



wwPDB EM Validation Summary Report ⓘ

Mar 31, 2025 – 06:36 PM JST

PDB ID : 7C9R / pdb_00007c9r
EMDB ID : EMD-30314
Title : STRUCTURE OF PHOTOSYNTHETIC LH1-RC SUPER-COMPLEX OF THIORHODOVIBRIO STRAIN 970
Authors : Tani, K.; Kanno, R.; Makino, Y.; Hall, M.; Takenouchi, M.; Imanishi, M.; Yu, L.-J.; Overmann, J.; Madigan, M.T.; Kimura, Y.; Mizoguchi, A.; Humbel, B.M.; Wang-Otomo, Z.-Y.
Deposited on : 2020-06-07
Resolution : 2.82 Å(reported)
Based on initial model : 5Y5S

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.dev117
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

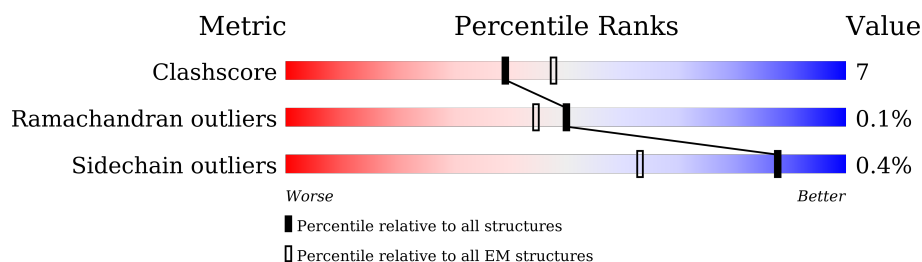
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.82 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.




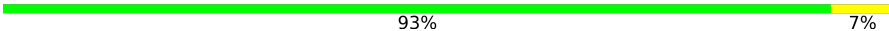









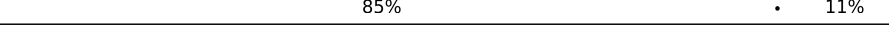

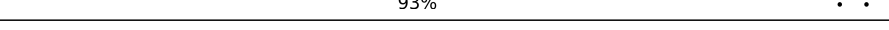





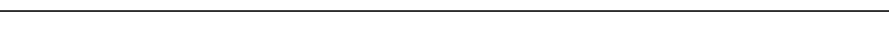

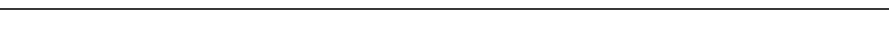
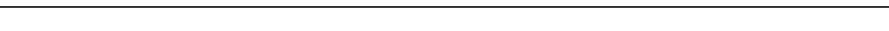


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	C	396	
2	L	273	
3	M	324	
4	H	258	
5	A	73	
5	D	73	
5	F	73	
5	I	73	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	K	73	 93% 5%
5	O	73	 93% 7%
6	4	46	 89% 7%
6	B	46	 80% 13% 7%
6	P	46	 89% 9%
7	0	46	 76% 11% 11%
7	2	46	 83% 7% 11%
7	6	46	 87% 7% 7%
7	8	46	 78% 11% 9%
7	E	46	 89% 9%
7	G	46	 83% 7% 11%
7	J	46	 85% 11%
7	N	46	 87% 9%
7	R	46	 93% 4%
7	T	46	 83% 11% 7%
7	V	46	 85% 9% 7%
7	X	46	 89% 11%
7	Z	46	 89% 9%
8	Q	81	 84% 12%
9	1	77	 86% 8% 6%
9	3	77	 88% 6% 5%
9	5	77	 90% 6%
9	7	77	 88% 6% 5%
9	S	77	 84% 8% 6%
9	U	77	 87% 6% 6%

Continued on next page...

Mol	Chain	Length	Quality of chain
9	W	77	<div><div style="width: 90%;"></div>90%<div><div style="width: 5%;"></div>• • 5%</div></div>
9	Y	77	<div><div style="width: 88%;"></div>88%<div><div style="width: 6%;"></div>6%<div style="width: 5%;"></div>5%</div></div>
10	9	86	<div><div style="width: 87%;"></div>87%<div><div style="width: 10%;"></div>10%<div style="width: 3%;"></div>•</div></div>

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 29228 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	311	Total	C	N	O	S	0	0
			2433	1536	423	458	16		

- Molecule 2 is a protein called L subunit of the reaction center.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	272	Total	C	N	O	S	0	0
			2161	1459	350	344	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
			2535	1700	408	416	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	257	Total	C	N	O	S	0	0
			2017	1298	348	366	5		

- Molecule 5 is a protein called Alpha subunit 1 of light-harvesting 1 complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	70	Total	C	N	O	S	0	0
			563	373	89	96	5		
5	D	72	Total	C	N	O	S	0	0
			580	382	93	100	5		
5	F	72	Total	C	N	O	S	0	0
			580	382	93	100	5		
5	I	73	Total	C	N	O	S	0	0
			588	387	94	101	6		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	72	Total	C	N	O	S	0	0
			580	382	93	100	5		
5	O	73	Total	C	N	O	S	0	0
			588	387	94	101	6		

- Molecule 6 is a protein called Antenna complex alpha/beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	43	Total	C	N	O	S	0	0
			352	236	55	58	3		
6	P	42	Total	C	N	O	S	0	0
			343	230	53	57	3		
6	4	44	Total	C	N	O	S	0	0
			361	241	56	61	3		

- Molecule 7 is a protein called Antenna complex alpha/beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	42	Total	C	N	O	S	0	0
			343	230	53	58	2		
7	G	41	Total	C	N	O	S	0	0
			337	227	52	56	2		
7	J	41	Total	C	N	O	S	0	0
			337	227	52	56	2		
7	N	42	Total	C	N	O	S	0	0
			343	230	53	58	2		
7	R	44	Total	C	N	O	S	0	0
			361	241	56	62	2		
7	T	43	Total	C	N	O	S	0	0
			352	236	55	59	2		
7	V	43	Total	C	N	O	S	0	0
			352	236	55	59	2		
7	X	41	Total	C	N	O	S	0	0
			337	227	52	56	2		
7	Z	42	Total	C	N	O	S	0	0
			343	230	53	58	2		
7	2	41	Total	C	N	O	S	0	0
			337	227	52	56	2		
7	6	43	Total	C	N	O	S	0	0
			352	236	55	59	2		
7	8	42	Total	C	N	O	S	0	0
			343	230	53	58	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
7	0	41	Total	C	N	O	S	0	0
			337	227	52	56	2		

- Molecule 8 is a protein called Antenna complex alpha/beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Q	78	Total	C	N	O	S	0	0
			628	416	101	107	4		

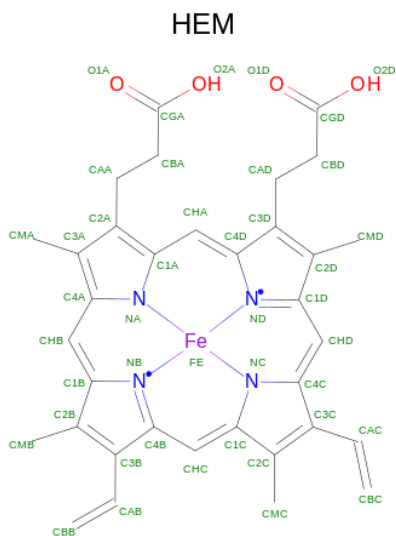
- Molecule 9 is a protein called LHC domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	S	72	Total	C	N	O	S	0	0
			579	382	92	99	6		
9	U	72	Total	C	N	O	S	0	0
			576	382	91	98	5		
9	W	73	Total	C	N	O	S	0	0
			584	386	92	101	5		
9	Y	73	Total	C	N	O	S	0	0
			584	386	92	101	5		
9	1	72	Total	C	N	O	S	0	0
			576	382	91	98	5		
9	3	73	Total	C	N	O	S	0	0
			584	386	93	100	5		
9	5	74	Total	C	N	O	S	0	0
			589	389	94	101	5		
9	7	73	Total	C	N	O	S	0	0
			584	386	93	100	5		

- Molecule 10 is a protein called Alpha subunit 2 of light-harvesting 1 complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	84	Total	C	N	O	S	0	0
			668	440	113	111	4		

- Molecule 11 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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

- Molecule 12 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
12	C	1	Total 1	Mg 1	0

- Molecule 13 is CALCIUM ION (CCD ID: CA) (formula: Ca).

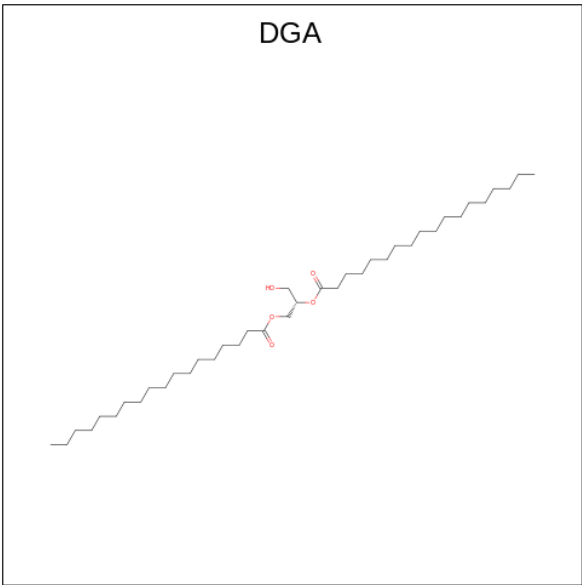
Mol	Chain	Residues	Atoms	AltConf
13	C	1	Total Ca 1 1	0
13	A	1	Total Ca 1 1	0
13	D	1	Total Ca 1 1	0
13	F	1	Total Ca 1 1	0

Continued on next page...

Continued from previous page...

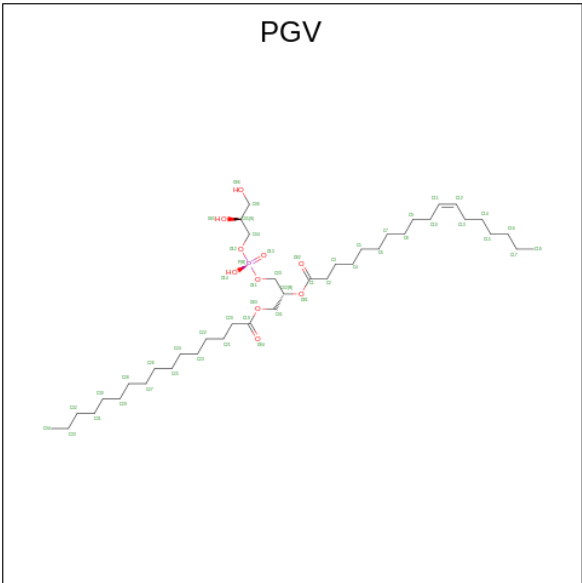
Mol	Chain	Residues	Atoms		AltConf
13	I	1	Total 1	Ca 1	0
13	K	1	Total 1	Ca 1	0
13	O	1	Total 1	Ca 1	0
13	Q	1	Total 1	Ca 1	0
13	S	1	Total 1	Ca 1	0
13	U	1	Total 1	Ca 1	0
13	W	1	Total 1	Ca 1	0
13	Y	1	Total 1	Ca 1	0
13	1	1	Total 1	Ca 1	0
13	3	1	Total 1	Ca 1	0
13	5	1	Total 1	Ca 1	0
13	7	1	Total 1	Ca 1	0
13	9	1	Total 1	Ca 1	0

- Molecule 14 is DIACYL GLYCEROL (CCD ID: DGA) (formula: C₃₉H₇₆O₅).



Mol	Chain	Residues	Atoms			AltConf
14	C	1	Total	C	O	0
			32	28	4	

- Molecule 15 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
15	C	1	Total	C	O	P	0
			16	9	6	1	
15	L	1	Total	C	O	P	0
			47	36	10	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf
15	M	1	Total	C	O	P	0
			39	28	10	1	
15	H	1	Total	C	O	P	0
			36	25	10	1	
15	A	1	Total	C	O	P	0
			23	12	10	1	
15	D	1	Total	C	O	P	0
			43	32	10	1	
15	F	1	Total	C	O	P	0
			34	25	8	1	
15	F	1	Total	C	O	P	0
			37	26	10	1	
15	I	1	Total	C	O	P	0
			41	32	8	1	
15	K	1	Total	C	O	P	0
			36	25	10	1	
15	K	1	Total	C	O	P	0
			19	10	8	1	
15	K	1	Total	C	O	P	0
			43	34	8	1	
15	O	1	Total	C	O	P	0
			44	33	10	1	
15	Q	1	Total	C	O	P	0
			38	27	10	1	
15	Y	1	Total	C	O	P	0
			27	18	8	1	
15	1	1	Total	C	O	P	0
			26	17	8	1	
15	3	1	Total	C	O	P	0
			47	36	10	1	
15	5	1	Total	C	O	P	0
			47	36	10	1	
15	9	1	Total	C	O	P	0
			47	36	10	1	

- Molecule 16 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: $C_{55}H_{74}MgN_4O_6$).



Continued on next page...

Continued from previous page...

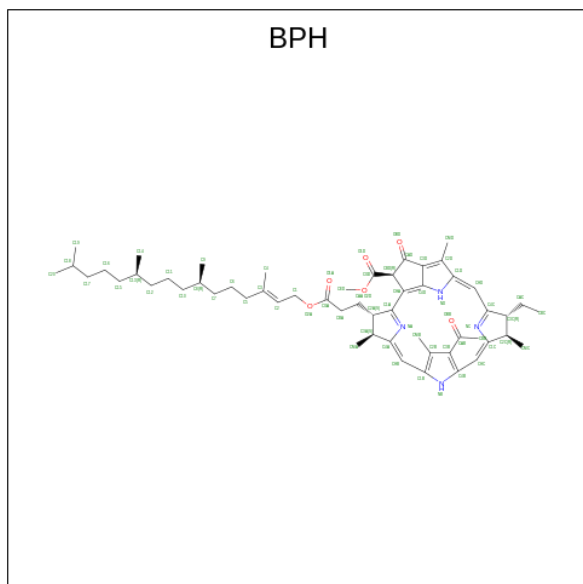
Mol	Chain	Residues	Atoms					AltConf
16	O	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	O	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	Q	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	Q	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	S	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	T	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	U	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	U	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	W	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	X	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	Y	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	Y	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	1	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	2	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	5	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	5	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	7	1	Total 61	C 50	Mg 1	N 4	O 6	0
16	7	1	Total 66	C 55	Mg 1	N 4	O 6	0
16	9	1	Total 66	C 55	Mg 1	N 4	O 6	0

Continued on next page...

Continued from previous page...

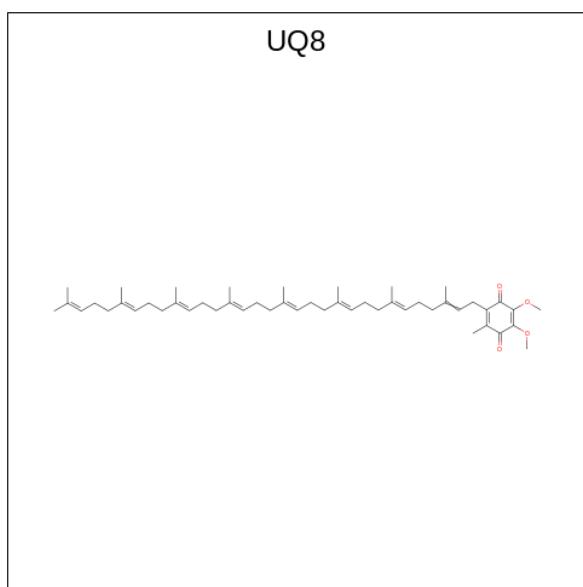
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
16	9	1	66	55	1	4	6	0

- Molecule 17 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$).



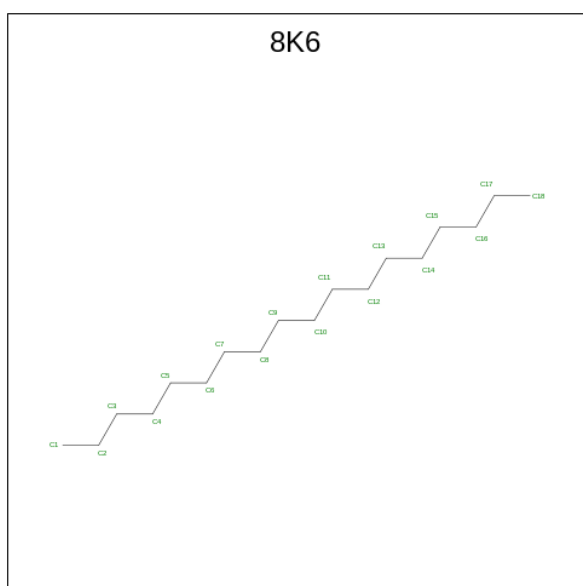
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
17	L	1	65	55	4	6	0
17	M	1	65	55	4	6	0

- Molecule 18 is Ubiquinone-8 (CCD ID: UQ8) (formula: $C_{49}H_{74}O_4$).



Mol	Chain	Residues	Atoms			AltConf
18	L	1	Total	C	O	0
			33	29	4	
18	L	1	Total	C	O	0
			33	29	4	

- Molecule 19 is Octadecane (CCD ID: 8K6) (formula: $C_{18}H_{38}$).

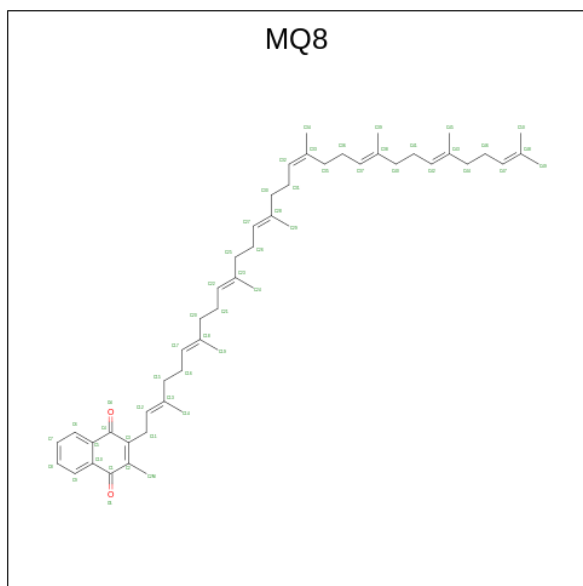


Mol	Chain	Residues	Atoms		AltConf
19	L	1	Total	C	0
			18	18	
19	5	1	Total	C	0
			15	15	

- Molecule 20 is FE (III) ION (CCD ID: FE) (formula: Fe).

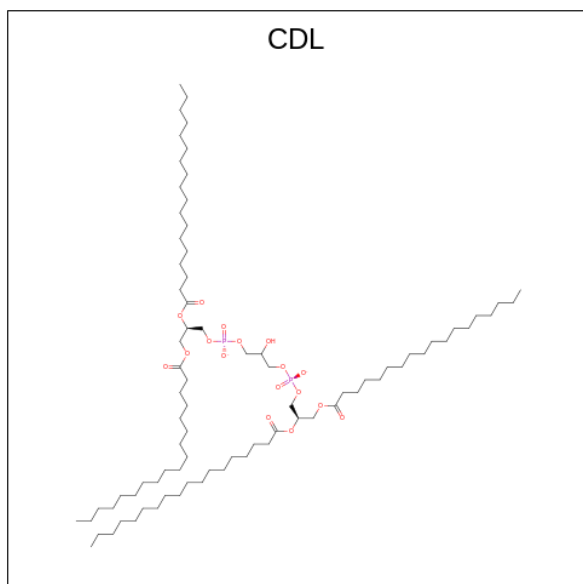
Mol	Chain	Residues	Atoms		AltConf
20	M	1	Total	Fe	0
			1	1	

- Molecule 21 is MENAQUINONE 8 (CCD ID: MQ8) (formula: $C_{51}H_{72}O_2$).



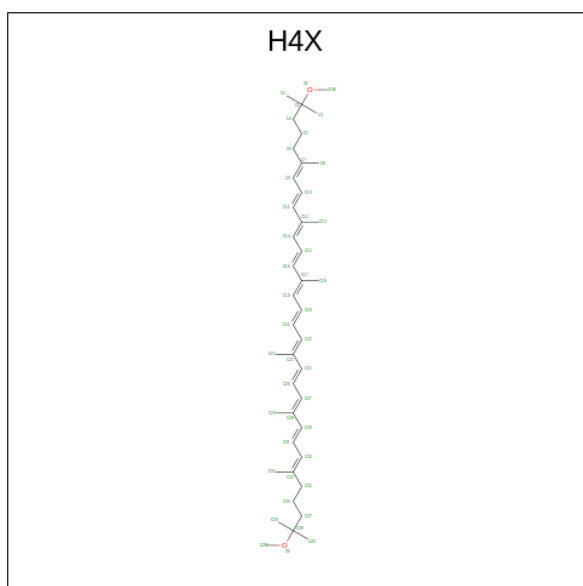
Mol	Chain	Residues	Atoms			AltConf
21	M	1	Total	C	O	0
			53	51	2	

- Molecule 22 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms				AltConf
22	H	1	Total	C	O	P	0
			73	54	17	2	
22	S	1	Total	C	O	P	0
			74	55	17	2	
22	Y	1	Total	C	O	P	0
			30	14	14	2	

- Molecule 23 is (6 {E},8 {E},10 {E},12 {E},14 {E},16 {E},18 {E},20 {E},22 {E},24 {E},26 {E})-2,31-dimethoxy-2,6,10,14,19,23,27,31-octamethyl-dotriaconta-6,8,10,12,14,16,18,20,22,24,26-undecaene (CCD ID: H4X) (formula: C₄₂H₆₄O₂).



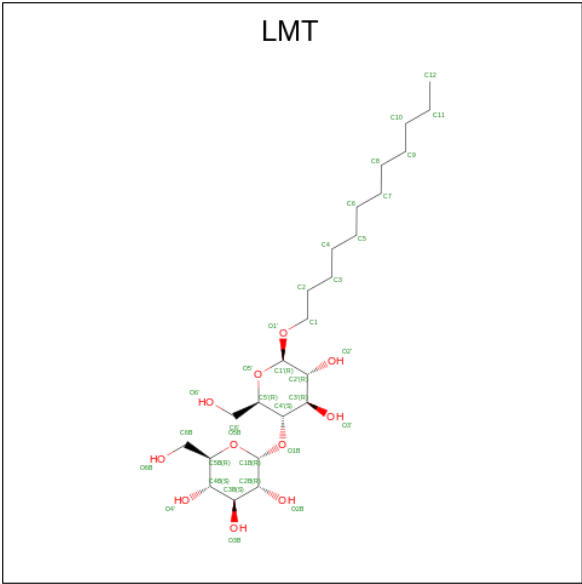
Mol	Chain	Residues	Atoms			AltConf
23	B	1	Total	C	O	0
			44	42	2	
23	E	1	Total	C	O	0
			44	42	2	
23	G	1	Total	C	O	0
			44	42	2	
23	K	1	Total	C	O	0
			44	42	2	
23	K	1	Total	C	O	0
			44	42	2	
23	O	1	Total	C	O	0
			44	42	2	
23	O	1	Total	C	O	0
			44	42	2	
23	P	1	Total	C	O	0
			44	42	2	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			AltConf
23	Q	1	Total	C	O	0
			44	42	2	
23	U	1	Total	C	O	0
			44	42	2	
23	V	1	Total	C	O	0
			44	42	2	
23	Z	1	Total	C	O	0
			44	42	2	
23	2	1	Total	C	O	0
			44	42	2	
23	4	1	Total	C	O	0
			44	42	2	
23	5	1	Total	C	O	0
			44	42	2	
23	6	1	Total	C	O	0
			44	42	2	
23	7	1	Total	C	O	0
			44	42	2	

- Molecule 24 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula: C₂₄H₄₆O₁₁).



Mol	Chain	Residues	Atoms			AltConf
24	B	1	Total	C	O	0
			35	24	11	
24	B	1	Total	C	O	0
			35	24	11	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			AltConf
24	E	1	Total	C	O	0
			35	24	11	
24	G	1	Total	C	O	0
			35	24	11	
24	J	1	Total	C	O	0
			35	24	11	
24	N	1	Total	C	O	0
			35	24	11	
24	P	1	Total	C	O	0
			35	24	11	
24	R	1	Total	C	O	0
			35	24	11	
24	T	1	Total	C	O	0
			35	24	11	
24	V	1	Total	C	O	0
			35	24	11	
24	X	1	Total	C	O	0
			35	24	11	
24	Z	1	Total	C	O	0
			35	24	11	
24	2	1	Total	C	O	0
			35	24	11	
24	4	1	Total	C	O	0
			35	24	11	
24	6	1	Total	C	O	0
			35	24	11	
24	8	1	Total	C	O	0
			35	24	11	
24	8	1	Total	C	O	0
			35	24	11	
24	0	1	Total	C	O	0
			35	24	11	

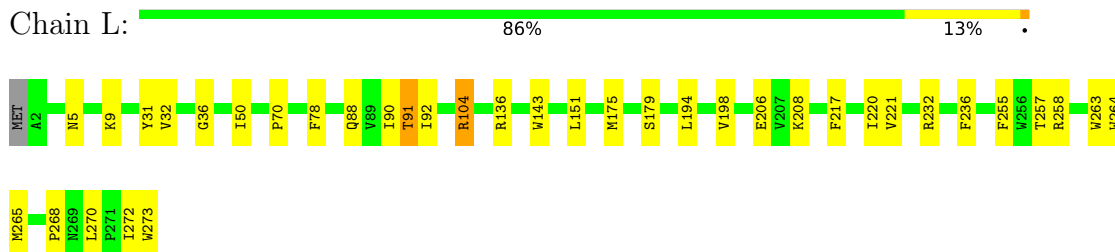
3 Residue-property plots [i](#)

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. 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. 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.

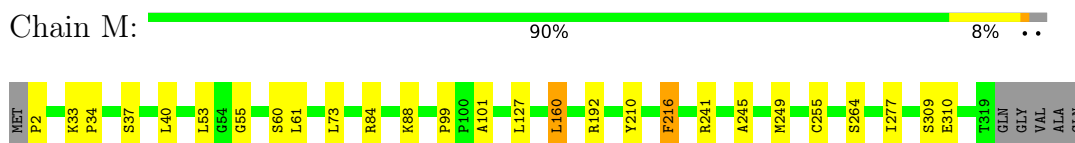
- Molecule 1: Photosynthetic reaction center cytochrome c subunit



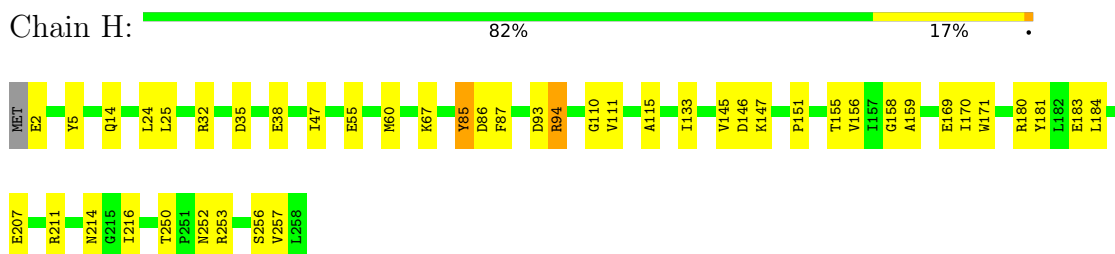
- Molecule 2: L subunit of the reaction center




- Molecule 3: Reaction center protein M chain



- Molecule 4: Photosynthetic reaction center, subunit H, bacterial



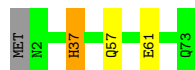
- Molecule 5: Alpha subunit 1 of light-harvesting 1 complex

Chain A:  86% 10% .




- Molecule 5: Alpha subunit 1 of light-harvesting 1 complex

Chain D:  95% ..



- Molecule 5: Alpha subunit 1 of light-harvesting 1 complex

Chain F:  90% 8% .



- Molecule 5: Alpha subunit 1 of light-harvesting 1 complex

Chain I:  99% .



- Molecule 5: Alpha subunit 1 of light-harvesting 1 complex

Chain K:  93% 5% .




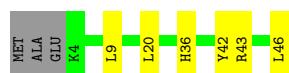
- Molecule 5: Alpha subunit 1 of light-harvesting 1 complex

Chain O:  93% 7%




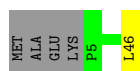
- Molecule 6: Antenna complex alpha/beta subunit

Chain B:  80% 13% 7%




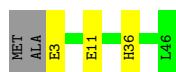
- Molecule 6: Antenna complex alpha/beta subunit

Chain P:  89% . 9%



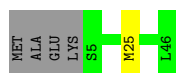
- Molecule 6: Antenna complex alpha/beta subunit

Chain 4:  89% 7% .




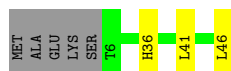
- Molecule 7: Antenna complex alpha/beta subunit

Chain E:  89% . 9%




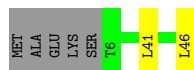
- Molecule 7: Antenna complex alpha/beta subunit

Chain G:  83% 7% 11%




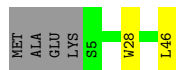
- Molecule 7: Antenna complex alpha/beta subunit

Chain J:  85% . 11%



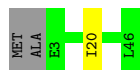
- Molecule 7: Antenna complex alpha/beta subunit

Chain N:  87% . 9%




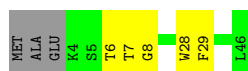
- Molecule 7: Antenna complex alpha/beta subunit

Chain R:  93% . .




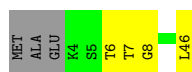
- Molecule 7: Antenna complex alpha/beta subunit

Chain T:  83% 11% 7%




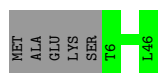
- Molecule 7: Antenna complex alpha/beta subunit

Chain V:  85% 9% 7%




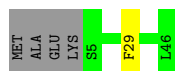
- Molecule 7: Antenna complex alpha/beta subunit

Chain X:  89% 11%




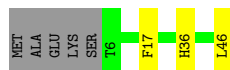
- Molecule 7: Antenna complex alpha/beta subunit

Chain Z:  89% 9% 2%




- Molecule 7: Antenna complex alpha/beta subunit

Chain 2:  83% 7% 11%



- Molecule 7: Antenna complex alpha/beta subunit

Chain 6:  87% 7% 7%




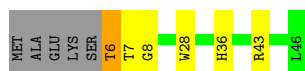
- Molecule 7: Antenna complex alpha/beta subunit

Chain 8:  78% 11% 11%




- Molecule 7: Antenna complex alpha/beta subunit

Chain 0:  76% 11% • 11%




- Molecule 8: Antenna complex alpha/beta subunit

Chain Q:  84% 12% •




- Molecule 9: LHC domain-containing protein

Chain S:  84% 8% • 6%



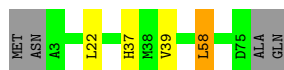
- Molecule 9: LHC domain-containing protein

Chain U:  87% 6% 6%




- Molecule 9: LHC domain-containing protein

Chain W:  90% • • 5%




- Molecule 9: LHC domain-containing protein

Chain Y:  88% 6% 5%




- Molecule 9: LHC domain-containing protein

Chain 1:  86% 8% 6%



- Molecule 9: LHC domain-containing protein

Chain 3:  88% 6% 5%




- Molecule 9: LHC domain-containing protein

Chain 5:  90% 6% .




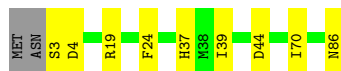
- Molecule 9: LHC domain-containing protein

Chain 7:  88% 6% 5%



- Molecule 10: Alpha subunit 2 of light-harvesting 1 complex

Chain 9:  87% 10% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	105234	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: H4X, FE, HEM, BPH, MG, UQ8, CA, PGV, 8K6, BCL, CDL, DGA, LMT, MQ8

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	0.75	3/2503 (0.1%)	0.95	7/3423 (0.2%)
2	L	0.67	1/2244 (0.0%)	0.92	5/3068 (0.2%)
3	M	0.63	0/2633	0.90	4/3599 (0.1%)
4	H	0.49	0/2069	0.87	3/2811 (0.1%)
5	A	0.67	0/579	0.83	0/787
5	D	0.62	0/596	0.85	1/810 (0.1%)
5	F	0.64	1/596 (0.2%)	0.79	0/810
5	I	0.56	0/604	0.76	0/820
5	K	0.57	0/596	0.76	0/810
5	O	0.64	0/604	0.81	0/820
6	4	0.59	0/374	0.67	0/506
6	B	1.07	3/365 (0.8%)	0.91	2/494 (0.4%)
6	P	0.58	0/356	0.70	0/482
7	0	0.64	0/349	0.83	1/474 (0.2%)
7	2	0.51	0/349	0.63	0/474
7	6	0.60	0/364	0.67	0/493
7	8	0.63	0/355	0.74	1/482 (0.2%)
7	E	0.62	0/355	0.66	0/482
7	G	0.62	0/349	0.65	0/474
7	J	0.60	0/349	0.71	1/474 (0.2%)
7	N	0.58	0/355	0.64	0/482
7	R	0.60	0/373	0.70	0/505
7	T	0.56	0/364	0.64	0/493
7	V	0.57	0/364	0.73	0/493
7	X	0.55	0/349	0.67	0/474
7	Z	0.53	0/355	0.61	0/482
8	Q	0.51	0/649	0.78	0/881
9	1	0.64	1/592 (0.2%)	0.74	0/805
9	3	0.57	0/600	0.76	0/816
9	5	0.61	0/605	0.73	0/823
9	7	0.67	0/600	0.95	2/816 (0.2%)
9	S	0.63	0/595	0.84	1/808 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	U	0.64	1/592 (0.2%)	0.75	0/805
9	W	0.59	0/600	0.75	0/816
9	Y	0.57	0/600	0.75	0/816
10	9	0.52	0/690	0.94	0/941
All	All	0.63	10/24872 (0.0%)	0.82	28/33849 (0.1%)

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
5	A	0	1
5	K	0	1
7	0	0	1
9	1	0	1
All	All	0	5

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	219	ARG	CZ-NH1	20.04	1.59	1.33
6	B	42	TYR	CZ-OH	14.18	1.61	1.37
1	C	219	ARG	NE-CZ	11.86	1.48	1.33
6	B	42	TYR	CE2-CZ	6.24	1.46	1.38
6	B	42	TYR	CD2-CE2	5.96	1.48	1.39

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	219	ARG	NE-CZ-NH1	-13.16	113.72	120.30
1	C	219	ARG	NE-CZ-NH2	10.65	125.63	120.30
3	M	216	PHE	CB-CG-CD1	10.00	127.80	120.80
6	B	43	ARG	NE-CZ-NH2	-7.75	116.42	120.30
9	7	3	ALA	N-CA-CB	-7.72	99.29	110.10

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	0	6	THR	Peptide
9	1	15	ILE	Mainchain
5	A	68	GLU	Mainchain
1	C	219	ARG	Sidechain
5	K	42	SER	Mainchain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2433	0	2339	58	0
2	L	2161	0	2138	31	0
3	M	2535	0	2502	23	0
4	H	2017	0	2015	39	0
5	A	563	0	565	7	0
5	D	580	0	579	2	0
5	F	580	0	579	4	0
5	I	588	0	591	1	0
5	K	580	0	579	7	0
5	O	588	0	591	6	0
6	4	361	0	354	3	0
6	B	352	0	348	4	0
6	P	343	0	336	1	0
7	0	337	0	332	10	0
7	2	337	0	332	3	0
7	6	352	0	350	3	0
7	8	343	0	337	5	0
7	E	343	0	337	1	0
7	G	337	0	332	3	0
7	J	337	0	332	1	0
7	N	343	0	337	2	0
7	R	361	0	356	2	0
7	T	352	0	350	4	0
7	V	352	0	350	3	0
7	X	337	0	332	0	0
7	Z	343	0	337	1	0
8	Q	628	0	617	8	0
9	1	576	0	578	5	0
9	3	584	0	584	5	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	5	589	0	586	5	0
9	7	584	0	584	3	0
9	S	579	0	583	8	0
9	U	576	0	578	4	0
9	W	584	0	582	4	0
9	Y	584	0	582	6	0
10	9	668	0	673	8	0
11	C	172	0	120	30	0
12	C	1	0	0	0	0
13	1	1	0	0	0	0
13	3	1	0	0	0	0
13	5	1	0	0	0	0
13	7	1	0	0	0	0
13	9	1	0	0	0	0
13	A	1	0	0	0	0
13	C	1	0	0	0	0
13	D	1	0	0	0	0
13	F	1	0	0	0	0
13	I	1	0	0	0	0
13	K	1	0	0	0	0
13	O	1	0	0	0	0
13	Q	1	0	0	0	0
13	S	1	0	0	0	0
13	U	1	0	0	0	0
13	W	1	0	0	0	0
13	Y	1	0	0	0	0
14	C	32	0	45	6	0
15	1	26	0	25	0	0
15	3	47	0	65	4	0
15	5	47	0	65	4	0
15	9	47	0	65	2	0
15	A	23	0	18	0	0
15	C	16	0	11	0	0
15	D	43	0	59	0	0
15	F	71	0	83	2	0
15	H	36	0	42	1	0
15	I	41	0	53	0	0
15	K	98	0	117	3	0
15	L	47	0	62	3	0
15	M	39	0	48	1	0
15	O	44	0	61	5	0
15	Q	38	0	46	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	Y	27	0	27	6	0
16	1	66	0	74	6	0
16	2	66	0	74	4	0
16	3	132	0	148	14	0
16	5	132	0	148	11	0
16	7	127	0	135	9	0
16	9	132	0	148	9	0
16	A	66	0	74	9	0
16	B	66	0	74	4	0
16	D	132	0	148	8	0
16	F	132	0	148	10	0
16	I	66	0	74	4	0
16	J	66	0	73	4	0
16	K	132	0	147	11	0
16	L	132	0	148	5	0
16	M	132	0	148	7	0
16	O	132	0	147	8	0
16	Q	132	0	147	12	0
16	S	66	0	74	6	0
16	T	66	0	74	4	0
16	U	132	0	147	9	0
16	W	66	0	74	3	0
16	X	66	0	74	4	0
16	Y	132	0	148	8	0
17	L	65	0	76	7	0
17	M	65	0	76	7	0
18	L	66	0	78	8	0
19	5	15	0	29	0	0
19	L	18	0	38	1	0
20	M	1	0	0	0	0
21	M	53	0	72	2	0
22	H	73	0	90	3	0
22	S	74	0	95	1	0
22	Y	30	0	17	0	0
23	2	44	0	0	0	0
23	4	44	0	0	0	0
23	5	44	0	0	0	0
23	6	44	0	0	0	0
23	7	44	0	0	0	0
23	B	44	0	0	0	0
23	E	44	0	0	1	0
23	G	44	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	K	88	0	0	1	0
23	O	88	0	0	1	0
23	P	44	0	0	0	0
23	Q	44	0	0	0	0
23	U	44	0	0	0	0
23	V	44	0	0	0	0
23	Z	44	0	0	0	0
24	0	35	0	46	1	0
24	2	35	0	46	2	0
24	4	35	0	46	3	0
24	6	35	0	46	2	0
24	8	70	0	92	5	0
24	B	70	0	92	3	0
24	E	35	0	46	2	0
24	G	35	0	46	1	0
24	J	35	0	46	2	0
24	N	35	0	46	3	0
24	P	35	0	46	2	0
24	R	35	0	46	2	0
24	T	35	0	46	2	0
24	V	35	0	46	1	0
24	X	35	0	46	2	0
24	Z	35	0	46	1	0
All	All	29228	0	28934	406	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 7.

