



wwPDB EM Validation Summary Report ⓘ

Dec 8, 2025 – 02:59 PM JST

PDB ID : 8ZP8 / pdb_00008zp8
EMDB ID : EMD-60329
Title : Respirasome open state 1 in presence of metformin(SC-MetO1)
Authors : Teng, F.; He, Z.X.; Hu, Y.Q.; Xu, C.Y.; Guo, R.Y.; Zhou, L.
Deposited on : 2024-05-29
Resolution : 2.97 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:

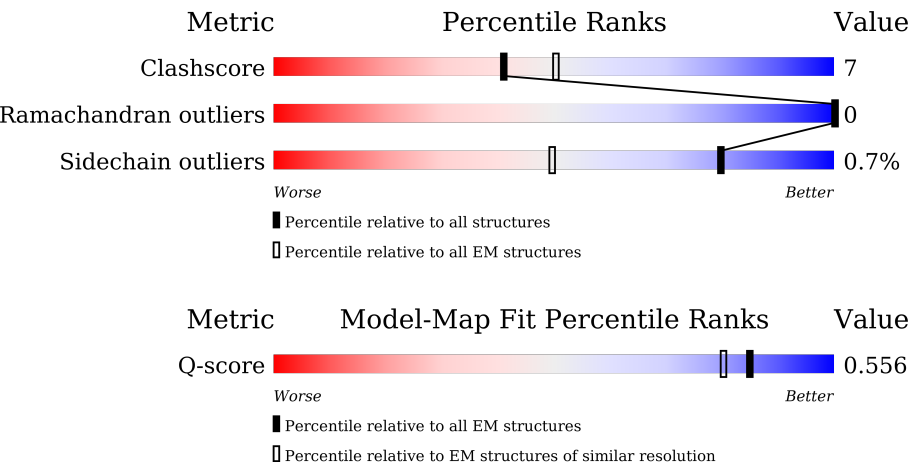
EMDB validation analysis : 0.0.1.dev129
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.47

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.97 Å.

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









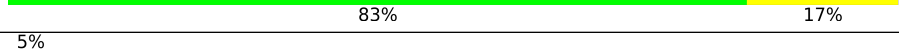
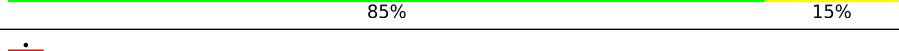
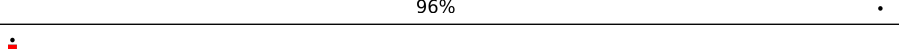
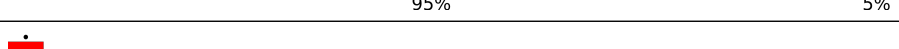
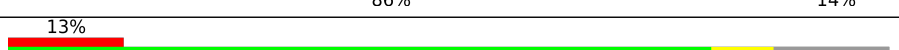

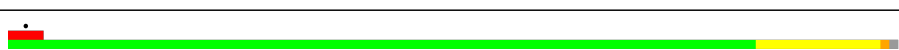
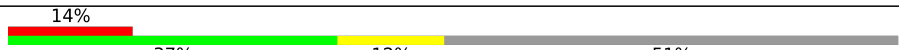
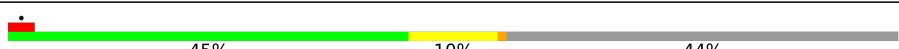





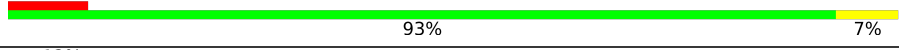
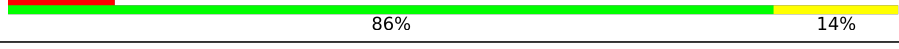

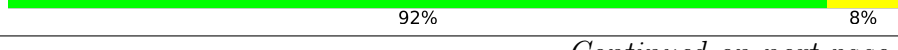

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	13205 (2.47 - 3.47)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	4L	98	<div><div></div><div>83%</div><div>17%</div></div>
2	5A	102	<div><div></div><div>84%</div><div>16%</div></div>
3	5B	95	<div><div>6%</div><div>85%</div><div>14%</div></div>
4	6A	76	<div><div>9%</div><div>89%</div><div>11%</div></div>

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Mol	Chain	Length	Quality of chain
5	6B	82	
6	6C	70	
7	7A	57	
8	7B	50	
9	7C	47	
10	8B	43	
11	A1	70	
12	A2	85	
13	A3	83	
14	A5	112	
15	A6	114	
16	A7	112	
17	A8	171	
18	A9	341	
19	AB	156	
19	AC	156	
20	AK	320	
21	AL	140	
22	AM	144	
23	AN	142	
24	B1	56	
25	B2	67	
26	B3	80	
27	B4	128	
28	B5	138	




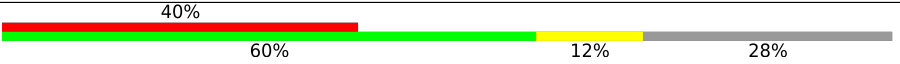
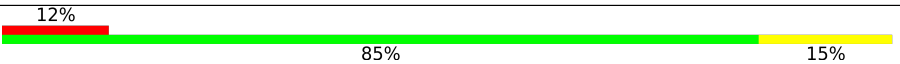

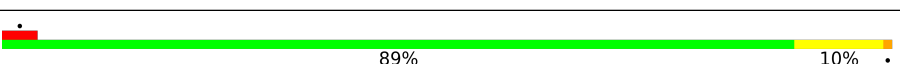
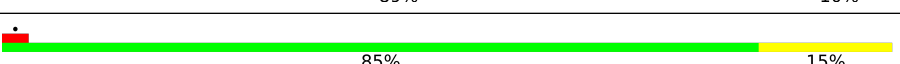
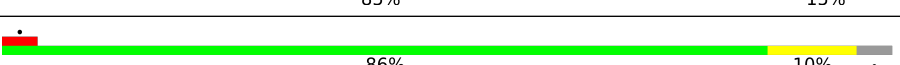
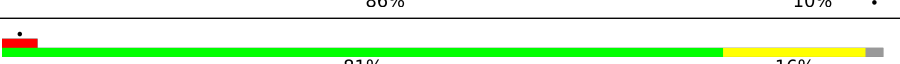
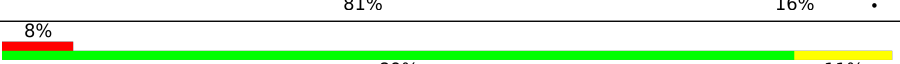
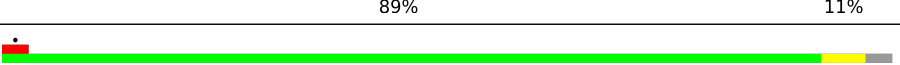
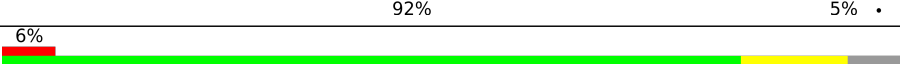
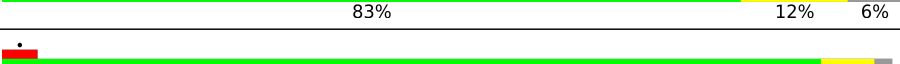
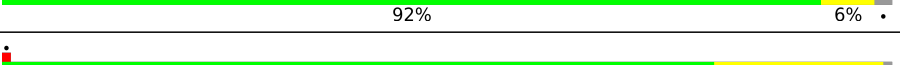


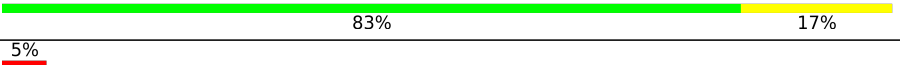

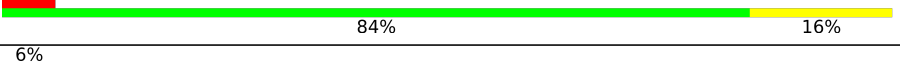
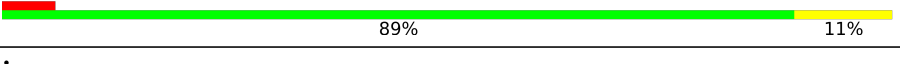


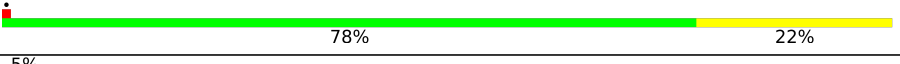

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Mol	Chain	Length	Quality of chain
29	B6	126	
30	B7	125	
31	B8	156	
32	B9	178	
33	BK	176	
34	BL	154	
35	C1	514	
36	C2	228	
37	C3	260	
38	C4	138	
39	CA	49	
40	CB	121	
41	N1	318	
42	N2	347	
43	N3	115	
44	N4	459	
45	N5	603	
46	N6	174	
47	QA	419	
47	Qa	419	
48	QB	446	
48	Qb	446	
49	QC	379	
49	Qc	379	
50	QD	326	

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Mol	Chain	Length	Quality of chain
50	Qd	326	
51	QE	274	
51	QK	274	
51	Qe	274	
52	QF	67	
52	Qf	67	
53	QG	101	
53	Qg	101	
54	QH	81	
54	Qh	81	
55	QI	62	
55	Qi	62	
56	QJ	52	
56	Qj	52	
57	S1	689	
58	S2	430	
59	S3	208	
60	S4	124	
61	S5	105	
62	S6	96	
63	S7	156	
64	S8	176	
65	V1	431	
66	V2	217	
67	V3	42	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
82	FES	QE	303	-	-	X	-
82	FES	Qe	301	-	-	X	-
83	SF4	S1	801	-	-	X	-

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 117250 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 NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	4L	98	Total	C	N	O	S	0	0
			748	493	113	128	14		

- Molecule 2 is a protein called Cytochrome c oxidase subunit 5A, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	102	Total	C	N	O	S	0	0
			825	528	139	156	2		

- Molecule 3 is a protein called Cytochrome c oxidase subunit 5B, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5B	95	Total	C	N	O	S	0	0
			724	449	128	141	6		

- Molecule 4 is a protein called Cytochrome c oxidase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6A	76	Total	C	N	O	S	0	0
			624	403	119	101	1		

- Molecule 5 is a protein called Cytochrome c oxidase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6B	82	Total	C	N	O	S	0	0
			684	431	125	123	5		

- Molecule 6 is a protein called Cytochrome c oxidase subunit 6C.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6C	70	Total	C	N	O	S	0	0
			574	375	101	95	3		

- Molecule 7 is a protein called Cytochrome c oxidase subunit 7A1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7A	57	Total	C	N	O	S	0	0
			447	287	76	81	3		

- Molecule 8 is a protein called Cytochrome c oxidase subunit 7B, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7B	50	Total	C	N	O	S	0	0
			392	254	66	71	1		

- Molecule 9 is a protein called Cytochrome c oxidase subunit 7C, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	7C	47	Total	C	N	O	S	0	0
			387	257	65	63	2		

- Molecule 10 is a protein called Cytochrome c oxidase subunit 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	8B	43	Total	C	N	O	0	0
			338	222	57	59		

- Molecule 11 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A1	70	Total	C	N	O	S	0	0
			562	361	101	94	6		

- Molecule 12 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A2	85	Total	C	N	O	S	0	0
			686	431	128	125	2		

- Molecule 13 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A3	83	Total	C	N	O	S	0	0
			643	417	110	115	1		

- Molecule 14 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	A5	112	Total	C	N	O	S	0	0
			910	588	154	165	3		

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	A6	114	Total	C	N	O	S	0	0
			967	617	178	167	5		

- Molecule 16 is a protein called Complex I-B14.5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	A7	97	Total	C	N	O	S	0	0
			780	491	147	139	3		

- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	A8	171	Total	C	N	O	S	0	0
			1398	887	250	251	10		

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	A9	337	Total	C	N	O	S	0	0
			2703	1750	472	472	9		

- Molecule 19 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AB	77	Total	C	N	O	S	0	0
			624	402	93	124	5		
19	AC	87	Total	C	N	O	S	0	0
			702	452	103	142	5		

- Molecule 20 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AK	320	Total	C	N	O	S	0	0
			2590	1649	440	491	10		

- Molecule 21 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AL	140	Total	C	N	O	S	0	0
			1021	651	174	190	6		

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AM	144	Total	C	N	O	S	0	0
			1204	770	218	212	4		

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AN	142	Total	C	N	O	S	0	0
			1173	755	203	206	9		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B1	56	Total	C	N	O	S	0	0
			479	311	88	79	1		

- Molecule 25 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B2	67	Total	C	N	O	S	0	0
			584	385	95	103	1		

- Molecule 26 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B3	80	Total	C	N	O	S	0	0
			641	418	108	114	1		

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B4	128	Total	C	N	O	S	0	0
			1062	691	182	189			

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B5	138	Total	C	N	O	S	0	0
			1151	754	195	199	3		

- Molecule 29 is a protein called Complex I-B17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B6	102	Total	C	N	O	S	0	0
			870	568	155	146	1		

- Molecule 30 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B7	125	Total	C	N	O	S	0	0
			1068	663	204	190	11		

- Molecule 31 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B8	156	Total	C	N	O	S	0	0
			1315	853	213	241	8		

- Molecule 32 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B9	178	Total	C	N	O	S	0	0
			1534	982	279	265	8		

- Molecule 33 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BK	174	Total	C	N	O	S	0	0
			1456	913	264	271	8		

- Molecule 34 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BL	99	Total	C	N	O	S	0	0
			828	531	137	156	4		

- Molecule 35 is a protein called Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	C1	514	Total	C	N	O	S	0	0
			4024	2692	625	675	32		

- Molecule 36 is a protein called Cytochrome c oxidase subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	C2	228	Total	C	N	O	S	0	0
			1833	1193	282	340	18		

- Molecule 37 is a protein called Cytochrome c oxidase subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	C3	260	Total	C	N	O	S	0	0
			2103	1403	337	353	10		

- Molecule 38 is a protein called Cytochrome c oxidase subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	C4	138	Total	C	N	O	S	0	0
			1153	751	188	210	4		

- Molecule 39 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	CA	49	Total	C	N	O	0	0
			417	276	71	70		

- Molecule 40 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	CB	121	Total	C	N	O	S	0	0
			1000	650	173	171	6		

- Molecule 41 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	N1	305	Total	C	N	O	S	0	0
			2411	1619	371	400	21		

- Molecule 42 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	N2	347	Total	C	N	O	S	0	0
			2710	1782	420	462	46		

- Molecule 43 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	N3	96	Total	C	N	O	S	0	0
			770	525	111	129	5		

- Molecule 44 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	N4	459	Total	C	N	O	S	0	0
			3631	2412	572	609	38		

- Molecule 45 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	N5	603	Total	C	N	O	S	0	0
			4785	3173	741	820	51		

- Molecule 46 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	N6	166	Total	C	N	O	S	0	0
			1259	844	180	224	11		

- Molecule 47 is a protein called Cytochrome b-c1 complex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	QA	419	Total	C	N	O	S	0	0
			3147	1971	557	611	8		
47	Qa	419	Total	C	N	O	S	0	0
			3147	1971	557	611	8		

- Molecule 48 is a protein called Cytochrome b-c1 complex subunit 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	QB	446	Total	C	N	O	S	0	0
			3459	2161	605	674	19		
48	Qb	433	Total	C	N	O	S	0	0
			3367	2103	592	653	19		

- Molecule 49 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	QC	379	Total	C	N	O	S	0	0
			3025	2031	471	502	21		
49	Qc	379	Total	C	N	O	S	0	0
			3025	2031	471	502	21		

- Molecule 50 is a protein called Cytochrome c1, heme protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	QD	241	Total	C	N	O	S	0	0
			1921	1225	330	350	16		
50	Qd	239	Total	C	N	O	S	0	0
			1904	1215	327	346	16		

- Molecule 51 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	QE	196	Total	C	N	O	S	0	0
			1517	955	265	290	7		
51	QK	73	Total	C	N	O	S	0	0
			520	328	98	92	2		
51	Qe	196	Total	C	N	O	S	0	0
			1517	955	265	290	7		

- Molecule 52 is a protein called Cytochrome b-c1 complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	QF	67	Total	C	N	O	S	0	0
			552	336	100	111	5		
52	Qf	64	Total	C	N	O	S	0	0
			528	320	97	106	5		

- Molecule 53 is a protein called Cytochrome b-c1 complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	QG	101	Total	C	N	O	S	0	0
			893	572	157	162	2		
53	Qg	101	Total	C	N	O	S	0	0
			893	572	157	162	2		

- Molecule 54 is a protein called Cytochrome b-c1 complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	QH	78	Total	C	N	O	S	0	0
			662	432	121	107	2		
54	Qh	79	Total	C	N	O	S	0	0
			666	434	122	108	2		

- Molecule 55 is a protein called Complex III subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	QI	62	Total	C	N	O	0	0
			507	331	90	86		
55	Qi	60	Total	C	N	O	0	0
			493	322	87	84		

- Molecule 56 is a protein called Cytochrome b-c1 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	QJ	49	Total	C	N	O	S	0	0
			405	269	71	63	2		
56	Qj	51	Total	C	N	O	S	0	0
			421	281	74	65	1		

- Molecule 57 is a protein called NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S1	685	Total	C	N	O	S	0	0
			5266	3303	918	1006	39		

- Molecule 58 is a protein called Complex I-49kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	S2	429	Total	C	N	O	S	0	0
			3452	2208	593	627	24		

- Molecule 59 is a protein called Complex I-30kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	S3	208	Total	C	N	O	S	0	0
			1738	1124	298	314	2		

- Molecule 60 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	S4	124	Total	C	N	O	S	0	0
			1007	637	179	188	3		

- Molecule 61 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	S5	105	Total	C	N	O	S	0	0
			867	550	161	150	6		

- Molecule 62 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	S6	96	Total	C	N	O	S	0	0
			741	452	140	146	3		

- Molecule 63 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	S7	156	Total	C	N	O	S	0	0
			1248	794	227	213	14		

- Molecule 64 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	S8	176	Total	C	N	O	S	0	0
			1412	887	243	269	13		

- Molecule 65 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	V1	431	Total	C	N	O	S	0	0
			3316	2092	592	612	20		

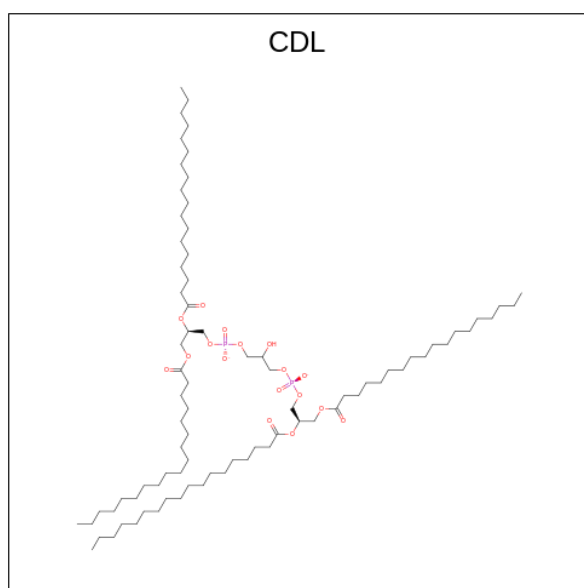
- Molecule 66 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	V2	217	Total	C	N	O	S	0	0
			1671	1065	281	315	10		

- Molecule 67 is a protein called Complex I-9kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	V3	42	Total	C	N	O	S	0	0
			355	219	67	68	1		

- Molecule 68 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).

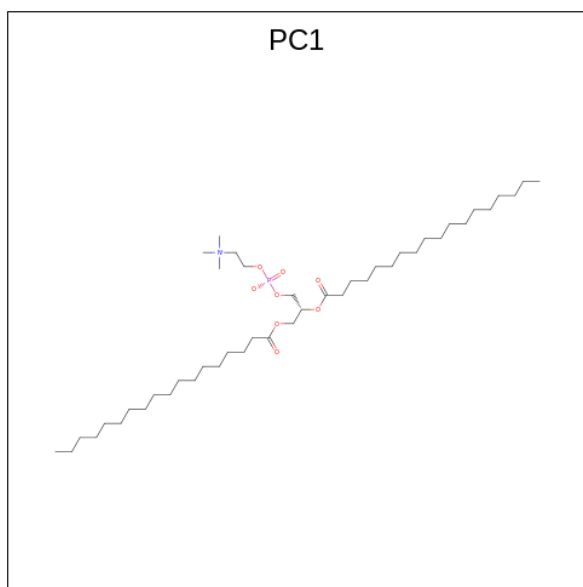


Mol	Chain	Residues	Atoms				AltConf
68	4L	1	Total	C	O	P	0
			92	73	17	2	
68	A1	1	Total	C	O	P	0
			94	75	17	2	
68	A8	1	Total	C	O	P	0
			77	58	17	2	
68	AL	1	Total	C	O	P	0
			94	75	17	2	
68	AL	1	Total	C	O	P	0
			90	71	17	2	
68	B4	1	Total	C	O	P	0
			62	43	17	2	
68	B5	1	Total	C	O	P	0
			98	79	17	2	
68	C1	1	Total	C	O	P	0
			77	58	17	2	
68	N2	1	Total	C	O	P	0
			68	49	17	2	
68	N2	1	Total	C	O	P	0
			100	81	17	2	
68	N5	1	Total	C	O	P	0
			82	63	17	2	
68	N5	1	Total	C	O	P	0
			100	81	17	2	
68	QB	1	Total	C	O	P	0
			61	42	17	2	
68	QC	1	Total	C	O	P	0
			55	36	17	2	
68	QD	1	Total	C	O	P	0
			64	45	17	2	
68	QE	1	Total	C	O	P	0
			100	81	17	2	
68	QH	1	Total	C	O	P	0
			61	42	17	2	
68	QH	1	Total	C	O	P	0
			64	45	17	2	
68	Qb	1	Total	C	O	P	0
			64	45	17	2	

- Molecule 69 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
69	5B	1	Total	Zn	0
			1	1	
69	S6	1	Total	Zn	0
			1	1	

- Molecule 70 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).



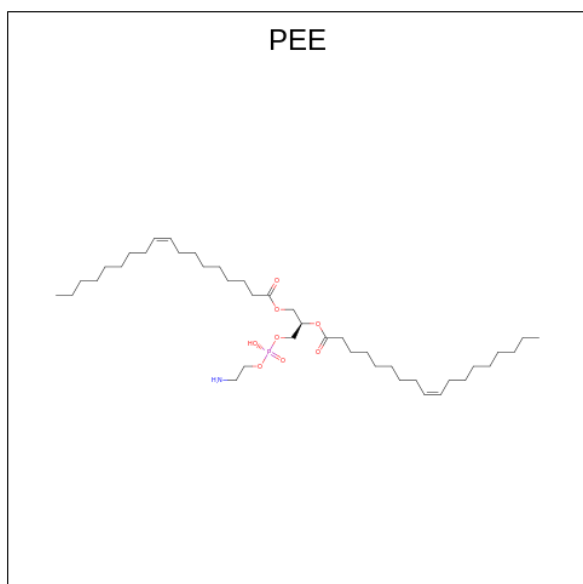
Mol	Chain	Residues	Atoms					AltConf
70	6A	1	Total	C	N	O	P	0
			45	35	1	8	1	
70	7C	1	Total	C	N	O	P	0
			52	42	1	8	1	
70	B5	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	B7	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	C1	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	C1	1	Total	C	N	O	P	0
			33	23	1	8	1	
70	C1	1	Total	C	N	O	P	0
			46	36	1	8	1	
70	C1	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	C1	1	Total	C	N	O	P	0
			50	40	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
70	C3	1	Total	C	N	O	P	0
			44	34	1	8	1	
70	C3	1	Total	C	N	O	P	0
			49	39	1	8	1	
70	N1	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	N1	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	N3	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	N5	1	Total	C	N	O	P	0
			31	21	1	8	1	
70	QJ	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	Qb	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	Qc	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	Qc	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	Qd	1	Total	C	N	O	P	0
			54	44	1	8	1	
70	Qh	1	Total	C	N	O	P	0
			54	44	1	8	1	

- Molecule 71 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: $C_{41}H_{78}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
71	6A	1	Total	C	N	O	P	0
			51	41	1	8	1	
71	6A	1	Total	C	N	O	P	0
			36	26	1	8	1	
71	8B	1	Total	C	N	O	P	0
			42	32	1	8	1	
71	A3	1	Total	C	N	O	P	0
			51	41	1	8	1	
71	AL	1	Total	C	N	O	P	0
			40	30	1	8	1	
71	B4	1	Total	C	N	O	P	0
			51	41	1	8	1	
71	C3	1	Total	C	N	O	P	0
			51	41	1	8	1	
71	N4	1	Total	C	N	O	P	0
			49	39	1	8	1	
71	N5	1	Total	C	N	O	P	0
			46	36	1	8	1	
71	N5	1	Total	C	N	O	P	0
			51	41	1	8	1	
71	QB	1	Total	C	N	O	P	0
			34	24	1	8	1	
71	QB	1	Total	C	N	O	P	0
			51	41	1	8	1	
71	QC	1	Total	C	N	O	P	0
			40	30	1	8	1	
71	QE	1	Total	C	N	O	P	0
			47	37	1	8	1	
71	Qc	1	Total	C	N	O	P	0
			51	41	1	8	1	
71	Qc	1	Total	C	N	O	P	0
			42	32	1	8	1	
71	Qd	1	Total	C	N	O	P	0
			24	14	1	8	1	
71	S2	1	Total	C	N	O	P	0
			48	38	1	8	1	
71	S8	1	Total	C	N	O	P	0
			51	41	1	8	1	

- Molecule 72 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$) (labeled as "Ligand of Interest" by depositor).



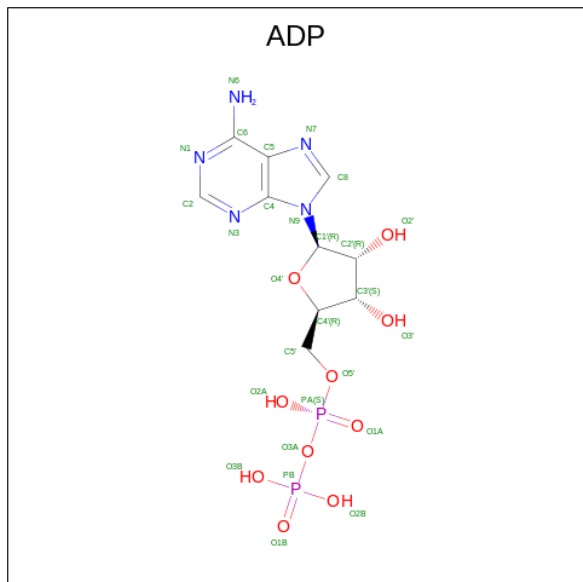
Mol	Chain	Residues	Atoms					AltCon
72	A9	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 73 is S-[2-({N-[(2S)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-alanyl}amino)ethyl] tetradecanethioate (CCD ID: ZMP) (formula: C₂₅H₄₉N₂O₈PS) (labeled as "Ligand of Interest" by depositor).



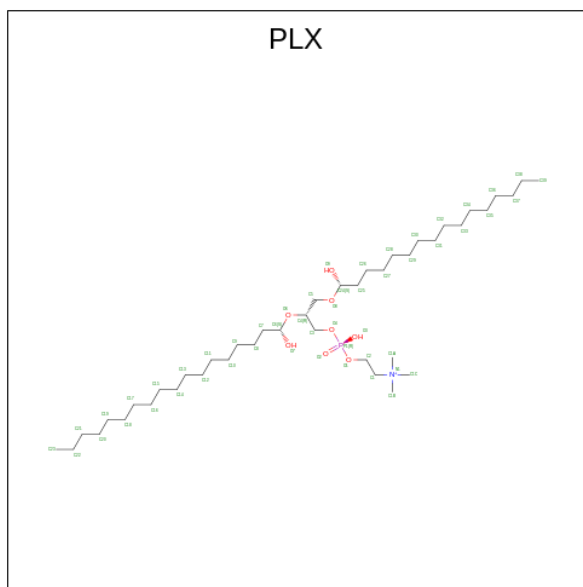
Mol	Chain	Residues	Atoms						AltConf
73	AB	1	Total 36	C 25	N 2	O 7	P 1	S 1	0
73	AC	1	Total 36	C 25	N 2	O 7	P 1	S 1	0

- Molecule 74 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



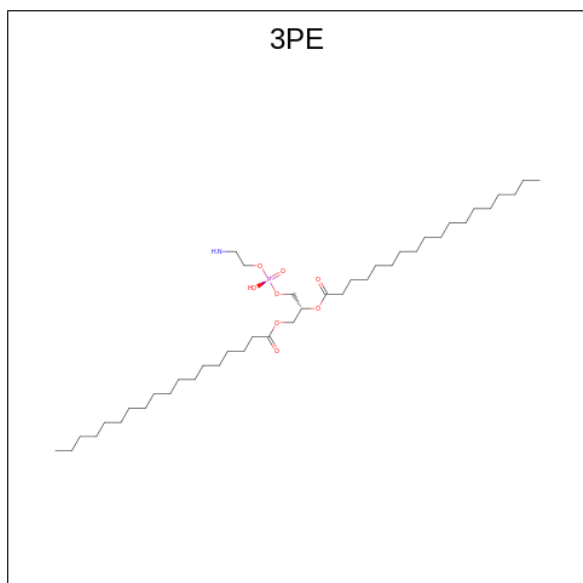
Mol	Chain	Residues	Atoms					AltConf
74	AK	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 75 is (9R,11S)-9-({[(1S)-1-HYDROXYHEXADECYL]OXY}METHYL)-2,2-DIMETHYL-5,7,10-TRIOXA-2LAMBDA 5 -AZA-6LAMBDA 5 -PHOSPHAOCTACOSANE-6,6,11-TRIOL (CCD ID: PLX) (formula: $C_{42}H_{89}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
75	AM	1	Total	C	N	O	P	0
			52	42	1	8	1	
75	AM	1	Total	C	N	O	P	0
			52	42	1	8	1	
75	B5	1	Total	C	N	O	P	0
			52	42	1	8	1	
75	C2	1	Total	C	N	O	P	0
			43	33	1	8	1	
75	CB	1	Total	C	N	O	P	0
			52	42	1	8	1	
75	N3	1	Total	C	N	O	P	0
			52	42	1	8	1	
75	N4	1	Total	C	N	O	P	0
			47	37	1	8	1	
75	N4	1	Total	C	N	O	P	0
			52	42	1	8	1	
75	QB	1	Total	C	N	O	P	0
			46	36	1	8	1	
75	QI	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 76 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).



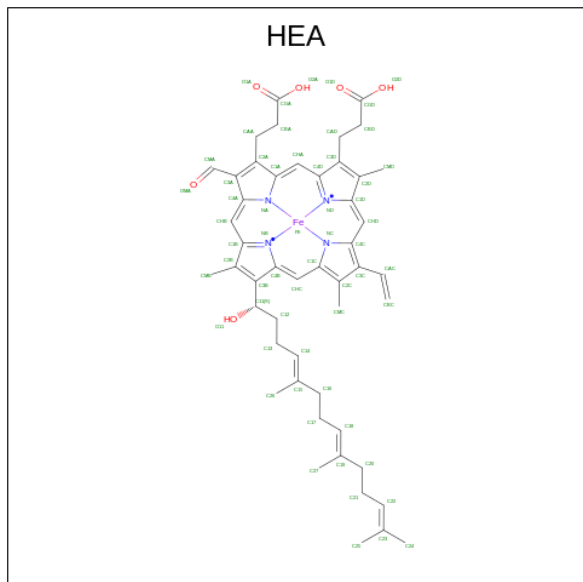
Mol	Chain	Residues	Atoms					AltConf
76	B4	1	Total	C	N	O	P	0
			51	41	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
76	B8	1	Total	C	N	O	P	0
			32	22	1	8	1	
76	C1	1	Total	C	N	O	P	0
			51	41	1	8	1	
76	C2	1	Total	C	N	O	P	0
			51	41	1	8	1	
76	CA	1	Total	C	N	O	P	0
			51	41	1	8	1	
76	QE	1	Total	C	N	O	P	0
			44	34	1	8	1	

- Molecule 77 is HEME-A (CCD ID: HEA) (formula: $C_{49}H_{56}FeN_4O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
77	C1	1	Total	C	Fe	N	O	0
			60	49	1	4	6	
77	C1	1	Total	C	Fe	N	O	0
			60	49	1	4	6	

- Molecule 78 is COPPER (II) ION (CCD ID: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
78	C1	1	Total	Cu	0
			1	1	

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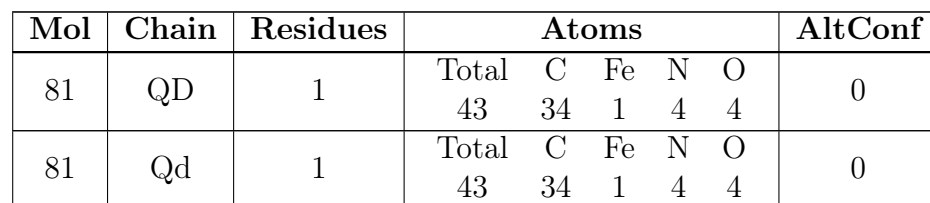
Mol	Chain	Residues	Atoms	AltConf
78	C2	2	Total Cu 2 2	0

- | Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|---------|---------|
| 79 | C1 | 1 | Total
1 | Mg
1 | 0 |
| 79 | S1 | 1 | Total
1 | Mg
1 | 0 |

- # HEM

Mol	Chain	Residues	Atoms					AltConf
80	QC	1	Total 43	C 34	Fe 1	N 4	O 4	0
80	QC	1	Total 43	C 34	Fe 1	N 4	O 4	0
80	Qc	1	Total 43	C 34	Fe 1	N 4	O 4	0
80	Qc	1	Total 43	C 34	Fe 1	N 4	O 4	0

- 



-
- Diagram illustrating the structure of a Ferredoxin Center (FES). The structure shows two Iron (Fe) atoms and two Sulfur (S) atoms arranged in a square. The top-left Sulfur atom is labeled S1, the top-right Iron atom is labeled FE2, the bottom-left Iron atom is labeled FE1, and the bottom-right Sulfur atom is labeled S2. The bonds between S1 and Fe, and between Fe and S2, are colored yellow. The bonds between S2 and Fe1, and between Fe1 and S1, are colored purple.

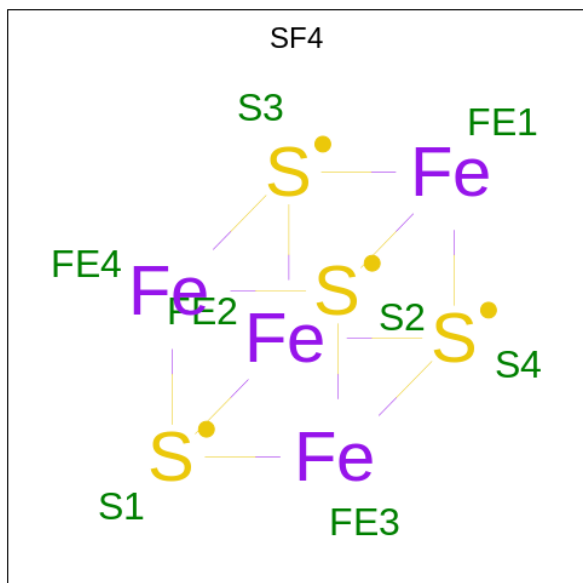
Mol	Chain	Residues	Atoms			AltConf
82	QE	1	Total 4	Fe 2	S 2	0
82	Qe	1	Total 4	Fe 2	S 2	0



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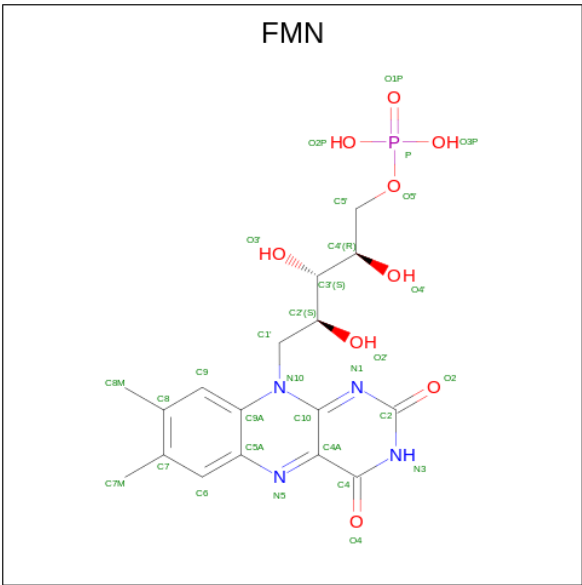
Mol	Chain	Residues	Atoms			AltConf
82	S1	1	Total	Fe	S	0
			4	2	2	
82	V2	1	Total	Fe	S	0
			4	2	2	

- Molecule 83 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
83	S1	1	Total	Fe	S	0
			8	4	4	
83	S1	1	Total	Fe	S	0
			8	4	4	
83	S7	1	Total	Fe	S	0
			8	4	4	
83	S8	1	Total	Fe	S	0
			8	4	4	
83	S8	1	Total	Fe	S	0
			8	4	4	
83	V1	1	Total	Fe	S	0
			8	4	4	

- Molecule 84 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $\text{C}_{17}\text{H}_{21}\text{N}_4\text{O}_9\text{P}$) (labeled as "Ligand of Interest" by depositor).




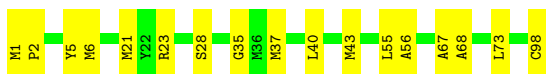
Mol	Chain	Residues	Atoms					AltConf
84	V1	1	Total	C	N	O	P	0
			31	17	4	9	1	

3 Residue-property plots [i](#)


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

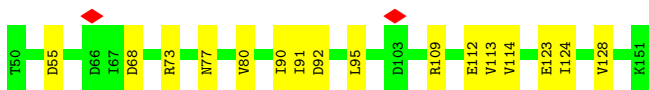
- Molecule 1: NADH-ubiquinone oxidoreductase chain 4L

Chain 4L:  83% 17%




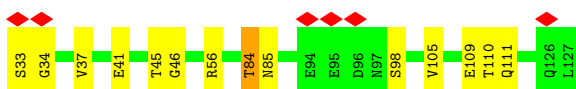
- Molecule 2: Cytochrome c oxidase subunit 5A, mitochondrial

Chain 5A:  84% 16%




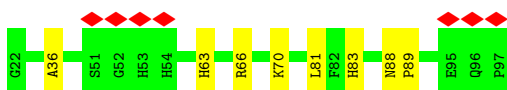
- Molecule 3: Cytochrome c oxidase subunit 5B, mitochondrial

Chain 5B:  6% 85% 14%




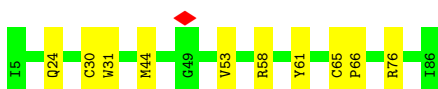
- Molecule 4: Cytochrome c oxidase subunit

Chain 6A:  9% 89% 11%




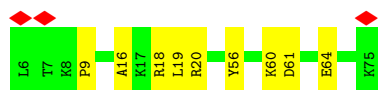
- Molecule 5: Cytochrome c oxidase subunit

Chain 6B:  88% 12%



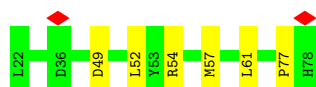
- Molecule 6: Cytochrome c oxidase subunit 6C

Chain 6C:  87% 13%




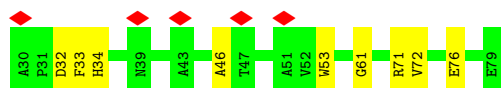
- Molecule 7: Cytochrome c oxidase subunit 7A1, mitochondrial

Chain 7A:  89% 11%




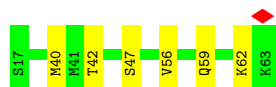
- Molecule 8: Cytochrome c oxidase subunit 7B, mitochondrial

Chain 7B:  82% 18% 10%




- Molecule 9: Cytochrome c oxidase subunit 7C, mitochondrial

Chain 7C:  87% 13%




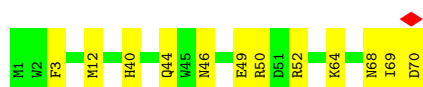
- Molecule 10: Cytochrome c oxidase subunit 8

Chain 8B:  86% 14%




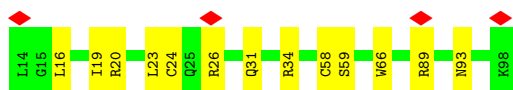
- Molecule 11: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1

Chain A1:  83% 17%

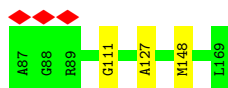


- Molecule 12: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2

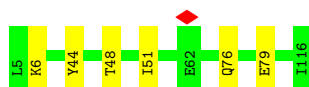
Chain A2:  85% 15% 5%



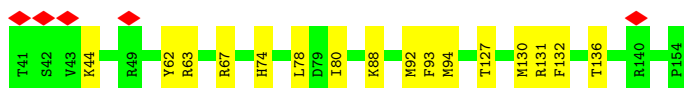
- Molecule 13: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3



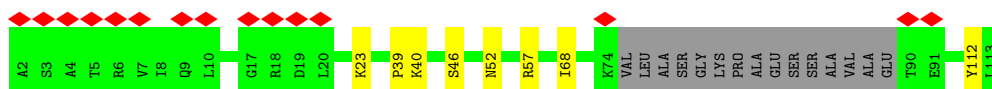
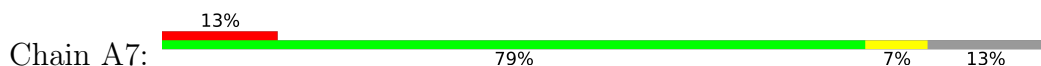
- Molecule 14: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5



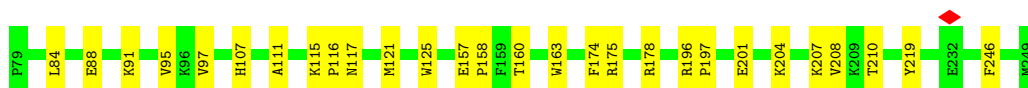
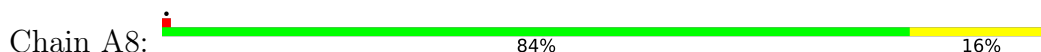
- Molecule 15: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



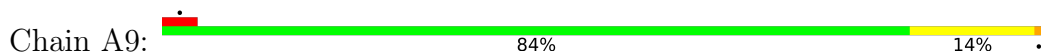
- Molecule 16: Complex I-B14.5a



- Molecule 17: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8

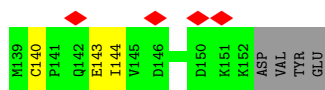
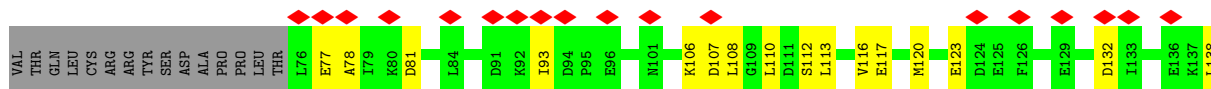
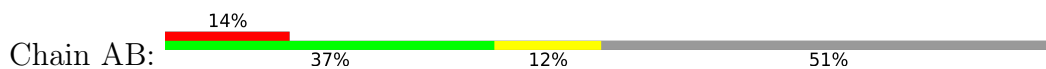


- Molecule 18: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial

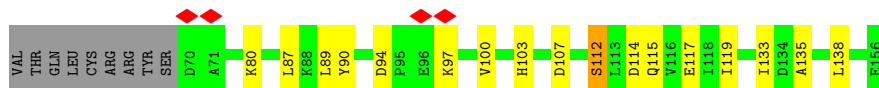
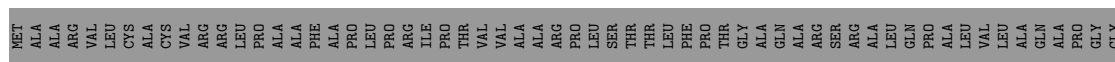




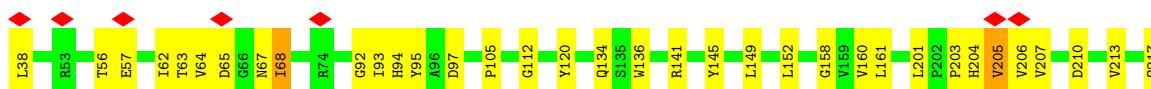
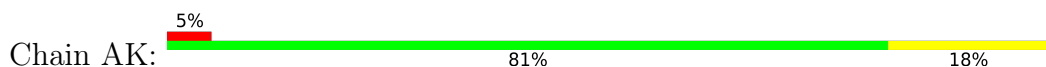
- Molecule 19: Acyl carrier protein



