



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2025 – 06:51 am GMT

PDB ID : 9F5X
EMDB ID : EMD-50202
Title : Structure of the Chlamydomonas reinhardtii respiratory supercomplex I1 III2 IV2
Authors : Waltz, F.; Righetto, R.; Kotecha, A.; Engel, B.D.
Deposited on : 2024-04-30
Resolution : 2.82 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.dev117
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.5

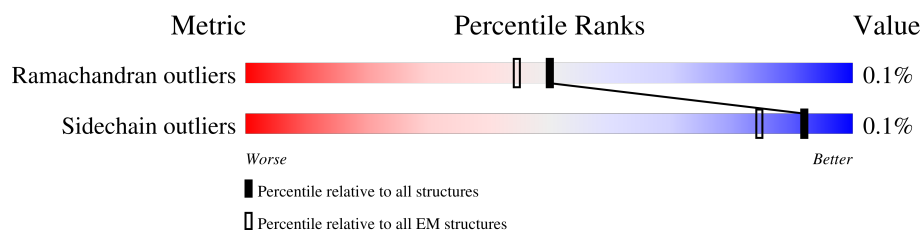
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.82 Å.

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



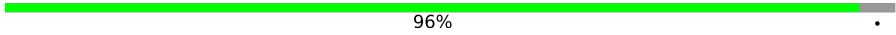
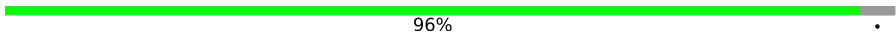
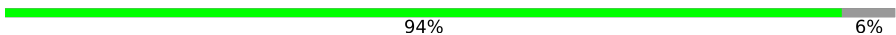








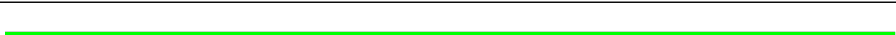

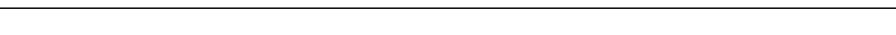
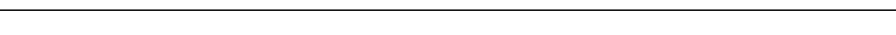
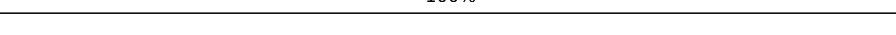
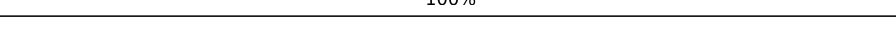
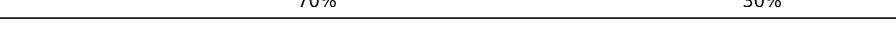

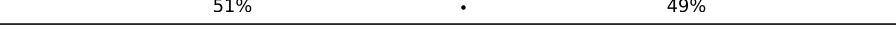
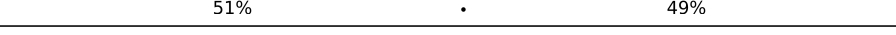




Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	1A	381	98% ..
1	1B	381	98% ..
2	1C	262	79% 21%
2	1D	262	79% 21%
3	1E	314	77% 23%
3	1F	314	77% 23%
4	1G	60	98% .
4	1H	60	98% .
5	1I	69	99% .
5	1J	69	99% .




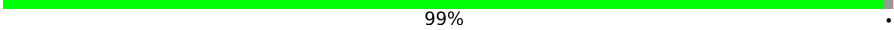
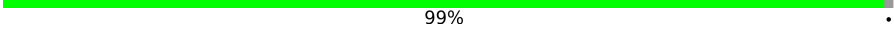






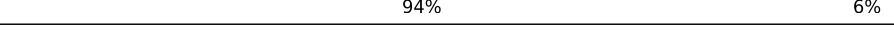


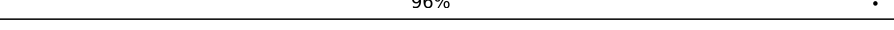




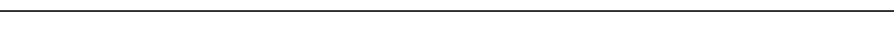

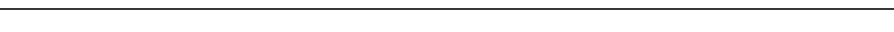
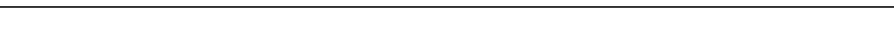


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Mol	Chain	Length	Quality of chain
6	1K	73	 96% .
6	1L	73	 96% .
7	1M	495	 94% 6%
7	1N	495	 93% . 6%
8	1O	59	 81% 19%
8	1P	59	 81% 19%
9	1Q	485	 90% . 9%
9	1S	485	 90% . 9%
10	1R	123	 99% .
10	1T	123	 99% .
11	2A	504	 100%
11	3A	504	 100%
12	2B	284	 50% 50%
12	3B	284	 50% 50%
13	2C	153	 100%
13	3C	153	 100%
14	2D	382	 70% 30%
14	3D	382	 70% 30%
15	2E	175	 51% . 49%
15	3E	175	 51% . 49%
16	2F	96	 90% 10%
16	3F	96	 90% 10%
17	2G	125	 72% . 27%
17	3G	125	 70% . 27%
18	2H	148	 77% 23%


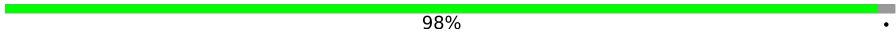
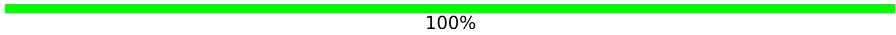

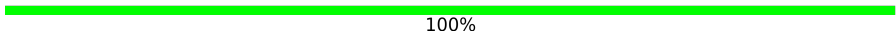

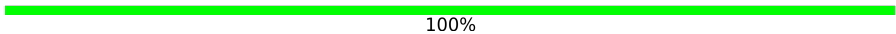
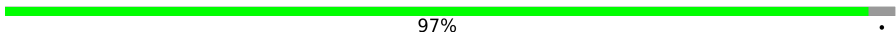







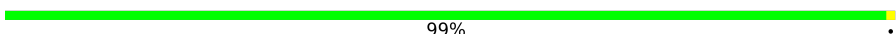
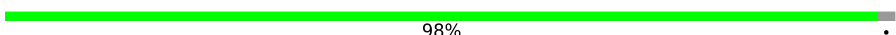


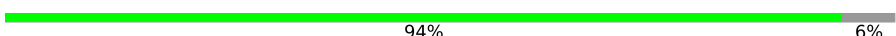
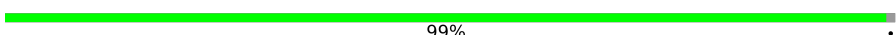
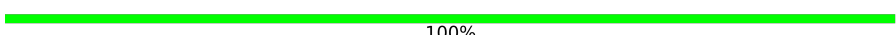
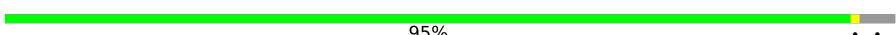
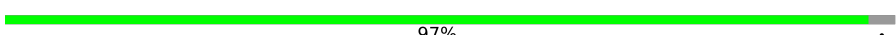
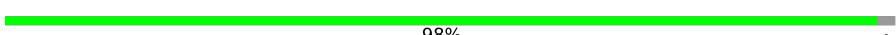
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Mol	Chain	Length	Quality of chain
18	3H	148	 77% 23%
19	2I	101	 71% 29%
19	3I	101	 71% 29%
20	2J	105	 99% .
20	3J	105	 99% .
21	2K	58	 81% 19%
21	3K	58	 81% 19%
22	2L	87	 87% 13%
22	3L	87	 90% 10%
23	A	282	 85% 15%
24	B	484	 90% 10%
25	C	733	 94% 6%
26	D	282	 77% 23%
27	E	467	 82% 18%
28	F	164	 96% .
29	G	231	 86% 14%
30	H	118	 75% . 24%
31	I	165	 82% 18%
32	J	128	 66% 34%
32	r	128	 69% 31%
33	K	138	 86% 14%
34	L	187	 88% 12%
35	M	154	 79% 21%
36	N	156	 96% .
37	O	101	 98% ..

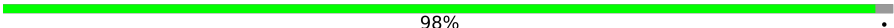
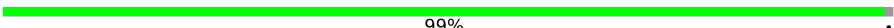



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Mol	Chain	Length	Quality of chain
38	P	397	
39	Q	292	
40	R	387	
41	S	279	
42	T	443	
43	U	227	
44	V	546	
45	W	162	
46	X	149	
47	Y	64	
48	Z	124	
49	a	129	
50	b	172	
51	c	67	
52	d	86	
53	e	219	
54	f	65	
55	g	55	
56	h	142	
57	i	81	
58	j	86	
59	k	117	
60	l	121	
61	m	142	
62	n	106	

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Mol	Chain	Length	Quality of chain
63	o	155	 98% .
64	p	130	 99% .
65	q	197	 80% 20%
66	s	312	 100%
67	t	279	 90% 9%
68	u	229	 100%
69	v	45	 100%
70	w	109	 59% 41%
71	x	157	 53% 47%
72	y	118	 97% .

2 Entry composition

There are 92 unique types of molecules in this entry. The entry contains 137999 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 Cytochrome b.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	376	Total	C	N	O	S	0	0
			2958	1984	466	491	17		
1	1B	376	Total	C	N	O	S	0	0
			2958	1984	466	491	17		

- Molecule 2 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1C	207	Total	C	N	O	S	0	0
			1602	1017	279	299	7		
2	1D	207	Total	C	N	O	S	0	0
			1602	1017	279	299	7		

- Molecule 3 is a protein called Cytochrome c1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1E	243	Total	C	N	O	S	0	0
			1898	1204	326	356	12		
3	1F	243	Total	C	N	O	S	0	0
			1898	1204	326	356	12		

- Molecule 4 is a protein called Complex III subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1G	59	Total	C	N	O	S	0	0
			486	316	79	88	3		
4	1H	59	Total	C	N	O	S	0	0
			486	316	79	88	3		

- Molecule 5 is a protein called Cytochrome b-c1 complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1I	68	Total	C	N	O	S	0	0
			550	347	92	105	6		
5	1J	68	Total	C	N	O	S	0	0
			550	347	92	105	6		

- Molecule 6 is a protein called Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1K	70	Total	C	N	O	S	0	0
			594	386	104	103	1		
6	1L	70	Total	C	N	O	S	0	0
			594	386	104	103	1		

- Molecule 7 is a protein called MPP-Beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1M	464	Total	C	N	O	S	0	0
			3646	2290	641	696	19		
7	1N	464	Total	C	N	O	S	0	0
			3646	2290	641	696	19		

- Molecule 8 is a protein called Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	1O	48	Total	C	N	O	S	0	0
			371	249	61	60	1		
8	1P	48	Total	C	N	O	S	0	0
			371	249	61	60	1		

- Molecule 9 is a protein called Alpha-MPP.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	1Q	441	Total	C	N	O	S	0	0
			3204	2018	562	619	5		
9	1S	441	Total	C	N	O	S	0	0
			3204	2018	562	619	5		

- Molecule 10 is a protein called Cytochrome b-c1 complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	1R	122	Total	C	N	O	S	0	0
			980	617	178	183	2		
10	1T	122	Total	C	N	O	S	0	0
			980	617	178	183	2		

- Molecule 11 is a protein called Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	2A	504	Total	C	N	O	S	0	0
			3888	2600	618	643	27		
11	3A	504	Total	C	N	O	S	0	0
			3888	2600	618	643	27		

- Molecule 12 is a protein called Cytochrome c oxidase polypeptide II.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	2B	141	Total	C	N	O	S	0	0
			1169	774	188	201	6		
12	3B	141	Total	C	N	O	S	0	0
			1169	774	188	201	6		

- Molecule 13 is a protein called cytochrome-c oxidase.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	2C	153	Total	C	N	O	S	0	0
			1212	776	206	223	7		
13	3C	153	Total	C	N	O	S	0	0
			1212	776	206	223	7		

- Molecule 14 is a protein called Cytochrome c oxidase subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2D	266	Total	C	N	O	S	0	0
			2079	1373	334	351	21		
14	3D	266	Total	C	N	O	S	0	0
			2079	1373	334	351	21		

- Molecule 15 is a protein called Cox5b.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2E	90	Total	C	N	O	S	0	0
			737	478	114	144	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
15	3E	90	Total	C	N	O	S	0	0
			737	478	114	144	1		

- Molecule 16 is a protein called Cox5c.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	2F	86	Total	C	N	O	S	0	0
			706	456	122	126	2		
16	3F	86	Total	C	N	O	S	0	0
			706	456	122	126	2		

- Molecule 17 is a protein called Cox6a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	2G	91	Total	C	N	O	S	0	0
			733	484	120	124	5		
17	3G	91	Total	C	N	O	S	0	0
			733	484	120	124	5		

- Molecule 18 is a protein called Cox6b.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2H	114	Total	C	N	O	S	0	0
			954	606	159	185	4		
18	3H	114	Total	C	N	O	S	0	0
			954	606	159	185	4		

- Molecule 19 is a protein called Cox7c.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	2I	72	Total	C	N	O	0	0
			594	393	98	103		
19	3I	72	Total	C	N	O	0	0
			594	393	98	103		

- Molecule 20 is a protein called Cytochrome c oxidase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2J	104	Total	C	N	O	S	0	0
			816	522	144	147	3		
20	3J	104	Total	C	N	O	S	0	0
			816	522	144	147	3		

- Molecule 21 is a protein called Cox7a.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	2K	47	Total	C	N	O	0	0
			382	249	63	70		
21	3K	47	Total	C	N	O	0	0
			382	249	63	70		

- Molecule 22 is a protein called CoxIn.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2L	76	Total	C	N	O	S	0	0
			605	390	100	111	4		
22	3L	78	Total	C	N	O	S	0	0
			627	405	104	114	4		

- Molecule 23 is a protein called NADH:ubiquinone oxidoreductase 24 kD subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A	239	Total	C	N	O	S	0	0
			1839	1165	311	352	11		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B	435	Total	C	N	O	S	0	0
			3331	2099	592	614	26		

- Molecule 25 is a protein called NADH:ubiquinone oxidoreductase 78 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	C	688	Total	C	N	O	S	0	0
			5175	3235	936	972	32		

- Molecule 26 is a protein called NADH:ubiquinone oxidoreductase 30kDa subunit domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	216	Total	C	N	O	S	0	0
			1790	1156	301	325	8		

- Molecule 27 is a protein called NADH:ubiquinone oxidoreductase 49 kD subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	383	Total	C	N	O	S	0	0
			3085	1971	537	554	23		

- Molecule 28 is a protein called NADH:ubiquinone oxidoreductase subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	157	Total	C	N	O	S	0	0
			1225	787	211	215	12		

- Molecule 29 is a protein called NADH:ubiquinone oxidoreductase subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	199	Total	C	N	O	S	0	0
			1615	1007	281	315	12		

- Molecule 30 is a protein called B14.5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	90	Total	C	N	O	S	0	0
			750	486	129	132	3		

- Molecule 31 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 18 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	135	Total	C	N	O	S	0	0
			1044	661	173	208	2		

- Molecule 32 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	84	Total	C	N	O	S	0	0
			640	404	100	133	3		
32	r	88	Total	C	N	O	S	0	0
			663	419	104	137	3		

- Molecule 33 is a protein called NADH:ubiquinone oxidoreductase B14 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	119	Total	C	N	O	S	0	0
			986	640	173	168	5		

- Molecule 34 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	164	Total	C	N	O	S	0	0
			1275	803	221	245	6		

- Molecule 35 is a protein called NADH:ubiquinone oxidoreductase 13 kD-like subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M	121	Total	C	N	O	S	0	0
			913	582	150	178	3		

- Molecule 36 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	N	150	Total	C	N	O	S	0	0
			1235	791	214	227	3		

- Molecule 37 is a protein called NADH:ubiquinone oxidoreductase B8 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	100	Total	C	N	O	S	0	0
			761	471	138	147	5		

- Molecule 38 is a protein called Putative NADH:ubiquinone oxidoreductase 39 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P	363	Total	C	N	O	S	0	0
			2823	1793	489	527	14		

- Molecule 39 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	286	Total	C	N	O	S	0	0
			2179	1448	338	374	19		

- Molecule 40 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	387	Total	C	N	O	S	0	0
			3014	2026	467	496	25		

- Molecule 41 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	134	Total	C	N	O	S	0	0
			1071	715	159	192	5		

- Molecule 42 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	T	443	Total	C	N	O	S	0	0
			3434	2321	526	557	30		

- Molecule 43 is a protein called NADH dehydrogenase subunit 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	U	105	Total	C	N	O	S	0	0
			805	524	124	146	11		

- Molecule 44 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	546	Total	C	N	O	S	0	0
			4152	2731	668	716	37		

- Molecule 45 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	W	157	Total	C	N	O	S	0	0
			1210	820	180	201	9		

- Molecule 46 is a protein called ASH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	X	125	Total	C	N	O	S	0	0
			1037	685	168	178	6		

- Molecule 47 is a protein called P9.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Y	54	Total	C	N	O	S	0	0
			405	256	74	74	1		

- Molecule 48 is a protein called KFYI.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Z	107	Total	C	N	O	S	0	0
			861	555	149	152	5		

- Molecule 49 is a protein called AGGG.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	a	82	Total	C	N	O	S	0	0
			674	440	109	123	2		

- Molecule 50 is a protein called ESSS.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	b	144	Total	C	N	O	S	0	0
			1169	756	192	214	7		

- Molecule 51 is a protein called B9.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	c	59	Total	C	N	O	S	0	0
			453	298	71	79	5		

- Molecule 52 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 10 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	d	85	Total	C	N	O	S	0	0
			699	456	120	120	3		

- Molecule 53 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 23 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	e	218	Total	C	N	O	S	0	0
			1639	1055	279	297	8		

- Molecule 54 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 7.5 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	f	64	Total	C	N	O	S	0	0
			532	345	93	92	2		

- Molecule 55 is a protein called Mitochondrial putative NADH:ubiquinone oxidoreductase 6.5

kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	g	50	Total	C	N	O	S	0	0
			416	277	73	65	1		

- Molecule 56 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 13 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	h	108	Total	C	N	O	S	0	0
			915	597	157	159	2		

- Molecule 57 is a protein called NADH:ubiquinone oxidoreductase 15 kDa subunit-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	i	76	Total	C	N	O	S	0	0
			633	387	122	116	8		

- Molecule 58 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	j	85	Total	C	N	O	S	0	0
			712	449	131	125	7		

- Molecule 59 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	k	117	Total	C	N	O	S	0	0
			984	631	176	173	4		

- Molecule 60 is a protein called NADH:ubiquinone oxidoreductase 20,9 kD-like subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	l	116	Total	C	N	O	S	0	0
			904	589	150	161	4		

- Molecule 61 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	m	138	Total	C	N	O	S	0	0
			1126	724	205	193	4		

- Molecule 62 is a protein called Putative NADH:ubiquinone oxidoreductase 12.5 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	n	104	Total	C	N	O	S	0	0
			864	547	152	159	6		

- Molecule 63 is a protein called Putative NADH:ubiquinone oxidoreductase 17.8 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	o	152	Total	C	N	O	S	0	0
			1240	771	238	228	3		

- Molecule 64 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 16 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	p	129	Total	C	N	O	S	0	0
			1069	670	192	204	3		

- Molecule 65 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 19 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	q	157	Total	C	N	O	S	0	0
			1268	818	217	229	4		

- Molecule 66 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 32 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	s	312	Total	C	N	O	S	0	0
			2302	1451	407	435	9		

- Molecule 67 is a protein called CAG2 - CA-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	t	253	Total	C	N	O	S	0	0
			1997	1268	357	367	5		

- Molecule 68 is a protein called CAG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	u	228	Total	C	N	O	S	0	0
			1698	1063	300	327	8		

- Molecule 69 is a protein called P10.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	v	45	Total	C	N	O	S	0	0
			361	233	61	66	1		

- Molecule 70 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 9 kDa sub-unit.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	w	64	Total	C	N	O	S	0	0
			508	334	78	91	5		

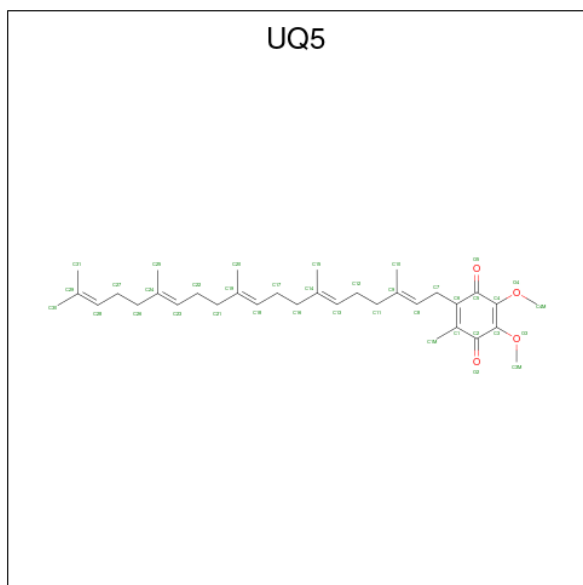
- Molecule 71 is a protein called NUOP8.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	x	83	Total	C	N	O	S	0	0
			699	467	110	121	1		

- Molecule 72 is a protein called NUOP7.

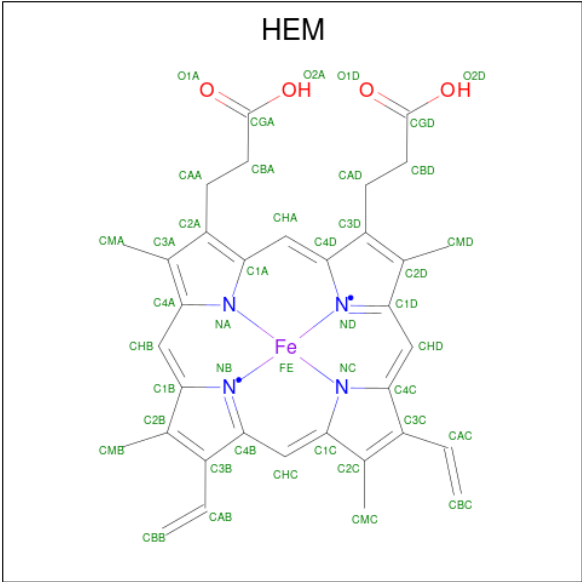
Mol	Chain	Residues	Atoms					AltConf	Trace
72	y	114	Total	C	N	O	S	0	0
			932	615	154	161	2		

- Molecule 73 is 2,3-DIMETHOXY-5-METHYL-6-(3,11,15,19-TETRAMETHYL-EICOSA-2,6,10,14,18-PENTAENYL)-[1,4]BENZOQUINONE (three-letter code: UQ5) (formula: C₃₄H₅₀O₄).



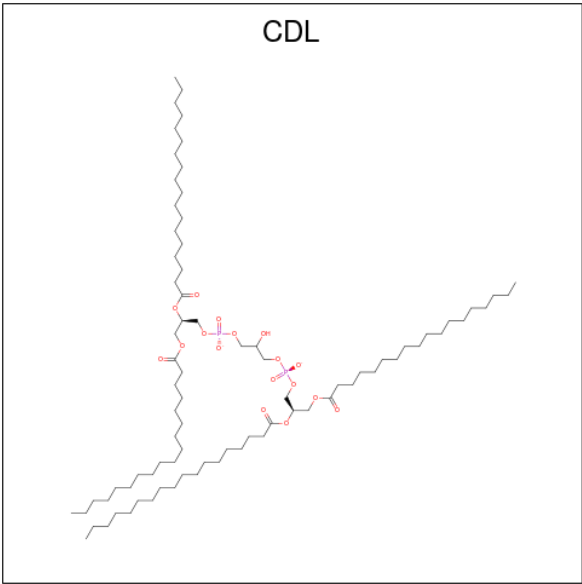
Mol	Chain	Residues	Atoms			AltConf
73	1A	1	Total	C	O	0
			38	34	4	
73	1A	1	Total	C	O	0
			38	34	4	
73	1B	1	Total	C	O	0
			38	34	4	
73	1B	1	Total	C	O	0
			38	34	4	
73	Q	1	Total	C	O	0
			38	34	4	

- Molecule 74 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



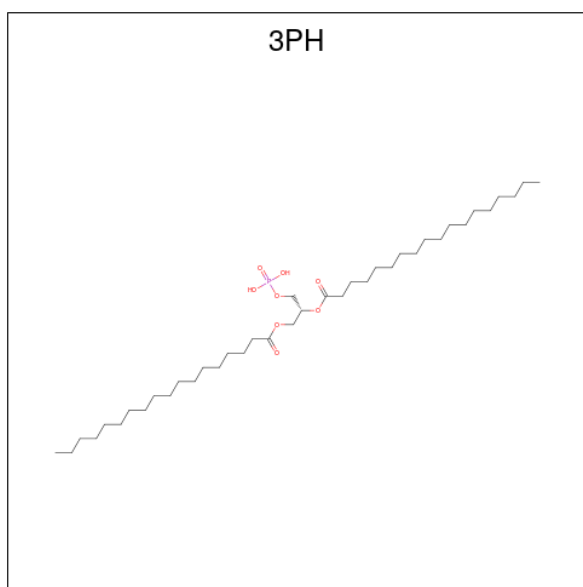
Mol	Chain	Residues	Atoms					AltConf
74	1A	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
74	1A	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
74	1B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
74	1B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 75 is CARDIOLIPIN (three-letter code: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



Mol	Chain	Residues	Atoms				AltConf
75	1A	1	Total	C	O	P	0
			59	40	17	2	
75	1B	1	Total	C	O	P	0
			64	45	17	2	
75	1B	1	Total	C	O	P	0
			71	52	17	2	
75	1E	1	Total	C	O	P	0
			53	34	17	2	
75	1F	1	Total	C	O	P	0
			56	37	17	2	
75	1K	1	Total	C	O	P	0
			79	60	17	2	
75	1L	1	Total	C	O	P	0
			59	40	17	2	
75	1M	1	Total	C	O	P	0
			54	35	17	2	
75	R	1	Total	C	O	P	0
			63	44	17	2	
75	V	1	Total	C	O	P	0
			64	45	17	2	
75	W	1	Total	C	O	P	0
			95	76	17	2	
75	h	1	Total	C	O	P	0
			77	58	17	2	
75	u	1	Total	C	O	P	0
			83	64	17	2	
75	u	1	Total	C	O	P	0
			71	52	17	2	
75	x	1	Total	C	O	P	0
			92	73	17	2	
75	y	1	Total	C	O	P	0
			55	36	17	2	

- Molecule 76 is 1,2-DIACYL-GLYCEROL-3-SN-PHOSPHATE (three-letter code: 3PH) (formula: C₃₉H₇₇O₈P).



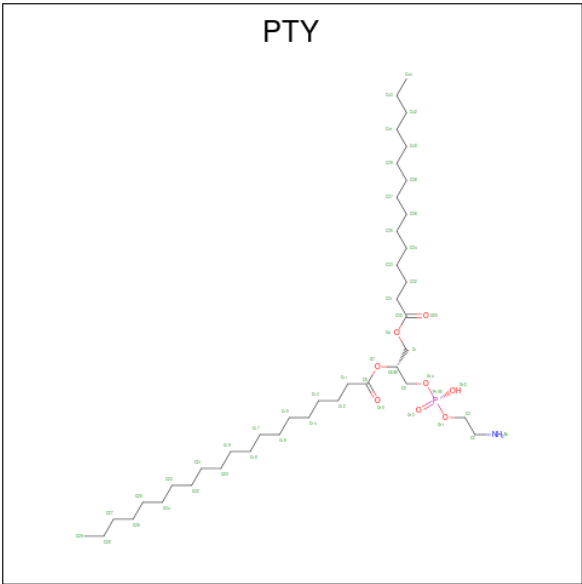
Mol	Chain	Residues	Atoms				AltConf
76	1A	1	Total	C	O	P	0
			31	22	8	1	
76	1B	1	Total	C	O	P	0
			48	39	8	1	
76	1B	1	Total	C	O	P	0
			48	39	8	1	
76	1E	1	Total	C	O	P	0
			40	31	8	1	
76	1K	1	Total	C	O	P	0
			48	39	8	1	
76	1R	1	Total	C	O	P	0
			37	28	8	1	
76	2D	1	Total	C	O	P	0
			32	23	8	1	
76	2I	1	Total	C	O	P	0
			42	33	8	1	
76	3D	1	Total	C	O	P	0
			32	23	8	1	
76	3I	1	Total	C	O	P	0
			42	33	8	1	
76	R	1	Total	C	O	P	0
			32	23	8	1	
76	S	1	Total	C	O	P	0
			37	28	8	1	
76	V	1	Total	C	O	P	0
			42	33	8	1	
76	V	1	Total	C	O	P	0
			41	32	8	1	

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Mol	Chain	Residues	Atoms				AltConf
76	c	1	Total	C	O	P	0
			48	39	8	1	
76	g	1	Total	C	O	P	0
			37	28	8	1	
76	h	1	Total	C	O	P	0
			45	36	8	1	
76	w	1	Total	C	O	P	0
			45	36	8	1	
76	y	1	Total	C	O	P	0
			32	23	8	1	

- Molecule 77 is PHOSPHATIDYLETHANOLAMINE (three-letter code: PTY) (formula: C₄₀H₈₀NO₈P).



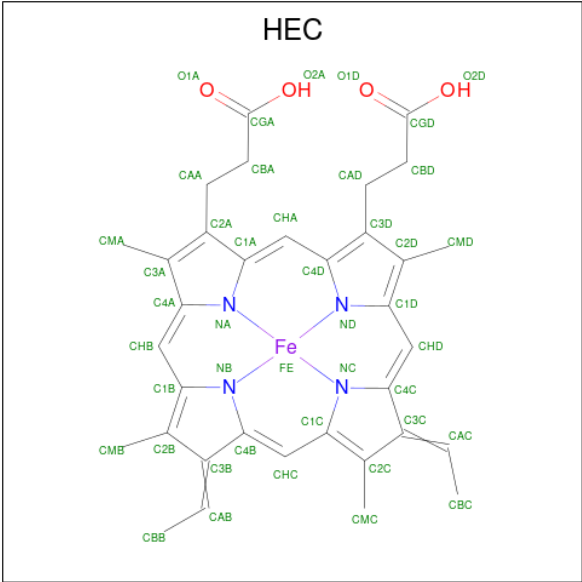
Mol	Chain	Residues	Atoms					AltConf
77	1E	1	Total	C	N	O	P	0
			34	24	1	8	1	
77	1F	1	Total	C	N	O	P	0
			38	28	1	8	1	
77	2D	1	Total	C	N	O	P	0
			35	25	1	8	1	
77	2F	1	Total	C	N	O	P	0
			34	24	1	8	1	
77	3D	1	Total	C	N	O	P	0
			35	25	1	8	1	
77	3F	1	Total	C	N	O	P	0
			34	24	1	8	1	

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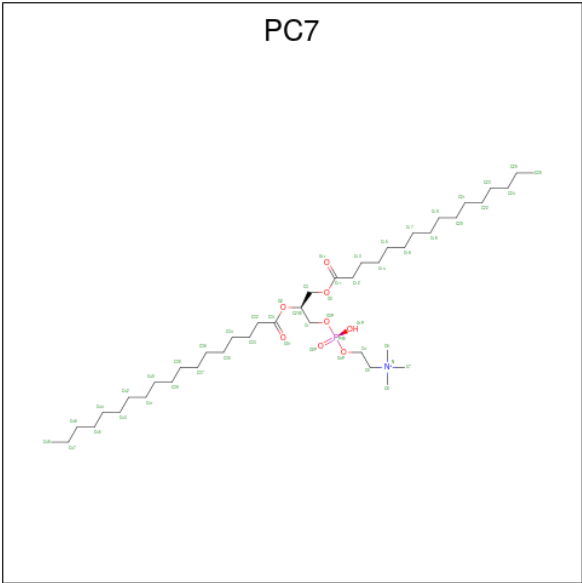
Mol	Chain	Residues	Atoms					AltConf
77	G	1	Total	C	N	O	P	0
			43	33	1	8	1	
77	R	1	Total	C	N	O	P	0
			34	24	1	8	1	
77	R	1	Total	C	N	O	P	0
			44	34	1	8	1	
77	R	1	Total	C	N	O	P	0
			40	30	1	8	1	
77	S	1	Total	C	N	O	P	0
			46	36	1	8	1	
77	T	1	Total	C	N	O	P	0
			50	40	1	8	1	
77	T	1	Total	C	N	O	P	0
			28	18	1	8	1	
77	T	1	Total	C	N	O	P	0
			26	16	1	8	1	
77	V	1	Total	C	N	O	P	0
			40	30	1	8	1	
77	V	1	Total	C	N	O	P	0
			50	40	1	8	1	
77	V	1	Total	C	N	O	P	0
			35	25	1	8	1	
77	e	1	Total	C	N	O	P	0
			25	15	1	8	1	
77	e	1	Total	C	N	O	P	0
			43	33	1	8	1	
77	h	1	Total	C	N	O	P	0
			46	36	1	8	1	
77	x	1	Total	C	N	O	P	0
			50	40	1	8	1	

- Molecule 78 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



Mol	Chain	Residues	Atoms					AltConf
78	1E	1	Total 43	C 34	Fe 1	N 4	O 4	0
78	1F	1	Total 43	C 34	Fe 1	N 4	O 4	0

- Molecule 79 is (7S)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSAN-1-AMINIUM 4-OXIDE (three-letter code: PC7) (formula: C₄₂H₈₅NO₈P).



Mol	Chain	Residues	Atoms					AltConf
79	1G	1	Total	C	N	O	P	0
			36	26	1	8	1	

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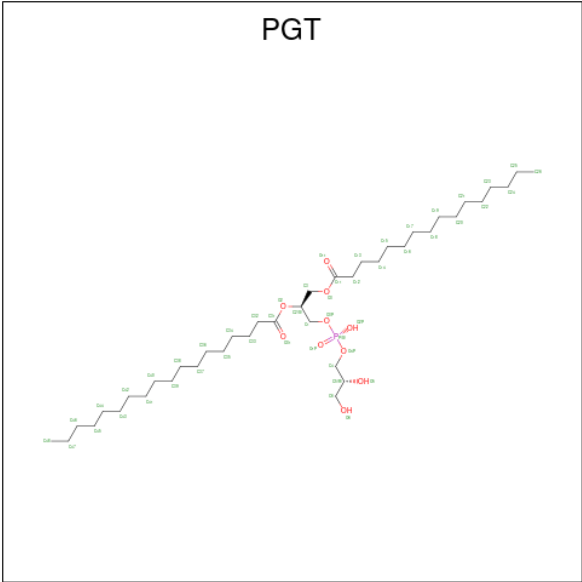
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Mol	Chain	Residues	Atoms					AltConf
79	1H	1	Total	C	N	O	P	0
			39	29	1	8	1	
79	2A	1	Total	C	N	O	P	0
			27	17	1	8	1	
79	3A	1	Total	C	N	O	P	0
			27	17	1	8	1	
79	Q	1	Total	C	N	O	P	0
			33	23	1	8	1	
79	R	1	Total	C	N	O	P	0
			44	34	1	8	1	
79	T	1	Total	C	N	O	P	0
			52	42	1	8	1	
79	u	1	Total	C	N	O	P	0
			42	32	1	8	1	

- Molecule 80 is ZINC ION (three-letter code: ZN) (formula: Zn).

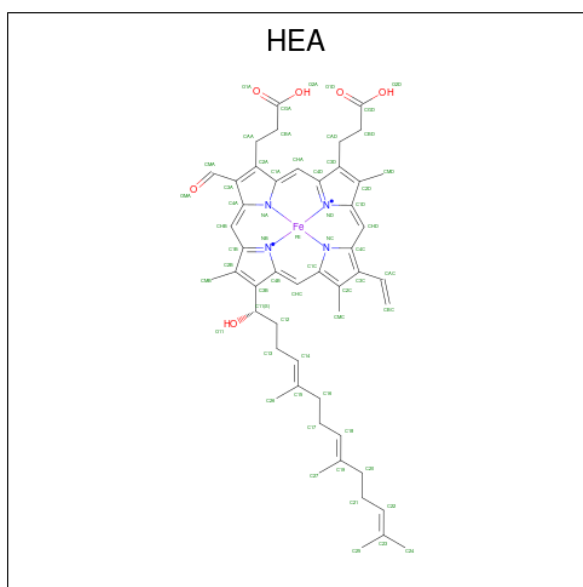
Mol	Chain	Residues	Atoms		AltConf
80	1M	1	Total	Zn	0
			1	1	
80	1N	1	Total	Zn	0
			1	1	
80	s	1	Total	Zn	0
			1	1	

- Molecule 81 is (1S)-2-{{[(2R)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL STEARATE (three-letter code: PGT) (formula: C₄₀H₇₉O₁₀P).



Mol	Chain	Residues	Atoms				AltConf
81	2A	1	Total	C	O	P	0
			33	22	10	1	
81	3A	1	Total	C	O	P	0
			33	22	10	1	
81	T	1	Total	C	O	P	0
			48	37	10	1	
81	T	1	Total	C	O	P	0
			40	29	10	1	
81	b	1	Total	C	O	P	0
			44	33	10	1	
81	l	1	Total	C	O	P	0
			51	40	10	1	

- Molecule 82 is HEME-A (three-letter code: HEA) (formula: C₄₉H₅₆FeN₄O₆).



Mol	Chain	Residues	Atoms					AltConf
82	2A	1	Total 60	C 49	Fe 1	N 4	O 6	0
82	2A	1	Total 60	C 49	Fe 1	N 4	O 6	0
82	3A	1	Total 60	C 49	Fe 1	N 4	O 6	0
82	3A	1	Total 60	C 49	Fe 1	N 4	O 6	0

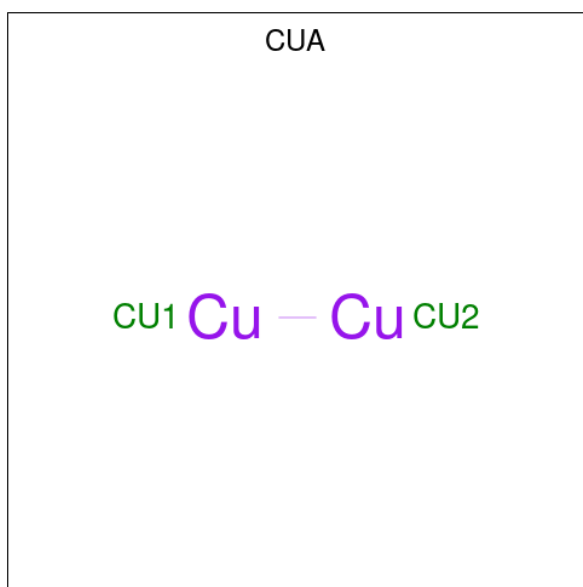
- Molecule 83 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		AltConf
83	2A	1	Total	Cu	0
			1	1	
83	3A	1	Total	Cu	0
			1	1	

- Molecule 84 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

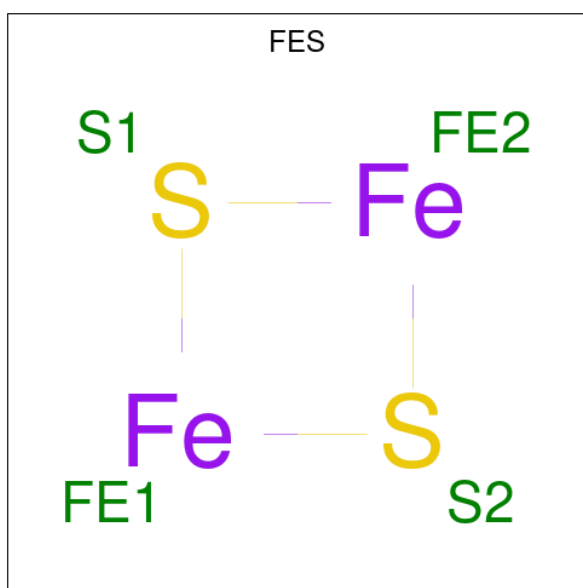
Mol	Chain	Residues	Atoms		AltConf
84	2A	1	Total	Mg	0
			1	1	
84	3A	1	Total	Mg	0
			1	1	

- Molecule 85 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu₂).



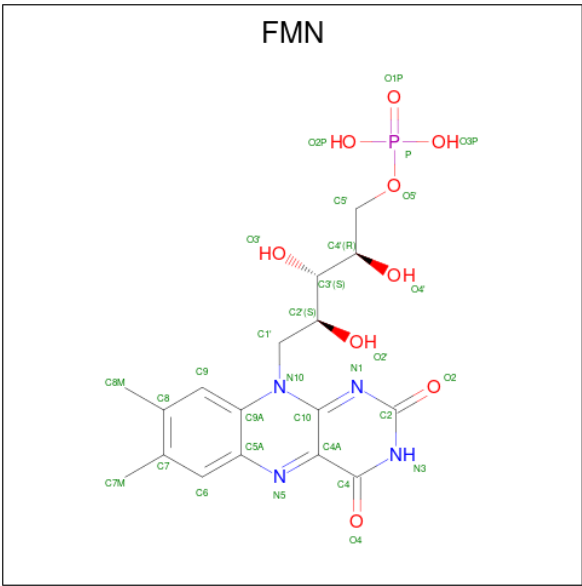
Mol	Chain	Residues	Atoms		AltConf
85	2C	1	Total	Cu	0
			2	2	
85	3C	1	Total	Cu	0
			2	2	

- Molecule 86 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



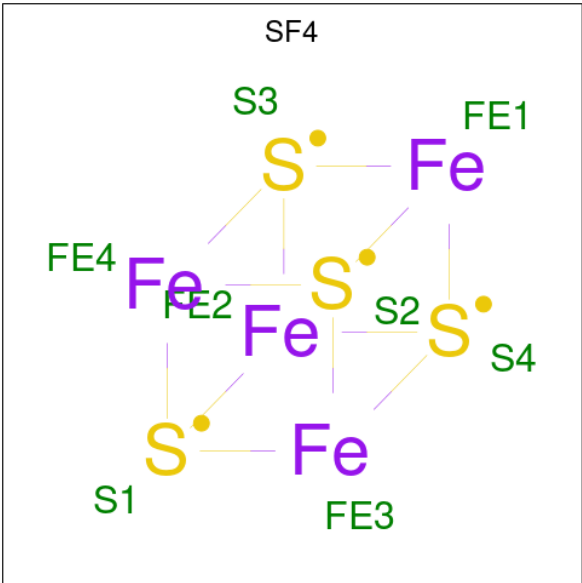
Mol	Chain	Residues	Atoms			AltConf
86	A	1	Total	Fe	S	0
			4	2	2	
86	C	1	Total	Fe	S	0
			4	2	2	

- Molecule 87 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).



Mol	Chain	Residues	Atoms					AltConf
87	B	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 88 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



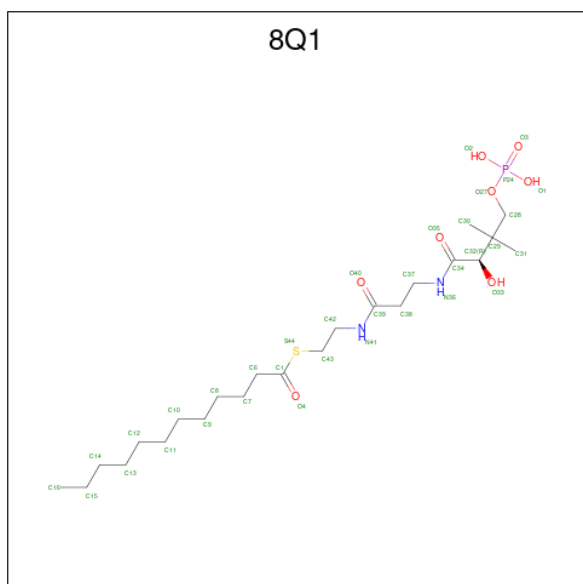
Mol	Chain	Residues	Atoms			AltConf
88	B	1	Total	Fe	S	0
			8	4	4	
88	C	1	Total	Fe	S	0
			8	4	4	

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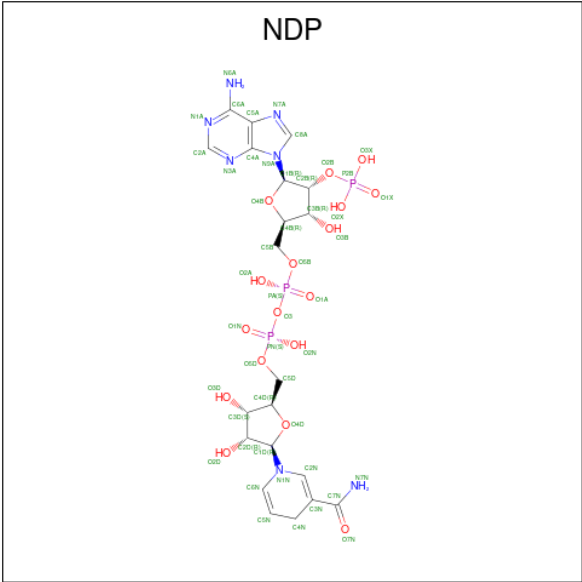
Mol	Chain	Residues	Atoms			AltConf
88	C	1	Total	Fe	S	0
			8	4	4	
88	F	1	Total	Fe	S	0
			8	4	4	
88	G	1	Total	Fe	S	0
			8	4	4	
88	G	1	Total	Fe	S	0
			8	4	4	

- Molecule 89 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-alanyl}amino)ethyl] dodecanethioate (three-letter code: 8Q1) (formula: C₂₃H₄₅N₂O₈PS).



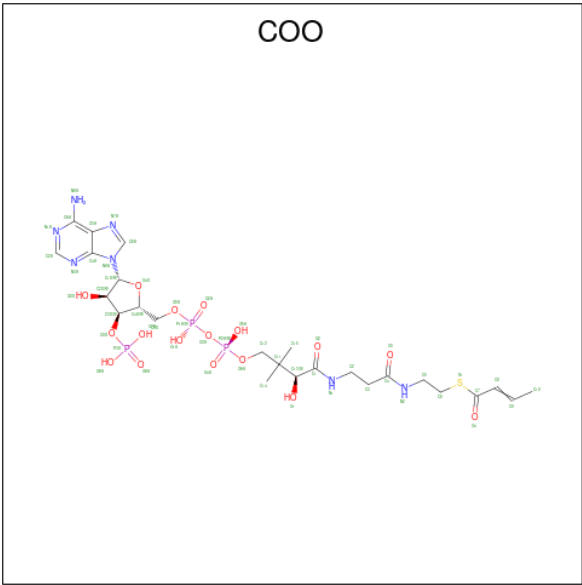
Mol	Chain	Residues	Atoms						AltConf
89	J	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	
89	r	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	

- Molecule 90 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					AltConf
90	P	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 91 is CROTONYL COENZYME A (three-letter code: COO) (formula: $C_{25}H_{40}N_7O_{17}P_3S$).



Mol	Chain	Residues	Atoms						AltConf
91	s	1	Total	C	N	O	P	S	0
			53	25	7	17	3	1	

- Molecule 92 is water.

