



wwPDB EM Validation Summary Report ⓘ

Aug 6, 2026 – 05:34 PM JST

PDB ID : 8GWA / pdb_00008gwa
EMDB ID : EMD-34307
Title : Structure of the intact photosynthetic light-harvesting antenna-reaction center complex from a green sulfur bacterium
Authors : Chen, J.H.; Zhang, X.
Deposited on : 2022-09-16
Resolution : 2.90 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

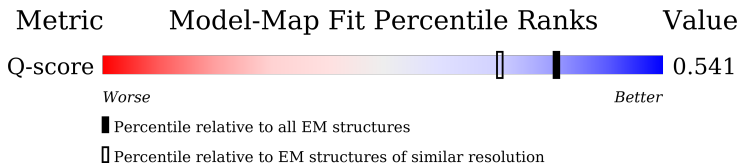
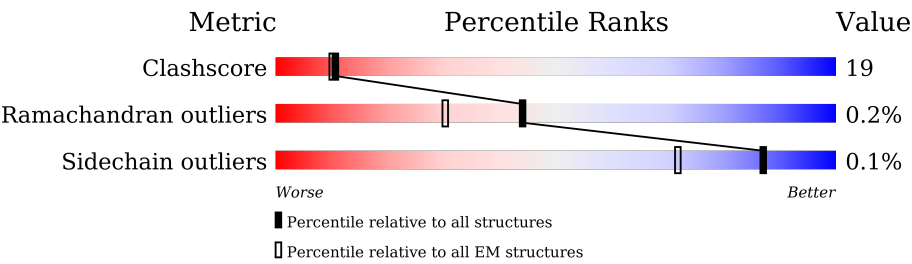
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 2.90 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	13054 (2.40 - 3.40)

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	1	366	63% 36% .
1	2	366	64% 33% .
1	3	366	64% 34% .
1	4	366	64% 34% .

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Mol	Chain	Length	Quality of chain
1	5	366	
1	6	366	
2	D	143	
3	B	230	
4	A	731	
4	a	731	
5	E	58	
6	F	58	
7	C	206	
7	c	206	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	SF4	B	302	-	-	X	-
13	F39	A	814	-	X	-	-
13	F39	A	815	-	X	-	-
13	F39	C	302	-	X	-	-
13	F39	a	816	-	X	-	-

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 37660 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 Bacteriochlorophyll a protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	362	Total	C	N	O	S	0	0
			2815	1783	501	524	7		
1	3	358	Total	C	N	O	S	0	0
			2789	1770	496	516	7		
1	2	358	Total	C	N	O	S	0	0
			2789	1770	496	516	7		
1	4	362	Total	C	N	O	S	0	0
			2815	1783	501	524	7		
1	6	358	Total	C	N	O	S	0	0
			2789	1770	496	516	7		
1	5	358	Total	C	N	O	S	0	0
			2789	1770	496	516	7		

- Molecule 2 is a protein called P840 reaction center 17 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	143	Total	C	N	O	S	0	0
			1167	741	208	212	6		

- Molecule 3 is a protein called Photosystem P840 reaction center iron-sulfur protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	102	Total	C	N	O	S	0	0
			798	510	132	147	9		

- Molecule 4 is a protein called Photosystem P840 reaction center, large subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	667	Total	C	N	O	S	0	0
			5344	3559	858	900	27		
4	a	662	Total	C	N	O	S	0	0
			5309	3538	852	893	26		

- Molecule 5 is a protein called unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	E	57	285	171	57	57	0	0

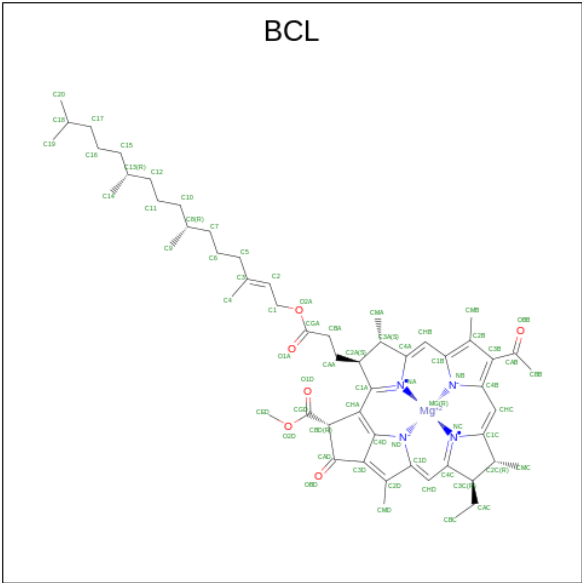
- Molecule 6 is a protein called Ric1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	50	379	253	62	61	3	0	0

- Molecule 7 is a protein called Cytochrome c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	C	113	875	587	137	144	7	0	0
7	c	113	875	587	137	144	7	0	0

- Molecule 8 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: C₅₅H₇₄MgN₄O₆).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
8	1	1	66	55	1	4	6	0
8	1	1	66	55	1	4	6	0

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Mol	Chain	Residues	Atoms					AltConf
8	1	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	1	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	1	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	1	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	1	1	Total 46	C 35	Mg 1	N 4	O 6	1
8	1	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	3	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	2	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	2	1	Total 46	C 35	Mg 1	N 4	O 6	1
8	2	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	2	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	2	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	2	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	2	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	2	1	Total 66	C 55	Mg 1	N 4	O 6	0

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Mol	Chain	Residues	Atoms					AltConf
8	2	1	Total	C	Mg	N	O	1
			46	35	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			56	45	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	A	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	a	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	a	1	Total	C	Mg	N	O	0
			56	45	1	4	6	
8	a	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	a	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	a	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	a	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	a	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	a	1	Total	C	Mg	N	O	0
			66	55	1	4	6	

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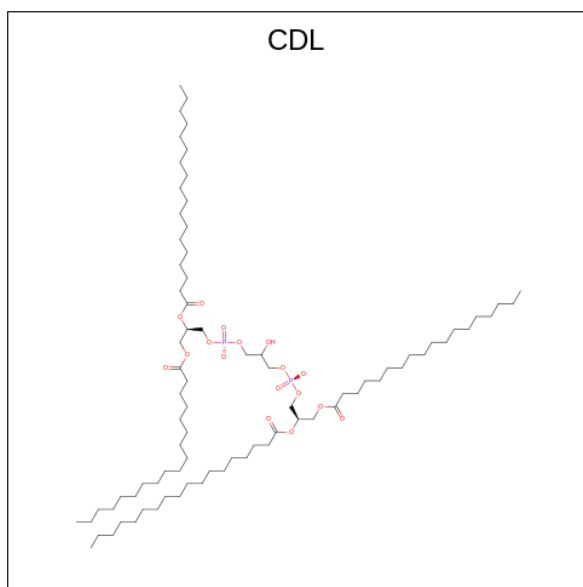
Mol	Chain	Residues	Atoms					AltConf
8	a	1	Total 46	C 35	Mg 1	N 4	O 6	0
8	a	1	Total 46	C 35	Mg 1	N 4	O 6	0
8	4	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	4	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	4	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	4	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	4	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	4	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	4	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	4	1	Total 46	C 35	Mg 1	N 4	O 6	1
8	4	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	4	1	Total 46	C 35	Mg 1	N 4	O 6	1
8	6	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	6	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	6	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	6	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	6	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	6	1	Total 46	C 35	Mg 1	N 4	O 6	1
8	6	1	Total 66	C 55	Mg 1	N 4	O 6	0
8	5	1	Total 66	C 55	Mg 1	N 4	O 6	0

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Mol	Chain	Residues	Atoms					AltConf
8	5	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	5	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	5	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	5	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	5	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
8	F	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	C	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
8	c	1	Total	C	Mg	N	O	0
			46	35	1	4	6	

- Molecule 9 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$) (labeled as "Ligand of Interest" by depositor).



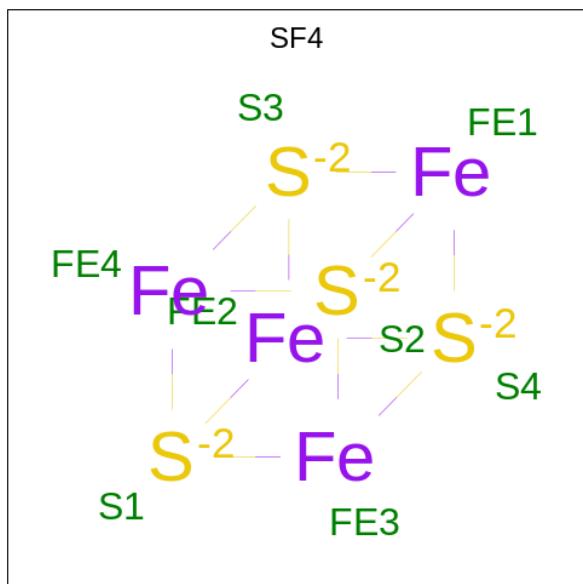
Mol	Chain	Residues	Atoms				AltConf
9	1	1	Total	C	O	P	0
			77	58	17	2	
9	a	1	Total	C	O	P	0
			70	51	17	2	
9	a	1	Total	C	O	P	0
			92	73	17	2	

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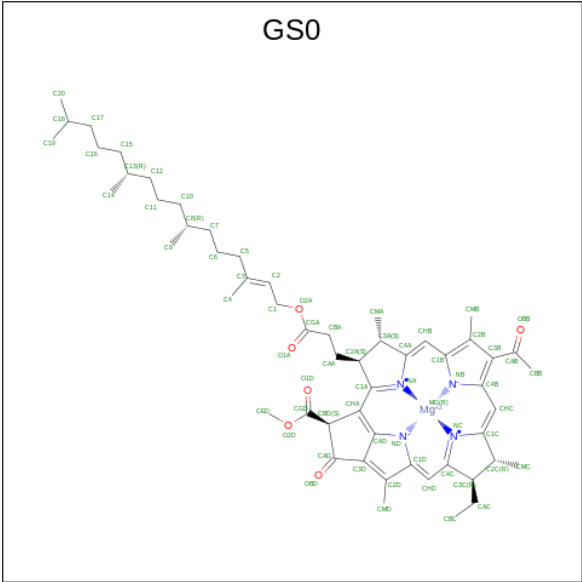
Mol	Chain	Residues	Atoms				AltConf
9	c	1	Total	C	O	P	0
			70	51	17	2	

- Molecule 10 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



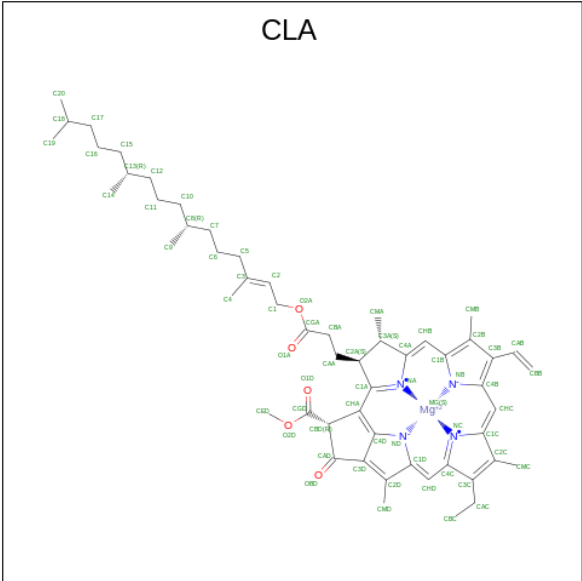
Mol	Chain	Residues	Atoms			AltConf
10	B	1	Total	Fe	S	0
			8	4	4	
10	B	1	Total	Fe	S	0
			8	4	4	
10	A	1	Total	Fe	S	0
			8	4	4	

- Molecule 11 is Bacteriochlorophyll A isomer (CCD ID: GS0) (formula: $\text{C}_{55}\text{H}_{74}\text{MgN}_4\text{O}_6$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 12 is CHLOROPHYLL A (CCD ID: CLA) (formula: $C_{55}H_{72}MgN_4O_5$) (labeled as "Ligand of Interest" by depositor).



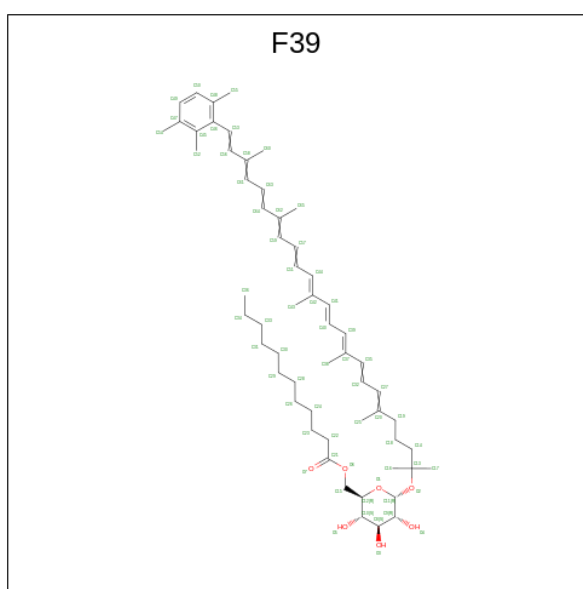
Mol	Chain	Residues	Atoms					AltConf
12	A	1	Total	C	Mg	N	O	0
			65	55	1	4	5	

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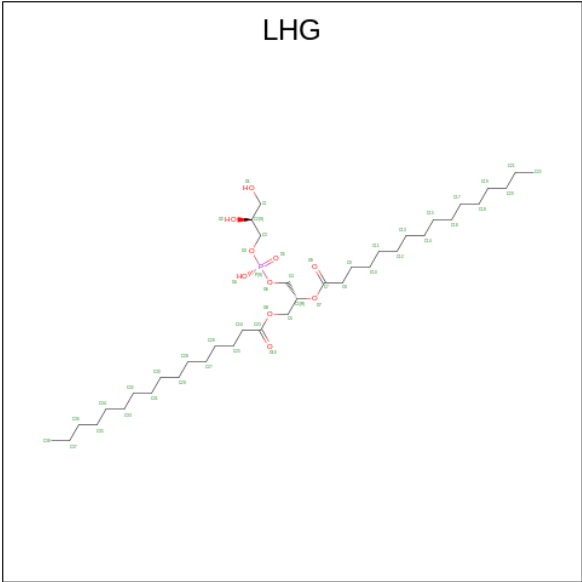
Mol	Chain	Residues	Atoms					AltConf
12	A	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	a	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	a	1	Total	C	Mg	N	O	0
			65	55	1	4	5	

- Molecule 13 is [(2R,3S,4S,5R,6R)-6-[(10E,12E,14E)-2,6,10,14,19,23-hexamethyl-25-(2,3,6-trimethylphenyl)pentacos-6,8,10,12,14,16,18,20,22,24-decaen-2-yl]oxy-3,4,5-tris(oxidanyl)oxan-2-yl]methyl dodecanoate (CCD ID: F39) (formula: C₅₈H₈₆O₇).



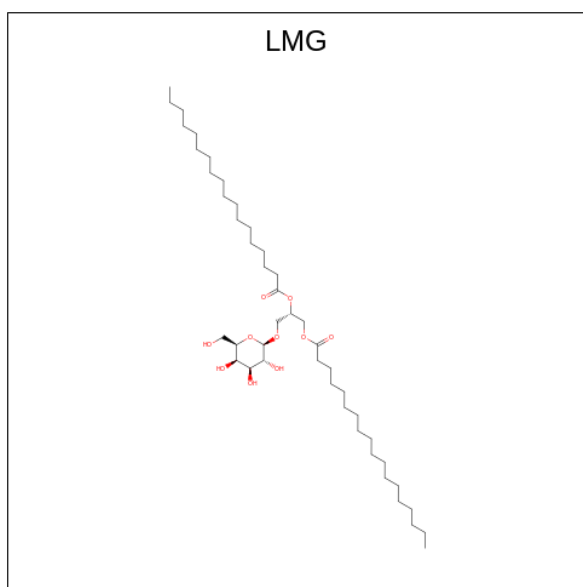
Mol	Chain	Residues	Atoms			AltConf
13	A	1	Total	C	O	0
			65	58	7	
13	A	1	Total	C	O	0
			65	58	7	
13	a	1	Total	C	O	0
			65	58	7	
13	C	1	Total	C	O	0
			65	58	7	

- Molecule 14 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: C₃₈H₇₅O₁₀P).



Mol	Chain	Residues	Atoms				AltConf
14	A	1	Total	C	O	P	0
			46	35	10	1	
14	A	1	Total	C	O	P	0
			49	38	10	1	
14	A	1	Total	C	O	P	0
			49	38	10	1	
14	a	1	Total	C	O	P	0
			46	35	10	1	
14	a	1	Total	C	O	P	0
			40	29	10	1	
14	a	1	Total	C	O	P	0
			42	31	10	1	
14	E	1	Total	C	O	P	0
			37	26	10	1	

- Molecule 15 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (CCD ID: LMG) (formula: C₄₅H₈₆O₁₀).

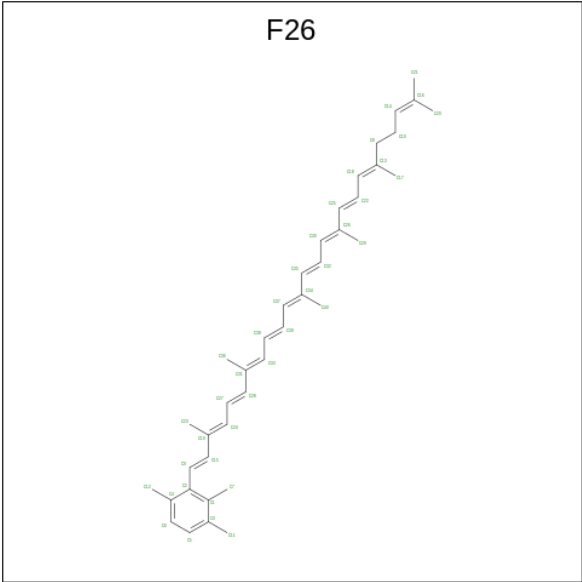


Mol	Chain	Residues	Atoms			AltConf
15	A	1	Total	C	O	0
			44	34	10	
15	a	1	Total	C	O	0
			44	34	10	

- Molecule 16 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
16	A	1	Total	Ca	0
			1	1	
16	a	1	Total	Ca	0
			1	1	

- Molecule 17 is 2-[(1E,3E,5E,7E,9E,11E,13E,15E,17E,19E)-3,7,12,16,20,24-hexamethylpentacos-1,3,5,7,9,11,13,15,17,19,23-undecaenyl]-1,3,4-trimethyl-benzene (CCD ID: F26) (formula: C₄₀H₅₂).

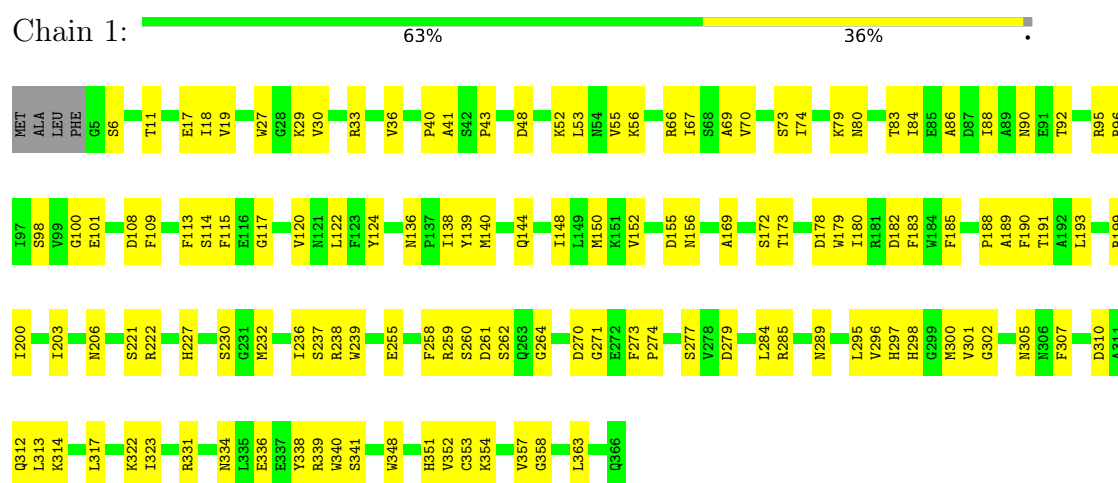


Mol	Chain	Residues	Atoms		AltConf
17	a	1	Total	C	0
			40	40	
17	c	1	Total	C	0
			40	40	

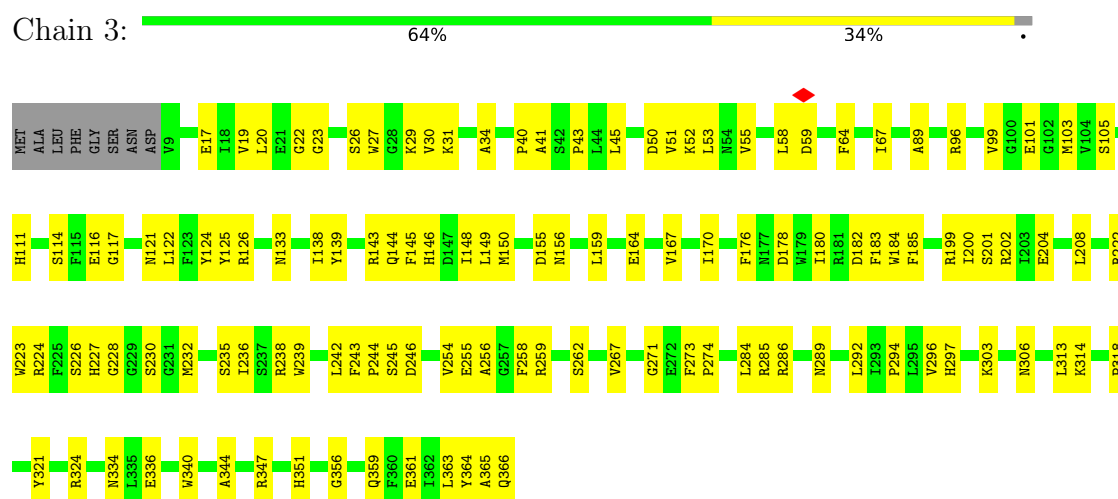
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Bacteriochlorophyll a protein

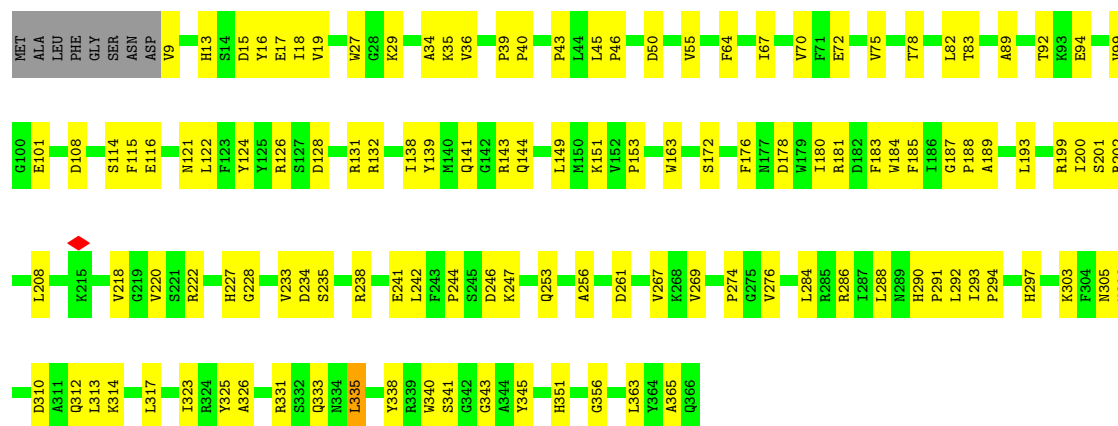


• Molecule 1: Bacteriochlorophyll a protein

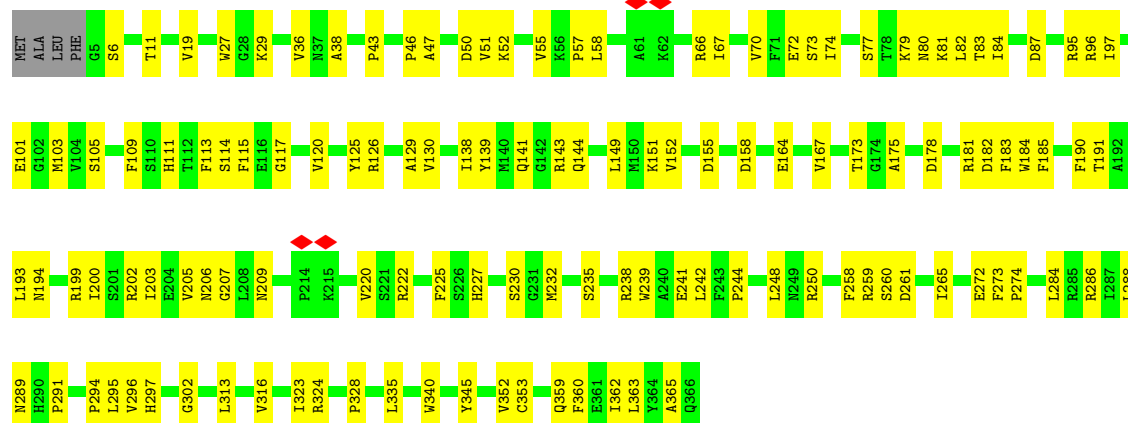


• Molecule 1: Bacteriochlorophyll a protein

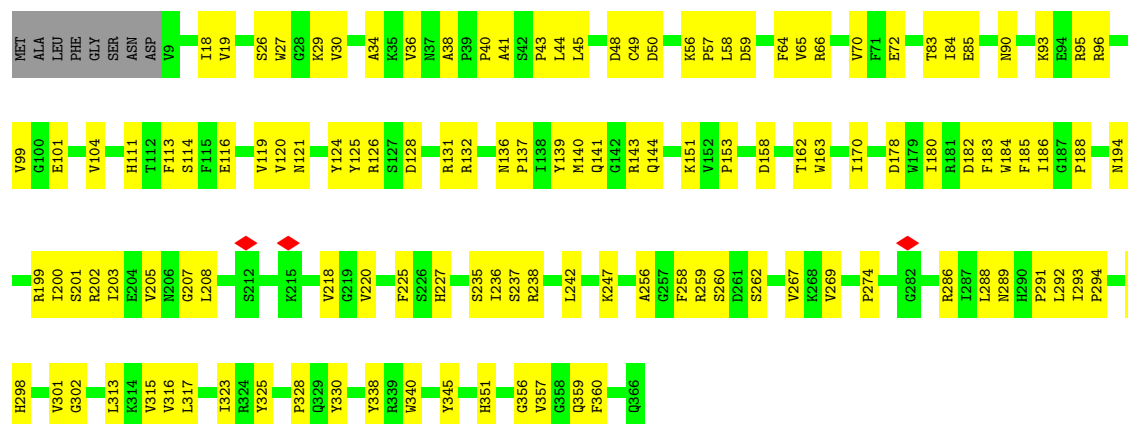




• Molecule 1: Bacteriochlorophyll a protein



• Molecule 1: Bacteriochlorophyll a protein



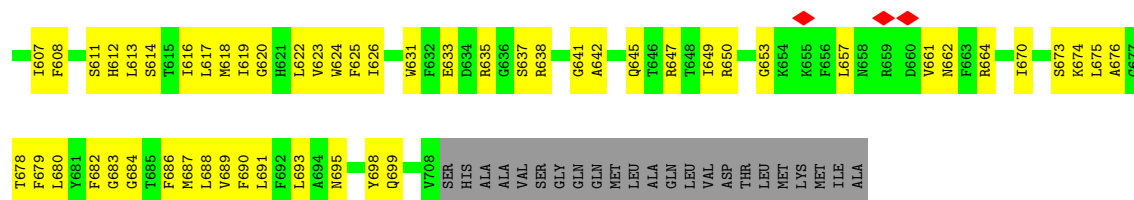
• Molecule 1: Bacteriochlorophyll a protein

K319	G216	E101	ALA	MET
G320	V233	G102	LEU	
Y321	D234	M103	PRO	
K322	S235	V104	GLY	
I323	I236	S105	SER	
K324			ASN	
	S237	T112	ASP	V9
Q333	R238	F113		
K334	P244	S114		
L335				
E336	K247	V120	I18	
E337		N121	V19	
Y338	Q253	L122	G22	
R339	V254	F123	G23	
W340	E255	Y124	S24	
		Y125	S25	
Y345	F258	R126	S26	
A346	R259		W27	
R347	S260	A129	G28	
			K29	
H351	V267	N136	A34	
	K268	P137	K35	
G356	E269		V36	
V357		R143		
	G271	Q144	P40	
E361	G272		A41	
I362	E273	N157	S42	
L363	F274	D158	P43	
Y364		L159	L44	
A365	S277			
Q366		N177	D50	
	G281	D178	V51	
			K52	
	L284	R181	L53	
	R285	D182	N54	
	R286	F183		
		Y184	D59	
	N289	F185	P60	
	H290	I186		
	P291		F64	
	L292	A189		
	I293	R190	V70	
	P294	T191	F71	
	L295	A192	E72	
	V296	L193	S73	
	H297	H194	I74	
	H298	E195		
			K79	
	V301	R199		
	N306	I200	T83	
	D310		T88	
	L313		K93	
	K314	G213	E94	
	V315	P214	R95	
				S08

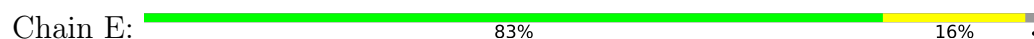
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| D85 | D86 | D87 | D88 | D89 | D90 | D91 | D92 | D93 | D94 | D95 | D96 | D97 | D98 | D99 | E00 | E01 | E02 | E03 | E04 | E05 | E06 | E07 | E08 | E09 | E10 | E11 | E12 | E13 | E14 | E15 | E16 | E17 | E18 | E19 | E20 | E21 | E22 | E23 | E24 | E25 | E26 | E27 | E28 | E29 | E30 | E31 | E32 | E33 | E34 | E35 | E36 | E37 | E38 | E39 | E40 | E41 | E42 | E43 | E44 | E45 | E46 | E47 | E48 | E49 | E50 | E51 | E52 | E53 | E54 | E55 | E56 | E57 | E58 | E59 | E60 | E61 | E62 | E63 | E64 | E65 | E66 | E67 | E68 | E69 | E70 | E71 | E72 | E73 | E74 | E75 | E76 | E77 | E78 | E79 | E80 | E81 | E82 | E83 | E84 | E85 | E86 | E87 | E88 | E89 | E90 | E91 | E92 | E93 | E94 | E95 | E96 | E97 | E98 | E99 | F00 | F01 | F02 | F03 | F04 | F05 | F06 | F07 | F08 | F09 | F10 | F11 | F12 | F13 | F14 | F15 | F16 | F17 | F18 | F19 | F20 | F21 | F22 | F23 | F24 | F25 | F26 | F27 | F28 | F29 | F30 | F31 | F32 | F33 | F34 | F35 | F36 | F37 | F38 | F39 | F40 | F41 | F42 | F43 | F44 | F45 | F46 | F47 | F48 | F49 | F50 | F51 | F52 | F53 | F54 | F55 | F56 | F57 | F58 | F59 | F60 | F61 | F62 | F63 | F64 | F65 | F66 | F67 | F68 | F69 | F70 | F71 | F72 | F73 | F74 | F75 | F76 | F77 | F78 | F79 | F80 | F81 | F82 | F83 | F84 | F85 | F86 | F87 | F88 | F89 | F90 | F91 | F92 | F93 | F94 | F95 | F96 | F97 | F98 | F99 | G00 | G01 | G02 | G03 | G04 | G05 | G06 | G07 | G08 | G09 | G10 | G11 | G12 | G13 | G14 | G15 | G16 | G17 | G18 | G19 | G20 | G21 | G22 | G23 | G24 | G25 | G26 | G27 | G28 | G29 | G30 | G31 | G32 | G33 | G34 | G35 | G36 | G37 | G38 | G39 | G40 | G41 | G42 | G43 | G44 | G45 | G46 | G47 | G48 | G49 | G50 | G51 | G52 | G53 | G54 | G55 | G56 | G57 | G58 | G59 | G60 | G61 | G62 | G63 | G64 | G65 | G66 | G67 | G68 | G69 | G70 | G71 | G72 | G73 | G74 | G75 | G76 | G77 | G78 | G79 | G80 | G81 | G82 | G83 | G84 | G85 | G86 | G87 | G88 | G89 | G90 | G91 | G92 | G93 | G94 | G95 | G96 | G97 | G98 | G99 | H00 | H01 | H02 | H03 | H04 | H05 | H06 | H07 | H08 | H09 | H10 | H11 | H12 | H13 | H14 | H15 | H16 | H17 | H18 | H19 | H20 | H21 | H22 | H23 | H24 | H25 | H26 | H27 | H28 | H29 | H30 | H31 | H32 | H33 | H34 | H35 | H36 | H37 | H38 | H39 | H40 | H41 | H42 | H43 | H44 | H45 | H46 | H47 | H48 | H49 | H50 | H51 | H52 | H53 | H54 | H55 | H56 | H57 | H58 | H59 | H60 | H61 | H62 | H63 | H64 | H65 | H66 | H67 | H68 | H69 | H70 | H71 | H72 | H73 | H74 | H75 | H76 | H77 | H78 | H79 | H80 | H81 | H82 | H83 | H84 | H85 | H86 | H87 | H88 | H89 | H90 | H91 | H92 | H93 | H94 | H95 | H96 | H97 | H98 | H99 | I00 | I01 | I02 | I03 | I04 | I05 | I06 | I07 | I08 | I09 | I10 | I11 | I12 | I13 | I14 | I15 | I16 | I17 | I18 | I19 | I20 | I21 | I22 | I23 | I24 | I25 | I26 | I27 | I28 | I29 | I30 | I31 | I32 | I33 | I34 | I35 | I36 | I37 | I38 | I39 | I40 | I41 | I42 | I43 | I44 | I45 | I46 | I47 | I48 | I49 | I50 | I51 | I52 | I53 | I54 | I55 | I56 | I57 | I58 | I59 | I60 | I61 | I62 | I63 | I64 | I65 | I66 | I67 | I68 | I69 | I70 | I71 | I72 | I73 | I74 | I75 | I76 | I77 | I78 | I79 | I80 | I81 | I82 | I83 | I84 | I85 | I86 | I87 | I88 | I89 | I90 | I91 | I92 | I93 | I94 | I95 | I96 | I97 | I98 | I99 | J00 | J01 | J02 | J03 | J04 | J05 | J06 | J07 | J08 | J09 | J10 | J11 | J12 | J13 | J14 | J15 | J16 | J17 | J18 | J19 | J20 | J21 | J22 | J23 | J24 | J25 | J26 | J27 | J28 | J29 | J30 | J31 | J32 | J33 | J34 | J35 | J36 | J37 | J38 | J39 | J40 | J41 | J42 | J43 | J44 | J45 | J46 | J47 | J48 | J49 | J50 | J51 | J52 | J53 | J54 | J55 | J56 | J57 | J58 | J59 | J60 | J61 | J62 | J63 | J64 | J65 | J66 | J67 | J68 |
|-----|

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|---------|------|------|------|------|------|---------|-----|-----|-----|
| P201 | D202 | G203 | E204 | V205 | L206 | D207 | P212 | E213 | E214 | R215 | L216 | D217 | R221 | F222 | L223 | H224 | R225 | F226 | H227 | R228 | E229 | A230 | | | |
| PRO VAL | ALA | ALA | LYS | ALA | ALA | PRO LYS | K129 | K130 | K131 | H132 | Y133 | F134 | I135 | I136 | F137 | N138 | L139 | C140 | K149 | C150 | F151 | P152 | K153 | V154 | N155 | A156 | I157 | Y162 | V165 | G166 | E167 | F170 | R171 | G172 | Y173 | I174 | D175 | S181 | C182 | S183 | A184 | C185 | F186 | S187 | E190 | C191 | P192 | S193 | E198 | V199 | L200 | | | |
| MET | ALA | GLU | PRO | VAL | GLU | ASN | LYS | LYS | GLN | ALA | PRO | ALA | GLY | GLN | VAL | PRO | LYS | GLY | ALA | PRO | ALA | LYS | GLY | ALA | LYS | VAL | PRO | GLY | ALA | ALA | VAL | ALA | LYS | PRO | GLY | ALA | ALA | GLY | ALA | LYS | PRO | ALA | ALA | GLY | ALA | ALA | LYS | ALA | GLN | ALA | ALA | GLY | ALA | LYS |

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|-----|
| MET | ALA | GLU | GLN | VAL | LYS | PRO | ALA | GLY | VAL | LYS | PRO | LYS | GLY | THR | VAL | PRO | PRO | PRO | LYS | LYS | ASN | GLN | ALA | ALA | ALA | ASN | GLY | PRO | PRO | GLY | GLY | ALA | SER | VAL | ILE | LYS | GLU | GLN | D42 | M46 | R47 | R48 | F49 | L50 | F51 | Q52 | R53 | T54 | E55 | T56 | K60 | Q63 | T66 |
|-----|



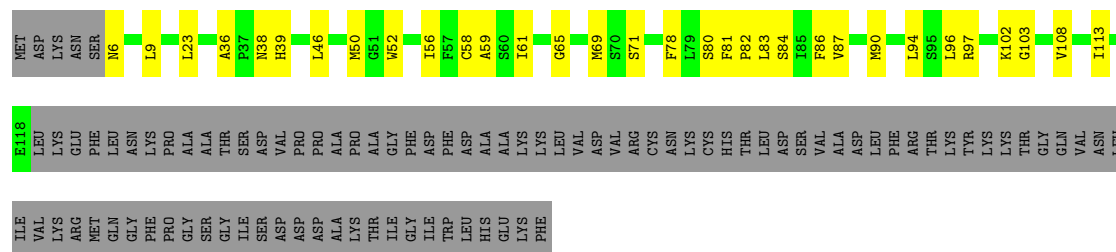
- Molecule 5: unknown protein



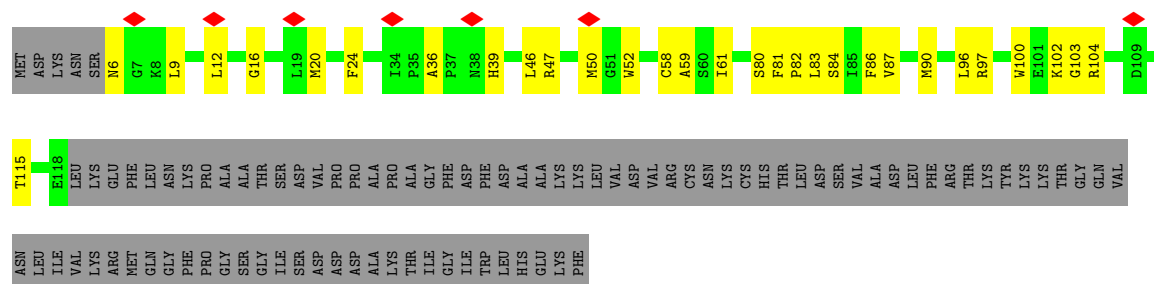
- Molecule 6: Ric1 protein



- Molecule 7: Cytochrome c



- Molecule 7: Cytochrome c



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	227038	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	152200	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.298	Depositor
Minimum map value	-0.557	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	312.80002, 312.80002, 312.80002	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9200001, 0.9200001, 0.9200001	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: CDL, GS0, F39, SF4, LMG, BCL, CA, CLA, LHG, F26

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	1	0.14	0/2885	0.35	0/3910
1	2	0.14	0/2859	0.33	0/3875
1	3	0.14	0/2859	0.34	0/3875
1	4	0.15	0/2885	0.37	0/3910
1	5	0.15	0/2859	0.38	0/3875
1	6	0.14	0/2859	0.35	0/3875
2	D	0.14	0/1191	0.39	0/1604
3	B	0.15	0/819	0.41	0/1106
4	A	0.15	0/5528	0.35	0/7527
4	a	0.15	0/5493	0.35	0/7481
6	F	0.12	0/386	0.38	0/525
7	C	0.14	0/898	0.37	0/1216
7	c	0.14	0/898	0.35	0/1216
All	All	0.15	0/32419	0.36	0/43995

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	1	2815	0	2749	108	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	2789	0	2731	105	0
1	3	2789	0	2731	109	0
1	4	2815	0	2749	101	0
1	5	2789	0	2731	112	0
1	6	2789	0	2731	115	0
2	D	1167	0	1188	62	0
3	B	798	0	752	62	0
4	A	5344	0	5236	247	0
4	a	5309	0	5202	220	0
5	E	285	0	60	5	0
6	F	379	0	418	9	0
7	C	875	0	915	28	0
7	c	875	0	915	26	0
8	1	508	0	551	59	0
8	2	554	0	586	60	0
8	3	462	0	516	57	0
8	4	620	0	660	63	0
8	5	396	0	442	48	0
8	6	508	0	551	69	0
8	A	596	0	548	42	0
8	C	46	0	35	4	0
8	F	46	0	35	3	0
8	a	596	0	547	34	0
8	c	46	0	35	6	0
9	1	77	0	103	7	0
9	a	162	0	216	13	0
9	c	70	0	82	3	0
10	A	8	0	0	0	0
10	B	16	0	0	2	0
11	A	66	0	0	5	0
11	a	66	0	0	2	0
12	A	130	0	142	21	0
12	a	130	0	142	26	0
13	A	130	0	0	0	0
13	C	65	0	0	0	0
13	a	65	0	0	1	0
14	A	144	0	211	8	0
14	E	37	0	44	1	0
14	a	128	0	172	10	0
15	A	44	0	57	4	0
15	a	44	0	57	1	0
16	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	a	1	0	0	0	0
17	a	40	0	0	0	0
17	c	40	0	0	0	0
All	All	37660	0	36840	1393	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 19.