The worst 5 of 406 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:247:CYS:SG	11:C:403:HEM:HAB	1.52	1.47
1:C:247:CYS:SG	11:C:403:HEM:CAB	2.07	1.42
1:C:307:CYS:SG	11:C:404:HEM:HAB	1.66	1.36
1:C:155:CYS:SG	11:C:402:HEM:HAC	1.73	1.29
1:C:310:CYS:SG	11:C:404:HEM:CAC	2.28	1.21

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	309/396 (78%)	287 (93%)	22 (7%)	0	100	100
2	L	270/273 (99%)	251 (93%)	19 (7%)	0	100	100
3	M	316/324 (98%)	303 (96%)	13 (4%)	0	100	100
4	H	255/258 (99%)	231 (91%)	21 (8%)	3 (1%)	11	32
5	A	68/73 (93%)	67 (98%)	1 (2%)	0	100	100
5	D	70/73 (96%)	70 (100%)	0	0	100	100
5	F	70/73 (96%)	68 (97%)	2 (3%)	0	100	100
5	I	71/73 (97%)	68 (96%)	3 (4%)	0	100	100
5	K	70/73 (96%)	69 (99%)	1 (1%)	0	100	100
5	O	71/73 (97%)	69 (97%)	2 (3%)	0	100	100
6	4	42/46 (91%)	40 (95%)	2 (5%)	0	100	100
6	B	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
6	P	40/46 (87%)	40 (100%)	0	0	100	100
7	0	39/46 (85%)	38 (97%)	1 (3%)	0	100	100
7	2	39/46 (85%)	38 (97%)	1 (3%)	0	100	100
7	6	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
7	8	40/46 (87%)	38 (95%)	1 (2%)	1 (2%)	4	15
7	E	40/46 (87%)	39 (98%)	1 (2%)	0	100	100
7	G	39/46 (85%)	38 (97%)	1 (3%)	0	100	100
7	J	39/46 (85%)	38 (97%)	1 (3%)	0	100	100
7	N	40/46 (87%)	39 (98%)	1 (2%)	0	100	100
7	R	42/46 (91%)	42 (100%)	0	0	100	100
7	T	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
7	V	41/46 (89%)	40 (98%)	1 (2%)	0	100	100
7	X	39/46 (85%)	38 (97%)	1 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	Z	40/46 (87%)	39 (98%)	1 (2%)	0	100	100
8	Q	76/81 (94%)	73 (96%)	3 (4%)	0	100	100
9	1	70/77 (91%)	69 (99%)	1 (1%)	0	100	100
9	3	71/77 (92%)	70 (99%)	1 (1%)	0	100	100
9	5	72/77 (94%)	72 (100%)	0	0	100	100
9	7	71/77 (92%)	71 (100%)	0	0	100	100
9	S	70/77 (91%)	68 (97%)	2 (3%)	0	100	100
9	U	70/77 (91%)	68 (97%)	2 (3%)	0	100	100
9	W	71/77 (92%)	71 (100%)	0	0	100	100
9	Y	71/77 (92%)	71 (100%)	0	0	100	100
10	9	82/86 (95%)	76 (93%)	6 (7%)	0	100	100
All	All	2937/3208 (92%)	2819 (96%)	114 (4%)	4 (0%)	50	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	H	86	ASP
7	8	6	THR
4	H	257	VAL
4	H	256	SER

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	266/314 (85%)	265 (100%)	1 (0%)	89	96
2	L	217/218 (100%)	216 (100%)	1 (0%)	86	95
3	M	256/260 (98%)	253 (99%)	3 (1%)	67	89
4	H	211/212 (100%)	209 (99%)	2 (1%)	75	92
5	A	62/65 (95%)	62 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	D	64/65 (98%)	64 (100%)	0	100	100
5	F	64/65 (98%)	64 (100%)	0	100	100
5	I	65/65 (100%)	65 (100%)	0	100	100
5	K	64/65 (98%)	64 (100%)	0	100	100
5	O	65/65 (100%)	65 (100%)	0	100	100
6	4	38/39 (97%)	38 (100%)	0	100	100
6	B	37/39 (95%)	36 (97%)	1 (3%)	40	72
6	P	36/39 (92%)	36 (100%)	0	100	100
7	0	35/39 (90%)	35 (100%)	0	100	100
7	2	35/39 (90%)	35 (100%)	0	100	100
7	6	37/39 (95%)	37 (100%)	0	100	100
7	8	36/39 (92%)	36 (100%)	0	100	100
7	E	36/39 (92%)	36 (100%)	0	100	100
7	G	35/39 (90%)	35 (100%)	0	100	100
7	J	35/39 (90%)	35 (100%)	0	100	100
7	N	36/39 (92%)	36 (100%)	0	100	100
7	R	38/39 (97%)	38 (100%)	0	100	100
7	T	37/39 (95%)	37 (100%)	0	100	100
7	V	37/39 (95%)	37 (100%)	0	100	100
7	X	35/39 (90%)	35 (100%)	0	100	100
7	Z	36/39 (92%)	36 (100%)	0	100	100
8	Q	67/70 (96%)	66 (98%)	1 (2%)	60	85
9	1	63/68 (93%)	63 (100%)	0	100	100
9	3	64/68 (94%)	64 (100%)	0	100	100
9	5	64/68 (94%)	64 (100%)	0	100	100
9	7	64/68 (94%)	64 (100%)	0	100	100
9	S	64/68 (94%)	64 (100%)	0	100	100
9	U	63/68 (93%)	63 (100%)	0	100	100
9	W	64/68 (94%)	63 (98%)	1 (2%)	58	84
9	Y	64/68 (94%)	64 (100%)	0	100	100
10	9	72/74 (97%)	72 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2562/2706 (95%)	2552 (100%)	10 (0%)	88 96

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	B	20	LEU
8	Q	69	MET
9	W	58	LEU
3	M	192	ARG
3	M	216	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
9	W	59	GLN
9	7	59	GLN
10	9	86	ASN
10	9	29	GLN
2	L	88	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 124 ligands modelled in this entry, 19 are monoatomic - leaving 105 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
17	BPH	M	404	-	51,70,70	0.78	2 (3%)	52,101,101	1.04	3 (5%)
15	PGV	K	106	-	42,42,50	1.06	2 (4%)	46,47,56	1.03	3 (6%)
16	BCL	T	101	-	64,74,74	1.94	16 (25%)	78,115,115	1.91	23 (29%)
23	H4X	O	106	-	43,43,43	2.44	17 (39%)	50,54,54	2.05	18 (36%)
23	H4X	5	105	-	43,43,43	2.24	12 (27%)	50,54,54	2.10	14 (28%)
16	BCL	K	108	-	64,74,74	1.93	14 (21%)	78,115,115	2.07	24 (30%)
24	LMT	X	102	-	36,36,36	0.75	1 (2%)	47,47,47	1.36	5 (10%)
16	BCL	Y	104	-	64,74,74	1.78	10 (15%)	78,115,115	1.92	22 (28%)
17	BPH	L	302	-	51,70,70	0.75	2 (3%)	52,101,101	0.97	1 (1%)
23	H4X	7	104	-	43,43,43	2.34	12 (27%)	50,54,54	2.18	14 (28%)
18	UQ8	L	306	-	33,33,53	1.67	2 (6%)	40,43,67	1.86	11 (27%)
24	LMT	T	102	-	36,36,36	0.91	2 (5%)	47,47,47	1.49	9 (19%)
24	LMT	R	101	-	36,36,36	0.85	2 (5%)	47,47,47	1.36	8 (17%)
15	PGV	I	103	-	40,40,50	1.01	2 (5%)	44,45,56	1.17	7 (15%)
16	BCL	1	102	-	64,74,74	1.82	13 (20%)	78,115,115	2.12	19 (24%)
24	LMT	B	102	-	36,36,36	0.53	0	47,47,47	1.16	3 (6%)
23	H4X	V	101	-	43,43,43	2.32	13 (30%)	50,54,54	2.67	17 (34%)
23	H4X	B	101	-	43,43,43	2.22	13 (30%)	50,54,54	2.06	19 (38%)
16	BCL	3	104	-	64,74,74	2.02	14 (21%)	78,115,115	2.02	25 (32%)
15	PGV	5	101	-	46,46,50	1.05	2 (4%)	49,52,56	1.03	3 (6%)
15	PGV	3	101	-	46,46,50	1.05	2 (4%)	48,52,56	1.40	8 (16%)
11	HEM	C	402	1	41,50,50	1.61	8 (19%)	45,82,82	2.15	15 (33%)
16	BCL	A	102	-	64,74,74	1.78	15 (23%)	78,115,115	2.26	16 (20%)
16	BCL	B	103	-	64,74,74	2.07	16 (25%)	78,115,115	2.02	26 (33%)
15	PGV	C	408	-	15,15,50	1.45	3 (20%)	18,19,56	2.34	5 (27%)
15	PGV	A	101	-	22,22,50	1.50	4 (18%)	23,27,56	1.55	6 (26%)
23	H4X	U	104	-	43,43,43	2.35	14 (32%)	50,54,54	2.05	14 (28%)
24	LMT	8	101	-	36,36,36	0.56	0	47,47,47	0.78	0
16	BCL	L	301	-	64,74,74	1.89	14 (21%)	78,115,115	2.25	28 (35%)
23	H4X	E	101	-	43,43,43	2.49	13 (30%)	50,54,54	2.18	15 (30%)
11	HEM	C	403	1	41,50,50	1.41	5 (12%)	45,82,82	2.51	19 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
16	BCL	U	103	-	64,74,74	2.15	13 (20%)	78,115,115	1.92	19 (24%)
15	PGV	Q	101	-	37,37,50	1.09	3 (8%)	40,43,56	1.47	6 (15%)
16	BCL	W	102	-	64,74,74	1.72	14 (21%)	78,115,115	2.05	18 (23%)
23	H4X	Z	101	-	43,43,43	2.28	11 (25%)	50,54,54	1.87	11 (22%)
16	BCL	D	103	-	64,74,74	1.70	14 (21%)	78,115,115	2.18	14 (17%)
16	BCL	L	304	-	64,74,74	1.91	14 (21%)	78,115,115	3.14	23 (29%)
24	LMT	V	102	-	36,36,36	0.90	0	47,47,47	1.72	7 (14%)
22	CDL	H	302	-	72,72,99	0.45	0	78,84,111	1.01	5 (6%)
16	BCL	7	103	-	64,74,74	2.00	13 (20%)	78,115,115	1.88	17 (21%)
11	HEM	C	404	1	41,50,50	1.44	6 (14%)	45,82,82	2.24	13 (28%)
23	H4X	Q	105	-	43,43,43	2.25	12 (27%)	50,54,54	2.30	22 (44%)
24	LMT	Z	102	-	36,36,36	0.83	1 (2%)	47,47,47	1.62	10 (21%)
16	BCL	9	104	-	64,74,74	2.03	12 (18%)	78,115,115	1.83	22 (28%)
16	BCL	F	103	-	64,74,74	1.65	11 (17%)	78,115,115	2.13	20 (25%)
24	LMT	6	102	-	36,36,36	0.94	3 (8%)	47,47,47	1.68	8 (17%)
16	BCL	I	102	-	64,74,74	1.60	13 (20%)	78,115,115	2.15	21 (26%)
16	BCL	5	104	-	64,74,74	1.86	13 (20%)	78,115,115	1.99	22 (28%)
14	DGA	C	407	1	31,31,43	0.61	0	33,33,45	0.77	1 (3%)
16	BCL	9	103	-	64,74,74	1.76	13 (20%)	78,115,115	2.13	20 (25%)
23	H4X	K	103	-	43,43,43	2.18	11 (25%)	50,54,54	2.00	21 (42%)
15	PGV	9	101	-	46,46,50	0.95	2 (4%)	48,52,56	1.12	4 (8%)
24	LMT	G	102	-	36,36,36	0.85	2 (5%)	47,47,47	1.69	8 (17%)
16	BCL	7	102	-	59,69,74	1.80	13 (22%)	72,109,115	2.13	19 (26%)
16	BCL	K	105	-	64,74,74	1.83	13 (20%)	78,115,115	1.89	20 (25%)
23	H4X	2	101	-	43,43,43	2.25	10 (23%)	50,54,54	1.90	16 (32%)
16	BCL	Q	103	-	64,74,74	1.70	12 (18%)	78,115,115	1.93	14 (17%)
15	PGV	O	102	-	43,43,50	0.93	2 (4%)	46,49,56	1.23	3 (6%)
16	BCL	5	103	-	64,74,74	1.79	13 (20%)	78,115,115	2.03	18 (23%)
24	LMT	B	104	-	36,36,36	1.13	3 (8%)	47,47,47	1.38	8 (17%)
24	LMT	P	102	-	36,36,36	0.92	1 (2%)	47,47,47	1.36	6 (12%)
16	BCL	Q	104	-	64,74,74	2.18	18 (28%)	78,115,115	2.20	29 (37%)
16	BCL	O	105	-	64,74,74	1.87	14 (21%)	78,115,115	2.08	24 (30%)
18	UQ8	L	303	-	33,33,53	1.70	4 (12%)	40,43,67	2.02	13 (32%)
15	PGV	K	102	-	18,18,50	1.27	1 (5%)	20,22,56	1.10	1 (5%)
23	H4X	K	107	-	43,43,43	2.20	11 (25%)	50,54,54	1.95	13 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	LMT	4	102	-	36,36,36	0.96	3 (8%)	47,47,47	1.76	9 (19%)
15	PGV	F	101	-	33,33,50	1.34	2 (6%)	36,38,56	1.65	10 (27%)
23	H4X	4	101	-	43,43,43	2.13	12 (27%)	50,54,54	1.90	16 (32%)
16	BCL	U	102	-	64,74,74	1.71	12 (18%)	78,115,115	2.25	20 (25%)
19	8K6	5	106	-	14,14,17	0.29	0	13,13,16	0.11	0
22	CDL	S	101	-	73,73,99	0.48	0	79,85,111	0.81	3 (3%)
24	LMT	0	101	-	36,36,36	0.83	2 (5%)	47,47,47	1.37	7 (14%)
23	H4X	G	101	-	43,43,43	2.29	14 (32%)	50,54,54	2.16	18 (36%)
16	BCL	3	103	-	64,74,74	1.79	15 (23%)	78,115,115	1.95	20 (25%)
15	PGV	1	103	-	25,25,50	1.37	2 (8%)	29,30,56	1.57	3 (10%)
22	CDL	Y	103	-	29,29,99	0.59	0	33,38,111	0.84	1 (3%)
11	HEM	C	401	1	41,50,50	1.50	11 (26%)	45,82,82	2.18	18 (40%)
24	LMT	N	101	-	36,36,36	0.83	1 (2%)	47,47,47	1.53	6 (12%)
15	PGV	F	104	-	36,36,50	1.11	2 (5%)	39,42,56	1.49	6 (15%)
21	MQ8	M	405	-	54,54,54	0.80	3 (5%)	66,69,69	0.85	1 (1%)
23	H4X	6	101	-	43,43,43	2.29	12 (27%)	50,54,54	2.19	19 (38%)
16	BCL	D	104	-	64,74,74	1.95	16 (25%)	78,115,115	1.83	16 (20%)
15	PGV	M	406	-	38,38,50	1.15	2 (5%)	41,44,56	1.19	3 (7%)
15	PGV	H	301	-	35,35,50	1.27	3 (8%)	38,41,56	1.92	5 (13%)
16	BCL	S	103	-	64,74,74	1.62	12 (18%)	78,115,115	2.00	16 (20%)
16	BCL	F	105	-	64,74,74	1.87	15 (23%)	78,115,115	1.90	17 (21%)
16	BCL	M	402	-	64,74,74	1.77	11 (17%)	78,115,115	2.35	18 (23%)
16	BCL	J	101	-	64,74,74	1.86	13 (20%)	78,115,115	1.97	23 (29%)
24	LMT	2	103	-	36,36,36	0.92	3 (8%)	47,47,47	1.91	13 (27%)
24	LMT	8	102	-	36,36,36	0.74	0	47,47,47	1.32	6 (12%)
16	BCL	M	403	-	64,74,74	1.71	11 (17%)	78,115,115	2.27	25 (32%)
16	BCL	Y	102	-	64,74,74	1.72	12 (18%)	78,115,115	2.15	19 (24%)
19	8K6	L	307	-	17,17,17	0.45	0	16,16,16	0.17	0
23	H4X	P	101	-	43,43,43	2.34	14 (32%)	50,54,54	1.92	17 (34%)
15	PGV	L	305	-	46,46,50	1.05	2 (4%)	49,52,56	1.45	6 (12%)
23	H4X	O	101	-	43,43,43	2.25	15 (34%)	50,54,54	2.50	19 (38%)
16	BCL	X	101	-	64,74,74	1.98	14 (21%)	78,115,115	1.99	20 (25%)
24	LMT	E	102	-	36,36,36	0.92	2 (5%)	47,47,47	1.53	9 (19%)
15	PGV	D	101	-	42,42,50	0.95	2 (4%)	45,48,56	1.52	7 (15%)
24	LMT	J	102	-	36,36,36	0.90	2 (5%)	47,47,47	1.75	11 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	PGV	Y	105	-	26,26,50	1.37	2 (7%)	30,31,56	1.28	5 (16%)
16	BCL	2	102	-	64,74,74	1.57	9 (14%)	78,115,115	2.07	22 (28%)
15	PGV	K	101	-	35,35,50	1.20	2 (5%)	38,41,56	1.14	5 (13%)
16	BCL	O	104	-	64,74,74	1.84	15 (23%)	78,115,115	1.97	19 (24%)

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
17	BPH	M	404	-	-	19/37/105/105	0/5/6/6
15	PGV	K	106	-	-	17/44/44/55	-
16	BCL	T	101	-	-	16/37/137/137	-
23	H4X	O	106	-	-	8/51/51/51	-
23	H4X	5	105	-	-	10/51/51/51	-
16	BCL	K	108	-	-	19/37/137/137	-
24	LMT	X	102	-	-	11/21/61/61	0/2/2/2
16	BCL	Y	104	-	-	18/37/137/137	-
17	BPH	L	302	-	-	17/37/105/105	0/5/6/6
23	H4X	7	104	-	-	7/51/51/51	-
18	UQ8	L	306	-	-	7/27/51/75	0/1/1/1
24	LMT	T	102	-	-	11/21/61/61	0/2/2/2
24	LMT	R	101	-	-	9/21/61/61	0/2/2/2
15	PGV	I	103	-	-	19/42/42/55	-
16	BCL	1	102	-	-	9/37/137/137	-
24	LMT	B	102	-	-	13/21/61/61	0/2/2/2
23	H4X	V	101	-	-	11/51/51/51	-
23	H4X	B	101	-	-	3/51/51/51	-
16	BCL	3	104	-	-	17/37/137/137	-
15	PGV	5	101	-	-	23/51/51/55	-
15	PGV	3	101	-	-	24/51/51/55	-
11	HEM	C	402	1	-	5/12/54/54	-
16	BCL	A	102	-	-	14/37/137/137	-
16	BCL	B	103	-	-	14/37/137/137	-
15	PGV	C	408	-	-	10/15/15/55	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	PGV	A	101	-	-	10/26/26/55	-
23	H4X	U	104	-	-	5/51/51/51	-
24	LMT	8	101	-	-	8/21/61/61	0/2/2/2
16	BCL	L	301	-	-	8/37/137/137	-
23	H4X	E	101	-	-	5/51/51/51	-
11	HEM	C	403	1	-	4/12/54/54	-
16	BCL	U	103	-	-	15/37/137/137	-
15	PGV	Q	101	-	-	21/42/42/55	-
16	BCL	W	102	-	-	6/37/137/137	-
23	H4X	Z	101	-	-	8/51/51/51	-
16	BCL	D	103	-	-	6/37/137/137	-
16	BCL	L	304	-	-	7/37/137/137	-
24	LMT	V	102	-	-	10/21/61/61	0/2/2/2
22	CDL	H	302	-	-	29/83/83/110	-
16	BCL	7	103	-	-	14/37/137/137	-
11	HEM	C	404	1	-	5/12/54/54	-
23	H4X	Q	105	-	-	11/51/51/51	-
24	LMT	Z	102	-	-	11/21/61/61	0/2/2/2
16	BCL	9	104	-	-	14/37/137/137	-
16	BCL	F	103	-	-	13/37/137/137	-
24	LMT	6	102	-	-	10/21/61/61	0/2/2/2
16	BCL	I	102	-	-	13/37/137/137	-
16	BCL	5	104	-	-	18/37/137/137	-
14	DGA	C	407	1	-	20/32/32/45	-
16	BCL	9	103	-	-	21/37/137/137	-
23	H4X	K	103	-	-	10/51/51/51	-
15	PGV	9	101	-	-	23/51/51/55	-
24	LMT	G	102	-	-	12/21/61/61	0/2/2/2
16	BCL	7	102	-	-	8/31/131/137	-
16	BCL	K	105	-	-	22/37/137/137	-
23	H4X	2	101	-	-	10/51/51/51	-
16	BCL	Q	103	-	-	17/37/137/137	-
15	PGV	O	102	-	-	23/48/48/55	-
16	BCL	5	103	-	-	14/37/137/137	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	LMT	B	104	-	-	12/21/61/61	0/2/2/2
24	LMT	P	102	-	-	12/21/61/61	0/2/2/2
16	BCL	Q	104	-	-	14/37/137/137	-
16	BCL	O	105	-	-	17/37/137/137	-
18	UQ8	L	303	-	-	6/27/51/75	0/1/1/1
15	PGV	K	102	-	-	5/20/20/55	-
23	H4X	K	107	-	-	9/51/51/51	-
24	LMT	4	102	-	-	11/21/61/61	0/2/2/2
15	PGV	F	101	-	-	13/35/35/55	-
23	H4X	4	101	-	-	10/51/51/51	-
16	BCL	U	102	-	-	14/37/137/137	-
19	8K6	5	106	-	-	4/12/12/15	-
22	CDL	S	101	-	-	35/84/84/110	-
24	LMT	0	101	-	-	11/21/61/61	0/2/2/2
23	H4X	G	101	-	-	7/51/51/51	-
16	BCL	3	103	-	-	17/37/137/137	-
15	PGV	1	103	-	-	11/27/27/55	-
22	CDL	Y	103	-	-	13/35/35/110	-
11	HEM	C	401	1	-	7/12/54/54	-
24	LMT	N	101	-	-	11/21/61/61	0/2/2/2
15	PGV	F	104	-	-	23/41/41/55	-
21	MQ8	M	405	-	-	10/47/67/67	0/2/2/2
23	H4X	6	101	-	-	5/51/51/51	-
16	BCL	D	104	-	-	16/37/137/137	-
15	PGV	M	406	-	-	21/43/43/55	-
15	PGV	H	301	-	-	17/40/40/55	-
16	BCL	S	103	-	-	5/37/137/137	-
16	BCL	F	105	-	-	14/37/137/137	-
16	BCL	M	402	-	-	15/37/137/137	-
16	BCL	J	101	-	-	15/37/137/137	-
24	LMT	2	103	-	-	10/21/61/61	0/2/2/2
24	LMT	8	102	-	-	11/21/61/61	0/2/2/2
16	BCL	M	403	-	-	13/37/137/137	-
16	BCL	Y	102	-	-	10/37/137/137	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	8K6	L	307	-	-	11/15/15/15	-
23	H4X	P	101	-	-	6/51/51/51	-
15	PGV	L	305	-	-	14/51/51/55	-
23	H4X	O	101	-	-	14/51/51/51	-
16	BCL	X	101	-	-	16/37/137/137	-
24	LMT	E	102	-	-	12/21/61/61	0/2/2/2
15	PGV	D	101	-	-	14/47/47/55	-
24	LMT	J	102	-	-	10/21/61/61	0/2/2/2
15	PGV	Y	105	-	-	9/28/28/55	-
16	BCL	2	102	-	-	15/37/137/137	-
15	PGV	K	101	-	-	18/40/40/55	-
16	BCL	O	104	-	-	13/37/137/137	-

The worst 5 of 809 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	L	306	UQ8	C6-C1	8.07	1.49	1.35
18	L	303	UQ8	C6-C1	7.22	1.48	1.35
16	U	103	BCL	C3D-C4D	-6.72	1.29	1.44
16	L	301	BCL	O2D-CGD	6.54	1.49	1.33
16	B	103	BCL	C3D-C4D	-6.29	1.30	1.44

The worst 5 of 1354 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	L	304	BCL	O2D-CGD-CBD	15.70	139.16	111.27
16	L	304	BCL	O2D-CGD-O1D	-13.24	97.96	123.84
23	V	101	H4X	C21-C22-C23	-9.25	114.11	127.31
16	M	402	BCL	CHD-C1D-ND	-9.00	116.19	124.45
16	F	103	BCL	CHD-C1D-ND	-8.72	116.44	124.45

There are no chirality outliers.

5 of 1338 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	C	401	HEM	C2B-C3B-CAB-CBB
11	C	401	HEM	C4B-C3B-CAB-CBB
11	C	404	HEM	C2B-C3B-CAB-CBB
14	C	407	DGA	CA2-CA1-OG1-CG1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
14	C	407	DGA	OA1-CA1-OG1-CG1

There are no ring outliers.

80 monomers are involved in 272 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	M	404	BPH	7	0
16	T	101	BCL	4	0
23	O	106	H4X	1	0
16	K	108	BCL	4	0
24	X	102	LMT	2	0
16	Y	104	BCL	5	0
17	L	302	BPH	7	0
18	L	306	UQ8	8	0
24	T	102	LMT	2	0
24	R	101	LMT	2	0
16	1	102	BCL	6	0
24	B	102	LMT	1	0
16	3	104	BCL	6	0
15	5	101	PGV	4	0
15	3	101	PGV	4	0
11	C	402	HEM	5	0
16	A	102	BCL	9	0
16	B	103	BCL	4	0
24	8	101	LMT	2	0
16	L	301	BCL	2	0
23	E	101	H4X	1	0
11	C	403	HEM	10	0
16	U	103	BCL	3	0
15	Q	101	PGV	1	0
16	W	102	BCL	3	0
16	D	103	BCL	5	0
16	L	304	BCL	3	0
24	V	102	LMT	1	0
22	H	302	CDL	3	0
16	7	103	BCL	4	0
11	C	404	HEM	9	0
24	Z	102	LMT	1	0
16	9	104	BCL	3	0
16	F	103	BCL	6	0
24	6	102	LMT	2	0
16	I	102	BCL	4	0

Continued on next page...

Continued from previous page...

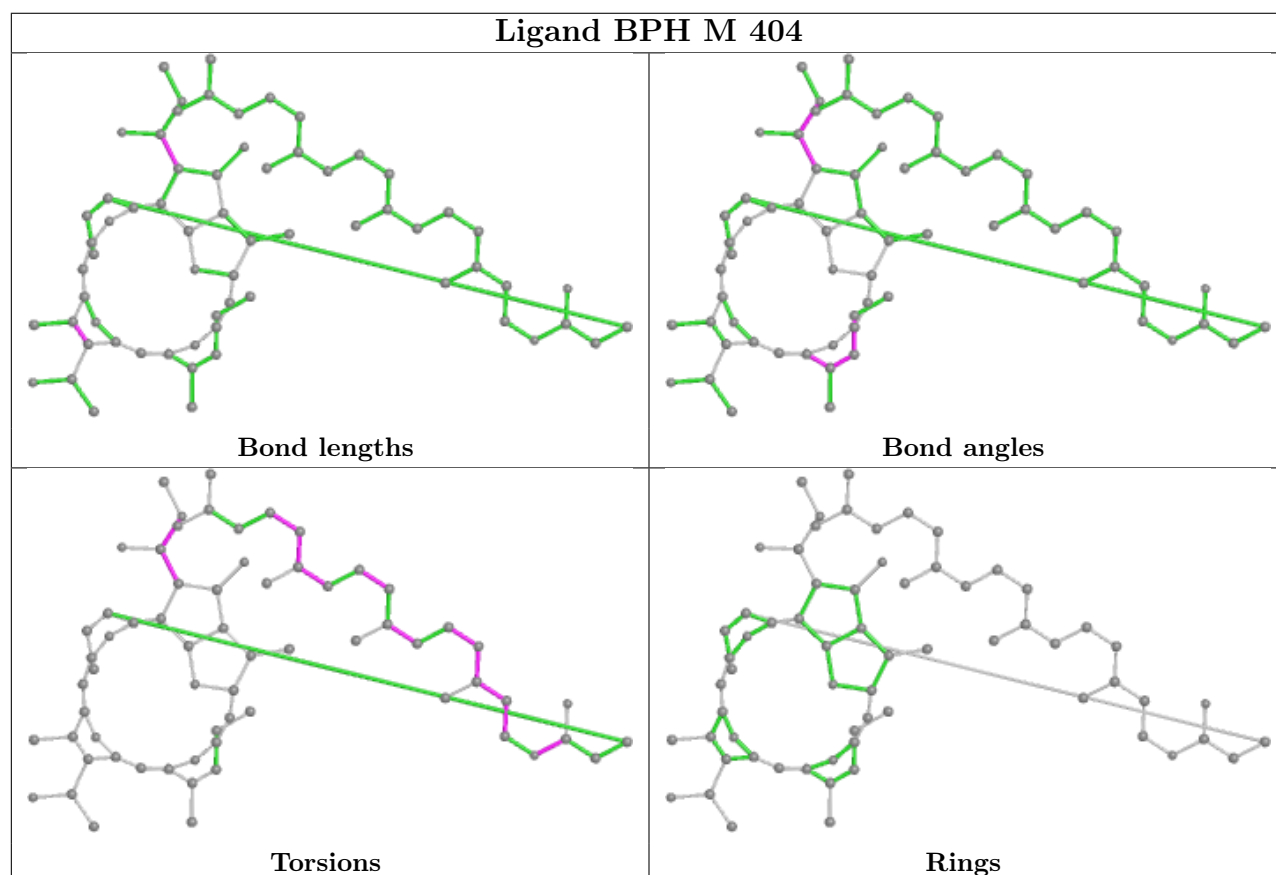
Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	5	104	BCL	3	0
14	C	407	DGA	6	0
16	9	103	BCL	6	0
23	K	103	H4X	1	0
15	9	101	PGV	2	0
24	G	102	LMT	1	0
16	7	102	BCL	5	0
16	K	105	BCL	7	0
16	Q	103	BCL	7	0
15	O	102	PGV	5	0
16	5	103	BCL	8	0
24	B	104	LMT	2	0
24	P	102	LMT	2	0
16	Q	104	BCL	5	0
16	O	105	BCL	4	0
24	4	102	LMT	3	0
16	U	102	BCL	6	0
22	S	101	CDL	1	0
24	0	101	LMT	1	0
16	3	103	BCL	8	0
11	C	401	HEM	6	0
24	N	101	LMT	3	0
15	F	104	PGV	2	0
21	M	405	MQ8	2	0
16	D	104	BCL	3	0
15	M	406	PGV	1	0
15	H	301	PGV	1	0
16	S	103	BCL	6	0
16	F	105	BCL	4	0
16	M	402	BCL	2	0
16	J	101	BCL	4	0
24	2	103	LMT	2	0
24	8	102	LMT	3	0
16	M	403	BCL	5	0
16	Y	102	BCL	3	0
19	L	307	8K6	1	0
15	L	305	PGV	3	0
16	X	101	BCL	4	0
24	E	102	LMT	2	0
24	J	102	LMT	2	0
15	Y	105	PGV	6	0
16	2	102	BCL	4	0

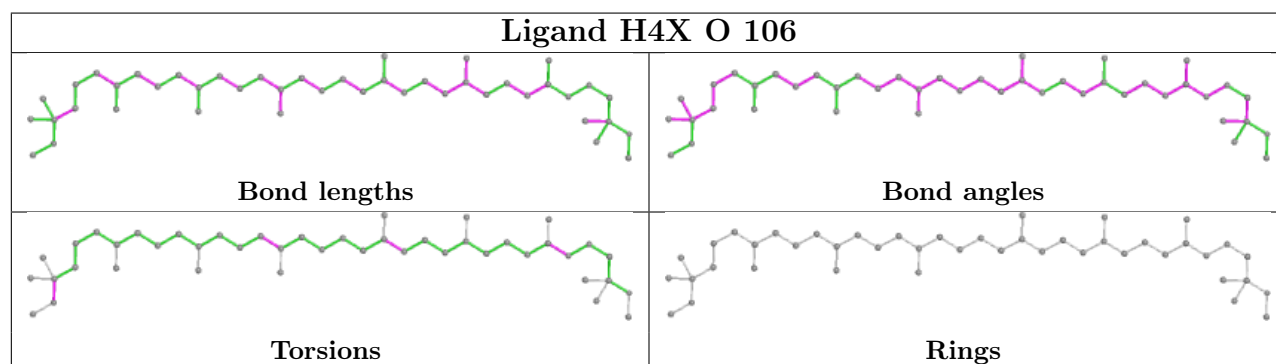
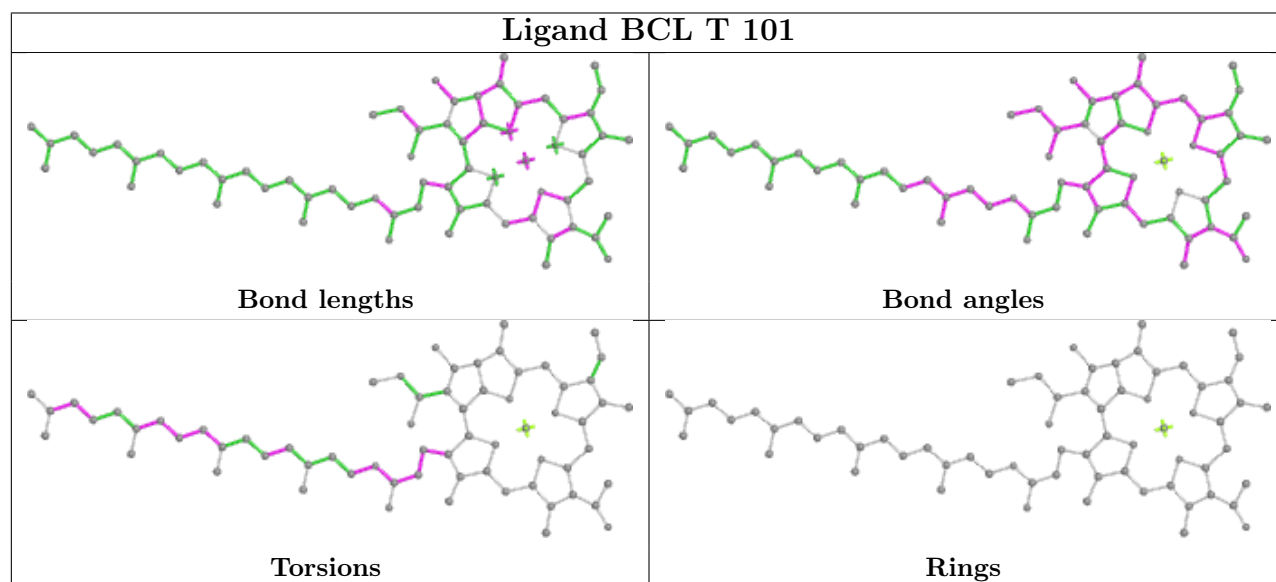
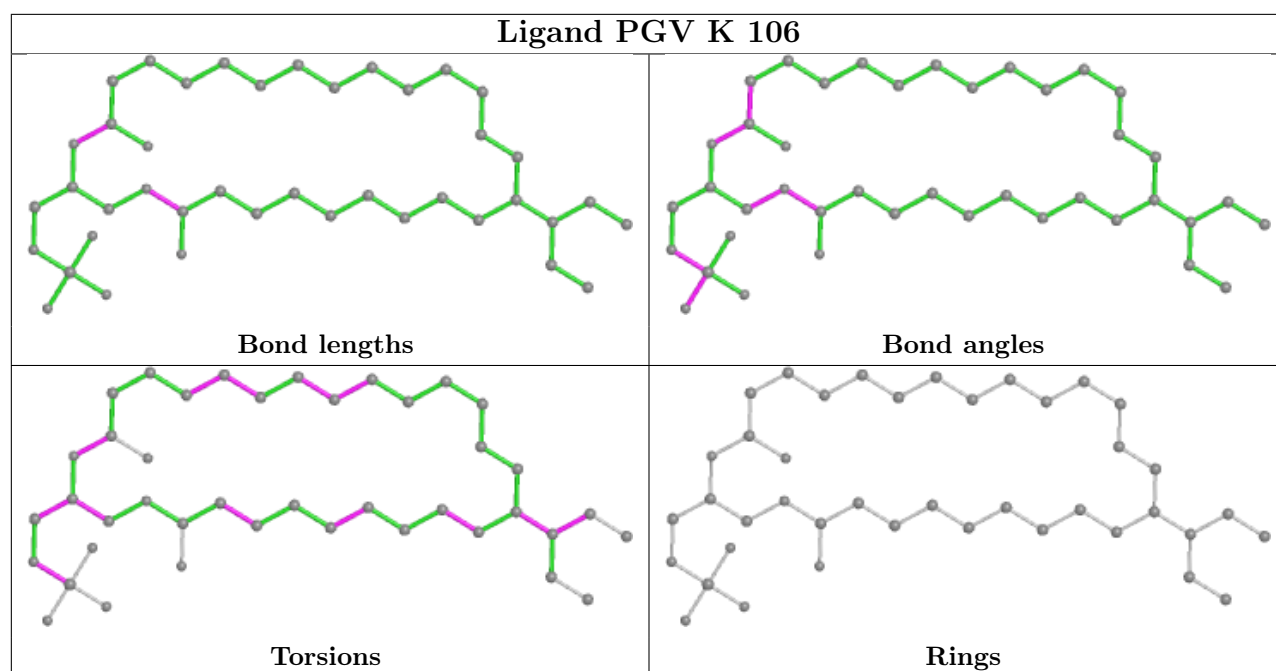
Continued on next page...