Mol	Chain	Residues	Atoms		AltConf
92	1A	48	Total 48	O 48	0
92	1B	52	Total 52	O 52	0
92	1C	13	Total 13	O 13	0
92	1D	12	Total 12	O 12	0
92	1E	51	Total 51	O 51	0
92	1F	34	Total 34	O 34	0
92	1G	7	Total 7	O 7	0
92	1H	9	Total 9	O 9	0
92	1I	11	Total 11	O 11	0
92	1J	3	Total 3	O 3	0
92	1K	12	Total 12	O 12	0
92	1L	12	Total 12	O 12	0
92	1M	76	Total 76	O 76	0
92	1N	74	Total 74	O 74	0
92	1O	4	Total 4	O 4	0
92	1P	6	Total 6	O 6	0
92	1Q	27	Total 27	O 27	0
92	1R	32	Total 32	O 32	0
92	1S	29	Total 29	O 29	0
92	1T	28	Total 28	O 28	0
92	A	24	Total 24	O 24	0
92	B	66	Total 66	O 66	0

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Mol	Chain	Residues	Atoms		AltConf
92	C	168	Total 168	O 168	0
92	D	66	Total 66	O 66	0
92	E	87	Total 87	O 87	0
92	F	39	Total 39	O 39	0
92	G	62	Total 62	O 62	0
92	H	16	Total 16	O 16	0
92	I	19	Total 19	O 19	0
92	K	16	Total 16	O 16	0
92	L	68	Total 68	O 68	0
92	M	30	Total 30	O 30	0
92	N	53	Total 53	O 53	0
92	O	6	Total 6	O 6	0
92	P	69	Total 69	O 69	0
92	Q	24	Total 24	O 24	0
92	R	64	Total 64	O 64	0
92	S	22	Total 22	O 22	0
92	T	85	Total 85	O 85	0
92	U	14	Total 14	O 14	0
92	V	99	Total 99	O 99	0
92	W	25	Total 25	O 25	0
92	X	50	Total 50	O 50	0

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Mol	Chain	Residues	Atoms		AltConf
92	Y	4	Total 4	O 4	0
92	Z	20	Total 20	O 20	0
92	a	6	Total 6	O 6	0
92	b	24	Total 24	O 24	0
92	c	1	Total 1	O 1	0
92	d	12	Total 12	O 12	0
92	e	55	Total 55	O 55	0
92	f	10	Total 10	O 10	0
92	g	7	Total 7	O 7	0
92	h	38	Total 38	O 38	0
92	i	30	Total 30	O 30	0
92	j	29	Total 29	O 29	0
92	k	51	Total 51	O 51	0
92	l	17	Total 17	O 17	0
92	m	32	Total 32	O 32	0
92	n	7	Total 7	O 7	0
92	o	51	Total 51	O 51	0
92	p	21	Total 21	O 21	0
92	q	24	Total 24	O 24	0
92	r	12	Total 12	O 12	0
92	s	39	Total 39	O 39	0

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Mol	Chain	Residues	Atoms		AltConf
92	t	55	Total 55	O 55	0
92	u	41	Total 41	O 41	0
92	v	2	Total 2	O 2	0
92	w	16	Total 16	O 16	0
92	x	22	Total 22	O 22	0
92	y	29	Total 29	O 29	0

Chain 1F:  77% 23%

MET ARG THR LEU ARG SER LEU GLY LYS GLY LEU GLY CYS ALA GLU ALA THR SER ARG VAL ALA GLN GLN THR MET PRO VAL VAL ALA MET SER SER SER ASP ALA GLU PRO THR SER LYS ALA ALA HIS THR ALA ALA LEU GLY VAL MET ALA

GLY ILE PHE GLY ALA SER CYS VAL ALA SER ALA N72 R314

- Molecule 4: Complex III subunit 9

Chain 1G:  98%

MET Y2 T60

- Molecule 4: Complex III subunit 9

Chain 1H:  98%

MET Y2 T60

- Molecule 5: Cytochrome b-c1 complex subunit 6

Chain 1I:  99%

MET Y2 K69

- Molecule 5: Cytochrome b-c1 complex subunit 6

Chain 1J:  99%

MET Y2 K69

- Molecule 6: Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 8

Chain 1K:  96%

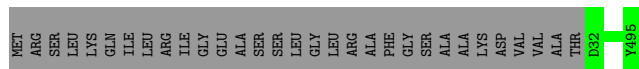
MET ALA PRO R4 Y73

- Molecule 6: Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 8

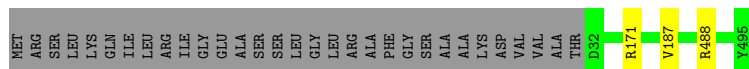
Chain 1L:  96%

MET ALA PRO R4 Y73


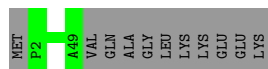
● Molecule 7: MPP-Beta

Chain 1M:  94% 6%


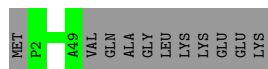
● Molecule 7: MPP-Beta

Chain 1N:  93% 6%

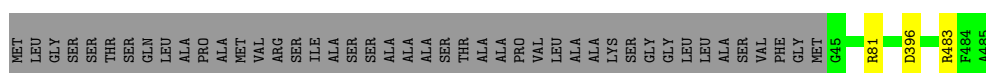
● Molecule 8: Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 10

Chain 1O:  81% 19%


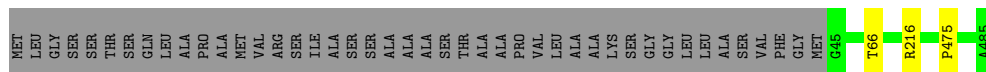
● Molecule 8: Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 10

Chain 1P:  81% 19%

● Molecule 9: Alpha-MPP

Chain 1Q:  90% 9%

● Molecule 9: Alpha-MPP

Chain 1S:  90% 9%

● Molecule 10: Cytochrome b-c1 complex subunit 7

Chain 1R:  99%

● Molecule 10: Cytochrome b-c1 complex subunit 7

MET	T2	D123
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-
- A diagram showing three vertical bars. The first bar is green and labeled 'M1'. The second bar is yellow and labeled 'L417'. The third bar is green and labeled 'S504'. Horizontal lines connect the top and bottom of the first bar to the second bar, and the second bar to the third bar.

-
- A diagram showing three vertical bars of different colors: a blue bar on the left labeled 'M1', a red bar in the middle labeled 'L417', and a blue bar on the right labeled 'S504'. The bars are connected by horizontal lines, suggesting a sequence or relationship between them.

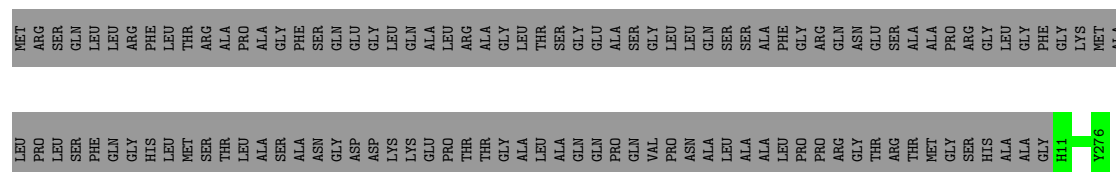
- [illegible]

- | | |
|------|-----|
| Lys | Ser |
| Lys | Ser |
| Val | Glu |
| Val | Gln |
| Leu | Ala |
| Lys | Ala |
| Ala | Gly |
| Ala | Leu |
| Ala | Ser |
| Ala | Ala |
| Ala | Ala |
| Leu | Asn |
| Leu | Lys |
| Ala | Lys |
| Ala | Arg |
| Ala | Arg |
| Leu | Gly |
| Gly | Leu |
| Leu | Ile |
| Thr | Gly |
| Thr | Ser |
| Thr | Gly |
| Thr | Met |
| Ala | Ser |
| Ala | Leu |
| Ala | Gln |
| Ala | Lys |
| D17 | Pro |
| K157 | Ser |
| | Ser |
| | Lys |
| | Pro |
| | Phe |
| | Leu |
| | Val |
| | Trp |
| | Asn |
| | Ala |
| | Ala |
| | Met |
| | Leu |
| | Ser |
| | Phe |
| | Ser |
| | Ser |
| | Lys |
| | Ala |
| | Glu |
| | Gly |
| | Ser |
| | Val |
| | Val |
| | Gln |
| | Gln |
| | Val |
| | Val |
| | Ser |
| | Ala |
| | Val |
| | Glu |
| | Ser |
| | Ala |
| | Ala |
| | Gly |
| | Gln |
| | Pro |
| | Ala |
| | Ala |
| | Val |
| | Gln |
| | Ala |
| | Rhe |

There are no outlier residues recorded for this chain.

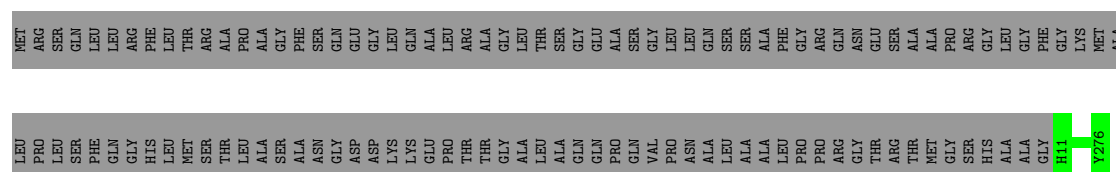
- Molecule 14: Cytochrome c oxidase subunit 3

Chain 2D:



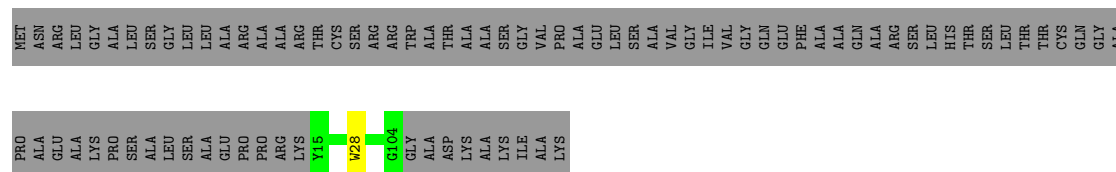
- Molecule 14: Cytochrome c oxidase subunit 3

Chain 3D:  70% 30%



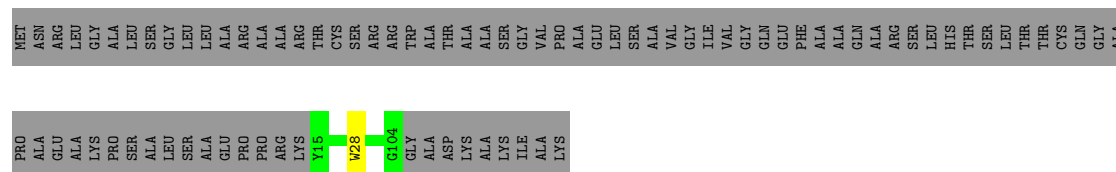
- Molecule 15: Cox5b

Chain 2E:  51% . 49%



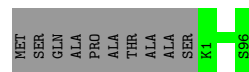
- Molecule 15: Cox5b

Chain 3E: 51% . 49%



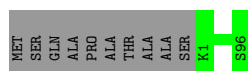
- Molecule 16: Cox5c

Chain 2F:  90% 10%



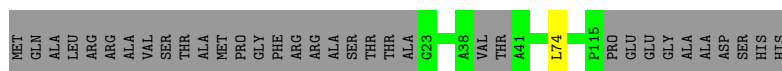
- Molecule 16: Cox5c

Chain 3F:  90% 10%



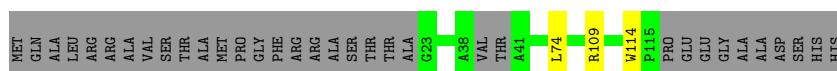
- Molecule 17: Cox6a

Chain 2G:  72% 27%




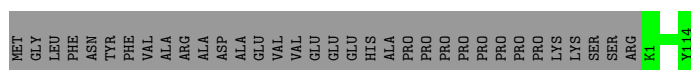
- Molecule 17: Cox6a

Chain 3G:  70% 27%




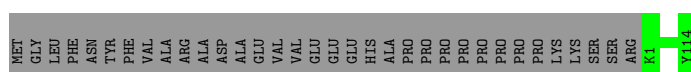
- Molecule 18: Cox6b

Chain 2H:  77% 23%



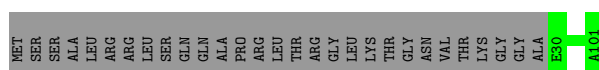
- Molecule 18: Cox6b

Chain 3H:  77% 23%



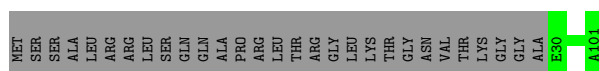
- Molecule 19: Cox7c

Chain 2I:  71% 29%



- Molecule 19: Cox7c

Chain 3I:  71% 29%



- Molecule 20: Cytochrome c oxidase subunit

Chain 2J:  99% .



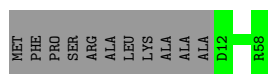
- Molecule 20: Cytochrome c oxidase subunit

Chain 3J: 99%



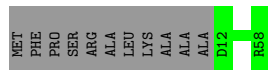
- Molecule 21: Cox7a

Chain 2K: 81% 19%



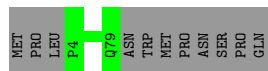
- Molecule 21: Cox7a

Chain 3K: 81% 19%



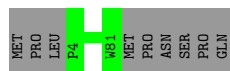
- Molecule 22: CoxIn

Chain 2L: 87% 13%



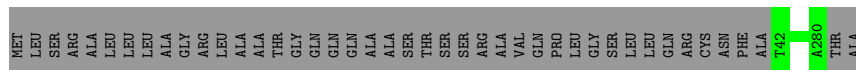
- Molecule 22: CoxIn

Chain 3L: 90% 10%



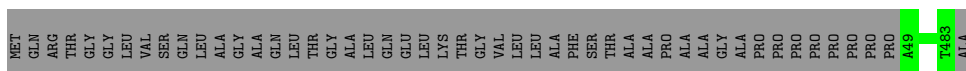
- Molecule 23: NADH:ubiquinone oxidoreductase 24 kD subunit

Chain A: 85% 15%

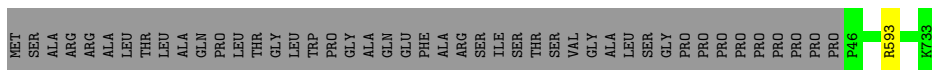


- Molecule 24: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial

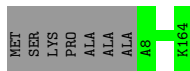
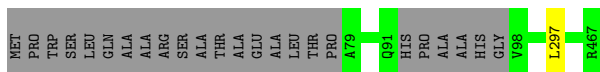
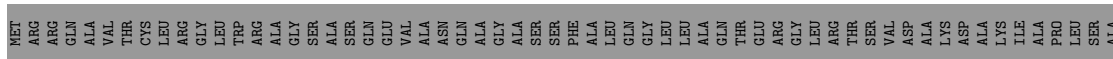
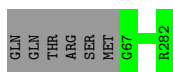
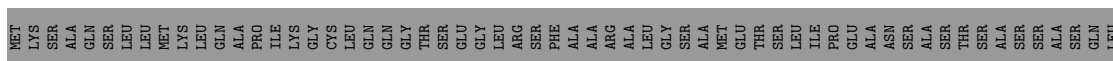
Chain B: 90% 10%



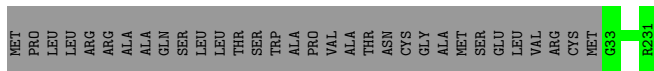
Chain C:  94% 6%



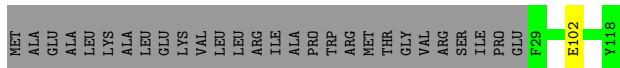
Chain D: 77% 23%




Chain G: 86% 14%

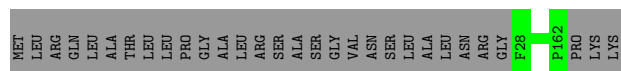


Chain H: 75% . 24%



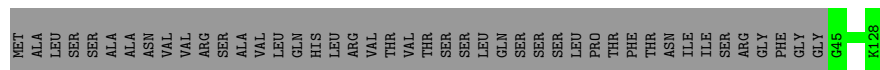
- Molecule 31: Mitochondrial NADH:ubiquinone oxidoreductase 18 kDa subunit

Chain I:  82% 18%



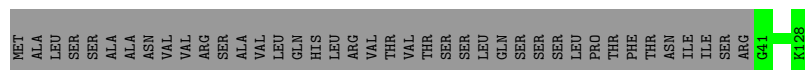
- Molecule 32: Acyl carrier protein

Chain J:  66% 34%




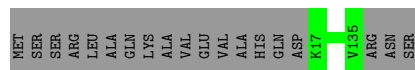
- Molecule 32: Acyl carrier protein

Chain r:  69% 31%




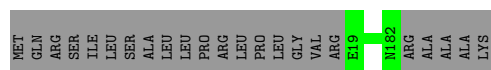
- Molecule 33: NADH:ubiquinone oxidoreductase B14 subunit

Chain K:  86% 14%




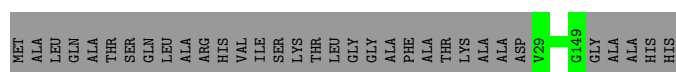
- Molecule 34: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

Chain L:  88% 12%



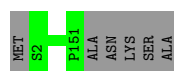
- Molecule 35: NADH:ubiquinone oxidoreductase 13 kD-like subunit

Chain M:  79% 21%

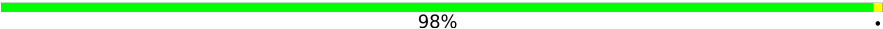


- Molecule 36: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

Chain N:  96%



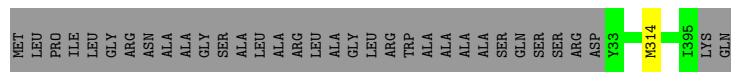
- Molecule 37: NADH:ubiquinone oxidoreductase B8 subunit

Chain O:  98% ..



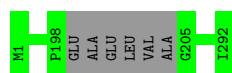
- Molecule 38: Putative NADH:ubiquinone oxidoreductase 39 kDa subunit

Chain P:  91% 9%



- Molecule 39: NADH-ubiquinone oxidoreductase chain 1

Chain Q:  98% .



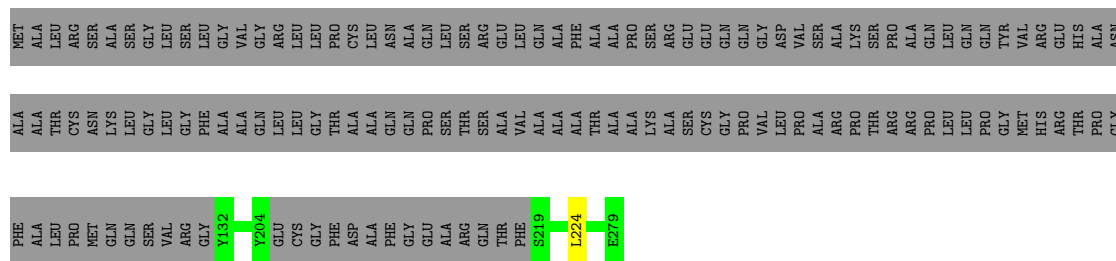
- Molecule 40: NADH-ubiquinone oxidoreductase chain 2

Chain R:  100%

There are no outlier residues recorded for this chain.

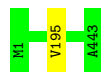
- Molecule 41: NADH-ubiquinone oxidoreductase chain 3

Chain S:  48% 52%



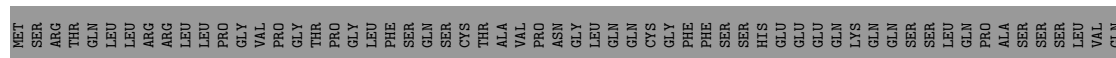
- Molecule 42: NADH-ubiquinone oxidoreductase chain 4

Chain T:  100%



- Molecule 43: NADH dehydrogenase subunit 4L

Chain U:  46% 54%





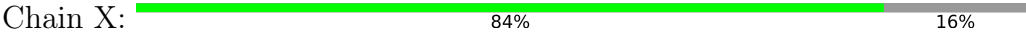
● Molecule 44: NADH-ubiquinone oxidoreductase chain 5



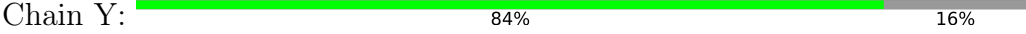
● Molecule 45: NADH-ubiquinone oxidoreductase chain 6



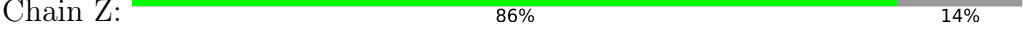
● Molecule 46: ASHI



● Molecule 47: P9



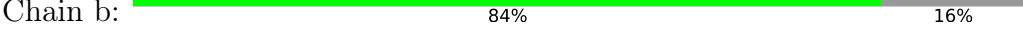
● Molecule 48: KFYI

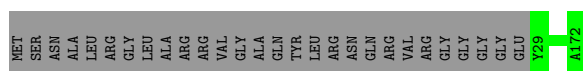


● Molecule 49: AGGG



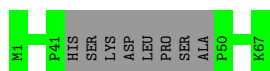
● Molecule 50: ESSS





- Molecule 51: B9

Chain c: 88% 12%



- Molecule 52: Mitochondrial NADH:ubiquinone oxidoreductase 10 kDa subunit

Chain d: 99%



- Molecule 53: Mitochondrial NADH:ubiquinone oxidoreductase 23 kDa subunit

Chain e: 99%



- Molecule 54: Mitochondrial NADH:ubiquinone oxidoreductase 7.5 kDa subunit

Chain f: 98%



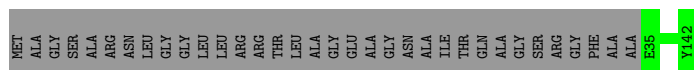
- Molecule 55: Mitochondrial putative NADH:ubiquinone oxidoreductase 6.5 kDa subunit

Chain g: 91% 9%



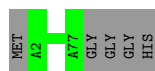
- Molecule 56: Mitochondrial NADH:ubiquinone oxidoreductase 13 kDa subunit

Chain h: 76% 24%



- Molecule 57: NADH:ubiquinone oxidoreductase 15 kDa subunit-like

Chain i: 94% 6%



- Molecule 58: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

Chain j: 99%



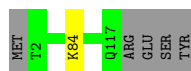
- Molecule 59: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

Chain k: 100%

There are no outlier residues recorded for this chain.

- Molecule 60: NADH:ubiquinone oxidoreductase 20,9 kD-like subunit

Chain l: 95%



- Molecule 61: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13

Chain m: 97%



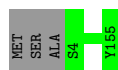
- Molecule 62: Putative NADH:ubiquinone oxidoreductase 12.5 kDa subunit

Chain n: 98%



- Molecule 63: Putative NADH:ubiquinone oxidoreductase 17.8 kDa subunit

Chain o: 98%



- Molecule 64: Mitochondrial NADH:ubiquinone oxidoreductase 16 kDa subunit

Chain p: 99%



- Molecule 66: Mitochondrial NADH:ubiquinone oxidoreductase 32 kDa subunit

- Molecule 67: CAG2 - CA-like

- Molecule 68: CAG1

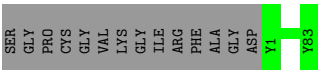
- Molecule 69: P10

There are no outlier residues recorded for this chain.

- Molecule 70: Mitochondrial NADH:ubiquinone oxidoreductase 9 kDa subunit

- Molecule 71: NUOP8





● Molecule 72: NUOP7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83443	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, HEM, CDL, PC7, PTY, SF4, ZN, CU, FMN, FES, HEC, HEA, 3PH, CUA, NDP, UQ5, 8Q1, PGT, COO

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	1A	0.34	0/3060	0.52	1/4187 (0.0%)
1	1B	0.35	0/3060	0.53	0/4187
2	1C	0.28	0/1643	0.50	0/2233
2	1D	0.28	0/1643	0.50	0/2233
3	1E	0.34	0/1953	0.53	1/2654 (0.0%)
3	1F	0.33	0/1953	0.52	0/2654
4	1G	0.32	0/496	0.54	0/667
4	1H	0.32	0/496	0.50	0/667
5	1I	0.31	0/567	0.50	0/766
5	1J	0.30	0/567	0.45	0/766
6	1K	0.33	0/609	0.54	0/817
6	1L	0.31	0/609	0.54	0/817
7	1M	0.31	0/3723	0.54	0/5046
7	1N	0.30	0/3723	0.54	0/5046
8	1O	0.28	0/385	0.53	0/531
8	1P	0.29	0/385	0.59	0/531
9	1Q	0.31	0/3258	0.54	0/4439
9	1S	0.30	0/3258	0.53	0/4439
10	1R	0.31	0/996	0.55	0/1349
10	1T	0.33	0/996	0.57	0/1349
11	2A	0.33	0/4011	0.54	1/5484 (0.0%)
11	3A	0.34	0/4011	0.56	1/5484 (0.0%)
12	2B	0.30	0/1204	0.51	0/1641
12	3B	0.30	0/1204	0.52	0/1641
13	2C	0.30	0/1237	0.53	0/1676
13	3C	0.32	0/1237	0.55	0/1676
14	2D	0.32	0/2152	0.49	0/2937
14	3D	0.32	0/2152	0.50	0/2937
15	2E	0.31	0/757	0.63	0/1029
15	3E	0.32	0/757	0.60	0/1029
16	2F	0.30	0/726	0.46	0/974

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	3F	0.30	0/726	0.46	0/974
17	2G	0.30	0/762	0.58	1/1038 (0.1%)
17	3G	0.30	0/762	0.55	1/1038 (0.1%)
18	2H	0.30	0/980	0.51	0/1325
18	3H	0.32	0/980	0.55	0/1325
19	2I	0.33	0/619	0.51	0/839
19	3I	0.31	0/619	0.50	0/839
20	2J	0.30	0/839	0.51	0/1143
20	3J	0.31	0/839	0.53	0/1143
21	2K	0.31	0/392	0.51	0/531
21	3K	0.32	0/392	0.51	0/531
22	2L	0.31	0/621	0.56	0/841
22	3L	0.30	0/645	0.55	0/875
23	A	0.31	0/1878	0.54	0/2549
24	B	0.33	0/3400	0.56	0/4573
25	C	0.31	0/5272	0.56	0/7143
26	D	0.36	0/1843	0.58	0/2506
27	E	0.38	0/3158	0.61	1/4270 (0.0%)
28	F	0.41	0/1258	0.57	0/1706
29	G	0.32	0/1648	0.60	0/2222
30	H	0.35	0/773	0.60	1/1046 (0.1%)
31	I	0.31	0/1061	0.49	0/1441
32	J	0.29	0/649	0.49	0/875
32	r	0.32	0/673	0.47	0/906
33	K	0.34	0/1007	0.59	0/1348
34	L	0.33	0/1306	0.59	0/1769
35	M	0.31	0/936	0.52	0/1276
36	N	0.32	0/1277	0.52	0/1735
37	O	0.28	0/772	0.60	1/1037 (0.1%)
38	P	0.30	0/2879	0.55	1/3905 (0.0%)
39	Q	0.36	0/2234	0.58	0/3034
40	R	0.36	0/3100	0.55	0/4226
41	S	0.37	0/1106	0.57	1/1512 (0.1%)
42	T	0.37	1/3533 (0.0%)	0.56	0/4825
43	U	0.34	0/819	0.53	0/1112
44	V	0.36	0/4258	0.57	2/5792 (0.0%)
45	W	0.34	0/1239	0.52	0/1686
46	X	0.36	0/1081	0.55	0/1479
47	Y	0.32	0/411	0.49	0/557
48	Z	0.33	0/894	0.53	0/1218
49	a	0.33	0/698	0.47	0/949
50	b	0.35	0/1201	0.56	0/1623
51	c	0.31	0/463	0.53	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
52	d	0.37	0/721	0.53	0/968
53	e	0.34	0/1688	0.54	0/2301
54	f	0.32	0/547	0.53	0/740
55	g	0.30	0/433	0.55	0/587
56	h	0.34	0/948	0.55	0/1285
57	i	0.32	0/644	0.60	0/860
58	j	0.34	0/732	0.54	0/983
59	k	0.32	0/1011	0.55	0/1361
60	l	0.33	0/936	0.49	0/1278
61	m	0.36	0/1155	0.56	0/1558
62	n	0.32	0/886	0.50	0/1188
63	o	0.33	0/1265	0.59	0/1705
64	p	0.32	0/1095	0.55	0/1480
65	q	0.32	0/1308	0.51	0/1779
66	s	0.32	0/2353	0.53	1/3202 (0.0%)
67	t	0.32	0/2043	0.56	0/2778
68	u	0.32	0/1730	0.54	0/2341
69	v	0.33	0/369	0.48	0/498
70	w	0.34	0/521	0.49	0/702
71	x	0.34	0/727	0.49	0/994
72	y	0.34	0/963	0.52	0/1313
All	All	0.33	1/134906 (0.0%)	0.54	14/183172 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1A	0	1
1	1B	0	1
17	3G	0	1
53	e	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	T	195	VAL	CB-CG1	-5.47	1.41	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	O	7	LEU	CA-CB-CG	7.19	131.83	115.30
27	E	297	LEU	CA-CB-CG	6.98	131.35	115.30
17	2G	74	LEU	CA-CB-CG	6.55	130.36	115.30
17	3G	74	LEU	CA-CB-CG	6.43	130.10	115.30
11	3A	417	LEU	CA-CB-CG	6.25	129.68	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1A	184	TYR	Sidechain
1	1B	184	TYR	Sidechain
17	3G	114	TRP	Peptide
53	e	147	MET	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1A	374/381 (98%)	363 (97%)	11 (3%)	0	100	100
1	1B	374/381 (98%)	366 (98%)	8 (2%)	0	100	100
2	1C	205/262 (78%)	194 (95%)	11 (5%)	0	100	100
2	1D	205/262 (78%)	201 (98%)	4 (2%)	0	100	100
3	1E	241/314 (77%)	236 (98%)	5 (2%)	0	100	100
3	1F	241/314 (77%)	235 (98%)	6 (2%)	0	100	100
4	1G	57/60 (95%)	57 (100%)	0	0	100	100
4	1H	57/60 (95%)	57 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	1I	66/69 (96%)	66 (100%)	0	0	100	100
5	1J	66/69 (96%)	64 (97%)	2 (3%)	0	100	100
6	1K	68/73 (93%)	67 (98%)	1 (2%)	0	100	100
6	1L	68/73 (93%)	65 (96%)	3 (4%)	0	100	100
7	1M	462/495 (93%)	454 (98%)	8 (2%)	0	100	100
7	1N	462/495 (93%)	456 (99%)	5 (1%)	1 (0%)	44	71
8	1O	46/59 (78%)	43 (94%)	3 (6%)	0	100	100
8	1P	46/59 (78%)	44 (96%)	2 (4%)	0	100	100
9	1Q	439/485 (90%)	418 (95%)	20 (5%)	1 (0%)	44	71
9	1S	439/485 (90%)	425 (97%)	12 (3%)	2 (0%)	25	54
10	1R	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
10	1T	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
11	2A	502/504 (100%)	489 (97%)	13 (3%)	0	100	100
11	3A	502/504 (100%)	490 (98%)	12 (2%)	0	100	100
12	2B	139/284 (49%)	136 (98%)	3 (2%)	0	100	100
12	3B	139/284 (49%)	135 (97%)	4 (3%)	0	100	100
13	2C	151/153 (99%)	144 (95%)	7 (5%)	0	100	100
13	3C	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
14	2D	264/382 (69%)	255 (97%)	9 (3%)	0	100	100
14	3D	264/382 (69%)	254 (96%)	10 (4%)	0	100	100
15	2E	88/175 (50%)	85 (97%)	2 (2%)	1 (1%)	12	35
15	3E	88/175 (50%)	85 (97%)	2 (2%)	1 (1%)	12	35
16	2F	84/96 (88%)	81 (96%)	3 (4%)	0	100	100
16	3F	84/96 (88%)	80 (95%)	4 (5%)	0	100	100
17	2G	87/125 (70%)	78 (90%)	9 (10%)	0	100	100
17	3G	87/125 (70%)	80 (92%)	7 (8%)	0	100	100
18	2H	112/148 (76%)	108 (96%)	4 (4%)	0	100	100
18	3H	112/148 (76%)	108 (96%)	4 (4%)	0	100	100
19	2I	70/101 (69%)	67 (96%)	3 (4%)	0	100	100
19	3I	70/101 (69%)	67 (96%)	3 (4%)	0	100	100
20	2J	102/105 (97%)	100 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	3J	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
21	2K	45/58 (78%)	44 (98%)	1 (2%)	0	100	100
21	3K	45/58 (78%)	44 (98%)	1 (2%)	0	100	100
22	2L	74/87 (85%)	70 (95%)	4 (5%)	0	100	100
22	3L	76/87 (87%)	72 (95%)	4 (5%)	0	100	100
23	A	237/282 (84%)	228 (96%)	9 (4%)	0	100	100
24	B	433/484 (90%)	417 (96%)	16 (4%)	0	100	100
25	C	686/733 (94%)	667 (97%)	19 (3%)	0	100	100
26	D	214/282 (76%)	204 (95%)	10 (5%)	0	100	100
27	E	379/467 (81%)	368 (97%)	11 (3%)	0	100	100
28	F	155/164 (94%)	149 (96%)	6 (4%)	0	100	100
29	G	197/231 (85%)	189 (96%)	8 (4%)	0	100	100
30	H	88/118 (75%)	81 (92%)	7 (8%)	0	100	100
31	I	133/165 (81%)	130 (98%)	3 (2%)	0	100	100
32	J	82/128 (64%)	76 (93%)	6 (7%)	0	100	100
32	r	86/128 (67%)	84 (98%)	2 (2%)	0	100	100
33	K	117/138 (85%)	115 (98%)	2 (2%)	0	100	100
34	L	162/187 (87%)	155 (96%)	7 (4%)	0	100	100
35	M	119/154 (77%)	111 (93%)	8 (7%)	0	100	100
36	N	148/156 (95%)	145 (98%)	3 (2%)	0	100	100
37	O	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
38	P	361/397 (91%)	350 (97%)	11 (3%)	0	100	100
39	Q	282/292 (97%)	274 (97%)	8 (3%)	0	100	100
40	R	385/387 (100%)	369 (96%)	16 (4%)	0	100	100
41	S	130/279 (47%)	128 (98%)	2 (2%)	0	100	100
42	T	441/443 (100%)	431 (98%)	10 (2%)	0	100	100
43	U	103/227 (45%)	102 (99%)	1 (1%)	0	100	100
44	V	544/546 (100%)	525 (96%)	18 (3%)	1 (0%)	44	71
45	W	155/162 (96%)	151 (97%)	4 (3%)	0	100	100
46	X	123/149 (83%)	117 (95%)	6 (5%)	0	100	100
47	Y	52/64 (81%)	52 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	Z	105/124 (85%)	100 (95%)	5 (5%)	0	100	100
49	a	80/129 (62%)	78 (98%)	1 (1%)	1 (1%)	10	30
50	b	142/172 (83%)	139 (98%)	3 (2%)	0	100	100
51	c	55/67 (82%)	52 (94%)	3 (6%)	0	100	100
52	d	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
53	e	216/219 (99%)	214 (99%)	1 (0%)	1 (0%)	25	54
54	f	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
55	g	48/55 (87%)	42 (88%)	6 (12%)	0	100	100
56	h	106/142 (75%)	97 (92%)	9 (8%)	0	100	100
57	i	74/81 (91%)	73 (99%)	1 (1%)	0	100	100
58	j	83/86 (96%)	80 (96%)	3 (4%)	0	100	100
59	k	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
60	l	114/121 (94%)	110 (96%)	4 (4%)	0	100	100
61	m	134/142 (94%)	133 (99%)	1 (1%)	0	100	100
62	n	102/106 (96%)	100 (98%)	2 (2%)	0	100	100
63	o	150/155 (97%)	145 (97%)	5 (3%)	0	100	100
64	p	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
65	q	155/197 (79%)	149 (96%)	6 (4%)	0	100	100
66	s	310/312 (99%)	303 (98%)	7 (2%)	0	100	100
67	t	251/279 (90%)	243 (97%)	8 (3%)	0	100	100
68	u	226/229 (99%)	220 (97%)	6 (3%)	0	100	100
69	v	43/45 (96%)	43 (100%)	0	0	100	100
70	w	62/109 (57%)	61 (98%)	1 (2%)	0	100	100
71	x	81/157 (52%)	81 (100%)	0	0	100	100
72	y	112/118 (95%)	111 (99%)	1 (1%)	0	100	100
All	All	16540/19385 (85%)	16027 (97%)	504 (3%)	9 (0%)	50	76

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	1Q	396	ASP
15	2E	28	TRP
15	3E	28	TRP

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Mol	Chain	Res	Type
49	a	43	TYR
9	1S	66	THR

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	1A	312/317 (98%)	311 (100%)	1 (0%)	91	97
1	1B	312/317 (98%)	309 (99%)	3 (1%)	73	91
2	1C	171/213 (80%)	170 (99%)	1 (1%)	84	94
2	1D	171/213 (80%)	171 (100%)	0	100	100
3	1E	191/238 (80%)	191 (100%)	0	100	100
3	1F	191/238 (80%)	191 (100%)	0	100	100
4	1G	52/53 (98%)	52 (100%)	0	100	100
4	1H	52/53 (98%)	52 (100%)	0	100	100
5	1I	58/59 (98%)	58 (100%)	0	100	100
5	1J	58/59 (98%)	58 (100%)	0	100	100
6	1K	62/64 (97%)	62 (100%)	0	100	100
6	1L	62/64 (97%)	62 (100%)	0	100	100
7	1M	390/413 (94%)	390 (100%)	0	100	100
7	1N	390/413 (94%)	388 (100%)	2 (0%)	86	95
8	1O	38/47 (81%)	38 (100%)	0	100	100
8	1P	38/47 (81%)	38 (100%)	0	100	100
9	1Q	333/362 (92%)	331 (99%)	2 (1%)	84	94
9	1S	333/362 (92%)	332 (100%)	1 (0%)	91	97
10	1R	106/107 (99%)	106 (100%)	0	100	100
10	1T	106/107 (99%)	106 (100%)	0	100	100
11	2A	408/408 (100%)	408 (100%)	0	100	100
11	3A	408/408 (100%)	408 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	2B	132/224 (59%)	132 (100%)	0	100	100
12	3B	132/224 (59%)	132 (100%)	0	100	100
13	2C	137/137 (100%)	137 (100%)	0	100	100
13	3C	137/137 (100%)	137 (100%)	0	100	100
14	2D	211/294 (72%)	211 (100%)	0	100	100
14	3D	211/294 (72%)	211 (100%)	0	100	100
15	2E	79/137 (58%)	79 (100%)	0	100	100
15	3E	79/137 (58%)	79 (100%)	0	100	100
16	2F	66/72 (92%)	66 (100%)	0	100	100
16	3F	66/72 (92%)	66 (100%)	0	100	100
17	2G	75/100 (75%)	75 (100%)	0	100	100
17	3G	75/100 (75%)	74 (99%)	1 (1%)	65	88
18	2H	103/132 (78%)	103 (100%)	0	100	100
18	3H	103/132 (78%)	103 (100%)	0	100	100
19	2I	58/80 (72%)	58 (100%)	0	100	100
19	3I	58/80 (72%)	58 (100%)	0	100	100
20	2J	83/84 (99%)	83 (100%)	0	100	100
20	3J	83/84 (99%)	83 (100%)	0	100	100
21	2K	39/46 (85%)	39 (100%)	0	100	100
21	3K	39/46 (85%)	39 (100%)	0	100	100
22	2L	63/74 (85%)	63 (100%)	0	100	100
22	3L	65/74 (88%)	65 (100%)	0	100	100
23	A	197/228 (86%)	197 (100%)	0	100	100
24	B	344/377 (91%)	344 (100%)	0	100	100
25	C	537/572 (94%)	536 (100%)	1 (0%)	92	97
26	D	196/248 (79%)	196 (100%)	0	100	100
27	E	329/388 (85%)	329 (100%)	0	100	100
28	F	129/133 (97%)	129 (100%)	0	100	100
29	G	172/198 (87%)	172 (100%)	0	100	100
30	H	82/105 (78%)	82 (100%)	0	100	100
31	I	111/134 (83%)	111 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	J	71/108 (66%)	71 (100%)	0	100	100
32	r	72/108 (67%)	72 (100%)	0	100	100
33	K	106/122 (87%)	106 (100%)	0	100	100
34	L	130/148 (88%)	130 (100%)	0	100	100
35	M	100/121 (83%)	100 (100%)	0	100	100
36	N	128/132 (97%)	128 (100%)	0	100	100
37	O	80/81 (99%)	80 (100%)	0	100	100
38	P	305/327 (93%)	305 (100%)	0	100	100
39	Q	230/234 (98%)	230 (100%)	0	100	100
40	R	321/321 (100%)	321 (100%)	0	100	100
41	S	111/217 (51%)	111 (100%)	0	100	100
42	T	374/374 (100%)	374 (100%)	0	100	100
43	U	84/180 (47%)	84 (100%)	0	100	100
44	V	439/439 (100%)	439 (100%)	0	100	100
45	W	131/135 (97%)	131 (100%)	0	100	100
46	X	105/122 (86%)	105 (100%)	0	100	100
47	Y	38/46 (83%)	38 (100%)	0	100	100
48	Z	93/102 (91%)	93 (100%)	0	100	100
49	a	68/98 (69%)	68 (100%)	0	100	100
50	b	119/138 (86%)	119 (100%)	0	100	100
51	c	49/56 (88%)	49 (100%)	0	100	100
52	d	63/64 (98%)	63 (100%)	0	100	100
53	e	163/164 (99%)	163 (100%)	0	100	100
54	f	52/53 (98%)	52 (100%)	0	100	100
55	g	40/45 (89%)	40 (100%)	0	100	100
56	h	91/110 (83%)	91 (100%)	0	100	100
57	i	65/67 (97%)	65 (100%)	0	100	100
58	j	72/73 (99%)	72 (100%)	0	100	100
59	k	102/102 (100%)	102 (100%)	0	100	100
60	l	94/99 (95%)	93 (99%)	1 (1%)	70	90
61	m	118/122 (97%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	n	92/94 (98%)	92 (100%)	0	100	100
63	o	130/132 (98%)	130 (100%)	0	100	100
64	p	109/110 (99%)	109 (100%)	0	100	100
65	q	135/165 (82%)	135 (100%)	0	100	100
66	s	243/243 (100%)	243 (100%)	0	100	100
67	t	212/233 (91%)	211 (100%)	1 (0%)	86	95
68	u	180/181 (99%)	180 (100%)	0	100	100
69	v	38/38 (100%)	38 (100%)	0	100	100
70	w	55/91 (60%)	55 (100%)	0	100	100
71	x	70/130 (54%)	70 (100%)	0	100	100
72	y	102/106 (96%)	102 (100%)	0	100	100
All	All	13813/15736 (88%)	13799 (100%)	14 (0%)	92	98

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	1Q	81	ARG
9	1Q	483	ARG
67	t	142	TYR
25	C	593	ARG
60	l	84	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	1B	261	ASN
25	C	279	ASN
25	C	297	ASN
25	C	618	GLN
60	l	41	ASN

5.3.3 RNA ⓘ

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 107 ligands modelled in this entry, 7 are monoatomic - leaving 100 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	$\# Z > 2$
88	SF4	C	803	25	0,12,12	-	-	-		
74	HEM	1A	403	1	41,50,50	1.42	4 (9%)	45,82,82	1.76	11 (24%)
81	PGT	T	502	-	47,47,50	0.53	0	50,53,56	0.56	1 (2%)
77	PTY	1E	403	-	33,33,49	0.55	0	36,38,54	0.50	0
77	PTY	T	501	-	49,49,49	0.46	0	52,54,54	0.62	1 (1%)
79	PC7	2A	606	-	26,26,51	0.66	0	32,34,59	0.70	0
77	PTY	T	504	-	27,27,49	0.65	0	30,32,54	0.48	0
82	HEA	3A	602	11	57,67,67	2.05	16 (28%)	61,103,103	2.43	25 (40%)
81	PGT	2A	601	-	32,32,50	0.61	0	35,38,56	0.60	0
79	PC7	T	503	-	51,51,51	0.50	0	57,59,59	0.59	0
79	PC7	1H	101	-	38,38,51	0.57	0	44,46,59	0.56	0
76	3PH	R	401	-	31,31,47	0.75	1 (3%)	35,36,52	0.73	2 (5%)
76	3PH	1A	406	-	30,30,47	0.78	1 (3%)	34,35,52	0.69	1 (2%)
77	PTY	V	604	-	39,39,49	0.54	0	42,44,54	0.50	0
77	PTY	V	605	-	49,49,49	0.46	0	52,54,54	0.38	0
82	HEA	2A	602	11	57,67,67	2.06	17 (29%)	61,103,103	2.43	25 (40%)
86	FES	C	801	25	0,4,4	-	-	-		
79	PC7	3A	606	-	26,26,51	0.66	0	32,34,59	0.65	0
86	FES	A	301	23	0,4,4	-	-	-		
76	3PH	y	201	-	31,31,47	0.78	1 (3%)	35,36,52	0.66	1 (2%)
81	PGT	3A	601	-	32,32,50	0.59	0	35,38,56	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
78	HEC	1E	404	3	32,50,50	2.19	3 (9%)	24,82,82	1.81	5 (20%)
75	CDL	1K	101	-	78,78,99	0.43	0	84,90,111	0.28	0
76	3PH	1R	201	-	36,36,47	0.71	1 (2%)	40,41,52	0.70	1 (2%)
79	PC7	u	601	-	41,41,51	0.55	0	47,49,59	0.68	2 (4%)
77	PTY	G	303	-	42,42,49	0.49	0	45,47,54	0.44	0
75	CDL	R	405	-	62,62,99	0.40	0	68,74,111	0.28	0
75	CDL	y	202	-	54,54,99	0.53	1 (1%)	60,66,111	0.32	0
75	CDL	x	101	-	91,91,99	0.40	1 (1%)	97,103,111	0.24	0
73	UQ5	1A	401	-	38,38,38	0.53	0	46,49,49	1.08	4 (8%)
89	8Q1	r	200	-	31,34,34	1.76	5 (16%)	40,43,43	1.88	10 (25%)
75	CDL	W	701	-	94,94,99	0.35	0	100,106,111	0.28	0
77	PTY	e	302	-	42,42,49	0.52	0	45,47,54	0.42	0
73	UQ5	1B	401	-	38,38,38	0.46	0	46,49,49	0.73	1 (2%)
76	3PH	h	201	-	44,44,47	0.65	1 (2%)	48,49,52	3.77	5 (10%)
76	3PH	V	601	-	41,41,47	0.66	1 (2%)	45,46,52	0.63	1 (2%)
75	CDL	1A	405	-	58,58,99	0.44	0	64,70,111	0.27	0
77	PTY	2D	301	-	34,34,49	0.56	0	37,39,54	0.56	0
75	CDL	1M	501	-	53,53,99	0.49	1 (1%)	59,65,111	0.26	0
75	CDL	1B	408	-	70,70,99	0.34	0	76,82,111	0.34	0
77	PTY	x	102	-	49,49,49	0.46	0	52,54,54	0.40	0
77	PTY	R	404	-	43,43,49	0.51	0	46,48,54	0.46	0
75	CDL	1B	405	-	63,63,99	0.44	1 (1%)	69,75,111	0.25	0
82	HEA	2A	603	11	57,67,67	2.08	16 (28%)	61,103,103	2.42	23 (37%)
75	CDL	V	603	-	63,63,99	0.41	0	69,75,111	0.25	0
73	UQ5	1B	402	-	38,38,38	0.51	0	46,49,49	1.51	6 (13%)
76	3PH	2D	302	-	31,31,47	0.77	1 (3%)	35,36,52	0.72	1 (2%)
75	CDL	u	602	-	82,82,99	0.38	0	88,94,111	0.30	0
75	CDL	1L	101	-	58,58,99	0.43	0	64,70,111	0.35	0
77	PTY	S	302	-	45,45,49	0.49	0	48,50,54	0.41	0
76	3PH	w	201	-	44,44,47	0.64	1 (2%)	48,49,52	0.75	3 (6%)
90	NDP	P	401	-	45,52,52	2.24	6 (13%)	53,80,80	1.65	13 (24%)
74	HEM	1B	404	1	41,50,50	1.45	3 (7%)	45,82,82	1.38	7 (15%)
76	3PH	1B	406	-	47,47,47	0.62	1 (2%)	51,52,52	0.60	1 (1%)
85	CUA	3C	301	-	0,1,1	-	-	-	-	-
77	PTY	T	506	-	25,25,49	0.64	0	28,30,54	0.47	0
77	PTY	2F	101	-	33,33,49	0.55	0	36,38,54	0.45	0
77	PTY	e	301	-	24,24,49	0.64	0	27,29,54	0.52	0
91	COO	s	401	-	45,55,55	0.82	1 (2%)	55,81,81	4.26	10 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
76	3PH	1E	402	-	39,39,47	0.69	1 (2%)	43,44,52	0.64	0
88	SF4	B	502	24	0,12,12	-	-	-		
85	CUA	2C	301	-	0,1,1	-	-	-		
73	UQ5	Q	301	-	38,38,38	0.51	0	46,49,49	0.83	3 (6%)
76	3PH	3D	302	-	31,31,47	0.75	1 (3%)	35,36,52	0.80	1 (2%)
74	HEM	1B	403	1	41,50,50	1.54	4 (9%)	45,82,82	1.51	7 (15%)
77	PTY	h	202	-	45,45,49	0.47	0	48,50,54	0.46	0
82	HEA	3A	603	11	57,67,67	2.06	15 (26%)	61,103,103	2.46	23 (37%)
88	SF4	G	302	29	0,12,12	-	-	-		
77	PTY	V	606	-	34,34,49	0.56	0	37,39,54	0.44	0
87	FMN	B	501	-	33,33,33	1.09	2 (6%)	48,50,50	1.25	8 (16%)
79	PC7	R	403	-	43,43,51	0.53	0	49,51,59	0.61	0
81	PGT	T	505	-	39,39,50	0.54	0	42,45,56	0.50	0
77	PTY	R	402	-	33,33,49	0.53	0	36,38,54	0.43	0
88	SF4	G	301	29	0,12,12	-	-	-		
77	PTY	3D	301	-	34,34,49	0.57	0	37,39,54	0.47	0
76	3PH	2I	201	-	41,41,47	0.67	1 (2%)	45,46,52	0.67	1 (2%)
75	CDL	u	603	-	70,70,99	0.43	0	76,82,111	0.28	0
77	PTY	1F	403	-	37,37,49	0.51	0	40,42,54	0.44	0
88	SF4	C	802	25	0,12,12	-	-	-		
76	3PH	1B	407	-	47,47,47	0.63	1 (2%)	51,52,52	0.60	0
79	PC7	1G	301	-	35,35,51	0.61	0	41,43,59	0.60	1 (2%)
81	PGT	l	701	-	50,50,50	0.48	0	53,56,56	0.59	1 (1%)
76	3PH	3I	201	-	41,41,47	0.65	1 (2%)	45,46,52	0.66	1 (2%)
76	3PH	S	301	-	36,36,47	0.71	1 (2%)	40,41,52	0.70	1 (2%)
76	3PH	c	101	-	47,47,47	0.62	1 (2%)	51,52,52	0.63	1 (1%)
75	CDL	1E	401	-	52,52,99	0.44	0	58,64,111	0.25	0
81	PGT	b	601	-	43,43,50	0.53	0	46,49,56	0.51	0
88	SF4	F	201	28	0,12,12	-	-	-		
75	CDL	h	203	-	76,76,99	0.37	0	82,88,111	0.25	0
73	UQ5	1A	402	-	38,38,38	0.52	0	46,49,49	0.66	1 (2%)
78	HEC	1F	402	3	32,50,50	2.08	3 (9%)	24,82,82	1.85	6 (25%)
76	3PH	V	602	-	40,40,47	0.67	1 (2%)	44,45,52	0.82	1 (2%)
74	HEM	1A	404	1	41,50,50	1.40	3 (7%)	45,82,82	1.52	7 (15%)
79	PC7	Q	302	-	32,32,51	0.59	0	38,40,59	0.69	0
76	3PH	g	101	-	36,36,47	0.71	1 (2%)	40,41,52	0.70	1 (2%)
77	PTY	R	406	-	39,39,49	0.53	0	42,44,54	0.51	0
89	8Q1	J	200	-	31,34,34	1.69	5 (16%)	40,43,43	1.71	5 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
77	PTY	3F	101	-	33,33,49	0.55	0	36,38,54	0.47	0
75	CDL	1F	401	-	55,55,99	0.42	0	61,67,111	0.27	0
76	3PH	1K	102	-	47,47,47	0.64	1 (2%)	51,52,52	0.60	2 (3%)