The worst 5 of 1393 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)
4:A:679:PHE:O	14:A:819:LHG:H223	1.73	0.87
12:A:822:CLA:H12	4:a:618:MET:HB3	1.58	0.85
4:A:553:LYS:HE2	12:A:822:CLA:NB	1.91	0.84
4:A:515:ASP:HB3	1:5:319:LYS:HG2	1.58	0.84
3:B:152:PRO:HG2	4:A:48:ARG:HB3	1.61	0.83

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	1	360/366 (98%)	349 (97%)	11 (3%)	0	100	100
1	2	356/366 (97%)	343 (96%)	12 (3%)	1 (0%)	36	65
1	3	356/366 (97%)	347 (98%)	9 (2%)	0	100	100
1	4	360/366 (98%)	346 (96%)	13 (4%)	1 (0%)	36	65
1	5	356/366 (97%)	349 (98%)	6 (2%)	1 (0%)	36	65
1	6	356/366 (97%)	349 (98%)	7 (2%)	0	100	100
2	D	141/143 (99%)	123 (87%)	16 (11%)	2 (1%)	9	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	100/230 (44%)	84 (84%)	16 (16%)	0	100	100
4	A	665/731 (91%)	607 (91%)	58 (9%)	0	100	100
4	a	660/731 (90%)	601 (91%)	57 (9%)	2 (0%)	36	65
6	F	48/58 (83%)	45 (94%)	3 (6%)	0	100	100
7	C	111/206 (54%)	101 (91%)	10 (9%)	0	100	100
7	c	111/206 (54%)	103 (93%)	8 (7%)	0	100	100
All	All	3980/4501 (88%)	3747 (94%)	226 (6%)	7 (0%)	44	72

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	123	GLU
4	a	334	GLU
1	5	336	GLU
1	4	335	LEU
1	2	335	LEU

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	1	299/302 (99%)	299 (100%)	0	100	100
1	2	296/302 (98%)	295 (100%)	1 (0%)	86	96
1	3	296/302 (98%)	296 (100%)	0	100	100
1	4	299/302 (99%)	299 (100%)	0	100	100
1	5	296/302 (98%)	295 (100%)	1 (0%)	86	96
1	6	296/302 (98%)	296 (100%)	0	100	100
2	D	128/128 (100%)	128 (100%)	0	100	100
3	B	86/161 (53%)	86 (100%)	0	100	100
4	A	553/599 (92%)	553 (100%)	0	100	100
4	a	550/599 (92%)	550 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	40/45 (89%)	40 (100%)	0	100	100
7	C	94/173 (54%)	94 (100%)	0	100	100
7	c	94/173 (54%)	94 (100%)	0	100	100
All	All	3327/3690 (90%)	3325 (100%)	2 (0%)	87	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	2	253	GLN
1	5	306	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	6	194	ASN
1	6	308	ASN
1	5	253	GLN
1	2	194	ASN
1	2	177	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 103 ligands modelled in this entry, 2 are monoatomic - leaving 101 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
8	BCL	2	402[B]	1	49,54,74	2.04	14 (28%)	59,91,115	2.27	23 (38%)
8	BCL	5	403	1	69,74,74	1.77	15 (21%)	83,115,115	2.17	29 (34%)
14	LHG	A	818	-	48,48,48	0.62	1 (2%)	51,54,54	1.25	6 (11%)
8	BCL	4	401	1	69,74,74	1.77	15 (21%)	83,115,115	2.31	28 (33%)
8	BCL	1	407[B]	1	49,54,74	2.04	13 (26%)	59,91,115	2.23	22 (37%)
8	BCL	2	407	1	69,74,74	1.77	16 (23%)	83,115,115	2.22	29 (34%)
8	BCL	a	812	4	69,74,74	1.76	15 (21%)	83,115,115	2.22	27 (32%)
10	SF4	A	821	4	0,12,12	-	-	-	-	-
8	BCL	1	406	1	69,74,74	1.75	15 (21%)	83,115,115	2.15	27 (32%)
13	F39	a	816	-	66,66,66	8.12	57 (86%)	79,85,85	4.15	29 (36%)
12	CLA	A	802	-	69,73,73	2.31	21 (30%)	83,113,113	1.27	8 (9%)
8	BCL	3	402	1	69,74,74	1.77	15 (21%)	83,115,115	2.12	27 (32%)
8	BCL	2	404	1	69,74,74	1.78	15 (21%)	83,115,115	2.15	27 (32%)
9	CDL	a	822	8	91,91,99	0.91	8 (8%)	97,103,111	1.09	4 (4%)
13	F39	A	814	4	66,66,66	8.14	55 (83%)	79,85,85	4.10	29 (36%)
10	SF4	B	301	3	0,12,12	-	-	-	-	-
9	CDL	1	409	1	76,76,99	0.99	8 (10%)	82,88,111	1.14	4 (4%)
8	BCL	6	407[B]	1	49,54,74	2.04	13 (26%)	59,91,115	2.25	23 (38%)
8	BCL	2	401	-	69,74,74	1.78	14 (20%)	83,115,115	2.14	27 (32%)
17	F26	a	815	-	40,40,40	2.00	15 (37%)	46,50,50	1.98	11 (23%)
15	LMG	a	818	4	44,44,55	0.79	0	52,52,63	1.37	4 (7%)
8	BCL	a	809	4	49,54,74	2.03	15 (30%)	59,91,115	2.41	23 (38%)
11	GS0	a	802	4	69,74,74	1.84	14 (20%)	83,115,115	2.24	29 (34%)
8	BCL	1	404	-	69,74,74	1.76	15 (21%)	83,115,115	2.16	30 (36%)
8	BCL	A	803	4	49,54,74	2.01	14 (28%)	59,91,115	2.35	23 (38%)
8	BCL	4	408[B]	1	49,54,74	2.04	14 (28%)	59,91,115	2.27	22 (37%)
8	BCL	a	804	4	49,54,74	2.01	14 (28%)	59,91,115	2.28	22 (37%)
8	BCL	6	402	1	69,74,74	1.79	15 (21%)	83,115,115	2.17	25 (30%)
10	SF4	B	302	3	0,12,12	-	-	-	-	-
14	LHG	a	817	-	45,45,48	0.64	1 (2%)	48,51,54	1.27	6 (12%)
8	BCL	C	301	7,4	49,54,74	2.03	14 (28%)	59,91,115	2.37	21 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	BCL	1	401	1	69,74,74	1.77	15 (21%)	83,115,115	2.31	28 (33%)
12	CLA	a	801	4	69,73,73	2.30	20 (28%)	83,113,113	1.32	9 (10%)
8	BCL	6	404	1	69,74,74	1.77	15 (21%)	83,115,115	2.16	26 (31%)
8	BCL	5	404	1	69,74,74	1.76	15 (21%)	83,115,115	2.14	29 (34%)
8	BCL	c	301	7,4	49,54,74	2.02	15 (30%)	59,91,115	2.40	21 (35%)
8	BCL	A	805	-	69,74,74	1.76	16 (23%)	83,115,115	2.20	28 (33%)
13	F39	C	302	-	66,66,66	8.14	59 (89%)	79,85,85	4.03	29 (36%)
8	BCL	a	810	4	49,54,74	1.97	12 (24%)	59,91,115	2.53	24 (40%)
8	BCL	5	401	1	69,74,74	1.77	15 (21%)	83,115,115	2.35	29 (34%)
8	BCL	A	810	4	69,74,74	1.76	15 (21%)	83,115,115	2.22	30 (36%)
8	BCL	4	409	-	69,74,74	1.78	14 (20%)	83,115,115	2.15	28 (33%)
8	BCL	4	402	-	69,74,74	1.78	15 (21%)	83,115,115	2.13	27 (32%)
14	LHG	A	819	4	48,48,48	0.60	0	51,54,54	1.24	6 (11%)
8	BCL	5	402	1	69,74,74	1.76	15 (21%)	83,115,115	2.18	25 (30%)
15	LMG	A	817	4	44,44,55	0.78	0	52,52,63	1.35	3 (5%)
8	BCL	5	405	1	69,74,74	1.77	15 (21%)	83,115,115	2.18	27 (32%)
8	BCL	A	806	4	49,54,74	2.04	15 (30%)	59,91,115	2.47	22 (37%)
8	BCL	4	404	1	69,74,74	1.77	15 (21%)	83,115,115	2.13	27 (32%)
14	LHG	E	101	-	36,36,48	0.70	0	39,42,54	1.26	4 (10%)
8	BCL	A	807	4	69,74,74	1.77	15 (21%)	83,115,115	2.23	30 (36%)
8	BCL	4	403	1	69,74,74	1.77	15 (21%)	83,115,115	2.14	27 (32%)
8	BCL	2	409[B]	1	49,54,74	2.05	14 (28%)	59,91,115	2.25	22 (37%)
11	GS0	A	801	4	69,74,74	1.81	15 (21%)	83,115,115	2.18	29 (34%)
8	BCL	4	410[B]	1	49,54,74	2.04	14 (28%)	59,91,115	2.27	22 (37%)
8	BCL	2	403	1	69,74,74	1.77	16 (23%)	83,115,115	2.29	28 (33%)
9	CDL	c	303	7	69,69,99	1.04	8 (11%)	75,81,111	1.14	4 (5%)
12	CLA	A	822	4	69,73,73	2.30	18 (26%)	83,113,113	1.31	8 (9%)
8	BCL	6	405	1	69,74,74	1.76	15 (21%)	83,115,115	2.17	27 (32%)
8	BCL	a	813	4	49,54,74	2.00	14 (28%)	59,91,115	2.47	26 (44%)
8	BCL	6	403	1	69,74,74	1.77	16 (23%)	83,115,115	2.18	28 (33%)
8	BCL	A	812	4	49,54,74	2.01	15 (30%)	59,91,115	2.48	23 (38%)
8	BCL	A	808	4	49,54,74	2.01	14 (28%)	59,91,115	2.41	23 (38%)
8	BCL	F	101	6,4	49,54,74	2.02	13 (26%)	59,91,115	2.47	24 (40%)
8	BCL	4	405	-	69,74,74	1.77	16 (23%)	83,115,115	2.14	30 (36%)
8	BCL	2	408	1	69,74,74	1.76	15 (21%)	83,115,115	2.16	27 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	BCL	1	403	1	69,74,74	1.76	14 (20%)	83,115,115	2.15	26 (31%)
8	BCL	4	406	1	69,74,74	1.77	16 (23%)	83,115,115	2.19	29 (34%)
8	BCL	5	406	1	69,74,74	1.76	16 (23%)	83,115,115	2.20	28 (33%)
8	BCL	a	814	4	49,54,74	2.00	14 (28%)	59,91,115	2.46	23 (38%)
8	BCL	a	808	4	69,74,74	1.77	15 (21%)	83,115,115	2.15	27 (32%)
8	BCL	2	406	1	69,74,74	1.76	15 (21%)	83,115,115	2.13	27 (32%)
8	BCL	3	403	1	69,74,74	1.77	15 (21%)	83,115,115	2.13	27 (32%)
8	BCL	a	806	9	69,74,74	1.77	16 (23%)	83,115,115	2.22	28 (33%)
8	BCL	6	406	1	69,74,74	1.76	15 (21%)	83,115,115	2.15	25 (30%)
8	BCL	4	407	1	69,74,74	1.77	16 (23%)	83,115,115	2.13	26 (31%)
8	BCL	A	809	4	49,54,74	1.97	12 (24%)	59,91,115	2.57	22 (37%)
13	F39	A	815	-	66,66,66	8.15	58 (87%)	79,85,85	4.10	29 (36%)
14	LHG	a	821	4	41,41,48	0.65	0	44,47,54	1.20	4 (9%)
8	BCL	3	407	-	69,74,74	1.78	15 (21%)	83,115,115	2.12	27 (32%)
8	BCL	3	404	-	69,74,74	1.76	15 (21%)	83,115,115	2.18	30 (36%)
8	BCL	A	804	-	59,64,74	1.89	16 (27%)	71,103,115	2.20	24 (33%)
9	CDL	a	820	-	69,69,99	1.04	8 (11%)	75,81,111	1.16	4 (5%)
8	BCL	2	405	1	69,74,74	1.76	15 (21%)	83,115,115	2.16	28 (33%)
8	BCL	1	402	1	69,74,74	1.78	14 (20%)	83,115,115	2.21	25 (30%)
8	BCL	A	813	4	49,54,74	2.03	13 (26%)	59,91,115	2.43	24 (40%)
8	BCL	3	401	1	69,74,74	1.76	14 (20%)	83,115,115	2.34	30 (36%)
8	BCL	a	805	-	59,64,74	1.89	16 (27%)	71,103,115	2.24	24 (33%)
8	BCL	3	405	1	69,74,74	1.74	14 (20%)	83,115,115	2.29	30 (36%)
17	F26	c	302	7	40,40,40	2.00	15 (37%)	46,50,50	2.15	9 (19%)
8	BCL	6	401	1	69,74,74	1.77	16 (23%)	83,115,115	2.30	30 (36%)
8	BCL	1	405	1	69,74,74	1.76	15 (21%)	83,115,115	2.19	28 (33%)
14	LHG	A	816	-	45,45,48	0.64	2 (4%)	48,51,54	1.26	6 (12%)
14	LHG	a	819	-	39,39,48	0.68	1 (2%)	42,45,54	1.25	4 (9%)
8	BCL	6	408	-	69,74,74	1.77	15 (21%)	83,115,115	2.15	28 (33%)
8	BCL	A	811	4	69,74,74	1.76	15 (21%)	83,115,115	2.16	26 (31%)
12	CLA	a	803	-	69,73,73	2.30	20 (28%)	83,113,113	1.31	9 (10%)
8	BCL	a	807	4	49,54,74	2.03	12 (24%)	59,91,115	2.56	23 (38%)
8	BCL	a	811	4	69,74,74	1.76	16 (23%)	83,115,115	2.27	29 (34%)
8	BCL	3	406	1	69,74,74	1.76	14 (20%)	83,115,115	2.15	29 (34%)
8	BCL	1	408	-	69,74,74	1.77	15 (21%)	83,115,115	2.13	28 (33%)

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
8	BCL	2	402[B]	1	-	7/17/113/137	-
8	BCL	5	403	1	-	14/41/137/137	-
14	LHG	A	818	-	-	24/53/53/53	-
8	BCL	4	401	1	-	12/41/137/137	-
8	BCL	1	407[B]	1	-	6/17/113/137	-
8	BCL	2	407	1	-	7/41/137/137	-
8	BCL	a	812	4	-	16/41/137/137	-
10	SF4	A	821	4	-	-	0/6/5/5
8	BCL	1	406	1	-	14/41/137/137	-
13	F39	a	816	-	-	38/58/78/78	0/2/2/2
12	CLA	A	802	-	-	23/39/115/115	-
8	BCL	3	402	1	-	12/41/137/137	-
8	BCL	2	404	1	-	16/41/137/137	-
9	CDL	a	822	8	-	49/102/102/110	-
13	F39	A	814	4	-	39/58/78/78	0/2/2/2
10	SF4	B	301	3	-	-	0/6/5/5
9	CDL	1	409	1	-	47/87/87/110	-
8	BCL	6	407[B]	1	-	5/17/113/137	-
8	BCL	2	401	-	-	21/41/137/137	-
17	F26	a	815	-	-	21/36/36/36	0/1/1/1
15	LMG	a	818	4	-	19/39/59/70	0/1/1/1
8	BCL	a	809	4	-	3/17/113/137	-
11	GS0	a	802	4	-	11/41/137/137	-
8	BCL	1	404	-	-	10/41/137/137	-
8	BCL	A	803	4	-	3/17/113/137	-
8	BCL	4	408[B]	1	-	5/17/113/137	-
8	BCL	a	804	4	-	9/17/113/137	-
8	BCL	6	402	1	-	17/41/137/137	-
14	LHG	a	817	-	-	20/50/50/53	-
10	SF4	B	302	3	-	-	0/6/5/5
8	BCL	C	301	7,4	-	5/17/113/137	-
8	BCL	1	401	1	-	12/41/137/137	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	CLA	a	801	4	-	20/39/115/115	-
8	BCL	6	404	1	-	12/41/137/137	-
8	BCL	5	404	1	-	11/41/137/137	-
8	BCL	c	301	7,4	-	5/17/113/137	-
8	BCL	A	805	-	-	11/41/137/137	-
13	F39	C	302	-	-	42/58/78/78	0/2/2/2
8	BCL	a	810	4	-	5/17/113/137	-
8	BCL	5	401	1	-	12/41/137/137	-
8	BCL	A	810	4	-	15/41/137/137	-
8	BCL	4	409	-	-	14/41/137/137	-
8	BCL	4	402	-	-	13/41/137/137	-
14	LHG	A	819	4	-	30/53/53/53	-
8	BCL	5	402	1	-	11/41/137/137	-
15	LMG	A	817	4	-	19/39/59/70	0/1/1/1
8	BCL	5	405	1	-	11/41/137/137	-
8	BCL	A	806	4	-	4/17/113/137	-
8	BCL	4	404	1	-	17/41/137/137	-
14	LHG	E	101	-	-	16/41/41/53	-
8	BCL	A	807	4	-	19/41/137/137	-
8	BCL	4	403	1	-	18/41/137/137	-
8	BCL	2	409[B]	1	-	1/17/113/137	-
11	GS0	A	801	4	-	10/41/137/137	-
8	BCL	4	410[B]	1	-	7/17/113/137	-
8	BCL	2	403	1	-	10/41/137/137	-
9	CDL	c	303	7	-	31/80/80/110	-
12	CLA	A	822	4	-	18/39/115/115	-
8	BCL	6	405	1	-	14/41/137/137	-
8	BCL	a	813	4	-	5/17/113/137	-
8	BCL	6	403	1	-	16/41/137/137	-
8	BCL	A	812	4	-	4/17/113/137	-
8	BCL	A	808	4	-	2/17/113/137	-
8	BCL	F	101	6,4	-	2/17/113/137	-
8	BCL	4	405	-	-	14/41/137/137	-
8	BCL	2	408	1	-	13/41/137/137	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	BCL	1	403	1	-	16/41/137/137	-
8	BCL	4	406	1	-	13/41/137/137	-
8	BCL	5	406	1	-	14/41/137/137	-
8	BCL	a	814	4	-	2/17/113/137	-
8	BCL	a	808	4	-	24/41/137/137	-
8	BCL	2	406	1	-	15/41/137/137	-
8	BCL	3	403	1	-	18/41/137/137	-
8	BCL	a	806	9	-	16/41/137/137	-
8	BCL	6	406	1	-	11/41/137/137	-
8	BCL	4	407	1	-	13/41/137/137	-
8	BCL	A	809	4	-	7/17/113/137	-
13	F39	A	815	-	-	41/58/78/78	0/2/2/2
14	LHG	a	821	4	-	26/46/46/53	-
8	BCL	3	407	-	-	15/41/137/137	-
8	BCL	3	404	-	-	16/41/137/137	-
8	BCL	A	804	-	-	12/29/125/137	-
9	CDL	a	820	-	-	40/80/80/110	-
8	BCL	2	405	1	-	16/41/137/137	-
8	BCL	1	402	1	-	10/41/137/137	-
8	BCL	A	813	4	-	3/17/113/137	-
8	BCL	3	401	1	-	12/41/137/137	-
8	BCL	a	805	-	-	11/29/125/137	-
8	BCL	3	405	1	-	11/41/137/137	-
17	F26	c	302	7	-	23/36/36/36	0/1/1/1
8	BCL	6	401	1	-	13/41/137/137	-
8	BCL	1	405	1	-	9/41/137/137	-
14	LHG	A	816	-	-	23/50/50/53	-
14	LHG	a	819	-	-	19/44/44/53	-
8	BCL	6	408	-	-	11/41/137/137	-
8	BCL	A	811	4	-	11/41/137/137	-
12	CLA	a	803	-	-	15/39/115/115	-
8	BCL	a	807	4	-	4/17/113/137	-
8	BCL	a	811	4	-	19/41/137/137	-
8	BCL	3	406	1	-	11/41/137/137	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	BCL	1	408	-	-	15/41/137/137	-

The worst 5 of 1478 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	815	F39	C27-C20	27.42	1.62	1.34
13	A	814	F39	C27-C20	27.38	1.62	1.34
13	a	816	F39	C27-C20	27.27	1.62	1.34
13	C	302	F39	C27-C20	27.06	1.62	1.34
13	A	815	F39	C39-C37	22.67	1.65	1.35

The worst 5 of 2201 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	a	816	F39	C40-C39-C37	-10.90	111.76	127.31
13	a	816	F39	C51-C44-C42	-10.79	111.92	127.31
13	A	814	F39	C57-C59-C62	-10.71	112.02	127.31
13	a	816	F39	C63-C61-C58	-10.63	112.14	127.31
13	A	815	F39	C40-C39-C37	-10.50	112.32	127.31

There are no chirality outliers.

5 of 1472 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	1	401	BCL	C1A-C2A-CAA-CBA
8	1	401	BCL	C3A-C2A-CAA-CBA
8	1	401	BCL	CBD-CGD-O2D-CED
8	1	401	BCL	O1D-CGD-O2D-CED
8	1	402	BCL	C2C-C3C-CAC-CBC

There are no ring outliers.

92 monomers are involved in 503 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	2	402[B]	BCL	3	0
8	5	403	BCL	6	0
14	A	818	LHG	2	0
8	4	401	BCL	9	0
8	1	407[B]	BCL	2	0
8	2	407	BCL	5	0
8	a	812	BCL	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	1	406	BCL	13	0
13	a	816	F39	1	0
12	A	802	CLA	9	0
8	3	402	BCL	7	0
8	2	404	BCL	8	0
9	a	822	CDL	8	0
9	1	409	CDL	7	0
8	2	401	BCL	10	0
15	a	818	LMG	1	0
8	a	809	BCL	1	0
11	a	802	GS0	2	0
8	1	404	BCL	3	0
8	A	803	BCL	3	0
8	4	408[B]	BCL	1	0
8	a	804	BCL	1	0
8	6	402	BCL	10	0
10	B	302	SF4	2	0
14	a	817	LHG	2	0
8	C	301	BCL	4	0
8	1	401	BCL	10	0
12	a	801	CLA	11	0
8	6	404	BCL	8	0
8	5	404	BCL	9	0
8	c	301	BCL	6	0
8	A	805	BCL	6	0
8	a	810	BCL	2	0
8	5	401	BCL	12	0
8	A	810	BCL	8	0
8	4	409	BCL	11	0
8	4	402	BCL	10	0
14	A	819	LHG	4	0
8	5	402	BCL	10	0
15	A	817	LMG	4	0
8	5	405	BCL	5	0
8	A	806	BCL	4	0
8	4	404	BCL	5	0
14	E	101	LHG	1	0
8	A	807	BCL	3	0
8	4	403	BCL	8	0
8	2	409[B]	BCL	3	0
11	A	801	GS0	5	0
8	4	410[B]	BCL	3	0

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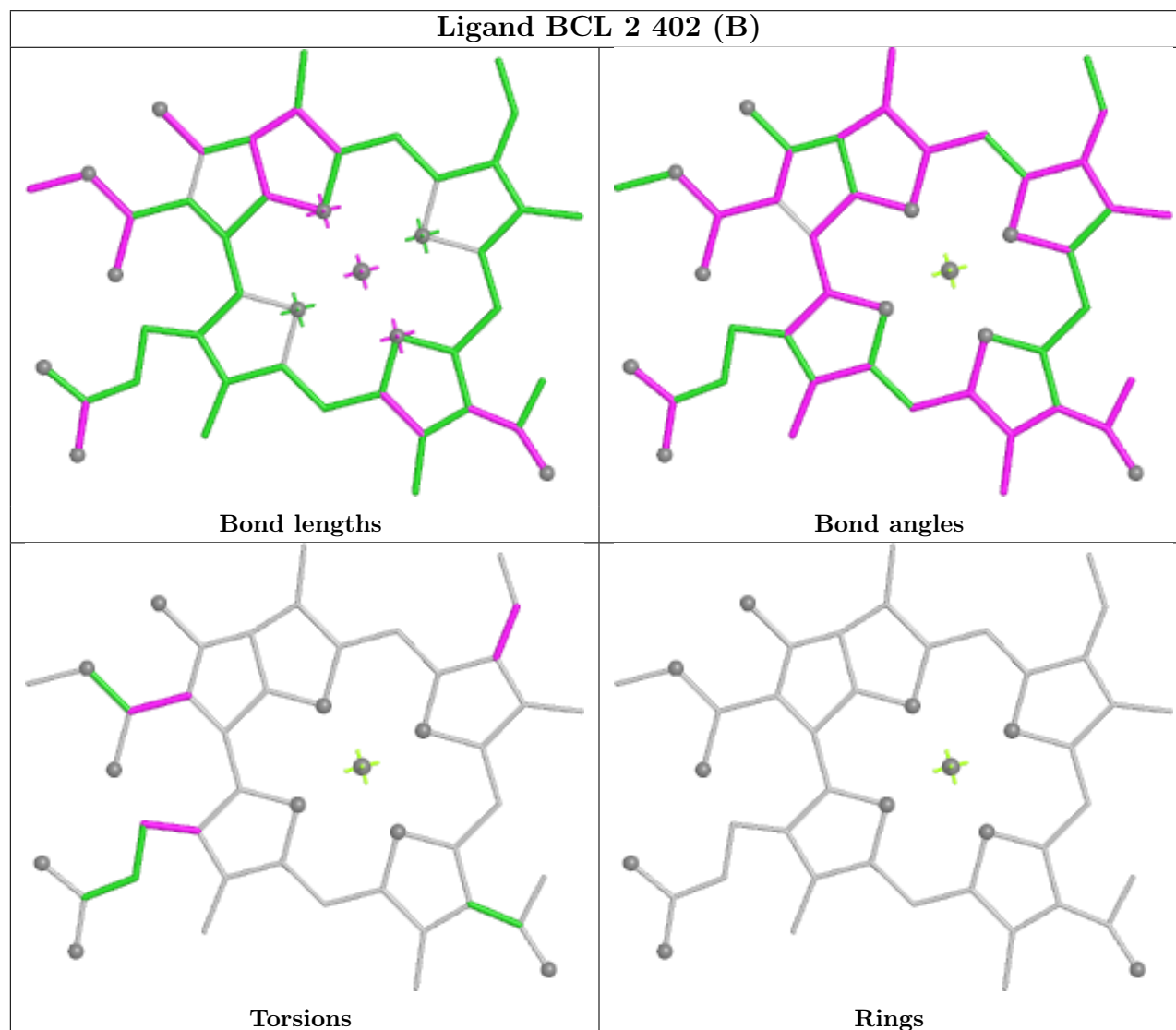
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	2	403	BCL	10	0
9	c	303	CDL	3	0
12	A	822	CLA	12	0
8	6	405	BCL	5	0
8	a	813	BCL	3	0
8	6	403	BCL	11	0
8	A	812	BCL	2	0
8	A	808	BCL	2	0
8	F	101	BCL	3	0
8	4	405	BCL	6	0
8	2	408	BCL	12	0
8	1	403	BCL	6	0
8	4	406	BCL	10	0
8	5	406	BCL	14	0
8	a	814	BCL	2	0
8	a	808	BCL	4	0
8	2	406	BCL	9	0
8	3	403	BCL	6	0
8	a	806	BCL	6	0
8	6	406	BCL	16	0
8	4	407	BCL	9	0
8	A	809	BCL	7	0
14	a	821	LHG	5	0
8	3	407	BCL	11	0
8	3	404	BCL	7	0
8	A	804	BCL	4	0
9	a	820	CDL	5	0
8	2	405	BCL	5	0
8	1	402	BCL	9	0
8	3	401	BCL	12	0
8	a	805	BCL	3	0
8	3	405	BCL	8	0
8	6	401	BCL	14	0
8	1	405	BCL	11	0
14	A	816	LHG	2	0
14	a	819	LHG	3	0
8	6	408	BCL	12	0
8	A	811	BCL	7	0
12	a	803	CLA	15	0
8	a	807	BCL	3	0
8	a	811	BCL	8	0
8	3	406	BCL	10	0

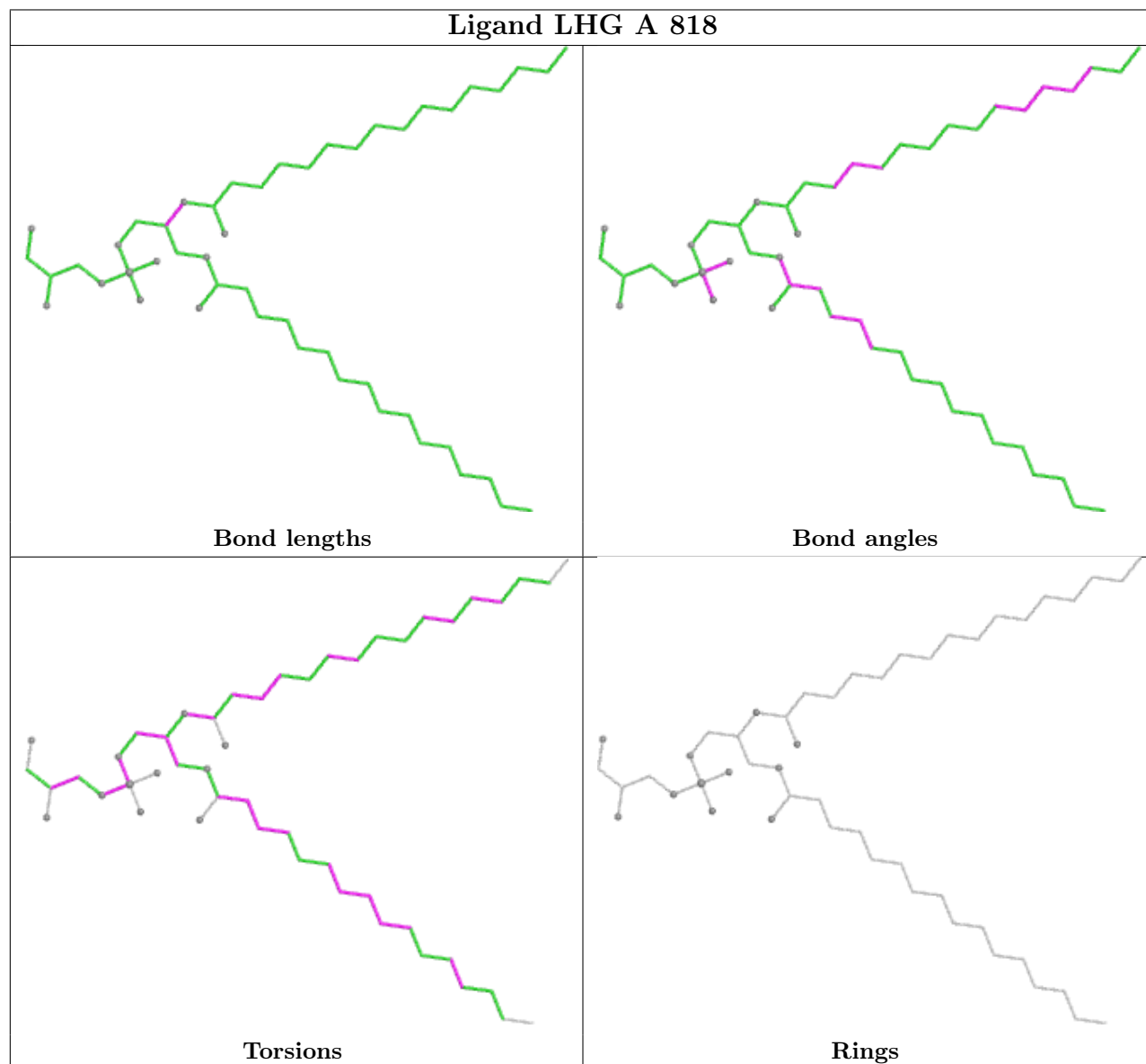
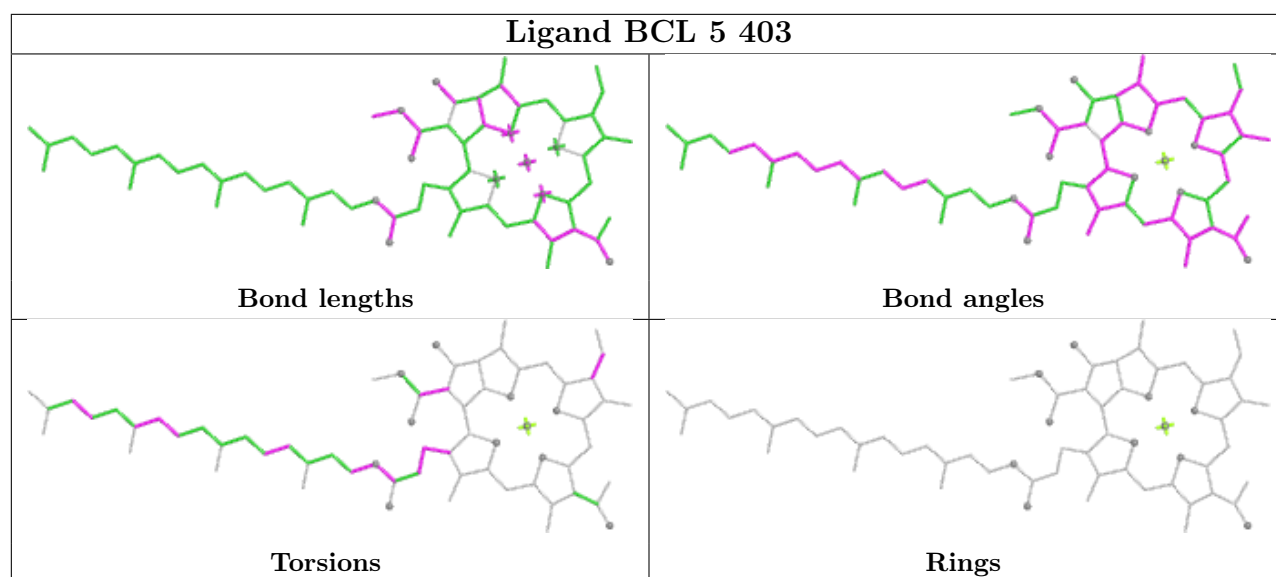
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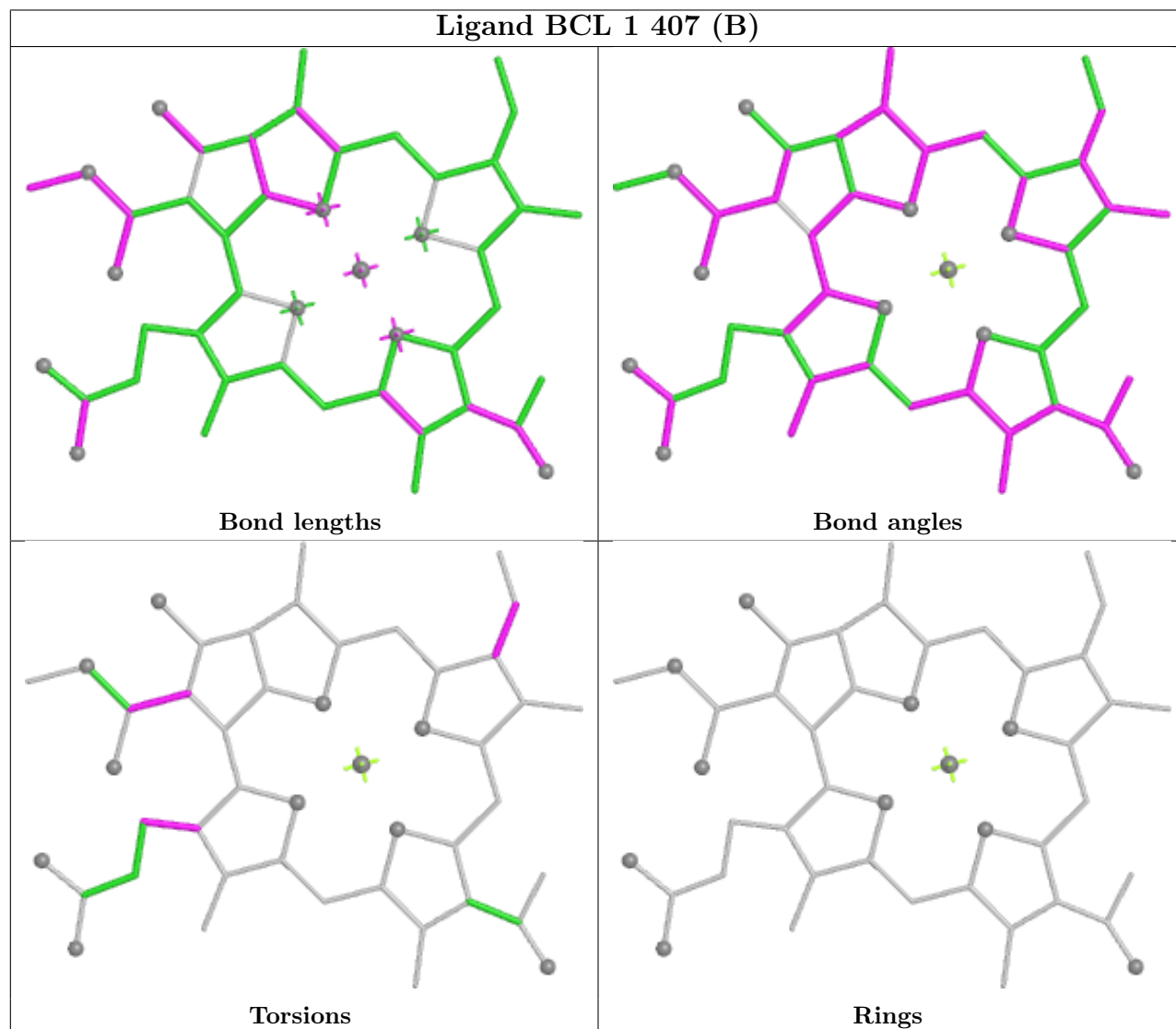
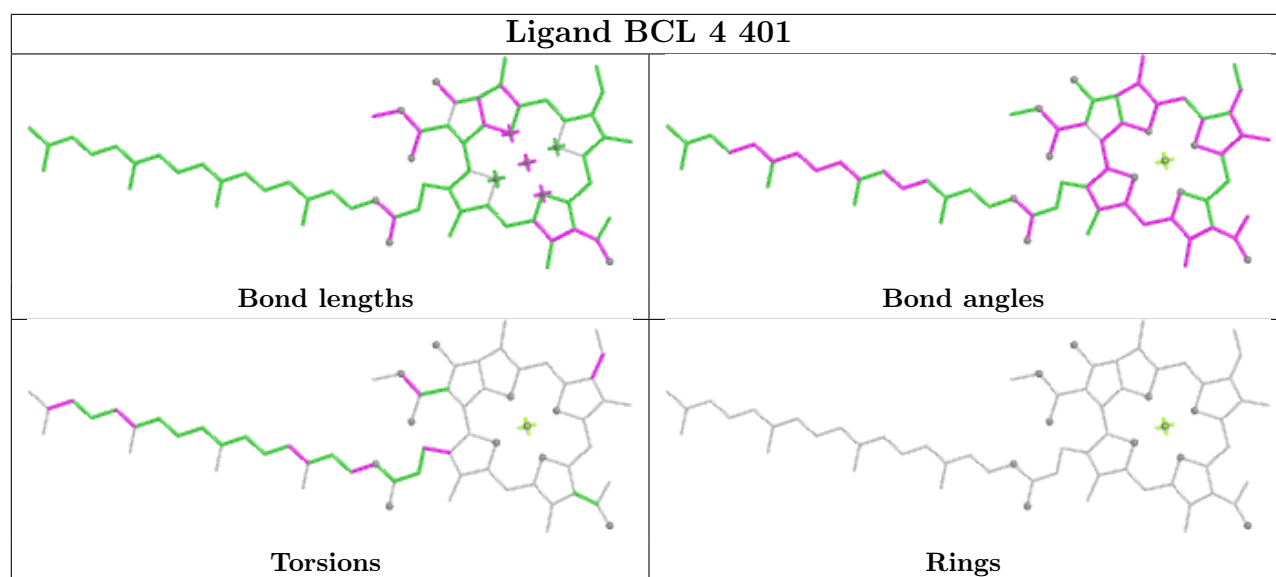
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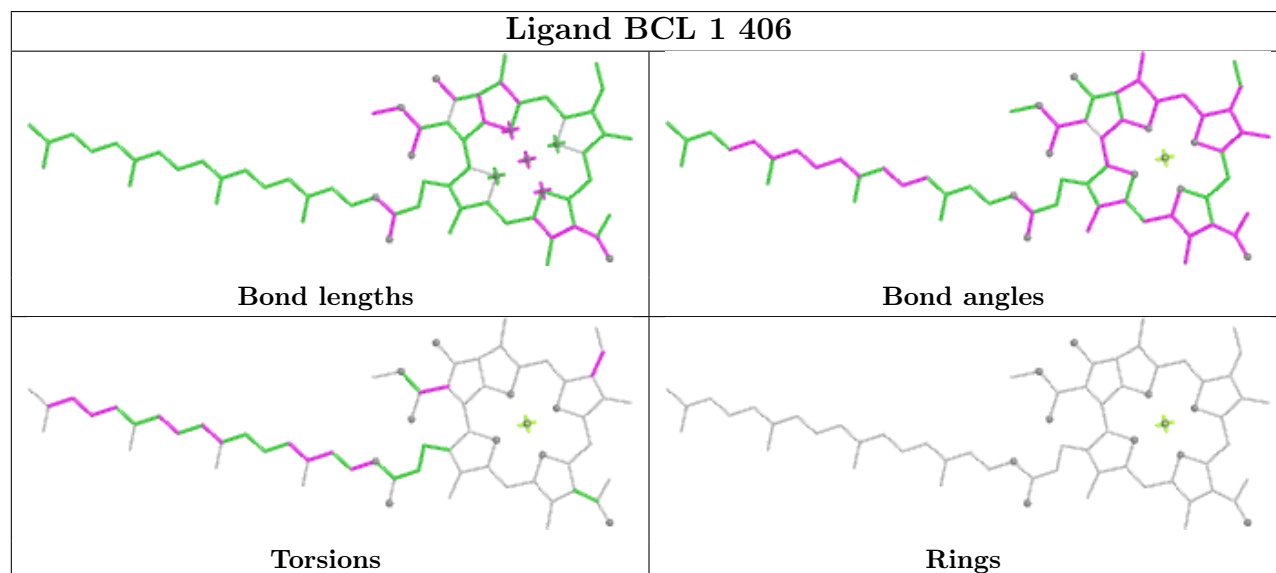
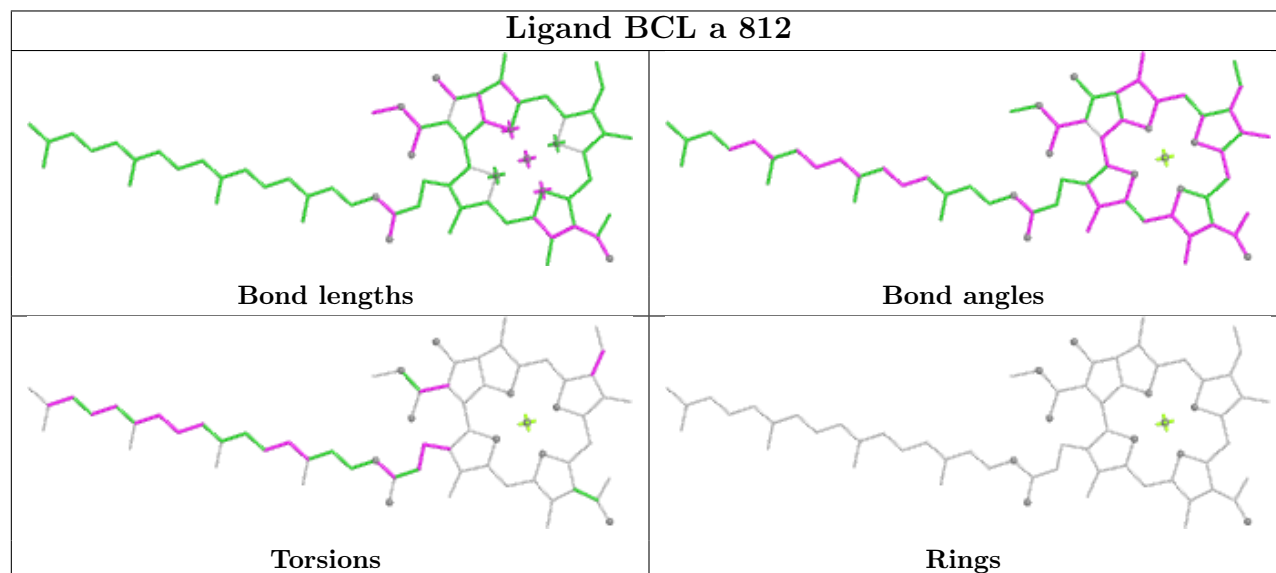
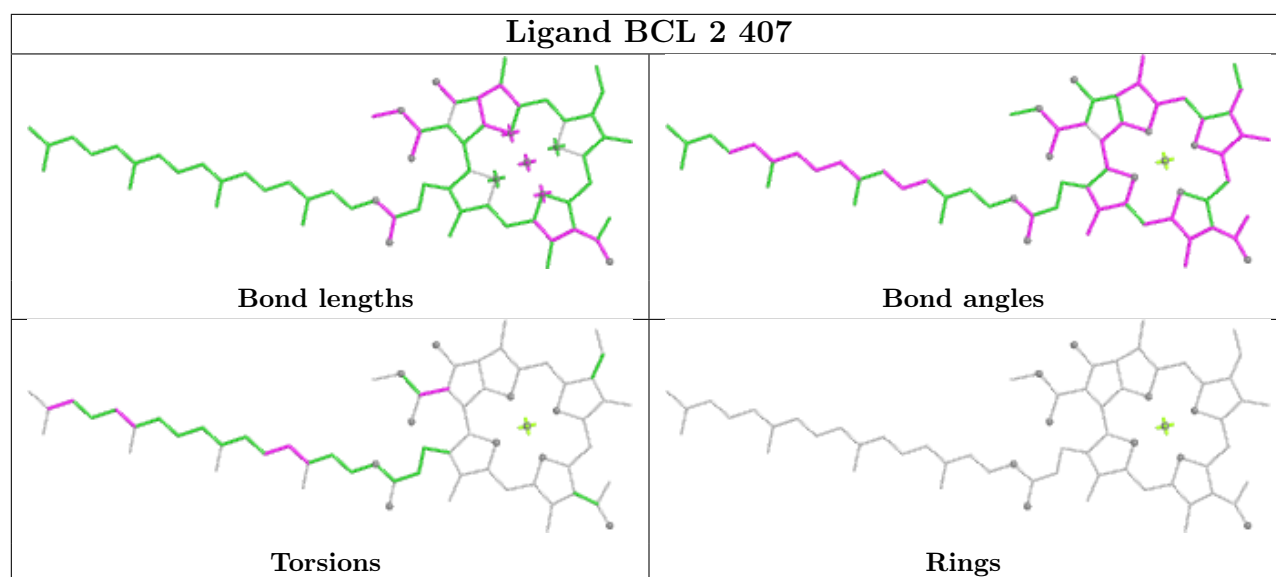
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	1	408	BCL	9	0