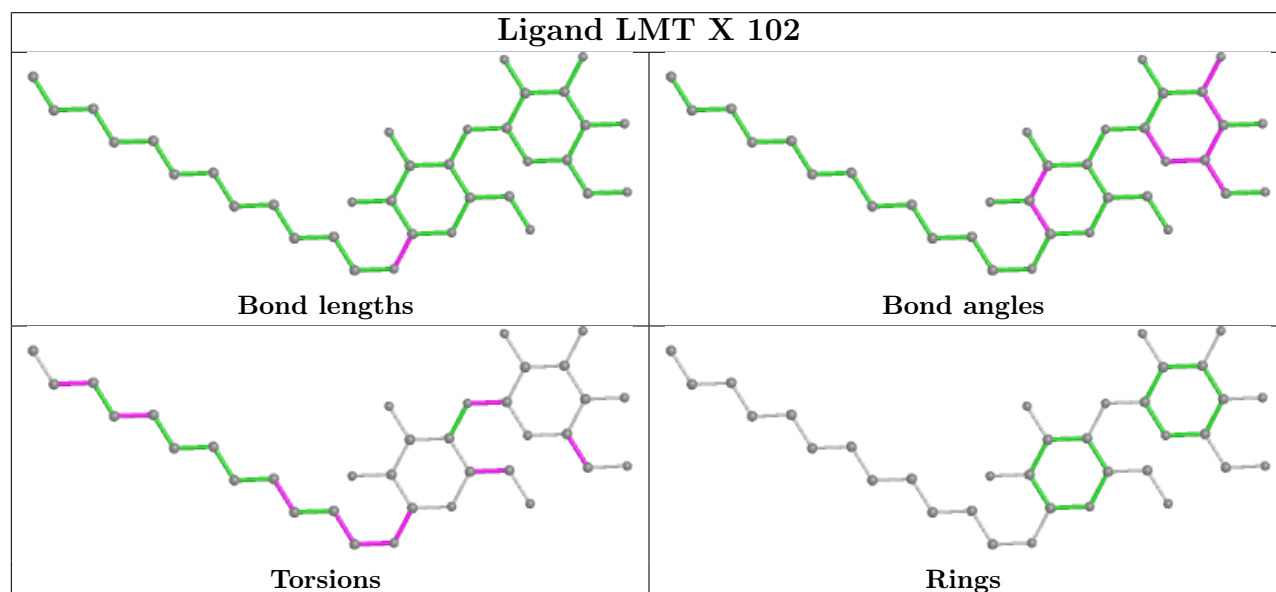
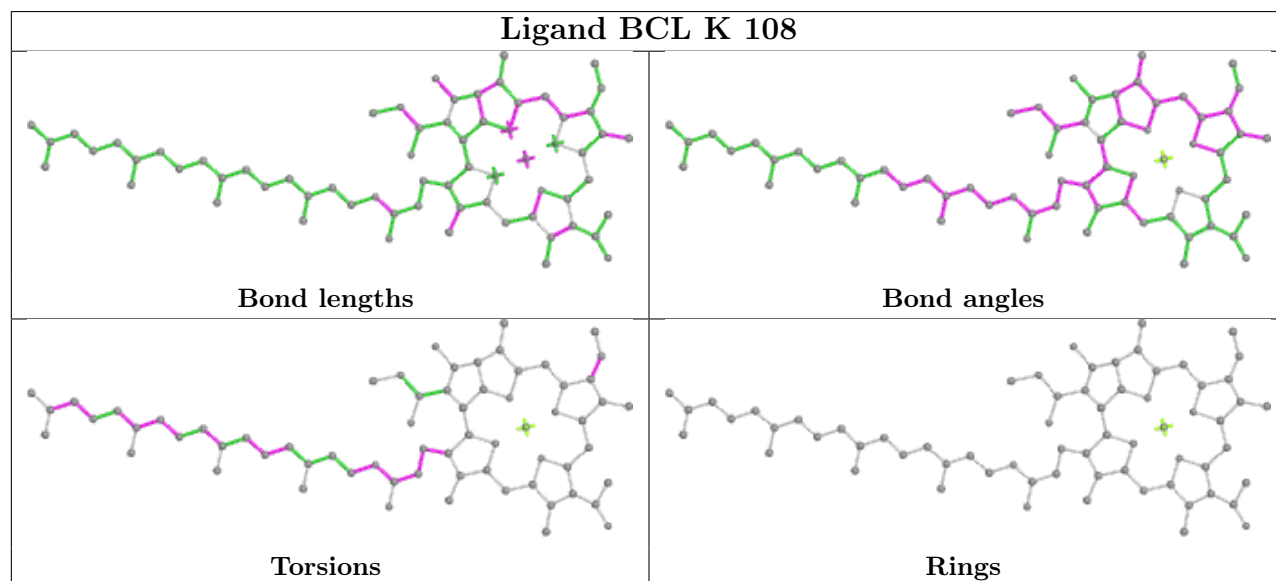
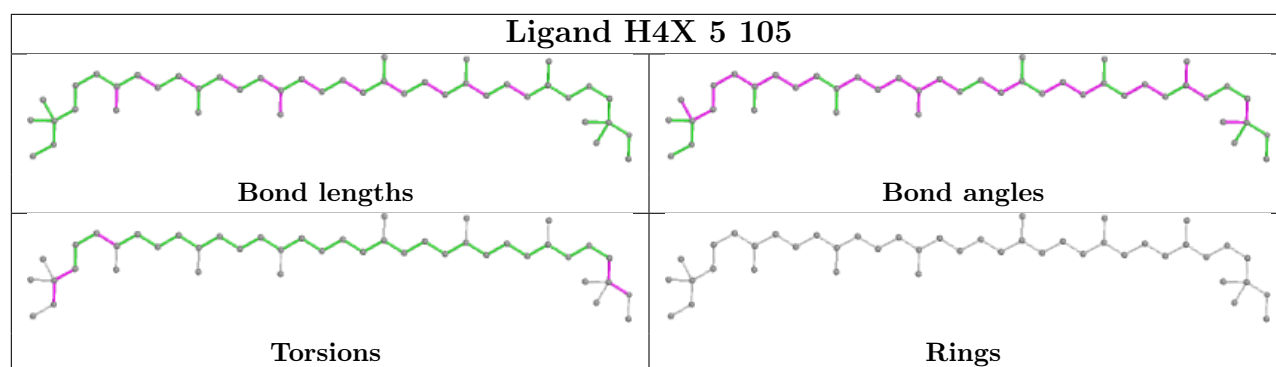
Continued from previous page...

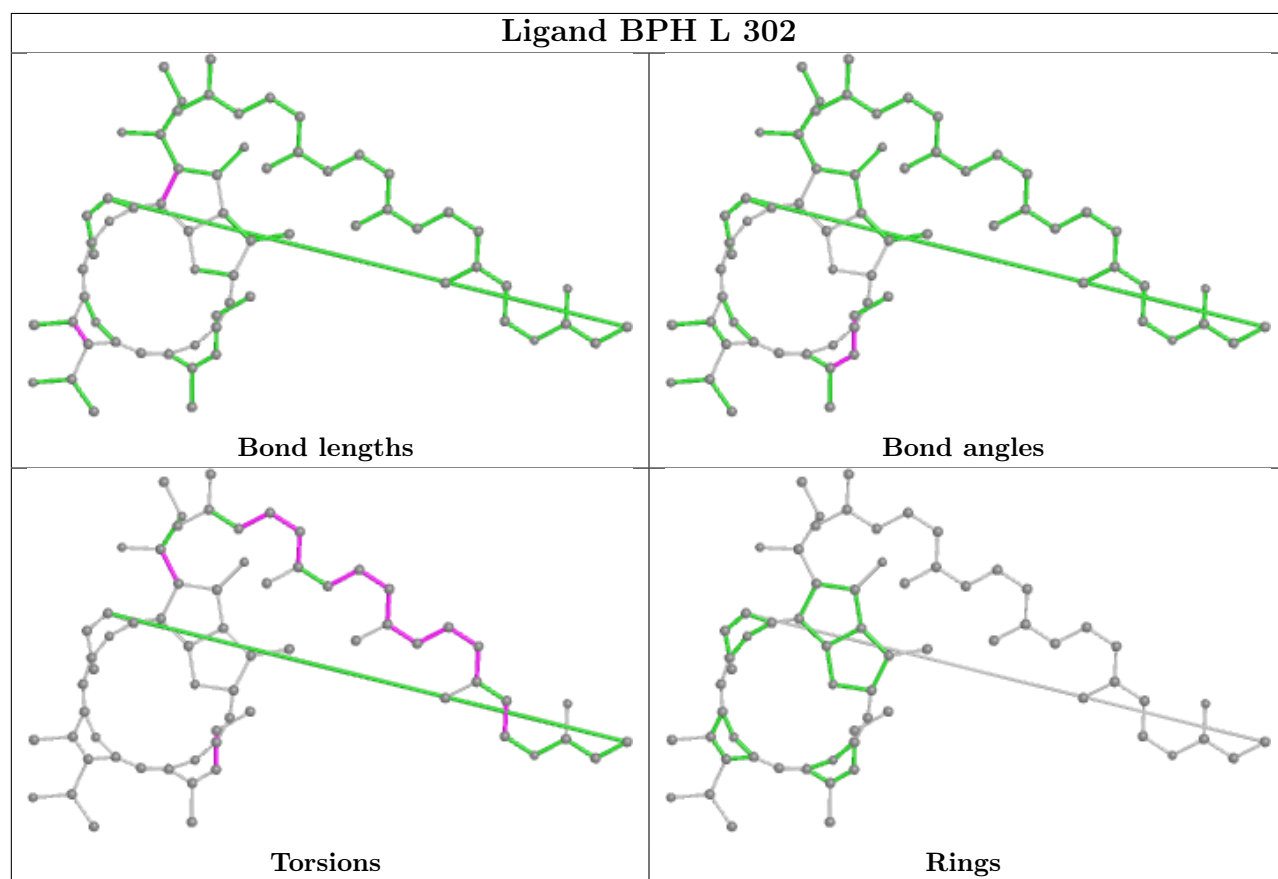
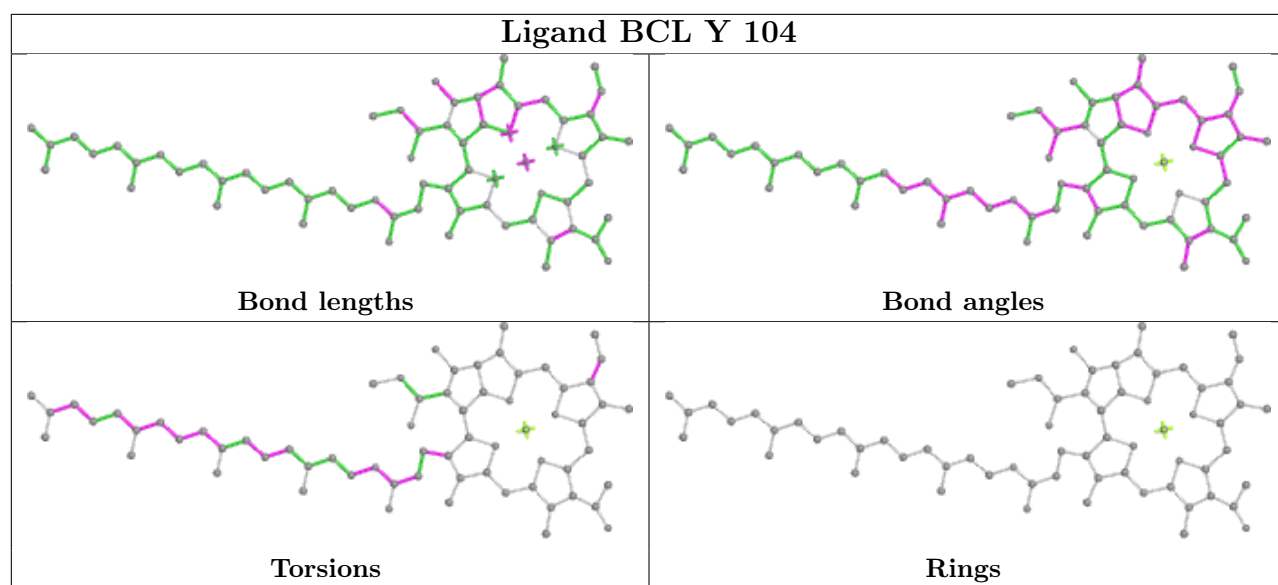
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	K	101	PGV	3	0
16	O	104	BCL	4	0

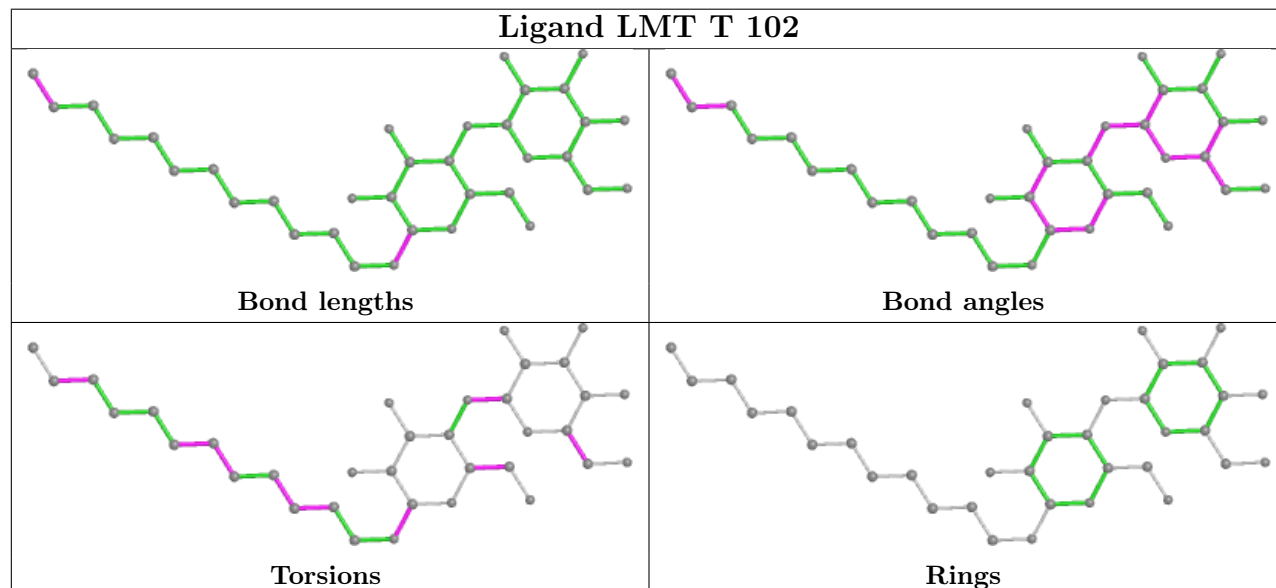
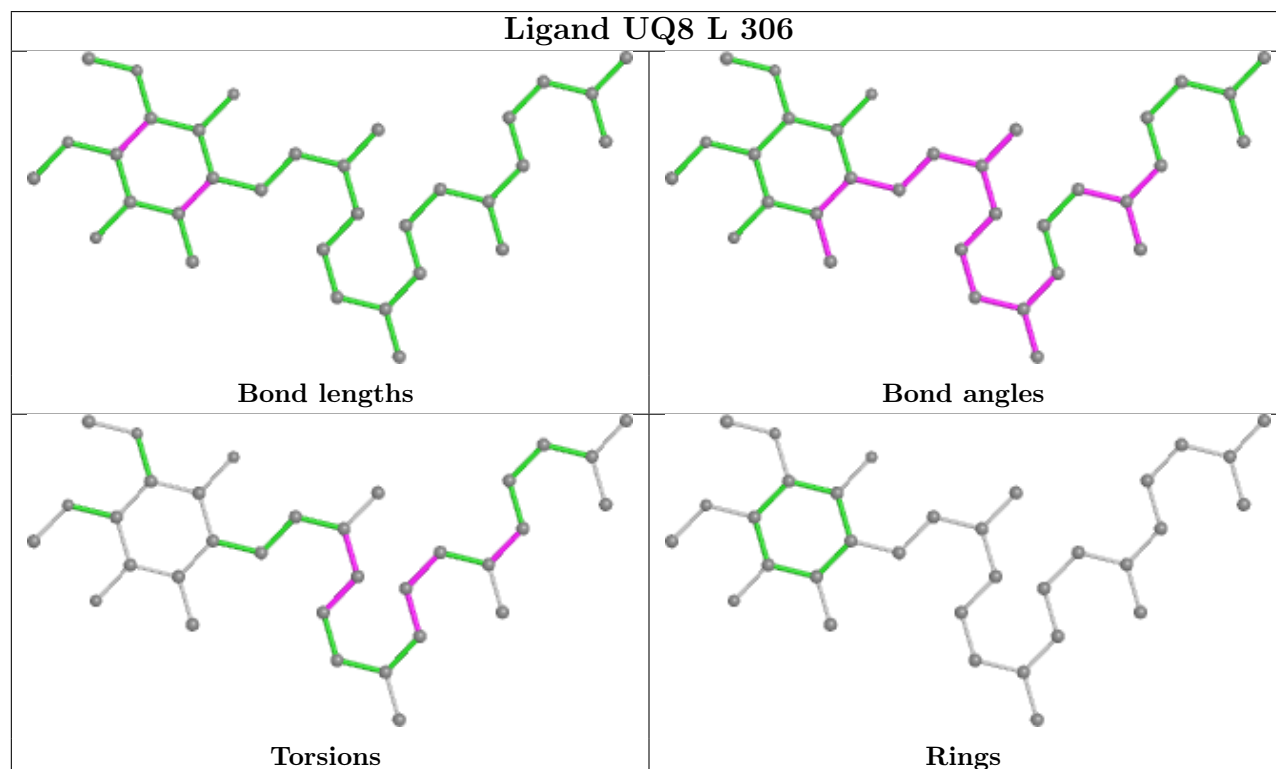
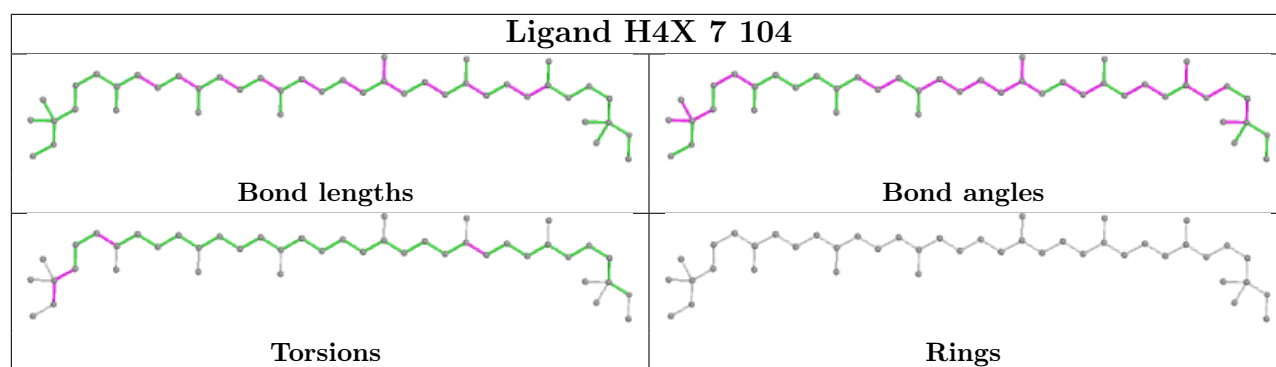
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

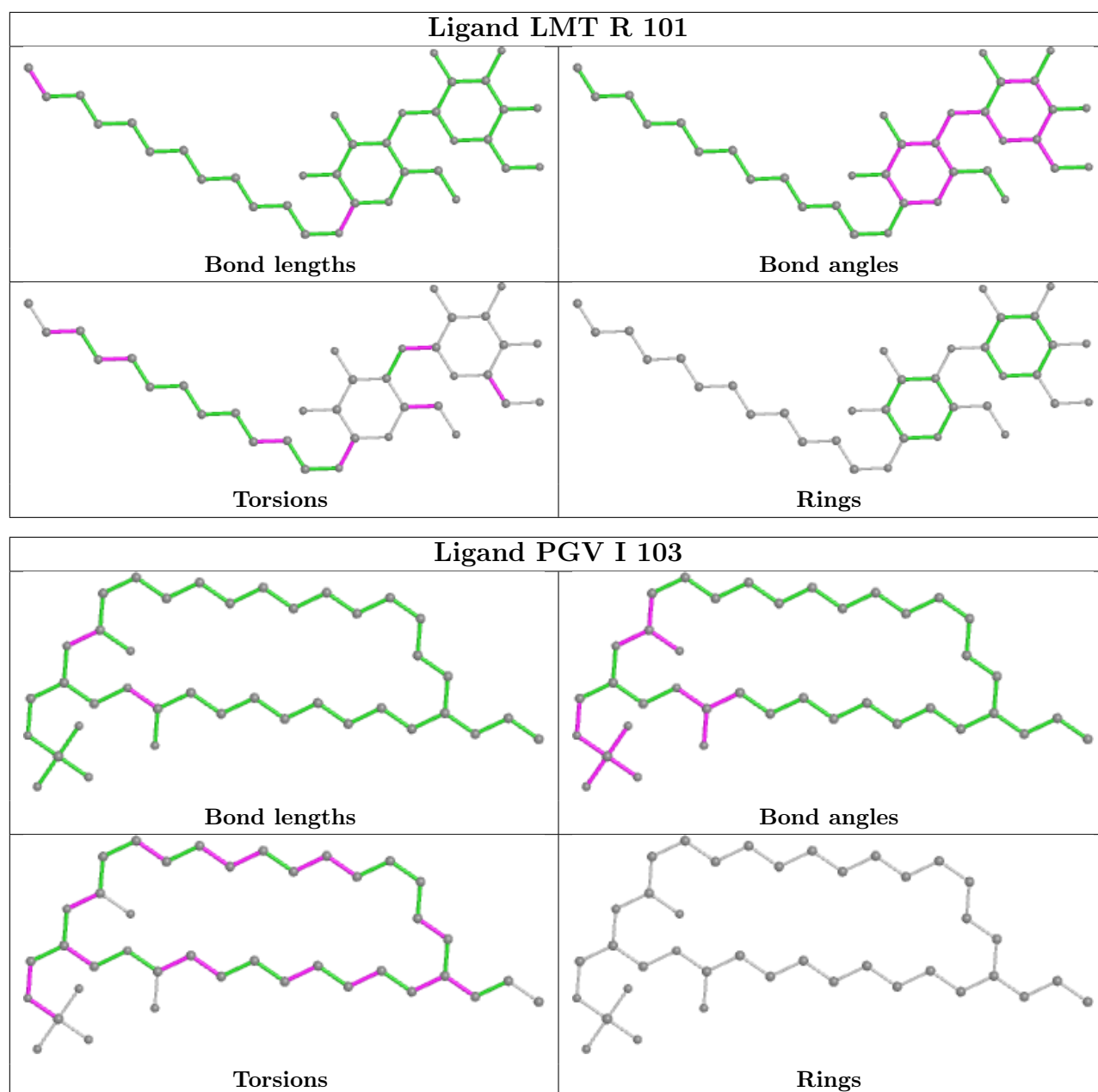


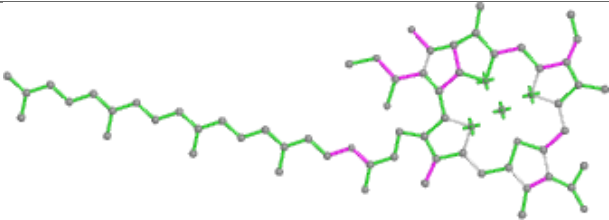
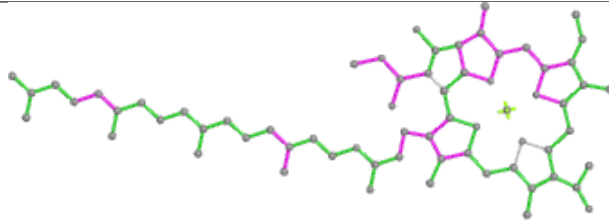
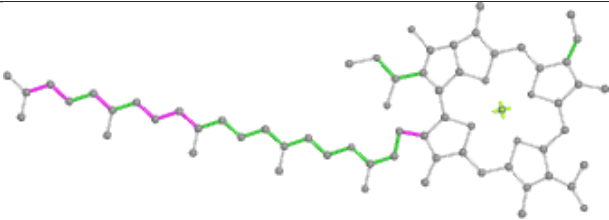
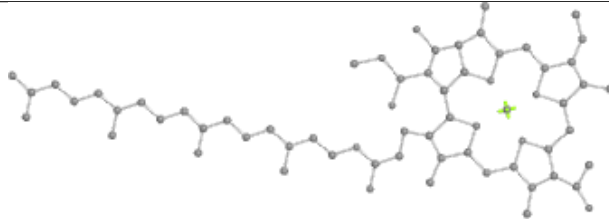


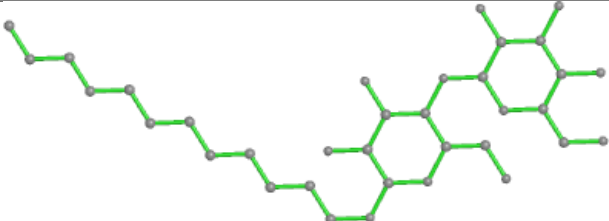
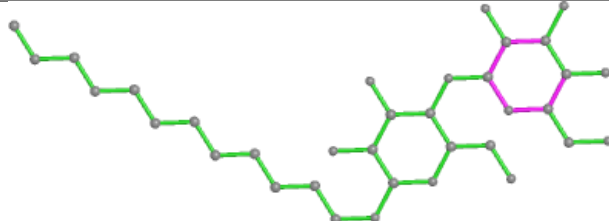
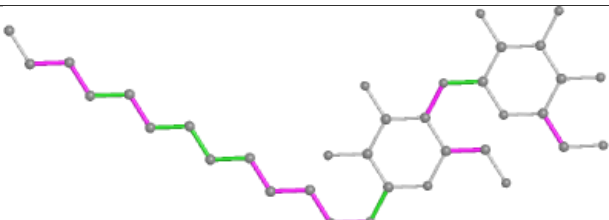
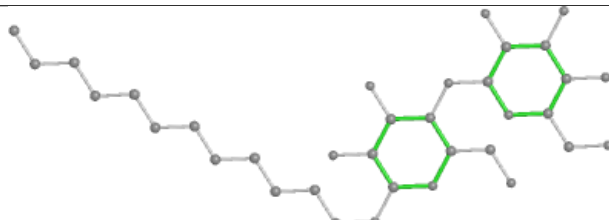


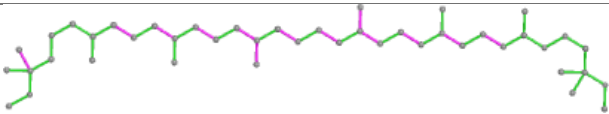
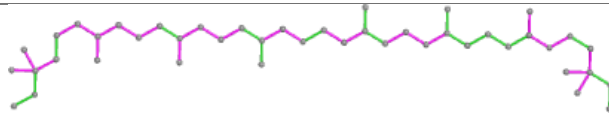
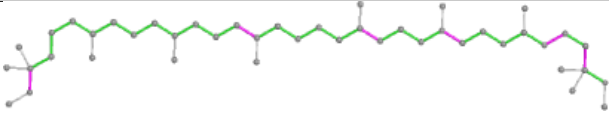
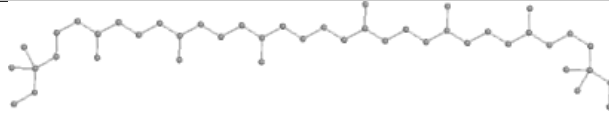


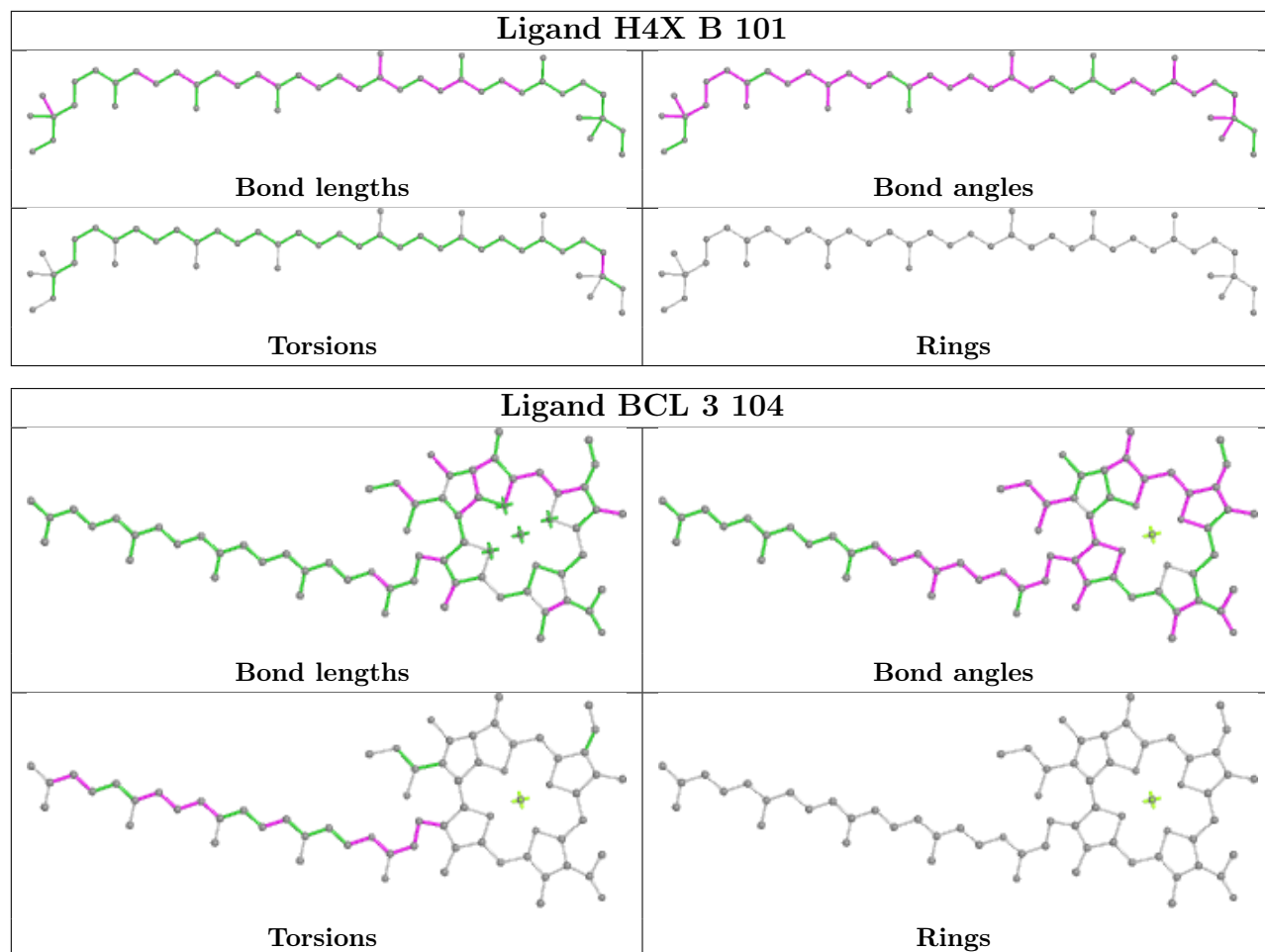


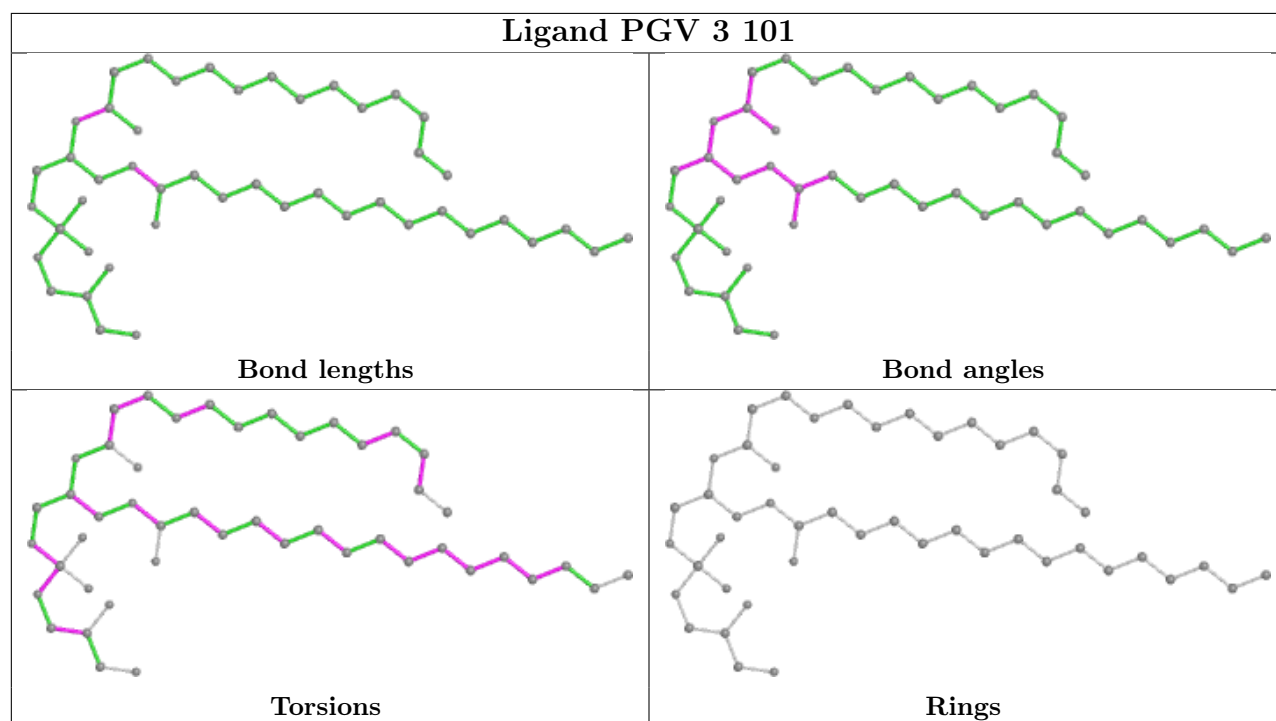
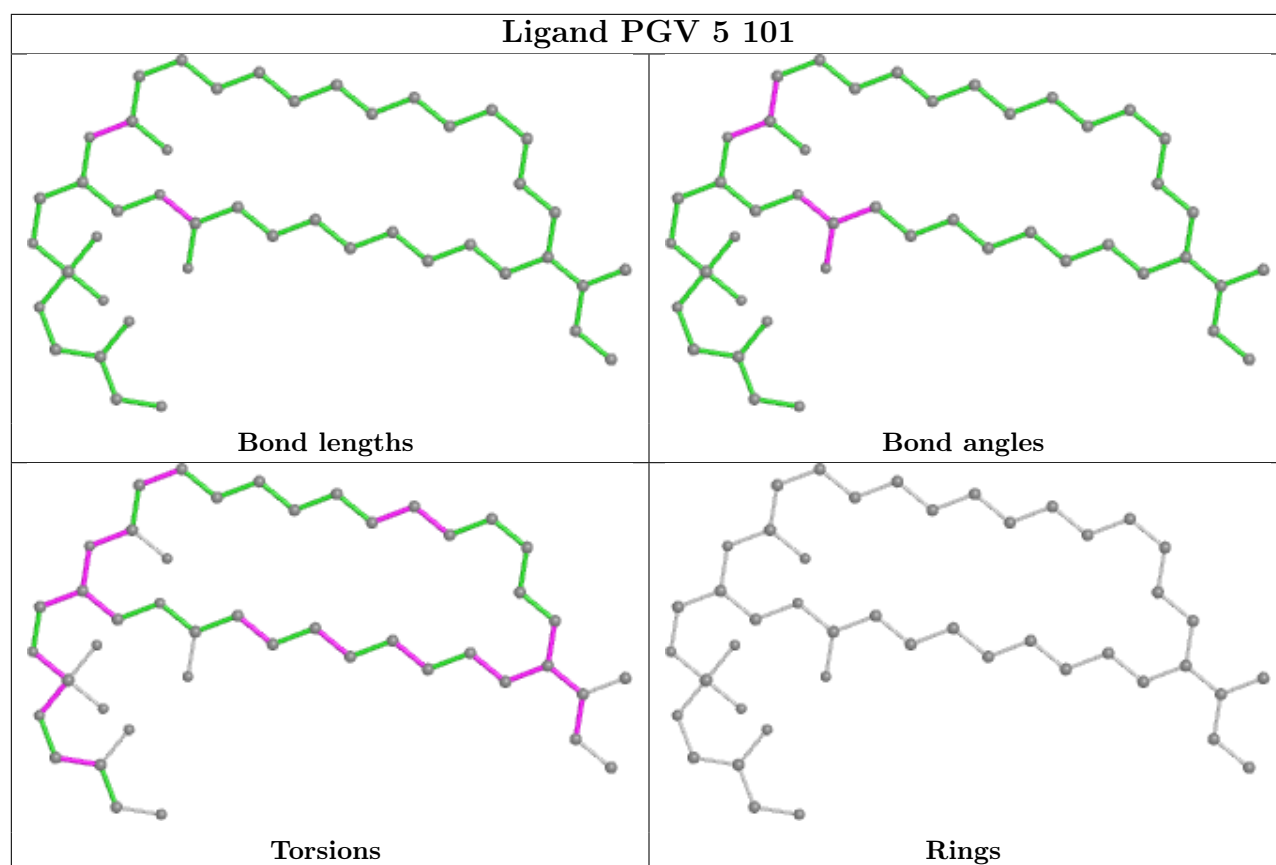


