



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:55 AM UTC

PDB ID : 7N61 / pdb_00007n61
EMDB ID : EMD-24191
Title : structure of C2 projections and MIPs
Authors : Han, L.; Zhang, K.
Deposited on : 2021-06-07
Resolution : 3.50 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:

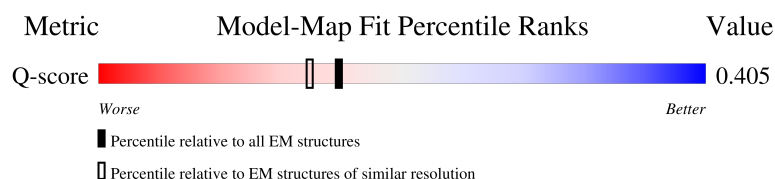
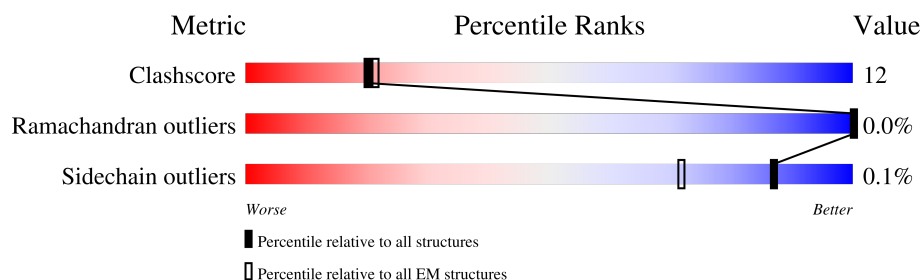
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	606	17% 54% 23% 23%
1	0B	606	10% 51% 26% 23%
1	0C	606	15% 52% 27% 21%
1	0D	606	34% 51% 27% 21%

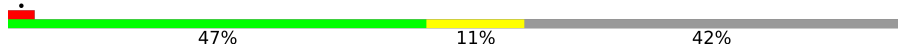
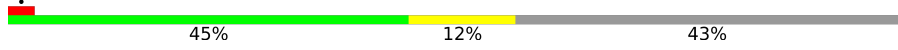
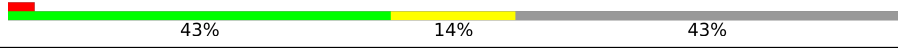
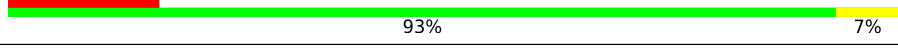
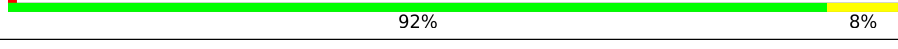
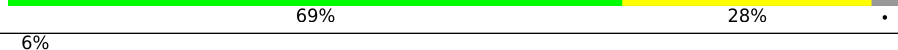
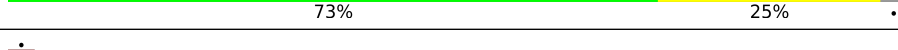
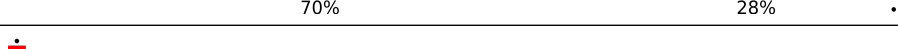
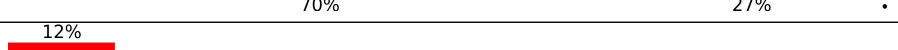
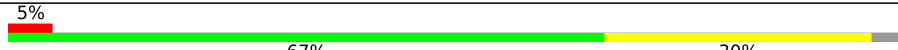
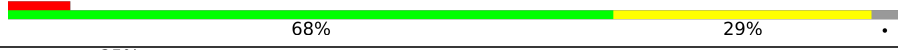
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Mol	Chain	Length	Quality of chain
2	0E	222	
2	0F	222	
2	0G	222	
2	0H	222	
3	0I	976	
3	0J	976	
4	0K	528	
4	0L	528	
5	0M	758	
5	0N	758	
6	0O	201	
6	0P	201	
7	0Q	618	
7	0S	618	
8	0T	169	
9	0U	170	
10	0V	160	
11	0W	39	
12	0X	776	
12	0Y	776	
12	0Z	776	
12	1A	776	
13	1B	2257	
13	1C	2257	
14	1D	1074	

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Mol	Chain	Length	Quality of chain
14	1E	1074	
14	1F	1074	
14	1G	1074	
15	1H	88	
16	1L	174	
16	1M	174	
17	1a	443	
17	1c	443	
17	1e	443	
17	1g	443	
17	2a	443	
17	2c	443	
17	2e	443	
17	2g	443	
17	3a	443	
17	3c	443	
17	3e	443	
17	3g	443	
17	4a	443	
17	4c	443	
17	4e	443	
17	4g	443	
17	5a	443	
17	5c	443	
17	5e	443	

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Mol	Chain	Length	Quality of chain
17	5g	443	
17	6a	443	
17	6c	443	
17	6e	443	
17	6g	443	
17	7a	443	
17	7c	443	
17	7e	443	
17	7g	443	
17	8a	443	
17	8c	443	
17	8e	443	
17	8g	443	
17	9a	443	
17	9c	443	
17	9e	443	
17	9g	443	
17	Aa	443	
17	Ac	443	
17	Ae	443	
17	Ag	443	
17	Ba	443	
17	Bc	443	
17	Be	443	
17	Bg	443	

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Mol	Chain	Length	Quality of chain
17	Ca	443	
17	Cc	443	
17	Ce	443	
17	Cg	443	
17	Da	443	
17	Dc	443	
17	De	443	
17	Dg	443	
18	1b	451	
18	1d	451	
18	1f	451	
18	1h	451	
18	2b	451	
18	2d	451	
18	2f	451	
18	2h	451	
18	3b	451	
18	3d	451	
18	3f	451	
18	3h	451	
18	4b	451	
18	4d	451	
18	4f	451	
18	4h	451	
18	5b	451	

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Mol	Chain	Length	Quality of chain
18	5d	451	
18	5f	451	
18	5h	451	
18	6b	451	
18	6d	451	
18	6f	451	
18	6h	451	
18	7b	451	
18	7d	451	
18	7f	451	
18	7h	451	
18	8b	451	
18	8d	451	
18	8f	451	
18	8h	451	
18	9b	451	
18	9d	451	
18	9f	451	
18	9h	451	
18	Ab	451	
18	Ad	451	
18	Af	451	
18	Ah	451	
18	Bb	451	
18	Bd	451	

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Mol	Chain	Length	Quality of chain
18	Bf	451	
18	Bh	451	
18	Cb	451	
18	Cd	451	
18	Cf	451	
18	Ch	451	
18	Db	451	
18	Dd	451	
18	Df	451	
18	Dh	451	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 443856 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 Flagellar WD repeat-containing protein Pf20.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0A	467	Total	C	N	O	S	0	0
			3656	2298	650	685	23		
1	0B	467	Total	C	N	O	S	0	0
			3656	2298	650	685	23		
1	0C	476	Total	C	N	O	S	0	0
			3726	2343	664	696	23		
1	0D	476	Total	C	N	O	S	0	0
			3726	2343	664	696	23		

- Molecule 2 is a protein called FAP178.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0E	128	Total	C	N	O	S	0	0
			1008	640	180	184	4		
2	0F	128	Total	C	N	O	S	0	0
			1008	640	180	184	4		
2	0G	128	Total	C	N	O	S	0	0
			1008	640	180	184	4		
2	0H	128	Total	C	N	O	S	0	0
			1008	640	180	184	4		

- Molecule 3 is a protein called FAP147.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	0I	448	Total	C	N	O	S	0	0
			3321	2062	633	616	10		
3	0J	448	Total	C	N	O	S	0	0
			3321	2062	633	616	10		

- Molecule 4 is a protein called FAP239.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	0K	166	Total	C	N	O	S	0	0
			1216	747	229	239	1		
4	0L	166	Total	C	N	O	S	0	0
			1216	747	229	239	1		

- Molecule 5 is a protein called FAP225.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	0M	515	Total	C	N	O	S	0	0
			4037	2487	769	768	13		
5	0N	515	Total	C	N	O	S	0	0
			4037	2487	769	768	13		

- Molecule 6 is a protein called FAP213.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	0O	188	Total	C	N	O	S	0	0
			1481	897	294	287	3		
6	0P	188	Total	C	N	O	S	0	0
			1481	897	294	287	3		

- Molecule 7 is a protein called FAP196.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	0Q	617	Total	C	N	O	S	0	0
			4537	2823	824	857	33		
7	0S	617	Total	C	N	O	S	0	0
			4537	2823	824	857	33		

- Molecule 8 is a protein called Unassigned protein-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	0T	169	Total	C	N	O	0	0
			845	507	169	169		

- Molecule 9 is a protein called Unassigned protein-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	0U	170	Total	C	N	O	0	0
			850	510	170	170		

- Molecule 10 is a protein called Unassigned protein-3.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	0V	160	Total	C	N	O	0	0
			800	480	160	160		

- Molecule 11 is a protein called Unassigned protein-4.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	0W	39	Total	C	N	O	0	0
			195	117	39	39		

- Molecule 12 is a protein called Kinesin-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	0X	420	Total	C	N	O	S	0	0
			3098	1921	561	608	8		
12	0Y	404	Total	C	N	O	S	0	0
			2903	1800	527	569	7		
12	0Z	420	Total	C	N	O	S	0	0
			3098	1921	561	608	8		
12	1A	404	Total	C	N	O	S	0	0
			2903	1800	527	569	7		

- Molecule 13 is a protein called FAP65.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	1B	630	Total	C	N	O	S	0	0
			4771	3018	865	874	14		
13	1C	630	Total	C	N	O	S	0	0
			4771	3018	865	874	14		

- Molecule 14 is a protein called FAP70.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	1D	623	Total	C	N	O	S	0	0
			4079	2527	756	781	15		
14	1E	623	Total	C	N	O	S	0	0
			4079	2527	756	781	15		
14	1F	614	Total	C	N	O	S	0	0
			4370	2725	808	821	16		
14	1G	614	Total	C	N	O	S	0	0
			4370	2725	808	821	16		

- Molecule 15 is a protein called Unassigned protein-5.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	1H	88	Total	C	N	O	0	0
			440	264	88	88		

- Molecule 16 is a protein called Unassigned protein-6.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	1M	174	Total	C	N	O	0	0
			870	522	174	174		
16	1L	174	Total	C	N	O	0	0
			870	522	174	174		

- Molecule 17 is a protein called Tubulin beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	1a	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	1c	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	1e	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	1g	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	2a	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	2c	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	2e	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	2g	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	3a	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	3c	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	3e	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	3g	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	4a	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	4c	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		
17	4e	431	Total	C	N	O	S	0	0
			3379	2121	579	649	30		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	4g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	5a	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	5c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	5e	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	5g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	6a	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	6c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	6e	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	6g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	7a	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	7c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	7e	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	7g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	8a	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	8c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	8e	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	8g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	9a	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	9c	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	9e	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	9g	431	Total 3379	C 2121	N 579	O 649	S 30	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	Aa	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Ac	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Ae	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Ag	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Ba	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Bc	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Be	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Bg	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Ca	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Cc	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Ce	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Cg	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Da	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Dc	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	De	431	Total 3379	C 2121	N 579	O 649	S 30	0	0
17	Dg	431	Total 3379	C 2121	N 579	O 649	S 30	0	0

- Molecule 18 is a protein called Tubulin alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	1b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	1d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	1f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
18	1h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	2b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	2d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	2f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	2h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	3b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	3d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	3f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	3h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	4b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	4d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	4f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	4h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	5b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	5d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	5f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	5h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	6b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	6d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	6f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	6h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0

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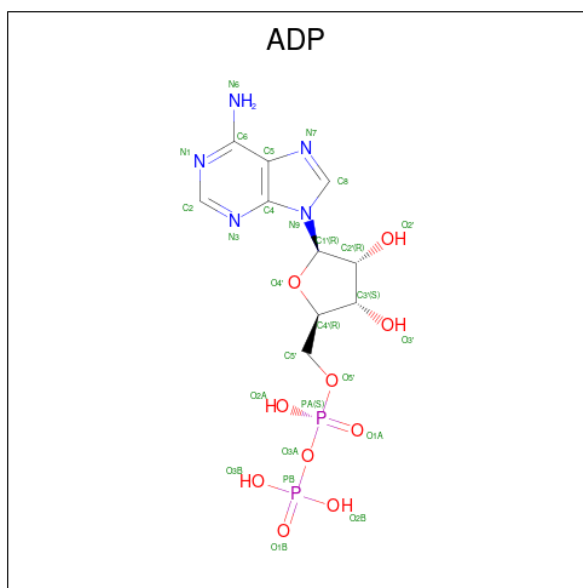
Mol	Chain	Residues	Atoms					AltConf	Trace
18	7b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	7d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	7f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	7h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	8b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	8d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	8f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	8h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	9b	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	9d	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	9f	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	9h	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	Ab	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	Ad	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	Af	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	Ah	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	Bb	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	Bd	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	Bf	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	Bh	430	Total 3339	C 2115	N 568	O 634	S 22	0	0
18	Cb	430	Total 3339	C 2115	N 568	O 634	S 22	0	0

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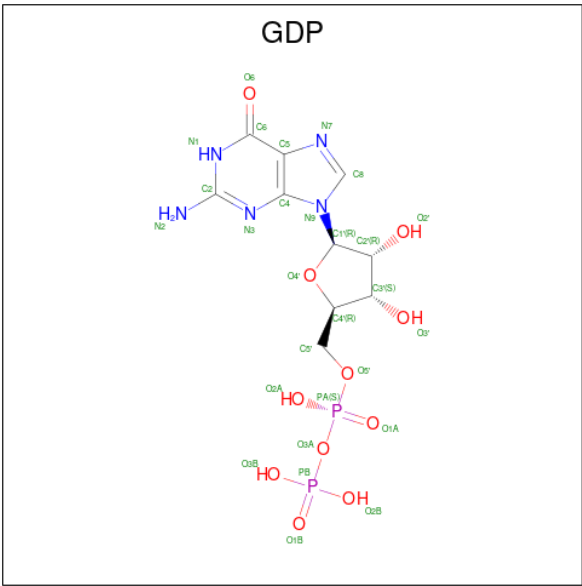
Mol	Chain	Residues	Atoms					AltConf	Trace
18	Cd	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
18	Cf	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
18	Ch	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
18	Db	430	Total	C	N	O	S	0	0
			3339	2115	568	634	22		
18	Dd	430	Total	C	N	O	S	0	0
			3339	2115	568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

- Molecule 19 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
19	0X	1	Total	C	N	O	P	0
			27	10	5	10	2	
19	0Y	1	Total	C	N	O	P	0
			27	10	5	10	2	
19	0Z	1	Total	C	N	O	P	0
			27	10	5	10	2	
19	1A	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 20 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
20	1a	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	1c	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	1e	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	1g	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	2a	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	2c	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	2e	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	2g	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	3a	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	3c	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	3e	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	3g	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	4a	1	Total	C	N	O	P	0
			28	10	5	11	2	

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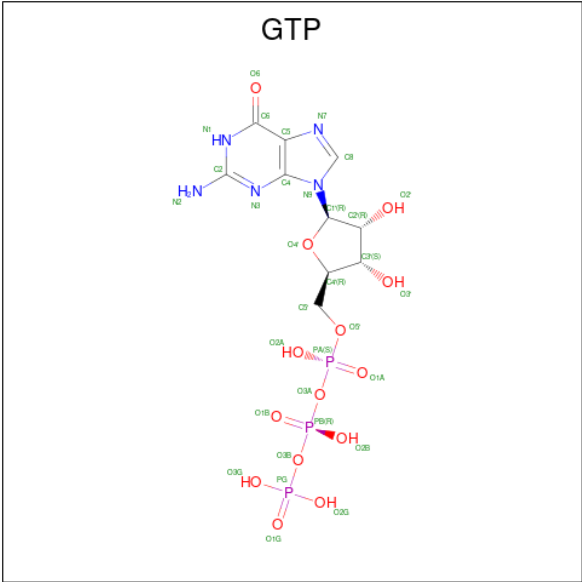
Mol	Chain	Residues	Atoms					AltConf
20	4c	1	Total 28	C 10	N 5	O 11	P 2	0
20	4e	1	Total 28	C 10	N 5	O 11	P 2	0
20	4g	1	Total 28	C 10	N 5	O 11	P 2	0
20	5a	1	Total 28	C 10	N 5	O 11	P 2	0
20	5c	1	Total 28	C 10	N 5	O 11	P 2	0
20	5e	1	Total 28	C 10	N 5	O 11	P 2	0
20	5g	1	Total 28	C 10	N 5	O 11	P 2	0
20	6a	1	Total 28	C 10	N 5	O 11	P 2	0
20	6c	1	Total 28	C 10	N 5	O 11	P 2	0
20	6e	1	Total 28	C 10	N 5	O 11	P 2	0
20	6g	1	Total 28	C 10	N 5	O 11	P 2	0
20	7a	1	Total 28	C 10	N 5	O 11	P 2	0
20	7c	1	Total 28	C 10	N 5	O 11	P 2	0
20	7e	1	Total 28	C 10	N 5	O 11	P 2	0
20	7g	1	Total 28	C 10	N 5	O 11	P 2	0
20	8a	1	Total 28	C 10	N 5	O 11	P 2	0
20	8c	1	Total 28	C 10	N 5	O 11	P 2	0
20	8e	1	Total 28	C 10	N 5	O 11	P 2	0
20	8g	1	Total 28	C 10	N 5	O 11	P 2	0
20	9a	1	Total 28	C 10	N 5	O 11	P 2	0
20	9c	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
20	9e	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	9g	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Aa	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Ac	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Ae	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Ag	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Ba	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Bc	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Be	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Bg	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Ca	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Cc	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Ce	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Cg	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Da	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Dc	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	De	1	Total	C	N	O	P	0
			28	10	5	11	2	
20	Dg	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 21 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
21	1b	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	1d	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	1f	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	1h	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	2b	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	2d	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	2f	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	2h	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	3b	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	3d	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	3f	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	3h	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	4b	1	Total	C	N	O	P	0
			32	10	5	14	3	
21	4d	1	Total	C	N	O	P	0
			32	10	5	14	3	

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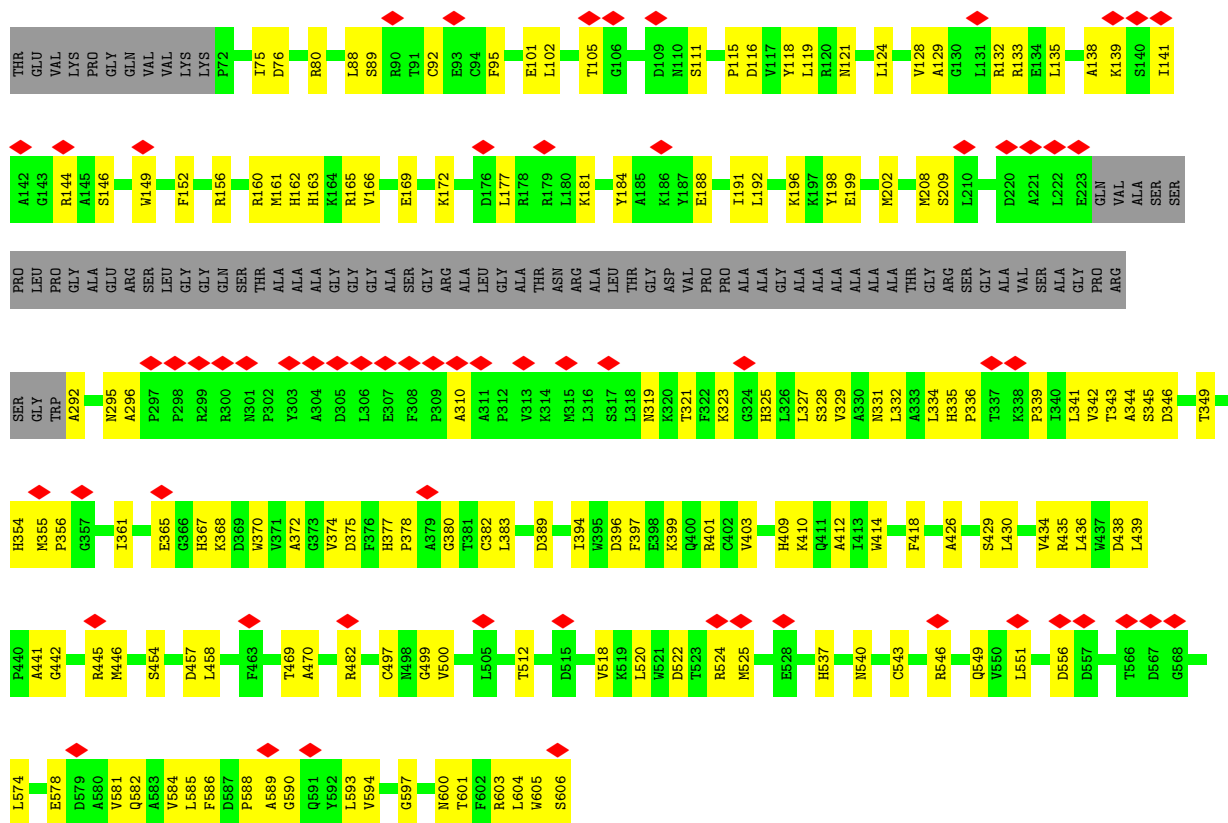
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Mol	Chain	Residues	Atoms					AltConf
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21	4h	1	Total 32	C 10	N 5	O 14	P 3	0
21	5b	1	Total 32	C 10	N 5	O 14	P 3	0
21	5d	1	Total 32	C 10	N 5	O 14	P 3	0
21	5f	1	Total 32	C 10	N 5	O 14	P 3	0
21	5h	1	Total 32	C 10	N 5	O 14	P 3	0
21	6b	1	Total 32	C 10	N 5	O 14	P 3	0
21	6d	1	Total 32	C 10	N 5	O 14	P 3	0
21	6f	1	Total 32	C 10	N 5	O 14	P 3	0
21	6h	1	Total 32	C 10	N 5	O 14	P 3	0
21	7b	1	Total 32	C 10	N 5	O 14	P 3	0
21	7d	1	Total 32	C 10	N 5	O 14	P 3	0
21	7f	1	Total 32	C 10	N 5	O 14	P 3	0
21	7h	1	Total 32	C 10	N 5	O 14	P 3	0
21	8b	1	Total 32	C 10	N 5	O 14	P 3	0
21	8d	1	Total 32	C 10	N 5	O 14	P 3	0
21	8f	1	Total 32	C 10	N 5	O 14	P 3	0
21	8h	1	Total 32	C 10	N 5	O 14	P 3	0
21	9b	1	Total 32	C 10	N 5	O 14	P 3	0
21	9d	1	Total 32	C 10	N 5	O 14	P 3	0
21	9f	1	Total 32	C 10	N 5	O 14	P 3	0

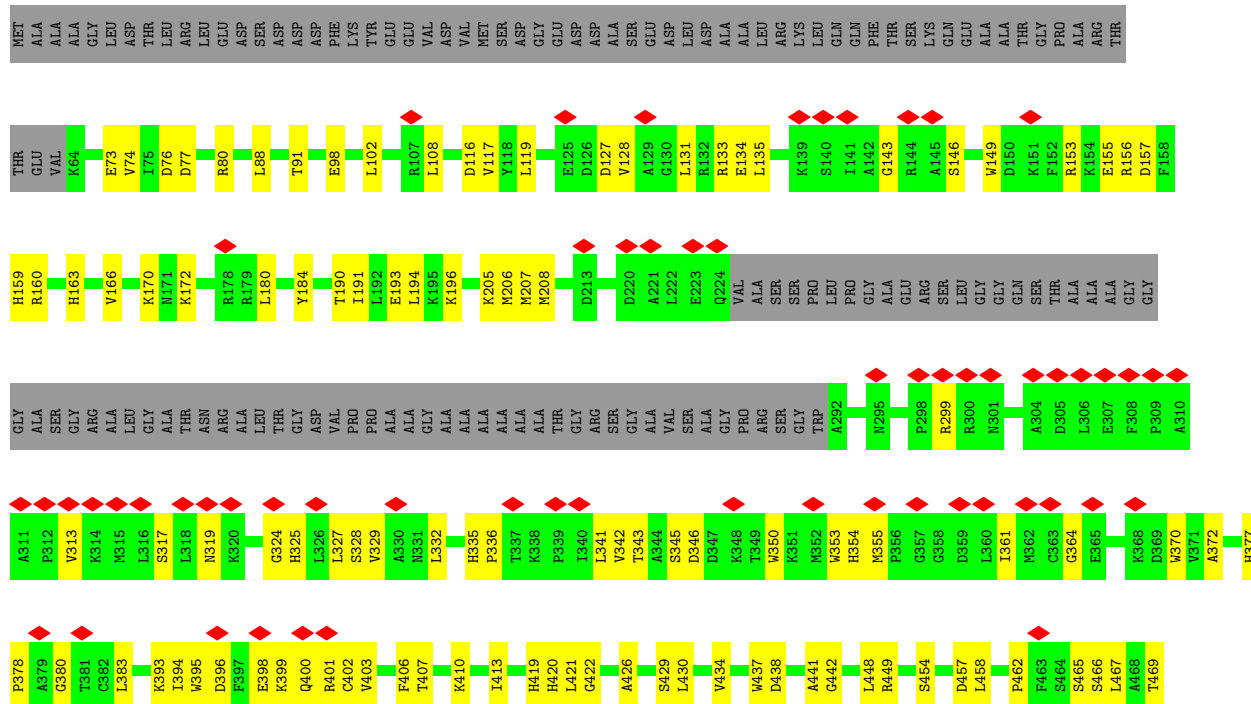
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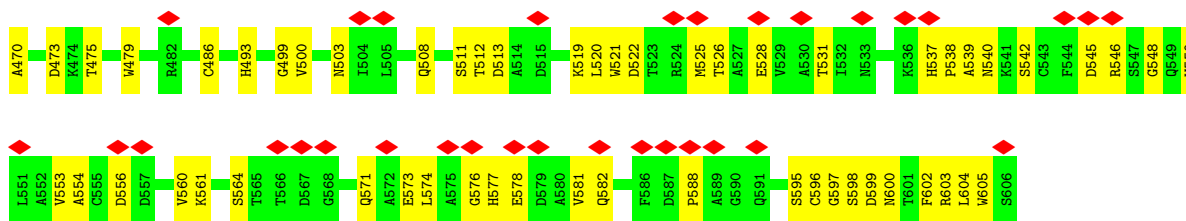
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Mol	Chain	Residues	Atoms					AltConf
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21	Ab	1	Total 32	C 10	N 5	O 14	P 3	0
21	Ad	1	Total 32	C 10	N 5	O 14	P 3	0
21	Af	1	Total 32	C 10	N 5	O 14	P 3	0
21	Ah	1	Total 32	C 10	N 5	O 14	P 3	0
21	Bb	1	Total 32	C 10	N 5	O 14	P 3	0
21	Bd	1	Total 32	C 10	N 5	O 14	P 3	0
21	Bf	1	Total 32	C 10	N 5	O 14	P 3	0
21	Bh	1	Total 32	C 10	N 5	O 14	P 3	0
21	Cb	1	Total 32	C 10	N 5	O 14	P 3	0
21	Cd	1	Total 32	C 10	N 5	O 14	P 3	0
21	Cf	1	Total 32	C 10	N 5	O 14	P 3	0
21	Ch	1	Total 32	C 10	N 5	O 14	P 3	0
21	Db	1	Total 32	C 10	N 5	O 14	P 3	0
21	Dd	1	Total 32	C 10	N 5	O 14	P 3	0
21	Df	1	Total 32	C 10	N 5	O 14	P 3	0
21	Dh	1	Total 32	C 10	N 5	O 14	P 3	0

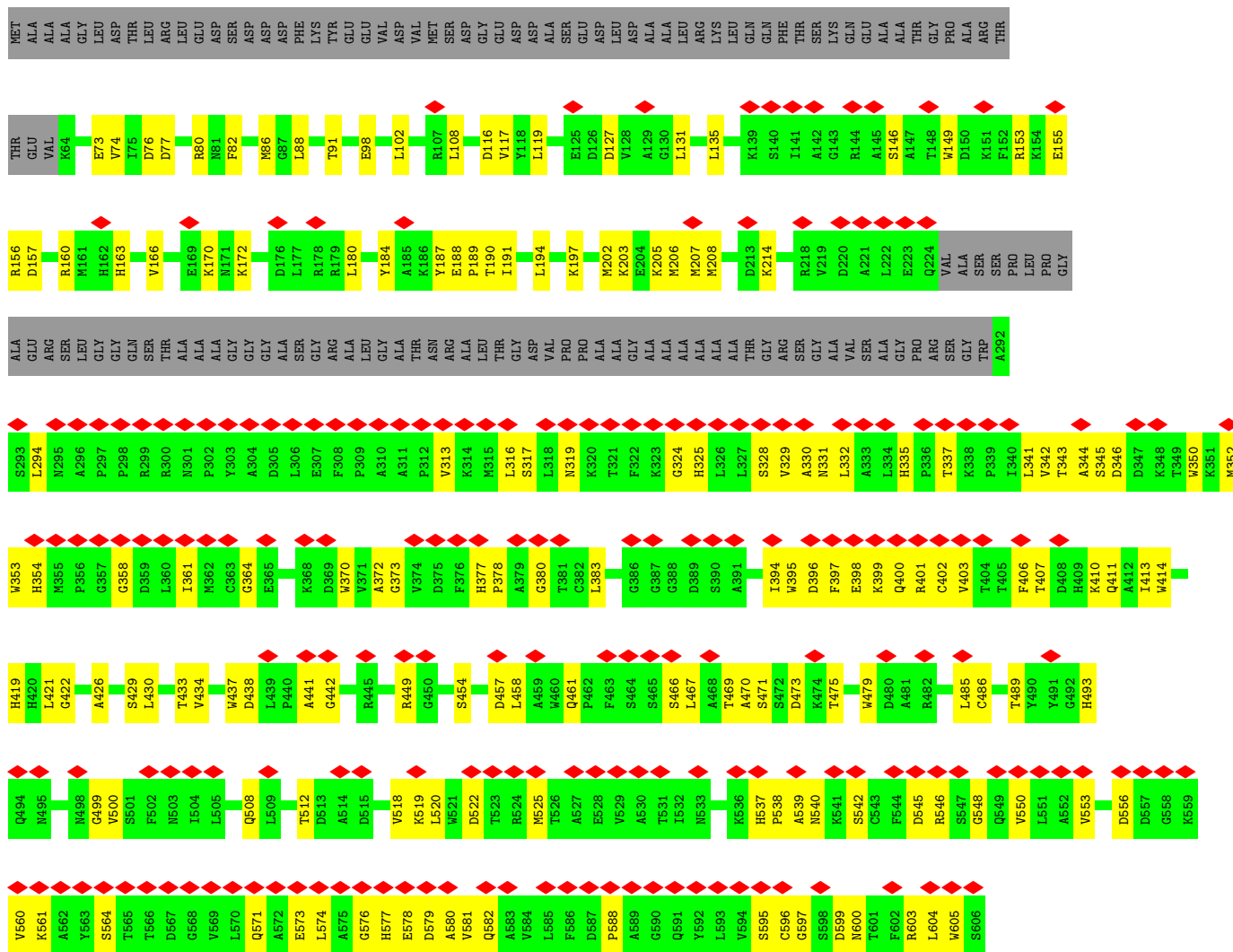


● Molecule 1: Flagellar WD repeat-containing protein Pf20

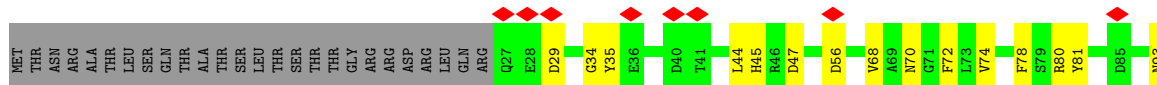




• Molecule 1: Flagellar WD repeat-containing protein Pf20



• Molecule 2: FAP178



Chain 0I:



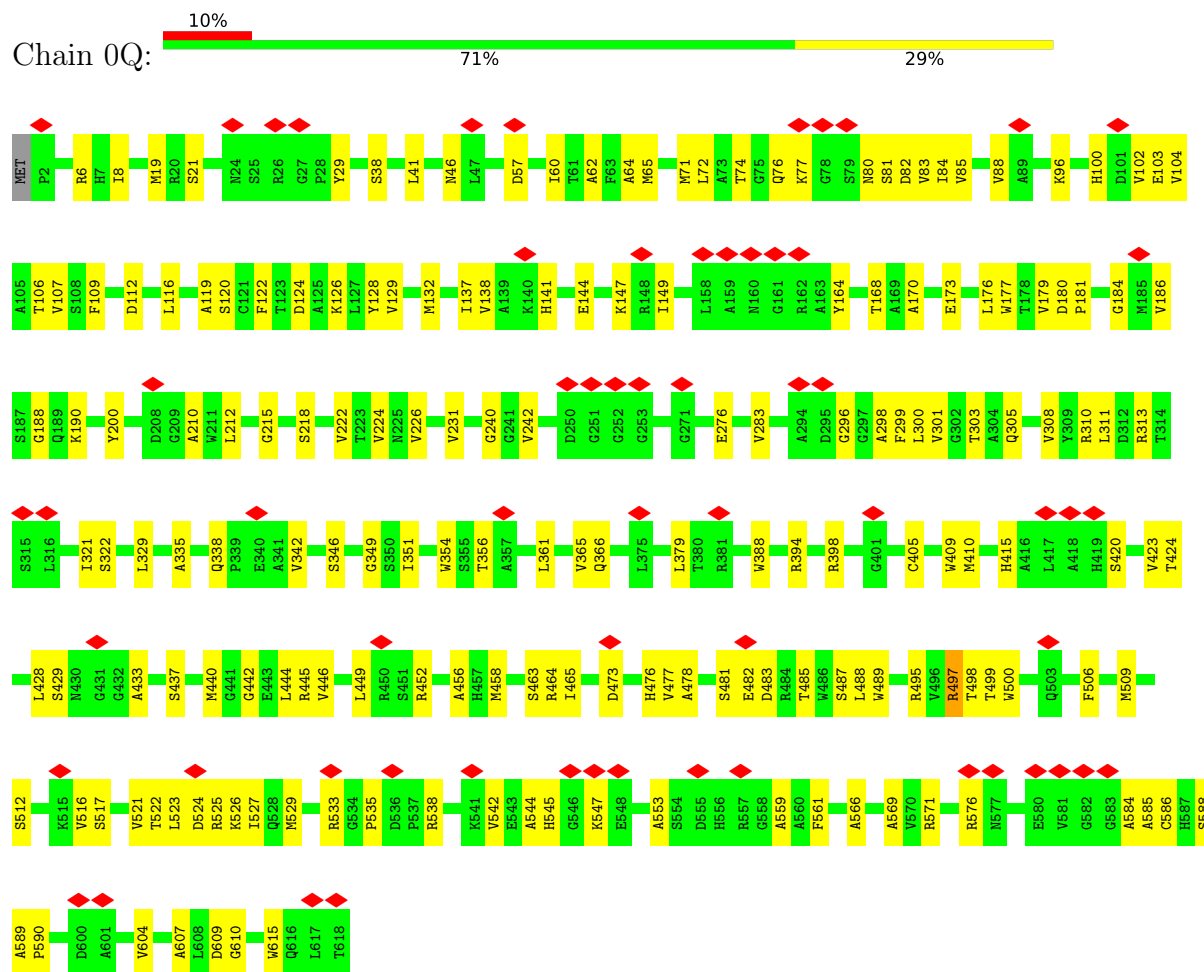
THR	GLU	THR	LEU	ALA	RE58	GLY	ARG	TRP	GLU	TRP	VAL	MET
LEU	LYS	ASP	LEU	LEU	A451	GLY	GLY	GLY	ASN	PHE	PHE	VAL
LEU	PRO	LEU	THR	ALA	A452	HIS	HIS	HIS	R129	R231	R232	GLY
ASP	GLY	GLU	GLU	ALA	A453	ALA	ALA	ALA	R234	R233	R234	PRO
GLU	ALA	ALA	LEU	ALA	A454	PRO	PRO	PRO	M135	R235	R235	SER
VAL	LYS	SER	ALA	LYS	A455	GLU	GLU	ALA	T141	R246	R246	GLU
ASP	GLY	ALA	ALA	LYS	A456	ALA	ALA	ALA	R142	R246	R246	PRO
ALA	GLY	ALA	ALA	PRO	A457	GLU	GLU	ALA	K143	P250	P250	LEU
ALA	GLY	ALA	ALA	SER	R458	GLU	GLU	ALA	K146	T263	T263	ASN
ALA	LYS	ASP	VAL	VAL	R459	ALA	ALA	ALA	F147	T264	T264	LYS
ALA	ASP	ALA	ALA	GLU	Q464	TYR	LYS	LYS	Q150	L265	L265	PRO
ALA	LYS	ALA	ALA	ASP	L482	ALA	ALA	ALA	Q153	L266	L266	LYS
ALA	LYS	ALA	ALA	ASP	Q483	VAL	VAL	VAL	L161	L267	L267	ALA
ALA	GLY	ALA	PRO	LYS	L487	GLY	ASP	GLY	R164	L268	L268	TYR
ALA	GLY	ALA	LEU	LYS	L488	GLU	GLU	GLU	R165	L269	L269	VAL
ALA	LYS	ALA	ALA	LYS	E582	GLU	GLU	GLU	G166	L270	L270	VAL
ALA	VAL	ALA	VAL	LYS	E583	GLU	GLU	GLU	R167	L271	L271	GLY
ALA	VAL	ALA	VAL	LYS	S583	GLU	GLU	GLU	L172	L272	L272	ASP
ALA	SER	ALA	ARG	LYS	A592	GLU	GLU	GLU	A173	L273	L273	VAL
ALA	HIS	ALA	ALA	GLU	V495	ALA	ALA	ALA	R176	L274	L274	GLY
ALA	THR	ALA	THR	THR	A496	GLN	GLN	GLN	V165	L275	L275	GLY
ALA	GLU	ALA	GLU	GLU	V497	LEU	LEU	LEU	G166	L276	L276	PHE
ALA	ASP	ALA	GLU	ALA	T498	ARG	ARG	ARG	R167	L277	L277	GLY
ALA	GLY	GLU	LYS	LYS	A503	ALA	ALA	ALA	L172	L278	L278	ASP
ALA	ASP	ALA	ALA	LYS	A504	ALA	ALA	ALA	A173	L279	L279	VAL
ALA	GLY	ALA	ARG	GLY	A505	LEU	LEU	LEU	R176	L280	L280	GLY
ALA	GLY	ASP	ALA	LYS	G505	GLU	GLU	GLU	G177	L281	L281	GLY
ALA	GLY	ALA	VAL	GLY	R508	GLU	GLU	GLU	P178	L282	L282	PHE
ALA	ALA	GLY	PRO	ASP	E512	GLU	GLU	GLU	R181	L283	L283	GLY
ALA	PRO	GLY	ASN	PRO	L513	GLN	GLN	GLN	T182	L284	L284	GLY
ALA	LEU	ALA	ASN	PRO	R516	ALA	ALA	ALA	E185	L285	L285	ALA
ALA	ASN	ALA	LYS	PRO	P517	ALA	ALA	ALA	A193	L286	L286	THR
ALA	VAL	TYR	VAL	PRO	P518	GLU	GLU	GLU	Q194	L287	L287	LEU
ALA	GLU	SER	LEU	PRO	S522	GLU	GLU	GLU	R196	L288	L288	PRO
ALA	GLY	VAL	ARG	LYS	T528	GLU	GLU	GLU	D197	L289	L289	PRO
ALA	HIS	VAL	ARG	TYR	L529	GLU	GLU	GLU	M104	L290	L290	LYS
ALA	GLY	GLY	ALA	ALA	A535	GLU	GLU	GLU	G105	L291	L291	ALA
ALA	GLY	GLY	ALA	ALA	E536	GLU	GLU	GLU	G106	L292	L292	PRO
ALA	GLY	GLY	ALA	ALA	V537	GLU	GLU	GLU	S107	L293	L293	GLU
ALA	VAL	VAL	VAL	VAL	R538	GLU	GLU	GLU	M108	L294	L294	ASN
ALA	VAL	VAL	VAL	VAL	GLU	VAL	VAL	VAL	G109	L295	L295	VAL
ALA	GLN	GLN	GLN	GLN	G544	GLU	GLU	GLU	P110	L296	L296	PHE
ALA	SER	GLU	VAL	ALA	R545	GLU	GLU	GLU	T208	L297	L297	ASN
ALA	GLY	GLY	ALA	ALA	L548	GLU	GLU	GLU	R211	L298	L298	ILE
ALA	GLY	ASP	ALA	ALA	E549	GLY	GLY	GLY	L212	L299	L299	SER
ALA	GLY	GLY	VAL	GLY	E550	GLY	GLY	GLY	R215	L300	L300	THR
ALA	GLY	GLY	GLY	CYS	A551	GLU	GLU	GLU	E216	L301	L301	SER
ALA	VAL	SER	VAL	VAL	L552	TYR	TYR	TYR	R217	L302	L302	GLY
ALA	LYS	LEU	LYS	LYS	A553	ALA	ALA	ALA	L218	L303	L303	PHE
ALA	LYS	LYS	PHE	ALA	E554	VAL	VAL	VAL	R219	L304	L304	GLY
ALA	GLY	GLY	ASN	VAL	E555	GLU	GLU	GLU	L219	L305	L305	PRO
ALA	GLY	GLY	VAL	VAL	E556	LEU	LEU	LEU	L220	L306	L306	PRO
ALA	ILE	ALA	ILE	ASP	E557	GLU	GLU	GLU	F225	L307	L307	ASP
ALA	ARG	LYS	ARG	GLU	X557	ALA	ALA	ALA	ALA	L308	L308	VAL

Chain 0J:

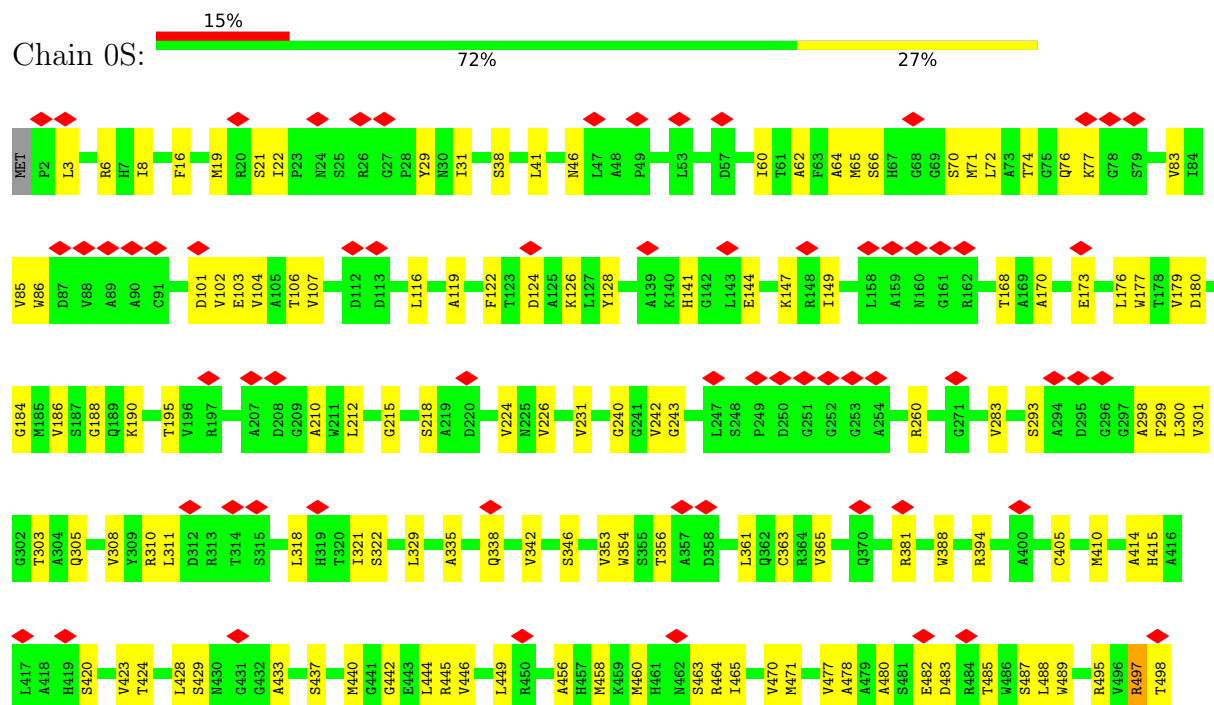


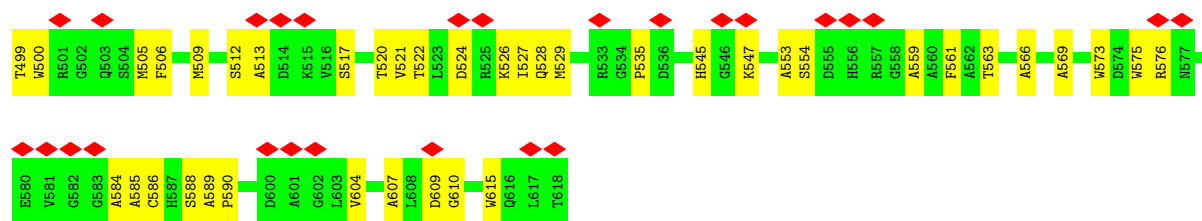
MET	VAL	GLY	GLY	PRO	SER	GLU	PRO	ALA	ALA	PRO	PRO	LYS	LYS	LEU	LEU	ASP	GLY	VAL	GLY	GLU	PHE	GLN	GLU	ARG	LEU	ALA	ALA	THR	LEU	PRO	PRO	PRO	PRO	LYS	ASN	ASN	VAL	PHE	ASN	ILE	SER	ASP	THR	SER	GLU	PHE	PRO	PRO	PRO	ASP	ALA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 7: FAP196

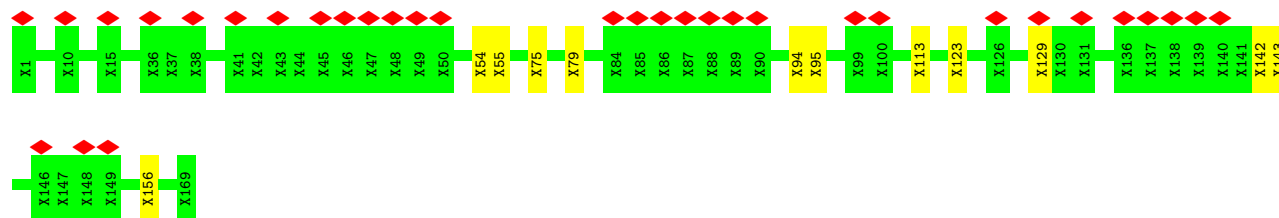


- Molecule 7: FAP196

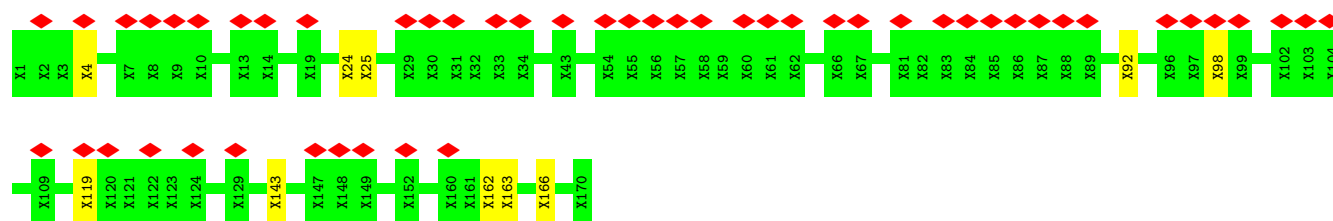




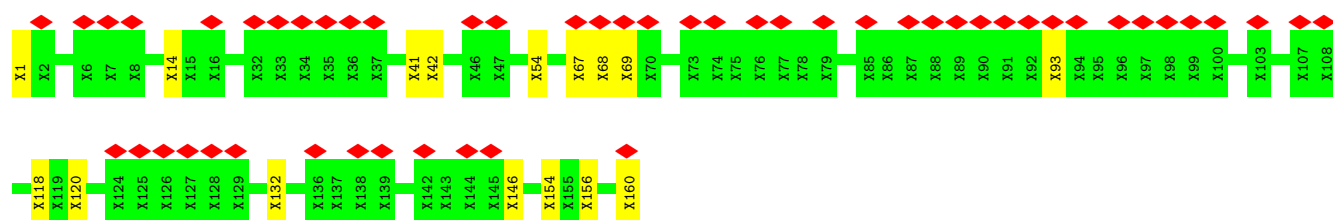
• Molecule 8: Unassigned protein-1



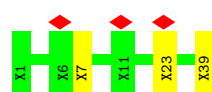
• Molecule 9: Unassigned protein-2



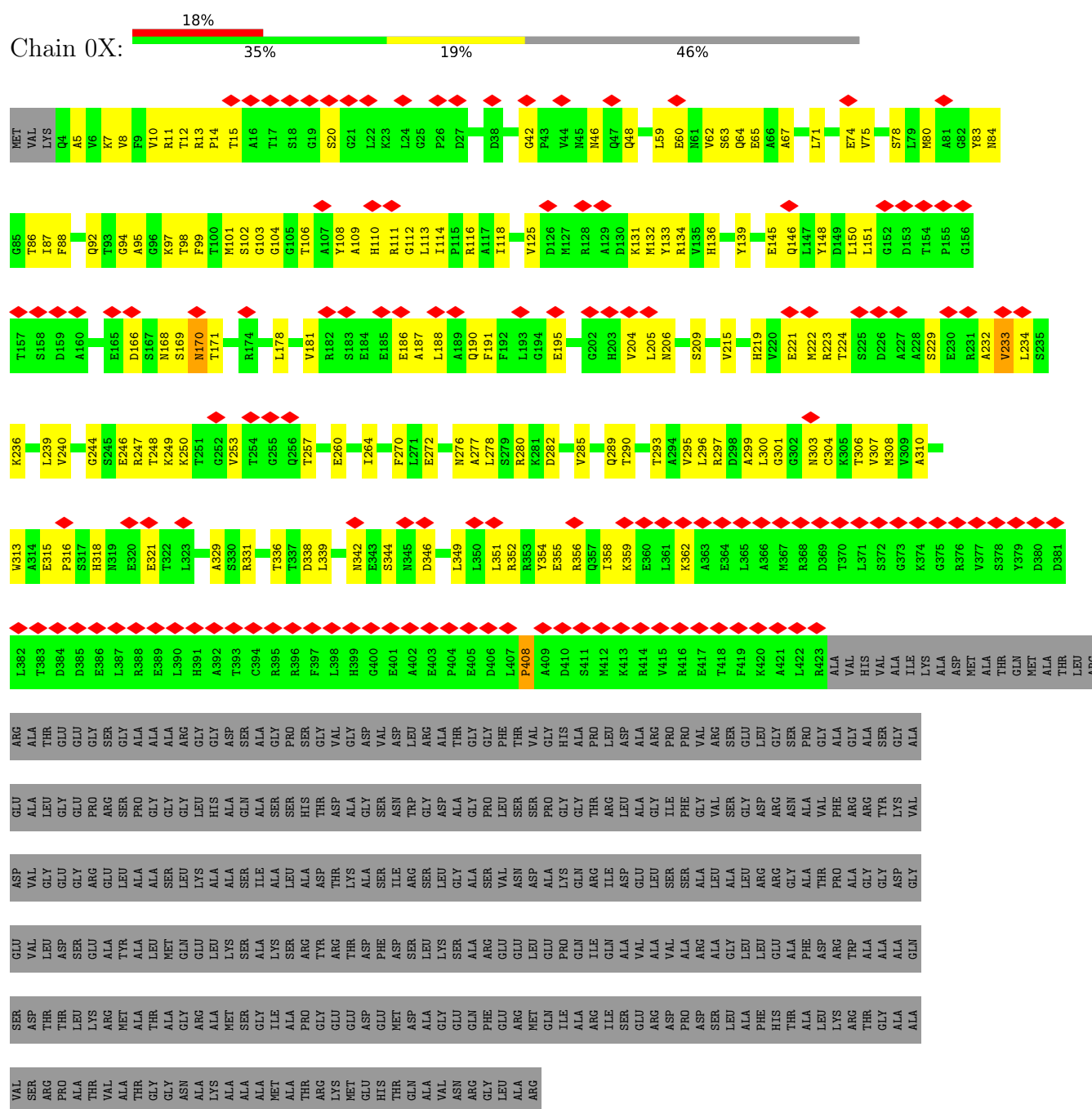
• Molecule 10: Unassigned protein-3



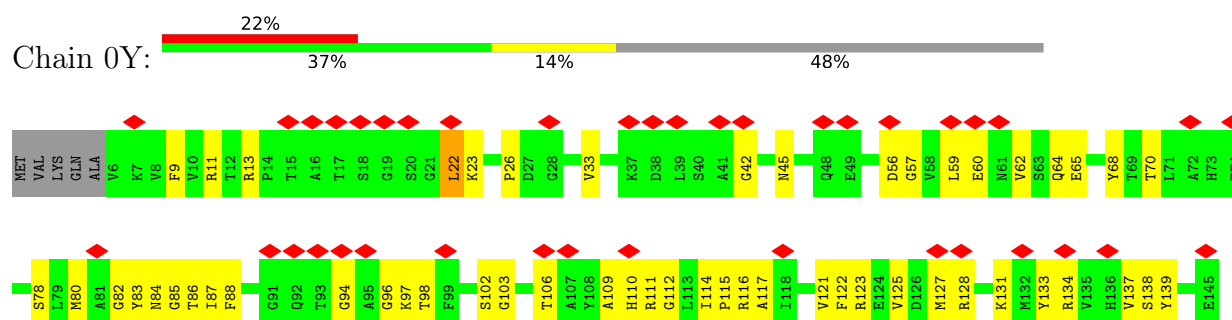
• Molecule 11: Unassigned protein-4

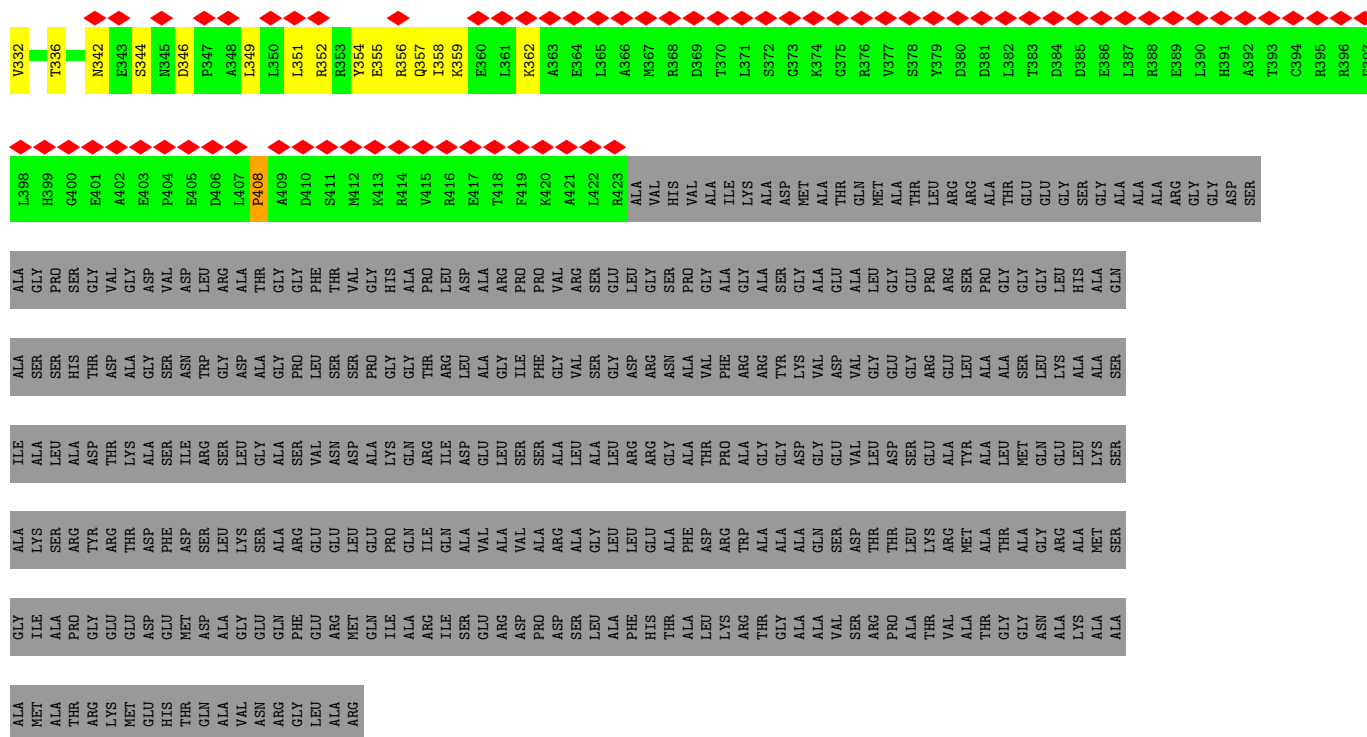


• Molecule 12: Kinesin-like protein

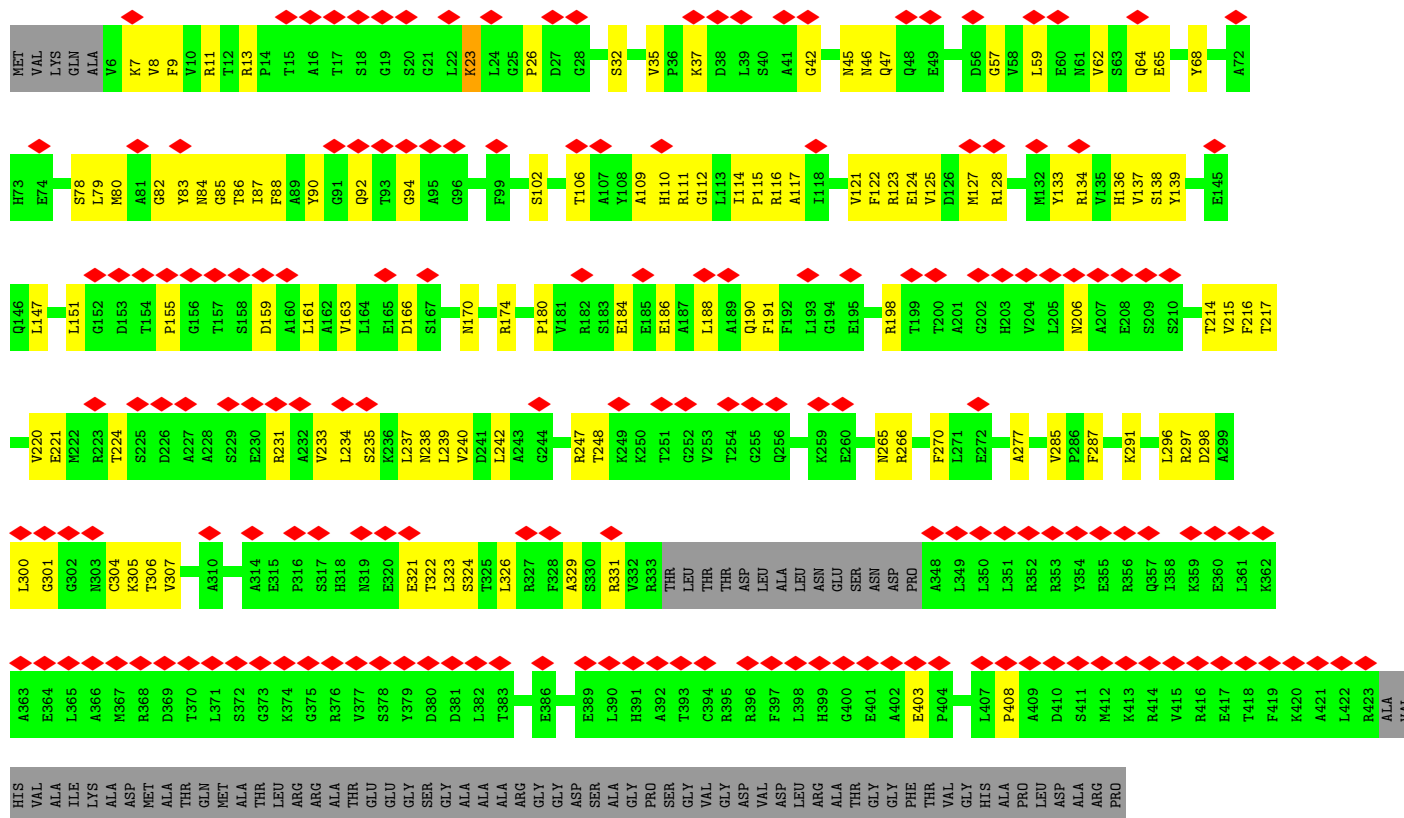
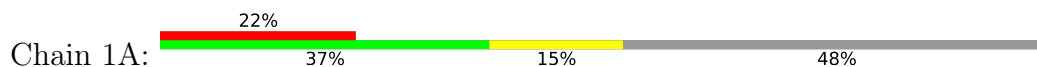


- Molecule 12: Kinesin-like protein





• Molecule 12: Kinesin-like protein



- Molecule 13: FAP65

[illegible]



- Molecule 13: FAP65

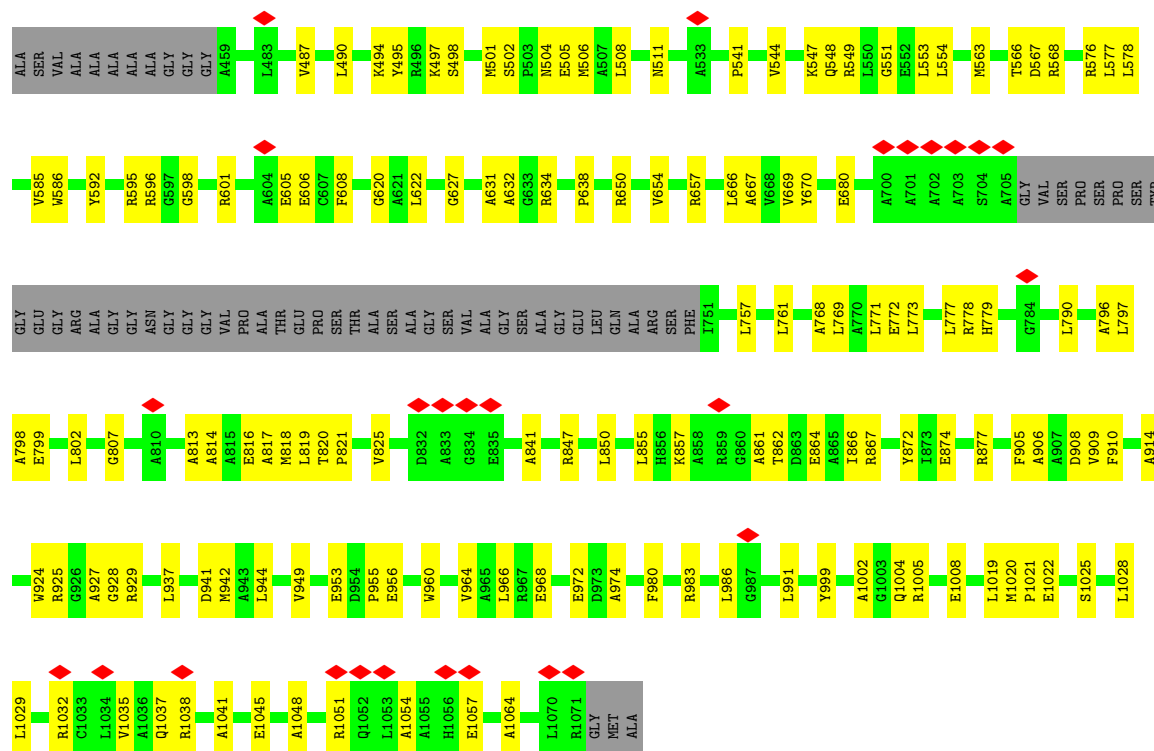
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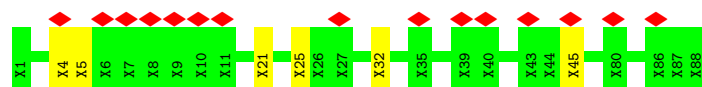


Frequency	Percentage
Daily	45%
Weekly	12%
Monthly	43%

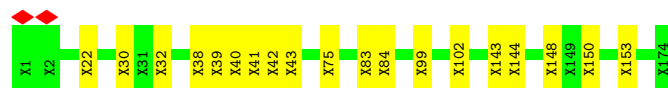




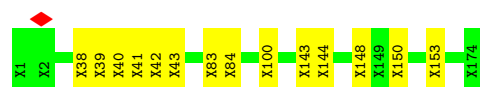
• Molecule 15: Unassigned protein-5



• Molecule 16: Unassigned protein-6

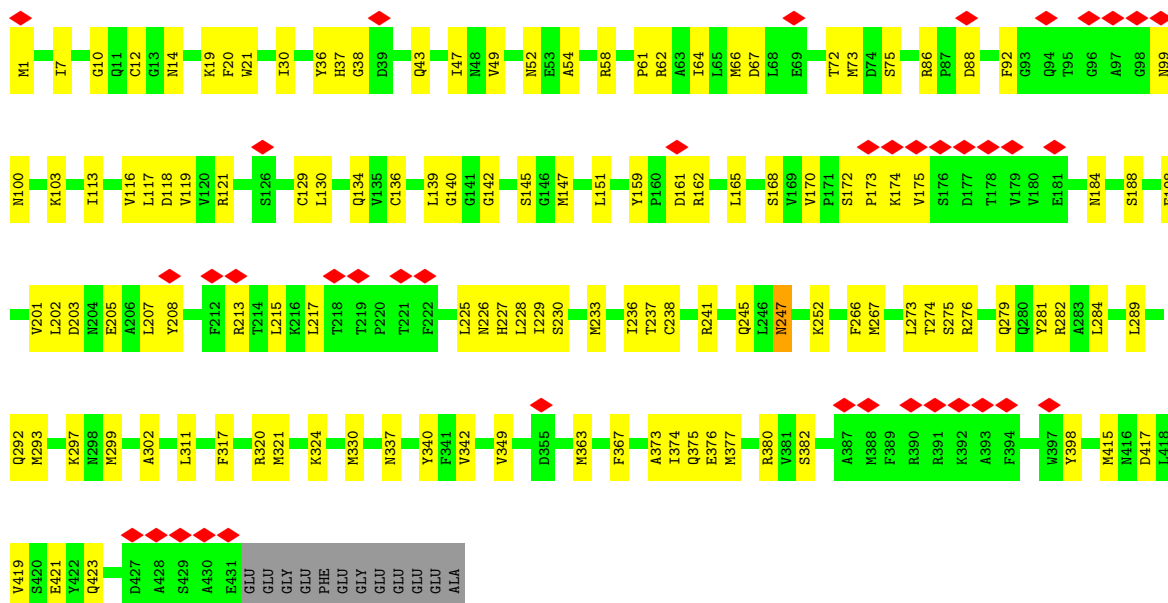


• Molecule 16: Unassigned protein-6

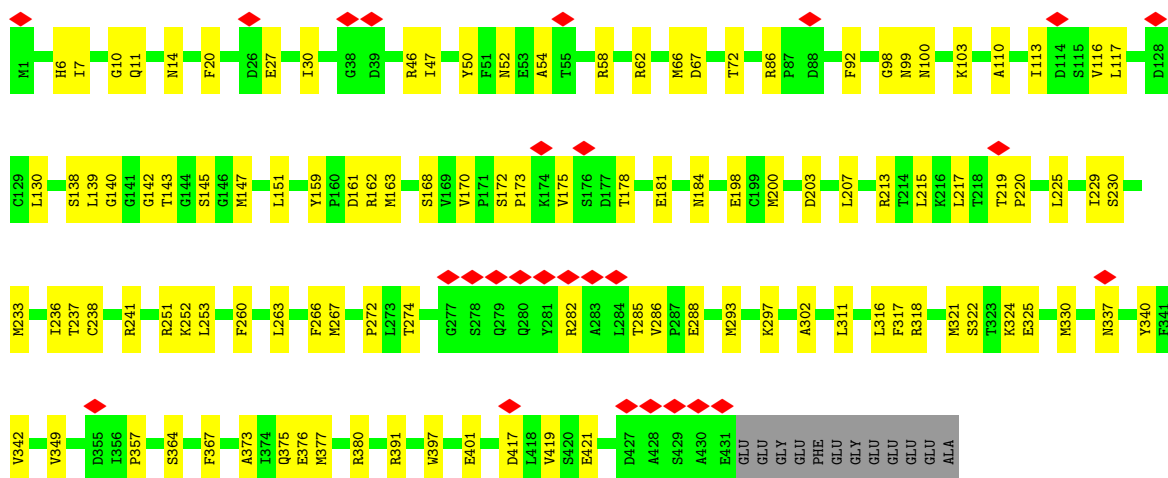
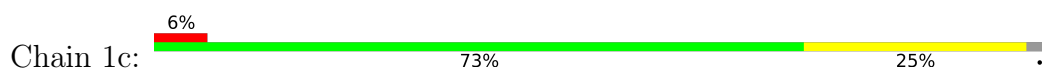


