



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:11 PM UTC

PDB ID : 7VRJ / pdb_00007vrj
EMDB ID : EMD-32100
Title : STRUCTURE OF PHOTOSYNTHETIC LH1-RC SUPER-COMPLEX OF
Allochromatium tepidum
Authors : Tani, K.; Kobayashi, K.; Hosogi, N.; Ji, X.-C.; Nagashima, S.; Nagashima,
K.V.P.; Tsukatani, Y.; Kanno, R.; Hall, M.; Yu, L.-J.; Ishikawa, I.; Okura,
Y.; Madigan, M.T.; Mizoguchi, A.; Humbel, B.M.; Kimura, Y.; Wang-Otomo,
Z.-Y.
Deposited on : 2021-10-23
Resolution : 2.81 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:

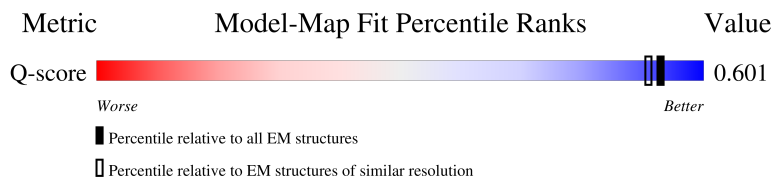
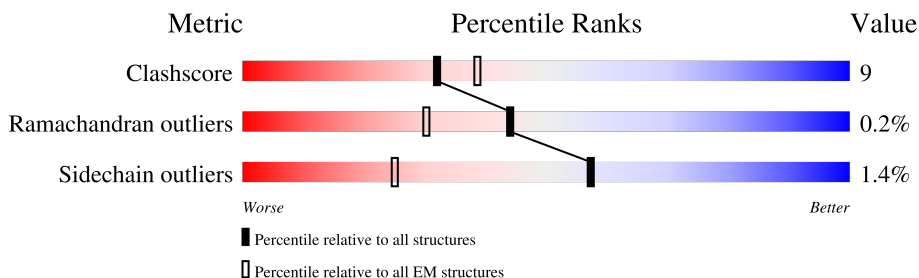
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.81 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11740 (2.31 - 3.31)

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	405	
2	L	277	

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
3	M	324	87% 11% ..
4	H	259	86% 13% .
5	1	44	75% 23% .
5	5	44	84% 14% .
5	7	44	80% 18% .
5	9	44	80% 18% .
5	A	44	84% 16%
5	I	44	82% 11% 7%
5	K	44	86% 14%
5	O	44	89% 11%
5	Q	44	75% 23% .
6	0	46	76% 15% 9%
6	2	46	65% 24% 11%
6	4	46	83% 9% 9%
6	6	46	74% 9% 17%
6	8	46	63% 15% . 20%
6	B	46	83% 13% .
6	J	46	65% 22% 13%
6	N	46	63% 17% . 17%
6	P	46	76% 15% 9%
6	R	46	74% 13% . 11%
7	D	64	61% 16% . 22%
7	F	64	61% 16% 23%
7	S	64	66% 14% . 19%
7	U	64	72% 6% . 20%

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Mol	Chain	Length	Quality of chain
7	W	64	
7	Y	64	
8	E	47	
8	G	47	
8	T	47	
8	V	47	
8	X	47	
8	Z	47	
9	3	67	

2 Entry composition [i](#)

There are 25 unique types of molecules in this entry. The entry contains 26309 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
			Total	C	N	O	S		
1	C	313	2450	1551	427	455	17	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	L	277	2212	1491	354	358	9	0	0

- Molecule 3 is a protein called Photosynthetic reaction center M subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	M	318	2539	1707	409	412	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	H	259	1989	1280	334	367	8	1	0

- Molecule 5 is a protein called Light-harvesting protein LH1 alpha2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A	44	366	251	59	55	1	0	0
5	I	44	366	251	59	55	1	0	0
5	K	44	366	251	59	55	1	0	0
5	O	44	366	251	59	55	1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	Q	44	Total	C	N	O	S	0	0
			366	251	59	55	1		
5	1	44	Total	C	N	O	S	0	0
			366	251	59	55	1		
5	5	43	Total	C	N	O	S	0	0
			355	245	57	52	1		
5	7	44	Total	C	N	O	S	0	0
			362	248	58	55	1		
5	9	43	Total	C	N	O	S	0	0
			359	248	58	52	1		

- Molecule 6 is a protein called Light-harvesting protein LH1 beta1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	44	Total	C	N	O	S	0	0
			359	238	58	61	2		
6	J	40	Total	C	N	O	S	0	0
			331	223	53	54	1		
6	N	38	Total	C	N	O	S	0	0
			320	217	51	51	1		
6	P	42	Total	C	N	O	S	0	0
			345	231	55	57	2		
6	R	41	Total	C	N	O	S	0	0
			339	228	54	55	2		
6	2	41	Total	C	N	O	S	0	0
			339	228	54	55	2		
6	4	42	Total	C	N	O	S	0	0
			345	231	55	57	2		
6	6	38	Total	C	N	O	S	0	0
			320	217	51	51	1		
6	8	37	Total	C	N	O	S	0	0
			312	211	50	50	1		
6	0	42	Total	C	N	O	S	0	0
			345	231	55	57	2		

- Molecule 7 is a protein called Light-harvesting protein LH1 alpha1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	50	Total	C	N	O	S	0	0
			411	279	63	67	2		
7	F	49	Total	C	N	O	S	0	0
			401	273	62	65	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	S	52	Total	C	N	O	S	0	0
			419	283	65	69	2		
7	U	51	Total	C	N	O	S	0	0
			416	282	64	68	2		
7	W	56	Total	C	N	O	S	0	0
			455	306	72	75	2		
7	Y	63	Total	C	N	O	S	0	0
			510	341	83	84	2		

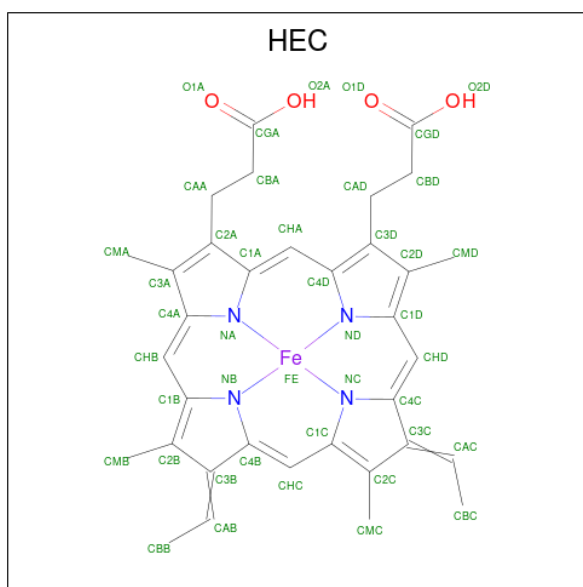
- Molecule 8 is a protein called Light-harvesting protein LH1 beta3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	43	Total	C	N	O	S	0	0
			353	236	55	59	3		
8	G	42	Total	C	N	O	S	0	0
			348	233	54	58	3		
8	T	42	Total	C	N	O	S	0	0
			348	233	54	58	3		
8	V	42	Total	C	N	O	S	0	0
			348	233	54	58	3		
8	X	42	Total	C	N	O	S	0	0
			348	233	54	58	3		
8	Z	41	Total	C	N	O	S	0	0
			342	230	53	56	3		

- Molecule 9 is a protein called Light-harvesting protein LH1 alpha3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	3	65	Total	C	N	O	S	0	0
			499	337	80	79	3		

- Molecule 10 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).

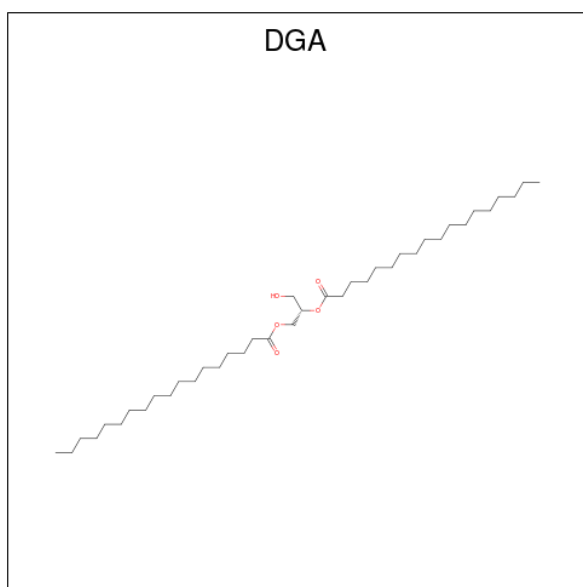


Mol	Chain	Residues	Atoms				AltConf	
10	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
10	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
10	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
10	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

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

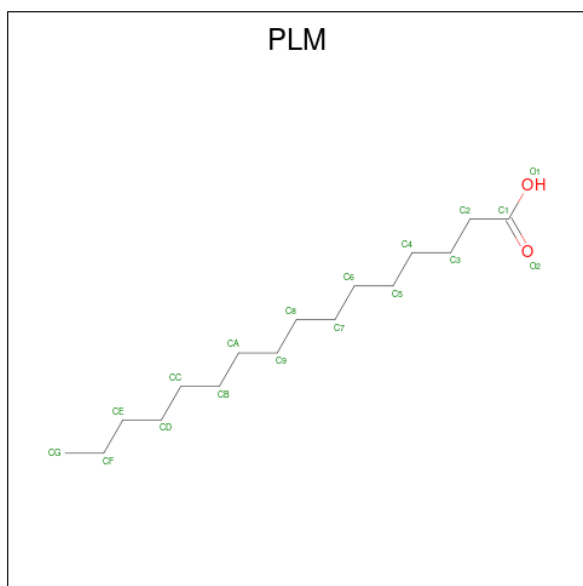
Mol	Chain	Residues	Atoms		AltConf
11	C	1	Total	Mg	0
			1	1	

- Molecule 12 is DIACYL GLYCEROL (CCD ID: DGA) (formula: C₃₉H₇₆O₅).



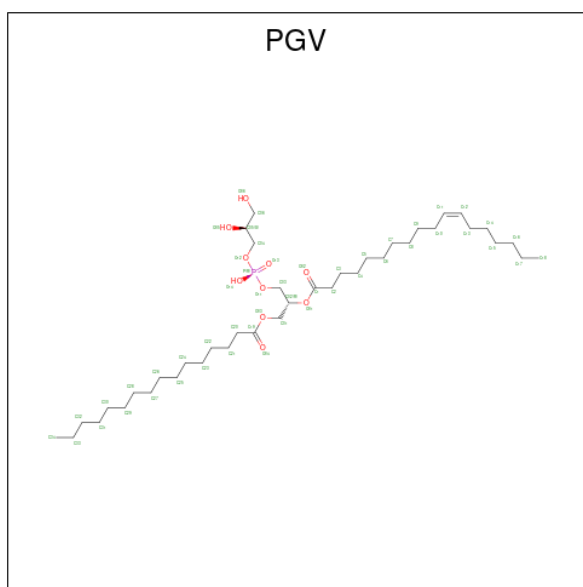
Mol	Chain	Residues	Atoms			AltConf
12	C	1	Total	C	O	0
			17	13	4	

- Molecule 13 is PALMITIC ACID (CCD ID: PLM) (formula: $C_{16}H_{32}O_2$).



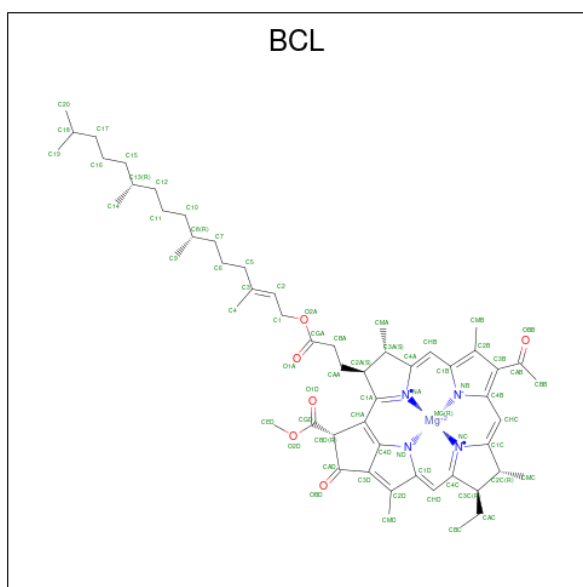
Mol	Chain	Residues	Atoms			AltConf
13	C	1	Total	C	O	0
			12	11	1	

- Molecule 14 is (1R)-2-{{[[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (CCD ID: PGV) (formula: $C_{40}H_{77}O_{10}P$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
14	C	1	31	20	10	1	0
14	L	1	17	8	8	1	0
14	L	1	29	18	10	1	0
14	L	1	39	28	10	1	0
14	L	1	33	22	10	1	0
14	M	1	37	26	10	1	0
14	M	1	31	22	8	1	0
14	M	1	36	25	10	1	0
14	H	1	36	25	10	1	0
14	D	1	35	24	10	1	0
14	1	1	27	18	8	1	0
14	5	1	44	33	10	1	0

- Molecule 15 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	
15	L	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	L	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	L	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	M	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	A	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	B	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	D	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	E	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	F	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	G	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	I	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	J	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	K	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
15	N	1	Total	C	Mg	N	O	0
			66	55	1	4	6	

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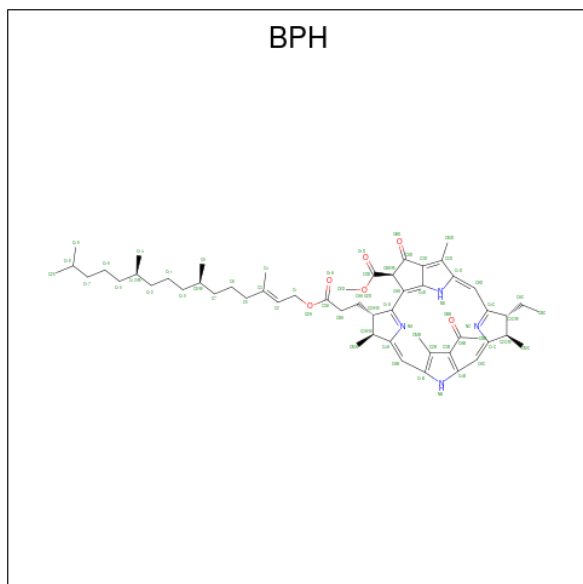
Mol	Chain	Residues	Atoms				AltConf	
			Total	C	Mg	N		O
15	O	1	66	55	1	4	6	0
15	P	1	66	55	1	4	6	0
15	Q	1	66	55	1	4	6	0
15	R	1	66	55	1	4	6	0
15	S	1	66	55	1	4	6	0
15	T	1	66	55	1	4	6	0
15	U	1	66	55	1	4	6	0
15	V	1	66	55	1	4	6	0
15	W	1	66	55	1	4	6	0
15	X	1	66	55	1	4	6	0
15	Y	1	66	55	1	4	6	0
15	Z	1	66	55	1	4	6	0
15	1	1	66	55	1	4	6	0
15	2	1	66	55	1	4	6	0
15	3	1	66	55	1	4	6	0
15	4	1	66	55	1	4	6	0
15	5	1	66	55	1	4	6	0
15	6	1	66	55	1	4	6	0
15	7	1	61	50	1	4	6	0
15	8	1	66	55	1	4	6	0
15	9	1	66	55	1	4	6	0

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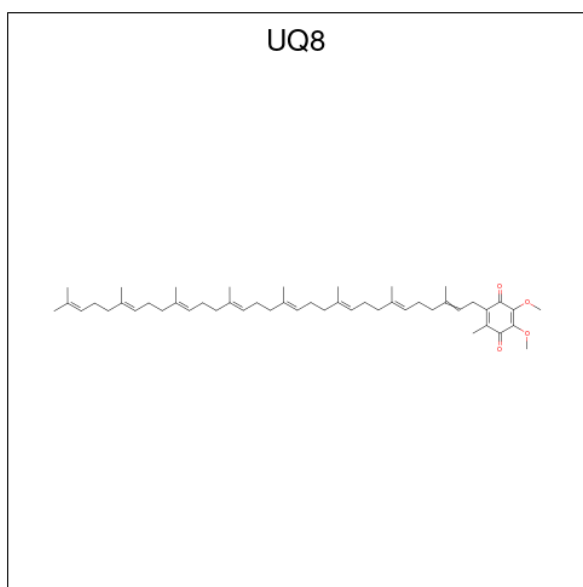
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
15	0	1	66	55	1	4	6	0

- Molecule 16 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$).



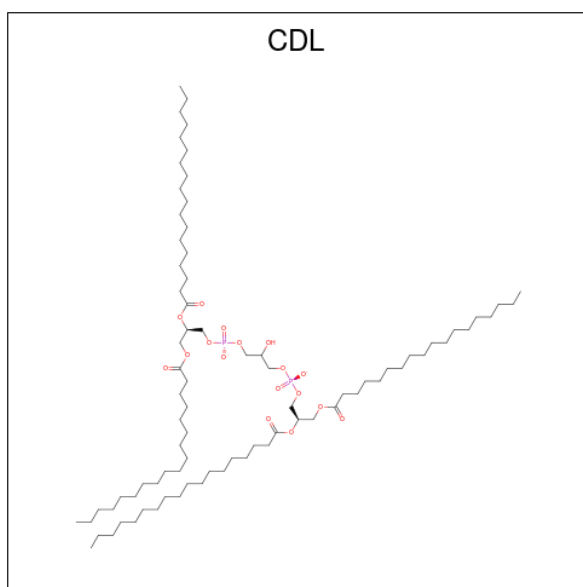
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
16	L	1	65	55	4	6	0
16	M	1	65	55	4	6	0

- Molecule 17 is Ubiquinone-8 (CCD ID: UQ8) (formula: $C_{49}H_{74}O_4$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
17	L	1	33	29	4	0
17	L	1	53	49	4	0
17	L	1	33	29	4	0

- Molecule 18 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
18	L	1	84	65	17	2	0

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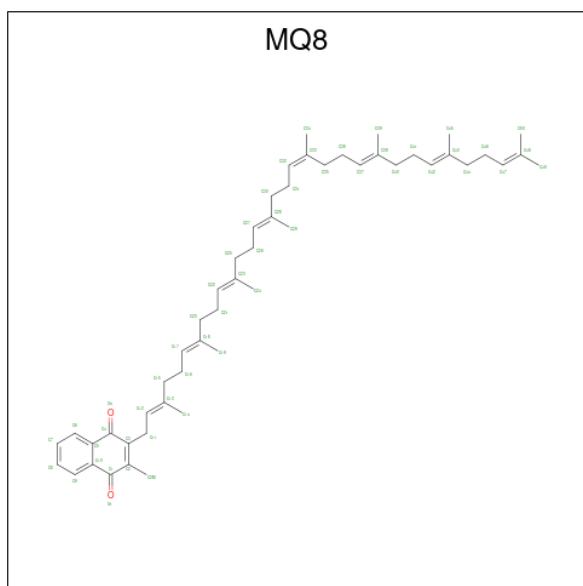
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
18	M	1	39	21	16	2	0
18	M	1	95	76	17	2	0
18	H	1	79	60	17	2	0
18	H	1	35	18	15	2	0
18	D	1	58	39	17	2	0
18	I	1	51	32	17	2	0
18	S	1	65	46	17	2	0

- Molecule 19 is FE (III) ION (CCD ID: FE) (formula: Fe).

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

- Molecule 20 is MENAQUINONE 8 (CCD ID: MQ8) (formula: C₅₁H₇₂O₂).



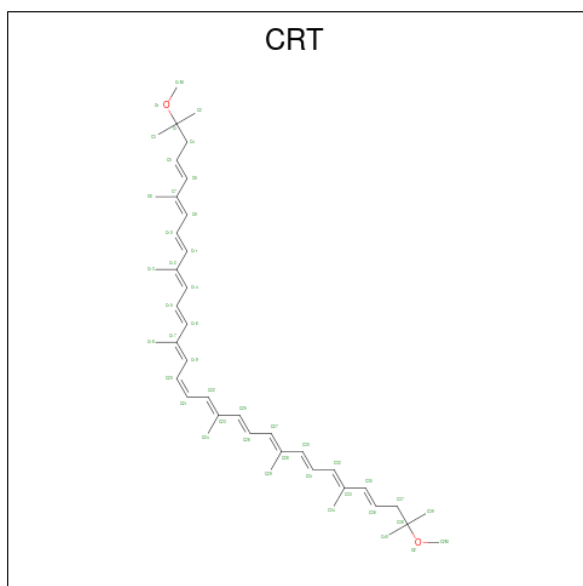
Mol	Chain	Residues	Atoms			AltConf
20	M	1	Total	C	O	0
			53	51	2	

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

- Molecule 21 is SPIRILLOXANTHIN (CCD ID: CRT) (formula: $C_{42}H_{60}O_2$).



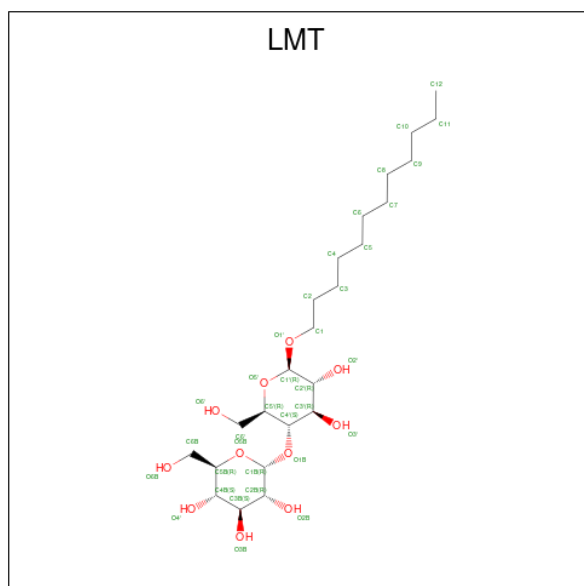
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
21	M	1	44	42	2	0
21	B	1	44	42	2	0
21	E	1	44	42	2	0
21	G	1	44	42	2	0
21	J	1	44	42	2	0
21	N	1	44	42	2	0
21	P	1	44	42	2	0
21	Q	1	44	42	2	0
21	R	1	44	42	2	0
21	S	1	44	42	2	0

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Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
21	X	1	44	42	2	0
21	1	1	44	42	2	0
21	2	1	44	42	2	0
21	4	1	44	42	2	0
21	6	1	44	42	2	0
21	7	1	44	42	2	0
21	8	1	44	42	2	0

- Molecule 22 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula: $C_{24}H_{46}O_{11}$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
22	H	1	35	24	11	0
22	B	1	35	24	11	0
22	E	1	35	24	11	0
22	G	1	35	24	11	0

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Mol	Chain	Residues	Atoms			AltConf
22	J	1	Total	C	O	0
			35	24	11	
22	J	1	Total	C	O	0
			35	24	11	
22	K	1	Total	C	O	0
			35	24	11	
22	N	1	Total	C	O	0
			35	24	11	
22	P	1	Total	C	O	0
			35	24	11	
22	T	1	Total	C	O	0
			35	24	11	
22	V	1	Total	C	O	0
			35	24	11	
22	X	1	Total	C	O	0
			35	24	11	
22	Z	1	Total	C	O	0
			35	24	11	
22	2	1	Total	C	O	0
			35	24	11	
22	4	1	Total	C	O	0
			35	24	11	
22	4	1	Total	C	O	0
			35	24	11	
22	8	1	Total	C	O	0
			35	24	11	
22	0	1	Total	C	O	0
			35	24	11	

- Molecule 23 is CALCIUM ION (CCD ID: CA) (formula: Ca).

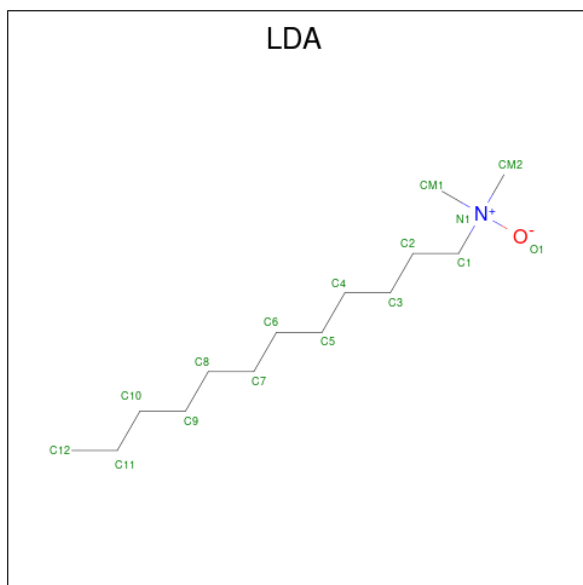
Mol	Chain	Residues	Atoms		AltConf
23	D	1	Total	Ca	0
			1	1	
23	F	1	Total	Ca	0
			1	1	
23	S	1	Total	Ca	0
			1	1	
23	U	1	Total	Ca	0
			1	1	
23	W	1	Total	Ca	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
23	Y	1	Total	Ca	0
			1	1	

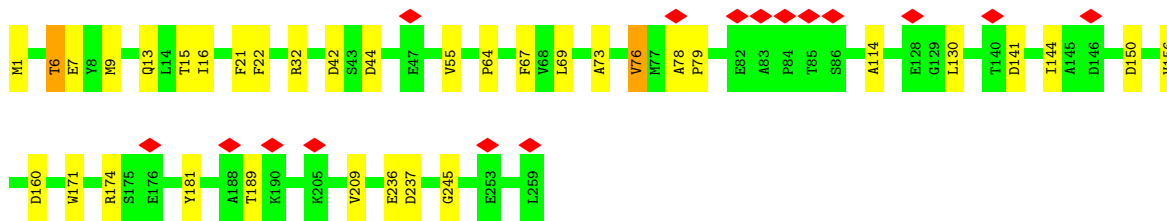
- Molecule 24 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: $C_{14}H_{31}NO$).



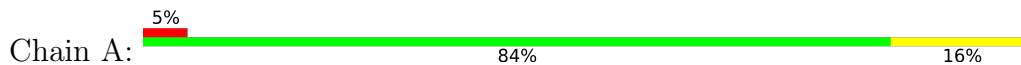
Mol	Chain	Residues	Atoms				AltConf
24	K	1	Total	C	N	O	0
			16	14	1	1	
24	O	1	Total	C	N	O	0
			16	14	1	1	

- Molecule 25 is water.

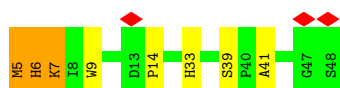
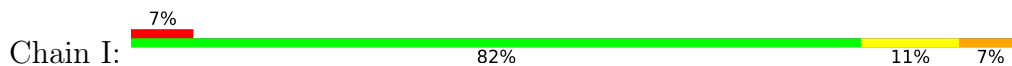
Mol	Chain	Residues	Atoms		AltConf
25	C	18	Total	O	0
			18	18	
25	L	13	Total	O	0
			13	13	
25	M	15	Total	O	0
			15	15	
25	Y	1	Total	O	0
			1	1	
25	3	1	Total	O	0
			1	1	



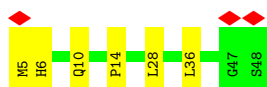
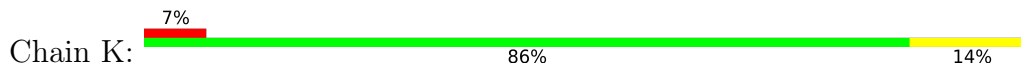
- Molecule 5: Light-harvesting protein LH1 alpha2



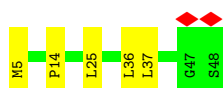
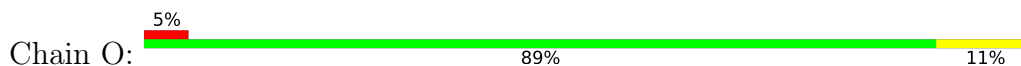
- Molecule 5: Light-harvesting protein LH1 alpha2



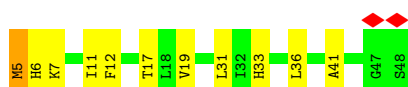
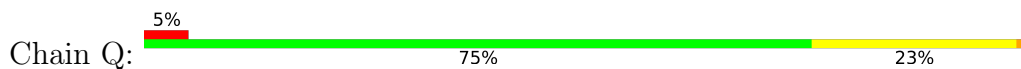
- Molecule 5: Light-harvesting protein LH1 alpha2



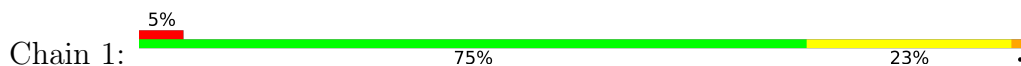
- Molecule 5: Light-harvesting protein LH1 alpha2



- Molecule 5: Light-harvesting protein LH1 alpha2

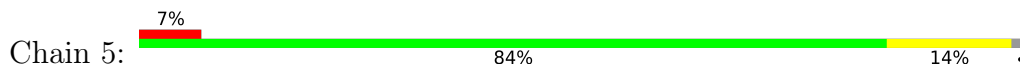


- Molecule 5: Light-harvesting protein LH1 alpha2

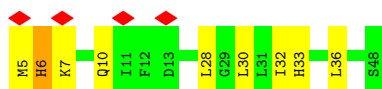
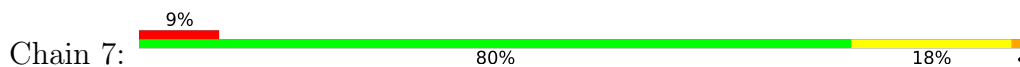




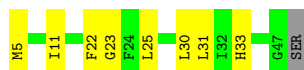
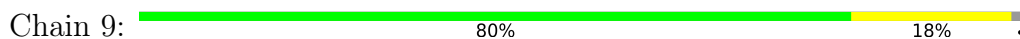
- Molecule 5: Light-harvesting protein LH1 alpha2



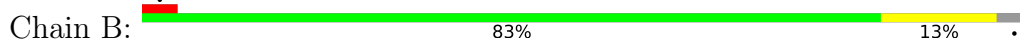
- Molecule 5: Light-harvesting protein LH1 alpha2



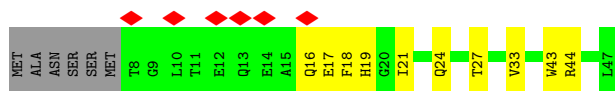
- Molecule 5: Light-harvesting protein LH1 alpha2



- Molecule 6: Light-harvesting protein LH1 beta1



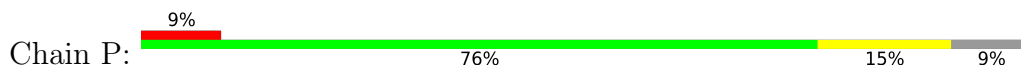
- Molecule 6: Light-harvesting protein LH1 beta1



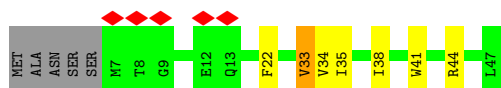
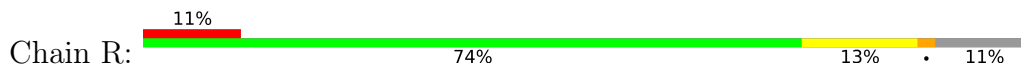
- Molecule 6: Light-harvesting protein LH1 beta1



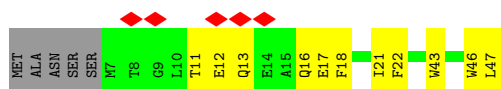
- Molecule 6: Light-harvesting protein LH1 beta1



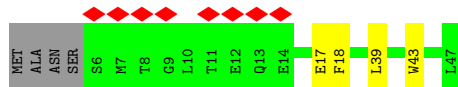
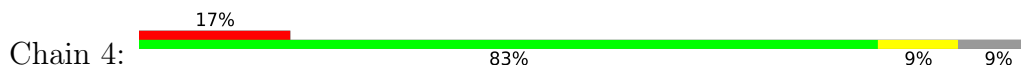
• Molecule 6: Light-harvesting protein LH1 beta1



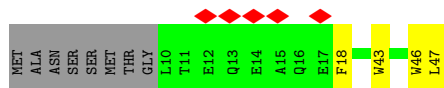
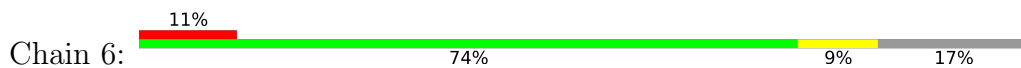
• Molecule 6: Light-harvesting protein LH1 beta1



• Molecule 6: Light-harvesting protein LH1 beta1



• Molecule 6: Light-harvesting protein LH1 beta1



• Molecule 6: Light-harvesting protein LH1 beta1



• Molecule 6: Light-harvesting protein LH1 beta1



• Molecule 7: Light-harvesting protein LH1 alpha1



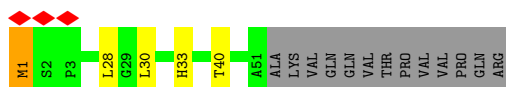
• Molecule 7: Light-harvesting protein LH1 alpha1



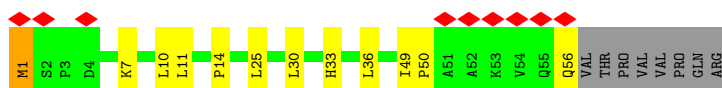
• Molecule 7: Light-harvesting protein LH1 alpha1



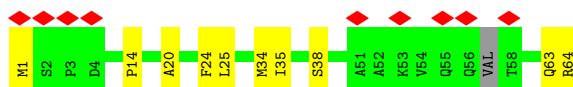
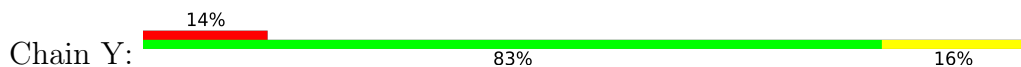
• Molecule 7: Light-harvesting protein LH1 alpha1



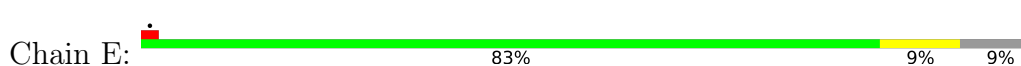
• Molecule 7: Light-harvesting protein LH1 alpha1

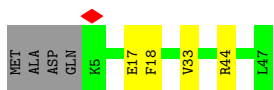


• Molecule 7: Light-harvesting protein LH1 alpha1

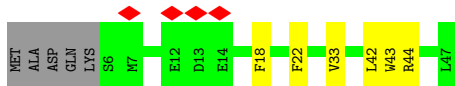
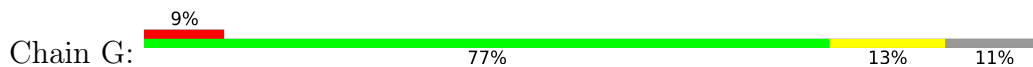


• Molecule 8: Light-harvesting protein LH1 beta3

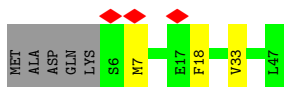
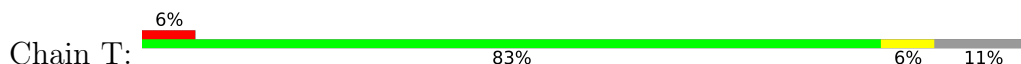




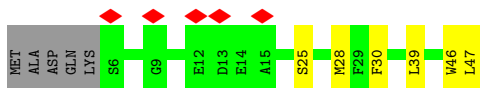
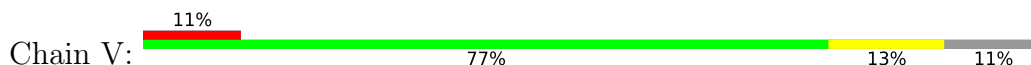
• Molecule 8: Light-harvesting protein LH1 beta3



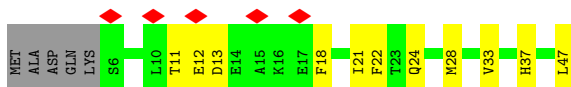
• Molecule 8: Light-harvesting protein LH1 beta3



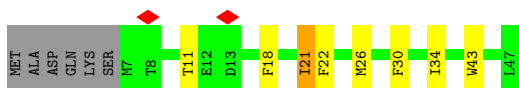
• Molecule 8: Light-harvesting protein LH1 beta3



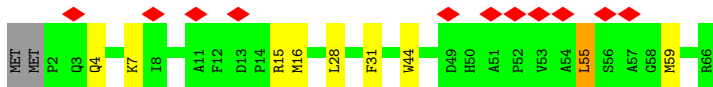
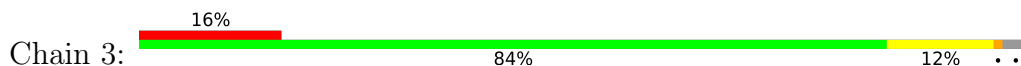
• Molecule 8: Light-harvesting protein LH1 beta3



• Molecule 8: Light-harvesting protein LH1 beta3



• Molecule 9: Light-harvesting protein LH1 alpha3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	156992	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	JEOL CRYO ARM 300	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	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.101	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0134	Depositor
Map size (\AA)	325.6, 325.6, 325.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.814, 0.814, 0.814	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: MQ8, MG, CDL, UQ8, FME, CRT, HEC, FE, DGA, LMT, PLM, LDA, BCL, CA, PGV, BPH

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	0.16	0/2524	0.32	0/3453
2	L	0.18	0/2297	0.38	0/3139
3	M	0.17	0/2639	0.32	0/3611
4	H	0.15	0/2045	0.32	0/2782
5	1	0.14	0/369	0.28	0/500
5	5	0.15	0/358	0.28	0/488
5	7	0.15	0/365	0.32	0/496
5	9	0.15	0/362	0.26	0/492
5	A	0.16	0/369	0.30	0/500
5	I	0.15	0/369	0.28	0/500
5	K	0.14	0/369	0.29	0/500
5	O	0.15	0/369	0.37	0/500
5	Q	0.15	0/369	0.28	0/500
6	0	0.15	0/357	0.26	0/485
6	2	0.15	0/351	0.28	0/477
6	4	0.14	0/357	0.25	0/485
6	6	0.13	0/332	0.30	0/452
6	8	0.15	0/324	0.33	0/441
6	B	0.17	0/371	0.33	0/504
6	J	0.15	0/343	0.28	0/467
6	N	0.14	0/332	0.30	0/452
6	P	0.14	0/357	0.28	0/485
6	R	0.16	0/351	0.31	0/477
7	D	0.15	0/413	0.31	0/566
7	F	0.15	0/413	0.30	0/566
7	S	0.15	0/421	0.36	0/577
7	U	0.15	0/418	0.35	0/573
7	W	0.13	0/457	0.29	0/625
7	Y	0.17	0/513	0.35	0/702
8	E	0.14	0/365	0.27	0/494
8	G	0.15	0/360	0.32	0/487
8	T	0.14	0/360	0.25	0/487

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	V	0.14	0/360	0.30	0/487
8	X	0.15	0/360	0.39	0/487
8	Z	0.14	0/354	0.24	0/479
9	3	0.13	0/517	0.26	0/704
All	All	0.16	0/21590	0.32	0/29420

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2450	0	2362	31	0
2	L	2212	0	2173	25	0
3	M	2539	0	2498	24	0
4	H	1989	0	1993	26	0
5	1	366	0	376	13	0
5	5	355	0	360	4	0
5	7	362	0	365	8	0
5	9	359	0	371	7	0
5	A	366	0	376	5	0
5	I	366	0	376	7	0
5	K	366	0	376	5	0
5	O	366	0	376	5	0
5	Q	366	0	376	10	0
6	0	345	0	334	7	0
6	2	339	0	329	10	0
6	4	345	0	334	4	0
6	6	320	0	310	4	0
6	8	312	0	299	9	0
6	B	359	0	345	6	0
6	J	331	0	320	11	0
6	N	320	0	310	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	P	345	0	334	5	0
6	R	339	0	329	6	0
7	D	411	0	430	9	0
7	F	401	0	419	9	0
7	S	419	0	433	10	0
7	U	416	0	435	5	0
7	W	455	0	478	10	0
7	Y	510	0	537	10	0
8	E	353	0	341	4	0
8	G	348	0	339	7	0
8	T	348	0	339	5	0
8	V	348	0	339	4	0
8	X	348	0	339	7	0
8	Z	342	0	334	8	0
9	3	499	0	506	7	0
10	C	172	0	126	23	0
11	C	1	0	0	0	0
12	C	17	0	15	0	0
13	C	12	0	18	1	0
14	1	27	0	25	2	0
14	5	44	0	56	4	0
14	C	31	0	32	3	0
14	D	35	0	40	0	0
14	H	36	0	42	3	0
14	L	118	0	122	4	0
14	M	104	0	124	3	0
15	0	66	0	74	6	0
15	1	66	0	74	5	0
15	2	66	0	74	5	0
15	3	66	0	74	3	0
15	4	66	0	74	5	0
15	5	66	0	74	3	0
15	6	66	0	74	3	0
15	7	61	0	61	0	0
15	8	66	0	74	8	0
15	9	66	0	74	4	0
15	A	66	0	74	0	0
15	B	66	0	74	5	0
15	D	66	0	74	3	0
15	E	66	0	74	4	0
15	F	66	0	74	4	0
15	G	66	0	74	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	I	66	0	74	1	0
15	J	66	0	74	2	0
15	K	66	0	74	6	0
15	L	198	0	222	8	0
15	M	66	0	74	3	0
15	N	66	0	74	5	0
15	O	66	0	74	3	0
15	P	66	0	74	8	0
15	Q	66	0	74	3	0
15	R	66	0	74	9	0
15	S	66	0	74	2	0
15	T	66	0	74	6	0
15	U	66	0	74	3	0
15	V	66	0	74	5	0
15	W	66	0	74	6	0
15	X	66	0	74	3	0
15	Y	66	0	74	6	0
15	Z	66	0	74	3	0
16	L	65	0	76	4	0
16	M	65	0	76	10	0
17	L	119	0	152	20	0
18	D	58	0	60	4	0
18	H	114	0	126	4	0
18	I	51	0	46	1	0
18	L	84	0	121	1	0
18	M	134	0	168	2	0
18	S	65	0	74	5	0
19	M	1	0	0	0	0
20	M	106	0	144	8	0
21	1	44	0	60	8	0
21	2	44	0	60	5	0
21	4	44	0	60	8	0
21	6	44	0	60	5	0
21	7	44	0	60	4	0
21	8	44	0	60	6	0
21	B	44	0	60	8	0
21	E	44	0	60	4	0
21	G	44	0	60	5	0
21	J	44	0	60	6	0
21	M	44	0	60	3	0
21	N	44	0	60	2	0
21	P	44	0	60	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	Q	44	0	60	6	0
21	R	44	0	60	5	0
21	S	44	0	60	2	0
21	X	44	0	60	5	0
22	0	35	0	46	3	0
22	2	35	0	46	2	0
22	4	70	0	92	4	0
22	8	35	0	46	1	0
22	B	35	0	46	1	0
22	E	35	0	46	0	0
22	G	35	0	46	3	0
22	H	35	0	46	1	0
22	J	70	0	92	1	0
22	K	35	0	46	1	0
22	N	35	0	46	0	0
22	P	35	0	46	1	0
22	T	35	0	46	0	0
22	V	35	0	46	3	0
22	X	35	0	46	0	0
22	Z	35	0	46	2	0
23	D	1	0	0	0	0
23	F	1	0	0	0	0
23	S	1	0	0	0	0
23	U	1	0	0	0	0
23	W	1	0	0	0	0
23	Y	1	0	0	0	0
24	K	16	0	31	1	0
24	O	16	0	31	2	0
25	3	1	0	0	0	0
25	C	18	0	0	0	0
25	L	13	0	0	0	0
25	M	15	0	0	1	0
25	Y	1	0	0	1	0
All	All	26309	0	27095	457	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 9.