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
88	SF4	C	803	25	-	-	0/6/5/5
74	HEM	1A	403	1	-	3/12/54/54	-
81	PGT	T	502	-	-	20/52/52/55	-
77	PTY	1E	403	-	-	15/37/37/53	-
77	PTY	T	501	-	-	19/53/53/53	-
79	PC7	2A	606	-	-	10/30/30/55	-
77	PTY	T	504	-	-	11/31/31/53	-
82	HEA	3A	602	11	-	7/32/76/76	-
81	PGT	2A	601	-	-	10/37/37/55	-
79	PC7	T	503	-	-	22/55/55/55	-
79	PC7	1H	101	-	-	19/42/42/55	-
76	3PH	R	401	-	-	13/33/33/49	-
76	3PH	1A	406	-	-	13/32/32/49	-
77	PTY	V	604	-	-	15/43/43/53	-
77	PTY	V	605	-	-	25/53/53/53	-
82	HEA	2A	602	11	-	7/32/76/76	-
86	FES	C	801	25	-	-	0/1/1/1
79	PC7	3A	606	-	-	22/30/30/55	-
86	FES	A	301	23	-	-	0/1/1/1
76	3PH	y	201	-	-	13/33/33/49	-
81	PGT	3A	601	-	-	12/37/37/55	-
78	HEC	1E	404	3	-	0/10/54/54	-
75	CDL	1K	101	-	-	59/89/89/110	-
76	3PH	1R	201	-	-	13/38/38/49	-
79	PC7	u	601	-	-	15/45/45/55	-
77	PTY	G	303	-	-	6/46/46/53	-
75	CDL	R	405	-	-	43/73/73/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
75	CDL	y	202	-	-	30/65/65/110	-
75	CDL	x	101	-	-	65/102/102/110	-
73	UQ5	1A	401	-	-	10/33/57/57	0/1/1/1
89	8Q1	r	200	-	-	19/41/41/41	-
75	CDL	W	701	-	-	62/105/105/110	-
77	PTY	e	302	-	-	22/46/46/53	-
73	UQ5	1B	401	-	-	7/33/57/57	0/1/1/1
76	3PH	h	201	-	-	19/46/46/49	-
76	3PH	V	601	-	-	18/43/43/49	-
75	CDL	1A	405	-	-	34/69/69/110	-
77	PTY	2D	301	-	-	13/38/38/53	-
75	CDL	1M	501	-	-	31/64/64/110	-
75	CDL	1B	408	-	-	45/81/81/110	-
77	PTY	x	102	-	-	18/53/53/53	-
77	PTY	R	404	-	-	21/47/47/53	-
75	CDL	1B	405	-	-	49/74/74/110	-
82	HEA	2A	603	11	-	5/32/76/76	-
75	CDL	V	603	-	-	42/74/74/110	-
73	UQ5	1B	402	-	-	10/33/57/57	0/1/1/1
76	3PH	2D	302	-	-	19/33/33/49	-
75	CDL	u	602	-	-	51/93/93/110	-
75	CDL	1L	101	-	-	43/69/69/110	-
77	PTY	S	302	-	-	21/49/49/53	-
76	3PH	w	201	-	-	21/46/46/49	-
90	NDP	P	401	-	-	11/30/77/77	0/5/5/5
74	HEM	1B	404	1	-	4/12/54/54	-
76	3PH	1B	406	-	-	22/49/49/49	-
77	PTY	T	506	-	-	15/29/29/53	-
77	PTY	2F	101	-	-	15/37/37/53	-
77	PTY	e	301	-	-	9/28/28/53	-
91	COO	s	401	-	-	22/50/70/70	0/3/3/3
76	3PH	1E	402	-	-	17/41/41/49	-
88	SF4	B	502	24	-	-	0/6/5/5
73	UQ5	Q	301	-	-	4/33/57/57	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
76	3PH	3D	302	-	-	10/33/33/49	-
74	HEM	1B	403	1	-	3/12/54/54	-
77	PTY	h	202	-	-	20/49/49/53	-
82	HEA	3A	603	11	-	4/32/76/76	-
88	SF4	G	302	29	-	-	0/6/5/5
77	PTY	V	606	-	-	18/38/38/53	-
87	FMN	B	501	-	-	4/18/18/18	0/3/3/3
79	PC7	R	403	-	-	15/47/47/55	-
81	PGT	T	505	-	-	18/44/44/55	-
77	PTY	R	402	-	-	11/37/37/53	-
88	SF4	G	301	29	-	-	0/6/5/5
77	PTY	3D	301	-	-	15/38/38/53	-
76	3PH	2I	201	-	-	14/43/43/49	-
75	CDL	u	603	-	-	57/81/81/110	-
77	PTY	1F	403	-	-	17/41/41/53	-
88	SF4	C	802	25	-	-	0/6/5/5
76	3PH	1B	407	-	-	18/49/49/49	-
79	PC7	1G	301	-	-	16/39/39/55	-
81	PGT	l	701	-	-	27/55/55/55	-
76	3PH	3I	201	-	-	9/43/43/49	-
76	3PH	S	301	-	-	13/38/38/49	-
76	3PH	c	101	-	-	13/49/49/49	-
75	CDL	1E	401	-	-	41/63/63/110	-
81	PGT	b	601	-	-	27/48/48/55	-
88	SF4	F	201	28	-	-	0/6/5/5
75	CDL	h	203	-	-	58/87/87/110	-
73	UQ5	1A	402	-	-	9/33/57/57	0/1/1/1
78	HEC	1F	402	3	-	0/10/54/54	-
76	3PH	V	602	-	-	17/42/42/49	-
74	HEM	1A	404	1	-	4/12/54/54	-
79	PC7	Q	302	-	-	14/36/36/55	-
76	3PH	g	101	-	-	10/38/38/49	-
77	PTY	R	406	-	-	15/43/43/53	-
89	8Q1	J	200	-	-	11/41/41/41	-
77	PTY	3F	101	-	-	10/37/37/53	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
75	CDL	1F	401	-	-	32/66/66/110	-
76	3PH	1K	102	-	-	15/49/49/49	-

The worst 5 of 126 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	P	401	NDP	P2B-O2B	12.34	1.82	1.59
78	1E	404	HEC	C3C-C2C	-6.90	1.33	1.40
78	1F	402	HEC	C3C-C2C	-6.31	1.34	1.40
78	1E	404	HEC	C2B-C3B	-6.05	1.34	1.40
89	r	200	8Q1	C34-N36	5.99	1.46	1.33

The worst 5 of 231 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	s	401	COO	C15-C11-C12	-19.13	77.03	108.23
76	h	201	3PH	O31-C31-O32	-17.93	78.33	123.59
91	s	401	COO	C15-C11-C13	-16.74	79.80	108.82
91	s	401	COO	C15-C11-C14	-15.18	78.23	109.17
76	h	201	3PH	O31-C31-C32	14.35	156.94	111.91

There are no chirality outliers.

5 of 1751 torsion outliers are listed below:

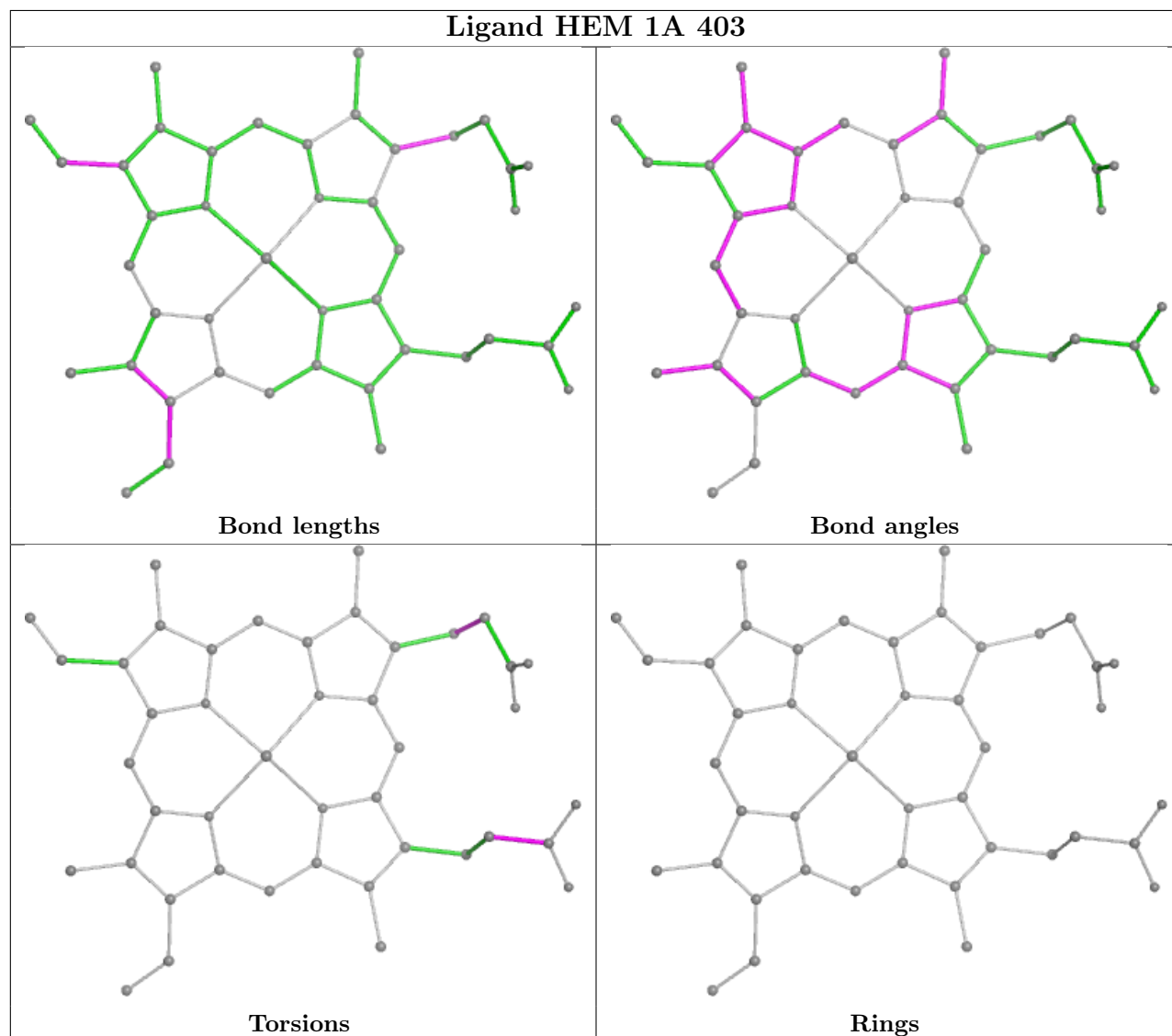
Mol	Chain	Res	Type	Atoms
73	1A	401	UQ5	C1-C6-C7-C8
73	1A	401	UQ5	C5-C6-C7-C8
73	1A	401	UQ5	C9-C11-C12-C13
73	1A	401	UQ5	C24-C26-C27-C28
73	1A	402	UQ5	C14-C16-C17-C18

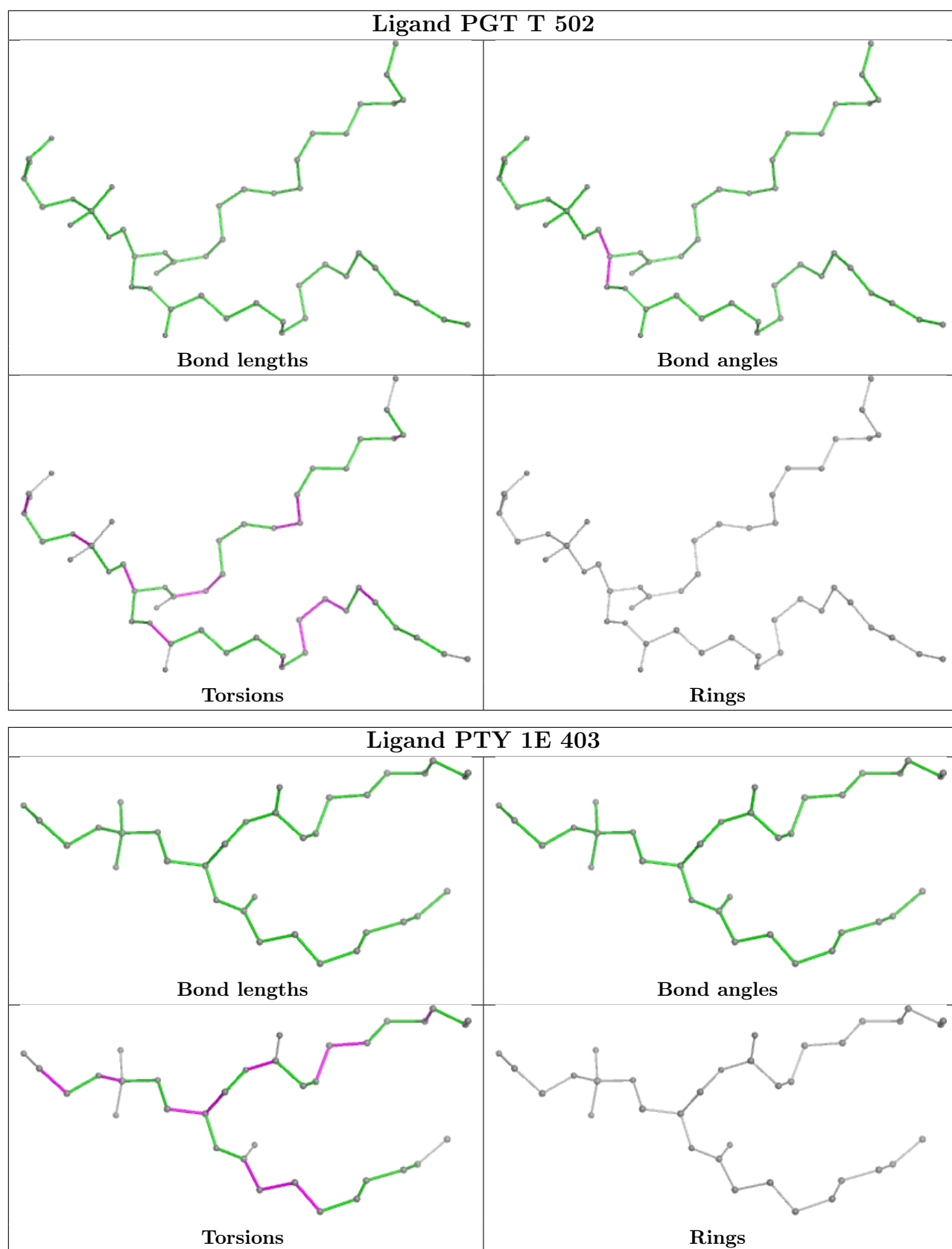
There are no ring outliers.

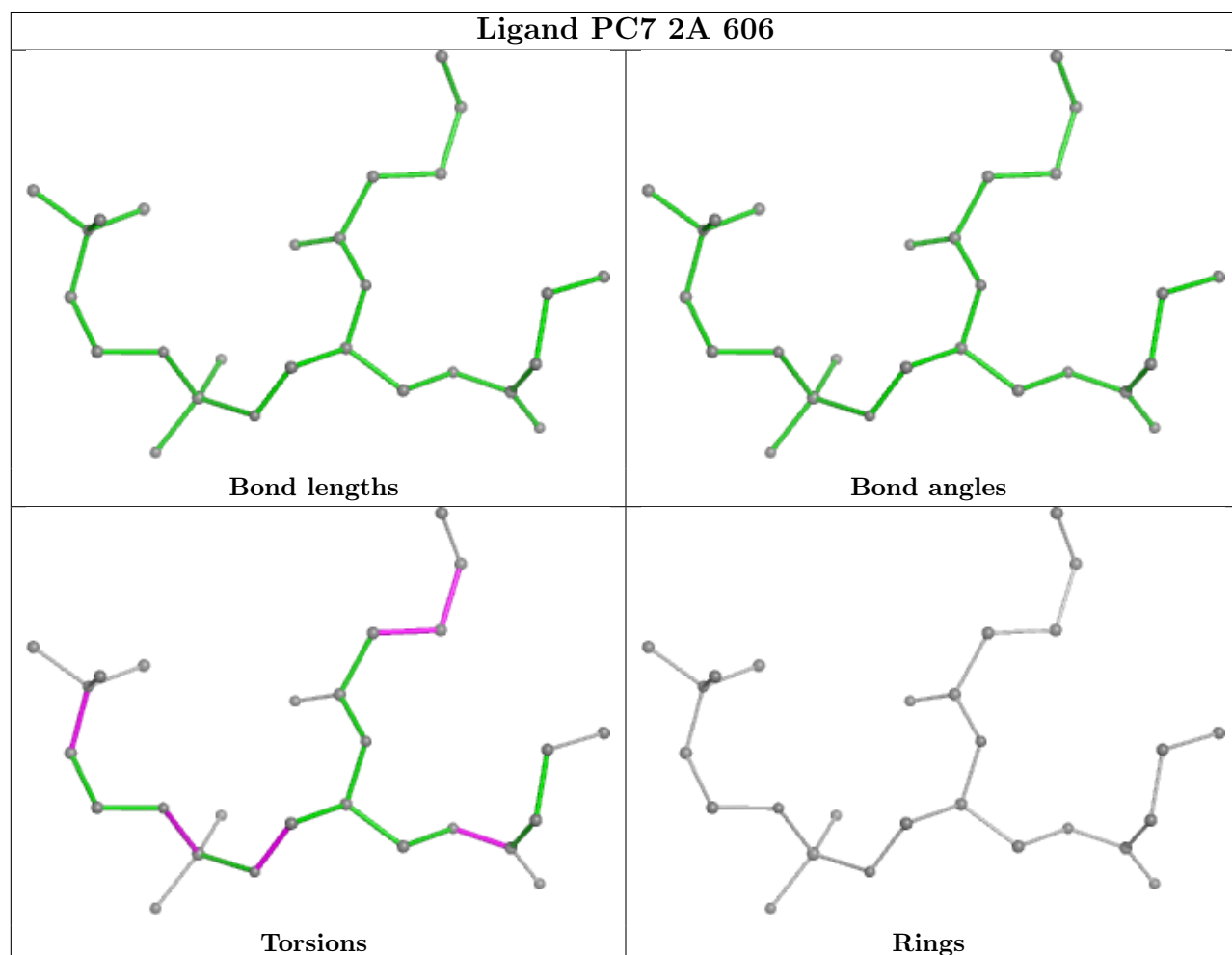
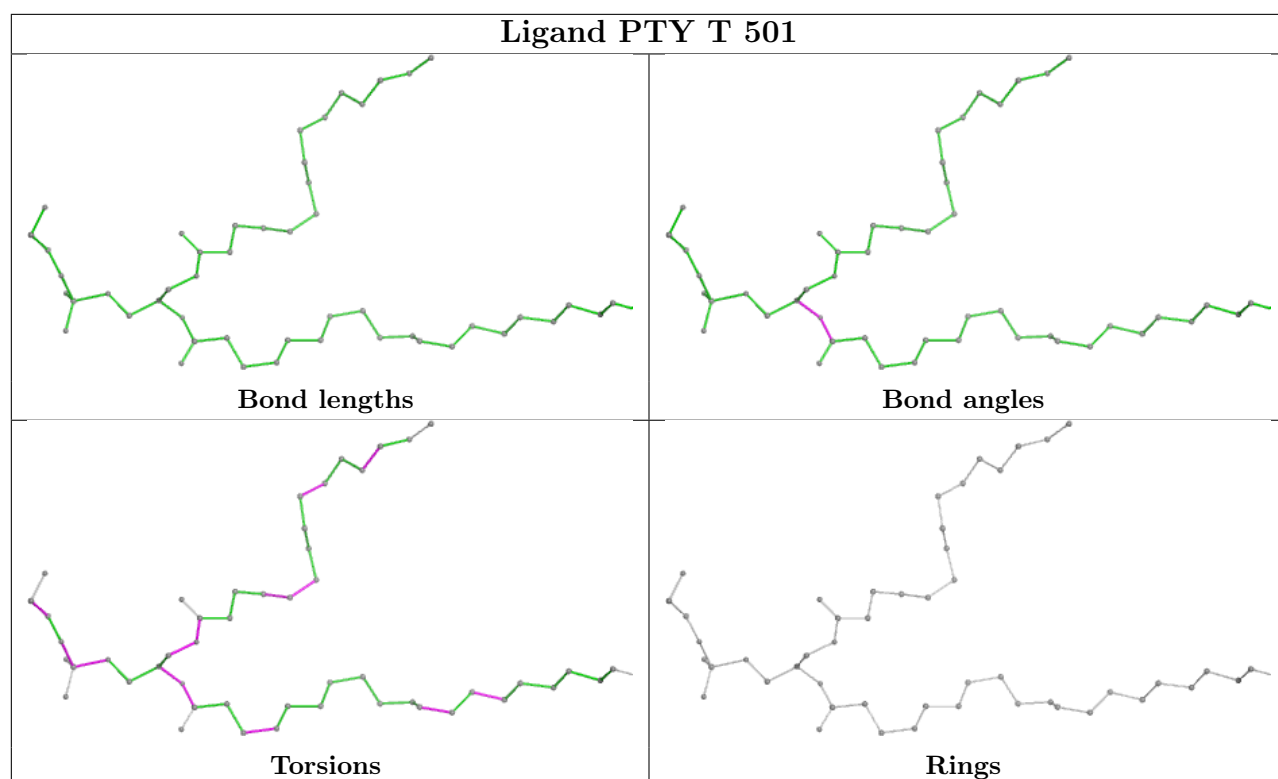
No monomer is involved in short contacts.

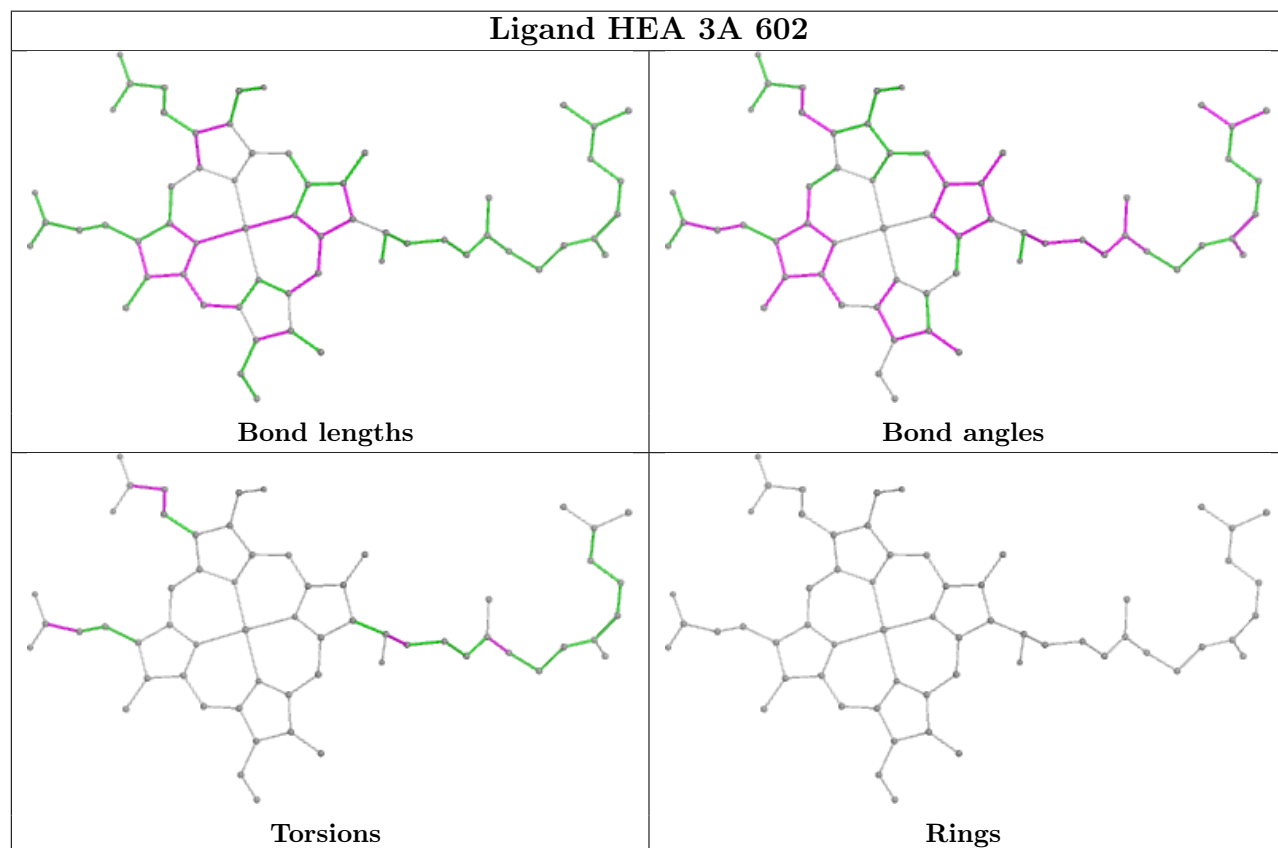
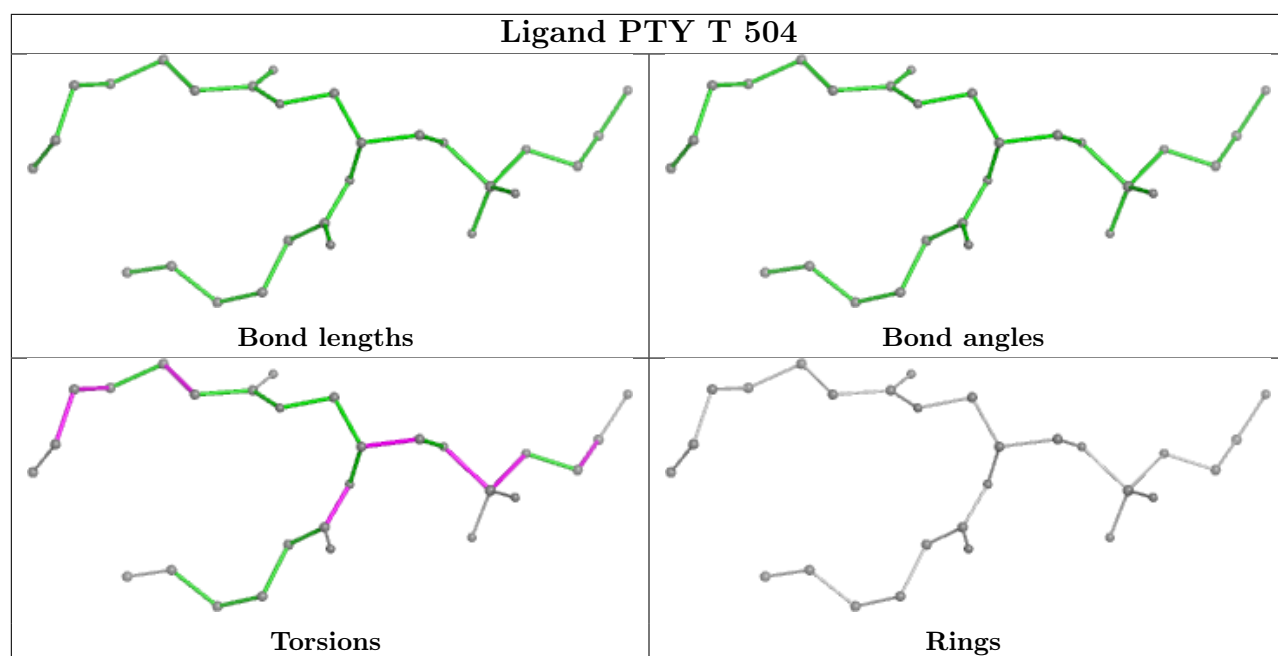
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

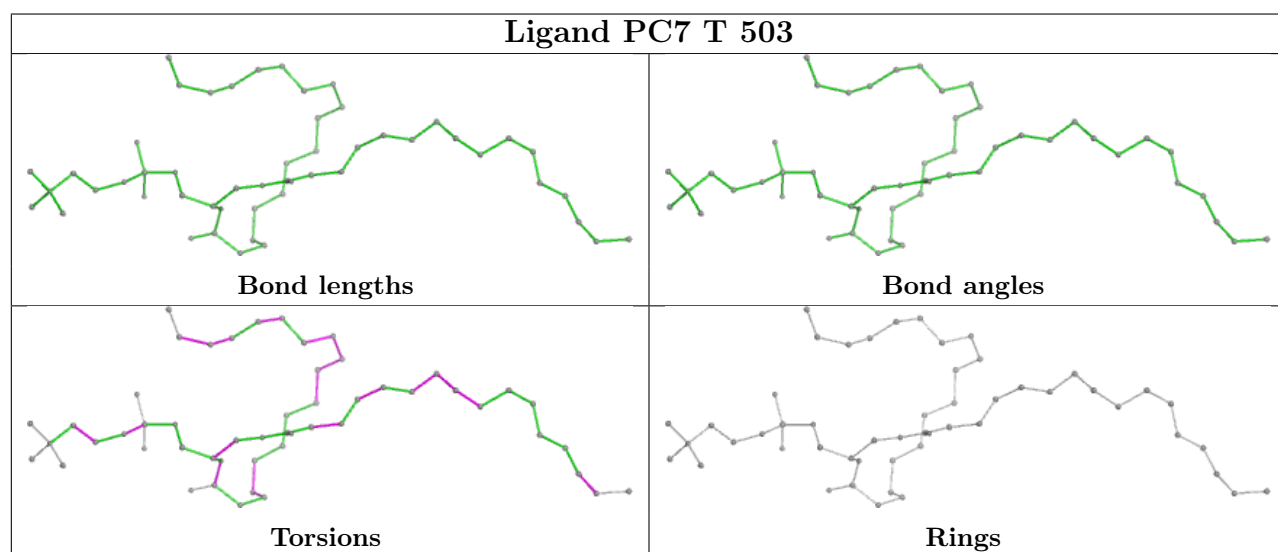
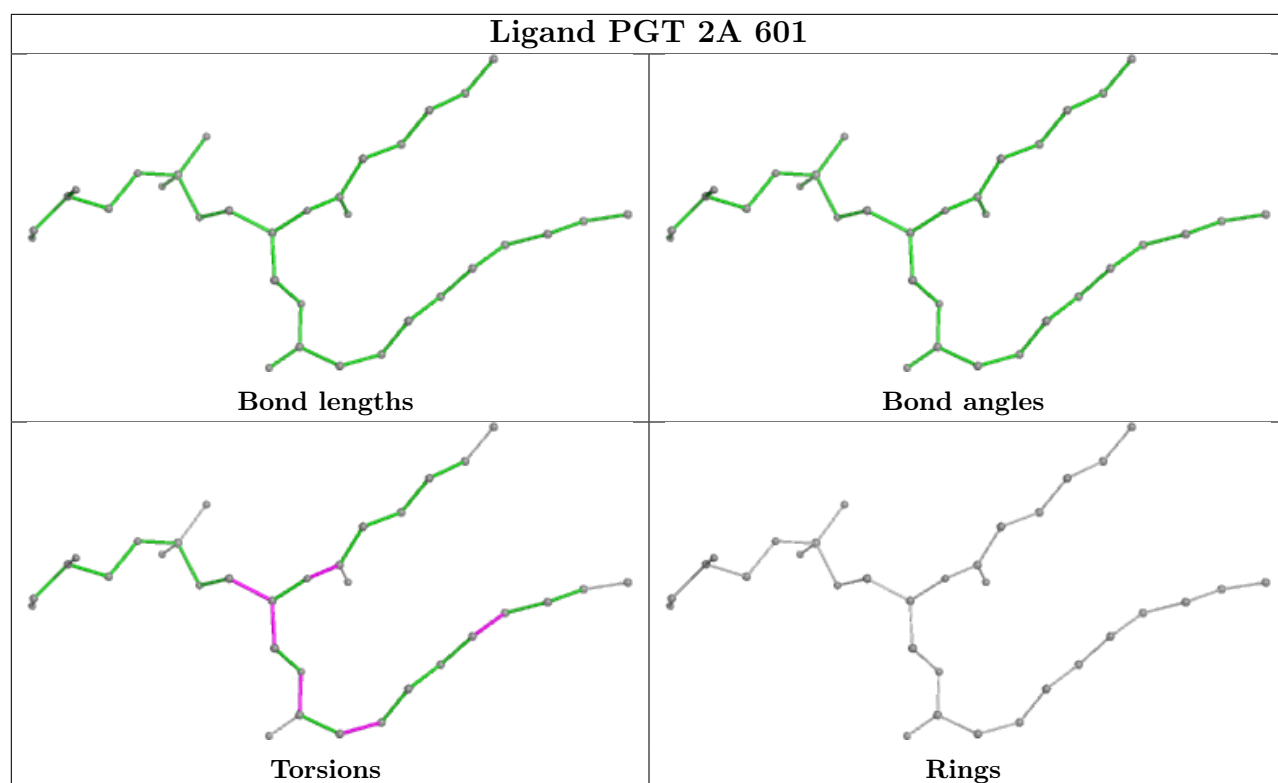
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

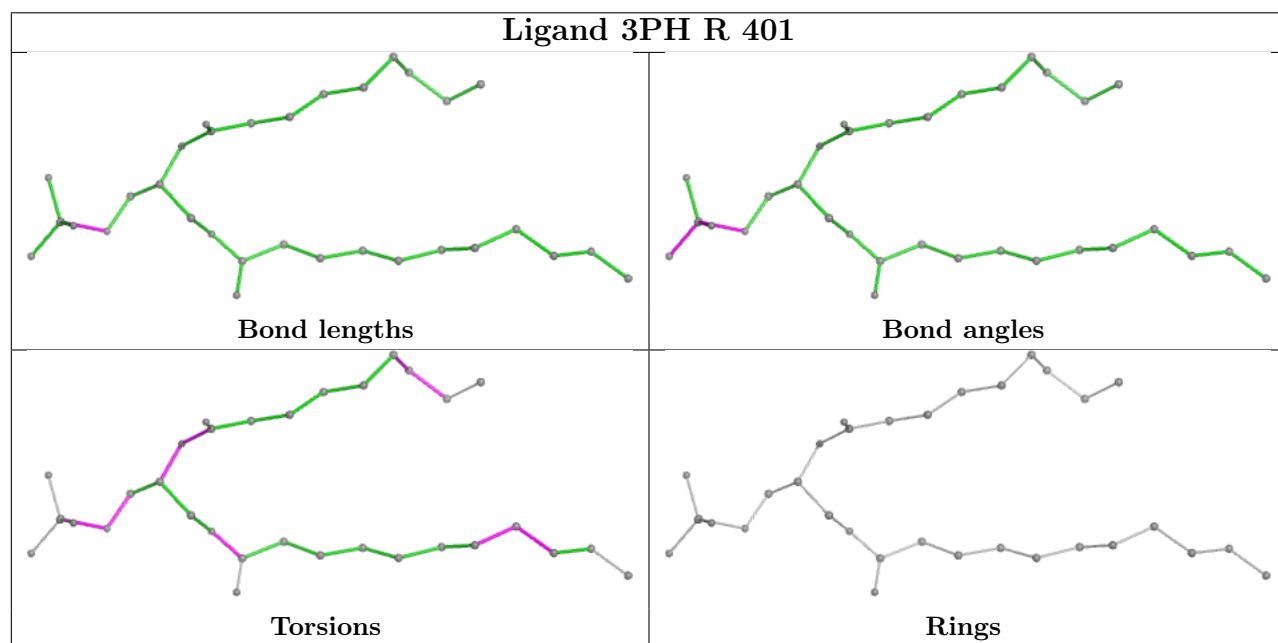
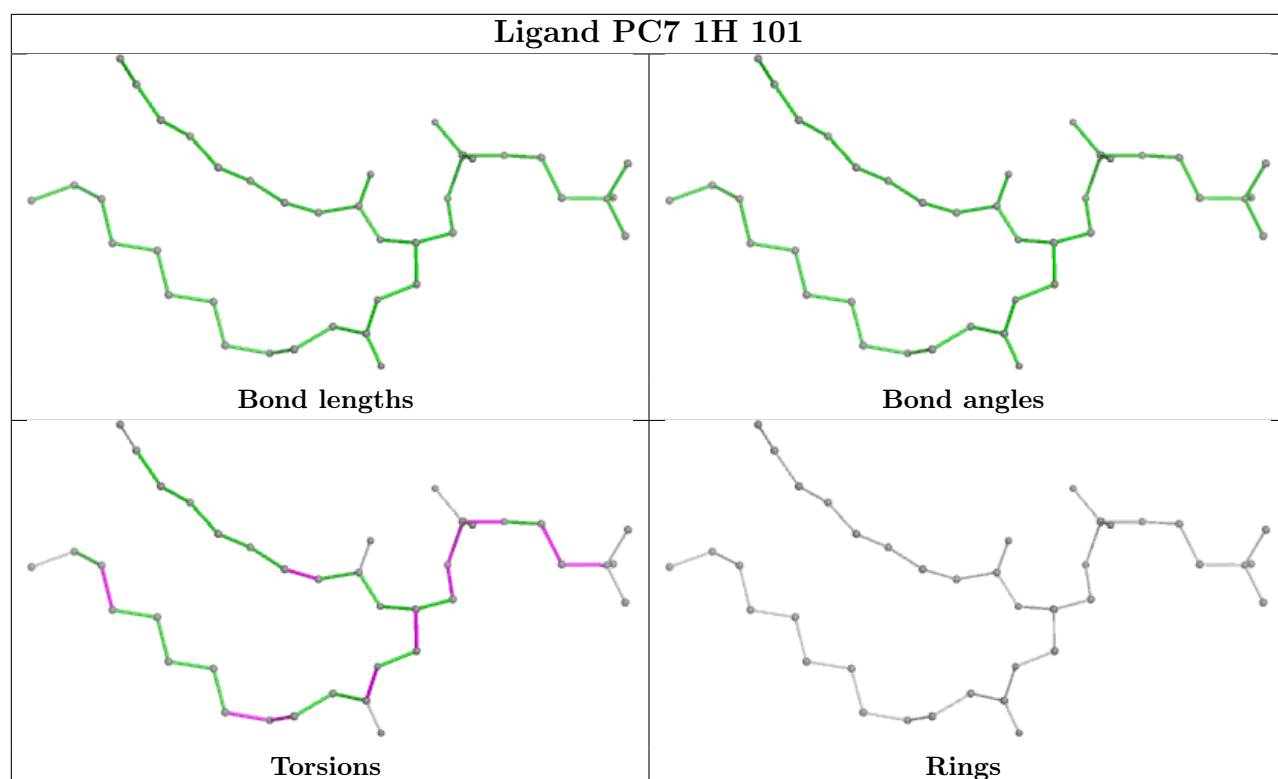


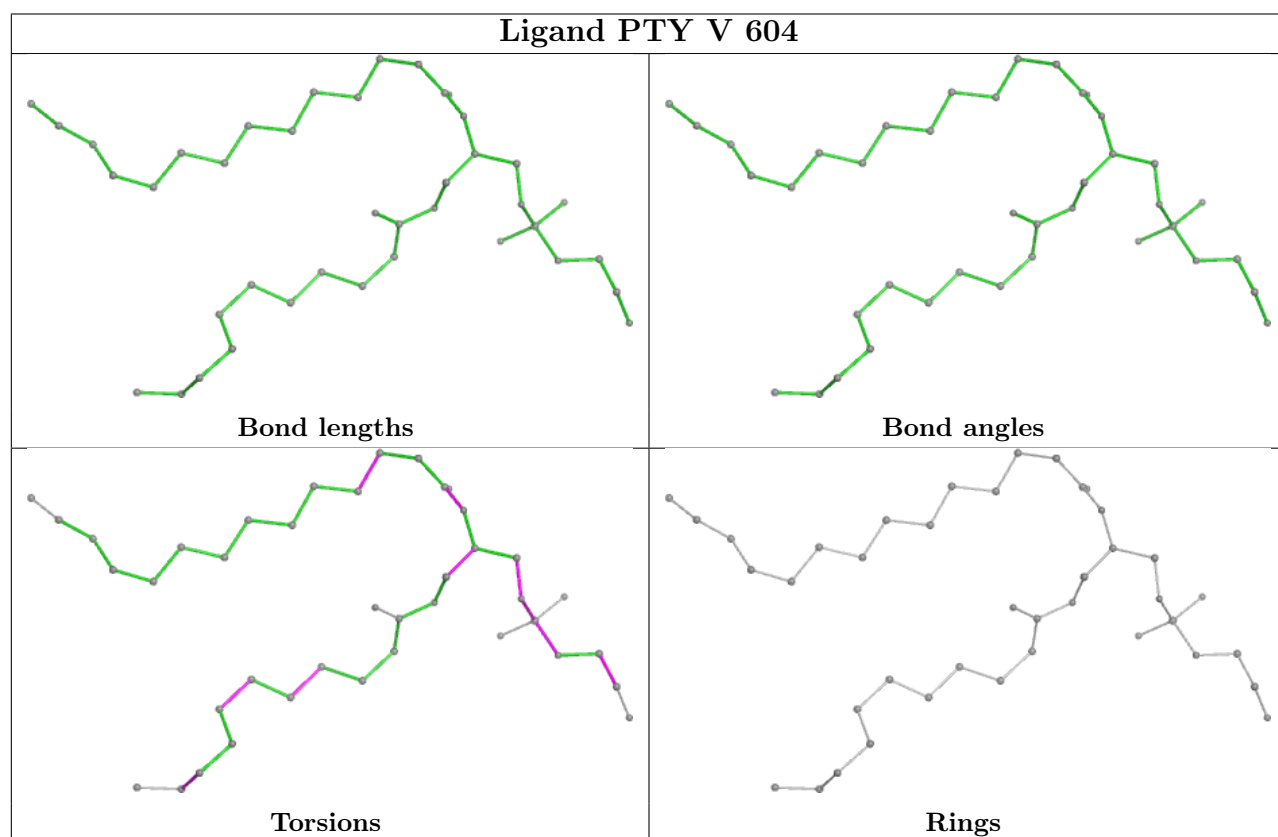
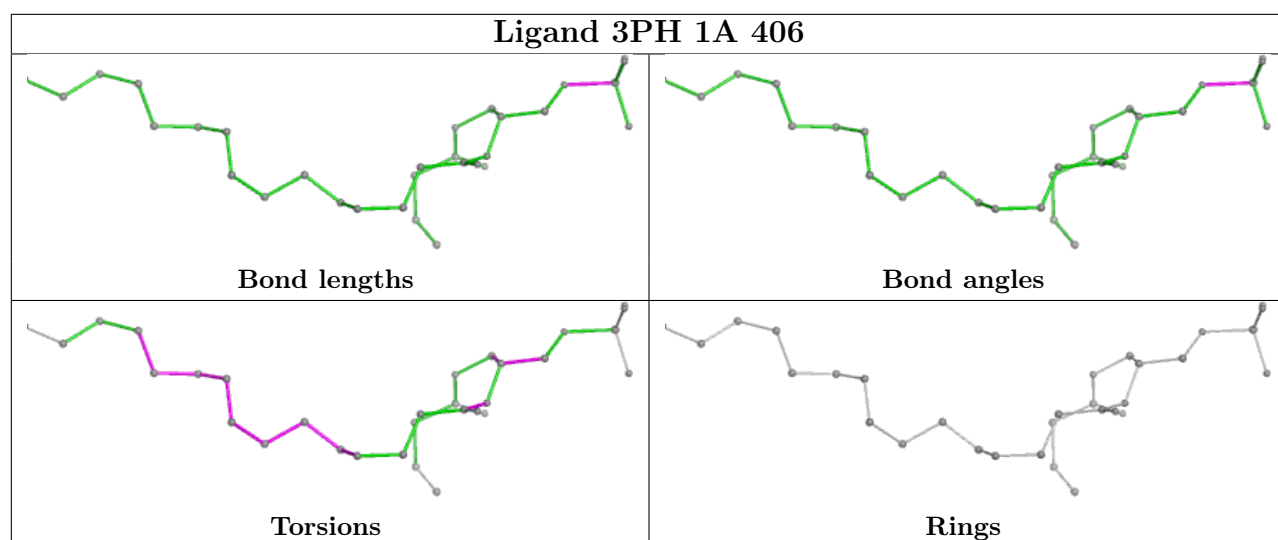