• Molecule 17: Tubulin beta





• Molecule 17: Tubulin beta

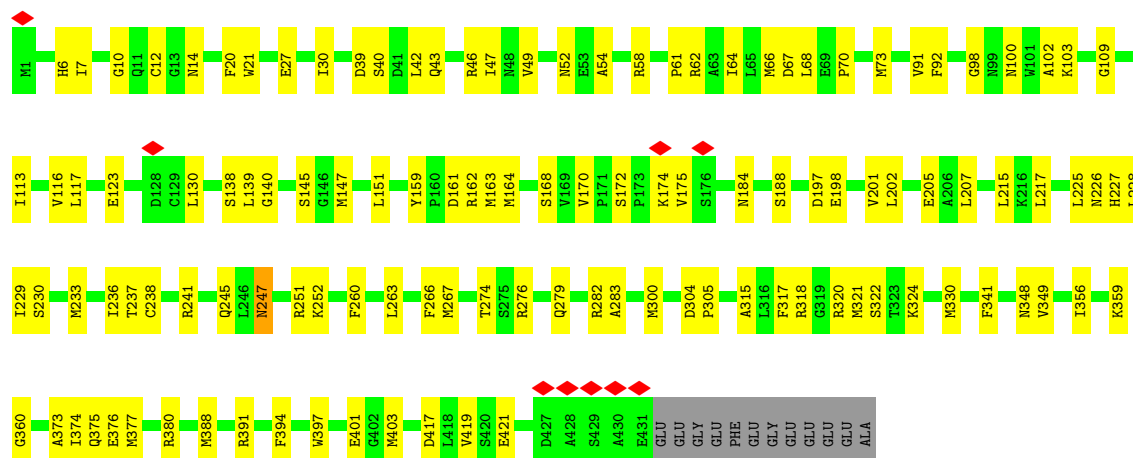


• Molecule 17: Tubulin beta

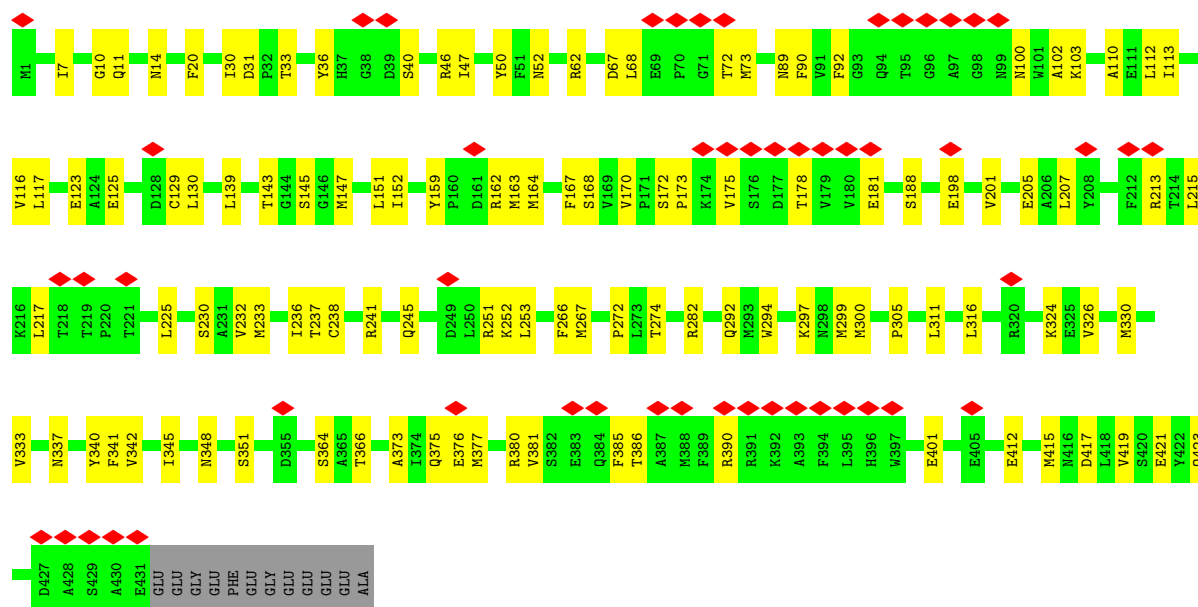
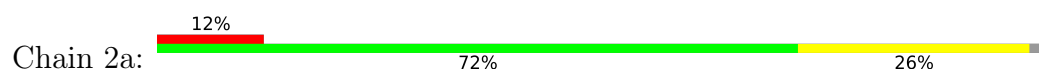




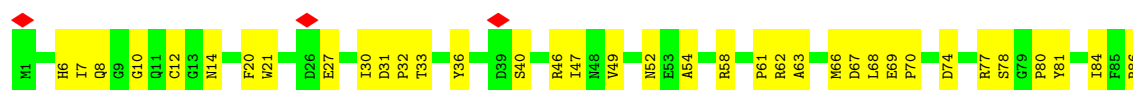
• Molecule 17: Tubulin beta

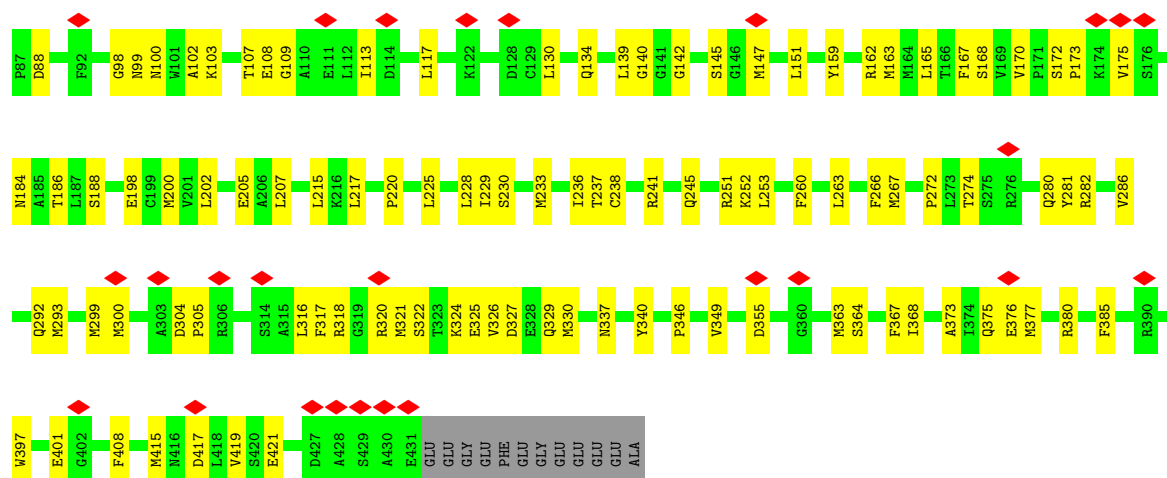


• Molecule 17: Tubulin beta

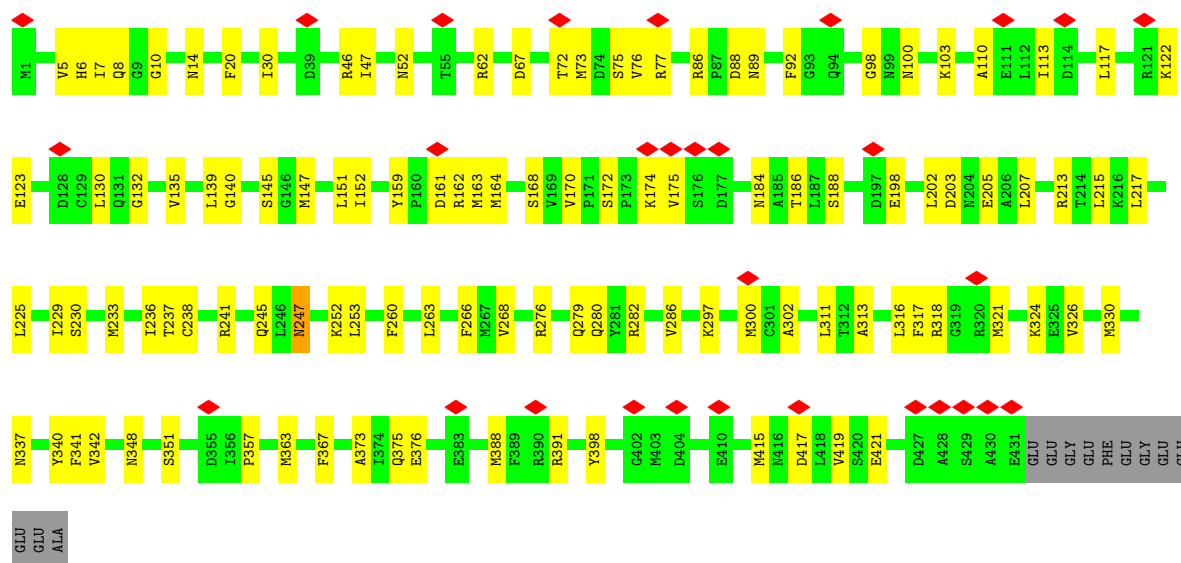
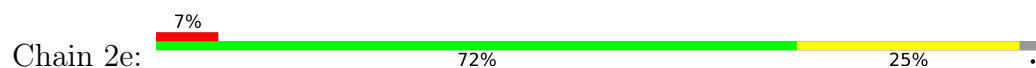


• Molecule 17: Tubulin beta

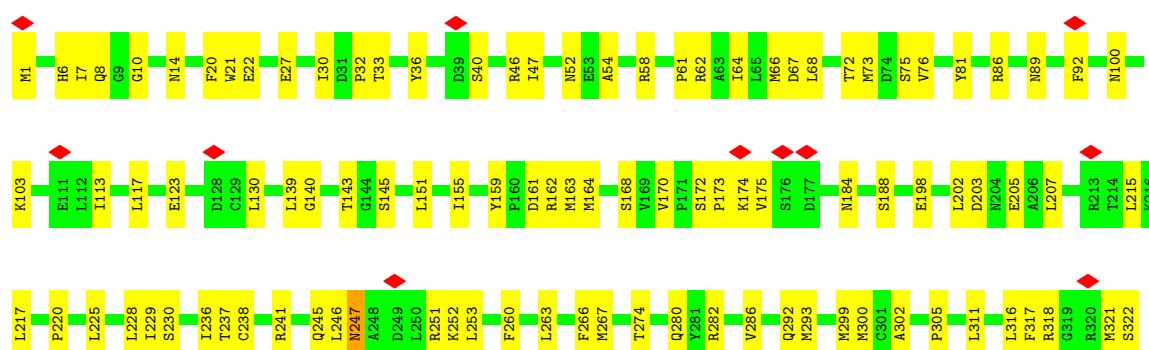


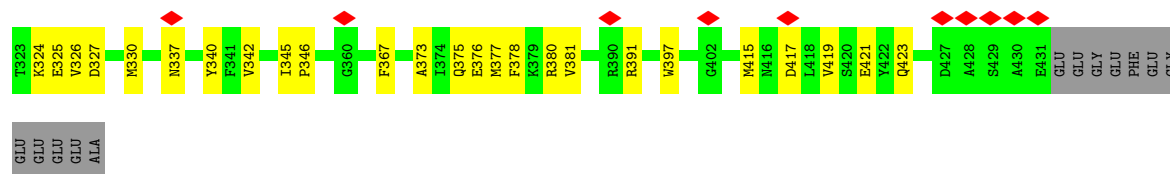


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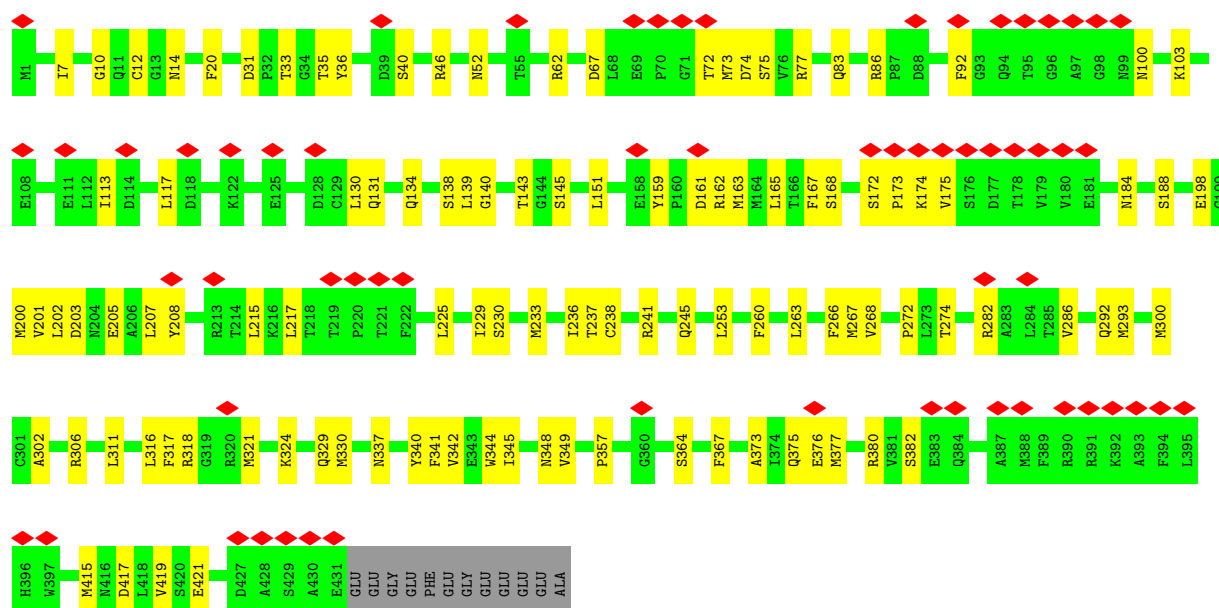
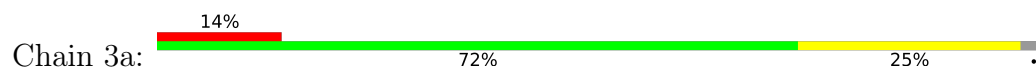


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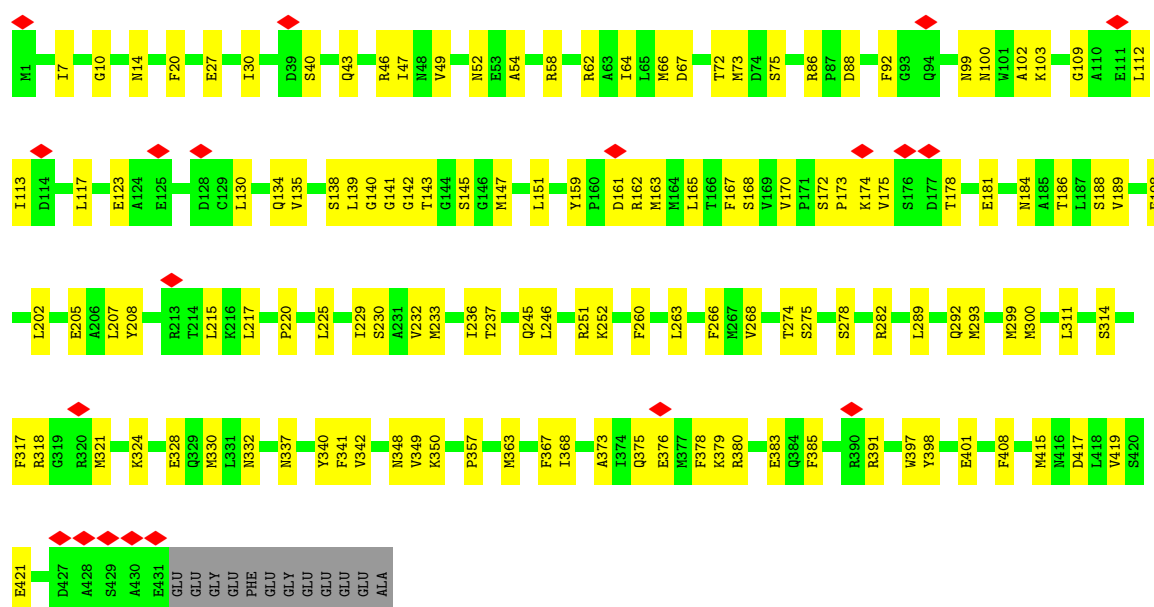




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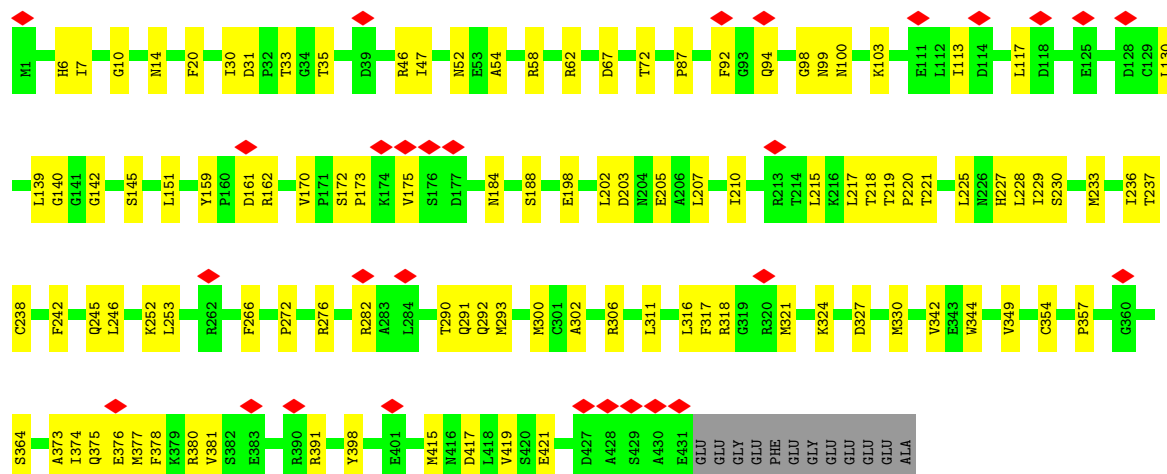


• Molecule 17: Tubulin beta



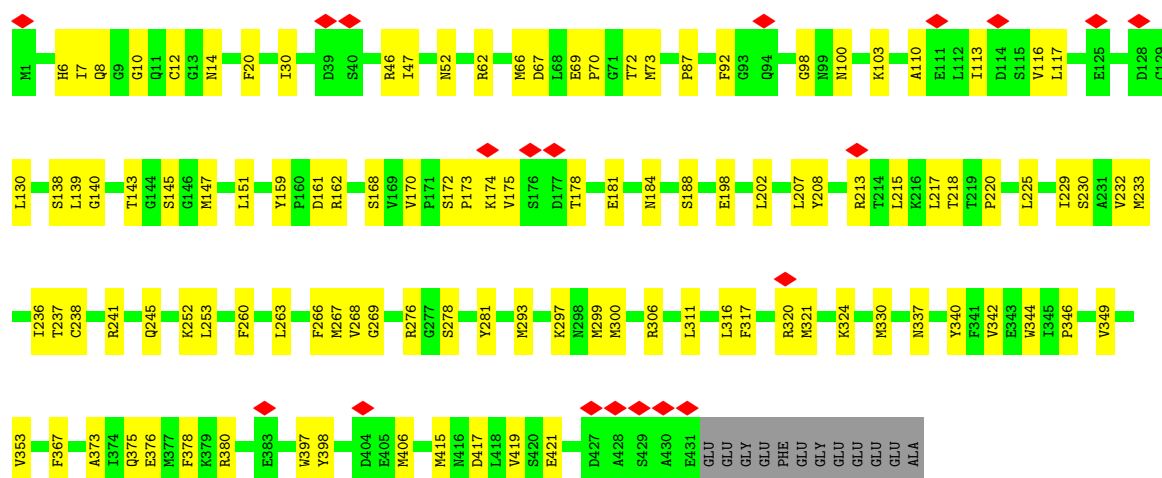
• Molecule 17: Tubulin beta

Chain 3e: 



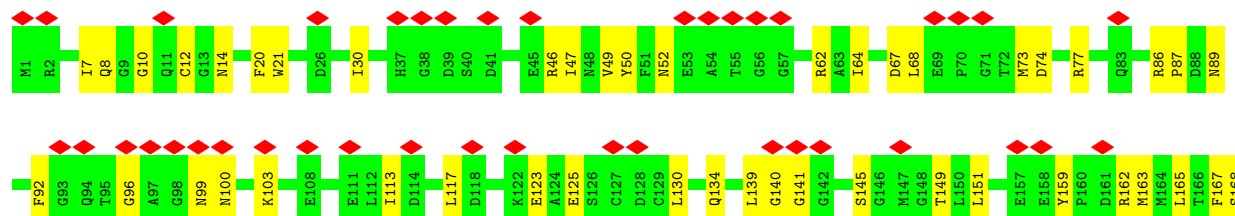
• Molecule 17: Tubulin beta

Chain 3g: 



• Molecule 17: Tubulin beta

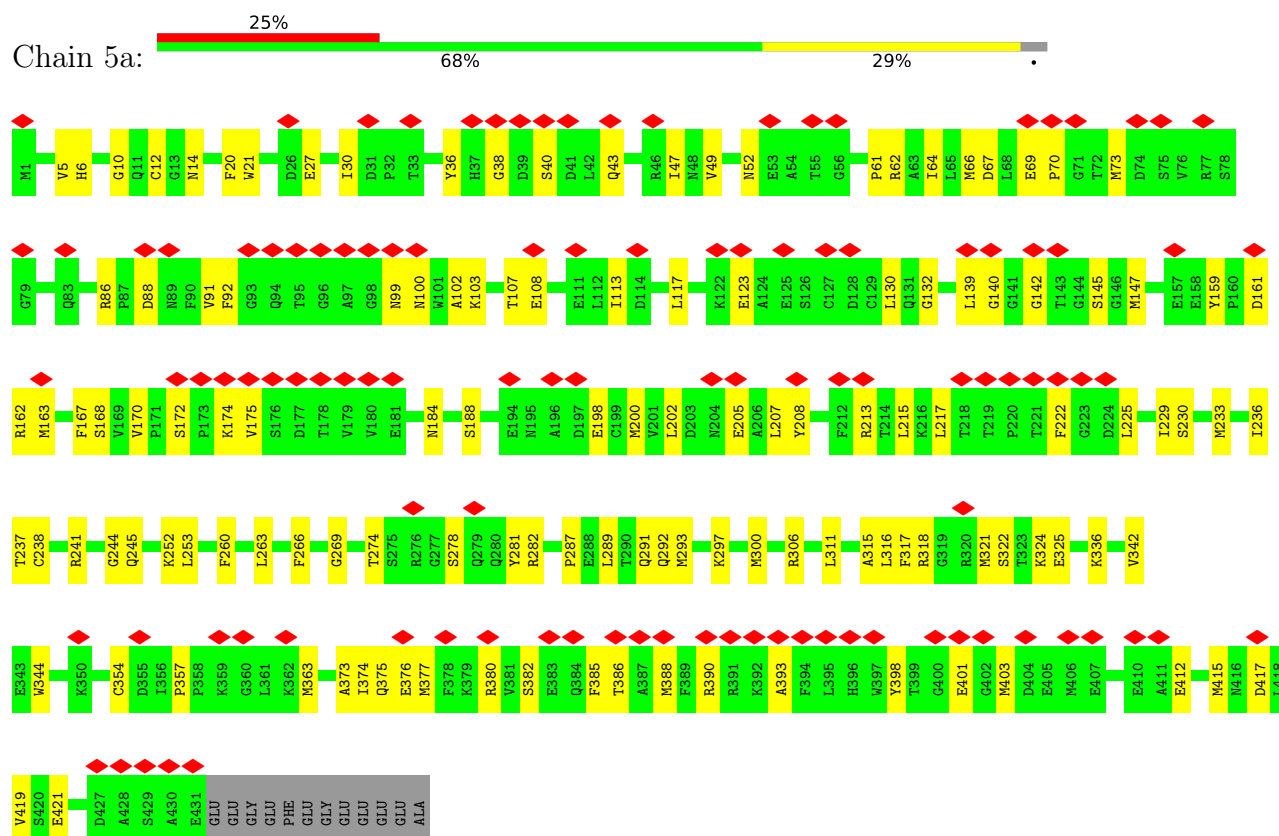
Chain 4a: 



- Molecule 17: Tubulin beta

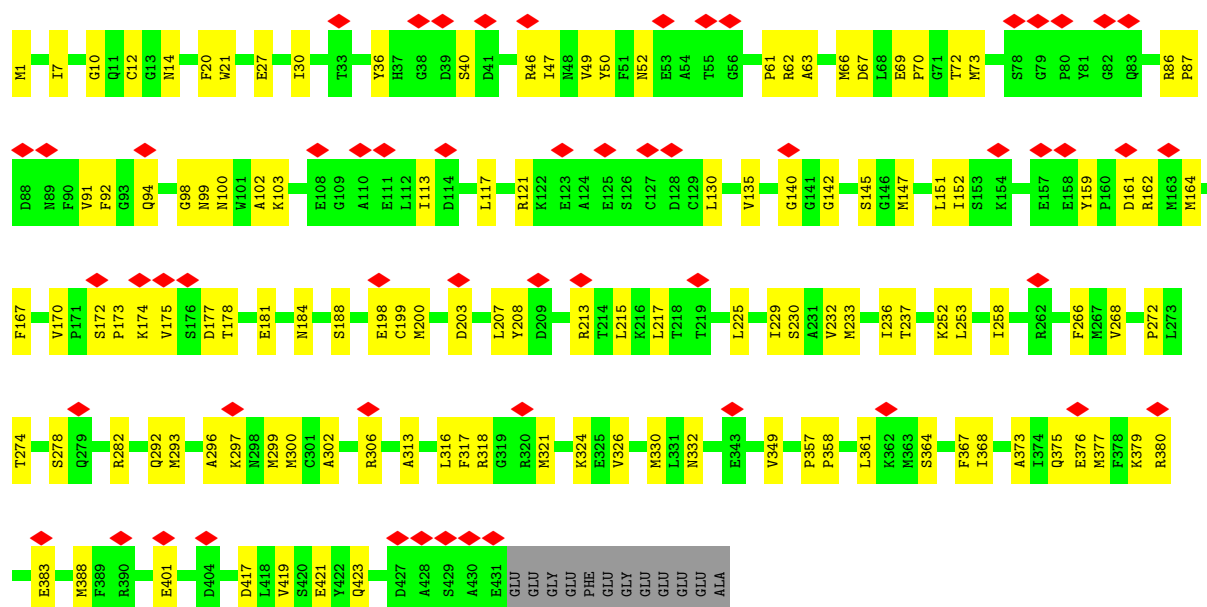


- Molecule 17: Tubulin beta



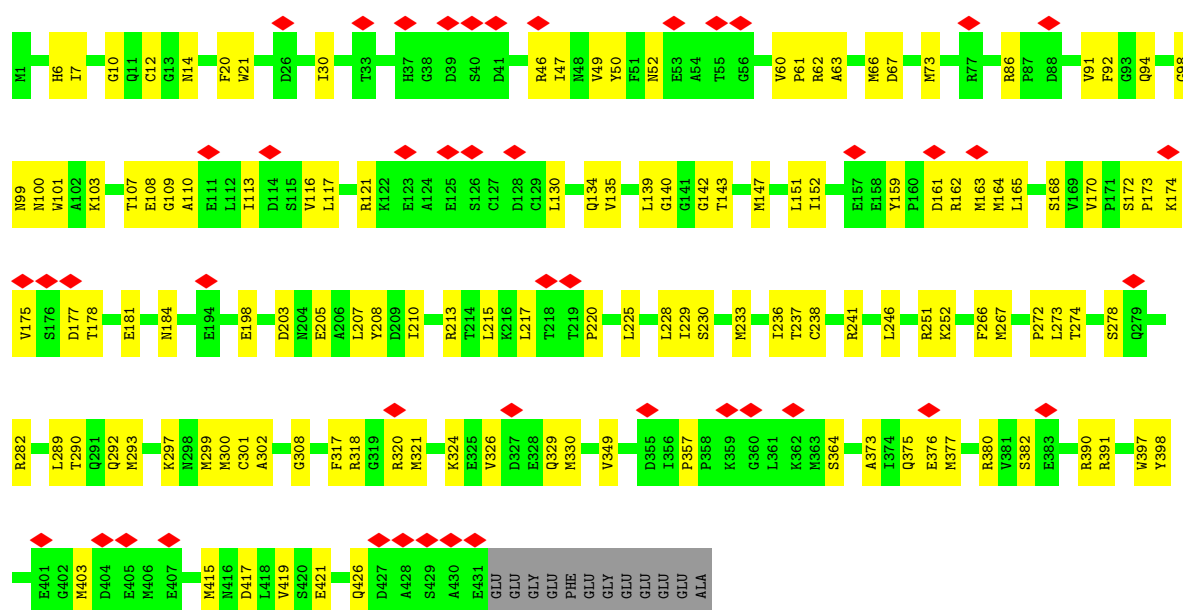
- Molecule 17: Tubulin beta

Chain 5c: 



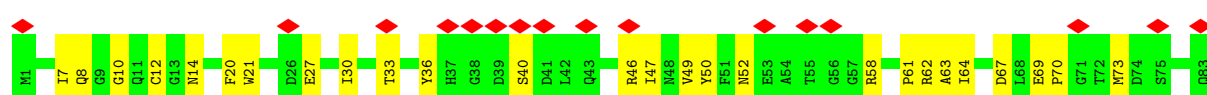
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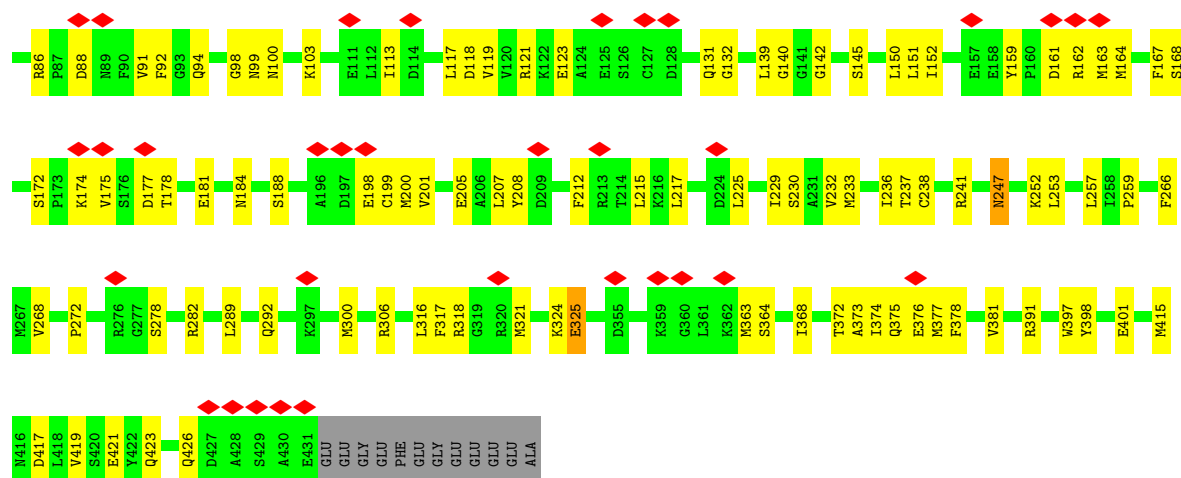
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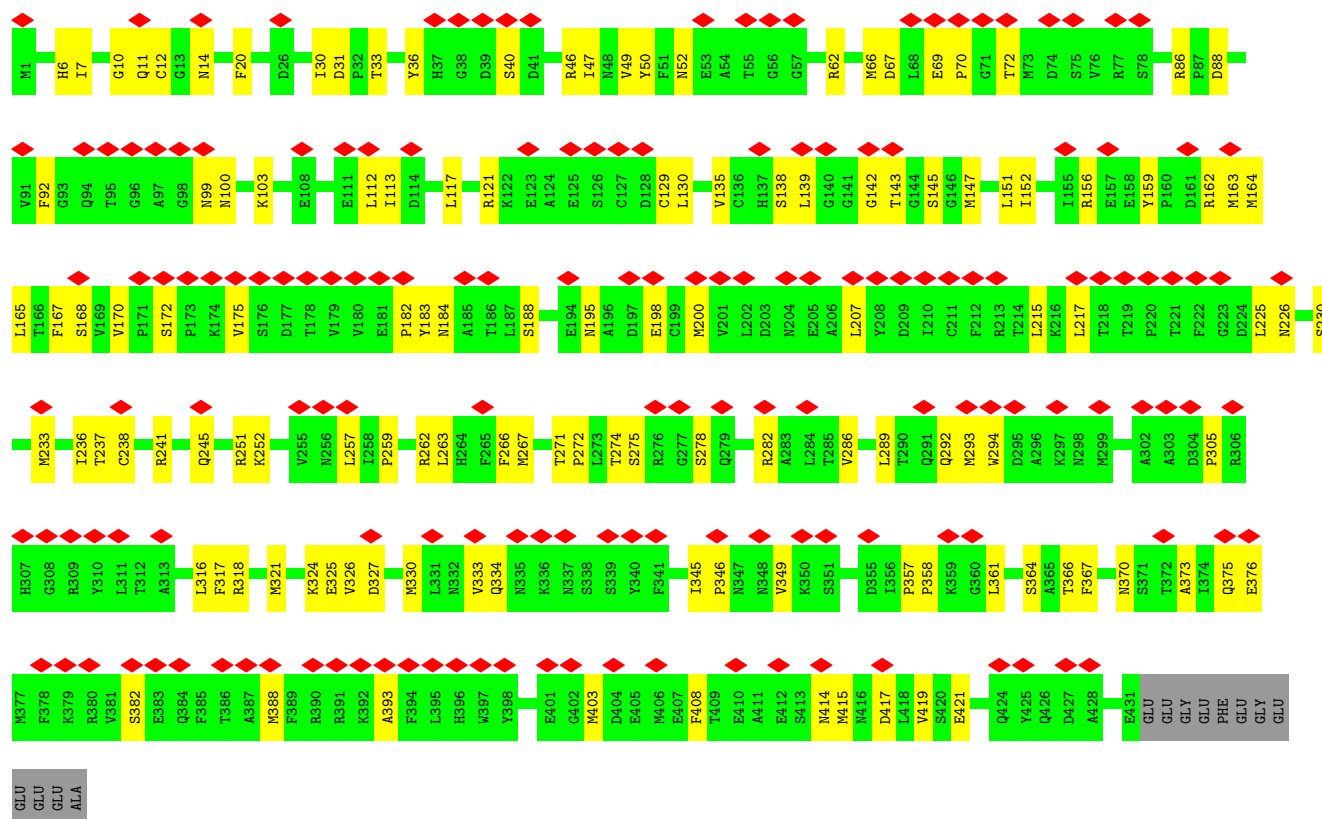
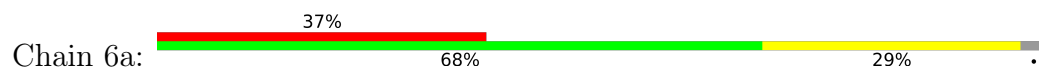
• Molecule 17: Tubulin beta

Chain 5g: 

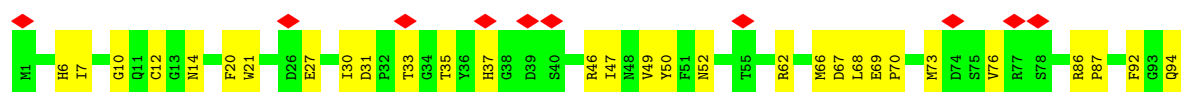


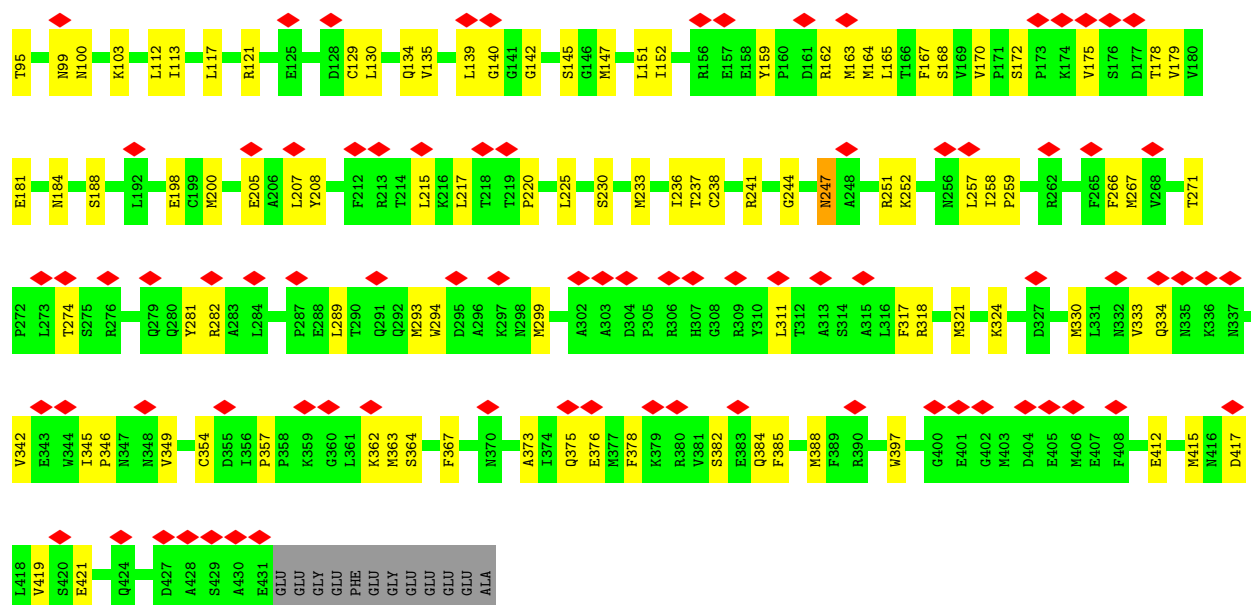


• Molecule 17: Tubulin beta

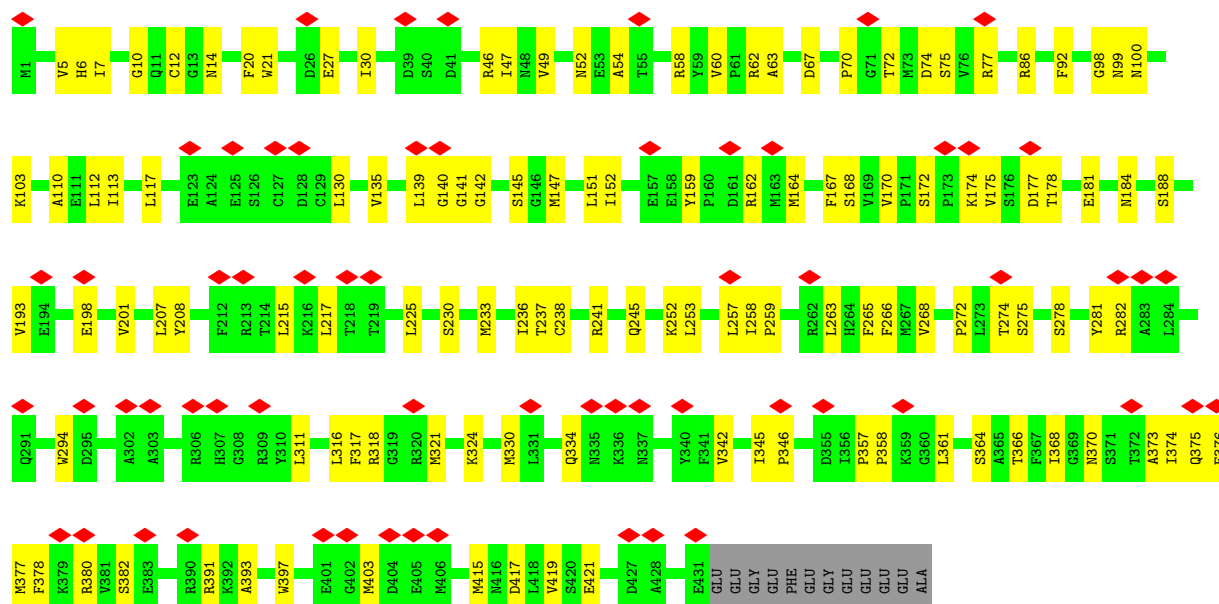


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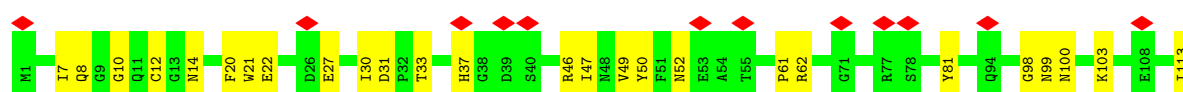


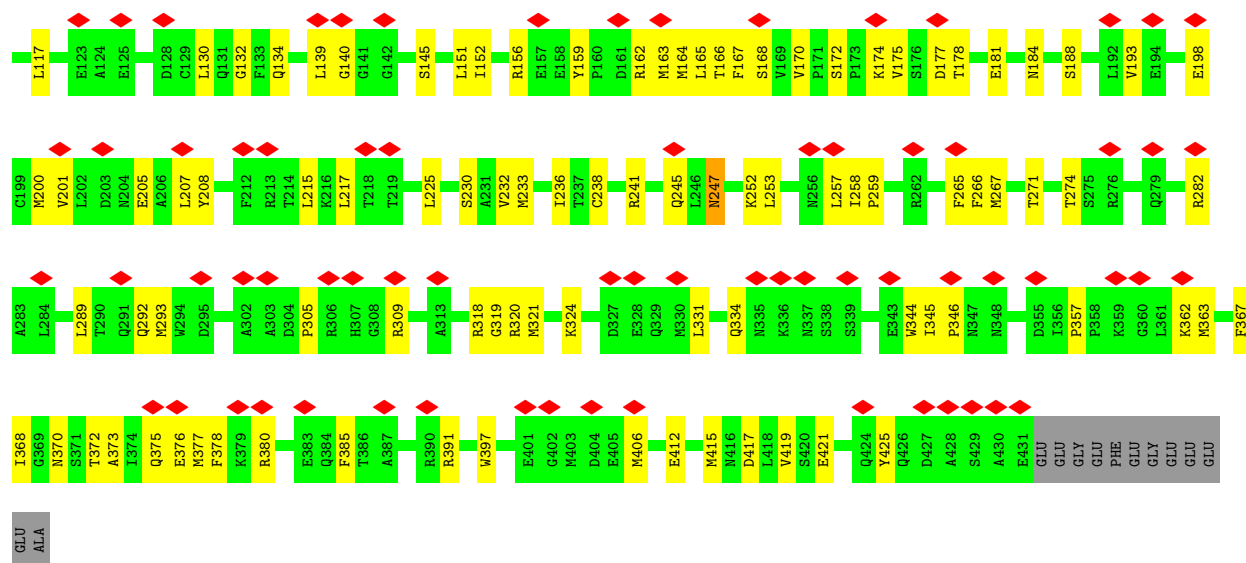


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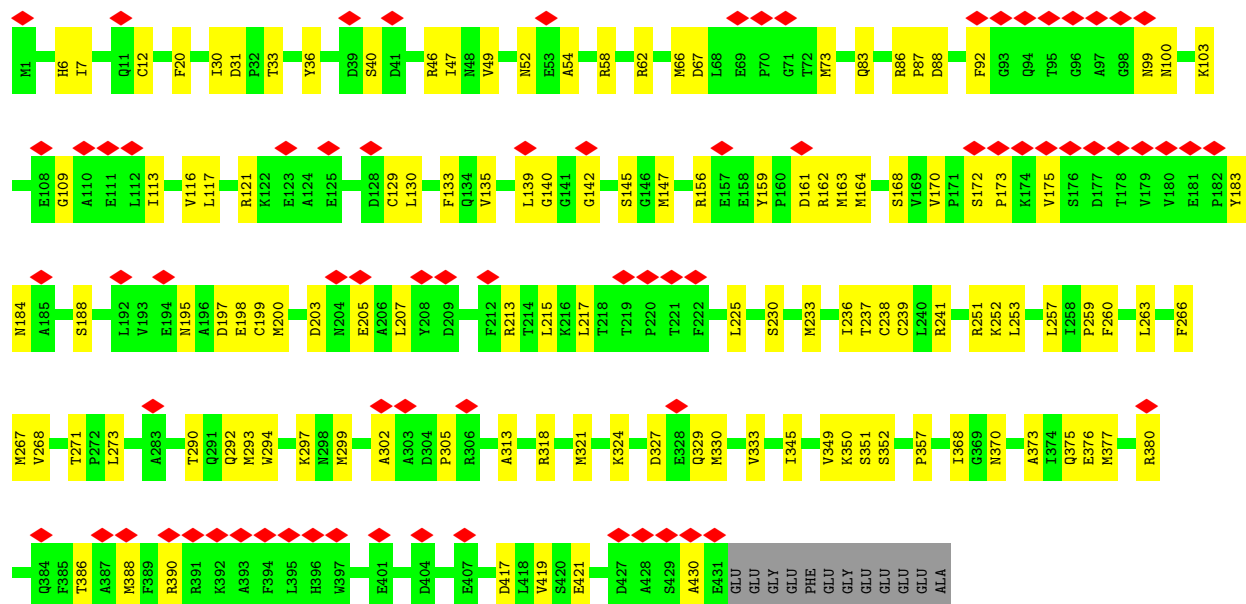


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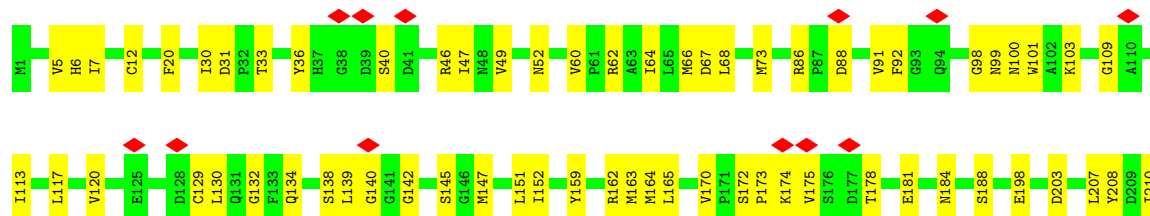


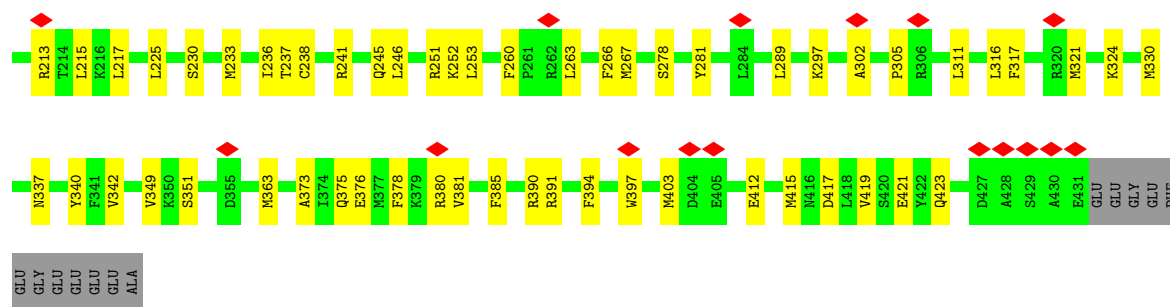


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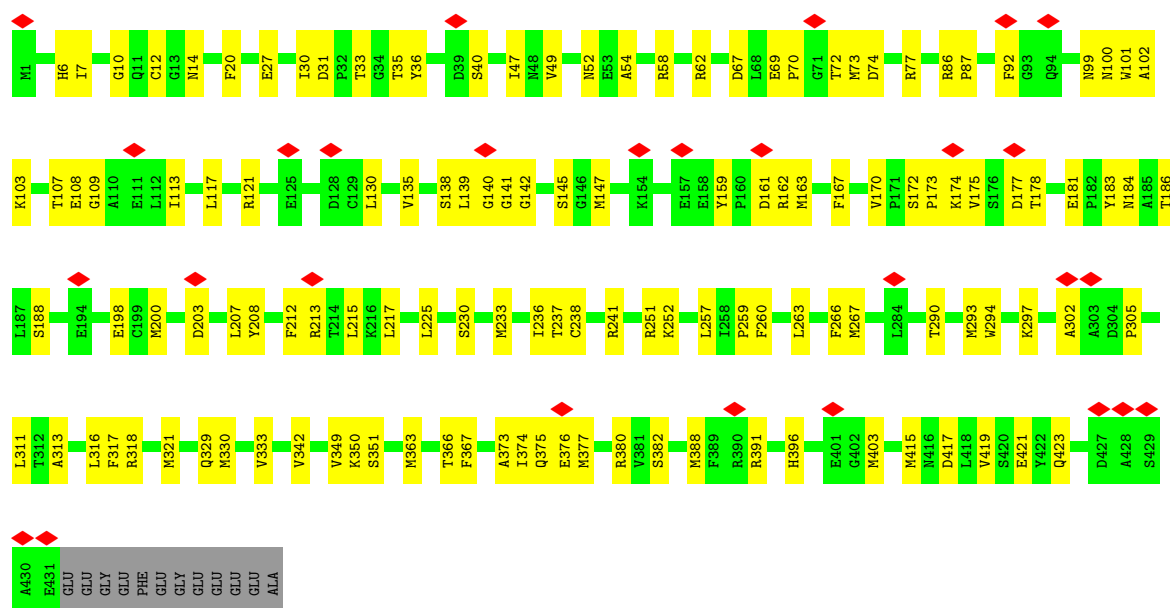


• Molecule 17: Tubulin beta

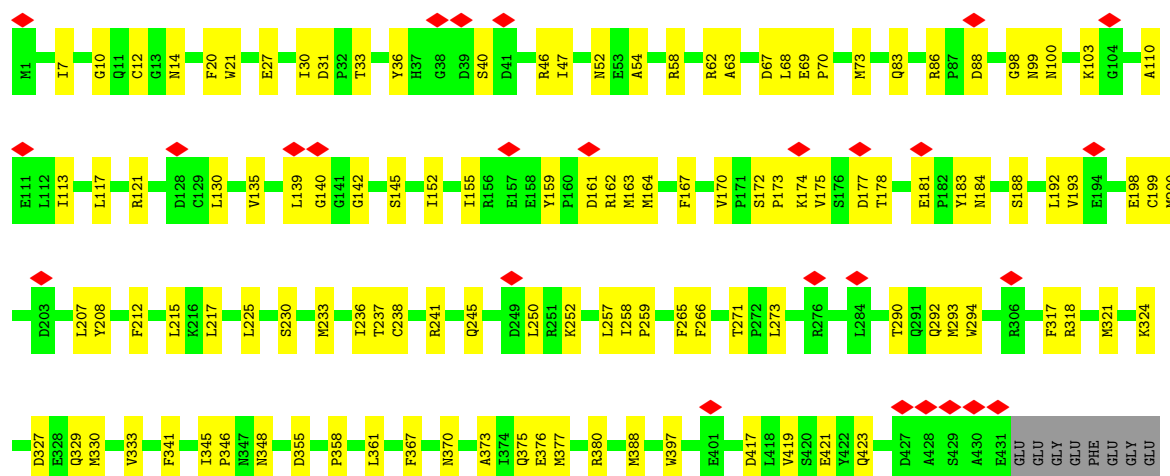




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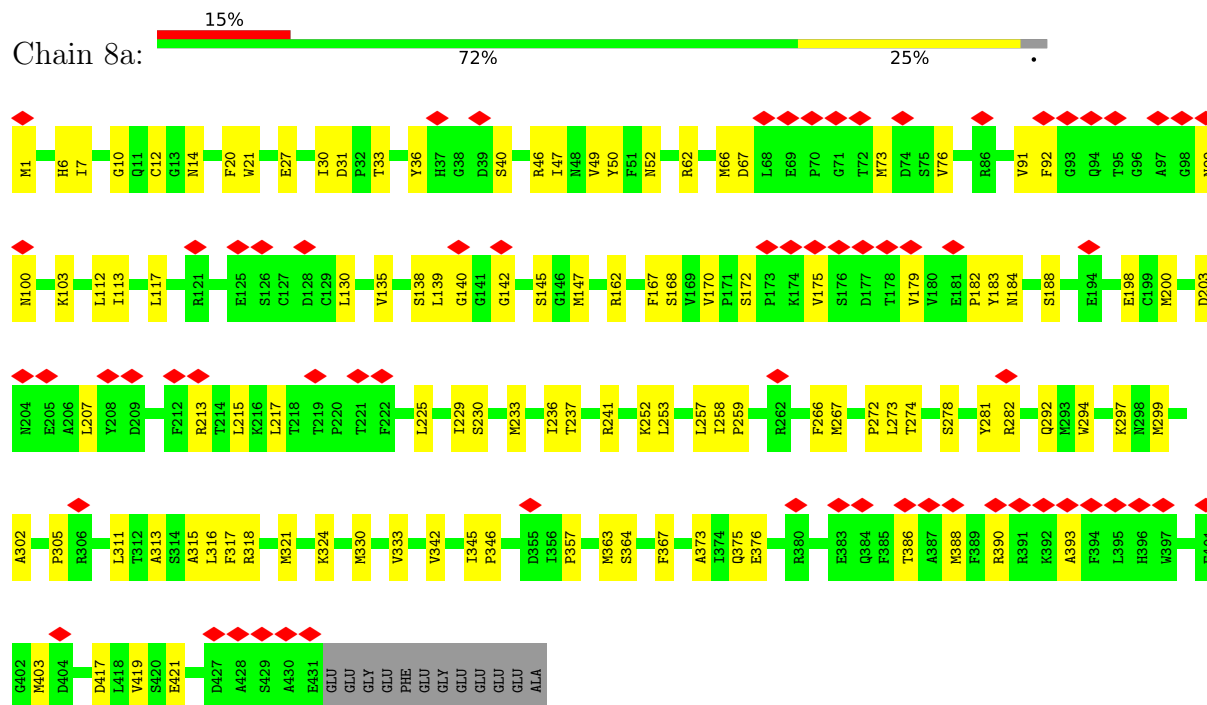


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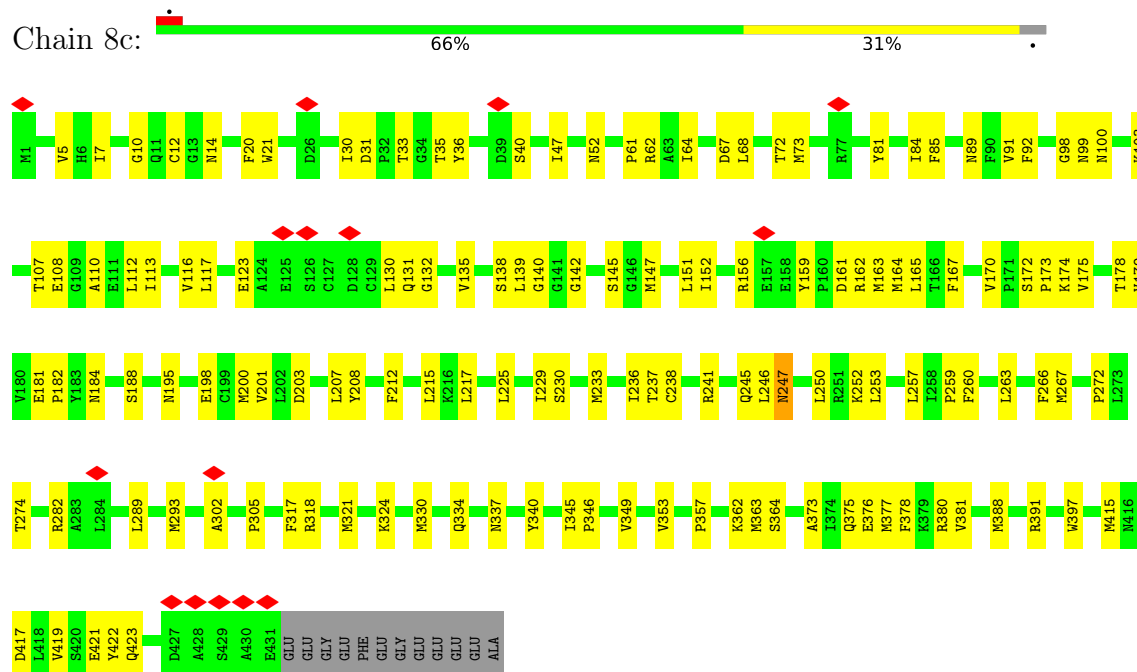


GLU
GLU
GLU
ALA

• Molecule 17: Tubulin beta

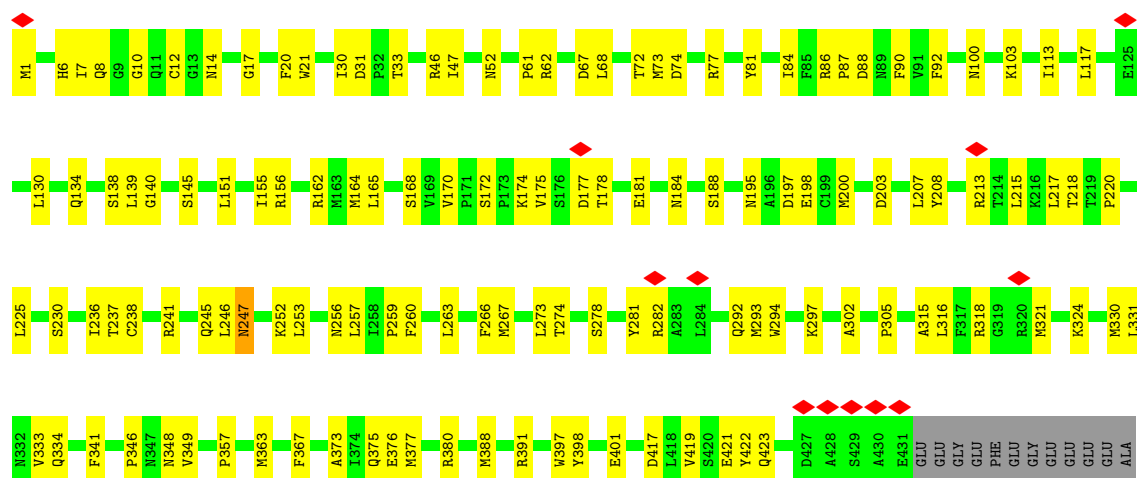


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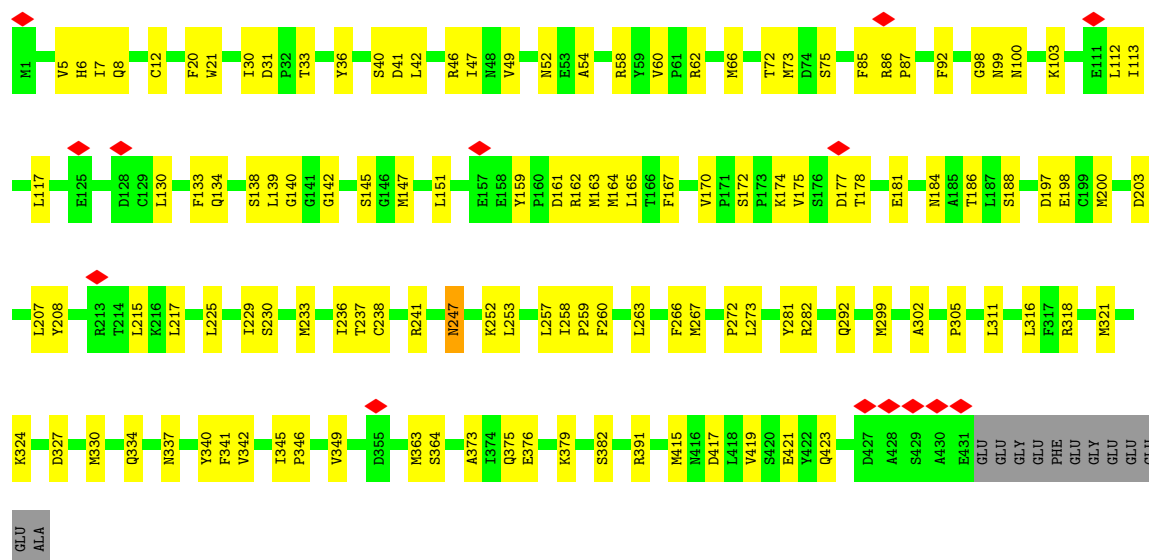


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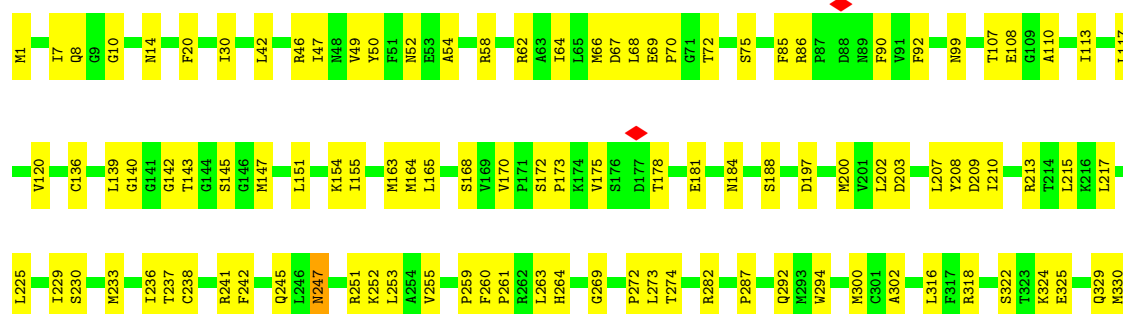


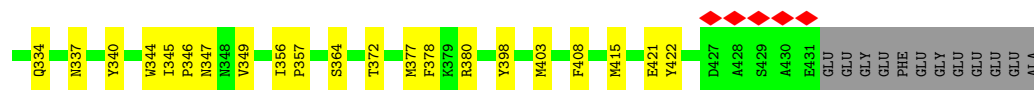


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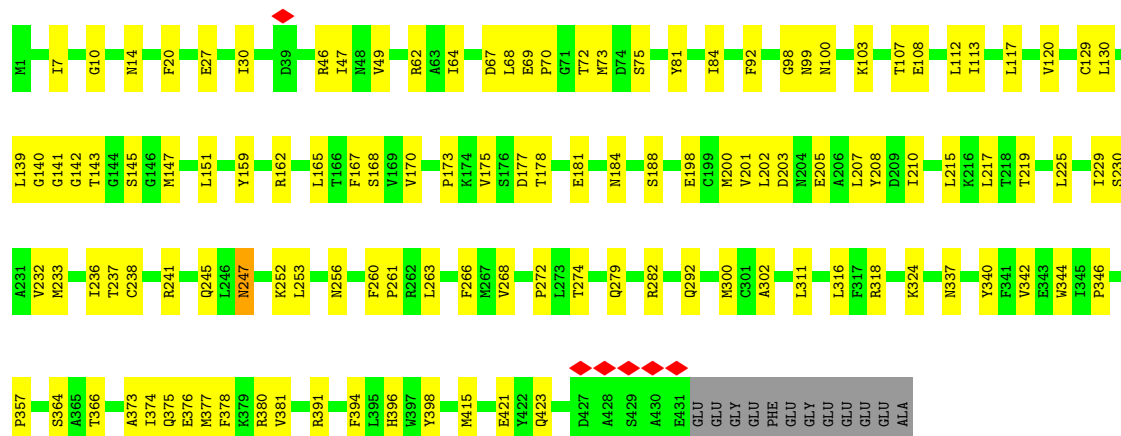


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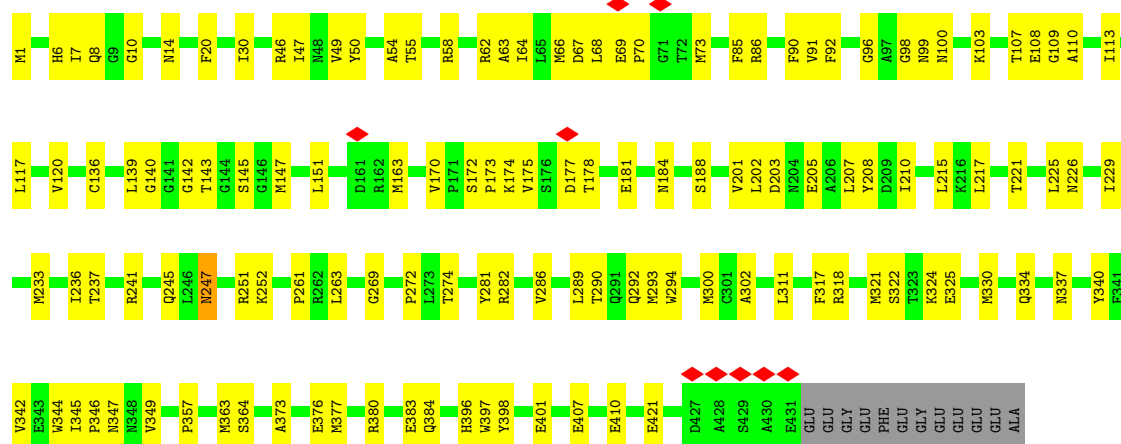




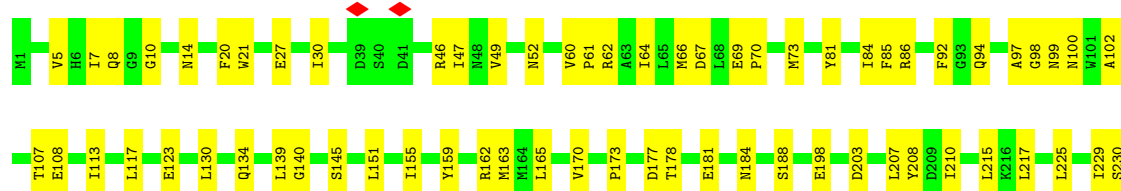
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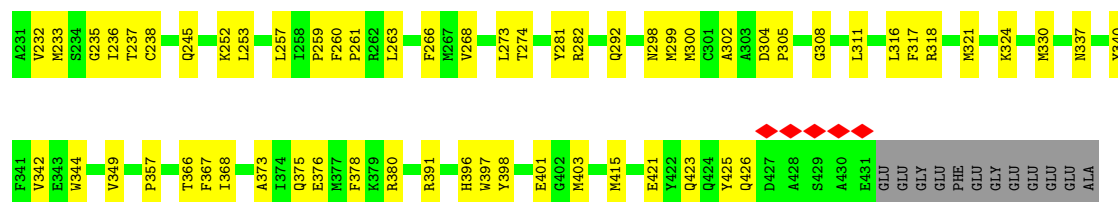


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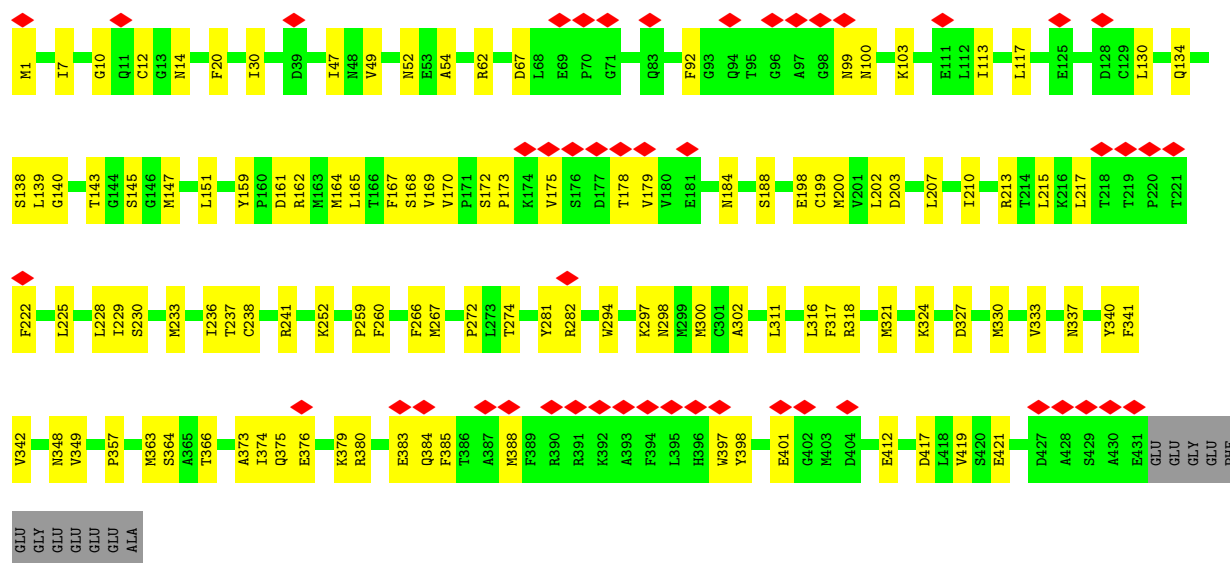
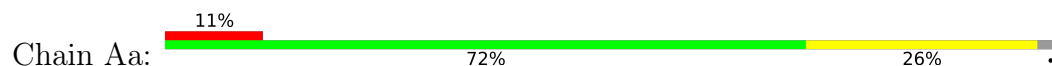