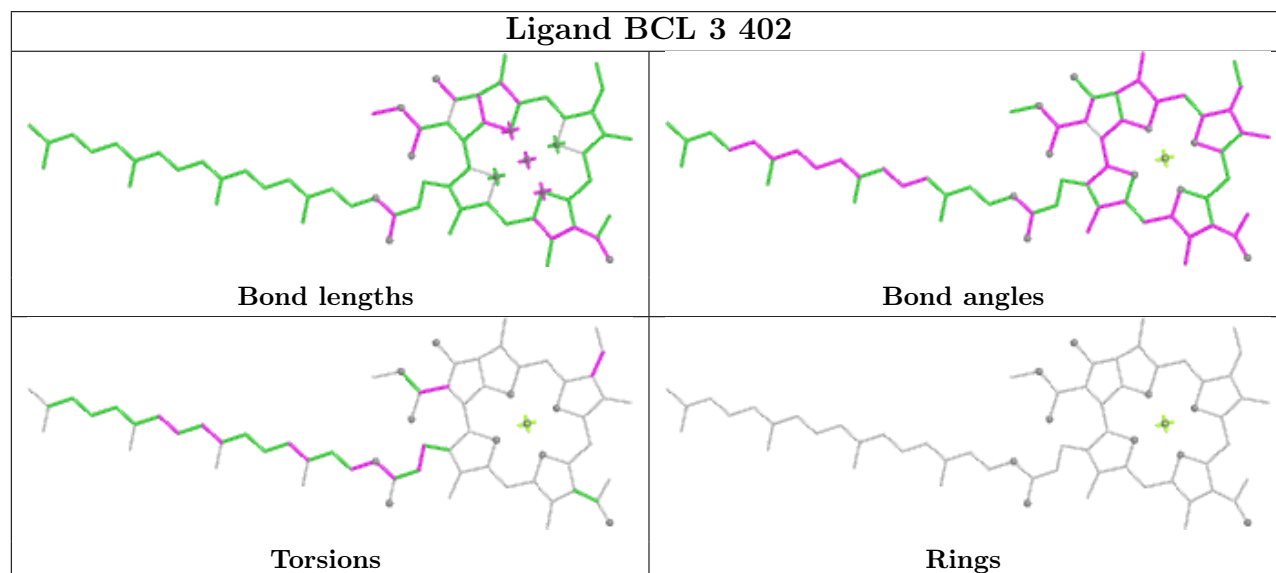
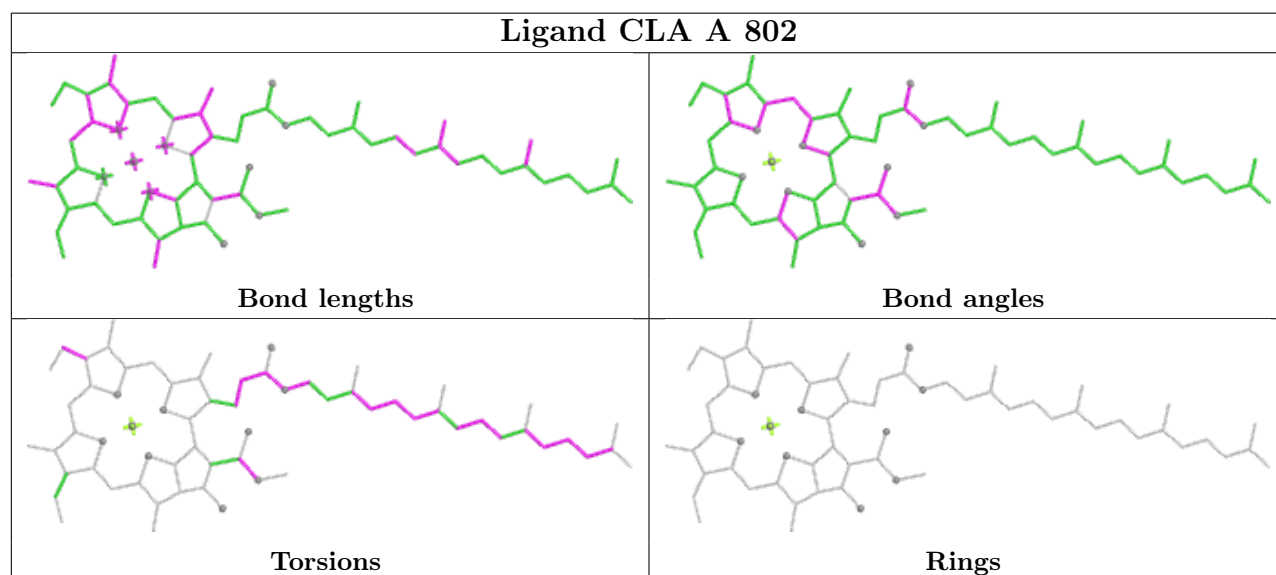
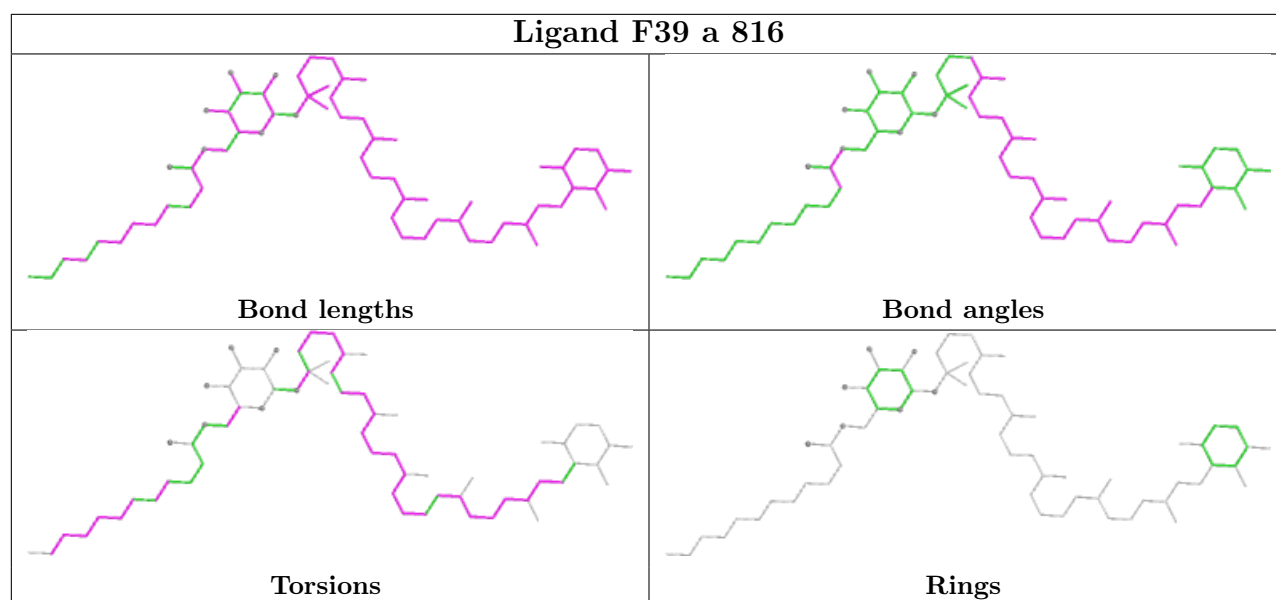
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

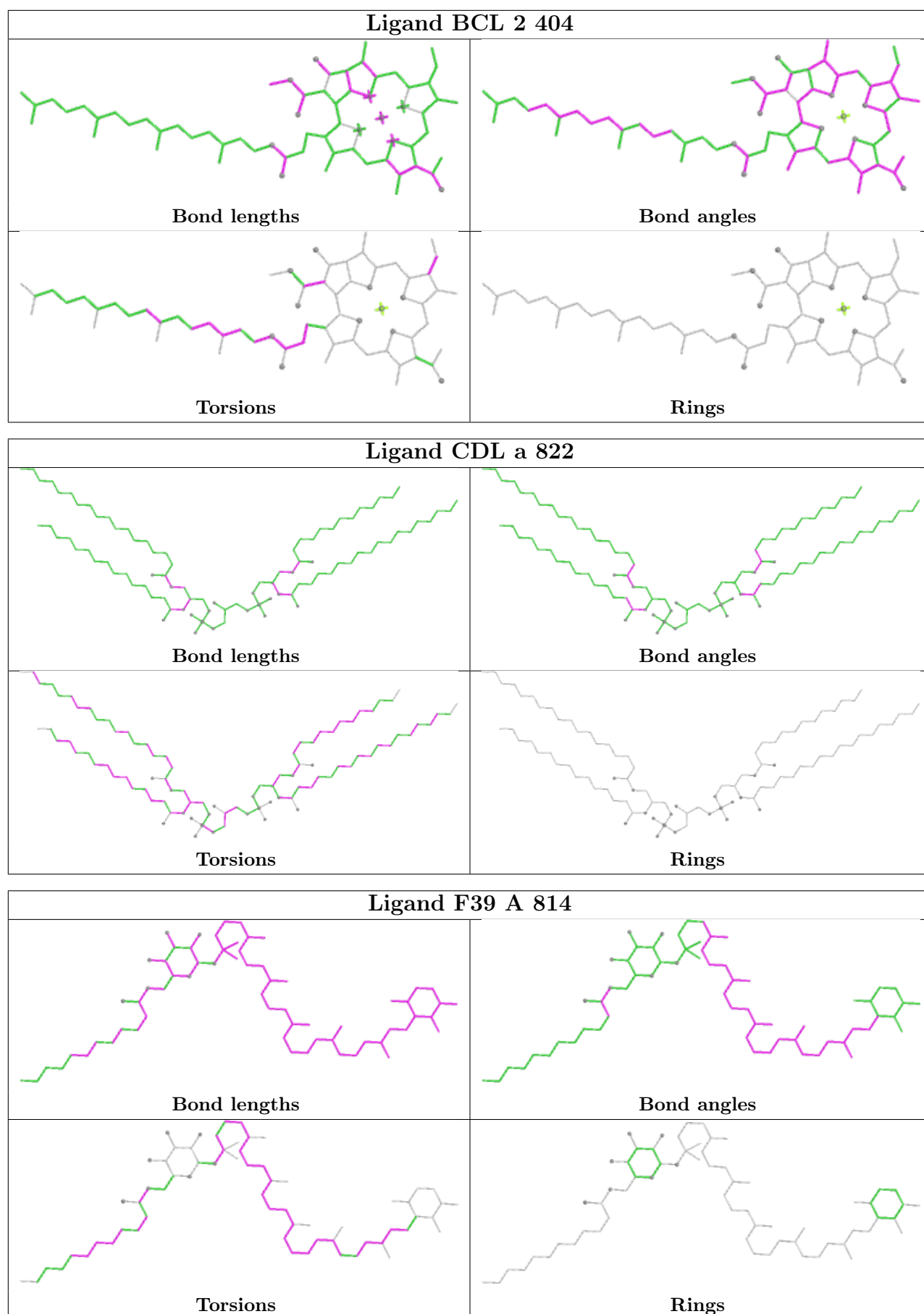


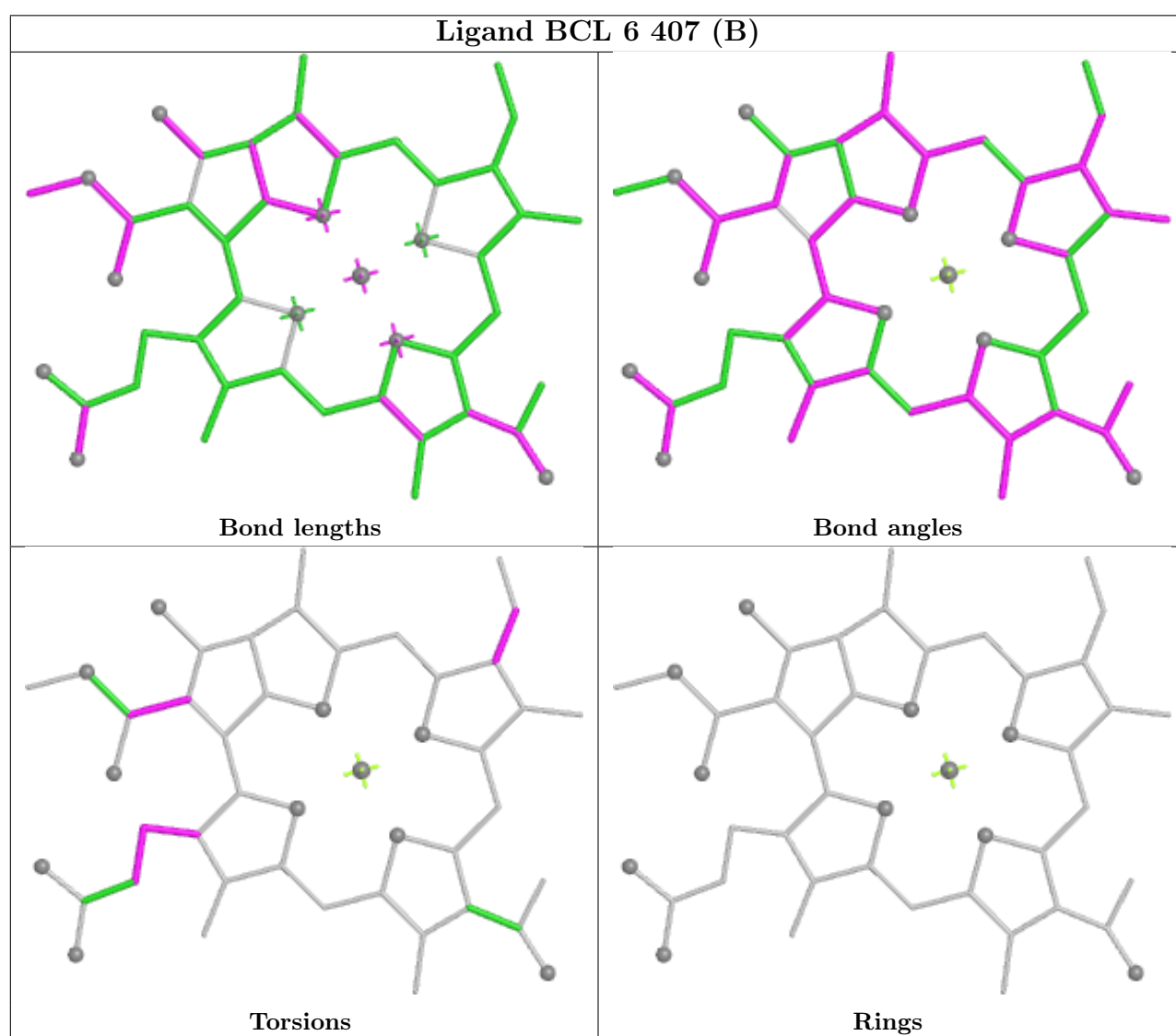
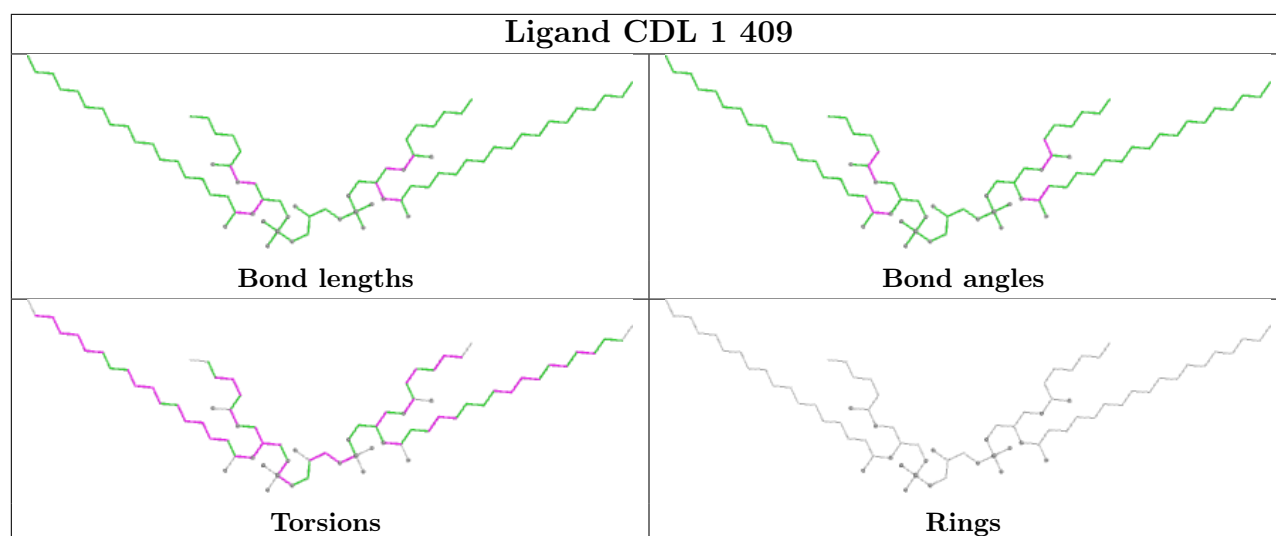


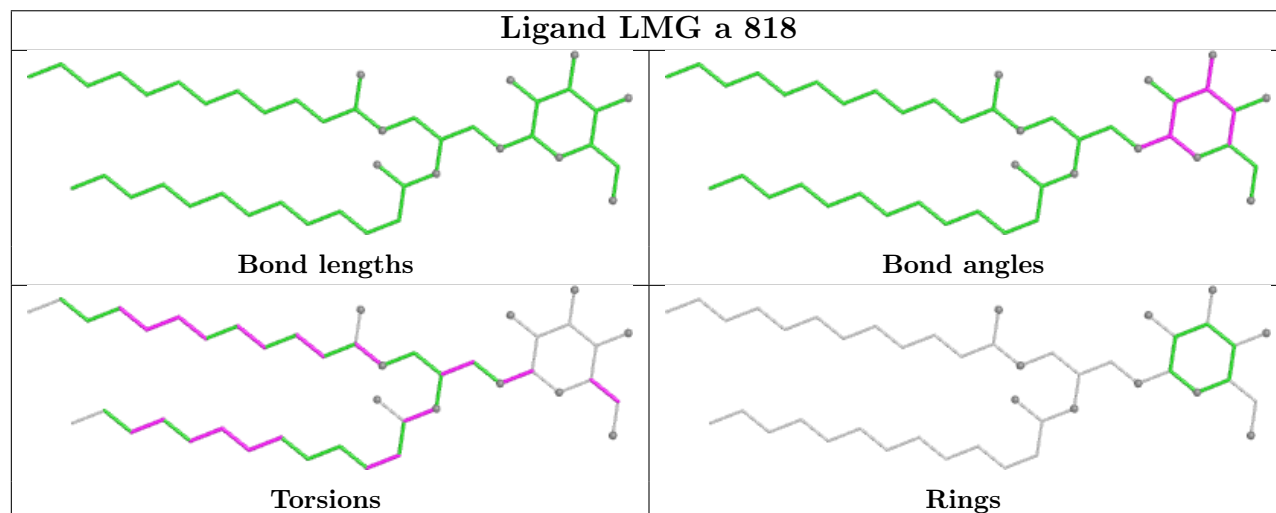
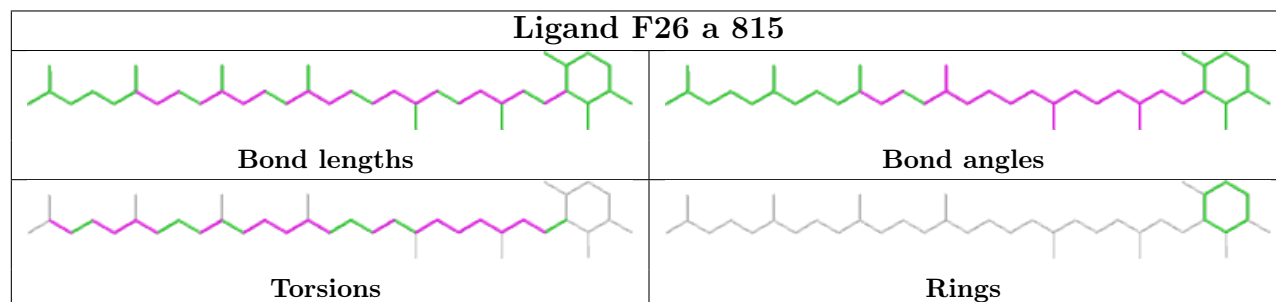
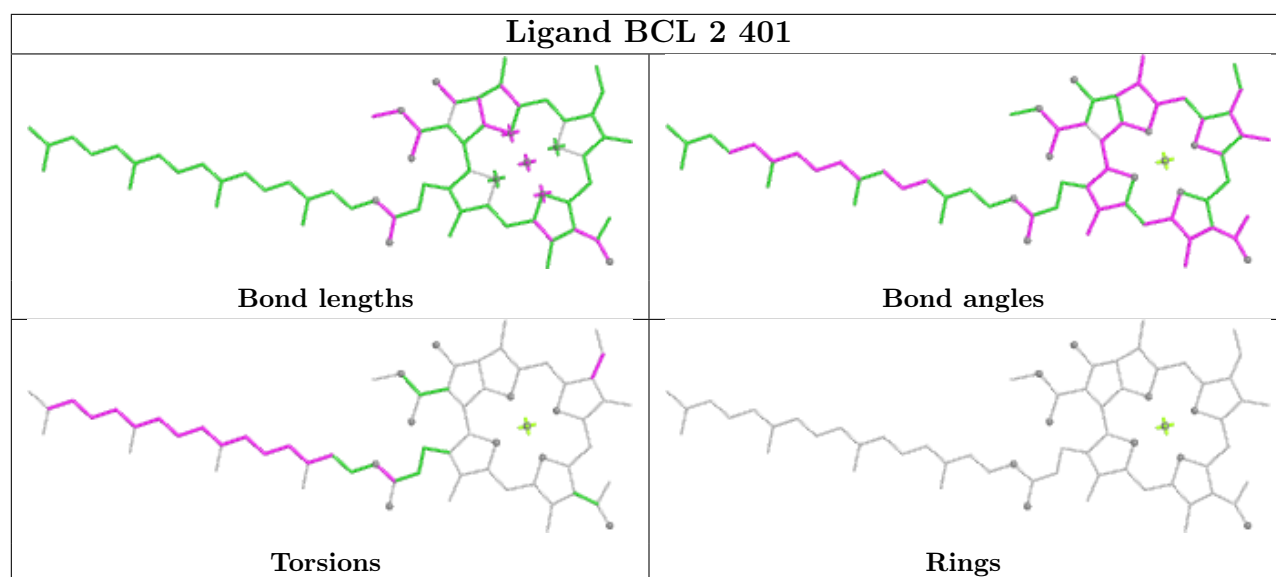


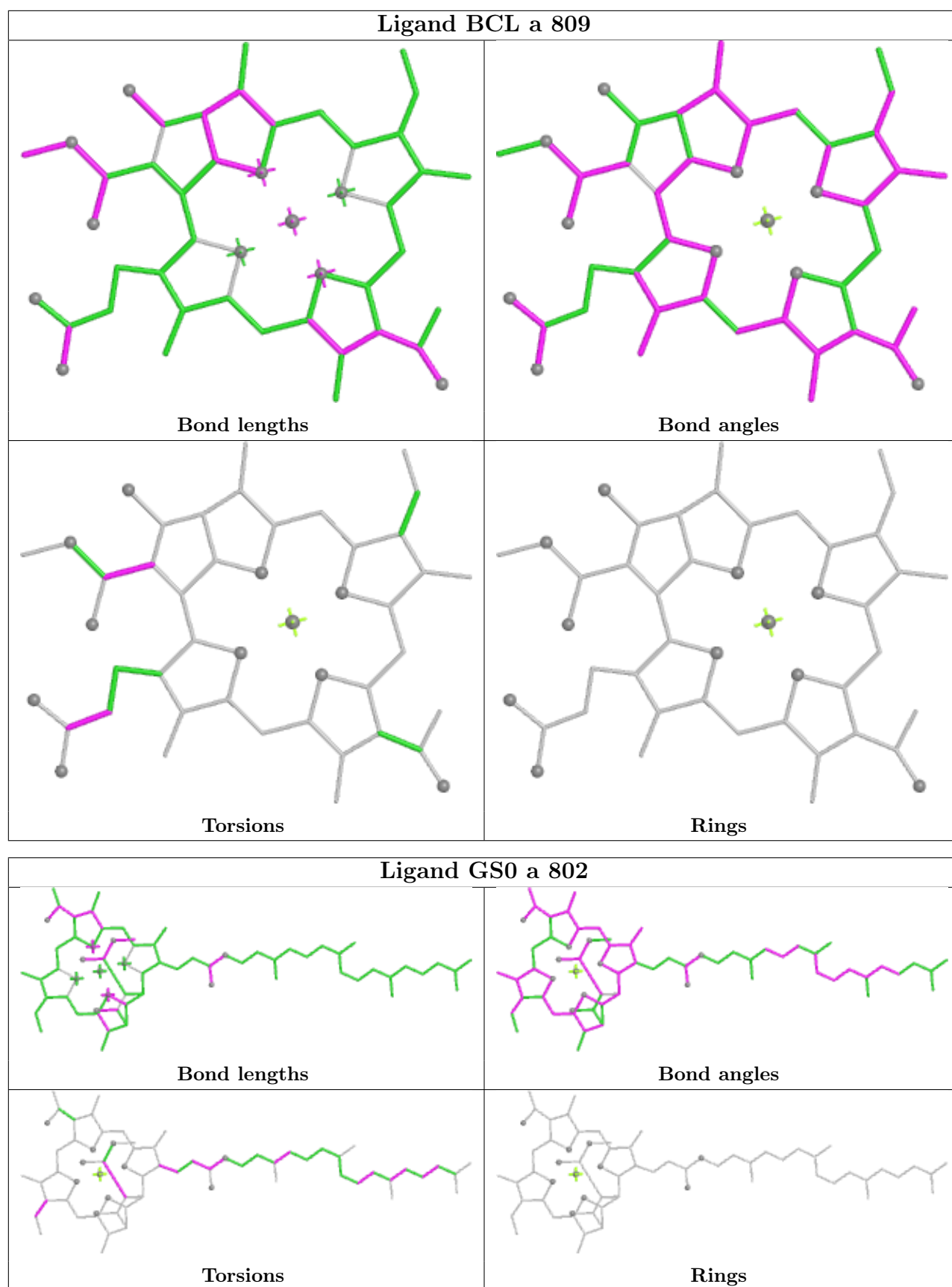


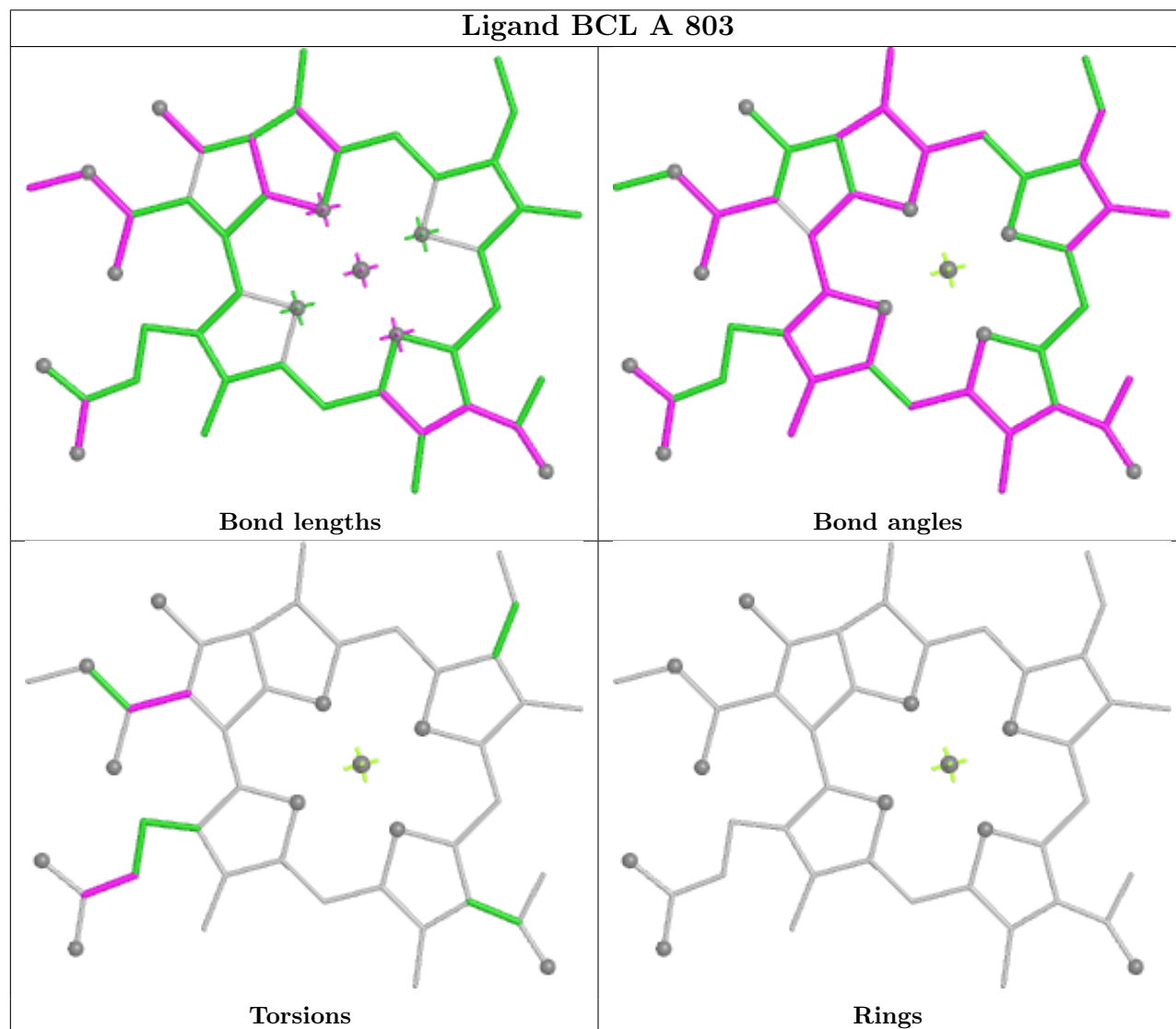
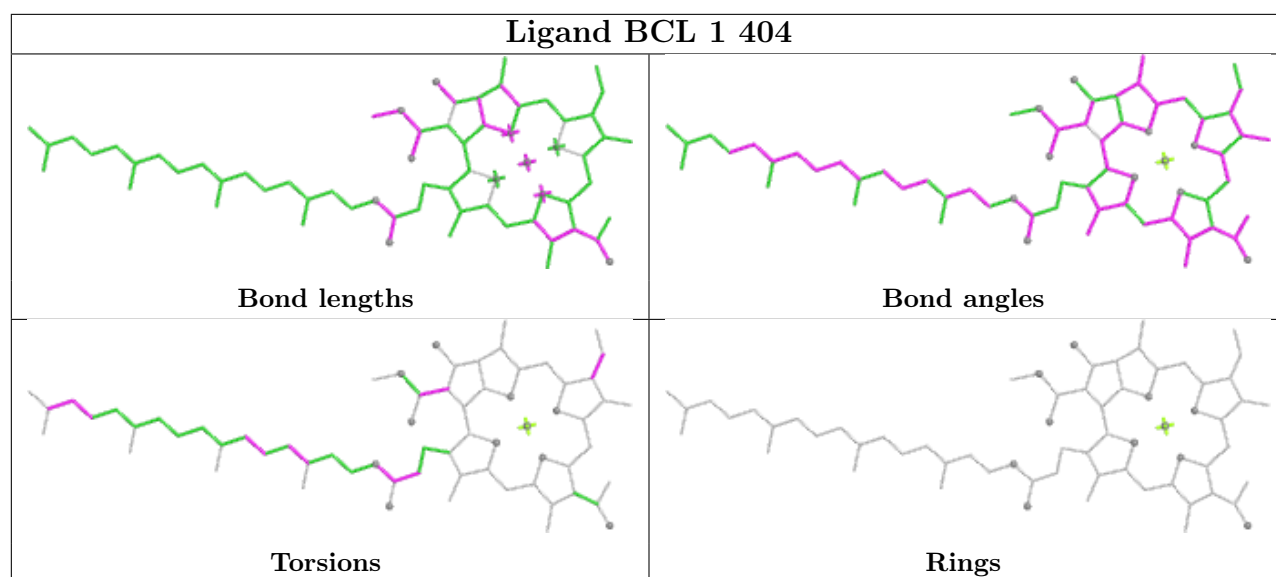