The worst 5 of 457 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:309:CYS:SG	10:C:504:HEC:HAB	1.53	1.48
1:C:252:CYS:SG	10:C:503:HEC:HAC	1.59	1.41
1:C:309:CYS:SG	10:C:504:HEC:CAB	2.07	1.40
1:C:110:CYS:SG	10:C:501:HEC:HAC	1.62	1.40
1:C:157:CYS:SG	10:C:502:HEC:HAC	1.64	1.38

There are no symmetry-related clashes.

5.3 Torsion angles [\(i\)](#)

5.3.1 Protein backbone [\(i\)](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	311/405 (77%)	297 (96%)	14 (4%)	0	100	100
2	L	275/277 (99%)	268 (98%)	7 (2%)	0	100	100
3	M	316/324 (98%)	309 (98%)	7 (2%)	0	100	100
4	H	258/259 (100%)	245 (95%)	13 (5%)	0	100	100
5	1	42/44 (96%)	40 (95%)	1 (2%)	1 (2%)	4	16
5	5	41/44 (93%)	40 (98%)	0	1 (2%)	4	16
5	7	42/44 (96%)	37 (88%)	4 (10%)	1 (2%)	4	16
5	9	41/44 (93%)	39 (95%)	2 (5%)	0	100	100
5	A	42/44 (96%)	42 (100%)	0	0	100	100
5	I	42/44 (96%)	40 (95%)	1 (2%)	1 (2%)	4	16
5	K	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
5	O	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
5	Q	42/44 (96%)	40 (95%)	1 (2%)	1 (2%)	4	16
6	0	40/46 (87%)	40 (100%)	0	0	100	100
6	2	39/46 (85%)	39 (100%)	0	0	100	100
6	4	40/46 (87%)	38 (95%)	2 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	6	36/46 (78%)	34 (94%)	2 (6%)	0	100	100
6	8	35/46 (76%)	34 (97%)	1 (3%)	0	100	100
6	B	42/46 (91%)	41 (98%)	1 (2%)	0	100	100
6	J	38/46 (83%)	37 (97%)	1 (3%)	0	100	100
6	N	36/46 (78%)	35 (97%)	1 (3%)	0	100	100
6	P	40/46 (87%)	40 (100%)	0	0	100	100
6	R	39/46 (85%)	39 (100%)	0	0	100	100
7	D	48/64 (75%)	46 (96%)	2 (4%)	0	100	100
7	F	47/64 (73%)	47 (100%)	0	0	100	100
7	S	50/64 (78%)	49 (98%)	1 (2%)	0	100	100
7	U	49/64 (77%)	48 (98%)	1 (2%)	0	100	100
7	W	54/64 (84%)	53 (98%)	1 (2%)	0	100	100
7	Y	59/64 (92%)	56 (95%)	3 (5%)	0	100	100
8	E	41/47 (87%)	40 (98%)	1 (2%)	0	100	100
8	G	40/47 (85%)	40 (100%)	0	0	100	100
8	T	40/47 (85%)	40 (100%)	0	0	100	100
8	V	40/47 (85%)	39 (98%)	1 (2%)	0	100	100
8	X	40/47 (85%)	39 (98%)	0	1 (2%)	4	15
8	Z	39/47 (83%)	39 (100%)	0	0	100	100
9	3	63/67 (94%)	59 (94%)	4 (6%)	0	100	100
All	All	2531/2854 (89%)	2451 (97%)	74 (3%)	6 (0%)	44	71

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	X	12	GLU
5	7	6	HIS
5	Q	6	HIS
5	5	6	HIS
5	1	6	HIS

5.3.2 Protein sidechains [i](#)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	265/322 (82%)	265 (100%)	0	100	100
2	L	224/224 (100%)	223 (100%)	1 (0%)	84	94
3	M	252/256 (98%)	246 (98%)	6 (2%)	43	75
4	H	208/208 (100%)	204 (98%)	4 (2%)	50	79
5	1	38/38 (100%)	38 (100%)	0	100	100
5	5	36/38 (95%)	36 (100%)	0	100	100
5	7	37/38 (97%)	37 (100%)	0	100	100
5	9	37/38 (97%)	37 (100%)	0	100	100
5	A	38/38 (100%)	38 (100%)	0	100	100
5	I	38/38 (100%)	37 (97%)	1 (3%)	40	73
5	K	38/38 (100%)	38 (100%)	0	100	100
5	O	38/38 (100%)	38 (100%)	0	100	100
5	Q	38/38 (100%)	37 (97%)	1 (3%)	40	73
6	0	35/38 (92%)	35 (100%)	0	100	100
6	2	34/38 (90%)	33 (97%)	1 (3%)	37	71
6	4	35/38 (92%)	35 (100%)	0	100	100
6	6	32/38 (84%)	32 (100%)	0	100	100
6	8	31/38 (82%)	29 (94%)	2 (6%)	15	42
6	B	37/38 (97%)	37 (100%)	0	100	100
6	J	33/38 (87%)	33 (100%)	0	100	100
6	N	32/38 (84%)	31 (97%)	1 (3%)	35	69
6	P	35/38 (92%)	32 (91%)	3 (9%)	10	29
6	R	34/38 (90%)	33 (97%)	1 (3%)	37	71
7	D	44/56 (79%)	43 (98%)	1 (2%)	44	76
7	F	44/56 (79%)	43 (98%)	1 (2%)	44	76
7	S	43/56 (77%)	42 (98%)	1 (2%)	44	76
7	U	44/56 (79%)	44 (100%)	0	100	100
7	W	48/56 (86%)	47 (98%)	1 (2%)	47	78
7	Y	55/56 (98%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	E	36/40 (90%)	36 (100%)	0	100	100
8	G	36/40 (90%)	36 (100%)	0	100	100
8	T	36/40 (90%)	36 (100%)	0	100	100
8	V	36/40 (90%)	36 (100%)	0	100	100
8	X	36/40 (90%)	34 (94%)	2 (6%)	19	48
8	Z	35/40 (88%)	33 (94%)	2 (6%)	18	47
9	3	49/51 (96%)	47 (96%)	2 (4%)	27	60
All	All	2167/2359 (92%)	2136 (99%)	31 (1%)	57	84

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	N	34	VAL
9	3	16	MET
6	P	38	ILE
6	8	18	PHE
8	Z	11	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
5	A	6	HIS
5	7	10	GLN
6	J	13	GLN
6	8	16	GLN
9	3	50	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

14 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	A	5	5	8,9,10	0.54	0	8,9,11	0.95	1 (12%)
5	FME	O	5	5	8,9,10	0.57	0	8,9,11	0.95	1 (12%)
7	FME	D	1	7	8,9,10	0.57	0	8,9,11	0.97	1 (12%)
5	FME	K	5	5	8,9,10	0.54	0	8,9,11	1.22	1 (12%)
5	FME	7	5	5	8,9,10	0.55	0	8,9,11	0.97	1 (12%)
7	FME	W	1	7	8,9,10	0.56	0	8,9,11	0.93	1 (12%)
5	FME	9	5	5	8,9,10	0.52	0	8,9,11	1.02	1 (12%)
7	FME	U	1	7	8,9,10	0.56	0	8,9,11	0.97	1 (12%)
5	FME	5	5	5	8,9,10	0.58	0	8,9,11	0.98	1 (12%)
7	FME	S	1	7	8,9,10	0.55	0	8,9,11	0.93	1 (12%)
7	FME	Y	1	7	8,9,10	0.56	0	8,9,11	0.96	1 (12%)
5	FME	I	5	5	8,9,10	0.54	0	8,9,11	1.05	1 (12%)
5	FME	1	5	5	8,9,10	0.54	0	8,9,11	1.00	1 (12%)
5	FME	Q	5	5	8,9,10	0.55	0	8,9,11	0.96	1 (12%)

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	A	5	5	-	2/7/9/11	-
5	FME	O	5	5	-	0/7/9/11	-
7	FME	D	1	7	-	1/7/9/11	-
5	FME	K	5	5	-	1/7/9/11	-
5	FME	7	5	5	-	0/7/9/11	-
7	FME	W	1	7	-	0/7/9/11	-
5	FME	9	5	5	-	1/7/9/11	-
7	FME	U	1	7	-	0/7/9/11	-
5	FME	5	5	5	-	3/7/9/11	-
7	FME	S	1	7	-	2/7/9/11	-
7	FME	Y	1	7	-	0/7/9/11	-
5	FME	I	5	5	-	1/7/9/11	-
5	FME	1	5	5	-	0/7/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FME	Q	5	5	-	1/7/9/11	-

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	K	5	FME	O-C-CA	-2.68	117.87	124.77
5	I	5	FME	O-C-CA	-2.67	117.91	124.77
5	Q	5	FME	O-C-CA	-2.59	118.11	124.77
5	7	5	FME	O-C-CA	-2.59	118.11	124.77
5	9	5	FME	O-C-CA	-2.57	118.16	124.77

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	5	FME	N-CA-CB-CG
5	K	5	FME	CB-CA-N-CN
5	Q	5	FME	O-C-CA-CB
5	5	5	FME	O1-CN-N-CA
5	5	5	FME	CB-CA-N-CN

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	1	FME	1	0
7	W	1	FME	1	0
7	U	1	FME	1	0
5	I	5	FME	1	0
5	Q	5	FME	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 114 ligands modelled in this entry, 8 are monoatomic - leaving 106 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	$\# Z > 2$
15	BCL	5	102	-	69,74,74	1.80	17 (24%)	79,115,115	2.25	25 (31%)
22	LMT	B	101	-	36,36,36	0.40	0	47,47,47	0.67	0
10	HEC	C	501	1	46,50,50	1.75	10 (21%)	58,82,82	1.58	10 (17%)
15	BCL	3	101	-	69,74,74	1.81	18 (26%)	79,115,115	2.15	20 (25%)
21	CRT	Q	102	-	43,43,43	0.63	0	48,54,54	2.12	15 (31%)
22	LMT	N	103	-	36,36,36	0.40	0	47,47,47	0.65	0
15	BCL	N	101	-	69,74,74	1.81	18 (26%)	79,115,115	2.20	24 (30%)
21	CRT	8	103	-	43,43,43	0.62	0	48,54,54	2.00	13 (27%)
15	BCL	B	102	-	69,74,74	1.78	17 (24%)	79,115,115	2.13	24 (30%)
22	LMT	4	104	-	36,36,36	0.40	0	47,47,47	0.71	1 (2%)
18	CDL	S	101	-	64,64,99	1.15	4 (6%)	70,76,111	1.16	6 (8%)
21	CRT	N	102	-	43,43,43	0.66	0	48,54,54	2.00	12 (25%)
18	CDL	H	301	-	78,78,99	1.03	4 (5%)	84,90,111	1.10	5 (5%)
15	BCL	G	102	-	69,74,74	1.77	17 (24%)	79,115,115	2.17	25 (31%)
14	PGV	M	411	-	35,35,50	1.08	2 (5%)	38,41,56	1.28	4 (10%)
15	BCL	1	403	-	69,74,74	1.78	17 (24%)	79,115,115	2.22	22 (27%)
18	CDL	D	102	-	57,57,99	1.12	4 (7%)	63,69,111	1.17	4 (6%)
12	DGA	C	506	1	16,16,43	1.77	3 (18%)	18,18,45	1.87	3 (16%)
15	BCL	Z	102	-	69,74,74	1.76	17 (24%)	79,115,115	2.19	23 (29%)
21	CRT	4	103	-	43,43,43	0.62	0	48,54,54	2.00	11 (22%)
15	BCL	V	102	-	69,74,74	1.77	18 (26%)	79,115,115	2.24	24 (30%)
21	CRT	R	102	-	43,43,43	0.63	0	48,54,54	1.99	15 (31%)
22	LMT	Z	101	-	36,36,36	0.39	0	47,47,47	0.80	0
24	LDA	O	501	-	13,15,15	2.18	2 (15%)	14,17,17	0.48	0
15	BCL	W	101	-	69,74,74	1.76	16 (23%)	79,115,115	2.34	25 (31%)
18	CDL	H	302	-	34,34,99	1.22	3 (8%)	39,44,111	1.08	3 (7%)
20	MQ8	M	406	-	54,54,54	1.35	2 (3%)	67,69,69	1.72	19 (28%)
17	UQ8	L	504	-	33,33,53	1.56	2 (6%)	42,43,67	1.53	8 (19%)
15	BCL	Y	101	-	69,74,74	1.79	16 (23%)	79,115,115	2.26	22 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	LMT	0	101	-	36,36,36	0.45	0	47,47,47	0.90	1 (2%)
10	HEC	C	502	1	46,50,50	1.73	11 (23%)	58,82,82	1.63	13 (22%)
10	HEC	C	504	1	46,50,50	1.75	10 (21%)	58,82,82	1.60	11 (18%)
24	LDA	K	101	-	13,15,15	2.19	2 (15%)	14,17,17	0.52	0
15	BCL	S	102	-	69,74,74	1.77	17 (24%)	79,115,115	2.21	22 (27%)
14	PGV	D	101	-	34,34,50	1.10	2 (5%)	37,40,56	1.07	2 (5%)
15	BCL	R	101	-	69,74,74	1.76	17 (24%)	79,115,115	2.17	23 (29%)
15	BCL	8	102	-	69,74,74	1.77	16 (23%)	79,115,115	2.20	25 (31%)
15	BCL	0	102	-	69,74,74	1.76	17 (24%)	79,115,115	2.21	24 (30%)
14	PGV	H	303	-	35,35,50	1.12	2 (5%)	38,41,56	1.10	2 (5%)
22	LMT	X	101	-	36,36,36	0.45	0	47,47,47	0.87	3 (6%)
21	CRT	X	103	-	43,43,43	0.64	0	48,54,54	2.11	13 (27%)
15	BCL	2	102	-	69,74,74	1.78	17 (24%)	79,115,115	2.15	23 (29%)
22	LMT	J	104	-	36,36,36	0.41	0	47,47,47	0.66	0
22	LMT	J	101	-	36,36,36	0.39	0	47,47,47	0.74	0
22	LMT	K	102	-	36,36,36	0.40	0	47,47,47	0.76	0
20	MQ8	M	404	-	54,54,54	1.32	2 (3%)	67,69,69	1.48	14 (20%)
21	CRT	J	103	-	43,43,43	0.66	0	48,54,54	2.23	15 (31%)
14	PGV	L	501	-	16,16,50	1.41	2 (12%)	19,21,56	1.36	3 (15%)
21	CRT	E	103	-	43,43,43	0.62	0	48,54,54	2.01	15 (31%)
15	BCL	L	502	-	69,74,74	1.78	17 (24%)	79,115,115	2.22	24 (30%)
15	BCL	L	509	-	69,74,74	1.78	17 (24%)	79,115,115	2.23	23 (29%)
21	CRT	1	402	-	43,43,43	0.65	0	48,54,54	1.99	16 (33%)
17	UQ8	L	512	-	33,33,53	1.60	2 (6%)	42,43,67	1.54	9 (21%)
14	PGV	M	409	-	30,30,50	1.22	2 (6%)	33,35,56	1.30	3 (9%)
18	CDL	M	408	-	38,38,99	1.29	3 (7%)	43,49,111	1.20	5 (11%)
14	PGV	L	507	-	38,38,50	1.02	2 (5%)	41,44,56	1.15	3 (7%)
21	CRT	6	102	-	43,43,43	0.63	0	48,54,54	2.14	17 (35%)
22	LMT	P	103	-	36,36,36	0.39	0	47,47,47	0.75	1 (2%)
15	BCL	A	101	-	69,74,74	1.78	18 (26%)	79,115,115	2.25	24 (30%)
15	BCL	M	402	-	69,74,74	1.80	17 (24%)	79,115,115	2.34	24 (30%)
15	BCL	E	102	-	69,74,74	1.77	18 (26%)	79,115,115	2.19	26 (32%)
22	LMT	2	101	-	36,36,36	0.42	0	47,47,47	0.69	0
15	BCL	Q	101	-	69,74,74	1.78	17 (24%)	79,115,115	2.26	22 (27%)
14	PGV	C	508	-	30,30,50	1.16	2 (6%)	33,36,56	1.30	4 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
14	PGV	L	506	-	28,28,50	1.21	2 (7%)	31,34,56	1.22	4 (12%)
22	LMT	E	101	-	36,36,36	0.43	0	47,47,47	0.93	3 (6%)
15	BCL	O	502	-	69,74,74	1.79	17 (24%)	79,115,115	2.24	22 (27%)
15	BCL	I	102	-	69,74,74	1.79	17 (24%)	79,115,115	2.18	21 (26%)
22	LMT	4	101	-	36,36,36	0.46	0	47,47,47	0.97	1 (2%)
18	CDL	I	101	-	50,50,99	1.29	4 (8%)	56,62,111	1.36	8 (14%)
10	HEC	C	503	1	46,50,50	1.76	11 (23%)	58,82,82	1.56	12 (20%)
22	LMT	V	101	-	36,36,36	0.44	0	47,47,47	0.69	1 (2%)
22	LMT	T	101	-	36,36,36	0.41	0	47,47,47	0.65	1 (2%)
16	BPH	M	403	-	59,70,70	0.78	3 (5%)	59,101,101	0.85	2 (3%)
21	CRT	B	103	-	43,43,43	0.64	0	48,54,54	2.06	14 (29%)
15	BCL	9	101	-	69,74,74	1.78	17 (24%)	79,115,115	2.26	23 (29%)
21	CRT	M	405	-	43,43,43	0.63	0	48,54,54	1.98	11 (22%)
17	UQ8	L	505	-	53,53,53	1.25	2 (3%)	66,67,67	1.79	21 (31%)
14	PGV	5	101	-	43,43,50	0.98	2 (4%)	46,49,56	1.04	2 (4%)
21	CRT	S	104	-	43,43,43	0.66	0	48,54,54	2.27	15 (31%)
15	BCL	7	101	-	64,69,74	1.82	16 (25%)	73,109,115	2.38	24 (32%)
16	BPH	L	503	-	59,70,70	0.78	2 (3%)	59,101,101	0.88	3 (5%)
22	LMT	8	101	-	36,36,36	0.41	0	47,47,47	0.75	1 (2%)
15	BCL	F	101	-	69,74,74	1.78	16 (23%)	79,115,115	2.33	24 (30%)
15	BCL	D	103	-	69,74,74	1.78	17 (24%)	79,115,115	2.23	21 (26%)
14	PGV	L	511	-	32,32,50	1.12	2 (6%)	35,38,56	1.28	5 (14%)
15	BCL	T	102	-	69,74,74	1.74	16 (23%)	79,115,115	2.17	23 (29%)
15	BCL	L	508	-	69,74,74	1.75	18 (26%)	79,115,115	2.28	21 (26%)
15	BCL	X	102	-	69,74,74	1.77	17 (24%)	79,115,115	2.23	24 (30%)
21	CRT	2	103	-	43,43,43	0.68	0	48,54,54	2.20	17 (35%)
15	BCL	P	101	-	69,74,74	1.78	17 (24%)	79,115,115	2.22	24 (30%)
15	BCL	4	102	-	69,74,74	1.78	17 (24%)	79,115,115	2.26	24 (30%)
15	BCL	J	102	-	69,74,74	1.77	17 (24%)	79,115,115	2.15	20 (25%)
22	LMT	H	304	-	36,36,36	0.42	0	47,47,47	0.71	1 (2%)
18	CDL	L	510	-	83,83,99	1.05	4 (4%)	89,95,111	1.24	8 (8%)
18	CDL	M	410	-	94,94,99	0.95	4 (4%)	100,106,111	1.09	7 (7%)
22	LMT	G	101	-	36,36,36	0.42	0	47,47,47	0.76	1 (2%)
15	BCL	U	101	-	69,74,74	1.80	18 (26%)	79,115,115	2.29	22 (27%)
14	PGV	1	401	-	26,26,50	1.30	2 (7%)	29,31,56	1.19	2 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
13	PLM	C	507	-	10,11,17	0.36	0	9,10,17	0.35	0
21	CRT	G	103	-	43,43,43	0.65	0	48,54,54	1.94	13 (27%)
15	BCL	6	101	-	69,74,74	1.77	17 (24%)	79,115,115	2.16	23 (29%)
15	BCL	K	103	-	69,74,74	1.80	16 (23%)	79,115,115	2.25	23 (29%)
21	CRT	P	102	-	43,43,43	0.67	0	48,54,54	2.21	11 (22%)
21	CRT	7	102	-	43,43,43	0.63	0	48,54,54	1.99	14 (29%)
14	PGV	M	407	-	36,36,50	1.06	2 (5%)	39,42,56	1.15	3 (7%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	BCL	5	102	-	-	17/41/137/137	-
22	LMT	B	101	-	-	7/21/61/61	0/2/2/2
10	HEC	C	501	1	-	6/14/54/54	-
15	BCL	3	101	-	-	12/41/137/137	-
21	CRT	Q	102	-	-	5/51/51/51	-
22	LMT	N	103	-	-	4/21/61/61	0/2/2/2
15	BCL	N	101	-	-	11/41/137/137	-
21	CRT	8	103	-	-	4/51/51/51	-
15	BCL	B	102	-	-	15/41/137/137	-
22	LMT	4	104	-	-	1/21/61/61	0/2/2/2
18	CDL	S	101	-	-	19/75/75/110	-
21	CRT	N	102	-	-	4/51/51/51	-
18	CDL	H	301	-	-	29/89/89/110	-
15	BCL	G	102	-	-	14/41/137/137	-
14	PGV	M	411	-	-	11/40/40/55	-
15	BCL	1	403	-	-	13/41/137/137	-
18	CDL	D	102	-	-	26/67/67/110	-
12	DGA	C	506	1	-	9/16/16/45	-
15	BCL	Z	102	-	-	18/41/137/137	-
21	CRT	4	103	-	-	4/51/51/51	-
15	BCL	V	102	-	-	19/41/137/137	-
21	CRT	R	102	-	-	2/51/51/51	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	LMT	Z	101	-	-	8/21/61/61	0/2/2/2
24	LDA	O	501	-	-	1/13/13/13	-
15	BCL	W	101	-	-	16/41/137/137	-
18	CDL	H	302	-	-	12/41/41/110	-
20	MQ8	M	406	-	-	7/47/67/67	0/2/2/2
17	UQ8	L	504	-	-	5/27/51/75	0/1/1/1
15	BCL	Y	101	-	-	17/41/137/137	-
22	LMT	0	101	-	-	4/21/61/61	0/2/2/2
10	HEC	C	502	1	-	8/14/54/54	-
10	HEC	C	504	1	-	6/14/54/54	-
24	LDA	K	101	-	-	5/13/13/13	-
15	BCL	S	102	-	-	12/41/137/137	-
14	PGV	D	101	-	-	14/39/39/55	-
15	BCL	R	101	-	-	11/41/137/137	-
15	BCL	8	102	-	-	15/41/137/137	-
15	BCL	0	102	-	-	11/41/137/137	-
14	PGV	H	303	-	-	9/40/40/55	-
22	LMT	X	101	-	-	1/21/61/61	0/2/2/2
21	CRT	X	103	-	-	6/51/51/51	-
15	BCL	2	102	-	-	12/41/137/137	-
22	LMT	J	104	-	-	1/21/61/61	0/2/2/2
22	LMT	J	101	-	-	5/21/61/61	0/2/2/2
22	LMT	K	102	-	-	4/21/61/61	0/2/2/2
20	MQ8	M	404	-	-	6/47/67/67	0/2/2/2
21	CRT	J	103	-	-	3/51/51/51	-
14	PGV	L	501	-	-	2/17/17/55	-
21	CRT	E	103	-	-	4/51/51/51	-
15	BCL	L	502	-	-	12/41/137/137	-
15	BCL	L	509	-	-	14/41/137/137	-
21	CRT	1	402	-	-	14/51/51/51	-
17	UQ8	L	512	-	-	5/27/51/75	0/1/1/1
14	PGV	M	409	-	-	6/32/32/55	-
18	CDL	M	408	-	-	16/48/48/110	-
14	PGV	L	507	-	-	17/43/43/55	-
21	CRT	6	102	-	-	8/51/51/51	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	LMT	P	103	-	-	4/21/61/61	0/2/2/2
15	BCL	A	101	-	-	14/41/137/137	-
15	BCL	M	402	-	-	22/41/137/137	-
15	BCL	E	102	-	-	17/41/137/137	-
22	LMT	2	101	-	-	1/21/61/61	0/2/2/2
15	BCL	Q	101	-	-	16/41/137/137	-
14	PGV	C	508	-	-	11/35/35/55	-
14	PGV	L	506	-	-	9/33/33/55	-
22	LMT	E	101	-	-	6/21/61/61	0/2/2/2
15	BCL	O	502	-	-	13/41/137/137	-
15	BCL	I	102	-	-	14/41/137/137	-
22	LMT	4	101	-	-	3/21/61/61	0/2/2/2
18	CDL	I	101	-	-	12/61/61/110	-
10	HEC	C	503	1	-	4/14/54/54	-
22	LMT	V	101	-	-	6/21/61/61	0/2/2/2
22	LMT	T	101	-	-	5/21/61/61	0/2/2/2
16	BPH	M	403	-	-	8/37/105/105	0/5/6/6
21	CRT	B	103	-	-	9/51/51/51	-
15	BCL	9	101	-	-	13/41/137/137	-
21	CRT	M	405	-	-	9/51/51/51	-
17	UQ8	L	505	-	-	15/51/75/75	0/1/1/1
14	PGV	5	101	-	-	13/48/48/55	-
21	CRT	S	104	-	-	9/51/51/51	-
15	BCL	7	101	-	-	7/35/131/137	-
16	BPH	L	503	-	-	4/37/105/105	0/5/6/6
22	LMT	8	101	-	-	3/21/61/61	0/2/2/2
15	BCL	F	101	-	-	13/41/137/137	-
15	BCL	D	103	-	-	14/41/137/137	-
14	PGV	L	511	-	-	9/37/37/55	-
15	BCL	T	102	-	-	12/41/137/137	-
15	BCL	L	508	-	-	10/41/137/137	-
15	BCL	X	102	-	-	17/41/137/137	-
21	CRT	2	103	-	-	5/51/51/51	-
15	BCL	P	101	-	-	23/41/137/137	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	BCL	4	102	-	-	19/41/137/137	-
15	BCL	J	102	-	-	13/41/137/137	-
22	LMT	H	304	-	-	1/21/61/61	0/2/2/2
18	CDL	L	510	-	-	29/93/93/110	-
18	CDL	M	410	-	-	34/105/105/110	-
22	LMT	G	101	-	-	5/21/61/61	0/2/2/2
15	BCL	U	101	-	-	15/41/137/137	-
14	PGV	1	401	-	-	12/30/30/55	-
13	PLM	C	507	-	-	1/9/9/15	-
21	CRT	G	103	-	-	7/51/51/51	-
15	BCL	6	101	-	-	17/41/137/137	-
15	BCL	K	103	-	-	14/41/137/137	-
21	CRT	P	102	-	-	8/51/51/51	-
21	CRT	7	102	-	-	4/51/51/51	-
14	PGV	M	407	-	-	4/41/41/55	-

The worst 5 of 730 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	L	512	UQ8	C6-C1	7.99	1.49	1.35
20	M	406	MQ8	C3-C2	7.97	1.49	1.35
20	M	404	MQ8	C3-C2	7.93	1.49	1.35
17	L	504	UQ8	C6-C1	7.78	1.49	1.35
17	L	505	UQ8	C6-C1	7.70	1.49	1.35

The worst 5 of 1293 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	M	402	BCL	CMD-C2D-C1D	8.63	139.92	124.73
15	7	101	BCL	CMD-C2D-C1D	8.39	139.51	124.73
15	1	403	BCL	CMD-C2D-C1D	8.31	139.37	124.73
15	U	101	BCL	CMD-C2D-C1D	8.26	139.27	124.73
15	O	502	BCL	CMD-C2D-C1D	8.24	139.23	124.73

There are no chirality outliers.

5 of 1080 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	C	501	HEC	C2B-C3B-CAB-CBB

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Mol	Chain	Res	Type	Atoms
10	C	501	HEC	C4B-C3B-CAB-CBB
10	C	501	HEC	C2C-C3C-CAC-CBC
10	C	501	HEC	C4C-C3C-CAC-CBC
10	C	502	HEC	C2B-C3B-CAB-CBB

There are no ring outliers.

93 monomers are involved in 340 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	5	102	BCL	3	0
22	B	101	LMT	1	0
10	C	501	HEC	5	0
15	3	101	BCL	3	0
21	Q	102	CRT	6	0
15	N	101	BCL	5	0
21	8	103	CRT	6	0
15	B	102	BCL	5	0
22	4	104	LMT	1	0
18	S	101	CDL	5	0
21	N	102	CRT	2	0
18	H	301	CDL	3	0
15	G	102	BCL	4	0
14	M	411	PGV	2	0
15	1	403	BCL	5	0
18	D	102	CDL	4	0
15	Z	102	BCL	3	0
21	4	103	CRT	8	0
15	V	102	BCL	5	0
21	R	102	CRT	5	0
22	Z	101	LMT	2	0
24	O	501	LDA	2	0
15	W	101	BCL	6	0
18	H	302	CDL	1	0
20	M	406	MQ8	4	0
17	L	504	UQ8	2	0
15	Y	101	BCL	6	0
22	0	101	LMT	3	0
10	C	502	HEC	4	0
10	C	504	HEC	10	0
24	K	101	LDA	1	0
15	S	102	BCL	2	0
15	R	101	BCL	9	0

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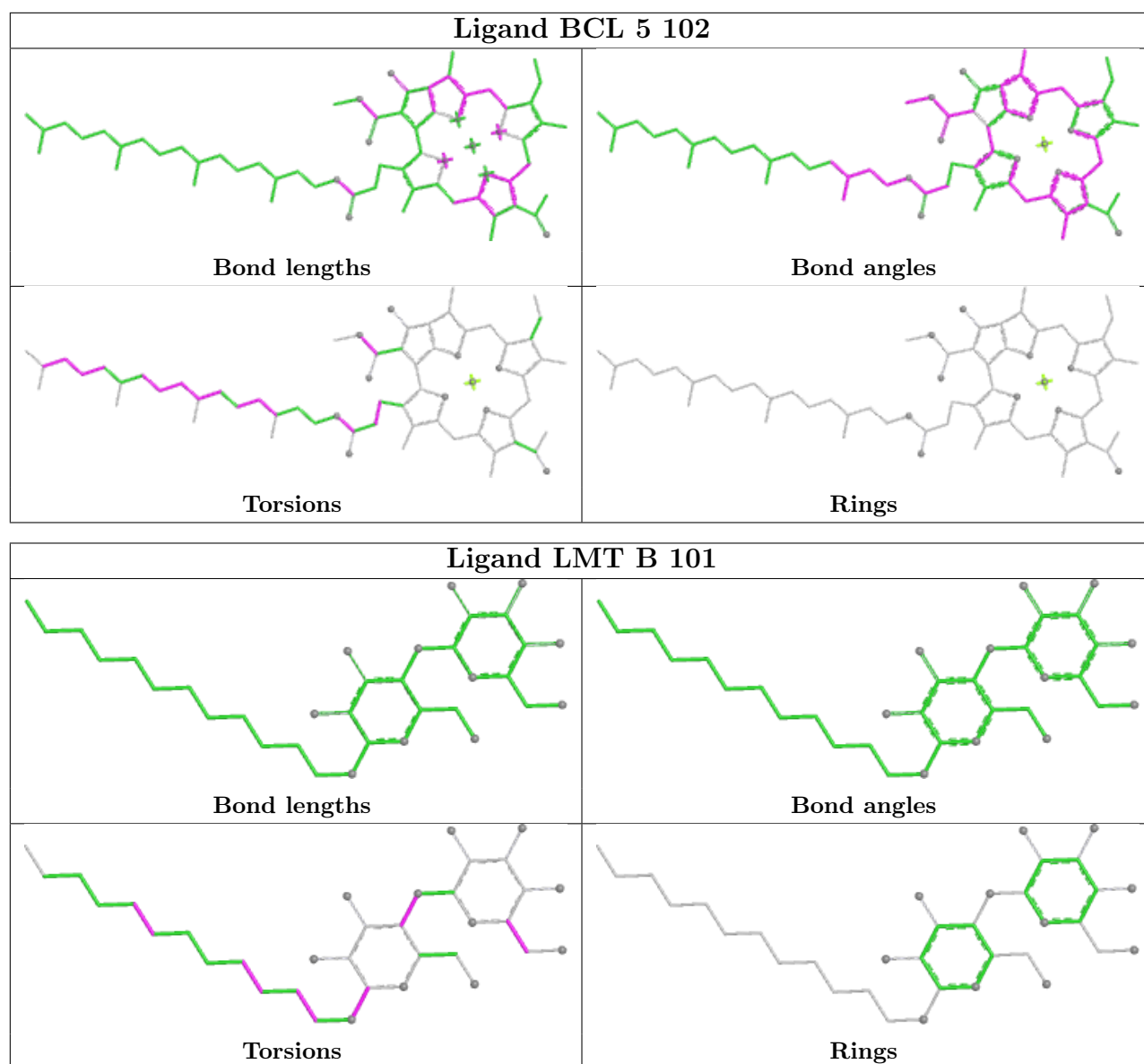
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	8	102	BCL	8	0
15	0	102	BCL	6	0
14	H	303	PGV	3	0
21	X	103	CRT	5	0
15	2	102	BCL	5	0
22	J	101	LMT	1	0
22	K	102	LMT	1	0
20	M	404	MQ8	4	0
21	J	103	CRT	6	0
21	E	103	CRT	4	0
15	L	502	BCL	2	0
15	L	509	BCL	2	0
21	1	402	CRT	8	0
17	L	512	UQ8	7	0
14	M	409	PGV	1	0
18	M	408	CDL	1	0
21	6	102	CRT	5	0
22	P	103	LMT	1	0
15	M	402	BCL	3	0
15	E	102	BCL	4	0
22	2	101	LMT	2	0
15	Q	101	BCL	3	0
14	C	508	PGV	3	0
14	L	506	PGV	4	0
15	O	502	BCL	3	0
15	I	102	BCL	1	0
22	4	101	LMT	3	0
18	I	101	CDL	1	0
10	C	503	HEC	4	0
22	V	101	LMT	3	0
16	M	403	BPH	10	0
21	B	103	CRT	8	0
15	9	101	BCL	4	0
21	M	405	CRT	3	0
17	L	505	UQ8	11	0
14	5	101	PGV	4	0
21	S	104	CRT	2	0
16	L	503	BPH	4	0
22	8	101	LMT	1	0
15	F	101	BCL	4	0
15	D	103	BCL	3	0
15	T	102	BCL	6	0