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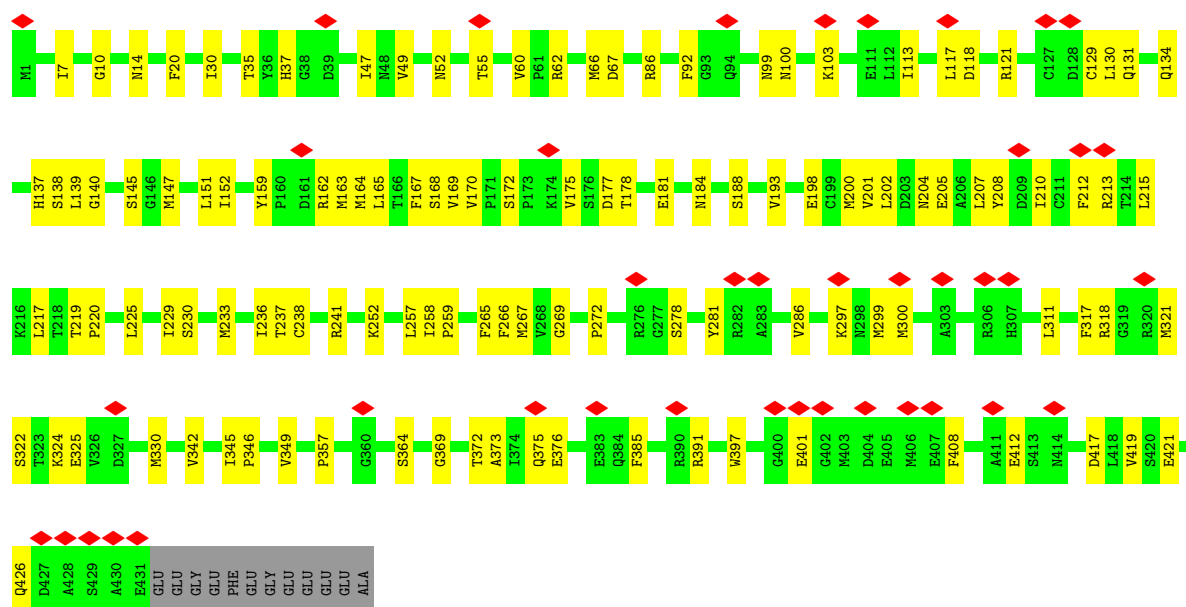




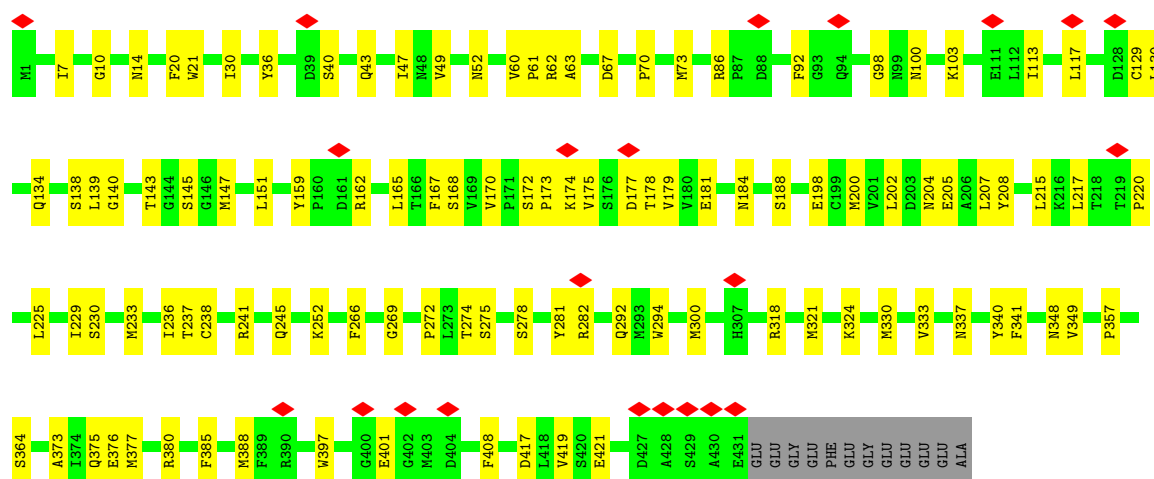
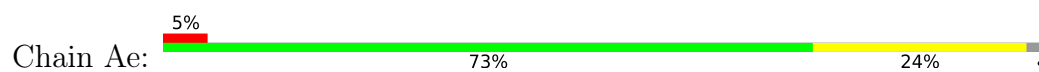
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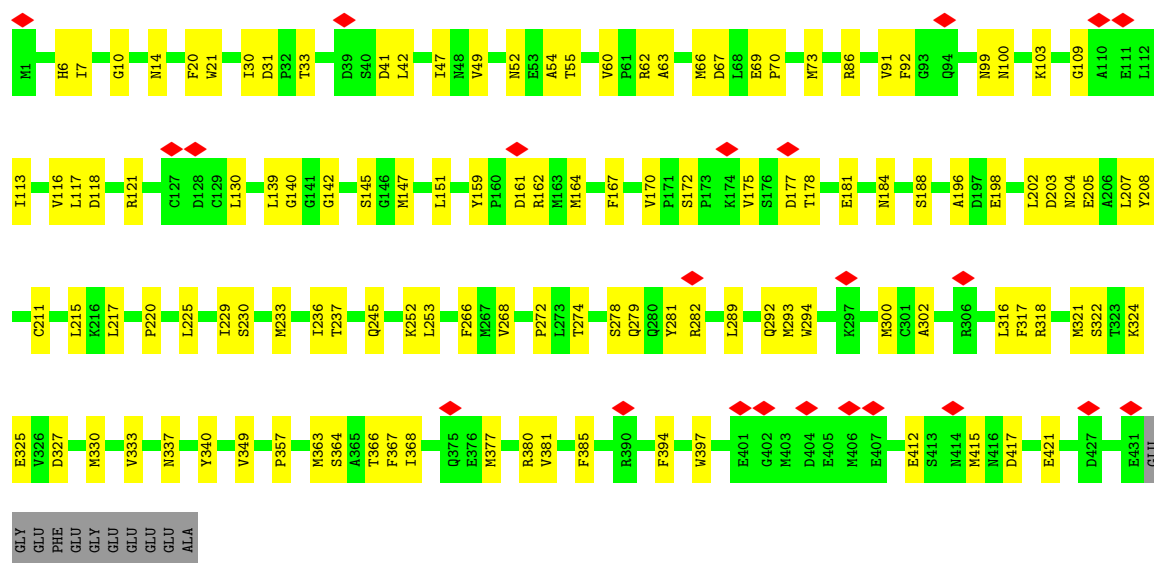
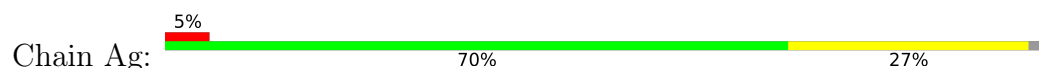
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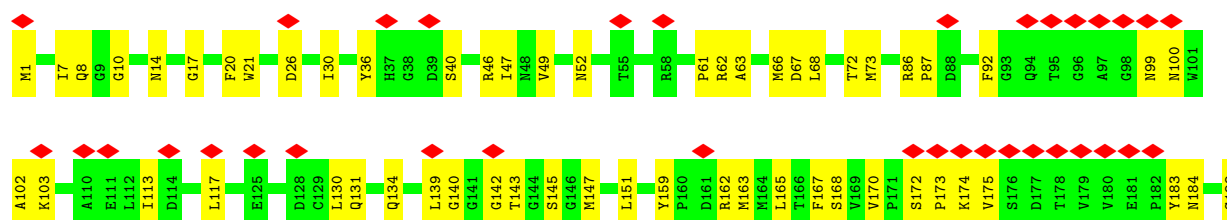
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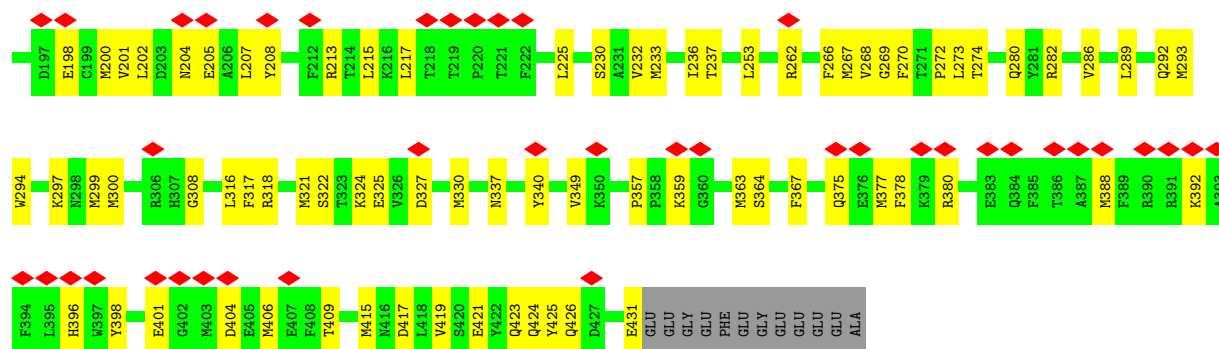


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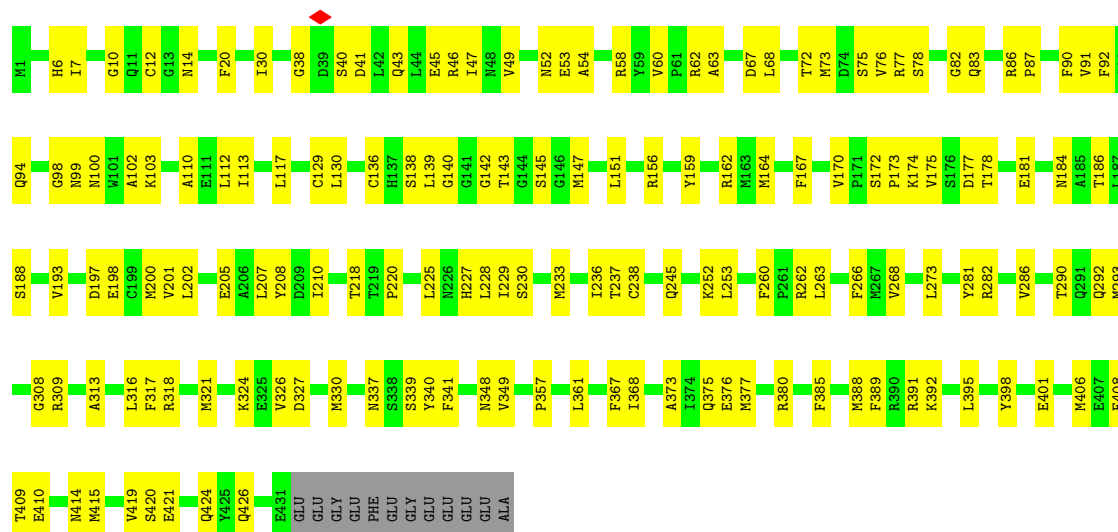


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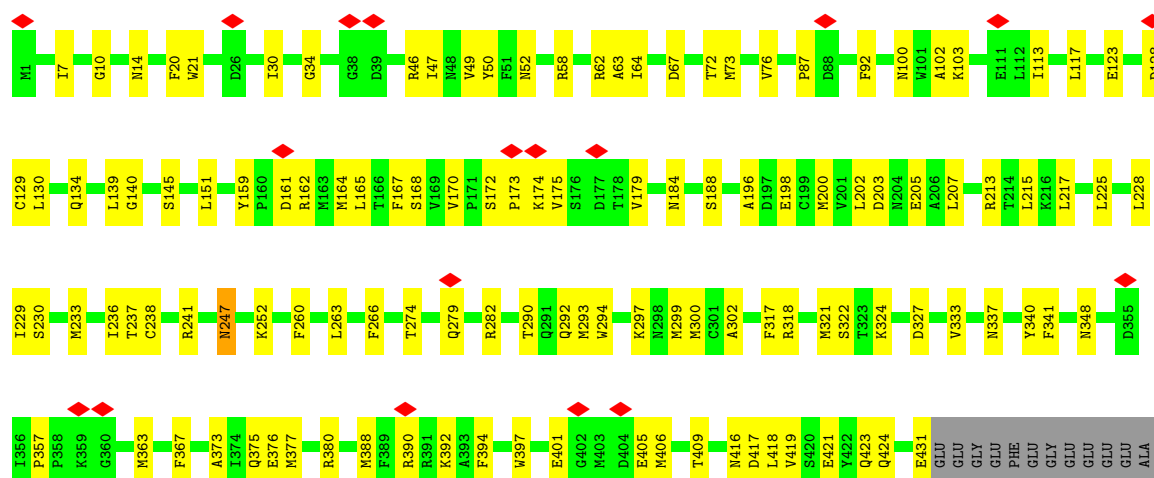




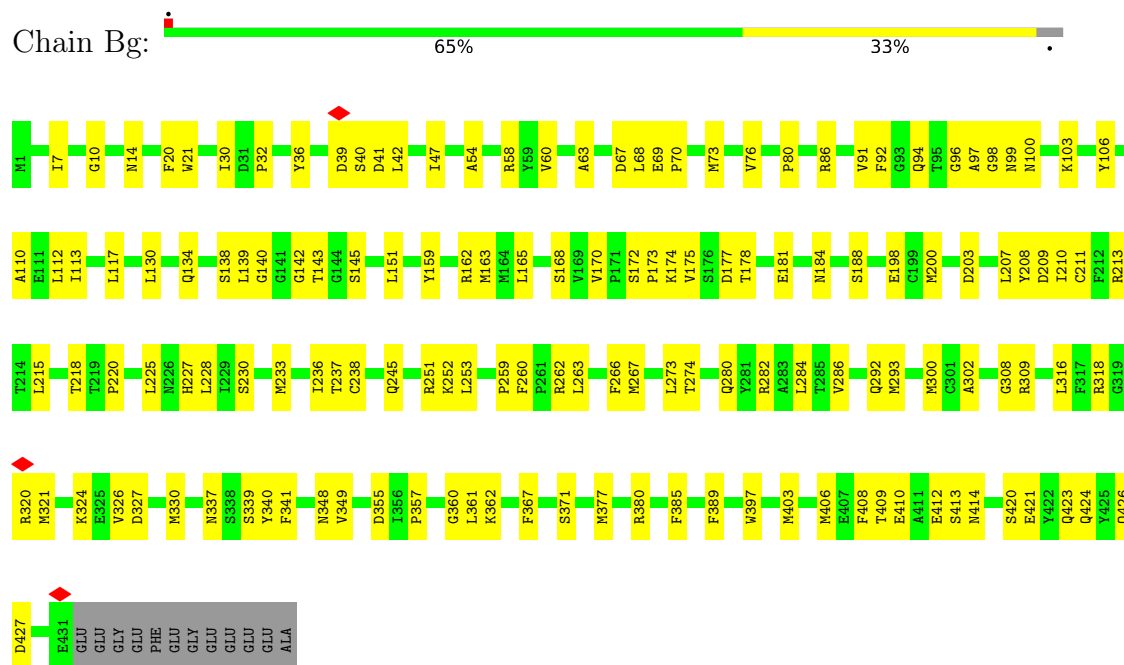
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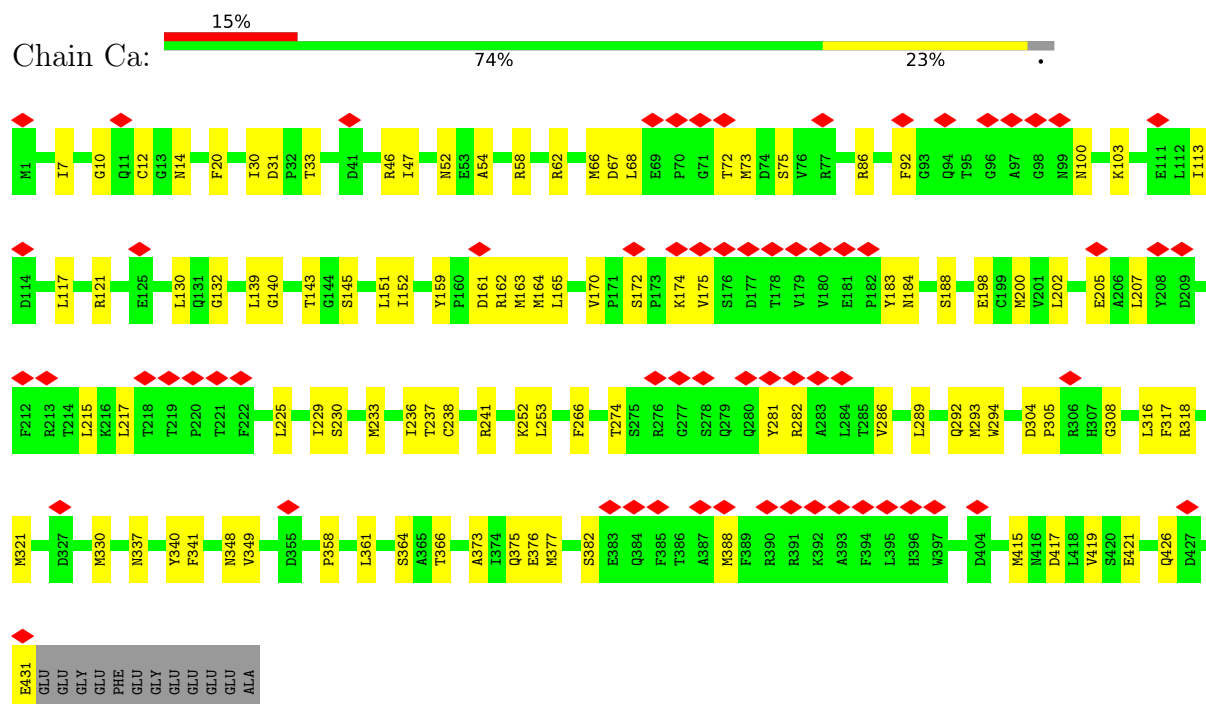
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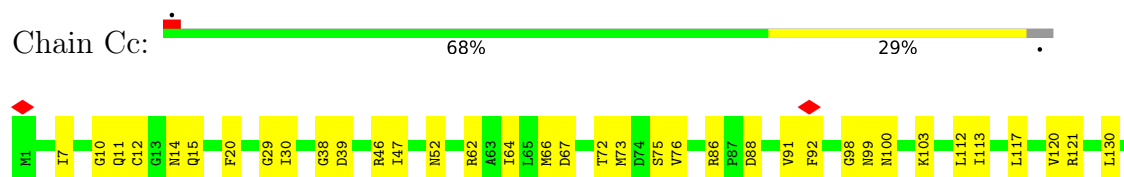
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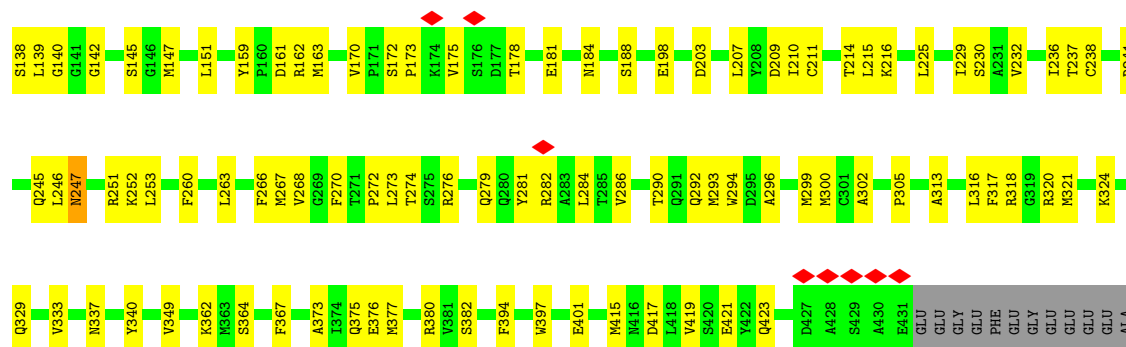


- Molecule 17: Tubulin beta

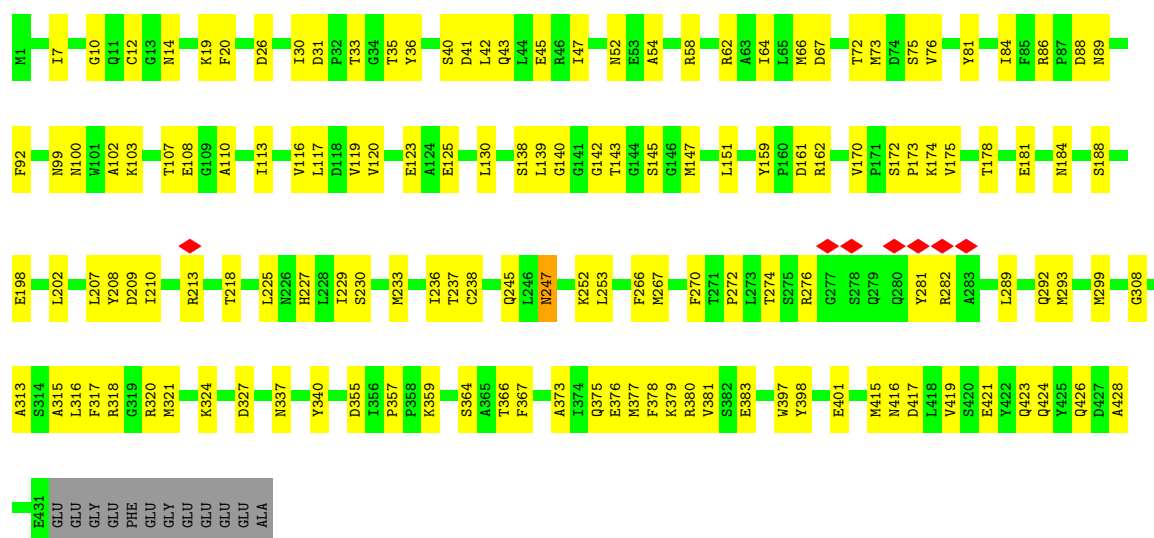


- Molecule 17: Tubulin beta

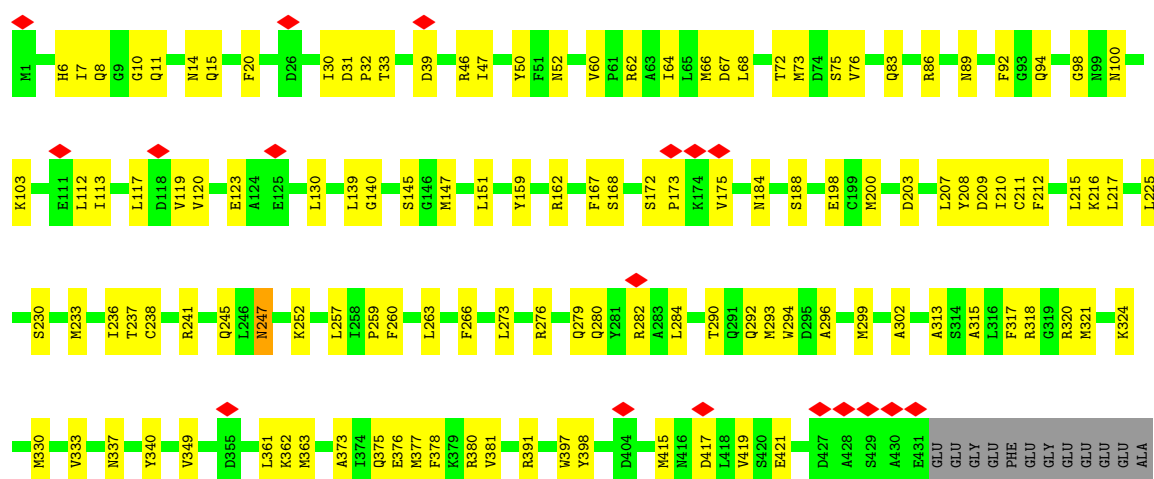




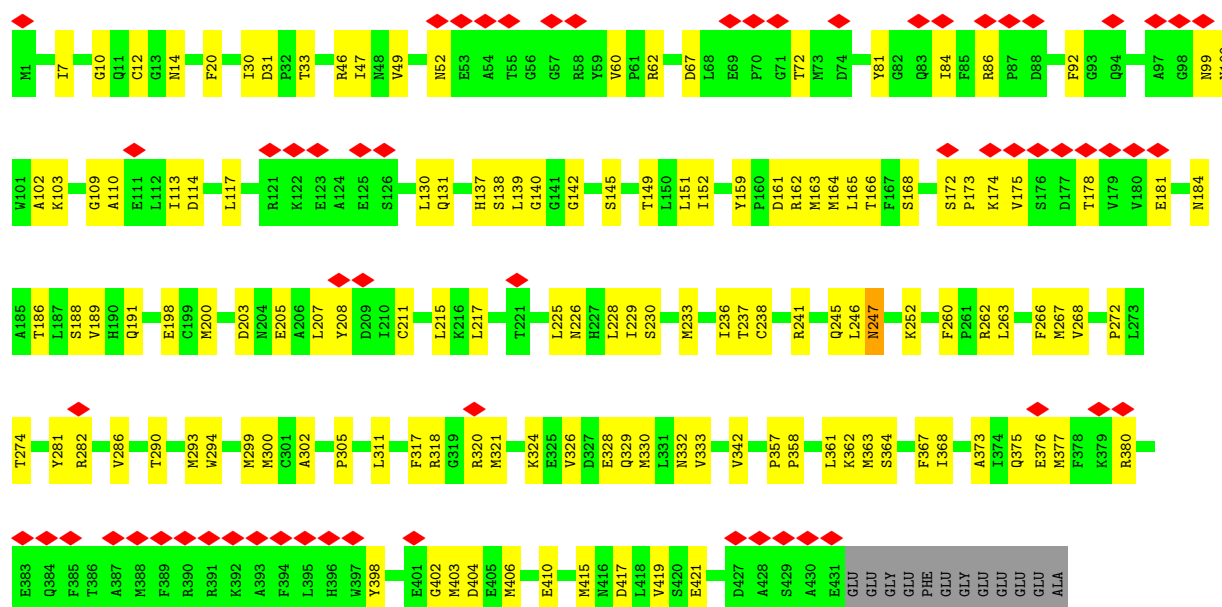
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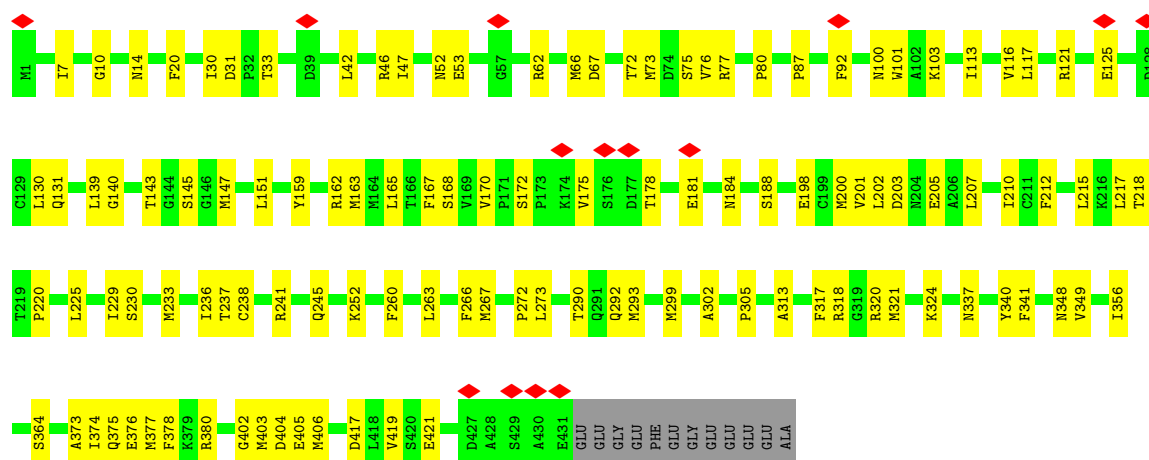
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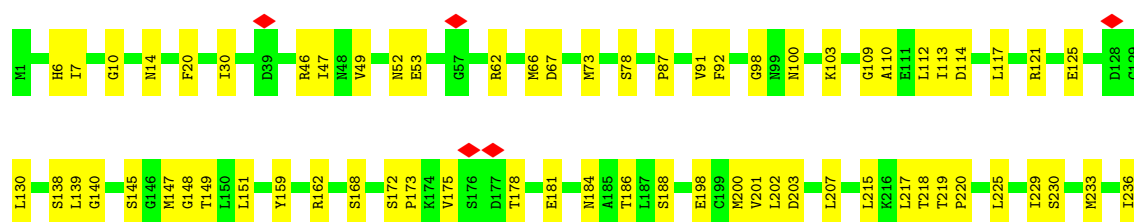
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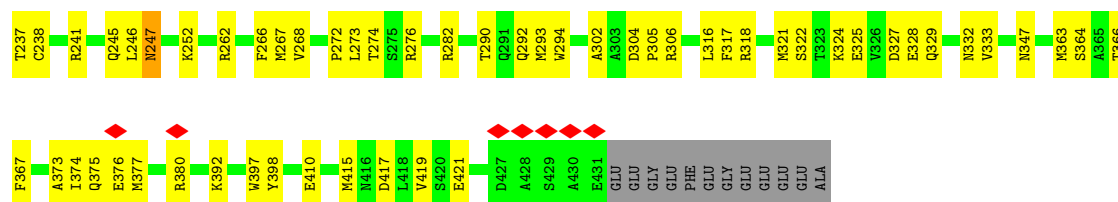


• Molecule 17: Tubulin beta

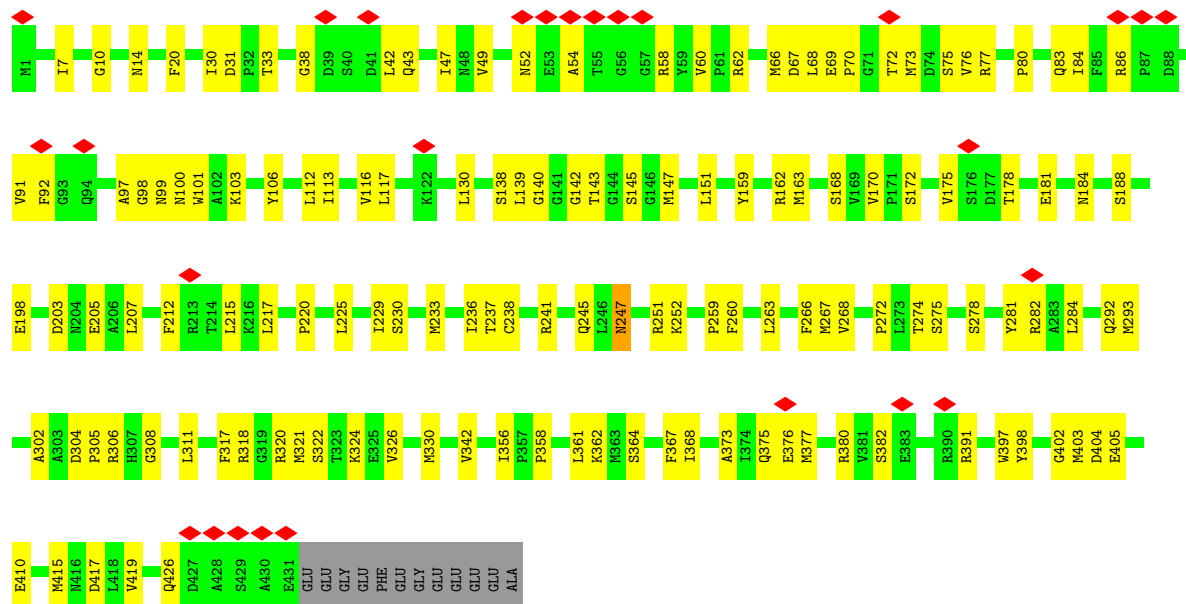


• Molecule 17: Tubulin beta

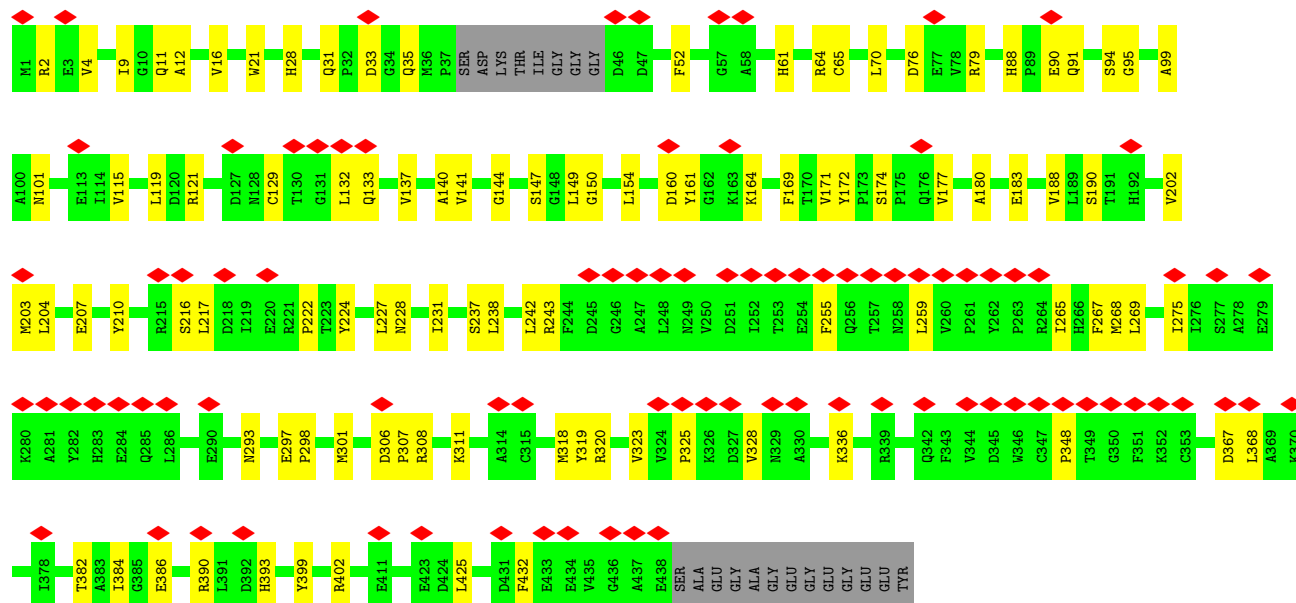
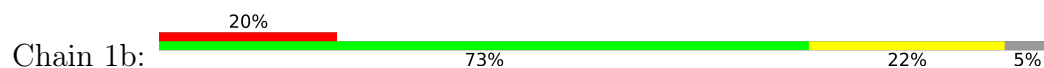




• Molecule 17: Tubulin beta

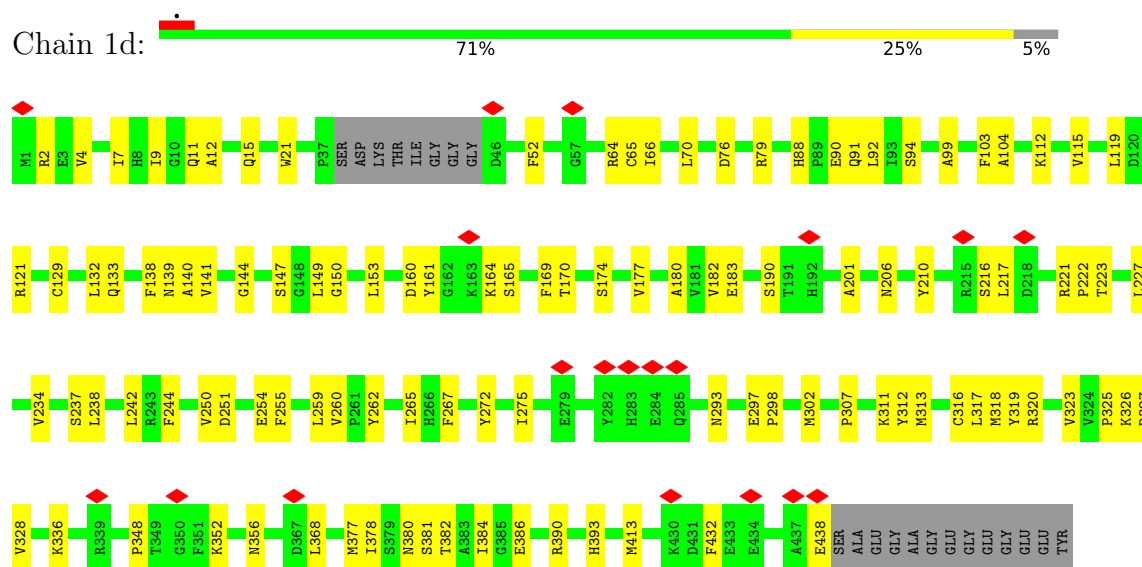


• Molecule 18: Tubulin alpha



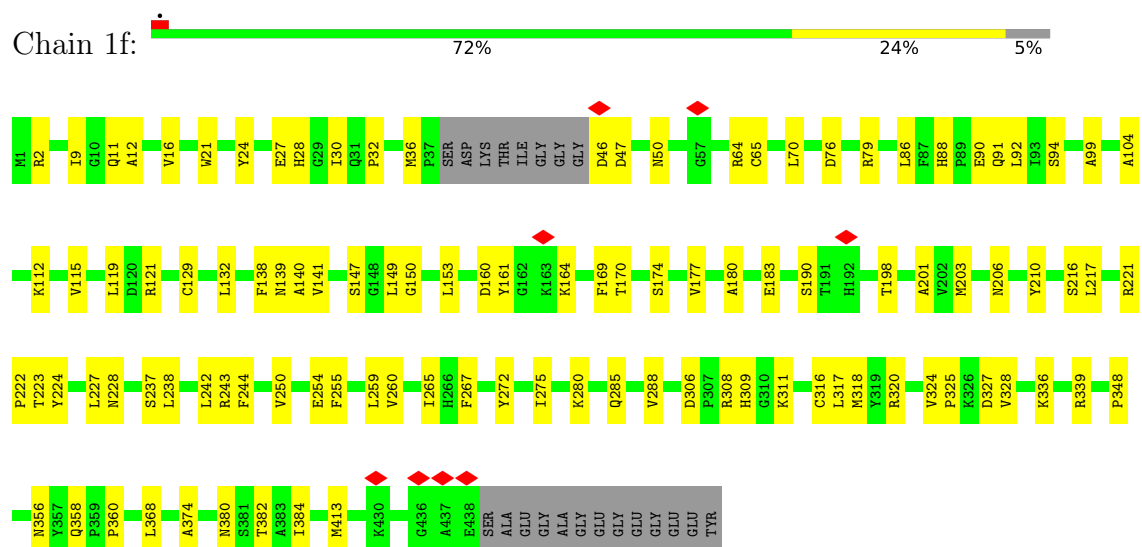
- Molecule 18: Tubulin alpha

Chain 1d:



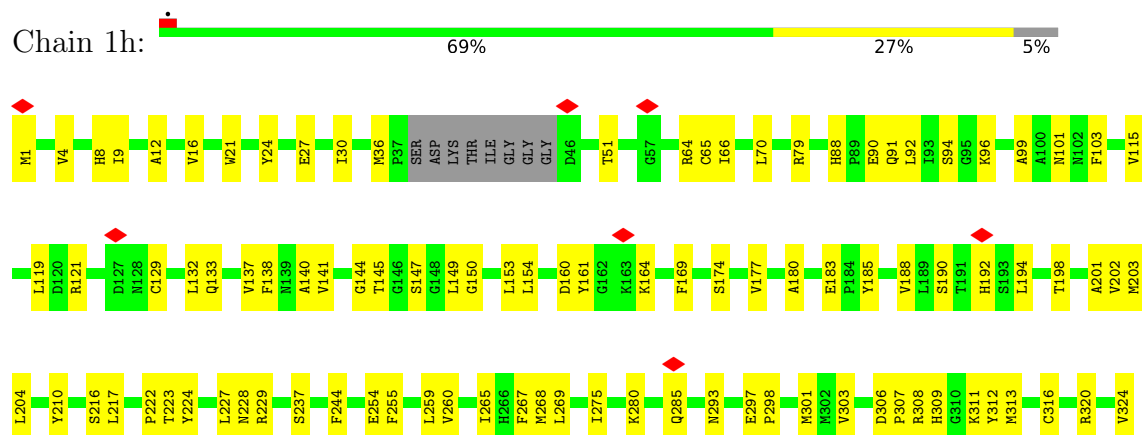
- Molecule 18: Tubulin alpha

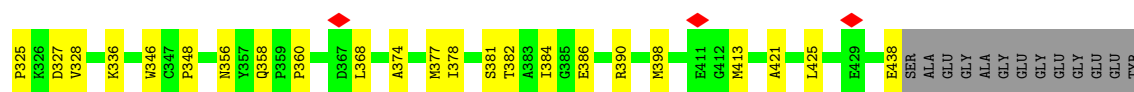
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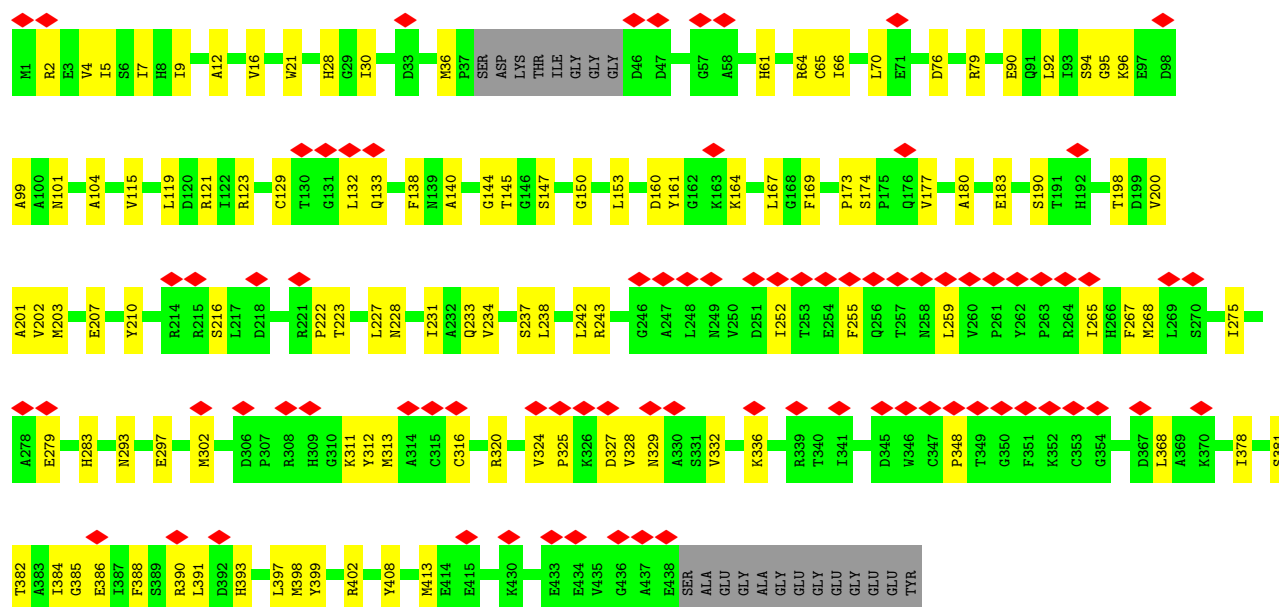
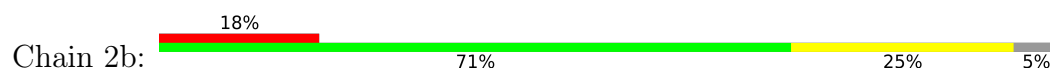
- Molecule 18: Tubulin alpha

Chain 1h:

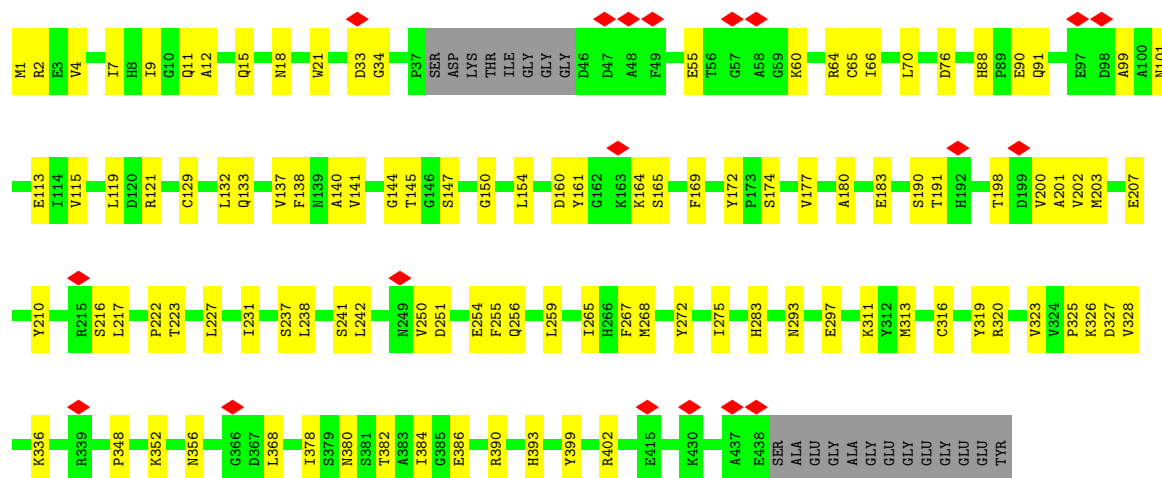




• Molecule 18: Tubulin alpha

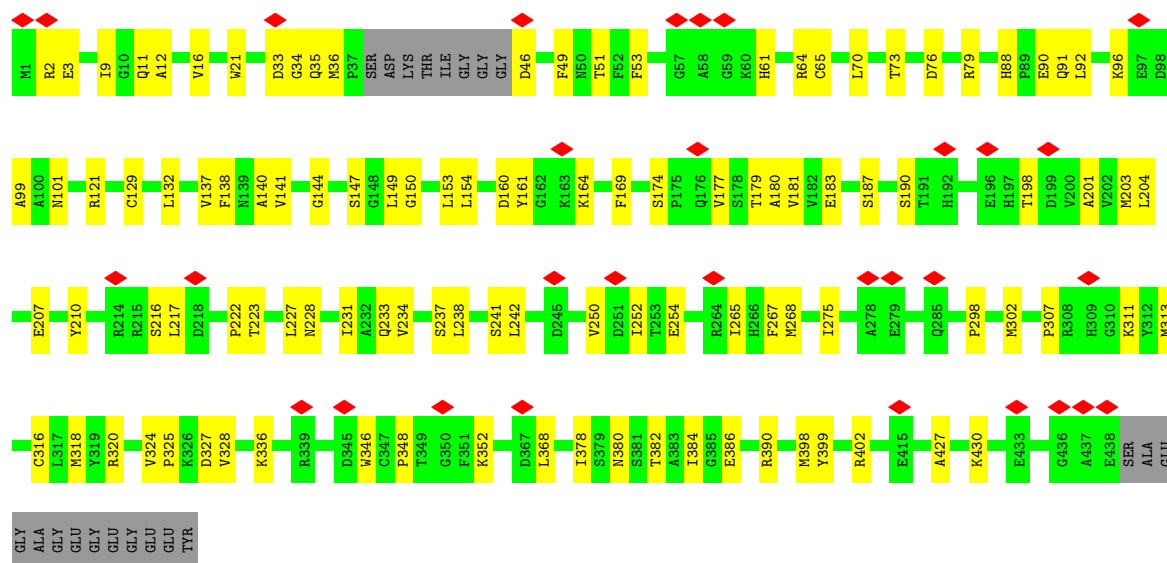


• Molecule 18: Tubulin alpha

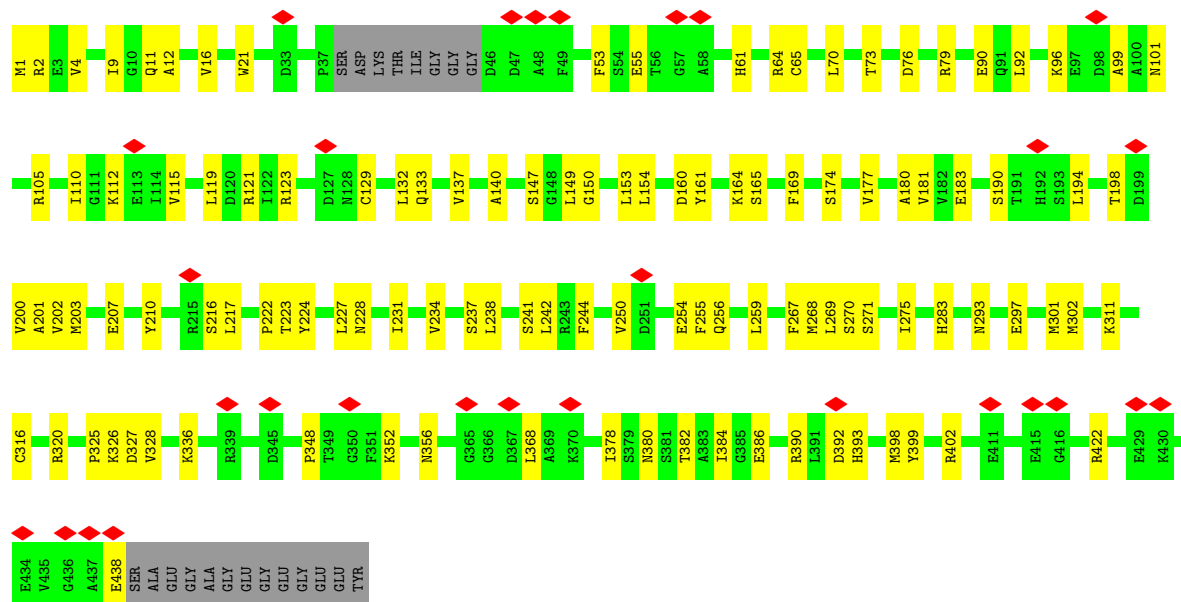


• Molecule 18: Tubulin alpha

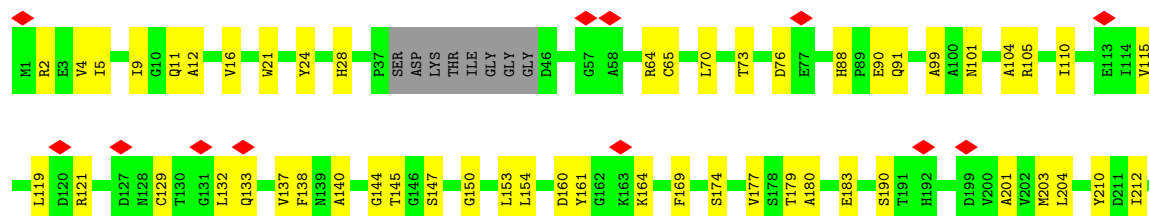
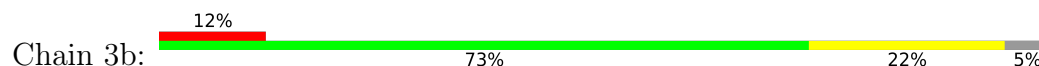


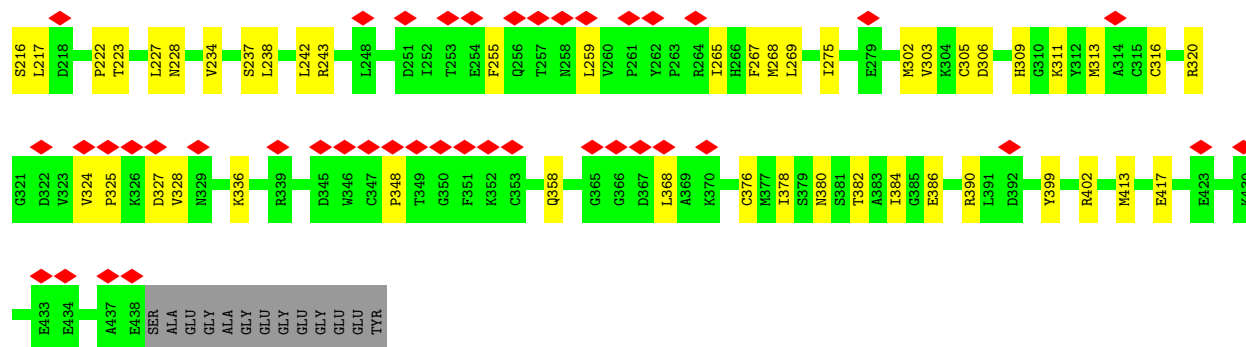


• Molecule 18: Tubulin alpha

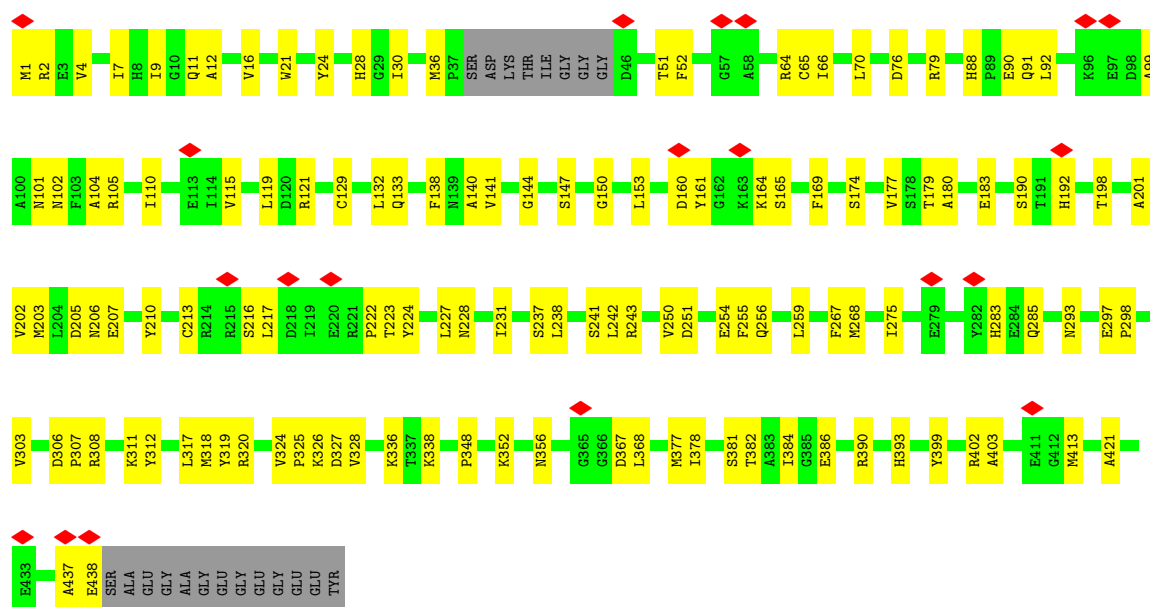


• Molecule 18: Tubulin alpha

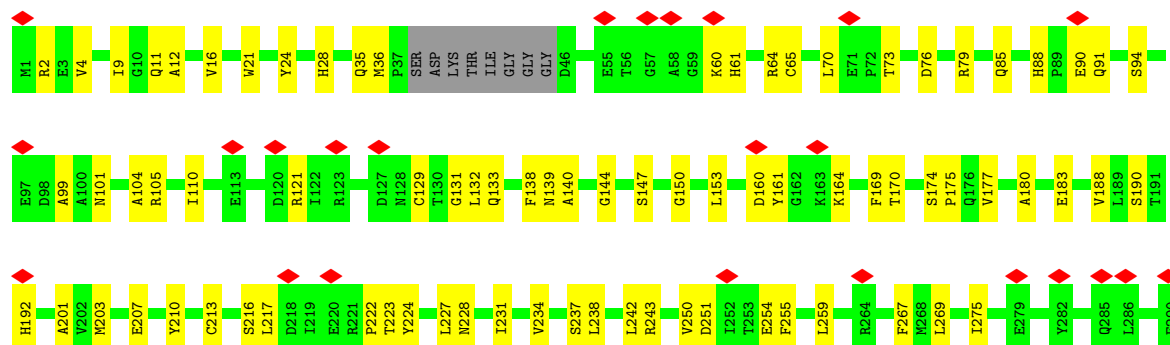


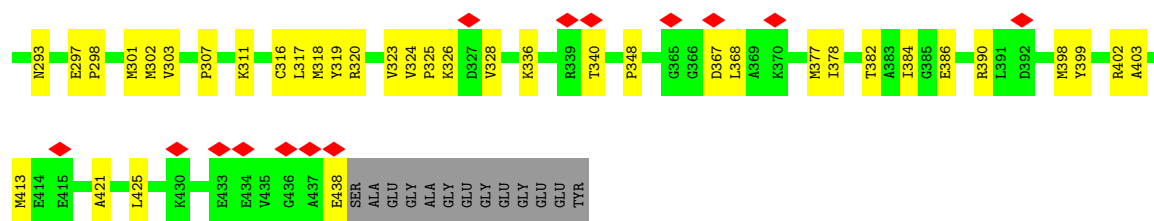


• Molecule 18: Tubulin alpha

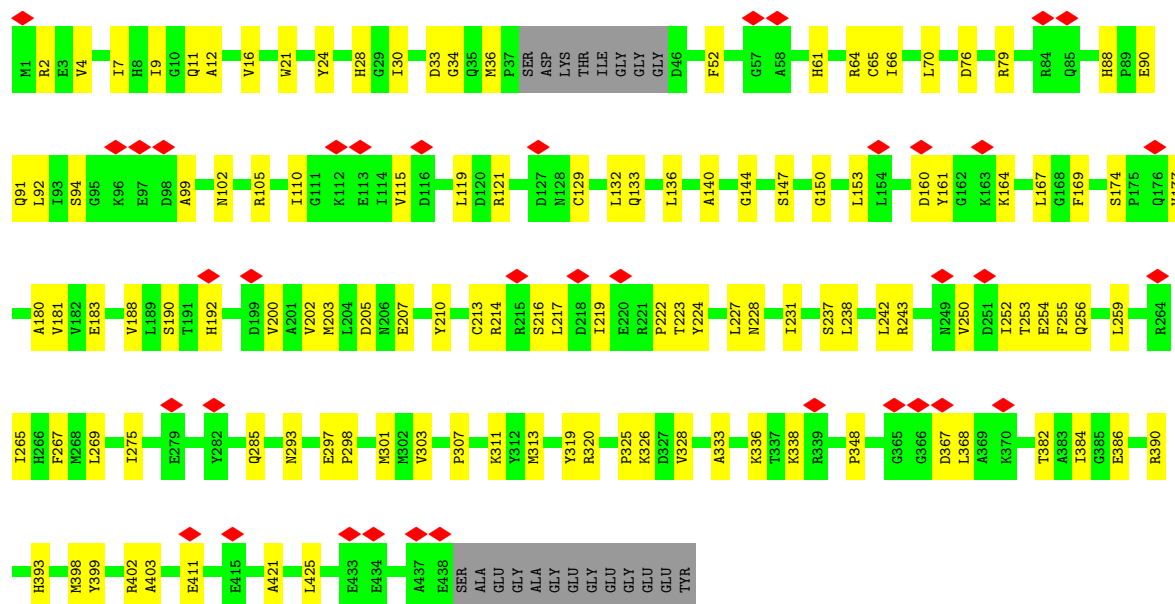


• Molecule 18: Tubulin alpha

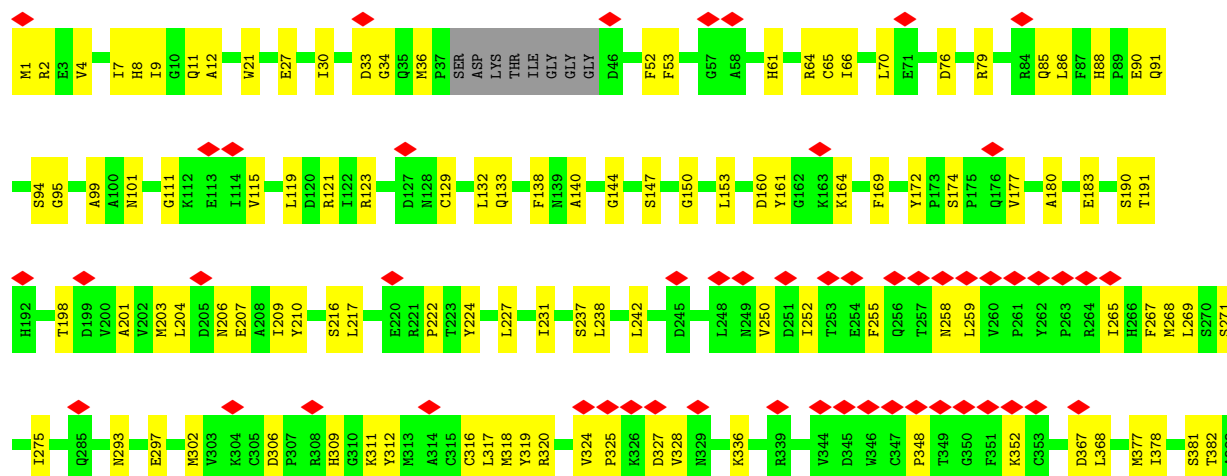


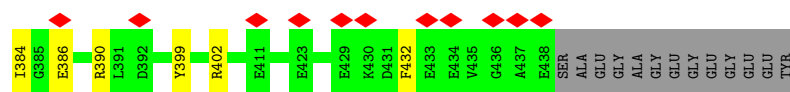


• Molecule 18: Tubulin alpha

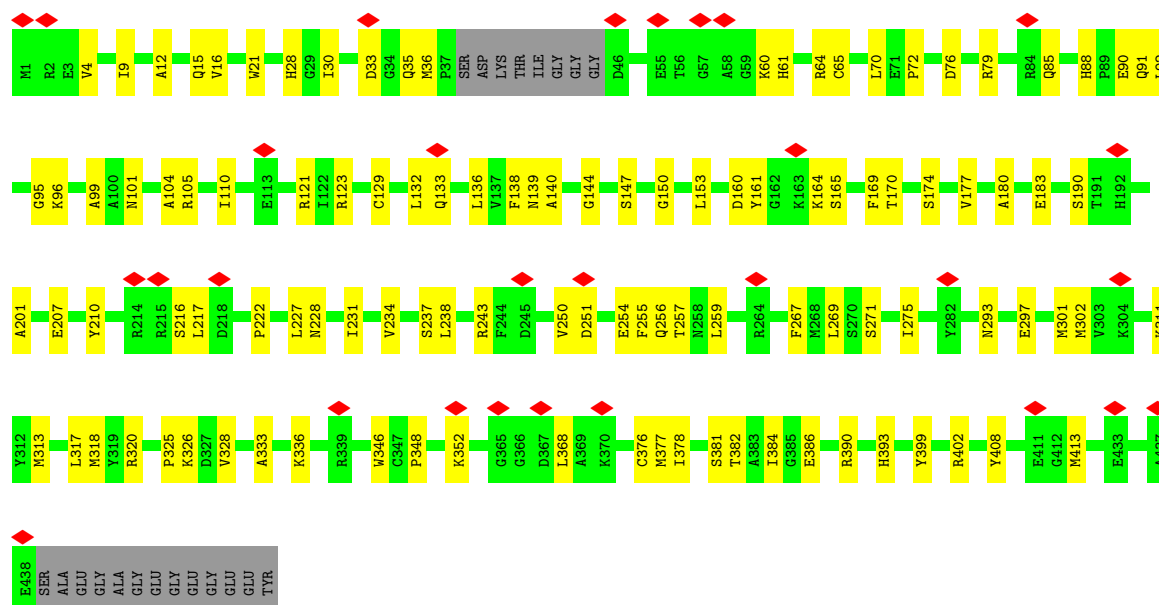


• Molecule 18: Tubulin alpha

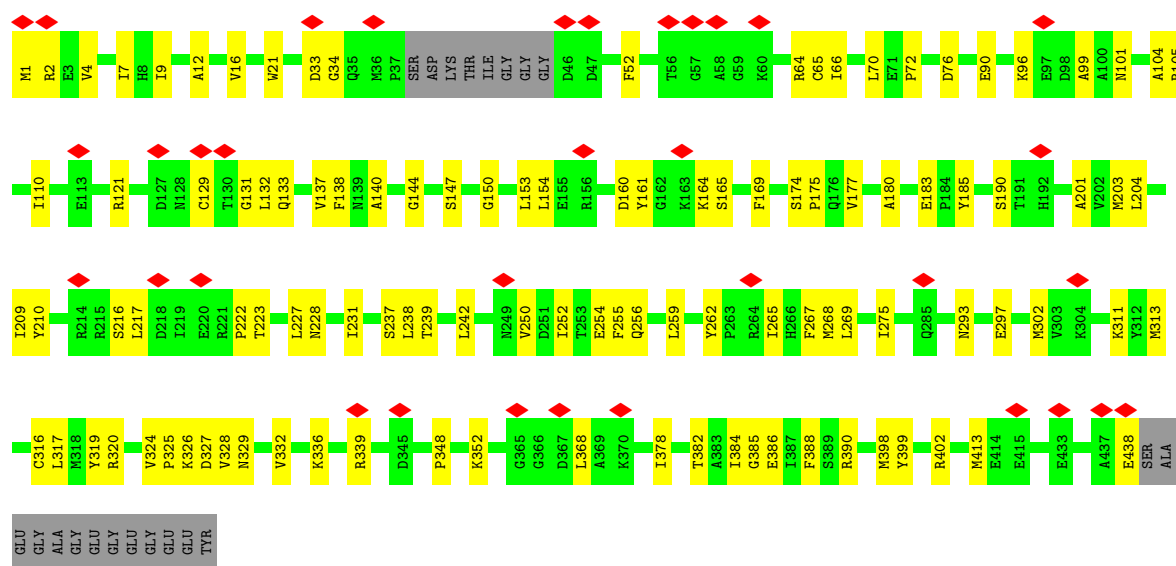




• Molecule 18: Tubulin alpha

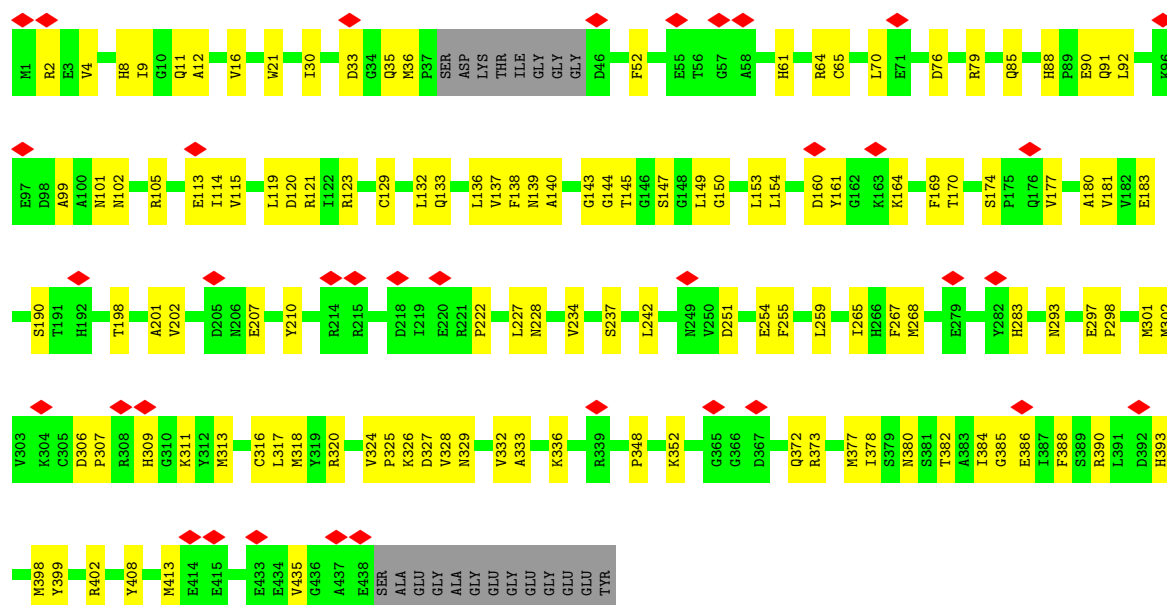


• Molecule 18: Tubulin alpha

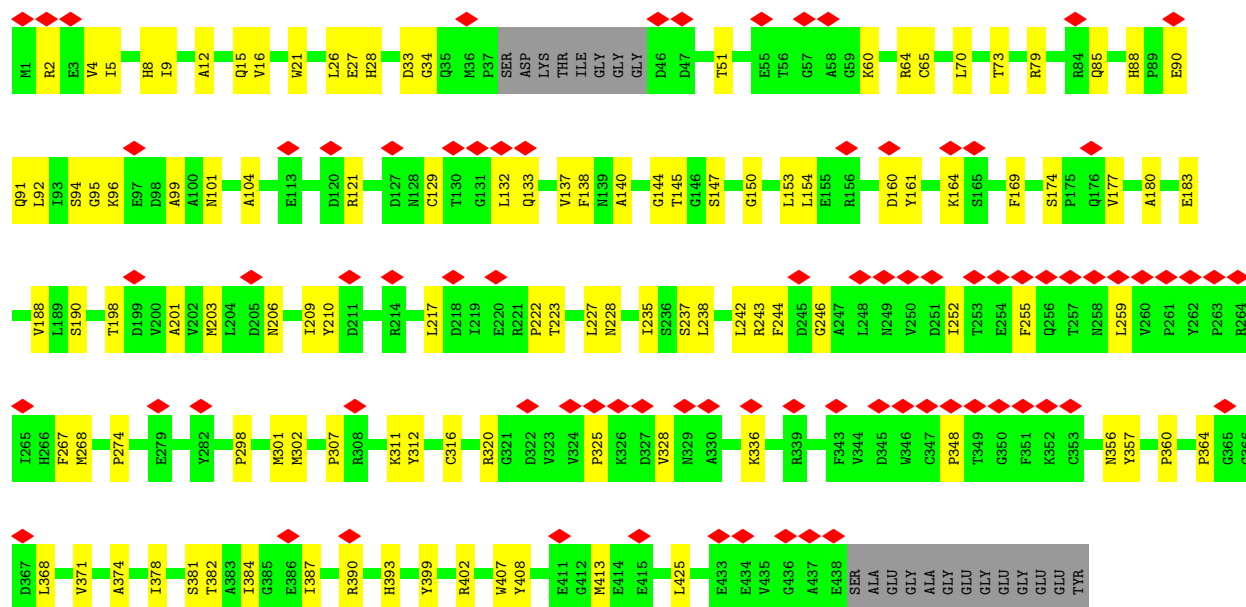


• Molecule 18: Tubulin alpha



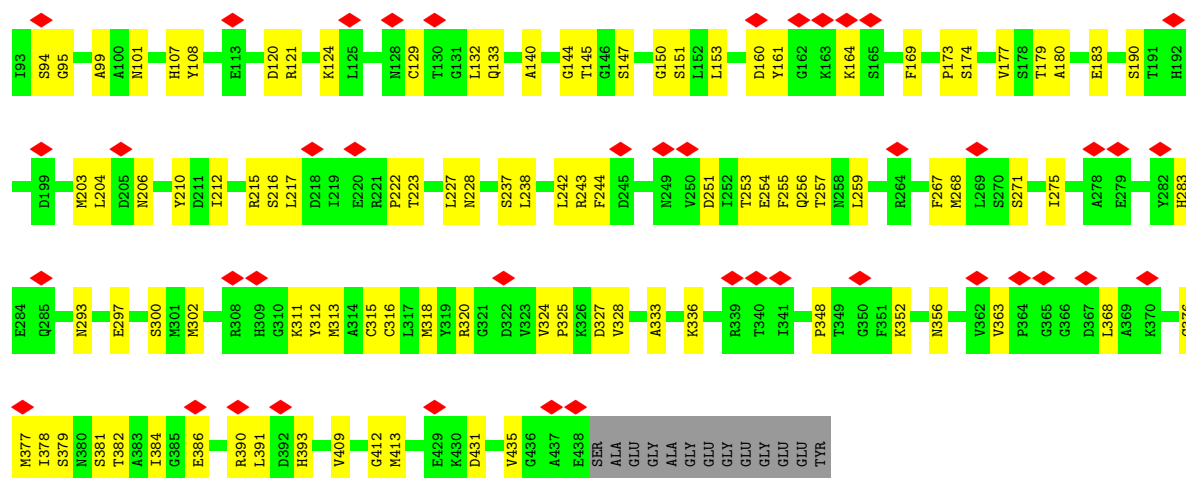


• Molecule 18: Tubulin alpha

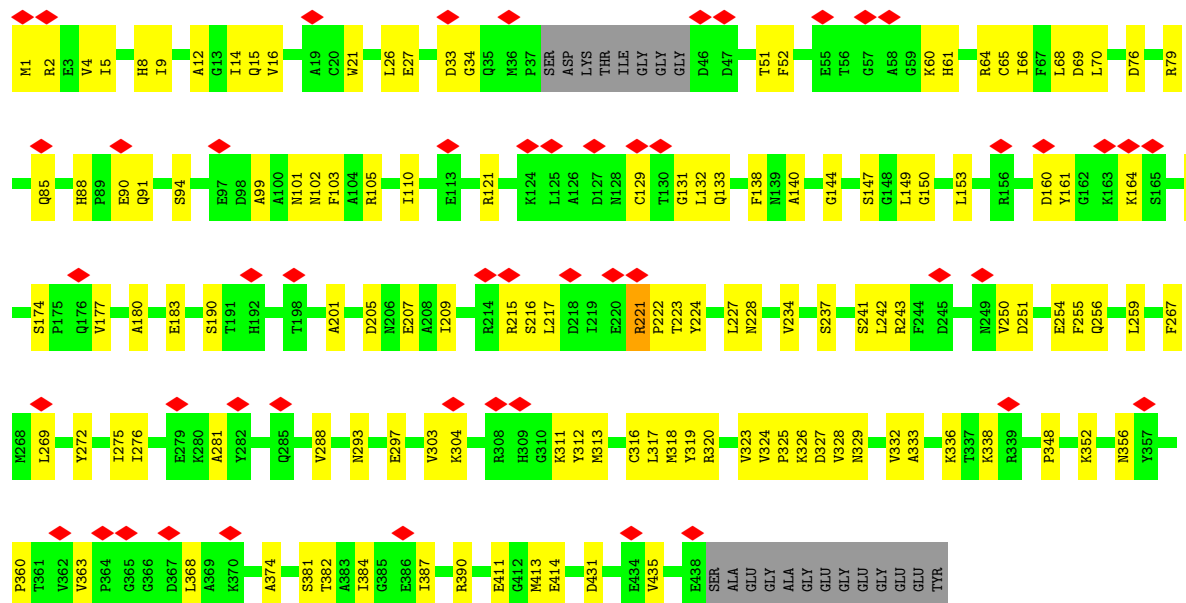


• Molecule 18: Tubulin alpha

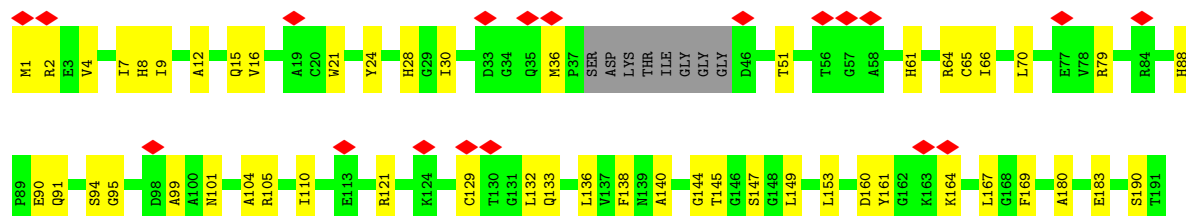


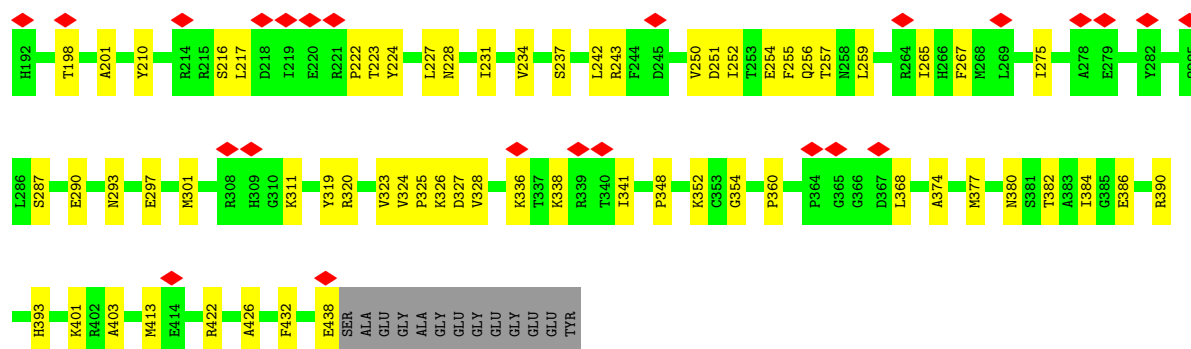


• Molecule 18: Tubulin alpha

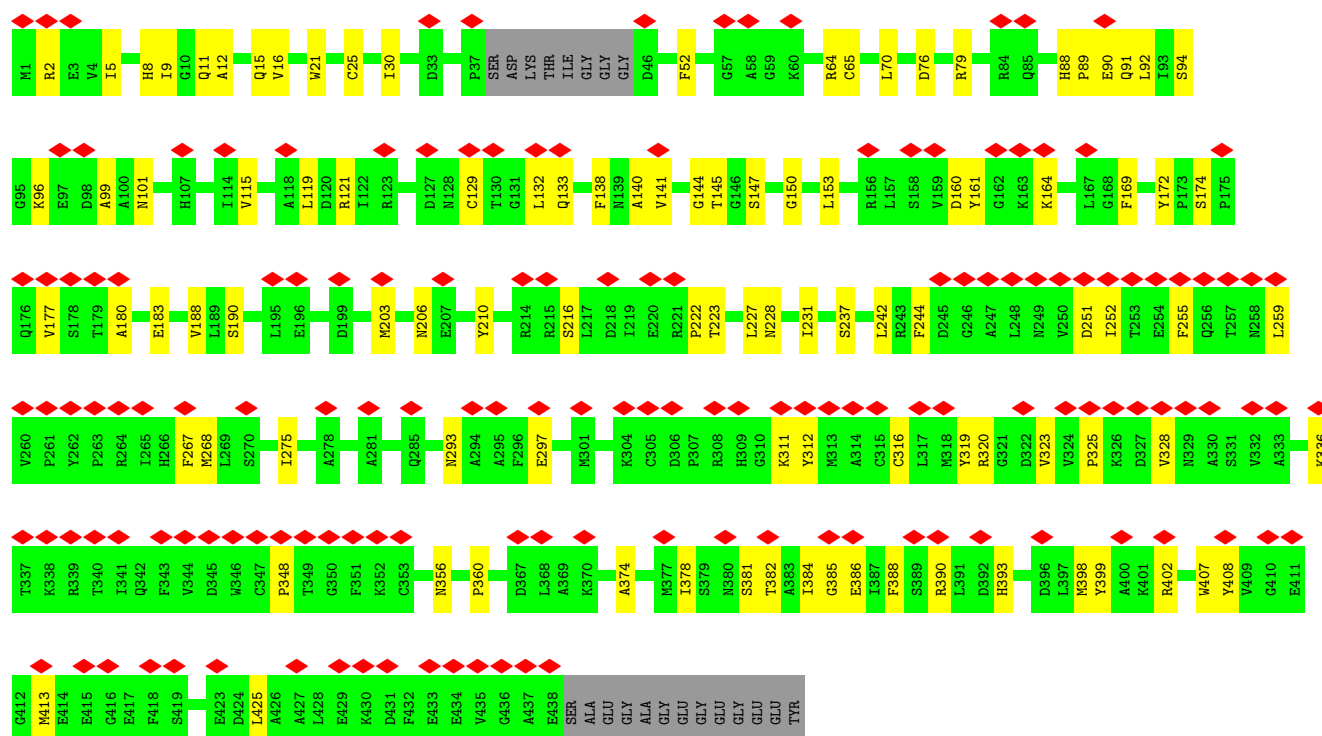
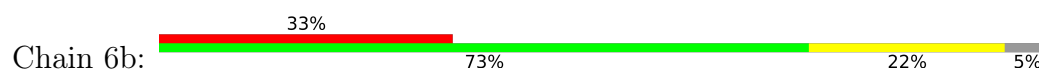