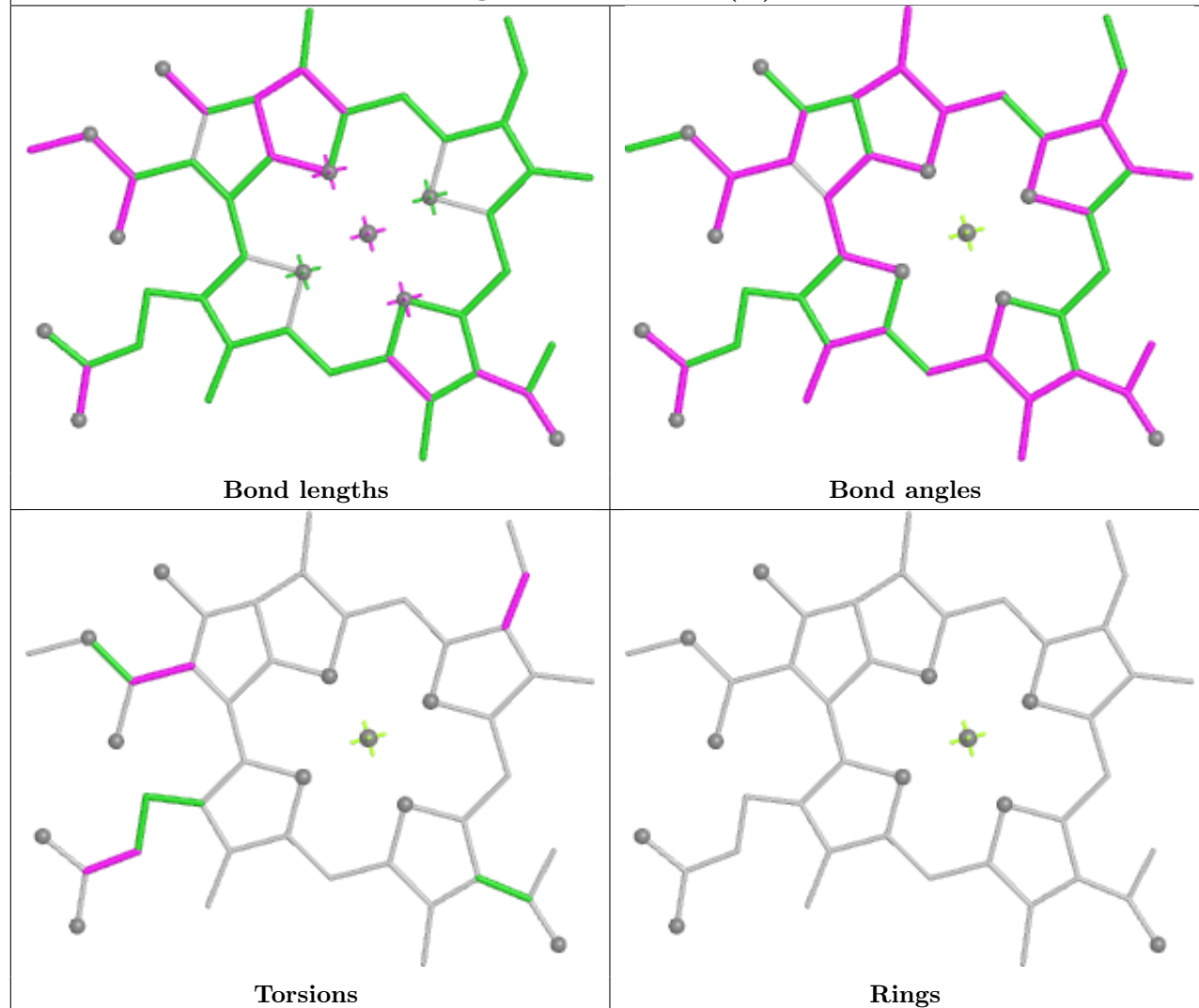


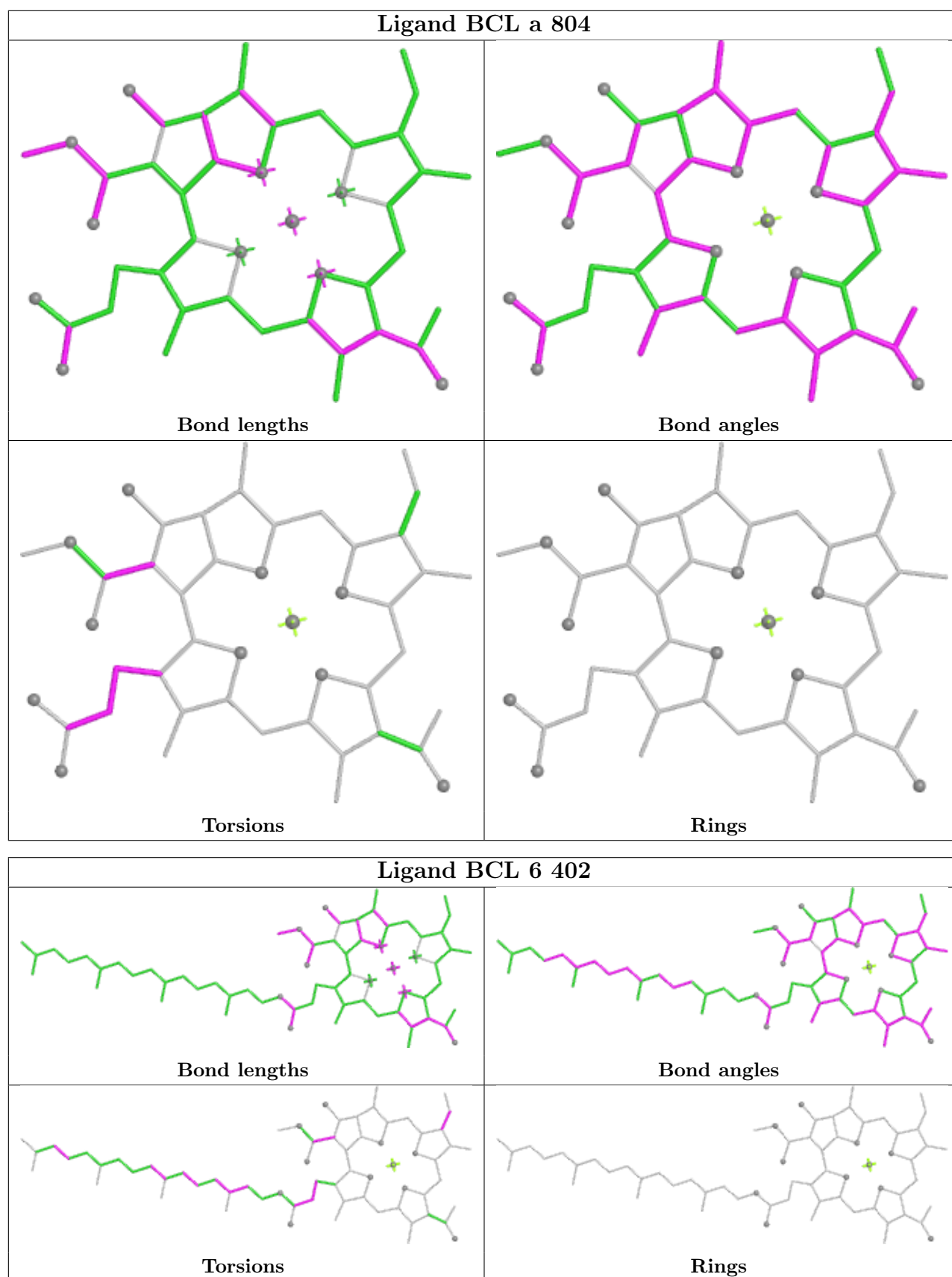


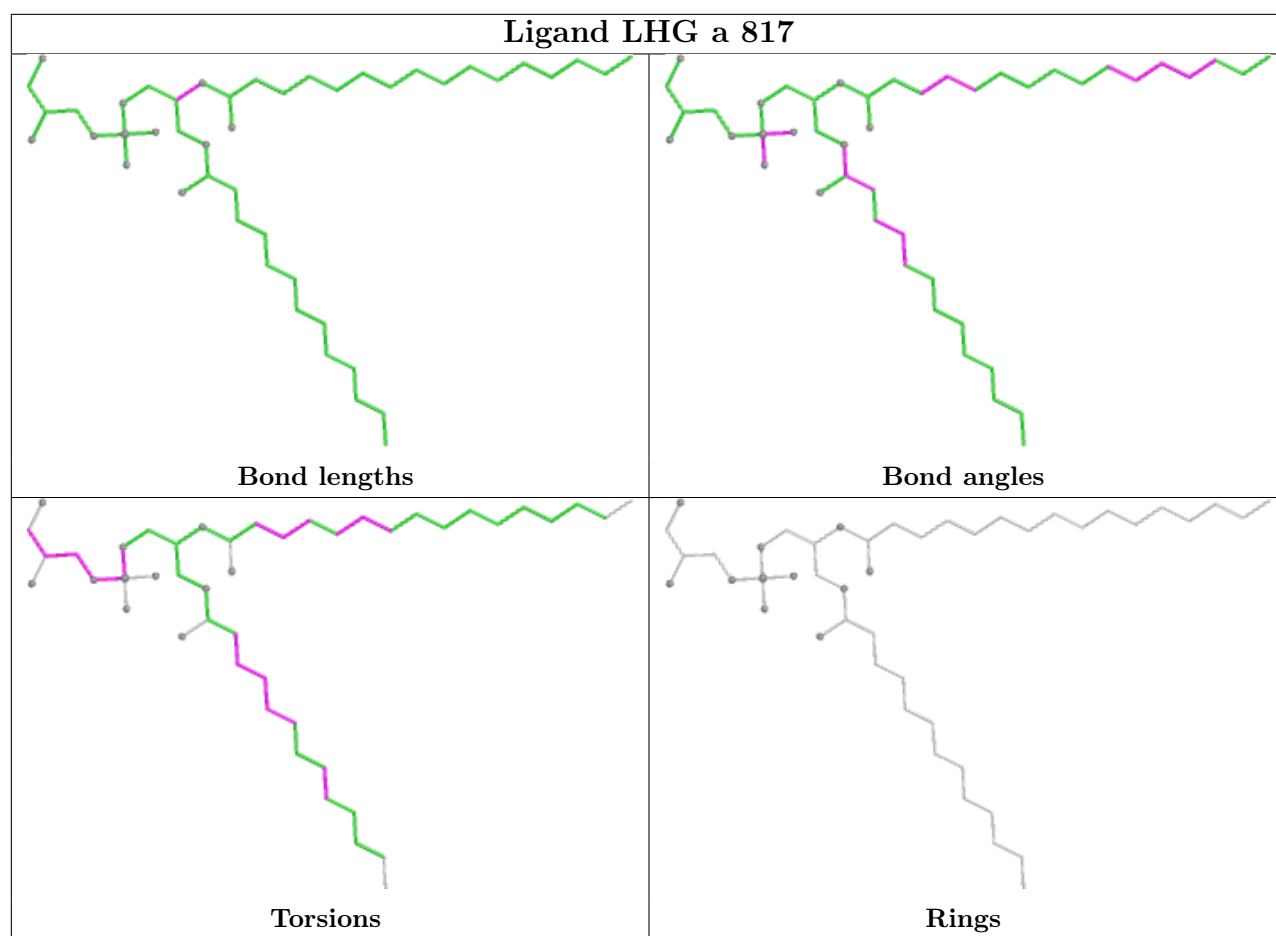


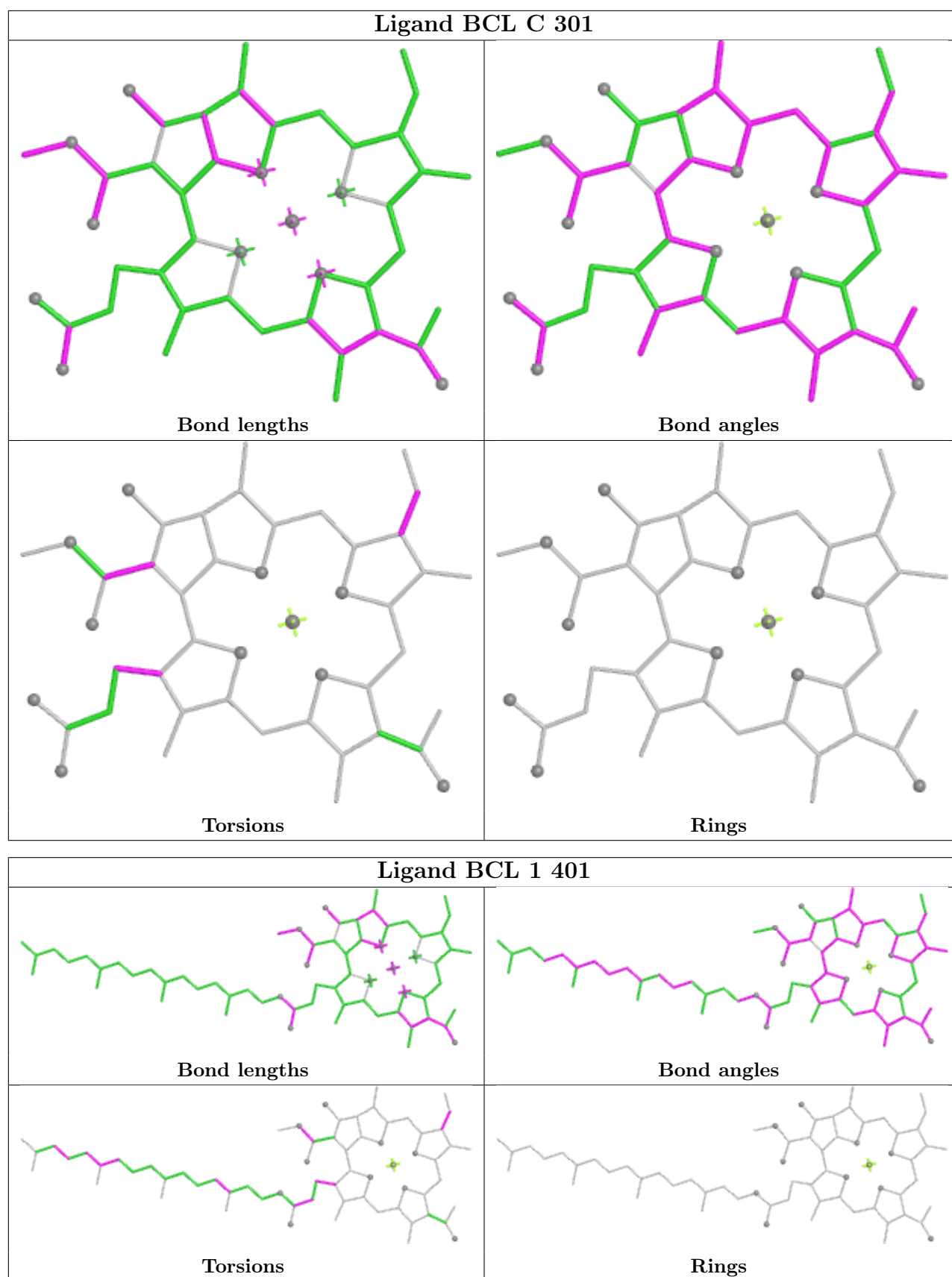


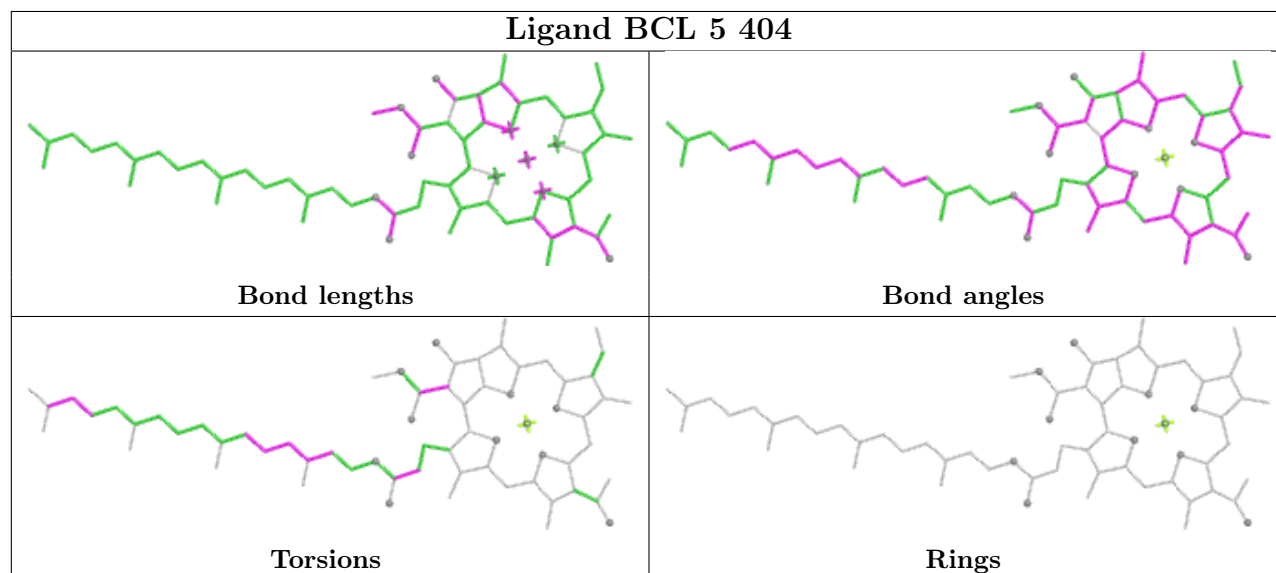
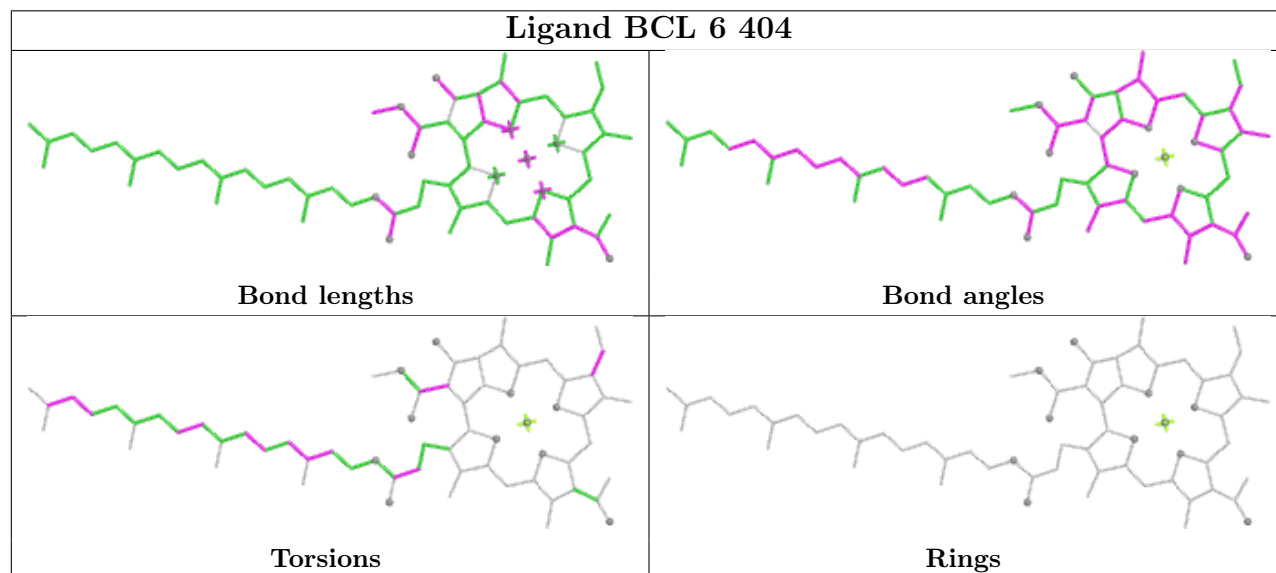
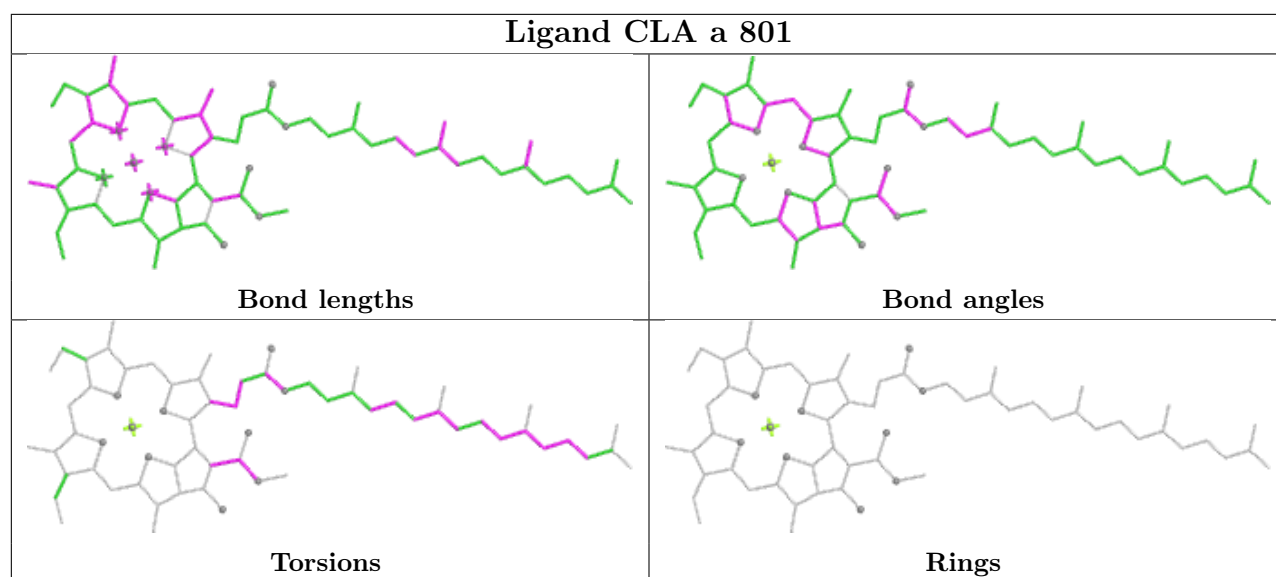
Ligand BCL 4 408 (B)

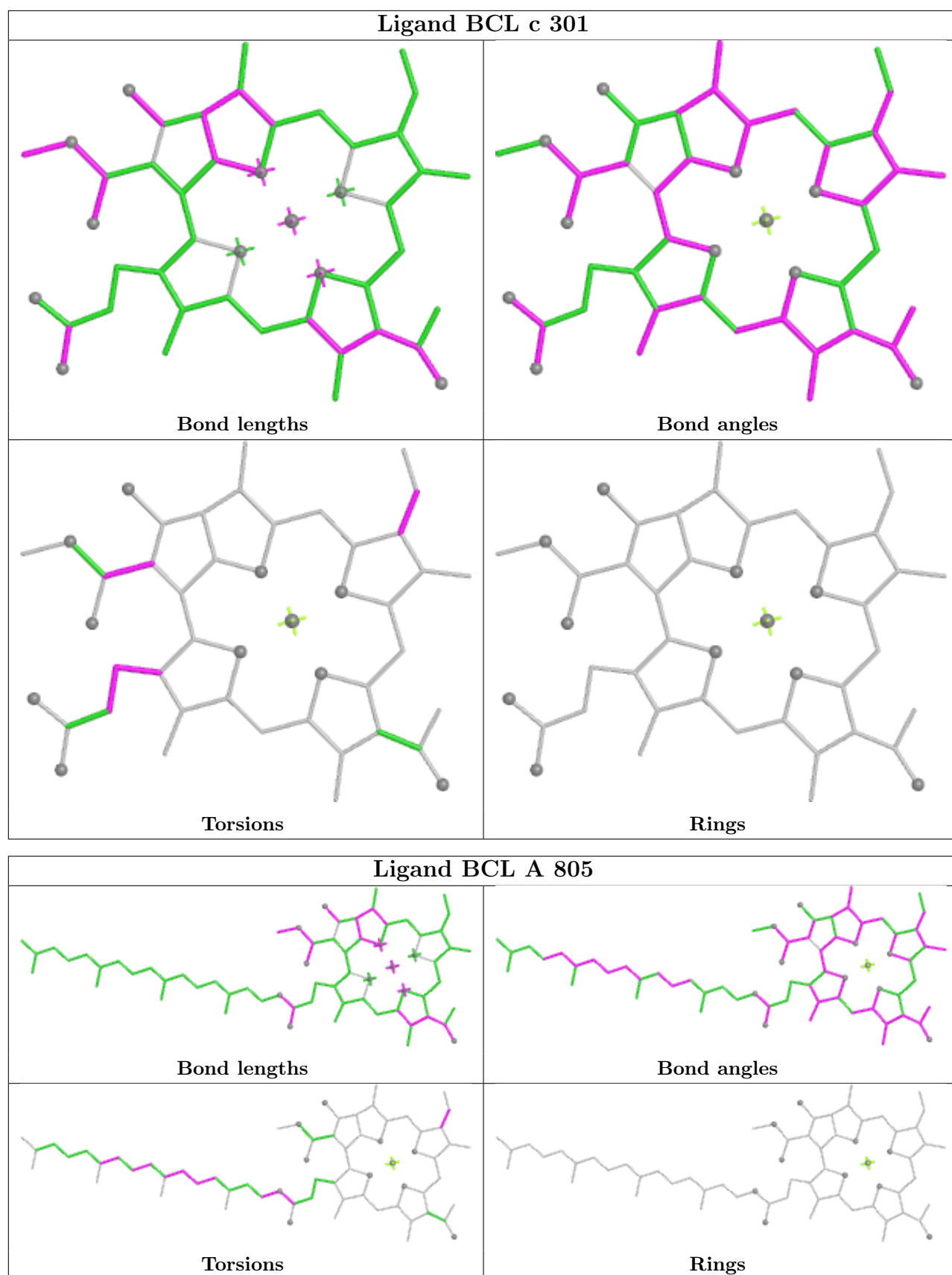


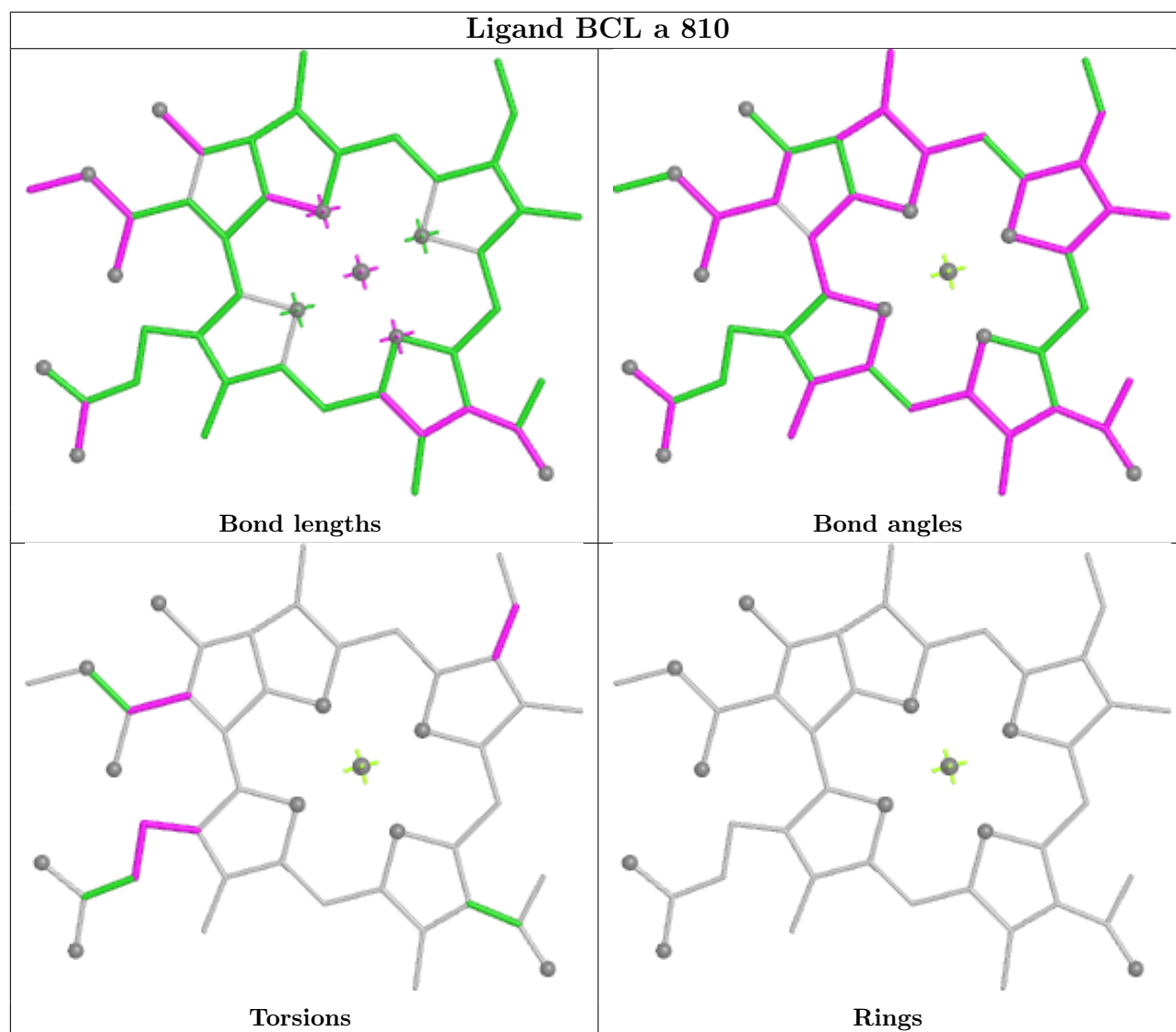
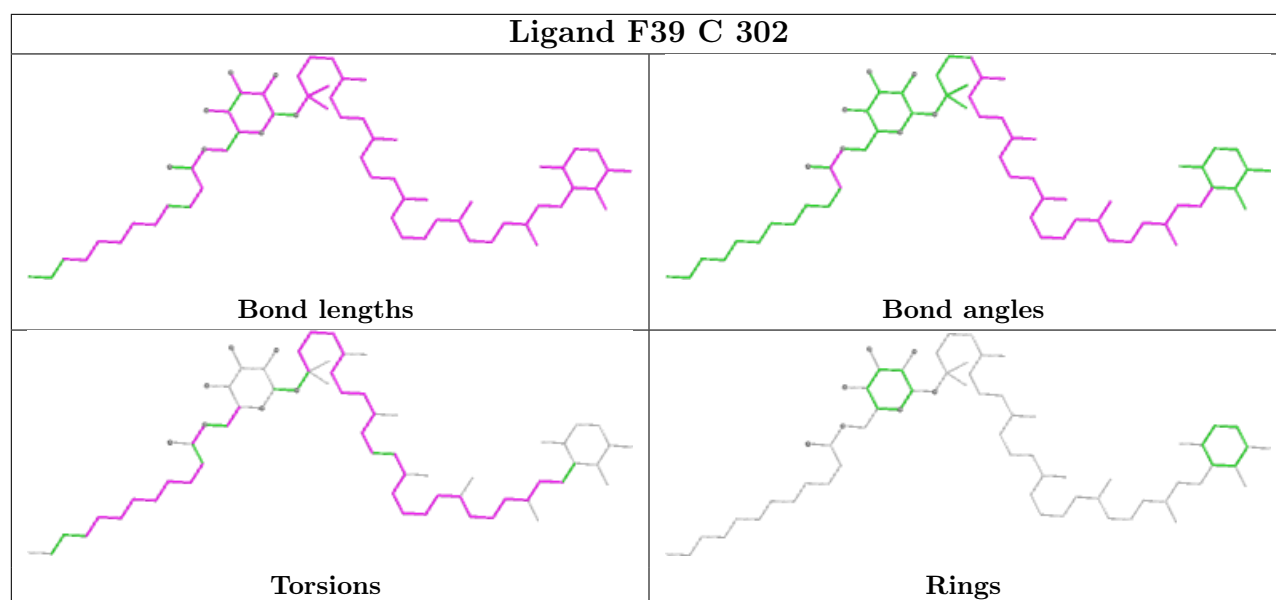


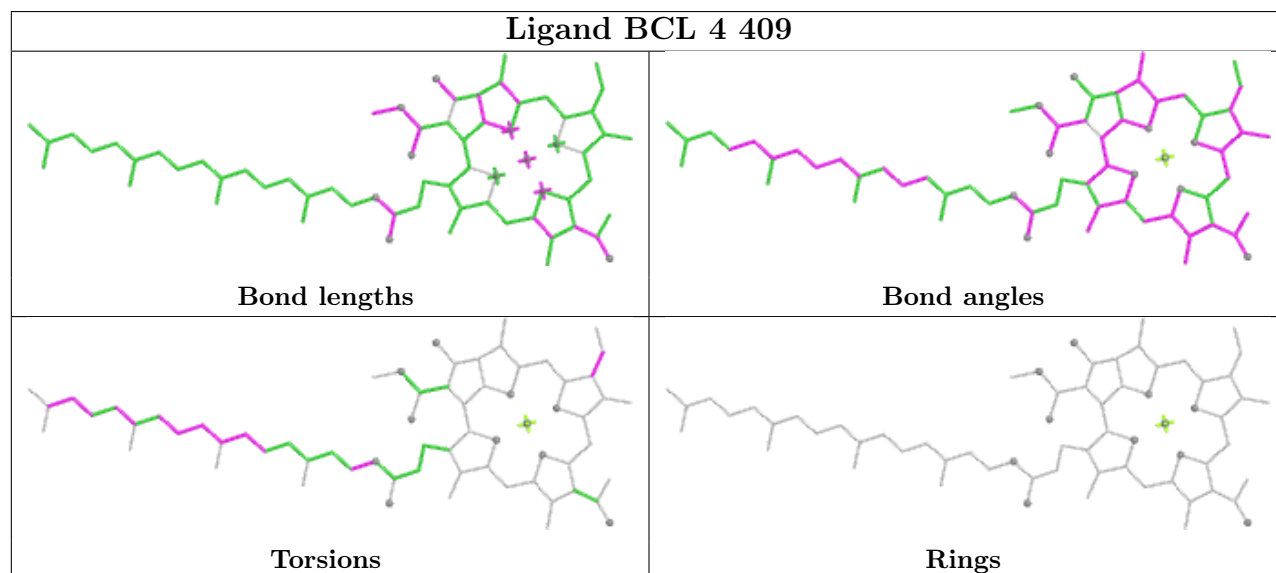
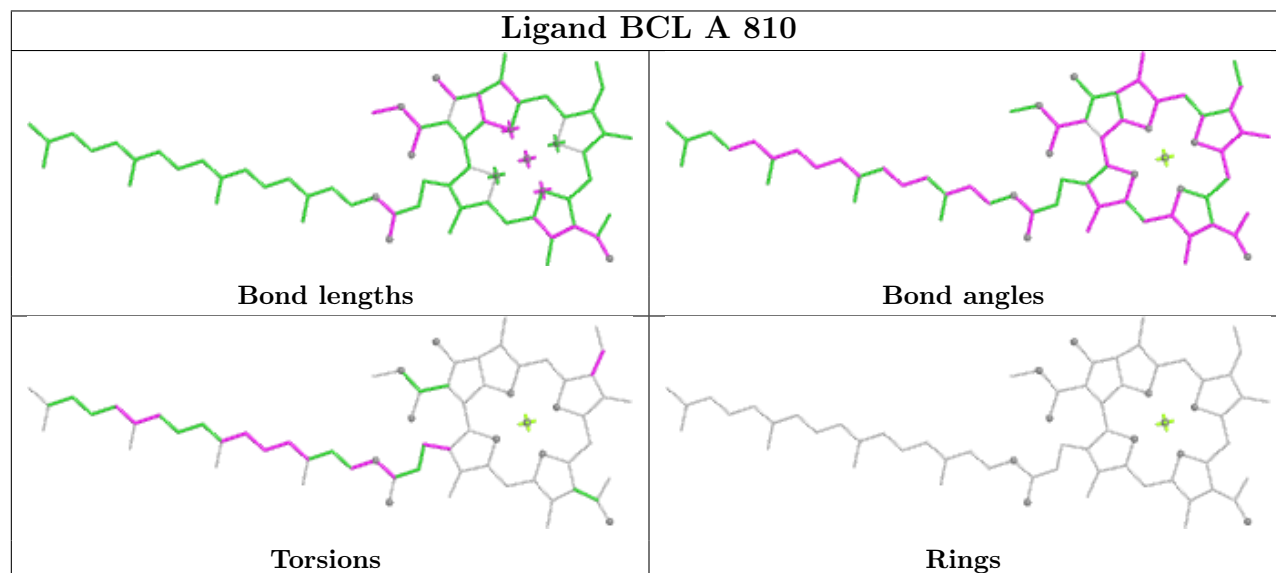
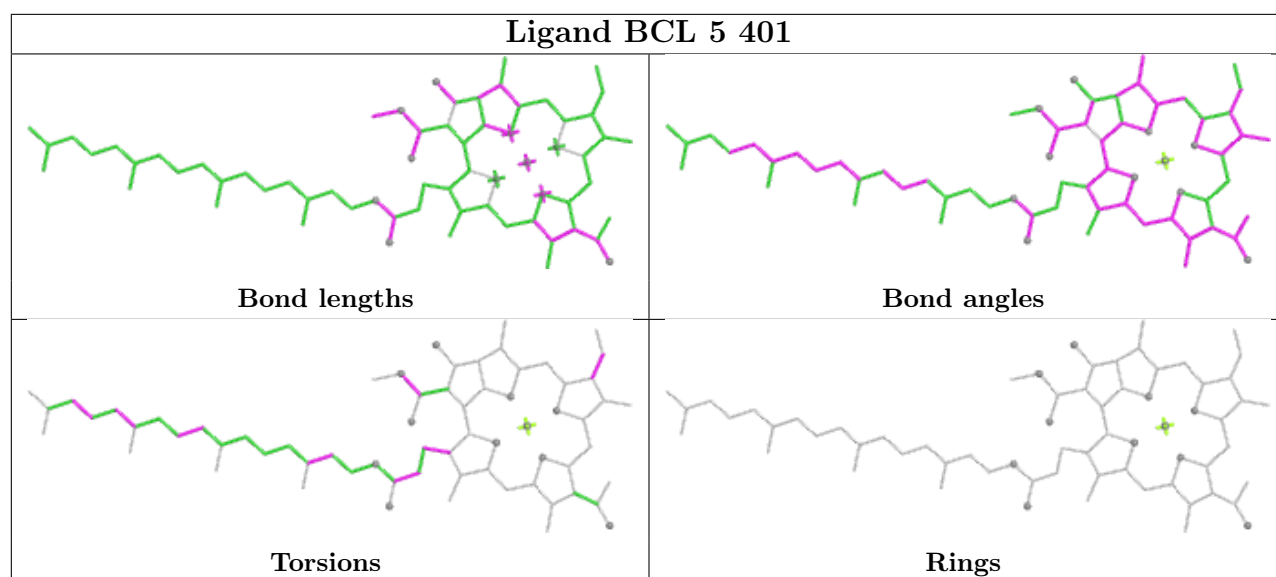


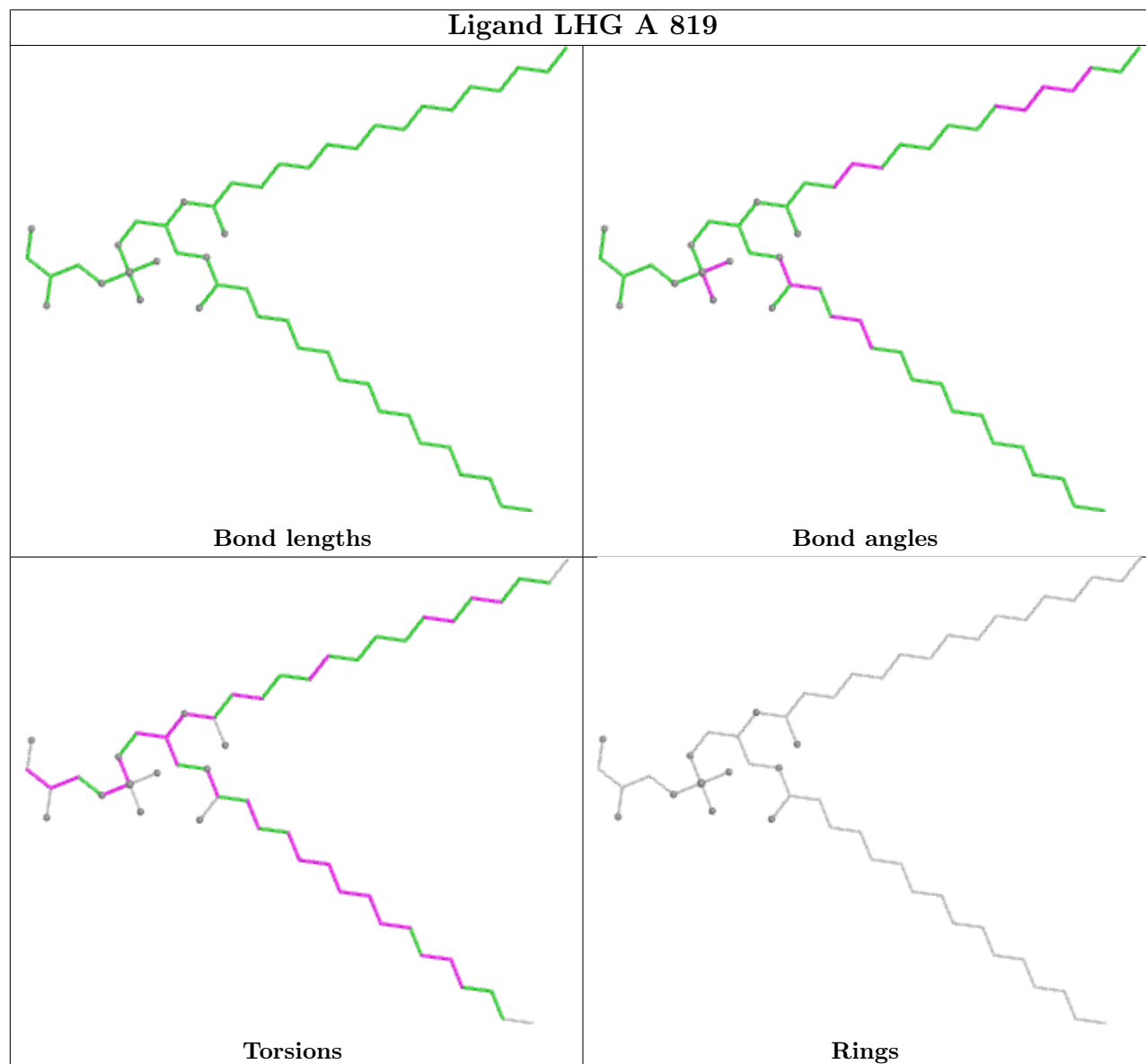
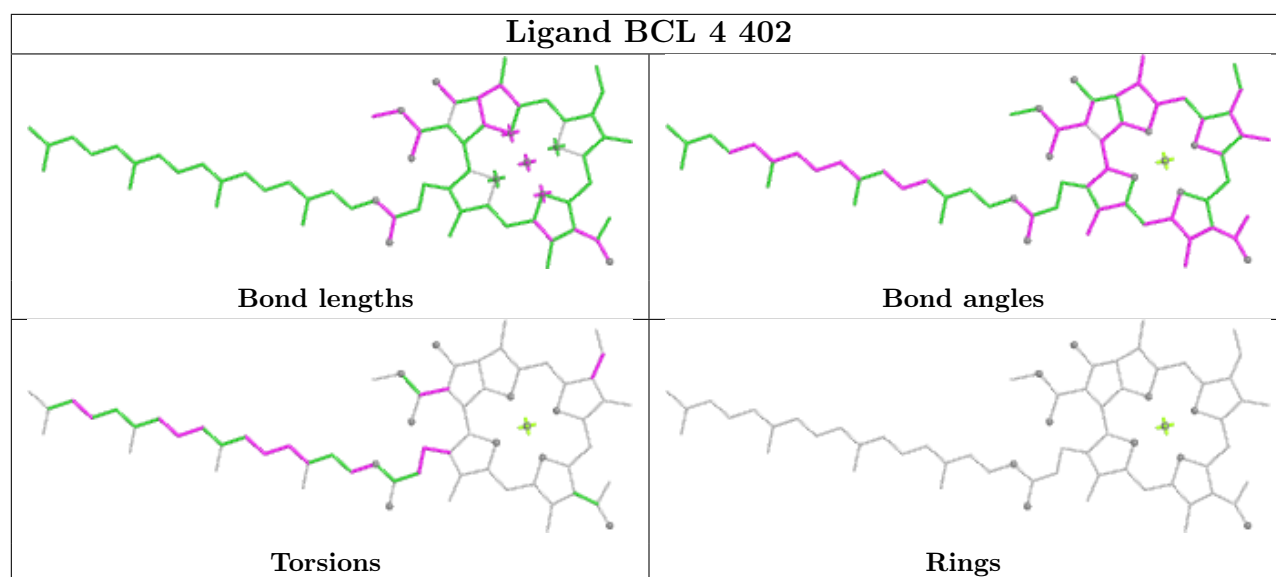


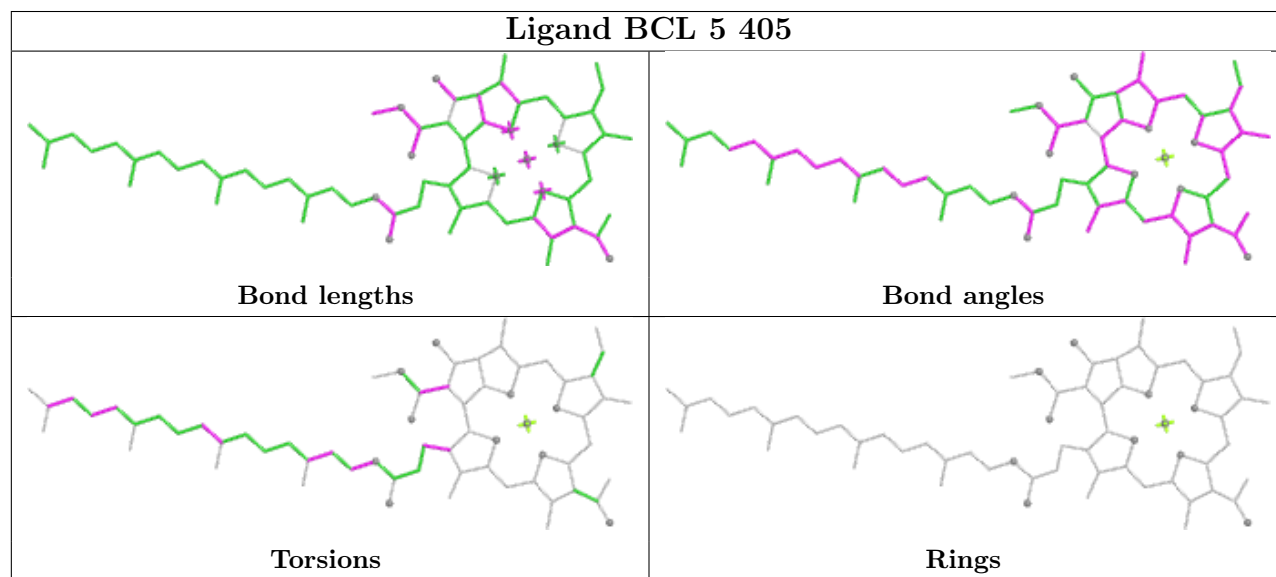
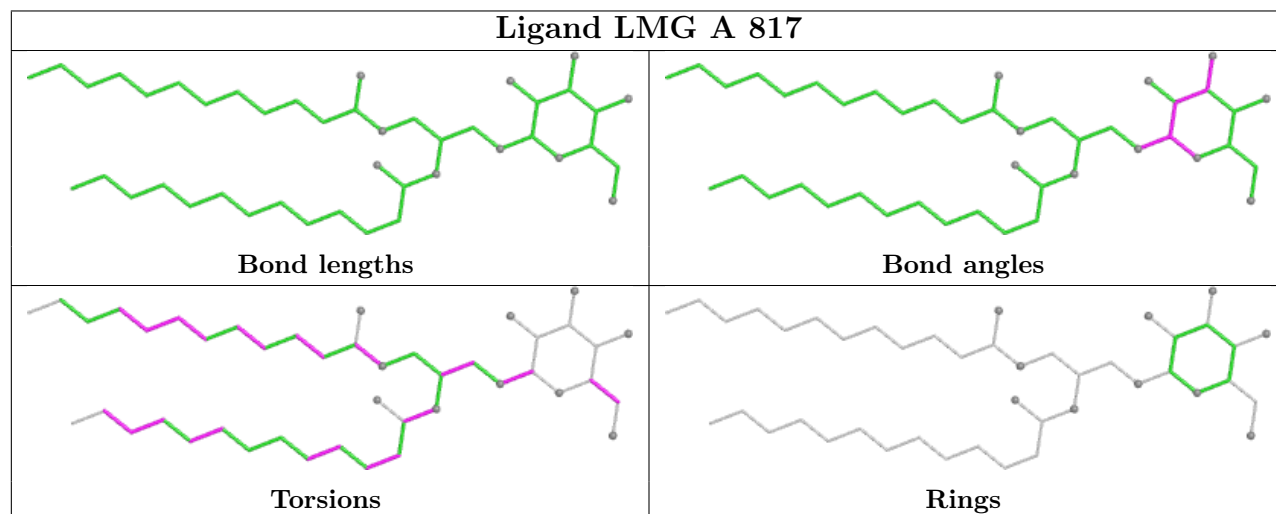
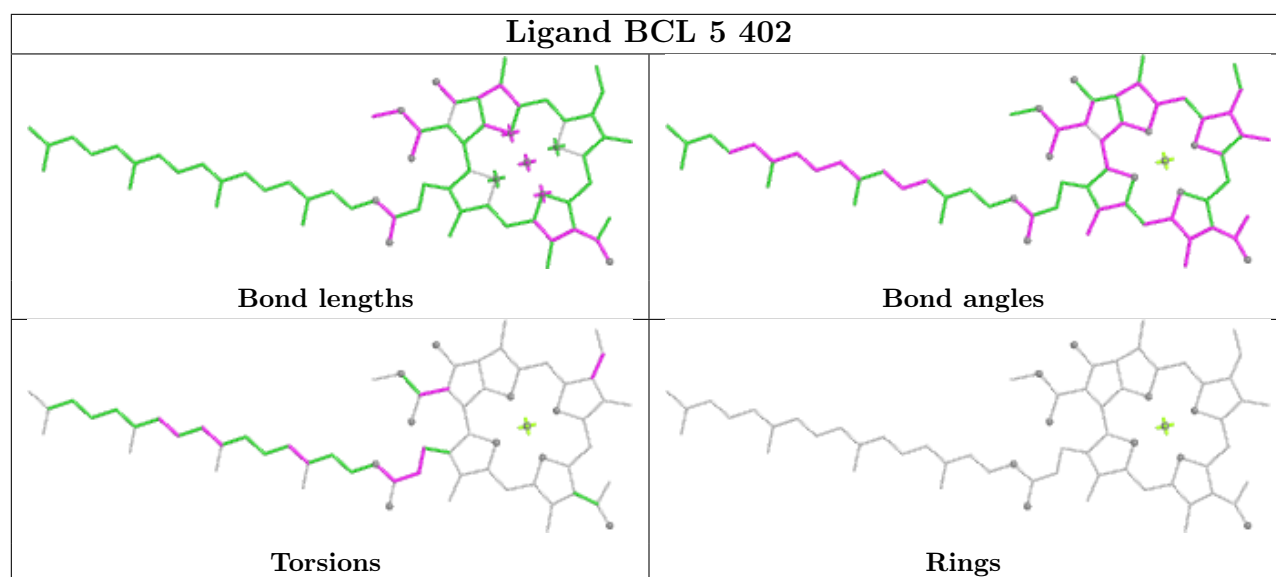