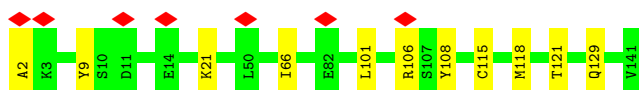
- Molecule 19: Acyl carrier protein



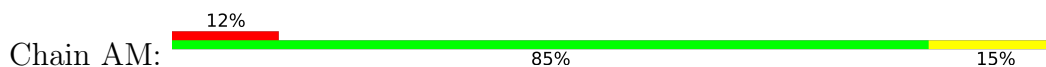
- Molecule 20: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial



- Molecule 21: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11

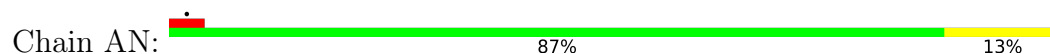


- Molecule 22: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

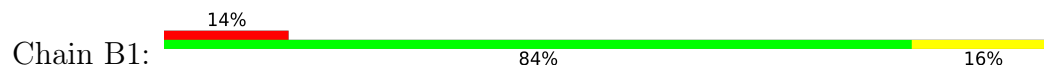




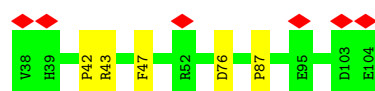
- Molecule 23: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13



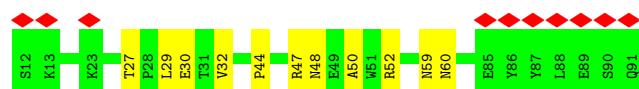
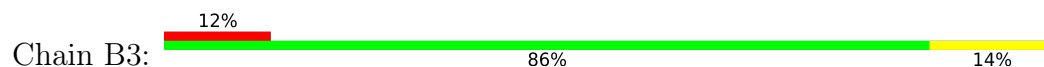
- Molecule 24: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1



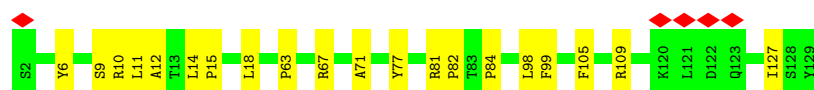
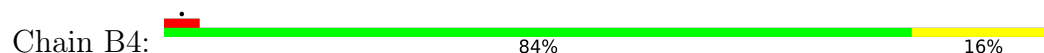
- Molecule 25: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial



- Molecule 26: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3



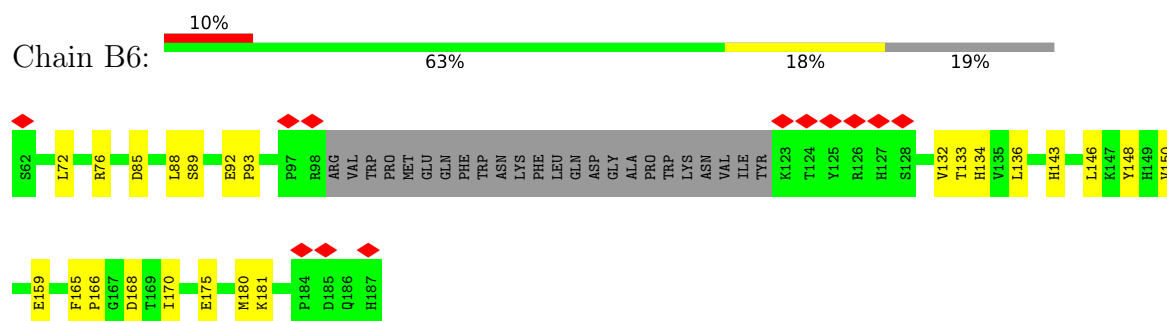
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4



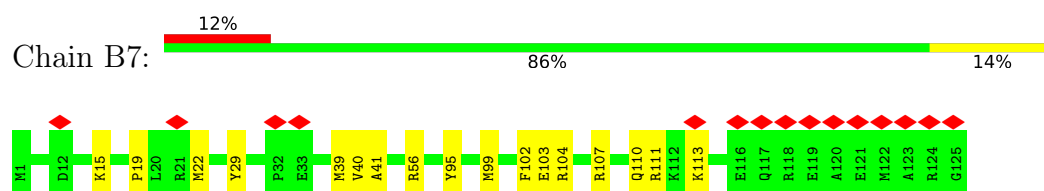
- Molecule 28: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial



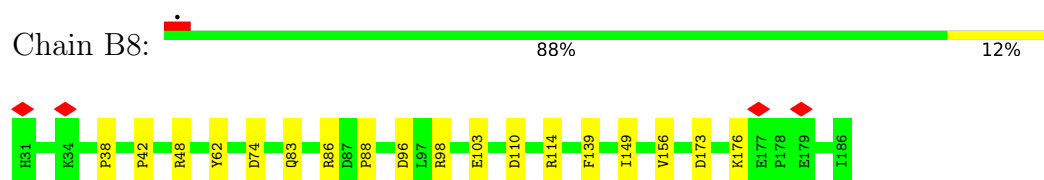
- Molecule 29: Complex I-B17



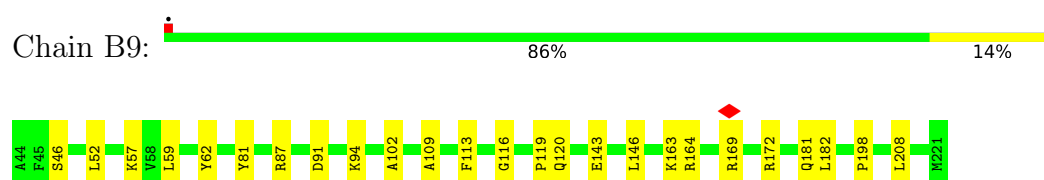
- Molecule 30: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



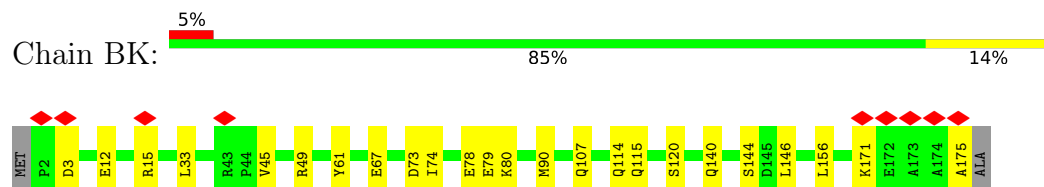
- Molecule 31: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial



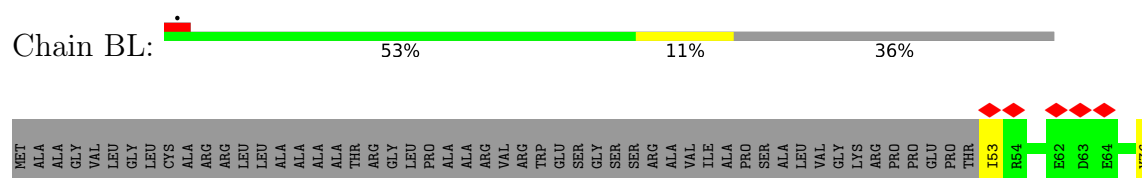
- Molecule 32: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9



- Molecule 33: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10



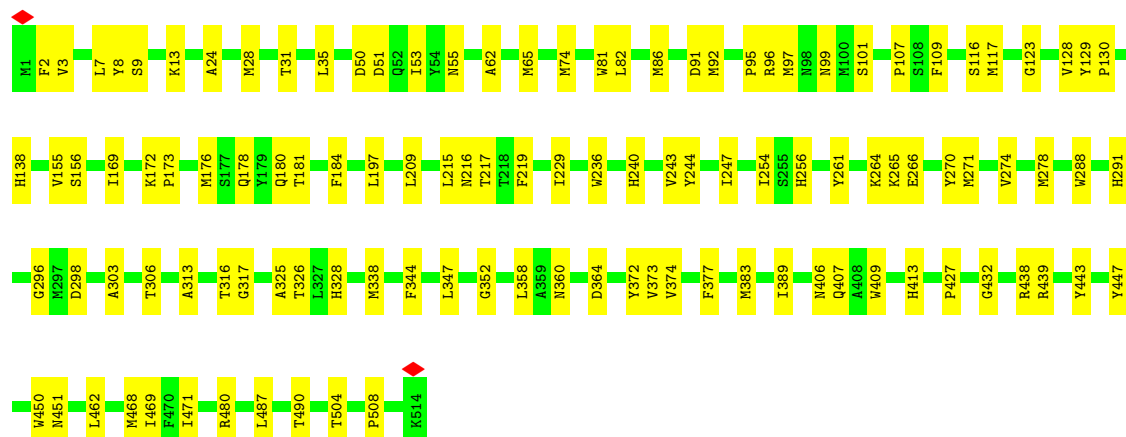
- Molecule 34: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial





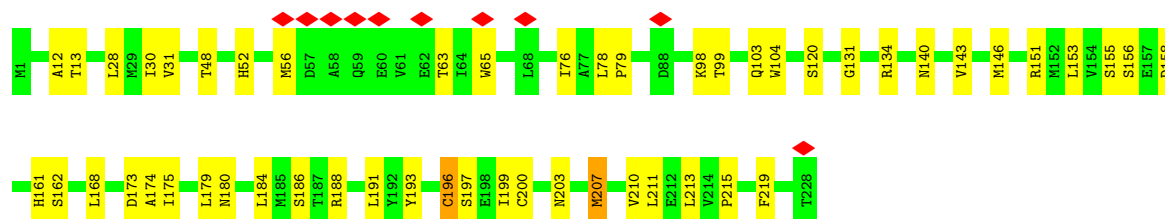
• Molecule 35: Cytochrome c oxidase subunit 1

Chain C1: 78% 22%



• Molecule 36: Cytochrome c oxidase subunit 2

Chain C2: 77% 22%



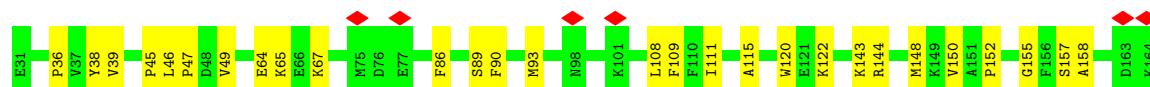
• Molecule 37: Cytochrome c oxidase subunit 3

Chain C3: 82% 18%



• Molecule 38: Cytochrome c oxidase subunit 4

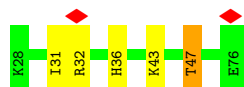
Chain C4: 80% 20%





- Molecule 39: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial

Chain CA: 90% 8%



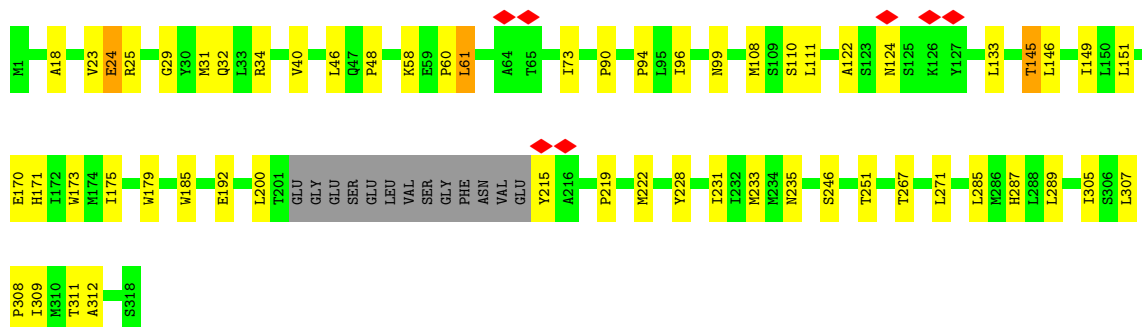
- Molecule 40: NADH dehydrogenase [ubiquinone] 1 subunit C2

Chain CB: 89% 11%



- Molecule 41: NADH-ubiquinone oxidoreductase chain 1

Chain N1: 78% 17%



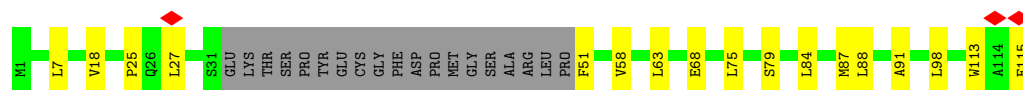
- Molecule 42: NADH-ubiquinone oxidoreductase chain 2

Chain N2: 78% 22%

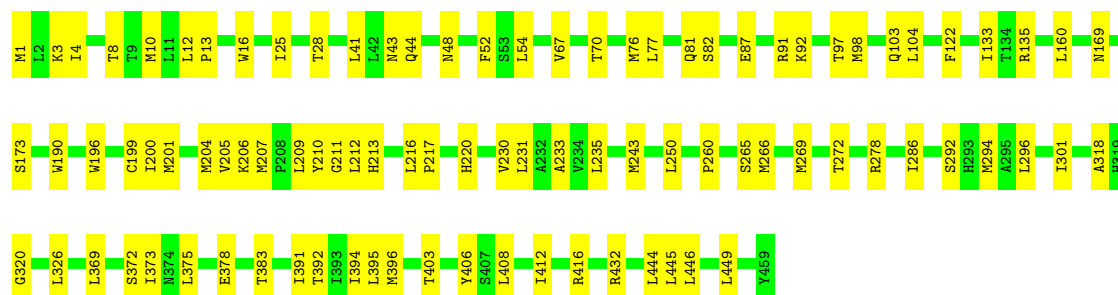
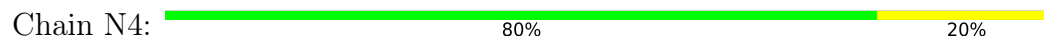


- Molecule 43: NADH-ubiquinone oxidoreductase chain 3

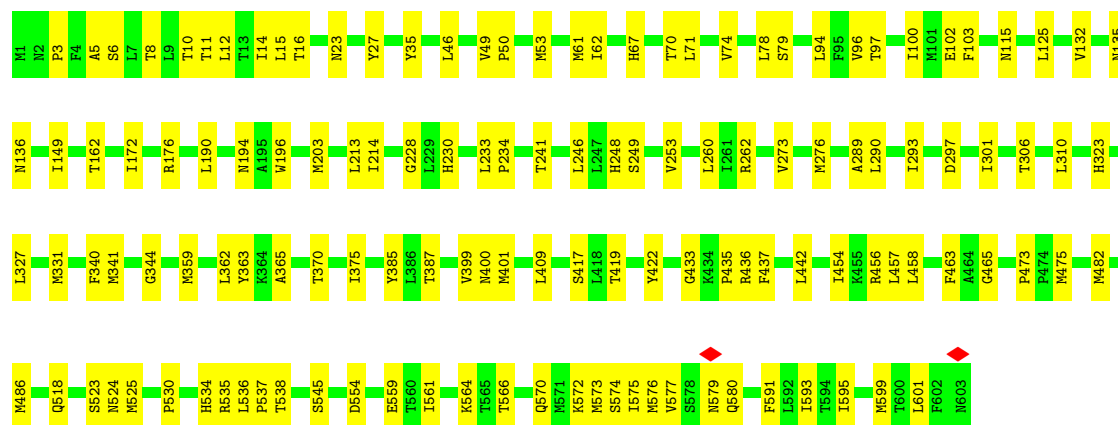
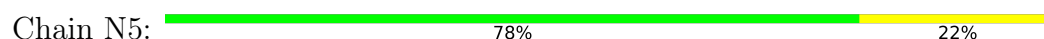
Chain N3: 69% 15% 17%



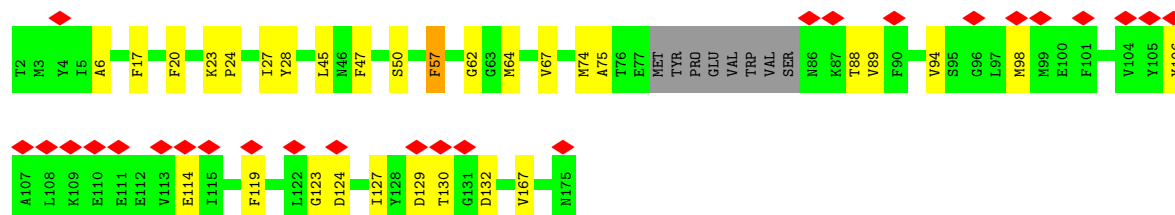
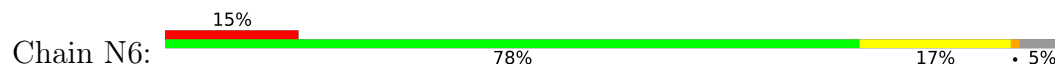
- Molecule 44: NADH-ubiquinone oxidoreductase chain 4



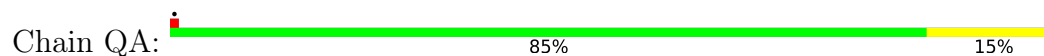
- Molecule 45: NADH-ubiquinone oxidoreductase chain 5



- Molecule 46: NADH-ubiquinone oxidoreductase chain 6

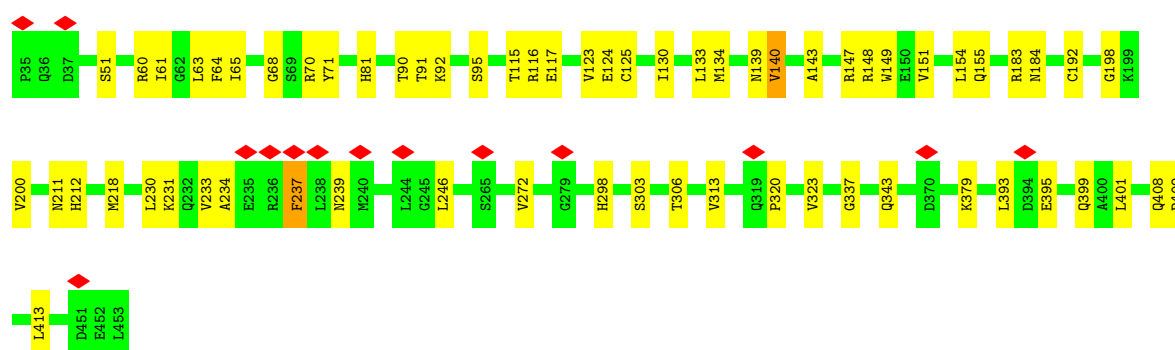
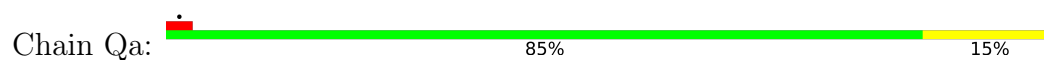


- Molecule 47: Cytochrome b-c1 complex subunit 2, mitochondrial

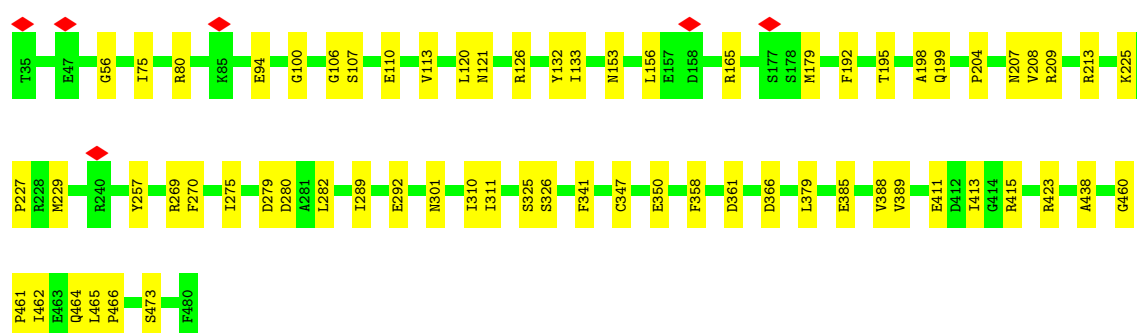
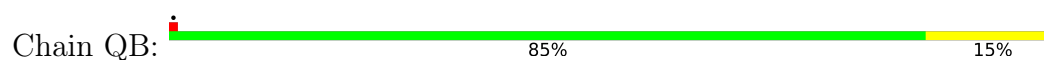




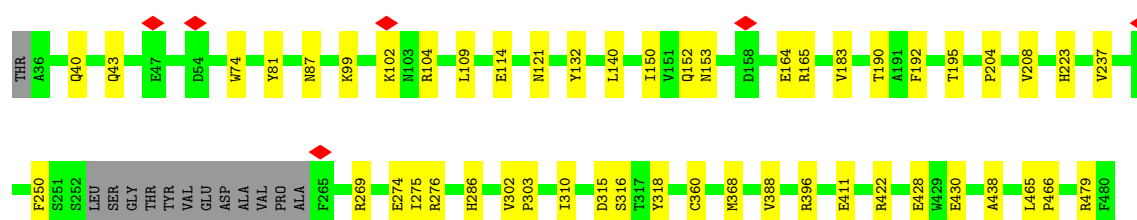
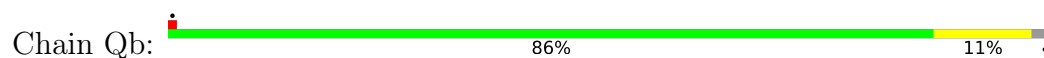
- Molecule 47: Cytochrome b-c1 complex subunit 2, mitochondrial




- Molecule 48: Cytochrome b-c1 complex subunit 1, mitochondrial



- Molecule 48: Cytochrome b-c1 complex subunit 1, mitochondrial




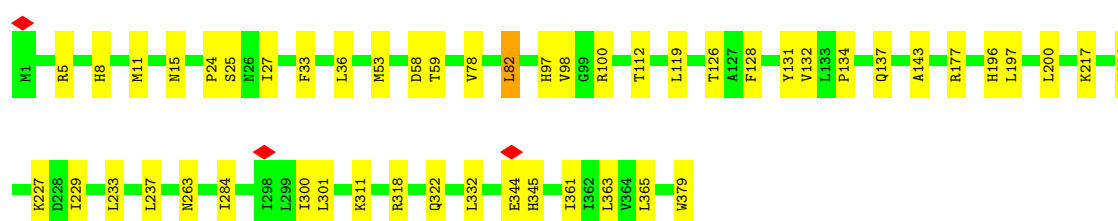
- Molecule 49: Cytochrome b

Chain QC:  87% 13%



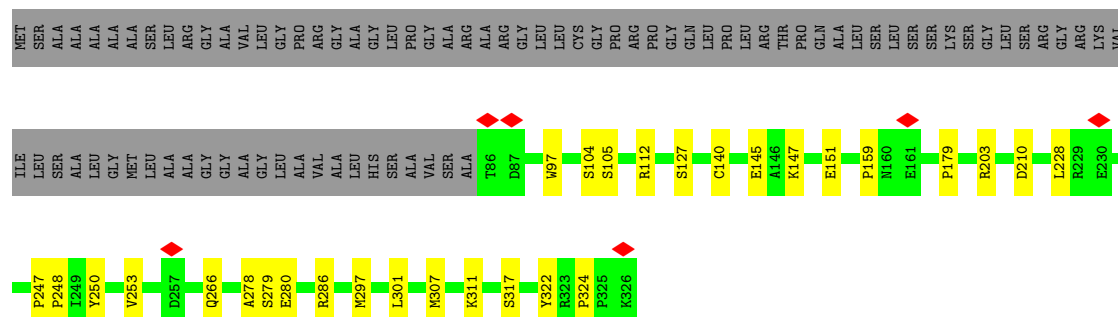
- Molecule 49: Cytochrome b

Chain Qc:  87% 13%



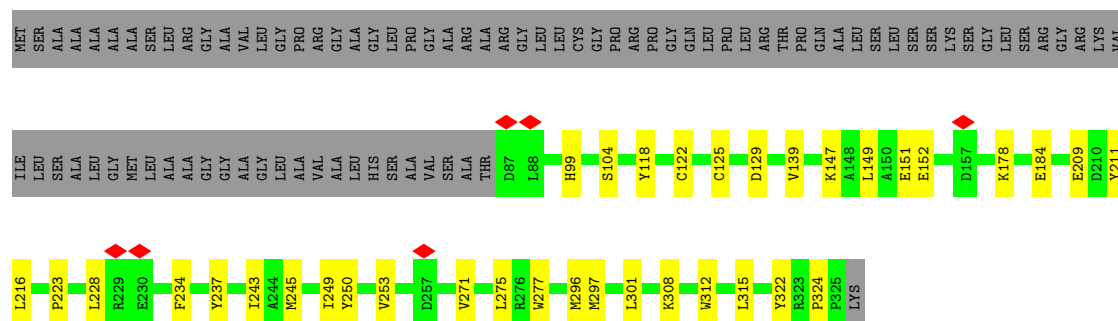
- Molecule 50: Cytochrome c1, heme protein, mitochondrial

Chain QD:  64% 10% 26%

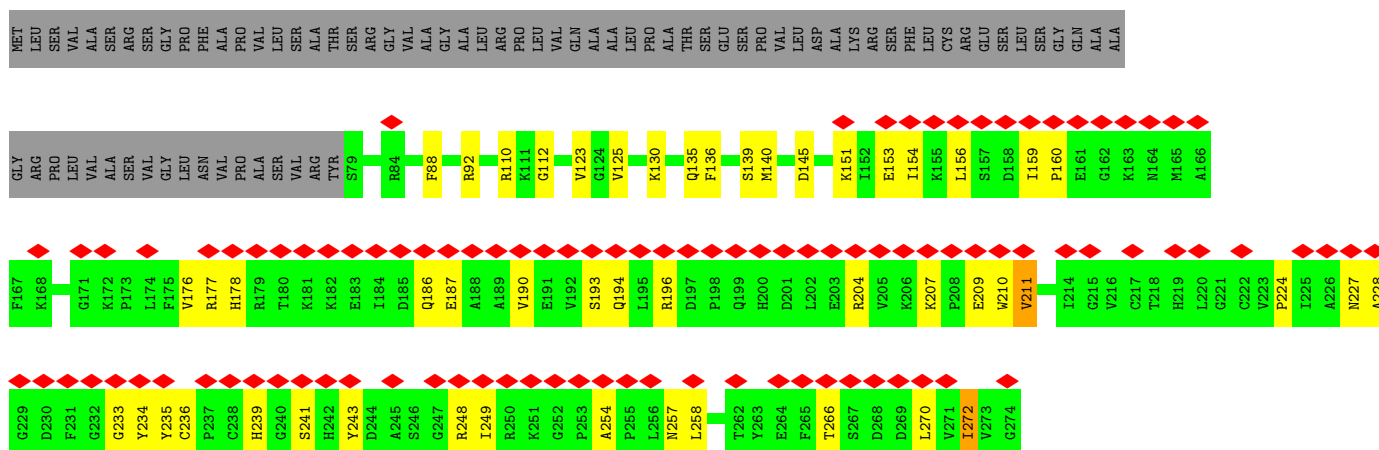
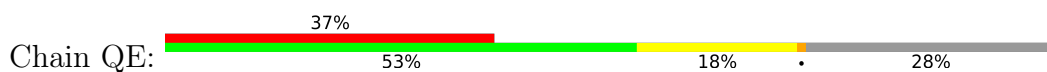


- Molecule 50: Cytochrome c1, heme protein, mitochondrial

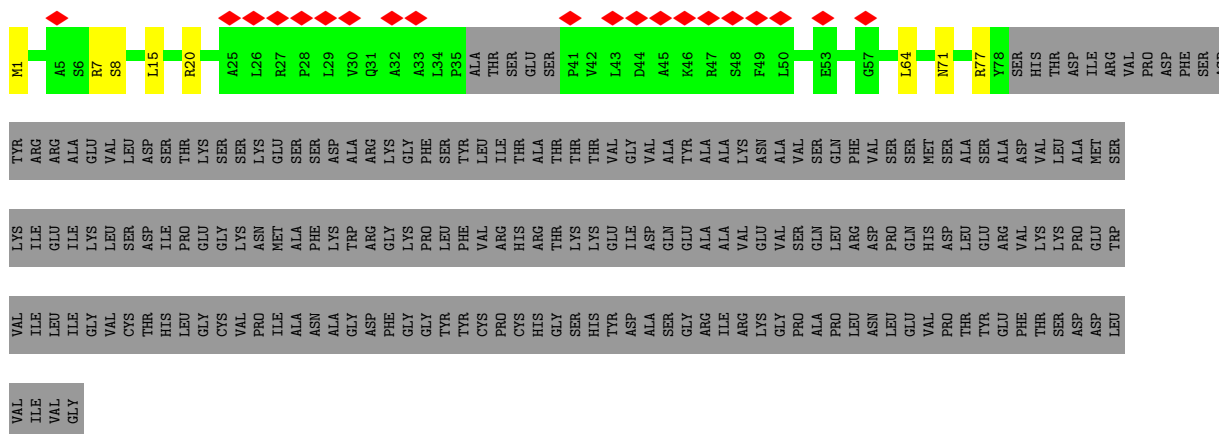
Chain Qd:  62% 11% 27%



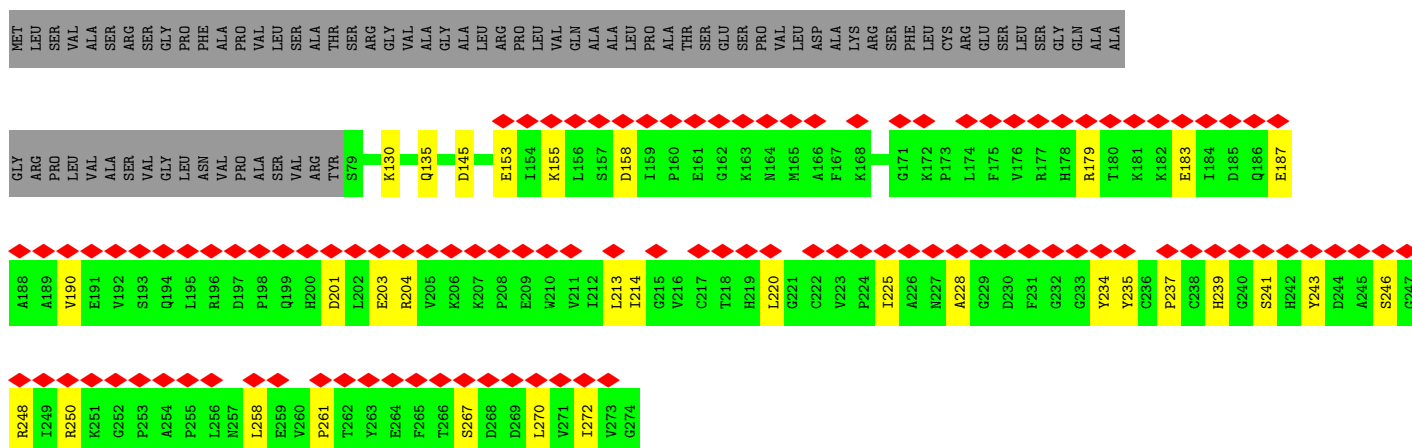
- Molecule 51: Cytochrome b-c1 complex subunit Rieske, mitochondrial



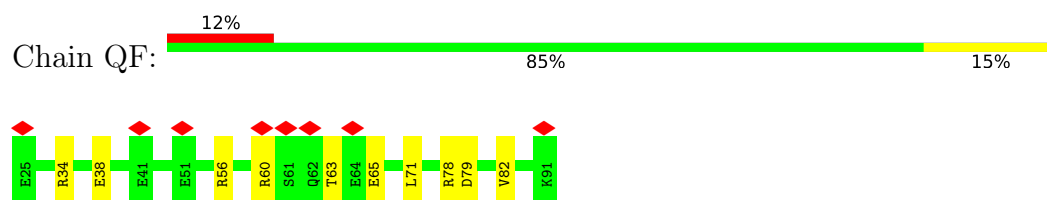
- Molecule 51: Cytochrome b-c1 complex subunit Rieske, mitochondrial



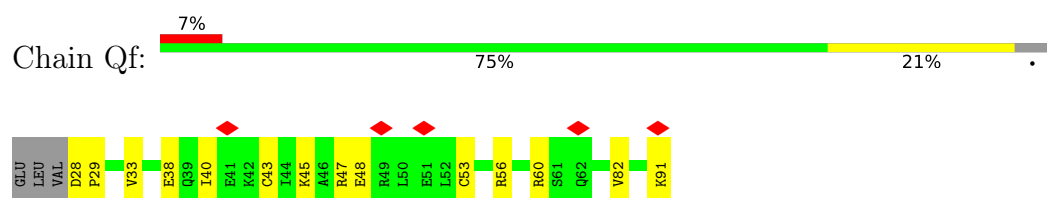
- Molecule 51: Cytochrome b-c1 complex subunit Rieske, mitochondrial



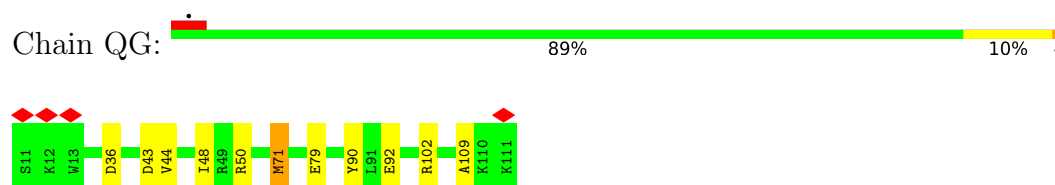
- Molecule 52: Cytochrome b-c1 complex subunit 6



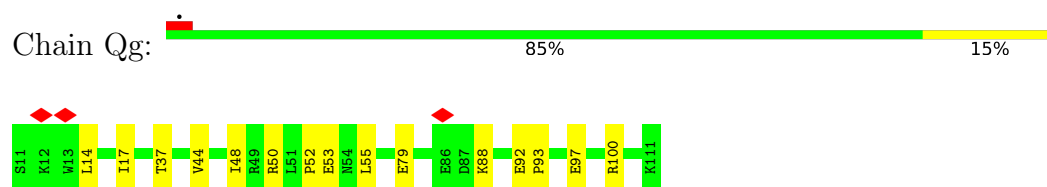
- Molecule 52: Cytochrome b-c1 complex subunit 6



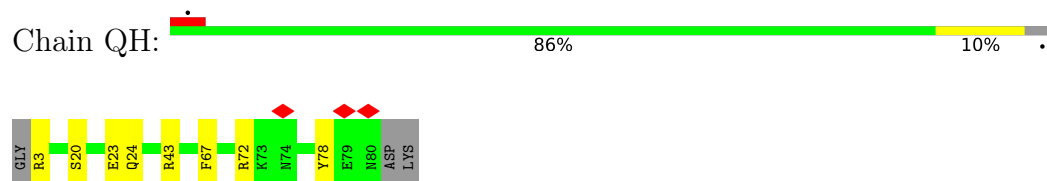
- Molecule 53: Cytochrome b-c1 complex subunit 7



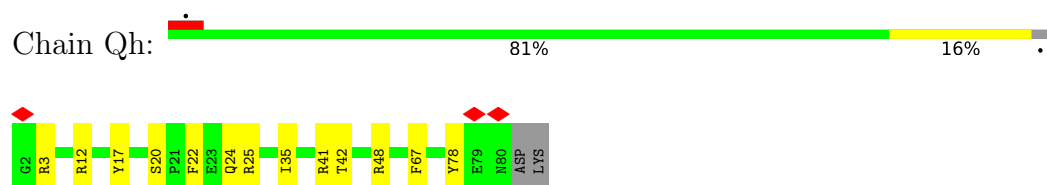
- Molecule 53: Cytochrome b-c1 complex subunit 7



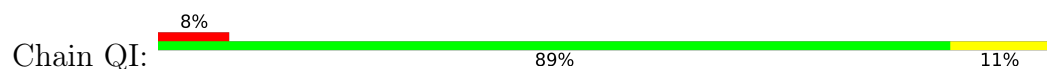
- Molecule 54: Cytochrome b-c1 complex subunit 8



- Molecule 54: Cytochrome b-c1 complex subunit 8

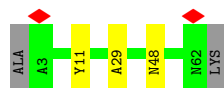


- Molecule 55: Complex III subunit 9

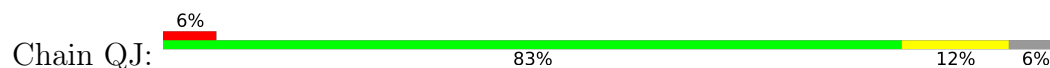




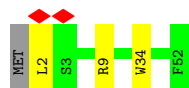
- Molecule 55: Complex III subunit 9



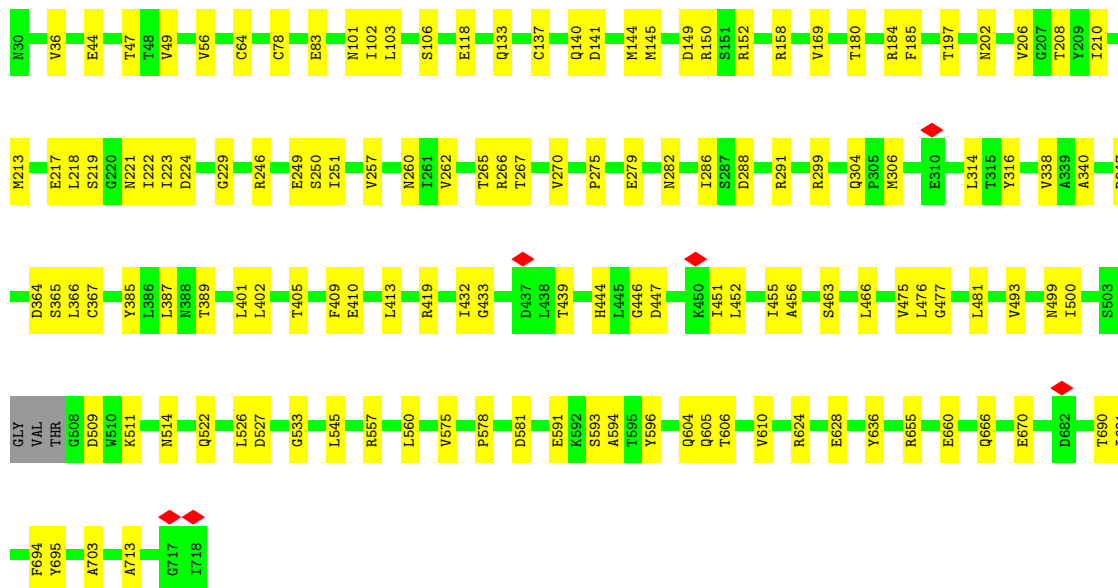
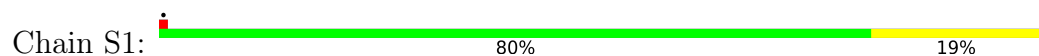
- Molecule 56: Cytochrome b-c1 complex subunit 10



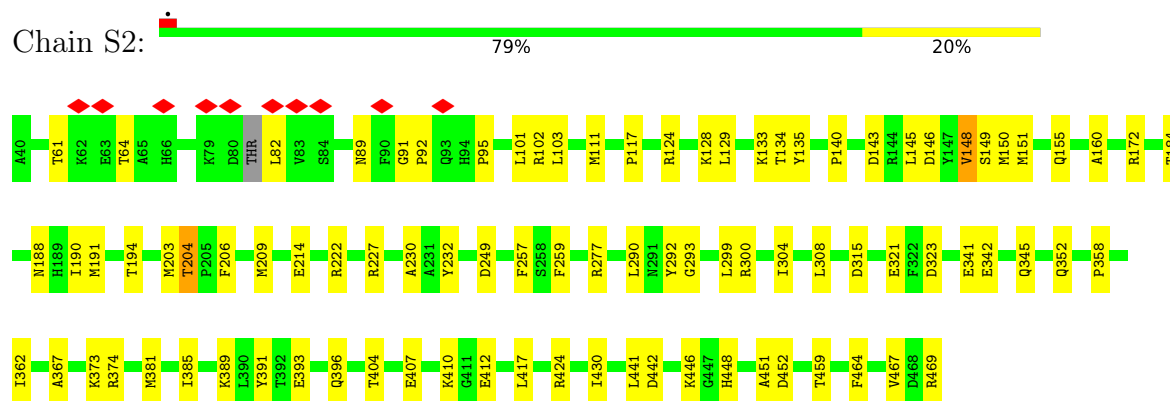
- Molecule 56: Cytochrome b-c1 complex subunit 10



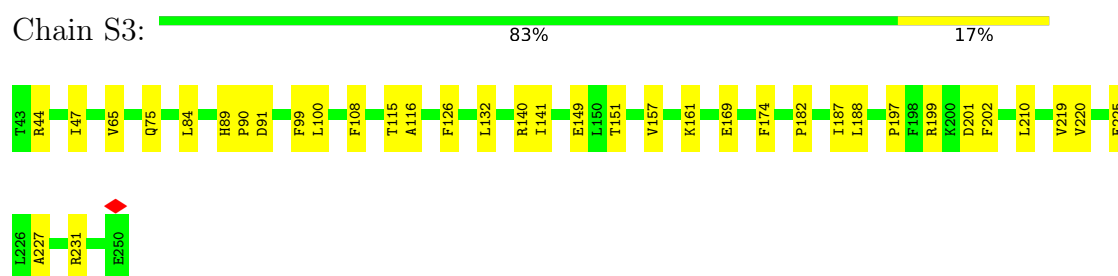
- Molecule 57: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial



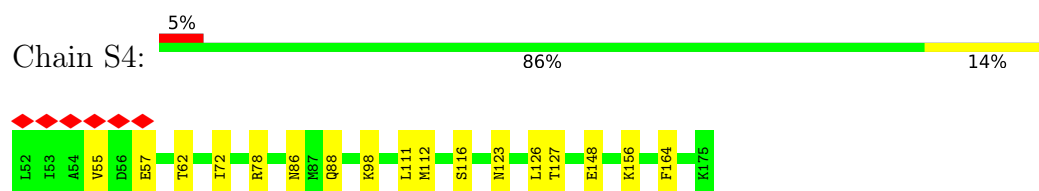
- Molecule 58: Complex I-49kD



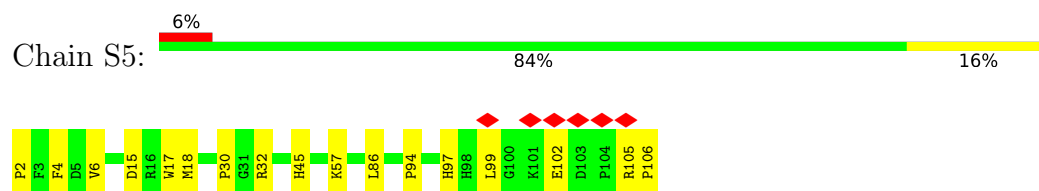
- Molecule 59: Complex I-30kD



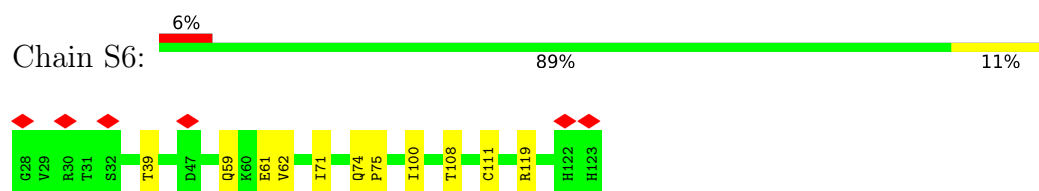
- Molecule 60: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial



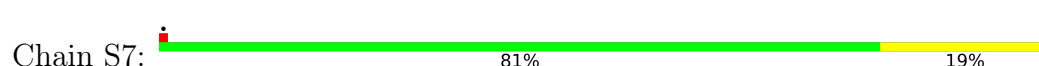
- Molecule 61: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5

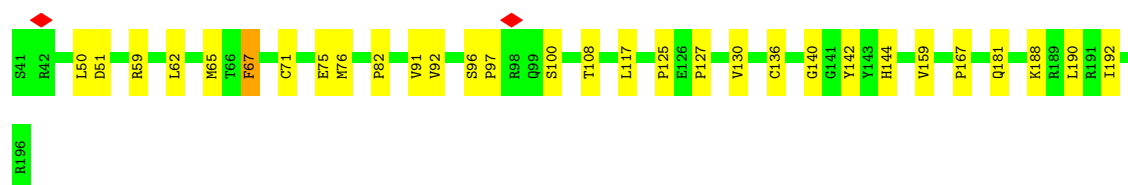


- Molecule 62: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial

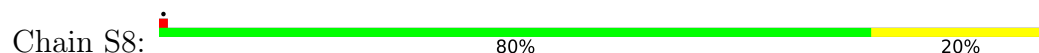


- Molecule 63: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial

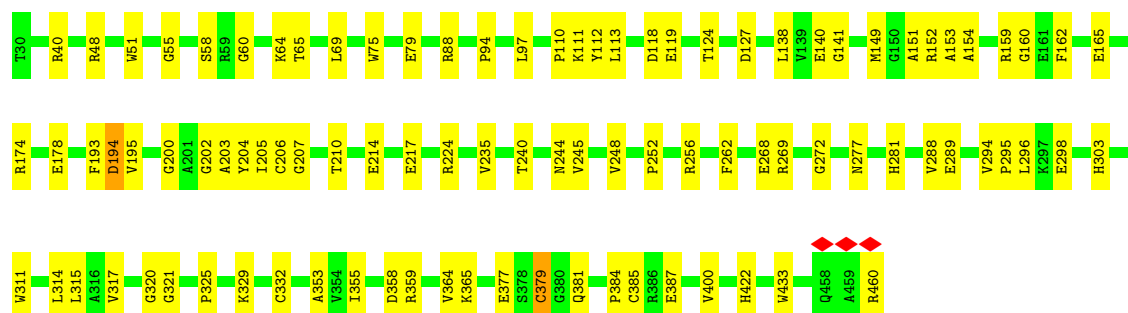
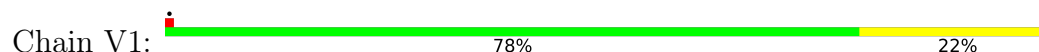