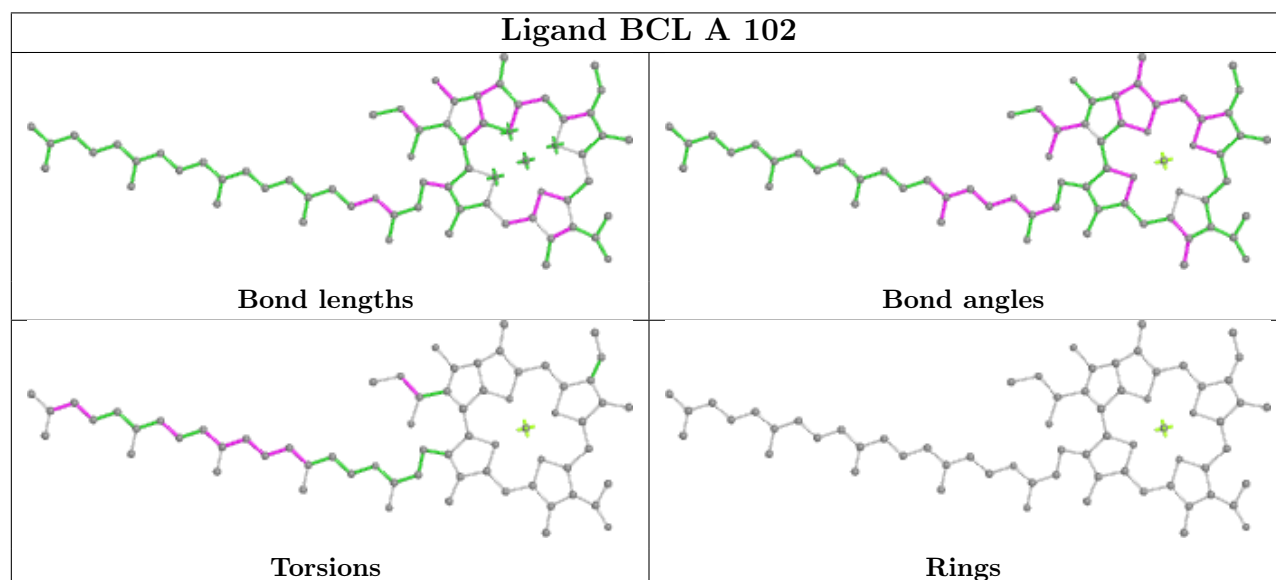
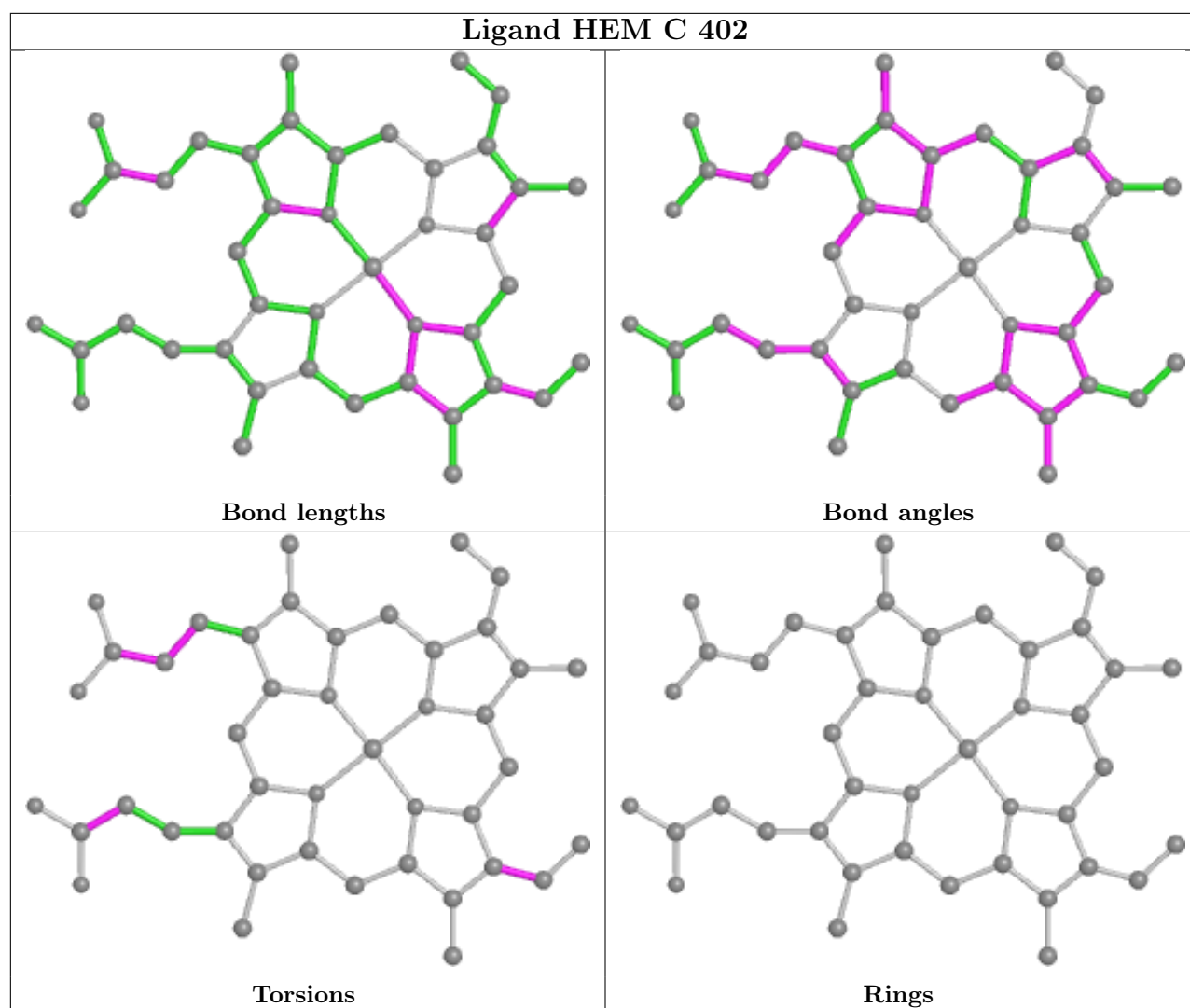
Ligand BCL 1 102	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand LMT B 102	
	
Bond lengths	Bond angles
	
Torsions	Rings

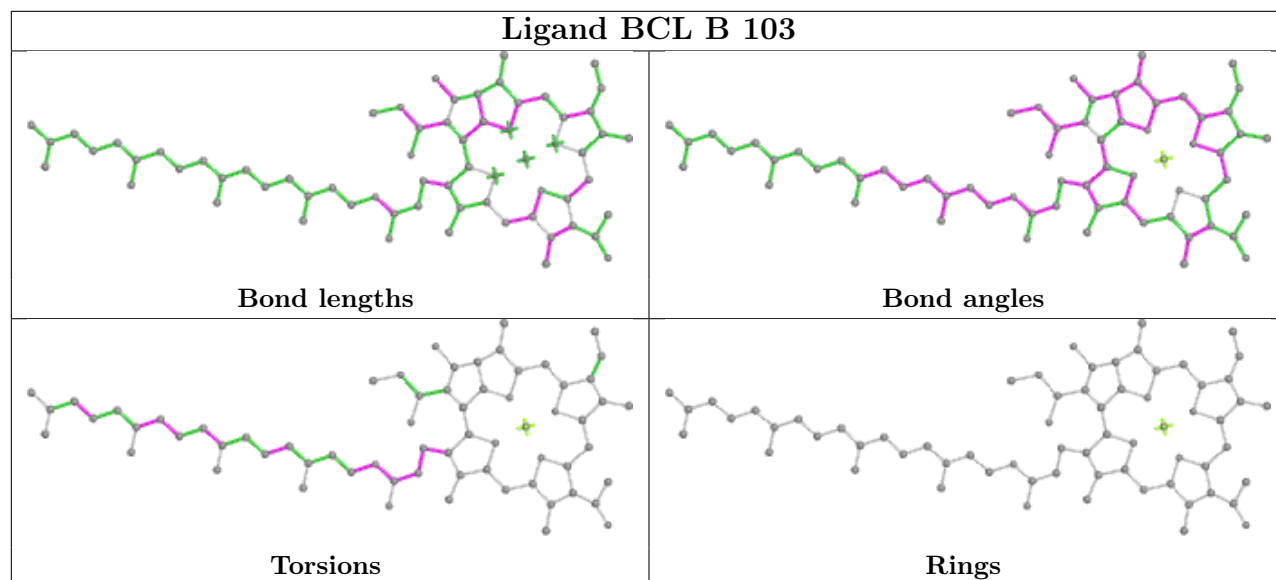
Ligand H4X V 101	
	
Bond lengths	Bond angles
	
Torsions	Rings



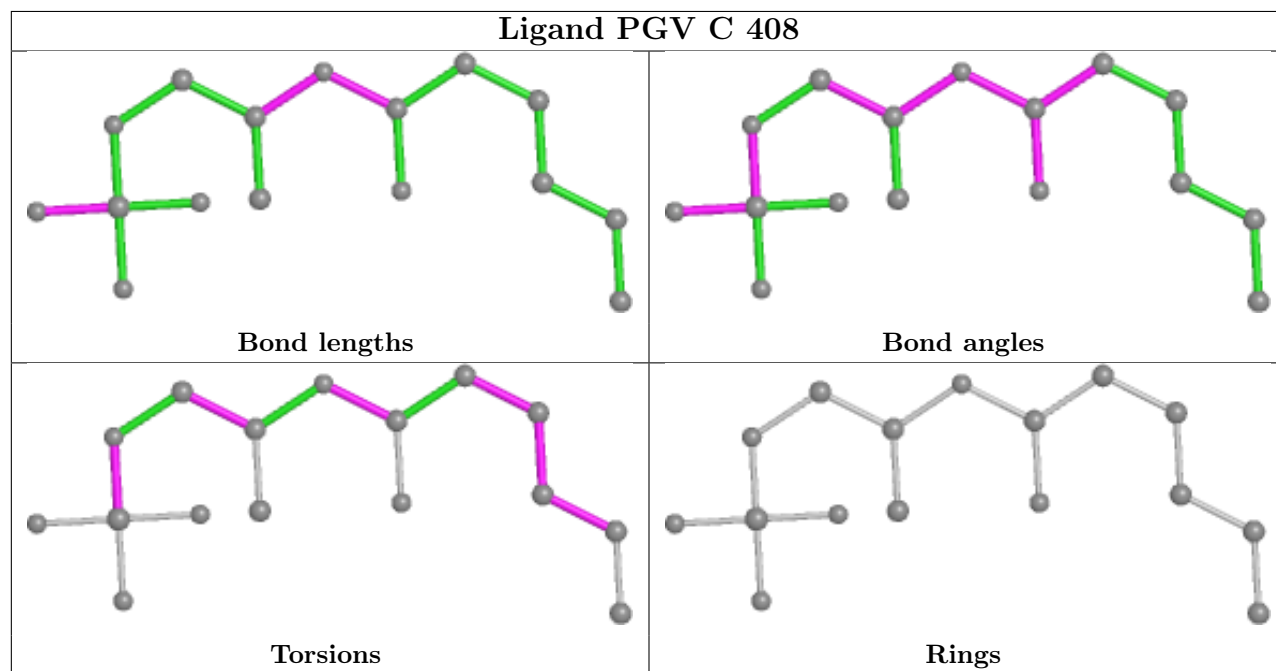


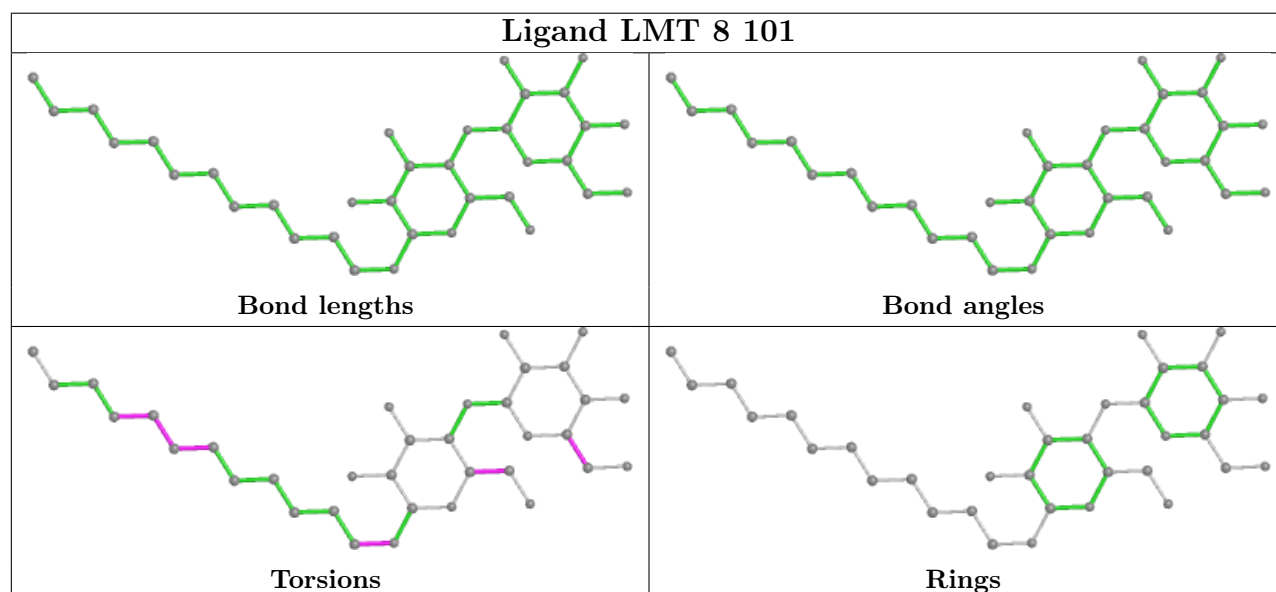
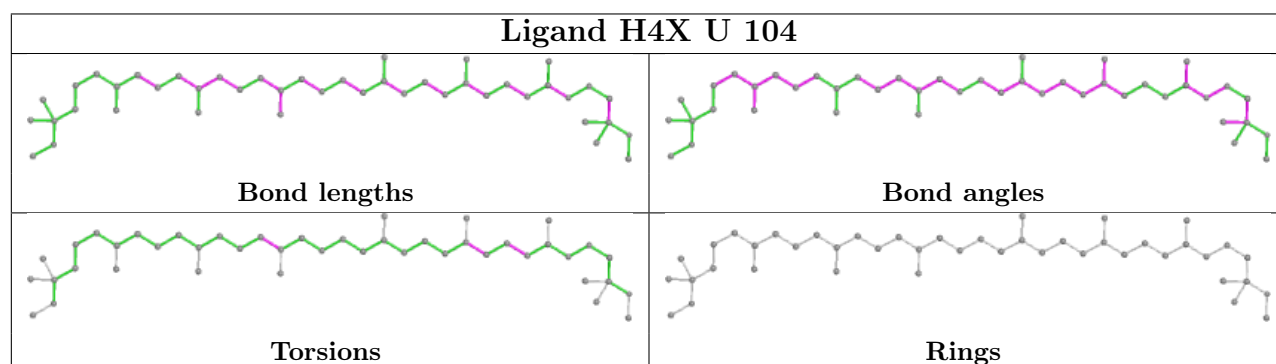
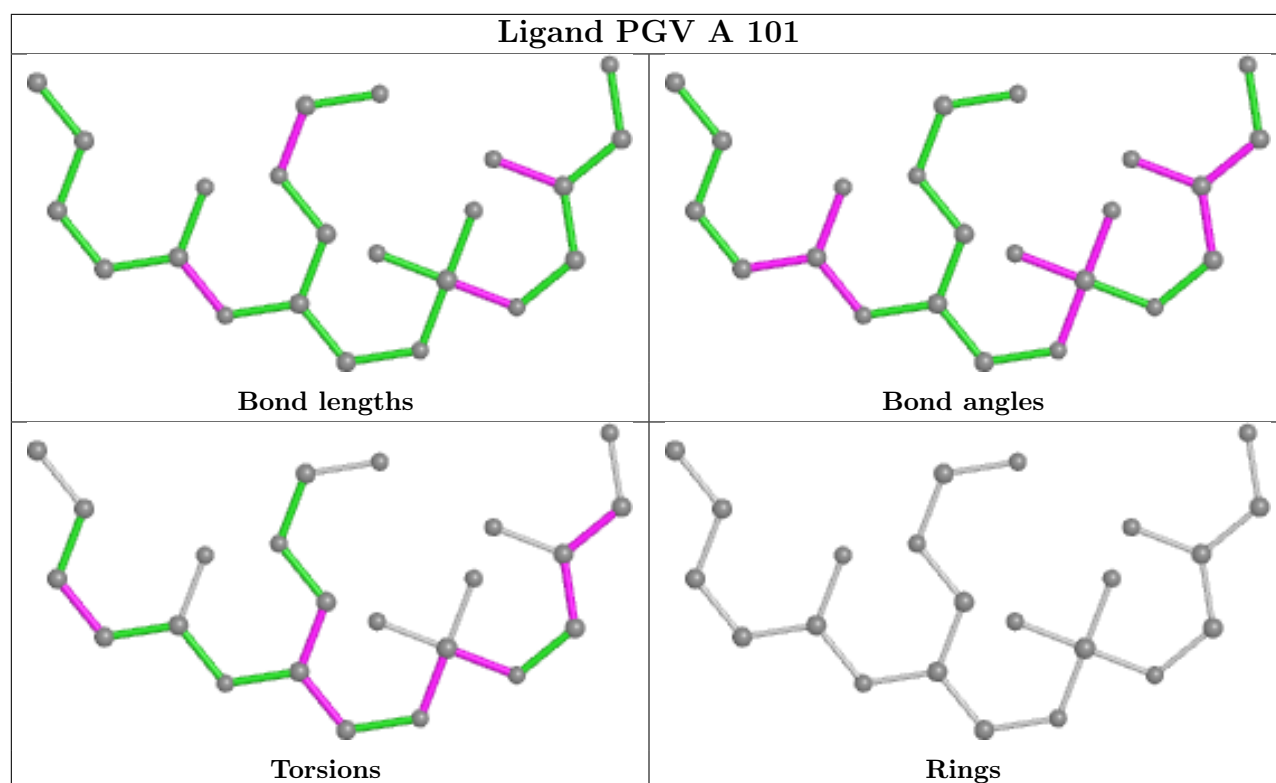


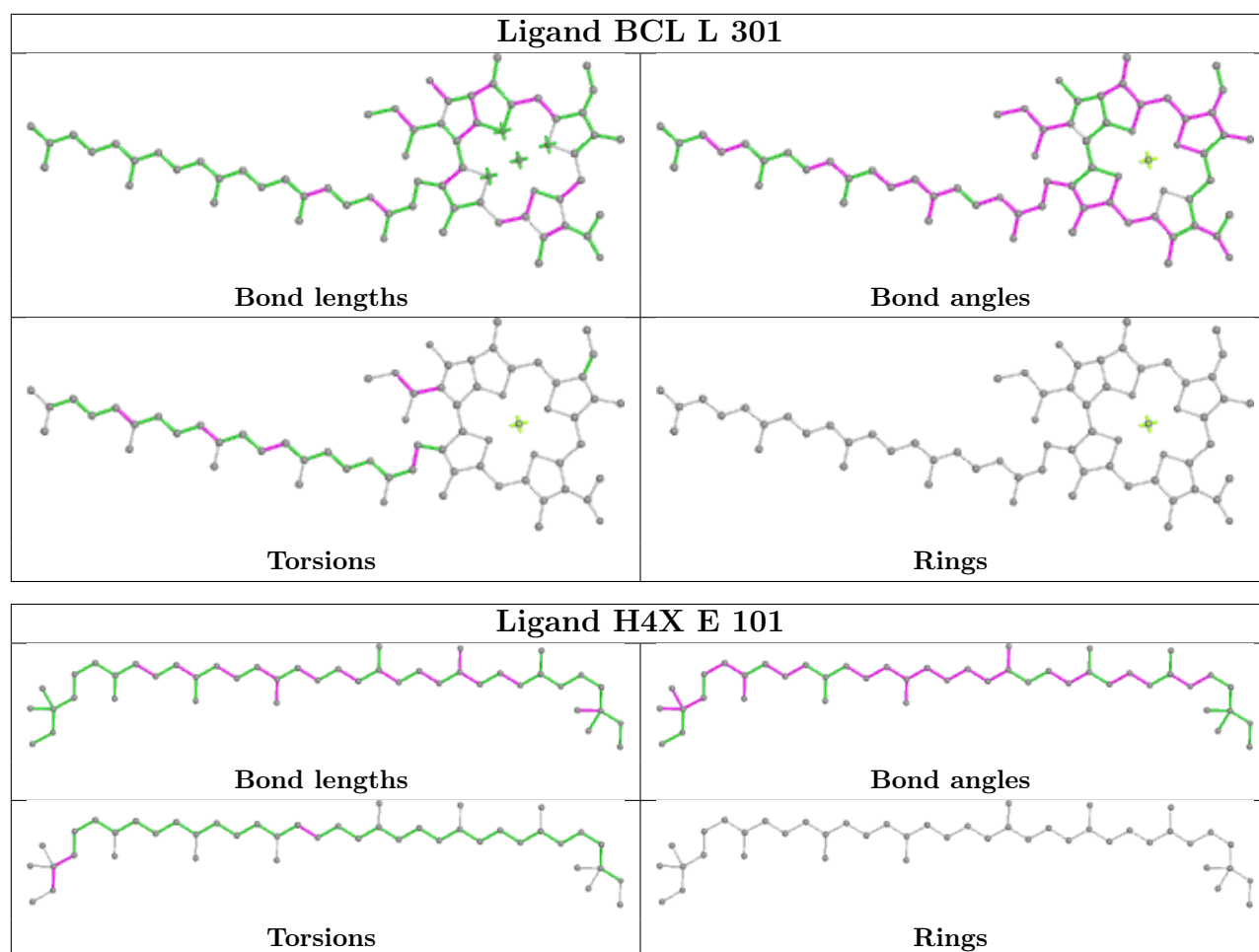
Ligand BCL B 103

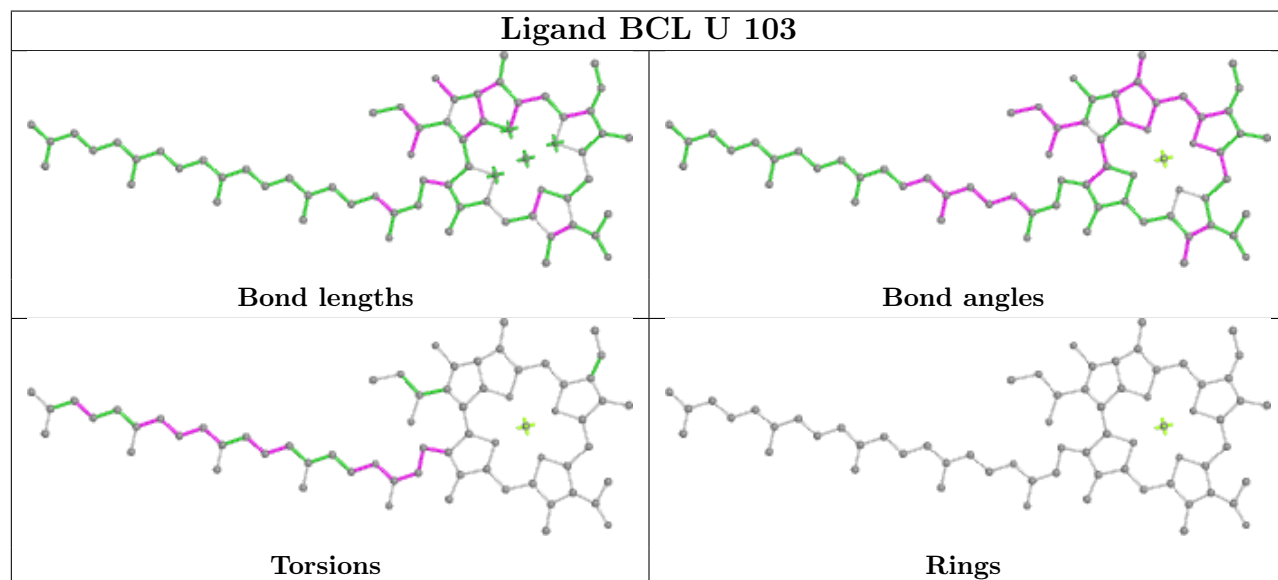
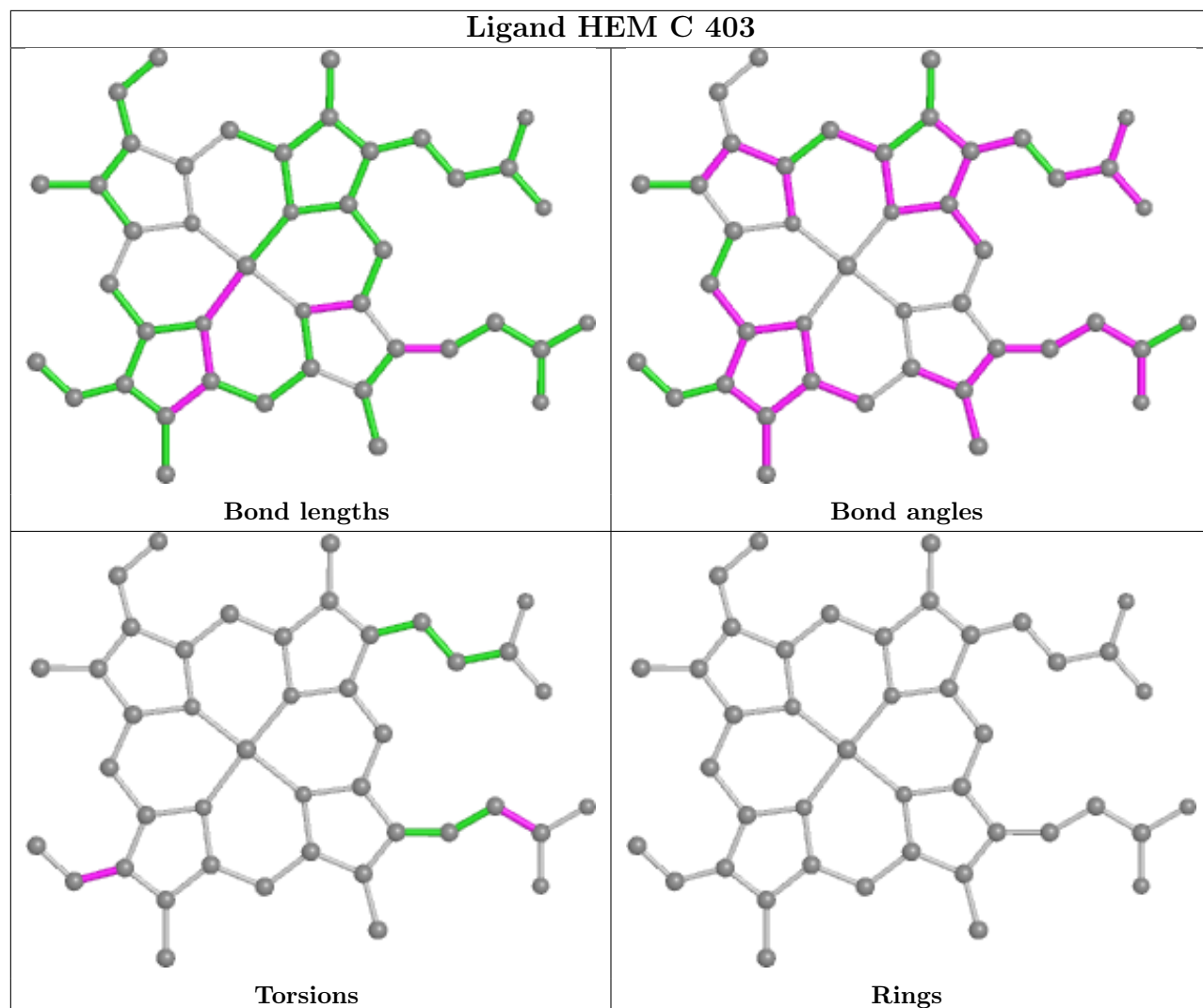


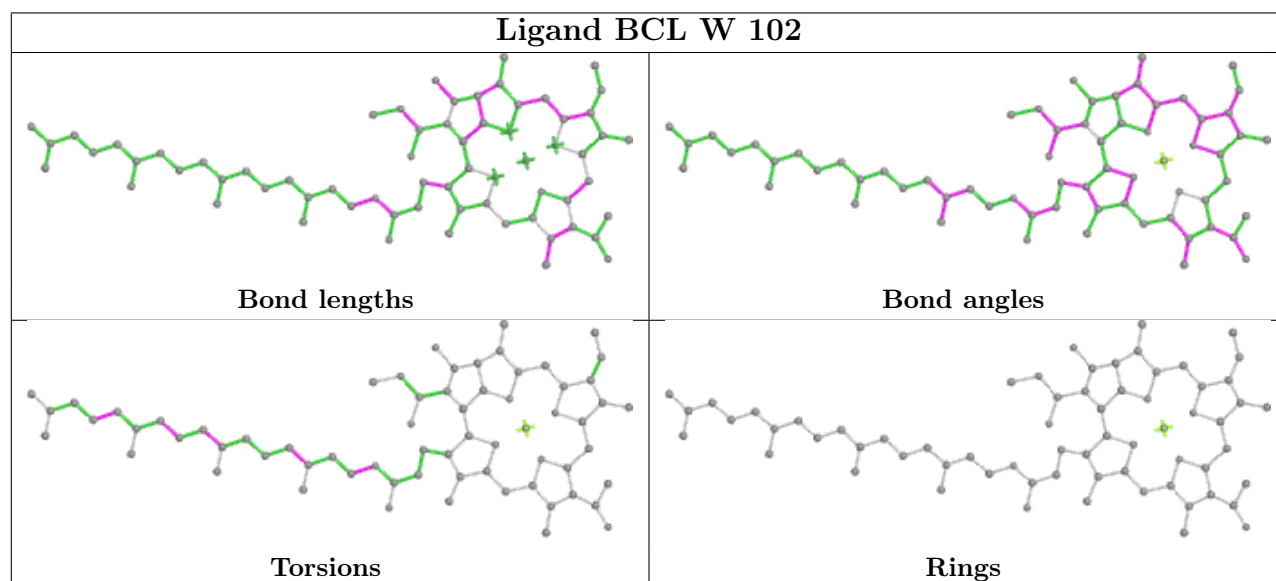
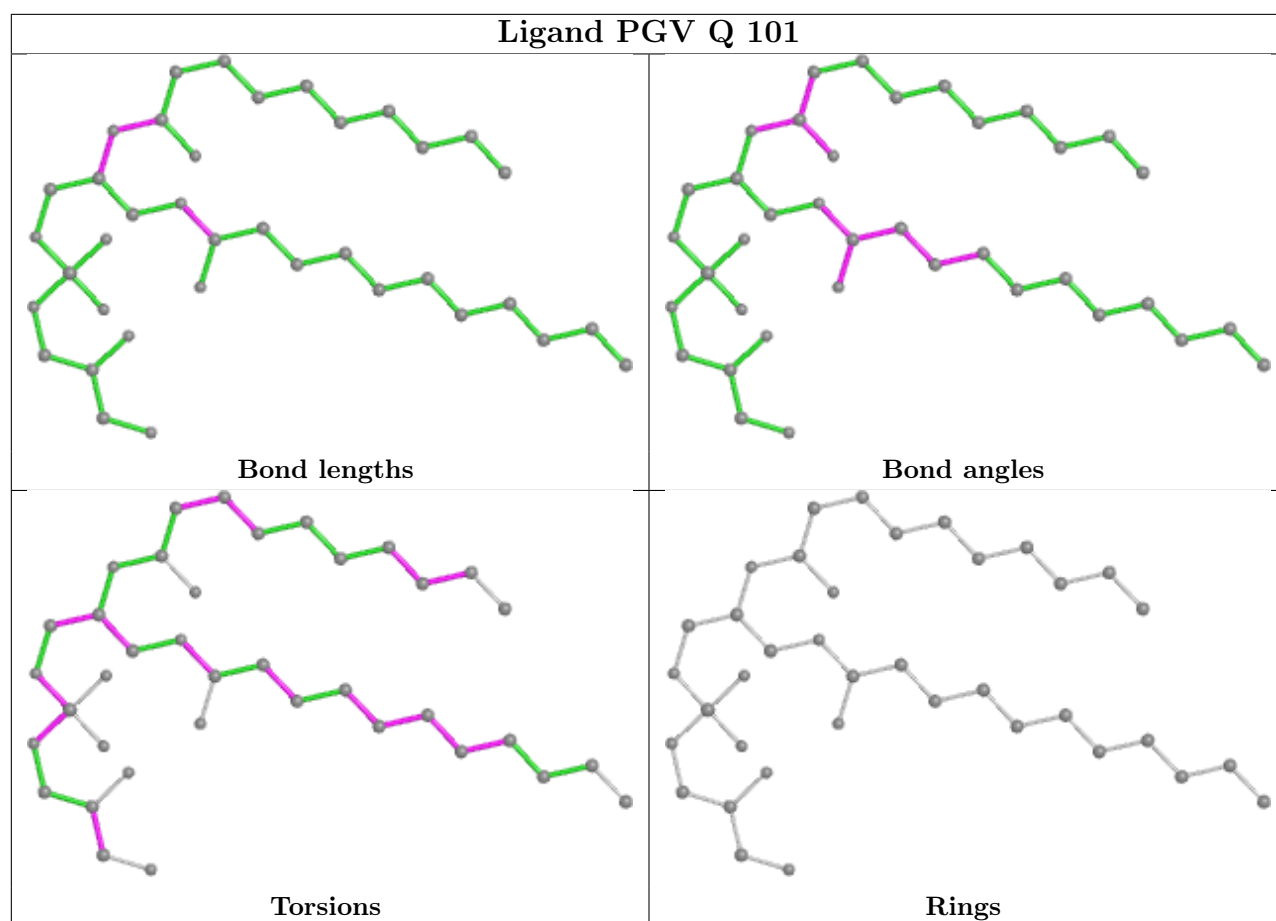
Ligand PGV C 408