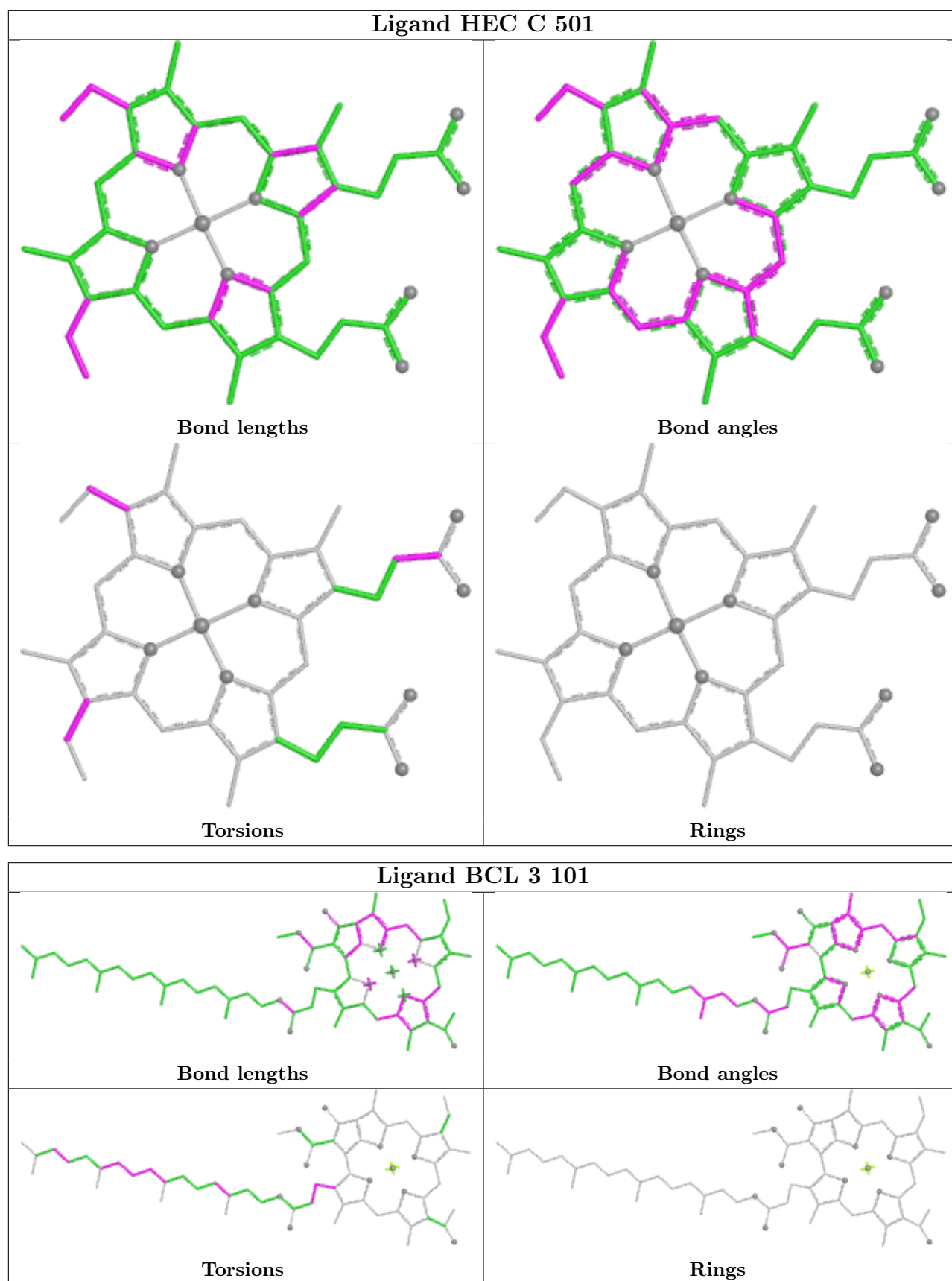
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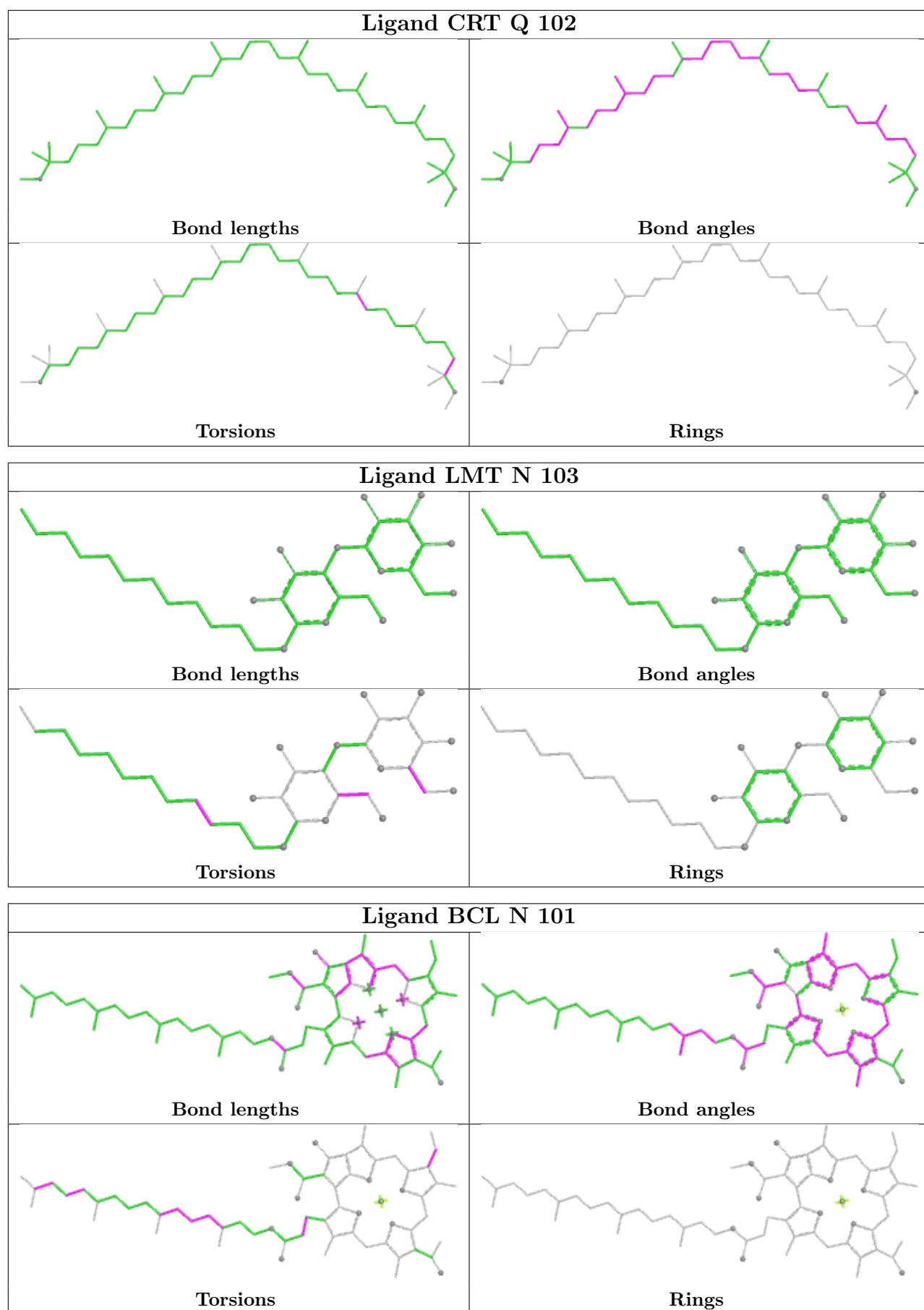
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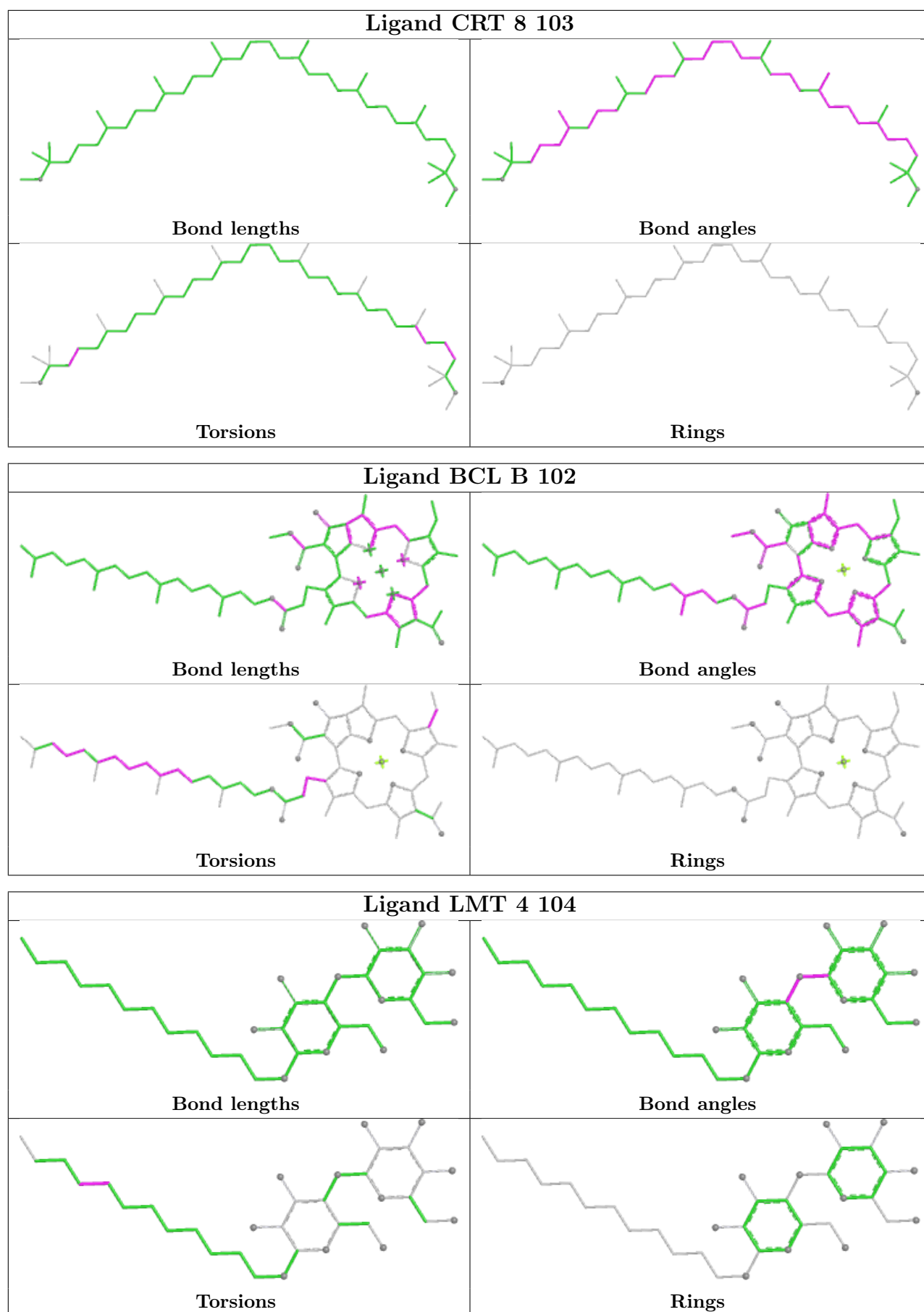
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	L	508	BCL	4	0
15	X	102	BCL	3	0
21	2	103	CRT	5	0
15	P	101	BCL	8	0
15	4	102	BCL	5	0
15	J	102	BCL	2	0
22	H	304	LMT	1	0
18	L	510	CDL	1	0
18	M	410	CDL	1	0
22	G	101	LMT	3	0
15	U	101	BCL	3	0
14	1	401	PGV	2	0
13	C	507	PLM	1	0
21	G	103	CRT	5	0
15	6	101	BCL	3	0
15	K	103	BCL	6	0
21	P	102	CRT	5	0
21	7	102	CRT	4	0

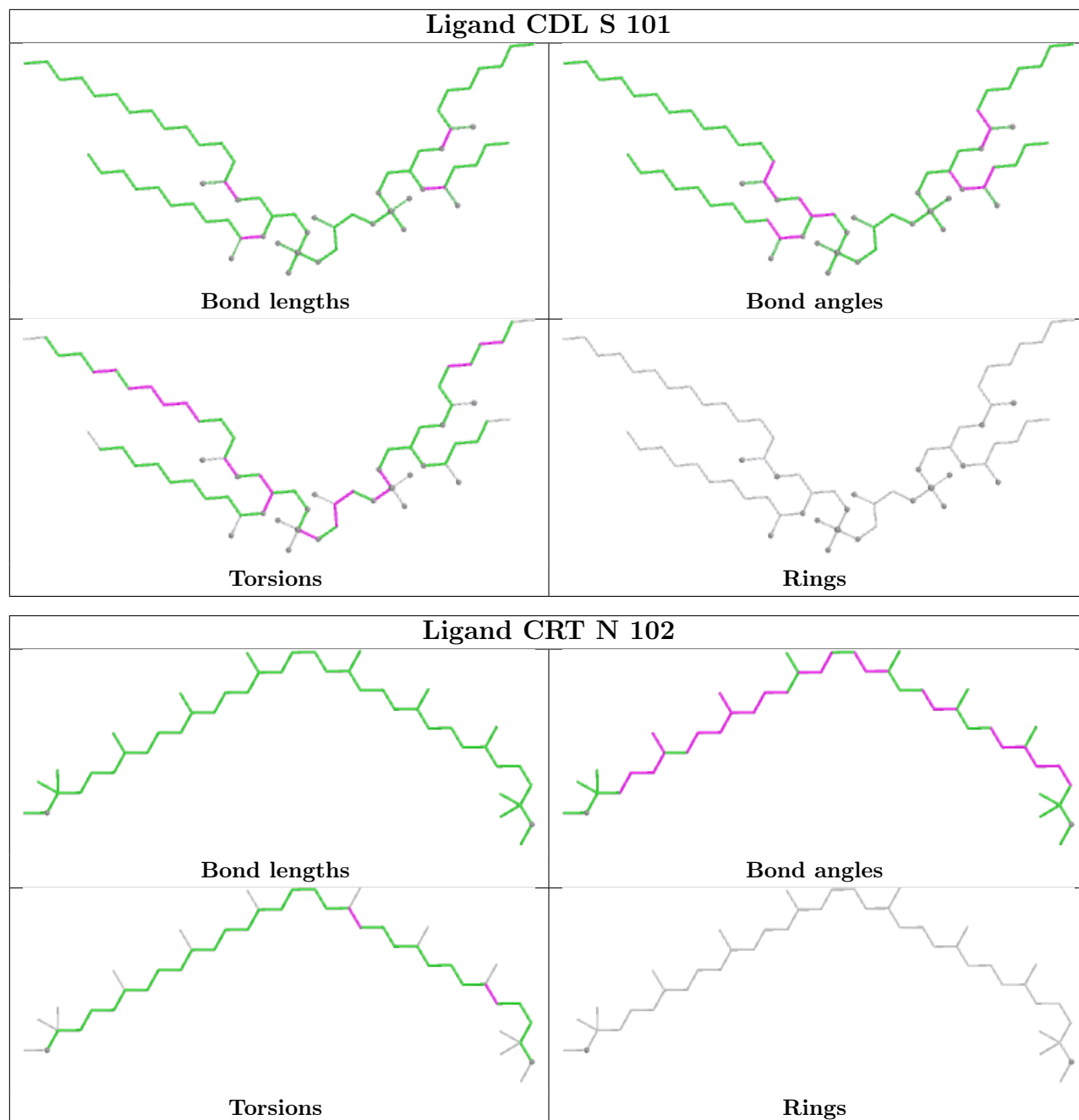
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