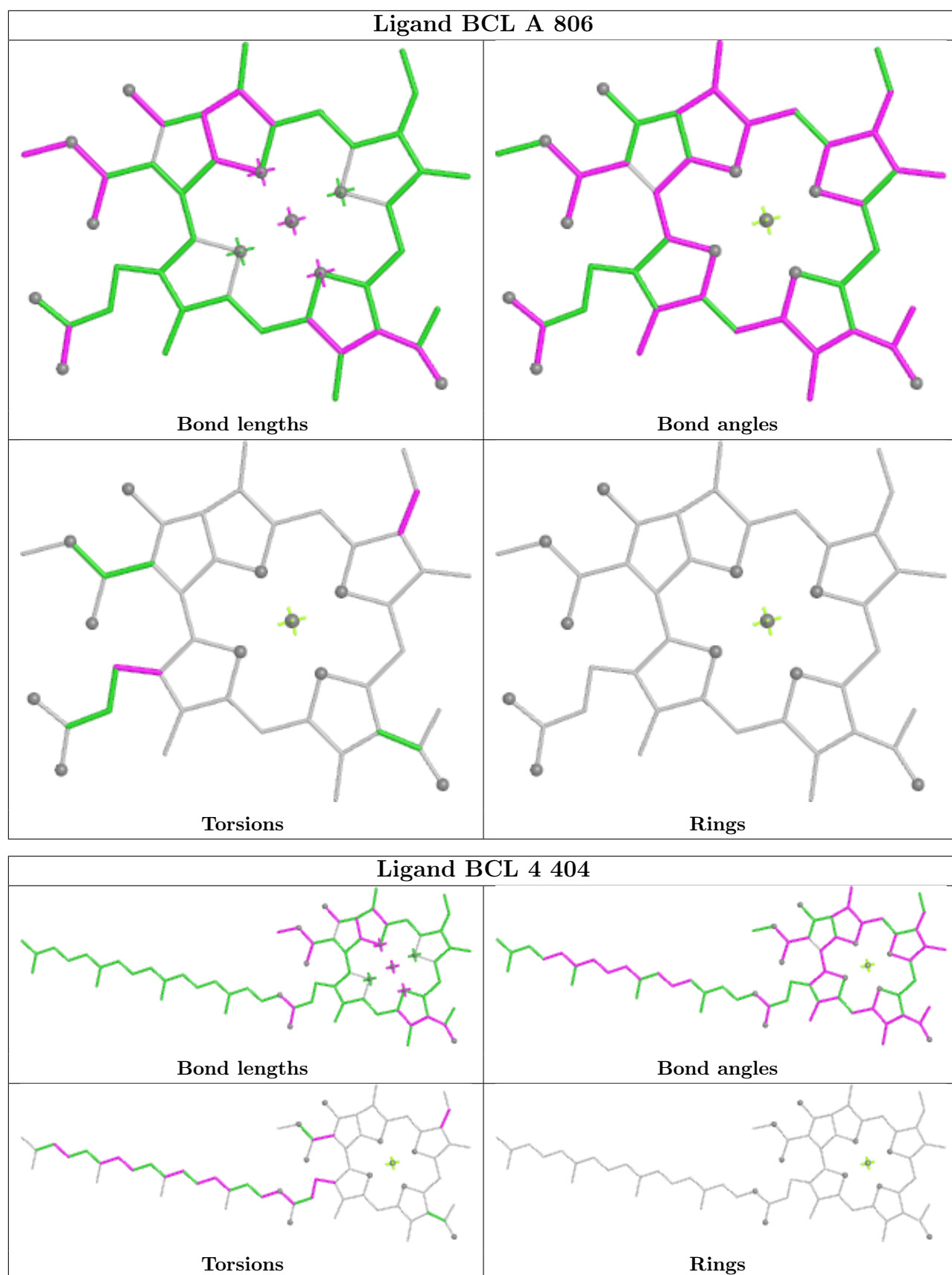


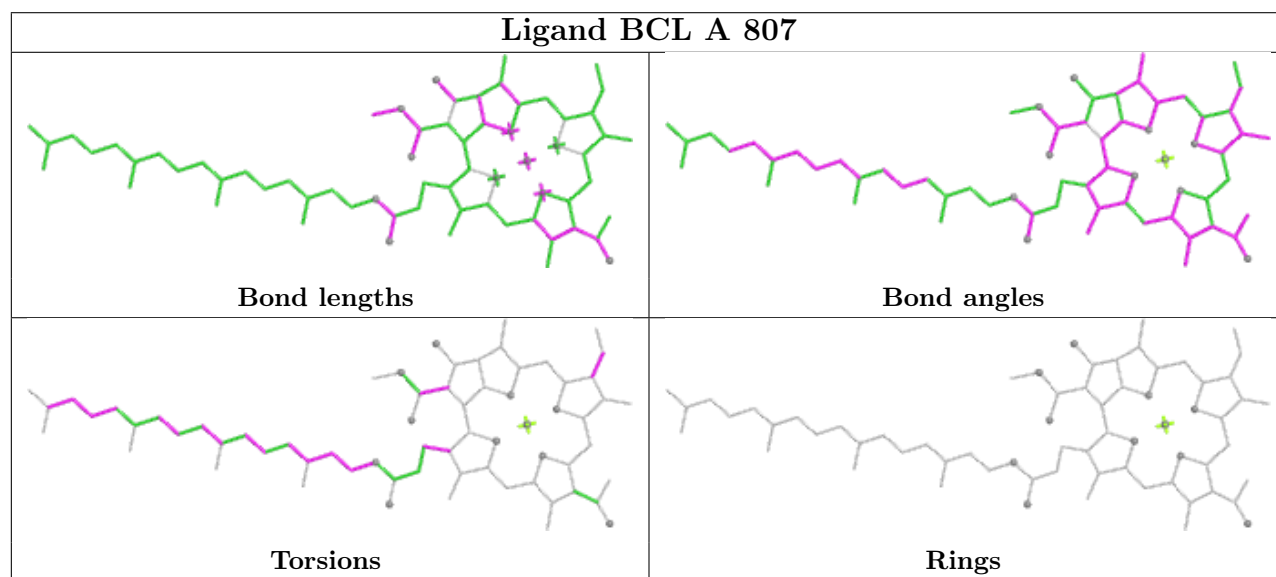
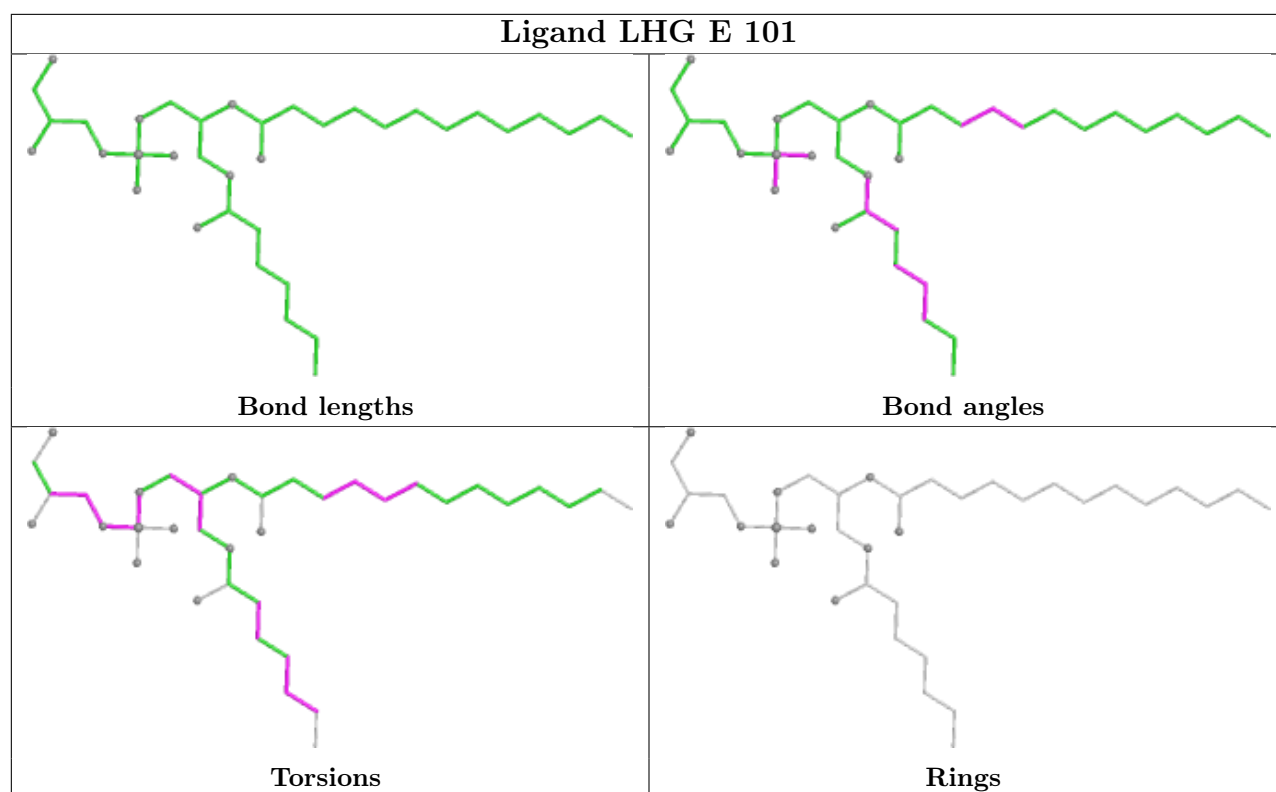


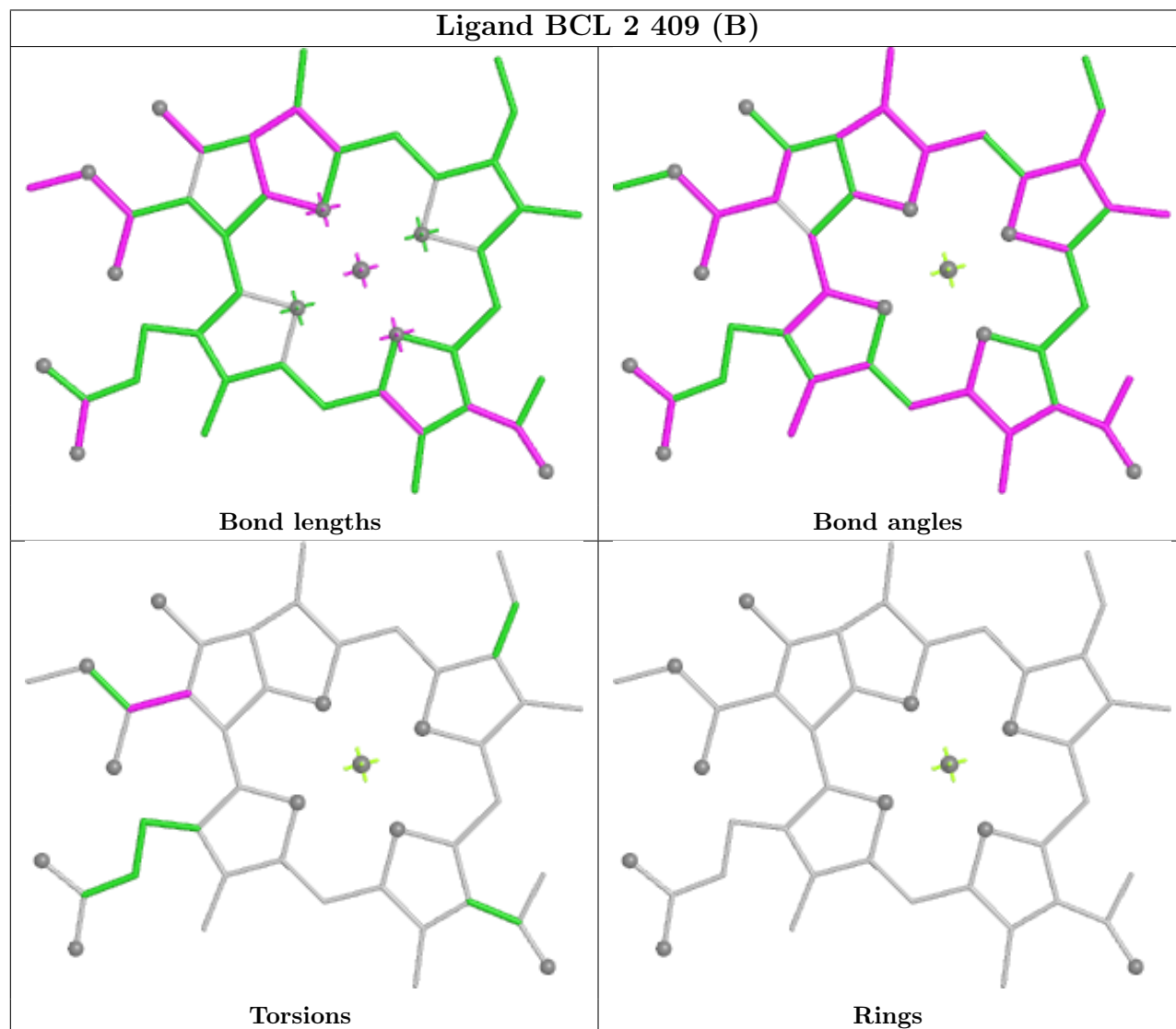
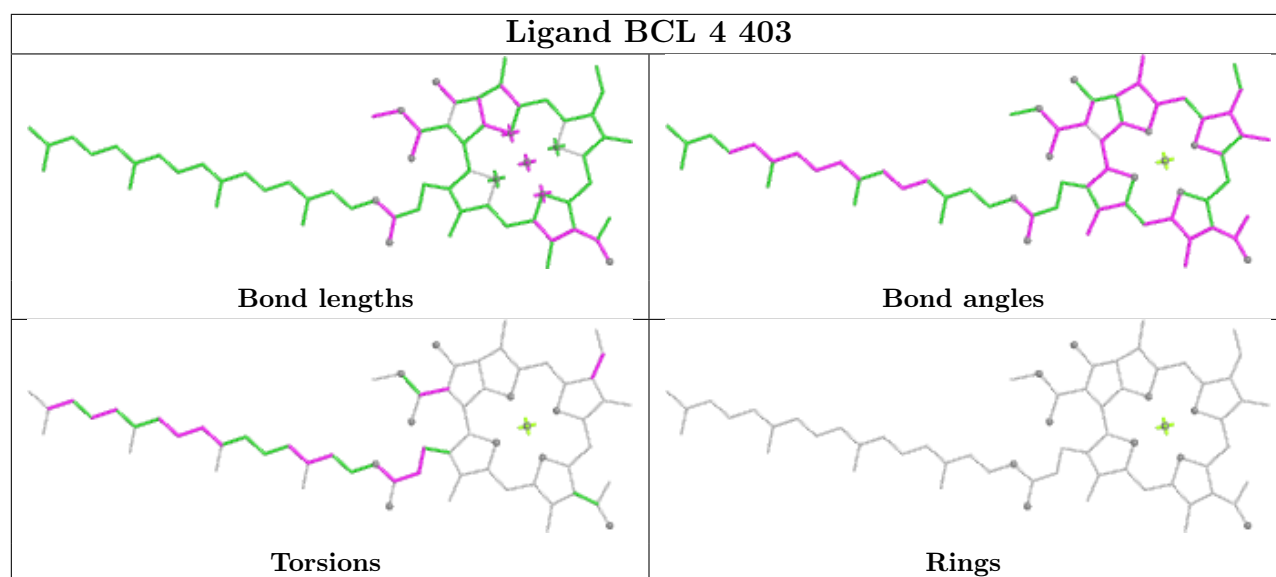


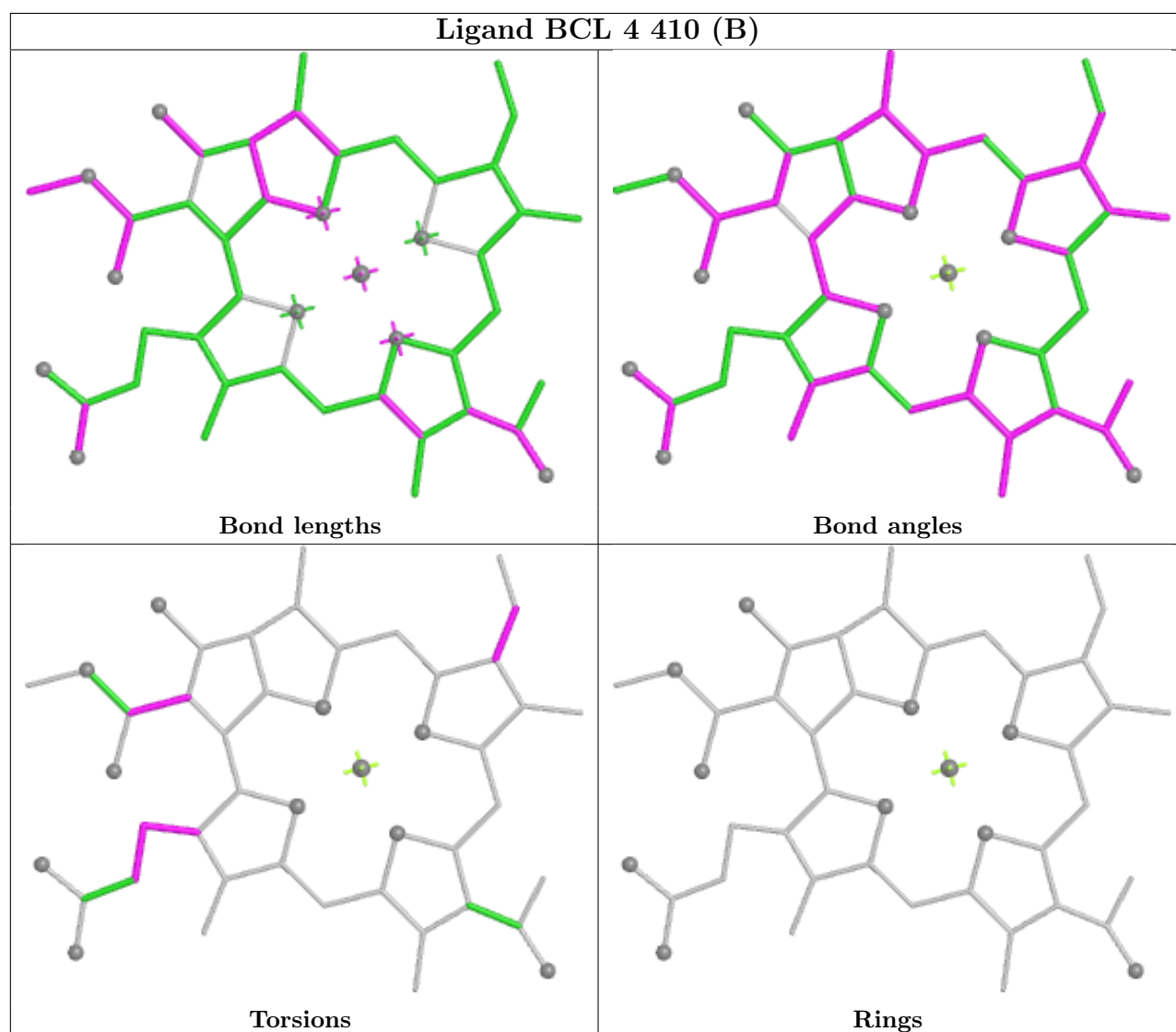
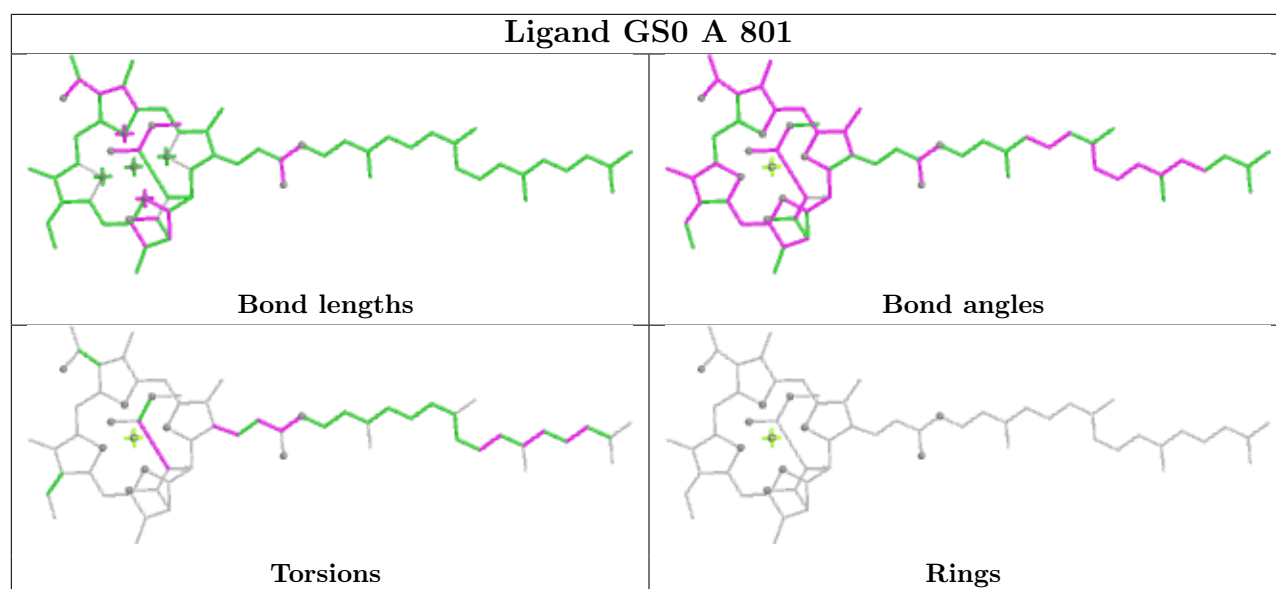


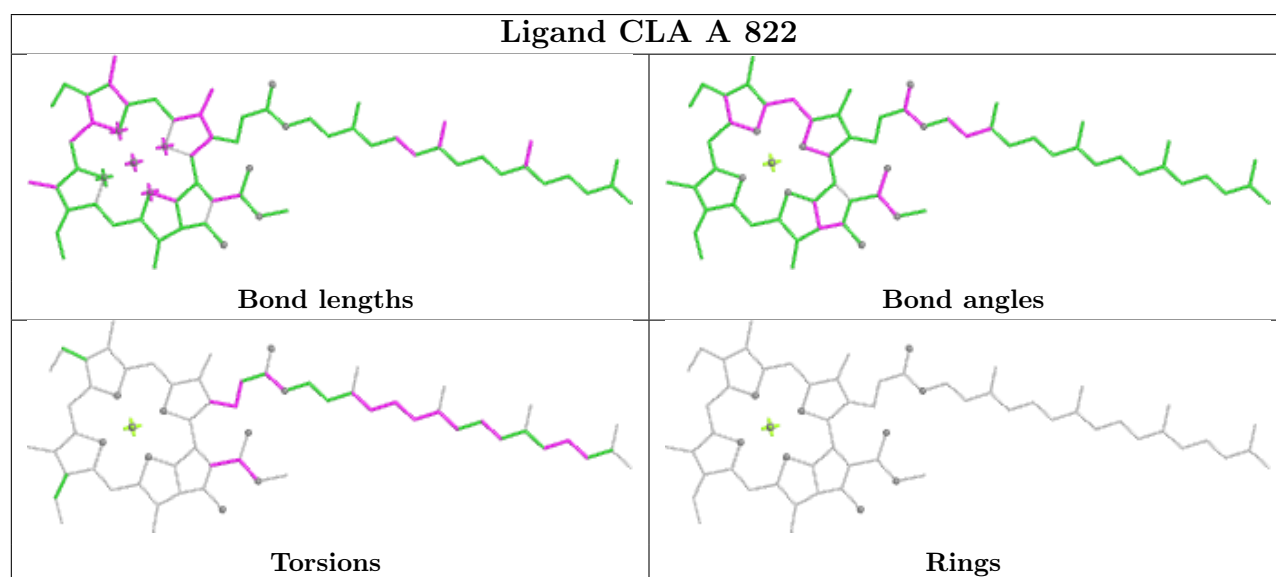
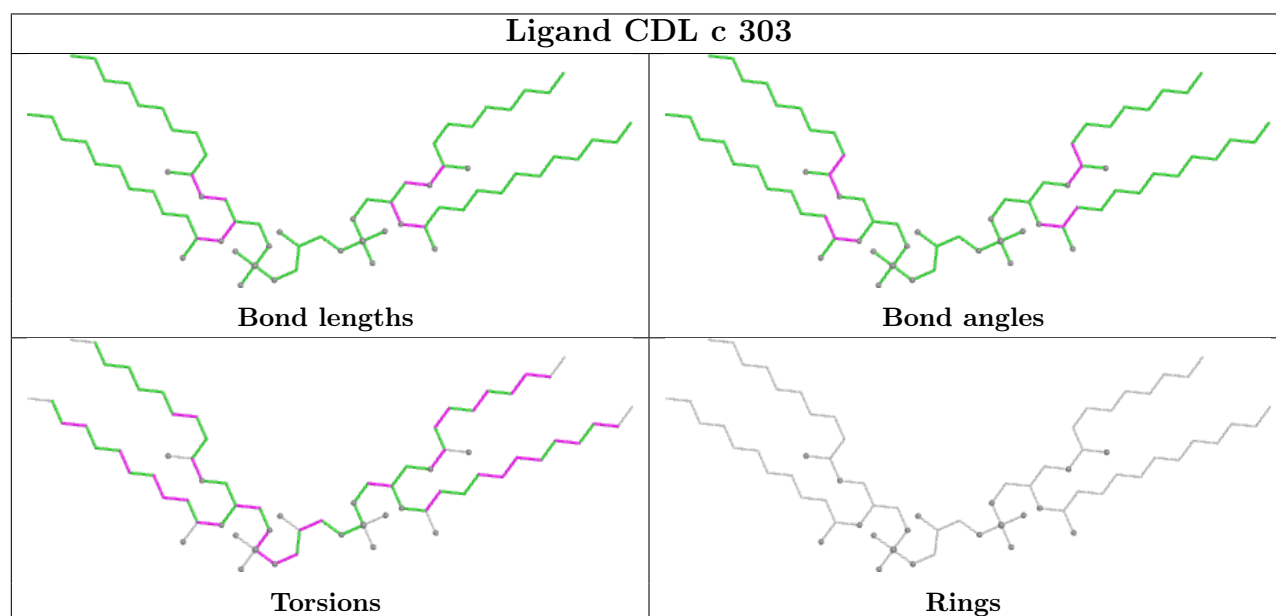
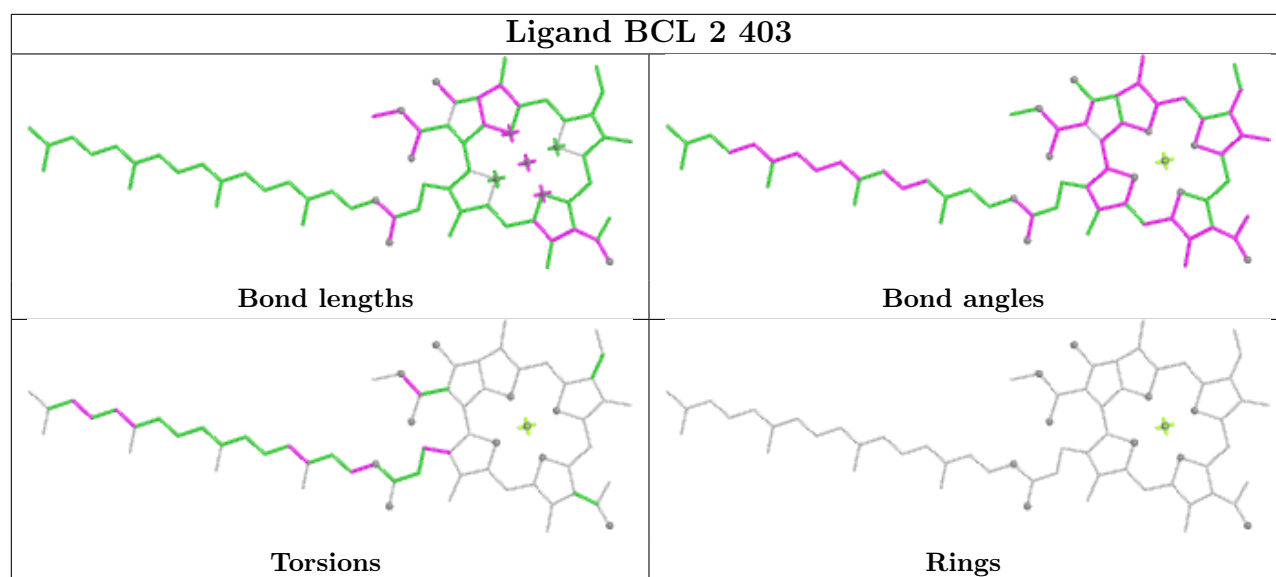


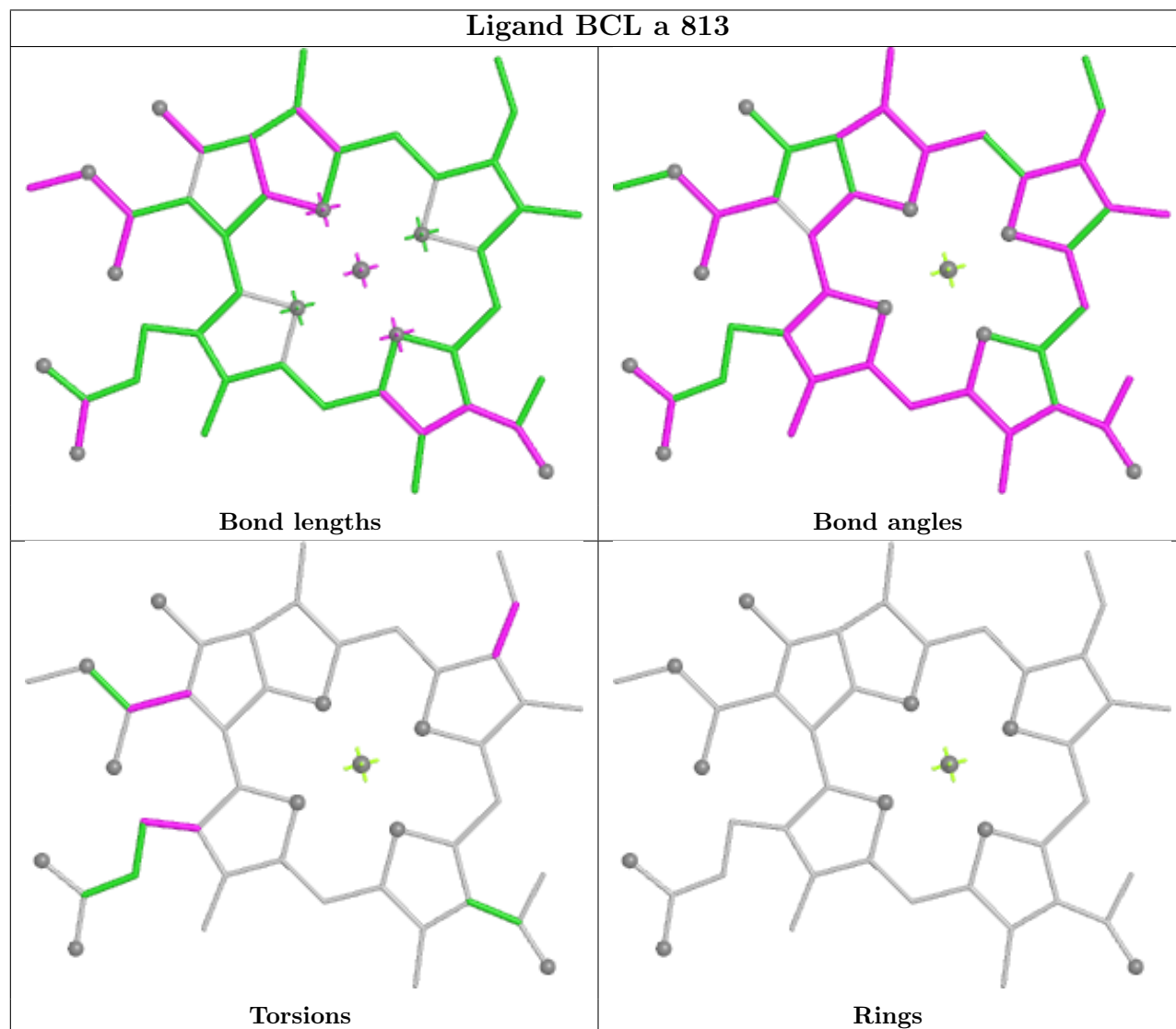
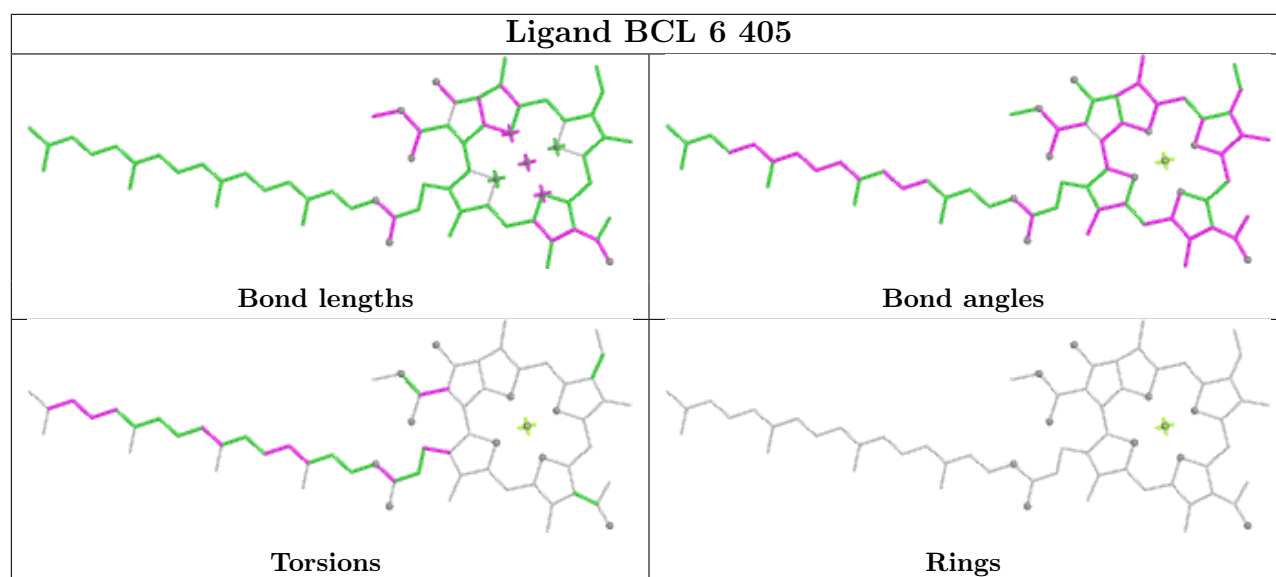


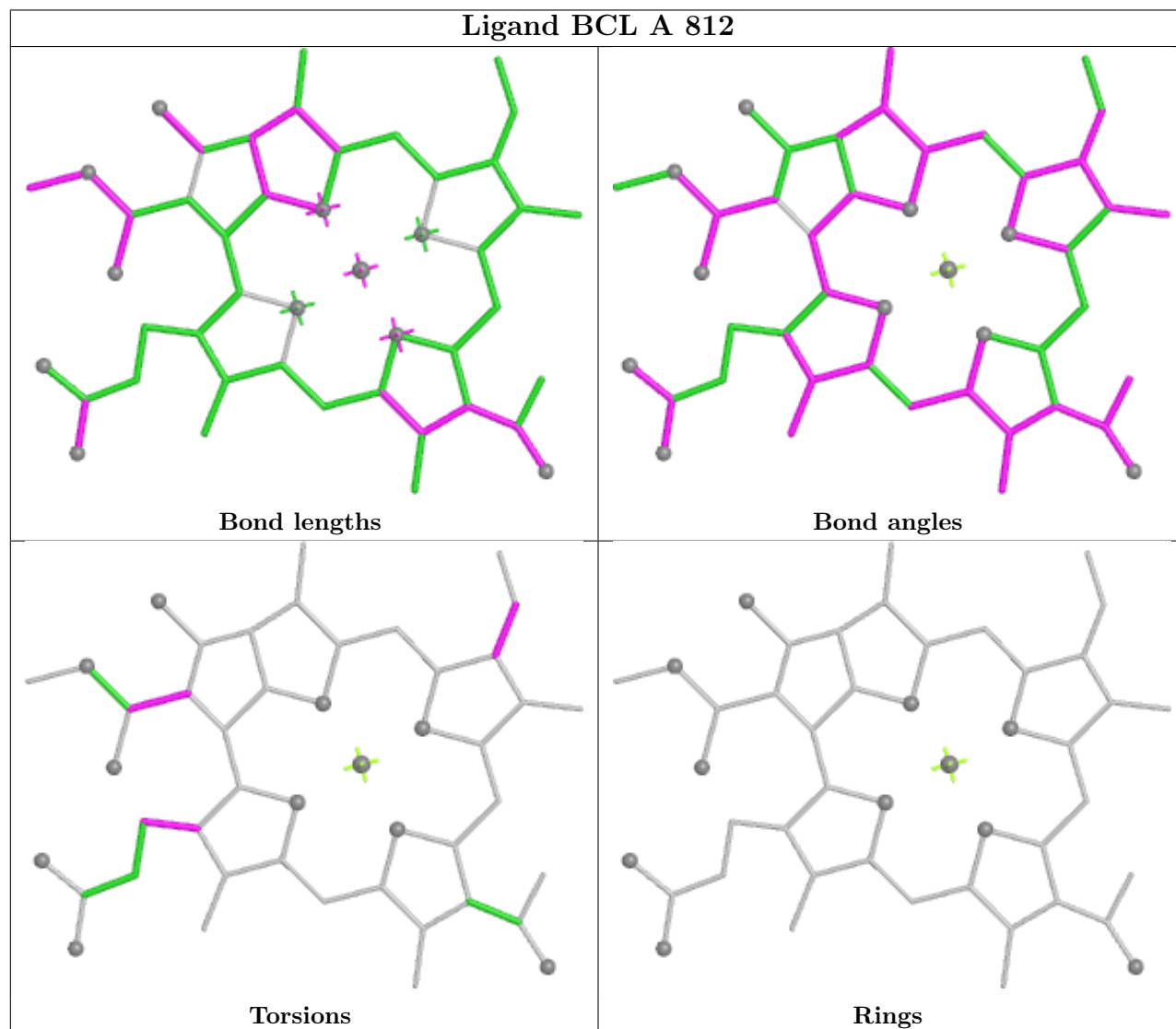
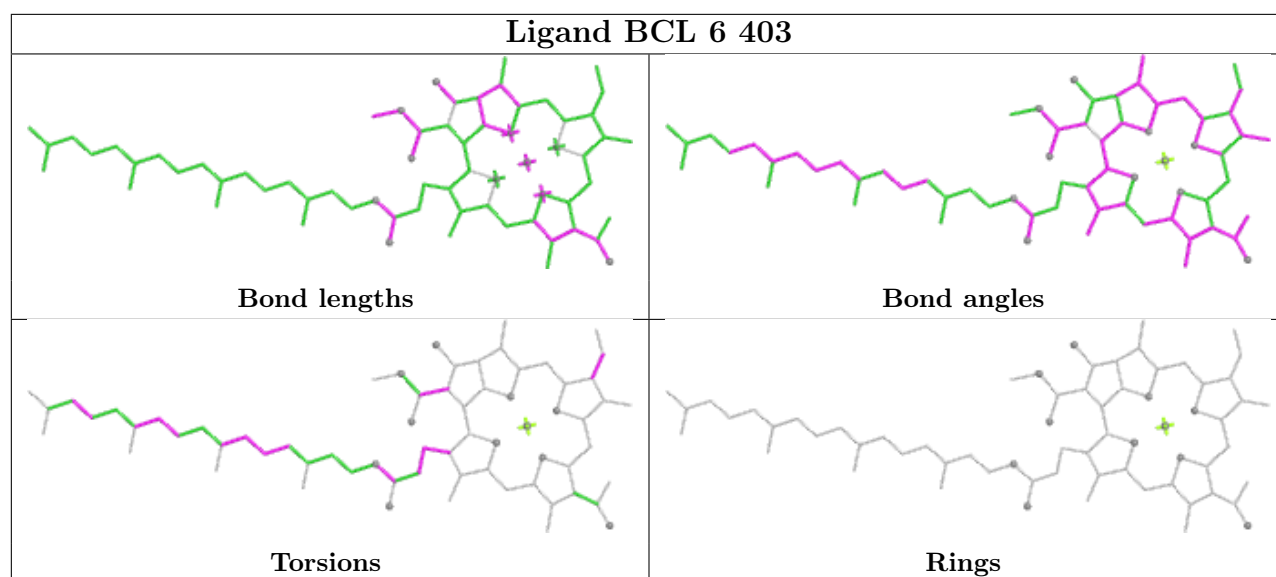




