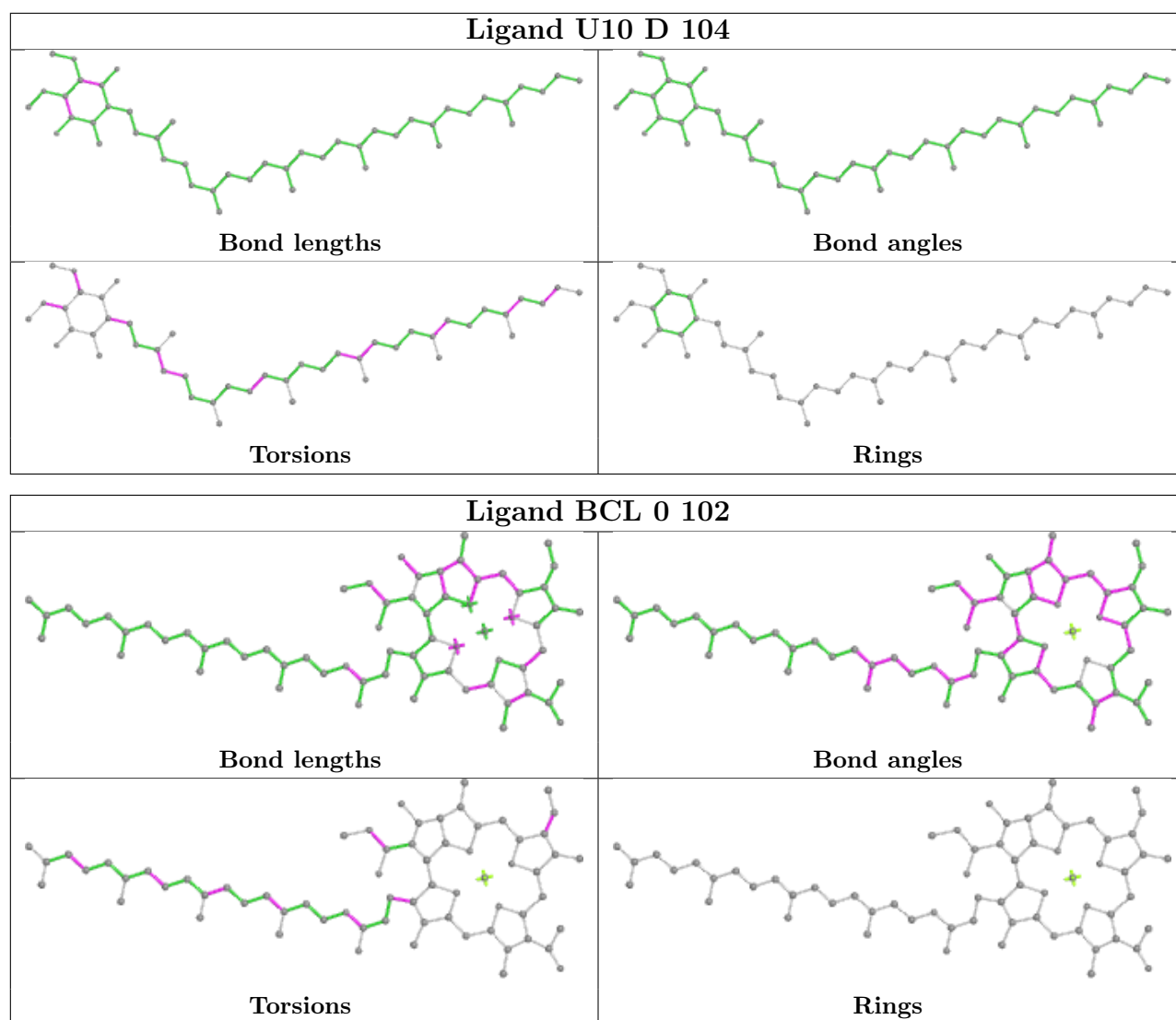


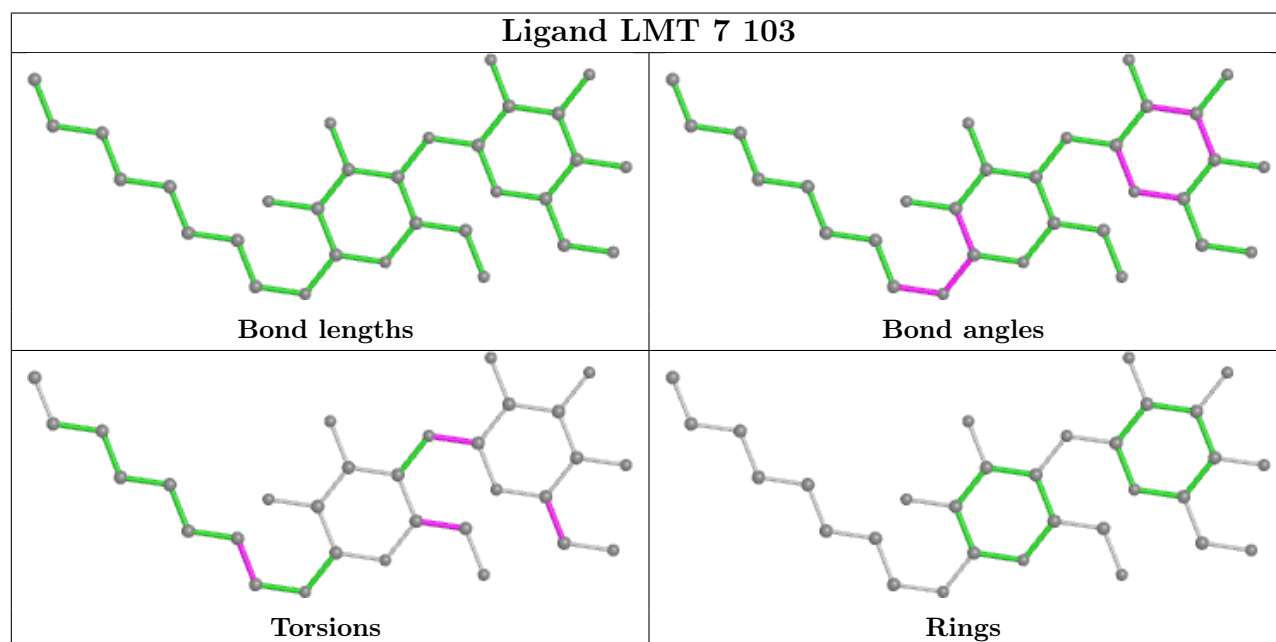
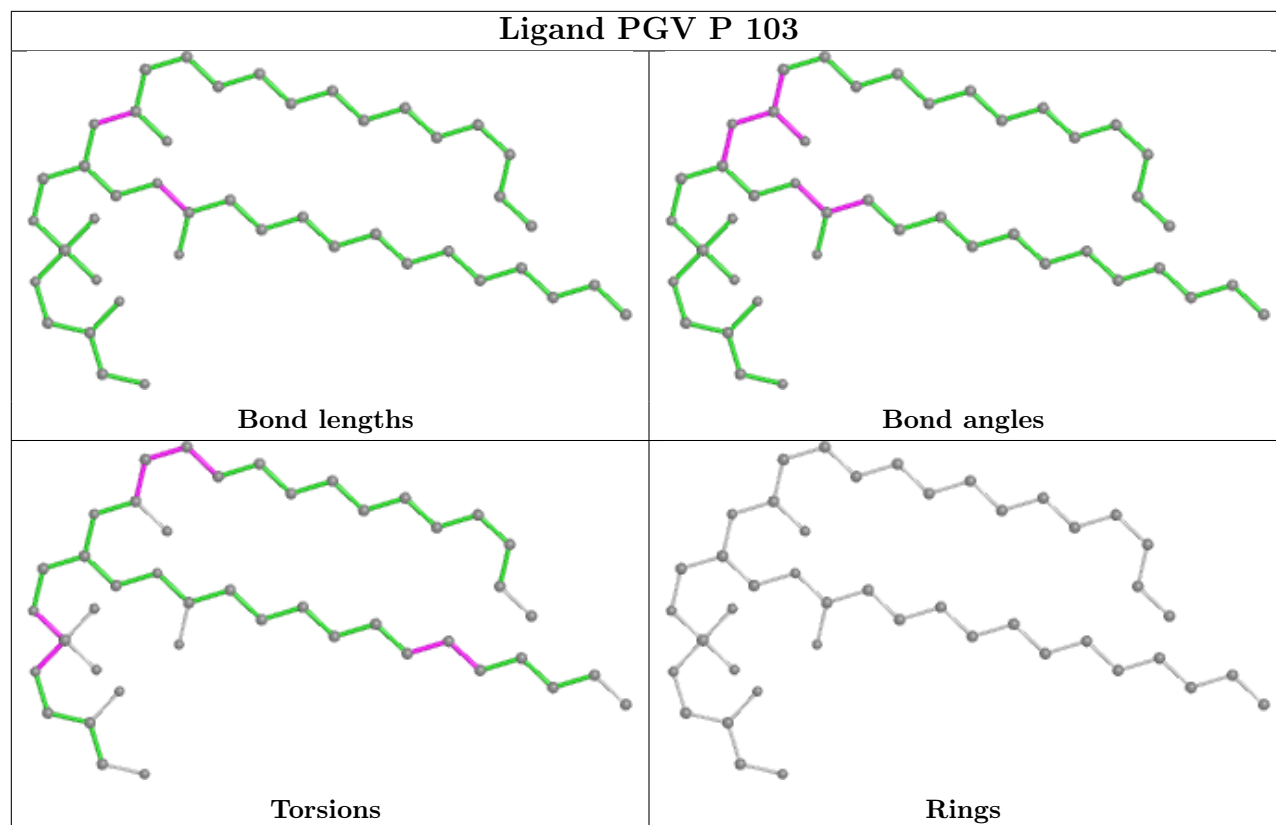


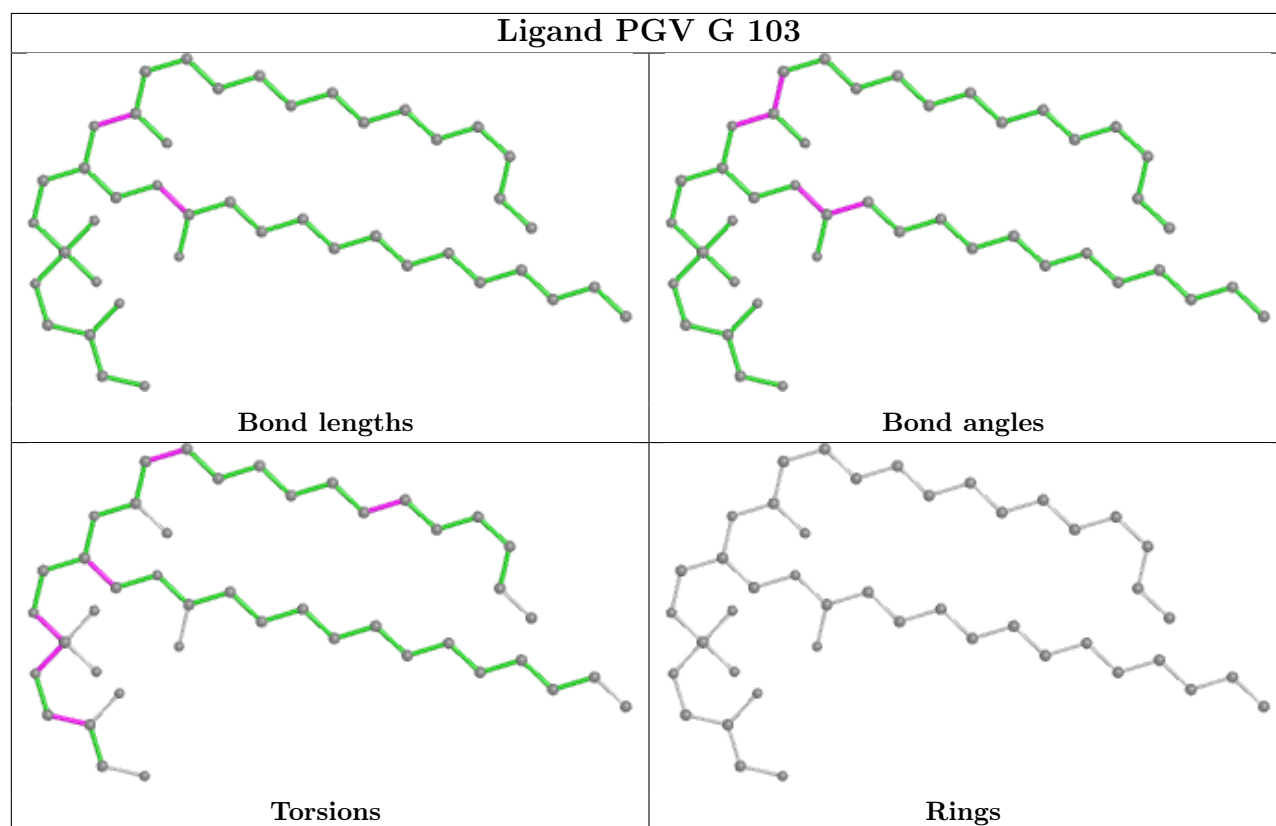
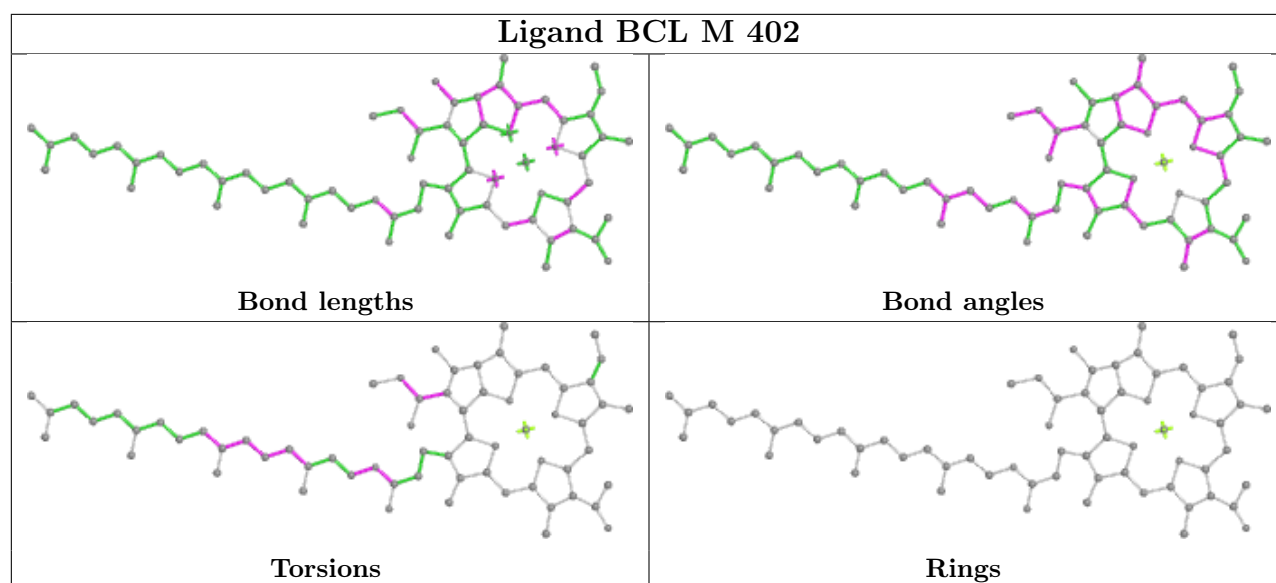


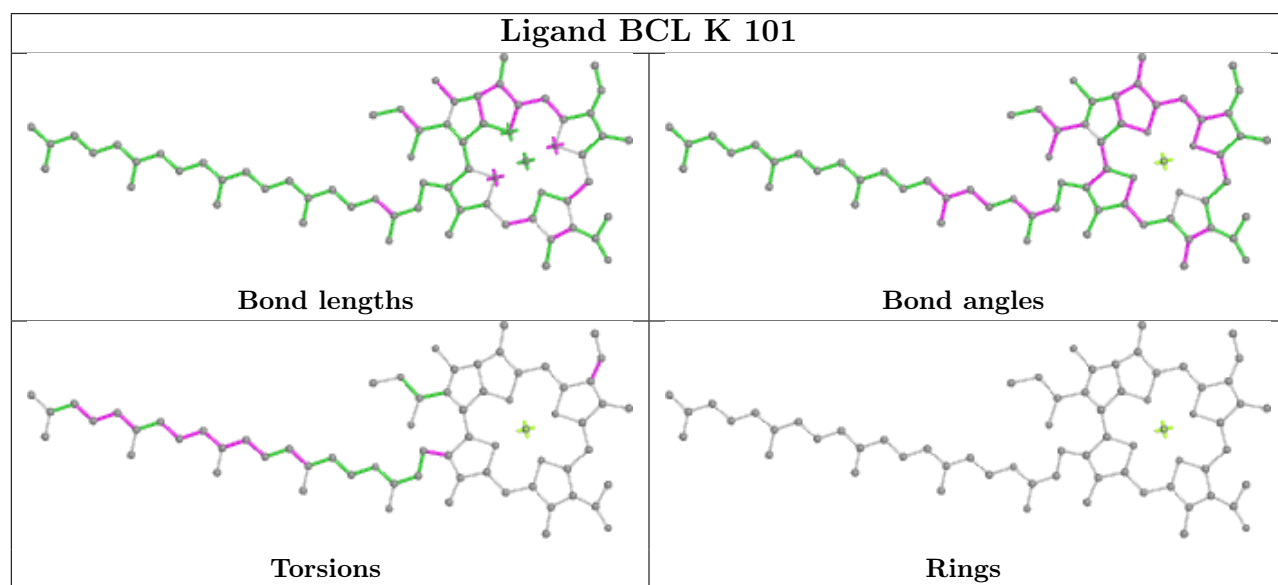
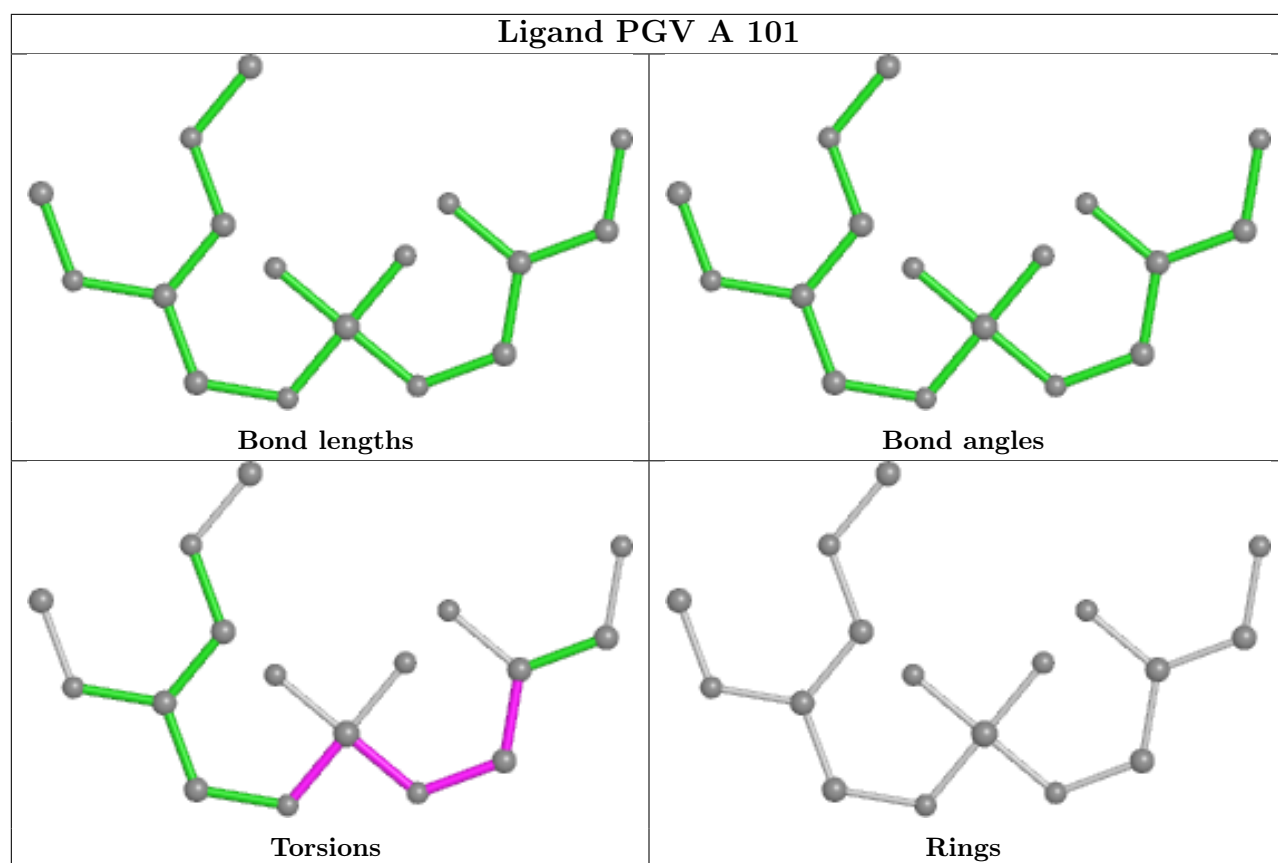


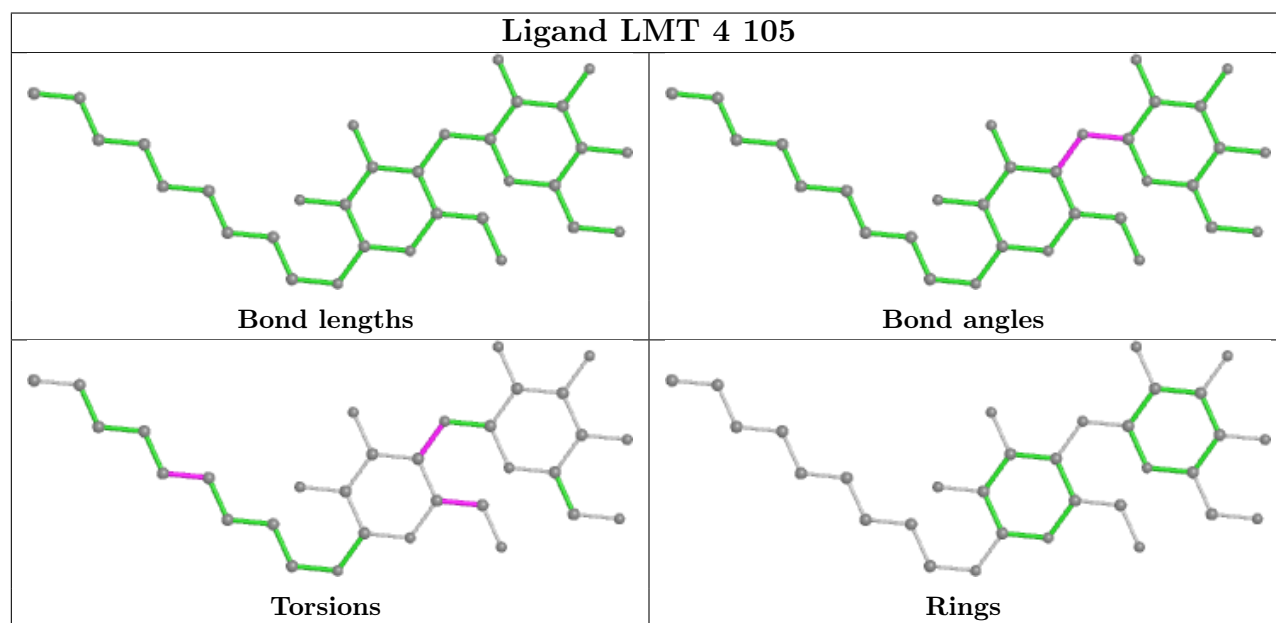
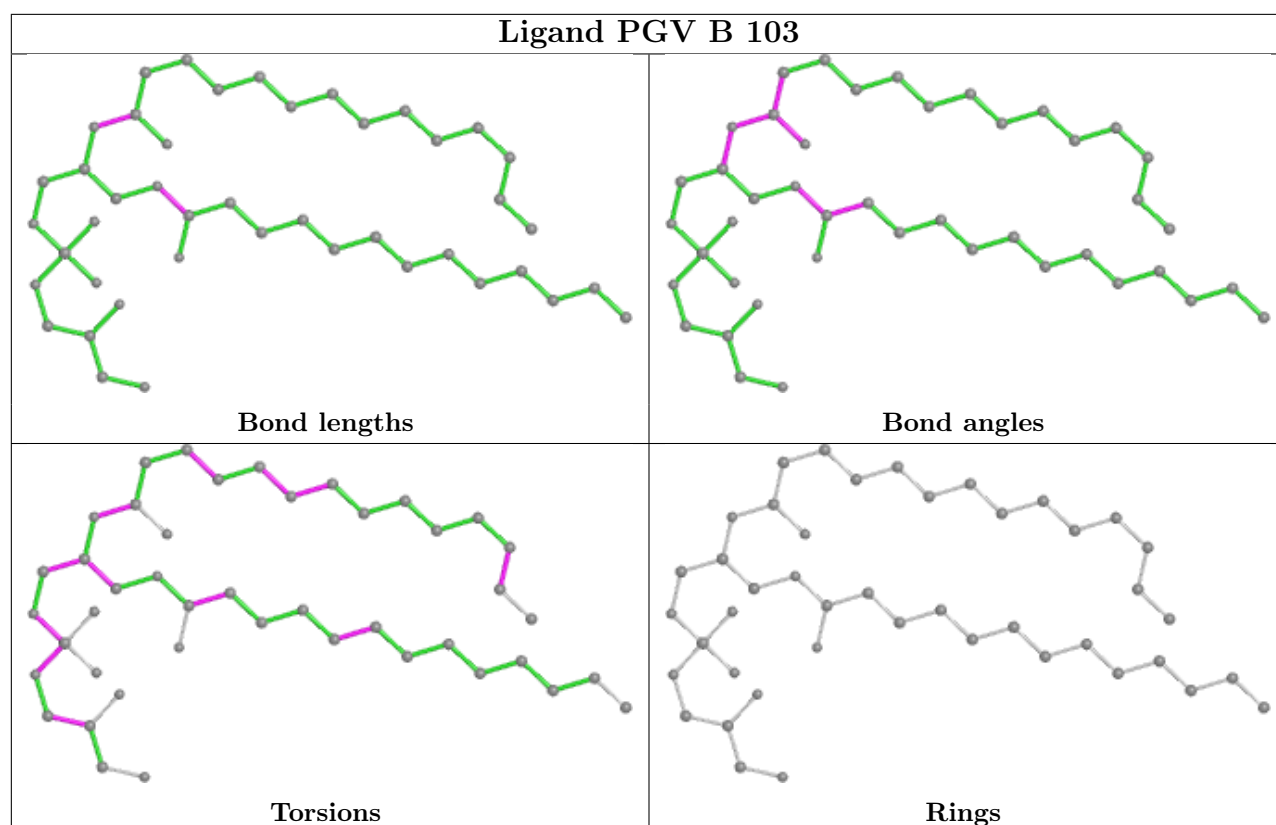