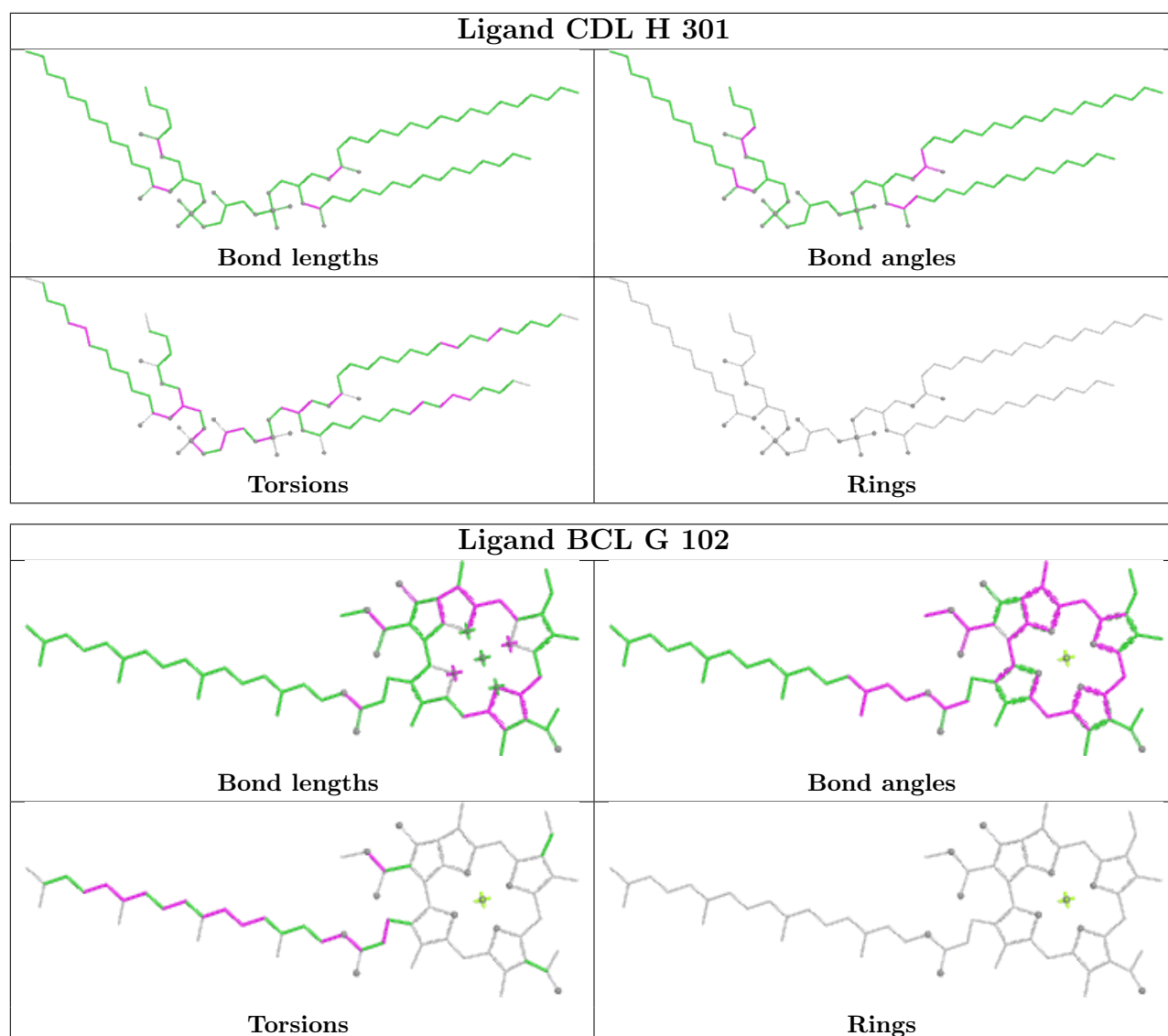


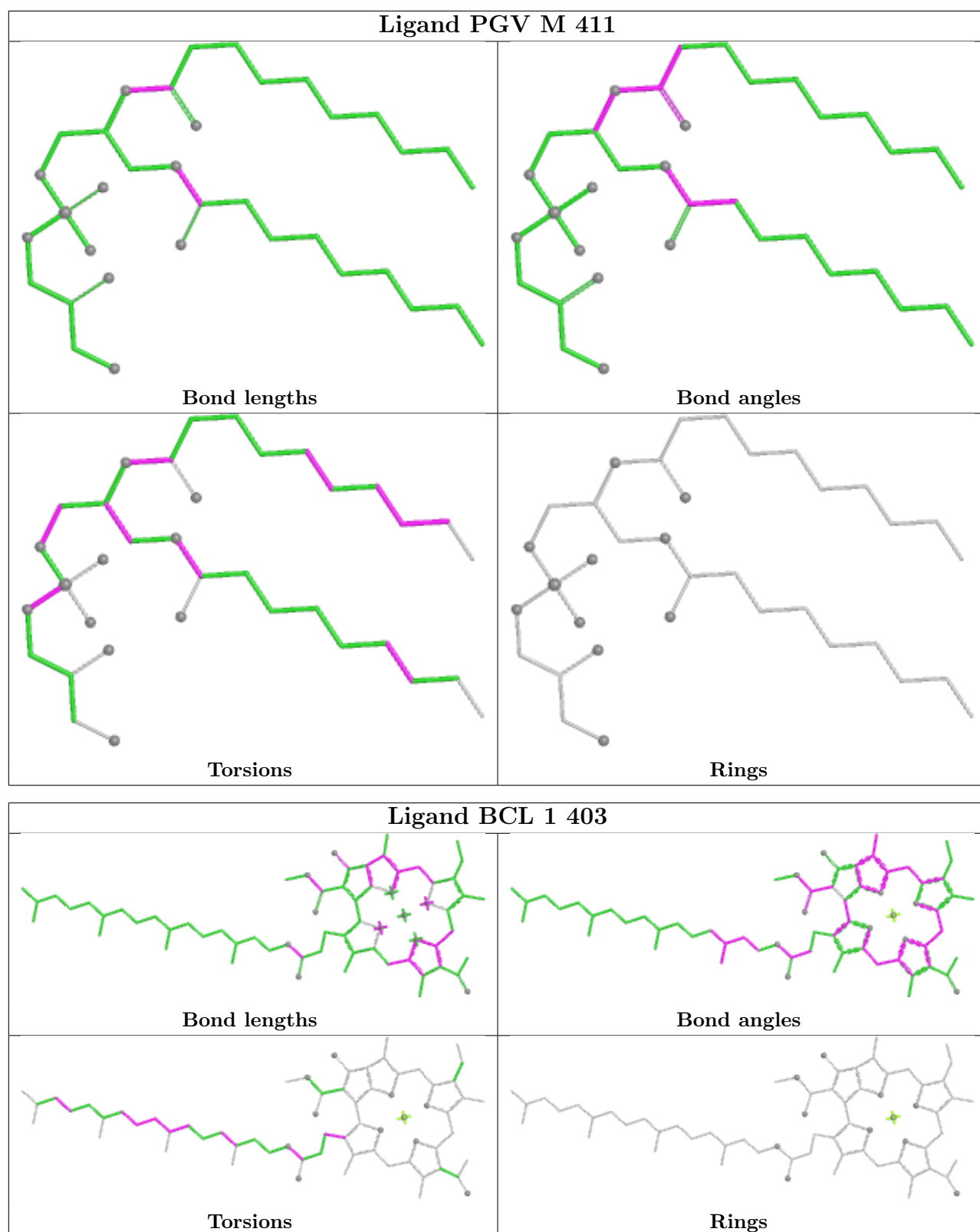


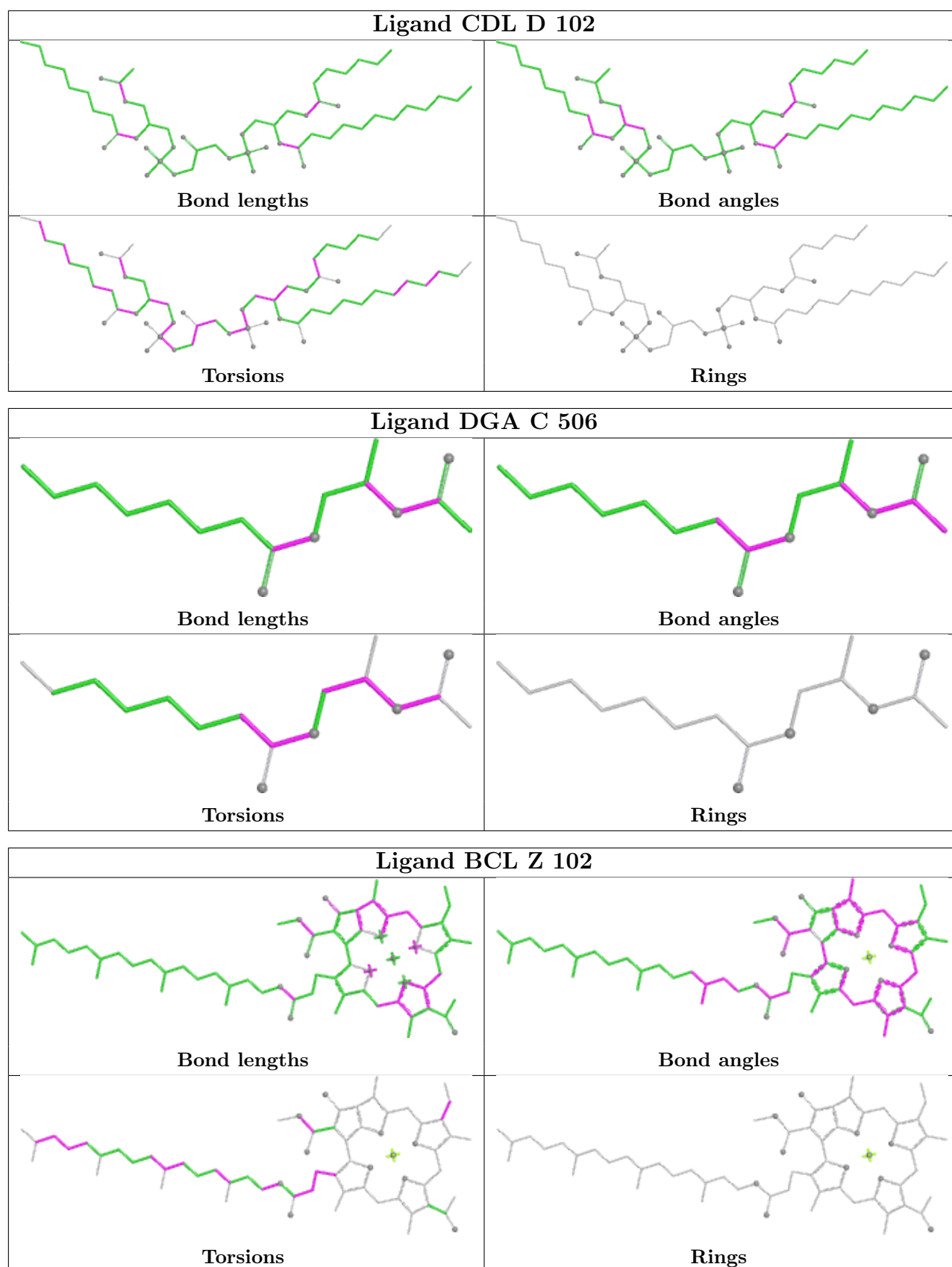


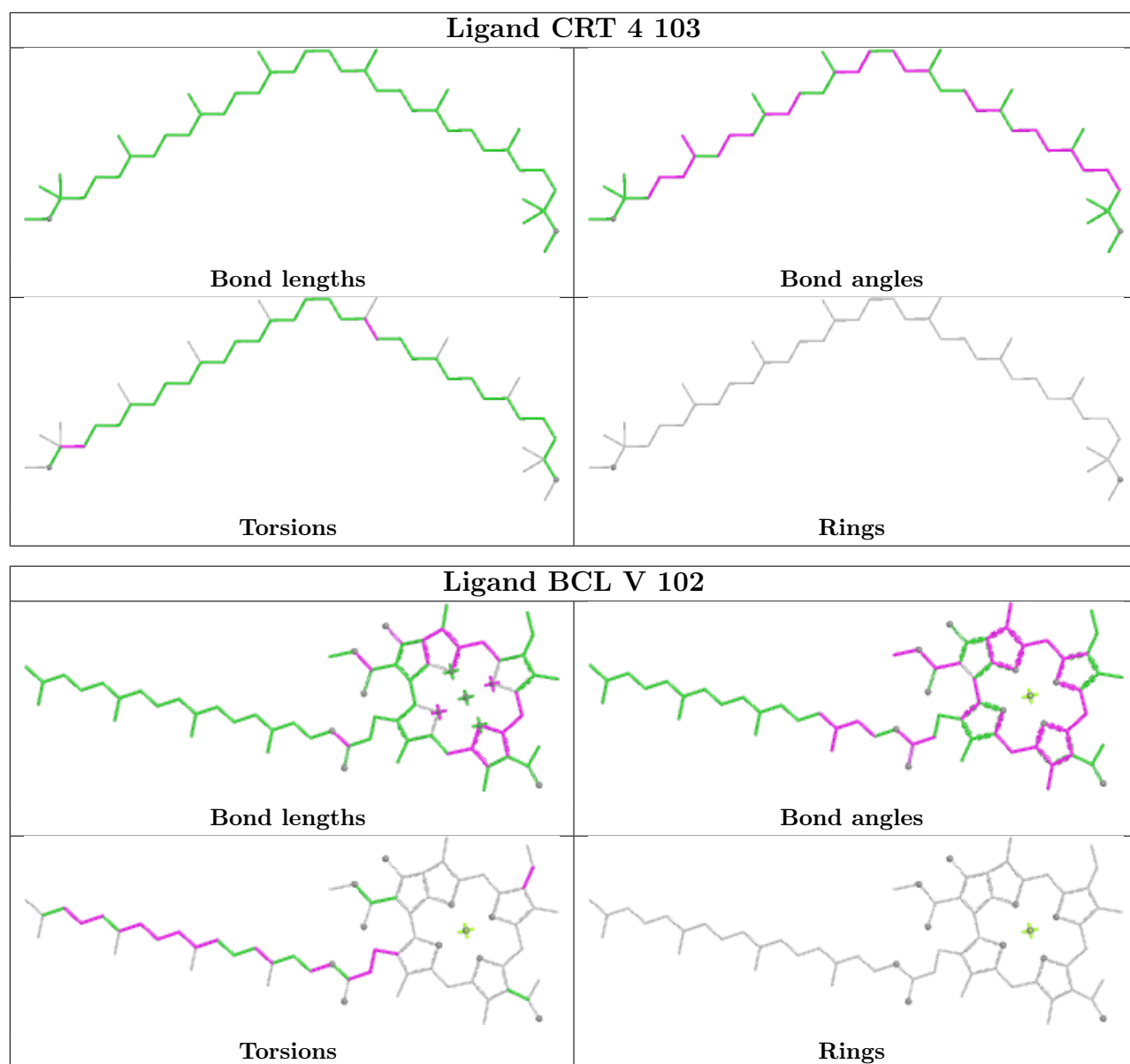


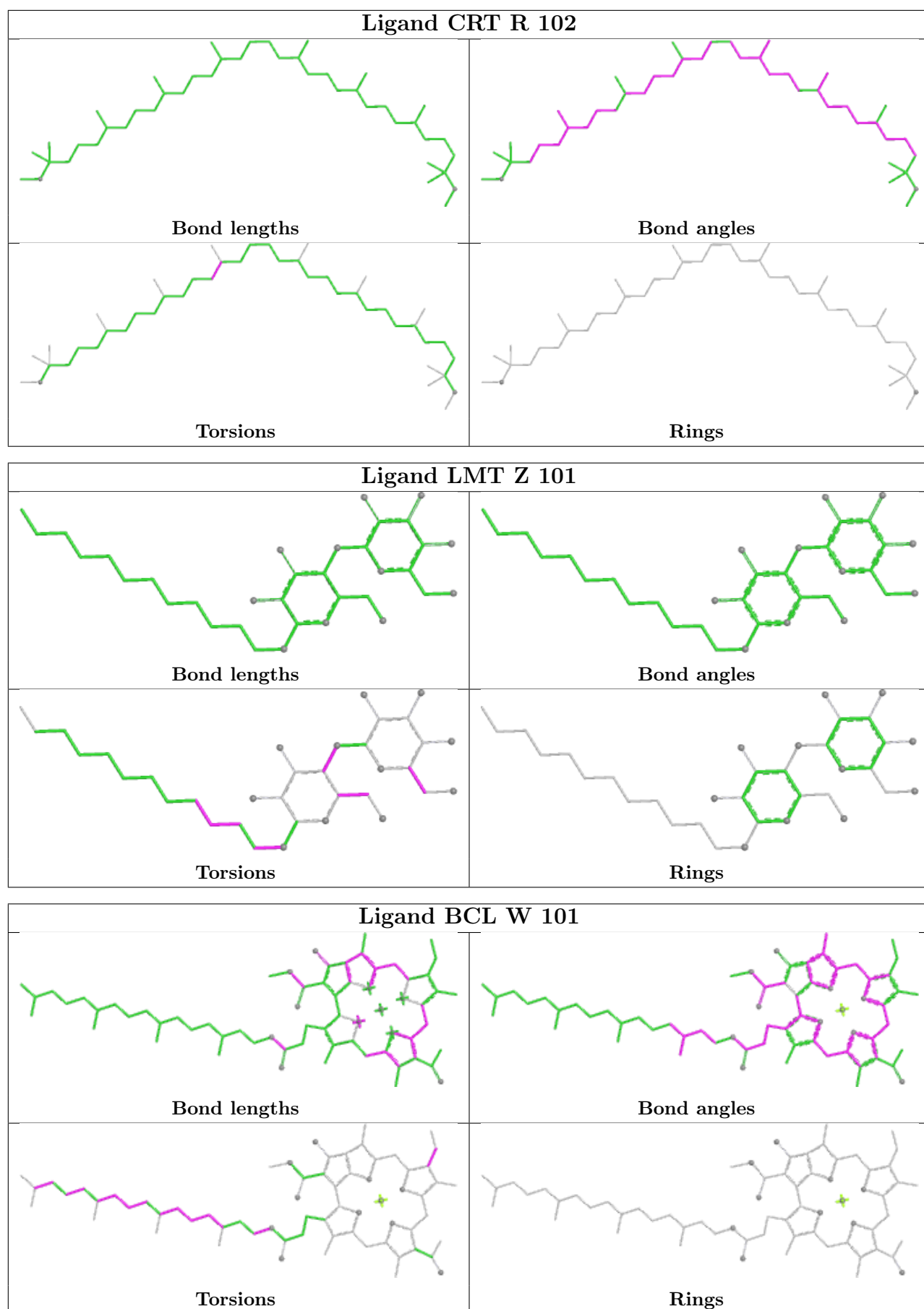


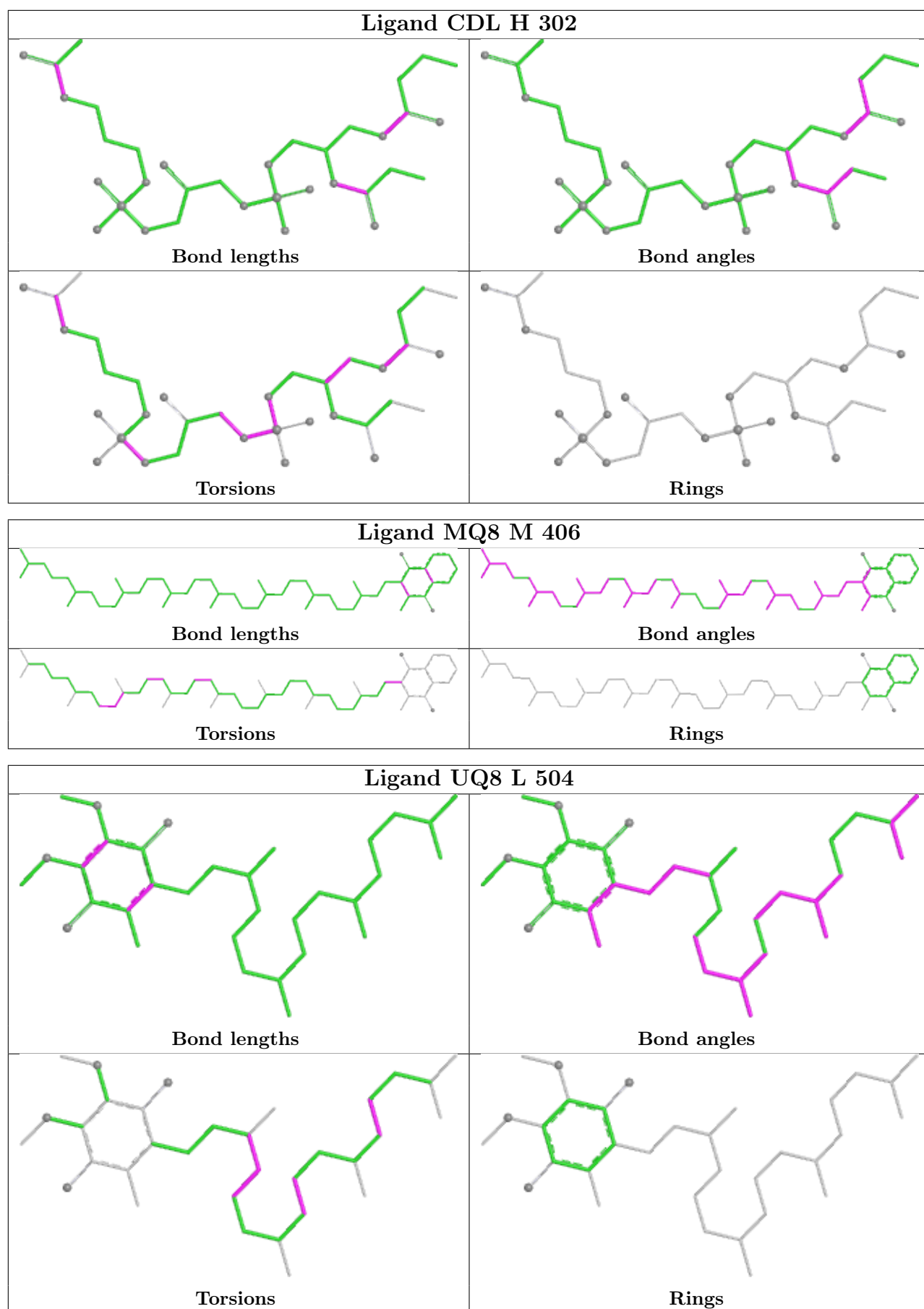


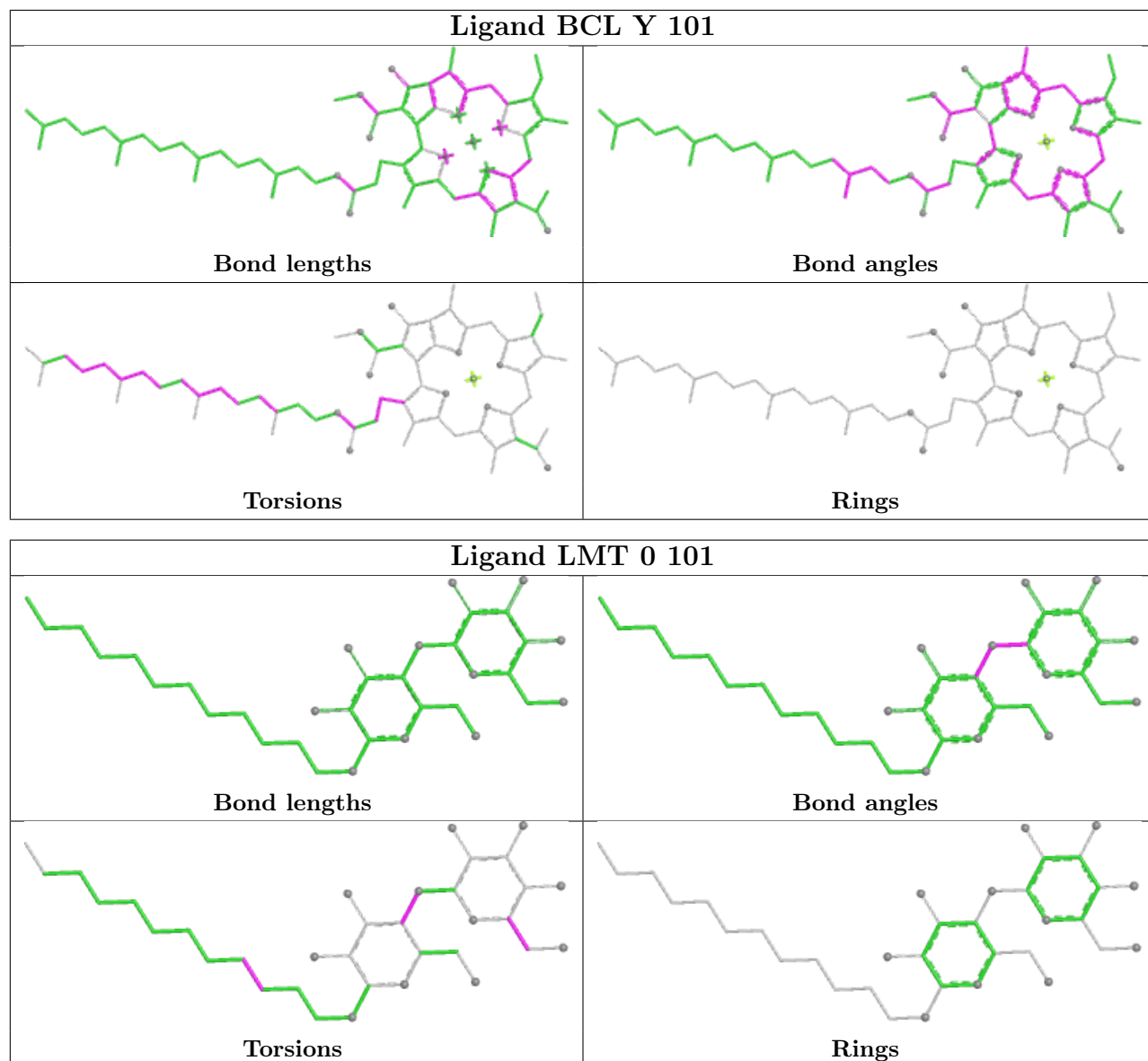


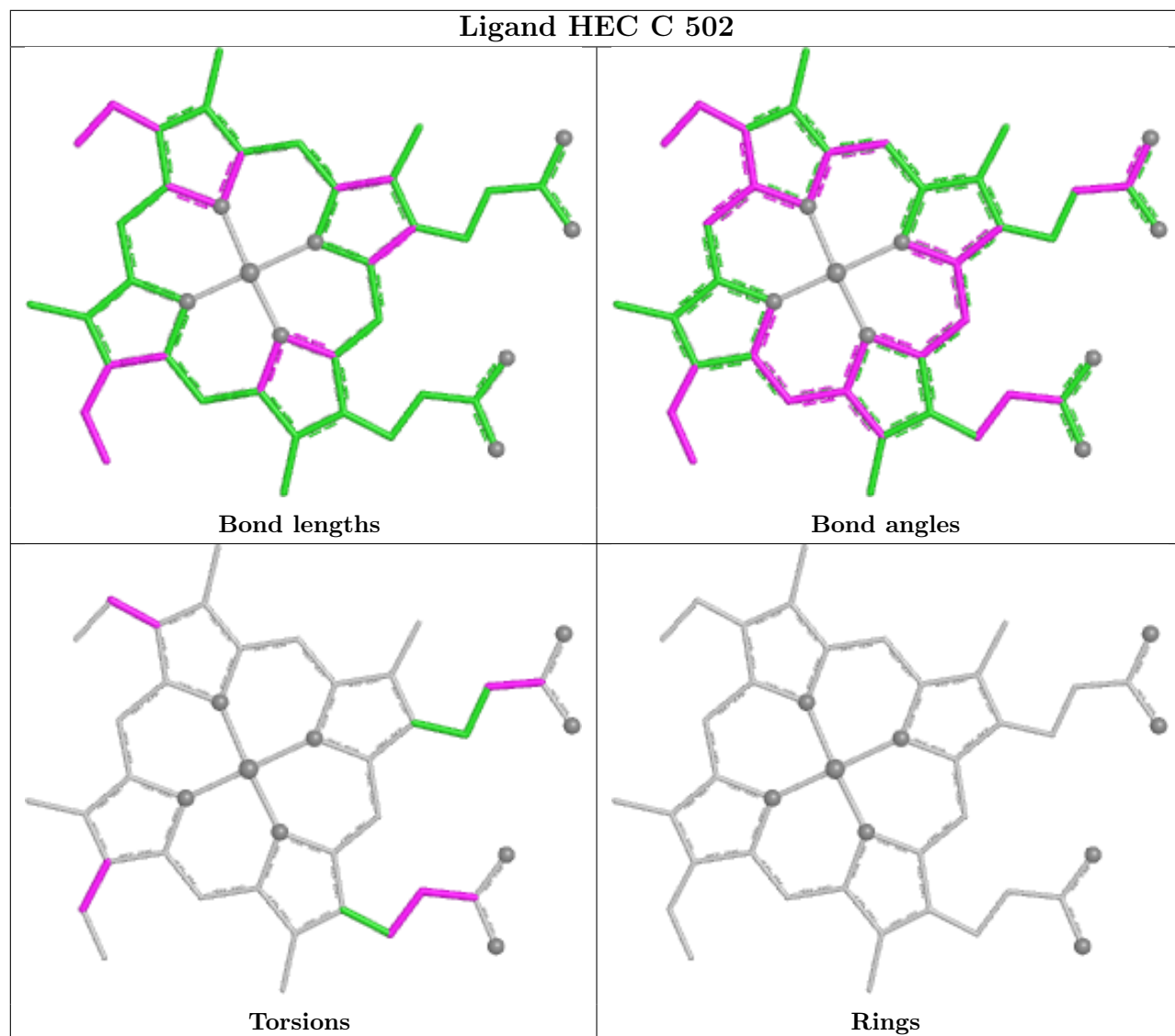


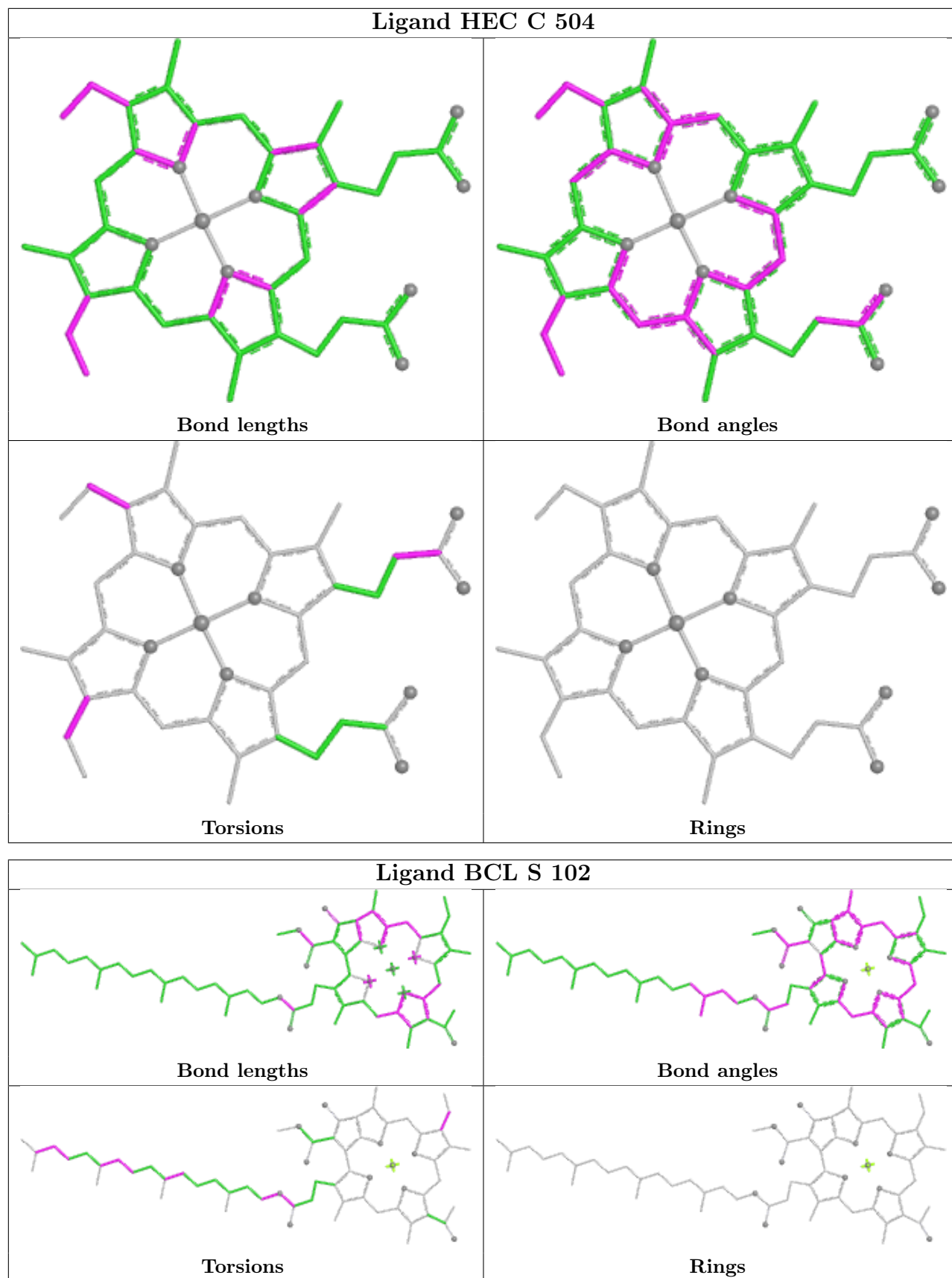


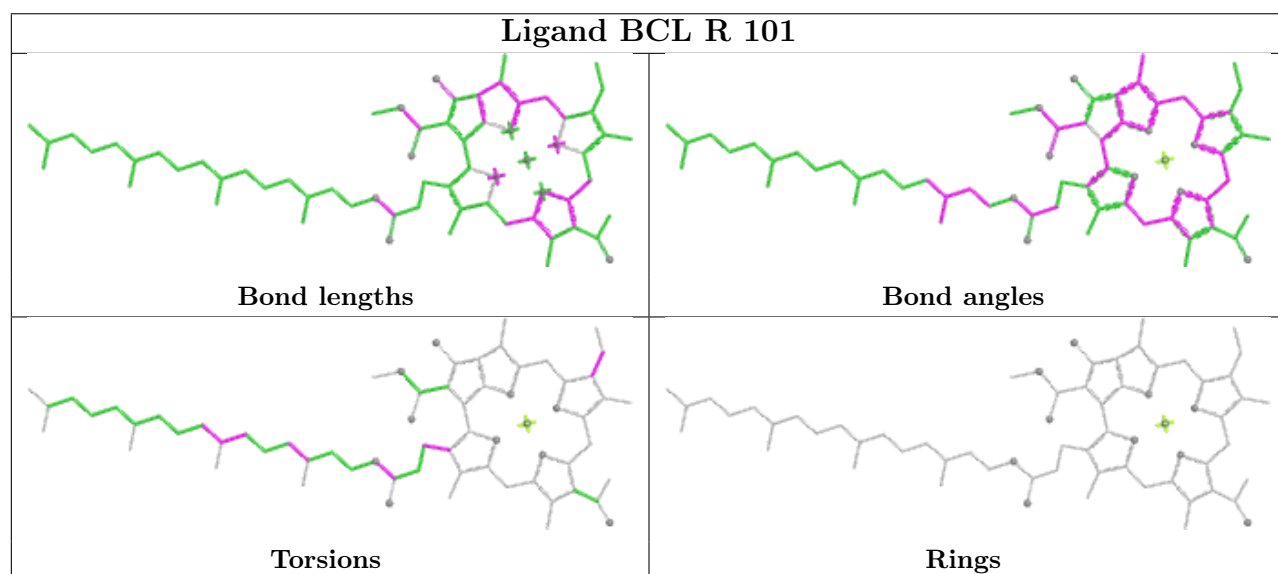
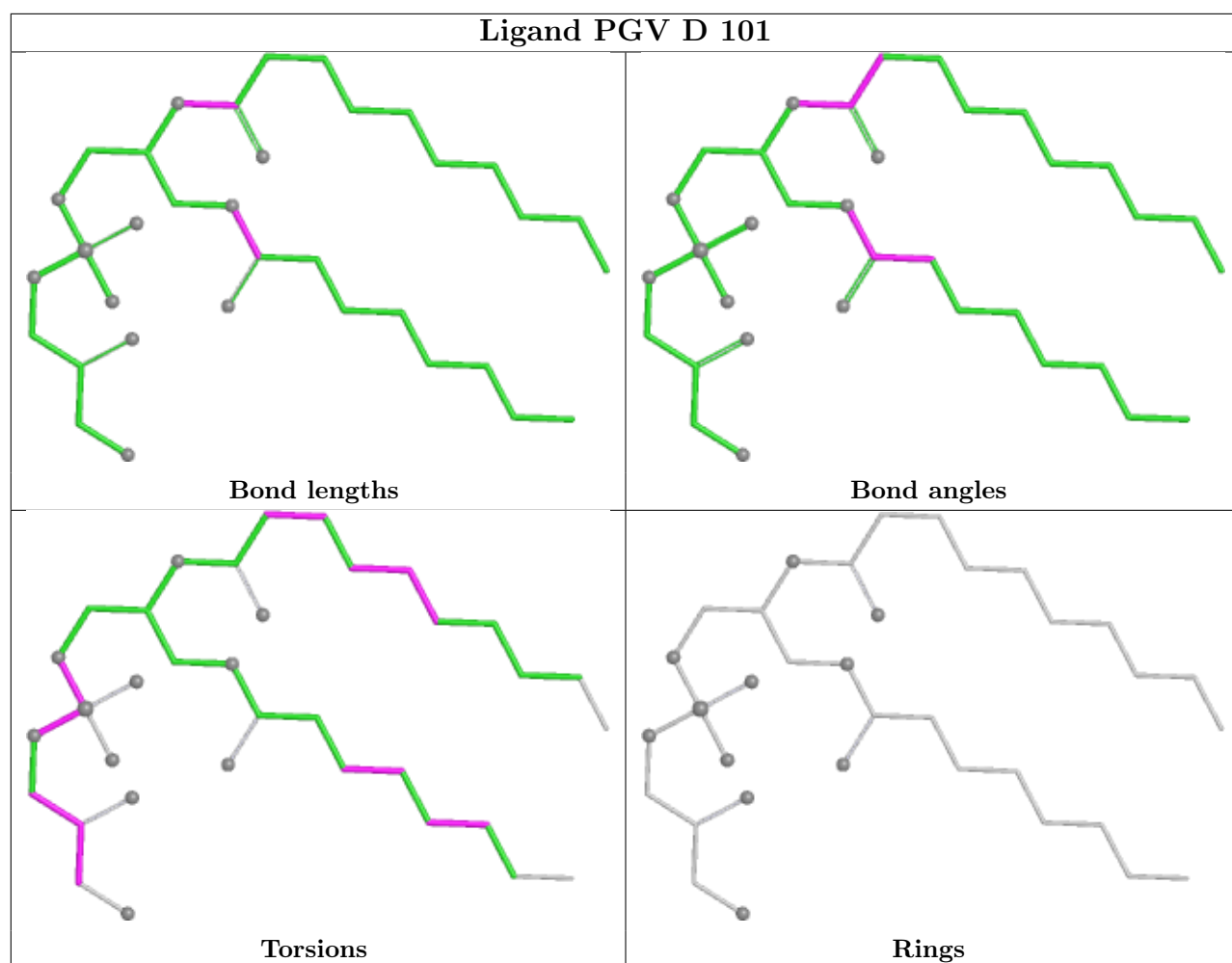


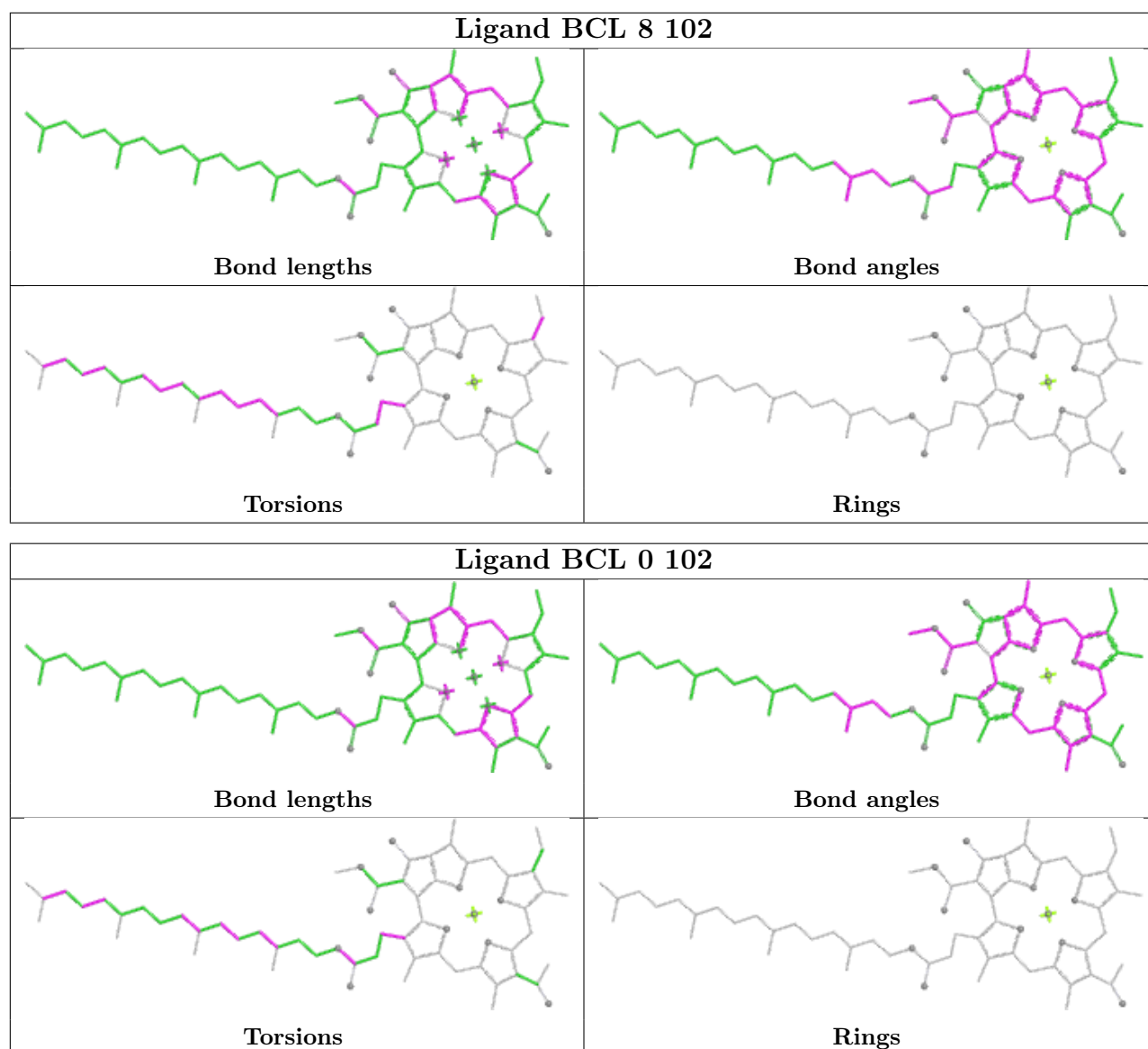


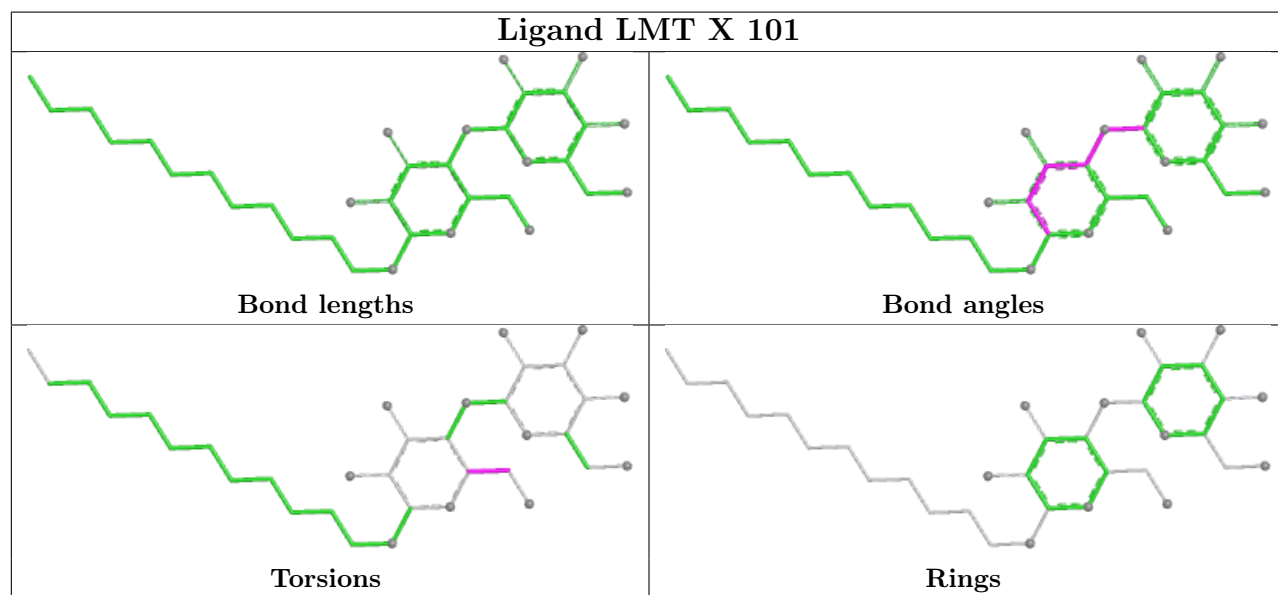
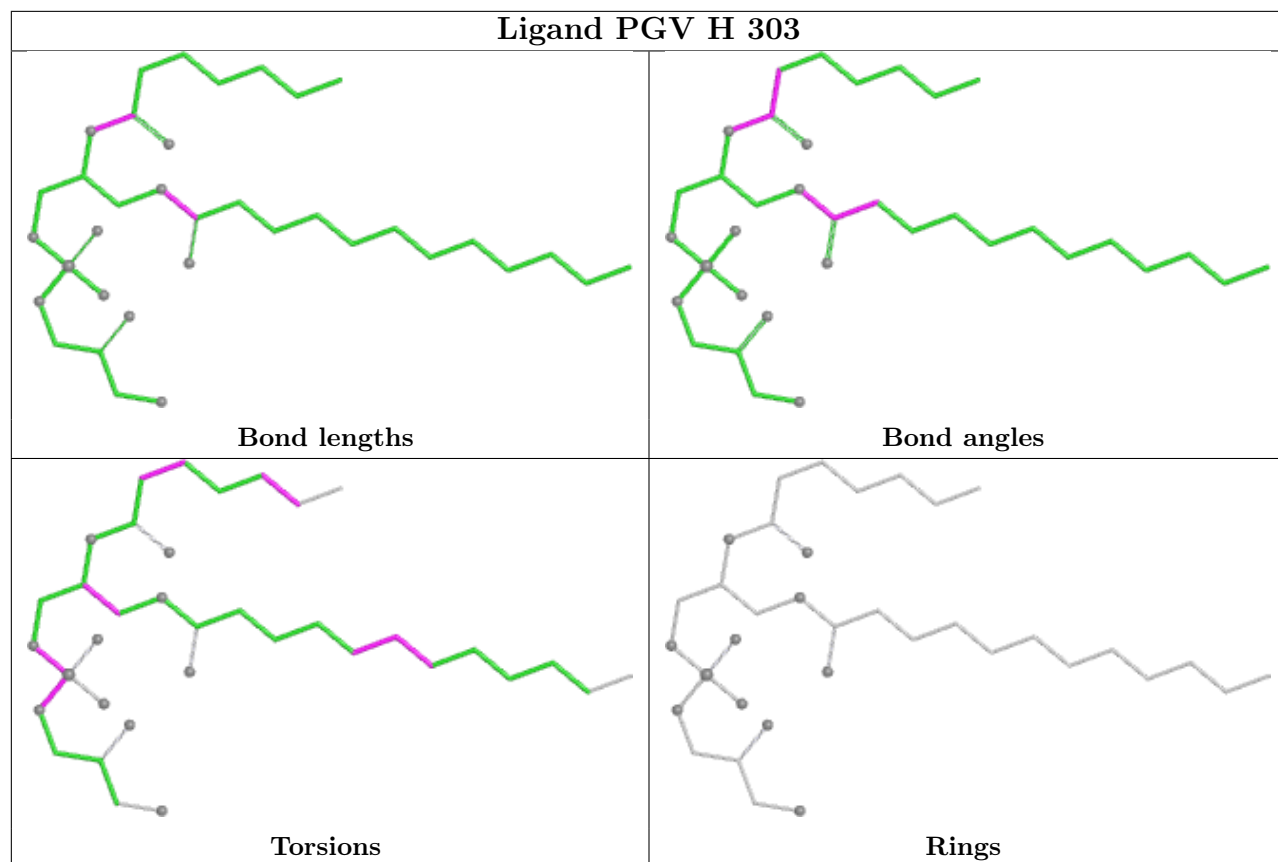


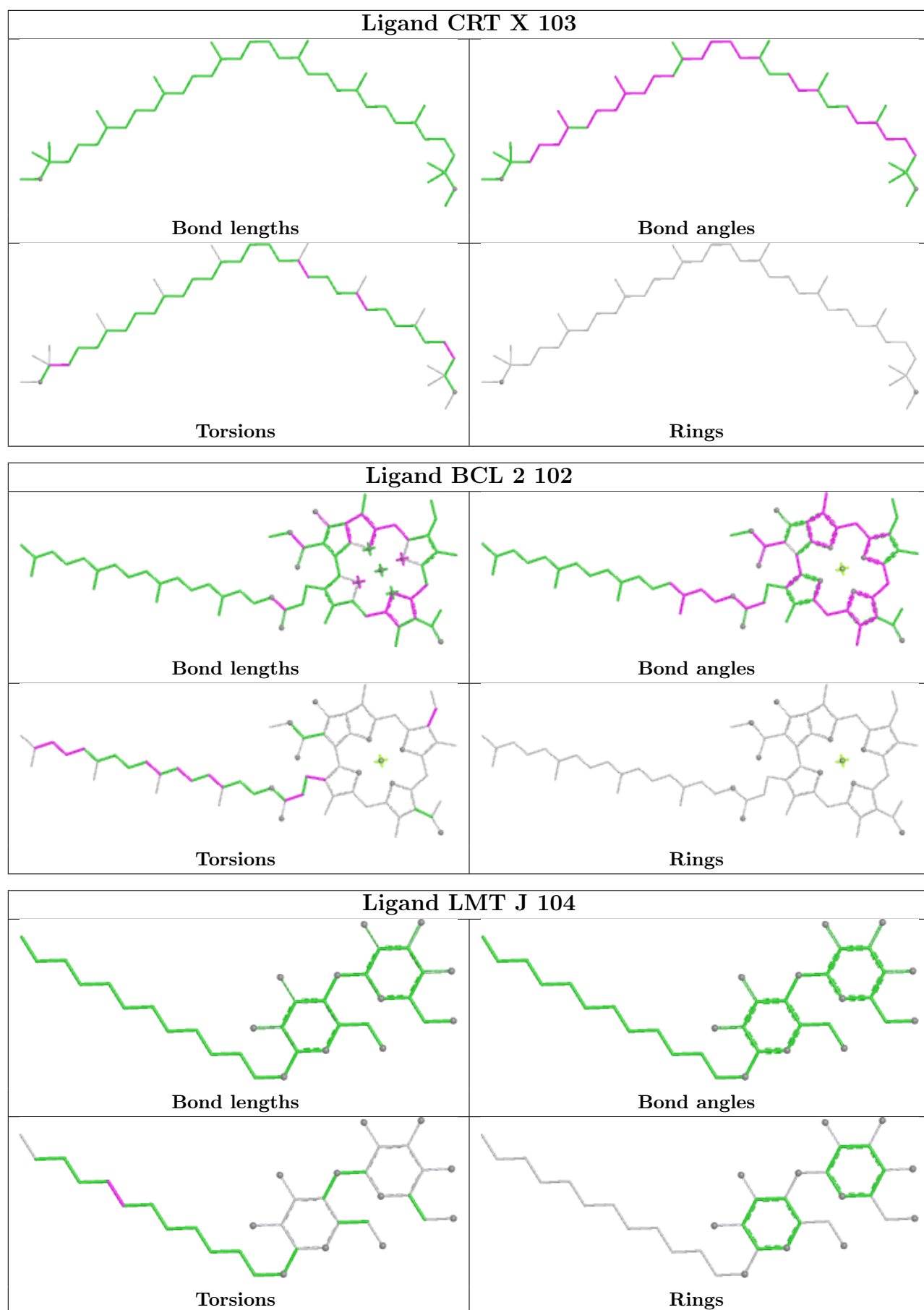


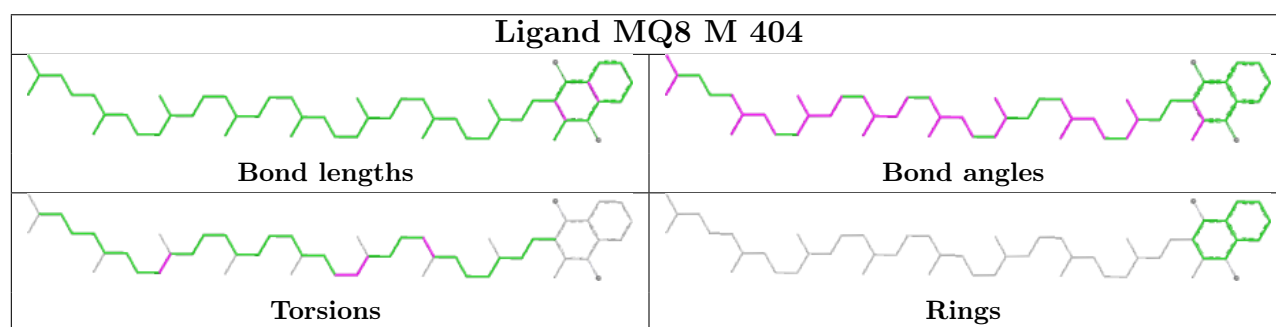
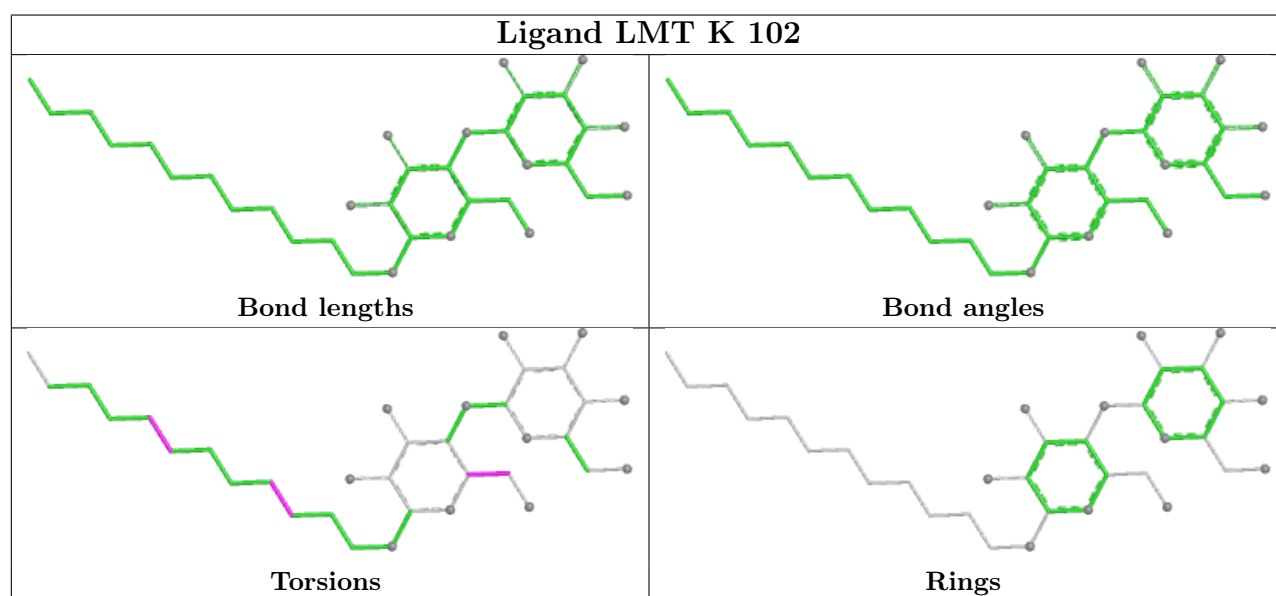
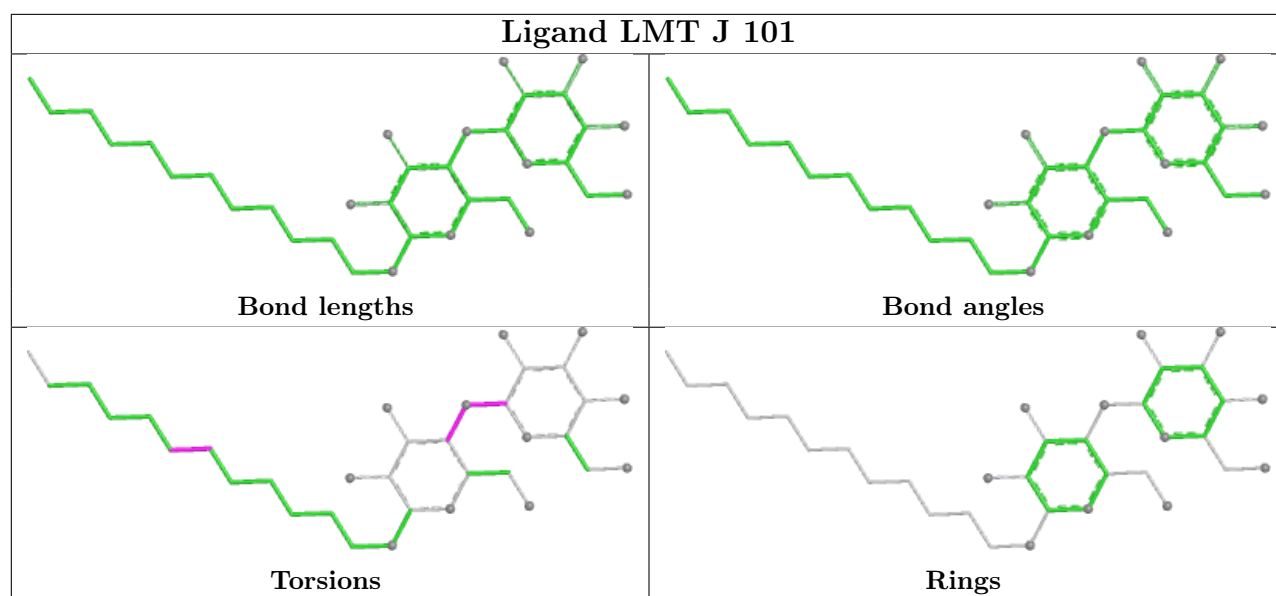


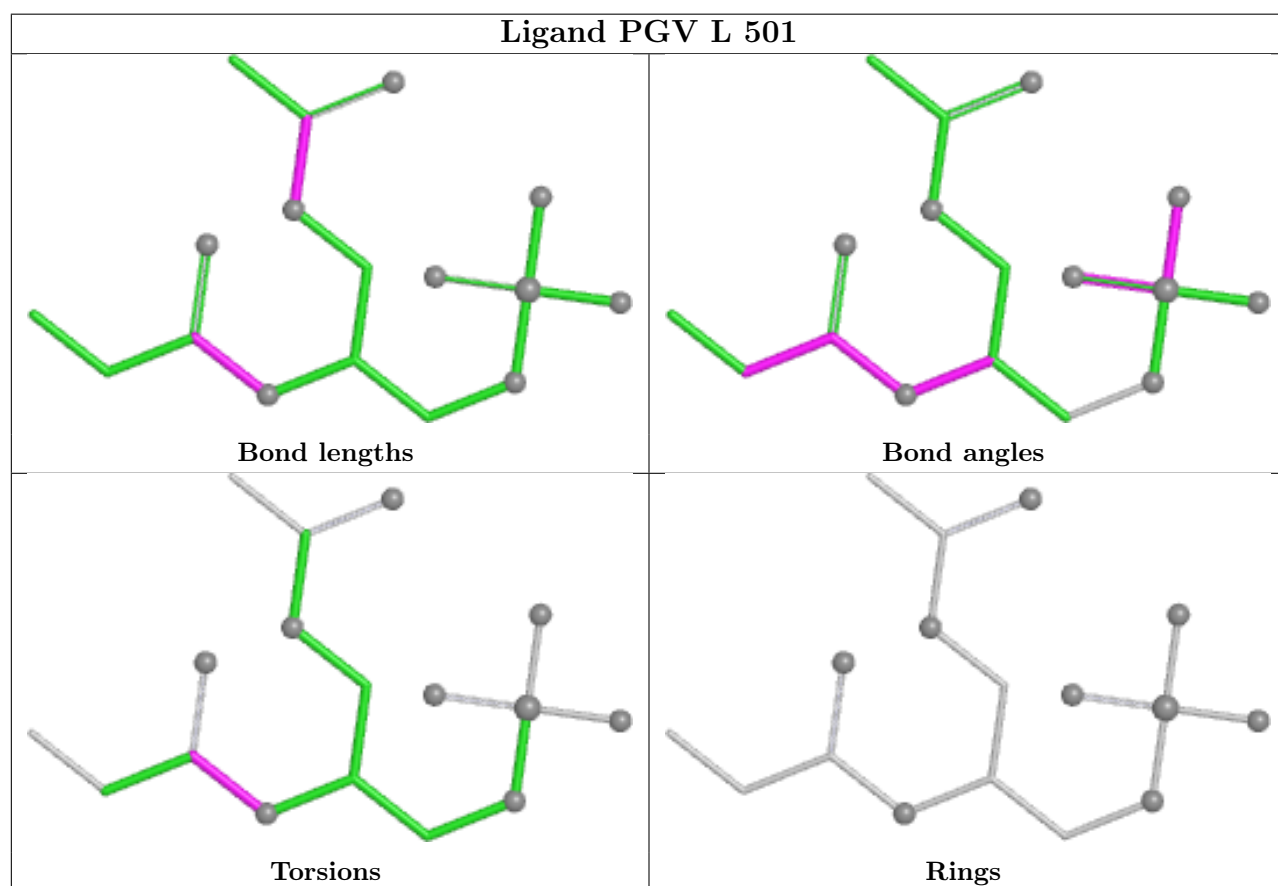
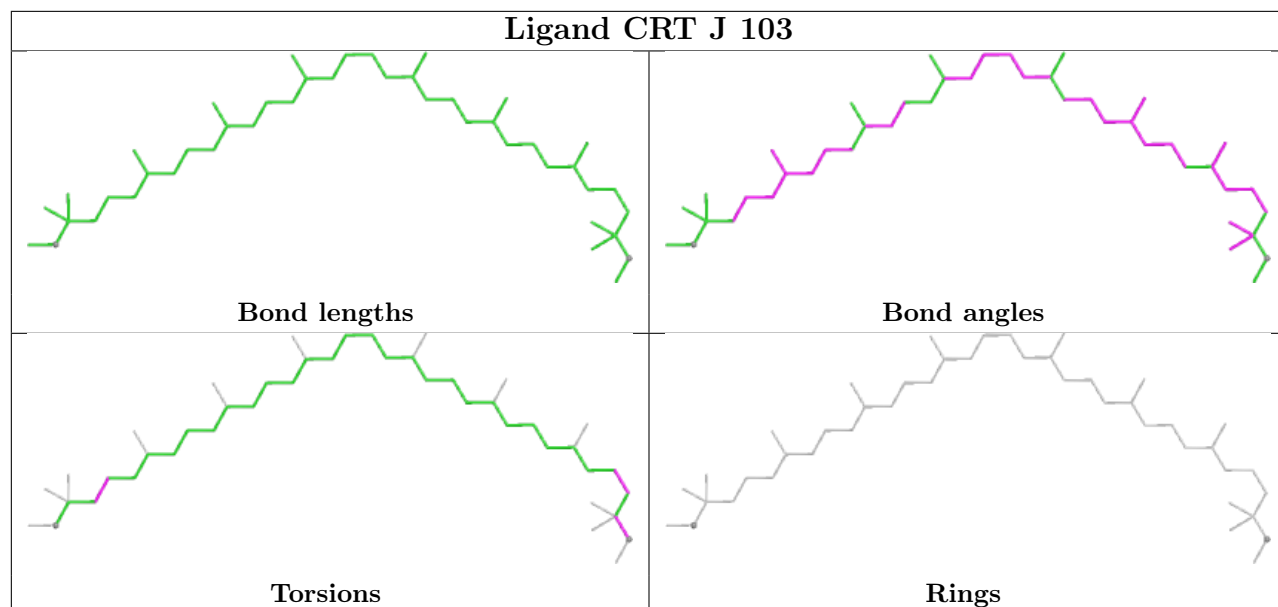