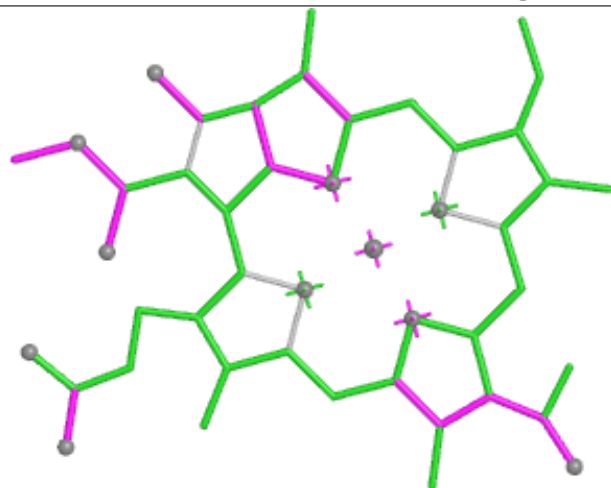




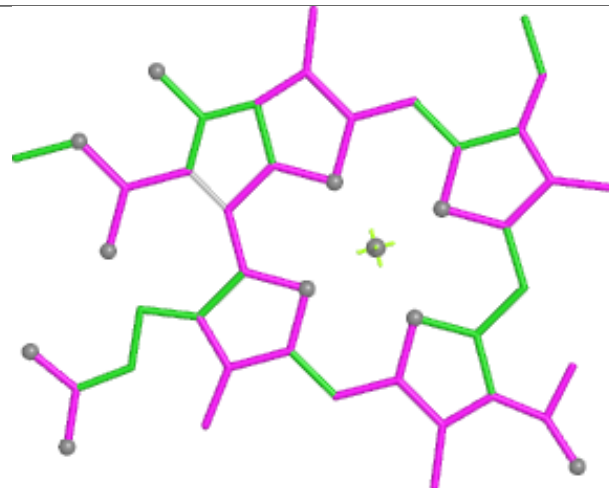




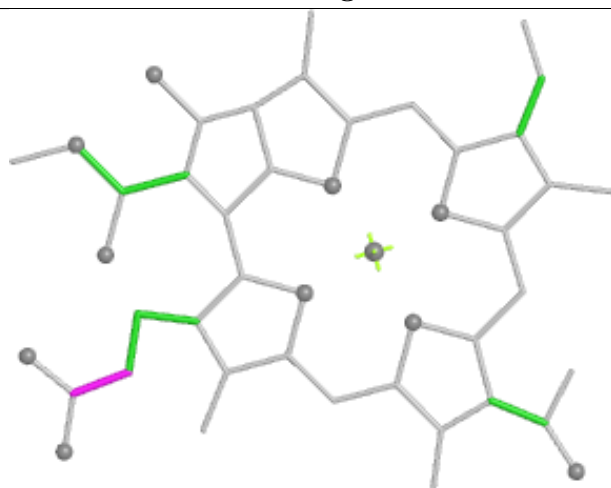
Ligand BCL A 808



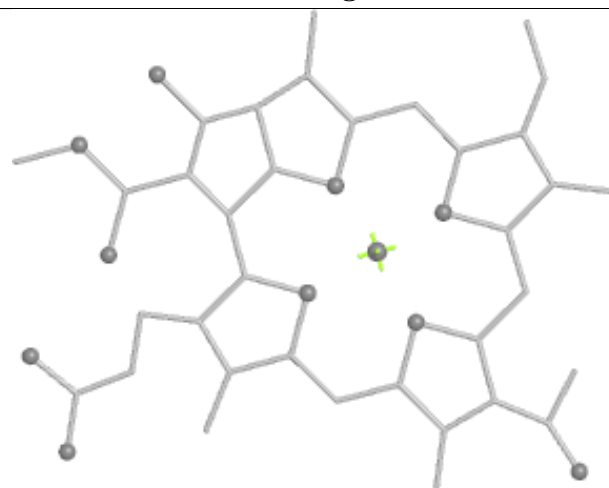
Bond lengths



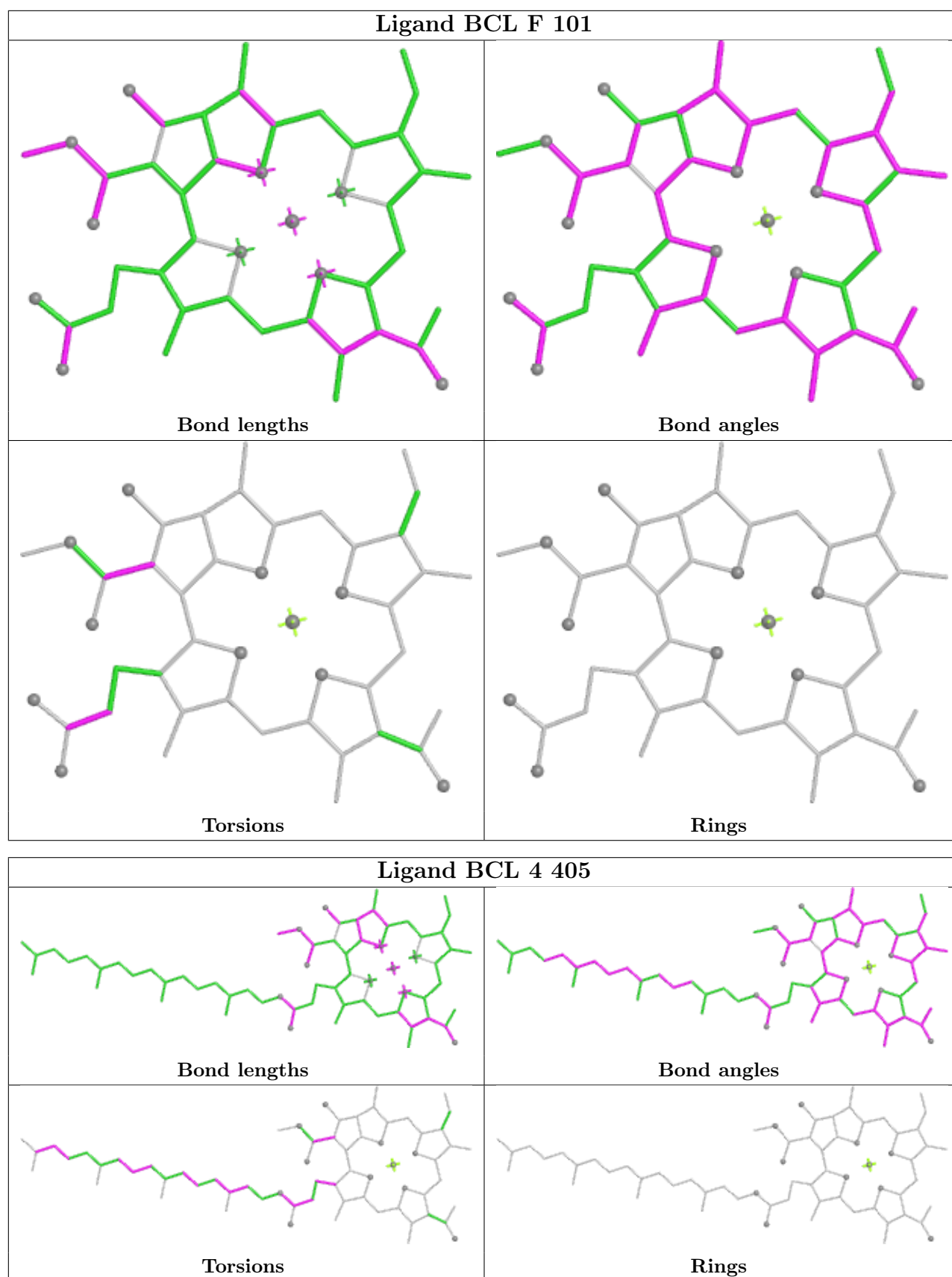
Bond angles

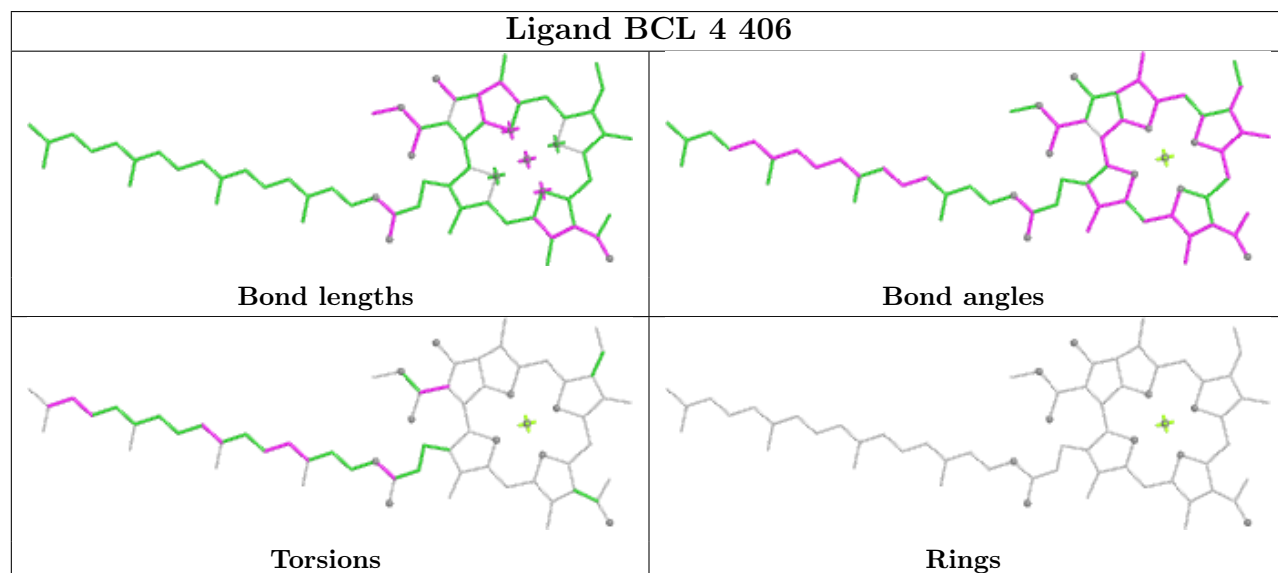
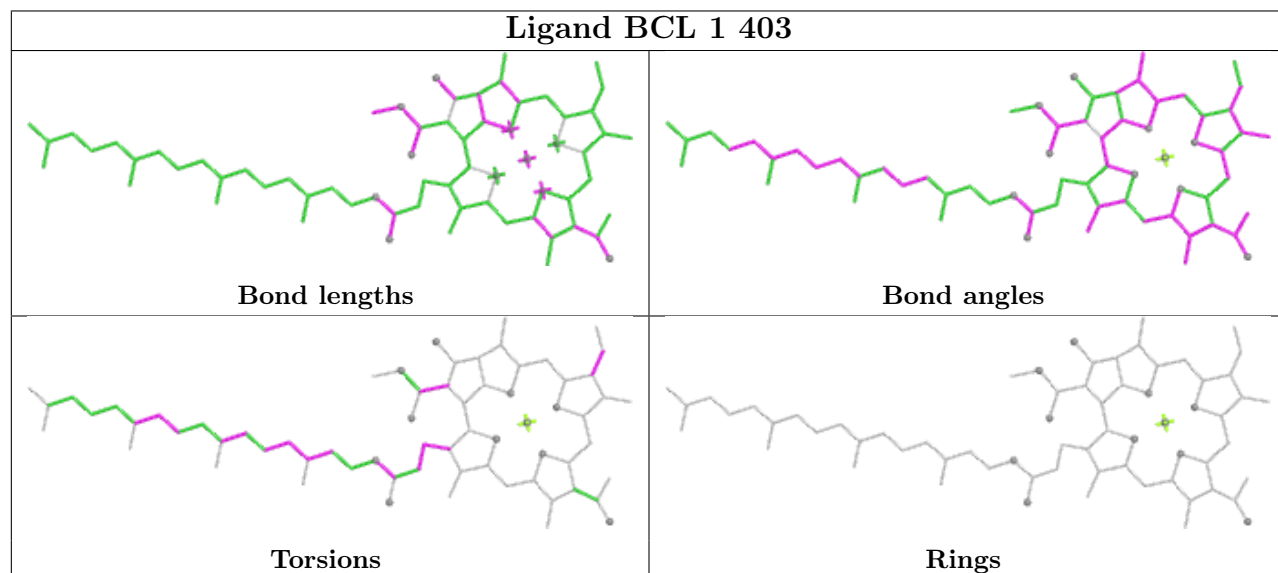
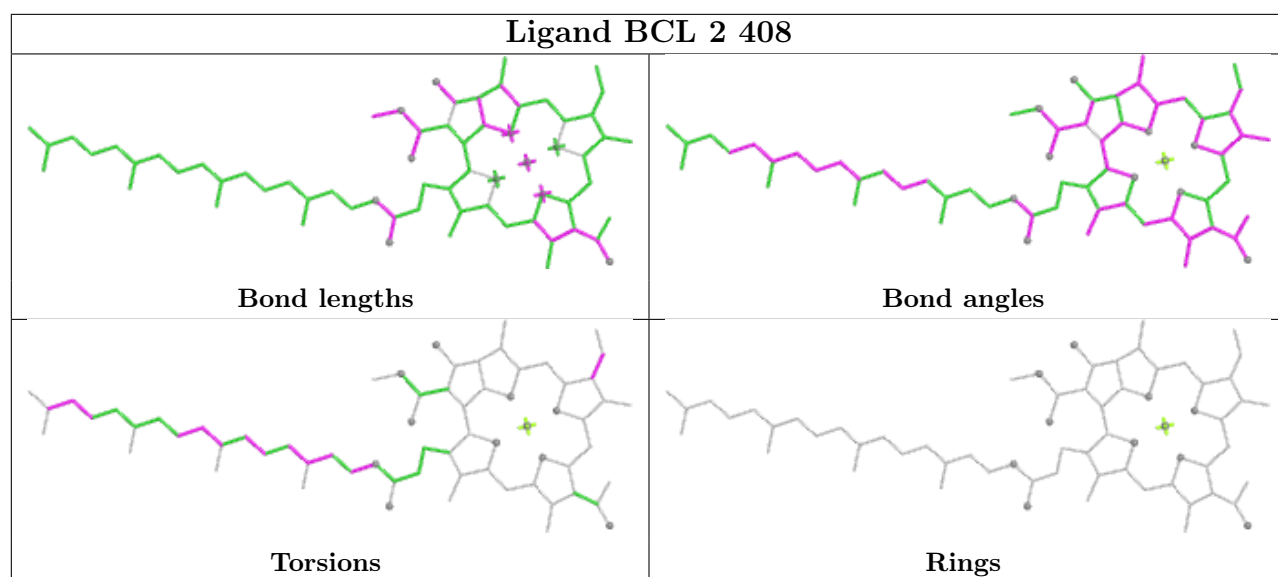


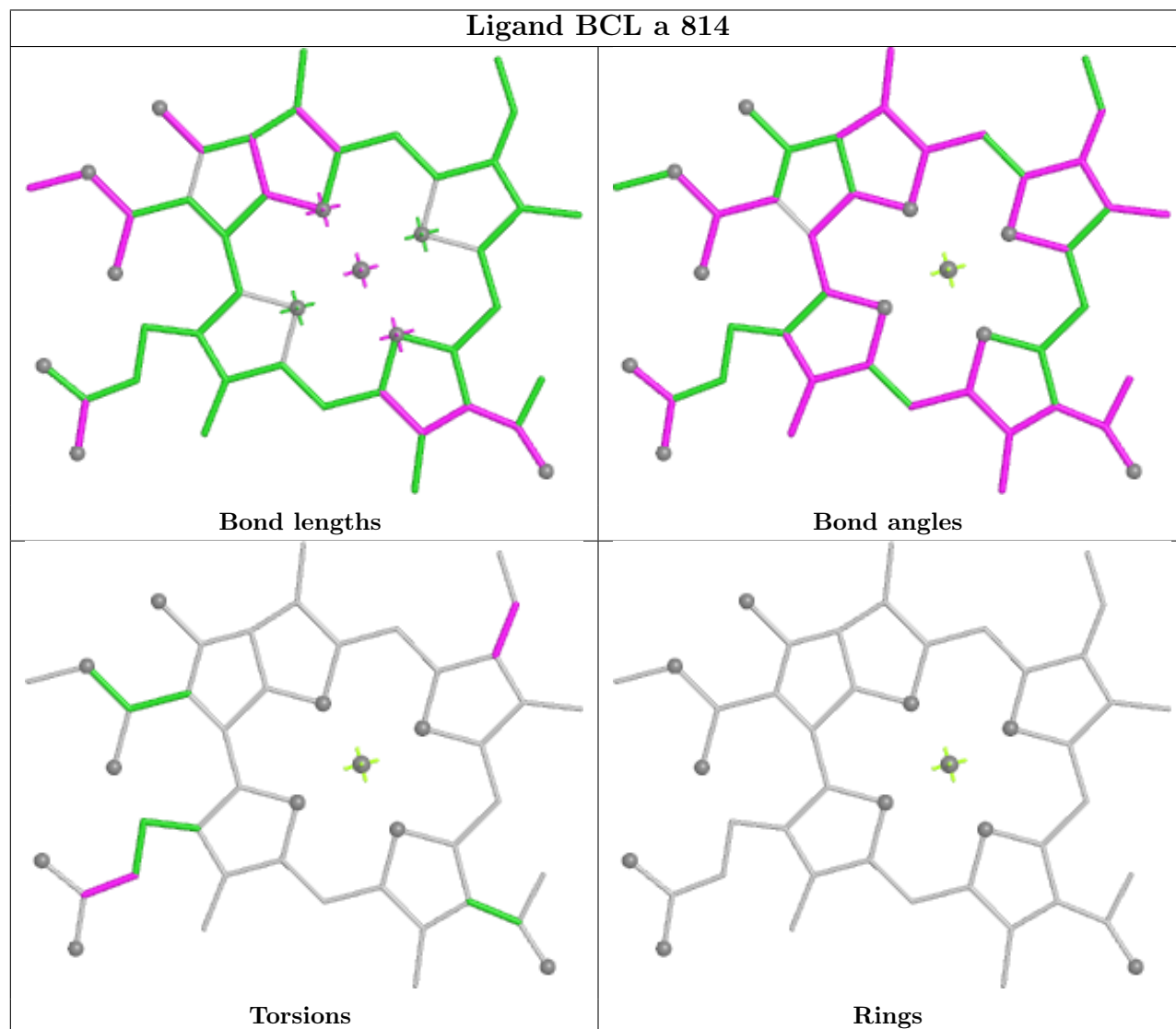
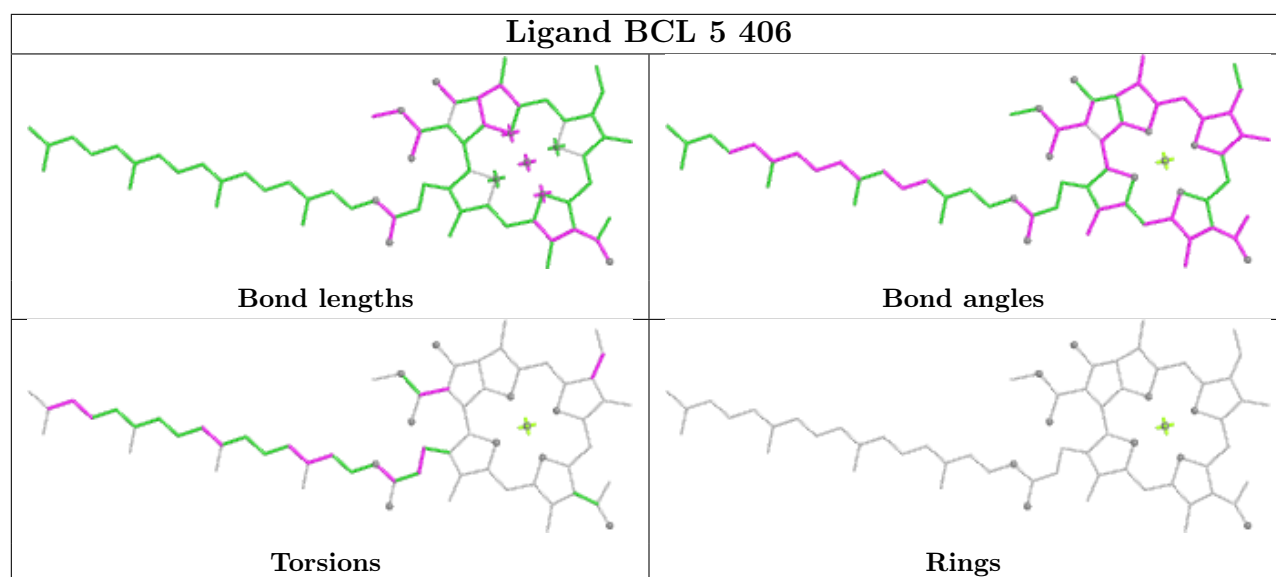
Torsions

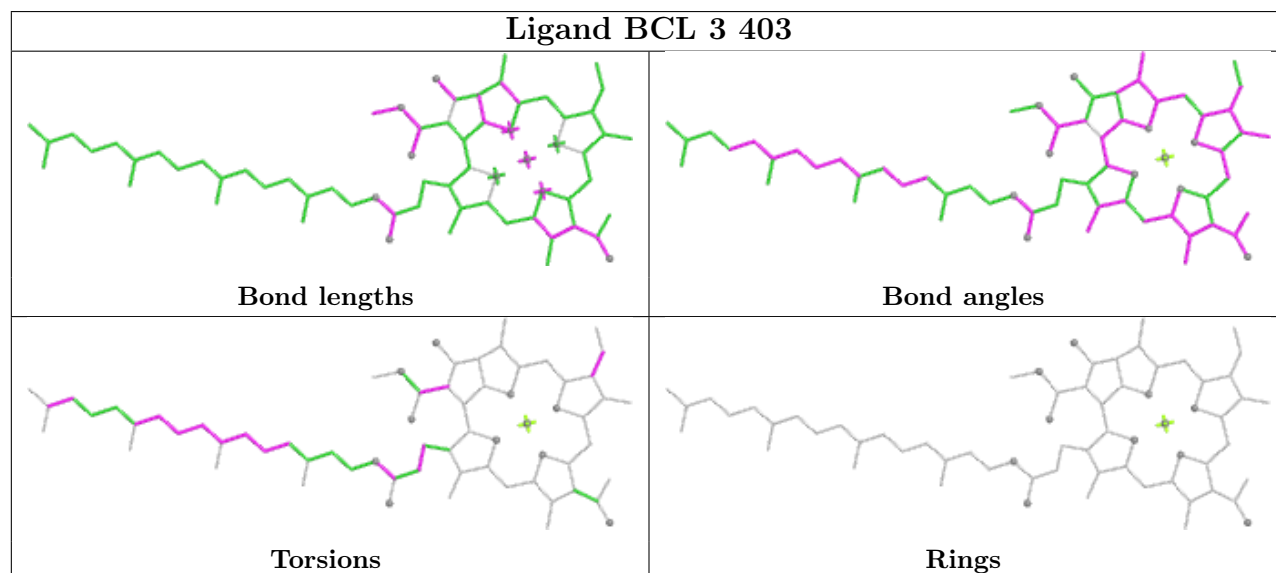
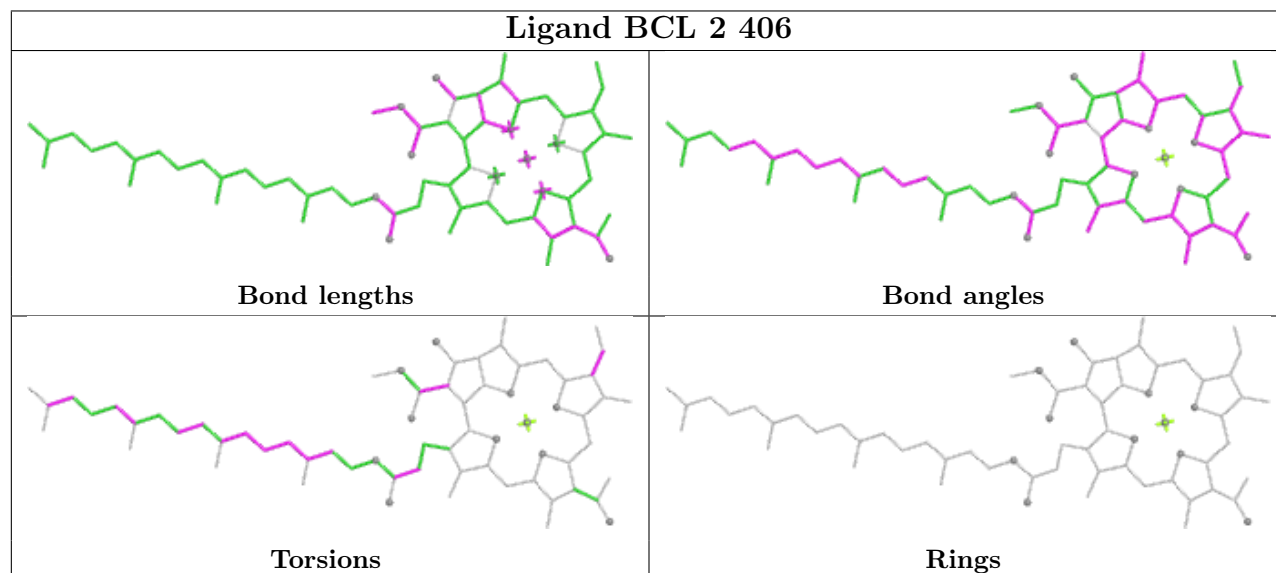
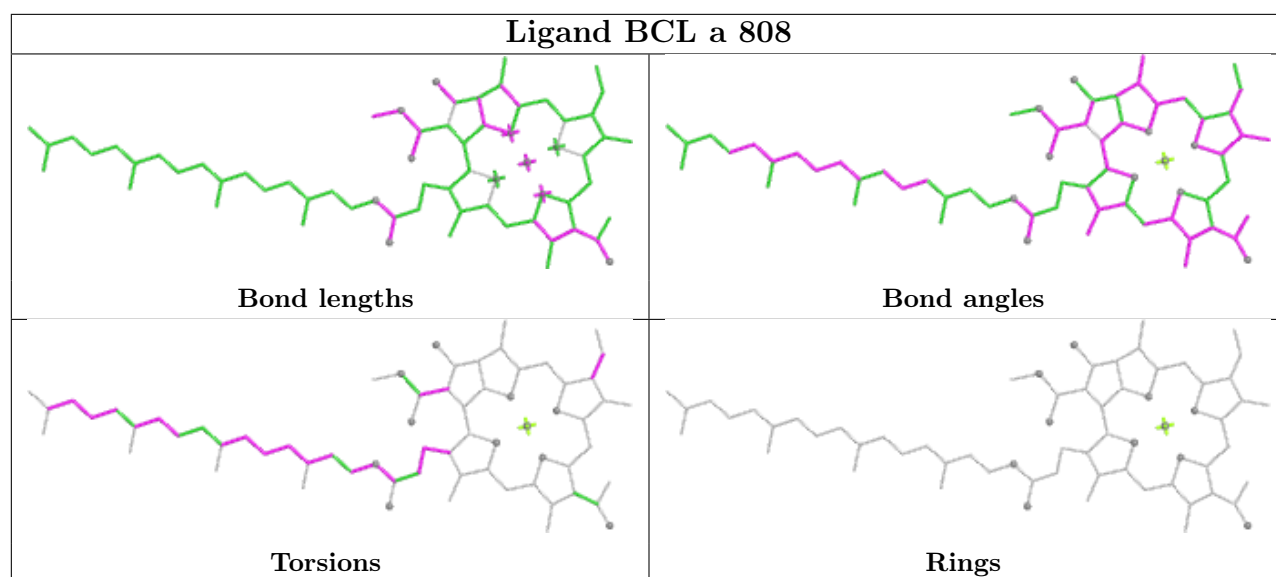


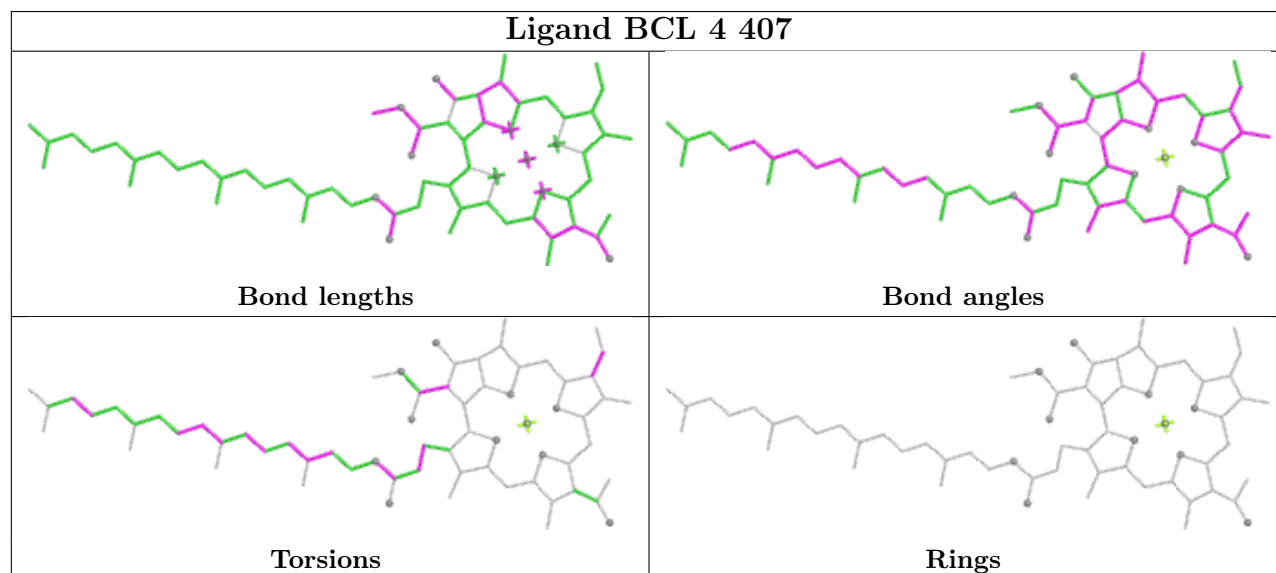
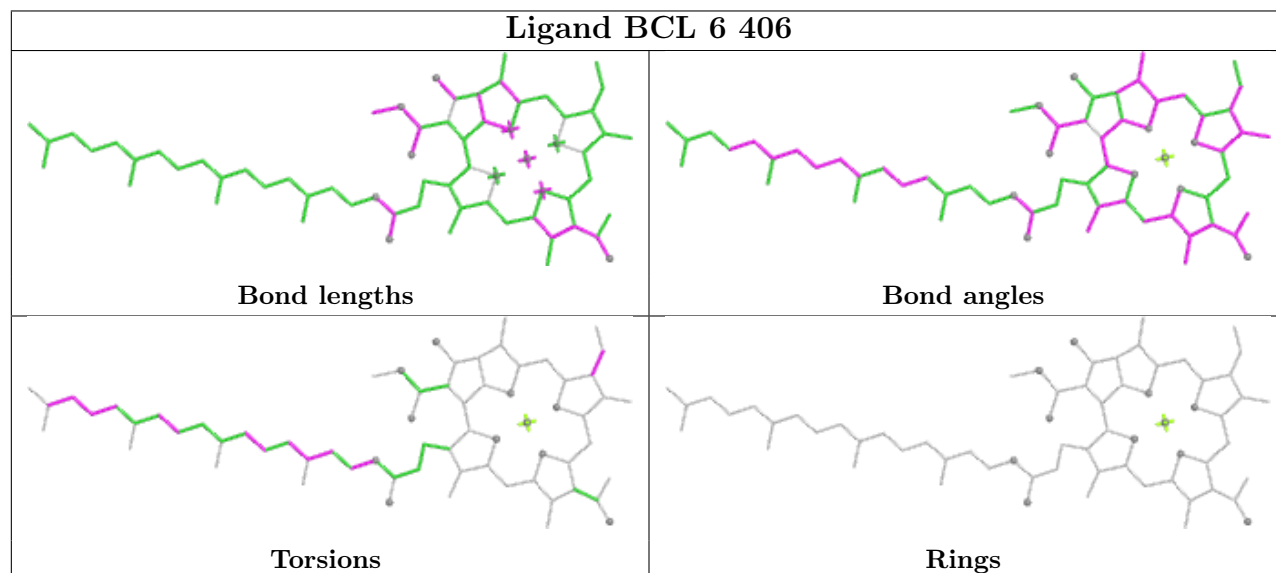
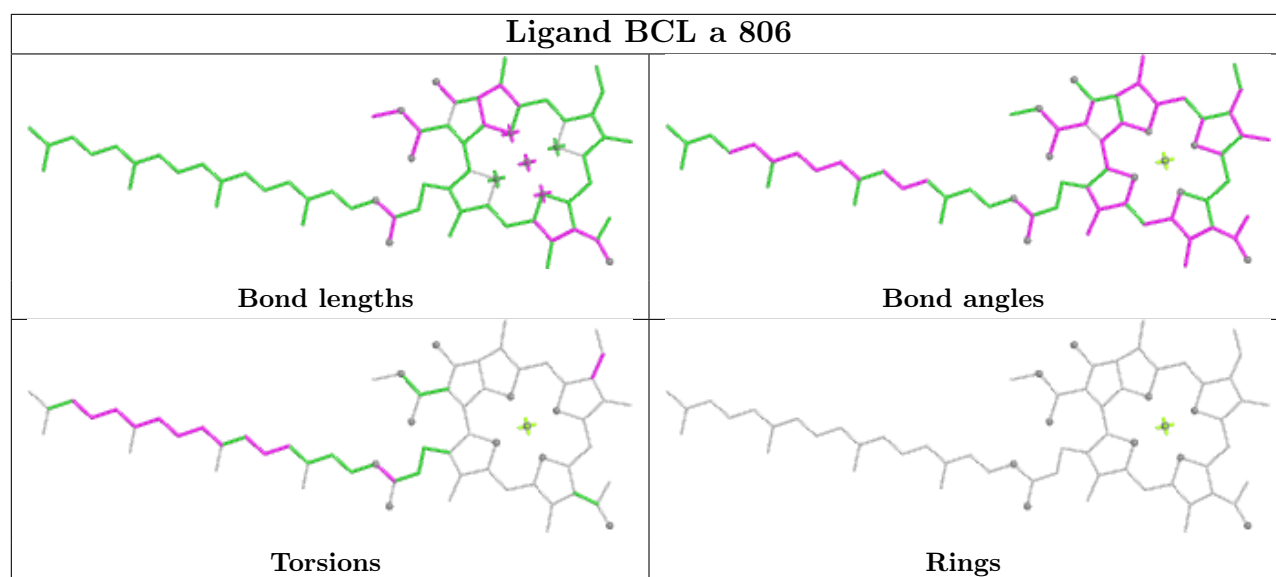
Rings

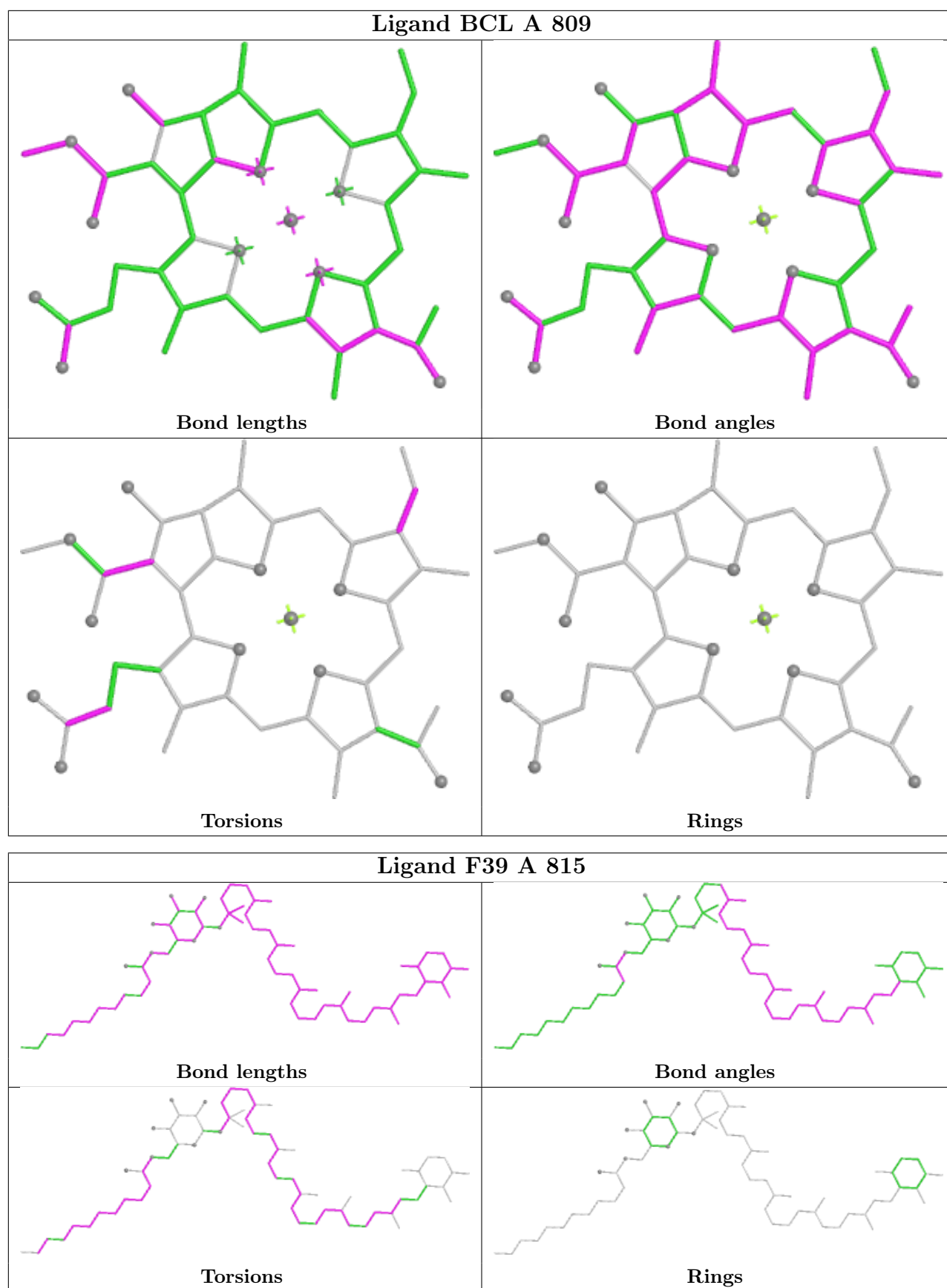


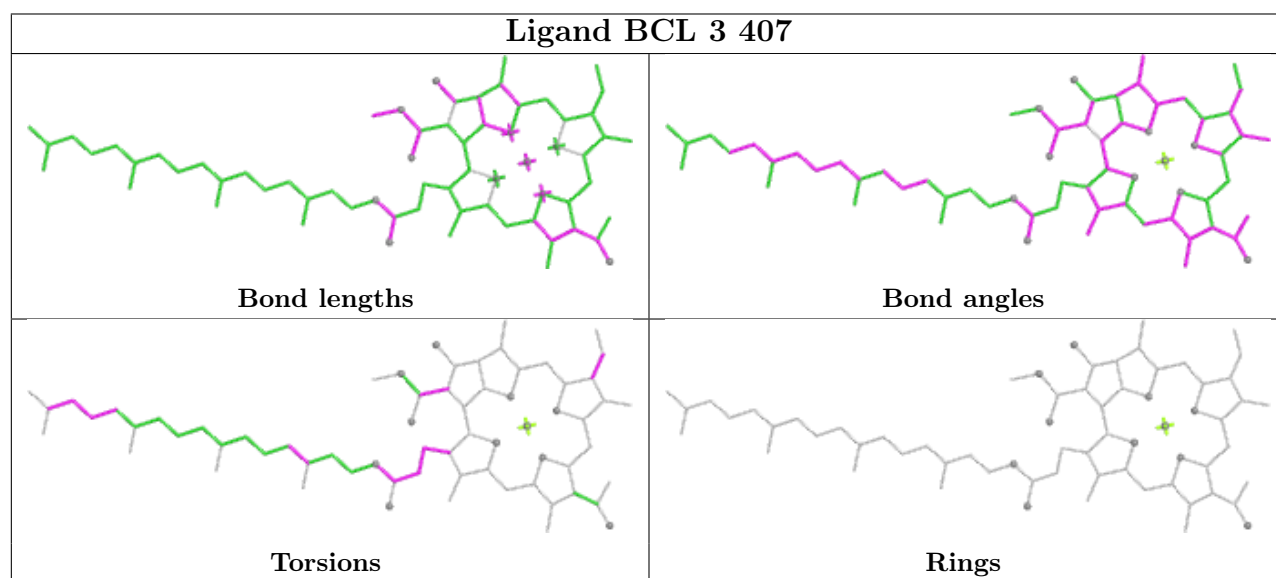
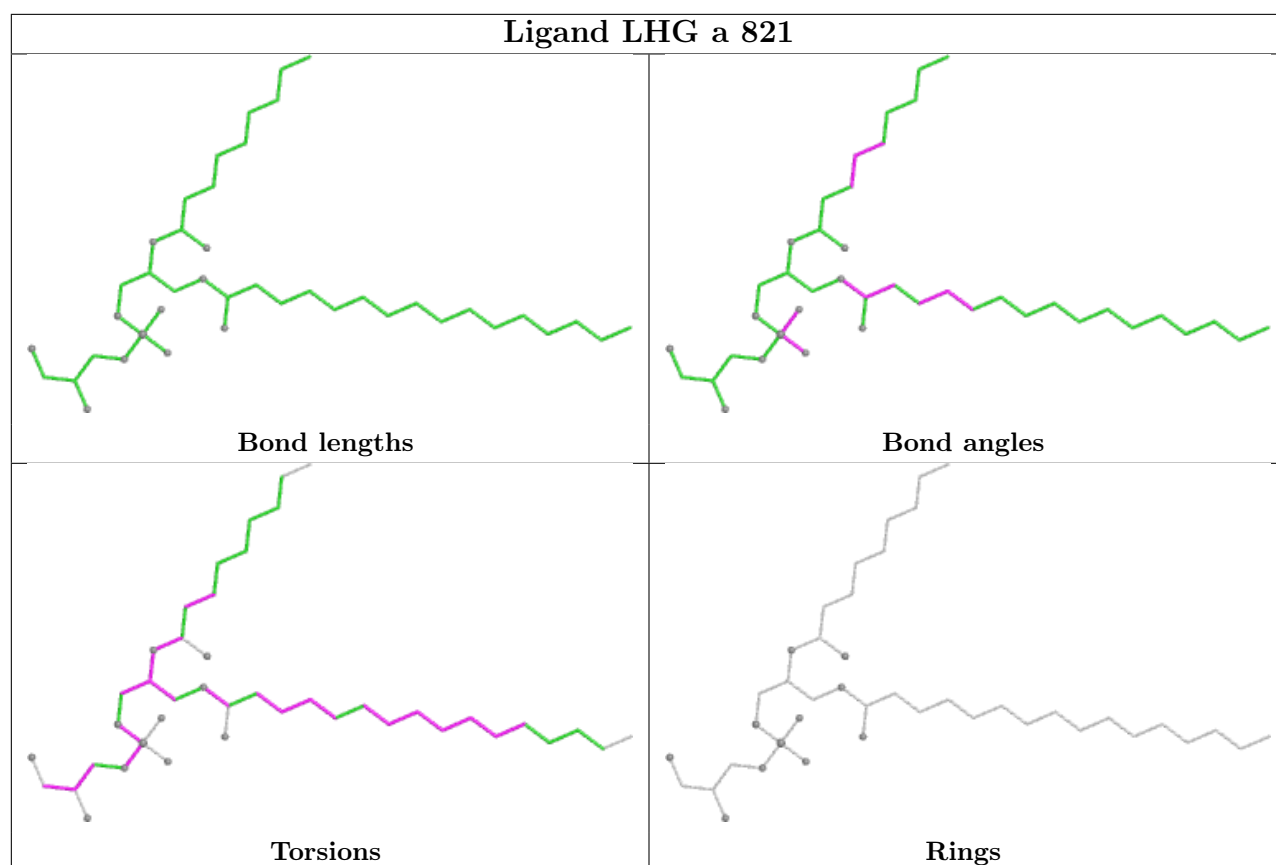


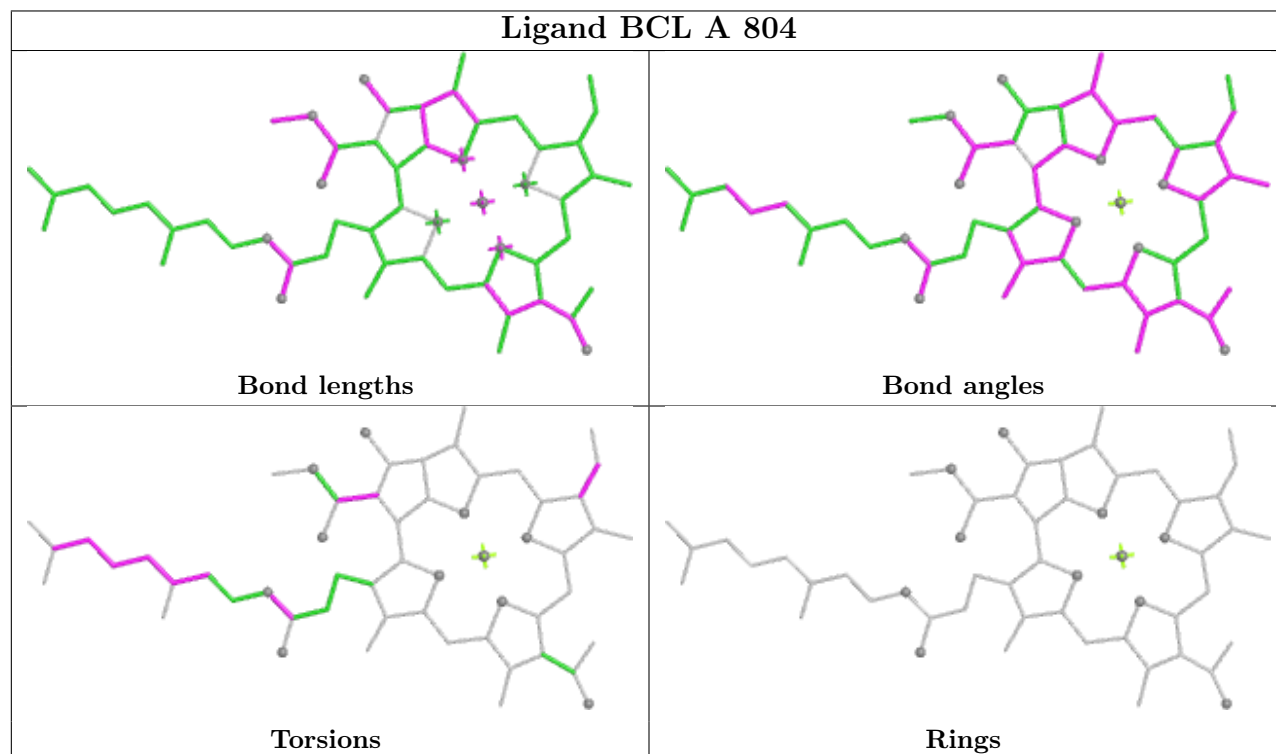
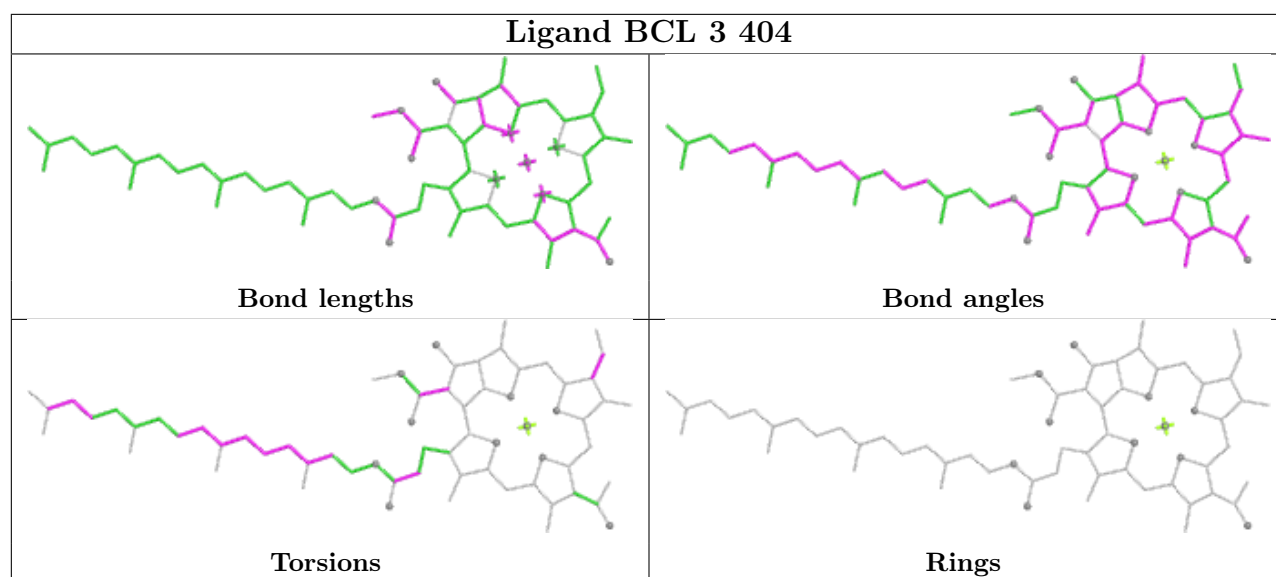