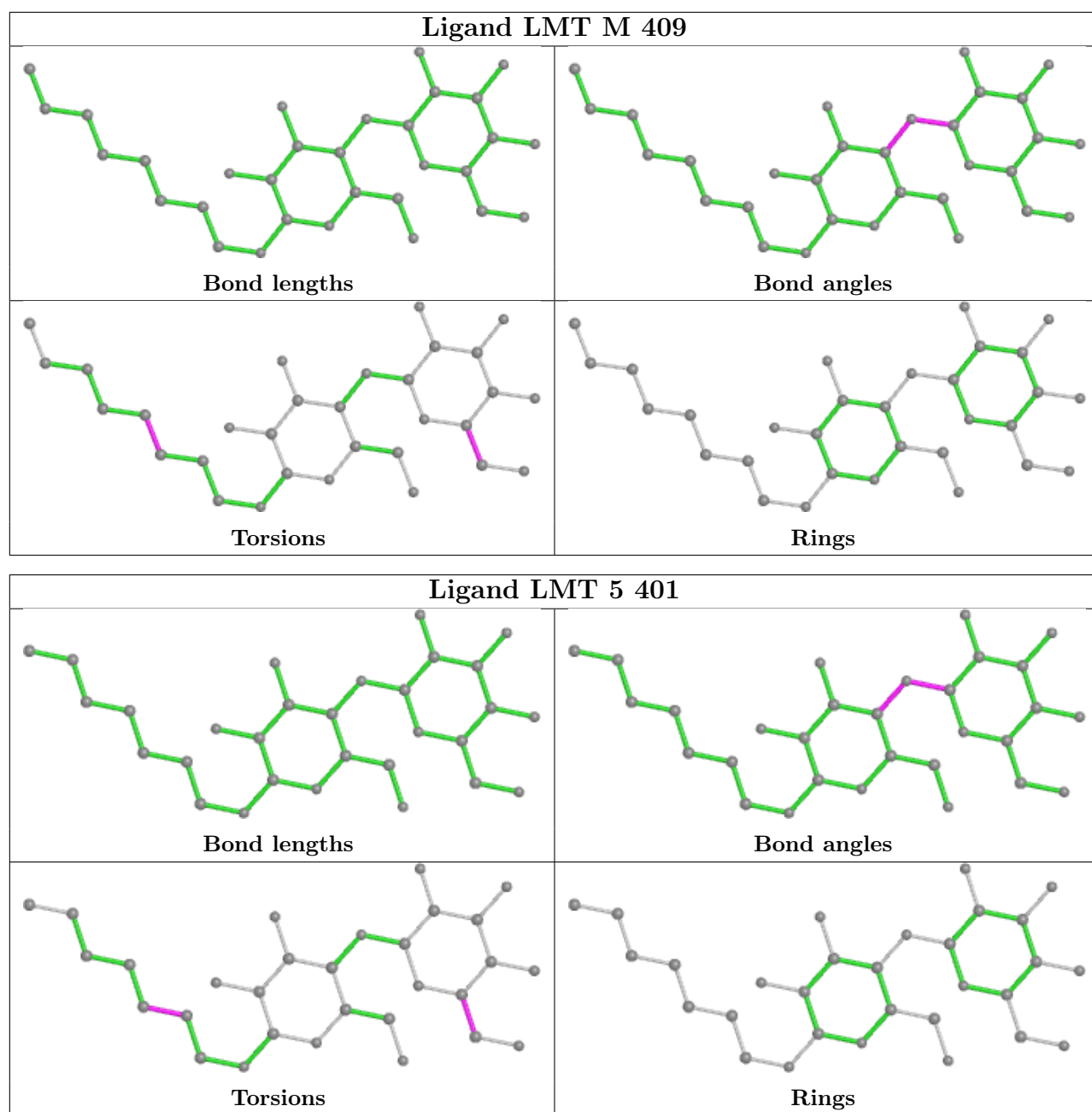




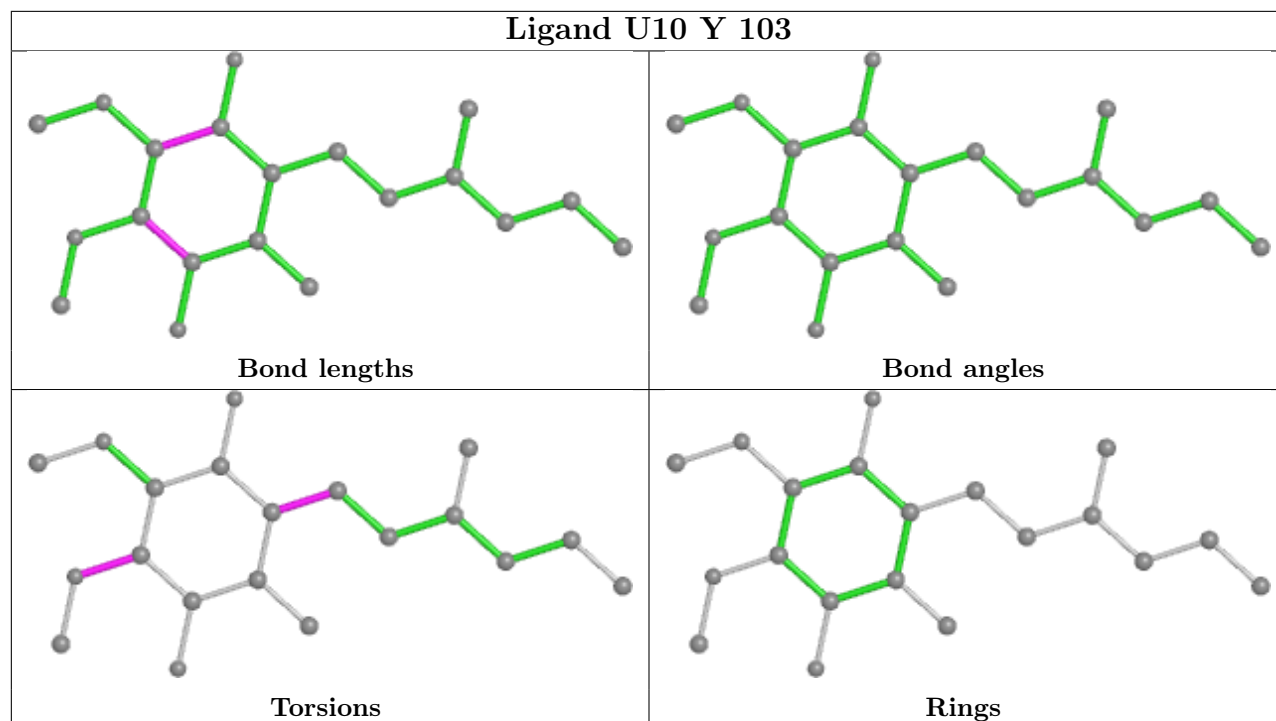




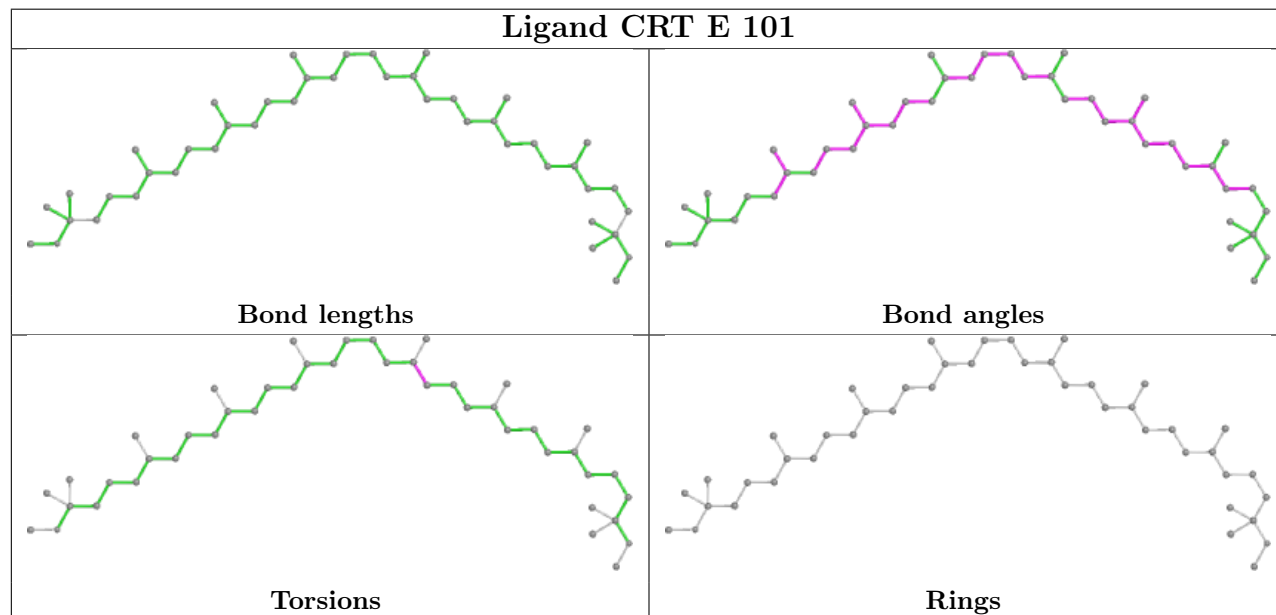


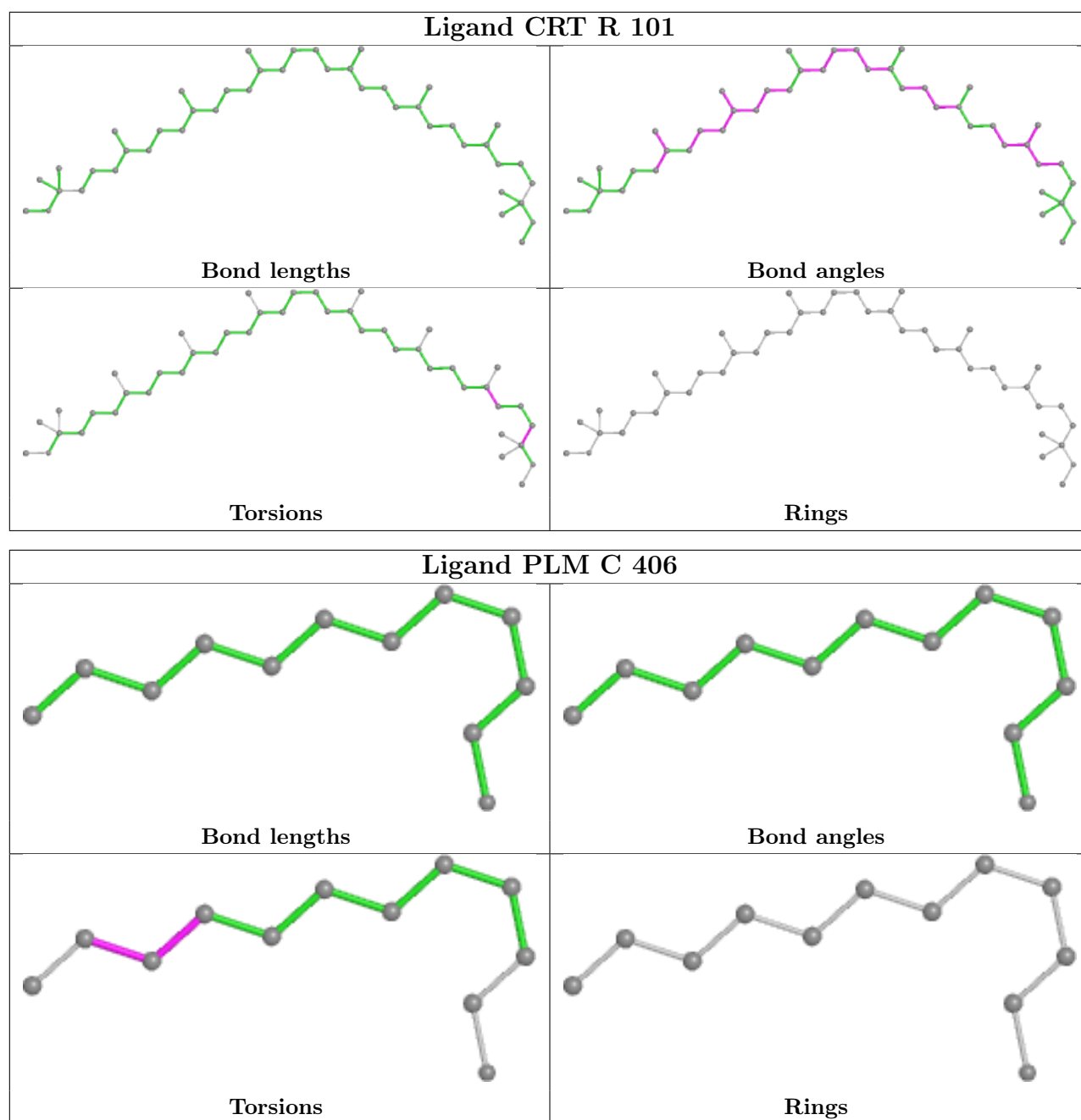


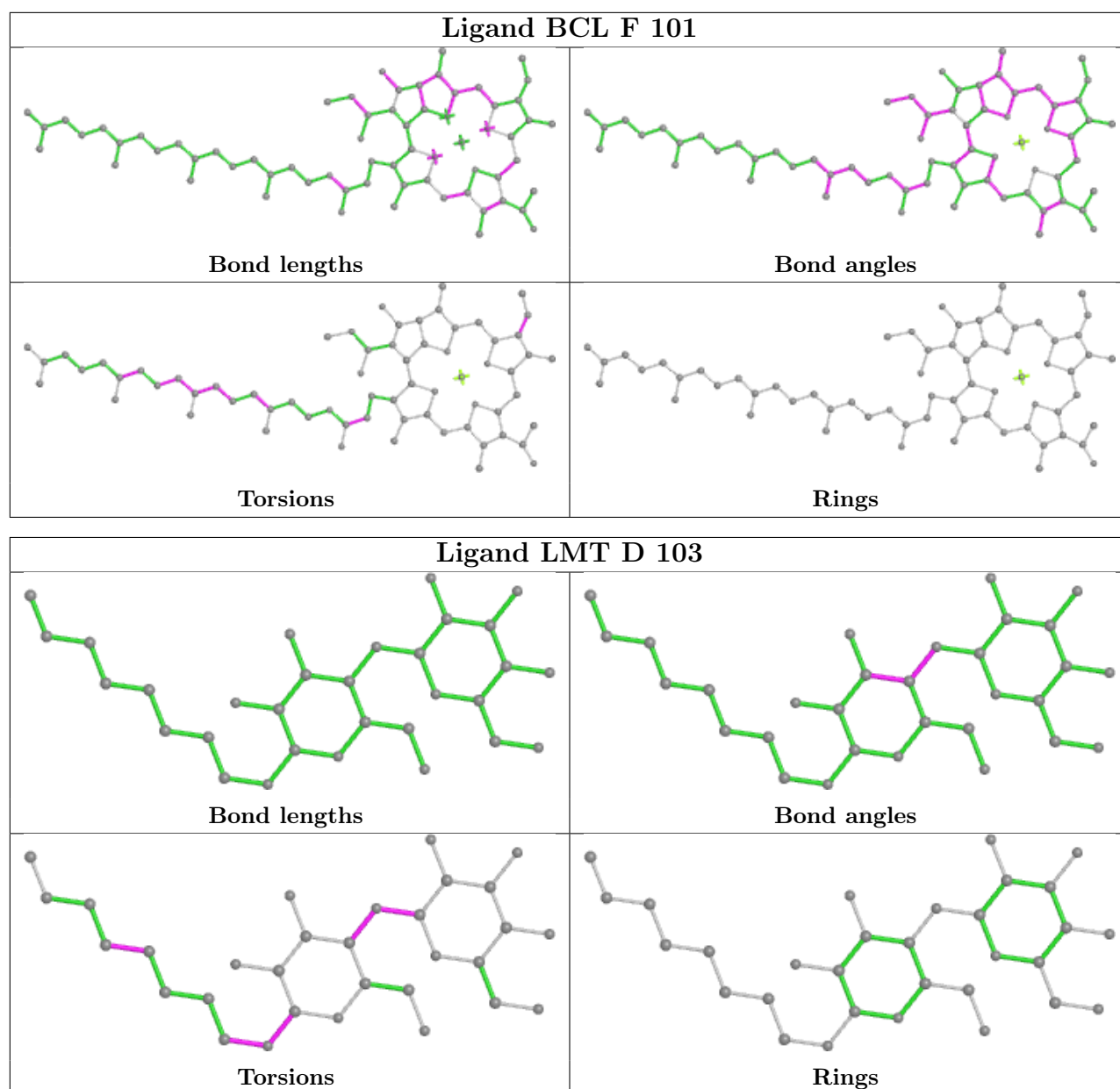
Ligand U10 Y 103

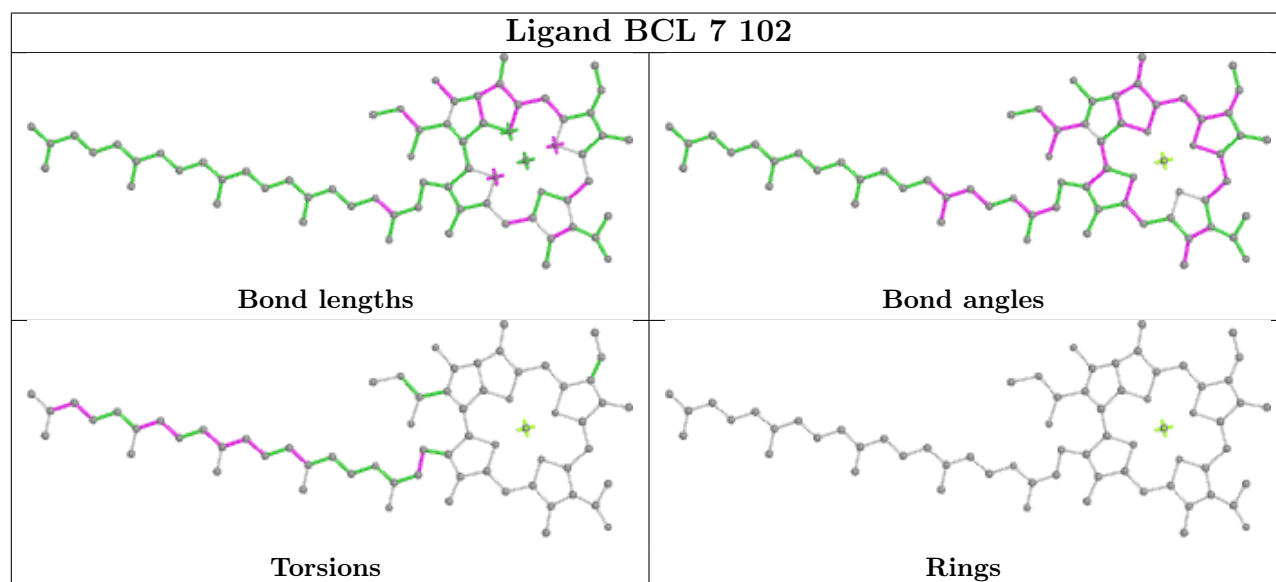
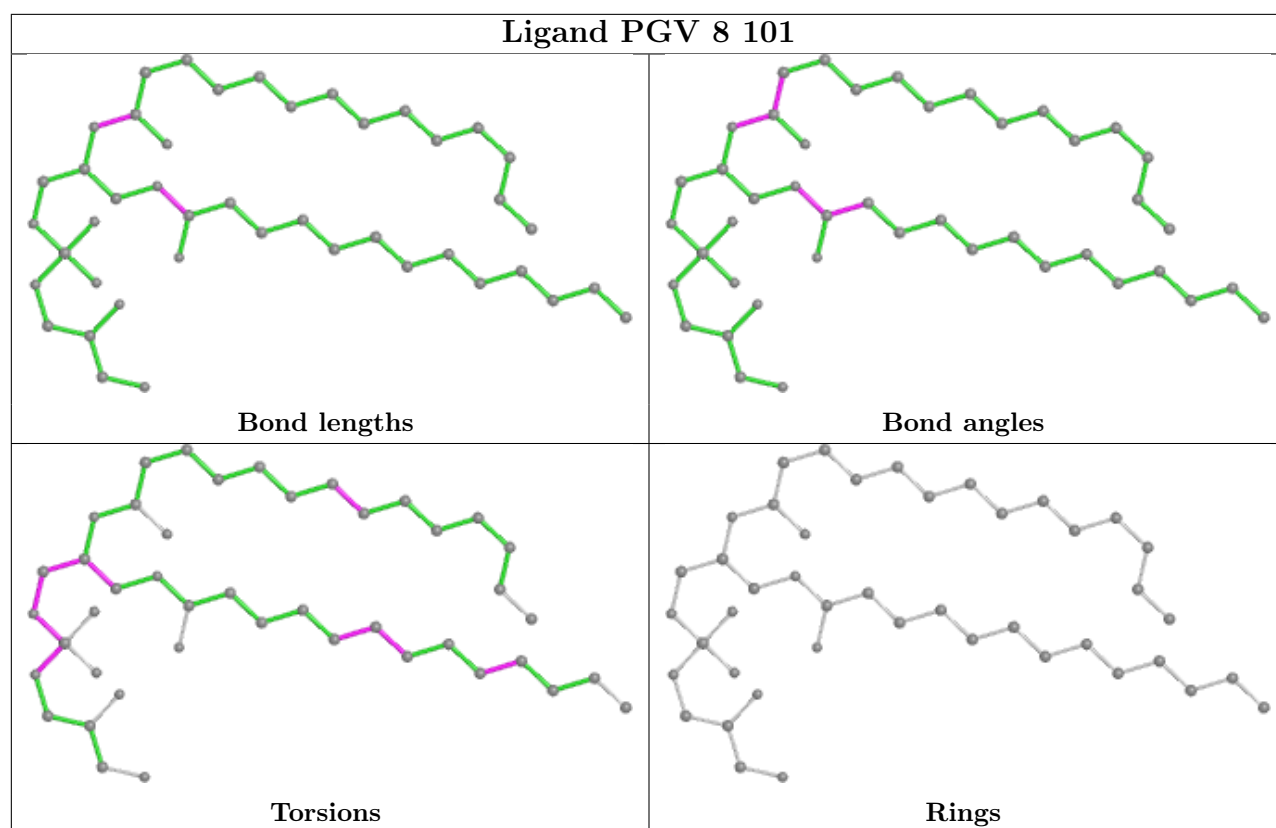


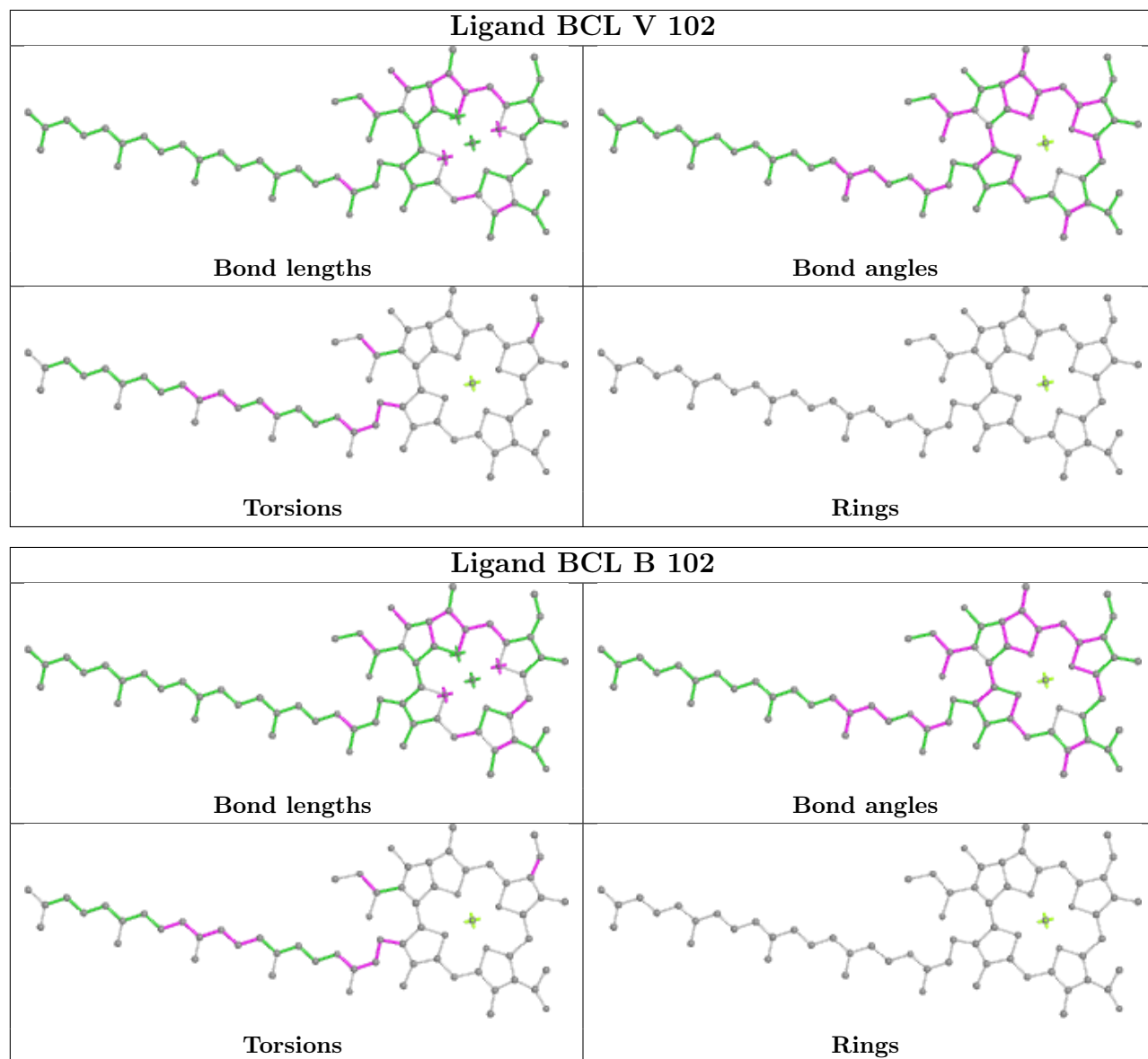
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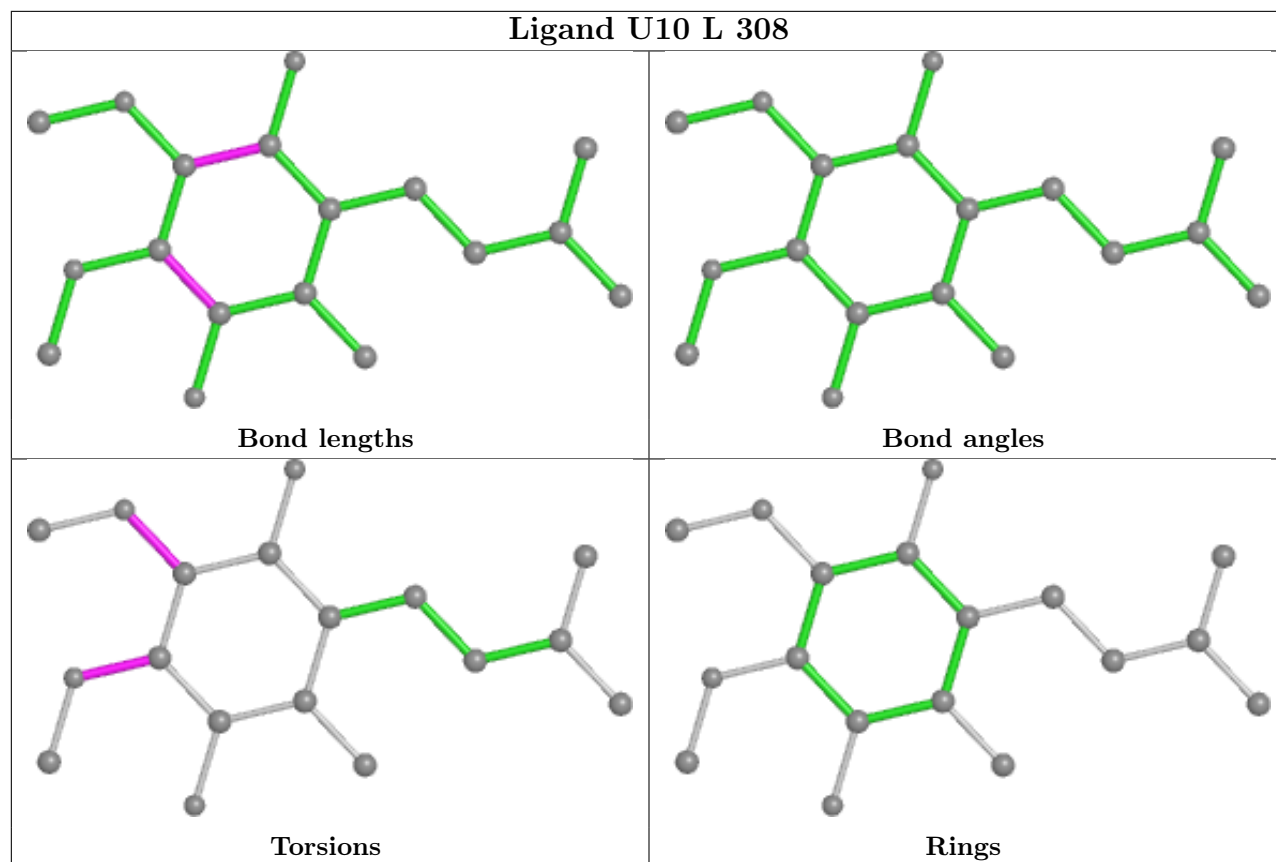




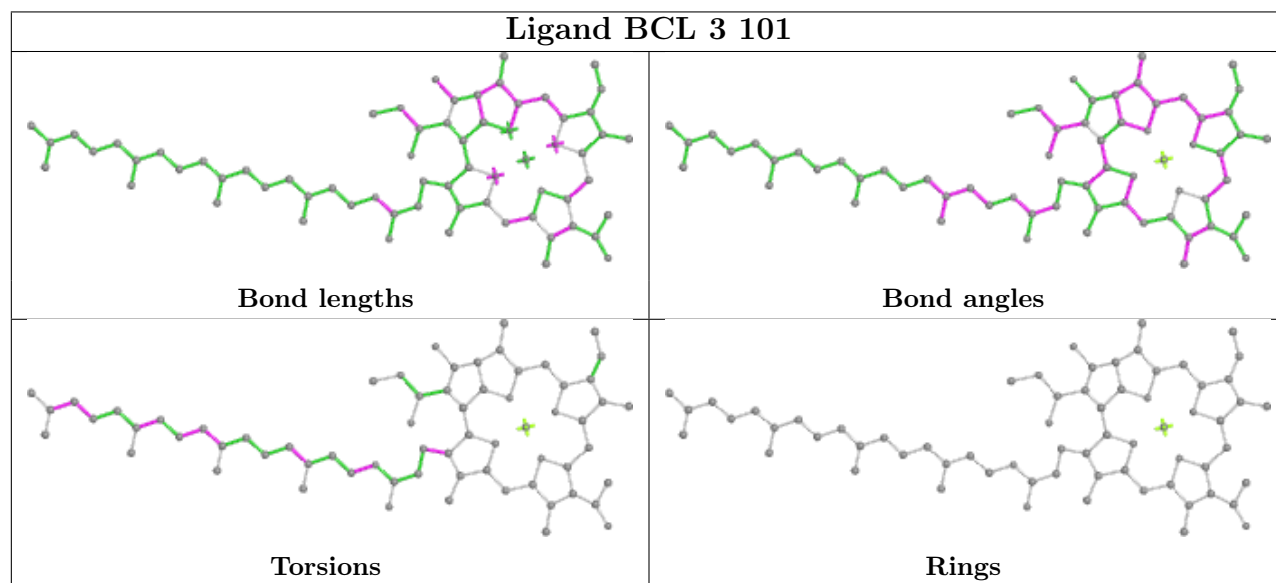


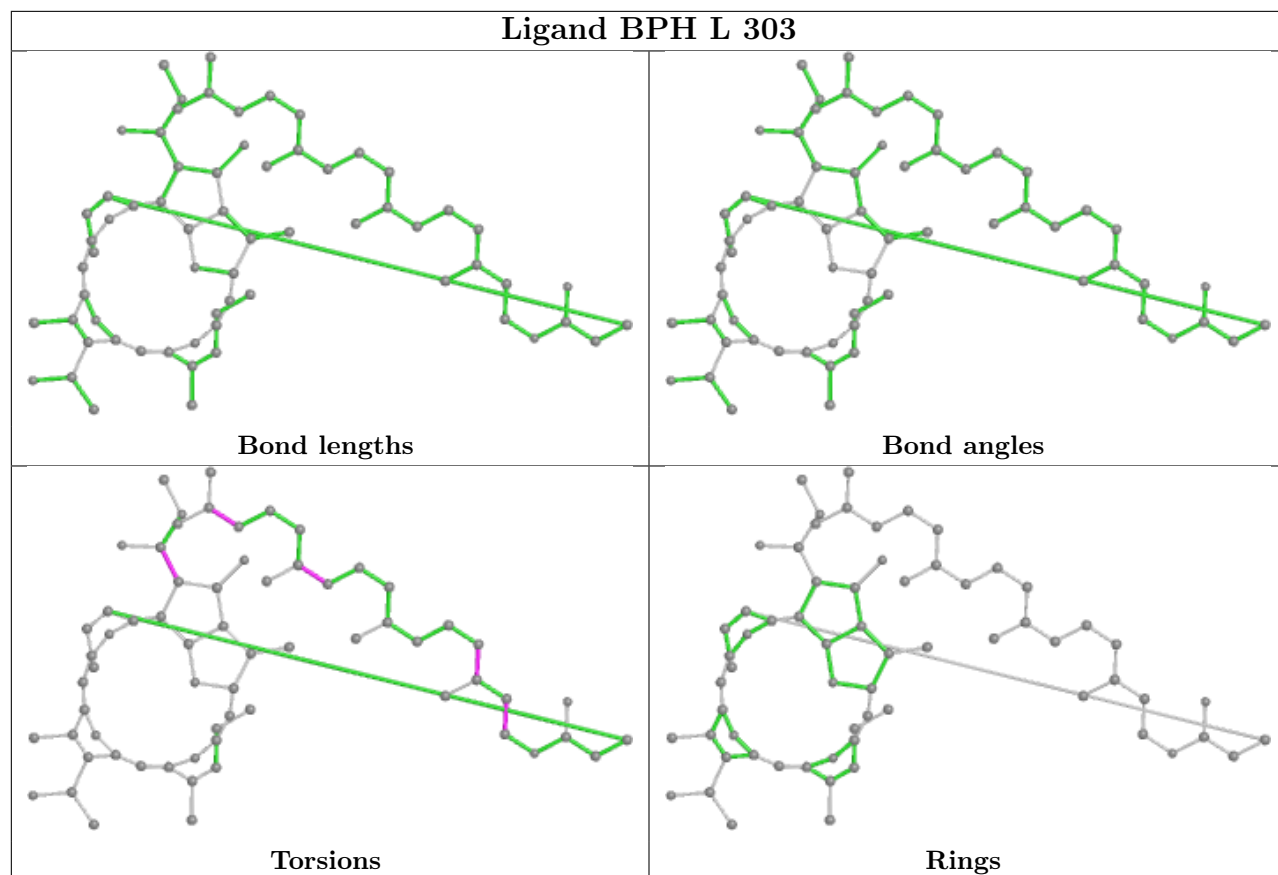
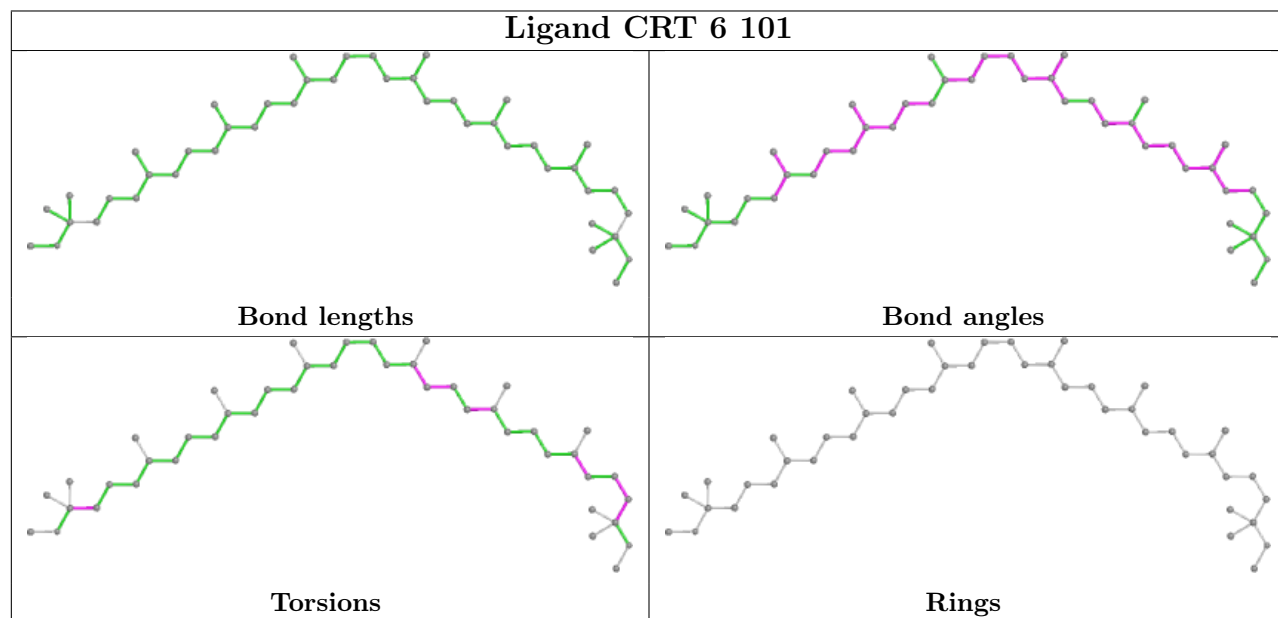


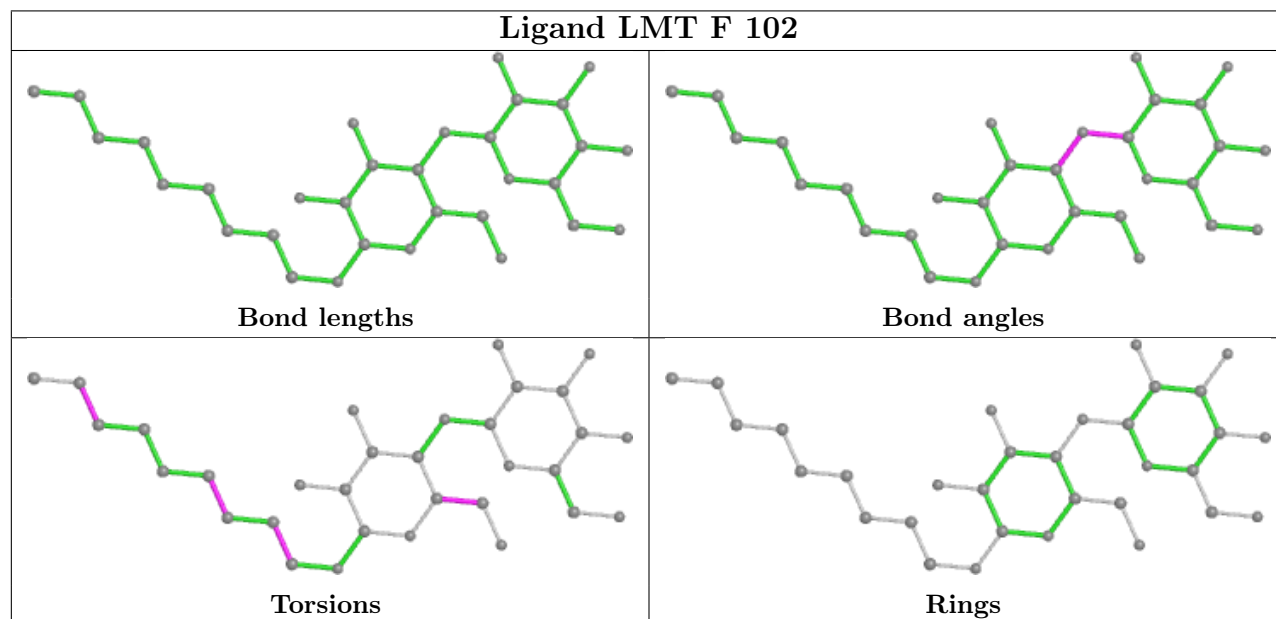
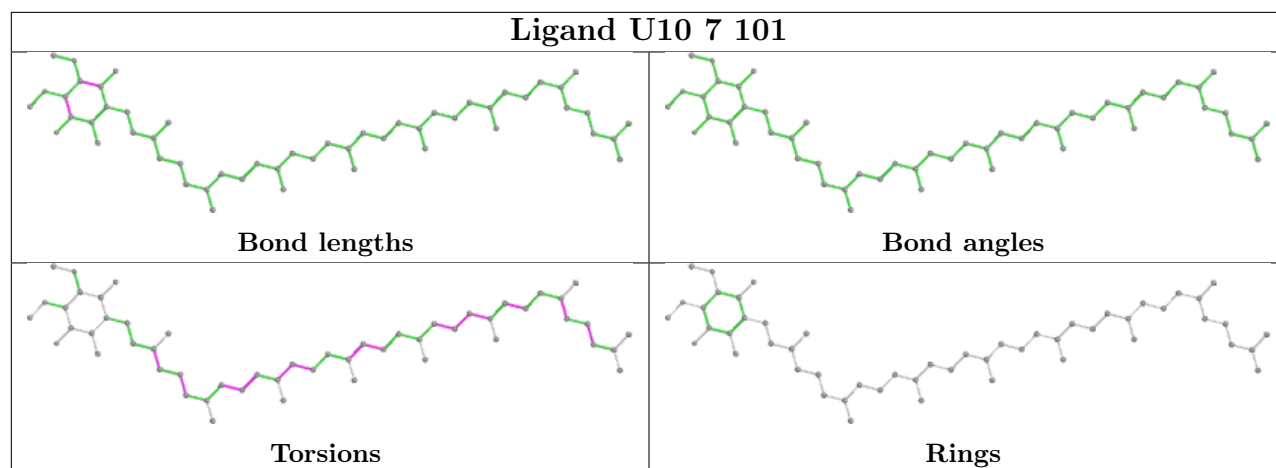
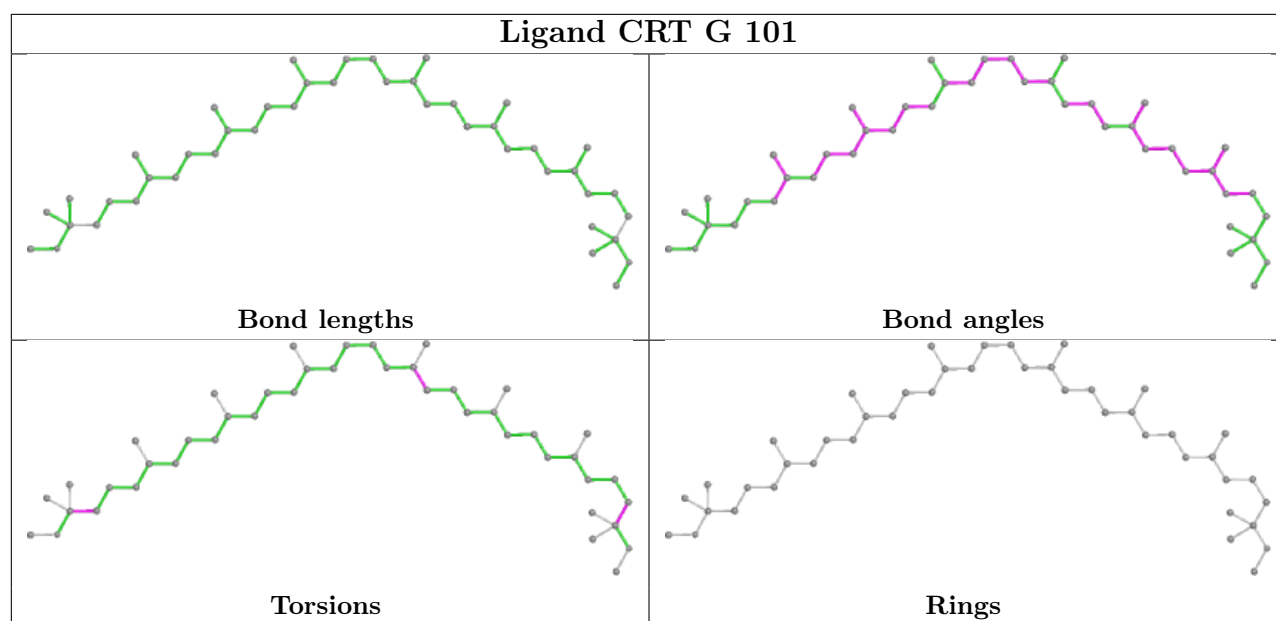
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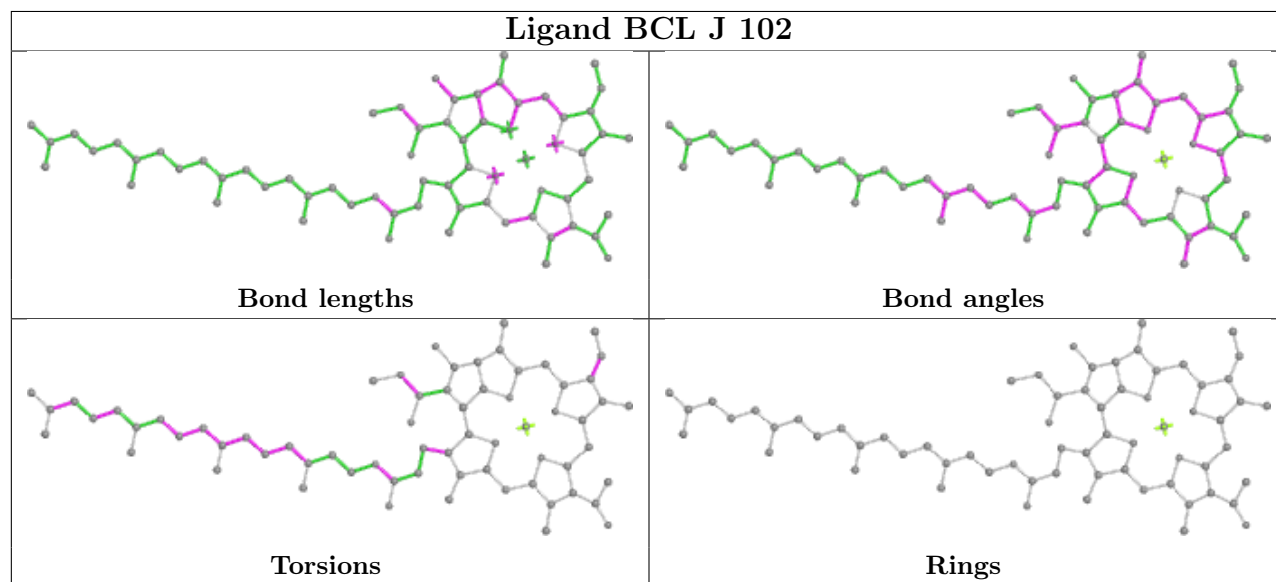
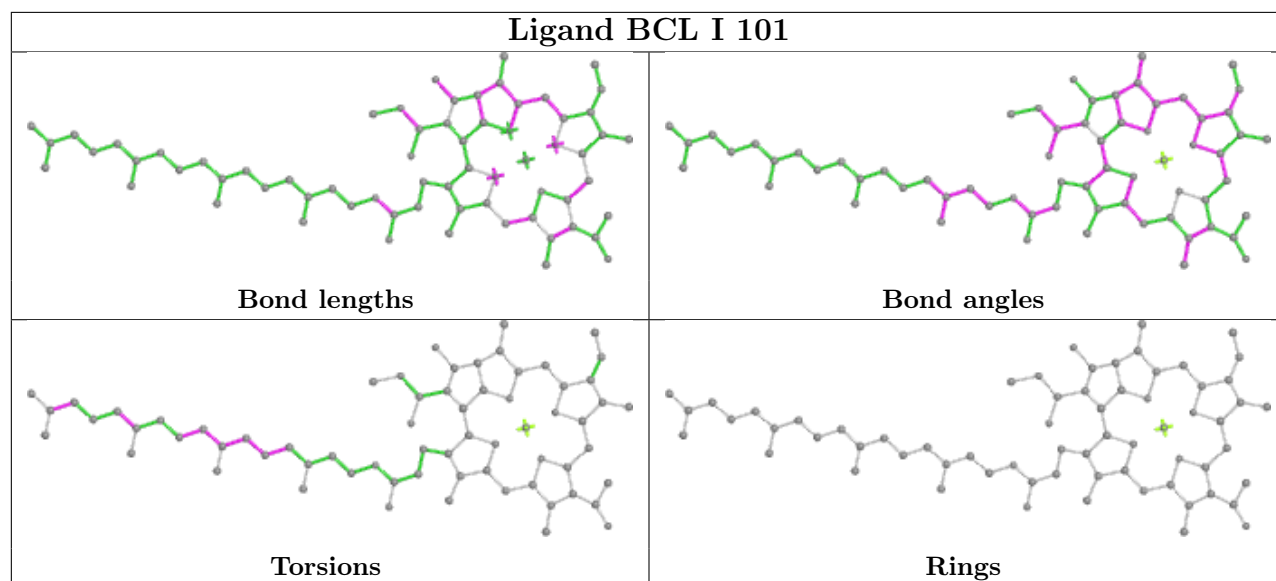
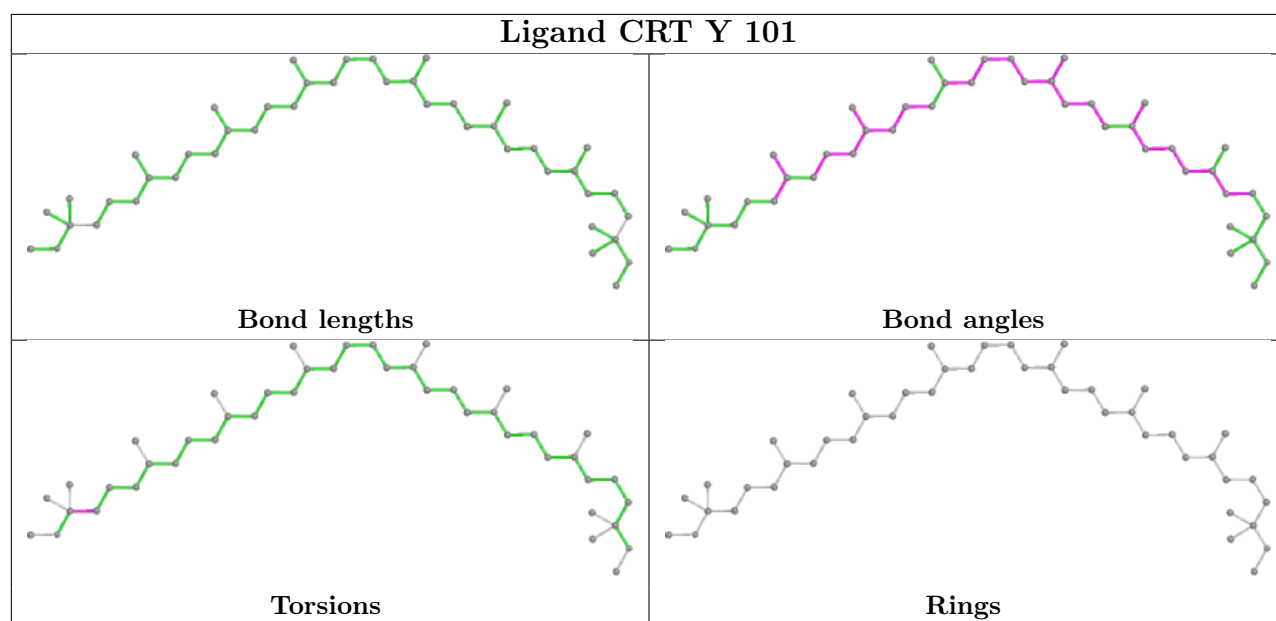