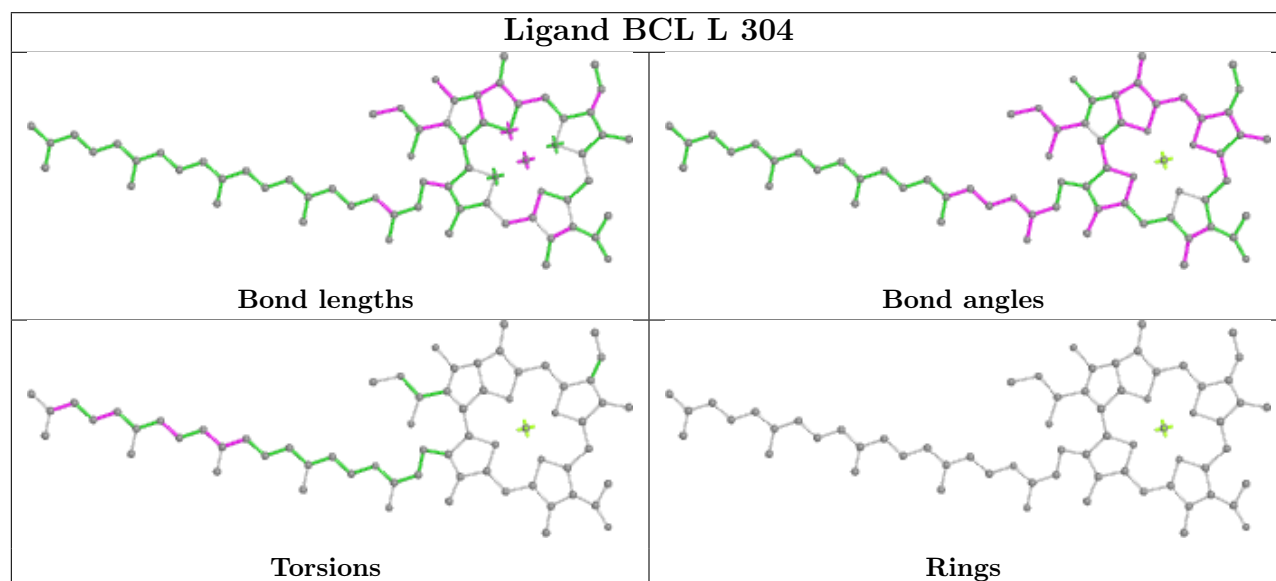
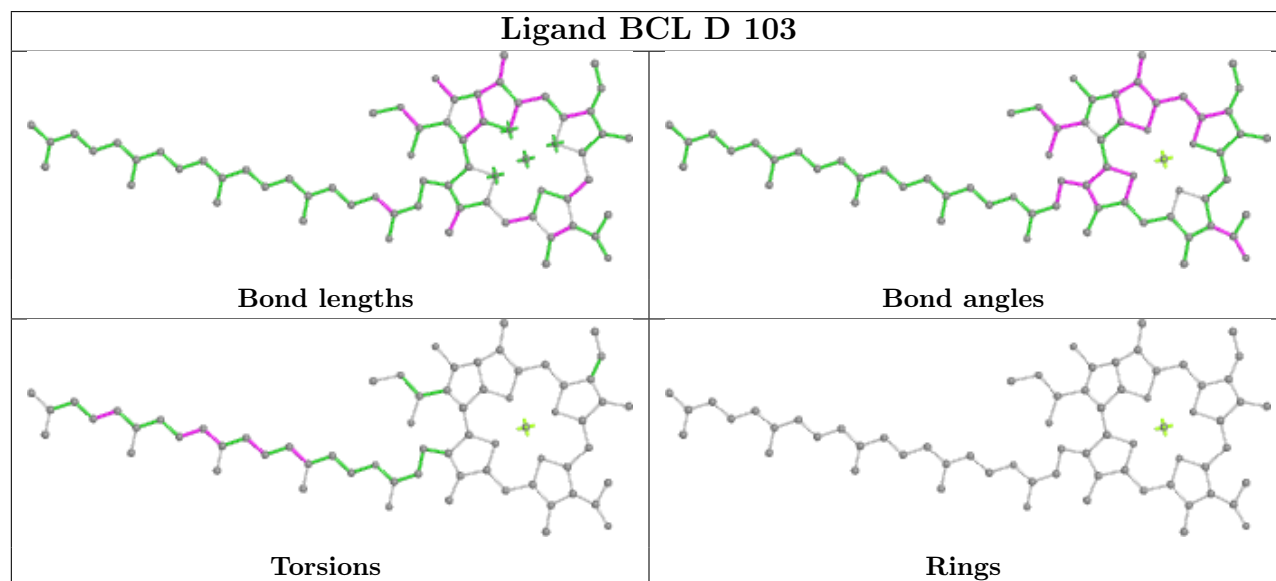
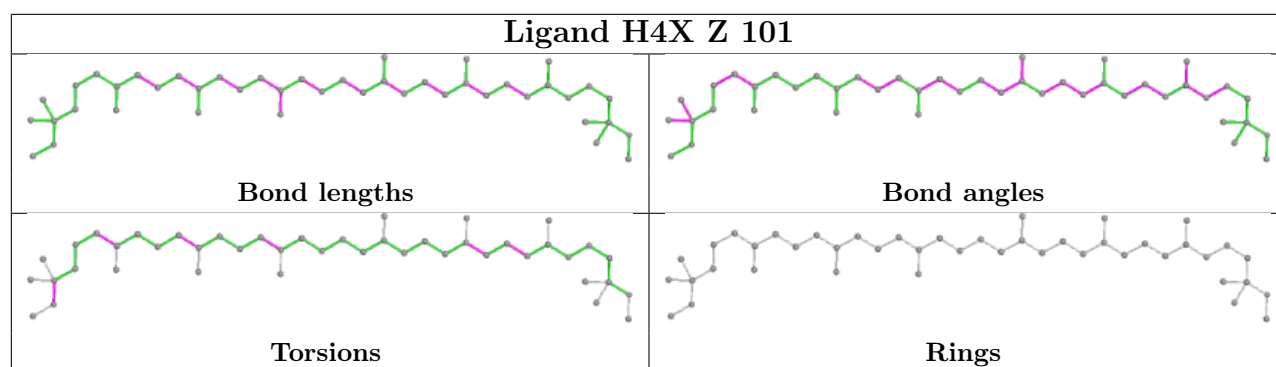


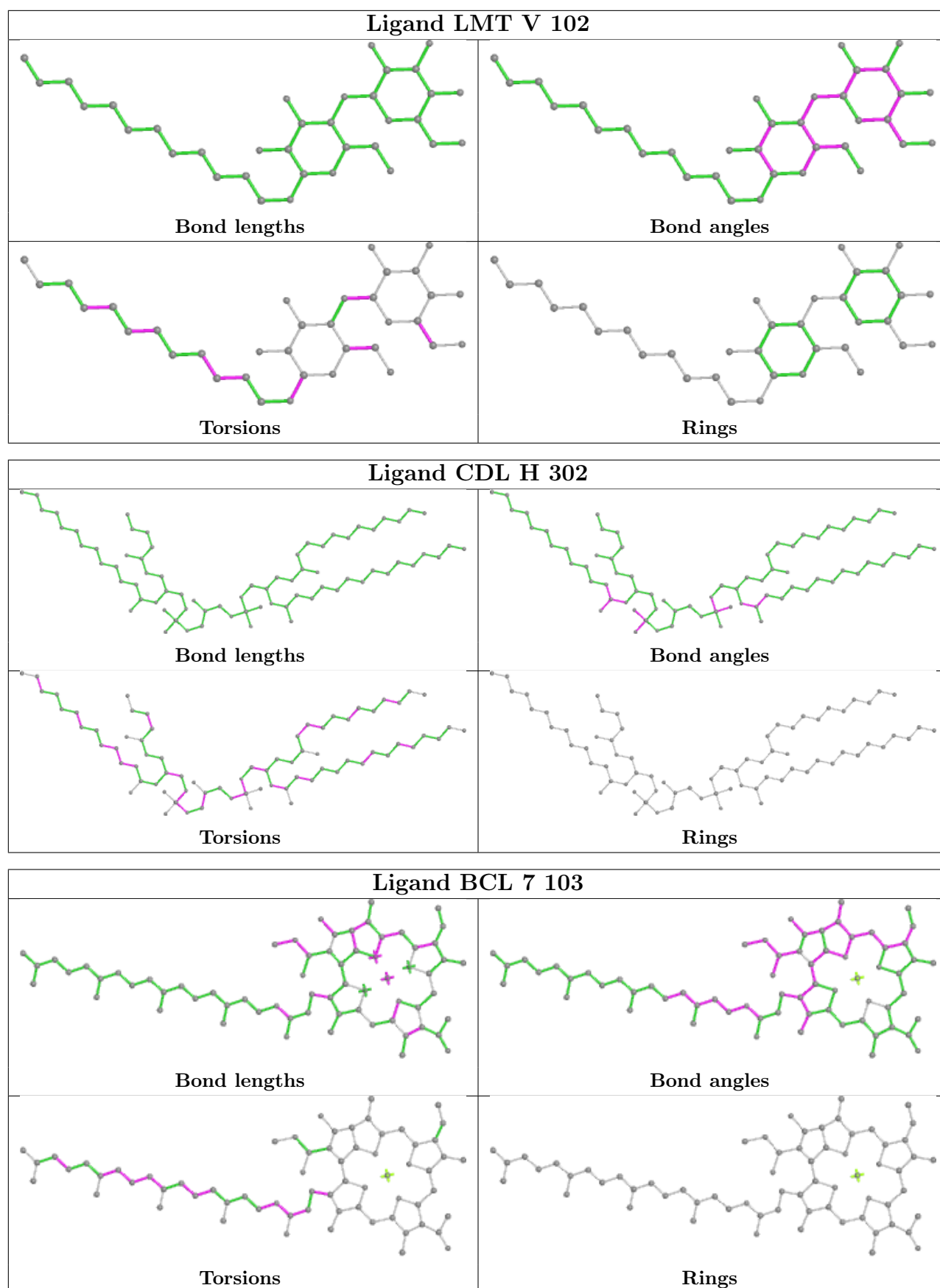


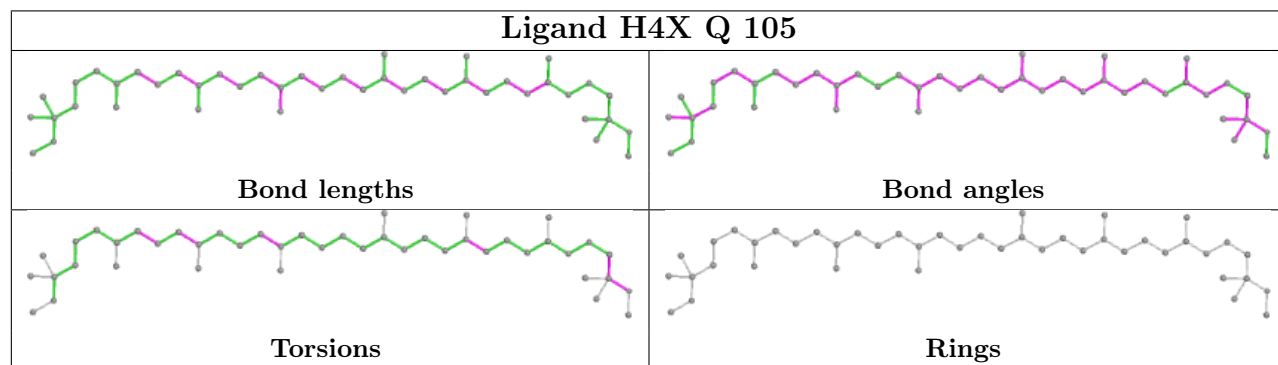
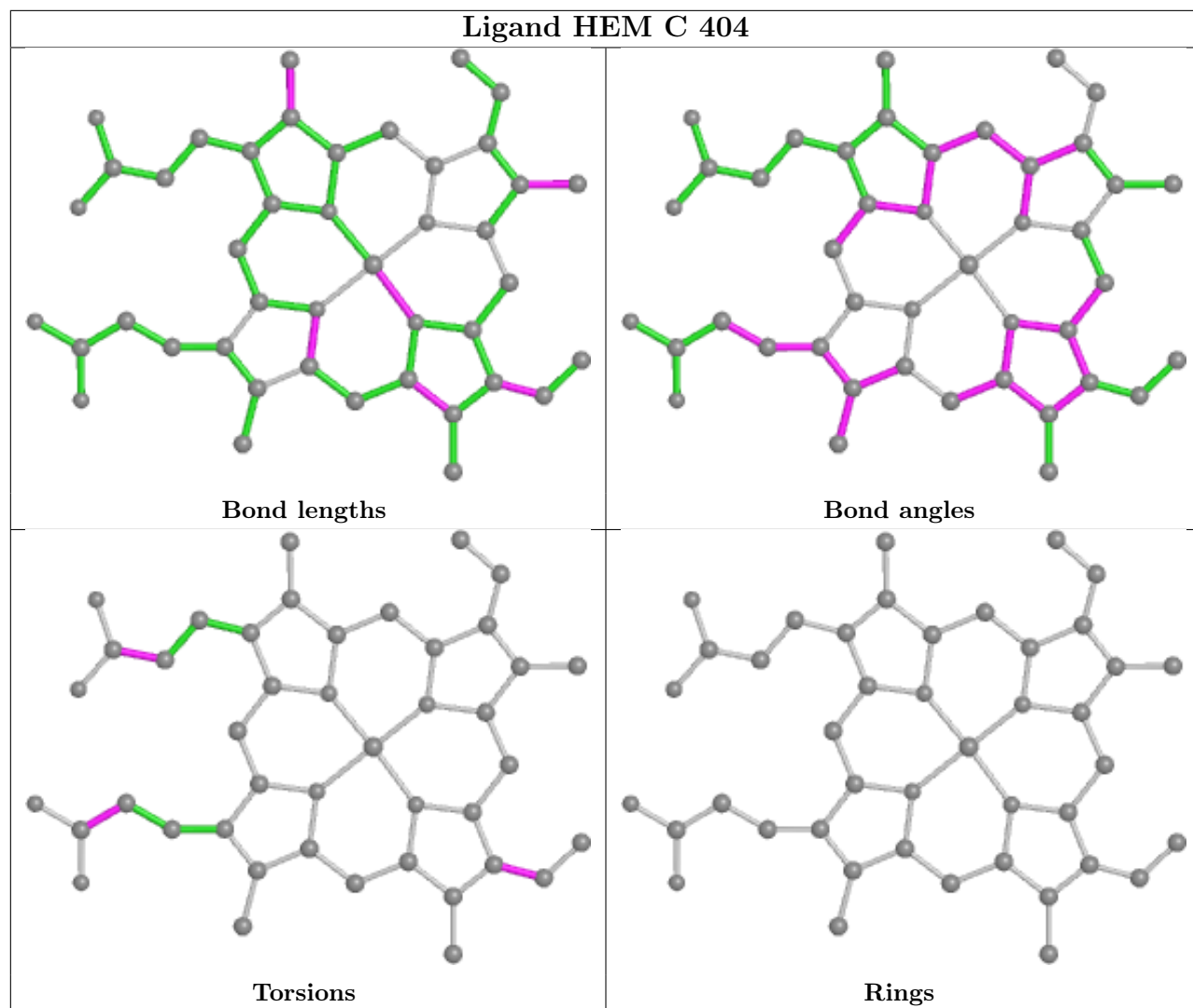


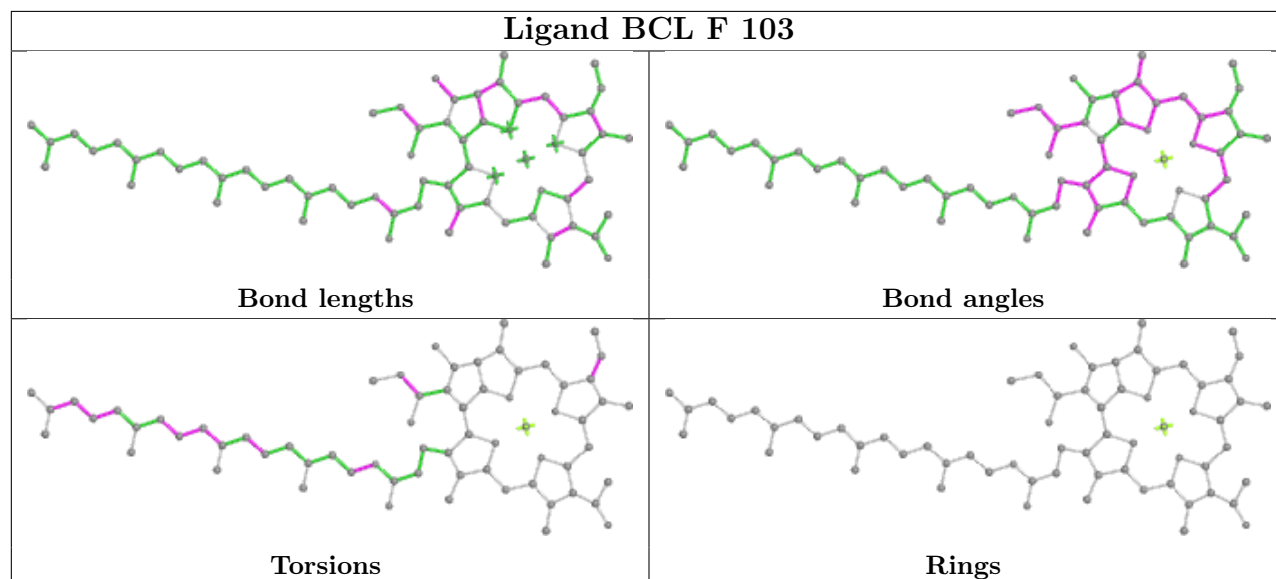
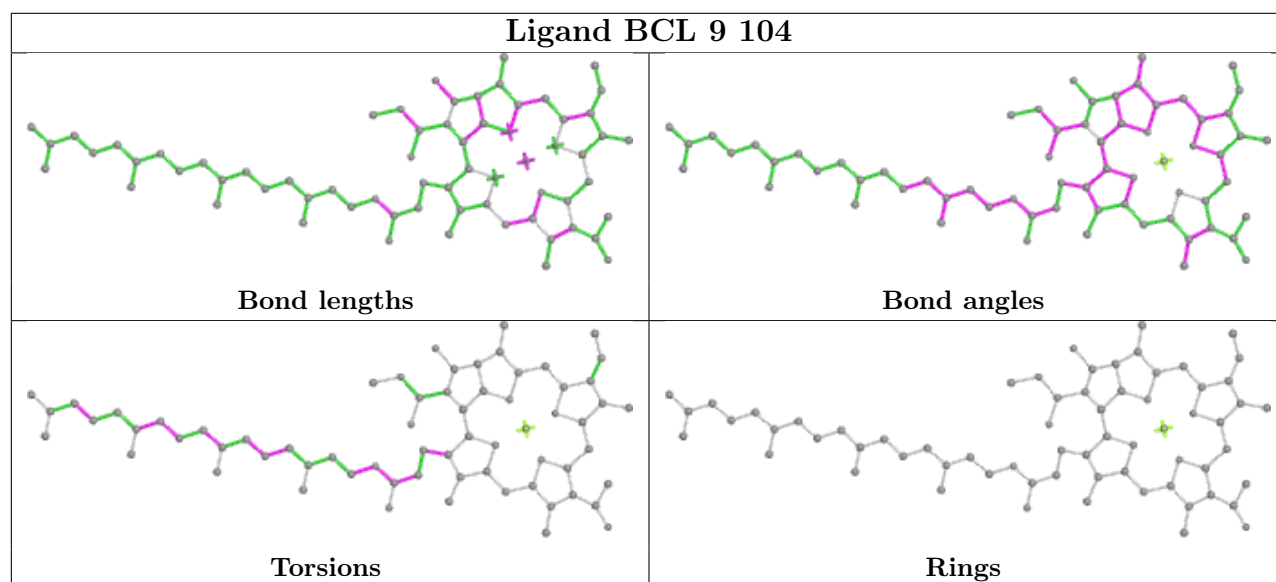
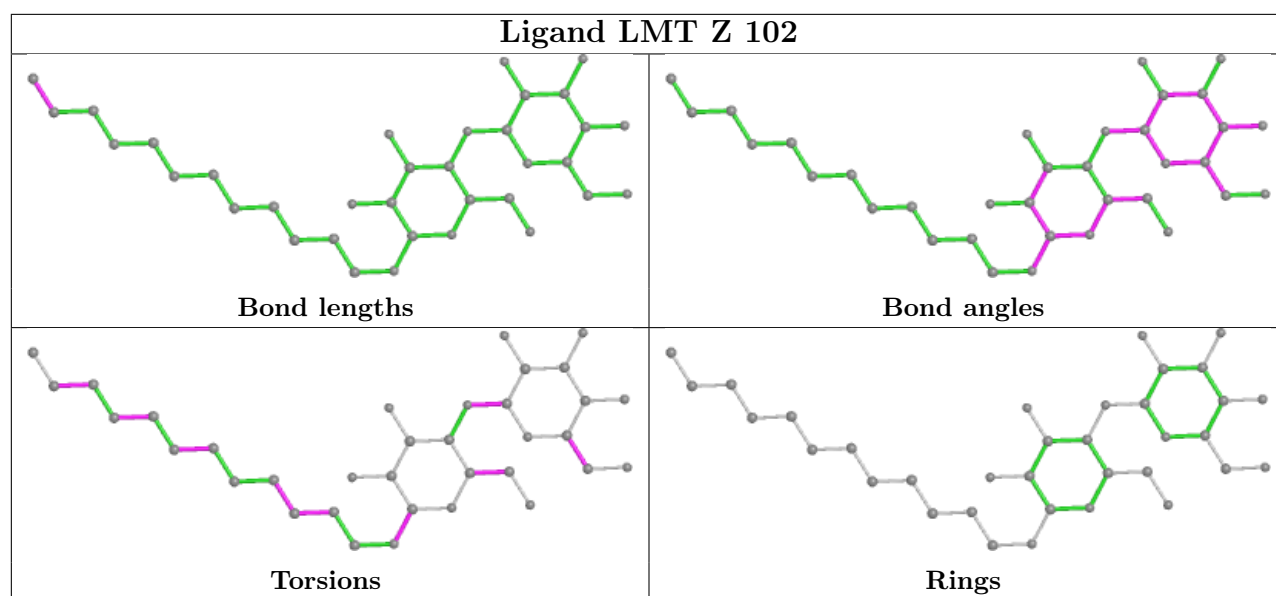


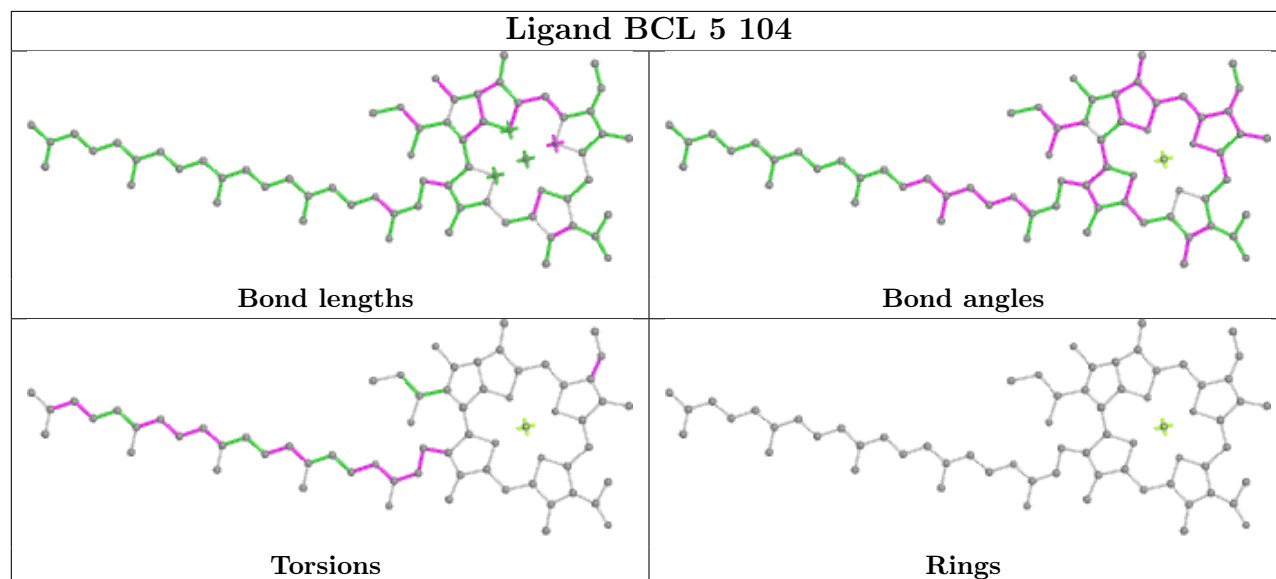
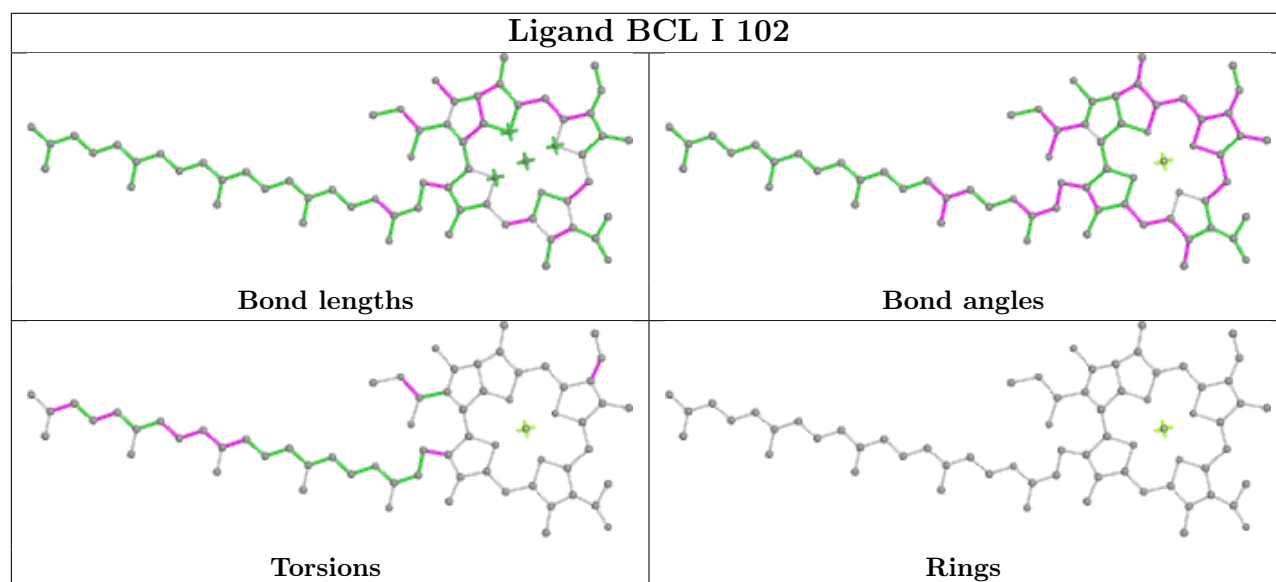
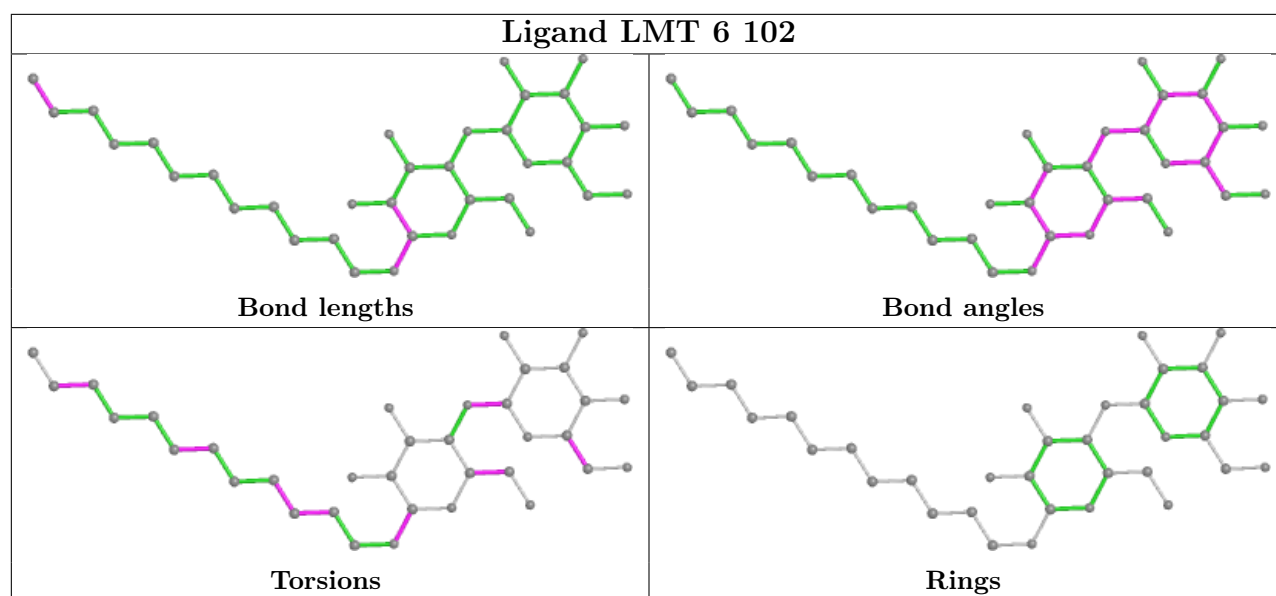


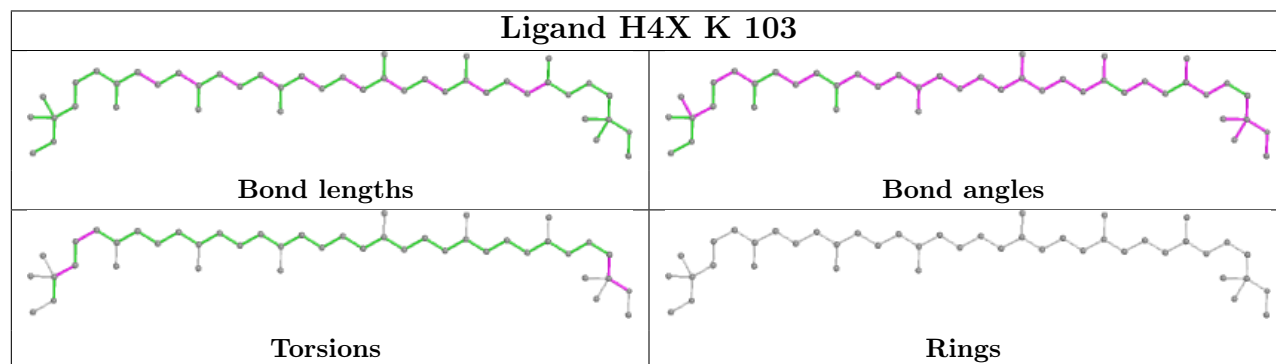
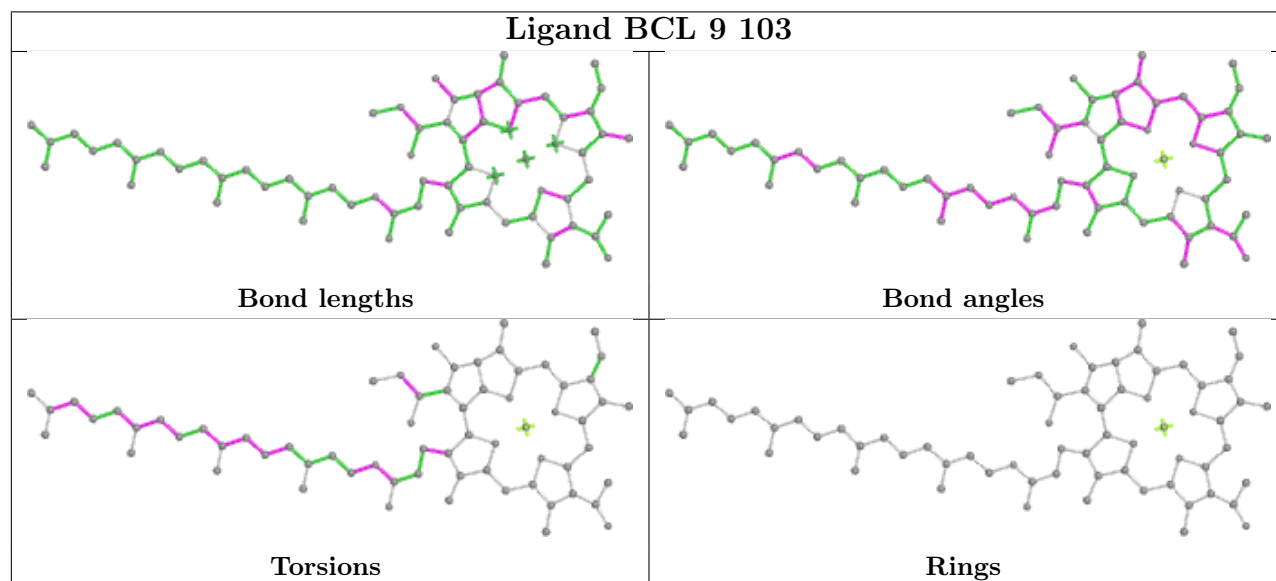
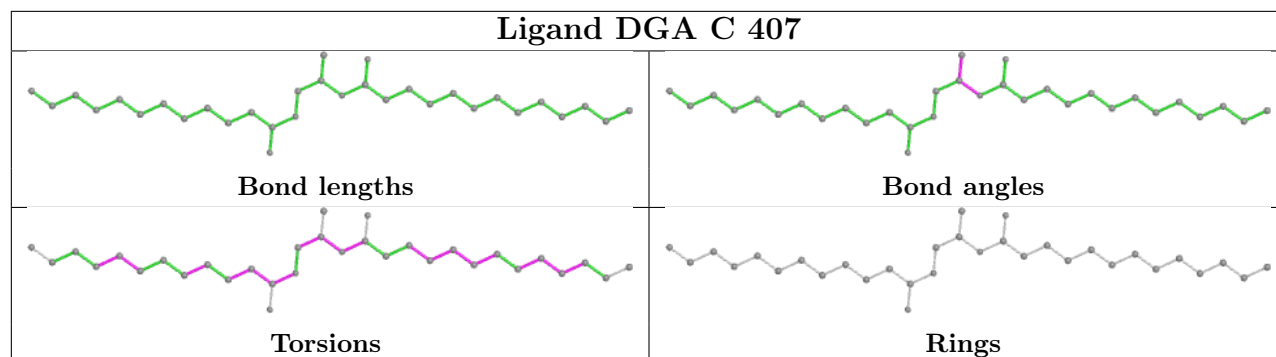


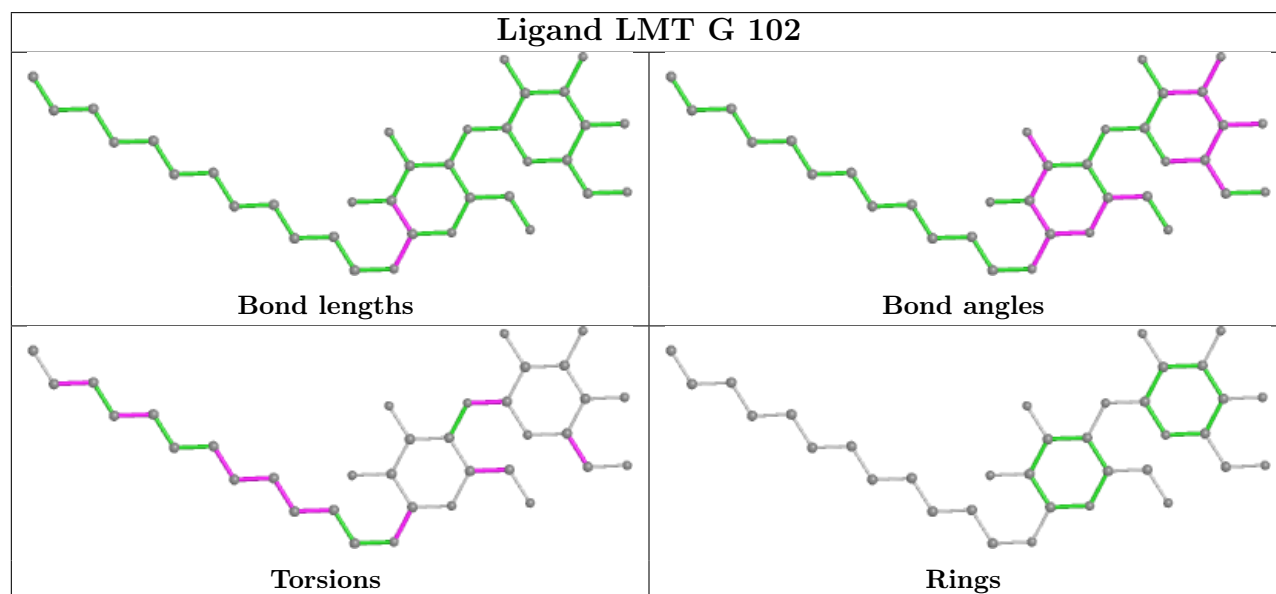
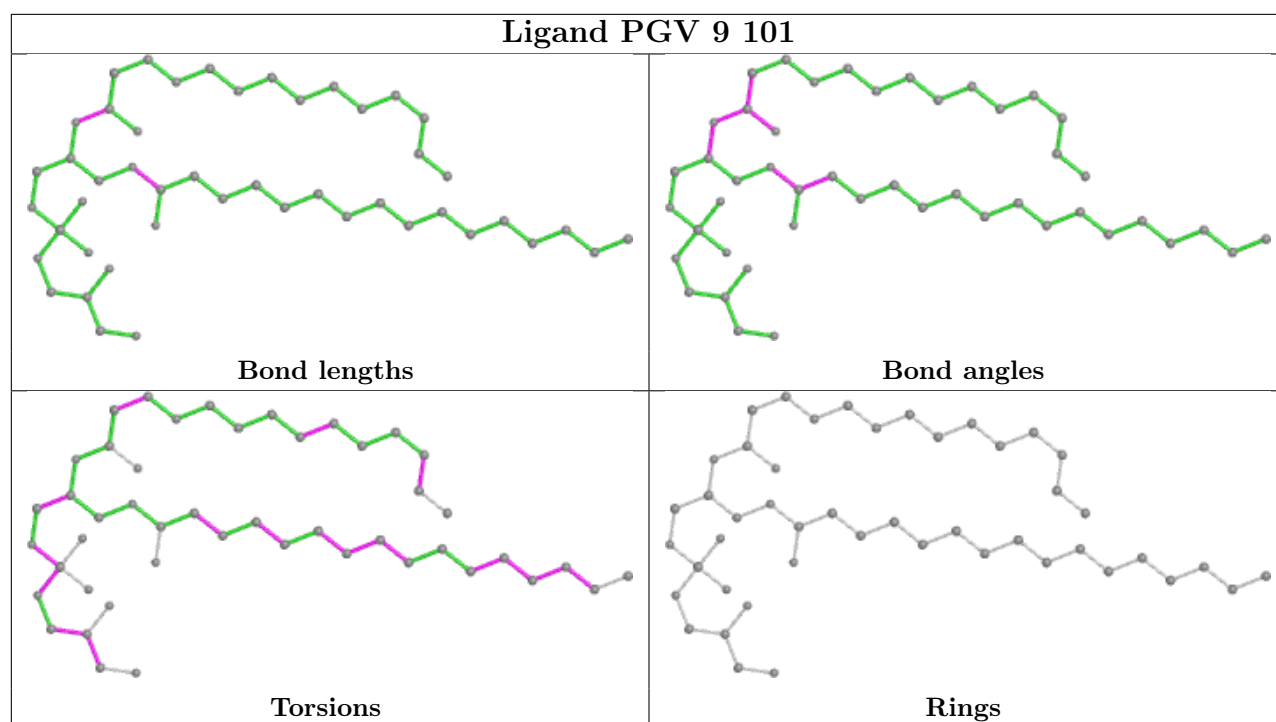


