



wwPDB EM Validation Summary Report ⓘ

Dec 17, 2024 – 02:25 AM EST

PDB ID : 7N6G
EMDB ID : EMD-24207
Title : C1 of central pair
Authors : Han, L.; Zhang, K.
Deposited on : 2021-06-08
Resolution : 3.60 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:

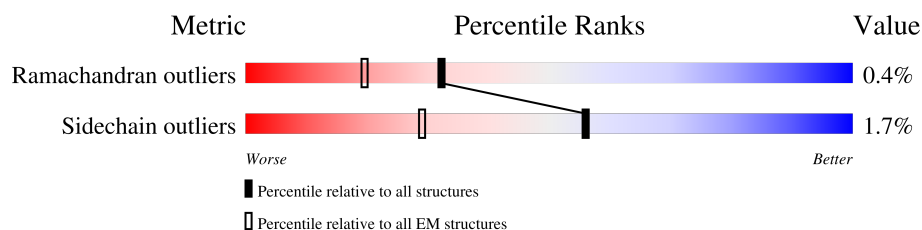
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 3.60 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	0A	512	<div> <div>11%</div> <div>96%</div> <div>..</div> </div>
1	0B	512	<div> <div>44%</div> <div>96%</div> <div>..</div> </div>
1	0C	512	<div> <div>15%</div> <div>97%</div> <div>.</div> </div>
1	0D	512	<div> <div>22%</div> <div>97%</div> <div>..</div> </div>
1	0E	512	<div> <div>15%</div> <div>97%</div> <div>.</div> </div>
1	0F	512	<div> <div>9%</div> <div>97%</div> <div>..</div> </div>
1	0G	512	<div> <div>24%</div> <div>96%</div> <div>..</div> </div>
1	0H	512	<div> <div>6%</div> <div>97%</div> <div>.</div> </div>
1	0I	512	<div> <div>21%</div> <div>97%</div> <div>..</div> </div>


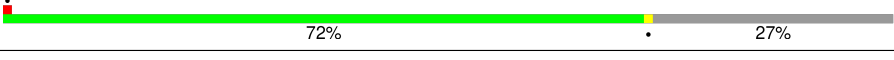
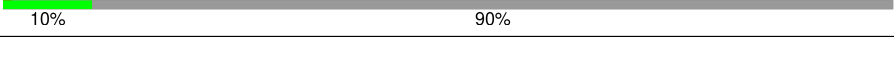
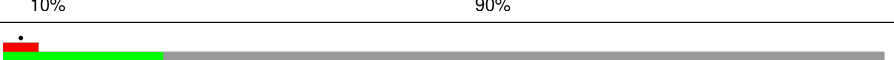
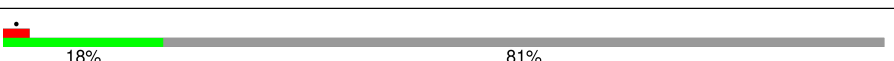


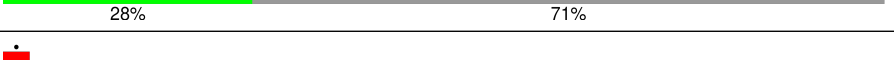
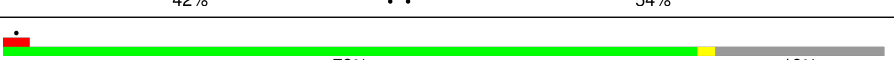
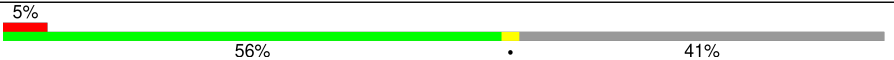

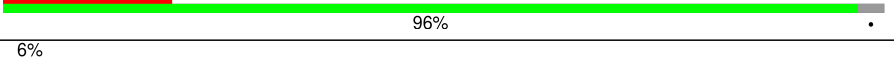
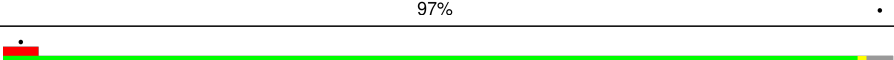
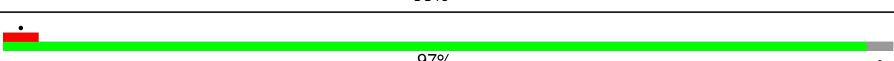
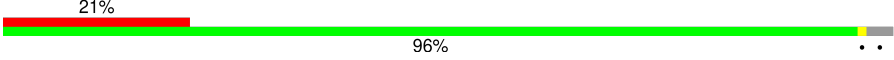
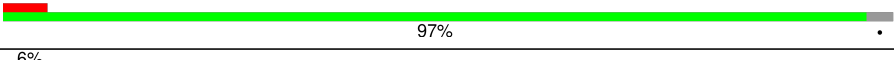
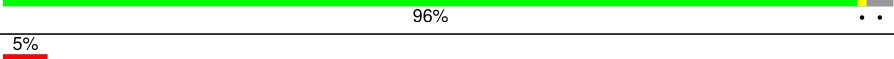
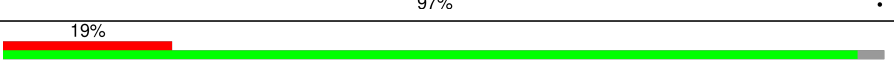
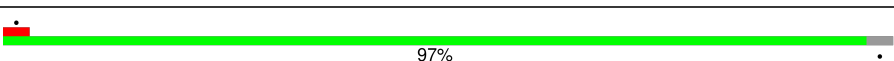
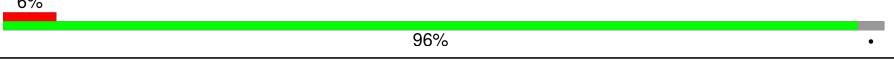
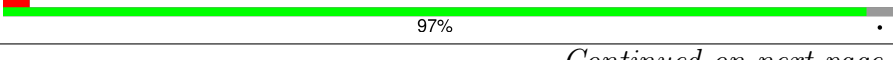



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Mol	Chain	Length	Quality of chain
1	0J	512	20% 97%
1	0K	512	11% 97%
1	0L	512	• 97%
1	0M	512	6% 97%
1	0N	512	• 97%
1	0O	512	5% 97%
1	0P	512	62% 97%
1	0Q	512	45% 97%
1	0R	512	7% 97%
1	0S	512	6% 97%
1	0T	512	5% 97%
1	0U	512	• 97%
1	0V	512	6% 97%
1	0W	512	10% 96%
1	0X	512	8% 97%
1	0Y	512	32% 96%
1	0Z	512	35% 97%
1	1A	512	13% 97%
1	1B	512	85% 97%
1	1C	512	70% 97%
2	1D	571	• 85% 12%
2	1E	571	43% 86% 12%
2	1F	571	• 88% 10%
2	1G	571	31% 88% 10%
3	1H	1102	• 71% 27%

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Mol	Chain	Length	Quality of chain
3	1I	1102	
3	6D	1102	
4	1J	3965	
4	1K	3965	
5	1L	2939	
5	1M	2939	
6	1N	2784	
7	1O	3225	
8	1P	1023	
9	1Q	945	
10	1R	446	
10	1S	446	
11	1T	1638	
12	1a	443	
12	1c	443	
12	1e	443	
12	1g	443	
12	2a	443	
12	2c	443	
12	2e	443	
12	2g	443	
12	3a	443	
12	3c	443	
12	3e	443	
12	3g	443	

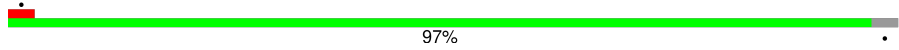
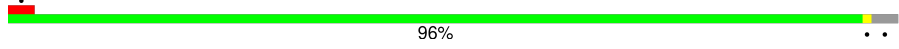
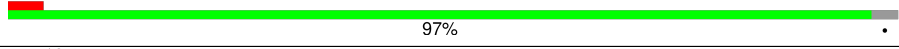
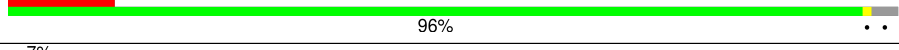
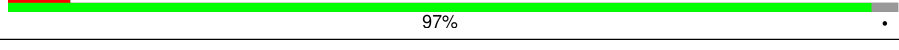
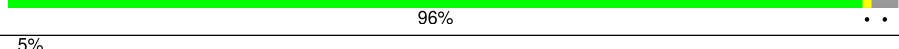
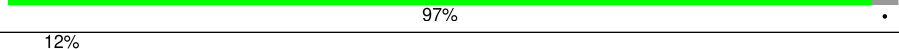
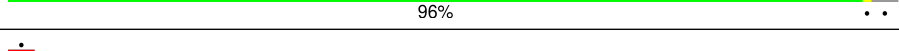
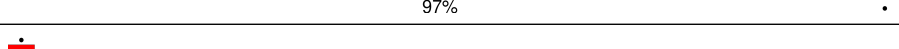
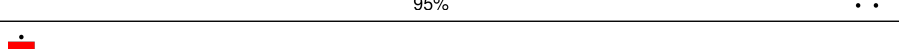
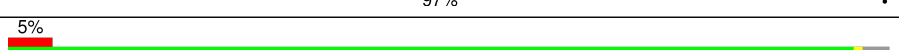
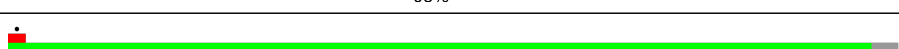
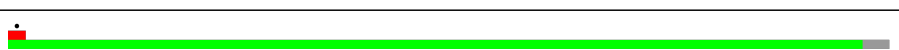
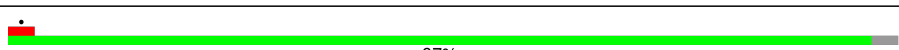
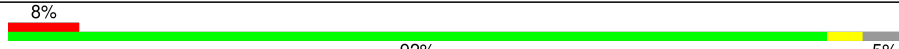


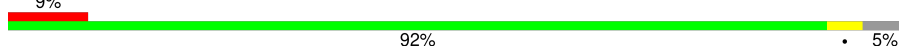
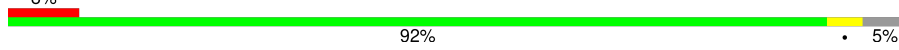
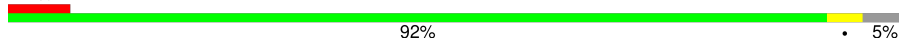
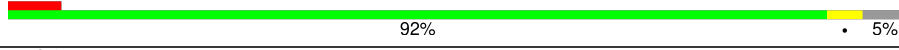
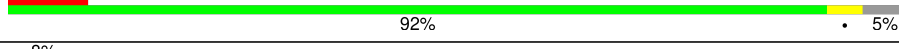
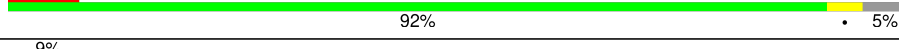
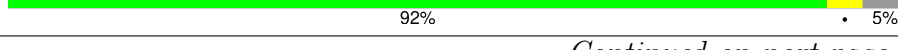

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Mol	Chain	Length	Quality of chain
12	4a	443	17% 95% ..
12	4c	443	5% 97% .
12	4e	443	. 96% .
12	4g	443	. 97% .
12	5a	443	27% 96% .
12	5c	443	6% 97% .
12	5e	443	. 96% ..
12	5g	443	6% 97% .
12	6a	443	30% 96% ..
12	6c	443	6% 97% .
12	6e	443	. 96% ..
12	6g	443	. 97% .
12	7a	443	23% 96% ..
12	7c	443	8% 97% .
12	7e	443	5% 96% ..
12	7g	443	. 97% .
12	8a	443	31% 96% ..
12	8c	443	5% 97% .
12	8e	443	6% 96% ..
12	8g	443	5% 97% .
12	9a	443	18% 95% ..
12	9c	443	. 97% .
12	9e	443	5% 96% ..
12	9g	443	5% 97% .
12	Aa	443	17% 96% ..

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Mol	Chain	Length	Quality of chain
12	Ac	443	
12	Ae	443	
12	Ag	443	
12	Ba	443	
12	Bc	443	
12	Be	443	
12	Bg	443	
12	Ca	443	
12	Cc	443	
12	Ce	443	
12	Cg	443	
12	Da	443	
12	Dc	443	
12	De	443	
12	Dg	443	
13	1b	451	
13	1d	451	
13	1f	451	
13	1h	451	
13	2b	451	
13	2d	451	
13	2f	451	
13	2h	451	
13	3b	451	
13	3d	451	

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Mol	Chain	Length	Quality of chain
13	3f	451	
13	3h	451	
13	4b	451	
13	4d	451	
13	4f	451	
13	4h	451	
13	5b	451	
13	5d	451	
13	5f	451	
13	5h	451	
13	6b	451	
13	6d	451	
13	6f	451	
13	6h	451	
13	7b	451	
13	7d	451	
13	7f	451	
13	7h	451	
13	8b	451	
13	8d	451	
13	8f	451	
13	8h	451	
13	9b	451	
13	9d	451	
13	9f	451	

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Mol	Chain	Length	Quality of chain
13	9h	451	
13	Ab	451	
13	Ad	451	
13	Af	451	
13	Ah	451	
13	Bb	451	
13	Bd	451	
13	Bf	451	
13	Bh	451	
13	Cb	451	
13	Cd	451	
13	Cf	451	
13	Ch	451	
13	Db	451	
13	Dd	451	
13	Df	451	
13	Dh	451	
14	2F	168	
14	2G	168	
15	2H	196	
16	2I	108	
17	2J	100	
17	2K	100	
18	2L	54	
19	2M	18	

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Mol	Chain	Length	Quality of chain
20	2N	52	
21	2O	47	
22	2P	106	
23	2Q	110	
23	2R	110	
24	2S	447	
24	2T	447	
24	2U	447	
24	2V	447	
25	2W	167	
25	2X	167	
26	2Y	65	
26	2Z	65	
27	3A	36	
27	3B	36	
28	3C	739	
29	3E	1471	
30	3F	795	
30	3G	795	
31	3H	1940	
31	3I	1940	
32	3J	749	
32	3K	749	
33	3L	401	
34	3M	507	

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Mol	Chain	Length	Quality of chain
34	3N	507	
34	3O	507	
34	3P	507	
34	3Q	507	
34	3R	507	
34	3S	507	
34	3T	507	
34	3U	507	
34	3V	507	
34	3W	507	
34	3X	507	
34	3Y	507	
34	3Z	507	
34	4A	507	
34	4B	507	
35	4C	2215	
36	4D	304	
37	4E	2301	
37	4F	2301	
37	4G	2301	
37	4H	2301	
38	4I	110	
38	4J	110	
38	4K	110	
38	4L	110	

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Mol	Chain	Length	Quality of chain
38	4M	110	
38	4N	110	
38	4O	110	
38	4P	110	
39	4Q	427	
39	4R	427	
39	4S	427	
40	4T	835	
40	4U	835	
40	4V	835	
41	4W	173	
41	4X	173	
41	4Y	173	
41	4Z	173	
41	5A	173	
41	5B	173	
41	5C	173	
41	5D	173	
42	5E	286	
42	5F	286	
42	5G	286	
42	5H	286	
43	5I	306	
43	5J	306	
43	5K	306	

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Mol	Chain	Length	Quality of chain
43	5L	306	
44	5M	163	
44	5N	163	
44	5O	163	
44	5P	163	
44	5Q	163	
44	5R	163	
44	5S	163	
44	5T	163	
44	5U	163	
44	5V	163	
45	5W	137	
45	5X	137	
45	5Y	137	
46	5Z	181	
47	6A	1929	
47	6B	1929	
48	6E	1138	
48	6F	1138	
49	6G	477	
49	6H	477	
49	6I	477	
49	6J	477	
50	6K	651	
50	6L	651	

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Mol	Chain	Length	Quality of chain
51	6M	2540	<div><div></div><div>41%</div><div></div><div>58%</div></div>
51	6N	2540	<div><div></div><div>41%</div><div></div><div>58%</div></div>
52	6O	89	<div><div></div><div>36%</div><div></div><div>96%</div></div>
52	6P	89	<div><div></div><div>30%</div><div></div><div>96%</div></div>
52	6Q	89	<div><div></div><div>18%</div><div></div><div>96%</div></div>

2 Entry composition [i](#)

There are 54 unique types of molecules in this entry. The entry contains 793756 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 PF16.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0A	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0B	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0C	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0D	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0E	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0F	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0G	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0L	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0M	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0N	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0O	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0P	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0Q	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0R	499	Total	C	N	O	S	0	0
			3526	2215	625	675	11		
1	0S	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0T	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0U	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	0V	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0X	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0Y	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0Z	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	1A	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	1B	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	1C	499	Total	C	N	O	S	0	0
			3524	2214	624	675	11		
1	0H	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0J	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0W	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0I	499	Total	C	N	O	S	0	0
			3528	2217	625	675	11		
1	0K	499	Total	C	N	O	S	0	0
			3524	2214	624	675	11		

- Molecule 2 is a protein called FAP194.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1D	504	Total	C	N	O	S	0	0
			3213	1978	593	625	17		
2	1E	504	Total	C	N	O	S	0	0
			3213	1978	593	625	17		
2	1F	516	Total	C	N	O	S	0	0
			3292	2028	606	641	17		
2	1G	516	Total	C	N	O	S	0	0
			3292	2028	606	641	17		

- Molecule 3 is a protein called FAP69.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1H	803	Total	C	N	O	S	0	0
			5778	3640	1042	1072	24		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	1I	803	Total	C	N	O	S	0	0
			5778	3640	1042	1072	24		
3	6D	801	Total	C	N	O	S	0	0
			6016	3811	1073	1105	27		

- Molecule 4 is a protein called HYDIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1J	396	Total	C	N	O	S	0	0
			2856	1798	498	552	8		
4	1K	396	Total	C	N	O	S	0	0
			2856	1798	498	552	8		

- Molecule 5 is a protein called FAP47.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1L	546	Total	C	N	O	S	0	0
			3368	2055	639	663	11		
5	1M	546	Total	C	N	O	S	0	0
			3368	2055	639	663	11		

- Molecule 6 is a protein called FAP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1N	2179	Total	C	N	O	S	1	0
			16109	10108	2968	2963	70		

- Molecule 7 is a protein called FAP54.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1O	2632	Total	C	N	O	S	0	0
			19593	12378	3583	3552	80		

- Molecule 8 is a protein called HTH_9 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	1P	295	Total	C	N	O	S	0	0
			2266	1435	393	431	7		

- Molecule 9 is a protein called FAP297.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	1Q	437	Total	C	N	O	S	0	0
			2335	1409	460	464	2		

- Molecule 10 is a protein called FAP108.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	1R	361	Total	C	N	O	S	0	0
			2753	1724	494	524	11		
10	1S	264	Total	C	N	O	S	0	0
			1984	1255	355	368	6		

- Molecule 11 is a protein called FAP76.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	1T	972	Total	C	N	O	0	0
			4804	2857	975	972		

- Molecule 12 is a protein called Tubulin beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	1a	428	Total	C	N	O	S	0	0
			3359	2110	576	643	30		
12	1c	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
12	1e	428	Total	C	N	O	S	0	0
			3359	2110	576	643	30		
12	1g	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
12	2a	428	Total	C	N	O	S	0	0
			3359	2110	576	643	30		
12	2c	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
12	2e	428	Total	C	N	O	S	0	0
			3359	2110	576	643	30		
12	2g	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
12	3a	428	Total	C	N	O	S	0	0
			3359	2110	576	643	30		
12	3c	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
12	3e	428	Total	C	N	O	S	0	0
			3359	2110	576	643	30		

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	3g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	4a	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	4c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	4e	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	4g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	5a	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	5c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	5e	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	5g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	6a	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	6c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	6e	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	6g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	7a	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	7c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	7e	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	7g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	8a	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	8c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	8e	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	8g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	9a	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	9c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	9e	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	9g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	Aa	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	Ac	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	Ae	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	Ag	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	Ba	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	Bc	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	Be	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	Bg	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	Ca	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	Cc	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	Ce	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	Cg	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	Da	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	Dc	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
12	De	428	Total 3359	C 2110	N 576	O 643	S 30	0	0
12	Dg	431	Total 3379	C 2121	N 579	O 649	S 30	0	0

- Molecule 13 is a protein called Tubulin alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	1b	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	1d	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	1f	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	1h	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	2b	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	2d	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	2f	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	2h	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	3b	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	3d	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	3f	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	3h	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	4b	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	4d	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	4f	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	4h	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	5b	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	5d	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	5f	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	5h	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	6b	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	6d	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	6f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	6h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	7b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	7d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	7f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	7h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	8b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	8d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	8f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	8h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	9b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	9d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	9f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	9h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	Ab	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	Ad	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	Af	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	Ah	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	Bb	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	Bd	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
13	Bf	430	Total 3339	C 2115	N 568	O 634	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	Bh	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	Cb	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	Cd	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	Cf	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	Ch	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	Db	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	Dd	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	Df	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
13	Dh	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		

- Molecule 14 is a protein called FAP275.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2F	161	Total	C	N	O	S	0	0
			1228	758	238	228	4		
14	2G	161	Total	C	N	O	S	0	0
			1228	758	238	228	4		

- Molecule 15 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	2H	196	Total	C	N	O	0	0
			980	588	196	196		

- Molecule 16 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	2I	108	Total	C	N	O	0	0
			540	324	108	108		

- Molecule 17 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	2J	100	Total	C	N	O	0	0
			500	300	100	100		
17	2K	100	Total	C	N	O	0	0
			500	300	100	100		

- Molecule 18 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	2L	54	Total	C	N	O	0	0
			270	162	54	54		

- Molecule 19 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	2M	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 20 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	2N	52	Total	C	N	O	0	0
			260	156	52	52		

- Molecule 21 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	2O	47	Total	C	N	O	0	0
			235	141	47	47		

- Molecule 22 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	2P	106	Total	C	N	O	0	0
			530	318	106	106		

- Molecule 23 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	2Q	110	Total	C	N	O	0	0
			550	330	110	110		
23	2R	110	Total	C	N	O	0	0
			550	330	110	110		

- Molecule 24 is a protein called FAP289.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	2S	105	Total	C	N	O	0	0
			522	312	105	105		
24	2T	109	Total	C	N	O	S	0
			868	530	176	159	3	0
24	2U	111	Total	C	N	O	S	0
			882	539	178	162	3	0
24	2V	109	Total	C	N	O	S	0
			868	530	176	159	3	0

- Molecule 25 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	2W	167	Total	C	N	O	0	0
			835	501	167	167		
25	2X	167	Total	C	N	O	0	0
			835	501	167	167		

- Molecule 26 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	2Y	65	Total	C	N	O	0	0
			325	195	65	65		
26	2Z	65	Total	C	N	O	0	0
			325	195	65	65		

- Molecule 27 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	3A	36	Total	C	N	O	0	0
			180	108	36	36		
27	3B	36	Total	C	N	O	0	0
			180	108	36	36		

- Molecule 28 is a protein called FAP216.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3C	61	Total	C	N	O	S	0	0
			480	291	96	92	1		

- Molecule 29 is a protein called FAP92.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	3E	87	Total	C	N	O	0	0
			671	406	142	123		

- Molecule 30 is a protein called FAP99.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3F	444	Total	C	N	O	S	0	0
			3386	2041	688	650	7		
30	3G	240	Total	C	N	O	S	0	0
			1904	1142	391	367	4		

- Molecule 31 is a protein called FAP74.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	3H	308	Total	C	N	O	S	0	0
			1958	1190	379	387	2		
31	3I	401	Total	C	N	O	S	0	0
			3118	1904	606	601	7		

- Molecule 32 is a protein called FAP360.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	3J	372	Total	C	N	O	S	0	0
			2792	1758	501	519	14		
32	3K	367	Total	C	N	O	S	0	0
			2767	1745	495	513	14		

- Molecule 33 is a protein called FAP279.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	3L	197	Total	C	N	O	S	0	0
			1572	1001	278	287	6		

- Molecule 34 is a protein called FAP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	3M	387	Total	C	N	O	S	0	0
			2989	1825	572	580	12		
34	3N	392	Total	C	N	O	S	0	0
			3040	1861	578	589	12		
34	3O	353	Total	C	N	O	S	0	0
			2775	1696	535	532	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
34	3P	355	Total	C	N	O	S	0	0
			2795	1712	537	534	12		
34	3Q	353	Total	C	N	O	S	0	0
			2775	1696	535	532	12		
34	3R	358	Total	C	N	O	S	0	0
			2814	1723	540	539	12		
34	3S	387	Total	C	N	O	S	0	0
			2989	1825	572	580	12		
34	3T	392	Total	C	N	O	S	0	0
			3040	1861	578	589	12		
34	3U	355	Total	C	N	O	S	0	0
			2795	1712	537	534	12		
34	3V	410	Total	C	N	O	S	0	0
			3192	1954	611	614	13		
34	3W	411	Total	C	N	O	S	0	0
			3198	1956	612	617	13		
34	3X	358	Total	C	N	O	S	0	0
			2814	1723	540	539	12		
34	3Y	358	Total	C	N	O	S	0	0
			2814	1723	540	539	12		
34	3Z	358	Total	C	N	O	S	0	0
			2814	1723	540	539	12		
34	4A	410	Total	C	N	O	S	0	0
			3192	1954	611	614	13		
34	4B	411	Total	C	N	O	S	0	0
			3198	1956	612	617	13		

- Molecule 35 is a protein called FAP81.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4C	634	Total	C	N	O	S	0	0
			4846	3052	870	902	22		

- Molecule 36 is a protein called FAP15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	4D	295	Total	C	N	O	S	0	0
			2372	1515	397	442	18		

- Molecule 37 is a protein called PF6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	4E	983	Total	C	N	O	S	0	0
			7227	4588	1245	1365	29		
37	4F	965	Total	C	N	O	S	0	0
			7056	4482	1212	1335	27		
37	4G	965	Total	C	N	O	S	0	0
			7056	4482	1212	1335	27		
37	4H	965	Total	C	N	O	S	0	0
			7056	4482	1212	1335	27		

- Molecule 38 is a protein called DPY30.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	4I	64	Total	C	N	O	S	0	0
			491	317	84	87	3		
38	4J	64	Total	C	N	O	S	0	0
			491	317	84	87	3		
38	4K	64	Total	C	N	O	S	0	0
			491	317	84	87	3		
38	4L	64	Total	C	N	O	S	0	0
			491	317	84	87	3		
38	4M	64	Total	C	N	O	S	0	0
			491	317	84	87	3		
38	4N	64	Total	C	N	O	S	0	0
			491	317	84	87	3		
38	4O	84	Total	C	N	O	S	0	0
			626	400	106	117	3		
38	4P	55	Total	C	N	O	S	0	0
			424	275	73	73	3		

- Molecule 39 is a protein called FAP305.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	4Q	216	Total	C	N	O	S	0	0
			1778	1127	344	302	5		
39	4R	216	Total	C	N	O	S	0	0
			1778	1127	344	302	5		
39	4S	216	Total	C	N	O	S	0	0
			1778	1127	344	302	5		

- Molecule 40 is a protein called FAP101.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	4T	602	Total	C	N	O	S	0	0
			4494	2824	814	839	17		
40	4U	602	Total	C	N	O	S	0	0
			4494	2824	814	839	17		
40	4V	602	Total	C	N	O	S	0	0
			4494	2824	814	839	17		

- Molecule 41 is a protein called FAP227.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	4W	124	Total	C	N	O	0	0
			597	349	124	124		
41	4X	124	Total	C	N	O	0	0
			597	349	124	124		
41	4Y	124	Total	C	N	O	0	0
			597	349	124	124		
41	4Z	124	Total	C	N	O	0	0
			597	349	124	124		
41	5A	123	Total	C	N	O	0	0
			592	346	123	123		
41	5B	123	Total	C	N	O	0	0
			592	346	123	123		
41	5C	123	Total	C	N	O	0	0
			592	346	123	123		
41	5D	123	Total	C	N	O	0	0
			592	346	123	123		

- Molecule 42 is a protein called FAP114.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5E	216	Total	C	N	O	S	0	0
			1562	993	272	292	5		
42	5F	216	Total	C	N	O	S	0	0
			1562	993	272	292	5		
42	5G	216	Total	C	N	O	S	0	0
			1562	993	272	292	5		
42	5H	165	Total	C	N	O	S	0	0
			1307	840	221	241	5		

- Molecule 43 is a protein called FAP119.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5I	211	Total	C	N	O	S	0	0
			1594	1020	276	292	6		
43	5J	211	Total	C	N	O	S	0	0
			1594	1020	276	292	6		
43	5K	211	Total	C	N	O	S	0	0
			1594	1020	276	292	6		
43	5L	211	Total	C	N	O	S	0	0
			1594	1020	276	292	6		

- Molecule 44 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5M	142	Total	C	N	O		0	0
			699	415	142	142			
44	5N	142	Total	C	N	O		0	0
			699	415	142	142			
44	5O	142	Total	C	N	O		0	0
			699	415	142	142			
44	5Q	146	Total	C	N	O	S	0	0
			1153	710	186	248	9		
44	5R	146	Total	C	N	O	S	0	0
			1153	710	186	248	9		
44	5S	145	Total	C	N	O	S	0	0
			1144	705	185	245	9		
44	5T	145	Total	C	N	O	S	0	0
			1144	705	185	245	9		
44	5U	145	Total	C	N	O	S	0	0
			1144	705	185	245	9		
44	5V	149	Total	C	N	O	S	0	0
			1166	714	190	253	9		
44	5P	146	Total	C	N	O	S	0	0
			1153	710	186	248	9		

- Molecule 45 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	5W	137	Total	C	N	O	0	0
			685	411	137	137		
45	5X	137	Total	C	N	O	0	0
			685	411	137	137		
45	5Y	137	Total	C	N	O	0	0
			685	411	137	137		

- Molecule 46 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5Z	181	Total	C	N	O	S	0	0
			978	603	191	181	3		

- Molecule 47 is a protein called CPC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	6A	1558	Total	C	N	O	S	0	0
			11821	7347	2181	2246	47		
47	6B	1558	Total	C	N	O	S	0	0
			11821	7347	2181	2246	47		

- Molecule 48 is a protein called FAP246.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	6E	904	Total	C	N	O	S	0	0
			6892	4372	1255	1236	29		
48	6F	904	Total	C	N	O	S	0	0
			6892	4372	1255	1236	29		

- Molecule 49 is a protein called Phosphopyruvate hydratase.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	6G	476	Total	C	N	O	S	0	0
			3606	2262	615	707	22		
49	6H	476	Total	C	N	O	S	0	0
			3606	2262	615	707	22		
49	6I	476	Total	C	N	O	S	0	0
			3606	2262	615	707	22		
49	6J	476	Total	C	N	O	S	0	0
			3606	2262	615	707	22		

- Molecule 50 is a protein called Heat shock protein 70A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	6K	609	Total	C	N	O	S	0	0
			4731	2963	821	927	20		
50	6L	609	Total	C	N	O	S	0	0
			4731	2963	821	927	20		

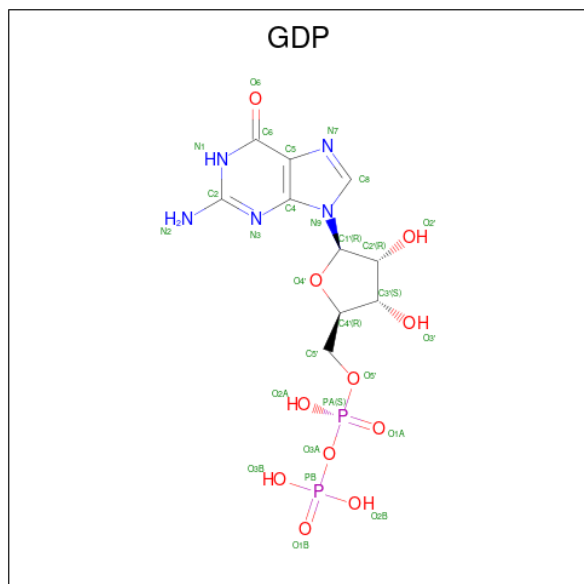
- Molecule 51 is a protein called FAP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	6M	1075	Total	C	N	O	S	0	0
			8050	5038	1459	1512	41		
51	6N	1075	Total	C	N	O	S	0	0
			8050	5038	1459	1512	41		

- Molecule 52 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	6O	89	Total	C	N	O	0	0
			444	266	89	89		
52	6P	89	Total	C	N	O	0	0
			444	266	89	89		
52	6Q	89	Total	C	N	O	0	0
			444	266	89	89		

- Molecule 53 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



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Mol	Chain	Residues	Atoms					AltConf
53	2a	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	2c	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	2e	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	2g	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	3a	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	3c	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	3e	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	3g	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	4a	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	4c	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	4e	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	4g	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	5a	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	5c	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	5e	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	5g	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	6a	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	6c	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	6e	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	6g	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	7a	1	Total	C	N	O	P	0
			28	10	5	11	2	

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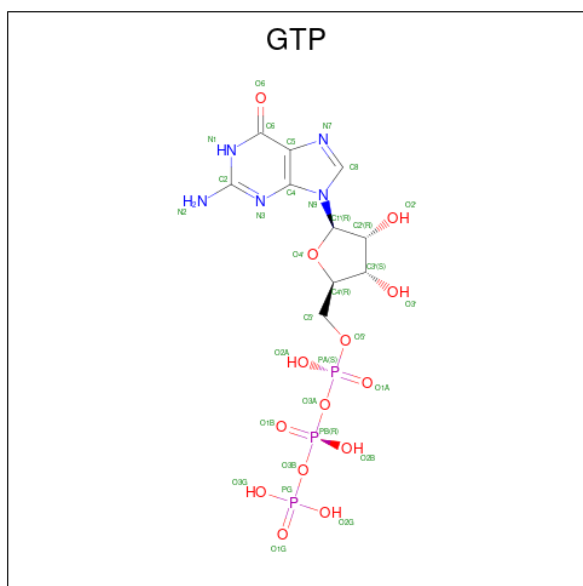
Mol	Chain	Residues	Atoms					AltConf
53	7c	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	7e	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	7g	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	8a	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	8c	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	8e	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	8g	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	9a	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	9c	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	9e	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	9g	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Aa	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Ac	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Ae	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Ag	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Ba	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Bc	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Be	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Bg	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Ca	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Cc	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
53	Ce	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Cg	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Da	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Dc	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	De	1	Total	C	N	O	P	0
			28	10	5	11	2	
53	Dg	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 54 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
54	1b	1	Total	C	N	O	P	0
			32	10	5	14	3	
54	1d	1	Total	C	N	O	P	0
			32	10	5	14	3	
54	1f	1	Total	C	N	O	P	0
			32	10	5	14	3	
54	1h	1	Total	C	N	O	P	0
			32	10	5	14	3	
54	2b	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
54	2d	1	32	10	5	14	3	0
54	2f	1	32	10	5	14	3	0
54	2h	1	32	10	5	14	3	0
54	3c	1	32	10	5	14	3	0
54	3d	1	32	10	5	14	3	0
54	3f	1	32	10	5	14	3	0
54	3h	1	32	10	5	14	3	0
54	4b	1	32	10	5	14	3	0
54	4d	1	32	10	5	14	3	0
54	4f	1	32	10	5	14	3	0
54	4h	1	32	10	5	14	3	0
54	5c	1	32	10	5	14	3	0
54	5d	1	32	10	5	14	3	0
54	5f	1	32	10	5	14	3	0
54	5h	1	32	10	5	14	3	0
54	6c	1	32	10	5	14	3	0
54	6e	1	32	10	5	14	3	0
54	6g	1	32	10	5	14	3	0
54	6h	1	32	10	5	14	3	0
54	7b	1	32	10	5	14	3	0
54	7e	1	32	10	5	14	3	0

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Mol	Chain	Residues	Atoms					AltConf
54	7f	1	Total 32	C 10	N 5	O 14	P 3	0
54	7h	1	Total 32	C 10	N 5	O 14	P 3	0
54	8b	1	Total 32	C 10	N 5	O 14	P 3	0
54	8d	1	Total 32	C 10	N 5	O 14	P 3	0
54	8f	1	Total 32	C 10	N 5	O 14	P 3	0
54	8h	1	Total 32	C 10	N 5	O 14	P 3	0
54	9b	1	Total 32	C 10	N 5	O 14	P 3	0
54	9e	1	Total 32	C 10	N 5	O 14	P 3	0
54	9f	1	Total 32	C 10	N 5	O 14	P 3	0
54	9h	1	Total 32	C 10	N 5	O 14	P 3	0
54	Ab	1	Total 32	C 10	N 5	O 14	P 3	0
54	Ae	1	Total 32	C 10	N 5	O 14	P 3	0
54	Af	1	Total 32	C 10	N 5	O 14	P 3	0
54	Ah	1	Total 32	C 10	N 5	O 14	P 3	0
54	Bb	1	Total 32	C 10	N 5	O 14	P 3	0
54	Bd	1	Total 32	C 10	N 5	O 14	P 3	0
54	Bf	1	Total 32	C 10	N 5	O 14	P 3	0
54	Bh	1	Total 32	C 10	N 5	O 14	P 3	0
54	Cc	1	Total 32	C 10	N 5	O 14	P 3	0
54	Cd	1	Total 32	C 10	N 5	O 14	P 3	0
54	Cf	1	Total 32	C 10	N 5	O 14	P 3	0

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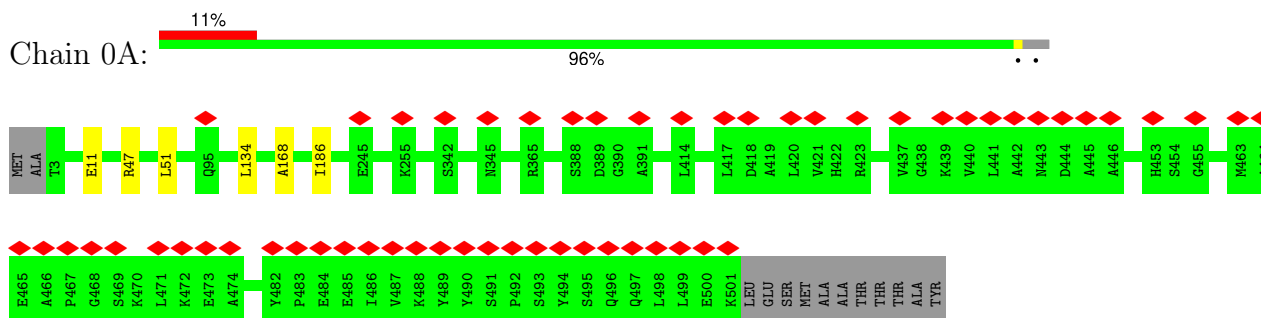
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Mol	Chain	Residues	Atoms					AltConf
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			32	10	5	14	3	
54	Db	1	Total	C	N	O	P	0
			32	10	5	14	3	
54	Dd	1	Total	C	N	O	P	0
			32	10	5	14	3	
54	Df	1	Total	C	N	O	P	0
			32	10	5	14	3	
54	Dh	1	Total	C	N	O	P	0
			32	10	5	14	3	

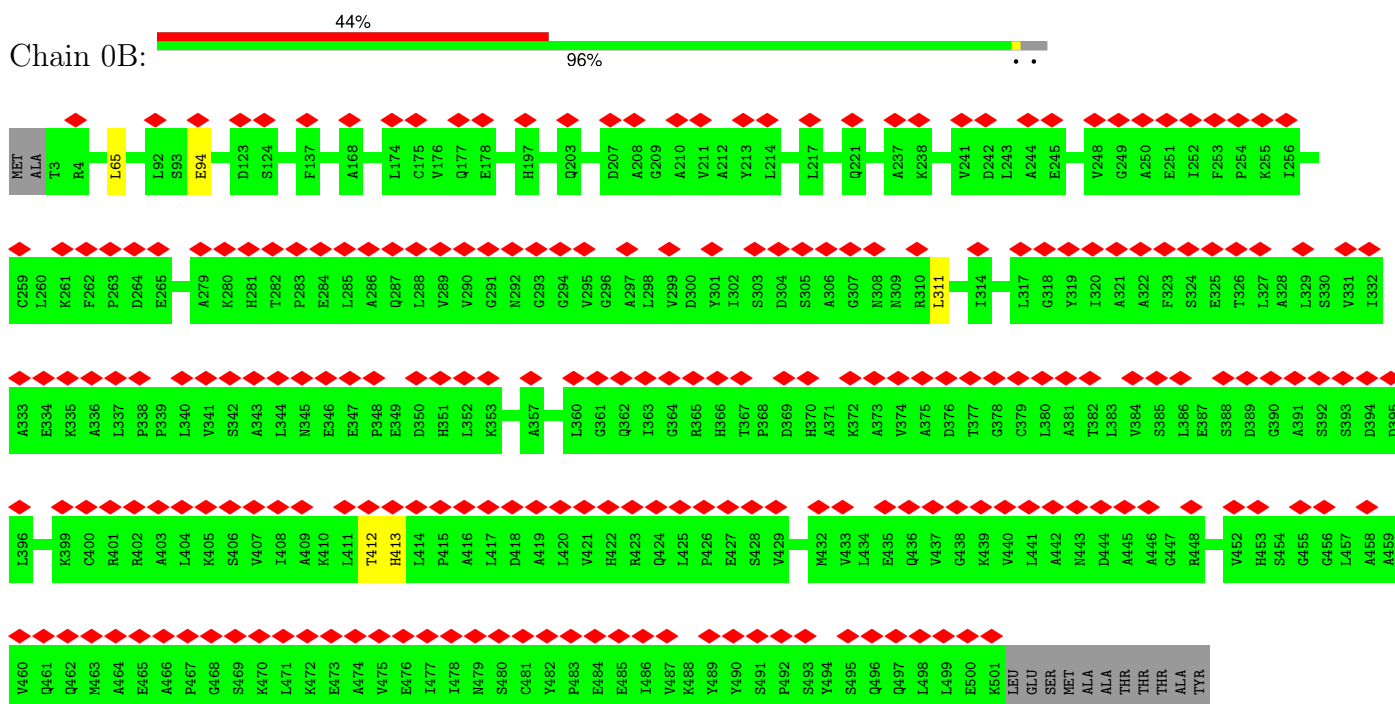
3 Residue-property plots

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: PF16

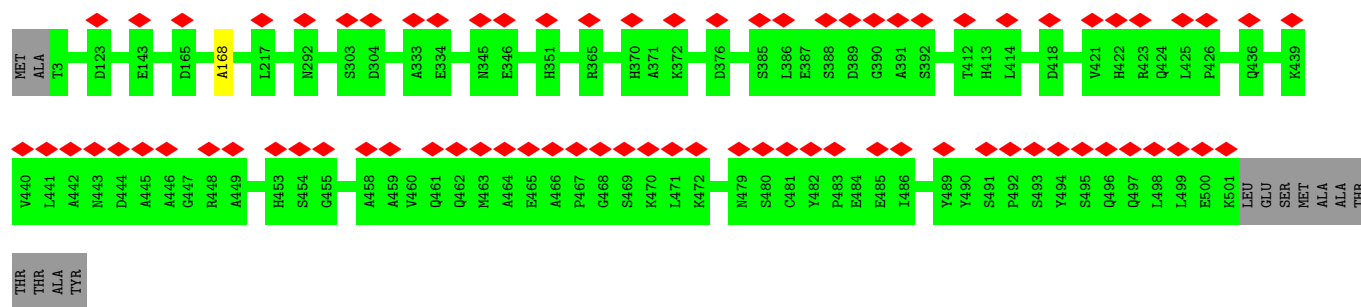


• Molecule 1: PF16

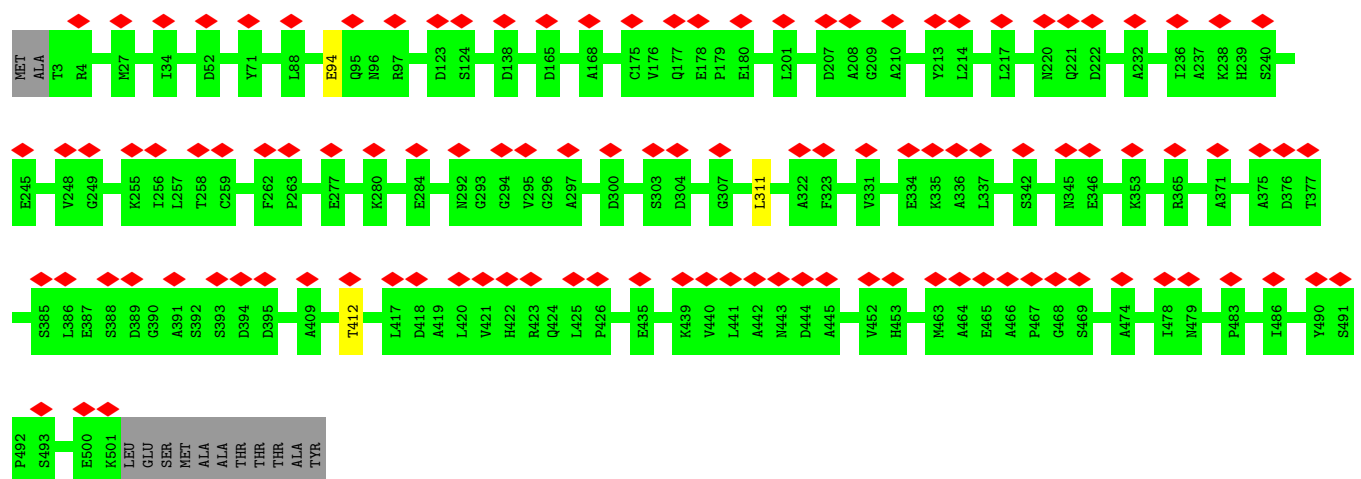


• Molecule 1: PF16

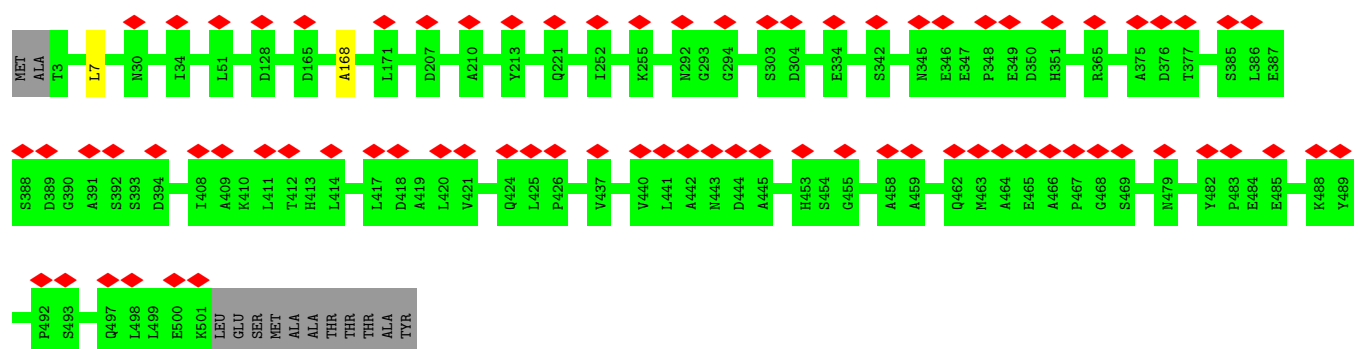




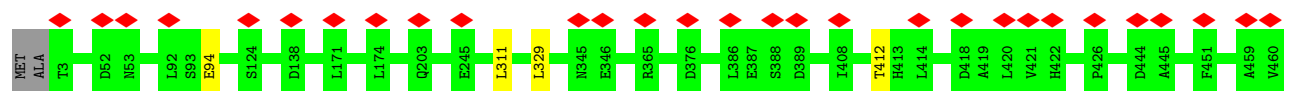
• Molecule 1: PF16



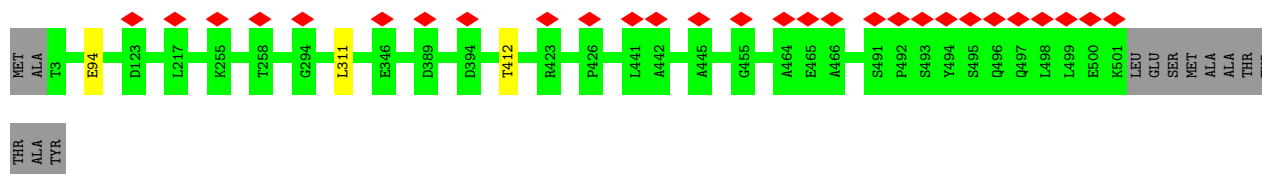
• Molecule 1: PF16



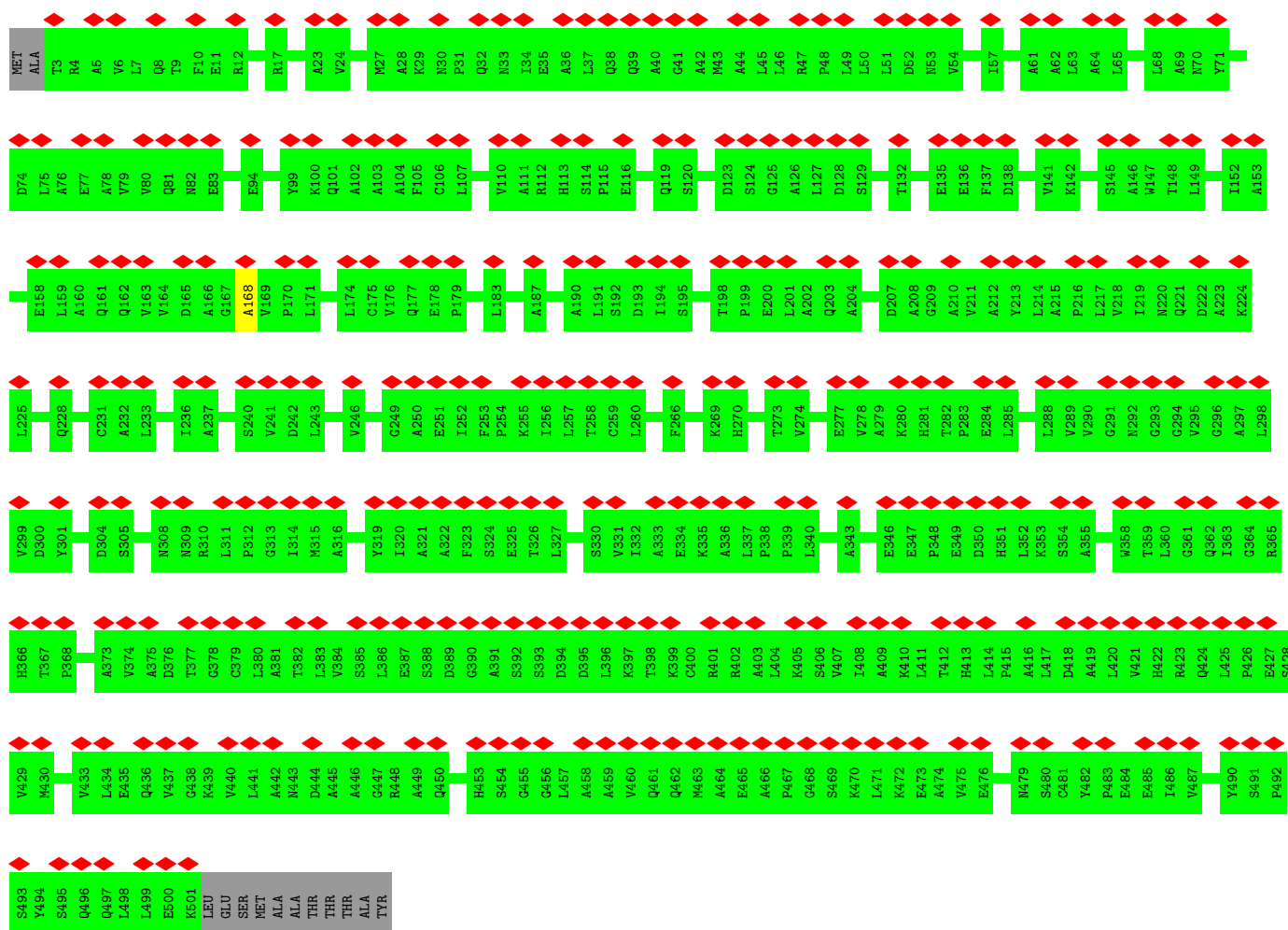
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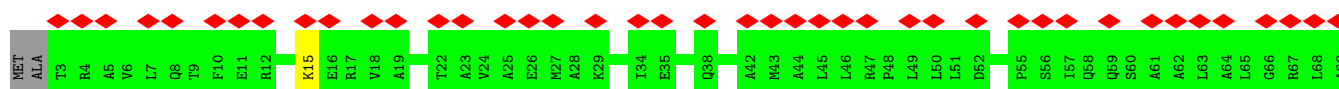


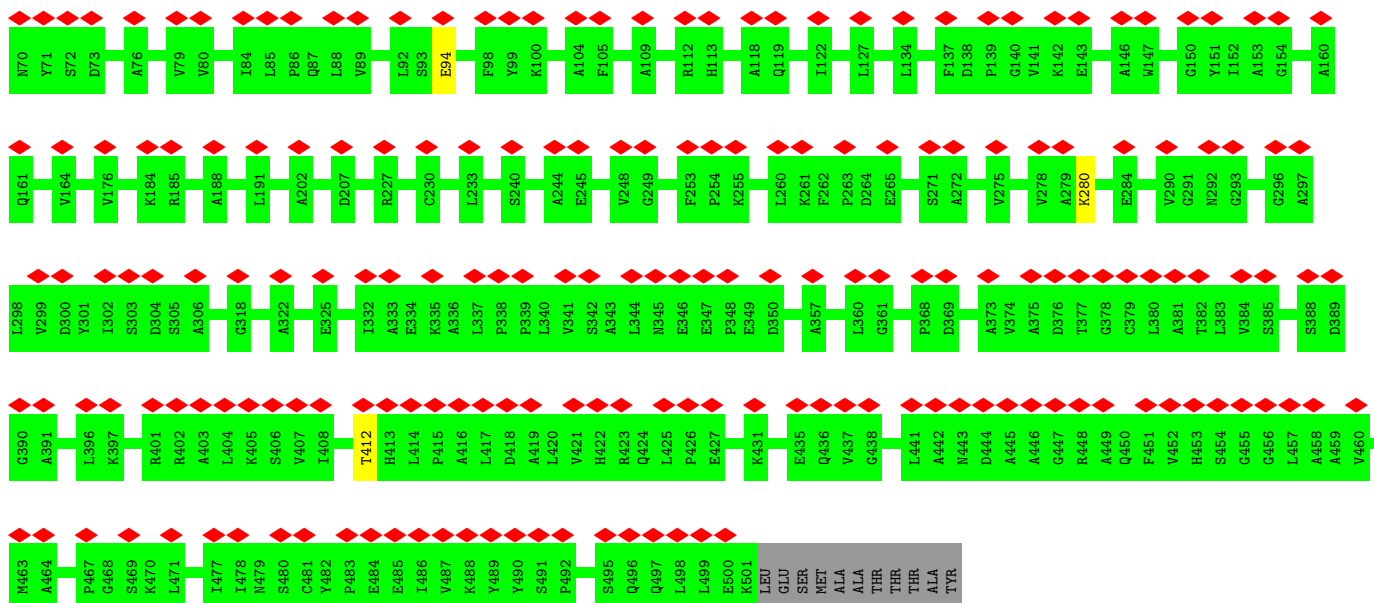


• Molecule 1: PF16

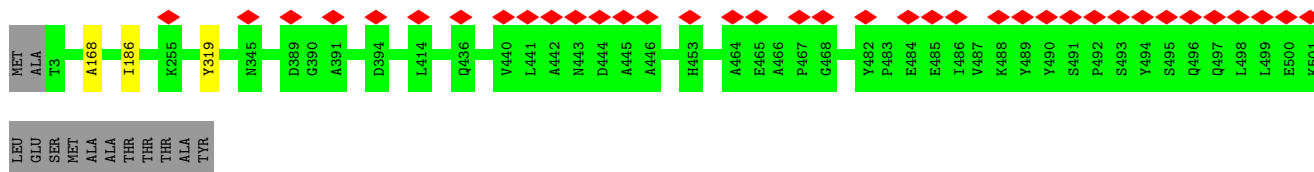


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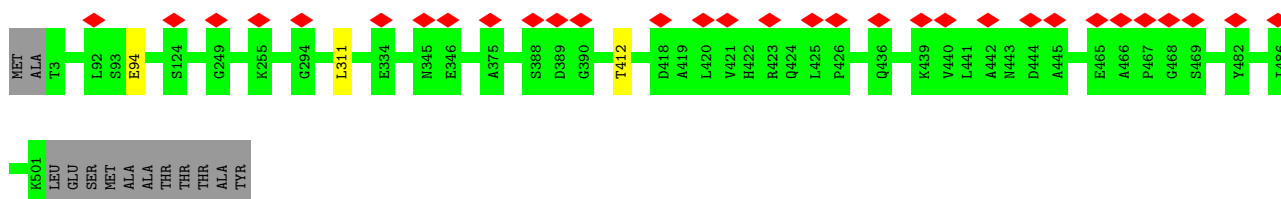




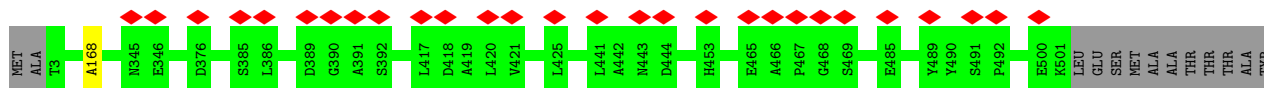
- Molecule 1: PF16



- Molecule 1: PF16

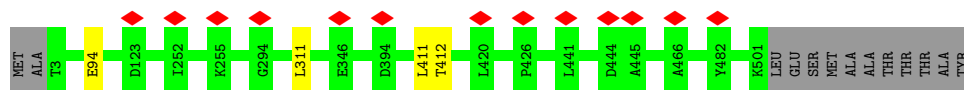


- Molecule 1: PF16

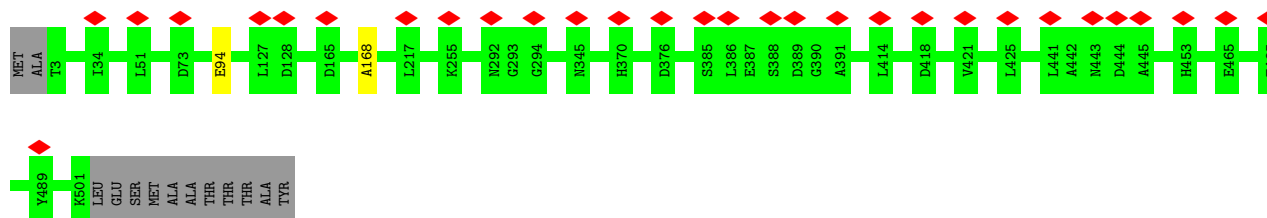


- Molecule 1: PF16

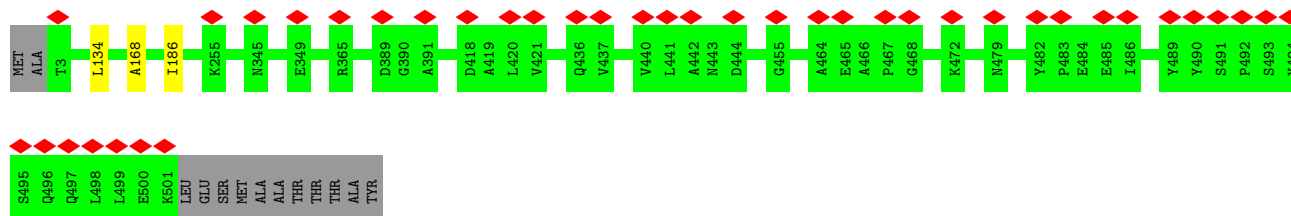




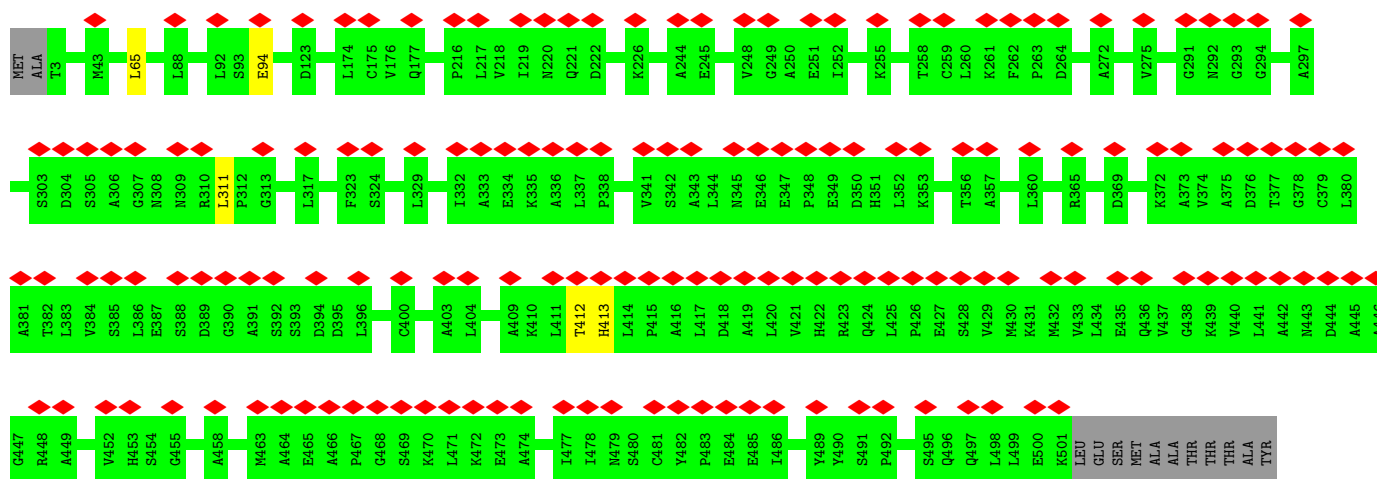
- Molecule 1: PF16



- Molecule 1: PF16



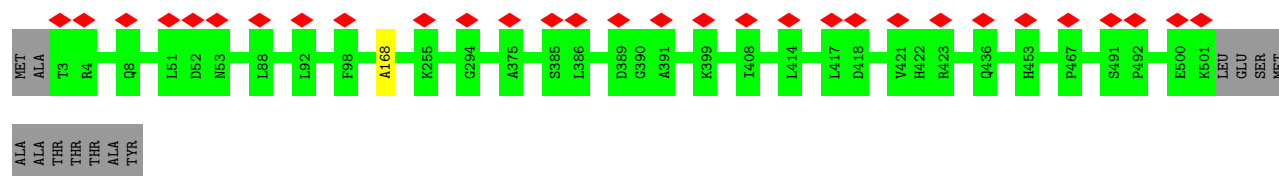
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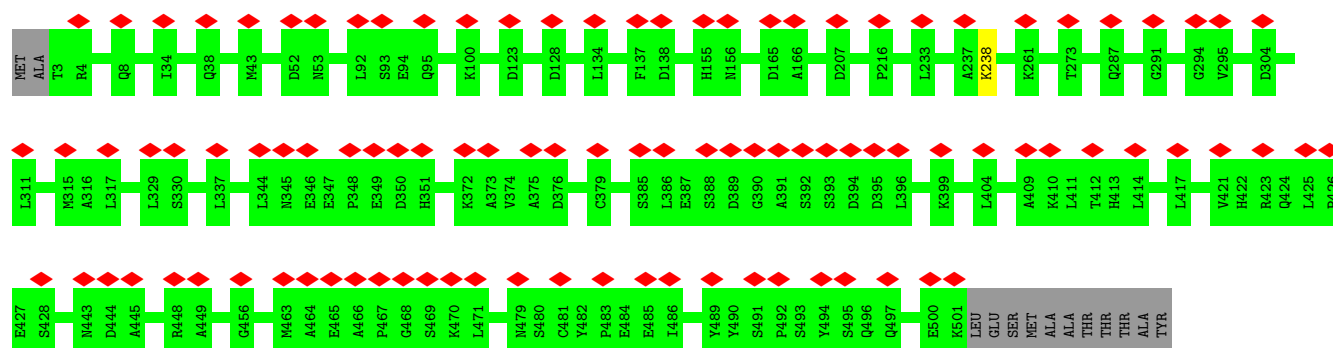
- Molecule 1: PF16



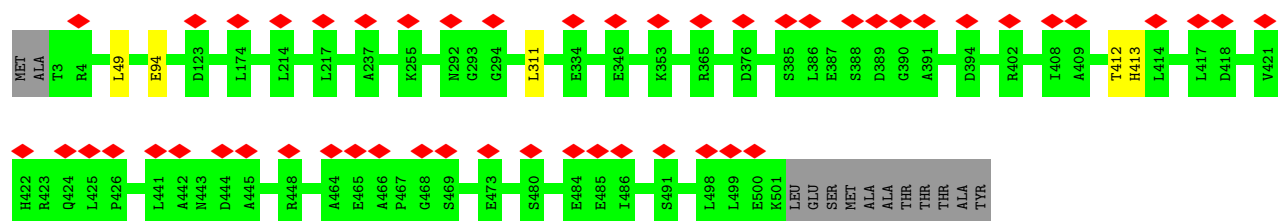




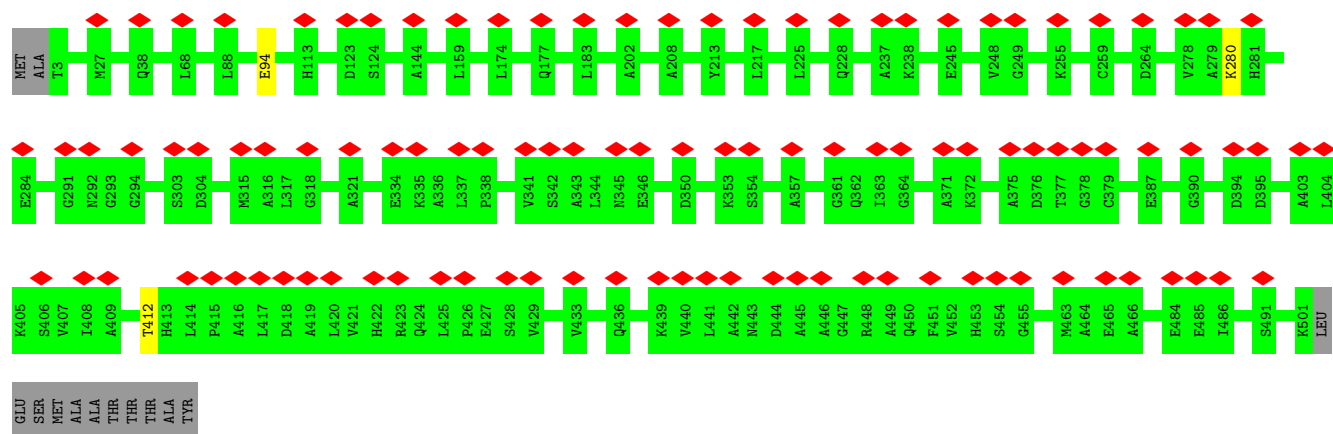
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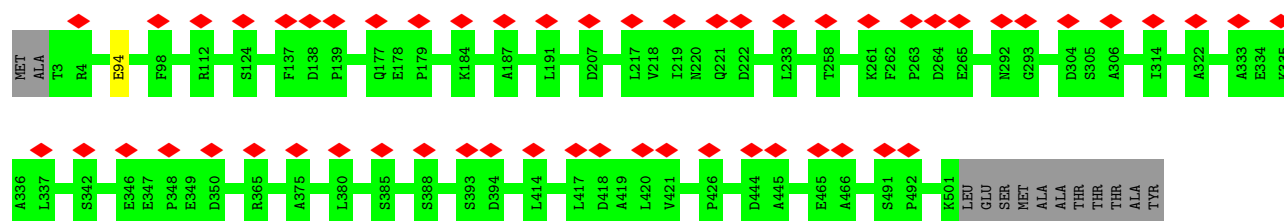
- Molecule 1: PF16



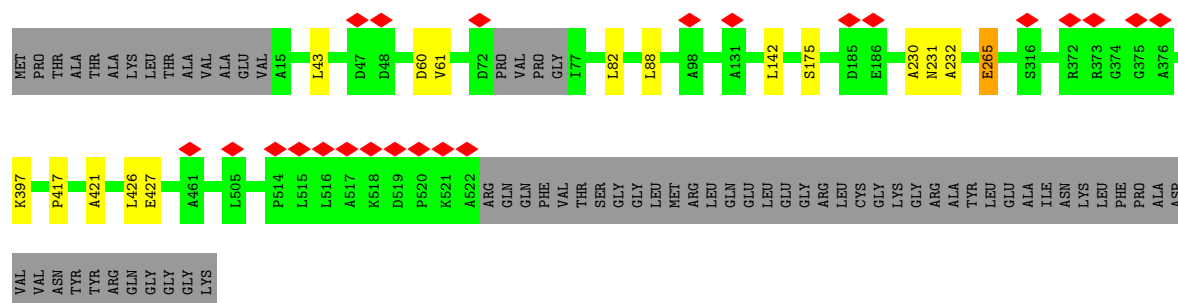
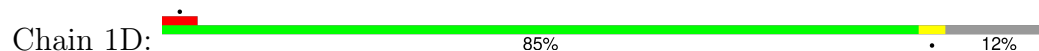
- Molecule 1: PF16



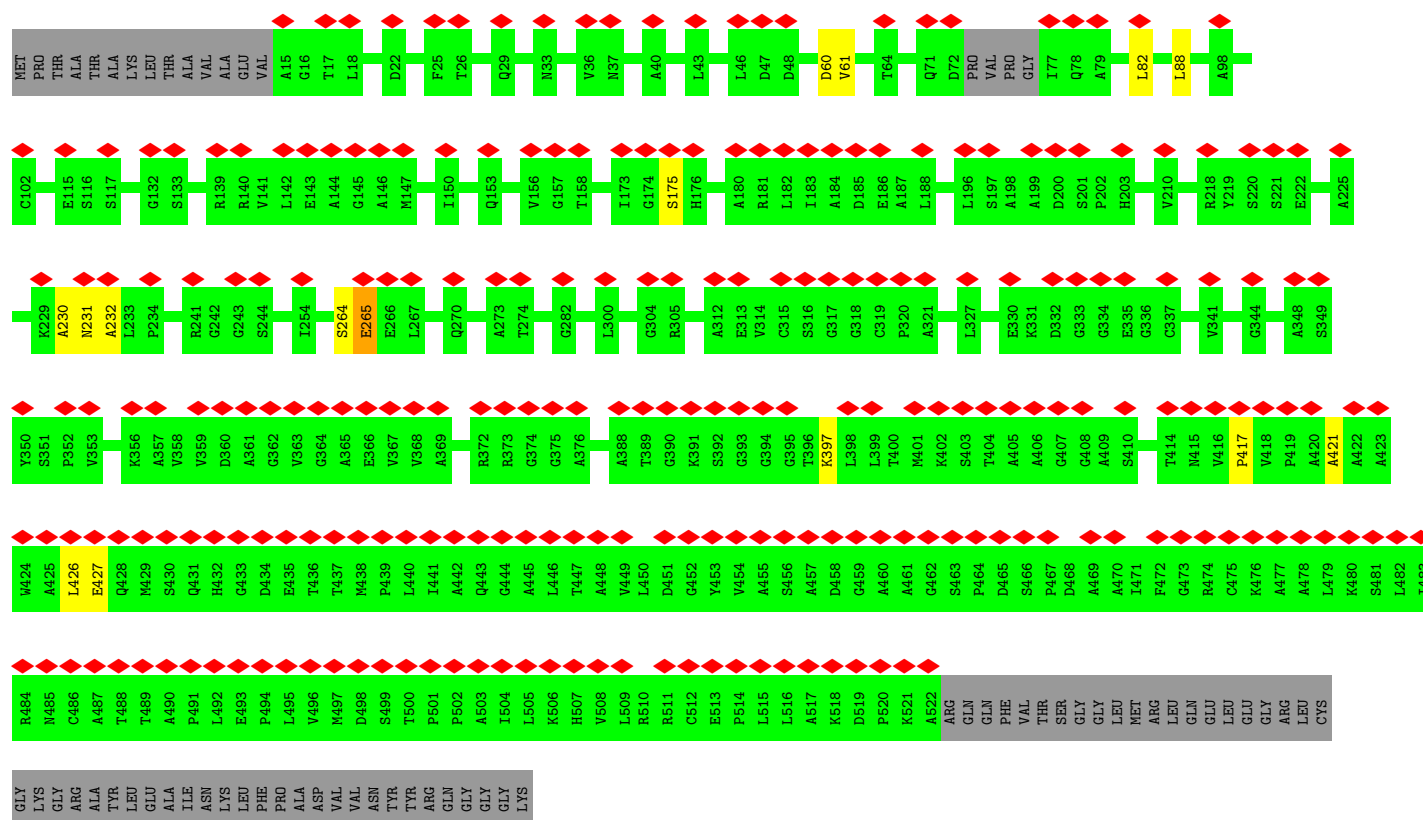
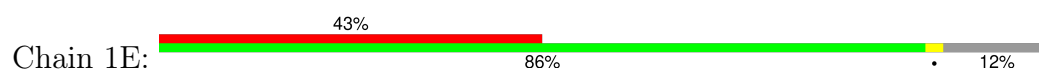
- Molecule 1: PF16



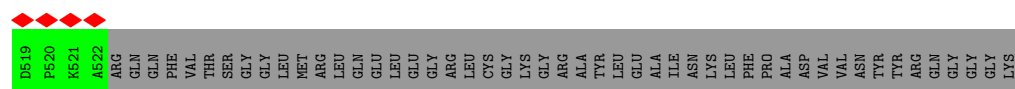
• Molecule 2: FAP194



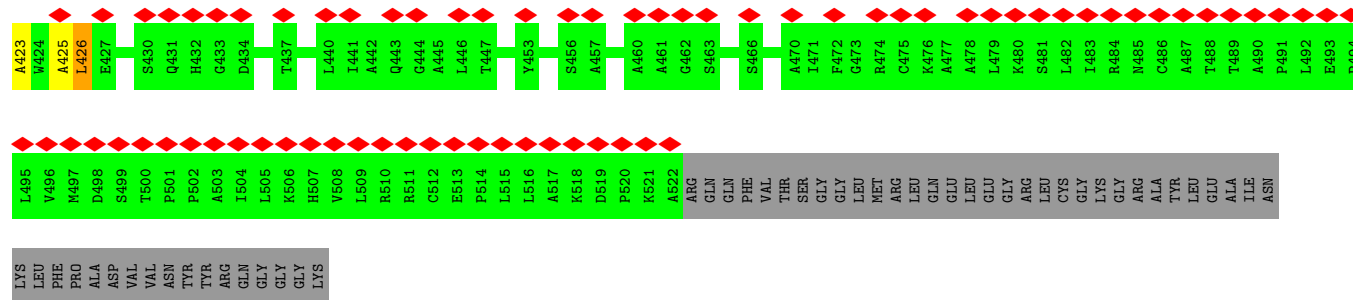
• Molecule 2: FAP194



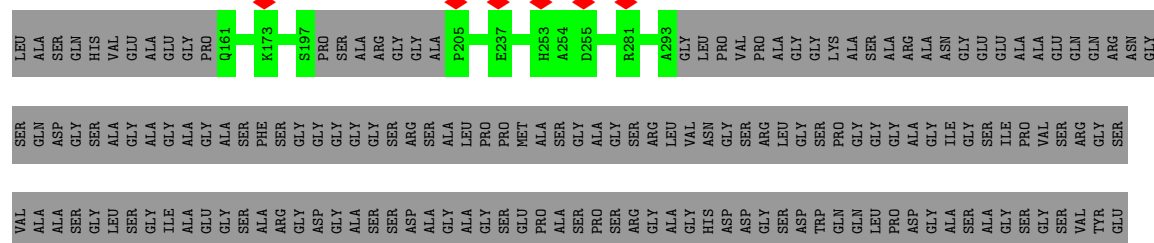
Chain 1F:

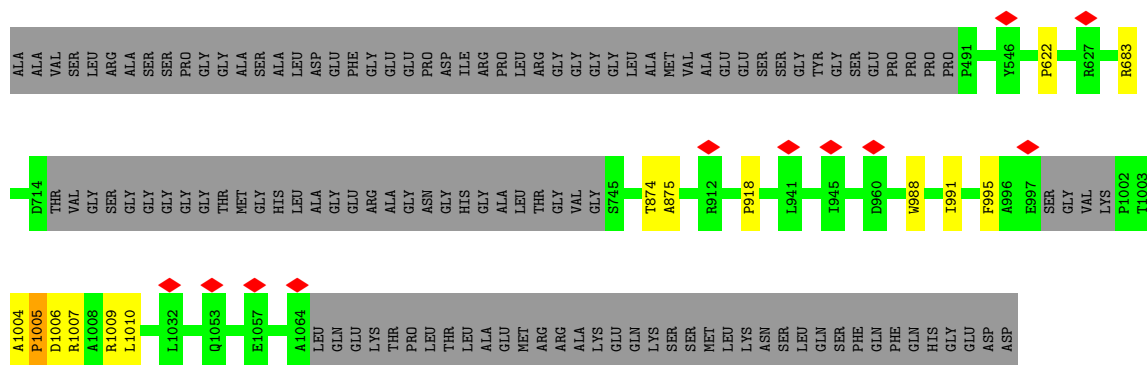


Chain 1G:

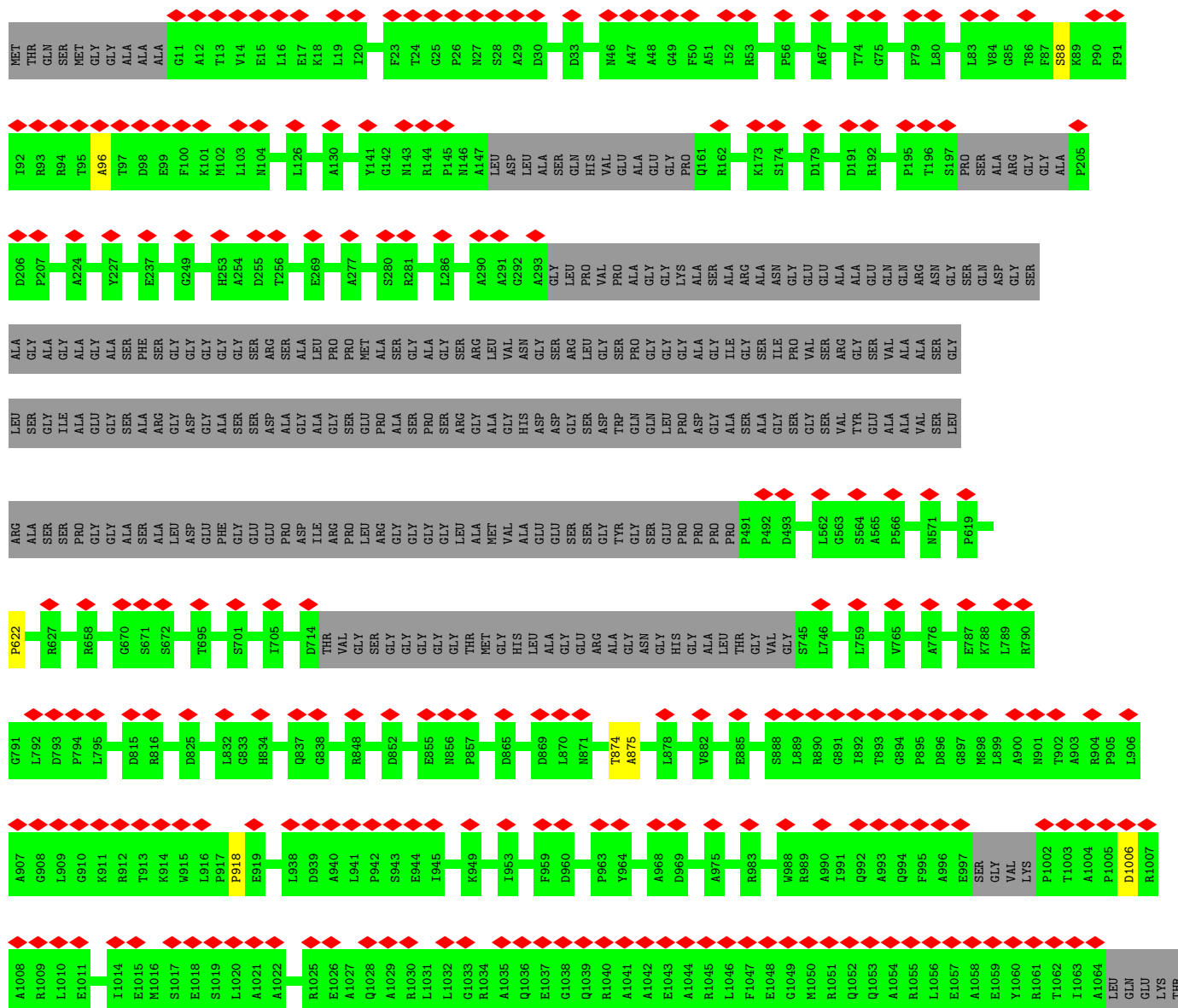


Chain 1H:





• Molecule 3: FAP69



Chain 6D: 72% 27%



Chain 1J: 10% 90%















ARG
ARG
ARG

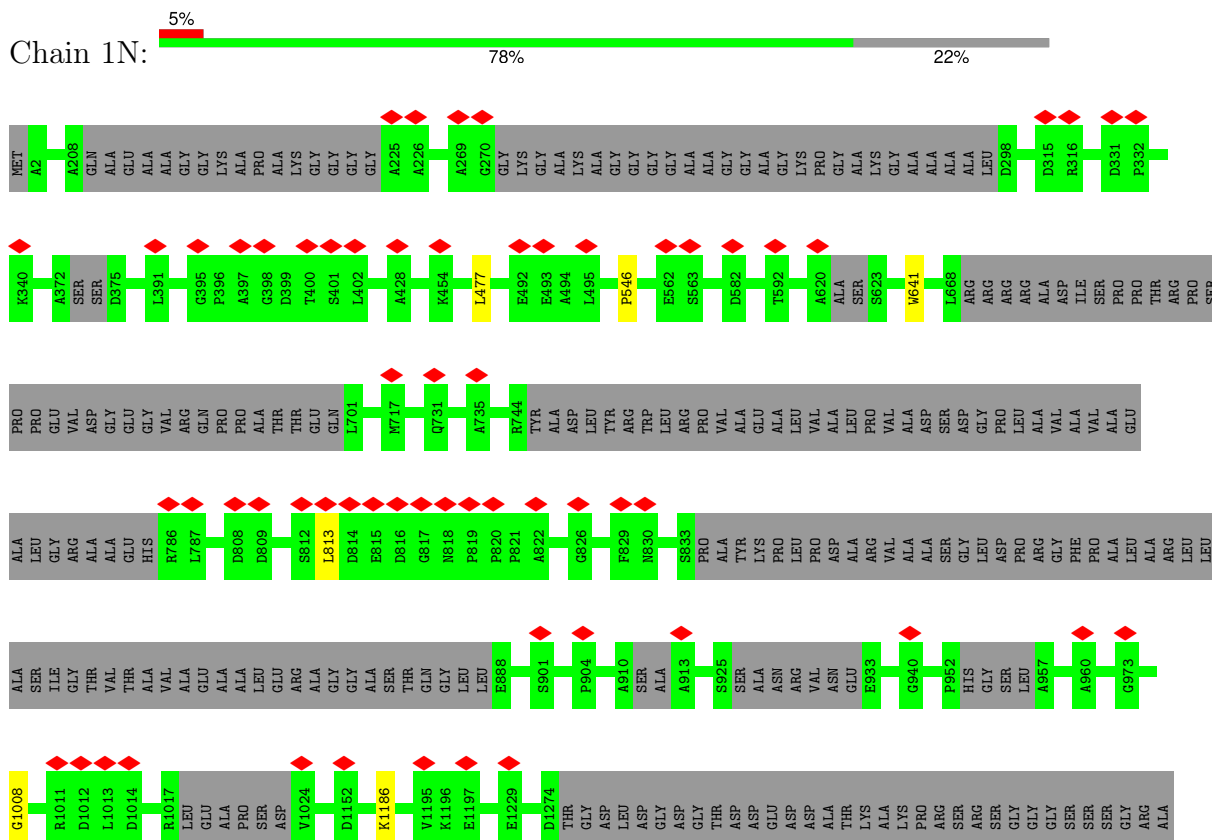
Chain 1M: 18% 81%

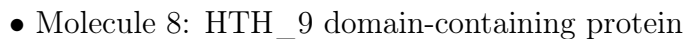


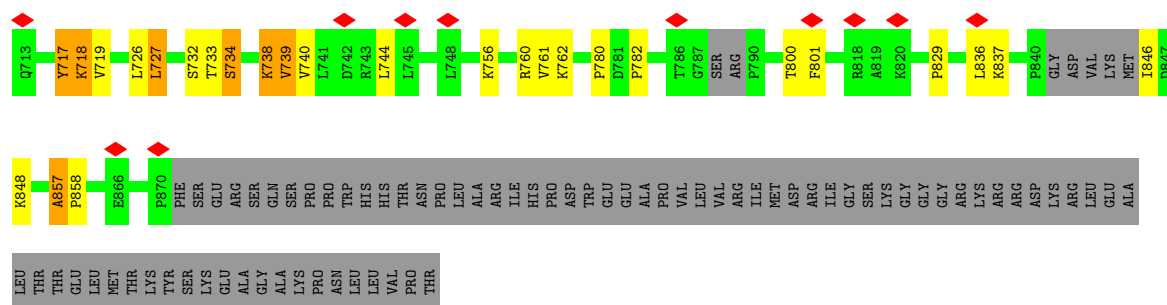


[illegible]