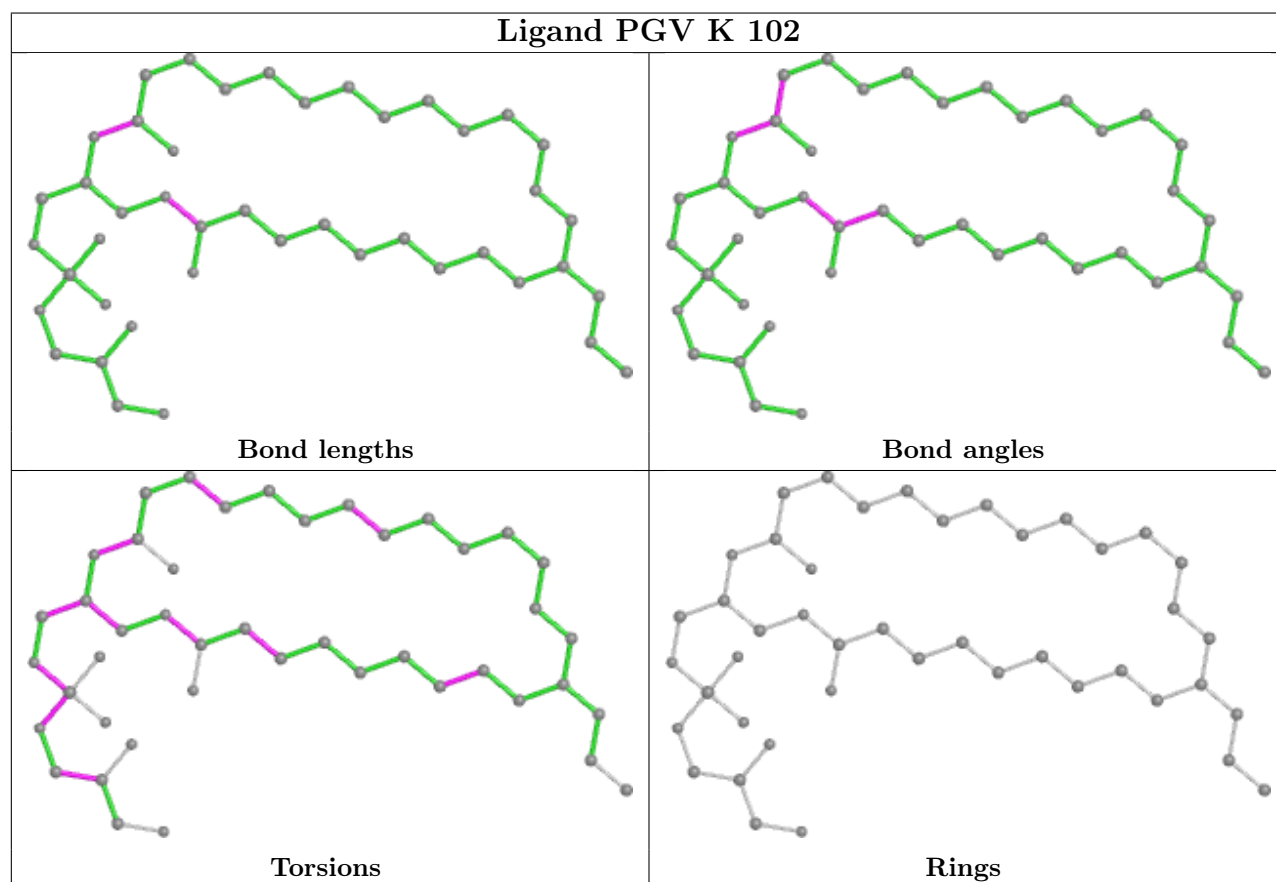
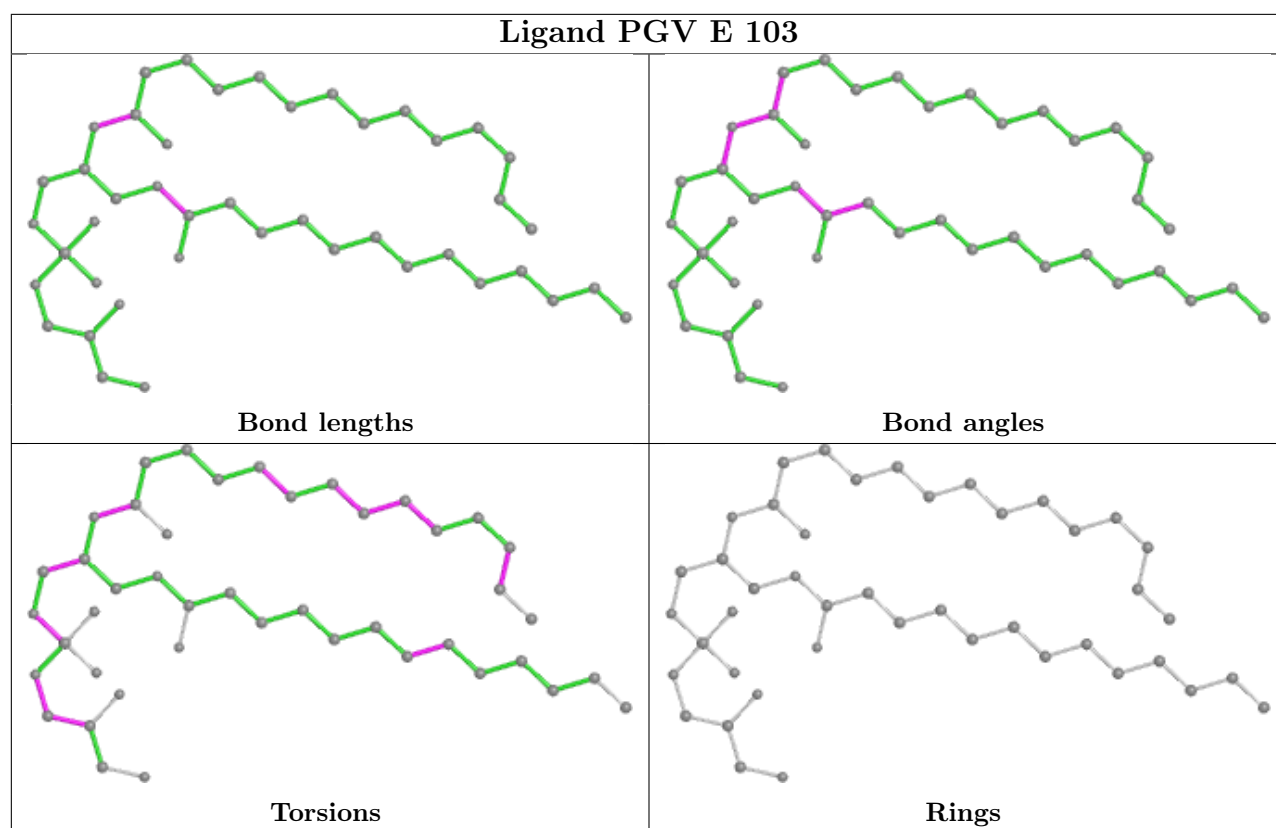
Ligand BCL 3 101

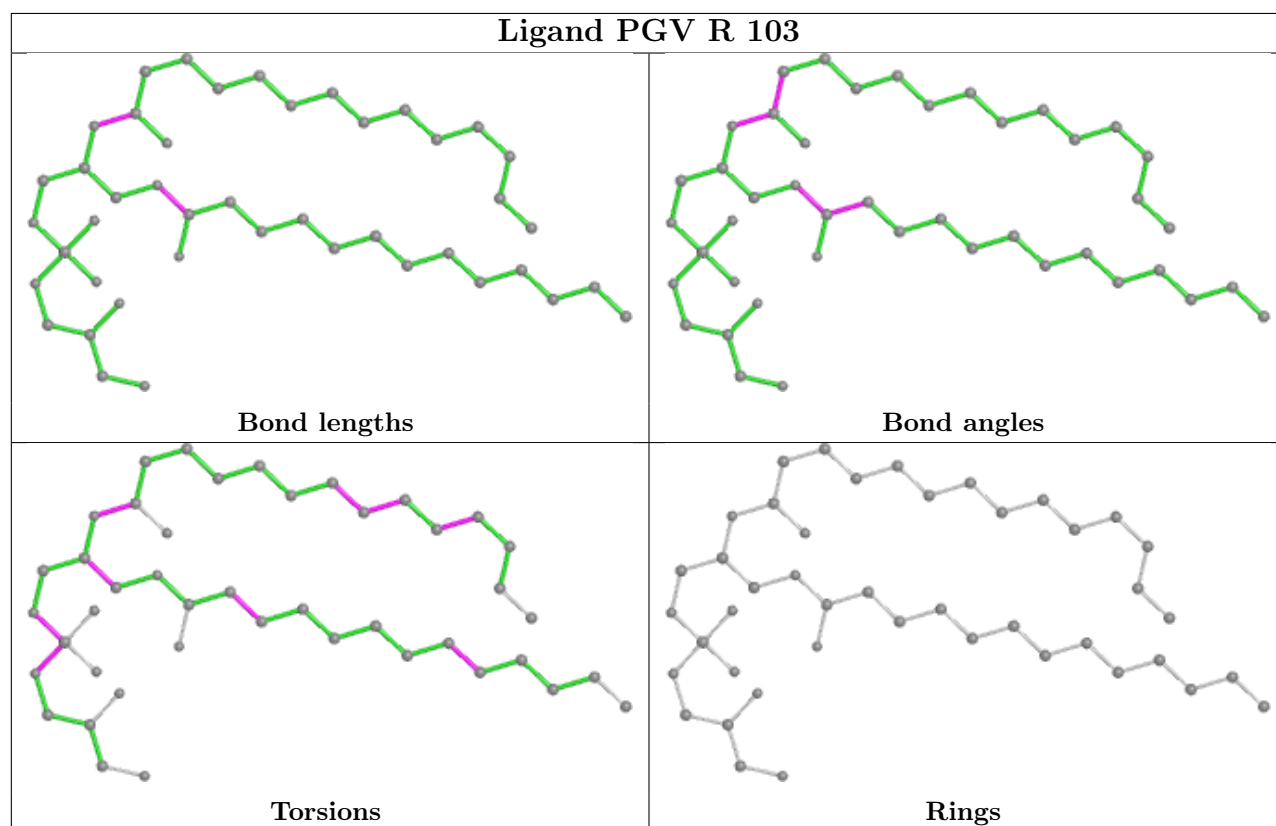
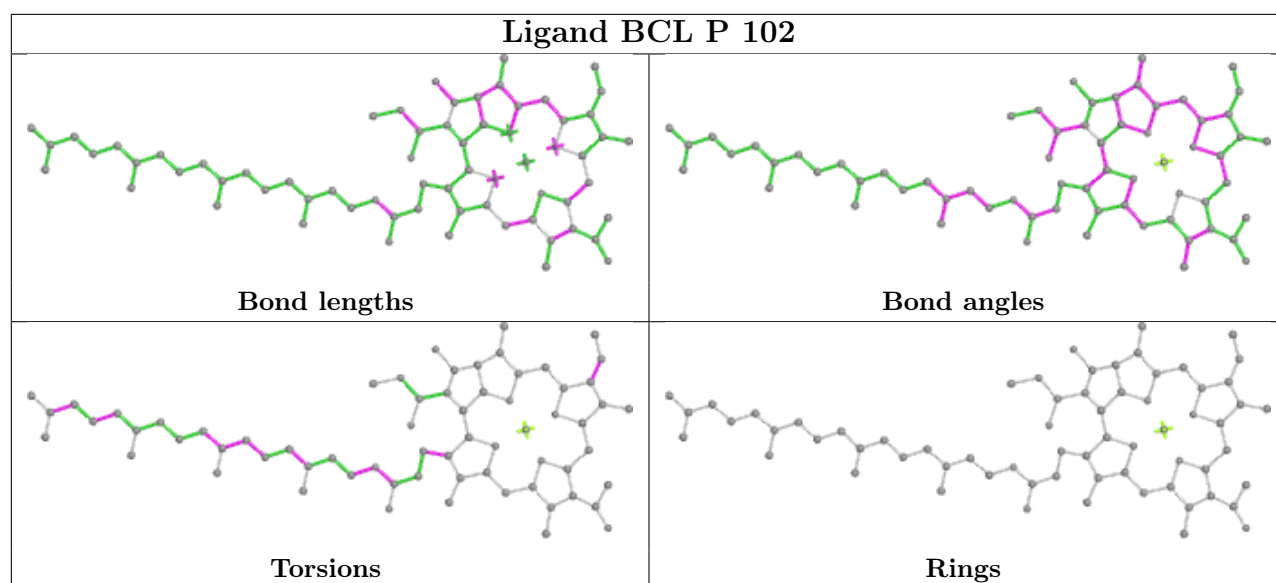


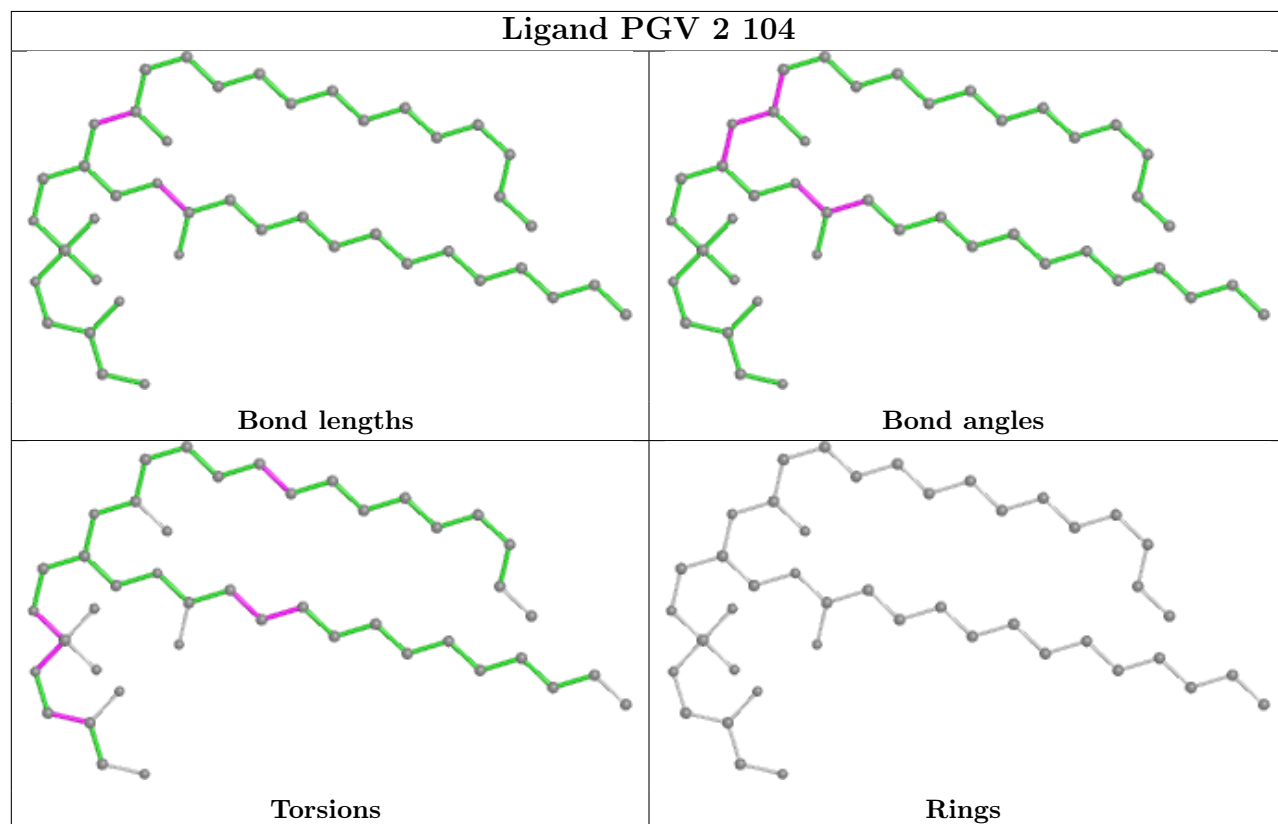
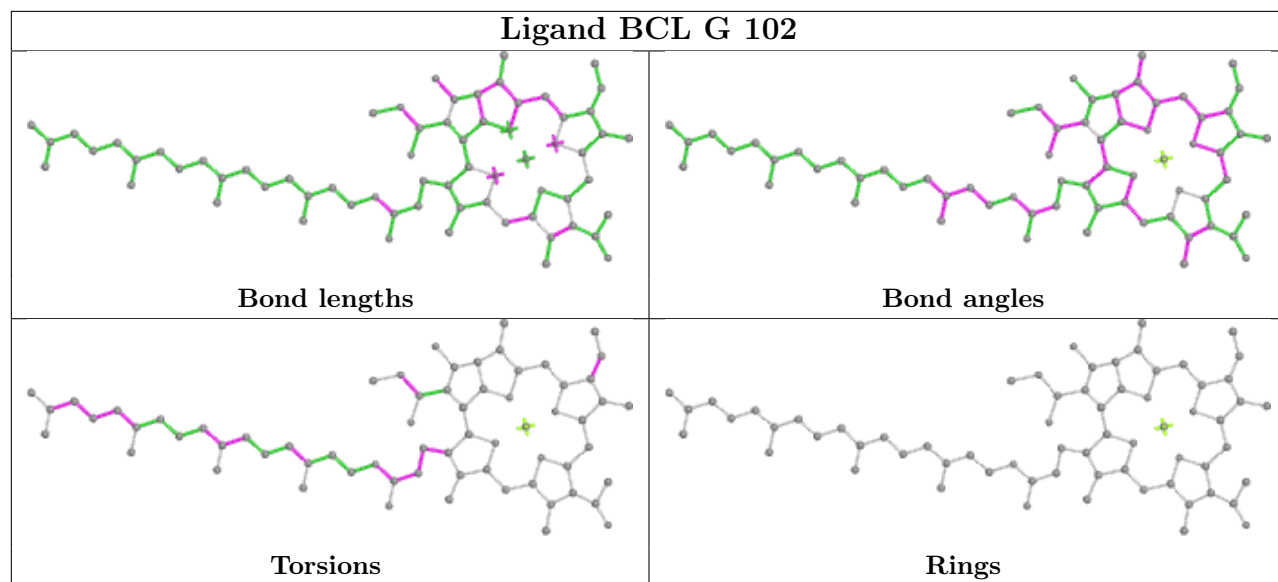
Ligand BPH L 303**Ligand CRT 6 101**

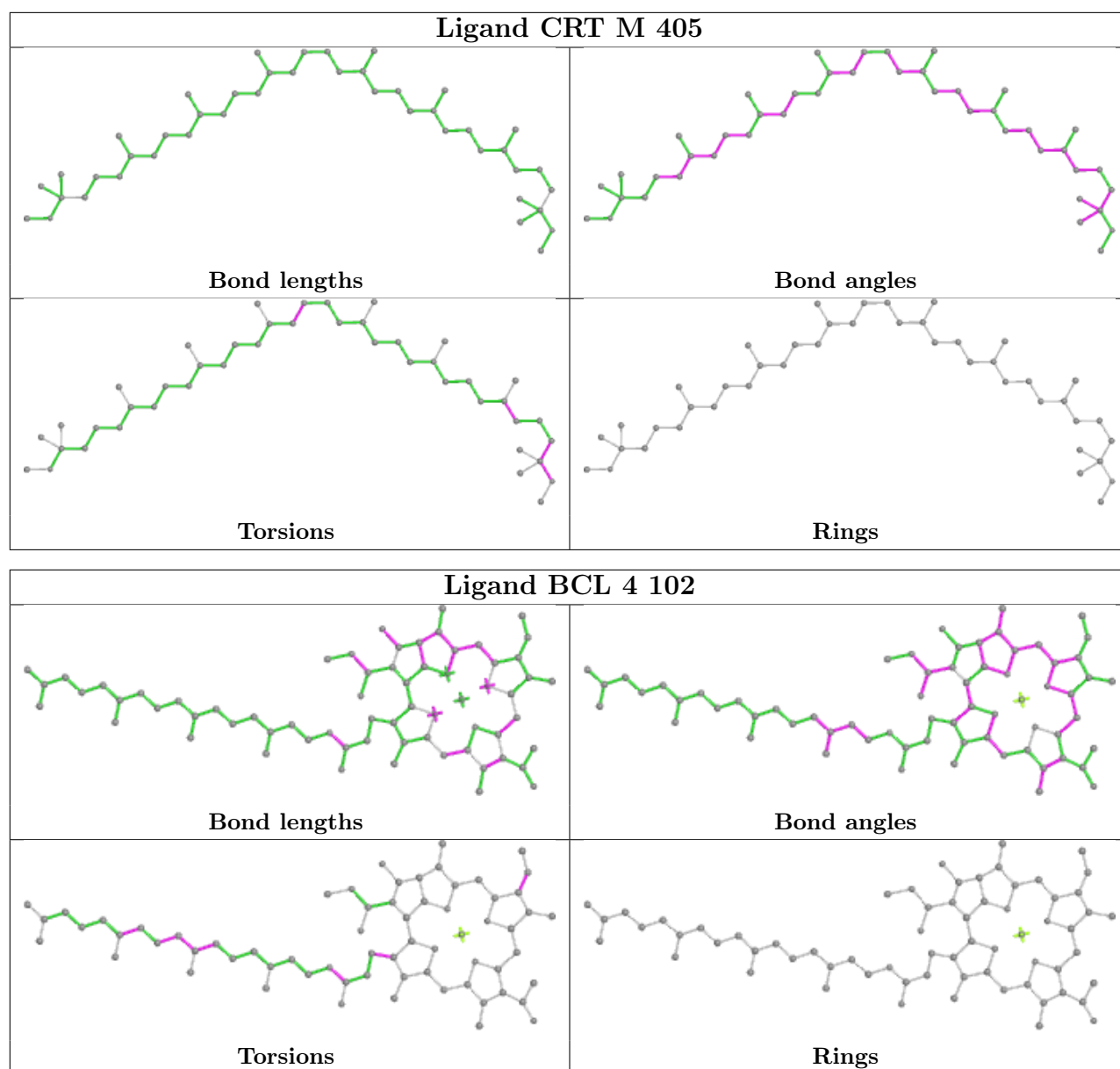


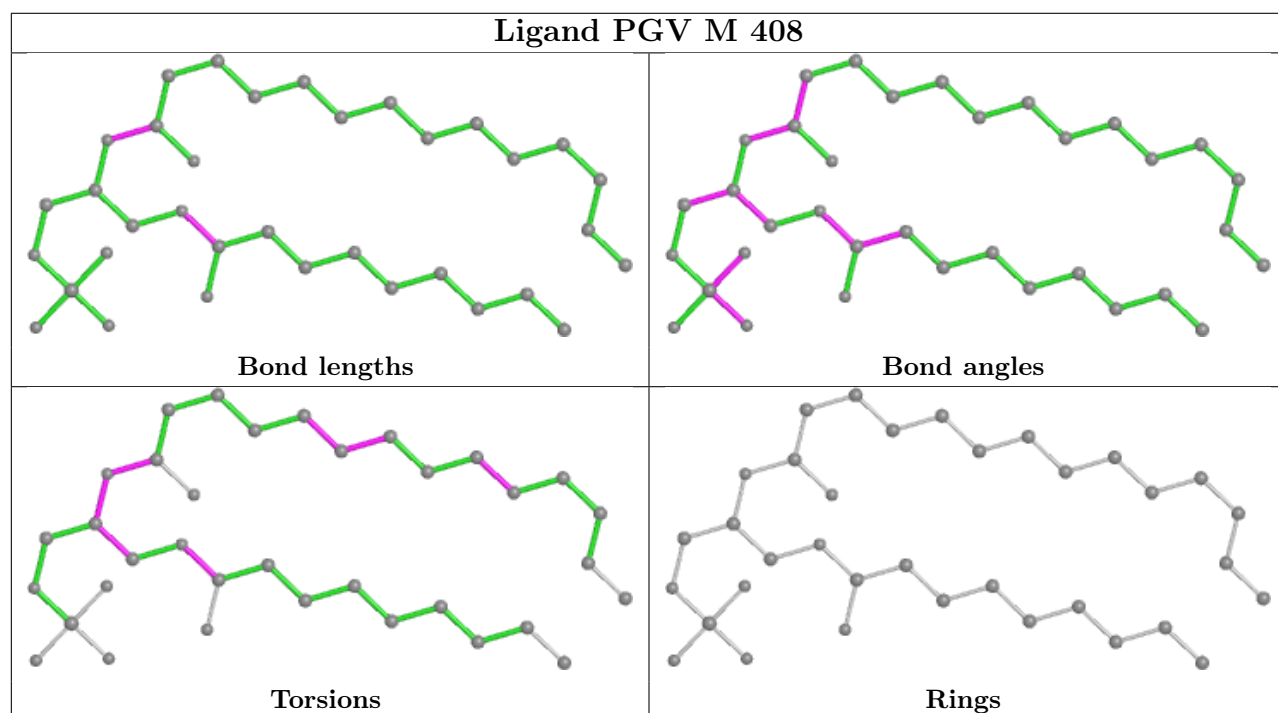
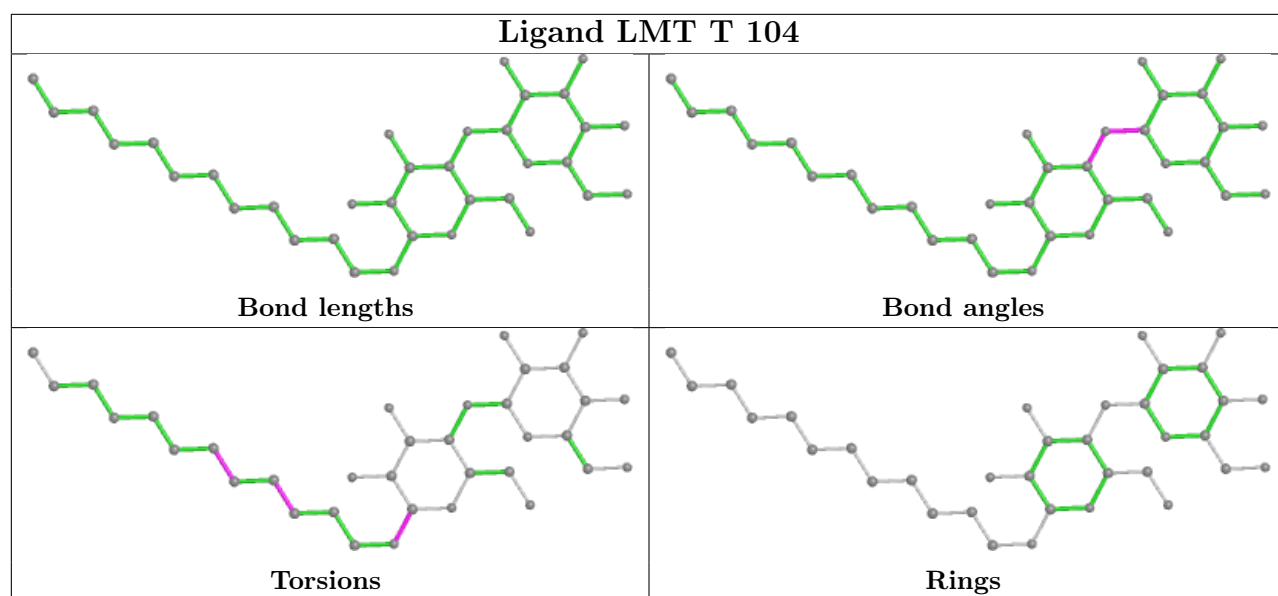


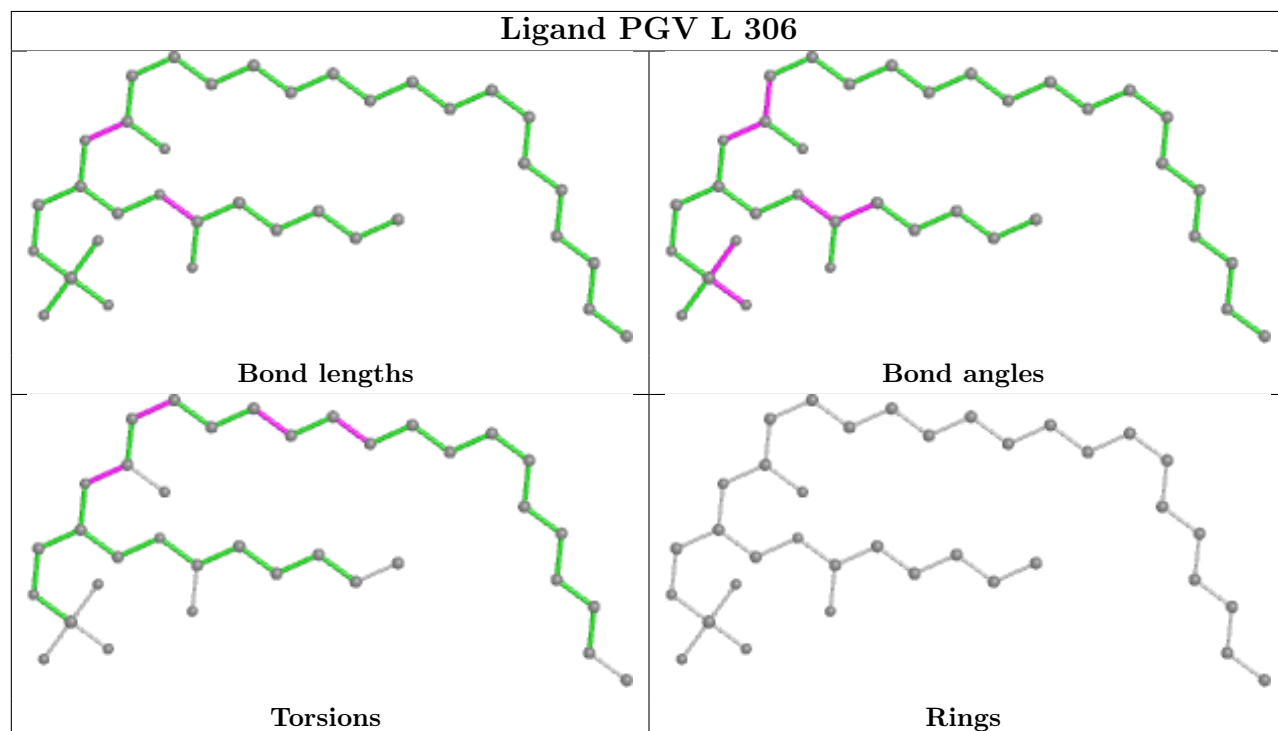
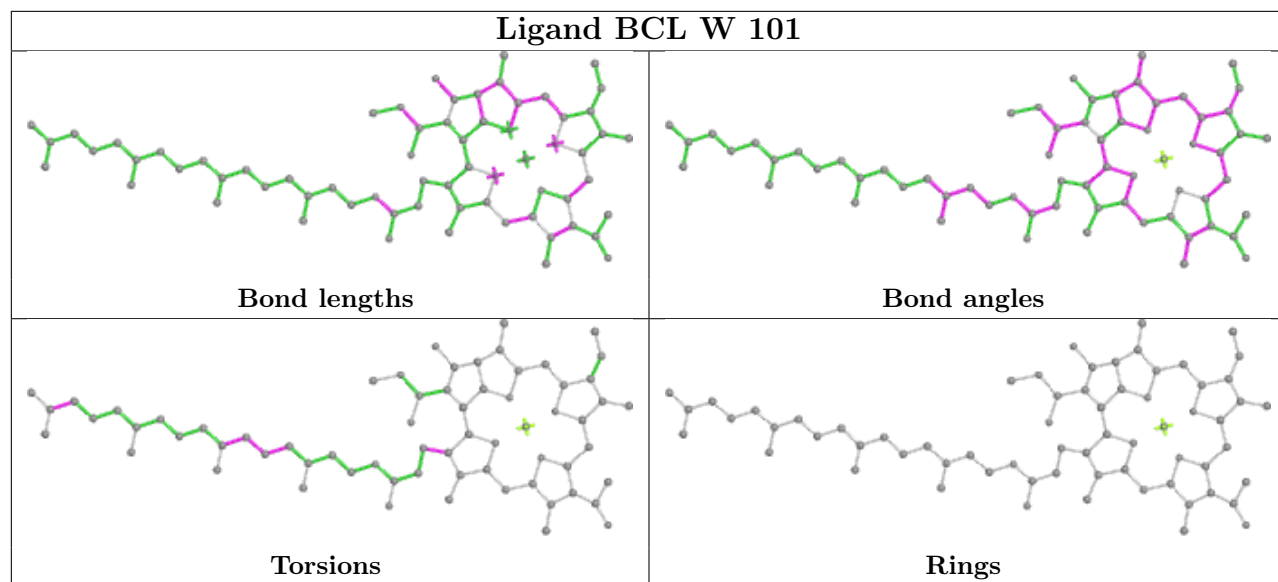