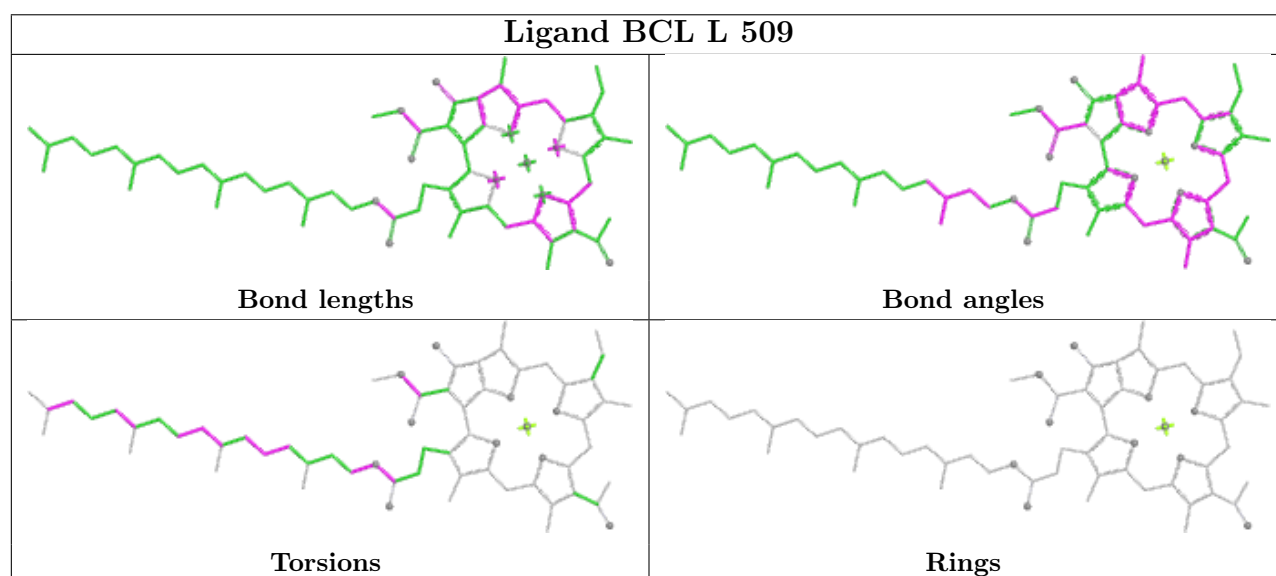
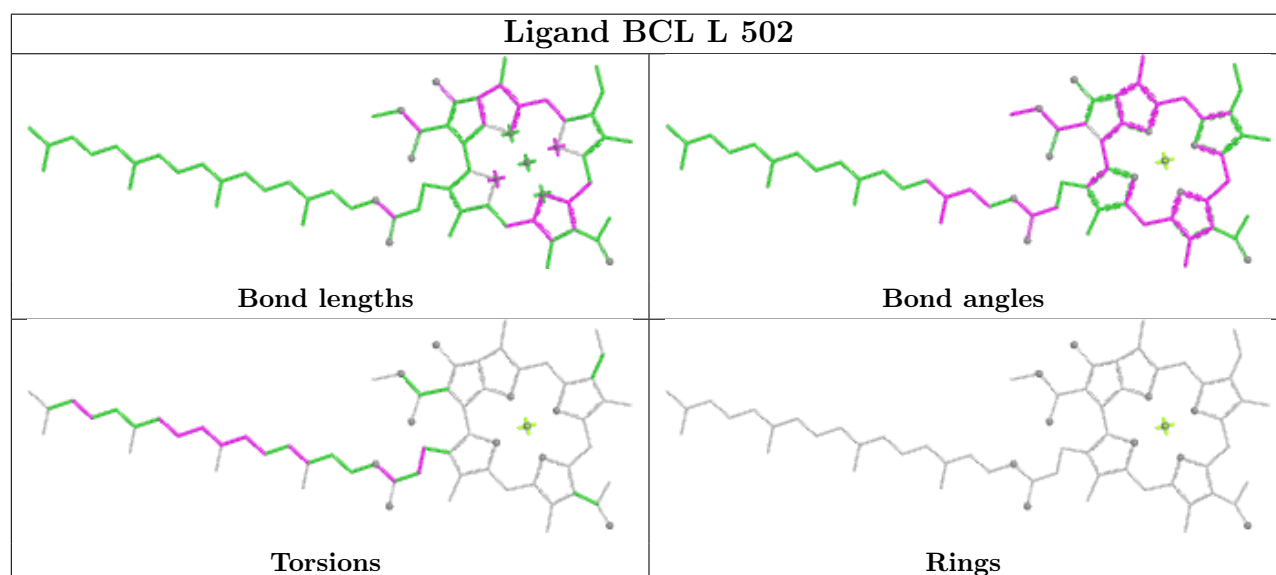
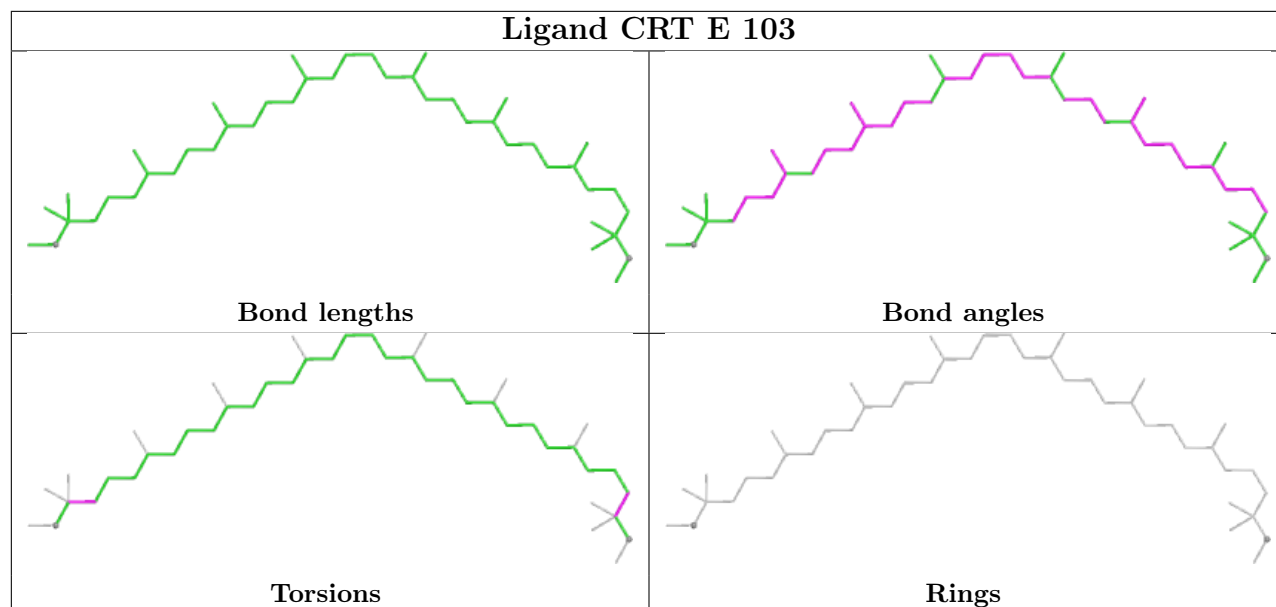


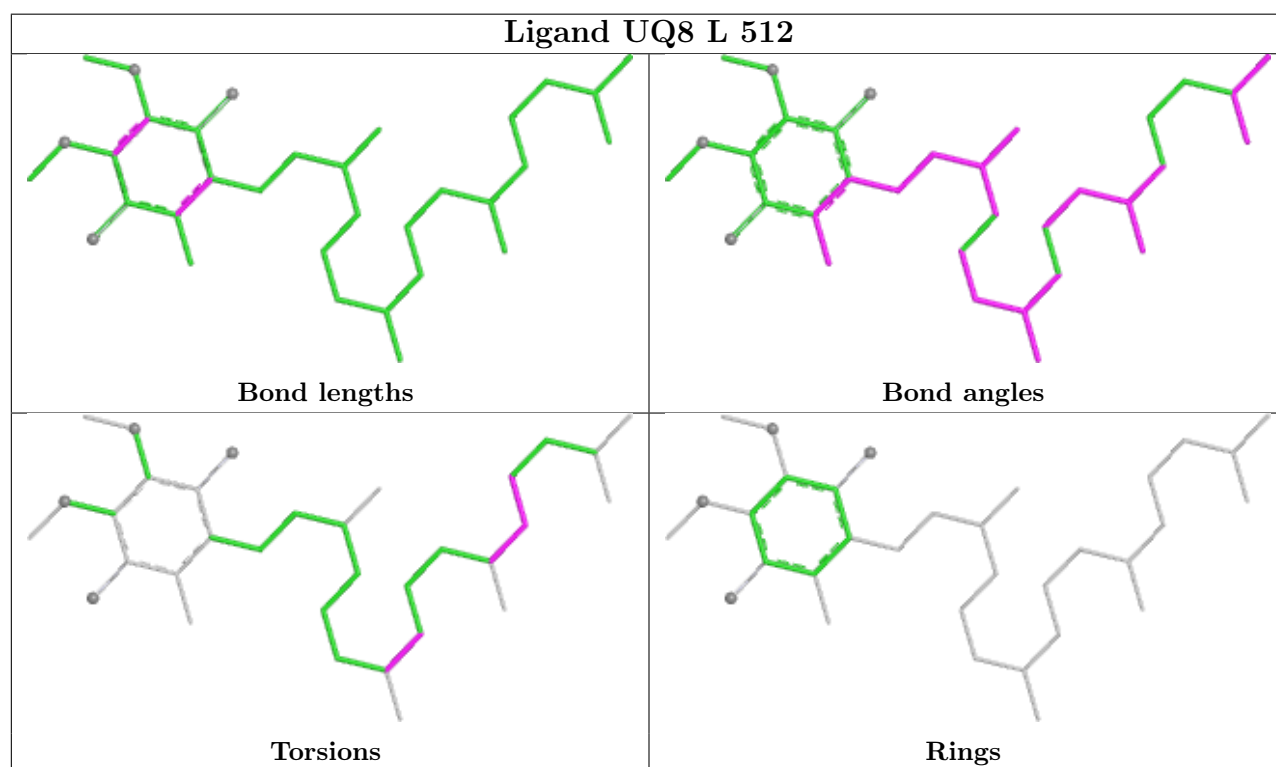
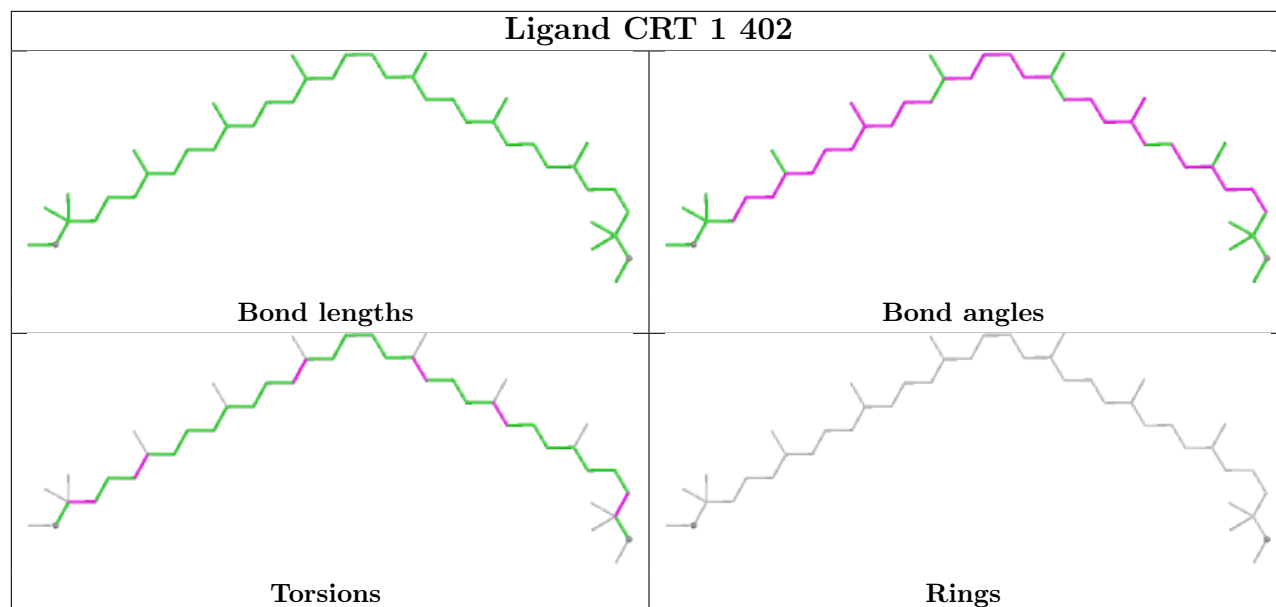


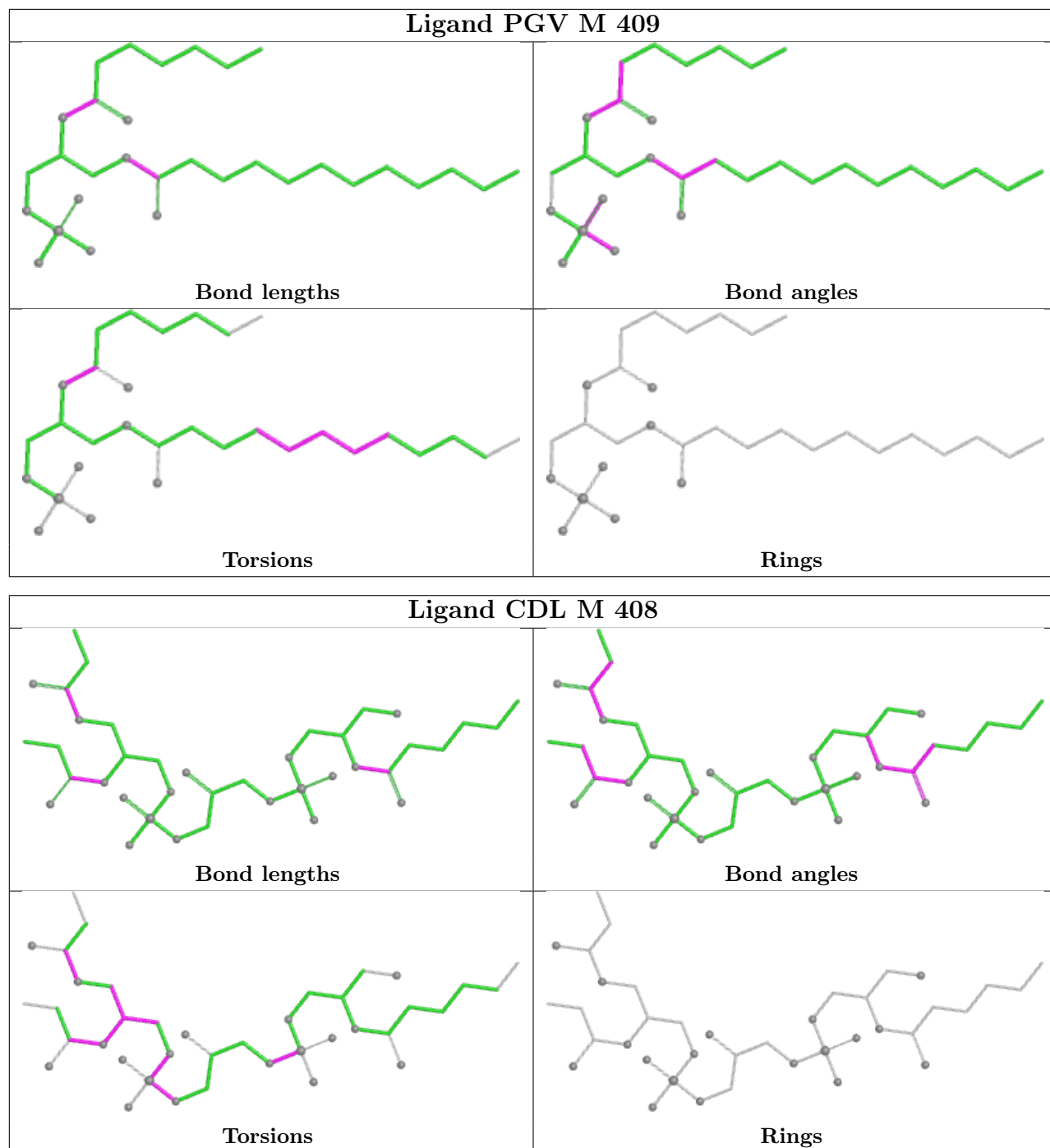


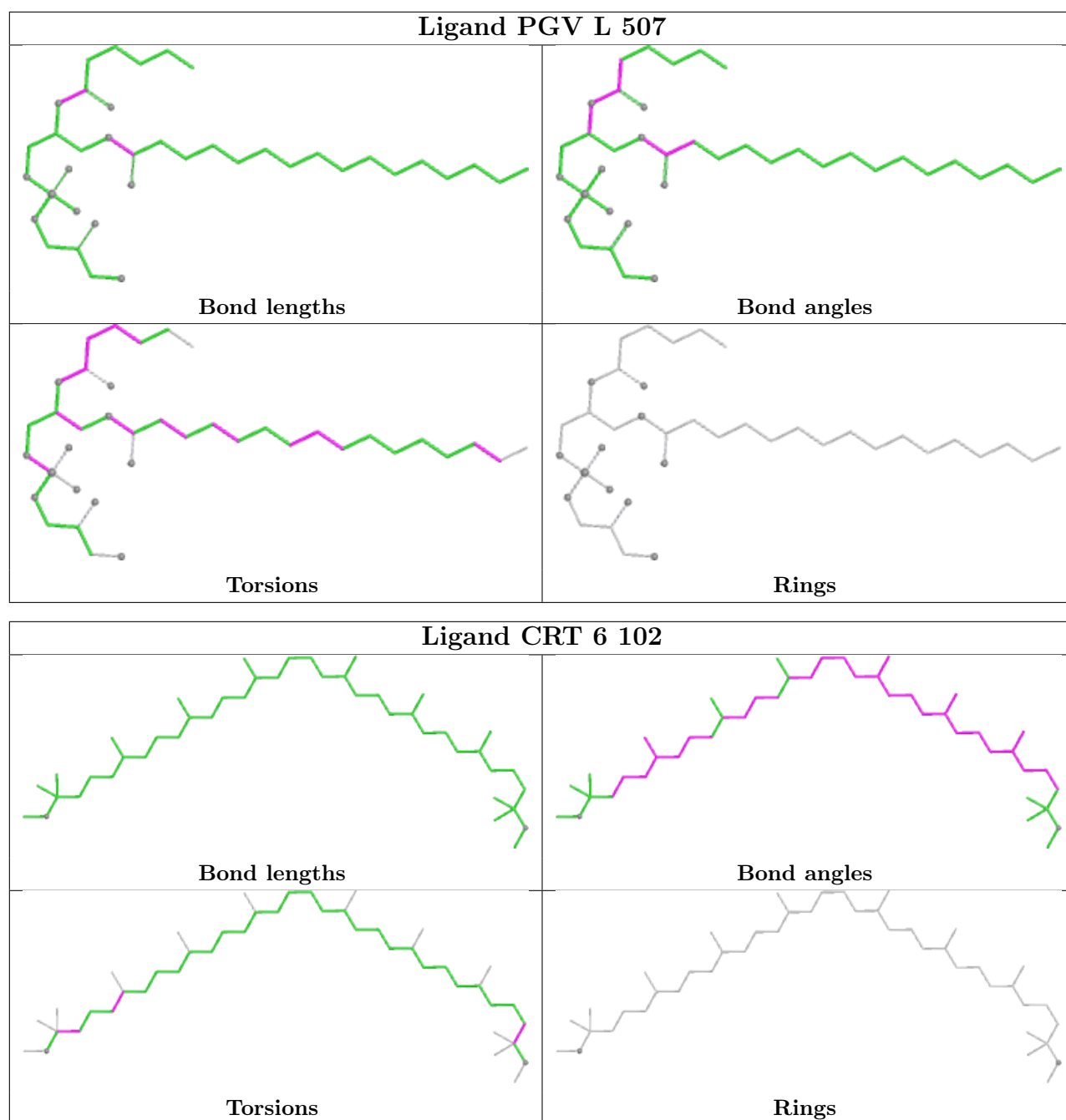


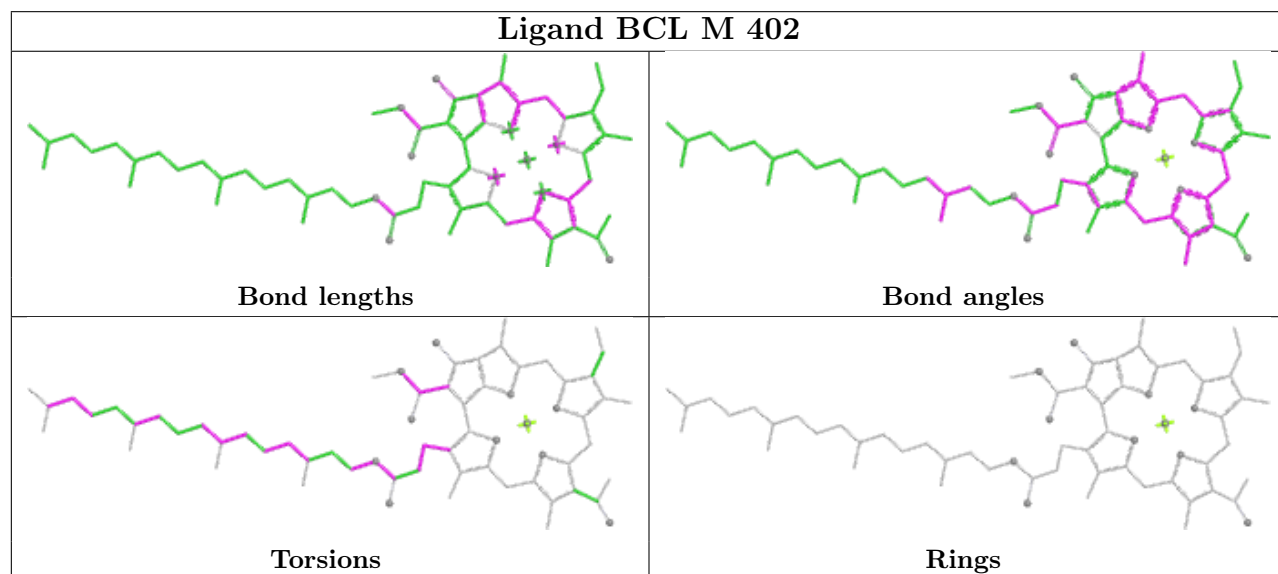
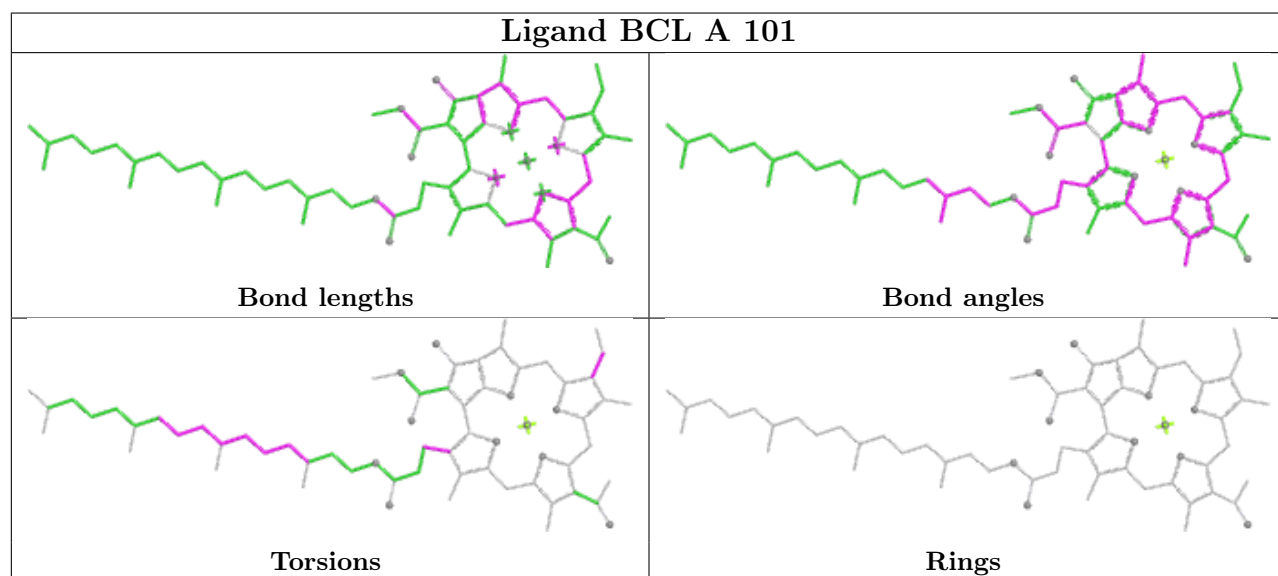
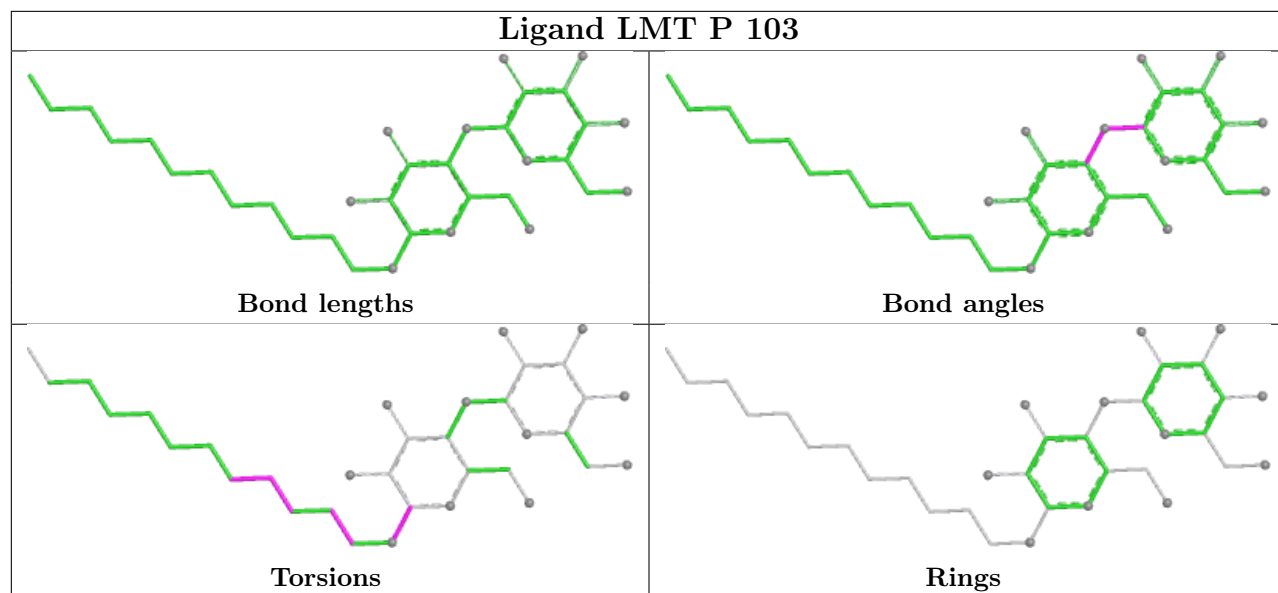


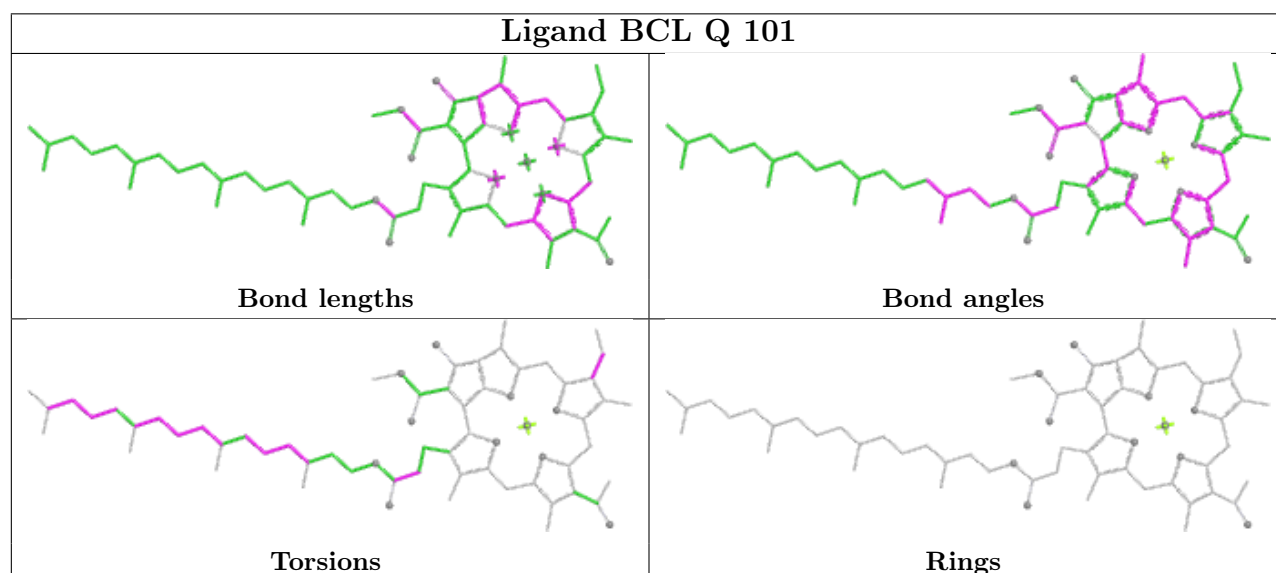
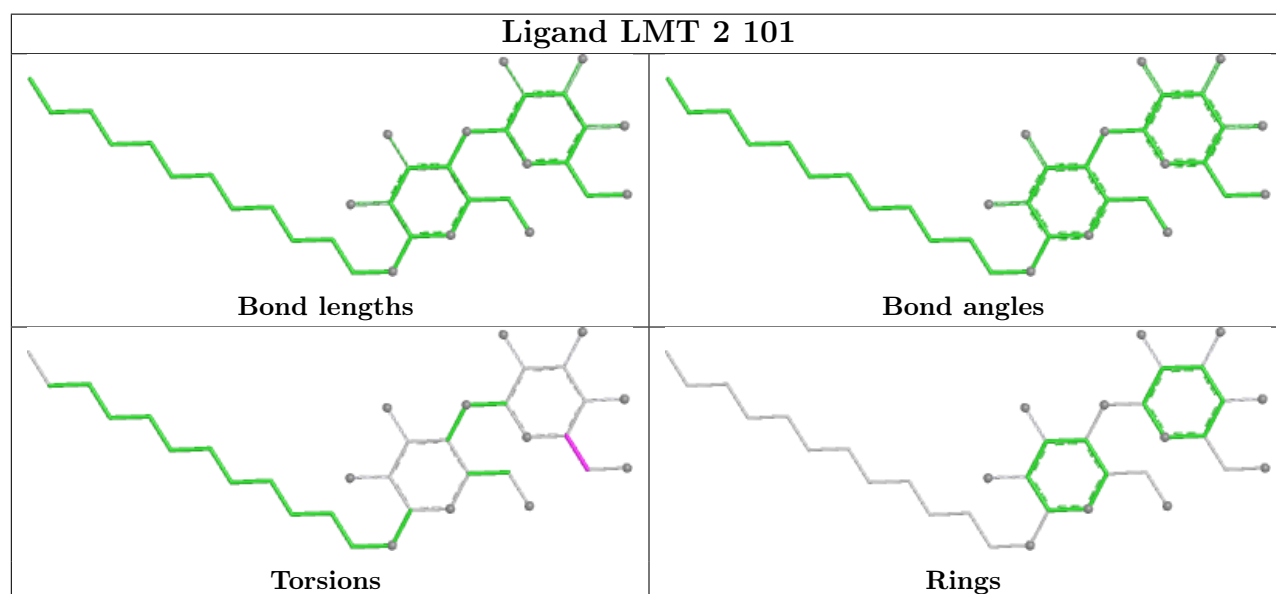
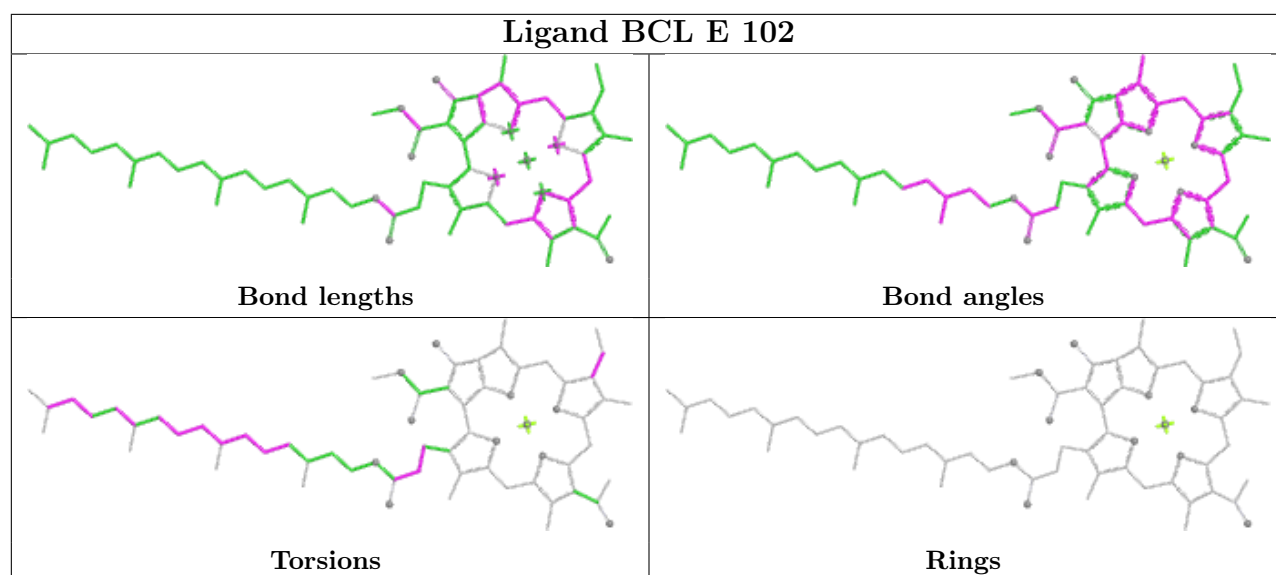