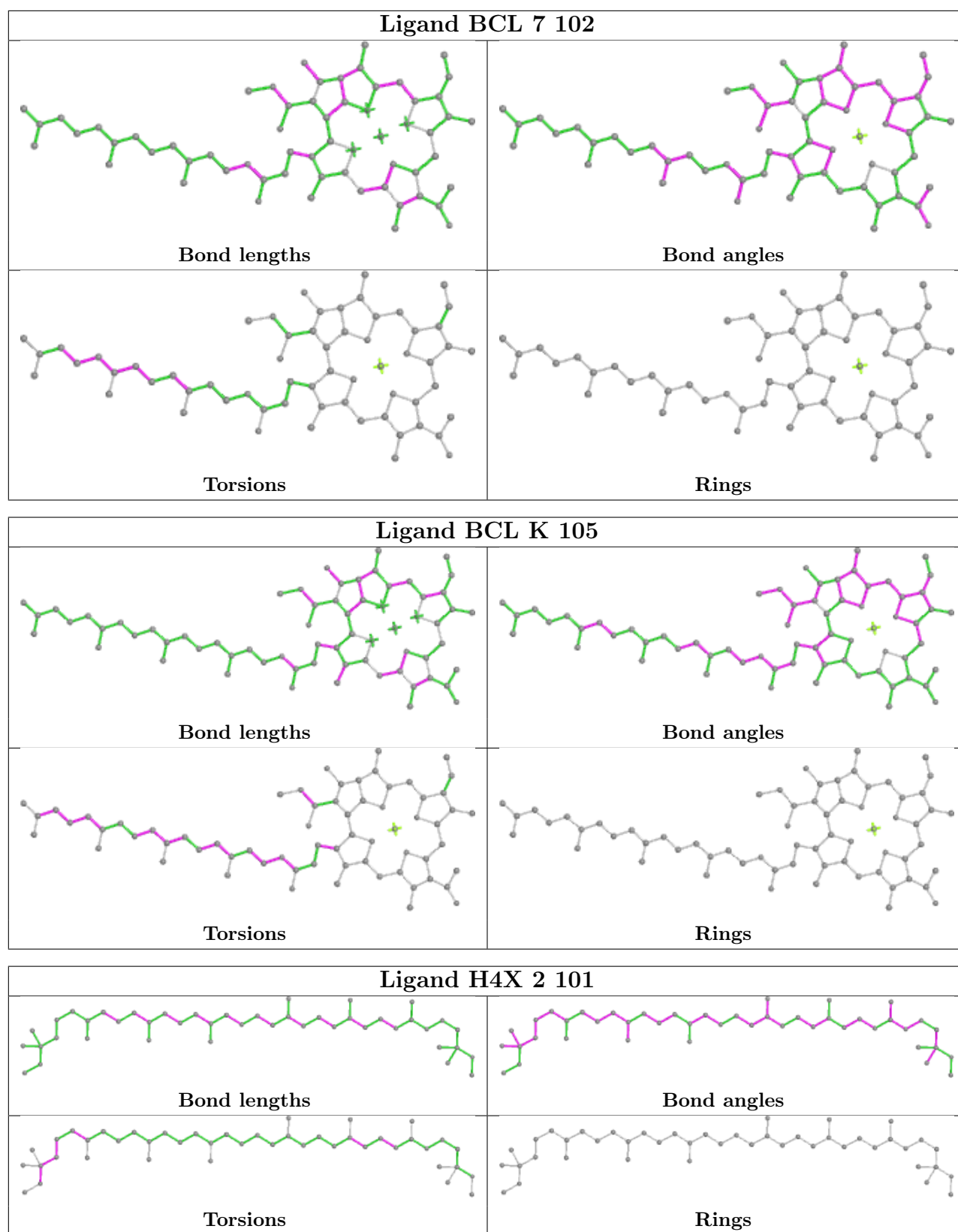


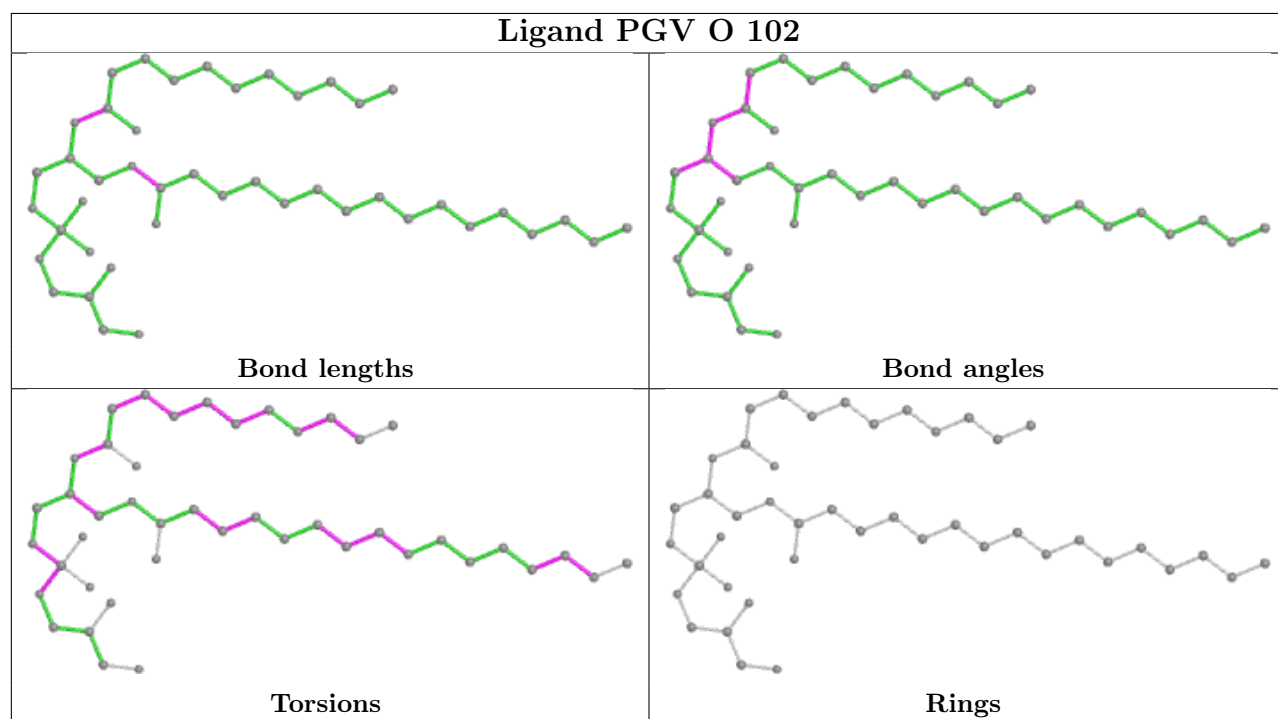
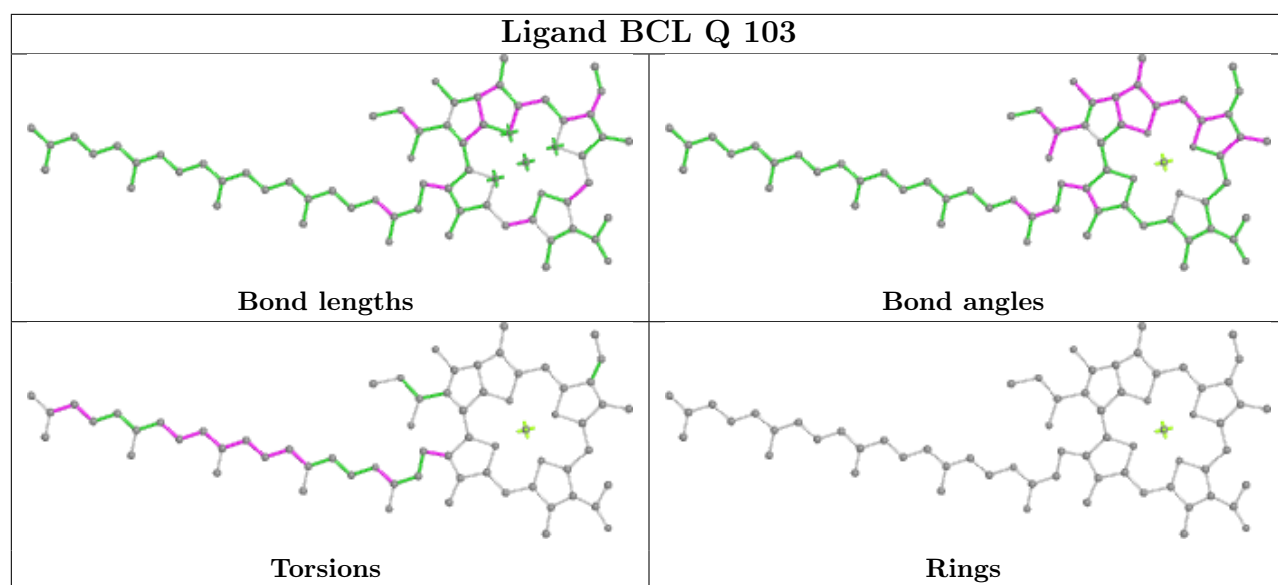


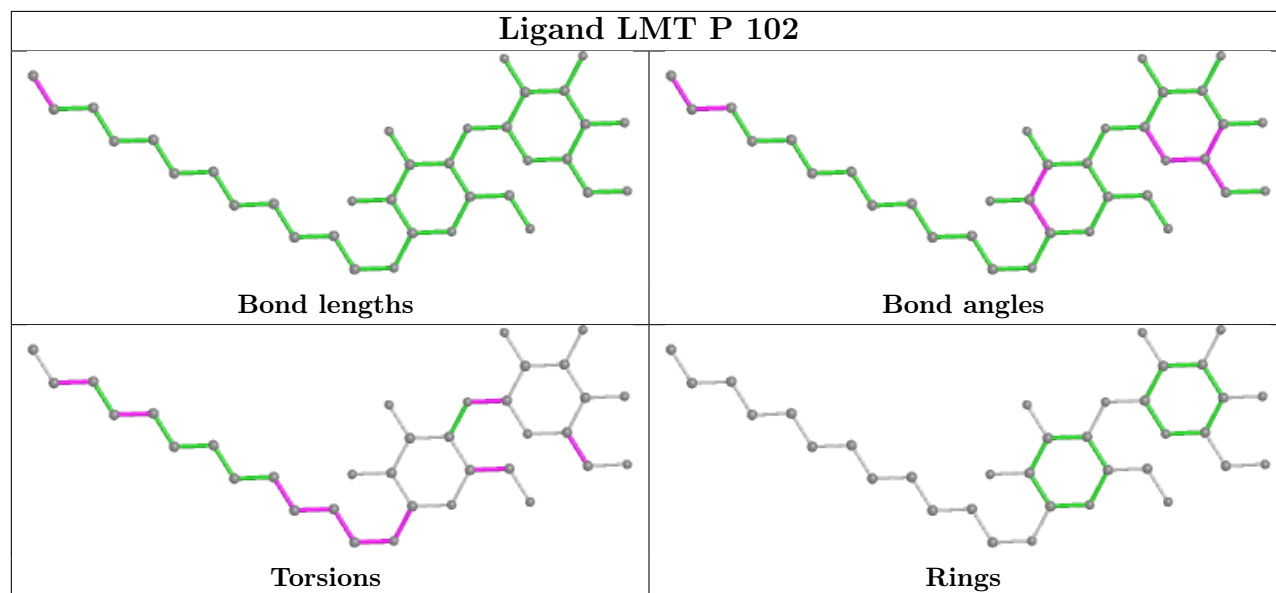
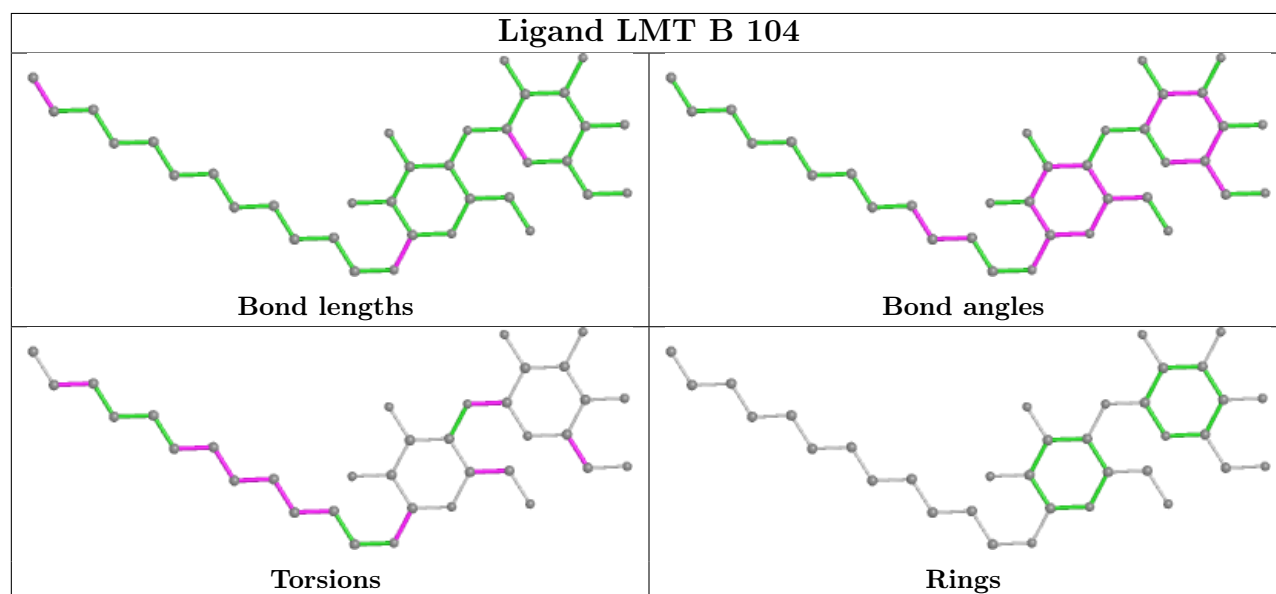
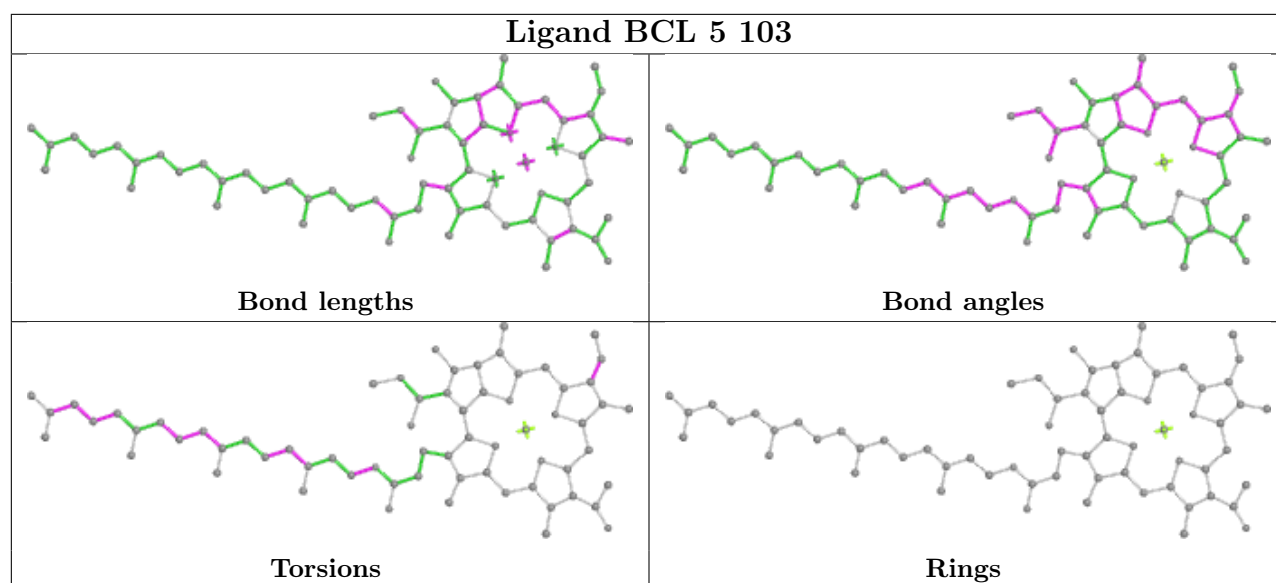


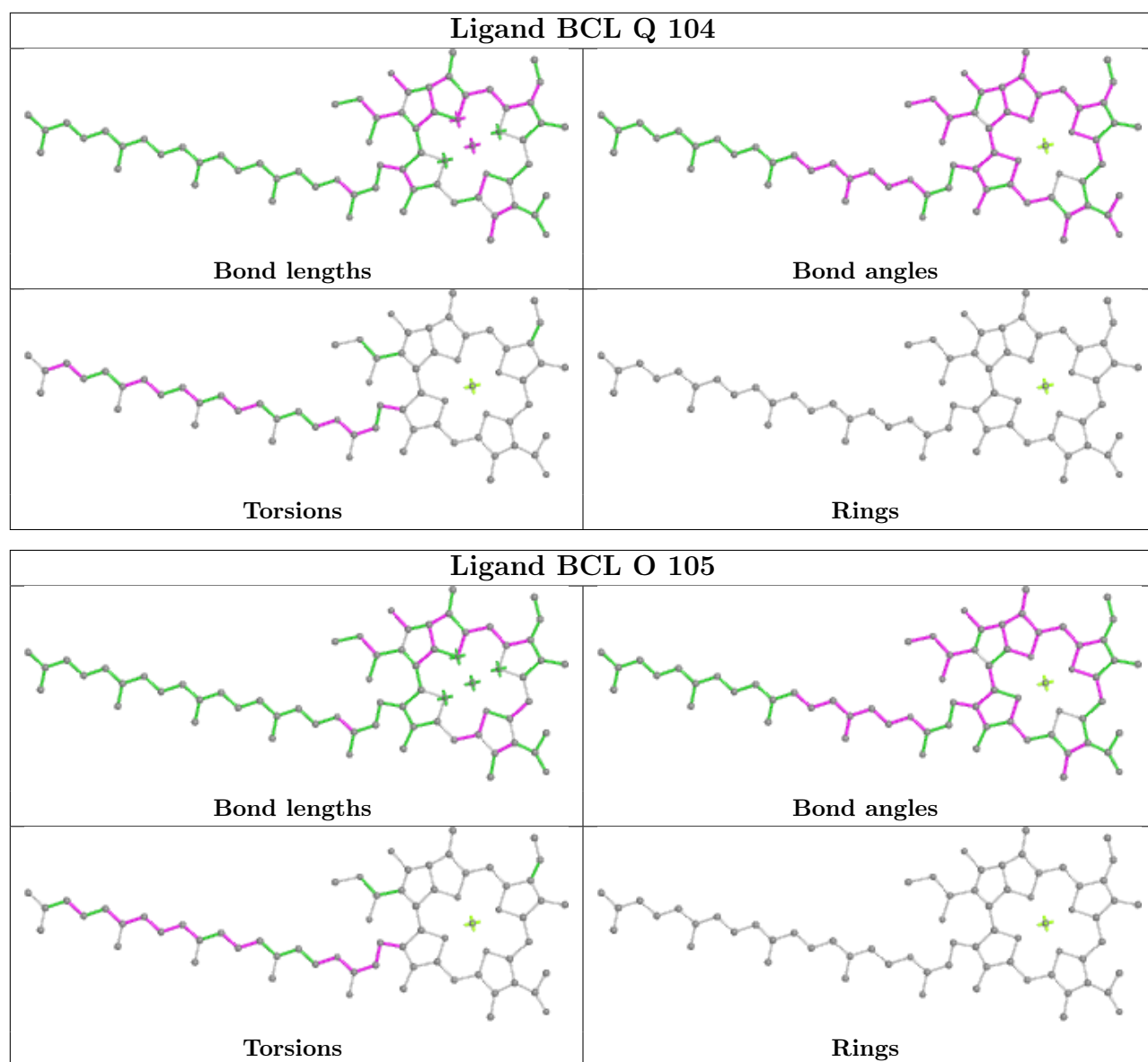


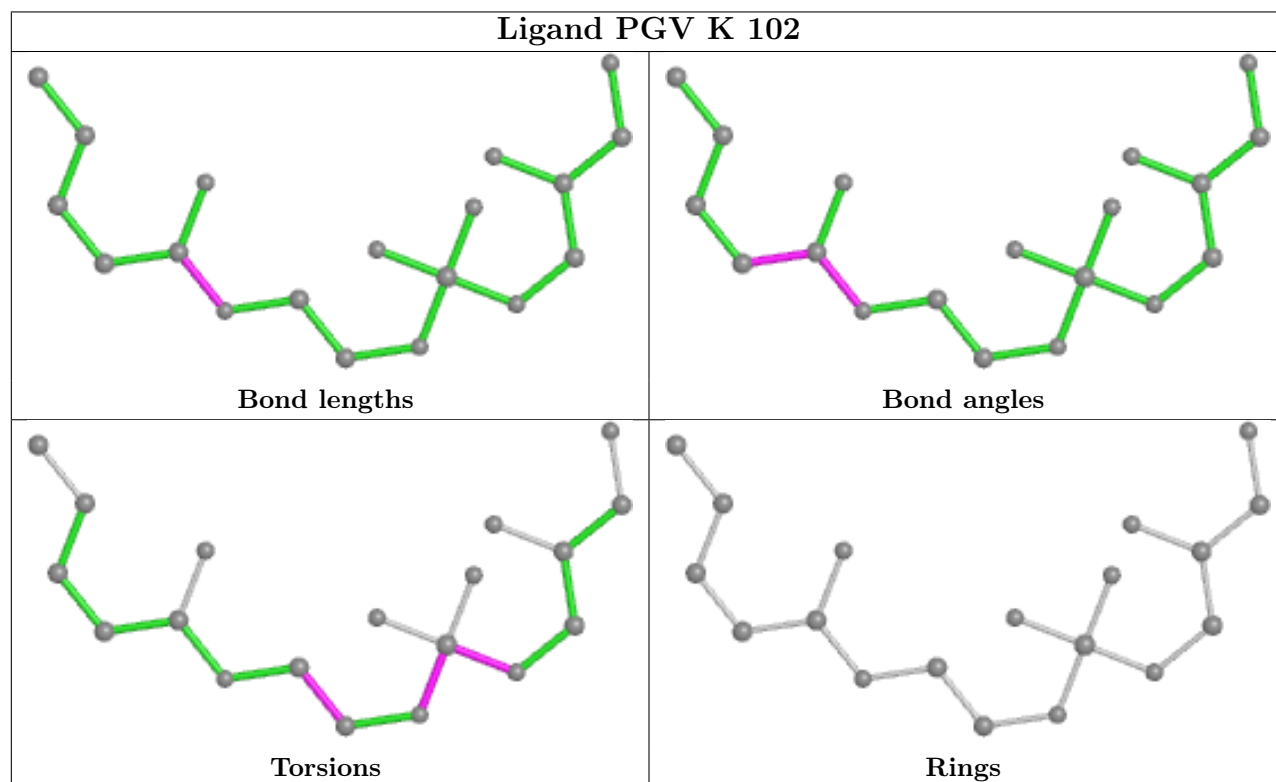
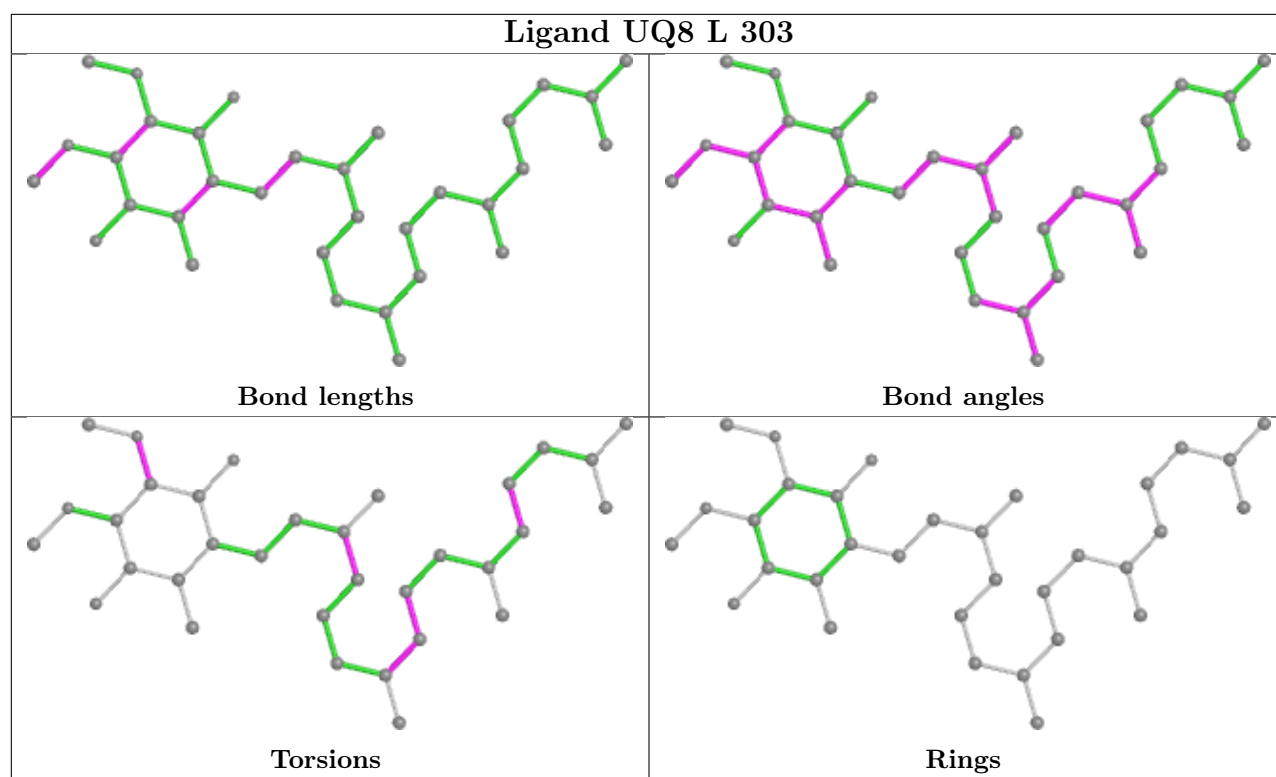


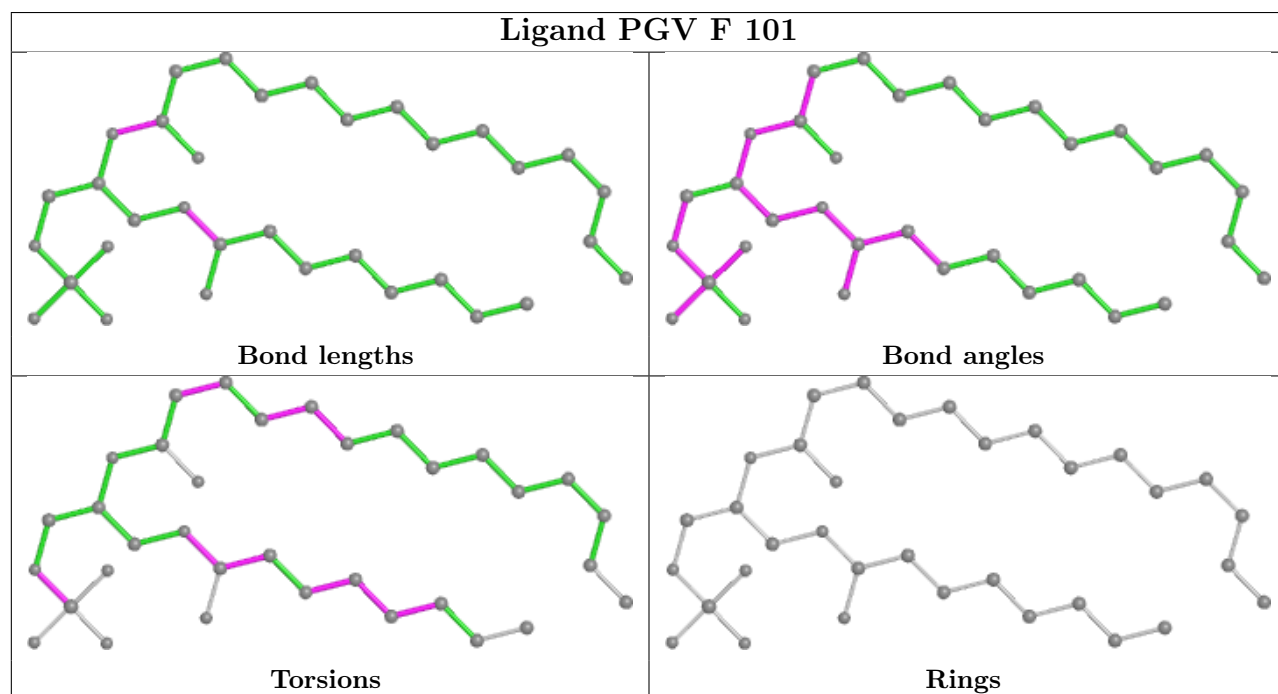
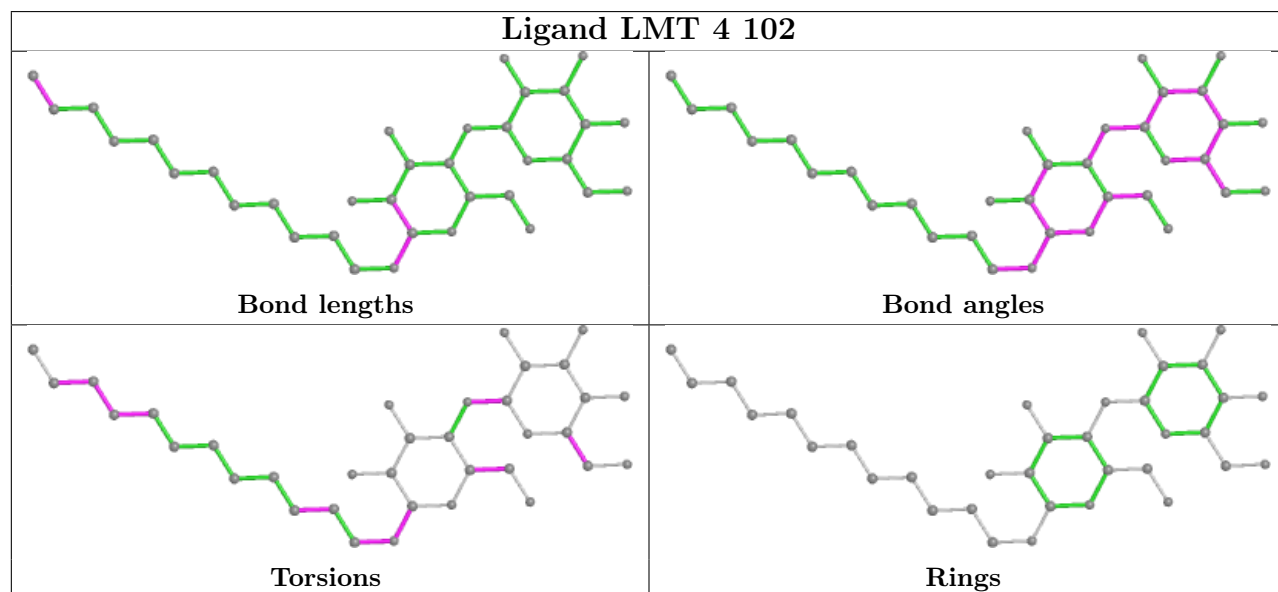
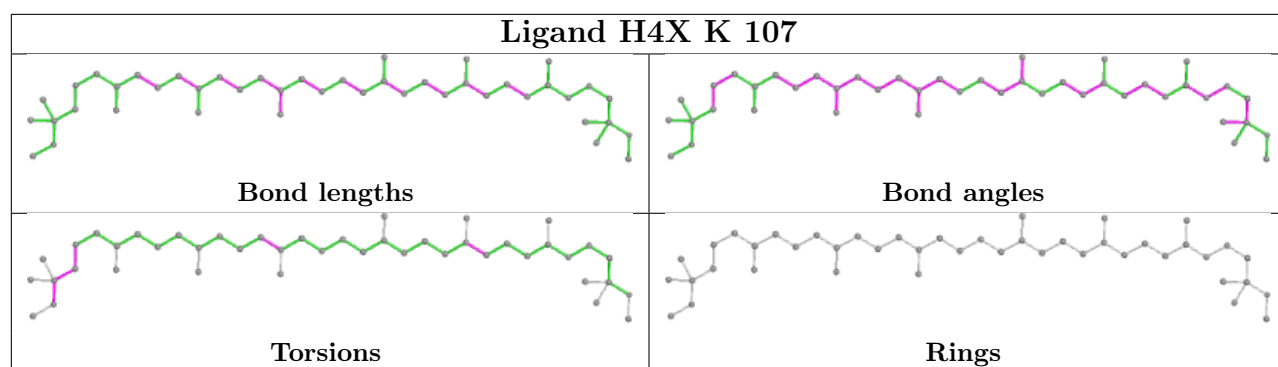


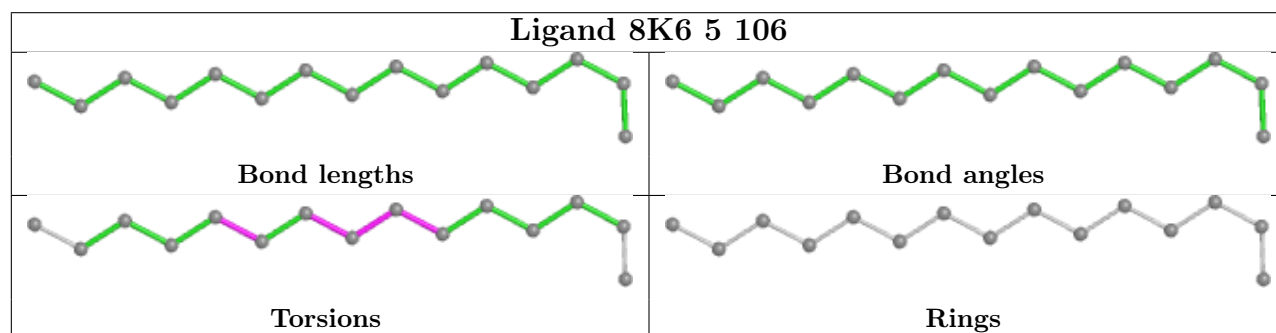
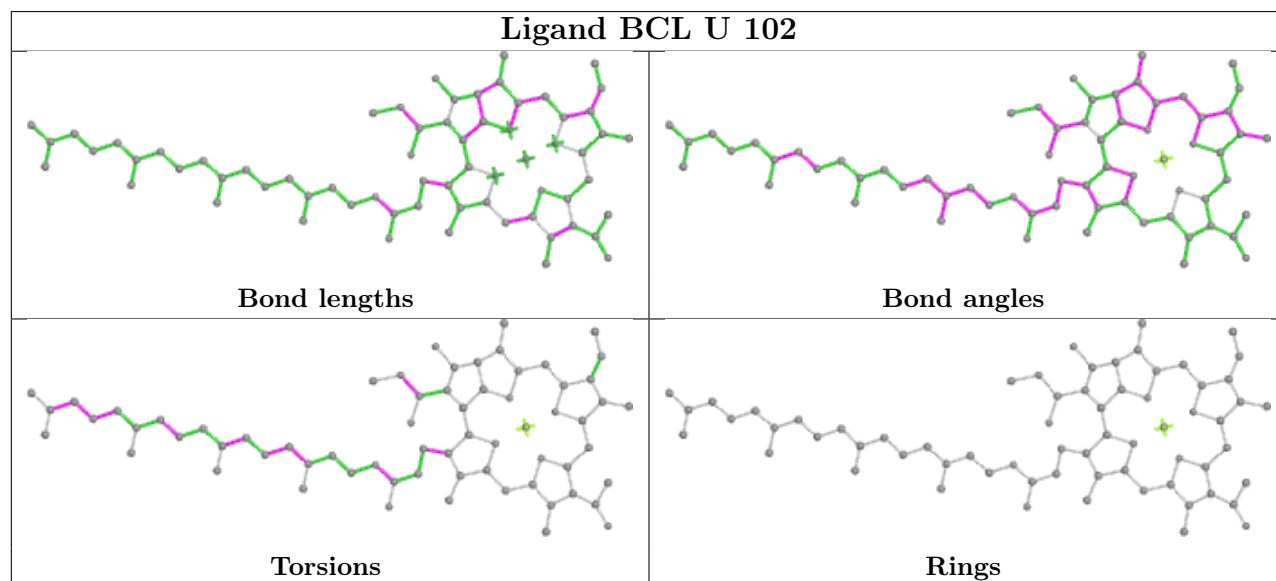
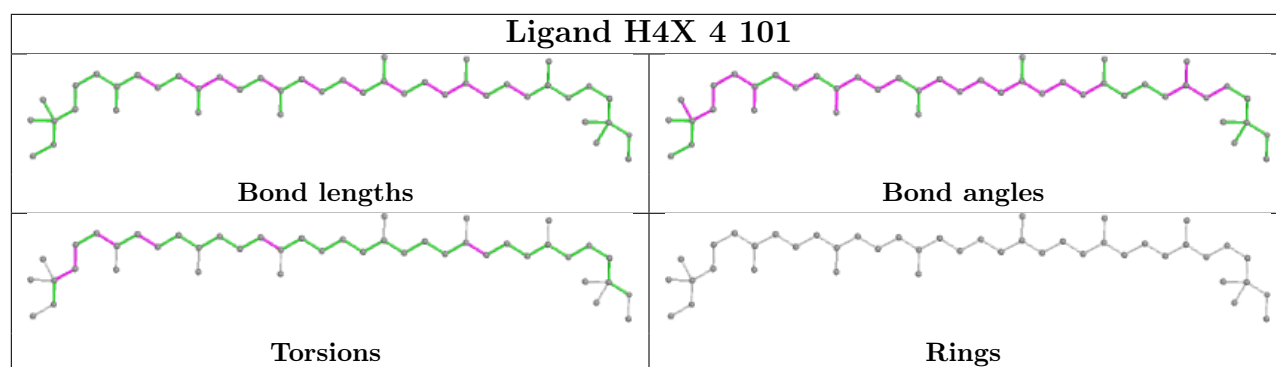