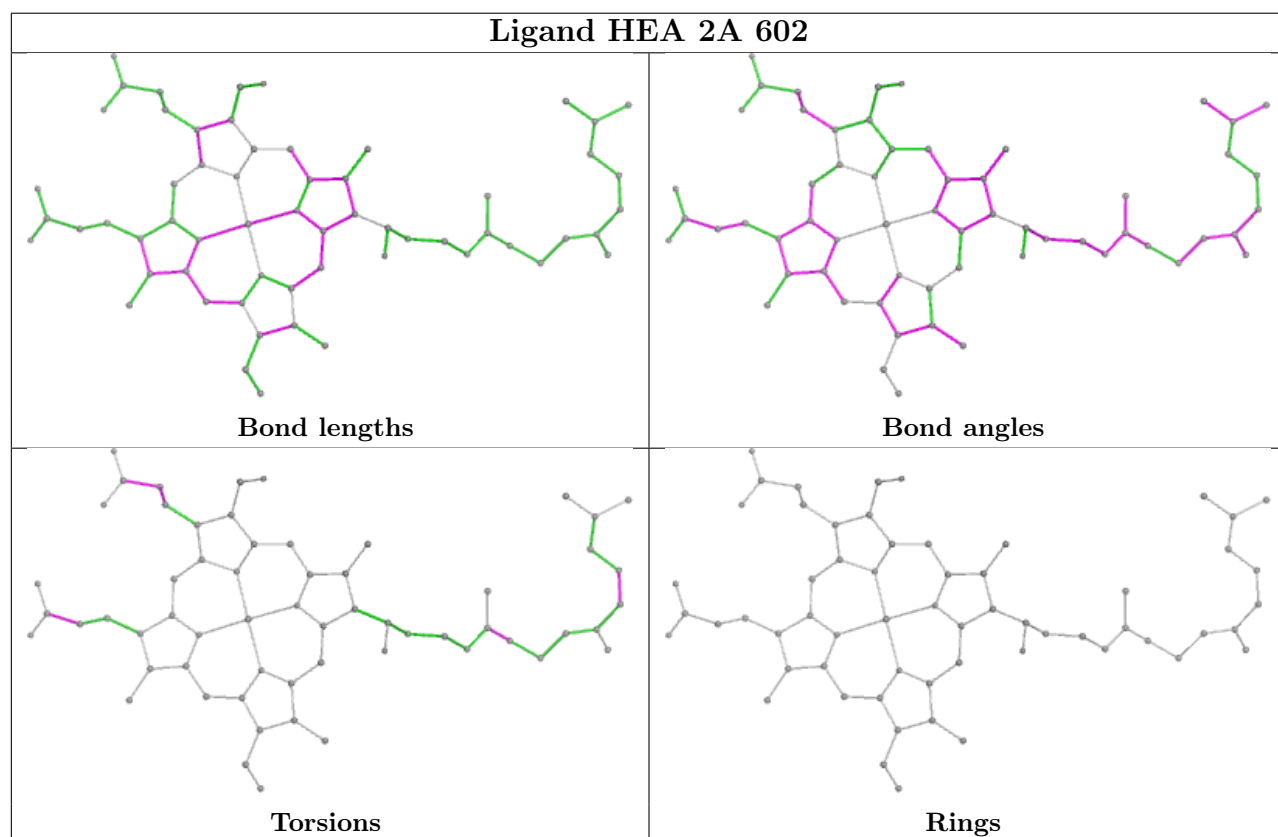
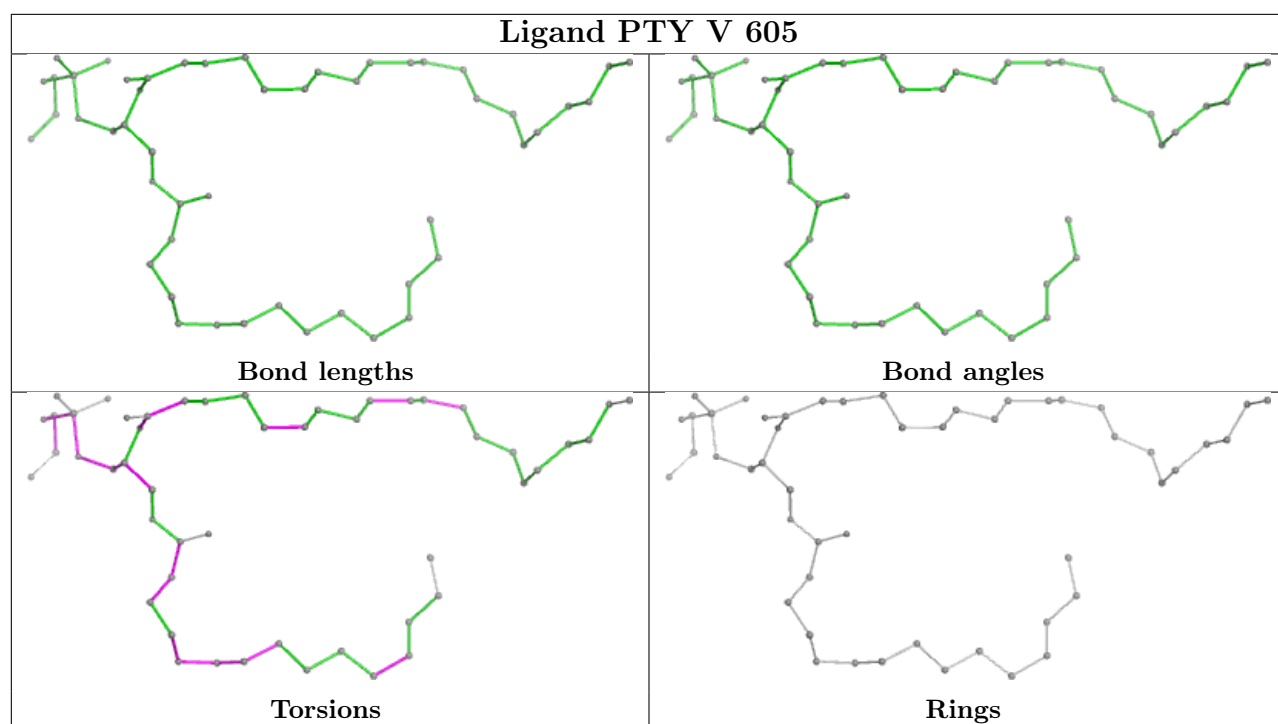


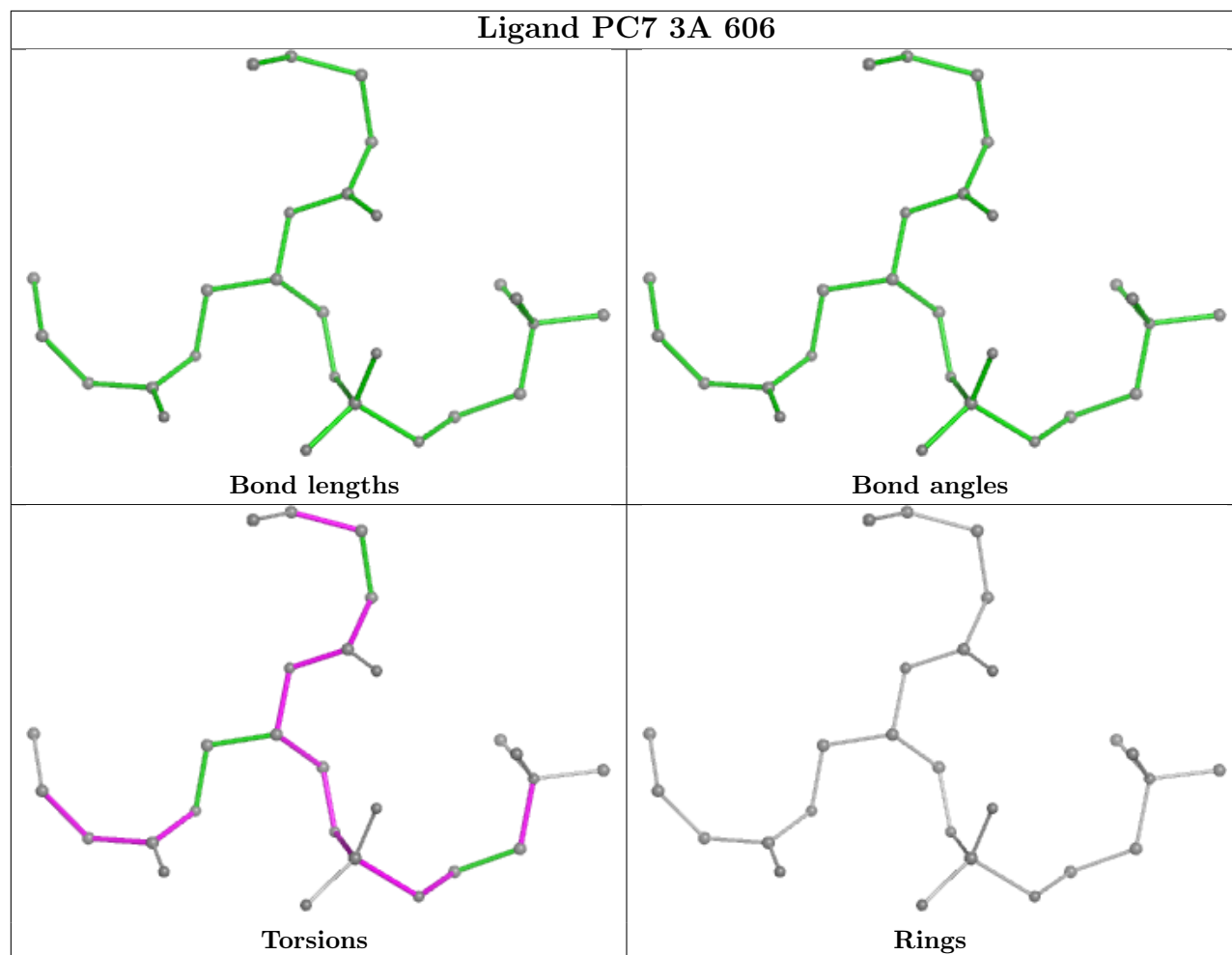


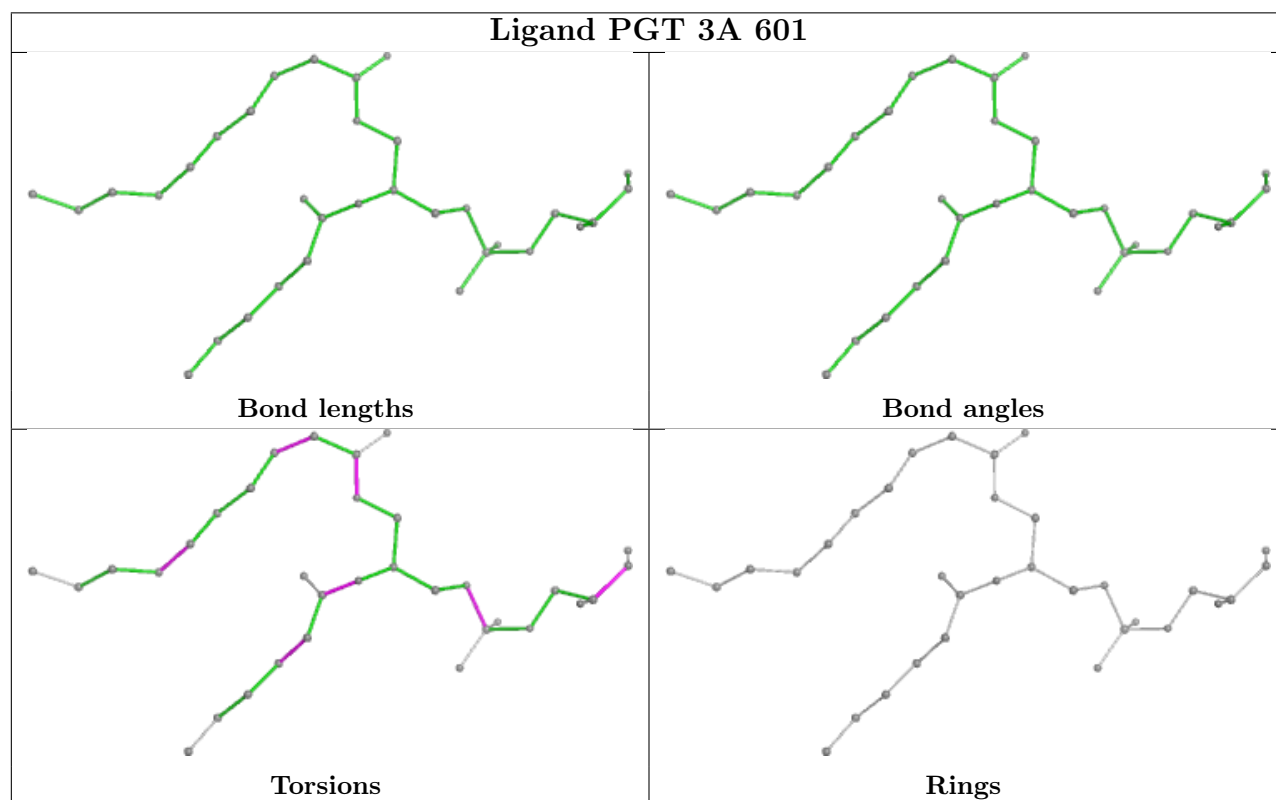
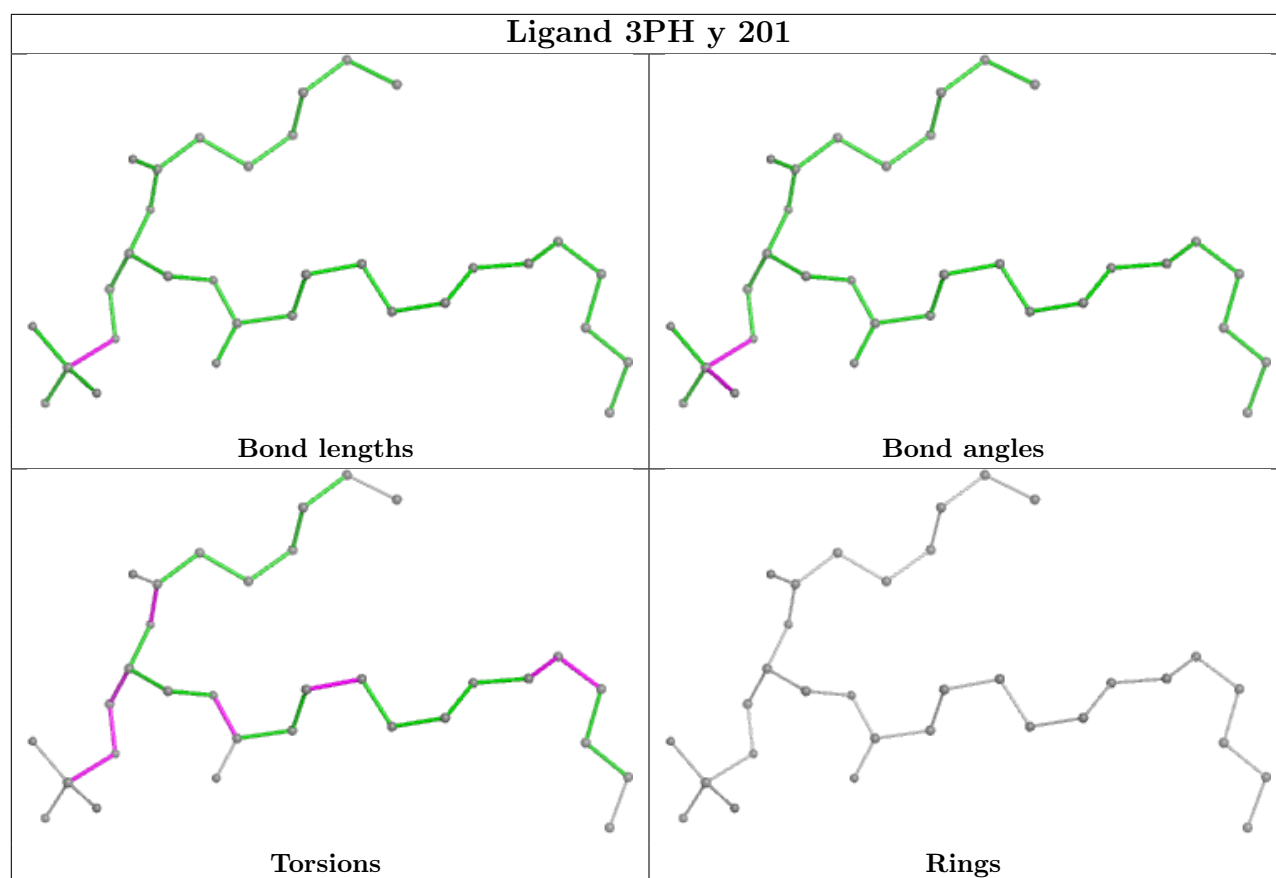


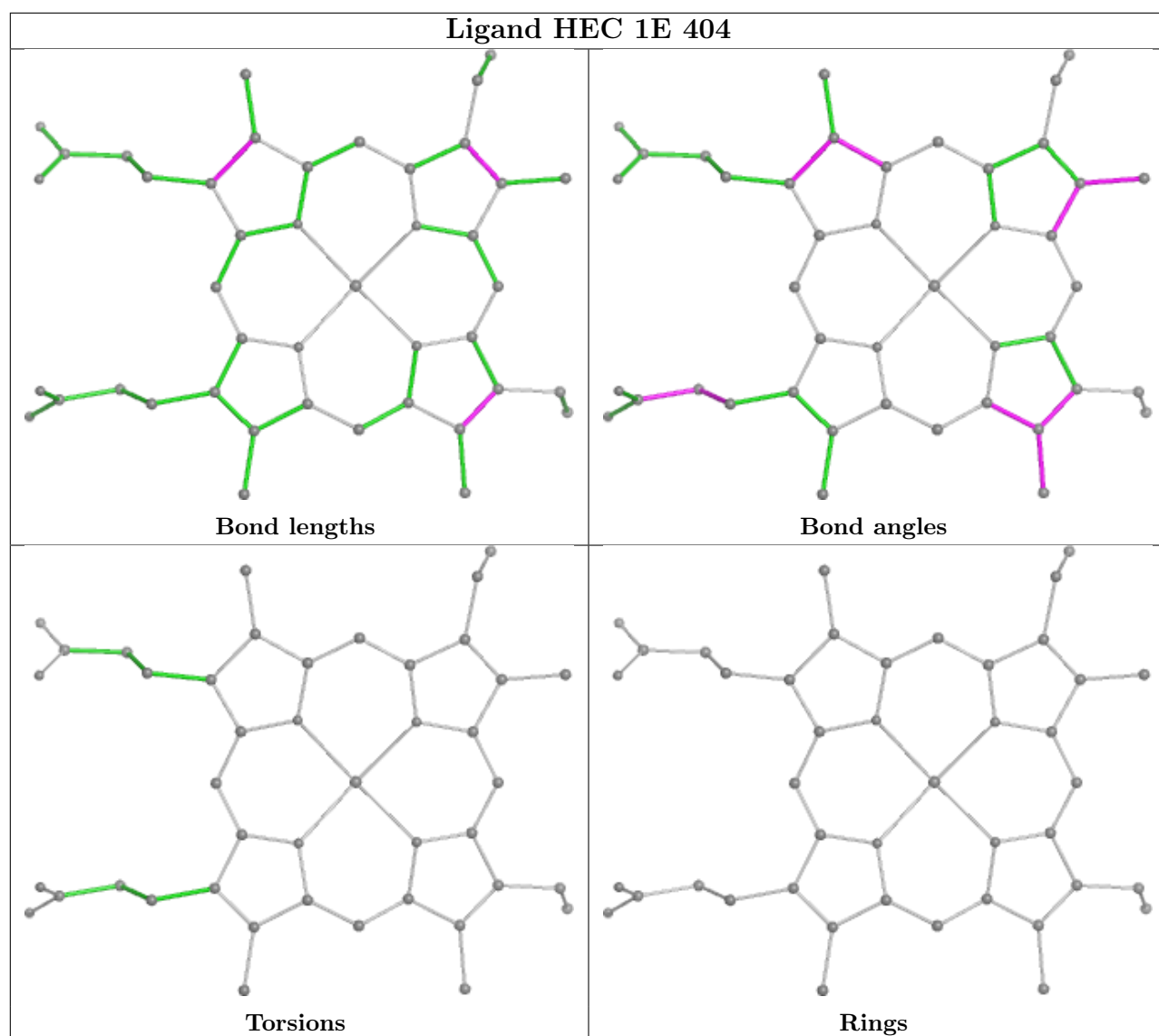


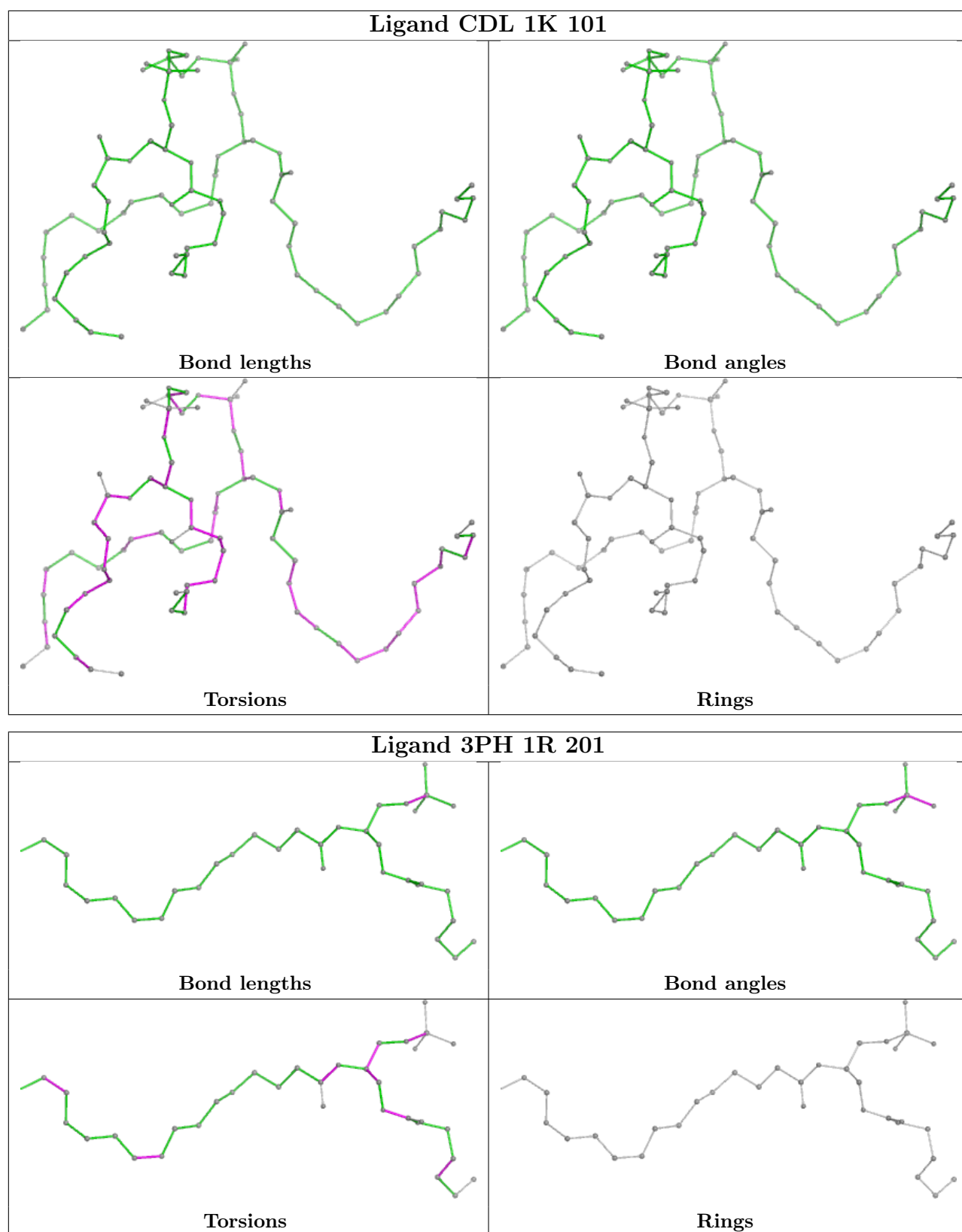


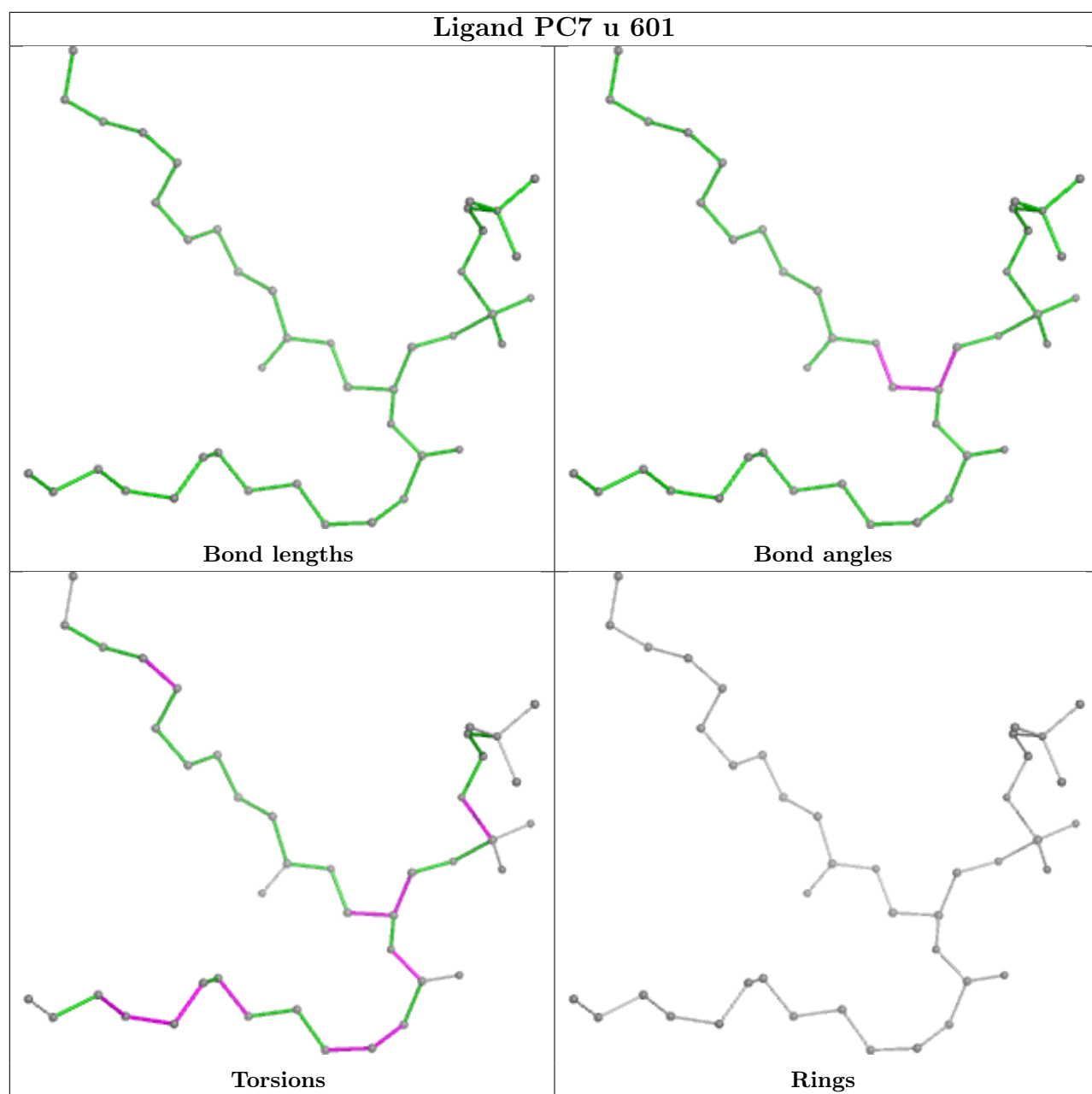


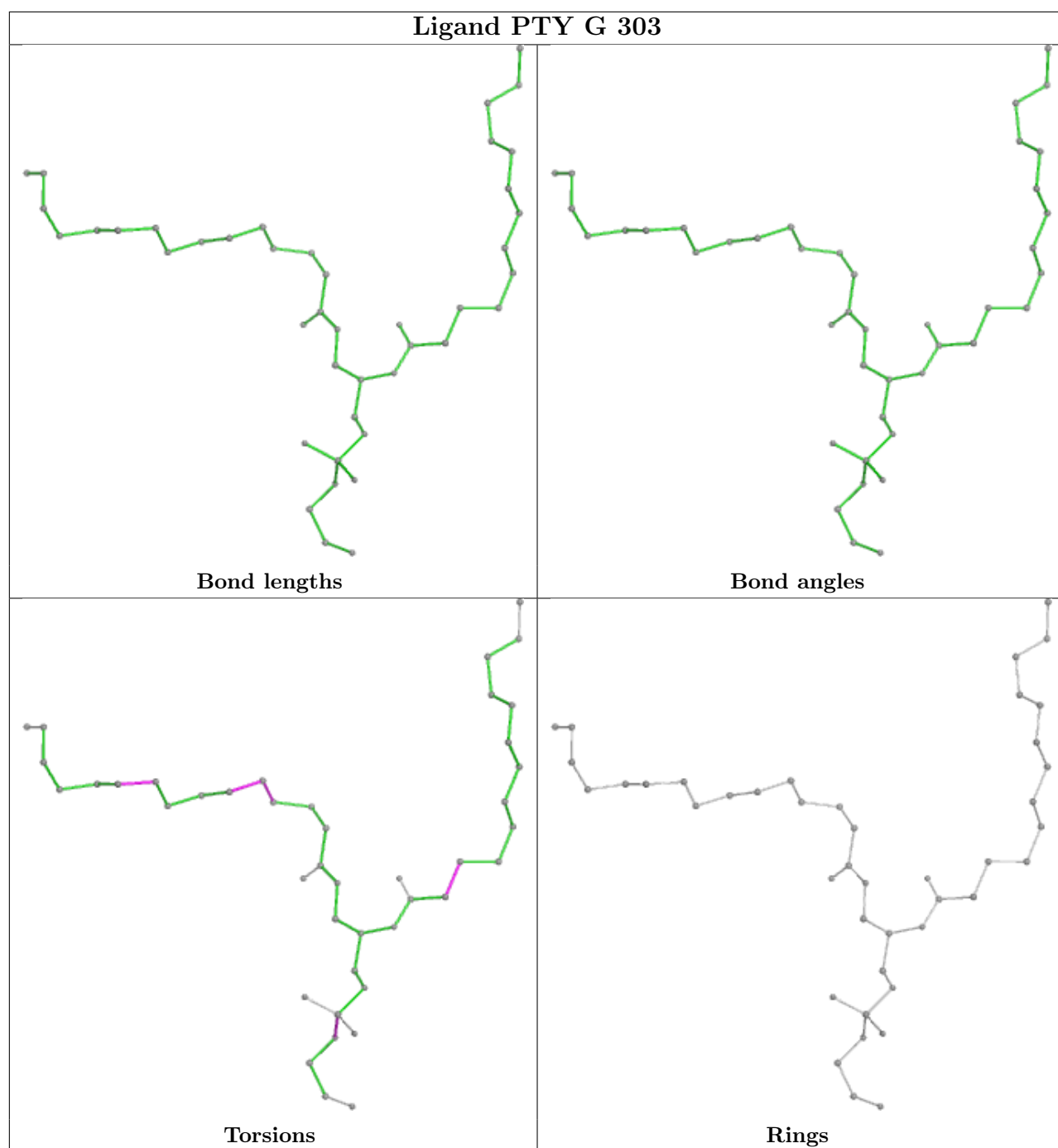


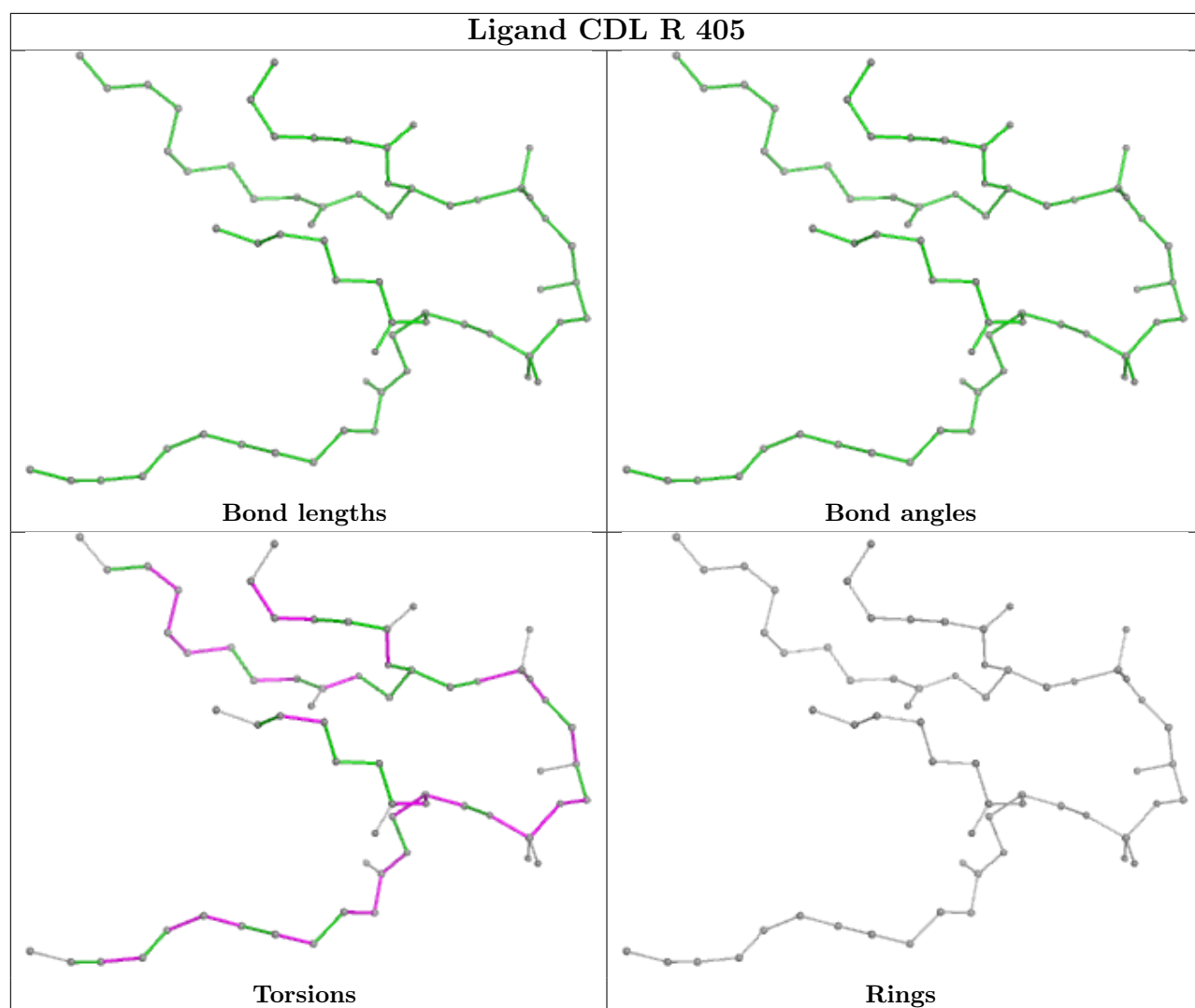


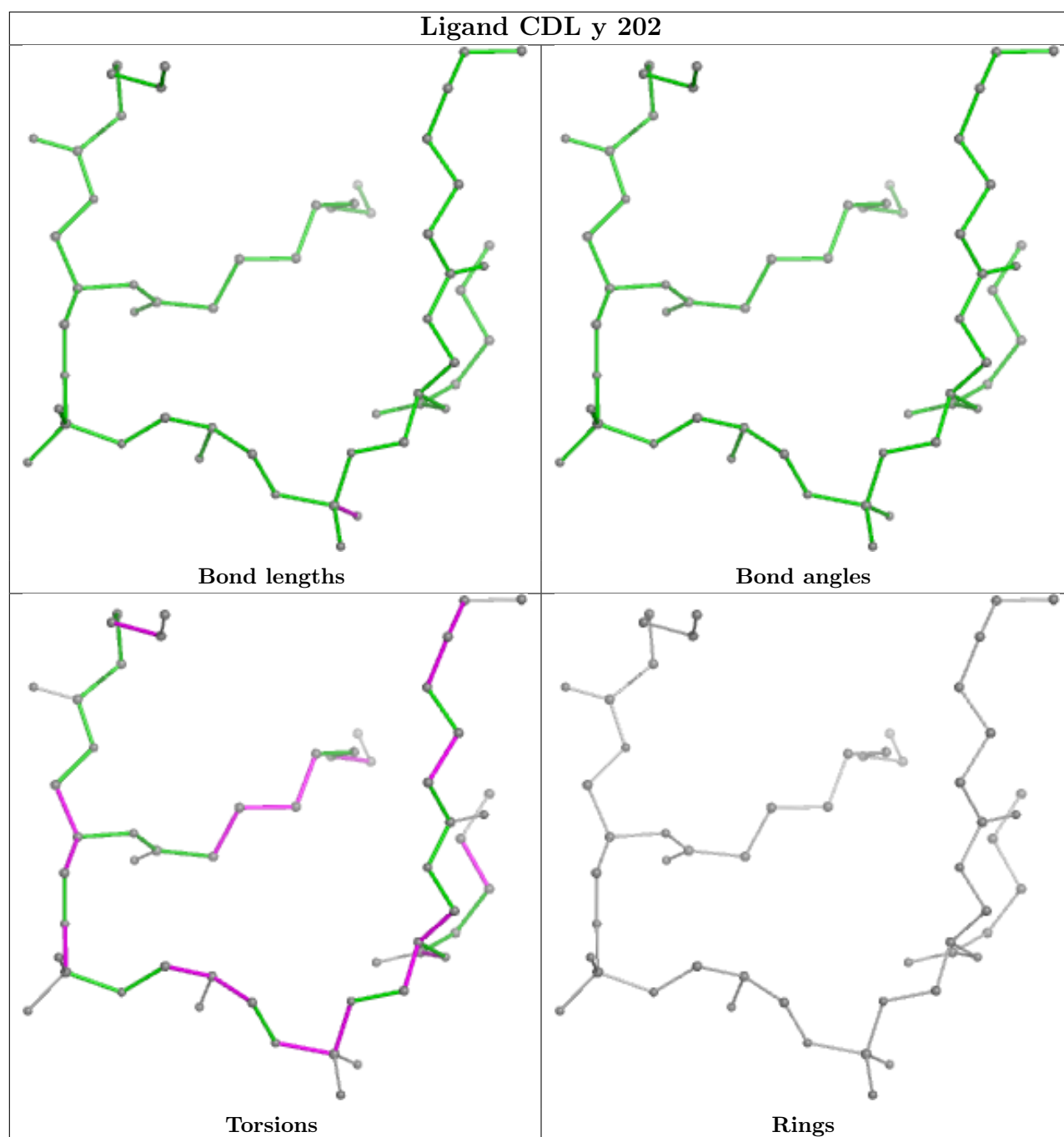


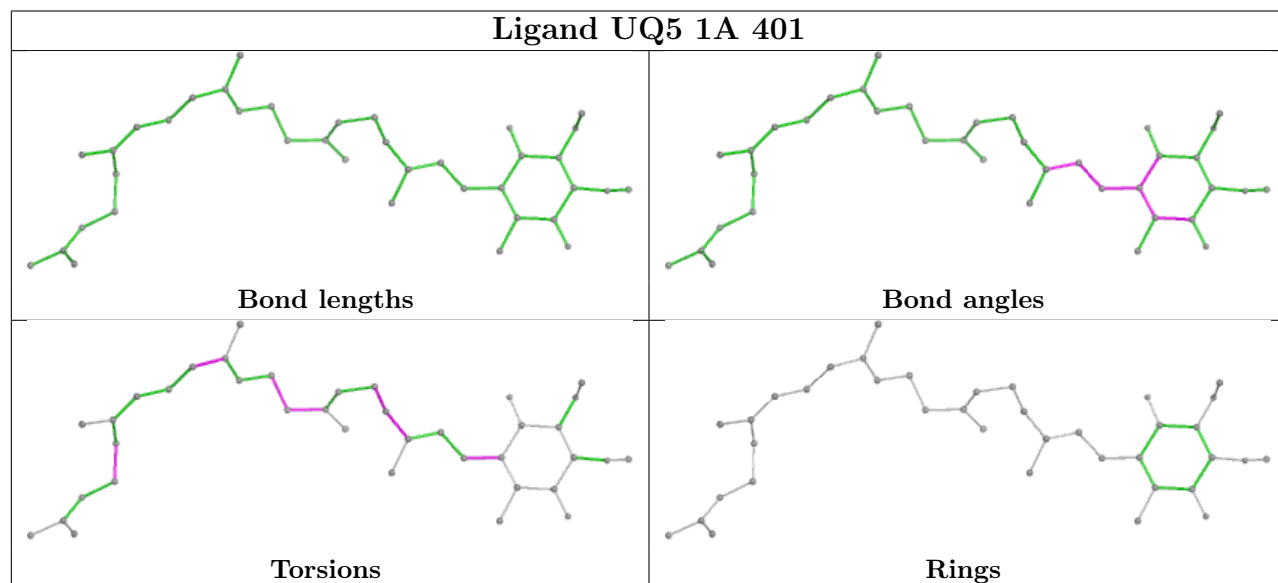
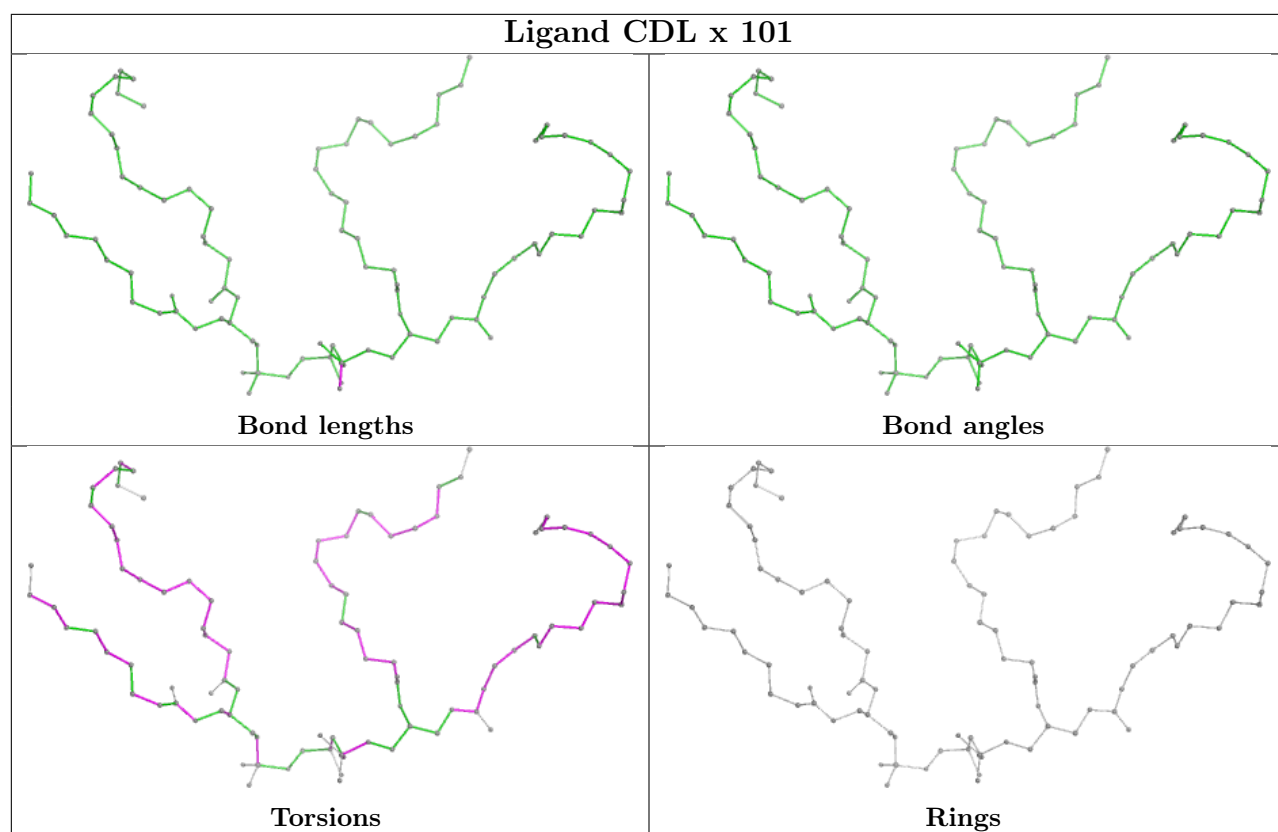


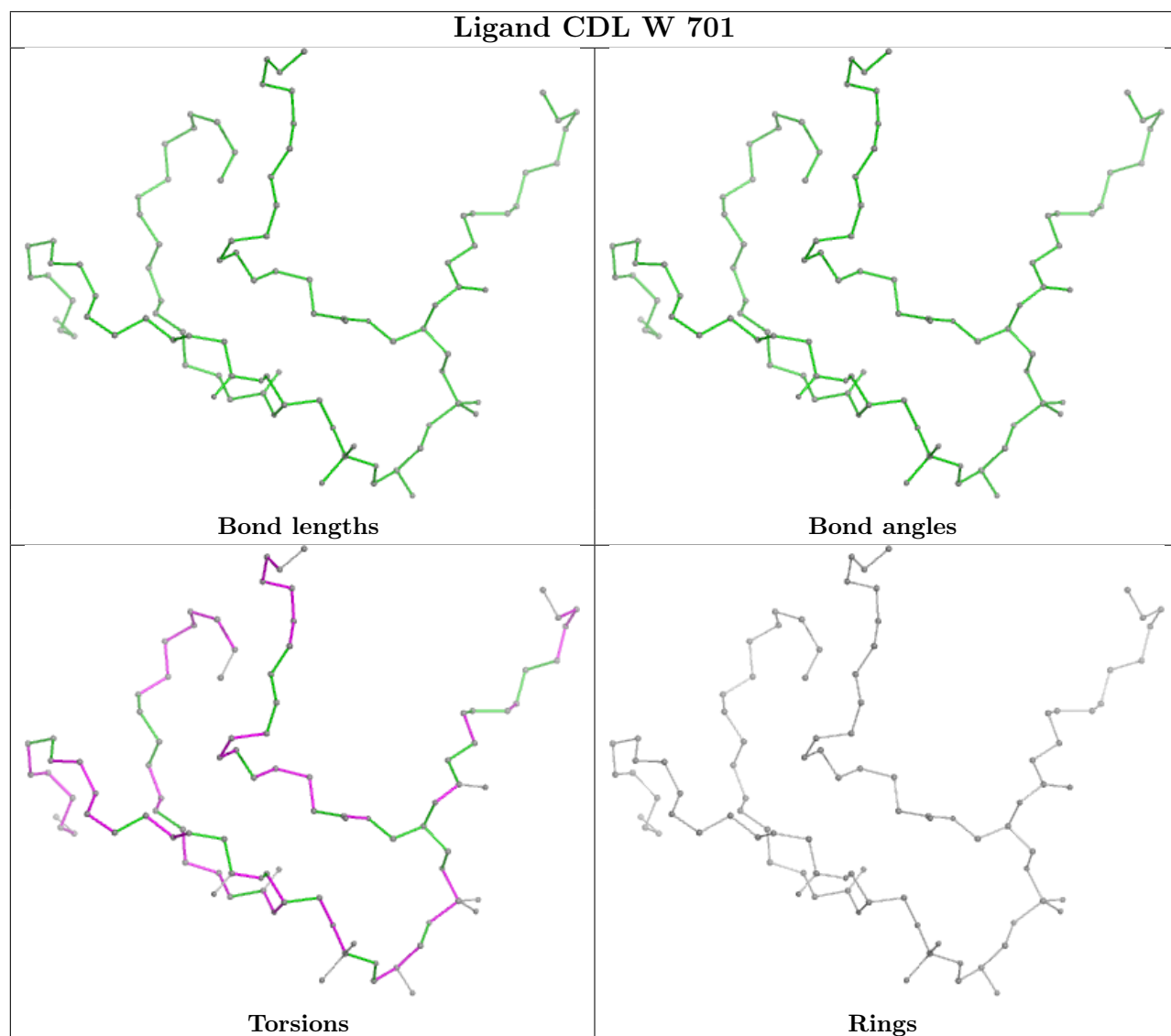
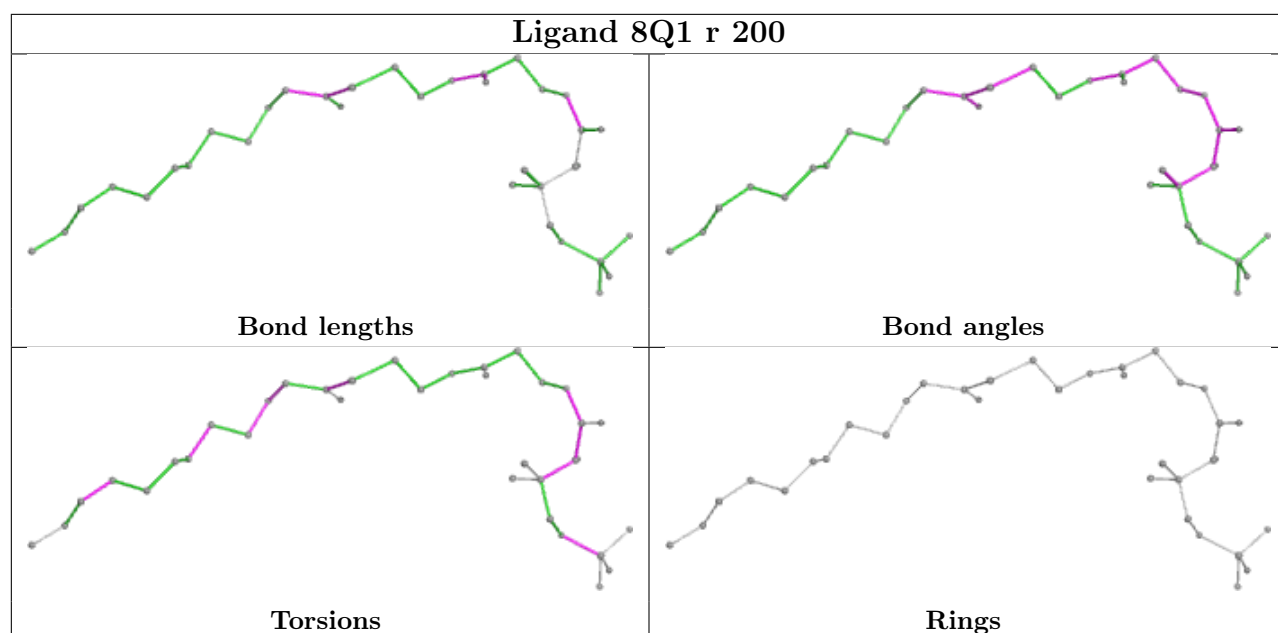


