



wwPDB EM Validation Summary Report ⓘ

Dec 29, 2024 – 09:12 PM EST

PDB ID : 7W5Z
EMDB ID : EMD-32325
Title : Cryo-EM structure of Tetrahymena thermophila mitochondrial complex IV, composite dimer model
Authors : Zhou, L.; Maldonado, M.; Padavannil, A.; Letts, J.
Deposited on : 2021-11-30
Resolution : 3.02 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:

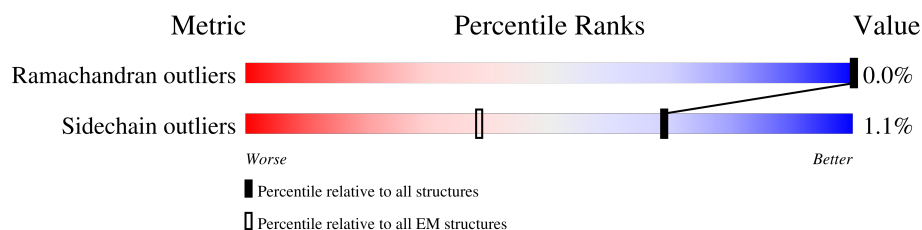
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

1 Overall quality at a glance

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

The reported resolution of this entry is 3.02 Å.

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




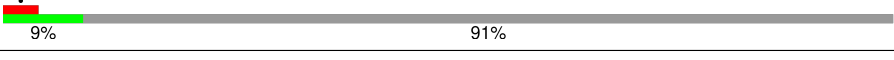
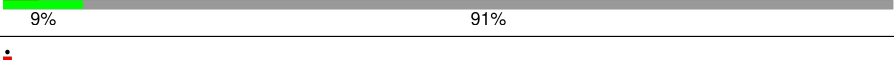
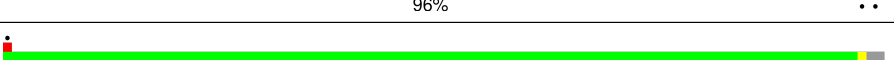
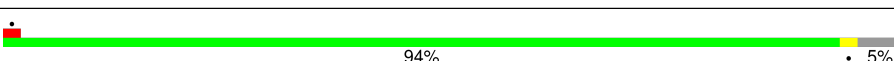
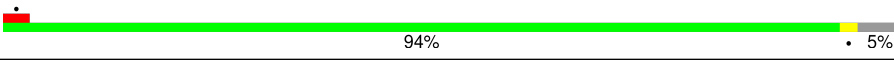
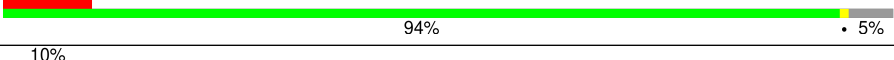
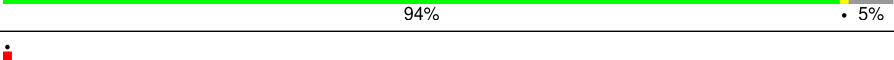
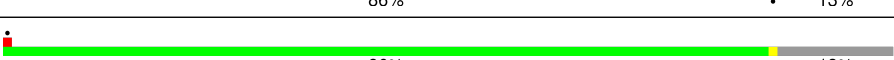
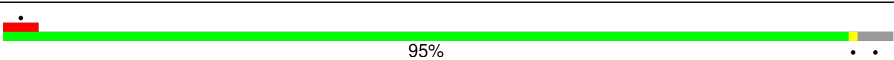
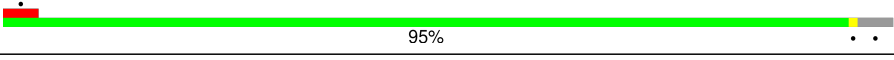
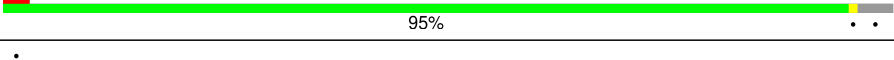
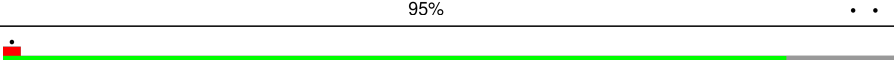
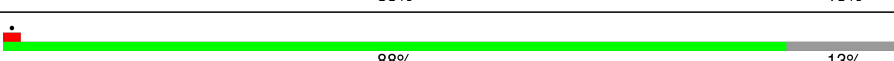
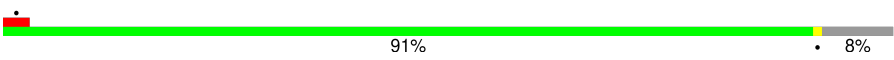
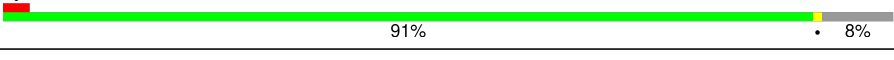
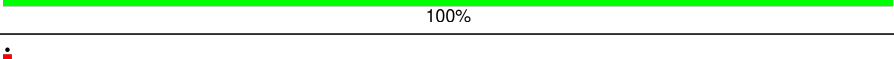
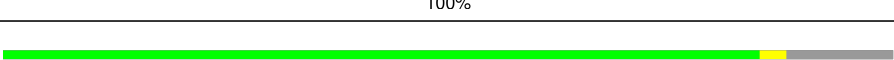






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	U1	98	100%
1	u1	98	100%
2	U2	3634	97%
2	u2	3634	97%
3	U3	34	85% 100%
3	u3	34	91% 100%
4	U4	30	93% 100%
4	u4	30	100%
5	U5	172	11% 19% 81%

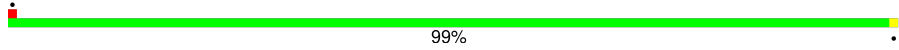
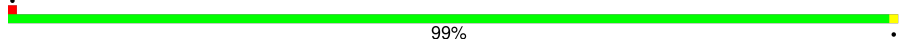
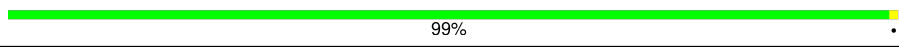
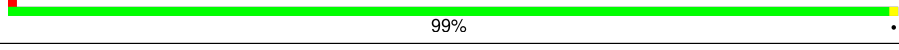
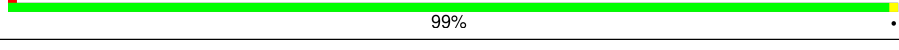
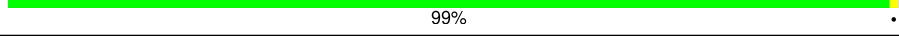
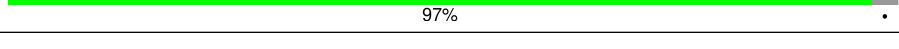
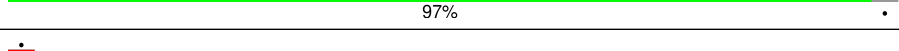
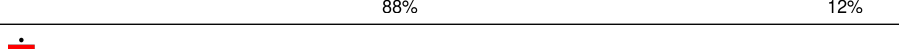
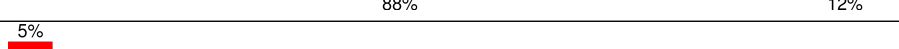
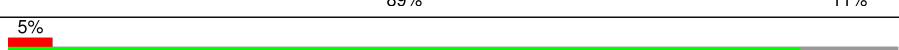

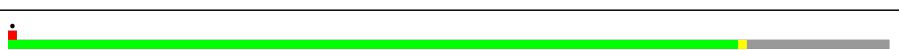

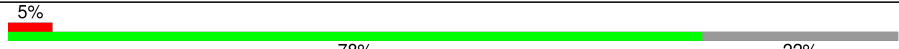
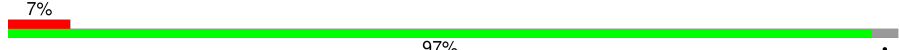



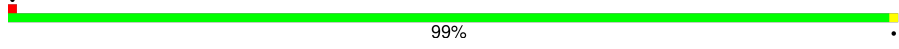
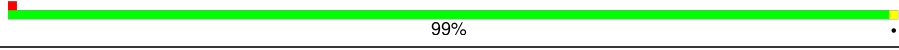
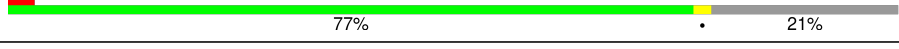



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Mol	Chain	Length	Quality of chain
5	u5	172	
6	U6	478	
6	u6	478	
7	C1	688	
7	c1	688	
8	C2	604	
8	c2	604	
9	C3	594	
9	c3	594	
10	5B	637	
10	5b	637	
11	6A	130	
11	6a	130	
12	6B	230	
12	6b	230	
13	6L	88	
13	6l	88	
14	6C	103	
14	6c	103	
15	7A	133	
15	7a	133	
16	7C	236	
16	7c	236	
17	7L	990	
17	7l	990	


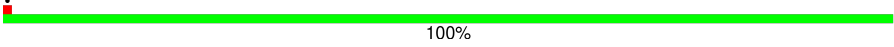
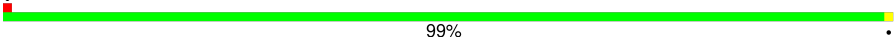
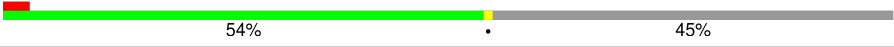
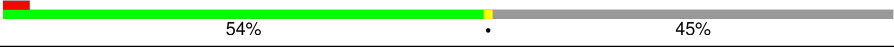
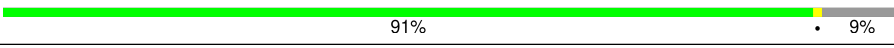
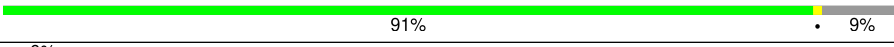
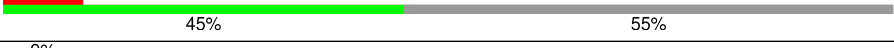

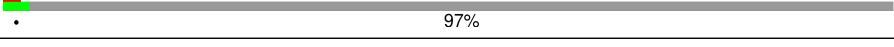
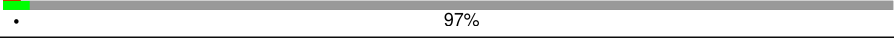

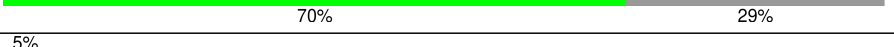
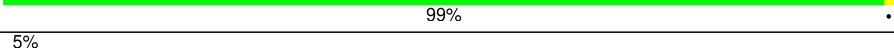
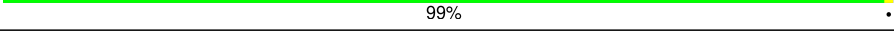
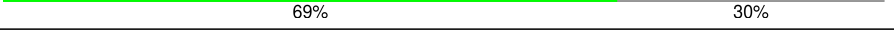
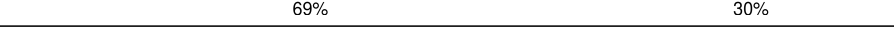

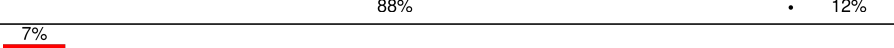
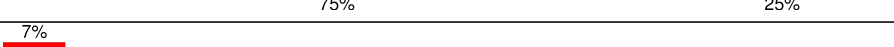
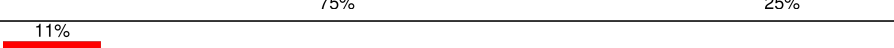




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Mol	Chain	Length	Quality of chain
18	M1	346	
18	m1	346	
19	M2	318	
19	m2	318	
20	M3	330	
20	m3	330	
21	T1	72	
21	t1	72	
22	T2	72	
22	t2	72	
23	T3	93	
23	t3	93	
24	T4	68	
24	t4	68	
25	T5	81	
25	t5	81	
26	T6	72	
26	t6	72	
27	BP	380	
27	bp	380	
28	FS	188	
28	fs	188	
29	AC	127	
29	ac	127	
30	Y7	453	







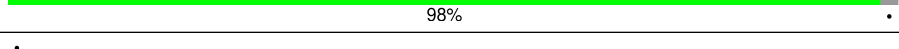
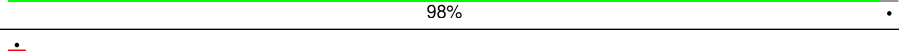
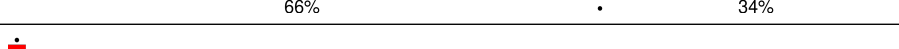
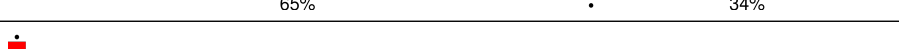
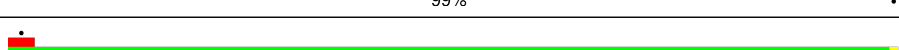
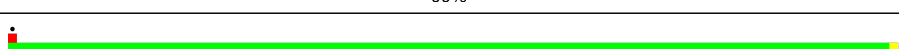
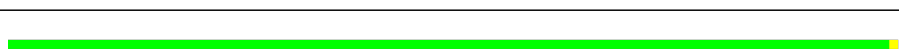
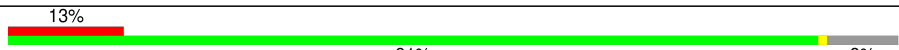
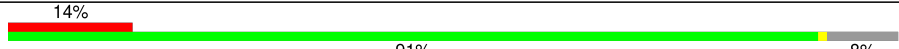


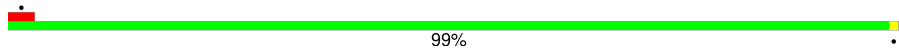
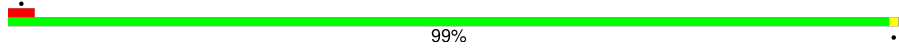
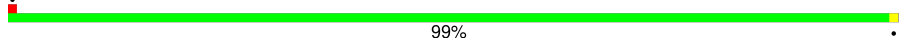
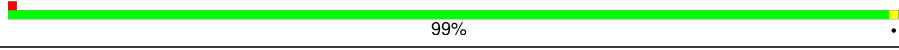
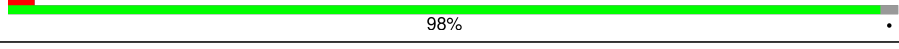
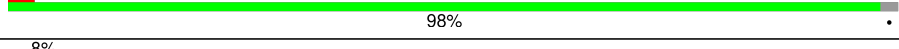


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Mol	Chain	Length	Quality of chain
30	y7	453	
31	Y0	89	
31	y0	89	
32	Y5	190	
32	y5	190	
33	A	490	
33	a	490	
34	B	473	
34	b	473	
35	C	1471	
35	c	1471	
36	D	402	
36	d	402	
37	E	385	
37	e	385	
38	F	348	
38	f	348	
39	G	318	
39	g	318	
40	H	318	
40	h	318	
41	I	252	
41	i	252	
42	J	234	
42	j	234	

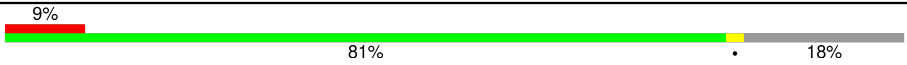
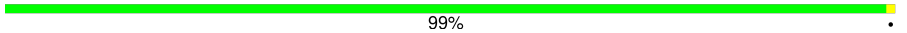
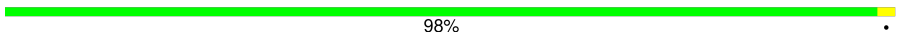
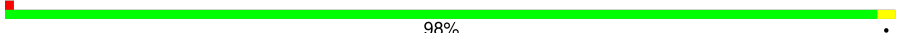
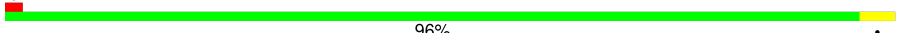


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Mol	Chain	Length	Quality of chain
43	K	231	
43	k	231	
44	L	222	
44	l	222	
45	M	220	
45	m	220	
46	N	210	
46	n	210	
47	O	193	
47	o	193	
48	P	175	
48	p	175	
49	Q	173	
49	q	173	
50	R	173	
50	r	173	
51	S	170	
51	s	170	
52	T	158	
52	t	158	
53	U	154	
53	u	154	
54	V	149	
54	v	149	
55	W	124	

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Mol	Chain	Length	Quality of chain
55	w	124	
56	X	122	
56	x	122	
57	Y	105	
57	y	105	
58	Z	90	
58	z	90	

2 Entry composition

There are 65 unique types of molecules in this entry. The entry contains 190448 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 Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	U1	98	Total	C	N	O	0	0
			490	294	98	98		
1	u1	98	Total	C	N	O	0	0
			490	294	98	98		

- Molecule 2 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	U2	127	Total	C	N	O	S	0	0
			743	456	139	143	5		
2	u2	127	Total	C	N	O	S	0	0
			743	456	139	143	5		

- Molecule 3 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	U3	34	Total	C	N	O	0	0
			170	102	34	34		
3	u3	34	Total	C	N	O	0	0
			170	102	34	34		

- Molecule 4 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	U4	30	Total	C	N	O	0	0
			150	90	30	30		
4	u4	30	Total	C	N	O	0	0
			150	90	30	30		

- Molecule 5 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	U5	33	Total	C	N	O	0	0
			242	160	40	42		
5	u5	33	Total	C	N	O	0	0
			242	160	40	42		

- Molecule 6 is a protein called Protein transporter Sec61 alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	U6	42	Total	C	N	O	S	0	0
			275	178	45	50	2		
6	u6	42	Total	C	N	O	S	0	0
			275	178	45	50	2		

- Molecule 7 is a protein called Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C1	672	Total	C	N	O	S	0	0
			5563	3722	908	897	36		
7	c1	672	Total	C	N	O	S	0	0
			5563	3722	908	897	36		

- Molecule 8 is a protein called Cytochrome c oxidase subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C2	576	Total	C	N	O	S	0	0
			4883	3186	841	846	10		
8	c2	576	Total	C	N	O	S	0	0
			4883	3186	841	846	10		

- Molecule 9 is a protein called Ymf68.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C3	563	Total	C	N	O	S	0	0
			4930	3354	763	805	8		
9	c3	563	Total	C	N	O	S	0	0
			4930	3354	763	805	8		

- Molecule 10 is a protein called Cytochrome C oxidase subunit Vb protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	5B	554	Total	C	N	O	P	S	0	0
			4624	2915	778	912	2	17		

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Mol	Chain	Residues	Atoms						AltConf	Trace
10	5b	554	Total	C	N	O	P	S	0	0
			4624	2915	778	912	2	17		

- Molecule 11 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	6A	125	Total	C	N	O	S		0	0
			1074	693	183	196	2			
11	6a	125	Total	C	N	O	S		0	0
			1074	693	183	196	2			

- Molecule 12 is a protein called Cytochrome c oxidase subunit 6B.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	6B	221	Total	C	N	O	S		0	0
			1904	1234	311	346	13			
12	6b	221	Total	C	N	O	S		0	0
			1904	1234	311	346	13			

- Molecule 13 is a protein called Cytochrome c oxidase subunit 6B-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	6L	77	Total	C	N	O	S		0	0
			638	408	108	116	6			
13	6l	77	Total	C	N	O	S		0	0
			638	408	108	116	6			

- Molecule 14 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	6C	95	Total	C	N	O	S		0	0
			841	545	151	143	2			
14	6c	95	Total	C	N	O	S		0	0
			841	545	151	143	2			

- Molecule 15 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	7A	133	Total	C	N	O	S		0	0
			1168	770	197	200	1			
15	7a	133	Total	C	N	O	S		0	0
			1168	770	197	200	1			

- Molecule 16 is a protein called Cytochrome c oxidase subunit 7C.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	7C	207	Total	C	N	O	P	S	0	0
			1789	1139	287	353	2	8		
16	7c	207	Total	C	N	O	P	S	0	0
			1789	1139	287	353	2	8		

- Molecule 17 is a protein called CTF/NF-I domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	7L	130	Total	C	N	O	S	0	0
			1070	693	174	195	8		
17	7l	130	Total	C	N	O	S	0	0
			1070	693	174	195	8		

- Molecule 18 is a protein called Oxoglutarate/malate translocator protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M1	346	Total	C	N	O	S	0	0
			2863	1890	469	491	13		
18	m1	346	Total	C	N	O	S	0	0
			2863	1890	469	491	13		

- Molecule 19 is a protein called 2-oxoglutarate/malate carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M2	318	Total	C	N	O	S	0	0
			2560	1666	440	450	4		
19	m2	318	Total	C	N	O	S	0	0
			2560	1666	440	450	4		

- Molecule 20 is a protein called Carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M3	329	Total	C	N	O	S	0	0
			2620	1700	446	470	4		
20	m3	329	Total	C	N	O	S	0	0
			2620	1700	446	470	4		

- Molecule 21 is a protein called Tim10/DDP family zinc finger protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T1	70	Total	C	N	O	S	0	0
			540	329	98	109	4		
21	t1	70	Total	C	N	O	S	0	0
			540	329	98	109	4		

- Molecule 22 is a protein called Cytochrome c oxidase small TIM subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T2	63	Total	C	N	O	S	0	0
			513	319	90	100	4		
22	t2	63	Total	C	N	O	S	0	0
			513	319	90	100	4		

- Molecule 23 is a protein called Cytochrome c oxidase small TIM subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T3	83	Total	C	N	O	S	0	0
			655	412	109	128	6		
23	t3	83	Total	C	N	O	S	0	0
			655	412	109	128	6		

- Molecule 24 is a protein called Cytochrome c oxidase small TIM subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T4	57	Total	C	N	O	S	0	0
			483	309	80	91	3		
24	t4	57	Total	C	N	O	S	0	0
			483	309	80	91	3		

- Molecule 25 is a protein called Cytochrome c oxidase small TIM subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T5	63	Total	C	N	O	S	0	0
			515	327	90	96	2		
25	t5	63	Total	C	N	O	S	0	0
			515	327	90	96	2		

- Molecule 26 is a protein called Cytochrome c oxidase small TIM subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T6	70	Total	C	N	O	S	0	0
			563	363	90	106	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	t6	70	Total	C	N	O	S	0	0
			563	363	90	106	4		

- Molecule 27 is a protein called Chromosome condensation regulator RCC1 repeat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BP	380	Total	C	N	O	S	0	0
			2916	1856	492	566	2		
27	bp	380	Total	C	N	O	S	0	0
			2916	1856	492	566	2		

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BP	413	GLU	-	expression tag	UNP Q22RF2
BP	414	THR	-	expression tag	UNP Q22RF2
BP	415	GLY	-	expression tag	UNP Q22RF2
BP	416	LYS	-	expression tag	UNP Q22RF2
BP	417	ILE	-	expression tag	UNP Q22RF2
BP	418	TYR	-	expression tag	UNP Q22RF2
BP	419	GLN	-	expression tag	UNP Q22RF2
BP	420	PHE	-	expression tag	UNP Q22RF2
BP	421	ASN	-	expression tag	UNP Q22RF2
BP	422	GLU	-	expression tag	UNP Q22RF2
BP	423	PHE	-	expression tag	UNP Q22RF2
BP	424	VAL	-	expression tag	UNP Q22RF2
BP	425	GLY	-	expression tag	UNP Q22RF2
BP	426	VAL	-	expression tag	UNP Q22RF2
BP	427	SER	-	expression tag	UNP Q22RF2
BP	428	THR	-	expression tag	UNP Q22RF2
BP	429	ASN	-	expression tag	UNP Q22RF2
BP	430	GLU	-	expression tag	UNP Q22RF2
BP	431	VAL	-	expression tag	UNP Q22RF2
BP	432	GLY	-	expression tag	UNP Q22RF2
BP	433	ASN	-	expression tag	UNP Q22RF2
BP	434	ASP	-	expression tag	UNP Q22RF2
BP	435	TYR	-	expression tag	UNP Q22RF2
BP	436	ASN	-	expression tag	UNP Q22RF2
BP	437	VAL	-	expression tag	UNP Q22RF2
BP	438	ALA	-	expression tag	UNP Q22RF2
BP	439	ASP	-	expression tag	UNP Q22RF2
BP	440	SER	-	expression tag	UNP Q22RF2

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Chain	Residue	Modelled	Actual	Comment	Reference
BP	441	LYS	-	expression tag	UNP Q22RF2
BP	442	ALA	-	expression tag	UNP Q22RF2
BP	443	PHE	-	expression tag	UNP Q22RF2
BP	444	GLU	-	expression tag	UNP Q22RF2
BP	445	GLY	-	expression tag	UNP Q22RF2
BP	446	LYS	-	expression tag	UNP Q22RF2
BP	447	VAL	-	expression tag	UNP Q22RF2
BP	448	VAL	-	expression tag	UNP Q22RF2
BP	449	ASP	-	expression tag	UNP Q22RF2
BP	450	LEU	-	expression tag	UNP Q22RF2
BP	451	GLY	-	expression tag	UNP Q22RF2
BP	452	GLY	-	expression tag	UNP Q22RF2
BP	453	SER	-	expression tag	UNP Q22RF2
BP	454	TYR	-	expression tag	UNP Q22RF2
BP	455	GLY	-	expression tag	UNP Q22RF2
BP	456	ILE	-	expression tag	UNP Q22RF2
BP	457	ARG	-	expression tag	UNP Q22RF2
BP	458	PHE	-	expression tag	UNP Q22RF2
BP	459	ALA	-	expression tag	UNP Q22RF2
BP	460	ILE	-	expression tag	UNP Q22RF2
BP	461	VAL	-	expression tag	UNP Q22RF2
BP	462	ASN	-	expression tag	UNP Q22RF2
bp	413	GLU	-	expression tag	UNP Q22RF2
bp	414	THR	-	expression tag	UNP Q22RF2
bp	415	GLY	-	expression tag	UNP Q22RF2
bp	416	LYS	-	expression tag	UNP Q22RF2
bp	417	ILE	-	expression tag	UNP Q22RF2
bp	418	TYR	-	expression tag	UNP Q22RF2
bp	419	GLN	-	expression tag	UNP Q22RF2
bp	420	PHE	-	expression tag	UNP Q22RF2
bp	421	ASN	-	expression tag	UNP Q22RF2
bp	422	GLU	-	expression tag	UNP Q22RF2
bp	423	PHE	-	expression tag	UNP Q22RF2
bp	424	VAL	-	expression tag	UNP Q22RF2
bp	425	GLY	-	expression tag	UNP Q22RF2
bp	426	VAL	-	expression tag	UNP Q22RF2
bp	427	SER	-	expression tag	UNP Q22RF2
bp	428	THR	-	expression tag	UNP Q22RF2
bp	429	ASN	-	expression tag	UNP Q22RF2
bp	430	GLU	-	expression tag	UNP Q22RF2
bp	431	VAL	-	expression tag	UNP Q22RF2
bp	432	GLY	-	expression tag	UNP Q22RF2

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Chain	Residue	Modelled	Actual	Comment	Reference
bp	433	ASN	-	expression tag	UNP Q22RF2
bp	434	ASP	-	expression tag	UNP Q22RF2
bp	435	TYR	-	expression tag	UNP Q22RF2
bp	436	ASN	-	expression tag	UNP Q22RF2
bp	437	VAL	-	expression tag	UNP Q22RF2
bp	438	ALA	-	expression tag	UNP Q22RF2
bp	439	ASP	-	expression tag	UNP Q22RF2
bp	440	SER	-	expression tag	UNP Q22RF2
bp	441	LYS	-	expression tag	UNP Q22RF2
bp	442	ALA	-	expression tag	UNP Q22RF2
bp	443	PHE	-	expression tag	UNP Q22RF2
bp	444	GLU	-	expression tag	UNP Q22RF2
bp	445	GLY	-	expression tag	UNP Q22RF2
bp	446	LYS	-	expression tag	UNP Q22RF2
bp	447	VAL	-	expression tag	UNP Q22RF2
bp	448	VAL	-	expression tag	UNP Q22RF2
bp	449	ASP	-	expression tag	UNP Q22RF2
bp	450	LEU	-	expression tag	UNP Q22RF2
bp	451	GLY	-	expression tag	UNP Q22RF2
bp	452	GLY	-	expression tag	UNP Q22RF2
bp	453	SER	-	expression tag	UNP Q22RF2
bp	454	TYR	-	expression tag	UNP Q22RF2
bp	455	GLY	-	expression tag	UNP Q22RF2
bp	456	ILE	-	expression tag	UNP Q22RF2
bp	457	ARG	-	expression tag	UNP Q22RF2
bp	458	PHE	-	expression tag	UNP Q22RF2
bp	459	ALA	-	expression tag	UNP Q22RF2
bp	460	ILE	-	expression tag	UNP Q22RF2
bp	461	VAL	-	expression tag	UNP Q22RF2
bp	462	ASN	-	expression tag	UNP Q22RF2

- Molecule 28 is a protein called Iron-binding zinc finger CDGSH type protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	FS	188	Total	C	N	O	S	0	0
			1509	978	260	257	14		
28	fs	188	Total	C	N	O	S	0	0
			1509	978	260	257	14		

- Molecule 29 is a protein called Cytochrome c oxidase acyl carrier-like subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AC	100	Total	C	N	O	S	0	0
			816	519	144	151	2		
29	ac	100	Total	C	N	O	S	0	0
			816	519	144	151	2		

- Molecule 30 is a protein called Ymf67.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y7	338	Total	C	N	O	S	0	0
			2895	1936	459	494	6		
30	y7	338	Total	C	N	O	S	0	0
			2895	1936	459	494	6		

- Molecule 31 is a protein called Ymf70.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y0	89	Total	C	N	O	S	0	0
			777	536	115	124	2		
31	y0	89	Total	C	N	O	S	0	0
			777	536	115	124	2		

- Molecule 32 is a protein called Ymf75.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y5	104	Total	C	N	O		0	0
			924	638	140	146			
32	y5	104	Total	C	N	O		0	0
			924	638	140	146			

- Molecule 33 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	A	448	Total	C	N	O	S	0	0
			3746	2402	635	700	9		
33	a	448	Total	C	N	O	S	0	0
			3746	2402	635	700	9		

- Molecule 34 is a protein called Protein phosphatase 2C, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B	214	Total	C	N	O	S	0	0
			1682	1087	287	307	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	214	Total	C	N	O	S	0	0
			1682	1087	287	307	1		

- Molecule 35 is a protein called Cyclic nucleotide-binding domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	C	46	Total	C	N	O	S	0	0
			383	261	60	60	2		
35	c	46	Total	C	N	O	S	0	0
			383	261	60	60	2		

- Molecule 36 is a protein called SURF1-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	D	284	Total	C	N	O	S	0	0
			2331	1504	395	427	5		
36	d	284	Total	C	N	O	S	0	0
			2331	1504	395	427	5		

- Molecule 37 is a protein called TraB family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	E	384	Total	C	N	O	S	0	0
			3178	2046	549	576	7		
37	e	384	Total	C	N	O	S	0	0
			3178	2046	549	576	7		

- Molecule 38 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	F	242	Total	C	N	O	S	0	0
			2014	1298	332	379	5		
38	f	242	Total	C	N	O	S	0	0
			2014	1298	332	379	5		

- Molecule 39 is a protein called Cytochrome c oxidase subunit TT7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	G	281	Total	C	N	O	S	0	0
			2364	1510	395	447	12		
39	g	281	Total	C	N	O	S	0	0
			2364	1510	395	447	12		

- Molecule 40 is a protein called SURF1-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	H	239	Total	C	N	O	S	0	0
			1915	1204	330	372	9		
40	h	239	Total	C	N	O	S	0	0
			1915	1204	330	372	9		

- Molecule 41 is a protein called Cytochrome c oxidase subunit TT9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	I	101	Total	C	N	O		0	0
			852	538	150	164			
41	i	101	Total	C	N	O		0	0
			852	538	150	164			

- Molecule 42 is a protein called Cytochrome c oxidase subunit TT10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	J	187	Total	C	N	O	S	0	0
			1575	1024	276	274	1		
42	j	187	Total	C	N	O	S	0	0
			1575	1024	276	274	1		

- Molecule 43 is a protein called Cytochrome c oxidase subunit TT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	K	208	Total	C	N	O	S	0	0
			1714	1090	302	319	3		
43	k	208	Total	C	N	O	S	0	0
			1714	1090	302	319	3		

- Molecule 44 is a protein called Cytochrome c oxidase subunit TT12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	L	194	Total	C	N	O	S	0	0
			1668	1089	284	293	2		
44	l	194	Total	C	N	O	S	0	0
			1668	1089	284	293	2		

- Molecule 45 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	M	183	Total	C	N	O	S	0	0
			1581	1030	264	276	11		
45	m	183	Total	C	N	O	S	0	0
			1581	1030	264	276	11		

- Molecule 46 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	N	206	Total	C	N	O	S	0	0
			1716	1117	286	306	7		
46	n	206	Total	C	N	O	S	0	0
			1716	1117	286	306	7		

- Molecule 47 is a protein called Cytochrome c oxidase subunit TT15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	O	128	Total	C	N	O	S	0	0
			1073	671	189	207	6		
47	o	128	Total	C	N	O	S	0	0
			1073	671	189	207	6		

- Molecule 48 is a protein called Cytochrome c oxidase subunit TT16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	P	175	Total	C	N	O	S	0	0
			1412	890	247	274	1		
48	p	175	Total	C	N	O	S	0	0
			1412	890	247	274	1		

- Molecule 49 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Q	173	Total	C	N	O	S	0	0
			1434	927	243	255	9		
49	q	173	Total	C	N	O	S	0	0
			1434	927	243	255	9		

- Molecule 50 is a protein called Cytochrome c oxidase subunit TT18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	R	159	Total	C	N	O	S	0	0
			1305	854	217	231	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	159	Total	C	N	O	S	0	0
			1305	854	217	231	3		

- Molecule 51 is a protein called Cytochrome c oxidase subunit TT19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S	143	Total	C	N	O	S	0	0
			1165	732	204	224	5		
51	s	143	Total	C	N	O	S	0	0
			1165	732	204	224	5		

- Molecule 52 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	T	157	Total	C	N	O	S	0	0
			1323	864	231	224	4		
52	t	157	Total	C	N	O	S	0	0
			1323	864	231	224	4		

- Molecule 53 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	U	153	Total	C	N	O	S	0	0
			1304	848	221	230	5		
53	u	153	Total	C	N	O	S	0	0
			1304	848	221	230	5		

- Molecule 54 is a protein called Cytochrome c oxidase subunit TT22.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	V	146	Total	C	N	O	S	0	0
			1234	802	217	213	2		
54	v	146	Total	C	N	O	S	0	0
			1234	802	217	213	2		

- Molecule 55 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	W	102	Total	C	N	O	S	0	0
			902	588	146	164	4		
55	w	102	Total	C	N	O	S	0	0
			902	588	146	164	4		

- Molecule 56 is a protein called Transmembrane protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X	122	Total	C	N	O	S	0	0
			1012	665	171	172	4		
56	x	122	Total	C	N	O	S	0	0
			1012	665	171	172	4		

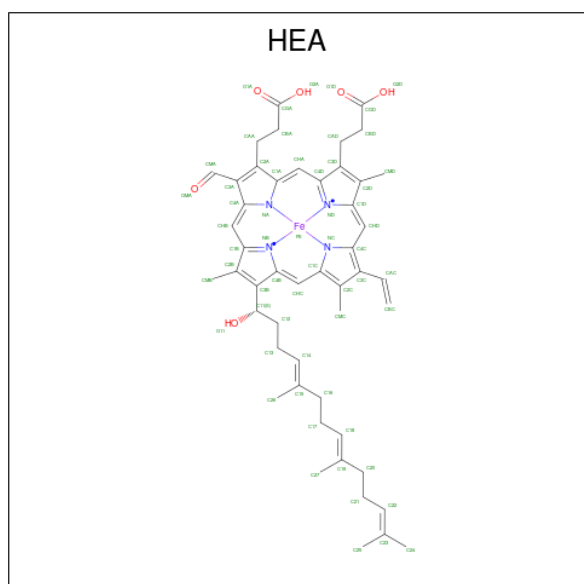
- Molecule 57 is a protein called Cytochrome c oxidase subunit TT25.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Y	105	Total	C	N	O	S	0	0
			859	540	157	153	9		
57	y	105	Total	C	N	O	S	0	0
			859	540	157	153	9		

- Molecule 58 is a protein called Cytochrome c oxidase subunit TT26.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	Z	60	Total	C	N	O	0	0
			479	310	85	84		
58	z	60	Total	C	N	O	0	0
			479	310	85	84		

- Molecule 59 is HEME-A (three-letter code: HEA) (formula: $C_{49}H_{56}FeN_4O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
59	C1	1	Total	C	Fe	N	O	0
			60	49	1	4	6	
59	C1	1	Total	C	Fe	N	O	0
			60	49	1	4	6	
59	c1	1	Total	C	Fe	N	O	0
			60	49	1	4	6	
59	c1	1	Total	C	Fe	N	O	0
			60	49	1	4	6	

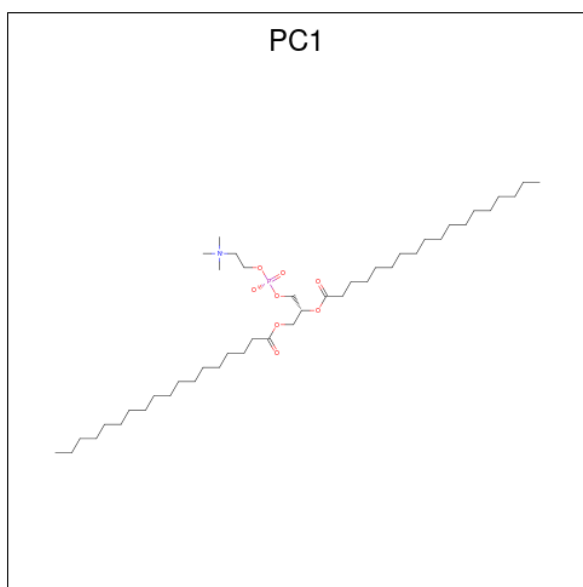
- Molecule 60 is COPPER (II) ION (three-letter code: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
60	C1	1	Total	Cu	0
			1	1	
60	C2	2	Total	Cu	0
			2	2	
60	c1	1	Total	Cu	0
			1	1	
60	c2	2	Total	Cu	0
			2	2	

- Molecule 61 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
61	C1	1	Total	Mg	0
			1	1	
61	c1	1	Total	Mg	0
			1	1	

- Molecule 62 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PC1) (formula: C₄₄H₈₈NO₈P).



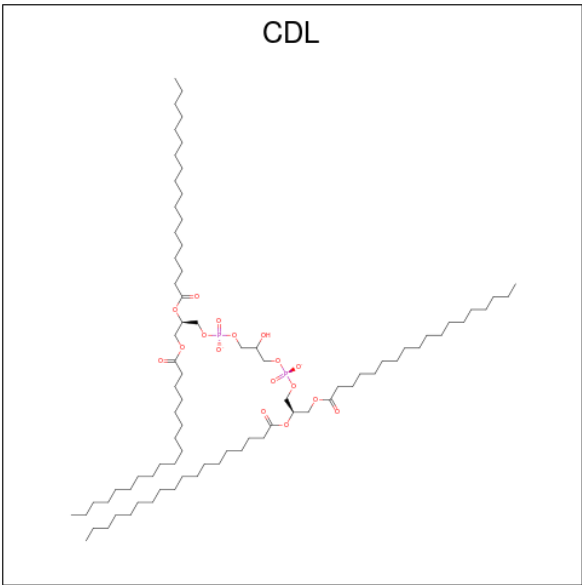
Mol	Chain	Residues	Atoms					AltConf
62	C1	1	Total	C	N	O	P	0
			49	39	1	8	1	
62	C3	1	Total	C	N	O	P	0
			52	42	1	8	1	
62	C3	1	Total	C	N	O	P	0
			39	29	1	8	1	
62	C3	1	Total	C	N	O	P	0
			31	21	1	8	1	
62	C3	1	Total	C	N	O	P	0
			41	31	1	8	1	
62	7C	1	Total	C	N	O	P	0
			54	44	1	8	1	
62	7C	1	Total	C	N	O	P	0
			43	33	1	8	1	
62	M1	1	Total	C	N	O	P	0
			35	25	1	8	1	
62	M2	1	Total	C	N	O	P	0
			32	22	1	8	1	
62	M2	1	Total	C	N	O	P	0
			41	31	1	8	1	
62	M2	1	Total	C	N	O	P	0
			54	44	1	8	1	
62	A	1	Total	C	N	O	P	0
			45	35	1	8	1	
62	A	1	Total	C	N	O	P	0
			41	31	1	8	1	
62	J	1	Total	C	N	O	P	0
			37	27	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
62	N	1	Total	C	N	O	P	0
			32	22	1	8	1	
62	N	1	Total	C	N	O	P	0
			36	26	1	8	1	
62	V	1	Total	C	N	O	P	0
			54	44	1	8	1	
62	c1	1	Total	C	N	O	P	0
			49	39	1	8	1	
62	c3	1	Total	C	N	O	P	0
			52	42	1	8	1	
62	c3	1	Total	C	N	O	P	0
			39	29	1	8	1	
62	c3	1	Total	C	N	O	P	0
			31	21	1	8	1	
62	c3	1	Total	C	N	O	P	0
			41	31	1	8	1	
62	7c	1	Total	C	N	O	P	0
			43	33	1	8	1	
62	m1	1	Total	C	N	O	P	0
			54	44	1	8	1	
62	m1	1	Total	C	N	O	P	0
			35	25	1	8	1	
62	m2	1	Total	C	N	O	P	0
			32	22	1	8	1	
62	m2	1	Total	C	N	O	P	0
			41	31	1	8	1	
62	m2	1	Total	C	N	O	P	0
			54	44	1	8	1	
62	a	1	Total	C	N	O	P	0
			45	35	1	8	1	
62	a	1	Total	C	N	O	P	0
			41	31	1	8	1	
62	j	1	Total	C	N	O	P	0
			37	27	1	8	1	
62	n	1	Total	C	N	O	P	0
			32	22	1	8	1	
62	n	1	Total	C	N	O	P	0
			36	26	1	8	1	
62	v	1	Total	C	N	O	P	0
			54	44	1	8	1	

- Molecule 63 is CARDIOLIPIN (three-letter code: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



Mol	Chain	Residues	Atoms				AltConf
63	C1	1	Total	C	O	P	0
			59	40	17	2	
63	C1	1	Total	C	O	P	0
			65	46	17	2	
63	C3	1	Total	C	O	P	0
			68	49	17	2	
63	5B	1	Total	C	O	P	0
			87	68	17	2	
63	5B	1	Total	C	O	P	0
			62	43	17	2	
63	5B	1	Total	C	O	P	0
			67	48	17	2	
63	7A	1	Total	C	O	P	0
			67	48	17	2	
63	7A	1	Total	C	O	P	0
			100	81	17	2	
63	7C	1	Total	C	O	P	0
			85	66	17	2	
63	7C	1	Total	C	O	P	0
			51	32	17	2	
63	M1	1	Total	C	O	P	0
			95	76	17	2	
63	M1	1	Total	C	O	P	0
			66	47	17	2	
63	M1	1	Total	C	O	P	0
			66	47	17	2	
63	M2	1	Total	C	O	P	0
			54	35	17	2	

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Mol	Chain	Residues	Atoms				AltConf
63	M2	1	Total	C	O	P	0
			66	47	17	2	
63	M2	1	Total	C	O	P	0
			74	55	17	2	
63	M3	1	Total	C	O	P	0
			94	75	17	2	
63	M3	1	Total	C	O	P	0
			51	32	17	2	
63	M3	1	Total	C	O	P	0
			63	44	17	2	
63	Y7	1	Total	C	O	P	0
			65	46	17	2	
63	Y0	1	Total	C	O	P	0
			64	45	17	2	
63	Y5	1	Total	C	O	P	0
			81	62	17	2	
63	A	1	Total	C	O	P	0
			51	32	17	2	
63	B	1	Total	C	O	P	0
			62	43	17	2	
63	E	1	Total	C	O	P	0
			60	41	17	2	
63	E	1	Total	C	O	P	0
			72	53	17	2	
63	F	1	Total	C	O	P	0
			100	81	17	2	
63	J	1	Total	C	O	P	0
			70	51	17	2	
63	L	1	Total	C	O	P	0
			74	55	17	2	
63	N	1	Total	C	O	P	0
			95	76	17	2	
63	T	1	Total	C	O	P	0
			68	49	17	2	
63	T	1	Total	C	O	P	0
			75	56	17	2	
63	U	1	Total	C	O	P	0
			82	63	17	2	
63	V	1	Total	C	O	P	0
			91	72	17	2	
63	c1	1	Total	C	O	P	0
			59	40	17	2	

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Mol	Chain	Residues	Atoms				AltConf
63	c1	1	Total	C	O	P	0
			65	46	17	2	
63	c3	1	Total	C	O	P	0
			68	49	17	2	
63	5b	1	Total	C	O	P	0
			87	68	17	2	
63	5b	1	Total	C	O	P	0
			67	48	17	2	
63	7a	1	Total	C	O	P	0
			67	48	17	2	
63	7a	1	Total	C	O	P	0
			100	81	17	2	
63	7c	1	Total	C	O	P	0
			85	66	17	2	
63	7c	1	Total	C	O	P	0
			51	32	17	2	
63	m1	1	Total	C	O	P	0
			95	76	17	2	
63	m1	1	Total	C	O	P	0
			66	47	17	2	
63	m1	1	Total	C	O	P	0
			66	47	17	2	
63	m2	1	Total	C	O	P	0
			54	35	17	2	
63	m2	1	Total	C	O	P	0
			66	47	17	2	
63	m2	1	Total	C	O	P	0
			74	55	17	2	
63	m3	1	Total	C	O	P	0
			94	75	17	2	
63	m3	1	Total	C	O	P	0
			51	32	17	2	
63	m3	1	Total	C	O	P	0
			63	44	17	2	
63	y7	1	Total	C	O	P	0
			65	46	17	2	
63	y0	1	Total	C	O	P	0
			64	45	17	2	
63	y5	1	Total	C	O	P	0
			81	62	17	2	
63	a	1	Total	C	O	P	0
			51	32	17	2	

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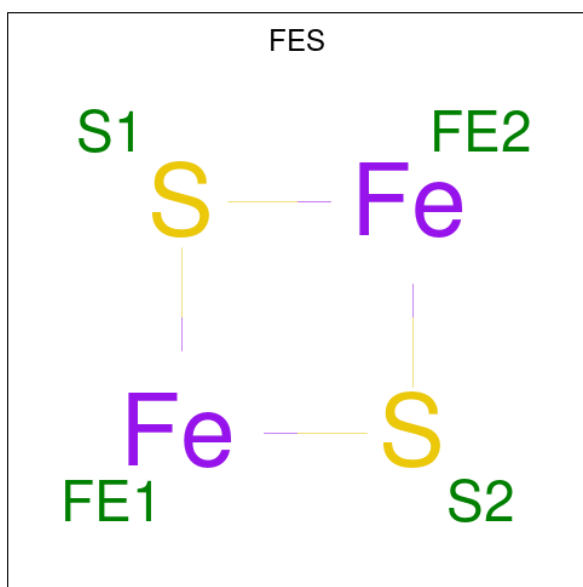
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Mol	Chain	Residues	Atoms				AltConf
63	b	1	Total	C	O	P	0
			62	43	17	2	
63	e	1	Total	C	O	P	0
			60	41	17	2	
63	e	1	Total	C	O	P	0
			72	53	17	2	
63	f	1	Total	C	O	P	0
			100	81	17	2	
63	j	1	Total	C	O	P	0
			70	51	17	2	
63	k	1	Total	C	O	P	0
			62	43	17	2	
63	l	1	Total	C	O	P	0
			74	55	17	2	
63	n	1	Total	C	O	P	0
			95	76	17	2	
63	t	1	Total	C	O	P	0
			68	49	17	2	
63	t	1	Total	C	O	P	0
			75	56	17	2	
63	u	1	Total	C	O	P	0
			82	63	17	2	
63	v	1	Total	C	O	P	0
			91	72	17	2	

- Molecule 64 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
64	5B	1	Total	Zn	0
			1	1	
64	M	1	Total	Zn	0
			1	1	
64	5b	1	Total	Zn	0
			1	1	
64	m	1	Total	Zn	0
			1	1	

- Molecule 65 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
65	FS	1	Total	Fe	S	0
			4	2	2	
65	FS	1	Total	Fe	S	0
			4	2	2	
65	fs	1	Total	Fe	S	0
			4	2	2	
65	fs	1	Total	Fe	S	0
			4	2	2	

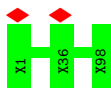
3 Residue-property plots

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

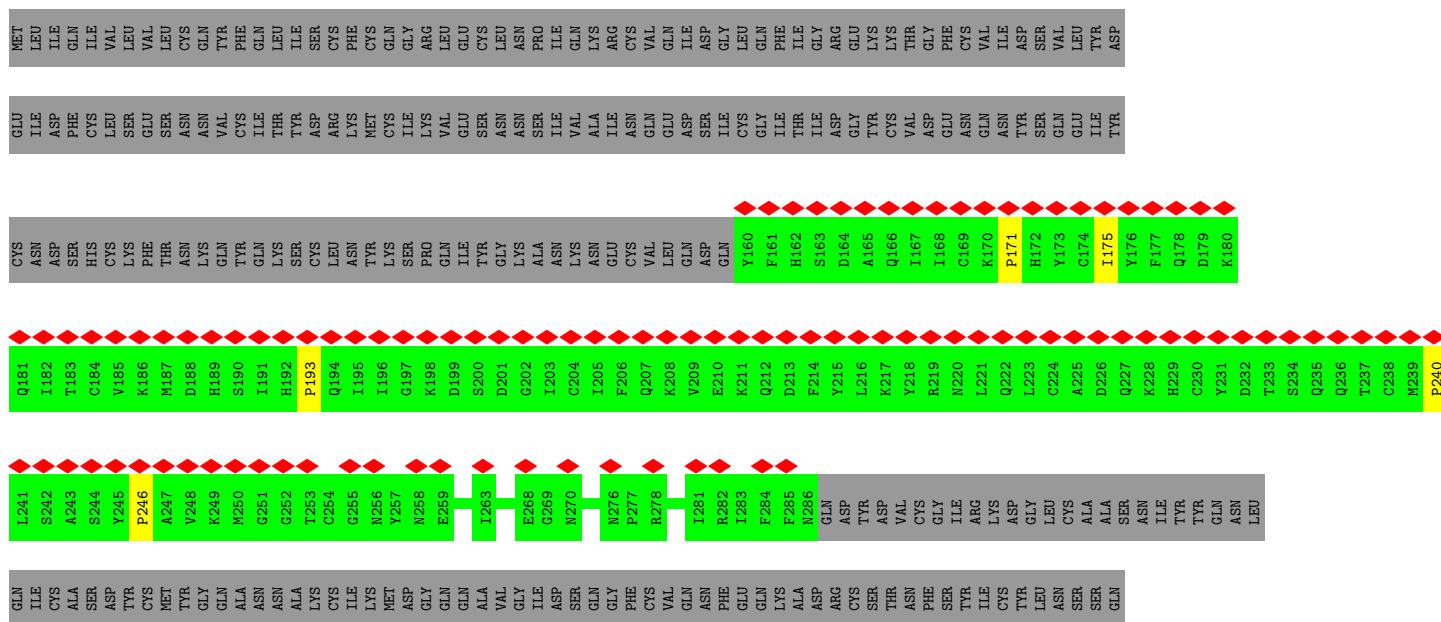
- Molecule 1: Unknown peptide



- Molecule 1: Unknown peptide



- Molecule 2: Transmembrane protein, putative







- Molecule 2: Transmembrane protein, putative

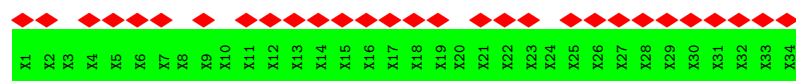
Chain u2: 97%

[illegible]