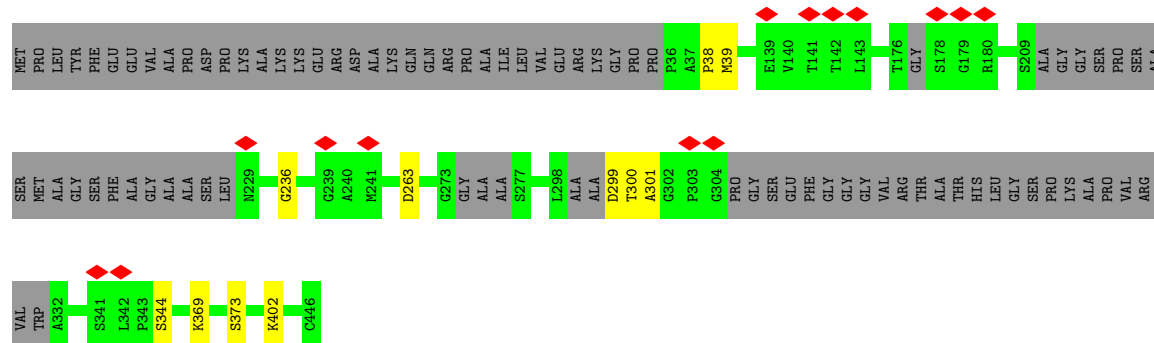
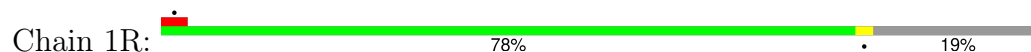
- Molecule 6: FAP46



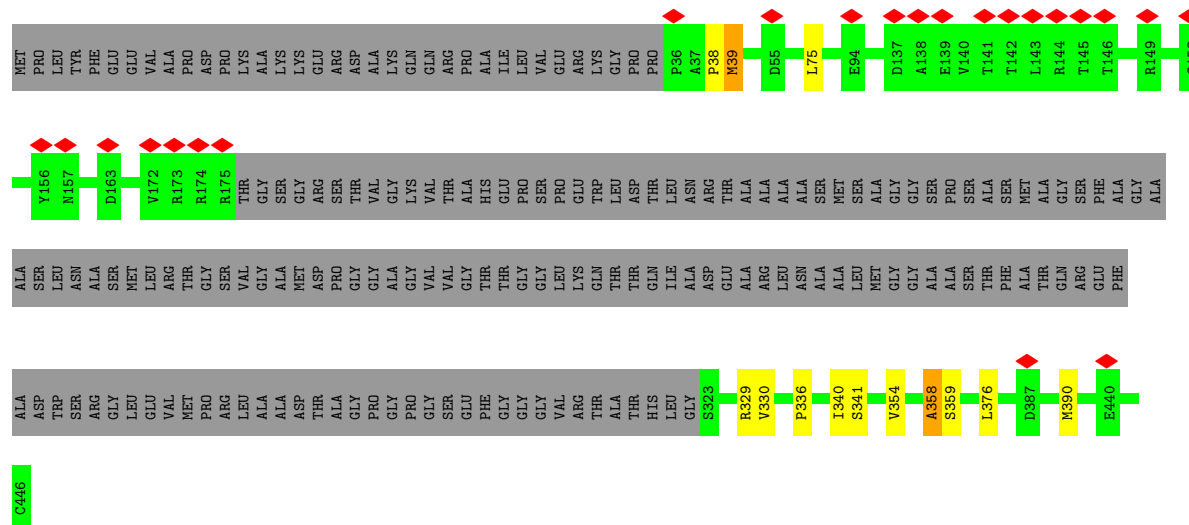




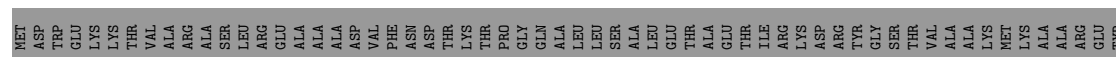
• Molecule 10: FAP108

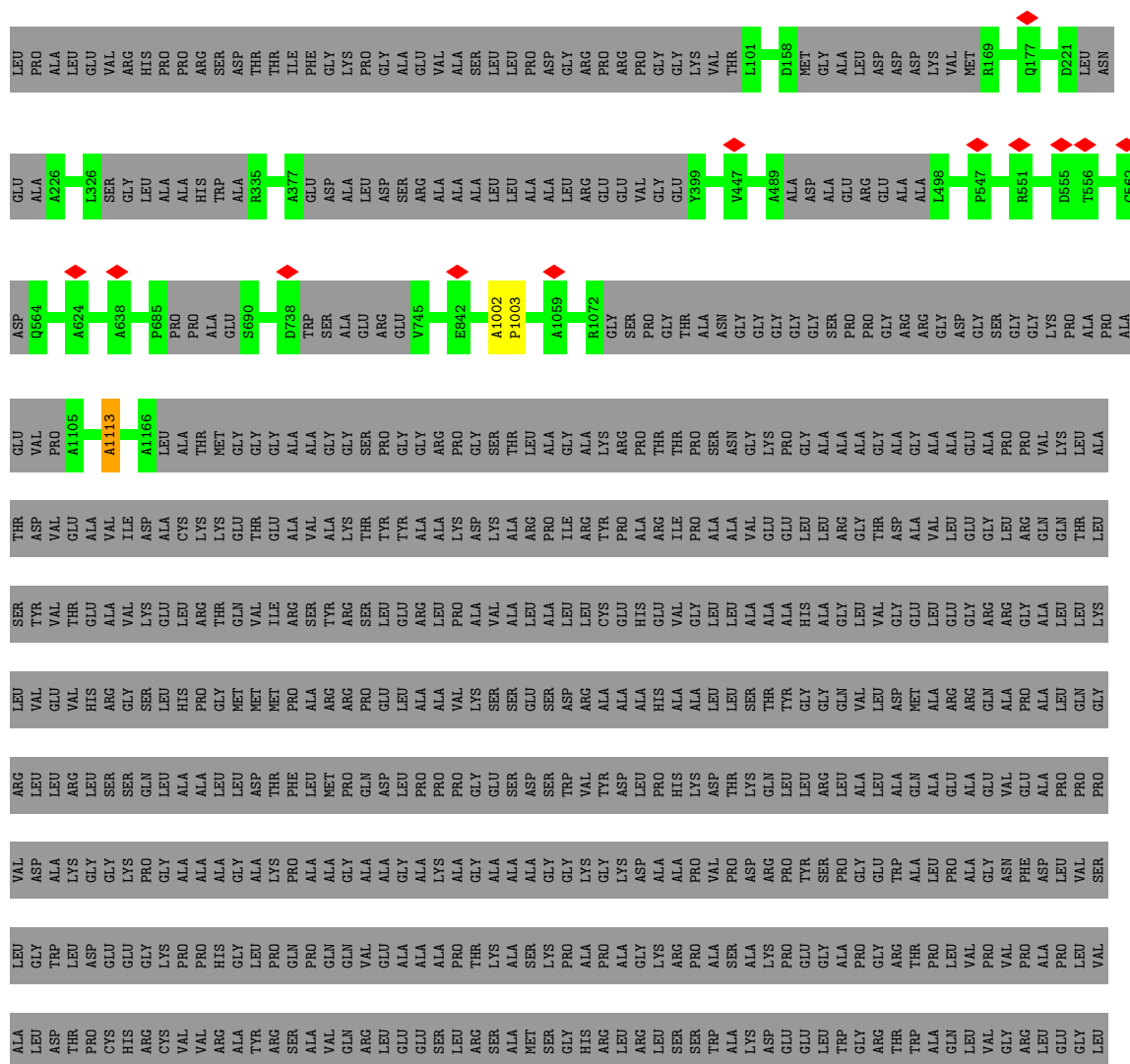


• Molecule 10: FAP108

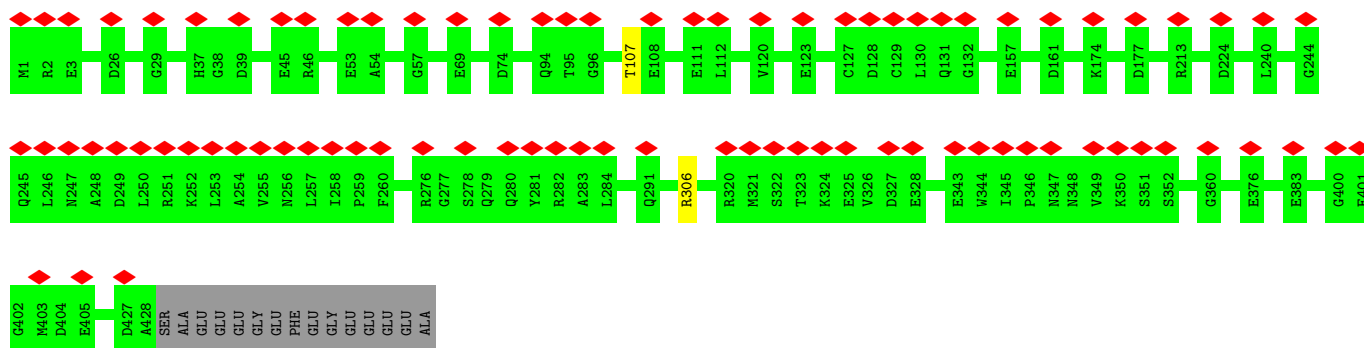


• Molecule 11: FAP76



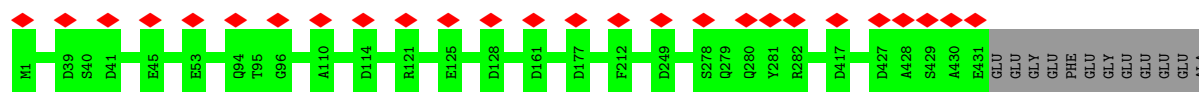


• Molecule 12: Tubulin beta



• Molecule 12: Tubulin beta





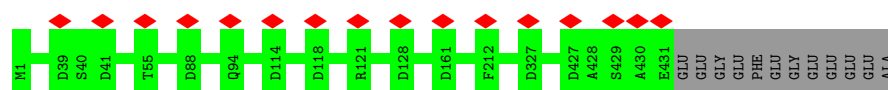
- Molecule 12: Tubulin beta

Chain 1e: 96%



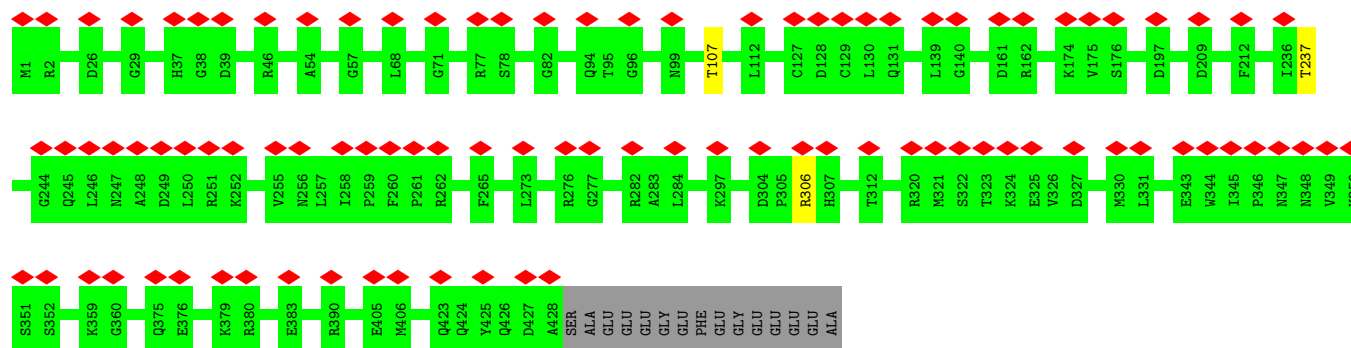
- Molecule 12: Tubulin beta

Chain 1g: 97%



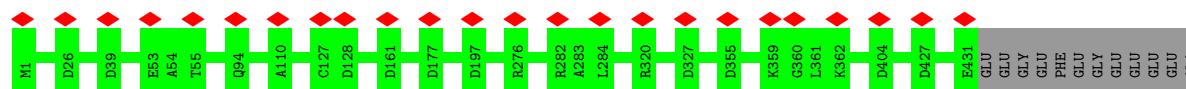
- Molecule 12: Tubulin beta

Chain 2a: 21% 96%



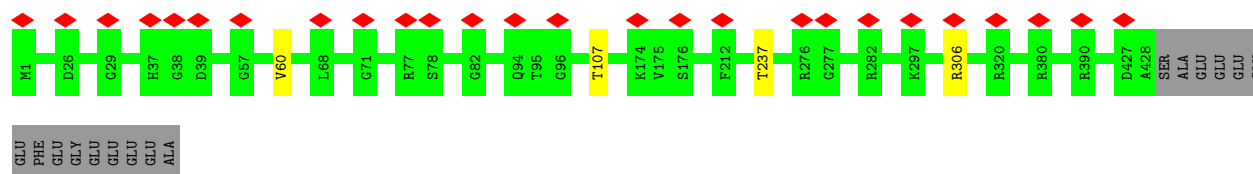
- Molecule 12: Tubulin beta

Chain 2c: 5% 97%

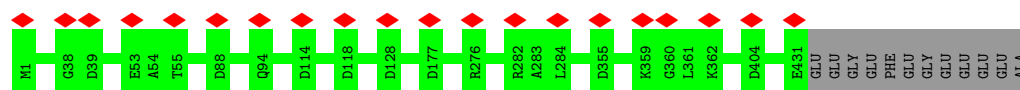


- Molecule 12: Tubulin beta

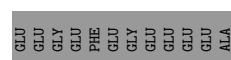
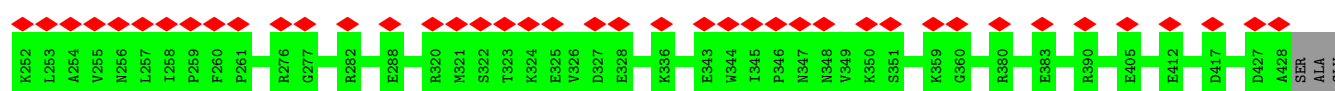
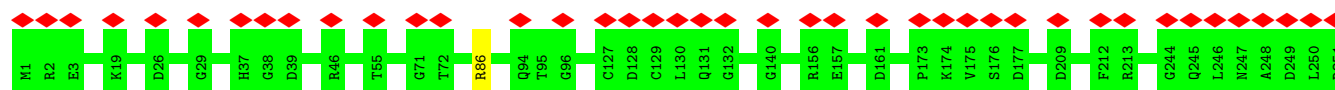
Chain 2e: 6% 96%



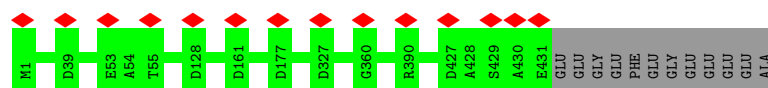
• Molecule 12: Tubulin beta



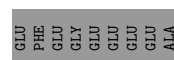
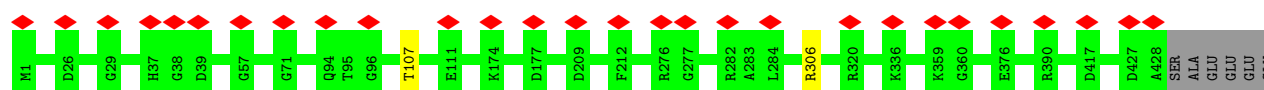
• Molecule 12: Tubulin beta



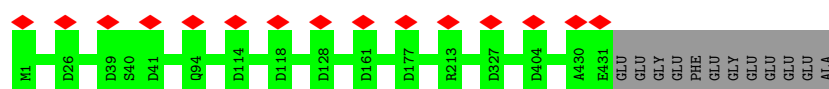
• Molecule 12: Tubulin beta



• Molecule 12: Tubulin beta

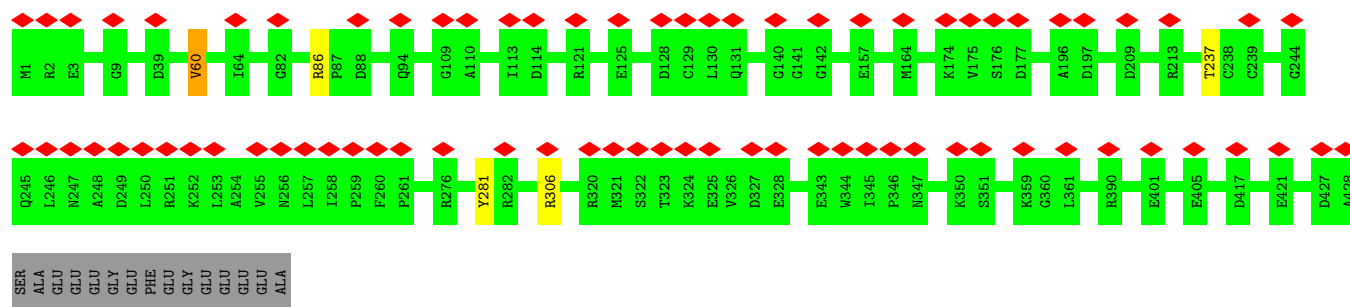


• Molecule 12: Tubulin beta

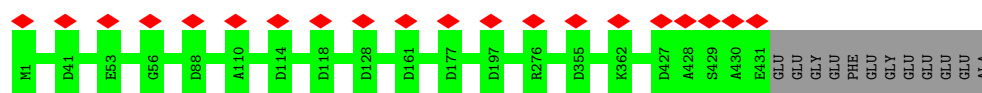


• Molecule 12: Tubulin beta

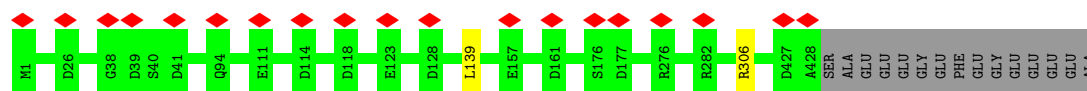




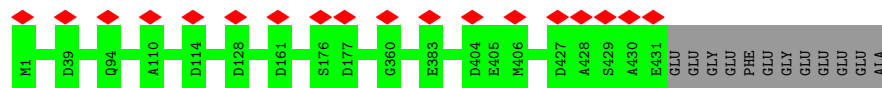
- Molecule 12: Tubulin beta



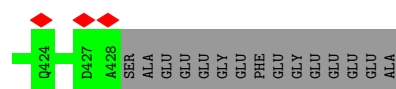
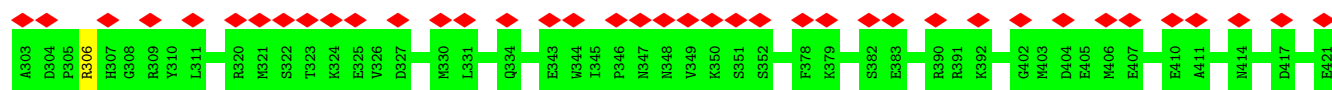
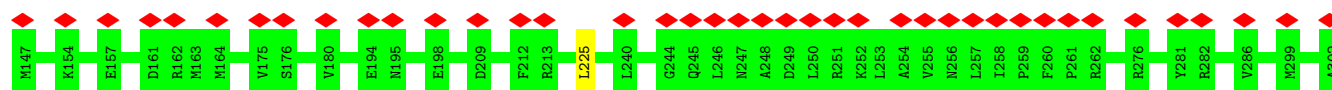
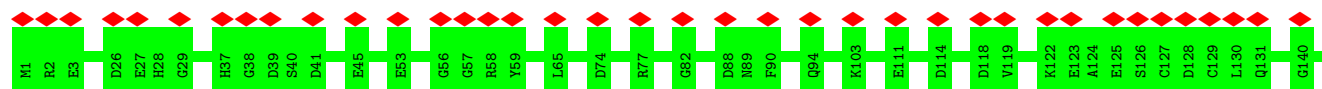
- Molecule 12: Tubulin beta



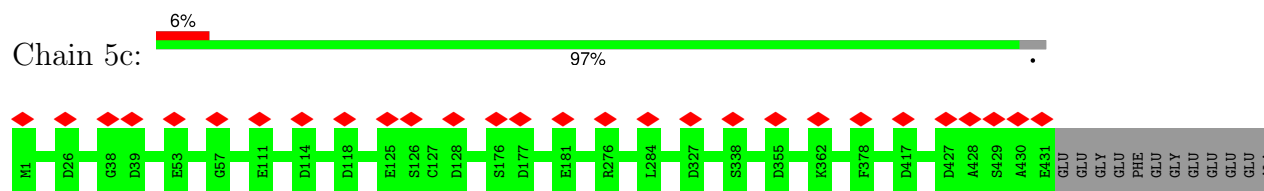
- Molecule 12: Tubulin beta



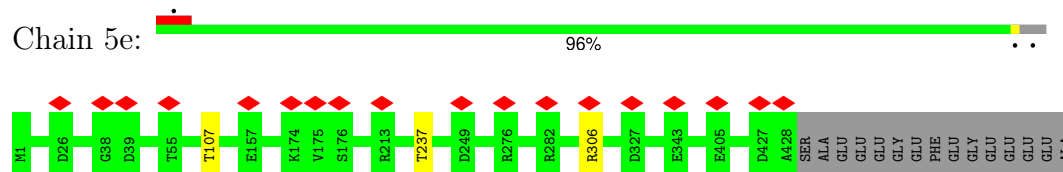
- Molecule 12: Tubulin beta



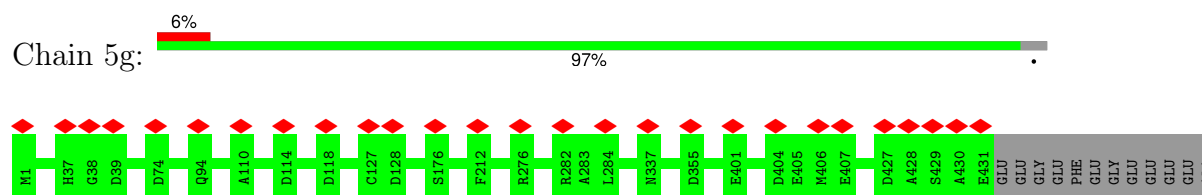
• Molecule 12: Tubulin beta



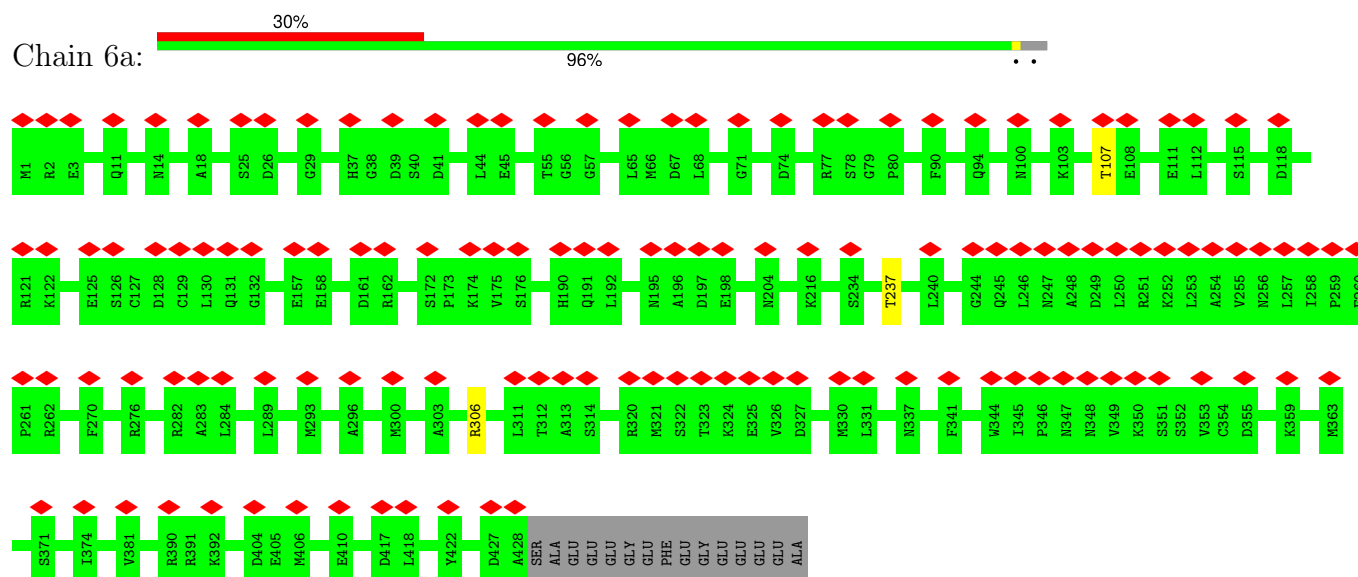
• Molecule 12: Tubulin beta



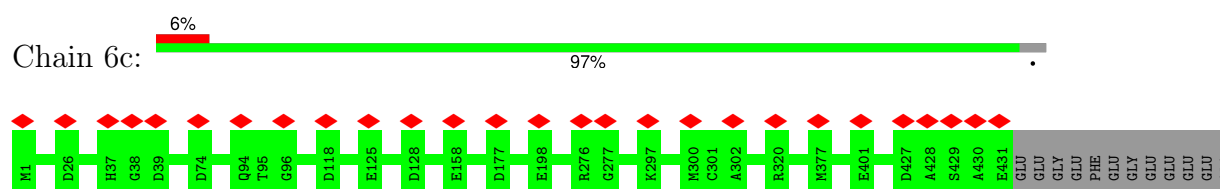
• Molecule 12: Tubulin beta



• Molecule 12: Tubulin beta

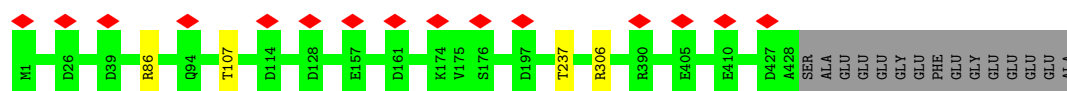


• Molecule 12: Tubulin beta



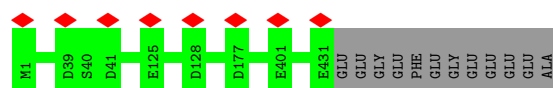
• Molecule 12: Tubulin beta

Chain 6e:  96%



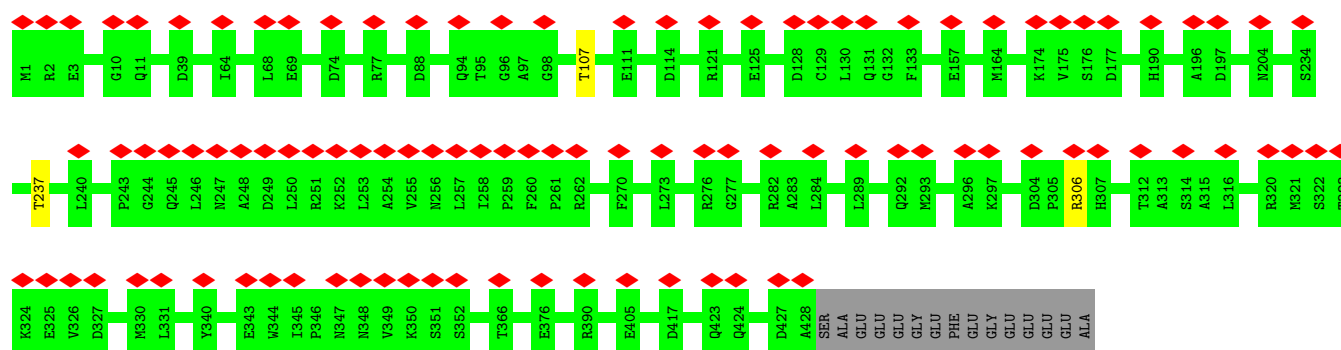
- Molecule 12: Tubulin beta

Chain 6g:  97%



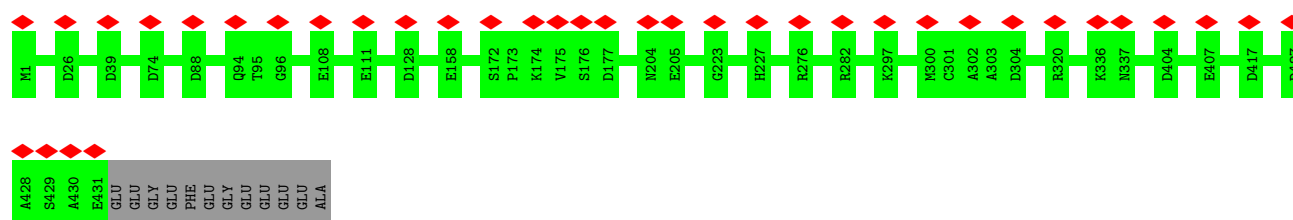
- Molecule 12: Tubulin beta

Chain 7a:  23% 96%



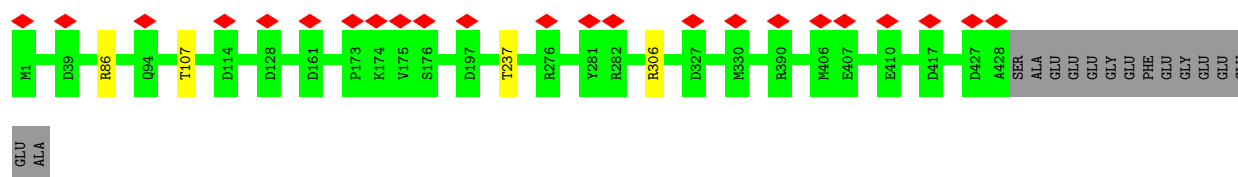
- Molecule 12: Tubulin beta

Chain 7c:  8% 97%



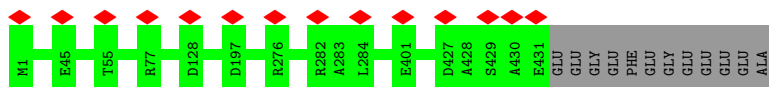
- Molecule 12: Tubulin beta

Chain 7e:  5% 96%



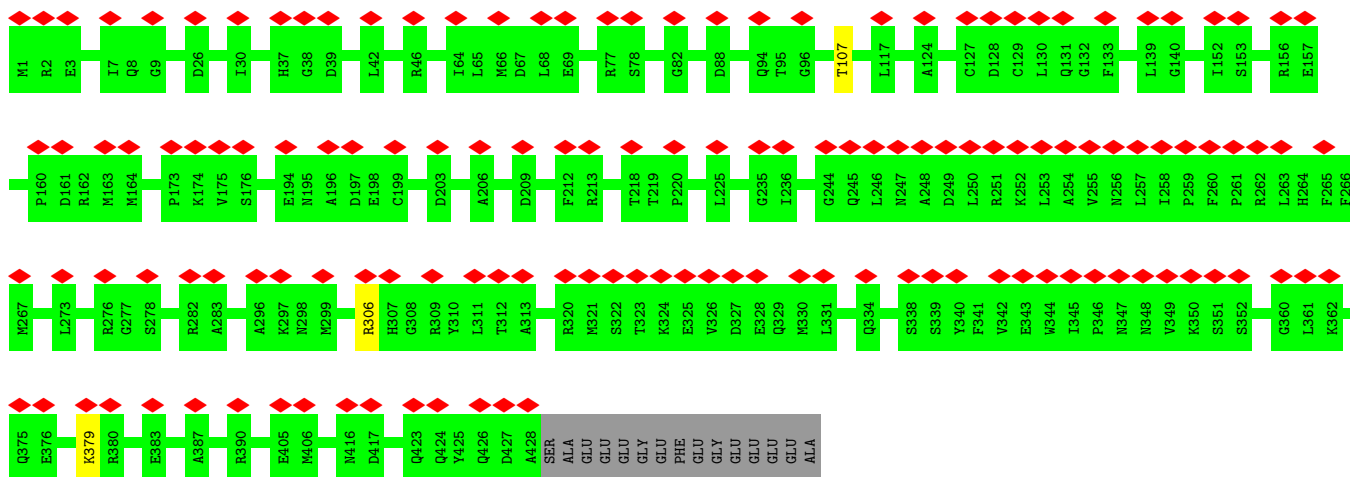
- Molecule 12: Tubulin beta

Chain 7g:  97%



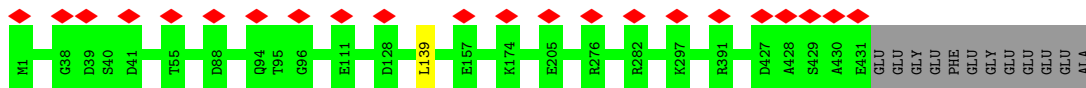
• Molecule 12: Tubulin beta

Chain 8a:  96%



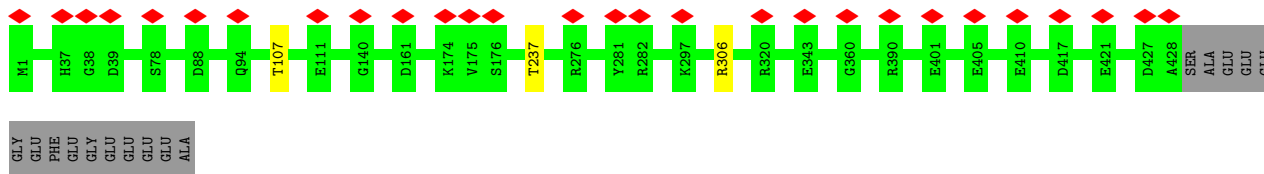
• Molecule 12: Tubulin beta

Chain 8c:  97%



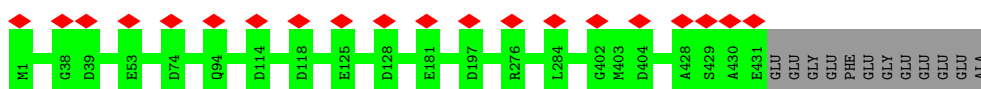
• Molecule 12: Tubulin beta

Chain 8e:  96%

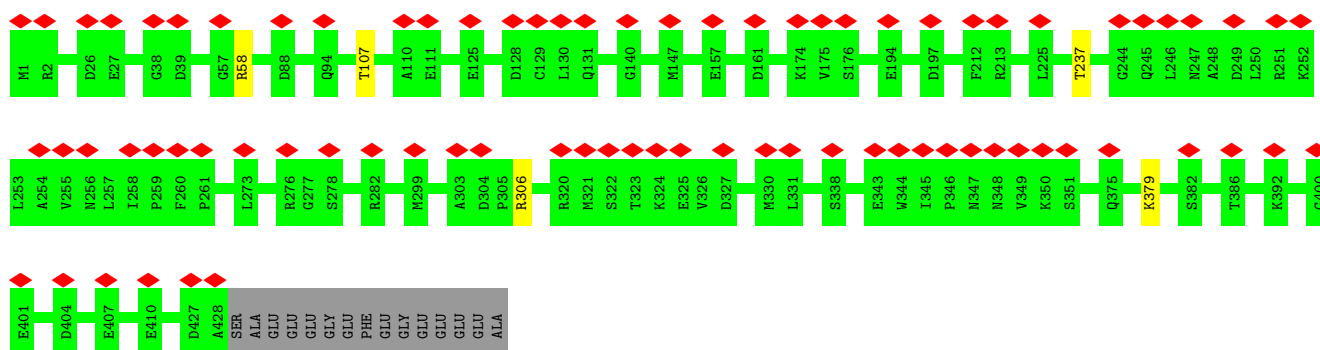


• Molecule 12: Tubulin beta

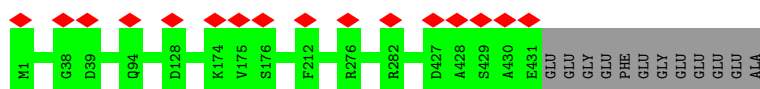
Chain 8g:  97%



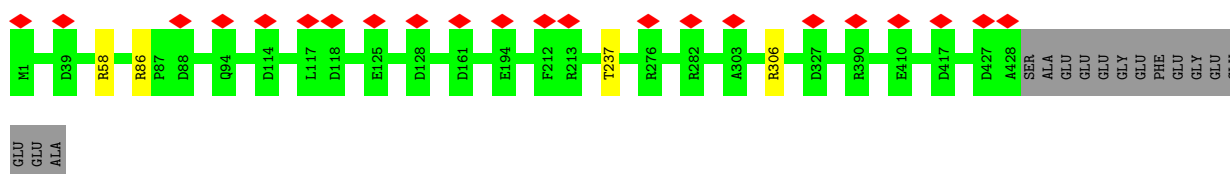
• Molecule 12: Tubulin beta



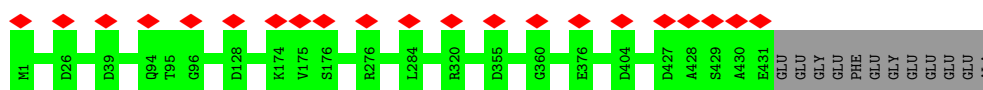
- Molecule 12: Tubulin beta



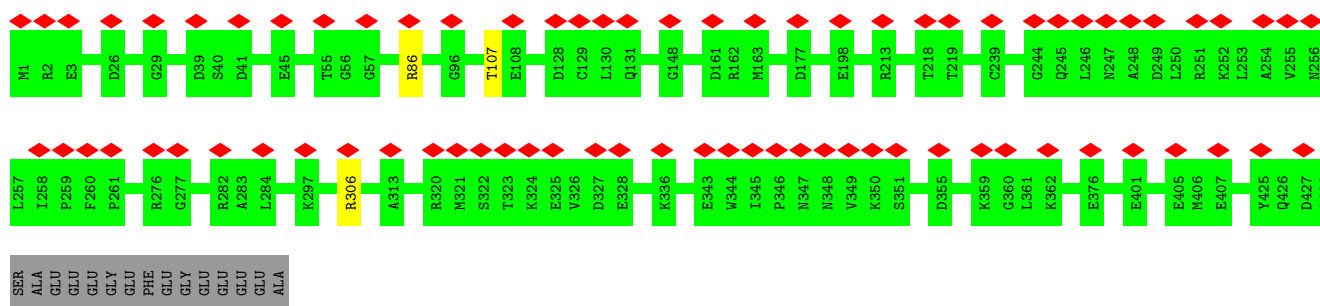
- Molecule 12: Tubulin beta



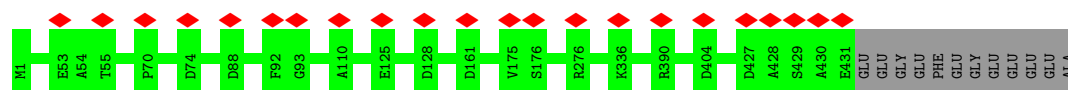
- Molecule 12: Tubulin beta



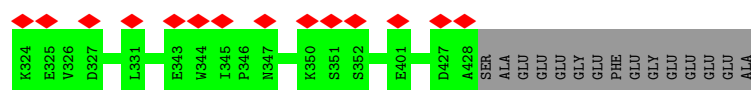
- Molecule 12: Tubulin beta



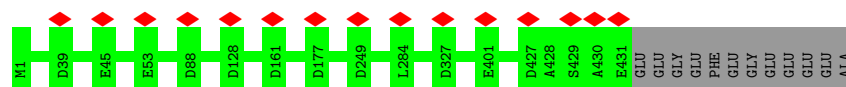
● Molecule 12: Tubulin beta



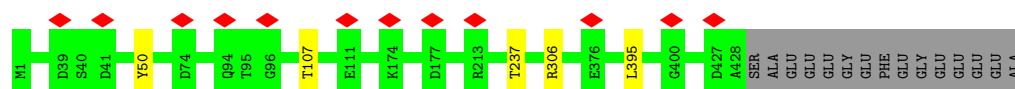
● Molecule 12: Tubulin beta



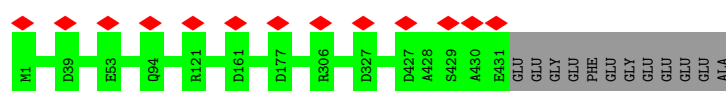
● Molecule 12: Tubulin beta



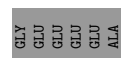
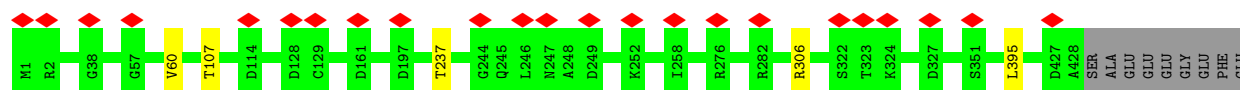
● Molecule 12: Tubulin beta



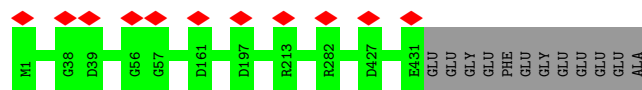
● Molecule 12: Tubulin beta



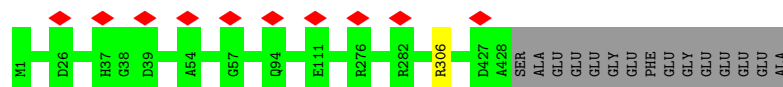
● Molecule 12: Tubulin beta



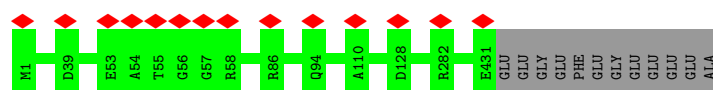
• Molecule 12: Tubulin beta

Chain Dc:  97%

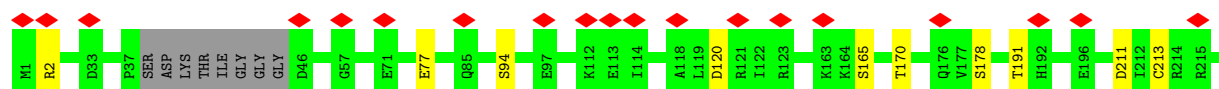
• Molecule 12: Tubulin beta

Chain De:  96%

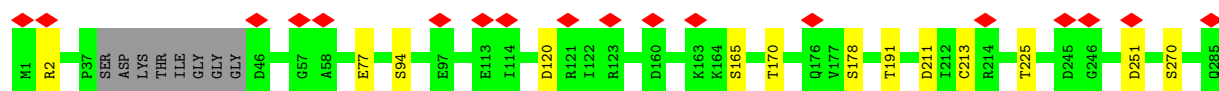
• Molecule 12: Tubulin beta

Chain Dg:  97%

• Molecule 13: Tubulin alpha

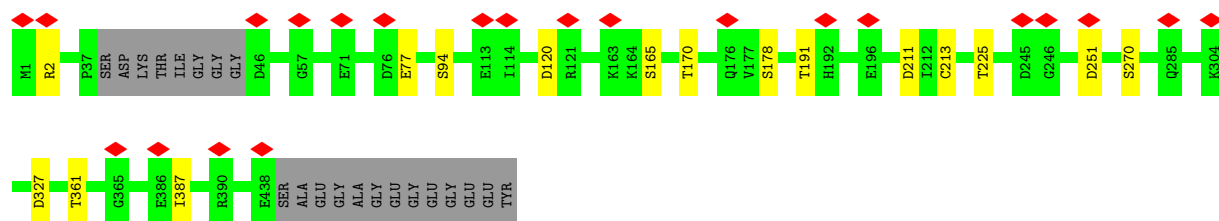
Chain 1b:  8% 92% 5%

• Molecule 13: Tubulin alpha

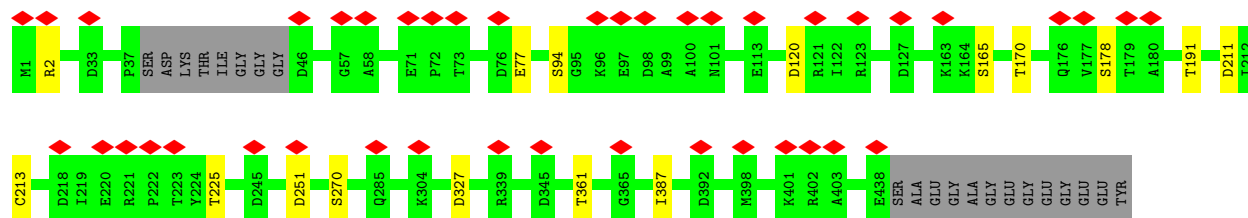
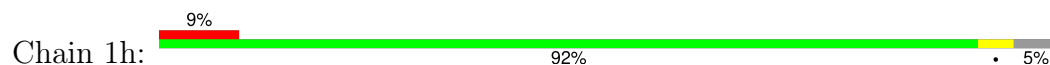
Chain 1d:  5% 92% 5%

• Molecule 13: Tubulin alpha

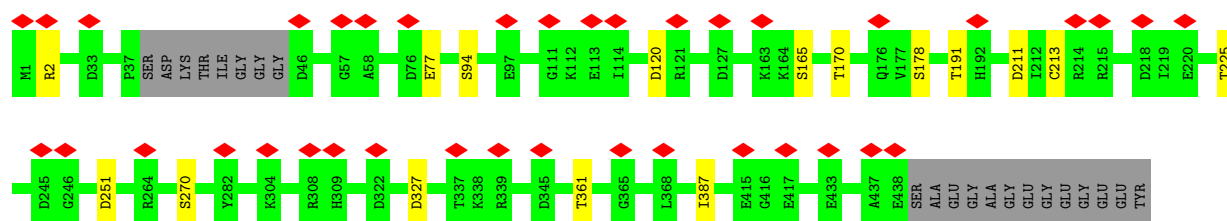
Chain 1f:  5% 92% 5%



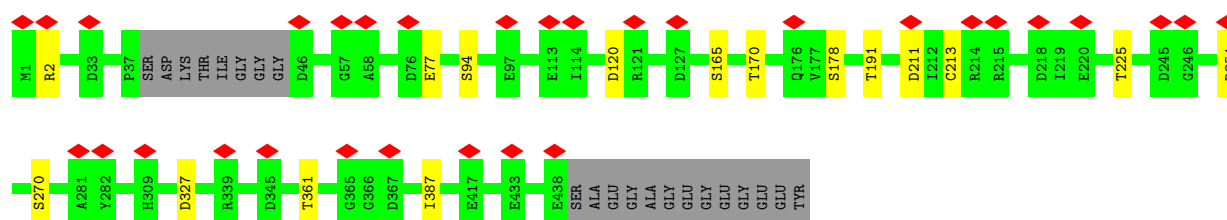
- Molecule 13: Tubulin alpha



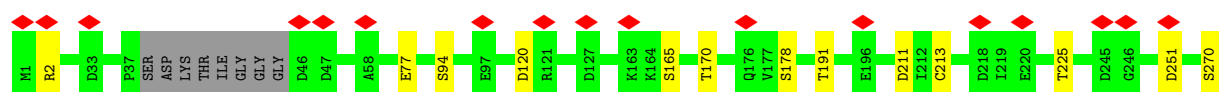
- Molecule 13: Tubulin alpha



- Molecule 13: Tubulin alpha

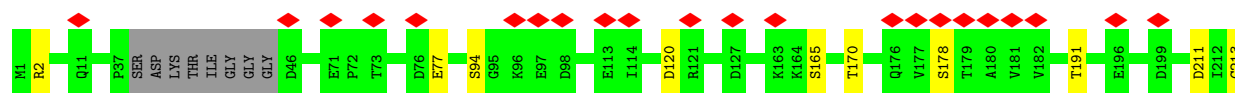
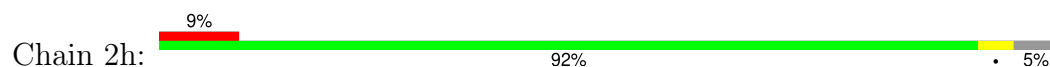


- Molecule 13: Tubulin alpha

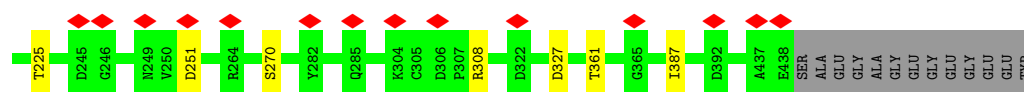
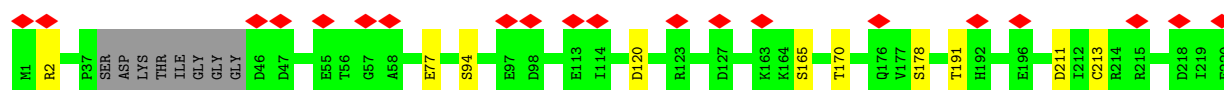




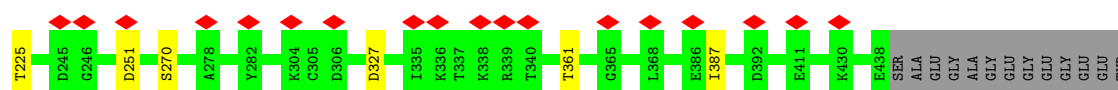
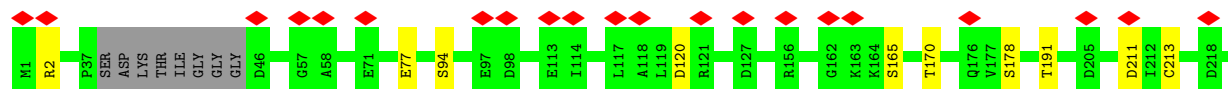
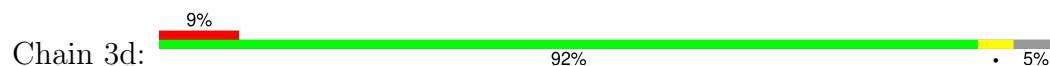
- Molecule 13: Tubulin alpha



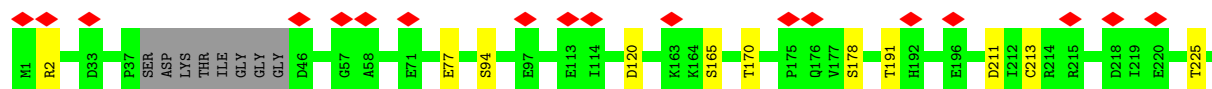
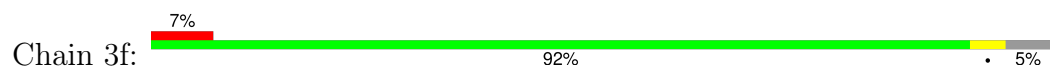
- Molecule 13: Tubulin alpha



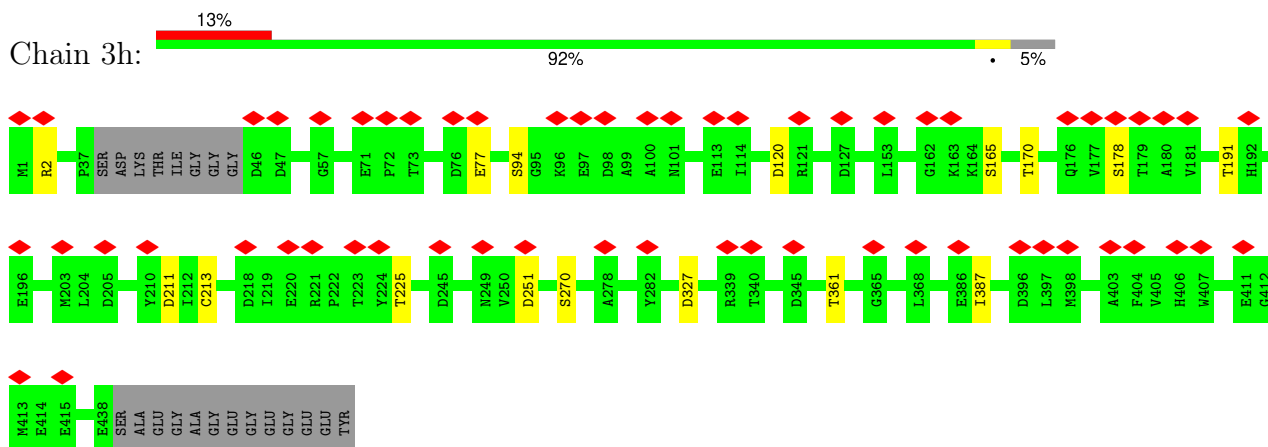
- Molecule 13: Tubulin alpha



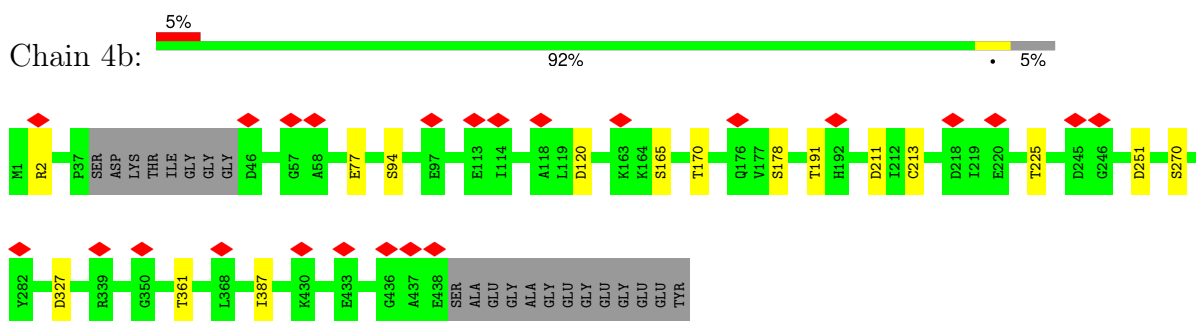
- Molecule 13: Tubulin alpha



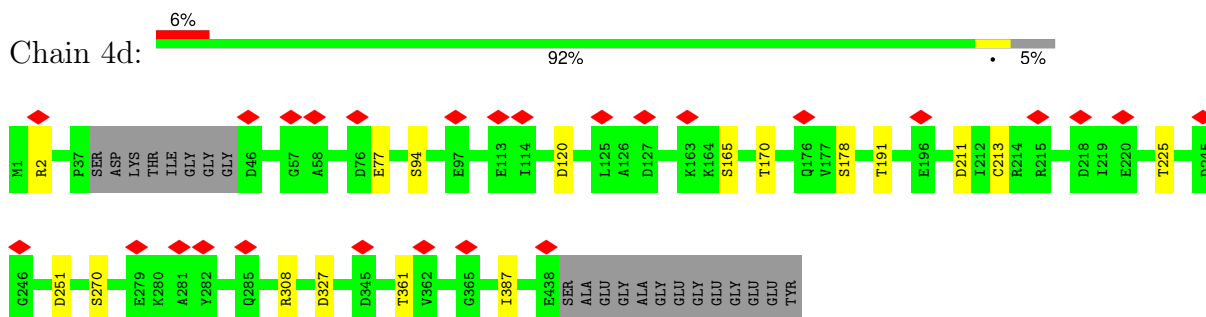
- Molecule 13: Tubulin alpha



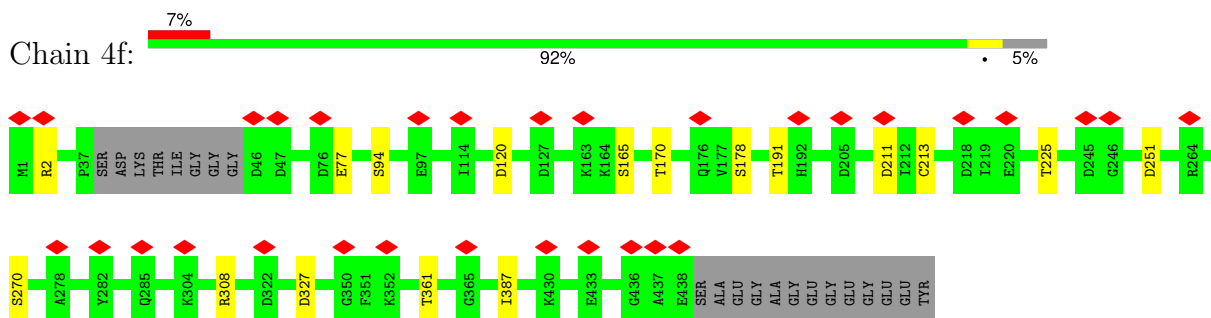
- Molecule 13: Tubulin alpha



- Molecule 13: Tubulin alpha

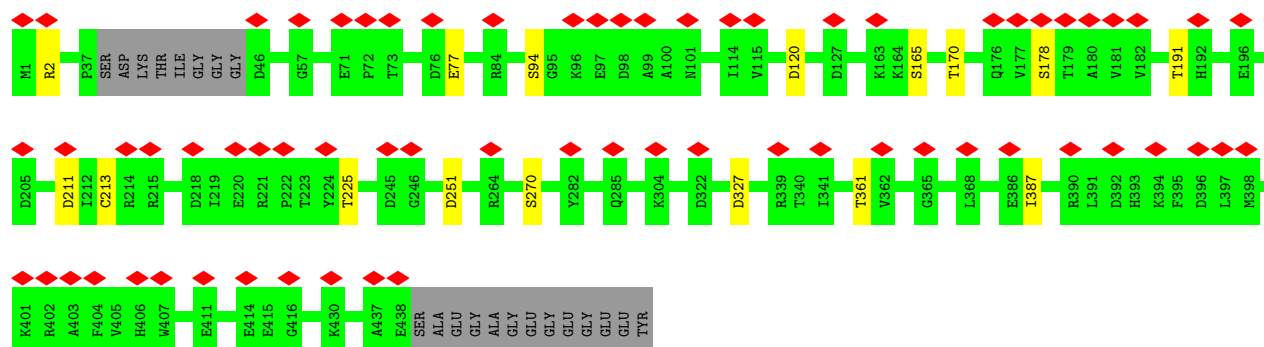


- Molecule 13: Tubulin alpha

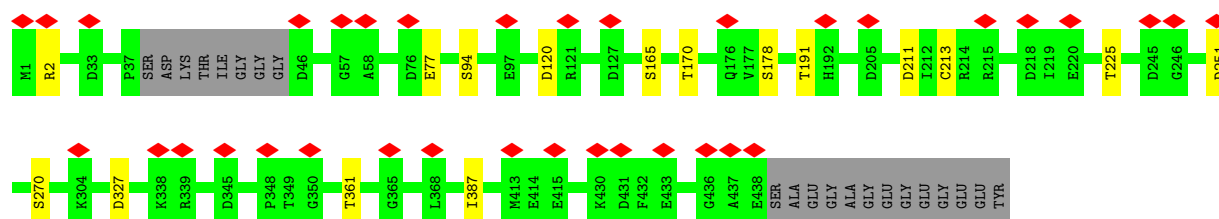
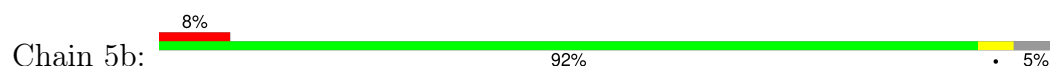


- Molecule 13: Tubulin alpha

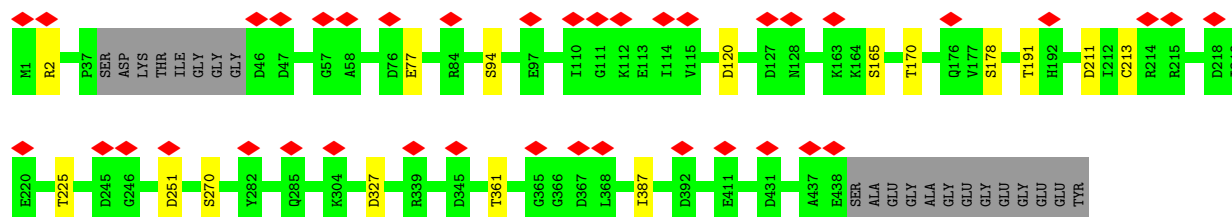
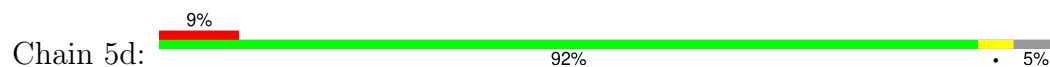




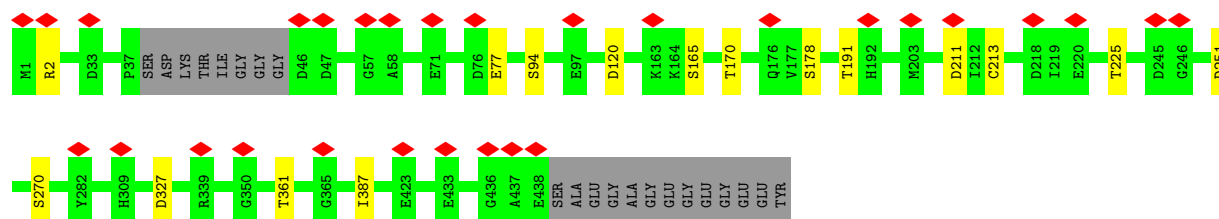
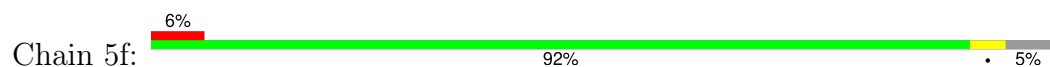
- Molecule 13: Tubulin alpha



- Molecule 13: Tubulin alpha

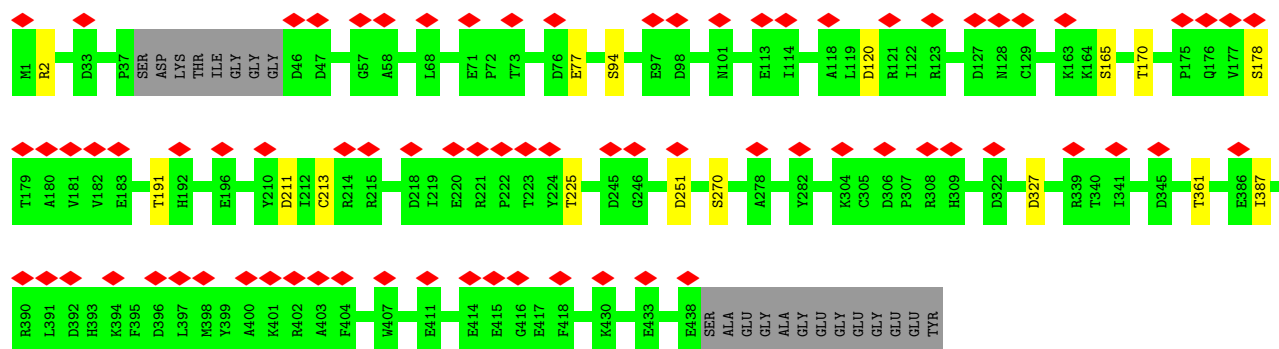


- Molecule 13: Tubulin alpha

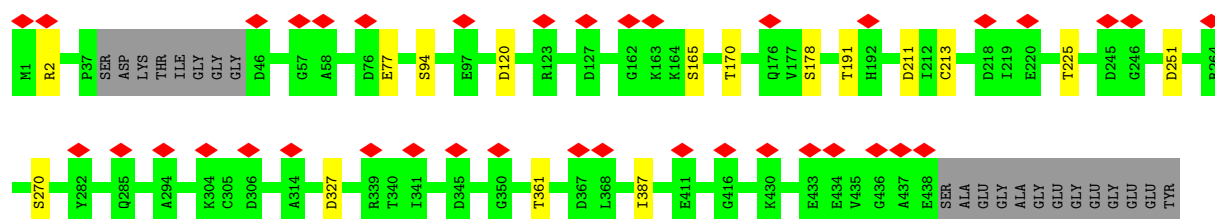
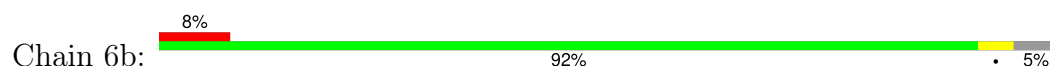


- Molecule 13: Tubulin alpha

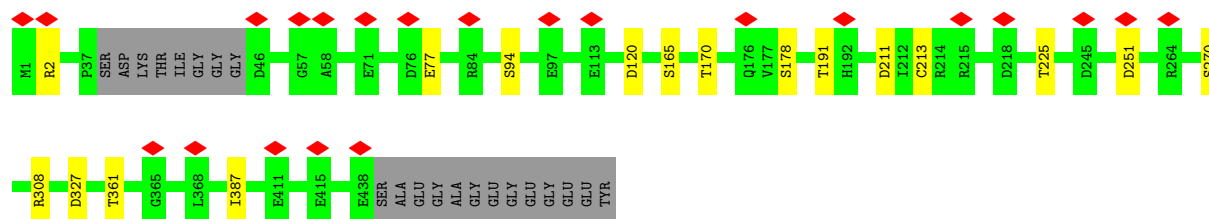
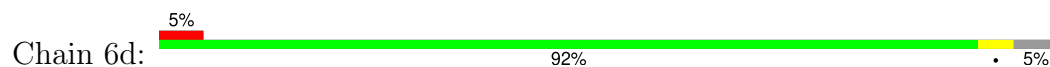




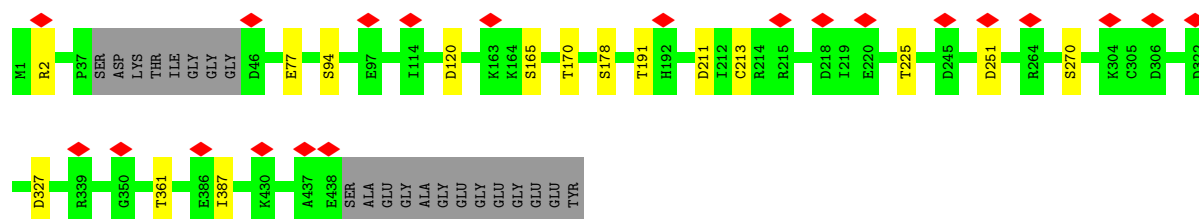
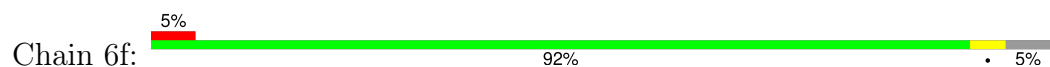
- Molecule 13: Tubulin alpha



- Molecule 13: Tubulin alpha

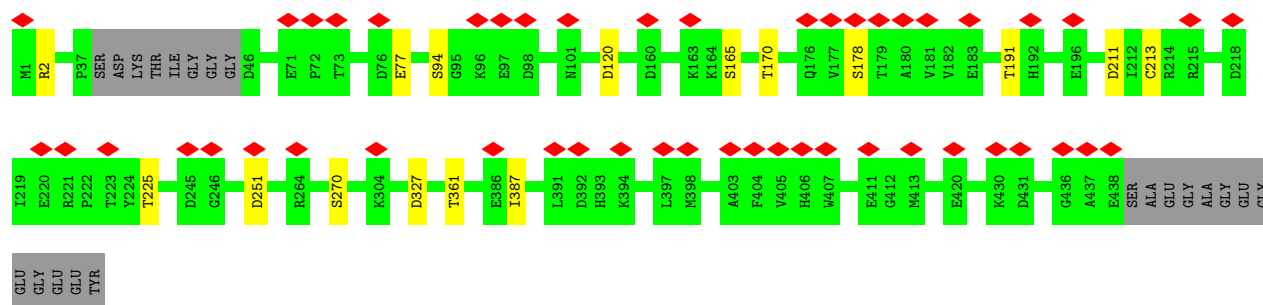


- Molecule 13: Tubulin alpha

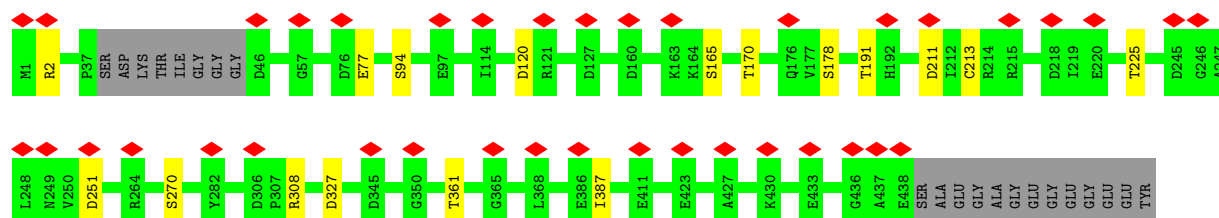
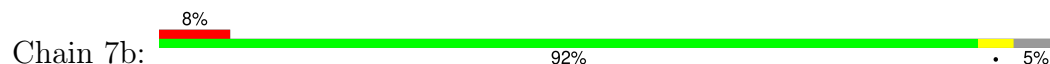


- Molecule 13: Tubulin alpha

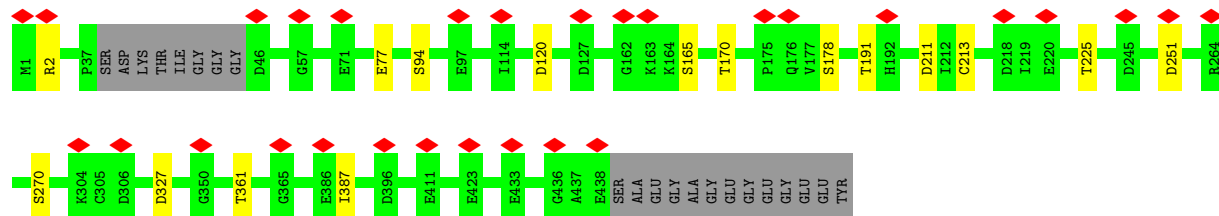
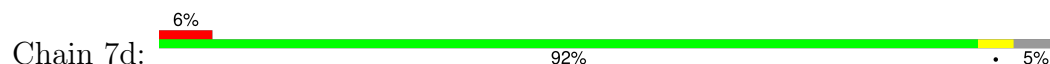




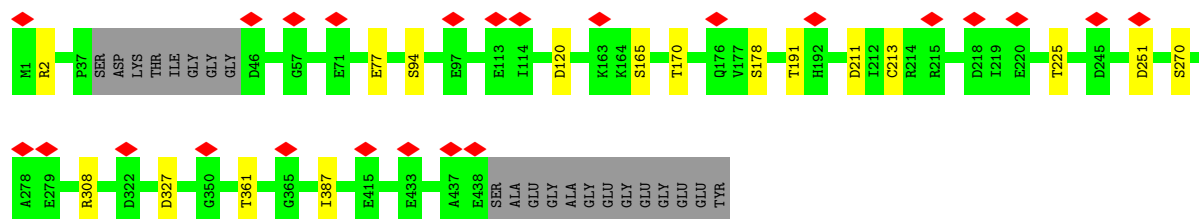
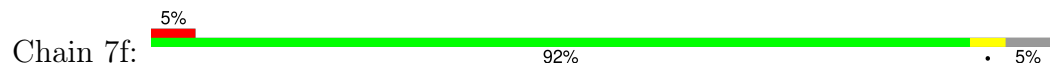
• Molecule 13: Tubulin alpha



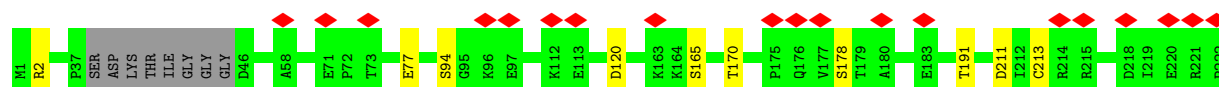
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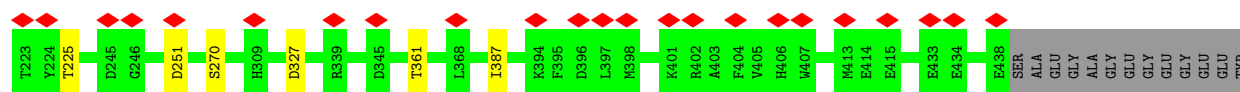


• Molecule 13: Tubulin alpha

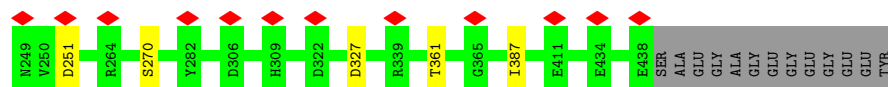
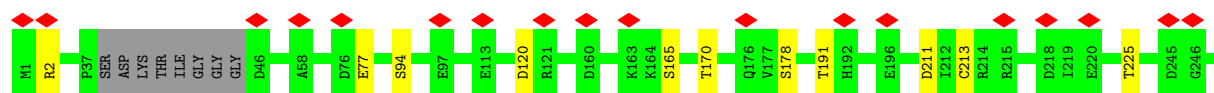
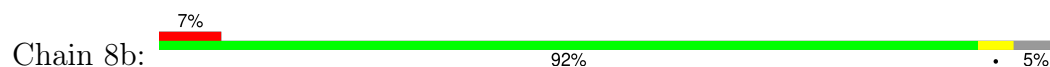


• Molecule 13: Tubulin alpha

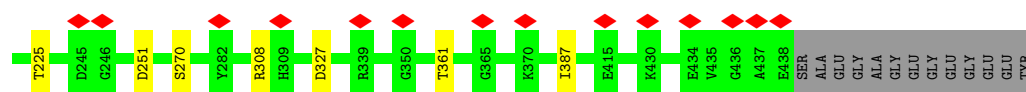
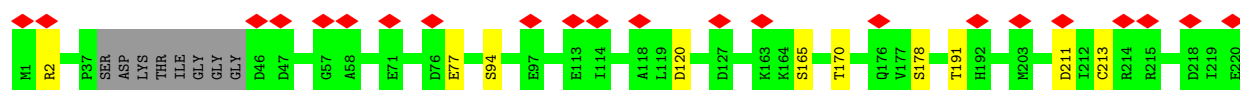
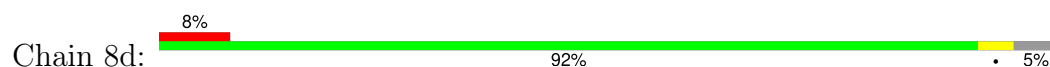




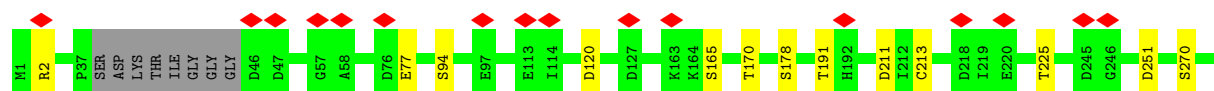
- Molecule 13: Tubulin alpha



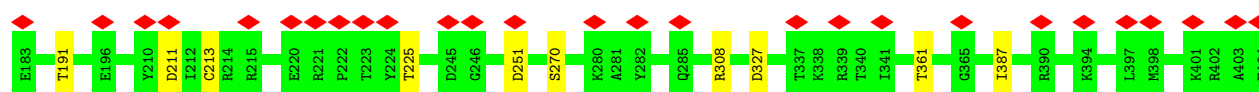
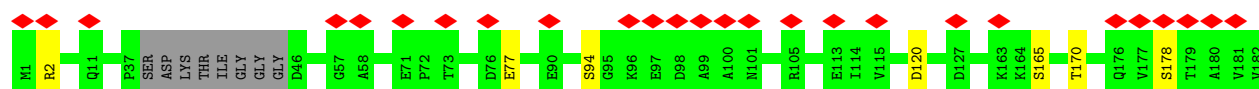
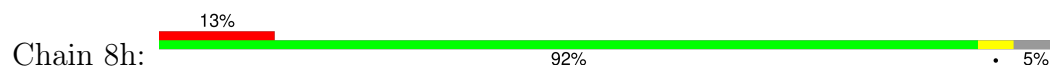
- Molecule 13: Tubulin alpha

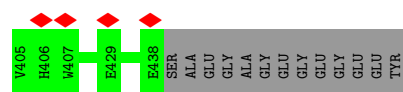


- Molecule 13: Tubulin alpha

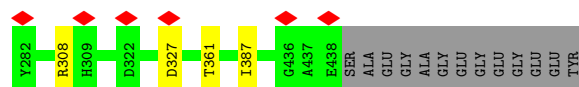
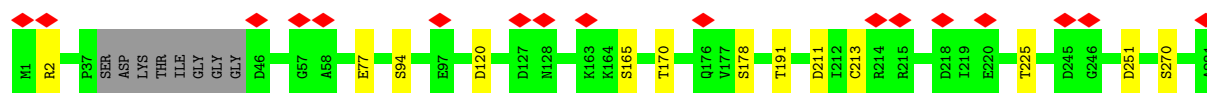
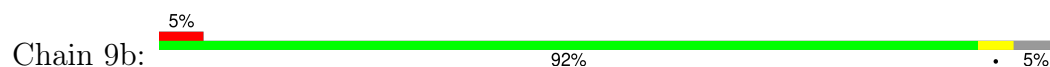


- Molecule 13: Tubulin alpha

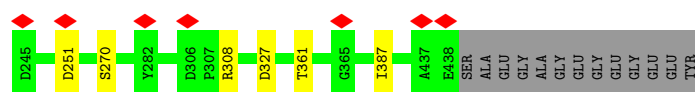
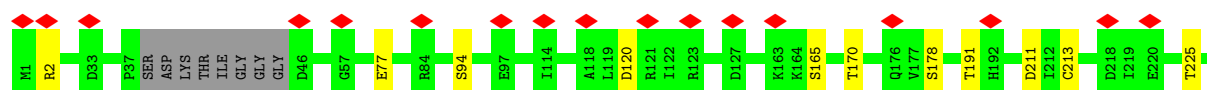
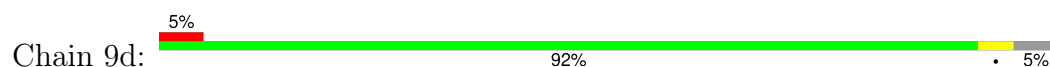




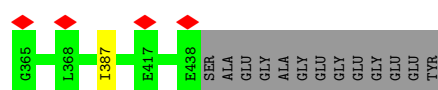
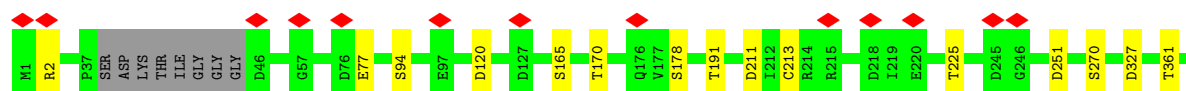
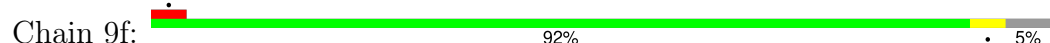
- Molecule 13: Tubulin alpha



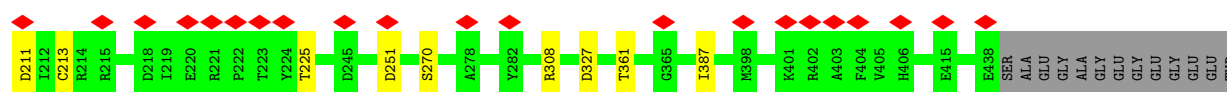
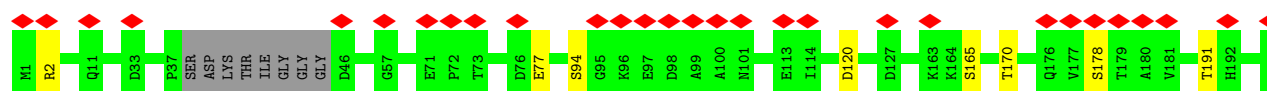
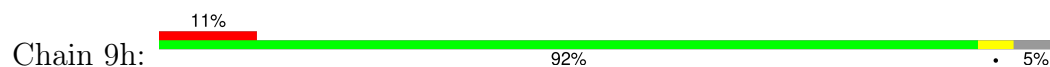
- Molecule 13: Tubulin alpha




- Molecule 13: Tubulin alpha

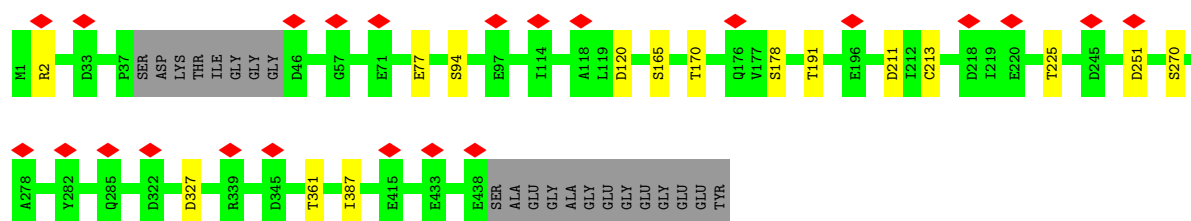


- Molecule 13: Tubulin alpha



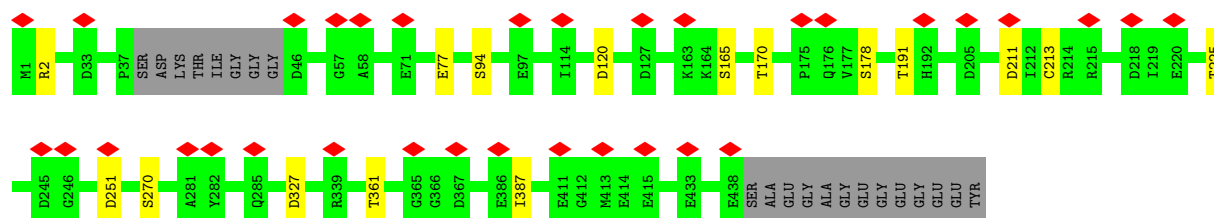
- Molecule 13: Tubulin alpha

Chain Ab:  5% 92% 5%



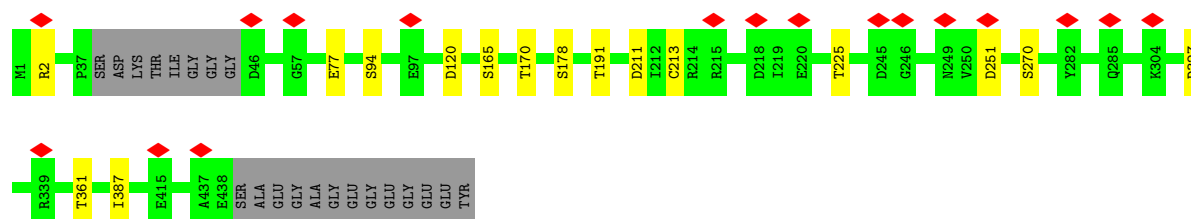
• Molecule 13: Tubulin alpha

Chain Ad:  7% 92% 5%




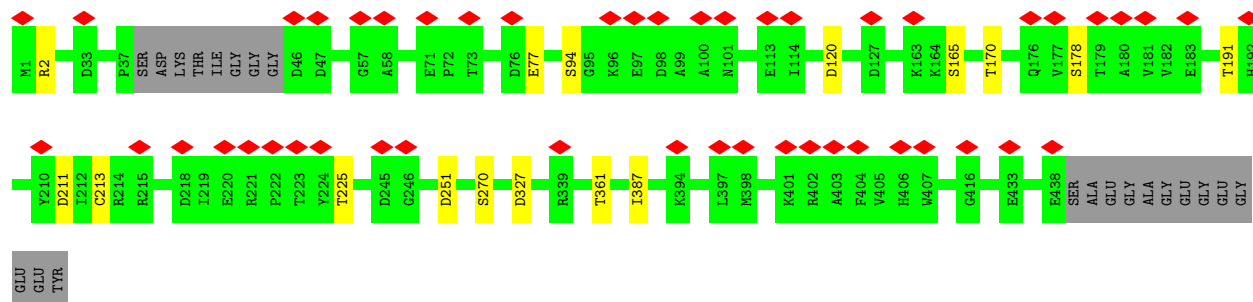
• Molecule 13: Tubulin alpha

Chain Af:  5% 92% 5%



• Molecule 13: Tubulin alpha

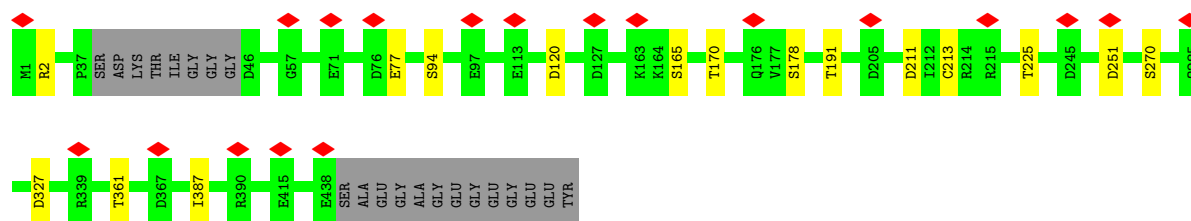
Chain Ah:  11% 92% 5%



• Molecule 13: Tubulin alpha

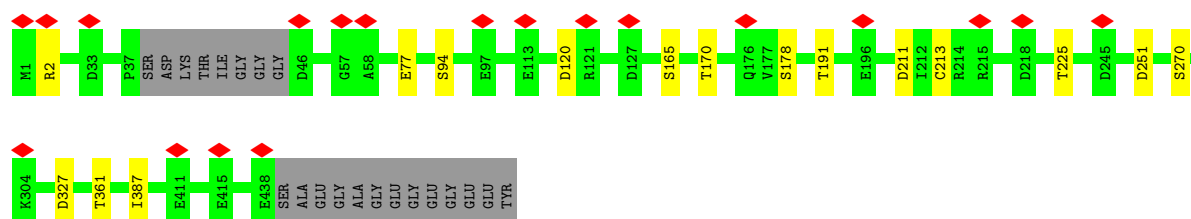
Chain Bb:  5% 92% 5%





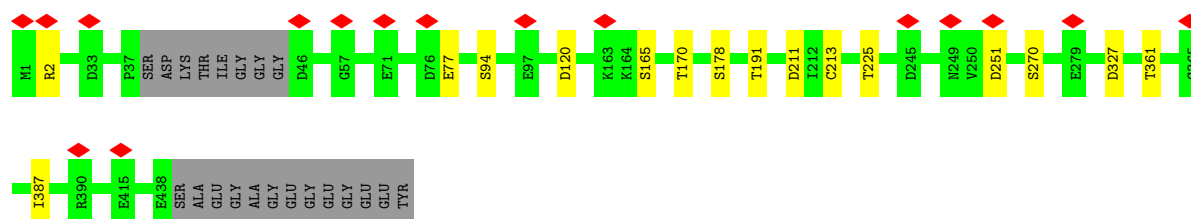
- Molecule 13: Tubulin alpha

Chain Bd: 92% 5%



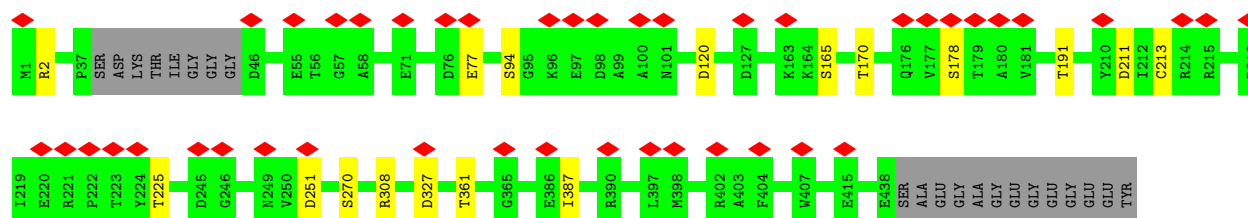
- Molecule 13: Tubulin alpha

Chain Bf: 92% 5%



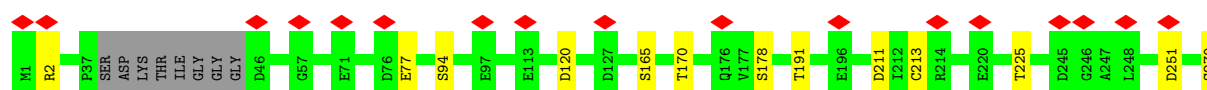
- Molecule 13: Tubulin alpha

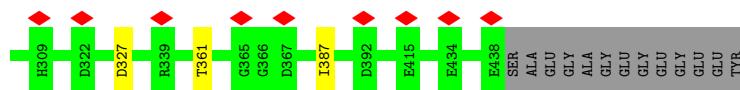
Chain Bh: 92% 10% 5%



- Molecule 13: Tubulin alpha

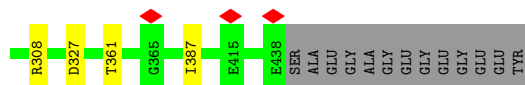
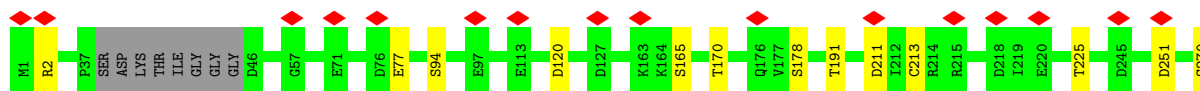
Chain Cb: 92% 6% 5%