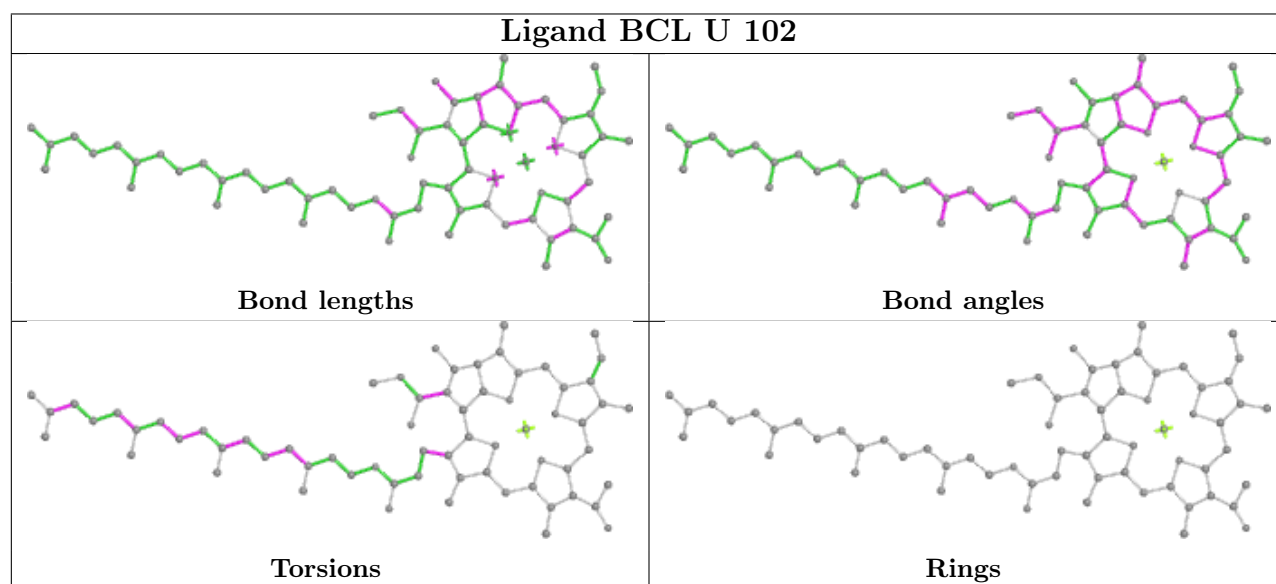
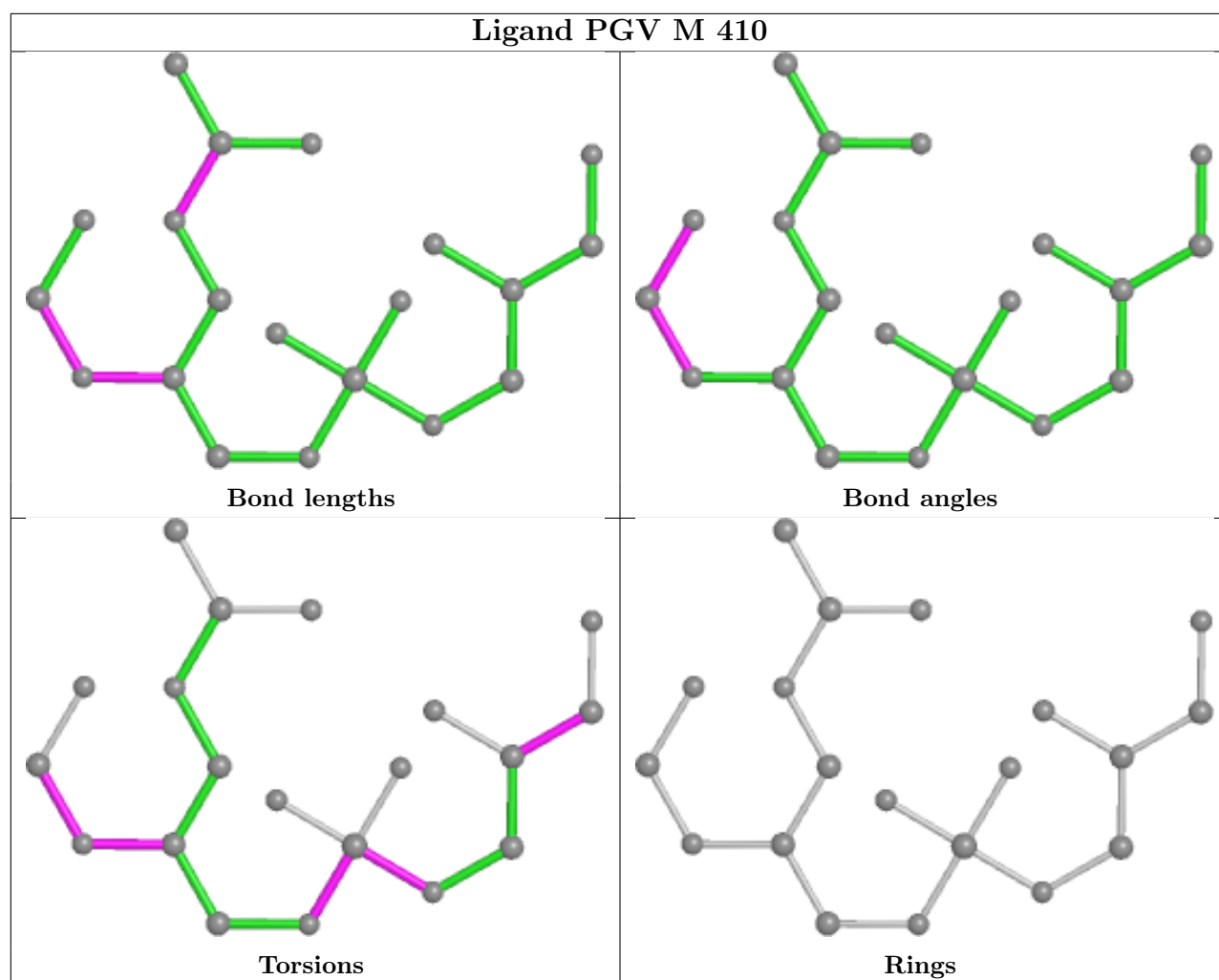


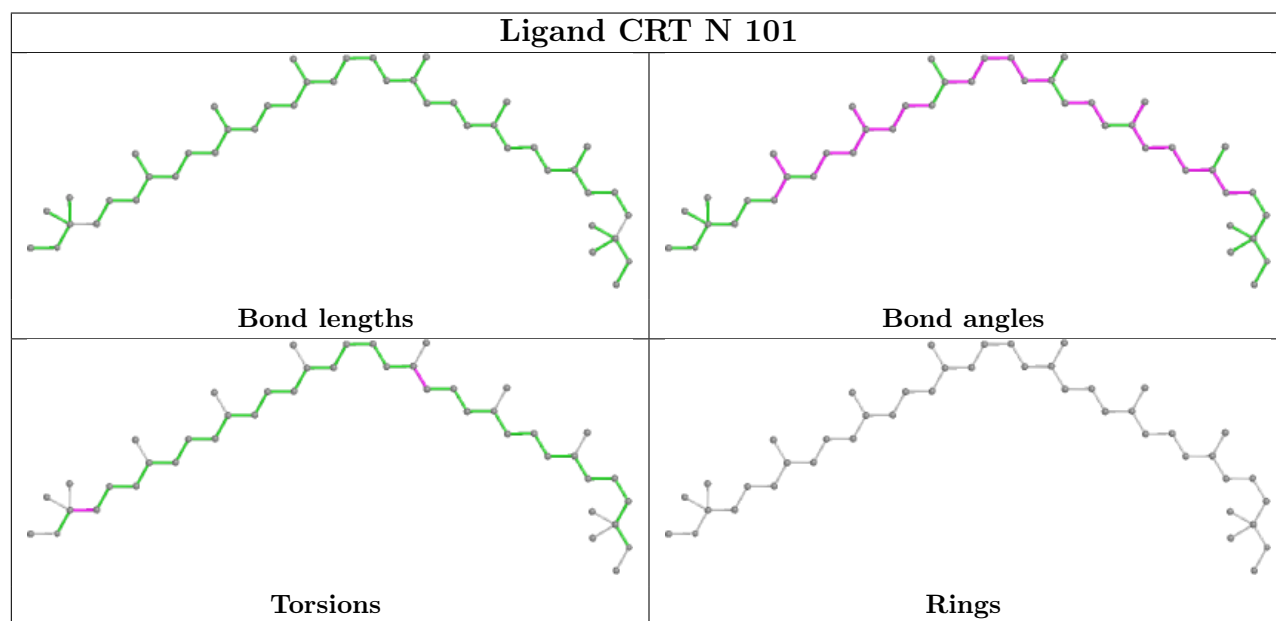
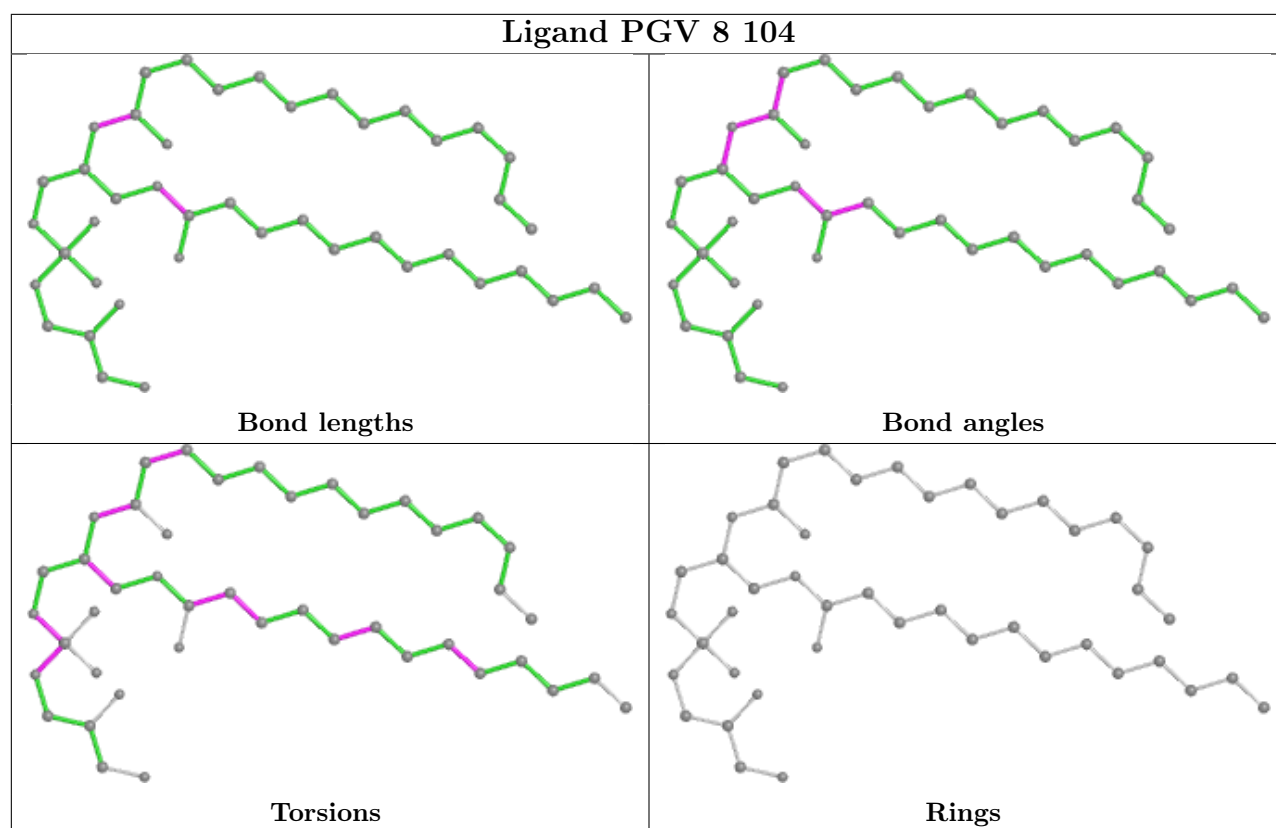


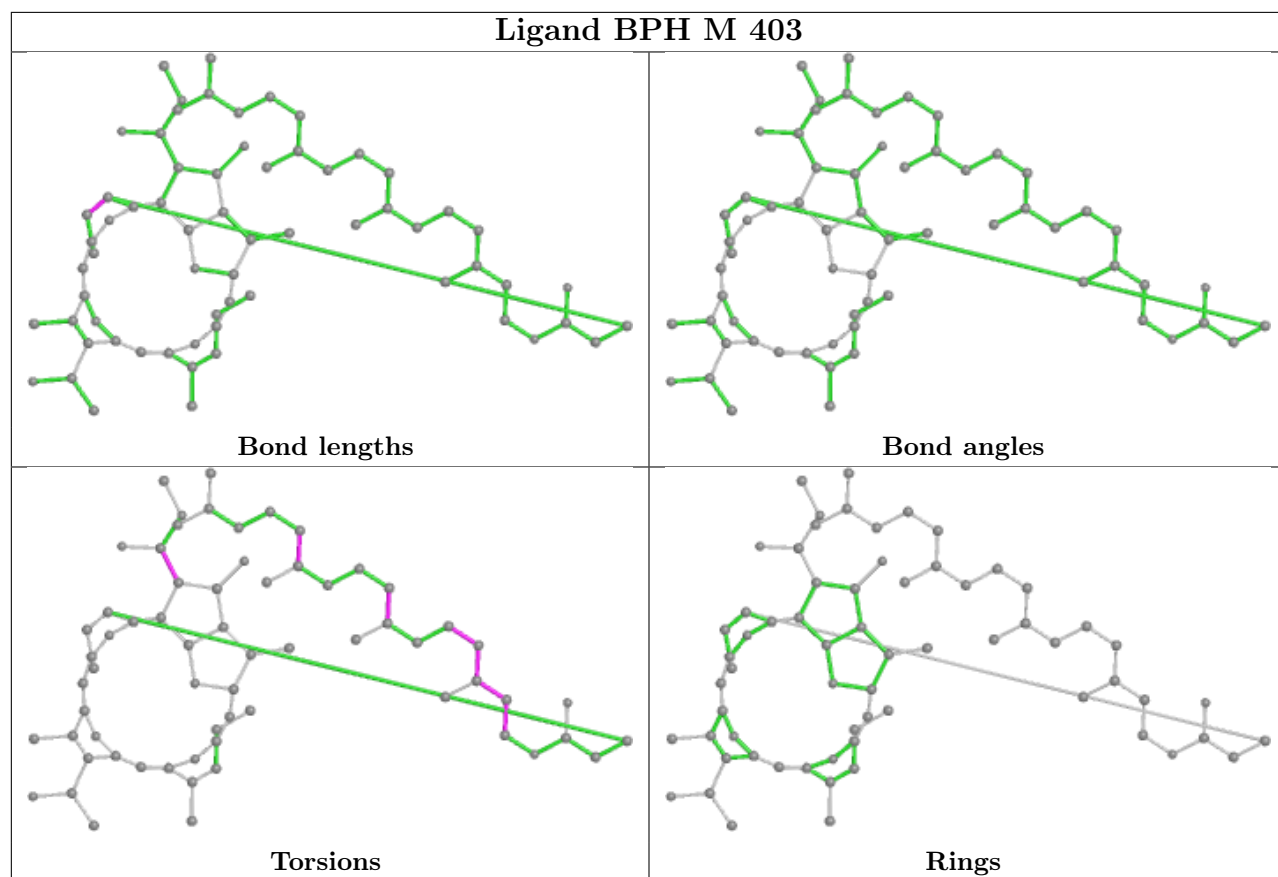
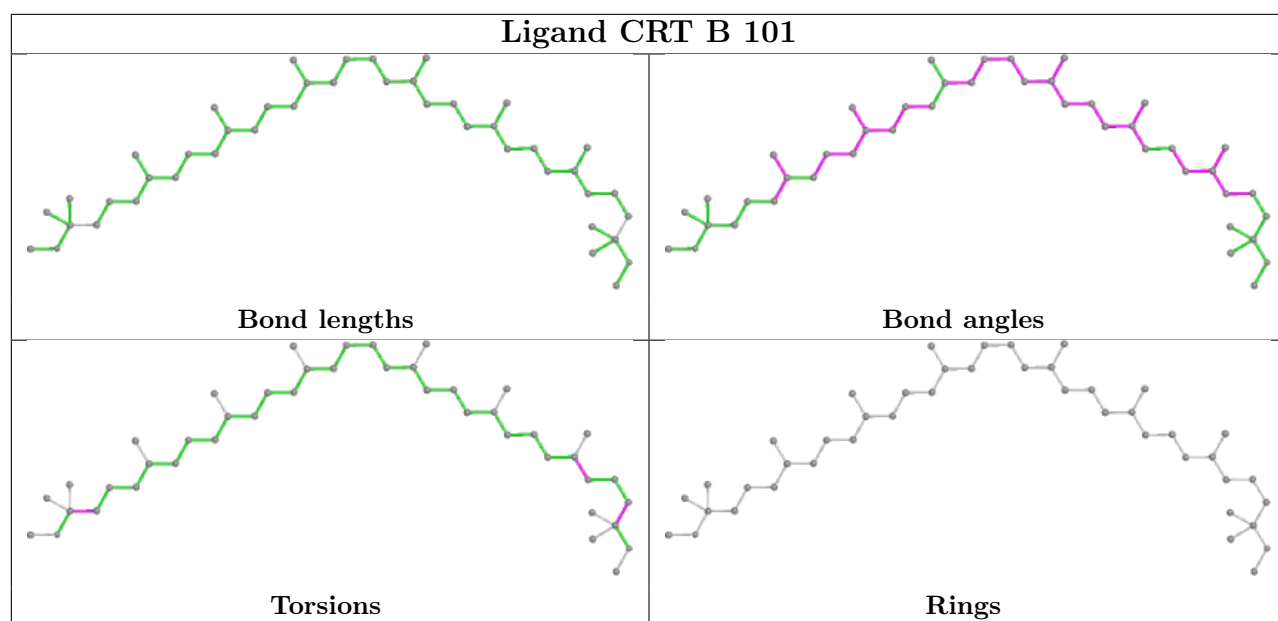


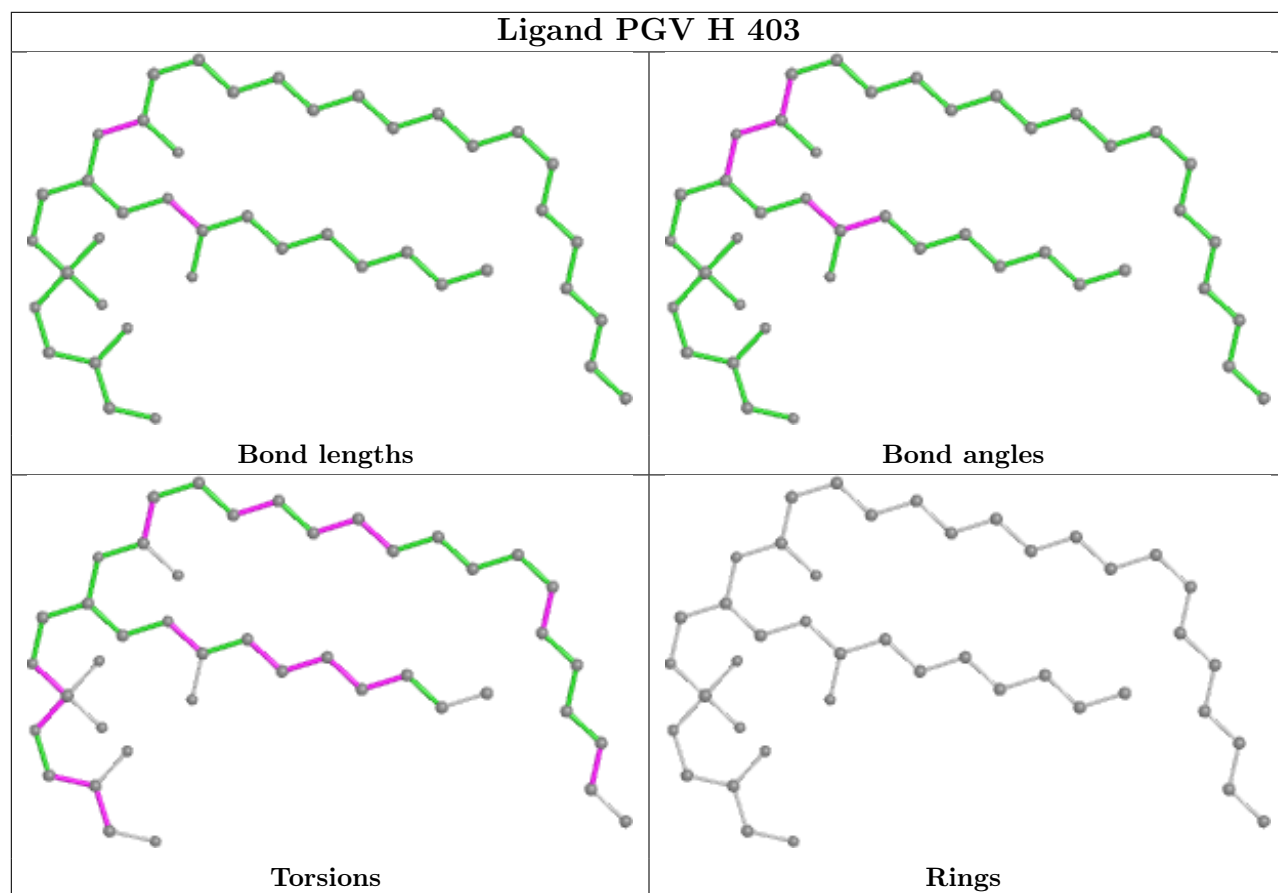
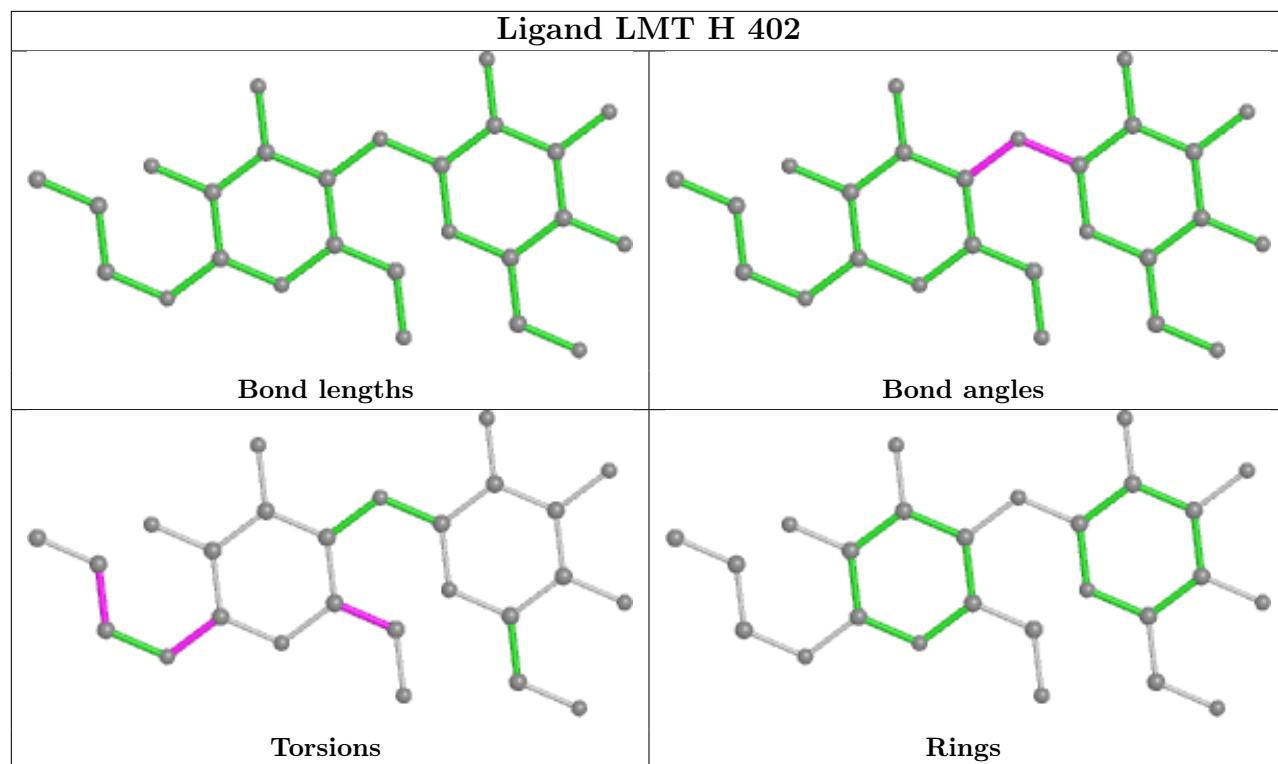