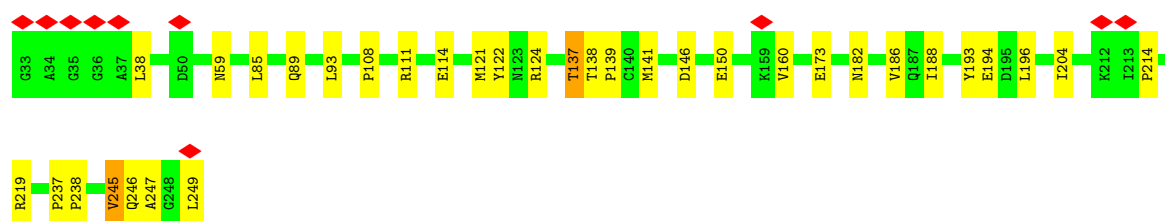
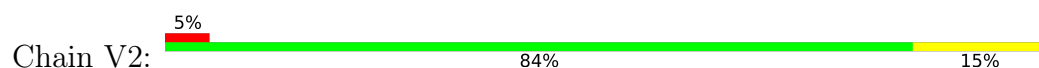
- Molecule 64: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial



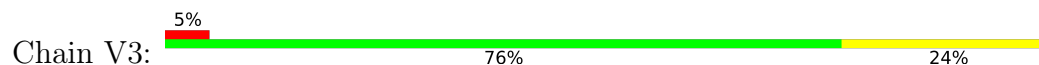
- Molecule 65: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



- Molecule 66: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial



- Molecule 67: Complex I-9kD



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	217871	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51.9	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	47.979	Depositor
Minimum map value	-21.464	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	1.073	Depositor
Recommended contour level	6	Depositor
Map size (Å)	576.0, 576.0, 576.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2, 1.2, 1.2	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PC1, HEC, PEE, HEA, 2MR, HEM, FES, 3PE, MG, PLX, CDL, SF4, NDP, CU, ADP, FMN, ZMP, ZN

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	4L	0.23	0/759	0.27	0/1029
2	5A	0.17	0/843	0.25	0/1145
3	5B	0.21	0/739	0.32	0/1002
4	6A	0.16	0/652	0.26	0/893
5	6B	0.20	0/704	0.25	0/951
6	6C	0.17	0/587	0.27	0/781
7	7A	0.17	0/457	0.27	0/620
8	7B	0.16	0/405	0.24	0/555
9	7C	0.23	0/400	0.26	0/536
10	8B	0.21	0/349	0.26	0/477
11	A1	0.20	0/577	0.28	0/777
12	A2	0.15	0/697	0.25	0/938
13	A3	0.17	0/664	0.24	0/912
14	A5	0.18	0/929	0.24	0/1258
15	A6	0.18	0/991	0.25	0/1335
16	A7	0.16	0/798	0.23	0/1079
17	A8	0.19	0/1436	0.26	0/1938
18	A9	0.18	0/2777	0.26	0/3762
19	AB	0.12	0/633	0.22	0/851
19	AC	0.21	0/714	0.25	0/965
20	AK	0.20	0/2650	0.36	2/3588 (0.1%)
21	AL	0.17	0/1042	0.22	0/1411
22	AM	0.16	0/1245	0.23	0/1694
23	AN	0.20	0/1204	0.25	0/1624
24	B1	0.18	0/491	0.24	0/663
25	B2	0.18	0/610	0.26	0/836
26	B3	0.17	0/660	0.27	0/892
27	B4	0.20	0/1092	0.26	0/1481
28	B5	0.22	0/1184	0.27	0/1603
29	B6	0.20	0/897	0.31	0/1219
30	B7	0.17	0/1092	0.25	0/1459

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	B8	0.20	0/1371	0.25	0/1875
32	B9	0.20	0/1590	0.28	0/2155
33	BK	0.20	0/1489	0.25	0/2008
34	BL	0.21	0/851	0.31	0/1155
35	C1	0.27	0/4164	0.34	0/5689
36	C2	0.24	0/1880	0.32	0/2564
37	C3	0.23	0/2186	0.29	0/2991
38	C4	0.18	0/1187	0.25	0/1606
39	CA	0.17	0/430	0.23	0/581
40	CB	0.22	0/1031	0.27	0/1394
41	N1	0.24	0/2482	0.36	0/3394
42	N2	0.26	0/2773	0.35	0/3768
43	N3	0.21	0/788	0.26	0/1076
44	N4	0.25	0/3723	0.34	0/5078
45	N5	0.23	0/4914	0.35	0/6683
46	N6	0.20	0/1289	0.31	0/1744
47	QA	0.21	0/3200	0.29	0/4333
47	Qa	0.21	0/3200	0.29	0/4333
48	QB	0.22	0/3531	0.31	0/4793
48	Qb	0.21	0/3436	0.28	0/4659
49	QC	0.24	0/3123	0.31	0/4269
49	Qc	0.24	0/3123	0.32	0/4269
50	QD	0.21	0/1979	0.27	0/2684
50	Qd	0.21	0/1962	0.28	0/2663
51	QE	0.16	0/1550	0.25	0/2098
51	QK	0.16	0/528	0.27	0/716
51	Qe	0.15	0/1550	0.28	0/2098
52	QF	0.16	0/558	0.23	0/747
52	Qf	0.17	0/534	0.25	0/714
53	QG	0.21	0/913	0.27	0/1223
53	Qg	0.21	0/913	0.28	0/1223
54	QH	0.20	0/684	0.32	0/926
54	Qh	0.20	0/688	0.29	0/931
55	QI	0.18	0/520	0.21	0/701
55	Qi	0.20	0/506	0.25	0/683
56	QJ	0.16	0/420	0.24	0/576
56	Qj	0.19	0/437	0.30	0/598
57	S1	0.22	0/5353	0.32	2/7251 (0.0%)
58	S2	0.25	0/3530	0.31	0/4783
59	S3	0.23	0/1789	0.29	0/2436
60	S4	0.22	0/1030	0.28	0/1391
61	S5	0.19	0/889	0.27	0/1190
62	S6	0.17	0/755	0.26	0/1018

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
63	S7	0.23	0/1279	0.27	0/1730
64	S8	0.24	0/1443	0.29	0/1952
65	V1	0.19	0/3391	0.30	0/4583
66	V2	0.17	0/1711	0.28	0/2328
67	V3	0.14	0/365	0.19	0/493
All	All	0.21	0/115316	0.29	4/156427 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	AK	204	HIS	CA-C-N	-5.99	114.71	123.10
20	AK	204	HIS	C-N-CA	-5.99	114.71	123.10
57	S1	364	ASP	CA-C-N	-5.66	113.83	122.21
57	S1	364	ASP	C-N-CA	-5.66	113.83	122.21

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	4L	748	0	799	16	0
2	5A	825	0	823	12	0
3	5B	724	0	705	10	0
4	6A	624	0	592	7	0
5	6B	684	0	649	8	0
6	6C	574	0	590	7	0
7	7A	447	0	443	5	0
8	7B	392	0	372	9	0
9	7C	387	0	385	7	0
10	8B	338	0	342	6	0
11	A1	562	0	557	9	0
12	A2	686	0	699	8	0
13	A3	643	0	642	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	A5	910	0	950	4	0
15	A6	967	0	972	18	0
16	A7	780	0	808	7	0
17	A8	1398	0	1372	20	0
18	A9	2703	0	2720	30	0
19	AB	624	0	625	15	0
19	AC	702	0	694	12	0
20	AK	2590	0	2553	44	0
21	AL	1021	0	1025	7	0
22	AM	1204	0	1162	16	0
23	AN	1173	0	1166	16	0
24	B1	479	0	486	6	0
25	B2	584	0	529	4	0
26	B3	641	0	620	9	0
27	B4	1062	0	1072	16	0
28	B5	1151	0	1164	11	0
29	B6	870	0	890	18	0
30	B7	1068	0	1041	13	0
31	B8	1315	0	1208	14	0
32	B9	1534	0	1470	19	0
33	BK	1456	0	1426	22	0
34	BL	828	0	788	12	0
35	C1	4024	0	4005	91	0
36	C2	1833	0	1843	38	0
37	C3	2103	0	2034	48	0
38	C4	1153	0	1130	24	0
39	CA	417	0	422	4	0
40	CB	1000	0	994	15	0
41	N1	2411	0	2522	49	0
42	N2	2710	0	2874	57	0
43	N3	770	0	816	17	0
44	N4	3631	0	3839	68	0
45	N5	4785	0	4933	99	0
46	N6	1259	0	1261	28	0
47	QA	3147	0	3129	40	0
47	Qa	3147	0	3129	40	0
48	QB	3459	0	3350	41	0
48	Qb	3367	0	3262	33	0
49	QC	3025	0	3090	36	0
49	Qc	3025	0	3090	39	0
50	QD	1921	0	1867	22	0
50	Qd	1904	0	1849	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	QE	1517	0	1500	37	0
51	QK	520	0	554	5	0
51	Qe	1517	0	1500	23	0
52	QF	552	0	536	9	0
52	Qf	528	0	510	8	0
53	QG	893	0	888	7	0
53	Qg	893	0	888	8	0
54	QH	662	0	660	7	0
54	Qh	666	0	663	12	0
55	QI	507	0	509	5	0
55	Qi	493	0	491	4	0
56	QJ	405	0	405	6	0
56	Qj	421	0	418	2	0
57	S1	5266	0	5296	81	0
58	S2	3452	0	3388	65	0
59	S3	1738	0	1693	26	0
60	S4	1007	0	1008	14	0
61	S5	867	0	871	16	0
62	S6	741	0	701	9	0
63	S7	1248	0	1254	19	0
64	S8	1412	0	1363	29	0
65	V1	3316	0	3272	60	0
66	V2	1671	0	1673	21	0
67	V3	355	0	329	9	0
68	4L	92	0	137	3	0
68	A1	94	0	141	5	0
68	A8	77	0	98	10	0
68	AL	184	0	268	9	0
68	B4	62	0	68	3	0
68	B5	98	0	149	3	0
68	C1	77	0	98	7	0
68	N2	168	0	236	13	0
68	N5	182	0	270	12	0
68	QB	61	0	66	1	0
68	QC	55	0	54	4	0
68	QD	64	0	72	1	0
68	QE	100	0	156	2	0
68	QH	125	0	138	4	0
68	Qb	64	0	72	6	0
69	5B	1	0	0	0	0
69	S6	1	0	0	0	0
70	6A	45	0	64	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	7C	52	0	81	4	0
70	B5	54	0	88	2	0
70	B7	54	0	88	1	0
70	C1	237	0	362	22	0
70	C3	93	0	140	9	0
70	N1	108	0	176	11	0
70	N3	54	0	88	3	0
70	N5	31	0	36	2	0
70	QJ	54	0	88	3	0
70	Qb	54	0	88	5	0
70	Qc	108	0	176	3	0
70	Qd	54	0	88	2	0
70	Qh	54	0	88	1	0
71	6A	87	0	131	5	0
71	8B	42	0	61	2	0
71	A3	51	0	82	3	0
71	AL	40	0	54	4	0
71	B4	51	0	82	4	0
71	C3	51	0	82	4	0
71	N4	49	0	75	3	0
71	N5	97	0	151	7	0
71	QB	85	0	124	3	0
71	QC	40	0	54	0	0
71	QE	47	0	71	1	0
71	Qc	93	0	143	6	0
71	Qd	24	0	22	1	0
71	S2	48	0	73	1	0
71	S8	51	0	82	0	0
72	A9	48	0	26	1	0
73	AB	36	0	47	1	0
73	AC	36	0	47	4	0
74	AK	27	0	12	4	0
75	AM	104	0	176	3	0
75	B5	52	0	88	0	0
75	C2	43	0	67	2	0
75	CB	52	0	88	3	0
75	N3	52	0	88	1	0
75	N4	99	0	163	16	0
75	QB	46	0	73	4	0
75	QI	52	0	88	5	0
76	B4	51	0	82	8	0
76	B8	32	0	38	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
76	C1	51	0	82	5	0
76	C2	51	0	82	2	0
76	CA	51	0	82	5	0
76	QE	44	0	65	0	0
77	C1	120	0	108	21	0
78	C1	1	0	0	0	0
78	C2	2	0	0	0	0
79	C1	1	0	0	0	0
79	S1	1	0	0	0	0
80	QC	86	0	60	9	0
80	Qc	86	0	60	10	0
81	QD	43	0	30	0	0
81	Qd	43	0	32	3	0
82	QE	4	0	0	2	0
82	Qe	4	0	0	2	0
82	S1	4	0	0	1	0
82	V2	4	0	0	0	0
83	S1	16	0	0	3	0
83	S7	8	0	0	0	0
83	S8	16	0	0	2	0
83	V1	8	0	0	1	0
84	V1	31	0	19	2	0
All	All	117250	0	118812	1573	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1573 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:B6:88:LEU:HD22	29:B6:92:GLU:HG2	1.59	0.85
36:C2:196:CYS:HB3	36:C2:207:MET:SD	2.18	0.82
42:N2:88:LYS:HG3	42:N2:148:SER:HB3	1.61	0.82
36:C2:196:CYS:CB	36:C2:207:MET:SD	2.68	0.82
7:7A:77:PRO:HG3	9:7C:62:LYS:HG3	1.61	0.80

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	4L	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
2	5A	100/102 (98%)	100 (100%)	0	0	100	100
3	5B	93/95 (98%)	88 (95%)	5 (5%)	0	100	100
4	6A	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
5	6B	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
6	6C	68/70 (97%)	65 (96%)	3 (4%)	0	100	100
7	7A	55/57 (96%)	54 (98%)	1 (2%)	0	100	100
8	7B	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
9	7C	45/47 (96%)	43 (96%)	2 (4%)	0	100	100
10	8B	41/43 (95%)	41 (100%)	0	0	100	100
11	A1	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
12	A2	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
13	A3	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
14	A5	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
15	A6	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
16	A7	93/112 (83%)	92 (99%)	1 (1%)	0	100	100
17	A8	169/171 (99%)	166 (98%)	3 (2%)	0	100	100
18	A9	333/341 (98%)	324 (97%)	9 (3%)	0	100	100
19	AB	75/156 (48%)	69 (92%)	6 (8%)	0	100	100
19	AC	85/156 (54%)	85 (100%)	0	0	100	100
20	AK	318/320 (99%)	306 (96%)	12 (4%)	0	100	100
21	AL	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
22	AM	142/144 (99%)	141 (99%)	1 (1%)	0	100	100
23	AN	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
24	B1	54/56 (96%)	52 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	B2	65/67 (97%)	64 (98%)	1 (2%)	0	100	100
26	B3	78/80 (98%)	75 (96%)	3 (4%)	0	100	100
27	B4	126/128 (98%)	125 (99%)	1 (1%)	0	100	100
28	B5	136/138 (99%)	133 (98%)	3 (2%)	0	100	100
29	B6	98/126 (78%)	95 (97%)	3 (3%)	0	100	100
30	B7	123/125 (98%)	120 (98%)	3 (2%)	0	100	100
31	B8	154/156 (99%)	152 (99%)	2 (1%)	0	100	100
32	B9	176/178 (99%)	173 (98%)	3 (2%)	0	100	100
33	BK	172/176 (98%)	166 (96%)	6 (4%)	0	100	100
34	BL	97/154 (63%)	91 (94%)	6 (6%)	0	100	100
35	C1	512/514 (100%)	497 (97%)	15 (3%)	0	100	100
36	C2	226/228 (99%)	216 (96%)	10 (4%)	0	100	100
37	C3	258/260 (99%)	248 (96%)	10 (4%)	0	100	100
38	C4	136/138 (99%)	131 (96%)	5 (4%)	0	100	100
39	CA	47/49 (96%)	47 (100%)	0	0	100	100
40	CB	119/121 (98%)	118 (99%)	1 (1%)	0	100	100
41	N1	301/318 (95%)	287 (95%)	14 (5%)	0	100	100
42	N2	345/347 (99%)	336 (97%)	9 (3%)	0	100	100
43	N3	92/115 (80%)	89 (97%)	3 (3%)	0	100	100
44	N4	457/459 (100%)	452 (99%)	5 (1%)	0	100	100
45	N5	601/603 (100%)	567 (94%)	34 (6%)	0	100	100
46	N6	162/174 (93%)	148 (91%)	14 (9%)	0	100	100
47	QA	417/419 (100%)	405 (97%)	12 (3%)	0	100	100
47	Qa	417/419 (100%)	406 (97%)	11 (3%)	0	100	100
48	QB	444/446 (100%)	432 (97%)	12 (3%)	0	100	100
48	Qb	429/446 (96%)	423 (99%)	6 (1%)	0	100	100
49	QC	377/379 (100%)	372 (99%)	5 (1%)	0	100	100
49	Qc	377/379 (100%)	369 (98%)	8 (2%)	0	100	100
50	QD	239/326 (73%)	231 (97%)	8 (3%)	0	100	100
50	Qd	237/326 (73%)	232 (98%)	5 (2%)	0	100	100
51	QE	194/274 (71%)	189 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	QK	69/274 (25%)	69 (100%)	0	0	100	100
51	Qe	194/274 (71%)	187 (96%)	7 (4%)	0	100	100
52	QF	65/67 (97%)	65 (100%)	0	0	100	100
52	Qf	62/67 (92%)	60 (97%)	2 (3%)	0	100	100
53	QG	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
53	Qg	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
54	QH	76/81 (94%)	73 (96%)	3 (4%)	0	100	100
54	Qh	77/81 (95%)	77 (100%)	0	0	100	100
55	QI	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
55	Qi	58/62 (94%)	58 (100%)	0	0	100	100
56	QJ	47/52 (90%)	46 (98%)	1 (2%)	0	100	100
56	Qj	49/52 (94%)	47 (96%)	2 (4%)	0	100	100
57	S1	681/689 (99%)	650 (95%)	31 (5%)	0	100	100
58	S2	424/430 (99%)	399 (94%)	25 (6%)	0	100	100
59	S3	206/208 (99%)	198 (96%)	8 (4%)	0	100	100
60	S4	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
61	S5	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
62	S6	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
63	S7	154/156 (99%)	149 (97%)	5 (3%)	0	100	100
64	S8	174/176 (99%)	171 (98%)	3 (2%)	0	100	100
65	V1	429/431 (100%)	413 (96%)	16 (4%)	0	100	100
66	V2	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
67	V3	40/42 (95%)	39 (98%)	1 (2%)	0	100	100
All	All	13910/14938 (93%)	13480 (97%)	430 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	4L	85/85 (100%)	85 (100%)	0	100	100
2	5A	89/89 (100%)	88 (99%)	1 (1%)	70	86
3	5B	80/80 (100%)	79 (99%)	1 (1%)	65	84
4	6A	66/66 (100%)	66 (100%)	0	100	100
5	6B	73/73 (100%)	73 (100%)	0	100	100
6	6C	57/57 (100%)	57 (100%)	0	100	100
7	7A	48/48 (100%)	48 (100%)	0	100	100
8	7B	39/39 (100%)	39 (100%)	0	100	100
9	7C	40/40 (100%)	40 (100%)	0	100	100
10	8B	37/37 (100%)	37 (100%)	0	100	100
11	A1	58/58 (100%)	58 (100%)	0	100	100
12	A2	76/76 (100%)	76 (100%)	0	100	100
13	A3	69/69 (100%)	69 (100%)	0	100	100
14	A5	99/99 (100%)	99 (100%)	0	100	100
15	A6	107/107 (100%)	107 (100%)	0	100	100
16	A7	87/97 (90%)	87 (100%)	0	100	100
17	A8	153/153 (100%)	153 (100%)	0	100	100
18	A9	291/295 (99%)	289 (99%)	2 (1%)	81	91
19	AB	71/132 (54%)	70 (99%)	1 (1%)	62	83
19	AC	80/132 (61%)	79 (99%)	1 (1%)	65	84
20	AK	283/283 (100%)	278 (98%)	5 (2%)	54	79
21	AL	101/101 (100%)	99 (98%)	2 (2%)	50	76
22	AM	130/130 (100%)	130 (100%)	0	100	100
23	AN	123/123 (100%)	123 (100%)	0	100	100
24	B1	53/53 (100%)	53 (100%)	0	100	100
25	B2	62/62 (100%)	62 (100%)	0	100	100
26	B3	62/62 (100%)	62 (100%)	0	100	100
27	B4	113/113 (100%)	113 (100%)	0	100	100
28	B5	121/121 (100%)	121 (100%)	0	100	100
29	B6	97/119 (82%)	97 (100%)	0	100	100
30	B7	112/112 (100%)	112 (100%)	0	100	100
31	B8	141/141 (100%)	141 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	B9	159/159 (100%)	159 (100%)	0	100	100
33	BK	155/156 (99%)	155 (100%)	0	100	100
34	BL	91/129 (70%)	90 (99%)	1 (1%)	70	86
35	C1	425/425 (100%)	420 (99%)	5 (1%)	67	85
36	C2	212/212 (100%)	208 (98%)	4 (2%)	52	77
37	C3	224/224 (100%)	224 (100%)	0	100	100
38	C4	123/123 (100%)	123 (100%)	0	100	100
39	CA	45/45 (100%)	44 (98%)	1 (2%)	47	74
40	CB	108/108 (100%)	108 (100%)	0	100	100
41	N1	264/275 (96%)	260 (98%)	4 (2%)	60	82
42	N2	311/311 (100%)	311 (100%)	0	100	100
43	N3	84/100 (84%)	84 (100%)	0	100	100
44	N4	410/410 (100%)	410 (100%)	0	100	100
45	N5	537/537 (100%)	533 (99%)	4 (1%)	81	91
46	N6	132/140 (94%)	129 (98%)	3 (2%)	45	73
47	QA	330/330 (100%)	330 (100%)	0	100	100
47	Qa	330/330 (100%)	323 (98%)	7 (2%)	48	75
48	QB	372/372 (100%)	370 (100%)	2 (0%)	86	94
48	Qb	362/372 (97%)	361 (100%)	1 (0%)	91	96
49	QC	332/332 (100%)	327 (98%)	5 (2%)	60	82
49	Qc	332/332 (100%)	329 (99%)	3 (1%)	75	88
50	QD	206/259 (80%)	206 (100%)	0	100	100
50	Qd	204/259 (79%)	204 (100%)	0	100	100
51	QE	166/225 (74%)	164 (99%)	2 (1%)	67	85
51	QK	55/225 (24%)	55 (100%)	0	100	100
51	Qe	166/225 (74%)	166 (100%)	0	100	100
52	QF	64/64 (100%)	64 (100%)	0	100	100
52	Qf	61/64 (95%)	61 (100%)	0	100	100
53	QG	93/93 (100%)	90 (97%)	3 (3%)	34	65
53	Qg	93/93 (100%)	91 (98%)	2 (2%)	47	74
54	QH	70/72 (97%)	69 (99%)	1 (1%)	62	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	Qh	70/72 (97%)	70 (100%)	0	100	100
55	QI	50/50 (100%)	50 (100%)	0	100	100
55	Qi	49/50 (98%)	49 (100%)	0	100	100
56	QJ	40/42 (95%)	40 (100%)	0	100	100
56	Qj	41/42 (98%)	40 (98%)	1 (2%)	44	72
57	S1	576/579 (100%)	573 (100%)	3 (0%)	86	94
58	S2	369/370 (100%)	364 (99%)	5 (1%)	62	83
59	S3	190/190 (100%)	190 (100%)	0	100	100
60	S4	112/112 (100%)	111 (99%)	1 (1%)	75	88
61	S5	93/93 (100%)	93 (100%)	0	100	100
62	S6	79/79 (100%)	79 (100%)	0	100	100
63	S7	132/132 (100%)	128 (97%)	4 (3%)	36	67
64	S8	151/151 (100%)	151 (100%)	0	100	100
65	V1	344/344 (100%)	337 (98%)	7 (2%)	50	76
66	V2	183/183 (100%)	181 (99%)	2 (1%)	70	86
67	V3	41/41 (100%)	41 (100%)	0	100	100
All	All	12139/12783 (95%)	12055 (99%)	84 (1%)	80	91

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	Qc	82	LEU
63	S7	67	PHE
53	Qg	79	GLU
58	S2	82	LEU
65	V1	178	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 260 such sidechains are listed below:

Mol	Chain	Res	Type
58	S2	229	HIS
59	S3	196	HIS
41	N1	171	HIS
39	CA	62	HIS
62	S6	59	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	2MR	S2	124	58	10,12,13	2.39	3 (30%)	5,13,15	1.11	0

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
58	2MR	S2	124	58	-	3/10/13/15	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	S2	124	2MR	CZ-NE	5.05	1.45	1.34
58	S2	124	2MR	CZ-NH2	4.89	1.44	1.33
58	S2	124	2MR	CQ1-NH1	-2.09	1.42	1.46

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	S2	124	2MR	NE-CD-CG-CB
58	S2	124	2MR	CA-CB-CG-CD
58	S2	124	2MR	CG-CD-NE-CZ

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 105 ligands modelled in this entry, 7 are monoatomic - leaving 98 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	$\# Z > 2$
75	PLX	C2	301	-	42,42,51	1.16	2 (4%)	46,50,59	0.88	1 (2%)
76	3PE	C2	302	-	50,50,50	0.30	0	53,55,55	0.33	0
81	HEC	Qd	401	50	32,50,50	2.08	4 (12%)	24,82,82	2.25	12 (50%)
70	PC1	C1	609	-	53,53,53	0.29	0	59,61,61	0.29	0
71	PEE	QB	503	-	50,50,50	1.32	5 (10%)	53,55,55	1.19	4 (7%)
70	PC1	N1	402	-	53,53,53	0.29	0	59,61,61	0.29	0
73	ZMP	AB	201	19	29,35,36	0.68	1 (3%)	34,42,45	0.73	0
82	FES	QE	303	51	0,4,4	-	-	-	-	-
68	CDL	N5	702	-	81,81,99	0.32	0	87,93,111	0.36	0
70	PC1	6A	101	-	44,44,53	0.33	0	50,52,61	0.33	0
83	SF4	S7	301	63	0,12,12	-	-	-	-	-
68	CDL	QH	102	-	63,63,99	0.37	0	69,75,111	0.41	0
83	SF4	V1	501	65	0,12,12	-	-	-	-	-
70	PC1	Qc	406	-	53,53,53	0.29	0	59,61,61	0.28	0
68	CDL	N5	703	-	99,99,99	0.30	0	105,111,111	0.29	0
82	FES	Qe	301	51	0,4,4	-	-	-	-	-
75	PLX	AM	201	-	51,51,51	1.11	4 (7%)	55,59,59	0.84	1 (1%)
83	SF4	S1	802	57	0,12,12	-	-	-	-	-
76	3PE	B4	201	-	50,50,50	0.30	0	53,55,55	0.37	0
81	HEC	QD	401	50	32,50,50	2.08	4 (12%)	24,82,82	2.42	15 (62%)
70	PC1	N3	202	-	53,53,53	0.29	0	59,61,61	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
73	ZMP	AC	201	19	29,35,36	0.70	1 (3%)	34,42,45	0.68	0
70	PC1	B7	201	-	53,53,53	0.30	0	59,61,61	0.29	0
70	PC1	C1	606	-	53,53,53	0.30	0	59,61,61	0.28	0
68	CDL	AL	201	-	93,93,99	0.30	0	99,105,111	0.34	0
82	FES	V2	301	66	0,4,4	-	-	-		
68	CDL	QE	304	-	99,99,99	0.31	0	105,111,111	0.32	0
75	PLX	CB	201	-	51,51,51	1.11	4 (7%)	55,59,59	0.89	1 (1%)
75	PLX	N4	502	-	46,46,51	1.15	5 (10%)	50,54,59	0.89	1 (2%)
70	PC1	Qd	402	-	53,53,53	0.29	0	59,61,61	0.28	0
68	CDL	C1	610	-	76,76,99	0.34	0	82,88,111	0.35	0
75	PLX	N4	503	-	51,51,51	1.12	3 (5%)	55,59,59	0.89	1 (1%)
70	PC1	Qc	405	-	53,53,53	0.29	0	59,61,61	0.29	0
75	PLX	AM	202	-	51,51,51	1.11	3 (5%)	55,59,59	0.92	1 (1%)
68	CDL	QB	501	-	60,60,99	0.39	0	66,72,111	0.43	0
70	PC1	C3	302	-	48,48,53	0.30	0	54,56,61	0.36	0
71	PEE	Qd	403	-	23,23,50	1.41	3 (13%)	26,28,55	1.41	2 (7%)
68	CDL	B4	203	-	61,61,99	0.38	0	67,73,111	0.37	0
72	NDP	A9	401	-	45,52,52	0.56	0	53,80,80	0.52	1 (1%)
80	HEM	QC	402	49	41,50,50	1.26	4 (9%)	45,82,82	1.73	8 (17%)
70	PC1	N1	401	-	53,53,53	0.29	0	59,61,61	0.32	0
70	PC1	Qh	101	-	53,53,53	0.30	0	59,61,61	0.29	0
68	CDL	N2	402	-	99,99,99	0.30	0	105,111,111	0.32	0
70	PC1	C1	611	-	49,49,53	0.31	0	55,57,61	0.33	0
68	CDL	AL	202	-	89,89,99	0.32	0	95,101,111	0.43	0
71	PEE	N5	704	-	50,50,50	1.31	5 (10%)	53,55,55	1.22	4 (7%)
80	HEM	Qc	404	49	41,50,50	1.27	4 (9%)	45,82,82	1.73	8 (17%)
77	HEA	C1	602	35	57,67,67	2.01	15 (26%)	61,103,103	2.67	26 (42%)
70	PC1	7C	101	-	51,51,53	0.30	0	57,59,61	0.30	0
70	PC1	B5	203	-	53,53,53	0.29	0	59,61,61	0.28	0
71	PEE	Qc	402	-	41,41,50	1.28	4 (9%)	44,46,55	1.16	3 (6%)
80	HEM	Qc	403	49	41,50,50	1.24	4 (9%)	45,82,82	1.67	8 (17%)
71	PEE	B4	202	-	50,50,50	1.32	5 (10%)	53,55,55	1.17	3 (5%)
68	CDL	4L	201	-	91,91,99	0.32	0	97,103,111	0.31	0
76	3PE	B8	201	-	31,31,50	0.38	0	34,36,55	0.35	0
77	HEA	C1	603	35	57,67,67	2.00	15 (26%)	61,103,103	2.63	26 (42%)
71	PEE	C3	303	-	50,50,50	1.32	6 (12%)	53,55,55	1.21	3 (5%)
71	PEE	S2	501	-	47,47,50	1.33	5 (10%)	50,52,55	1.24	4 (8%)
68	CDL	A1	101	-	93,93,99	0.31	0	99,105,111	0.29	0
84	FMN	V1	502	-	33,33,33	0.32	0	48,50,50	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
71	PEE	6A	103	-	35,35,50	1.37	4 (11%)	38,40,55	1.24	3 (7%)
70	PC1	C1	608	-	45,45,53	0.31	0	51,53,61	0.36	0
68	CDL	Qb	501	-	63,63,99	0.38	0	69,75,111	0.51	0
68	CDL	A8	301	-	76,76,99	0.34	0	82,88,111	0.43	0
68	CDL	N2	401	-	67,67,99	0.35	0	73,79,111	0.37	0
76	3PE	C1	601	-	50,50,50	0.30	0	53,55,55	0.35	0
75	PLX	B5	201	-	51,51,51	1.11	4 (7%)	55,59,59	0.88	1 (1%)
82	FES	S1	803	57	0,4,4	-	-	-	-	-
70	PC1	N5	705	-	30,30,53	0.37	0	36,38,61	0.44	0
71	PEE	QB	502	-	33,33,50	1.40	4 (12%)	36,38,55	1.14	3 (8%)
71	PEE	AL	203	-	39,39,50	1.48	5 (12%)	41,44,55	1.17	3 (7%)
70	PC1	C3	301	-	43,43,53	0.31	0	49,51,61	0.32	0
71	PEE	QE	301	-	46,46,50	1.35	5 (10%)	49,51,55	1.30	5 (10%)
71	PEE	A3	201	-	50,50,50	1.30	5 (10%)	53,55,55	1.18	4 (7%)
76	3PE	CA	101	-	50,50,50	0.31	0	53,55,55	0.32	0
83	SF4	S8	301	64	0,12,12	-	-	-	-	-
80	HEM	QC	401	49	41,50,50	1.25	4 (9%)	45,82,82	1.71	9 (20%)
71	PEE	QC	403	-	39,39,50	1.30	4 (10%)	42,44,55	1.20	3 (7%)
70	PC1	QJ	101	-	53,53,53	0.30	0	59,61,61	0.36	0
71	PEE	6A	102	-	50,50,50	1.31	5 (10%)	53,55,55	1.20	5 (9%)
71	PEE	Qc	401	-	50,50,50	1.32	5 (10%)	53,55,55	1.09	3 (5%)
71	PEE	S8	303	-	50,50,50	1.30	5 (10%)	53,55,55	1.20	3 (5%)
75	PLX	N3	201	-	51,51,51	1.11	5 (9%)	55,59,59	0.89	2 (3%)
71	PEE	N5	701	-	45,45,50	1.37	5 (11%)	48,50,55	1.20	4 (8%)
83	SF4	S1	801	57	0,12,12	-	-	-	-	-
71	PEE	8B	201	-	41,41,50	1.29	4 (9%)	44,46,55	1.13	2 (4%)
68	CDL	QH	101	-	60,60,99	0.38	0	66,72,111	0.40	0
75	PLX	QB	504	-	45,45,51	1.17	3 (6%)	49,53,59	0.92	2 (4%)
68	CDL	B5	202	-	97,97,99	0.30	0	103,109,111	0.29	0
68	CDL	QC	404	-	54,54,99	0.40	0	60,66,111	0.42	0
74	ADP	AK	401	-	24,29,29	0.92	1 (4%)	29,45,45	1.40	4 (13%)
75	PLX	QI	301	-	51,51,51	1.12	3 (5%)	55,59,59	0.89	1 (1%)
71	PEE	N4	501	-	48,48,50	1.34	5 (10%)	51,53,55	1.18	4 (7%)
70	PC1	C1	607	-	32,32,53	0.36	0	38,40,61	0.33	0
70	PC1	Qb	502	-	53,53,53	0.30	0	59,61,61	0.39	0
68	CDL	QD	402	-	63,63,99	0.38	0	69,75,111	0.63	2 (2%)
76	3PE	QE	302	-	43,43,50	0.32	0	46,48,55	0.31	0
83	SF4	S8	302	64	0,12,12	-	-	-	-	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
75	PLX	C2	301	-	-	17/46/46/55	-
76	3PE	C2	302	-	-	19/54/54/54	-
81	HEC	Qd	401	50	-	2/10/54/54	-
70	PC1	C1	609	-	-	15/57/57/57	-
71	PEE	QB	503	-	-	27/54/54/54	-
70	PC1	N1	402	-	-	15/57/57/57	-
73	ZMP	AB	201	19	-	19/40/42/43	-
82	FES	QE	303	51	-	-	0/1/1/1
68	CDL	N5	702	-	-	30/92/92/110	-
70	PC1	6A	101	-	-	13/48/48/57	-
83	SF4	S7	301	63	-	-	0/6/5/5
68	CDL	QH	102	-	-	22/74/74/110	-
83	SF4	V1	501	65	-	-	0/6/5/5
70	PC1	Qc	406	-	-	16/57/57/57	-
68	CDL	N5	703	-	-	25/110/110/110	-
82	FES	Qe	301	51	-	-	0/1/1/1
75	PLX	AM	201	-	-	24/55/55/55	-
83	SF4	S1	802	57	-	-	0/6/5/5
76	3PE	B4	201	-	-	11/54/54/54	-
81	HEC	QD	401	50	-	2/10/54/54	-
70	PC1	N3	202	-	-	12/57/57/57	-
73	ZMP	AC	201	19	-	14/40/42/43	-
70	PC1	B7	201	-	-	8/57/57/57	-
70	PC1	C1	606	-	-	14/57/57/57	-
68	CDL	AL	201	-	-	21/104/104/110	-
82	FES	V2	301	66	-	-	0/1/1/1
68	CDL	QE	304	-	-	30/110/110/110	-
75	PLX	CB	201	-	-	23/55/55/55	-
75	PLX	N4	502	-	-	33/50/50/55	-
70	PC1	Qd	402	-	-	10/57/57/57	-
68	CDL	C1	610	-	-	23/87/87/110	-
75	PLX	N4	503	-	-	22/55/55/55	-
70	PC1	Qc	405	-	-	10/57/57/57	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
75	PLX	AM	202	-	-	19/55/55/55	-
68	CDL	QB	501	-	-	17/71/71/110	-
70	PC1	C3	302	-	-	10/52/52/57	-
71	PEE	Qd	403	-	-	8/27/27/54	-
68	CDL	B4	203	-	-	12/72/72/110	-
72	NDP	A9	401	-	-	10/30/77/77	0/5/5/5
80	HEM	QC	402	49	-	4/12/54/54	-
70	PC1	N1	401	-	-	19/57/57/57	-
70	PC1	Qh	101	-	-	20/57/57/57	-
68	CDL	N2	402	-	-	22/110/110/110	-
70	PC1	C1	611	-	-	8/53/53/57	-
68	CDL	AL	202	-	-	17/100/100/110	-
71	PEE	N5	704	-	-	27/54/54/54	-
80	HEM	Qc	404	49	-	9/12/54/54	-
77	HEA	C1	602	35	-	11/32/76/76	-
70	PC1	7C	101	-	-	10/55/55/57	-
70	PC1	B5	203	-	-	18/57/57/57	-
71	PEE	Qc	402	-	-	19/45/45/54	-
80	HEM	Qc	403	49	-	7/12/54/54	-
71	PEE	B4	202	-	-	28/54/54/54	-
68	CDL	4L	201	-	-	25/102/102/110	-
76	3PE	B8	201	-	-	6/35/35/54	-
77	HEA	C1	603	35	-	12/32/76/76	-
71	PEE	C3	303	-	-	27/54/54/54	-
71	PEE	S2	501	-	-	17/51/51/54	-
68	CDL	A1	101	-	-	30/104/104/110	-
84	FMN	V1	502	-	-	5/18/18/18	0/3/3/3
71	PEE	6A	103	-	-	17/39/39/54	-
70	PC1	C1	608	-	-	9/49/49/57	-
68	CDL	Qb	501	-	-	14/74/74/110	-
68	CDL	A8	301	-	-	29/87/87/110	-
68	CDL	N2	401	-	-	25/78/78/110	-
76	3PE	C1	601	-	-	8/54/54/54	-
75	PLX	B5	201	-	-	22/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	FES	S1	803	57	-	-	0/1/1/1
70	PC1	N5	705	-	-	8/34/34/57	-
71	PEE	QB	502	-	-	22/37/37/54	-
71	PEE	AL	203	-	-	26/43/43/54	-
70	PC1	C3	301	-	-	13/47/47/57	-
71	PEE	QE	301	-	-	21/50/50/54	-
71	PEE	A3	201	-	-	27/54/54/54	-
76	3PE	CA	101	-	-	18/54/54/54	-
83	SF4	S8	301	64	-	-	0/6/5/5
80	HEM	QC	401	49	-	7/12/54/54	-
71	PEE	QC	403	-	-	23/43/43/54	-
70	PC1	QJ	101	-	-	22/57/57/57	-
71	PEE	6A	102	-	-	27/54/54/54	-
71	PEE	Qc	401	-	-	39/54/54/54	-
71	PEE	S8	303	-	-	25/54/54/54	-
75	PLX	N3	201	-	-	17/55/55/55	-
71	PEE	N5	701	-	-	23/49/49/54	-
83	SF4	S1	801	57	-	-	0/6/5/5
71	PEE	8B	201	-	-	27/45/45/54	-
68	CDL	QH	101	-	-	22/71/71/110	-
75	PLX	QB	504	-	-	17/49/49/55	-
68	CDL	B5	202	-	-	27/108/108/110	-
68	CDL	QC	404	-	-	12/65/65/110	-
74	ADP	AK	401	-	-	2/12/32/32	0/3/3/3
75	PLX	QI	301	-	-	24/55/55/55	-
71	PEE	N4	501	-	-	27/52/52/54	-
70	PC1	C1	607	-	-	16/36/36/57	-
70	PC1	Qb	502	-	-	11/57/57/57	-
68	CDL	QD	402	-	-	21/74/74/110	-
76	3PE	QE	302	-	-	9/47/47/54	-
83	SF4	S8	302	64	-	-	0/6/5/5

The worst 5 of 182 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	Qd	401	HEC	C3C-C2C	-6.88	1.33	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	QD	401	HEC	C3C-C2C	-6.78	1.33	1.40
81	QD	401	HEC	C2B-C3B	-6.49	1.34	1.40
81	Qd	401	HEC	C2B-C3B	-6.47	1.34	1.40
77	C1	602	HEA	C3B-C2B	5.19	1.46	1.34

The worst 5 of 196 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	C1	603	HEA	CAD-CBD-CGD	-7.97	96.44	113.60
77	C1	602	HEA	CAD-CBD-CGD	-7.50	97.46	113.60
77	C1	603	HEA	C3D-C4D-ND	5.82	115.99	110.36
77	C1	602	HEA	C3D-C4D-ND	5.73	115.91	110.36
77	C1	602	HEA	C13-C12-C11	-5.43	106.20	114.35

There are no chirality outliers.

5 of 1551 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
68	4L	201	CDL	CA2-OA2-PA1-OA3
68	4L	201	CDL	CB2-OB2-PB2-OB3
68	4L	201	CDL	CB3-OB5-PB2-OB2
68	4L	201	CDL	CB3-OB5-PB2-OB3
68	4L	201	CDL	CB3-OB5-PB2-OB4

There are no ring outliers.