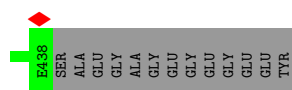
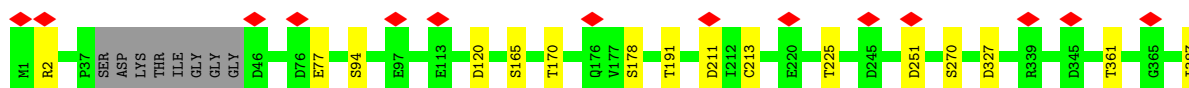
- Molecule 13: Tubulin alpha

Chain Cd: 92% 5%



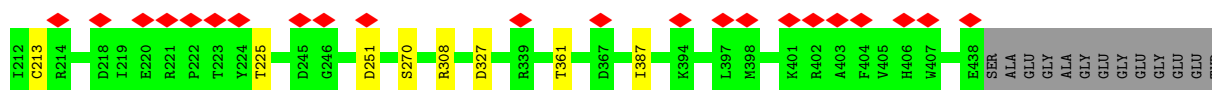
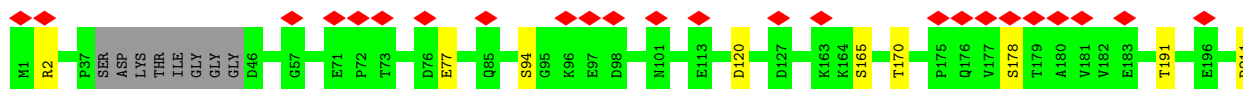
- Molecule 13: Tubulin alpha

Chain Cf: 92% 5%



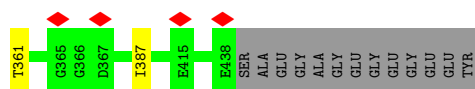
- Molecule 13: Tubulin alpha

Chain Ch: 10% 92% 5%



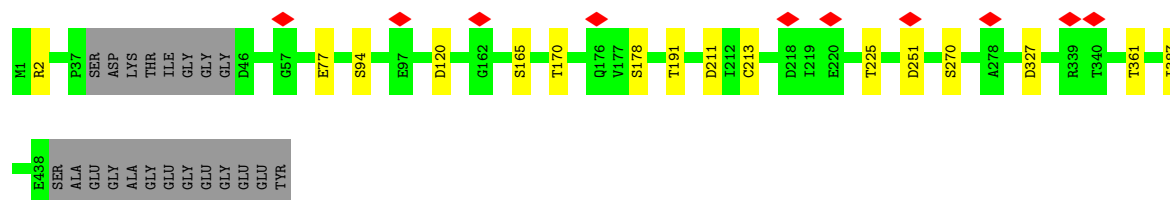
- Molecule 13: Tubulin alpha

Chain Db: 92% 5%




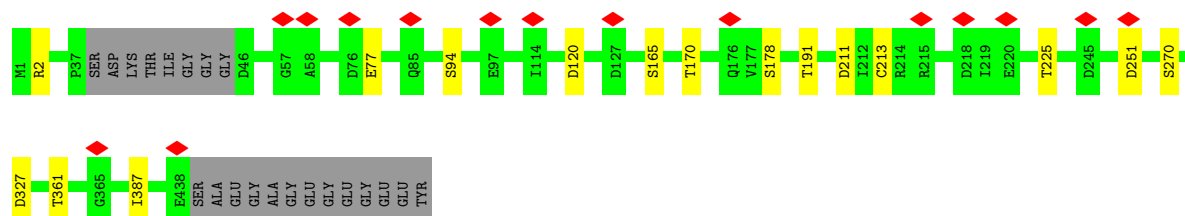
- Molecule 13: Tubulin alpha

Chain Dd:  92% 5%

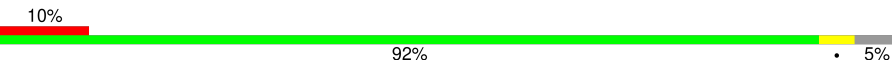


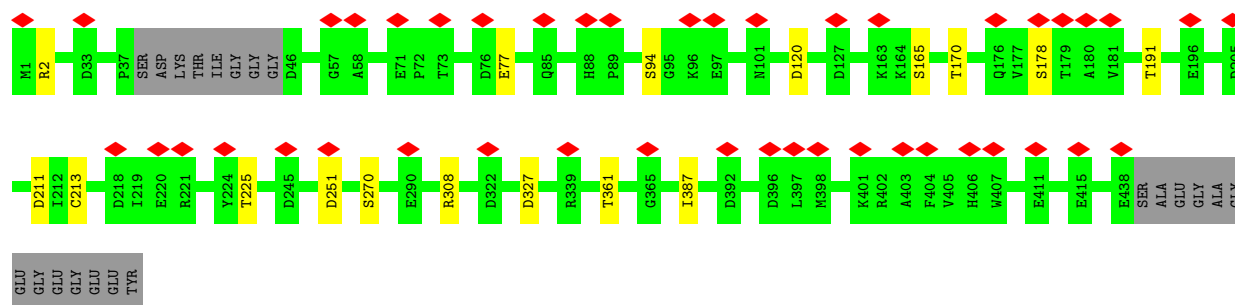
• Molecule 13: Tubulin alpha

Chain Df:  92% 5%




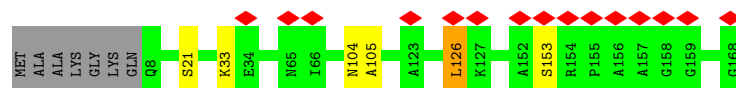
• Molecule 13: Tubulin alpha

Chain Dh:  10% 92% 5%



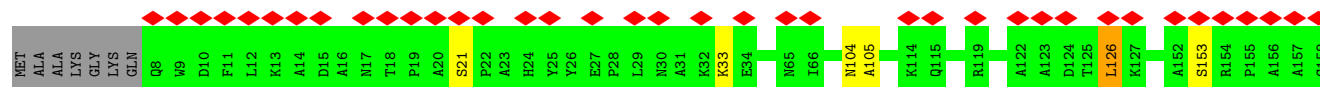
• Molecule 14: FAP275

Chain 2F:  9% 92% 5%



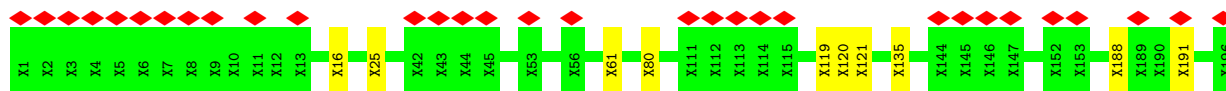
• Molecule 14: FAP275

Chain 2G:  24% 92% 5%

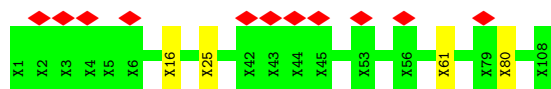




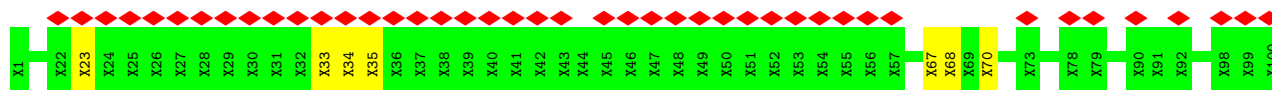
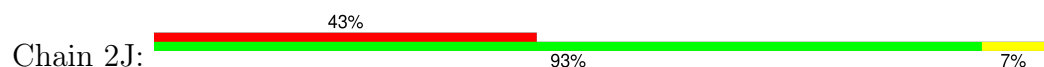
- Molecule 15: Unknown protein



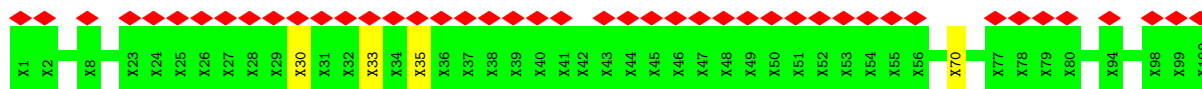
- Molecule 16: Unknown protein



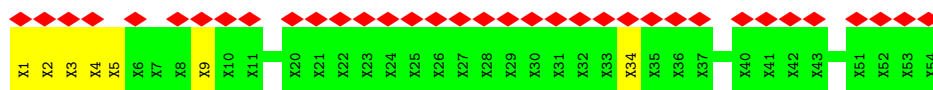
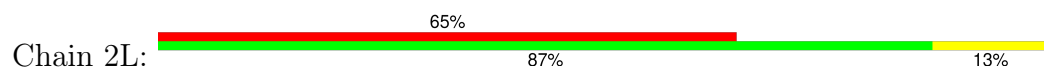
- Molecule 17: Unknown protein



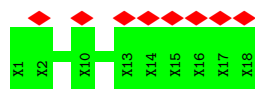
- Molecule 17: Unknown protein



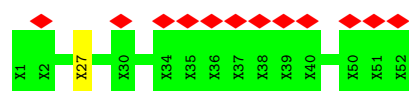
- Molecule 18: Unknown protein



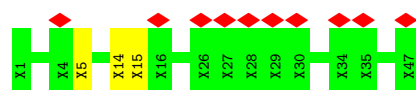
- Molecule 19: Unknown protein



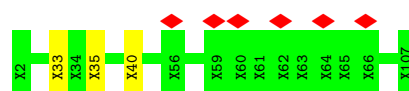
- Molecule 20: Unknown protein



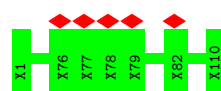
- Molecule 21: Unknown protein



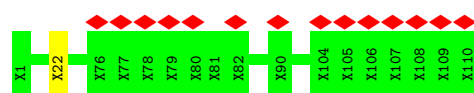
- Molecule 22: Unknown protein



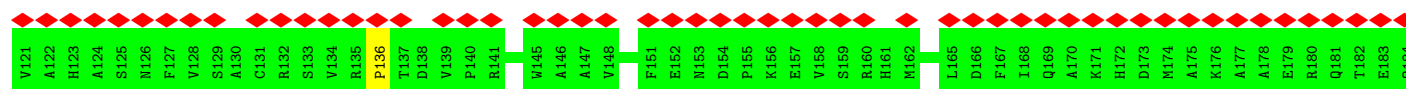
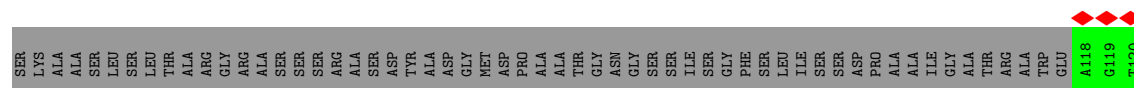
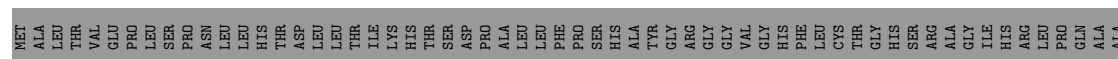
- Molecule 23: Unknown protein



- Molecule 23: Unknown protein

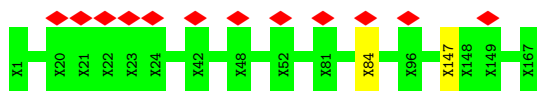


- Molecule 24: FAP289

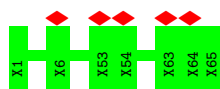




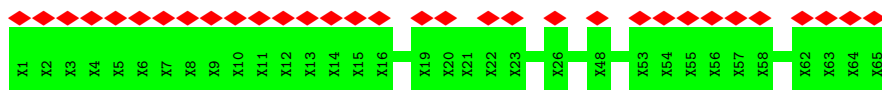
- Molecule 25: Unknown protein



- Molecule 26: Unknown protein



- Molecule 26: Unknown protein

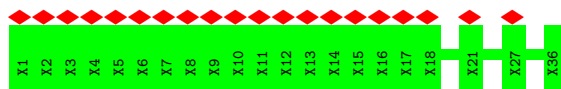


- Molecule 27: Unknown protein



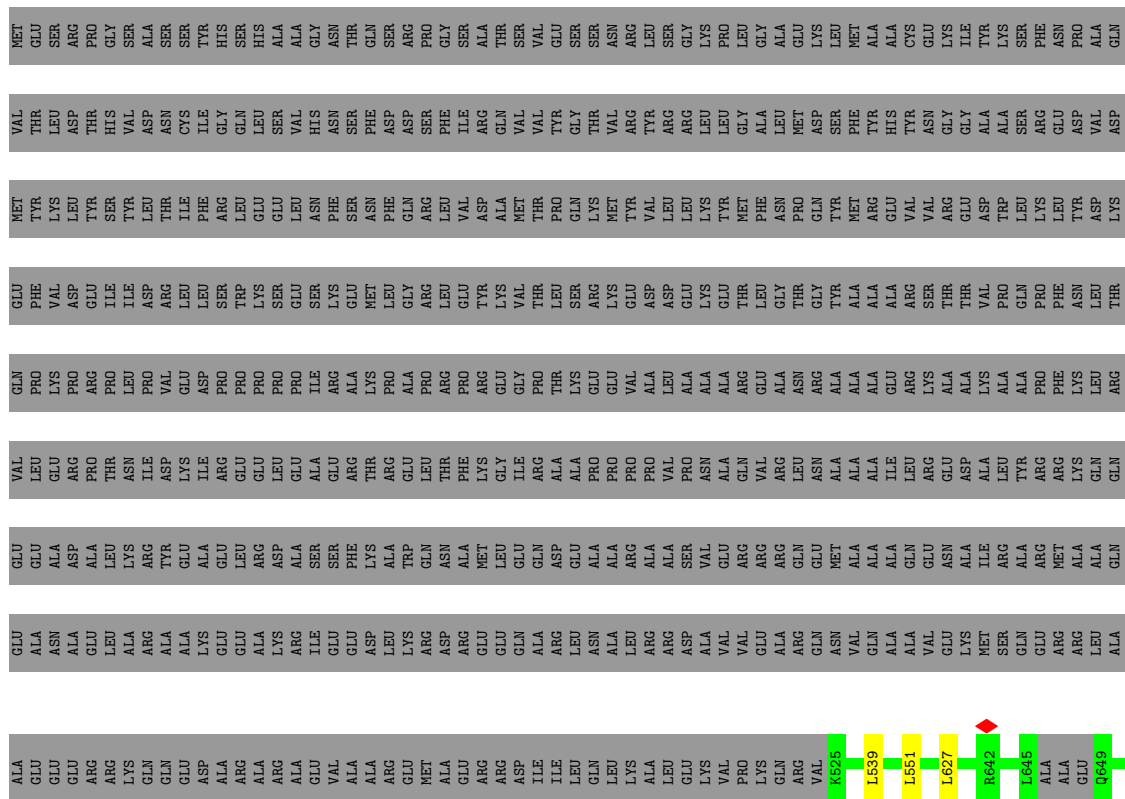
There are no outlier residues recorded for this chain.

- Molecule 27: Unknown protein



- Molecule 28: FAP216

[illegible]



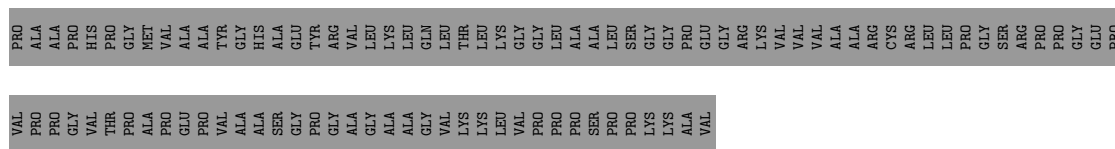
LYS	LEU	ALA	ALA	GLN	PHE	GLU	ARG	LEU	ALA	ASP	GLY
LEU	GLY	ALA	GLY	ALA	THR	ALA	VAL	HIS	PRO	ALA	GLY
VAL	TRP	ALA	GLY	ALA	PRO	ALA	MET	GLN	ALA	GLU	ALA
PRO	GLY	ALA	VAL	ALA	PHE	ALA	VAL	CYS	ALA	ALA	ALA
PRO	LEU	VAL	ALA	SER	SER	ARG	SER	HIS	SER	GLU	GLY
PRO	ALA	THR	LEU	GLN	GLN	THR	PHE	CYS	ALA	ALA	ALA
SER	ASP	GLY	PRO	ARG	ARG	LEU	THR	LEU	PRO	ALA	ASP
PRO	LEU	GLY	GLY	THR	THR	VAL	GLN	PHE	ASP	GLU	GLY
PRO	LEU	PRO	PRO	SER	TYR	THR	ALA	ASP	GLY	ALA	GLY
LYS	GLY	ALA	SER	SER	GLU	ASN	ARG	PRO	ALA	GLU	ASP
ALA	PRO	GLY	GLY	GLY	ASP	VAL	THR	VAL	SER	GLN	GLY
VAL	ALA	GLY	VAL	GLY	VAL	CYS	THR	PRO	GLY	ARG	GLY
	GLY	GLY	GLY	GLY	GLN	PRO	TYR	VAL	ALA	THR	ALA
	ARG	THR	ALA	PHE	GLN	PHE	TYR	GLY	ALA	ALA	GLY
	ALA	LEU	ALA	GLN	LEU	PRO	GLU	GLN	ALA	LEU	HIS
	LYS	GLY	ALA	VAL	VAL	LEU	VAL	ARG	ALA	ALA	TYR
	VAL	LYS	ALA	GLY	VAL	SER	LEU	VAL	ALA	LEU	LEU
	VAL	VAL	GLY	VAL	VAL	THR	LEU	VAL	ALA	ALA	PRO
	VAL	VAL	GLY	GLY	PRO	PHE	VAL	VAL	LEU	VAL	VAL
	ALA	PRO	GLY	GLY	ASN	THR	ARG	GLY	ALA	ASP	ASP
	ALA	PRO	ALA	PRO	PRO	THR	LEU	ARG	LYS	VAL	ASN
	ALA	PRO	ALA	ALA	ASN	THR	LEU	ARG	LYS	VAL	ASP
	ARG	ALA	ILE	VAL	GLN	MET	SER	LEU	ALA	ILE	GLY
	ALA	TYR	ALA	ALA	ASP	LEU	ALA	GLU	SER	GLN	SER
	GLY	GLY	PRO	ALA	GLN	ALA	ARG	LEU	SER	SER	PRO
	LEU	GLY	GLY	ALA	GLY	GLY	THR	LEU	GLY	MET	ASP
	LEU	ARG	ALA	ALA	LEU	LYS	ARG	ASN	PRO	GLY	SER
	PRO	GLY	VAL	ALA	LEU	ALA	LEU	GLU	ALA	GLY	GLY
	GLY	PRO	ALA	GLY	PRO	SER	LEU	GLY	ALA	GLY	LYS
	SER	ILE	THR	ASP	LEU	LEU	ARG	GLU	ALA	ASP	ASP
	ARG	THR	ALA	LYS	ARG	ALA	ALA	GLU	PRO	PRO	ALA
	PRO	LEU	SER	PRO	ALA	ASP	LEU	PRO	GLY	GLY	SER
	PRO	LEU	PHE	SER	ARG	PRO	LEU	LEU	PRO	SER	SER
	GLY	TYR	GLY	THR	GLY	THR	GLY	VAL	TRP	TYR	HIS
	GLU	SER	VAL	PRO	ARG	PRO	ALA	LEU	GLU	ARG	THR
	PRO	ALA	GLY	ALA	ARG	THR	GLY	GLY	ILE	TRP	ASP
	VAL	PRO	SER	PRO	GLU	MET	THR	ALA	HIS	ARG	SER
	PRO	ALA	LEU	GLY	ARG	ALA	ILE	GLU	LEU	GLY	ASP
	ALA	ALA	LYS	ILE	ALA	ASP	LEU	ASP	ALA	ILE	GLN
	THR	PRO	PRO	PRO	ALA	CYS	GLN	SER	THR	CYS	GLY
	PRO	GLY	SER	ALA	THR	GLY	LEU	ARG	TYR	GLY	PRO
	ALA	MET	GLY	THR	PRO	HIS	GLY	GLU	ALA	TYR	ARG
	VAL	VAL	SER	PRO	ASP	PRO	PRO	VAL	VAL	ILE	VAL
	GLU	ALA	ALA	ALA	THR	ALA	GLU	PHE	LYS	GLY	ARG
	PRO	ALA	ALA	GLY	PRO	GLY	GLY	GLY	PRO	LEU	ALA
	VAL	VAL	GLY	GLY	GLY	GLY	VAL	LEU	ASP	GLN	SER
	ALA	GLY	GLY	ALA	PRO	THR	THR	VAL	SER	PRO	PRO
	ALA	HIS	ALA	SER	GLN	LEU	ALA	ASN	VAL	GLN	VAL
	SER	GLY	GLY	LYS	ALA	ALA	THR	ALA	GLN	GLN	GLY
	GLY	ALA	ALA	GLY	ASP	LEU	THR	VAL	ASN	GLN	VAL
	GLY	GLY	GLY	GLY	THR	GLY	LEU	ARG	LEU	GLY	ARG
	GLY	GLY	GLY	GLY	LEU	VAL	VAL	VAL	PRO	VAL	GLY
	GLY	GLY	GLY	GLY	LEU	ARG	ARG	ARG	ASP	GLY	ARG
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
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	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
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	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
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	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
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	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
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	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
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	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
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	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
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	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY
	GLY	GLY	GLY	GLY							

- Molecule 31: FAP74

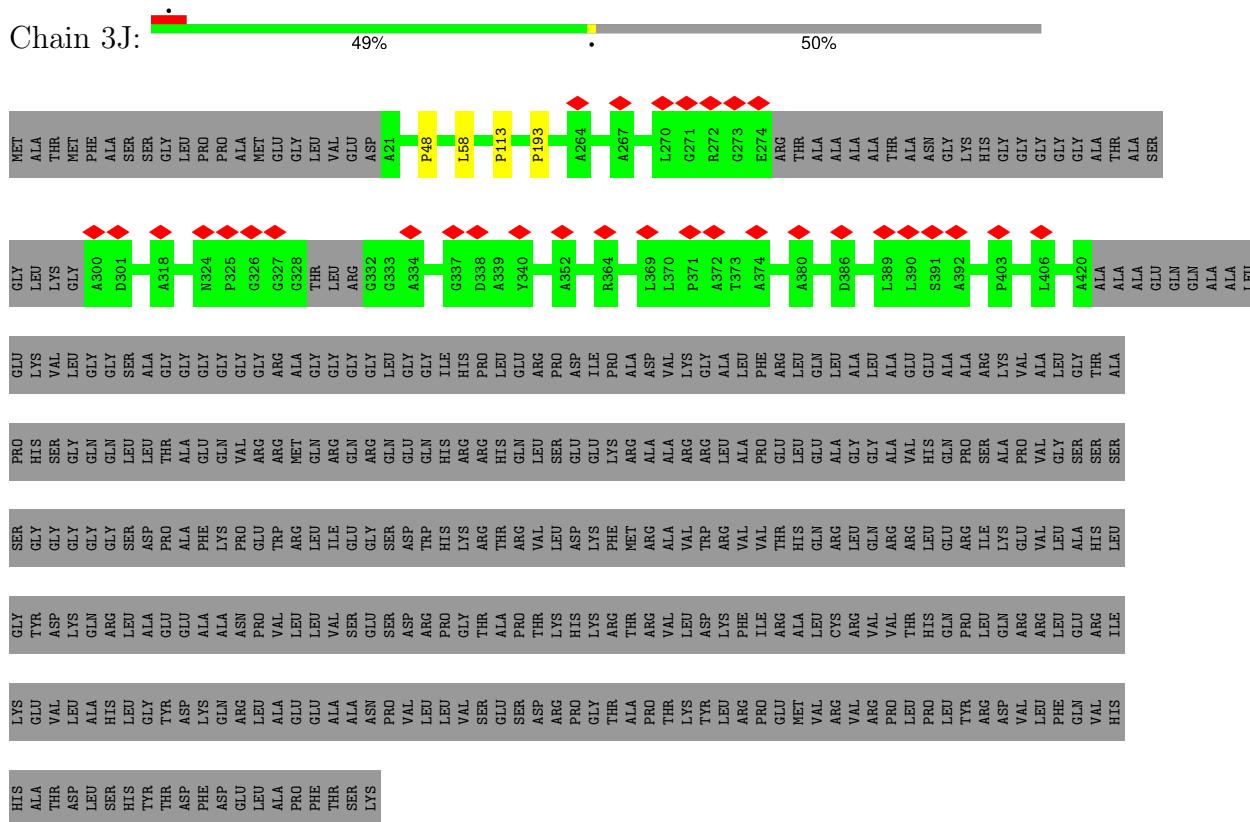
Chain 3I:

[illegible]

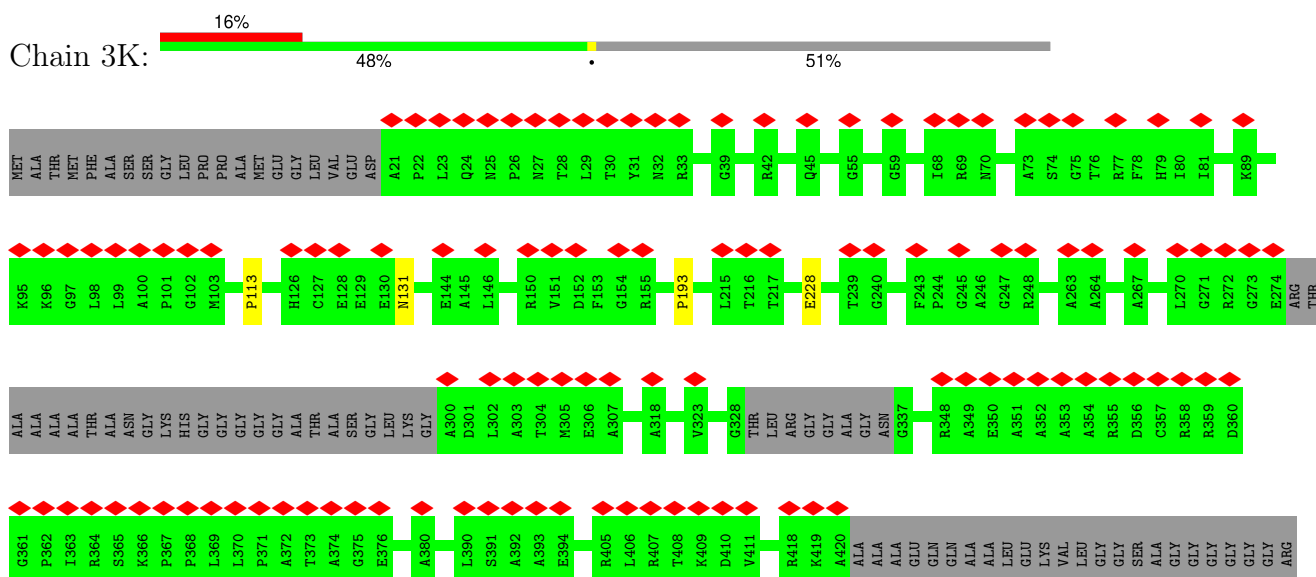




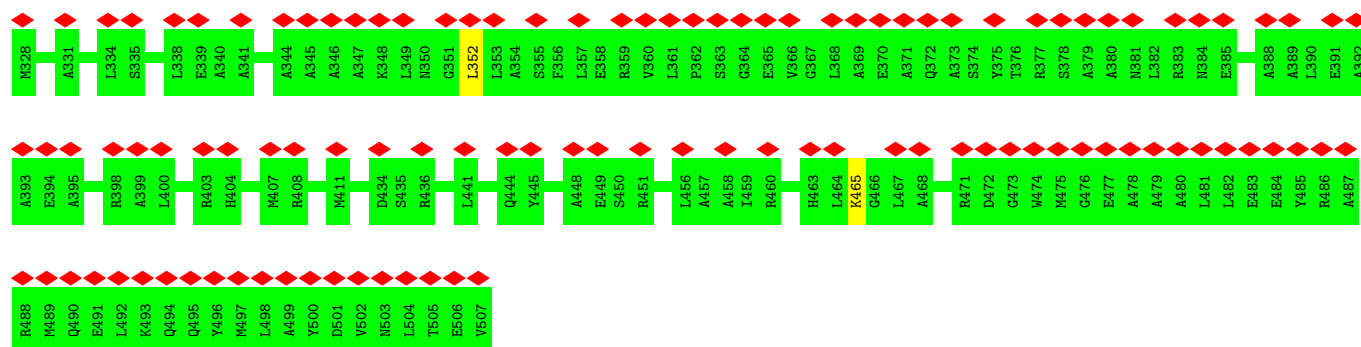
- Molecule 32: FAP360



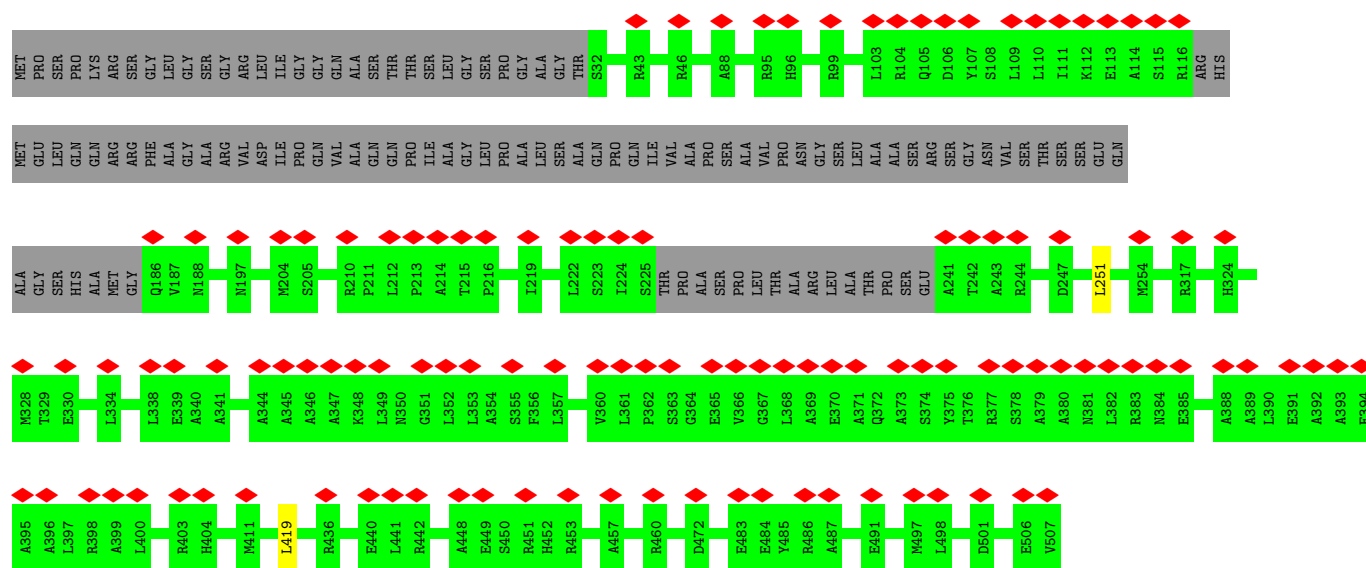
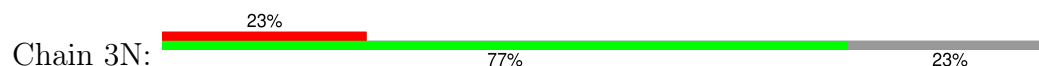
- Molecule 32: FAP360



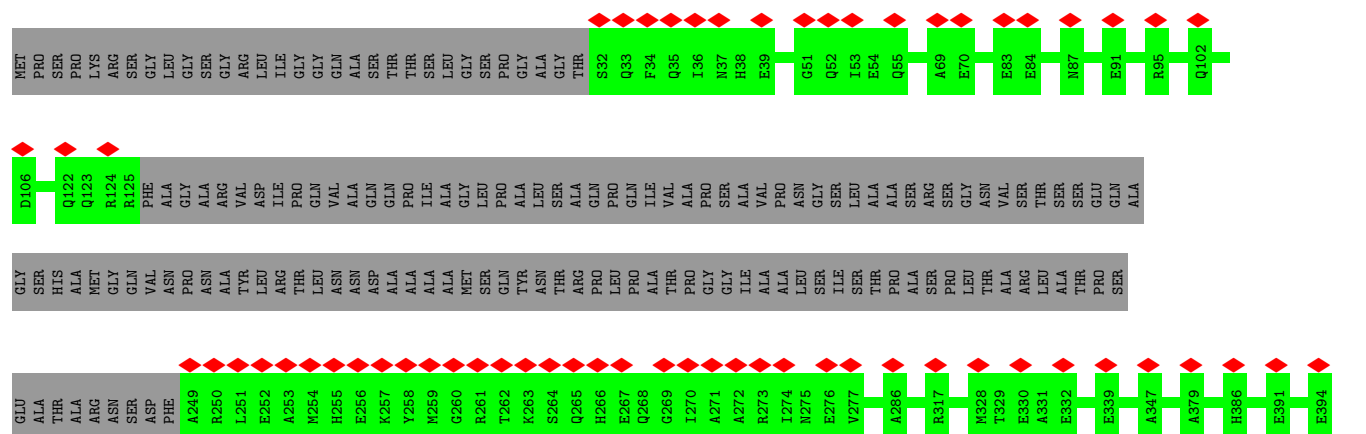


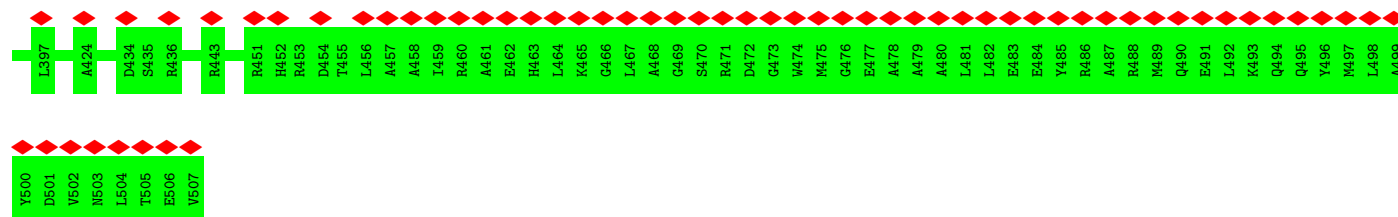


• Molecule 34: FAP7

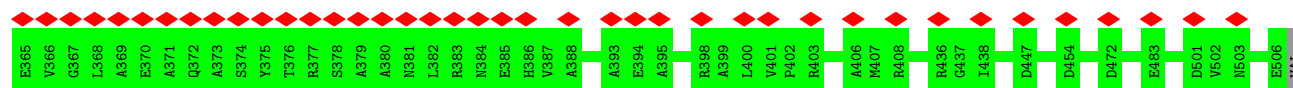
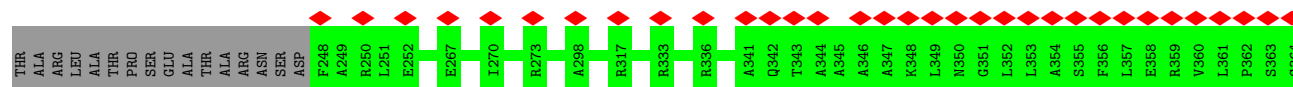
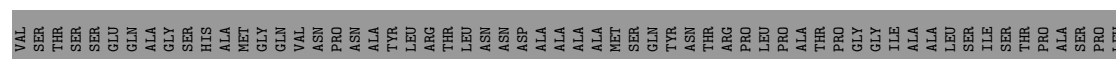
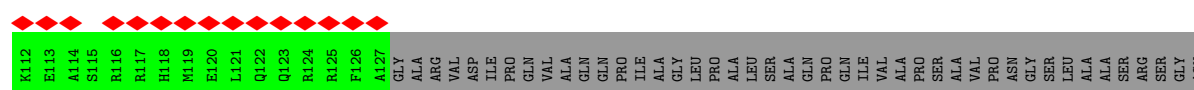
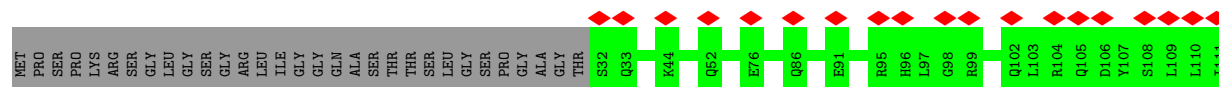


• Molecule 34: FAP7

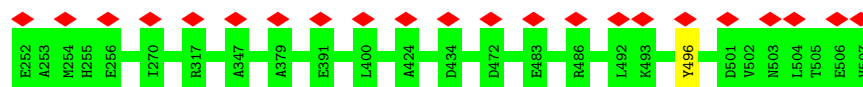
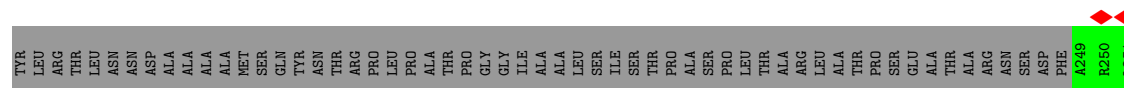
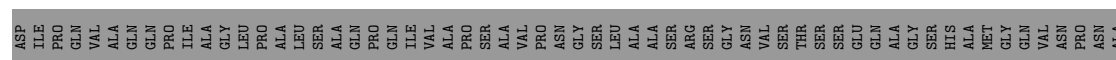
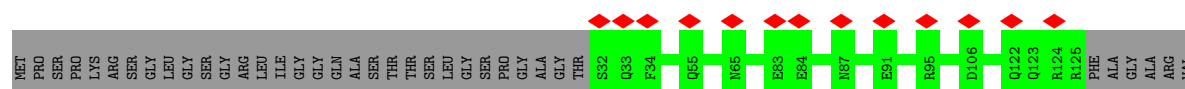




• Molecule 34: FAP7



• Molecule 34: FAP7



• Molecule 34: FAP7



Chain 3W:



Chain 3X:

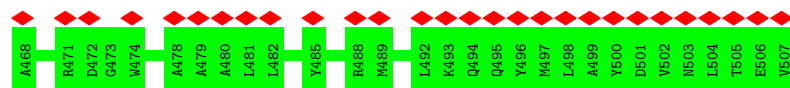


Chain 3Y:

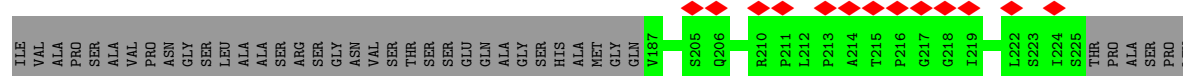
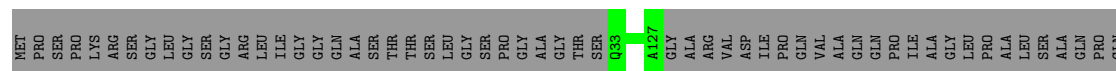
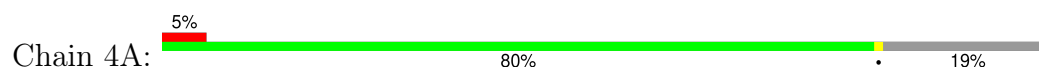


Chain 3Z:

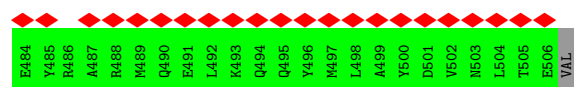
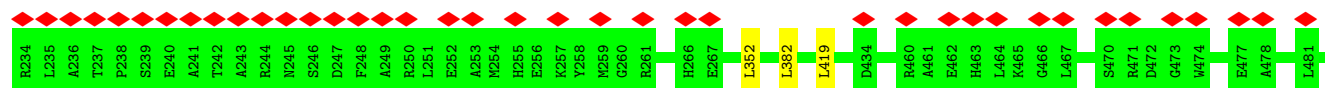
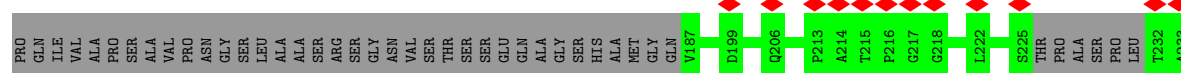
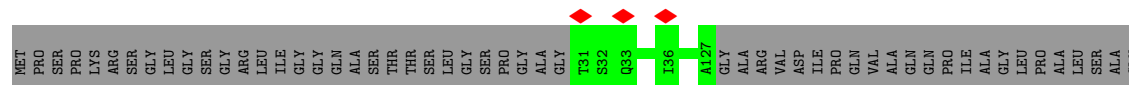
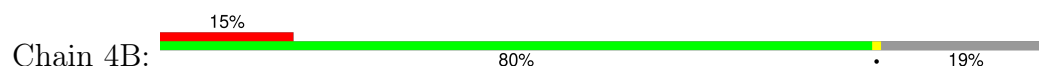




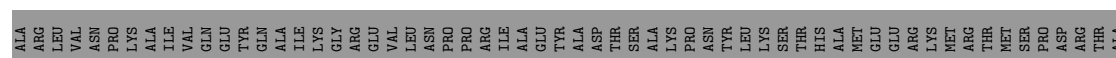
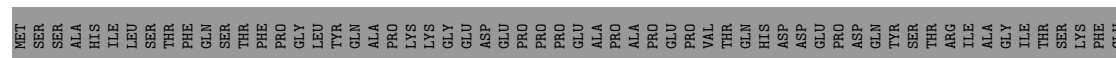
- Molecule 34: FAP7



- Molecule 34: FAP7



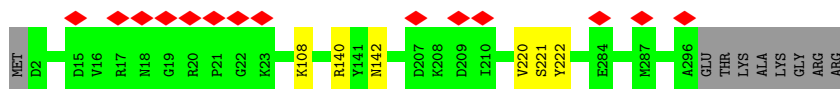
- Molecule 35: FAP81





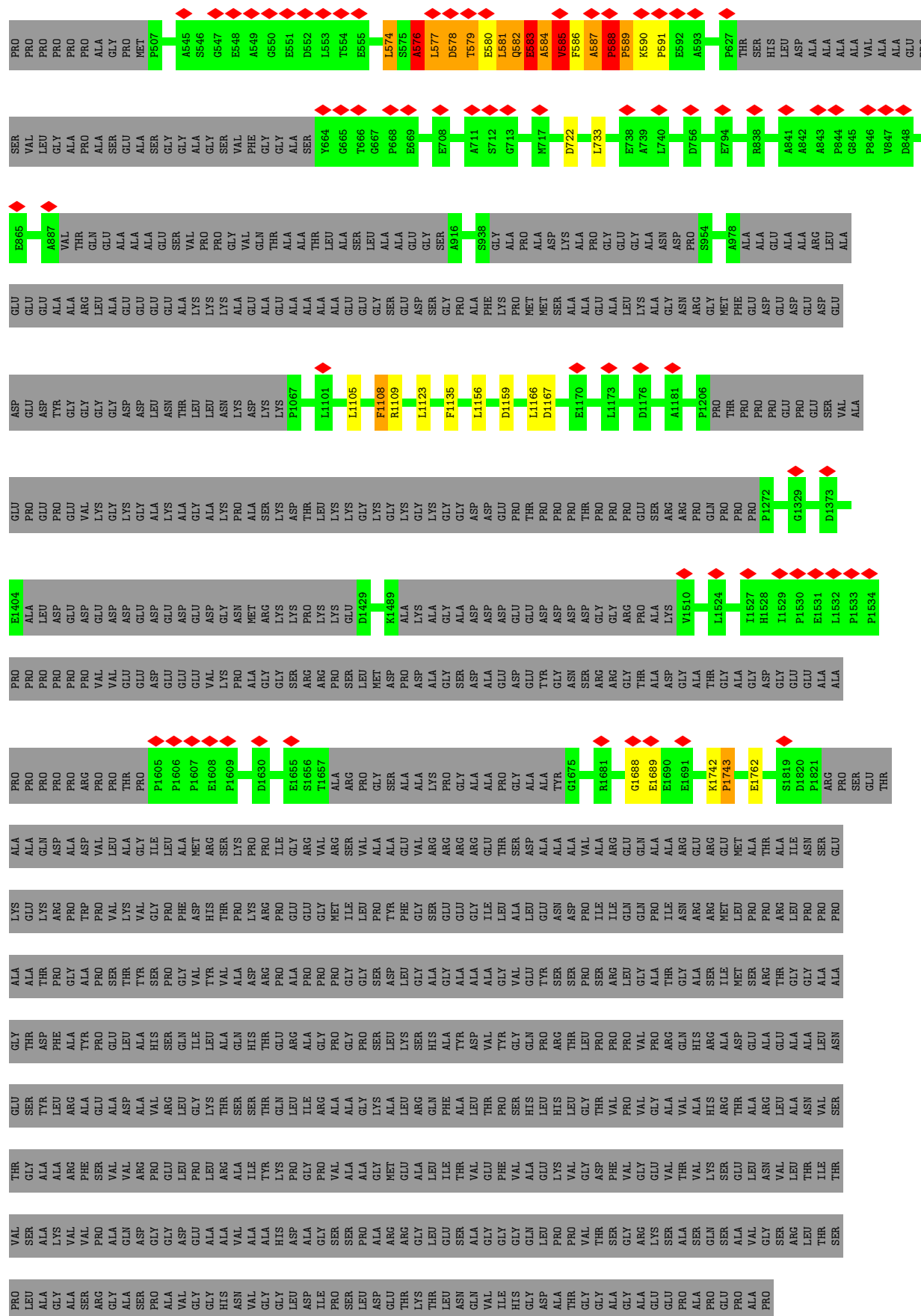
[illegible]

- Molecule 36: FAP15

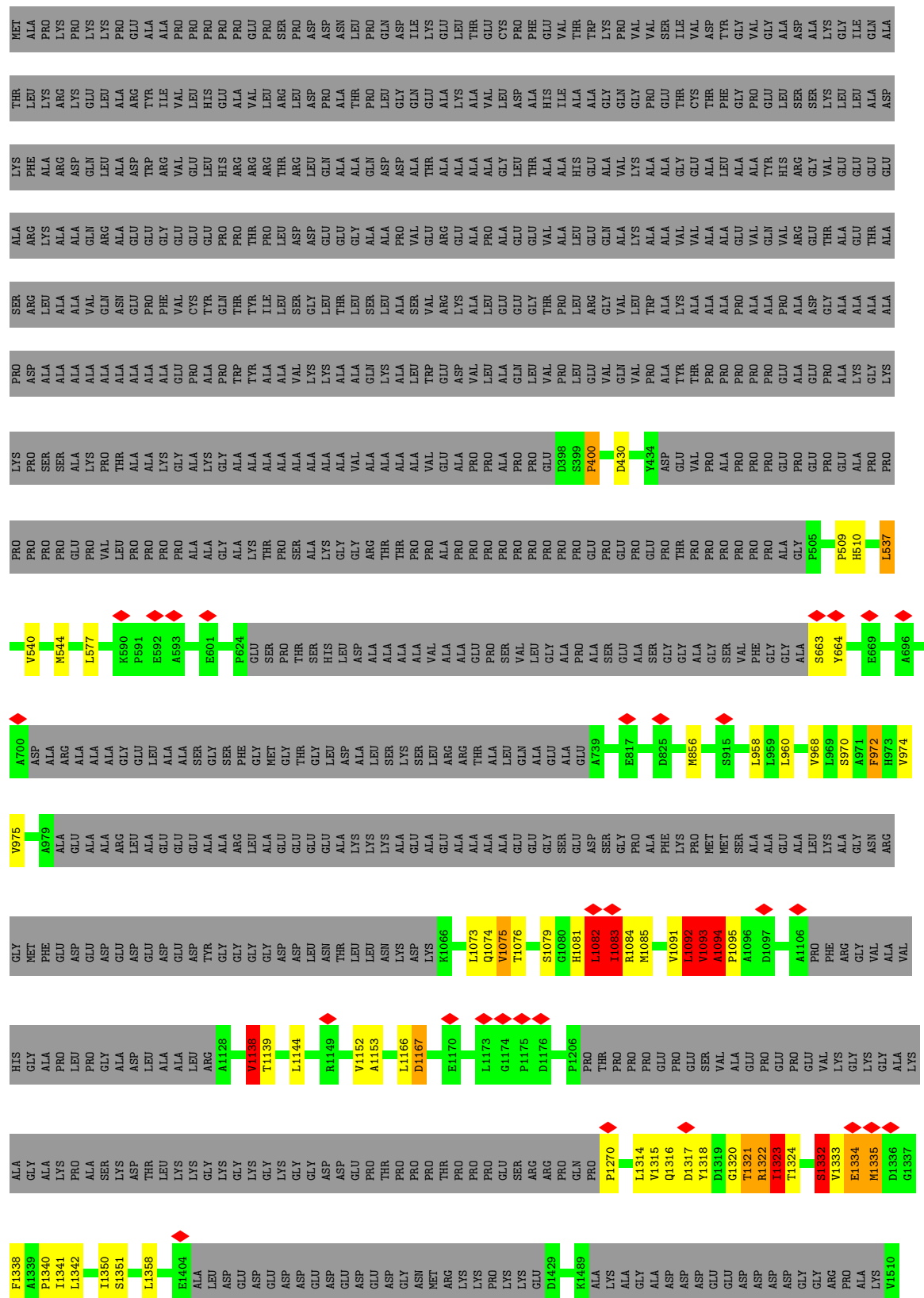


- Molecule 37: PF₆

[illegible]




Chain 4F:

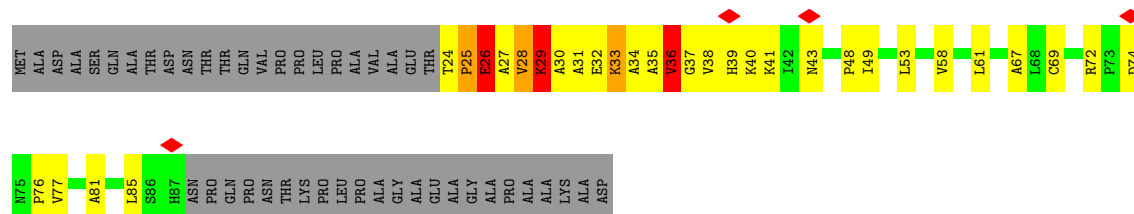







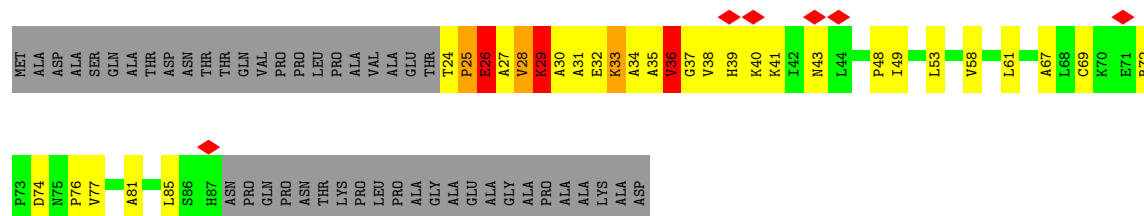
- Molecule 38: DPY30

Chain 4J: 




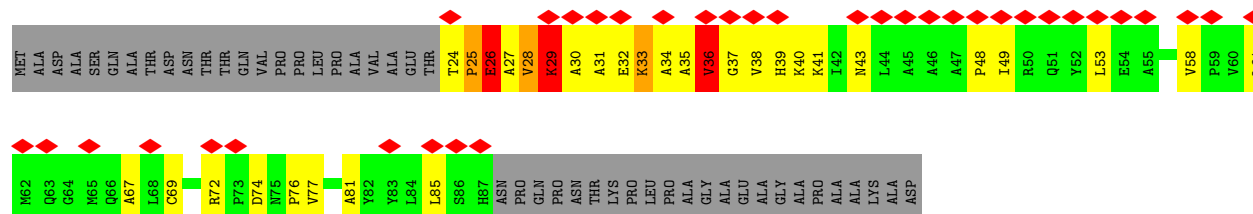
- Molecule 38: DPY30

Chain 4K: 




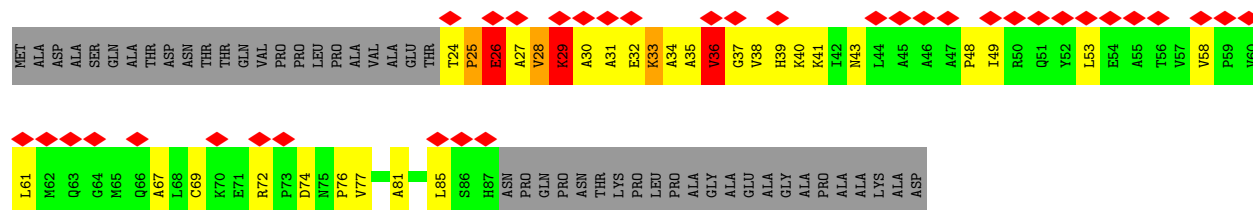
- Molecule 38: DPY30

Chain 4L: 




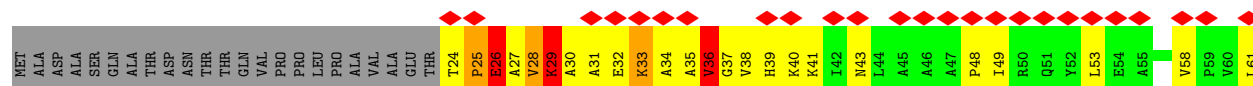
- Molecule 38: DPY30

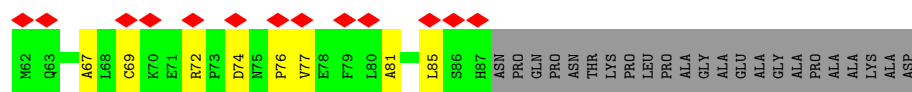
Chain 4M: 



- Molecule 38: DPY30

Chain 4N: 

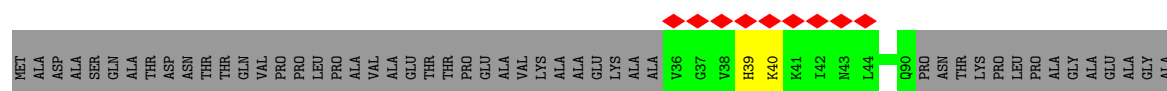




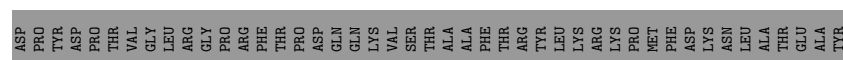
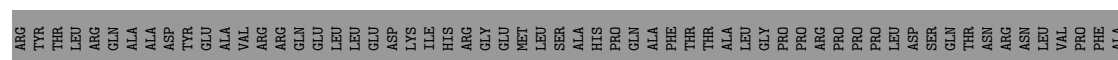
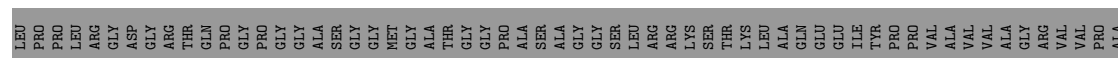
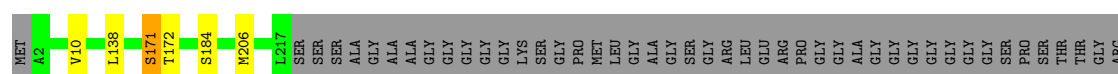
• Molecule 38: DPY30



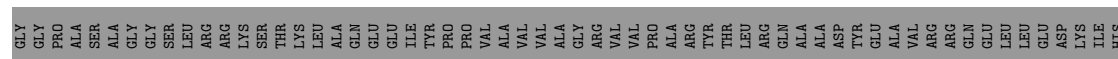
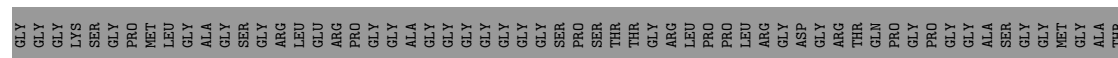
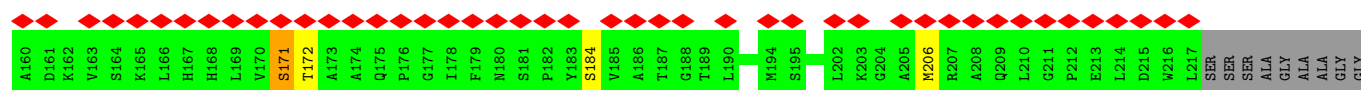
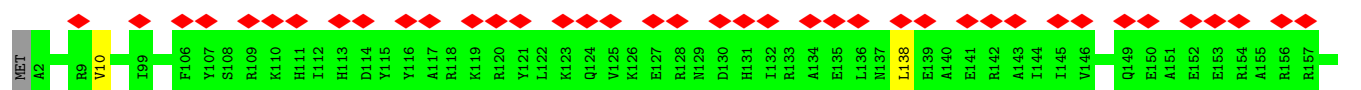
• Molecule 38: DPY30



• Molecule 39: FAP305

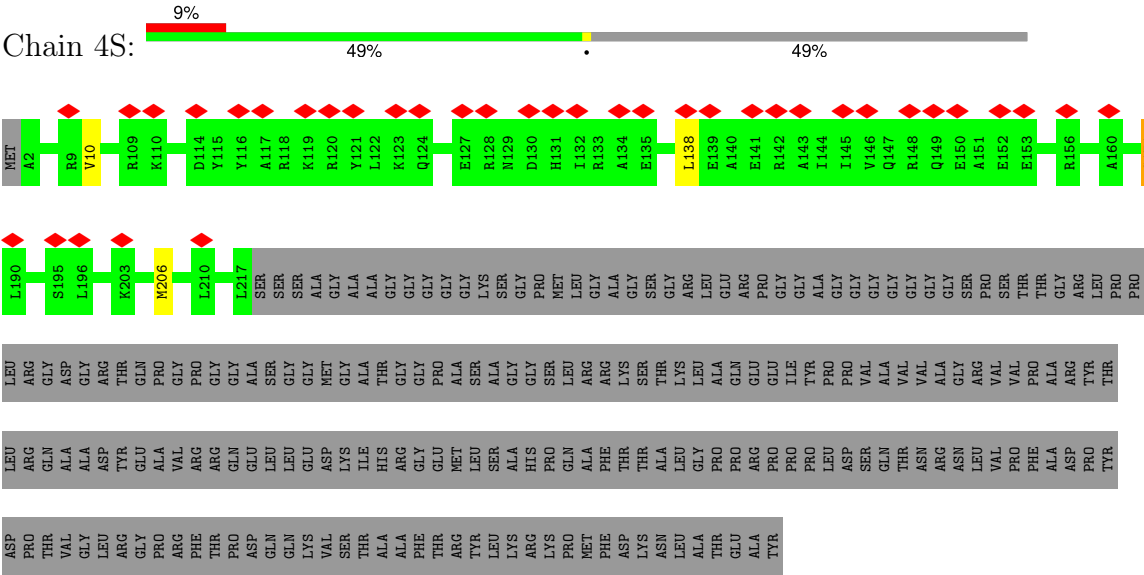


• Molecule 39: FAP305

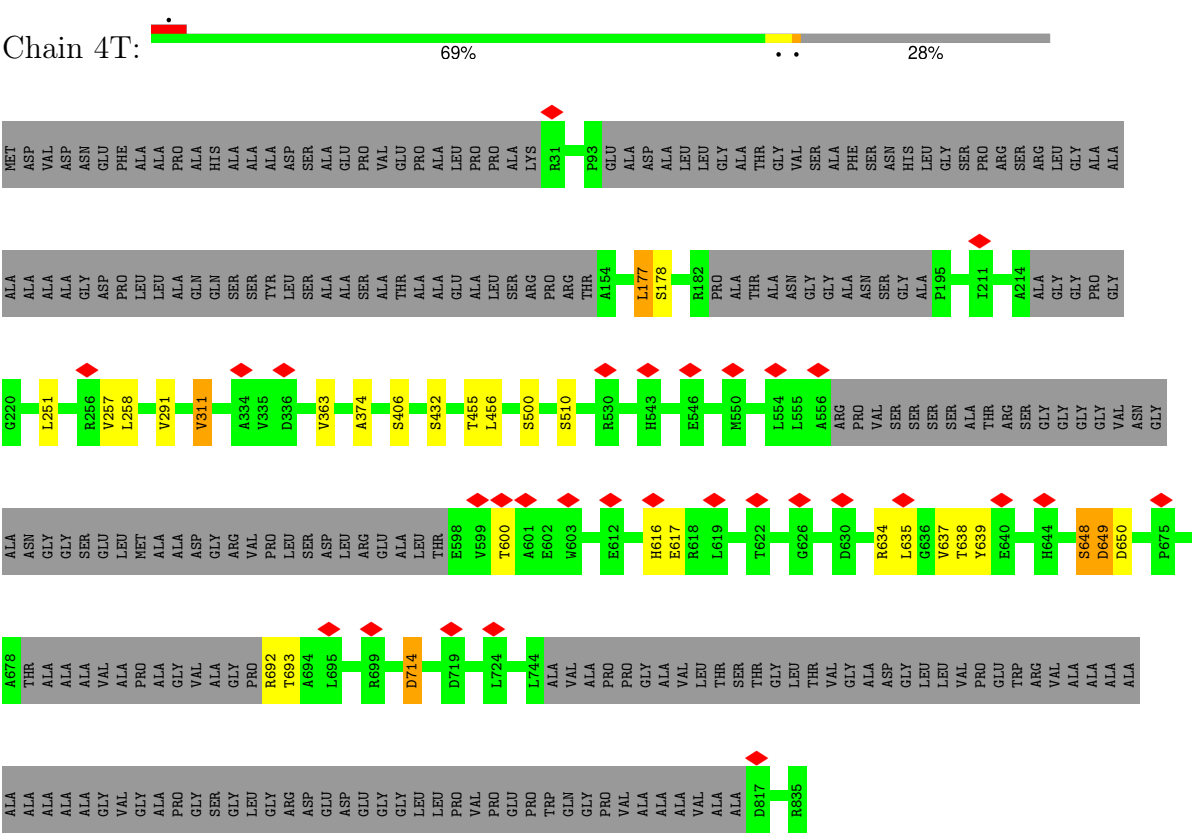


ALA	PHE	THR	ARG	TYR	LEU	LYS	ARG	PRO	LYS	PRO	PHE	ASP	LYS	ASN	LEU	ALA	GLY	THR	GLU	ALA	TYR																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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• Molecule 39: FAP305



• Molecule 40: FAP101

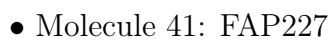


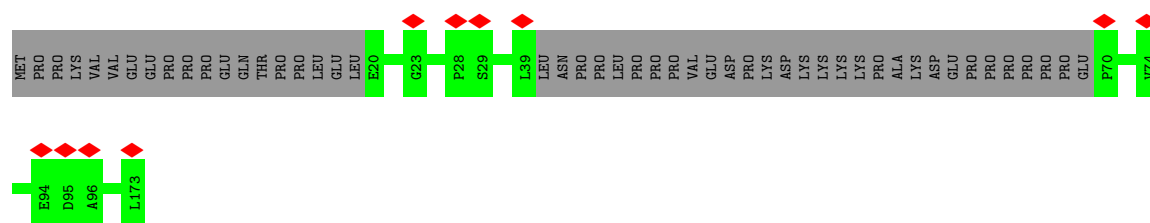
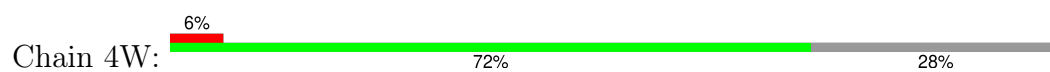
• Molecule 40: FAP101

Frequency	Percentage
Daily	69%
Sometimes	28%
Never	3%

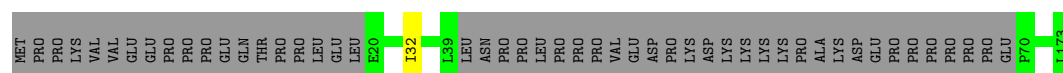


Frequency	Percentage
Daily	69%
Sometimes	28%
Never	3%

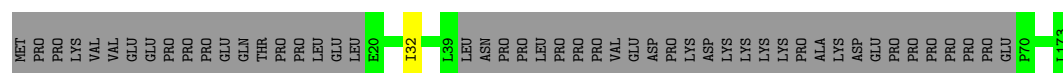




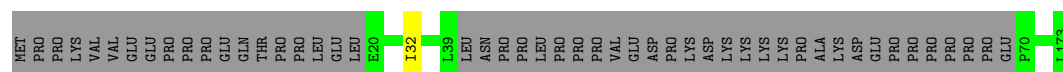
- Molecule 41: FAP227



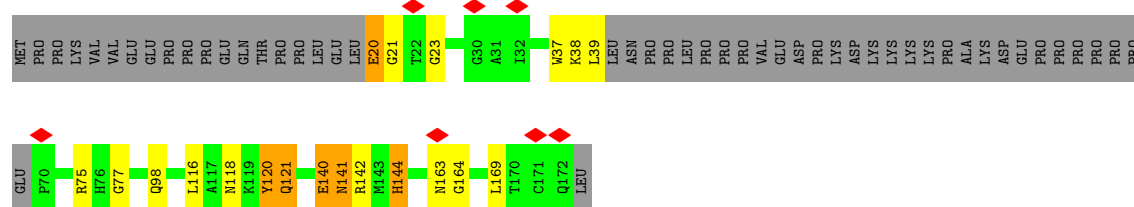
- Molecule 41: FAP227



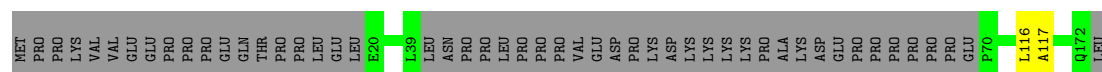
- Molecule 41: FAP227



- Molecule 41: FAP227

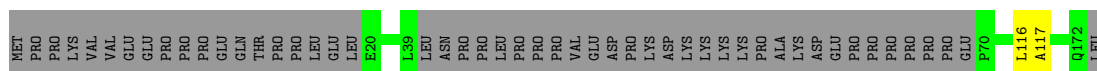


- Molecule 41: FAP227



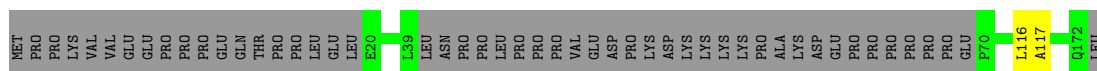
- Molecule 41: FAP227

Chain 5C:  70% 29%




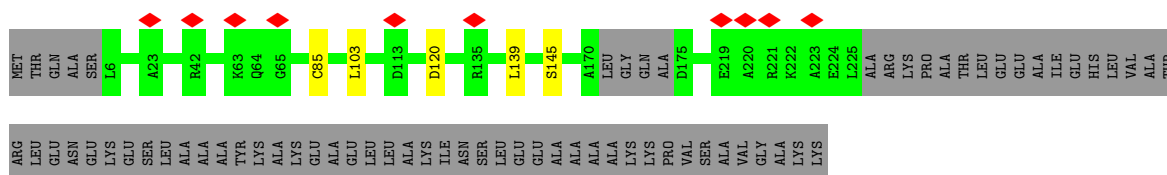
- Molecule 41: FAP227

Chain 5D:  70% 29%




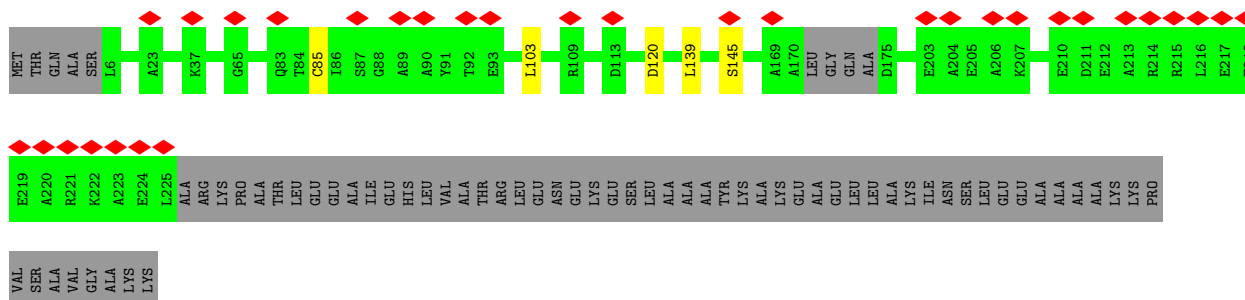
- Molecule 42: FAP114

Chain 5E:  74% 24%




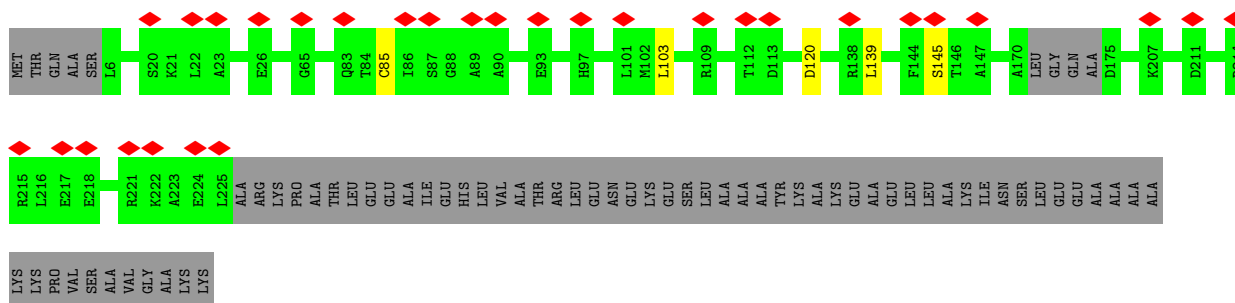
- Molecule 42: FAP114

Chain 5F:  11% 74% 24%



- Molecule 42: FAP114

Chain 5G:  10% 74% 24%



- Molecule 42: FAP114

Frequency	Percentage
Often	48%
Sometimes	6%
Never	42%



Response	Percentage
Yes	56%
No	10%
Don't know	31%



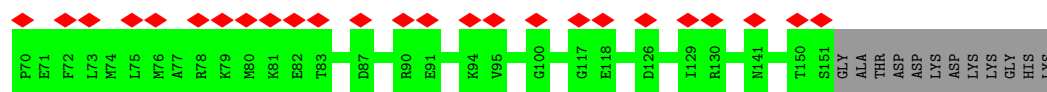
Category	Percentage
Very bad	10%
Bad	56%
Average	10%
Good	31%
Very good	0%



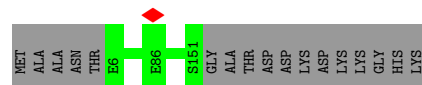
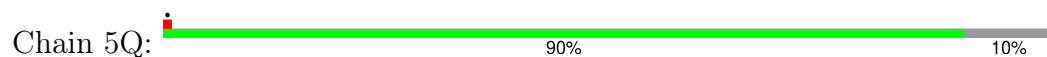
Frequency	Percentage
Daily	56%
Sometimes	10%
Never	31%



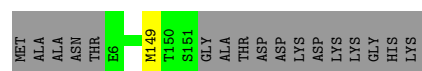
[illegible]



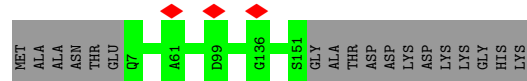
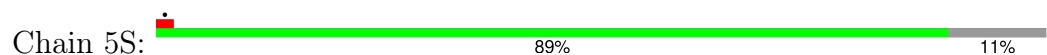
- Molecule 44: Calmodulin



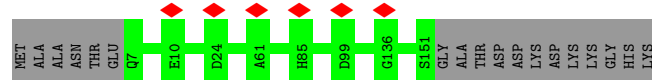
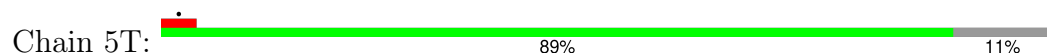
- Molecule 44: Calmodulin



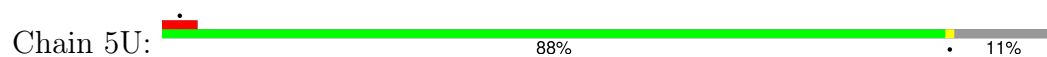
- Molecule 44: Calmodulin



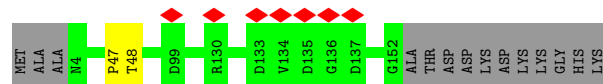
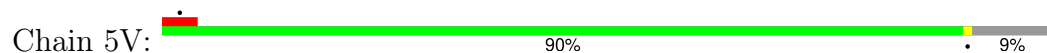
- Molecule 44: Calmodulin



- Molecule 44: Calmodulin

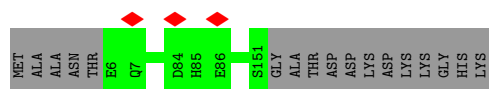


- Molecule 44: Calmodulin



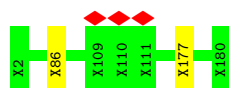
- Molecule 44: Calmodulin

Chain 5P:  90% 10%



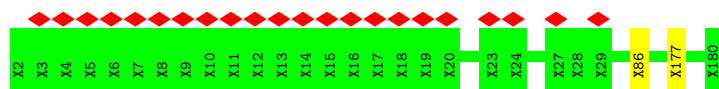
- Molecule 45: Unknown protein

Chain 5W:  99%



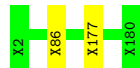
- Molecule 45: Unknown protein

Chain 5X:  16% 99%



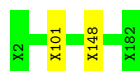
- Molecule 45: Unknown protein

Chain 5Y:  99%




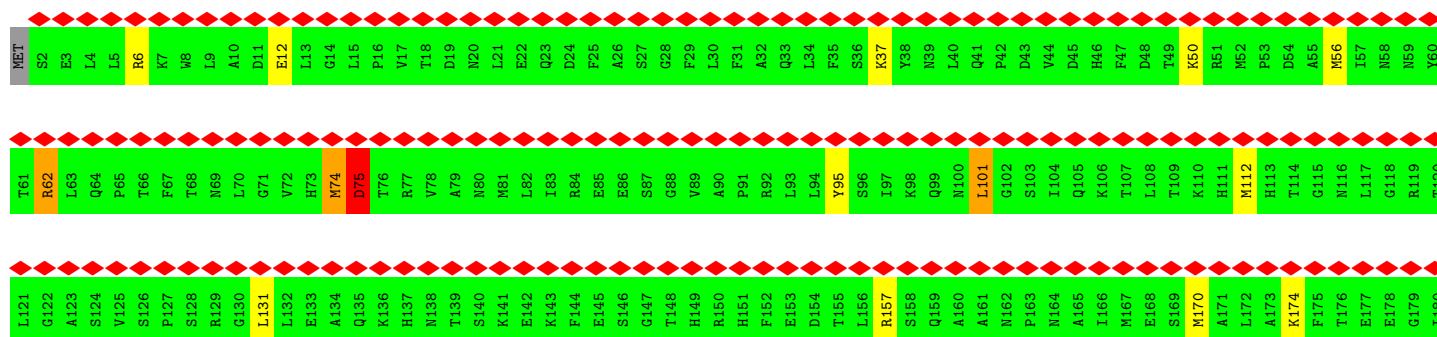
- Molecule 46: Unknown protein

Chain 5Z:  99%

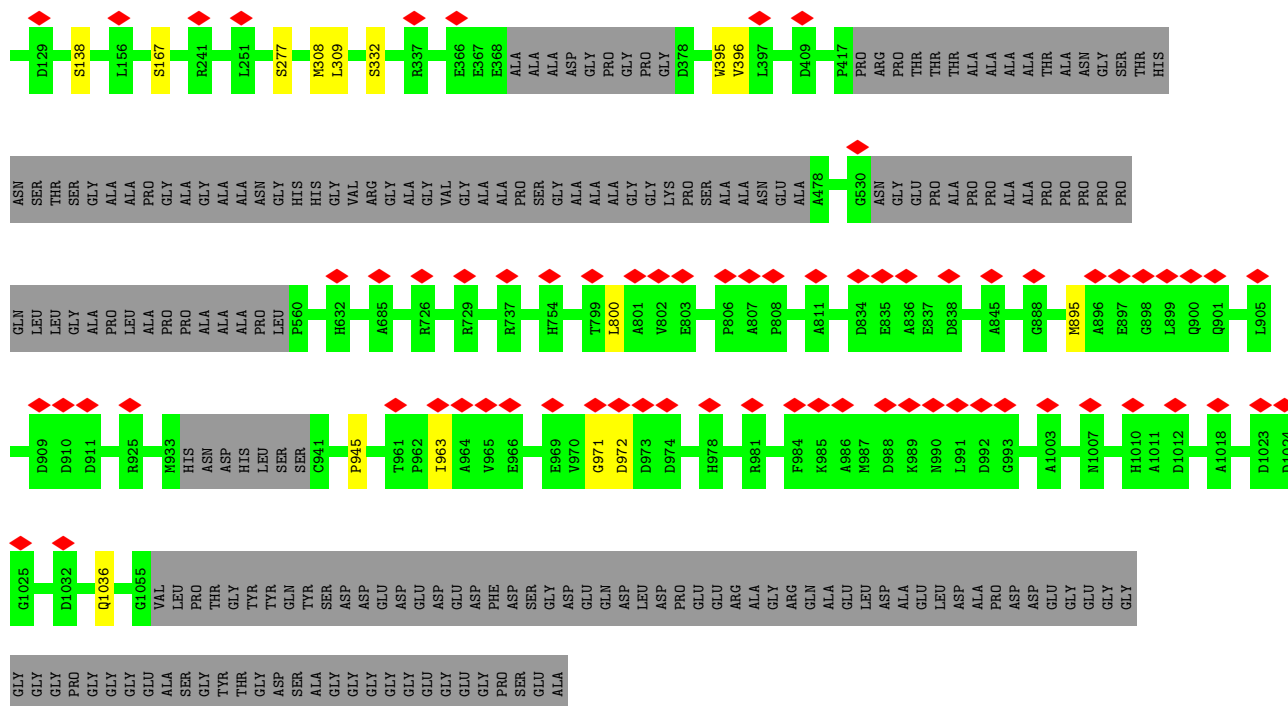


- Molecule 47: CPC1

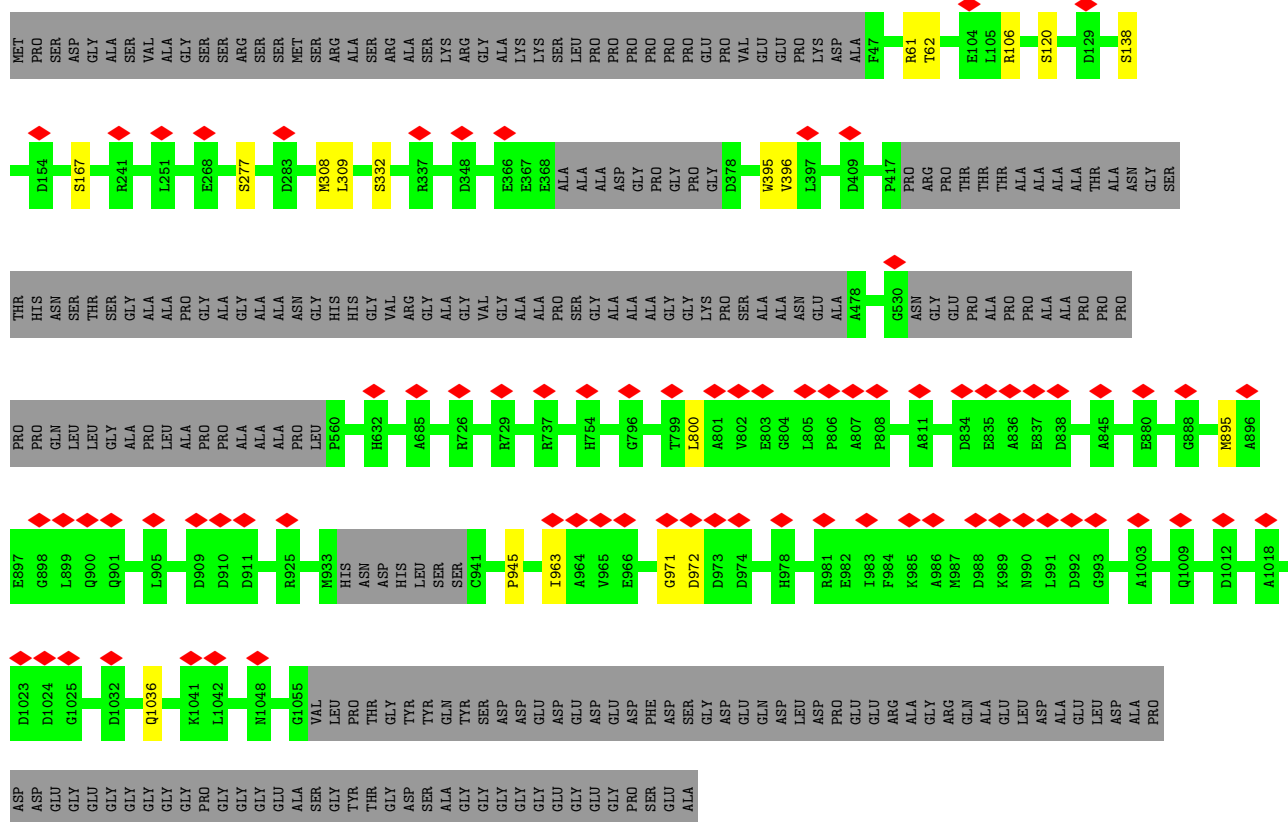
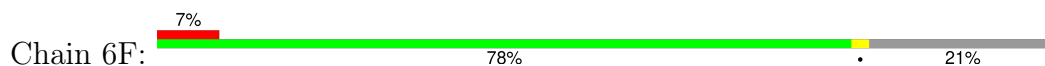
Chain 6A:  20% 78% 19%