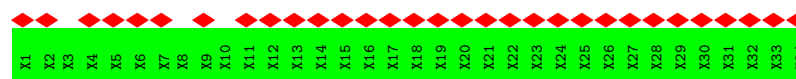




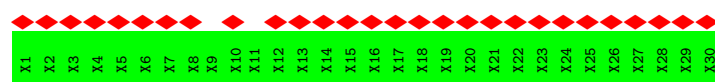




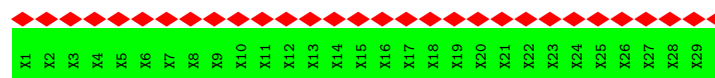
- Molecule 3: Unknown peptide



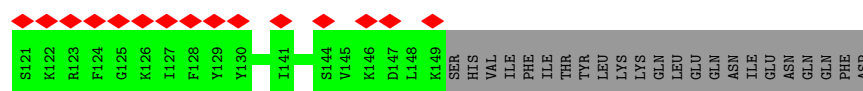
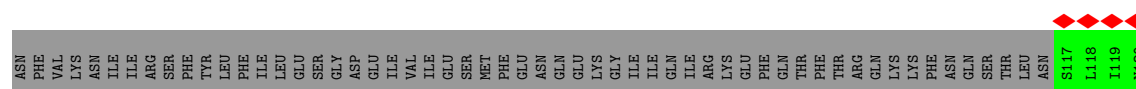
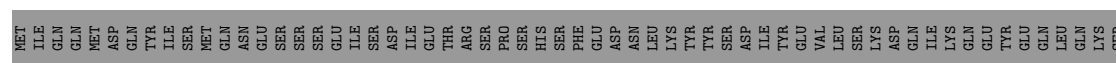
- Molecule 4: Unknown peptide



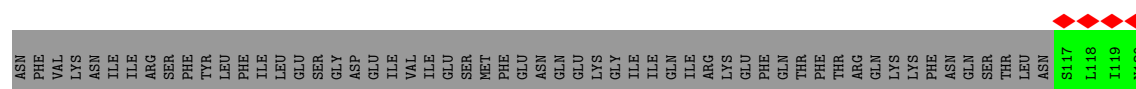
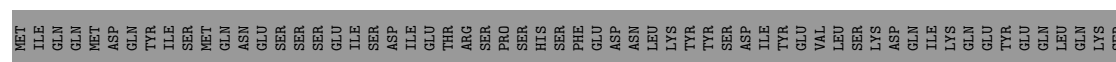
- Molecule 4: Unknown peptide



- Molecule 5: Uncharacterized protein

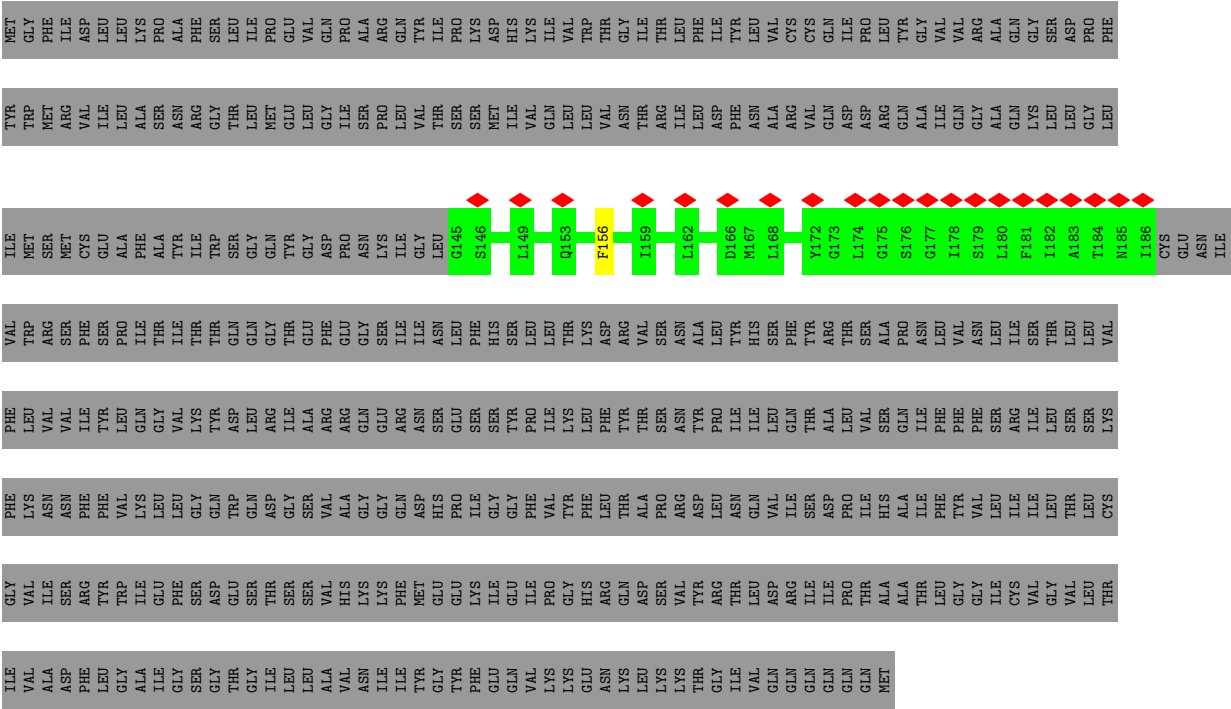


- Molecule 5: Uncharacterized protein





• Molecule 6: Protein transporter Sec61 alpha subunit



• Molecule 6: Protein transporter Sec61 alpha subunit



ILE VAL ALA ASP PHE LEU GLY ALA ILE SER SER SER SER THR THR GLY ILE LEU LEU VAL ALA VAL ASN ILE ILE TYR GLY TYR PHE GLU GLN VAL LYS LYS GLU ASN LYS LEU LYS THR GLY ILE VAL GLN GLN GLN GLN MET

• Molecule 7: Cytochrome c oxidase subunit 1

Chain C1:  96%

MET TRP VAL ASP PHE ILE ASP GLN THR LYS SER SER LEU LYS VAL SER V16 Y57 R164 N189 D190 K217 K263 C264 S265 T275 R318 R329 F404 T414 Y432 F503 H591 M621 R672 E687 LYS

• Molecule 7: Cytochrome c oxidase subunit 1

Chain c1:  96%

MET TRP VAL ASP PHE ILE ASP GLN THR LYS SER SER LEU LYS VAL SER V16 Y57 R164 N189 D190 K217 K263 C264 S265 T275 F310 R318 R329 T414 Y432 F503 H591 D592 M621 R672 E687 LYS

• Molecule 8: Cytochrome c oxidase subunit 2

Chain C2:  94% • 5%

H1 R59 G75 K76 W77 G78 D79 F80 K210 S211 L212 F224 D228 L229 Y230 D234 Y238 D242 D274 F291 T335 R348 L409 Y431 LYS ASP ASP ASN GLY ASN LYS T439 D440 L441 V501 D526 T536 H559 K583 MET LEU

ASN THR VAL SER ARG LYS ARG PHE GLU THR HIS TYR GLU LEU ARG LYS SER TRP

• Molecule 8: Cytochrome c oxidase subunit 2

Chain c2:  94% • 5%

H1 R59 G75 K76 W77 G78 D79 F80 L81 A82 K210 F224 D228 L229 Y230 Y238 D242 D274 F291 D333 Y334 T335 R348 L409 Y431 LYS ASP ASP ASN GLY ASN LYS T439 D440 L441 V501 D526 T536 H559 K583 MET LEU

ASN THR VAL SER ARG LYS ARG PHE GLU THR HIS TYR GLU LEU ARG LYS SER TRP

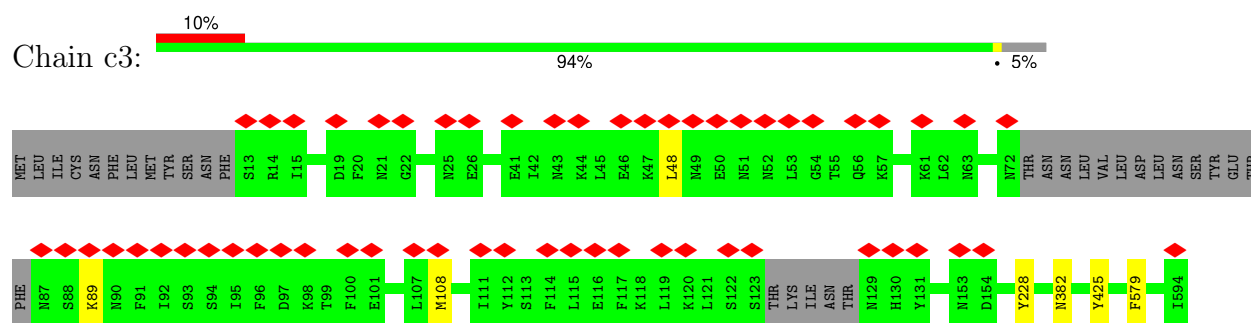
• Molecule 9: Ymf68

Chain C3:  94% • 5%

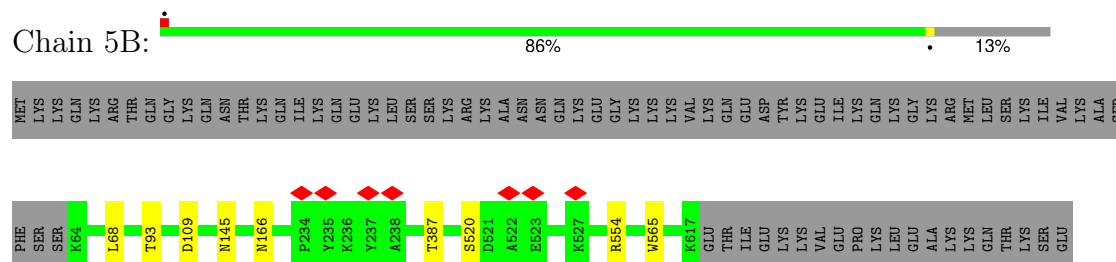
MET LEU ILE CYS ASN PHE LEU MET TYR SER ASN PHE S13 R14 I15 D19 F20 N21 G22 N25 E26 E41 I42 M43 K44 L45 E46 K47 L48 M49 E50 N51 N52 L53 Q54 T55 Q56 K57 K61 L62 M63 D69 N72 THR ASN ASN LEU VAL LEU ASP MET LEU ASN SER TYR

GLU THR PHE M87 S88 K89 N90 F91 I92 S93 S94 I95 F96 D97 K98 T99 F100 E101 L107 M108 I111 Y112 S113 F114 L115 E116 L119 K120 L121 S122 S123 THR LYS ILE ASN THR M129 H130 Y131 M143 M153 D154 Y228 N382 Y425 F579 I594

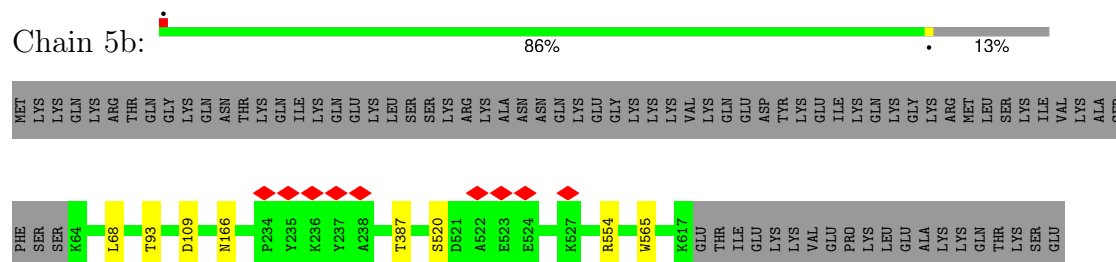
• Molecule 9: Ymf68



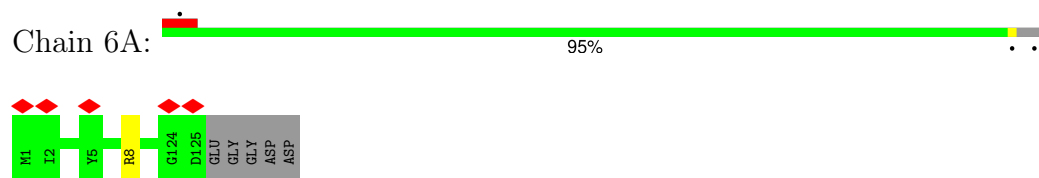
- Molecule 10: Cytochrome C oxidase subunit Vb protein



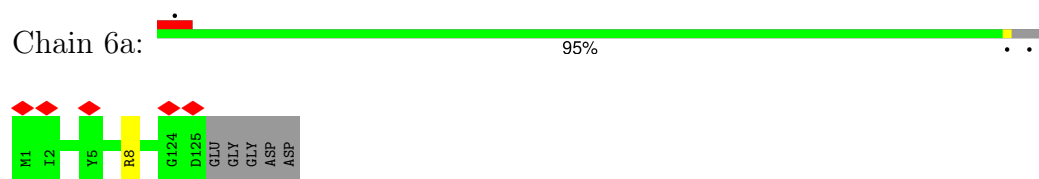
- Molecule 10: Cytochrome C oxidase subunit Vb protein



- Molecule 11: Transmembrane protein, putative

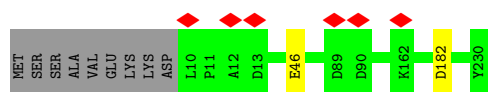


- Molecule 11: Transmembrane protein, putative



- Molecule 12: Cytochrome c oxidase subunit 6B

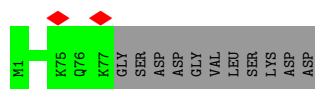




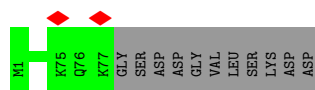
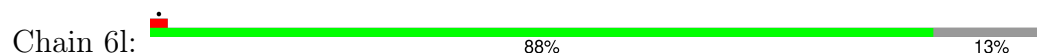
- Molecule 12: Cytochrome c oxidase subunit 6B



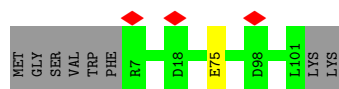
- Molecule 13: Cytochrome c oxidase subunit 6B-like



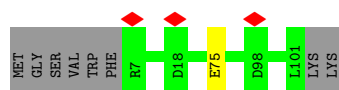
- Molecule 13: Cytochrome c oxidase subunit 6B-like



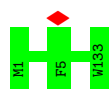
- Molecule 14: Transmembrane protein, putative



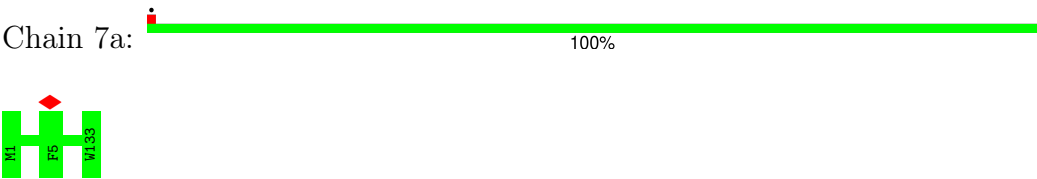
- Molecule 14: Transmembrane protein, putative



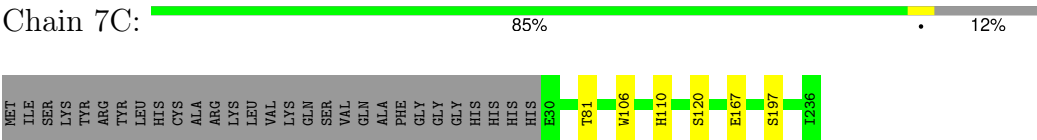
- Molecule 15: Transmembrane protein, putative



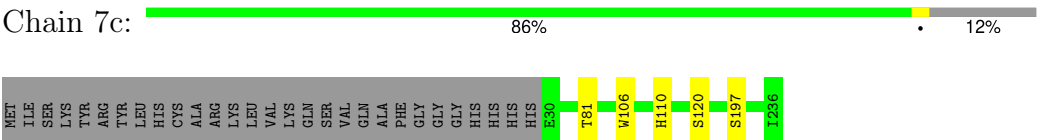
- Molecule 15: Transmembrane protein, putative



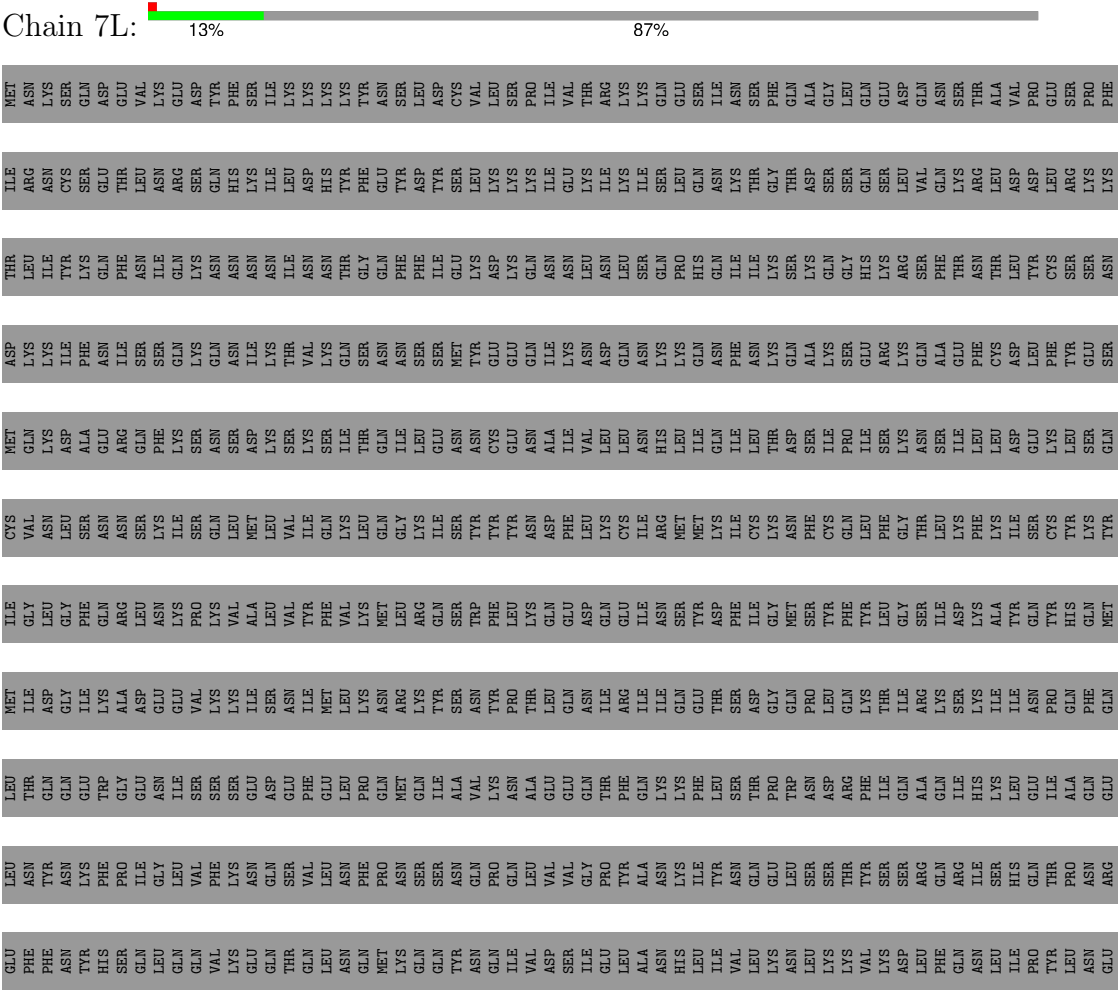
- Molecule 16: Cytochrome c oxidase subunit 7C



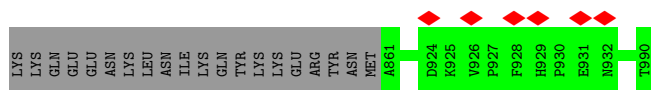
- Molecule 16: Cytochrome c oxidase subunit 7C



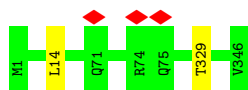
- Molecule 17: CTF/NF-I domain-containing protein



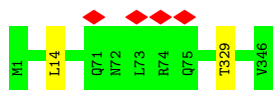




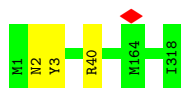
- Molecule 18: Oxoglutarate/malate translocator protein, putative



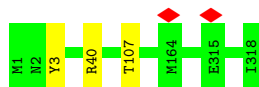
- Molecule 18: Oxoglutarate/malate translocator protein, putative



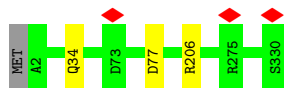
- Molecule 19: 2-oxoglutarate/malate carrier protein



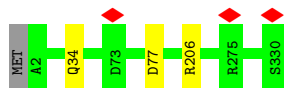
- Molecule 19: 2-oxoglutarate/malate carrier protein



- Molecule 20: Carrier protein



- Molecule 20: Carrier protein



- Molecule 21: Tim10/DDP family zinc finger protein

Chain T1:  97%




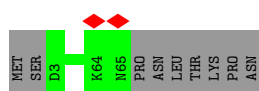
- Molecule 21: Tim10/DDP family zinc finger protein

Chain t1:  97%




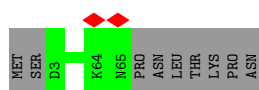
- Molecule 22: Cytochrome c oxidase small TIM subunit 2

Chain T2:  88% 12%




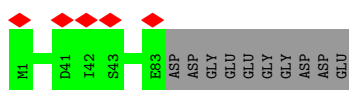
- Molecule 22: Cytochrome c oxidase small TIM subunit 2

Chain t2:  88% 12%




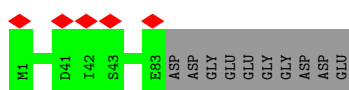
- Molecule 23: Cytochrome c oxidase small TIM subunit 3

Chain T3:  5% 89% 11%




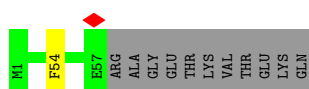
- Molecule 23: Cytochrome c oxidase small TIM subunit 3

Chain t3:  5% 89% 11%

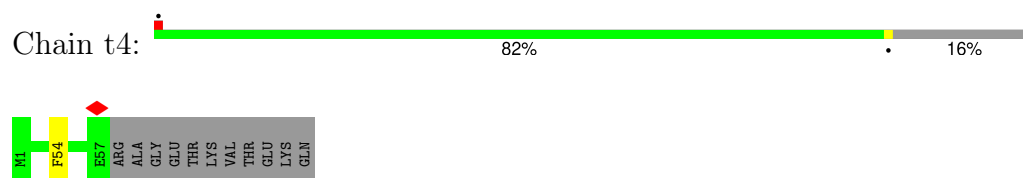


- Molecule 24: Cytochrome c oxidase small TIM subunit 4

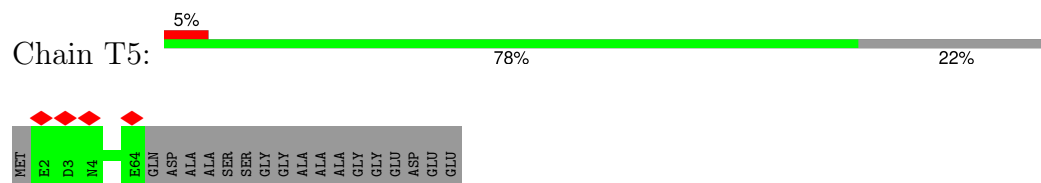
Chain T4:  82% 16%



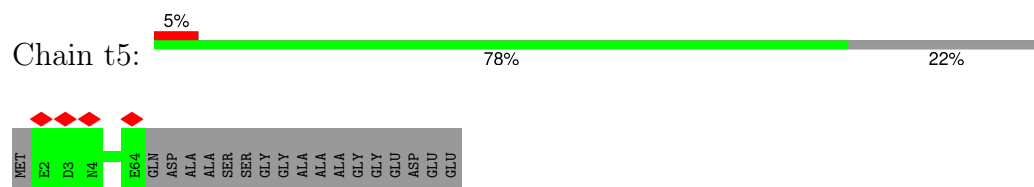
- Molecule 24: Cytochrome c oxidase small TIM subunit 4



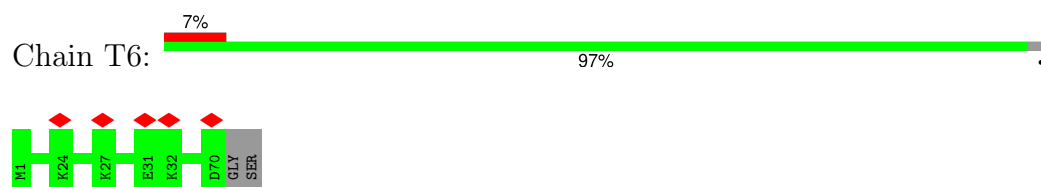
- Molecule 25: Cytochrome c oxidase small TIM subunit 5



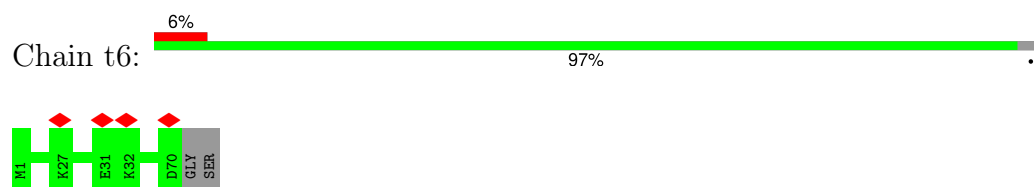
- Molecule 25: Cytochrome c oxidase small TIM subunit 5



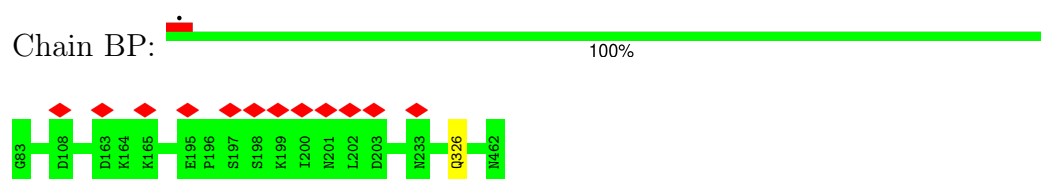
- Molecule 26: Cytochrome c oxidase small TIM subunit 6



- Molecule 26: Cytochrome c oxidase small TIM subunit 6



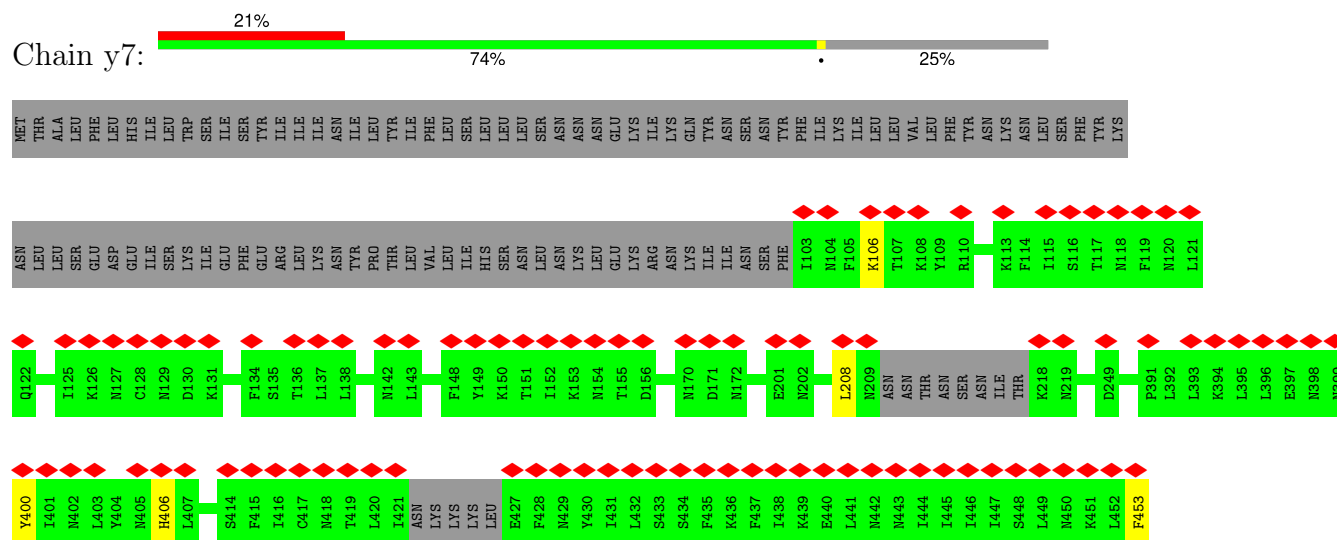
- Molecule 27: Chromosome condensation regulator RCC1 repeat protein



- Molecule 27: Chromosome condensation regulator RCC1 repeat protein



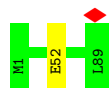
- Molecule 30: Ymf67



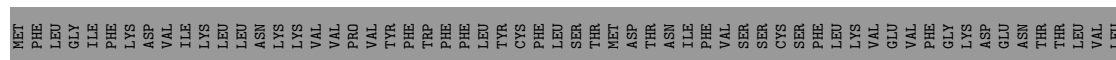
- Molecule 31: Ymf70



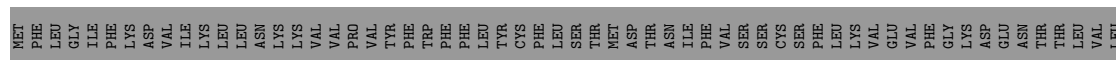
- Molecule 31: Ymf70

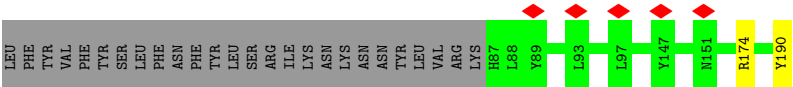


- Molecule 32: Ymf75

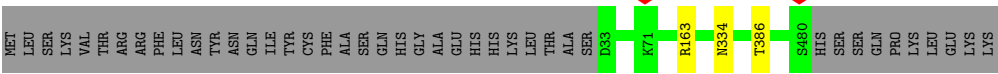
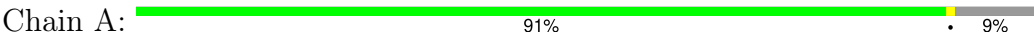


- Molecule 32: Ymf75

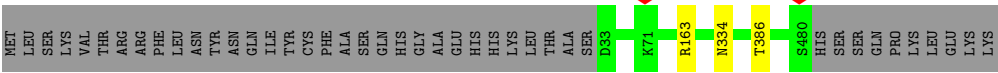
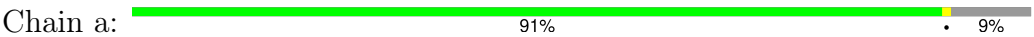




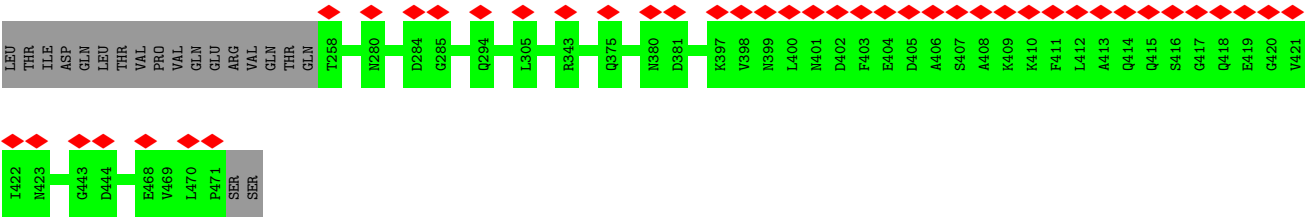
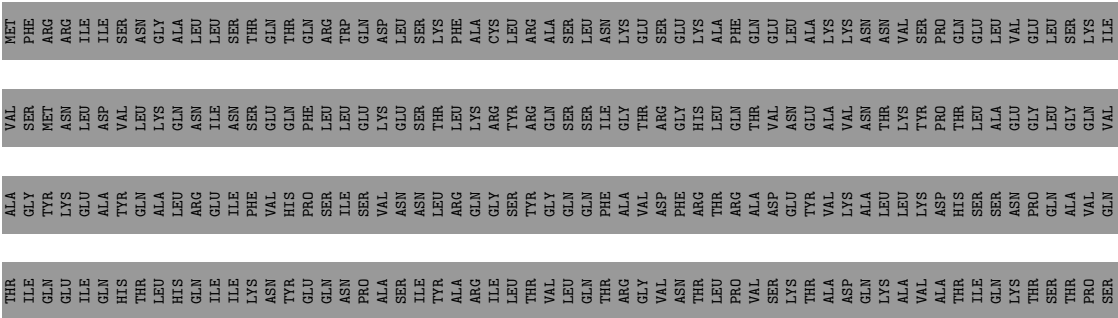
● Molecule 33: Transmembrane protein, putative



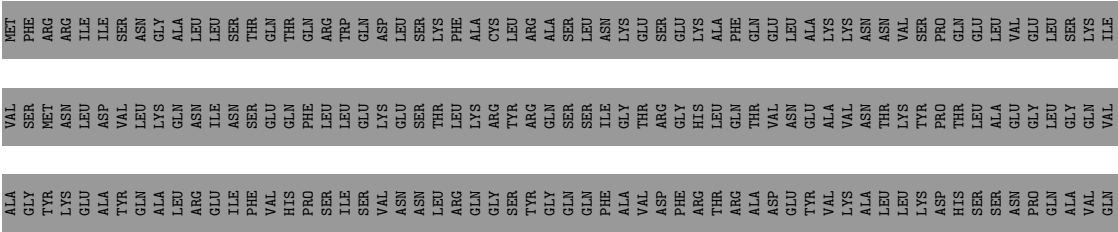
● Molecule 33: Transmembrane protein, putative



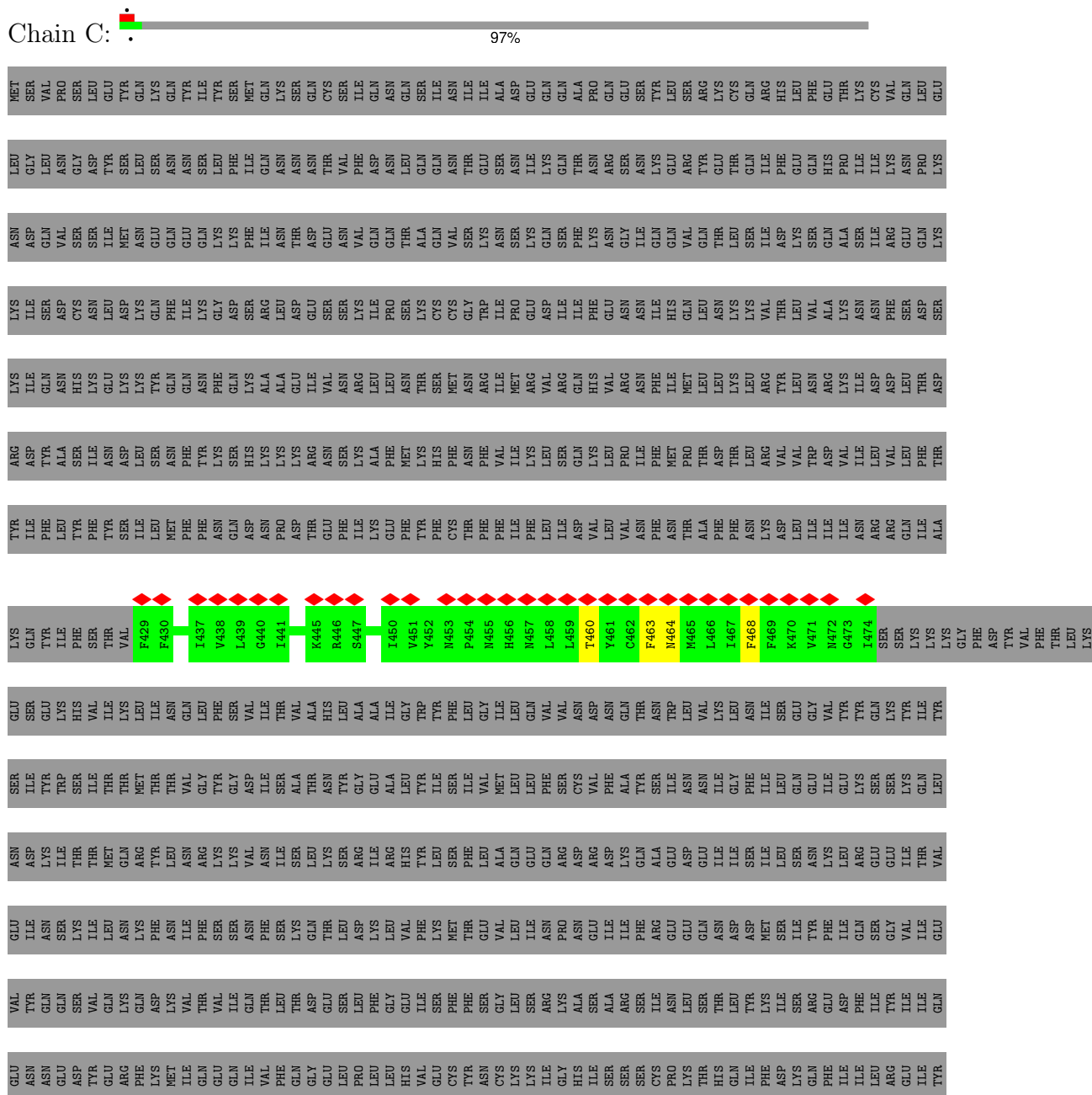
● Molecule 34: Protein phosphatase 2C, putative



● Molecule 34: Protein phosphatase 2C, putative



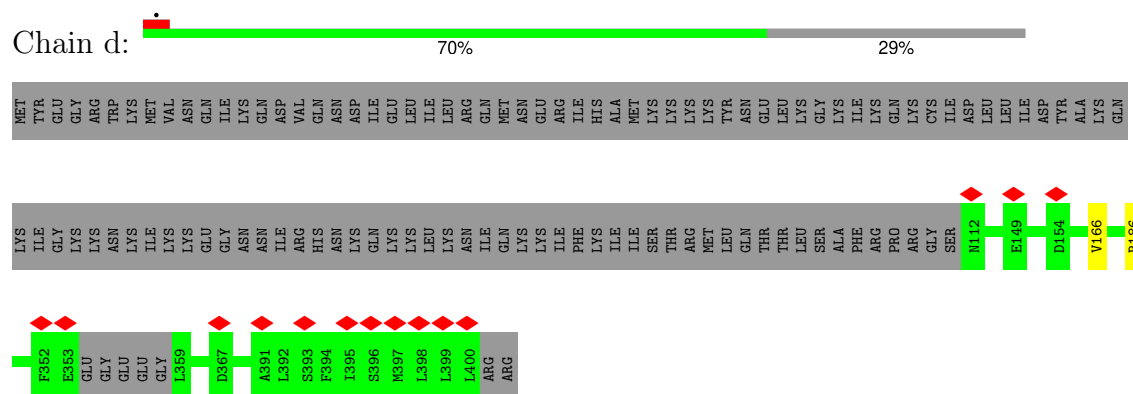
- Molecule 35: Cyclic nucleotide-binding domain protein



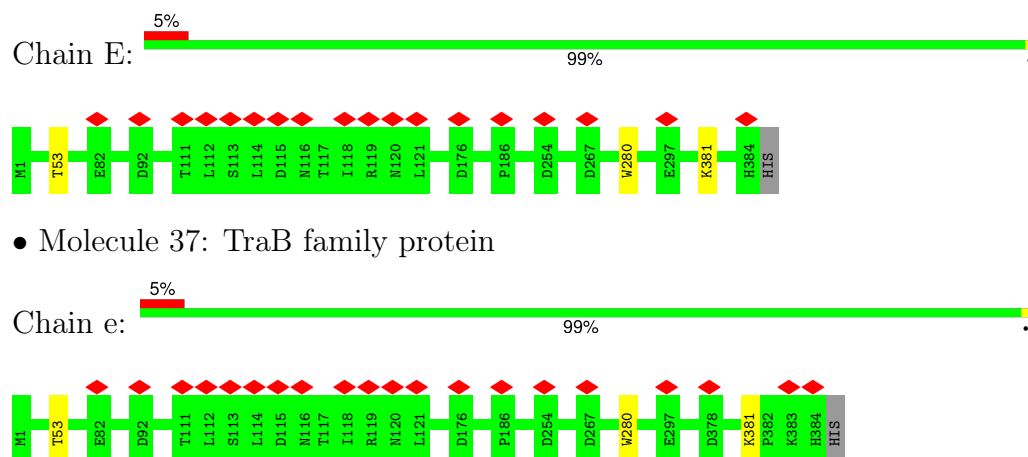
- Molecule 36: SURF1-like protein

29%

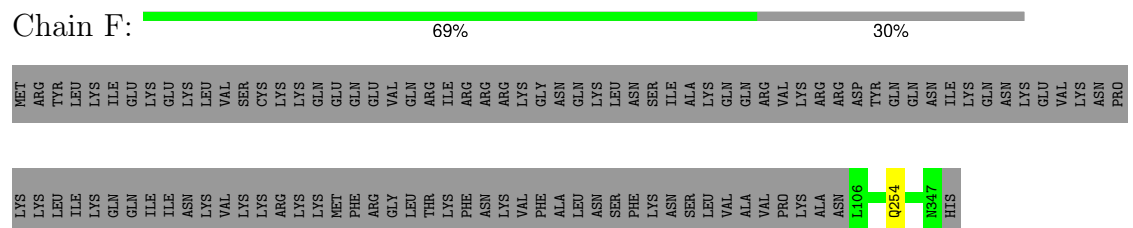
- Molecule 36: SURF1-like protein



- Molecule 37: TraB family protein

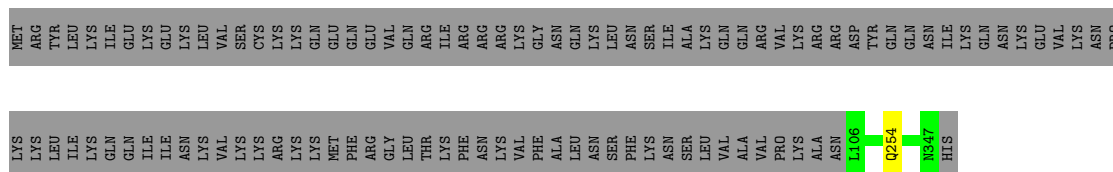


- Molecule 38: Transmembrane protein, putative




- Molecule 38: Transmembrane protein, putative

Chain f:  69% 30%




- Molecule 39: Cytochrome c oxidase subunit TT7

Chain G:  88% 12%




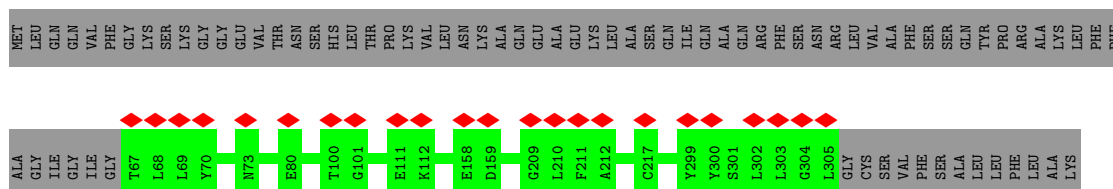
- Molecule 39: Cytochrome c oxidase subunit TT7

Chain g:  88% 12%




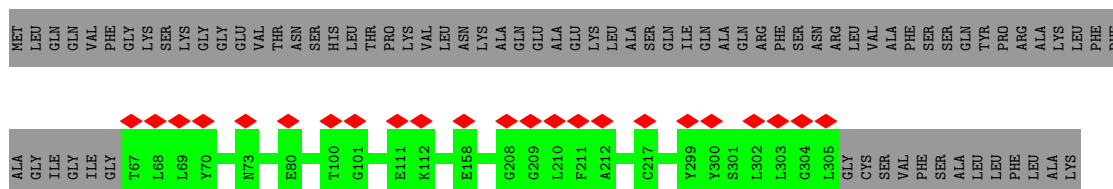
- Molecule 40: SURF1-like protein

Chain H:  7% 75% 25%



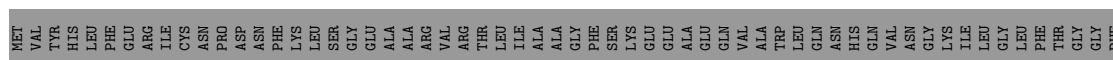
- Molecule 40: SURF1-like protein

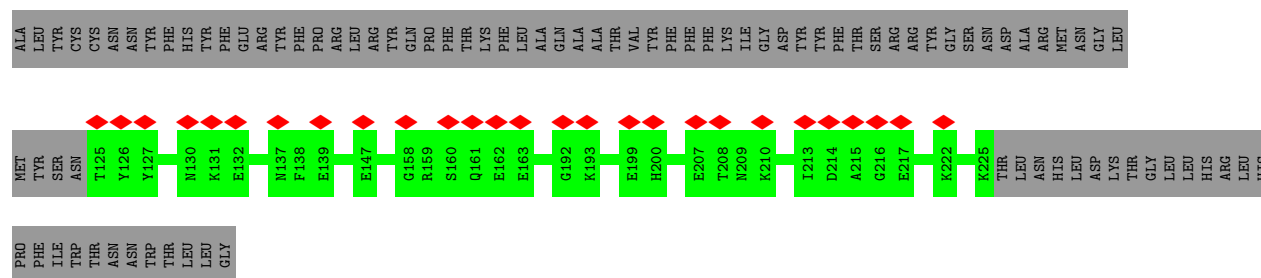
Chain h:  7% 75% 25%



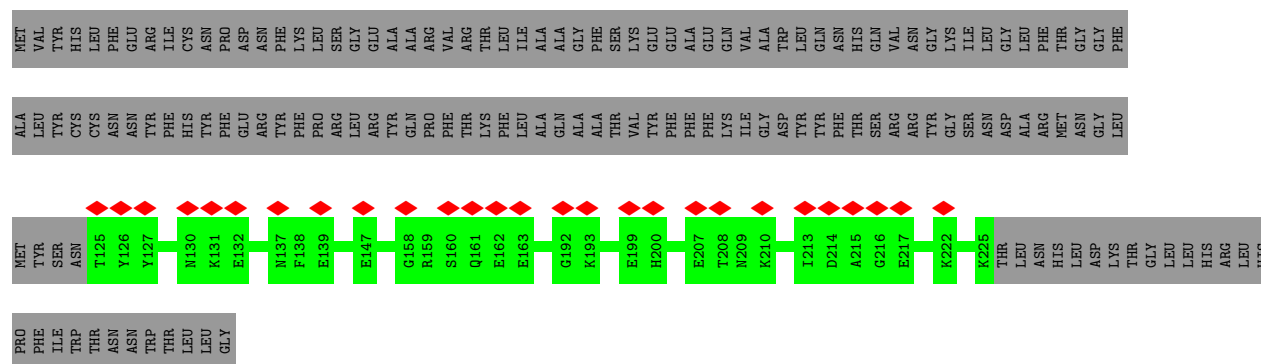
- Molecule 41: Cytochrome c oxidase subunit TT9

Chain I:  11% 40% 60%

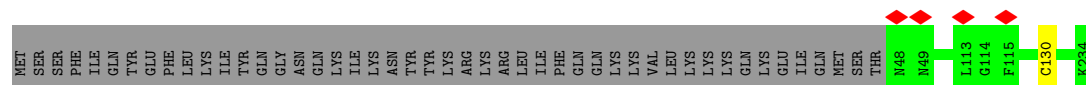
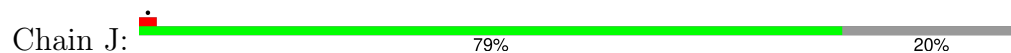




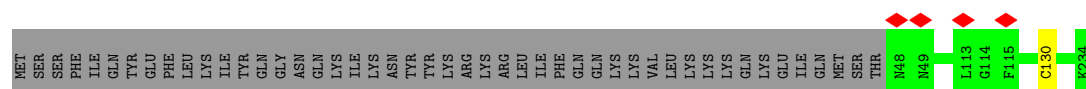
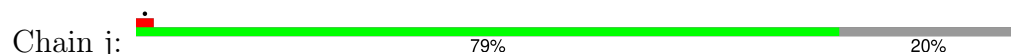
- Molecule 41: Cytochrome c oxidase subunit TT9



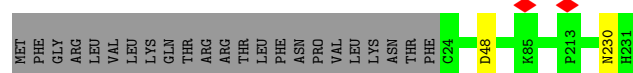
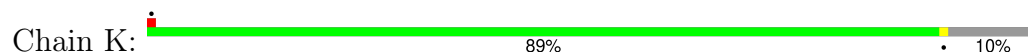
- Molecule 42: Cytochrome c oxidase subunit TT10



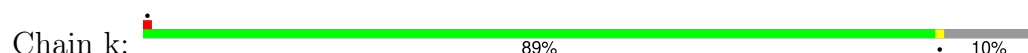
- Molecule 42: Cytochrome c oxidase subunit TT10

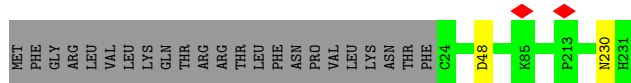


- Molecule 43: Cytochrome c oxidase subunit TT11

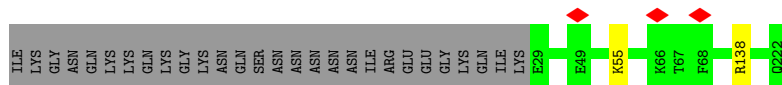
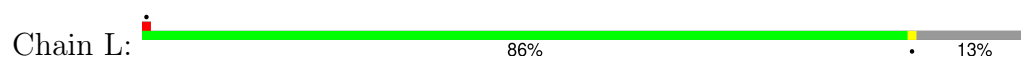


- Molecule 43: Cytochrome c oxidase subunit TT11

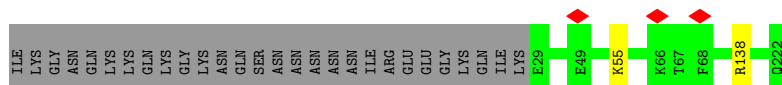
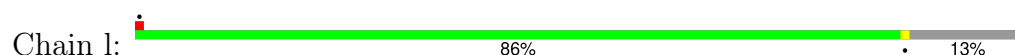




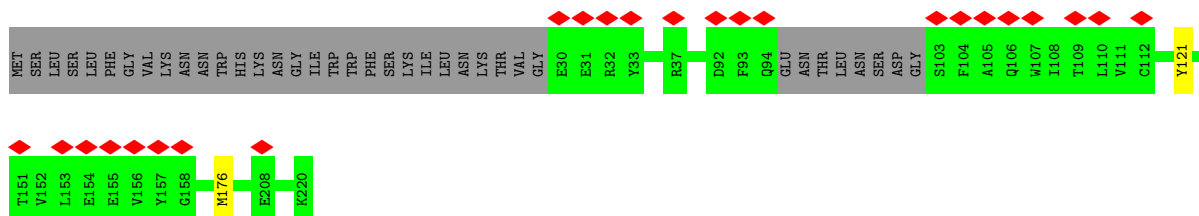
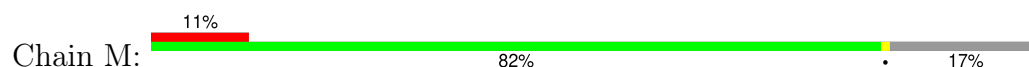
- Molecule 44: Cytochrome c oxidase subunit TT12



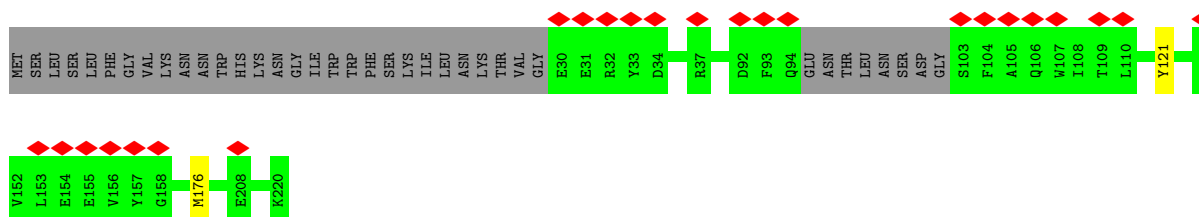
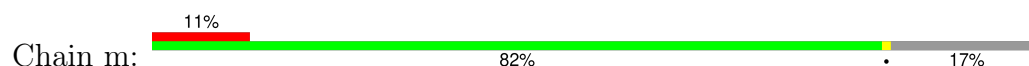
- Molecule 44: Cytochrome c oxidase subunit TT12