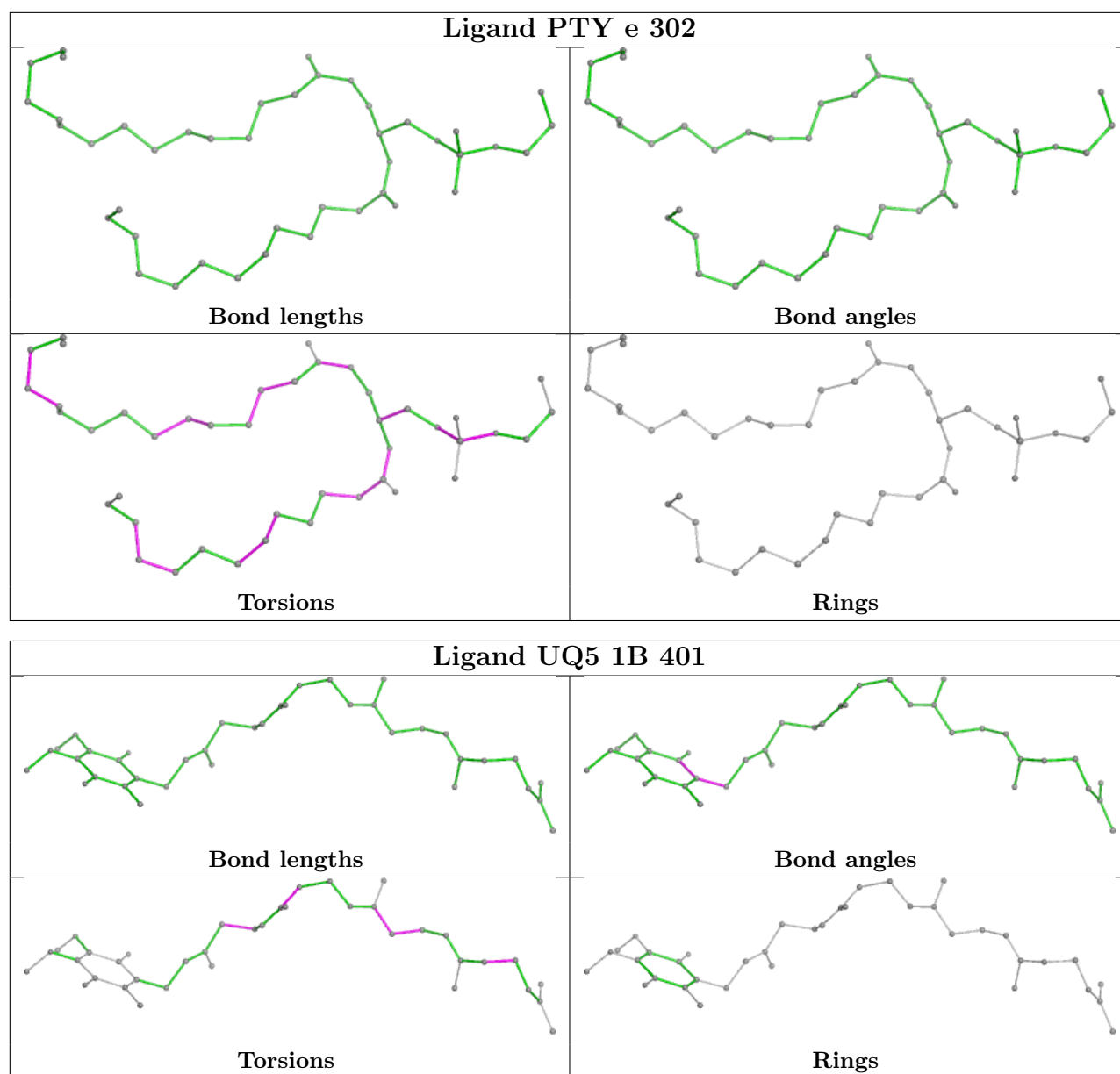


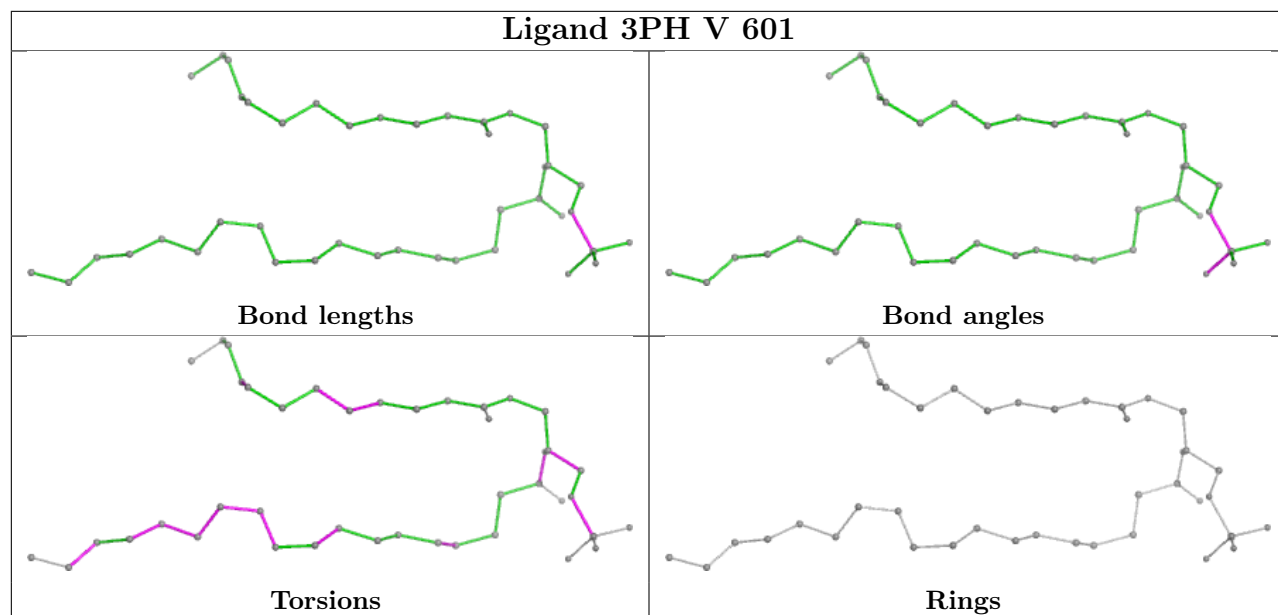
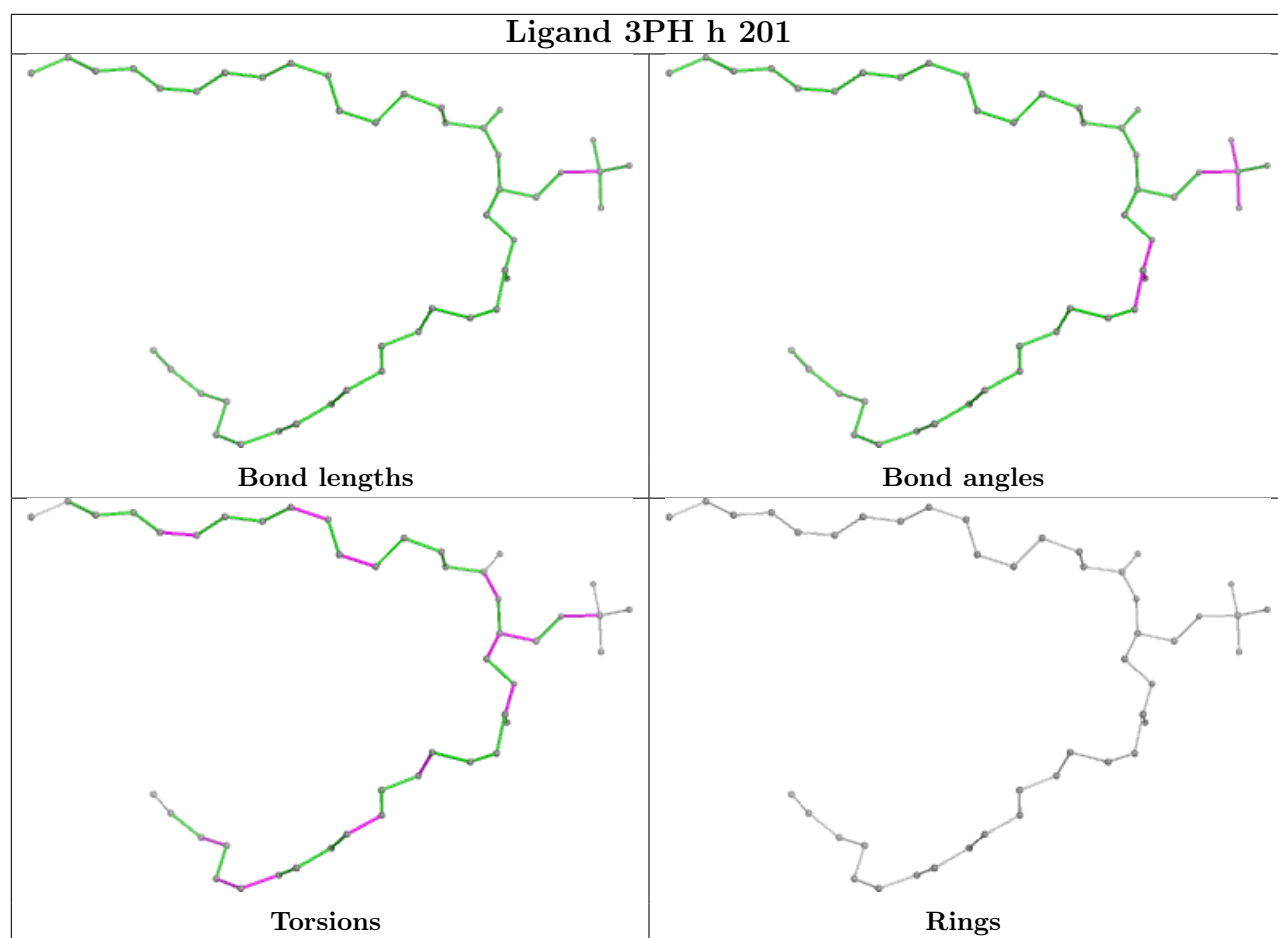


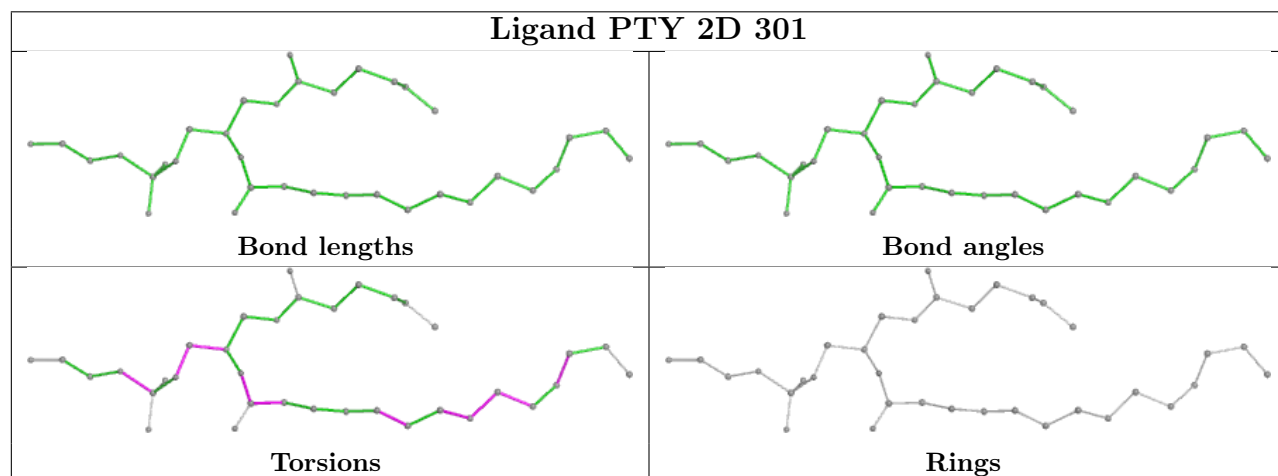
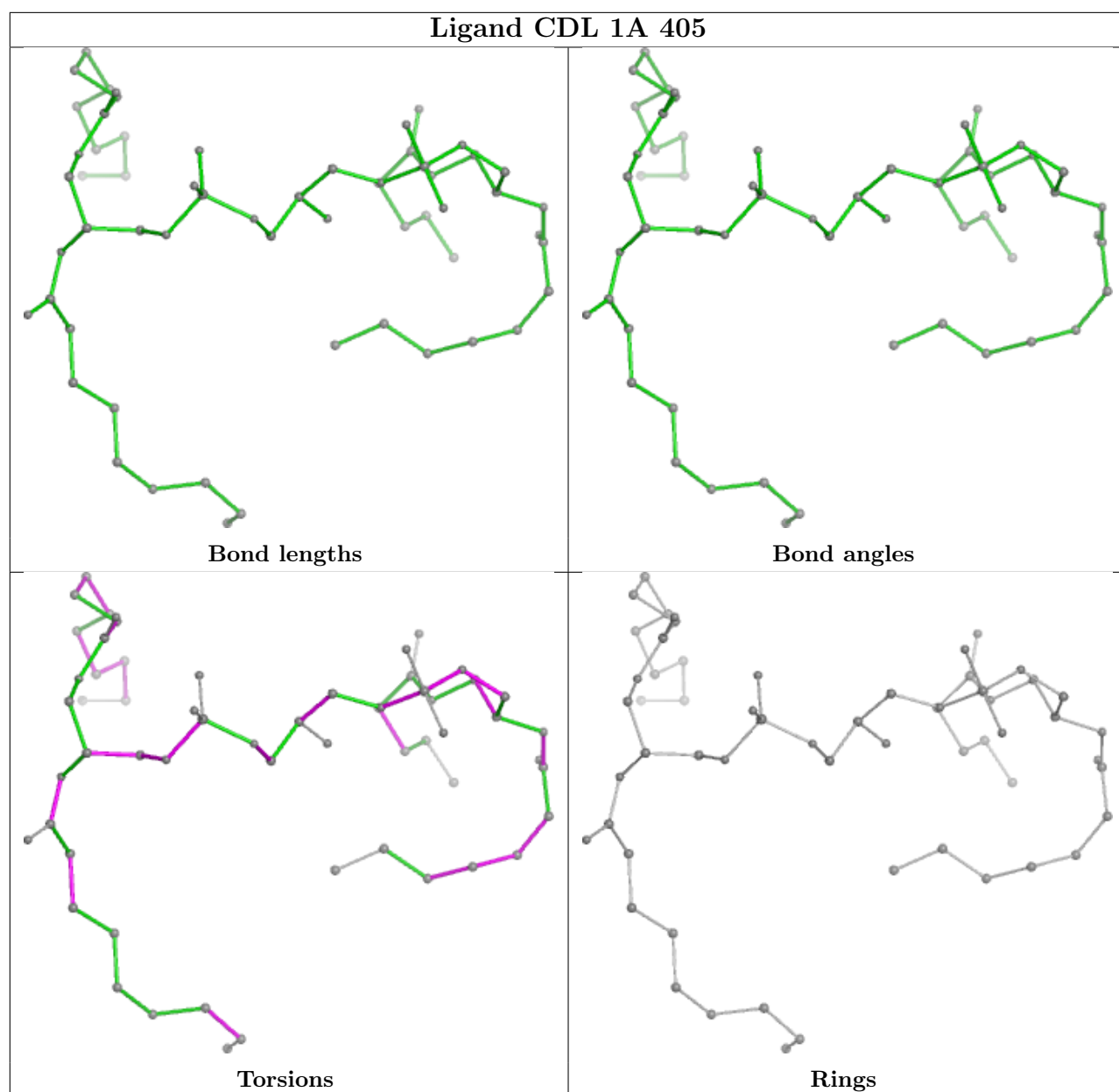


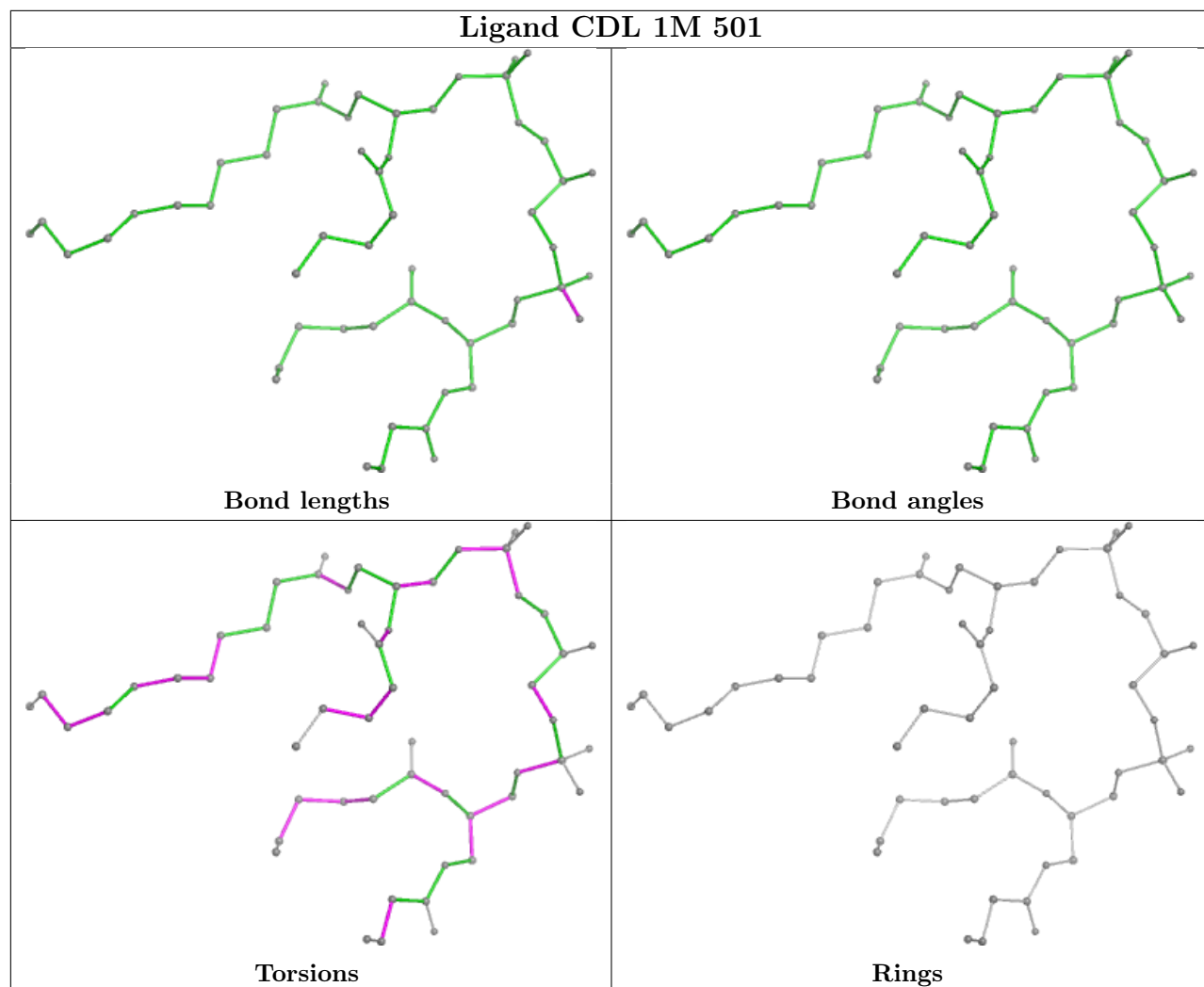


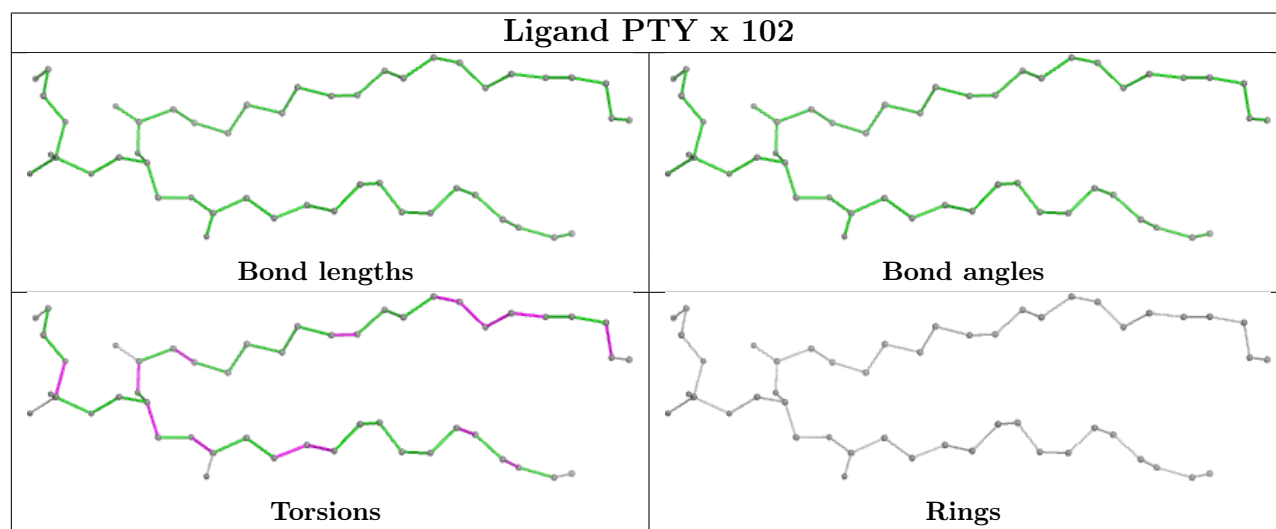
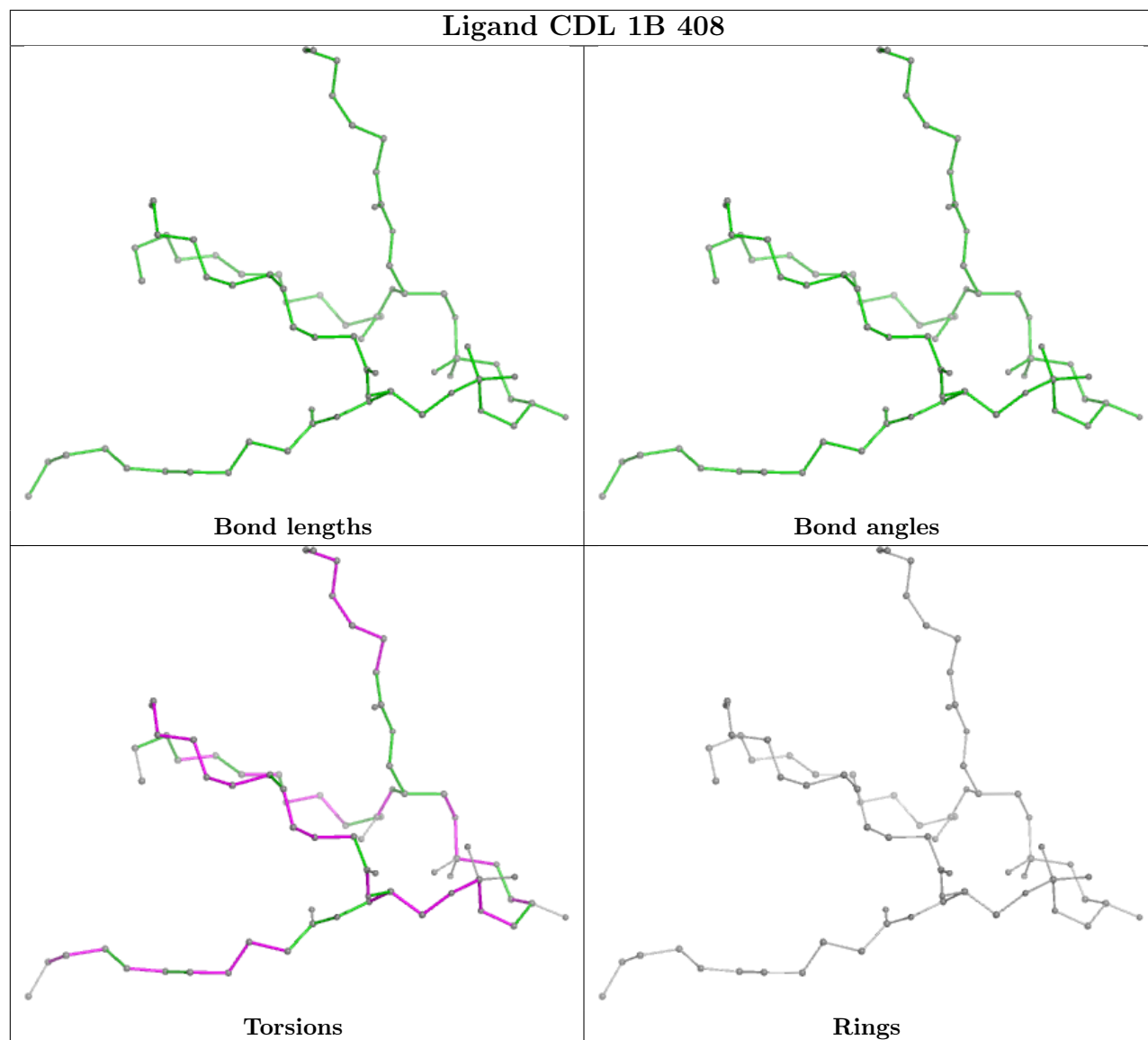


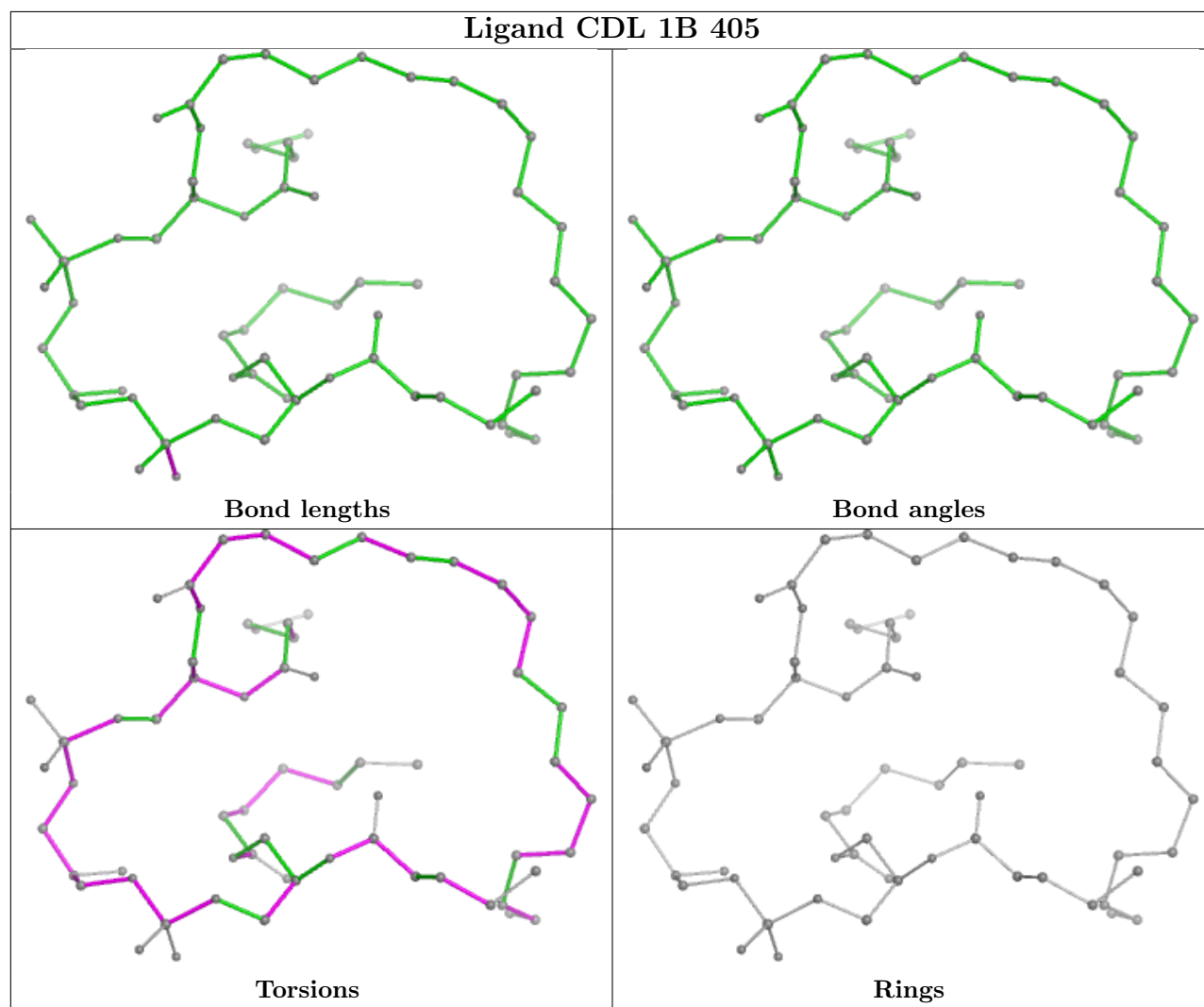
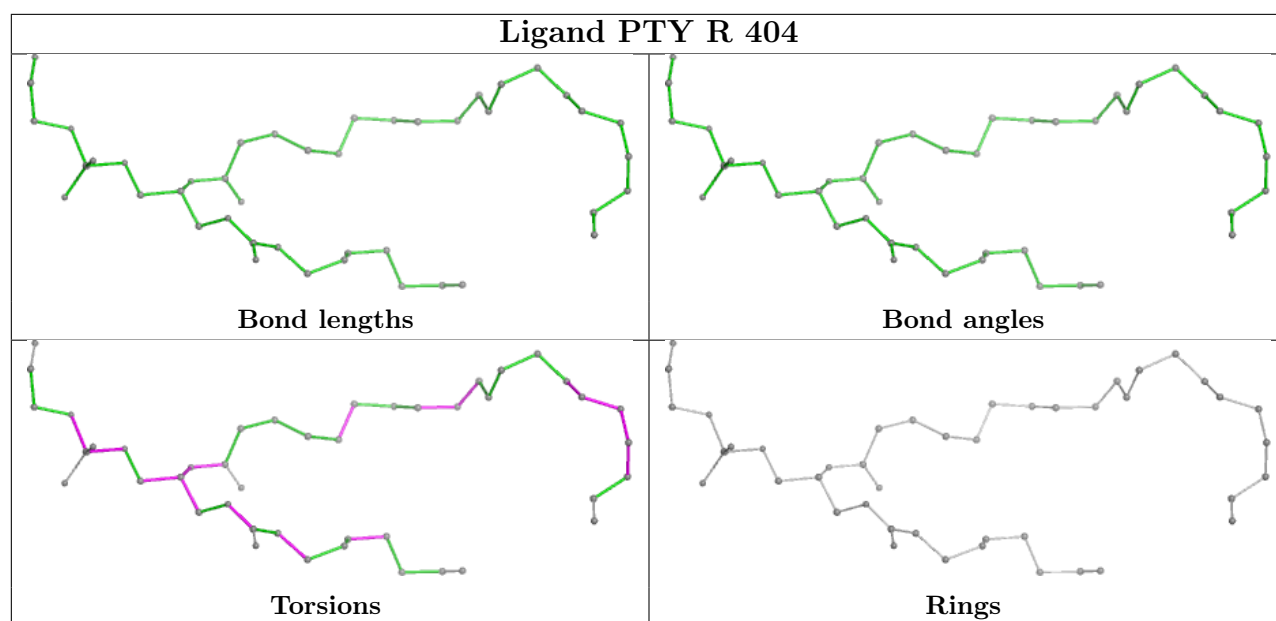


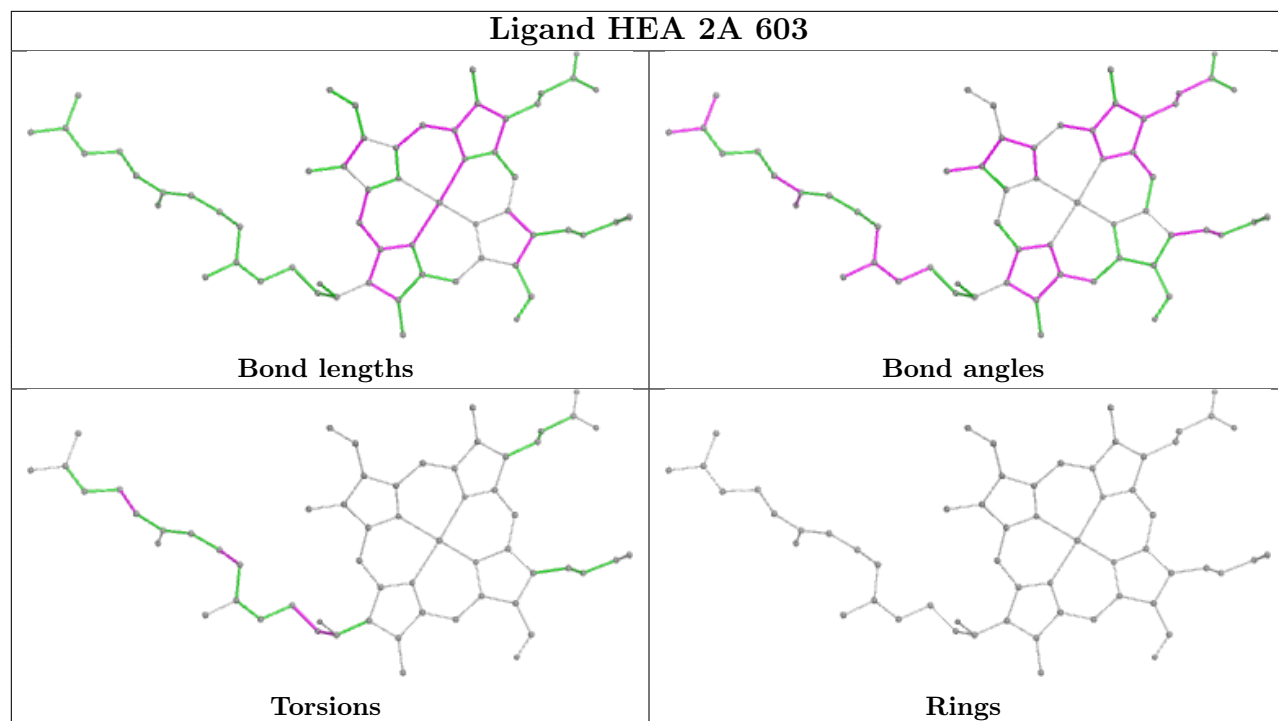
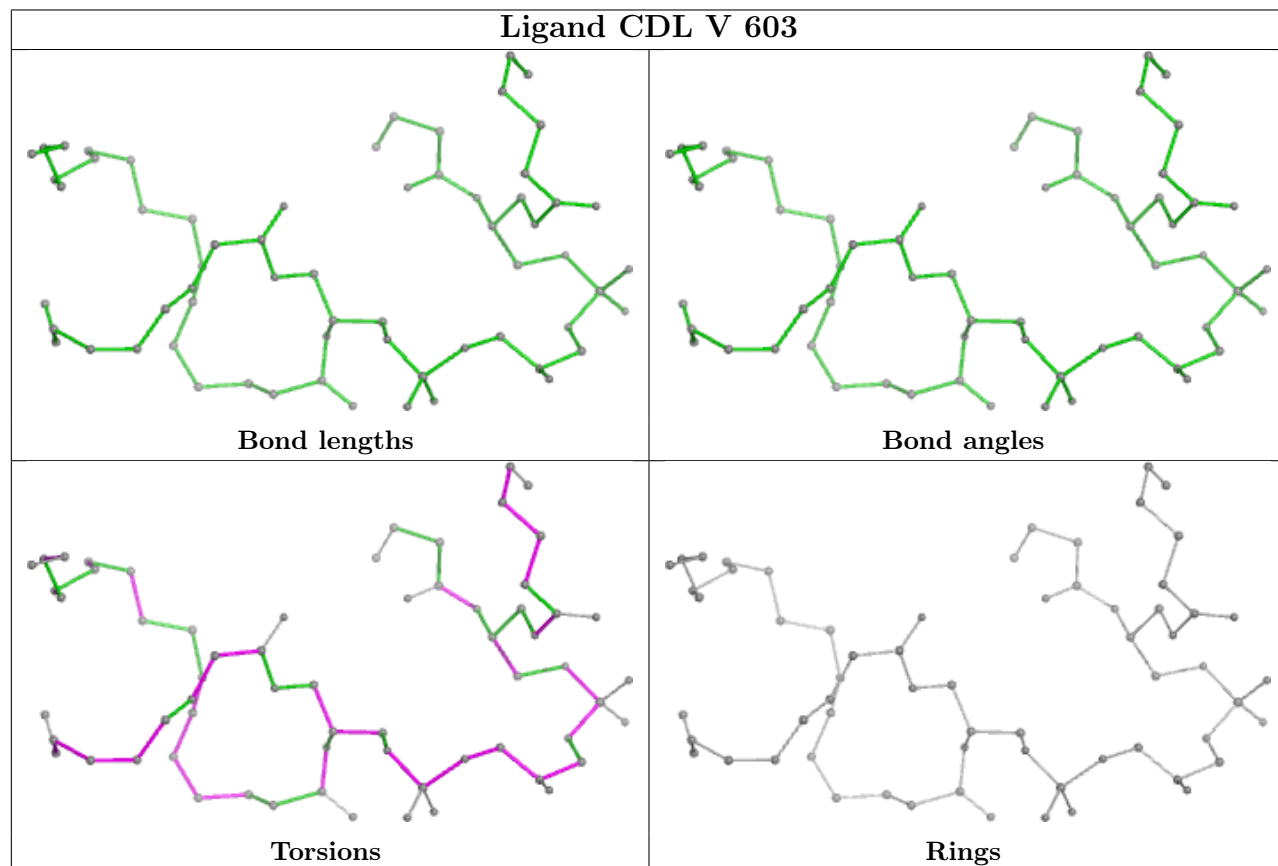


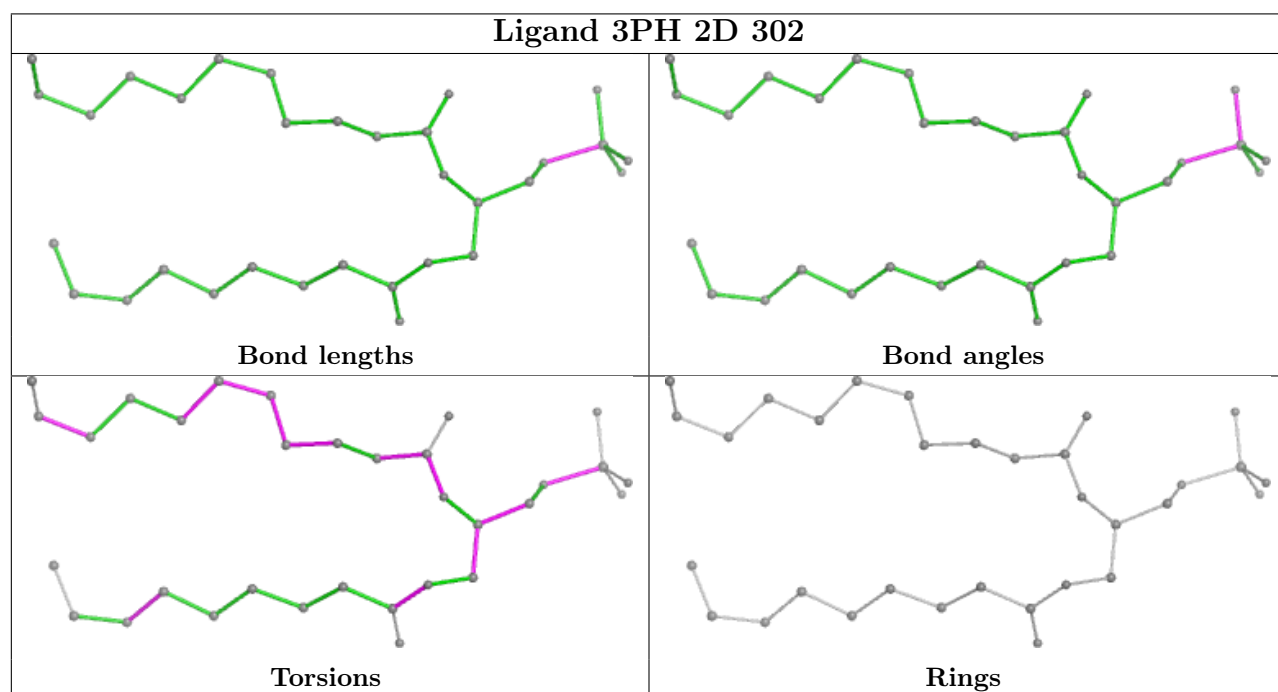
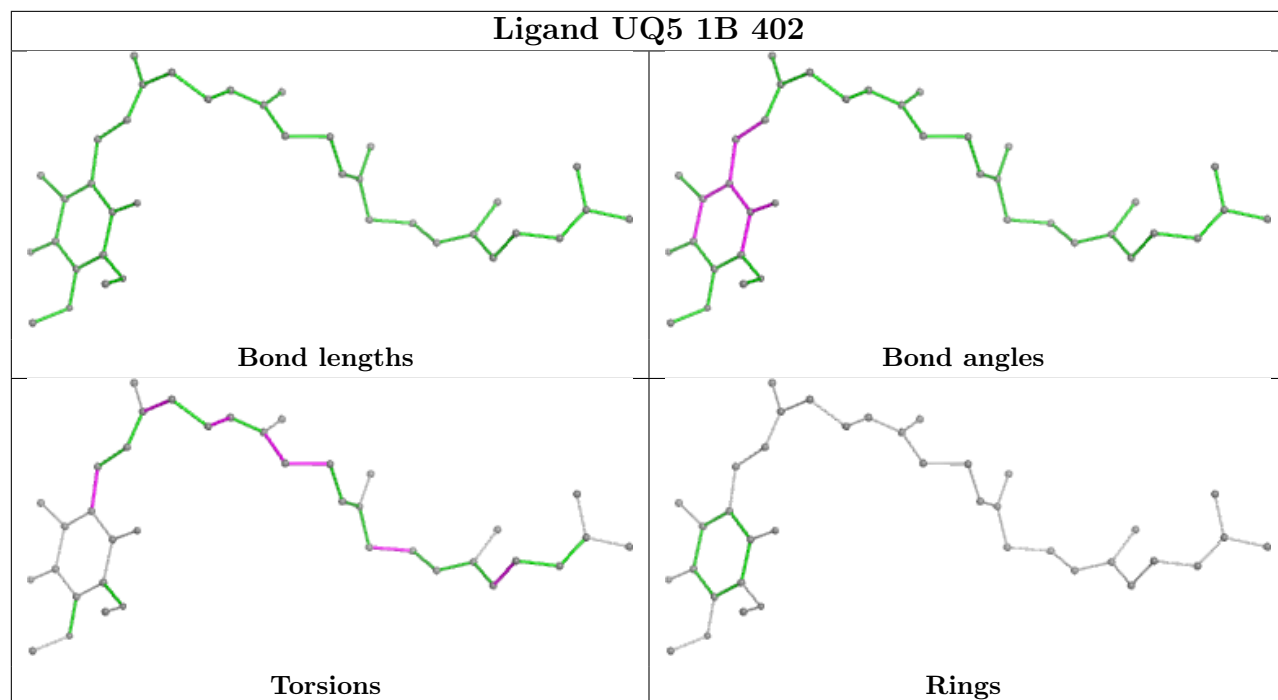