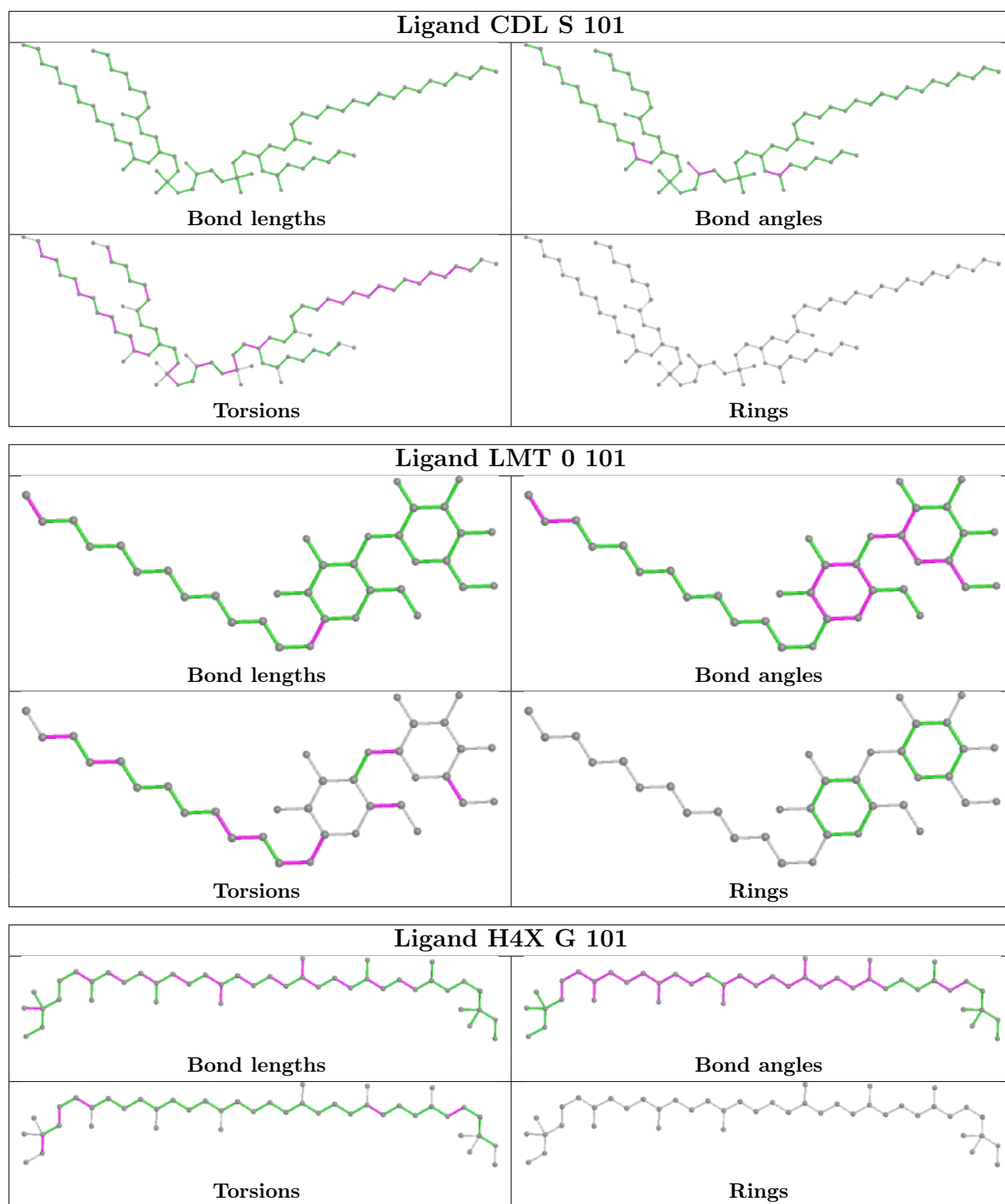


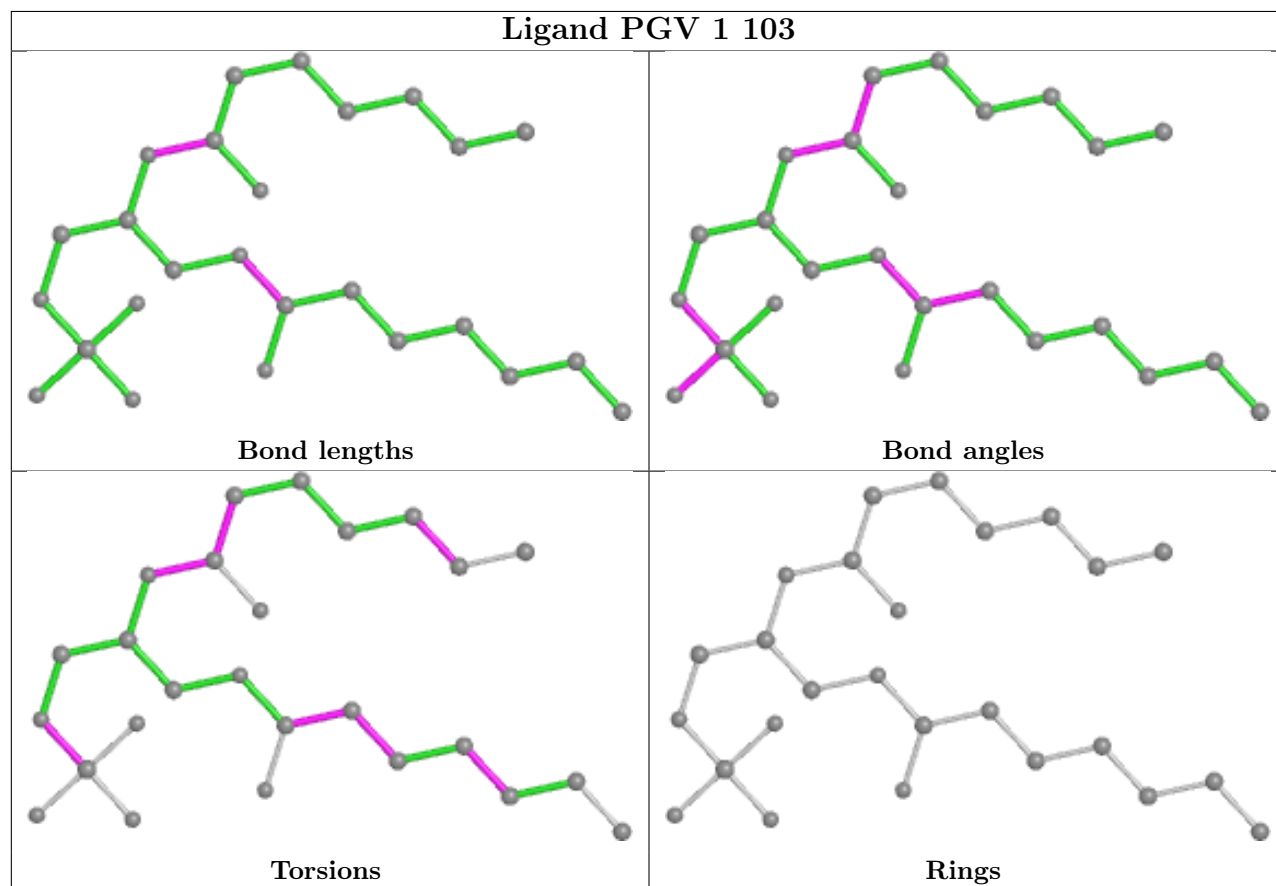
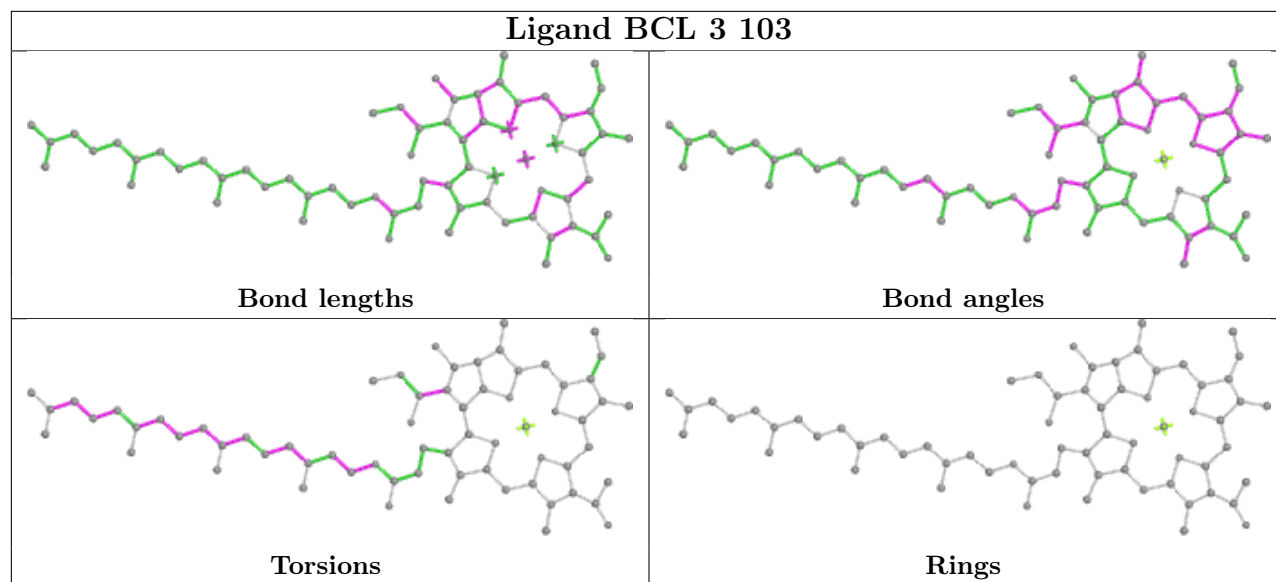




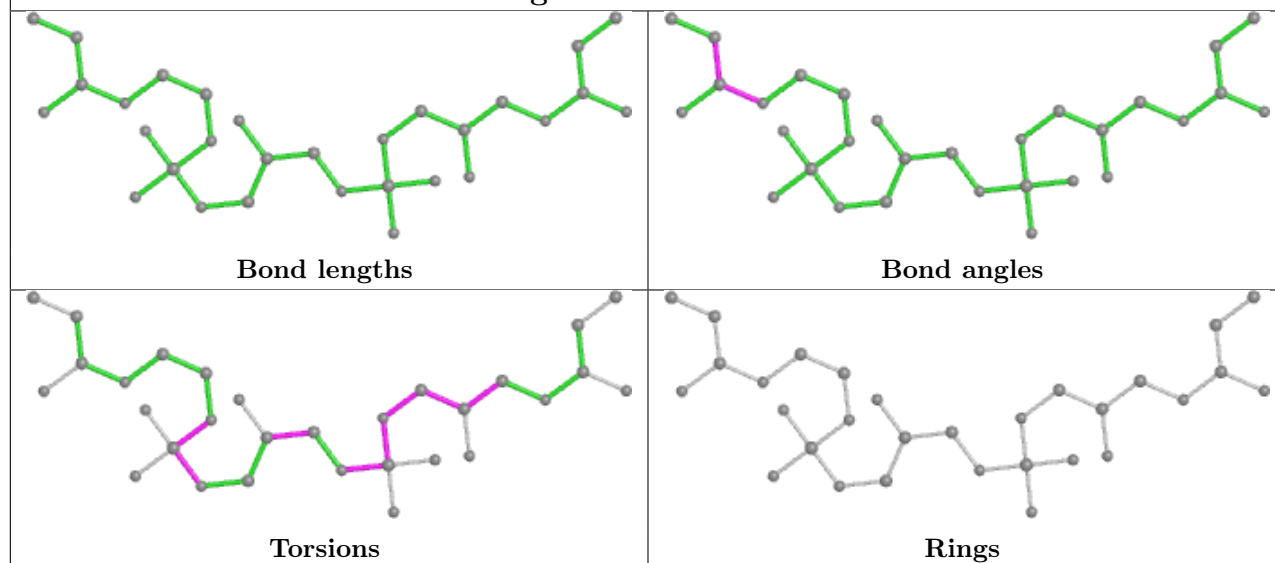




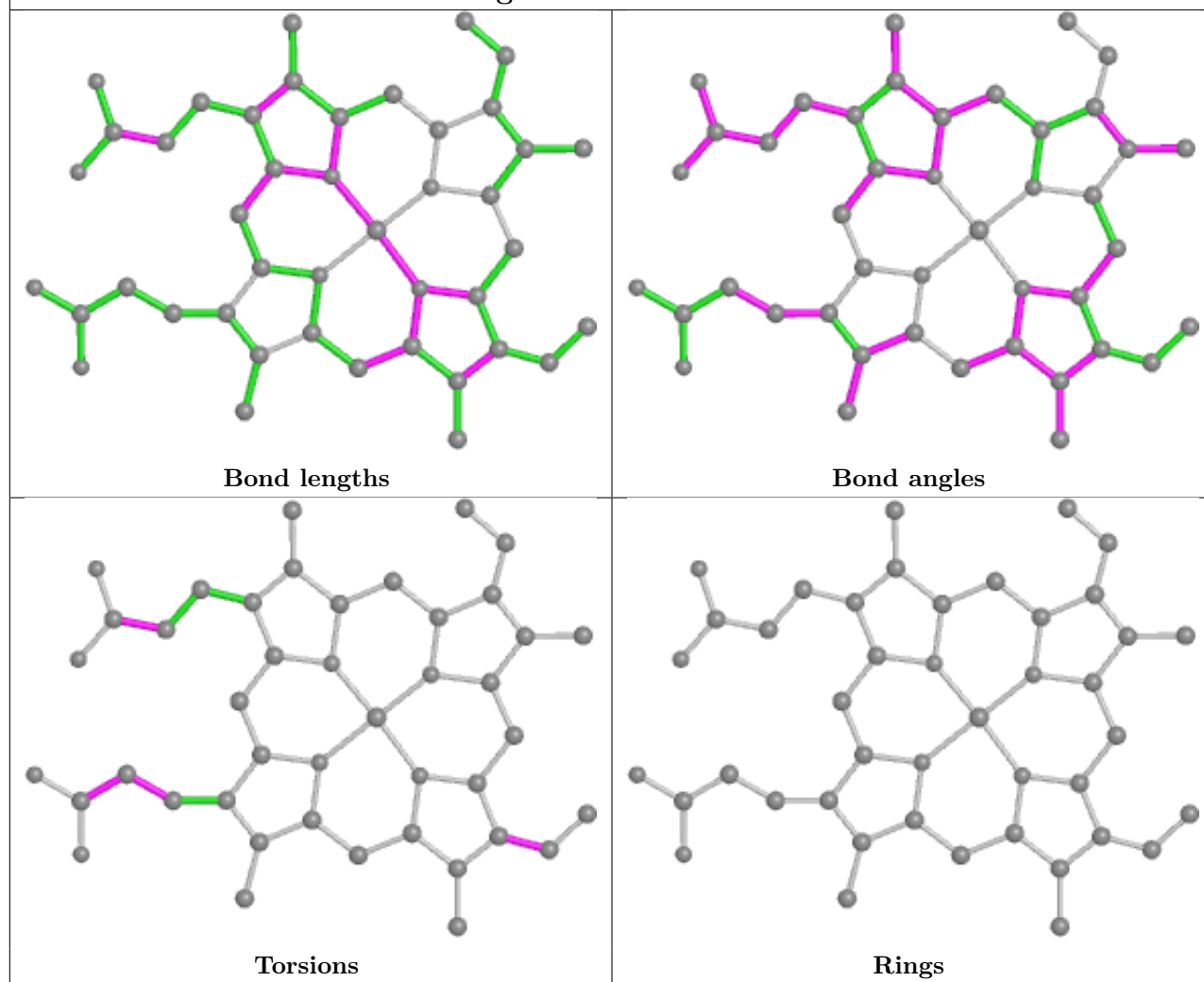


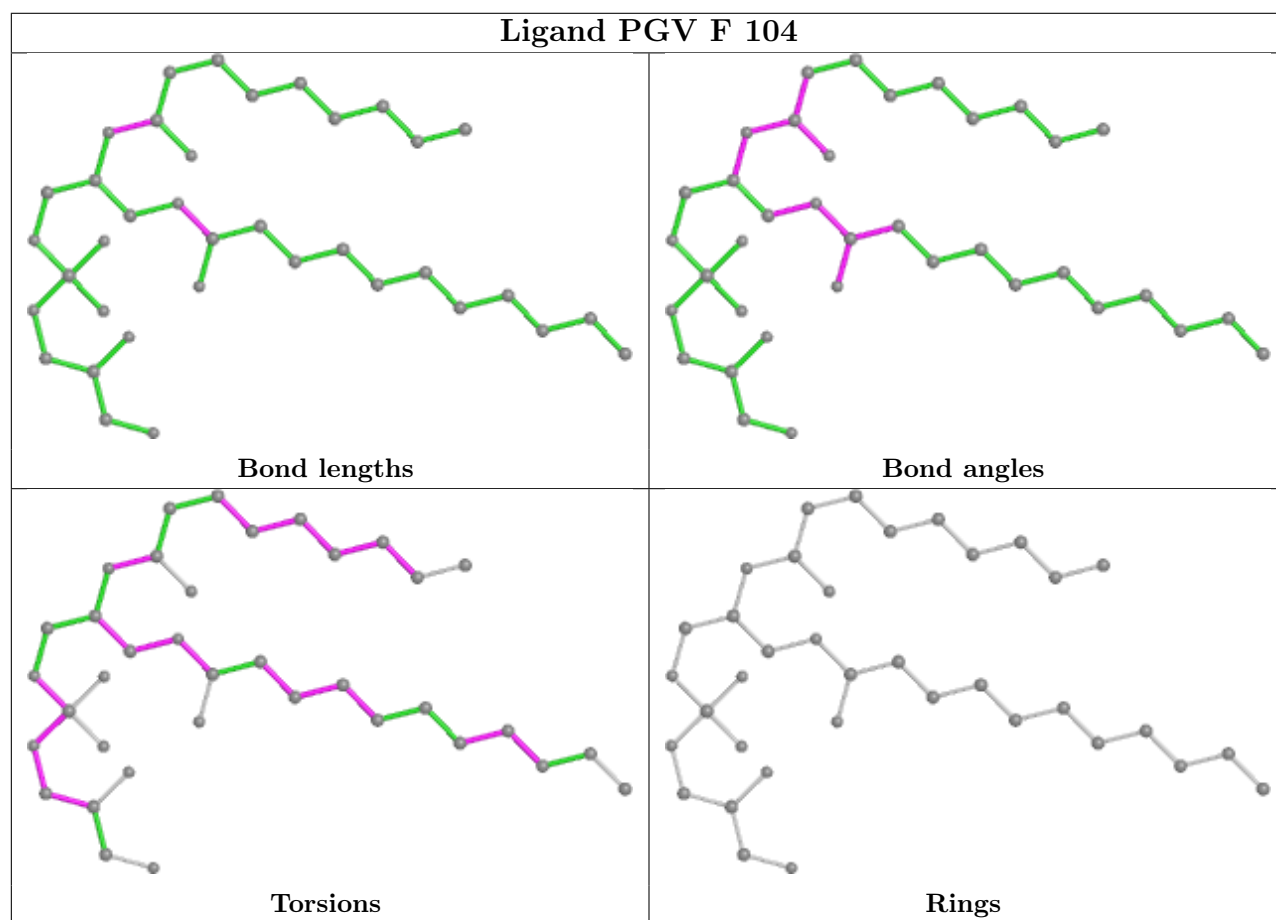
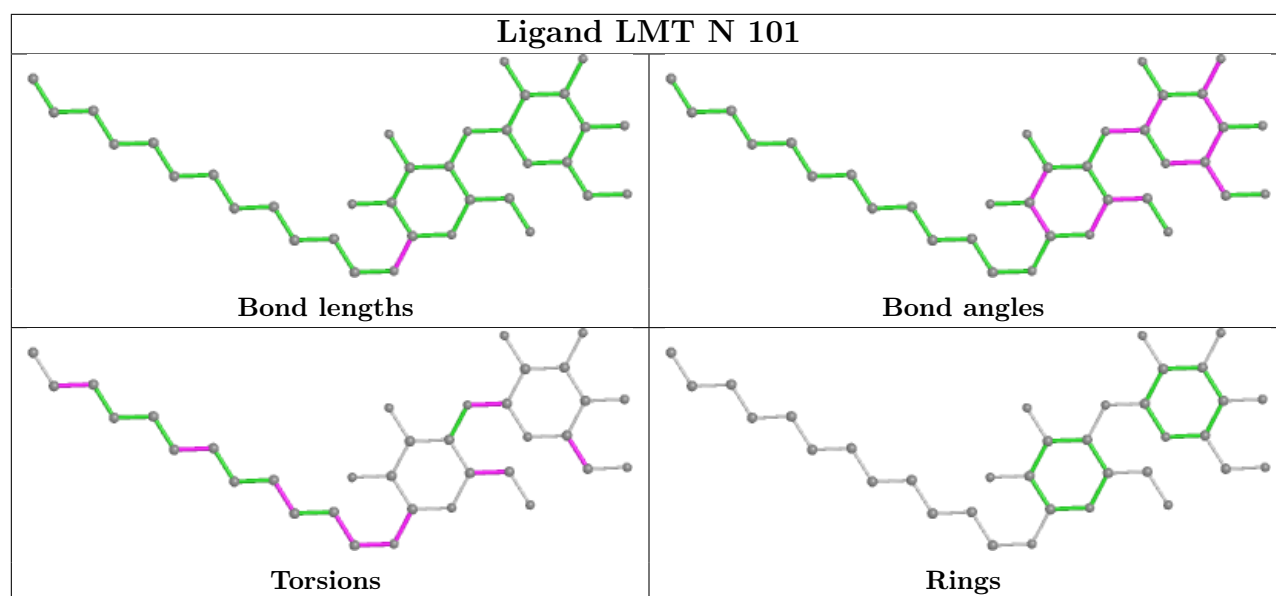


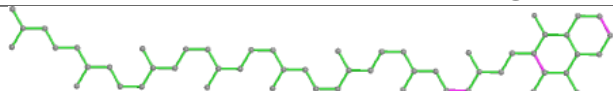
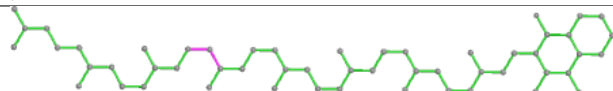
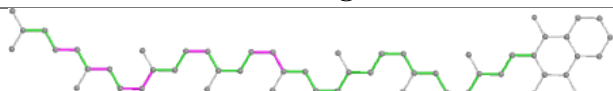
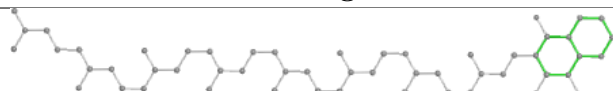
Ligand CDL Y 103

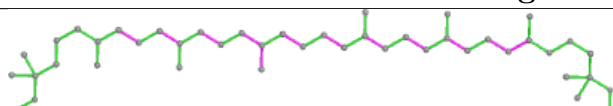
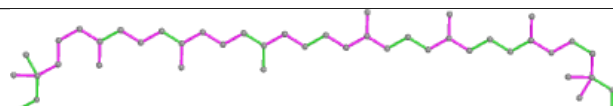
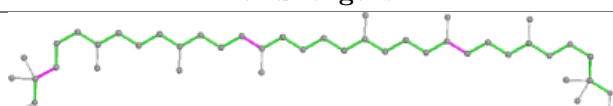
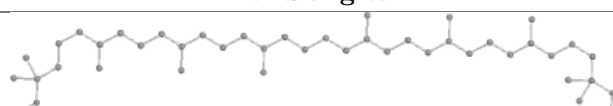


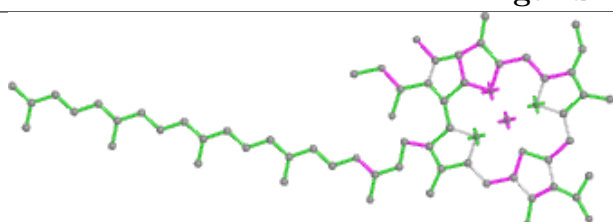
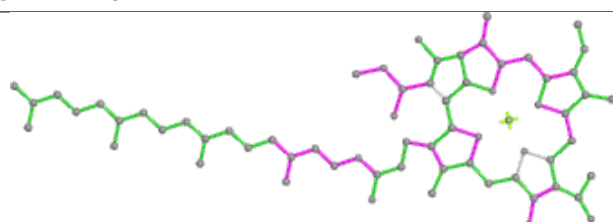
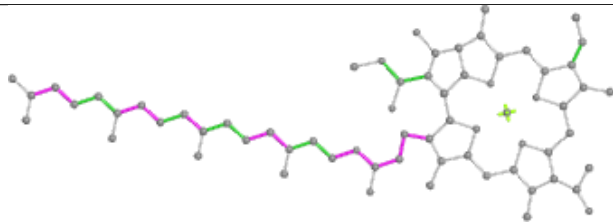
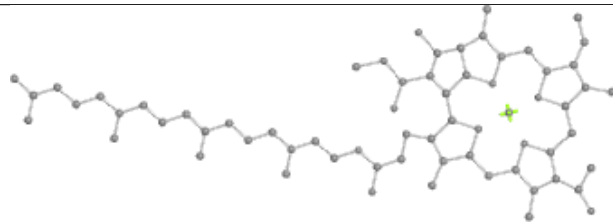
Ligand HEM C 401

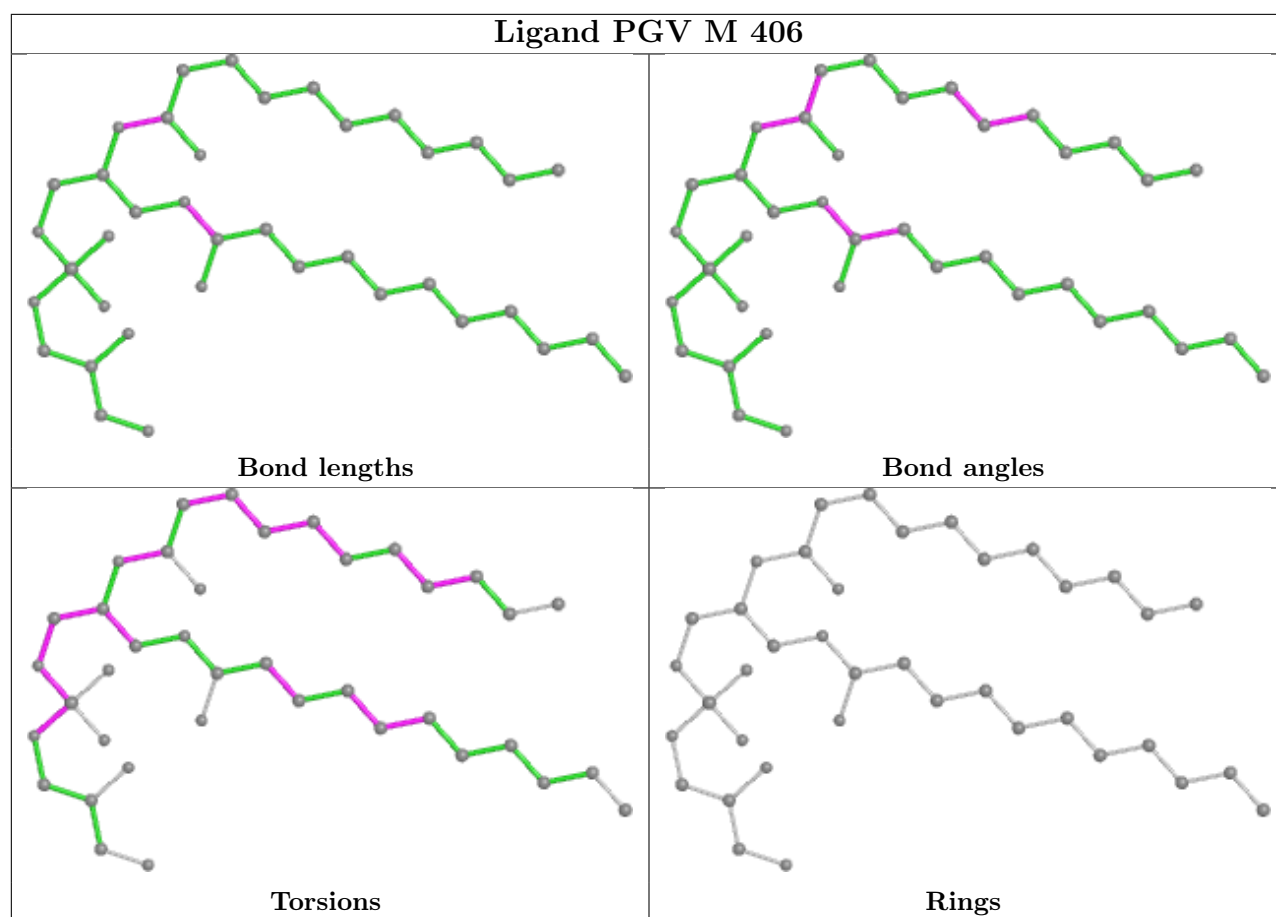


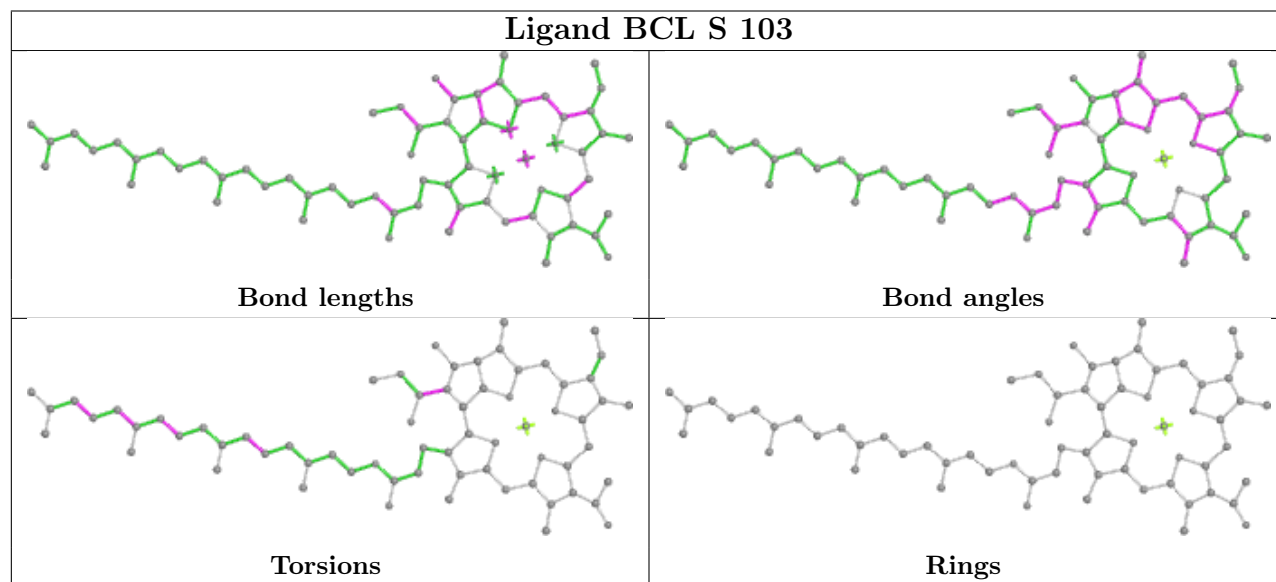
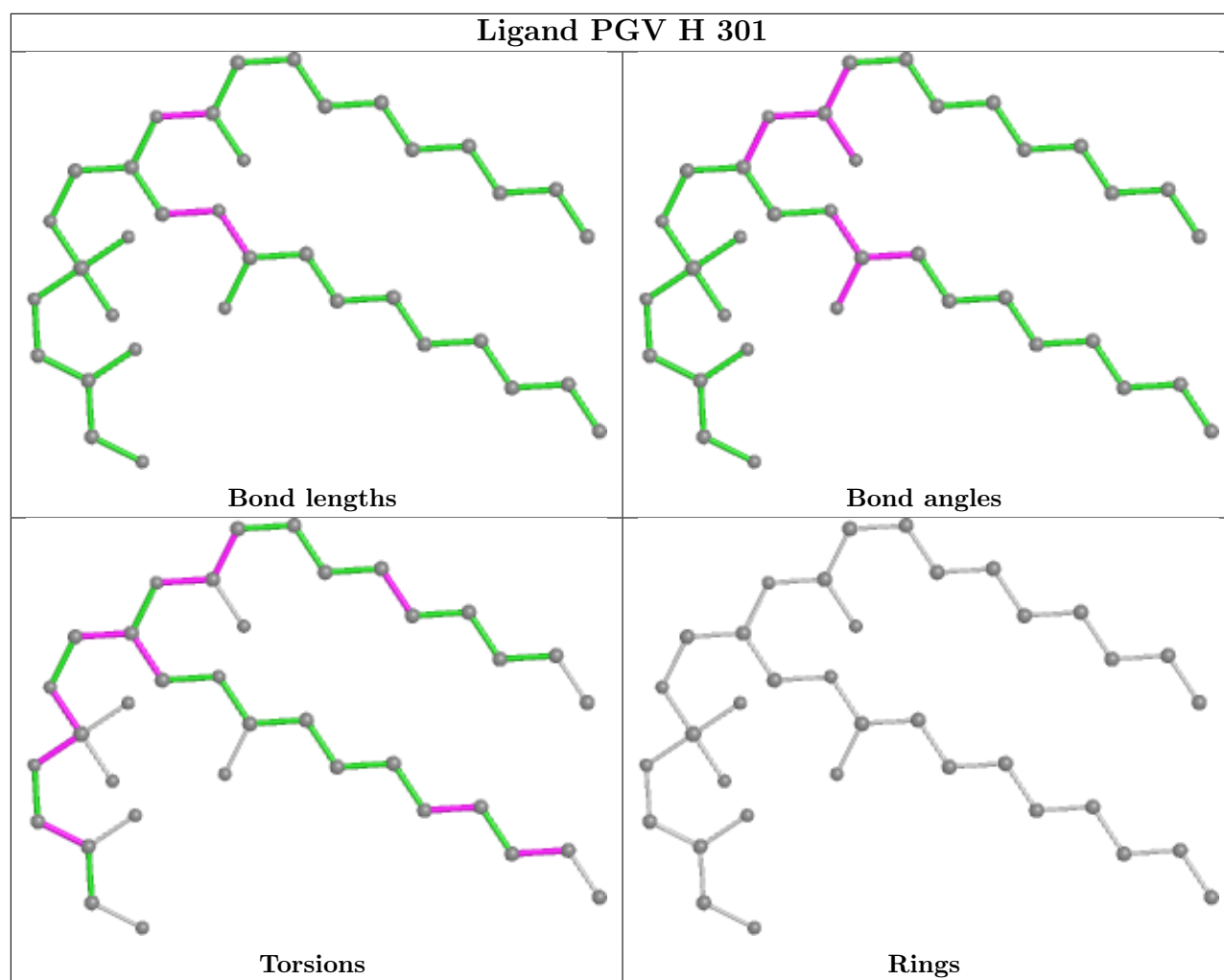