91 monomers are involved in 306 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
75	C2	301	PLX	2	0
76	C2	302	3PE	2	0
81	Qd	401	HEC	3	0
70	C1	609	PC1	4	0
71	QB	503	PEE	1	0
70	N1	402	PC1	2	0
73	AB	201	ZMP	1	0
82	QE	303	FES	2	0
68	N5	702	CDL	7	0
70	6A	101	PC1	10	0
68	QH	102	CDL	3	0
83	V1	501	SF4	1	0
70	Qc	406	PC1	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
68	N5	703	CDL	5	0
82	Qe	301	FES	2	0
75	AM	201	PLX	1	0
83	S1	802	SF4	1	0
76	B4	201	3PE	8	0
70	N3	202	PC1	3	0
73	AC	201	ZMP	4	0
70	B7	201	PC1	1	0
70	C1	606	PC1	4	0
68	AL	201	CDL	7	0
68	QE	304	CDL	2	0
75	CB	201	PLX	3	0
75	N4	502	PLX	9	0
70	Qd	402	PC1	2	0
68	C1	610	CDL	7	0
75	N4	503	PLX	7	0
70	Qc	405	PC1	1	0
75	AM	202	PLX	3	0
68	QB	501	CDL	1	0
70	C3	302	PC1	8	0
71	Qd	403	PEE	1	0
68	B4	203	CDL	3	0
72	A9	401	NDP	1	0
80	QC	402	HEM	8	0
70	N1	401	PC1	9	0
70	Qh	101	PC1	1	0
68	N2	402	CDL	12	0
70	C1	611	PC1	10	0
68	AL	202	CDL	3	0
71	N5	704	PEE	1	0
80	Qc	404	HEM	8	0
77	C1	602	HEA	11	0
70	7C	101	PC1	4	0
70	B5	203	PC1	2	0
71	Qc	402	PEE	4	0
80	Qc	403	HEM	2	0
71	B4	202	PEE	4	0
68	4L	201	CDL	3	0
76	B8	201	3PE	1	0
77	C1	603	HEA	10	0
71	C3	303	PEE	4	0
71	S2	501	PEE	1	0

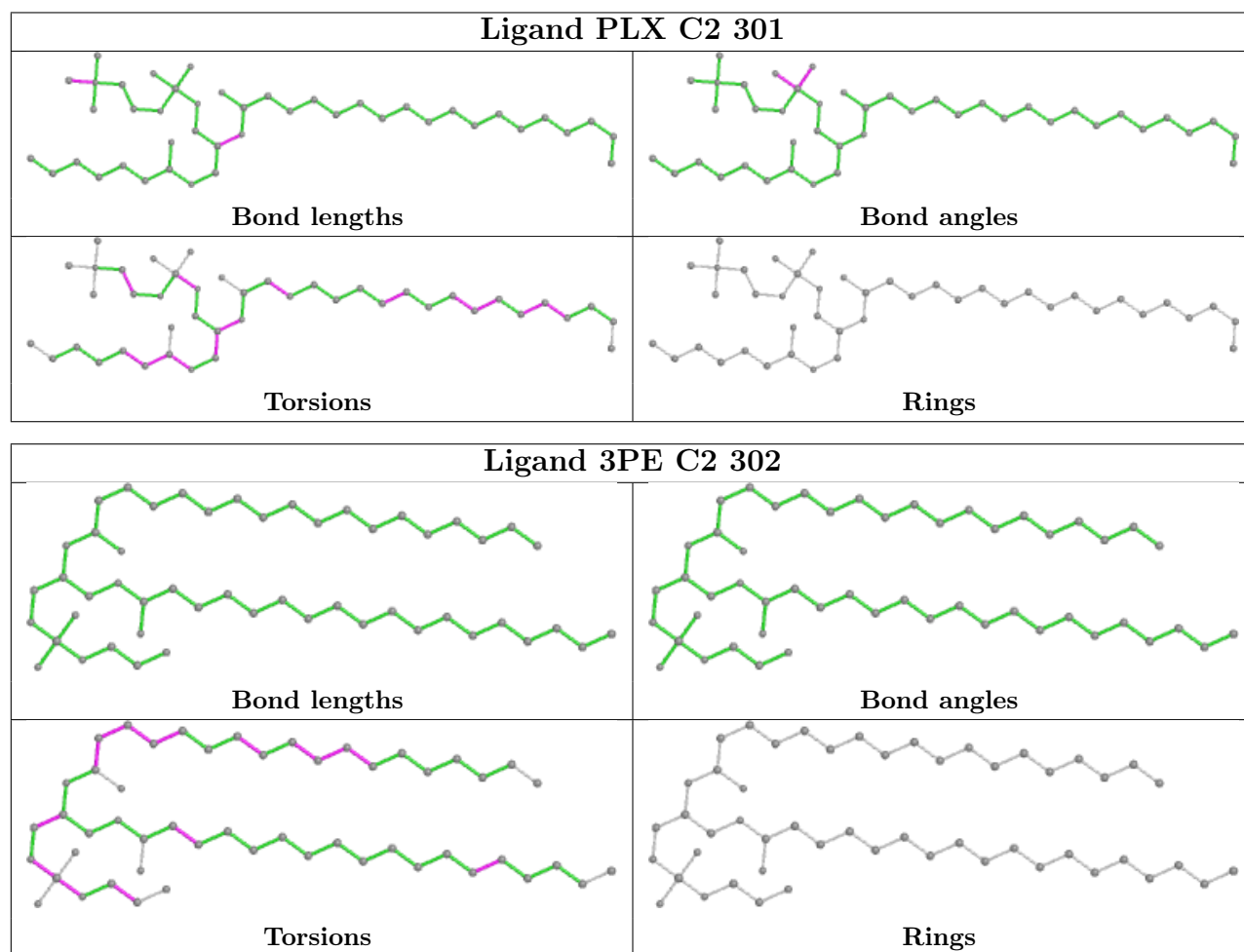
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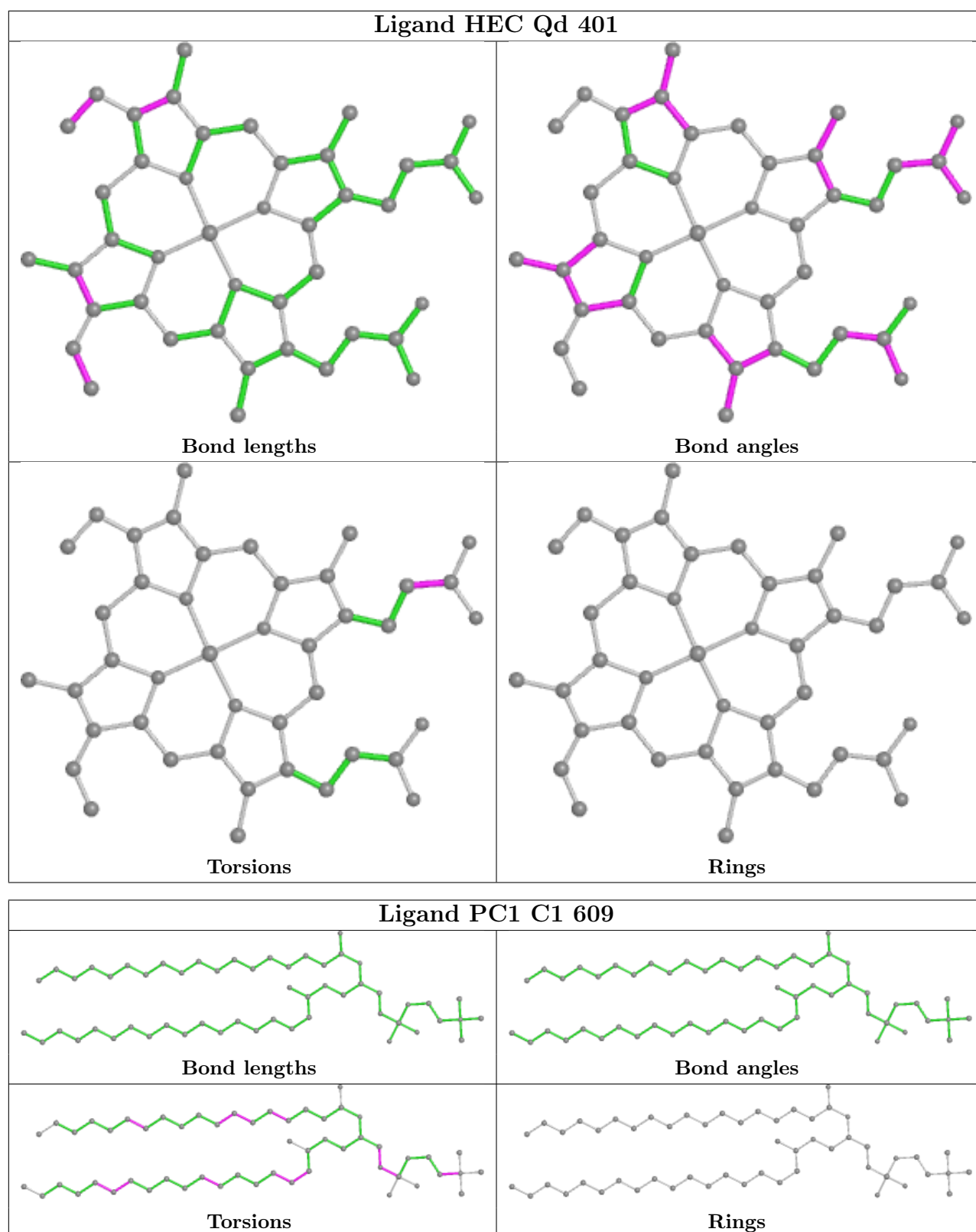
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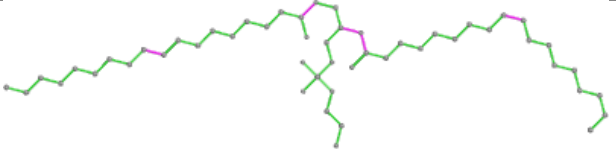
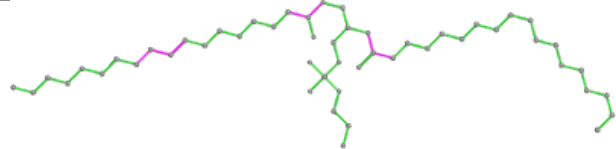
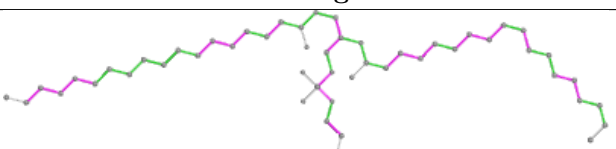
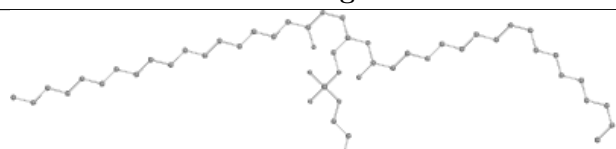
Mol	Chain	Res	Type	Clashes	Symm-Clashes
68	A1	101	CDL	5	0
84	V1	502	FMN	2	0
71	6A	103	PEE	1	0
70	C1	608	PC1	1	0
68	Qb	501	CDL	6	0
68	A8	301	CDL	10	0
68	N2	401	CDL	1	0
76	C1	601	3PE	5	0
82	S1	803	FES	1	0
70	N5	705	PC1	2	0
71	QB	502	PEE	2	0
71	AL	203	PEE	4	0
70	C3	301	PC1	1	0
71	QE	301	PEE	1	0
71	A3	201	PEE	3	0
76	CA	101	3PE	5	0
83	S8	301	SF4	1	0
80	QC	401	HEM	1	0
70	QJ	101	PC1	3	0
71	6A	102	PEE	4	0
71	Qc	401	PEE	2	0
75	N3	201	PLX	1	0
71	N5	701	PEE	6	0
83	S1	801	SF4	2	0
71	8B	201	PEE	2	0
68	QH	101	CDL	2	0
75	QB	504	PLX	4	0
68	B5	202	CDL	3	0
68	QC	404	CDL	4	0
74	AK	401	ADP	4	0
75	QI	301	PLX	5	0
71	N4	501	PEE	3	0
70	C1	607	PC1	3	0
70	Qb	502	PC1	5	0
68	QD	402	CDL	1	0
83	S8	302	SF4	1	0

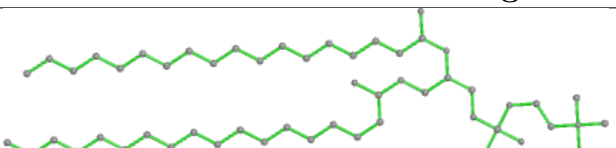
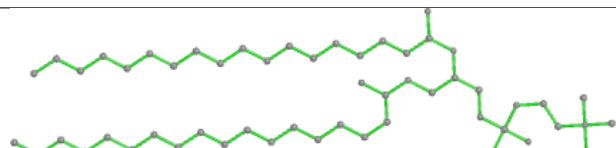
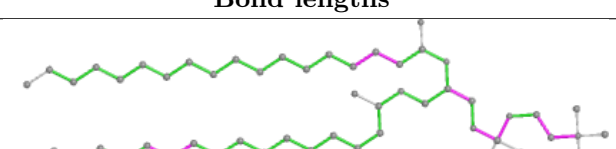
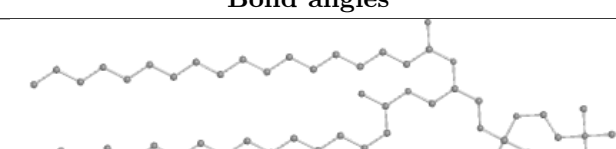
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

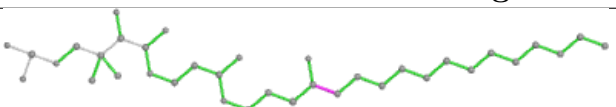

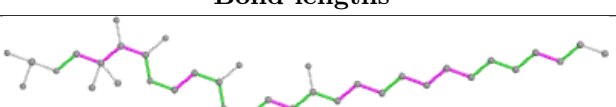
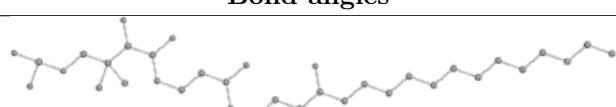
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified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

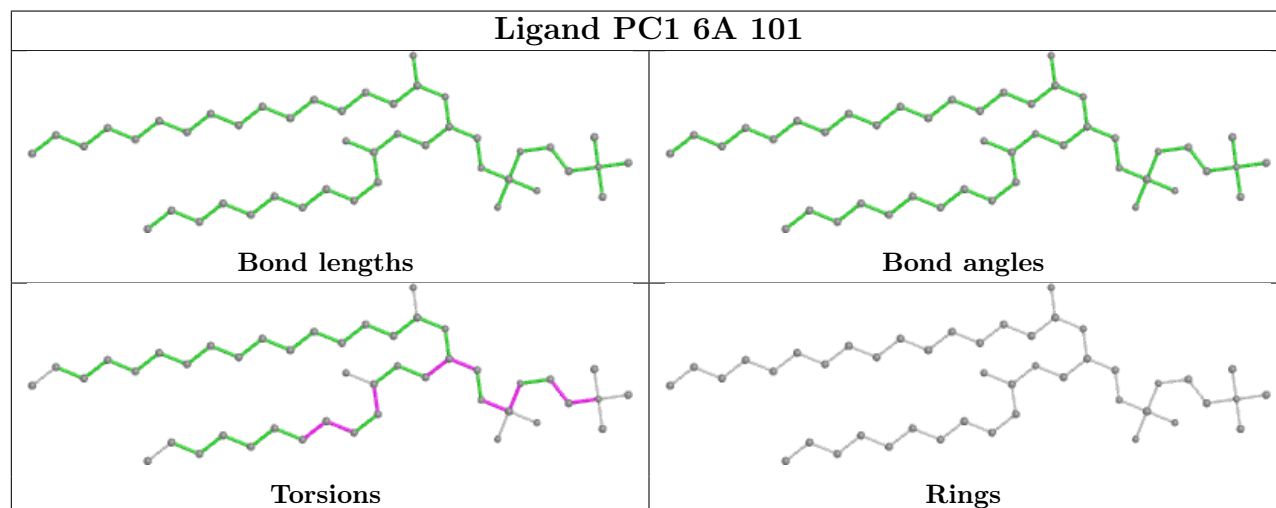
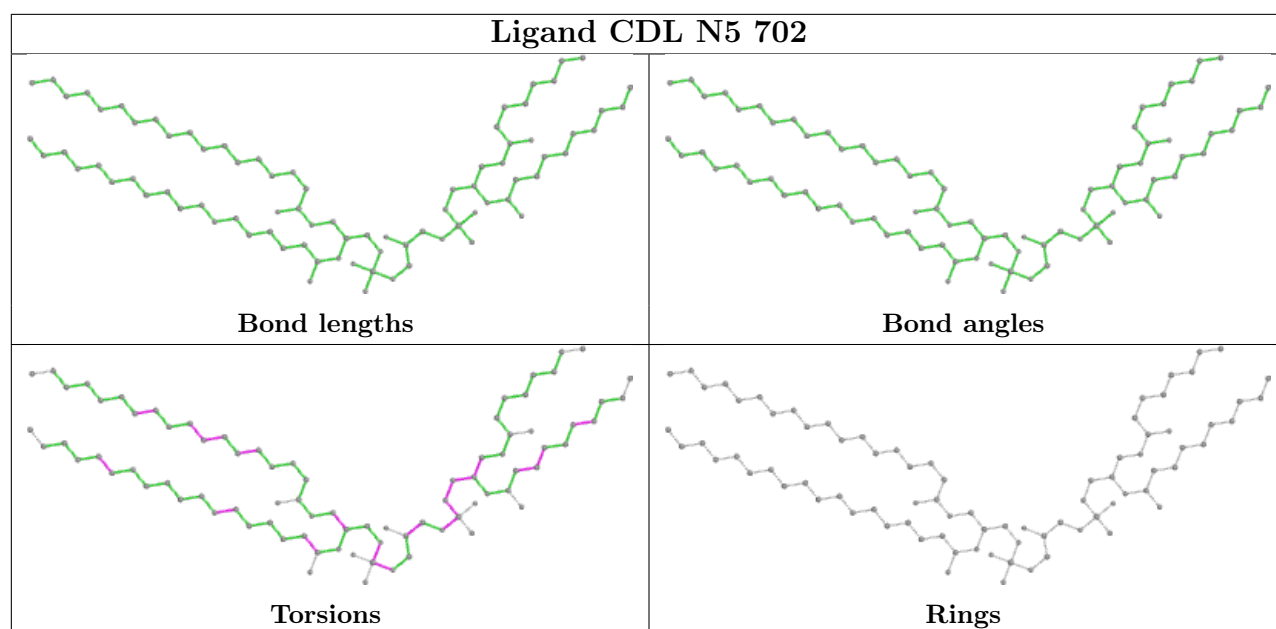


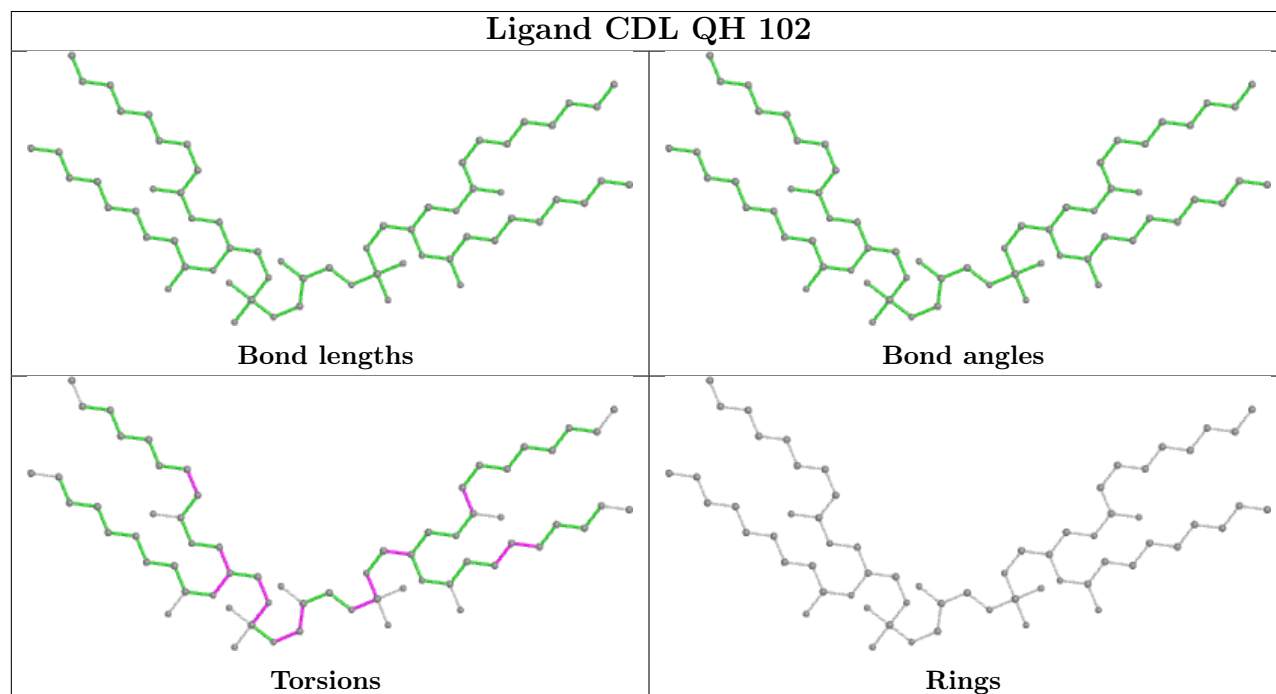
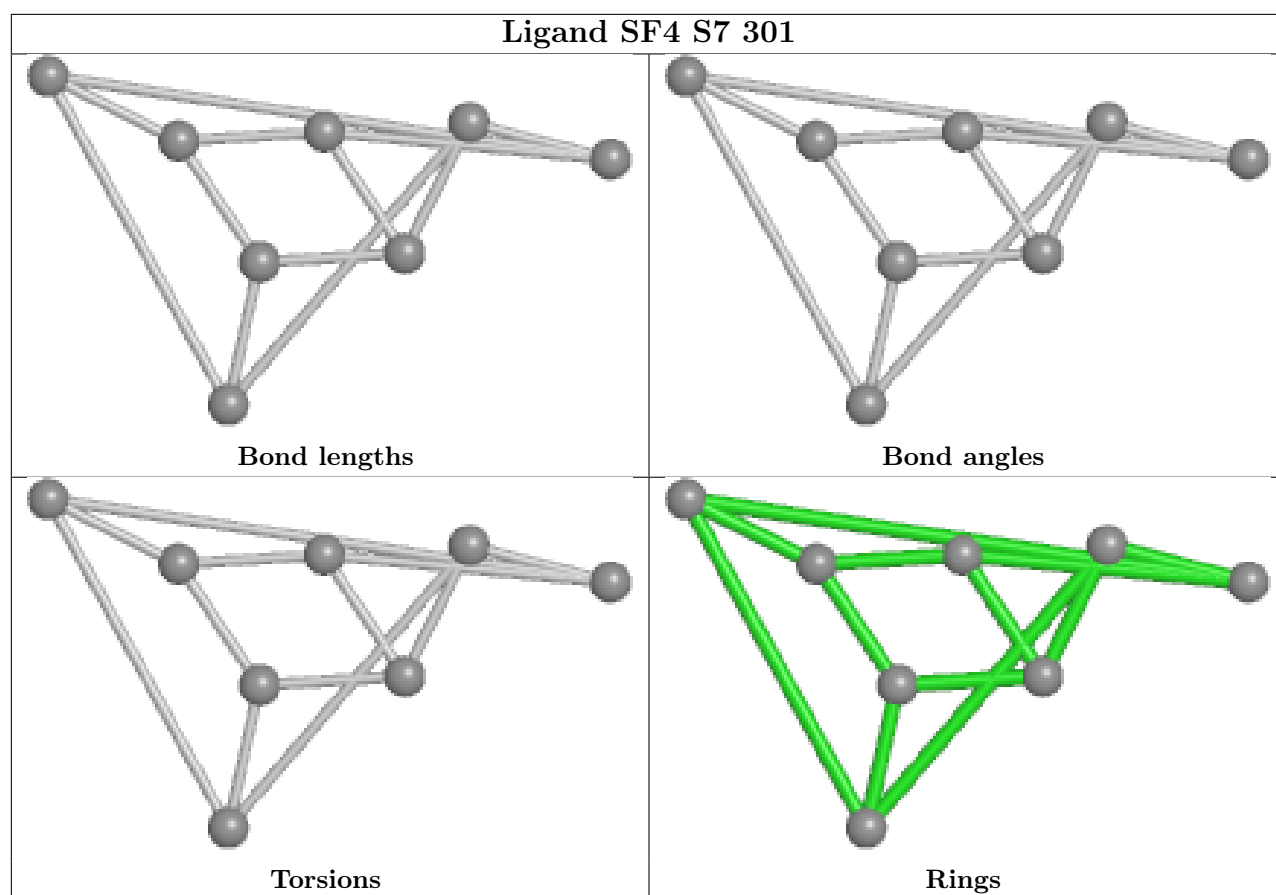


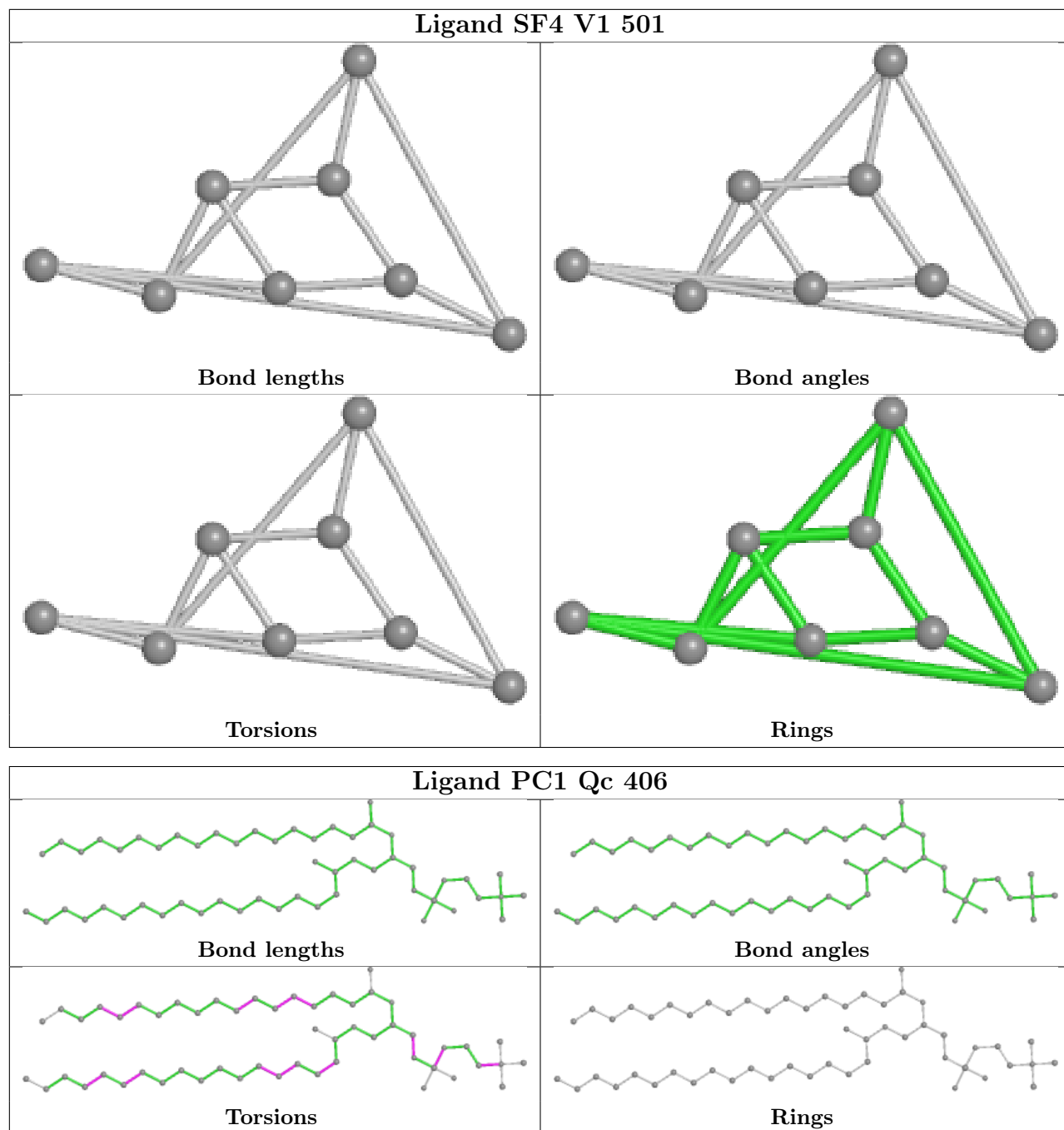
Ligand PEE QB 503	
	
Bond lengths	Bond angles
	
Torsions	Rings

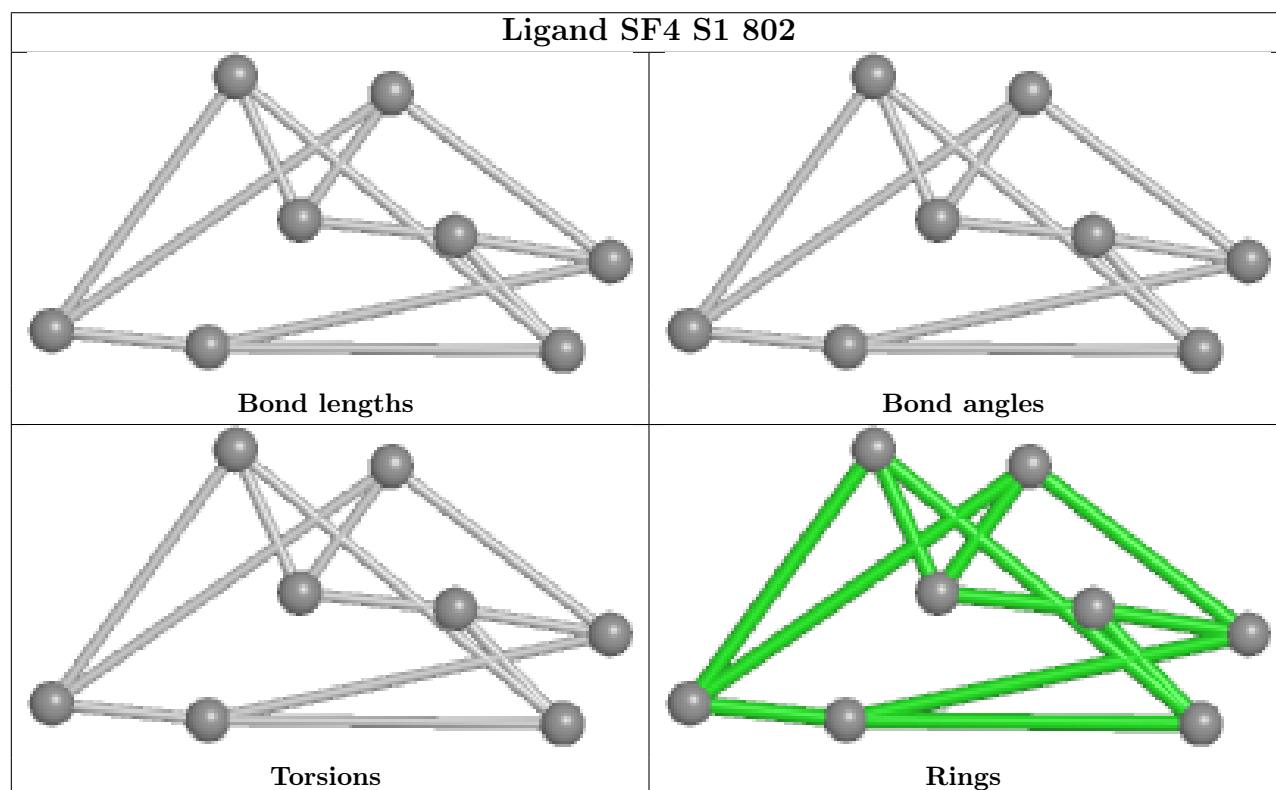
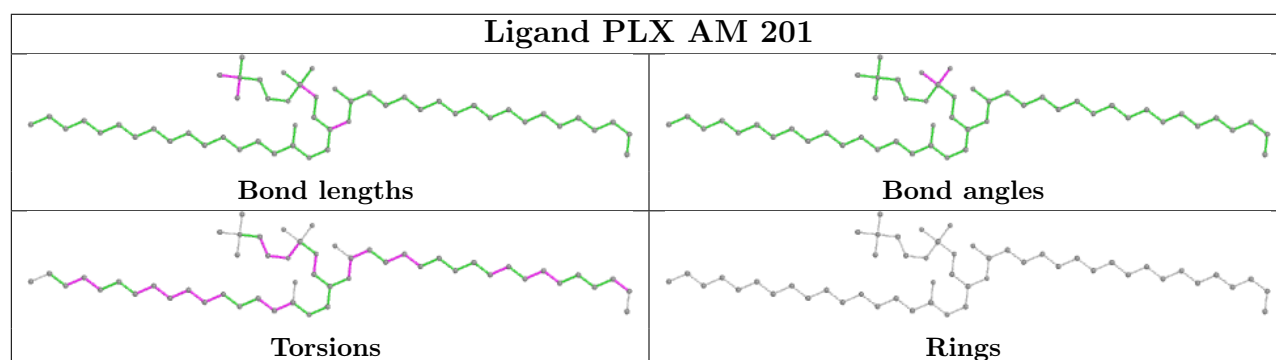
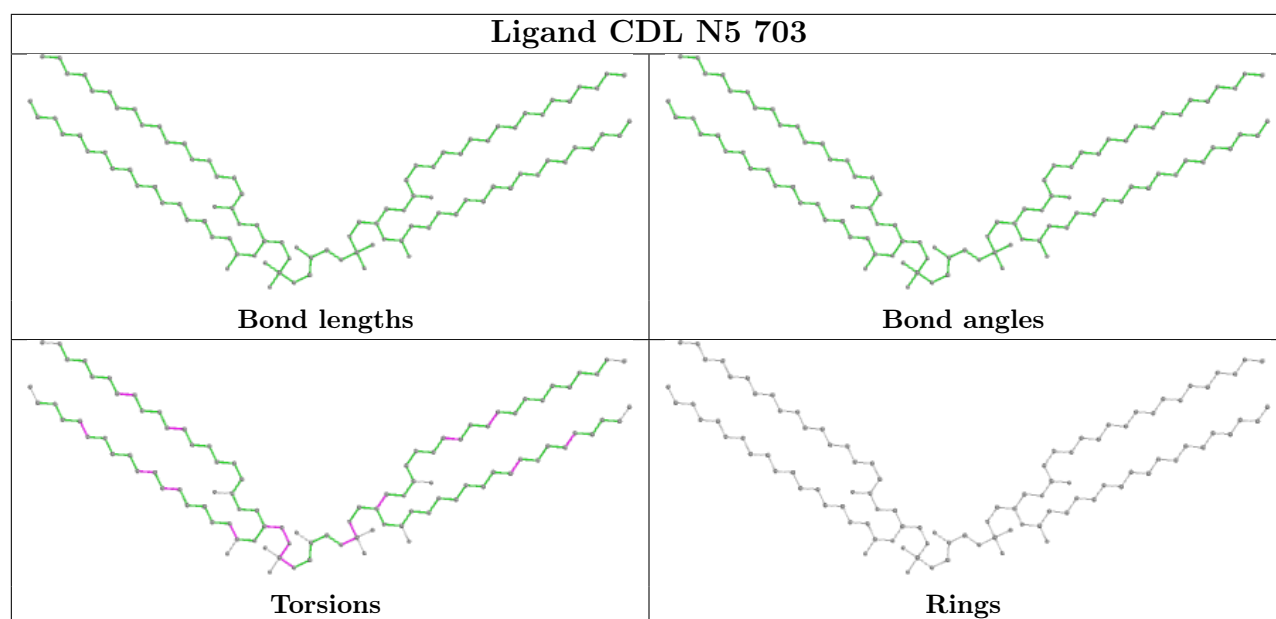
Ligand PC1 N1 402	
	
Bond lengths	Bond angles
	
Torsions	Rings

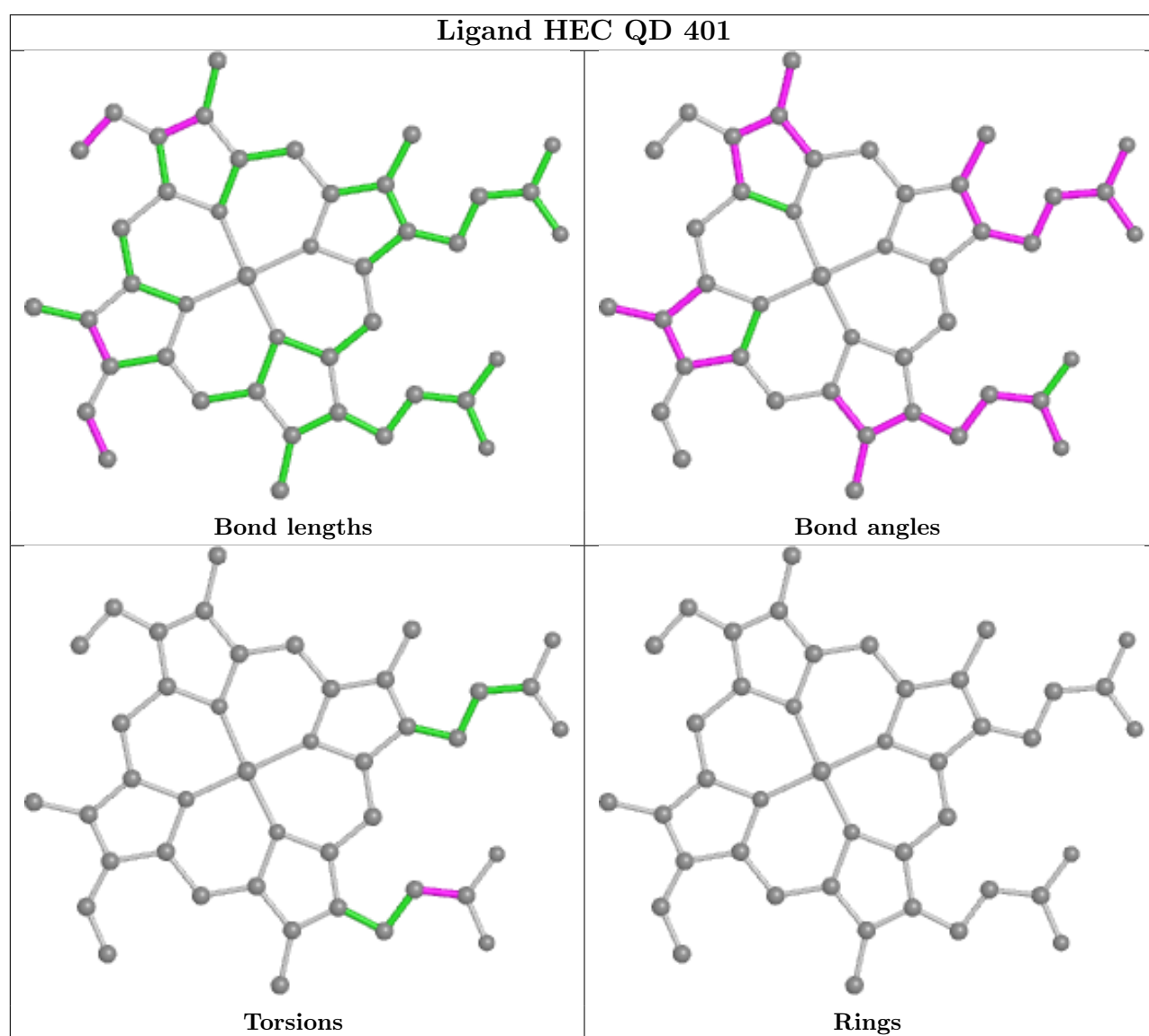
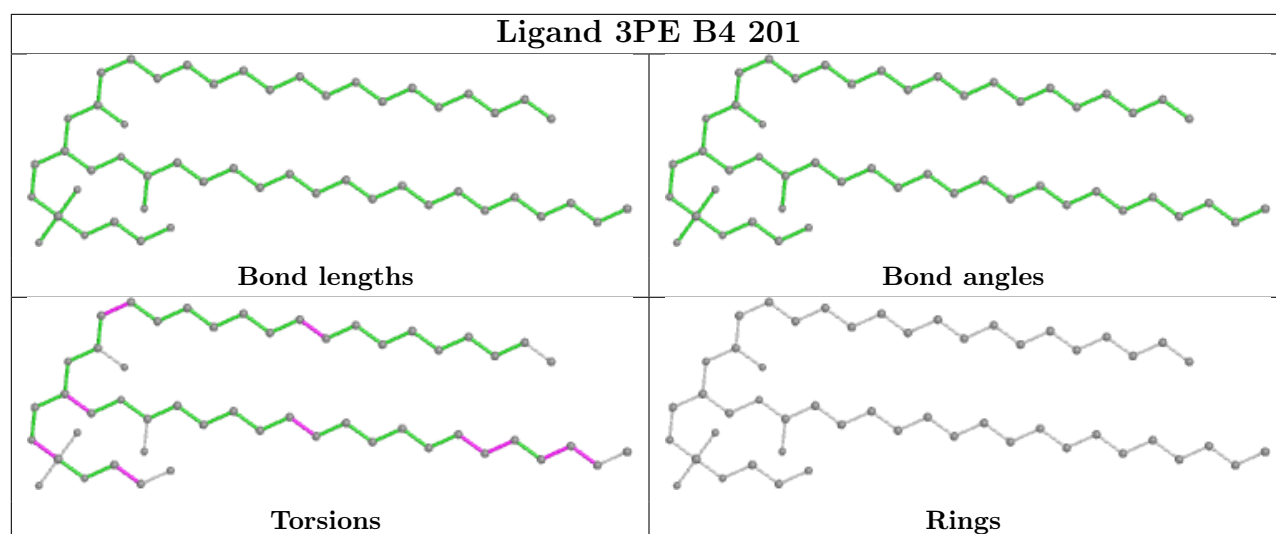
Ligand ZMP AB 201	
	