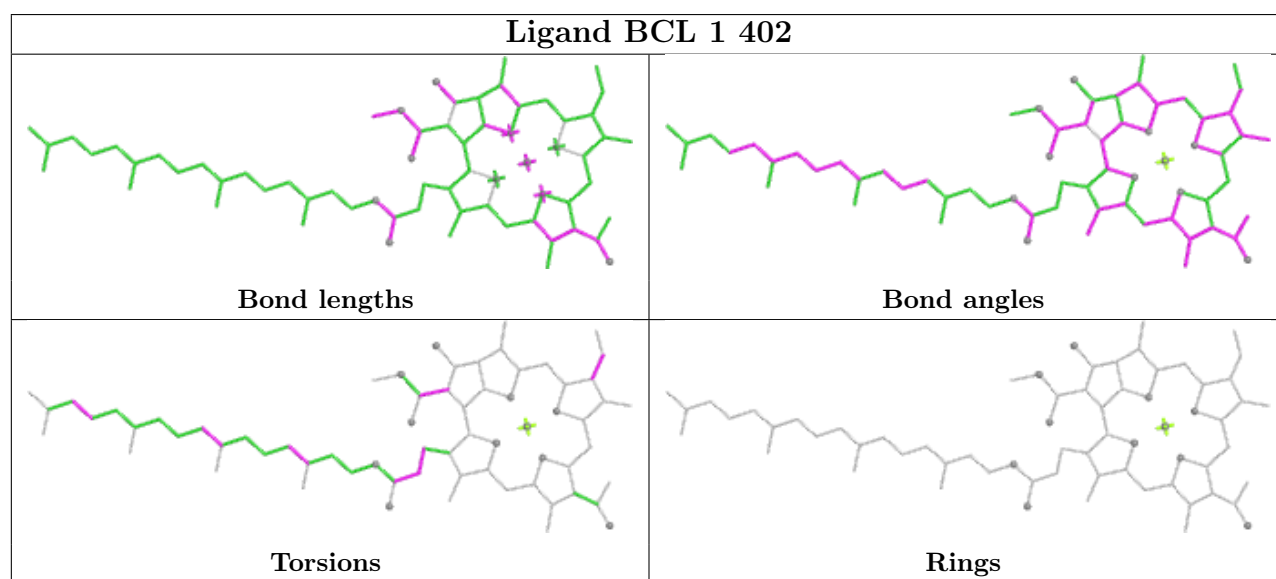
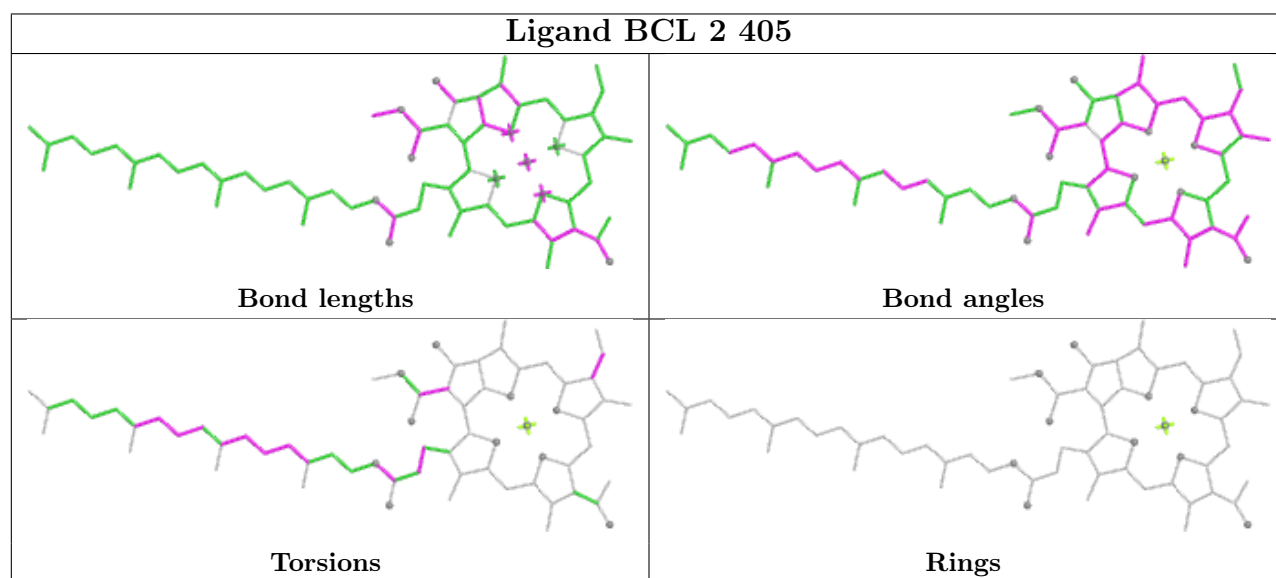
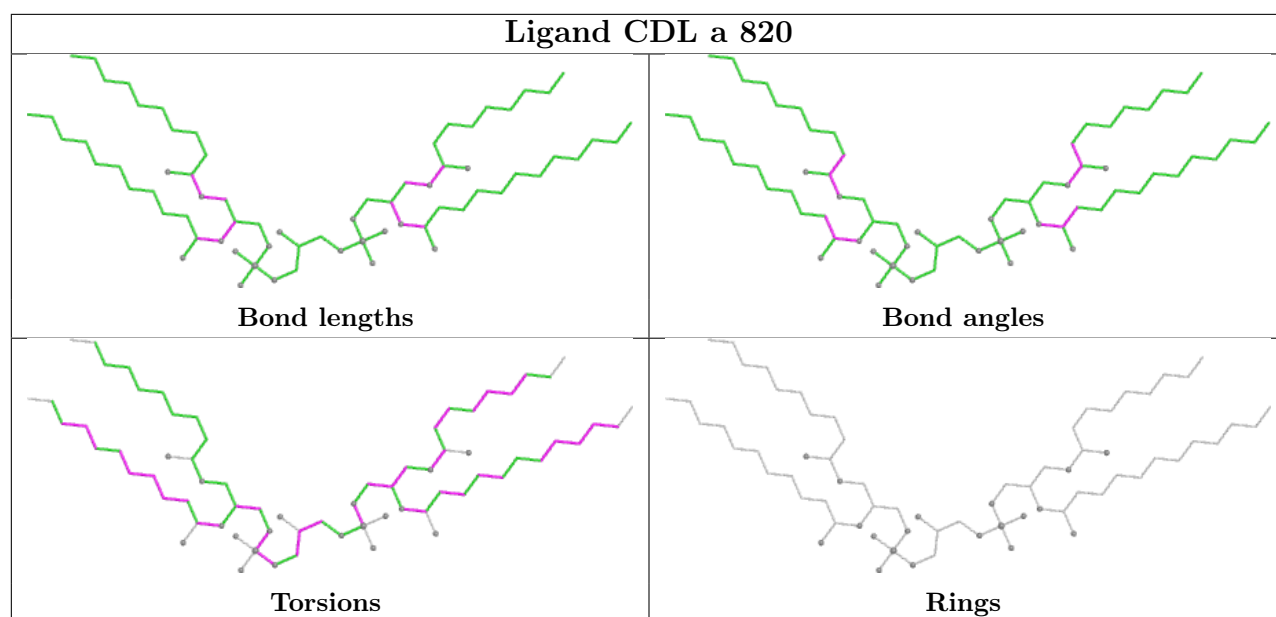


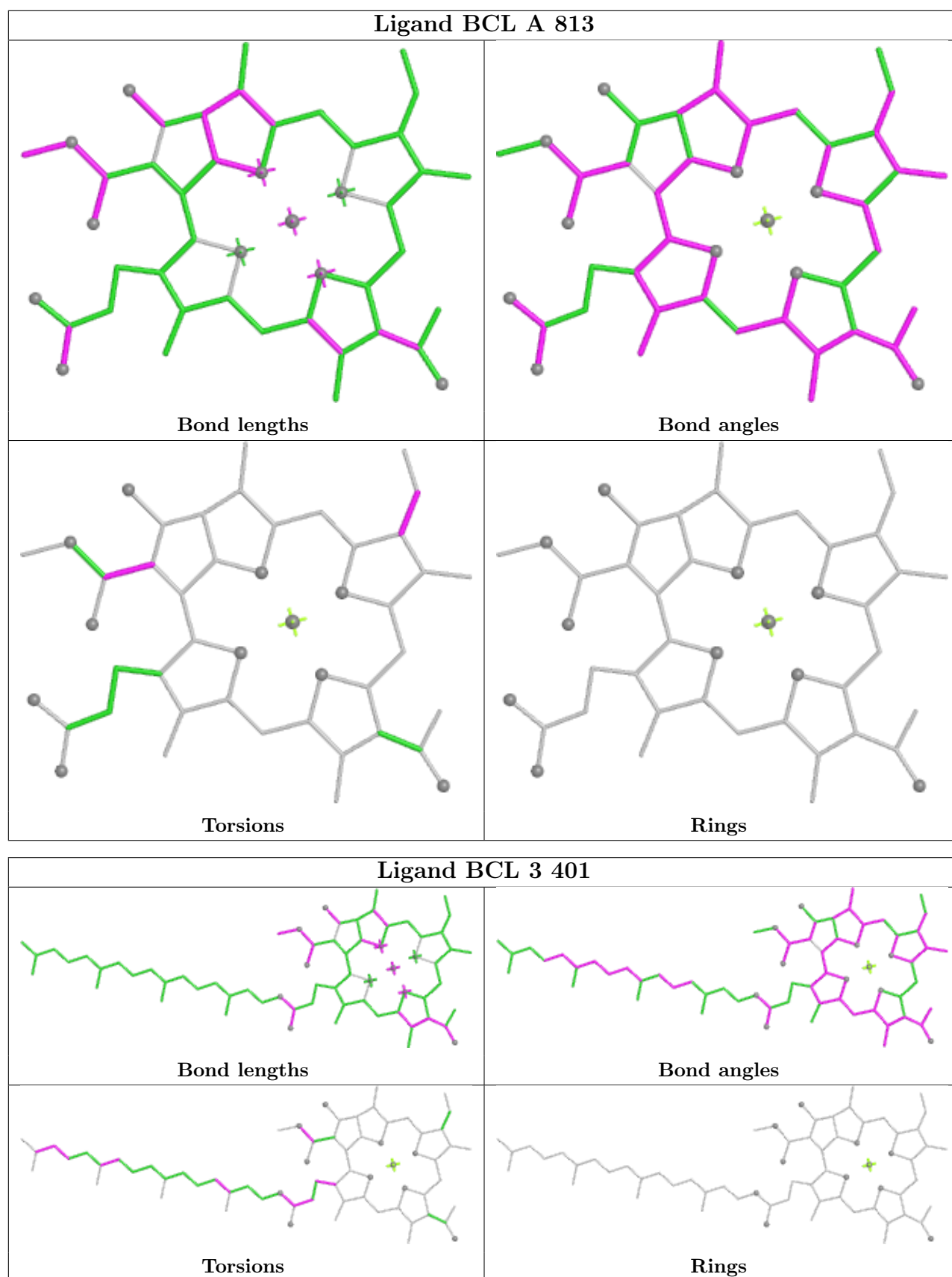


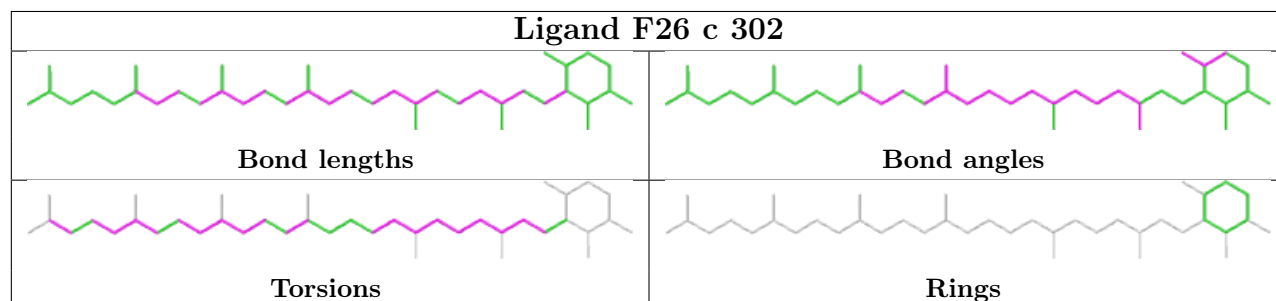
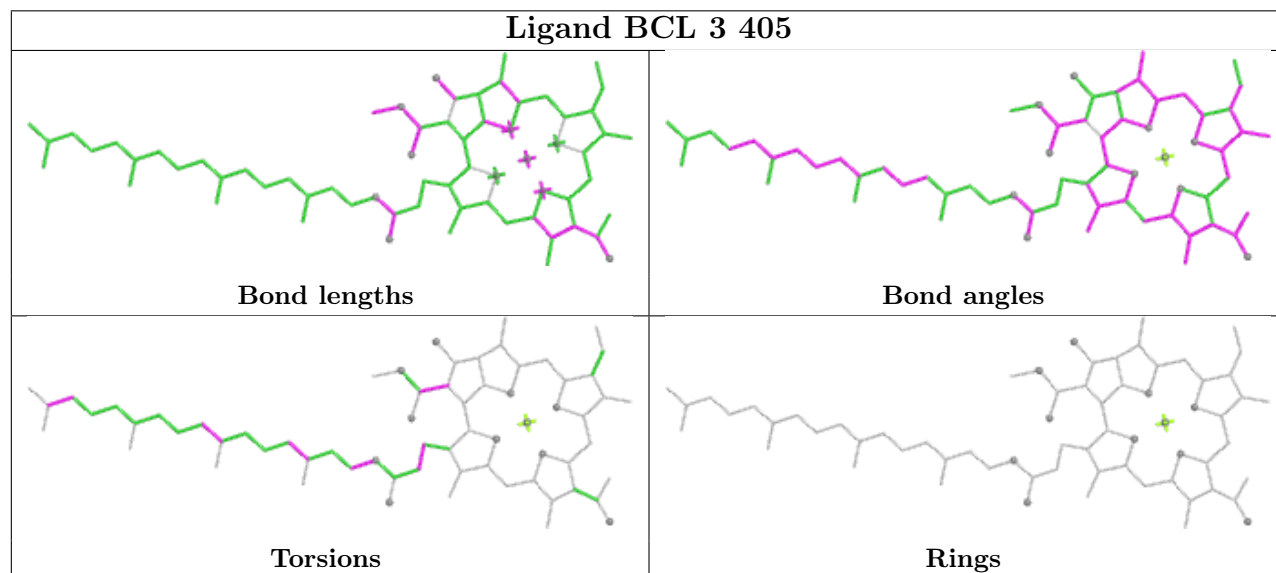
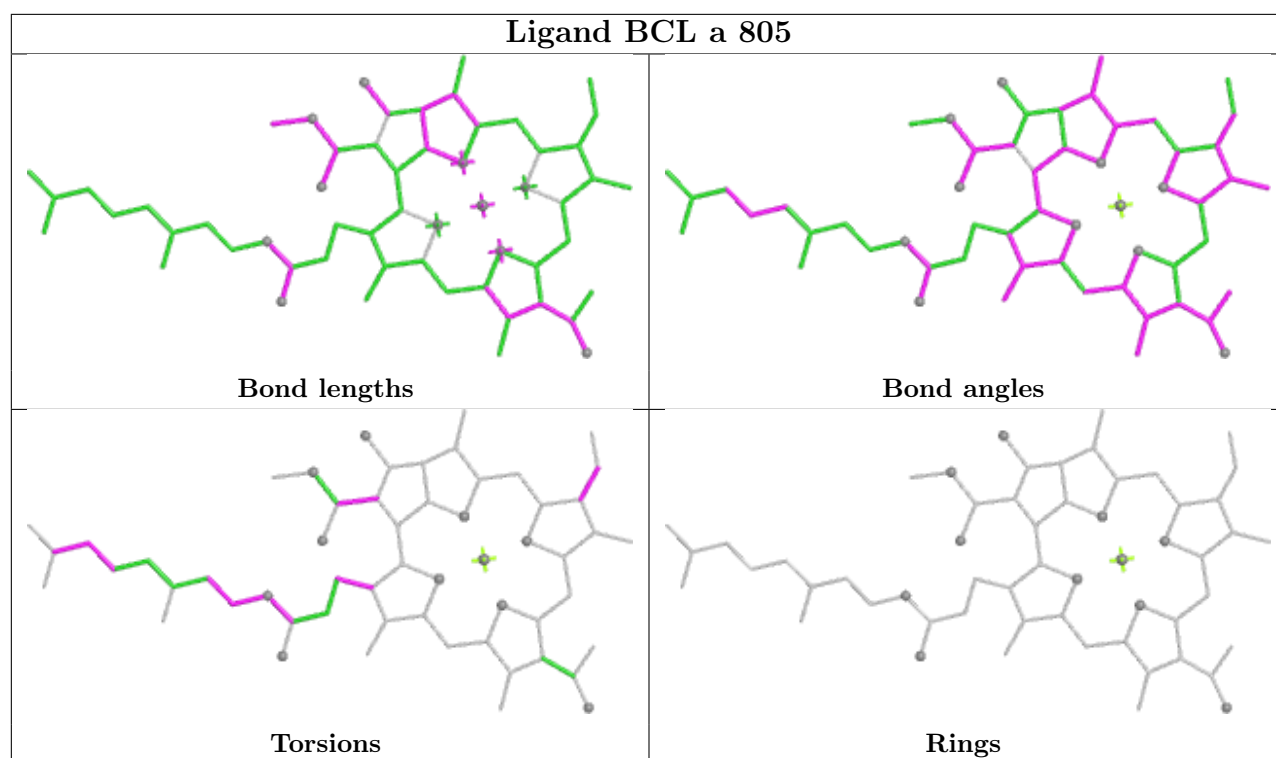


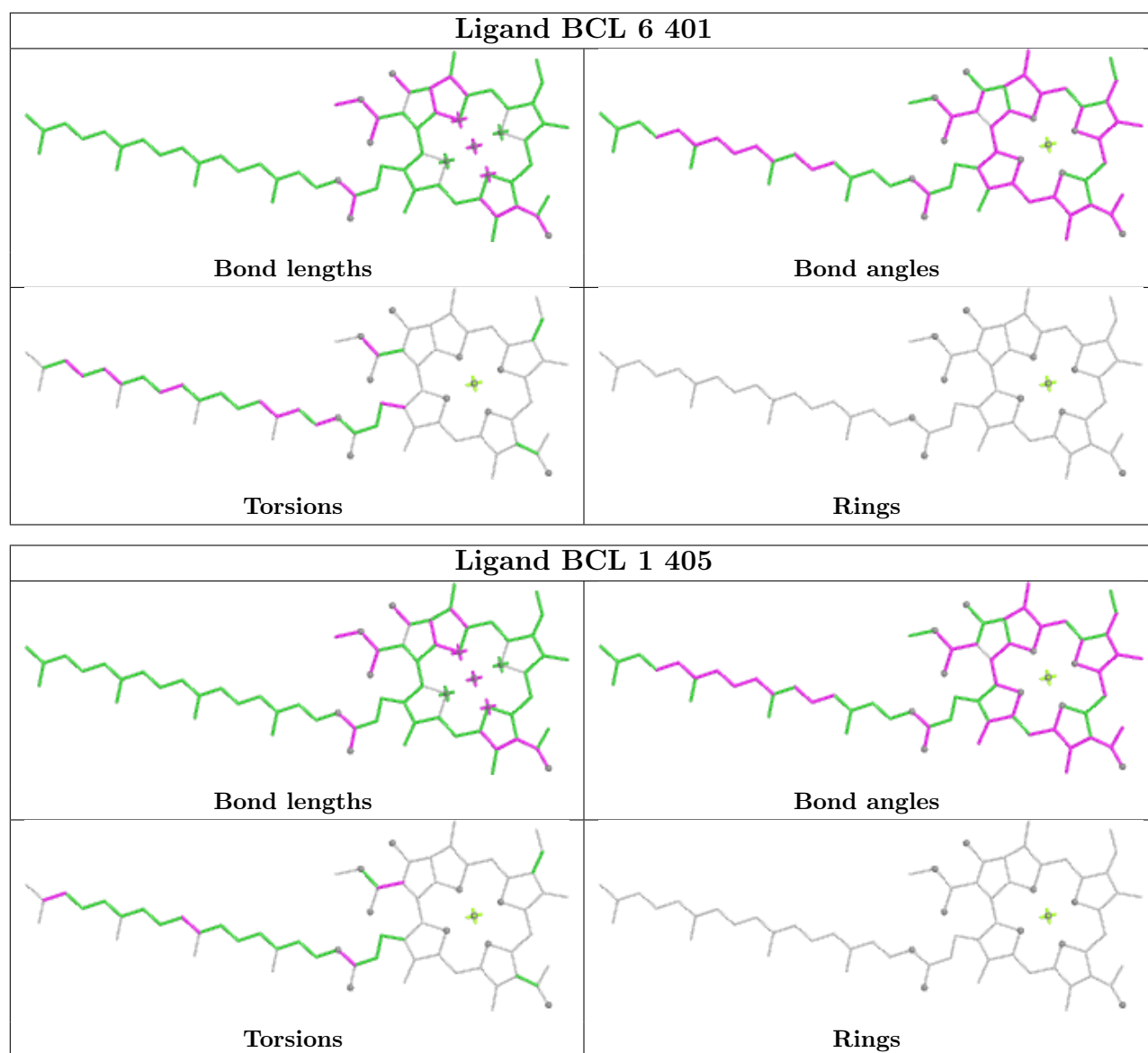


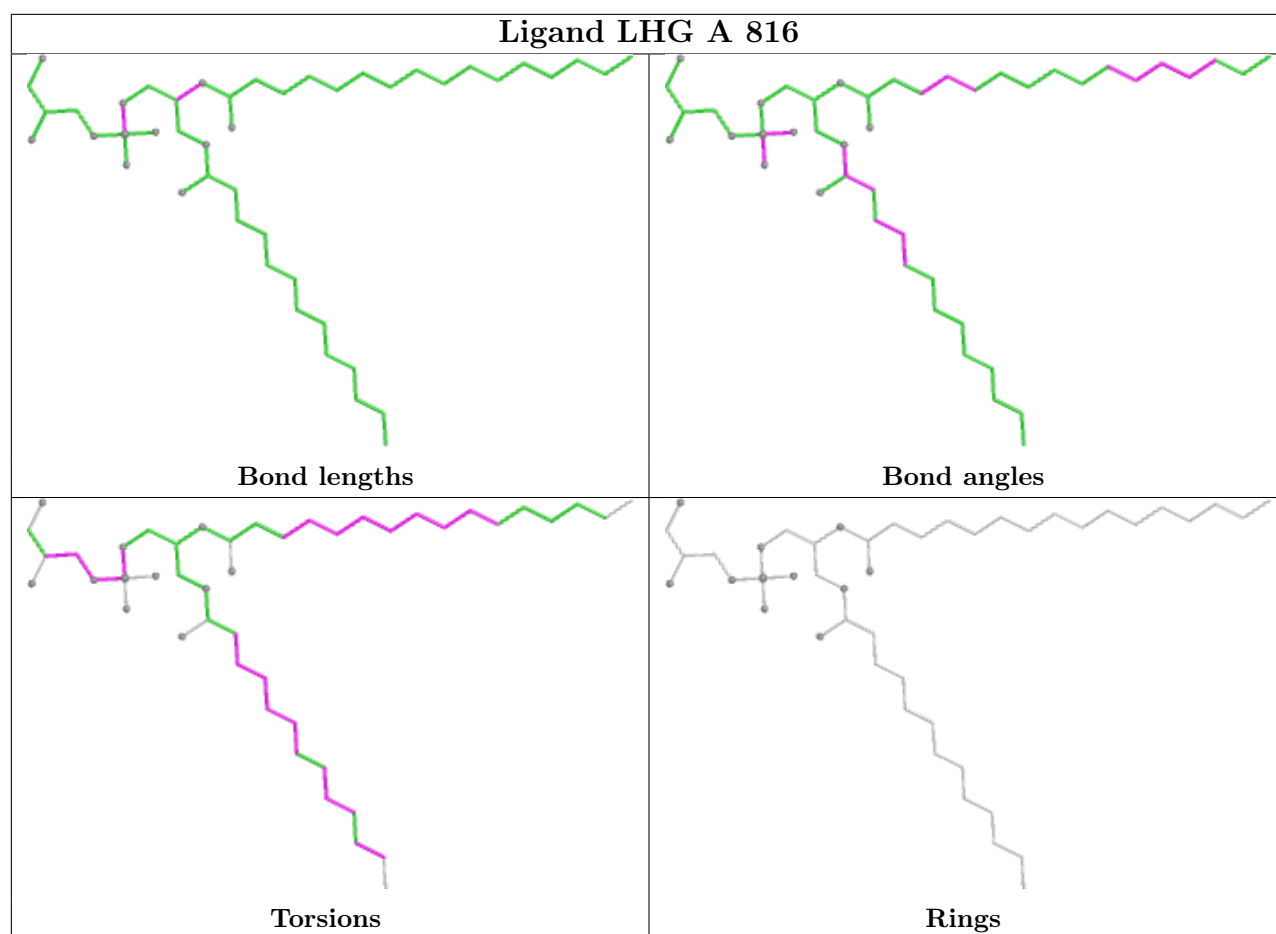


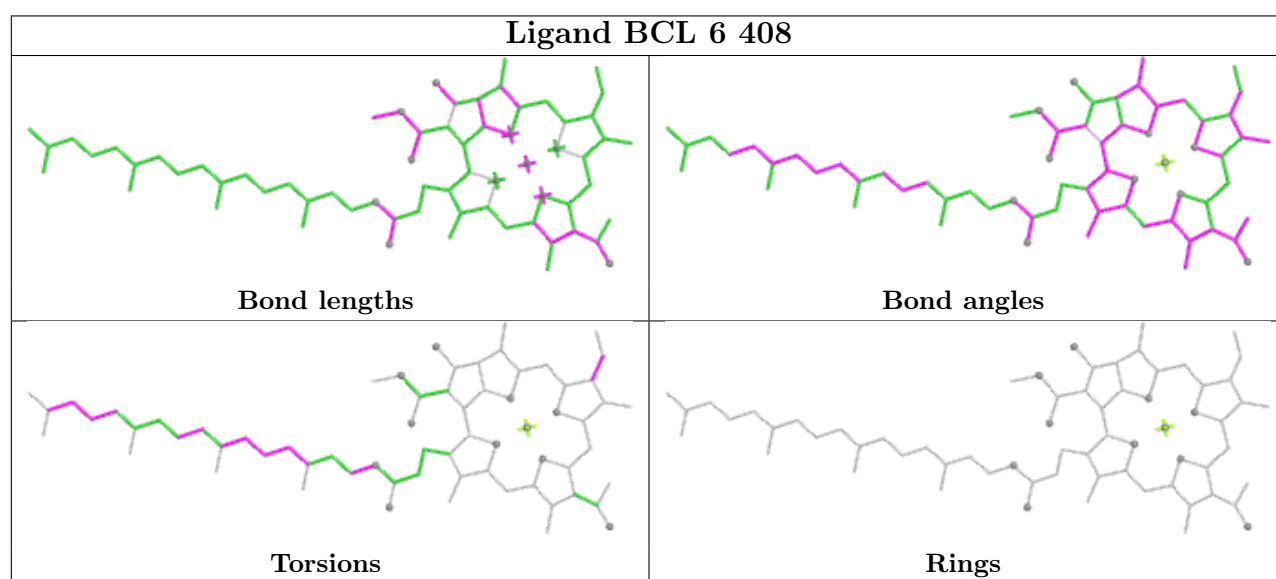
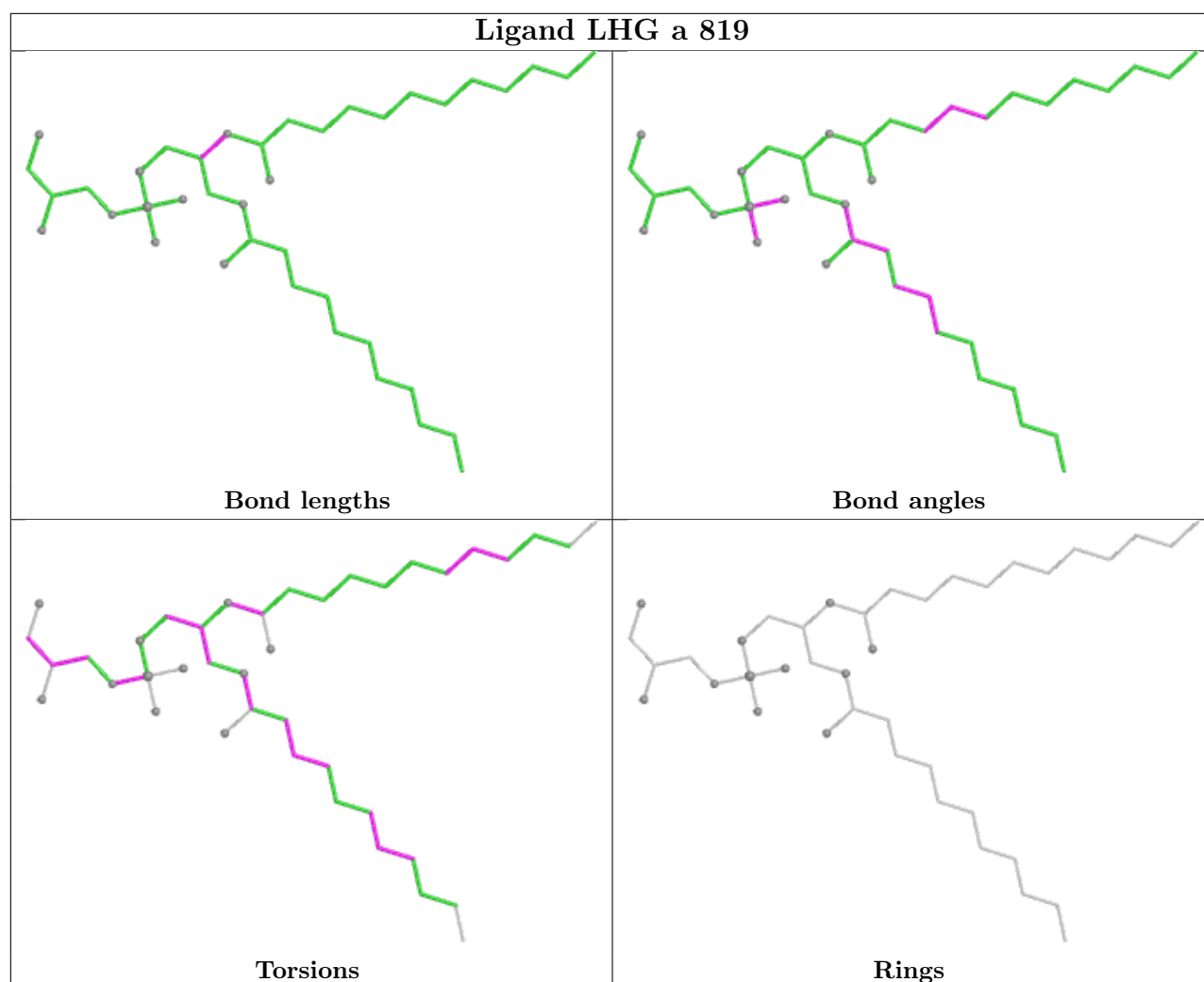


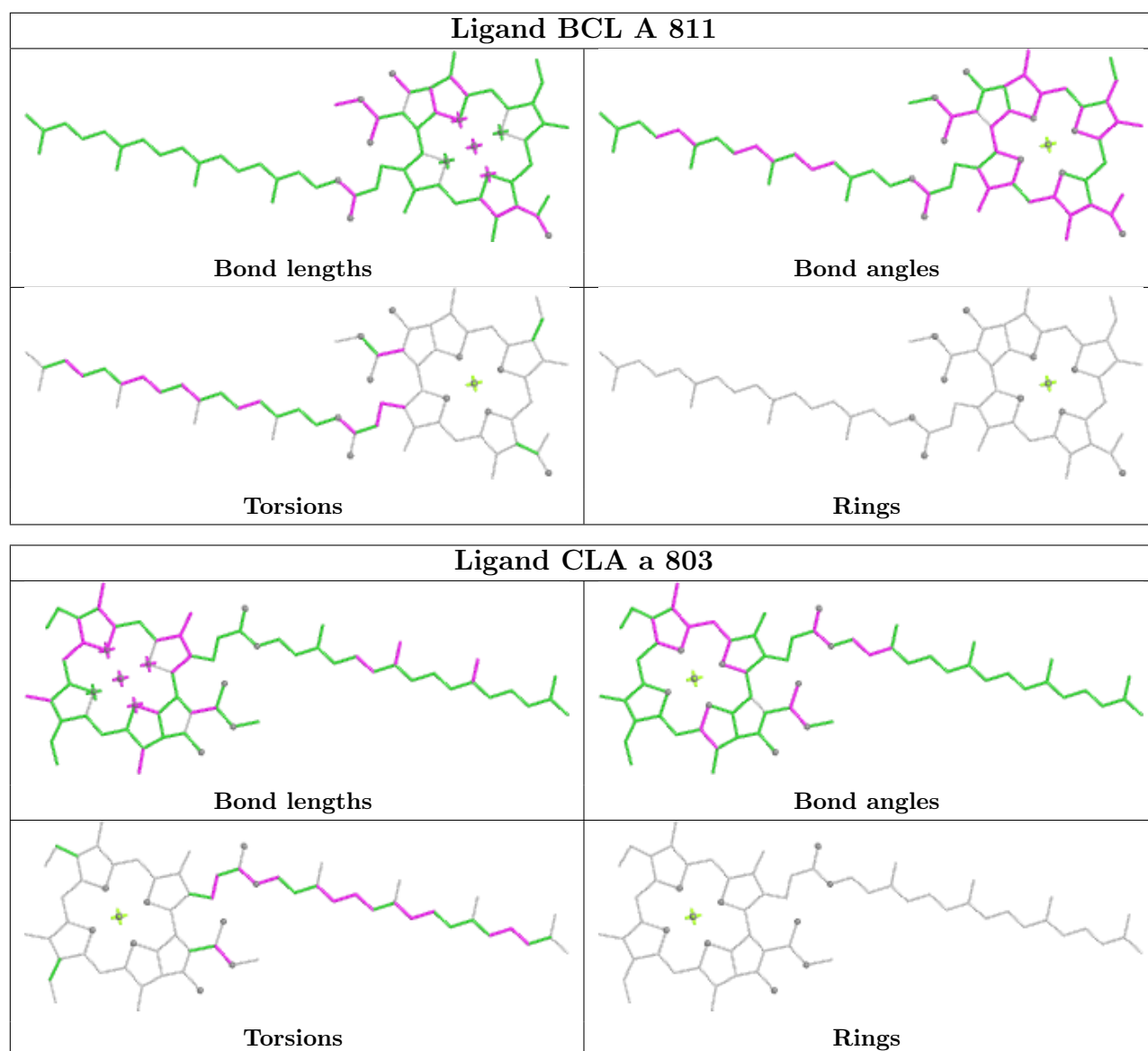


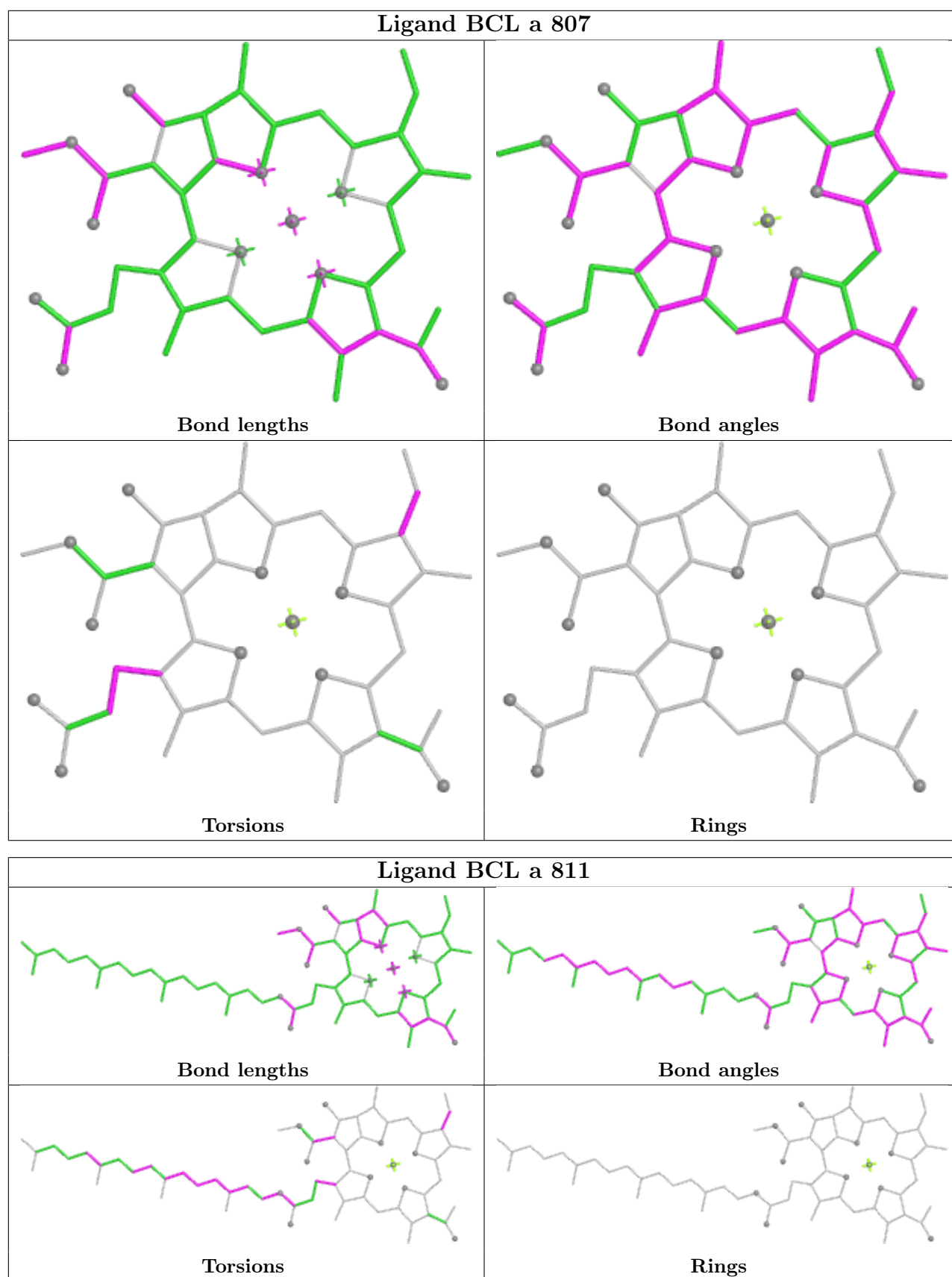


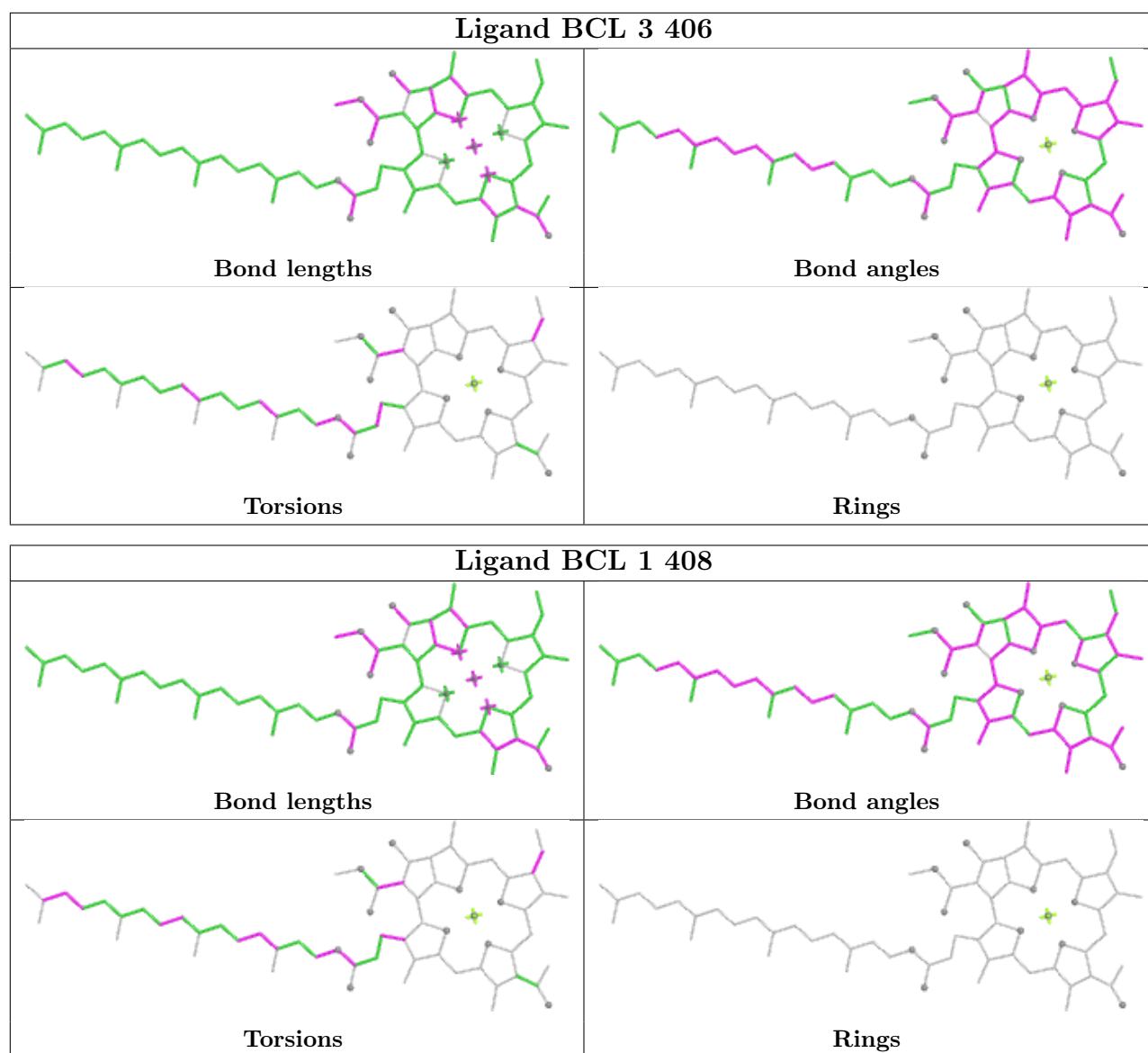












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

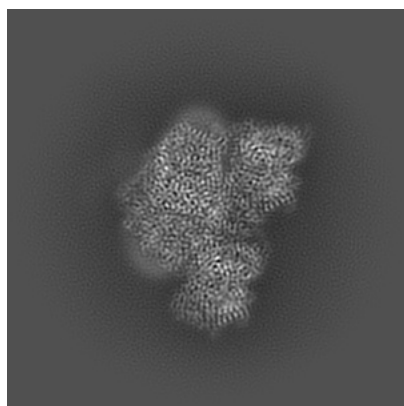
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34307. These allow visual inspection of the internal detail of the map and identification of artifacts.