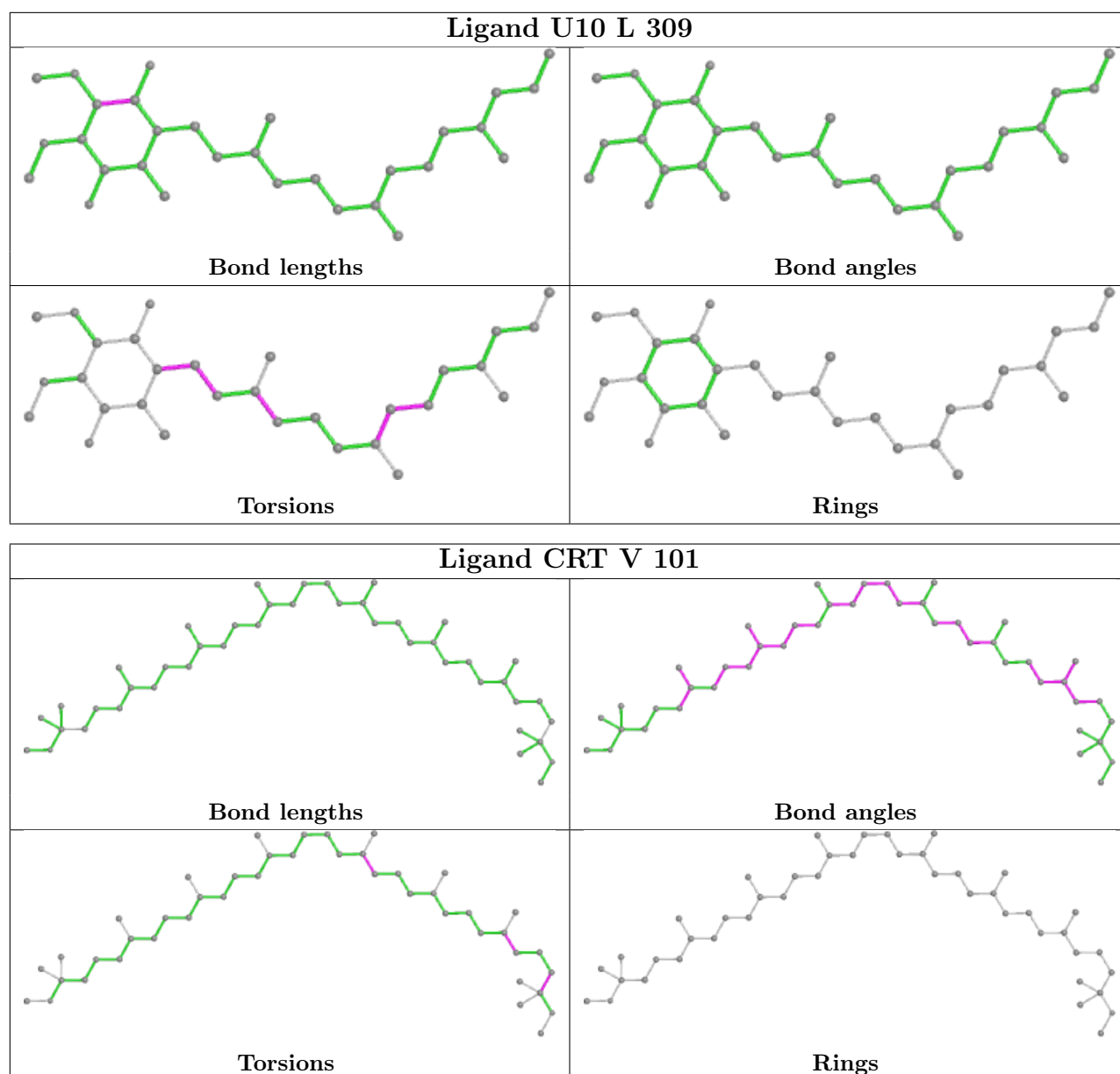




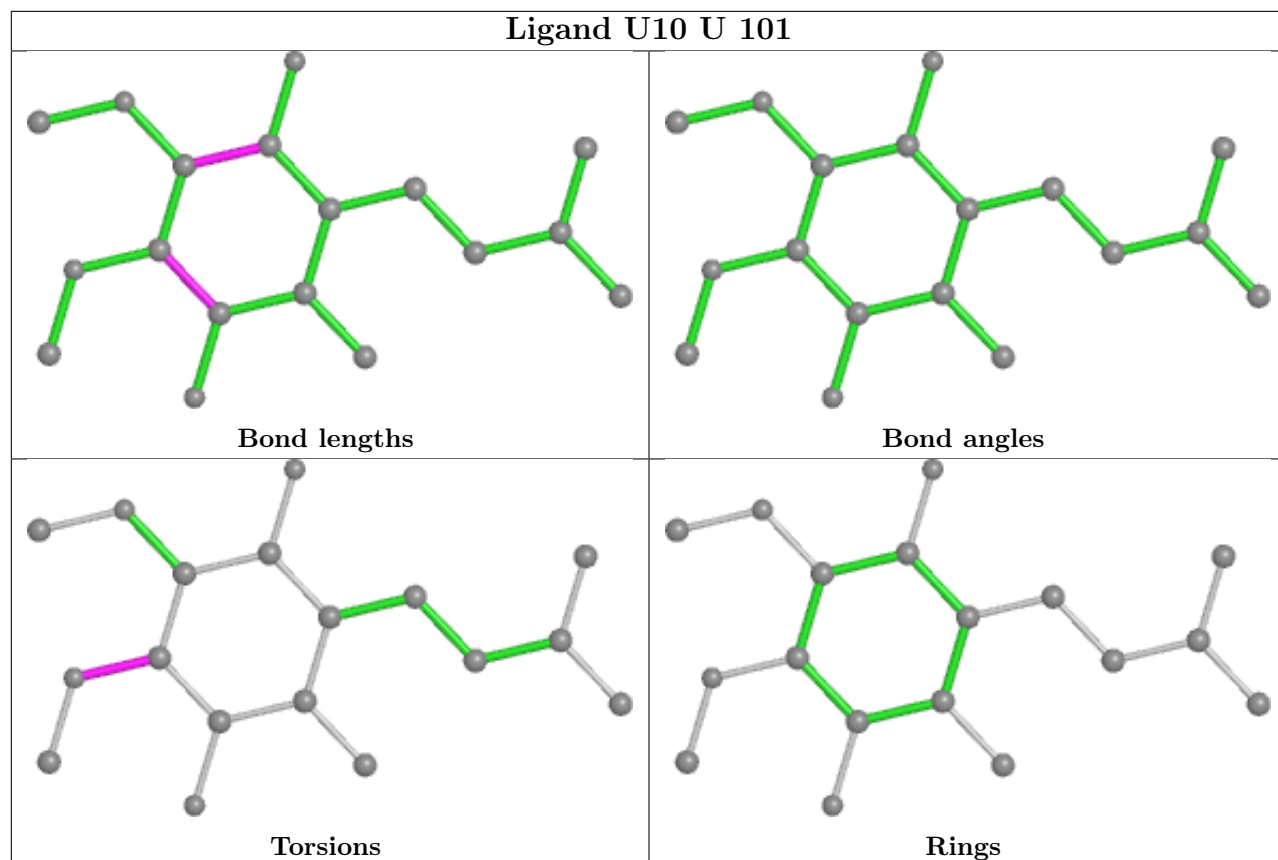




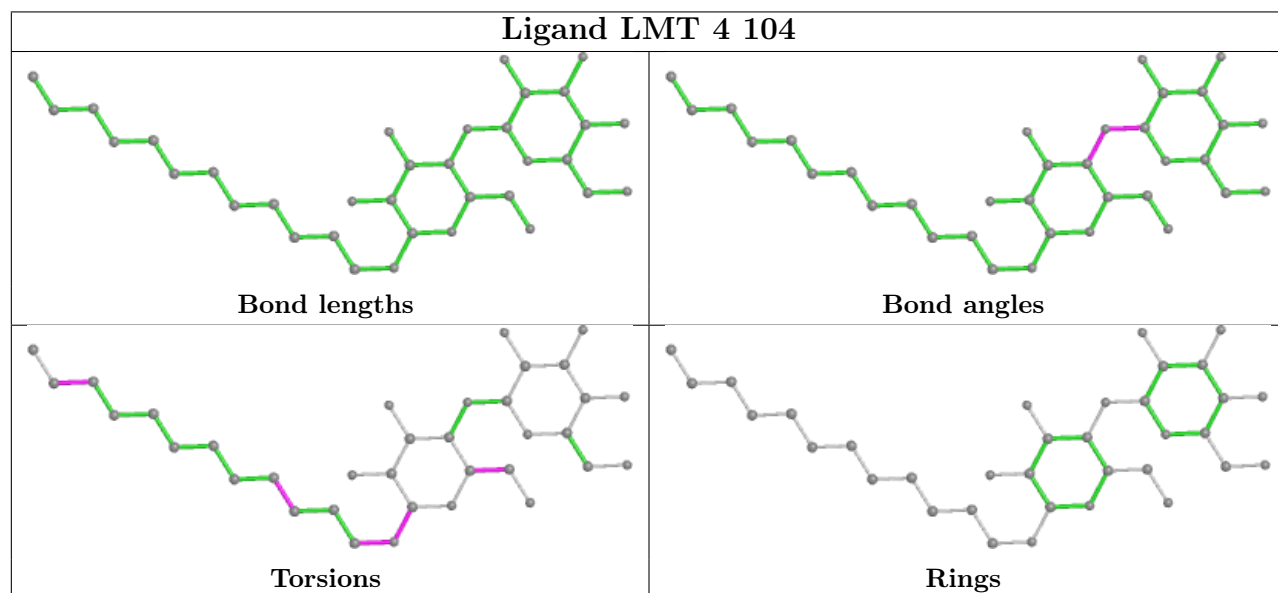


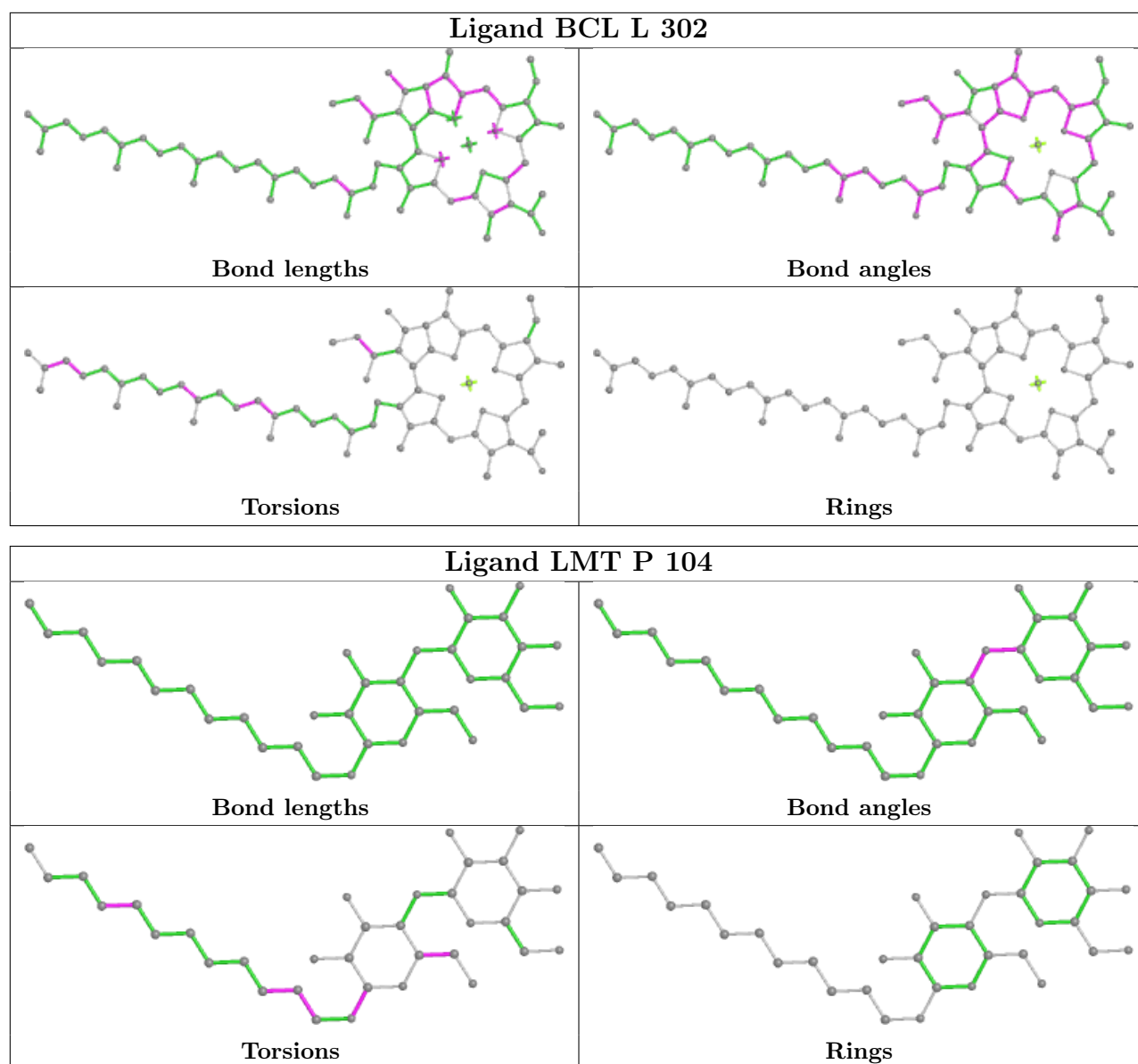


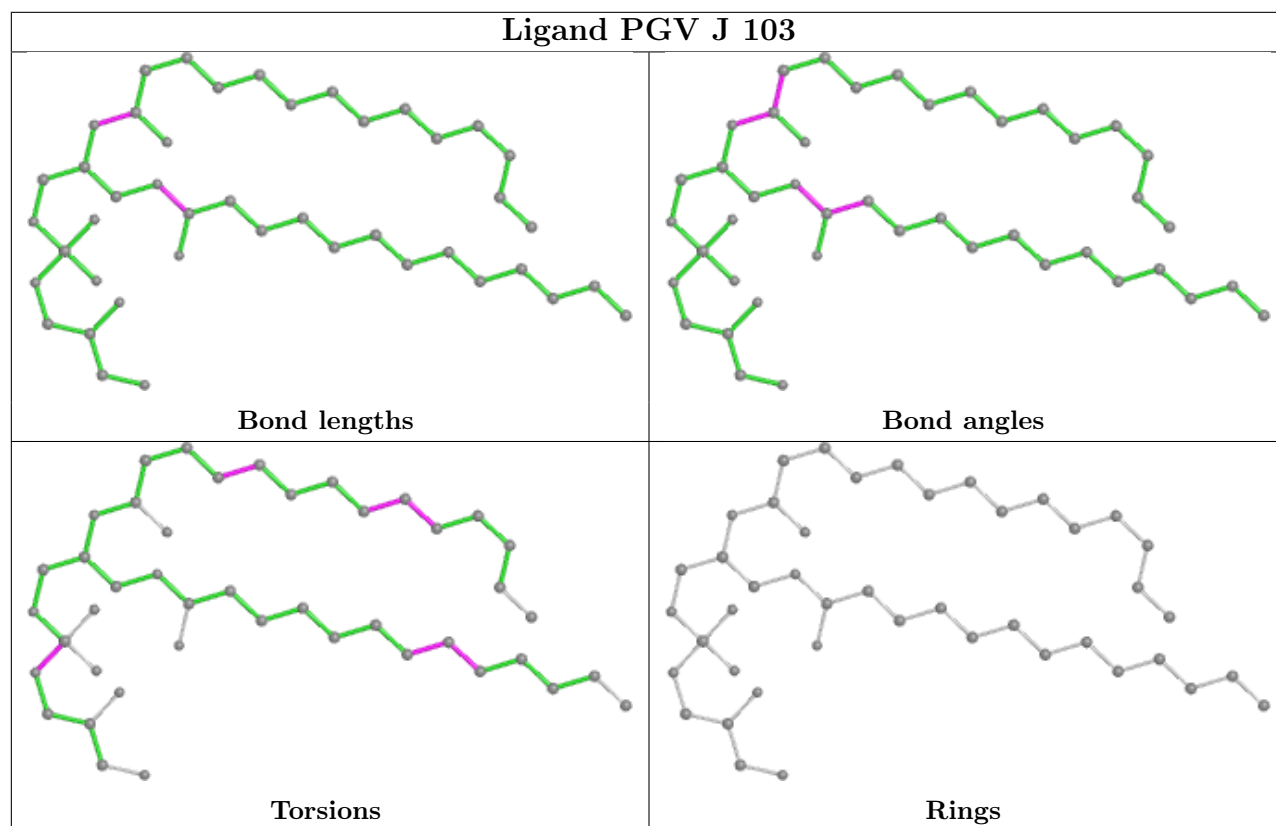
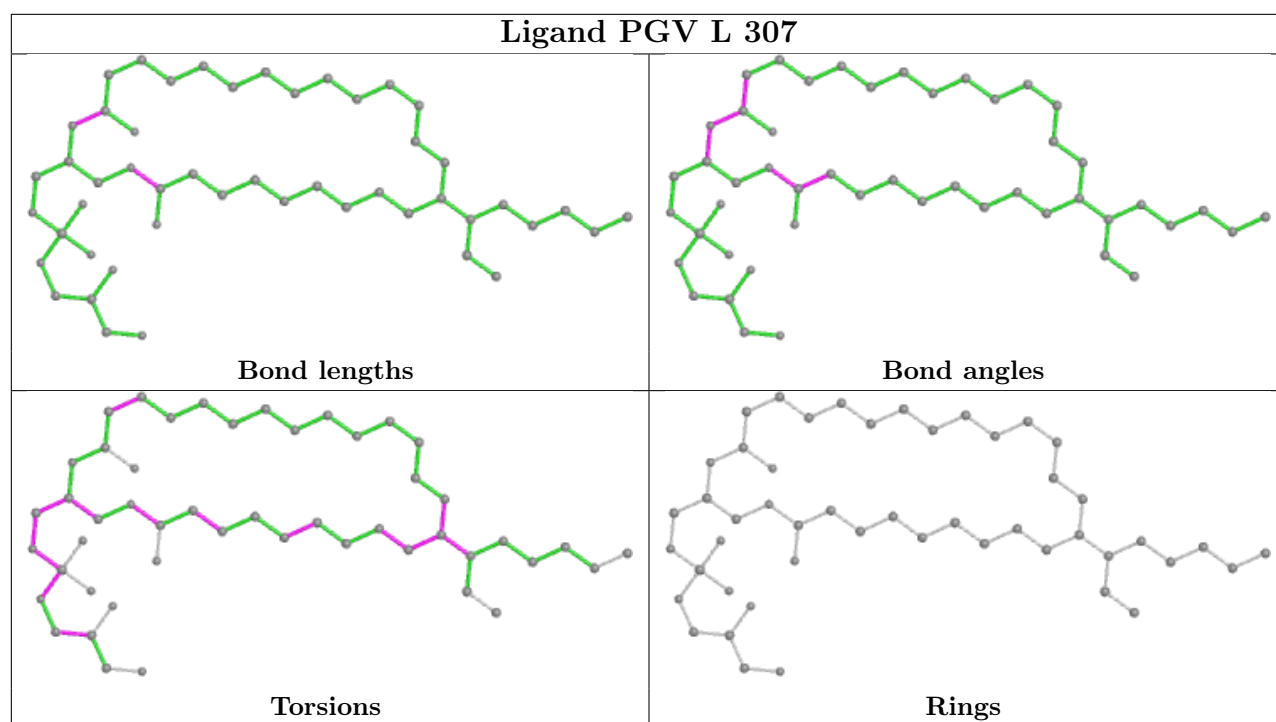
Ligand U10 U 101

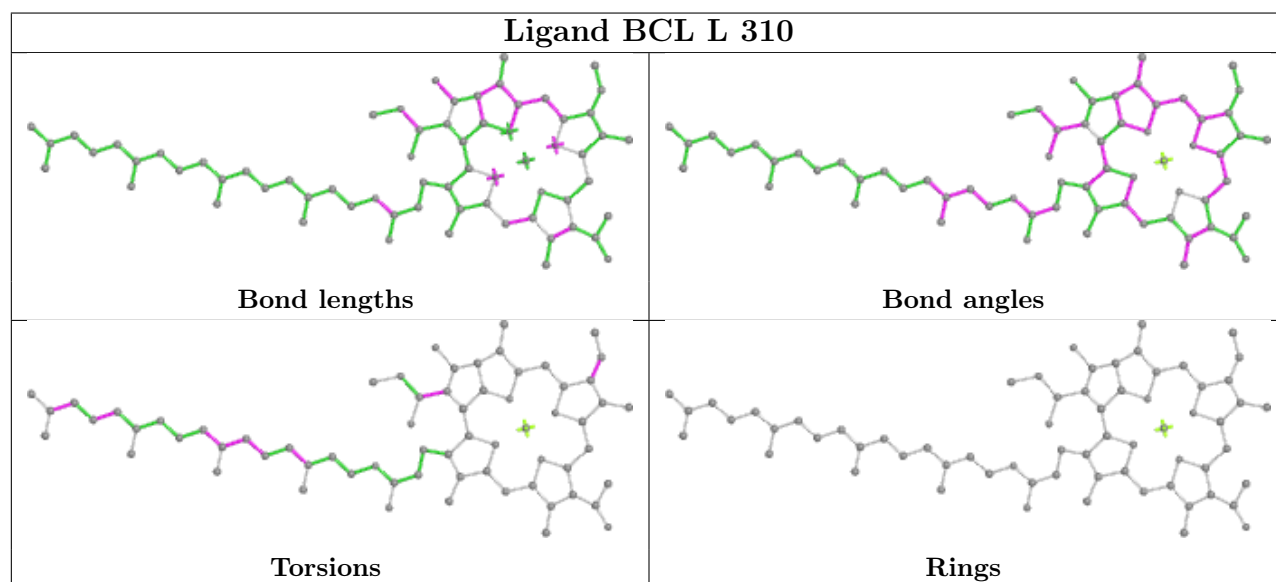
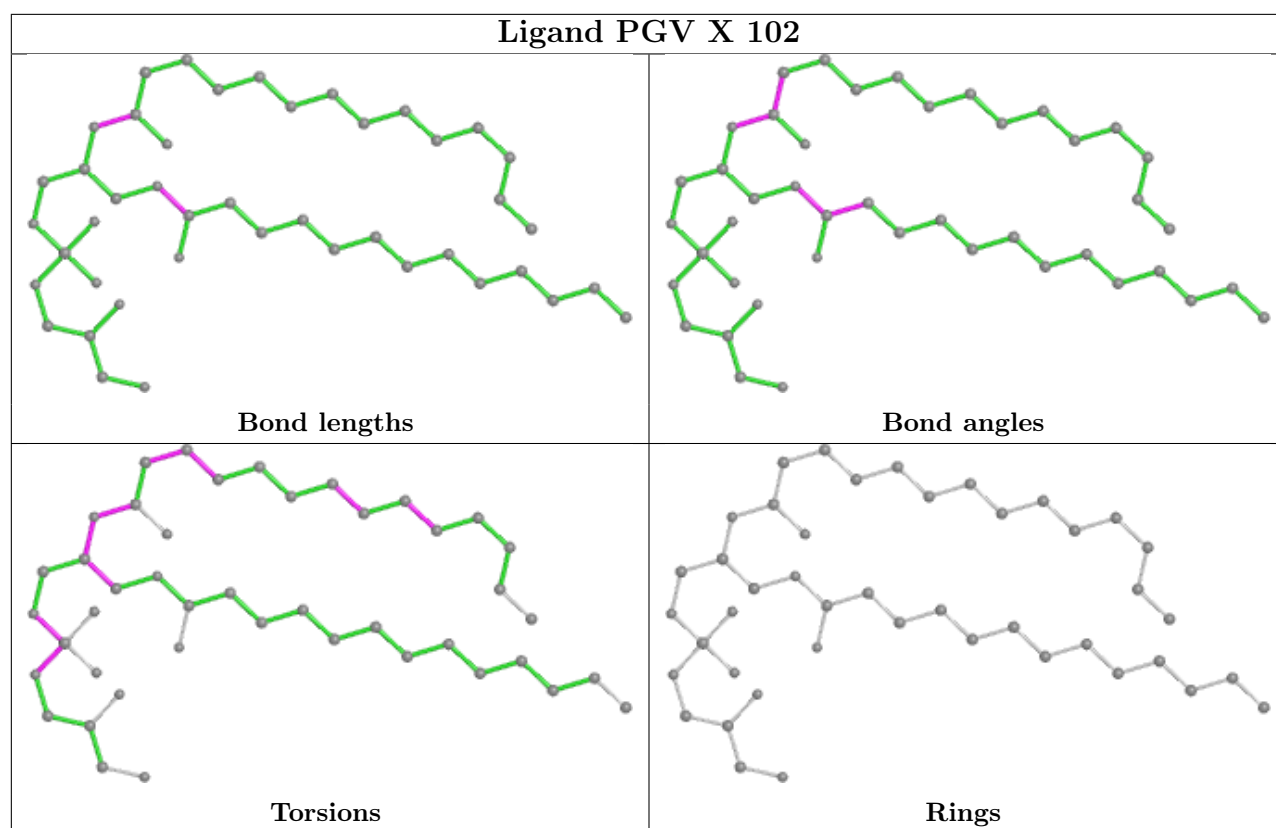


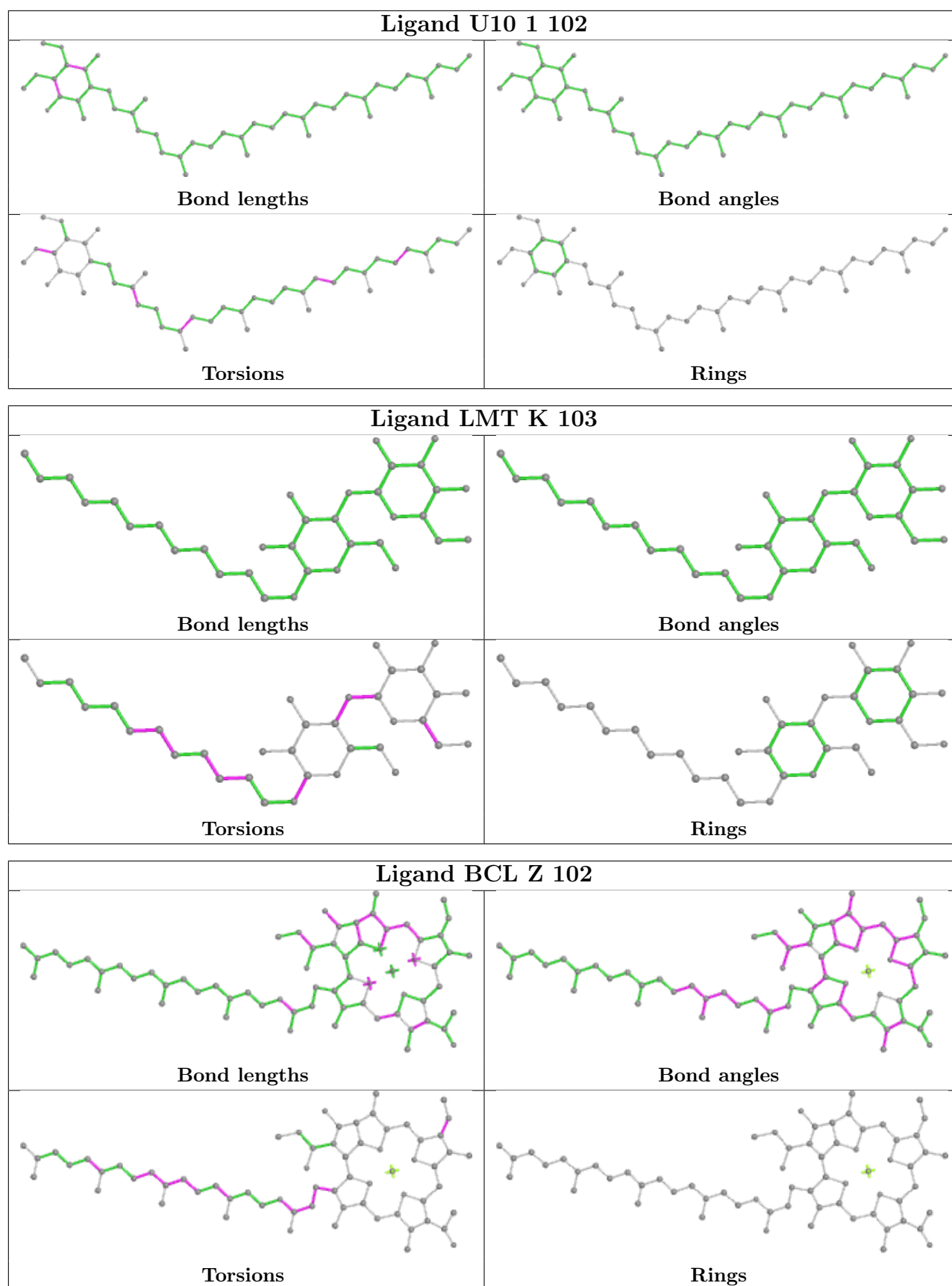
Ligand LMT 4 104

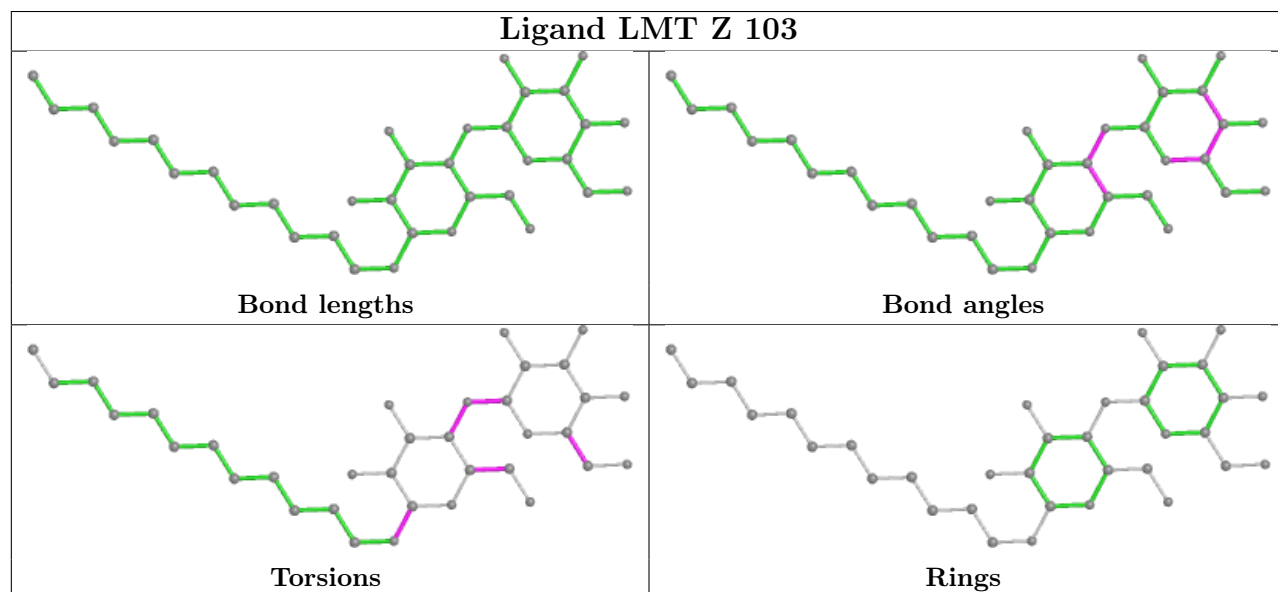
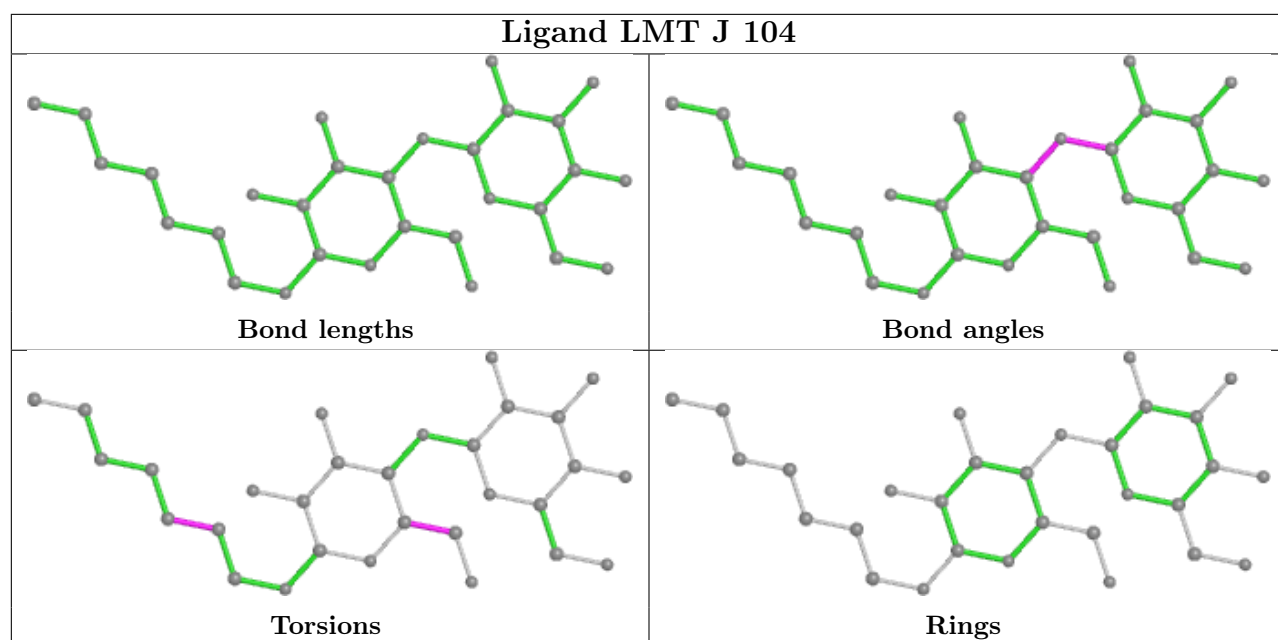


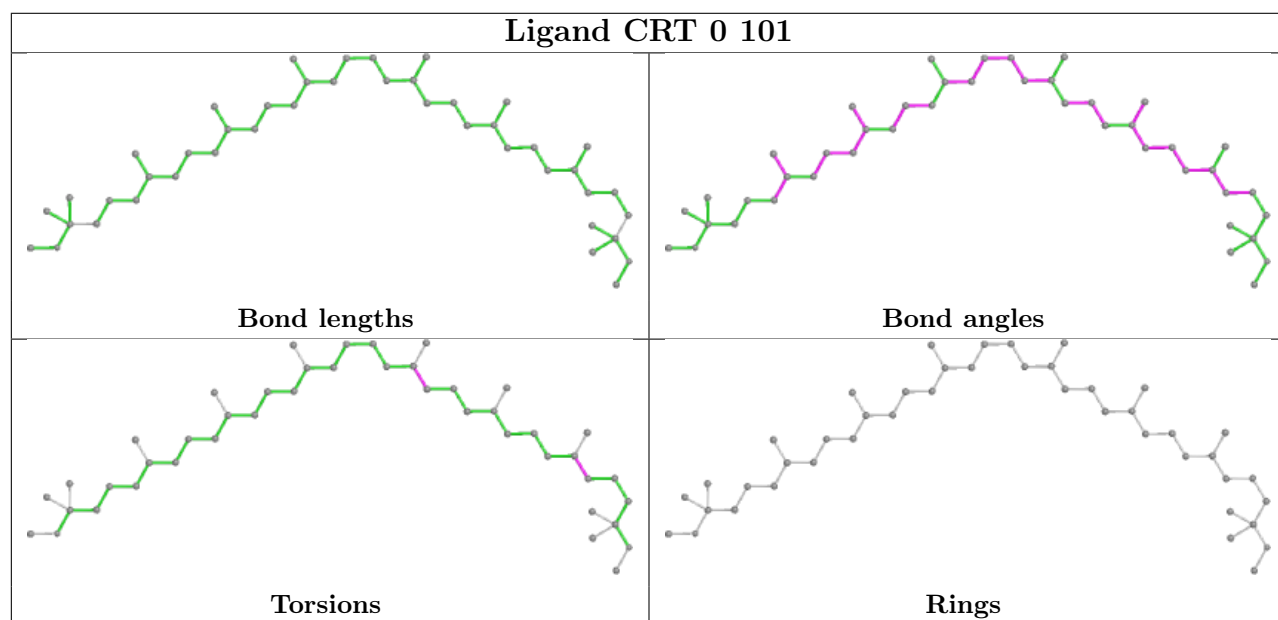
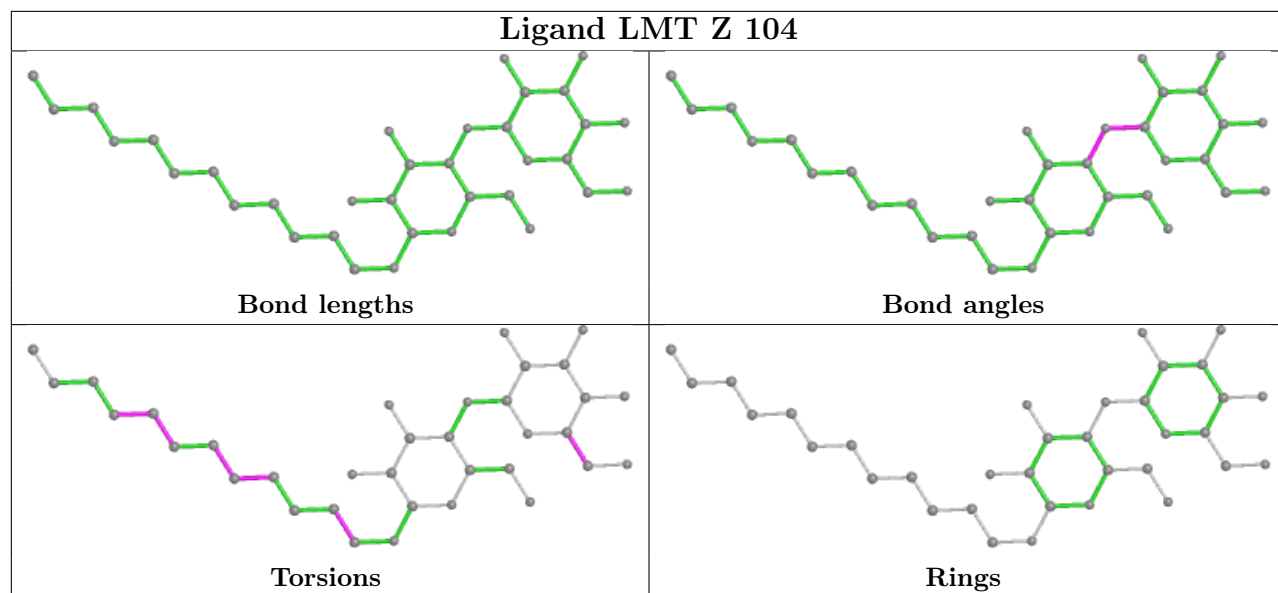


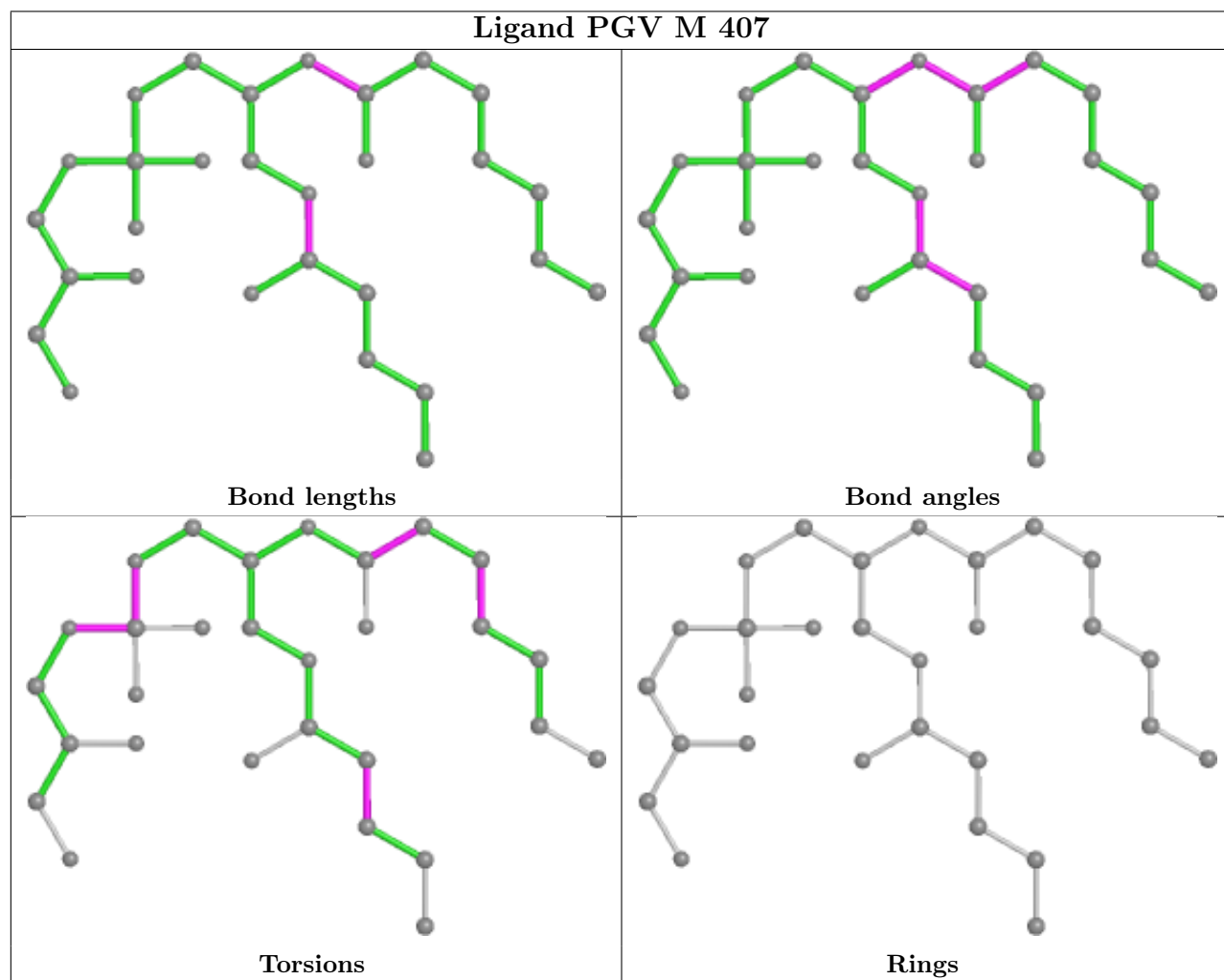
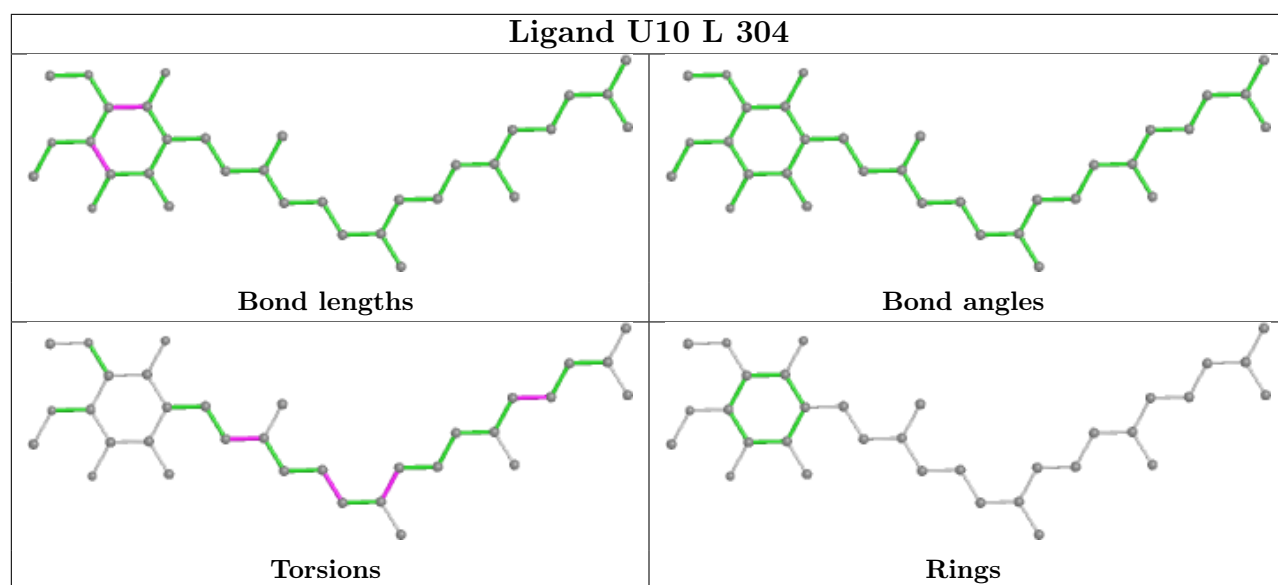