Bond lengths	Bond angles
	
Torsions	Rings

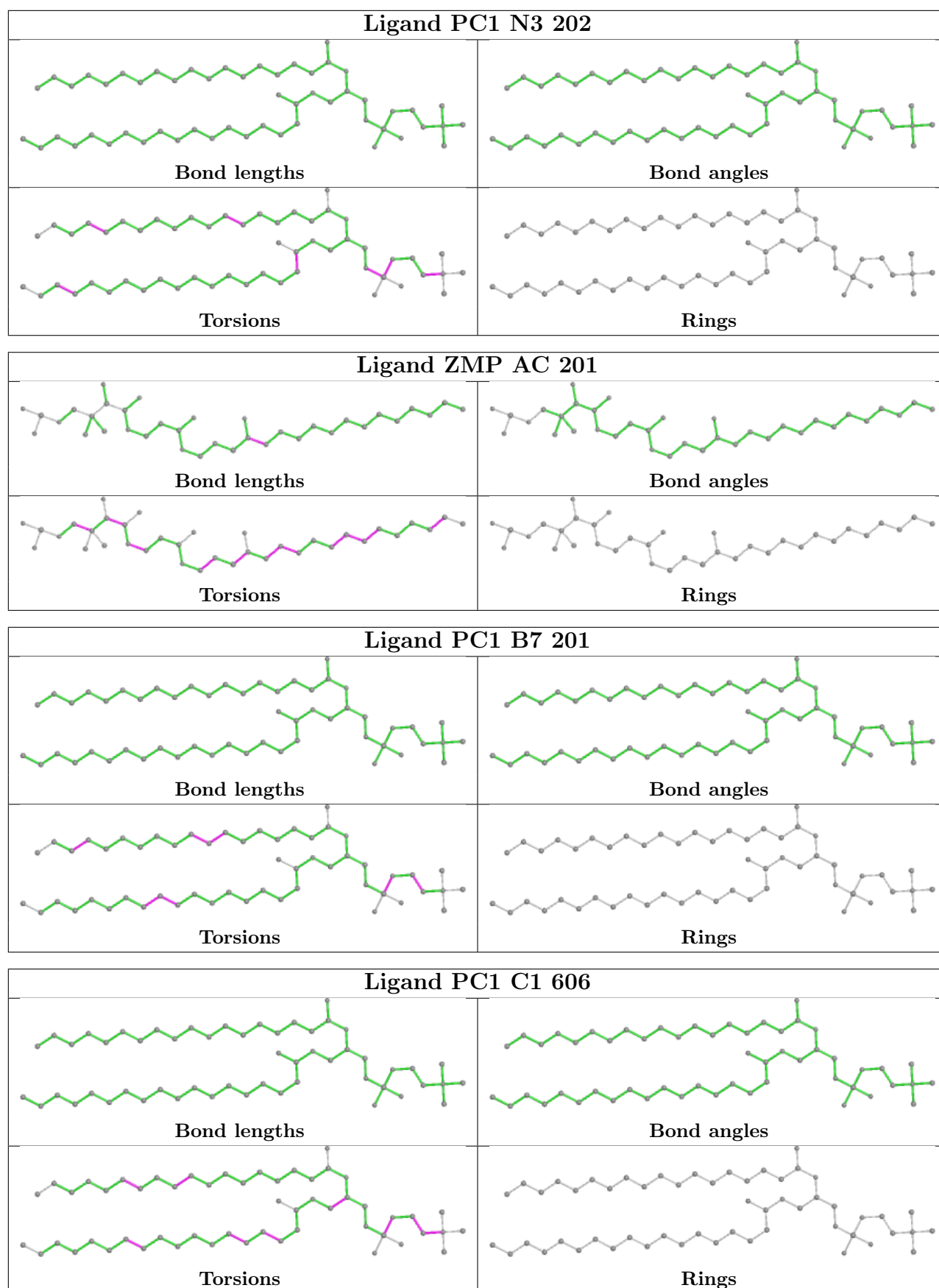


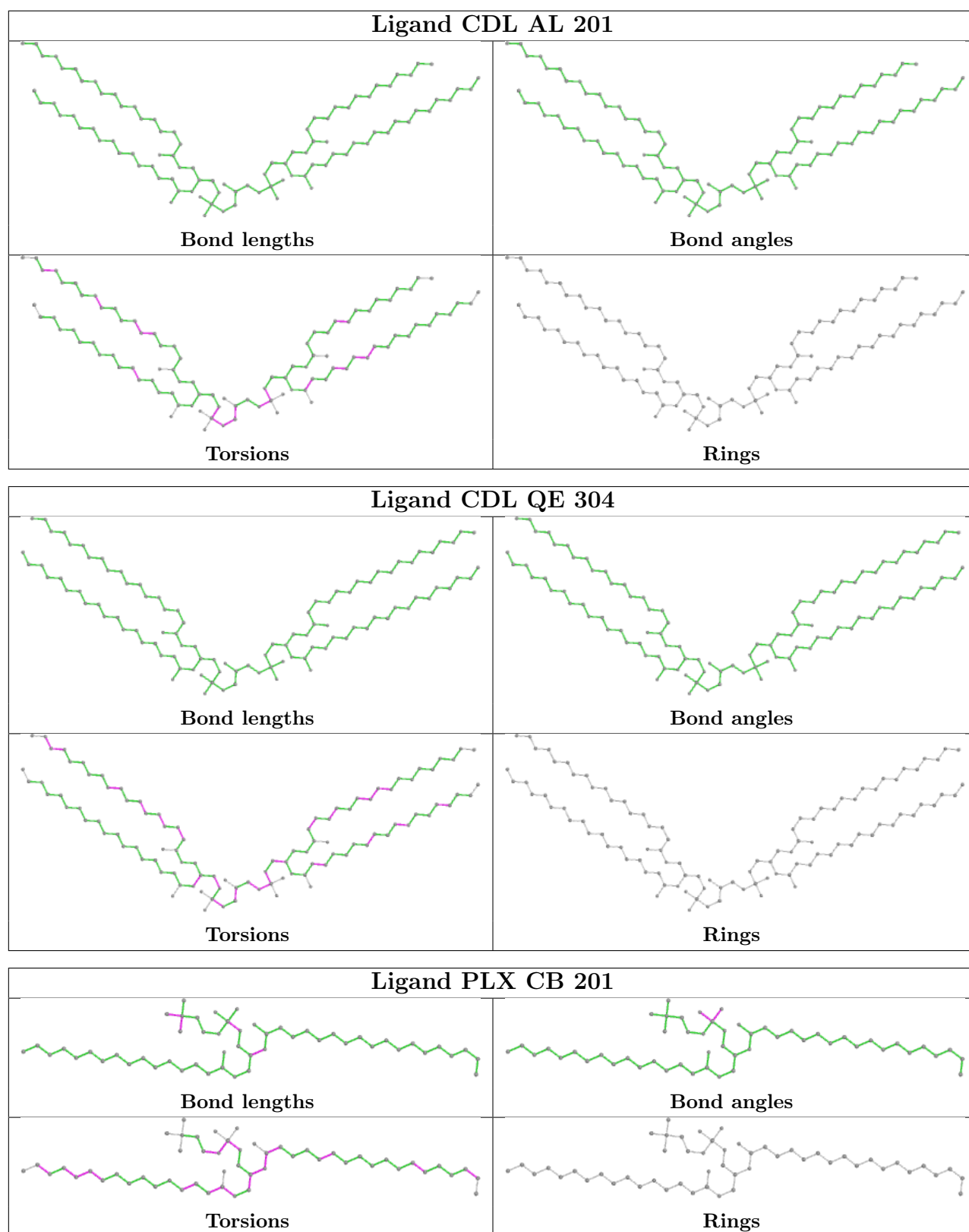


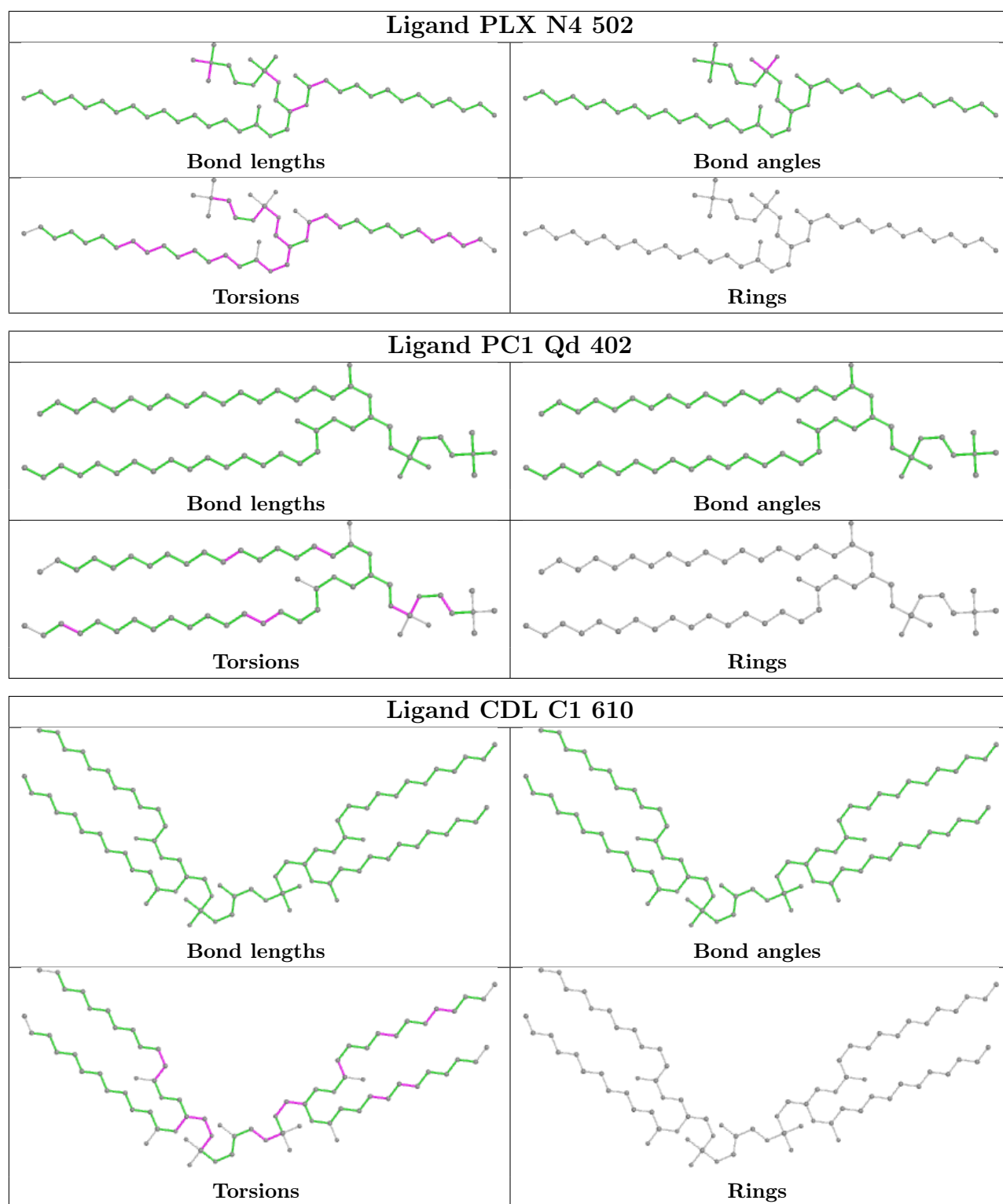


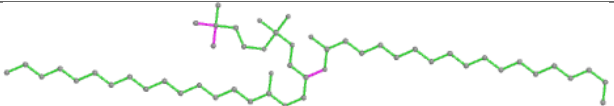
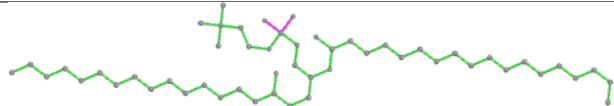
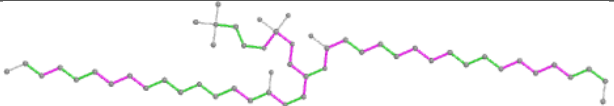
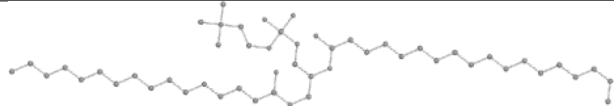


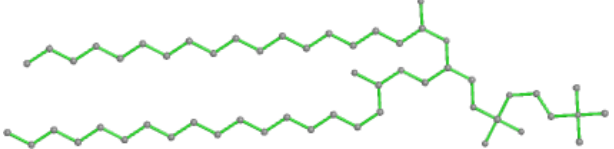
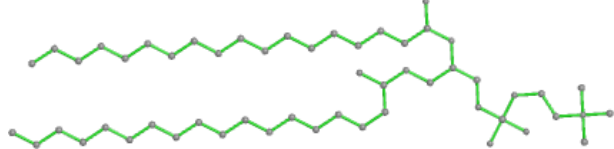
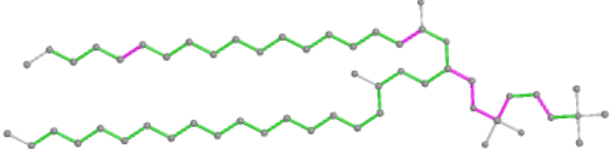
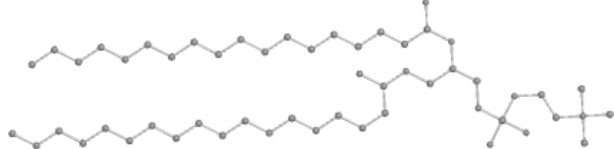


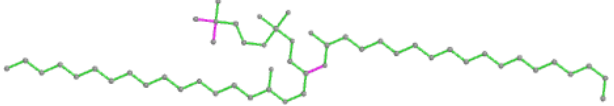
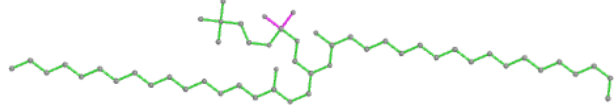
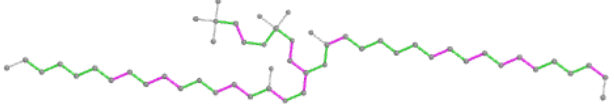
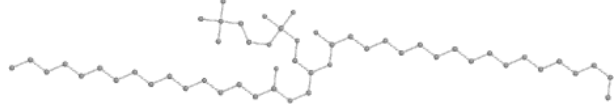


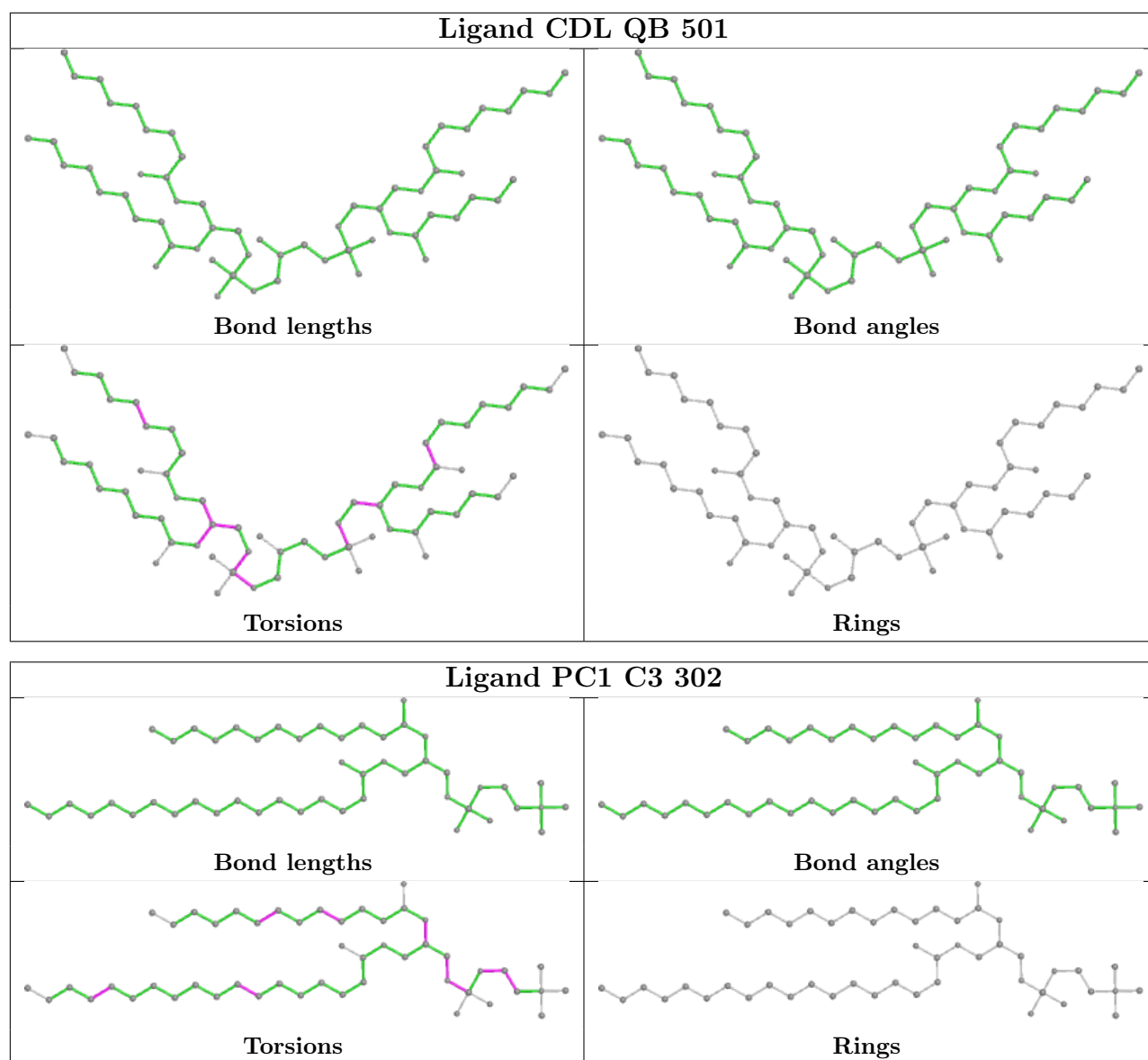


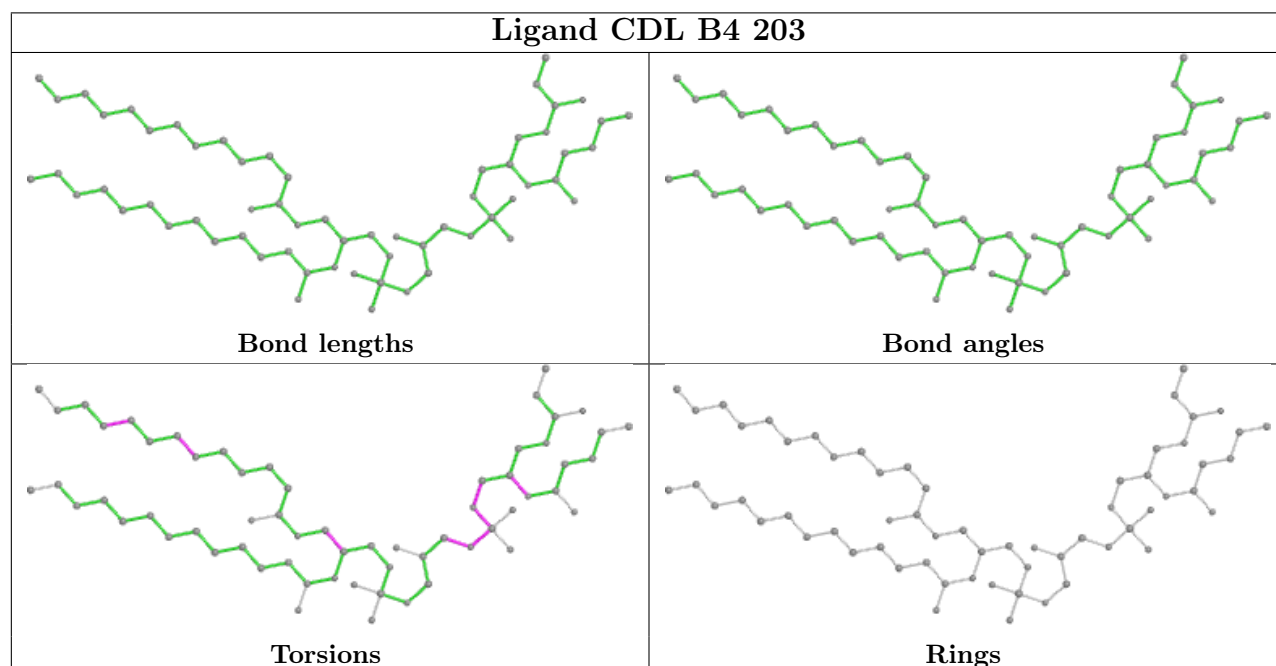
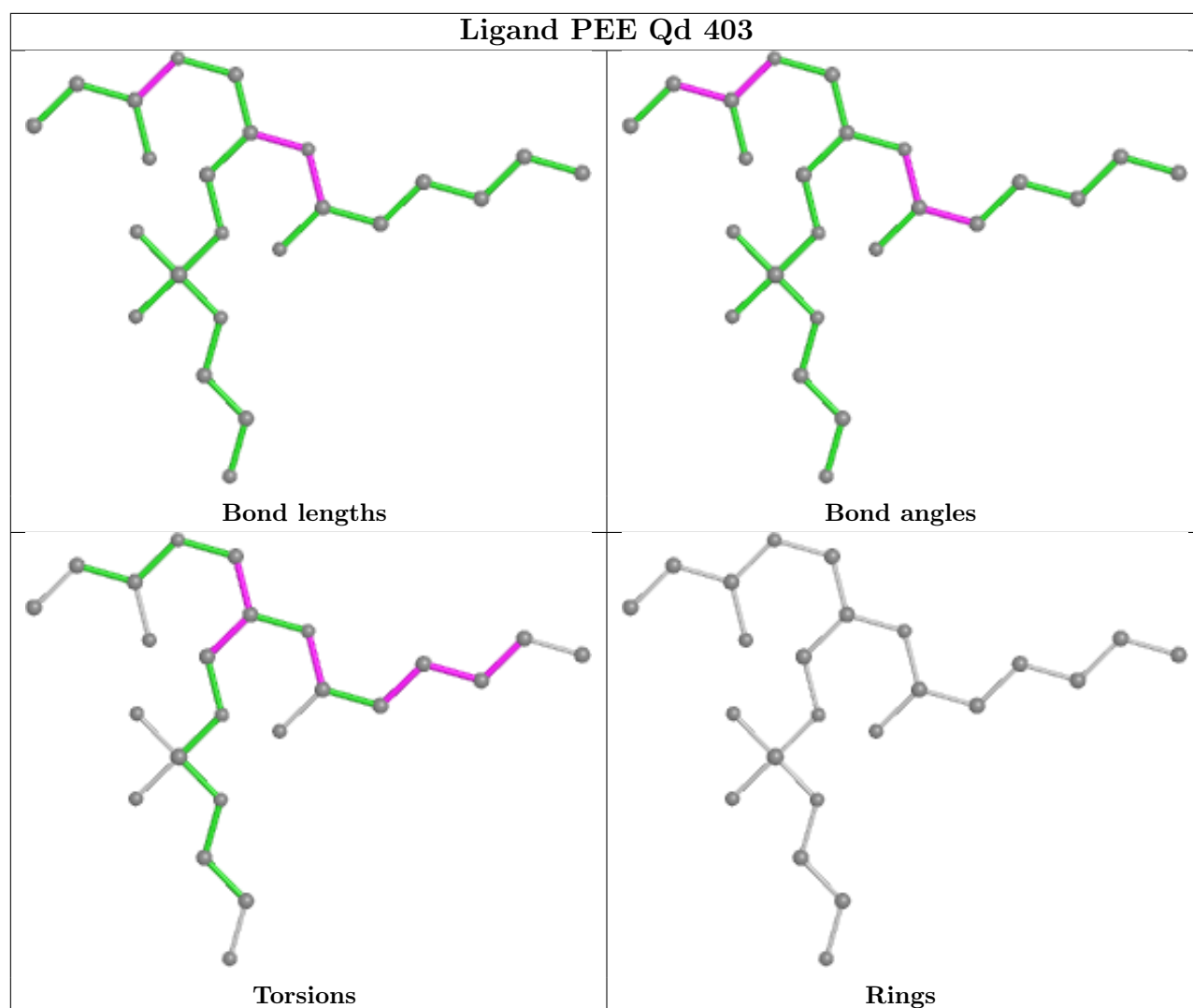


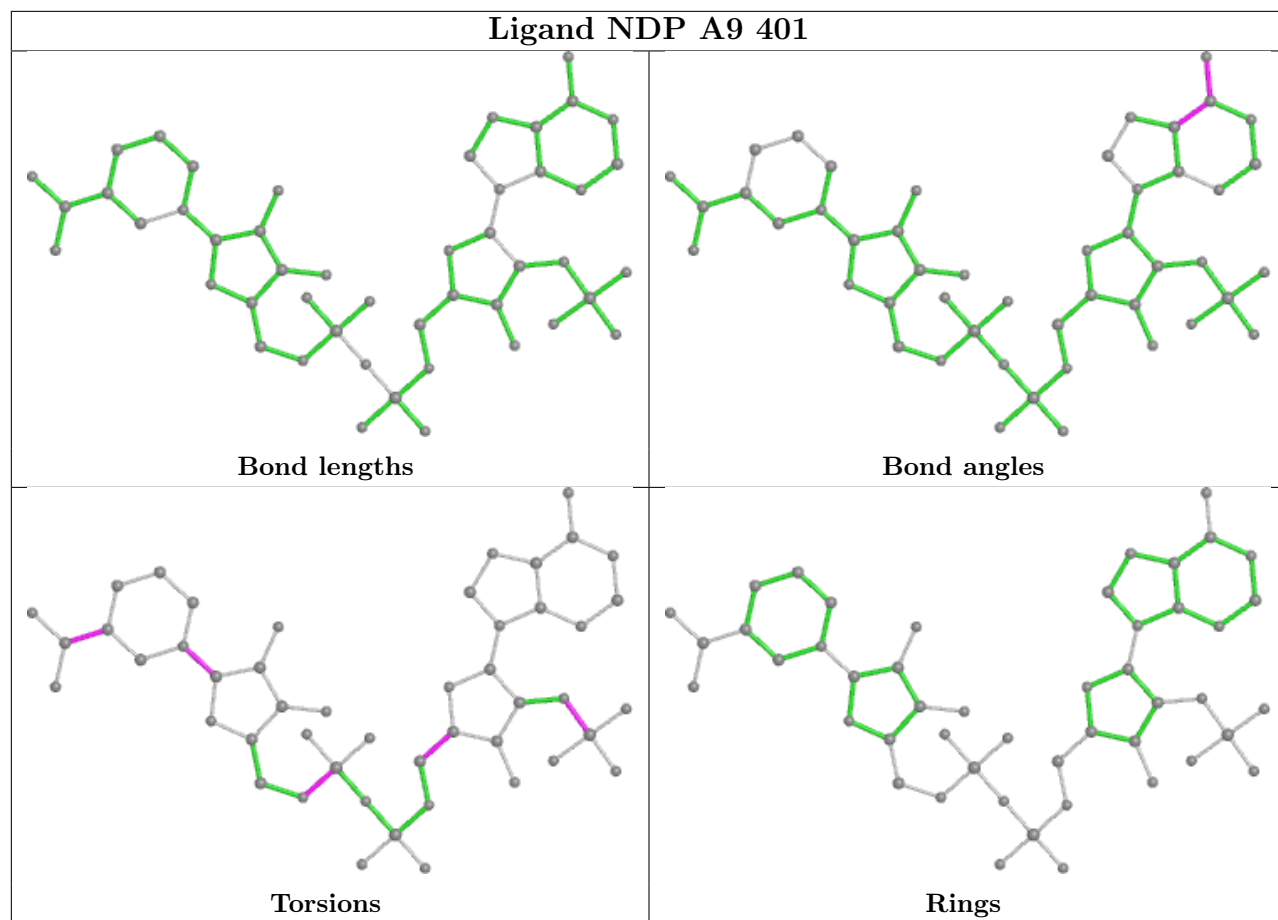
Ligand PLX N4 503	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PC1 Qc 405	
	