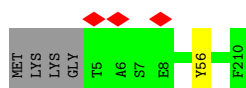
- Molecule 45: Transmembrane protein, putative



- Molecule 45: Transmembrane protein, putative

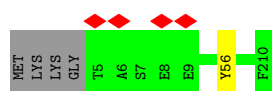


- Molecule 46: Transmembrane protein, putative



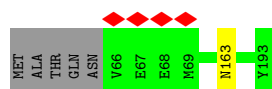
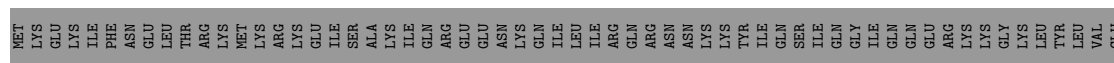
- Molecule 46: Transmembrane protein, putative

Chain n:  98%



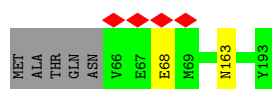
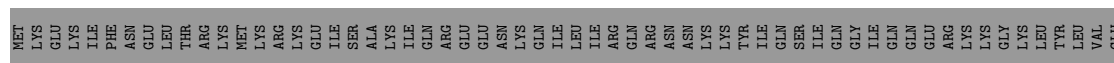
- Molecule 47: Cytochrome c oxidase subunit TT15

Chain O:  66%



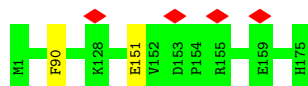
- Molecule 47: Cytochrome c oxidase subunit TT15

Chain o:  65%



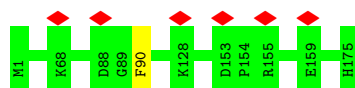
- Molecule 48: Cytochrome c oxidase subunit TT16

Chain P:  99%



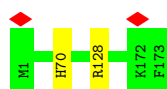
- Molecule 48: Cytochrome c oxidase subunit TT16

Chain p:  99%



- Molecule 49: Transmembrane protein, putative

Chain Q:  99%

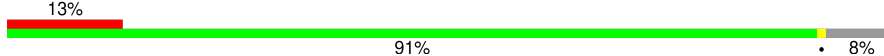


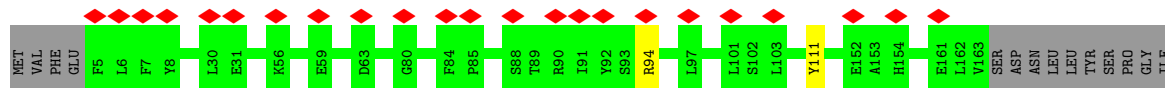
- Molecule 49: Transmembrane protein, putative

Chain q:  99%




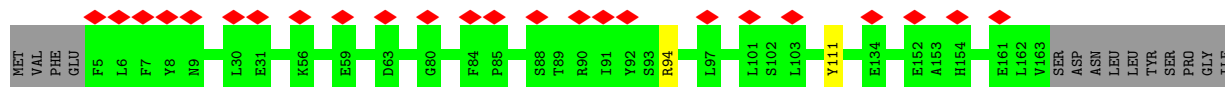
- Molecule 50: Cytochrome c oxidase subunit TT18

Chain R:  91% 13% 8%




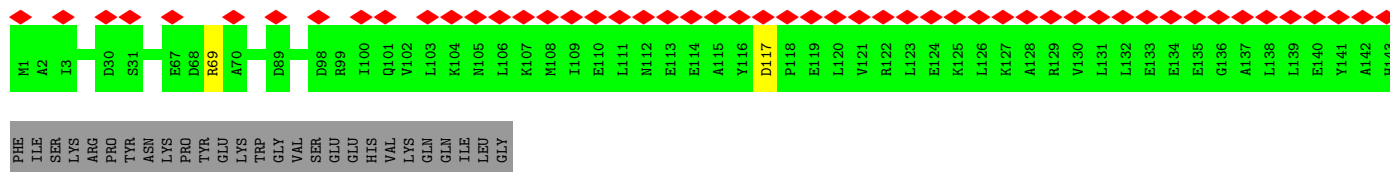
- Molecule 50: Cytochrome c oxidase subunit TT18

Chain r:  91% 14% 8%




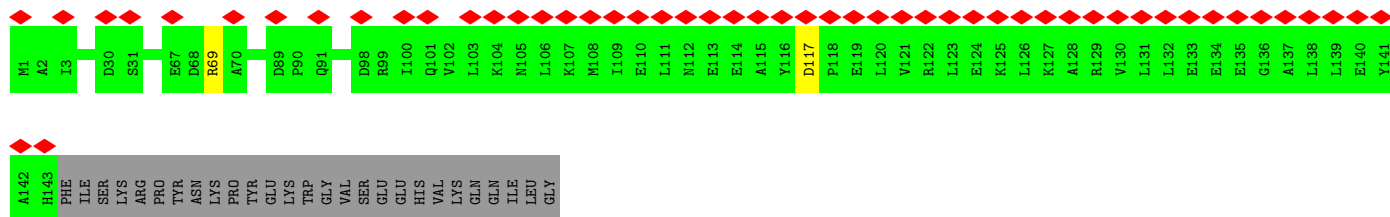
- Molecule 51: Cytochrome c oxidase subunit TT19

Chain S:  83% 30% 16%



- Molecule 51: Cytochrome c oxidase subunit TT19

Chain s:  83% 31% 16%



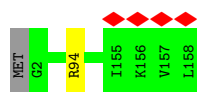
- Molecule 52: Transmembrane protein, putative

Chain T:  99%



- Molecule 52: Transmembrane protein, putative

Chain t:  99%



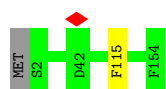
- Molecule 53: Transmembrane protein, putative

Chain U:  99%



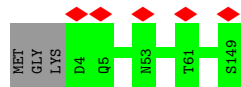
- Molecule 53: Transmembrane protein, putative

Chain u:  99%



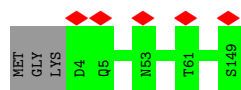
- Molecule 54: Cytochrome c oxidase subunit TT22

Chain V:  98%




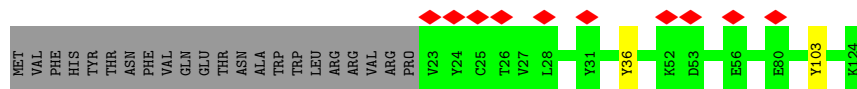
- Molecule 54: Cytochrome c oxidase subunit TT22

Chain v:  98%




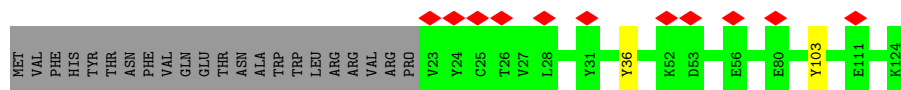
- Molecule 55: Transmembrane protein, putative

Chain W:  8% 81% 18%



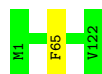
- Molecule 55: Transmembrane protein, putative

Chain w:  9% 81% 18%



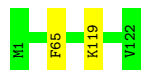
- Molecule 56: Transmembrane protein, putative

Chain X:  99%



- Molecule 56: Transmembrane protein, putative

Chain x:  98%



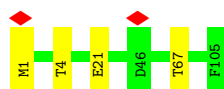
- Molecule 57: Cytochrome c oxidase subunit TT25

Chain Y:  98%



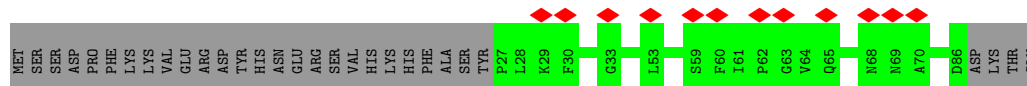
- Molecule 57: Cytochrome c oxidase subunit TT25

Chain y:  96%



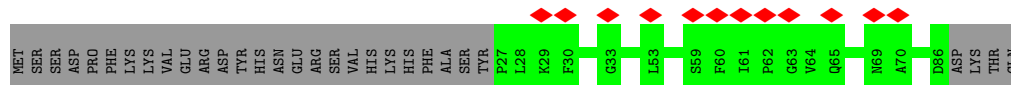
- Molecule 58: Cytochrome c oxidase subunit TT26

Chain Z:  13% 67% 33%



- Molecule 58: Cytochrome c oxidase subunit TT26

Chain z:  13% 67% 33%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	394262	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	56818	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	33.161	Depositor
Minimum map value	-22.263	Depositor
Average map value	-0.020	Depositor
Map value standard deviation	1.223	Depositor
Recommended contour level	5	Depositor
Map size (Å)	450.56, 450.56, 450.56	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.88, 0.88, 0.88	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CU, MG, ZN, FES, CDL, TPO, FME, PC1, SEP, HEA

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
2	U2	0.26	0/749	0.56	4/1031 (0.4%)
2	u2	0.25	0/749	0.56	4/1031 (0.4%)
5	U5	0.25	0/247	0.37	0/335
5	u5	0.25	0/247	0.36	0/335
6	U6	0.27	0/276	0.37	0/373
6	u6	0.26	0/276	0.35	0/373
7	C1	0.29	0/5752	0.47	0/7801
7	c1	0.29	0/5752	0.47	0/7801
8	C2	0.27	0/5027	0.47	0/6818
8	c2	0.27	0/5027	0.47	0/6818
9	C3	0.29	0/5098	0.44	0/6922
9	c3	0.29	0/5098	0.44	0/6922
10	5B	0.28	0/4706	0.46	0/6349
10	5b	0.28	0/4706	0.45	0/6349
11	6A	0.28	0/1107	0.44	0/1500
11	6a	0.28	0/1107	0.44	0/1500
12	6B	0.29	0/1968	0.46	0/2662
12	6b	0.29	0/1968	0.46	0/2662
13	6L	0.27	0/641	0.42	0/861
13	6l	0.26	0/641	0.42	0/861
14	6C	0.28	0/873	0.46	0/1184
14	6c	0.27	0/873	0.46	0/1184
15	7A	0.30	0/1198	0.48	0/1621
15	7a	0.30	0/1198	0.48	0/1621
16	7C	0.28	0/1830	0.44	0/2487
16	7c	0.28	0/1830	0.44	0/2487
17	7L	0.27	0/1099	0.44	0/1495
17	7l	0.28	0/1099	0.44	0/1495
18	M1	0.29	0/2958	0.46	0/4013
18	m1	0.29	0/2958	0.46	0/4013
19	M2	0.27	0/2621	0.47	0/3554
19	m2	0.28	0/2621	0.47	0/3554

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
20	M3	0.27	0/2689	0.44	0/3657
20	m3	0.27	0/2689	0.45	0/3657
21	T1	0.26	0/546	0.41	0/735
21	t1	0.26	0/546	0.41	0/735
22	T2	0.26	0/518	0.44	0/694
22	t2	0.26	0/518	0.44	0/694
23	T3	0.26	0/662	0.43	0/888
23	t3	0.26	0/662	0.44	0/888
24	T4	0.29	0/483	0.44	0/652
24	t4	0.30	0/483	0.44	0/652
25	T5	0.27	0/523	0.43	0/705
25	t5	0.27	0/523	0.43	0/705
26	T6	0.27	0/565	0.42	0/760
26	t6	0.27	0/565	0.42	0/760
27	BP	0.28	0/2984	0.47	0/4047
27	bp	0.28	0/2984	0.47	0/4047
28	FS	0.29	0/1562	0.46	0/2123
28	fs	0.29	0/1562	0.46	0/2123
29	AC	0.26	0/836	0.48	0/1133
29	ac	0.26	0/836	0.48	0/1133
30	Y7	0.28	0/2968	0.40	0/4014
30	y7	0.28	0/2968	0.40	0/4014
31	Y0	0.29	0/793	0.45	0/1077
31	y0	0.29	0/793	0.44	0/1077
32	Y5	0.28	0/951	0.39	0/1284
32	y5	0.28	0/951	0.39	0/1284
33	A	0.29	0/3863	0.46	0/5258
33	a	0.29	0/3863	0.46	0/5258
34	B	0.25	0/1712	0.44	0/2318
34	b	0.26	0/1712	0.44	0/2318
35	C	0.27	0/393	0.43	0/531
35	c	0.27	0/393	0.43	0/531
36	D	0.28	0/2394	0.47	0/3254
36	d	0.27	0/2394	0.47	0/3254
37	E	0.27	0/3258	0.46	0/4425
37	e	0.27	0/3258	0.46	0/4425
38	F	0.28	0/2066	0.45	0/2809
38	f	0.28	0/2066	0.45	0/2809
39	G	0.29	0/2439	0.47	0/3328
39	g	0.29	0/2439	0.47	0/3328
40	H	0.26	0/1960	0.47	0/2656
40	h	0.27	0/1960	0.47	0/2656
41	I	0.24	0/873	0.44	0/1173

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
41	i	0.24	0/873	0.43	0/1173
42	J	0.26	0/1621	0.46	0/2201
42	j	0.26	0/1621	0.46	0/2201
43	K	0.26	0/1755	0.44	0/2376
43	k	0.26	0/1755	0.43	0/2376
44	L	0.26	0/1718	0.44	0/2333
44	l	0.26	0/1718	0.44	0/2333
45	M	0.28	0/1640	0.45	0/2227
45	m	0.27	0/1640	0.45	0/2227
46	N	0.28	0/1770	0.43	0/2391
46	n	0.28	0/1770	0.43	0/2391
47	O	0.27	0/1090	0.46	0/1466
47	o	0.27	0/1090	0.45	0/1466
48	P	0.26	0/1428	0.45	0/1931
48	p	0.26	0/1428	0.44	0/1931
49	Q	0.29	0/1478	0.48	0/2005
49	q	0.29	0/1478	0.48	0/2005
50	R	0.25	0/1336	0.42	0/1808
50	r	0.25	0/1336	0.42	0/1808
51	S	0.24	0/1178	0.43	0/1588
51	s	0.25	0/1178	0.44	0/1588
52	T	0.28	0/1367	0.46	0/1853
52	t	0.28	0/1367	0.46	0/1853
53	U	0.27	0/1335	0.46	0/1794
53	u	0.27	0/1335	0.46	0/1794
54	V	0.28	0/1277	0.47	0/1735
54	v	0.28	0/1277	0.47	0/1735
55	W	0.26	0/933	0.43	0/1266
55	w	0.26	0/933	0.43	0/1266
56	X	0.28	0/1043	0.45	0/1413
56	x	0.28	0/1043	0.45	0/1413
57	Y	0.28	0/882	0.46	0/1192
57	y	0.29	0/882	0.46	0/1192
58	Z	0.25	0/491	0.44	0/664
58	z	0.25	0/491	0.44	0/664
All	All	0.28	0/187060	0.45	8/253540 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	U2	171	PRO	N-CA-CB	5.87	110.34	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	u2	171	PRO	N-CA-CB	5.87	110.34	103.30
2	U2	193	PRO	N-CA-CB	5.71	110.15	103.30
2	U2	240	PRO	N-CA-CB	5.68	110.12	103.30
2	u2	246	PRO	N-CA-CB	5.68	110.12	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	U2	125/3634 (3%)	115 (92%)	9 (7%)	1 (1%)	16	49
2	u2	125/3634 (3%)	114 (91%)	10 (8%)	1 (1%)	16	49
5	U5	31/172 (18%)	31 (100%)	0	0	100	100
5	u5	31/172 (18%)	31 (100%)	0	0	100	100
6	U6	40/478 (8%)	39 (98%)	1 (2%)	0	100	100
6	u6	40/478 (8%)	39 (98%)	1 (2%)	0	100	100
7	C1	670/688 (97%)	638 (95%)	32 (5%)	0	100	100
7	c1	670/688 (97%)	638 (95%)	32 (5%)	0	100	100
8	C2	572/604 (95%)	547 (96%)	25 (4%)	0	100	100
8	c2	572/604 (95%)	547 (96%)	25 (4%)	0	100	100
9	C3	557/594 (94%)	542 (97%)	15 (3%)	0	100	100
9	c3	557/594 (94%)	543 (98%)	14 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	5B	550/637 (86%)	539 (98%)	11 (2%)	0	100	100
10	5b	550/637 (86%)	540 (98%)	10 (2%)	0	100	100
11	6A	123/130 (95%)	117 (95%)	6 (5%)	0	100	100
11	6a	123/130 (95%)	117 (95%)	6 (5%)	0	100	100
12	6B	219/230 (95%)	215 (98%)	4 (2%)	0	100	100
12	6b	219/230 (95%)	216 (99%)	3 (1%)	0	100	100
13	6L	75/88 (85%)	75 (100%)	0	0	100	100
13	6l	75/88 (85%)	75 (100%)	0	0	100	100
14	6C	93/103 (90%)	91 (98%)	2 (2%)	0	100	100
14	6c	93/103 (90%)	91 (98%)	2 (2%)	0	100	100
15	7A	131/133 (98%)	124 (95%)	7 (5%)	0	100	100
15	7a	131/133 (98%)	125 (95%)	6 (5%)	0	100	100
16	7C	203/236 (86%)	198 (98%)	5 (2%)	0	100	100
16	7c	203/236 (86%)	198 (98%)	5 (2%)	0	100	100
17	7L	128/990 (13%)	120 (94%)	8 (6%)	0	100	100
17	7l	128/990 (13%)	120 (94%)	8 (6%)	0	100	100
18	M1	344/346 (99%)	330 (96%)	14 (4%)	0	100	100
18	m1	344/346 (99%)	330 (96%)	14 (4%)	0	100	100
19	M2	316/318 (99%)	311 (98%)	5 (2%)	0	100	100
19	m2	316/318 (99%)	311 (98%)	5 (2%)	0	100	100
20	M3	327/330 (99%)	312 (95%)	15 (5%)	0	100	100
20	m3	327/330 (99%)	313 (96%)	14 (4%)	0	100	100
21	T1	68/72 (94%)	68 (100%)	0	0	100	100
21	t1	68/72 (94%)	68 (100%)	0	0	100	100
22	T2	61/72 (85%)	61 (100%)	0	0	100	100
22	t2	61/72 (85%)	61 (100%)	0	0	100	100
23	T3	81/93 (87%)	79 (98%)	2 (2%)	0	100	100
23	t3	81/93 (87%)	79 (98%)	2 (2%)	0	100	100
24	T4	55/68 (81%)	53 (96%)	2 (4%)	0	100	100
24	t4	55/68 (81%)	53 (96%)	2 (4%)	0	100	100
25	T5	61/81 (75%)	60 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	t5	61/81 (75%)	60 (98%)	1 (2%)	0	100	100
26	T6	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
26	t6	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
27	BP	378/380 (100%)	361 (96%)	17 (4%)	0	100	100
27	bp	378/380 (100%)	359 (95%)	19 (5%)	0	100	100
28	FS	186/188 (99%)	177 (95%)	9 (5%)	0	100	100
28	fs	186/188 (99%)	178 (96%)	8 (4%)	0	100	100
29	AC	98/127 (77%)	97 (99%)	1 (1%)	0	100	100
29	ac	98/127 (77%)	98 (100%)	0	0	100	100
30	Y7	332/453 (73%)	326 (98%)	6 (2%)	0	100	100
30	y7	332/453 (73%)	325 (98%)	7 (2%)	0	100	100
31	Y0	87/89 (98%)	84 (97%)	3 (3%)	0	100	100
31	y0	87/89 (98%)	84 (97%)	3 (3%)	0	100	100
32	Y5	102/190 (54%)	99 (97%)	3 (3%)	0	100	100
32	y5	102/190 (54%)	99 (97%)	3 (3%)	0	100	100
33	A	446/490 (91%)	431 (97%)	15 (3%)	0	100	100
33	a	446/490 (91%)	432 (97%)	14 (3%)	0	100	100
34	B	212/473 (45%)	203 (96%)	9 (4%)	0	100	100
34	b	212/473 (45%)	203 (96%)	9 (4%)	0	100	100
35	C	44/1471 (3%)	43 (98%)	1 (2%)	0	100	100
35	c	44/1471 (3%)	43 (98%)	1 (2%)	0	100	100
36	D	280/402 (70%)	275 (98%)	5 (2%)	0	100	100
36	d	280/402 (70%)	275 (98%)	5 (2%)	0	100	100
37	E	382/385 (99%)	361 (94%)	21 (6%)	0	100	100
37	e	382/385 (99%)	361 (94%)	21 (6%)	0	100	100
38	F	240/348 (69%)	232 (97%)	8 (3%)	0	100	100
38	f	240/348 (69%)	233 (97%)	7 (3%)	0	100	100
39	G	279/318 (88%)	270 (97%)	9 (3%)	0	100	100
39	g	279/318 (88%)	271 (97%)	8 (3%)	0	100	100
40	H	237/318 (74%)	233 (98%)	4 (2%)	0	100	100
40	h	237/318 (74%)	234 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	I	99/252 (39%)	98 (99%)	1 (1%)	0	100	100
41	i	99/252 (39%)	98 (99%)	1 (1%)	0	100	100
42	J	185/234 (79%)	182 (98%)	3 (2%)	0	100	100
42	j	185/234 (79%)	182 (98%)	3 (2%)	0	100	100
43	K	206/231 (89%)	194 (94%)	12 (6%)	0	100	100
43	k	206/231 (89%)	195 (95%)	11 (5%)	0	100	100
44	L	192/222 (86%)	186 (97%)	6 (3%)	0	100	100
44	l	192/222 (86%)	186 (97%)	6 (3%)	0	100	100
45	M	179/220 (81%)	176 (98%)	3 (2%)	0	100	100
45	m	179/220 (81%)	176 (98%)	3 (2%)	0	100	100
46	N	204/210 (97%)	200 (98%)	4 (2%)	0	100	100
46	n	204/210 (97%)	198 (97%)	6 (3%)	0	100	100
47	O	126/193 (65%)	125 (99%)	1 (1%)	0	100	100
47	o	126/193 (65%)	126 (100%)	0	0	100	100
48	P	173/175 (99%)	169 (98%)	4 (2%)	0	100	100
48	p	173/175 (99%)	169 (98%)	4 (2%)	0	100	100
49	Q	171/173 (99%)	170 (99%)	1 (1%)	0	100	100
49	q	171/173 (99%)	170 (99%)	1 (1%)	0	100	100
50	R	157/173 (91%)	153 (98%)	4 (2%)	0	100	100
50	r	157/173 (91%)	153 (98%)	4 (2%)	0	100	100
51	S	141/170 (83%)	137 (97%)	4 (3%)	0	100	100
51	s	141/170 (83%)	137 (97%)	4 (3%)	0	100	100
52	T	155/158 (98%)	152 (98%)	3 (2%)	0	100	100
52	t	155/158 (98%)	152 (98%)	3 (2%)	0	100	100
53	U	151/154 (98%)	146 (97%)	5 (3%)	0	100	100
53	u	151/154 (98%)	146 (97%)	5 (3%)	0	100	100
54	V	144/149 (97%)	139 (96%)	5 (4%)	0	100	100
54	v	144/149 (97%)	139 (96%)	5 (4%)	0	100	100
55	W	100/124 (81%)	99 (99%)	1 (1%)	0	100	100
55	w	100/124 (81%)	100 (100%)	0	0	100	100
56	X	120/122 (98%)	118 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	x	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
57	Y	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
57	y	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
58	Z	58/90 (64%)	58 (100%)	0	0	100	100
58	z	58/90 (64%)	58 (100%)	0	0	100	100
All	All	21730/37912 (57%)	21056 (97%)	672 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	U2	175	ILE
2	u2	175	ILE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	U2	35/3358 (1%)	35 (100%)	0	100	100
2	u2	35/3358 (1%)	35 (100%)	0	100	100
5	U5	19/169 (11%)	19 (100%)	0	100	100
5	u5	19/169 (11%)	19 (100%)	0	100	100
6	U6	24/419 (6%)	23 (96%)	1 (4%)	25	58
6	u6	24/419 (6%)	23 (96%)	1 (4%)	25	58
7	C1	597/613 (97%)	588 (98%)	9 (2%)	60	82
7	c1	597/613 (97%)	587 (98%)	10 (2%)	56	80
8	C2	542/569 (95%)	531 (98%)	11 (2%)	50	77
8	c2	542/569 (95%)	531 (98%)	11 (2%)	50	77
9	C3	534/565 (94%)	527 (99%)	7 (1%)	65	84
9	c3	534/565 (94%)	527 (99%)	7 (1%)	65	84
10	5B	502/579 (87%)	495 (99%)	7 (1%)	62	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	5b	502/579 (87%)	496 (99%)	6 (1%)	67	85
11	6A	113/116 (97%)	112 (99%)	1 (1%)	75	89
11	6a	113/116 (97%)	112 (99%)	1 (1%)	75	89
12	6B	199/207 (96%)	197 (99%)	2 (1%)	73	88
12	6b	199/207 (96%)	196 (98%)	3 (2%)	60	82
13	6L	71/80 (89%)	71 (100%)	0	100	100
13	6l	71/80 (89%)	71 (100%)	0	100	100
14	6C	81/88 (92%)	80 (99%)	1 (1%)	67	85
14	6c	81/88 (92%)	80 (99%)	1 (1%)	67	85
15	7A	119/119 (100%)	119 (100%)	0	100	100
15	7a	119/119 (100%)	119 (100%)	0	100	100
16	7C	193/217 (89%)	189 (98%)	4 (2%)	48	76
16	7c	193/217 (89%)	190 (98%)	3 (2%)	58	81
17	7L	121/943 (13%)	121 (100%)	0	100	100
17	7l	121/943 (13%)	121 (100%)	0	100	100
18	M1	294/294 (100%)	292 (99%)	2 (1%)	81	91
18	m1	294/294 (100%)	292 (99%)	2 (1%)	81	91
19	M2	259/259 (100%)	256 (99%)	3 (1%)	67	85
19	m2	259/259 (100%)	256 (99%)	3 (1%)	67	85
20	M3	275/276 (100%)	272 (99%)	3 (1%)	70	87
20	m3	275/276 (100%)	272 (99%)	3 (1%)	70	87
21	T1	61/63 (97%)	61 (100%)	0	100	100
21	t1	61/63 (97%)	61 (100%)	0	100	100
22	T2	58/67 (87%)	58 (100%)	0	100	100
22	t2	58/67 (87%)	58 (100%)	0	100	100
23	T3	76/83 (92%)	76 (100%)	0	100	100
23	t3	76/83 (92%)	76 (100%)	0	100	100
24	T4	53/62 (86%)	52 (98%)	1 (2%)	52	78
24	t4	53/62 (86%)	52 (98%)	1 (2%)	52	78
25	T5	57/66 (86%)	57 (100%)	0	100	100
25	t5	57/66 (86%)	57 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	T6	61/62 (98%)	61 (100%)	0	100	100
26	t6	61/62 (98%)	61 (100%)	0	100	100
27	BP	308/308 (100%)	307 (100%)	1 (0%)	91	96
27	bp	308/308 (100%)	307 (100%)	1 (0%)	91	96
28	FS	164/164 (100%)	163 (99%)	1 (1%)	84	92
28	fs	164/164 (100%)	162 (99%)	2 (1%)	67	85
29	AC	87/113 (77%)	85 (98%)	2 (2%)	45	74
29	ac	87/113 (77%)	85 (98%)	2 (2%)	45	74
30	Y7	328/442 (74%)	324 (99%)	4 (1%)	67	85
30	y7	328/442 (74%)	323 (98%)	5 (2%)	60	82
31	Y0	83/83 (100%)	83 (100%)	0	100	100
31	y0	83/83 (100%)	82 (99%)	1 (1%)	67	85
32	Y5	101/185 (55%)	99 (98%)	2 (2%)	50	77
32	y5	101/185 (55%)	99 (98%)	2 (2%)	50	77
33	A	409/447 (92%)	406 (99%)	3 (1%)	81	91
33	a	409/447 (92%)	406 (99%)	3 (1%)	81	91
34	B	182/413 (44%)	182 (100%)	0	100	100
34	b	182/413 (44%)	182 (100%)	0	100	100
35	C	44/1405 (3%)	40 (91%)	4 (9%)	7	28
35	c	44/1405 (3%)	40 (91%)	4 (9%)	7	28
36	D	250/358 (70%)	248 (99%)	2 (1%)	79	90
36	d	250/358 (70%)	248 (99%)	2 (1%)	79	90
37	E	341/342 (100%)	338 (99%)	3 (1%)	75	89
37	e	341/342 (100%)	338 (99%)	3 (1%)	75	89
38	F	218/318 (69%)	217 (100%)	1 (0%)	86	94
38	f	218/318 (69%)	217 (100%)	1 (0%)	86	94
39	G	260/289 (90%)	258 (99%)	2 (1%)	79	90
39	g	260/289 (90%)	258 (99%)	2 (1%)	79	90
40	H	209/272 (77%)	209 (100%)	0	100	100
40	h	209/272 (77%)	209 (100%)	0	100	100
41	I	90/219 (41%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	i	90/219 (41%)	90 (100%)	0	100	100
42	J	170/216 (79%)	169 (99%)	1 (1%)	84	92
42	j	170/216 (79%)	169 (99%)	1 (1%)	84	92
43	K	191/213 (90%)	189 (99%)	2 (1%)	73	88
43	k	191/213 (90%)	189 (99%)	2 (1%)	73	88
44	L	181/206 (88%)	179 (99%)	2 (1%)	70	87
44	l	181/206 (88%)	179 (99%)	2 (1%)	70	87
45	M	166/199 (83%)	164 (99%)	2 (1%)	67	85
45	m	166/199 (83%)	164 (99%)	2 (1%)	67	85
46	N	178/181 (98%)	177 (99%)	1 (1%)	84	92
46	n	178/181 (98%)	177 (99%)	1 (1%)	84	92
47	O	119/180 (66%)	118 (99%)	1 (1%)	79	90
47	o	119/180 (66%)	117 (98%)	2 (2%)	56	80
48	P	156/156 (100%)	154 (99%)	2 (1%)	65	84
48	p	156/156 (100%)	155 (99%)	1 (1%)	84	92
49	Q	157/157 (100%)	155 (99%)	2 (1%)	65	84
49	q	157/157 (100%)	155 (99%)	2 (1%)	65	84
50	R	144/157 (92%)	142 (99%)	2 (1%)	62	83
50	r	144/157 (92%)	142 (99%)	2 (1%)	62	83
51	S	129/154 (84%)	127 (98%)	2 (2%)	58	81
51	s	129/154 (84%)	127 (98%)	2 (2%)	58	81
52	T	138/139 (99%)	137 (99%)	1 (1%)	81	91
52	t	138/139 (99%)	137 (99%)	1 (1%)	81	91
53	U	137/138 (99%)	136 (99%)	1 (1%)	81	91
53	u	137/138 (99%)	136 (99%)	1 (1%)	81	91
54	V	133/135 (98%)	133 (100%)	0	100	100
54	v	133/135 (98%)	133 (100%)	0	100	100
55	W	92/113 (81%)	90 (98%)	2 (2%)	47	75
55	w	92/113 (81%)	90 (98%)	2 (2%)	47	75
56	X	105/105 (100%)	104 (99%)	1 (1%)	73	88
56	x	105/105 (100%)	103 (98%)	2 (2%)	52	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	Y	88/88 (100%)	86 (98%)	2 (2%)	45	74
57	y	88/88 (100%)	84 (96%)	4 (4%)	23	56
58	Z	51/80 (64%)	51 (100%)	0	100	100
58	z	51/80 (64%)	51 (100%)	0	100	100
All	All	19506/34498 (56%)	19298 (99%)	208 (1%)	69	87

5 of 208 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	c2	291	PHE
16	7c	110	HIS
56	x	119	LYS
8	c2	501	VAL
10	5b	68	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
27	bp	260	ASN
30	y7	172	ASN
35	c	456	HIS
30	y7	118	ASN
30	y7	191	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

24 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	FME	M2	1	19	8,9,10	0.98	0	8,9,11	0.99	0
15	FME	7a	1	15	8,9,10	0.98	0	8,9,11	0.87	0
16	SEP	7c	197	16	8,9,10	1.57	1 (12%)	7,12,14	1.81	1 (14%)
16	SEP	7C	197	16	8,9,10	1.59	1 (12%)	7,12,14	1.85	1 (14%)
15	FME	7A	1	15	8,9,10	0.99	0	8,9,11	0.87	0
24	FME	T4	1	24	8,9,10	0.96	0	8,9,11	0.87	0
37	FME	e	1	37	8,9,10	0.98	0	8,9,11	0.96	0
37	FME	E	1	37	8,9,10	0.98	0	8,9,11	0.95	0
16	SEP	7C	120	16	8,9,10	1.55	1 (12%)	7,12,14	1.33	1 (14%)
26	FME	T6	1	26	8,9,10	0.97	0	8,9,11	0.81	0
13	FME	6l	1	13	8,9,10	0.97	0	8,9,11	0.93	0
10	SEP	5B	520	10	8,9,10	1.58	1 (12%)	7,12,14	1.25	1 (14%)
10	TPO	5b	387	10	8,10,11	1.60	1 (12%)	10,14,16	2.11	1 (10%)
48	FME	P	1	48	8,9,10	0.96	0	8,9,11	1.01	0
31	FME	Y0	1	31	8,9,10	1.00	0	8,9,11	0.86	0
24	FME	t4	1	24	8,9,10	0.95	0	8,9,11	0.89	0
31	FME	y0	1	31	8,9,10	0.98	0	8,9,11	0.87	0
16	SEP	7c	120	16	8,9,10	1.56	1 (12%)	7,12,14	1.25	1 (14%)
48	FME	p	1	48	8,9,10	0.95	0	8,9,11	1.03	0
26	FME	t6	1	26	8,9,10	0.97	0	8,9,11	0.79	0
10	SEP	5b	520	10	8,9,10	1.59	1 (12%)	7,12,14	1.26	1 (14%)
13	FME	6L	1	13	8,9,10	0.99	0	8,9,11	0.91	0
19	FME	m2	1	19	8,9,10	0.98	0	8,9,11	0.95	0
10	TPO	5B	387	10	8,10,11	1.06	0	10,14,16	2.09	1 (10%)

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
19	FME	M2	1	19	-	4/7/9/11	-
15	FME	7a	1	15	-	4/7/9/11	-
16	SEP	7c	197	16	-	0/6/8/10	-
16	SEP	7C	197	16	-	2/6/8/10	-
15	FME	7A	1	15	-	4/7/9/11	-
24	FME	T4	1	24	-	4/7/9/11	-
37	FME	e	1	37	-	5/7/9/11	-
37	FME	E	1	37	-	5/7/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	SEP	7C	120	16	-	0/6/8/10	-
26	FME	T6	1	26	-	5/7/9/11	-
13	FME	6l	1	13	-	6/7/9/11	-
10	SEP	5B	520	10	-	3/6/8/10	-
10	TPO	5b	387	10	-	1/9/11/13	-
48	FME	P	1	48	-	3/7/9/11	-
31	FME	Y0	1	31	-	5/7/9/11	-
24	FME	t4	1	24	-	4/7/9/11	-
31	FME	y0	1	31	-	5/7/9/11	-
16	SEP	7c	120	16	-	0/6/8/10	-
48	FME	p	1	48	-	3/7/9/11	-
26	FME	t6	1	26	-	5/7/9/11	-
10	SEP	5b	520	10	-	3/6/8/10	-
13	FME	6L	1	13	-	5/7/9/11	-
19	FME	m2	1	19	-	4/7/9/11	-
10	TPO	5B	387	10	-	1/9/11/13	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	7C	197	SEP	P-O1P	3.49	1.61	1.50
10	5b	520	SEP	P-O1P	3.47	1.61	1.50
10	5B	520	SEP	P-O1P	3.46	1.61	1.50
16	7c	120	SEP	P-O1P	3.43	1.61	1.50
10	5b	387	TPO	P-O1P	3.42	1.61	1.50

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	5b	387	TPO	P-OG1-CB	-6.12	106.70	123.33
10	5B	387	TPO	P-OG1-CB	-6.02	106.98	123.33
16	7C	197	SEP	OG-CB-CA	4.32	112.35	108.14
16	7c	197	SEP	OG-CB-CA	4.18	112.21	108.14
16	7C	120	SEP	OG-CB-CA	2.99	111.05	108.14

There are no chirality outliers.

5 of 81 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	5B	387	TPO	O-C-CA-CB
10	5B	520	SEP	CB-OG-P-O1P
10	5B	520	SEP	CB-OG-P-O2P
10	5B	520	SEP	CB-OG-P-O3P
13	6L	1	FME	O1-CN-N-CA

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 122 ligands modelled in this entry, 12 are monoatomic - leaving 110 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	$\# Z > 2$
59	HEA	C1	702	7	58,67,67	1.17	5 (8%)	63,103,103	1.62	15 (23%)
63	CDL	c1	706	-	58,58,99	0.38	0	64,70,111	0.41	0
63	CDL	M1	401	-	94,94,99	0.31	0	100,106,111	0.32	0
62	PC1	A	501	-	44,44,53	0.31	0	50,52,61	0.36	0
62	PC1	n	302	-	35,35,53	0.36	0	41,43,61	0.35	0
63	CDL	7c	302	-	50,50,99	0.41	0	56,62,111	0.34	0
62	PC1	a	501	-	44,44,53	0.31	0	50,52,61	0.36	0
63	CDL	a	503	-	50,50,99	0.41	0	56,62,111	0.51	0
63	CDL	v	201	-	90,90,99	0.32	0	96,102,111	0.37	0
63	CDL	7c	301	-	84,84,99	0.32	0	90,96,111	0.34	0
63	CDL	7C	301	-	84,84,99	0.32	0	90,96,111	0.34	0
62	PC1	C3	602	-	38,38,53	0.33	0	44,46,61	0.34	0
62	PC1	m1	402	-	53,53,53	0.29	0	59,61,61	0.35	0
63	CDL	5b	703	-	66,66,99	0.36	0	72,78,111	0.33	0
62	PC1	c1	705	-	48,48,53	0.31	0	54,56,61	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
63	CDL	M3	403	-	62,62,99	0.37	0	68,74,111	0.34	0
63	CDL	y5	201	-	80,80,99	0.33	0	86,92,111	0.28	0
62	PC1	C3	601	-	51,51,53	0.29	0	57,59,61	0.38	0
63	CDL	M3	402	-	50,50,99	0.41	0	56,62,111	0.35	0
63	CDL	M2	401	-	53,53,99	0.40	0	59,65,111	0.39	0
63	CDL	Y0	101	-	63,63,99	0.37	0	69,75,111	0.34	0
63	CDL	b	501	-	61,61,99	0.37	0	67,73,111	0.33	0
63	CDL	M1	403	-	65,65,99	0.36	0	71,77,111	0.30	0
62	PC1	n	301	-	31,31,53	0.36	0	37,39,61	0.36	0
63	CDL	M3	401	-	93,93,99	0.30	0	99,105,111	0.34	0
63	CDL	5B	703	-	61,61,99	0.37	0	67,73,111	0.33	0
63	CDL	7A	201	-	66,66,99	0.36	0	72,78,111	0.38	0
62	PC1	A	502	-	40,40,53	0.33	0	46,48,61	0.39	0
63	CDL	Y7	501	-	64,64,99	0.37	0	70,76,111	0.37	0
62	PC1	M2	402	-	31,31,53	0.37	0	37,39,61	0.37	0
62	PC1	M1	404	-	34,34,53	0.35	0	40,42,61	0.33	0
63	CDL	5B	702	-	86,86,99	0.32	0	92,98,111	0.33	0
63	CDL	m1	403	-	65,65,99	0.36	0	71,77,111	0.32	0
62	PC1	7C	304	-	42,42,53	0.32	0	48,50,61	0.30	0
63	CDL	C3	604	-	67,67,99	0.36	0	73,79,111	0.30	0
63	CDL	T	201	-	67,67,99	0.36	0	73,79,111	0.35	0
63	CDL	t	202	-	74,74,99	0.34	0	80,86,111	0.35	0
62	PC1	J	302	-	36,36,53	0.34	0	42,44,61	0.33	0
62	PC1	c3	601	-	51,51,53	0.30	0	57,59,61	0.38	0
63	CDL	k	301	-	61,61,99	0.37	0	67,73,111	0.33	0
63	CDL	m2	401	-	53,53,99	0.40	0	59,65,111	0.40	0
59	HEA	c1	701	7	58,67,67	1.12	5 (8%)	63,103,103	1.61	15 (23%)
63	CDL	7a	202	-	99,99,99	0.30	0	105,111,111	0.30	0
63	CDL	l	301	-	73,73,99	0.34	0	79,85,111	0.29	0
63	CDL	T	202	-	74,74,99	0.34	0	80,86,111	0.35	0
63	CDL	j	301	-	69,69,99	0.35	0	75,81,111	0.30	0
62	PC1	C3	603	-	30,30,53	0.37	0	36,38,61	0.39	0
62	PC1	v	202	-	53,53,53	0.29	0	59,61,61	0.33	0
63	CDL	E	401	-	59,59,99	0.38	0	65,71,111	0.38	0
63	CDL	c1	707	-	64,64,99	0.36	0	70,76,111	0.31	0
63	CDL	f	401	-	99,99,99	0.29	0	105,111,111	0.35	0
65	FES	fs	201	28	0,4,4	-	-	-	-	-
63	CDL	U	201	-	81,81,99	0.32	0	87,93,111	0.32	0
62	PC1	m2	405	-	40,40,53	0.33	0	46,48,61	0.33	0
63	CDL	m2	404	-	73,73,99	0.34	0	79,85,111	0.35	0
62	PC1	m1	405	-	34,34,53	0.35	0	40,42,61	0.32	0
63	CDL	m1	404	-	65,65,99	0.36	0	71,77,111	0.30	0
62	PC1	j	302	-	36,36,53	0.34	0	42,44,61	0.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
63	CDL	m3	401	-	93,93,99	0.30	0	99,105,111	0.33	0
59	HEA	C1	701	7	58,67,67	1.12	5 (8%)	63,103,103	1.62	15 (23%)
62	PC1	C3	605	-	40,40,53	0.33	0	46,48,61	0.42	0
62	PC1	7c	303	-	42,42,53	0.32	0	48,50,61	0.30	0
65	FES	fs	202	28	0,4,4	-	-	-		
63	CDL	F	401	-	99,99,99	0.29	0	105,111,111	0.36	0
62	PC1	M2	405	-	40,40,53	0.33	0	46,48,61	0.34	0
63	CDL	y7	501	-	64,64,99	0.37	0	70,76,111	0.37	0
62	PC1	M2	406	-	53,53,53	0.29	0	59,61,61	0.28	0
62	PC1	7C	302	-	53,53,53	0.29	0	59,61,61	0.36	0
62	PC1	m2	402	-	31,31,53	0.37	0	37,39,61	0.37	0
63	CDL	t	201	-	67,67,99	0.36	0	73,79,111	0.35	0
65	FES	FS	201	28	0,4,4	-	-	-		
62	PC1	c3	602	-	38,38,53	0.33	0	44,46,61	0.34	0
63	CDL	C1	706	-	58,58,99	0.38	0	64,70,111	0.40	0
63	CDL	L	301	-	73,73,99	0.34	0	79,85,111	0.29	0
63	CDL	V	201	-	90,90,99	0.32	0	96,102,111	0.37	0
62	PC1	N	302	-	35,35,53	0.36	0	41,43,61	0.35	0
63	CDL	7A	202	-	99,99,99	0.30	0	105,111,111	0.29	0
63	CDL	B	501	-	61,61,99	0.37	0	67,73,111	0.33	0
62	PC1	a	502	-	40,40,53	0.34	0	46,48,61	0.40	0
65	FES	FS	202	28	0,4,4	-	-	-		
62	PC1	c3	605	-	40,40,53	0.33	0	46,48,61	0.42	0
62	PC1	C1	705	-	48,48,53	0.31	0	54,56,61	0.31	0
63	CDL	u	201	-	81,81,99	0.32	0	87,93,111	0.32	0
63	CDL	M2	404	-	73,73,99	0.34	0	79,85,111	0.35	0
63	CDL	5B	704	-	66,66,99	0.36	0	72,78,111	0.34	0
63	CDL	e	402	-	71,71,99	0.34	0	77,83,111	0.34	0
63	CDL	m2	403	-	65,65,99	0.36	0	71,77,111	0.32	0
62	PC1	m2	406	-	53,53,53	0.29	0	59,61,61	0.28	0
63	CDL	Y5	201	-	80,80,99	0.33	0	86,92,111	0.28	0
63	CDL	5b	702	-	86,86,99	0.32	0	92,98,111	0.33	0
62	PC1	c3	603	-	30,30,53	0.37	0	36,38,61	0.39	0
63	CDL	e	401	-	59,59,99	0.38	0	65,71,111	0.38	0
63	CDL	c3	604	-	67,67,99	0.36	0	73,79,111	0.31	0
63	CDL	N	303	-	94,94,99	0.31	0	100,106,111	0.36	0
59	HEA	c1	702	7	58,67,67	1.17	5 (8%)	63,103,103	1.62	16 (25%)
63	CDL	7a	201	-	66,66,99	0.36	0	72,78,111	0.38	0
63	CDL	m1	401	-	94,94,99	0.31	0	100,106,111	0.32	0
63	CDL	7C	303	-	50,50,99	0.41	0	56,62,111	0.35	0
62	PC1	N	301	-	31,31,53	0.36	0	37,39,61	0.36	0
63	CDL	E	402	-	71,71,99	0.34	0	77,83,111	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
63	CDL	M1	402	-	65,65,99	0.36	0	71,77,111	0.32	0
63	CDL	y0	101	-	63,63,99	0.37	0	69,75,111	0.34	0
62	PC1	V	202	-	53,53,53	0.29	0	59,61,61	0.33	0
63	CDL	J	301	-	69,69,99	0.35	0	75,81,111	0.30	0
63	CDL	C1	707	-	64,64,99	0.36	0	70,76,111	0.31	0
63	CDL	m3	403	-	62,62,99	0.37	0	68,74,111	0.34	0
63	CDL	m3	402	-	50,50,99	0.41	0	56,62,111	0.35	0
63	CDL	A	503	-	50,50,99	0.41	0	56,62,111	0.50	0
63	CDL	n	303	-	94,94,99	0.31	0	100,106,111	0.37	0
63	CDL	M2	403	-	65,65,99	0.36	0	71,77,111	0.32	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
59	HEA	C1	702	7	-	10/32/76/76	-
63	CDL	c1	706	-	-	19/69/69/110	-
63	CDL	M1	401	-	-	27/105/105/110	-
62	PC1	A	501	-	-	11/48/48/57	-
62	PC1	n	302	-	-	4/39/39/57	-
63	CDL	7c	302	-	-	15/61/61/110	-
62	PC1	a	501	-	-	13/48/48/57	-
63	CDL	a	503	-	-	12/61/61/110	-
63	CDL	v	201	-	-	13/101/101/110	-
63	CDL	7c	301	-	-	24/95/95/110	-
63	CDL	7C	301	-	-	22/95/95/110	-
62	PC1	C3	602	-	-	10/42/42/57	-
62	PC1	m1	402	-	-	16/57/57/57	-
63	CDL	5b	703	-	-	11/77/77/110	-
62	PC1	c1	705	-	-	9/52/52/57	-
63	CDL	M3	403	-	-	17/73/73/110	-
63	CDL	y5	201	-	-	15/91/91/110	-
62	PC1	C3	601	-	-	12/55/55/57	-
63	CDL	M3	402	-	-	13/61/61/110	-
63	CDL	M2	401	-	-	15/64/64/110	-
63	CDL	Y0	101	-	-	17/74/74/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
63	CDL	b	501	-	-	14/72/72/110	-
63	CDL	M1	403	-	-	9/76/76/110	-
62	PC1	n	301	-	-	13/35/35/57	-
63	CDL	M3	401	-	-	20/104/104/110	-
63	CDL	5B	703	-	-	14/72/72/110	-
63	CDL	7A	201	-	-	12/77/77/110	-
62	PC1	A	502	-	-	11/44/44/57	-
63	CDL	Y7	501	-	-	11/75/75/110	-
62	PC1	M2	402	-	-	4/35/35/57	-
62	PC1	M1	404	-	-	8/38/38/57	-
63	CDL	5B	702	-	-	23/97/97/110	-
63	CDL	m1	403	-	-	15/76/76/110	-
62	PC1	7C	304	-	-	12/46/46/57	-
63	CDL	C3	604	-	-	9/78/78/110	-
63	CDL	T	201	-	-	12/78/78/110	-
63	CDL	t	202	-	-	14/85/85/110	-
62	PC1	J	302	-	-	7/40/40/57	-
62	PC1	c3	601	-	-	12/55/55/57	-
63	CDL	k	301	-	-	14/72/72/110	-
63	CDL	m2	401	-	-	18/64/64/110	-
59	HEA	c1	701	7	-	16/32/76/76	-
63	CDL	7a	202	-	-	23/110/110/110	-
63	CDL	l	301	-	-	21/84/84/110	-
63	CDL	T	202	-	-	13/85/85/110	-
63	CDL	j	301	-	-	13/80/80/110	-
62	PC1	C3	603	-	-	10/34/34/57	-
62	PC1	v	202	-	-	9/57/57/57	-
63	CDL	E	401	-	-	17/70/70/110	-
63	CDL	c1	707	-	-	10/75/75/110	-
63	CDL	f	401	-	-	17/110/110/110	-
65	FES	fs	201	28	-	-	0/1/1/1
63	CDL	U	201	-	-	17/92/92/110	-
62	PC1	m2	405	-	-	6/44/44/57	-
63	CDL	m2	404	-	-	16/84/84/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	PC1	m1	405	-	-	8/38/38/57	-
63	CDL	m1	404	-	-	10/76/76/110	-
62	PC1	j	302	-	-	8/40/40/57	-
63	CDL	m3	401	-	-	19/104/104/110	-
59	HEA	C1	701	7	-	15/32/76/76	-
62	PC1	C3	605	-	-	10/44/44/57	-
62	PC1	7c	303	-	-	13/46/46/57	-
65	FES	fs	202	28	-	-	0/1/1/1
63	CDL	F	401	-	-	19/110/110/110	-
62	PC1	M2	405	-	-	11/44/44/57	-
63	CDL	y7	501	-	-	10/75/75/110	-
62	PC1	M2	406	-	-	8/57/57/57	-
62	PC1	7C	302	-	-	17/57/57/57	-
62	PC1	m2	402	-	-	3/35/35/57	-
63	CDL	t	201	-	-	10/78/78/110	-
65	FES	FS	201	28	-	-	0/1/1/1
62	PC1	c3	602	-	-	9/42/42/57	-
63	CDL	C1	706	-	-	17/69/69/110	-
63	CDL	L	301	-	-	21/84/84/110	-
63	CDL	V	201	-	-	14/101/101/110	-
62	PC1	N	302	-	-	4/39/39/57	-
63	CDL	7A	202	-	-	19/110/110/110	-
63	CDL	B	501	-	-	14/72/72/110	-
62	PC1	a	502	-	-	9/44/44/57	-
65	FES	FS	202	28	-	-	0/1/1/1
62	PC1	c3	605	-	-	9/44/44/57	-
62	PC1	C1	705	-	-	12/52/52/57	-
63	CDL	u	201	-	-	15/92/92/110	-
63	CDL	M2	404	-	-	17/84/84/110	-
63	CDL	5B	704	-	-	9/77/77/110	-
63	CDL	e	402	-	-	14/82/82/110	-
63	CDL	m2	403	-	-	15/76/76/110	-
62	PC1	m2	406	-	-	8/57/57/57	-
63	CDL	Y5	201	-	-	16/91/91/110	-
63	CDL	5b	702	-	-	23/97/97/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	PC1	c3	603	-	-	10/34/34/57	-
63	CDL	e	401	-	-	16/70/70/110	-
63	CDL	c3	604	-	-	9/78/78/110	-
63	CDL	N	303	-	-	22/105/105/110	-
59	HEA	c1	702	7	-	11/32/76/76	-
63	CDL	7a	201	-	-	13/77/77/110	-
63	CDL	m1	401	-	-	26/105/105/110	-
63	CDL	7C	303	-	-	15/61/61/110	-
62	PC1	N	301	-	-	13/35/35/57	-
63	CDL	E	402	-	-	14/82/82/110	-
63	CDL	M1	402	-	-	15/76/76/110	-
63	CDL	y0	101	-	-	21/74/74/110	-
62	PC1	V	202	-	-	10/57/57/57	-
63	CDL	J	301	-	-	12/80/80/110	-
63	CDL	C1	707	-	-	11/75/75/110	-
63	CDL	m3	403	-	-	18/73/73/110	-
63	CDL	m3	402	-	-	13/61/61/110	-
63	CDL	A	503	-	-	8/61/61/110	-
63	CDL	n	303	-	-	22/105/105/110	-
63	CDL	M2	403	-	-	15/76/76/110	-

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	c1	702	HEA	C3A-C2A	-3.76	1.35	1.40
59	C1	702	HEA	C3A-C2A	-3.73	1.35	1.40
59	c1	702	HEA	C4D-C3D	3.26	1.50	1.45
59	C1	702	HEA	C4D-C3D	3.25	1.50	1.45
59	c1	701	HEA	C3A-C2A	-2.96	1.36	1.40

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	C1	702	HEA	C13-C12-C11	-4.84	106.65	114.39
59	c1	702	HEA	C13-C12-C11	-4.80	106.73	114.39
59	C1	701	HEA	C13-C12-C11	-3.67	108.53	114.39
59	c1	701	HEA	C13-C12-C11	-3.61	108.63	114.39
59	c1	702	HEA	CMC-C2C-C1C	-3.40	123.47	128.46

There are no chirality outliers.