• Molecule 18: Tubulin alpha

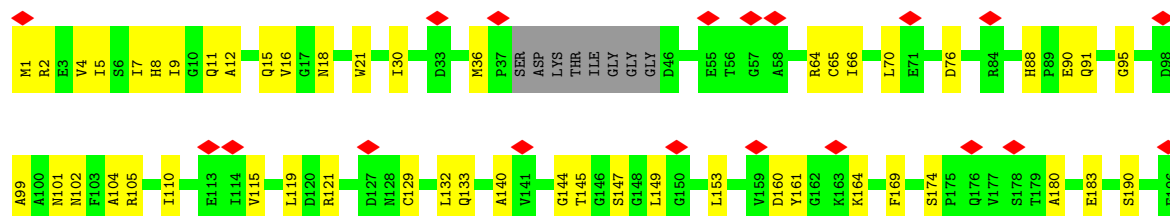


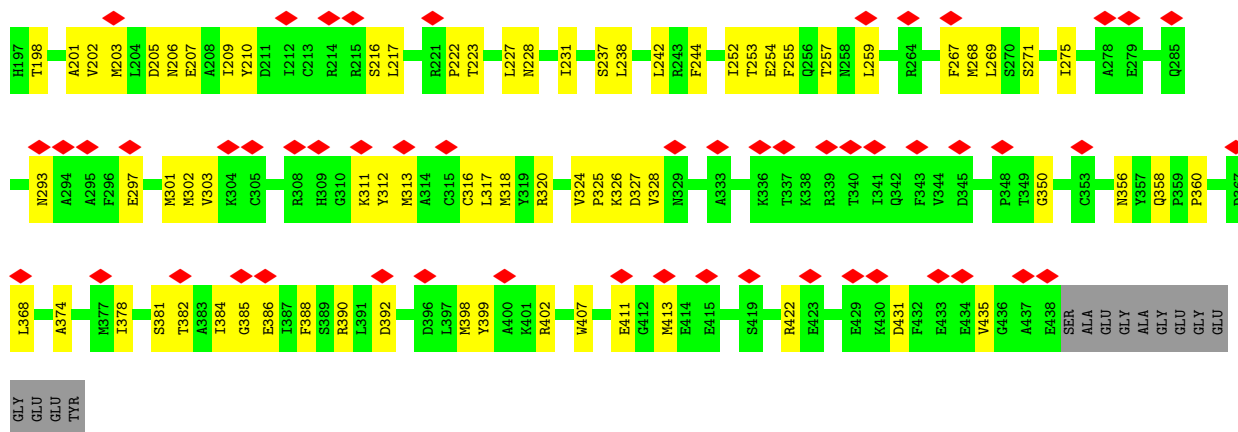


• Molecule 18: Tubulin alpha



• Molecule 18: Tubulin alpha



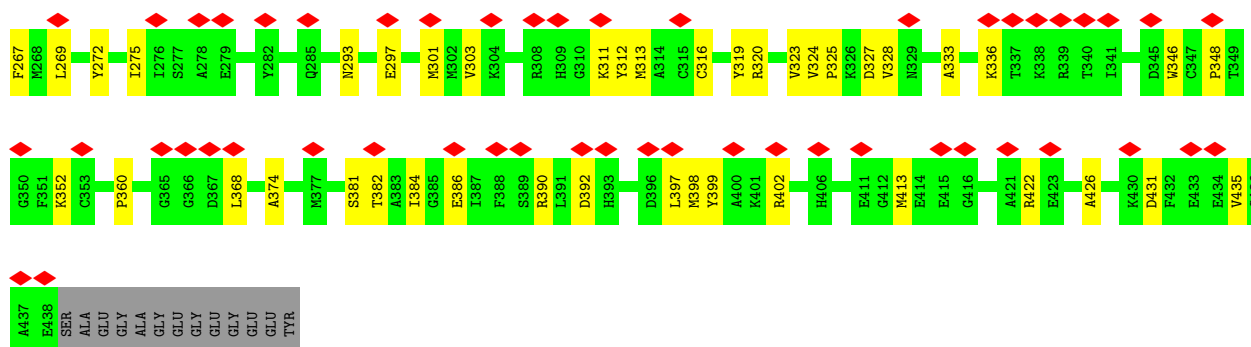


• Molecule 18: Tubulin alpha

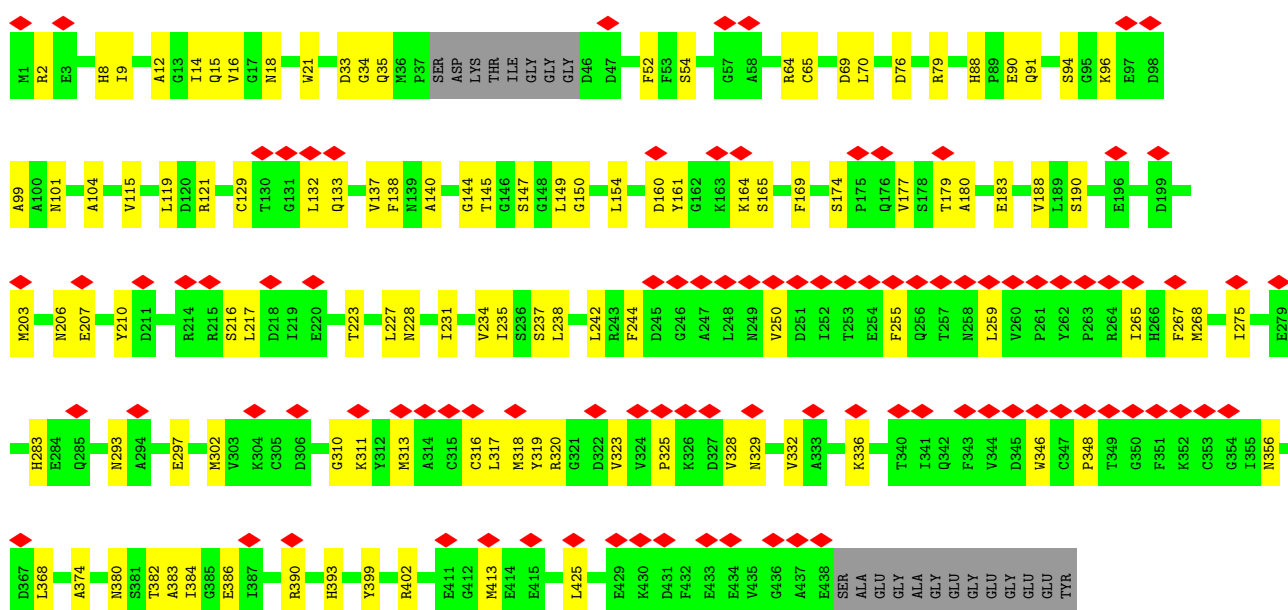
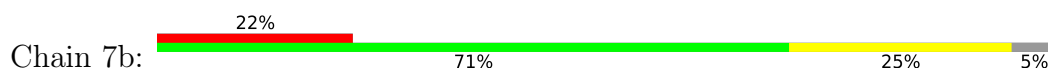


• Molecule 18: Tubulin alpha

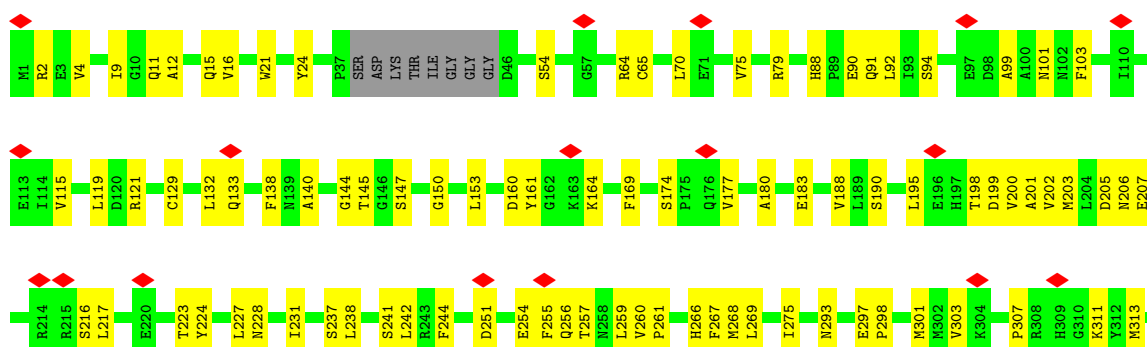


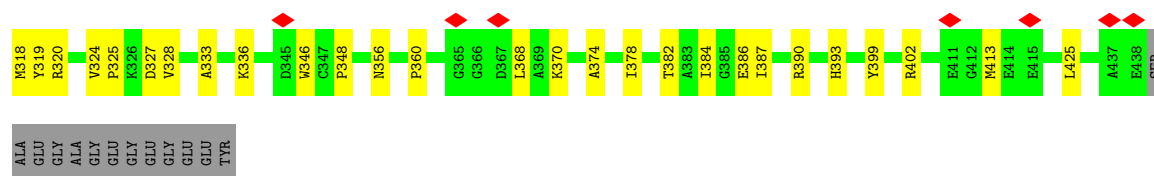


• Molecule 18: Tubulin alpha

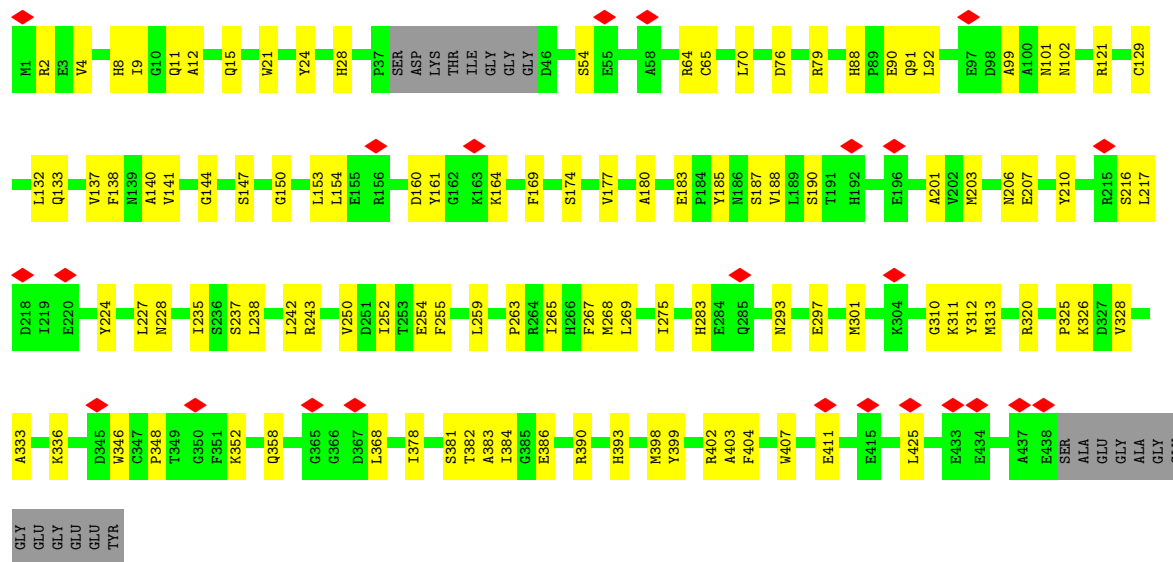


• Molecule 18: Tubulin alpha

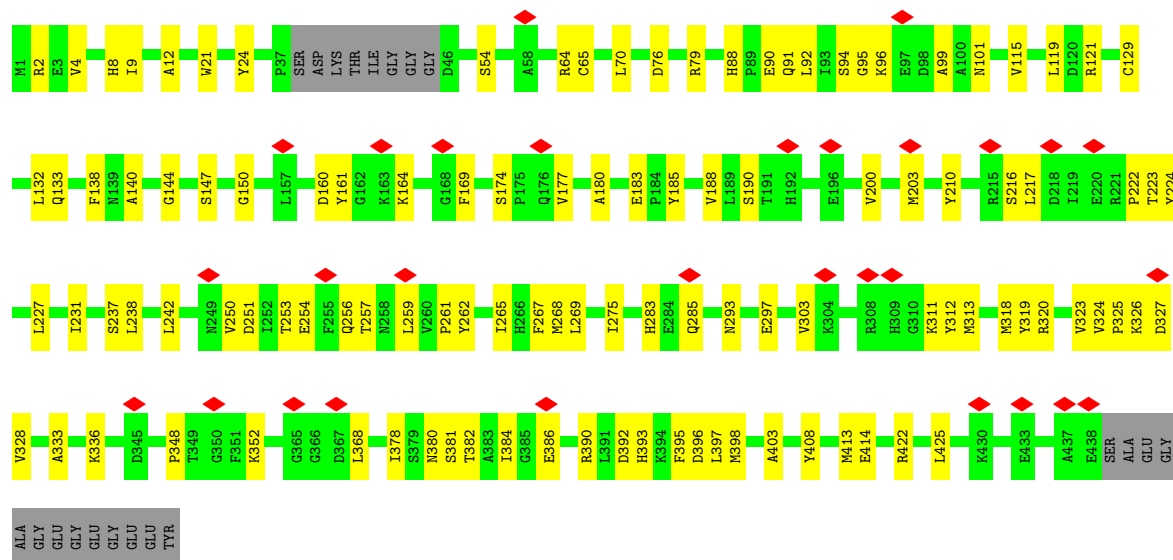




• Molecule 18: Tubulin alpha

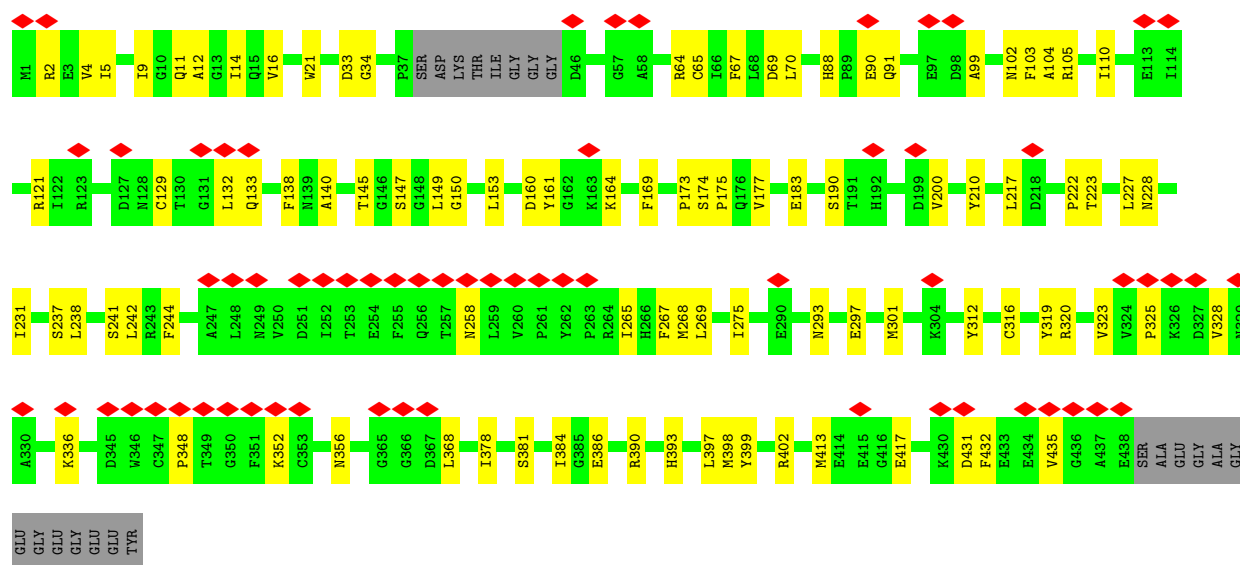


• Molecule 18: Tubulin alpha



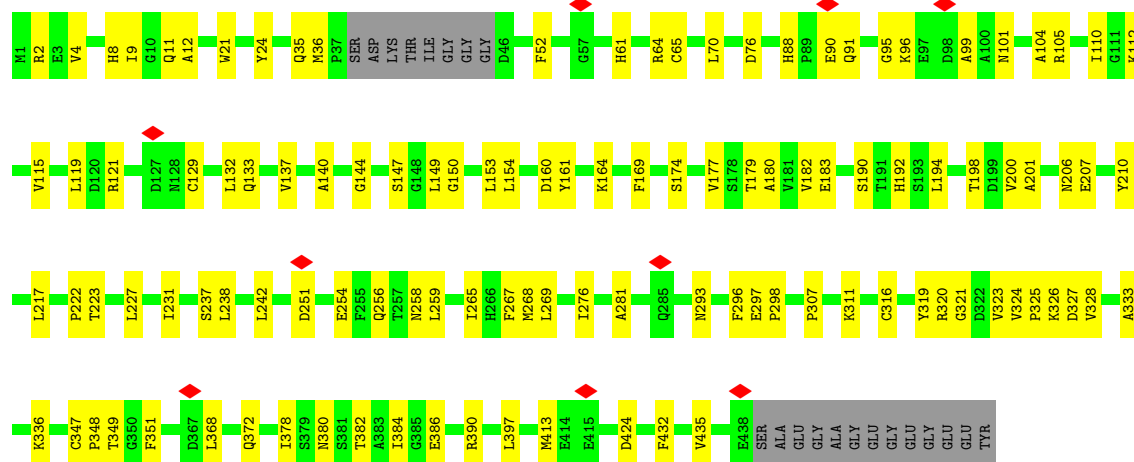
• Molecule 18: Tubulin alpha

Chain 8b: 



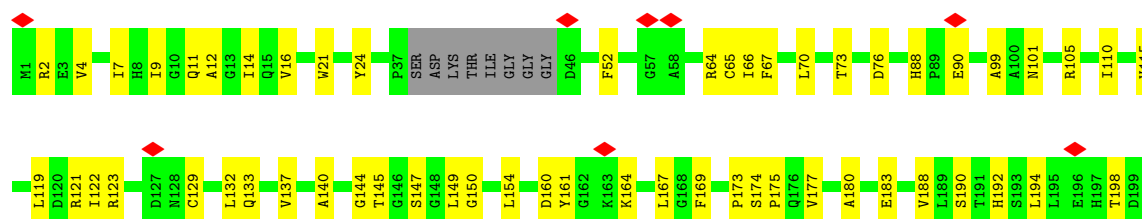
• Molecule 18: Tubulin alpha

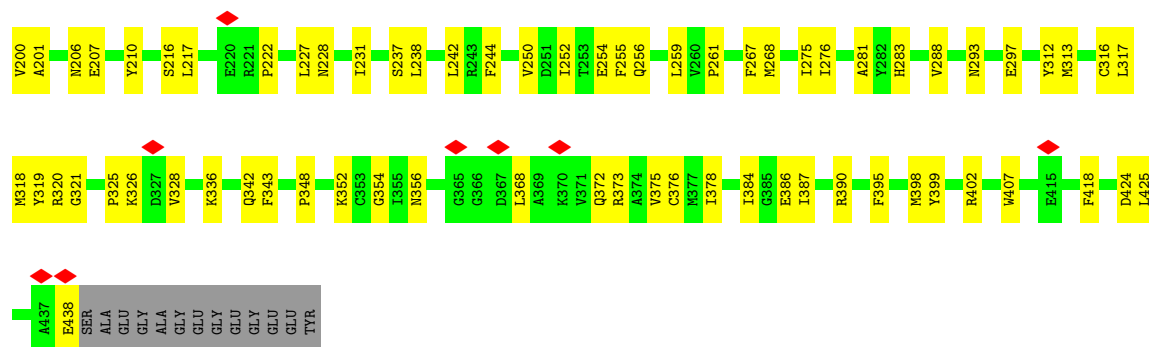
Chain 8d: 



• Molecule 18: Tubulin alpha

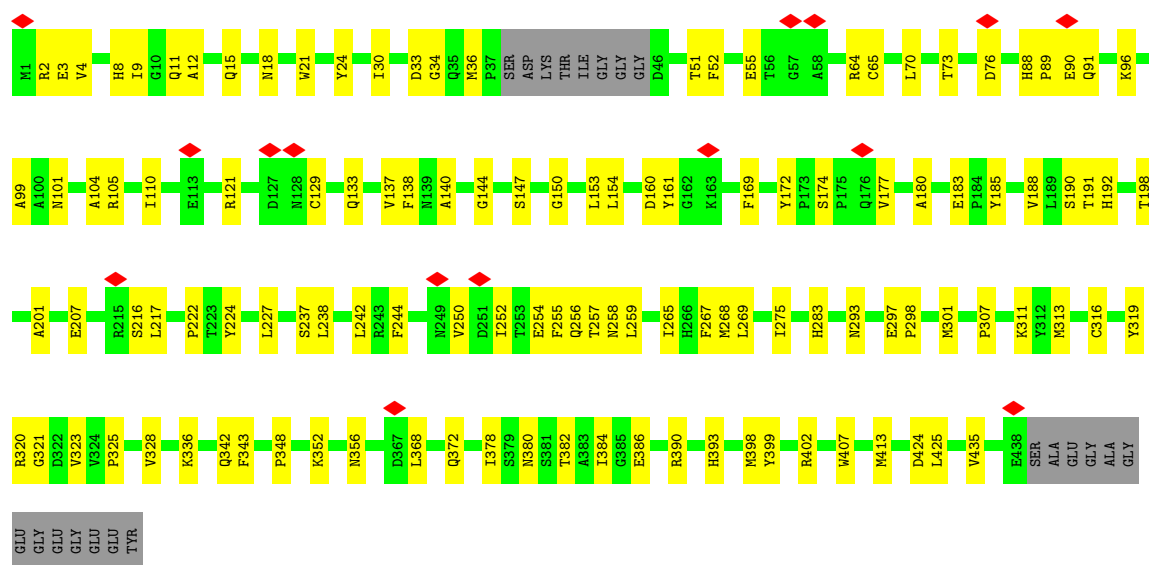
Chain 8f: 





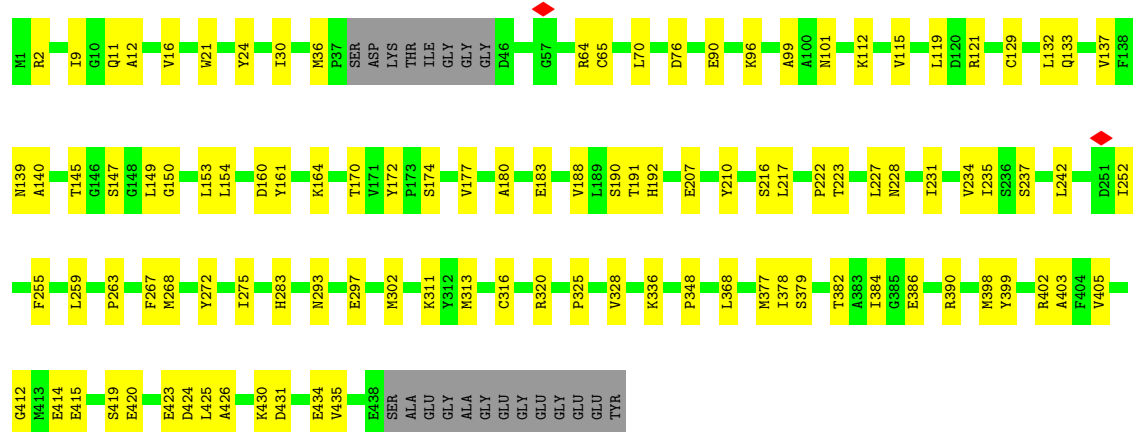
- Molecule 18: Tubulin alpha

Chain 8h: 69% 27% 5%

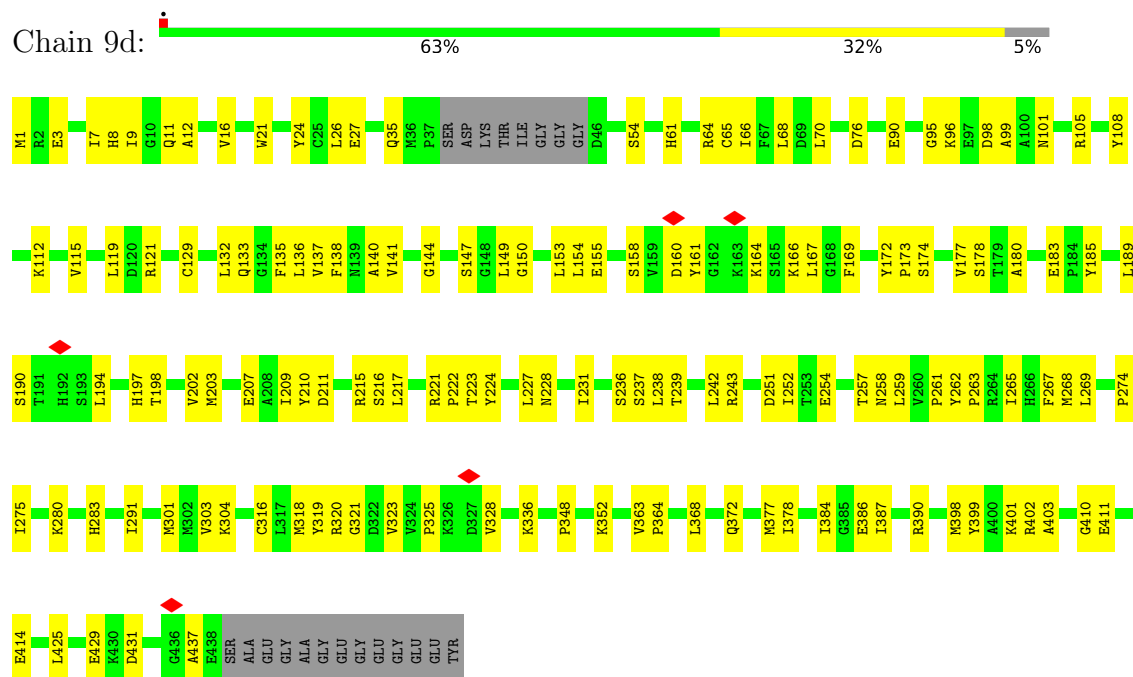


- Molecule 18: Tubulin alpha

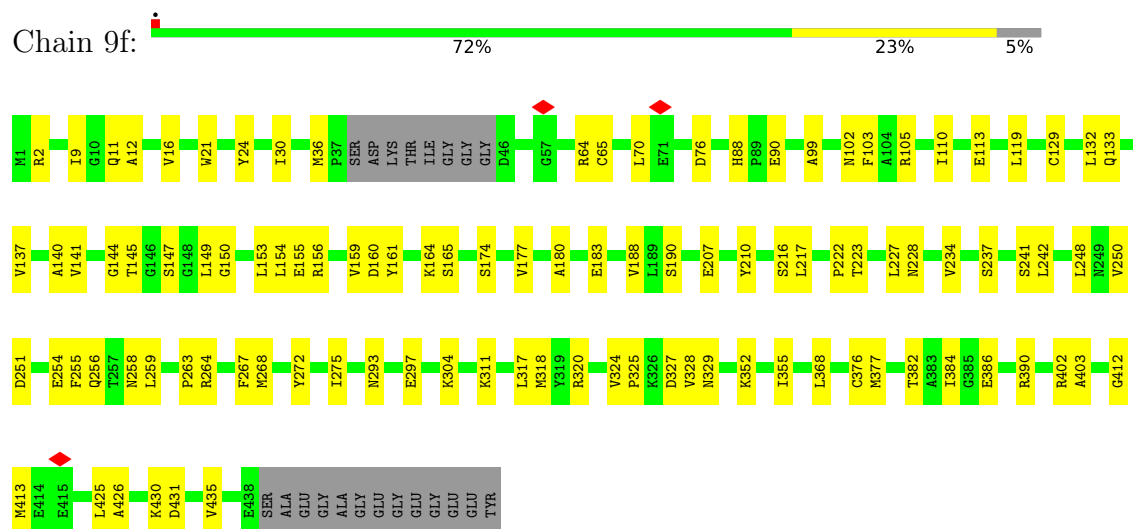
Chain 9b: 72% 23% 5%



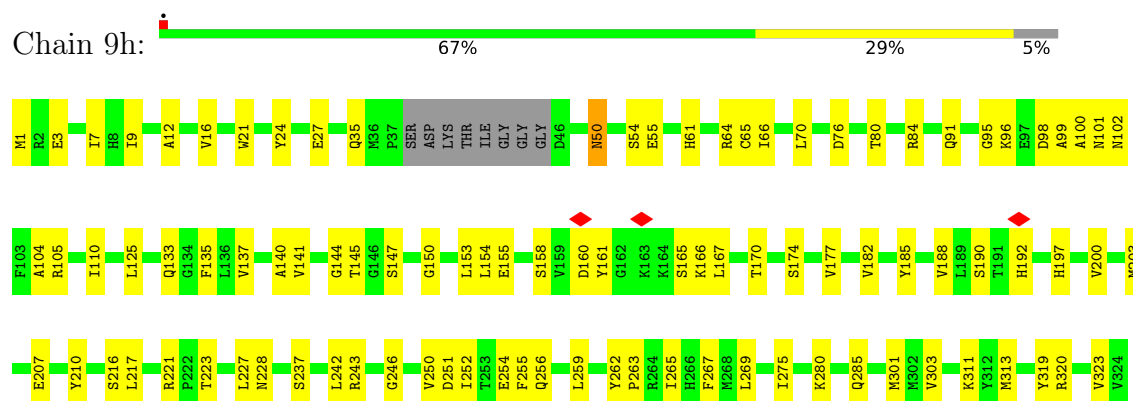
- Molecule 18: Tubulin alpha

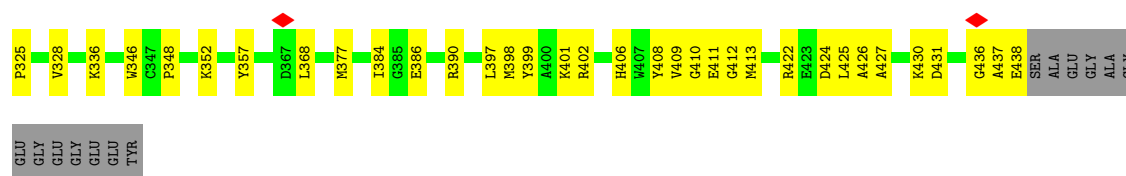


• Molecule 18: Tubulin alpha



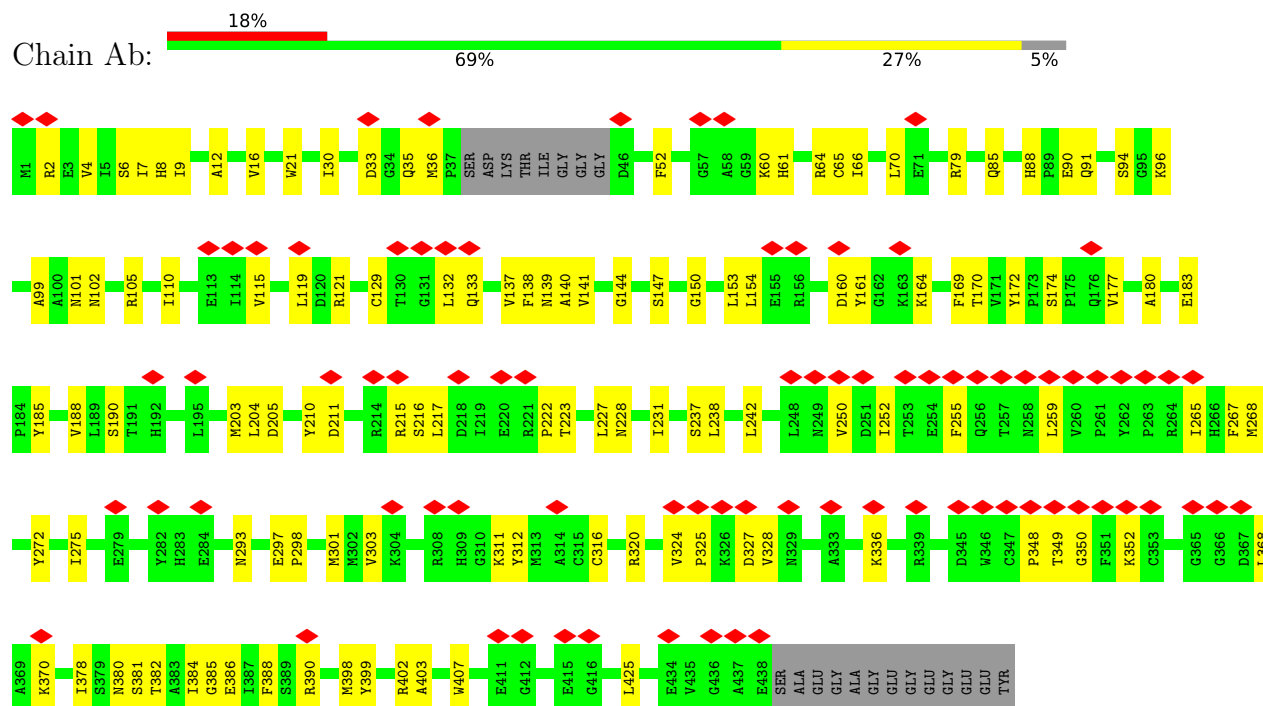
• Molecule 18: Tubulin alpha





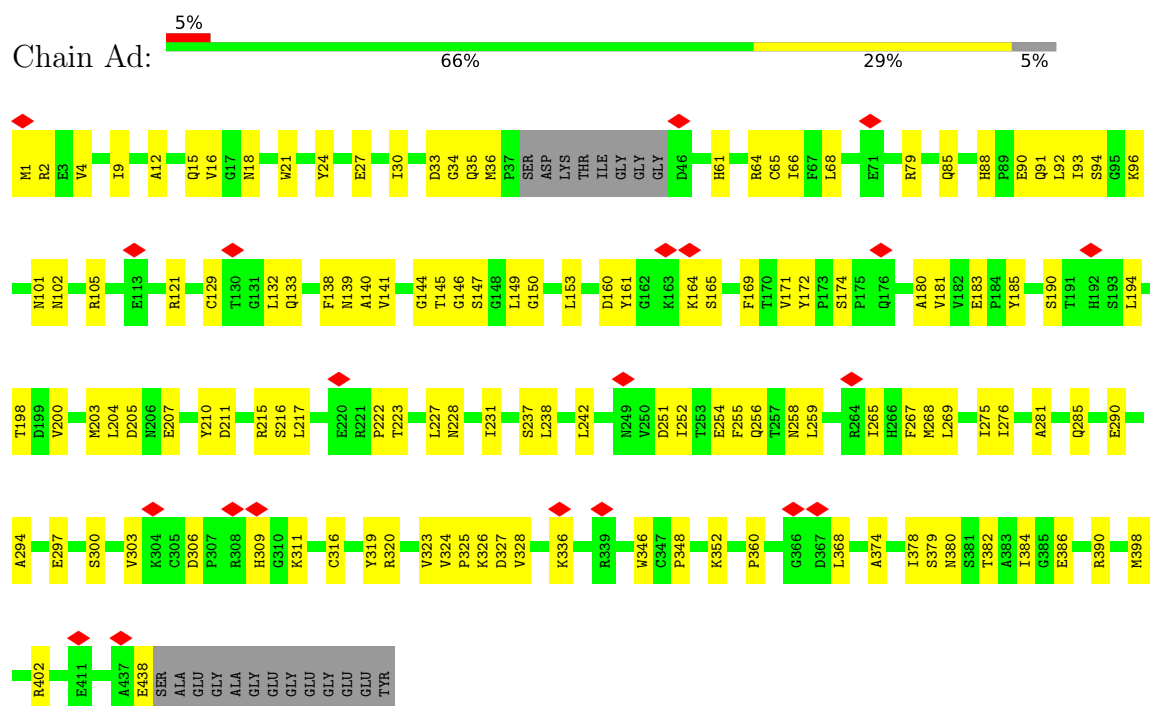
• Molecule 18: Tubulin alpha

Chain Ab:

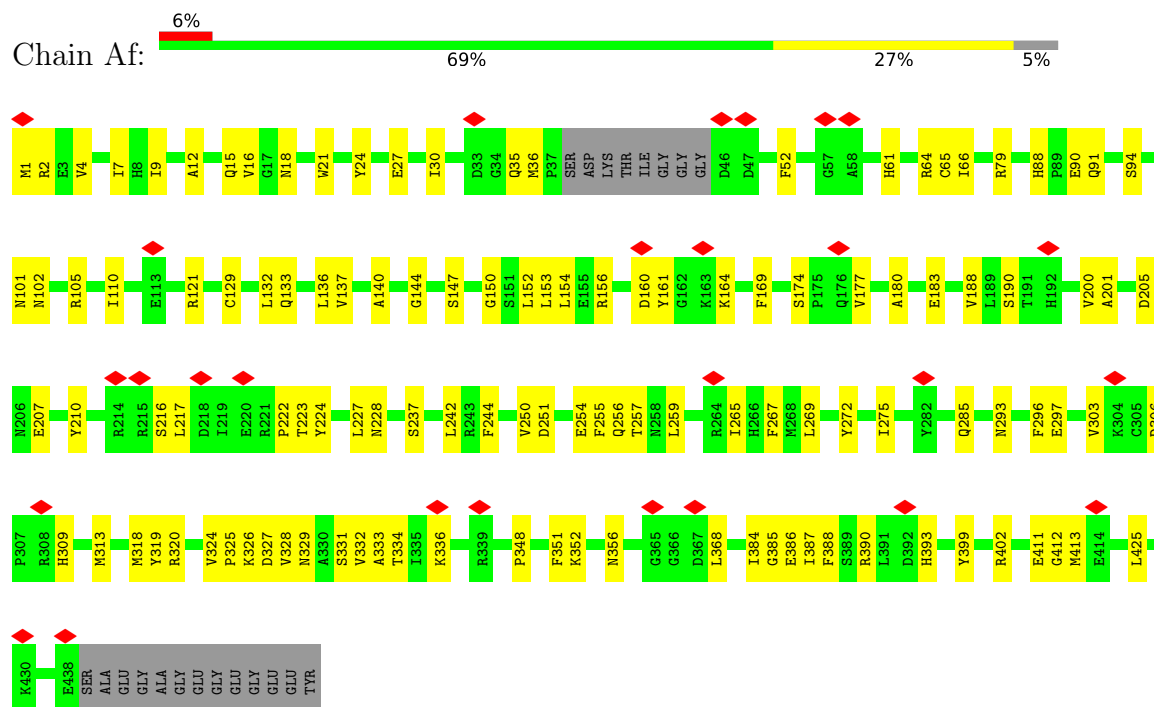


• Molecule 18: Tubulin alpha

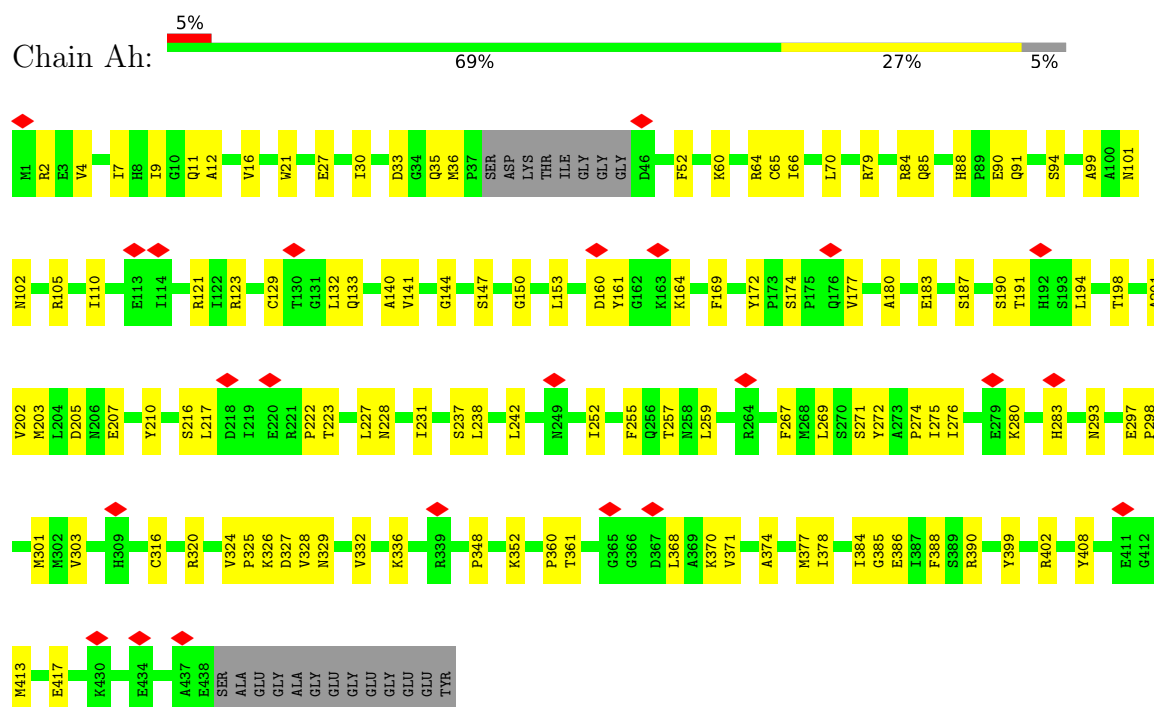
Chain Ad:



• Molecule 18: Tubulin alpha

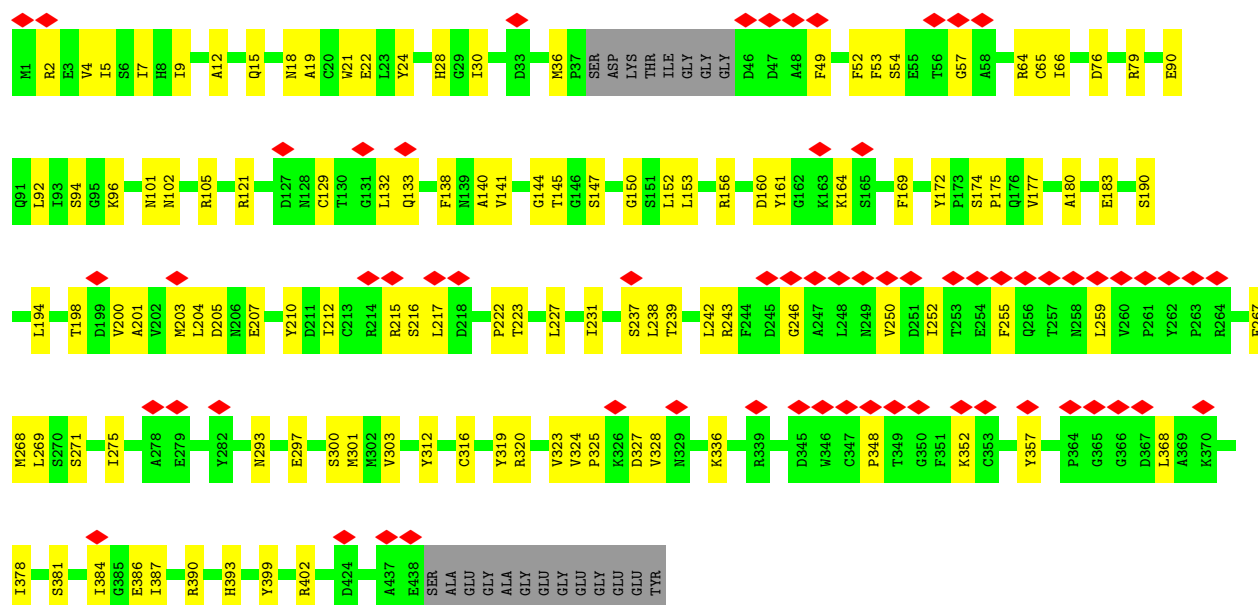


• Molecule 18: Tubulin alpha



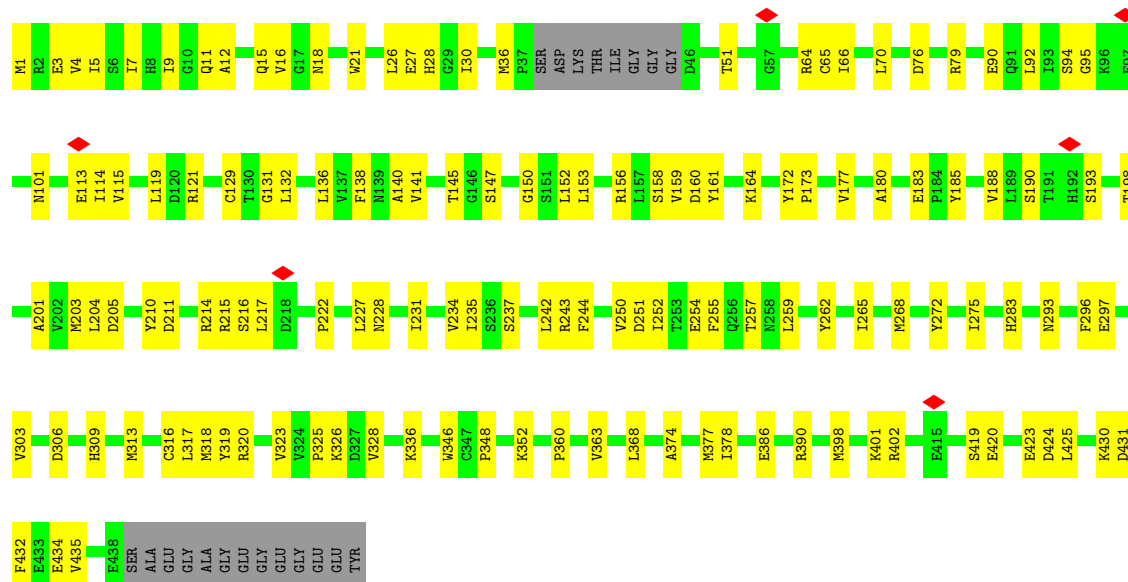
• Molecule 18: Tubulin alpha





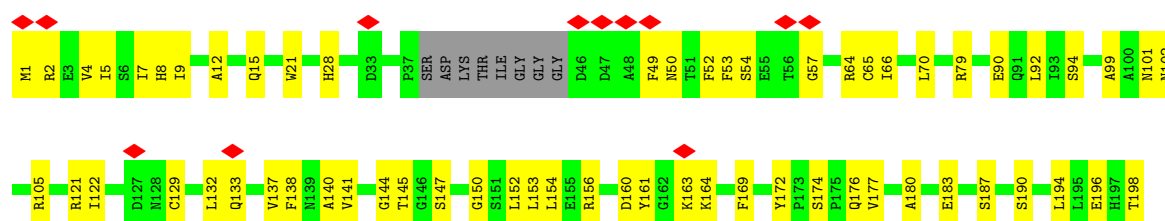
• Molecule 18: Tubulin alpha

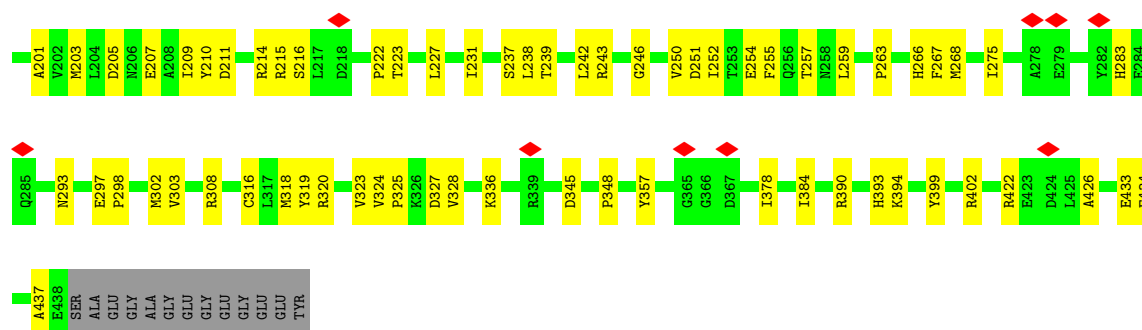
Chain Bd: 65% 30% 5%



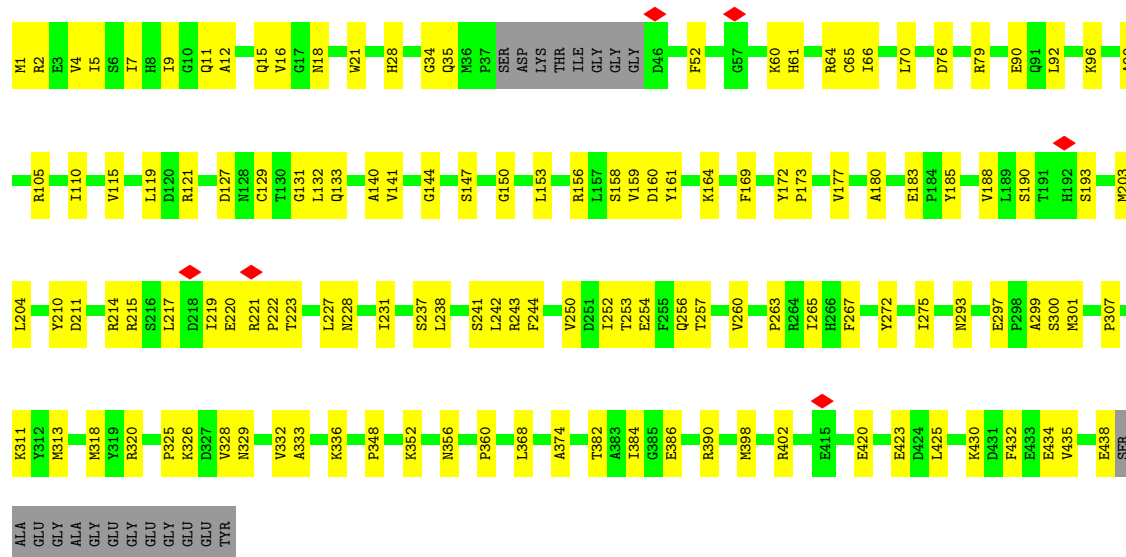
• Molecule 18: Tubulin alpha

Chain Bf: 67% 28% 5%

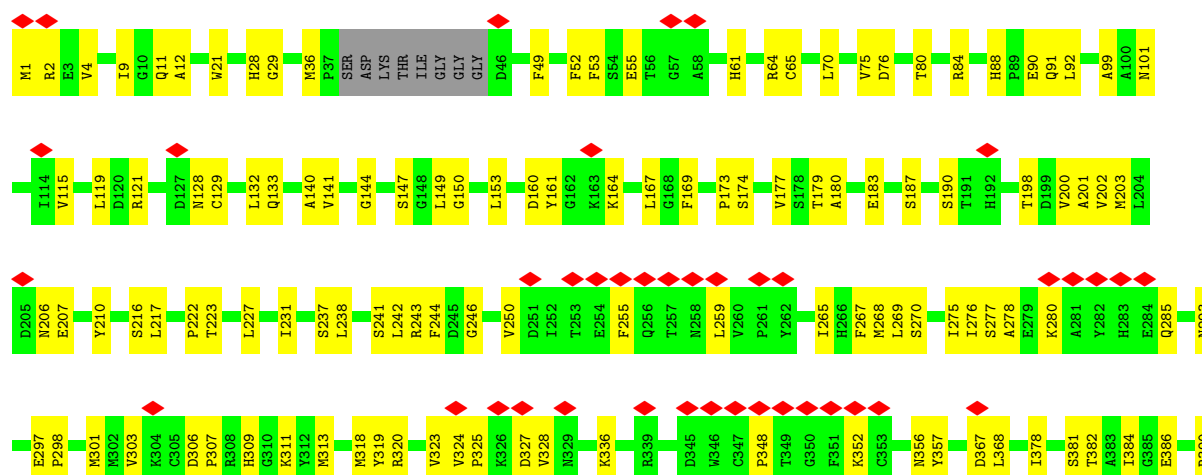


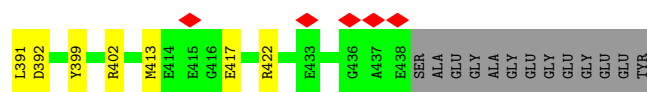


• Molecule 18: Tubulin alpha

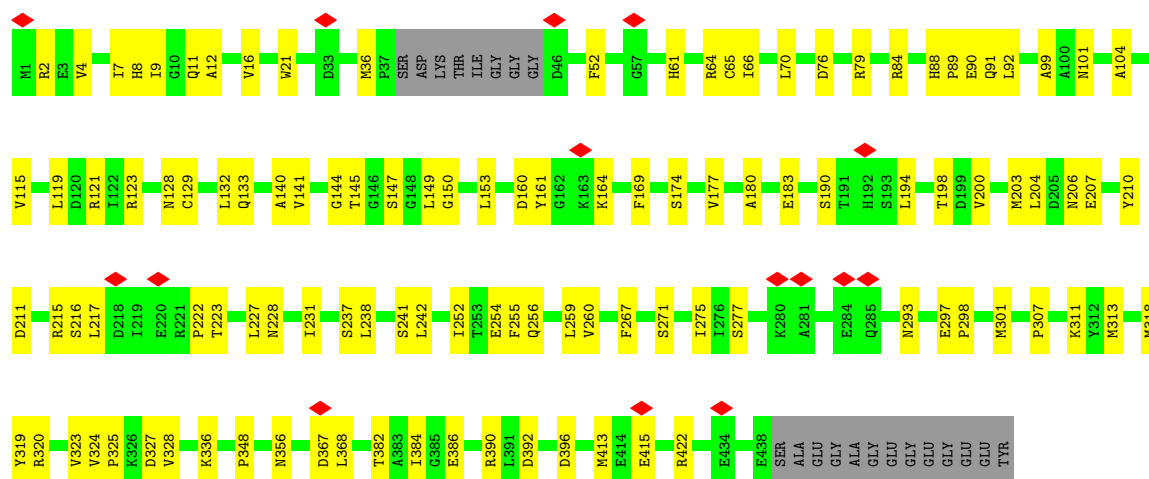


• Molecule 18: Tubulin alpha

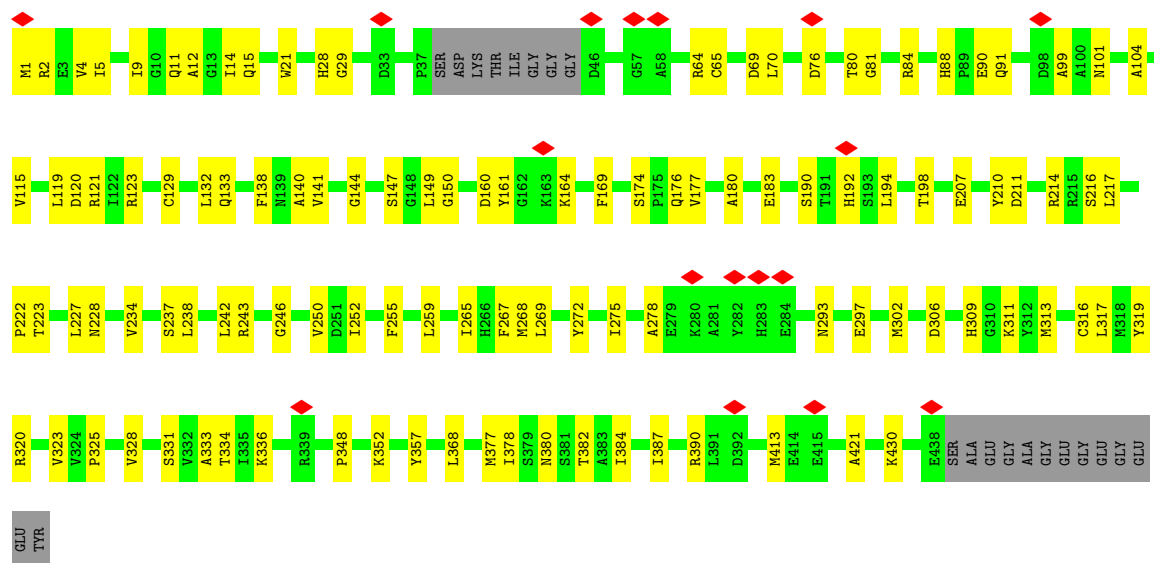




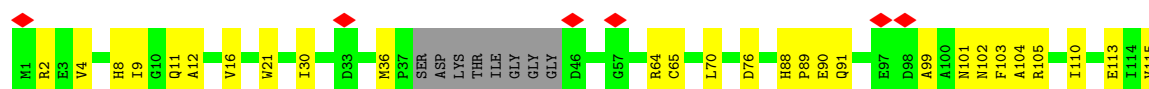
• Molecule 18: Tubulin alpha

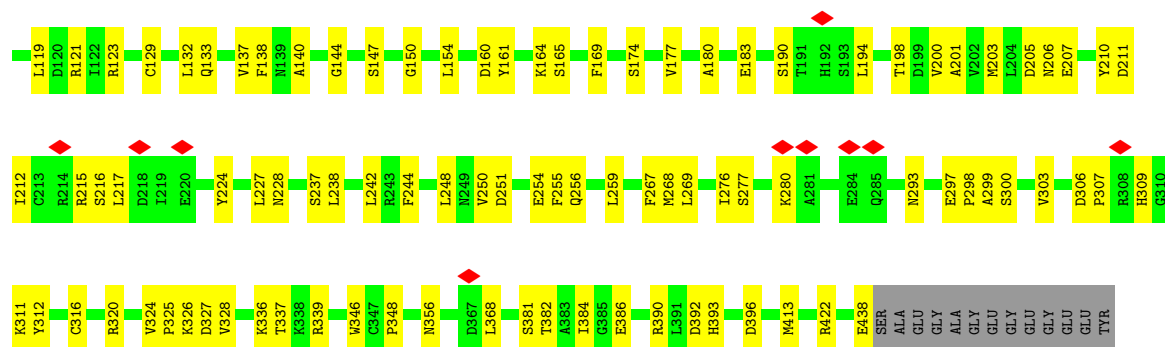


• Molecule 18: Tubulin alpha

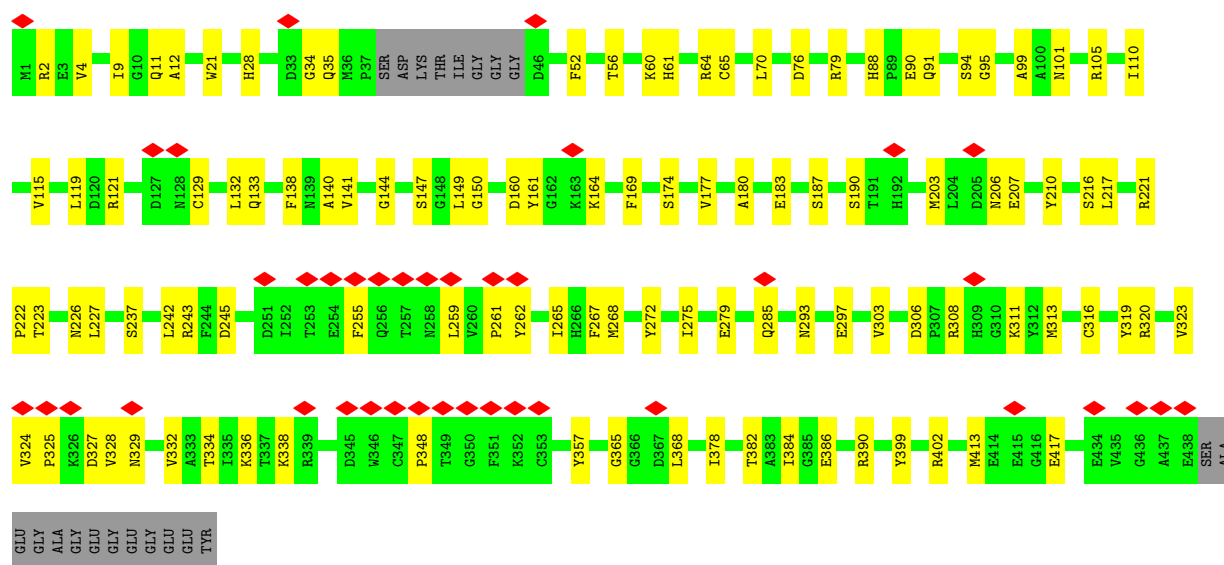


• Molecule 18: Tubulin alpha

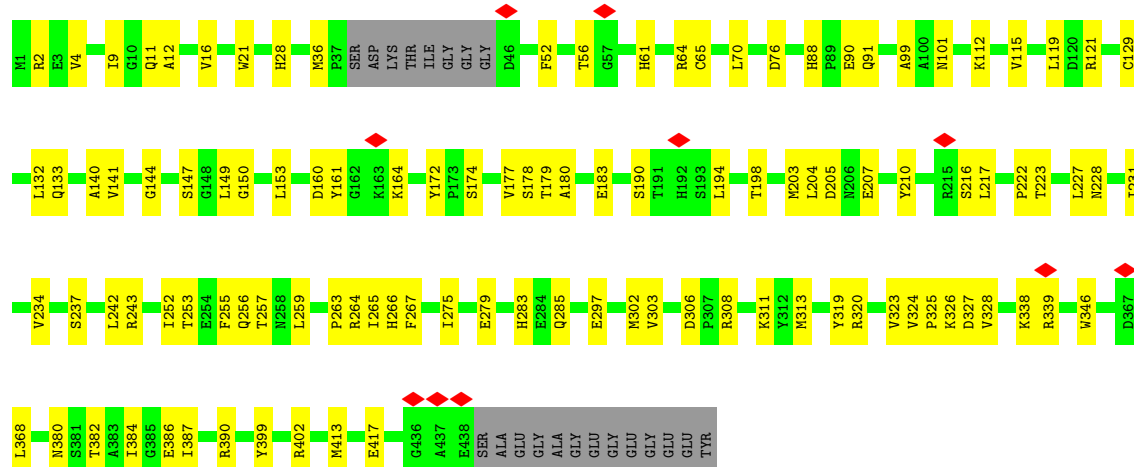




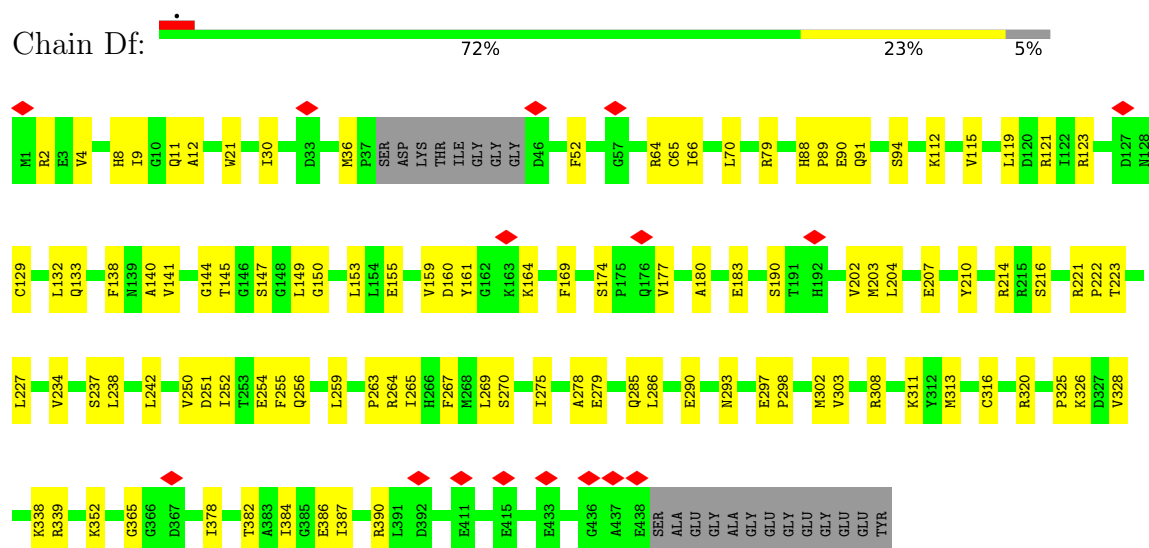
• Molecule 18: Tubulin alpha



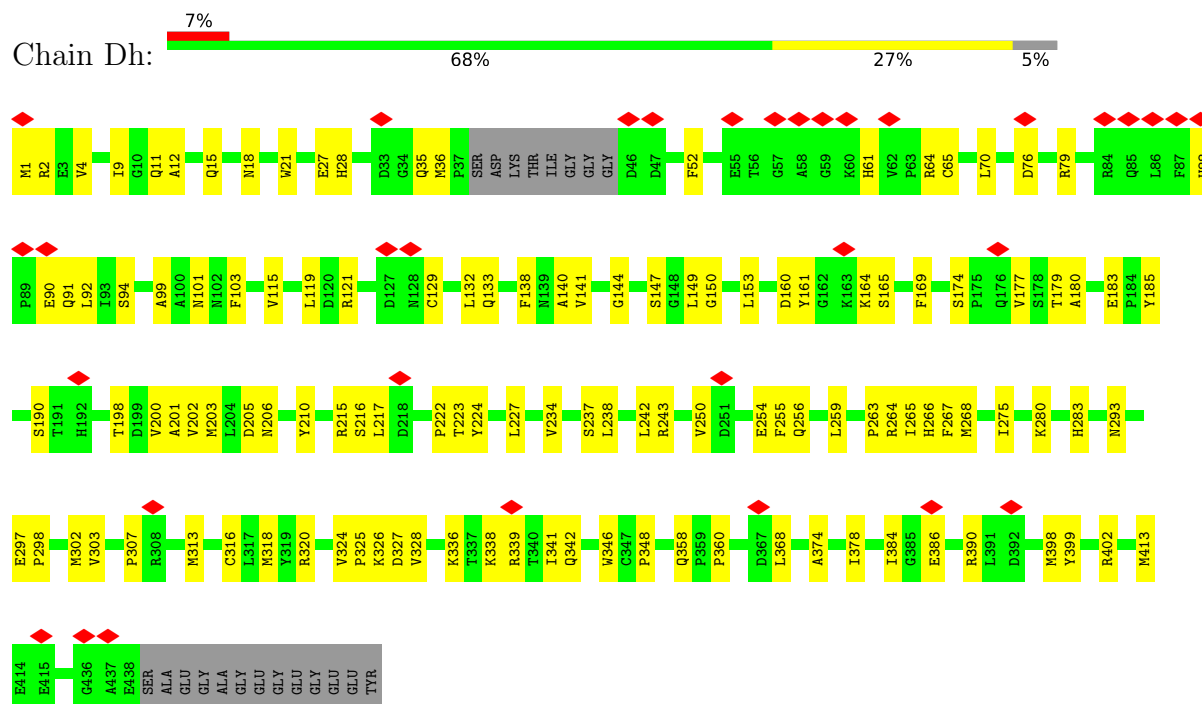
• Molecule 18: Tubulin alpha



• Molecule 18: Tubulin alpha



• Molecule 18: Tubulin alpha



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	192253	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	9.616	Depositor
Minimum map value	0.000	Depositor
Average map value	0.046	Depositor
Map value standard deviation	0.138	Depositor
Recommended contour level	0.5	Depositor
Map size ($\text{\AA}$)	805.9794, 699.57947, 699.57947	wwPDB
Map dimensions	606, 526, 526	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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: GTP, ADP, GDP