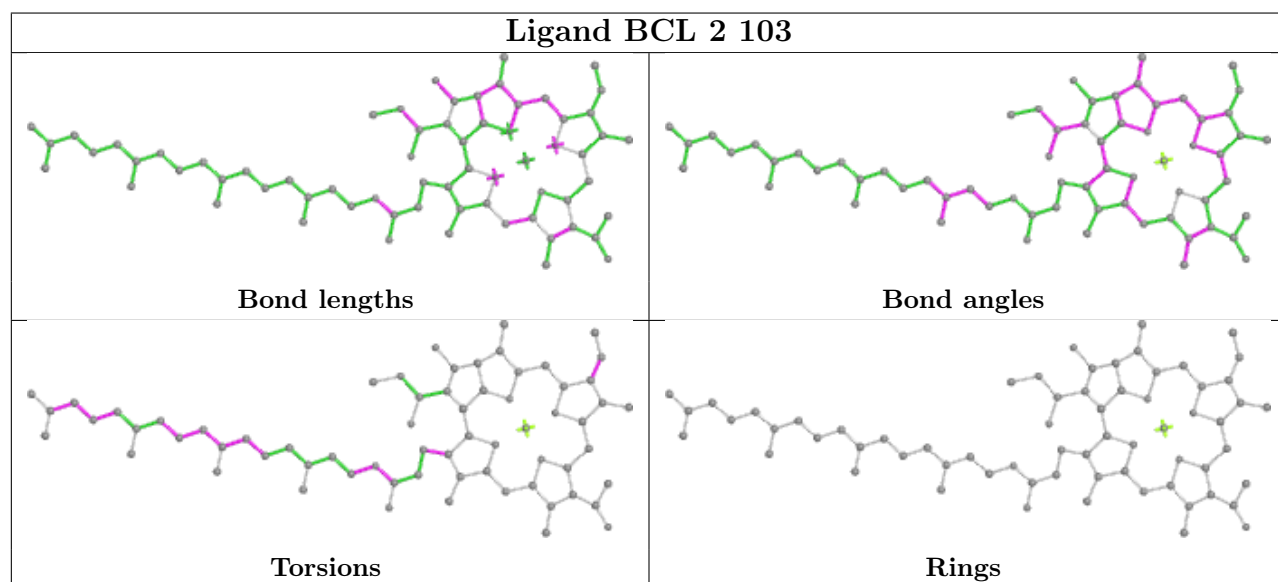
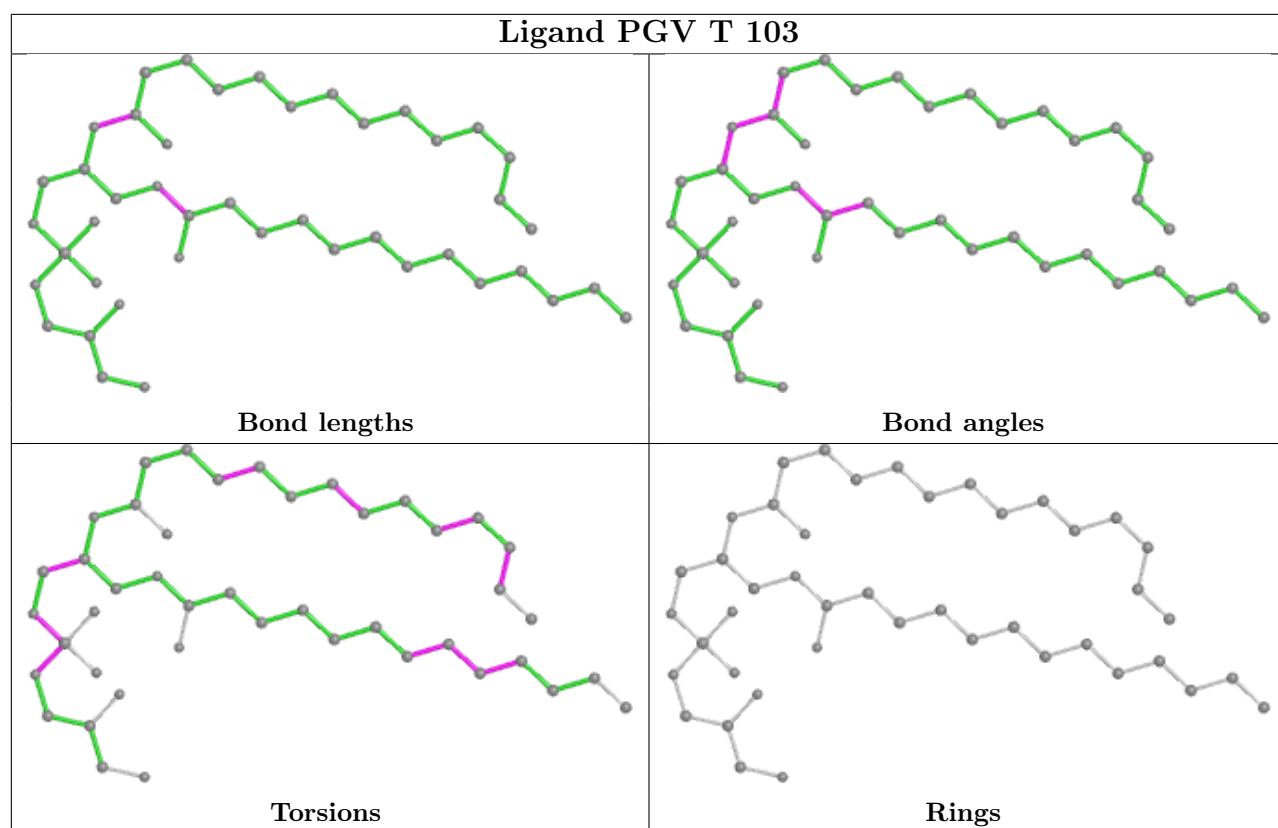


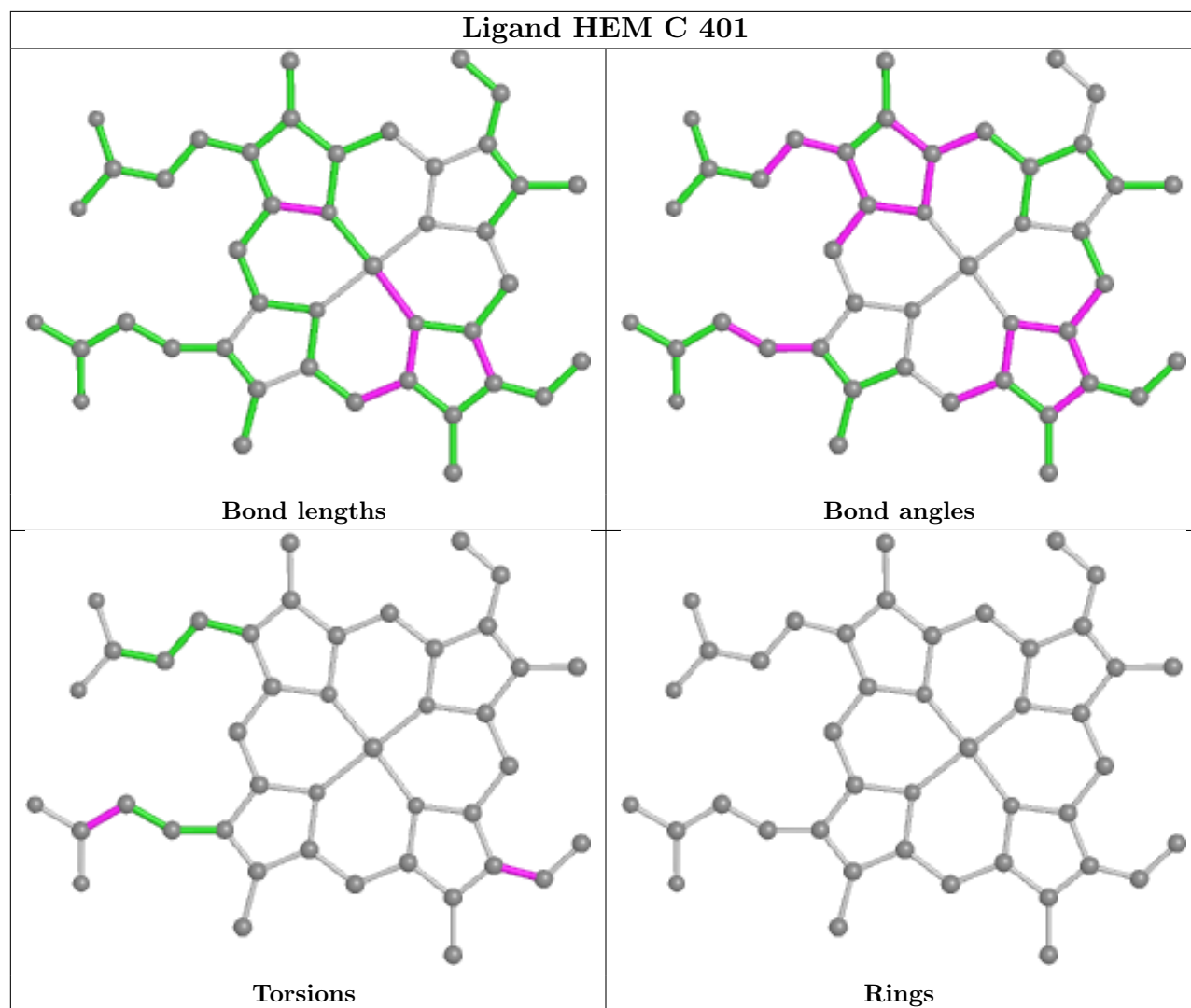
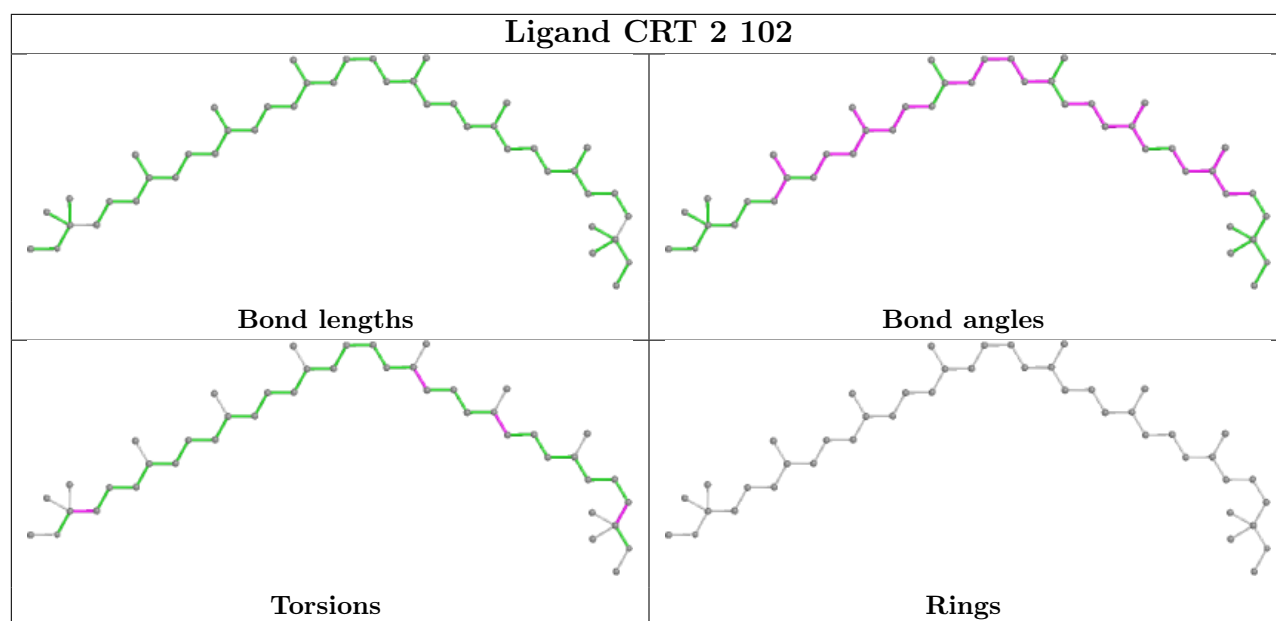


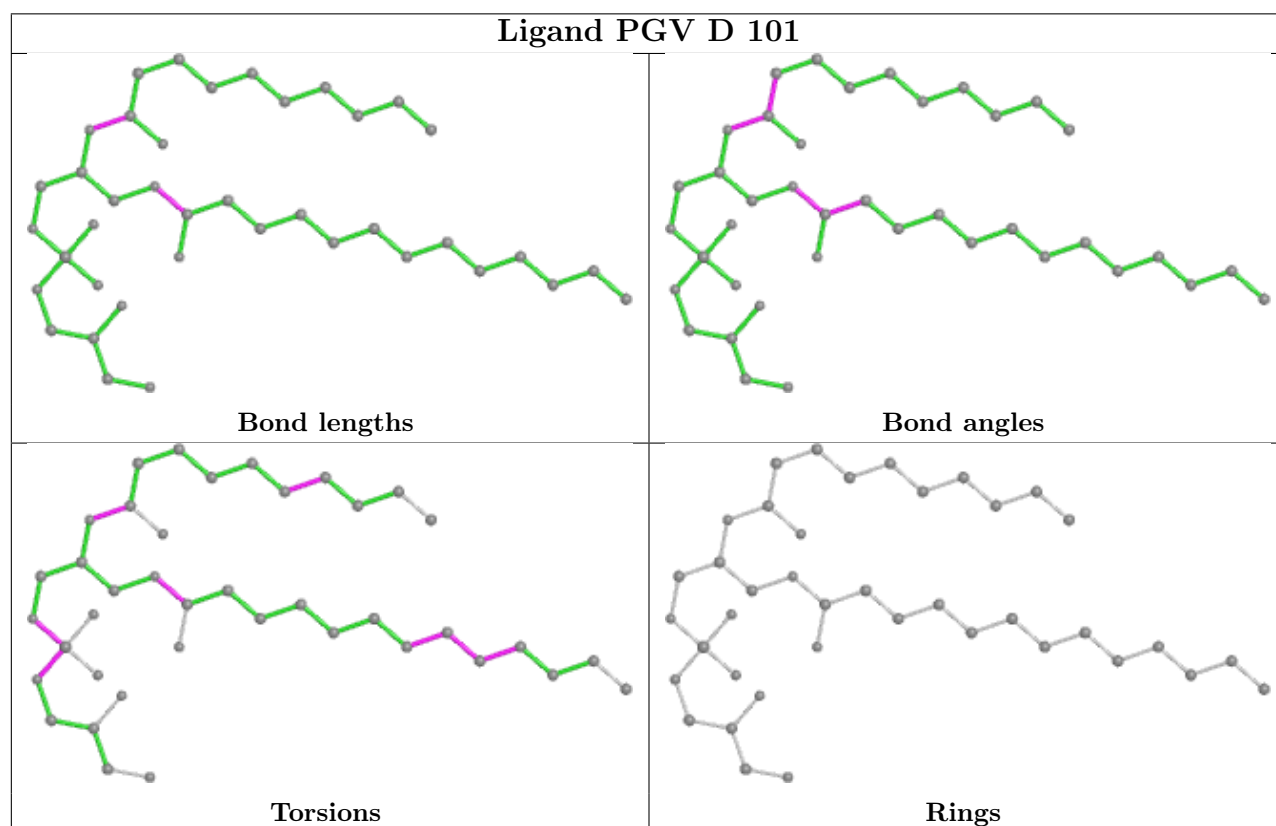
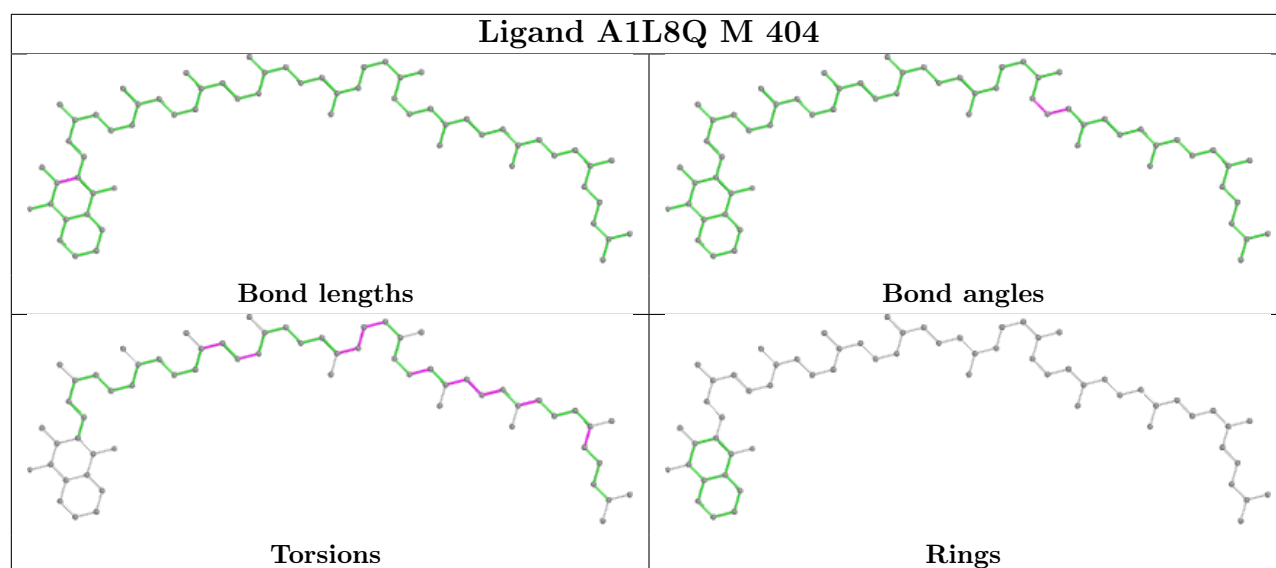


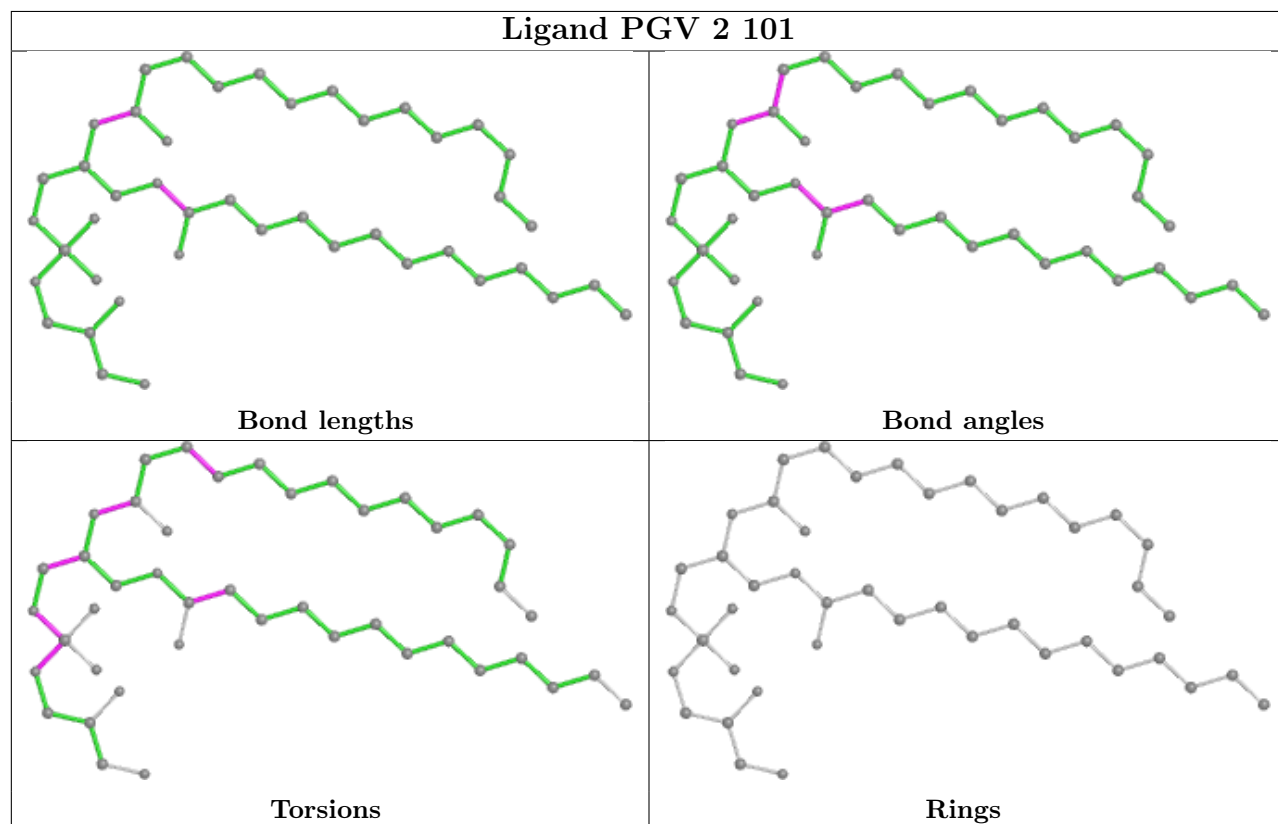
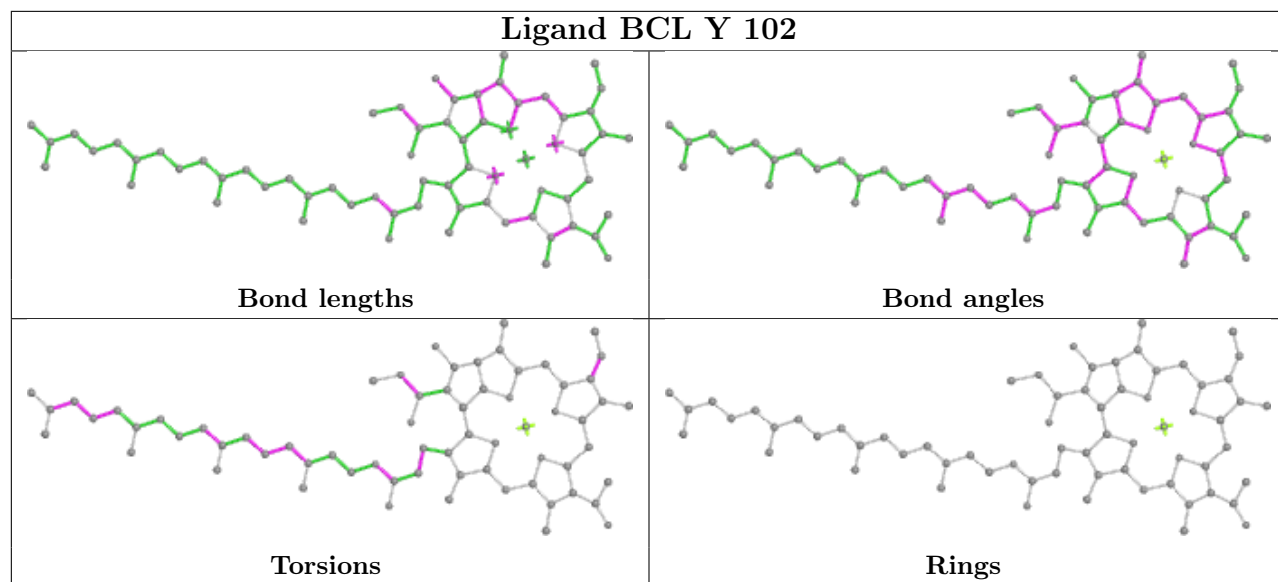


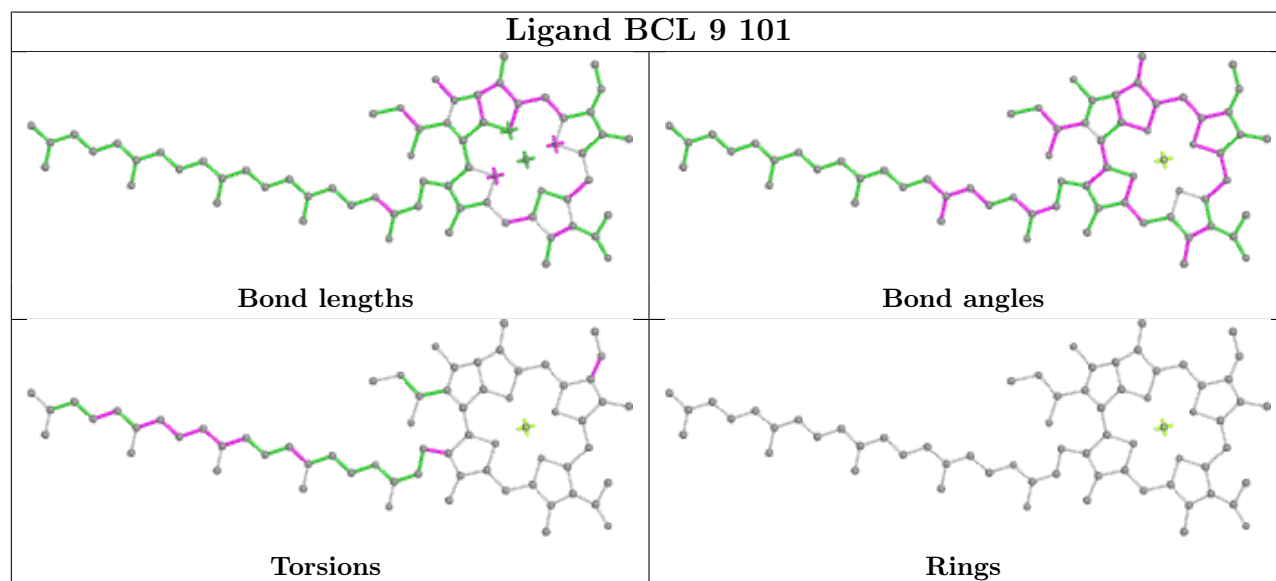
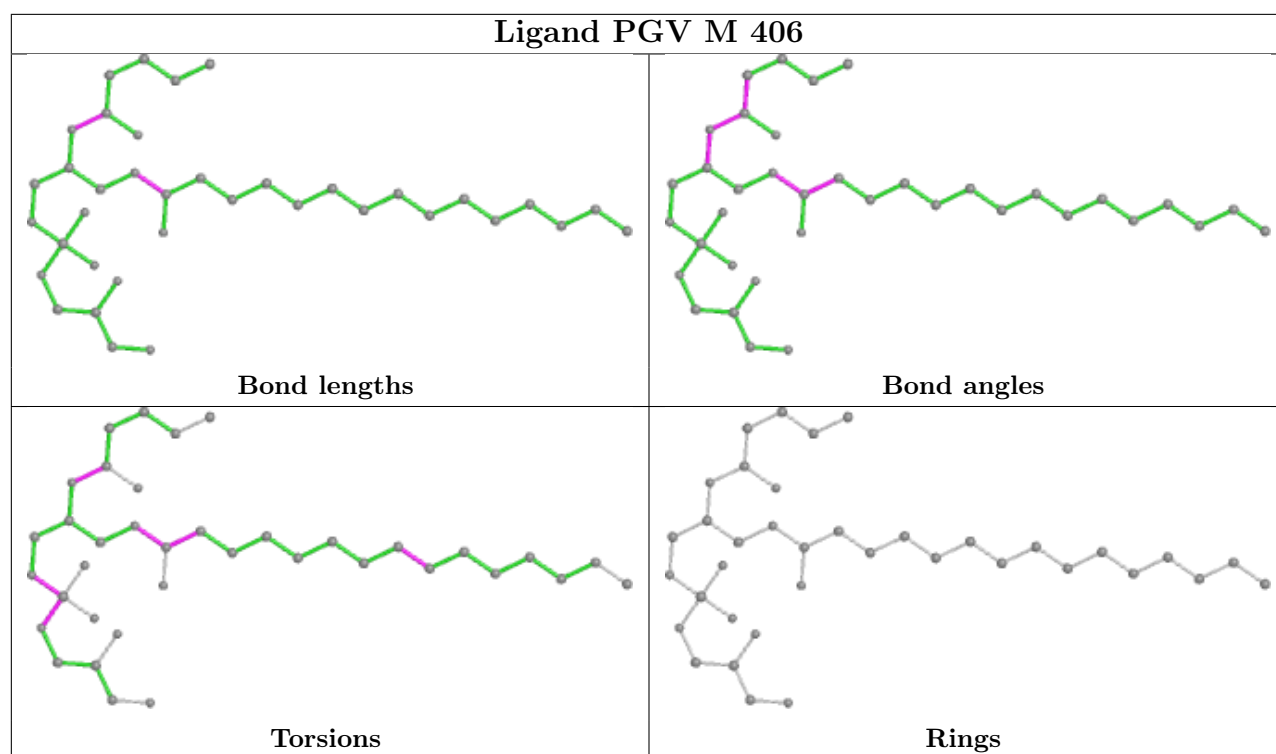


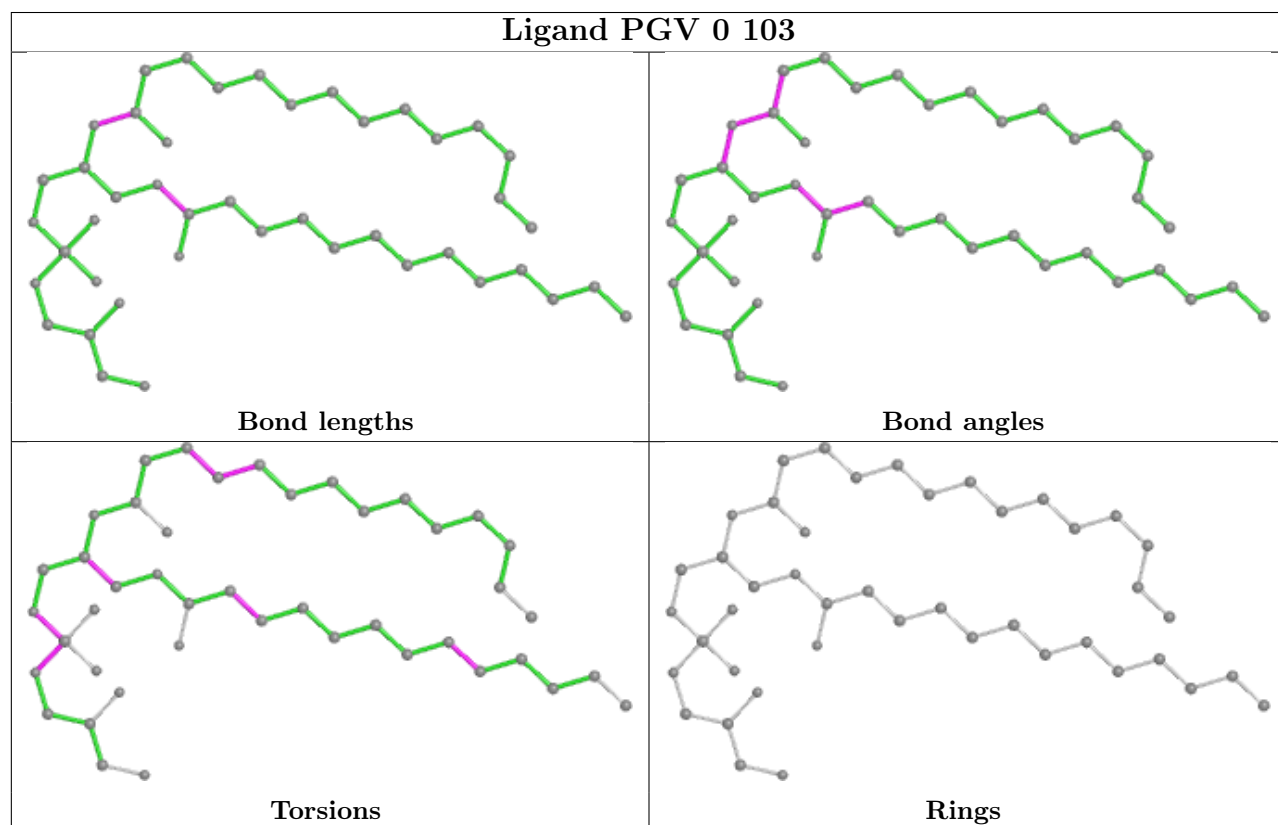
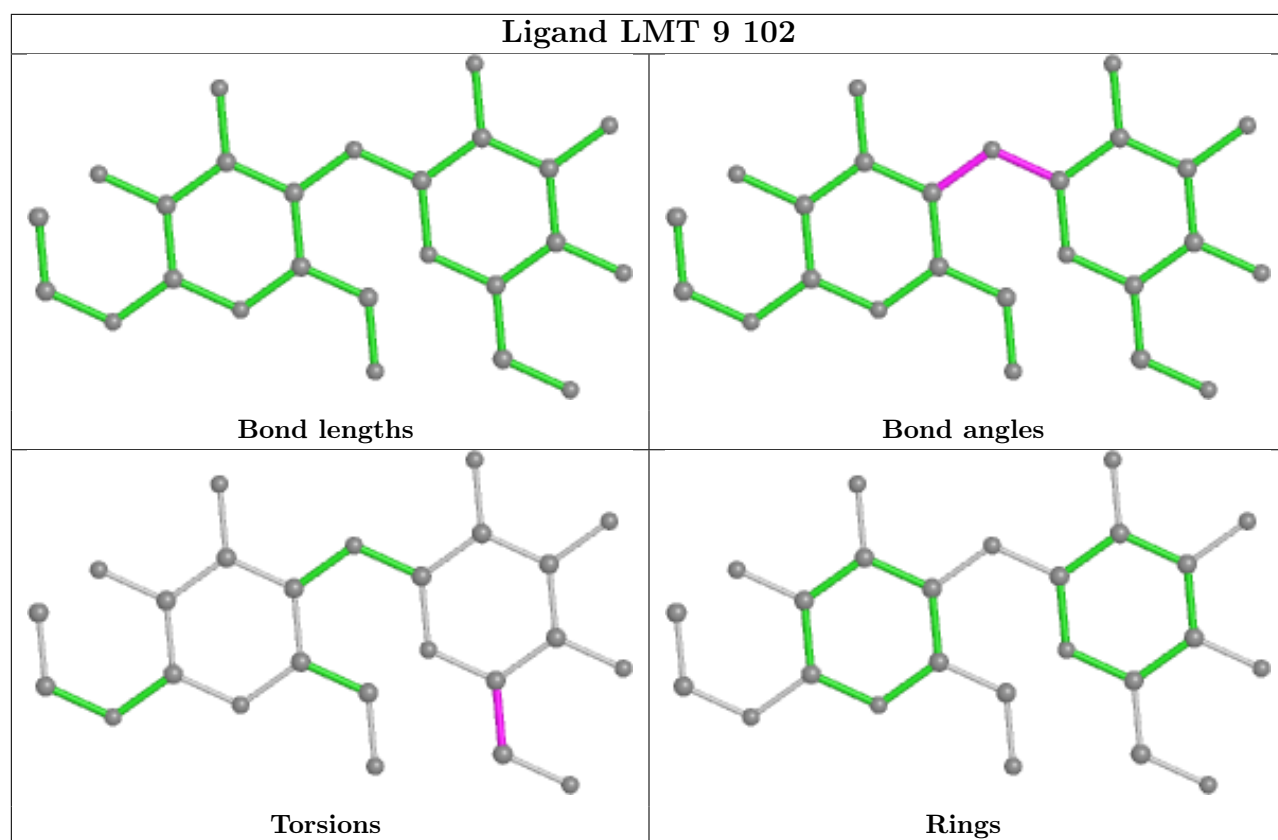


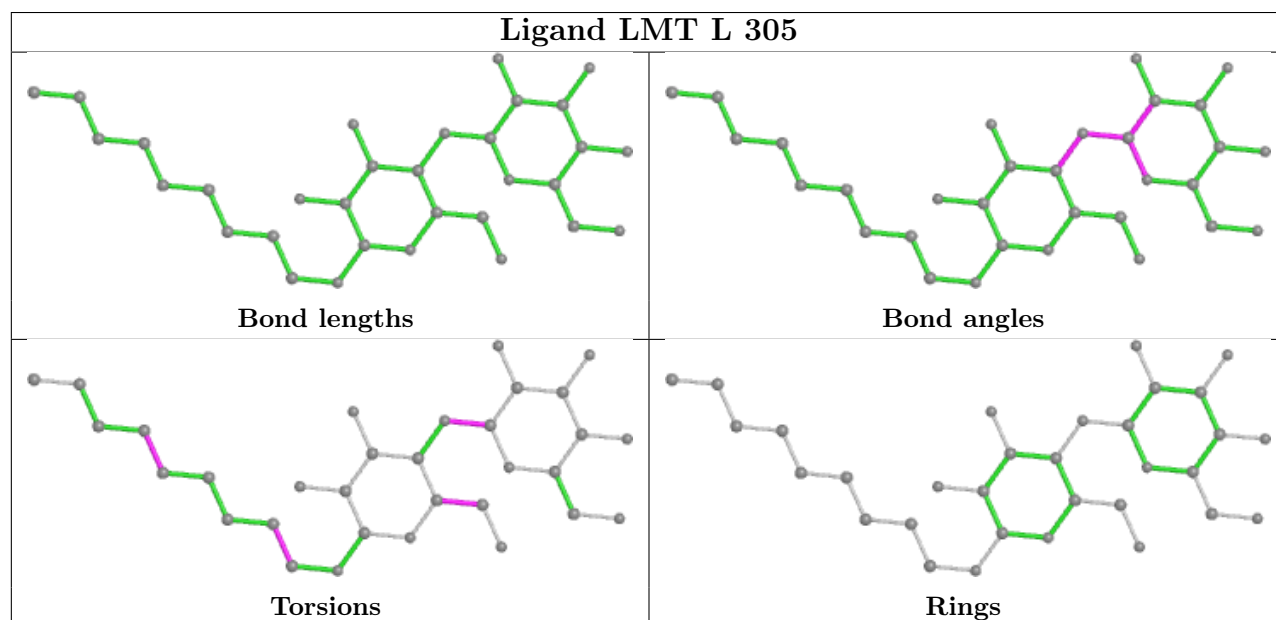
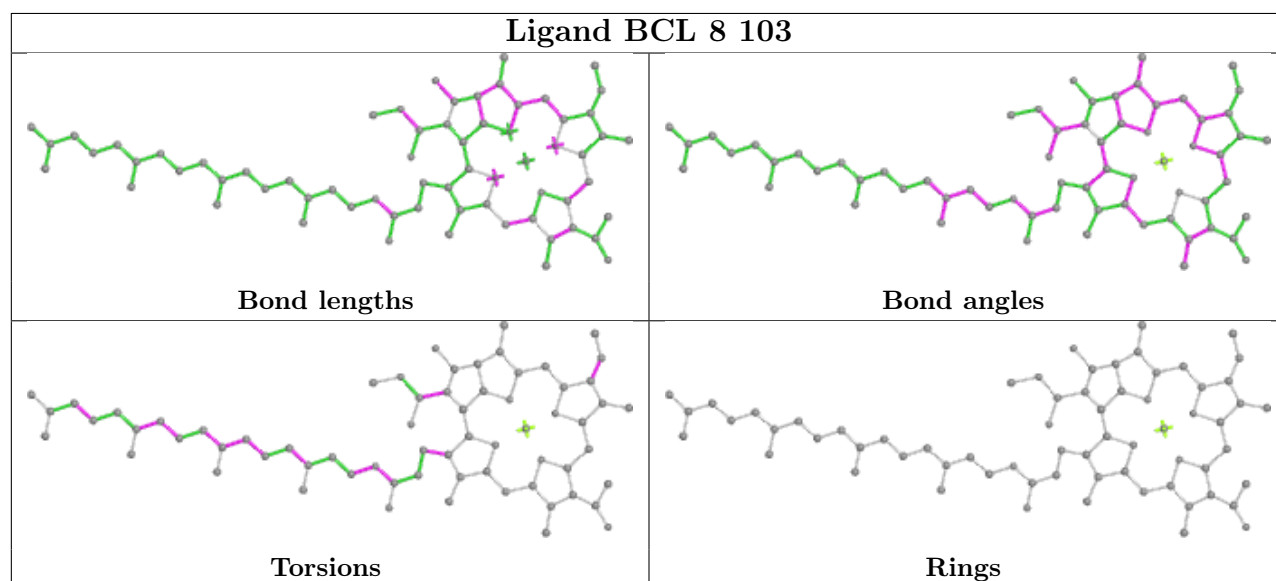
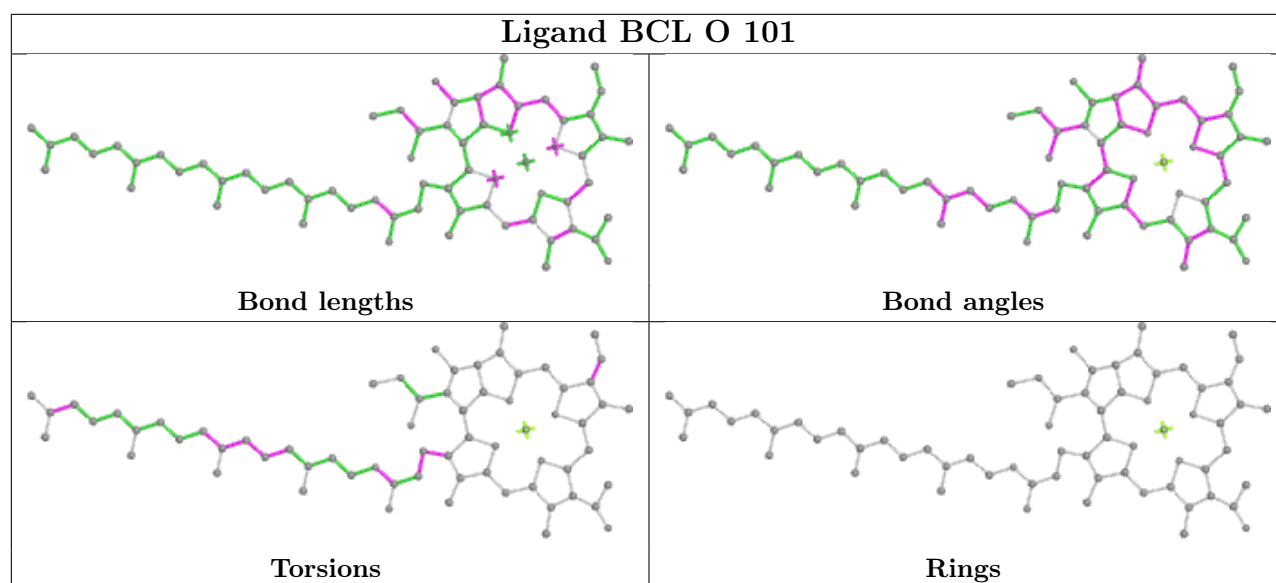