Bond lengths	Bond angles
	
Torsions	Rings

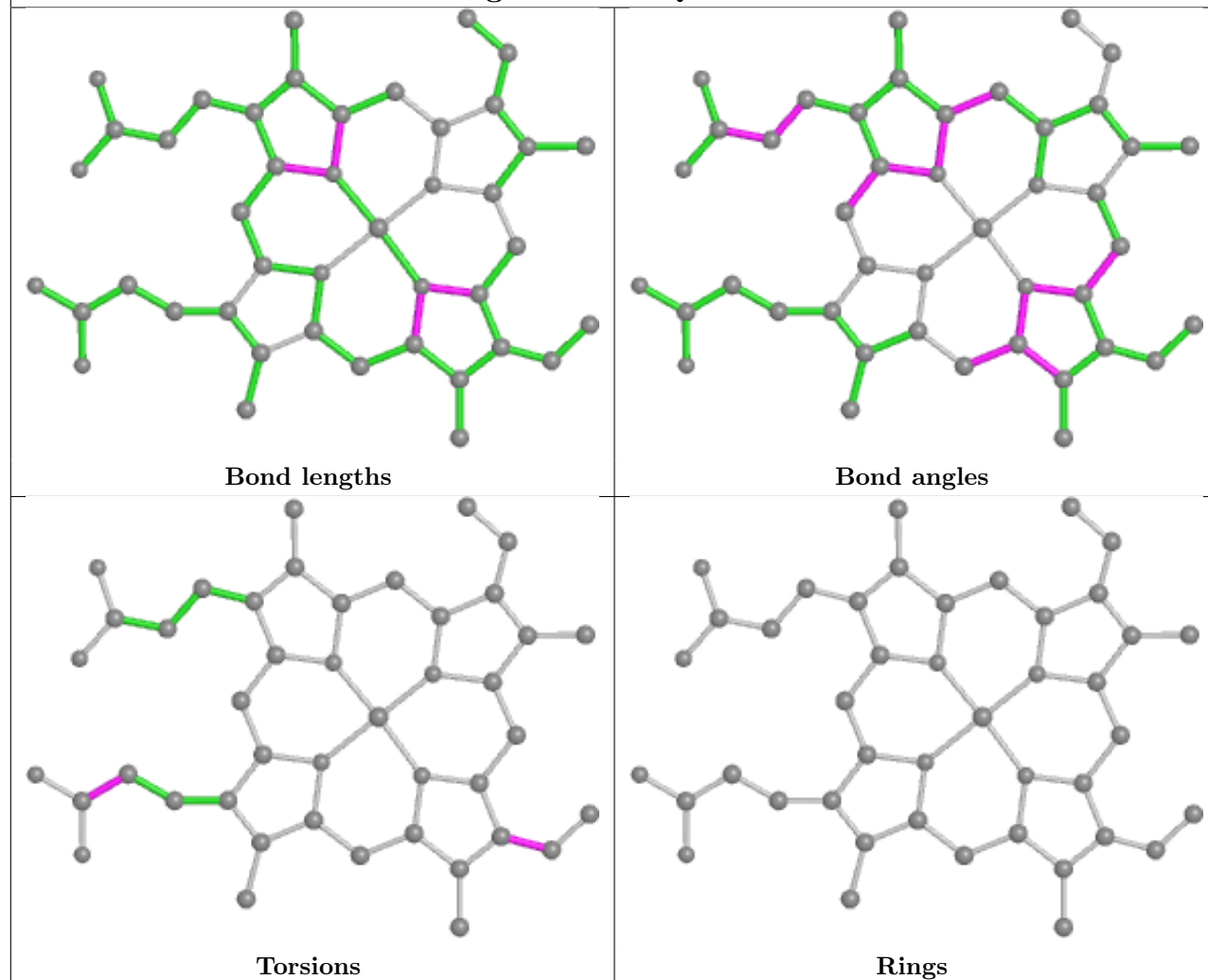
Ligand PLX AM 202	
	
Bond lengths	Bond angles
	
Torsions	Rings



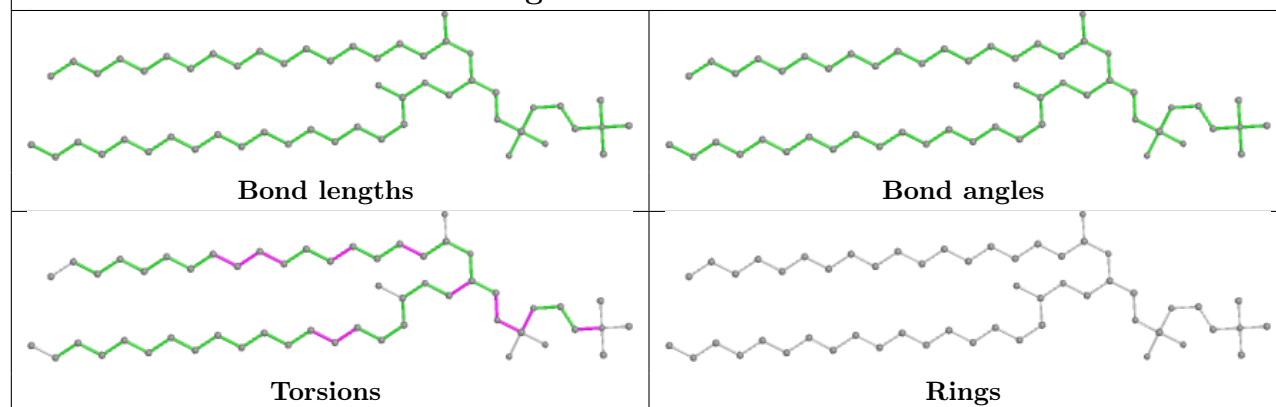


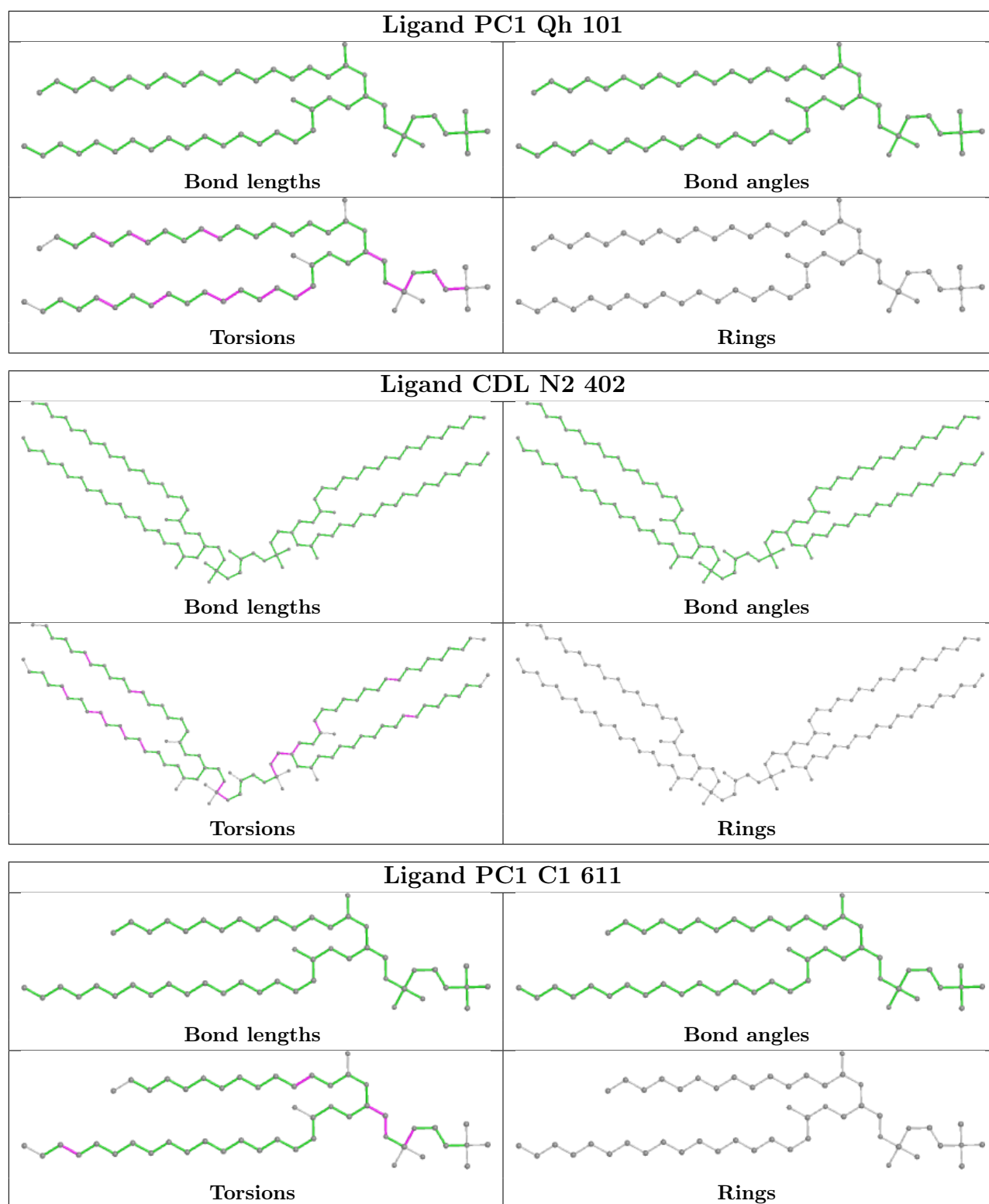


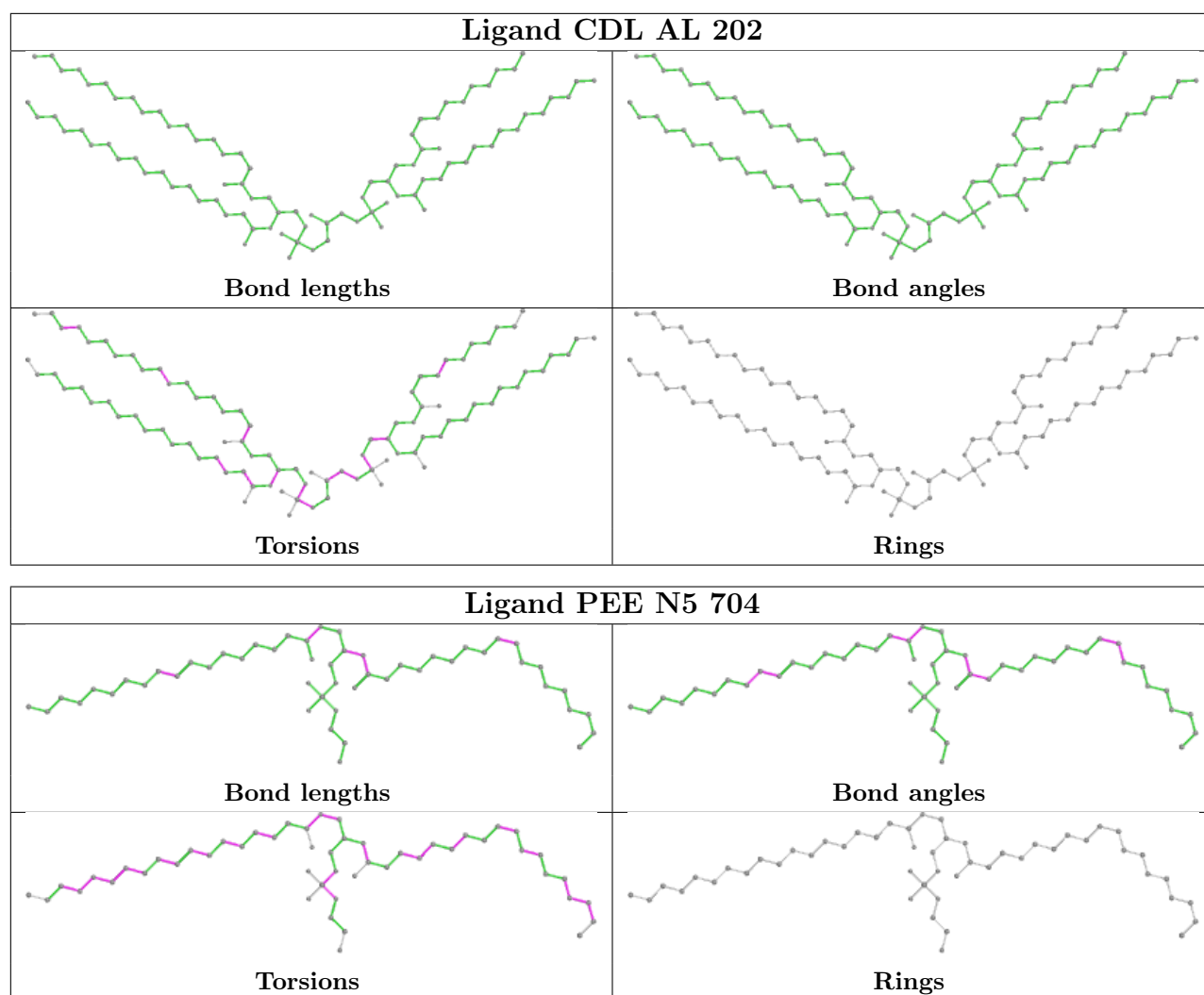
Ligand HEM QC 402

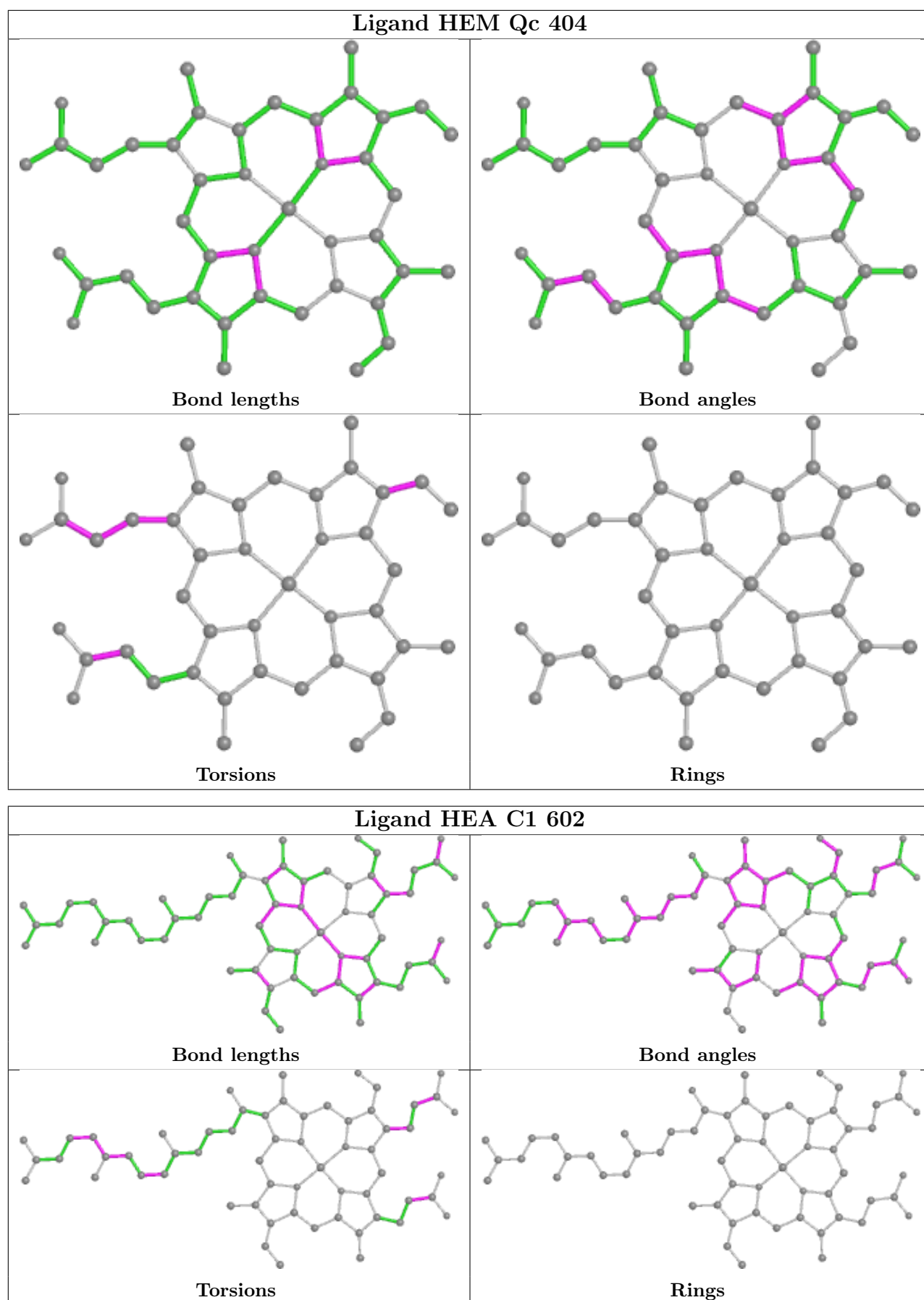


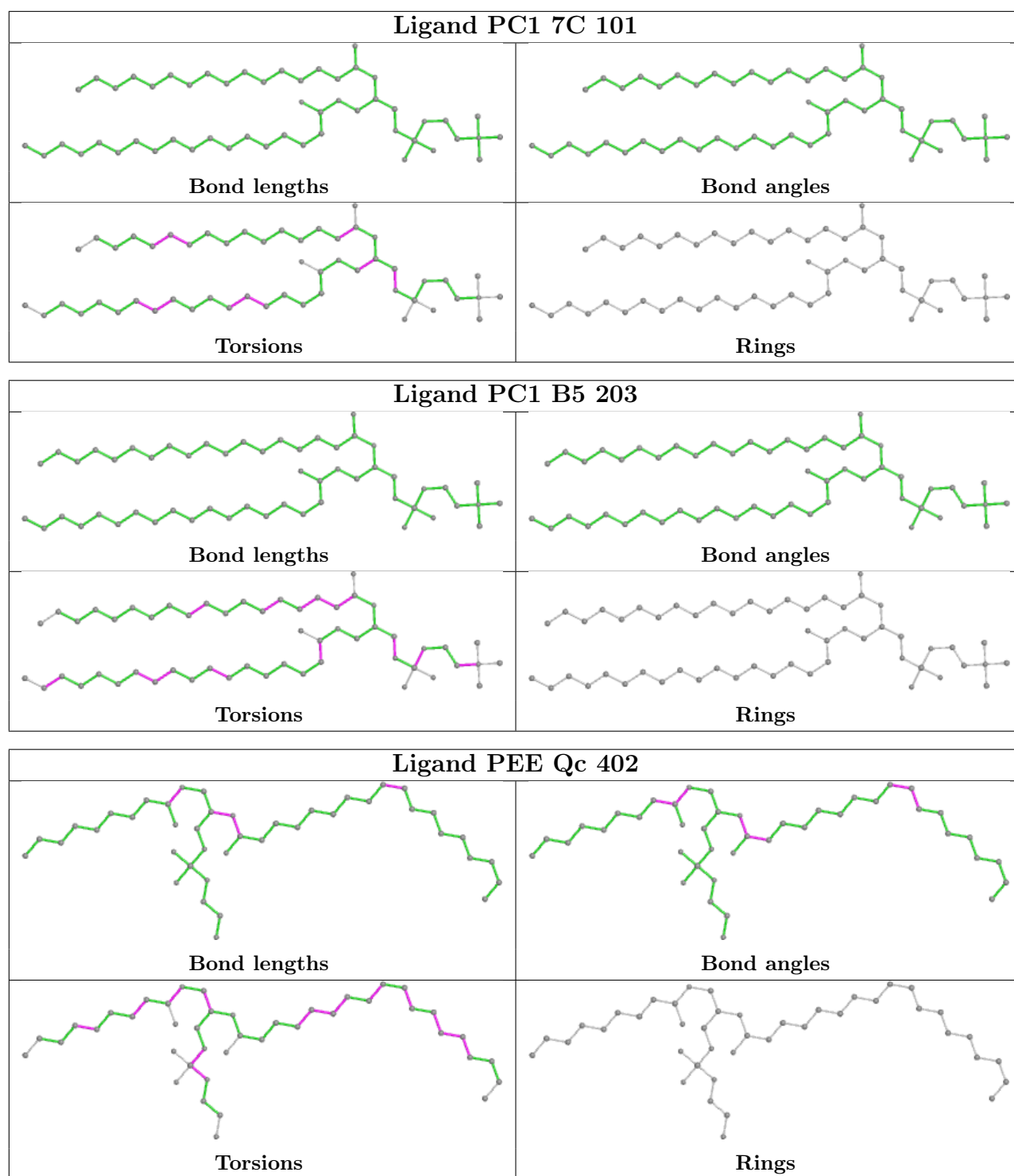
Ligand PC1 N1 401



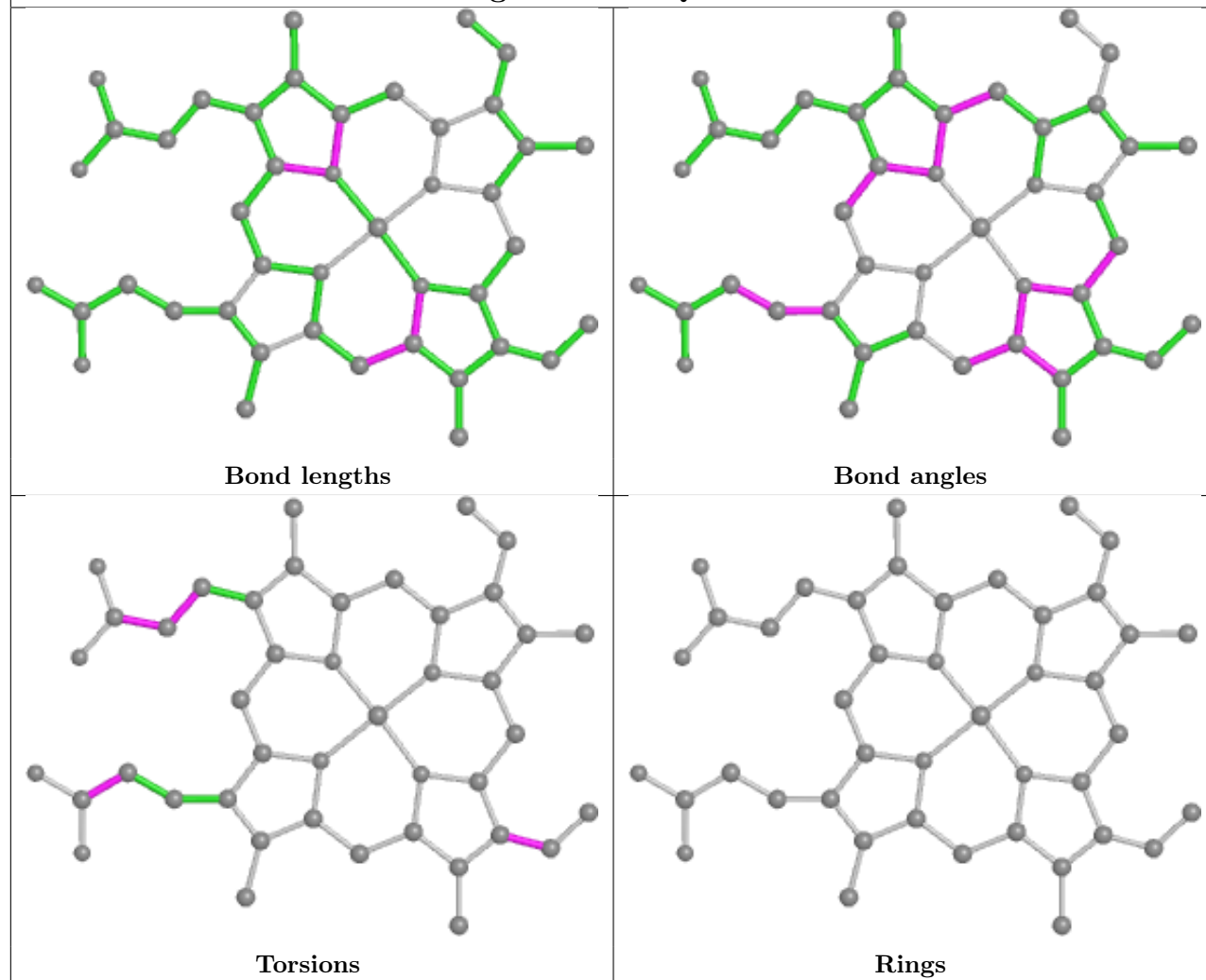




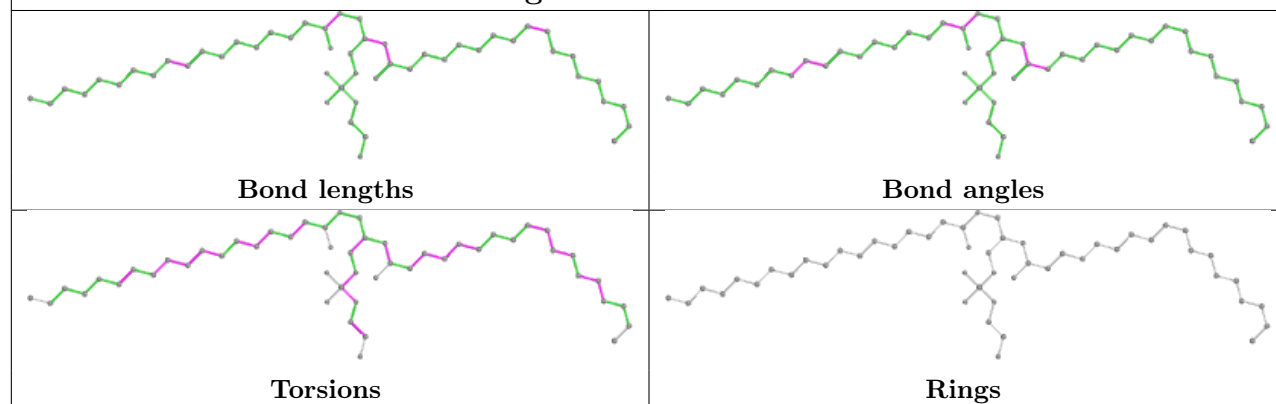


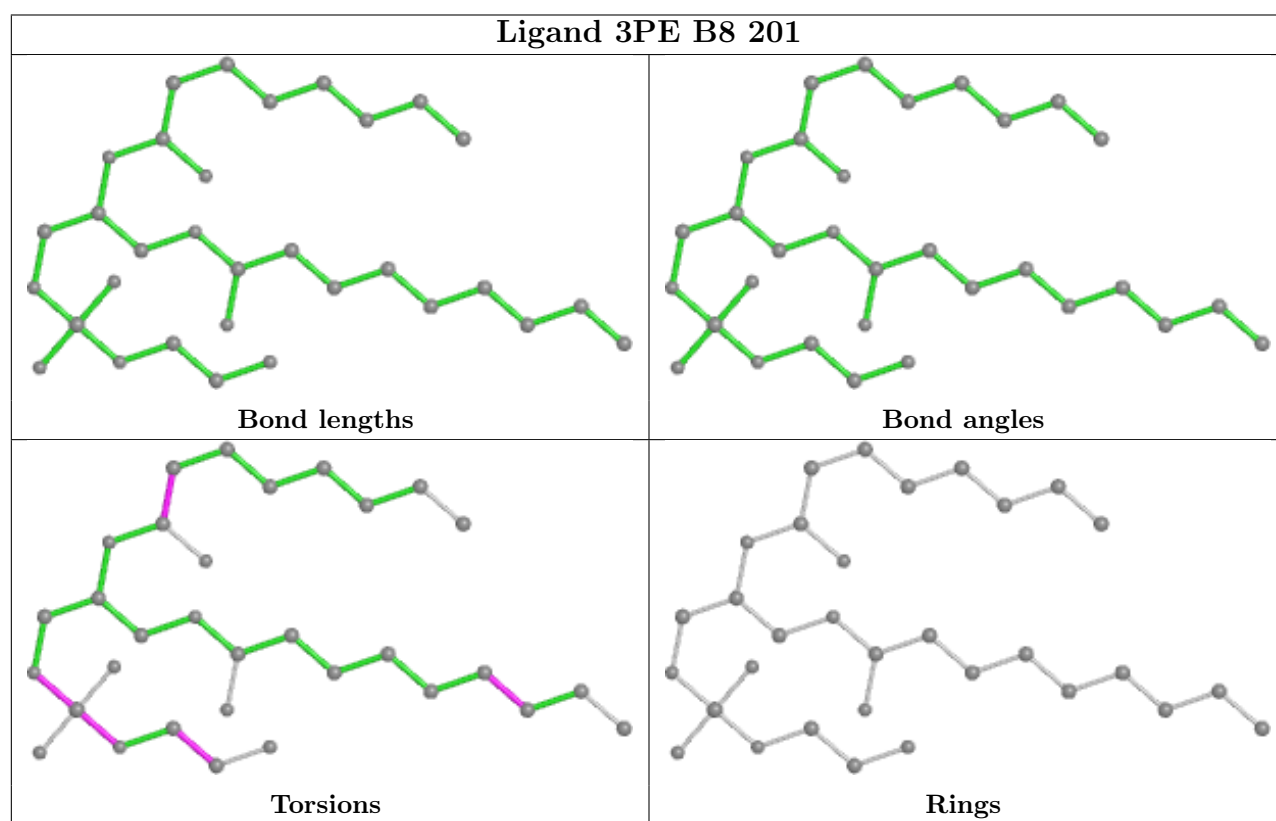
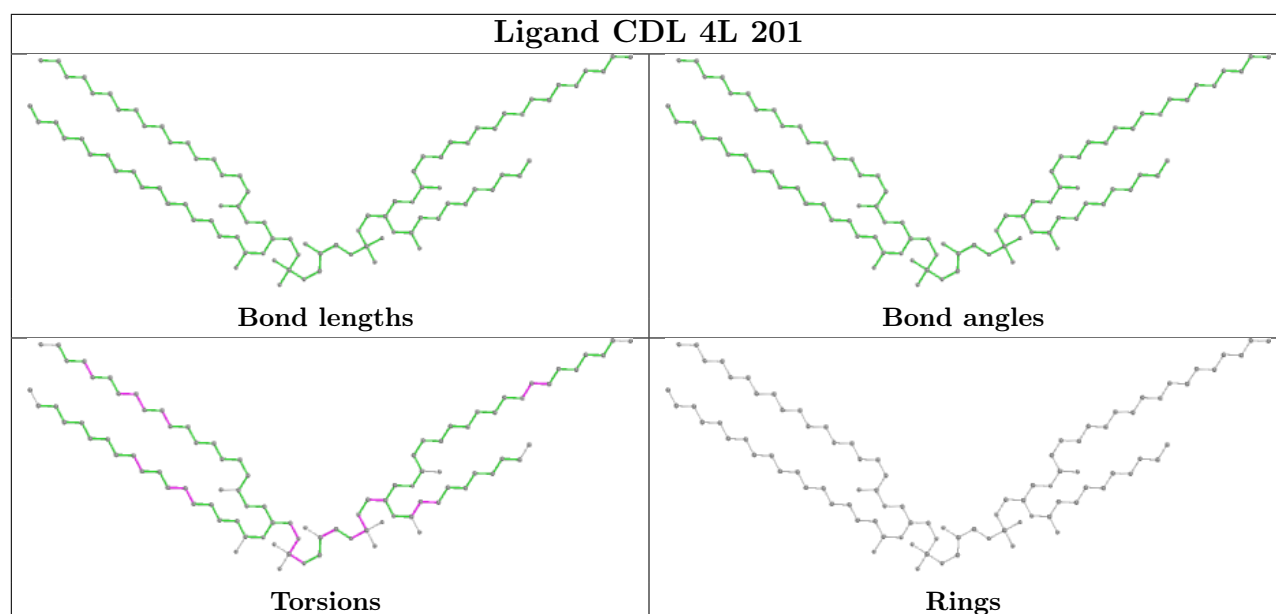


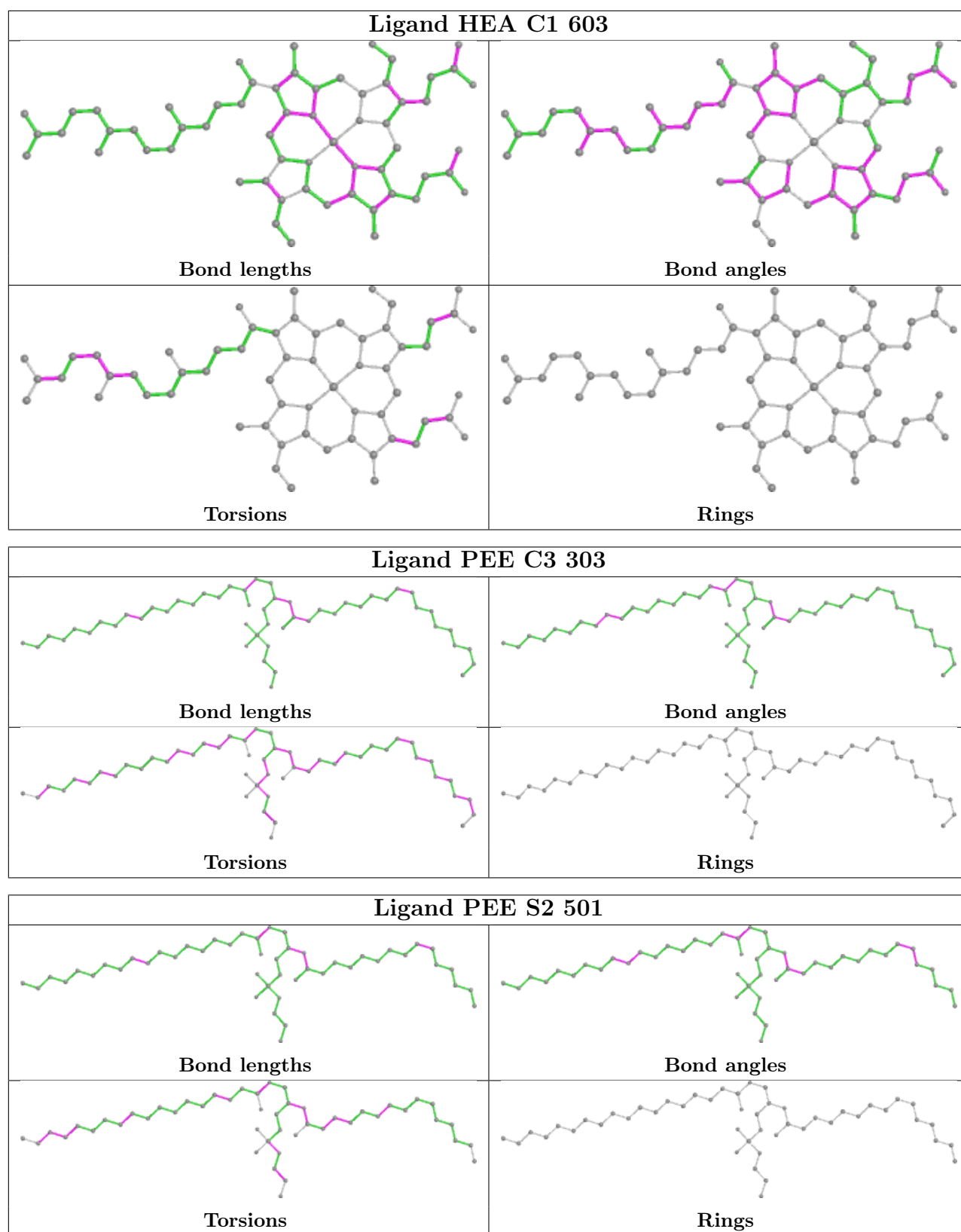
Ligand HEM Qc 403

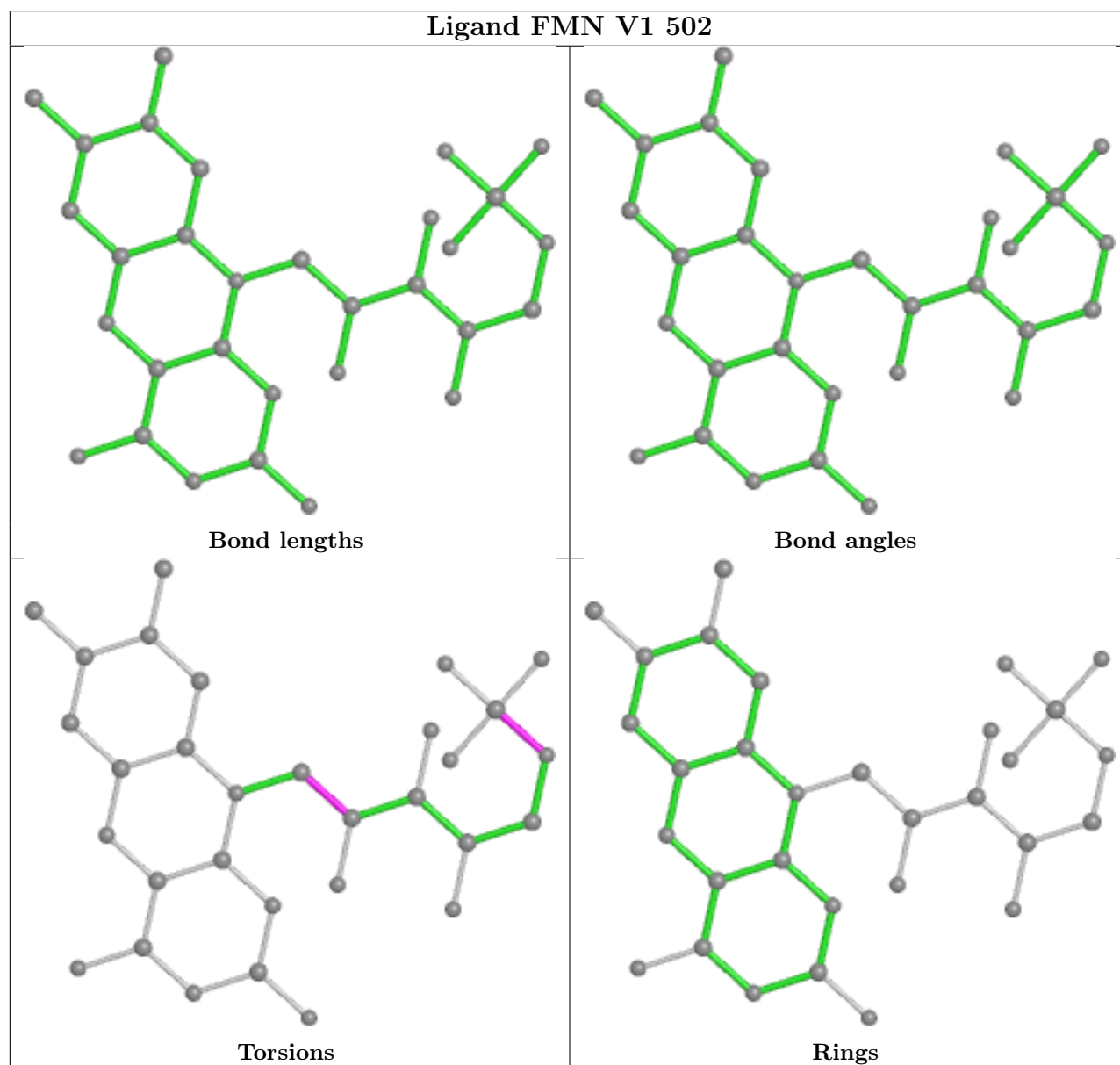
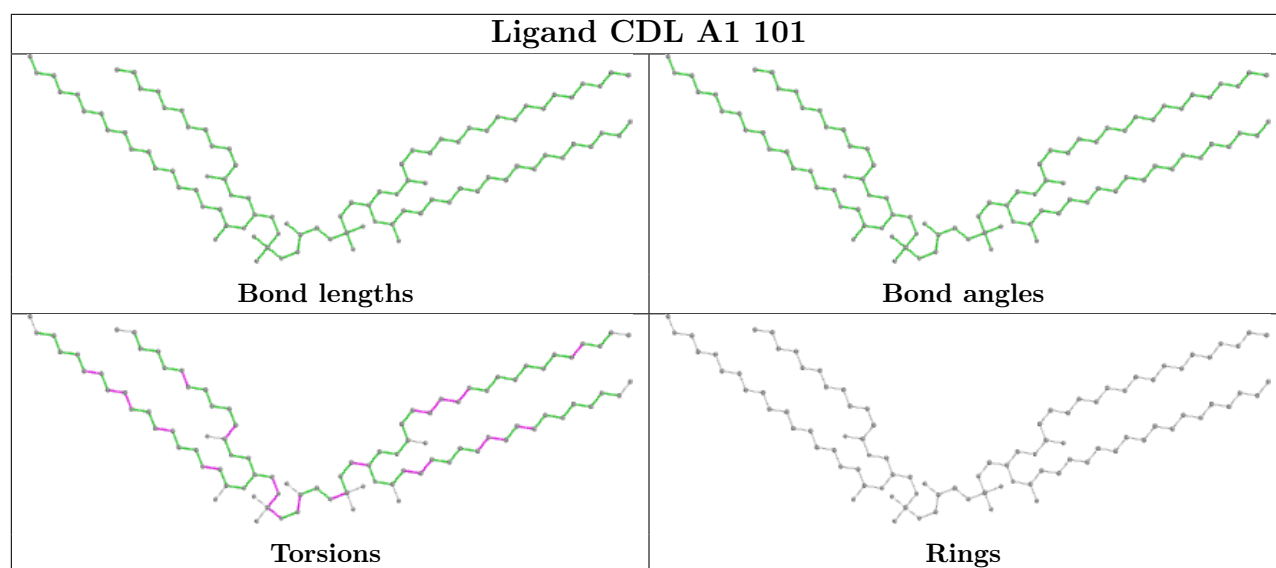


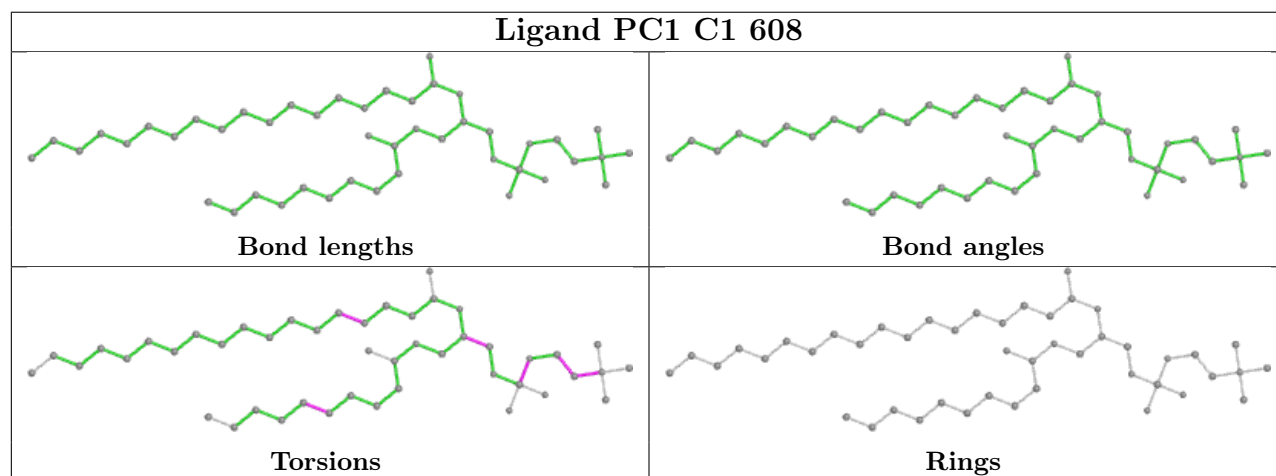
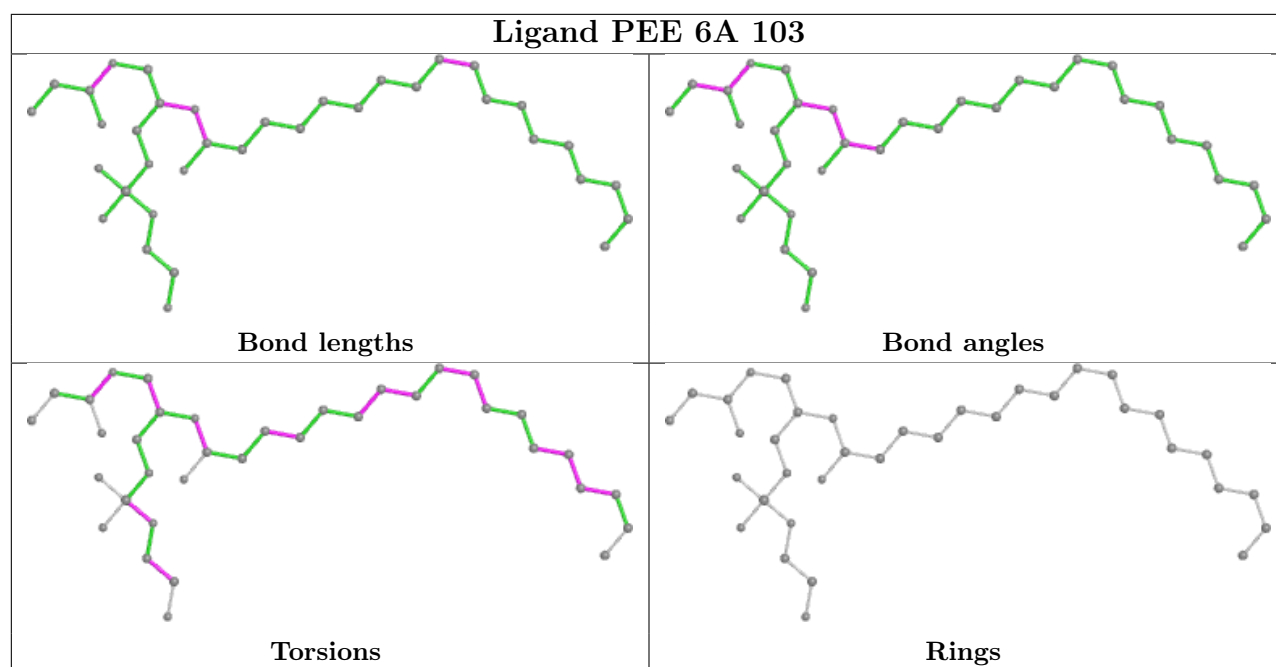
Ligand PEE B4 202

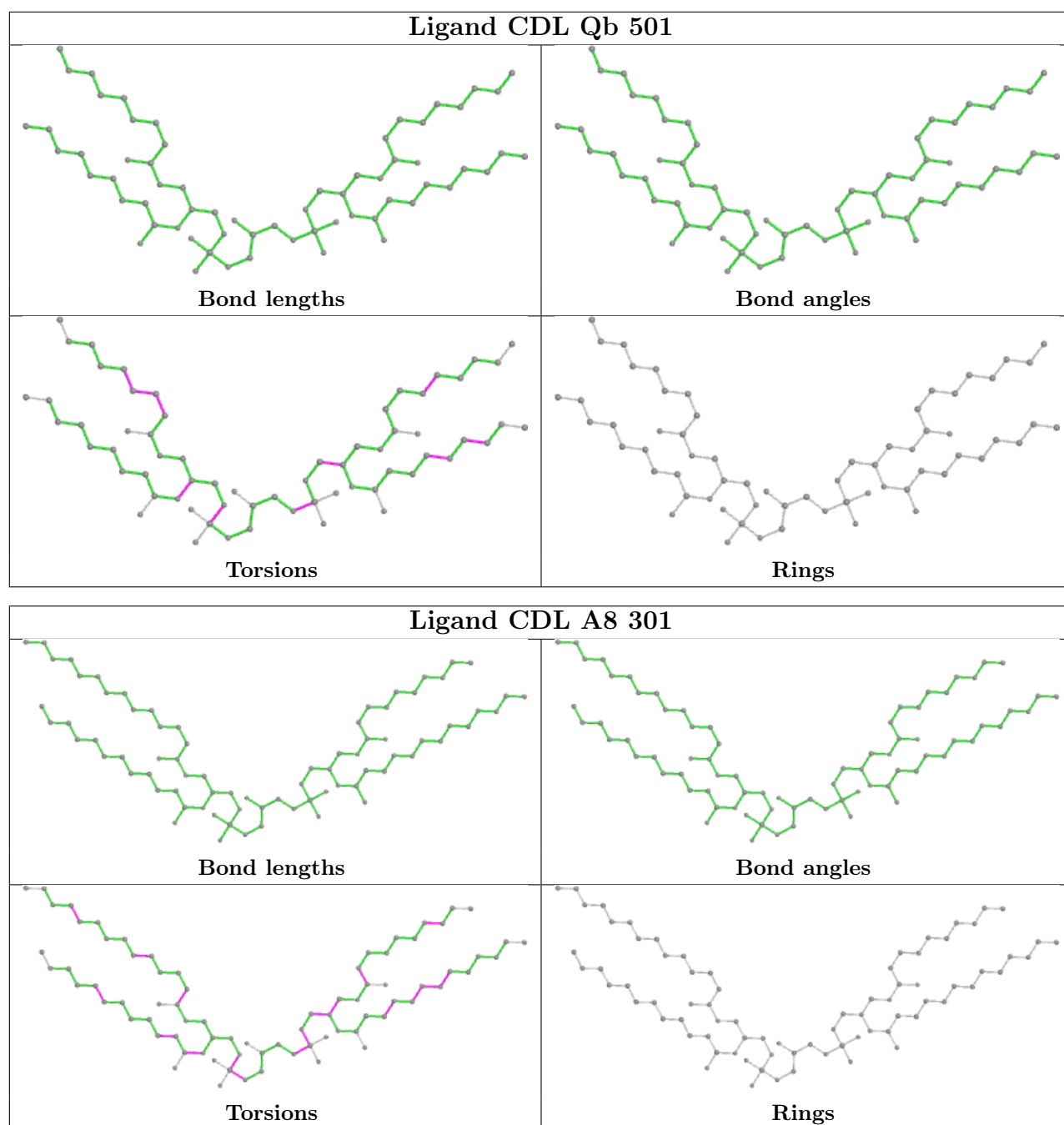


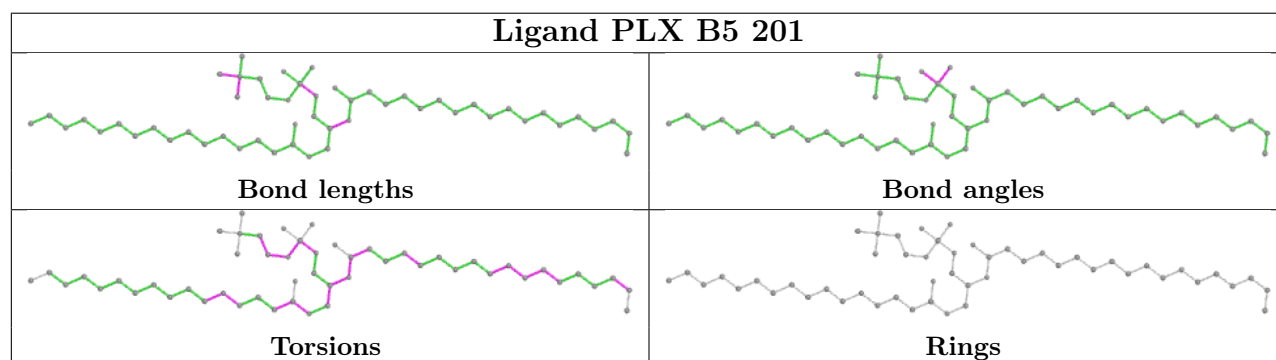
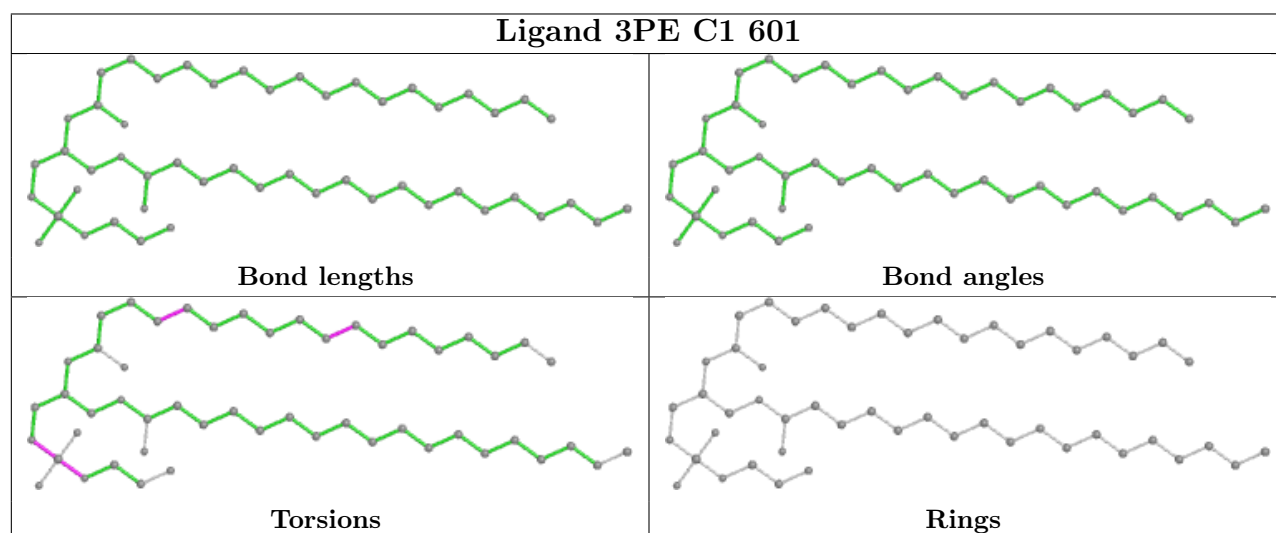
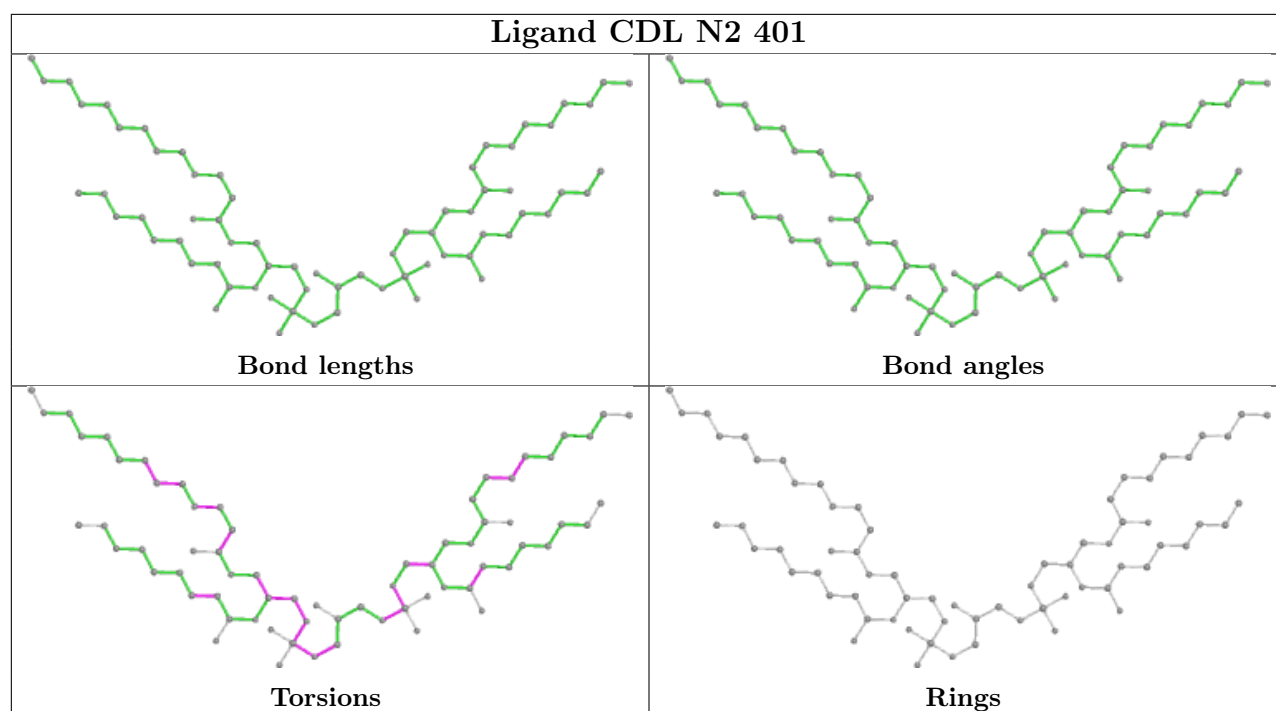


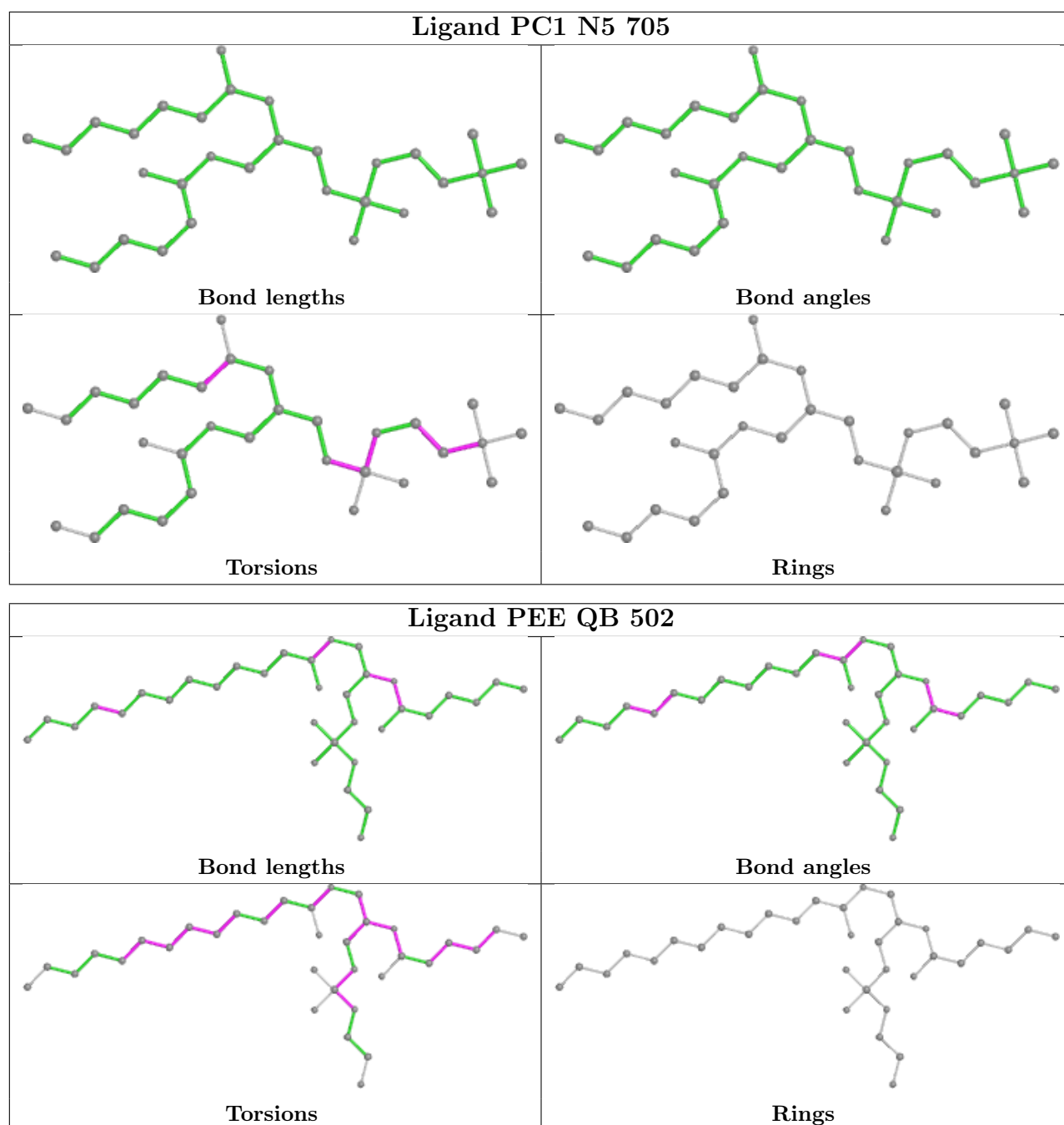


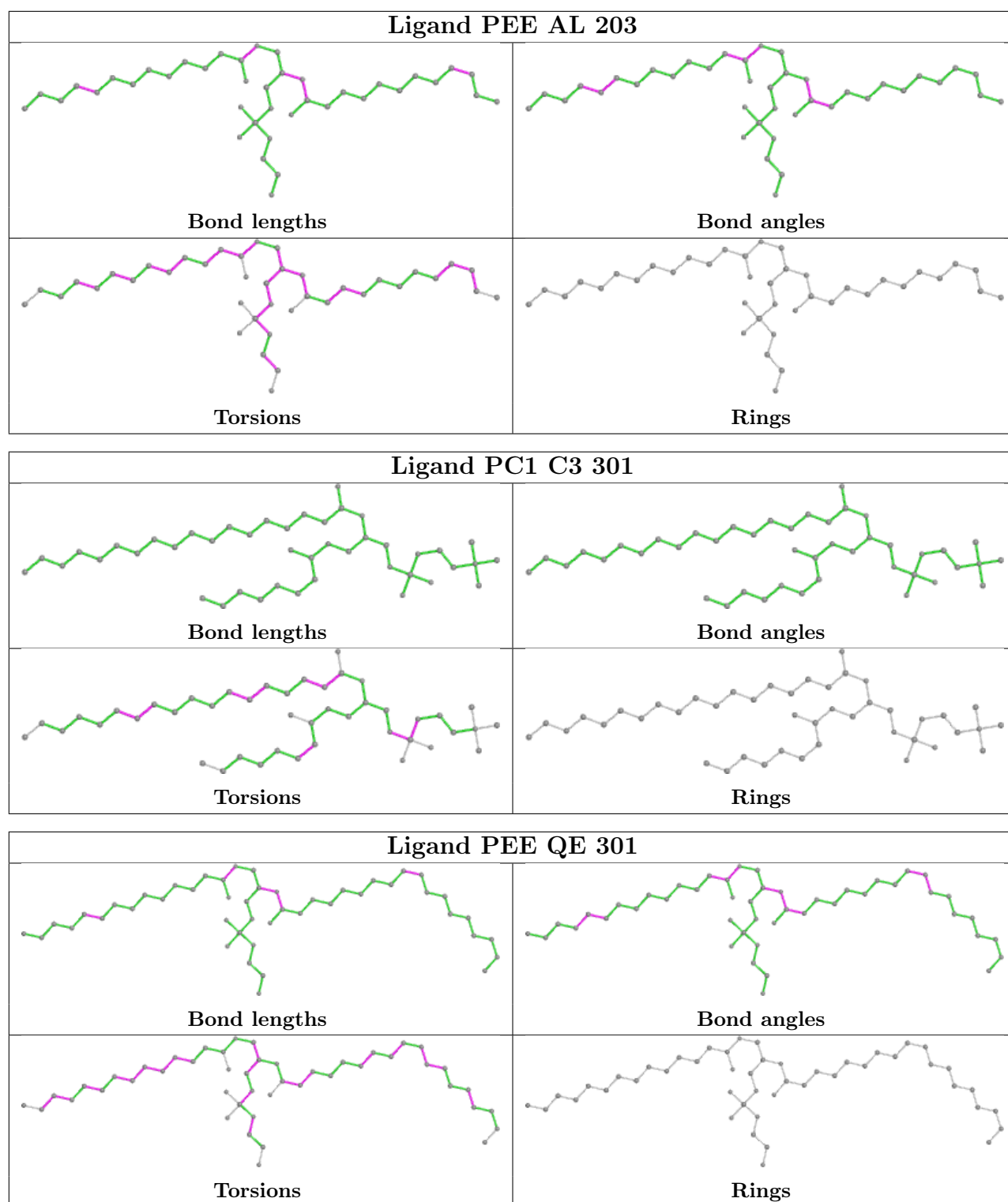


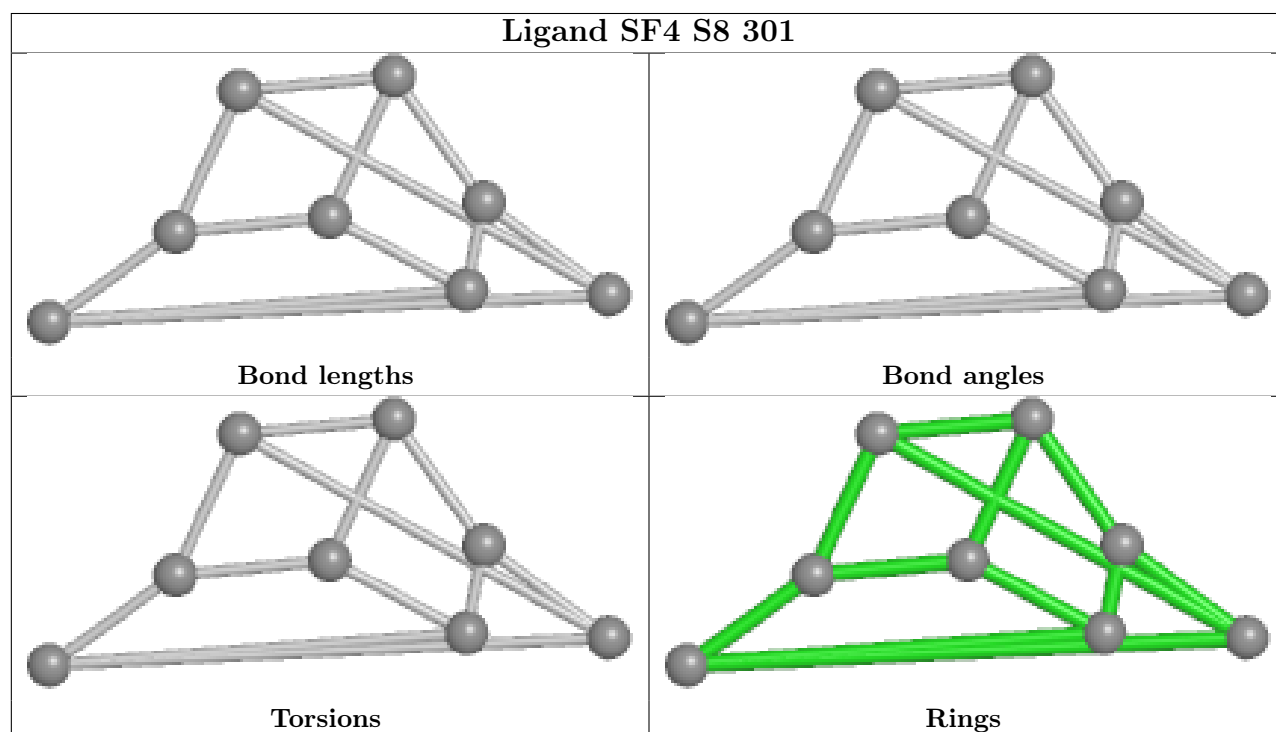
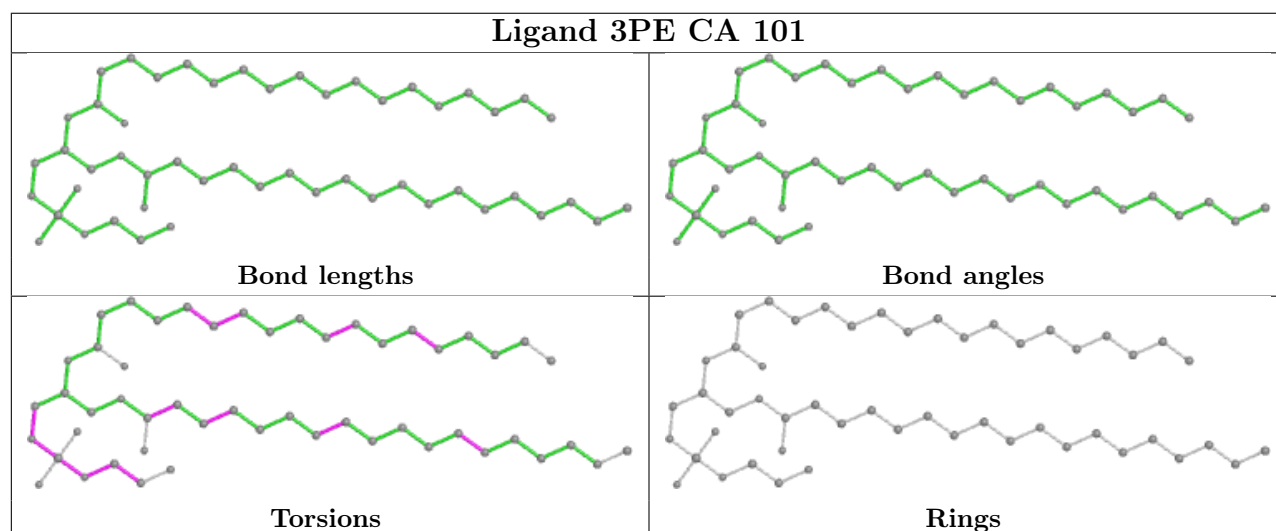
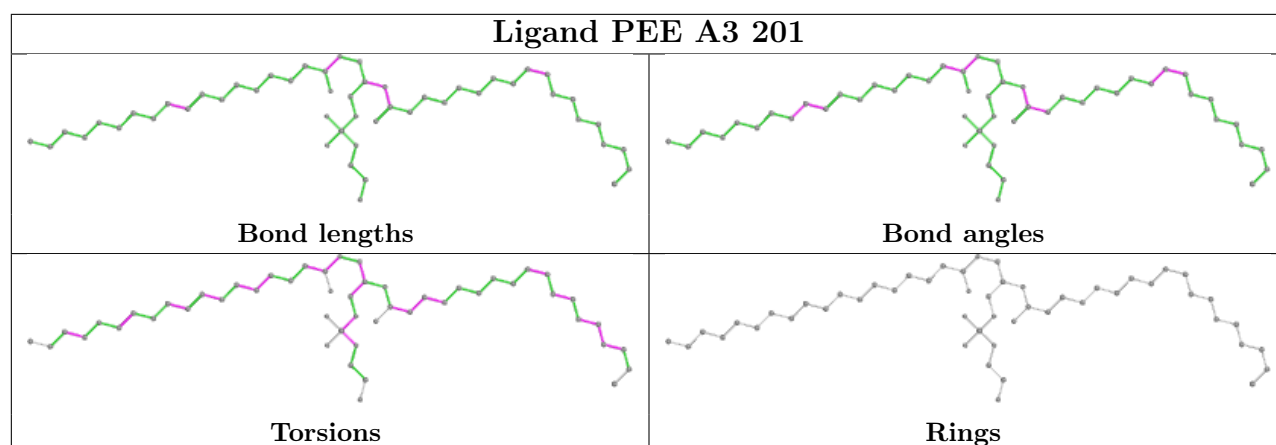