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	0.25	0/3738	0.41	0/5058
1	0B	0.16	0/3738	0.38	0/5058
1	0C	0.15	0/3809	0.34	0/5153
1	0D	0.14	0/3809	0.34	0/5153
2	0E	0.16	0/1033	0.32	0/1399
2	0F	0.16	0/1033	0.32	0/1399
2	0G	0.15	0/1033	0.34	0/1399
2	0H	0.22	0/1033	0.39	0/1399
3	0I	0.19	0/3391	0.37	0/4613
3	0J	0.19	0/3391	0.39	0/4613
4	0K	0.15	0/1231	0.40	1/1674 (0.1%)
4	0L	0.13	0/1231	0.38	1/1674 (0.1%)
5	0M	0.14	0/4111	0.31	0/5556
5	0N	0.13	0/4111	0.30	0/5556
6	0O	0.13	0/1501	0.27	0/2016
6	0P	0.15	0/1501	0.30	0/2016
7	0Q	0.15	0/4634	0.36	1/6298 (0.0%)
7	0S	0.14	0/4634	0.37	1/6298 (0.0%)
12	0X	0.17	0/3143	0.41	1/4267 (0.0%)
12	0Y	0.25	0/2945	0.45	0/4003
12	0Z	0.16	0/3143	0.40	1/4267 (0.0%)
12	1A	0.23	0/2945	0.43	0/4003
13	1B	0.16	0/4891	0.34	0/6694
13	1C	0.18	0/4891	0.35	0/6694
14	1D	0.19	0/4141	0.41	0/5670
14	1E	0.15	0/4141	0.35	0/5670
14	1F	0.16	0/4441	0.35	1/6044 (0.0%)
14	1G	0.17	0/4441	0.40	0/6044
17	1a	0.16	0/3453	0.33	0/4673
17	1c	0.17	0/3453	0.32	0/4673
17	1e	0.19	0/3453	0.35	0/4673
17	1g	0.19	0/3453	0.34	0/4673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	2a	0.22	0/3453	0.37	0/4673
17	2c	0.16	0/3453	0.32	0/4673
17	2e	0.16	0/3453	0.31	0/4673
17	2g	0.17	0/3453	0.31	0/4673
17	3a	0.15	0/3453	0.32	0/4673
17	3c	0.17	0/3453	0.32	0/4673
17	3e	0.16	0/3453	0.32	0/4673
17	3g	0.17	0/3453	0.33	0/4673
17	4a	0.15	0/3453	0.32	0/4673
17	4c	0.15	0/3453	0.31	0/4673
17	4e	0.16	0/3453	0.32	0/4673
17	4g	0.16	0/3453	0.32	0/4673
17	5a	0.14	0/3453	0.32	0/4673
17	5c	0.15	0/3453	0.31	0/4673
17	5e	0.15	0/3453	0.33	0/4673
17	5g	0.19	0/3453	0.34	0/4673
17	6a	0.15	0/3453	0.36	0/4673
17	6c	0.14	0/3453	0.33	0/4673
17	6e	0.15	0/3453	0.32	0/4673
17	6g	0.15	0/3453	0.33	0/4673
17	7a	0.14	0/3453	0.32	0/4673
17	7c	0.15	0/3453	0.31	0/4673
17	7e	0.14	0/3453	0.32	0/4673
17	7g	0.15	0/3453	0.33	0/4673
17	8a	0.15	0/3453	0.32	0/4673
17	8c	0.16	0/3453	0.33	0/4673
17	8e	0.16	0/3453	0.32	0/4673
17	8g	0.16	0/3453	0.33	0/4673
17	9a	0.24	0/3453	0.38	0/4673
17	9c	0.22	0/3453	0.35	0/4673
17	9e	0.22	0/3453	0.39	0/4673
17	9g	0.23	0/3453	0.36	0/4673
17	Aa	0.16	0/3453	0.35	0/4673
17	Ac	0.16	0/3453	0.34	0/4673
17	Ae	0.16	0/3453	0.33	0/4673
17	Ag	0.17	0/3453	0.34	0/4673
17	Ba	0.17	0/3453	0.37	0/4673
17	Bc	0.24	0/3453	0.39	0/4673
17	Be	0.17	0/3453	0.34	0/4673
17	Bg	0.23	0/3453	0.37	0/4673
17	Ca	0.16	0/3453	0.32	0/4673
17	Cc	0.20	0/3453	0.36	0/4673
17	Ce	0.19	0/3453	0.34	0/4673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	Cg	0.19	0/3453	0.35	0/4673
17	Da	0.17	0/3453	0.34	0/4673
17	Dc	0.18	0/3453	0.33	0/4673
17	De	0.19	0/3453	0.34	0/4673
17	Dg	0.19	0/3453	0.35	0/4673
18	1b	0.14	0/3410	0.32	0/4623
18	1d	0.17	0/3410	0.33	0/4623
18	1f	0.17	0/3410	0.33	0/4623
18	1h	0.16	0/3410	0.32	0/4623
18	2b	0.15	0/3410	0.31	0/4623
18	2d	0.16	0/3410	0.32	0/4623
18	2f	0.16	0/3410	0.32	0/4623
18	2h	0.16	0/3410	0.31	0/4623
18	3b	0.16	0/3410	0.32	0/4623
18	3d	0.17	0/3410	0.33	0/4623
18	3f	0.15	0/3410	0.33	0/4623
18	3h	0.16	0/3410	0.32	0/4623
18	4b	0.14	0/3410	0.31	0/4623
18	4d	0.15	0/3410	0.33	0/4623
18	4f	0.14	0/3410	0.32	0/4623
18	4h	0.15	0/3410	0.33	0/4623
18	5b	0.14	0/3410	0.33	0/4623
18	5d	0.14	0/3410	0.34	0/4623
18	5f	0.23	0/3410	0.39	0/4623
18	5h	0.15	0/3410	0.34	0/4623
18	6b	0.14	0/3410	0.31	0/4623
18	6d	0.24	0/3410	0.40	0/4623
18	6f	0.16	0/3410	0.33	0/4623
18	6h	0.22	0/3410	0.36	0/4623
18	7b	0.14	0/3410	0.32	0/4623
18	7d	0.23	0/3410	0.37	0/4623
18	7f	0.14	0/3410	0.32	0/4623
18	7h	0.16	0/3410	0.34	0/4623
18	8b	0.15	0/3410	0.32	0/4623
18	8d	0.22	0/3410	0.38	0/4623
18	8f	0.17	0/3410	0.35	0/4623
18	8h	0.15	0/3410	0.31	0/4623
18	9b	0.21	0/3410	0.35	0/4623
18	9d	0.24	0/3410	0.40	0/4623
18	9f	0.22	0/3410	0.36	0/4623
18	9h	0.23	0/3410	0.40	0/4623
18	Ab	0.15	0/3410	0.32	0/4623
18	Ad	0.16	0/3410	0.33	0/4623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	Af	0.16	0/3410	0.32	0/4623
18	Ah	0.15	0/3410	0.32	0/4623
18	Bb	0.17	0/3410	0.33	0/4623
18	Bd	0.21	0/3410	0.38	0/4623
18	Bf	0.19	0/3410	0.37	0/4623
18	Bh	0.21	0/3410	0.37	0/4623
18	Cb	0.17	0/3410	0.33	0/4623
18	Cd	0.18	0/3410	0.33	0/4623
18	Cf	0.18	0/3410	0.34	0/4623
18	Ch	0.19	0/3410	0.34	0/4623
18	Db	0.16	0/3410	0.33	0/4623
18	Dd	0.18	0/3410	0.34	0/4623
18	Df	0.18	0/3410	0.33	0/4623
18	Dh	0.17	0/3410	0.32	0/4623
All	All	0.17	0/444960	0.34	7/603080 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	0X	408	PRO	N-CA-CB	7.43	111.06	103.25
12	0Z	408	PRO	N-CA-CB	7.42	111.04	103.25
4	0K	220	PRO	N-CA-CB	7.02	110.25	103.51
4	0L	220	PRO	N-CA-CB	6.32	110.22	103.52
7	0S	497	ARG	CB-CA-C	-6.32	109.27	116.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0A	3656	0	3589	120	0
1	0B	3656	0	3589	127	0
1	0C	3726	0	3671	139	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0D	3726	0	3671	149	0
2	0E	1008	0	980	31	0
2	0F	1008	0	980	22	0
2	0G	1008	0	980	33	0
2	0H	1008	0	980	21	0
3	0I	3321	0	3319	135	0
3	0J	3321	0	3319	145	0
4	0K	1216	0	1136	50	0
4	0L	1216	0	1136	31	0
5	0M	4037	0	3964	117	0
5	0N	4037	0	3964	91	0
6	0O	1481	0	1456	29	0
6	0P	1481	0	1456	43	0
7	0Q	4537	0	4426	124	0
7	0S	4537	0	4426	130	0
8	0T	845	0	185	13	0
9	0U	850	0	188	11	0
10	0V	800	0	171	18	0
11	0W	195	0	42	3	0
12	0X	3098	0	2933	115	0
12	0Y	2903	0	2675	86	0
12	0Z	3098	0	2933	98	0
12	1A	2903	0	2675	80	0
13	1B	4771	0	4774	170	0
13	1C	4771	0	4774	166	0
14	1D	4079	0	3607	97	0
14	1E	4079	0	3607	84	0
14	1F	4370	0	4195	97	0
14	1G	4370	0	4195	126	0
15	1H	440	0	97	7	0
16	1L	870	0	195	10	0
16	1M	870	0	195	23	0
17	1a	3379	0	3265	94	0
17	1c	3379	0	3265	74	0
17	1e	3379	0	3265	96	0
17	1g	3379	0	3265	97	0
17	2a	3379	0	3265	77	0
17	2c	3379	0	3265	97	0
17	2e	3379	0	3265	80	0
17	2g	3379	0	3265	93	0
17	3a	3379	0	3265	76	0
17	3c	3379	0	3265	101	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	3e	3379	0	3265	78	0
17	3g	3379	0	3265	87	0
17	4a	3379	0	3265	79	0
17	4c	3379	0	3265	71	0
17	4e	3379	0	3265	91	0
17	4g	3379	0	3265	97	0
17	5a	3379	0	3265	93	0
17	5c	3379	0	3265	98	0
17	5e	3379	0	3265	96	0
17	5g	3379	0	3265	90	0
17	6a	3379	0	3265	95	0
17	6c	3379	0	3265	103	0
17	6e	3379	0	3265	91	0
17	6g	3379	0	3265	90	0
17	7a	3379	0	3265	91	0
17	7c	3379	0	3265	89	0
17	7e	3379	0	3265	82	0
17	7g	3379	0	3265	88	0
17	8a	3379	0	3265	78	0
17	8c	3379	0	3265	108	0
17	8e	3379	0	3265	93	0
17	8g	3379	0	3265	101	0
17	9a	3379	0	3265	95	0
17	9c	3379	0	3265	85	0
17	9e	3379	0	3265	108	0
17	9g	3379	0	3265	94	0
17	Aa	3379	0	3265	76	0
17	Ac	3379	0	3265	97	0
17	Ae	3379	0	3265	84	0
17	Ag	3379	0	3265	101	0
17	Ba	3379	0	3265	99	0
17	Bc	3379	0	3265	129	0
17	Be	3379	0	3265	89	0
17	Bg	3379	0	3265	125	0
17	Ca	3379	0	3265	69	0
17	Cc	3379	0	3265	101	0
17	Ce	3379	0	3265	108	0
17	Cg	3379	0	3265	101	0
17	Da	3379	0	3265	95	0
17	Dc	3379	0	3265	83	0
17	De	3379	0	3265	92	0
17	Dg	3379	0	3265	104	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	1b	3339	0	3277	67	0
18	1d	3339	0	3277	83	0
18	1f	3339	0	3277	70	0
18	1h	3339	0	3277	84	0
18	2b	3339	0	3277	73	0
18	2d	3339	0	3277	79	0
18	2f	3339	0	3277	80	0
18	2h	3339	0	3277	80	0
18	3b	3339	0	3277	66	0
18	3d	3339	0	3277	92	0
18	3f	3339	0	3277	81	0
18	3h	3339	0	3277	86	0
18	4b	3339	0	3277	76	0
18	4d	3339	0	3277	78	0
18	4f	3339	0	3277	79	0
18	4h	3339	0	3277	86	0
18	5b	3339	0	3277	76	0
18	5d	3339	0	3277	80	0
18	5f	3339	0	3277	88	0
18	5h	3339	0	3277	80	0
18	6b	3339	0	3277	77	0
18	6d	3339	0	3277	91	0
18	6f	3339	0	3277	91	0
18	6h	3339	0	3277	87	0
18	7b	3339	0	3277	73	0
18	7d	3339	0	3277	79	0
18	7f	3339	0	3277	77	0
18	7h	3339	0	3277	89	0
18	8b	3339	0	3277	66	0
18	8d	3339	0	3277	84	0
18	8f	3339	0	3277	95	0
18	8h	3339	0	3277	84	0
18	9b	3339	0	3277	68	0
18	9d	3339	0	3277	121	0
18	9f	3339	0	3277	74	0
18	9h	3339	0	3277	105	0
18	Ab	3339	0	3277	80	0
18	Ad	3339	0	3277	98	0
18	Af	3339	0	3277	84	0
18	Ah	3339	0	3277	80	0
18	Bb	3339	0	3277	79	0
18	Bd	3339	0	3277	110	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Bf	3339	0	3277	107	0
18	Bh	3339	0	3277	109	0
18	Cb	3339	0	3277	90	0
18	Cd	3339	0	3277	77	0
18	Cf	3339	0	3277	78	0
18	Ch	3339	0	3277	97	0
18	Db	3339	0	3277	71	0
18	Dd	3339	0	3277	80	0
18	Df	3339	0	3277	81	0
18	Dh	3339	0	3277	85	0
19	0X	27	0	12	2	0
19	0Y	27	0	12	4	0
19	0Z	27	0	12	2	0
19	1A	27	0	12	1	0
20	1a	28	0	12	2	0
20	1c	28	0	12	1	0
20	1e	28	0	12	0	0
20	1g	28	0	12	3	0
20	2a	28	0	12	1	0
20	2c	28	0	12	1	0
20	2e	28	0	12	0	0
20	2g	28	0	12	0	0
20	3a	28	0	12	0	0
20	3c	28	0	12	1	0
20	3e	28	0	12	0	0
20	3g	28	0	12	0	0
20	4a	28	0	12	1	0
20	4c	28	0	12	1	0
20	4e	28	0	12	0	0
20	4g	28	0	12	0	0
20	5a	28	0	12	2	0
20	5c	28	0	12	1	0
20	5e	28	0	12	1	0
20	5g	28	0	12	1	0
20	6a	28	0	12	3	0
20	6c	28	0	12	1	0
20	6e	28	0	12	2	0
20	6g	28	0	12	1	0
20	7a	28	0	12	1	0
20	7c	28	0	12	1	0
20	7e	28	0	12	2	0
20	7g	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	8a	28	0	12	2	0
20	8c	28	0	12	1	0
20	8e	28	0	12	1	0
20	8g	28	0	12	1	0
20	9a	28	0	12	0	0
20	9c	28	0	12	3	0
20	9e	28	0	12	1	0
20	9g	28	0	12	0	0
20	Aa	28	0	12	1	0
20	Ac	28	0	12	0	0
20	Ae	28	0	12	0	0
20	Ag	28	0	12	0	0
20	Ba	28	0	12	0	0
20	Bc	28	0	12	0	0
20	Be	28	0	12	0	0
20	Bg	28	0	12	0	0
20	Ca	28	0	12	1	0
20	Cc	28	0	12	2	0
20	Ce	28	0	12	1	0
20	Cg	28	0	12	1	0
20	Da	28	0	12	2	0
20	Dc	28	0	12	0	0
20	De	28	0	12	1	0
20	Dg	28	0	12	1	0
21	1b	32	0	12	3	0
21	1d	32	0	12	4	0
21	1f	32	0	12	3	0
21	1h	32	0	12	2	0
21	2b	32	0	12	2	0
21	2d	32	0	12	5	0
21	2f	32	0	12	4	0
21	2h	32	0	12	3	0
21	3b	32	0	12	4	0
21	3d	32	0	12	5	0
21	3f	32	0	12	4	0
21	3h	32	0	12	2	0
21	4b	32	0	12	4	0
21	4d	32	0	12	2	0
21	4f	32	0	12	2	0
21	4h	32	0	12	2	0
21	5b	32	0	12	2	0
21	5d	32	0	12	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	5f	32	0	12	1	0
21	5h	32	0	12	3	0
21	6b	32	0	12	6	0
21	6d	32	0	12	6	0
21	6f	32	0	12	3	0
21	6h	32	0	12	4	0
21	7b	32	0	12	4	0
21	7d	32	0	12	3	0
21	7f	32	0	12	3	0
21	7h	32	0	12	2	0
21	8b	32	0	12	3	0
21	8d	32	0	12	4	0
21	8f	32	0	12	6	0
21	8h	32	0	12	4	0
21	9b	32	0	12	3	0
21	9d	32	0	12	4	0
21	9f	32	0	12	4	0
21	9h	32	0	12	4	0
21	Ab	32	0	12	2	0
21	Ad	32	0	12	1	0
21	Af	32	0	12	2	0
21	Ah	32	0	12	3	0
21	Bb	32	0	12	4	0
21	Bd	32	0	12	3	0
21	Bf	32	0	12	4	0
21	Bh	32	0	12	2	0
21	Cb	32	0	12	5	0
21	Cd	32	0	12	5	0
21	Cf	32	0	12	4	0
21	Ch	32	0	12	4	0
21	Db	32	0	12	5	0
21	Dd	32	0	12	3	0
21	Df	32	0	12	4	0
21	Dh	32	0	12	3	0
All	All	443856	0	425963	10696	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 10696 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1B:1659:ALA:HB2	16:1M:22:UNK:CB	1.25	1.57
13:1B:1659:ALA:CB	16:1M:22:UNK:CB	2.19	1.20
13:1B:1650:GLU:OE1	16:1M:30:UNK:O	1.69	1.10
17:5e:220:PRO:HG2	18:5f:326:LYS:HE2	1.39	1.00
18:Bh:215:ARG:HH22	18:Bh:300:SER:HA	1.27	0.97

There are no symmetry-related clashes.

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	463/606 (76%)	447 (96%)	16 (4%)	0	100	100
1	0B	463/606 (76%)	449 (97%)	14 (3%)	0	100	100
1	0C	472/606 (78%)	454 (96%)	18 (4%)	0	100	100
1	0D	472/606 (78%)	458 (97%)	14 (3%)	0	100	100
2	0E	126/222 (57%)	122 (97%)	4 (3%)	0	100	100
2	0F	126/222 (57%)	121 (96%)	5 (4%)	0	100	100
2	0G	126/222 (57%)	122 (97%)	4 (3%)	0	100	100
2	0H	126/222 (57%)	121 (96%)	5 (4%)	0	100	100
3	0I	442/976 (45%)	424 (96%)	17 (4%)	1 (0%)	43	74
3	0J	442/976 (45%)	426 (96%)	15 (3%)	1 (0%)	43	74
4	0K	164/528 (31%)	162 (99%)	2 (1%)	0	100	100
4	0L	164/528 (31%)	161 (98%)	3 (2%)	0	100	100
5	0M	507/758 (67%)	488 (96%)	19 (4%)	0	100	100
5	0N	507/758 (67%)	491 (97%)	16 (3%)	0	100	100
6	0O	184/201 (92%)	180 (98%)	4 (2%)	0	100	100
6	0P	184/201 (92%)	180 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	0Q	615/618 (100%)	564 (92%)	51 (8%)	0	100	100
7	0S	615/618 (100%)	566 (92%)	49 (8%)	0	100	100
12	0X	418/776 (54%)	390 (93%)	26 (6%)	2 (0%)	24	57
12	0Y	400/776 (52%)	371 (93%)	25 (6%)	4 (1%)	12	44
12	0Z	418/776 (54%)	390 (93%)	26 (6%)	2 (0%)	24	57
12	1A	400/776 (52%)	373 (93%)	24 (6%)	3 (1%)	16	49
13	1B	624/2257 (28%)	595 (95%)	29 (5%)	0	100	100
13	1C	624/2257 (28%)	595 (95%)	29 (5%)	0	100	100
14	1D	617/1074 (57%)	584 (95%)	33 (5%)	0	100	100
14	1E	617/1074 (57%)	584 (95%)	33 (5%)	0	100	100
14	1F	608/1074 (57%)	576 (95%)	32 (5%)	0	100	100
14	1G	608/1074 (57%)	573 (94%)	35 (6%)	0	100	100
17	1a	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	1c	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	1e	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	1g	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	2a	429/443 (97%)	418 (97%)	11 (3%)	0	100	100
17	2c	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	2e	429/443 (97%)	418 (97%)	11 (3%)	0	100	100
17	2g	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	3a	429/443 (97%)	422 (98%)	7 (2%)	0	100	100
17	3c	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	3e	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	3g	429/443 (97%)	422 (98%)	7 (2%)	0	100	100
17	4a	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	4c	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	4e	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	4g	429/443 (97%)	418 (97%)	11 (3%)	0	100	100
17	5a	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	5c	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	5e	429/443 (97%)	418 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	5g	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	6a	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	6c	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	6e	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	6g	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	7a	429/443 (97%)	418 (97%)	11 (3%)	0	100	100
17	7c	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	7e	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	7g	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	8a	429/443 (97%)	418 (97%)	11 (3%)	0	100	100
17	8c	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	8e	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	8g	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	9a	429/443 (97%)	418 (97%)	11 (3%)	0	100	100
17	9c	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	9e	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	9g	429/443 (97%)	417 (97%)	12 (3%)	0	100	100
17	Aa	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	Ac	429/443 (97%)	422 (98%)	7 (2%)	0	100	100
17	Ae	429/443 (97%)	422 (98%)	7 (2%)	0	100	100
17	Ag	429/443 (97%)	422 (98%)	7 (2%)	0	100	100
17	Ba	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	Bc	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	Be	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	Bg	429/443 (97%)	420 (98%)	9 (2%)	0	100	100
17	Ca	429/443 (97%)	422 (98%)	7 (2%)	0	100	100
17	Cc	429/443 (97%)	418 (97%)	11 (3%)	0	100	100
17	Ce	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	Cg	429/443 (97%)	414 (96%)	15 (4%)	0	100	100
17	Da	429/443 (97%)	421 (98%)	8 (2%)	0	100	100
17	Dc	429/443 (97%)	420 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	De	429/443 (97%)	419 (98%)	10 (2%)	0	100	100
17	Dg	429/443 (97%)	418 (97%)	11 (3%)	0	100	100
18	1b	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	1d	426/451 (94%)	416 (98%)	10 (2%)	0	100	100
18	1f	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	1h	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
18	2b	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	2d	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
18	2f	426/451 (94%)	411 (96%)	15 (4%)	0	100	100
18	2h	426/451 (94%)	416 (98%)	10 (2%)	0	100	100
18	3b	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
18	3d	426/451 (94%)	413 (97%)	13 (3%)	0	100	100
18	3f	426/451 (94%)	417 (98%)	9 (2%)	0	100	100
18	3h	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
18	4b	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	4d	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	4f	426/451 (94%)	416 (98%)	10 (2%)	0	100	100
18	4h	426/451 (94%)	411 (96%)	15 (4%)	0	100	100
18	5b	426/451 (94%)	416 (98%)	10 (2%)	0	100	100
18	5d	426/451 (94%)	416 (98%)	10 (2%)	0	100	100
18	5f	426/451 (94%)	420 (99%)	6 (1%)	0	100	100
18	5h	426/451 (94%)	411 (96%)	15 (4%)	0	100	100
18	6b	426/451 (94%)	417 (98%)	9 (2%)	0	100	100
18	6d	426/451 (94%)	413 (97%)	13 (3%)	0	100	100
18	6f	426/451 (94%)	416 (98%)	10 (2%)	0	100	100
18	6h	426/451 (94%)	416 (98%)	10 (2%)	0	100	100
18	7b	426/451 (94%)	417 (98%)	9 (2%)	0	100	100
18	7d	426/451 (94%)	417 (98%)	9 (2%)	0	100	100
18	7f	426/451 (94%)	412 (97%)	14 (3%)	0	100	100
18	7h	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
18	8b	426/451 (94%)	416 (98%)	10 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	8d	426/451 (94%)	416 (98%)	10 (2%)	0	100	100
18	8f	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	8h	426/451 (94%)	417 (98%)	9 (2%)	0	100	100
18	9b	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
18	9d	426/451 (94%)	413 (97%)	13 (3%)	0	100	100
18	9f	426/451 (94%)	412 (97%)	14 (3%)	0	100	100
18	9h	426/451 (94%)	411 (96%)	15 (4%)	0	100	100
18	Ab	426/451 (94%)	417 (98%)	9 (2%)	0	100	100
18	Ad	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
18	Af	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	Ah	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
18	Bb	426/451 (94%)	419 (98%)	7 (2%)	0	100	100
18	Bd	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	Bf	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
18	Bh	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	Cb	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	Cd	426/451 (94%)	418 (98%)	8 (2%)	0	100	100
18	Cf	426/451 (94%)	418 (98%)	8 (2%)	0	100	100
18	Ch	426/451 (94%)	412 (97%)	14 (3%)	0	100	100
18	Db	426/451 (94%)	419 (98%)	7 (2%)	0	100	100
18	Dd	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
18	Df	426/451 (94%)	416 (98%)	10 (2%)	0	100	100
18	Dh	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
All	All	55992/67876 (82%)	54371 (97%)	1608 (3%)	13 (0%)	100	100

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	0X	233	VAL
12	0X	408	PRO
12	0Y	408	PRO
12	0Z	233	VAL
12	0Z	408	PRO

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	389/482 (81%)	388 (100%)	1 (0%)	86	83
1	0B	389/482 (81%)	389 (100%)	0	100	100
1	0C	397/482 (82%)	397 (100%)	0	100	100
1	0D	397/482 (82%)	397 (100%)	0	100	100
2	0E	106/166 (64%)	106 (100%)	0	100	100
2	0F	106/166 (64%)	106 (100%)	0	100	100
2	0G	106/166 (64%)	106 (100%)	0	100	100
2	0H	106/166 (64%)	106 (100%)	0	100	100
3	0I	325/697 (47%)	324 (100%)	1 (0%)	86	83
3	0J	325/697 (47%)	325 (100%)	0	100	100
4	0K	113/410 (28%)	113 (100%)	0	100	100
4	0L	113/410 (28%)	113 (100%)	0	100	100
5	0M	426/598 (71%)	426 (100%)	0	100	100
5	0N	426/598 (71%)	426 (100%)	0	100	100
6	0O	152/159 (96%)	152 (100%)	0	100	100
6	0P	152/159 (96%)	152 (100%)	0	100	100
7	0Q	461/462 (100%)	461 (100%)	0	100	100
7	0S	461/462 (100%)	461 (100%)	0	100	100
12	0X	306/600 (51%)	305 (100%)	1 (0%)	86	83
12	0Y	274/600 (46%)	272 (99%)	2 (1%)	76	78
12	0Z	306/600 (51%)	306 (100%)	0	100	100
12	1A	274/600 (46%)	273 (100%)	1 (0%)	84	81
13	1B	487/1666 (29%)	487 (100%)	0	100	100
13	1C	487/1666 (29%)	487 (100%)	0	100	100
14	1D	291/753 (39%)	290 (100%)	1 (0%)	86	83
14	1E	291/753 (39%)	291 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	1F	373/753 (50%)	373 (100%)	0	100	100
14	1G	373/753 (50%)	373 (100%)	0	100	100
17	1a	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	1c	370/379 (98%)	370 (100%)	0	100	100
17	1e	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	1g	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	2a	370/379 (98%)	370 (100%)	0	100	100
17	2c	370/379 (98%)	370 (100%)	0	100	100
17	2e	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	2g	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	3a	370/379 (98%)	370 (100%)	0	100	100
17	3c	370/379 (98%)	370 (100%)	0	100	100
17	3e	370/379 (98%)	370 (100%)	0	100	100
17	3g	370/379 (98%)	370 (100%)	0	100	100
17	4a	370/379 (98%)	370 (100%)	0	100	100
17	4c	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	4e	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	4g	370/379 (98%)	370 (100%)	0	100	100
17	5a	370/379 (98%)	370 (100%)	0	100	100
17	5c	370/379 (98%)	370 (100%)	0	100	100
17	5e	370/379 (98%)	370 (100%)	0	100	100
17	5g	370/379 (98%)	368 (100%)	2 (0%)	81	80
17	6a	370/379 (98%)	370 (100%)	0	100	100
17	6c	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	6e	370/379 (98%)	370 (100%)	0	100	100
17	6g	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	7a	370/379 (98%)	370 (100%)	0	100	100
17	7c	370/379 (98%)	370 (100%)	0	100	100
17	7e	370/379 (98%)	370 (100%)	0	100	100
17	7g	370/379 (98%)	370 (100%)	0	100	100
17	8a	370/379 (98%)	370 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	8c	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	8e	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	8g	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	9a	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	9c	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	9e	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	9g	370/379 (98%)	370 (100%)	0	100	100
17	Aa	370/379 (98%)	370 (100%)	0	100	100
17	Ac	370/379 (98%)	370 (100%)	0	100	100
17	Ae	370/379 (98%)	370 (100%)	0	100	100
17	Ag	370/379 (98%)	370 (100%)	0	100	100
17	Ba	370/379 (98%)	370 (100%)	0	100	100
17	Bc	370/379 (98%)	370 (100%)	0	100	100
17	Be	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	Bg	370/379 (98%)	370 (100%)	0	100	100
17	Ca	370/379 (98%)	370 (100%)	0	100	100
17	Cc	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	Ce	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	Cg	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	Da	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	Dc	370/379 (98%)	370 (100%)	0	100	100
17	De	370/379 (98%)	369 (100%)	1 (0%)	86	83
17	Dg	370/379 (98%)	369 (100%)	1 (0%)	86	83
18	1b	361/374 (96%)	361 (100%)	0	100	100
18	1d	361/374 (96%)	361 (100%)	0	100	100
18	1f	361/374 (96%)	361 (100%)	0	100	100
18	1h	361/374 (96%)	361 (100%)	0	100	100
18	2b	361/374 (96%)	361 (100%)	0	100	100
18	2d	361/374 (96%)	361 (100%)	0	100	100
18	2f	361/374 (96%)	361 (100%)	0	100	100
18	2h	361/374 (96%)	361 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	3b	361/374 (96%)	361 (100%)	0	100	100
18	3d	361/374 (96%)	361 (100%)	0	100	100
18	3f	361/374 (96%)	361 (100%)	0	100	100
18	3h	361/374 (96%)	361 (100%)	0	100	100
18	4b	361/374 (96%)	361 (100%)	0	100	100
18	4d	361/374 (96%)	361 (100%)	0	100	100
18	4f	361/374 (96%)	361 (100%)	0	100	100
18	4h	361/374 (96%)	361 (100%)	0	100	100
18	5b	361/374 (96%)	361 (100%)	0	100	100
18	5d	361/374 (96%)	361 (100%)	0	100	100
18	5f	361/374 (96%)	358 (99%)	3 (1%)	73	77
18	5h	361/374 (96%)	361 (100%)	0	100	100
18	6b	361/374 (96%)	361 (100%)	0	100	100
18	6d	361/374 (96%)	361 (100%)	0	100	100
18	6f	361/374 (96%)	360 (100%)	1 (0%)	86	83
18	6h	361/374 (96%)	361 (100%)	0	100	100
18	7b	361/374 (96%)	361 (100%)	0	100	100
18	7d	361/374 (96%)	361 (100%)	0	100	100
18	7f	361/374 (96%)	361 (100%)	0	100	100
18	7h	361/374 (96%)	361 (100%)	0	100	100
18	8b	361/374 (96%)	361 (100%)	0	100	100
18	8d	361/374 (96%)	361 (100%)	0	100	100
18	8f	361/374 (96%)	361 (100%)	0	100	100
18	8h	361/374 (96%)	361 (100%)	0	100	100
18	9b	361/374 (96%)	361 (100%)	0	100	100
18	9d	361/374 (96%)	361 (100%)	0	100	100
18	9f	361/374 (96%)	361 (100%)	0	100	100
18	9h	361/374 (96%)	360 (100%)	1 (0%)	86	83
18	Ab	361/374 (96%)	361 (100%)	0	100	100
18	Ad	361/374 (96%)	361 (100%)	0	100	100
18	Af	361/374 (96%)	361 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	Ah	361/374 (96%)	361 (100%)	0	100	100
18	Bb	361/374 (96%)	361 (100%)	0	100	100
18	Bd	361/374 (96%)	361 (100%)	0	100	100
18	Bf	361/374 (96%)	361 (100%)	0	100	100
18	Bh	361/374 (96%)	361 (100%)	0	100	100
18	Cb	361/374 (96%)	361 (100%)	0	100	100
18	Cd	361/374 (96%)	361 (100%)	0	100	100
18	Cf	361/374 (96%)	361 (100%)	0	100	100
18	Ch	361/374 (96%)	361 (100%)	0	100	100
18	Db	361/374 (96%)	361 (100%)	0	100	100
18	Dd	361/374 (96%)	361 (100%)	0	100	100
18	Df	361/374 (96%)	361 (100%)	0	100	100
18	Dh	361/374 (96%)	361 (100%)	0	100	100
All	All	46424/55144 (84%)	46388 (100%)	36 (0%)	87	87

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	9h	50	ASN
17	Dg	247	ASN
17	Be	247	ASN
17	Cg	247	ASN
17	4c	247	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 581 such sidechains are listed below:

Mol	Chain	Res	Type
18	Bb	50	ASN
17	Dg	347	ASN
18	Bd	31	GLN
18	Bb	31	GLN
17	Ce	134	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

108 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	$\# Z > 2$
20	GDP	8e	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.75	7 (15%)
21	GTP	9b	501	-	33,34,34	0.98	3 (9%)	50,54,54	1.61	9 (18%)
21	GTP	Df	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.59	10 (20%)
21	GTP	7d	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.57	9 (18%)
20	GDP	3g	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
21	GTP	5b	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.58	9 (18%)
20	GDP	2a	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
20	GDP	4a	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
20	GDP	9g	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
21	GTP	9d	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.61	9 (18%)
20	GDP	6c	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.74	7 (15%)
21	GTP	1h	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.58	9 (18%)
21	GTP	6d	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.59	10 (20%)
19	ADP	0Y	801	-	28,29,29	1.41	4 (14%)	43,45,45	1.82	9 (20%)
21	GTP	2b	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.59	8 (16%)
20	GDP	Bg	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
20	GDP	6g	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
21	GTP	6h	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.57	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	GTP	9f	501	-	33,34,34	0.99	3 (9%)	50,54,54	1.61	10 (20%)
19	ADP	0X	801	-	28,29,29	1.39	4 (14%)	43,45,45	1.81	8 (18%)
21	GTP	Ad	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.59	10 (20%)
20	GDP	Da	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
20	GDP	4e	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
20	GDP	8c	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.75	7 (15%)
20	GDP	6a	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
21	GTP	4f	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.57	9 (18%)
21	GTP	4b	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.58	9 (18%)
21	GTP	4h	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.57	10 (20%)
21	GTP	3b	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.62	10 (20%)
21	GTP	2d	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.58	9 (18%)
20	GDP	De	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
20	GDP	4c	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
20	GDP	Ac	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
21	GTP	Bb	501	-	33,34,34	0.93	2 (6%)	50,54,54	1.59	9 (18%)
20	GDP	2e	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
20	GDP	Ca	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.75	7 (15%)
21	GTP	5h	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.60	9 (18%)
21	GTP	6b	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.58	9 (18%)
20	GDP	1c	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
20	GDP	7c	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
20	GDP	5e	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
21	GTP	1d	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.59	9 (18%)
21	GTP	Db	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.58	10 (20%)
21	GTP	5d	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.58	10 (20%)
20	GDP	5c	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
21	GTP	Ah	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.58	9 (18%)
21	GTP	2h	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.56	9 (18%)
21	GTP	Cb	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.58	10 (20%)
20	GDP	Ba	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
21	GTP	3d	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.59	10 (20%)
21	GTP	Ab	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.59	10 (20%)
20	GDP	Dc	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
20	GDP	1e	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
20	GDP	6e	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
20	GDP	7e	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.75	6 (13%)
19	ADP	1A	801	-	28,29,29	1.41	4 (14%)	43,45,45	1.82	9 (20%)
20	GDP	9a	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
20	GDP	1g	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.72	7 (15%)
20	GDP	3a	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
19	ADP	0Z	801	-	28,29,29	1.39	4 (14%)	43,45,45	1.81	8 (18%)
20	GDP	1a	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
21	GTP	9h	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.61	8 (16%)
20	GDP	Ae	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
21	GTP	Cf	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.58	9 (18%)
21	GTP	2f	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.59	10 (20%)
21	GTP	7b	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.57	9 (18%)
20	GDP	2c	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
20	GDP	Aa	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.76	7 (15%)
20	GDP	7g	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
21	GTP	6f	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.57	8 (16%)
20	GDP	2g	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
20	GDP	3e	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
21	GTP	Bf	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.60	9 (18%)
21	GTP	Cd	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.62	9 (18%)
20	GDP	9e	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	6 (13%)
21	GTP	1f	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.59	9 (18%)
21	GTP	Ch	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.61	10 (20%)
21	GTP	5f	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.58	9 (18%)
20	GDP	Cc	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.79	7 (15%)
21	GTP	Af	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.60	10 (20%)
20	GDP	Cg	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
21	GTP	7h	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.58	9 (18%)
20	GDP	8a	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
21	GTP	Dd	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.59	9 (18%)
20	GDP	Bc	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
21	GTP	3f	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.58	10 (20%)
21	GTP	3h	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.55	10 (20%)
21	GTP	8f	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.56	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
20	GDP	3c	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
21	GTP	1b	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.57	9 (18%)
20	GDP	5a	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.80	7 (15%)
21	GTP	Bh	501	-	33,34,34	1.01	3 (9%)	50,54,54	1.59	9 (18%)
20	GDP	Ag	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
20	GDP	Dg	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
20	GDP	4g	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
21	GTP	Bd	501	-	33,34,34	1.01	3 (9%)	50,54,54	1.61	10 (20%)
21	GTP	8b	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.59	10 (20%)
20	GDP	7a	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
21	GTP	8h	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.57	9 (18%)
21	GTP	7f	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.57	8 (16%)
21	GTP	4d	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.60	8 (16%)
20	GDP	5g	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.79	7 (15%)
21	GTP	Dh	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.60	9 (18%)
20	GDP	Be	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
20	GDP	8g	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
20	GDP	9c	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.77	7 (15%)
20	GDP	Ce	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
21	GTP	8d	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.59	10 (20%)

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
20	GDP	8e	501	-	-	3/16/32/32	0/3/3/3
21	GTP	9b	501	-	-	3/22/38/38	0/3/3/3
21	GTP	Df	501	-	-	3/22/38/38	0/3/3/3
21	GTP	7d	501	-	-	3/22/38/38	0/3/3/3
20	GDP	3g	501	-	-	3/16/32/32	0/3/3/3
21	GTP	5b	501	-	-	3/22/38/38	0/3/3/3
20	GDP	2a	501	-	-	3/16/32/32	0/3/3/3
20	GDP	4a	501	-	-	3/16/32/32	0/3/3/3
20	GDP	9g	501	-	-	3/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	GTP	9d	501	-	-	3/22/38/38	0/3/3/3
20	GDP	6c	501	-	-	3/16/32/32	0/3/3/3
21	GTP	1h	501	-	-	2/22/38/38	0/3/3/3
21	GTP	6d	501	-	-	3/22/38/38	0/3/3/3
19	ADP	0Y	801	-	-	9/16/32/32	0/3/3/3
21	GTP	2b	501	-	-	2/22/38/38	0/3/3/3
20	GDP	Bg	501	-	-	3/16/32/32	0/3/3/3
20	GDP	6g	501	-	-	3/16/32/32	0/3/3/3
21	GTP	6h	501	-	-	3/22/38/38	0/3/3/3
21	GTP	9f	501	-	-	3/22/38/38	0/3/3/3
19	ADP	0X	801	-	-	5/16/32/32	0/3/3/3
21	GTP	Ad	501	-	-	3/22/38/38	0/3/3/3
20	GDP	Da	501	-	-	3/16/32/32	0/3/3/3
20	GDP	4e	501	-	-	3/16/32/32	0/3/3/3
20	GDP	8c	501	-	-	3/16/32/32	0/3/3/3
20	GDP	6a	501	-	-	3/16/32/32	0/3/3/3
21	GTP	4f	501	-	-	3/22/38/38	0/3/3/3
21	GTP	4b	501	-	-	3/22/38/38	0/3/3/3
21	GTP	4h	501	-	-	2/22/38/38	0/3/3/3
21	GTP	3b	501	-	-	2/22/38/38	0/3/3/3
21	GTP	2d	501	-	-	3/22/38/38	0/3/3/3
20	GDP	De	501	-	-	3/16/32/32	0/3/3/3
20	GDP	4c	501	-	-	3/16/32/32	0/3/3/3
20	GDP	Ac	501	-	-	3/16/32/32	0/3/3/3
21	GTP	Bb	501	-	-	3/22/38/38	0/3/3/3
20	GDP	2e	501	-	-	3/16/32/32	0/3/3/3
20	GDP	Ca	501	-	-	3/16/32/32	0/3/3/3
21	GTP	5h	501	-	-	3/22/38/38	0/3/3/3
21	GTP	6b	501	-	-	3/22/38/38	0/3/3/3
20	GDP	1c	501	-	-	3/16/32/32	0/3/3/3
20	GDP	7c	501	-	-	3/16/32/32	0/3/3/3
20	GDP	5e	501	-	-	3/16/32/32	0/3/3/3
21	GTP	1d	501	-	-	2/22/38/38	0/3/3/3
21	GTP	Db	501	-	-	3/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	GTP	5d	501	-	-	3/22/38/38	0/3/3/3
20	GDP	5c	501	-	-	3/16/32/32	0/3/3/3
21	GTP	Ah	501	-	-	2/22/38/38	0/3/3/3
21	GTP	2h	501	-	-	2/22/38/38	0/3/3/3
21	GTP	Cb	501	-	-	3/22/38/38	0/3/3/3
20	GDP	Ba	501	-	-	3/16/32/32	0/3/3/3
21	GTP	3d	501	-	-	3/22/38/38	0/3/3/3
21	GTP	Ab	501	-	-	3/22/38/38	0/3/3/3
20	GDP	Dc	501	-	-	3/16/32/32	0/3/3/3
20	GDP	1e	501	-	-	3/16/32/32	0/3/3/3
20	GDP	6e	501	-	-	3/16/32/32	0/3/3/3
20	GDP	7e	501	-	-	3/16/32/32	0/3/3/3
19	ADP	1A	801	-	-	7/16/32/32	0/3/3/3
20	GDP	9a	501	-	-	3/16/32/32	0/3/3/3
20	GDP	1g	501	-	-	3/16/32/32	0/3/3/3
20	GDP	3a	501	-	-	3/16/32/32	0/3/3/3
19	ADP	0Z	801	-	-	5/16/32/32	0/3/3/3
20	GDP	1a	501	-	-	3/16/32/32	0/3/3/3
21	GTP	9h	501	-	-	3/22/38/38	0/3/3/3
20	GDP	Ae	501	-	-	3/16/32/32	0/3/3/3
21	GTP	Cf	501	-	-	3/22/38/38	0/3/3/3
21	GTP	2f	501	-	-	3/22/38/38	0/3/3/3
21	GTP	7b	501	-	-	3/22/38/38	0/3/3/3
20	GDP	2c	501	-	-	3/16/32/32	0/3/3/3
20	GDP	Aa	501	-	-	3/16/32/32	0/3/3/3
20	GDP	7g	501	-	-	3/16/32/32	0/3/3/3
21	GTP	6f	501	-	-	3/22/38/38	0/3/3/3
20	GDP	2g	501	-	-	3/16/32/32	0/3/3/3
20	GDP	3e	501	-	-	3/16/32/32	0/3/3/3
21	GTP	Bf	501	-	-	3/22/38/38	0/3/3/3
21	GTP	Cd	501	-	-	2/22/38/38	0/3/3/3
20	GDP	9e	501	-	-	3/16/32/32	0/3/3/3
21	GTP	1f	501	-	-	2/22/38/38	0/3/3/3
21	GTP	Ch	501	-	-	3/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	GTP	5f	501	-	-	3/22/38/38	0/3/3/3
20	GDP	Cc	501	-	-	3/16/32/32	0/3/3/3
21	GTP	Af	501	-	-	3/22/38/38	0/3/3/3
20	GDP	Cg	501	-	-	3/16/32/32	0/3/3/3
21	GTP	7h	501	-	-	3/22/38/38	0/3/3/3
20	GDP	8a	501	-	-	3/16/32/32	0/3/3/3
21	GTP	Dd	501	-	-	2/22/38/38	0/3/3/3
20	GDP	Bc	501	-	-	3/16/32/32	0/3/3/3
21	GTP	3f	501	-	-	3/22/38/38	0/3/3/3
21	GTP	3h	501	-	-	3/22/38/38	0/3/3/3
21	GTP	8f	501	-	-	3/22/38/38	0/3/3/3
20	GDP	3c	501	-	-	3/16/32/32	0/3/3/3
21	GTP	1b	501	-	-	3/22/38/38	0/3/3/3
20	GDP	5a	501	-	-	3/16/32/32	0/3/3/3
21	GTP	Bh	501	-	-	3/22/38/38	0/3/3/3
20	GDP	Ag	501	-	-	3/16/32/32	0/3/3/3
20	GDP	Dg	501	-	-	3/16/32/32	0/3/3/3
20	GDP	4g	501	-	-	3/16/32/32	0/3/3/3
21	GTP	Bd	501	-	-	2/22/38/38	0/3/3/3
21	GTP	8b	501	-	-	3/22/38/38	0/3/3/3
20	GDP	7a	501	-	-	3/16/32/32	0/3/3/3
21	GTP	8h	501	-	-	3/22/38/38	0/3/3/3
21	GTP	7f	501	-	-	2/22/38/38	0/3/3/3
21	GTP	4d	501	-	-	3/22/38/38	0/3/3/3
20	GDP	5g	501	-	-	2/16/32/32	0/3/3/3
21	GTP	Dh	501	-	-	2/22/38/38	0/3/3/3
20	GDP	Be	501	-	-	3/16/32/32	0/3/3/3
20	GDP	8g	501	-	-	3/16/32/32	0/3/3/3
20	GDP	9c	501	-	-	3/16/32/32	0/3/3/3
20	GDP	Ce	501	-	-	3/16/32/32	0/3/3/3
21	GTP	8d	501	-	-	3/22/38/38	0/3/3/3

The worst 5 of 253 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	1A	801	ADP	C5-C4	4.69	1.47	1.39
19	0Y	801	ADP	C5-C4	4.66	1.47	1.39
19	0Z	801	ADP	C5-C4	4.63	1.47	1.39
19	0X	801	ADP	C5-C4	4.62	1.47	1.39
20	5a	501	GDP	C5-C4	3.15	1.47	1.38

The worst 5 of 876 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	5a	501	GDP	C5-C4-N3	-6.38	118.24	128.39
20	Cc	501	GDP	C5-C4-N3	-6.33	118.31	128.39
20	5c	501	GDP	C5-C4-N3	-6.26	118.42	128.39
20	5g	501	GDP	C5-C4-N3	-6.25	118.44	128.39
20	6a	501	GDP	C5-C4-N3	-6.24	118.46	128.39

There are no chirality outliers.

5 of 324 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	0Y	801	ADP	PA-O3A-PB-O2B
19	0Y	801	ADP	PA-O3A-PB-O3B
19	1A	801	ADP	PA-O3A-PB-O2B
20	1a	501	GDP	C5'-O5'-PA-O3A
20	1a	501	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

90 monomers are involved in 233 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	8e	501	GDP	1	0
21	9b	501	GTP	3	0
21	Df	501	GTP	4	0
21	7d	501	GTP	3	0
21	5b	501	GTP	2	0
20	2a	501	GDP	1	0
20	4a	501	GDP	1	0
21	9d	501	GTP	4	0
20	6c	501	GDP	1	0
21	1h	501	GTP	2	0
21	6d	501	GTP	6	0
19	0Y	801	ADP	4	0
21	2b	501	GTP	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	6g	501	GDP	1	0
21	6h	501	GTP	4	0
21	9f	501	GTP	4	0
19	0X	801	ADP	2	0
21	Ad	501	GTP	1	0
20	Da	501	GDP	2	0
20	8c	501	GDP	1	0
20	6a	501	GDP	3	0
21	4f	501	GTP	2	0
21	4b	501	GTP	4	0
21	4h	501	GTP	2	0
21	3b	501	GTP	4	0
21	2d	501	GTP	5	0
20	De	501	GDP	1	0
20	4c	501	GDP	1	0
21	Bb	501	GTP	4	0
20	Ca	501	GDP	1	0
21	5h	501	GTP	3	0
21	6b	501	GTP	6	0
20	1c	501	GDP	1	0
20	7c	501	GDP	1	0
20	5e	501	GDP	1	0
21	1d	501	GTP	4	0
21	Db	501	GTP	5	0
21	5d	501	GTP	3	0
20	5c	501	GDP	1	0
21	Ah	501	GTP	3	0
21	2h	501	GTP	3	0
21	Cb	501	GTP	5	0
21	3d	501	GTP	5	0
21	Ab	501	GTP	2	0
20	6e	501	GDP	2	0
20	7e	501	GDP	2	0
19	1A	801	ADP	1	0
20	1g	501	GDP	3	0
19	0Z	801	ADP	2	0
20	1a	501	GDP	2	0
21	9h	501	GTP	4	0
21	Cf	501	GTP	4	0
21	2f	501	GTP	4	0
21	7b	501	GTP	4	0
20	2c	501	GDP	1	0

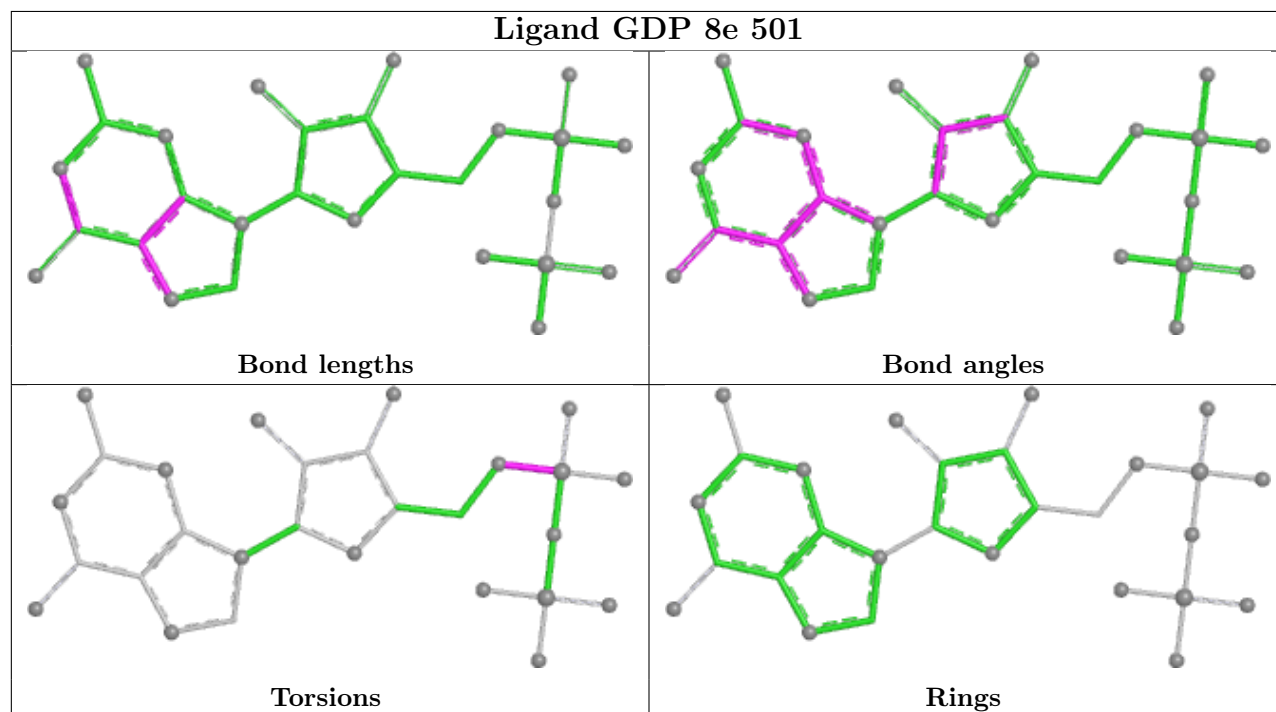
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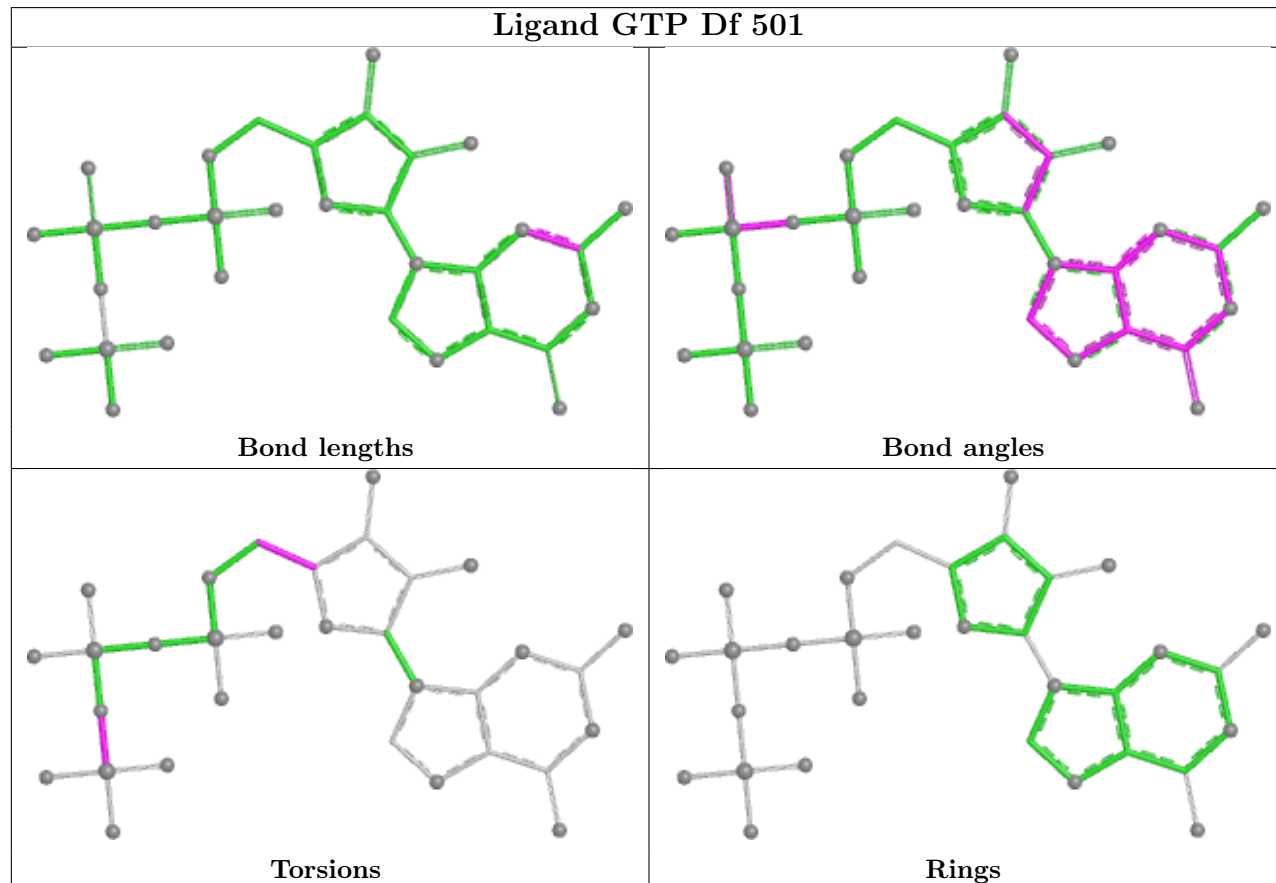
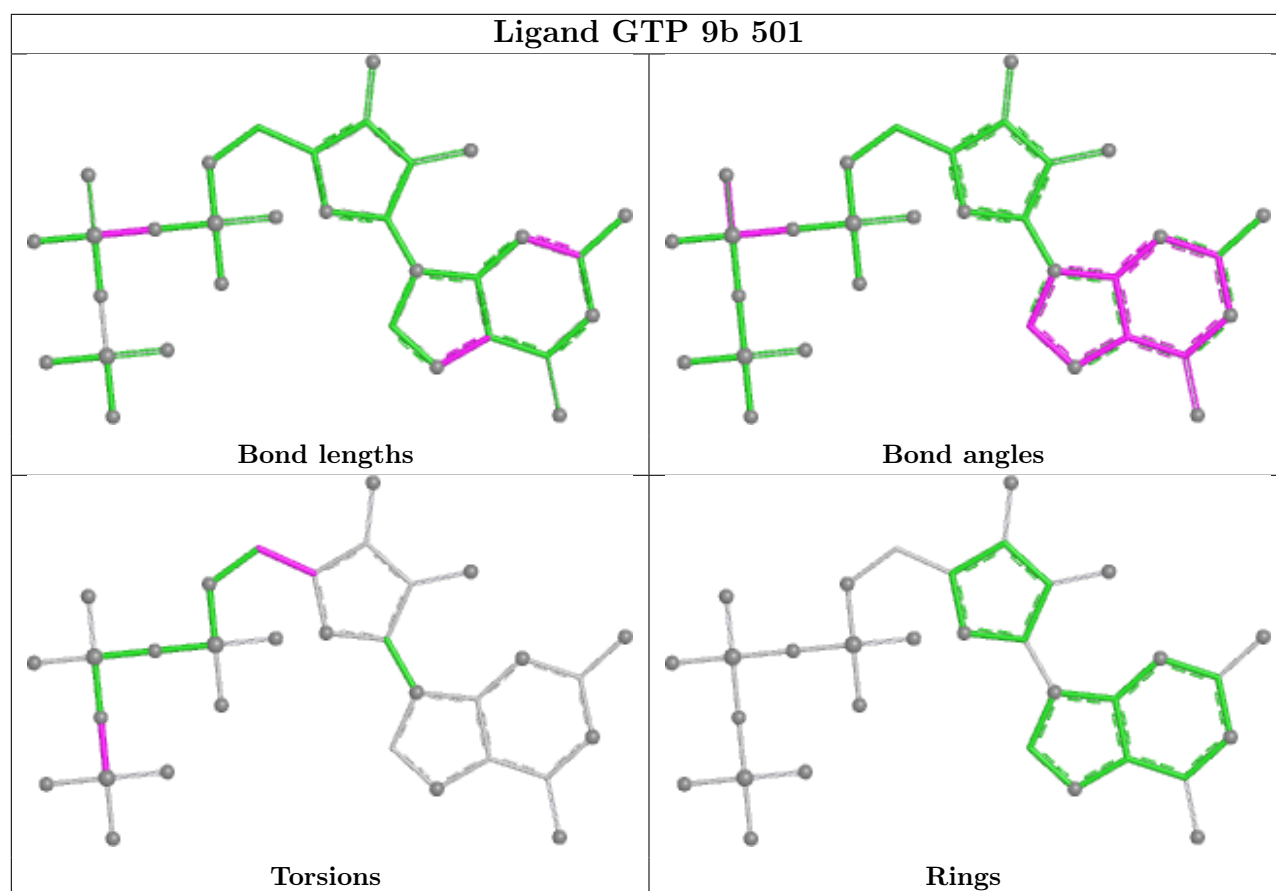
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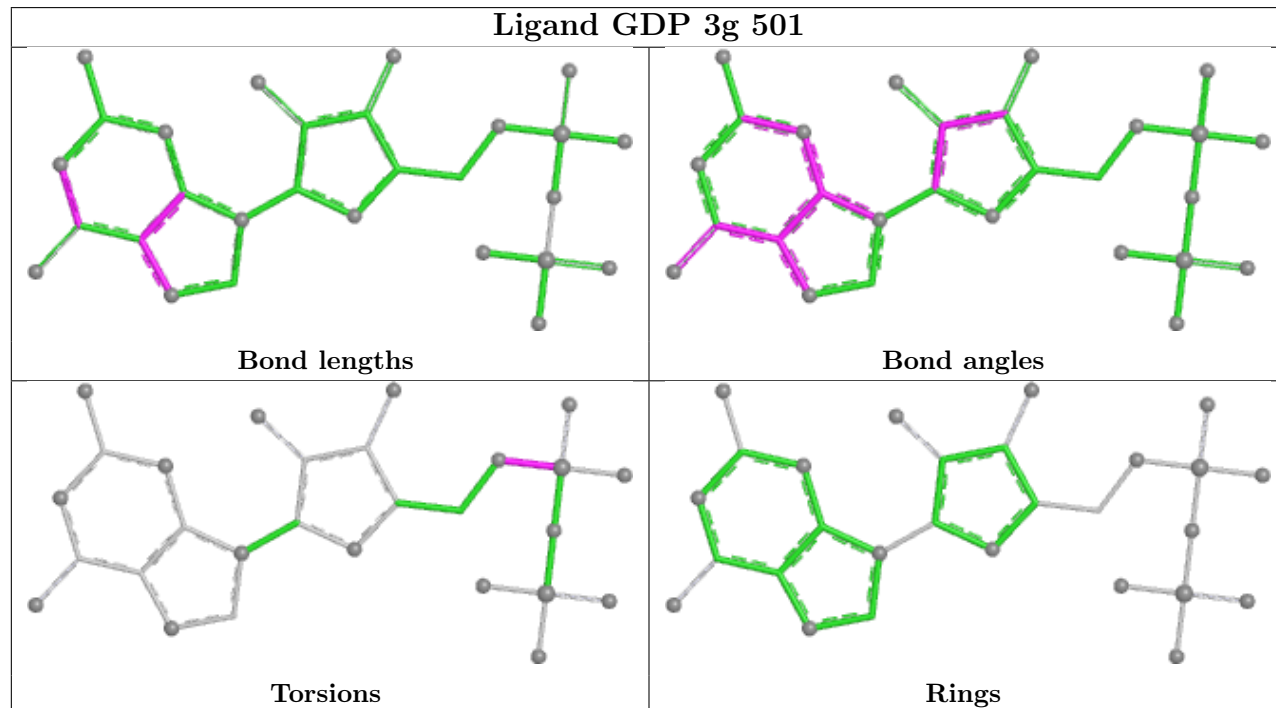
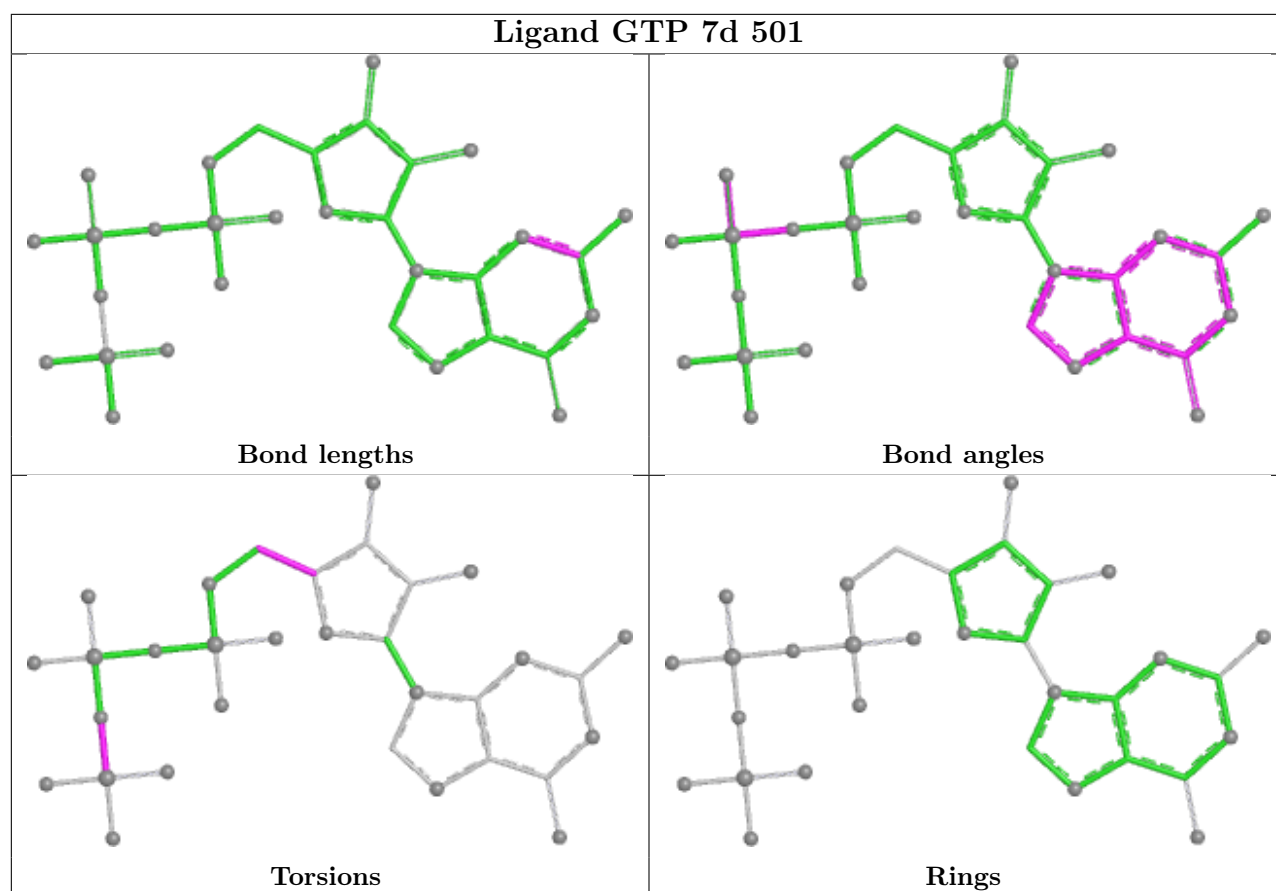
Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	Aa	501	GDP	1	0
20	7g	501	GDP	1	0
21	6f	501	GTP	3	0
21	Bf	501	GTP	4	0
21	Cd	501	GTP	5	0
20	9e	501	GDP	1	0
21	1f	501	GTP	3	0
21	Ch	501	GTP	4	0
21	5f	501	GTP	1	0
20	Cc	501	GDP	2	0
21	Af	501	GTP	2	0
20	Cg	501	GDP	1	0
21	7h	501	GTP	2	0
20	8a	501	GDP	2	0
21	Dd	501	GTP	3	0
21	3f	501	GTP	4	0
21	3h	501	GTP	2	0
21	8f	501	GTP	6	0
20	3c	501	GDP	1	0
21	1b	501	GTP	3	0
20	5a	501	GDP	2	0
21	Bh	501	GTP	2	0
20	Dg	501	GDP	1	0
21	Bd	501	GTP	3	0
21	8b	501	GTP	3	0
20	7a	501	GDP	1	0
21	8h	501	GTP	4	0
21	7f	501	GTP	3	0
21	4d	501	GTP	2	0
20	5g	501	GDP	1	0
21	Dh	501	GTP	3	0
20	8g	501	GDP	1	0
20	9c	501	GDP	3	0
20	Ce	501	GDP	1	0
21	8d	501	GTP	4	0