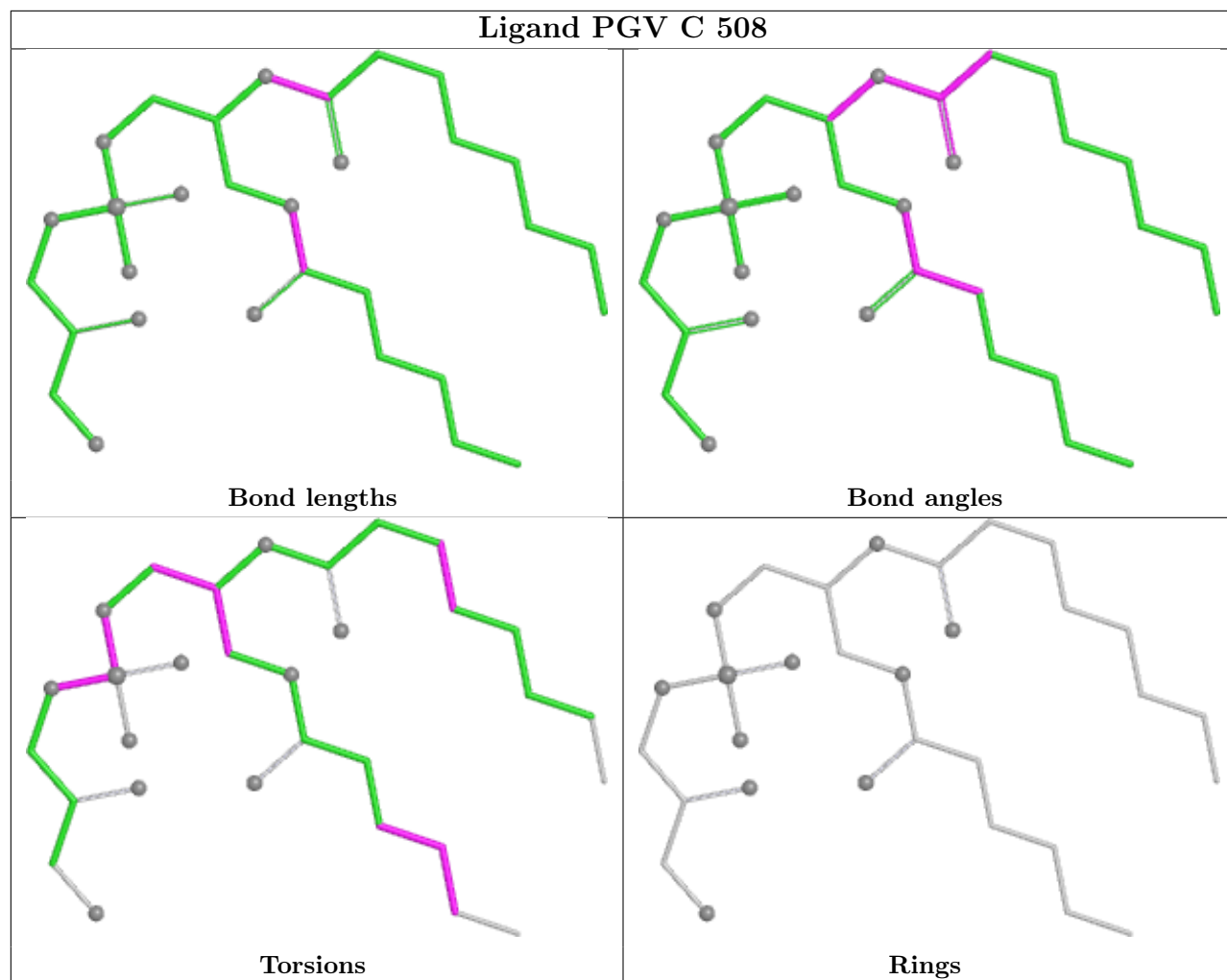


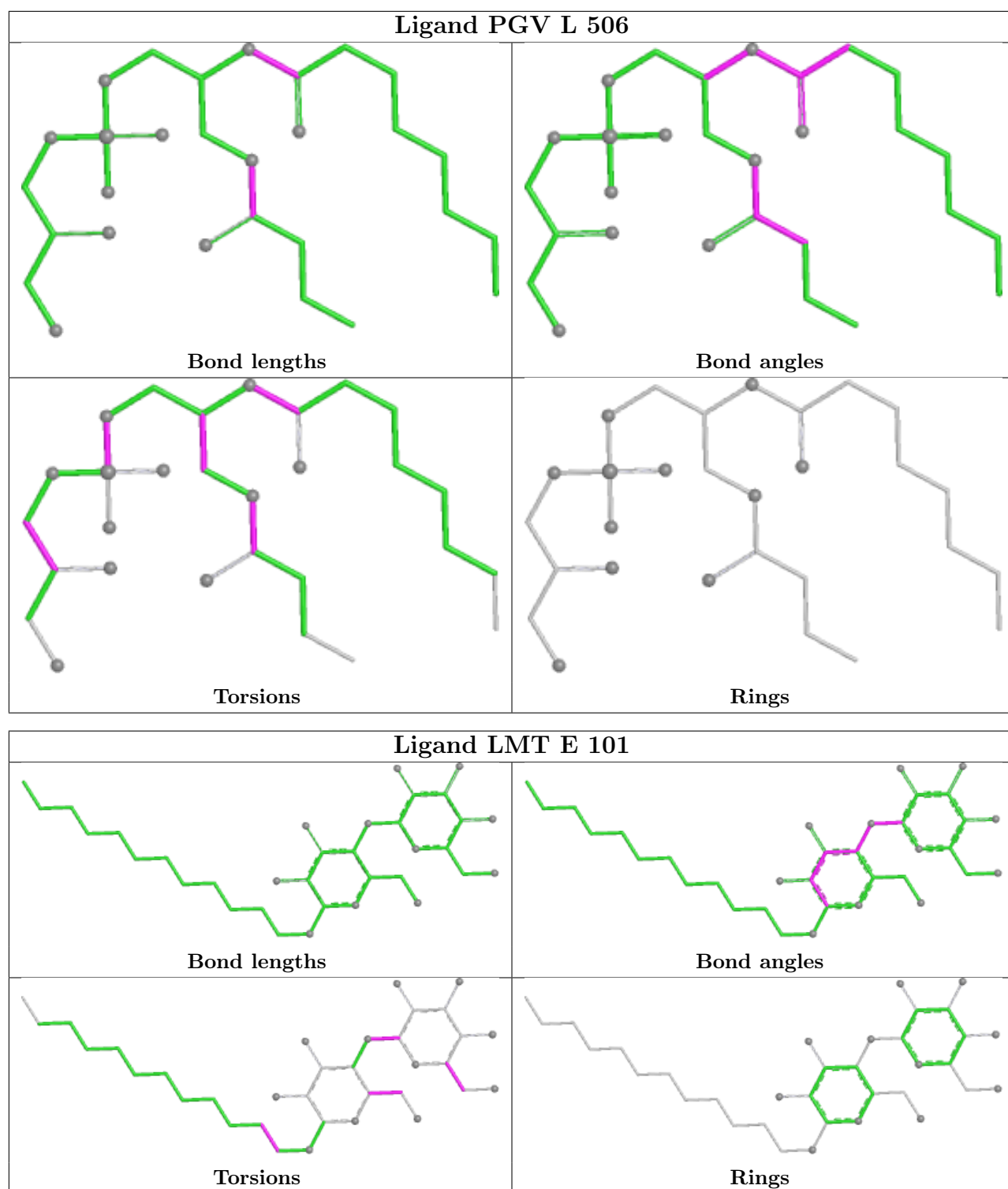


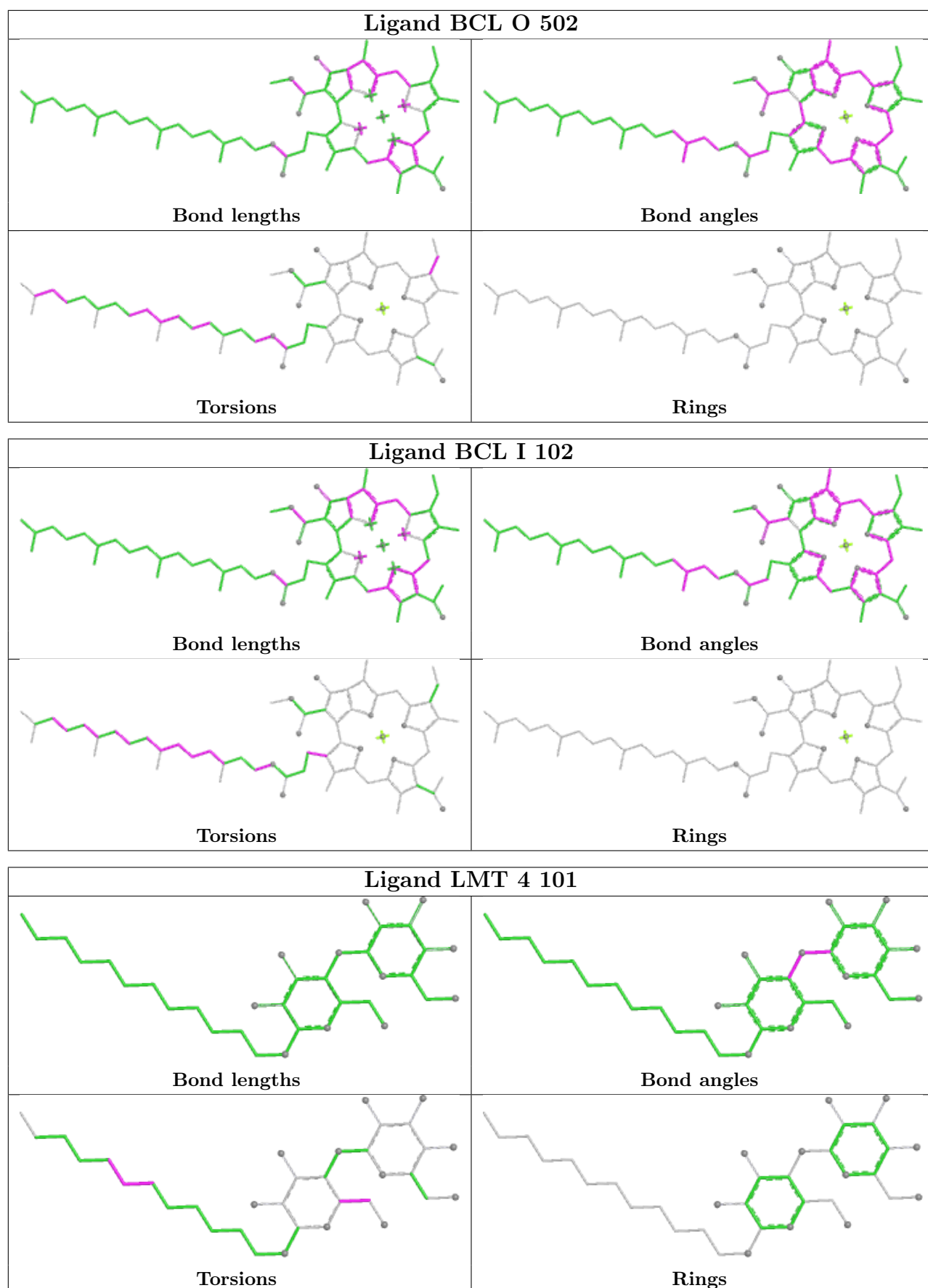


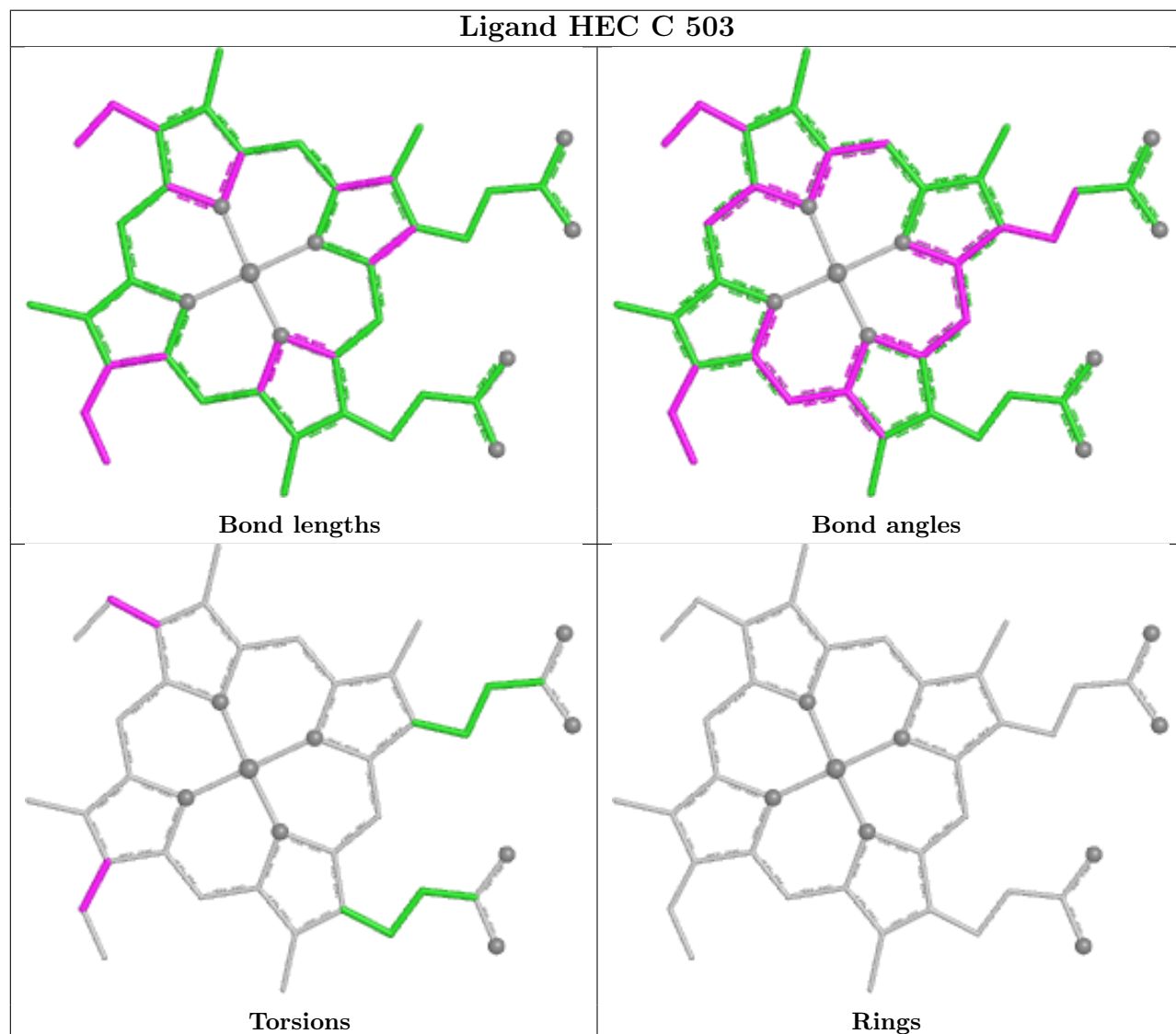
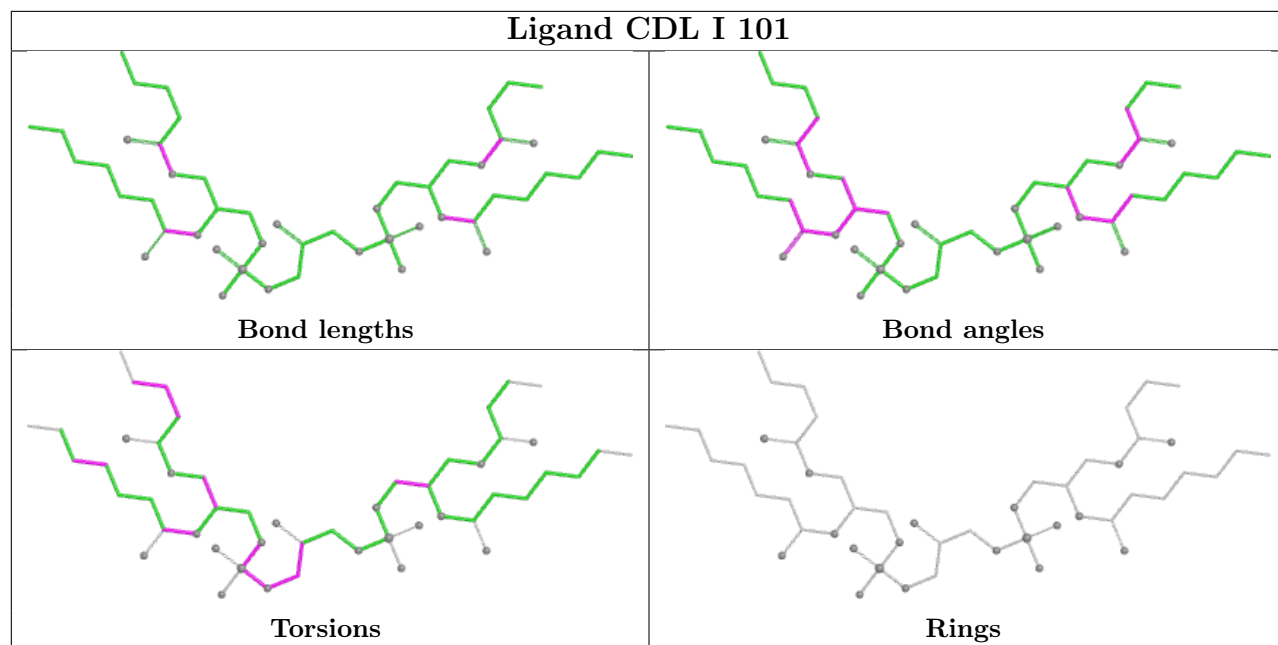


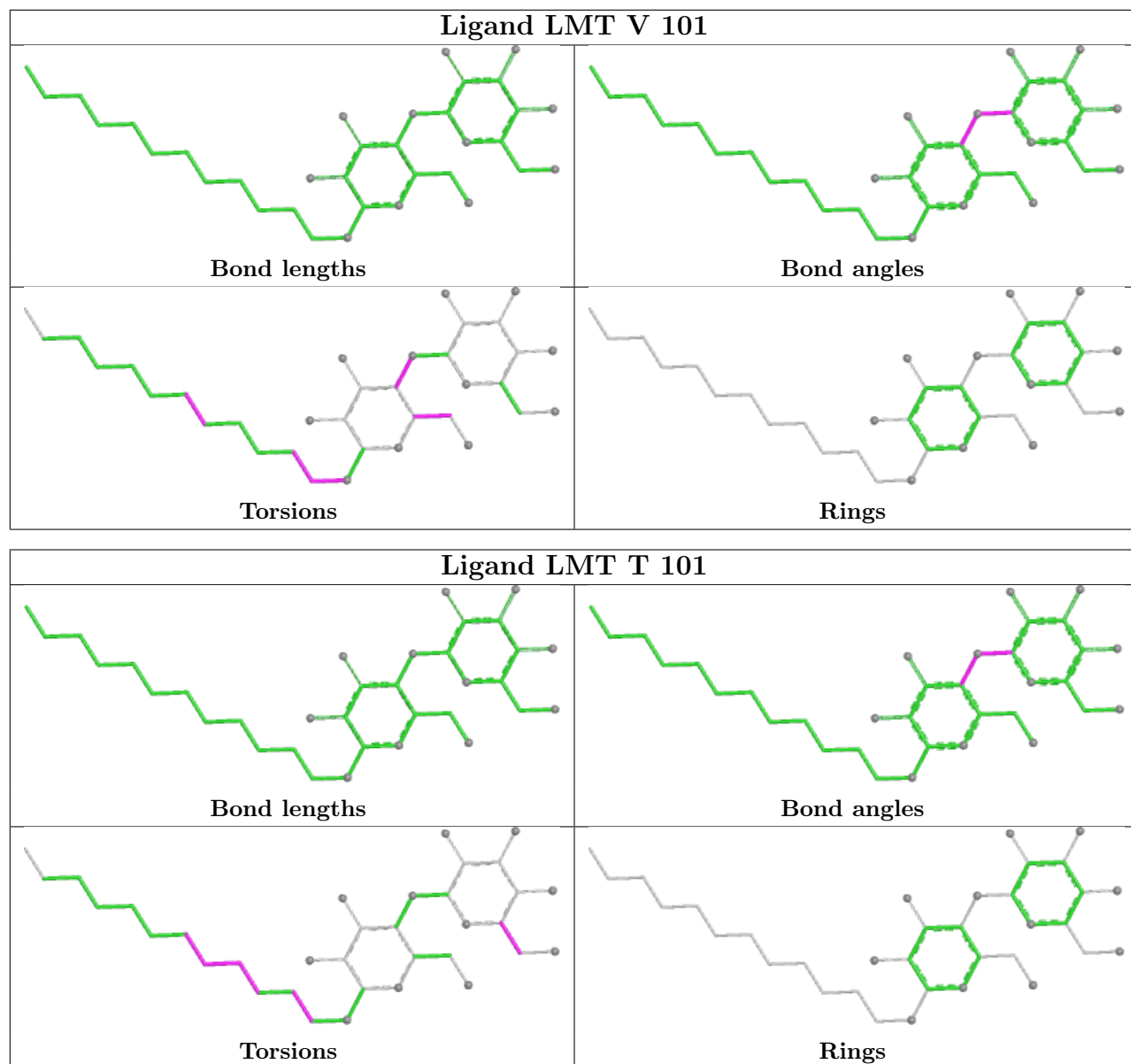


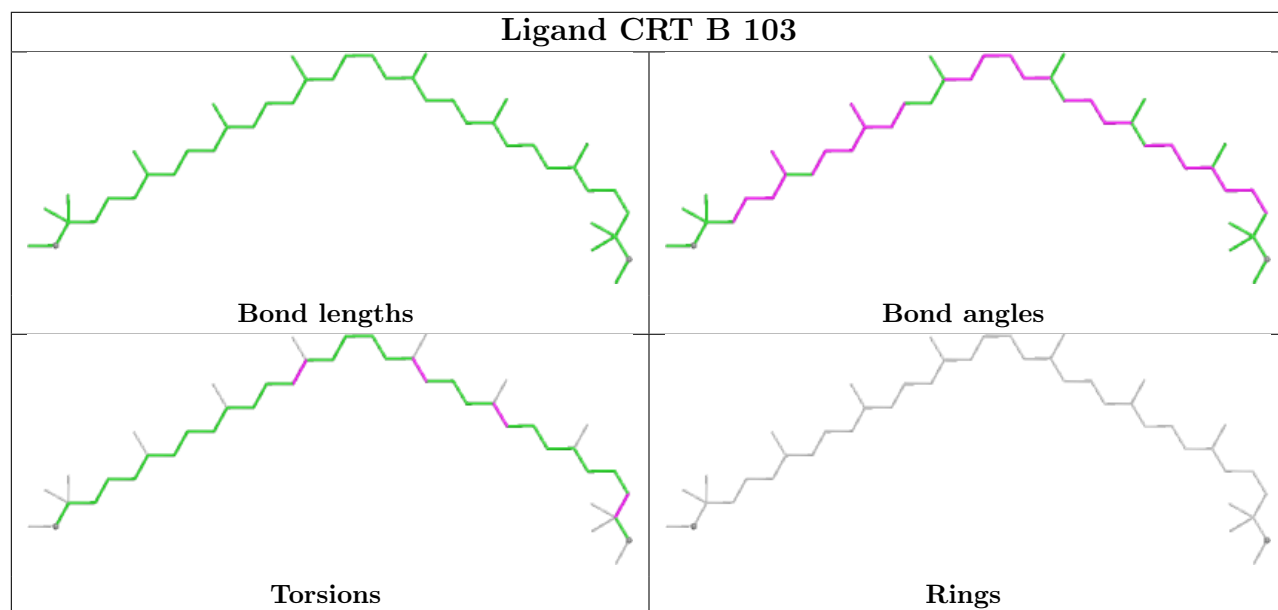
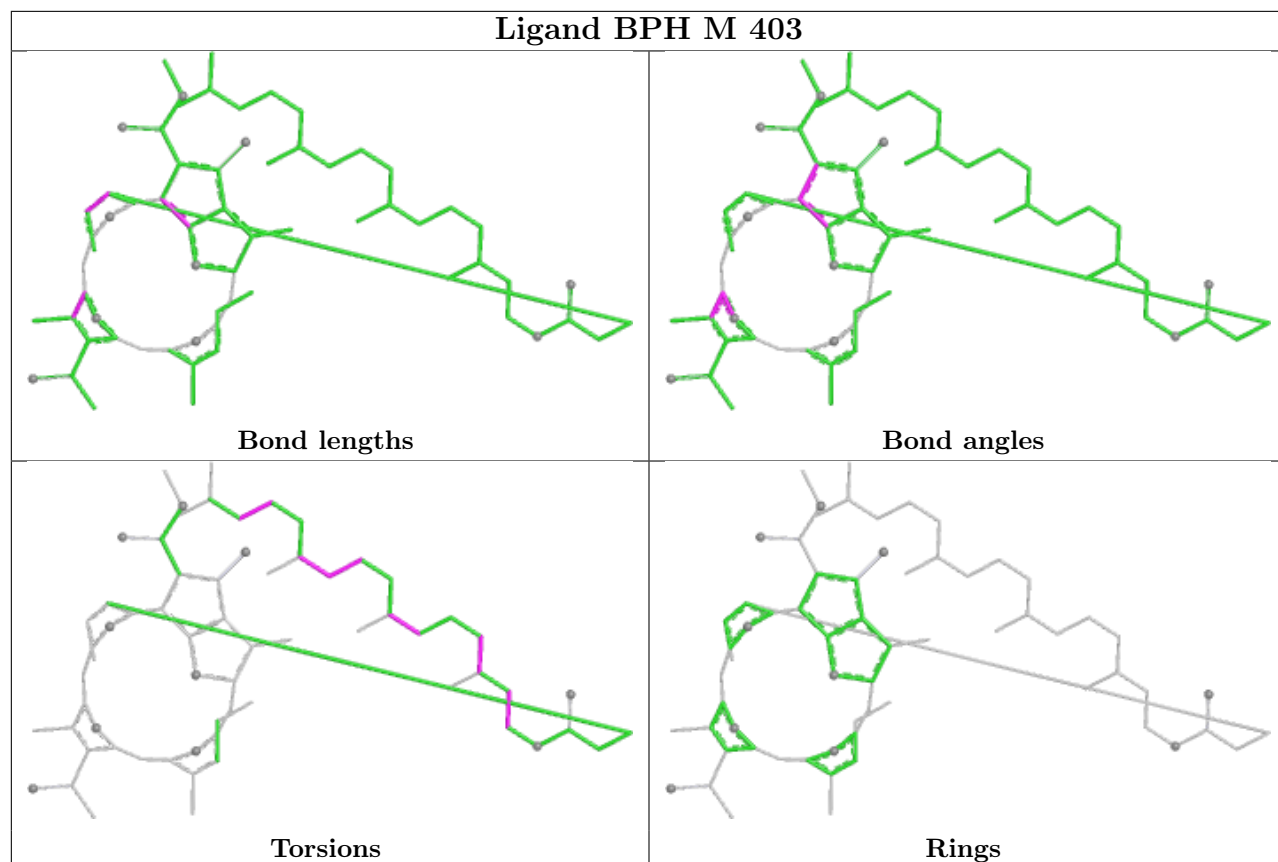


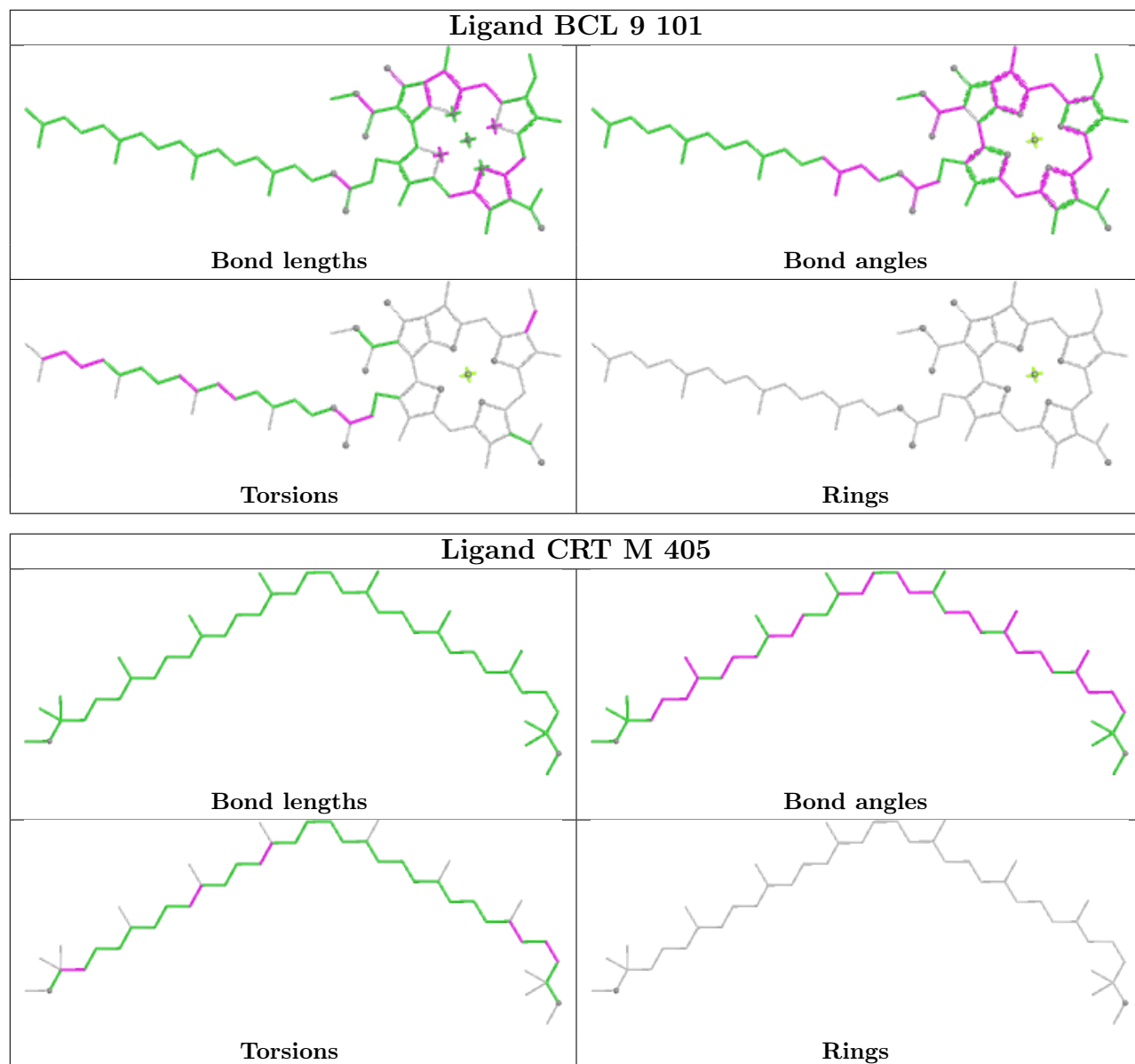


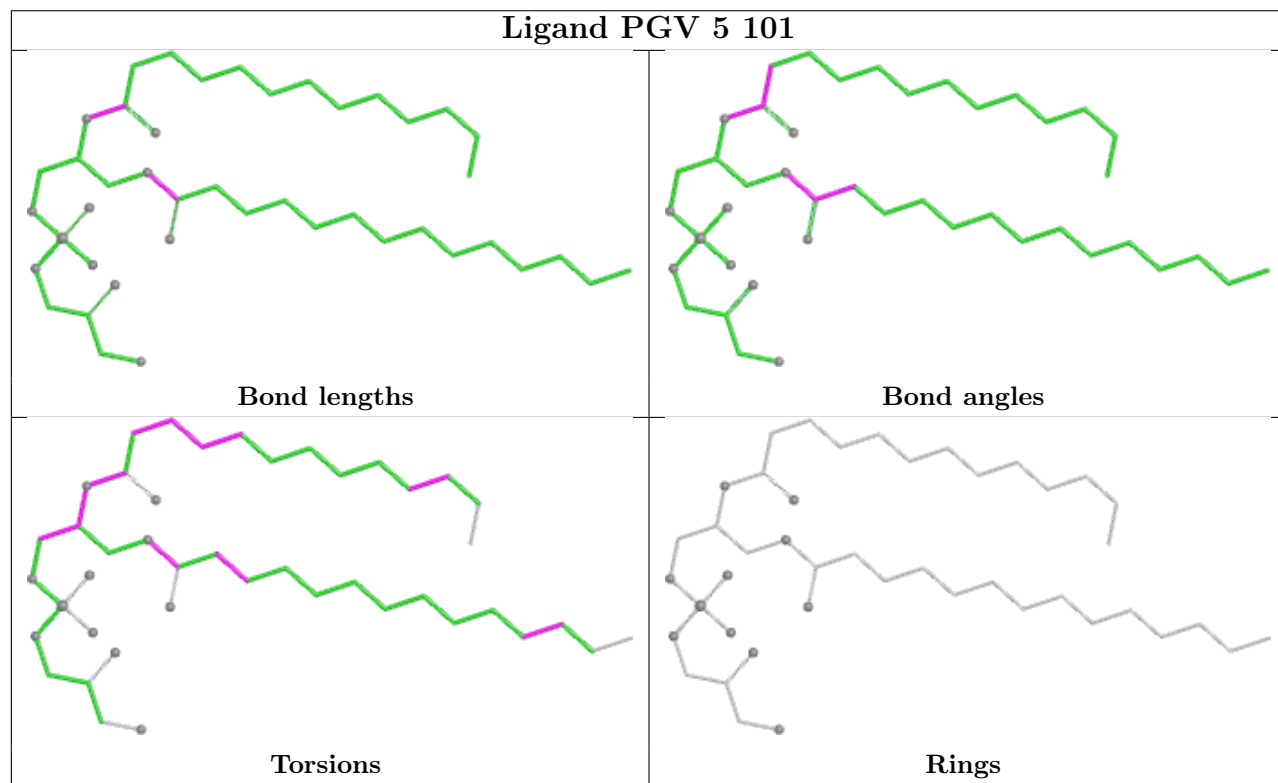
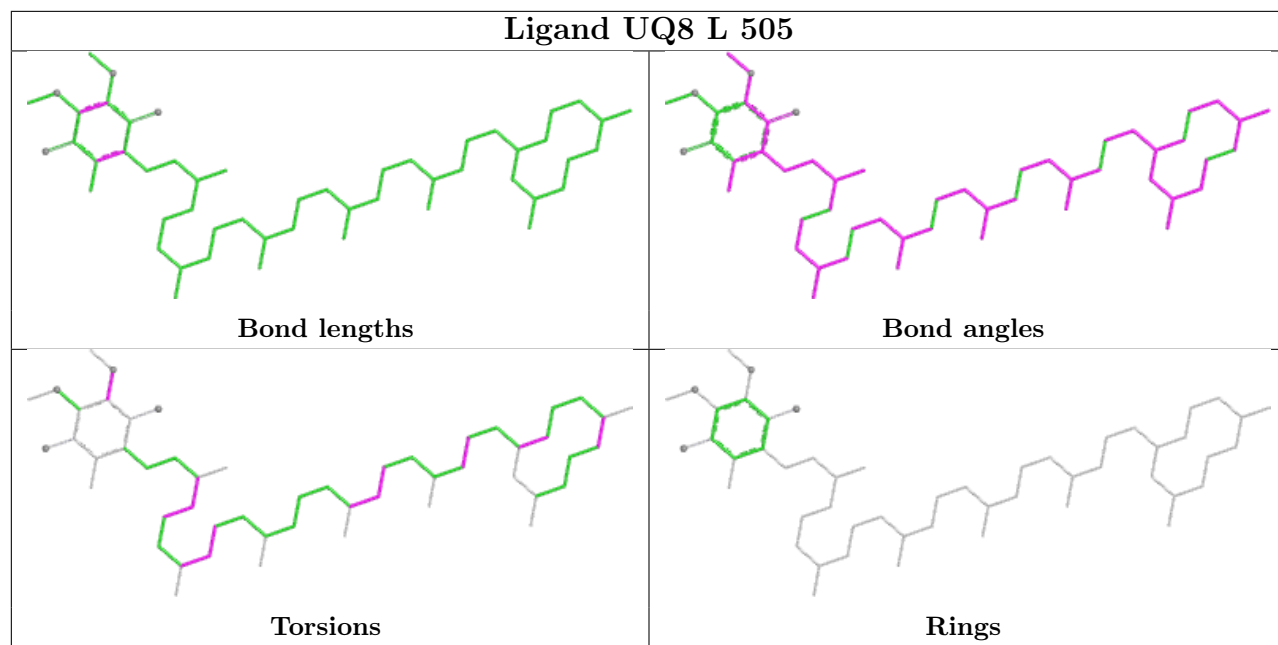


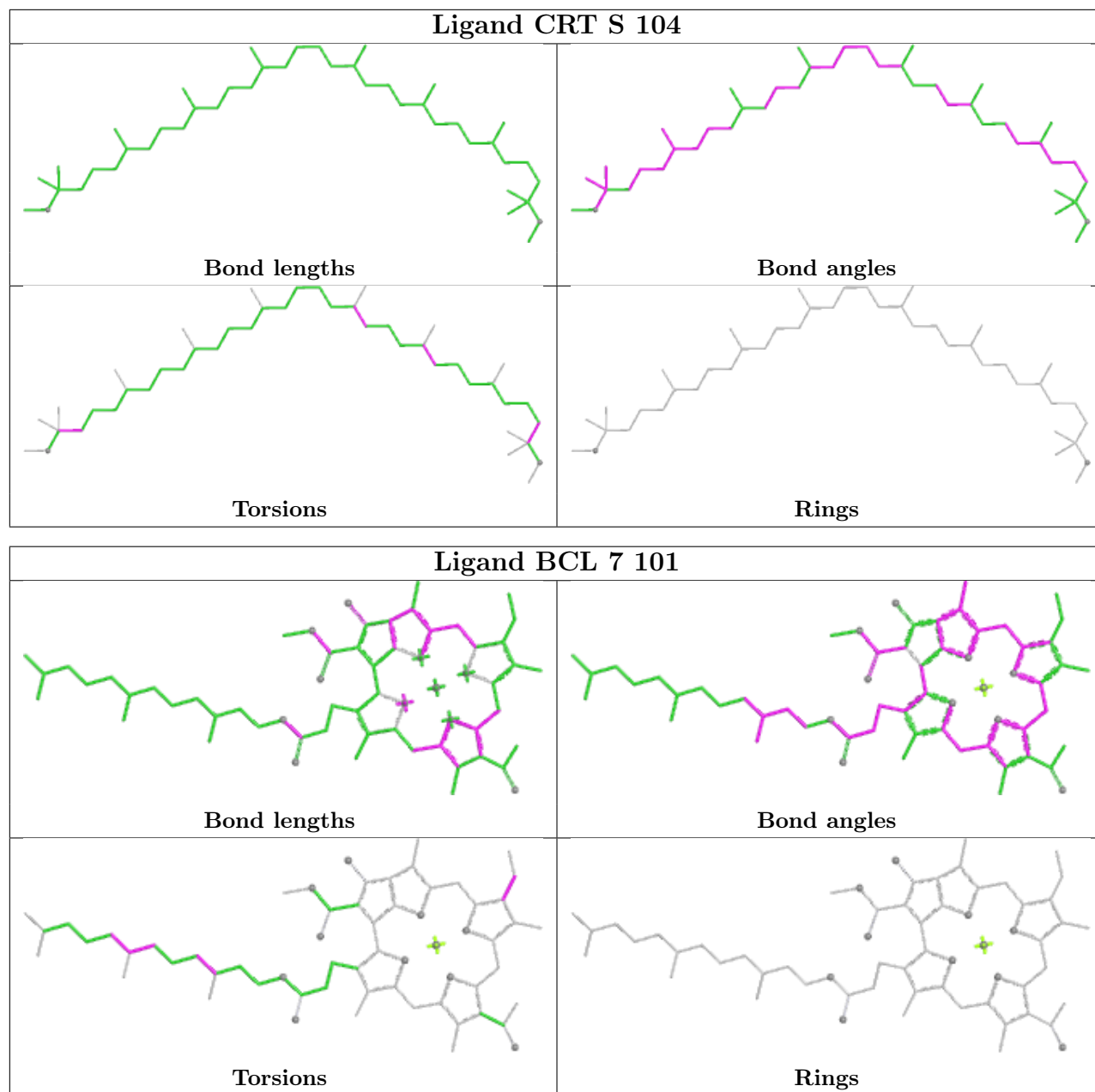


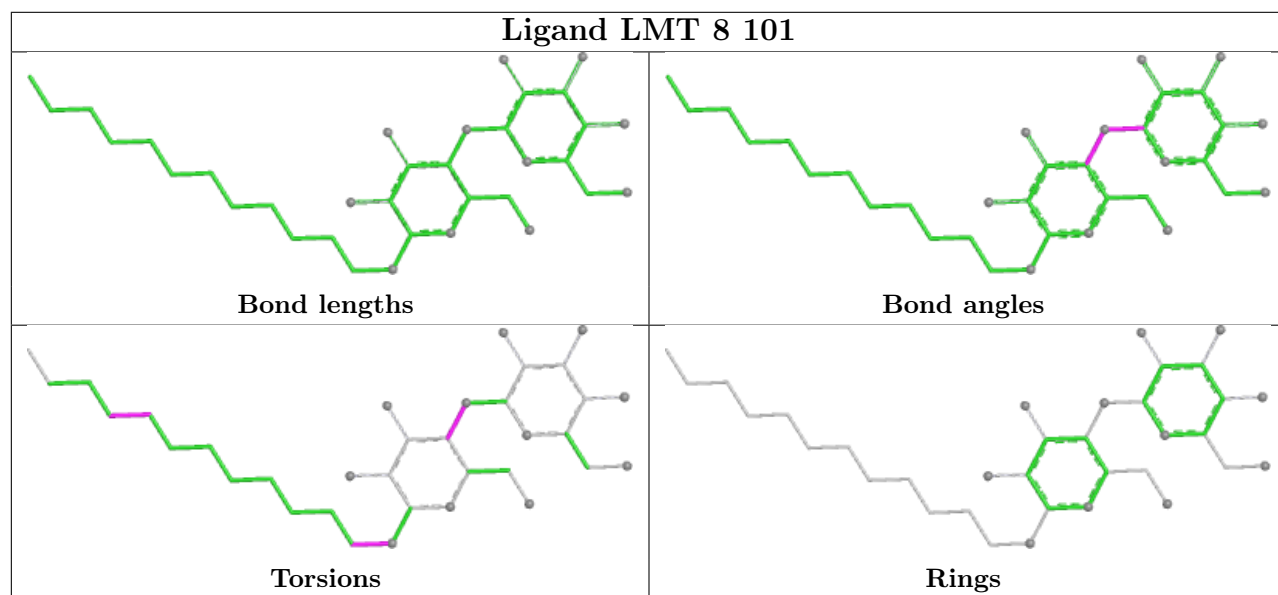
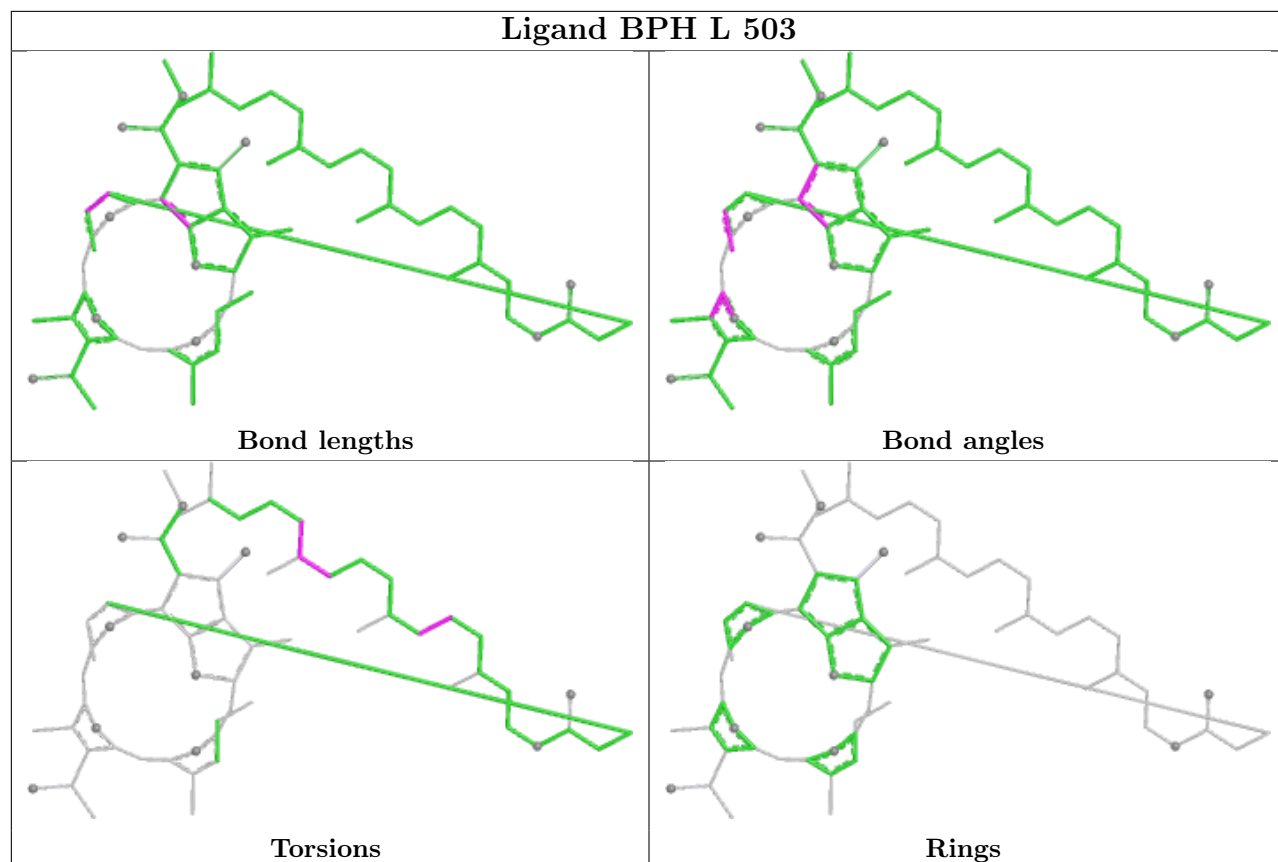