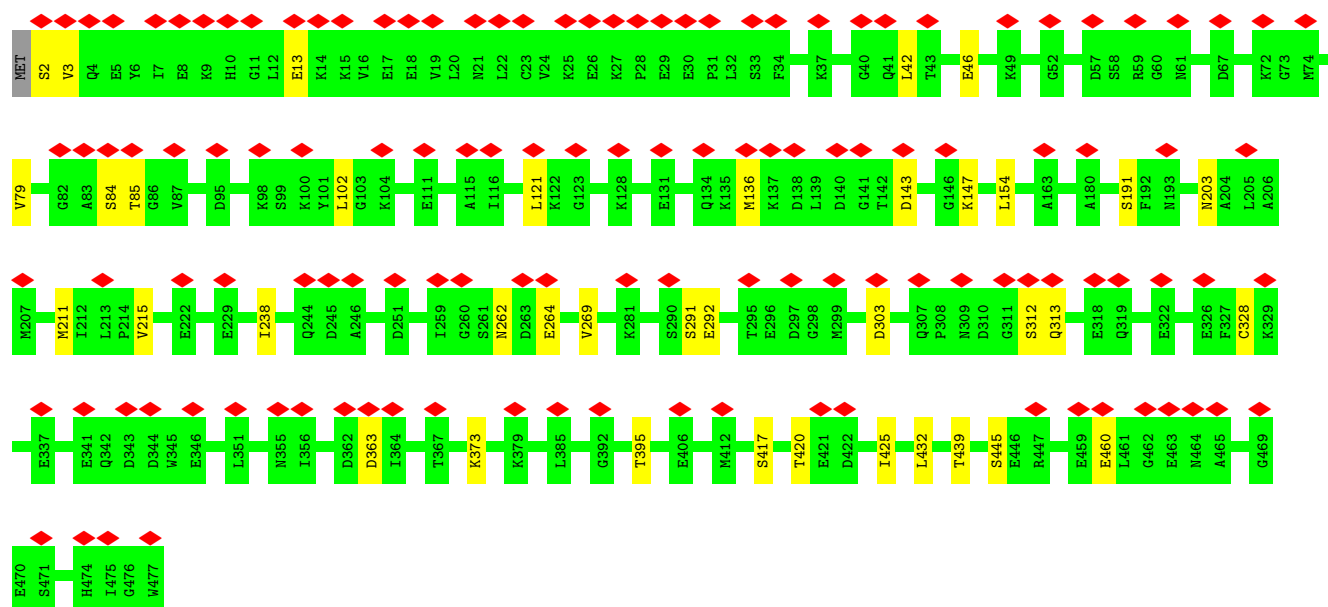




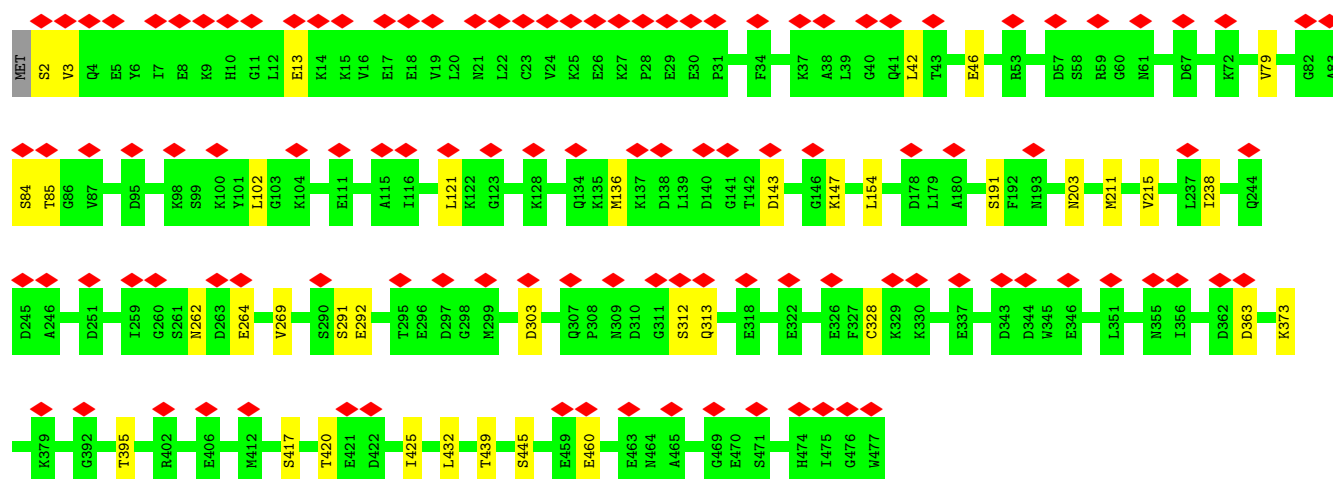
• Molecule 48: FAP246



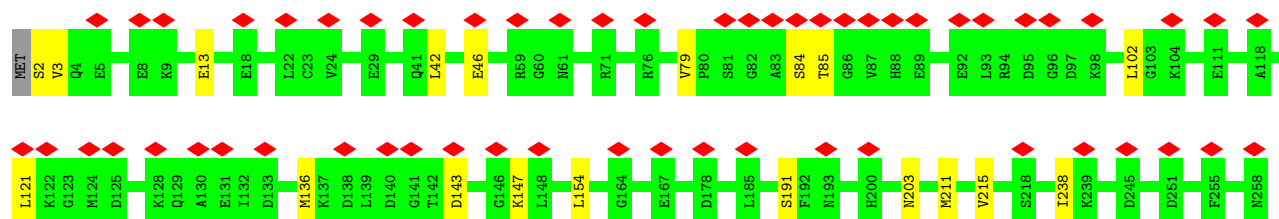
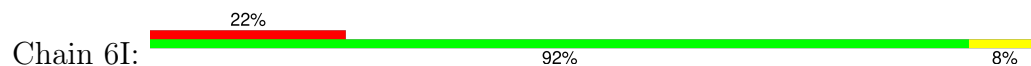
• Molecule 49: Phosphopyruvate hydratase

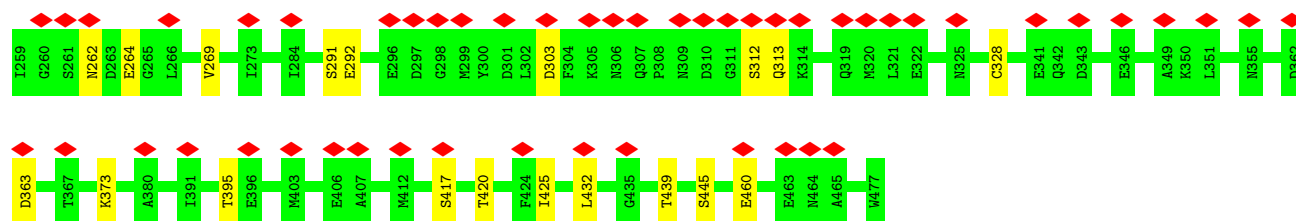


• Molecule 49: Phosphopyruvate hydratase

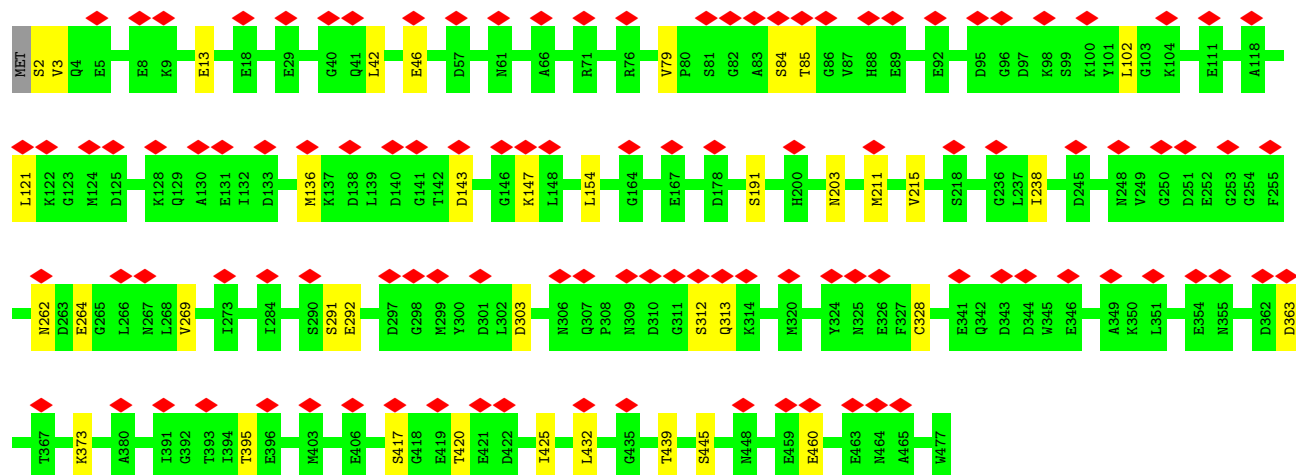
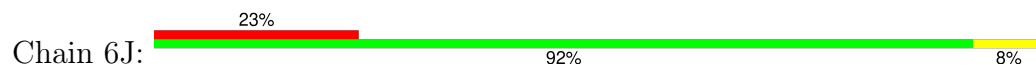


• Molecule 49: Phosphopyruvate hydratase

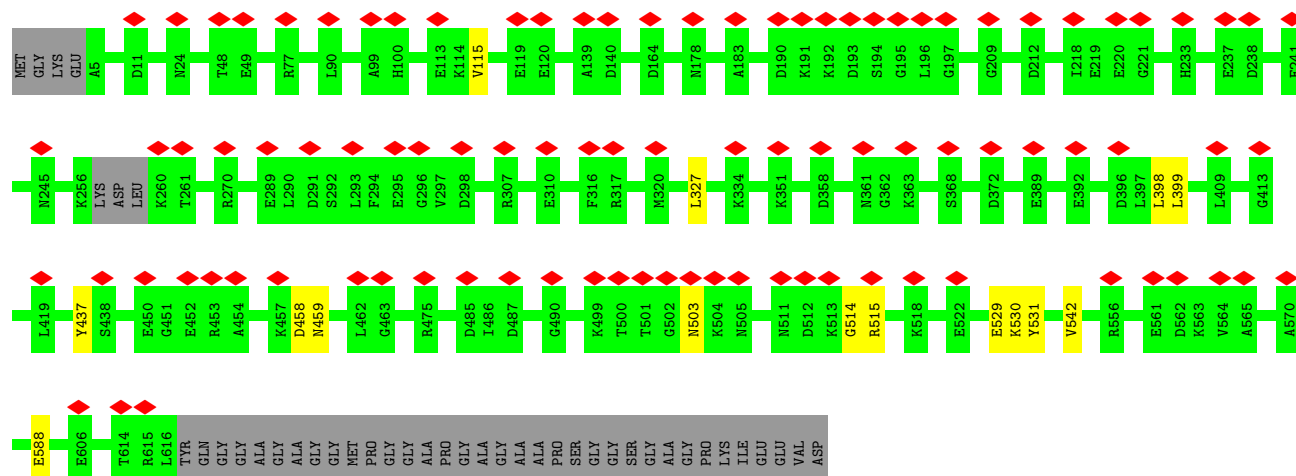
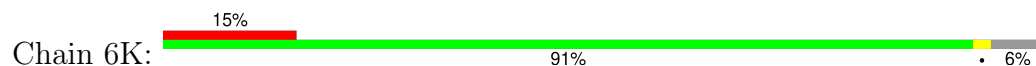




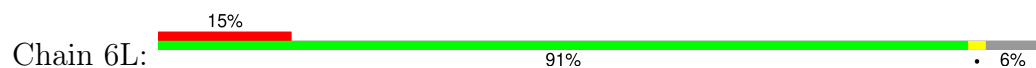
• Molecule 49: Phosphopyruvate hydratase



• Molecule 50: Heat shock protein 70A



• Molecule 50: Heat shock protein 70A





WORLDWIDE
PDB
PROTEIN DATA BANK

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	190727	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38.6	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	9.598	Depositor
Minimum map value	0.000	Depositor
Average map value	0.037	Depositor
Map value standard deviation	0.103	Depositor
Recommended contour level	0.5	Depositor
Map size (\AA)	1169.0691, 795.33936, 764.7494	wwPDB
Map dimensions	879, 598, 575	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.329999, 1.329999, 1.329999	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, GTP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0A	0.42	2/3578 (0.1%)	0.52	4/4885 (0.1%)
1	0B	0.30	0/3578	0.49	2/4885 (0.0%)
1	0C	0.29	0/3578	0.45	0/4885
1	0D	0.29	0/3578	0.47	1/4885 (0.0%)
1	0E	0.35	0/3578	0.50	1/4885 (0.0%)
1	0F	0.33	0/3578	0.50	2/4885 (0.0%)
1	0G	0.30	0/3578	0.47	2/4885 (0.0%)
1	0H	0.29	0/3578	0.46	0/4885
1	0I	0.31	0/3578	0.46	0/4885
1	0J	0.29	0/3578	0.45	0/4885
1	0K	0.30	0/3574	0.45	0/4881
1	0L	0.30	0/3578	0.46	0/4885
1	0M	0.29	0/3578	0.45	0/4885
1	0N	0.32	0/3578	0.54	2/4885 (0.0%)
1	0O	0.29	0/3578	0.46	1/4885 (0.0%)
1	0P	0.30	0/3578	0.46	0/4885
1	0Q	0.33	0/3578	0.48	0/4885
1	0R	0.40	2/3575 (0.1%)	0.51	3/4880 (0.1%)
1	0S	0.29	0/3578	0.47	1/4885 (0.0%)
1	0T	0.29	0/3578	0.44	0/4885
1	0U	0.29	0/3578	0.47	2/4885 (0.0%)
1	0V	0.31	0/3578	0.46	0/4885
1	0W	0.30	0/3578	0.47	2/4885 (0.0%)
1	0X	0.31	0/3578	0.46	2/4885 (0.0%)
1	0Y	0.30	0/3578	0.49	2/4885 (0.0%)
1	0Z	0.30	0/3578	0.45	0/4885
1	1A	0.31	0/3578	0.48	2/4885 (0.0%)
1	1B	0.36	0/3578	0.52	1/4885 (0.0%)
1	1C	0.31	0/3574	0.46	0/4881
2	1D	0.31	0/3240	0.63	5/4420 (0.1%)
2	1E	0.31	0/3240	0.61	3/4420 (0.1%)
2	1F	0.34	1/3319 (0.0%)	0.73	4/4529 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	1G	0.31	0/3319	0.63	2/4529 (0.0%)
3	1H	0.40	2/5878 (0.0%)	0.57	10/8010 (0.1%)
3	1I	0.30	0/5878	0.46	0/8010
3	6D	0.38	2/6127 (0.0%)	0.55	7/8328 (0.1%)
4	1J	0.30	0/2918	0.56	0/3984
4	1K	0.30	0/2918	0.56	0/3984
5	1L	0.28	0/3404	0.56	0/4660
5	1M	0.28	0/3404	0.56	0/4660
6	1N	0.31	2/16403 (0.0%)	0.47	5/22333 (0.0%)
7	1O	0.29	0/19999	0.45	3/27280 (0.0%)
8	1P	0.30	0/2329	0.51	2/3190 (0.1%)
9	1Q	0.30	0/2347	0.65	1/3241 (0.0%)
10	1R	0.36	0/2816	0.60	2/3832 (0.1%)
10	1S	0.43	0/2034	0.67	2/2779 (0.1%)
11	1T	0.27	0/4794	0.35	0/6657
12	1a	0.31	0/3433	0.47	0/4646
12	1c	0.27	0/3453	0.45	0/4673
12	1e	0.32	0/3433	0.48	1/4646 (0.0%)
12	1g	0.28	0/3453	0.45	0/4673
12	2a	0.30	0/3433	0.47	1/4646 (0.0%)
12	2c	0.29	0/3453	0.45	0/4673
12	2e	0.32	0/3433	0.46	2/4646 (0.0%)
12	2g	0.28	0/3453	0.45	0/4673
12	3a	0.35	2/3433 (0.1%)	0.50	3/4646 (0.1%)
12	3c	0.27	0/3453	0.44	0/4673
12	3e	0.30	0/3433	0.46	0/4646
12	3g	0.27	0/3453	0.44	0/4673
12	4a	0.35	2/3433 (0.1%)	0.51	4/4646 (0.1%)
12	4c	0.28	0/3453	0.45	0/4673
12	4e	0.28	0/3433	0.47	1/4646 (0.0%)
12	4g	0.27	0/3453	0.44	0/4673
12	5a	0.31	0/3433	0.48	1/4646 (0.0%)
12	5c	0.28	0/3453	0.45	0/4673
12	5e	0.33	0/3433	0.48	1/4646 (0.0%)
12	5g	0.27	0/3453	0.45	0/4673
12	6a	0.31	0/3433	0.49	1/4646 (0.0%)
12	6c	0.28	0/3453	0.46	0/4673
12	6e	0.34	0/3433	0.57	4/4646 (0.1%)
12	6g	0.28	0/3453	0.45	0/4673
12	7a	0.32	0/3433	0.48	1/4646 (0.0%)
12	7c	0.28	0/3453	0.45	0/4673
12	7e	0.33	0/3433	0.51	2/4646 (0.0%)
12	7g	0.29	0/3453	0.46	0/4673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
12	8a	0.31	0/3433	0.47	0/4646
12	8c	0.27	0/3453	0.46	1/4673 (0.0%)
12	8e	0.32	0/3433	0.49	1/4646 (0.0%)
12	8g	0.28	0/3453	0.45	0/4673
12	9a	0.32	0/3433	0.51	2/4646 (0.0%)
12	9c	0.27	0/3453	0.44	0/4673
12	9e	0.32	0/3433	0.50	2/4646 (0.0%)
12	9g	0.28	0/3453	0.44	0/4673
12	Aa	0.35	0/3433	0.51	1/4646 (0.0%)
12	Ac	0.29	0/3453	0.49	2/4673 (0.0%)
12	Ae	0.33	0/3433	0.49	2/4646 (0.0%)
12	Ag	0.27	0/3453	0.44	0/4673
12	Ba	0.34	0/3433	0.53	4/4646 (0.1%)
12	Bc	0.28	0/3453	0.44	0/4673
12	Be	0.34	0/3433	0.51	1/4646 (0.0%)
12	Bg	0.30	0/3453	0.46	0/4673
12	Ca	0.36	1/3433 (0.0%)	0.49	1/4646 (0.0%)
12	Cc	0.29	0/3453	0.45	0/4673
12	Ce	0.35	1/3433 (0.0%)	0.50	2/4646 (0.0%)
12	Cg	0.28	0/3453	0.46	0/4673
12	Da	0.35	1/3433 (0.0%)	0.51	3/4646 (0.1%)
12	Dc	0.28	0/3453	0.44	0/4673
12	De	0.31	0/3433	0.48	0/4646
12	Dg	0.28	0/3453	0.45	0/4673
13	1b	0.27	0/3410	0.43	0/4623
13	1d	0.27	0/3410	0.43	0/4623
13	1f	0.27	0/3410	0.43	0/4623
13	1h	0.27	0/3410	0.43	0/4623
13	2b	0.27	0/3410	0.43	0/4623
13	2d	0.27	0/3410	0.43	0/4623
13	2f	0.27	0/3410	0.43	0/4623
13	2h	0.27	0/3410	0.43	0/4623
13	3b	0.27	0/3410	0.43	0/4623
13	3d	0.27	0/3410	0.43	0/4623
13	3f	0.27	0/3410	0.43	0/4623
13	3h	0.27	0/3410	0.43	0/4623
13	4b	0.27	0/3410	0.43	0/4623
13	4d	0.27	0/3410	0.43	0/4623
13	4f	0.27	0/3410	0.43	0/4623
13	4h	0.27	0/3410	0.43	0/4623
13	5b	0.27	0/3410	0.43	0/4623
13	5d	0.27	0/3410	0.43	0/4623
13	5f	0.27	0/3410	0.43	0/4623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
13	5h	0.27	0/3410	0.43	0/4623
13	6b	0.27	0/3410	0.43	0/4623
13	6d	0.27	0/3410	0.43	0/4623
13	6f	0.27	0/3410	0.43	0/4623
13	6h	0.27	0/3410	0.43	0/4623
13	7b	0.27	0/3410	0.43	0/4623
13	7d	0.27	0/3410	0.43	0/4623
13	7f	0.27	0/3410	0.43	0/4623
13	7h	0.27	0/3410	0.43	0/4623
13	8b	0.27	0/3410	0.43	0/4623
13	8d	0.27	0/3410	0.43	0/4623
13	8f	0.27	0/3410	0.43	0/4623
13	8h	0.27	0/3410	0.43	0/4623
13	9b	0.27	0/3410	0.43	0/4623
13	9d	0.27	0/3410	0.43	0/4623
13	9f	0.27	0/3410	0.43	0/4623
13	9h	0.27	0/3410	0.43	0/4623
13	Ab	0.27	0/3410	0.43	0/4623
13	Ad	0.27	0/3410	0.43	0/4623
13	Af	0.27	0/3410	0.43	0/4623
13	Ah	0.27	0/3410	0.43	0/4623
13	Bb	0.27	0/3410	0.43	0/4623
13	Bd	0.27	0/3410	0.43	0/4623
13	Bf	0.27	0/3410	0.43	0/4623
13	Bh	0.27	0/3410	0.43	0/4623
13	Cb	0.27	0/3410	0.43	0/4623
13	Cd	0.27	0/3410	0.43	0/4623
13	Cf	0.27	0/3410	0.43	0/4623
13	Ch	0.27	0/3410	0.43	0/4623
13	Db	0.27	0/3410	0.43	0/4623
13	Dd	0.27	0/3410	0.43	0/4623
13	Df	0.27	0/3410	0.43	0/4623
13	Dh	0.27	0/3410	0.43	0/4623
14	2F	0.34	0/1257	0.58	1/1700 (0.1%)
14	2G	0.34	0/1257	0.58	1/1700 (0.1%)
24	2S	0.27	0/521	0.38	0/726
24	2T	0.42	1/886 (0.1%)	0.52	0/1193
24	2U	0.42	0/900	0.51	0/1213
24	2V	0.35	0/886	0.51	0/1193
28	3C	0.30	0/484	0.45	0/651
29	3E	0.50	1/682 (0.1%)	0.53	0/926
30	3F	0.43	3/3405 (0.1%)	0.56	7/4572 (0.2%)
30	3G	0.32	0/1911	0.51	4/2553 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	3H	0.29	0/1966	0.40	0/2686
31	3I	0.30	0/3146	0.50	4/4233 (0.1%)
32	3J	0.35	0/2849	0.54	1/3878 (0.0%)
32	3K	0.35	1/2824 (0.0%)	0.49	0/3845
33	3L	0.36	0/1597	0.50	0/2147
34	3M	0.32	0/3035	0.49	1/4097 (0.0%)
34	3N	0.30	0/3089	0.49	2/4173 (0.0%)
34	3O	0.32	0/2819	0.48	0/3798
34	3P	0.33	0/2841	0.49	0/3827
34	3Q	0.33	1/2819 (0.0%)	0.48	0/3798
34	3R	0.33	0/2860	0.47	0/3853
34	3S	0.31	0/3035	0.48	2/4097 (0.0%)
34	3T	0.33	0/3089	0.51	1/4173 (0.0%)
34	3U	0.36	2/2841 (0.1%)	0.48	0/3827
34	3V	0.32	0/3244	0.49	1/4381 (0.0%)
34	3W	0.31	0/3250	0.49	4/4389 (0.1%)
34	3X	0.31	0/2860	0.46	0/3853
34	3Y	0.32	0/2860	0.46	1/3853 (0.0%)
34	3Z	0.30	0/2860	0.48	1/3853 (0.0%)
34	4A	0.29	0/3244	0.50	2/4381 (0.0%)
34	4B	0.29	0/3250	0.54	3/4389 (0.1%)
35	4C	0.35	0/4954	0.61	4/6754 (0.1%)
36	4D	0.43	1/2424 (0.0%)	0.58	2/3278 (0.1%)
37	4E	0.96	52/7406 (0.7%)	0.98	70/10145 (0.7%)
37	4F	1.18	59/7235 (0.8%)	1.25	114/9923 (1.1%)
37	4G	1.65	66/7235 (0.9%)	1.33	121/9923 (1.2%)
37	4H	1.06	46/7235 (0.6%)	1.25	100/9923 (1.0%)
38	4I	2.05	17/501 (3.4%)	1.99	22/681 (3.2%)
38	4J	2.05	17/501 (3.4%)	1.99	22/681 (3.2%)
38	4K	2.05	17/501 (3.4%)	1.99	22/681 (3.2%)
38	4L	2.05	17/501 (3.4%)	1.99	22/681 (3.2%)
38	4M	2.05	17/501 (3.4%)	1.99	22/681 (3.2%)
38	4N	2.05	17/501 (3.4%)	1.99	22/681 (3.2%)
38	4O	0.47	0/639	0.75	2/876 (0.2%)
38	4P	0.35	0/433	0.55	0/589
39	4Q	0.29	0/1813	0.53	1/2442 (0.0%)
39	4R	0.29	0/1813	0.53	1/2442 (0.0%)
39	4S	0.29	0/1813	0.53	1/2442 (0.0%)
40	4T	0.30	0/4582	0.55	3/6245 (0.0%)
40	4U	0.30	0/4582	0.55	3/6245 (0.0%)
40	4V	0.30	0/4582	0.55	3/6245 (0.0%)
41	4W	0.29	0/595	0.54	0/816
41	4X	0.25	0/595	0.52	0/816

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
41	4Y	0.25	0/595	0.53	0/816
41	4Z	0.26	0/595	0.54	0/816
41	5A	1.59	11/590 (1.9%)	1.95	23/809 (2.8%)
41	5B	0.24	0/590	0.54	0/809
41	5C	0.25	0/590	0.54	0/809
41	5D	0.25	0/590	0.55	0/809
42	5E	0.32	0/1599	0.53	3/2187 (0.1%)
42	5F	0.32	0/1599	0.53	3/2187 (0.1%)
42	5G	0.32	0/1599	0.53	3/2187 (0.1%)
42	5H	3.32	53/1345 (3.9%)	2.44	74/1833 (4.0%)
43	5I	1.35	15/1631 (0.9%)	1.41	37/2219 (1.7%)
43	5J	1.35	15/1631 (0.9%)	1.41	37/2219 (1.7%)
43	5K	1.35	15/1631 (0.9%)	1.41	37/2219 (1.7%)
43	5L	1.35	15/1631 (0.9%)	1.41	37/2219 (1.7%)
44	5M	0.26	0/698	0.38	0/969
44	5N	0.26	0/698	0.38	0/969
44	5O	0.26	0/698	0.38	0/969
44	5P	0.32	0/1166	0.47	0/1563
44	5Q	0.32	0/1166	0.47	0/1563
44	5R	0.33	0/1166	0.48	1/1563 (0.1%)
44	5S	0.32	0/1157	0.48	0/1551
44	5T	0.33	0/1157	0.48	0/1551
44	5U	0.35	0/1157	0.52	2/1551 (0.1%)
44	5V	0.37	0/1178	0.49	0/1580
46	5Z	0.27	0/270	0.37	0/367
47	6A	0.37	0/12005	0.69	23/16230 (0.1%)
47	6B	0.37	0/12005	0.69	25/16230 (0.2%)
48	6E	0.29	0/7053	0.57	3/9607 (0.0%)
48	6F	0.29	0/7053	0.57	3/9607 (0.0%)
49	6G	0.34	0/3663	0.64	3/4941 (0.1%)
49	6H	0.34	0/3663	0.64	3/4941 (0.1%)
49	6I	0.34	0/3663	0.64	3/4941 (0.1%)
49	6J	0.34	0/3663	0.64	3/4941 (0.1%)
50	6K	0.31	0/4798	0.57	0/6478
50	6L	0.31	0/4798	0.57	0/6478
51	6M	0.30	0/8204	0.53	2/11178 (0.0%)
51	6N	0.30	0/8204	0.53	2/11178 (0.0%)
52	6O	0.29	0/33	0.78	0/44
52	6P	0.29	0/33	0.78	0/44
52	6Q	0.29	0/33	0.77	0/44
All	All	0.44	477/793581 (0.1%)	0.58	1040/1077552 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0B	0	1
1	0D	0	1
1	0F	0	1
1	0G	0	1
1	0I	0	1
1	0K	0	1
1	0M	0	1
1	0O	0	1
1	0Q	0	1
1	0S	0	1
1	0U	0	1
1	0V	0	1
1	0W	0	1
1	0Y	0	1
1	1A	0	1
1	1C	0	1
2	1D	0	4
2	1E	0	4
2	1F	0	4
2	1G	0	4
3	1H	0	3
3	1I	0	3
3	6D	0	2
4	1J	0	7
4	1K	0	7
5	1L	0	8
5	1M	0	8
6	1N	0	2
7	1O	0	8
8	1P	0	1
9	1Q	0	16
10	1R	0	4
10	1S	0	7
11	1T	0	2
12	1a	0	1
12	1e	0	1
12	2a	0	1
12	2e	0	1
12	3e	0	1
12	5e	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
12	6a	0	1
12	6e	0	1
12	7a	0	1
12	7e	0	1
12	8a	0	1
12	8e	0	1
12	9a	0	1
12	Aa	0	1
12	Be	0	1
12	Ce	0	1
12	Da	0	1
14	2F	0	2
14	2G	0	2
15	2H	0	10
16	2I	0	4
17	2J	0	7
17	2K	0	4
18	2L	0	7
20	2N	0	1
21	2O	0	3
22	2P	0	3
23	2R	0	1
24	2T	0	1
24	2U	0	1
24	2V	0	1
25	2W	0	3
25	2X	0	2
30	3F	0	2
31	3I	0	1
32	3J	0	3
32	3K	0	2
33	3L	0	2
35	4C	0	8
36	4D	0	1
37	4E	0	18
37	4F	0	20
37	4G	1	24
37	4H	0	25
38	4I	0	8
38	4J	0	8
38	4K	0	8
38	4L	0	8

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Mol	Chain	#Chirality outliers	#Planarity outliers
38	4M	0	8
38	4N	0	8
38	4O	0	4
38	4P	0	1
40	4T	0	8
40	4U	0	8
40	4V	0	8
41	4X	0	1
41	4Y	0	1
41	4Z	0	1
41	5A	0	7
41	5B	0	1
41	5C	0	1
41	5D	0	1
42	5H	0	13
43	5I	0	5
43	5J	0	5
43	5K	0	5
43	5L	0	5
44	5V	0	1
45	5W	0	2
45	5X	0	2
45	5Y	0	2
46	5Z	0	2
47	6A	0	12
47	6B	0	12
48	6E	0	6
48	6F	0	6
49	6G	0	1
49	6H	0	1
49	6I	0	1
49	6J	0	1
50	6K	0	5
50	6L	0	5
51	6M	0	6
51	6N	0	6
52	6O	0	4
52	6P	0	4
52	6Q	0	4
All	All	1	491

The worst 5 of 477 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	4G	690	CYS	CB-SG	84.81	3.26	1.82
37	4G	854	TYR	CD2-CE2	60.16	2.29	1.39
42	5H	137	TYR	CB-CG	58.22	2.38	1.51
42	5H	135	ARG	CB-CG	55.04	3.01	1.52
42	5H	135	ARG	CG-CD	43.96	2.61	1.51

The worst 5 of 1040 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	5H	135	ARG	NE-CZ-NH1	-39.92	100.34	120.30
37	4G	854	TYR	CD1-CE1-CZ	29.02	145.92	119.80
37	4H	1144	LEU	CB-CG-CD2	-29.02	61.67	111.00
42	5H	134	LEU	CB-CG-CD1	-28.89	61.89	111.00
37	4H	1333	VAL	CA-CB-CG1	-28.06	68.80	110.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
37	4G	793	THR	CB

5 of 491 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0B	94	GLU	Peptide
1	0D	94	GLU	Peptide
1	0F	94	GLU	Peptide
1	0G	94	GLU	Peptide
1	0M	94	GLU	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0A	497/512 (97%)	486 (98%)	10 (2%)	1 (0%)	44	73
1	0B	497/512 (97%)	485 (98%)	10 (2%)	2 (0%)	30	63
1	0C	497/512 (97%)	488 (98%)	8 (2%)	1 (0%)	44	73
1	0D	497/512 (97%)	486 (98%)	10 (2%)	1 (0%)	44	73
1	0E	497/512 (97%)	486 (98%)	10 (2%)	1 (0%)	44	73
1	0F	497/512 (97%)	484 (97%)	12 (2%)	1 (0%)	44	73
1	0G	497/512 (97%)	484 (97%)	11 (2%)	2 (0%)	30	63
1	0H	497/512 (97%)	484 (97%)	12 (2%)	1 (0%)	44	73
1	0I	497/512 (97%)	486 (98%)	10 (2%)	1 (0%)	44	73
1	0J	497/512 (97%)	489 (98%)	8 (2%)	0	100	100
1	0K	497/512 (97%)	492 (99%)	5 (1%)	0	100	100
1	0L	497/512 (97%)	487 (98%)	9 (2%)	1 (0%)	44	73
1	0M	497/512 (97%)	485 (98%)	10 (2%)	2 (0%)	30	63
1	0N	497/512 (97%)	487 (98%)	9 (2%)	1 (0%)	44	73
1	0O	497/512 (97%)	488 (98%)	8 (2%)	1 (0%)	44	73
1	0P	497/512 (97%)	484 (97%)	12 (2%)	1 (0%)	44	73
1	0Q	497/512 (97%)	486 (98%)	10 (2%)	1 (0%)	44	73
1	0R	497/512 (97%)	486 (98%)	10 (2%)	1 (0%)	44	73
1	0S	497/512 (97%)	485 (98%)	11 (2%)	1 (0%)	44	73
1	0T	497/512 (97%)	488 (98%)	8 (2%)	1 (0%)	44	73
1	0U	497/512 (97%)	487 (98%)	9 (2%)	1 (0%)	44	73
1	0V	497/512 (97%)	487 (98%)	9 (2%)	1 (0%)	44	73
1	0W	497/512 (97%)	485 (98%)	10 (2%)	2 (0%)	30	63
1	0X	497/512 (97%)	487 (98%)	9 (2%)	1 (0%)	44	73
1	0Y	497/512 (97%)	484 (97%)	11 (2%)	2 (0%)	30	63
1	0Z	497/512 (97%)	488 (98%)	8 (2%)	1 (0%)	44	73
1	1A	497/512 (97%)	487 (98%)	9 (2%)	1 (0%)	44	73
1	1B	497/512 (97%)	488 (98%)	9 (2%)	0	100	100
1	1C	497/512 (97%)	491 (99%)	6 (1%)	0	100	100
2	1D	500/571 (88%)	453 (91%)	39 (8%)	8 (2%)	8	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	1E	500/571 (88%)	454 (91%)	37 (7%)	9 (2%)	7	35
2	1F	512/571 (90%)	464 (91%)	43 (8%)	5 (1%)	13	46
2	1G	512/571 (90%)	464 (91%)	41 (8%)	7 (1%)	9	40
3	1H	791/1102 (72%)	764 (97%)	22 (3%)	5 (1%)	22	55
3	1I	791/1102 (72%)	769 (97%)	18 (2%)	4 (0%)	25	59
3	6D	787/1102 (71%)	766 (97%)	18 (2%)	3 (0%)	30	63
4	1J	392/3965 (10%)	344 (88%)	39 (10%)	9 (2%)	5	31
4	1K	392/3965 (10%)	344 (88%)	39 (10%)	9 (2%)	5	31
5	1L	540/2939 (18%)	476 (88%)	61 (11%)	3 (1%)	22	55
5	1M	540/2939 (18%)	476 (88%)	61 (11%)	3 (1%)	22	55
6	1N	2132/2784 (77%)	2080 (98%)	51 (2%)	1 (0%)	100	100
7	1O	2594/3225 (80%)	2506 (97%)	84 (3%)	4 (0%)	44	73
8	1P	291/1023 (28%)	274 (94%)	15 (5%)	2 (1%)	19	53
9	1Q	423/945 (45%)	336 (79%)	59 (14%)	28 (7%)	1	12
10	1R	351/446 (79%)	326 (93%)	21 (6%)	4 (1%)	12	45
10	1S	260/446 (58%)	237 (91%)	17 (6%)	6 (2%)	5	31
11	1T	952/1638 (58%)	942 (99%)	8 (1%)	2 (0%)	44	73
12	1a	426/443 (96%)	410 (96%)	16 (4%)	0	100	100
12	1c	429/443 (97%)	408 (95%)	21 (5%)	0	100	100
12	1e	426/443 (96%)	411 (96%)	15 (4%)	0	100	100
12	1g	429/443 (97%)	406 (95%)	23 (5%)	0	100	100
12	2a	426/443 (96%)	410 (96%)	16 (4%)	0	100	100
12	2c	429/443 (97%)	407 (95%)	22 (5%)	0	100	100
12	2e	426/443 (96%)	412 (97%)	14 (3%)	0	100	100
12	2g	429/443 (97%)	407 (95%)	22 (5%)	0	100	100
12	3a	426/443 (96%)	411 (96%)	15 (4%)	0	100	100
12	3c	429/443 (97%)	406 (95%)	23 (5%)	0	100	100
12	3e	426/443 (96%)	411 (96%)	15 (4%)	0	100	100
12	3g	429/443 (97%)	406 (95%)	23 (5%)	0	100	100
12	4a	426/443 (96%)	408 (96%)	18 (4%)	0	100	100
12	4c	429/443 (97%)	403 (94%)	26 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	4e	426/443 (96%)	410 (96%)	16 (4%)	0	100	100
12	4g	429/443 (97%)	406 (95%)	23 (5%)	0	100	100
12	5a	426/443 (96%)	409 (96%)	17 (4%)	0	100	100
12	5c	429/443 (97%)	404 (94%)	25 (6%)	0	100	100
12	5e	426/443 (96%)	411 (96%)	15 (4%)	0	100	100
12	5g	429/443 (97%)	403 (94%)	26 (6%)	0	100	100
12	6a	426/443 (96%)	408 (96%)	18 (4%)	0	100	100
12	6c	429/443 (97%)	404 (94%)	25 (6%)	0	100	100
12	6e	426/443 (96%)	408 (96%)	18 (4%)	0	100	100
12	6g	429/443 (97%)	405 (94%)	24 (6%)	0	100	100
12	7a	426/443 (96%)	410 (96%)	16 (4%)	0	100	100
12	7c	429/443 (97%)	403 (94%)	26 (6%)	0	100	100
12	7e	426/443 (96%)	405 (95%)	21 (5%)	0	100	100
12	7g	429/443 (97%)	403 (94%)	26 (6%)	0	100	100
12	8a	426/443 (96%)	408 (96%)	18 (4%)	0	100	100
12	8c	429/443 (97%)	405 (94%)	24 (6%)	0	100	100
12	8e	426/443 (96%)	410 (96%)	16 (4%)	0	100	100
12	8g	429/443 (97%)	408 (95%)	21 (5%)	0	100	100
12	9a	426/443 (96%)	407 (96%)	19 (4%)	0	100	100
12	9c	429/443 (97%)	404 (94%)	25 (6%)	0	100	100
12	9e	426/443 (96%)	408 (96%)	18 (4%)	0	100	100
12	9g	429/443 (97%)	407 (95%)	22 (5%)	0	100	100
12	Aa	426/443 (96%)	412 (97%)	14 (3%)	0	100	100
12	Ac	429/443 (97%)	405 (94%)	24 (6%)	0	100	100
12	Ae	426/443 (96%)	413 (97%)	13 (3%)	0	100	100
12	Ag	429/443 (97%)	408 (95%)	21 (5%)	0	100	100
12	Ba	426/443 (96%)	408 (96%)	18 (4%)	0	100	100
12	Bc	429/443 (97%)	407 (95%)	22 (5%)	0	100	100
12	Be	426/443 (96%)	407 (96%)	19 (4%)	0	100	100
12	Bg	429/443 (97%)	403 (94%)	26 (6%)	0	100	100
12	Ca	426/443 (96%)	414 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	Cc	429/443 (97%)	406 (95%)	23 (5%)	0	100	100
12	Ce	426/443 (96%)	408 (96%)	18 (4%)	0	100	100
12	Cg	429/443 (97%)	410 (96%)	19 (4%)	0	100	100
12	Da	426/443 (96%)	412 (97%)	14 (3%)	0	100	100
12	Dc	429/443 (97%)	407 (95%)	22 (5%)	0	100	100
12	De	426/443 (96%)	409 (96%)	17 (4%)	0	100	100
12	Dg	429/443 (97%)	404 (94%)	25 (6%)	0	100	100
13	1b	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	1d	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	1f	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	1h	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	2b	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	2d	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	2f	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	2h	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	3b	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	3d	426/451 (94%)	410 (96%)	16 (4%)	0	100	100
13	3f	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	3h	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	4b	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	4d	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	4f	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	4h	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	5b	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	5d	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	5f	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	5h	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	6b	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	6d	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	6f	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	6h	426/451 (94%)	409 (96%)	17 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	7b	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	7d	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	7f	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	7h	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	8b	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	8d	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	8f	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	8h	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	9b	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	9d	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	9f	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	9h	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Ab	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Ad	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Af	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Ah	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Bb	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Bd	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Bf	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Bh	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Cb	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Cd	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Cf	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Ch	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Db	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Dd	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Df	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
13	Dh	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
14	2F	159/168 (95%)	144 (91%)	14 (9%)	1 (1%)	22	55
14	2G	159/168 (95%)	144 (91%)	14 (9%)	1 (1%)	22	55
24	2S	103/447 (23%)	100 (97%)	2 (2%)	1 (1%)	13	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	2T	107/447 (24%)	104 (97%)	3 (3%)	0	100	100
24	2U	109/447 (24%)	100 (92%)	9 (8%)	0	100	100
24	2V	107/447 (24%)	103 (96%)	4 (4%)	0	100	100
28	3C	59/739 (8%)	59 (100%)	0	0	100	100
29	3E	85/1471 (6%)	79 (93%)	6 (7%)	0	100	100
30	3F	440/795 (55%)	426 (97%)	11 (2%)	3 (1%)	19	53
30	3G	236/795 (30%)	231 (98%)	5 (2%)	0	100	100
31	3H	304/1940 (16%)	304 (100%)	0	0	100	100
31	3I	399/1940 (21%)	393 (98%)	6 (2%)	0	100	100
32	3J	366/749 (49%)	349 (95%)	17 (5%)	0	100	100
32	3K	361/749 (48%)	345 (96%)	15 (4%)	1 (0%)	37	67
33	3L	193/401 (48%)	184 (95%)	7 (4%)	2 (1%)	13	46
34	3M	381/507 (75%)	369 (97%)	12 (3%)	0	100	100
34	3N	386/507 (76%)	379 (98%)	7 (2%)	0	100	100
34	3O	349/507 (69%)	342 (98%)	7 (2%)	0	100	100
34	3P	351/507 (69%)	347 (99%)	4 (1%)	0	100	100
34	3Q	349/507 (69%)	344 (99%)	5 (1%)	0	100	100
34	3R	354/507 (70%)	351 (99%)	3 (1%)	0	100	100
34	3S	381/507 (75%)	371 (97%)	10 (3%)	0	100	100
34	3T	386/507 (76%)	378 (98%)	8 (2%)	0	100	100
34	3U	351/507 (69%)	348 (99%)	3 (1%)	0	100	100
34	3V	404/507 (80%)	397 (98%)	6 (2%)	1 (0%)	44	73
34	3W	405/507 (80%)	399 (98%)	6 (2%)	0	100	100
34	3X	354/507 (70%)	349 (99%)	5 (1%)	0	100	100
34	3Y	354/507 (70%)	352 (99%)	2 (1%)	0	100	100
34	3Z	354/507 (70%)	349 (99%)	5 (1%)	0	100	100
34	4A	404/507 (80%)	396 (98%)	7 (2%)	1 (0%)	44	73
34	4B	405/507 (80%)	401 (99%)	4 (1%)	0	100	100
35	4C	618/2215 (28%)	585 (95%)	29 (5%)	4 (1%)	22	55
36	4D	293/304 (96%)	285 (97%)	6 (2%)	2 (1%)	19	53
37	4E	961/2301 (42%)	923 (96%)	28 (3%)	10 (1%)	13	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	4F	943/2301 (41%)	874 (93%)	49 (5%)	20 (2%)	5	33
37	4G	943/2301 (41%)	872 (92%)	57 (6%)	14 (2%)	8	39
37	4H	943/2301 (41%)	881 (93%)	47 (5%)	15 (2%)	8	38
38	4I	62/110 (56%)	41 (66%)	16 (26%)	5 (8%)	1	8
38	4J	62/110 (56%)	41 (66%)	16 (26%)	5 (8%)	1	8
38	4K	62/110 (56%)	41 (66%)	16 (26%)	5 (8%)	1	8
38	4L	62/110 (56%)	41 (66%)	16 (26%)	5 (8%)	1	8
38	4M	62/110 (56%)	41 (66%)	16 (26%)	5 (8%)	1	8
38	4N	62/110 (56%)	41 (66%)	16 (26%)	5 (8%)	1	8
38	4O	82/110 (74%)	71 (87%)	9 (11%)	2 (2%)	5	30
38	4P	53/110 (48%)	49 (92%)	3 (6%)	1 (2%)	6	35
39	4Q	214/427 (50%)	207 (97%)	5 (2%)	2 (1%)	14	48
39	4R	214/427 (50%)	207 (97%)	5 (2%)	2 (1%)	14	48
39	4S	214/427 (50%)	207 (97%)	5 (2%)	2 (1%)	14	48
40	4T	588/835 (70%)	544 (92%)	31 (5%)	13 (2%)	5	32
40	4U	588/835 (70%)	544 (92%)	31 (5%)	13 (2%)	5	32
40	4V	588/835 (70%)	544 (92%)	31 (5%)	13 (2%)	5	32
41	4W	120/173 (69%)	118 (98%)	2 (2%)	0	100	100
41	4X	120/173 (69%)	108 (90%)	12 (10%)	0	100	100
41	4Y	120/173 (69%)	107 (89%)	13 (11%)	0	100	100
41	4Z	120/173 (69%)	107 (89%)	13 (11%)	0	100	100
41	5A	119/173 (69%)	101 (85%)	12 (10%)	6 (5%)	1	17
41	5B	119/173 (69%)	106 (89%)	12 (10%)	1 (1%)	16	51
41	5C	119/173 (69%)	106 (89%)	12 (10%)	1 (1%)	16	51
41	5D	119/173 (69%)	106 (89%)	12 (10%)	1 (1%)	16	51
42	5E	212/286 (74%)	210 (99%)	2 (1%)	0	100	100
42	5F	212/286 (74%)	210 (99%)	2 (1%)	0	100	100
42	5G	212/286 (74%)	210 (99%)	2 (1%)	0	100	100
42	5H	163/286 (57%)	139 (85%)	16 (10%)	8 (5%)	2	17
43	5I	207/306 (68%)	179 (86%)	23 (11%)	5 (2%)	5	30
43	5J	207/306 (68%)	179 (86%)	23 (11%)	5 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	5K	207/306 (68%)	179 (86%)	23 (11%)	5 (2%)	5	30
43	5L	207/306 (68%)	179 (86%)	23 (11%)	5 (2%)	5	30
44	5M	140/163 (86%)	137 (98%)	3 (2%)	0	100	100
44	5N	140/163 (86%)	137 (98%)	3 (2%)	0	100	100
44	5O	140/163 (86%)	137 (98%)	3 (2%)	0	100	100
44	5P	144/163 (88%)	139 (96%)	5 (4%)	0	100	100
44	5Q	144/163 (88%)	139 (96%)	5 (4%)	0	100	100
44	5R	144/163 (88%)	140 (97%)	4 (3%)	0	100	100
44	5S	143/163 (88%)	141 (99%)	2 (1%)	0	100	100
44	5T	143/163 (88%)	142 (99%)	1 (1%)	0	100	100
44	5U	143/163 (88%)	141 (99%)	2 (1%)	0	100	100
44	5V	147/163 (90%)	143 (97%)	3 (2%)	1 (1%)	19	53
46	5Z	39/181 (22%)	39 (100%)	0	0	100	100
47	6A	1536/1929 (80%)	1453 (95%)	64 (4%)	19 (1%)	11	43
47	6B	1536/1929 (80%)	1453 (95%)	64 (4%)	19 (1%)	11	43
48	6E	894/1138 (79%)	839 (94%)	52 (6%)	3 (0%)	37	67
48	6F	894/1138 (79%)	839 (94%)	52 (6%)	3 (0%)	37	67
49	6G	474/477 (99%)	456 (96%)	17 (4%)	1 (0%)	44	73
49	6H	474/477 (99%)	456 (96%)	17 (4%)	1 (0%)	44	73
49	6I	474/477 (99%)	456 (96%)	17 (4%)	1 (0%)	44	73
49	6J	474/477 (99%)	456 (96%)	17 (4%)	1 (0%)	44	73
50	6K	605/651 (93%)	580 (96%)	21 (4%)	4 (1%)	19	53
50	6L	605/651 (93%)	580 (96%)	21 (4%)	4 (1%)	19	53
51	6M	1059/2540 (42%)	1011 (96%)	40 (4%)	8 (1%)	16	51
51	6N	1059/2540 (42%)	1011 (96%)	40 (4%)	8 (1%)	16	51
52	6O	7/89 (8%)	6 (86%)	1 (14%)	0	100	100
52	6P	7/89 (8%)	6 (86%)	1 (14%)	0	100	100
52	6Q	7/89 (8%)	6 (86%)	1 (14%)	0	100	100
All	All	102979/147699 (70%)	98412 (96%)	4161 (4%)	406 (0%)	32	63

5 of 406 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1D	61	VAL
2	1D	265	GLU
2	1D	427	GLU
2	1E	61	VAL
2	1E	265	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0A	333/408 (82%)	333 (100%)	0	100	100
1	0B	333/408 (82%)	333 (100%)	0	100	100
1	0C	333/408 (82%)	333 (100%)	0	100	100
1	0D	333/408 (82%)	333 (100%)	0	100	100
1	0E	333/408 (82%)	333 (100%)	0	100	100
1	0F	333/408 (82%)	333 (100%)	0	100	100
1	0G	333/408 (82%)	333 (100%)	0	100	100
1	0H	333/408 (82%)	333 (100%)	0	100	100
1	0I	333/408 (82%)	332 (100%)	1 (0%)	91	96
1	0J	333/408 (82%)	332 (100%)	1 (0%)	91	96
1	0K	332/408 (81%)	332 (100%)	0	100	100
1	0L	333/408 (82%)	333 (100%)	0	100	100
1	0M	333/408 (82%)	333 (100%)	0	100	100
1	0N	333/408 (82%)	333 (100%)	0	100	100
1	0O	333/408 (82%)	333 (100%)	0	100	100
1	0P	333/408 (82%)	333 (100%)	0	100	100
1	0Q	333/408 (82%)	331 (99%)	2 (1%)	84	92
1	0R	332/408 (81%)	332 (100%)	0	100	100
1	0S	333/408 (82%)	333 (100%)	0	100	100
1	0T	333/408 (82%)	333 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0U	333/408 (82%)	333 (100%)	0	100	100
1	0V	333/408 (82%)	333 (100%)	0	100	100
1	0W	333/408 (82%)	333 (100%)	0	100	100
1	0X	333/408 (82%)	333 (100%)	0	100	100
1	0Y	333/408 (82%)	333 (100%)	0	100	100
1	0Z	333/408 (82%)	333 (100%)	0	100	100
1	1A	333/408 (82%)	333 (100%)	0	100	100
1	1B	333/408 (82%)	332 (100%)	1 (0%)	91	96
1	1C	332/408 (81%)	332 (100%)	0	100	100
2	1D	256/415 (62%)	255 (100%)	1 (0%)	89	95
2	1E	256/415 (62%)	255 (100%)	1 (0%)	89	95
2	1F	263/415 (63%)	263 (100%)	0	100	100
2	1G	263/415 (63%)	263 (100%)	0	100	100
3	1H	547/811 (67%)	547 (100%)	0	100	100
3	1I	547/811 (67%)	547 (100%)	0	100	100
3	6D	620/811 (76%)	620 (100%)	0	100	100
4	1J	278/3239 (9%)	275 (99%)	3 (1%)	70	83
4	1K	278/3239 (9%)	276 (99%)	2 (1%)	81	90
5	1L	201/2456 (8%)	196 (98%)	5 (2%)	42	66
5	1M	201/2456 (8%)	196 (98%)	5 (2%)	42	66
6	1N	1553/1962 (79%)	1552 (100%)	1 (0%)	92	97
7	1O	1932/2270 (85%)	1932 (100%)	0	100	100
8	1P	236/790 (30%)	236 (100%)	0	100	100
9	1Q	55/728 (8%)	55 (100%)	0	100	100
10	1R	295/353 (84%)	294 (100%)	1 (0%)	91	96
10	1S	195/353 (55%)	195 (100%)	0	100	100
11	1T	1/1185 (0%)	1 (100%)	0	100	100
12	1a	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	1c	370/379 (98%)	370 (100%)	0	100	100
12	1e	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	1g	370/379 (98%)	370 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	2a	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	2c	370/379 (98%)	370 (100%)	0	100	100
12	2e	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	2g	370/379 (98%)	370 (100%)	0	100	100
12	3a	368/379 (97%)	368 (100%)	0	100	100
12	3c	370/379 (98%)	370 (100%)	0	100	100
12	3e	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	3g	370/379 (98%)	370 (100%)	0	100	100
12	4a	368/379 (97%)	366 (100%)	2 (0%)	86	93
12	4c	370/379 (98%)	370 (100%)	0	100	100
12	4e	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	4g	370/379 (98%)	370 (100%)	0	100	100
12	5a	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	5c	370/379 (98%)	370 (100%)	0	100	100
12	5e	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	5g	370/379 (98%)	370 (100%)	0	100	100
12	6a	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	6c	370/379 (98%)	370 (100%)	0	100	100
12	6e	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	6g	370/379 (98%)	370 (100%)	0	100	100
12	7a	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	7c	370/379 (98%)	370 (100%)	0	100	100
12	7e	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	7g	370/379 (98%)	370 (100%)	0	100	100
12	8a	368/379 (97%)	366 (100%)	2 (0%)	86	93
12	8c	370/379 (98%)	370 (100%)	0	100	100
12	8e	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	8g	370/379 (98%)	370 (100%)	0	100	100
12	9a	368/379 (97%)	366 (100%)	2 (0%)	86	93
12	9c	370/379 (98%)	370 (100%)	0	100	100
12	9e	368/379 (97%)	366 (100%)	2 (0%)	86	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	9g	370/379 (98%)	370 (100%)	0	100	100
12	Aa	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	Ac	370/379 (98%)	370 (100%)	0	100	100
12	Ae	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	Ag	370/379 (98%)	370 (100%)	0	100	100
12	Ba	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	Bc	370/379 (98%)	370 (100%)	0	100	100
12	Be	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	Bg	370/379 (98%)	370 (100%)	0	100	100
12	Ca	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	Cc	370/379 (98%)	370 (100%)	0	100	100
12	Ce	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	Cg	370/379 (98%)	370 (100%)	0	100	100
12	Da	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	Dc	370/379 (98%)	370 (100%)	0	100	100
12	De	368/379 (97%)	367 (100%)	1 (0%)	91	96
12	Dg	370/379 (98%)	370 (100%)	0	100	100
13	1b	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	1d	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	1f	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	1h	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	2b	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	2d	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	2f	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	2h	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	3b	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	3d	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	3f	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	3h	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	4b	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	4d	361/374 (96%)	344 (95%)	17 (5%)	22	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	4f	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	4h	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	5b	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	5d	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	5f	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	5h	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	6b	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	6d	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	6f	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	6h	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	7b	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	7d	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	7f	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	7h	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	8b	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	8d	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	8f	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	8h	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	9b	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	9d	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	9f	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	9h	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	Ab	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Ad	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Af	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Ah	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Bb	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Bd	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Bf	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Bh	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	Cb	361/374 (96%)	345 (96%)	16 (4%)	24	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	Cd	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	Cf	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Ch	361/374 (96%)	344 (95%)	17 (5%)	22	51
13	Db	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Dd	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Df	361/374 (96%)	345 (96%)	16 (4%)	24	53
13	Dh	361/374 (96%)	344 (95%)	17 (5%)	22	51
14	2F	115/119 (97%)	112 (97%)	3 (3%)	41	65
14	2G	115/119 (97%)	112 (97%)	3 (3%)	41	65
24	2T	85/313 (27%)	84 (99%)	1 (1%)	67	82
24	2U	87/313 (28%)	86 (99%)	1 (1%)	70	83
24	2V	85/313 (27%)	85 (100%)	0	100	100
28	3C	45/580 (8%)	45 (100%)	0	100	100
29	3E	59/1095 (5%)	59 (100%)	0	100	100
30	3F	303/642 (47%)	301 (99%)	2 (1%)	81	90
30	3G	187/642 (29%)	187 (100%)	0	100	100
31	3H	114/1457 (8%)	114 (100%)	0	100	100
31	3I	301/1457 (21%)	301 (100%)	0	100	100
32	3J	286/576 (50%)	286 (100%)	0	100	100
32	3K	285/576 (50%)	285 (100%)	0	100	100
33	3L	165/318 (52%)	165 (100%)	0	100	100
34	3M	291/386 (75%)	289 (99%)	2 (1%)	81	90
34	3N	302/386 (78%)	302 (100%)	0	100	100
34	3O	275/386 (71%)	275 (100%)	0	100	100
34	3P	276/386 (72%)	276 (100%)	0	100	100
34	3Q	275/386 (71%)	275 (100%)	0	100	100
34	3R	278/386 (72%)	278 (100%)	0	100	100
34	3S	291/386 (75%)	290 (100%)	1 (0%)	91	96
34	3T	302/386 (78%)	302 (100%)	0	100	100
34	3U	276/386 (72%)	276 (100%)	0	100	100
34	3V	317/386 (82%)	317 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	3W	318/386 (82%)	318 (100%)	0	100	100
34	3X	278/386 (72%)	278 (100%)	0	100	100
34	3Y	278/386 (72%)	278 (100%)	0	100	100
34	3Z	278/386 (72%)	278 (100%)	0	100	100
34	4A	317/386 (82%)	317 (100%)	0	100	100
34	4B	318/386 (82%)	318 (100%)	0	100	100
35	4C	525/1698 (31%)	525 (100%)	0	100	100
36	4D	260/267 (97%)	259 (100%)	1 (0%)	89	95
37	4E	743/1694 (44%)	740 (100%)	3 (0%)	89	95
37	4F	722/1694 (43%)	715 (99%)	7 (1%)	73	85
37	4G	722/1694 (43%)	709 (98%)	13 (2%)	54	74
37	4H	722/1694 (43%)	711 (98%)	11 (2%)	60	78
38	4I	51/83 (61%)	42 (82%)	9 (18%)	1	9
38	4J	51/83 (61%)	42 (82%)	9 (18%)	1	9
38	4K	51/83 (61%)	42 (82%)	9 (18%)	1	9
38	4L	51/83 (61%)	42 (82%)	9 (18%)	1	9
38	4M	51/83 (61%)	42 (82%)	9 (18%)	1	9
38	4N	51/83 (61%)	42 (82%)	9 (18%)	1	9
38	4O	65/83 (78%)	65 (100%)	0	100	100
38	4P	44/83 (53%)	44 (100%)	0	100	100
39	4Q	178/330 (54%)	174 (98%)	4 (2%)	47	69
39	4R	178/330 (54%)	174 (98%)	4 (2%)	47	69
39	4S	178/330 (54%)	174 (98%)	4 (2%)	47	69
40	4T	464/605 (77%)	454 (98%)	10 (2%)	47	69
40	4U	464/605 (77%)	454 (98%)	10 (2%)	47	69
40	4V	464/605 (77%)	454 (98%)	10 (2%)	47	69
42	5E	132/215 (61%)	129 (98%)	3 (2%)	45	68
42	5F	132/215 (61%)	129 (98%)	3 (2%)	45	68
42	5G	132/215 (61%)	129 (98%)	3 (2%)	45	68
42	5H	132/215 (61%)	127 (96%)	5 (4%)	28	57
43	5I	155/247 (63%)	139 (90%)	16 (10%)	6	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	5J	155/247 (63%)	139 (90%)	16 (10%)	6	27
43	5K	155/247 (63%)	139 (90%)	16 (10%)	6	27
43	5L	155/247 (63%)	139 (90%)	16 (10%)	6	27
44	5P	125/137 (91%)	125 (100%)	0	100	100
44	5Q	125/137 (91%)	125 (100%)	0	100	100
44	5R	125/137 (91%)	125 (100%)	0	100	100
44	5S	124/137 (90%)	124 (100%)	0	100	100
44	5T	124/137 (90%)	124 (100%)	0	100	100
44	5U	124/137 (90%)	124 (100%)	0	100	100
44	5V	126/137 (92%)	126 (100%)	0	100	100
46	5Z	22/22 (100%)	22 (100%)	0	100	100
47	6A	1147/1408 (82%)	1124 (98%)	23 (2%)	50	72
47	6B	1147/1408 (82%)	1124 (98%)	23 (2%)	50	72
48	6E	710/864 (82%)	702 (99%)	8 (1%)	70	83
48	6F	710/864 (82%)	702 (99%)	8 (1%)	70	83
49	6G	383/384 (100%)	349 (91%)	34 (9%)	8	32
49	6H	383/384 (100%)	349 (91%)	34 (9%)	8	32
49	6I	383/384 (100%)	349 (91%)	34 (9%)	8	32
49	6J	383/384 (100%)	349 (91%)	34 (9%)	8	32
50	6K	511/533 (96%)	505 (99%)	6 (1%)	67	82
50	6L	511/533 (96%)	505 (99%)	6 (1%)	67	82
51	6M	827/1940 (43%)	820 (99%)	7 (1%)	79	88
51	6N	827/1940 (43%)	820 (99%)	7 (1%)	79	88
All	All	78493/114873 (68%)	77144 (98%)	1349 (2%)	56	75

5 of 1349 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	7h	165	SER
13	Bb	2	ARG
13	8b	327	ASP
13	7h	120	ASP
13	9d	308	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1246 such sidechains are listed below:

Mol	Chain	Res	Type
12	6c	256	ASN
12	Ce	245	GLN
13	7b	15	GLN
12	6c	247	ASN
12	9g	83	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

104 ligands 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	$\# Z > 2$
53	GDP	4e	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.00	1 (3%)
53	GDP	1c	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.02	2 (6%)
53	GDP	Cc	502	-	25,30,30	0.97	1 (4%)	30,47,47	1.06	2 (6%)
54	GTP	Af	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	3c	502	-	25,30,30	0.98	1 (4%)	30,47,47	1.02	2 (6%)
53	GDP	De	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.03	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	GTP	Bh	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	3d	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	2g	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.04	2 (6%)
53	GDP	7a	501	-	25,30,30	0.99	2 (8%)	30,47,47	1.03	2 (6%)
53	GDP	9c	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.01	2 (6%)
53	GDP	5g	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.02	2 (6%)
54	GTP	Ch	501	-	29,34,34	1.29	4 (13%)	35,54,54	1.25	4 (11%)
53	GDP	3a	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.04	2 (6%)
54	GTP	1f	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	1a	501	-	25,30,30	1.01	2 (8%)	30,47,47	1.02	2 (6%)
54	GTP	3f	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	8d	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.24	4 (11%)
54	GTP	Bb	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	7g	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.02	2 (6%)
53	GDP	6g	502	-	25,30,30	0.98	1 (4%)	30,47,47	1.01	2 (6%)
54	GTP	3h	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	5e	501	-	25,30,30	0.99	1 (4%)	30,47,47	0.99	2 (6%)
54	GTP	1d	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	5a	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.01	2 (6%)
53	GDP	Dc	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.03	2 (6%)
54	GTP	9f	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	1b	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.24	4 (11%)
54	GTP	Bd	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	Ca	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.03	2 (6%)
54	GTP	4f	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	6h	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	2d	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	8f	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	6e	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.24	4 (11%)
53	GDP	Dg	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.05	2 (6%)
54	GTP	7f	501	-	29,34,34	1.27	2 (6%)	35,54,54	1.24	4 (11%)
54	GTP	Ae	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.24	4 (11%)
54	GTP	Bf	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	5d	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.24	4 (11%)
54	GTP	3c	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	GTP	5h	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	Be	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.00	2 (6%)
53	GDP	7e	502	-	25,30,30	1.00	1 (4%)	30,47,47	1.00	2 (6%)
54	GTP	6g	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	2h	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.24	4 (11%)
53	GDP	Da	501	-	25,30,30	0.99	2 (8%)	30,47,47	1.06	2 (6%)
53	GDP	6a	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.01	1 (3%)
54	GTP	Ah	501	-	29,34,34	1.28	4 (13%)	35,54,54	1.24	4 (11%)
54	GTP	4d	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.24	4 (11%)
53	GDP	8c	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.04	2 (6%)
54	GTP	4h	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	Df	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	4b	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	8b	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	Bc	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.04	2 (6%)
54	GTP	5f	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.24	4 (11%)
54	GTP	6c	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	Dd	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	Ae	502	-	25,30,30	1.00	2 (8%)	30,47,47	1.02	2 (6%)
54	GTP	8h	501	-	29,34,34	1.28	4 (13%)	35,54,54	1.25	4 (11%)
53	GDP	4g	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.01	2 (6%)
53	GDP	8g	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.01	2 (6%)
53	GDP	9e	502	-	25,30,30	0.99	1 (4%)	30,47,47	1.00	2 (6%)
54	GTP	2f	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	Ac	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.02	2 (6%)
53	GDP	Cg	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.03	2 (6%)
53	GDP	2a	501	-	25,30,30	1.00	1 (4%)	30,47,47	0.99	2 (6%)
53	GDP	6c	502	-	25,30,30	0.98	1 (4%)	30,47,47	1.01	2 (6%)
53	GDP	6e	502	-	25,30,30	0.99	1 (4%)	30,47,47	0.98	2 (6%)
53	GDP	4c	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.01	2 (6%)
53	GDP	Aa	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.03	2 (6%)
53	GDP	7c	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.02	2 (6%)
53	GDP	4a	501	-	25,30,30	1.00	2 (8%)	30,47,47	0.98	2 (6%)
53	GDP	8e	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.00	2 (6%)
54	GTP	9e	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.25	4 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	GTP	7b	501	-	29,34,34	1.29	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	Ag	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.02	2 (6%)
53	GDP	5c	502	-	25,30,30	0.98	1 (4%)	30,47,47	1.01	2 (6%)
53	GDP	1g	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.03	2 (6%)
53	GDP	9a	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.00	2 (6%)
54	GTP	7e	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	Cd	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	Cf	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.24	4 (11%)
54	GTP	9b	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.24	4 (11%)
53	GDP	2e	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.02	1 (3%)
54	GTP	Dh	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	1e	501	-	25,30,30	0.99	2 (8%)	30,47,47	1.05	2 (6%)
53	GDP	2c	501	-	25,30,30	0.96	1 (4%)	30,47,47	1.05	2 (6%)
53	GDP	Bg	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.04	2 (6%)
53	GDP	Ba	501	-	25,30,30	0.99	1 (4%)	30,47,47	0.99	2 (6%)
53	GDP	8a	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.00	2 (6%)
53	GDP	9g	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.03	2 (6%)
54	GTP	Db	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.24	4 (11%)
53	GDP	3e	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.04	2 (6%)
53	GDP	Ce	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.03	2 (6%)
54	GTP	1h	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	2b	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	Cc	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	5c	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
53	GDP	3g	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.04	2 (6%)
54	GTP	7h	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	Ab	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.25	4 (11%)
54	GTP	9h	501	-	29,34,34	1.28	3 (10%)	35,54,54	1.25	4 (11%)

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
53	GDP	4e	501	-	-	3/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
53	GDP	1c	501	-	-	3/12/32/32	0/3/3/3
53	GDP	Cc	502	-	-	3/12/32/32	0/3/3/3
54	GTP	Af	501	-	-	2/18/38/38	0/3/3/3
53	GDP	3c	502	-	-	3/12/32/32	0/3/3/3
53	GDP	De	501	-	-	3/12/32/32	0/3/3/3
54	GTP	Bh	501	-	-	2/18/38/38	0/3/3/3
54	GTP	3d	501	-	-	2/18/38/38	0/3/3/3
53	GDP	2g	501	-	-	3/12/32/32	0/3/3/3
53	GDP	7a	501	-	-	3/12/32/32	0/3/3/3
53	GDP	9c	501	-	-	3/12/32/32	0/3/3/3
53	GDP	5g	501	-	-	3/12/32/32	0/3/3/3
54	GTP	Ch	501	-	-	2/18/38/38	0/3/3/3
53	GDP	3a	501	-	-	3/12/32/32	0/3/3/3
54	GTP	1f	501	-	-	2/18/38/38	0/3/3/3
53	GDP	1a	501	-	-	3/12/32/32	0/3/3/3
54	GTP	3f	501	-	-	2/18/38/38	0/3/3/3
54	GTP	8d	501	-	-	2/18/38/38	0/3/3/3
54	GTP	Bb	501	-	-	2/18/38/38	0/3/3/3
53	GDP	7g	501	-	-	3/12/32/32	0/3/3/3
53	GDP	6g	502	-	-	3/12/32/32	0/3/3/3
54	GTP	3h	501	-	-	2/18/38/38	0/3/3/3
53	GDP	5e	501	-	-	3/12/32/32	0/3/3/3
54	GTP	1d	501	-	-	2/18/38/38	0/3/3/3
53	GDP	5a	501	-	-	3/12/32/32	0/3/3/3
53	GDP	Dc	501	-	-	3/12/32/32	0/3/3/3
54	GTP	9f	501	-	-	2/18/38/38	0/3/3/3
54	GTP	1b	501	-	-	2/18/38/38	0/3/3/3
54	GTP	Bd	501	-	-	2/18/38/38	0/3/3/3
53	GDP	Ca	501	-	-	3/12/32/32	0/3/3/3
54	GTP	4f	501	-	-	2/18/38/38	0/3/3/3
54	GTP	6h	501	-	-	2/18/38/38	0/3/3/3
54	GTP	2d	501	-	-	2/18/38/38	0/3/3/3
54	GTP	8f	501	-	-	2/18/38/38	0/3/3/3
54	GTP	6e	501	-	-	2/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
53	GDP	Dg	501	-	-	3/12/32/32	0/3/3/3
54	GTP	7f	501	-	-	2/18/38/38	0/3/3/3
54	GTP	Ae	501	-	-	2/18/38/38	0/3/3/3
54	GTP	Bf	501	-	-	2/18/38/38	0/3/3/3
54	GTP	5d	501	-	-	2/18/38/38	0/3/3/3
54	GTP	3c	501	-	-	2/18/38/38	0/3/3/3
54	GTP	5h	501	-	-	2/18/38/38	0/3/3/3
53	GDP	Be	501	-	-	3/12/32/32	0/3/3/3
53	GDP	7e	502	-	-	3/12/32/32	0/3/3/3
54	GTP	6g	501	-	-	2/18/38/38	0/3/3/3
54	GTP	2h	501	-	-	2/18/38/38	0/3/3/3
53	GDP	Da	501	-	-	3/12/32/32	0/3/3/3
53	GDP	6a	501	-	-	3/12/32/32	0/3/3/3
54	GTP	Ah	501	-	-	2/18/38/38	0/3/3/3
54	GTP	4d	501	-	-	2/18/38/38	0/3/3/3
53	GDP	8c	501	-	-	3/12/32/32	0/3/3/3
54	GTP	4h	501	-	-	2/18/38/38	0/3/3/3
54	GTP	Df	501	-	-	2/18/38/38	0/3/3/3
54	GTP	4b	501	-	-	2/18/38/38	0/3/3/3
54	GTP	8b	501	-	-	2/18/38/38	0/3/3/3
53	GDP	Bc	501	-	-	3/12/32/32	0/3/3/3
54	GTP	5f	501	-	-	2/18/38/38	0/3/3/3
54	GTP	6c	501	-	-	2/18/38/38	0/3/3/3
54	GTP	Dd	501	-	-	2/18/38/38	0/3/3/3
53	GDP	Ae	502	-	-	3/12/32/32	0/3/3/3
54	GTP	8h	501	-	-	2/18/38/38	0/3/3/3
53	GDP	4g	501	-	-	3/12/32/32	0/3/3/3
53	GDP	8g	501	-	-	3/12/32/32	0/3/3/3
53	GDP	9e	502	-	-	3/12/32/32	0/3/3/3
54	GTP	2f	501	-	-	2/18/38/38	0/3/3/3
53	GDP	Ac	501	-	-	3/12/32/32	0/3/3/3
53	GDP	Cg	501	-	-	3/12/32/32	0/3/3/3
53	GDP	2a	501	-	-	3/12/32/32	0/3/3/3
53	GDP	6c	502	-	-	3/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
53	GDP	6e	502	-	-	3/12/32/32	0/3/3/3
53	GDP	4c	501	-	-	3/12/32/32	0/3/3/3
53	GDP	Aa	501	-	-	3/12/32/32	0/3/3/3
53	GDP	7c	501	-	-	3/12/32/32	0/3/3/3
53	GDP	4a	501	-	-	3/12/32/32	0/3/3/3
53	GDP	8e	501	-	-	3/12/32/32	0/3/3/3
54	GTP	9e	501	-	-	2/18/38/38	0/3/3/3
54	GTP	7b	501	-	-	2/18/38/38	0/3/3/3
53	GDP	Ag	501	-	-	3/12/32/32	0/3/3/3
53	GDP	5c	502	-	-	3/12/32/32	0/3/3/3
53	GDP	1g	501	-	-	3/12/32/32	0/3/3/3
53	GDP	9a	501	-	-	3/12/32/32	0/3/3/3
54	GTP	7e	501	-	-	2/18/38/38	0/3/3/3
54	GTP	Cd	501	-	-	2/18/38/38	0/3/3/3
54	GTP	Cf	501	-	-	2/18/38/38	0/3/3/3
54	GTP	9b	501	-	-	2/18/38/38	0/3/3/3
53	GDP	2e	501	-	-	3/12/32/32	0/3/3/3
54	GTP	Dh	501	-	-	2/18/38/38	0/3/3/3
53	GDP	1e	501	-	-	3/12/32/32	0/3/3/3
53	GDP	2c	501	-	-	3/12/32/32	0/3/3/3
53	GDP	Bg	501	-	-	3/12/32/32	0/3/3/3
53	GDP	Ba	501	-	-	3/12/32/32	0/3/3/3
53	GDP	8a	501	-	-	3/12/32/32	0/3/3/3
53	GDP	9g	501	-	-	3/12/32/32	0/3/3/3
54	GTP	Db	501	-	-	2/18/38/38	0/3/3/3
53	GDP	3e	501	-	-	3/12/32/32	0/3/3/3
53	GDP	Ce	501	-	-	3/12/32/32	0/3/3/3
54	GTP	1h	501	-	-	2/18/38/38	0/3/3/3
54	GTP	2b	501	-	-	2/18/38/38	0/3/3/3
54	GTP	Cc	501	-	-	2/18/38/38	0/3/3/3
54	GTP	5c	501	-	-	2/18/38/38	0/3/3/3
53	GDP	3g	501	-	-	3/12/32/32	0/3/3/3
54	GTP	7h	501	-	-	2/18/38/38	0/3/3/3
54	GTP	Ab	501	-	-	2/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	GTP	9h	501	-	-	2/18/38/38	0/3/3/3

The worst 5 of 218 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	6c	501	GTP	C5-C6	-4.20	1.39	1.47
54	Af	501	GTP	C5-C6	-4.19	1.39	1.47
54	7b	501	GTP	C5-C6	-4.19	1.39	1.47
54	8b	501	GTP	C5-C6	-4.19	1.39	1.47
54	7h	501	GTP	C5-C6	-4.19	1.39	1.47

The worst 5 of 308 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	9e	501	GTP	C8-N7-C5	3.67	108.81	102.55
54	6g	501	GTP	C8-N7-C5	3.67	108.80	102.55
54	Bh	501	GTP	C8-N7-C5	3.67	108.79	102.55
54	Ch	501	GTP	C8-N7-C5	3.66	108.79	102.55
54	3d	501	GTP	C8-N7-C5	3.66	108.78	102.55

There are no chirality outliers.

5 of 260 torsion outliers are listed below:

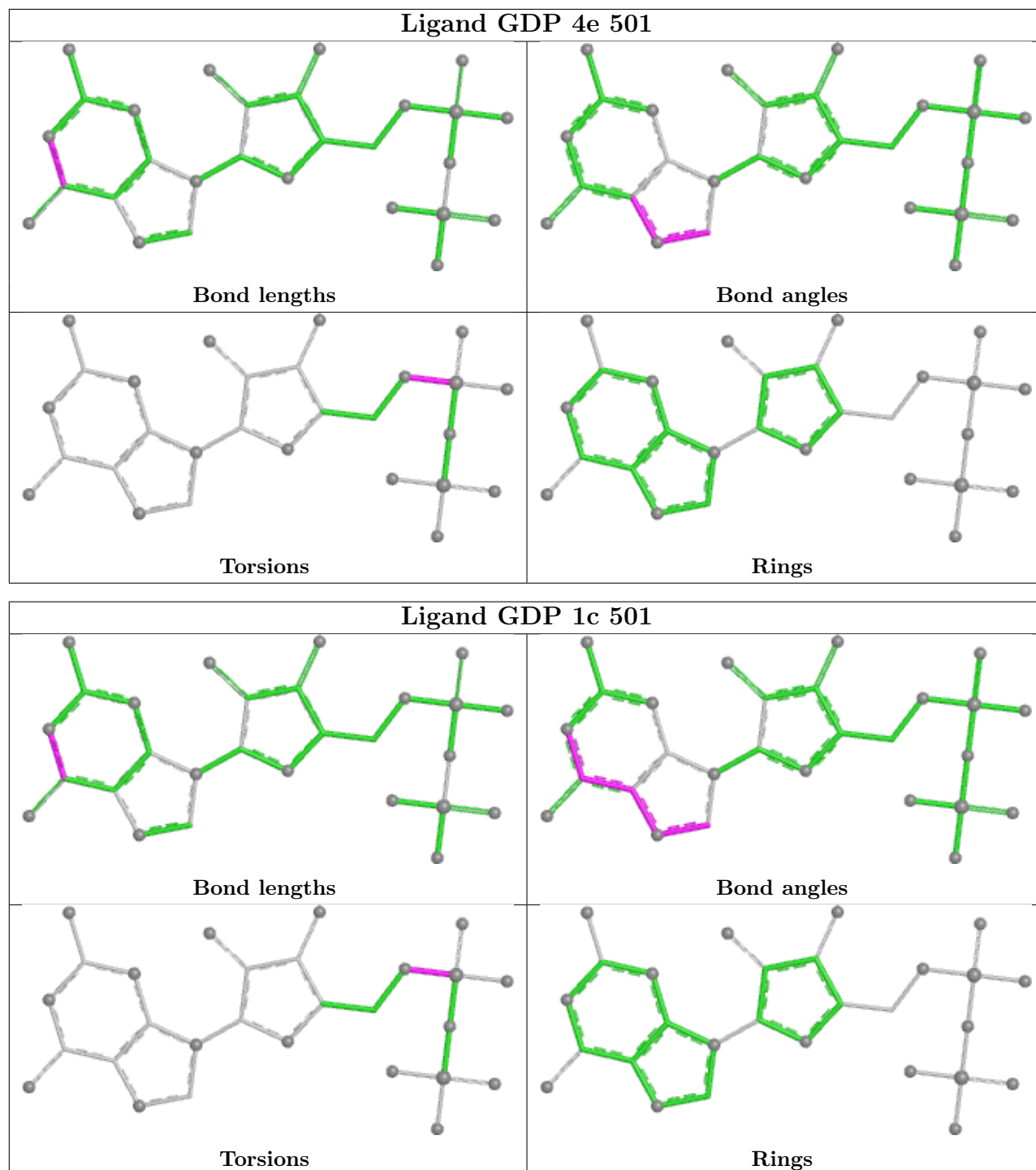
Mol	Chain	Res	Type	Atoms
53	1a	501	GDP	C5'-O5'-PA-O3A
53	1a	501	GDP	C5'-O5'-PA-O1A
53	1a	501	GDP	C5'-O5'-PA-O2A
53	1c	501	GDP	C5'-O5'-PA-O3A
53	1c	501	GDP	C5'-O5'-PA-O1A

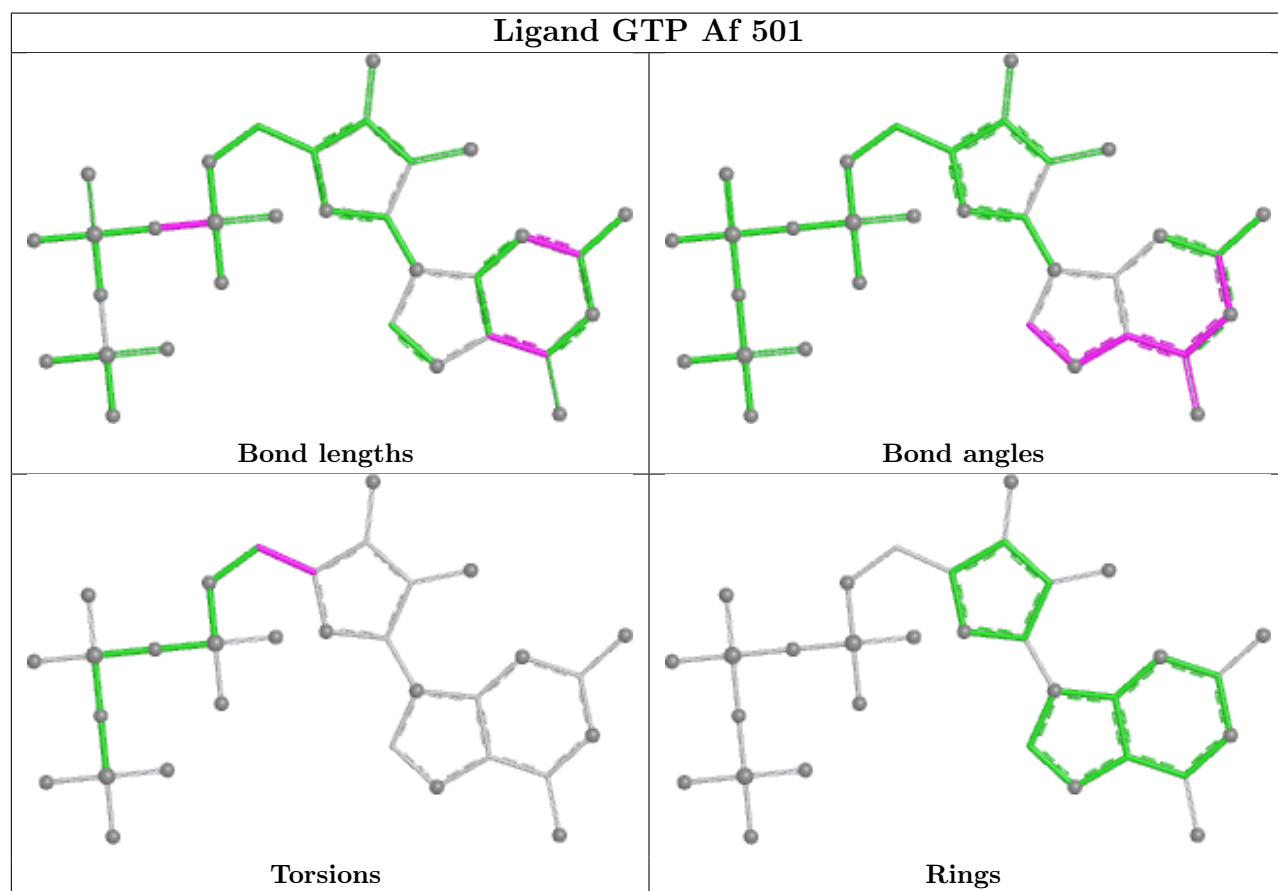
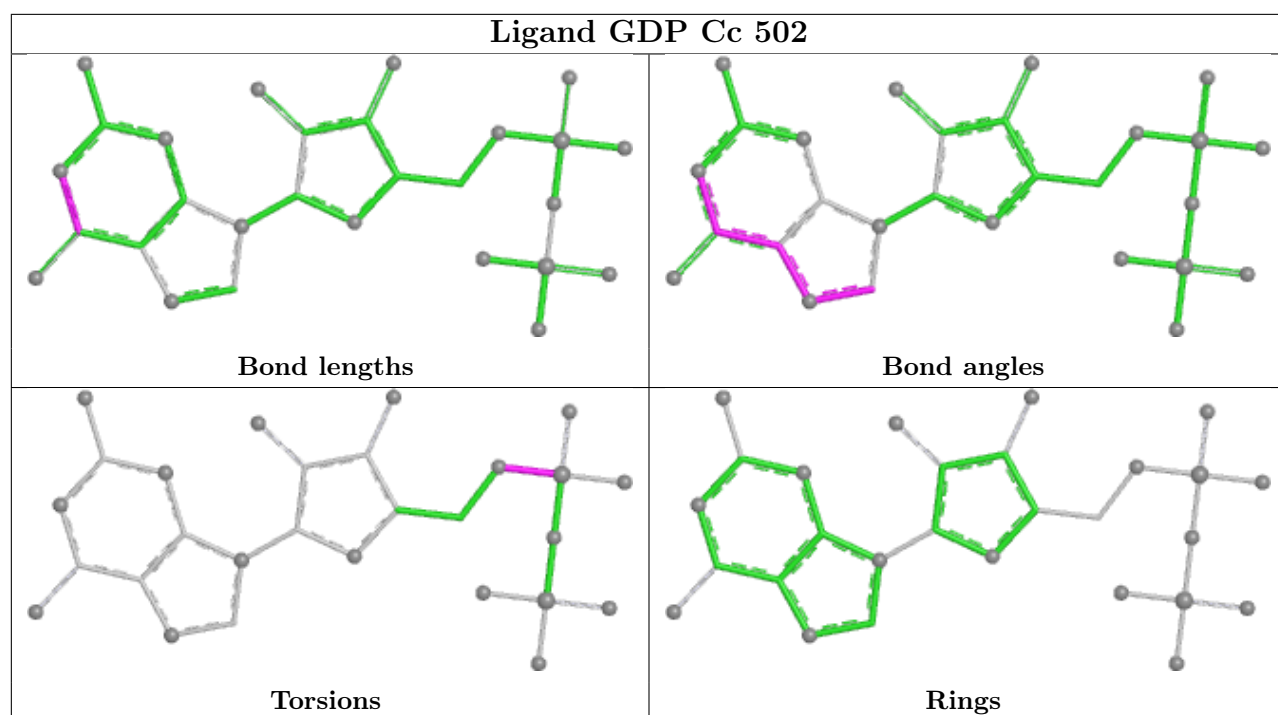
There are no ring outliers.