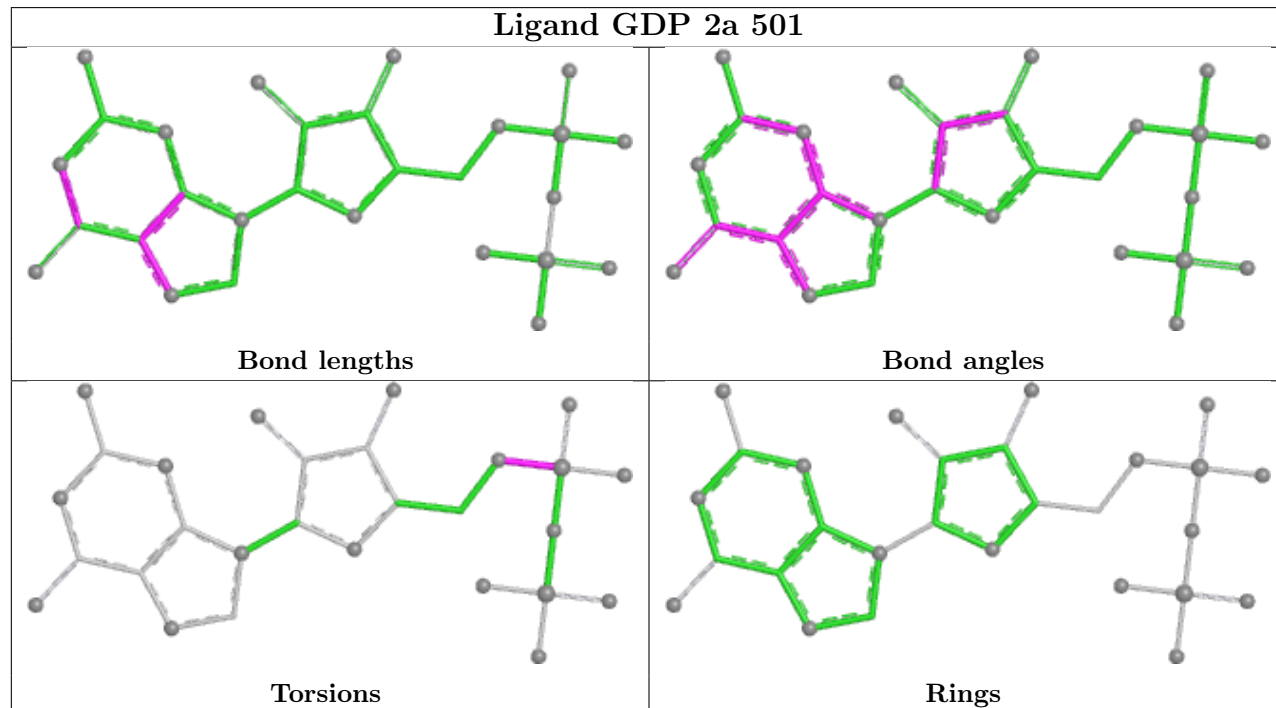
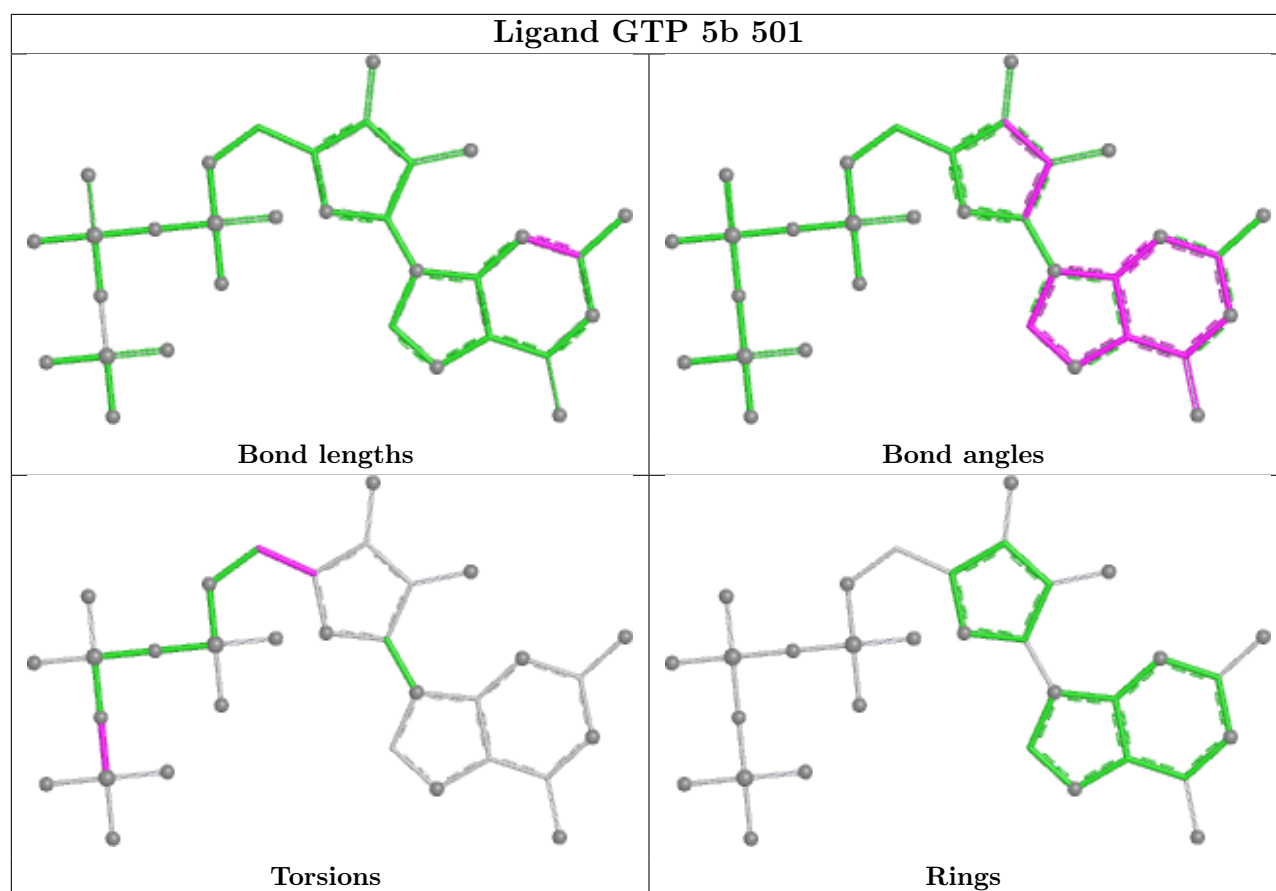
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

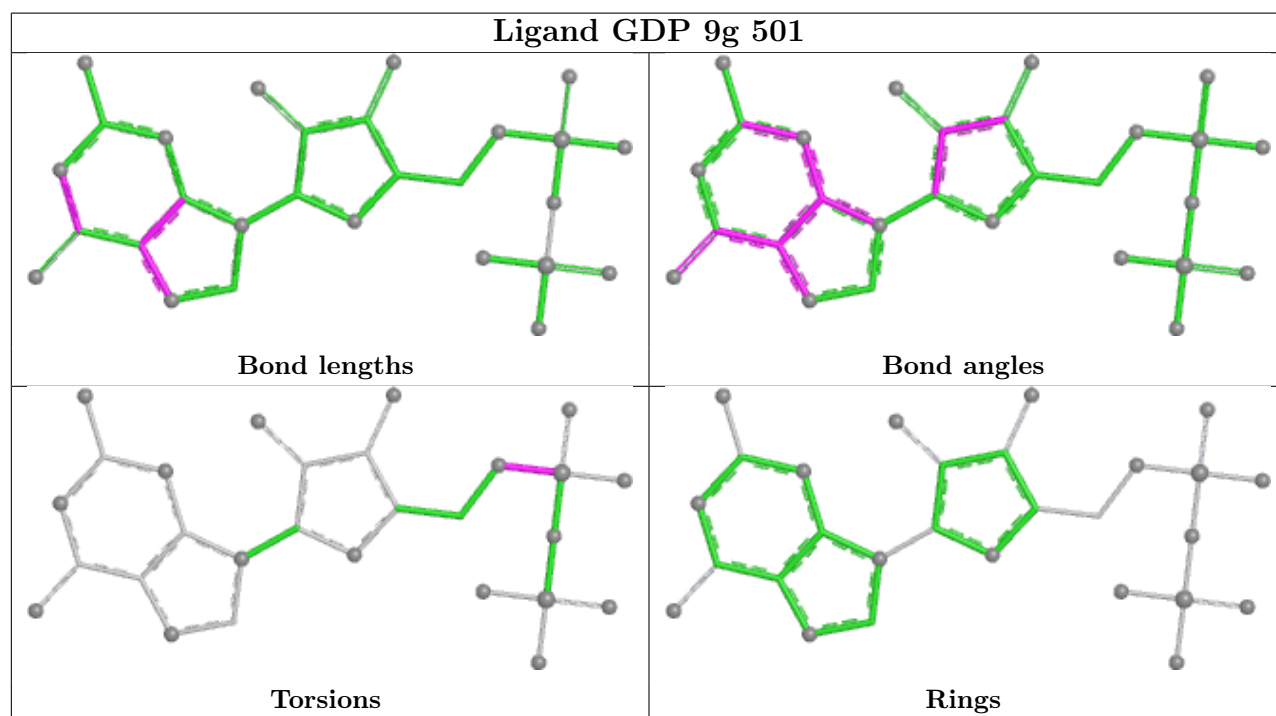
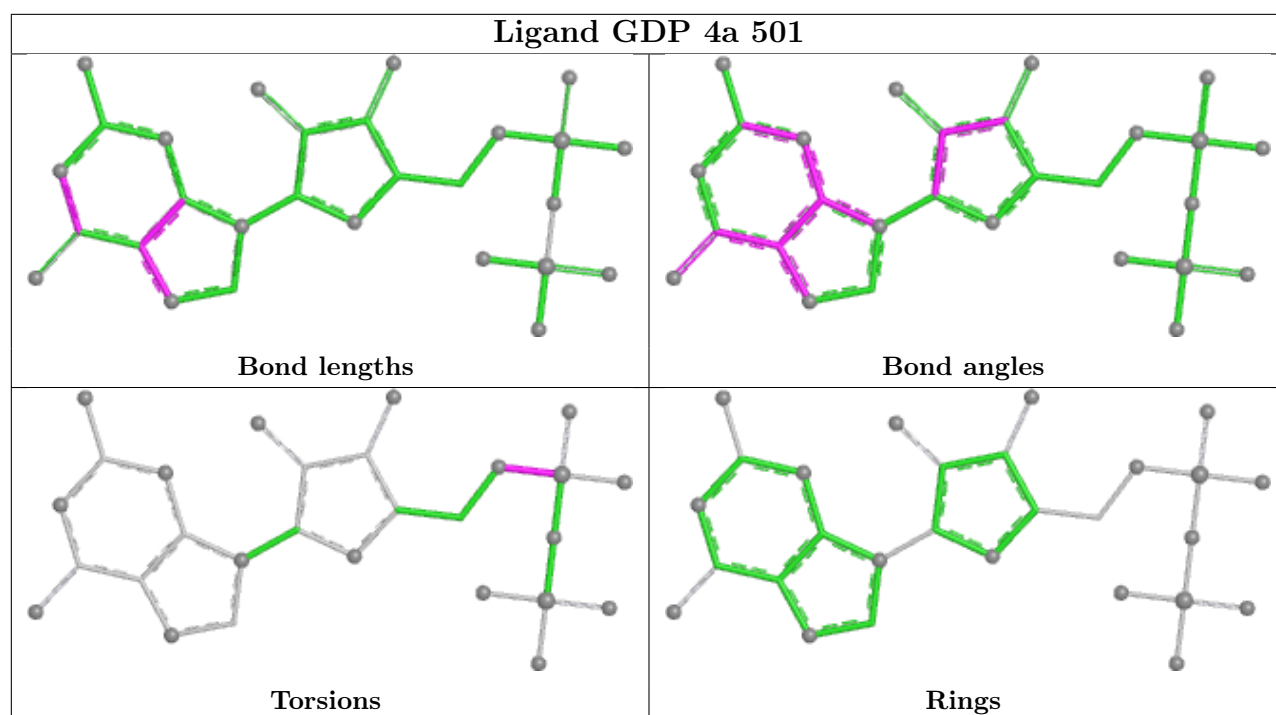
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers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

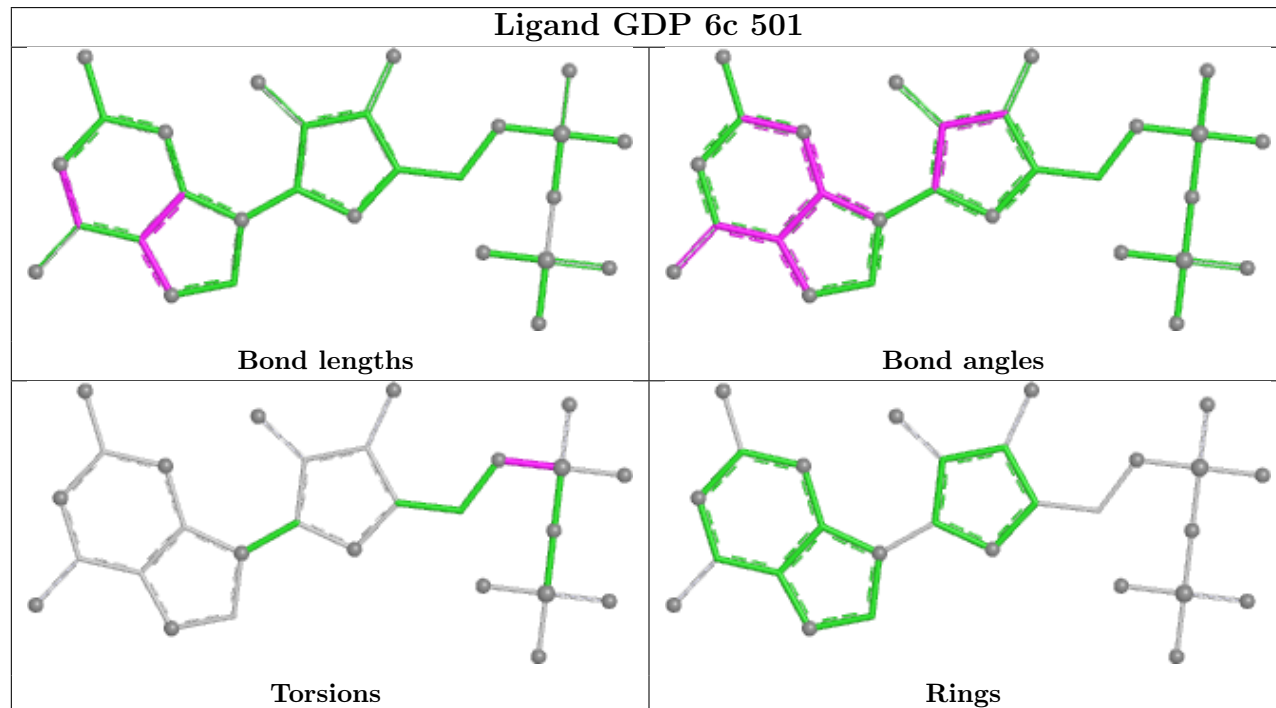
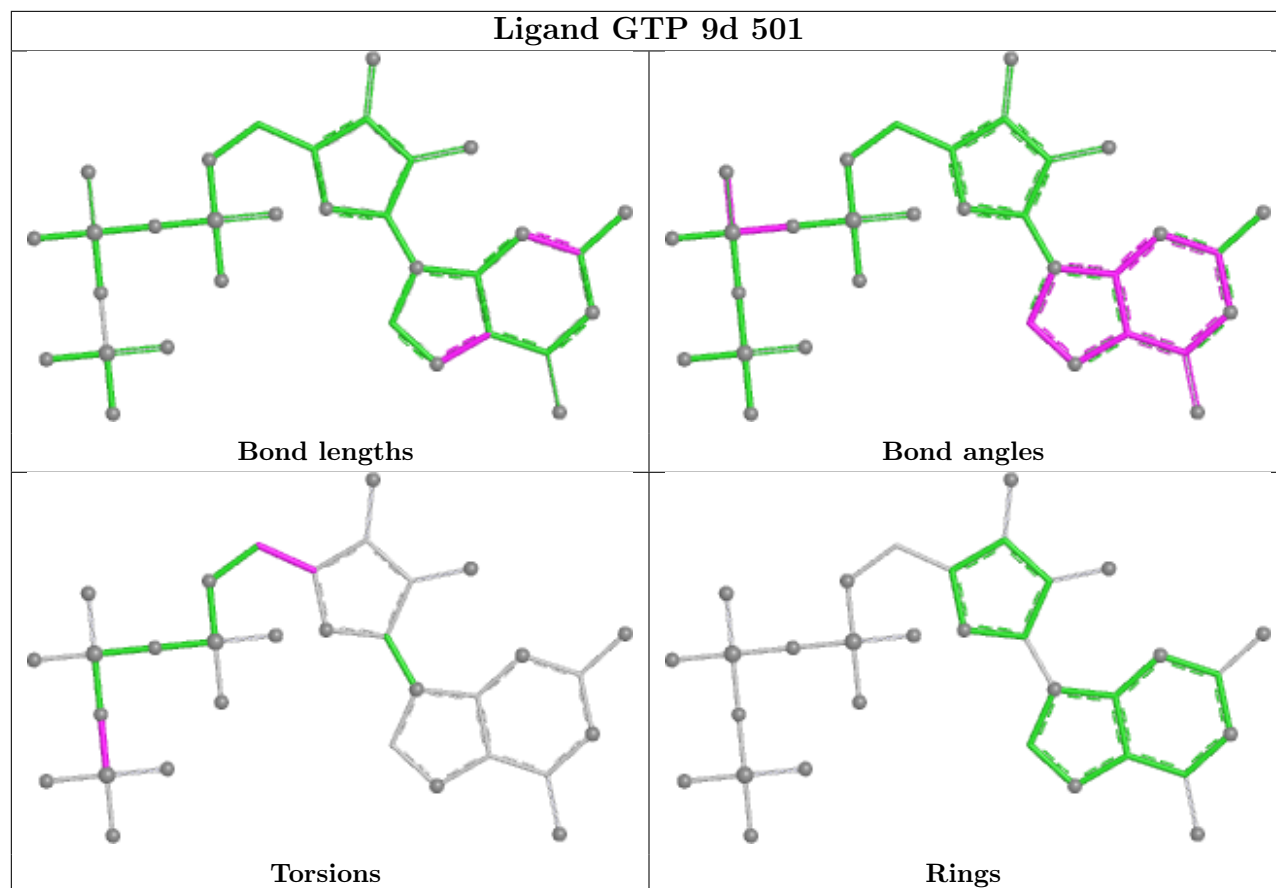


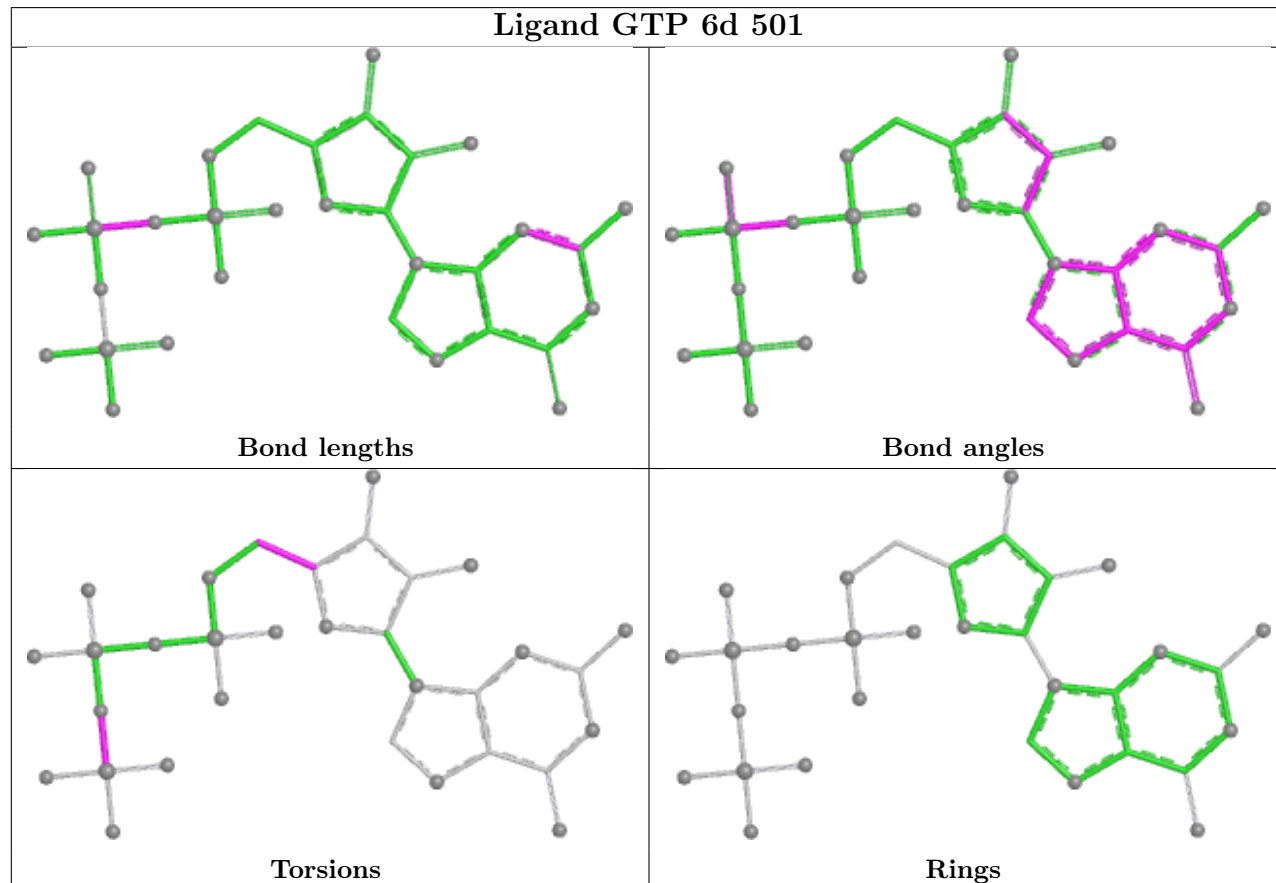
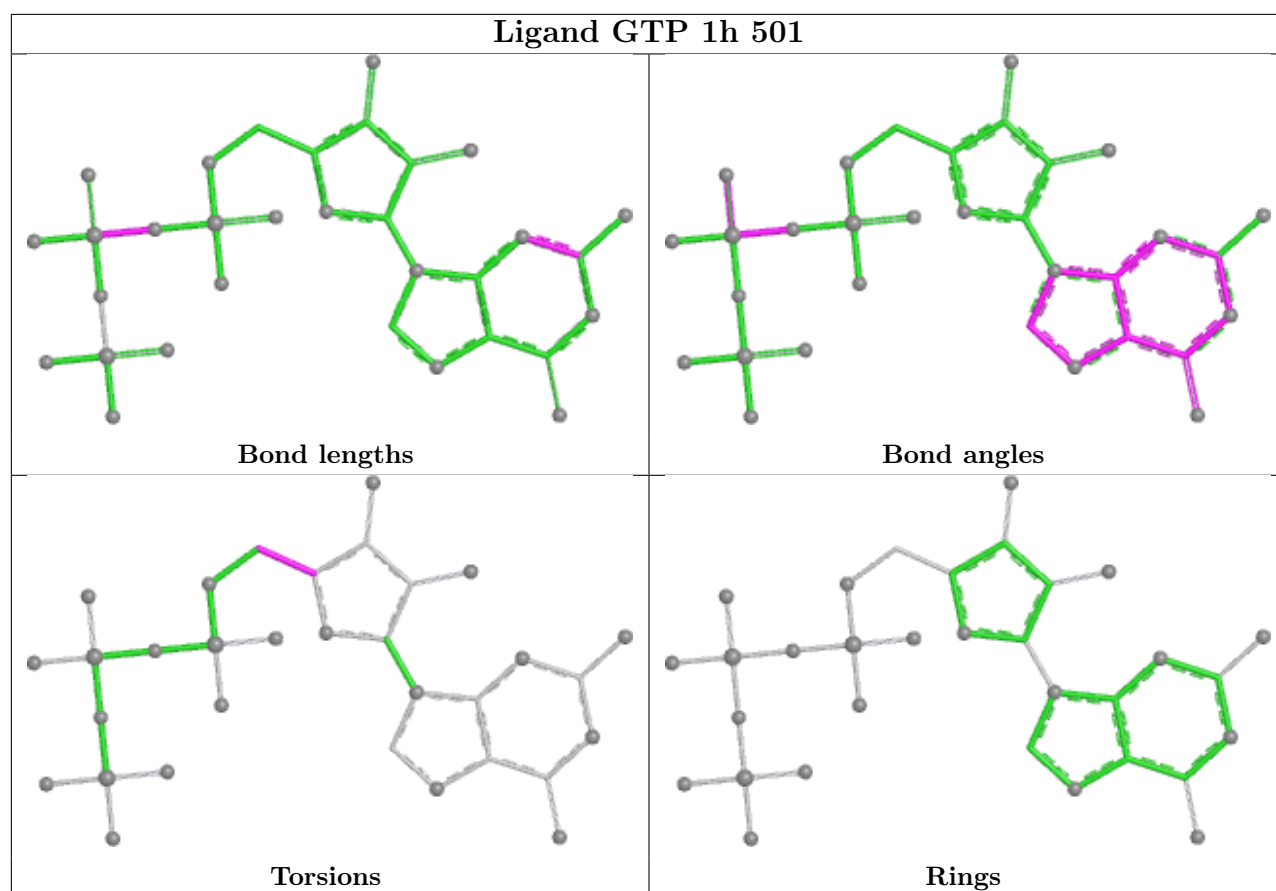


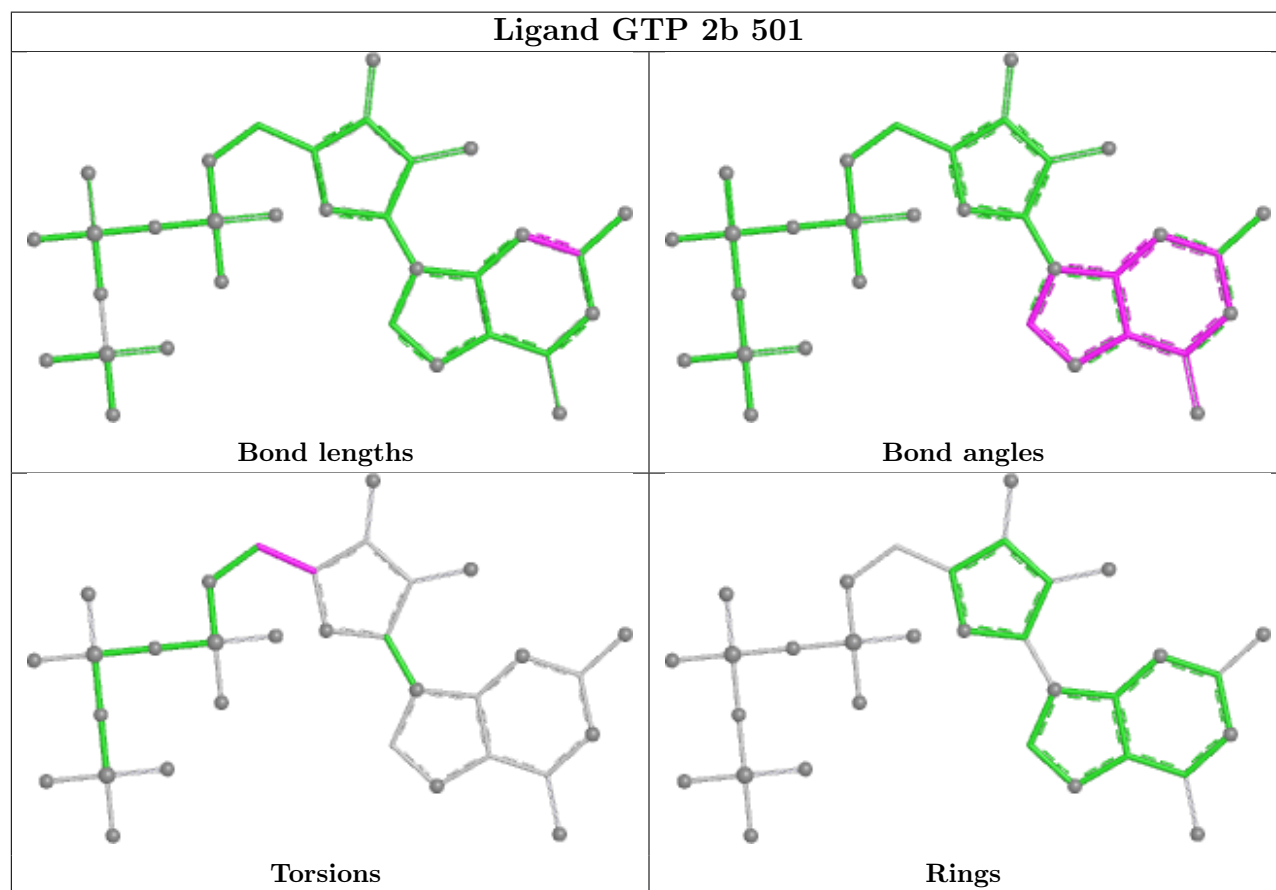
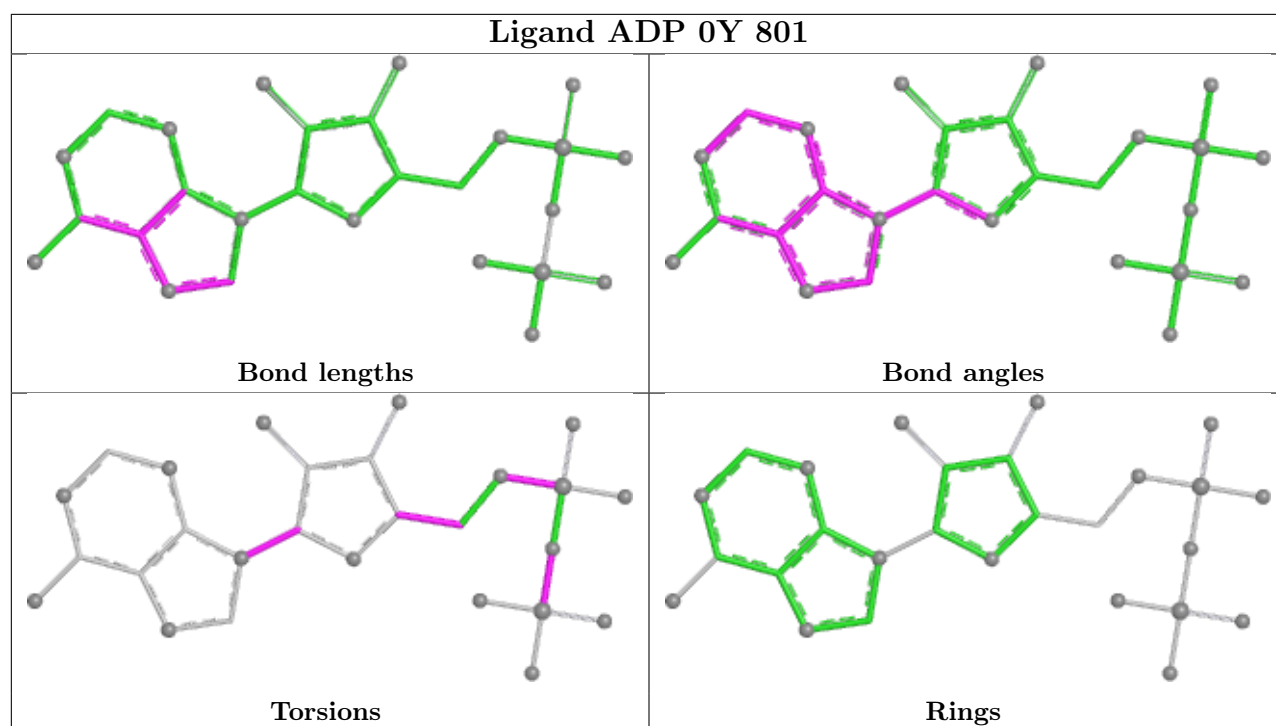


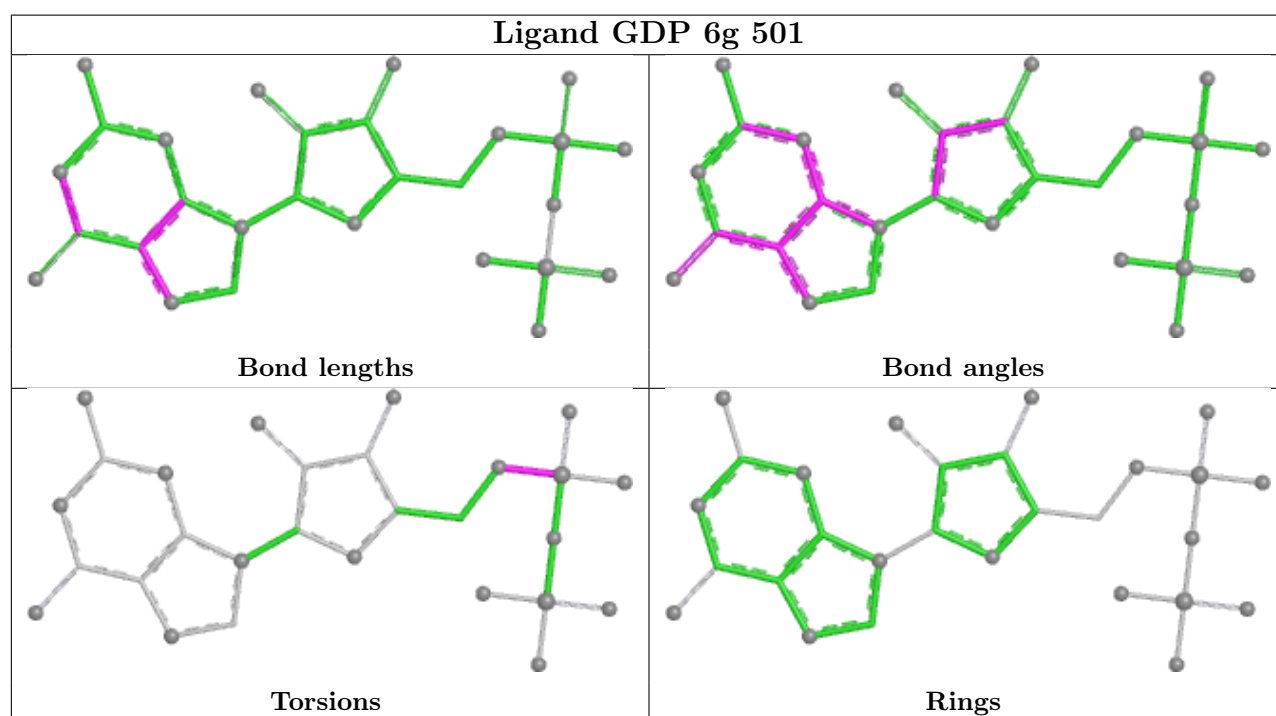
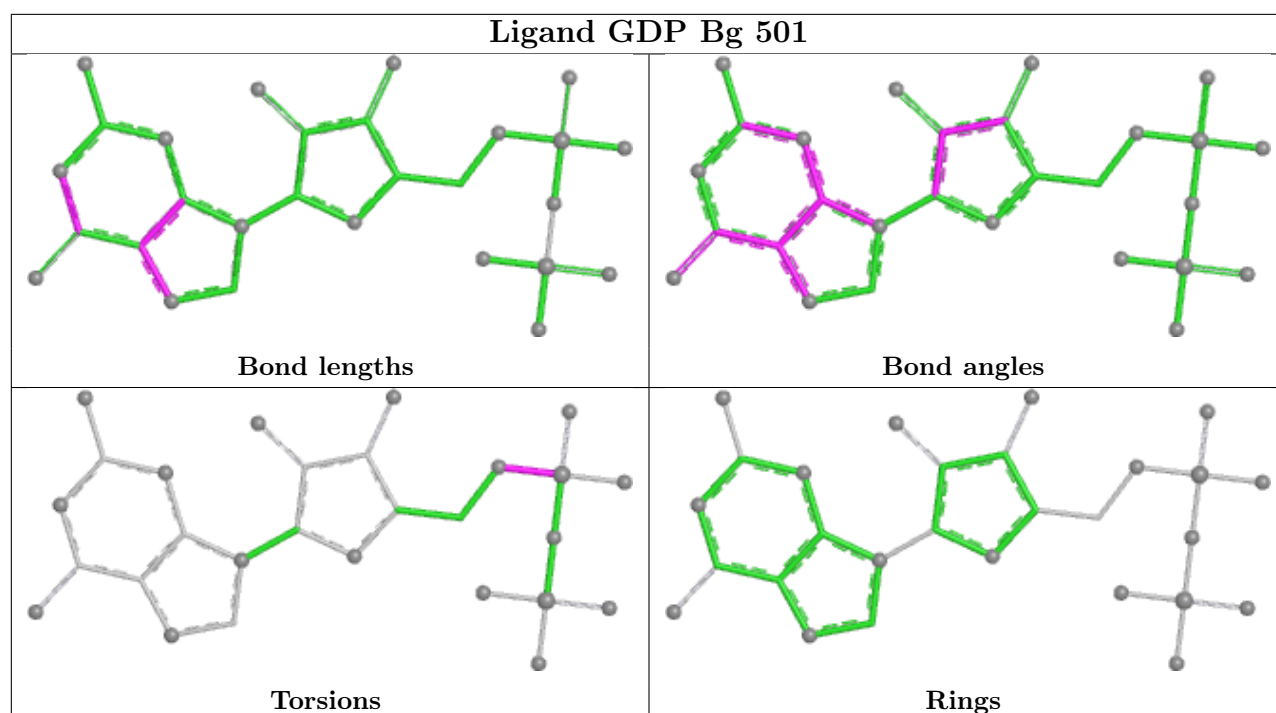


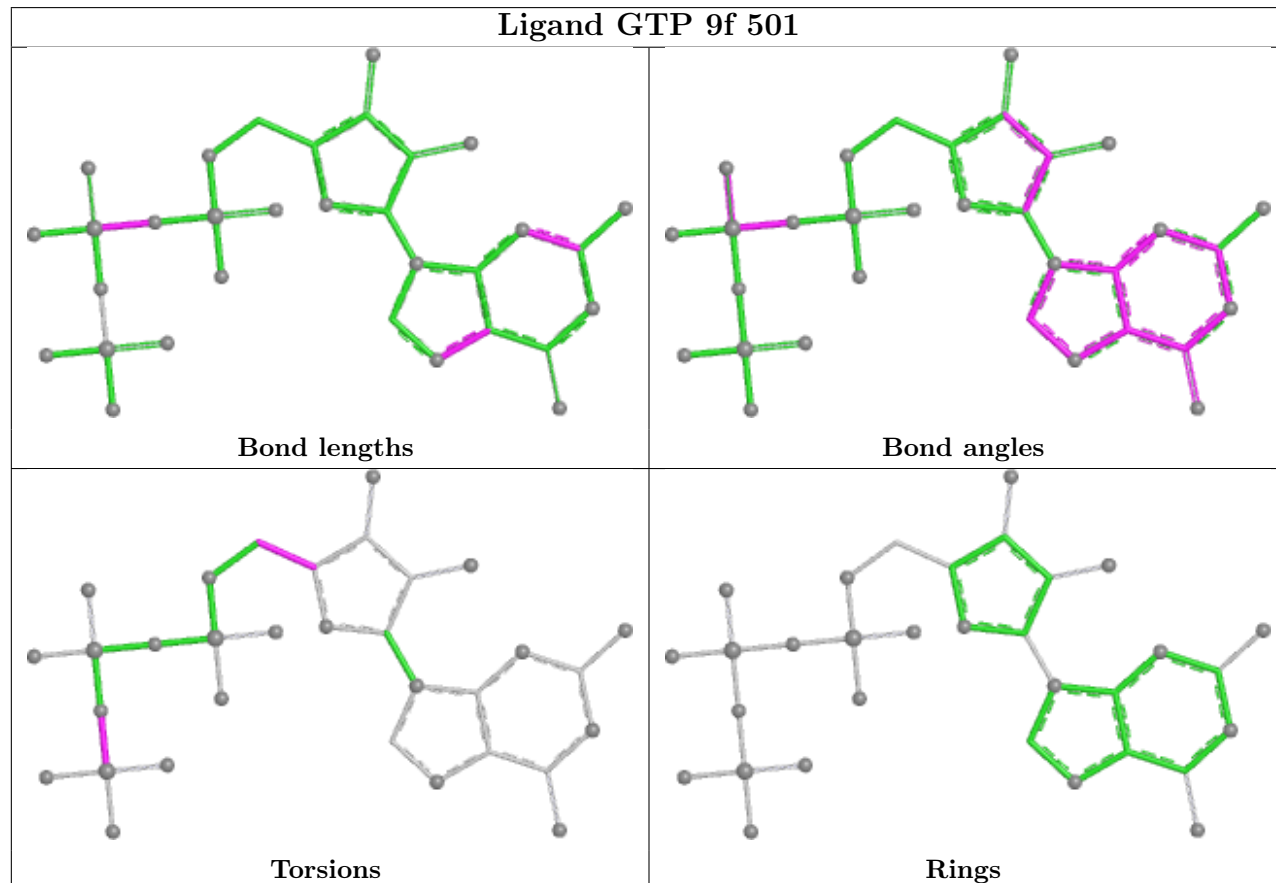
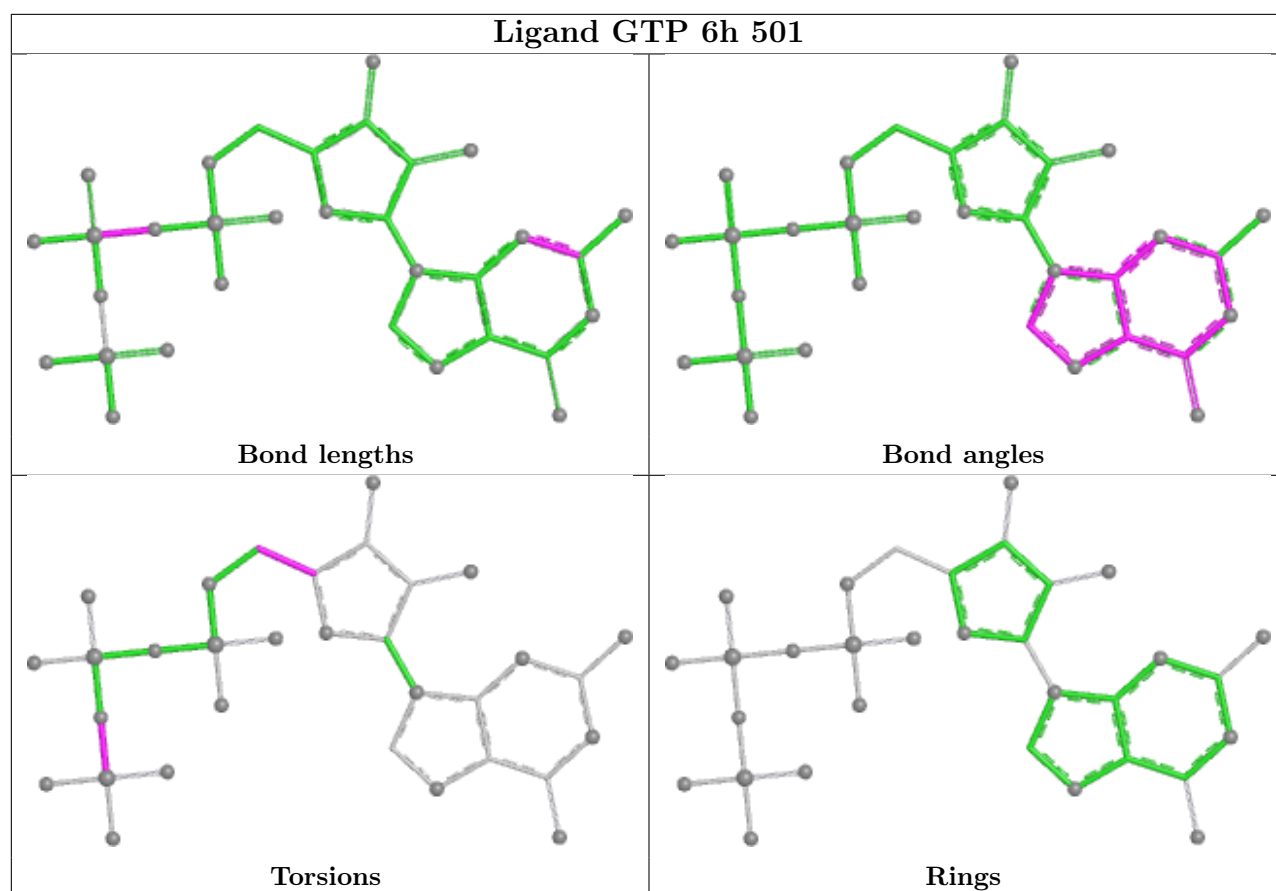


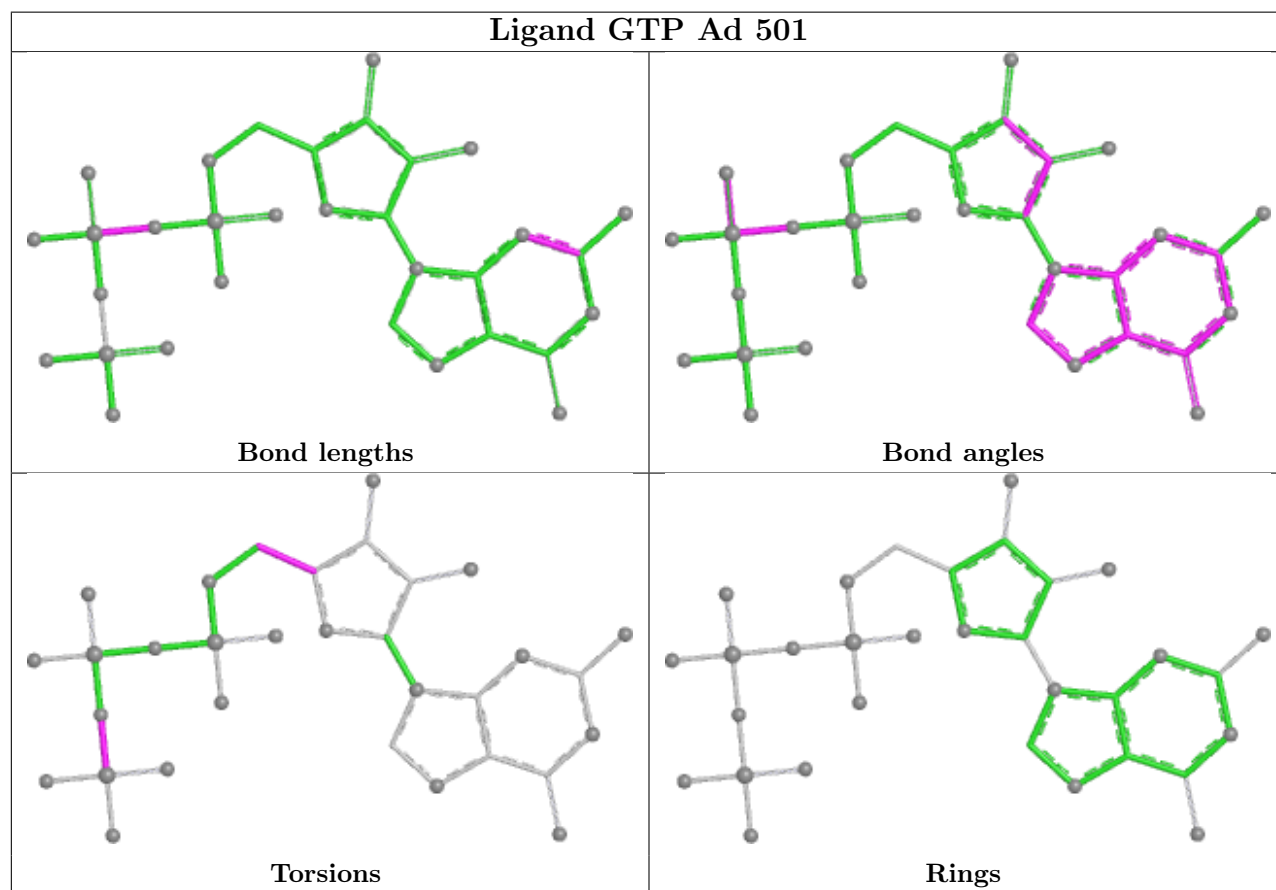
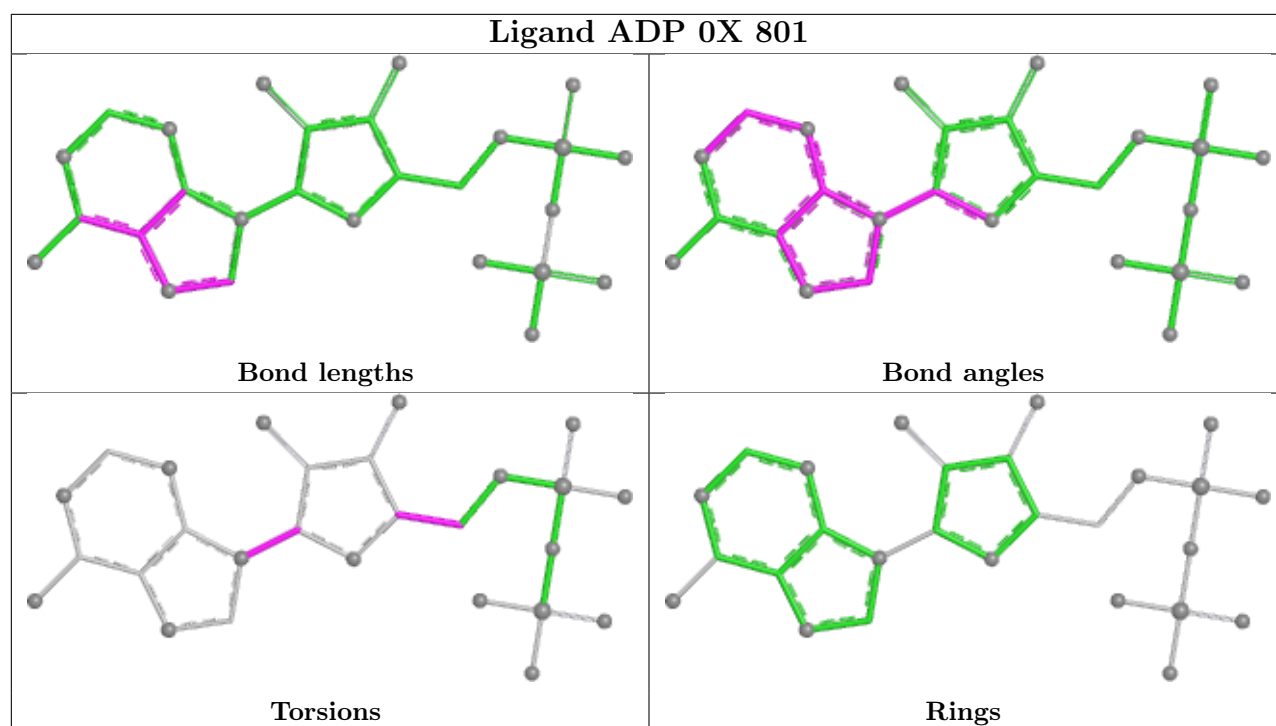


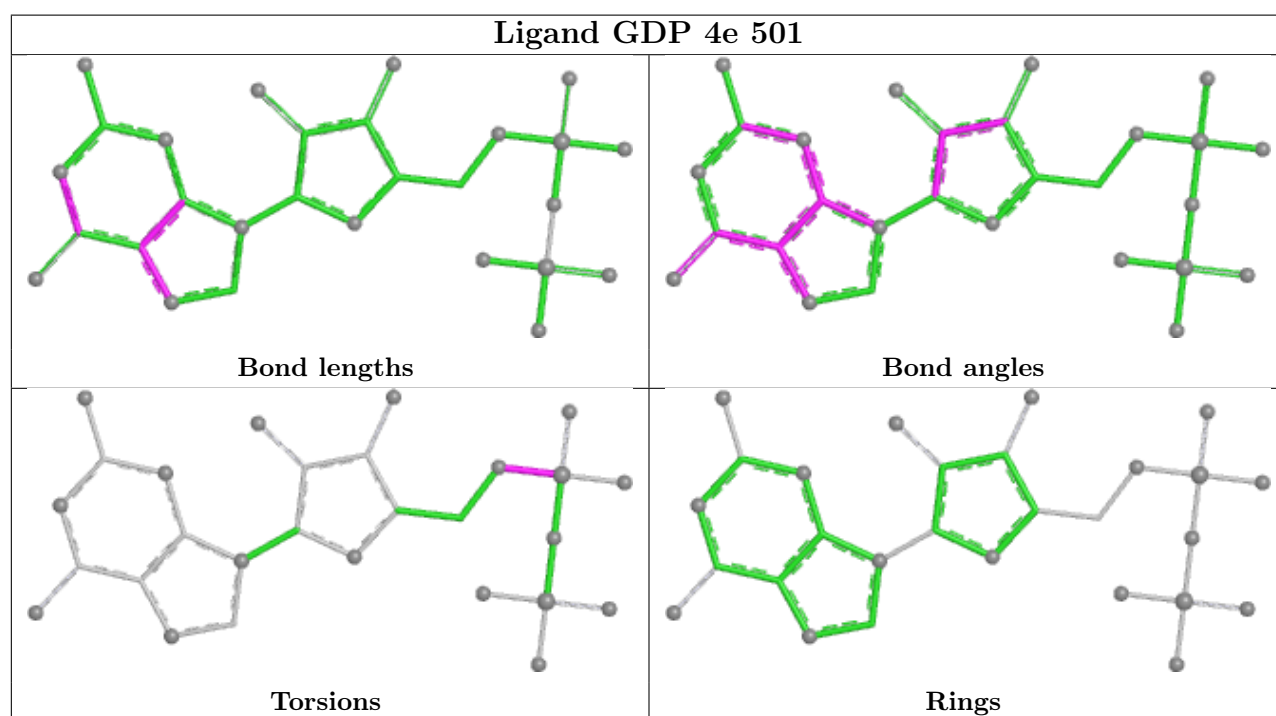
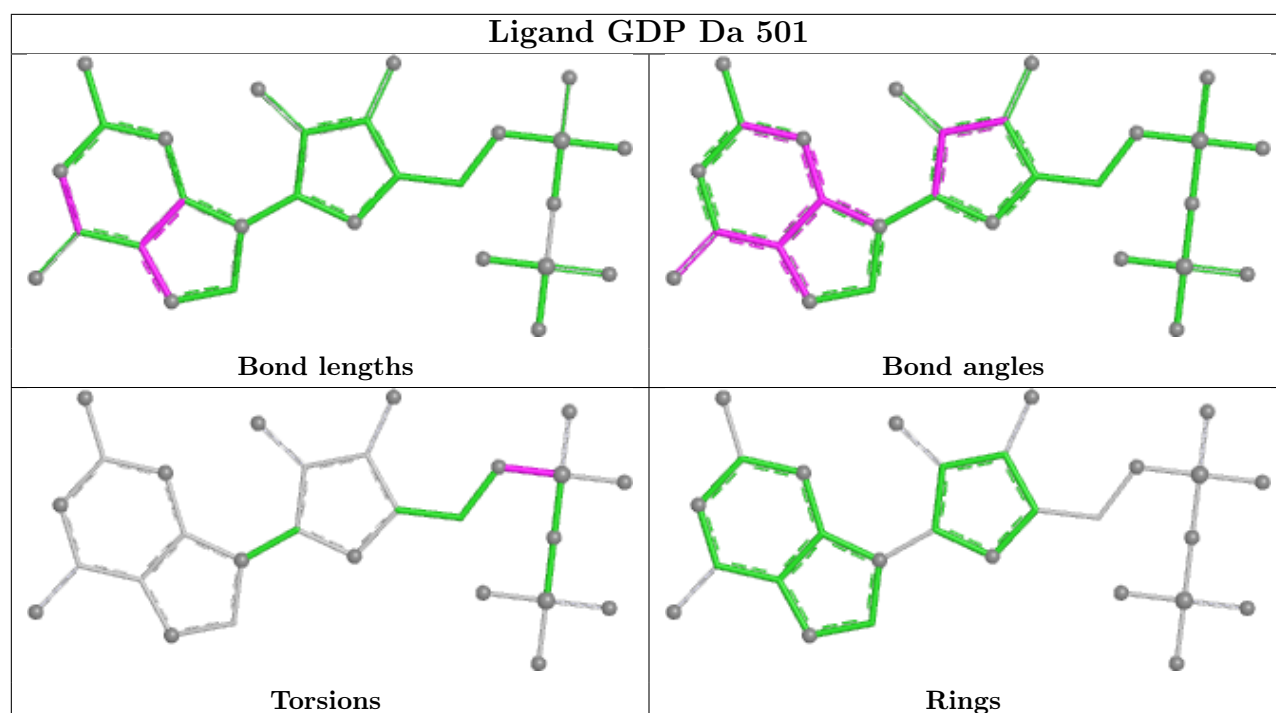


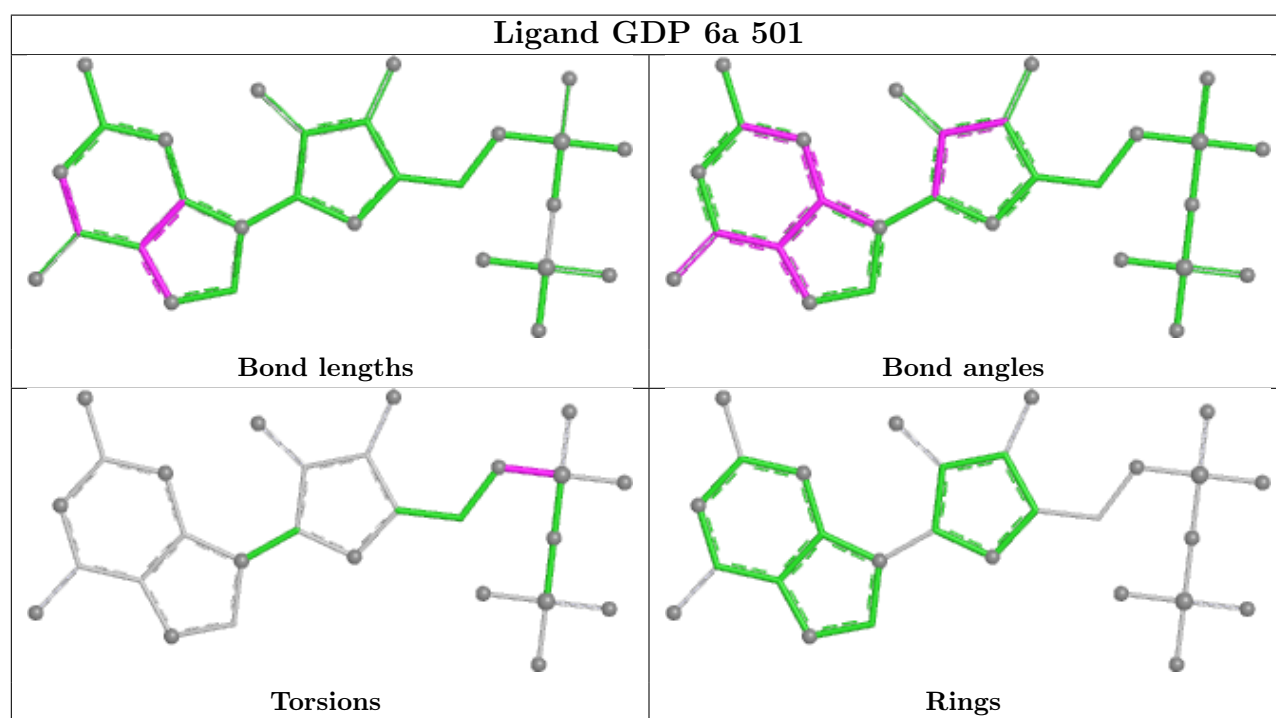
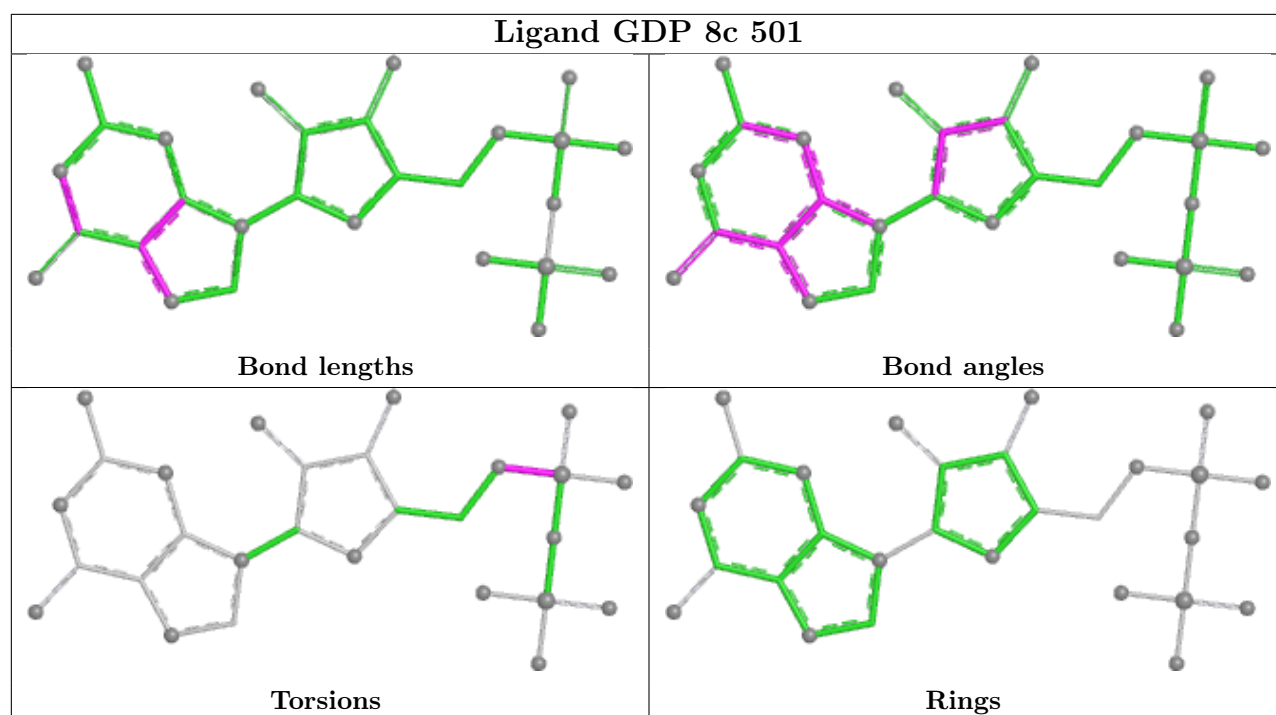