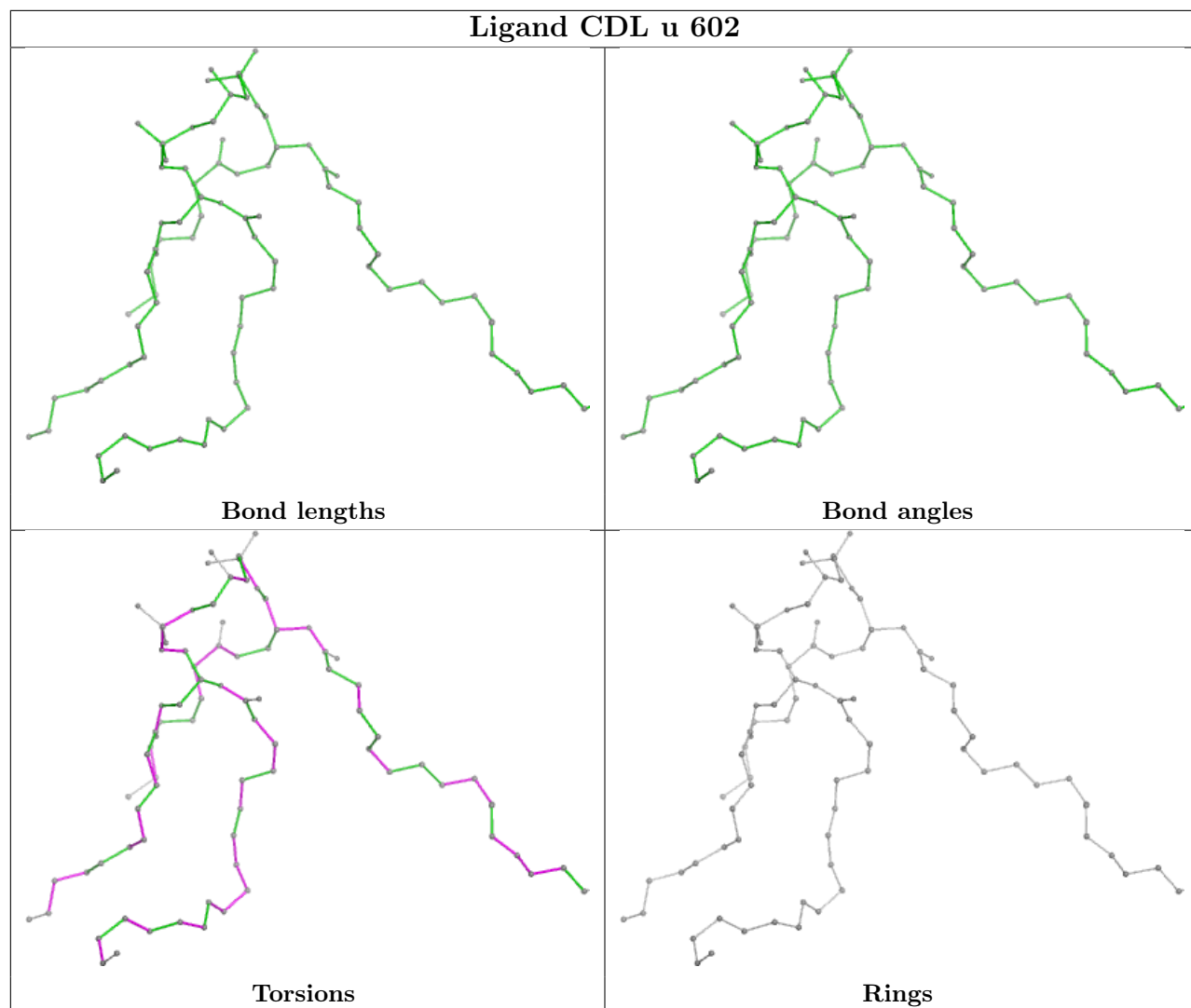


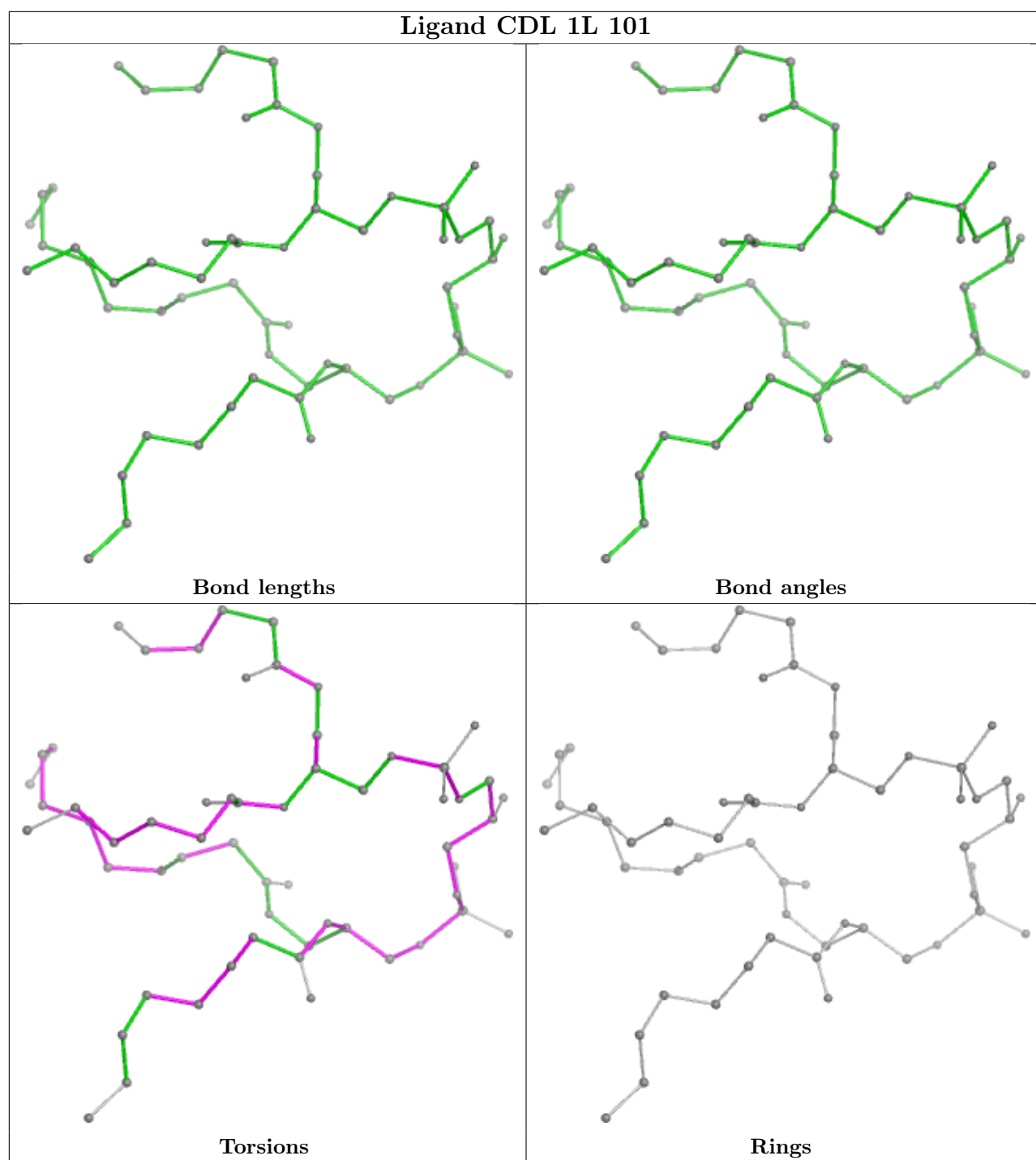


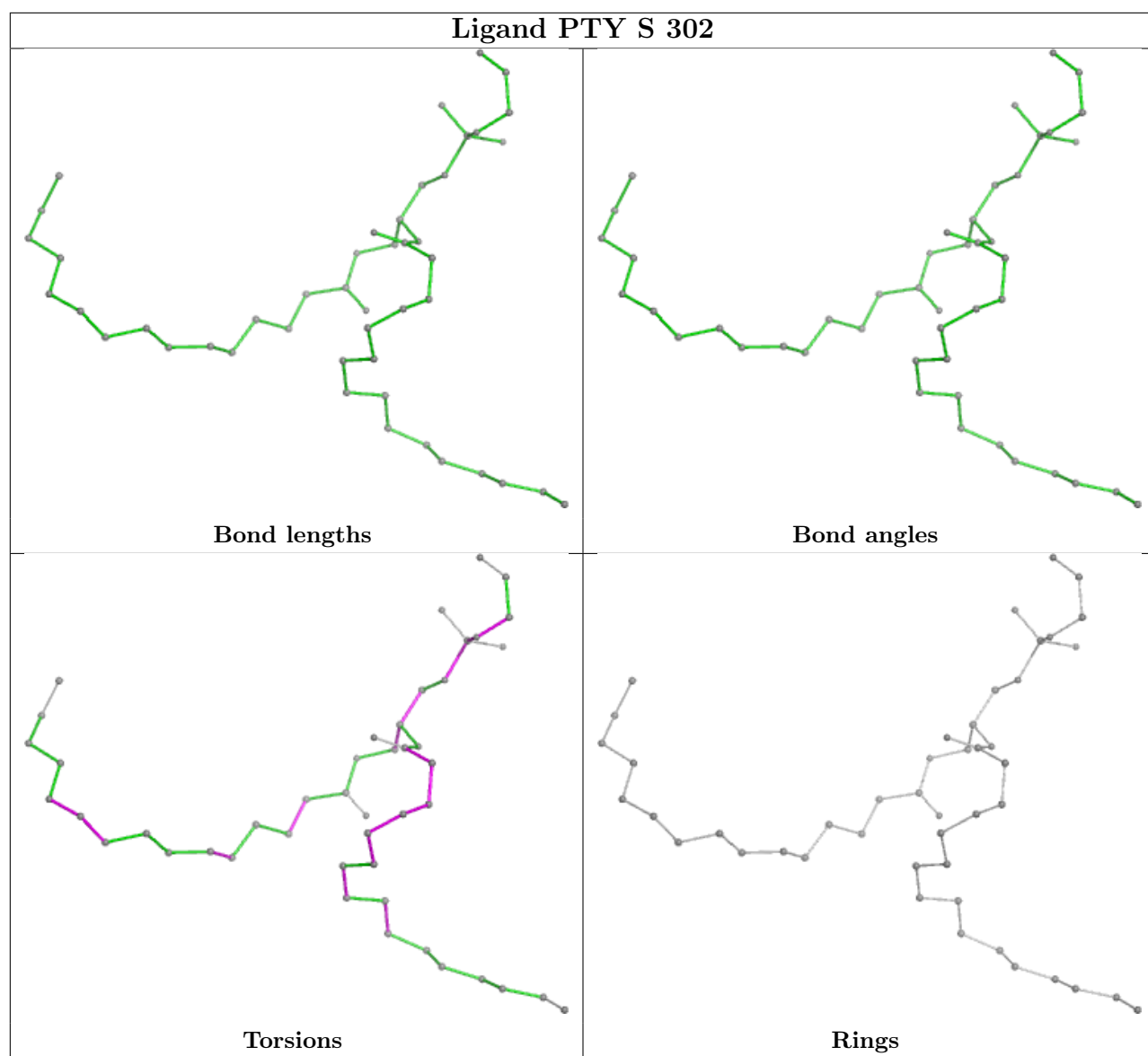


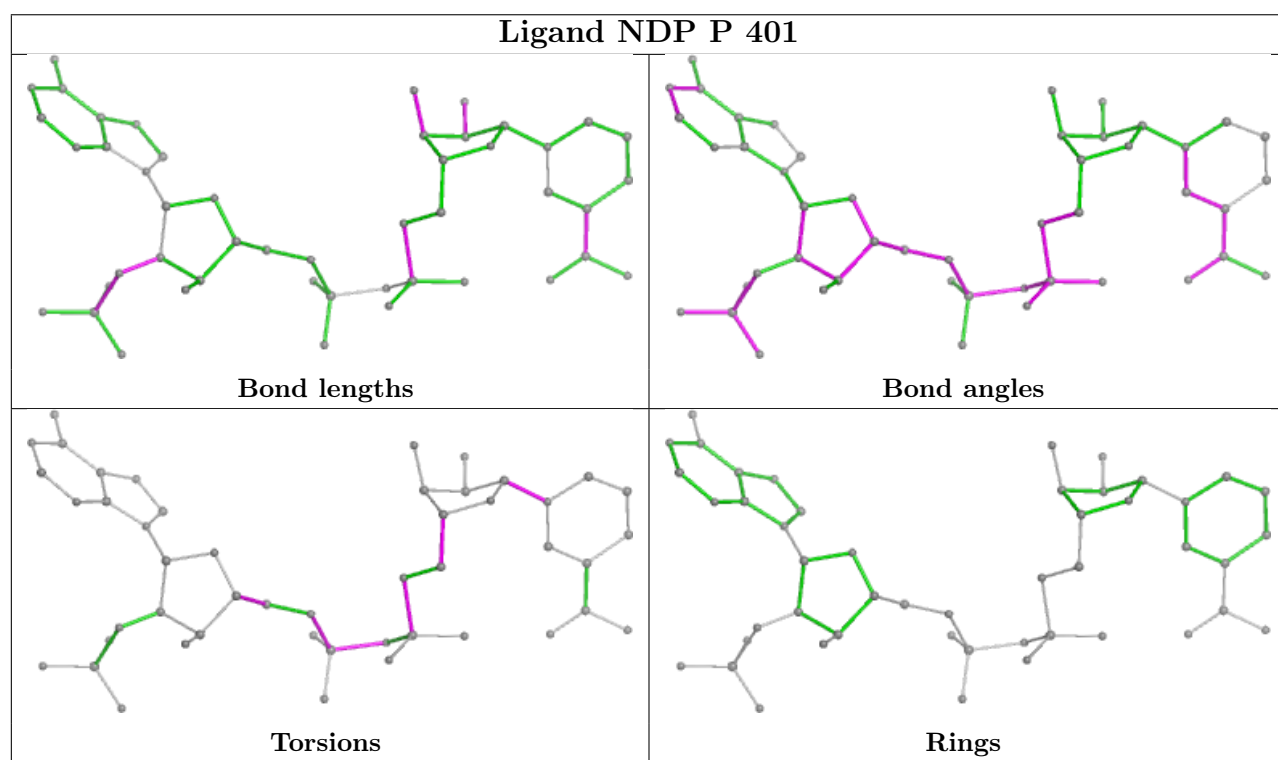
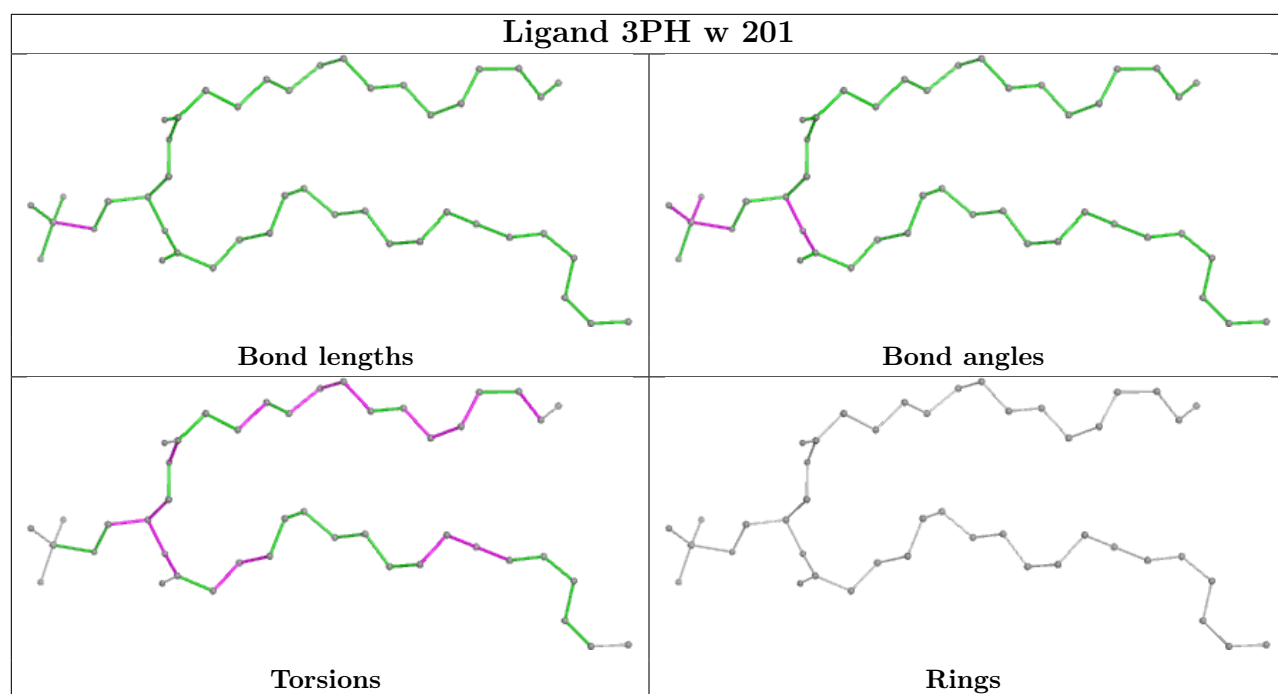
Ligand HEA 2A 603**Ligand CDL V 603**



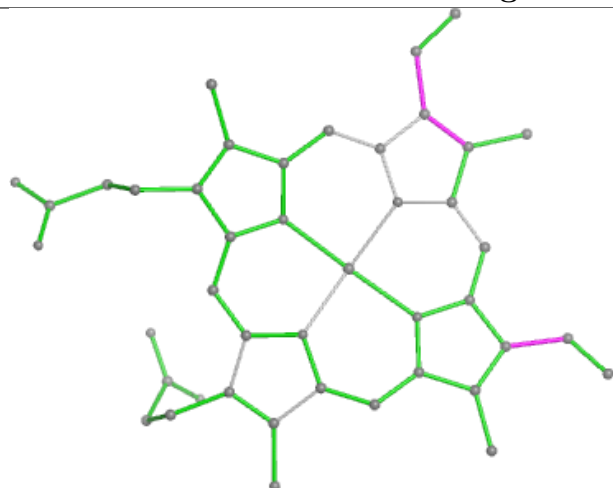




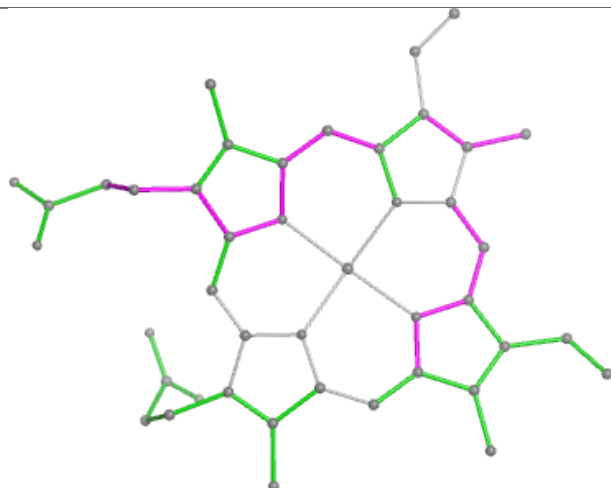




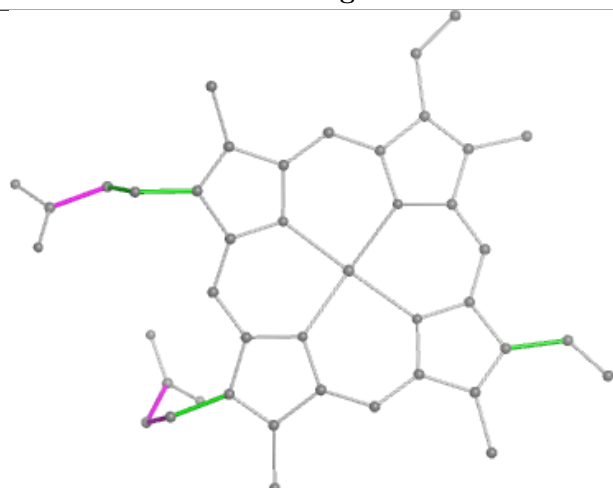
Ligand HEM 1B 404



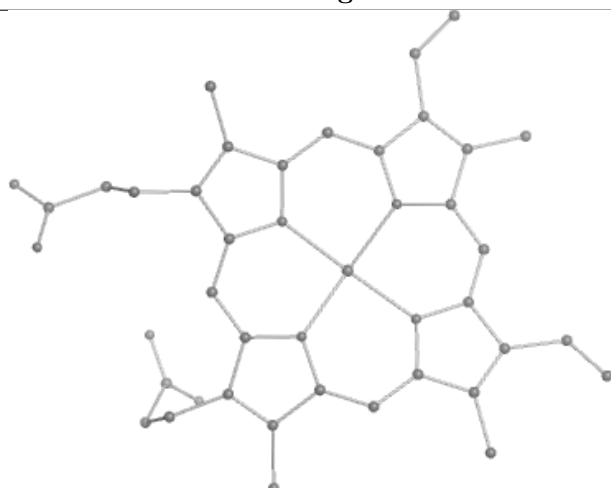
Bond lengths



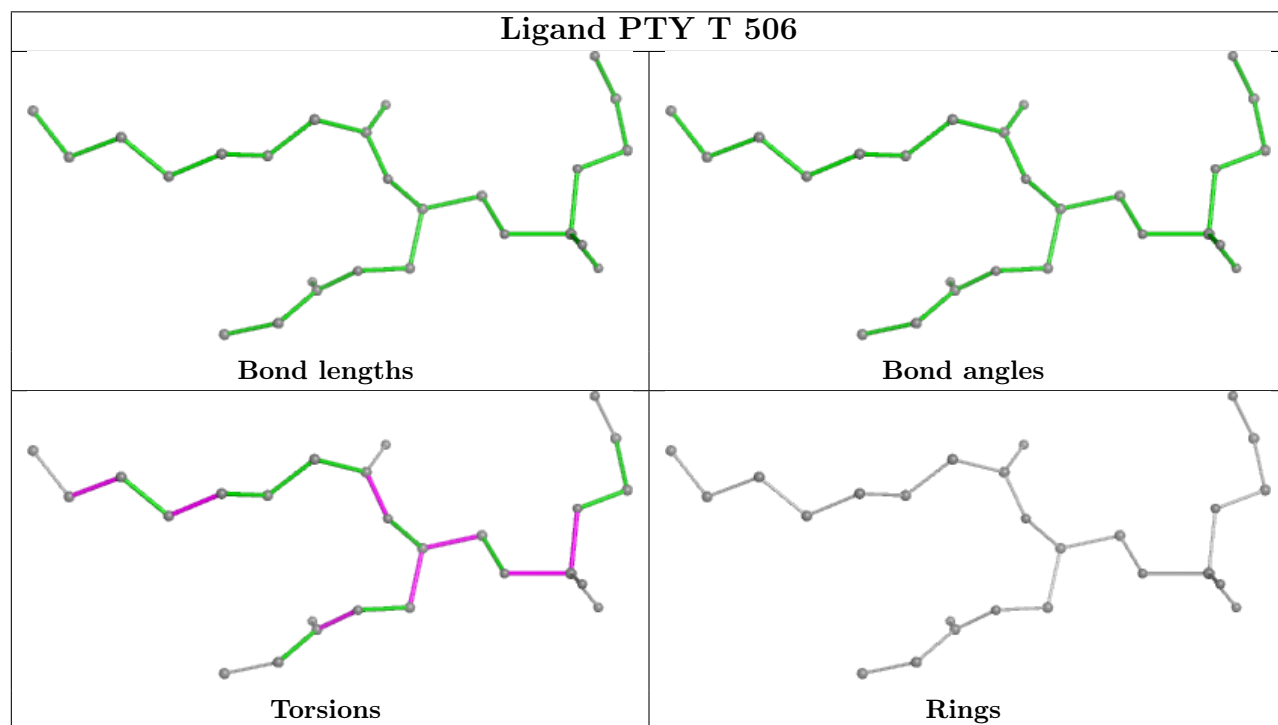
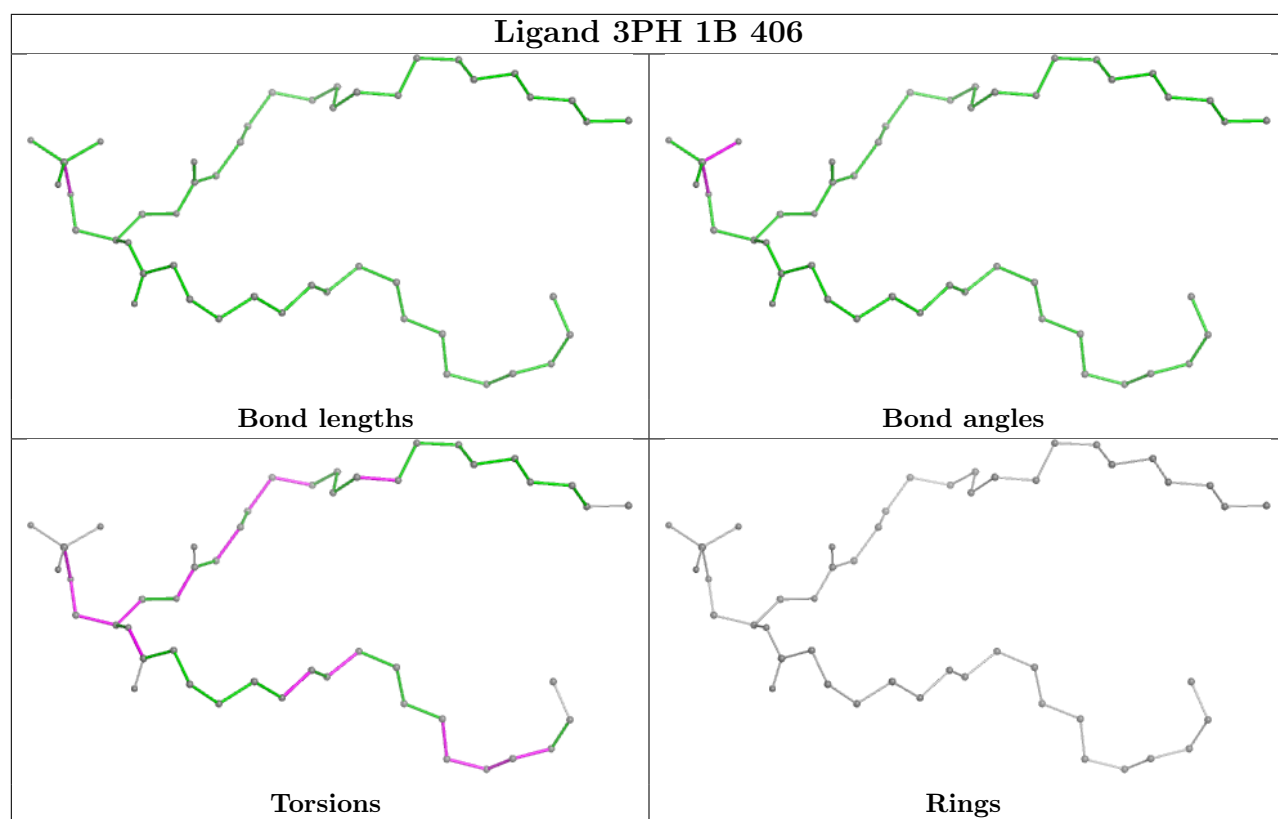
Bond angles

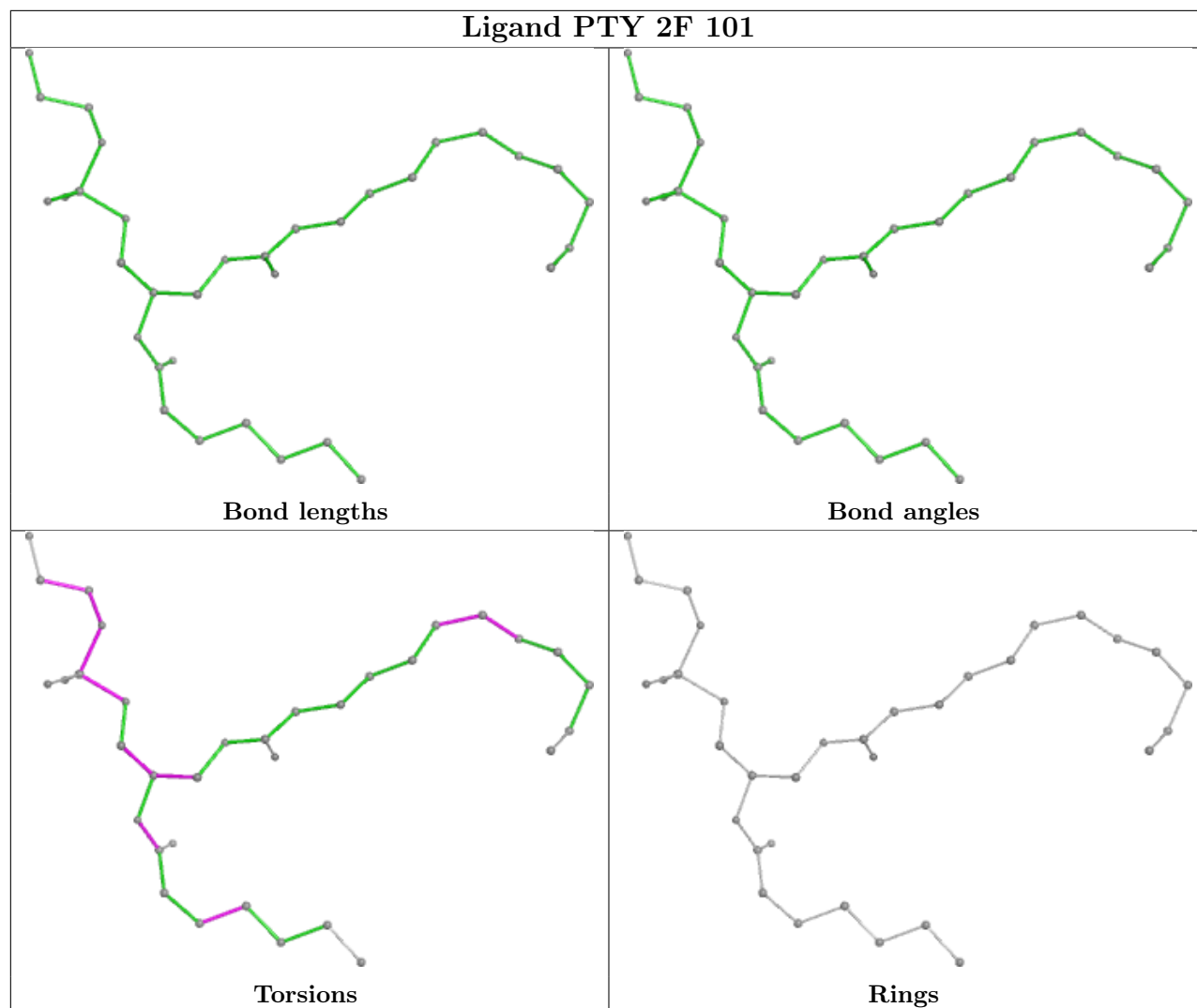


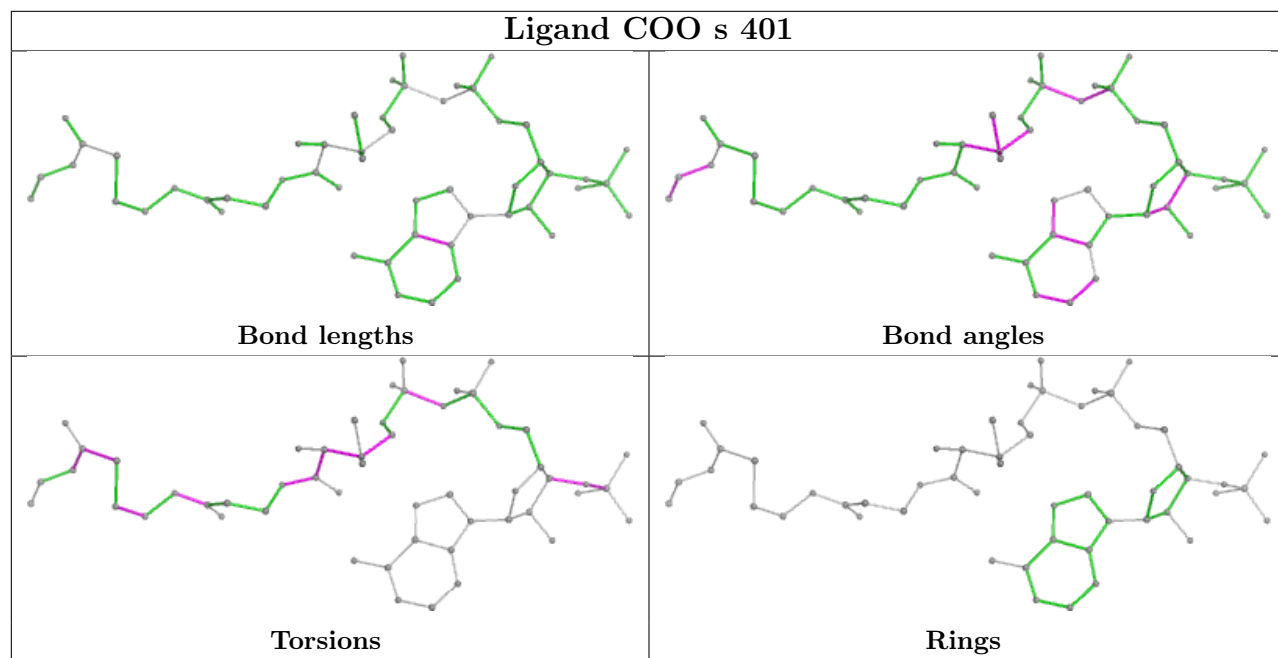
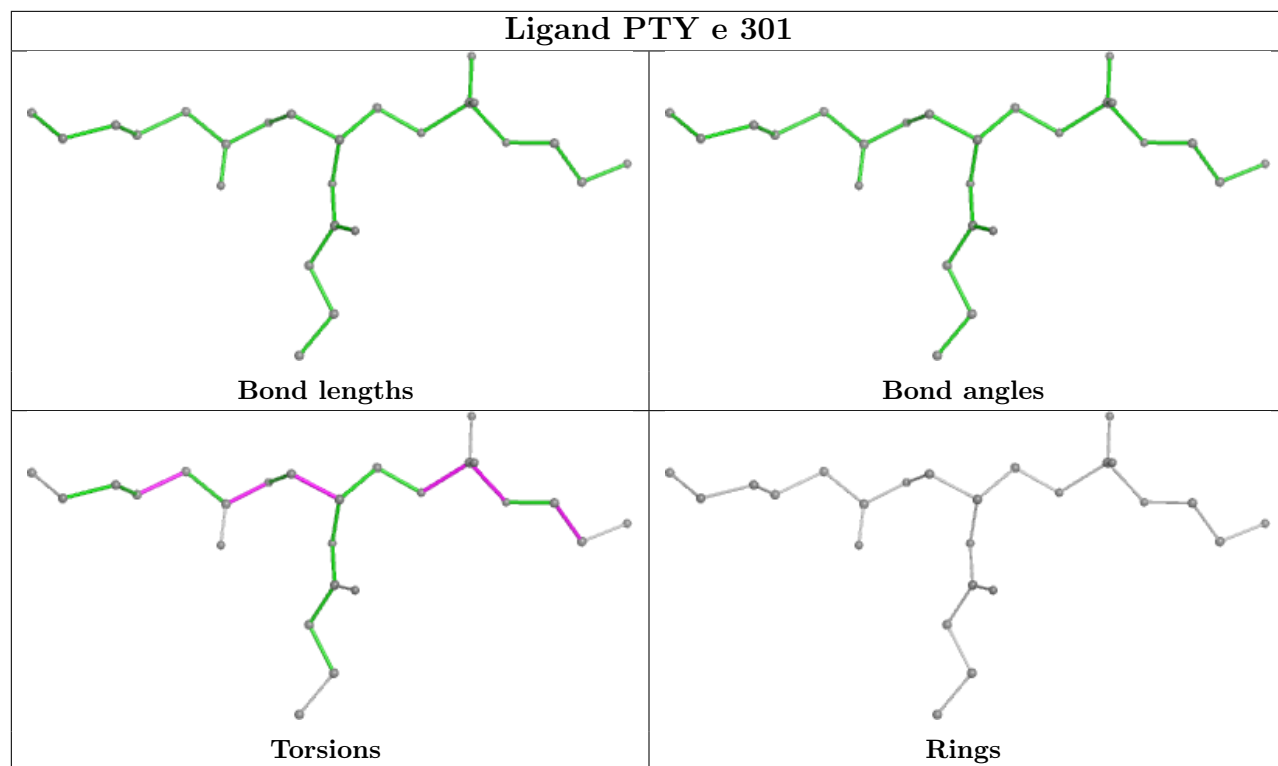
Torsions

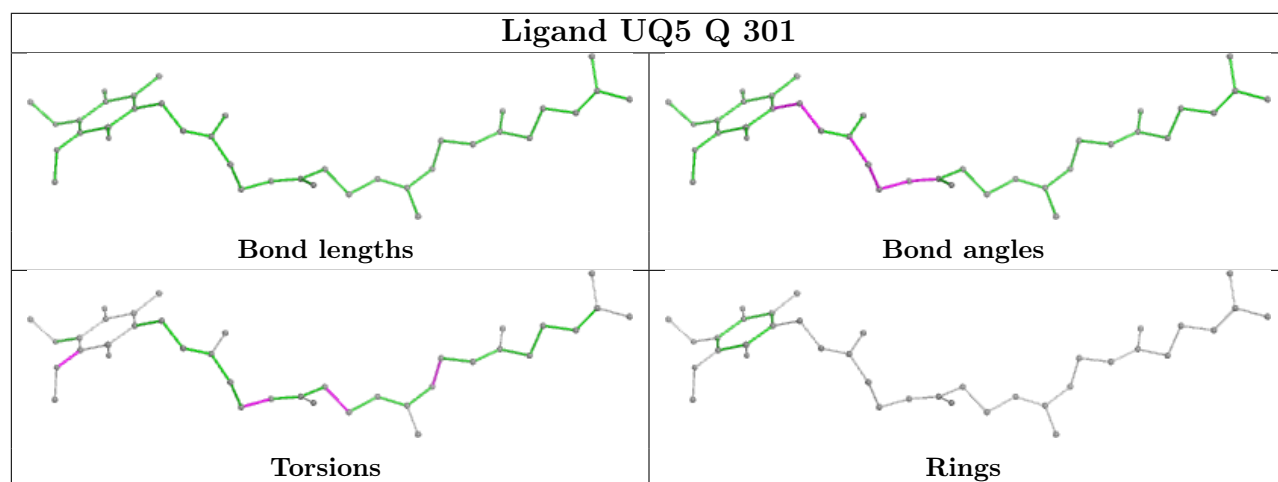
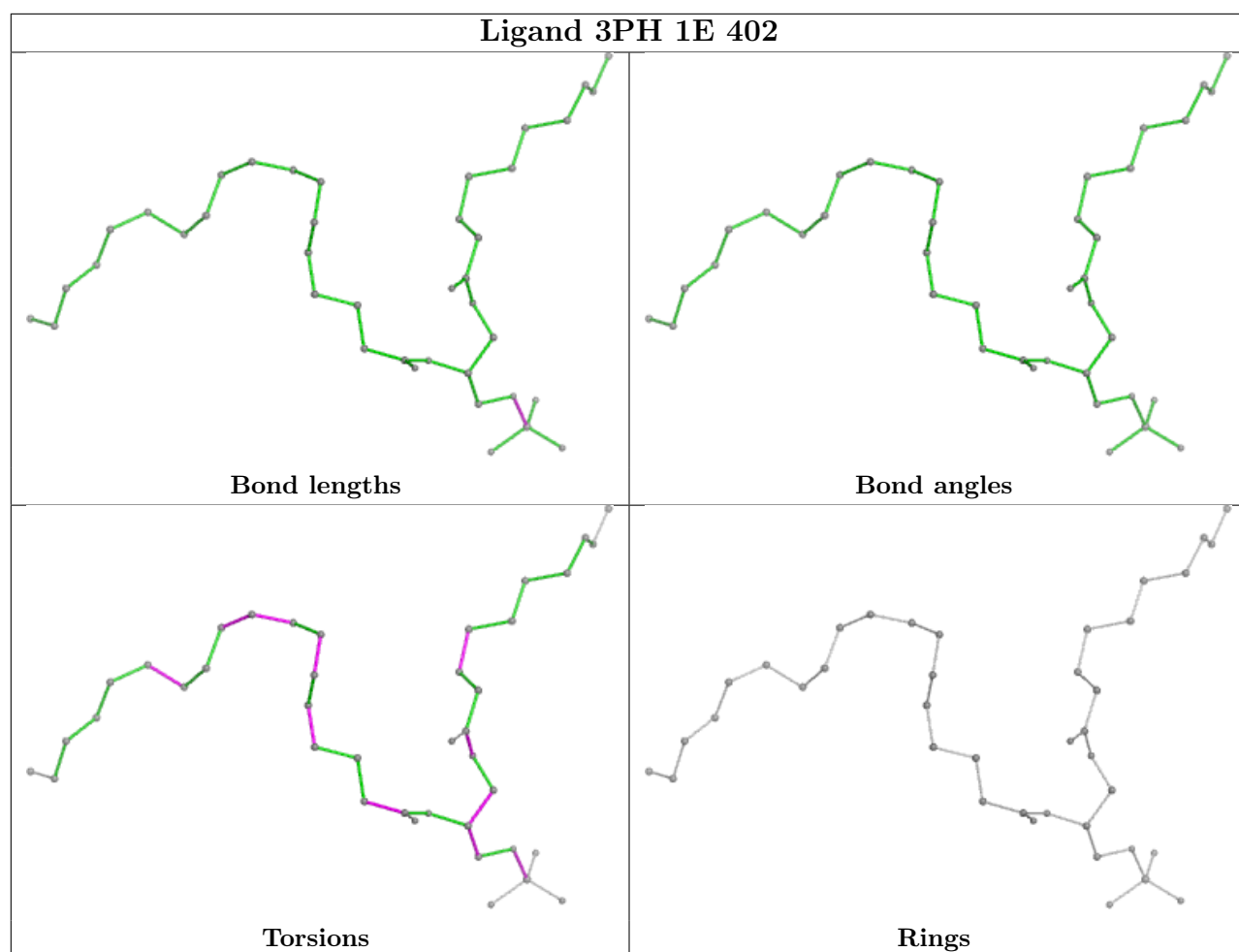


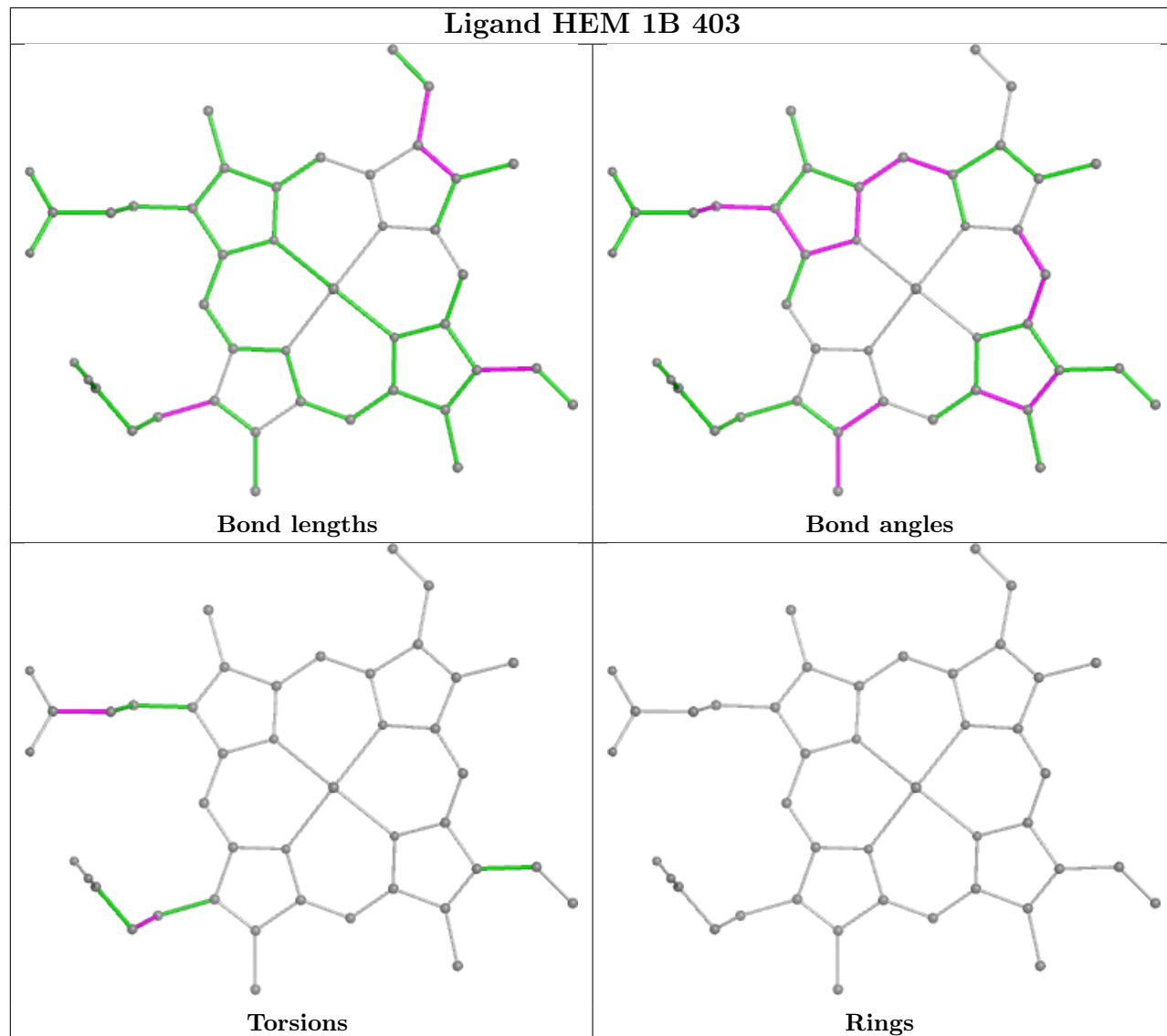
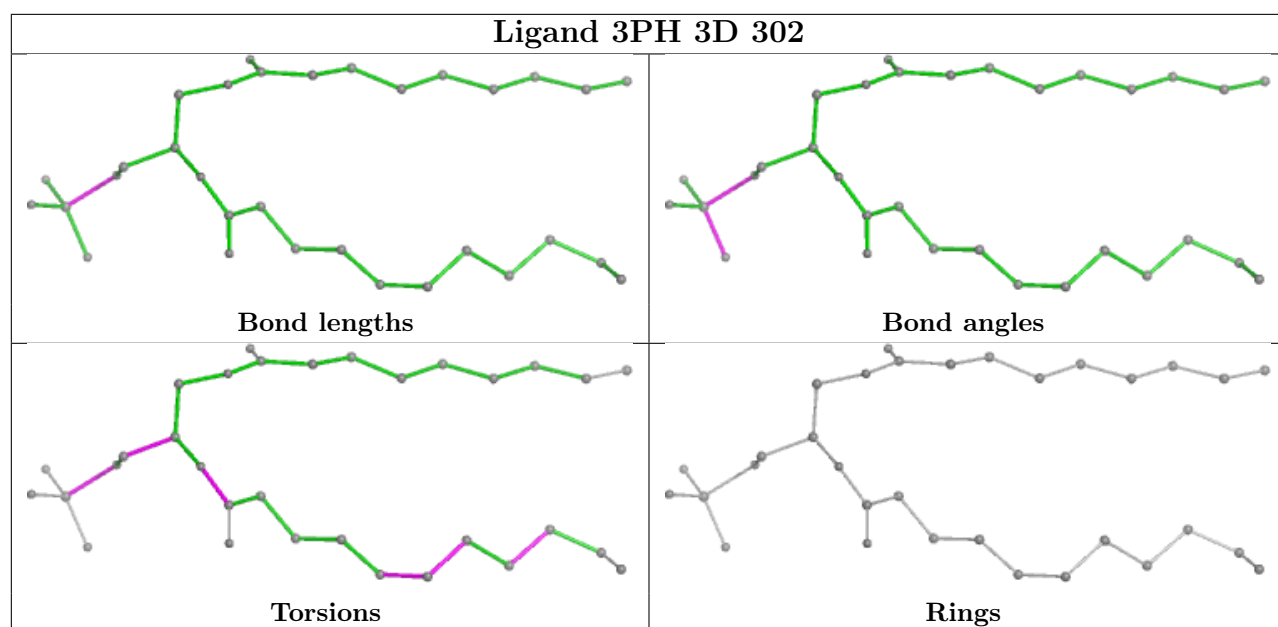
Rings