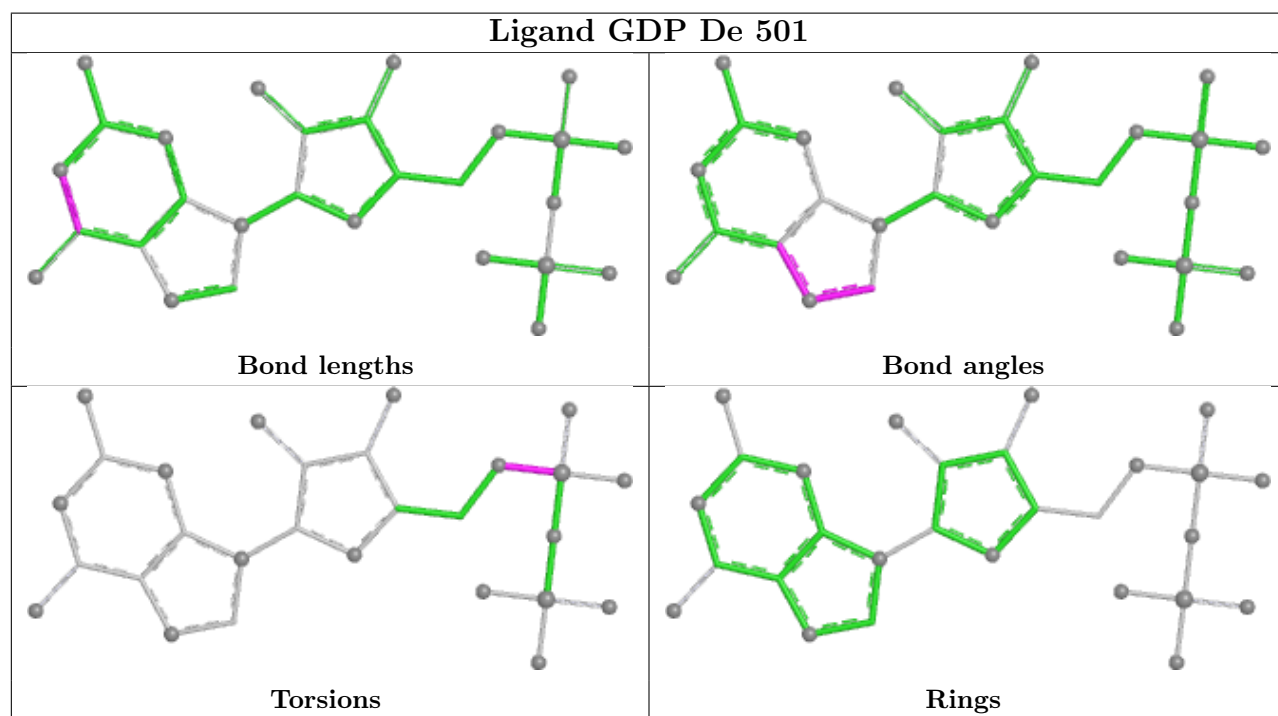
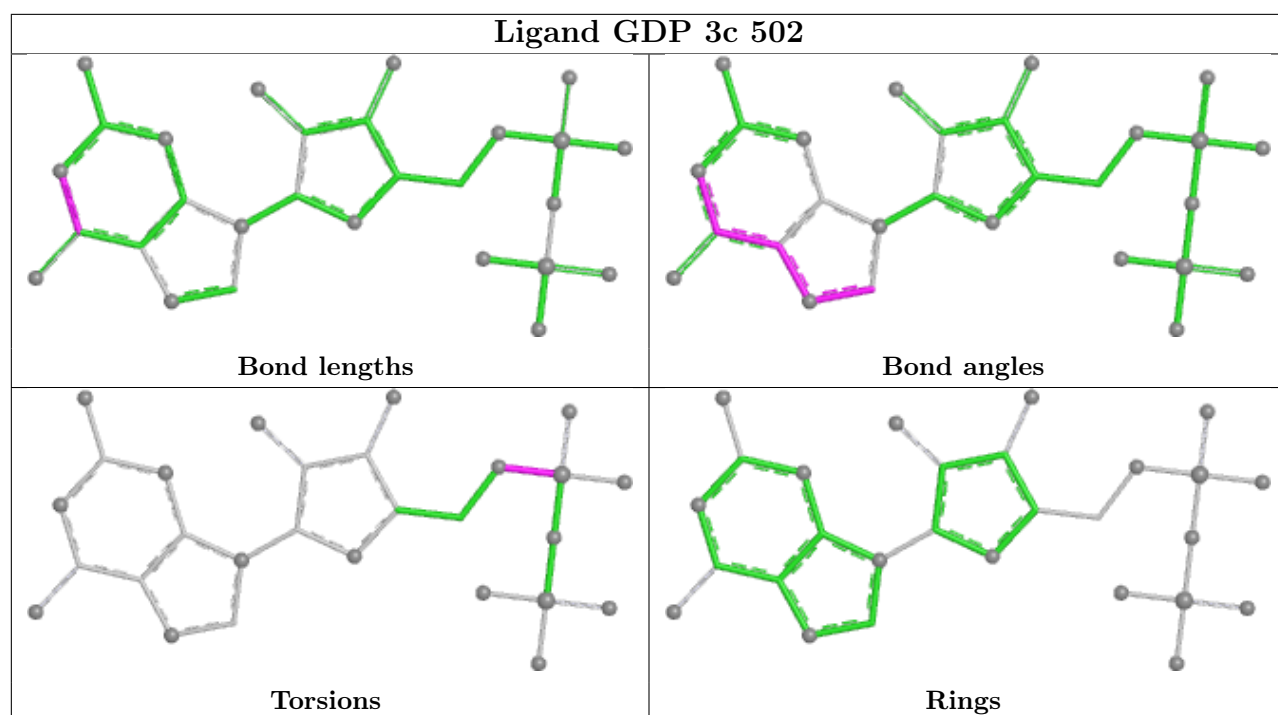
No monomer is involved in short contacts.

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

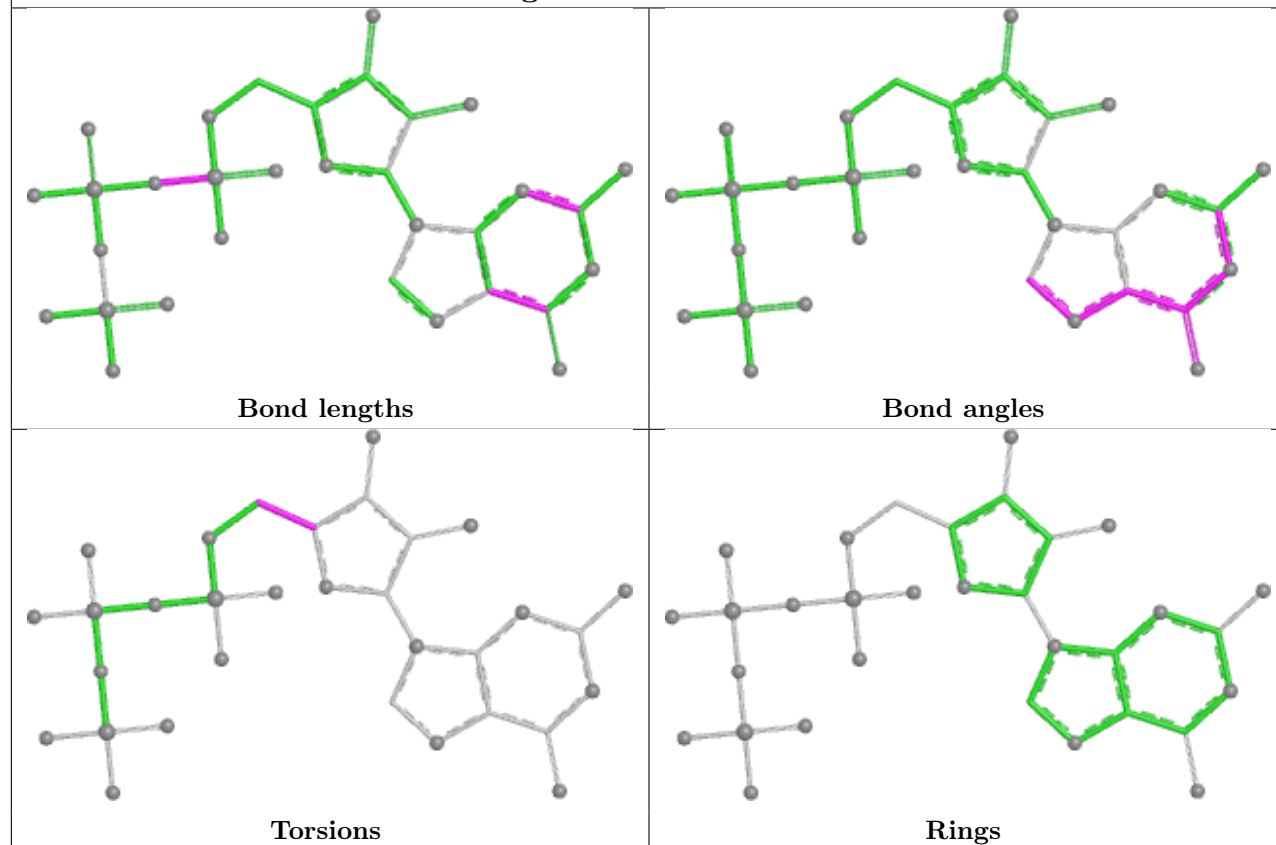
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



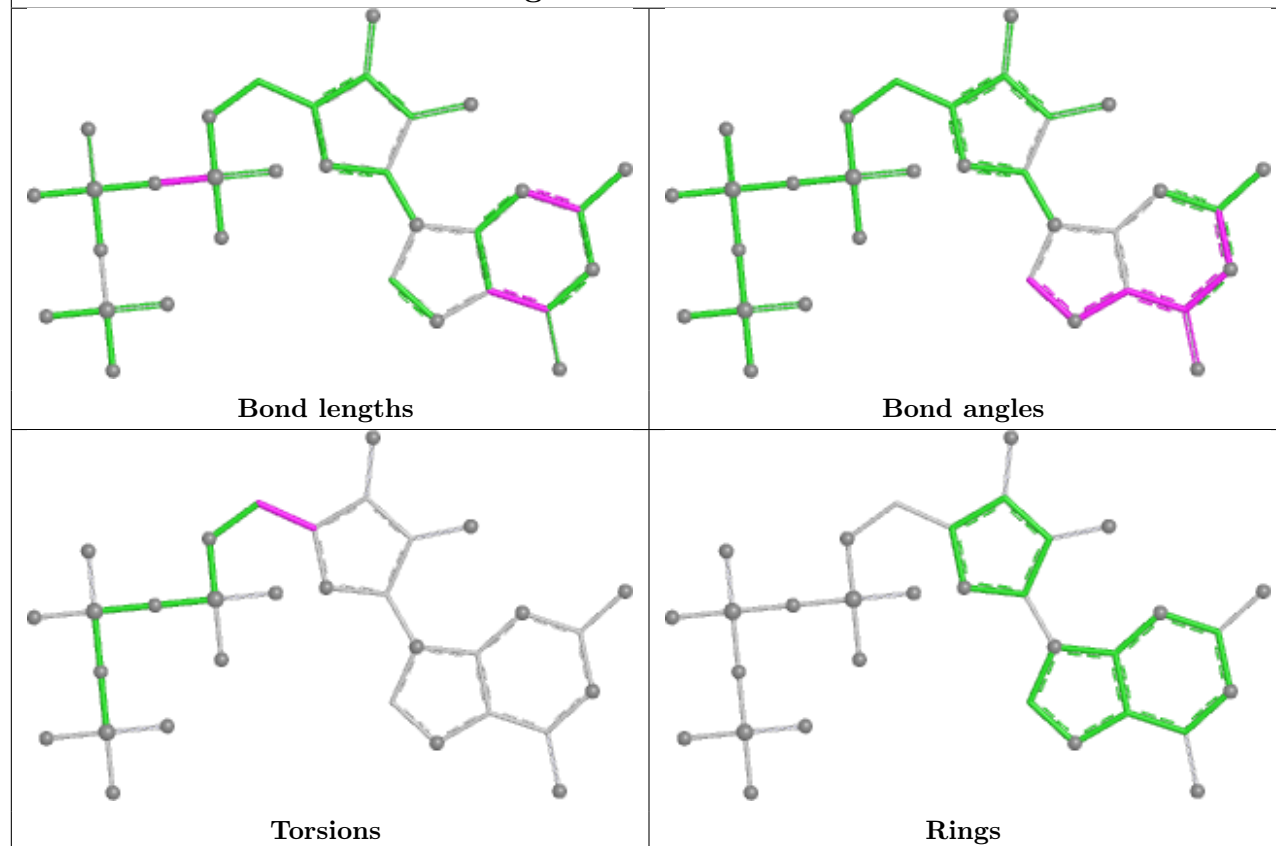


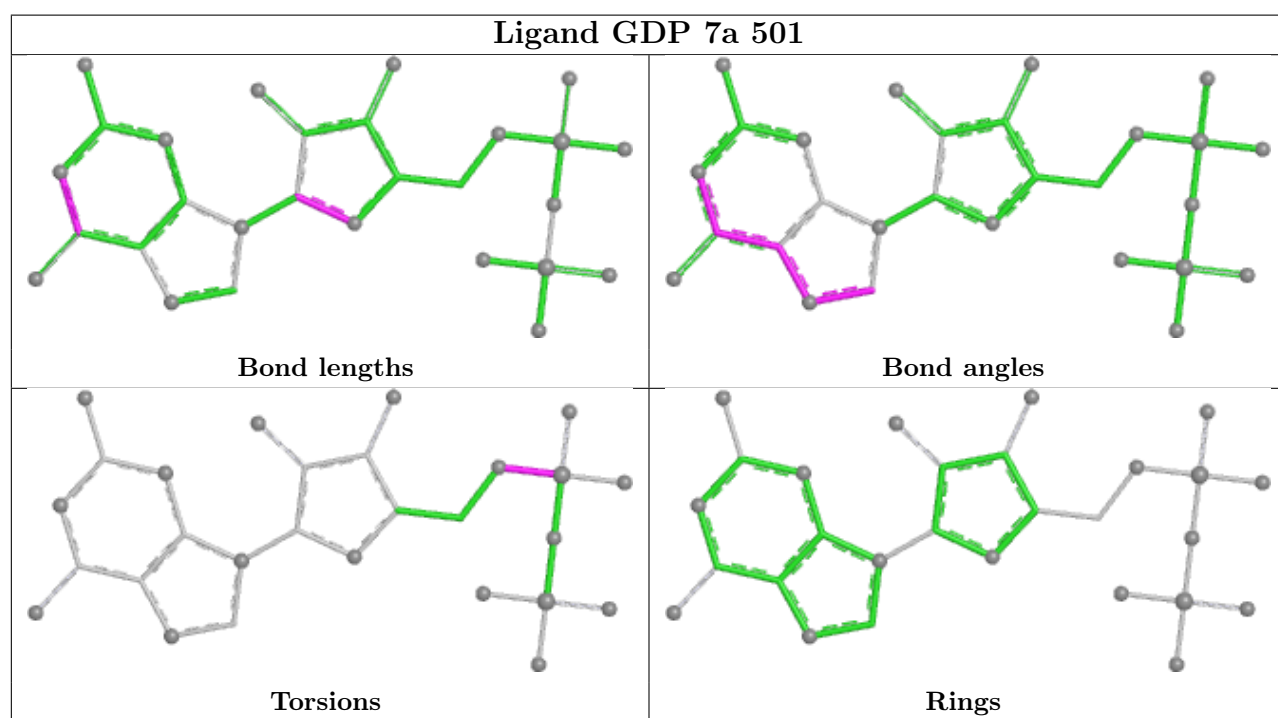
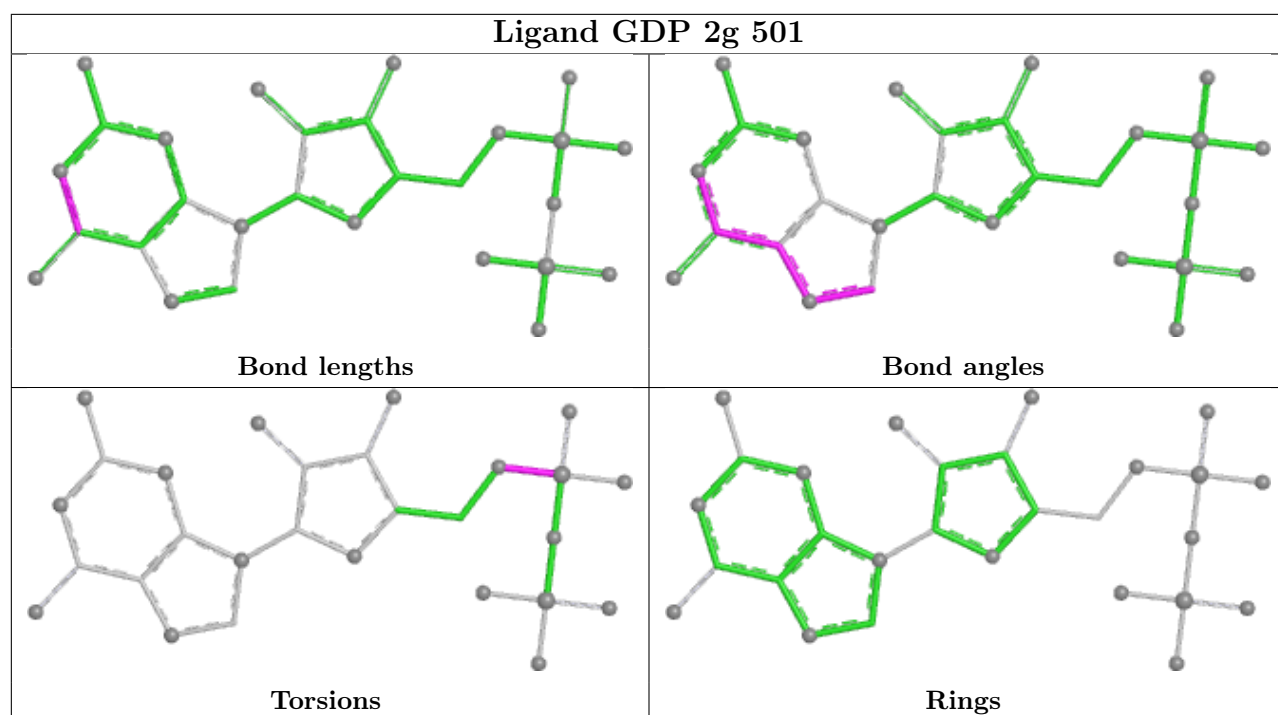


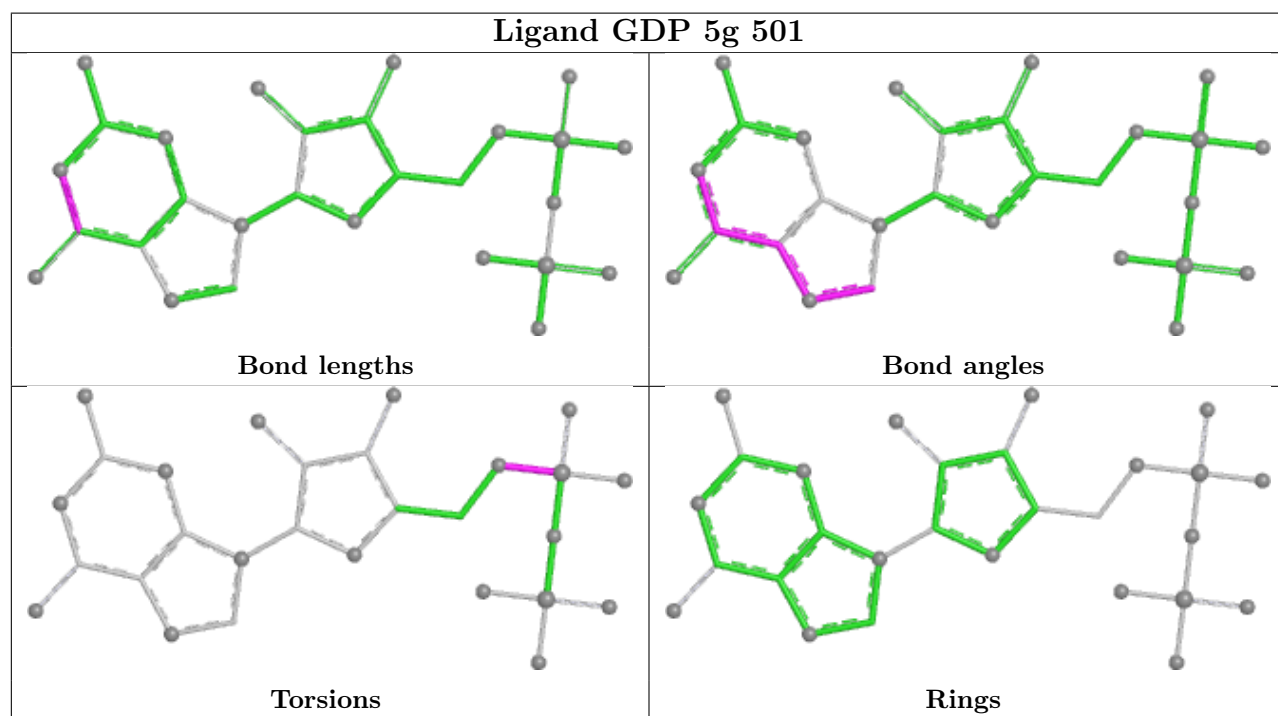
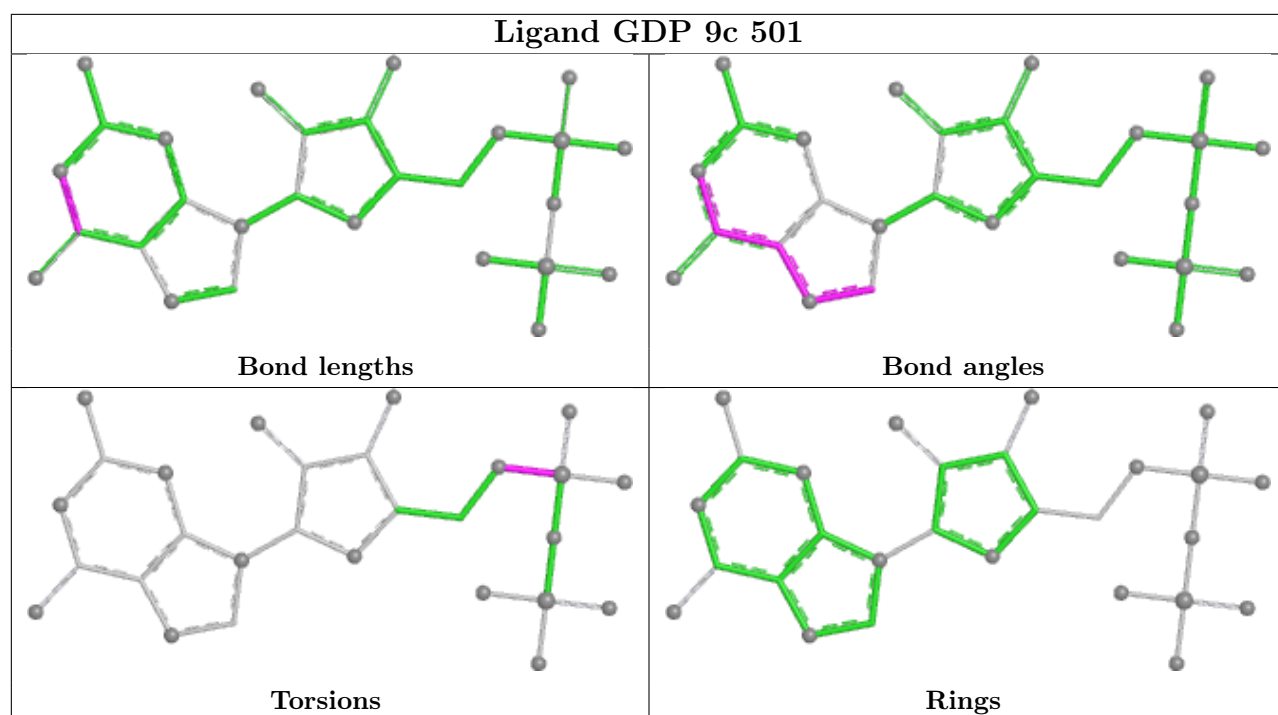
Ligand GTP Bh 501

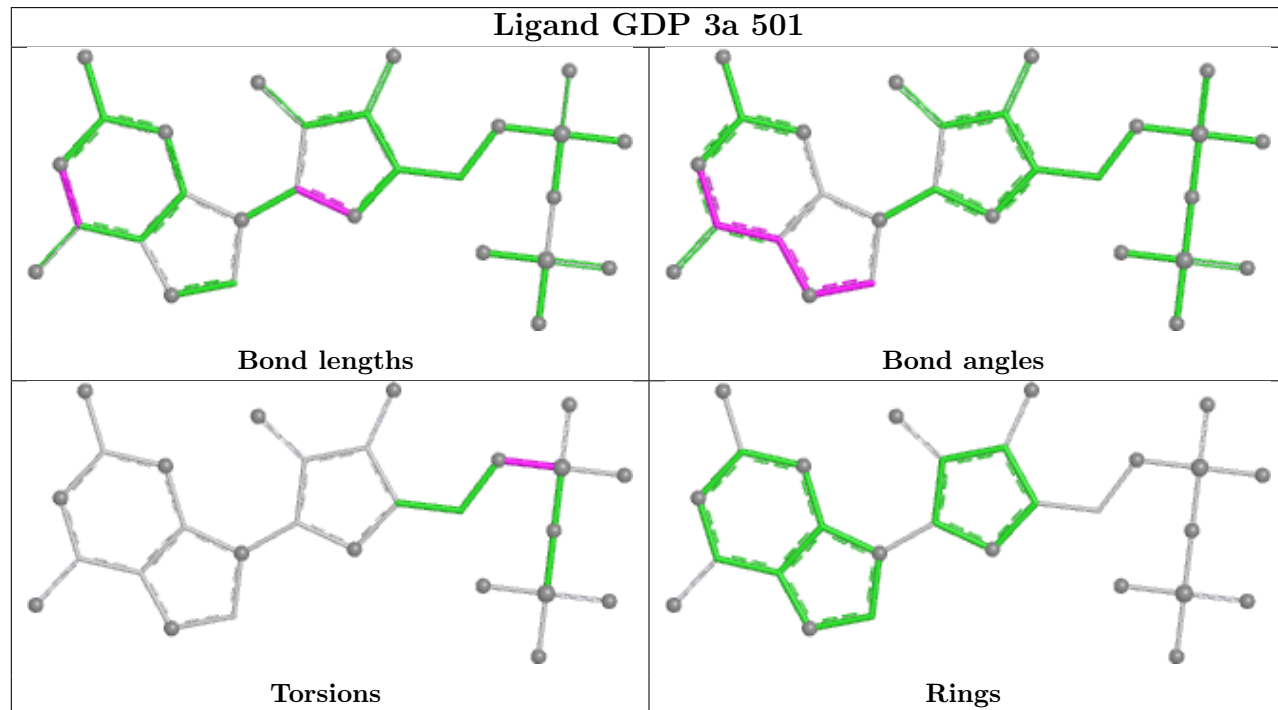
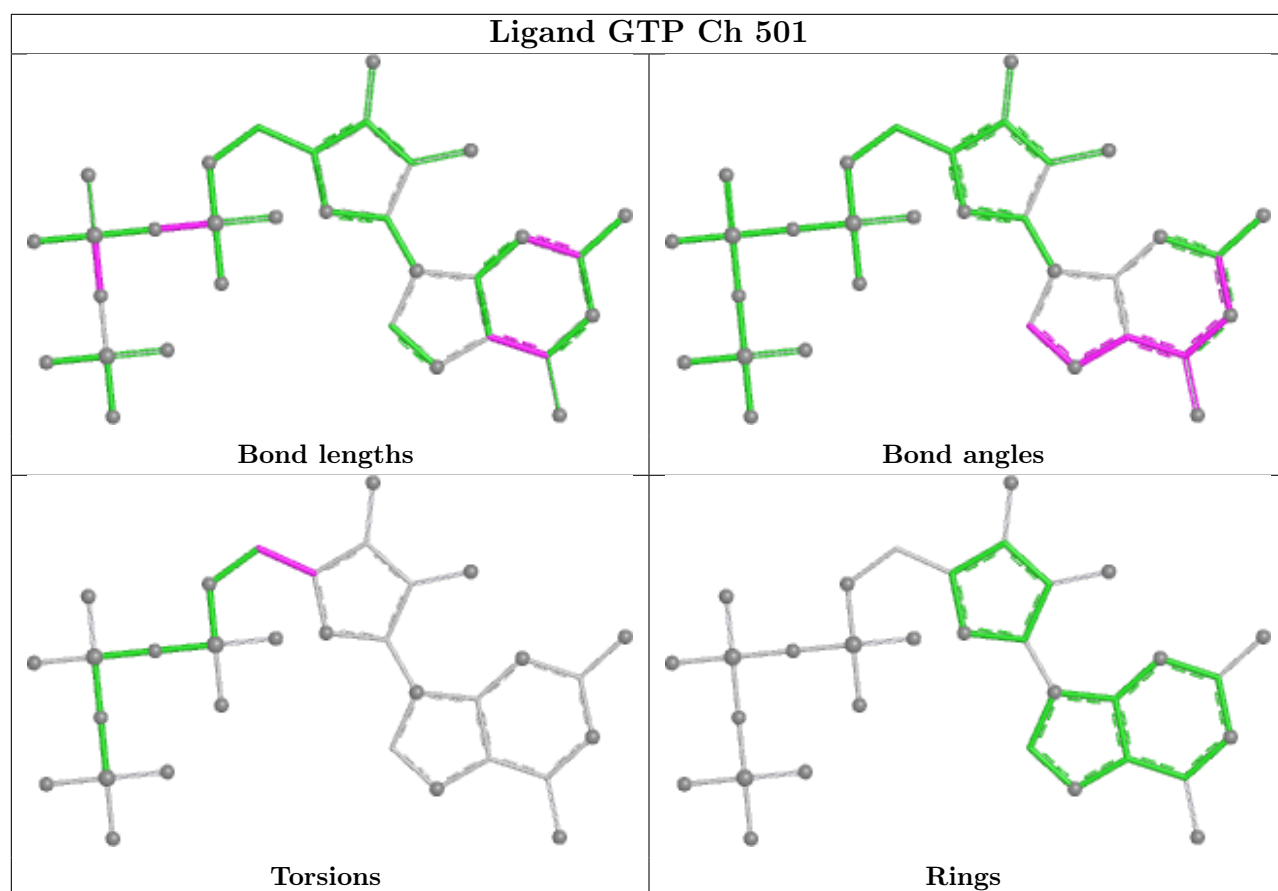


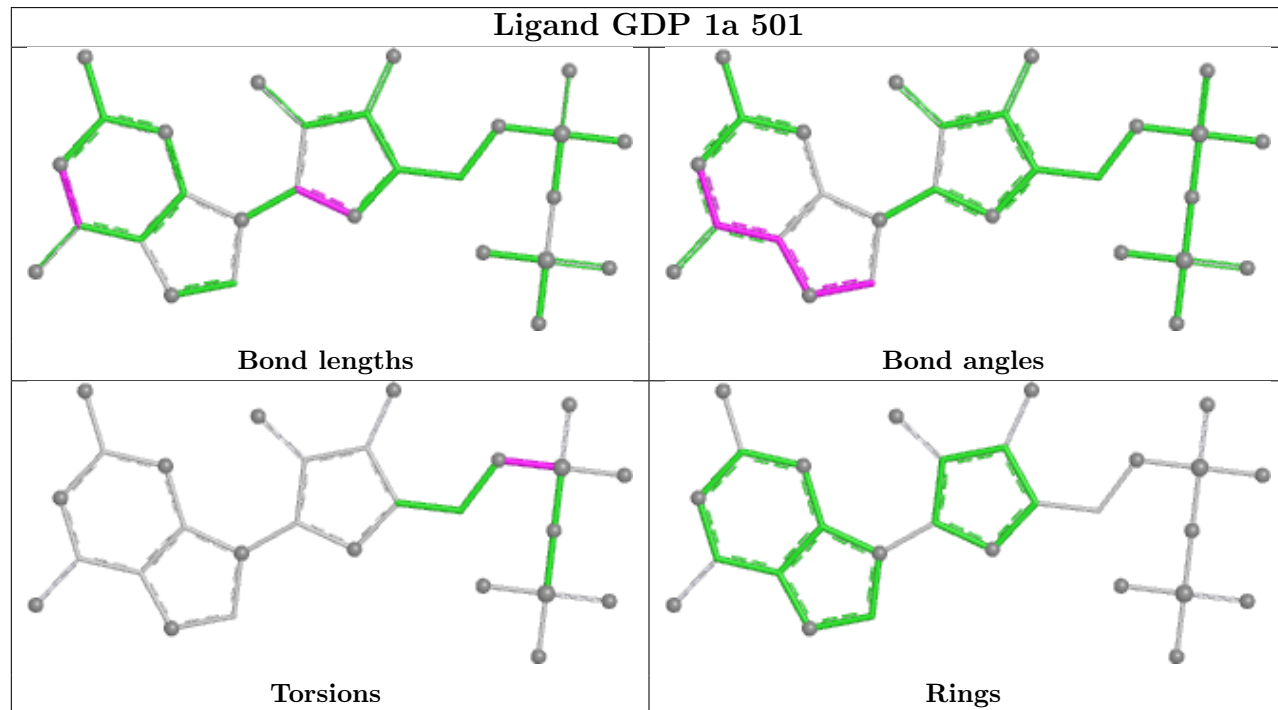
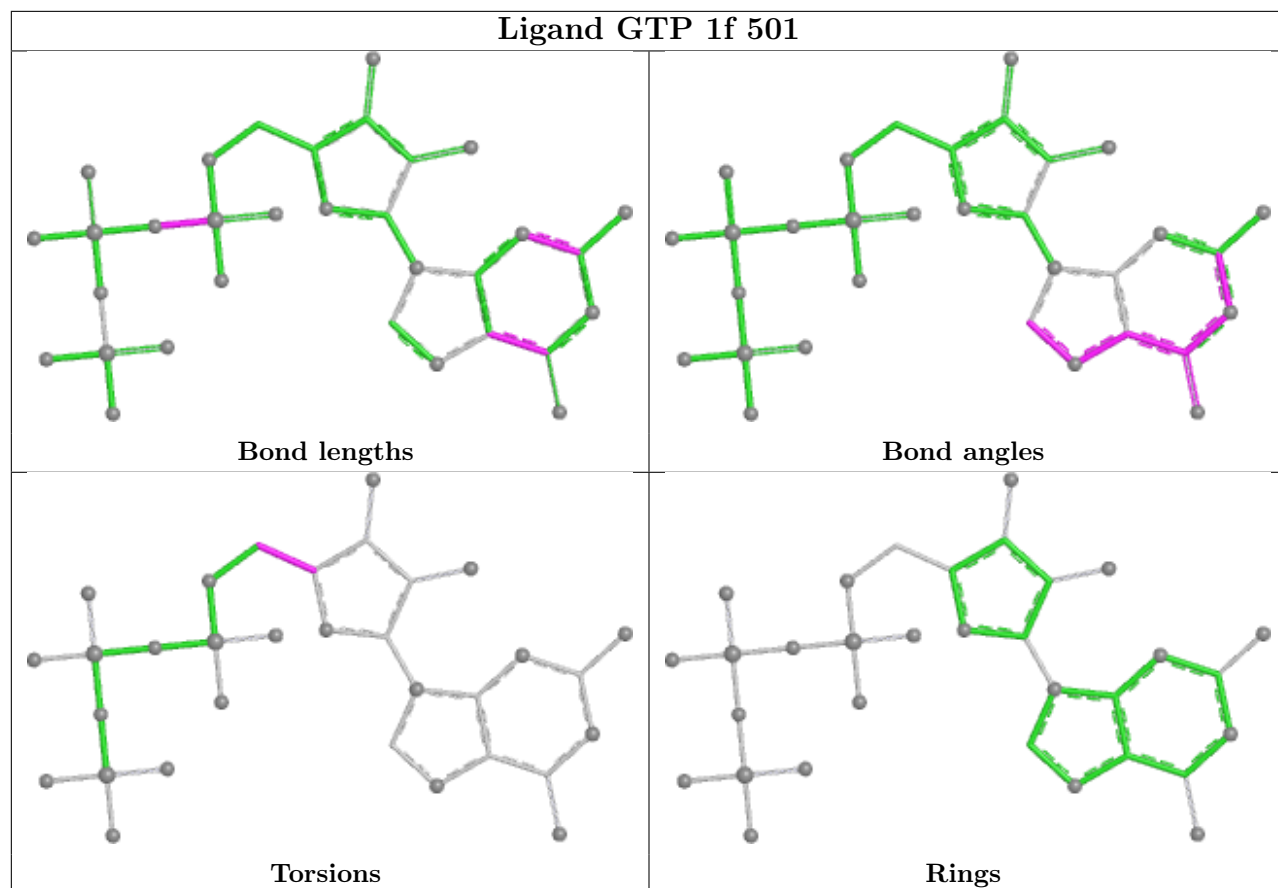
Ligand GTP 3d 501

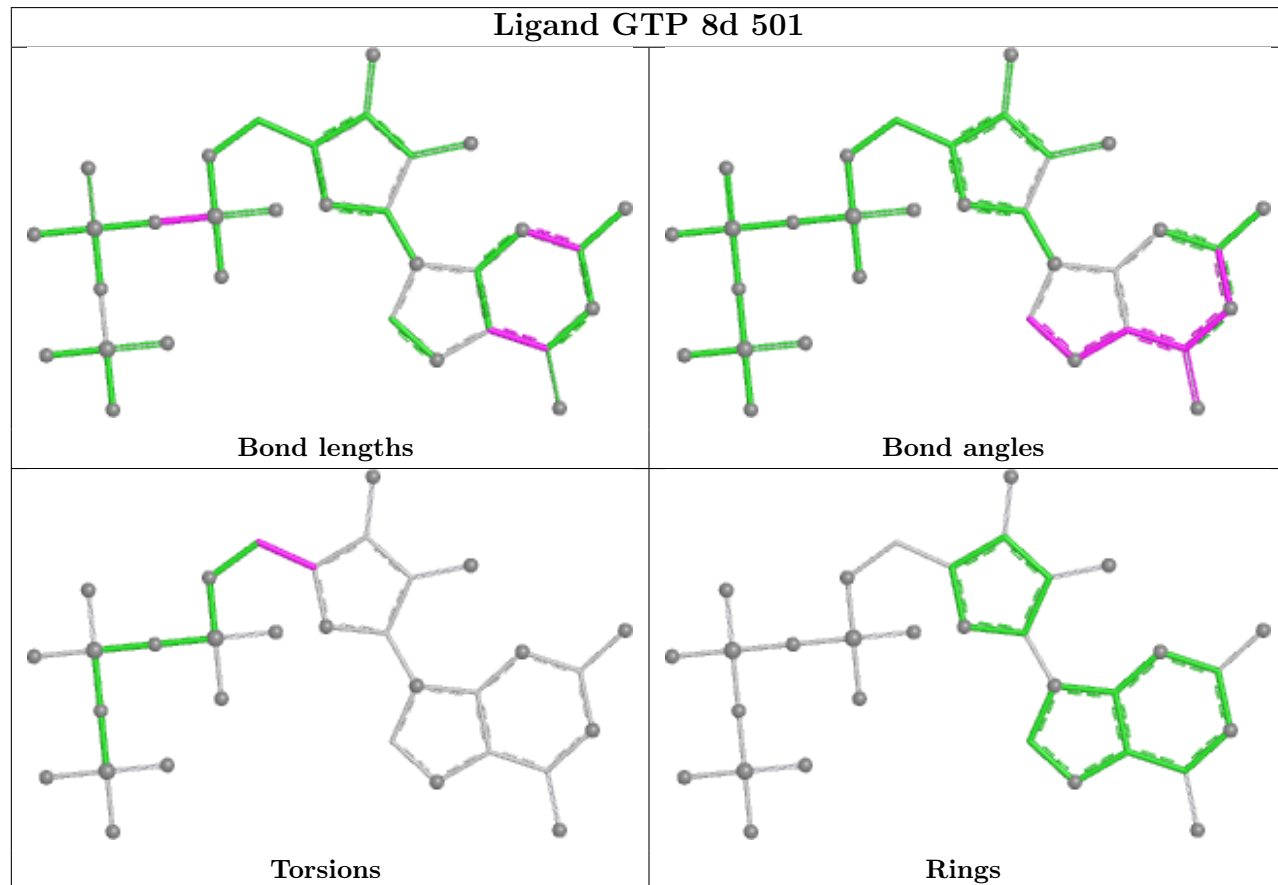
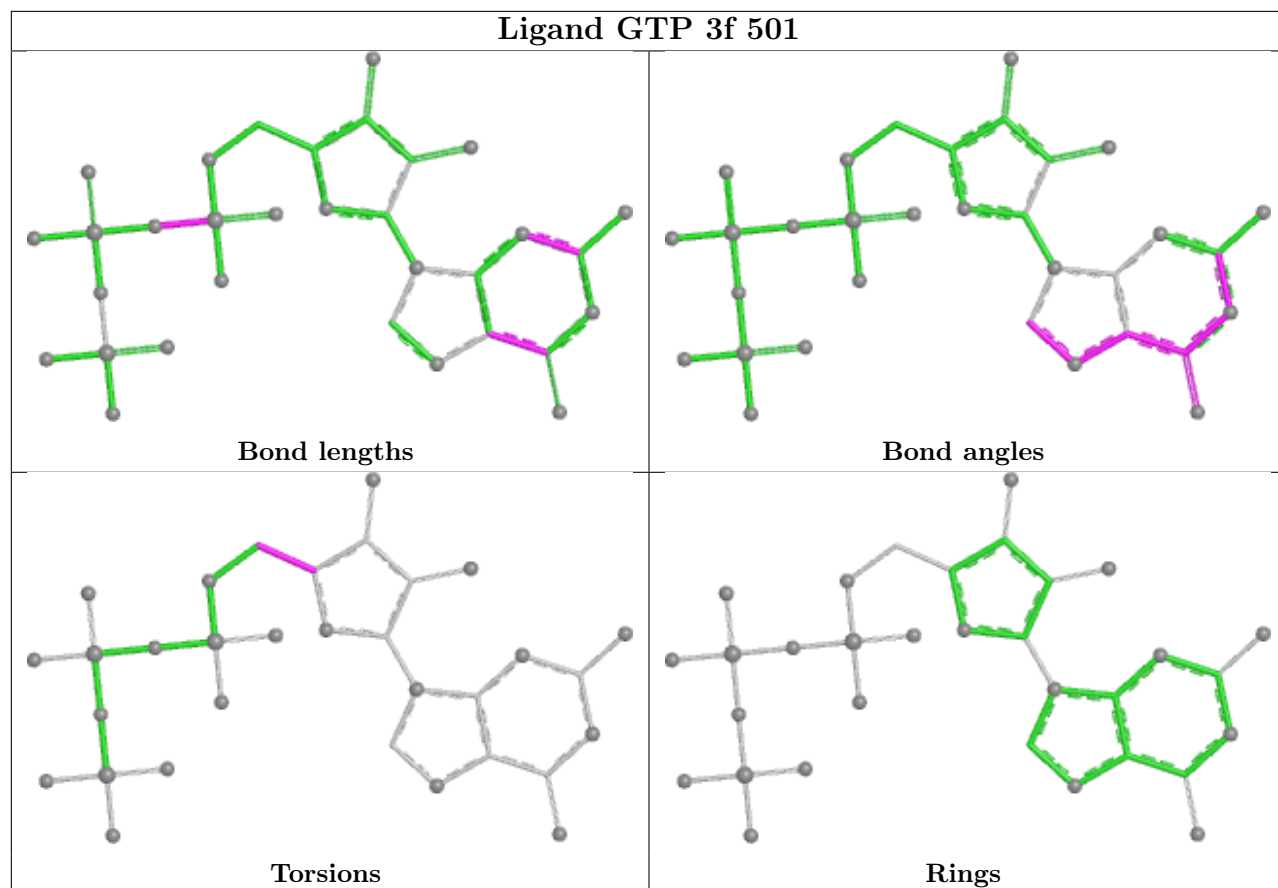


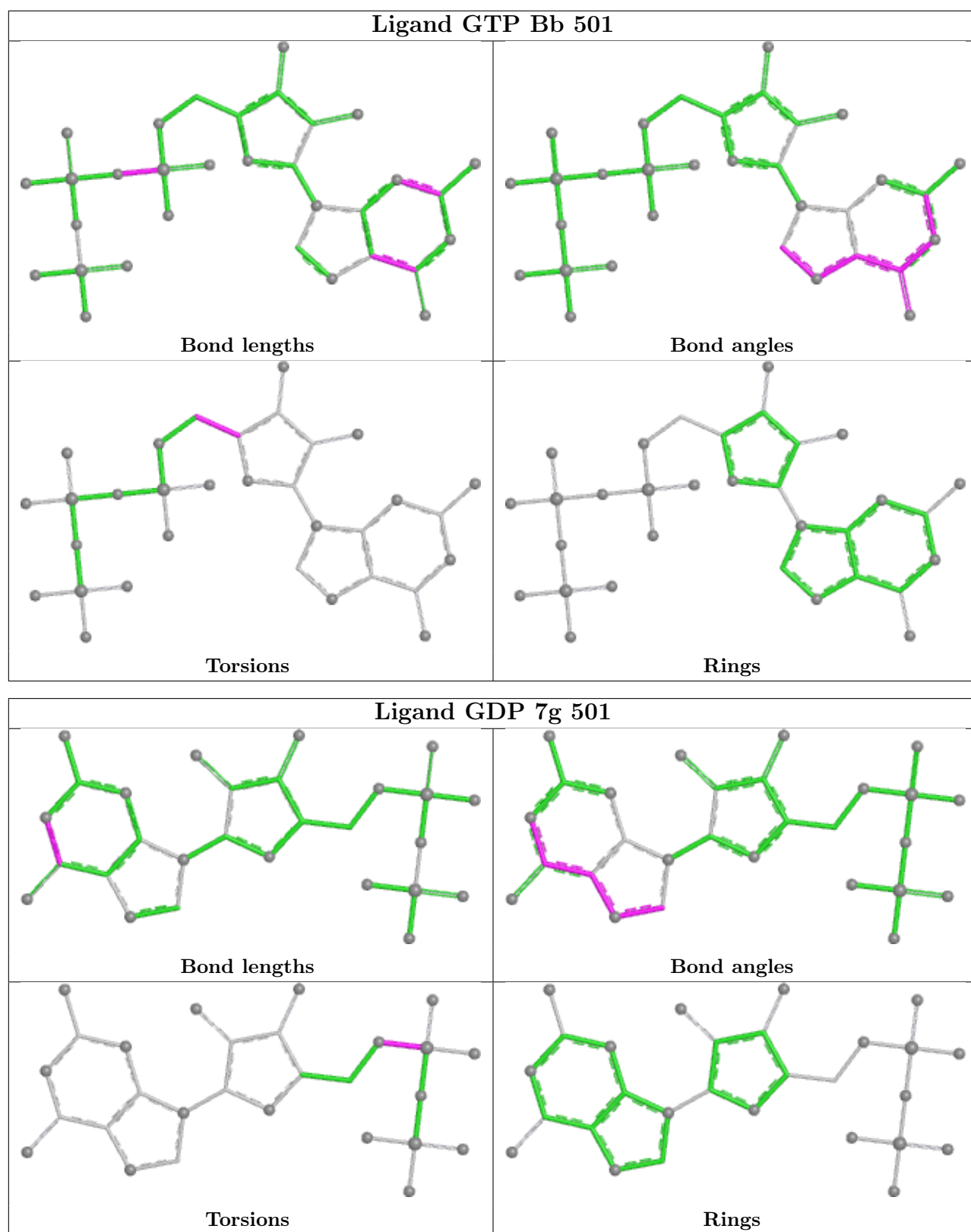


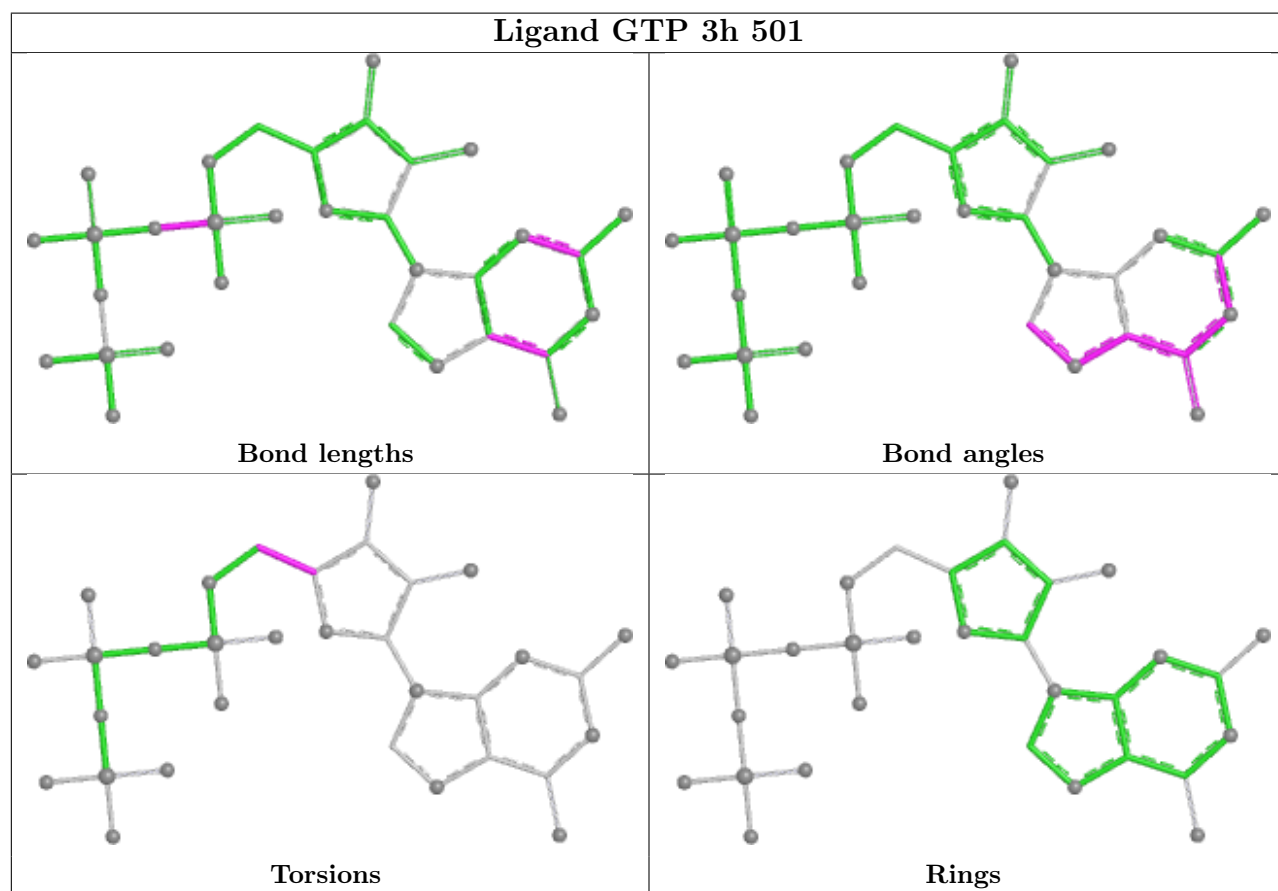
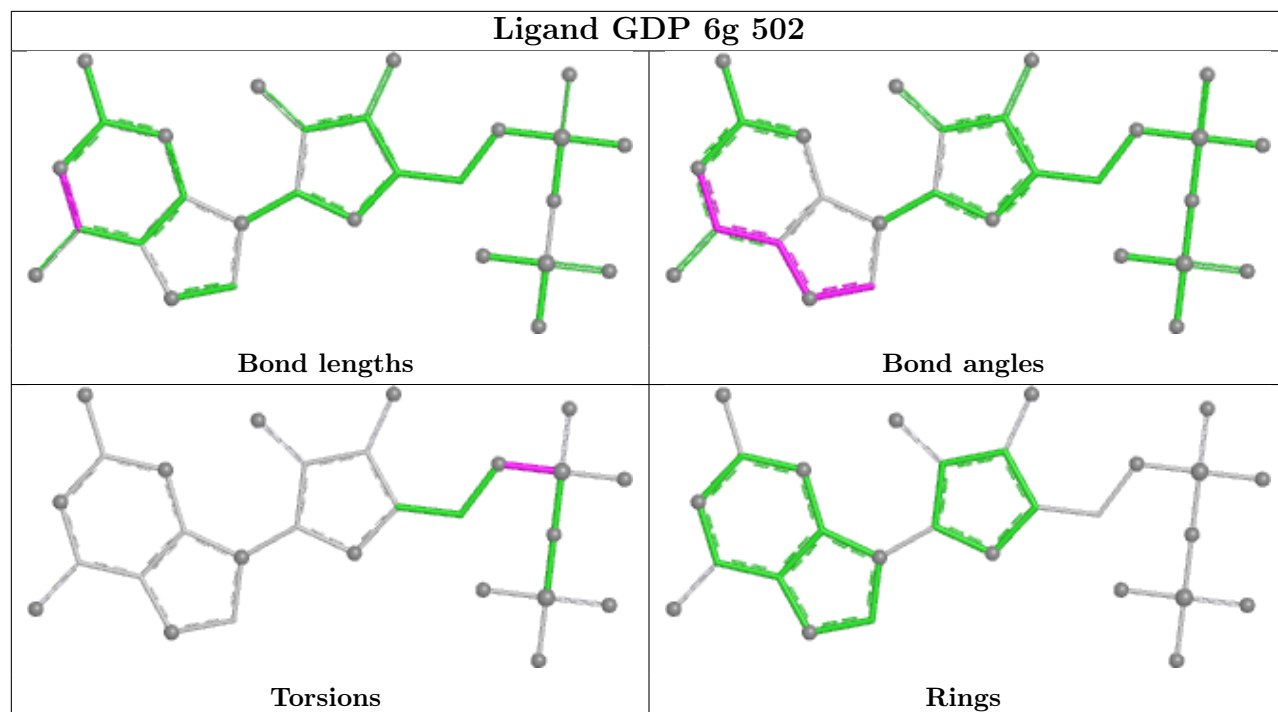


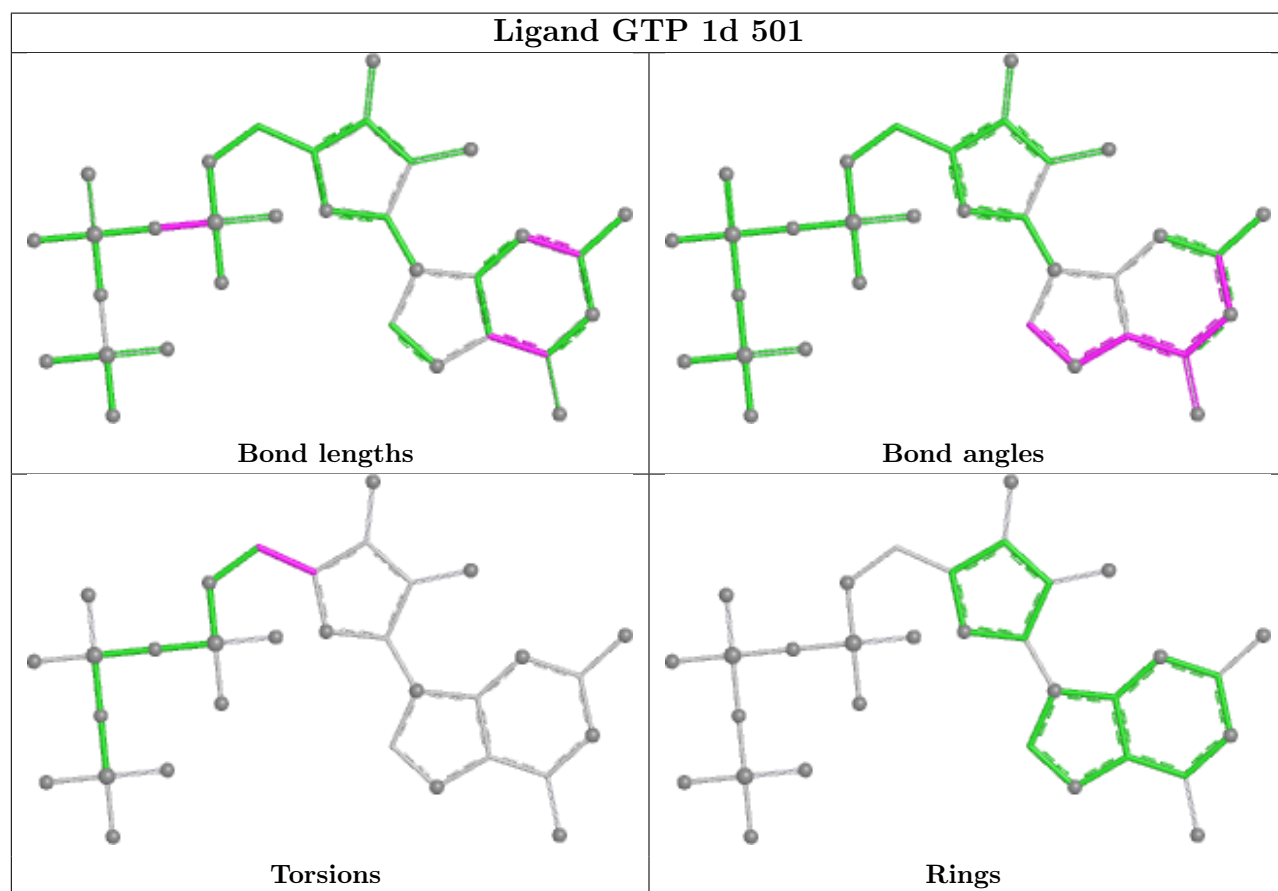
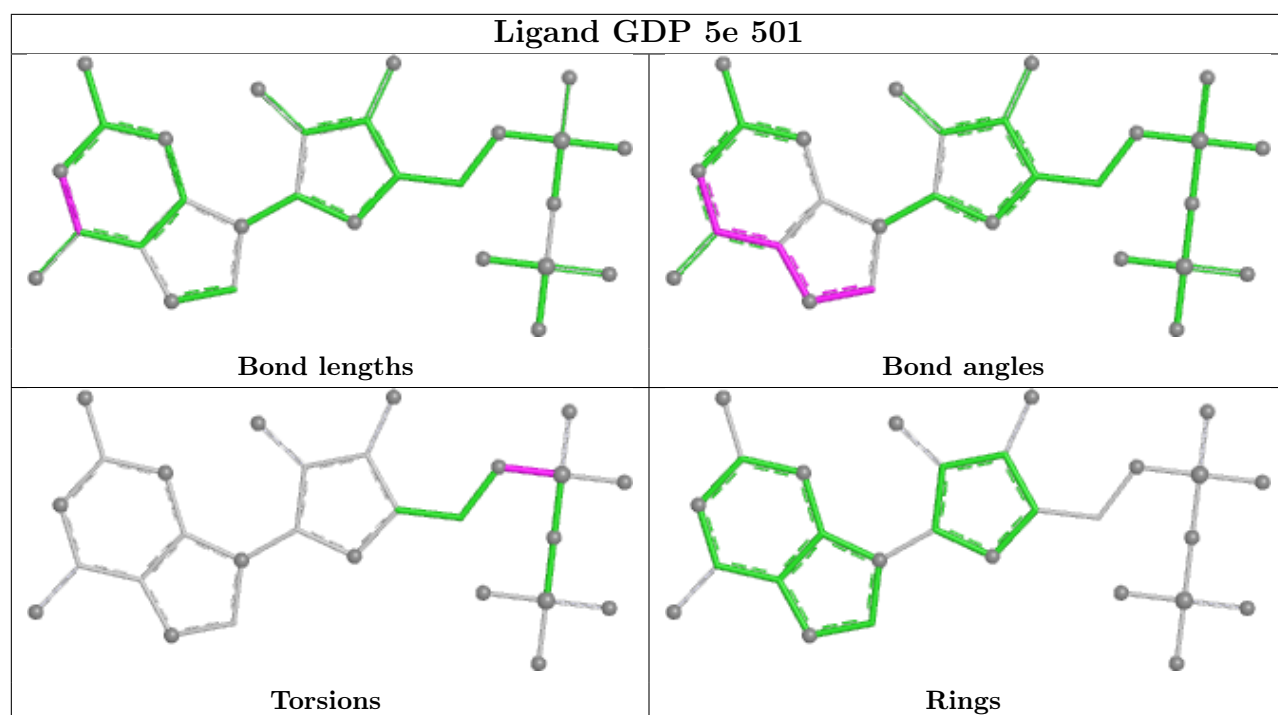


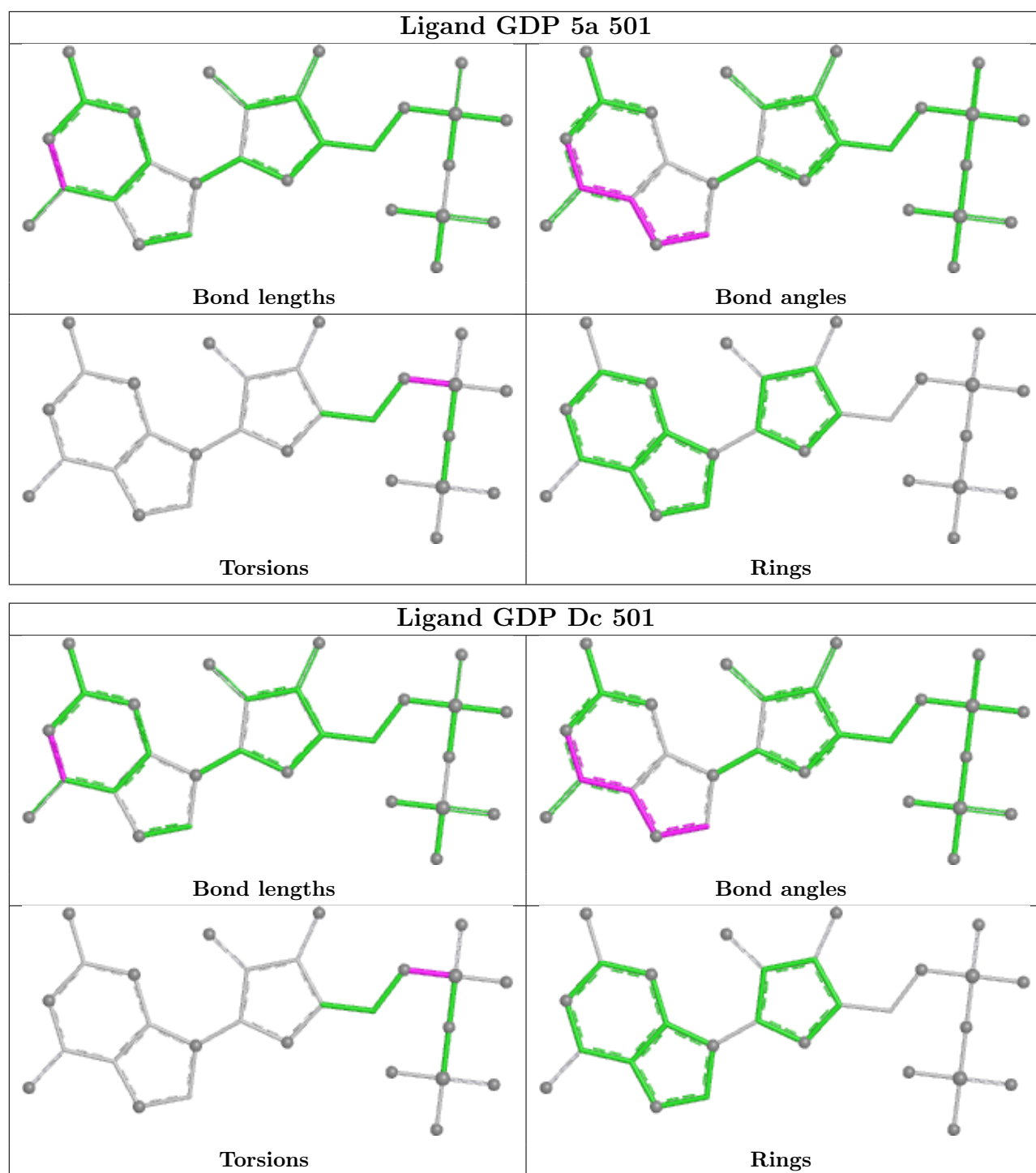


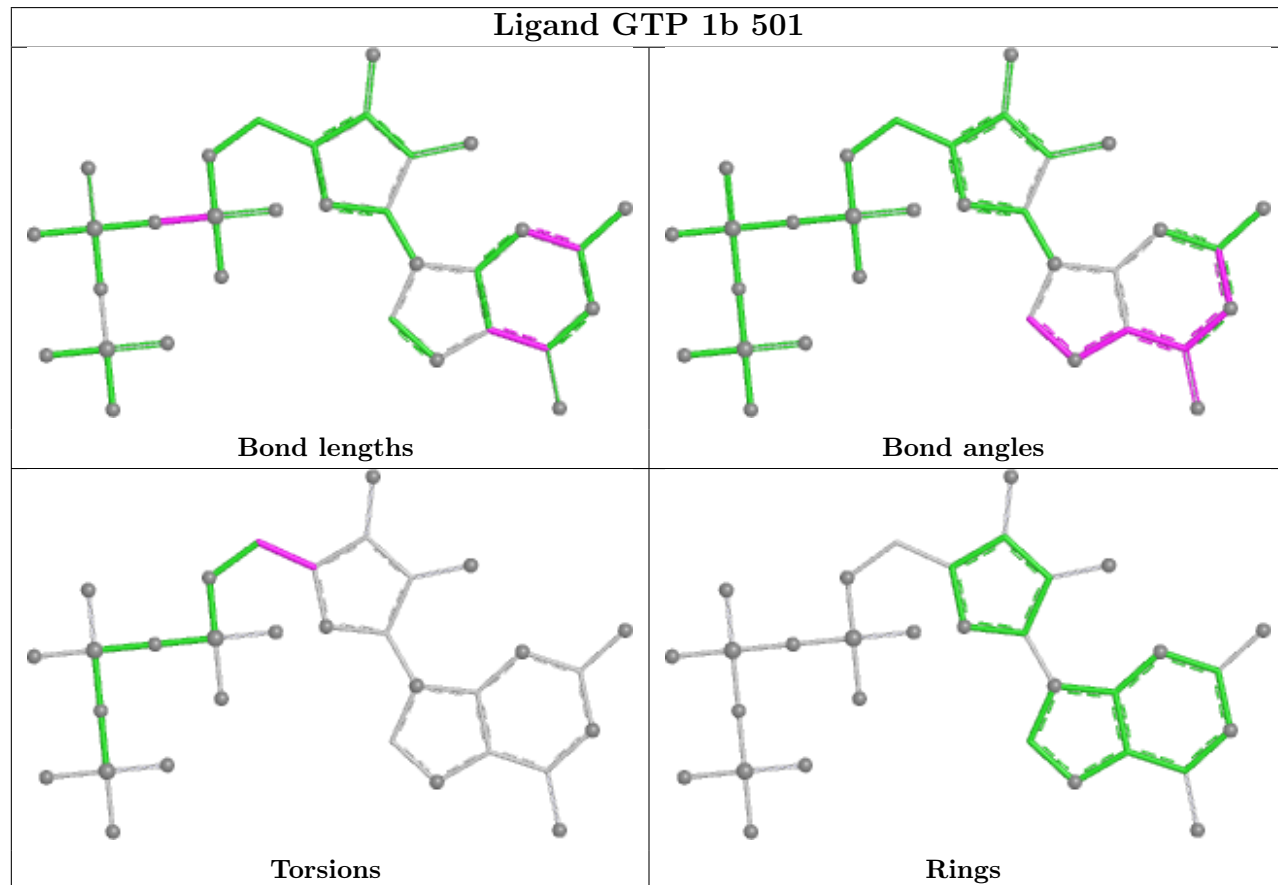
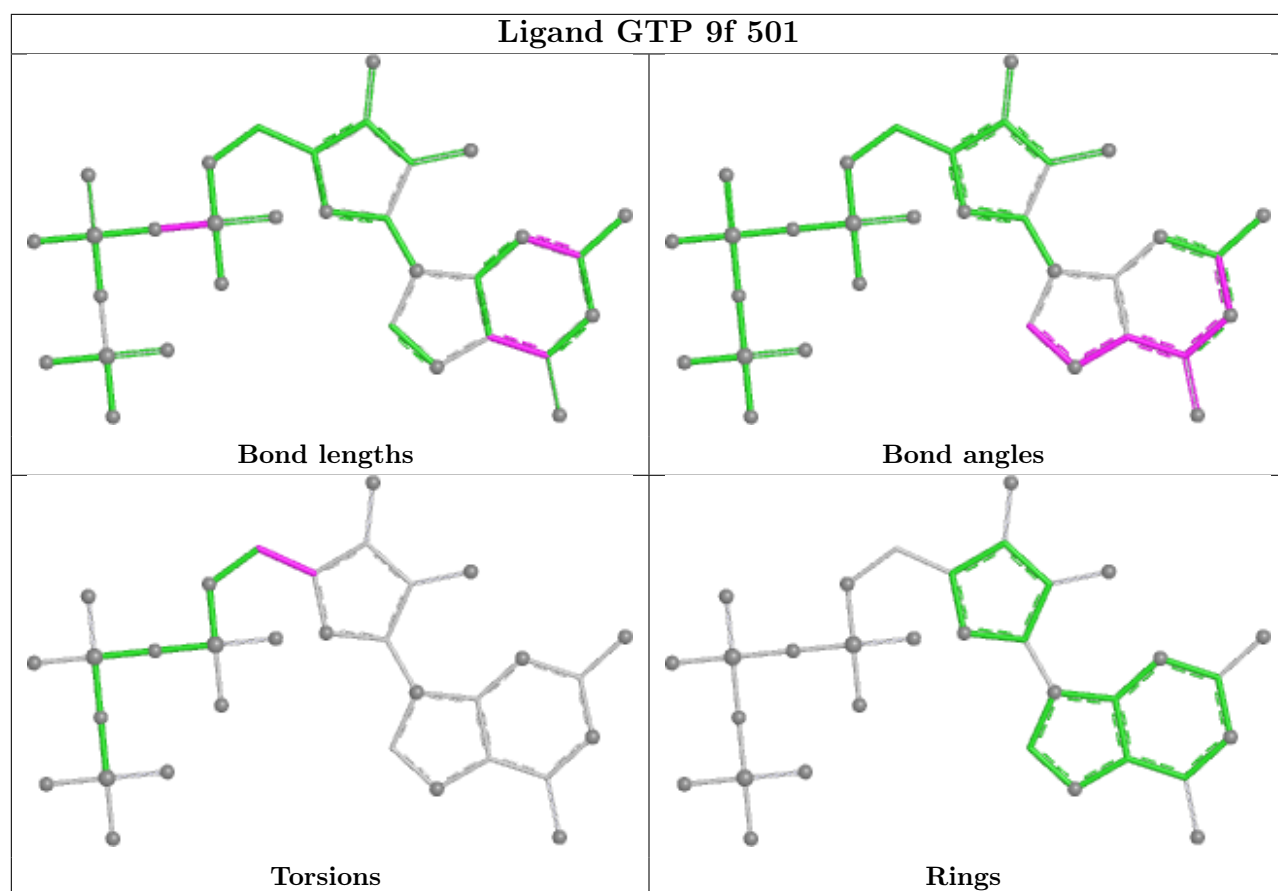


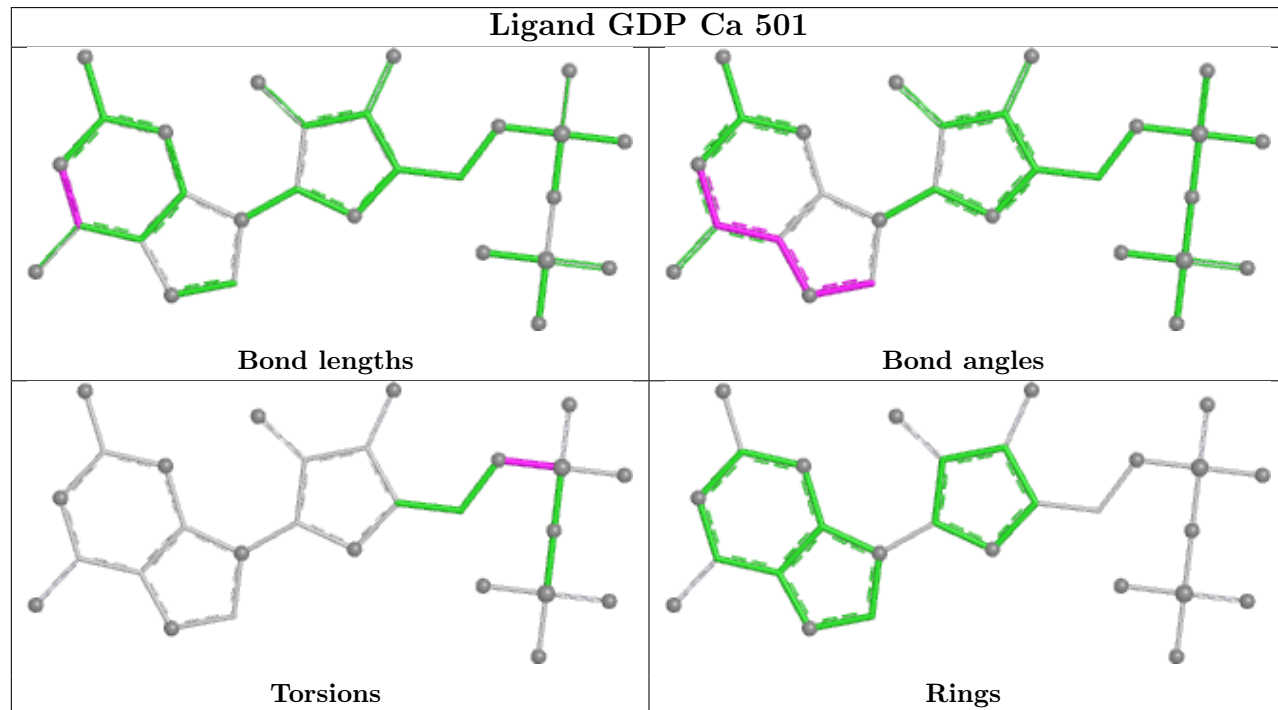
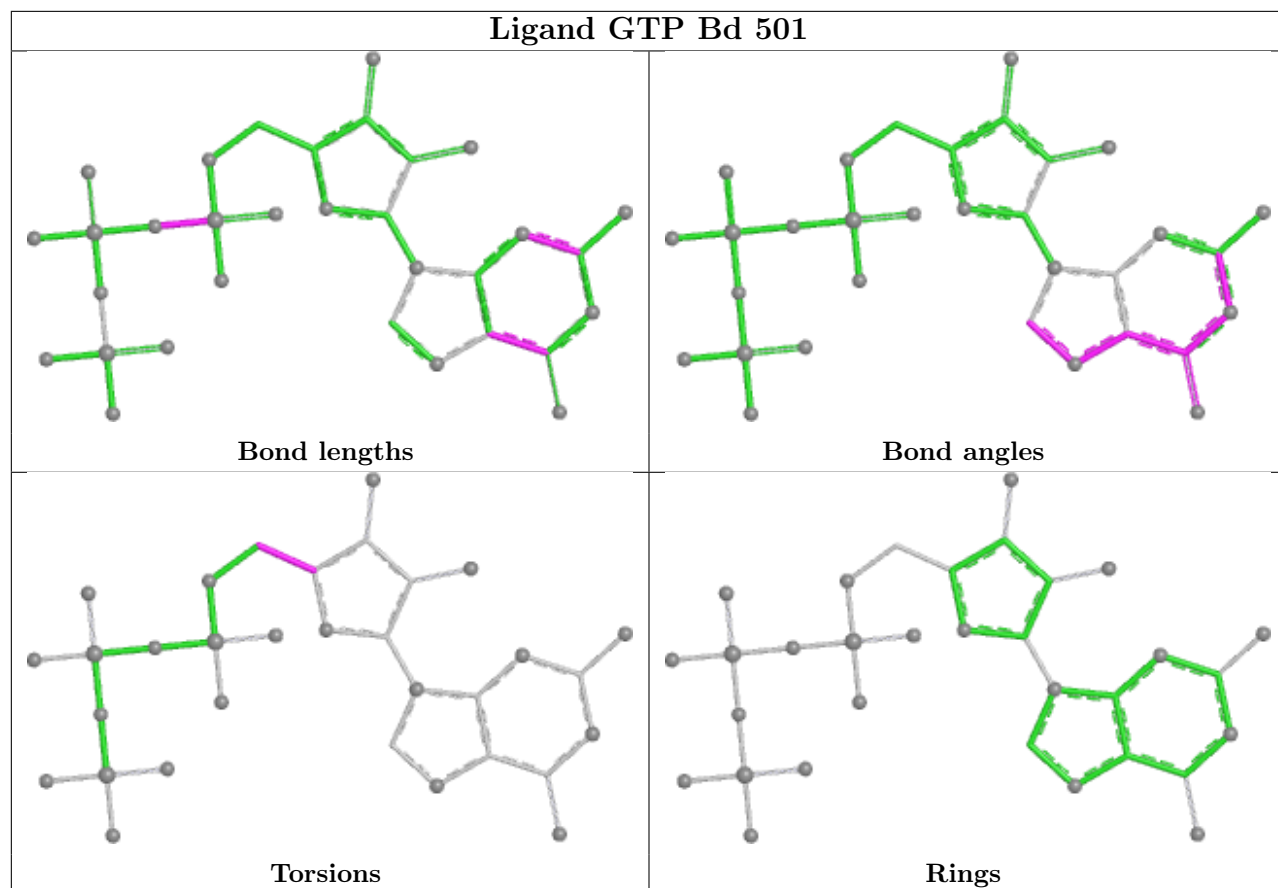


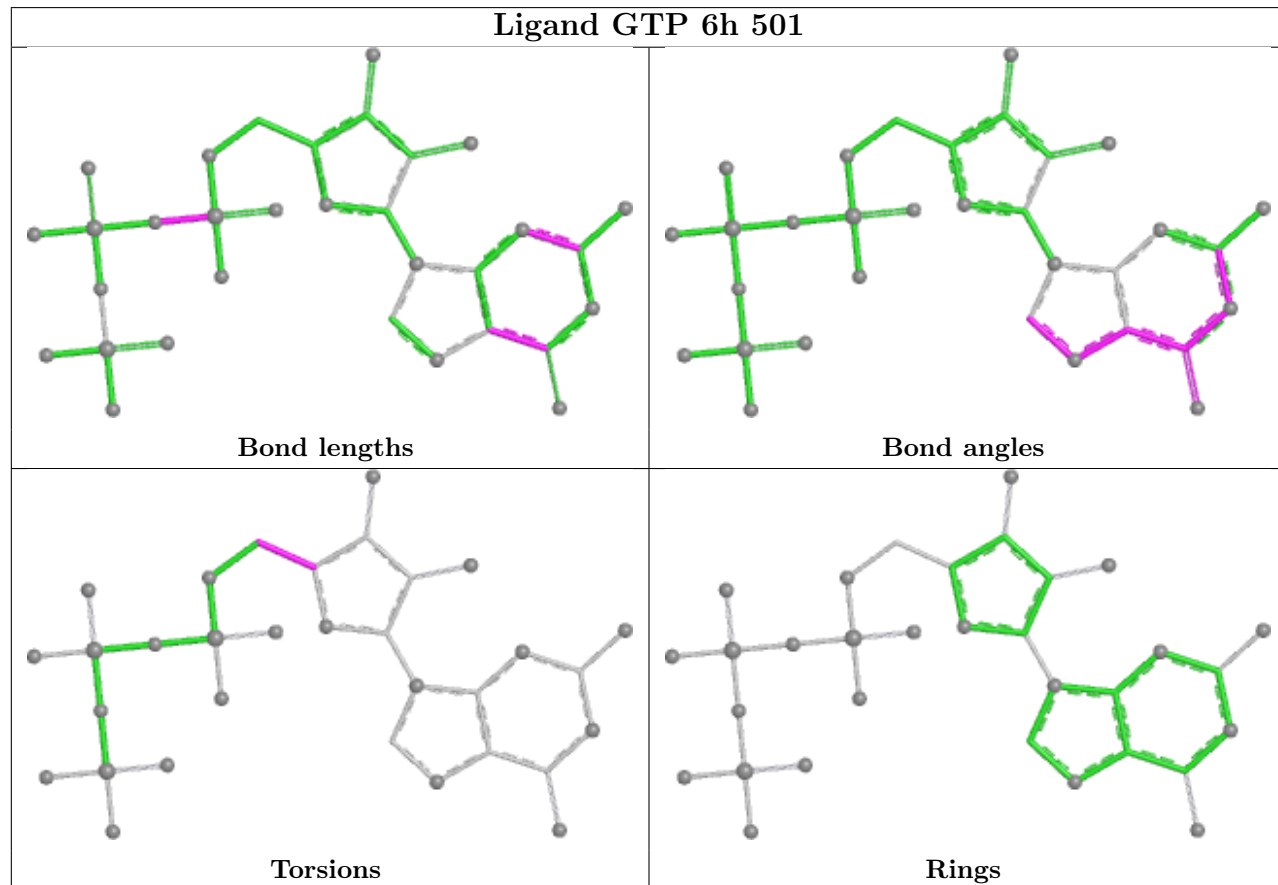
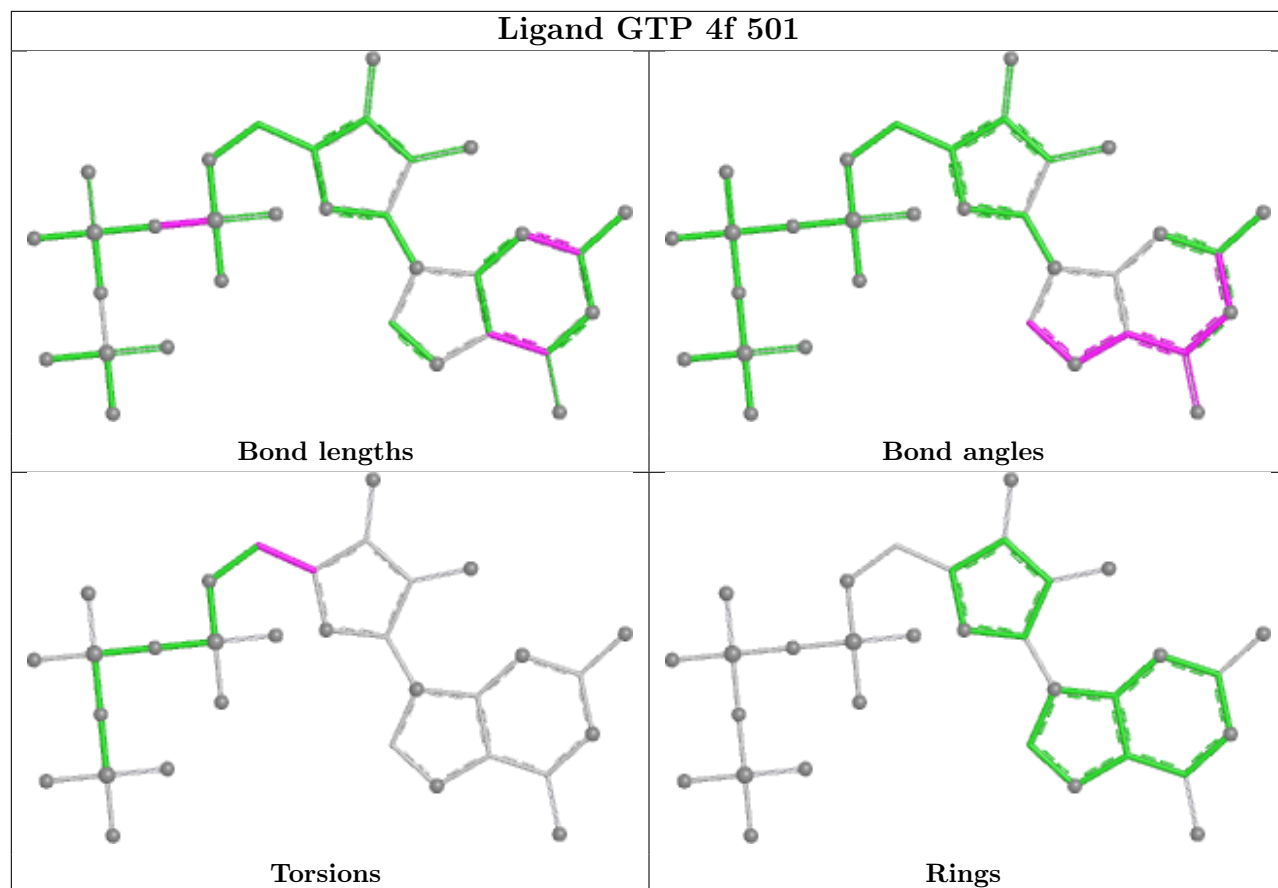