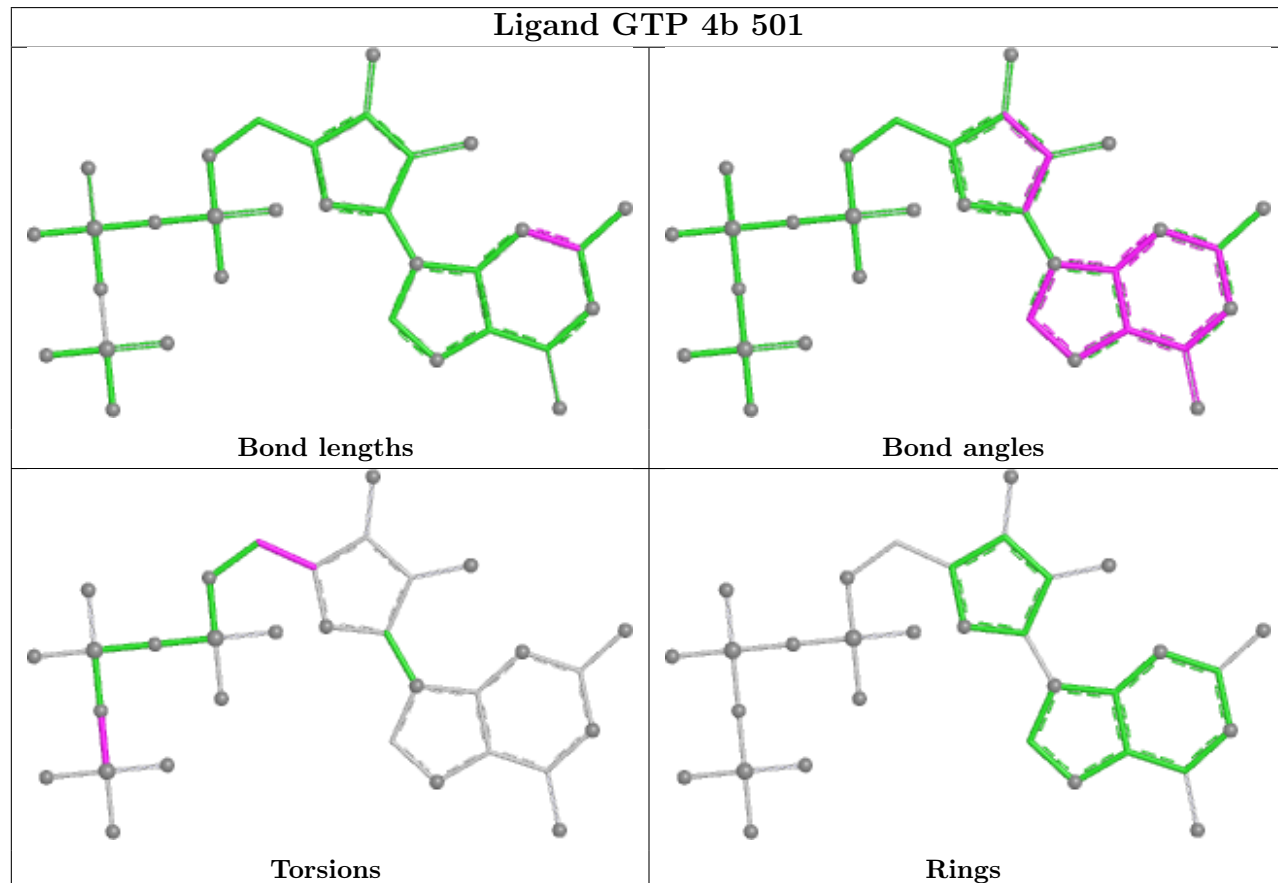
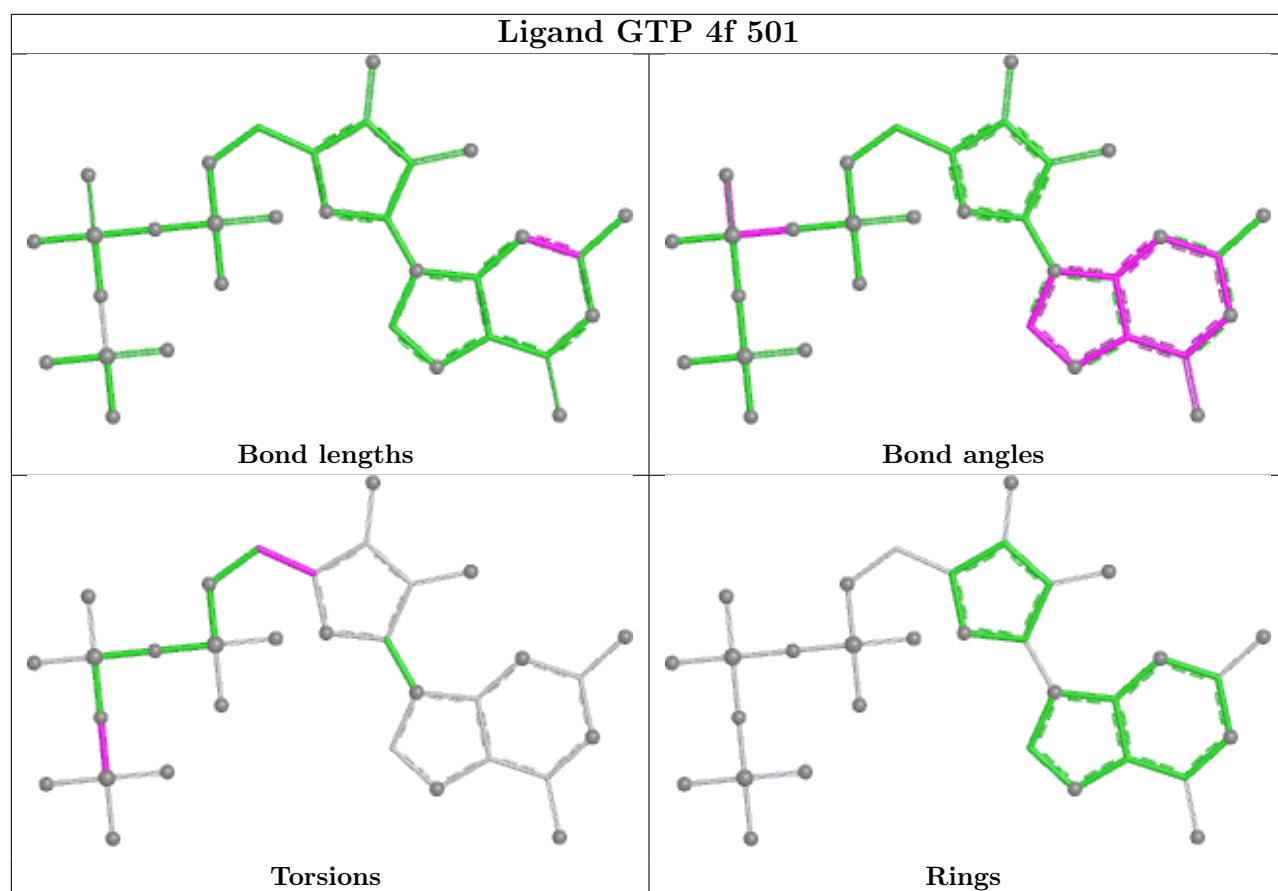


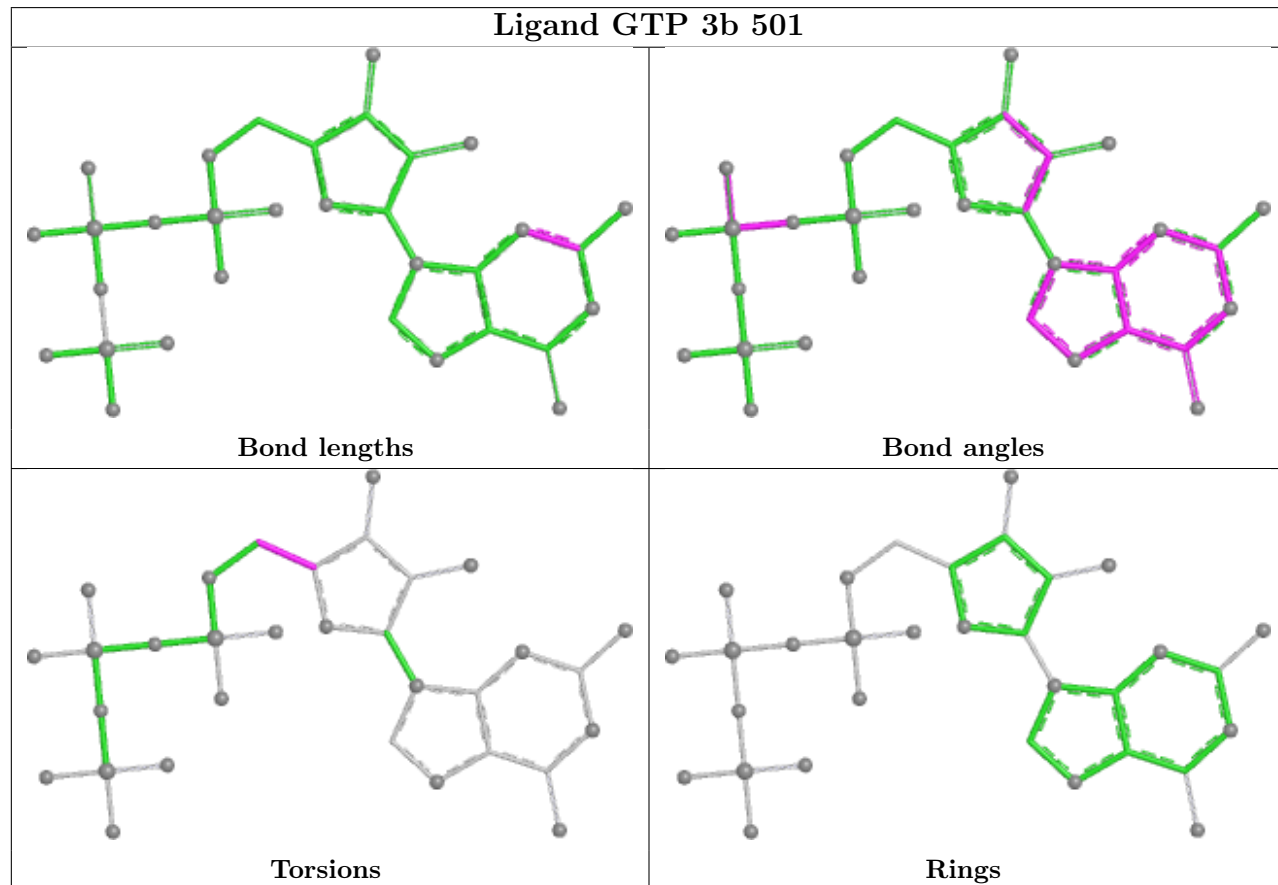
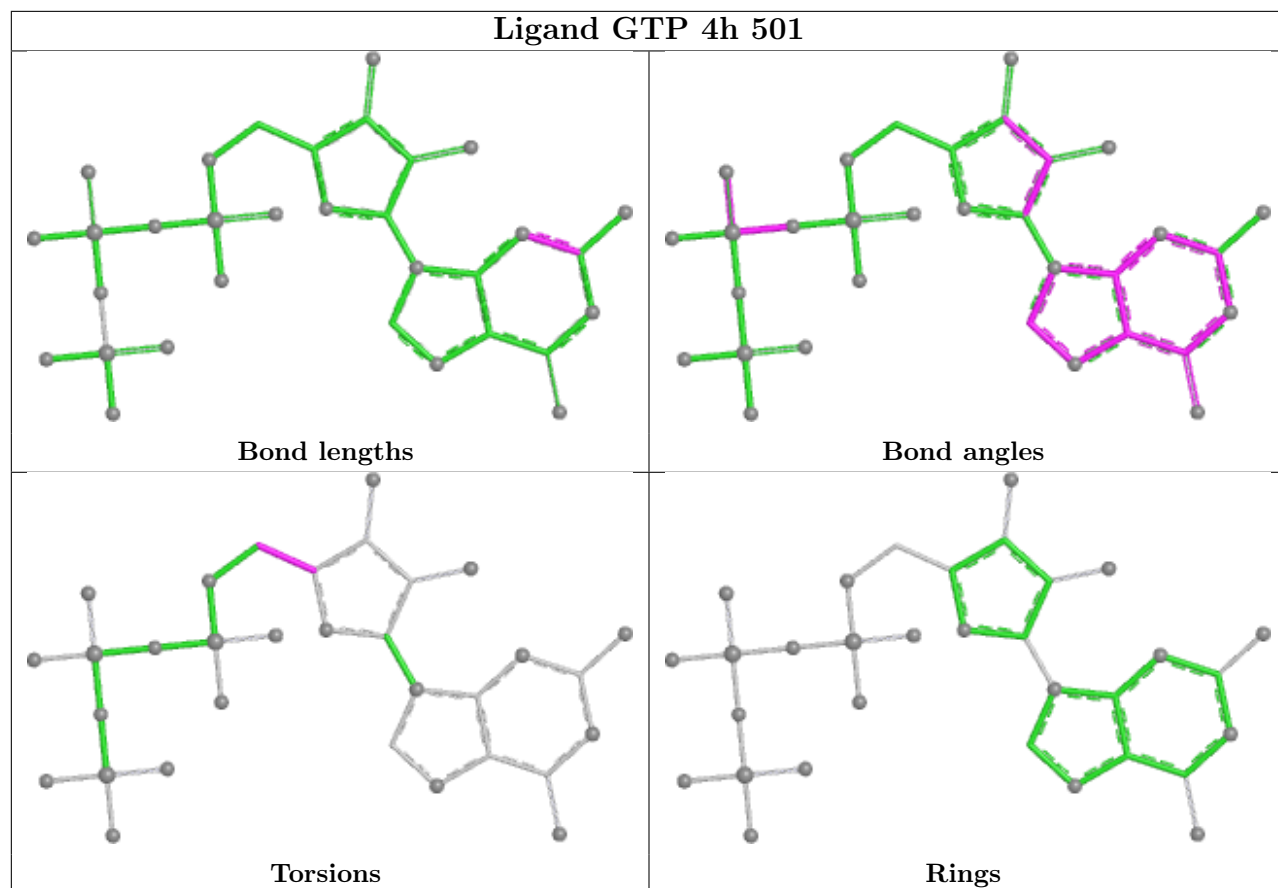


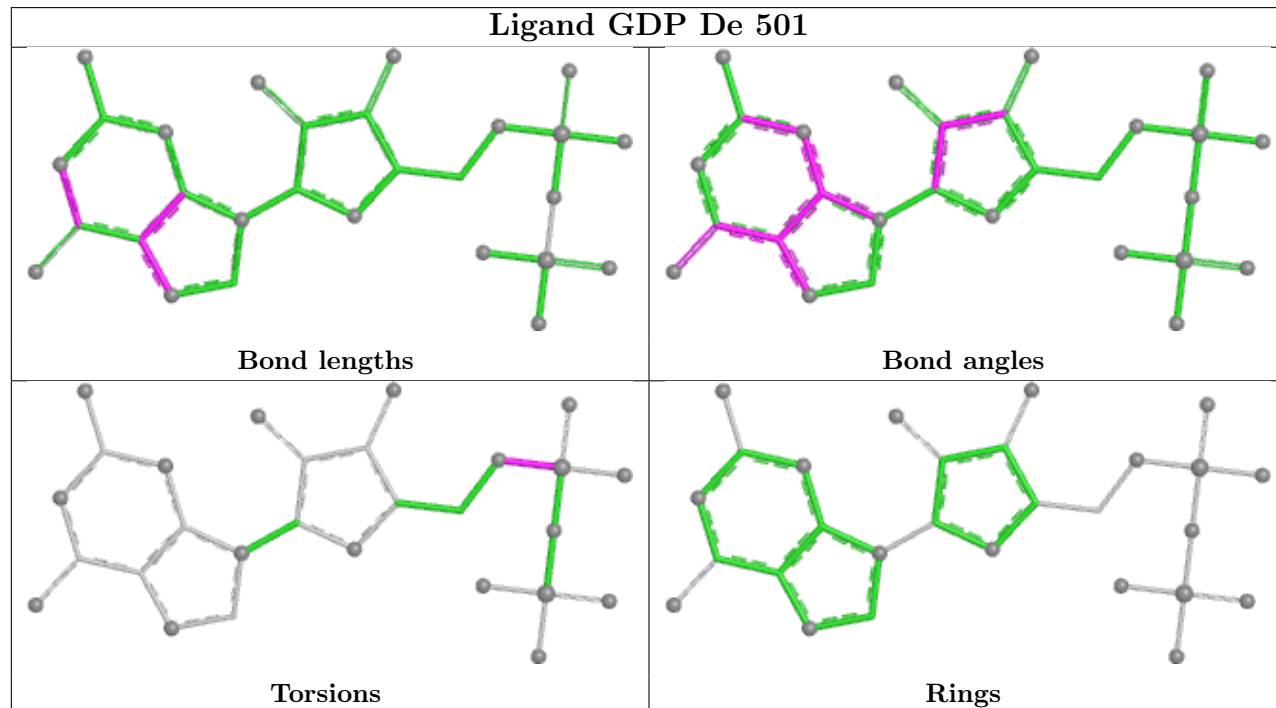
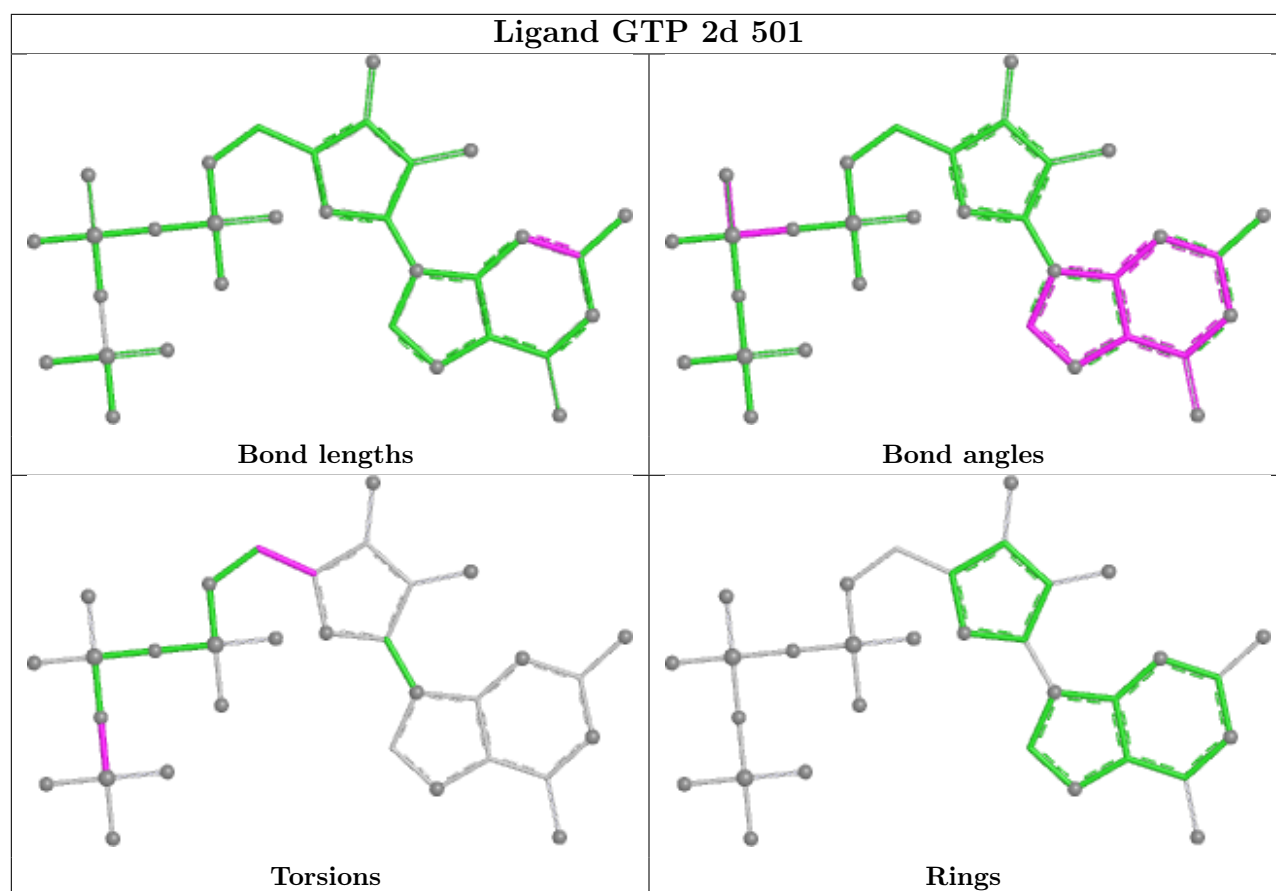


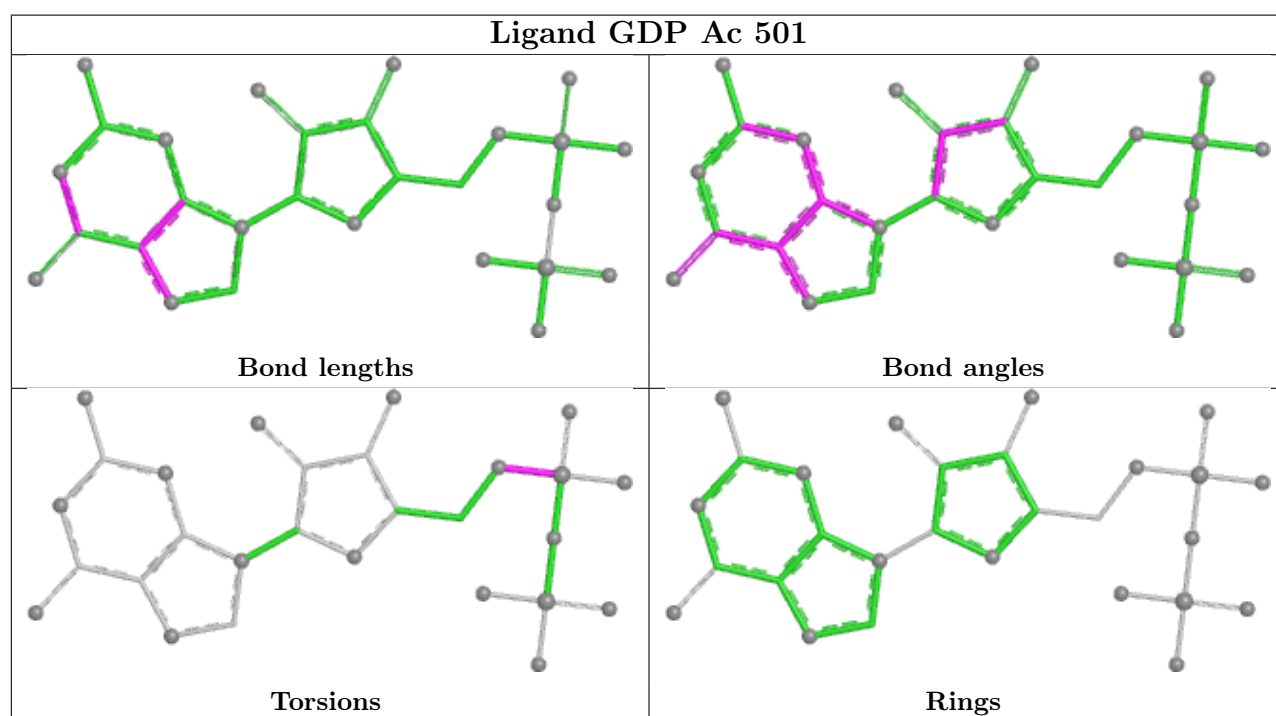
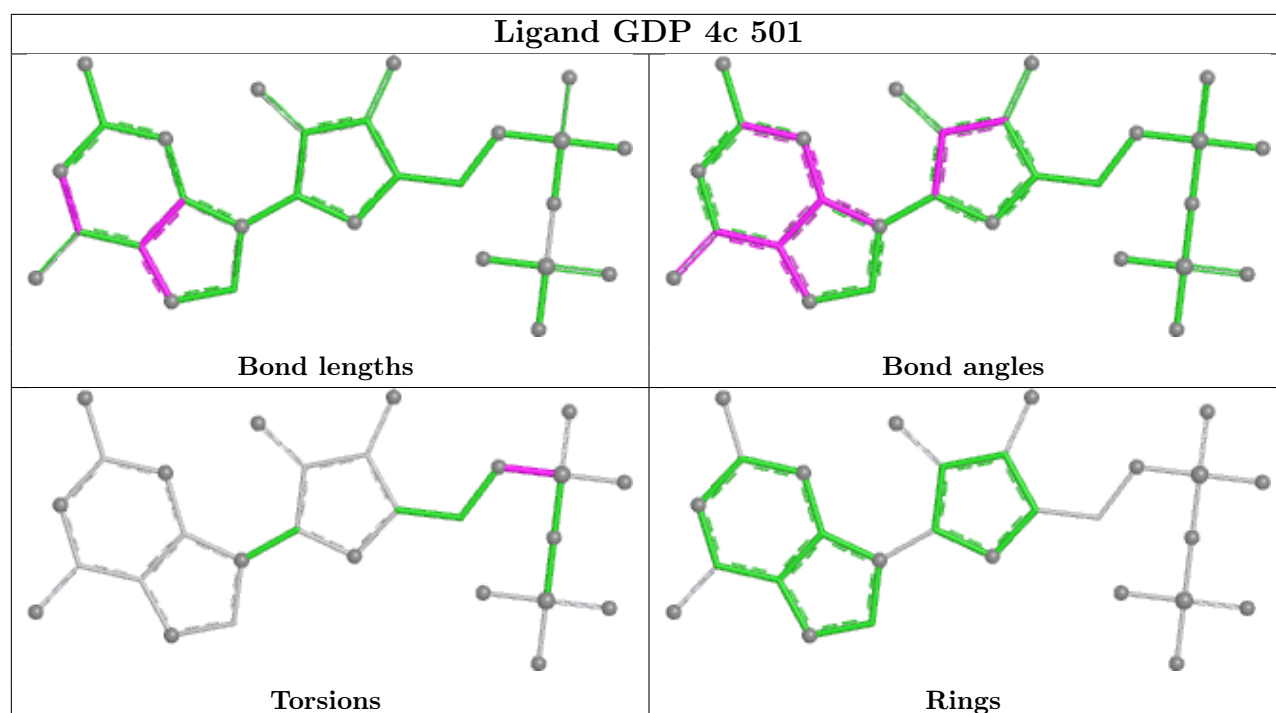


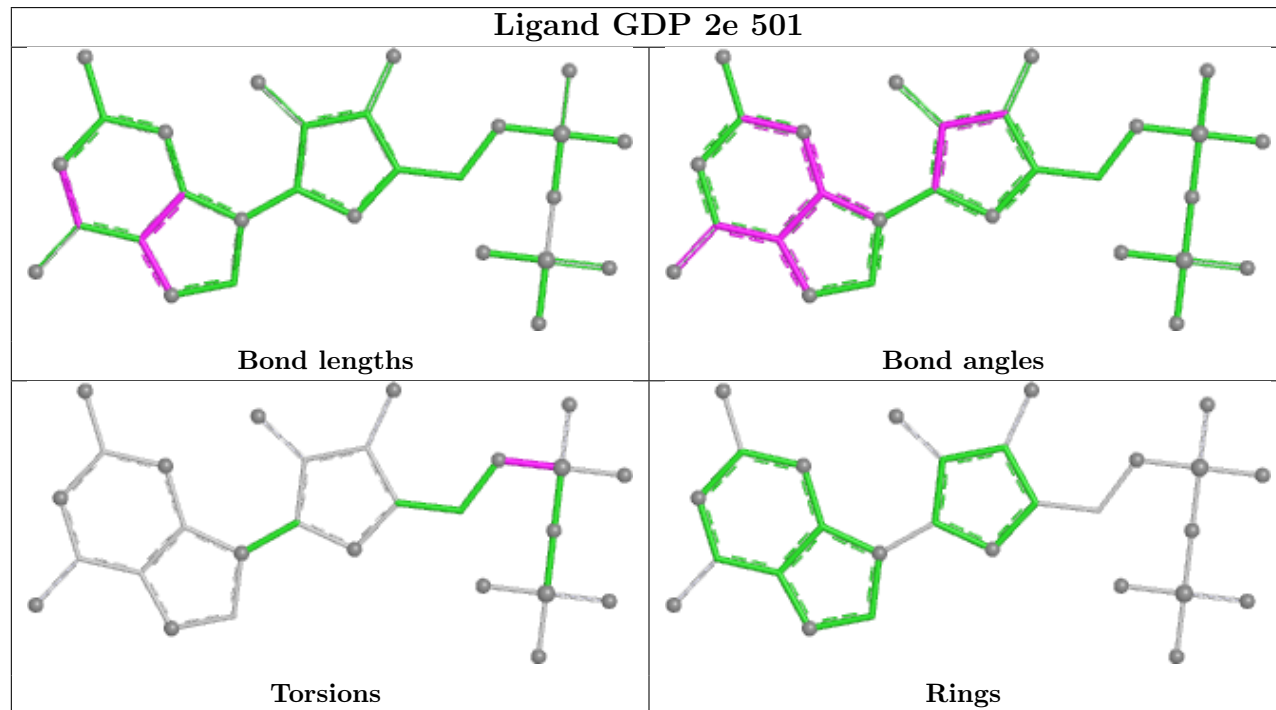
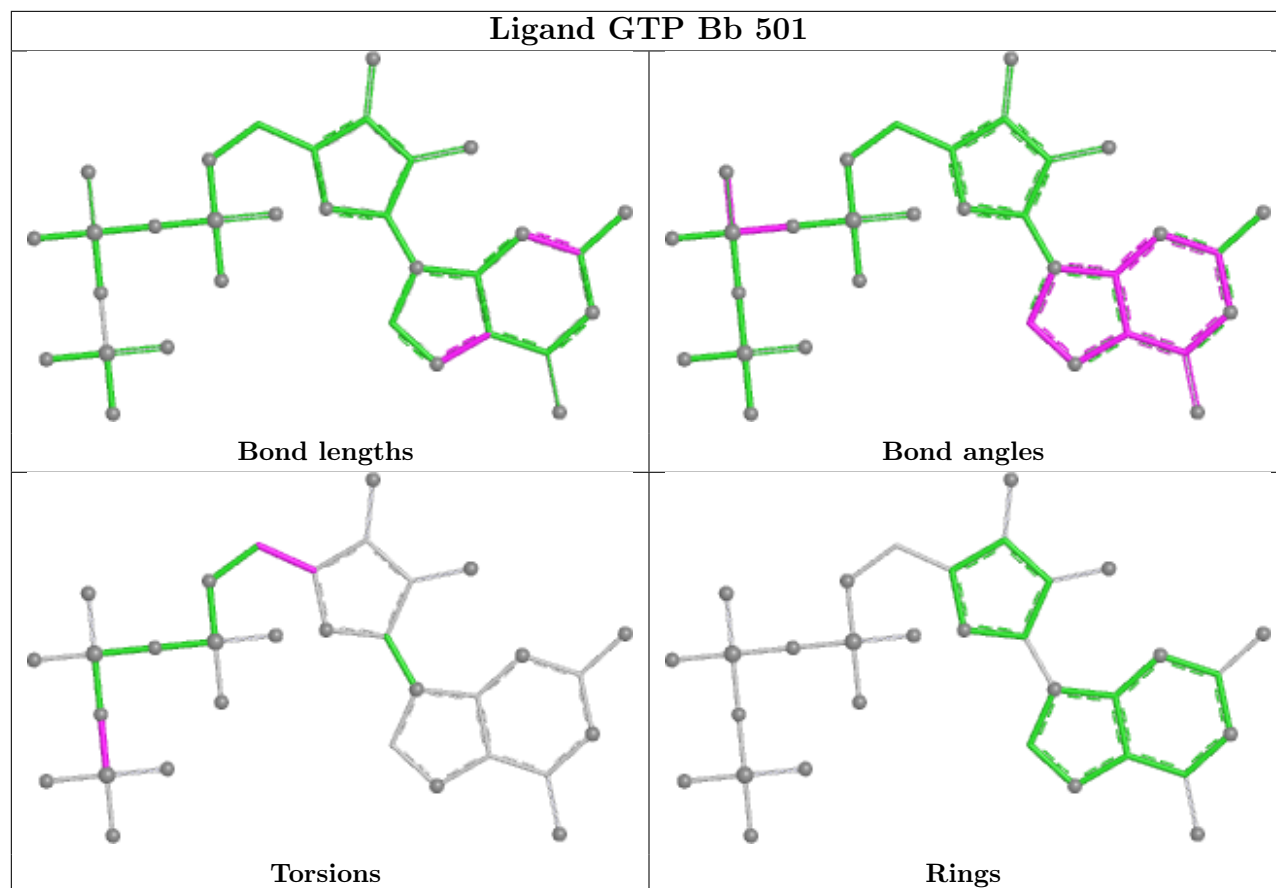


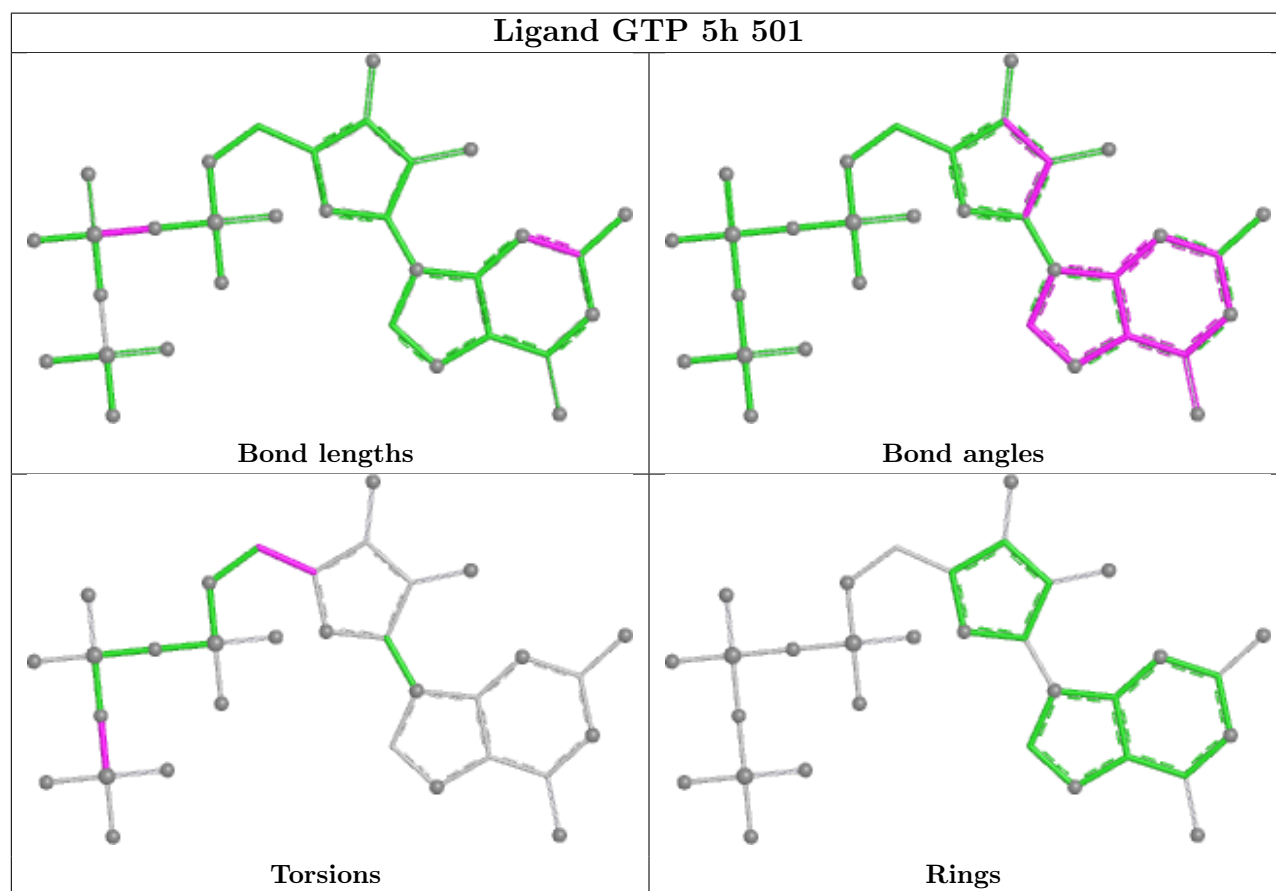
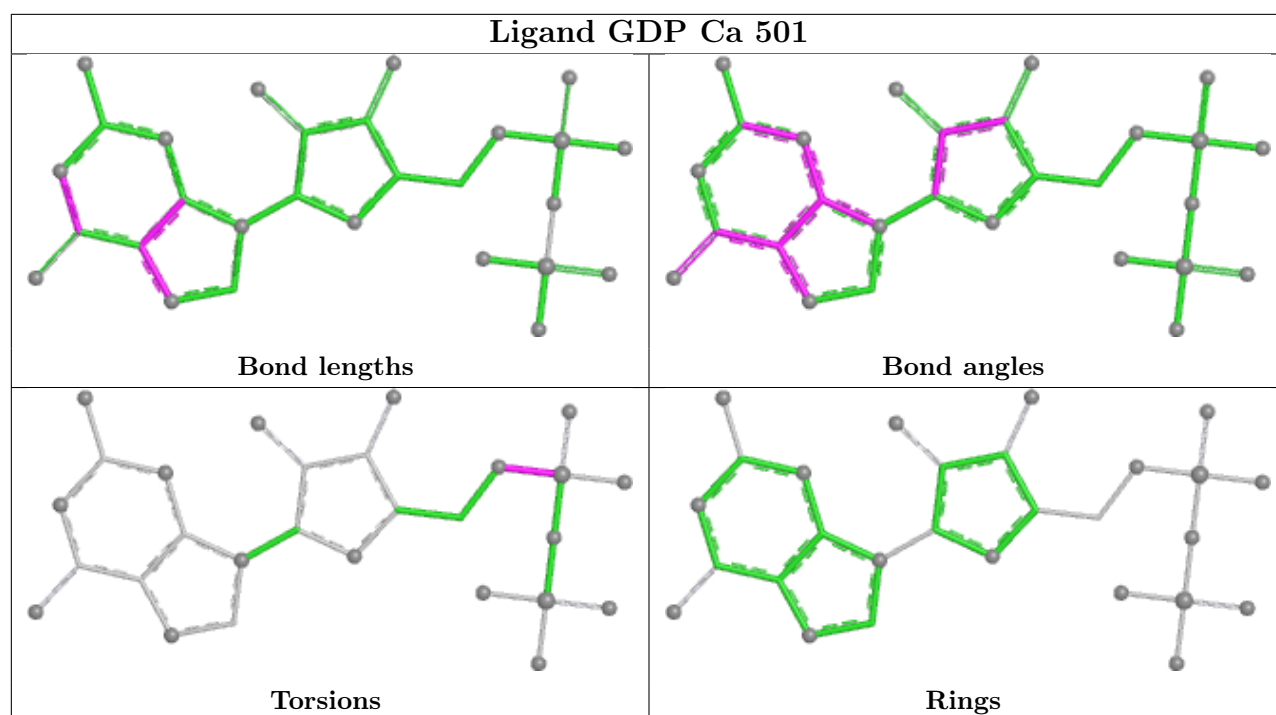


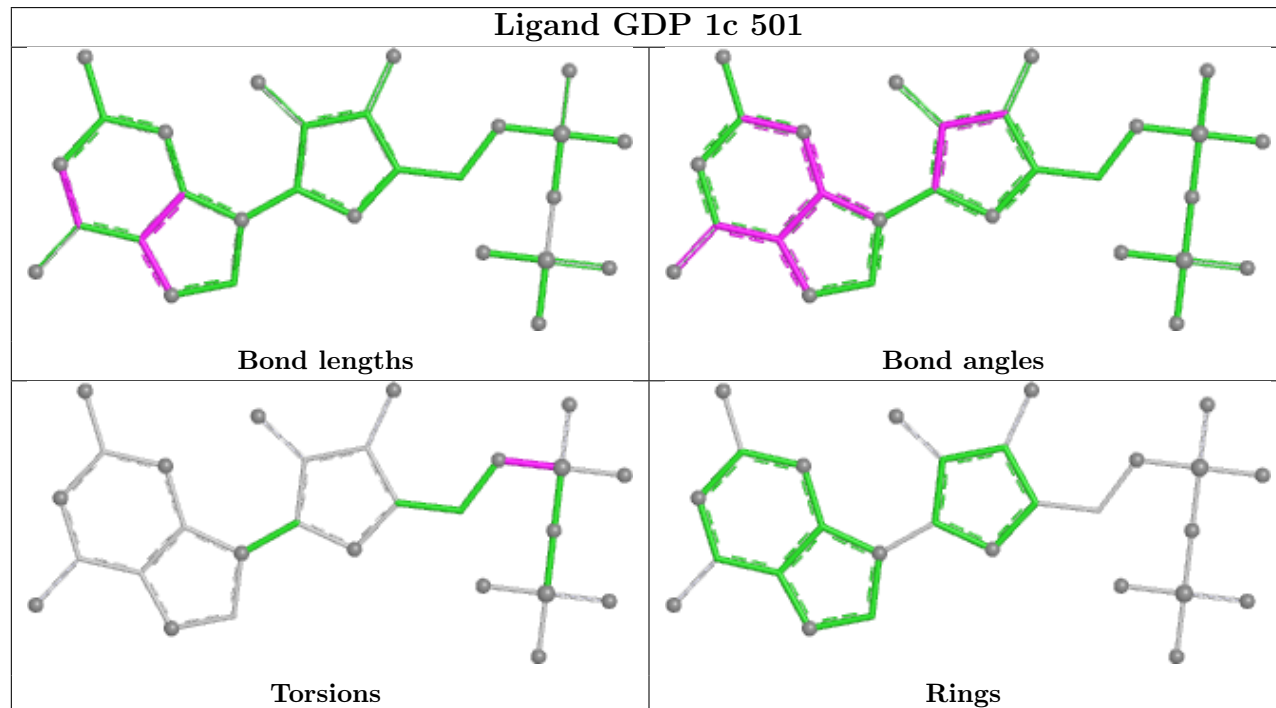
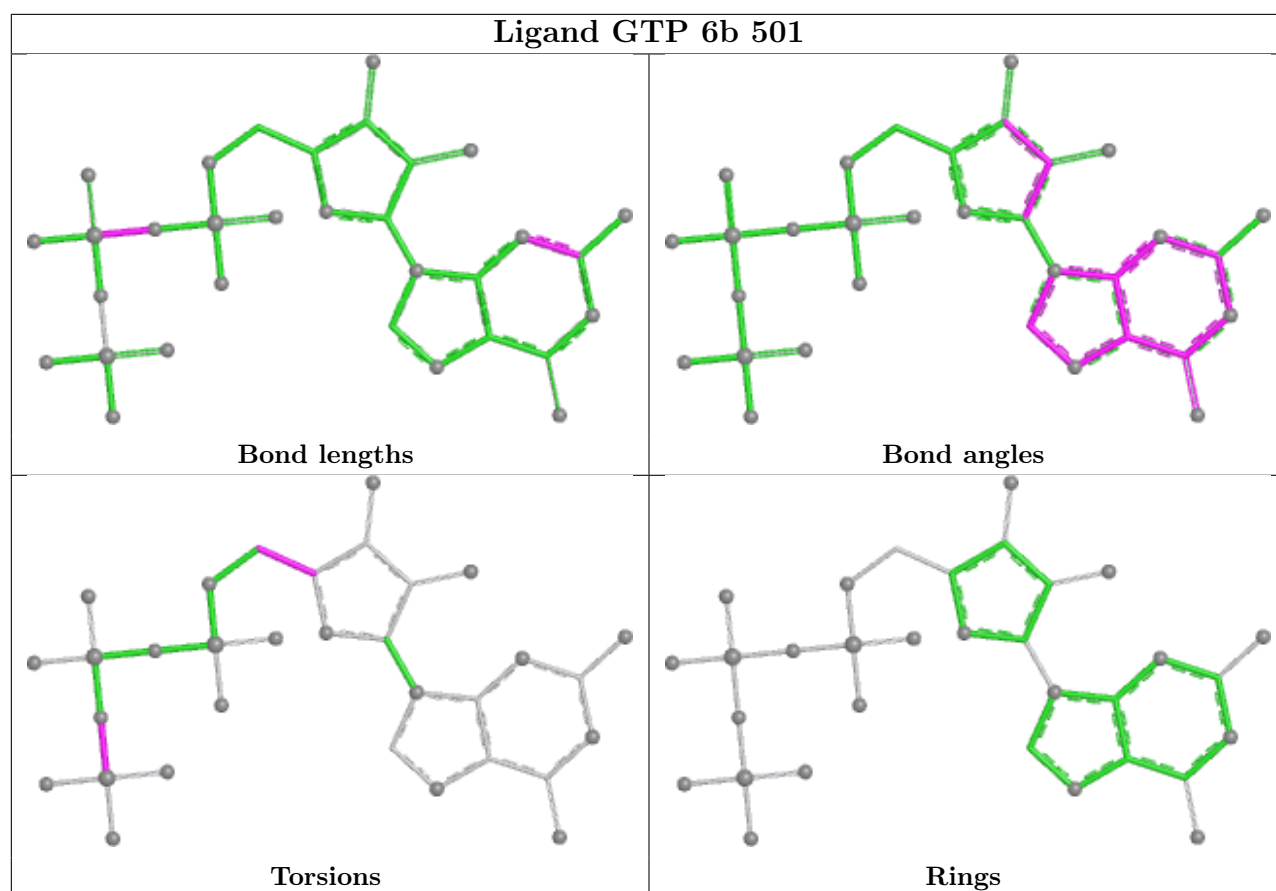


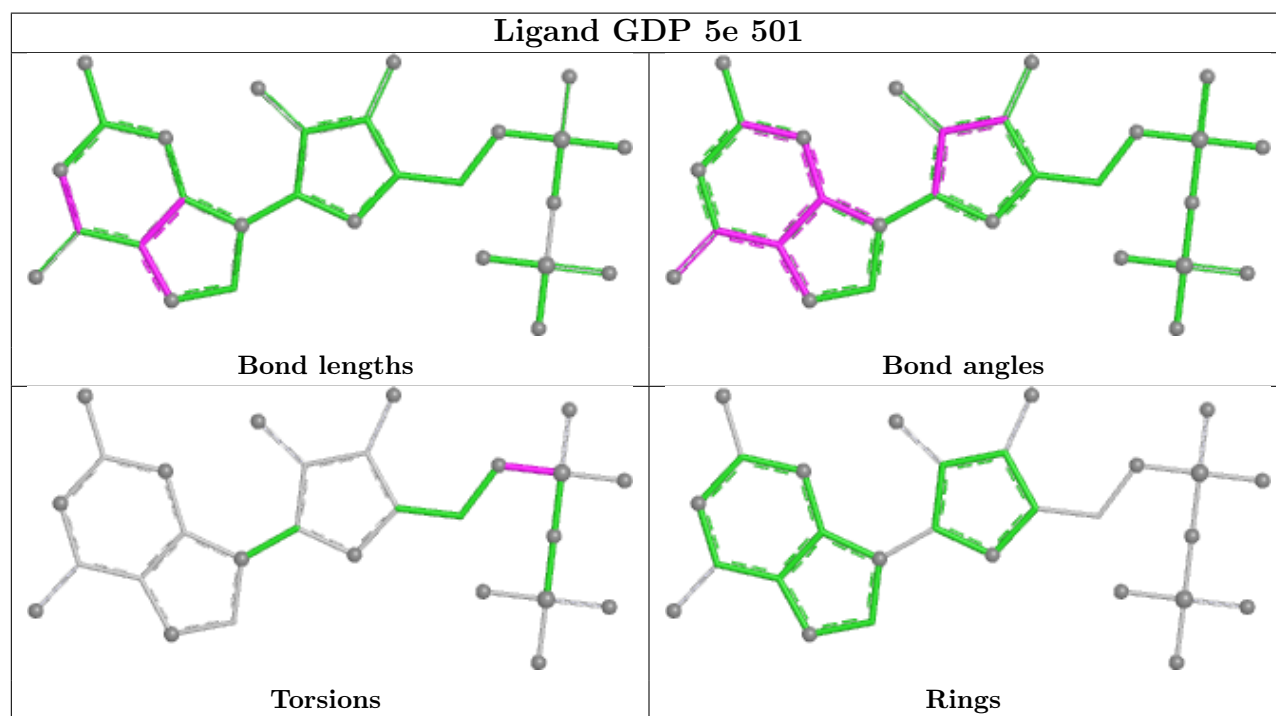
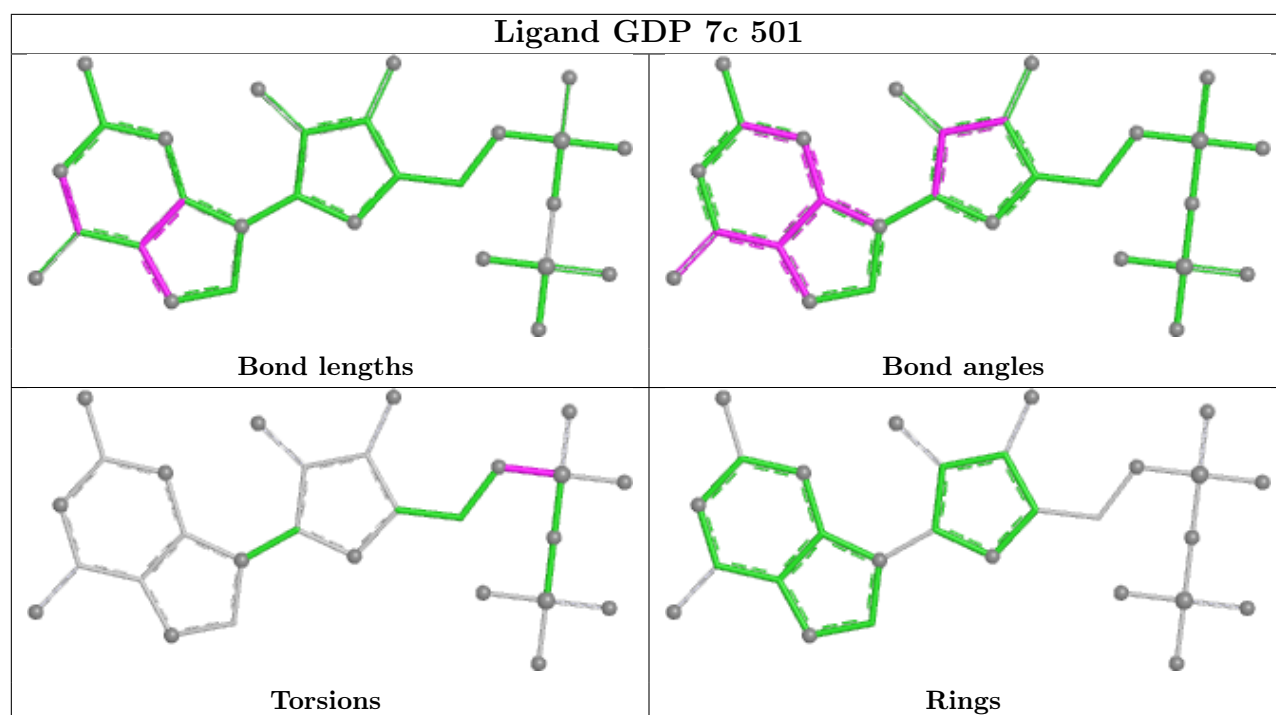


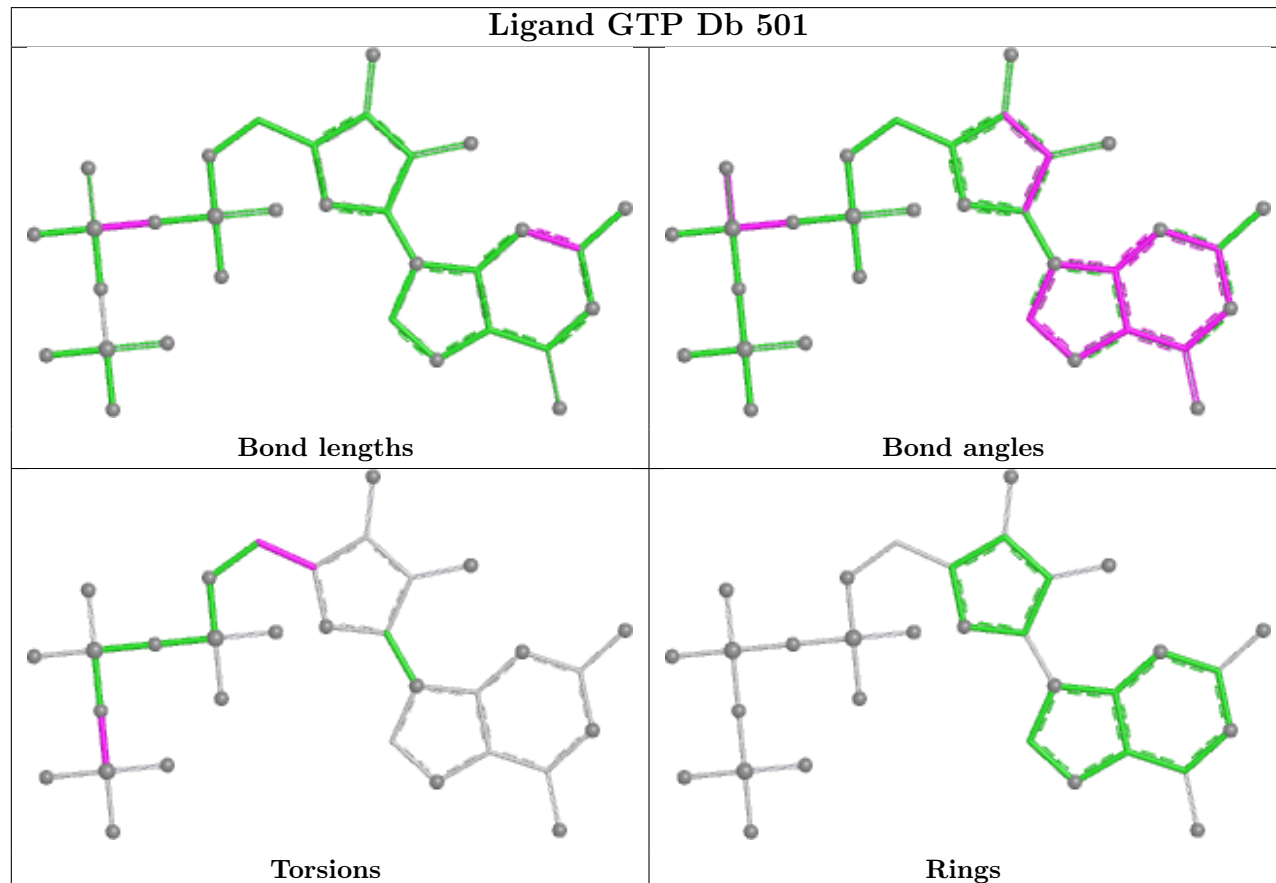
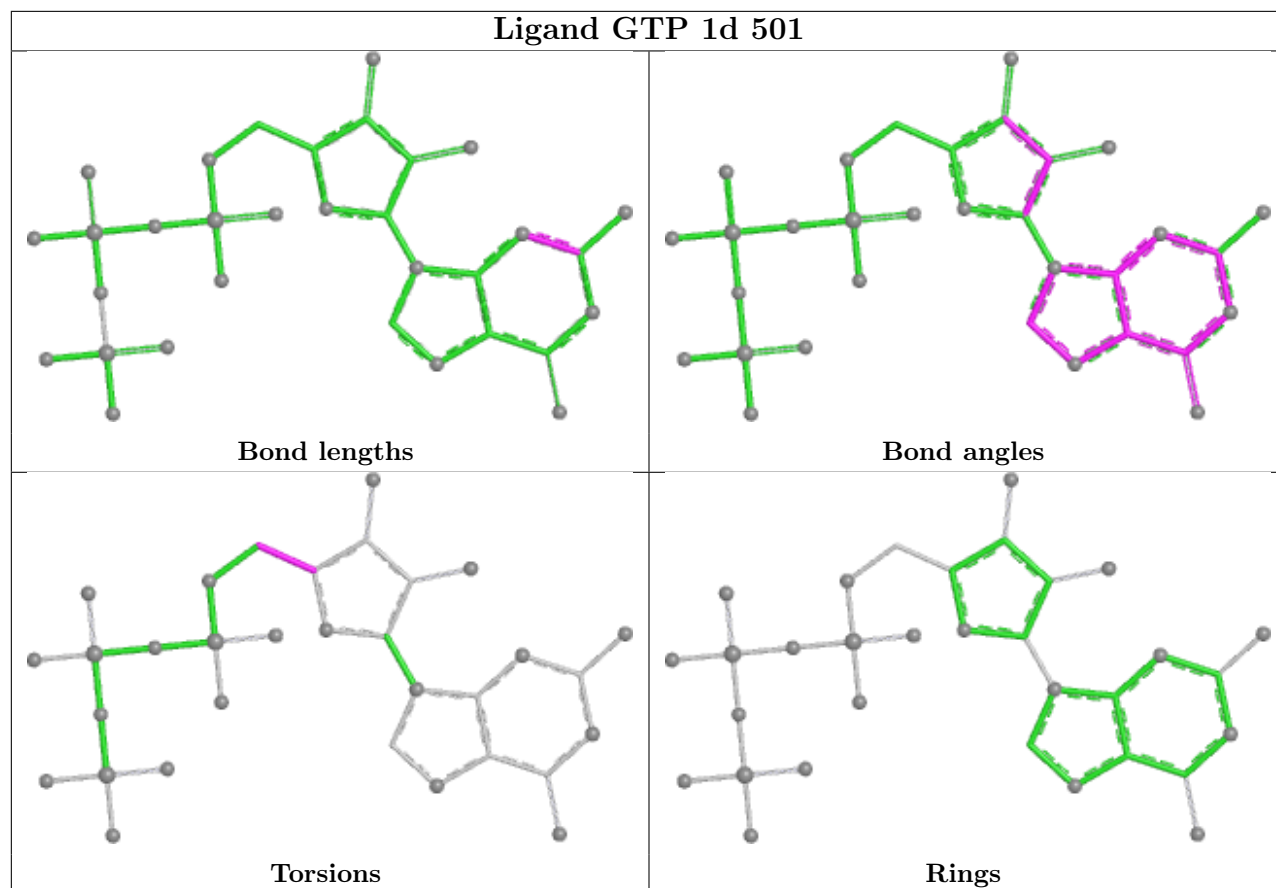


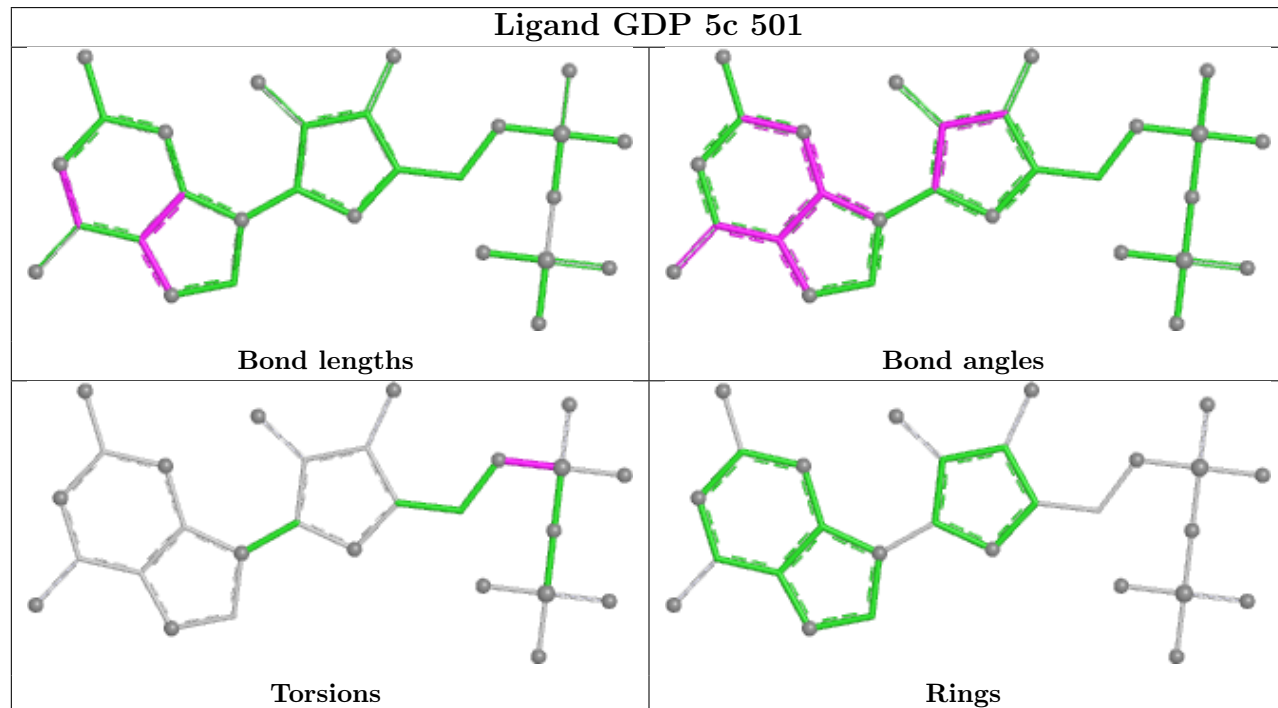
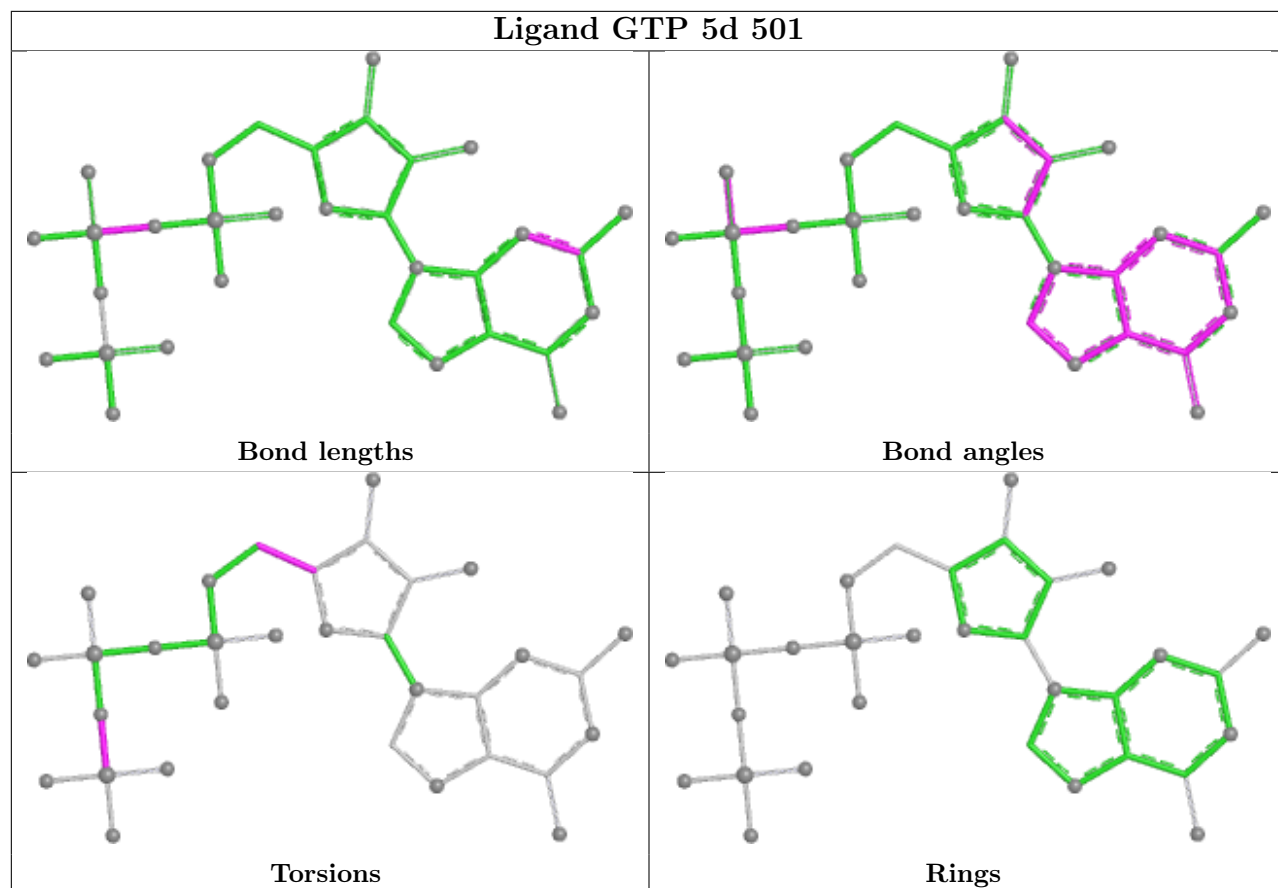