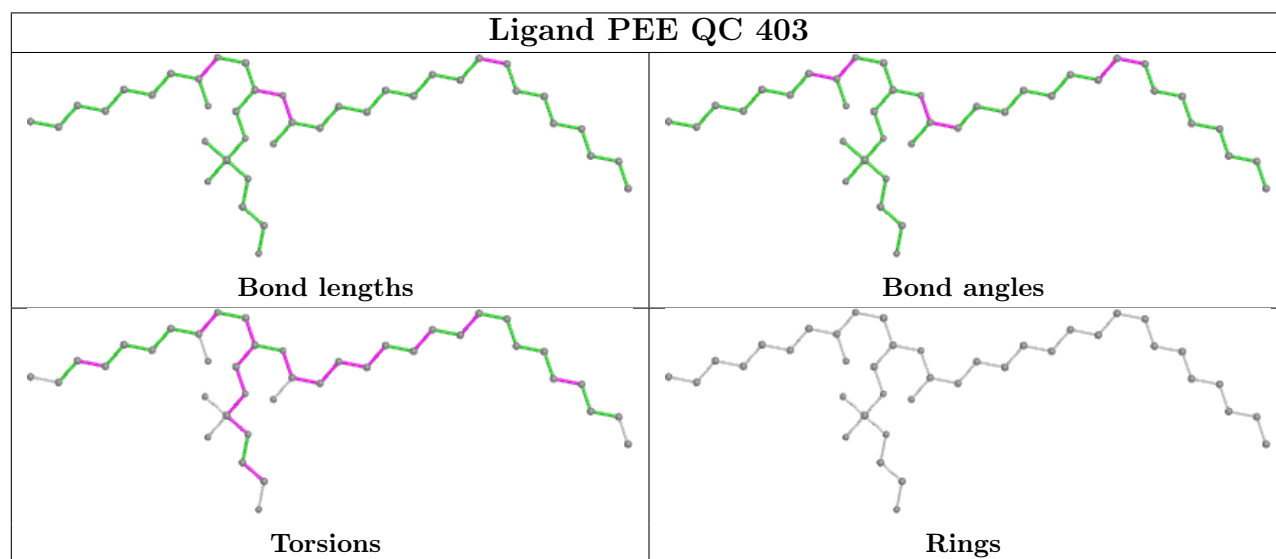
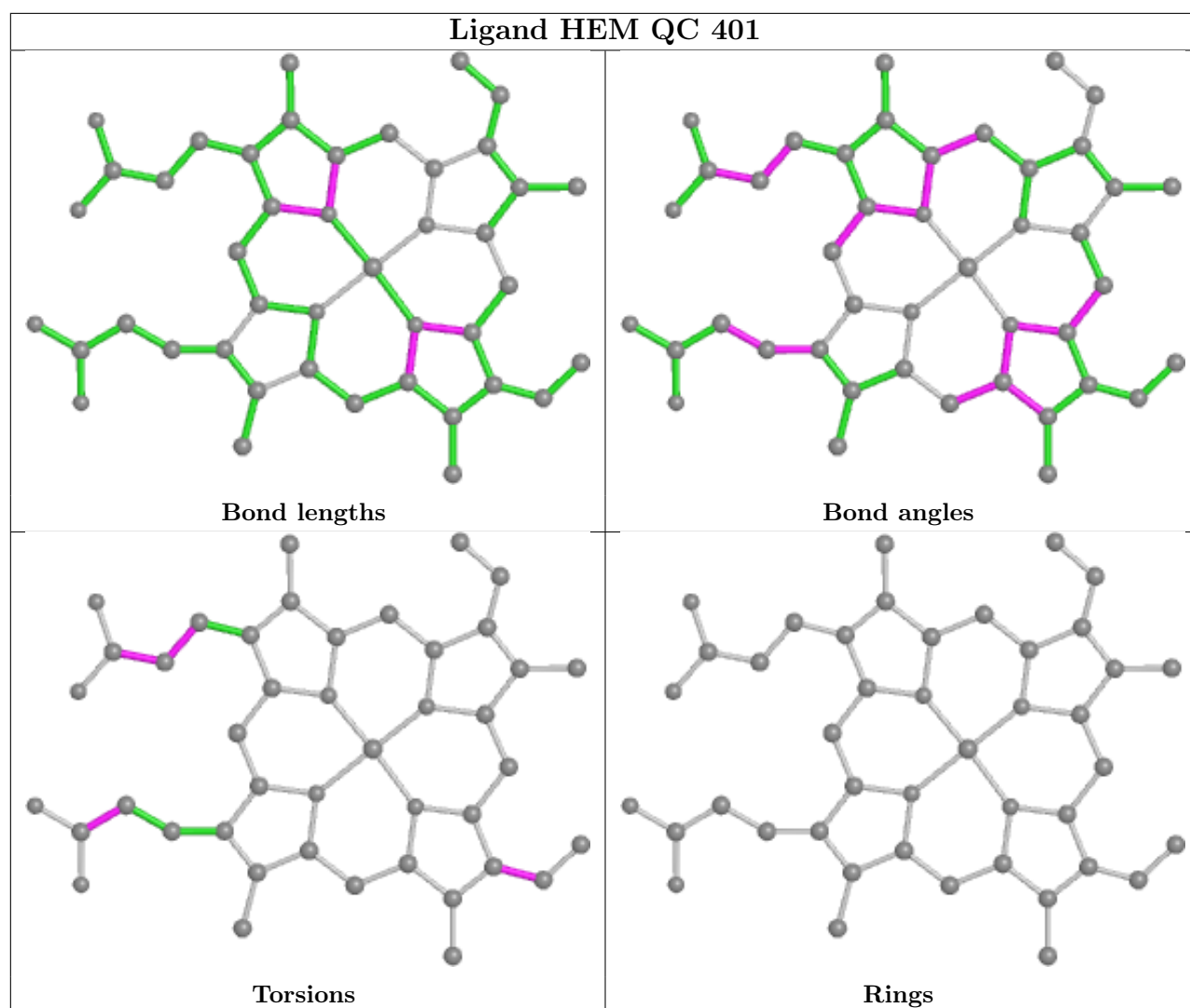


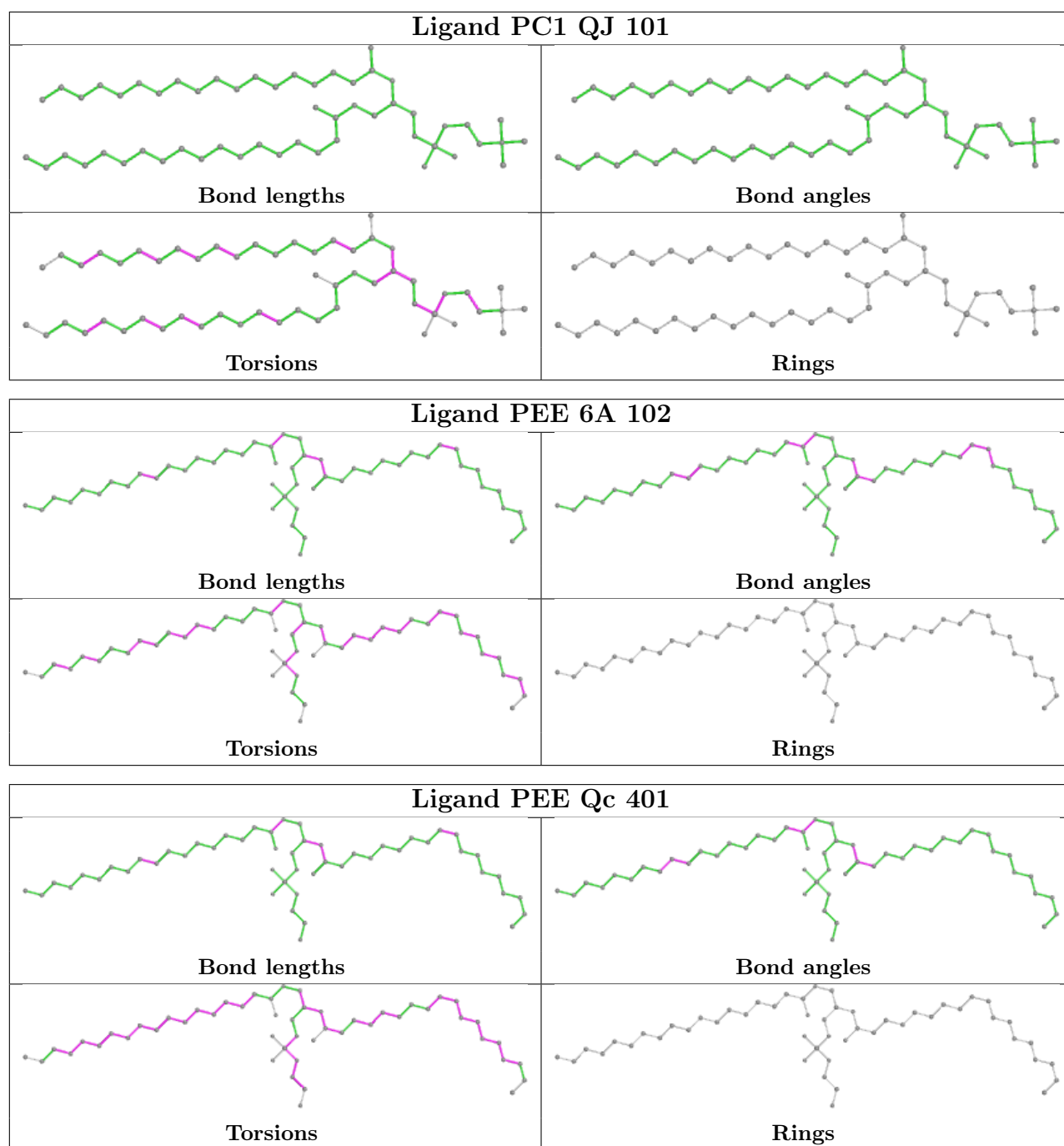


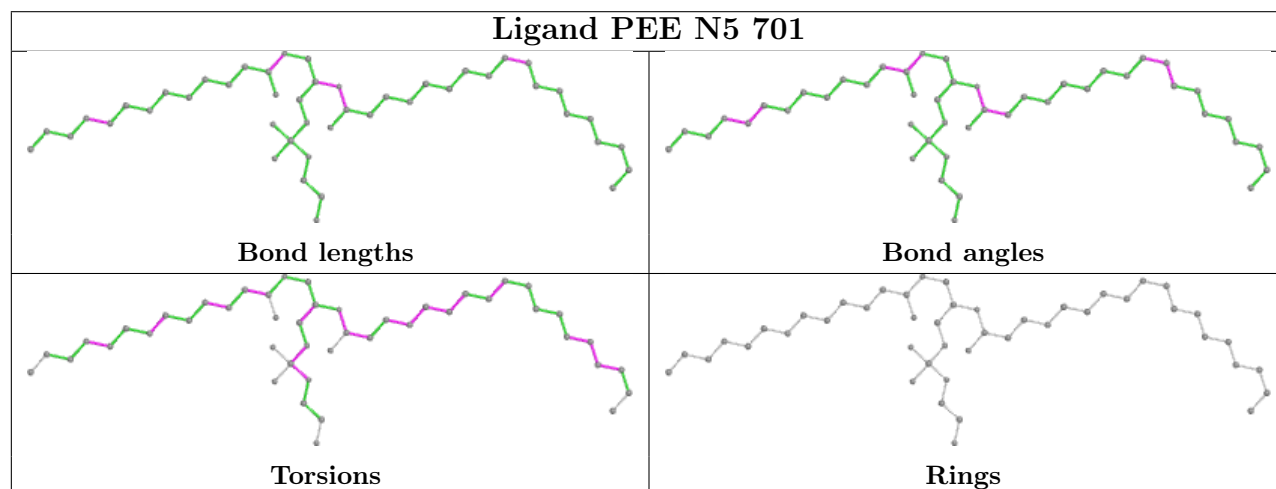
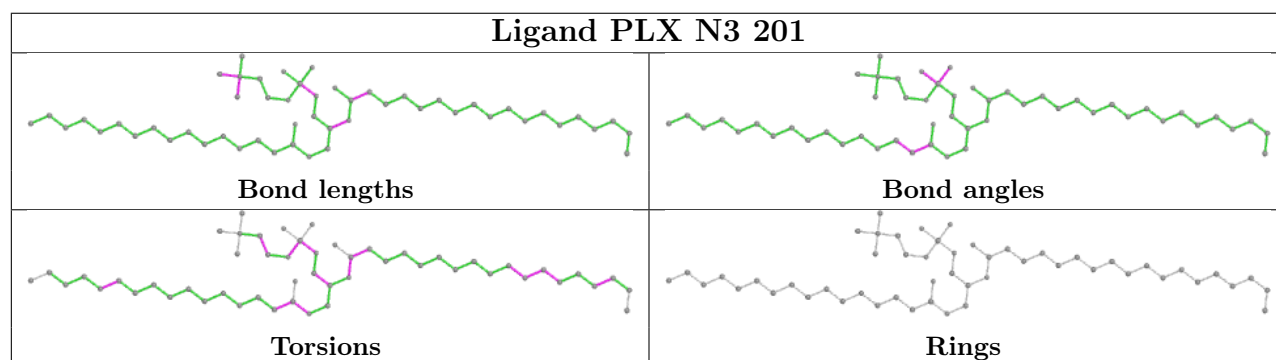
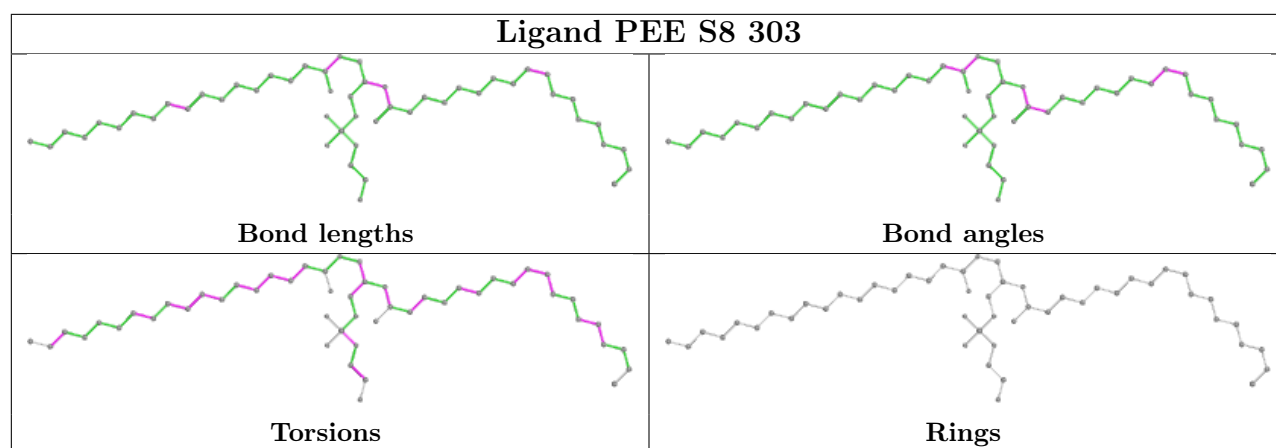


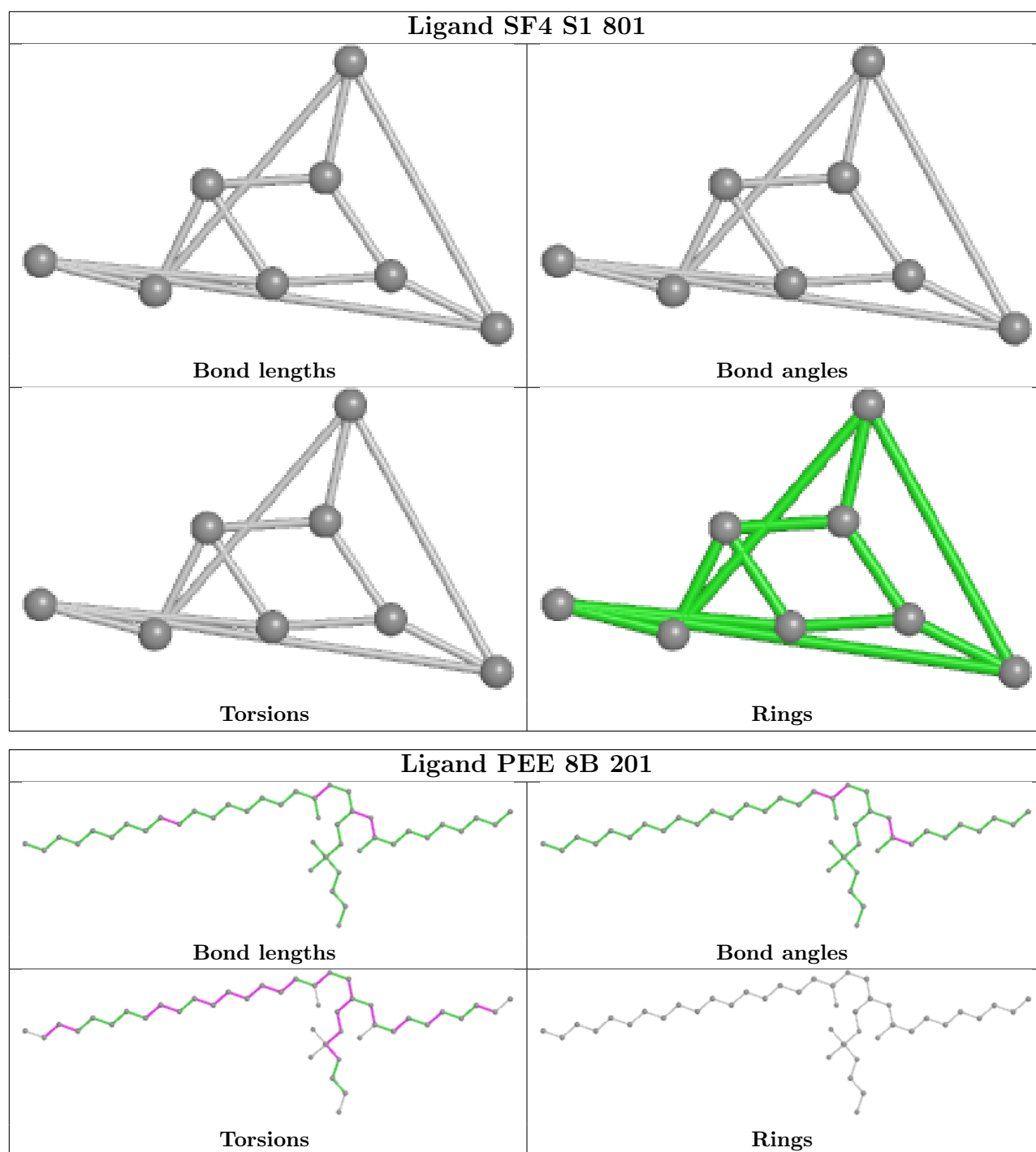


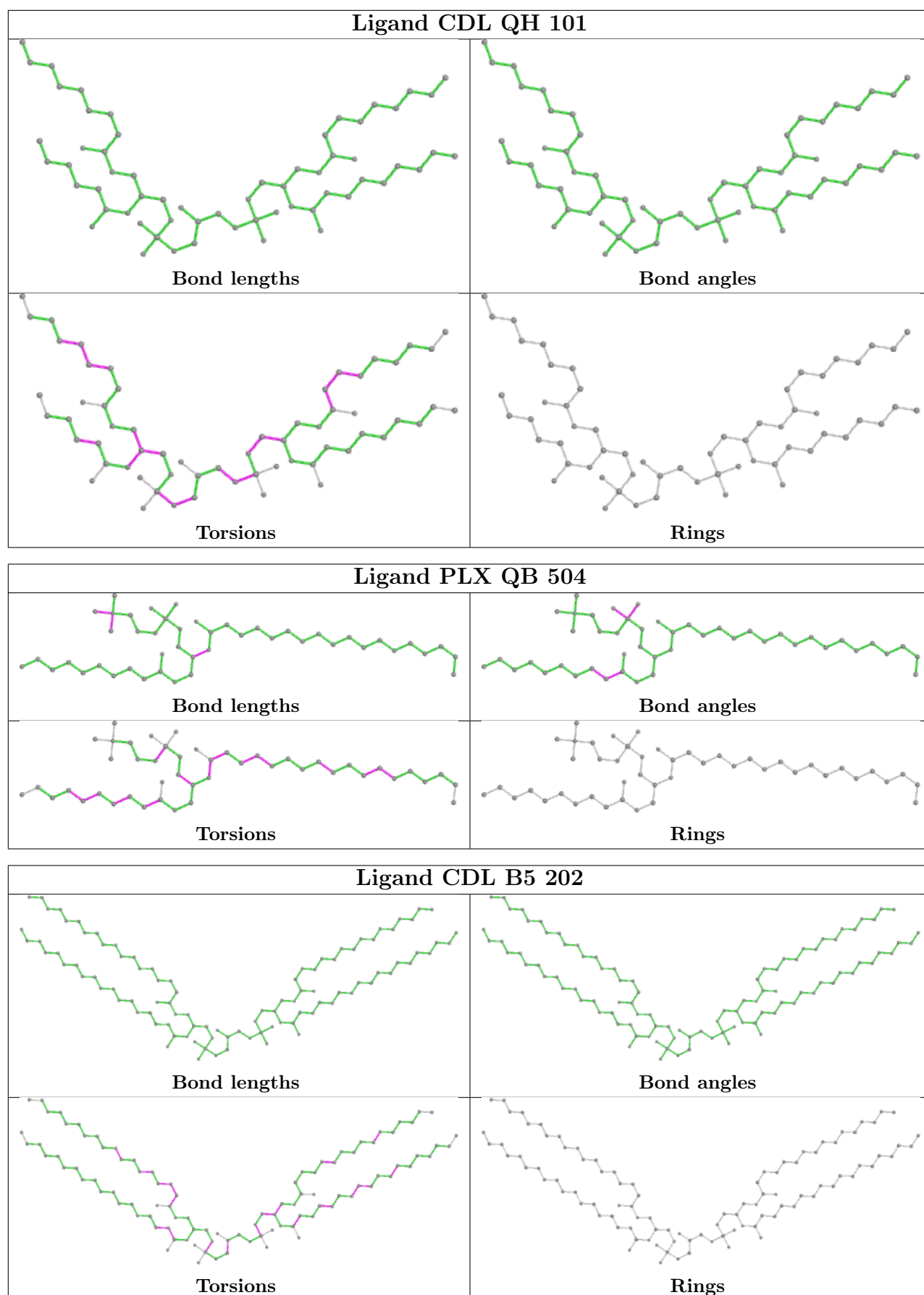


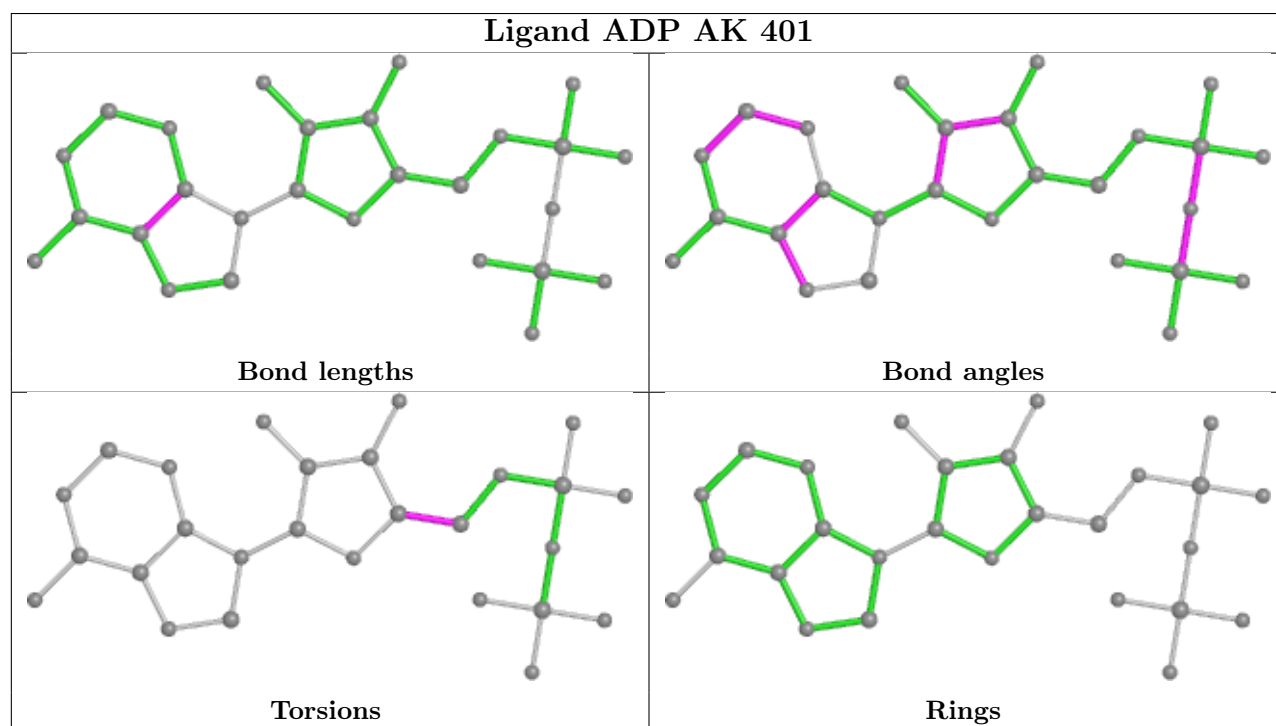
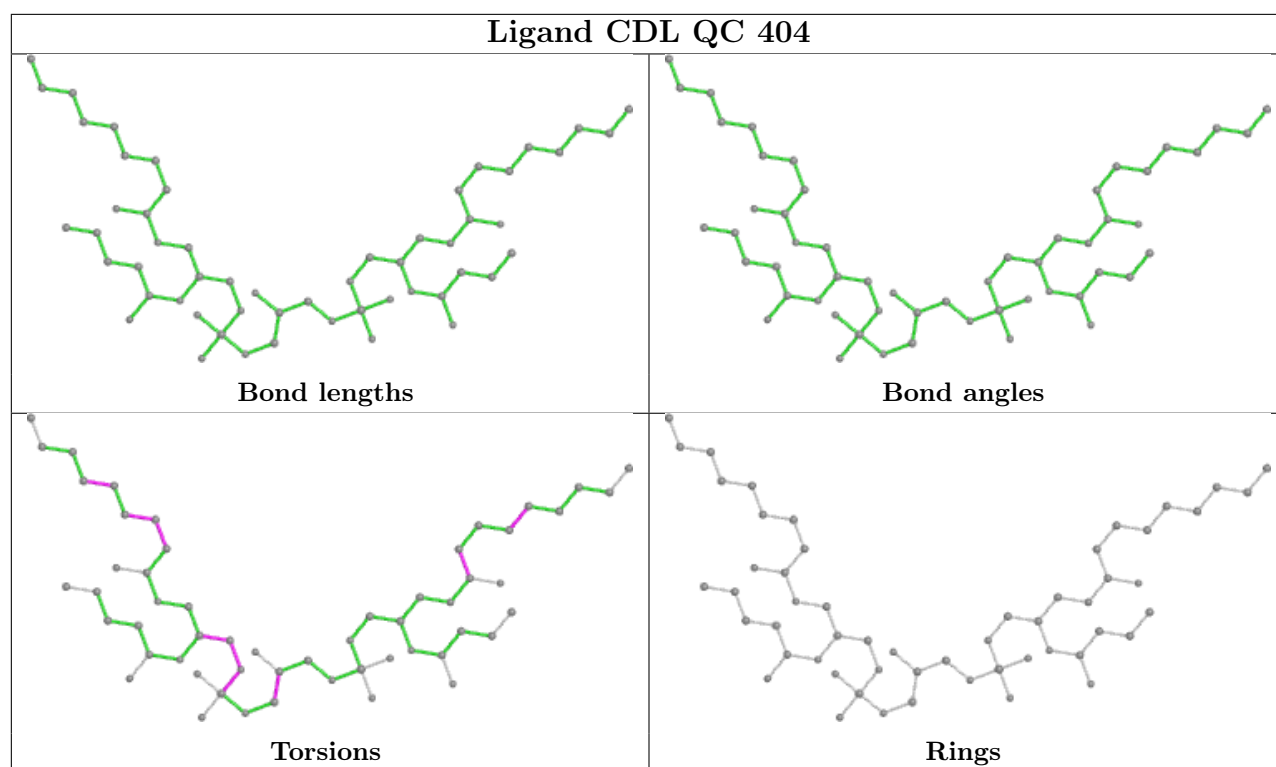


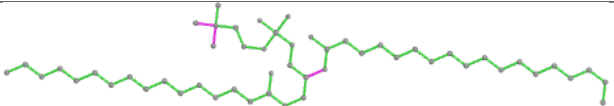
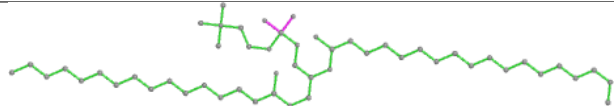
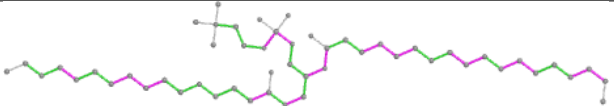
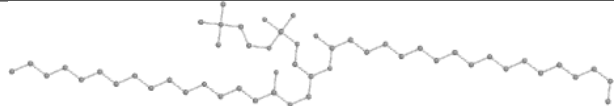


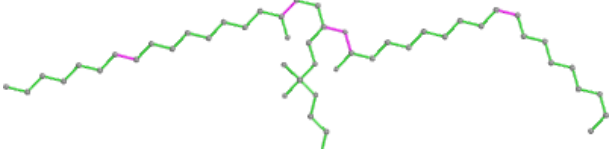
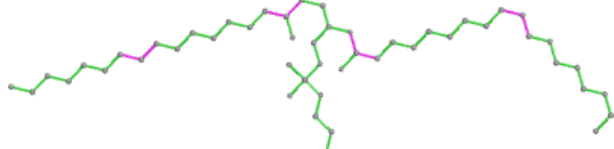
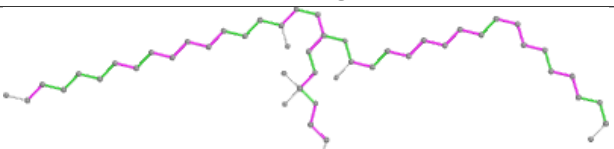
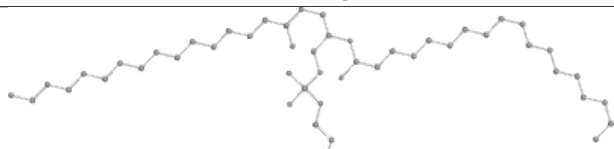


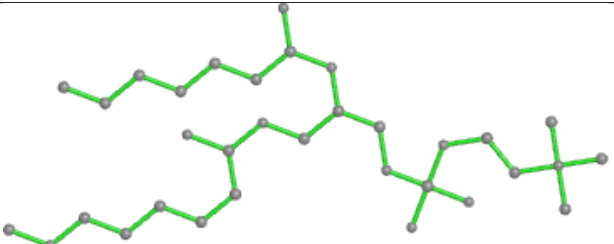
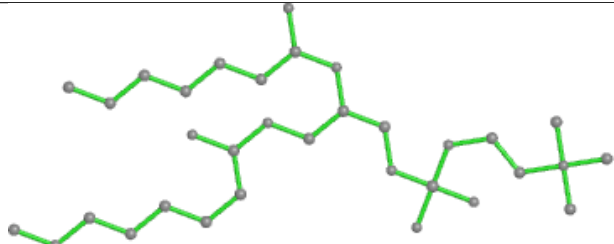
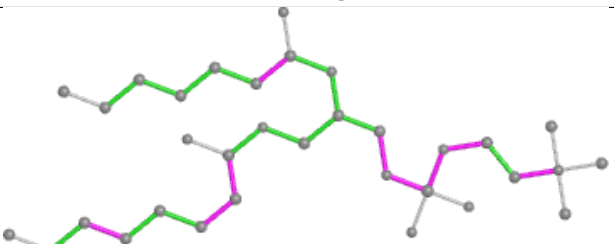
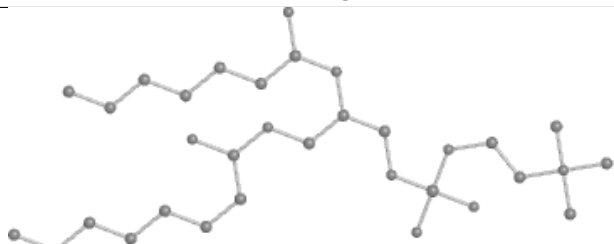


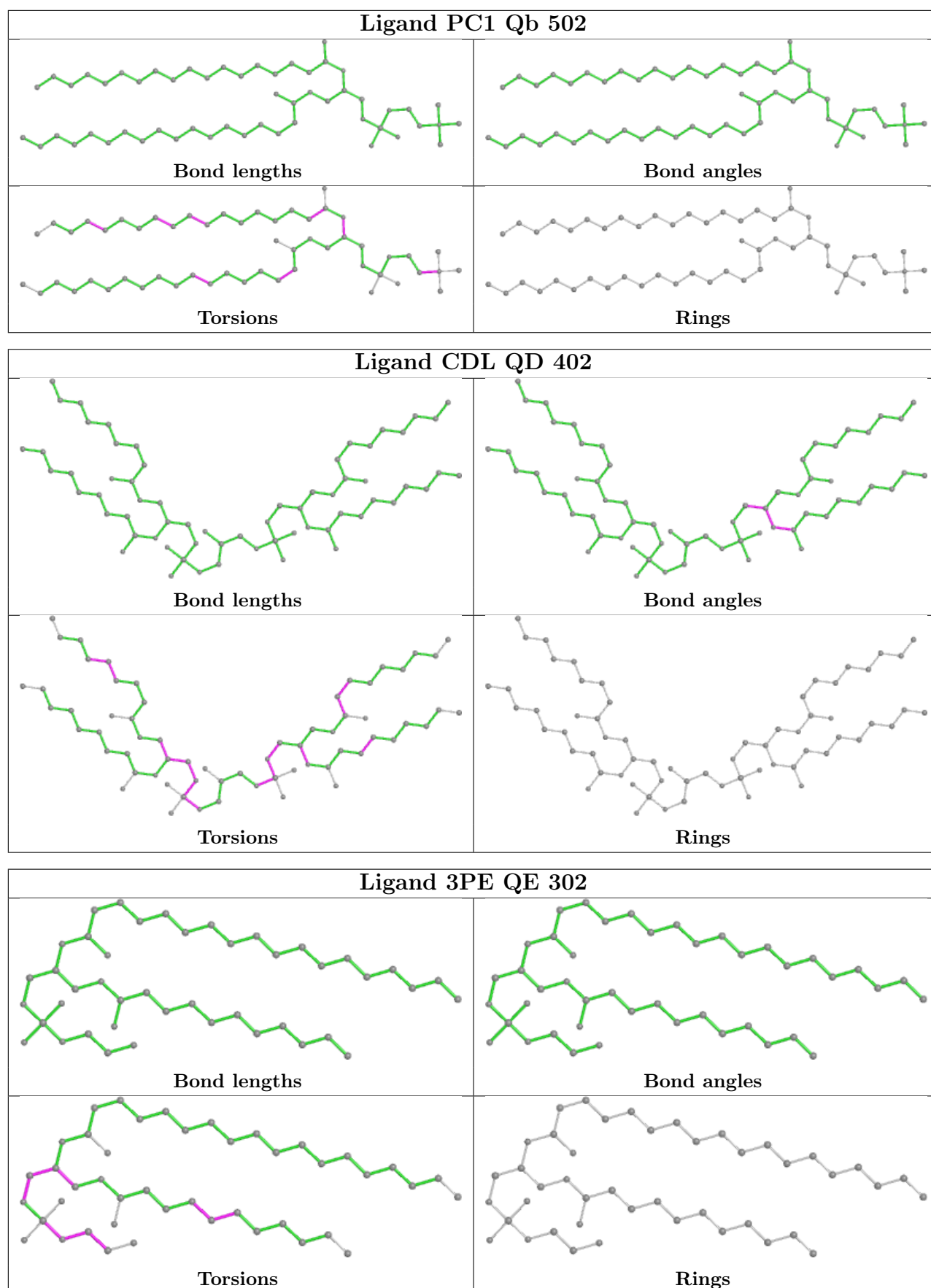


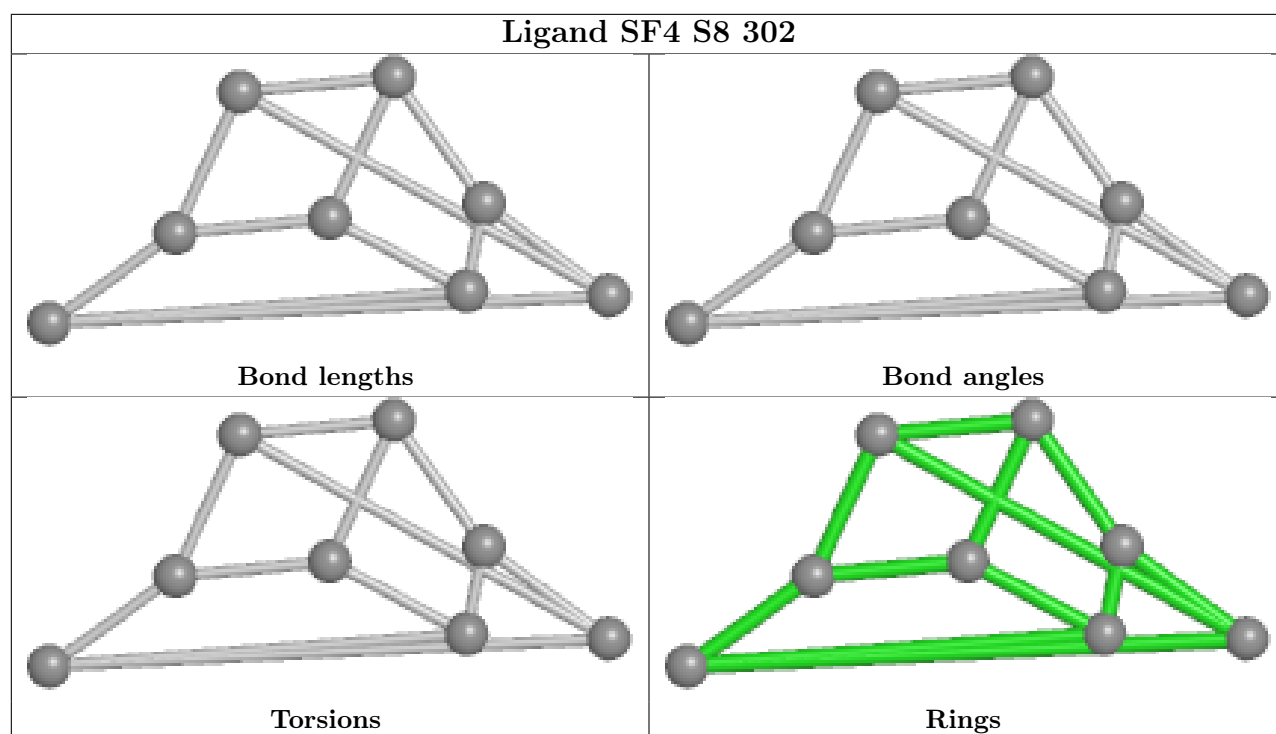


Ligand PLX QI 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PEE N4 501	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PC1 C1 607	
	
Bond lengths	Bond angles
	
Torsions	Rings





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

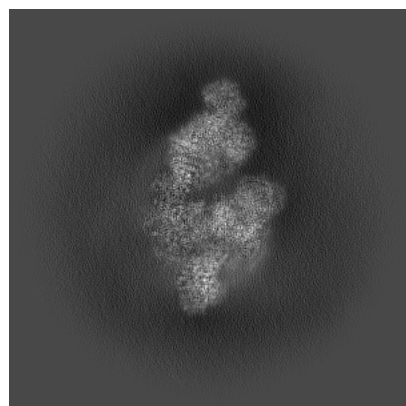
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60329. These allow visual inspection of the internal detail of the map and identification of artifacts.