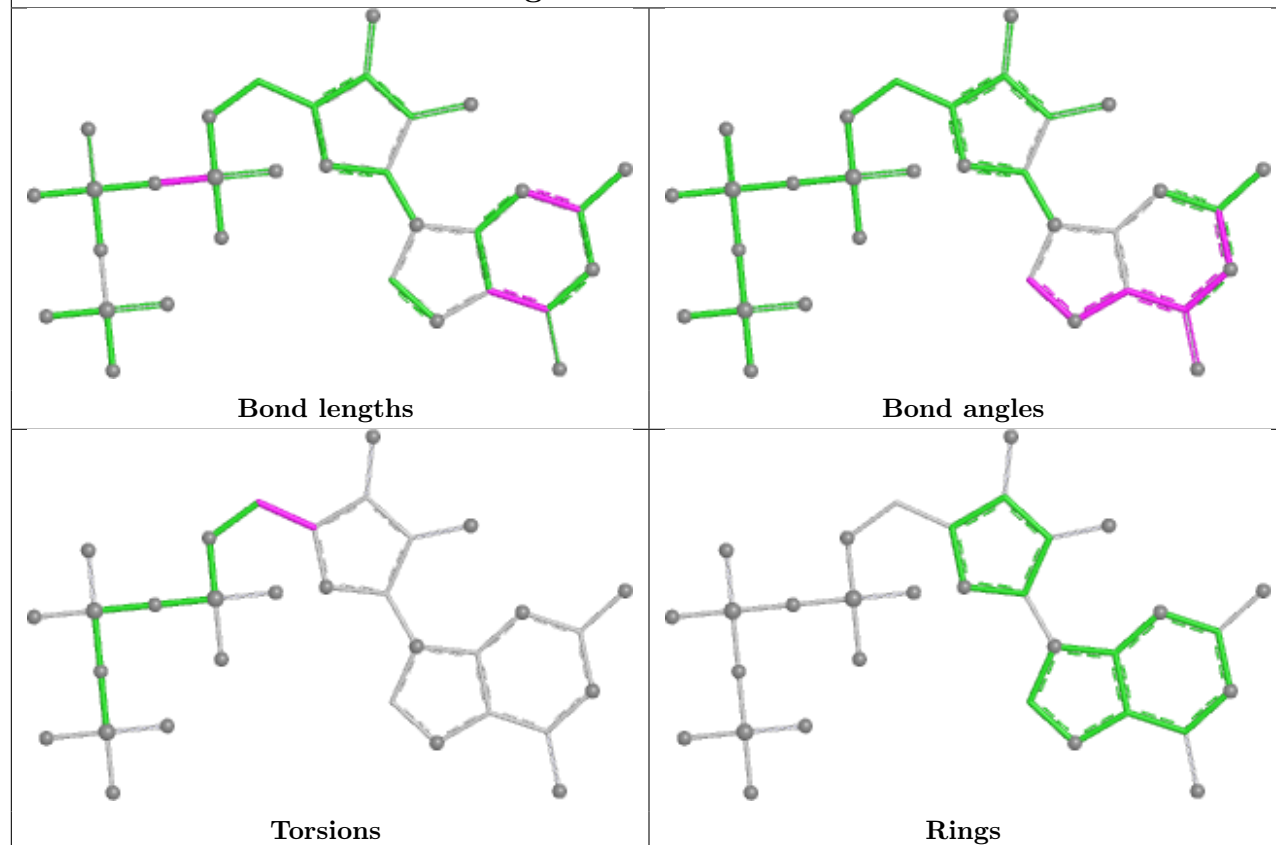




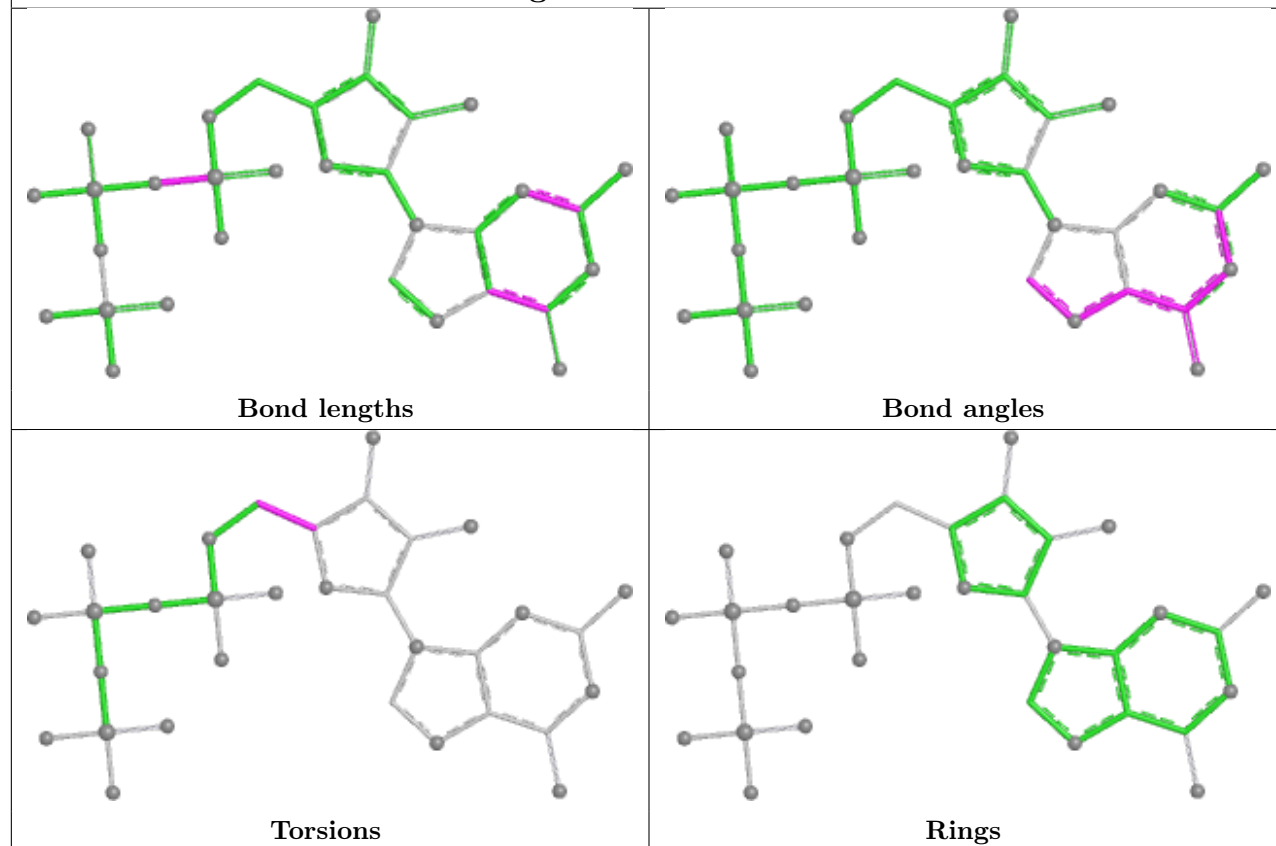


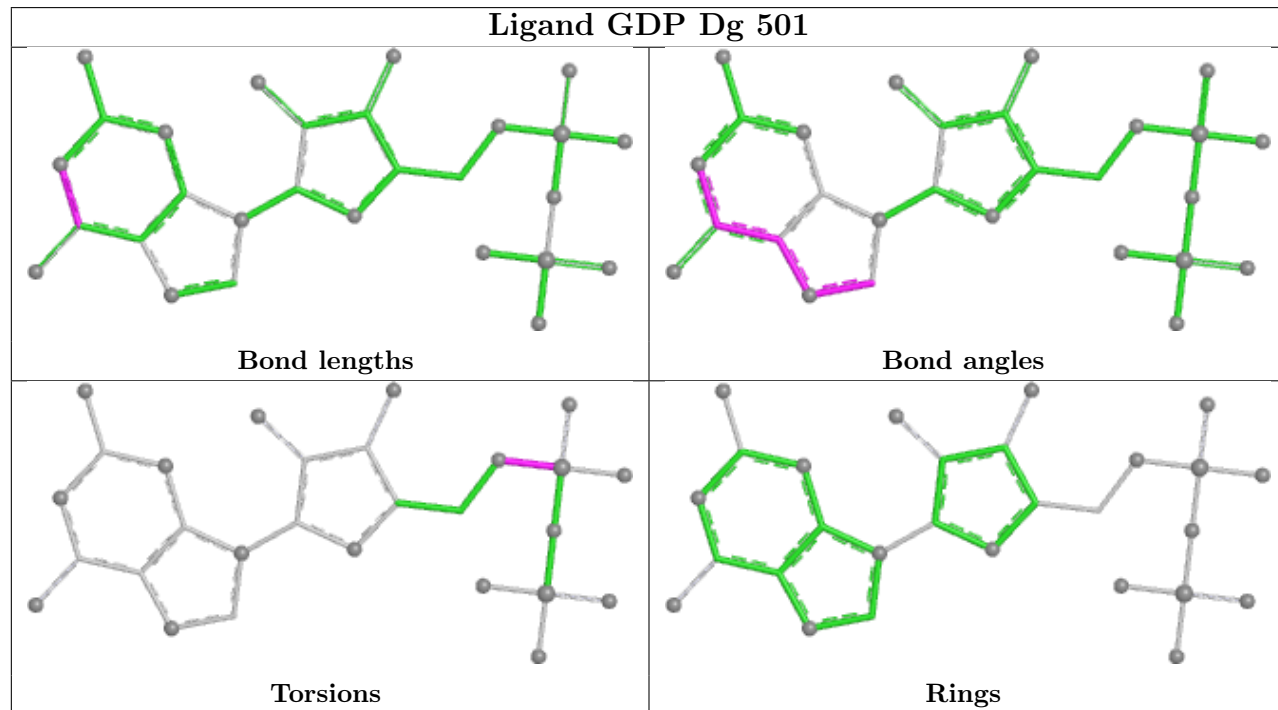
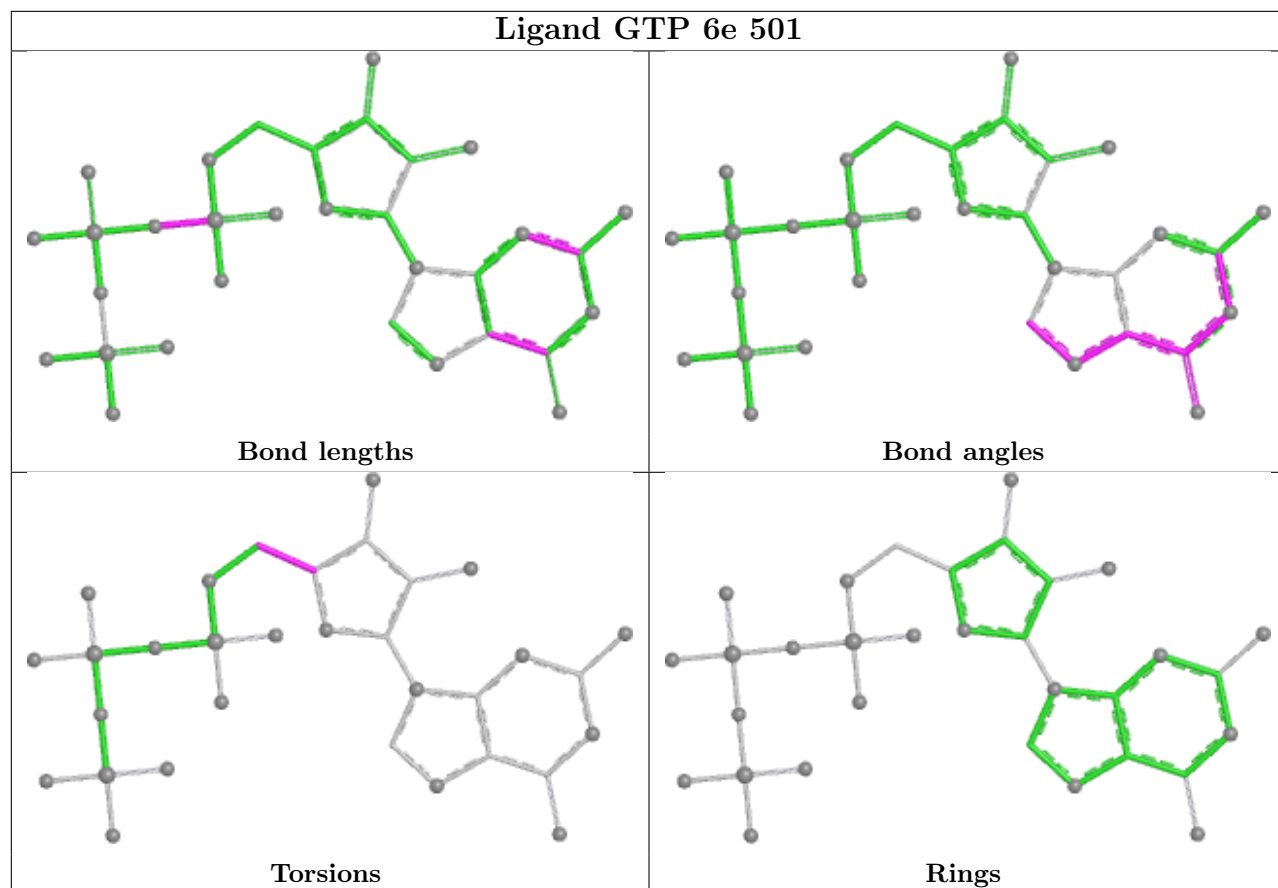


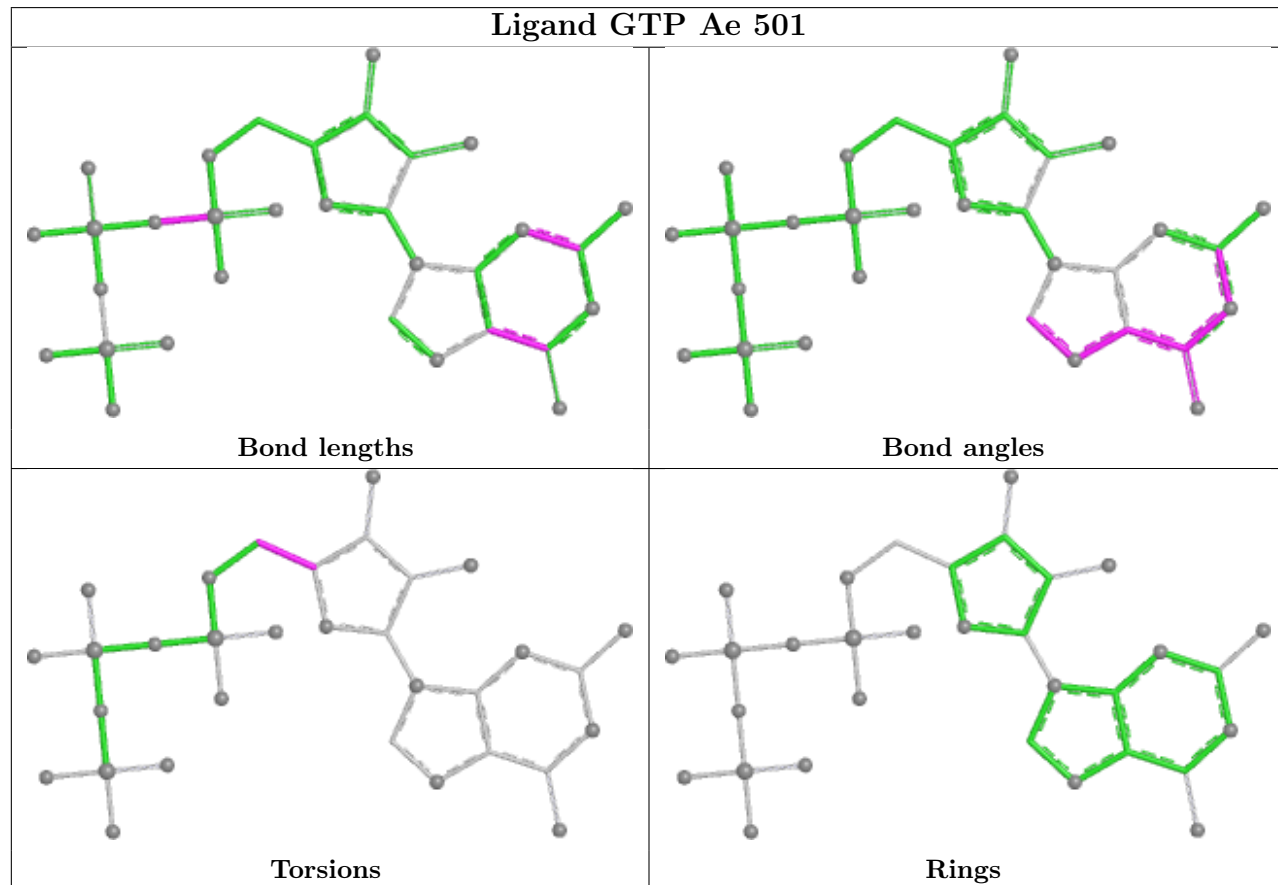
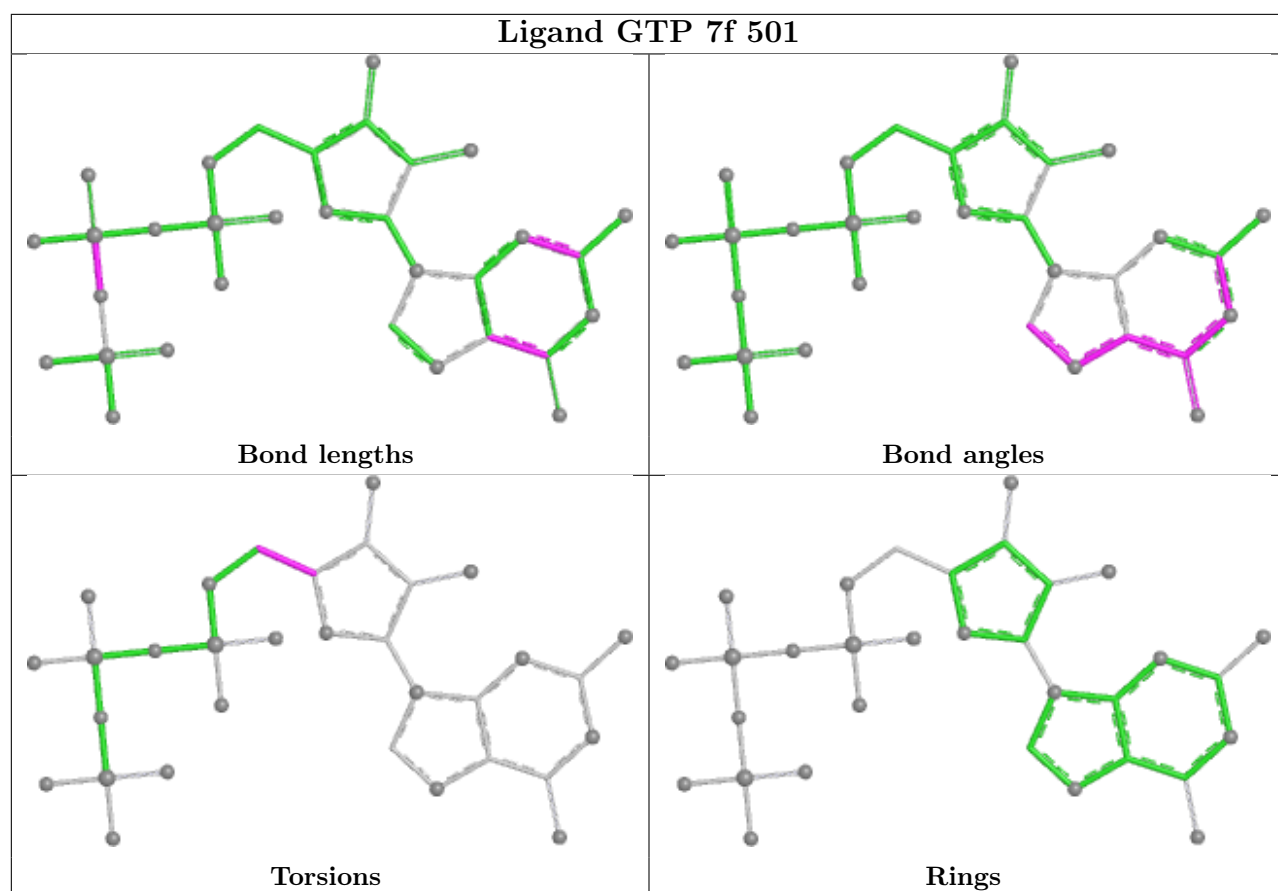
Ligand GTP 2d 501

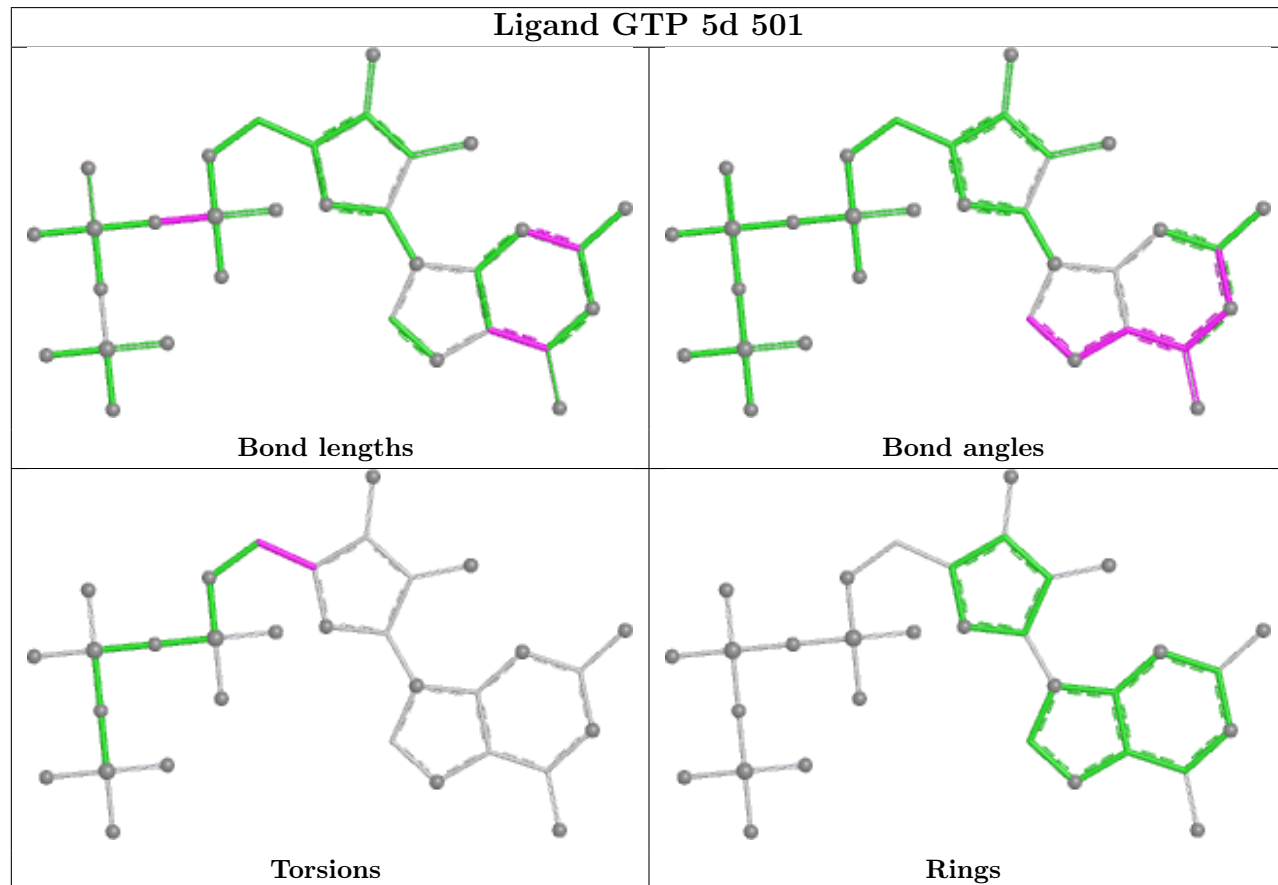
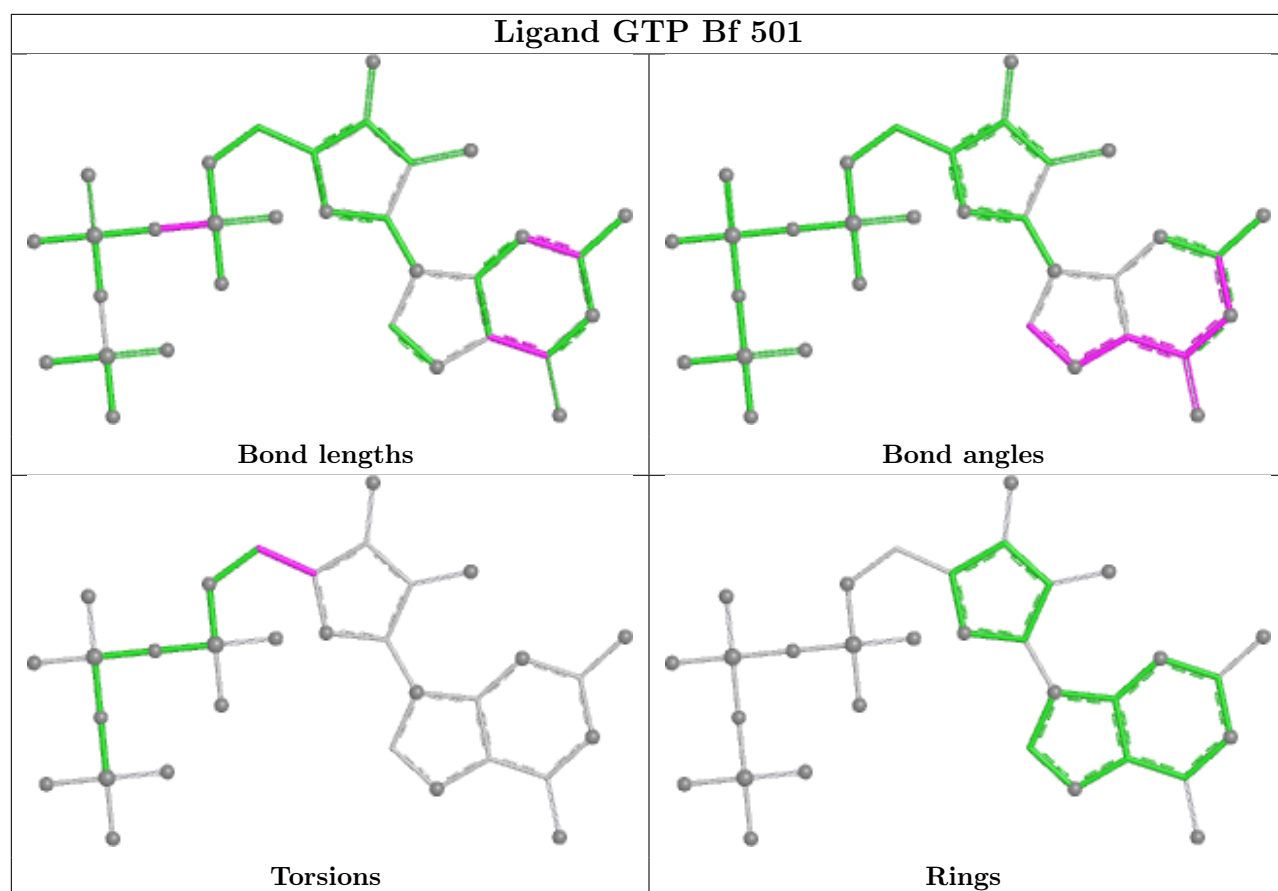


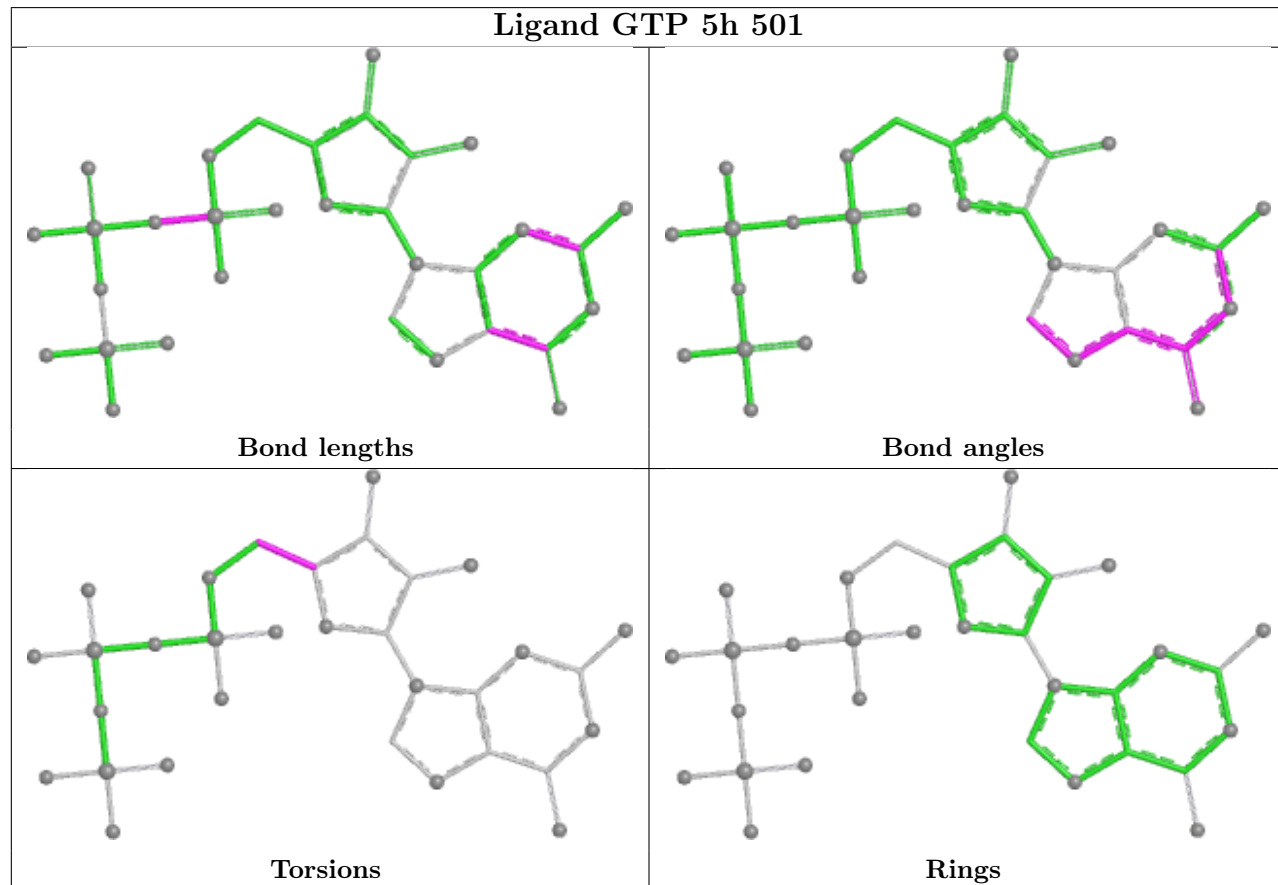
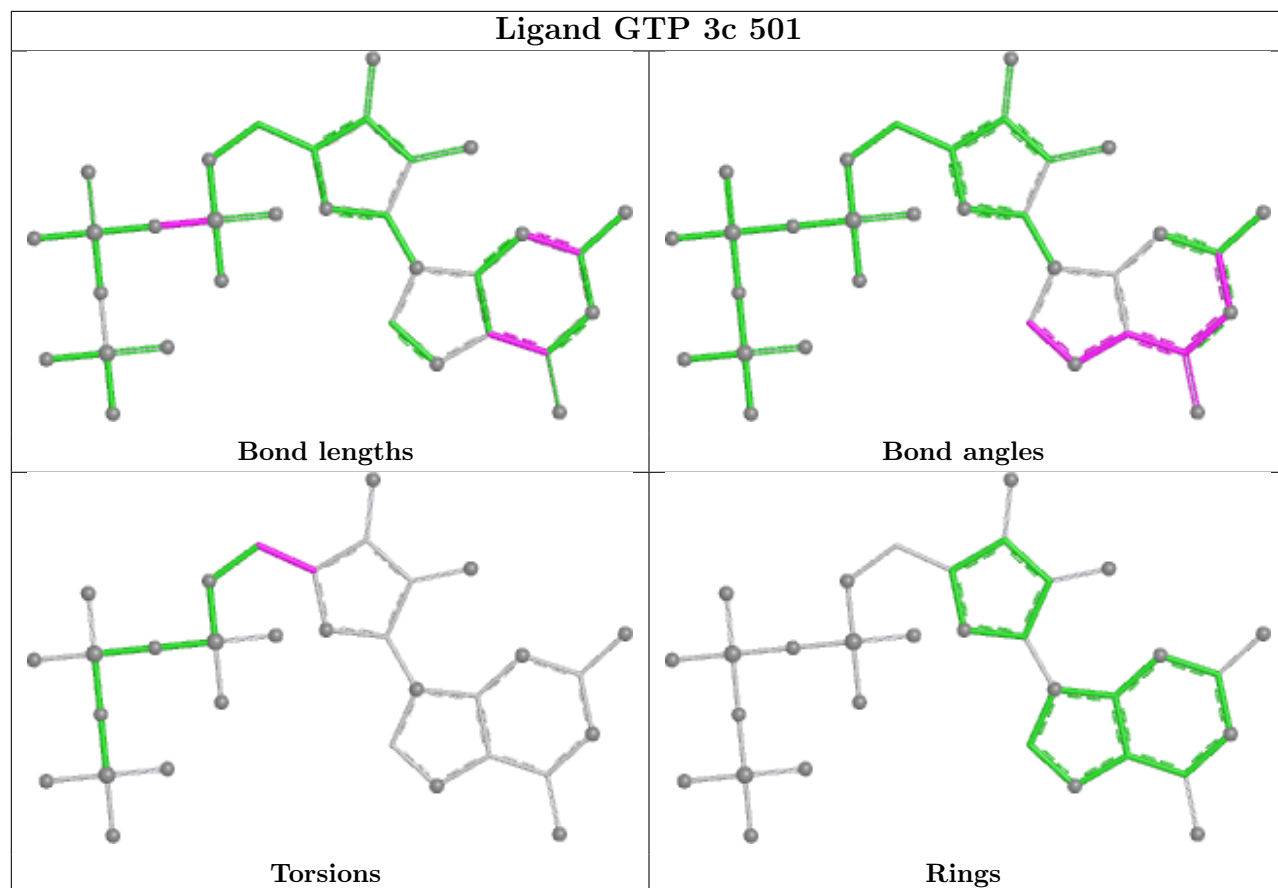
Ligand GTP 8f 501

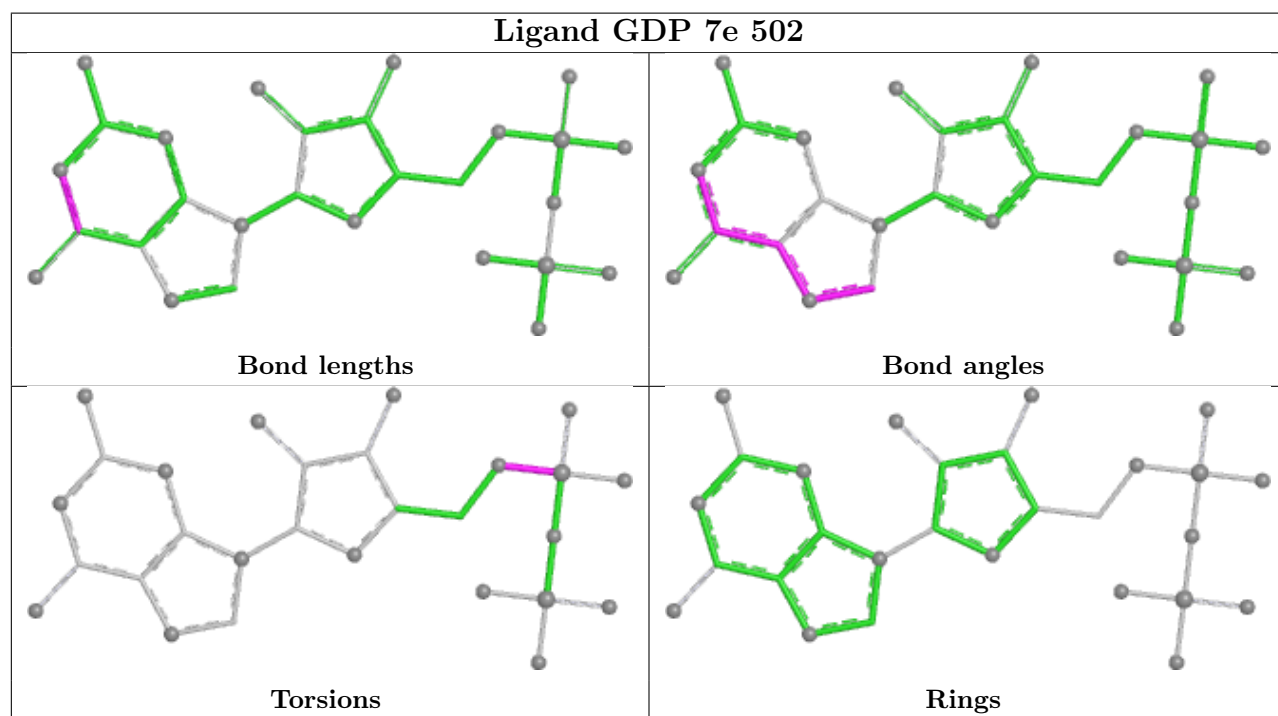
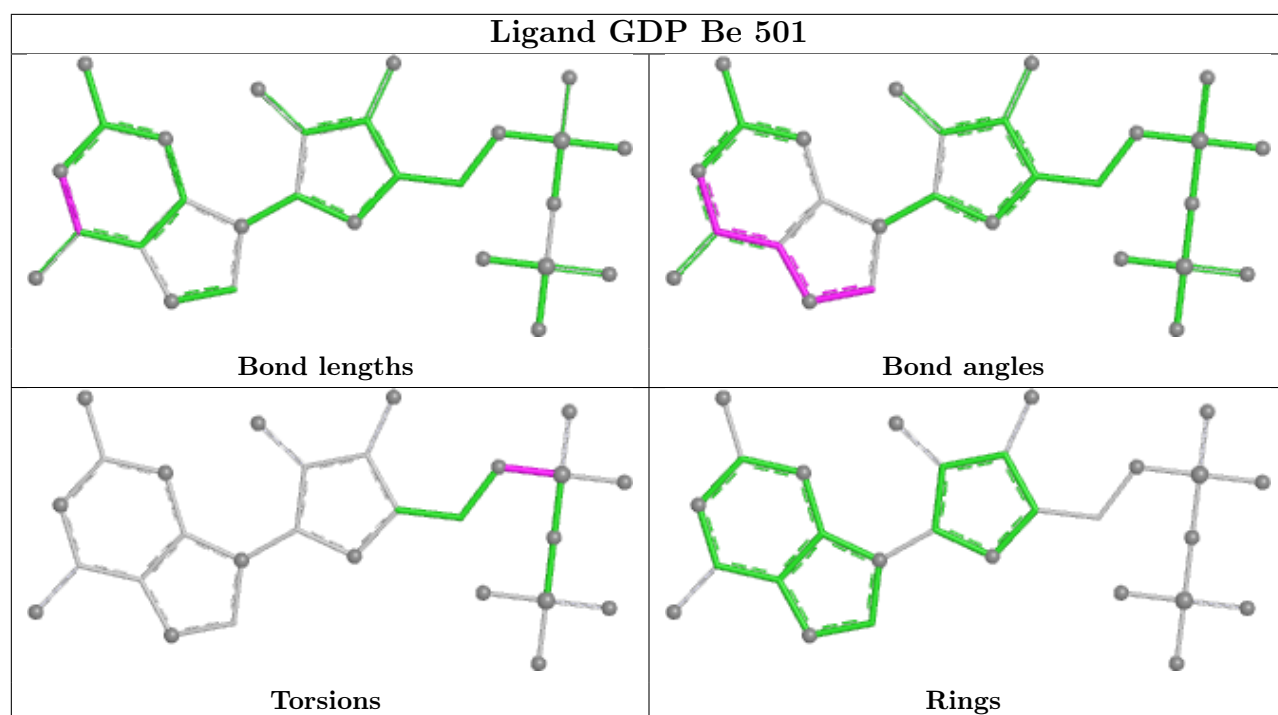


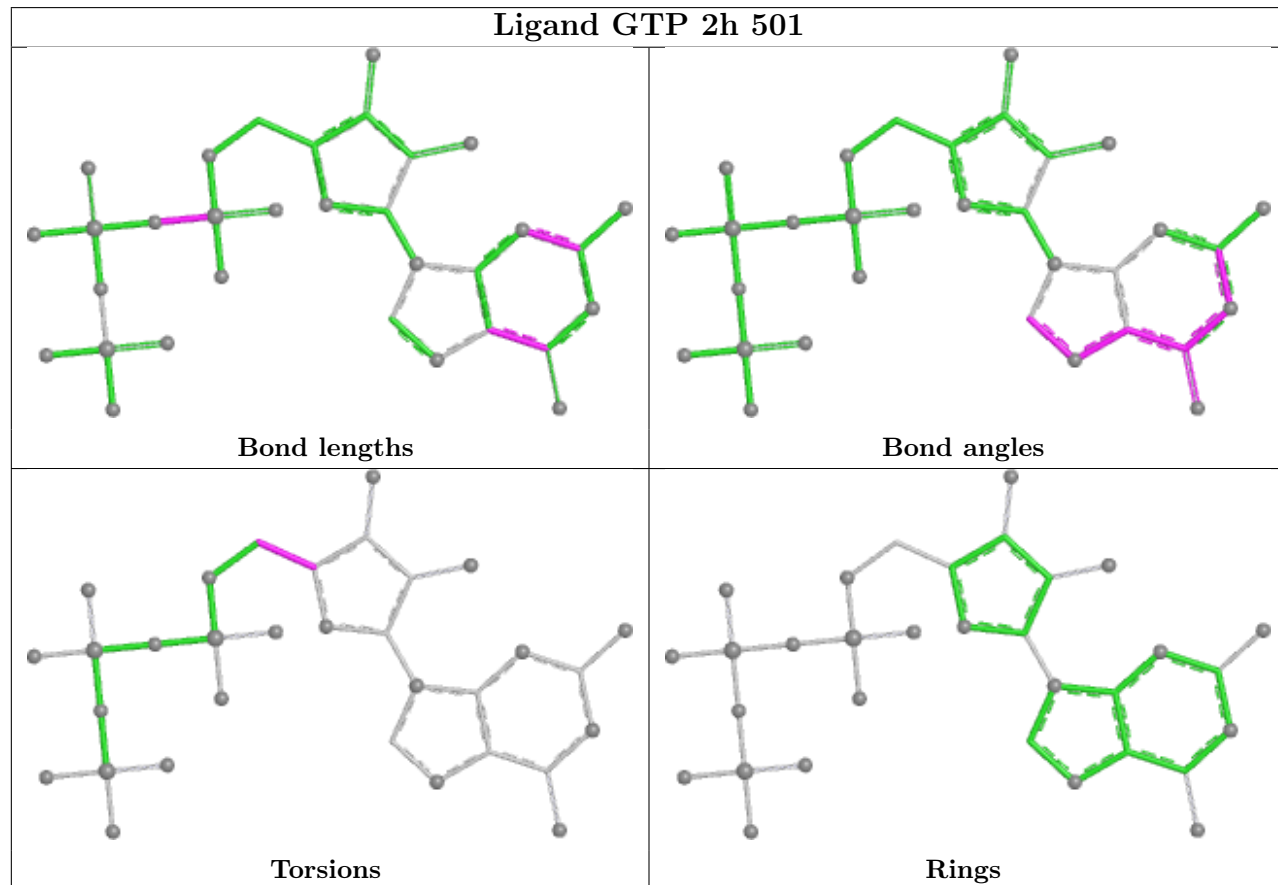
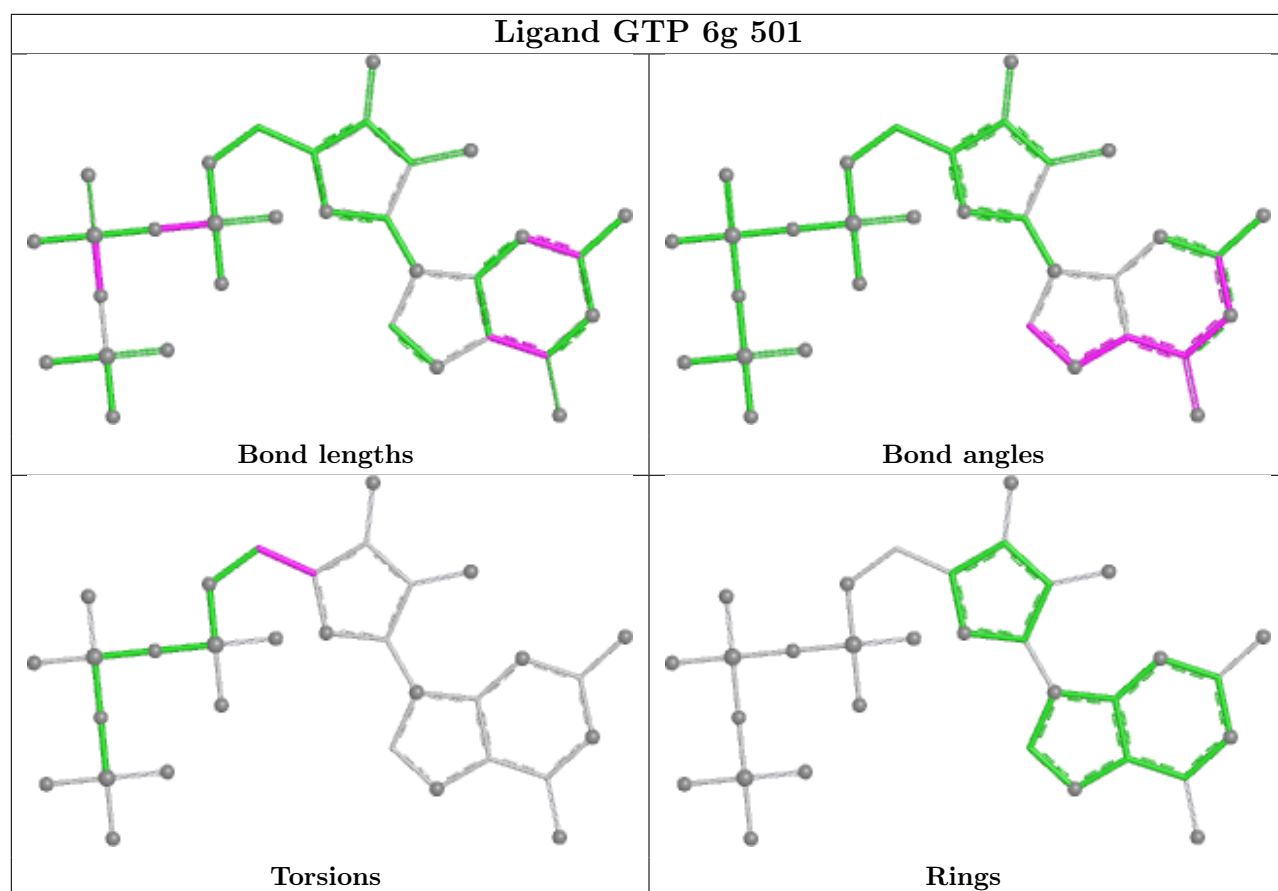


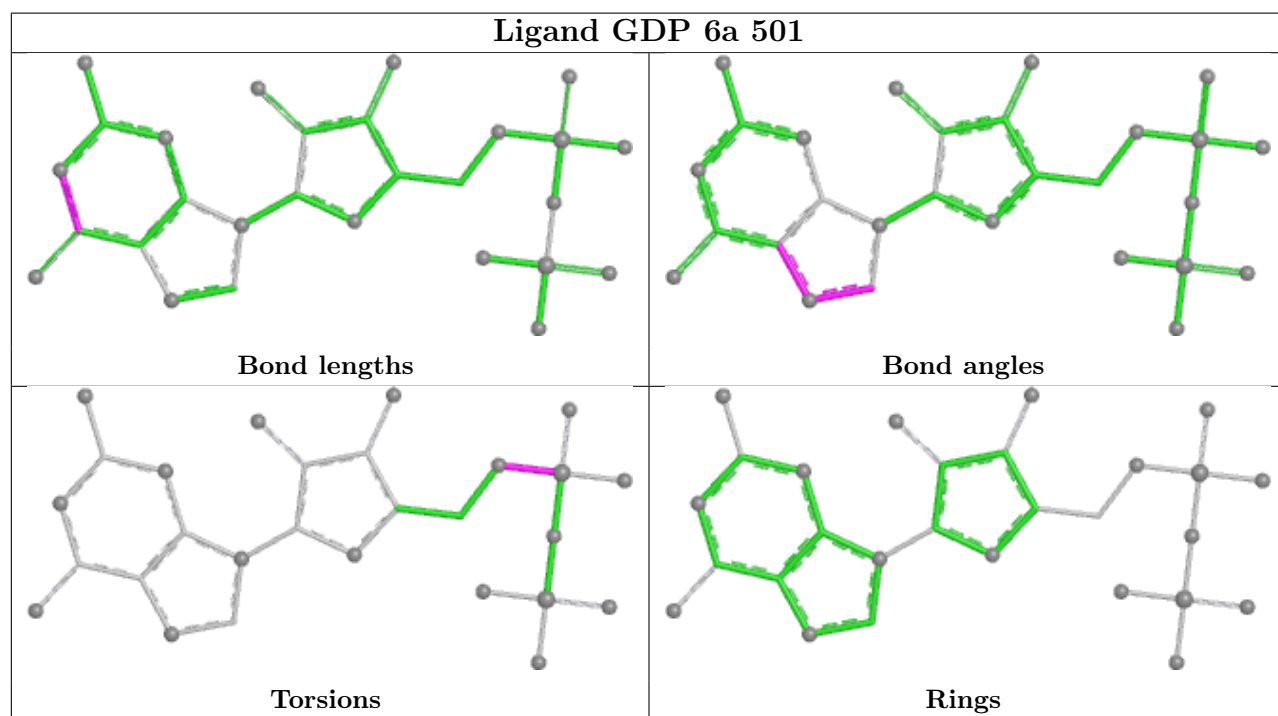
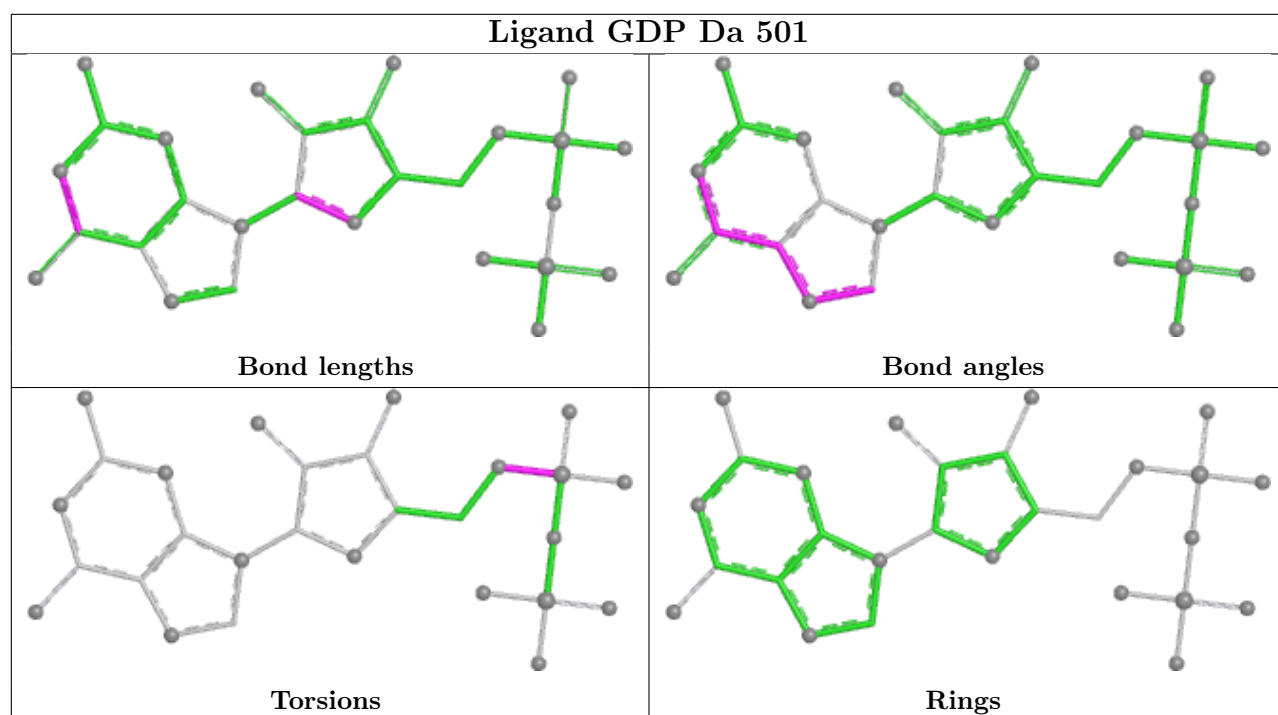




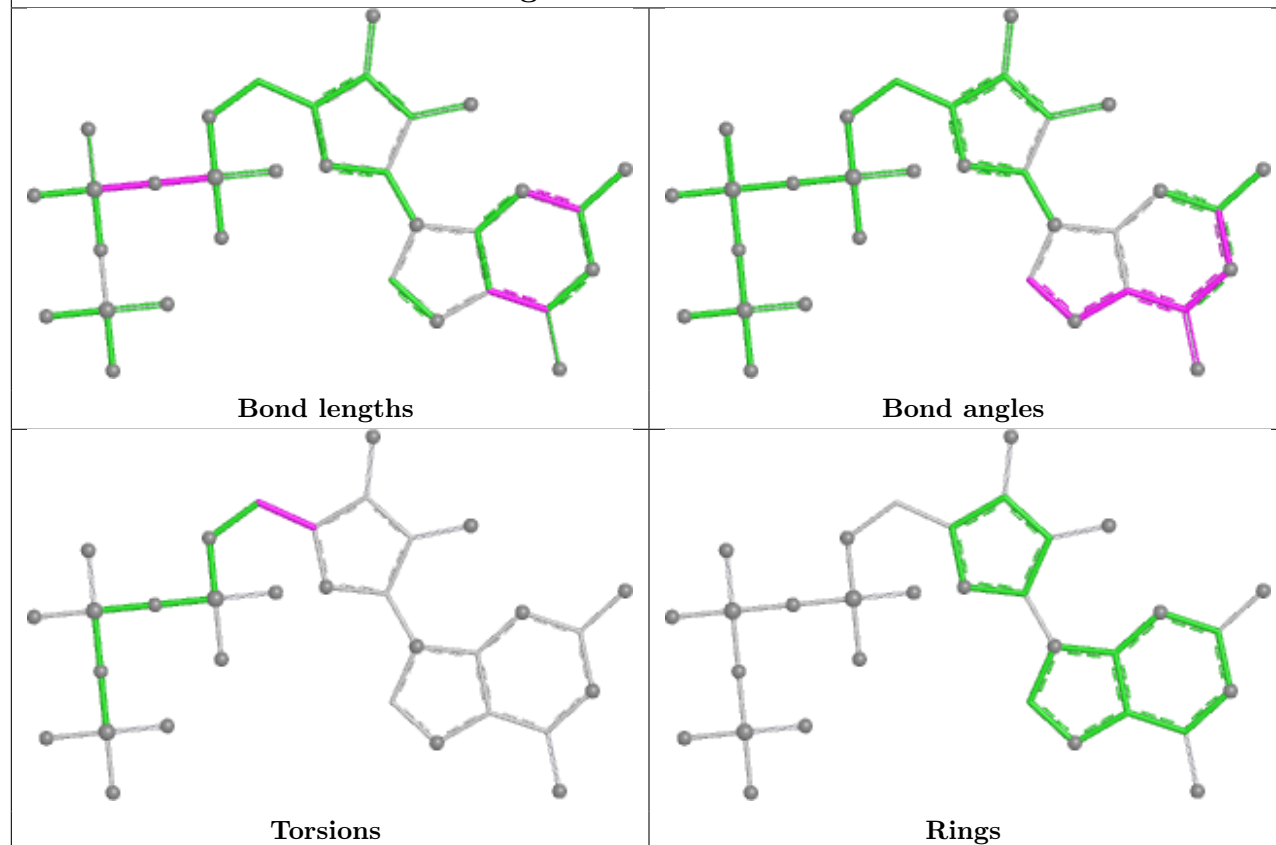




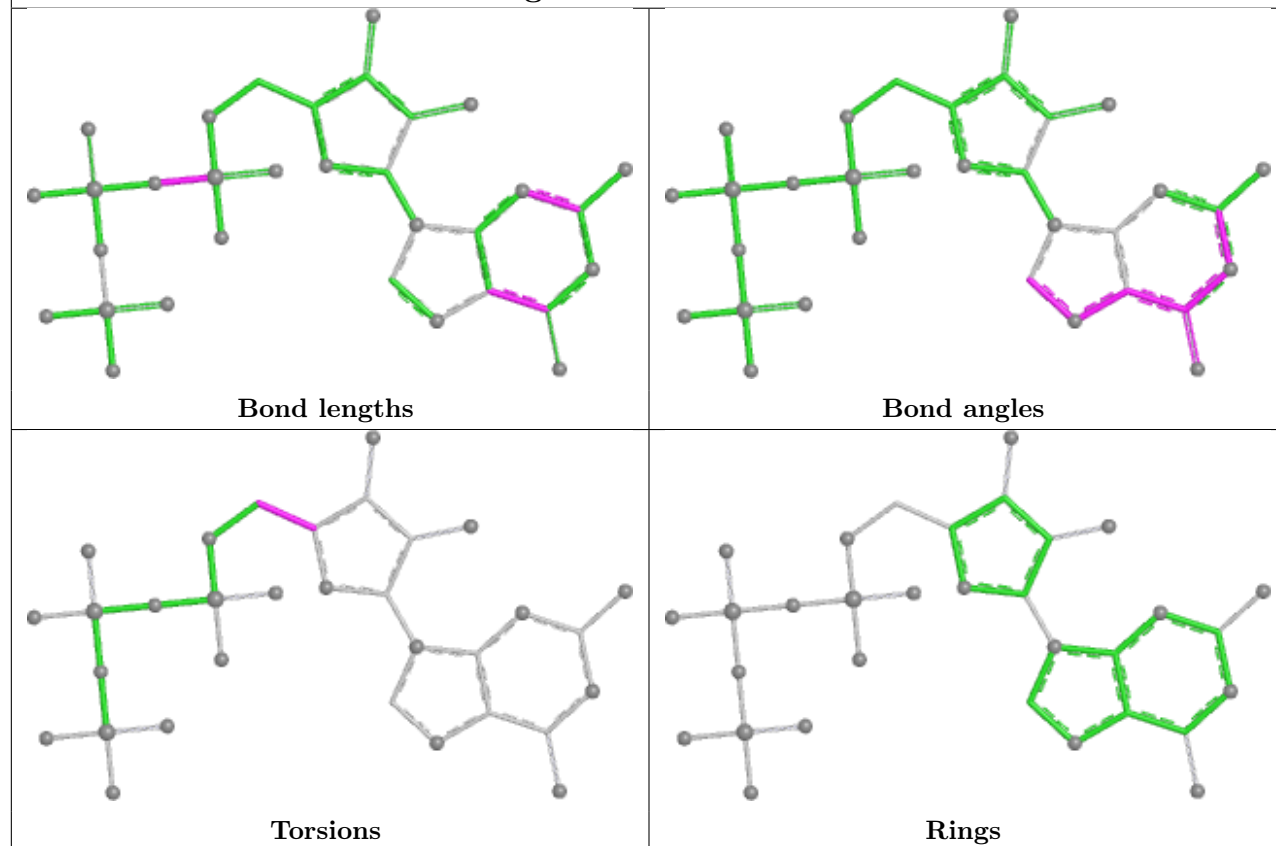


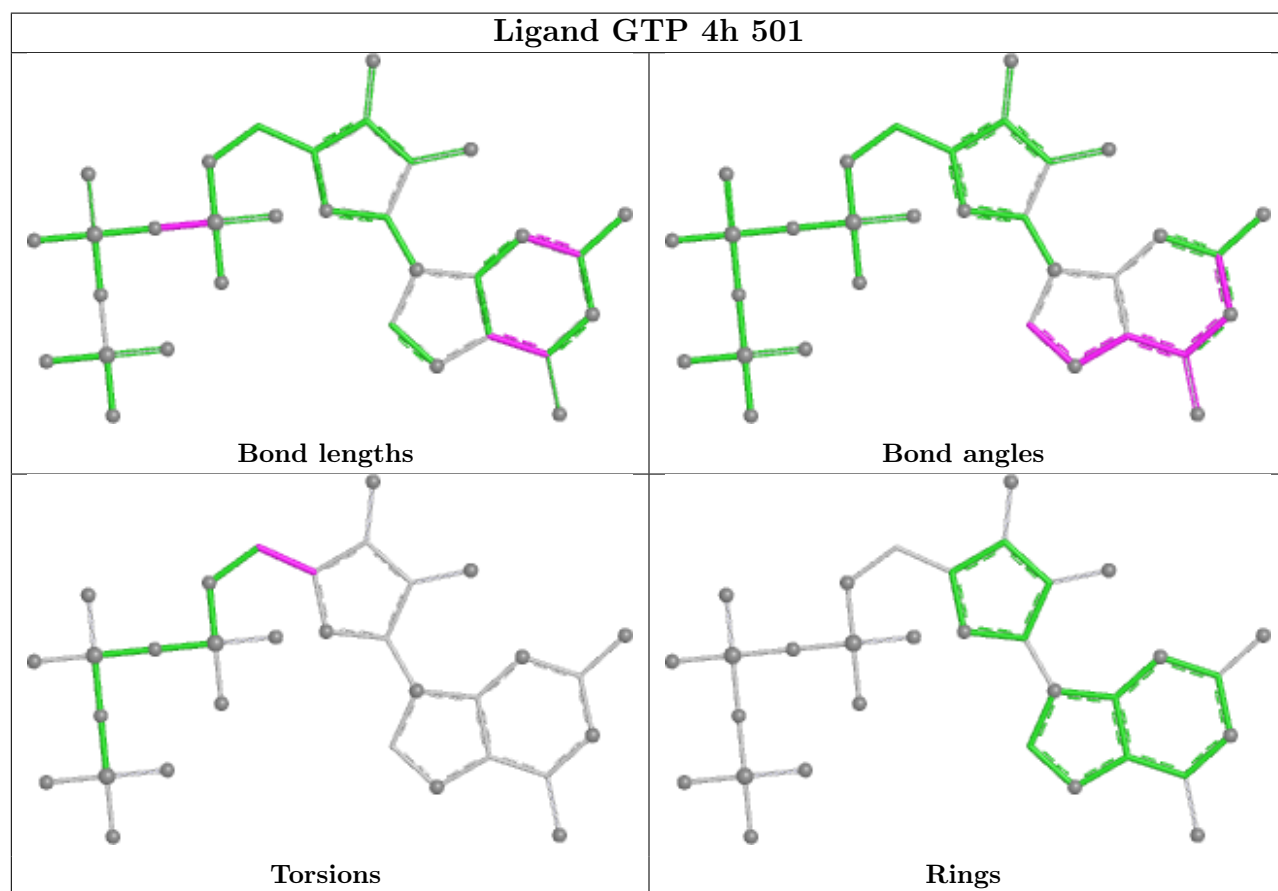
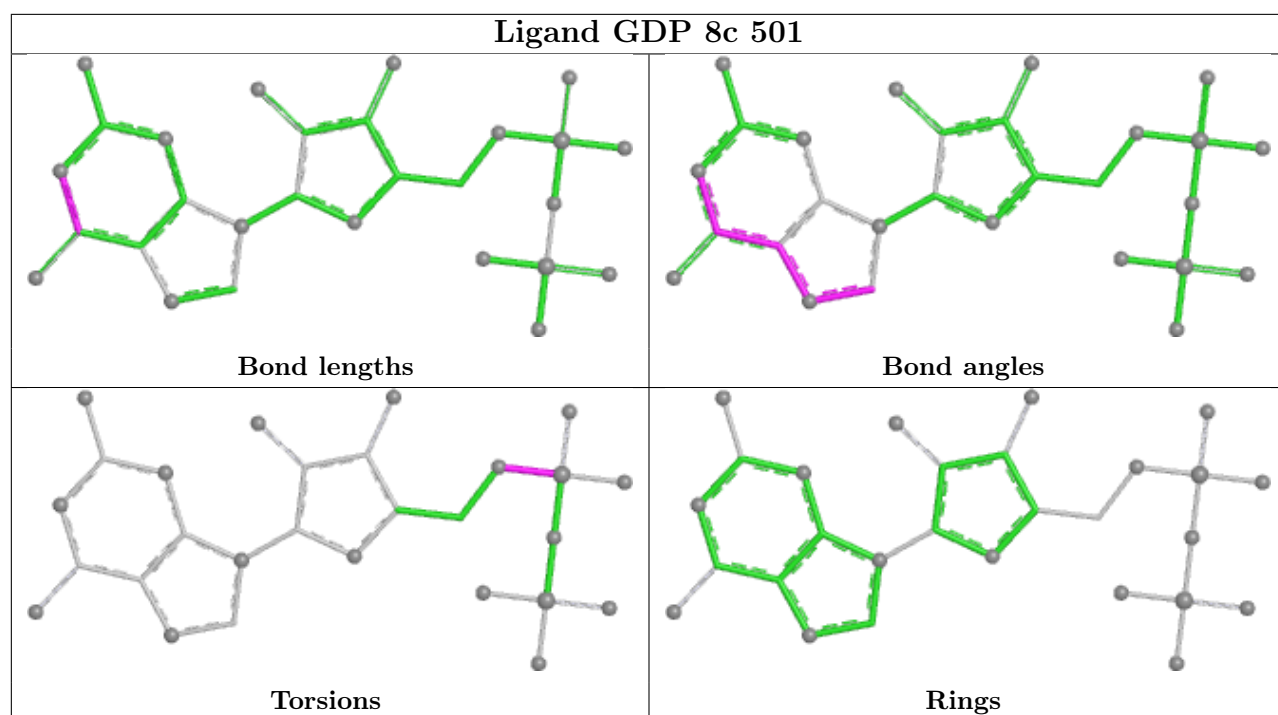


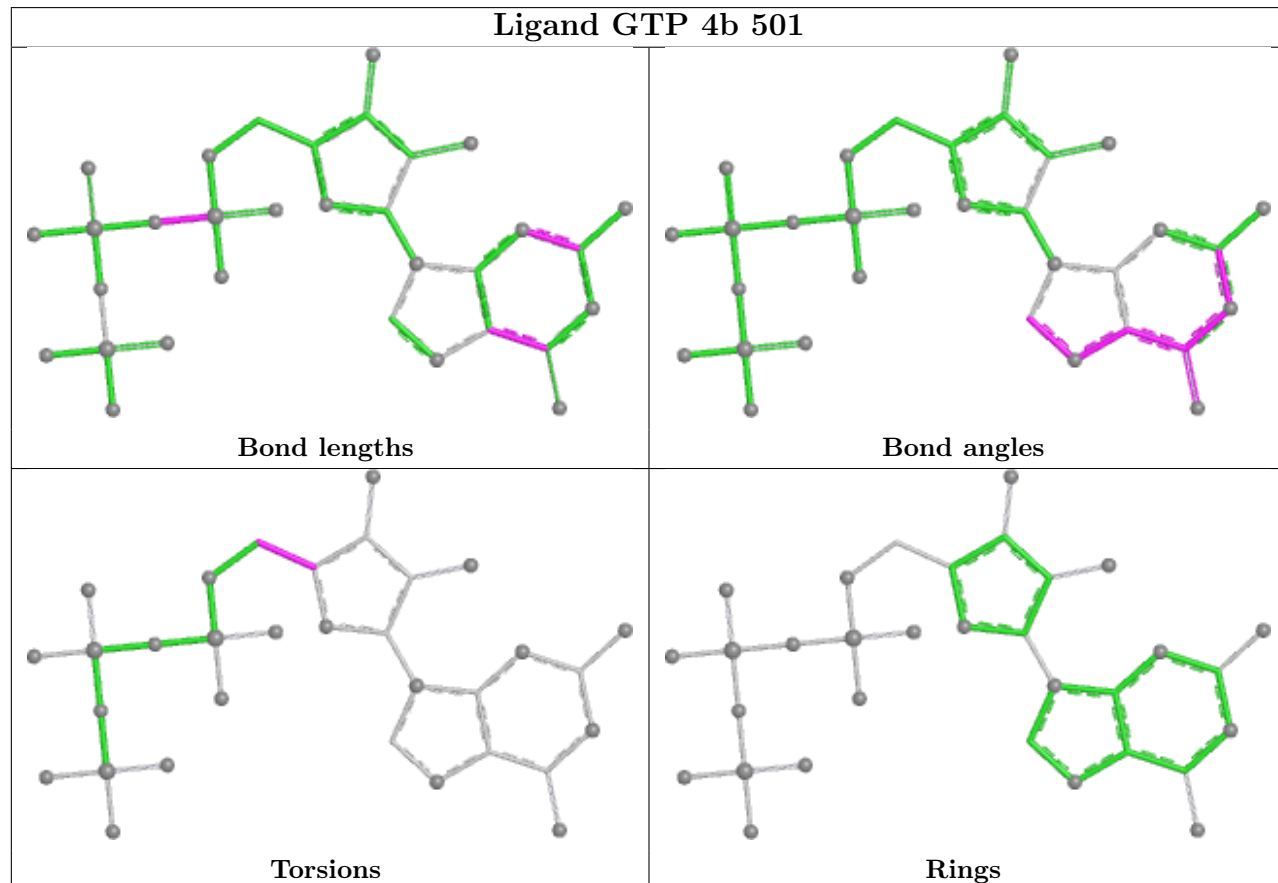
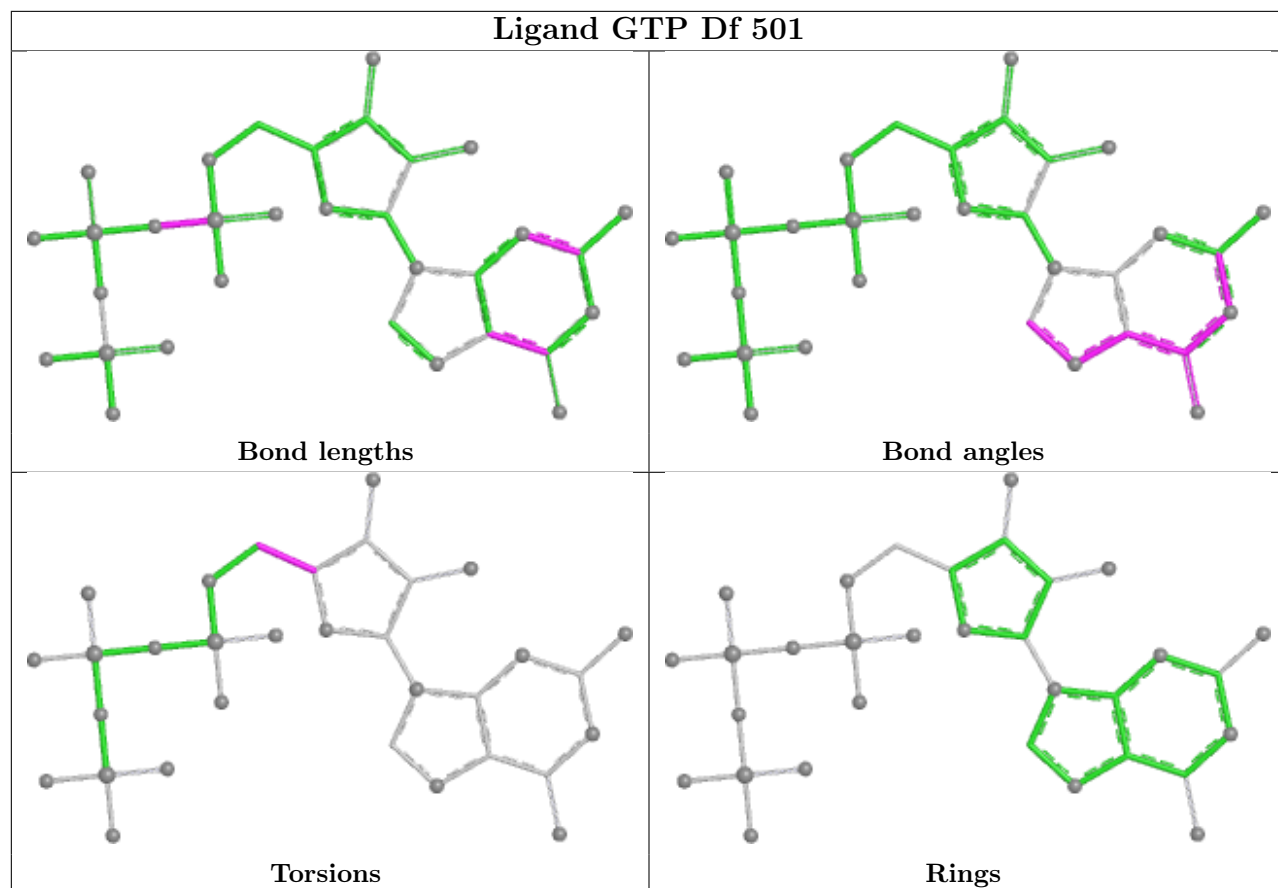
Ligand GTP Ah 501

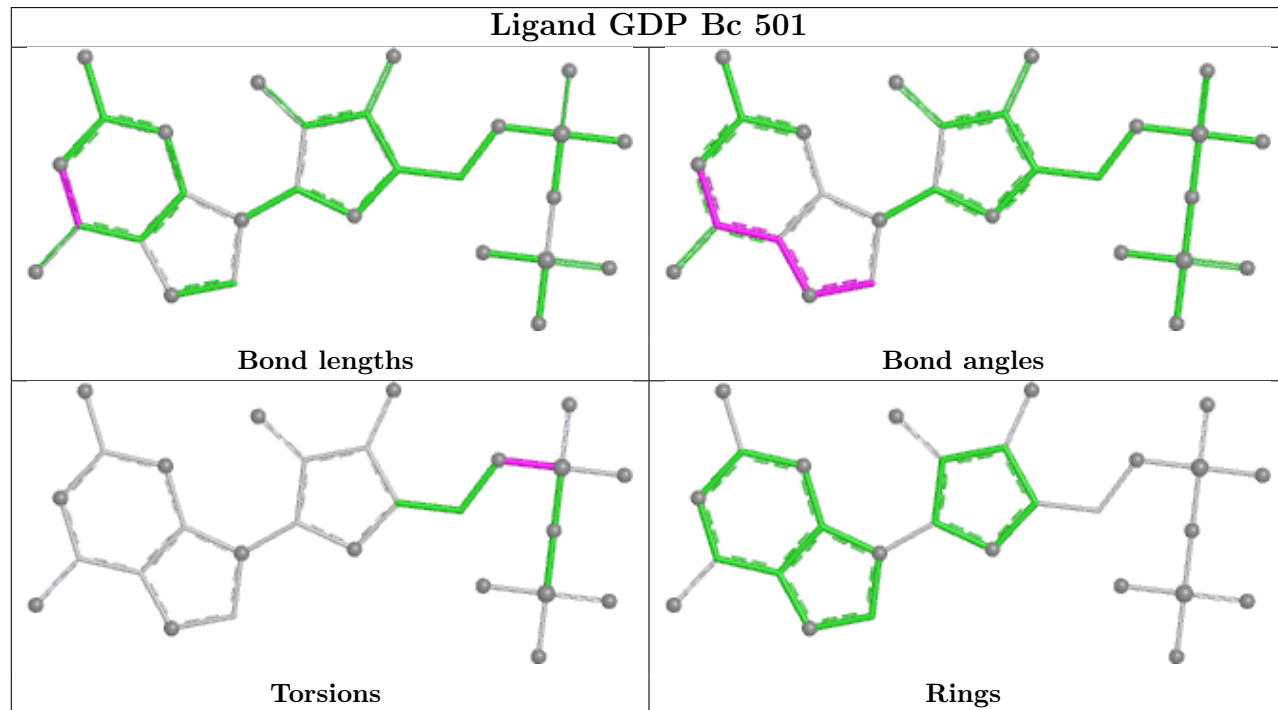
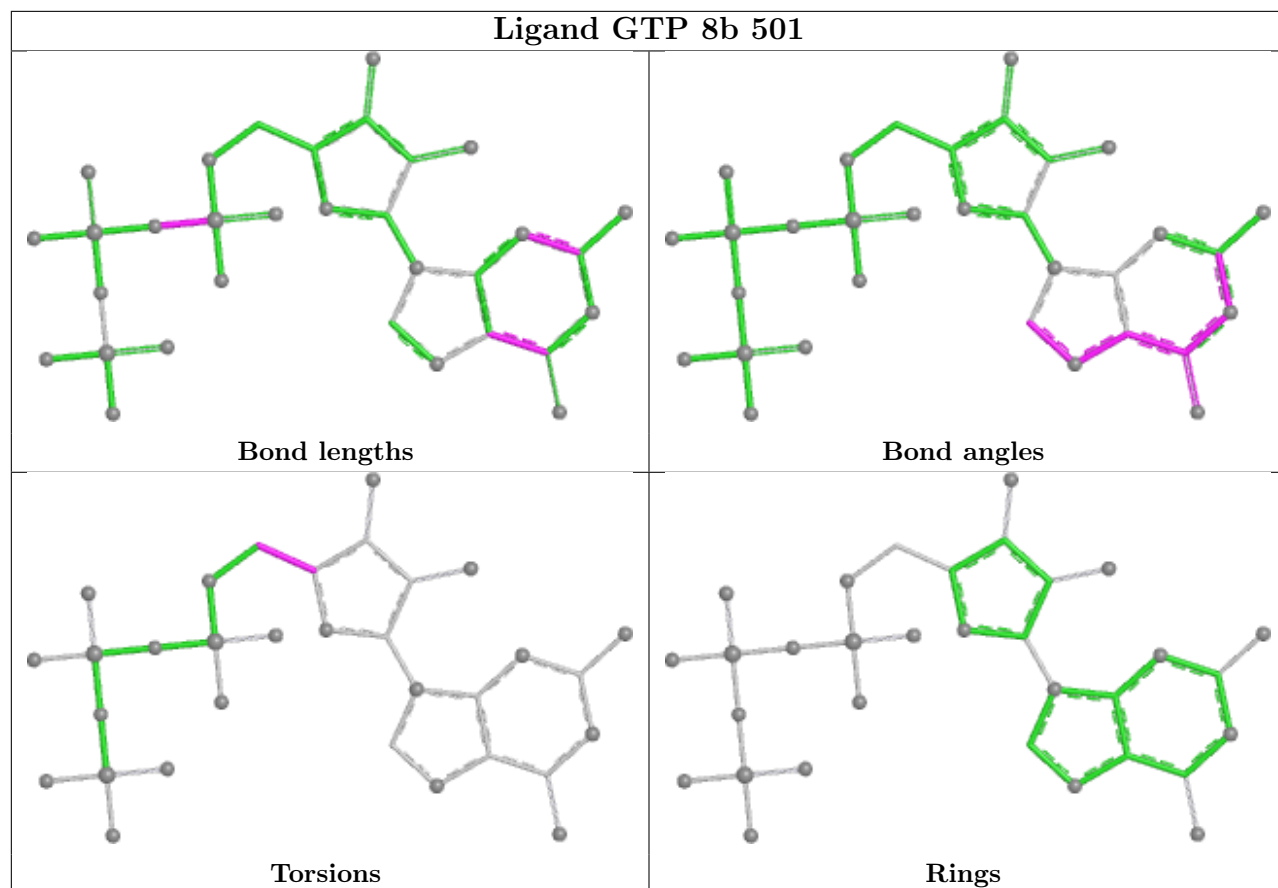


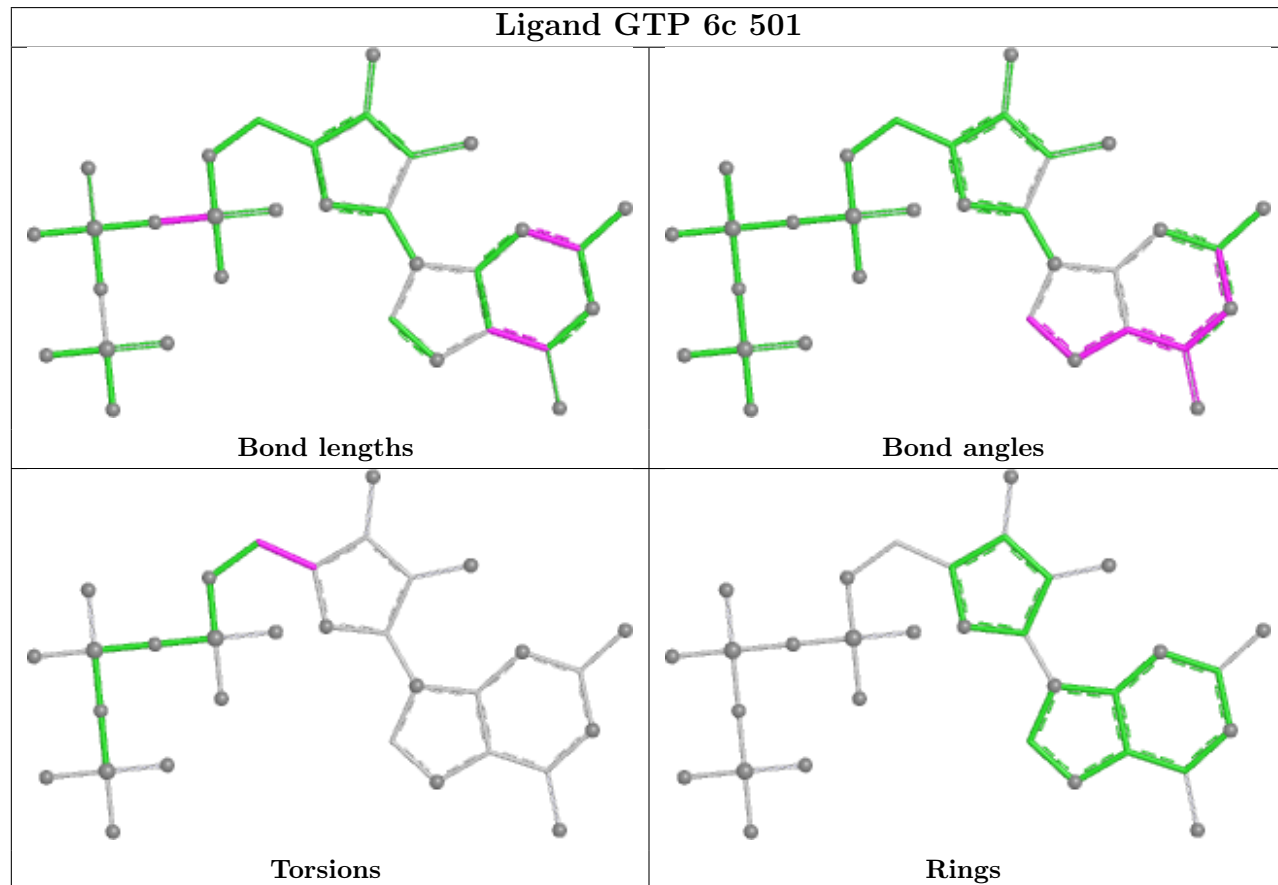
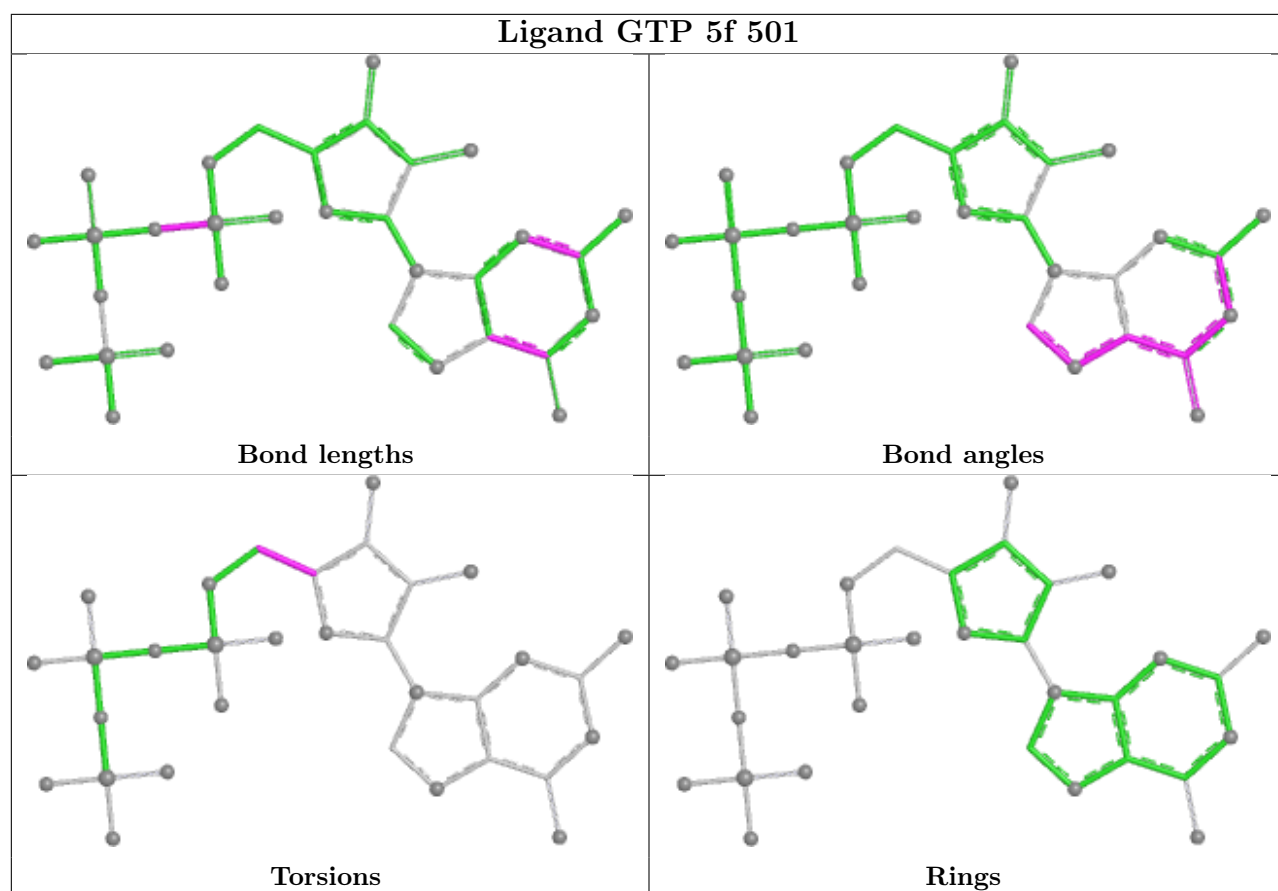
Ligand GTP 4d 501