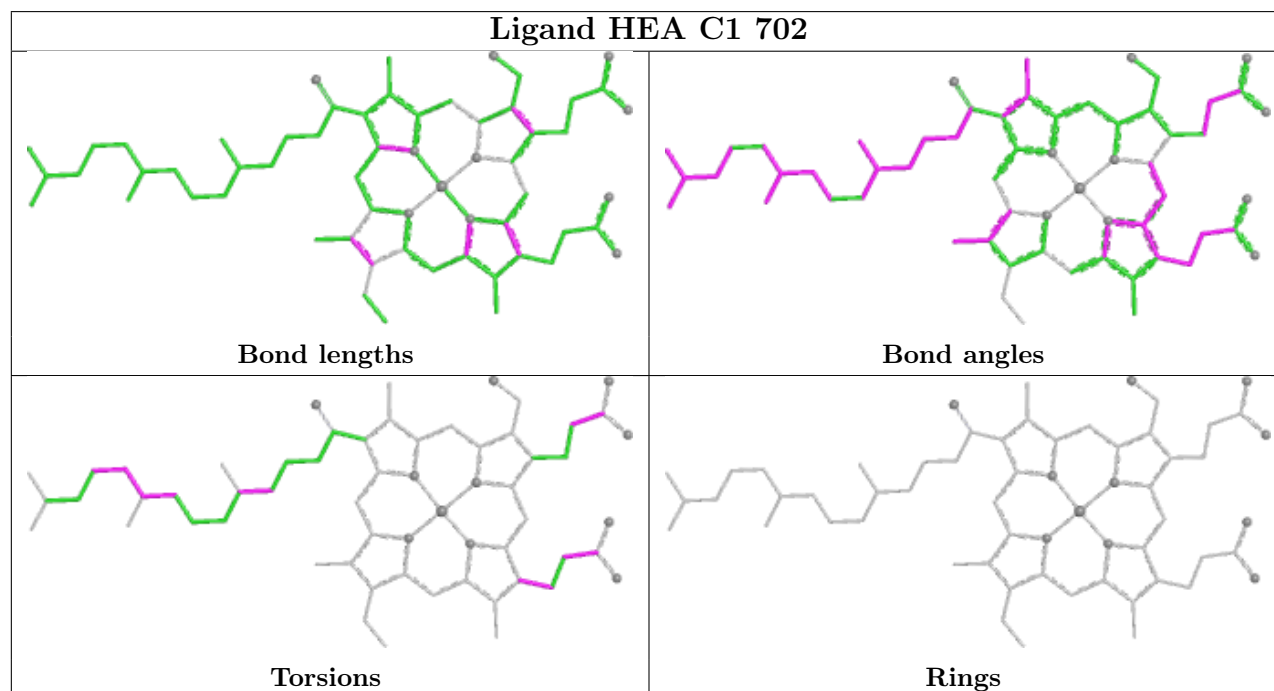
5 of 1445 torsion outliers are listed below:

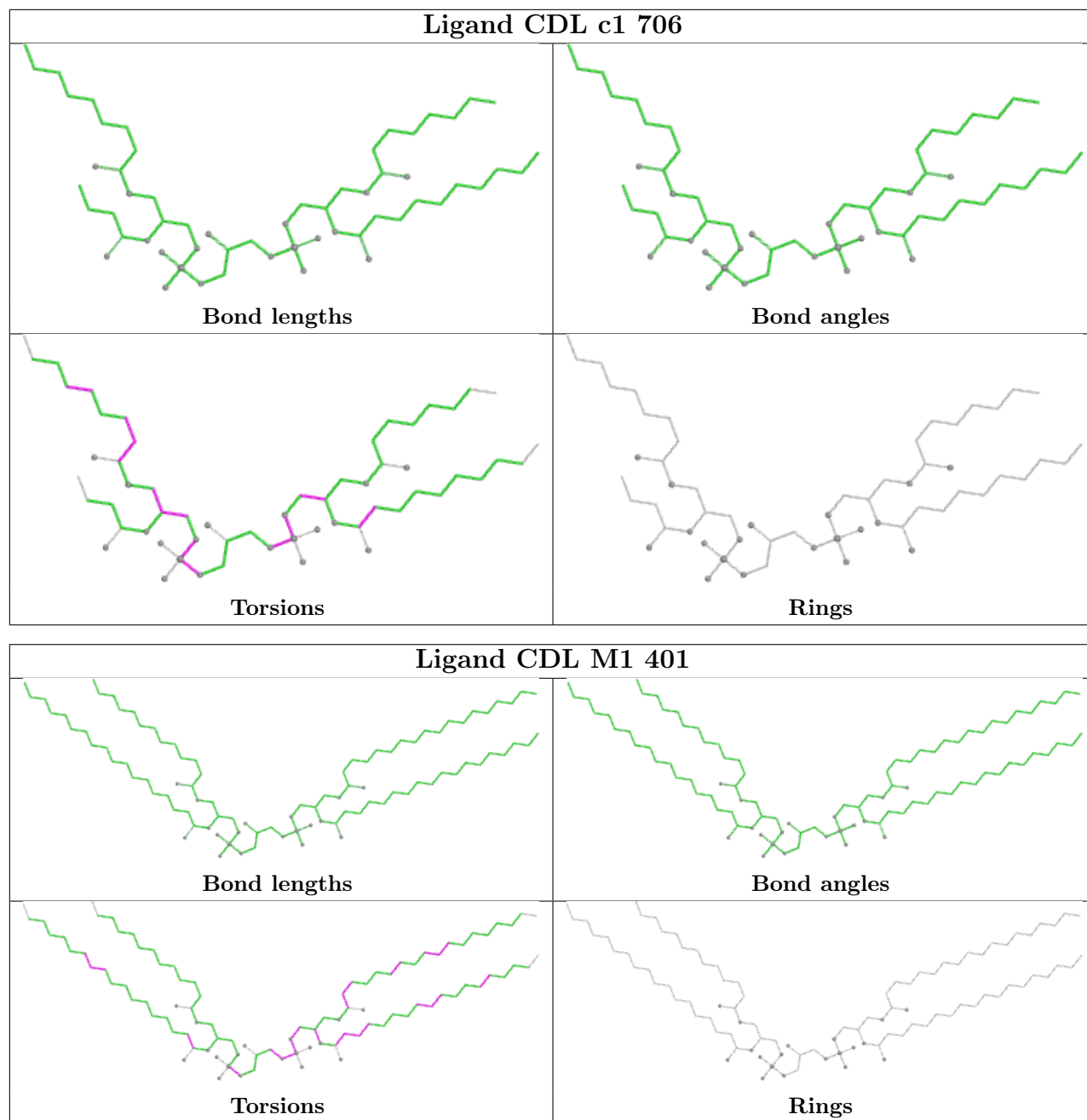
Mol	Chain	Res	Type	Atoms
59	C1	701	HEA	C1A-C2A-CAA-CBA
59	C1	701	HEA	C3A-C2A-CAA-CBA
59	C1	701	HEA	C26-C15-C16-C17
59	C1	701	HEA	C15-C16-C17-C18
59	C1	701	HEA	C17-C18-C19-C20

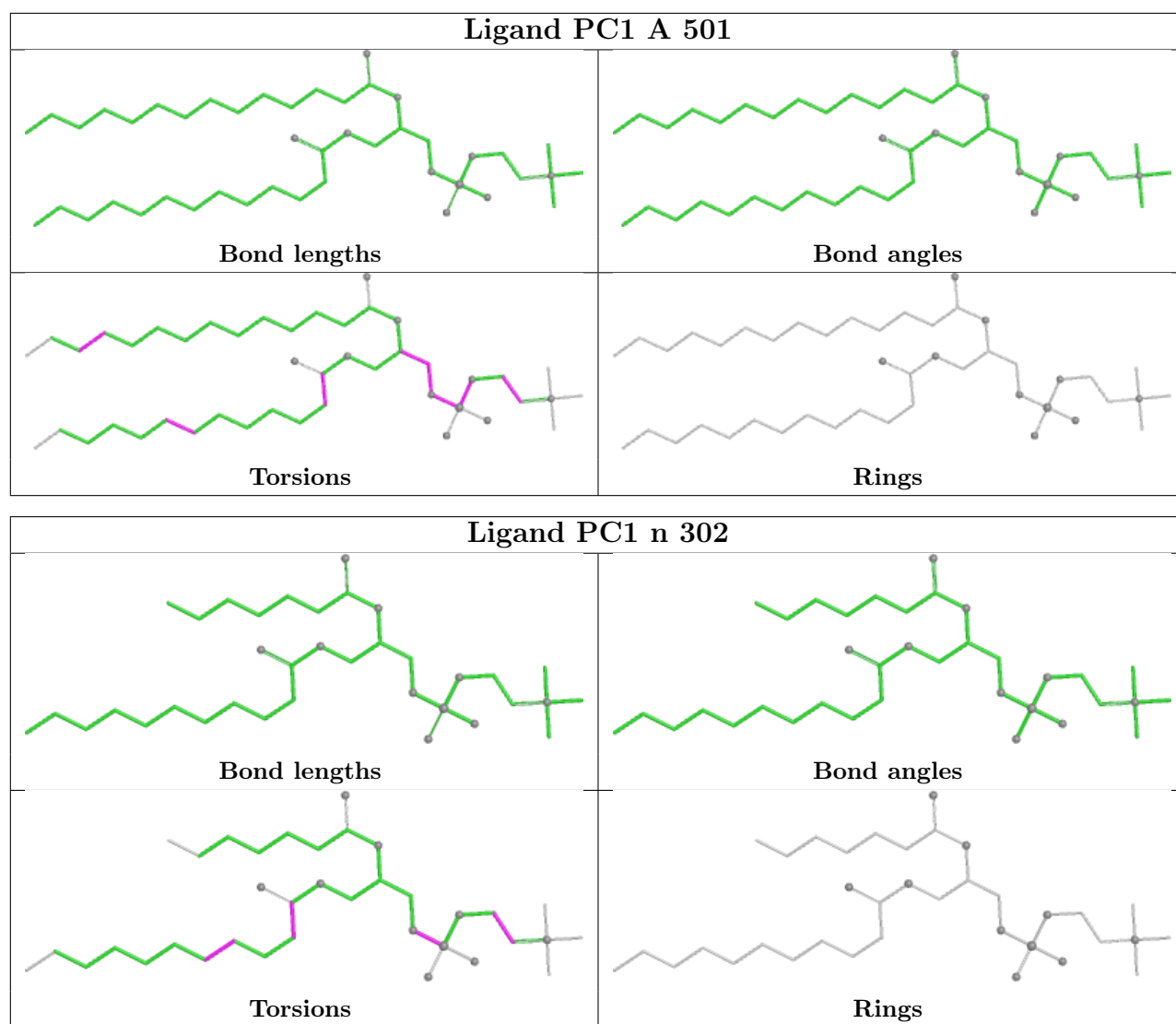
There are no ring outliers.

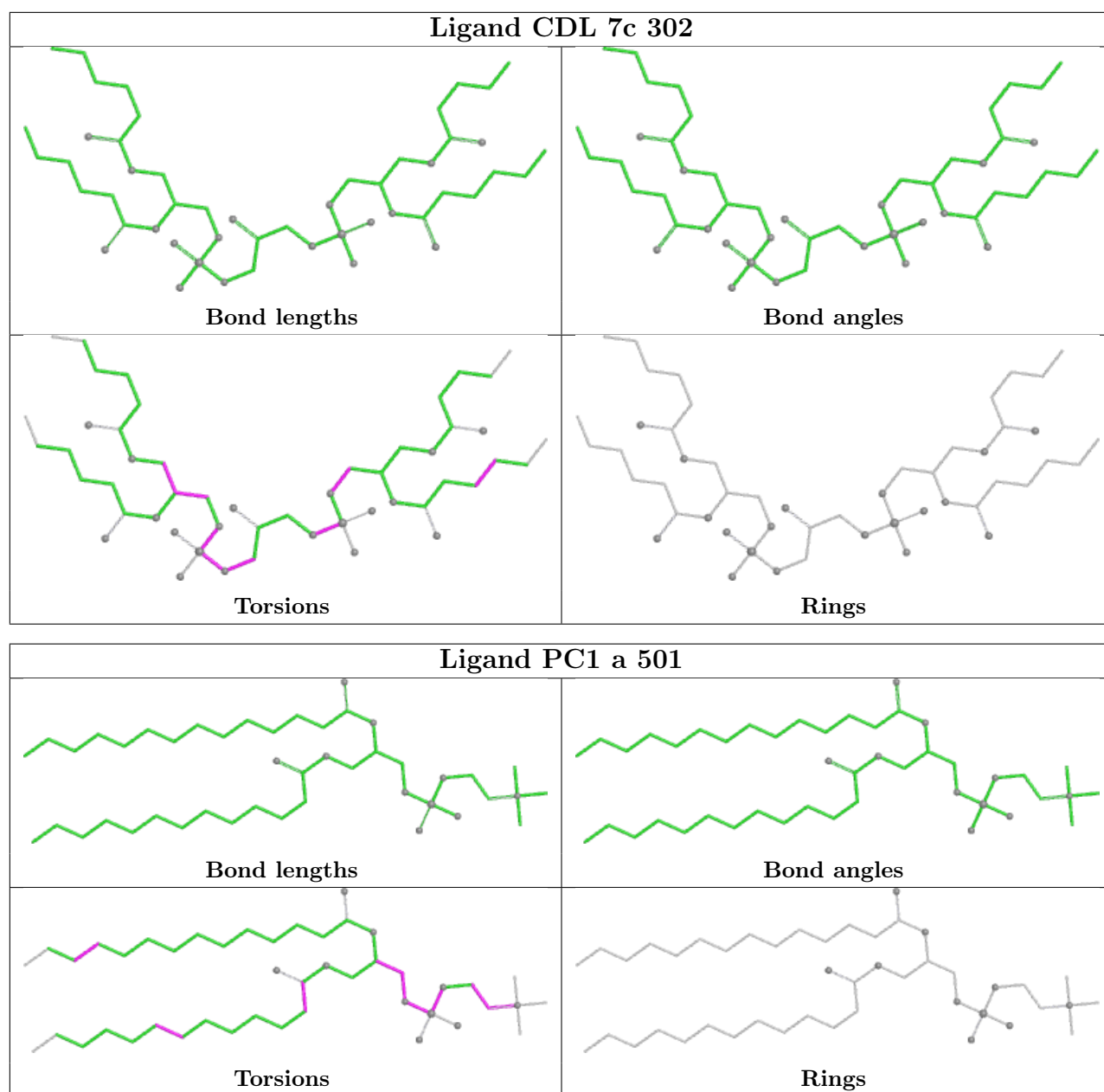
No monomer is involved in short contacts.

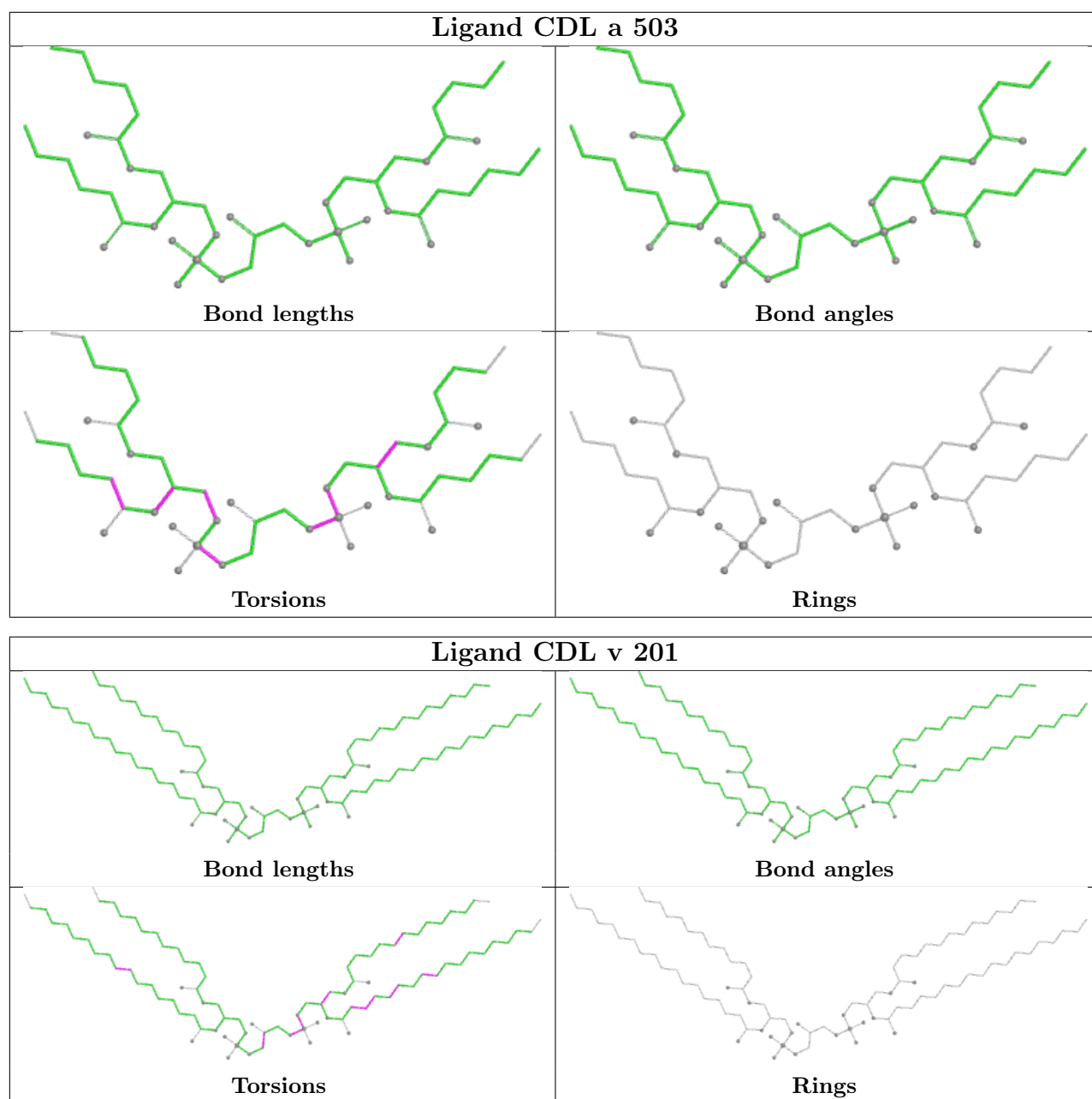
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

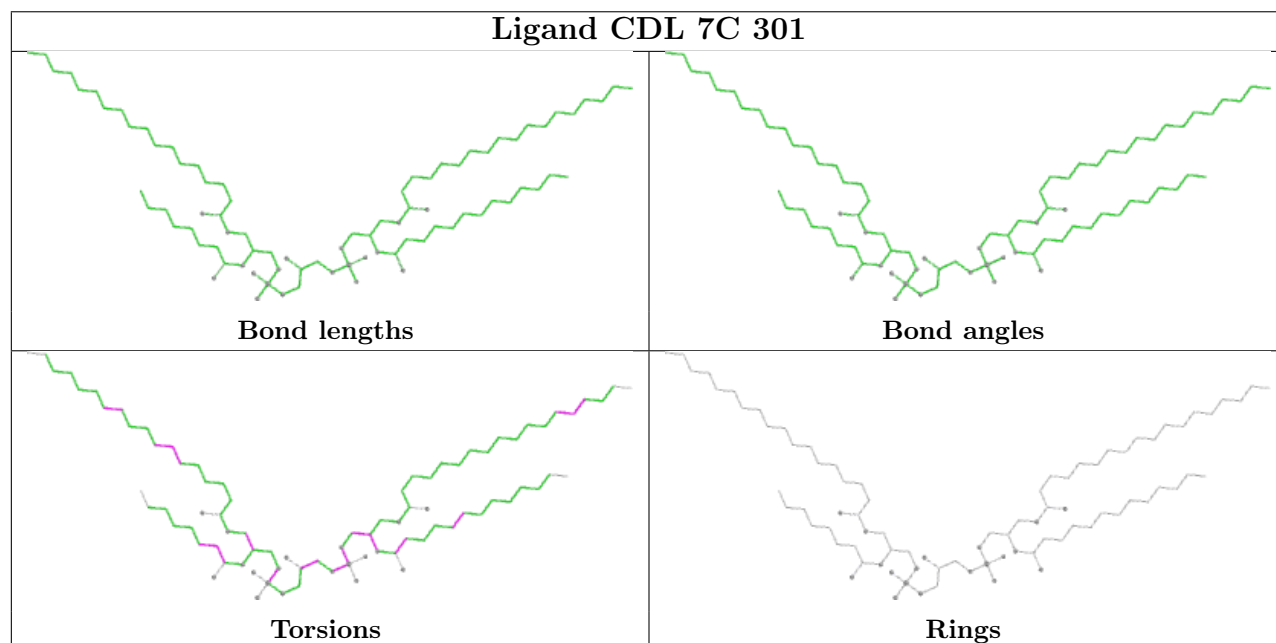
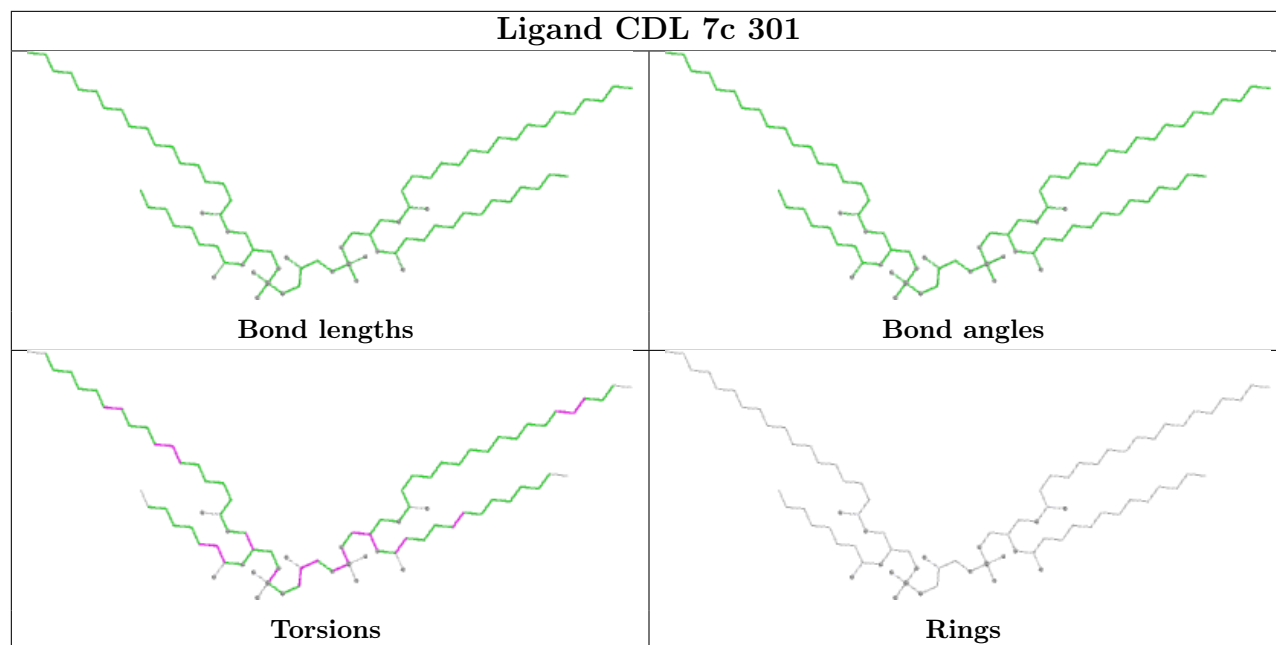


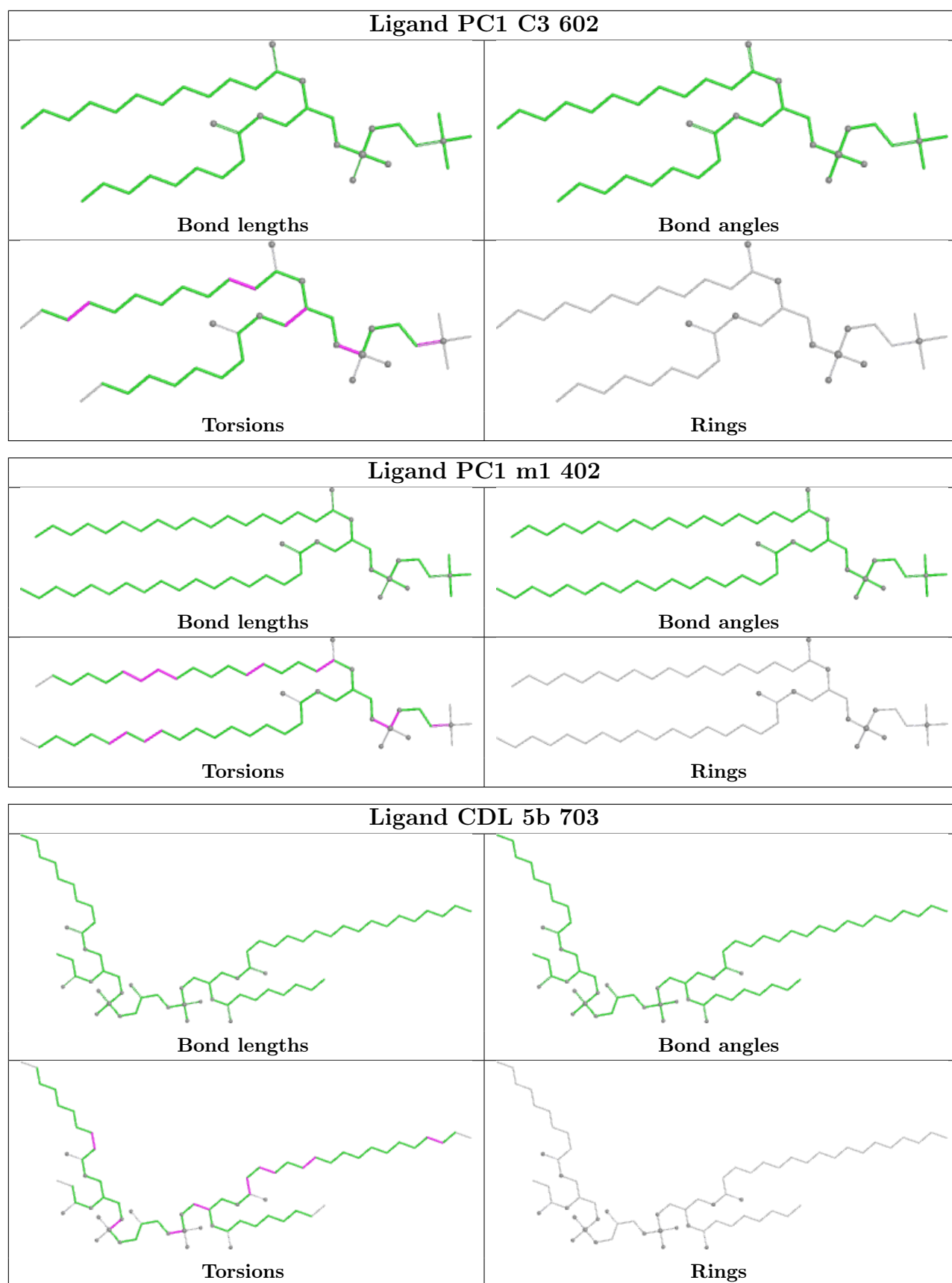


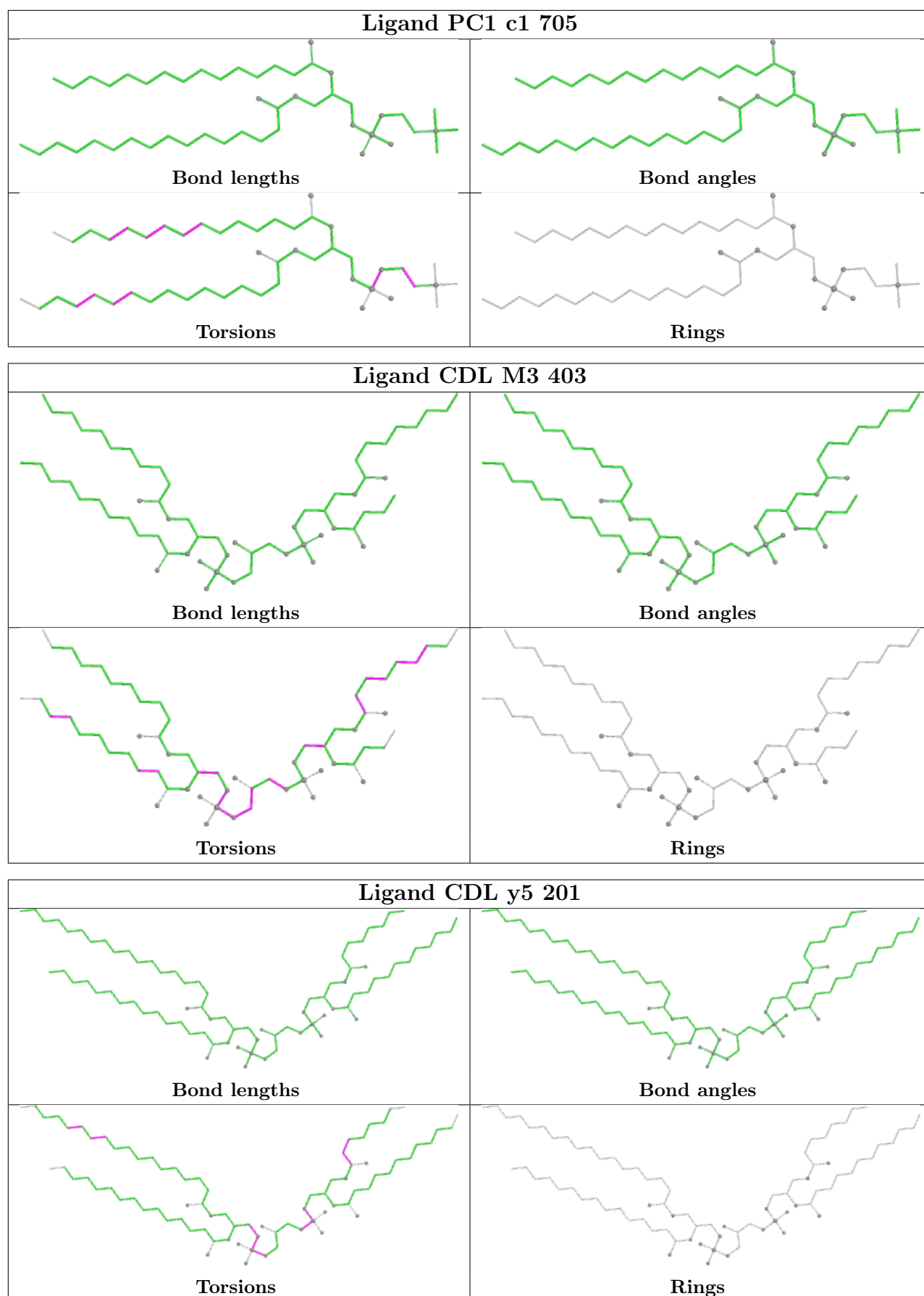


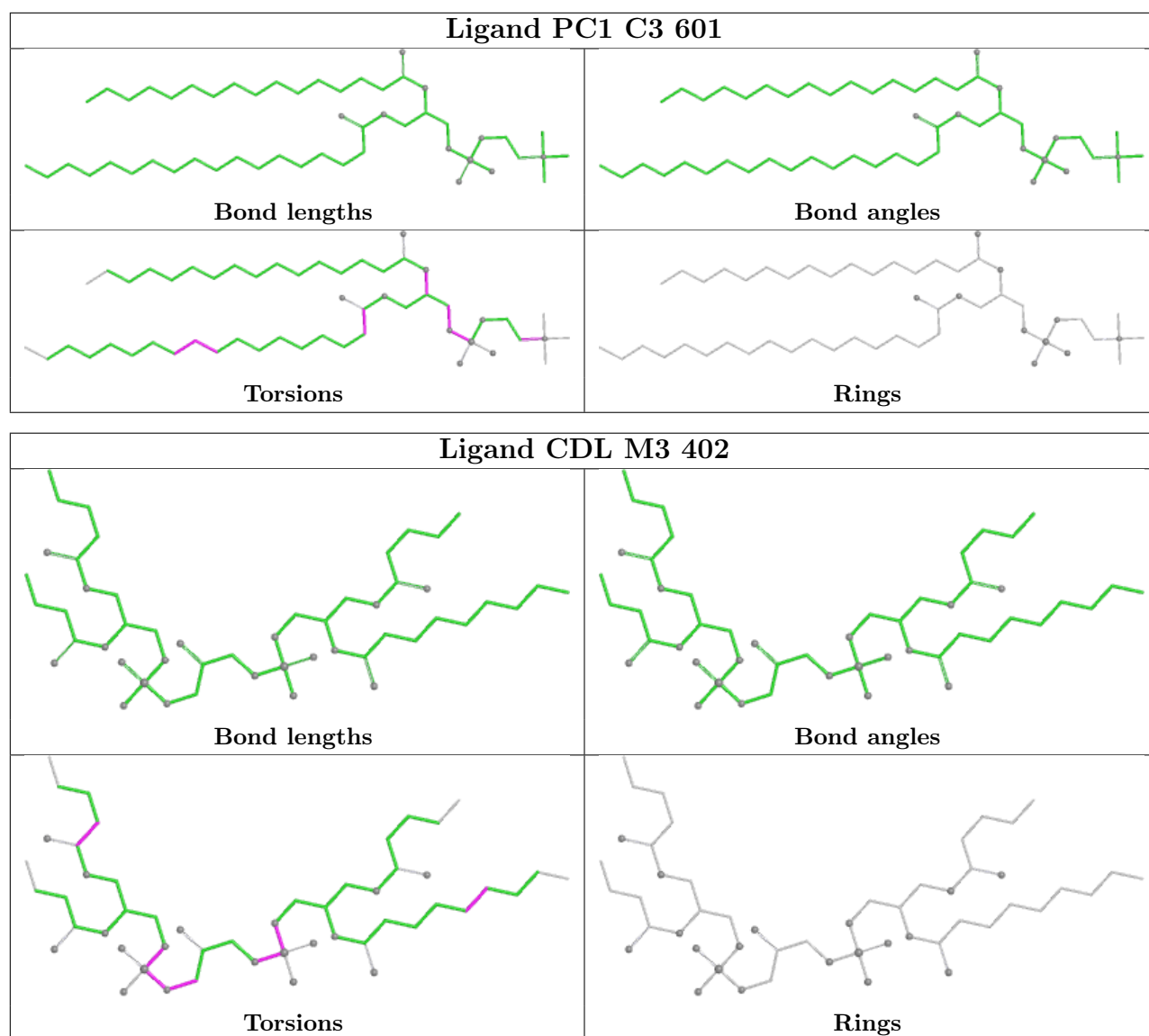


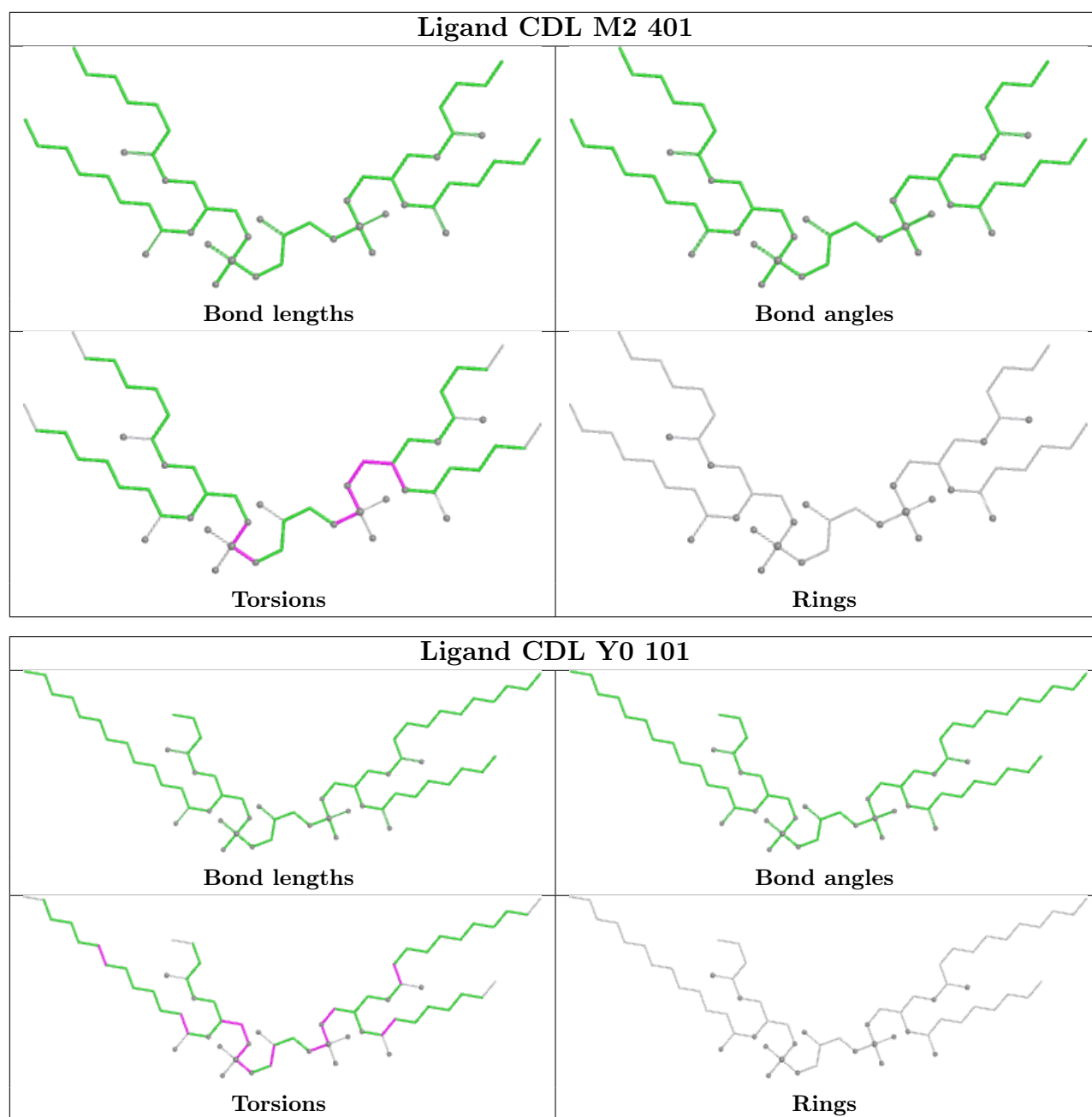


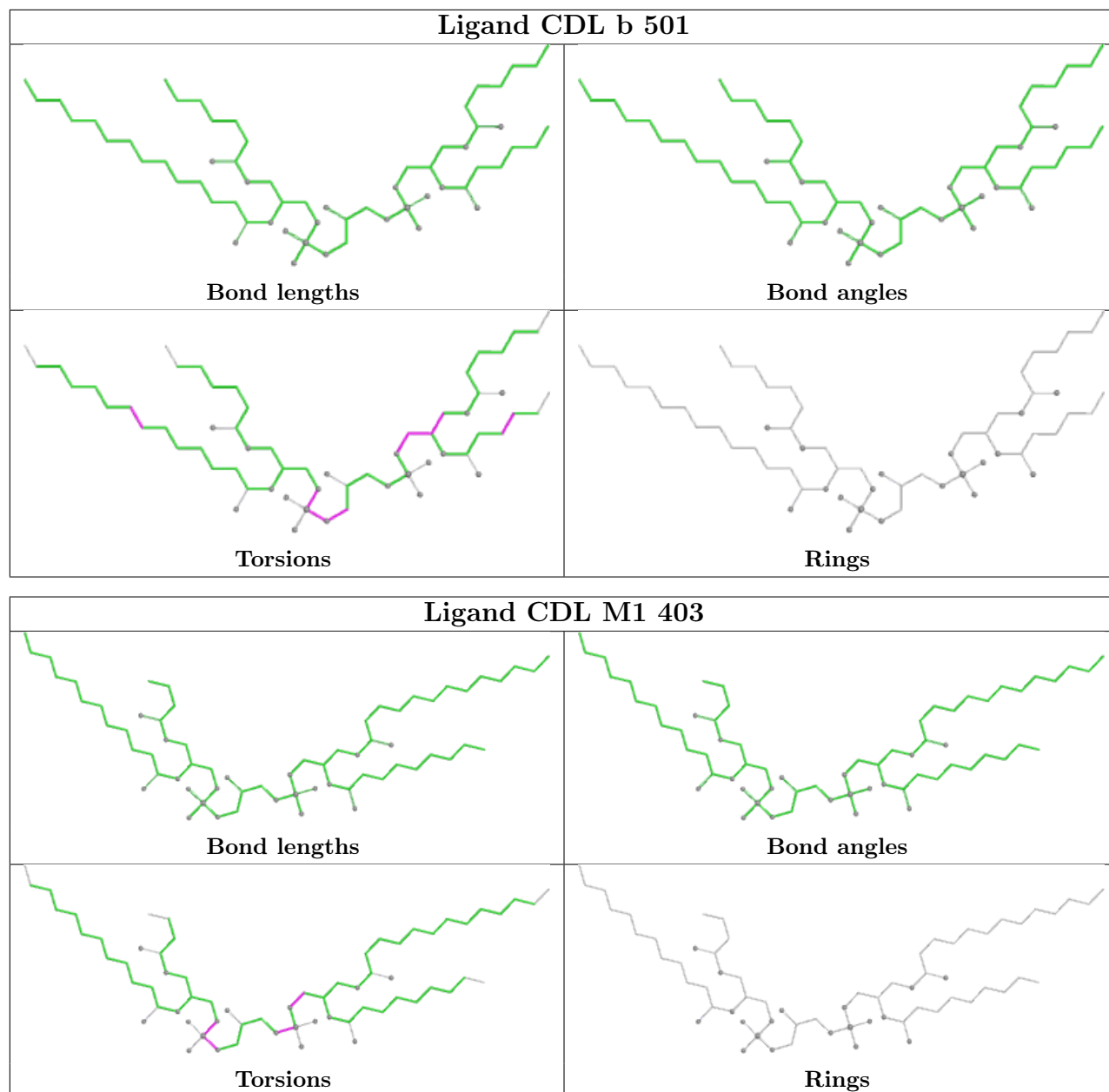


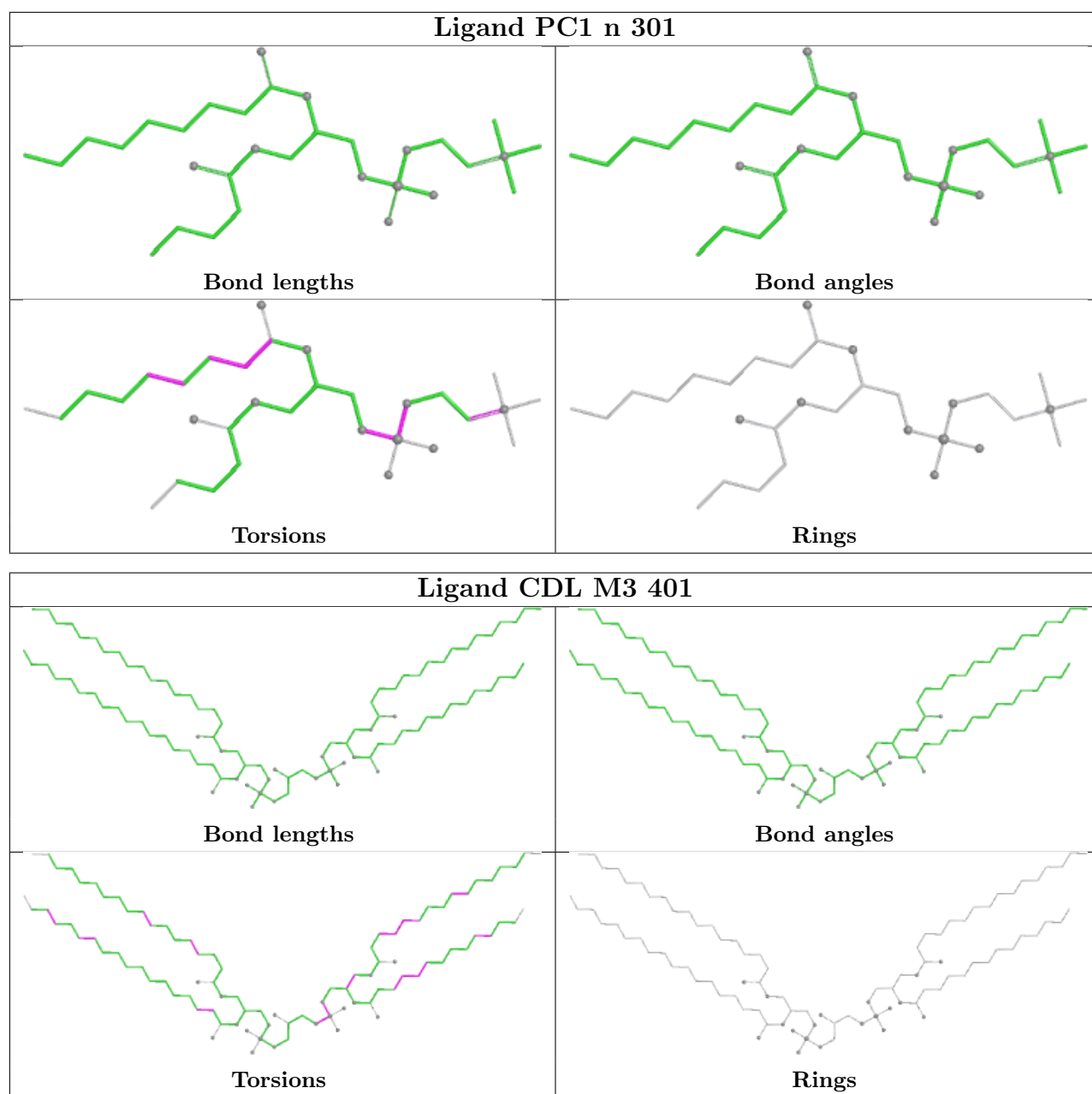


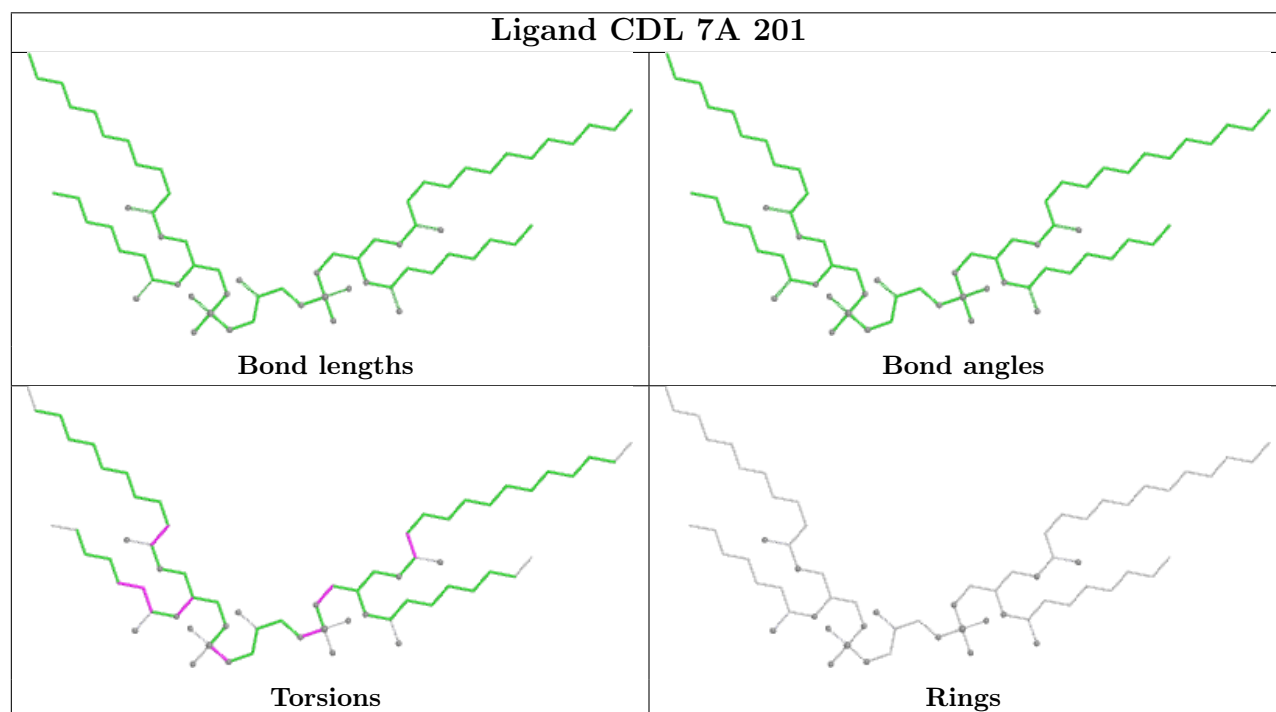
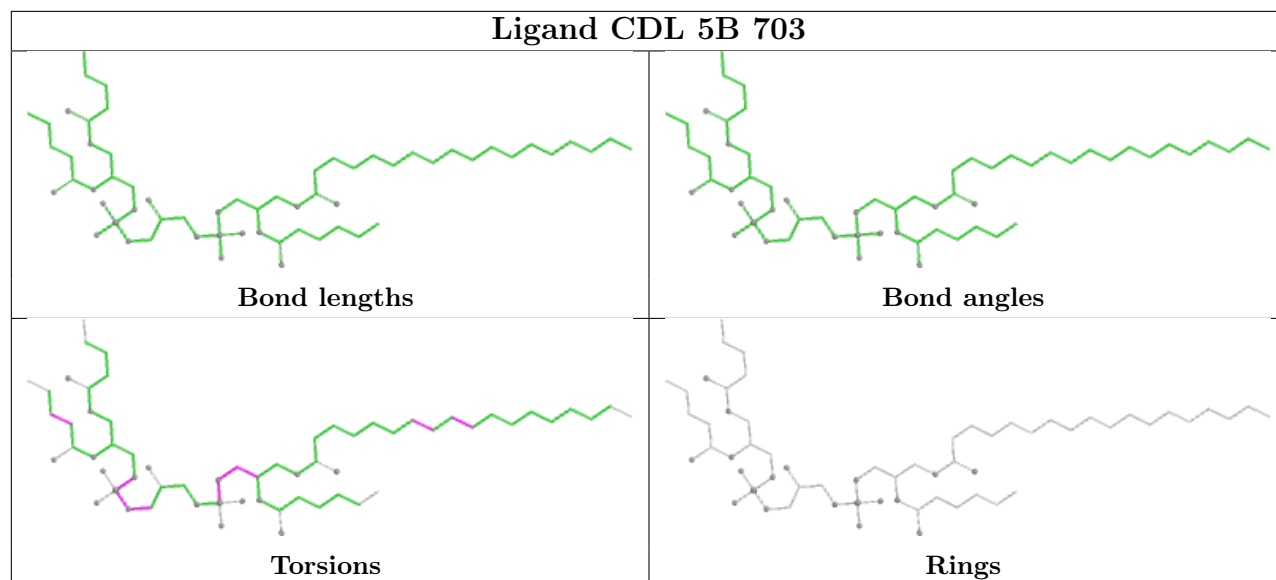