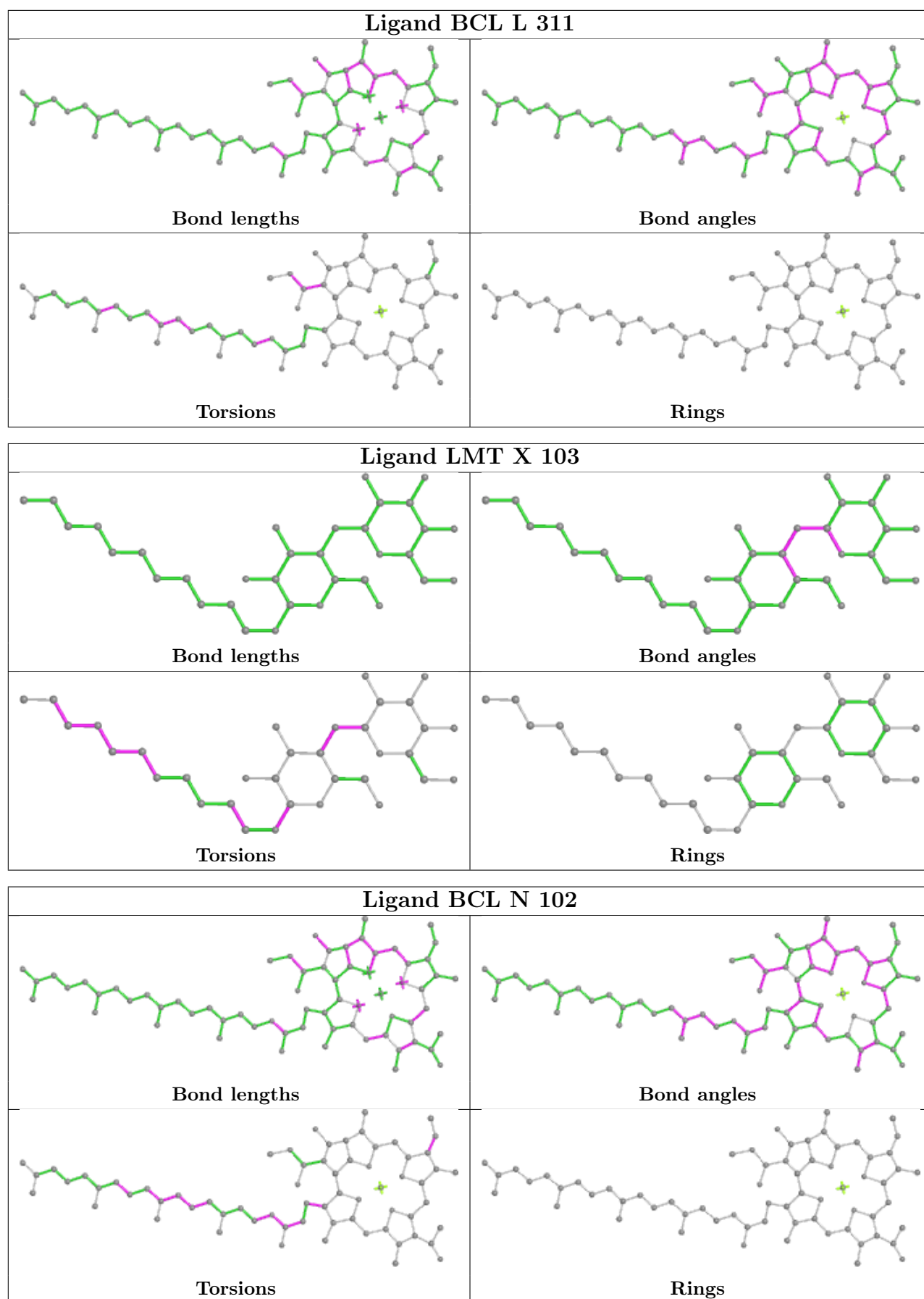




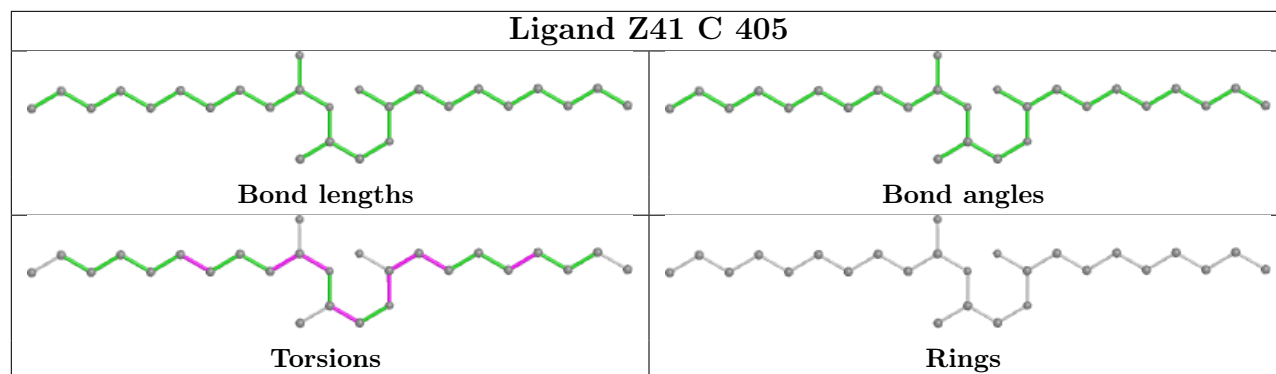




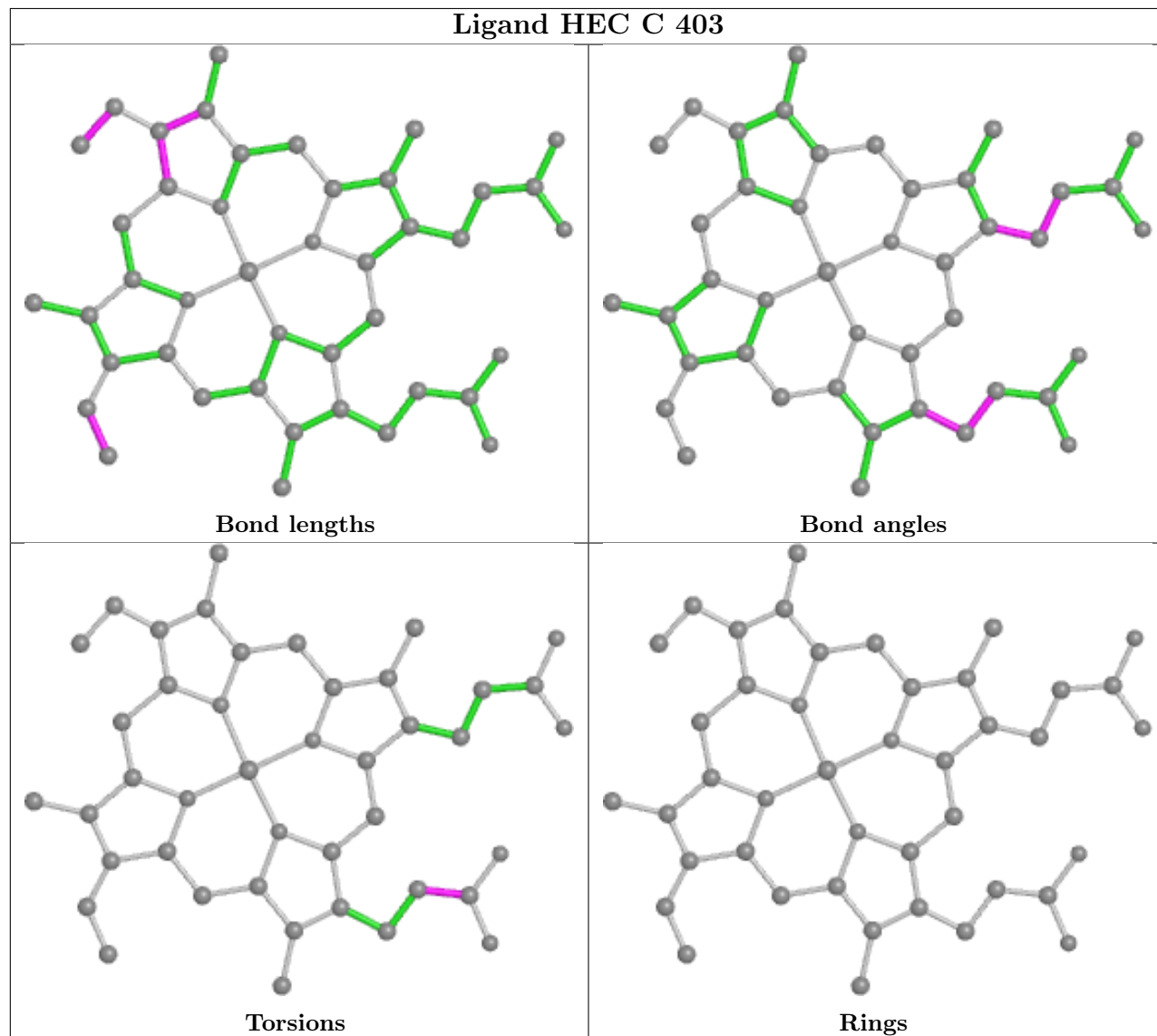


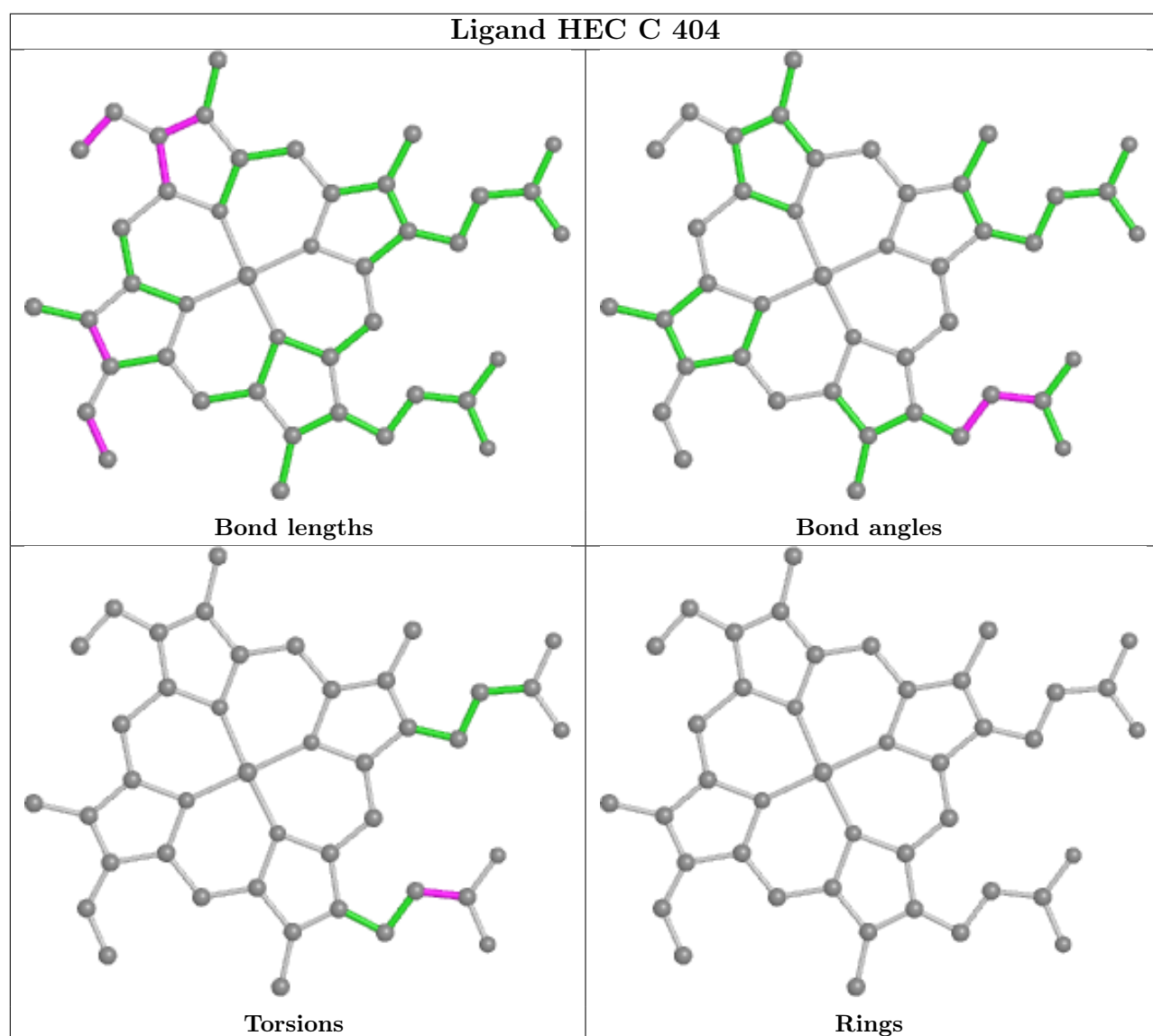
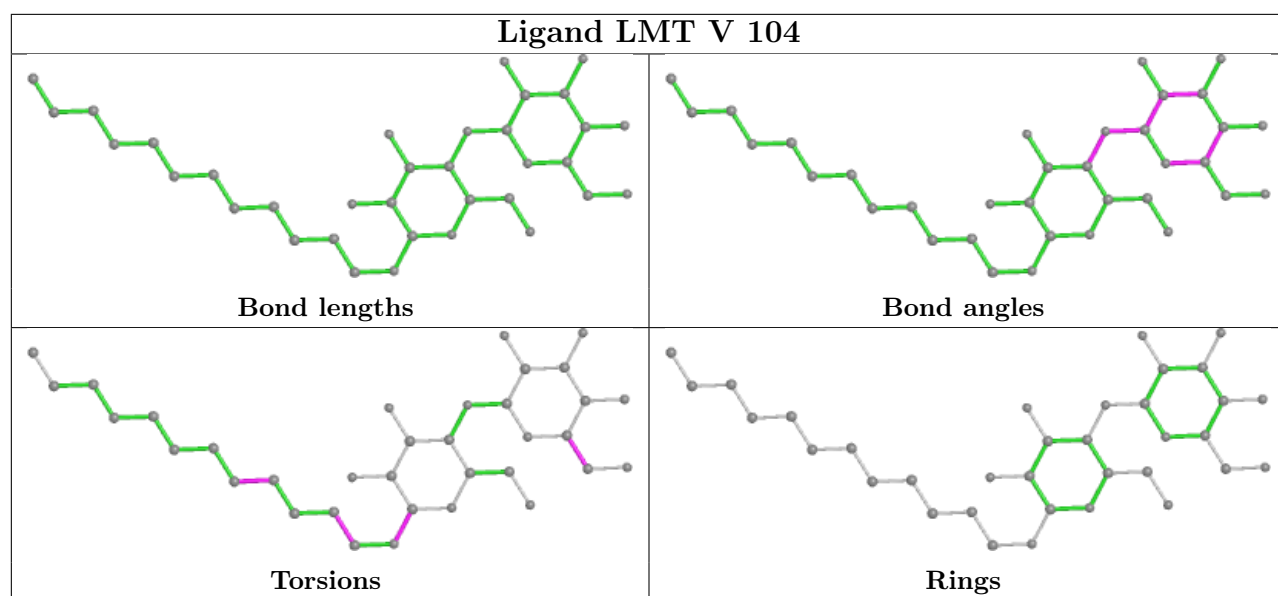


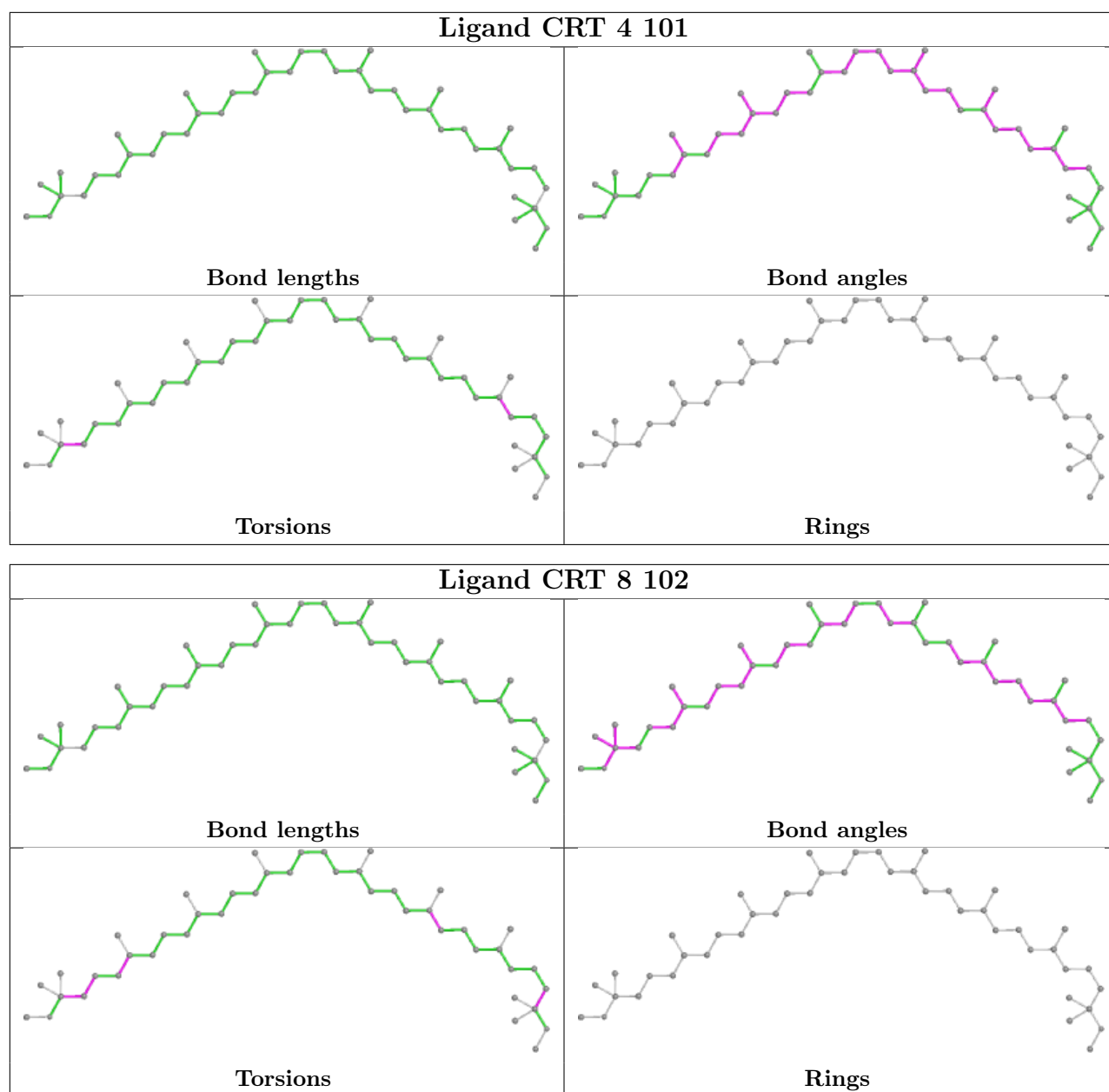
Ligand Z41 C 405

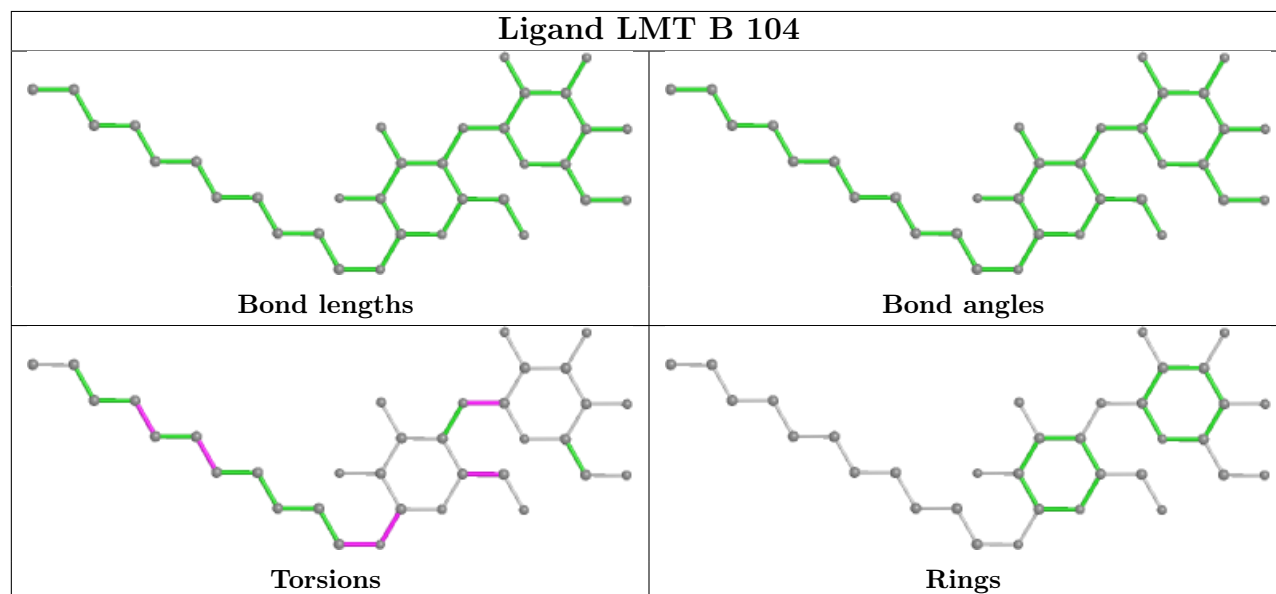
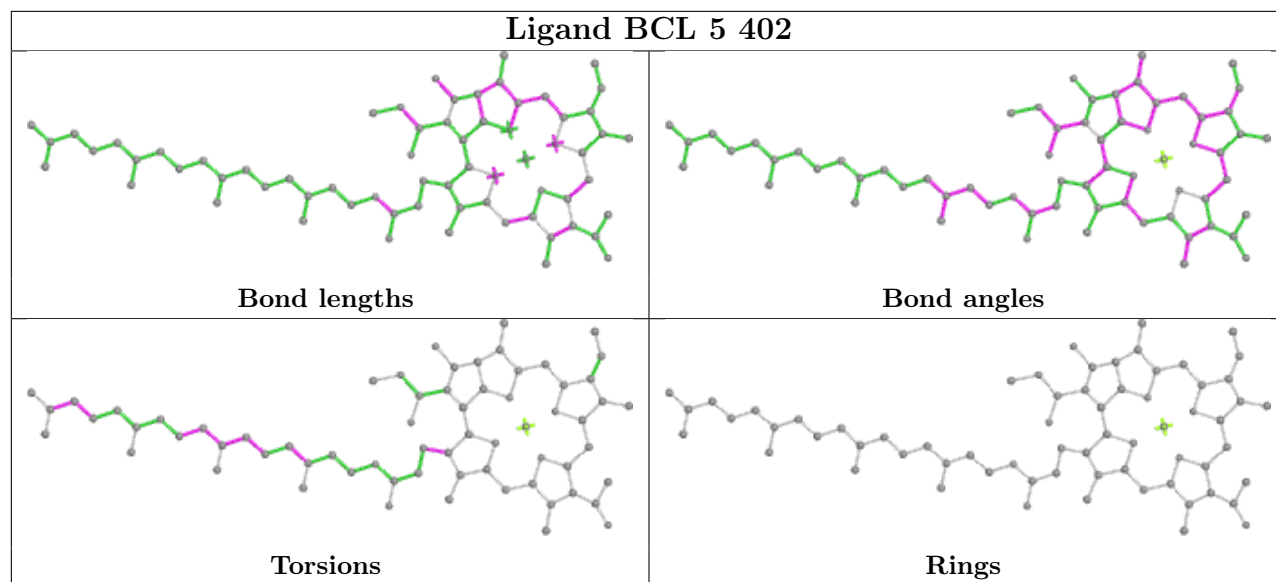


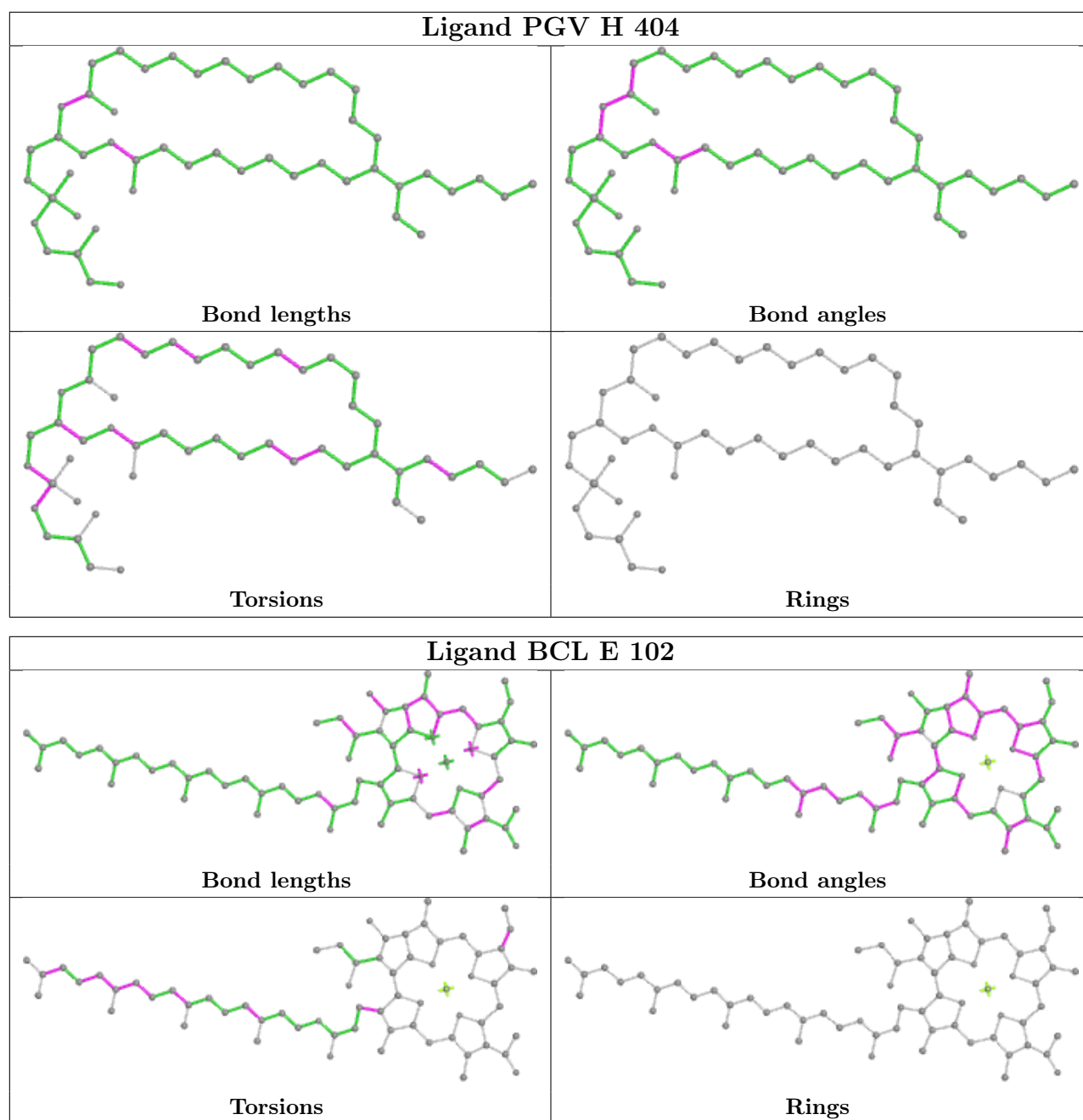
Ligand HEC C 403











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

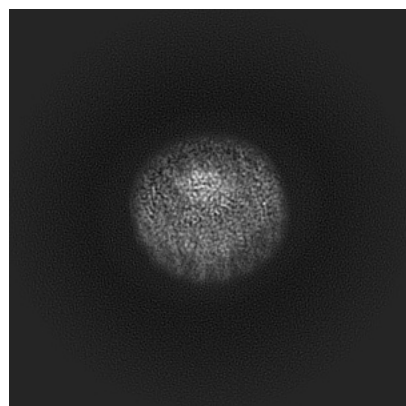
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63714. These allow visual inspection of the internal detail of the map and identification of artifacts.