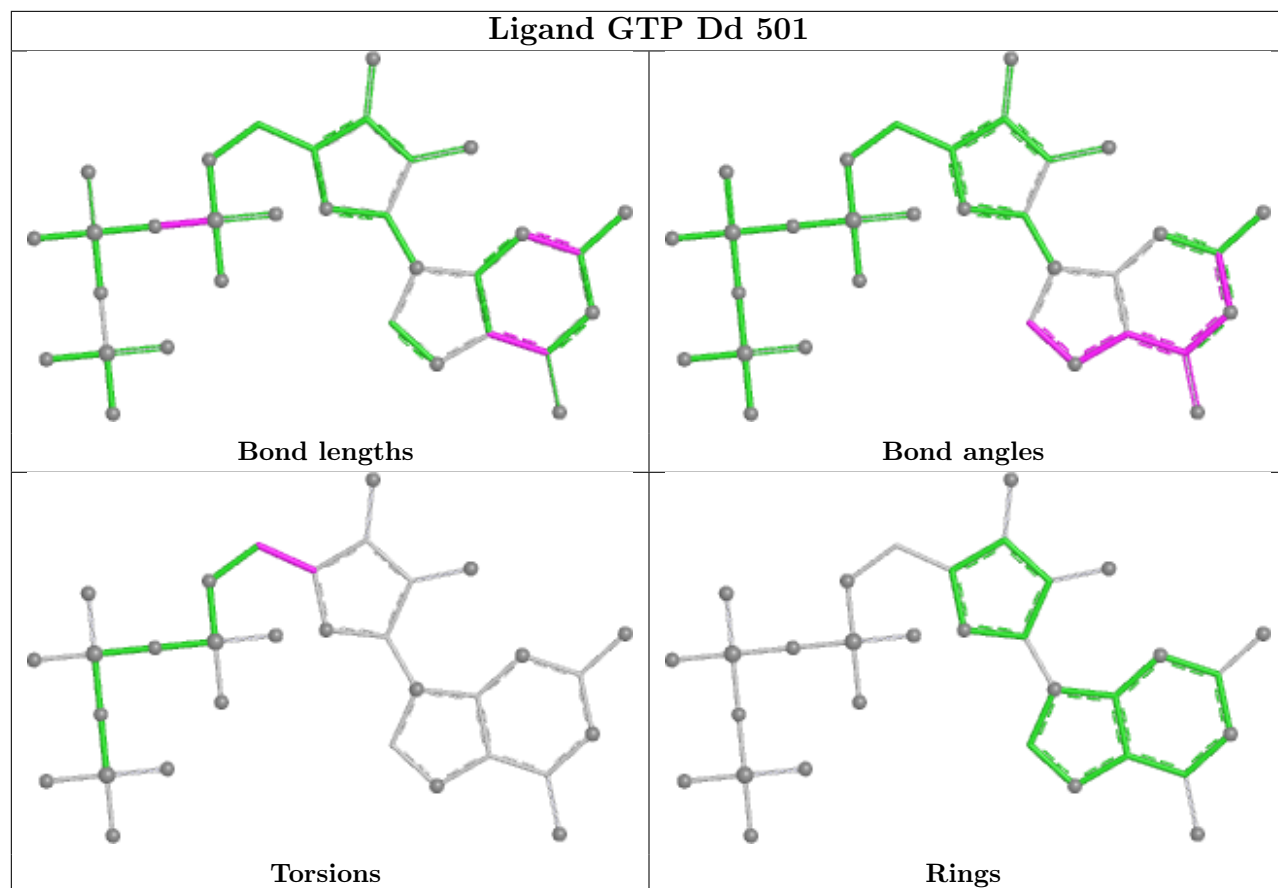




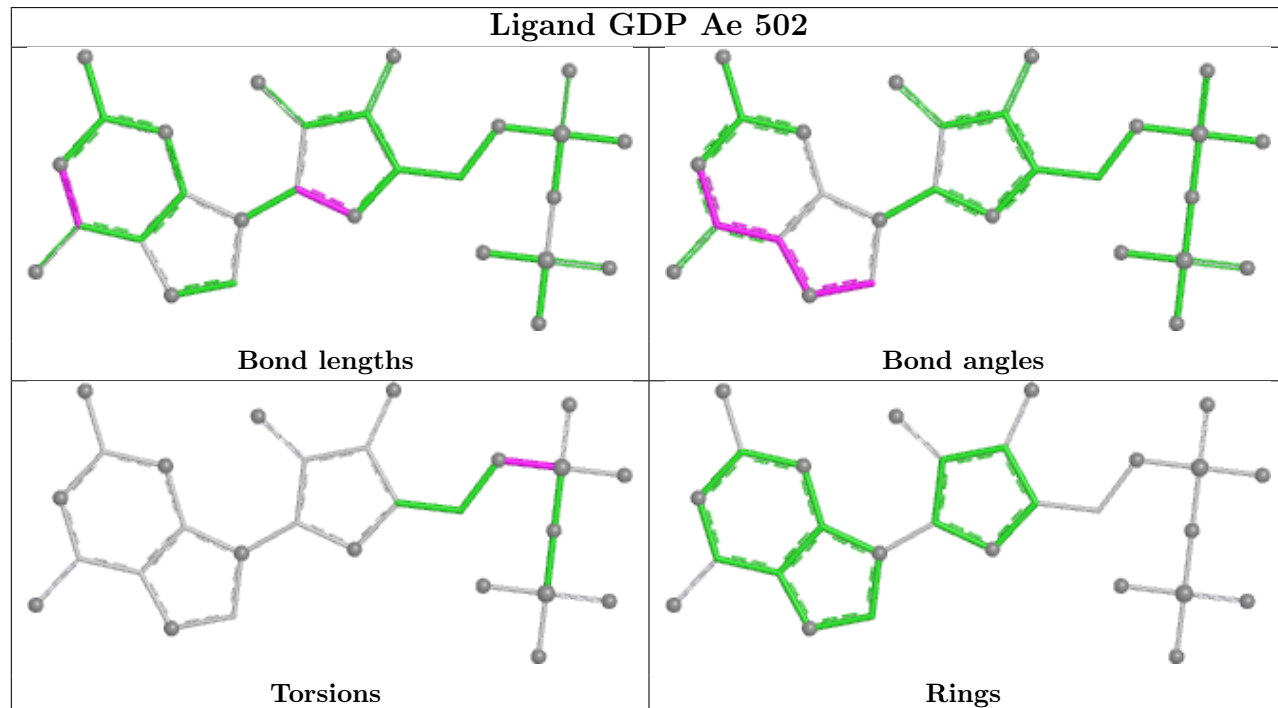


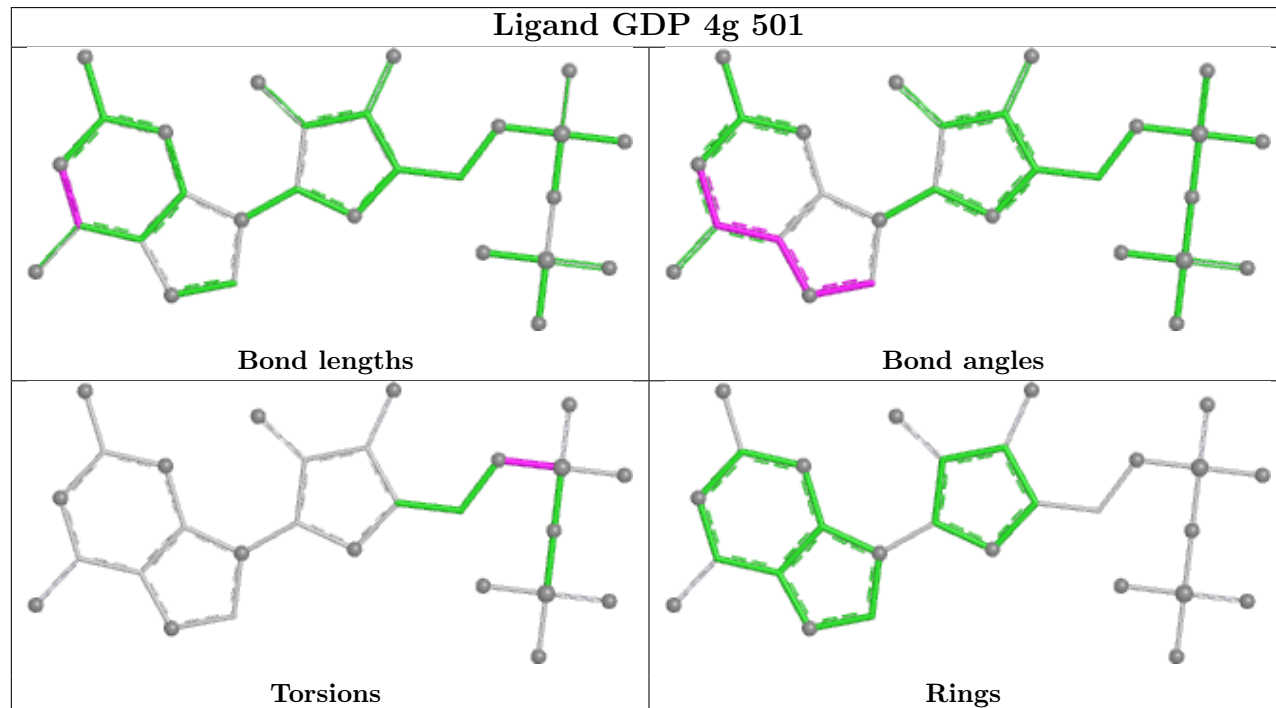
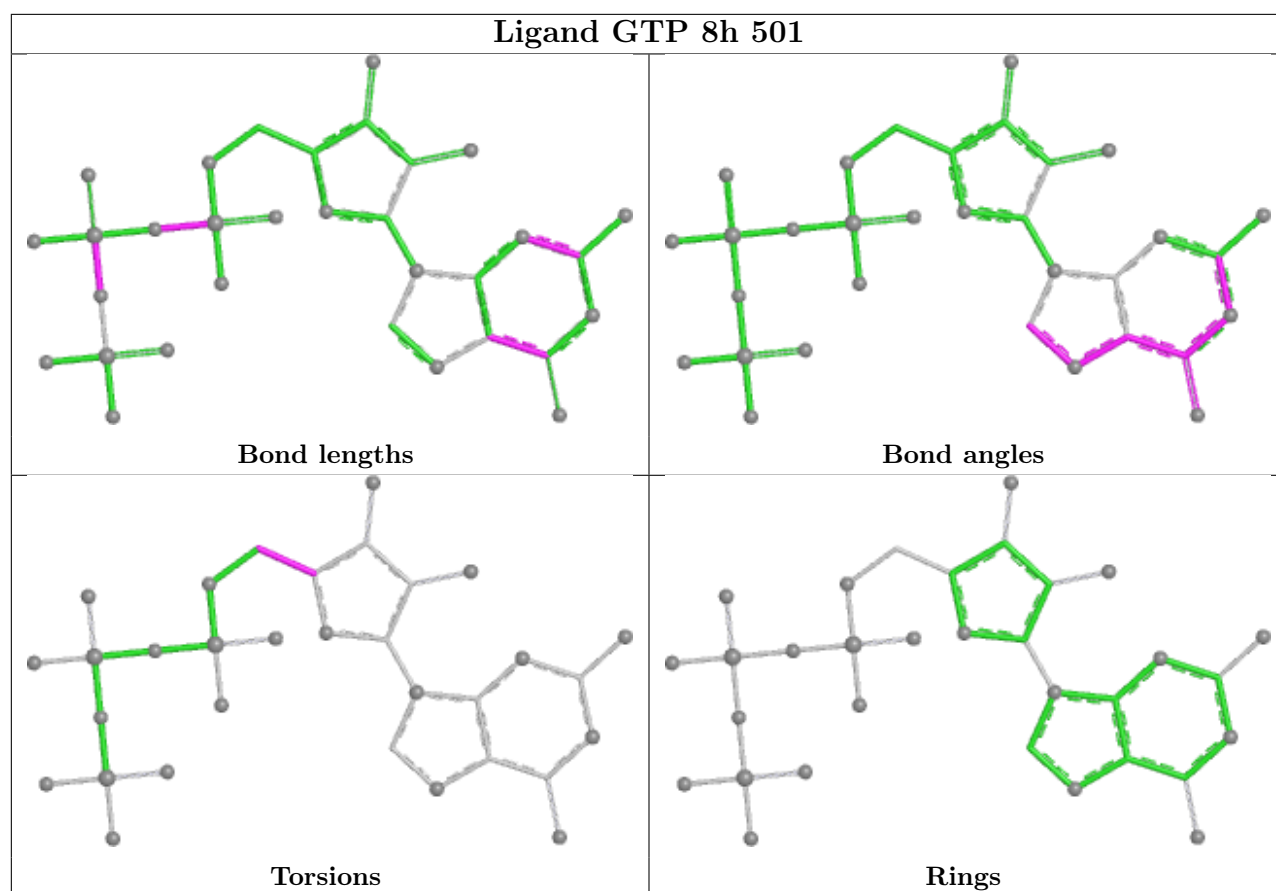


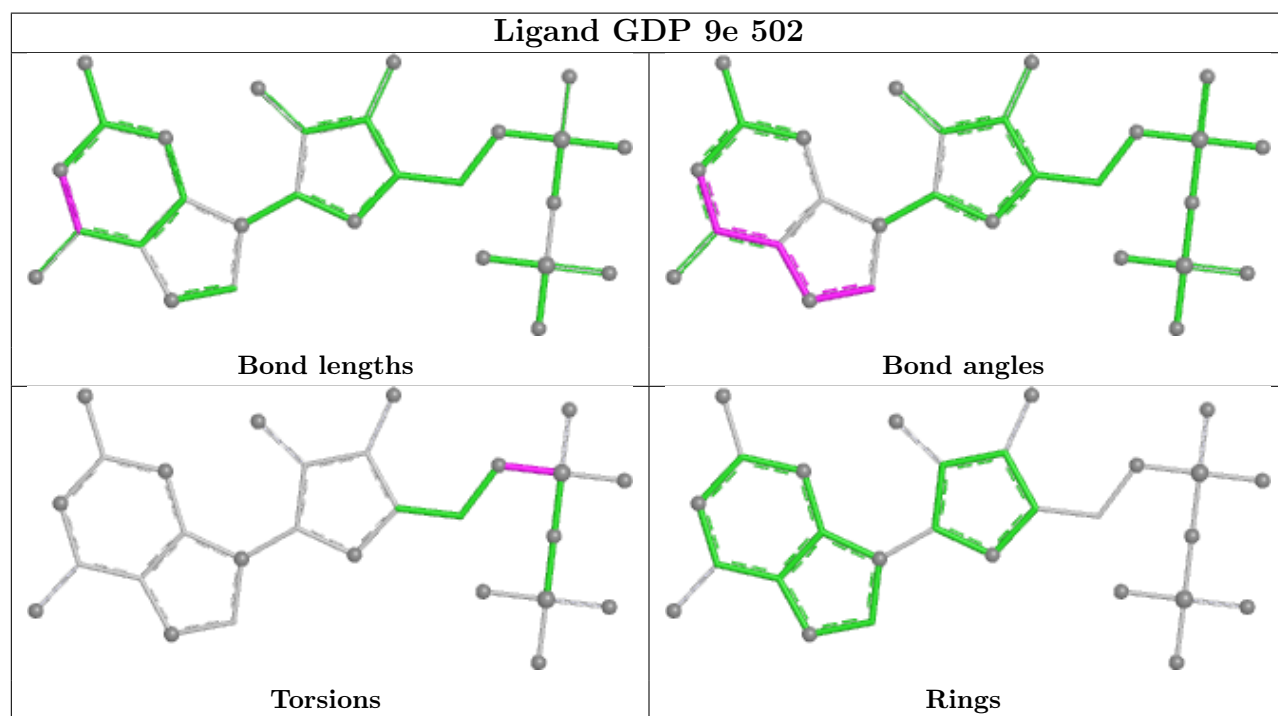
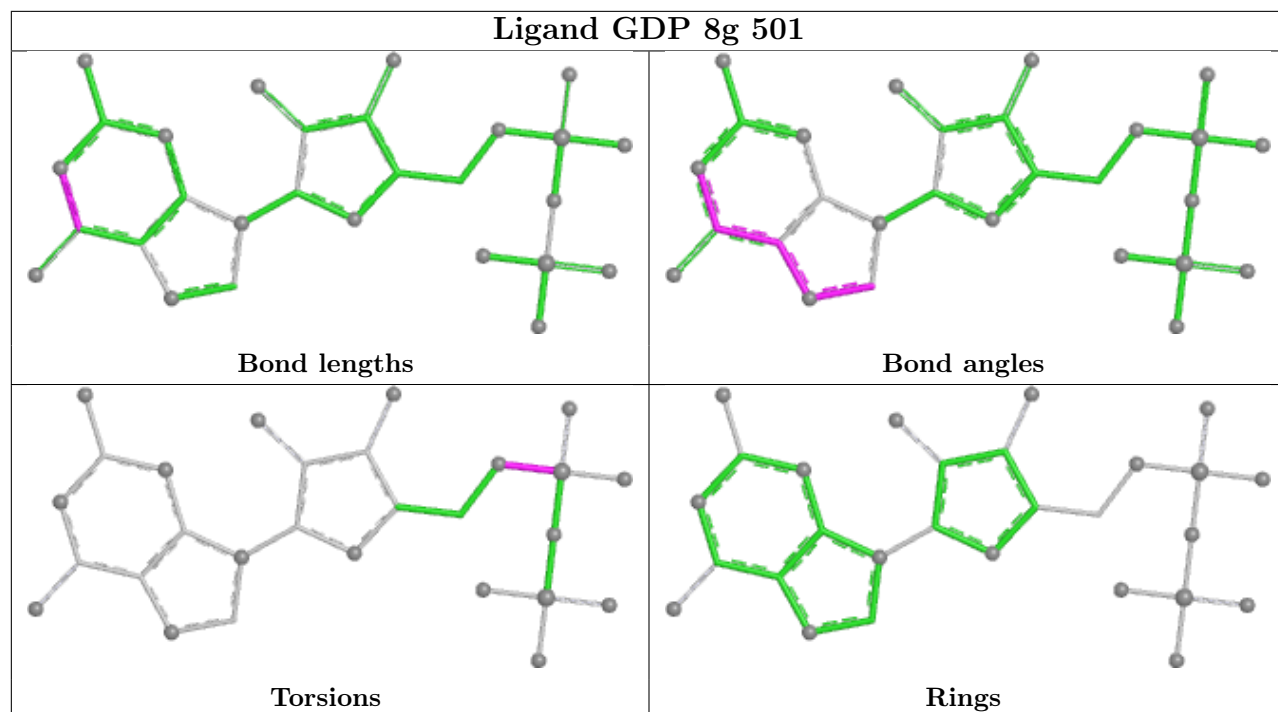
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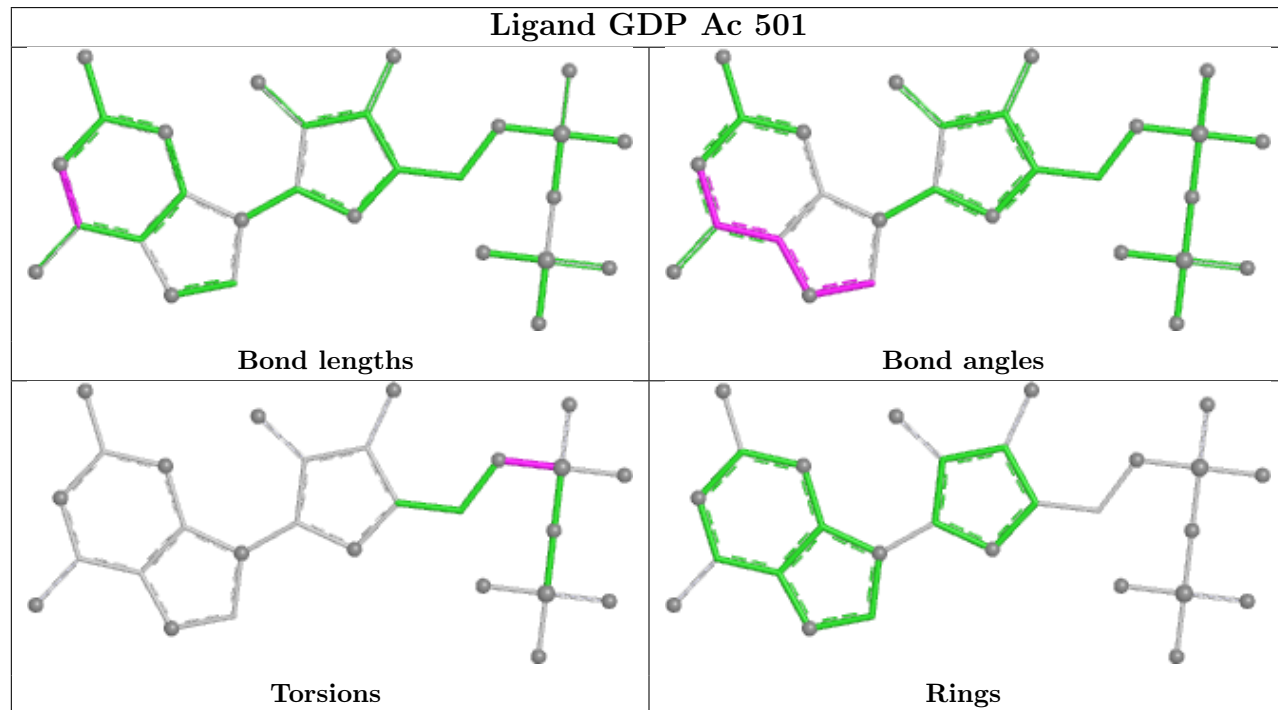
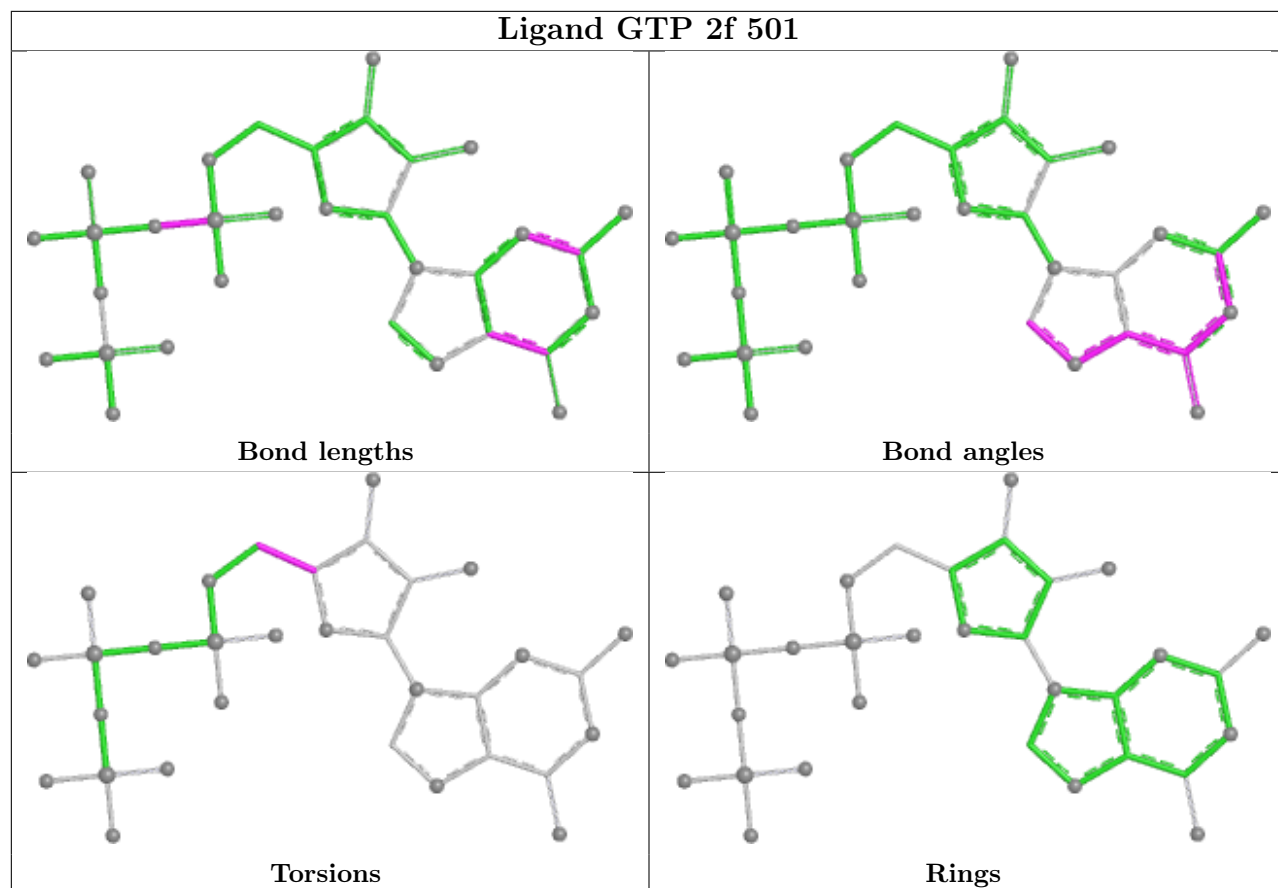


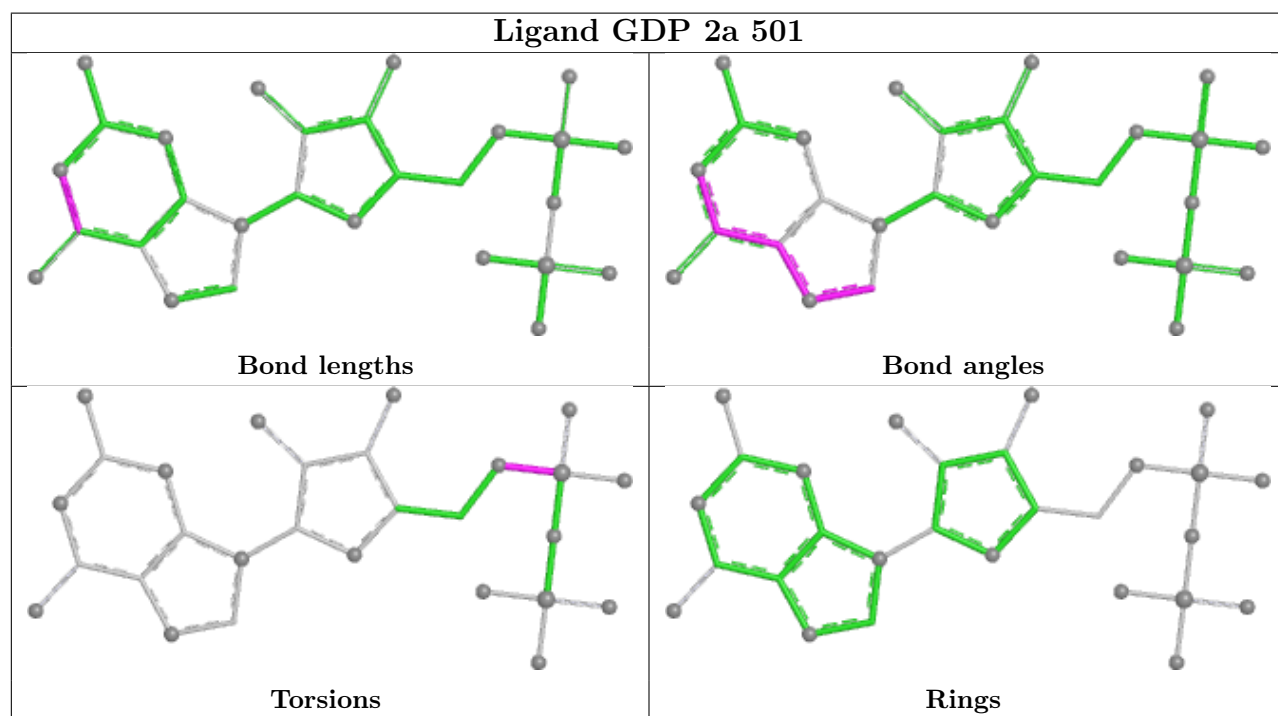
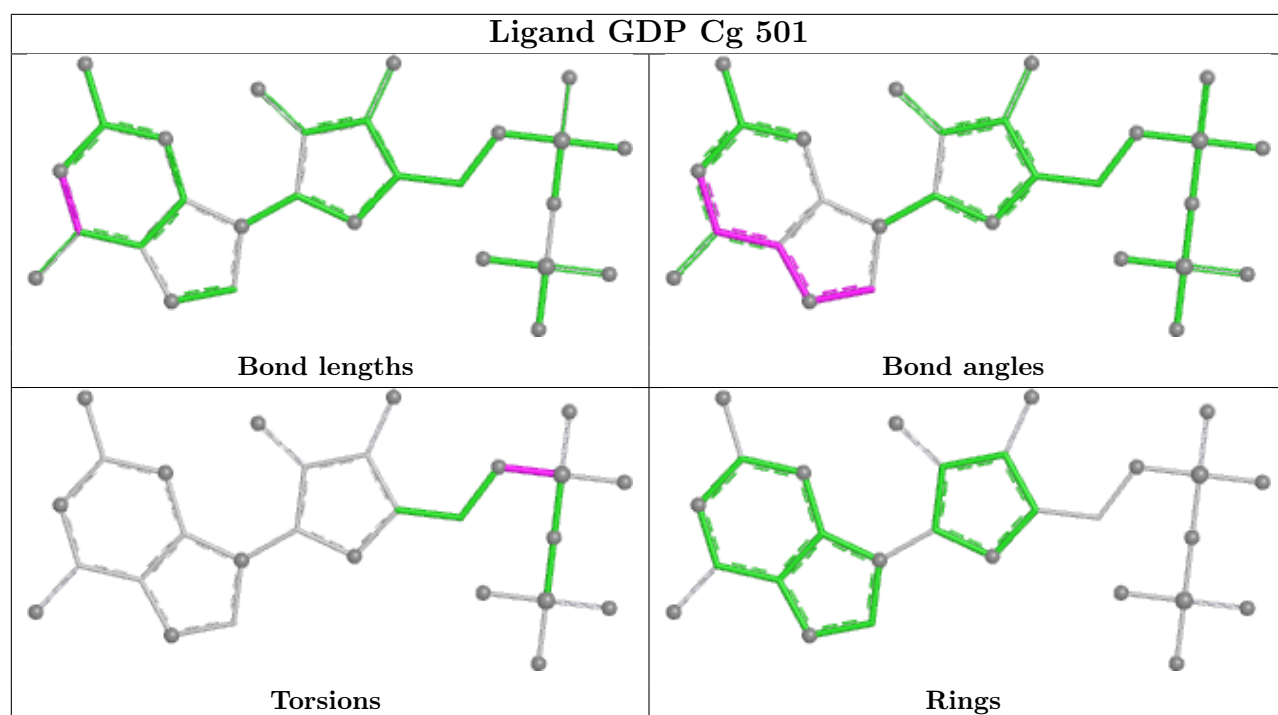
Ligand GDP Ae 502

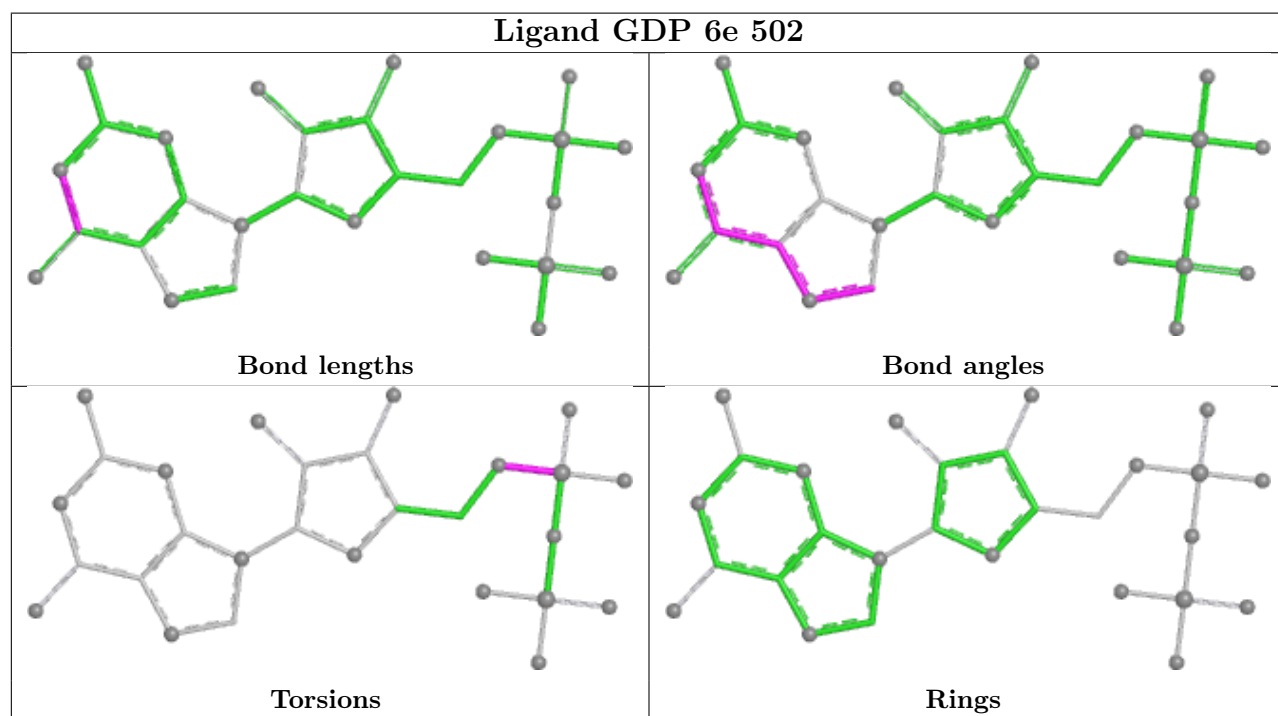
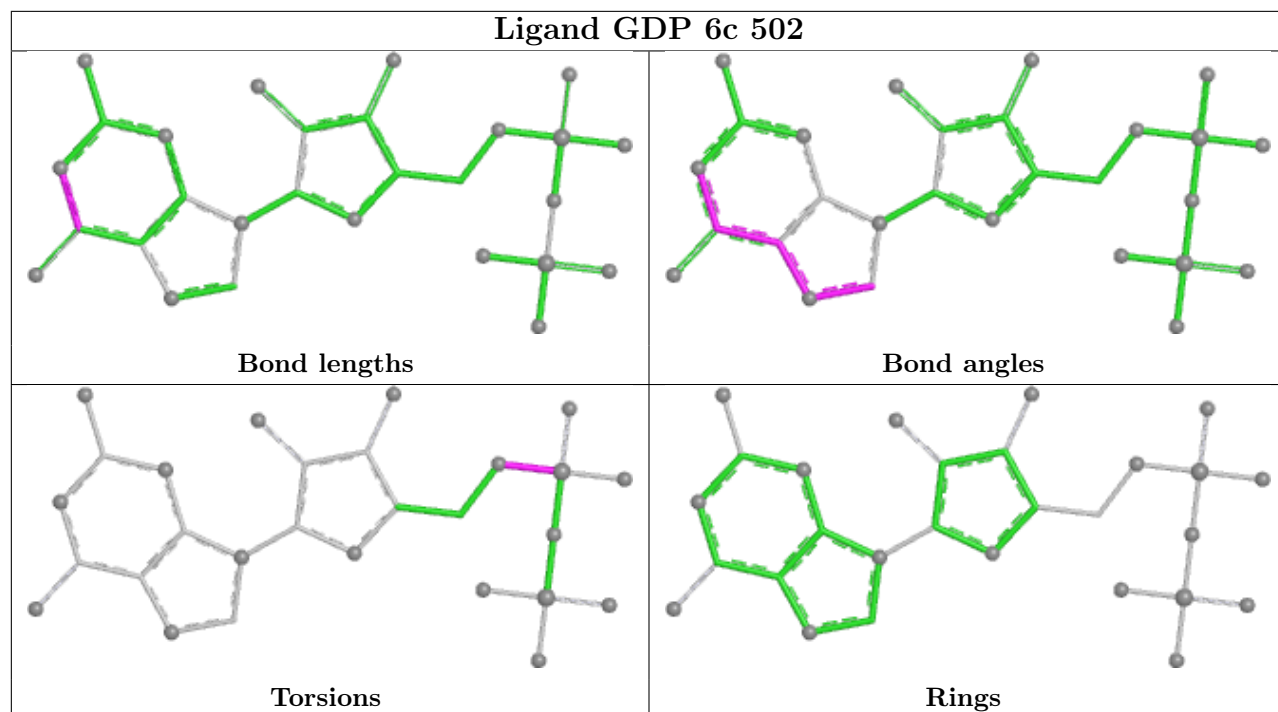


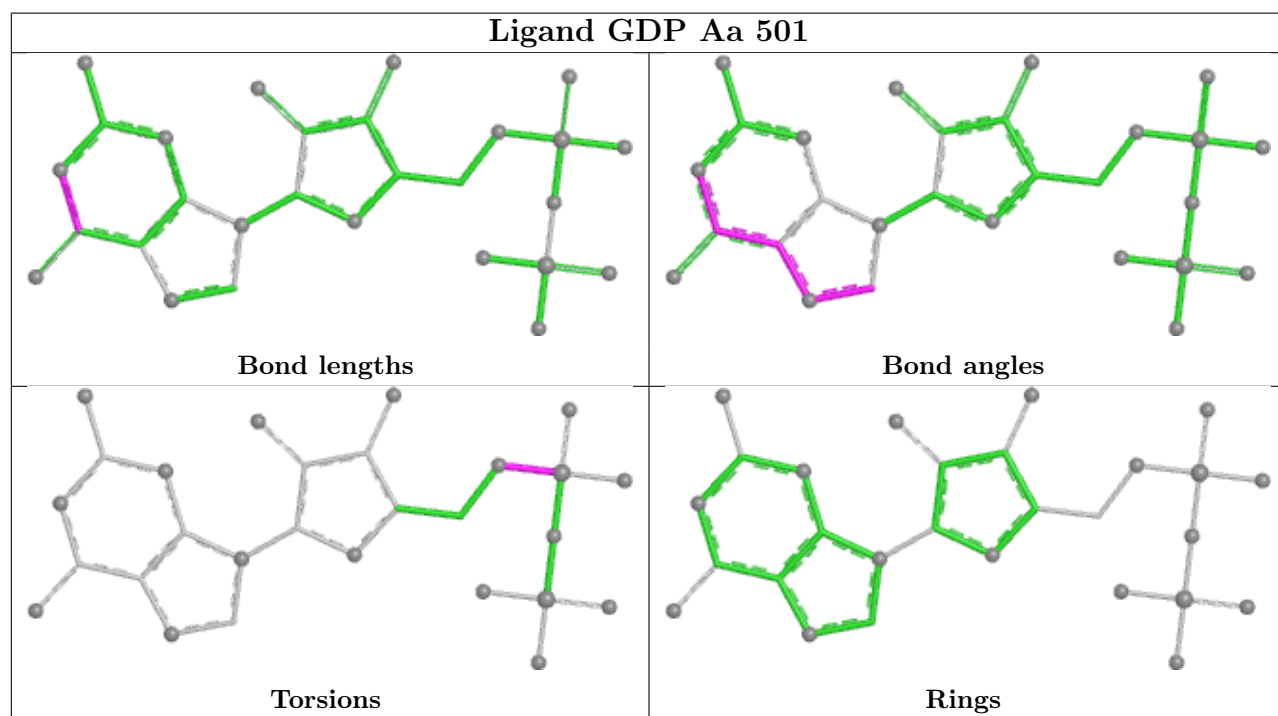
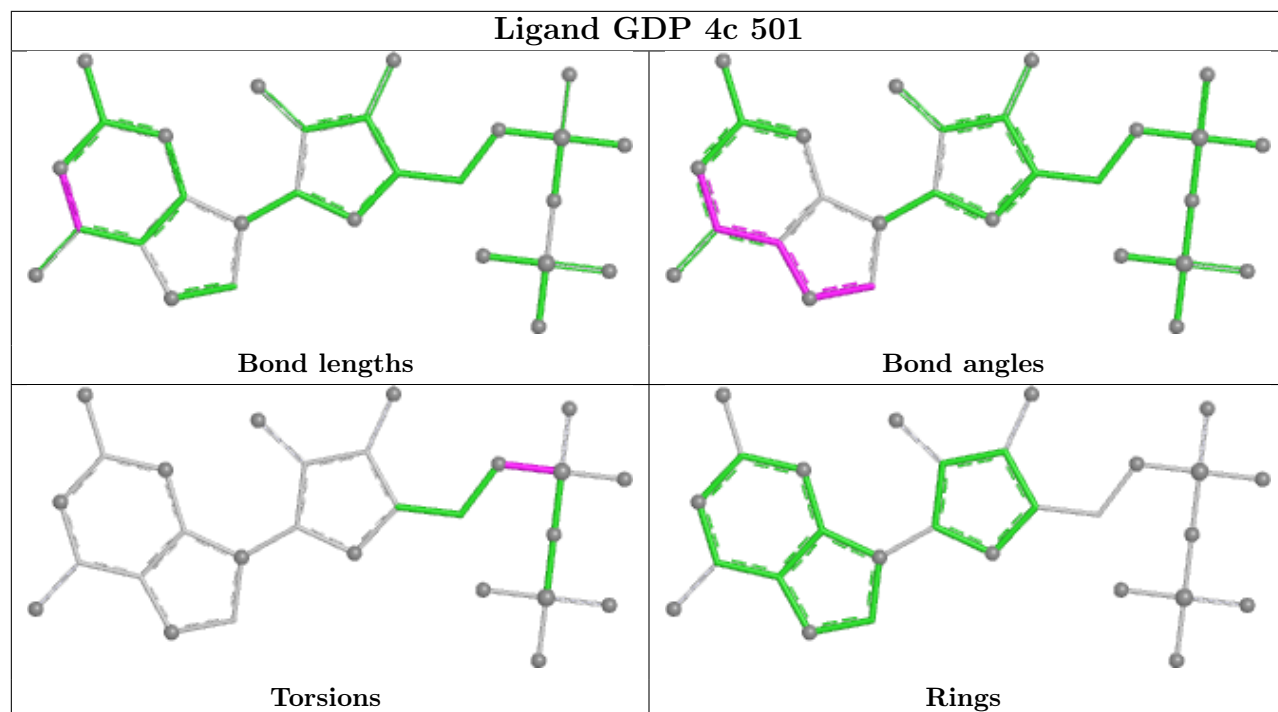


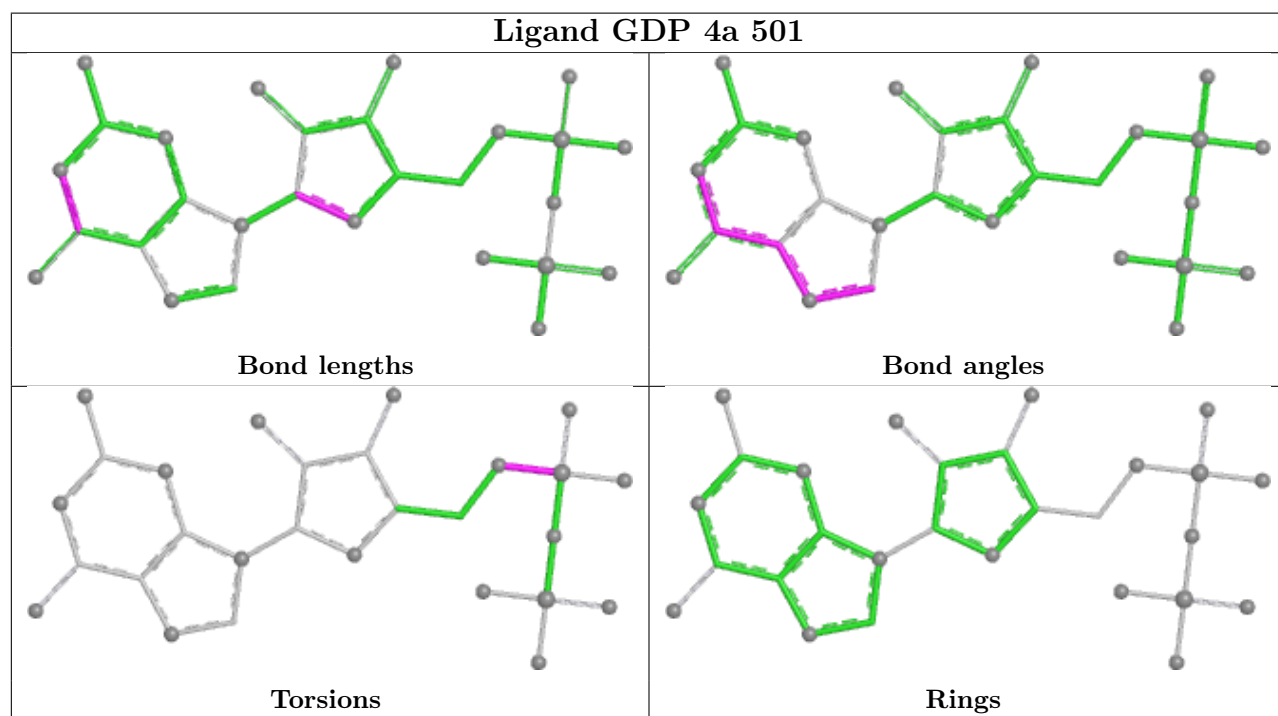
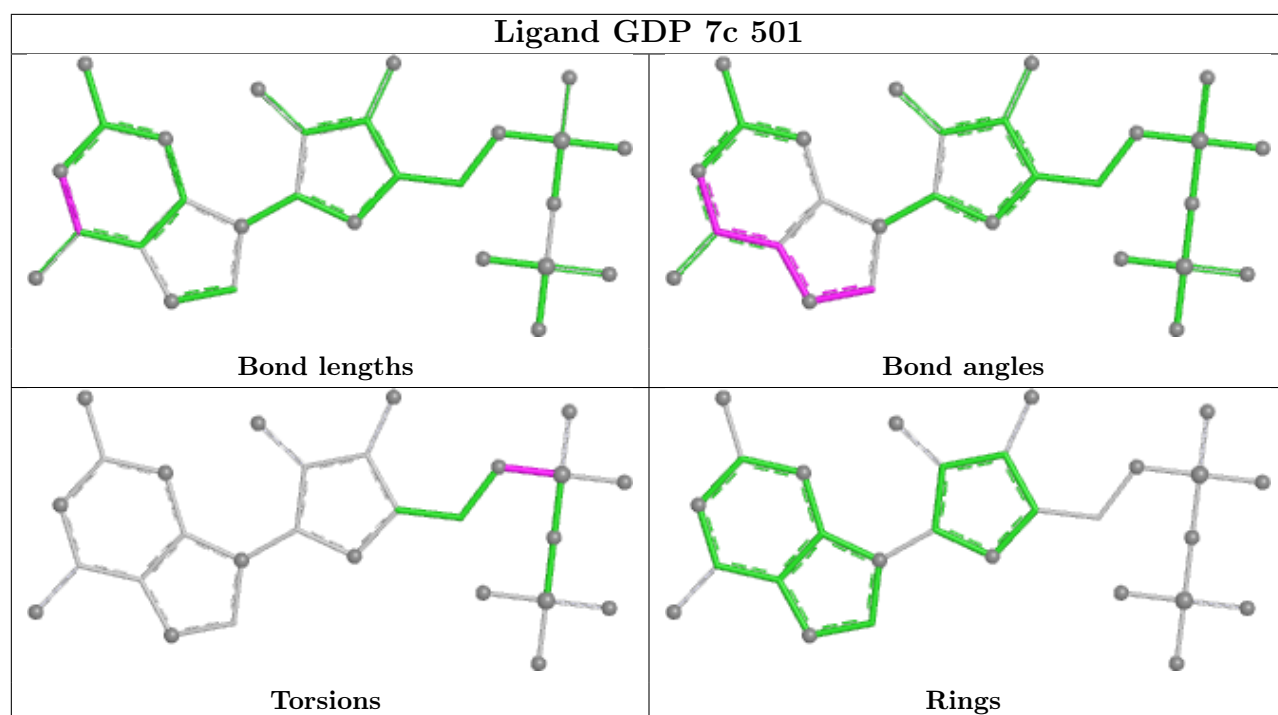


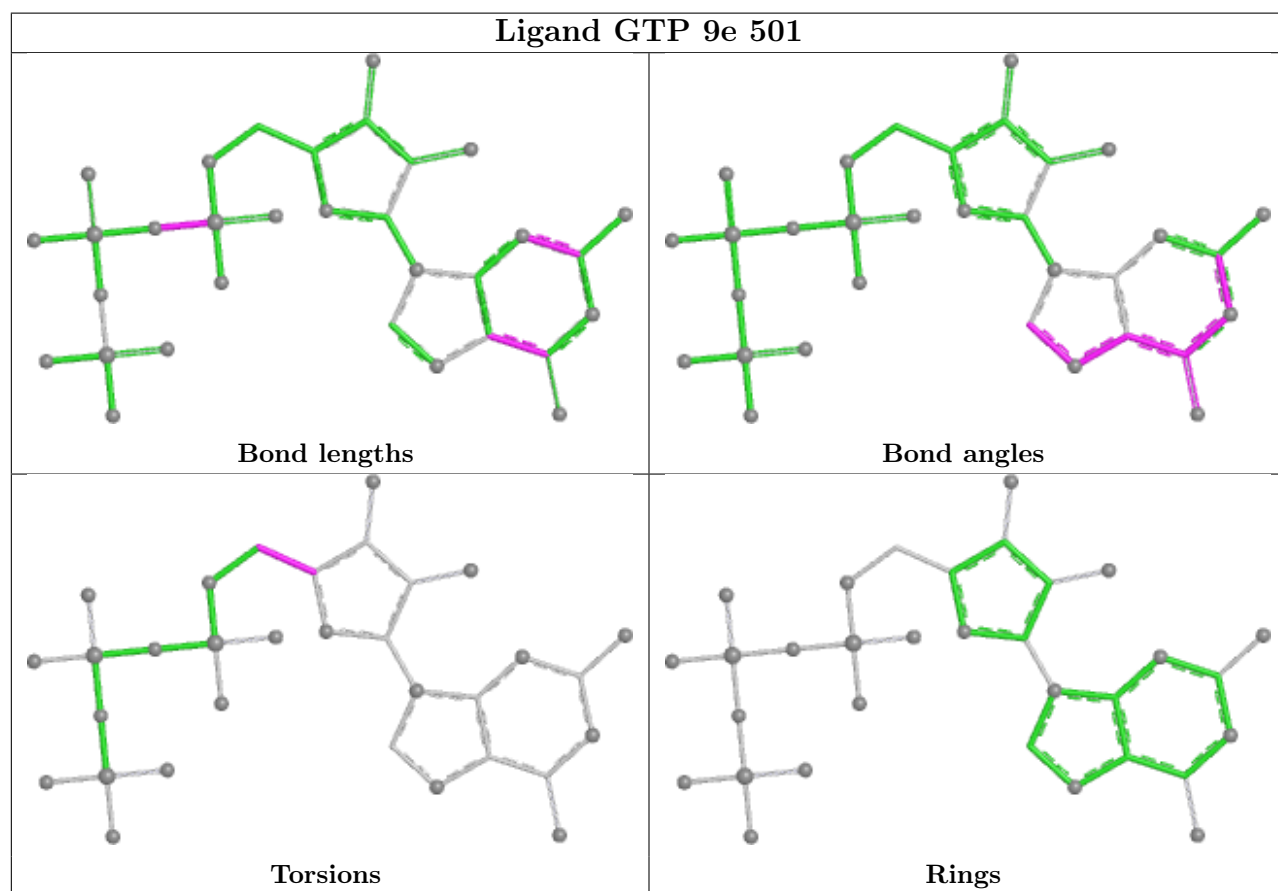
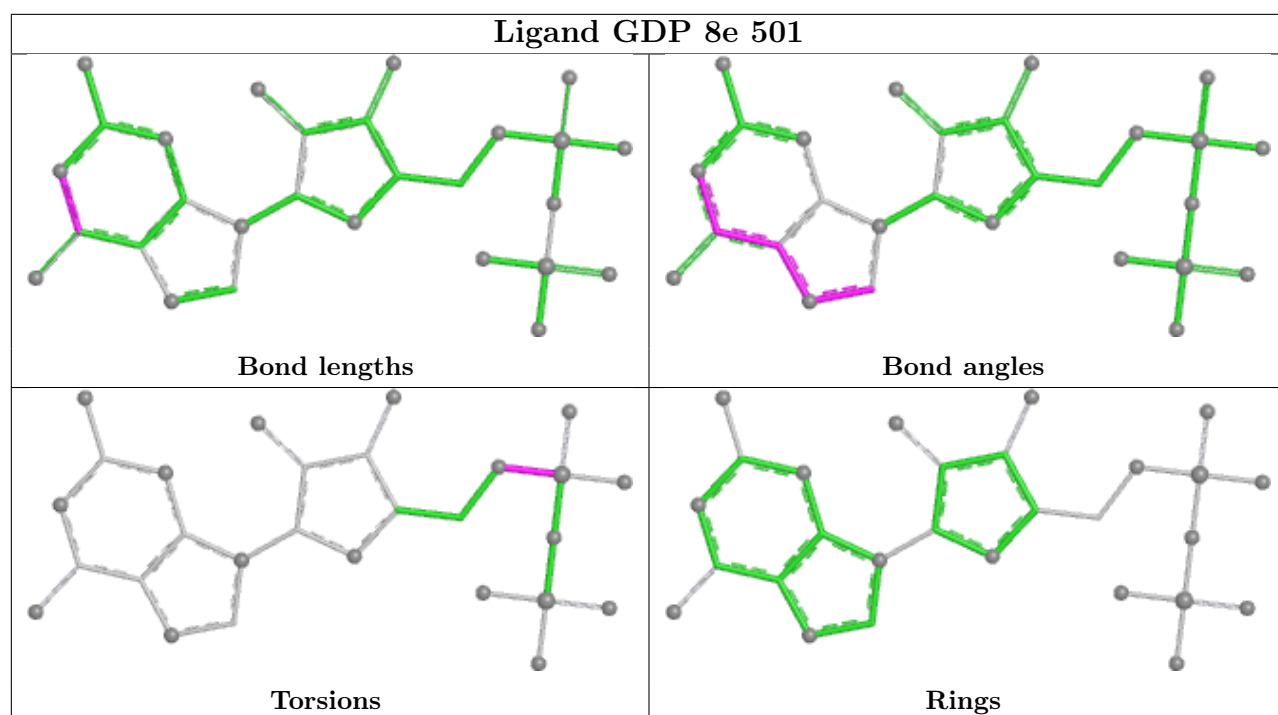


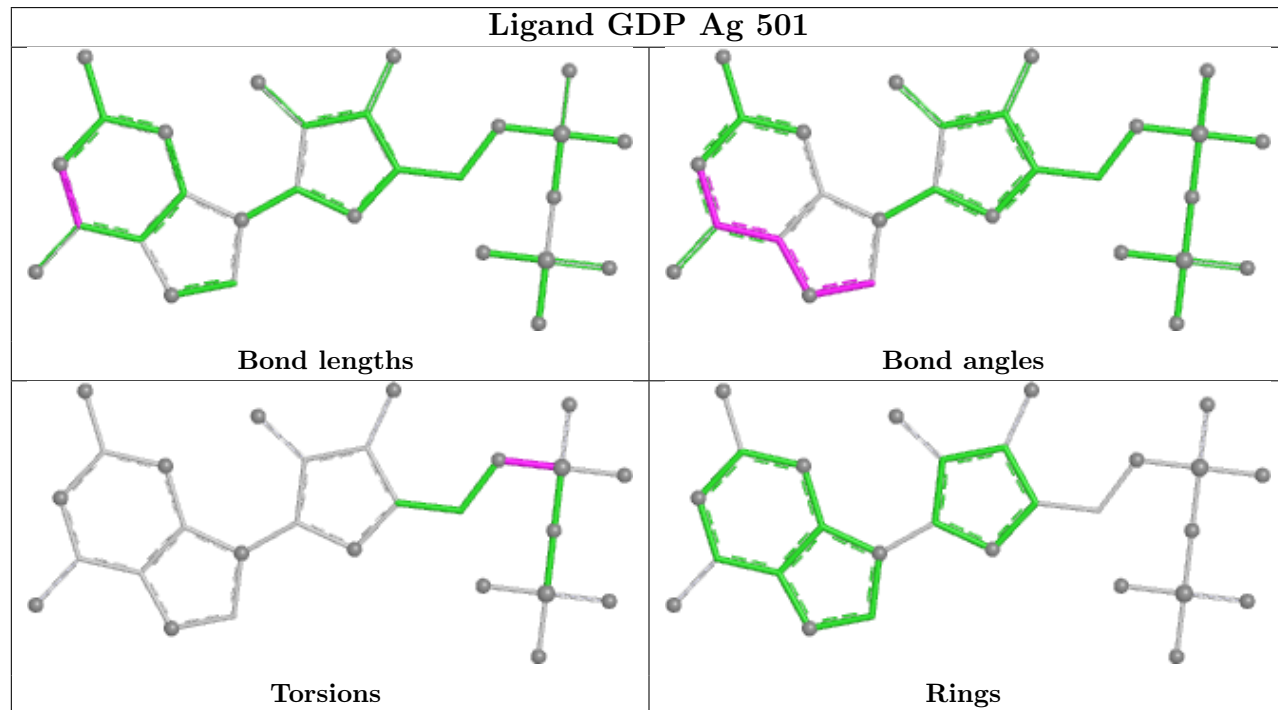
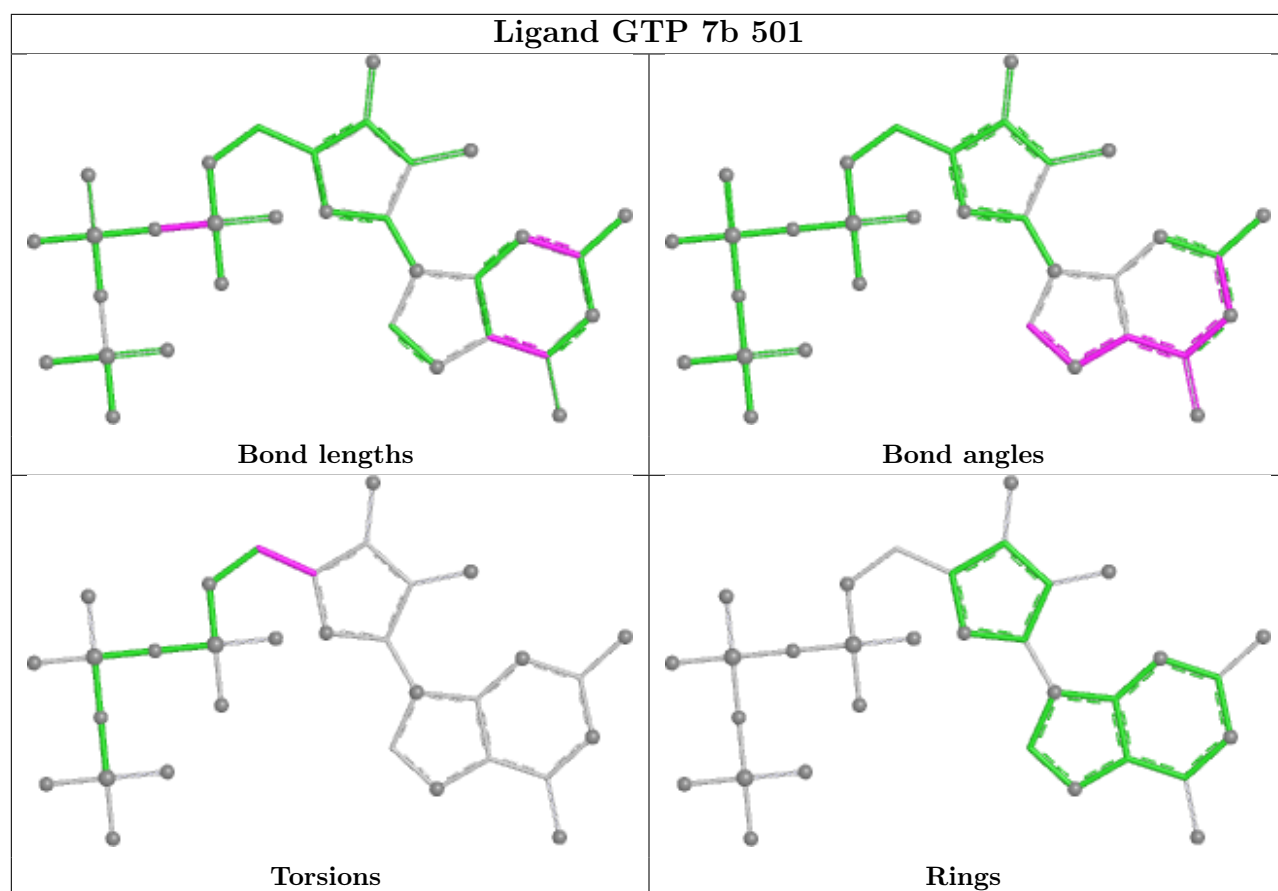


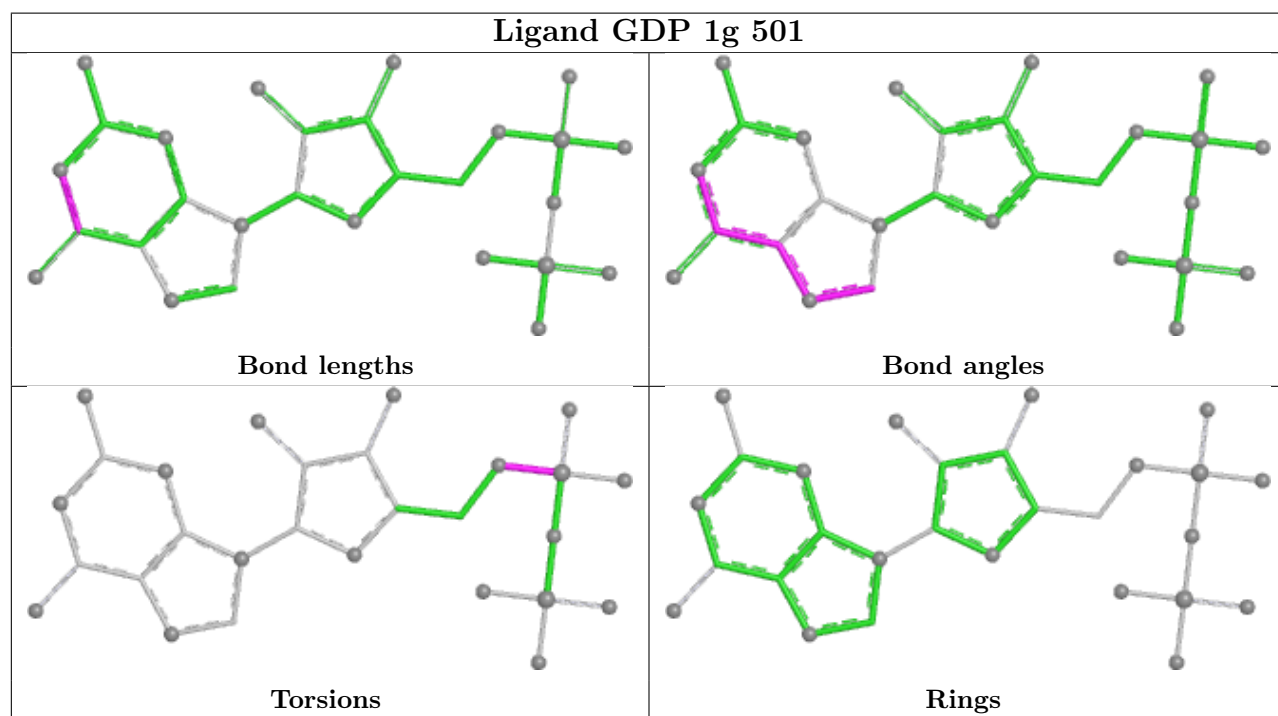
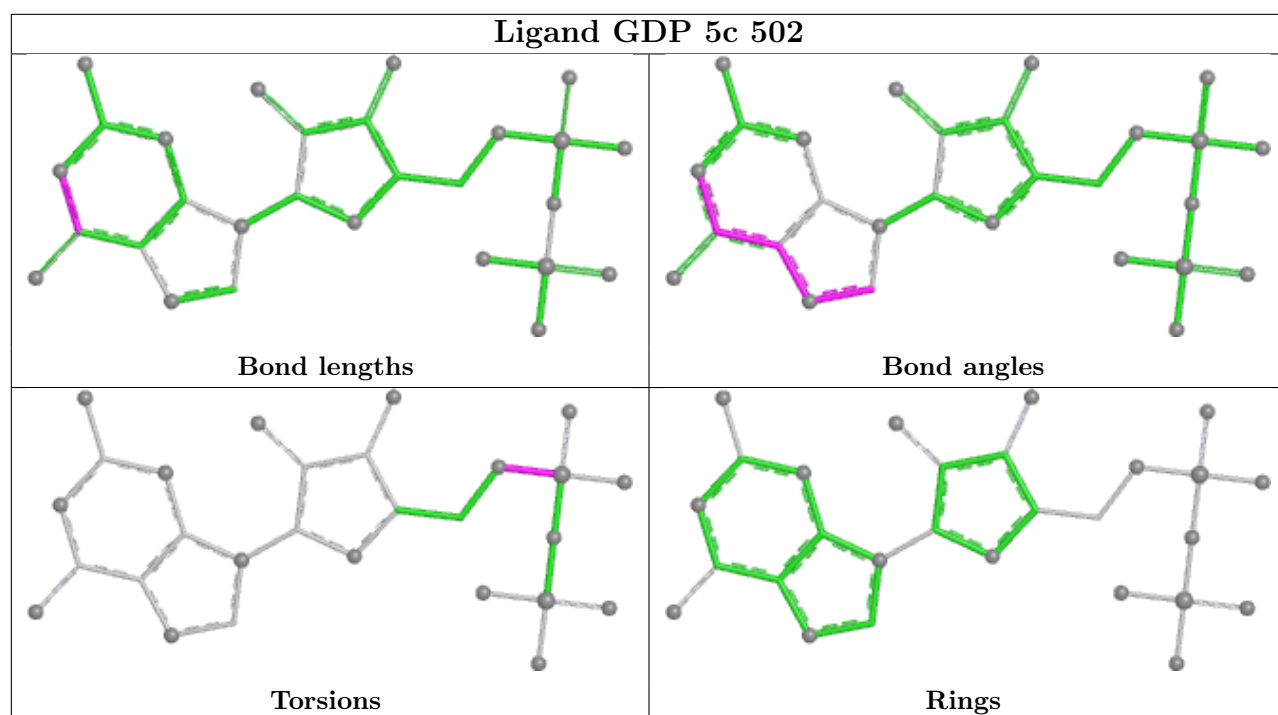


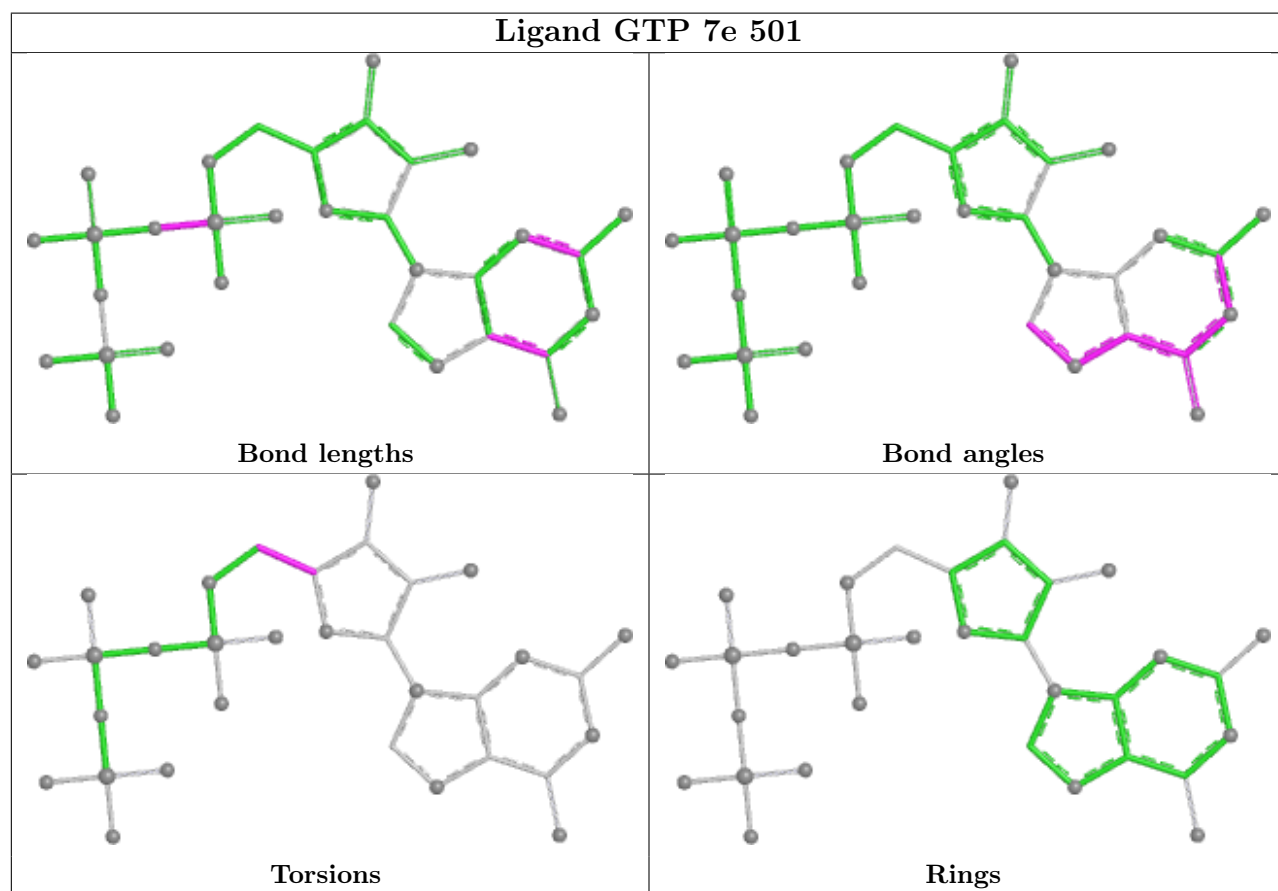
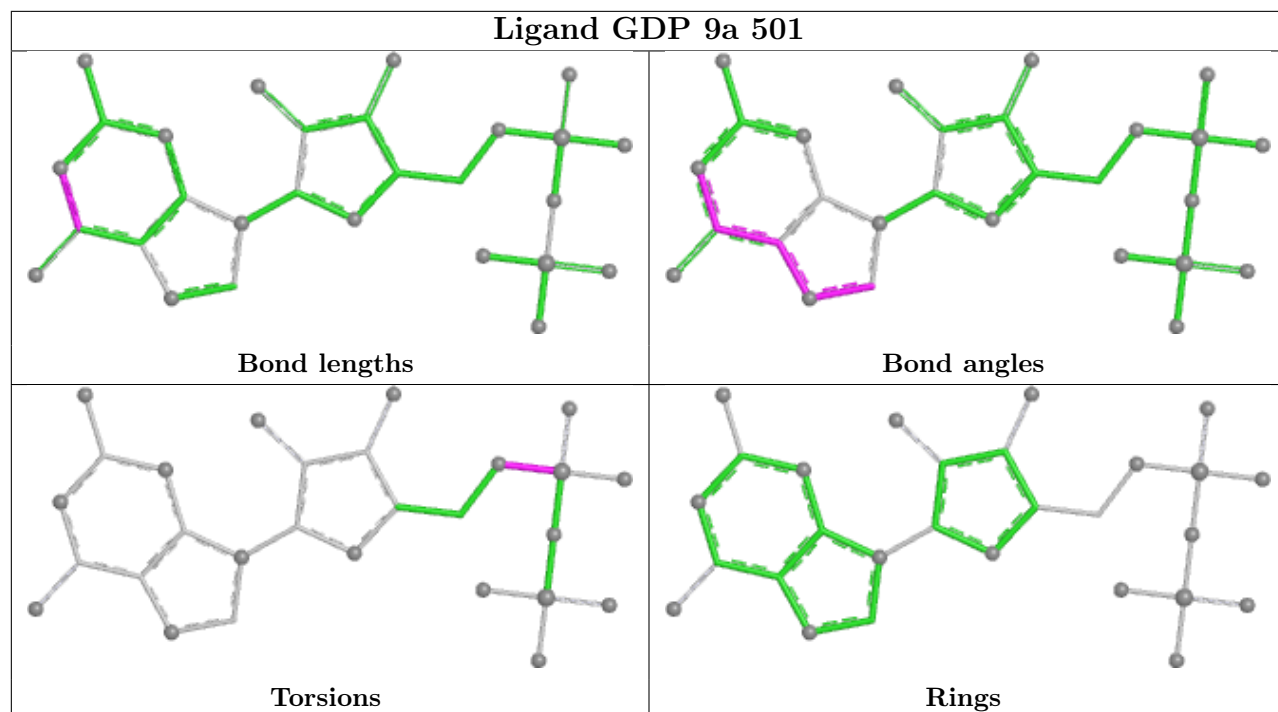