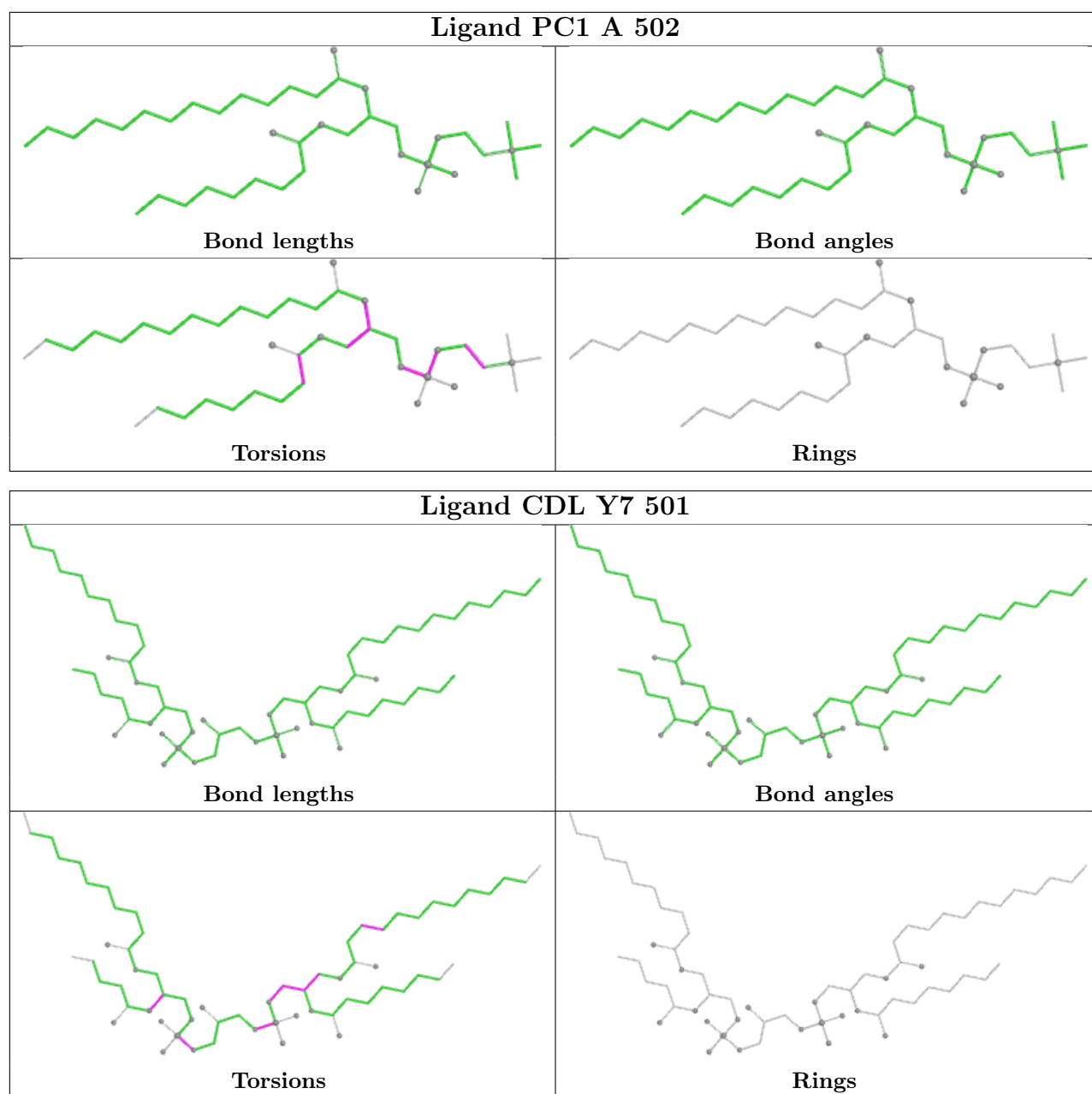


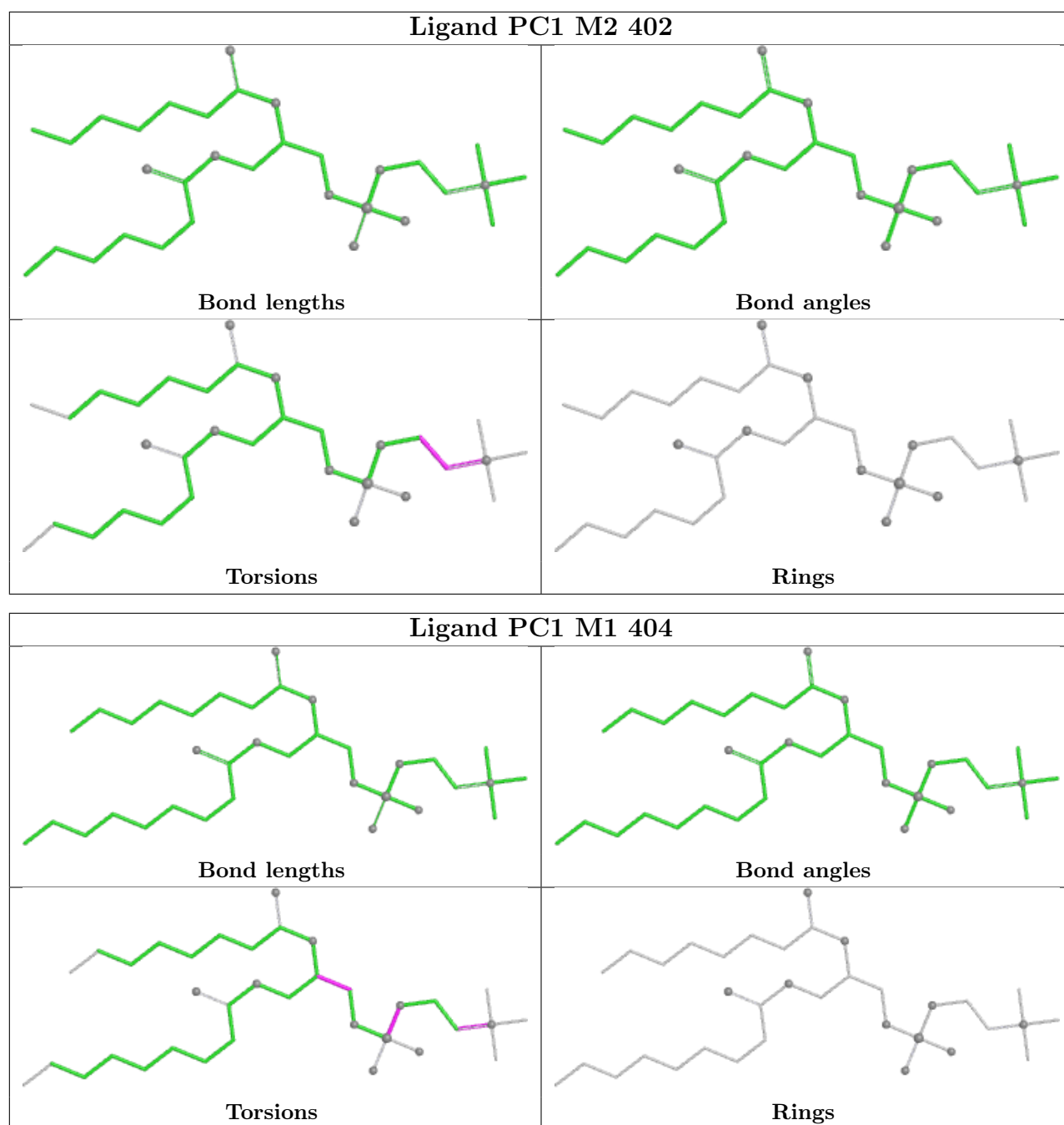


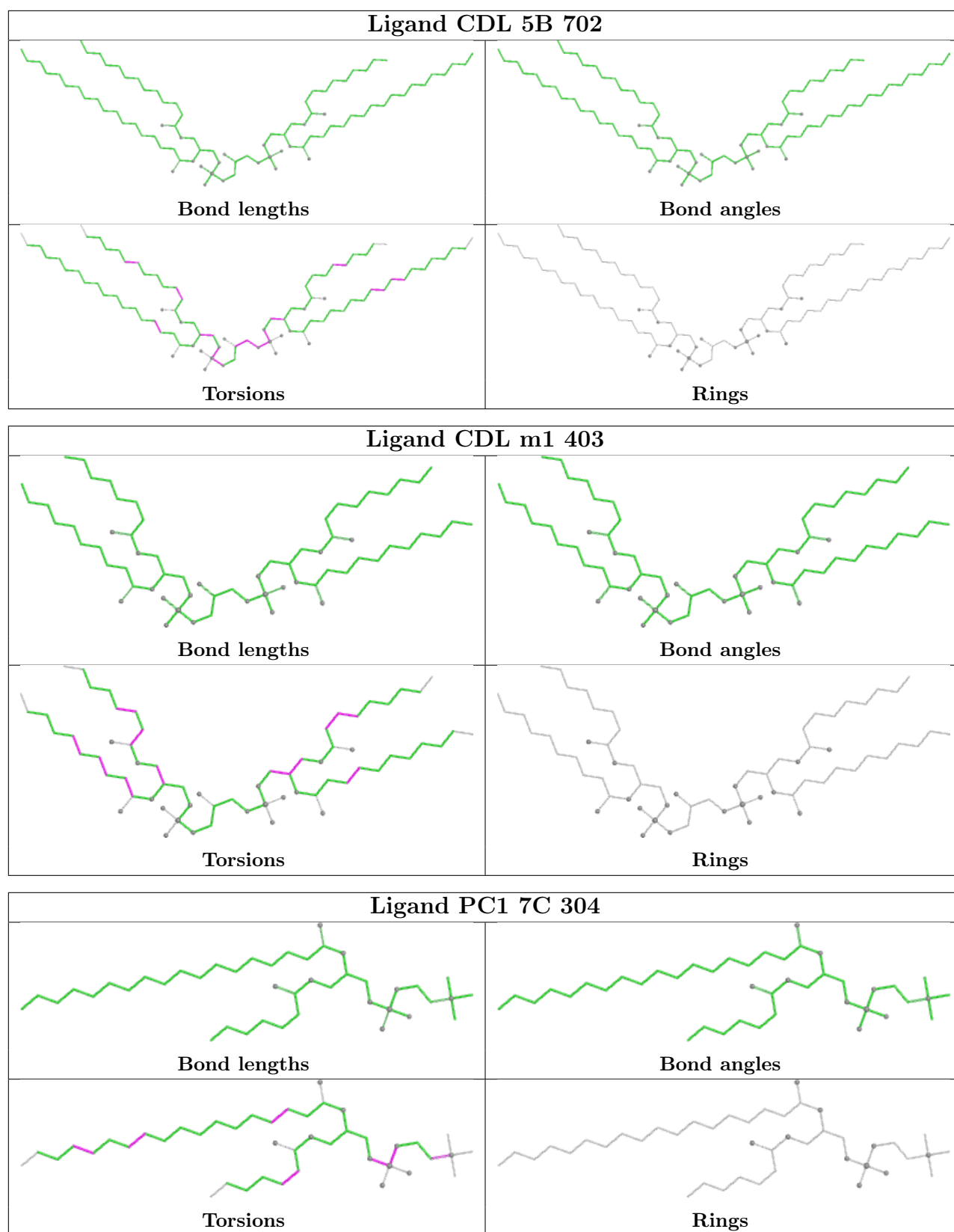


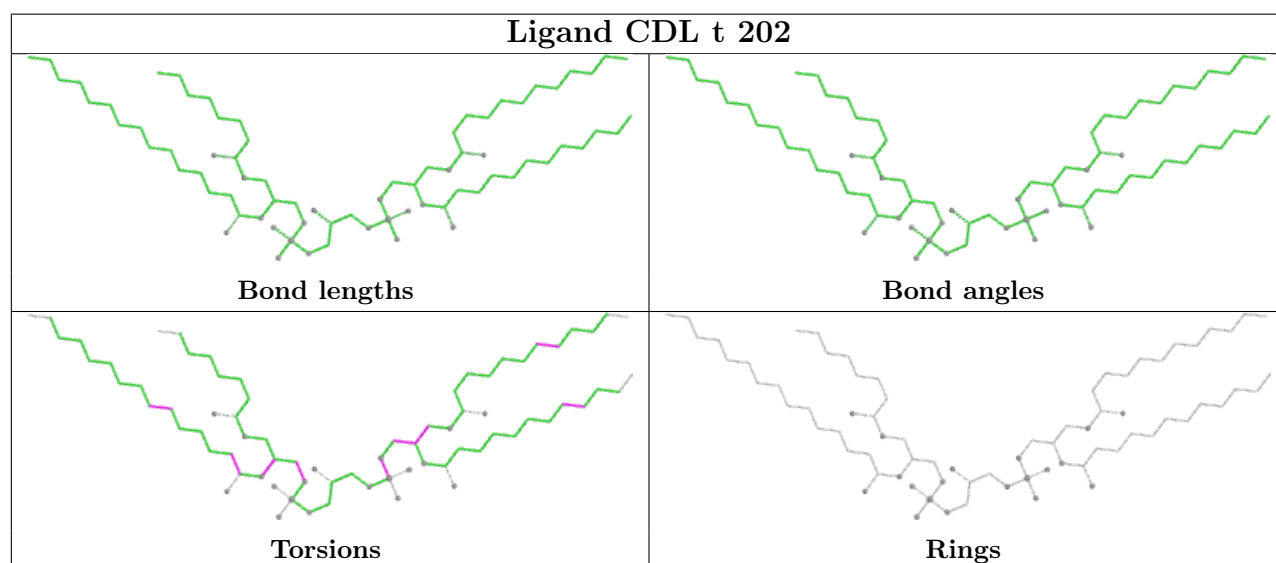
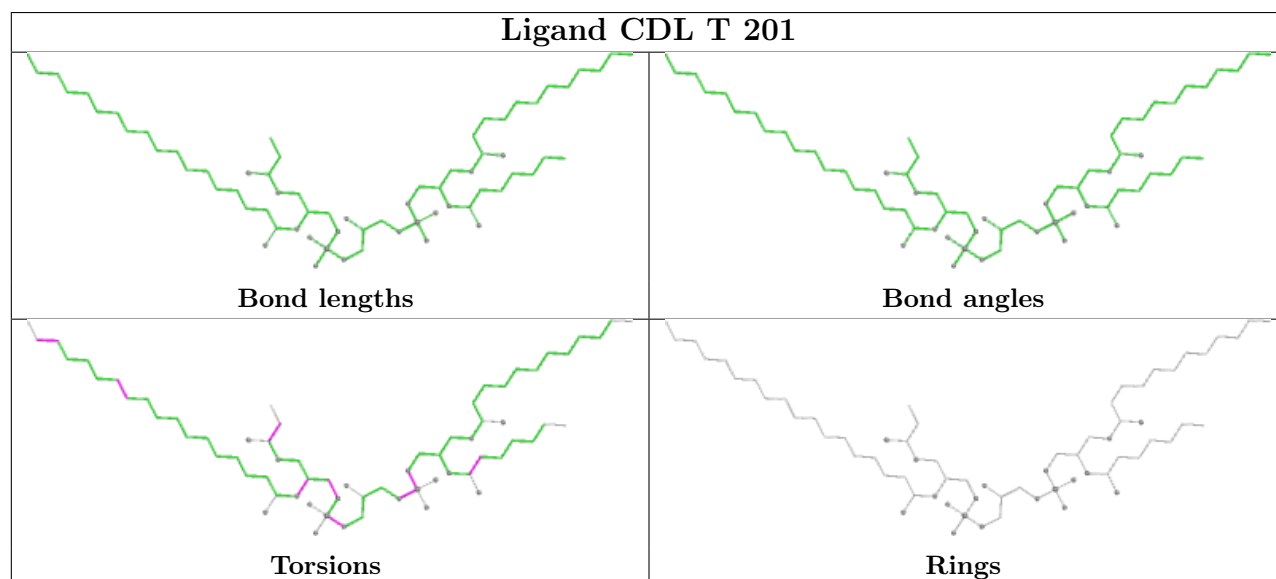
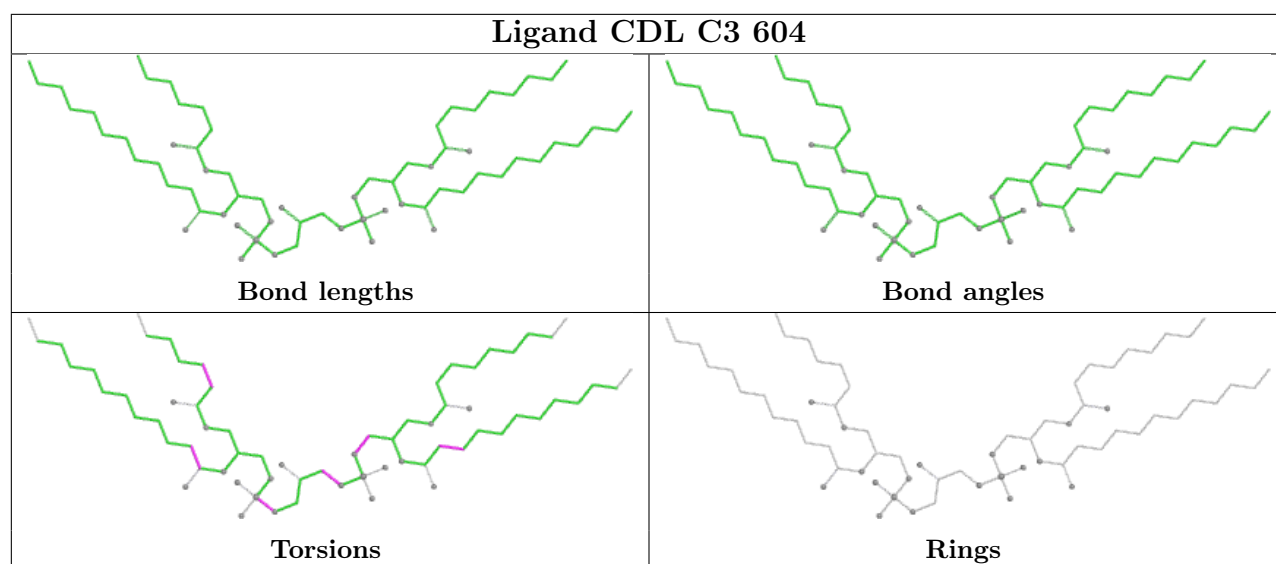


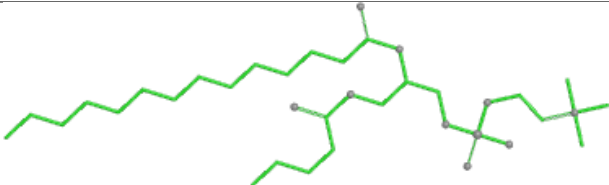
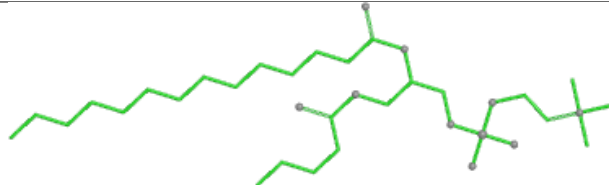
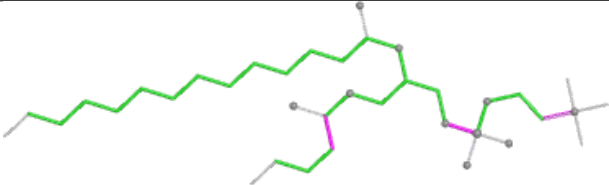
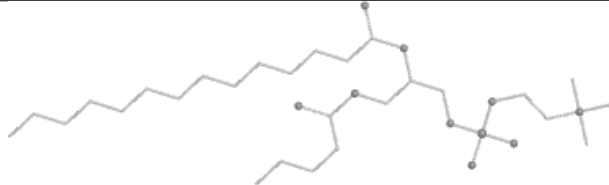


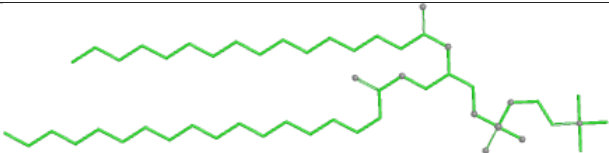
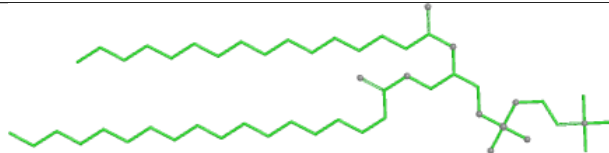
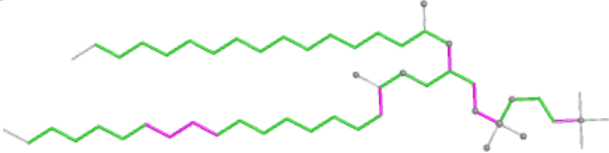
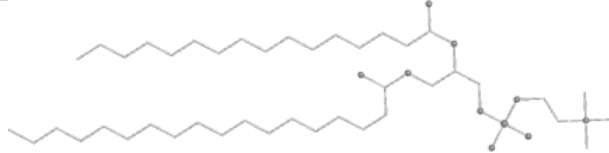


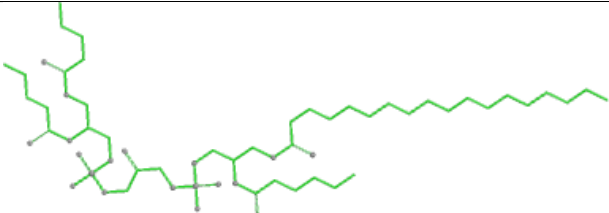
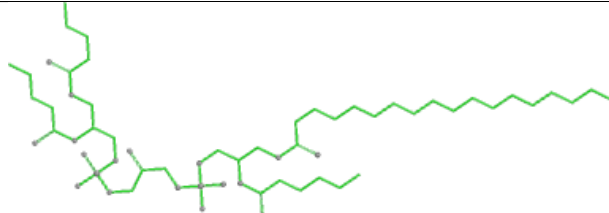
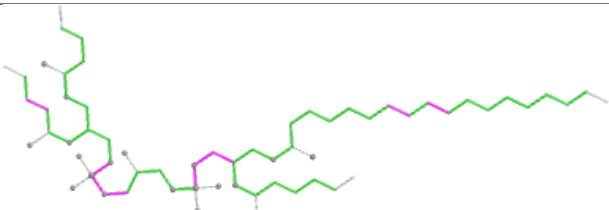
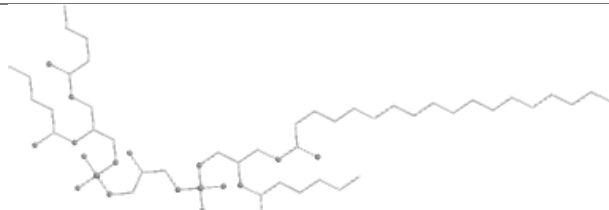


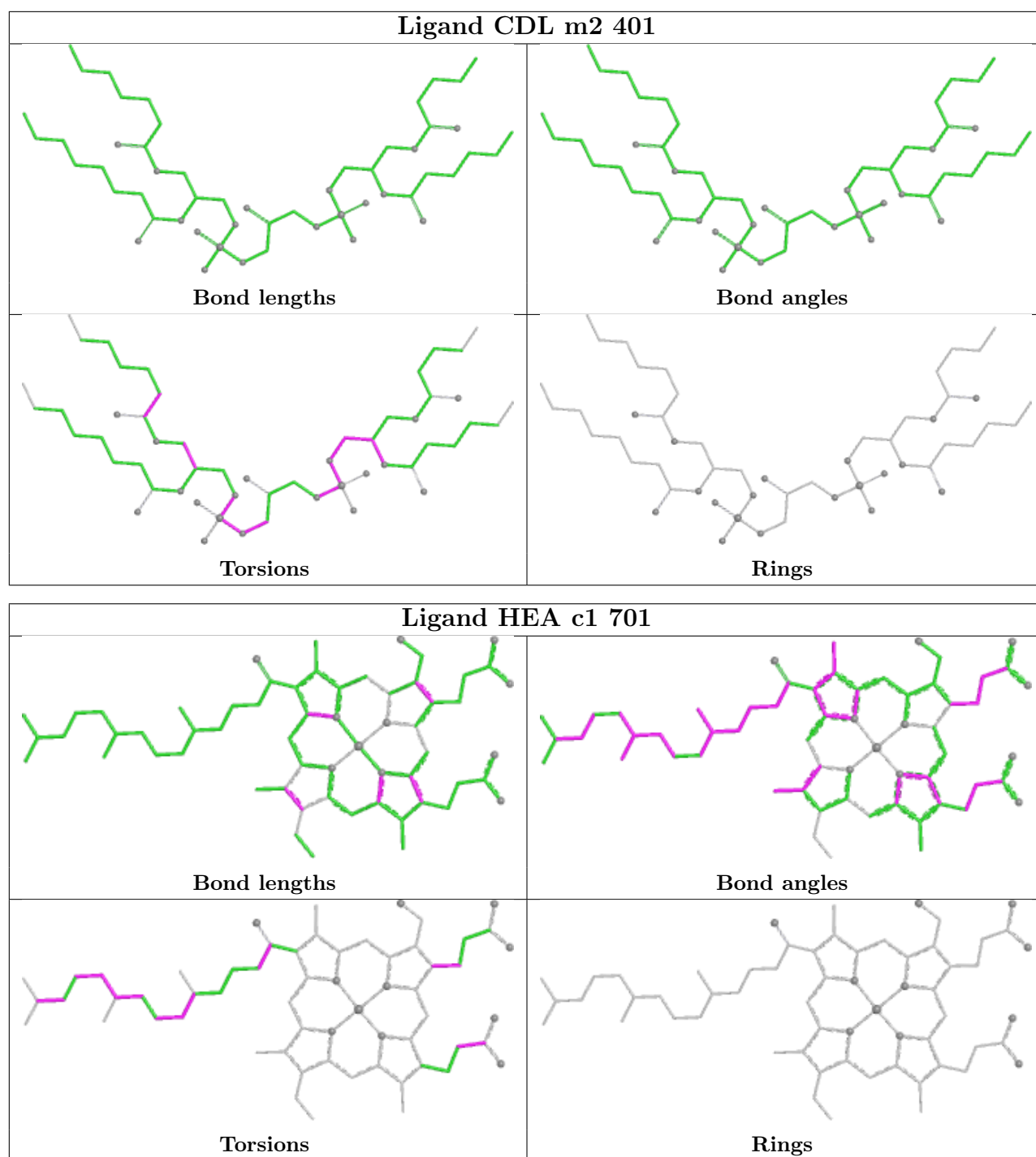


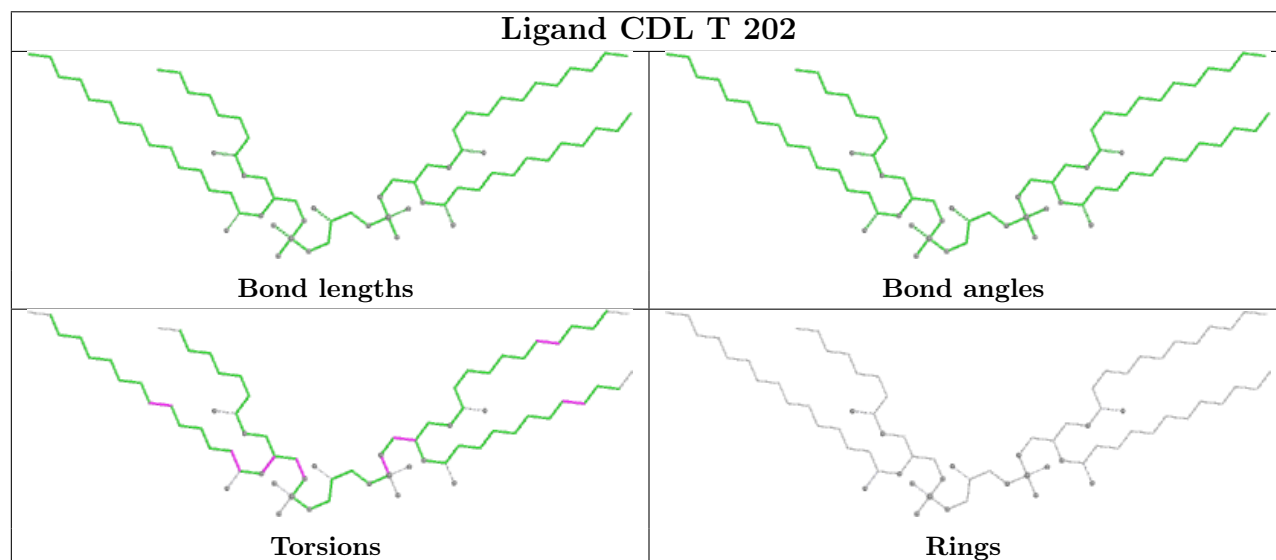
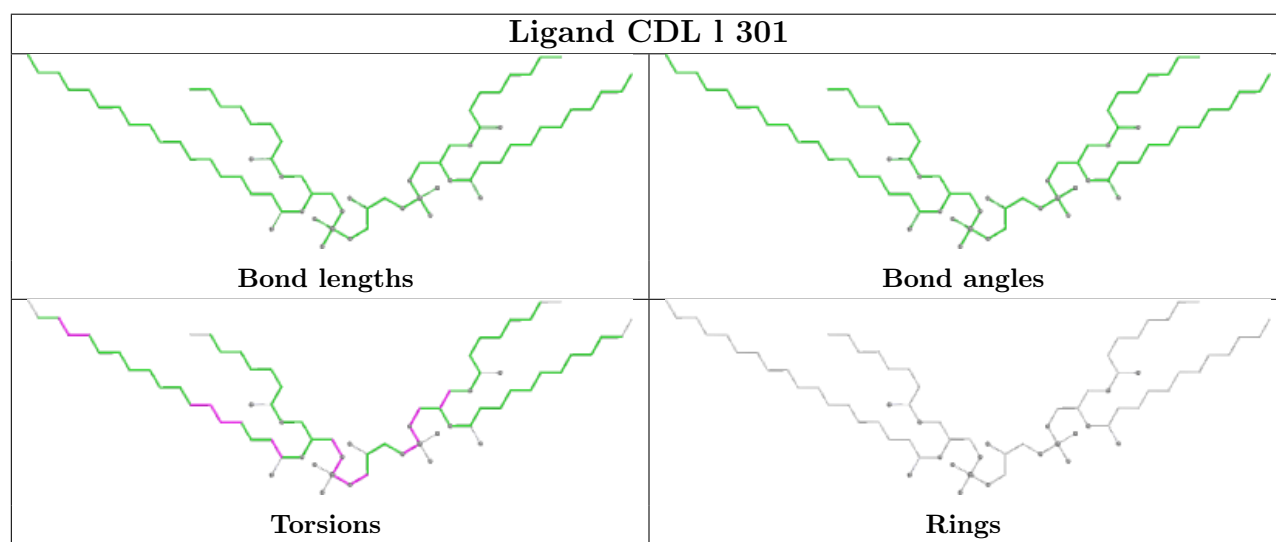
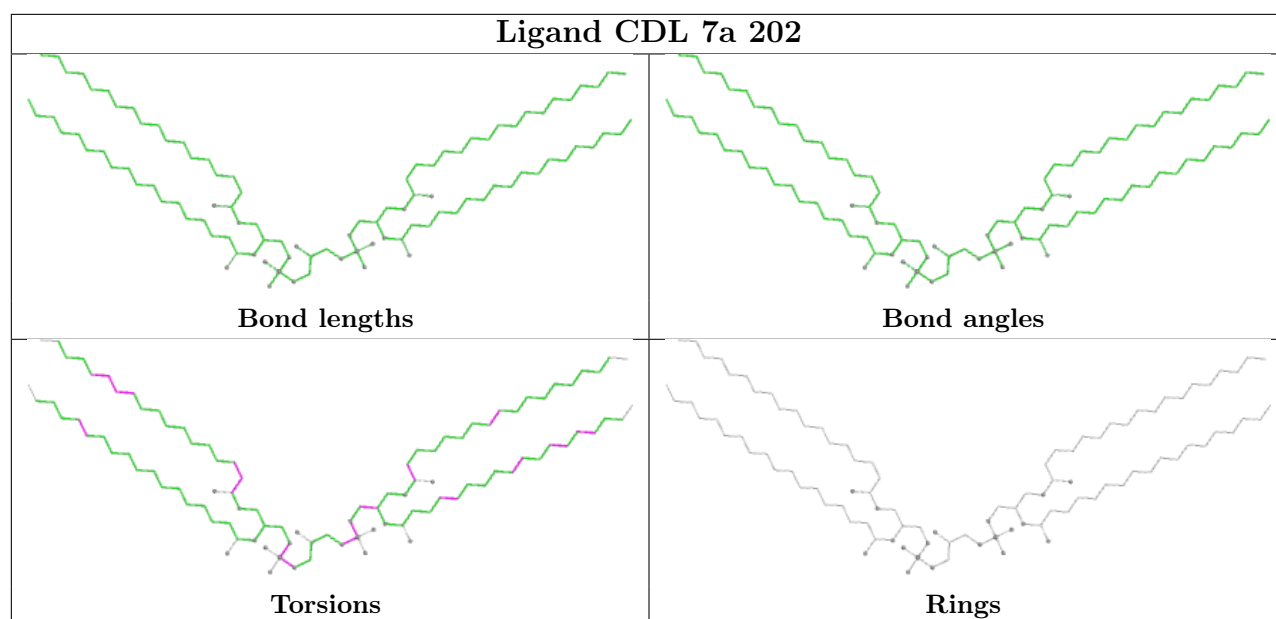


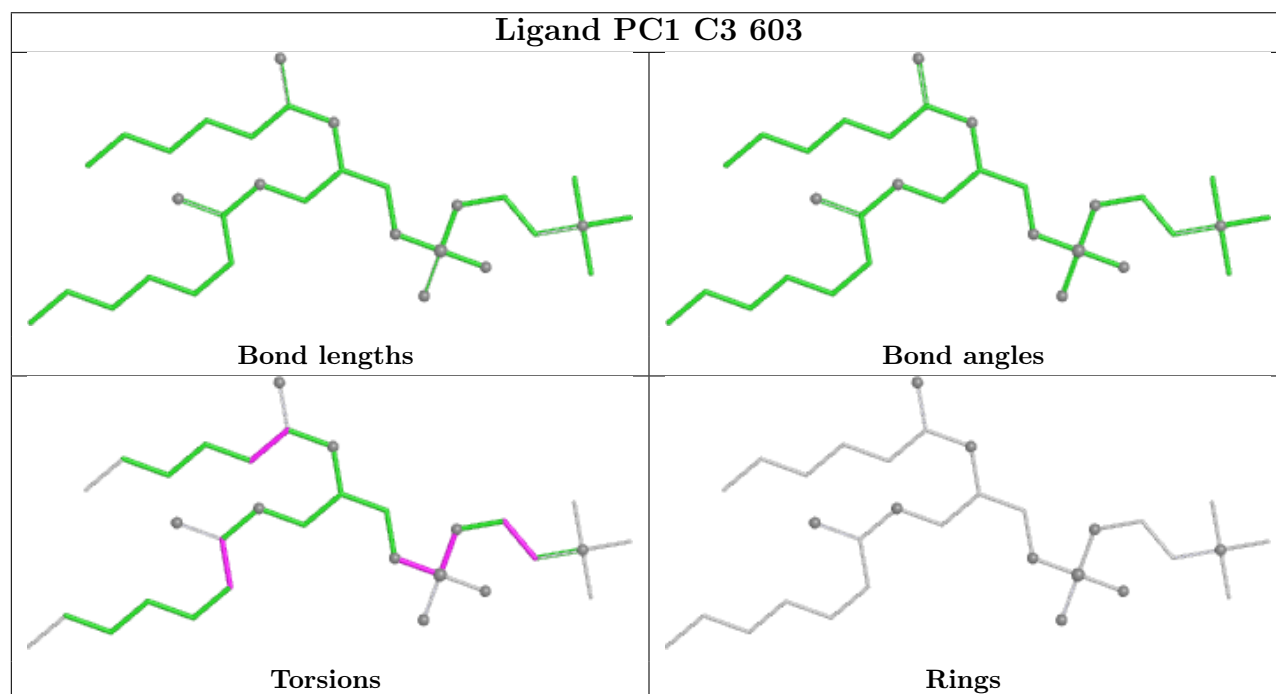
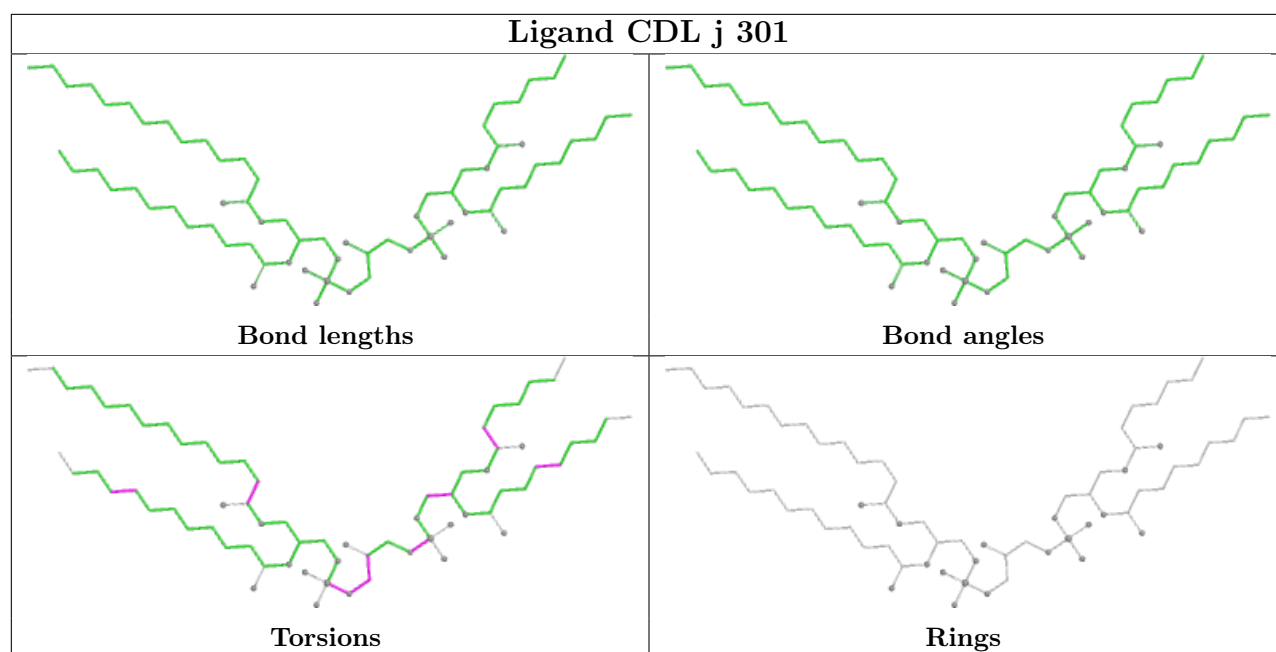
Ligand PC1 J 302	
	
Bond lengths	Bond angles
	
Torsions	Rings

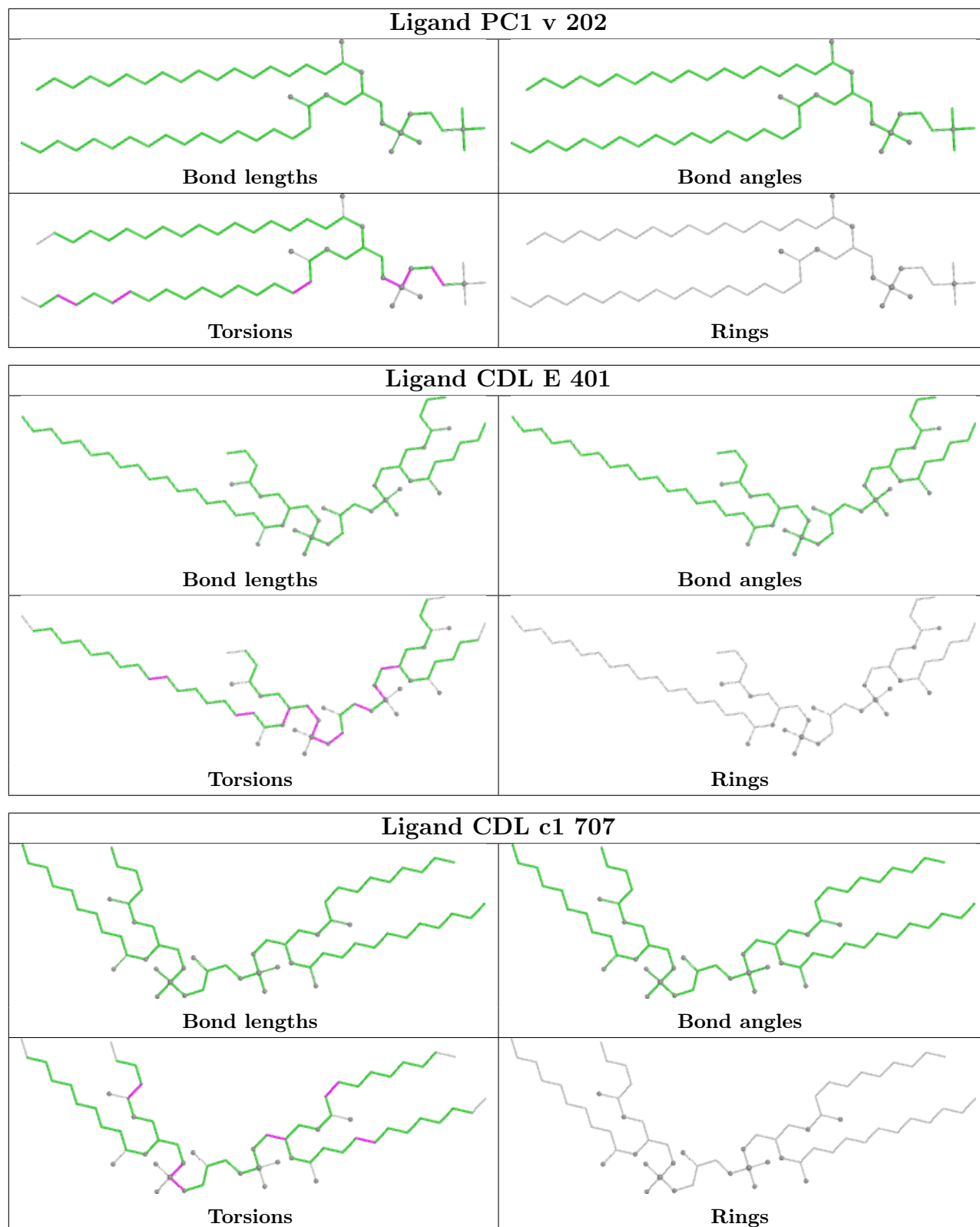
Ligand PC1 c3 601	
	
Bond lengths	Bond angles
	
Torsions	Rings

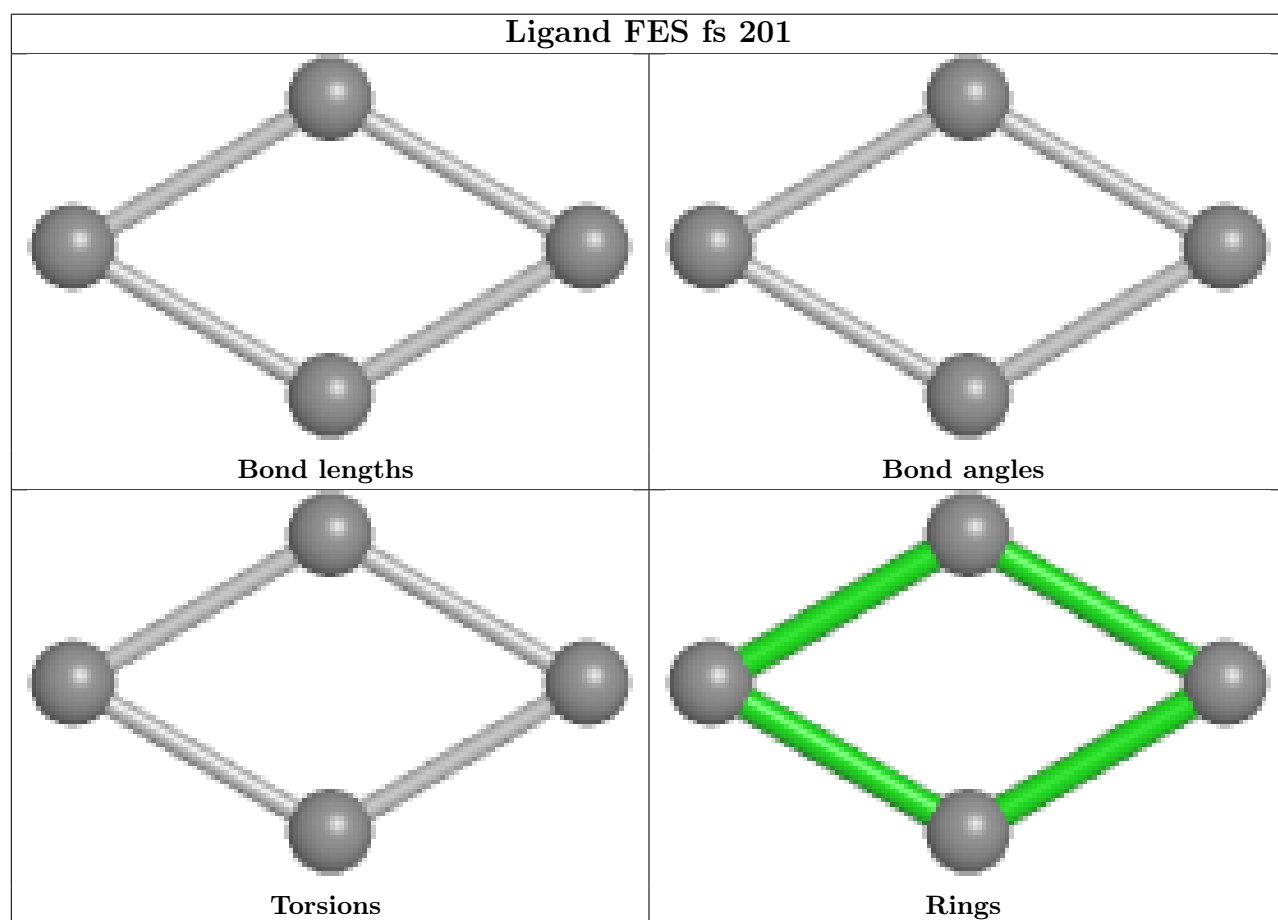
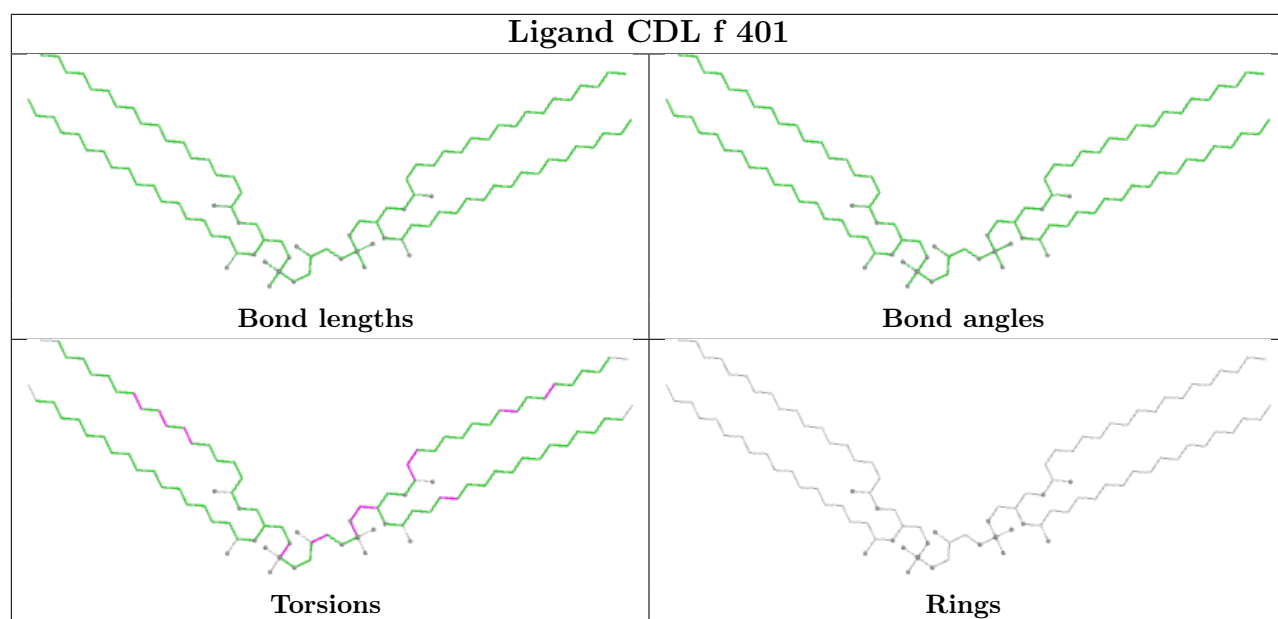
Ligand CDL k 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