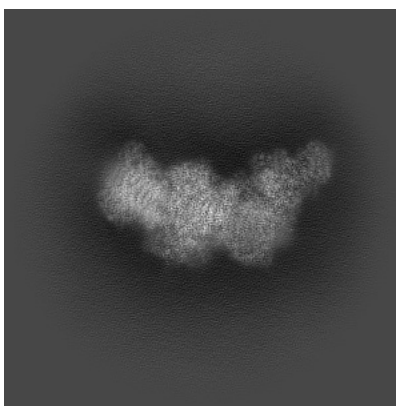
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

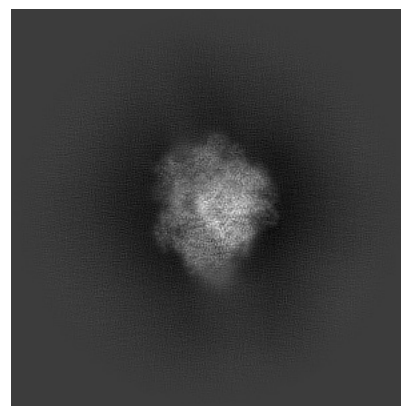
6.1.1 Primary map



X

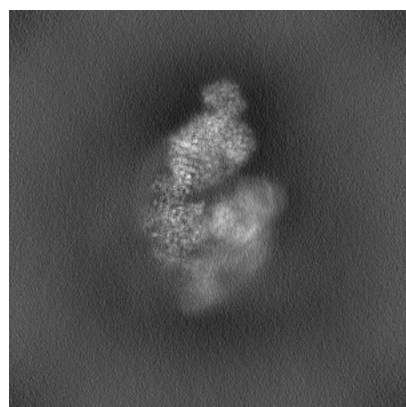


Y

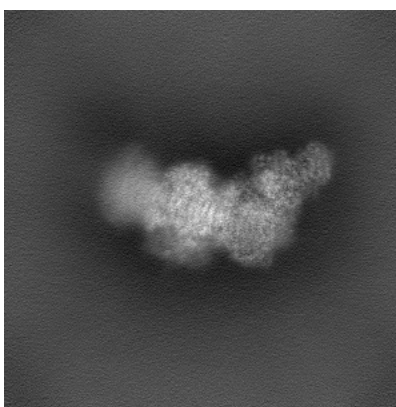


Z

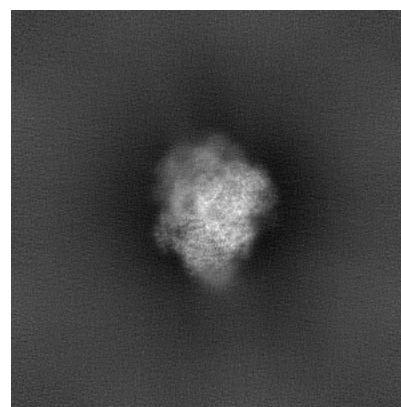
6.1.2 Raw map



X



Y

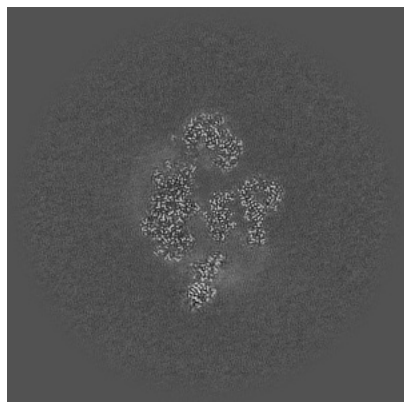


Z

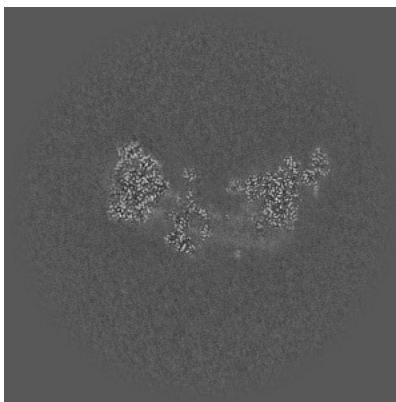
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

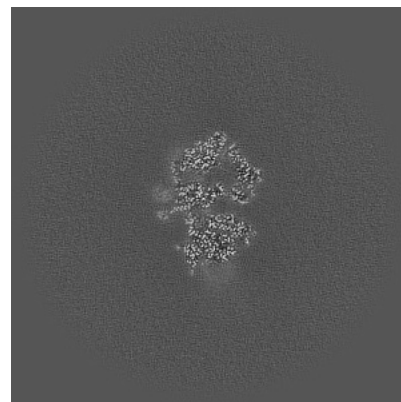
6.2.1 Primary map



X Index: 240

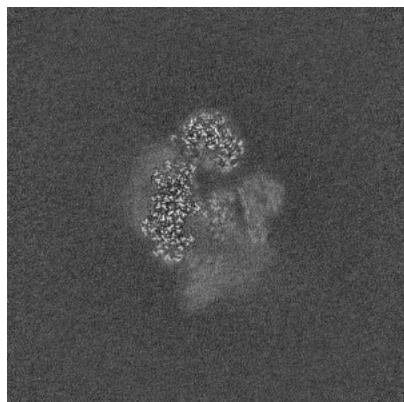


Y Index: 240

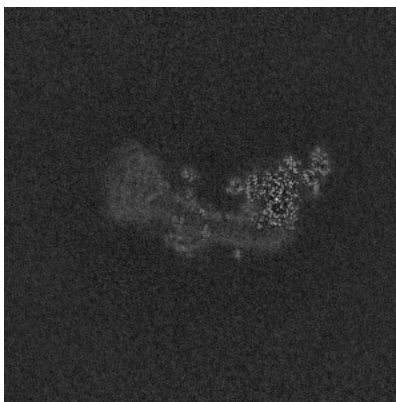


Z Index: 240

6.2.2 Raw map



X Index: 240



Y Index: 240

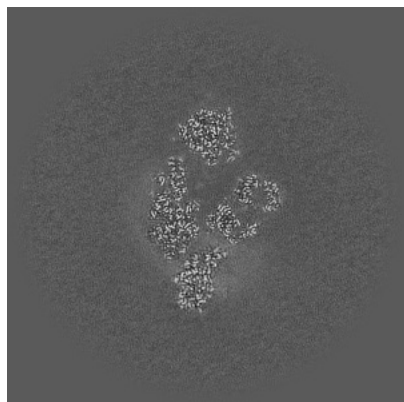


Z Index: 240

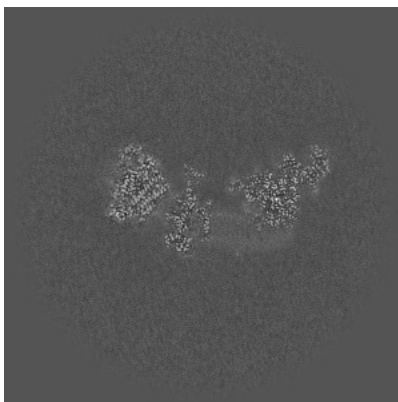
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

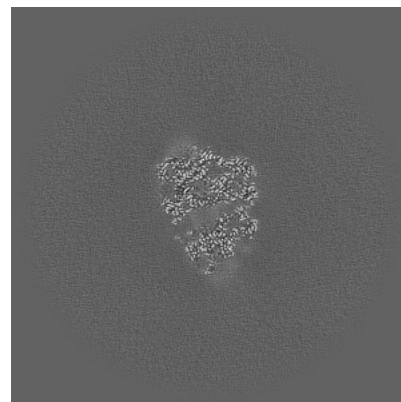
6.3.1 Primary map



X Index: 252

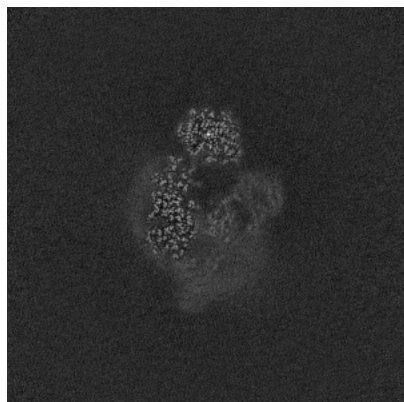


Y Index: 242

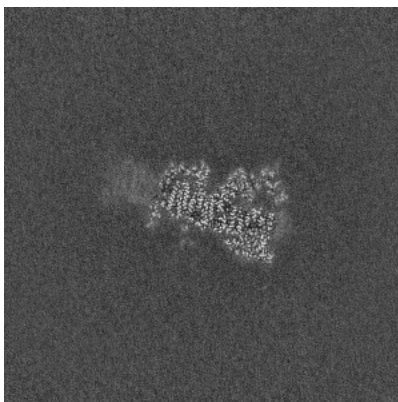


Z Index: 217

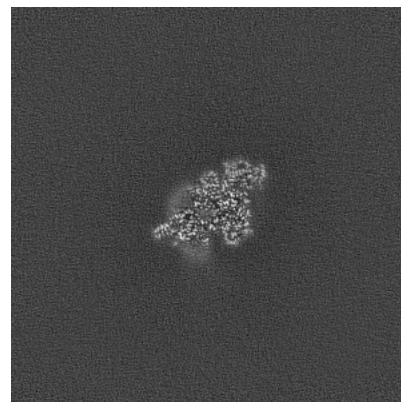
6.3.2 Raw map



X Index: 248



Y Index: 206

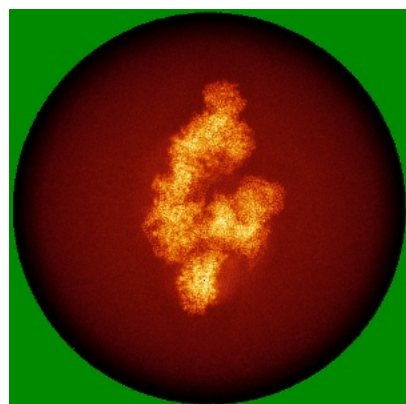


Z Index: 317

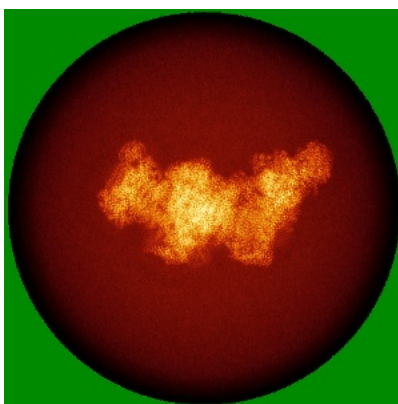
The images above show the largest variance slices of the map in three orthogonal directions.

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

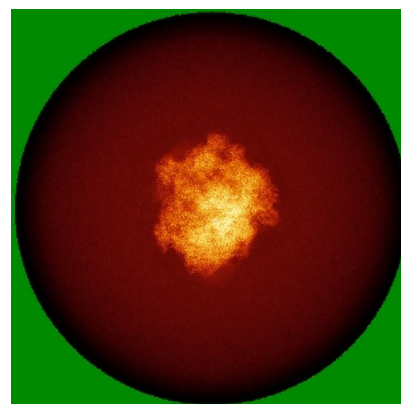
6.4.1 Primary map



X

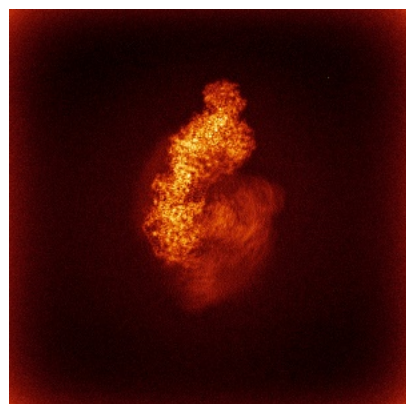


Y

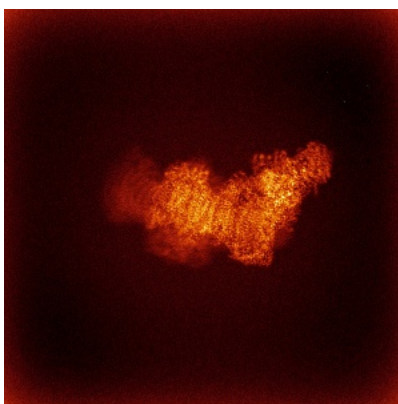


Z

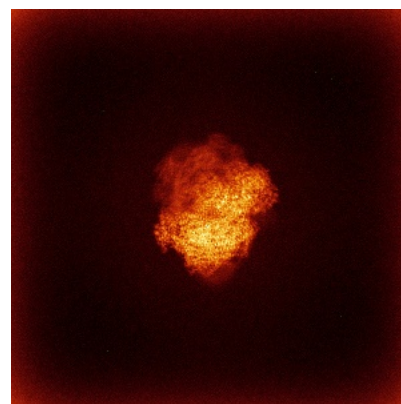
6.4.2 Raw map



X



Y

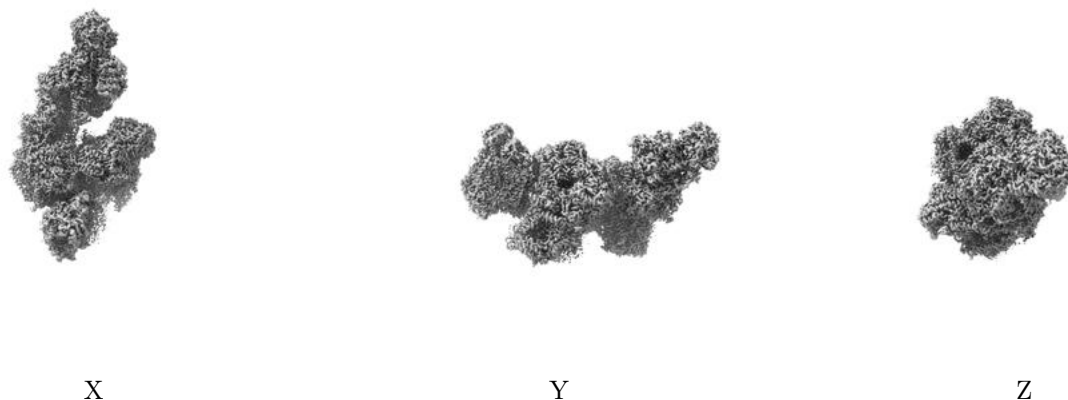


Z

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

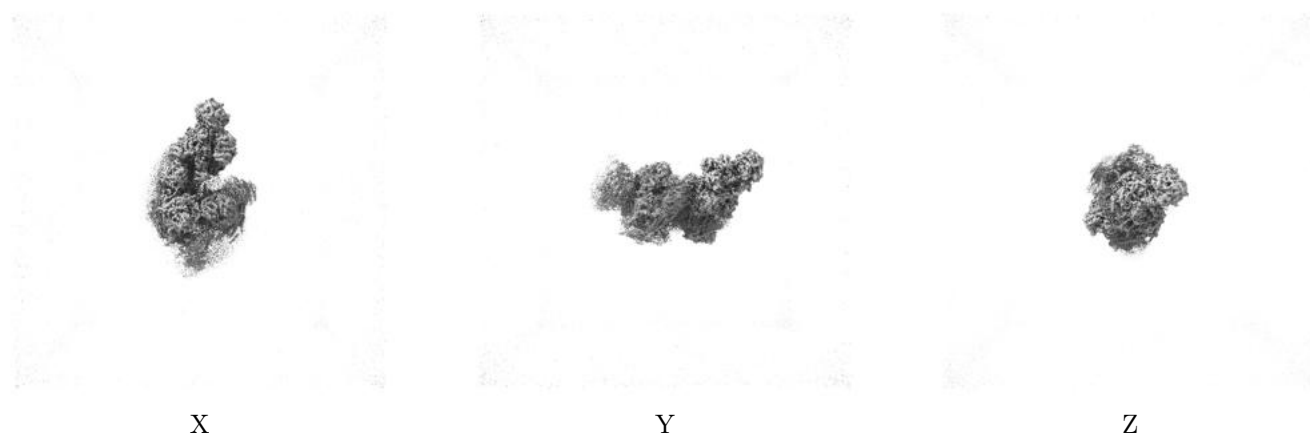
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 6.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

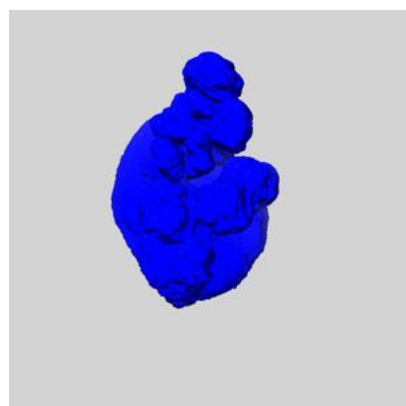
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

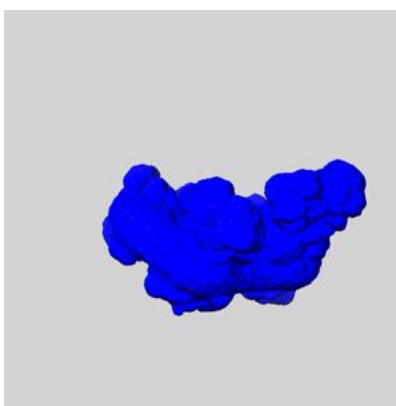
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

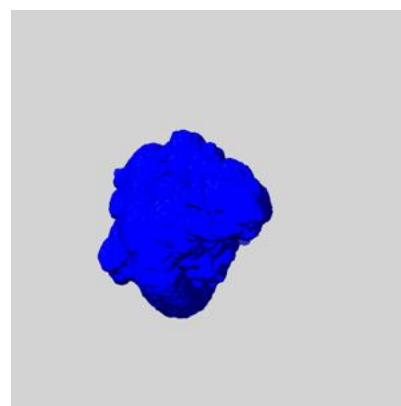
6.6.1 emd_60329_msk_1.map [i](#)



X



Y

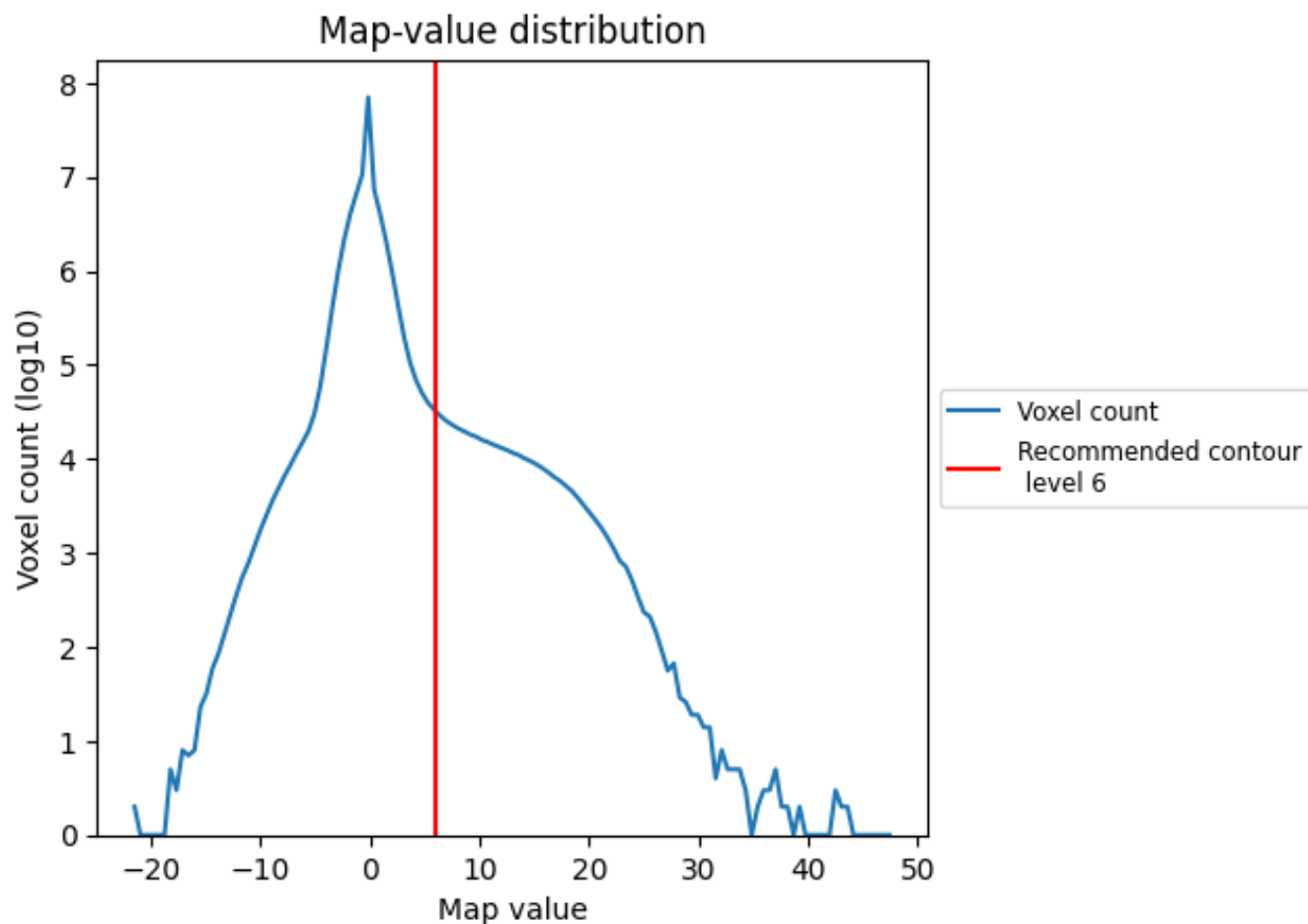


Z

7 Map analysis [i](#)

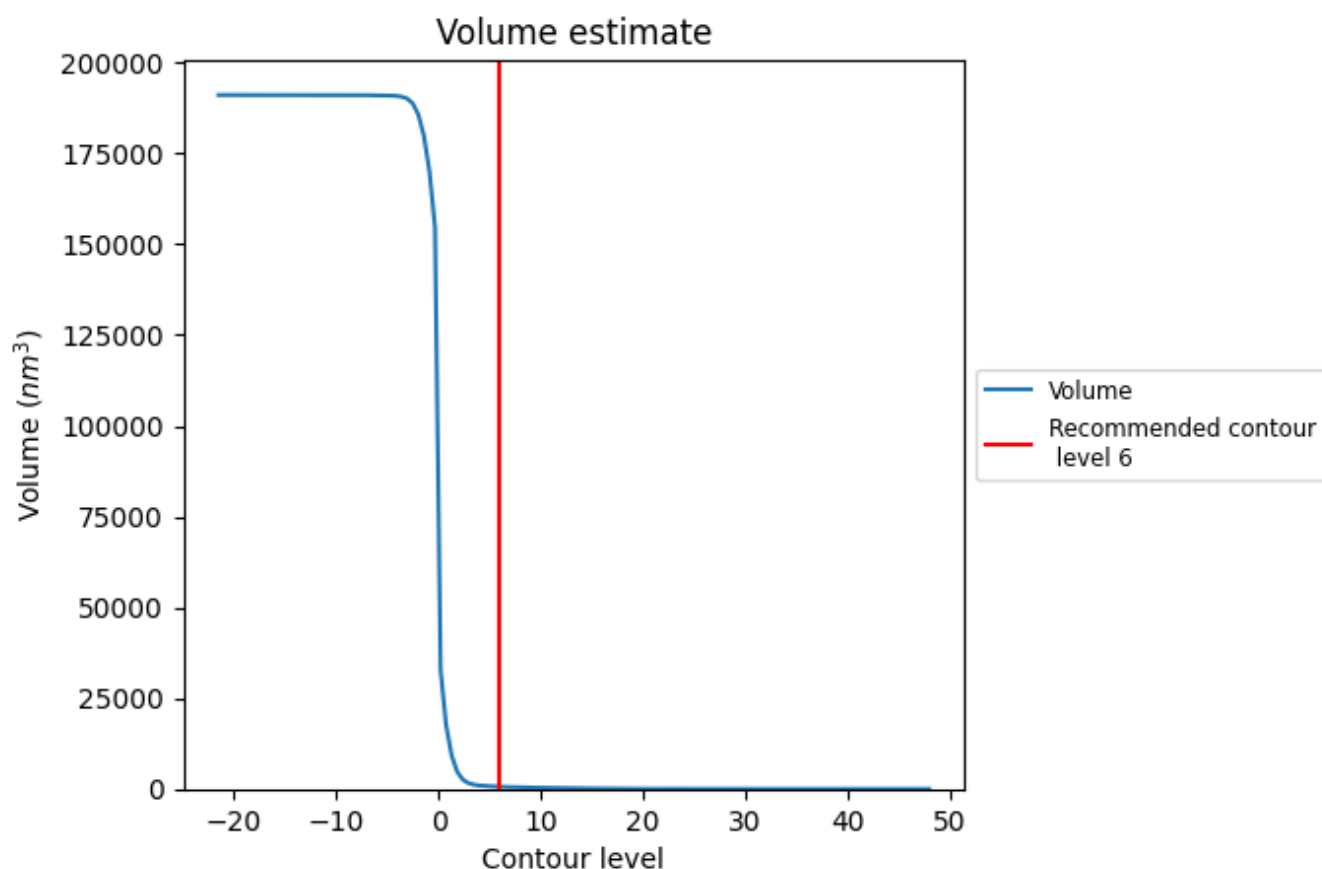
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

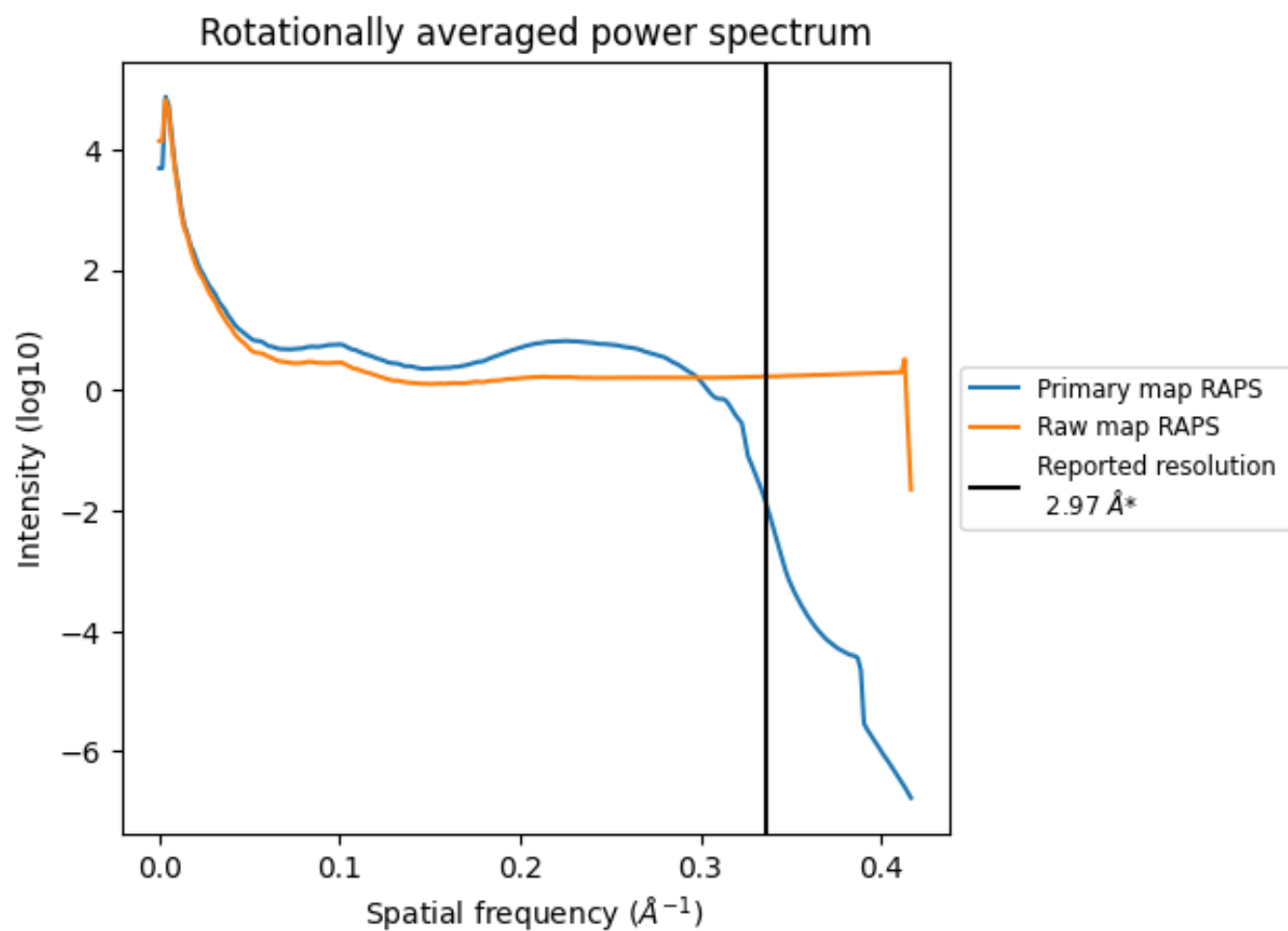
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 620 nm^3 ; this corresponds to an approximate mass of 560 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

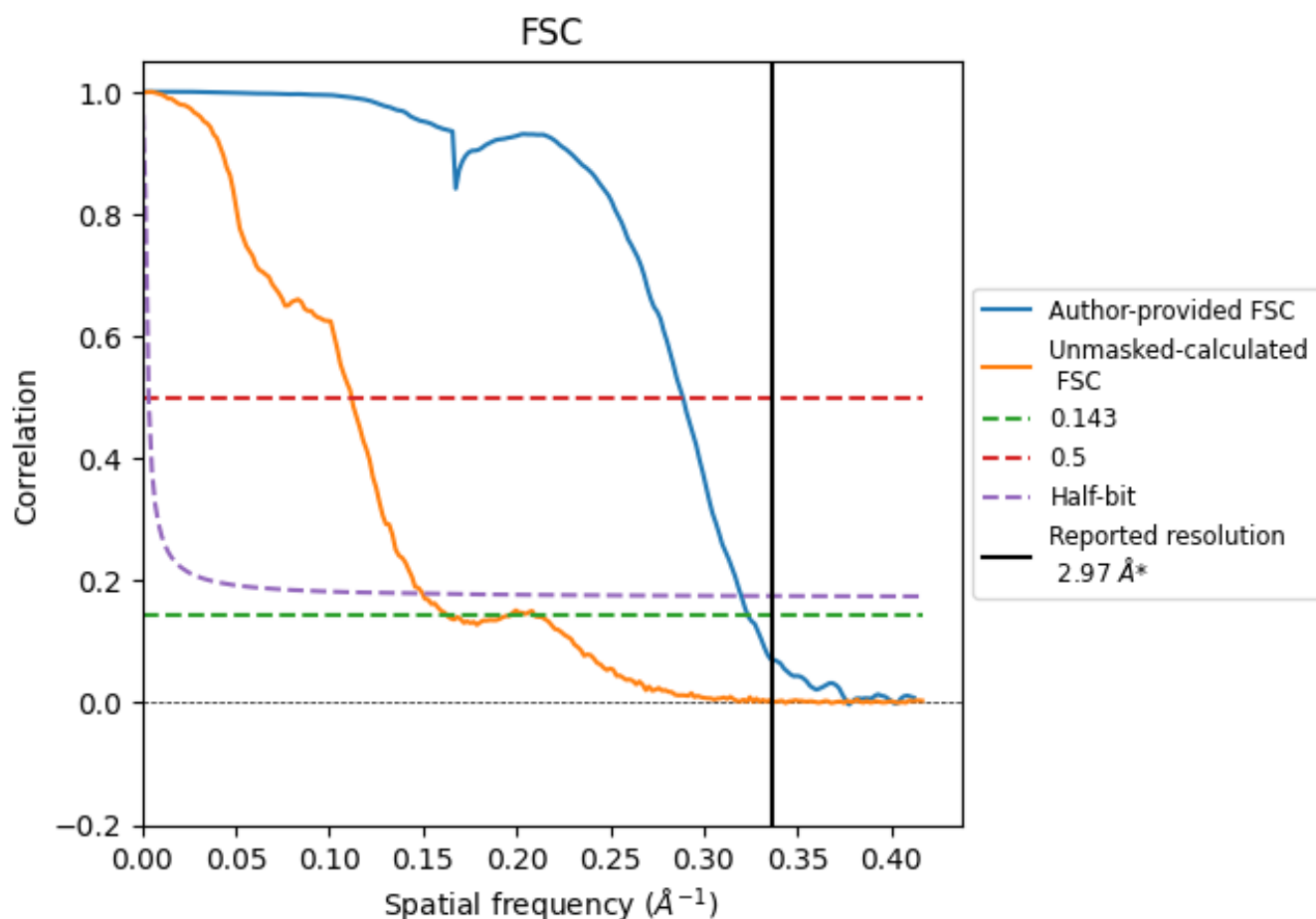


*Reported resolution corresponds to spatial frequency of 0.337 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.337 Å⁻¹

8.2 Resolution estimates [i](#)

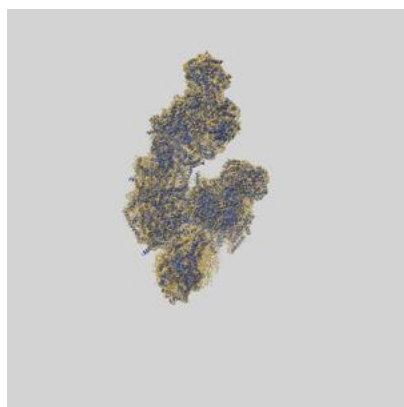
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.97	-	-
Author-provided FSC curve	3.09	3.46	3.12
Unmasked-calculated*	6.14	8.94	6.68

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.14 differs from the reported value 2.97 by more than 10 %

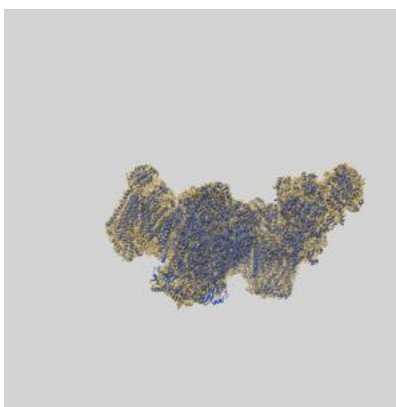
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60329 and PDB model 8ZP8. Per-residue inclusion information can be found in section [3](#) on page [30](#).

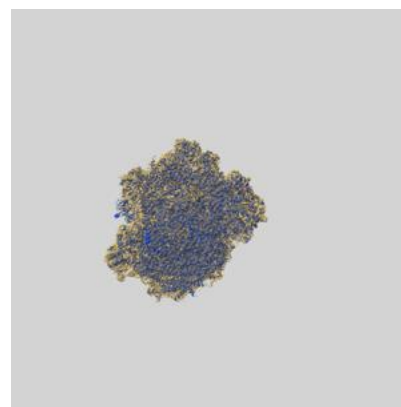
9.1 Map-model overlay [i](#)



X



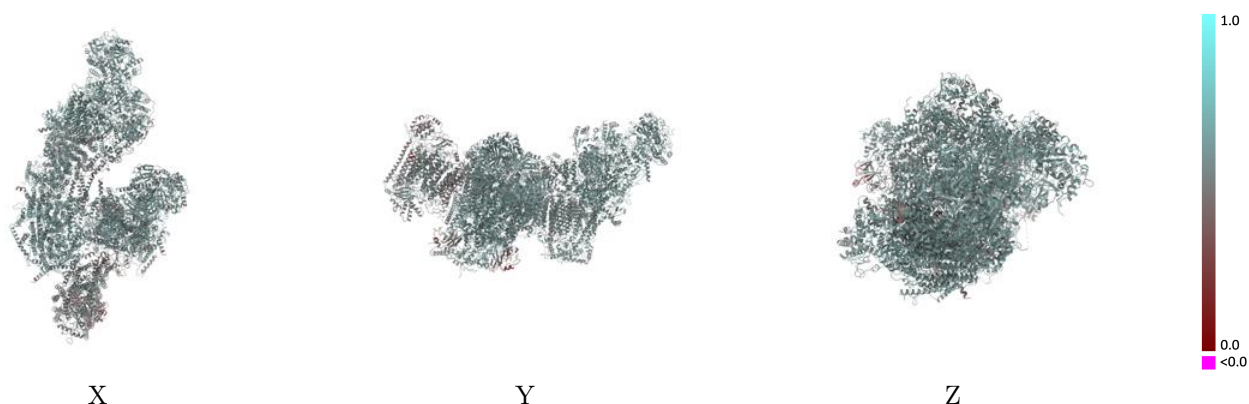
Y



Z

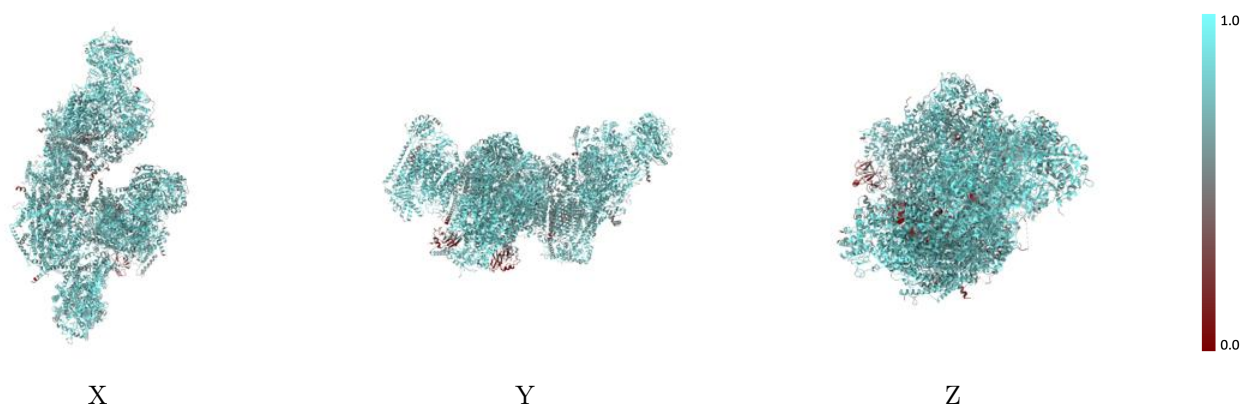
The images above show the 3D surface view of the map at the recommended contour level 6.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



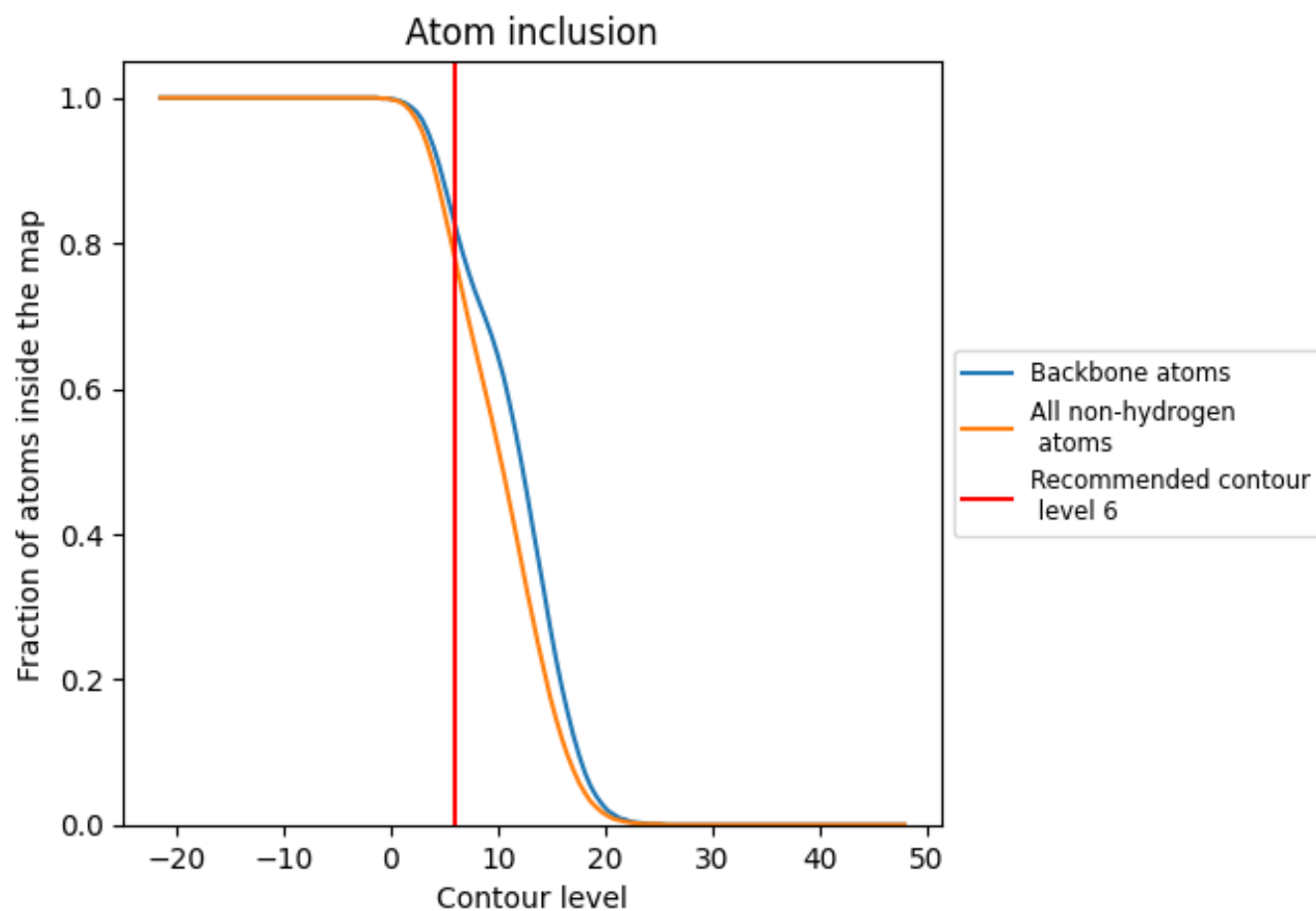
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (6).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7800	 0.5560
4L	 0.7630	 0.5730
5A	 0.7340	 0.4440
5B	 0.7710	 0.4480
6A	 0.7530	 0.4640
6B	 0.8310	 0.4680
6C	 0.7150	 0.4600
7A	 0.7400	 0.4690
7B	 0.6710	 0.4820
7C	 0.8280	 0.5000
8B	 0.7910	 0.5020
A1	 0.7330	 0.5610
A2	 0.7170	 0.5510
A3	 0.7810	 0.5650
A5	 0.7590	 0.5610
A6	 0.7540	 0.5650
A7	 0.6940	 0.5620
A8	 0.8060	 0.5690
A9	 0.7610	 0.5610
AB	 0.5630	 0.4900
AC	 0.7940	 0.5810
AK	 0.7530	 0.5440
AL	 0.6600	 0.5510
AM	 0.6660	 0.5550
AN	 0.8130	 0.5670
B1	 0.6940	 0.5520
B2	 0.7730	 0.5750
B3	 0.7280	 0.5510
B4	 0.7100	 0.5760
B5	 0.8200	 0.5920
B6	 0.7230	 0.5550
B7	 0.7230	 0.5670
B8	 0.7960	 0.5840
B9	 0.8250	 0.5870
BK	 0.7740	 0.5750









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Chain	Atom inclusion	Q-score
BL	 0.7890	 0.5740
C1	 0.8580	 0.5230
C2	 0.7970	 0.5000
C3	 0.8360	 0.4970
C4	 0.7730	 0.4690
CA	 0.7300	 0.5600
CB	 0.8320	 0.5810
N1	 0.7940	 0.5660
N2	 0.8340	 0.5810
N3	 0.6970	 0.5550
N4	 0.8460	 0.5890
N5	 0.8270	 0.5880
N6	 0.6690	 0.5170
QA	 0.7980	 0.5610
QB	 0.7930	 0.5660
QC	 0.8440	 0.5760
QD	 0.8150	 0.5700
QE	 0.4380	 0.4700
QF	 0.6430	 0.5010
QG	 0.7910	 0.5610
QH	 0.7390	 0.5530
QI	 0.7510	 0.5580
QJ	 0.6390	 0.5230
QK	 0.5660	 0.5290
Qa	 0.7680	 0.5620
Qb	 0.7930	 0.5680
Qc	 0.8230	 0.5730
Qd	 0.8100	 0.5720
Qe	 0.3750	 0.4230
Qf	 0.6360	 0.5190
Qg	 0.7920	 0.5650
Qh	 0.7590	 0.5640
Qi	 0.8090	 0.5720
Qj	 0.7770	 0.5460
S1	 0.8170	 0.5720
S2	 0.8350	 0.5810
S3	 0.8720	 0.5980
S4	 0.8050	 0.5840
S5	 0.7710	 0.5660
S6	 0.7700	 0.5740
S7	 0.8500	 0.5820
S8	 0.8970	 0.5910

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Chain	Atom inclusion	Q-score
V1	 0.8000	 0.5630
V2	 0.7540	 0.5580
V3	 0.7440	 0.5670