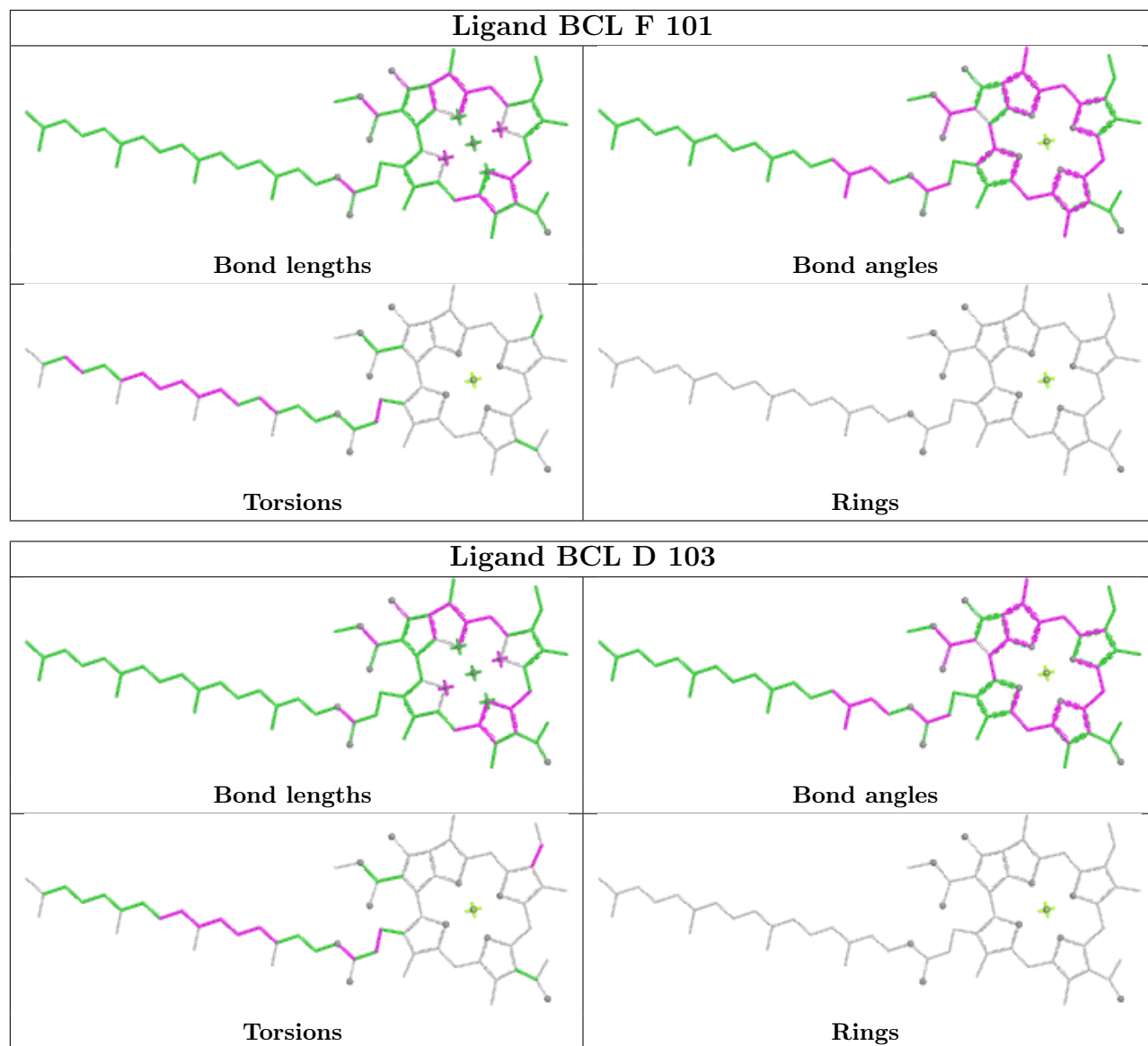


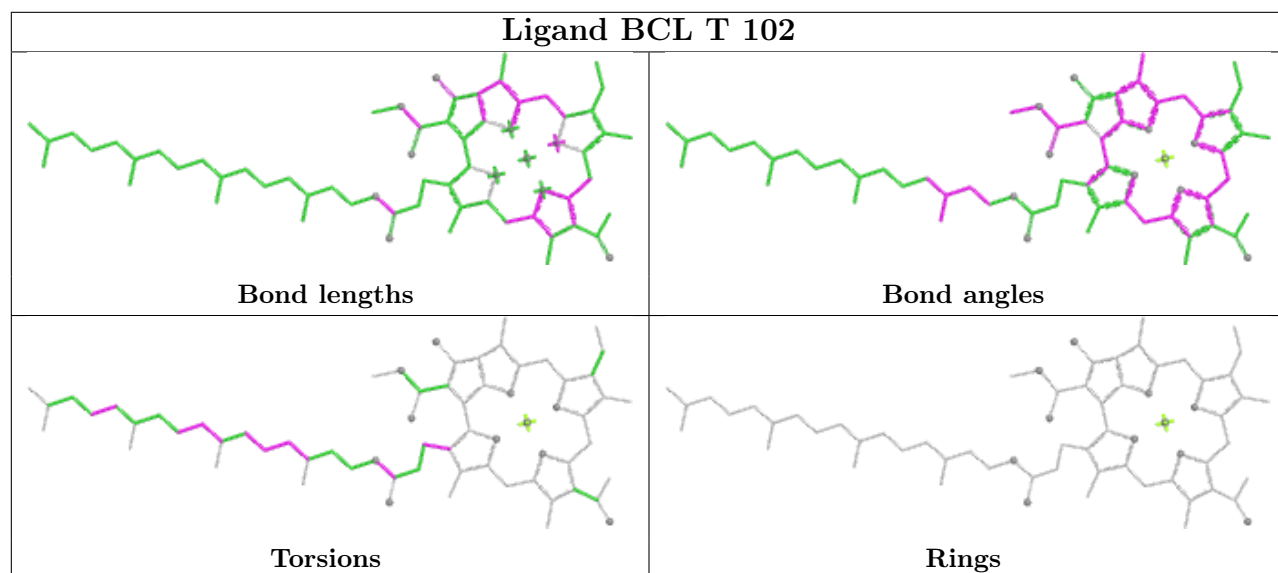
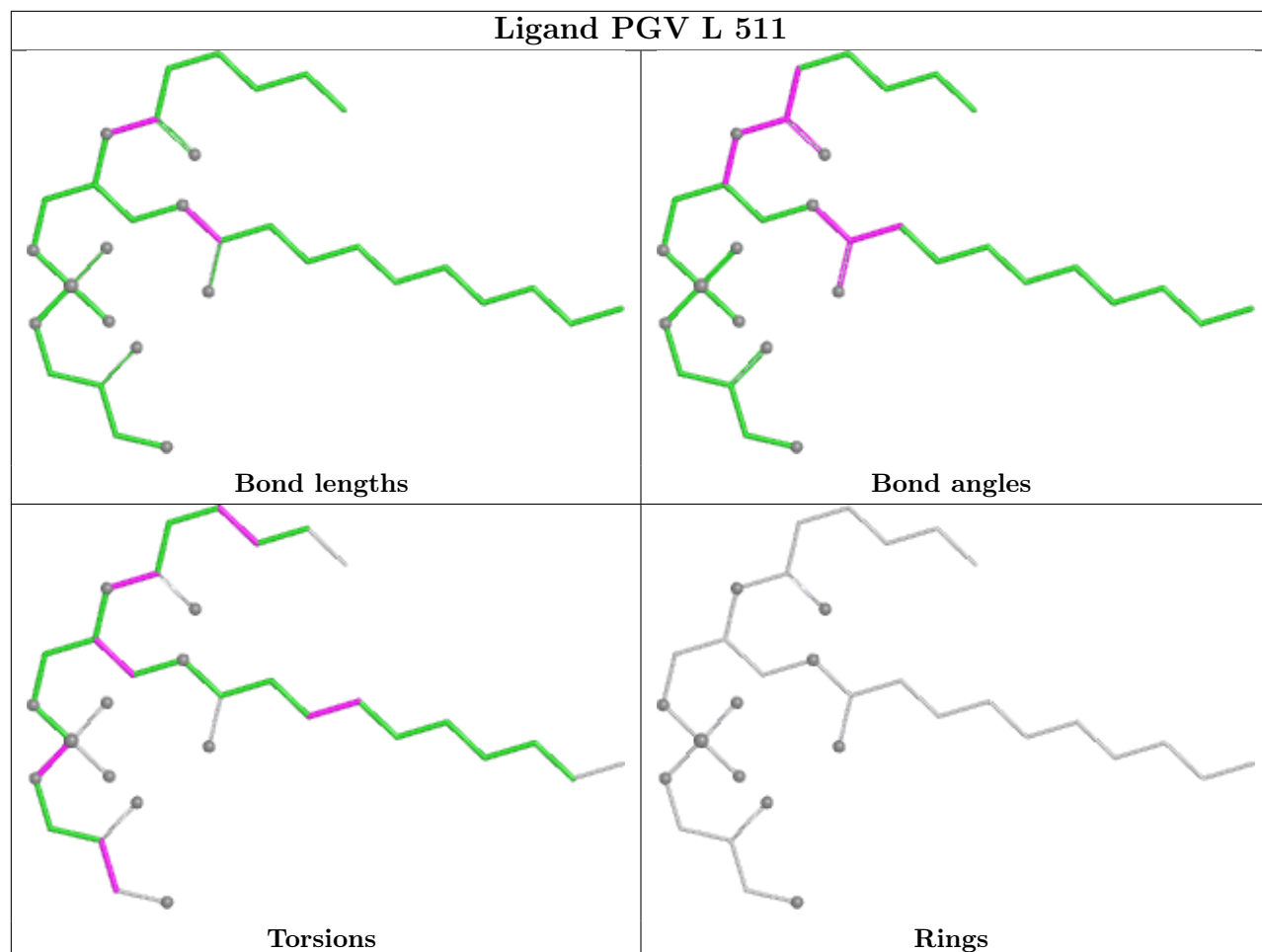


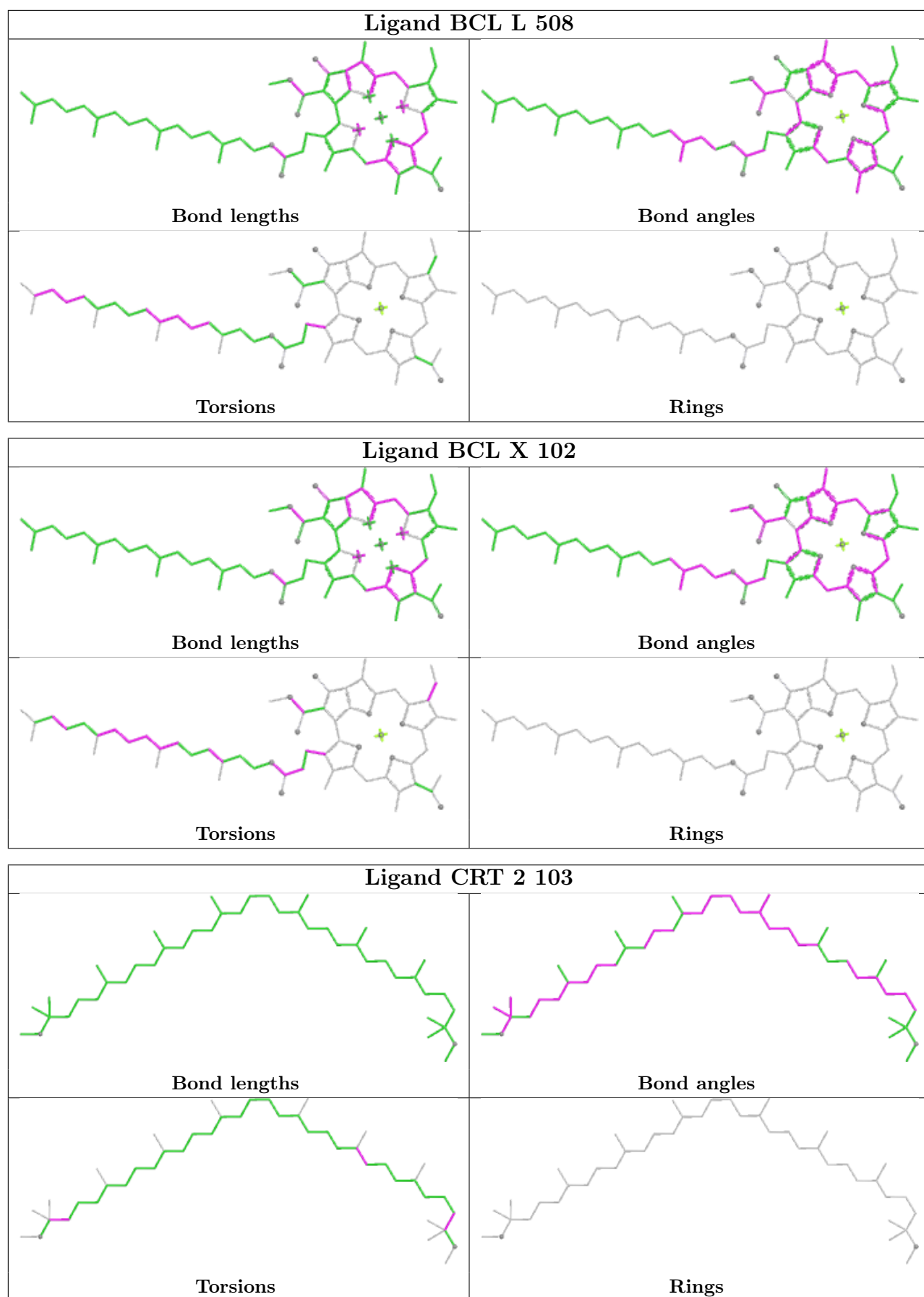


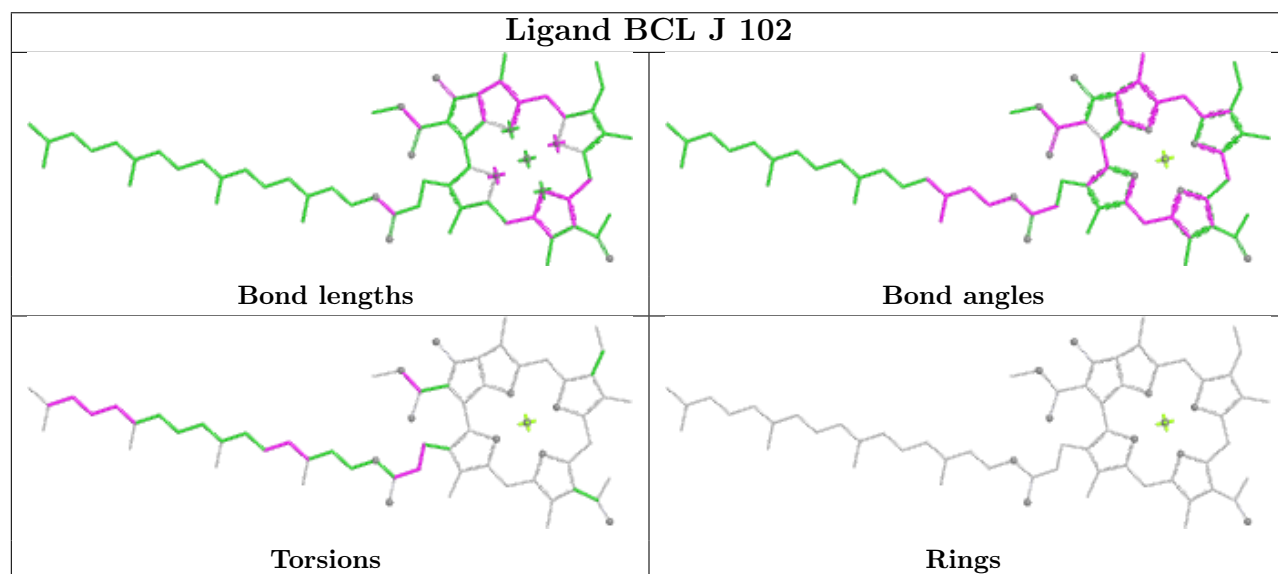
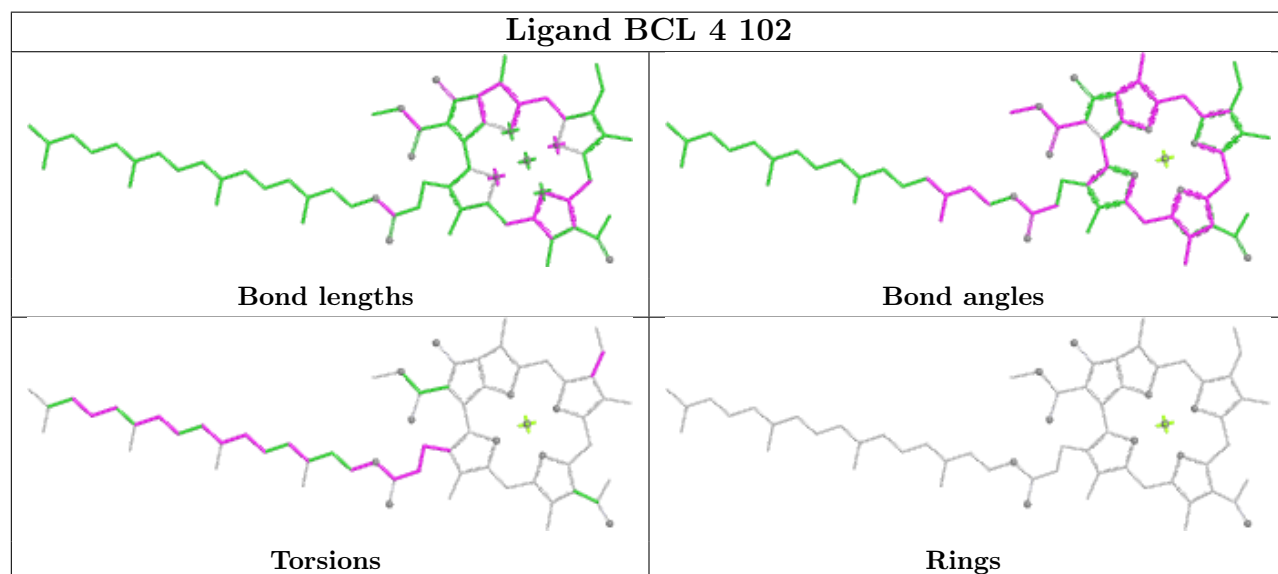
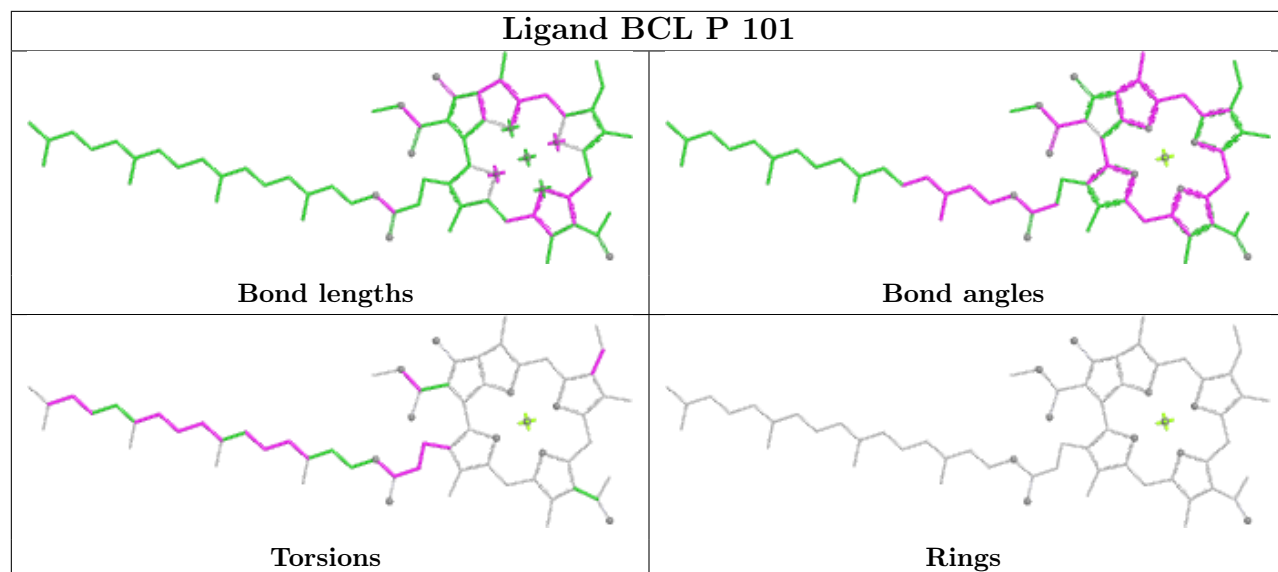


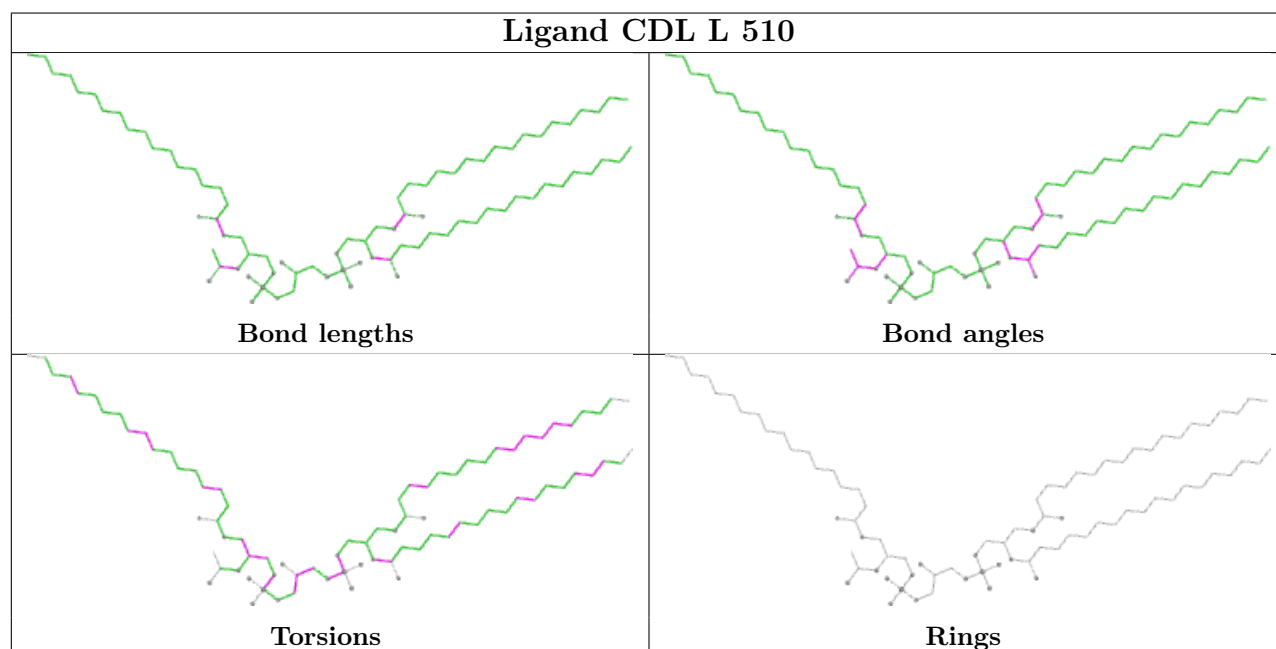
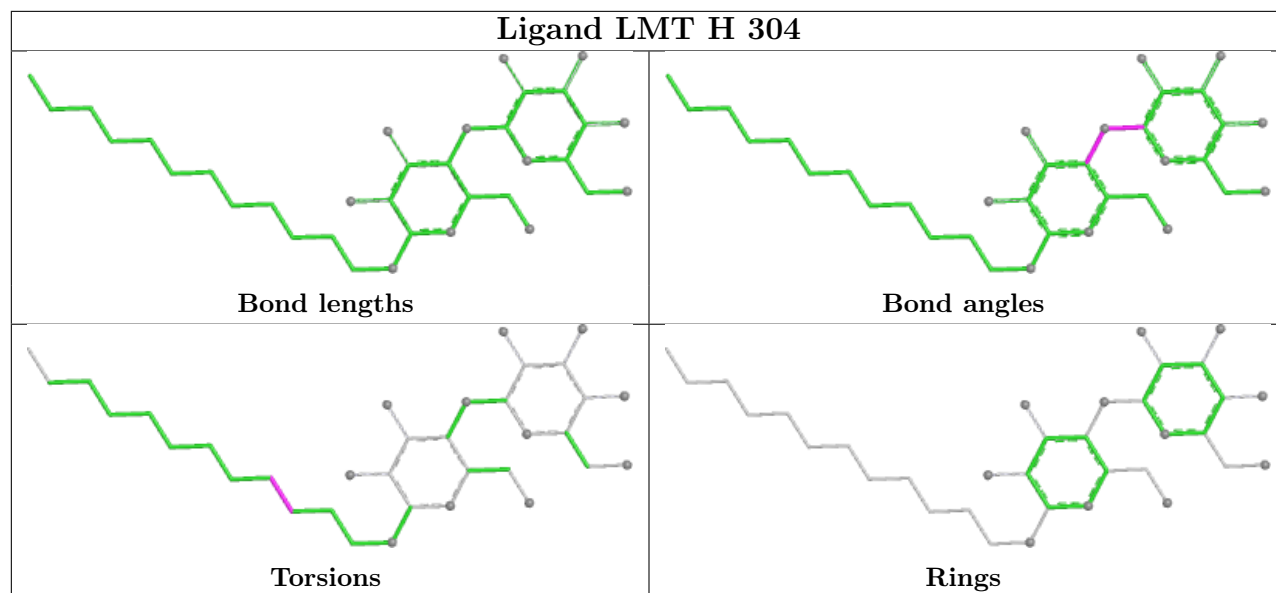


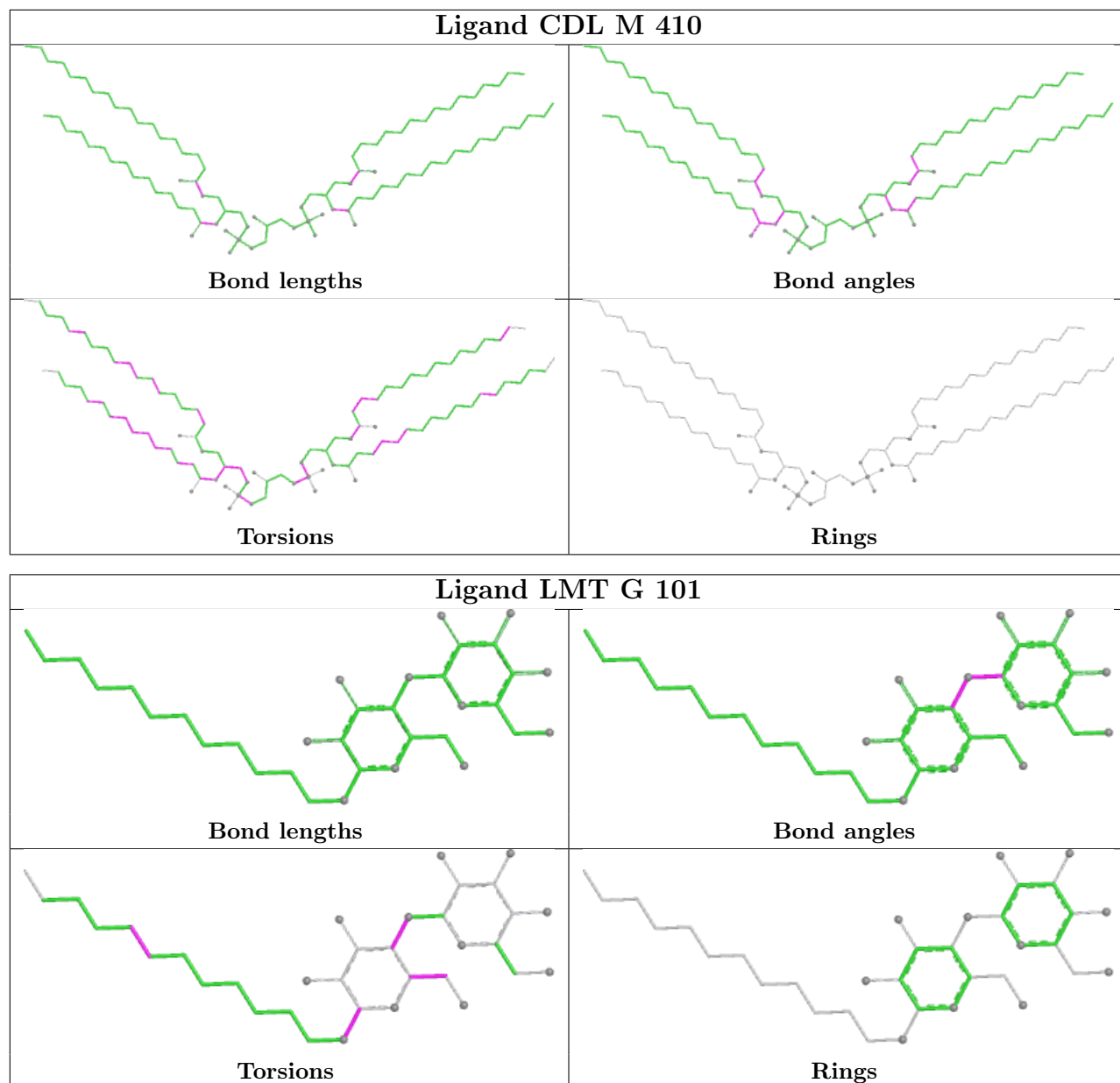


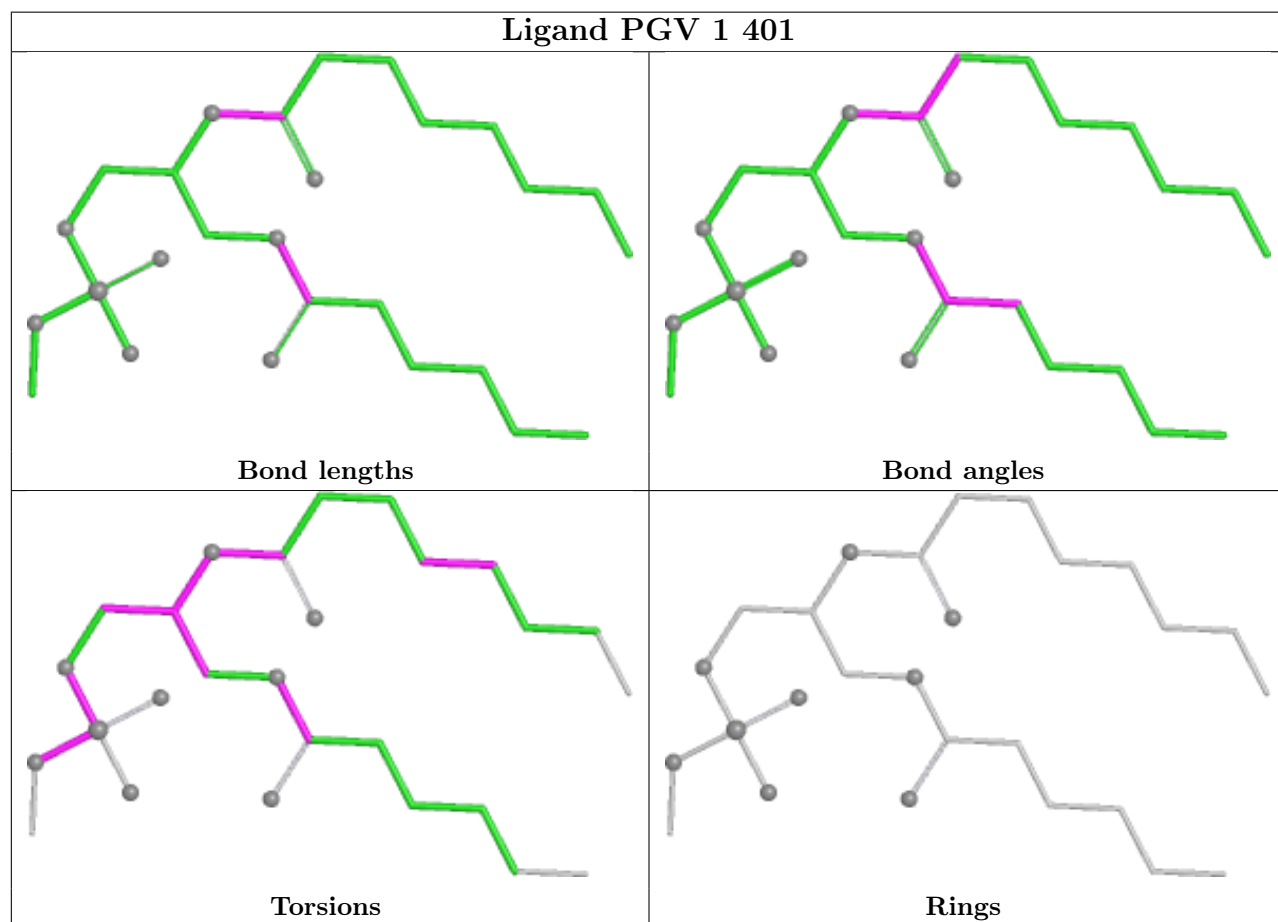
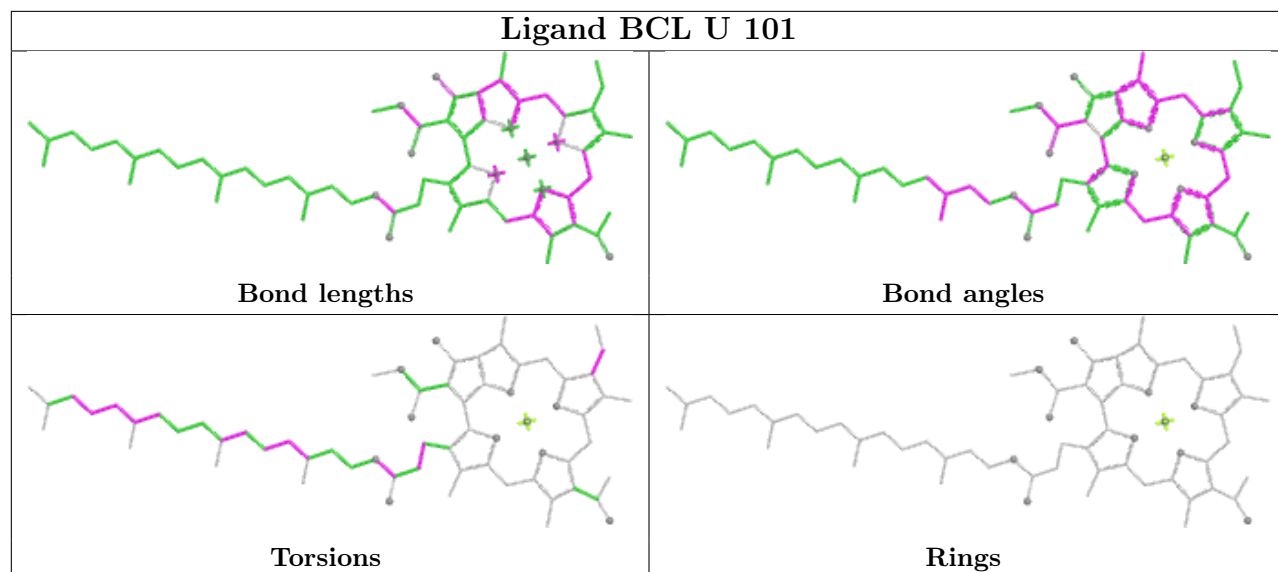