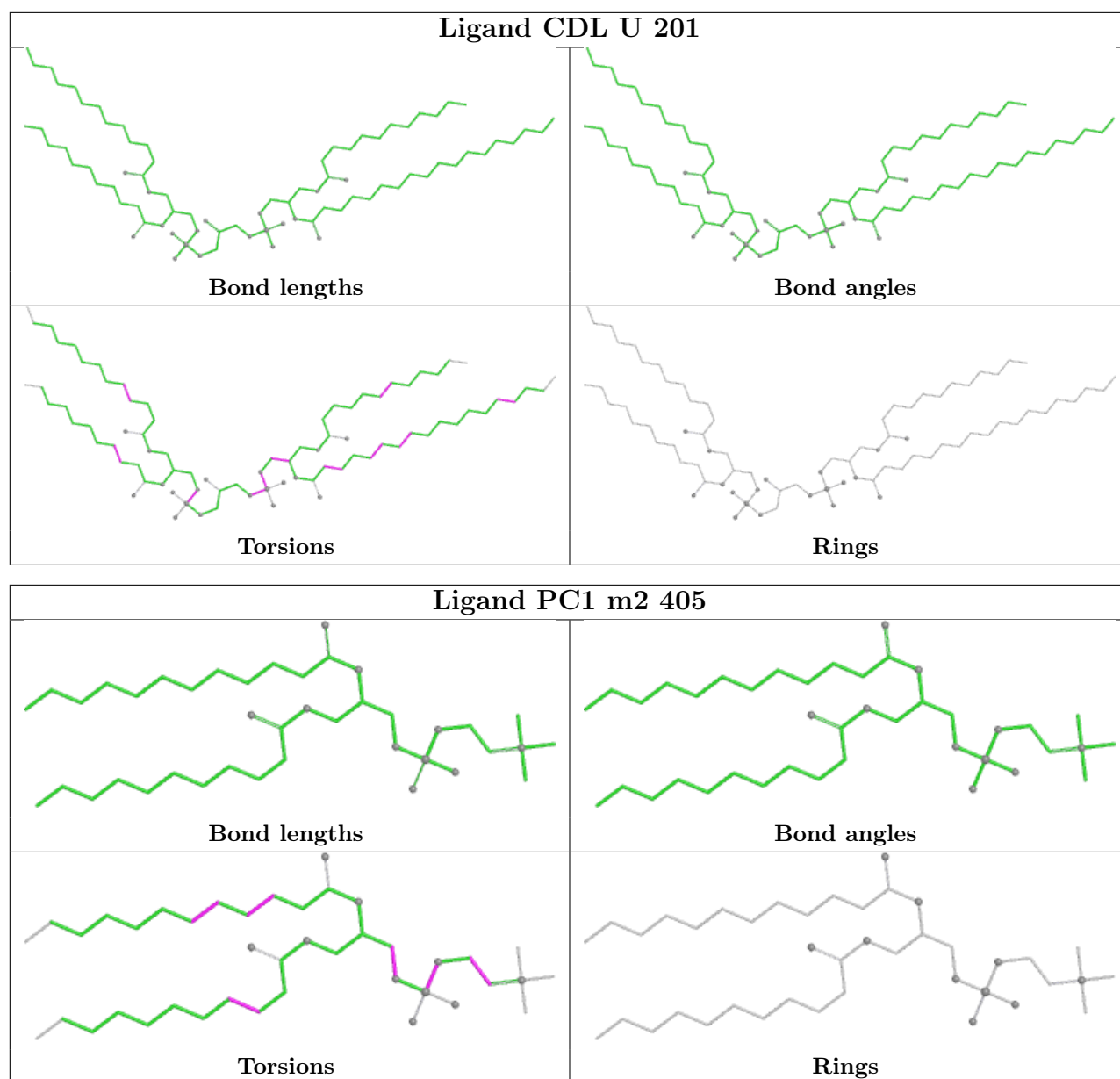


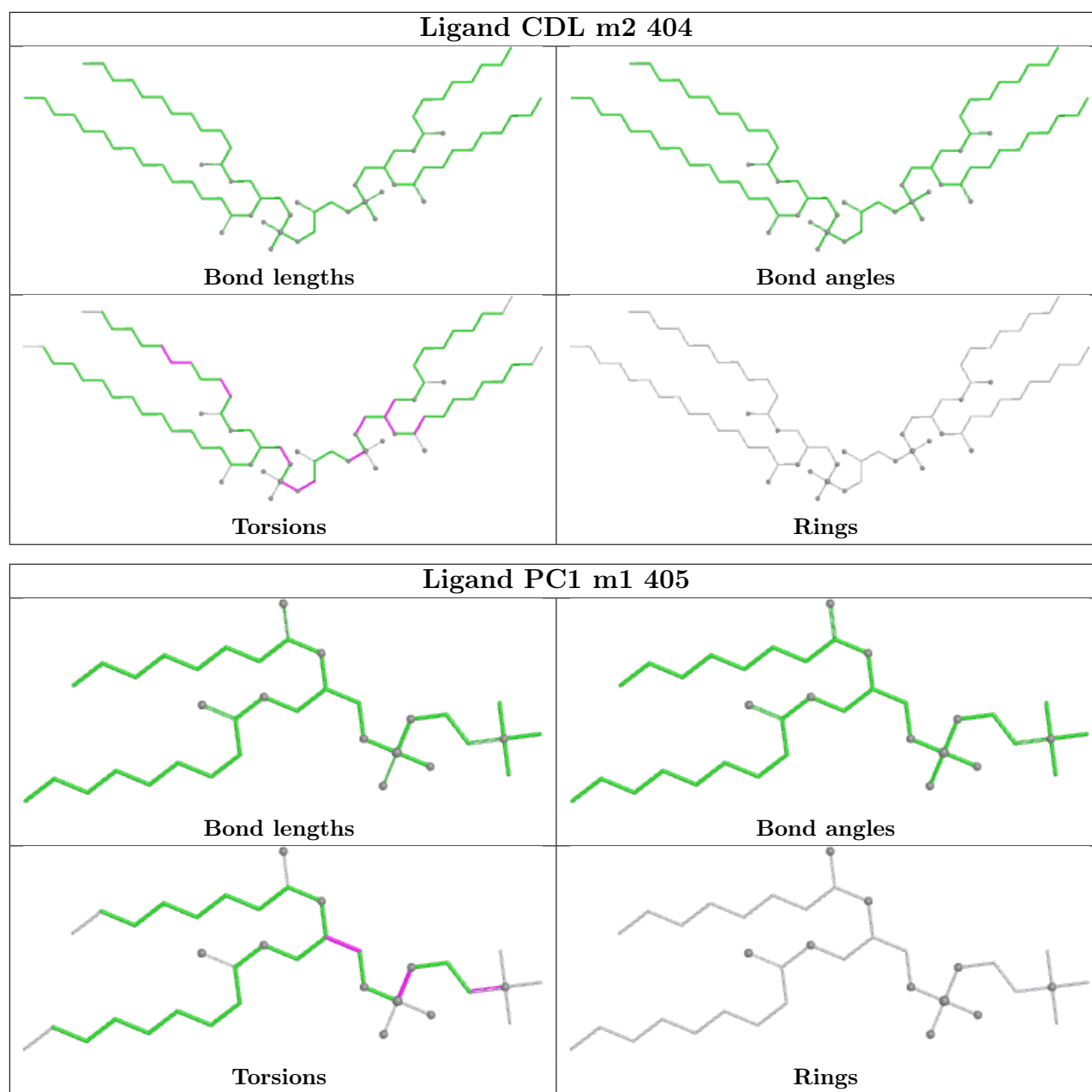


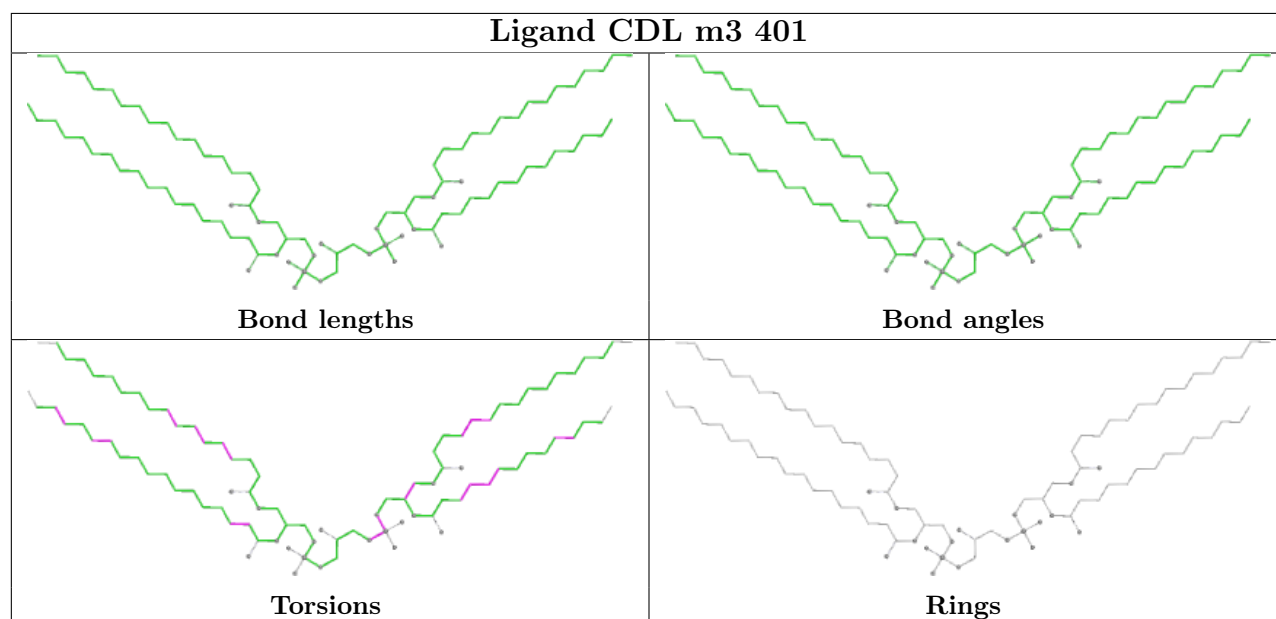
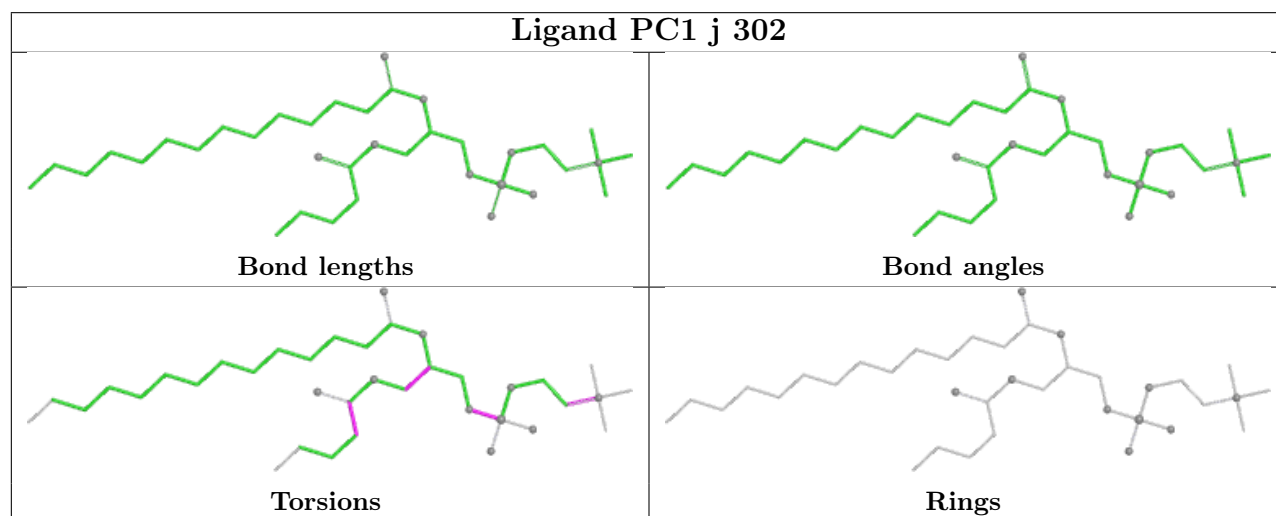
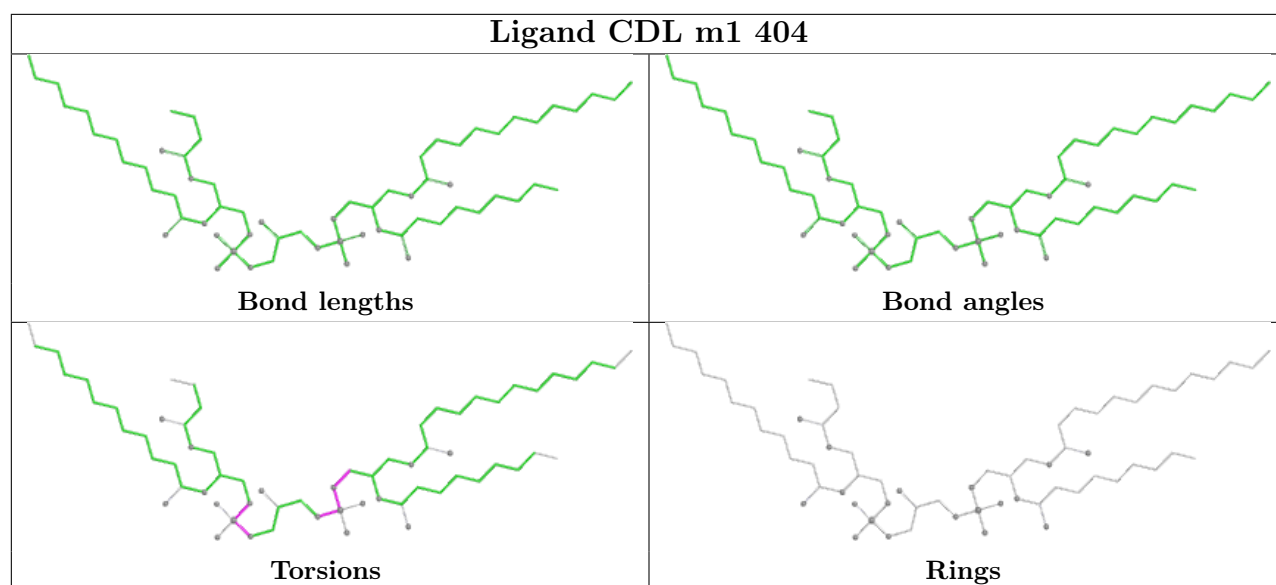


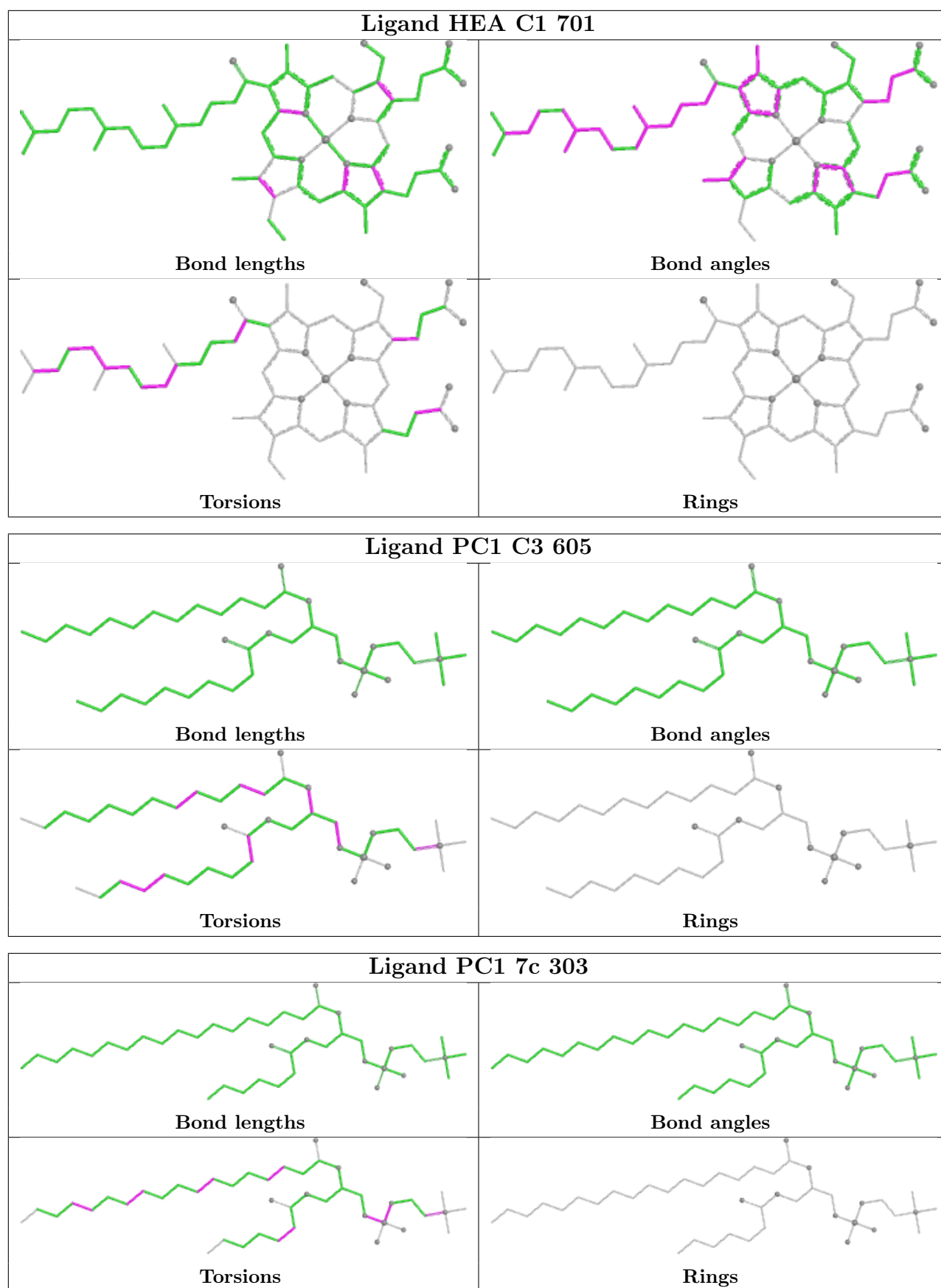


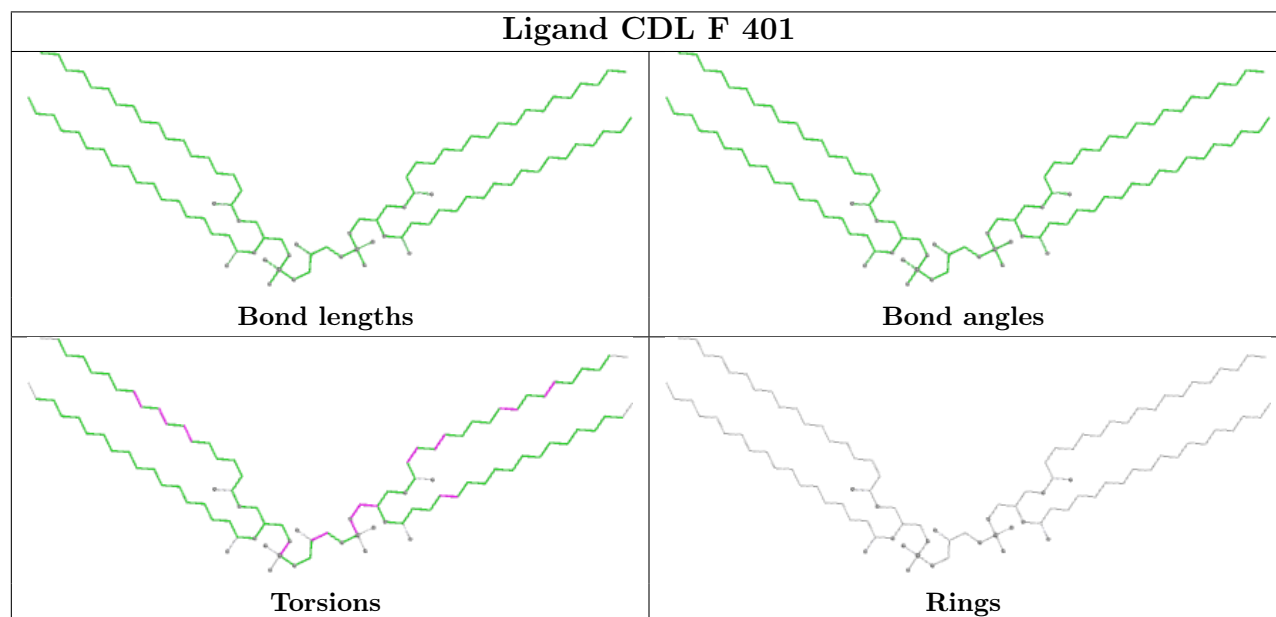
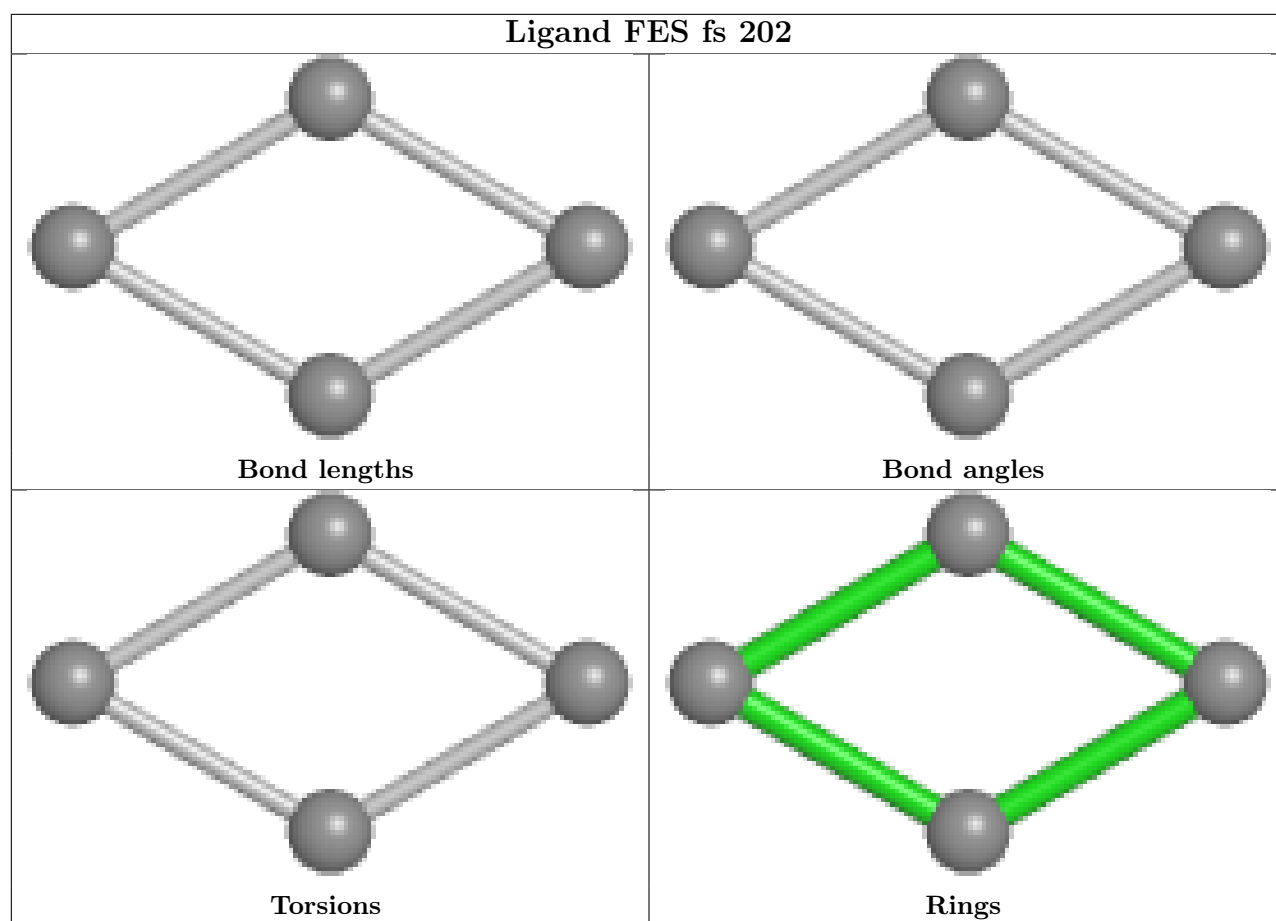


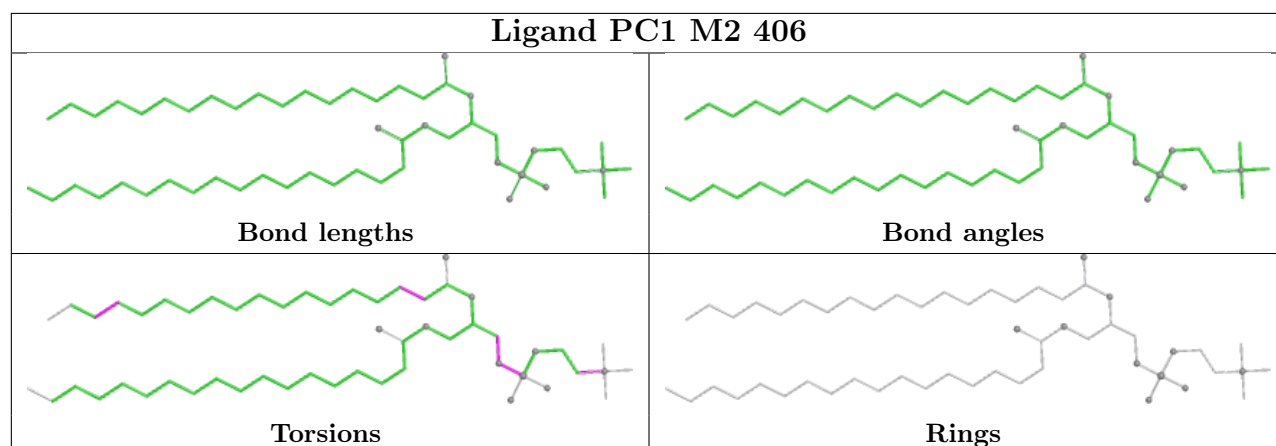
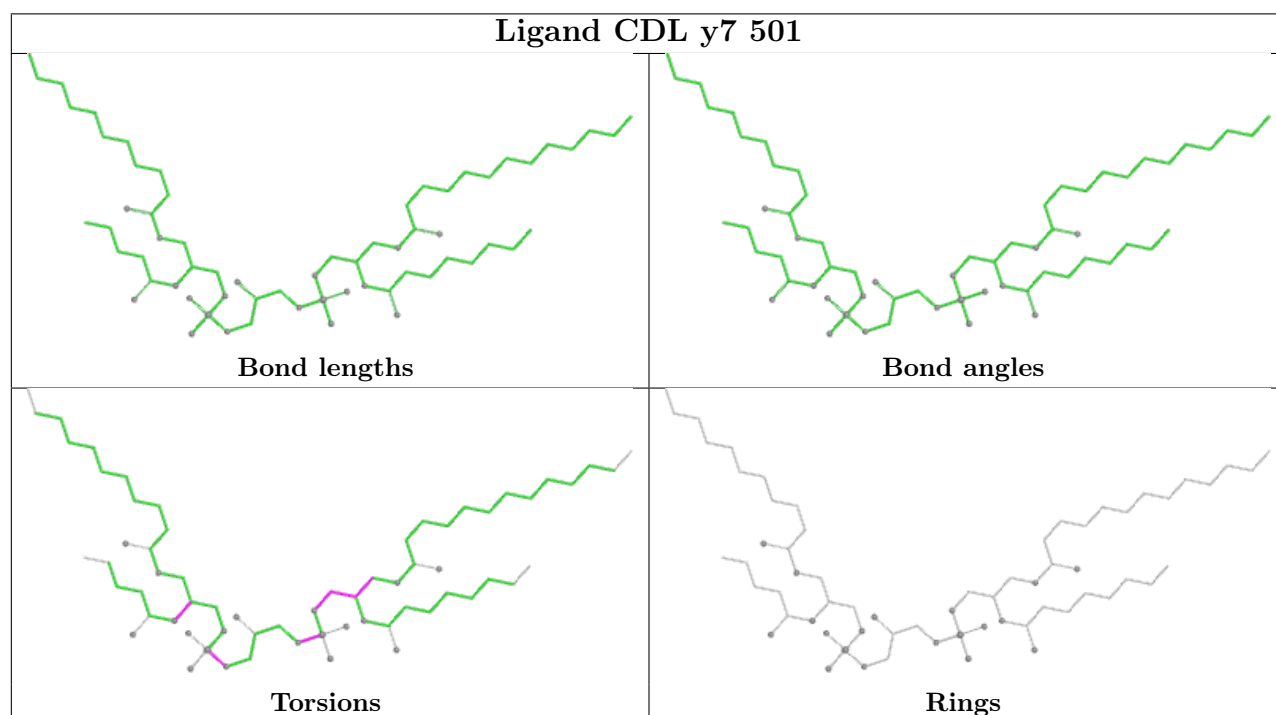
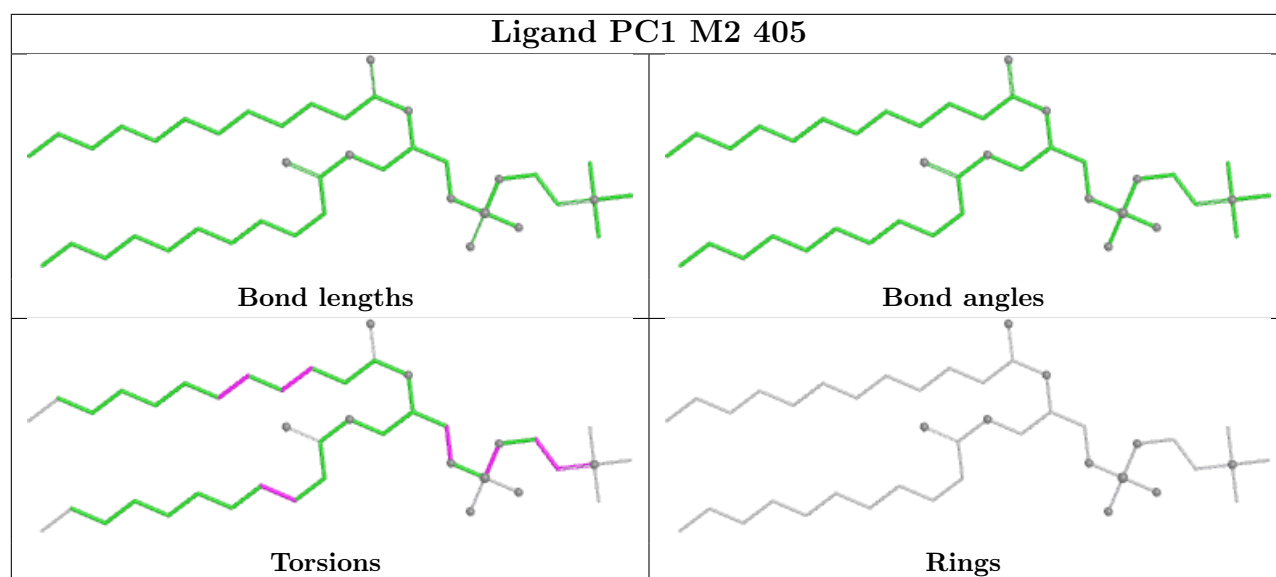


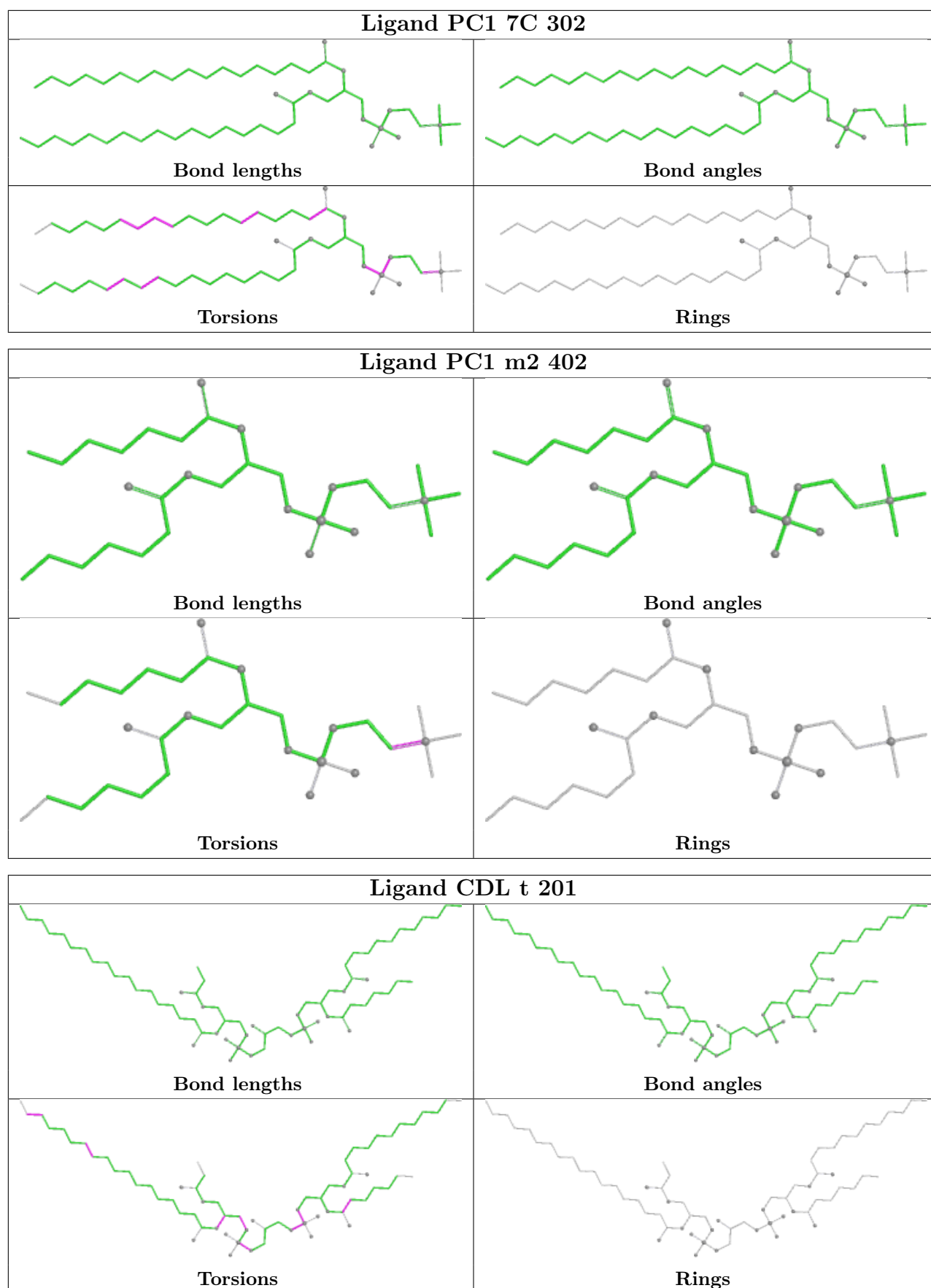


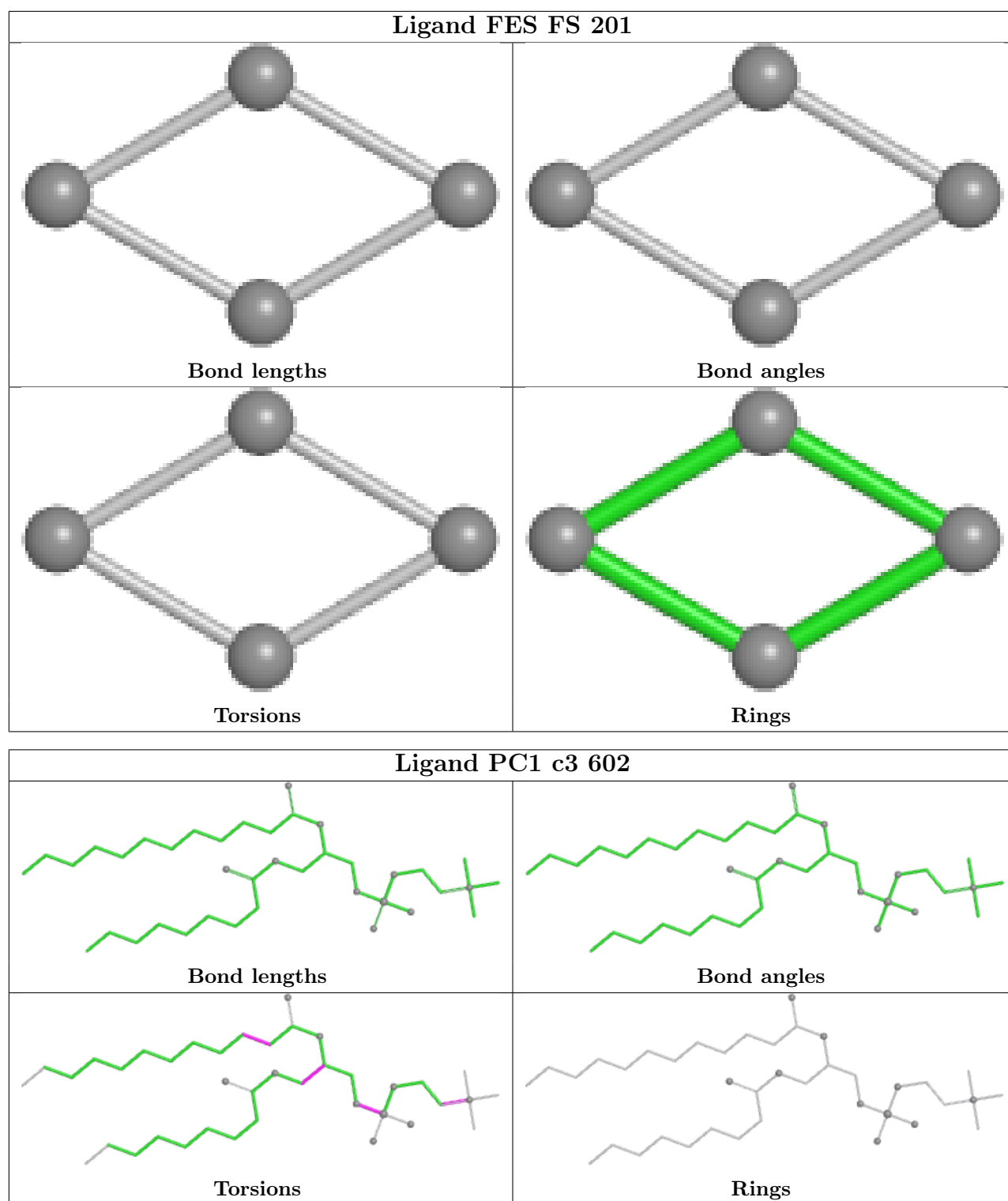


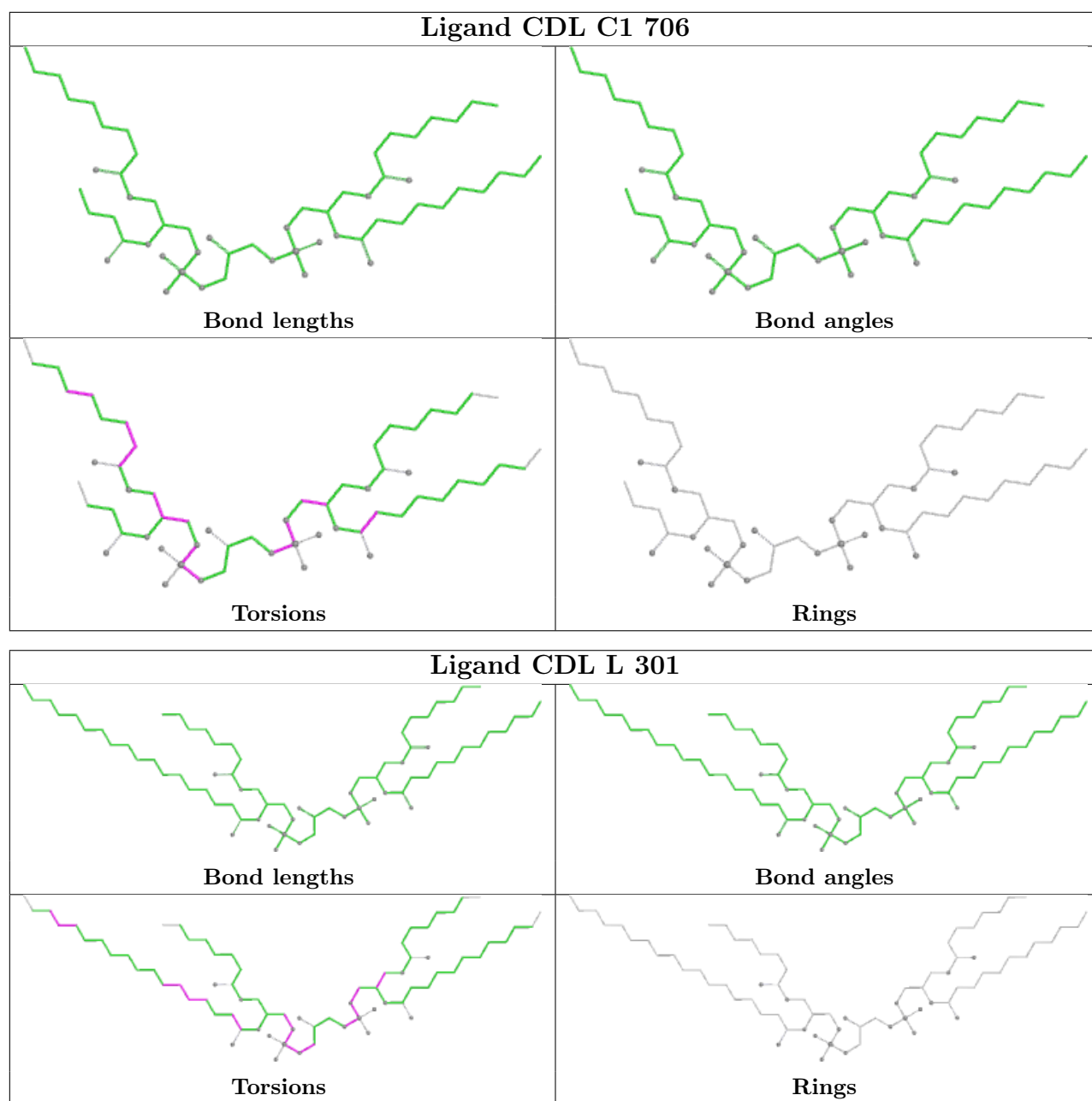


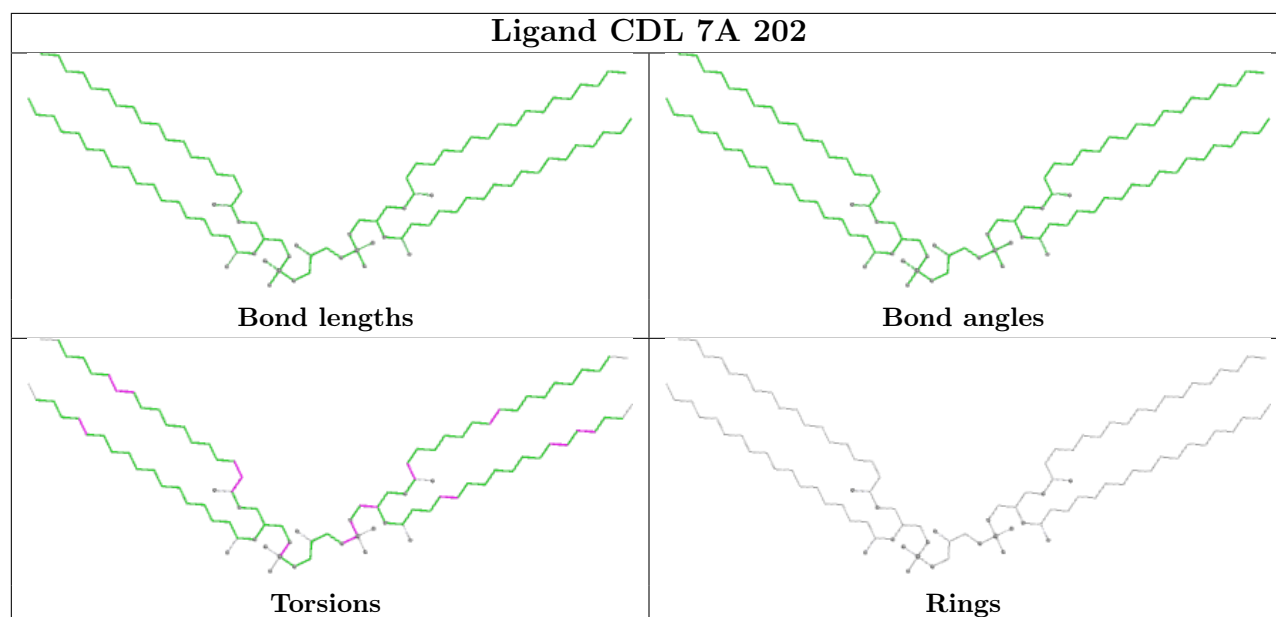
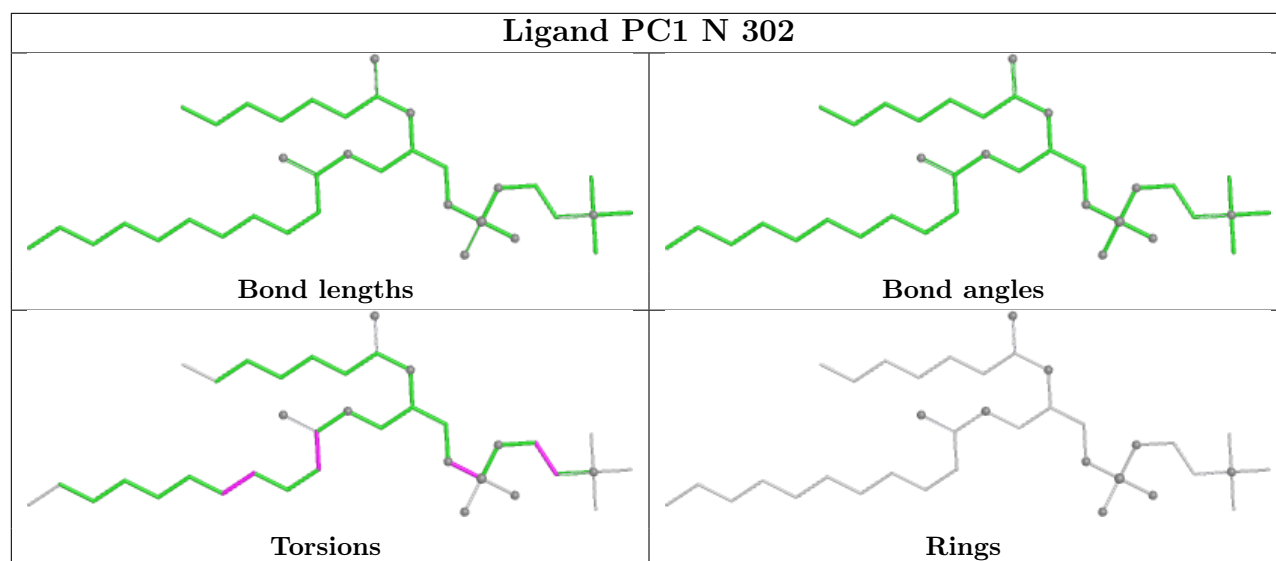
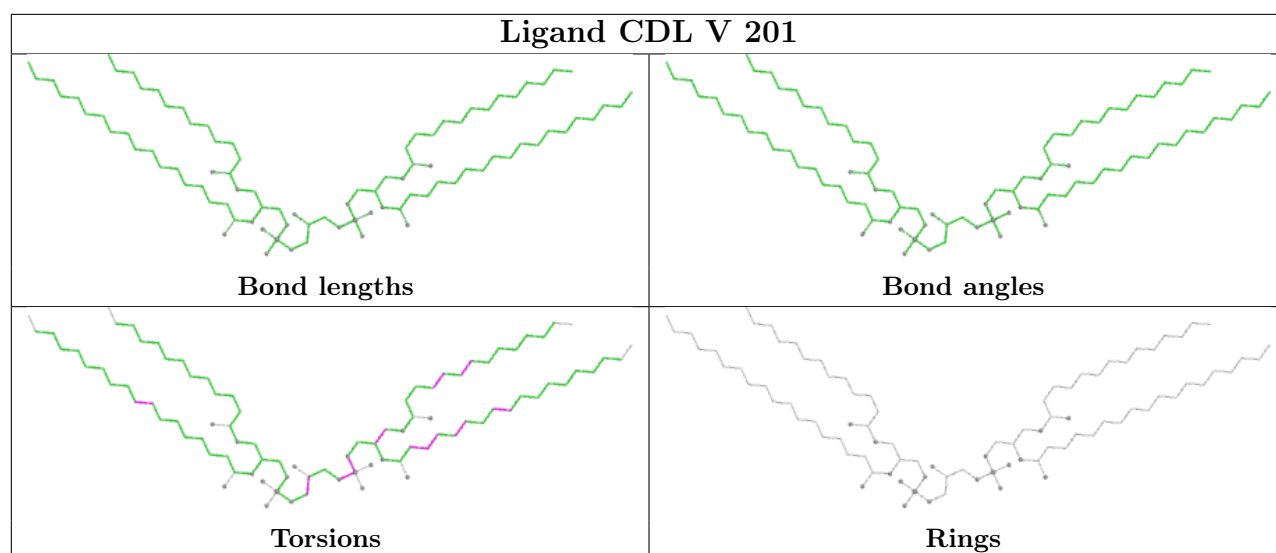