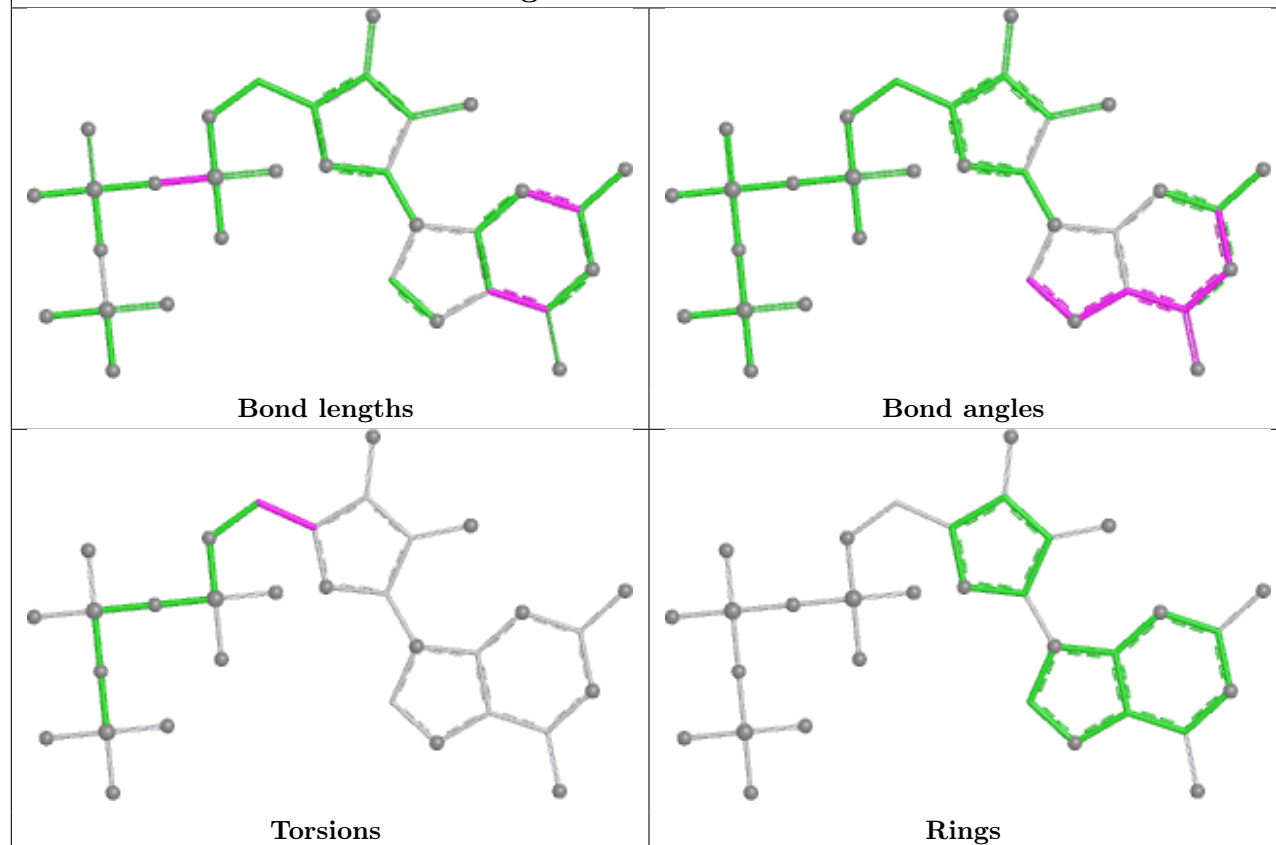




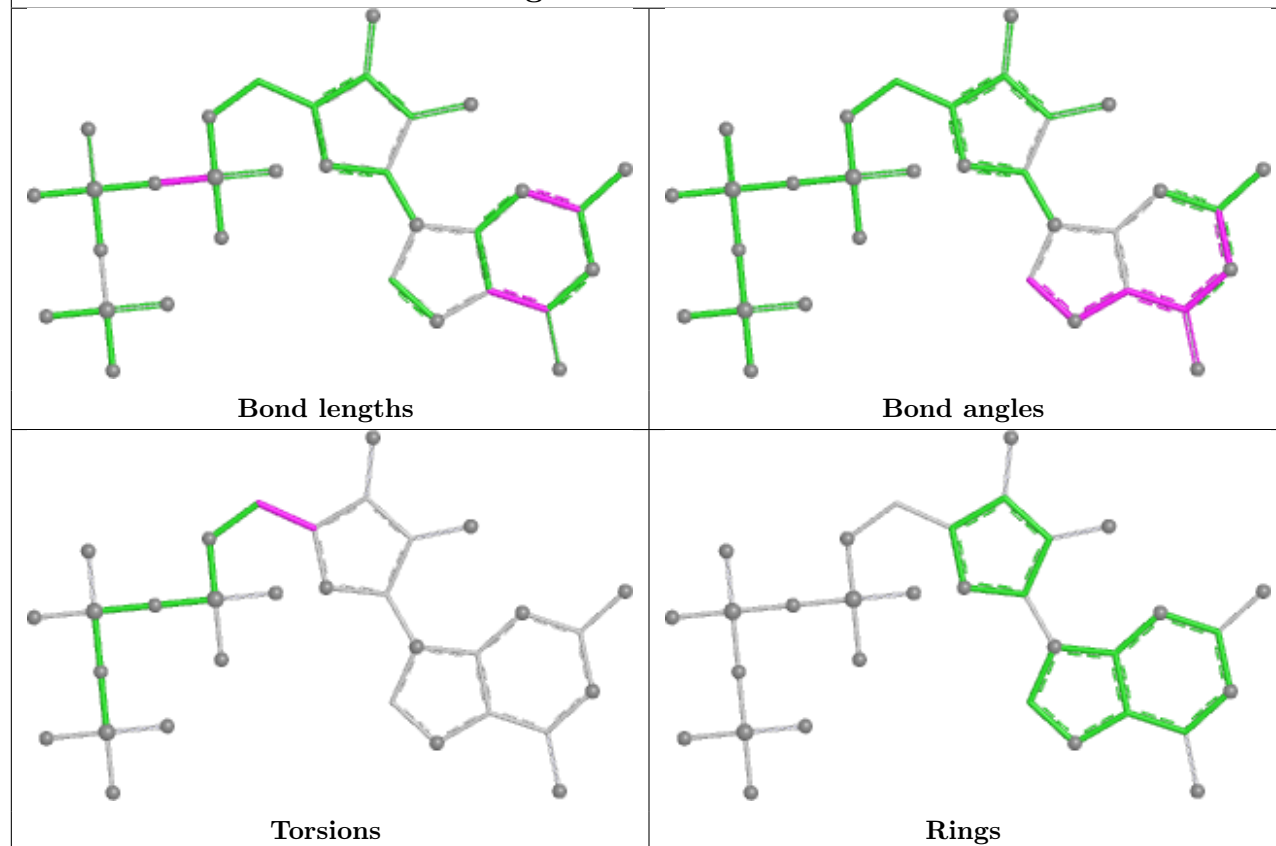


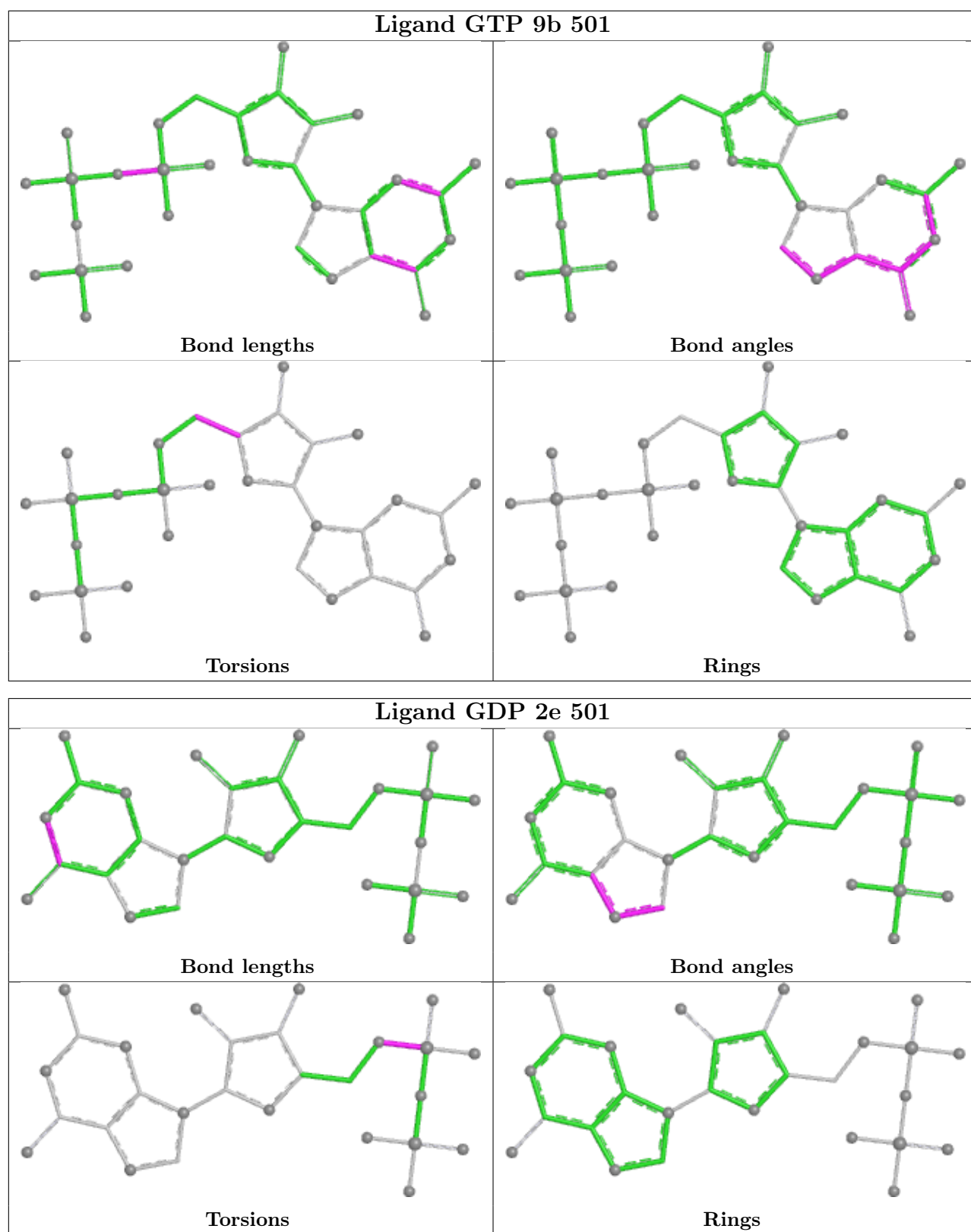


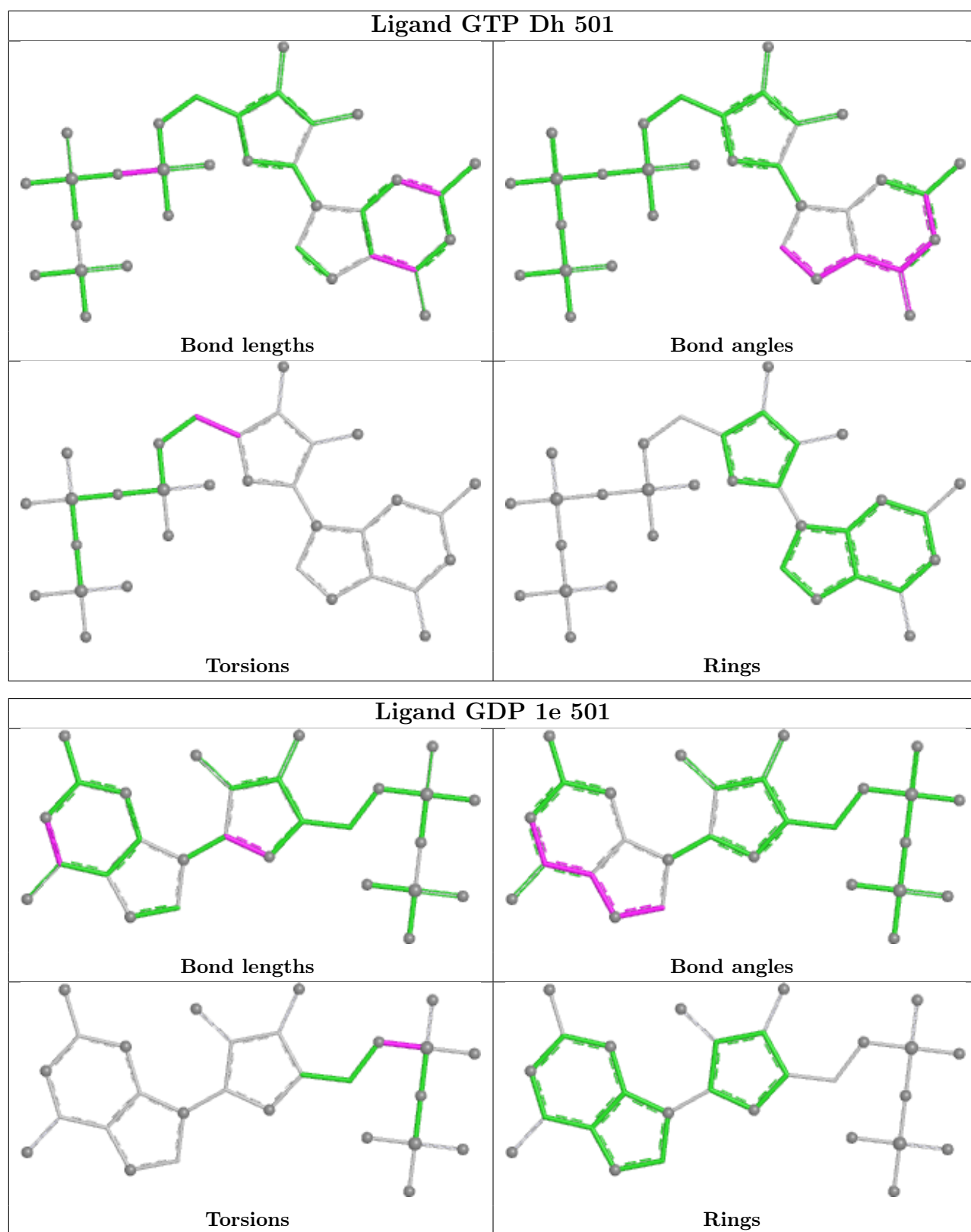
Ligand GTP Cd 501

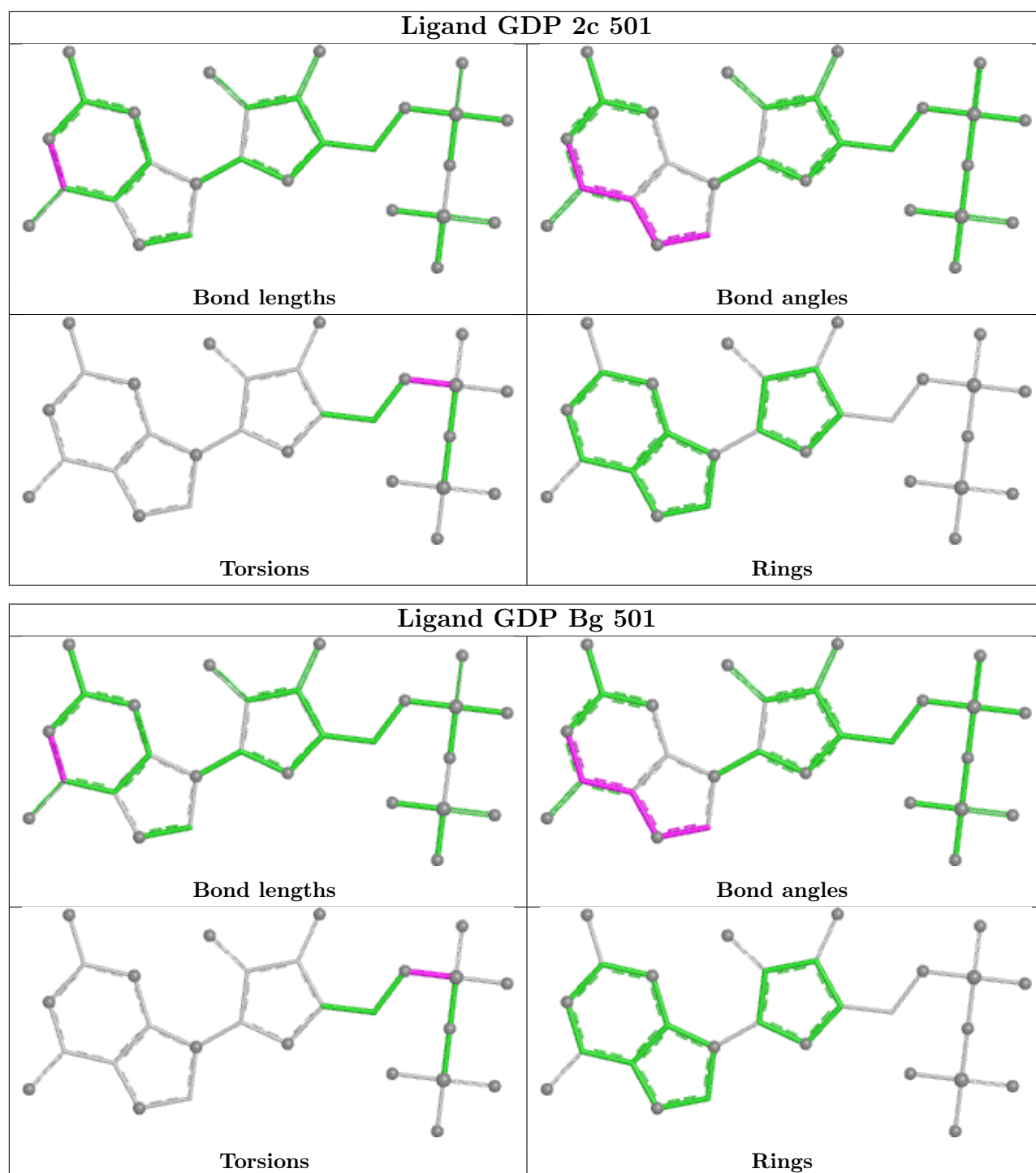


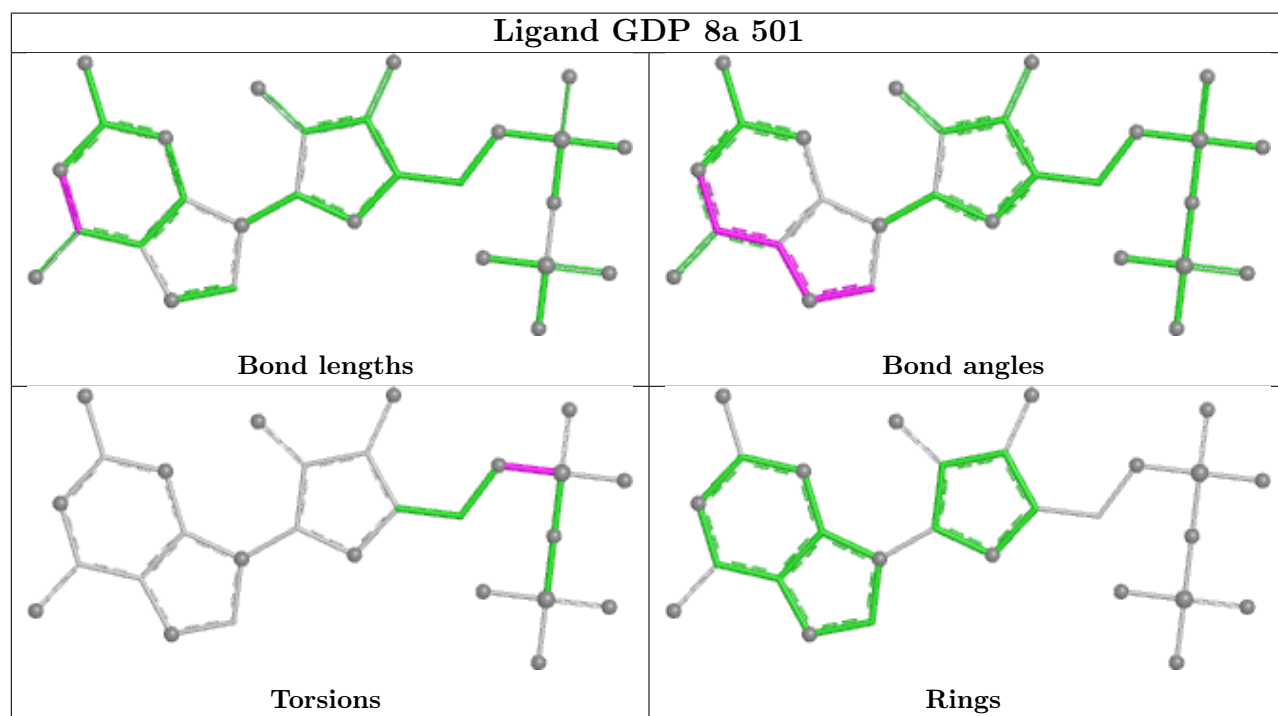
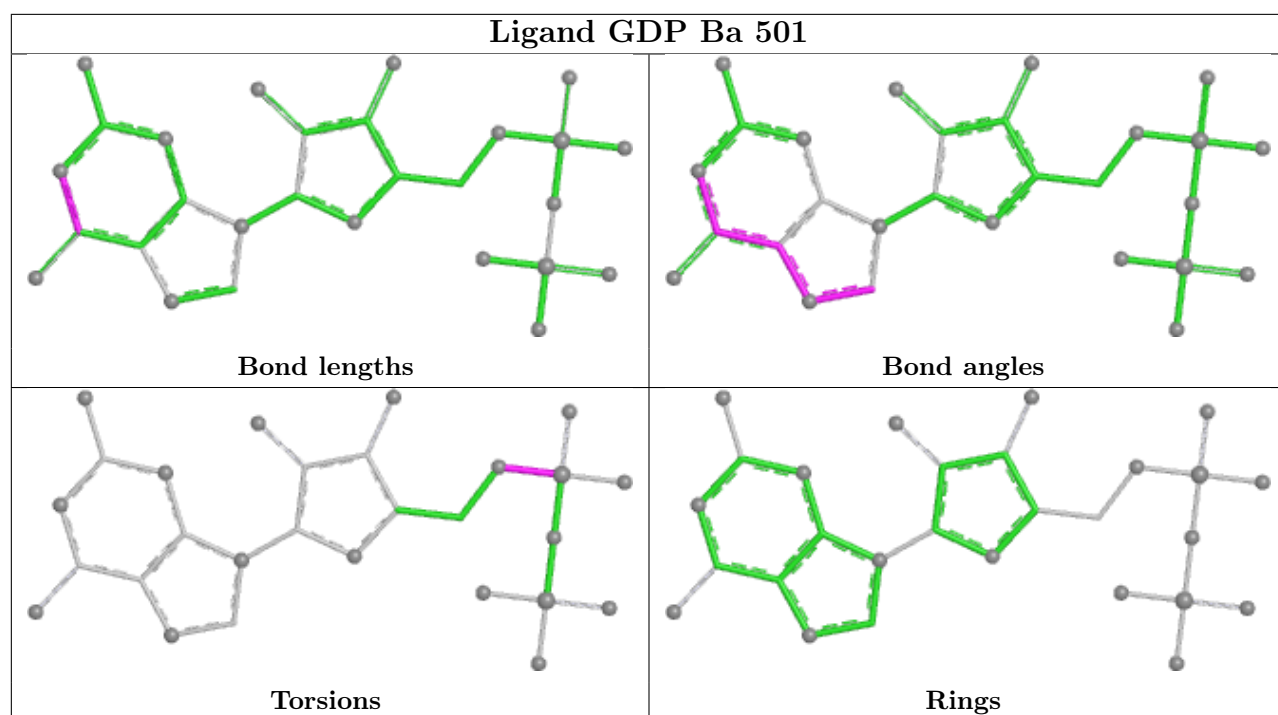
Ligand GTP Cf 501

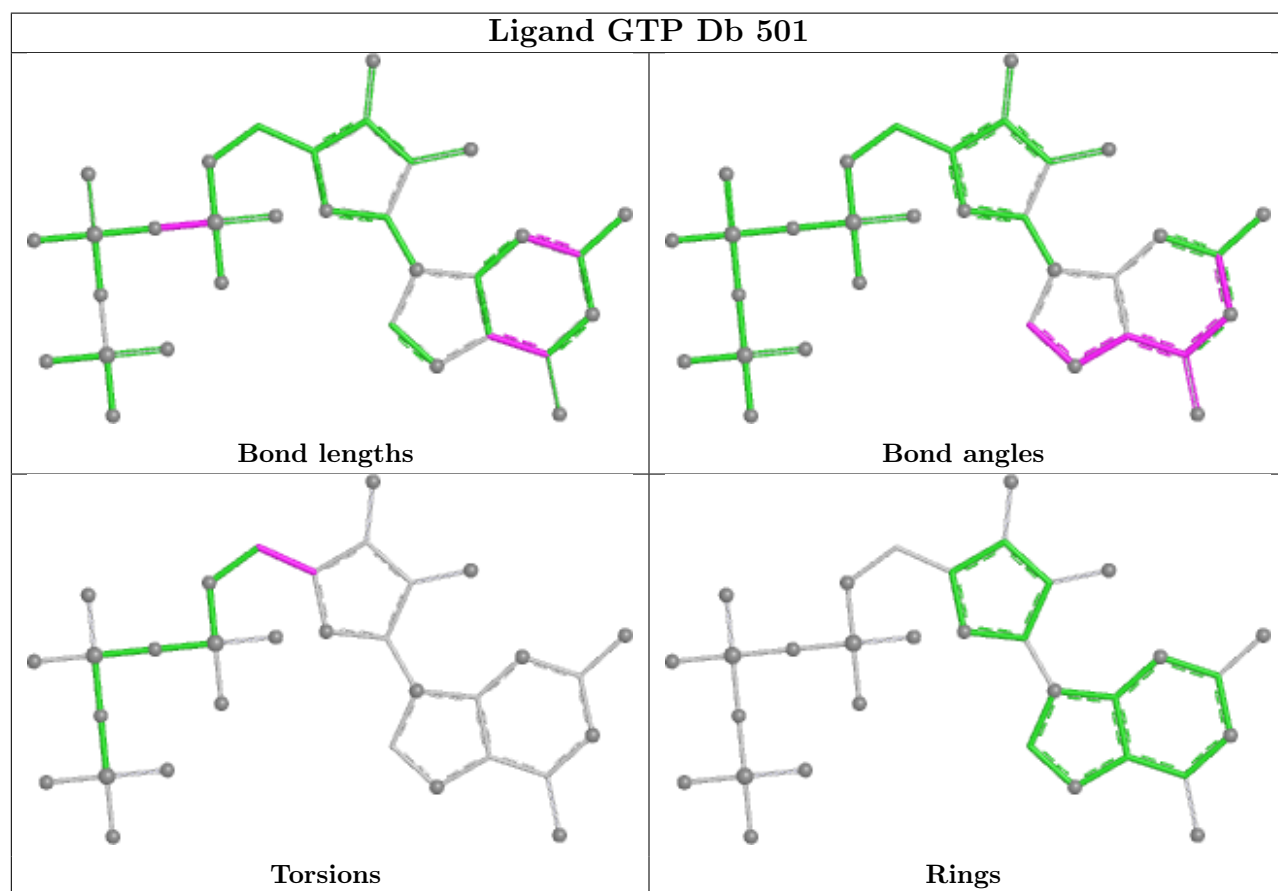
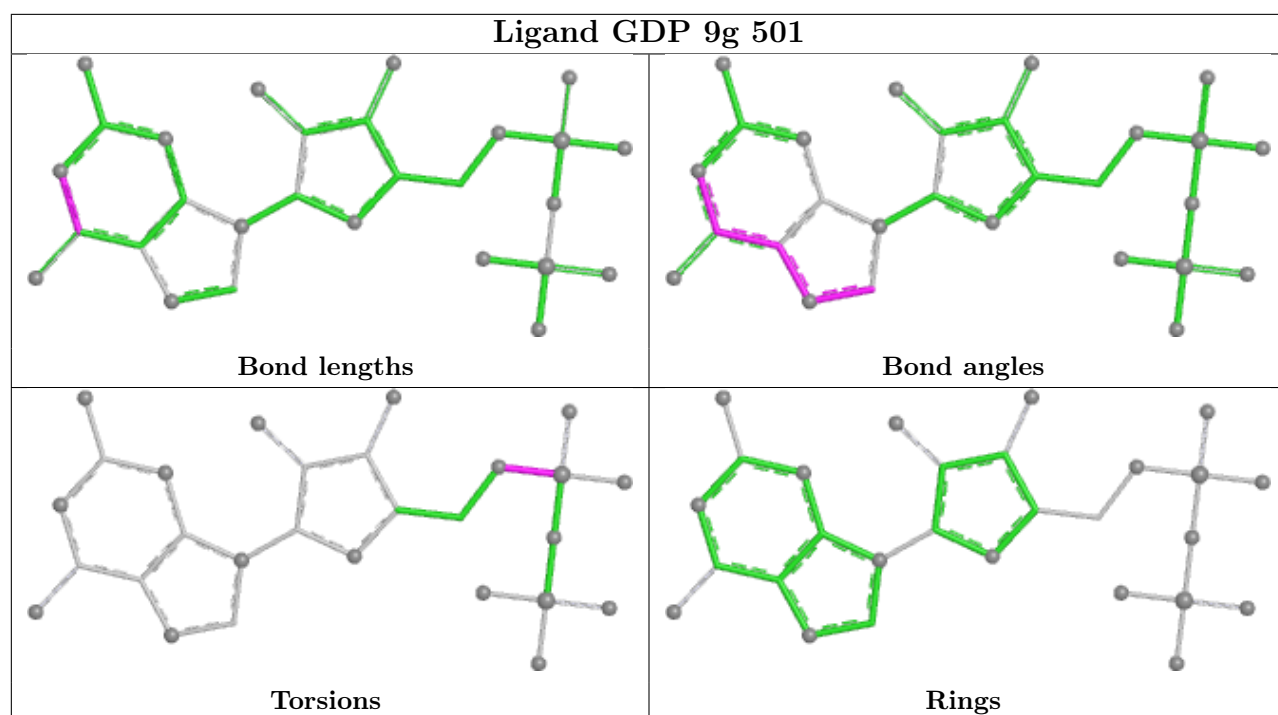


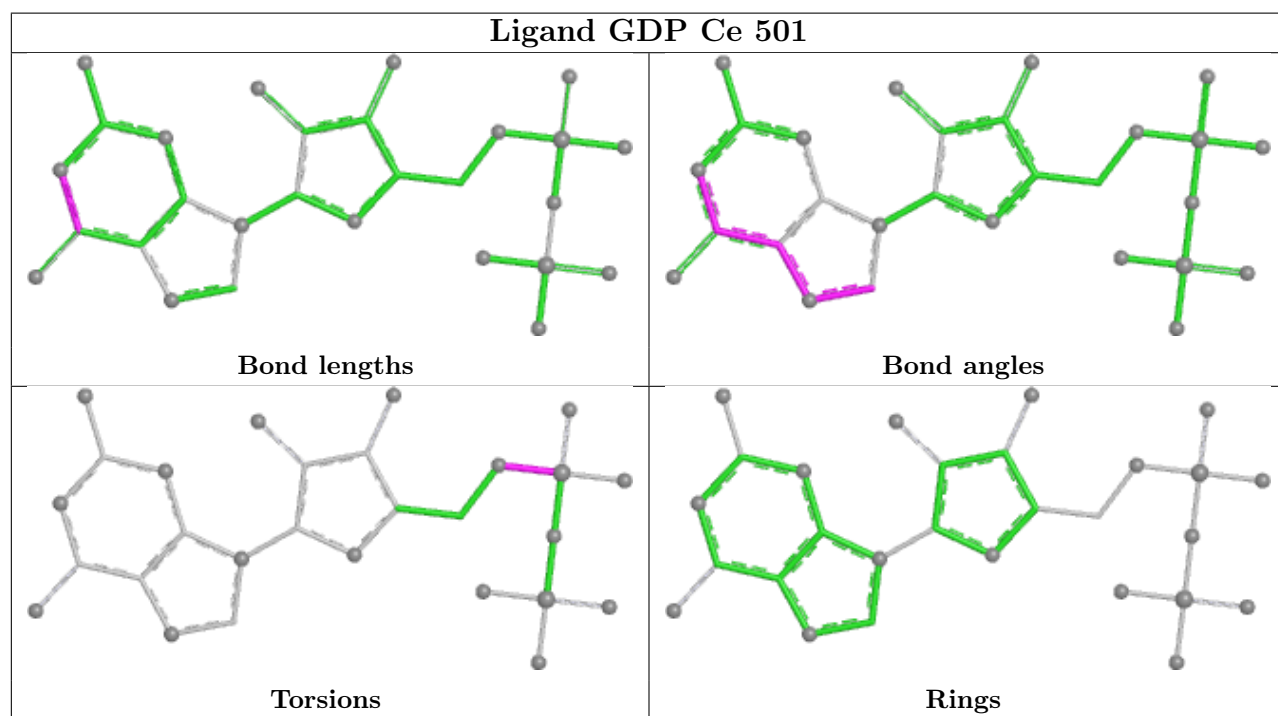
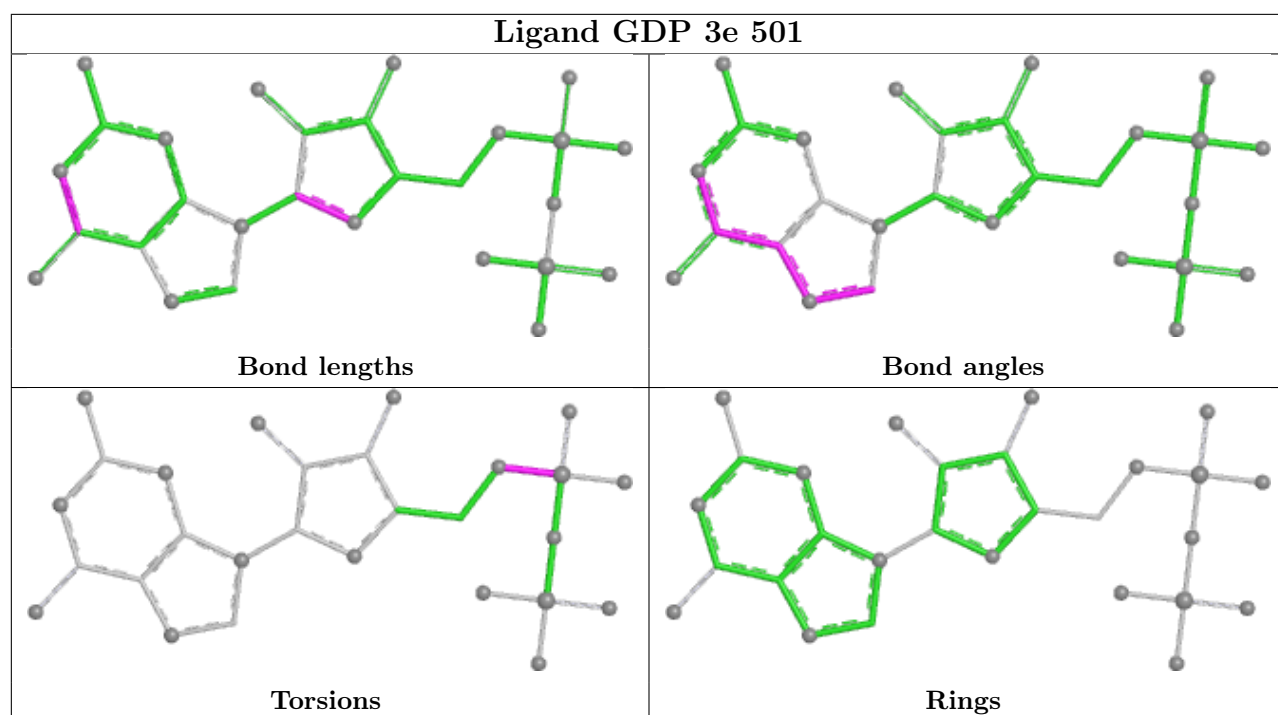


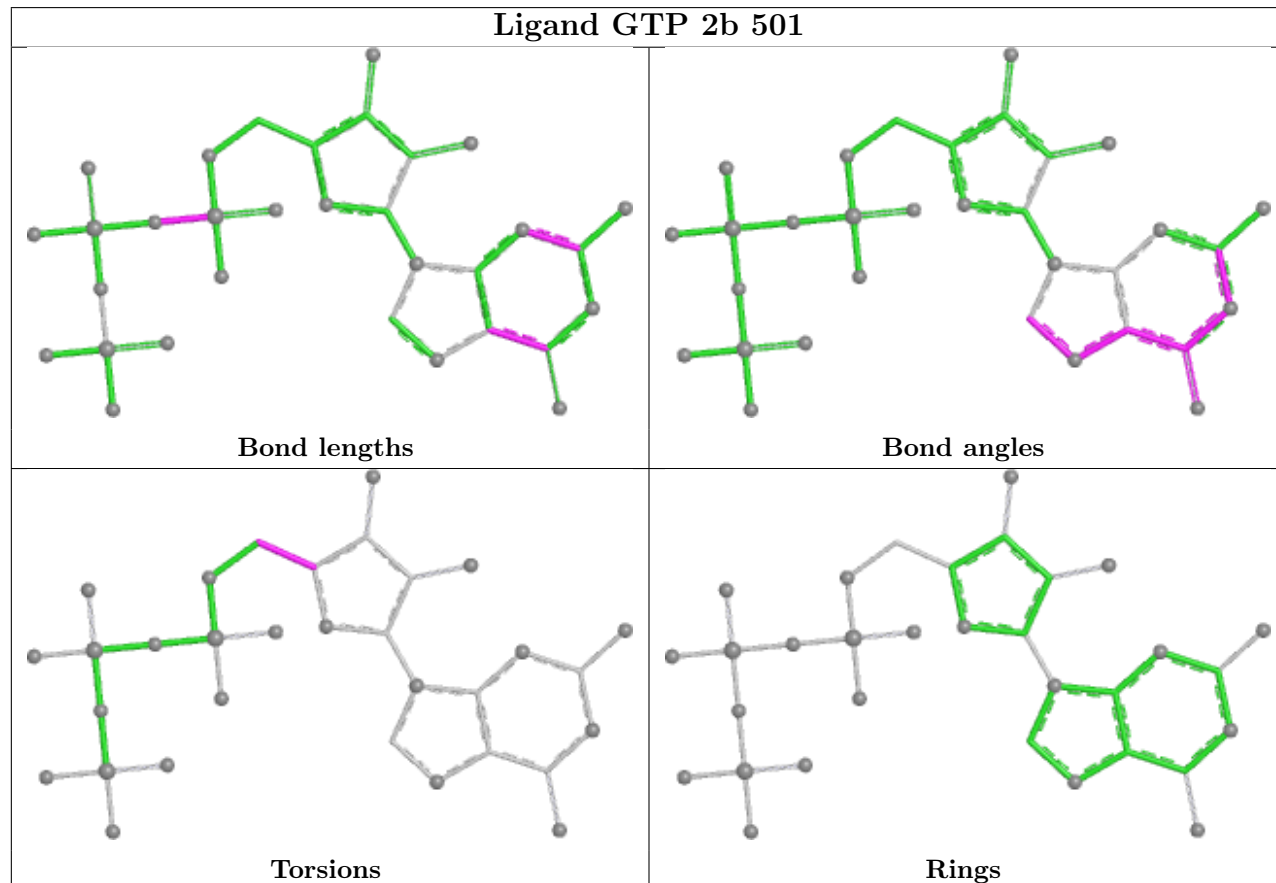
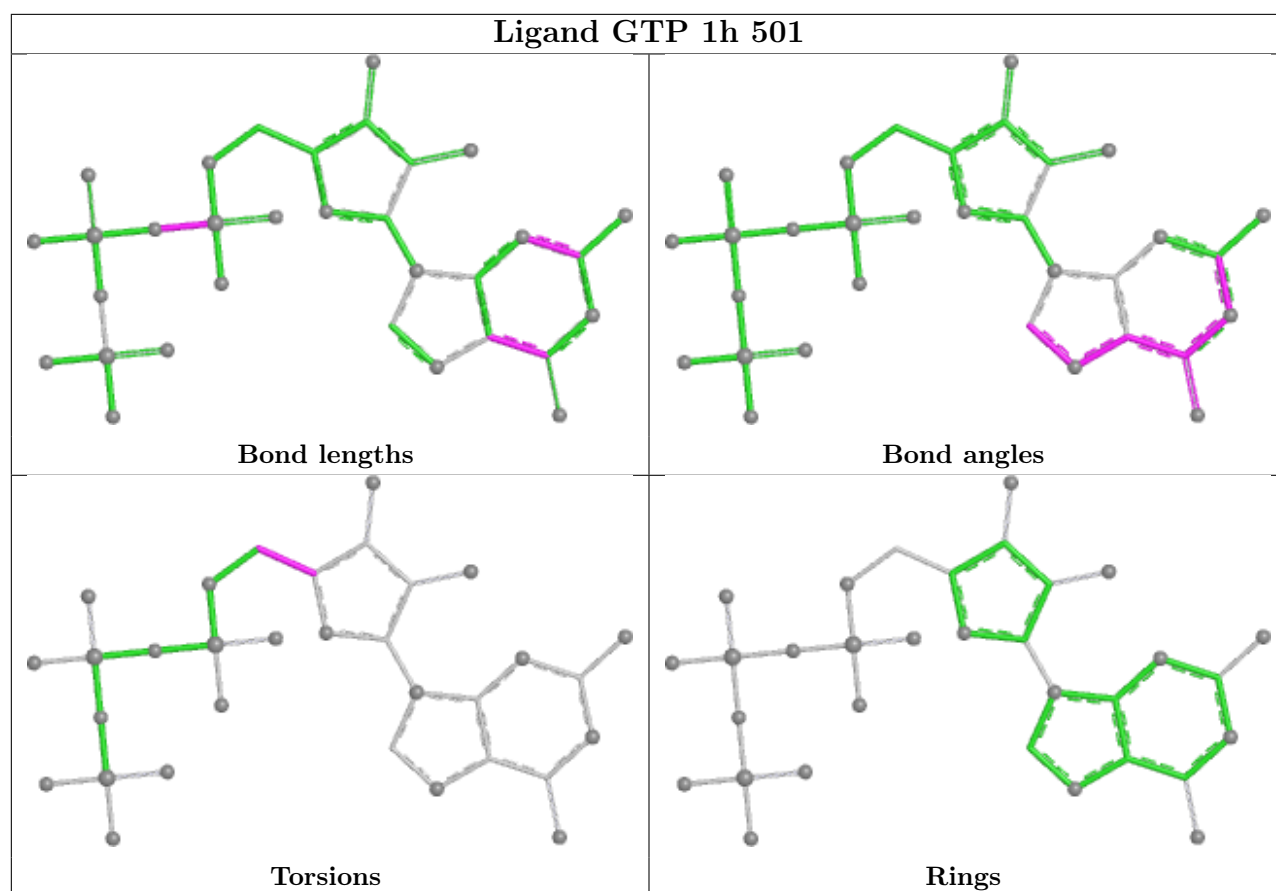




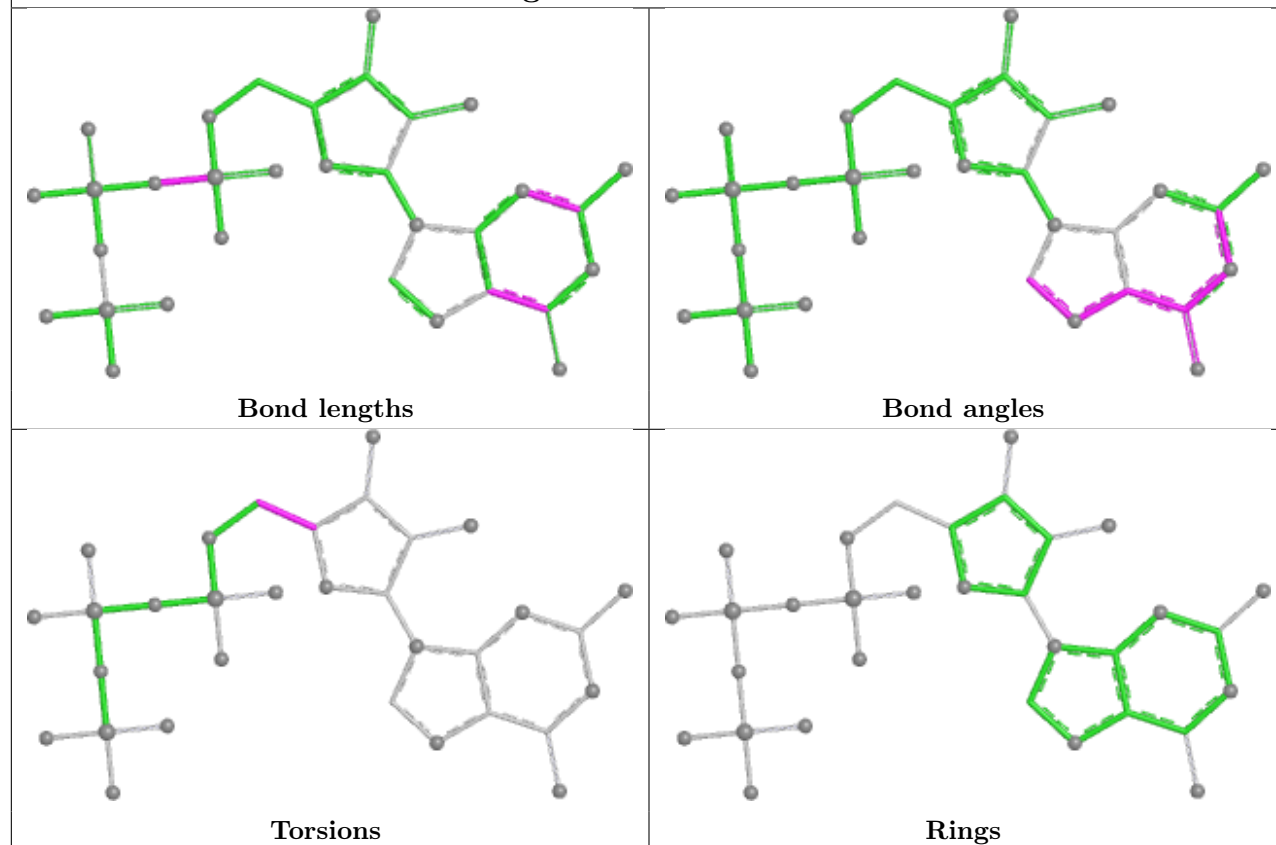




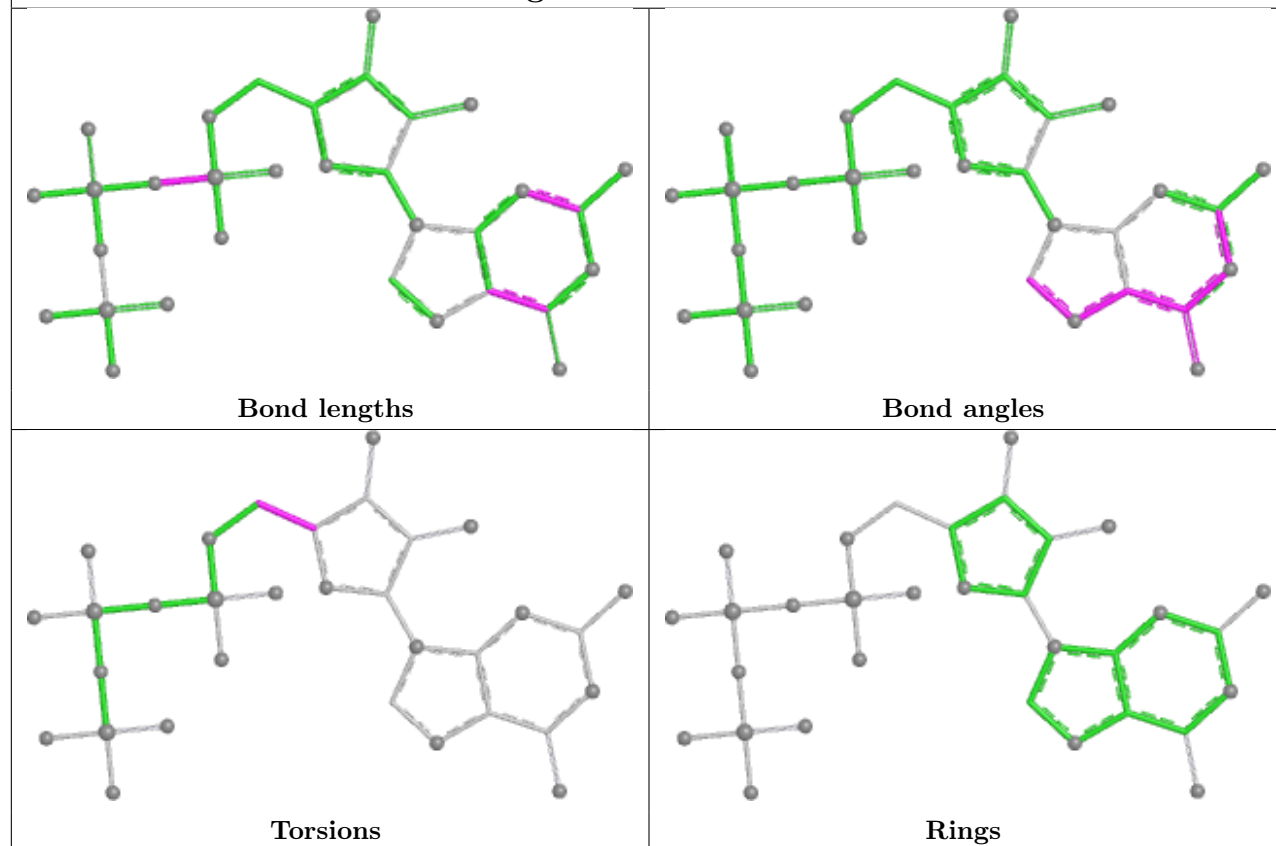


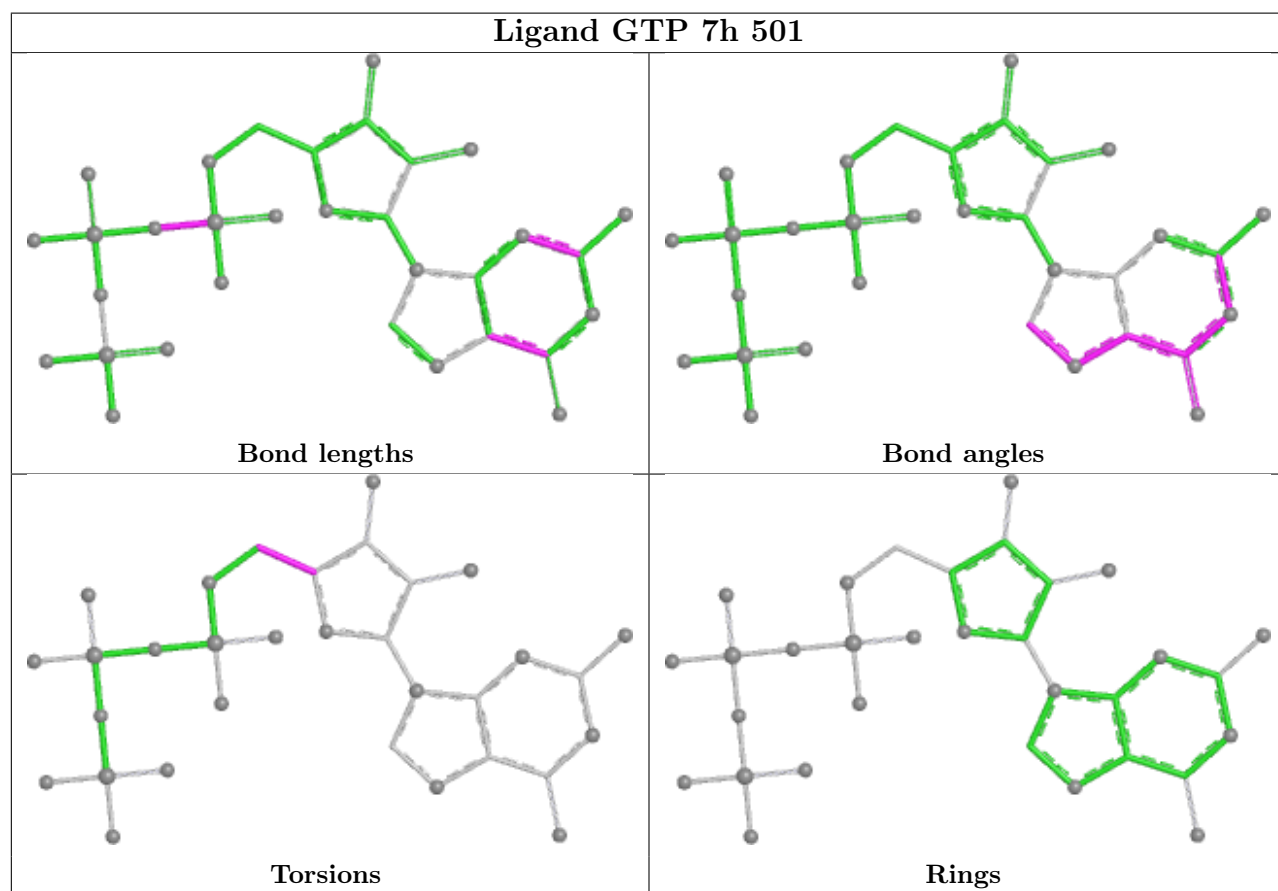
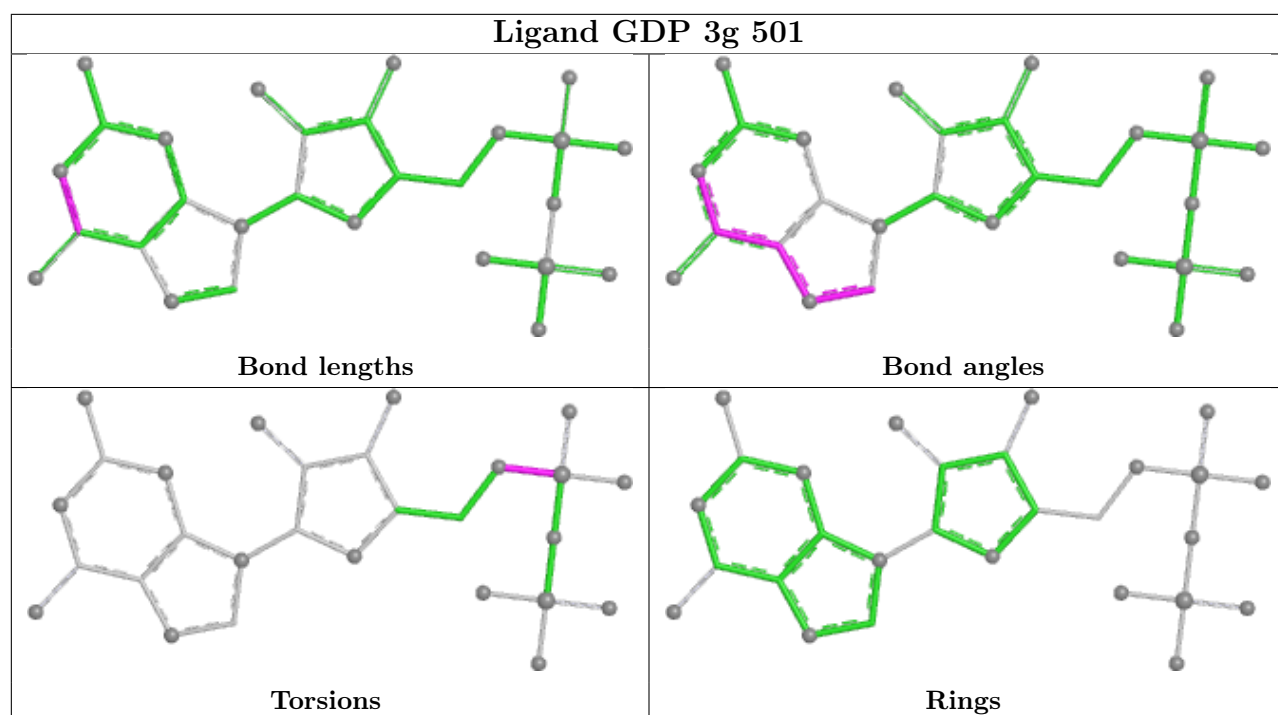


Ligand GTP Cc 501

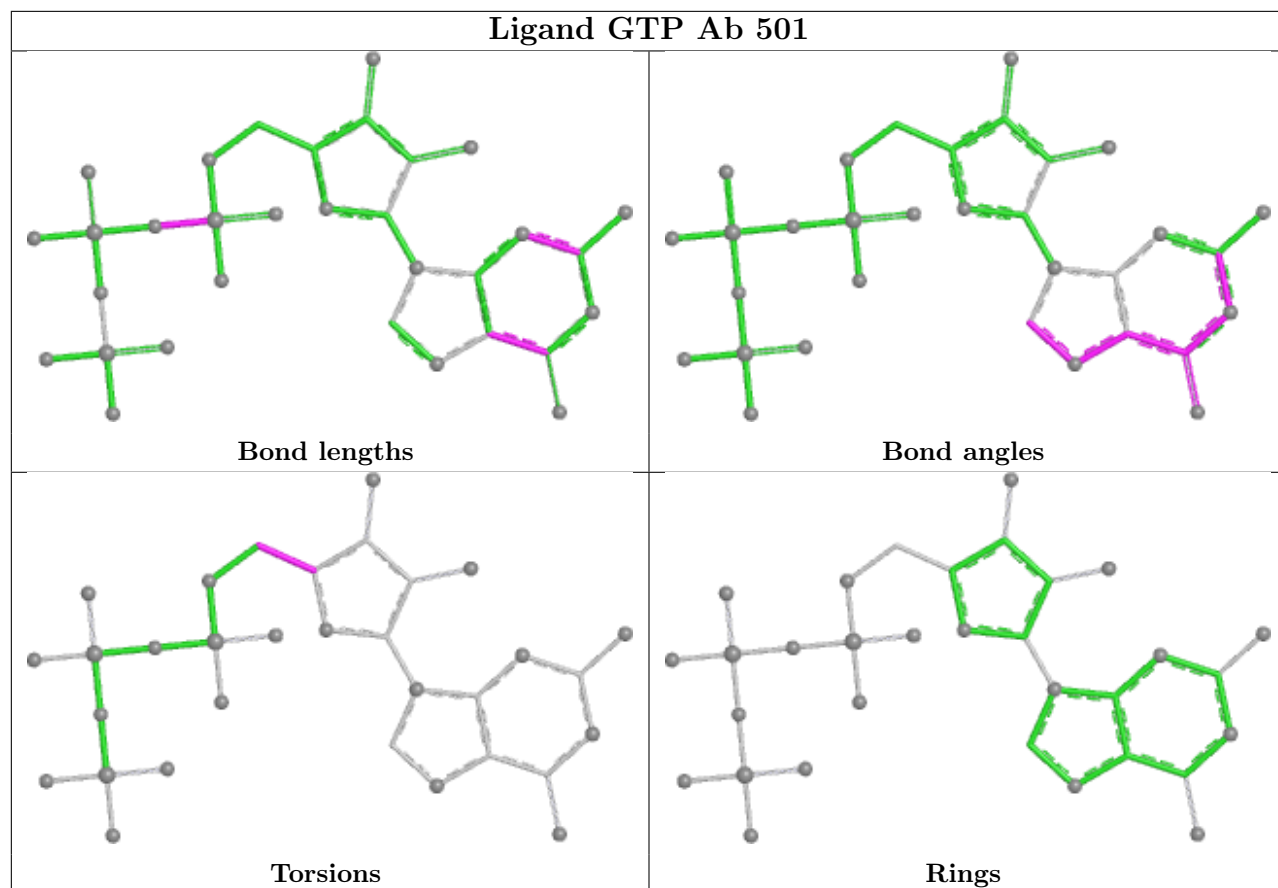


Ligand GTP 5c 501

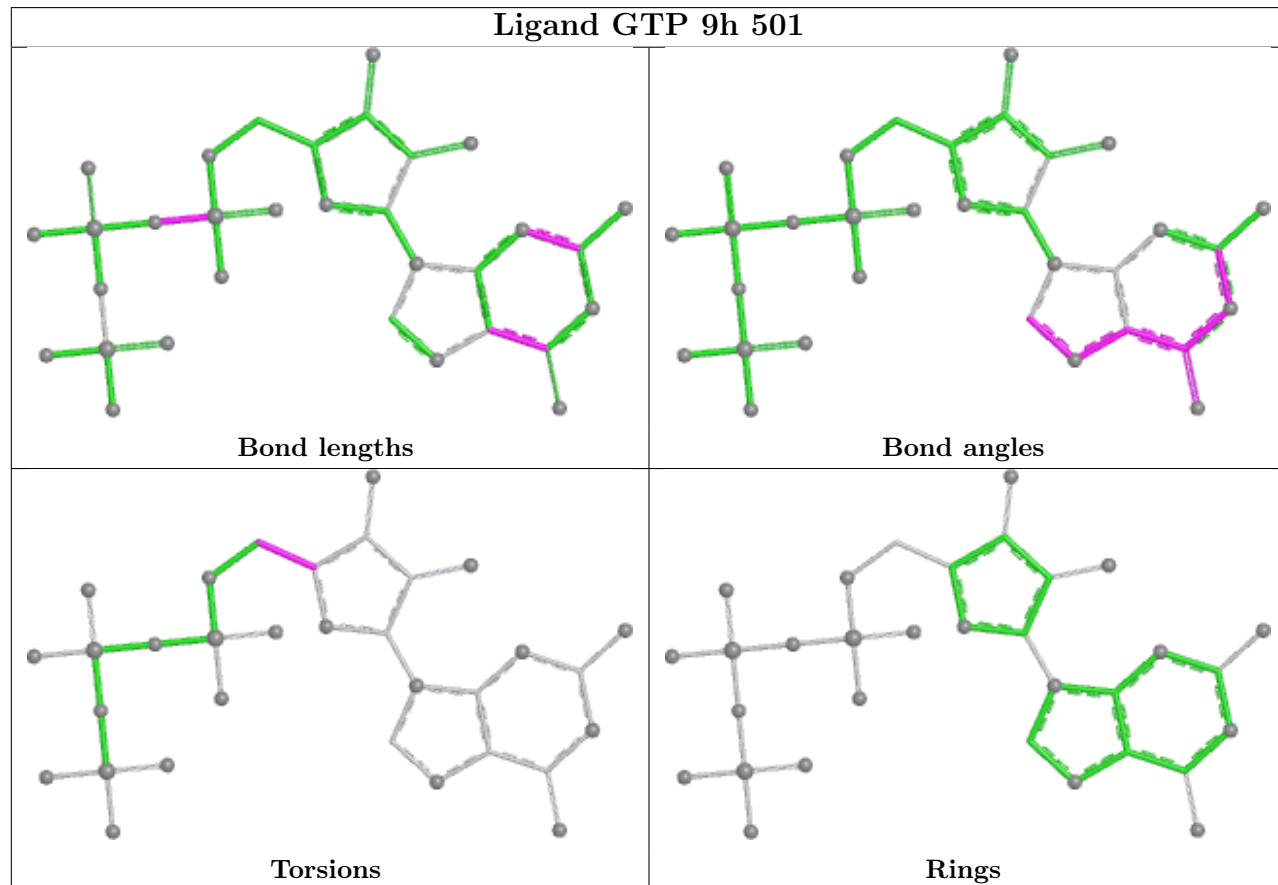




Ligand GTP Ab 501



Ligand GTP 9h 501



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
37	4F	5
37	4E	3
46	5Z	2
45	5W	1
45	5X	1
45	5Y	1
43	5I	1
43	5J	1
43	5L	1
43	5K	1
37	4G	1
41	5A	1

The worst 5 of 19 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5W	111:UNK	C	154:UNK	N	23.64
1	5X	111:UNK	C	154:UNK	N	23.64
1	5Y	111:UNK	C	154:UNK	N	23.64
1	5Z	14:UNK	C	15:UNK	N	3.57
1	5Z	44:UNK	C	45:UNK	N	3.20

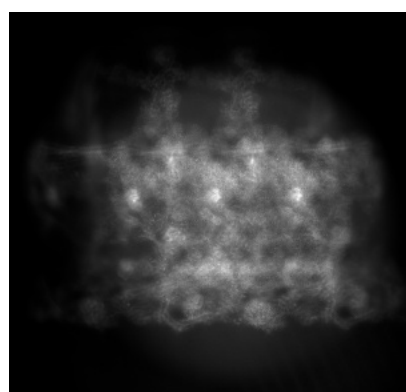
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24207. These allow visual inspection of the internal detail of the map and identification of artifacts.

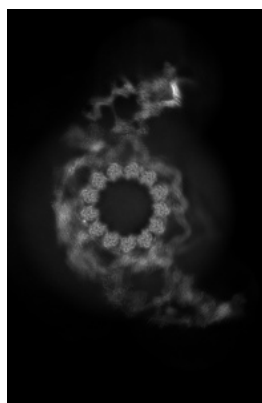
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

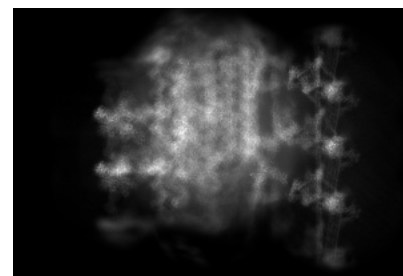
6.1.1 Primary map



X



Y

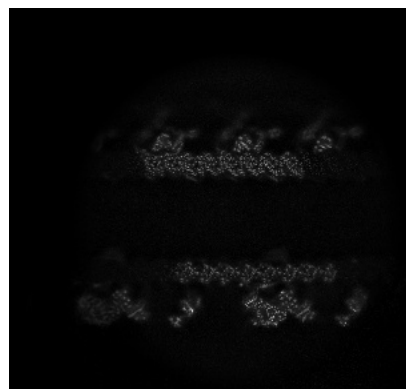


Z

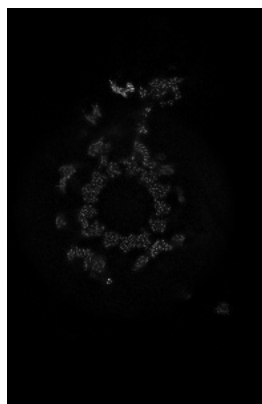
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

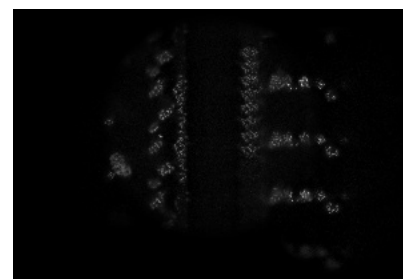
6.2.1 Primary map



X Index: 439



Y Index: 299

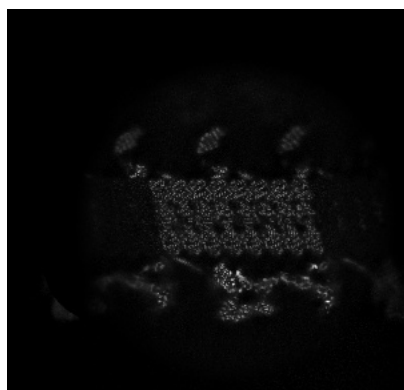


Z Index: 287

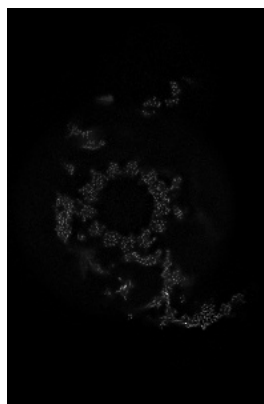
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

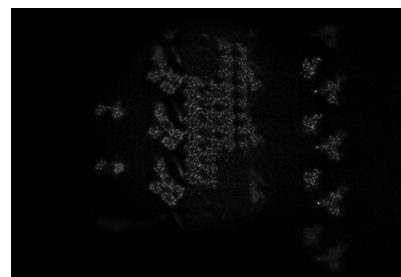
6.3.1 Primary map



X Index: 373



Y Index: 362

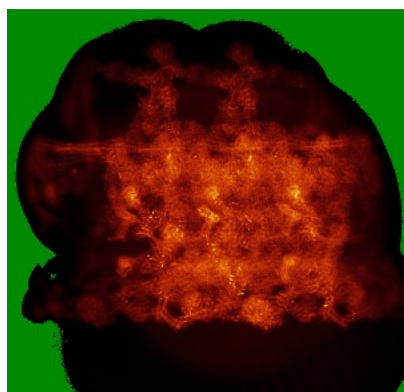


Z Index: 325

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

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

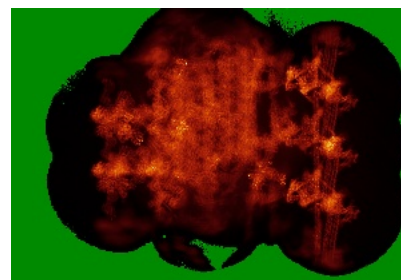
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

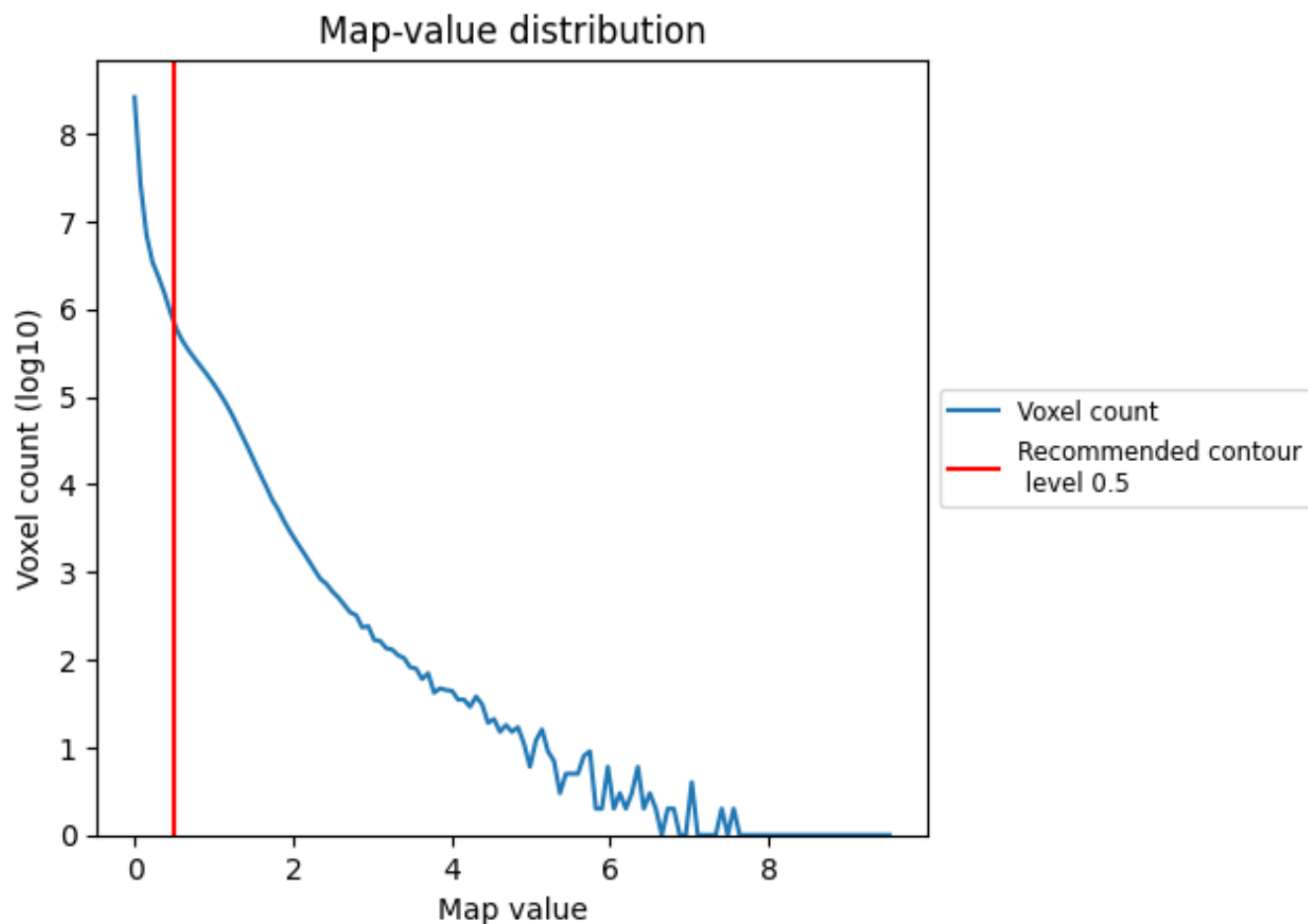
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

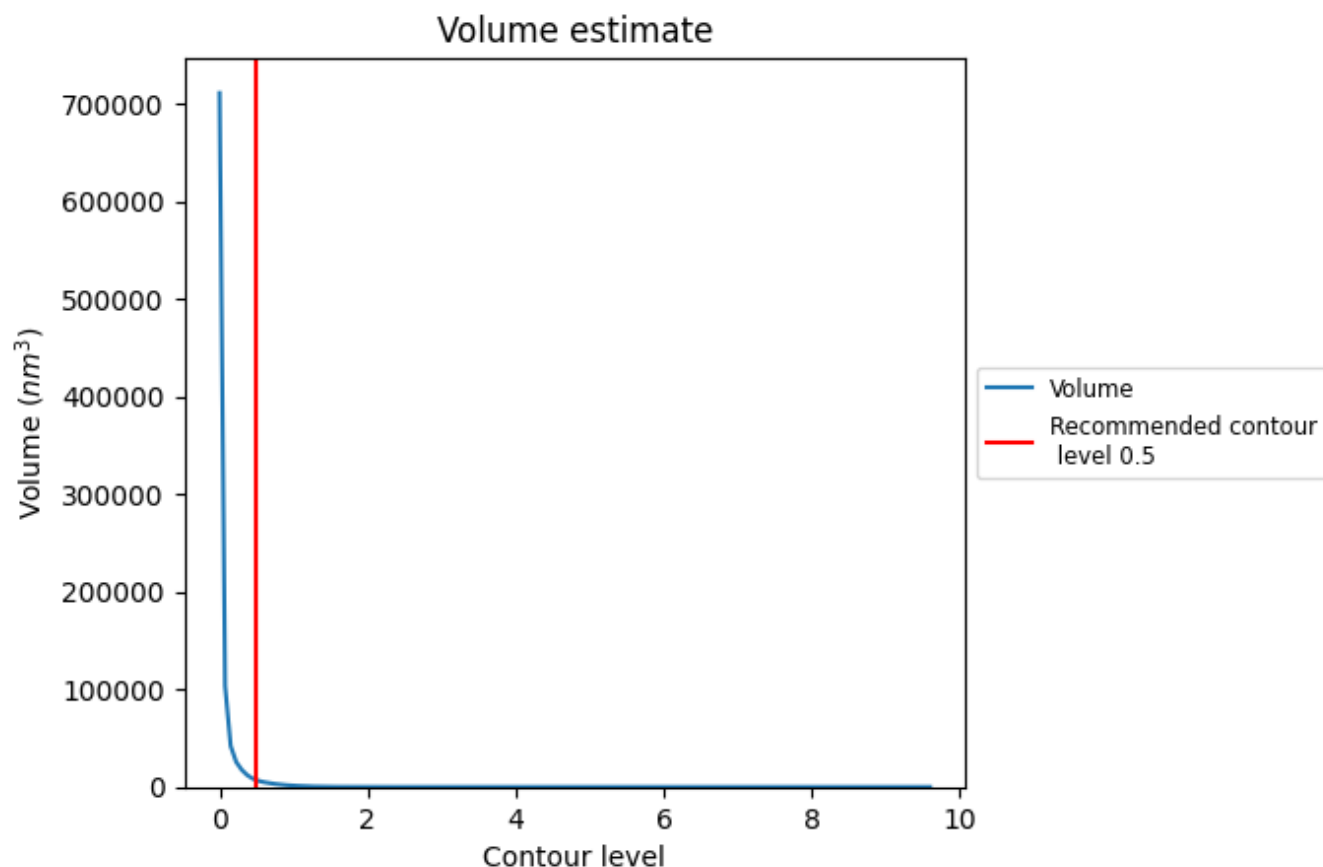
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 7012 nm³; this corresponds to an approximate mass of 6334 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

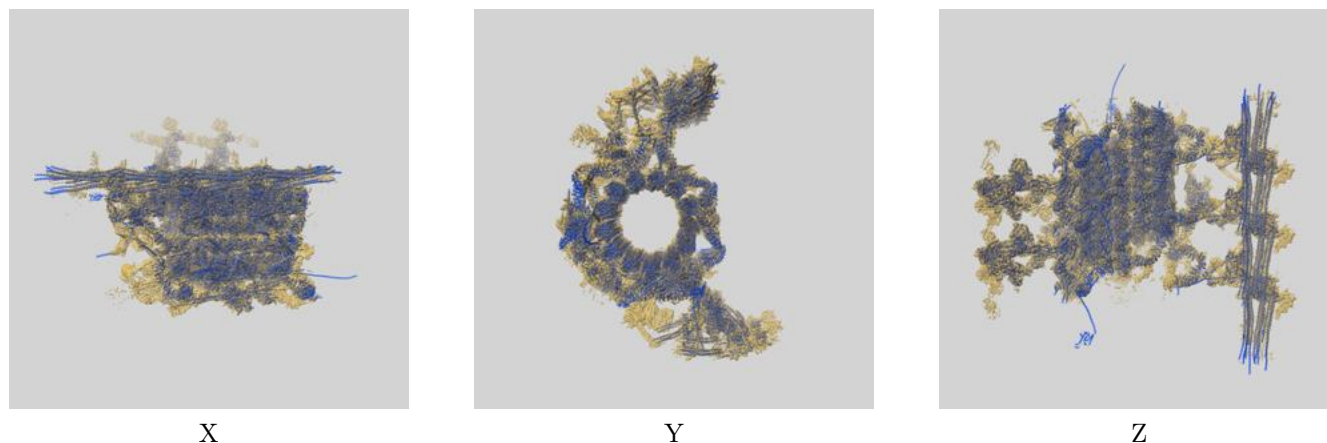
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

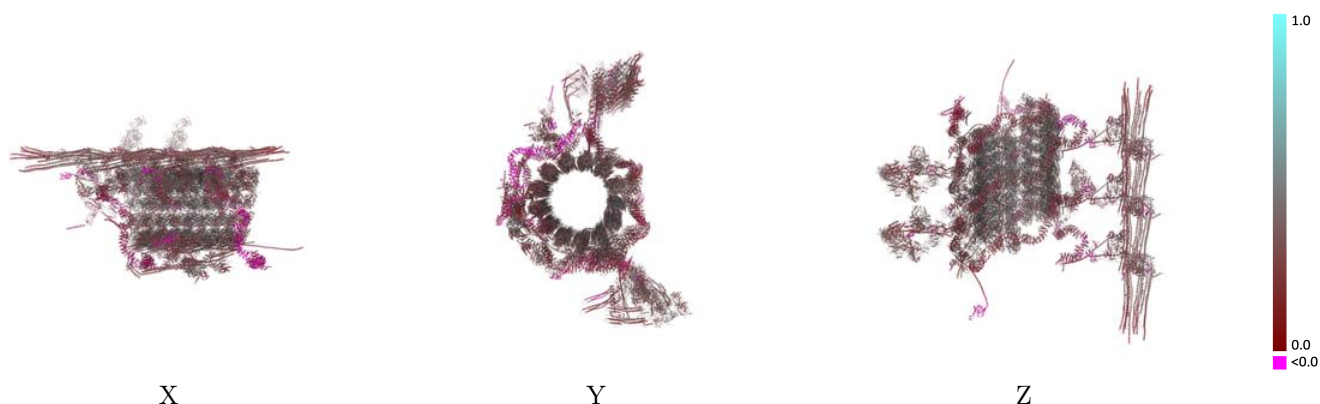
This section contains information regarding the fit between EMDB map EMD-24207 and PDB model 7N6G. Per-residue inclusion information can be found in section [3](#) on page [38](#).

9.1 Map-model overlay [i](#)



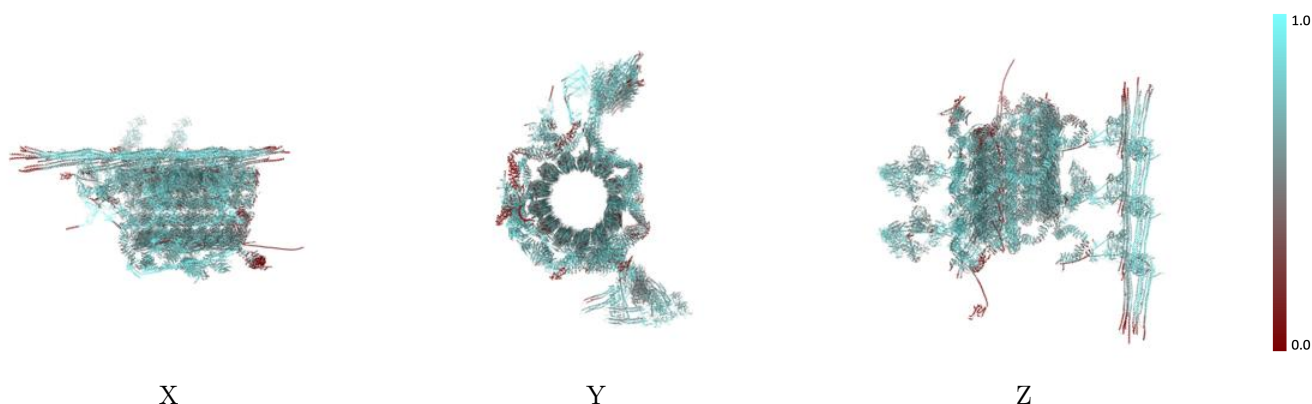
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



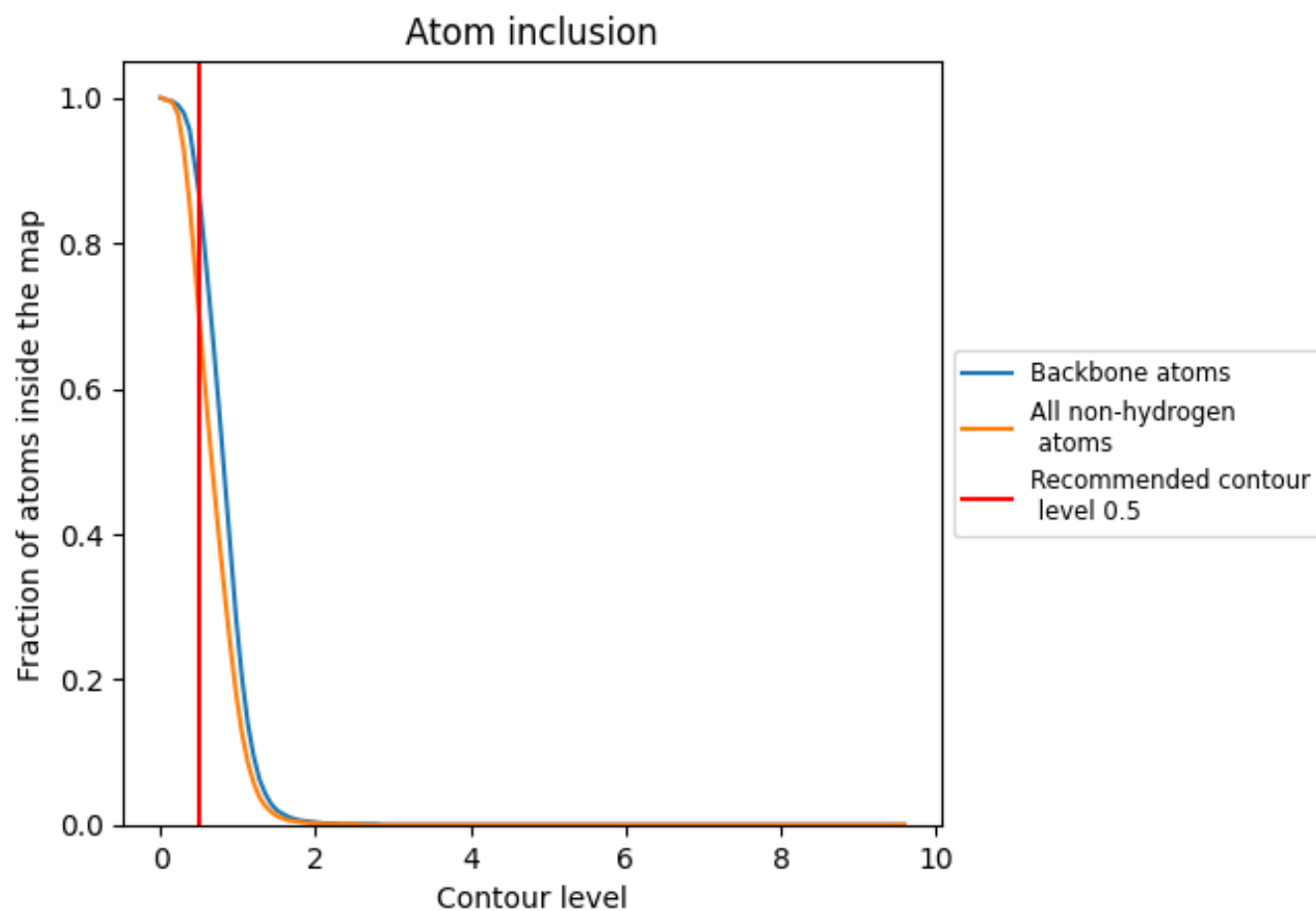
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6960	 0.3180
0A	 0.7500	 0.2650
0B	 0.4550	 0.2100
0C	 0.6700	 0.2090
0D	 0.5900	 0.2200
0E	 0.6450	 0.2060
0F	 0.7680	 0.1910
0G	 0.6020	 0.1330
0H	 0.7430	 0.1760
0I	 0.6340	 0.1160
0J	 0.6820	 0.1290
0K	 0.7380	 0.1500
0L	 0.8380	 0.2400
0M	 0.7780	 0.2260
0N	 0.8270	 0.2890
0O	 0.8100	 0.2820
0P	 0.3490	 0.0250
0Q	 0.4880	 0.0040
0R	 0.7990	 0.2820
0S	 0.7650	 0.2540
0T	 0.7850	 0.2600
0U	 0.8390	 0.2950
0V	 0.7750	 0.2540
0W	 0.7460	 0.2130
0X	 0.7530	 0.2590
0Y	 0.5600	 0.2060
0Z	 0.5210	 0.1890
1A	 0.7210	 0.2450
1B	 0.1150	 0.0410
1C	 0.2580	 0.0910
1D	 0.8500	 0.2490
1E	 0.4590	 0.1400
1F	 0.8270	 0.2670
1G	 0.5340	 0.1640
1H	 0.7510	 0.2730























































































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Chain	Atom inclusion	Q-score
1I	 0.5270	 0.2020
1J	 0.7930	 0.3180
1K	 0.8360	 0.3780
1L	 0.6760	 0.3030
1M	 0.7230	 0.2800
1N	 0.7710	 0.2690
1O	 0.8370	 0.3480
1P	 0.7480	 0.2890
1Q	 0.8610	 0.3240
1R	 0.7810	 0.3770
1S	 0.7220	 0.3510
1T	 0.9540	 0.2390
1a	 0.5810	 0.3640
1b	 0.6930	 0.3740
1c	 0.7180	 0.4100
1d	 0.7270	 0.4010
1e	 0.7370	 0.3940
1f	 0.7380	 0.3980
1g	 0.7530	 0.4240
1h	 0.7000	 0.4050
2F	 0.6800	 0.3690
2G	 0.5980	 0.3540
2H	 0.7460	 0.4360
2I	 0.8300	 0.4640
2J	 0.4780	 0.3790
2K	 0.5120	 0.4210
2L	 0.2930	 0.3280
2M	 0.4440	 0.3760
2N	 0.7190	 0.4510
2O	 0.7280	 0.3910
2P	 0.8360	 0.4620
2Q	 0.8730	 0.4280
2R	 0.8070	 0.4500
2S	 0.2160	 0.3650
2T	 0.0950	 0.2800
2U	 0.2200	 0.3280
2V	 0.2560	 0.3120
2W	 0.8800	 0.4280
2X	 0.8160	 0.4210
2Y	 0.8120	 0.3760
2Z	 0.4890	 0.3490
2a	 0.5660	 0.3220





















































































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Chain	Atom inclusion	Q-score
2b	 0.7120	 0.3890
2c	 0.7380	 0.4000
2d	 0.7280	 0.4040
2e	 0.7040	 0.3520
2f	 0.7400	 0.4020
2g	 0.7580	 0.4150
2h	 0.6870	 0.4000
3A	 0.8110	 0.3150
3B	 0.4170	 0.2640
3C	 0.7290	 0.3540
3E	 0.5680	 0.3030
3F	 0.4460	 0.2260
3G	 0.7000	 0.2620
3H	 0.7530	 0.3050
3I	 0.6460	 0.2630
3J	 0.7750	 0.3570
3K	 0.5320	 0.2870
3L	 0.7380	 0.2520
3M	 0.3960	 0.2500
3N	 0.5050	 0.2670
3O	 0.4690	 0.2650
3P	 0.4890	 0.2650
3Q	 0.6330	 0.2930
3R	 0.6270	 0.2790
3S	 0.5110	 0.2690
3T	 0.3670	 0.2580
3U	 0.6340	 0.2820
3V	 0.6330	 0.2710
3W	 0.7740	 0.3370
3X	 0.7780	 0.3250
3Y	 0.7830	 0.3240
3Z	 0.6600	 0.2850
3a	 0.5670	 0.3380
3b	 0.6940	 0.3860
3c	 0.7580	 0.4050
3d	 0.7050	 0.3890
3e	 0.7140	 0.3830
3f	 0.7160	 0.3950
3g	 0.7560	 0.4240
3h	 0.6470	 0.3860
4A	 0.7600	 0.3150
4B	 0.6350	 0.2930





















































































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Chain	Atom inclusion	Q-score
4C	 0.7520	 0.3040
4D	 0.7410	 0.2810
4E	 0.7300	 0.2730
4F	 0.7550	 0.3670
4G	 0.7590	 0.3660
4H	 0.7570	 0.3710
4I	 0.4340	 0.0160
4J	 0.6900	 0.2770
4K	 0.6710	 0.2600
4L	 0.3640	 -0.0330
4M	 0.3550	 -0.0260
4N	 0.3590	 -0.0290
4O	 0.7110	 0.2630
4P	 0.6930	 0.2780
4Q	 0.8390	 0.3110
4R	 0.5310	 0.1910
4S	 0.6980	 0.2050
4T	 0.7240	 0.3110
4U	 0.7230	 0.2980
4V	 0.7170	 0.3050
4W	 0.8510	 0.3030
4X	 0.9970	 0.3010
4Y	 0.9900	 0.2330
4Z	 0.9950	 0.2190
4a	 0.6040	 0.3270
4b	 0.7130	 0.3790
4c	 0.7460	 0.4040
4d	 0.7230	 0.3970
4e	 0.7260	 0.3990
4f	 0.7340	 0.3820
4g	 0.7520	 0.4110
4h	 0.6350	 0.3530
5A	 0.8630	 0.1960
5B	 1.0000	 0.2960
5C	 0.9870	 0.1560
5D	 0.9950	 0.1740
5E	 0.8180	 0.3270
5F	 0.7170	 0.2200
5G	 0.7330	 0.2050
5H	 0.7770	 0.2400
5I	 0.8210	 0.3050
5J	 0.7320	 0.2860





















































































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Chain	Atom inclusion	Q-score
5K	 0.7840	 0.2660
5L	 0.3860	 -0.0190
5M	 0.8910	 0.2500
5N	 0.6780	 0.1350
5O	 0.5380	 0.1390
5P	 0.7090	 0.2840
5Q	 0.8310	 0.2110
5R	 0.8460	 0.2190
5S	 0.7590	 0.3020
5T	 0.7410	 0.2960
5U	 0.7430	 0.2920
5V	 0.7660	 0.2950
5W	 0.9610	 0.2070
5X	 0.7900	 0.3030
5Y	 0.9940	 0.2860
5Z	 0.9180	 0.3220
5a	 0.5220	 0.2690
5b	 0.6960	 0.3700
5c	 0.7250	 0.3810
5d	 0.7120	 0.3840
5e	 0.7060	 0.3660
5f	 0.7290	 0.3770
5g	 0.7290	 0.3600
5h	 0.6290	 0.3390
6A	 0.5910	 0.1920
6B	 0.7190	 0.2660
6D	 0.8090	 0.3340
6E	 0.7320	 0.3210
6F	 0.7260	 0.3150
6G	 0.5100	 0.2830
6H	 0.5140	 0.2820
6I	 0.5360	 0.3380
6J	 0.5370	 0.3450
6K	 0.5900	 0.3200
6L	 0.5880	 0.3230
6M	 0.6980	 0.3180
6N	 0.6940	 0.3250
6O	 0.6130	 0.1910
6P	 0.6550	 0.1850
6Q	 0.7770	 0.2210
6a	 0.5320	 0.2520
6b	 0.6940	 0.3470









































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Chain	Atom inclusion	Q-score
6c	 0.7050	 0.3350
6d	 0.7170	 0.3820
6e	 0.7360	 0.3800
6f	 0.7350	 0.3740
6g	 0.7710	 0.3940
6h	 0.6550	 0.3590
7a	 0.5520	 0.2620
7b	 0.6890	 0.3570
7c	 0.6930	 0.3500
7d	 0.6890	 0.3600
7e	 0.7100	 0.3520
7f	 0.7500	 0.3800
7g	 0.7700	 0.4040
7h	 0.6850	 0.3800
8a	 0.4880	 0.2030
8b	 0.6950	 0.3660
8c	 0.7040	 0.3770
8d	 0.6830	 0.3650
8e	 0.6910	 0.3670
8f	 0.7250	 0.3570
8g	 0.7400	 0.3760
8h	 0.6410	 0.3520
9a	 0.5970	 0.3180
9b	 0.7240	 0.3890
9c	 0.7390	 0.3950
9d	 0.7120	 0.3780
9e	 0.7110	 0.3630
9f	 0.7430	 0.3920
9g	 0.7340	 0.3810
9h	 0.6700	 0.3700
Aa	 0.6200	 0.3240
Ab	 0.7200	 0.3880
Ac	 0.7560	 0.4150
Ad	 0.7180	 0.3880
Ae	 0.7500	 0.4060
Af	 0.7560	 0.4000
Ag	 0.7560	 0.4130
Ah	 0.6720	 0.3740
Ba	 0.6750	 0.4000
Bb	 0.7550	 0.4110
Bc	 0.7460	 0.3610
Bd	 0.7530	 0.4020

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Chain	Atom inclusion	Q-score
Be	 0.7620	 0.4010
Bf	 0.7700	 0.4060
Bg	 0.7530	 0.3840
Bh	 0.7010	 0.3960
Ca	 0.6860	 0.4150
Cb	 0.7430	 0.4180
Cc	 0.7710	 0.4190
Cd	 0.7560	 0.4180
Ce	 0.7650	 0.4000
Cf	 0.7660	 0.4210
Cg	 0.7590	 0.4260
Ch	 0.6860	 0.4070
Da	 0.7310	 0.4170
Db	 0.7830	 0.4210
Dc	 0.8150	 0.4470
Dd	 0.7790	 0.4220
De	 0.7820	 0.4110
Df	 0.7750	 0.4200
Dg	 0.7880	 0.4240
Dh	 0.6840	 0.3920