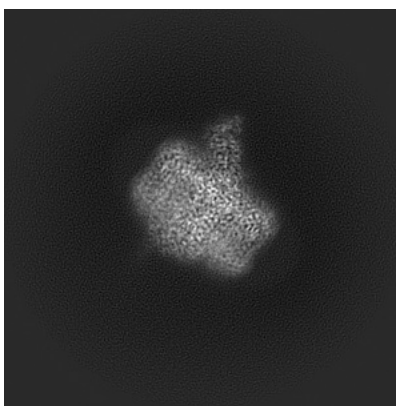
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

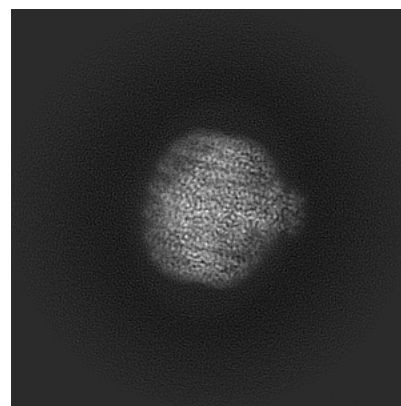
6.1.1 Primary map



X

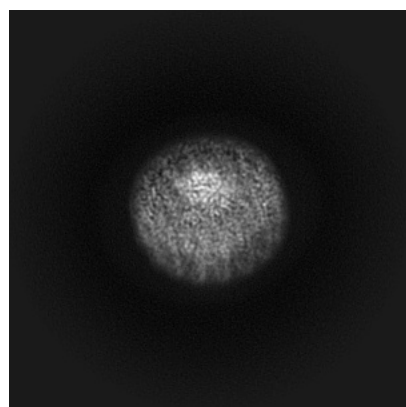


Y

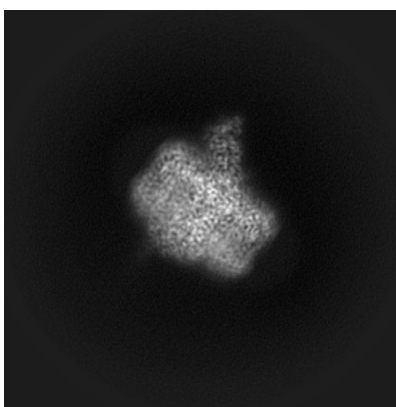


Z

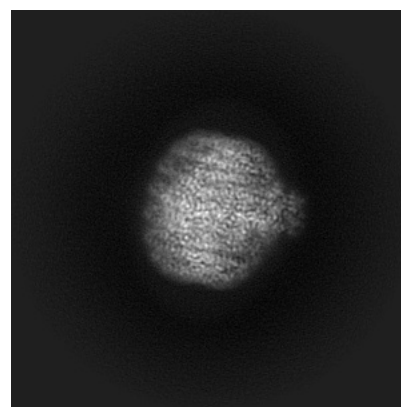
6.1.2 Raw map



X



Y

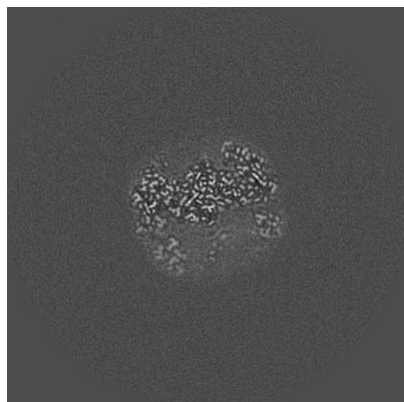


Z

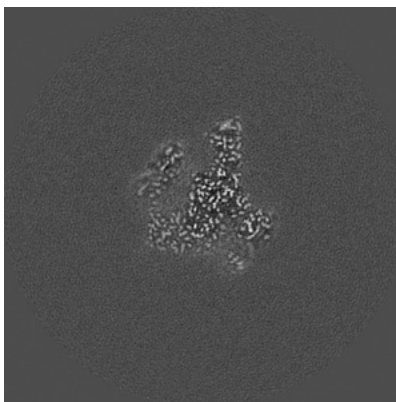
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

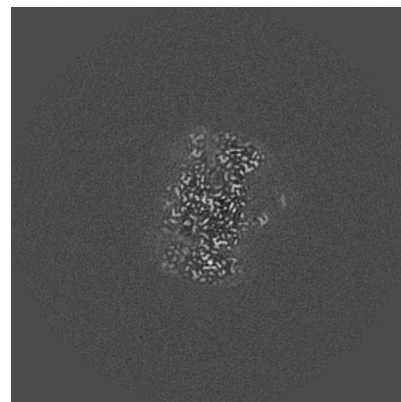
6.2.1 Primary map



X Index: 190

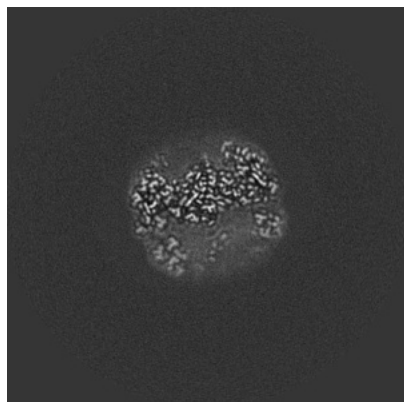


Y Index: 190

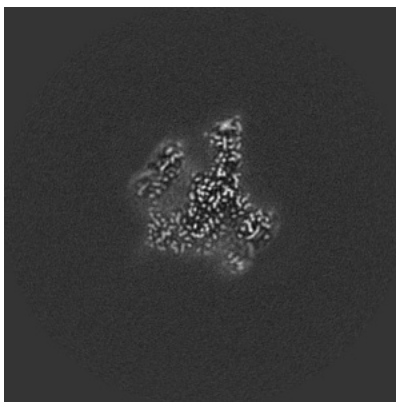


Z Index: 190

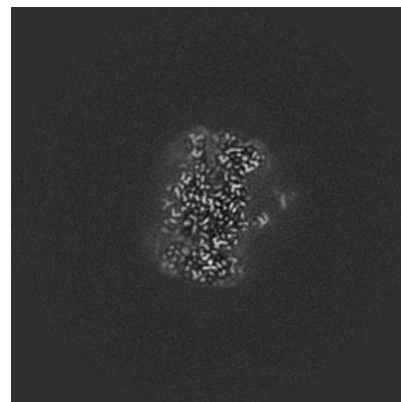
6.2.2 Raw map



X Index: 190



Y Index: 190

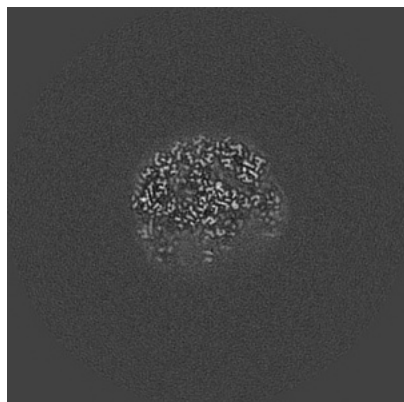


Z Index: 190

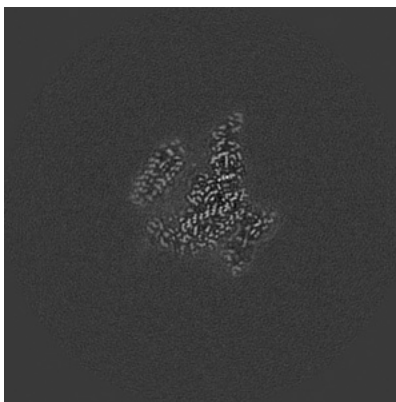
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

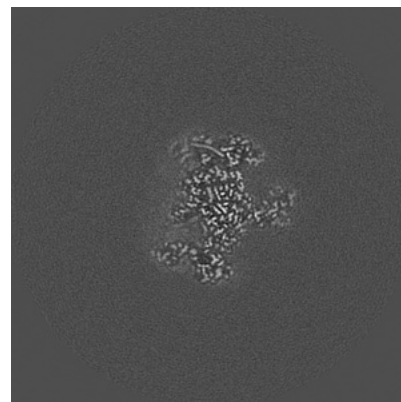
6.3.1 Primary map



X Index: 182

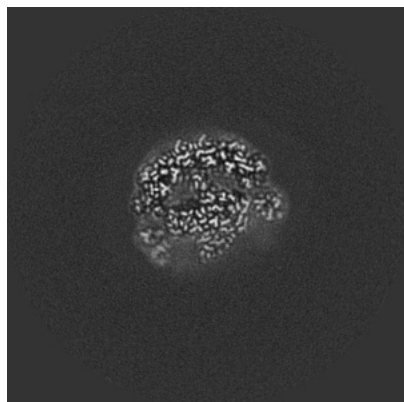


Y Index: 184

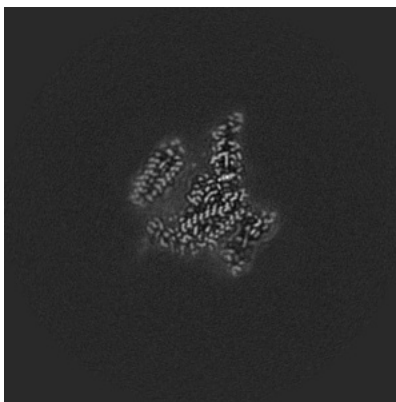


Z Index: 198

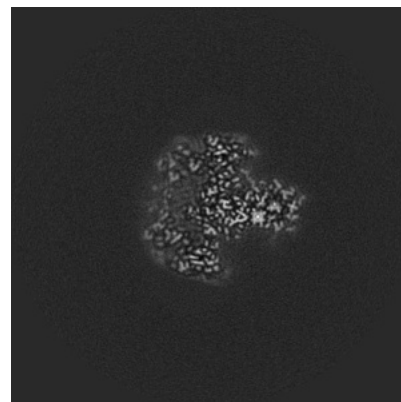
6.3.2 Raw map



X Index: 177



Y Index: 184

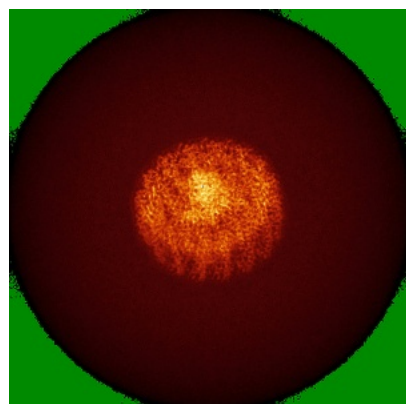


Z Index: 210

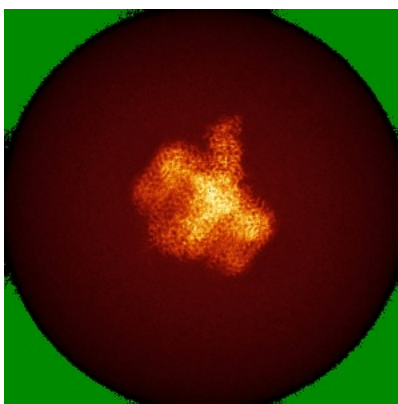
The images above show the largest variance slices of the map in three orthogonal directions.

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

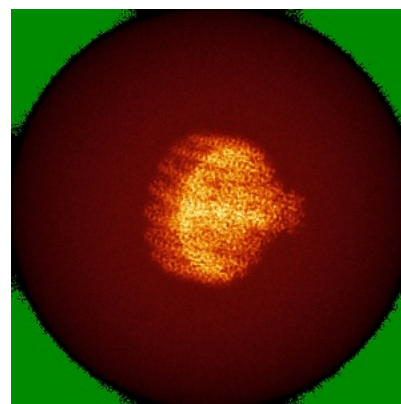
6.4.1 Primary map



X

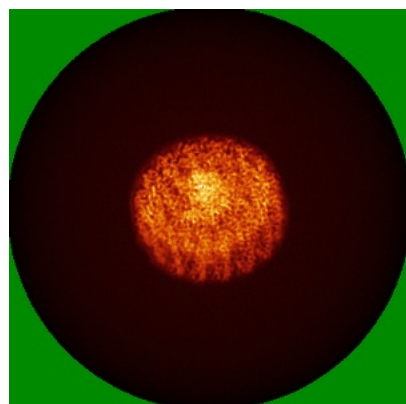


Y

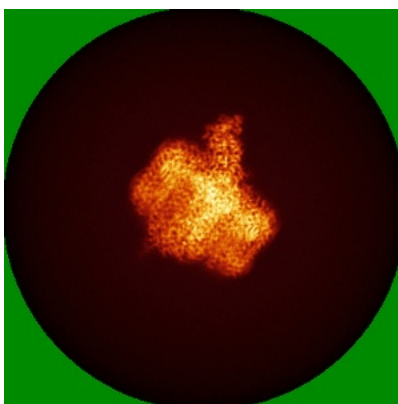


Z

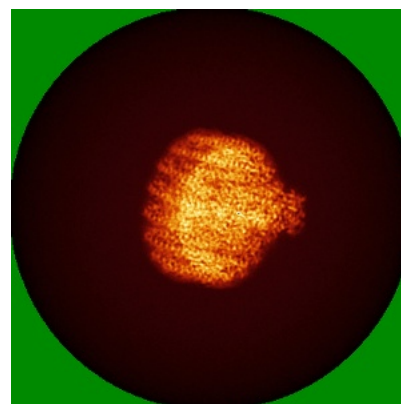
6.4.2 Raw map



X



Y

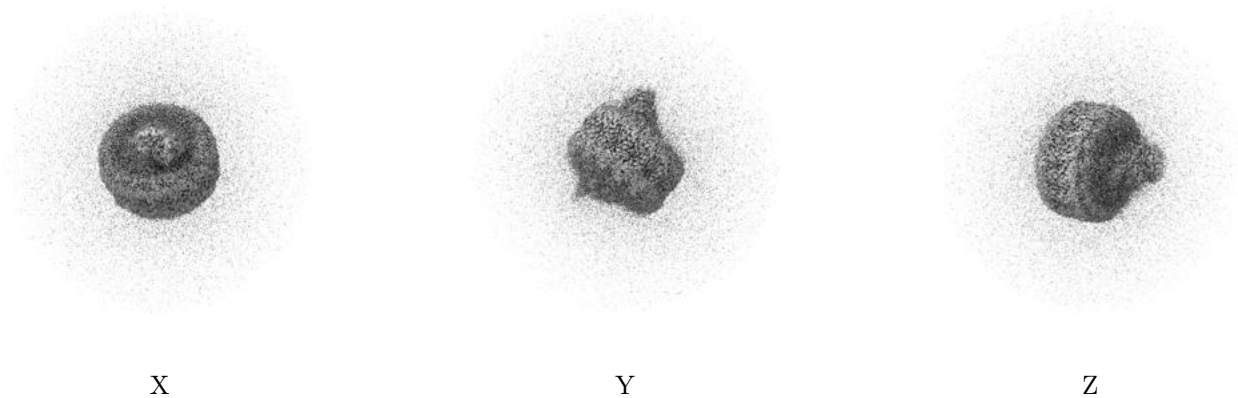


Z

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

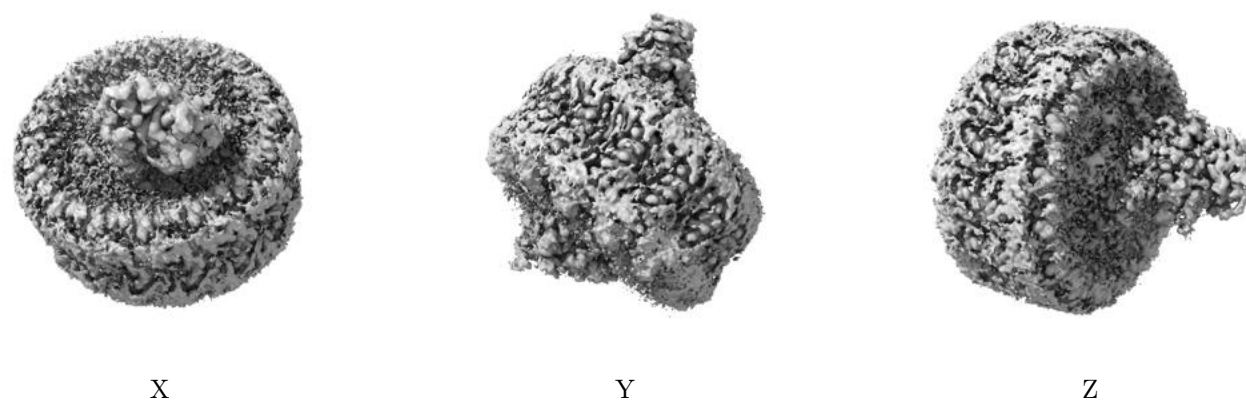
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

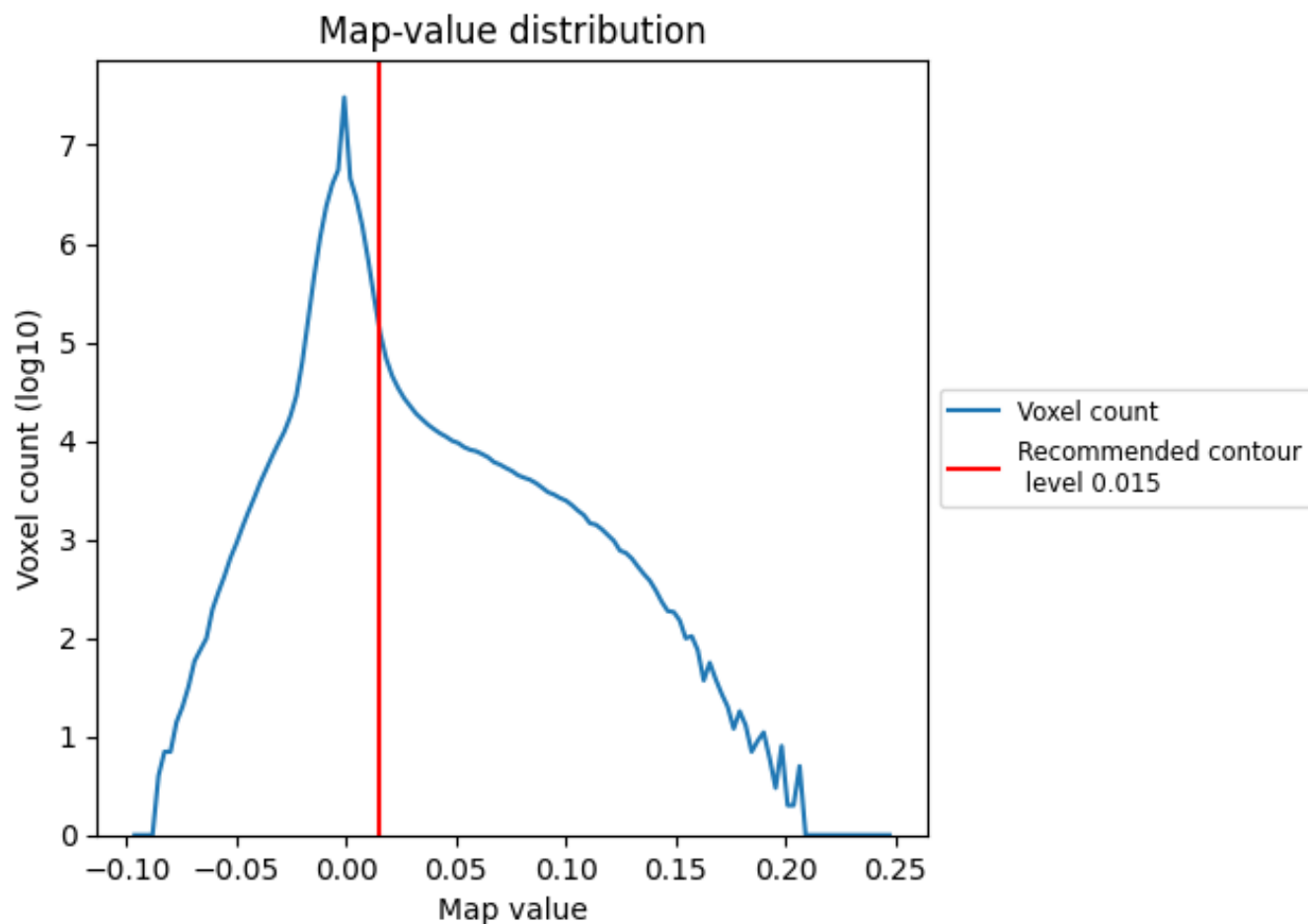
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

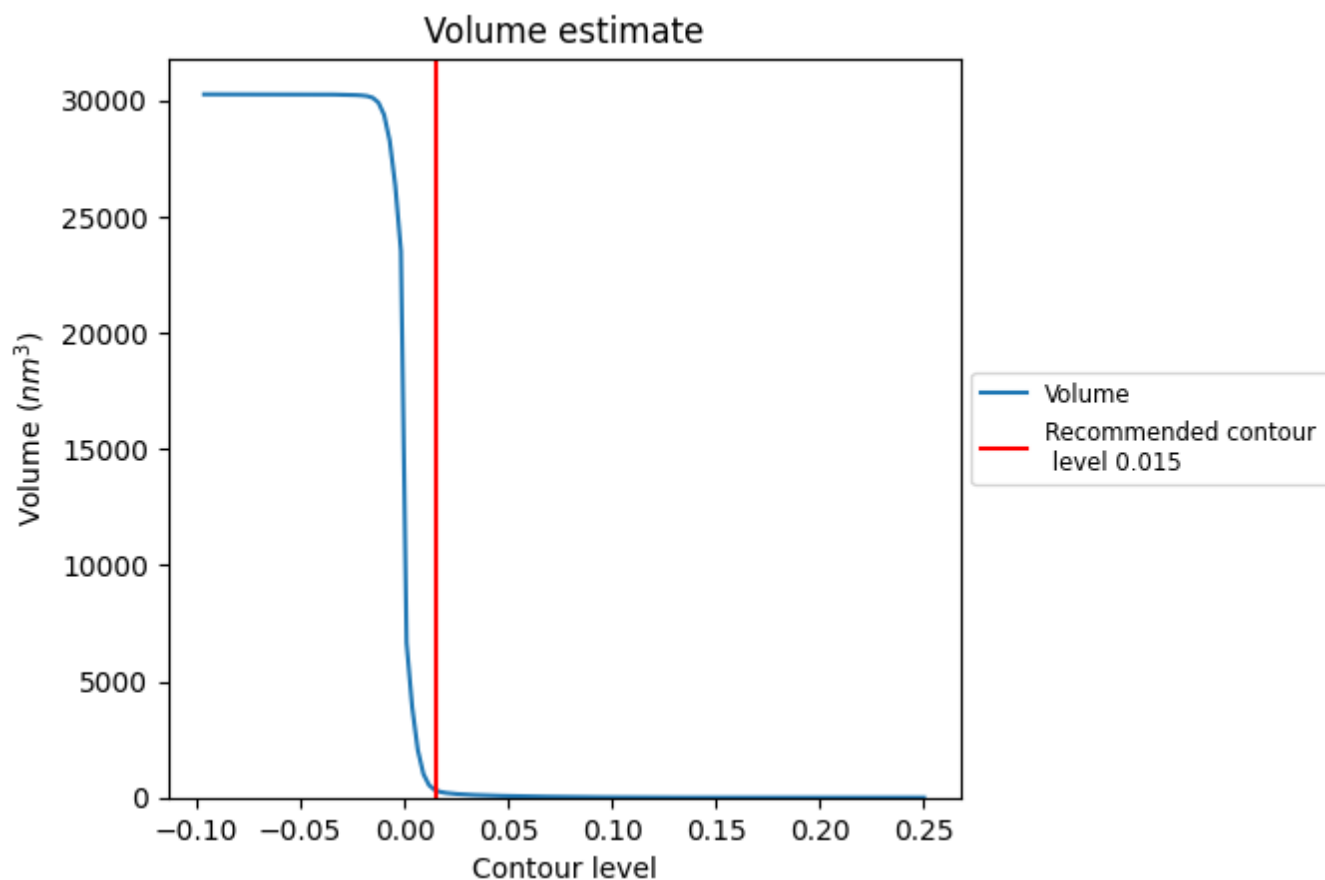
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

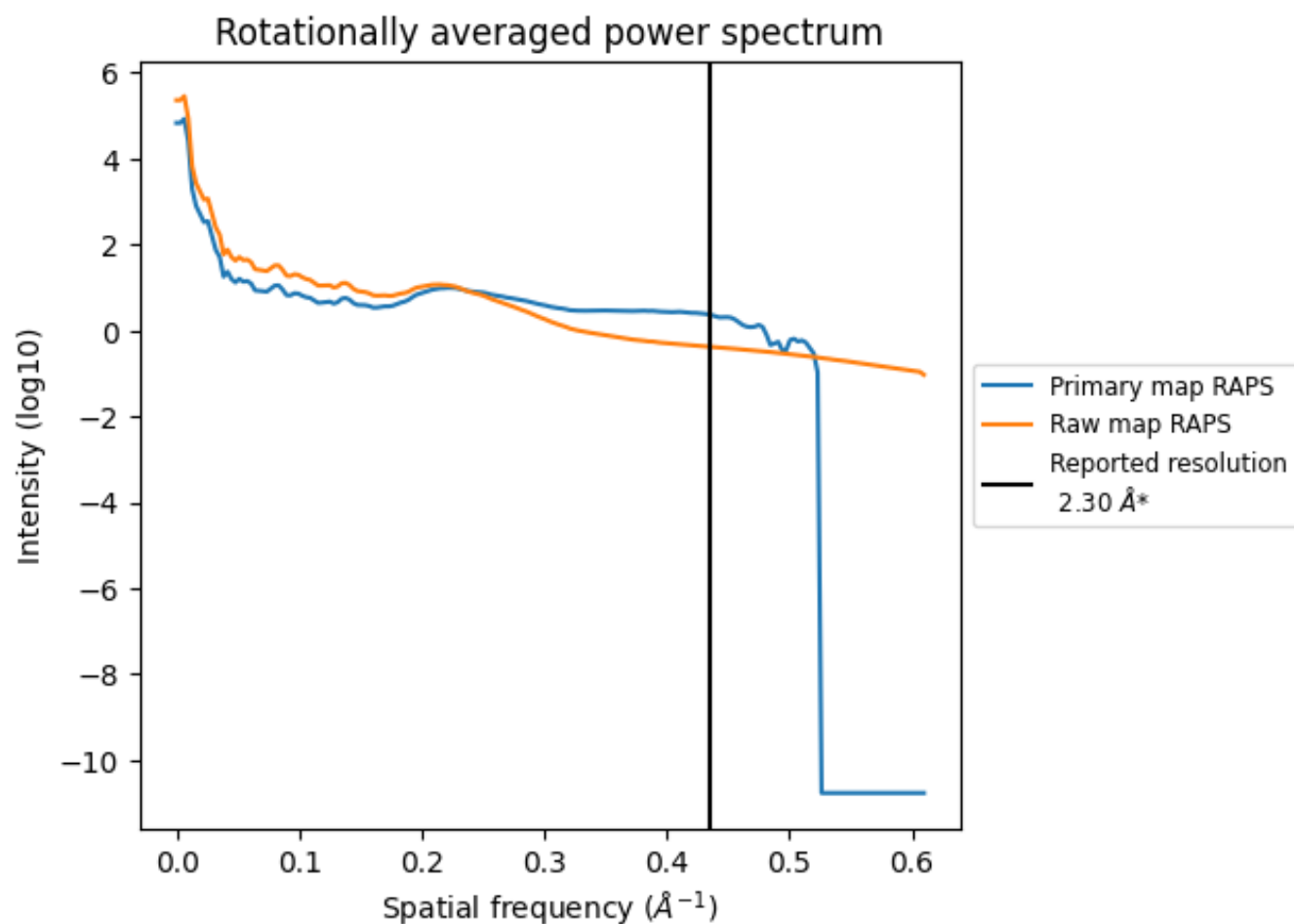
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 318 nm^3 ; this corresponds to an approximate mass of 287 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

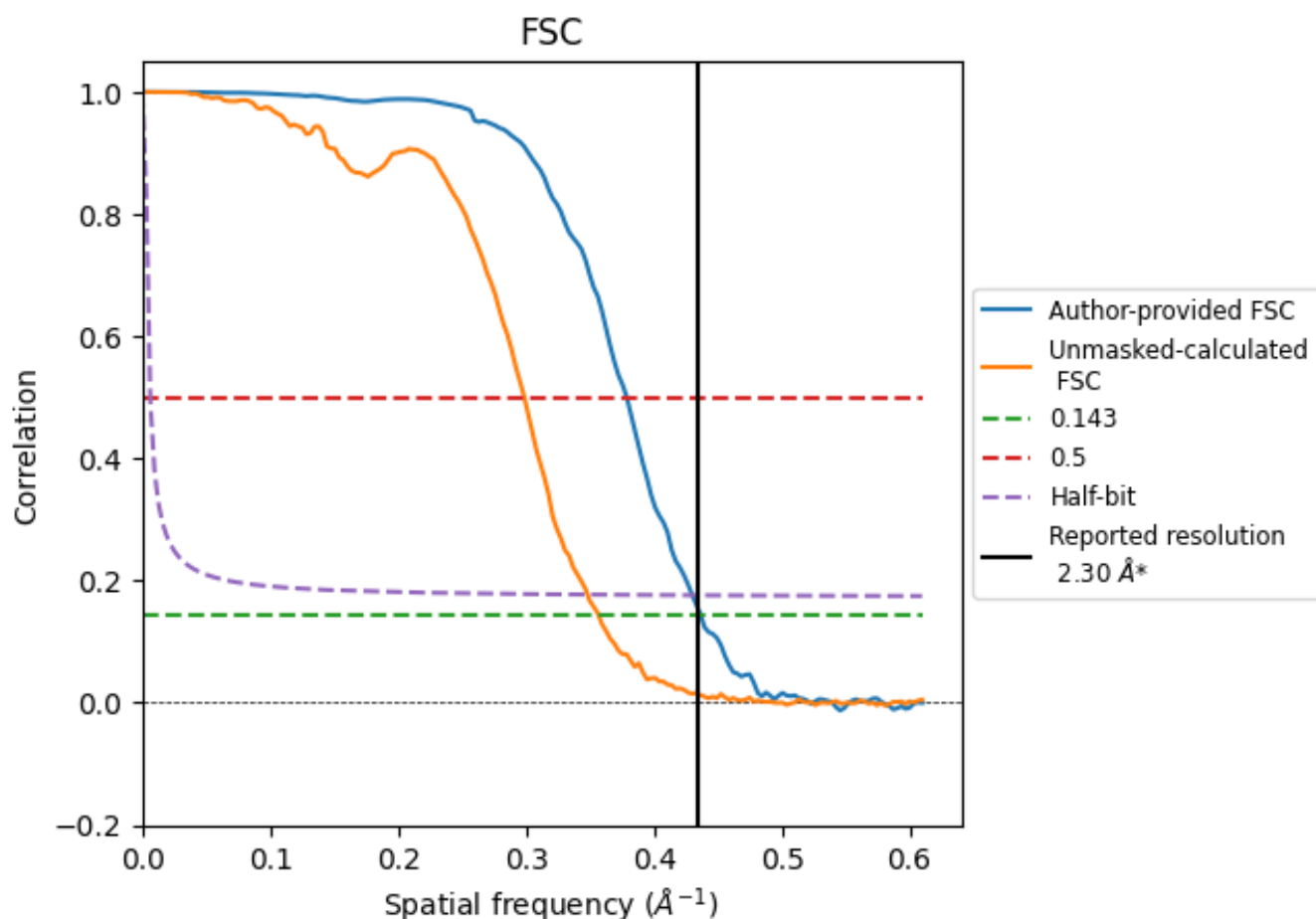


*Reported resolution corresponds to spatial frequency of 0.435 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.435 \AA^{-1}

8.2 Resolution estimates [i](#)

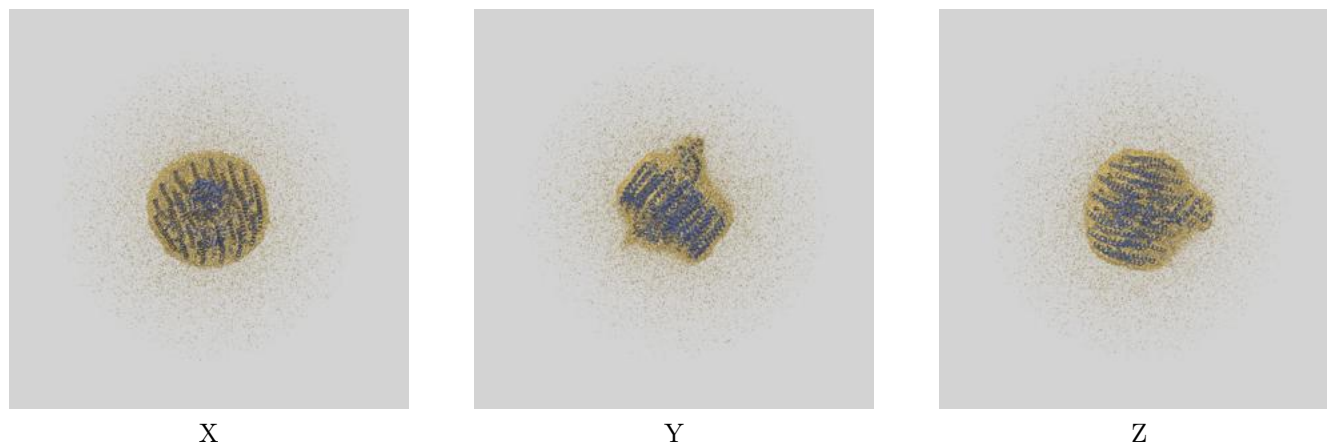
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.30	-	-
Author-provided FSC curve	2.29	2.64	2.33
Unmasked-calculated*	2.80	3.35	2.87

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.80 differs from the reported value 2.3 by more than 10 %

9 Map-model fit [i](#)

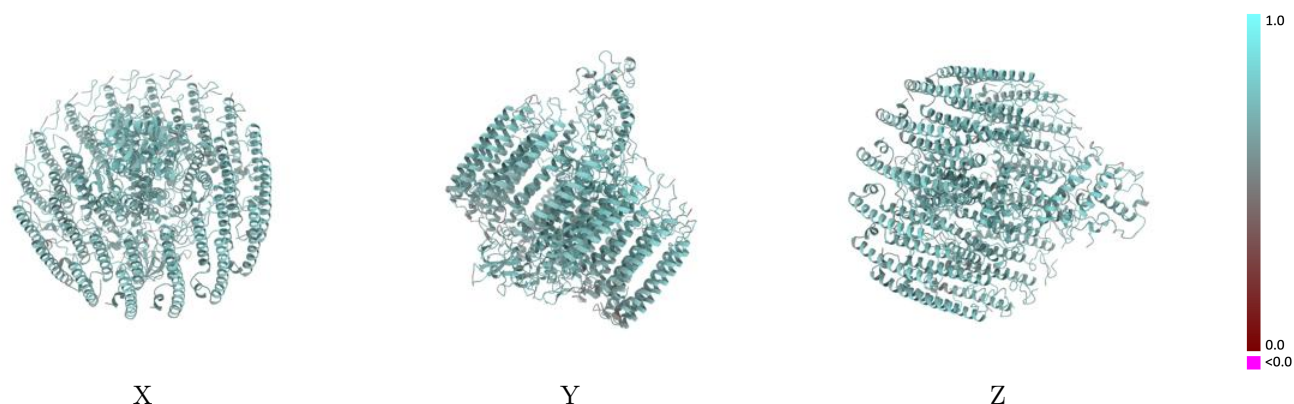
This section contains information regarding the fit between EMDB map EMD-63714 and PDB model 9M8M. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



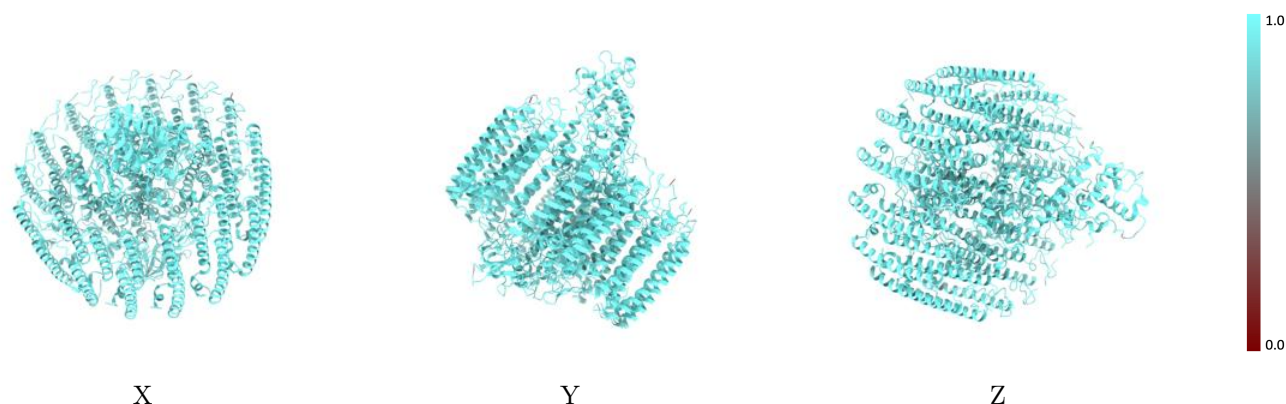
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



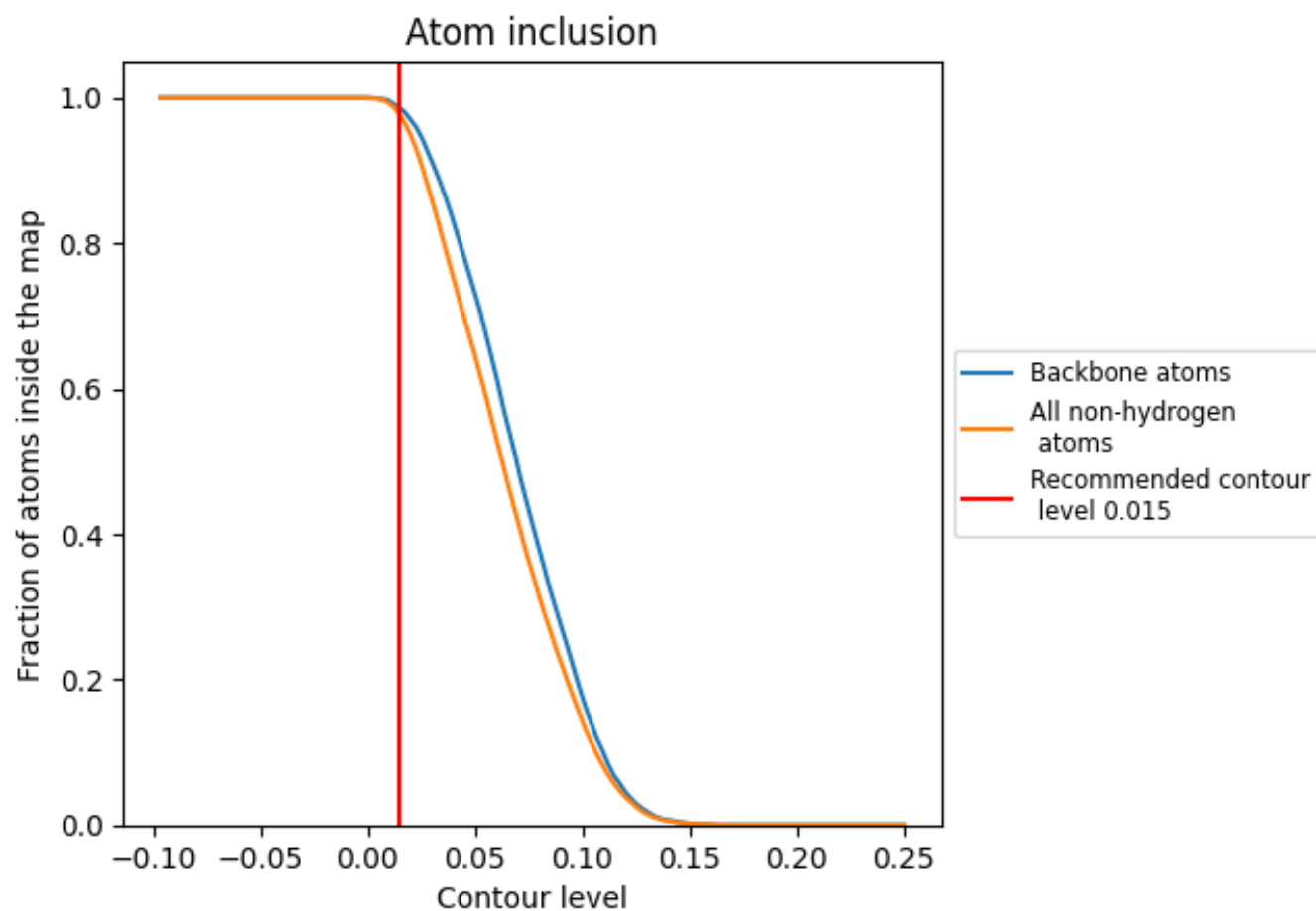
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9770	 0.6660
0	 0.9770	 0.6730
1	 0.9800	 0.6490
2	 0.9540	 0.6320
3	 0.9870	 0.6560
4	 0.9460	 0.6250
5	 0.9760	 0.6340
6	 0.9630	 0.6240
7	 0.9640	 0.6190
8	 0.9550	 0.6220
9	 0.9880	 0.6790
A	 0.9860	 0.6770
B	 0.9640	 0.6410
C	 0.9830	 0.6820
D	 0.9710	 0.6410
E	 0.9730	 0.6430
F	 0.9840	 0.6680
G	 0.9750	 0.6640
H	 0.9700	 0.6590
I	 0.9940	 0.6770
J	 0.9670	 0.6390
K	 0.9710	 0.6380
L	 0.9860	 0.7090
M	 0.9910	 0.7120
N	 0.9570	 0.6320
O	 0.9680	 0.6470
P	 0.9670	 0.6290
Q	 0.9830	 0.6870
R	 0.9710	 0.6630
S	 0.9830	 0.6730
T	 0.9730	 0.6540
U	 0.9860	 0.6780
V	 0.9590	 0.6370
W	 0.9870	 0.6750
X	 0.9670	 0.6330



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Chain	Atom inclusion	Q-score
Y	 0.9850	 0.6670
Z	 0.9440	 0.6300