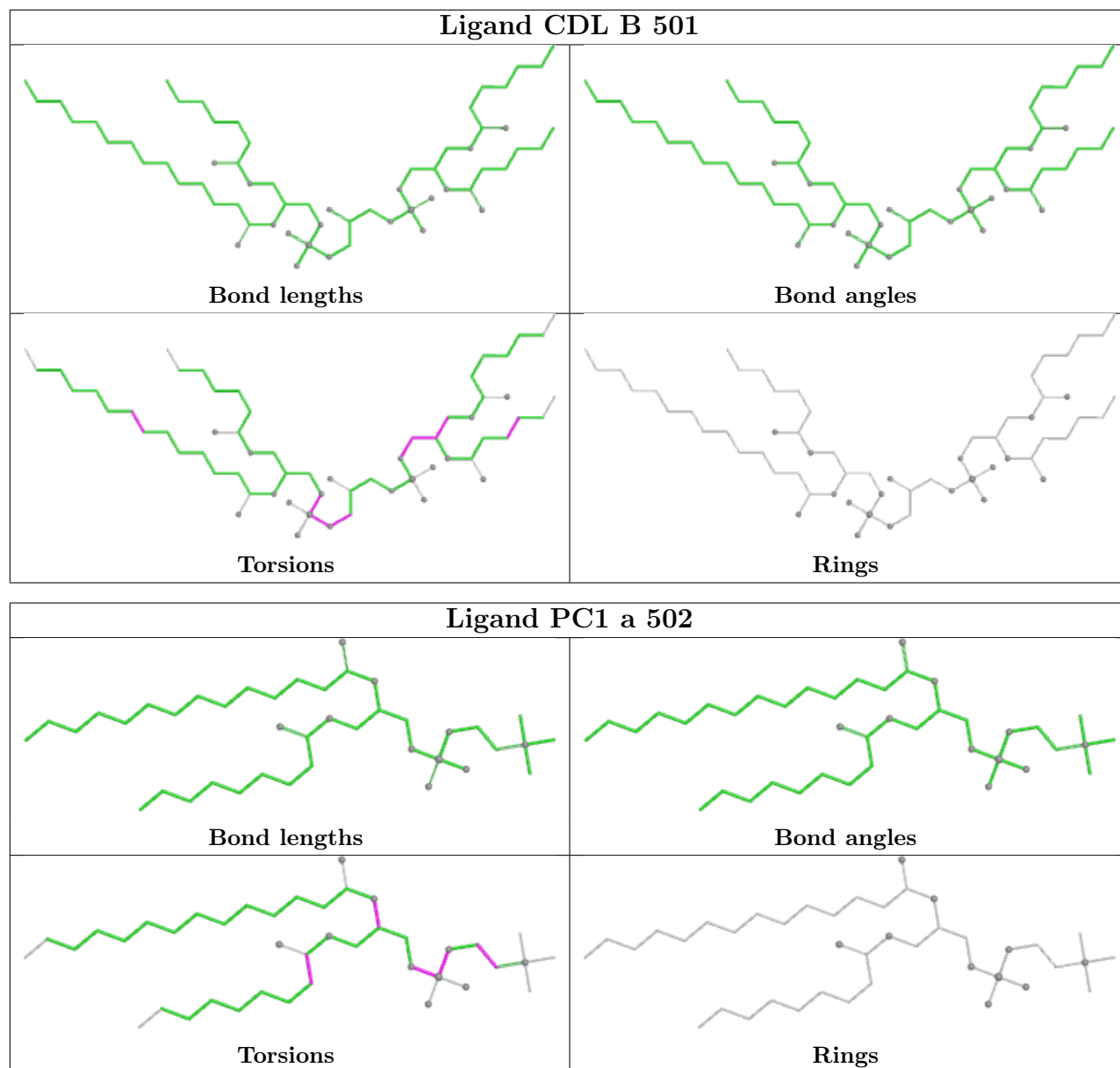


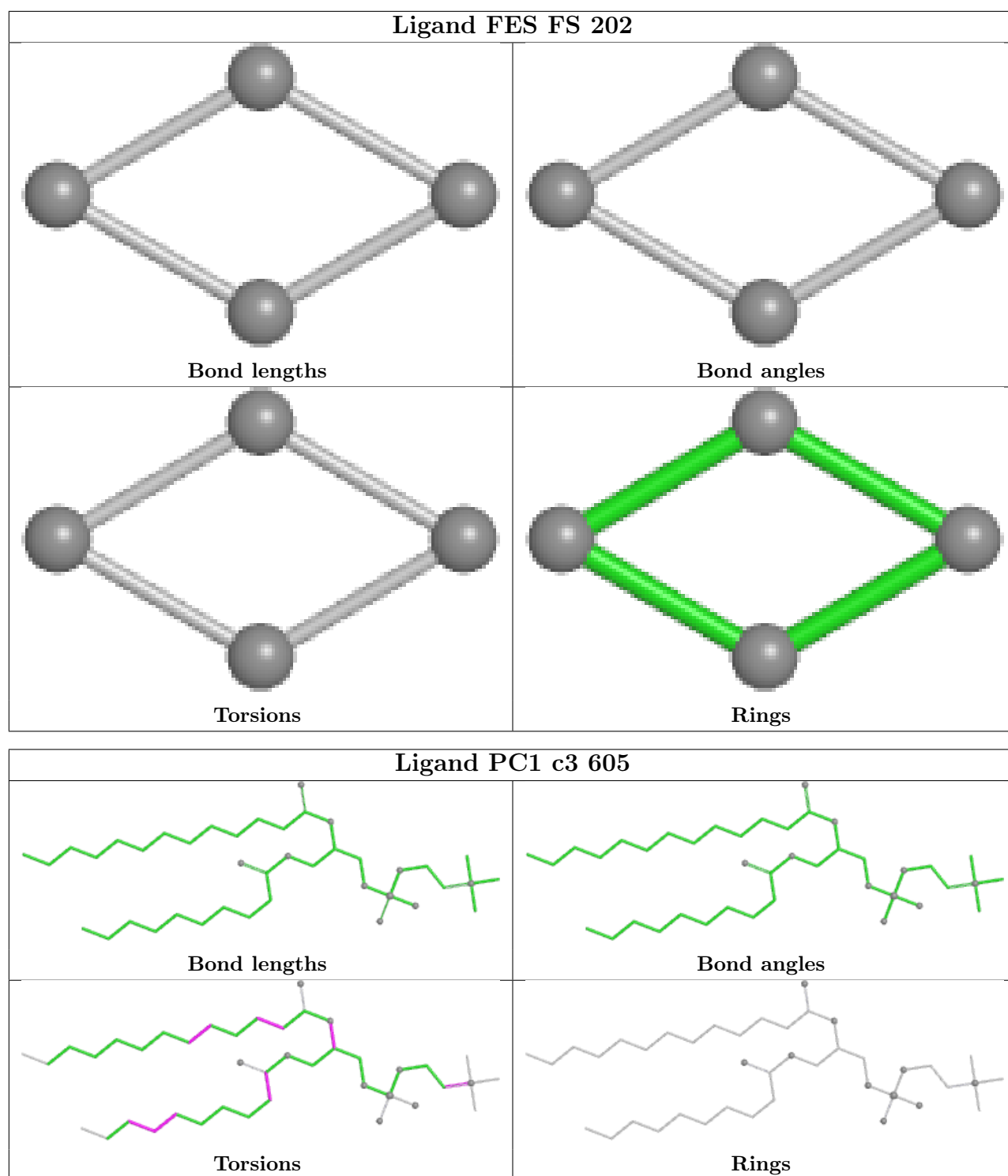


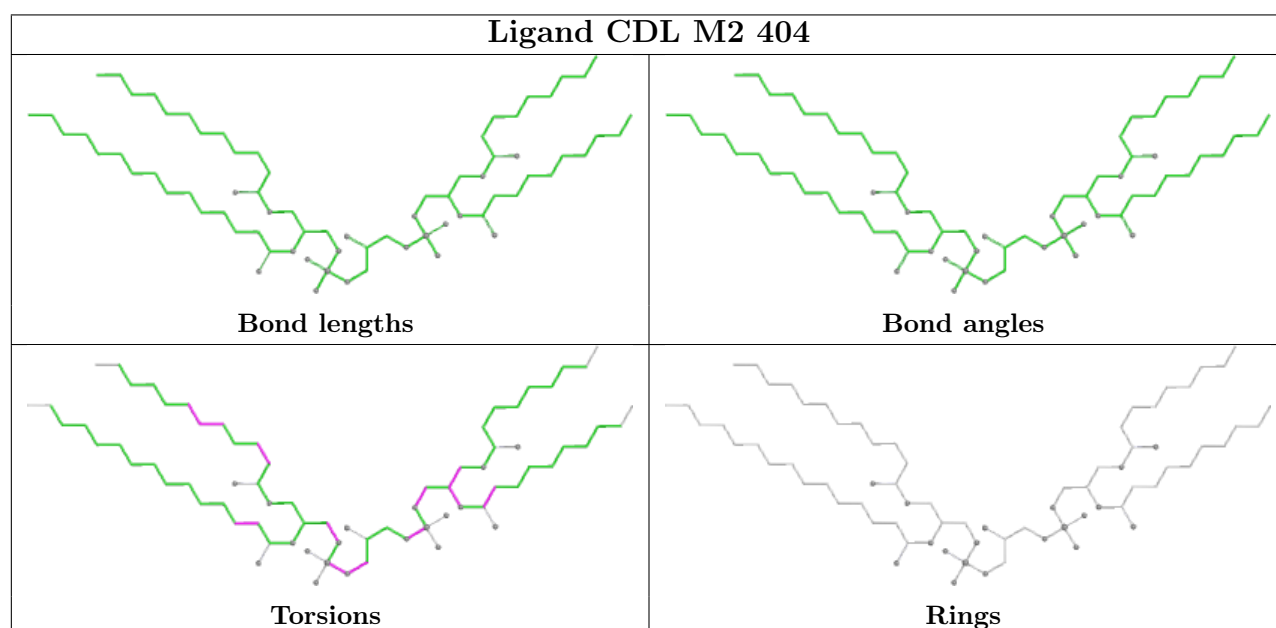
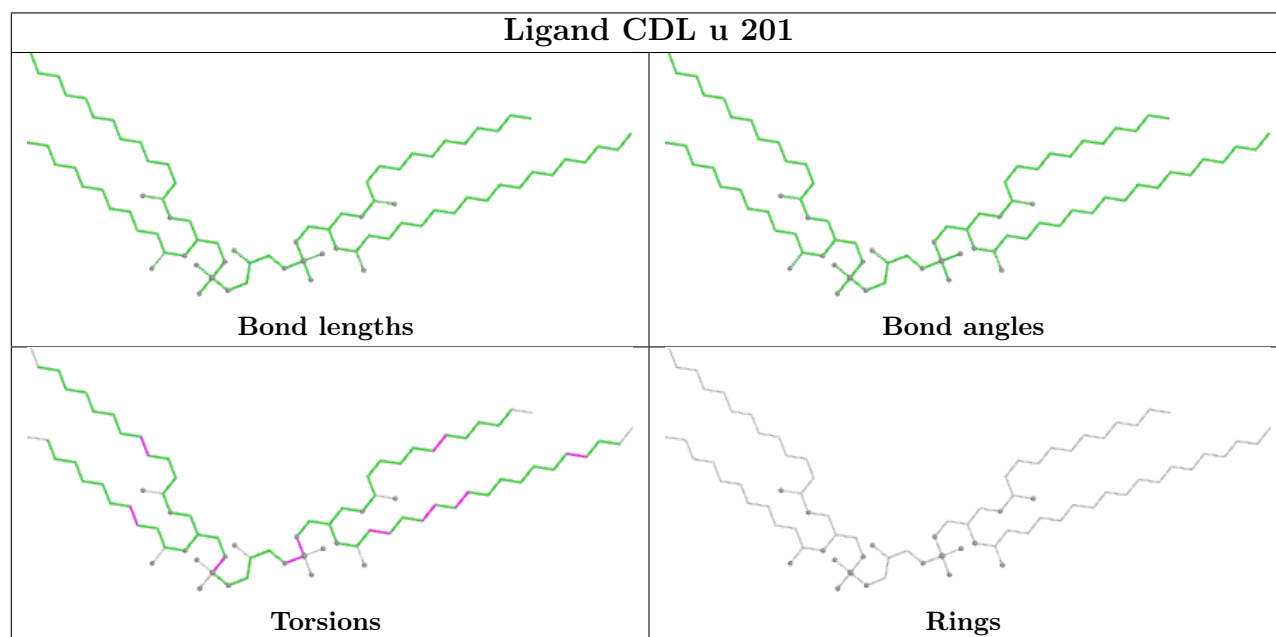
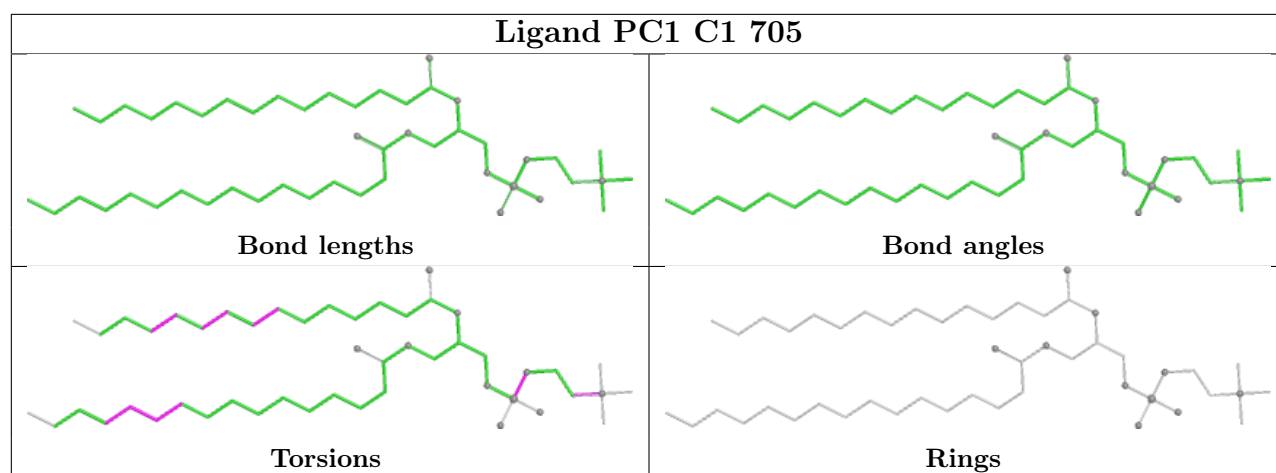


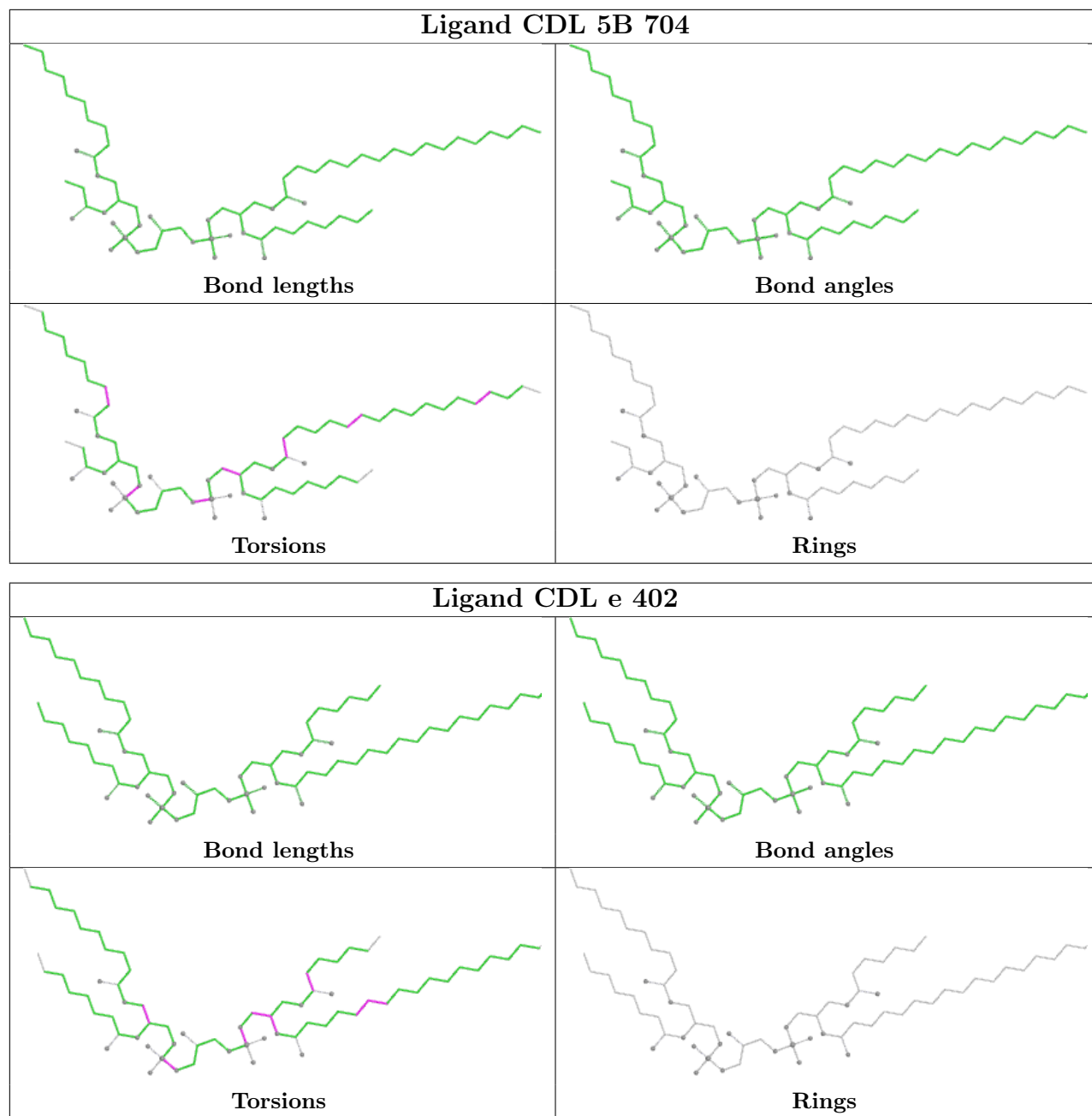


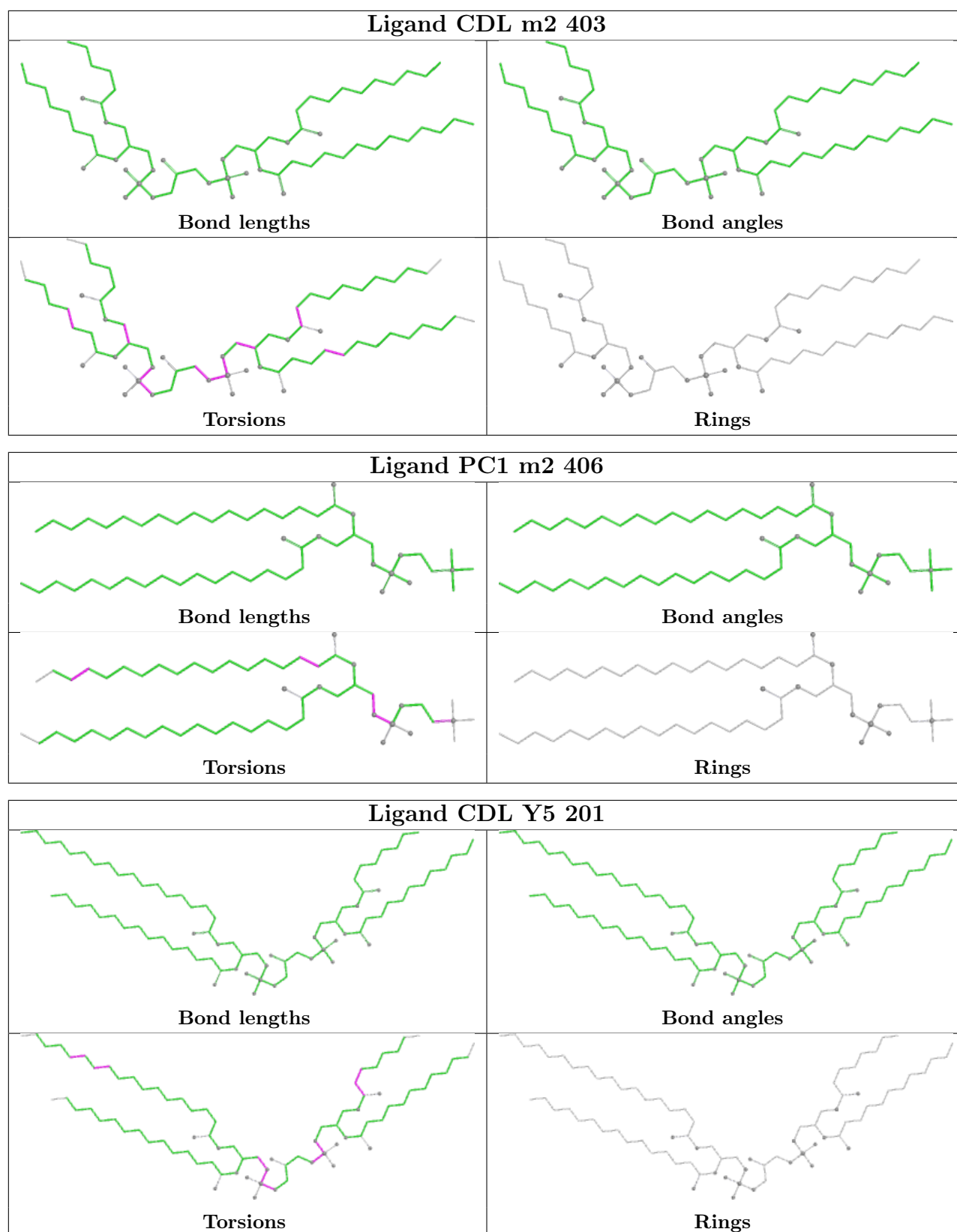


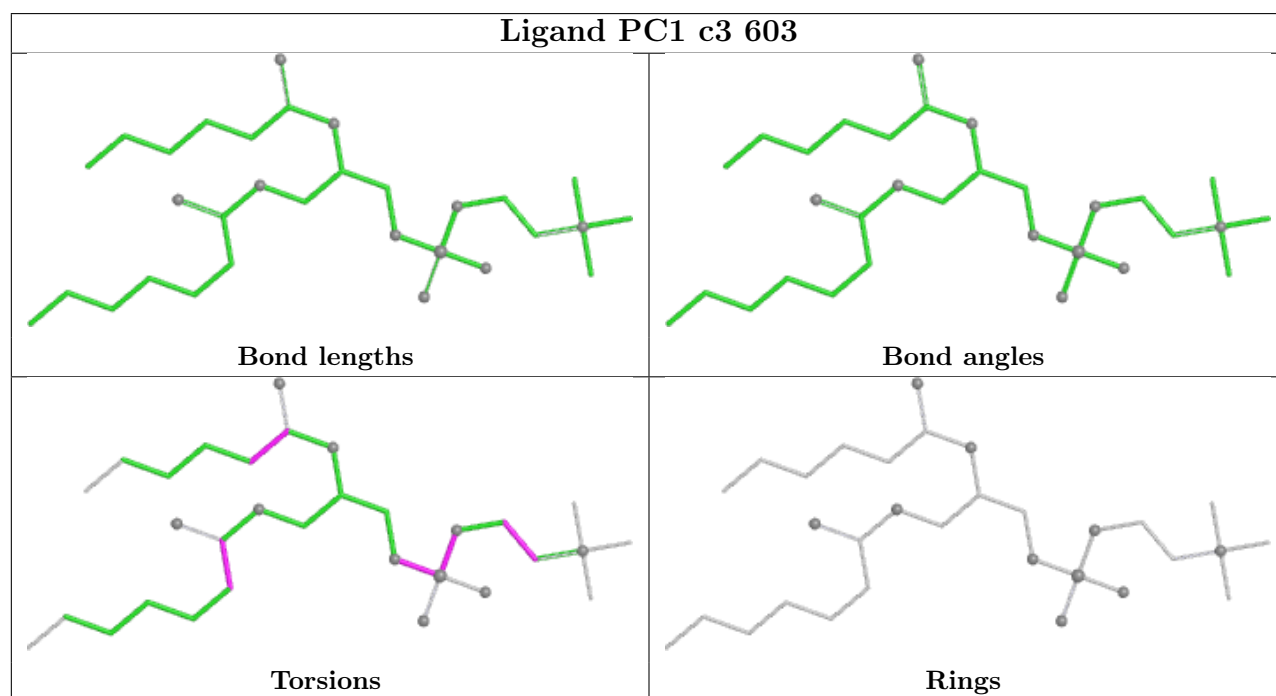
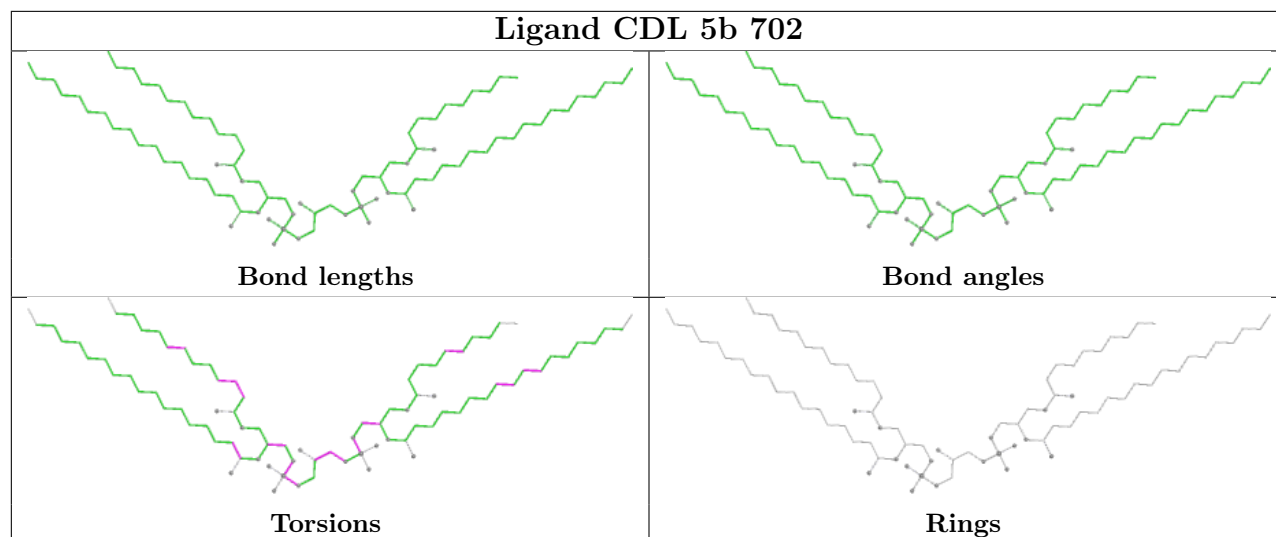


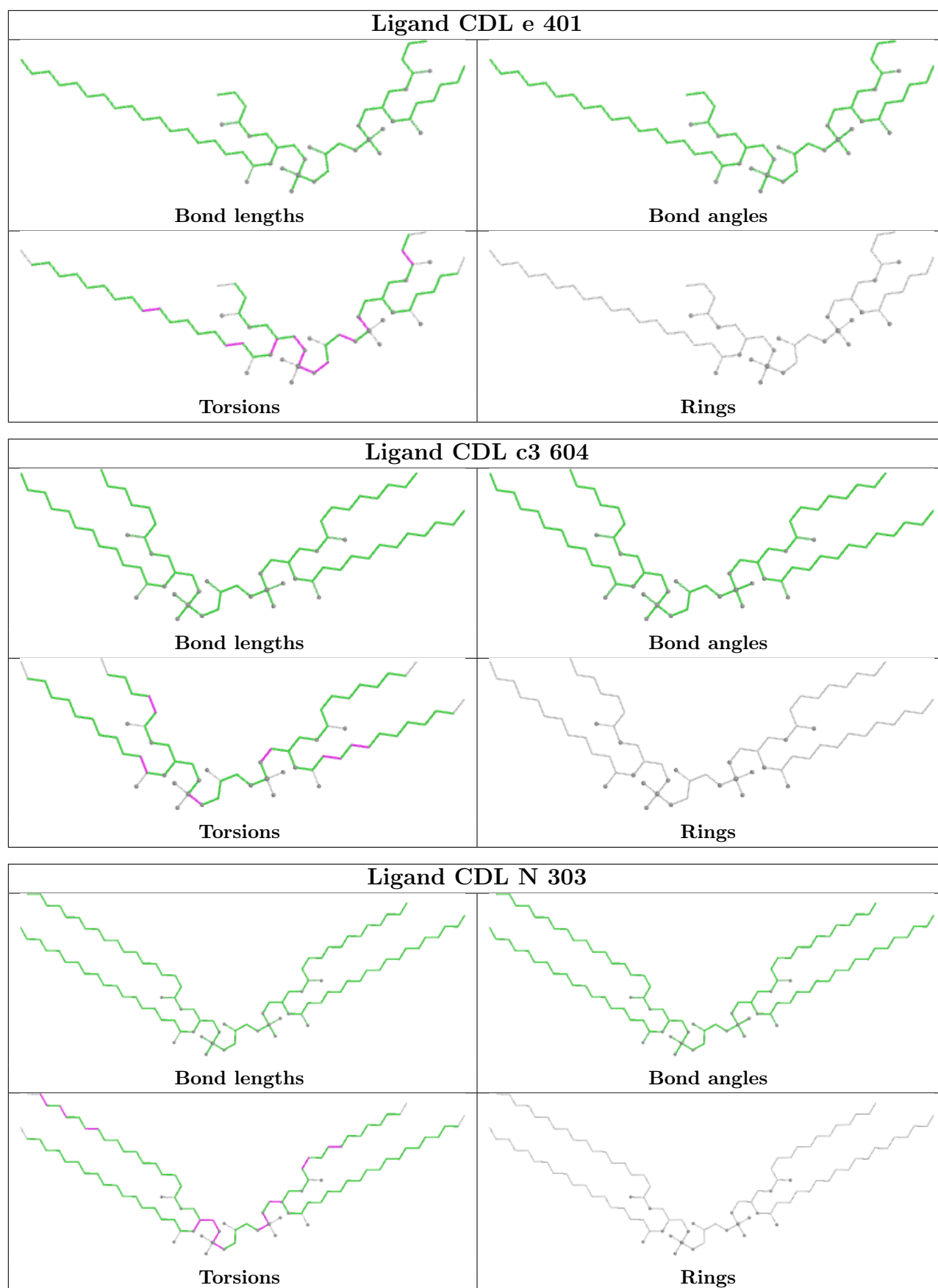


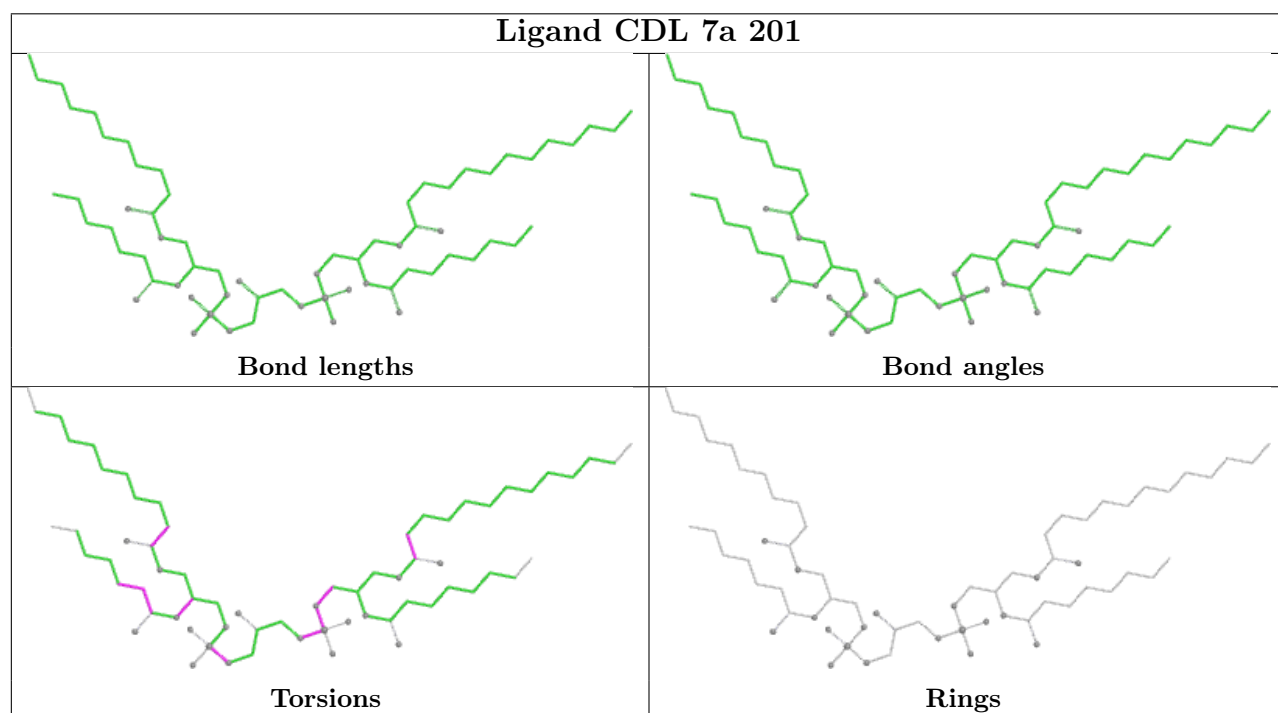
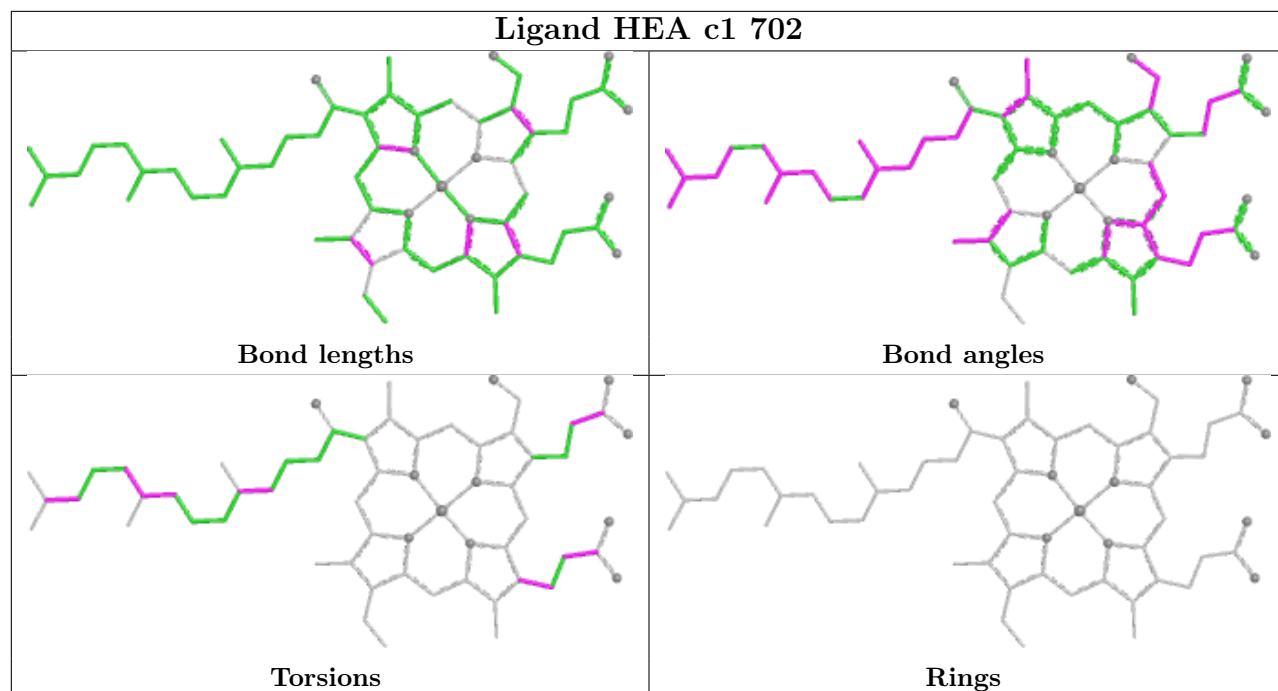


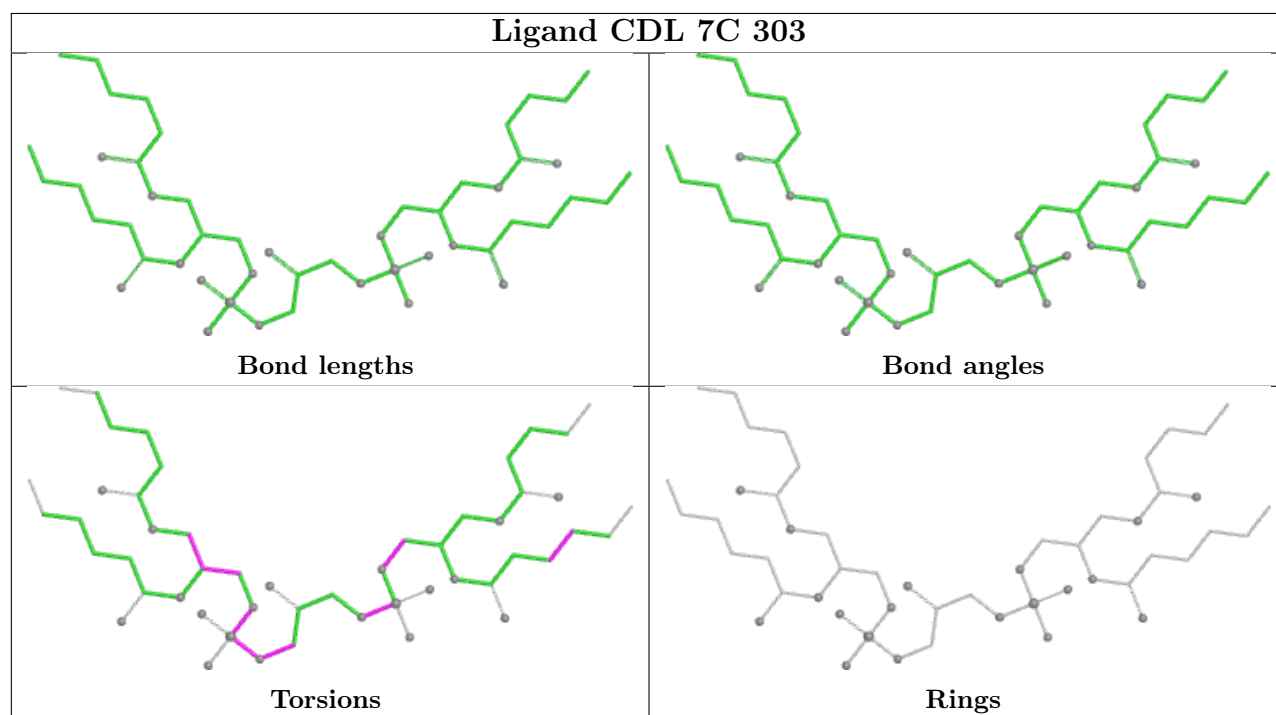
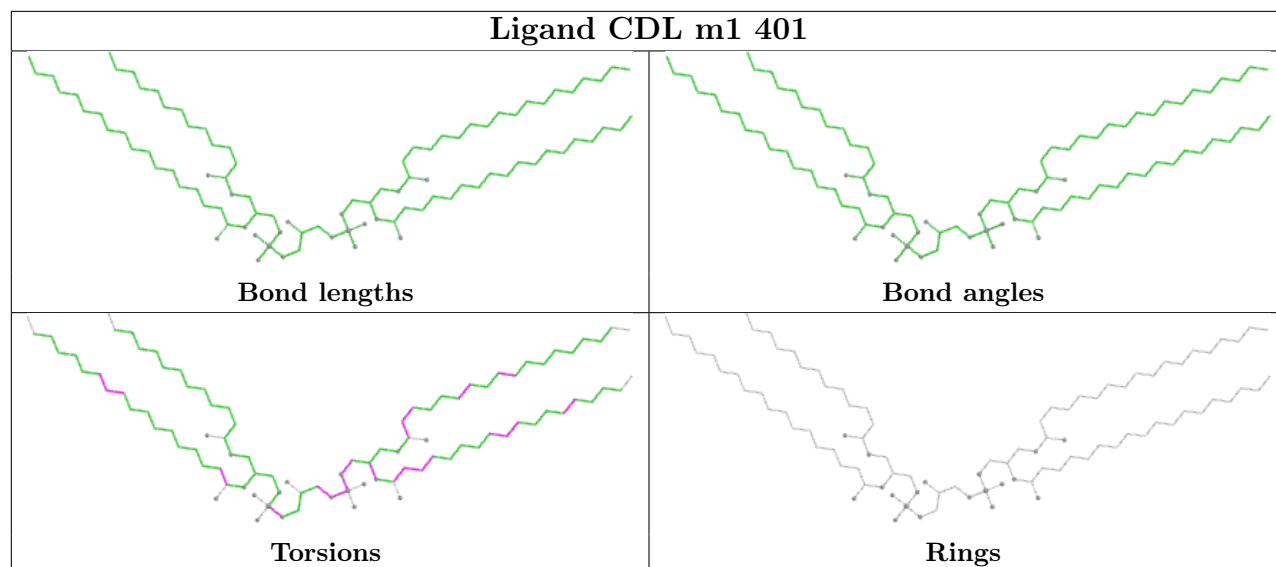


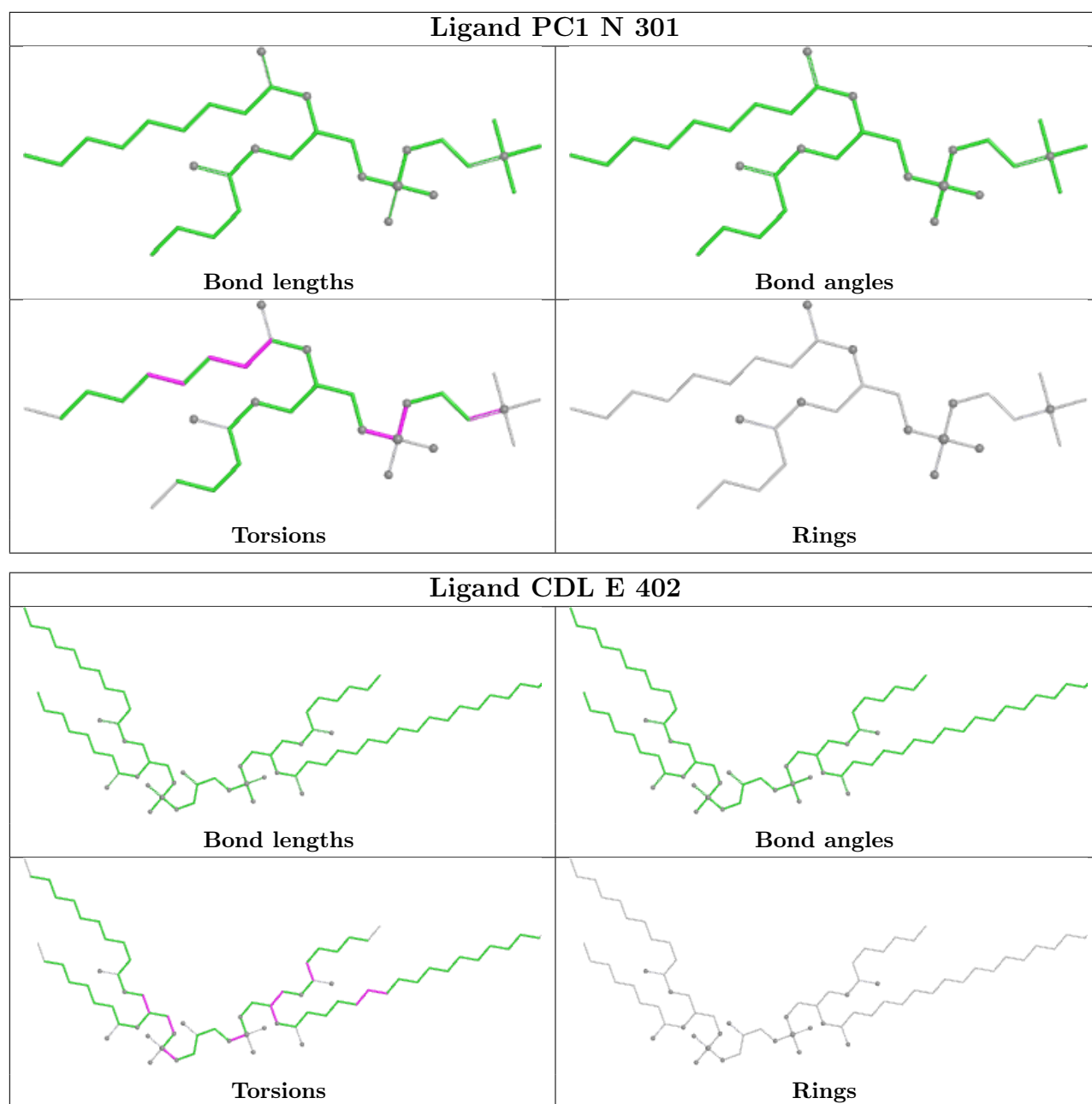


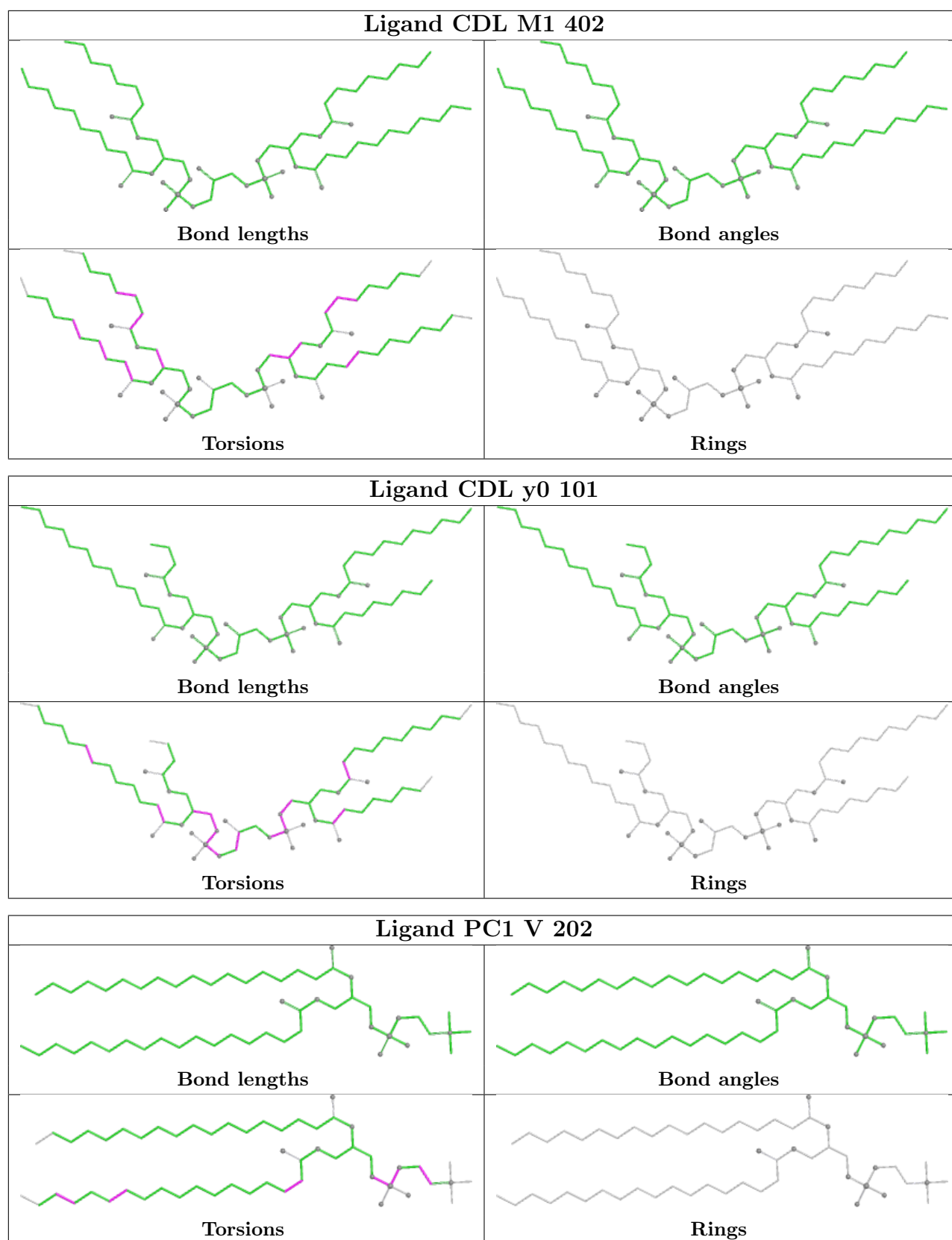


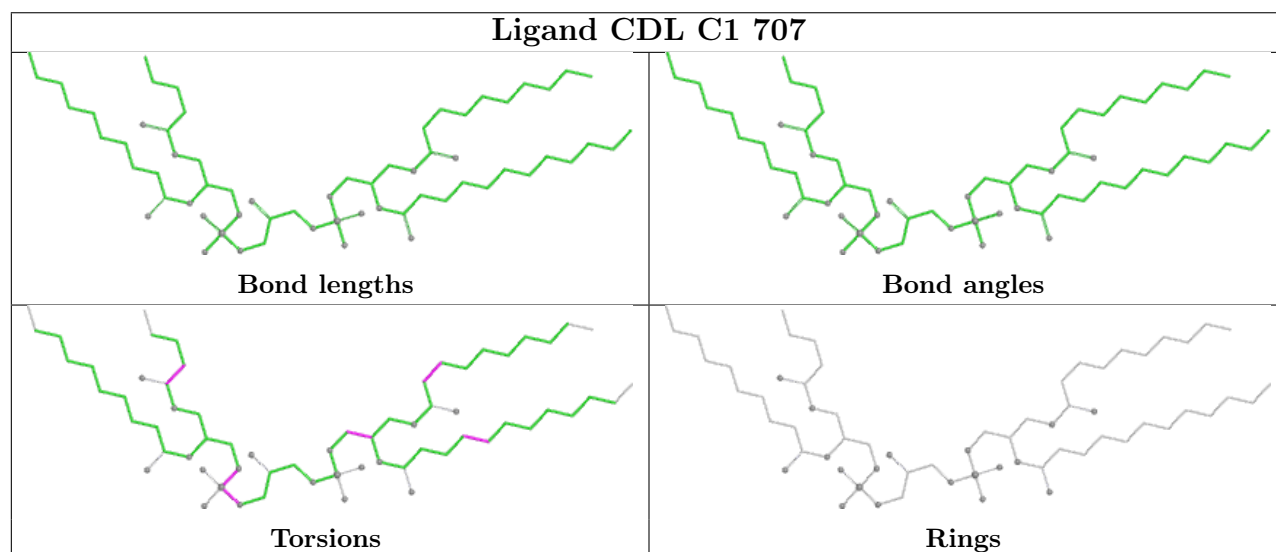
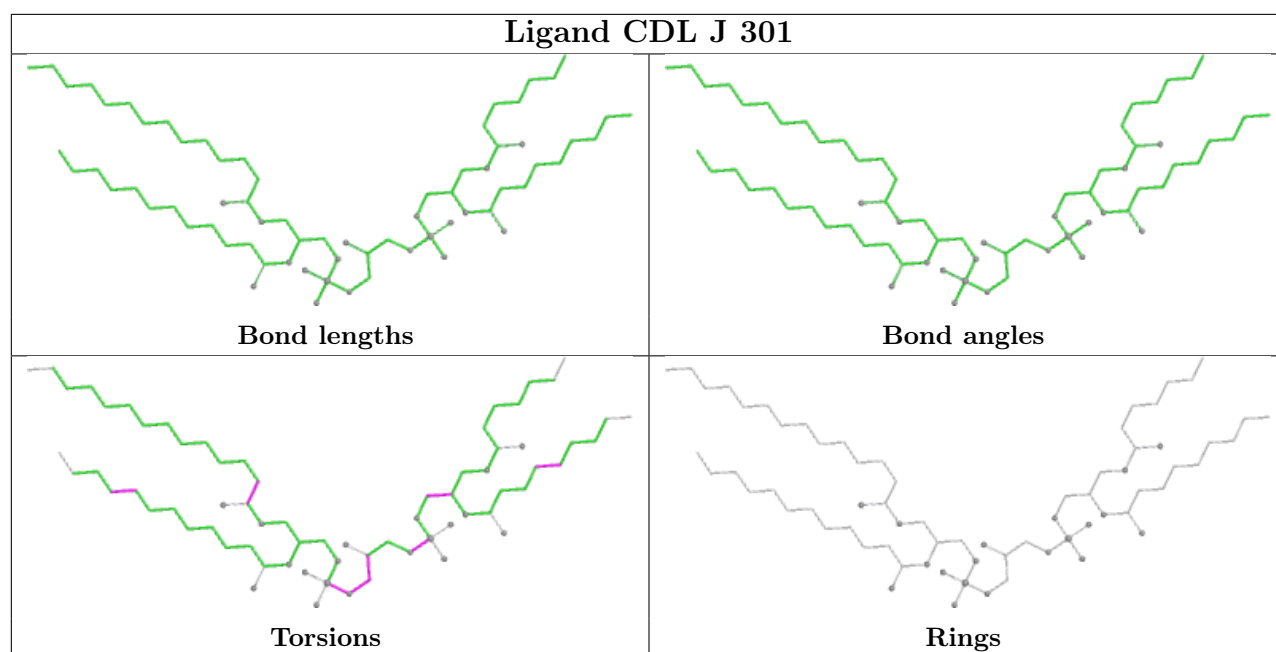


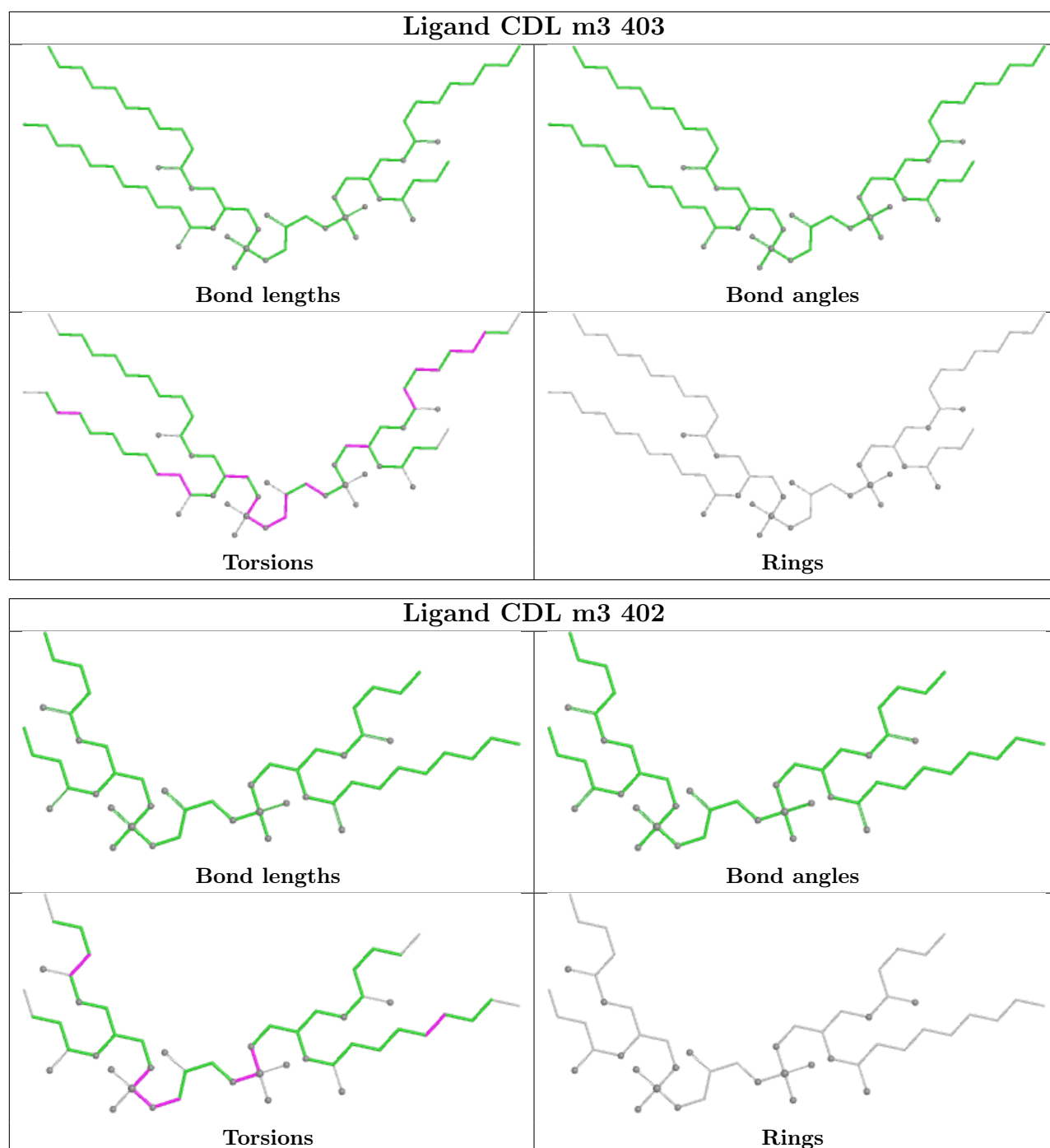


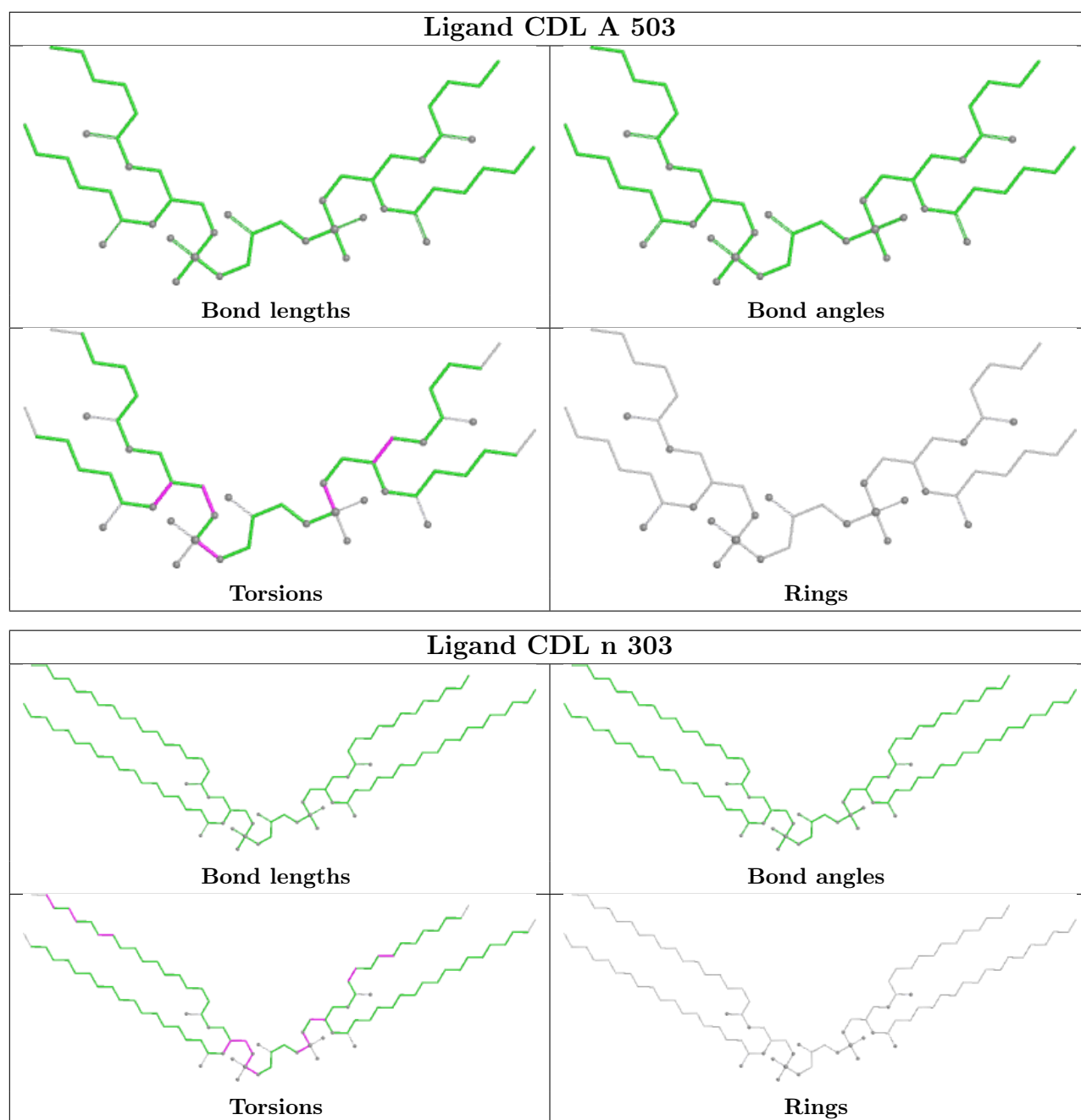


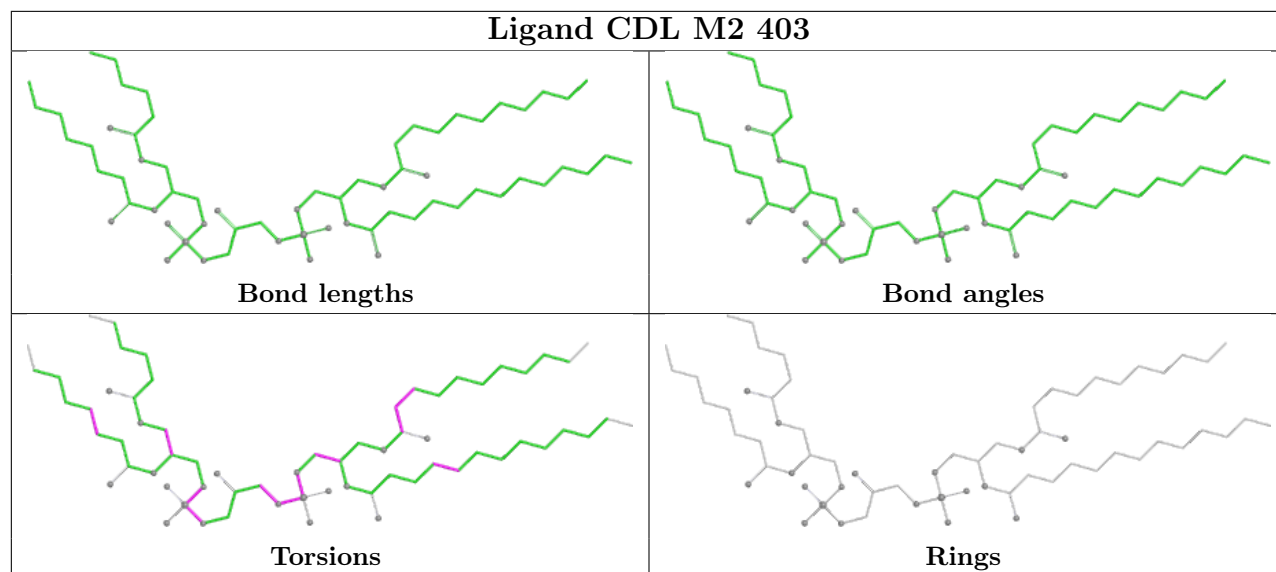












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

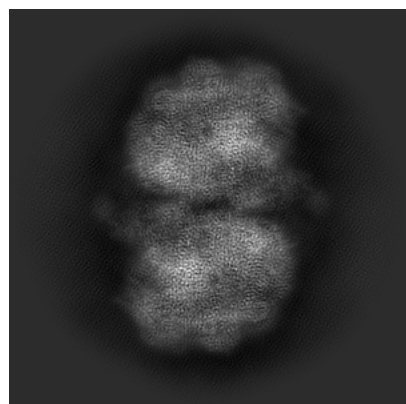
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32325. These allow visual inspection of the internal detail of the map and identification of artifacts.