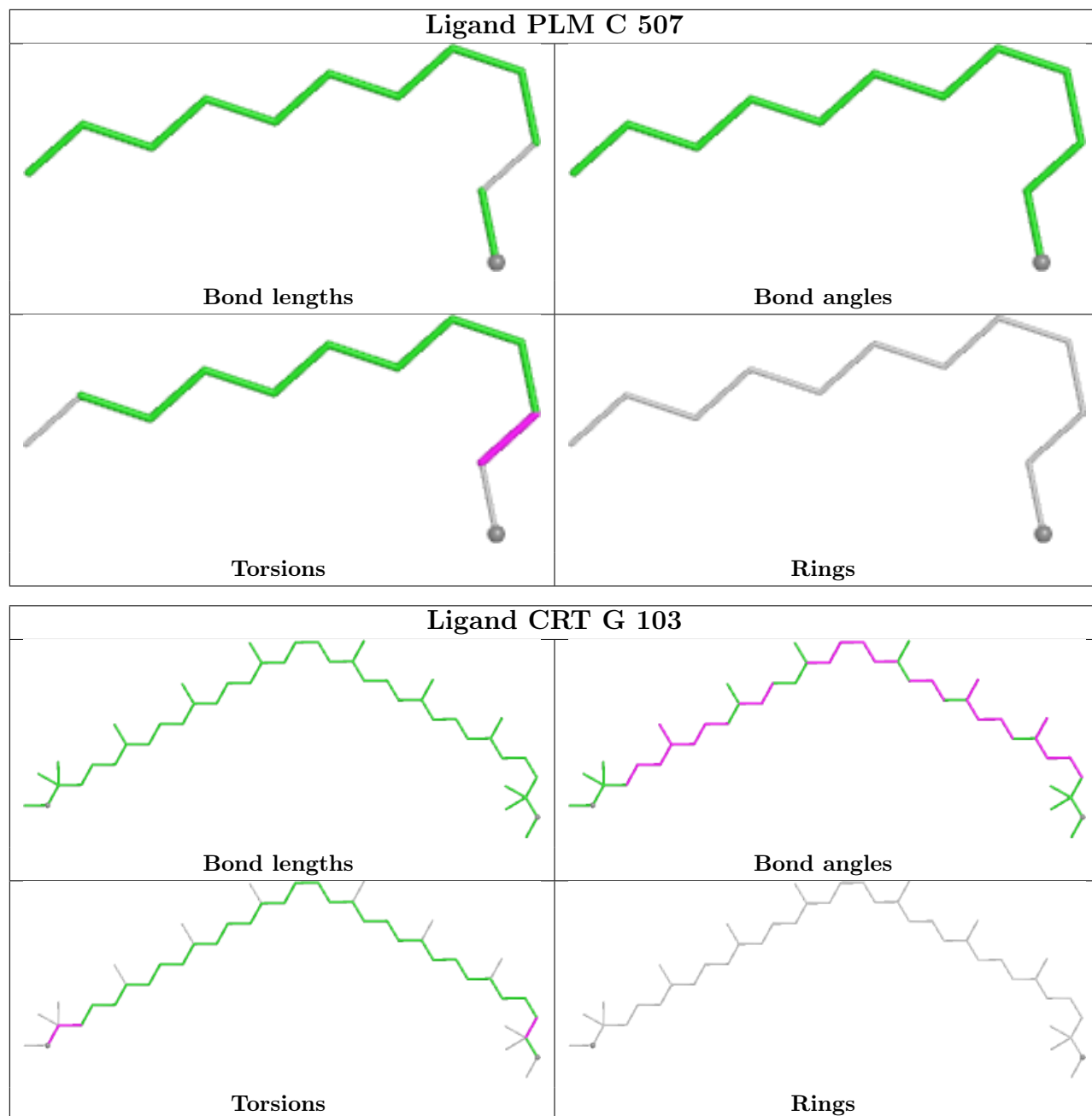


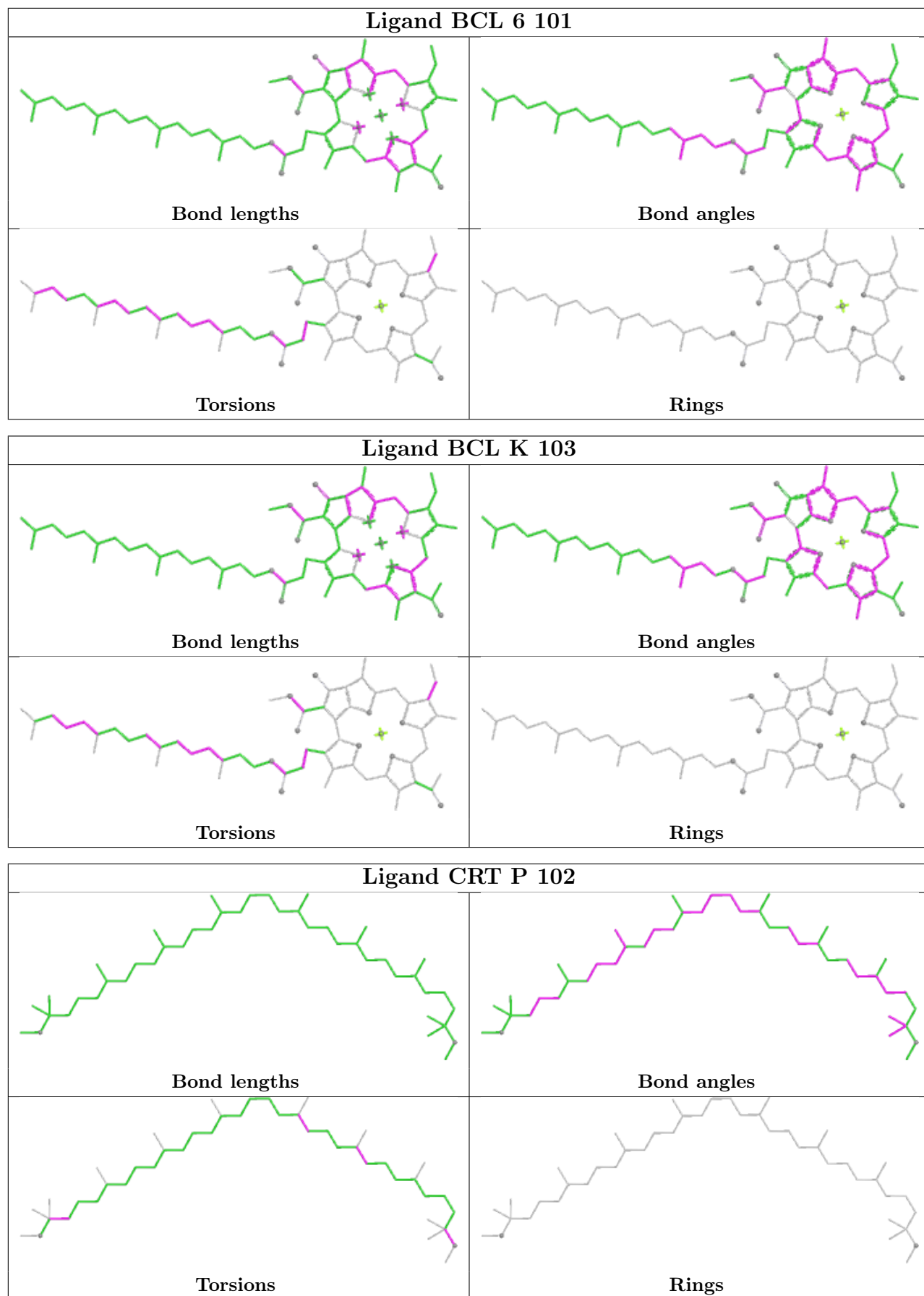


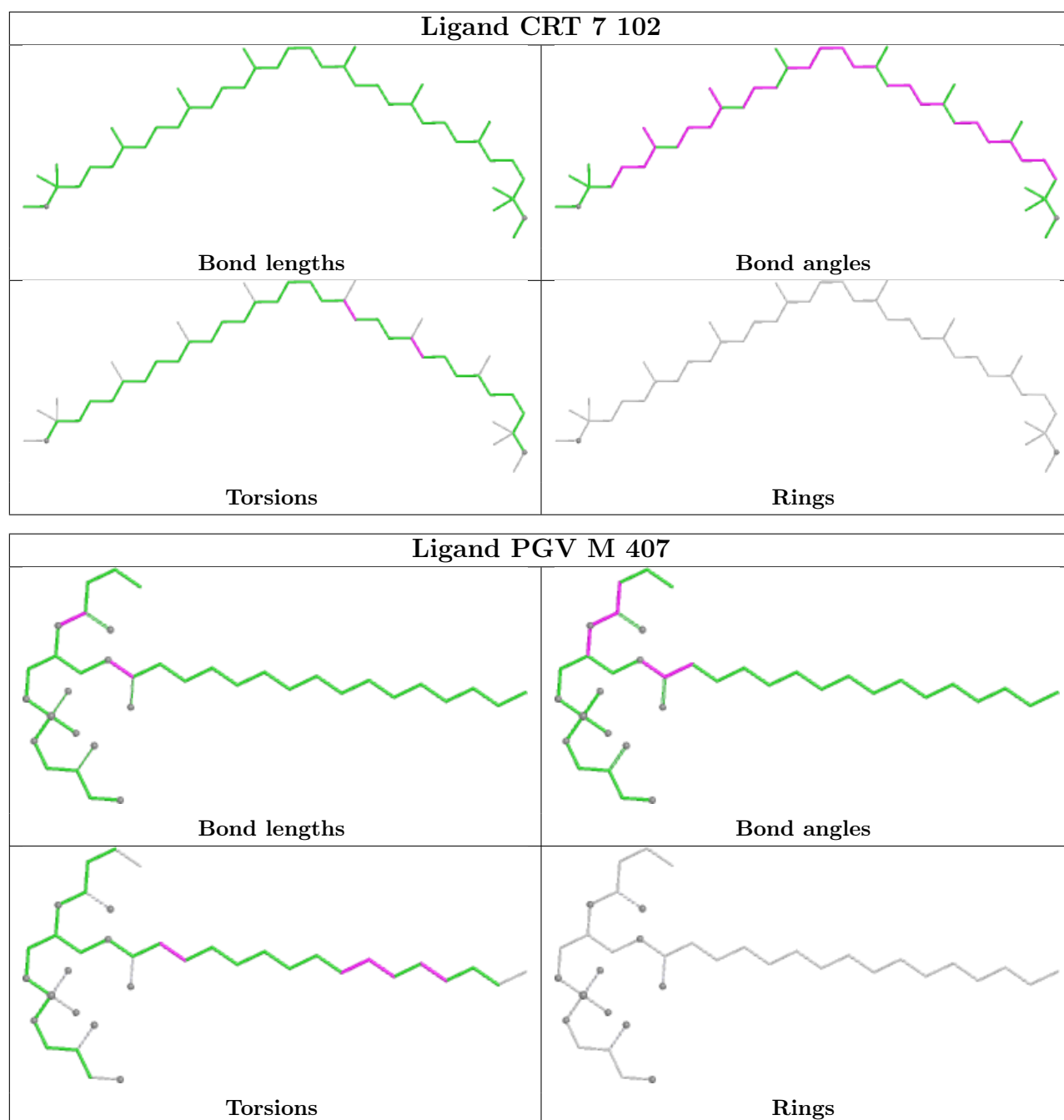












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

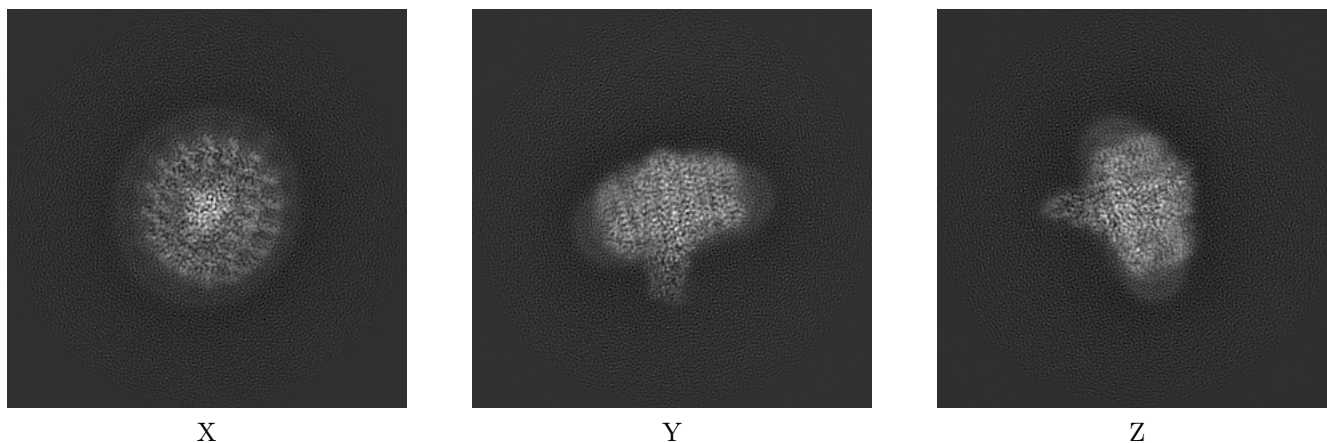
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32100. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

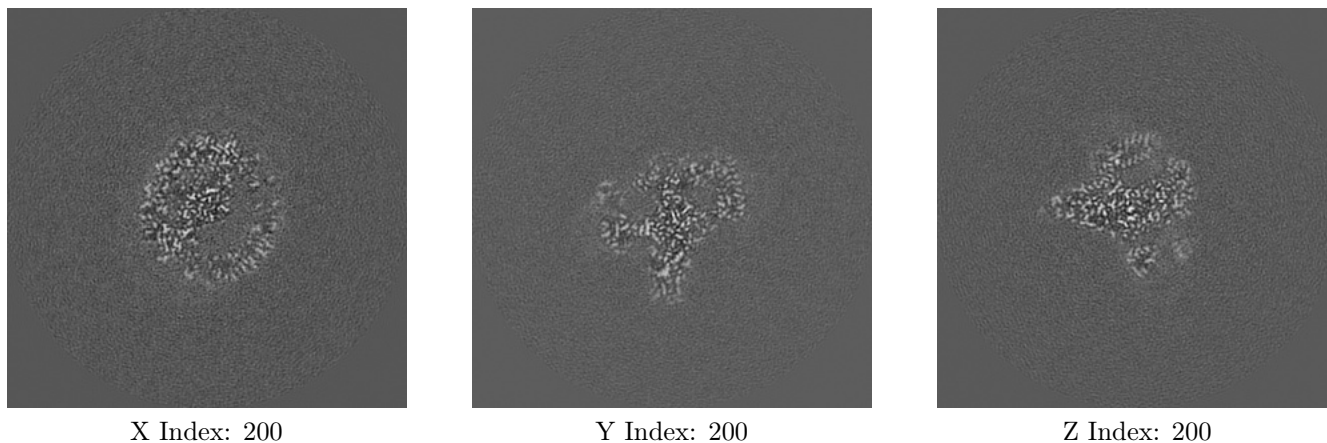
6.1.1 Primary map



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

6.2 Central slices [i](#)

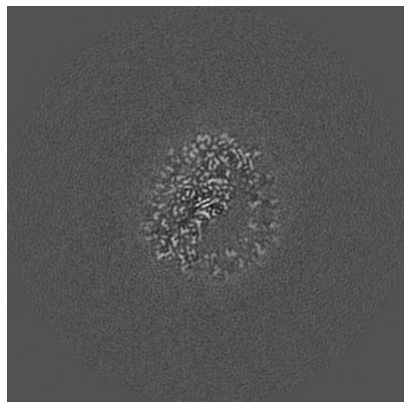
6.2.1 Primary map



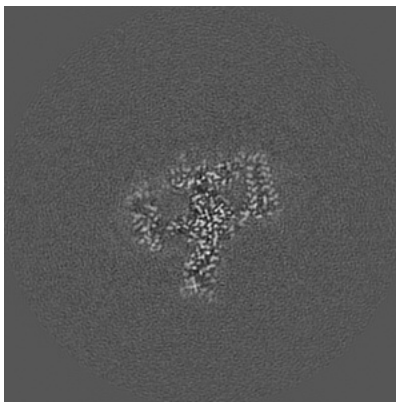
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

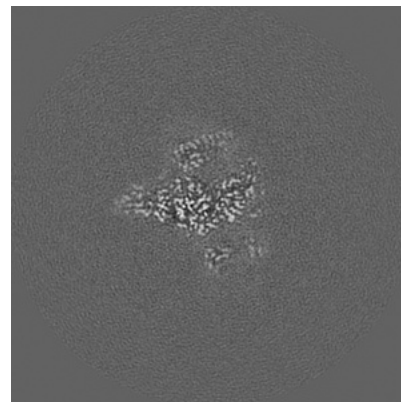
6.3.1 Primary map



X Index: 193



Y Index: 203

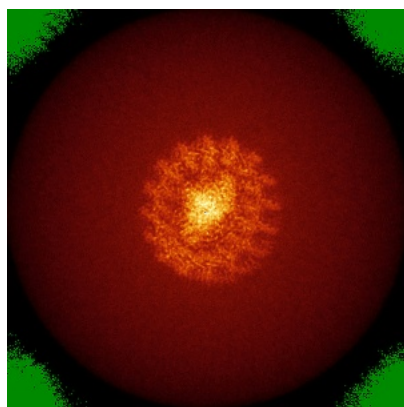


Z Index: 205

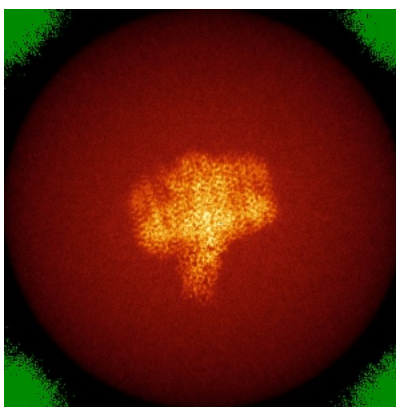
The images above show the largest variance slices of the map in three orthogonal directions.

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

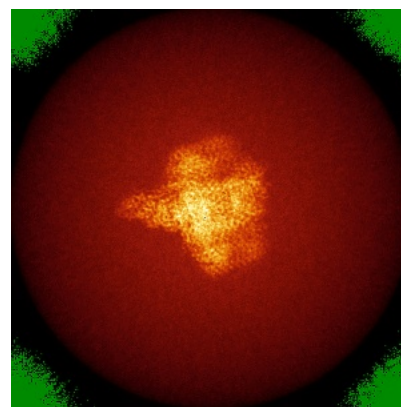
6.4.1 Primary map



X



Y

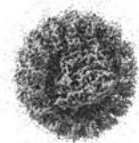


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0134. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

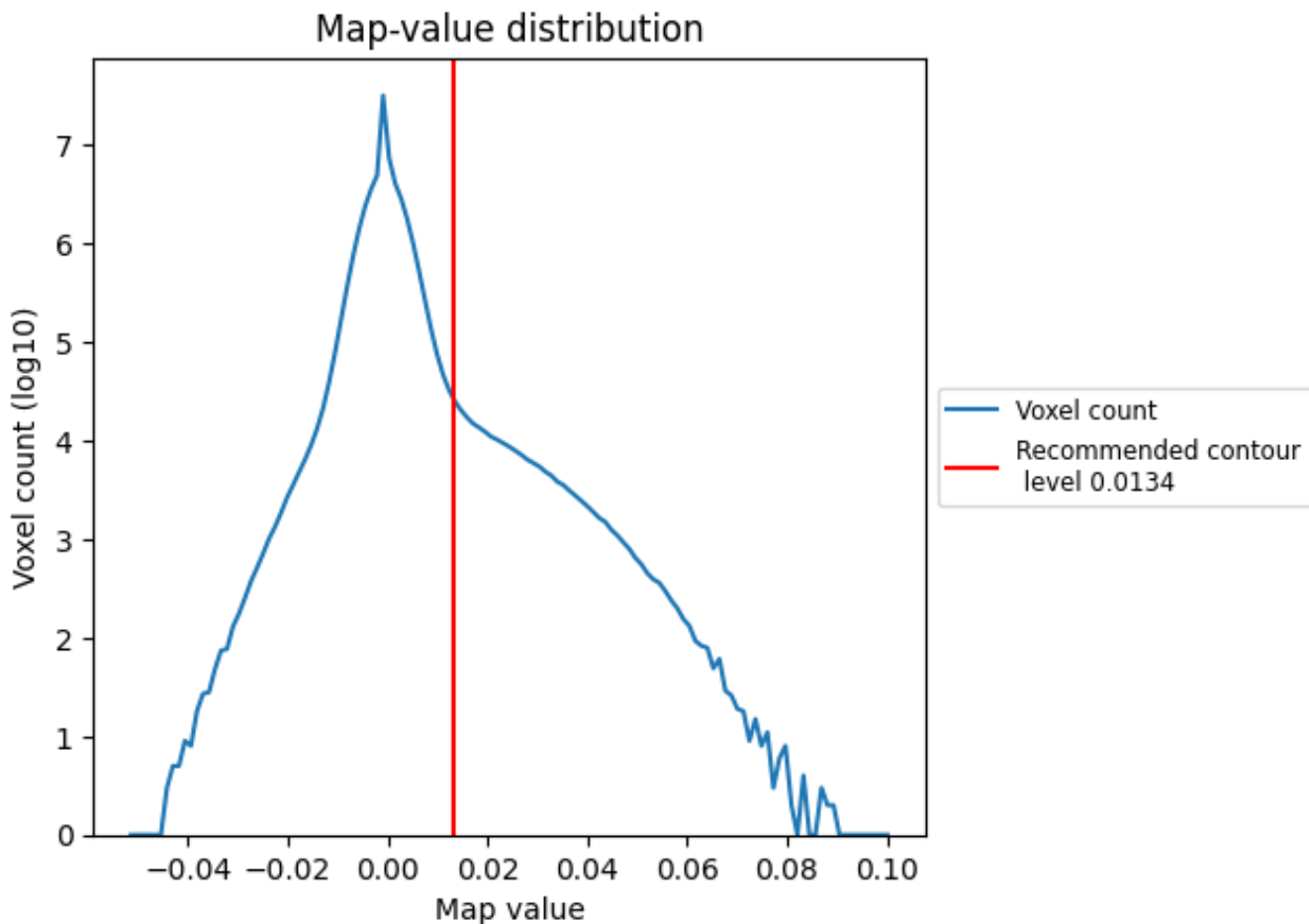
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

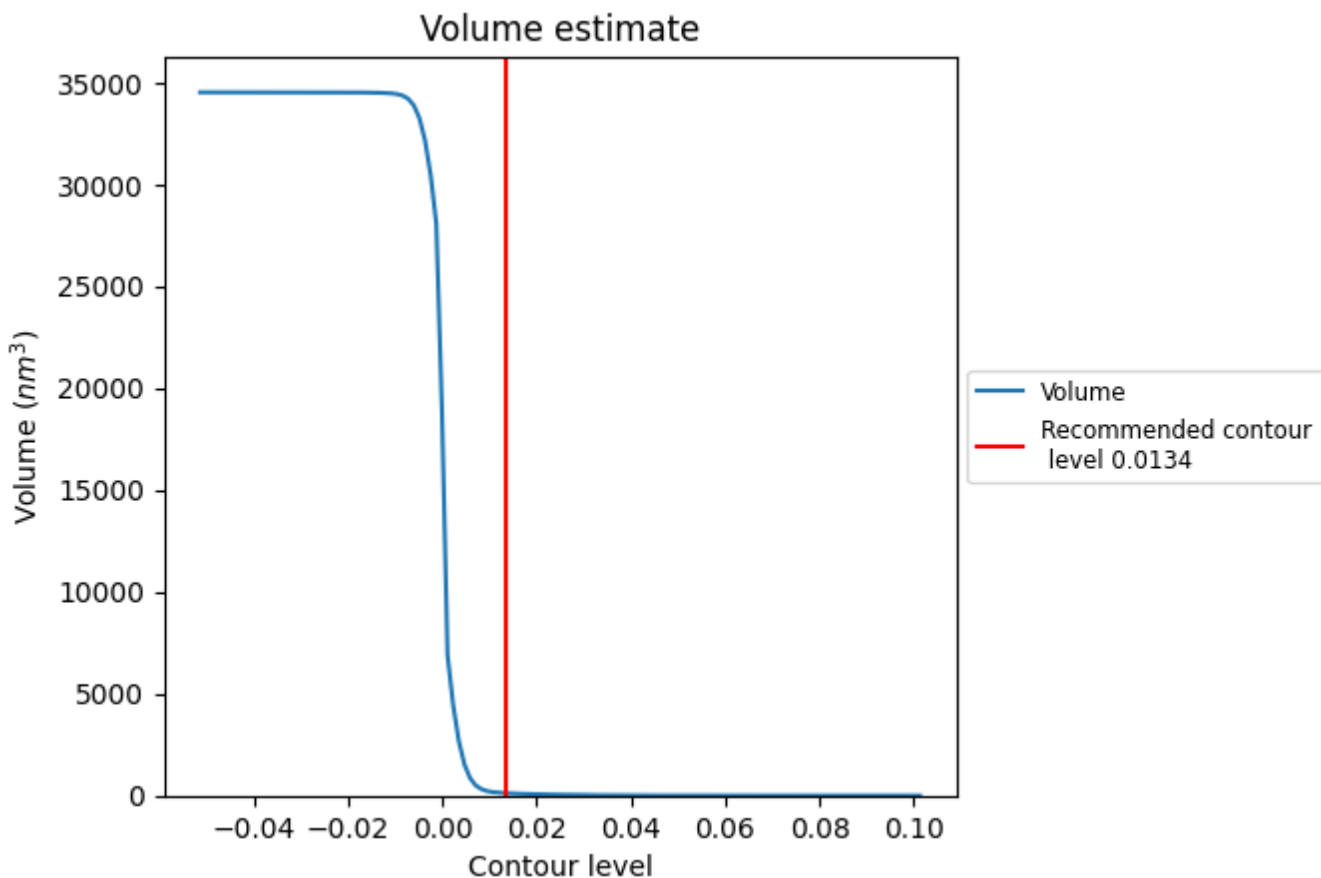
This section contains the results of statistical analysis of the map.

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.

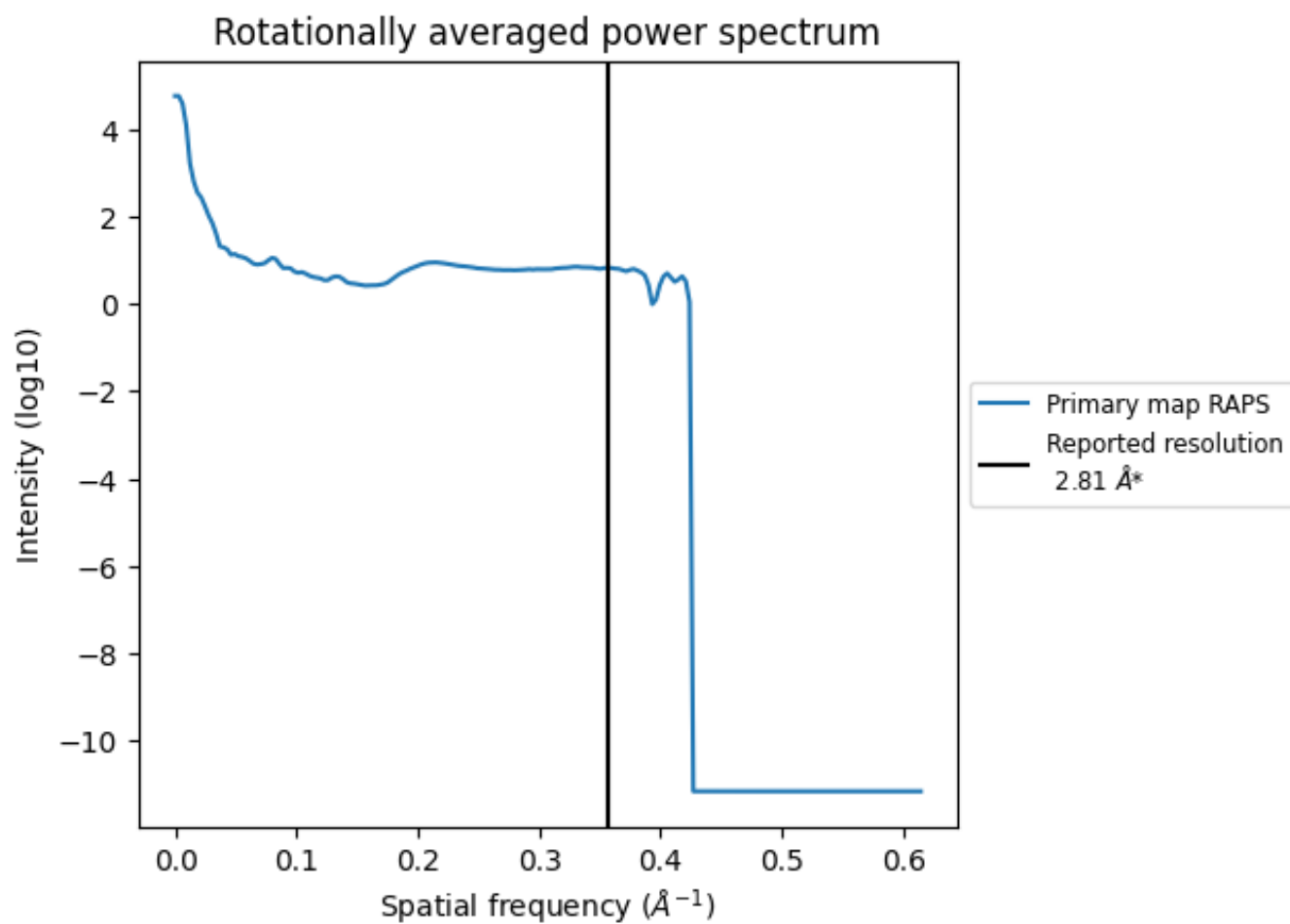
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 119 nm^3 ; this corresponds to an approximate mass of 107 kDa.

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

7.3 Rotationally averaged power spectrum [\(i\)](#)

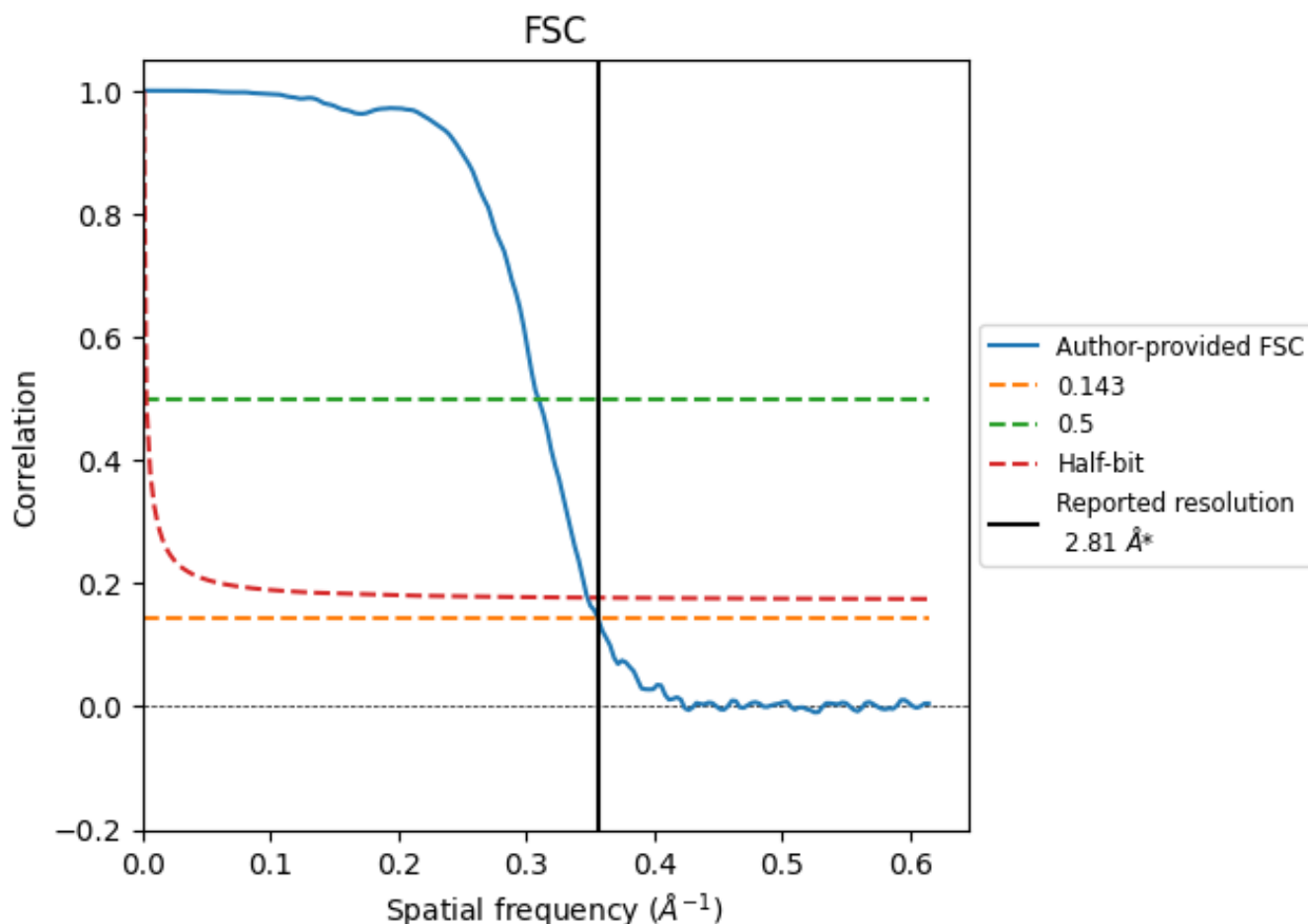


*Reported resolution corresponds to spatial frequency of 0.356 Å⁻¹

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 0.356 Å⁻¹

8.2 Resolution estimates [i](#)

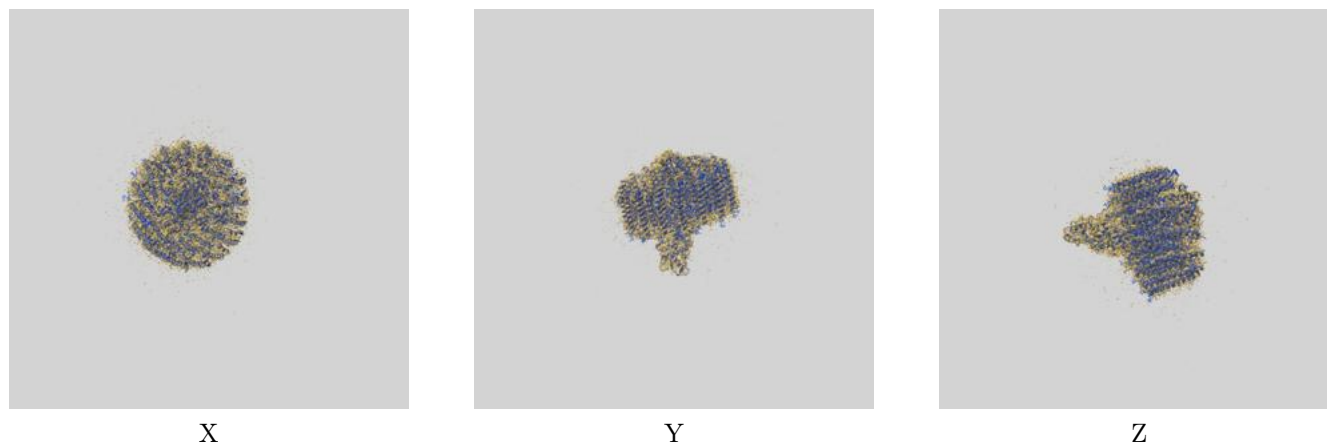
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.81	-	-
Author-provided FSC curve	2.81	3.23	2.88
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

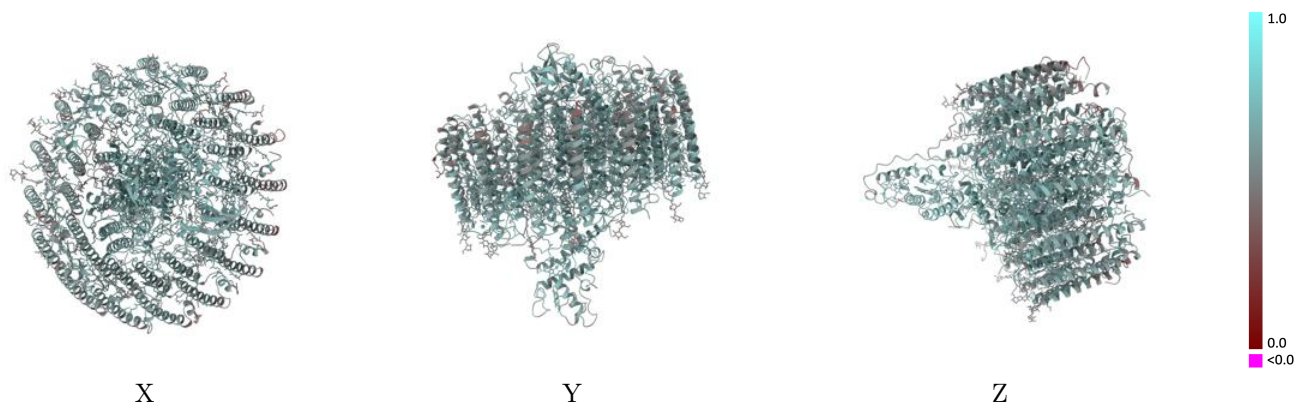
This section contains information regarding the fit between EMDB map EMD-32100 and PDB model 7VRJ. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0134 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](#)

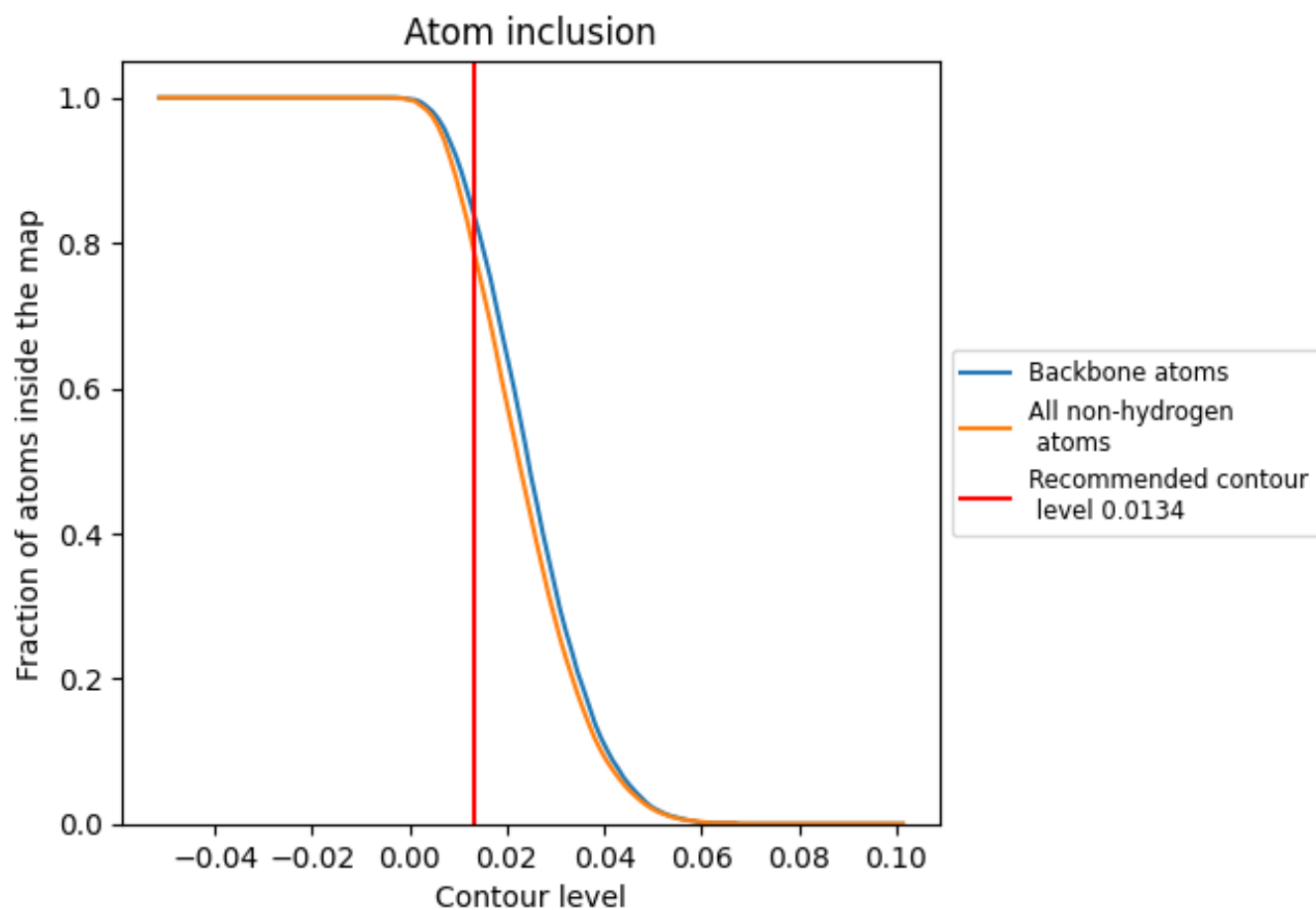


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 78% 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 (0.0134) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7830	 0.6010
0	 0.7690	 0.5950
1	 0.6790	 0.5680
2	 0.6650	 0.5520
3	 0.6910	 0.5680
4	 0.5990	 0.5280
5	 0.6990	 0.5870
6	 0.6580	 0.5420
7	 0.7350	 0.5770
8	 0.6940	 0.5620
9	 0.8360	 0.6280
A	 0.8480	 0.6200
B	 0.7560	 0.5840
C	 0.8850	 0.6370
D	 0.7800	 0.6070
E	 0.7610	 0.5900
F	 0.7750	 0.5920
G	 0.7150	 0.5660
H	 0.7570	 0.5950
I	 0.6830	 0.5630
J	 0.6530	 0.5400
K	 0.6720	 0.5660
L	 0.8890	 0.6500
M	 0.8850	 0.6510
N	 0.6690	 0.5590
O	 0.7650	 0.5980
P	 0.6970	 0.5620
Q	 0.8030	 0.6110
R	 0.7520	 0.5790
S	 0.7190	 0.5810
T	 0.7340	 0.5790
U	 0.7750	 0.5870
V	 0.7050	 0.5640
W	 0.7400	 0.5890
X	 0.6980	 0.5650



Continued on next page...

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Chain	Atom inclusion	Q-score
Y	 0.6970	 0.5770
Z	 0.7030	 0.5600