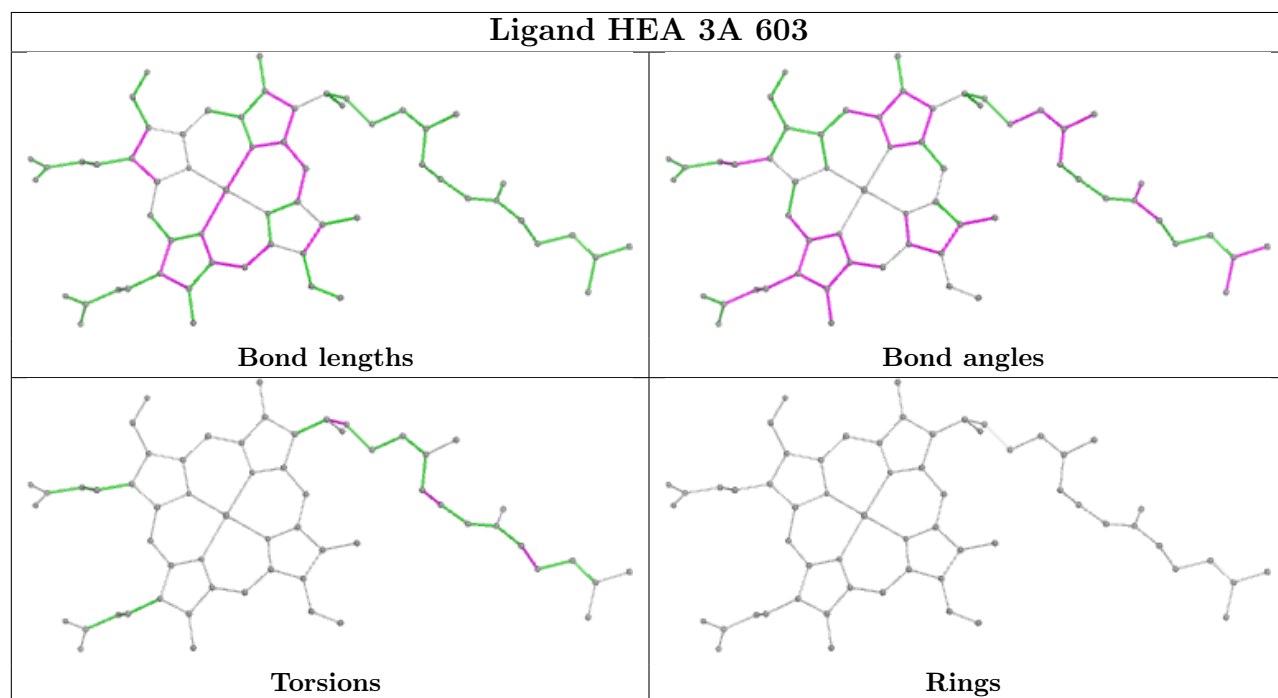
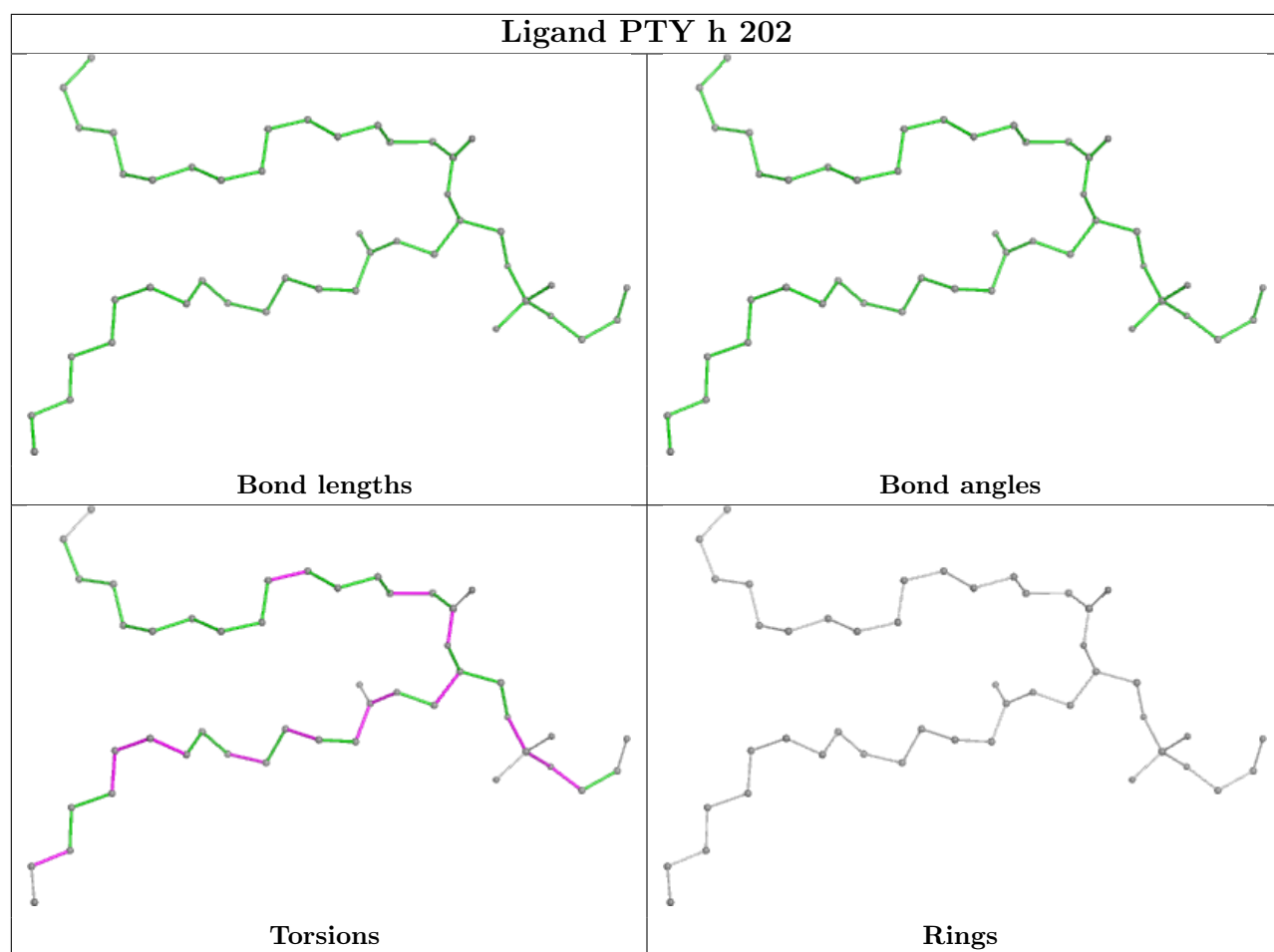


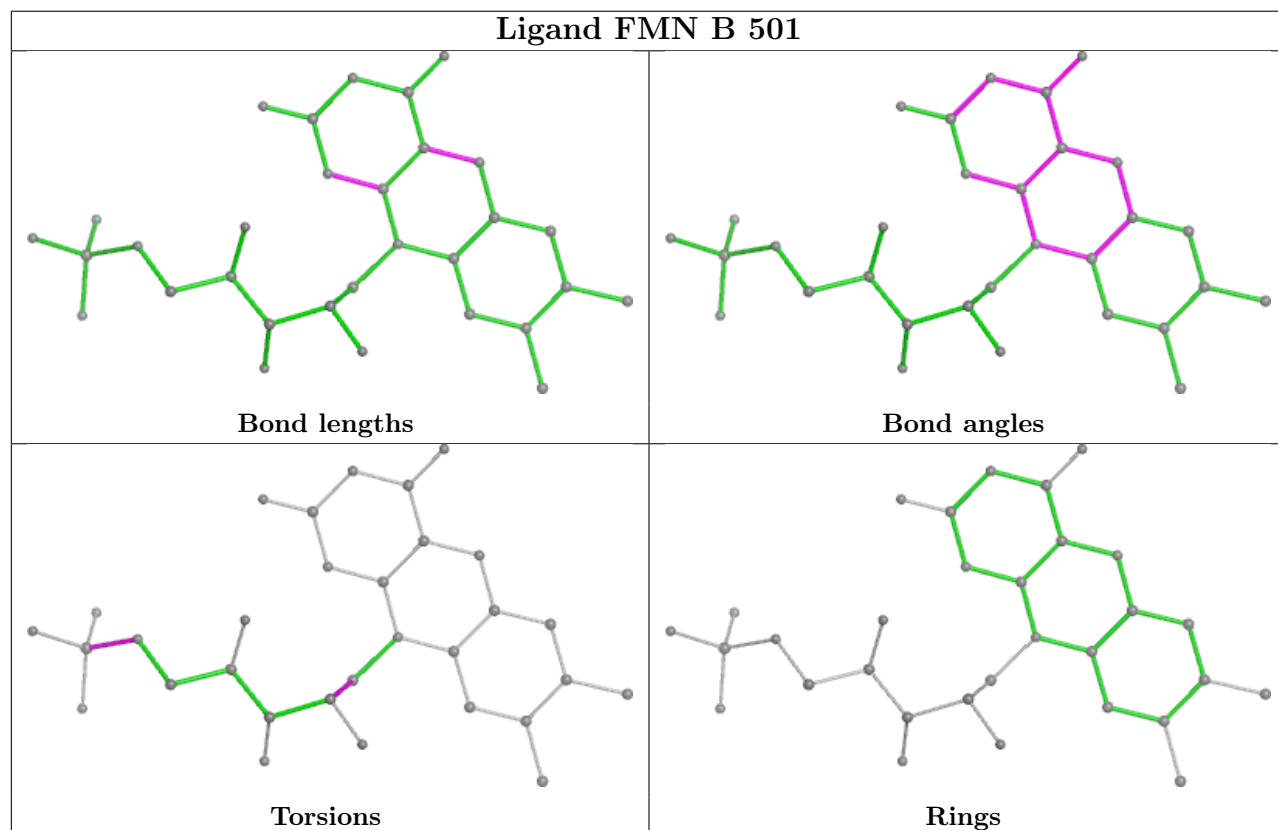
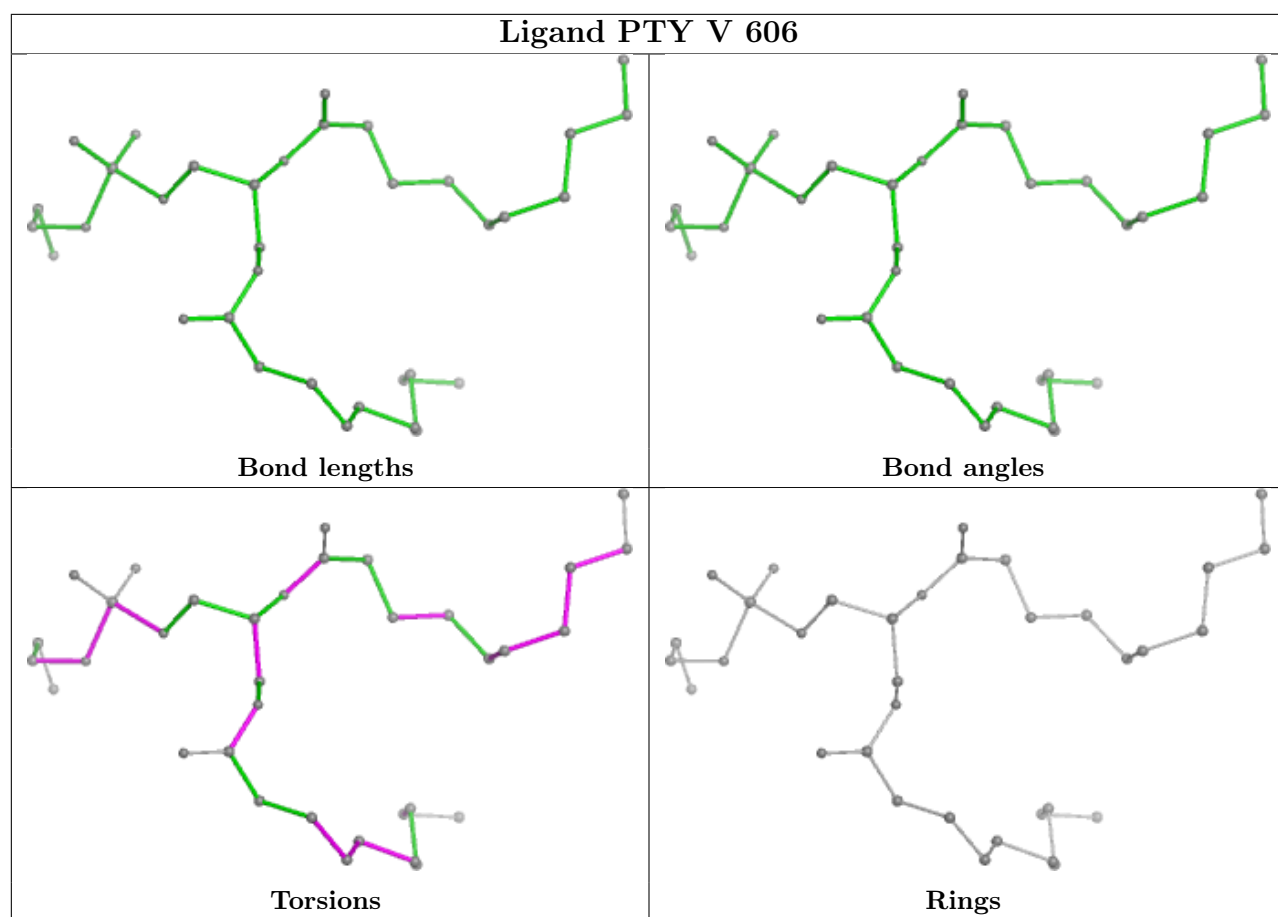


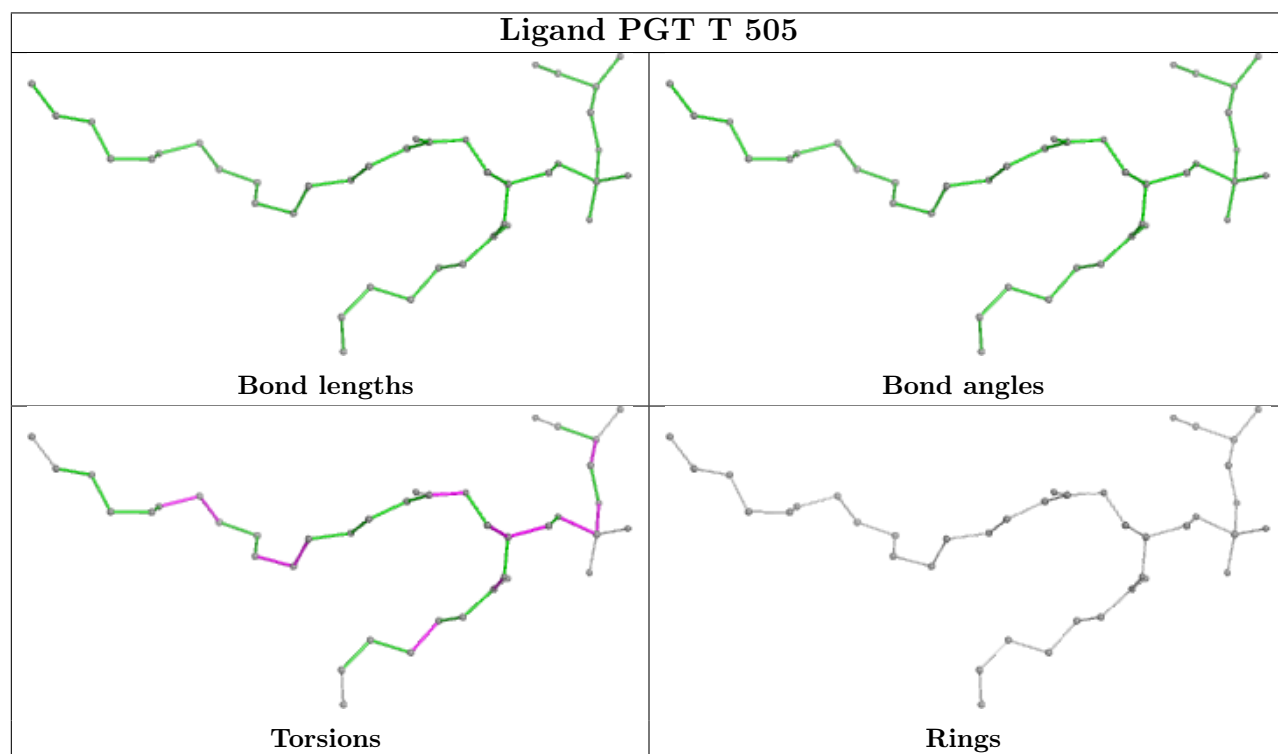
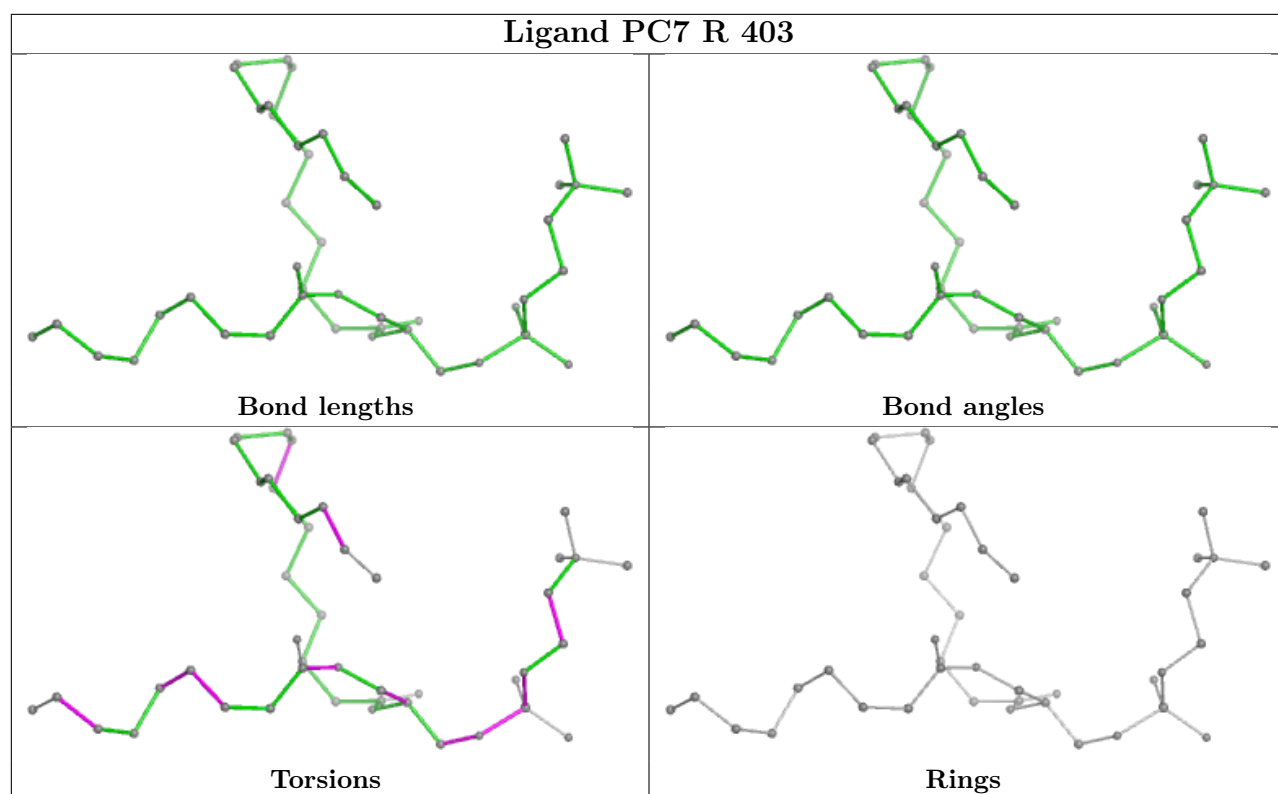


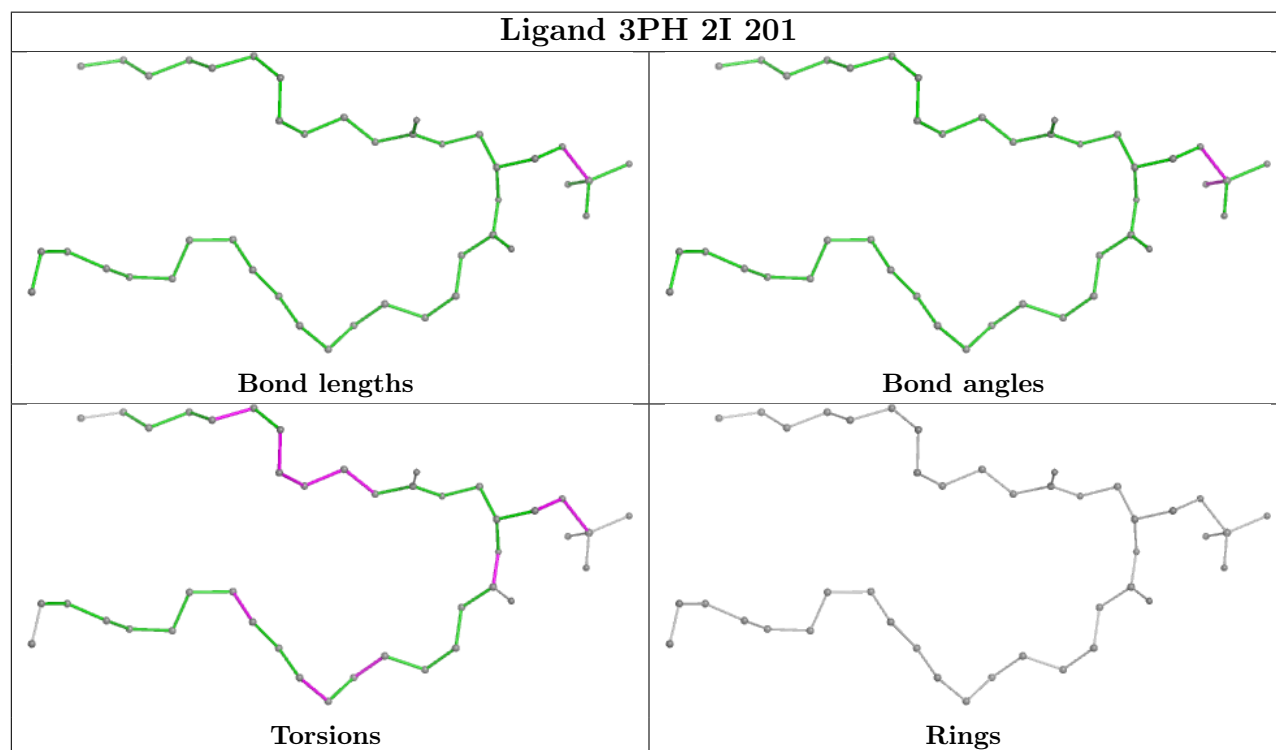
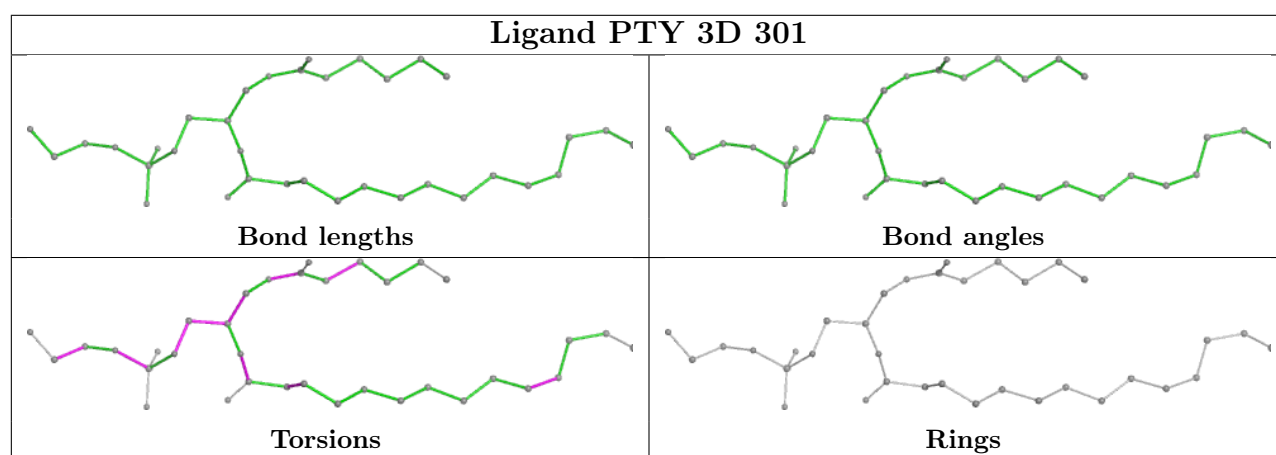
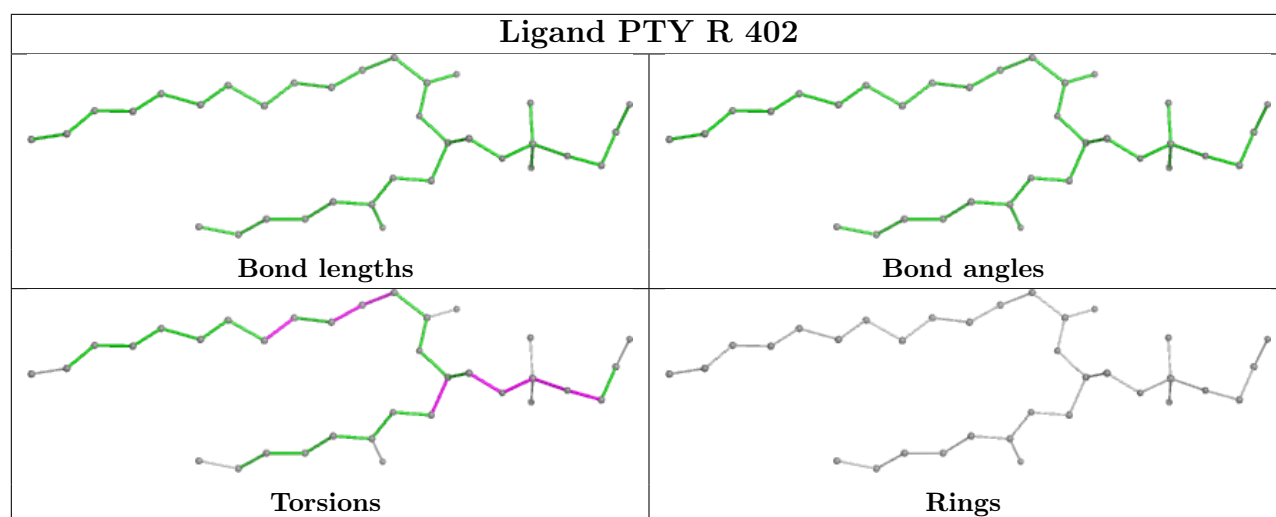


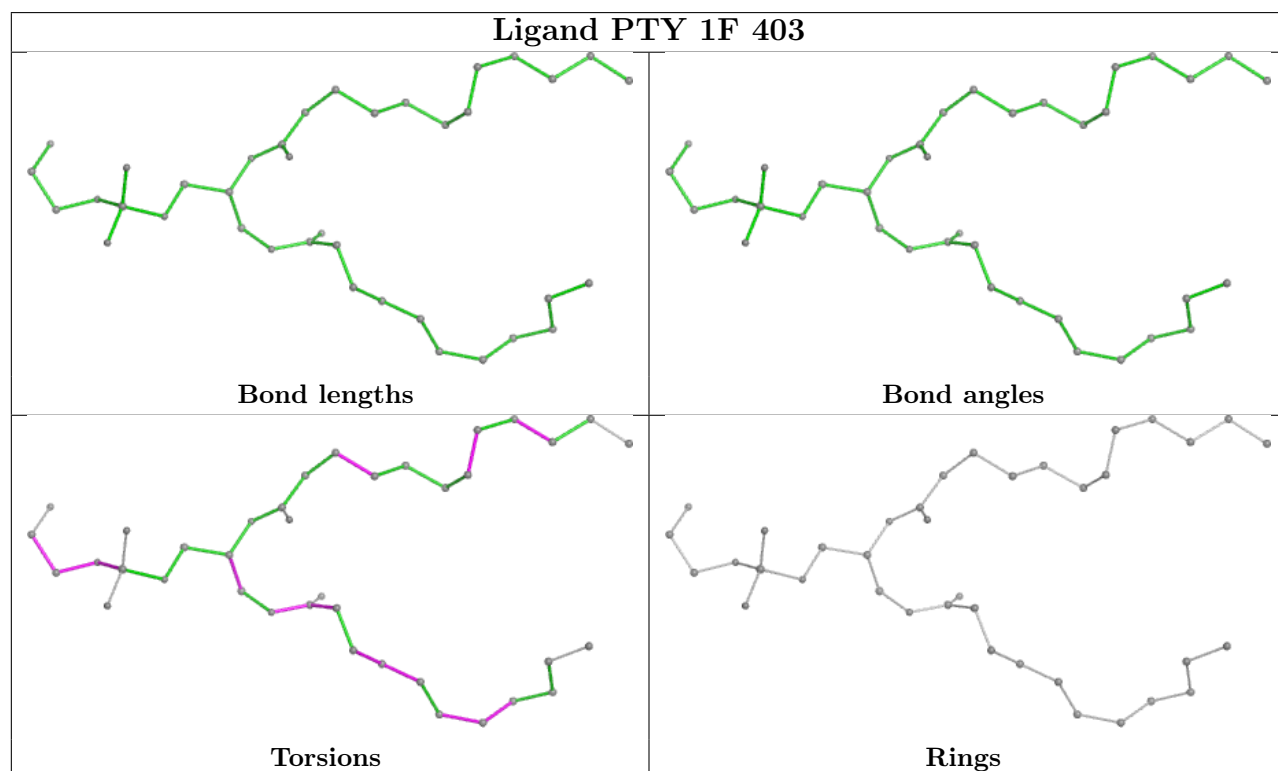
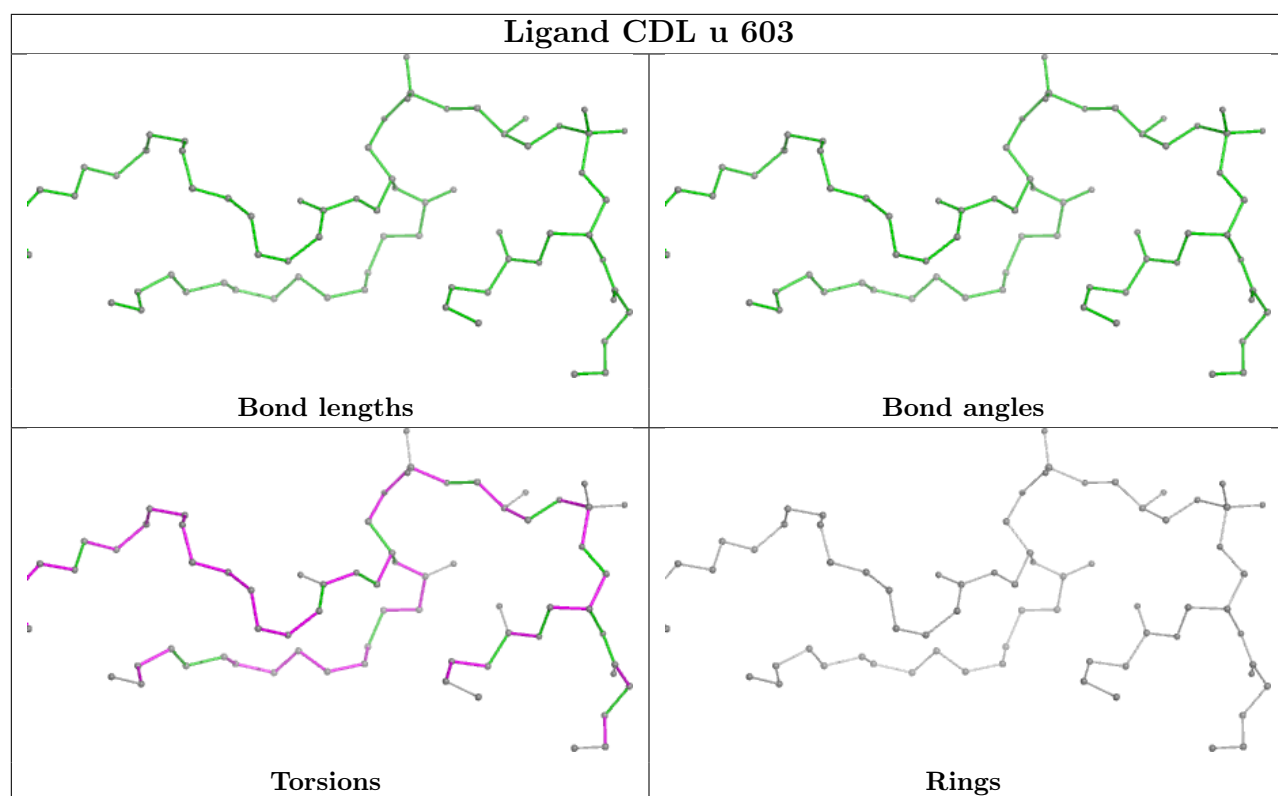


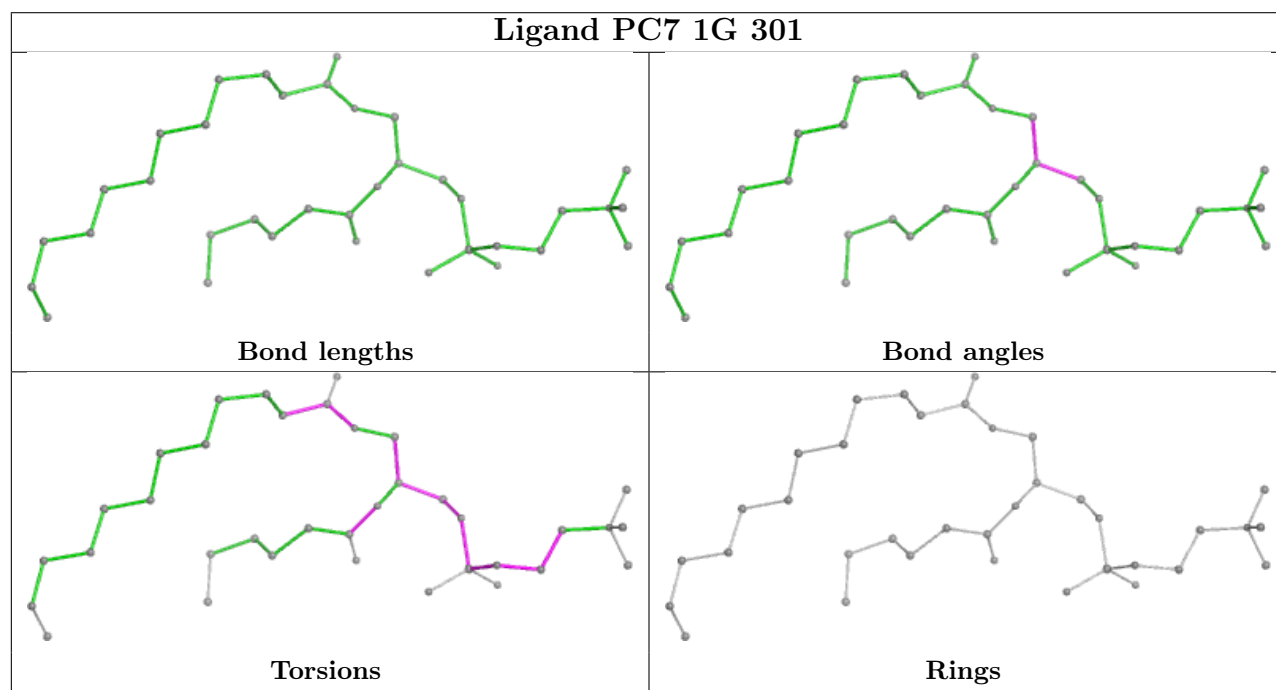
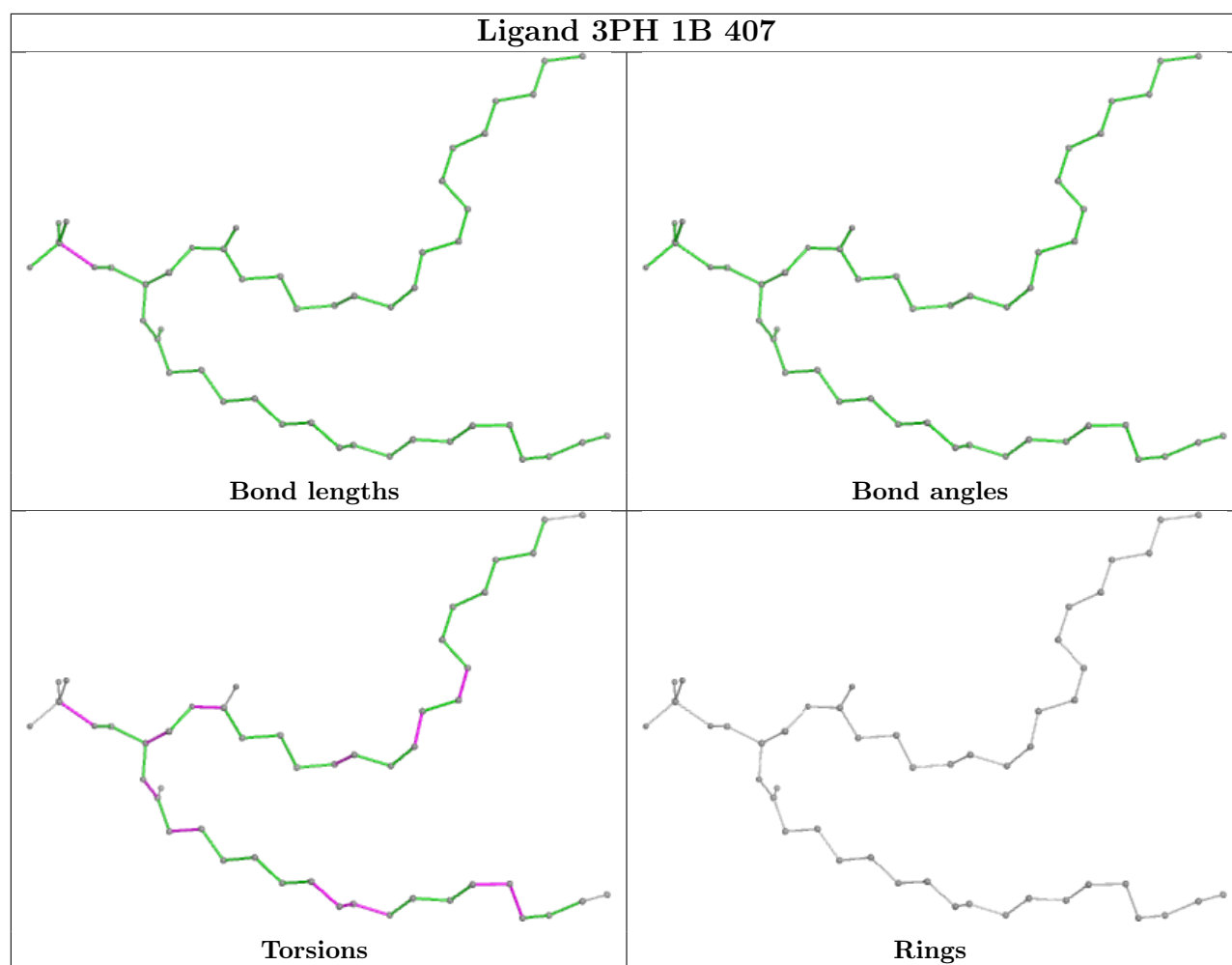


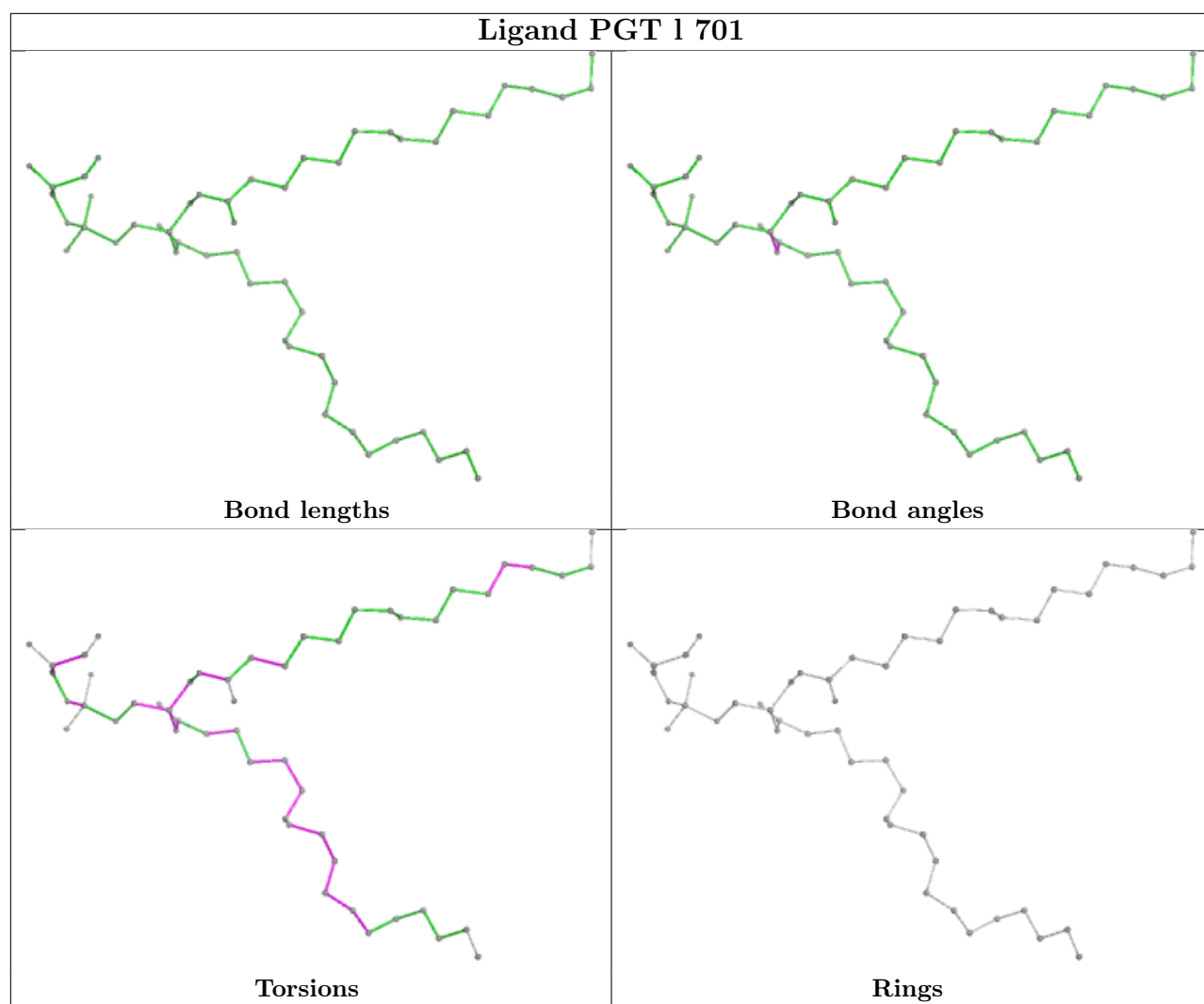


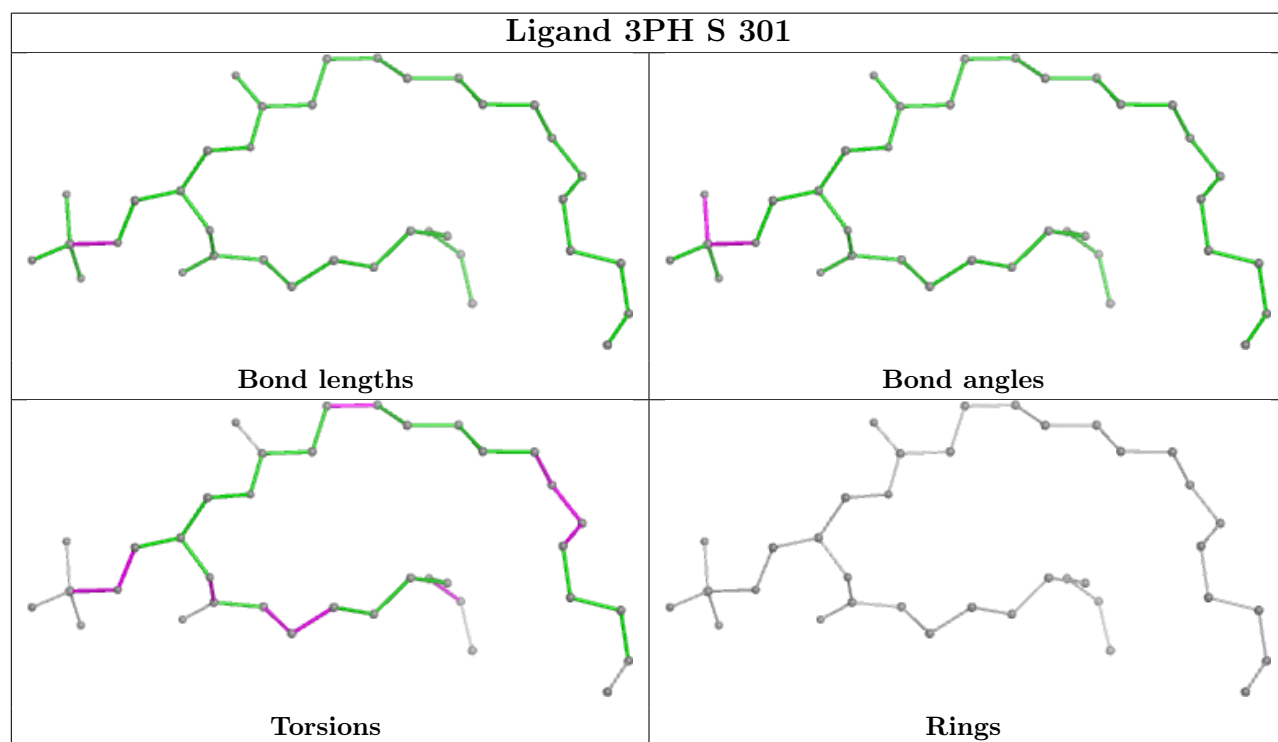
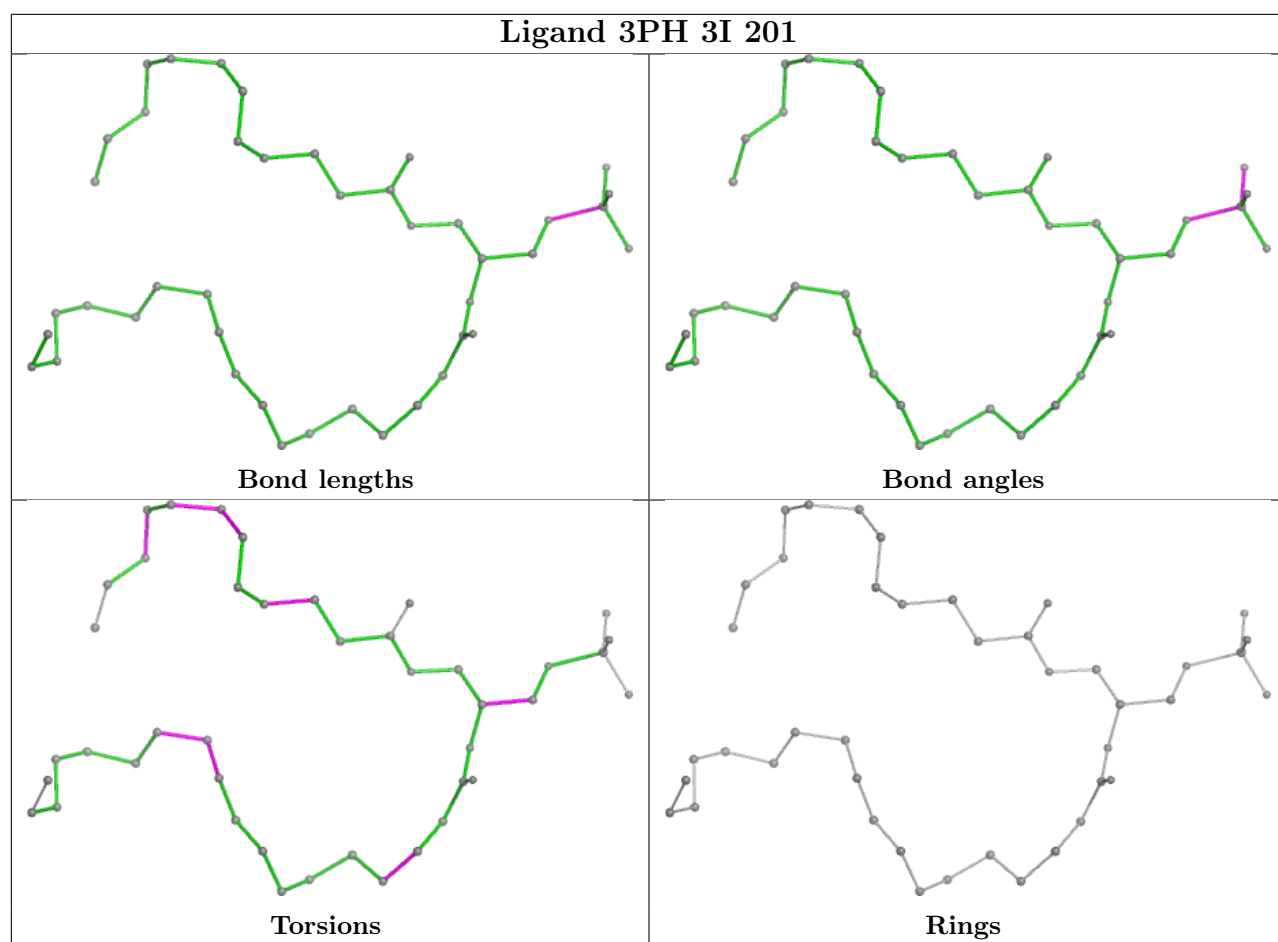