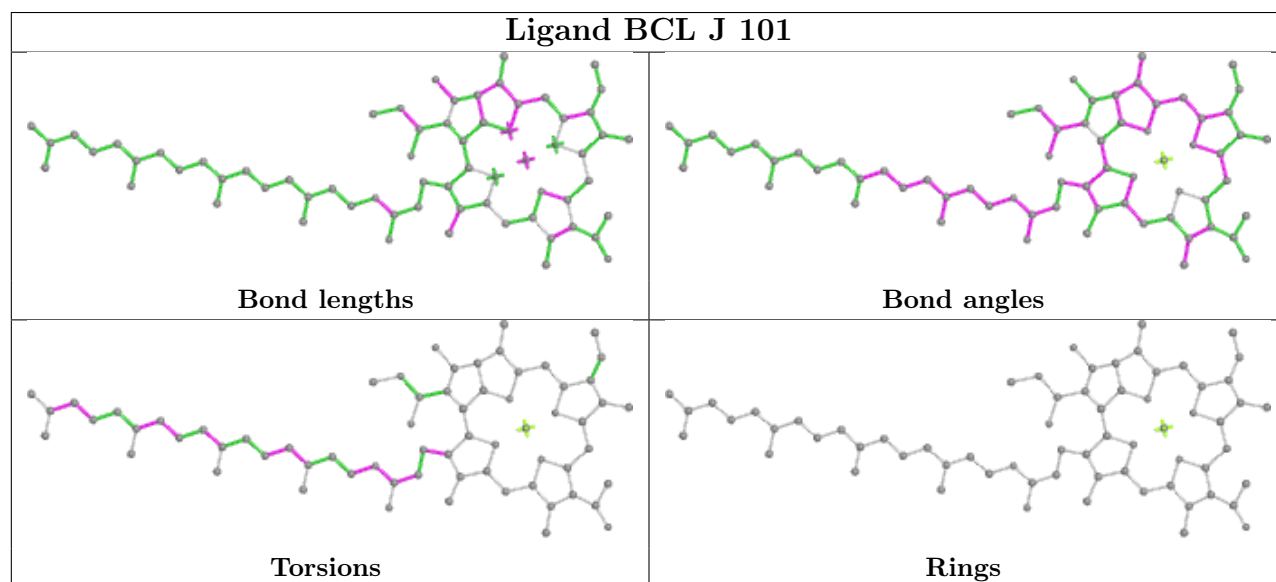
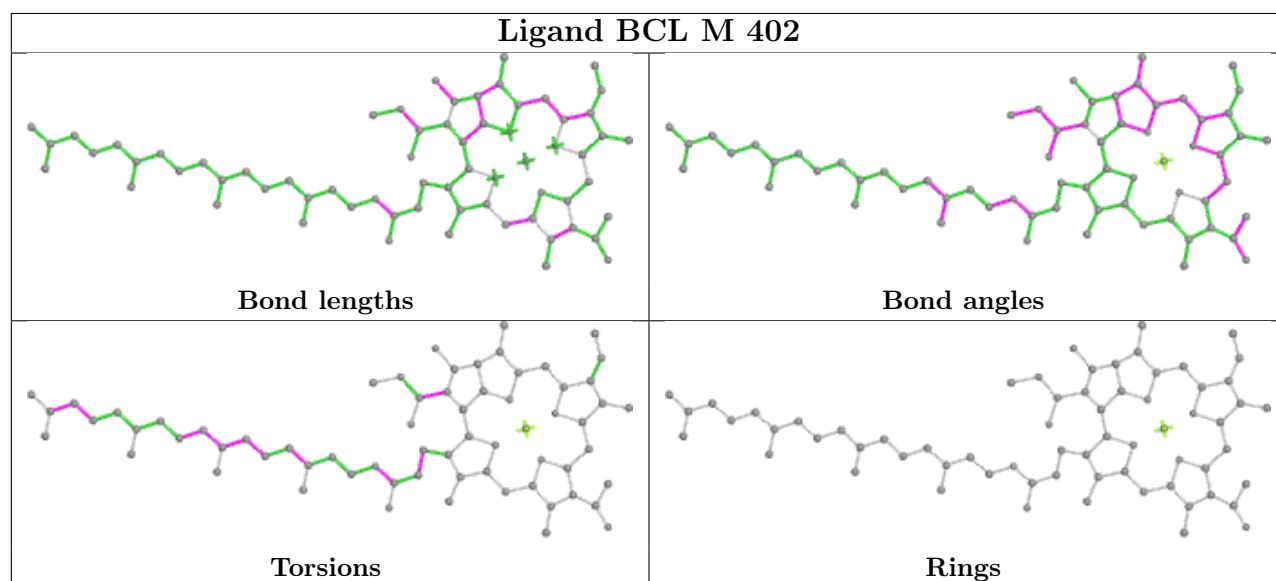
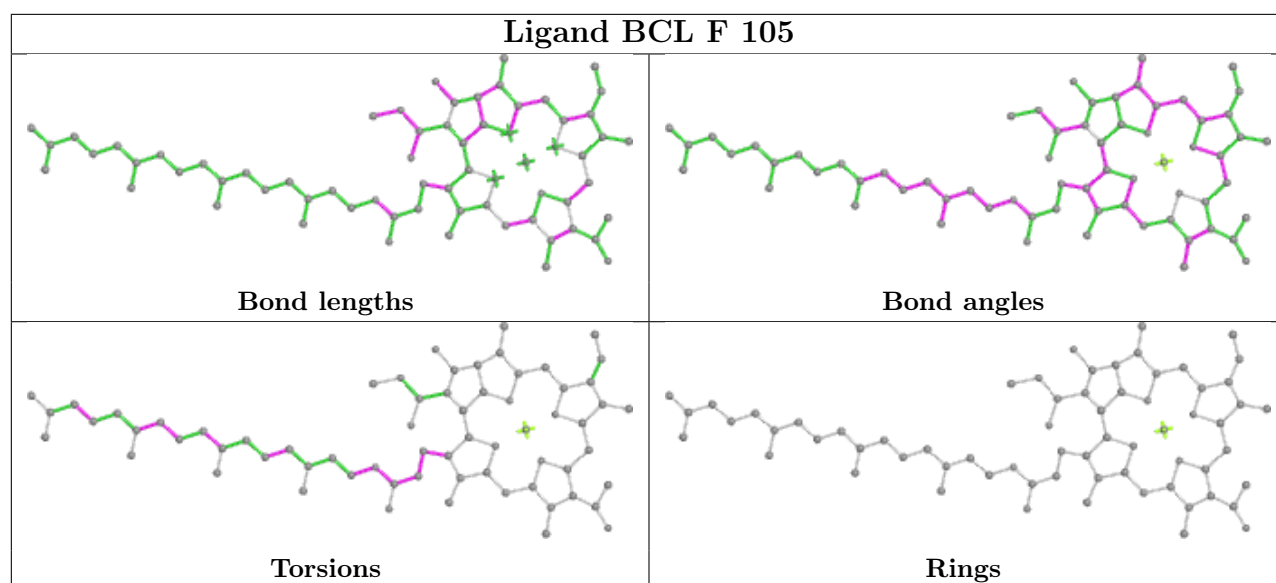
Ligand MQ8 M 405	
	
Bond lengths	Bond angles
	
Torsions	Rings

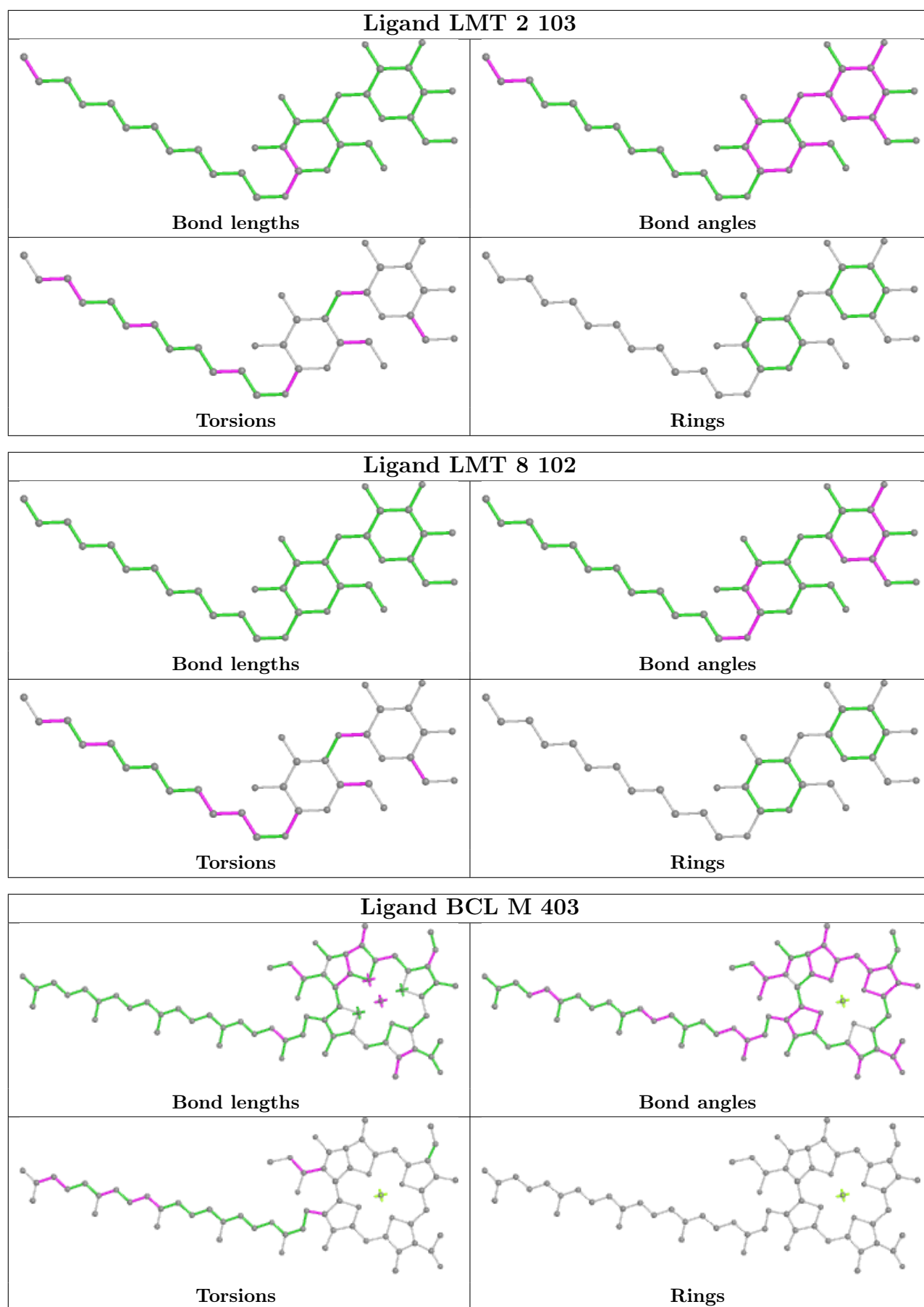
Ligand H4X 6 101	
	
Bond lengths	Bond angles
	
Torsions	Rings

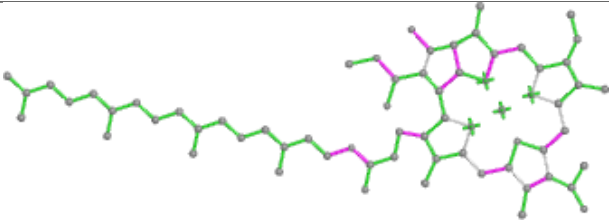
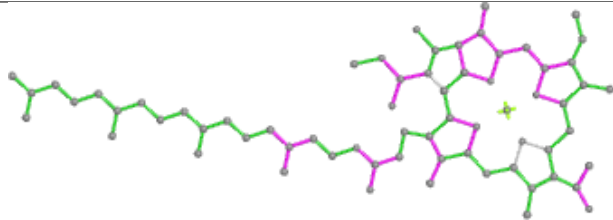
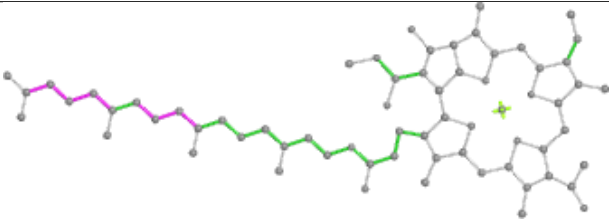
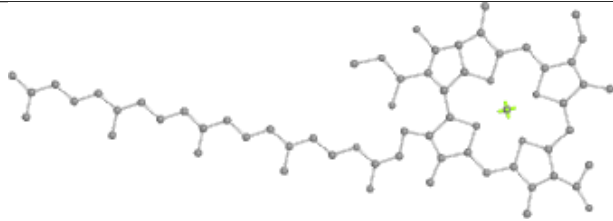
Ligand BCL D 104	
	
Bond lengths	Bond angles
	
Torsions	Rings


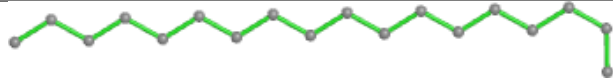
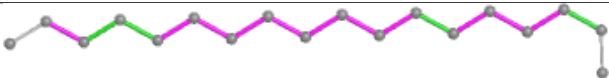
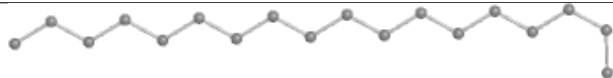


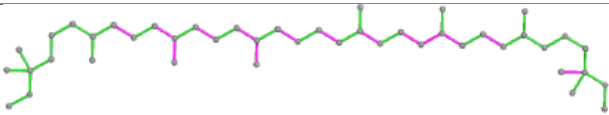
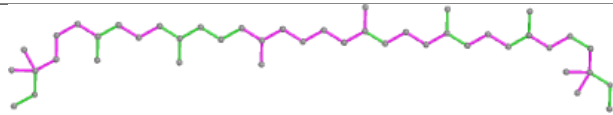
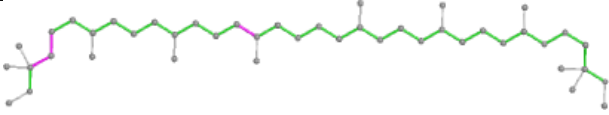
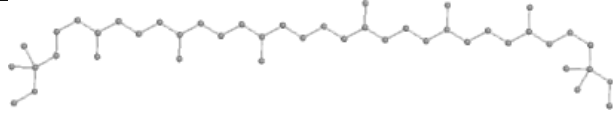


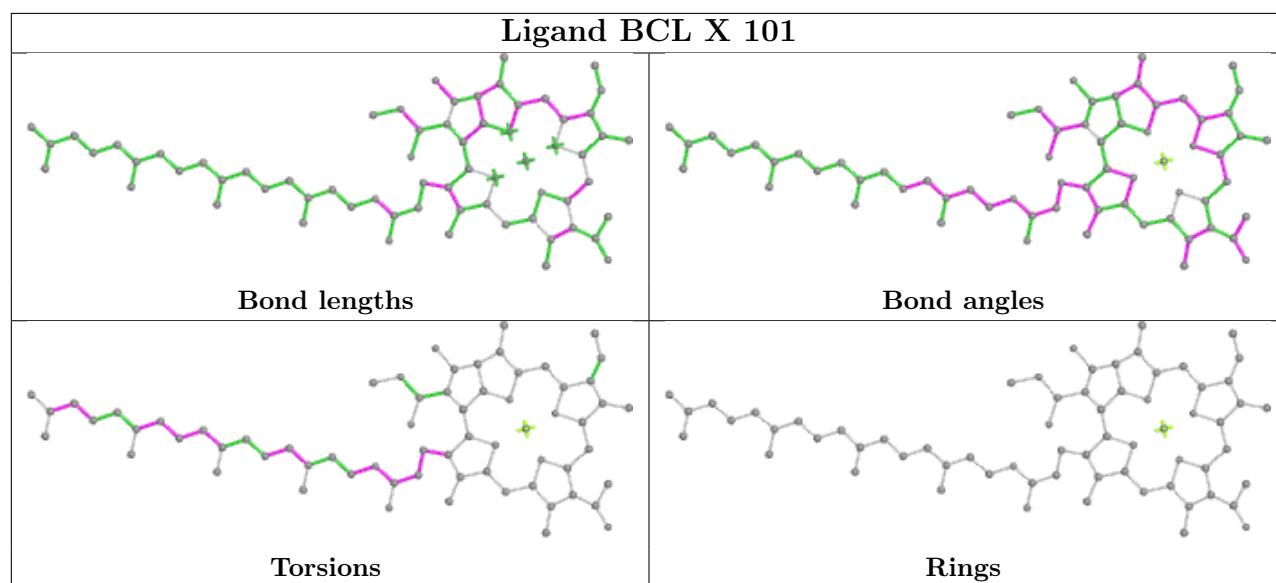
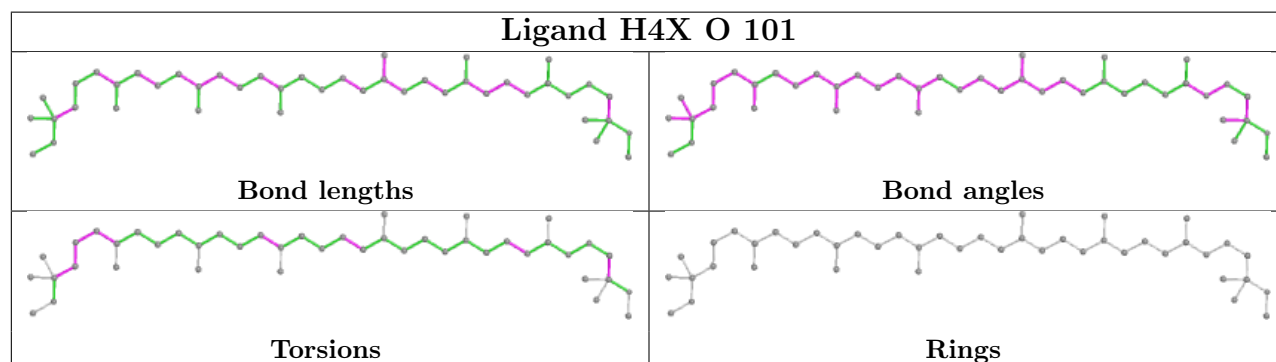
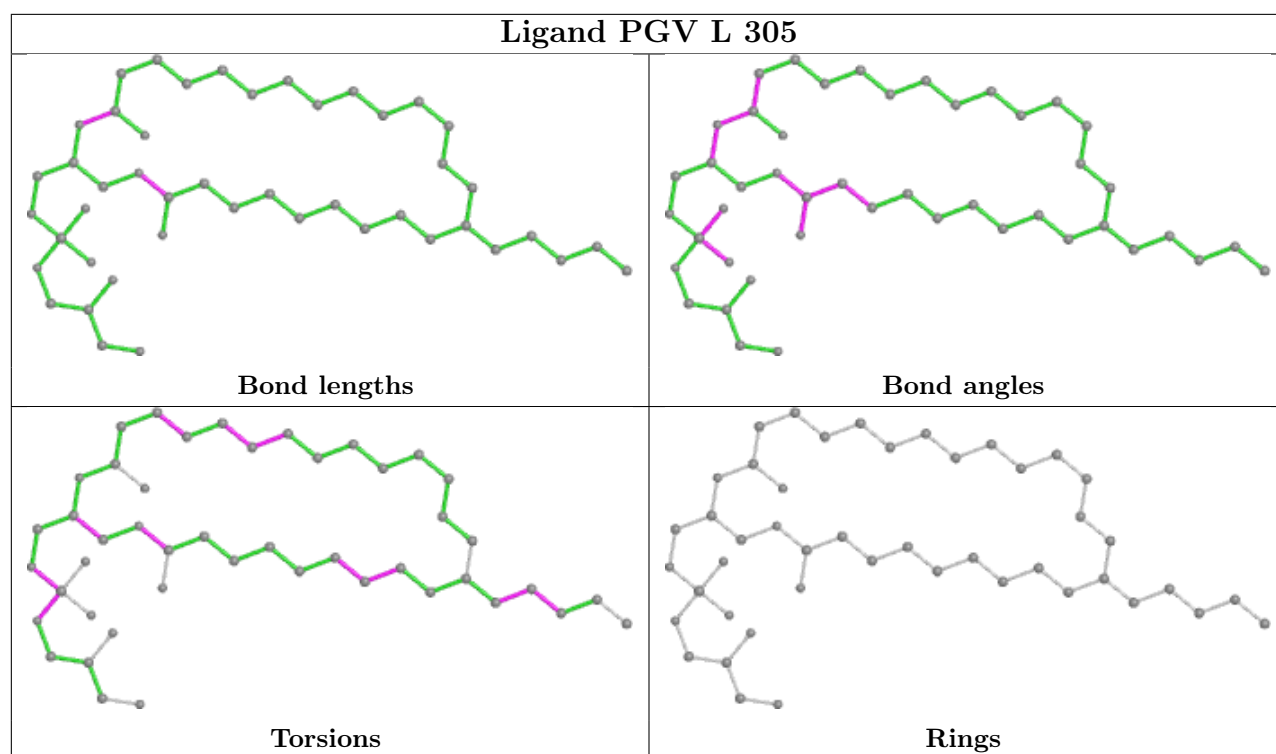


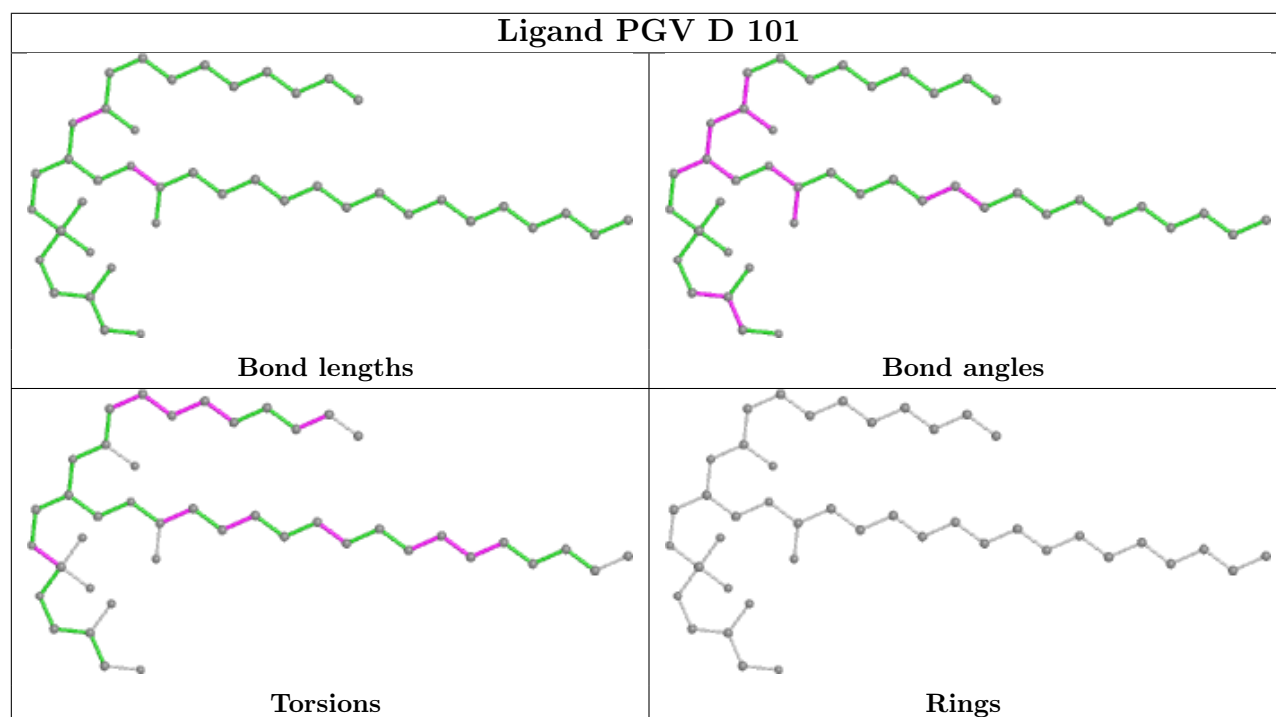
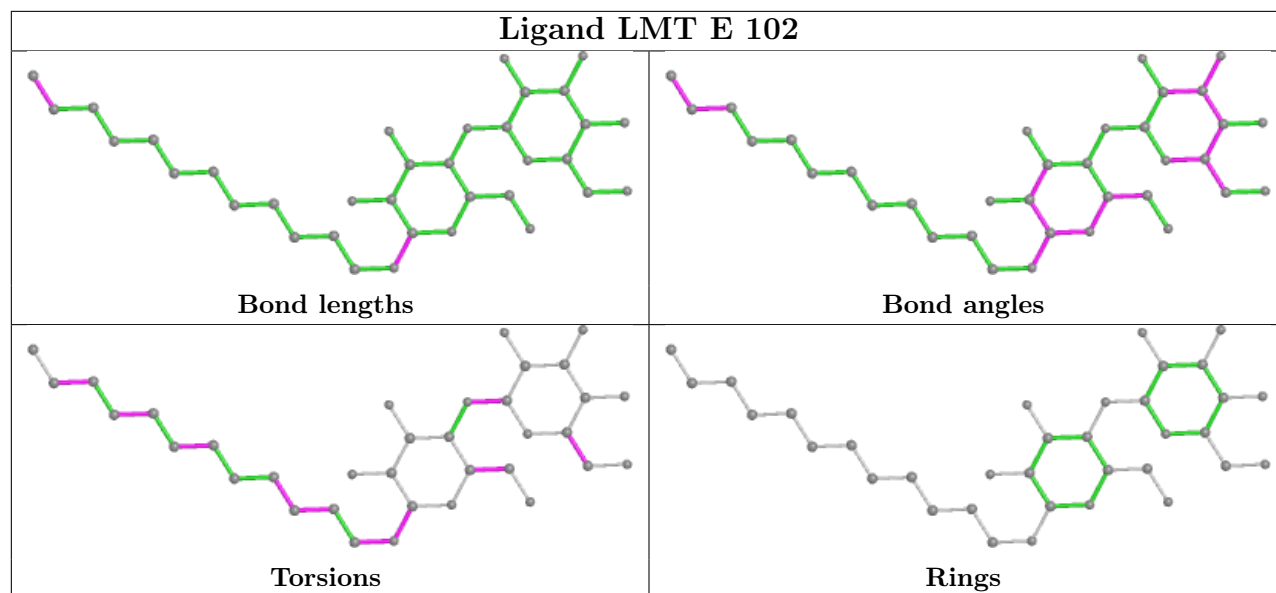


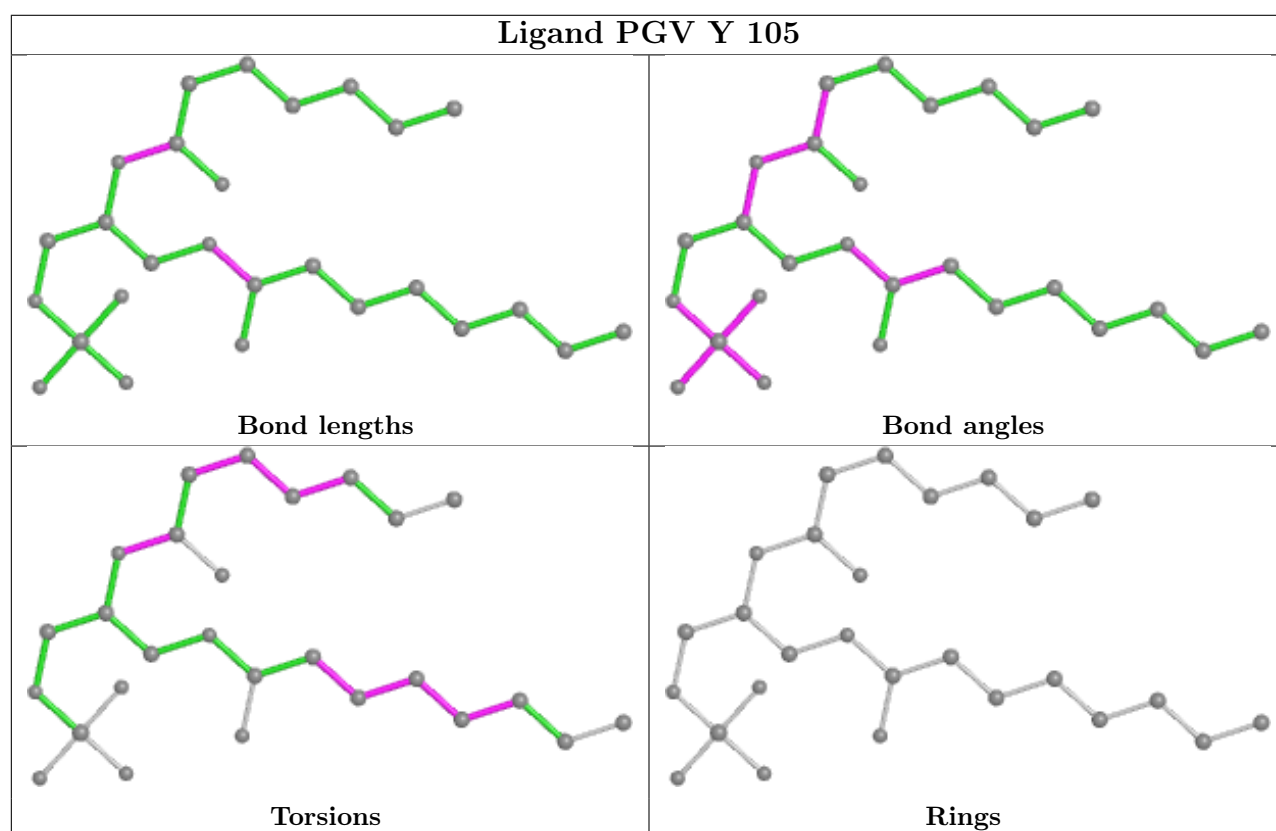
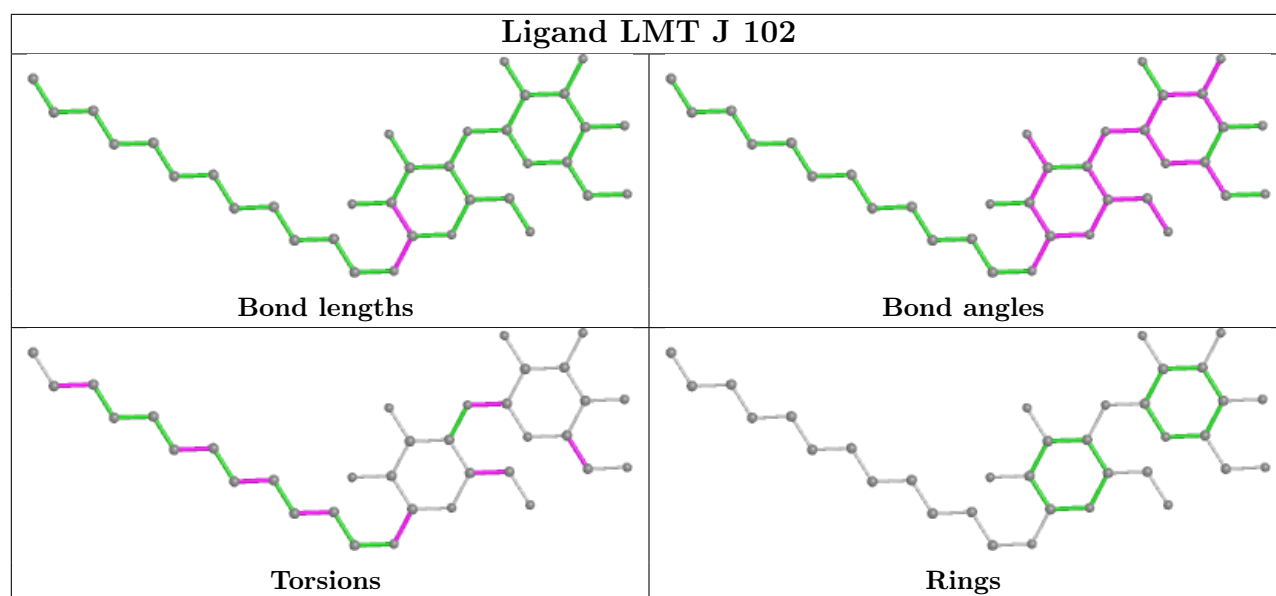
Ligand BCL Y 102	
	
Bond lengths	Bond angles
	
Torsions	Rings

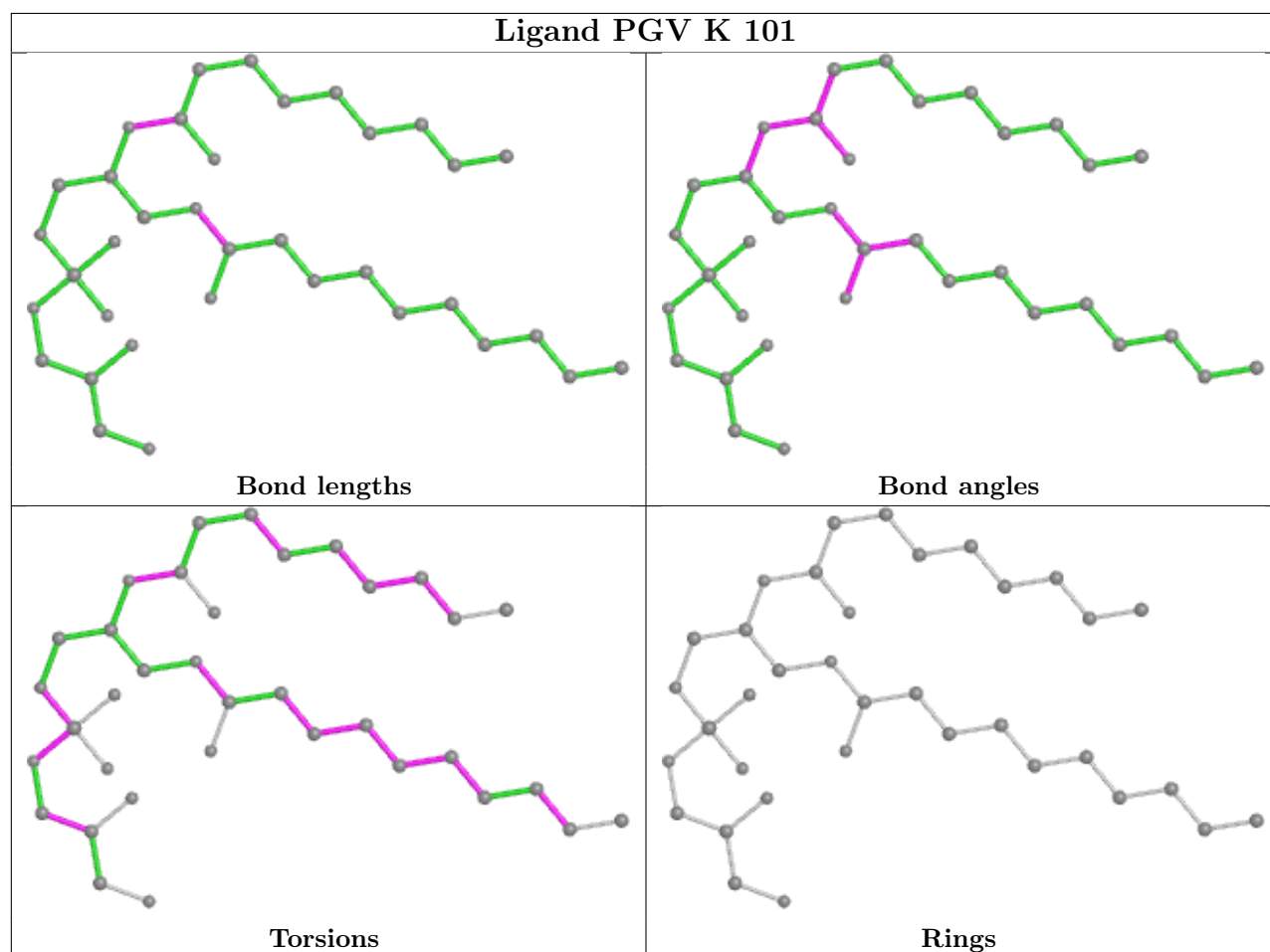
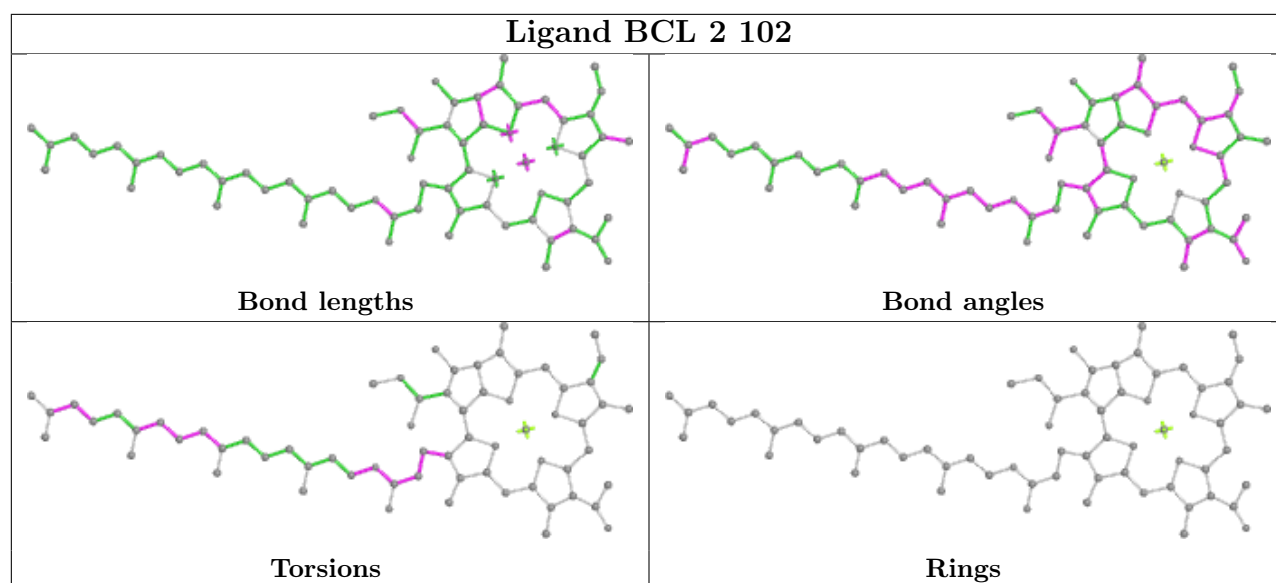
Ligand 8K6 L 307	
	
Bond lengths	Bond angles
	
Torsions	Rings

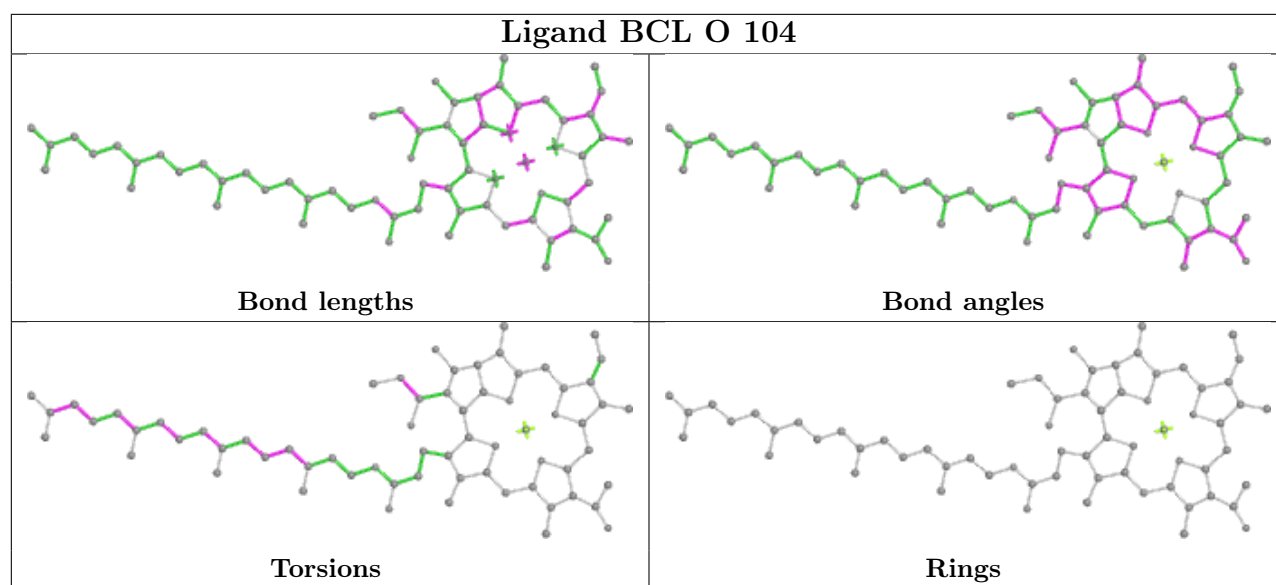
Ligand H4X P 101	
	
Bond lengths	Bond angles
	
Torsions	Rings











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

This section contains visualisations of the EMDB entry EMD-30314. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.