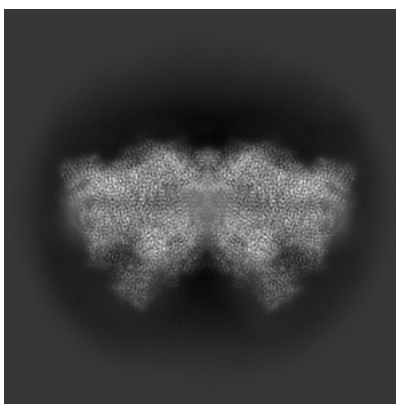
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

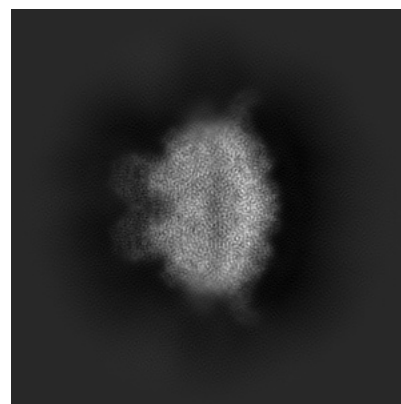
6.1.1 Primary map



X

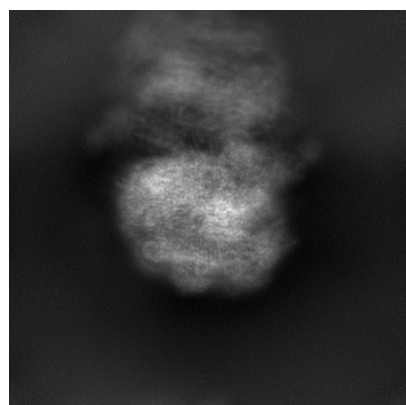


Y

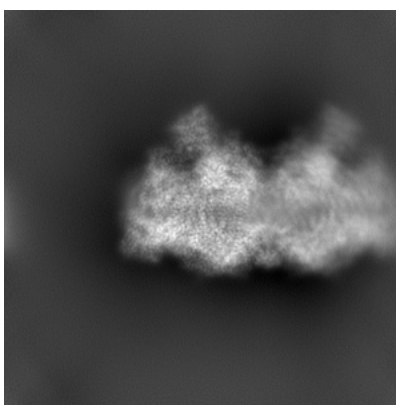


Z

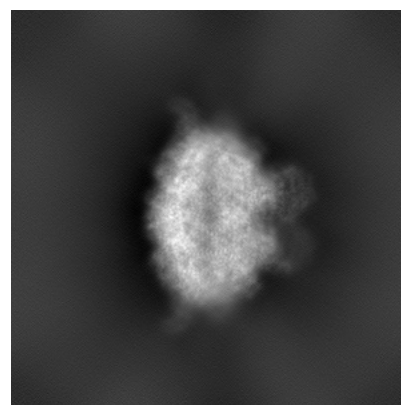
6.1.2 Raw map



X



Y

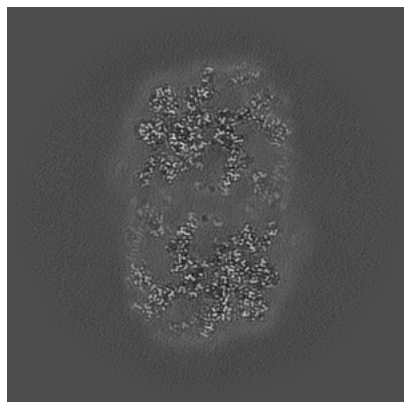


Z

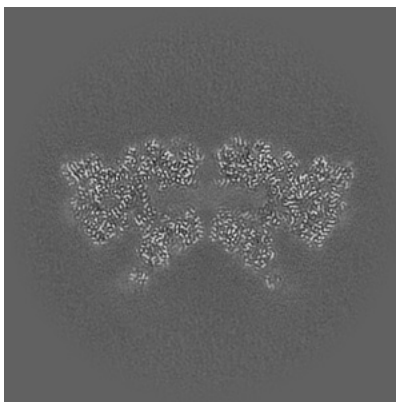
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

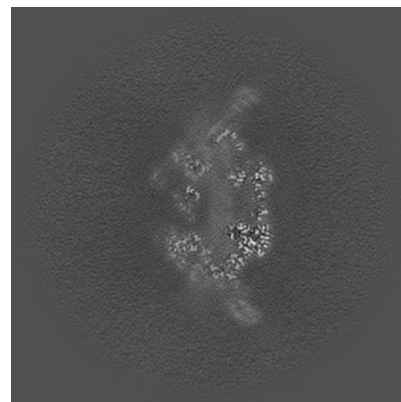
6.2.1 Primary map



X Index: 256

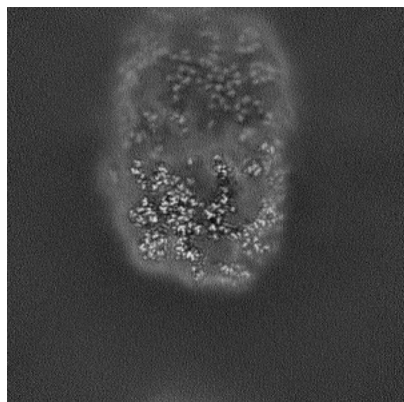


Y Index: 256

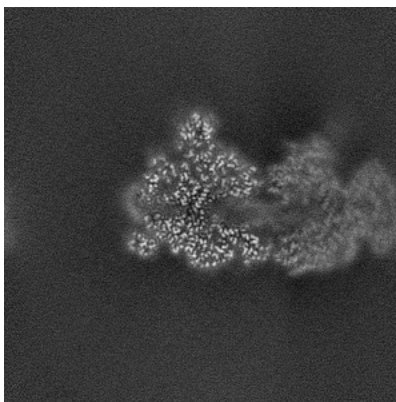


Z Index: 256

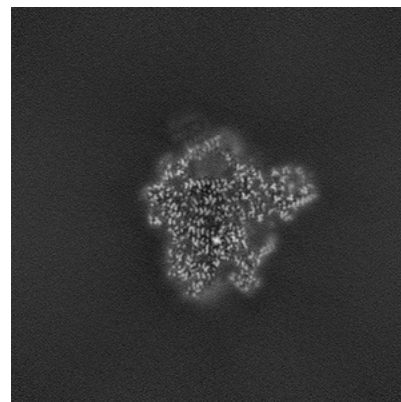
6.2.2 Raw map



X Index: 256



Y Index: 256

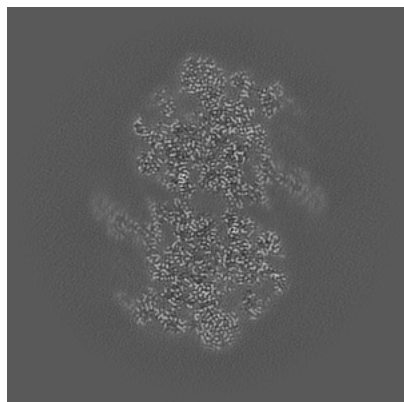


Z Index: 256

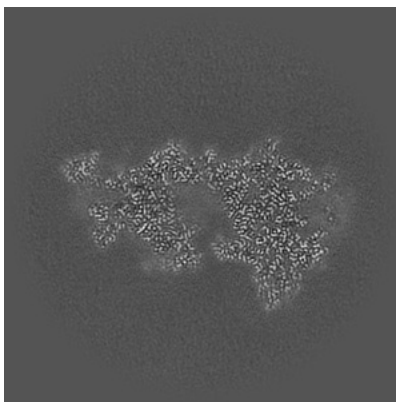
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

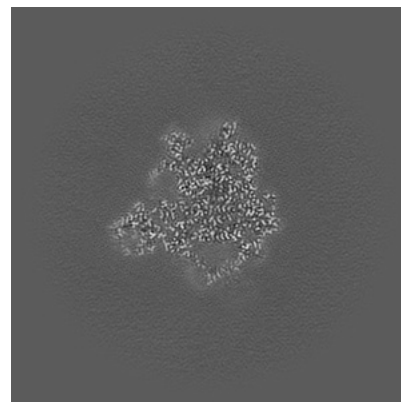
6.3.1 Primary map



X Index: 297

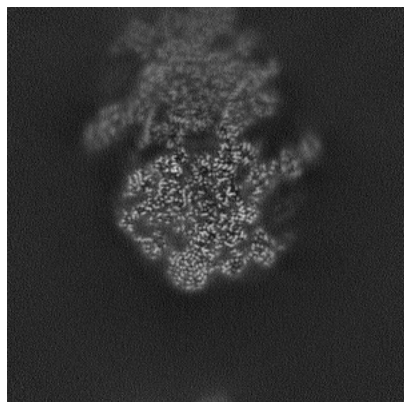


Y Index: 286

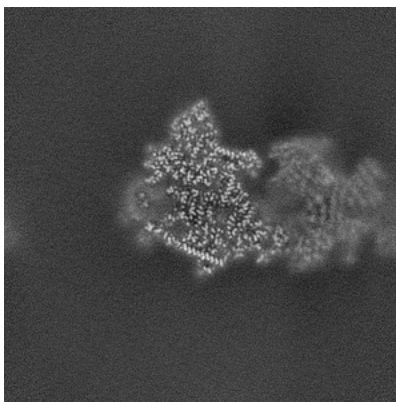


Z Index: 180

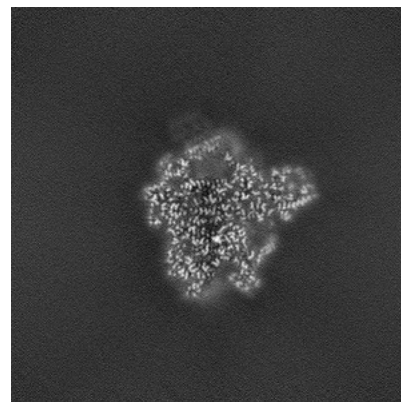
6.3.2 Raw map



X Index: 217



Y Index: 273

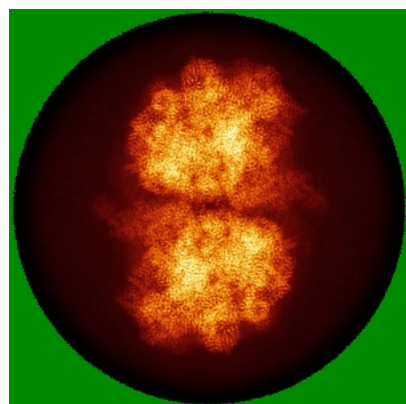


Z Index: 257

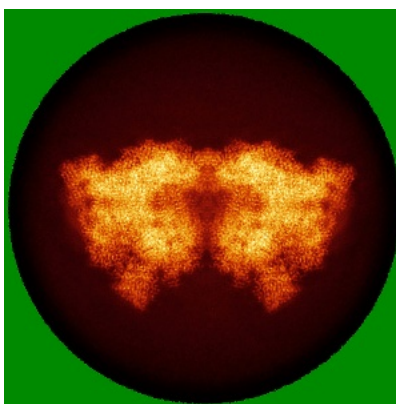
The images above show the largest variance slices of the map in three orthogonal directions.

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

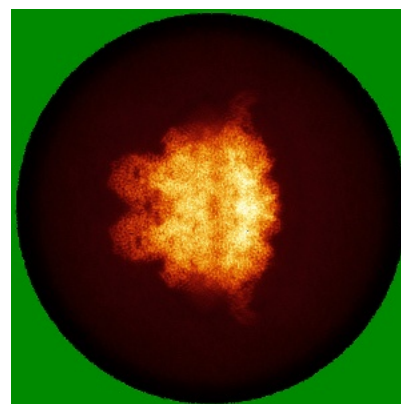
6.4.1 Primary map



X

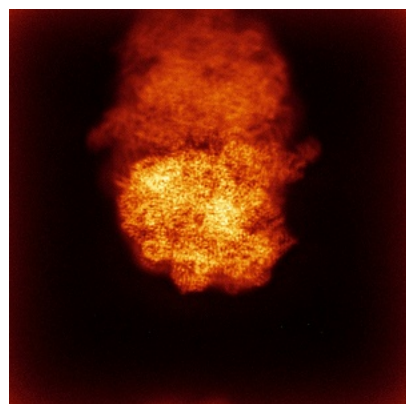


Y

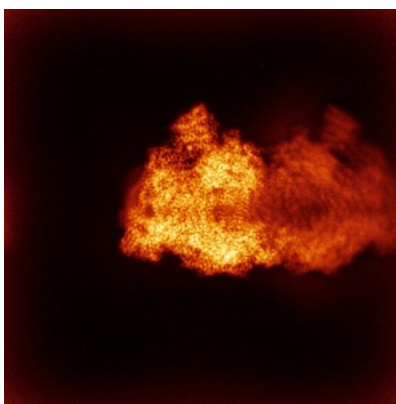


Z

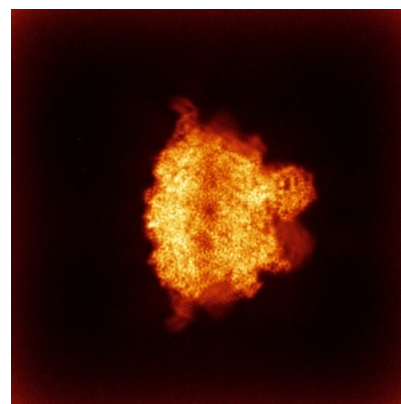
6.4.2 Raw map



X



Y

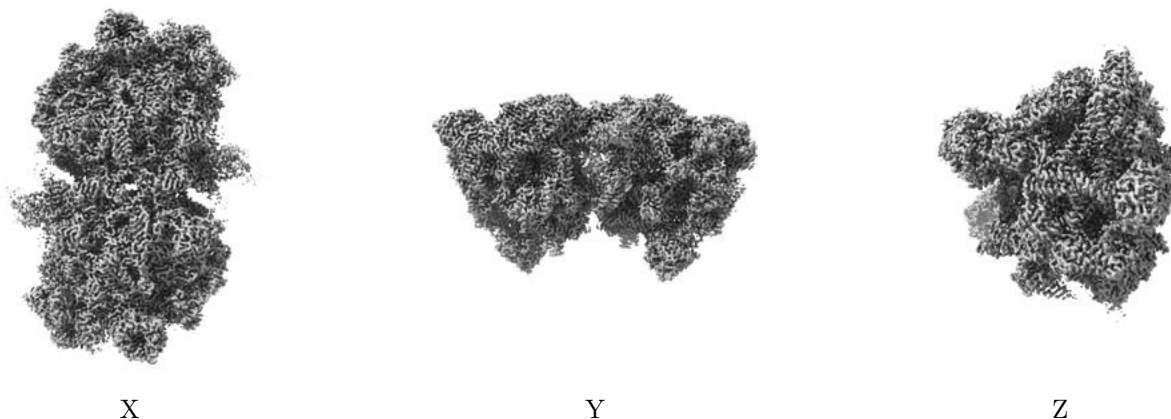


Z

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.

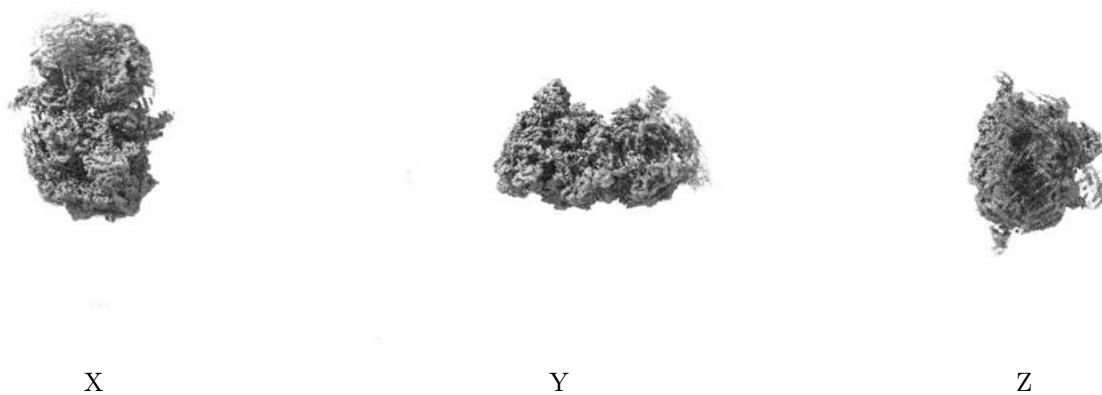
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.0. 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.

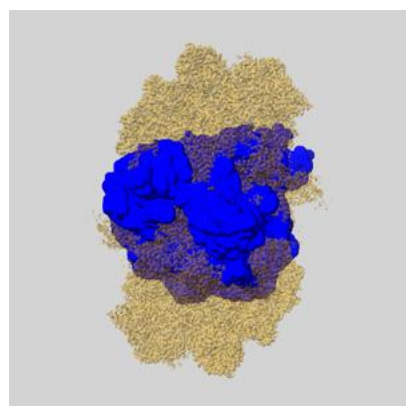
6.6 Mask visualisation [i](#)

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

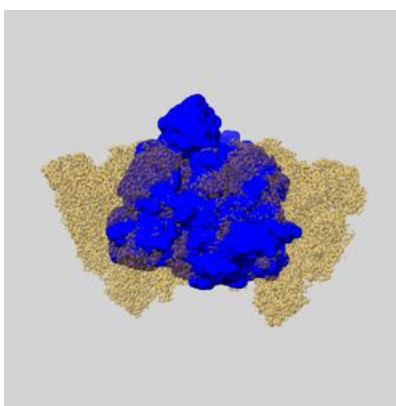
A mask typically either:

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

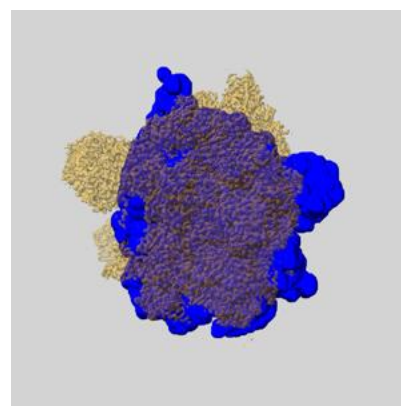
6.6.1 emd_32325_msk_1.map [i](#)



X



Y

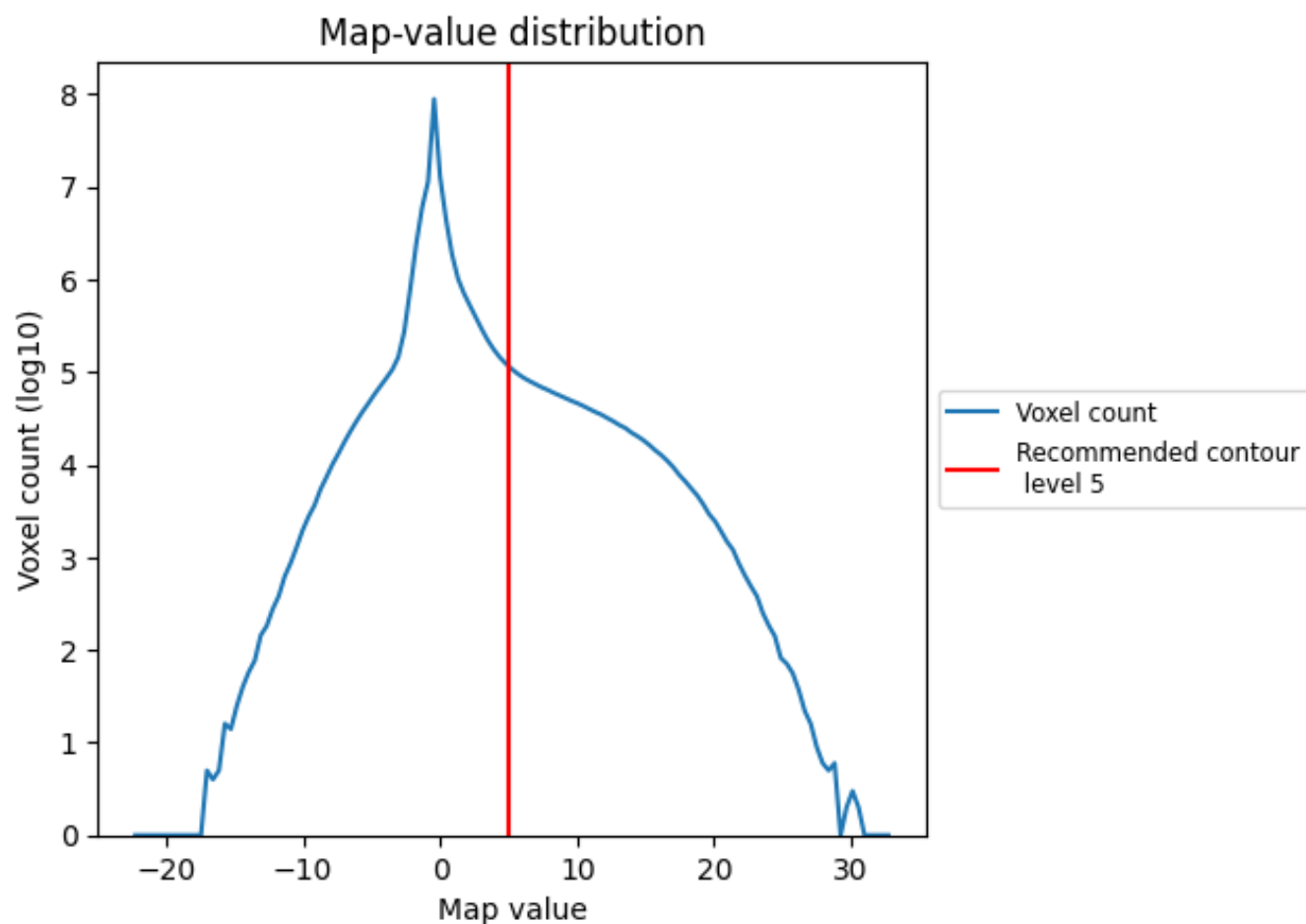


Z

7 Map analysis [i](#)

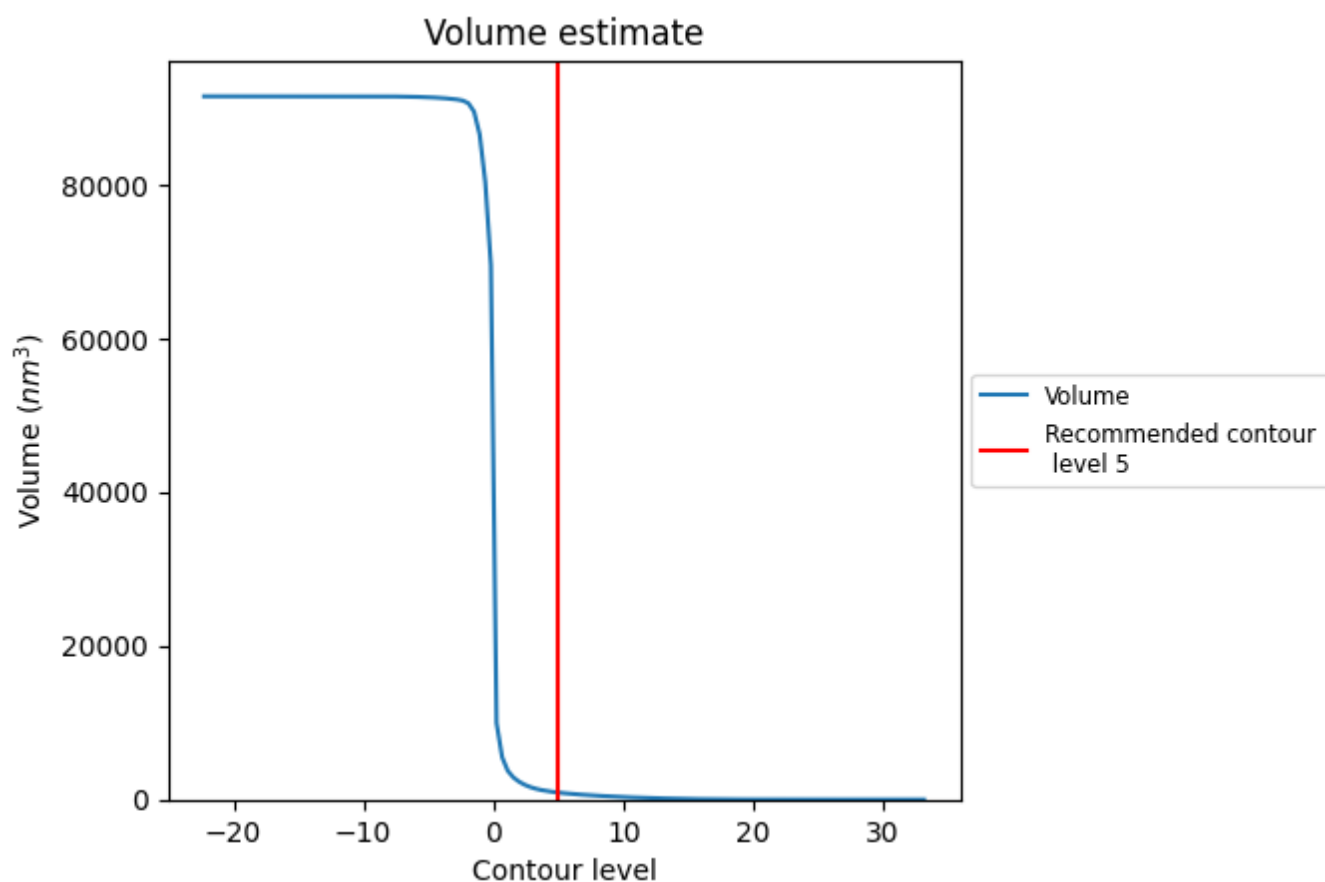
This section contains the results of statistical analysis of the map.

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.

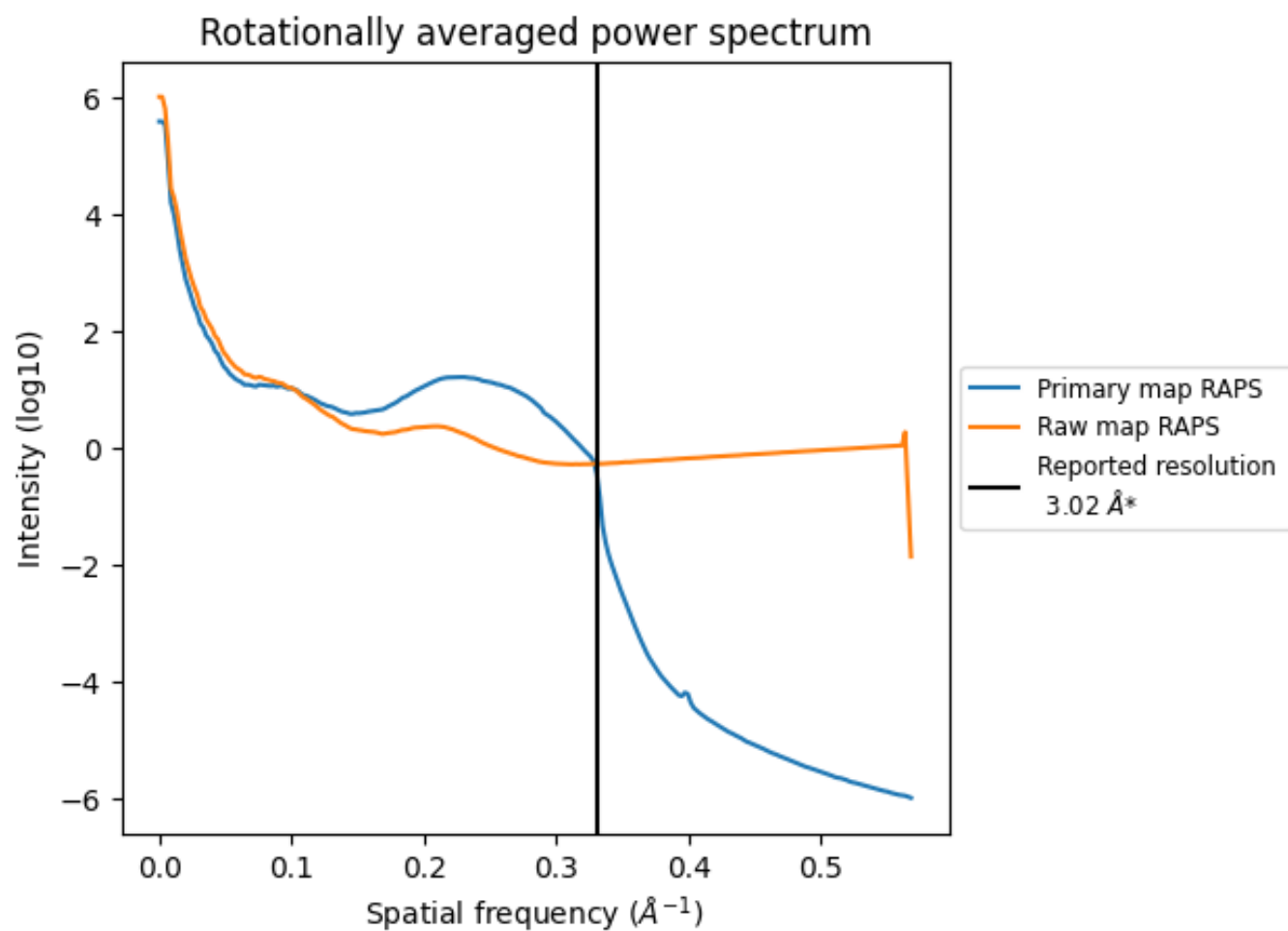
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 911 nm³; this corresponds to an approximate mass of 823 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 ⓘ

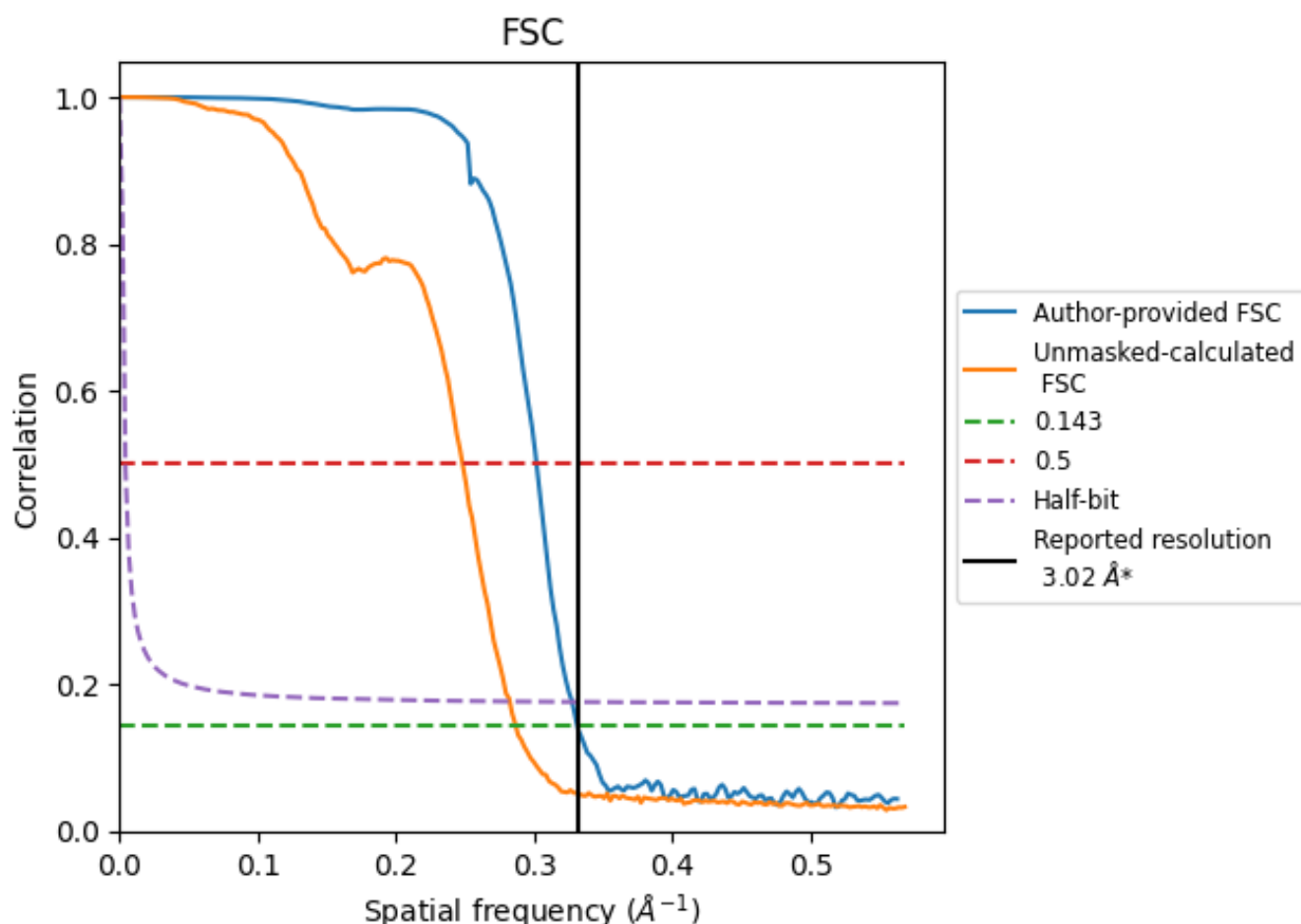


*Reported resolution corresponds to spatial frequency of 0.331 \AA^{-1}

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 0.331 \AA^{-1}

8.2 Resolution estimates [i](#)

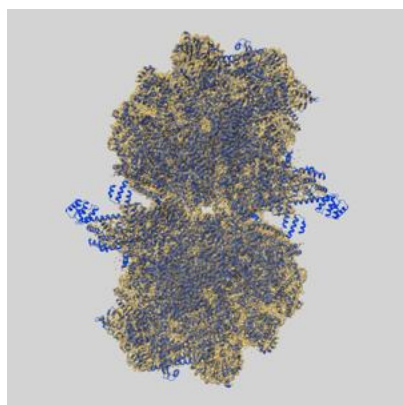
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.02	-	-
Author-provided FSC curve	3.02	3.31	3.05
Unmasked-calculated*	3.49	4.03	3.54

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.49 differs from the reported value 3.02 by more than 10 %

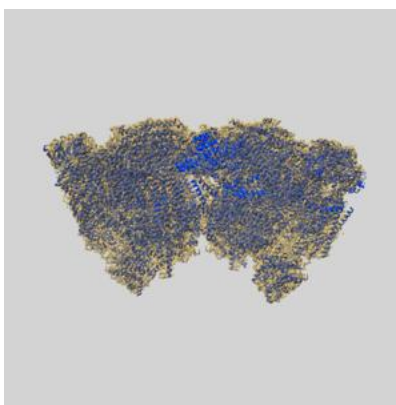
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32325 and PDB model 7W5Z. Per-residue inclusion information can be found in section 3 on page 30.

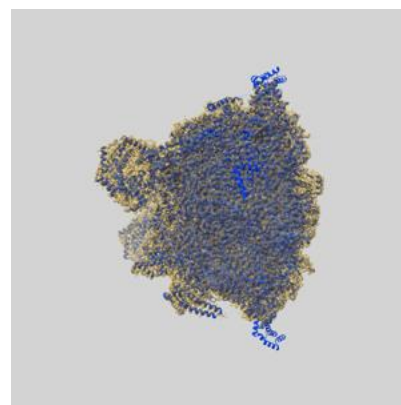
9.1 Map-model overlay [i](#)



X



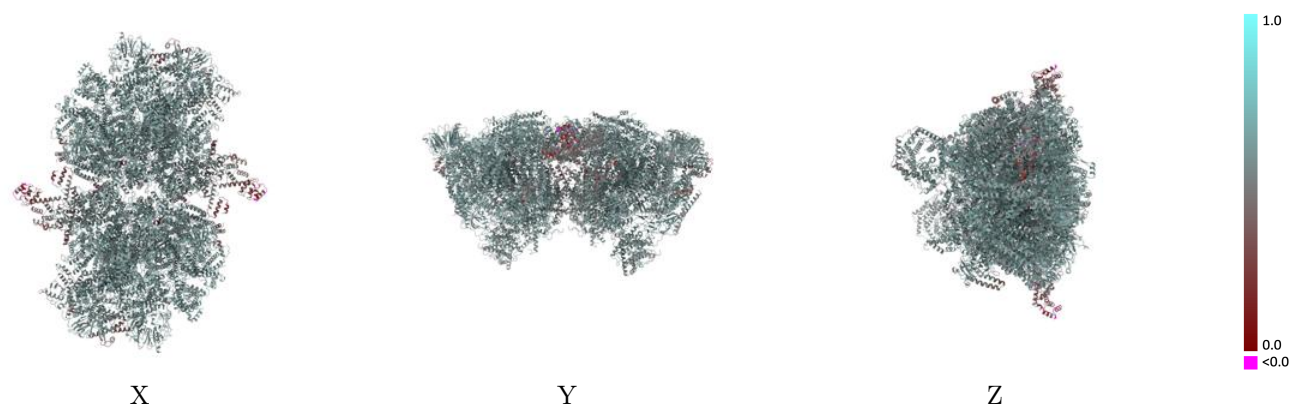
Y



Z

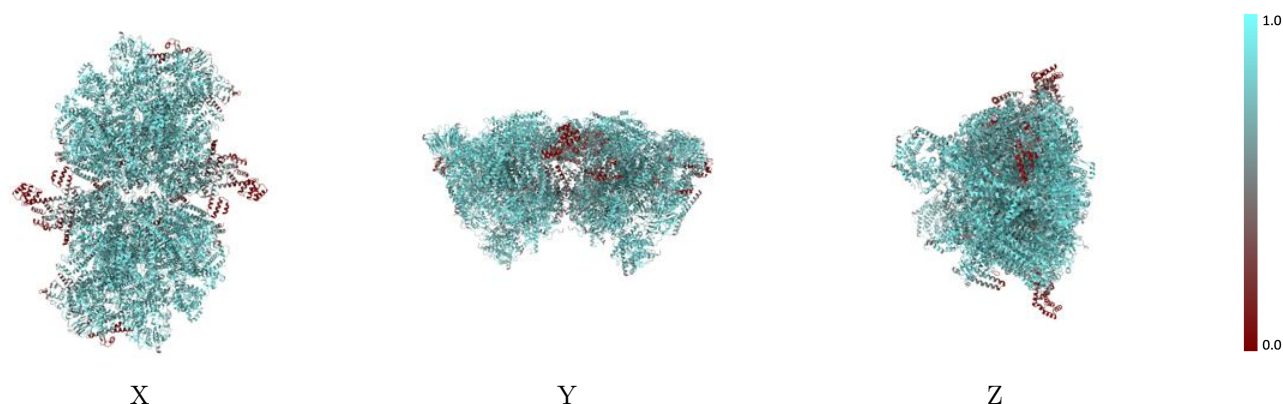
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



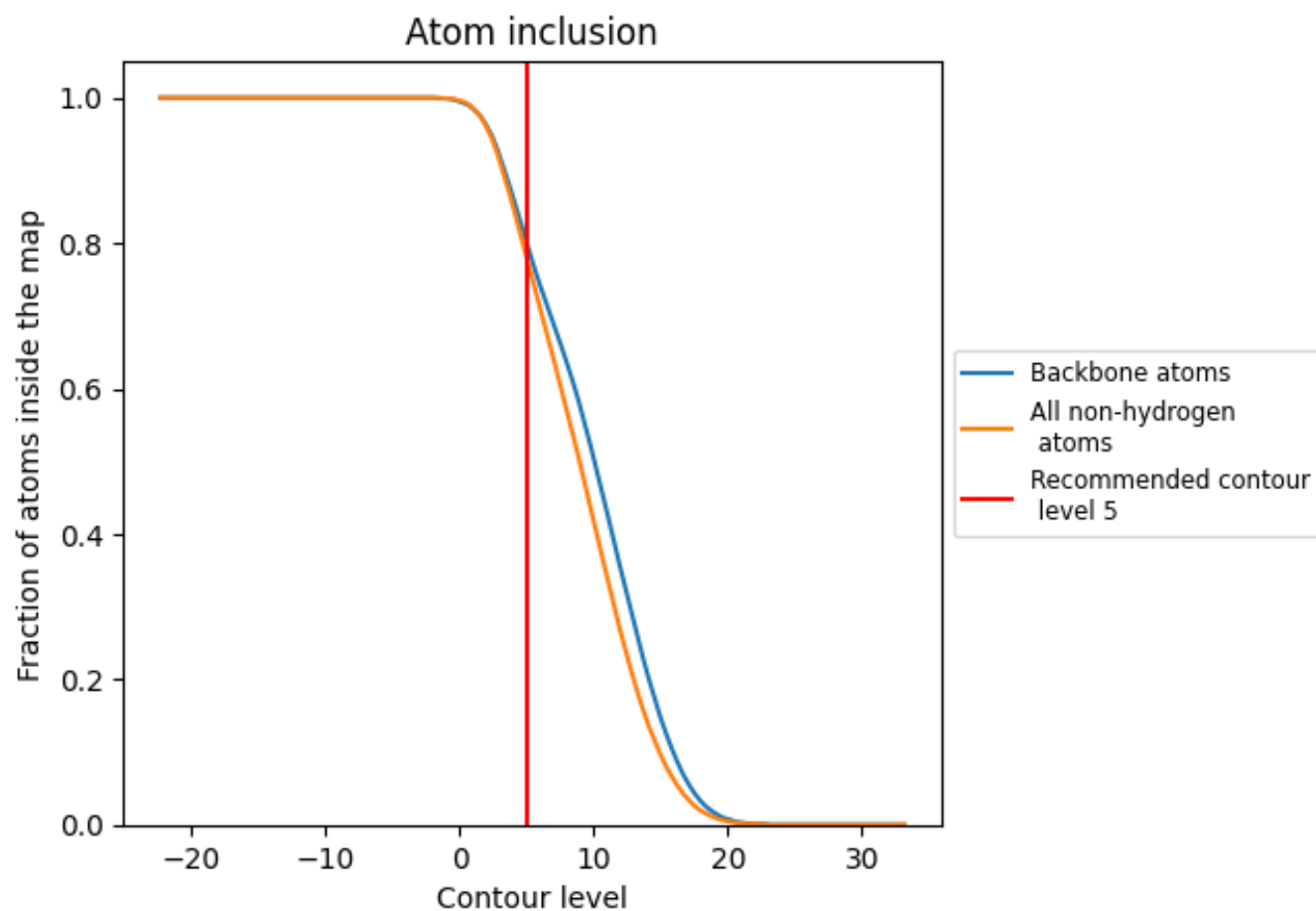
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7810	 0.5680
5B	 0.8080	 0.5800
5b	 0.8080	 0.5790
6A	 0.8120	 0.5890
6B	 0.8530	 0.5890
6C	 0.8020	 0.5790
6L	 0.8290	 0.5640
6a	 0.8100	 0.5880
6b	 0.8580	 0.5900
6c	 0.8000	 0.5790
6l	 0.8230	 0.5640
7A	 0.8530	 0.6040
7C	 0.8460	 0.5920
7L	 0.8010	 0.5590
7a	 0.8500	 0.6030
7c	 0.8420	 0.5900
7l	 0.8010	 0.5590
A	 0.8400	 0.5910
AC	 0.8350	 0.5970
B	 0.5960	 0.5200
BP	 0.8080	 0.5750
C	 0.2690	 0.4150
C1	 0.8480	 0.5900
C2	 0.8260	 0.5800
C3	 0.7670	 0.5690
D	 0.7750	 0.5640
E	 0.7780	 0.5730
F	 0.8510	 0.5820
FS	 0.8390	 0.5810
G	 0.8750	 0.5890
H	 0.7430	 0.5450
I	 0.5910	 0.5130
J	 0.8190	 0.5820
K	 0.8380	 0.5780
L	 0.7810	 0.5690



















































































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Chain	Atom inclusion	Q-score
M	 0.7180	 0.5520
M1	 0.8400	 0.5800
M2	 0.8440	 0.5870
M3	 0.7890	 0.5770
N	 0.8300	 0.5870
O	 0.8080	 0.5760
P	 0.7950	 0.5670
Q	 0.8470	 0.5900
R	 0.6280	 0.5160
S	 0.4690	 0.4540
T	 0.7560	 0.5810
T1	 0.8120	 0.5690
T2	 0.7560	 0.5490
T3	 0.7430	 0.5210
T4	 0.8170	 0.5560
T5	 0.7710	 0.5390
T6	 0.7910	 0.5410
U	 0.8170	 0.5790
U1	 0.7550	 0.5310
U2	 0.1760	 0.3210
U3	 0.2820	 0.3910
U4	 0.1600	 0.3930
U5	 0.4150	 0.4690
U6	 0.4110	 0.4220
V	 0.8100	 0.5780
W	 0.7220	 0.5520
X	 0.8520	 0.5930
Y	 0.8760	 0.5940
Y0	 0.8460	 0.5900
Y5	 0.7020	 0.5520
Y7	 0.6180	 0.5230
Z	 0.5880	 0.5160
a	 0.8440	 0.5900
ac	 0.8330	 0.5960
b	 0.6000	 0.5200
bp	 0.8060	 0.5740
c	 0.2800	 0.4160
c1	 0.8500	 0.5910
c2	 0.8300	 0.5800
c3	 0.7680	 0.5690
d	 0.7740	 0.5670
e	 0.7800	 0.5730

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Chain	Atom inclusion	Q-score
f	 0.8550	 0.5840
fs	 0.8410	 0.5810
g	 0.8760	 0.5890
h	 0.7450	 0.5470
i	 0.5980	 0.5140
j	 0.8190	 0.5810
k	 0.8340	 0.5780
l	 0.7790	 0.5700
m	 0.7250	 0.5520
m1	 0.8330	 0.5810
m2	 0.8420	 0.5870
m3	 0.7920	 0.5760
n	 0.8300	 0.5870
o	 0.8090	 0.5760
p	 0.7900	 0.5680
q	 0.8470	 0.5880
r	 0.6350	 0.5160
s	 0.4680	 0.4530
t	 0.7560	 0.5810
t1	 0.8180	 0.5640
t2	 0.7680	 0.5500
t3	 0.7380	 0.5210
t4	 0.8100	 0.5580
t5	 0.7790	 0.5430
t6	 0.7870	 0.5420
u	 0.8080	 0.5770
u1	 0.7470	 0.5330
u2	 0.1820	 0.3190
u3	 0.2530	 0.4000
u4	 0.1530	 0.4160
u5	 0.4190	 0.4830
u6	 0.4070	 0.4350
v	 0.8090	 0.5800
w	 0.7230	 0.5530
x	 0.8560	 0.5950
y	 0.8800	 0.5940
y0	 0.8370	 0.5880
y5	 0.7010	 0.5510
y7	 0.6150	 0.5240
z	 0.5940	 0.5200