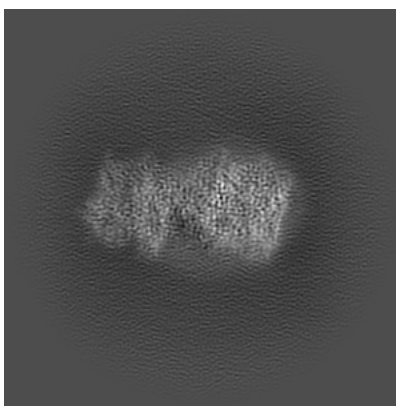
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

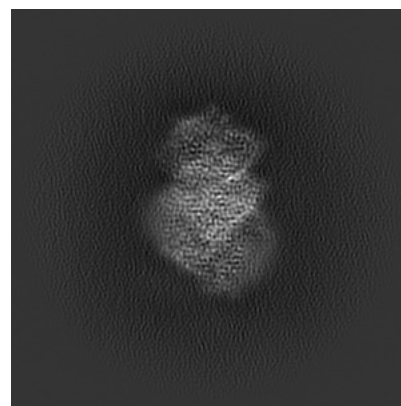
6.1.1 Primary map



X

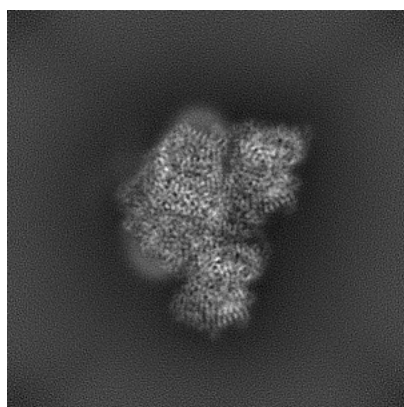


Y

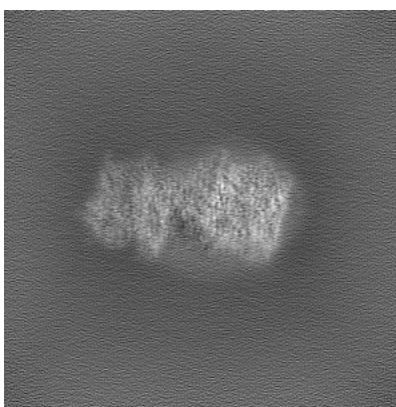


Z

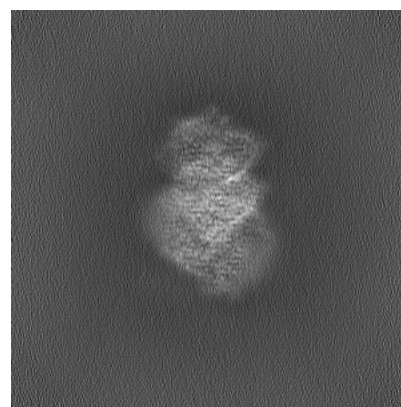
6.1.2 Raw map



X



Y

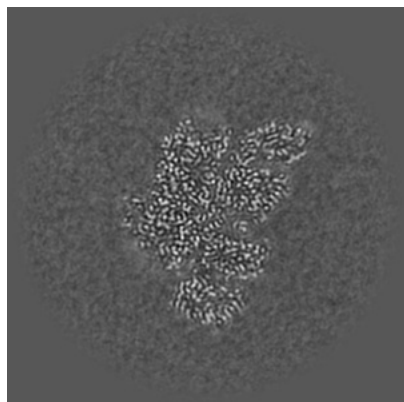


Z

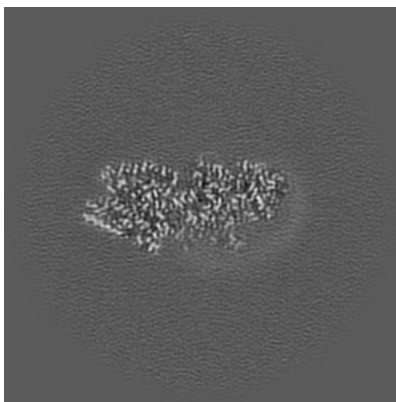
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

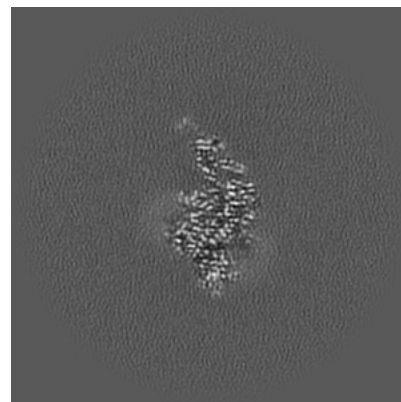
6.2.1 Primary map



X Index: 170

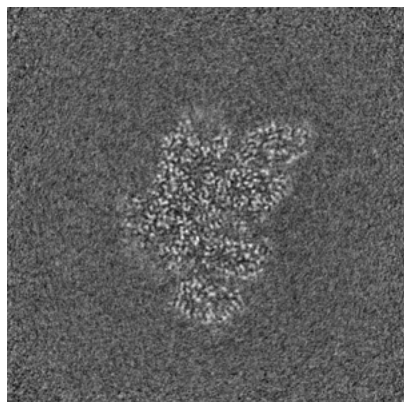


Y Index: 170

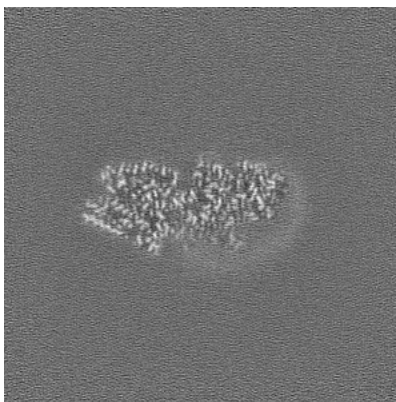


Z Index: 170

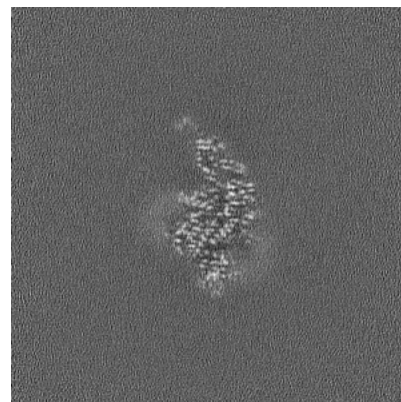
6.2.2 Raw map



X Index: 170



Y Index: 170

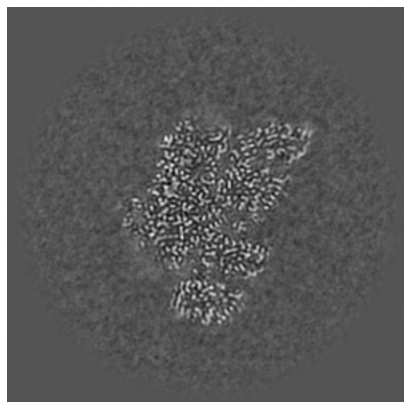


Z Index: 170

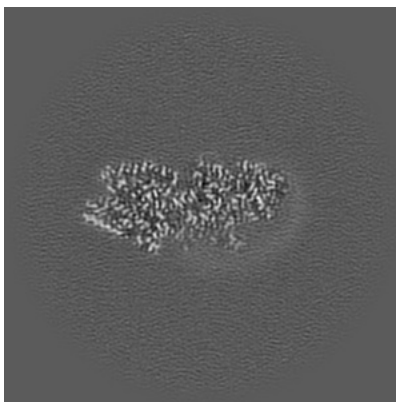
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

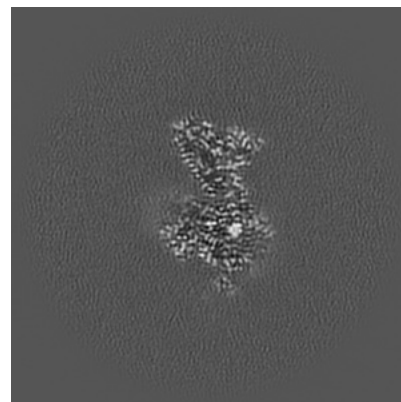
6.3.1 Primary map



X Index: 171

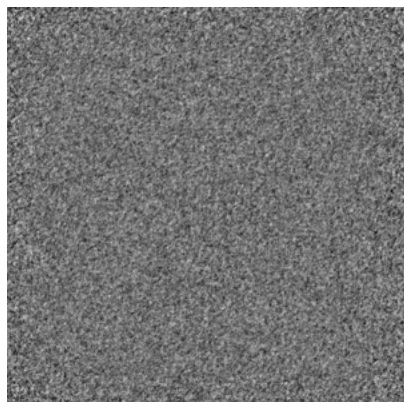


Y Index: 170

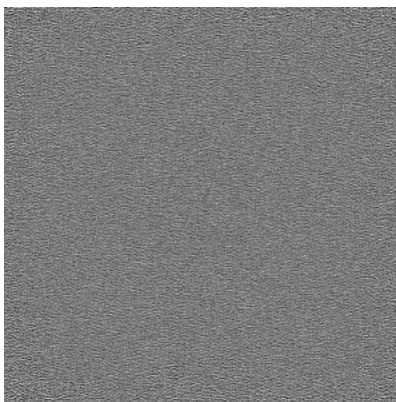


Z Index: 185

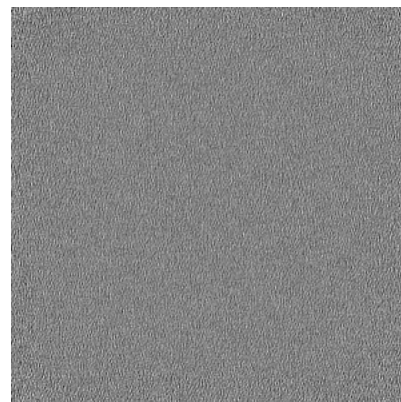
6.3.2 Raw map



X Index: 0



Y Index: 0

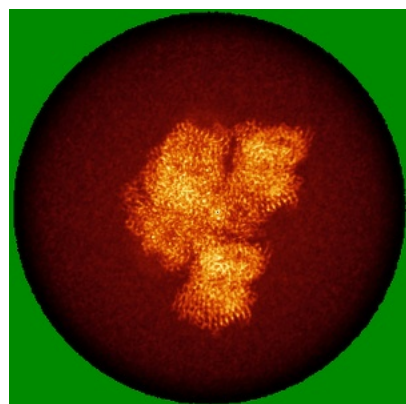


Z Index: 0

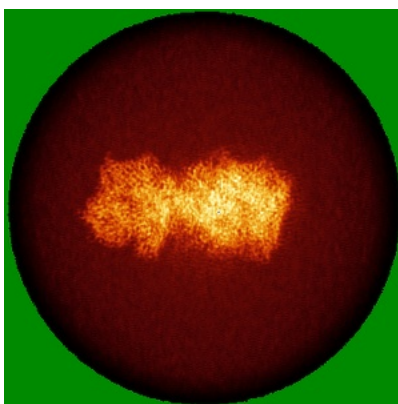
The images above show the largest variance slices of the map in three orthogonal directions.

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

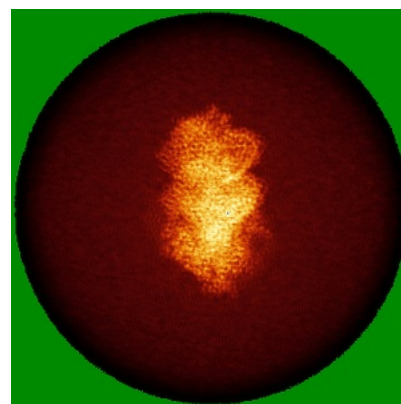
6.4.1 Primary map



X

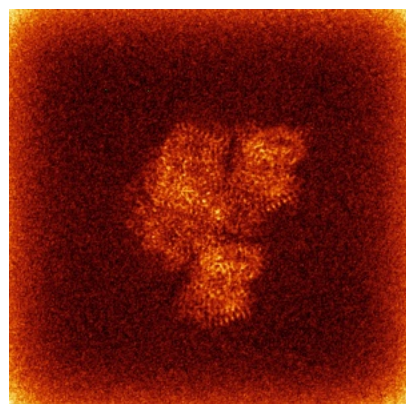


Y

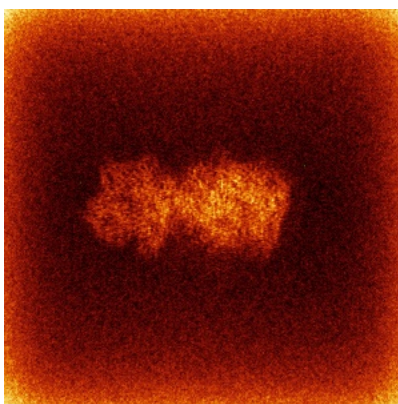


Z

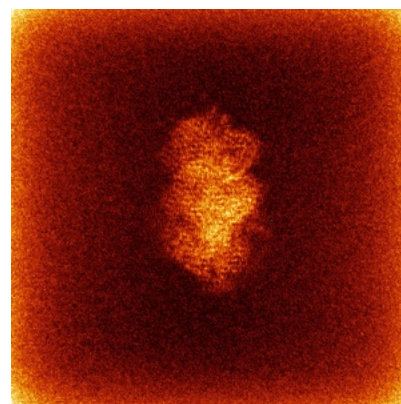
6.4.2 Raw map



X



Y

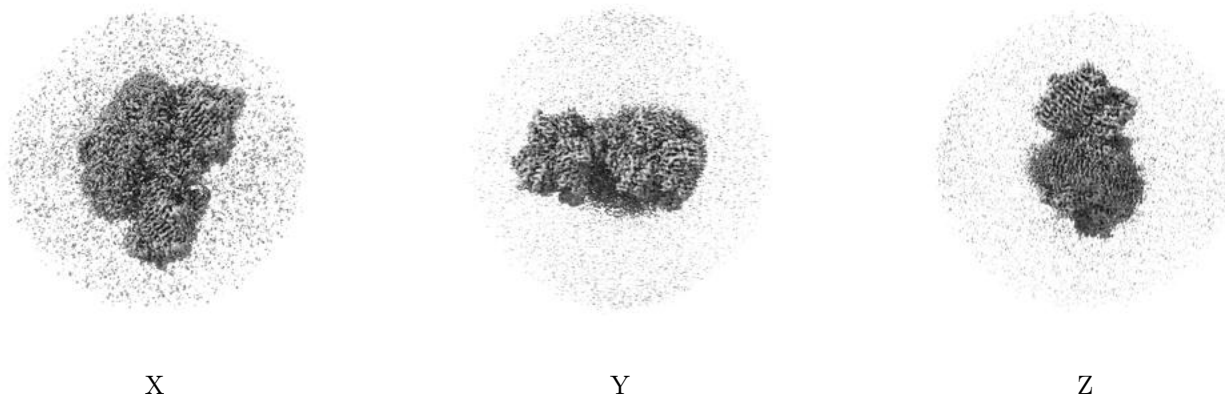


Z

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

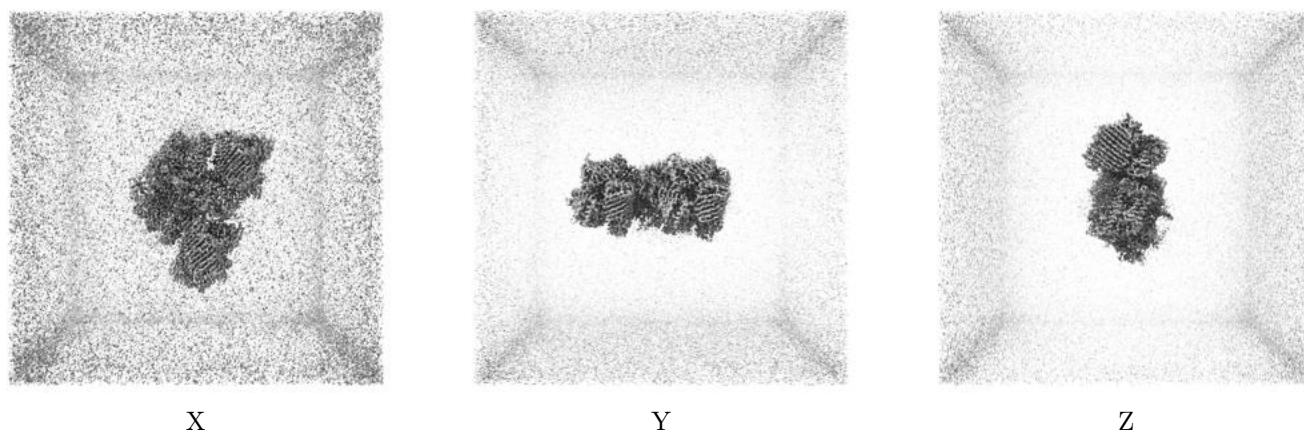
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

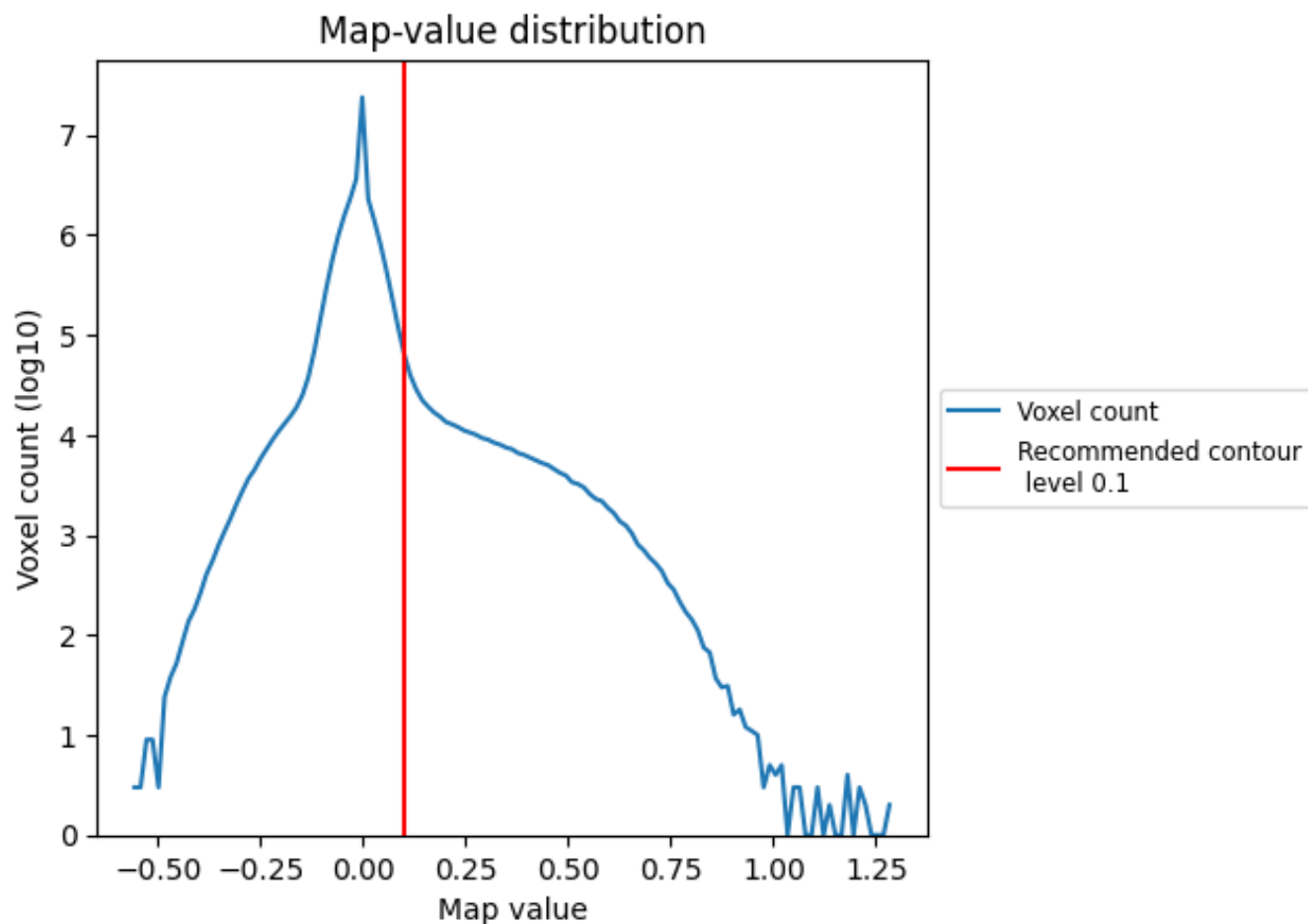
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

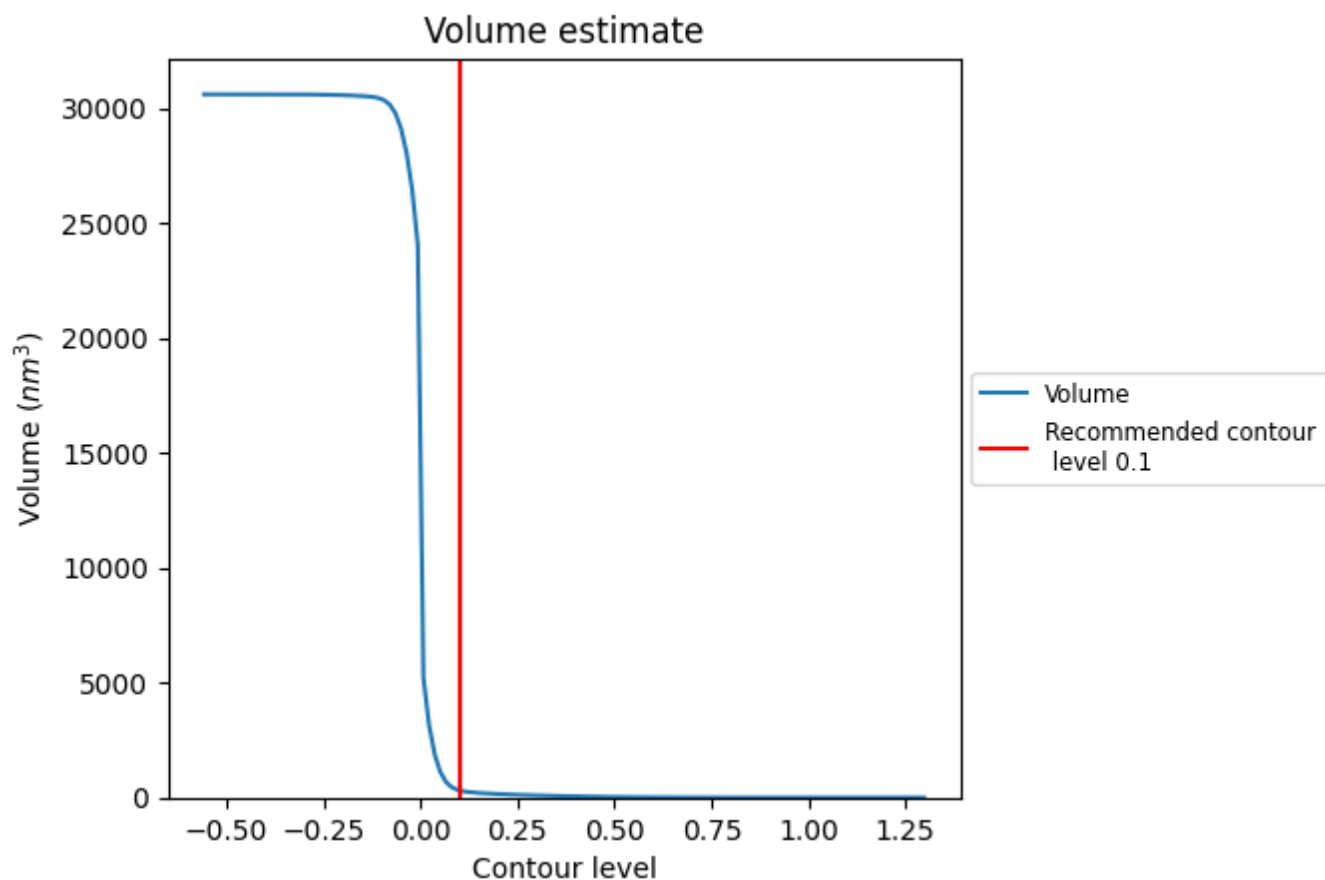
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

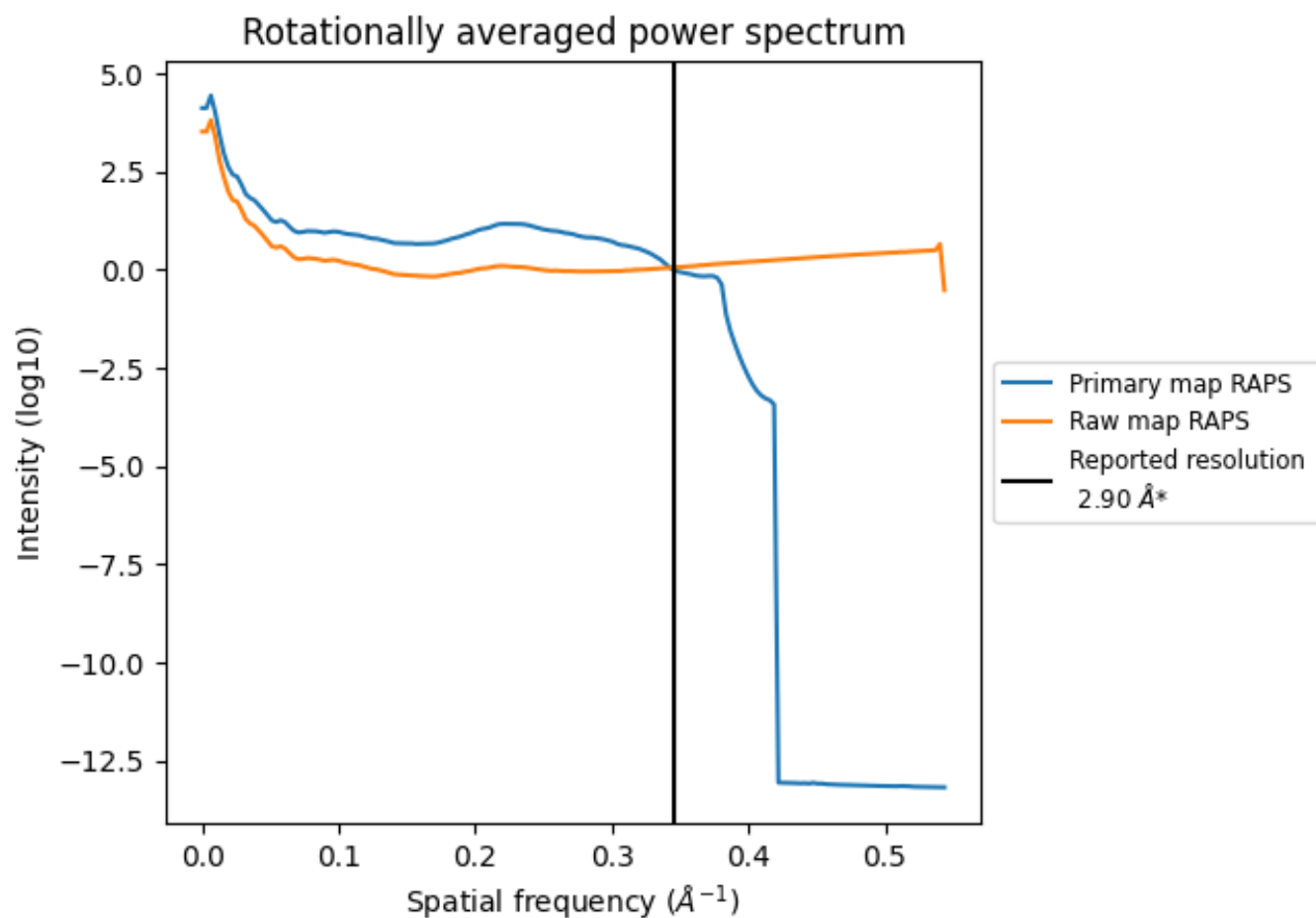
7.2 Volume estimate [i](#)



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

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

7.3 Rotationally averaged power spectrum ⓘ

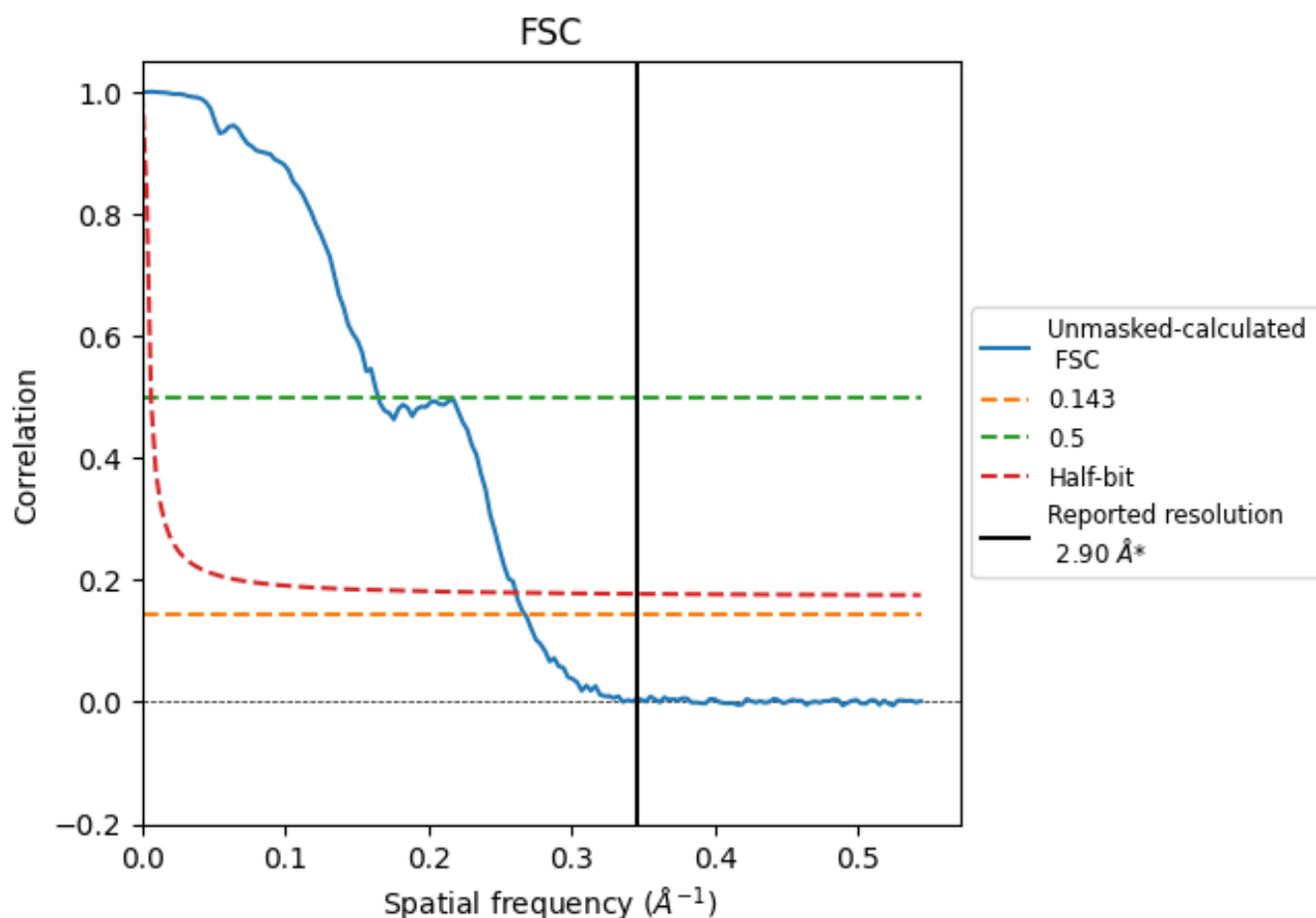


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

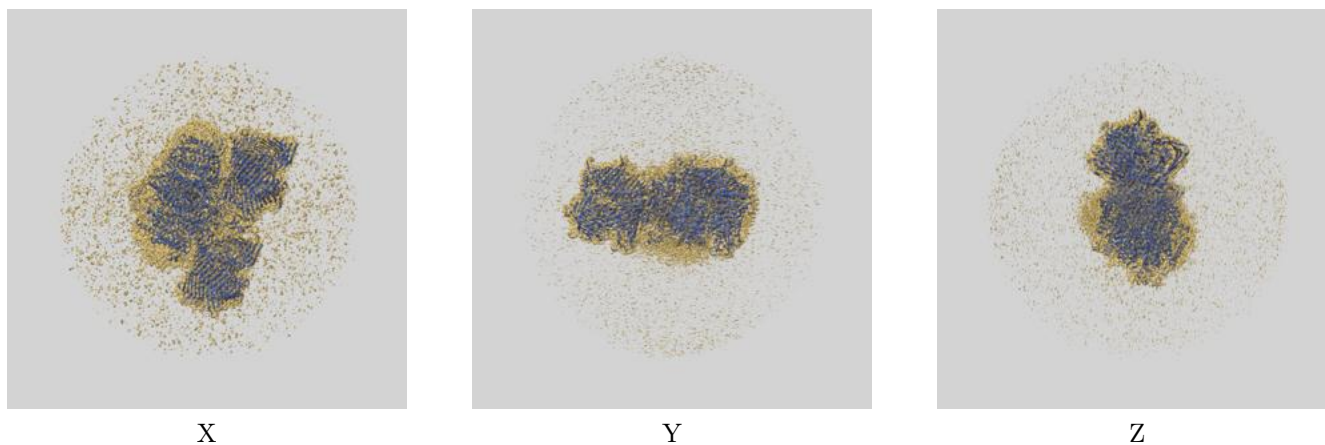
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.74	6.06	3.83

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.74 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

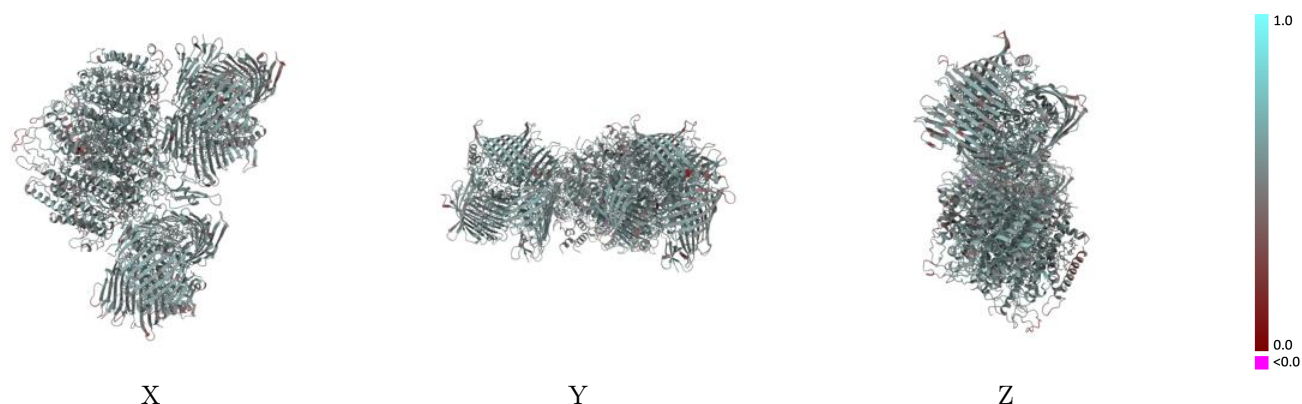
This section contains information regarding the fit between EMDB map EMD-34307 and PDB model 8GWA. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



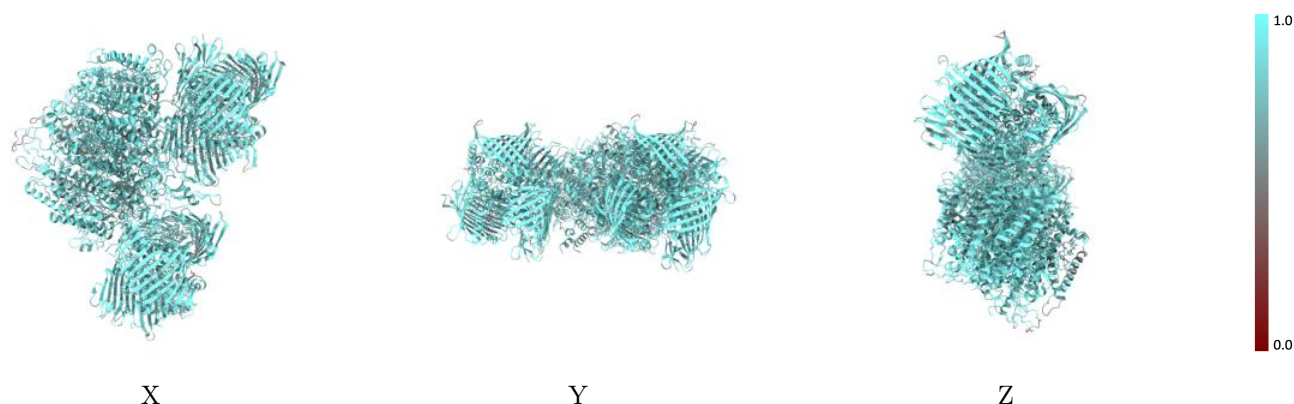
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



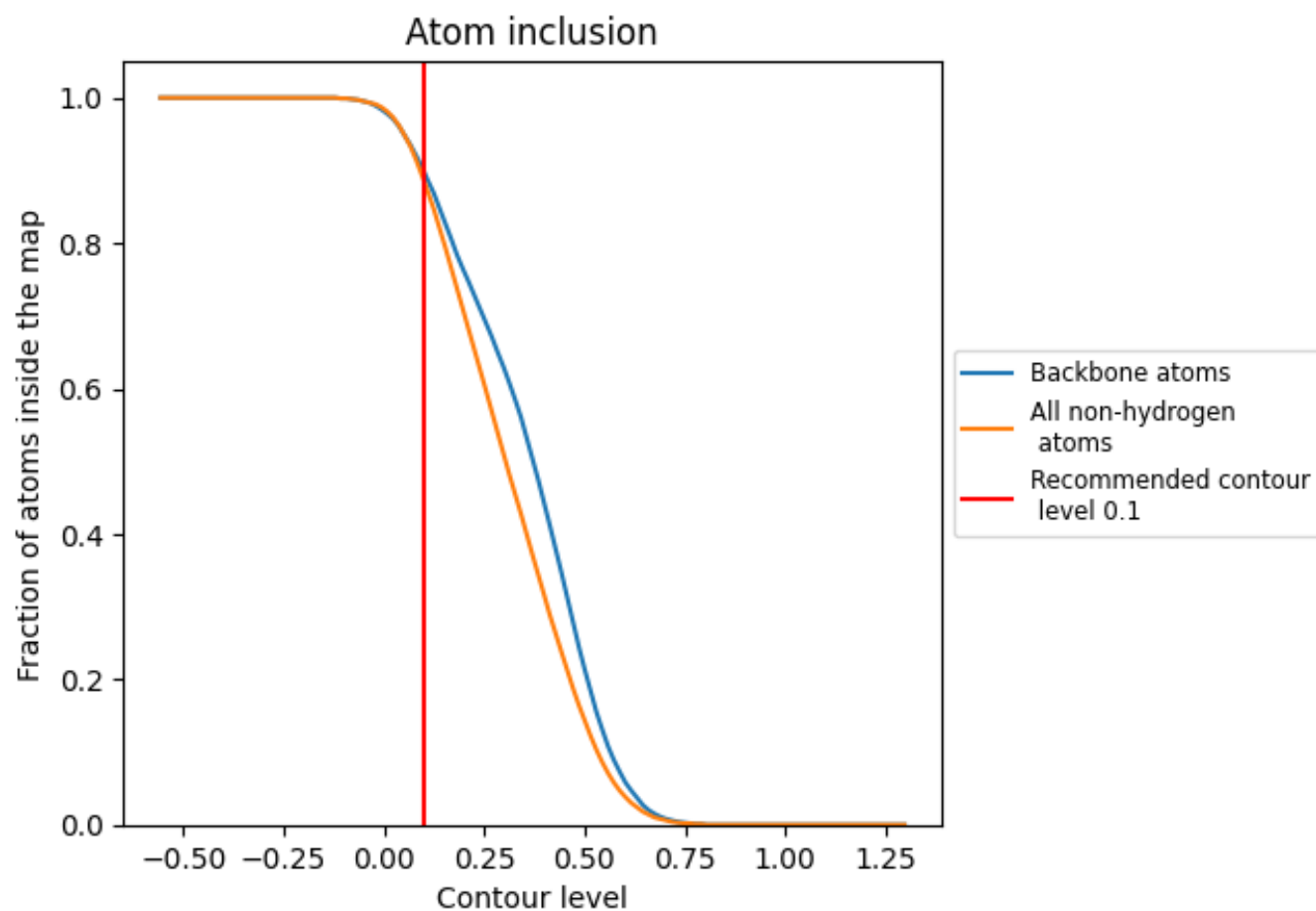
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 88% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8850	0.5410
1	0.9110	0.5550
2	0.8980	0.5550
3	0.8900	0.5330
4	0.8750	0.5370
5	0.8850	0.5500
6	0.8910	0.5270
A	0.8900	0.5480
B	0.8960	0.5320
C	0.8730	0.5320
D	0.8610	0.5330
E	0.8630	0.5060
F	0.7900	0.4990
a	0.8970	0.5480
c	0.7470	0.4760

1.0

0.0

<0.0