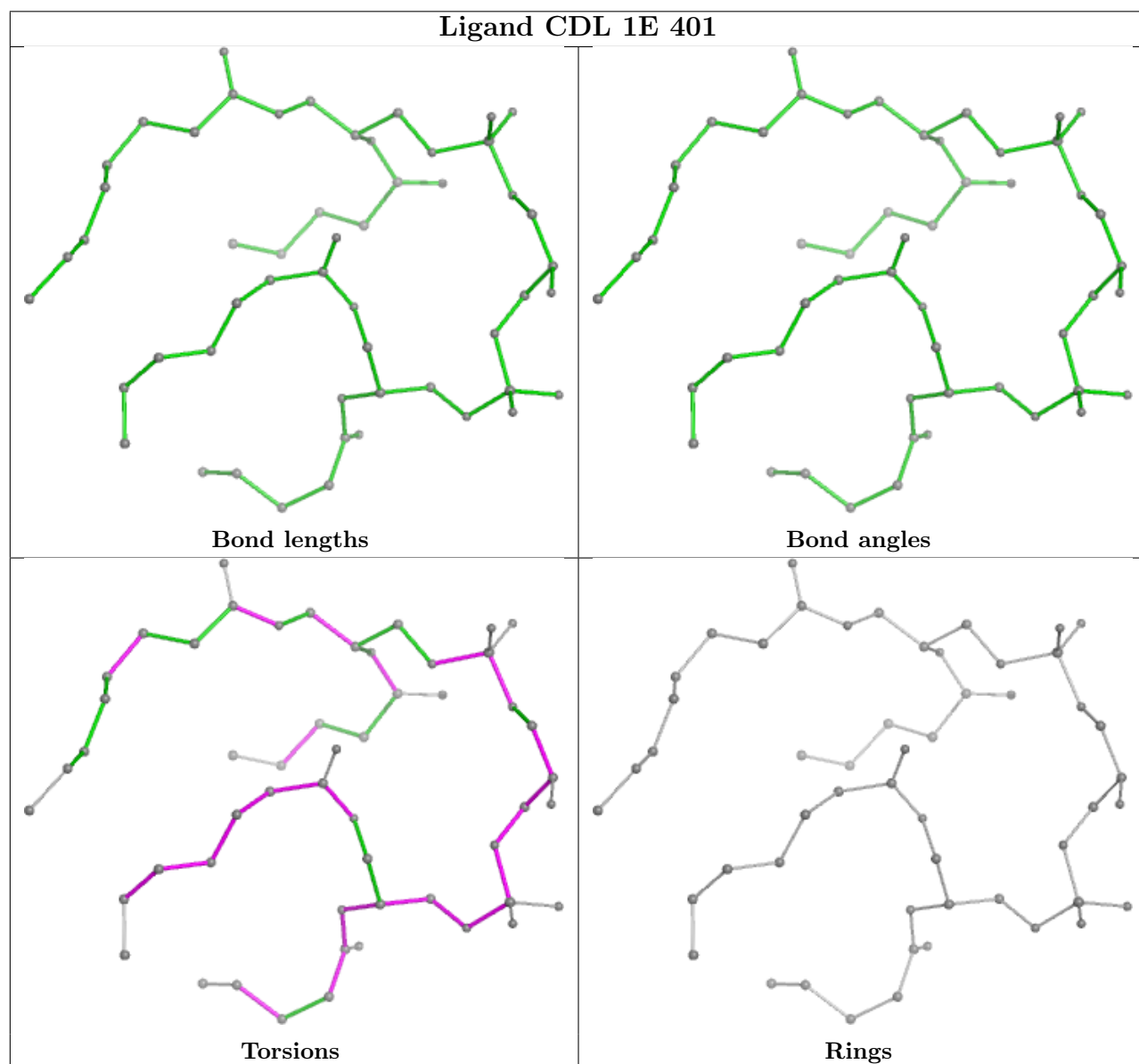
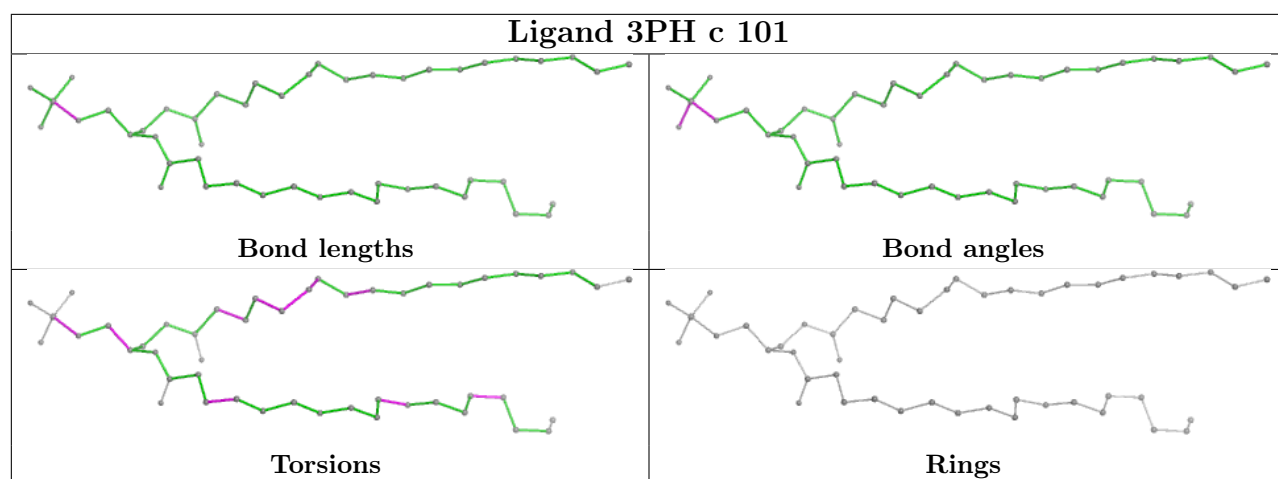


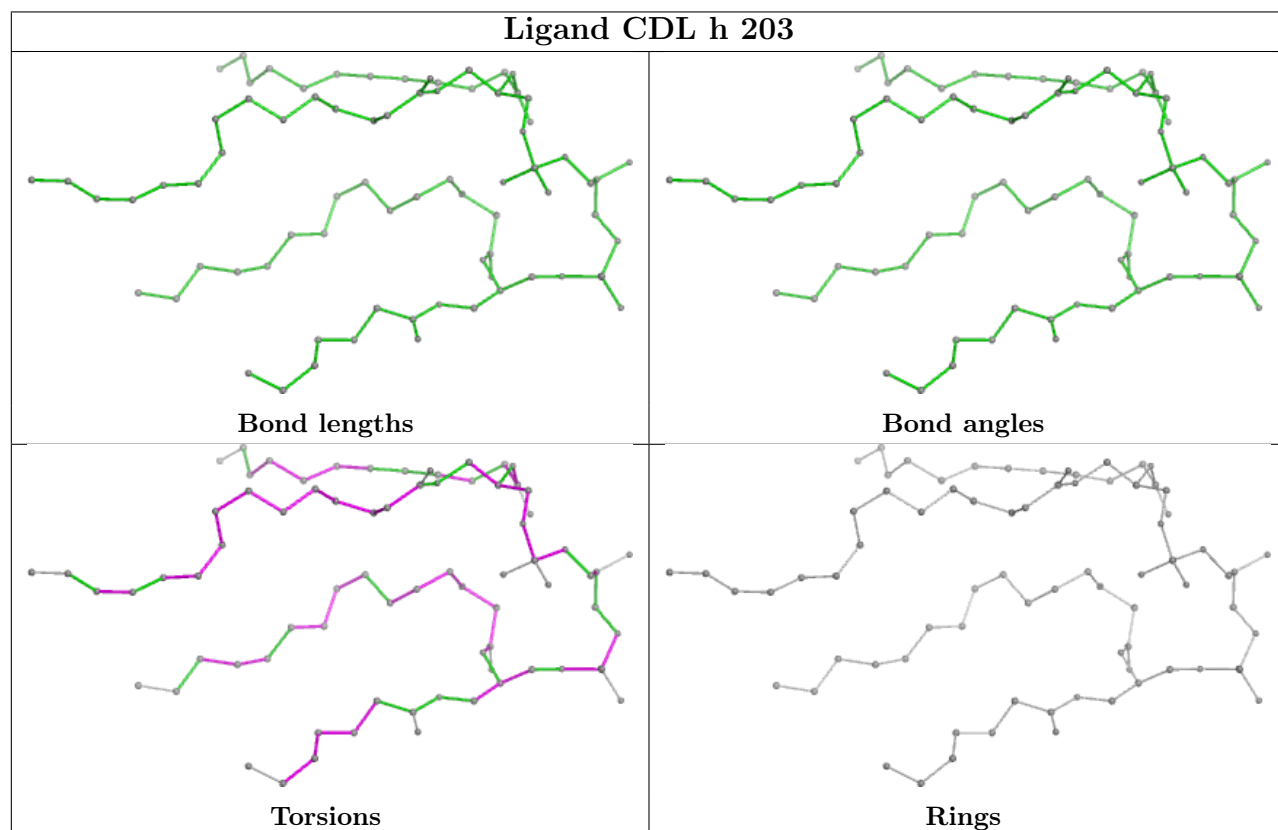
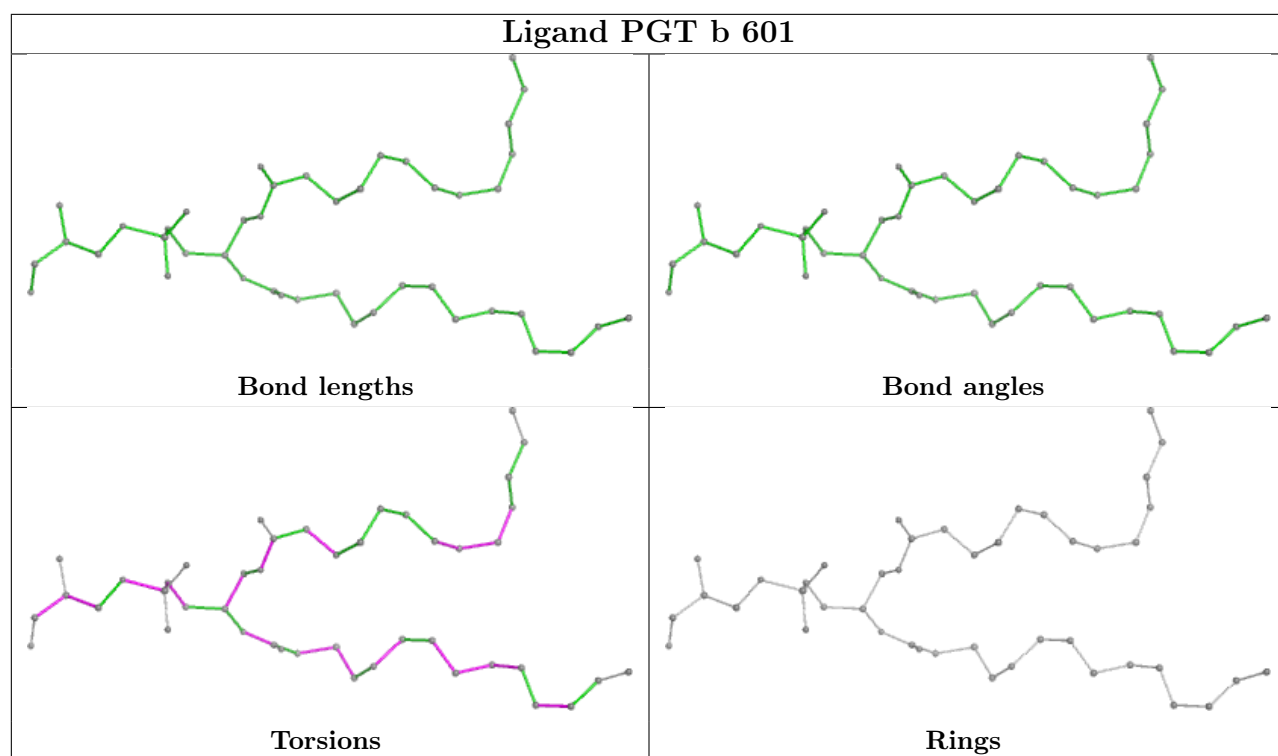


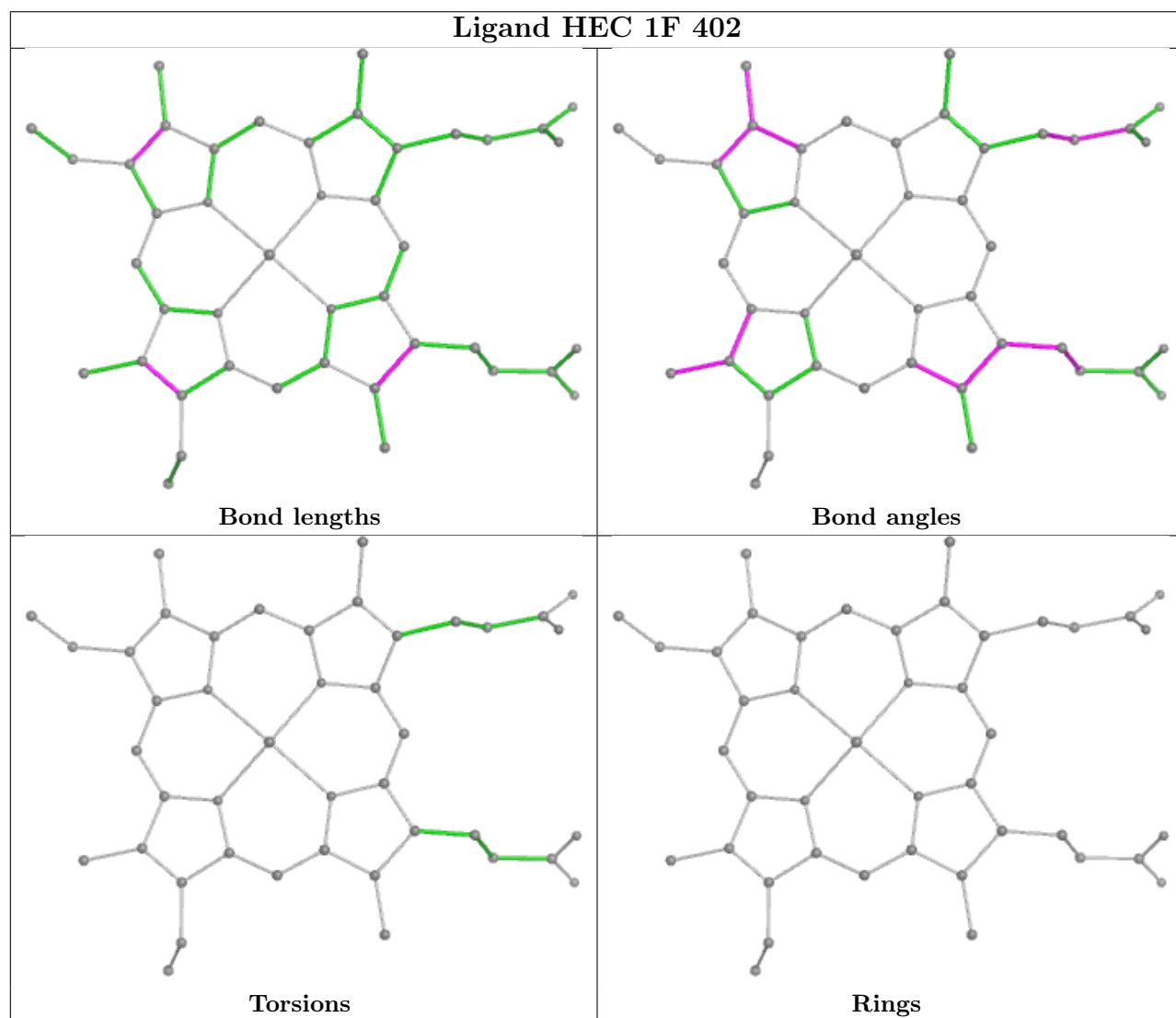
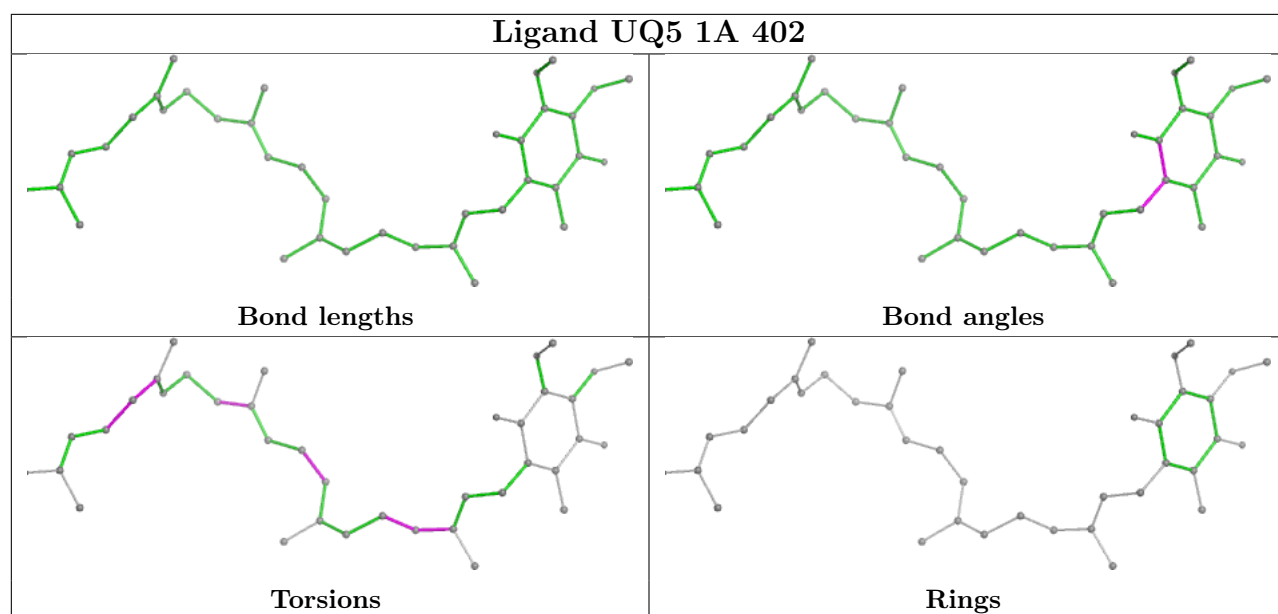


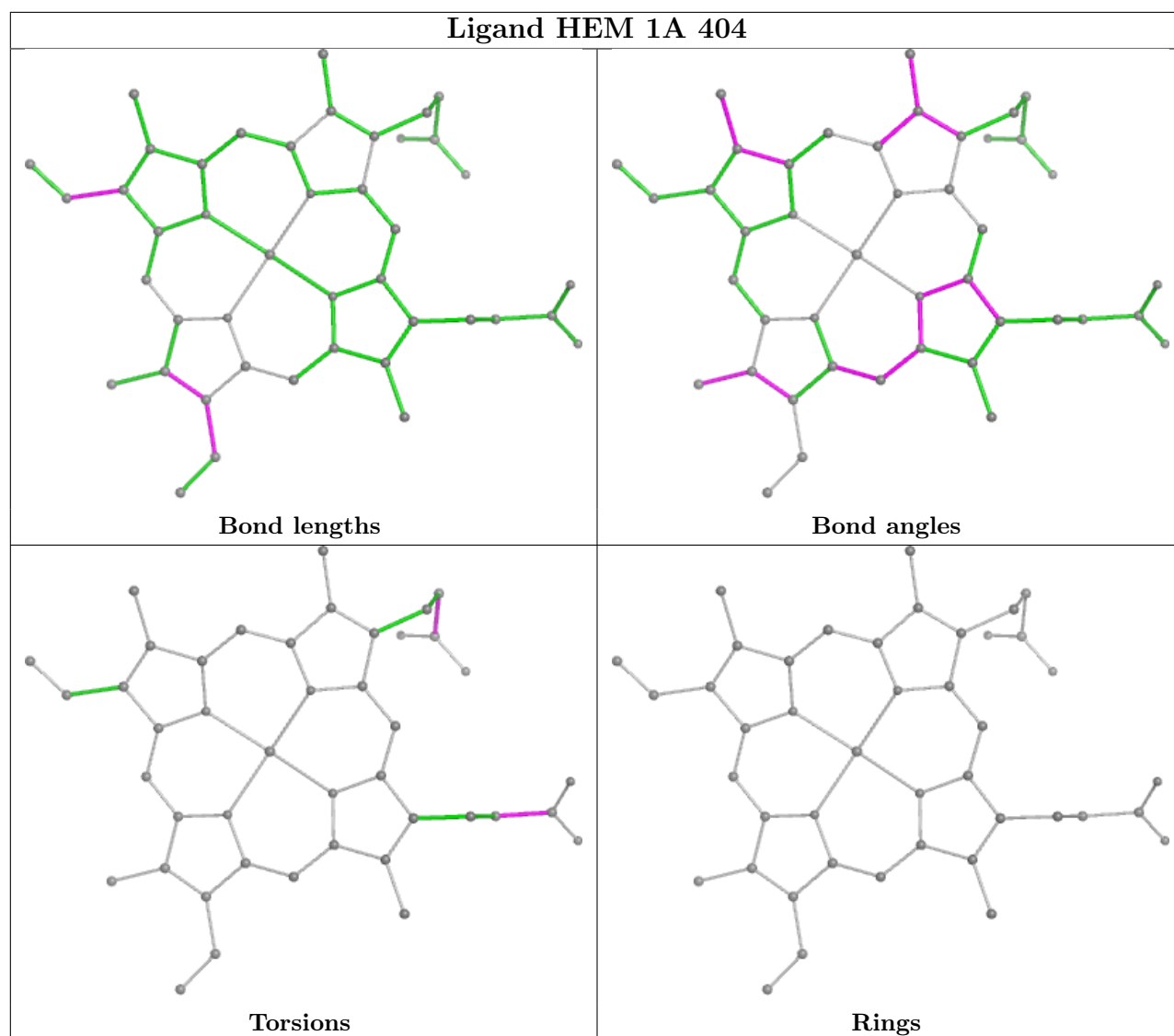
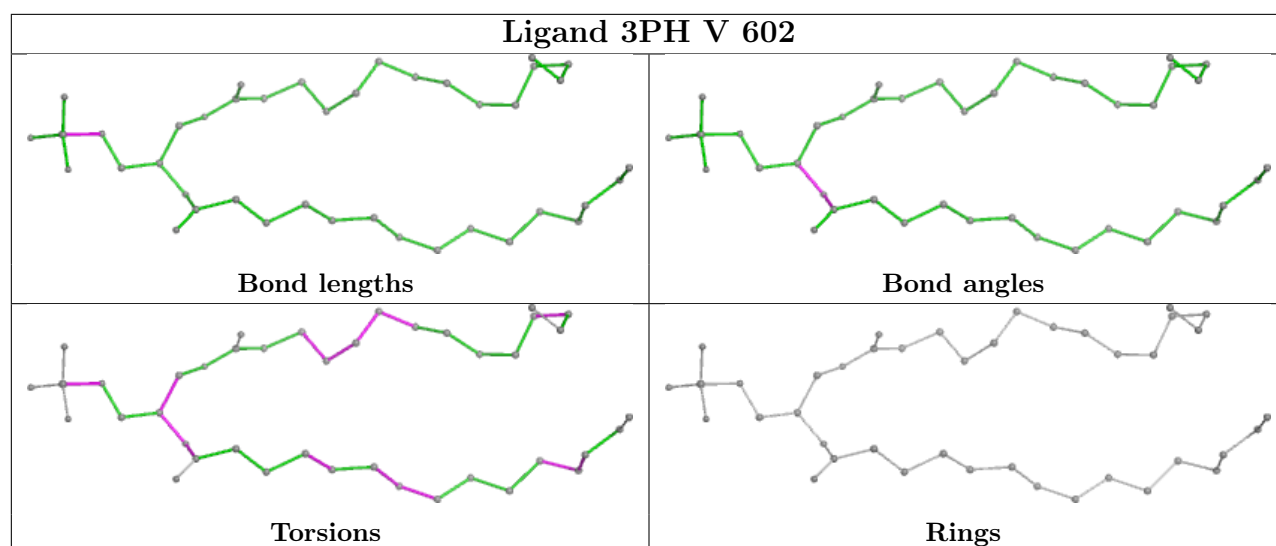


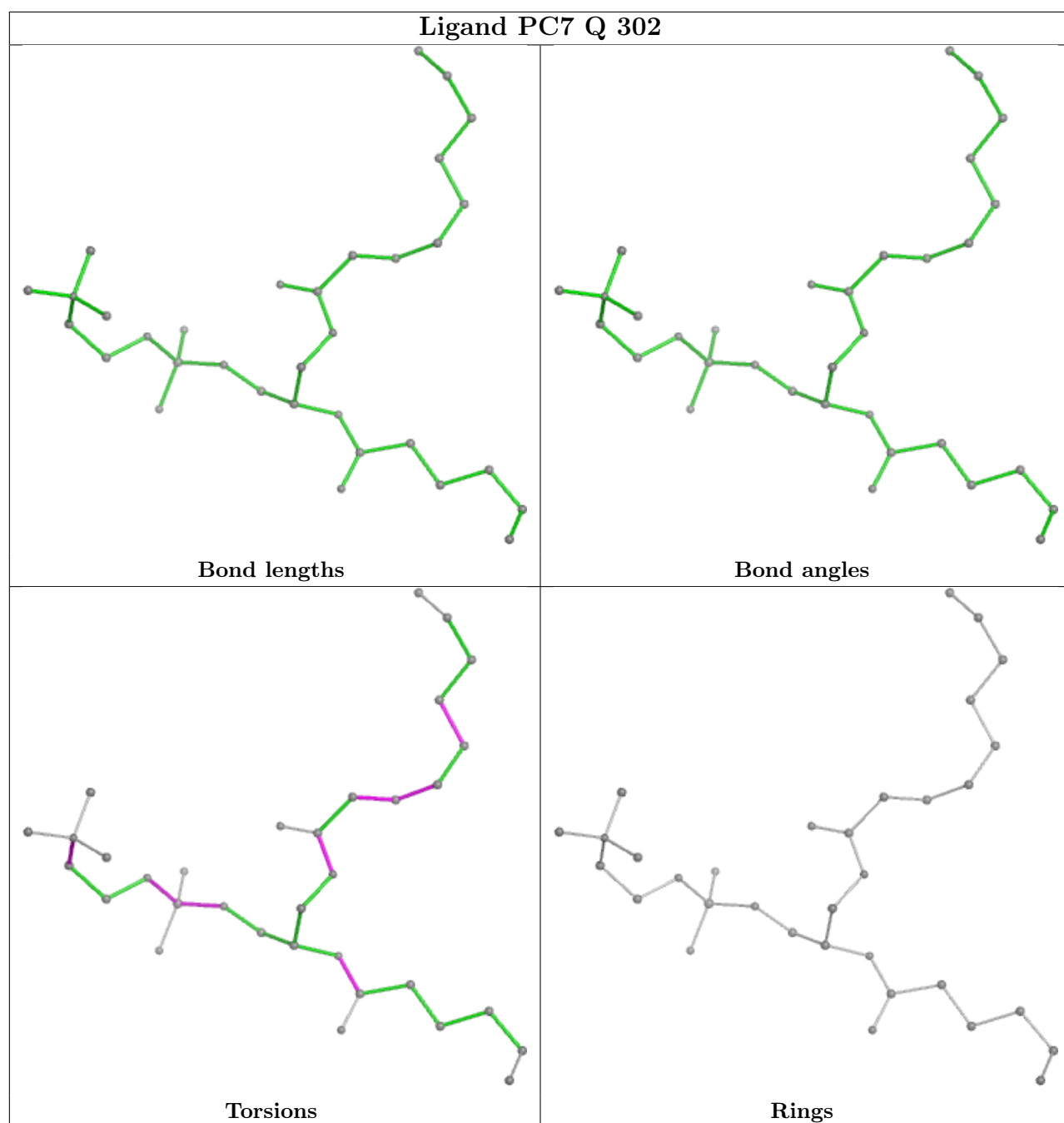


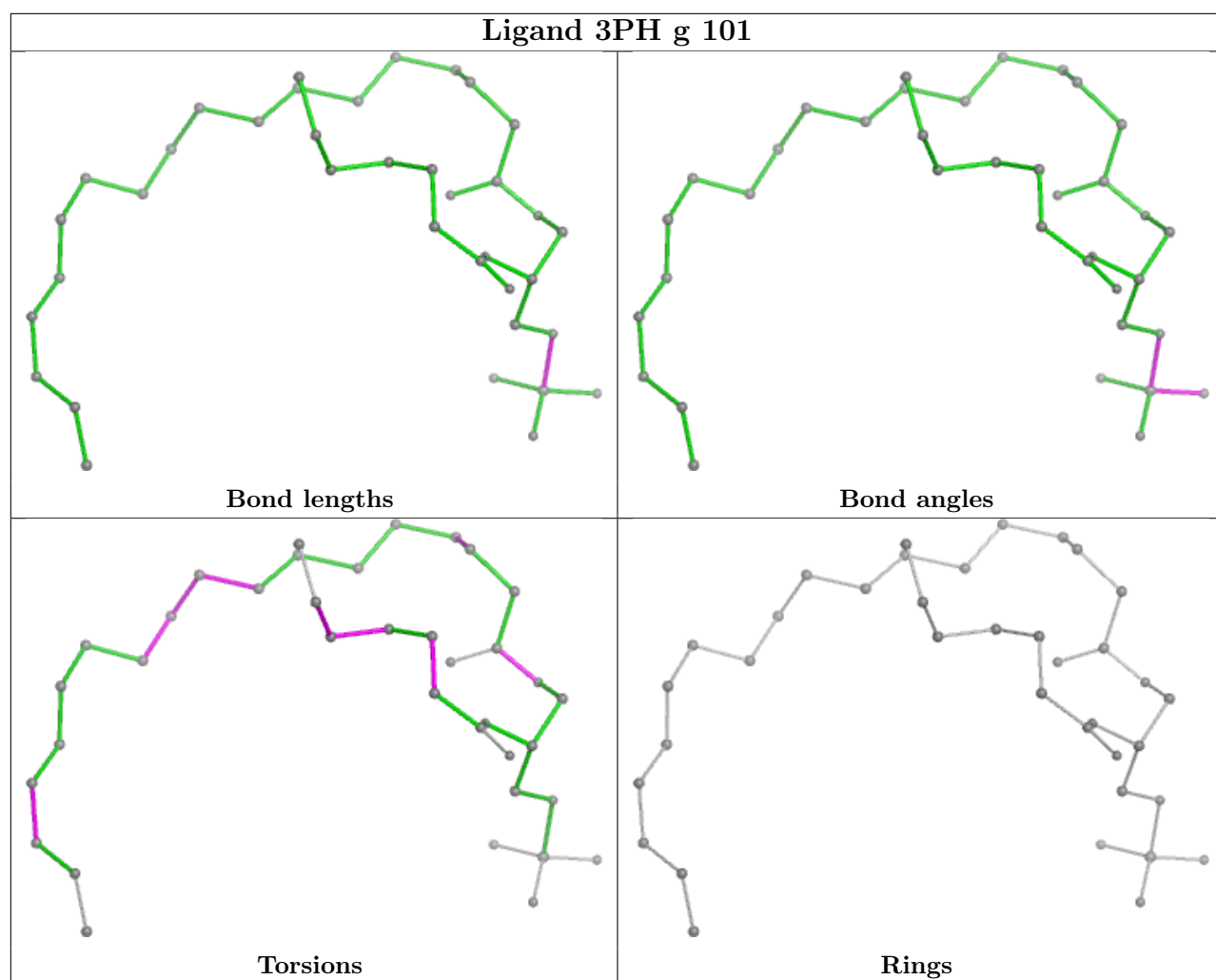


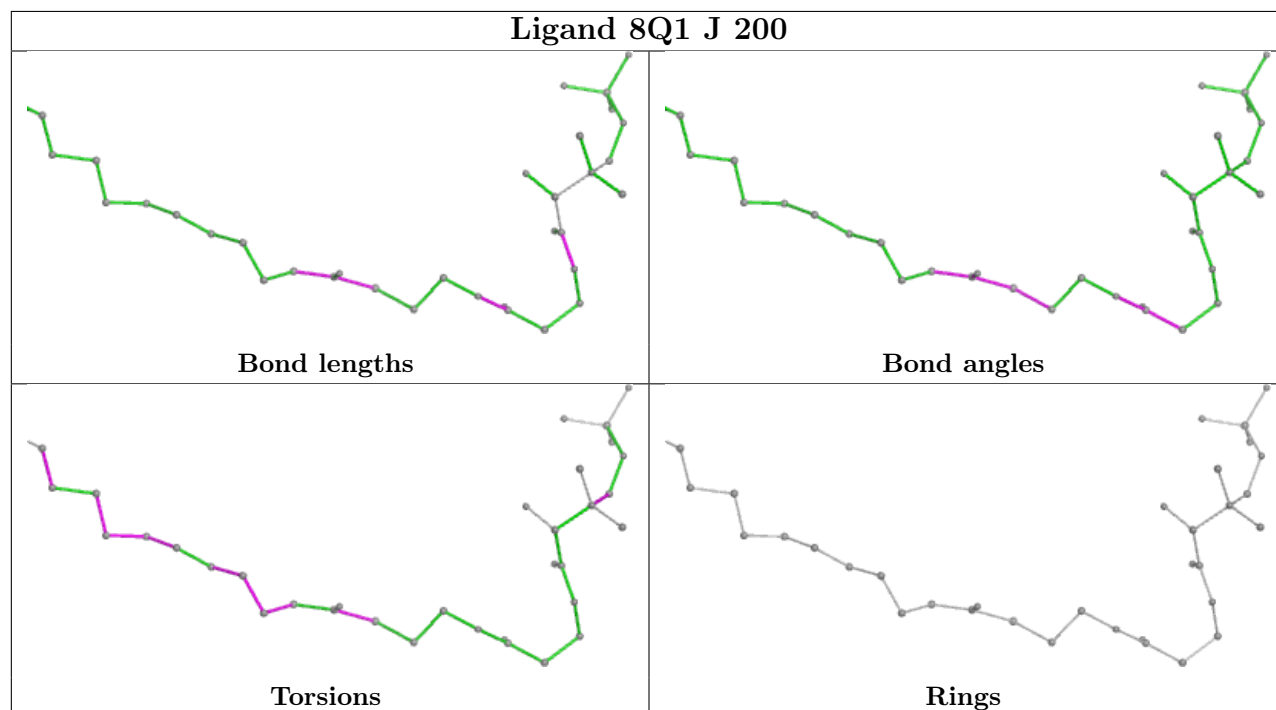
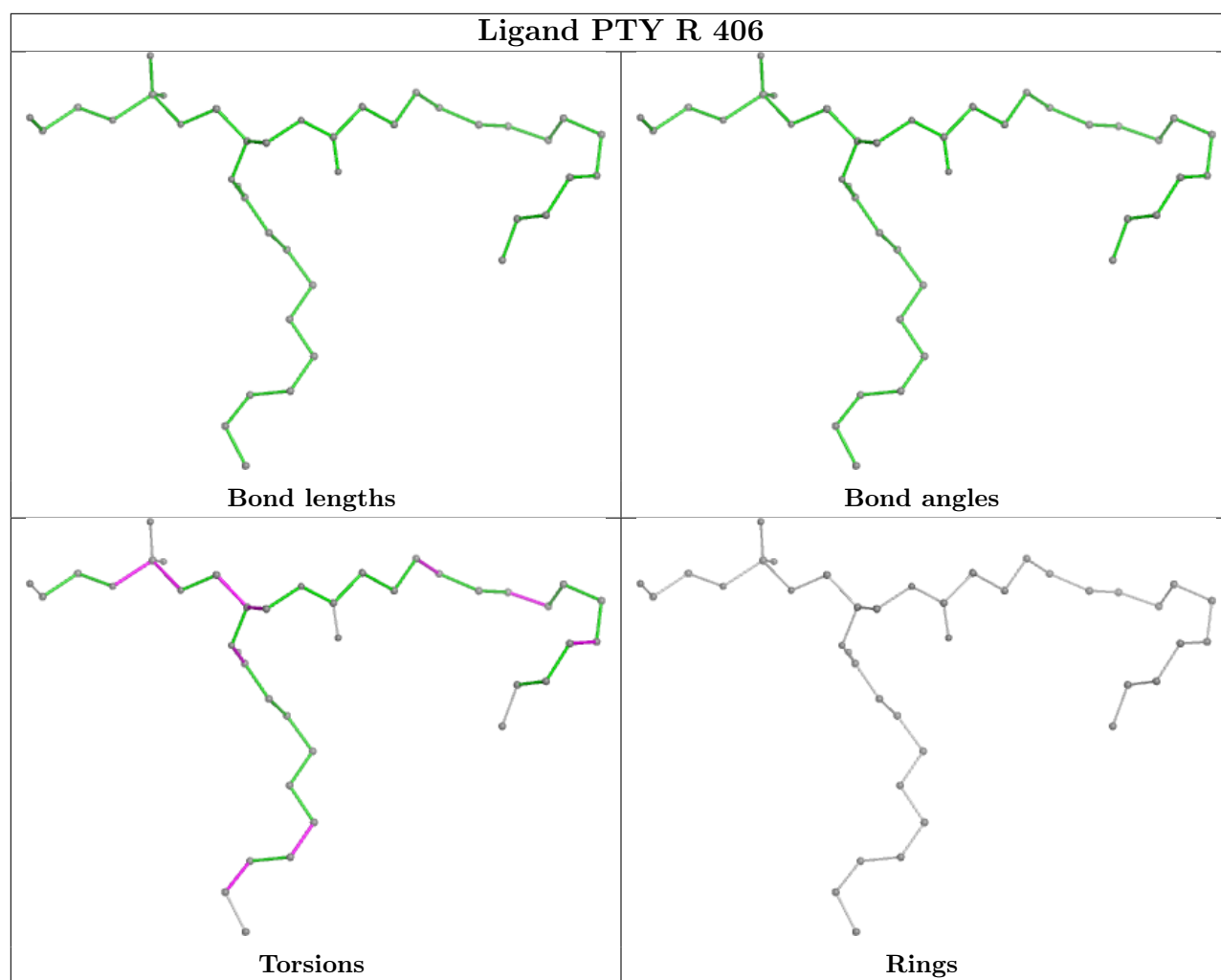


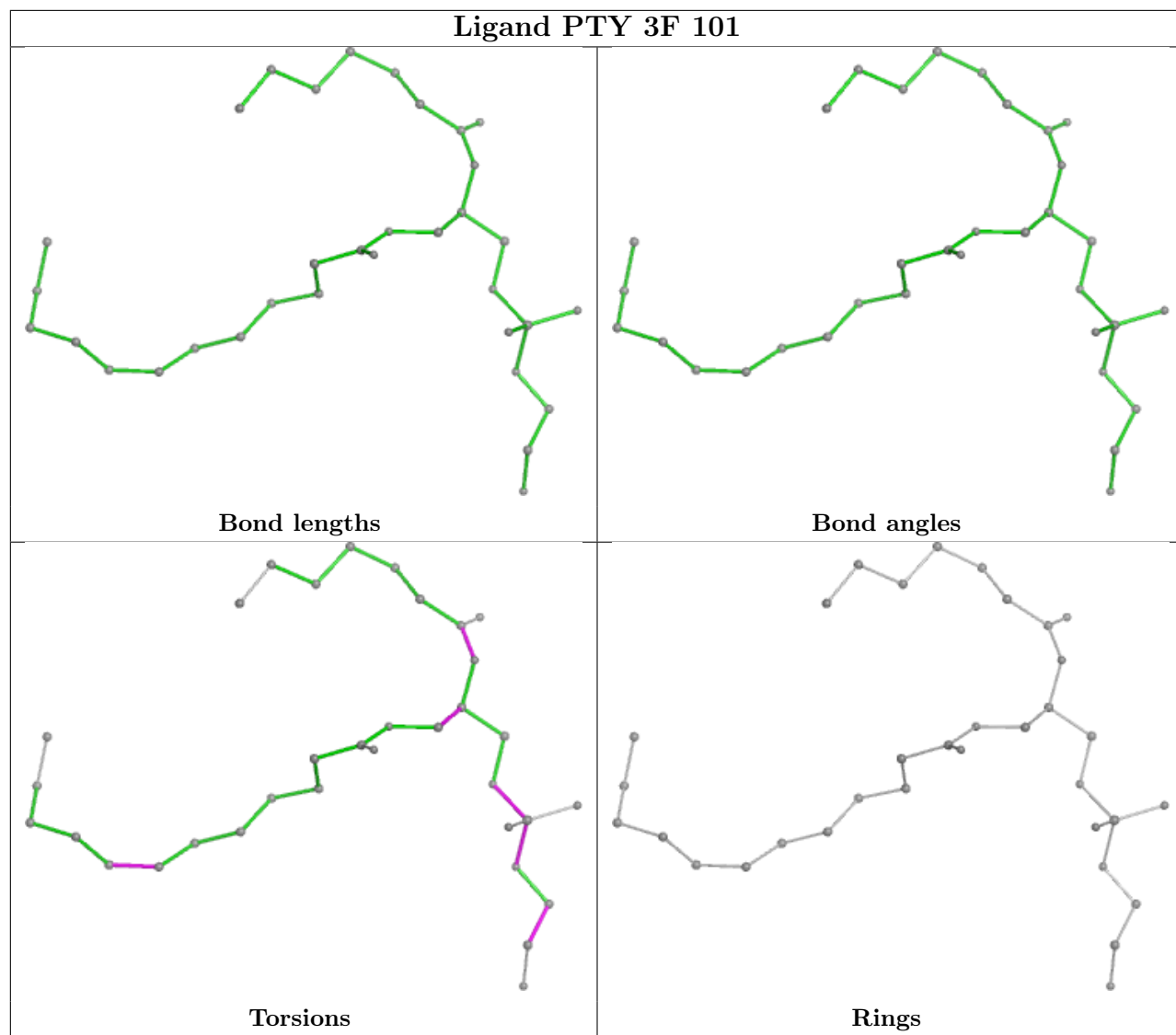


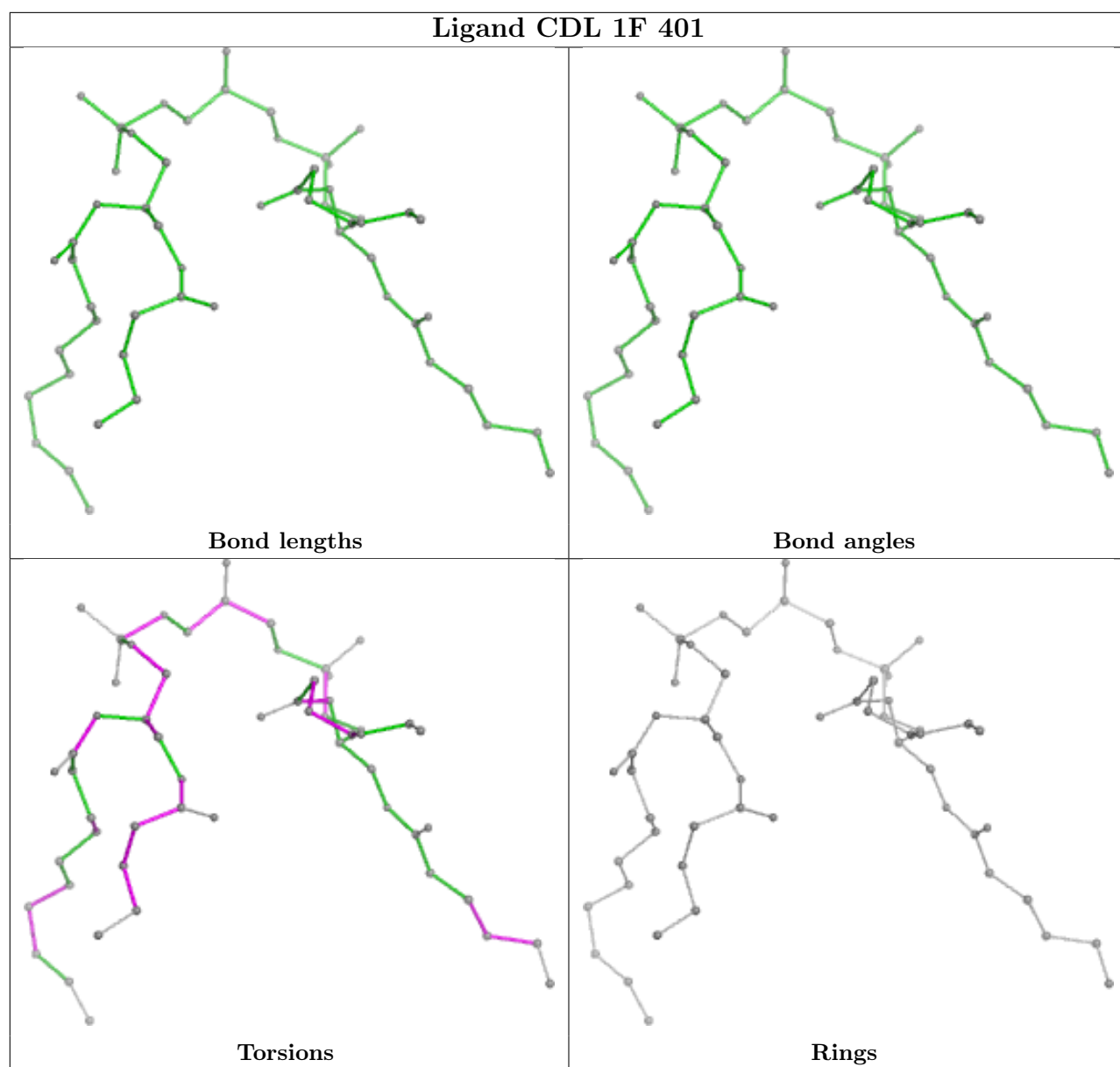


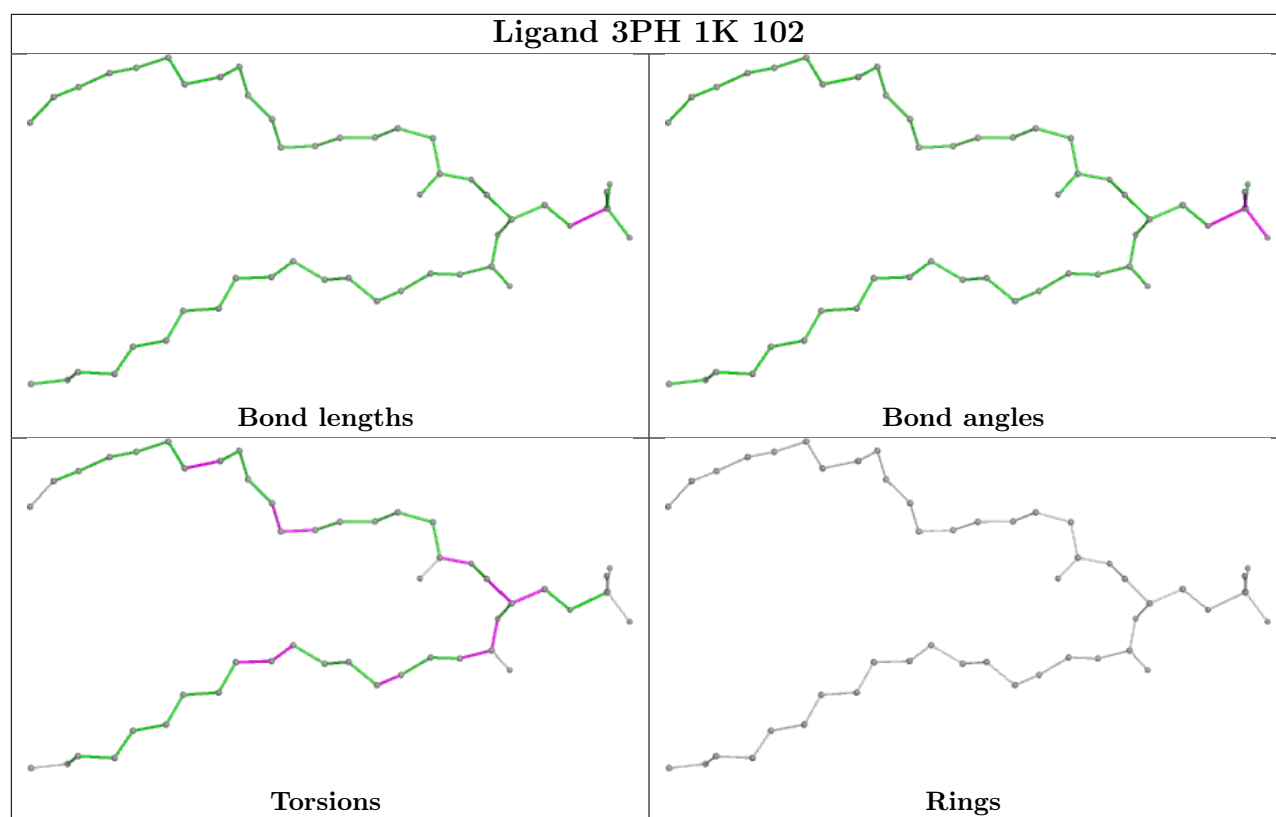












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-50202. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

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

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.