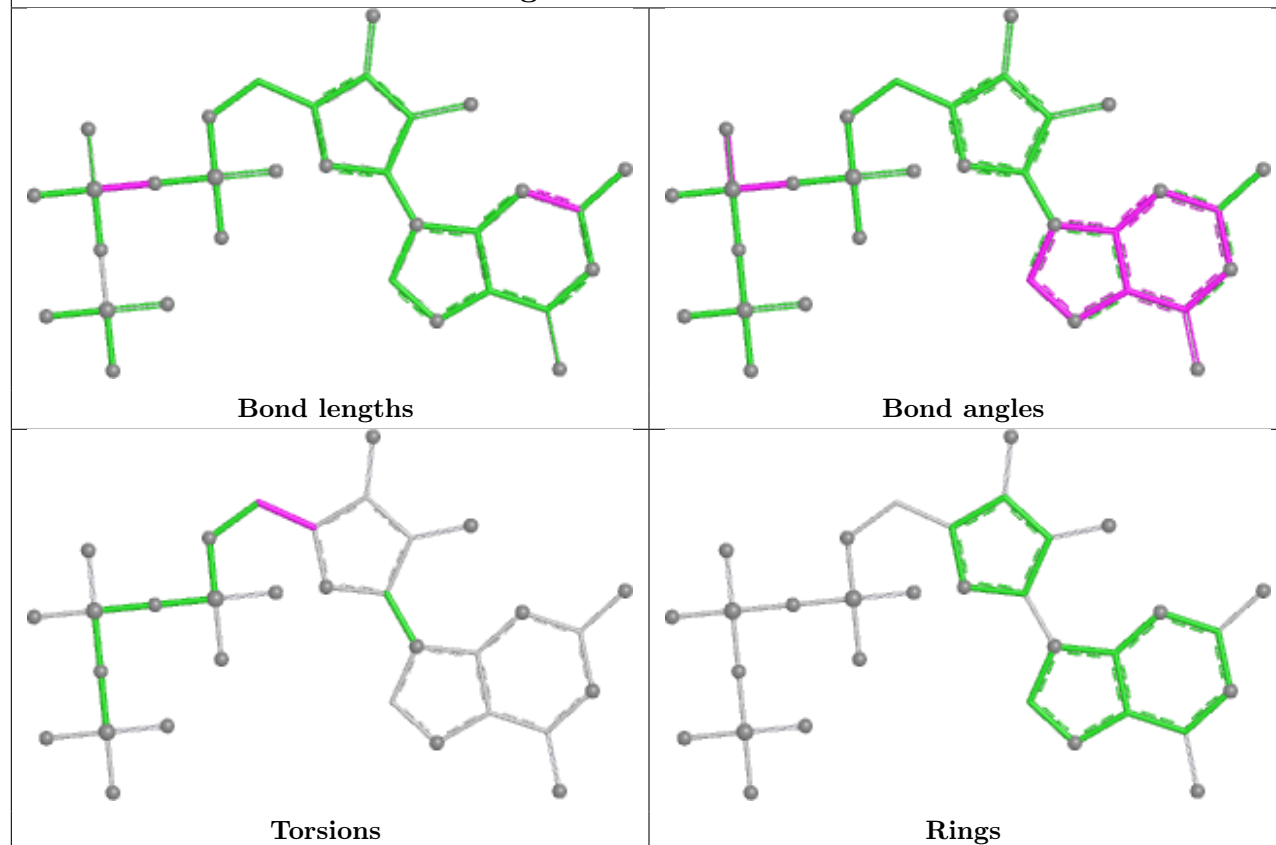




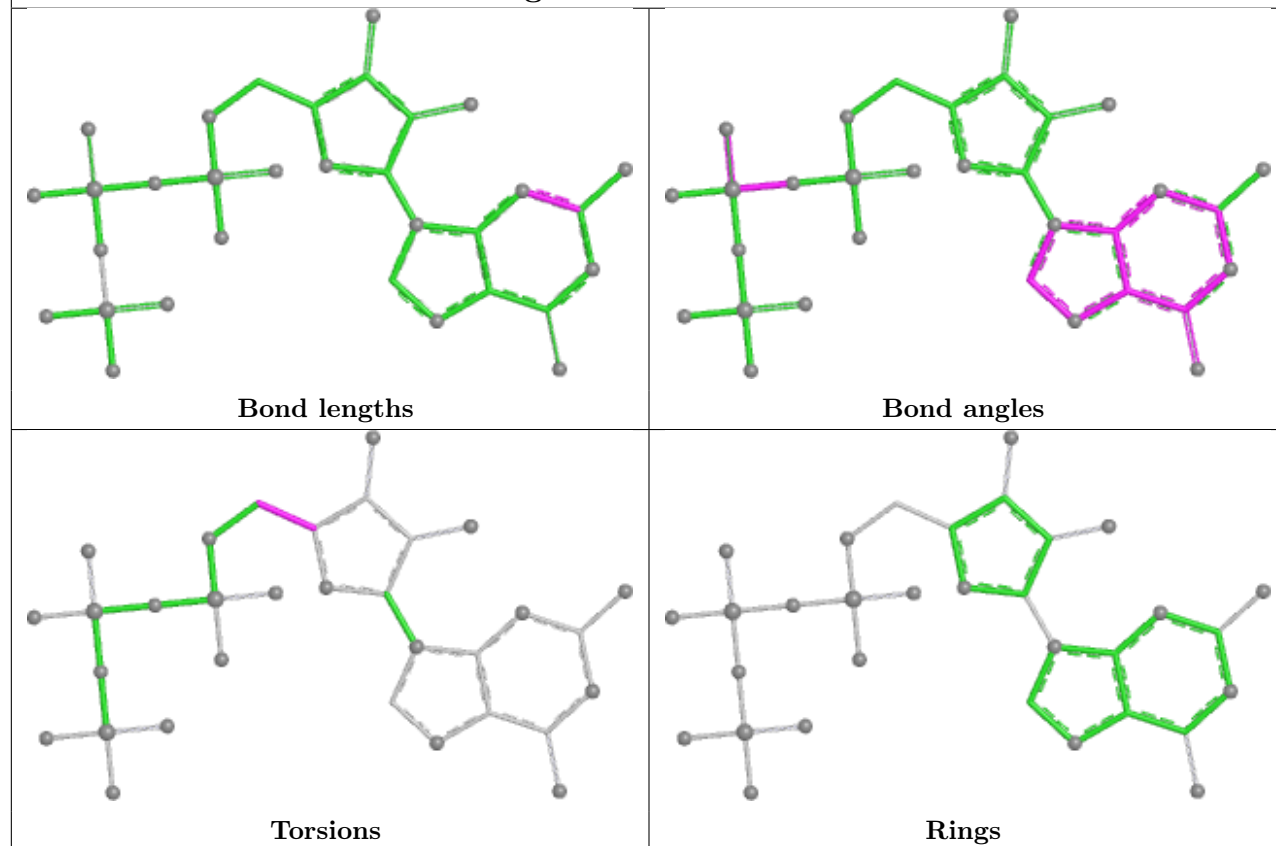


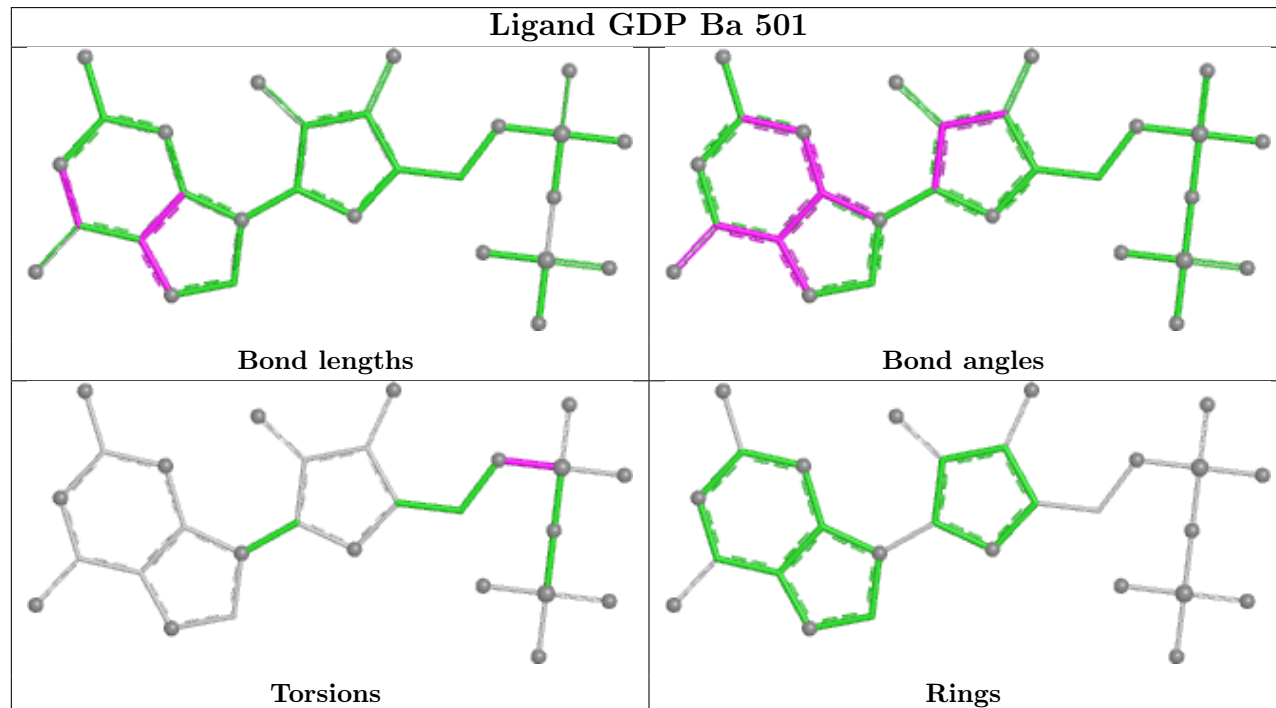
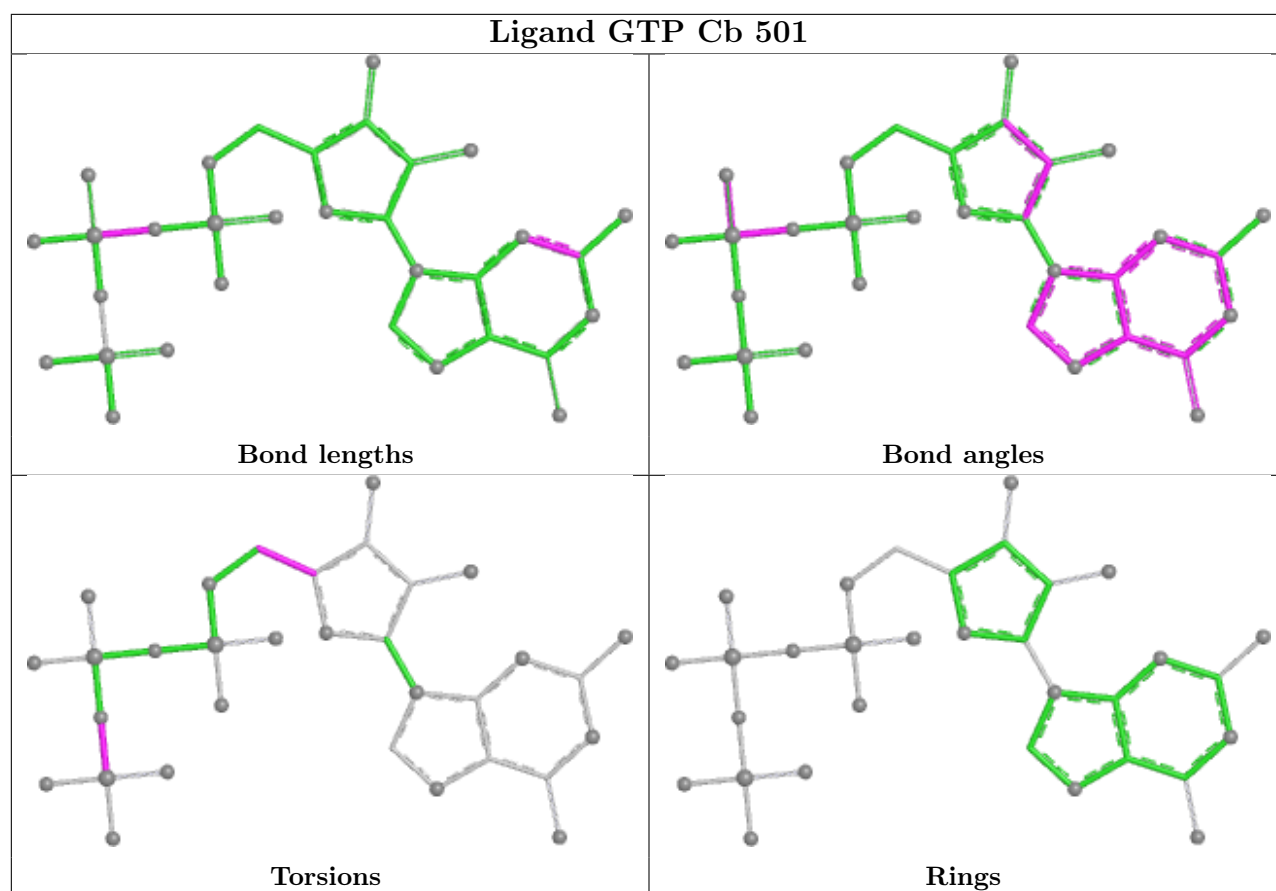


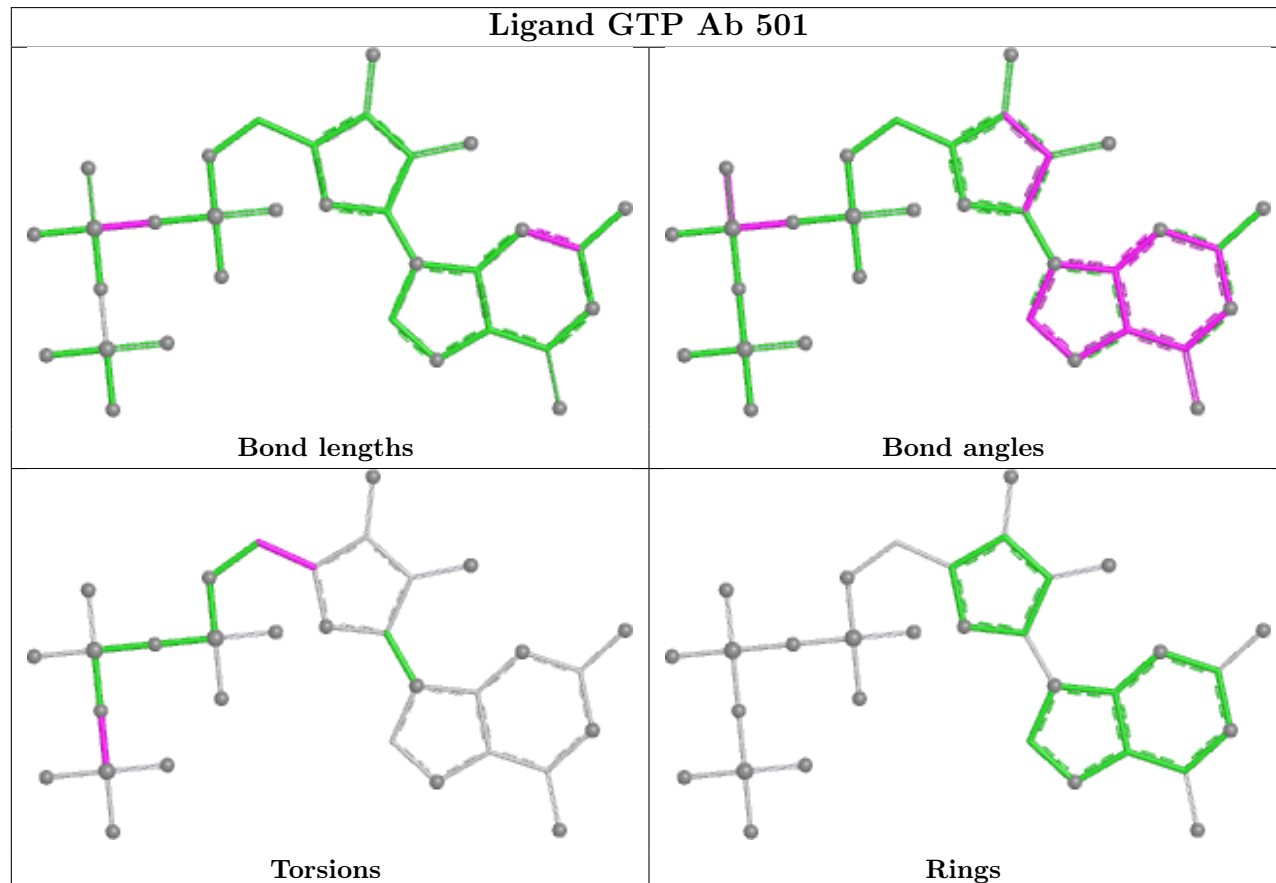
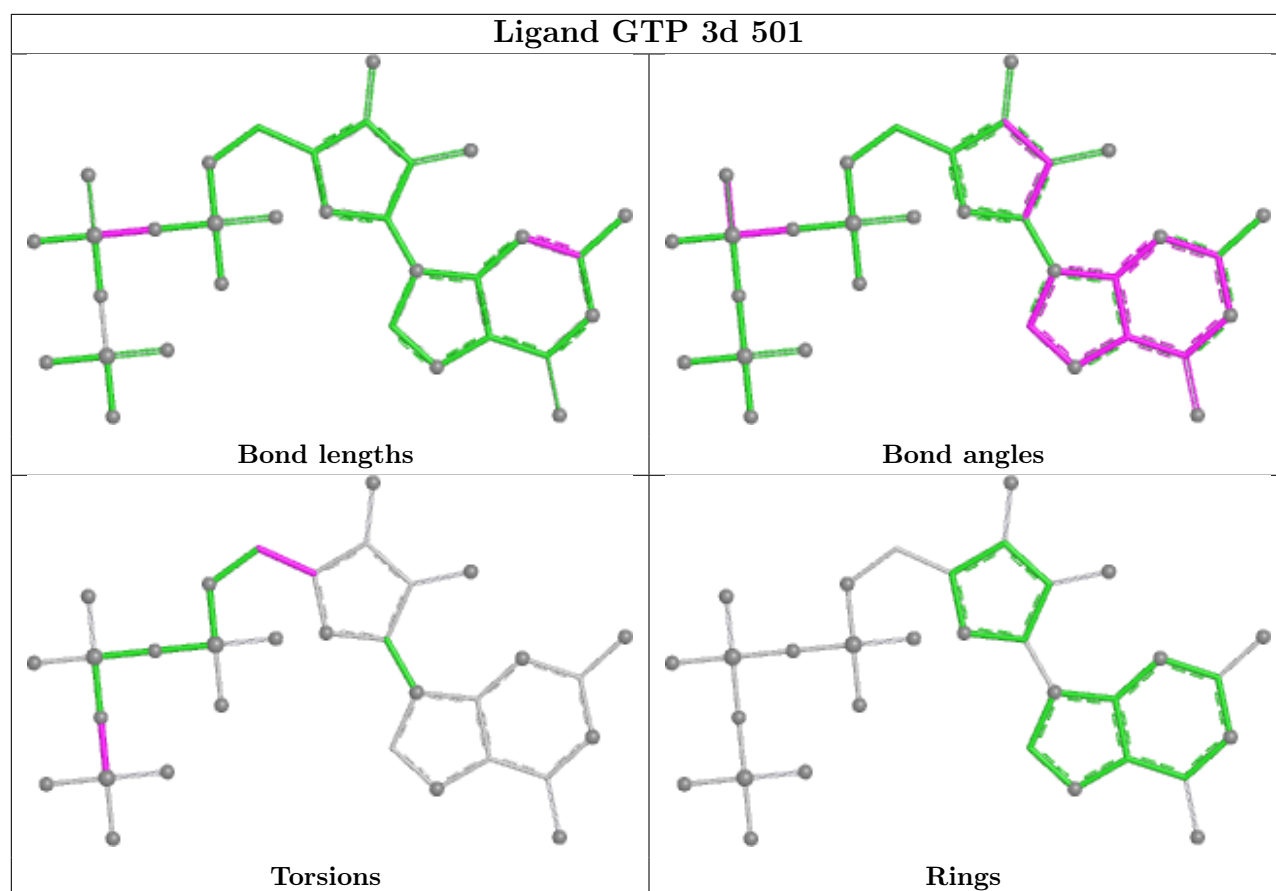
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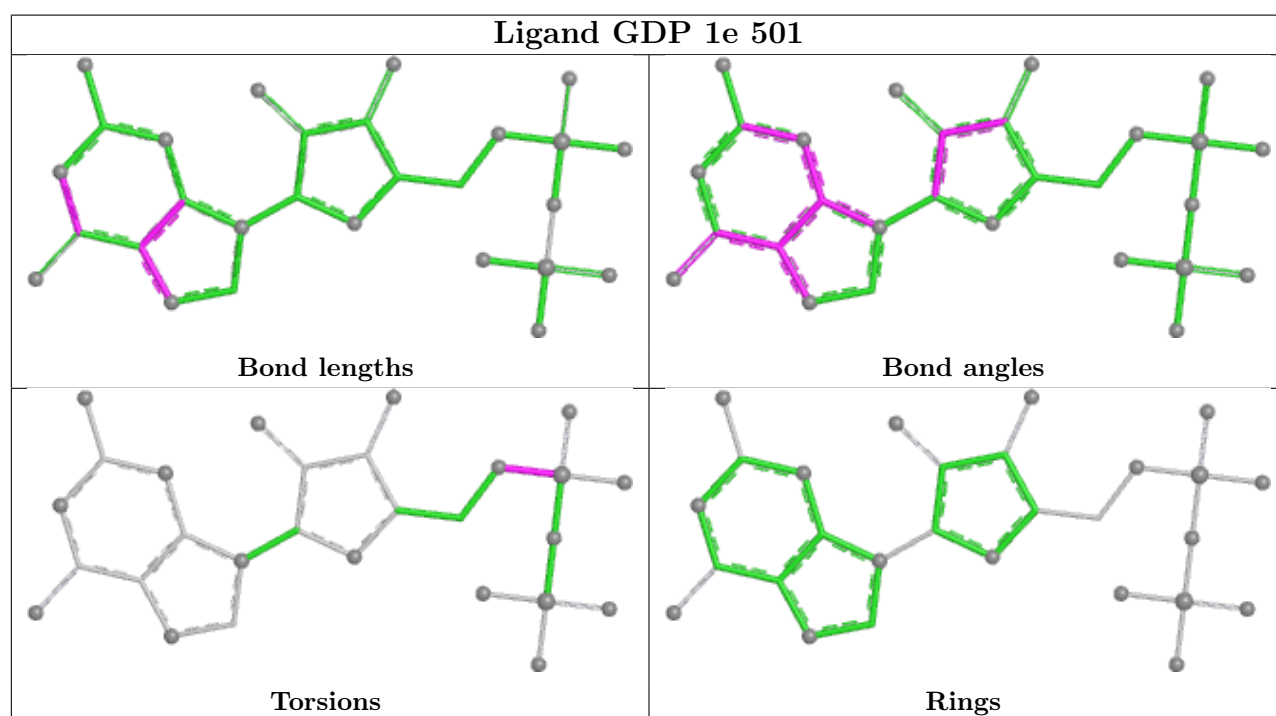
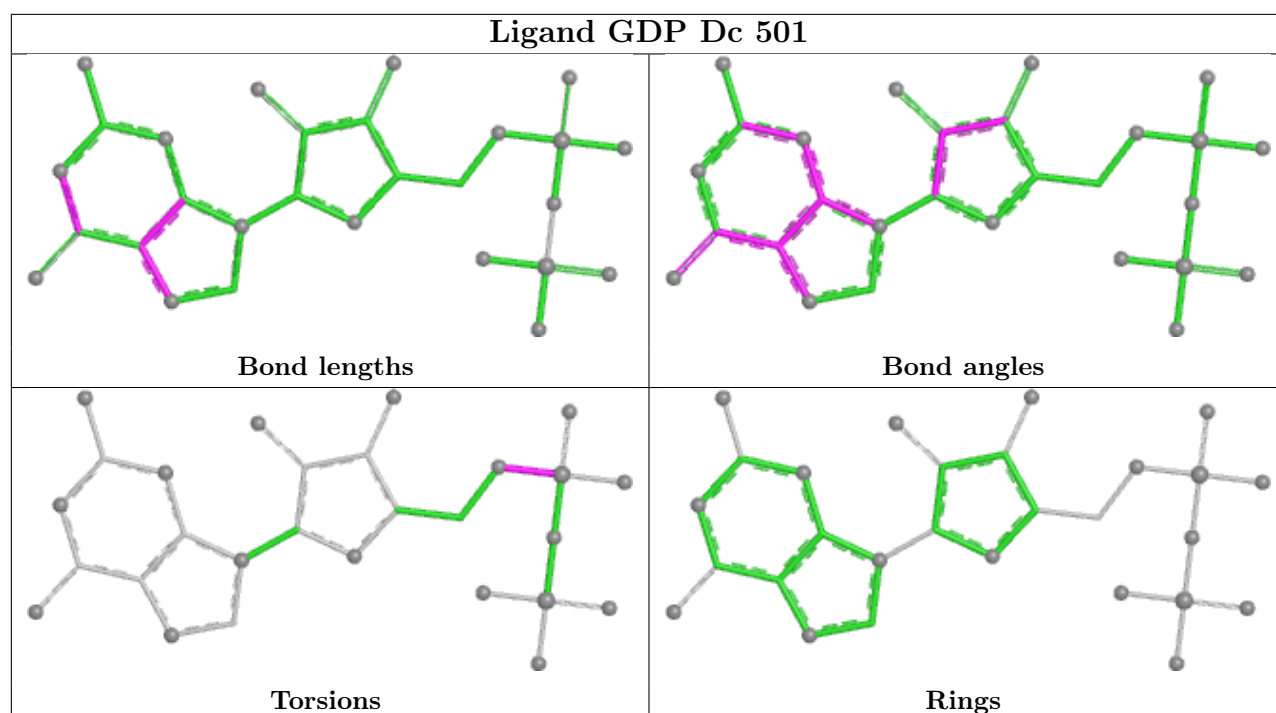


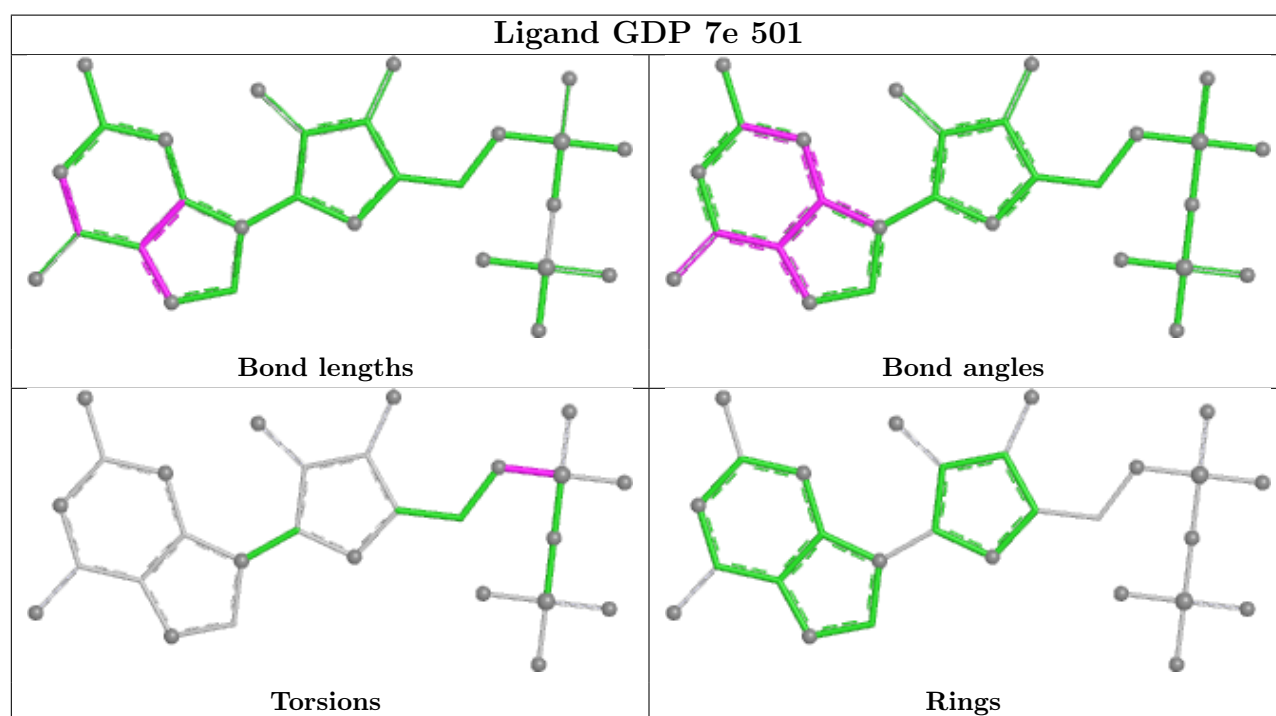
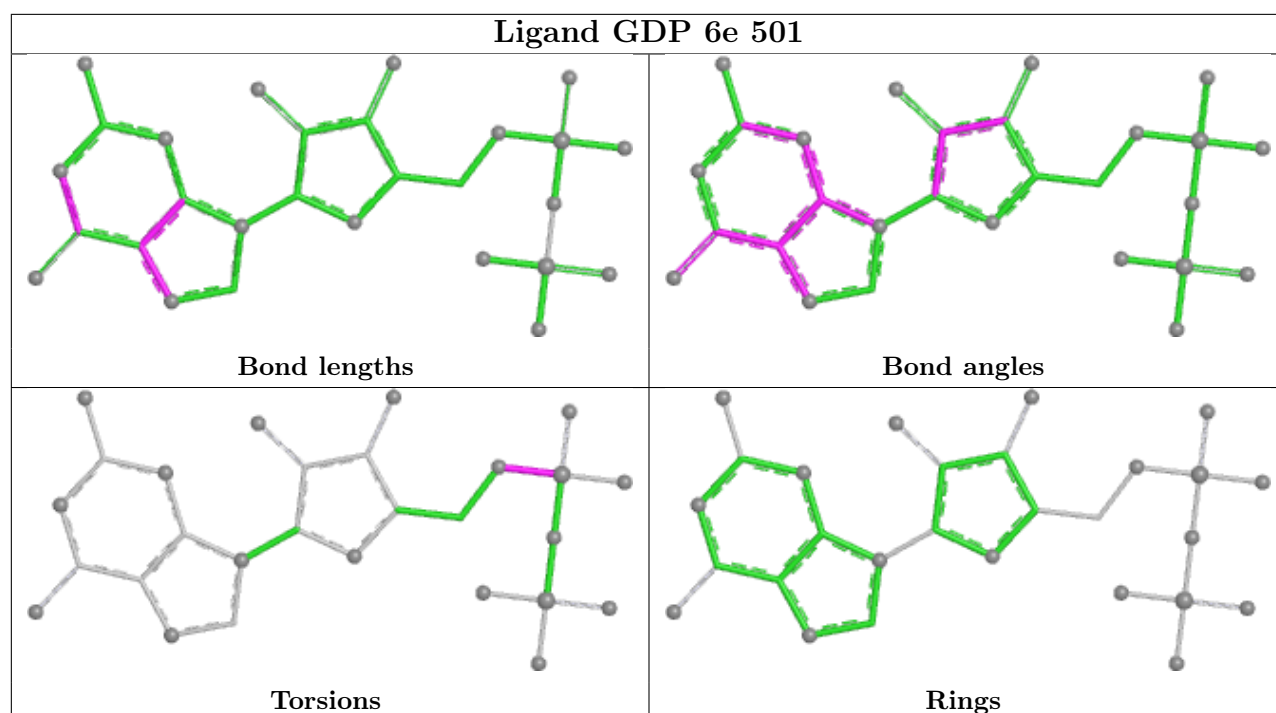
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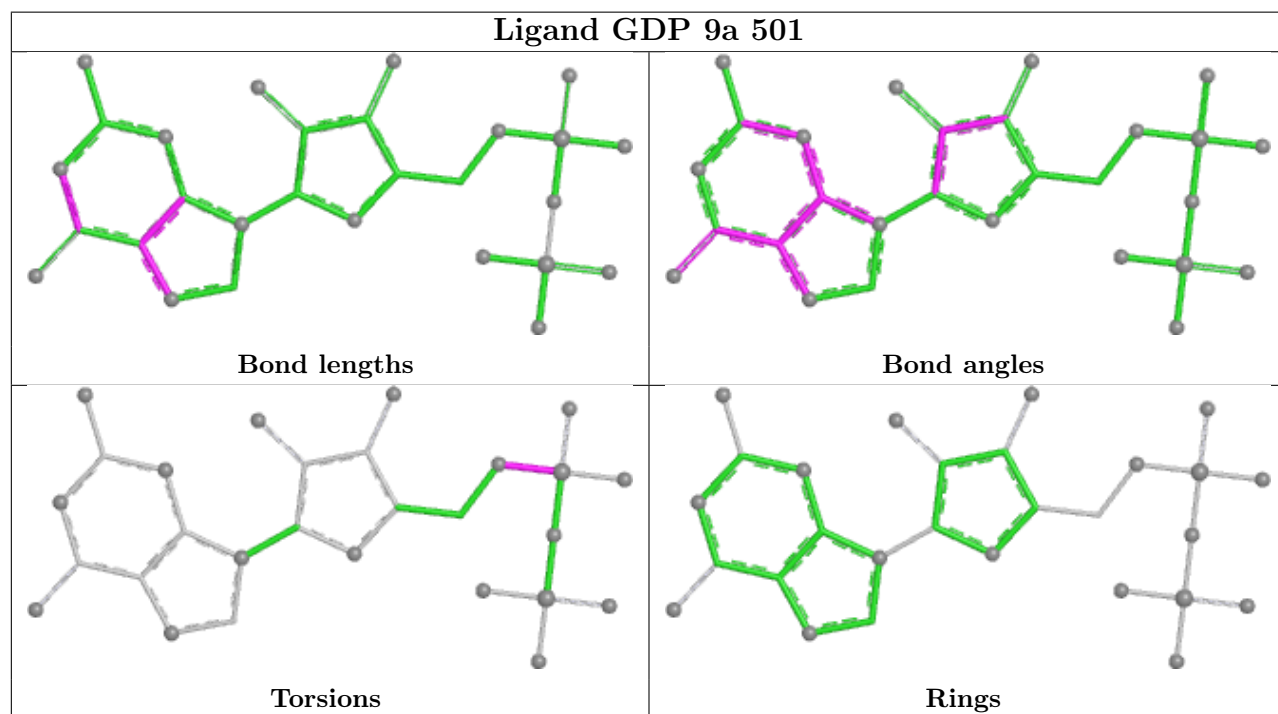
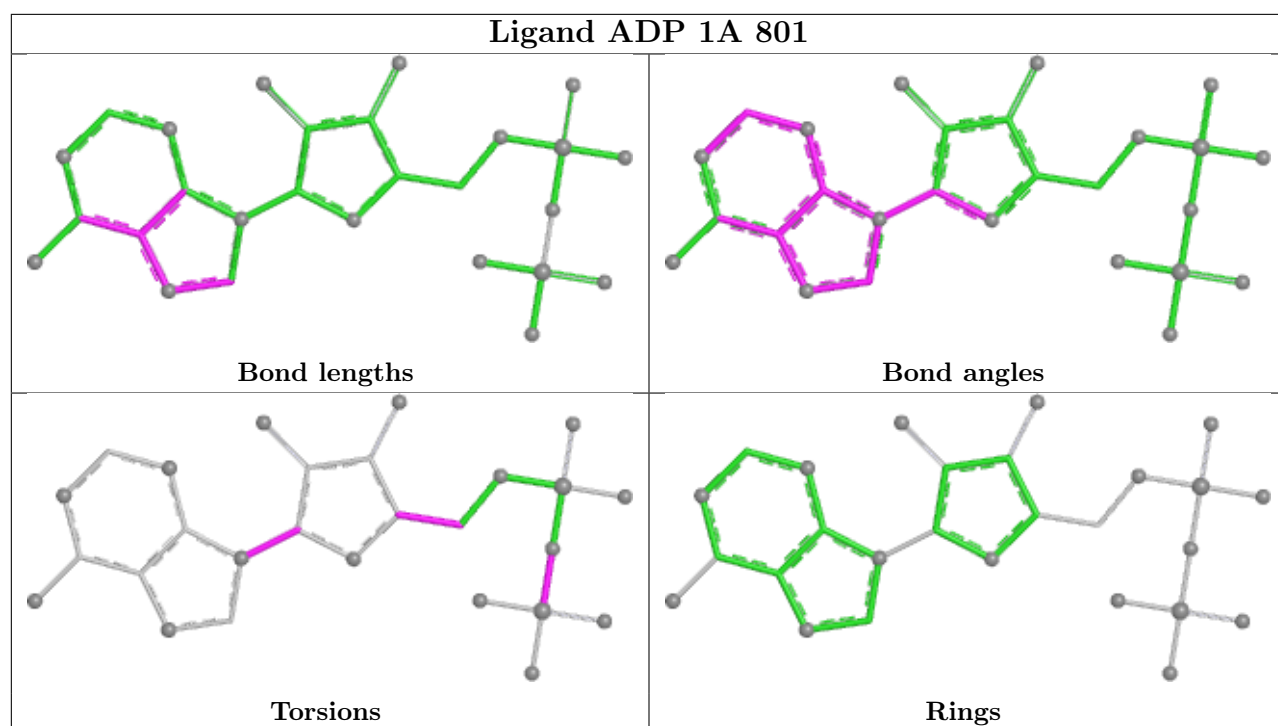


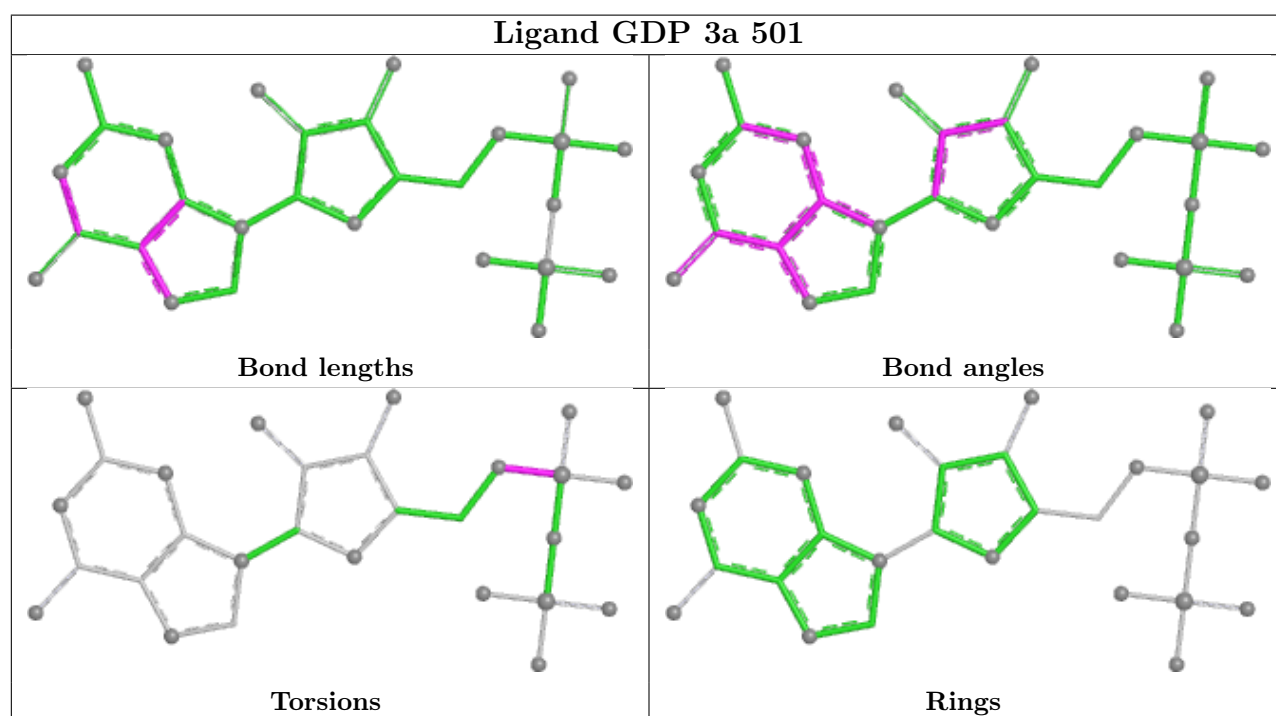
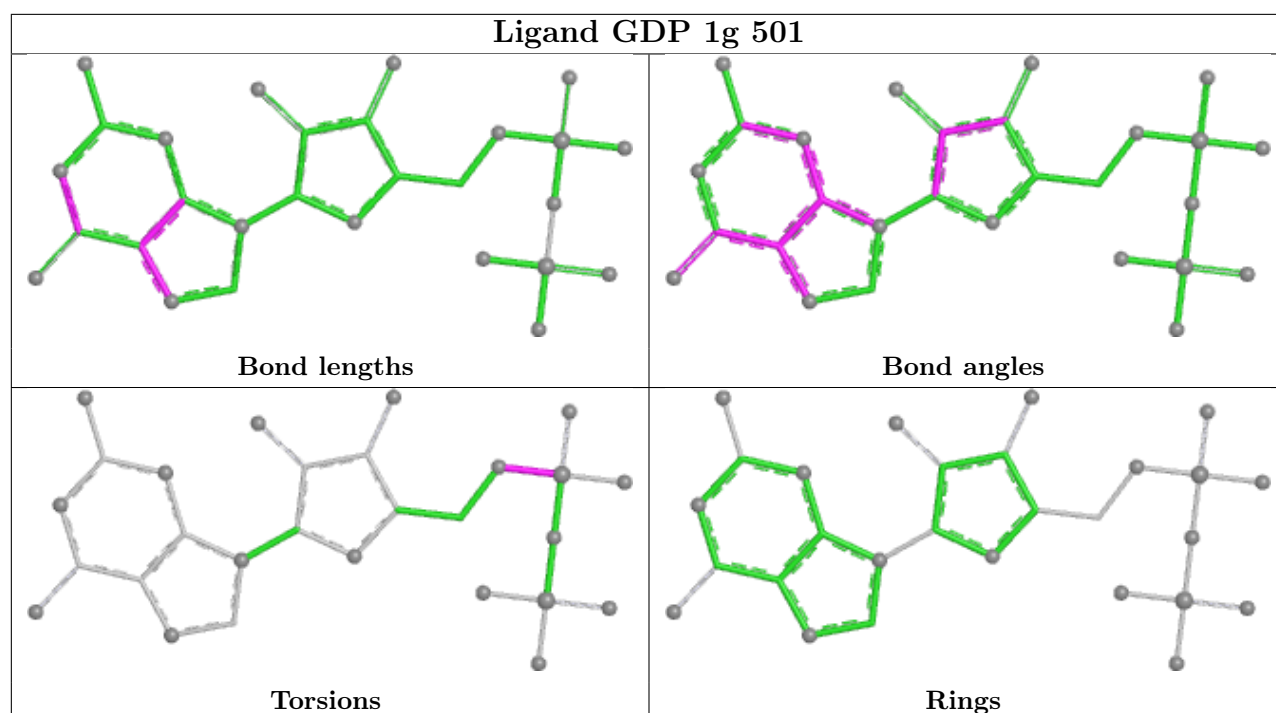


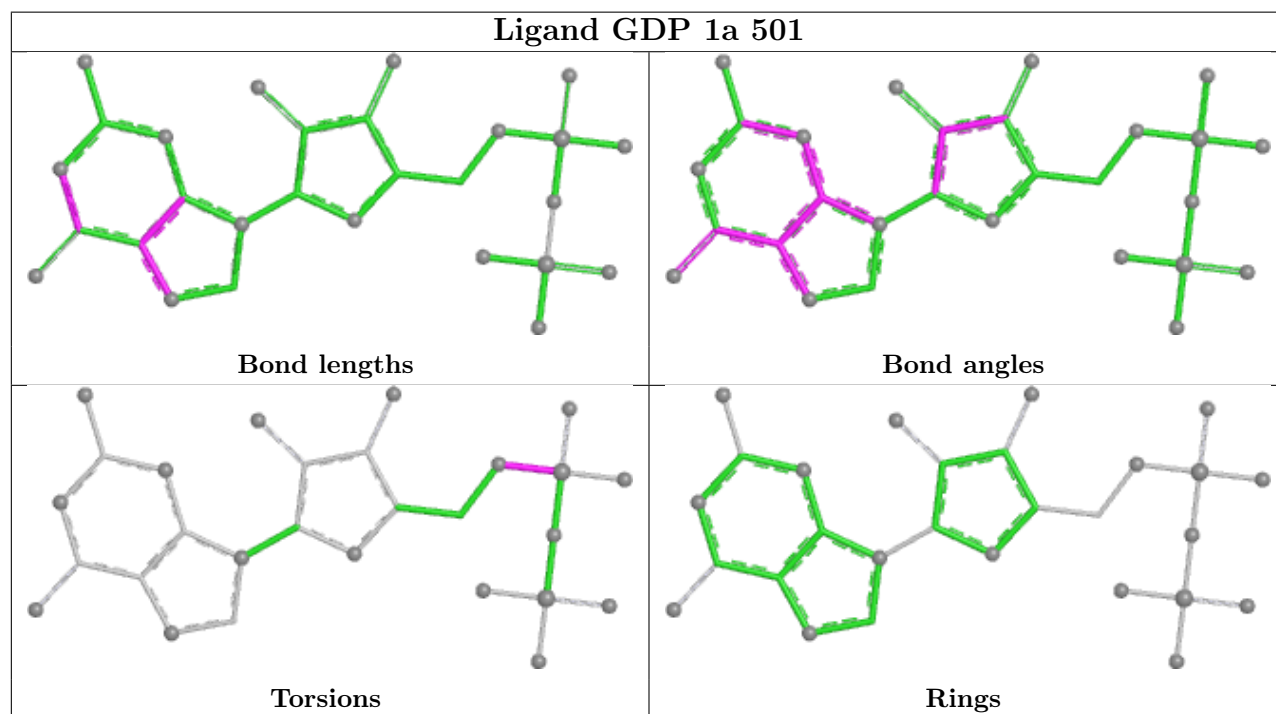
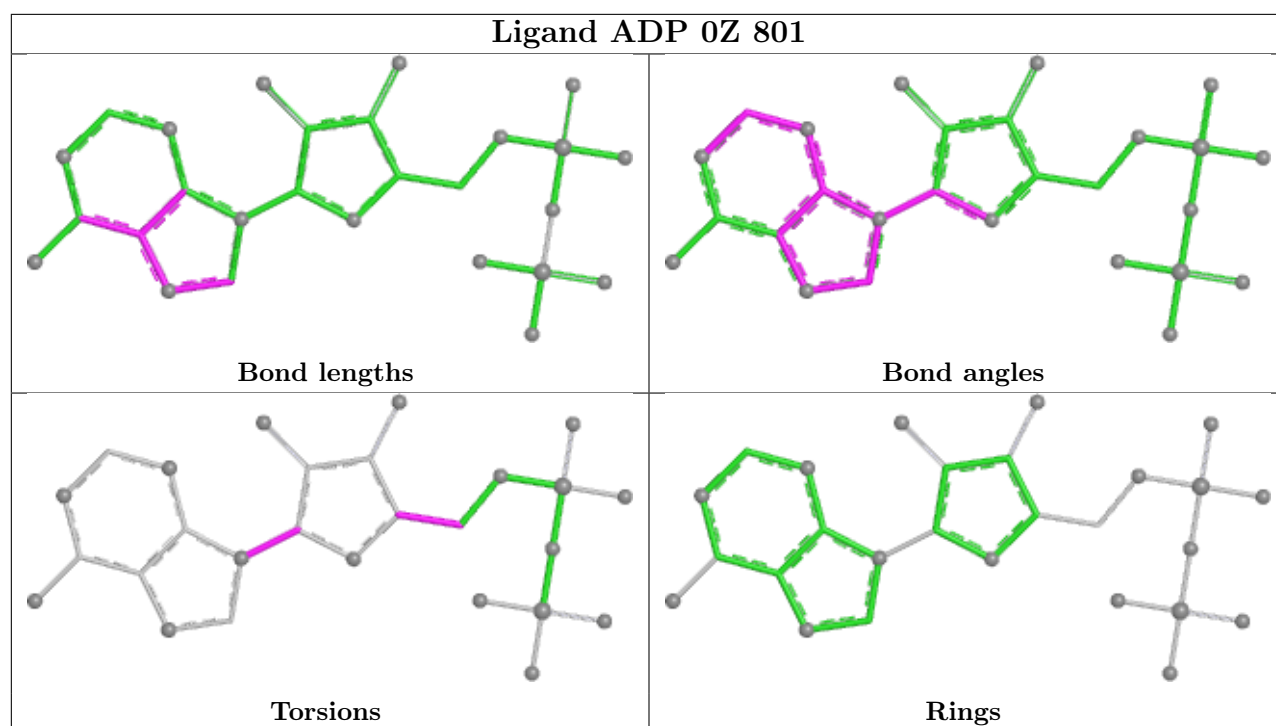


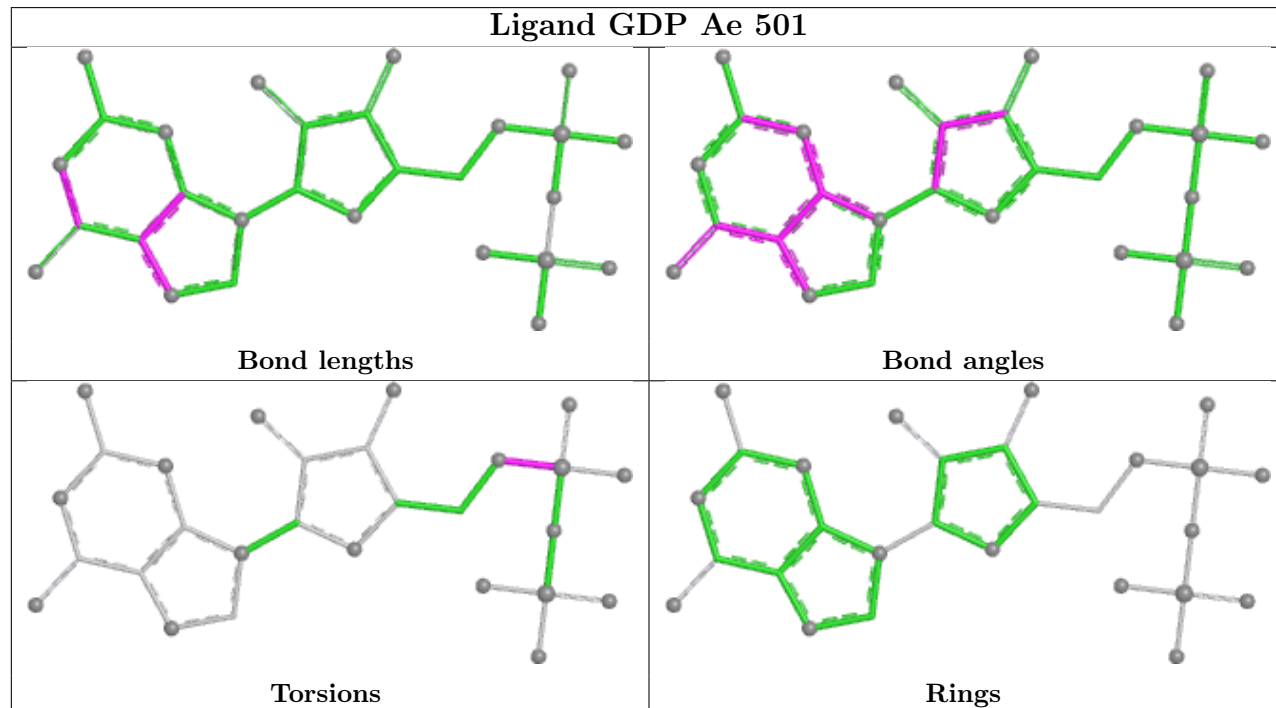
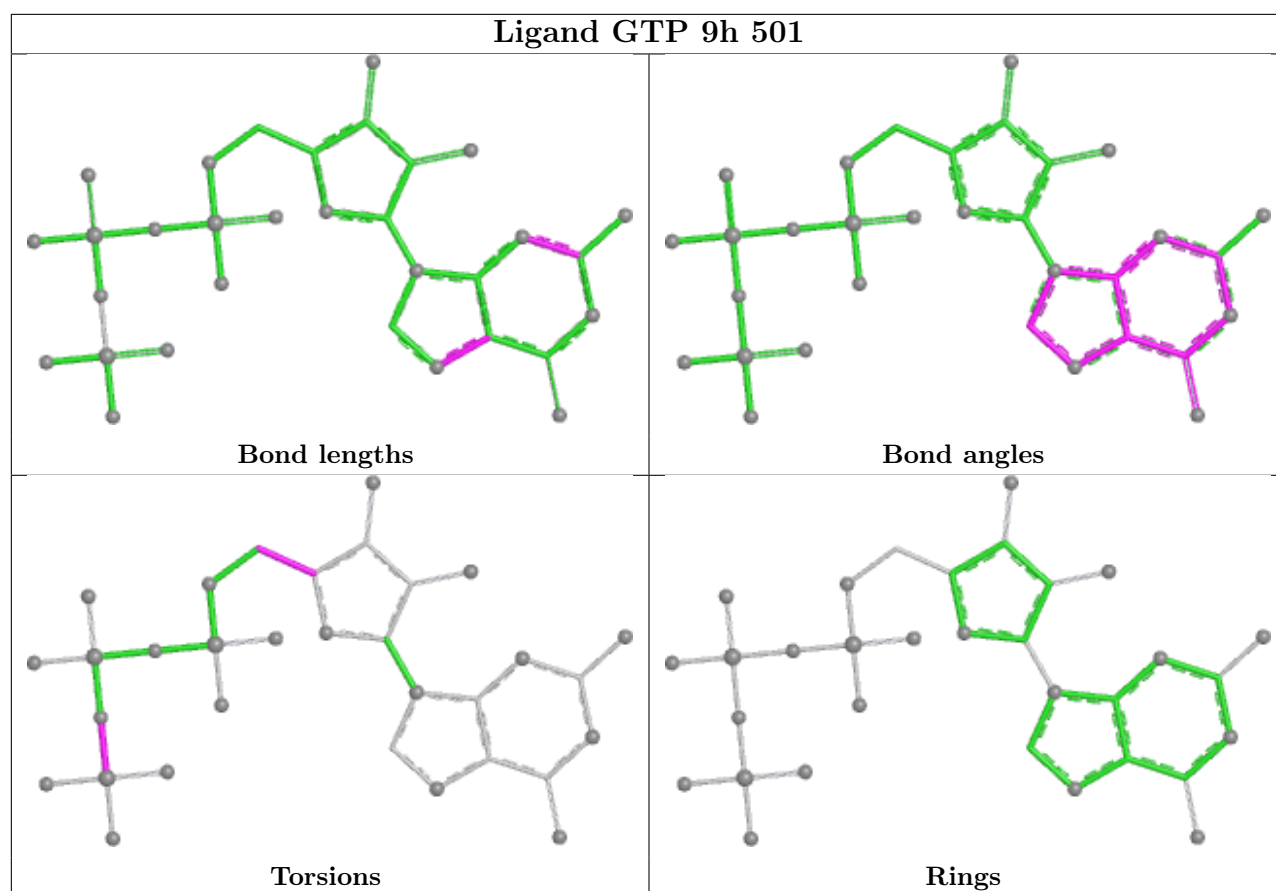


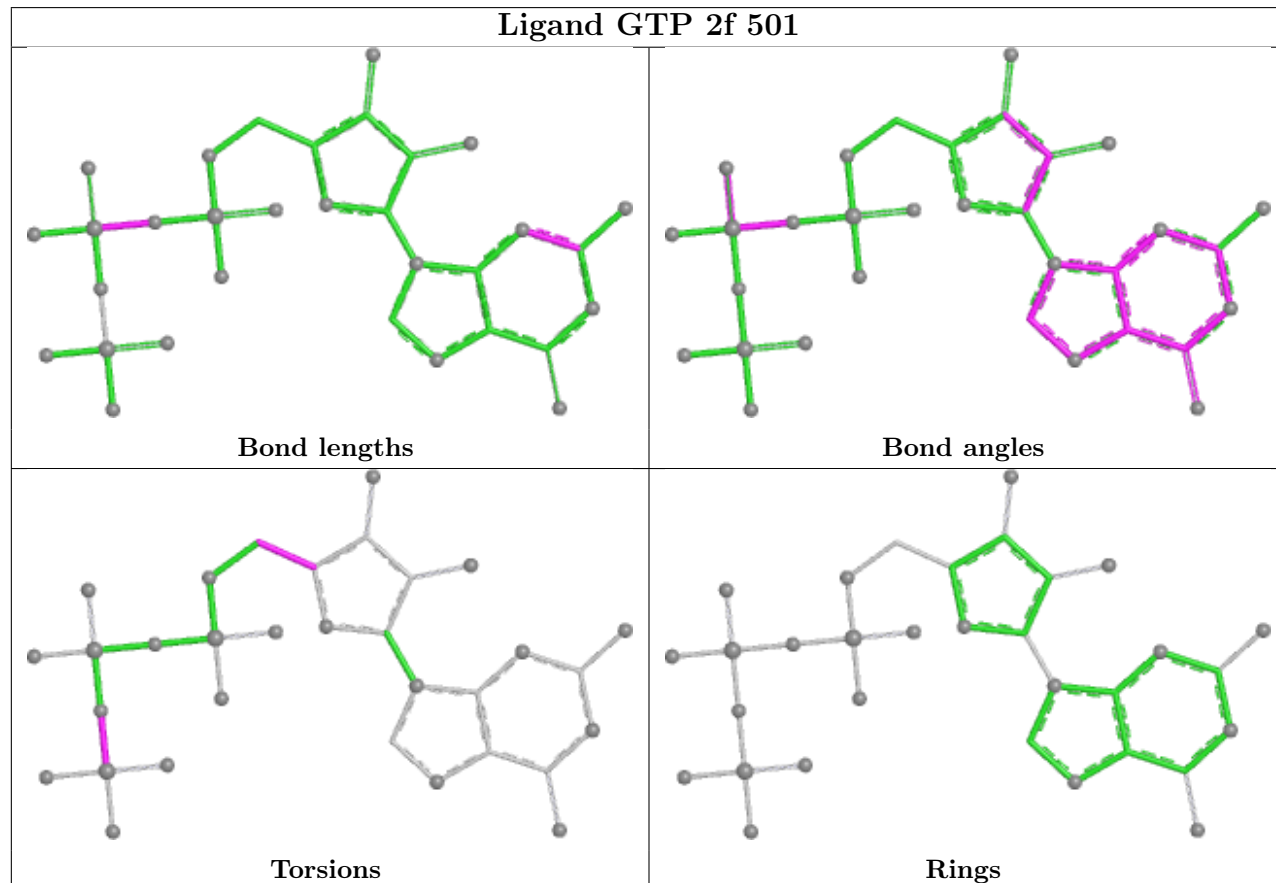
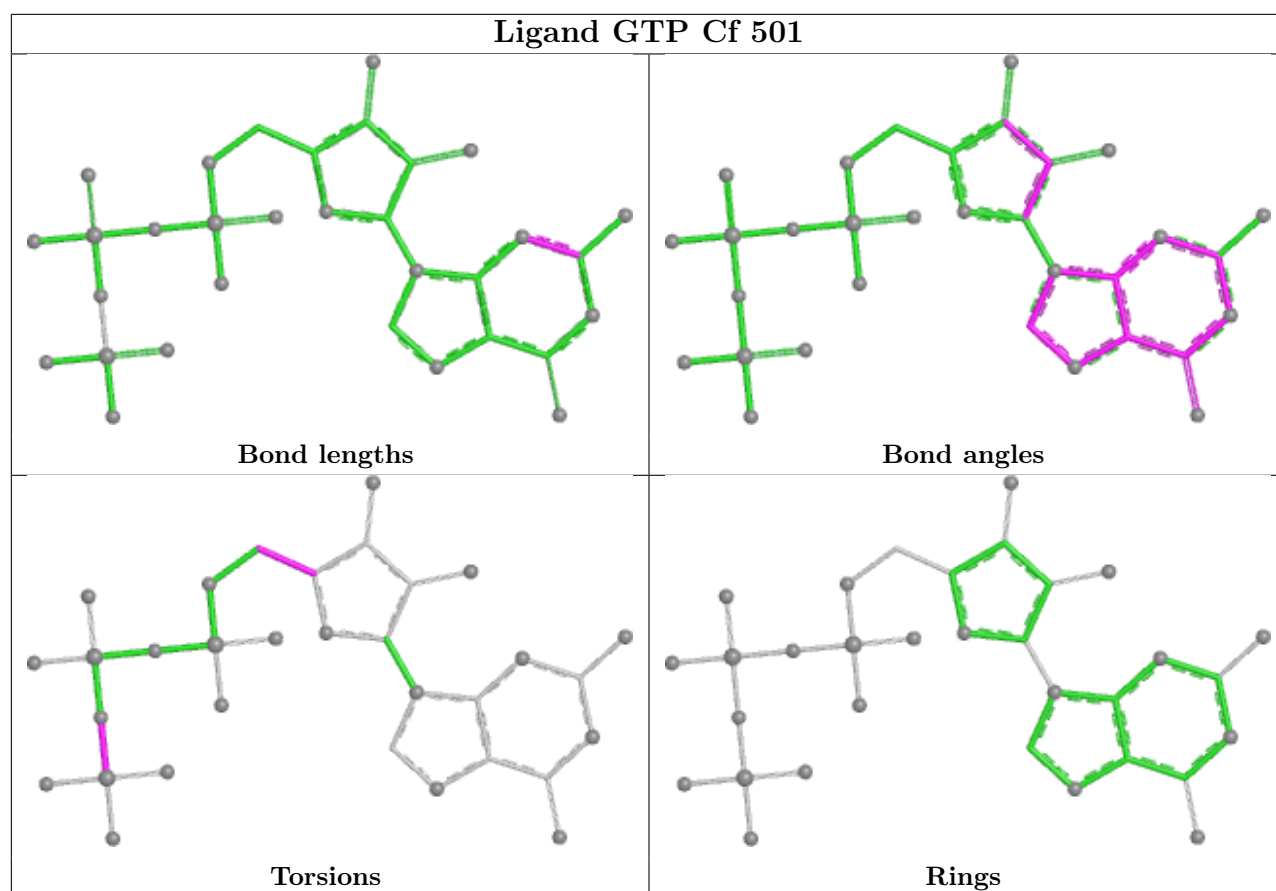


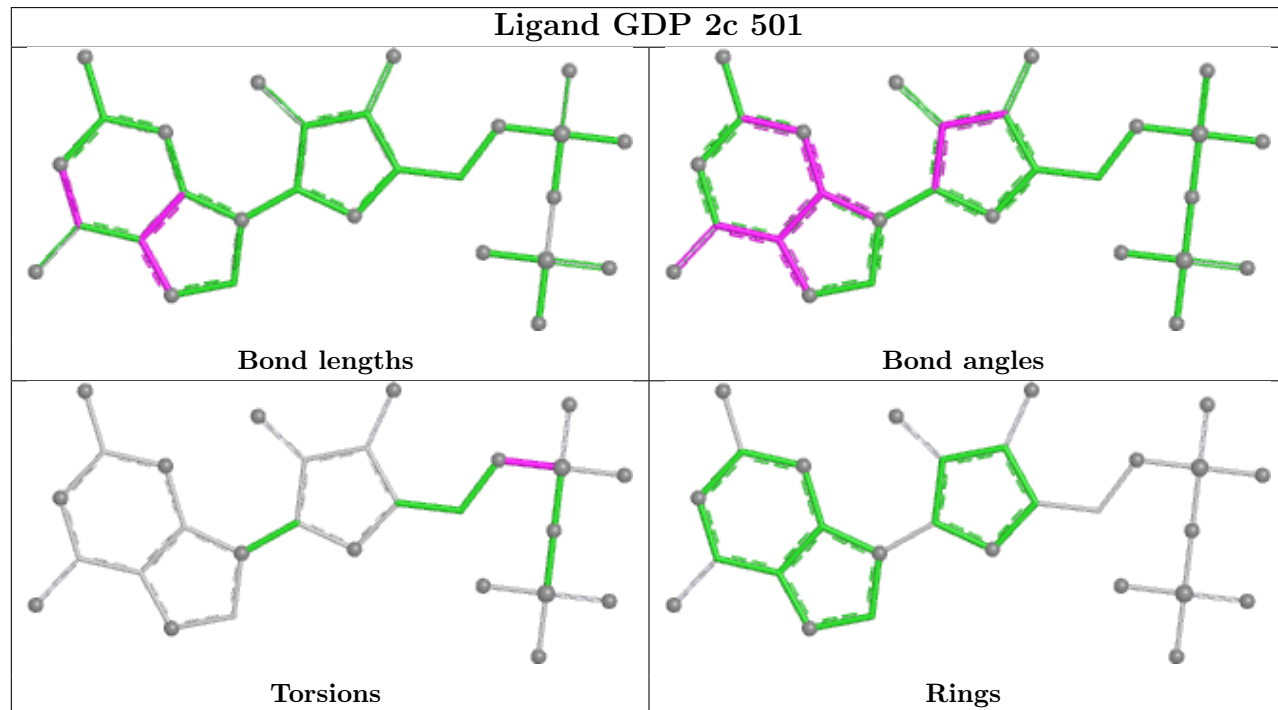
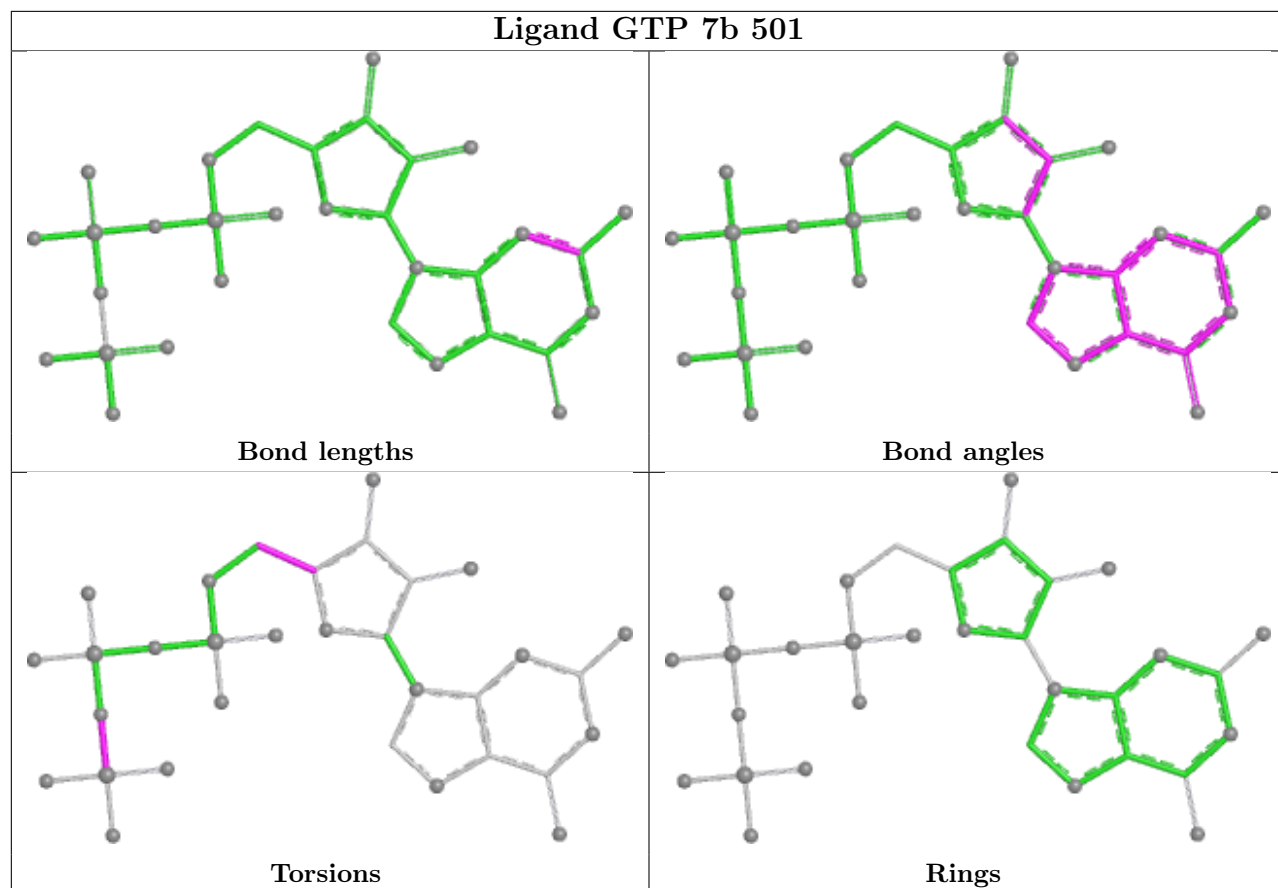


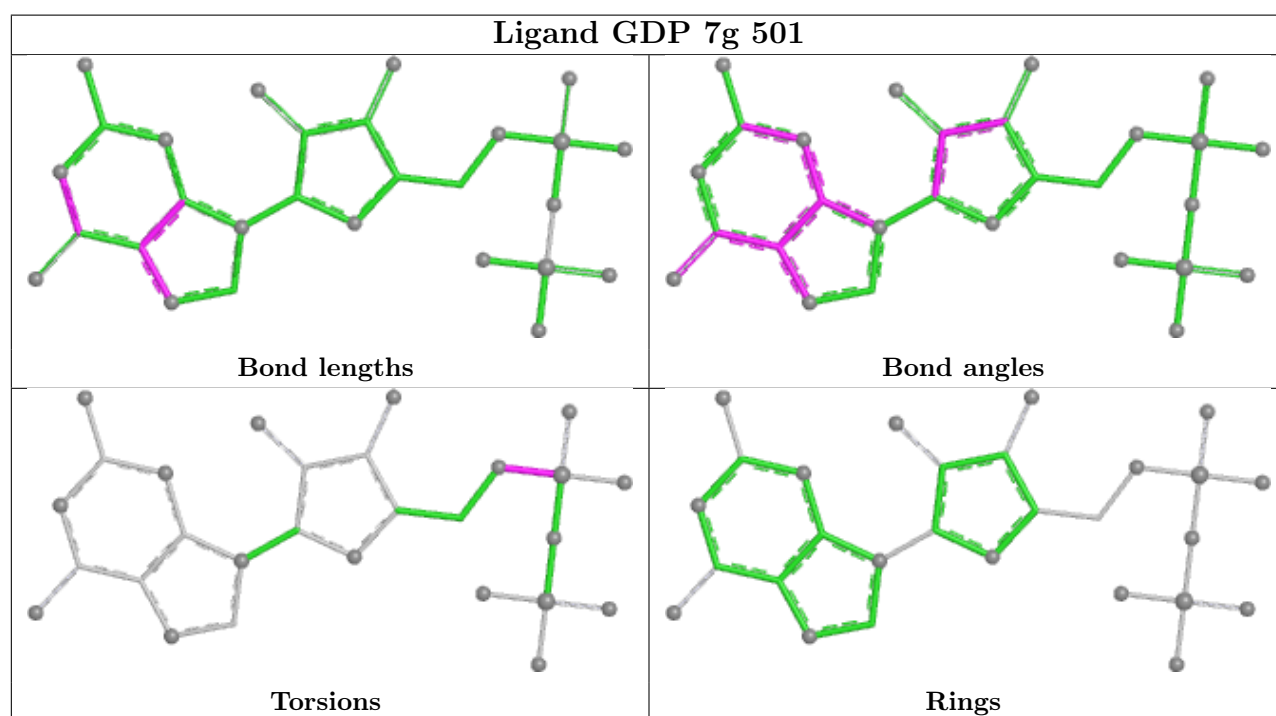
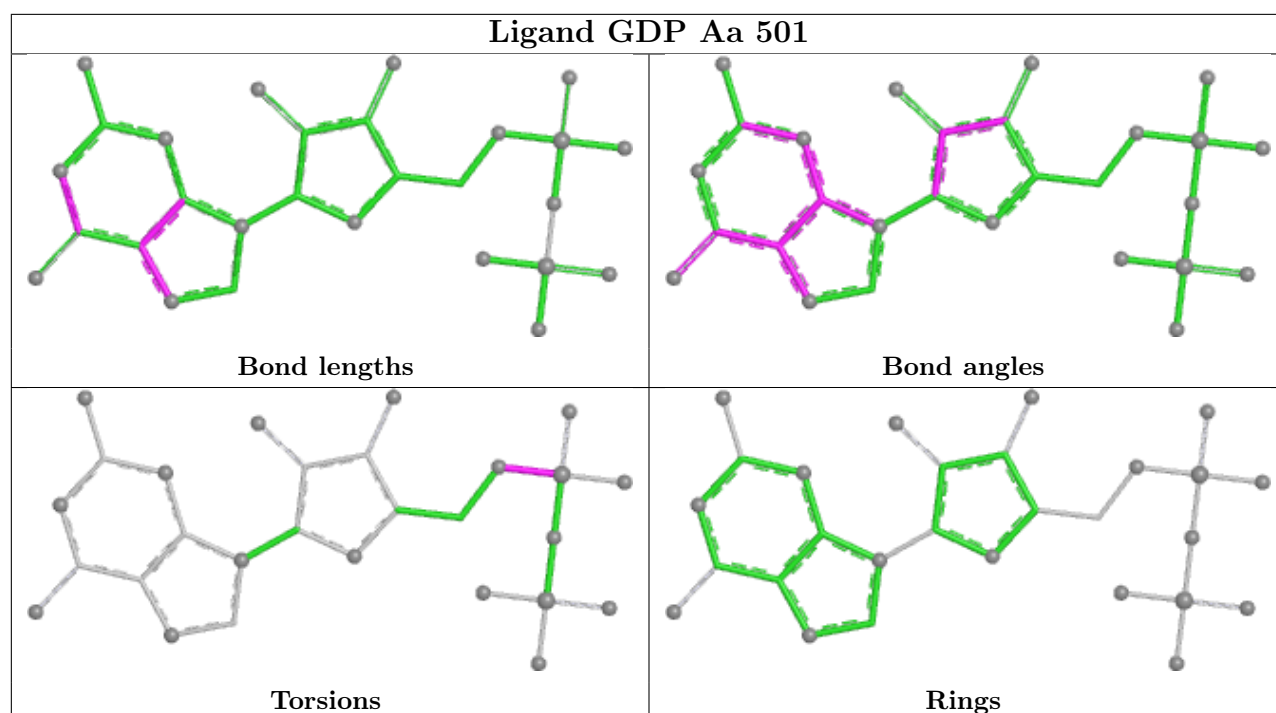


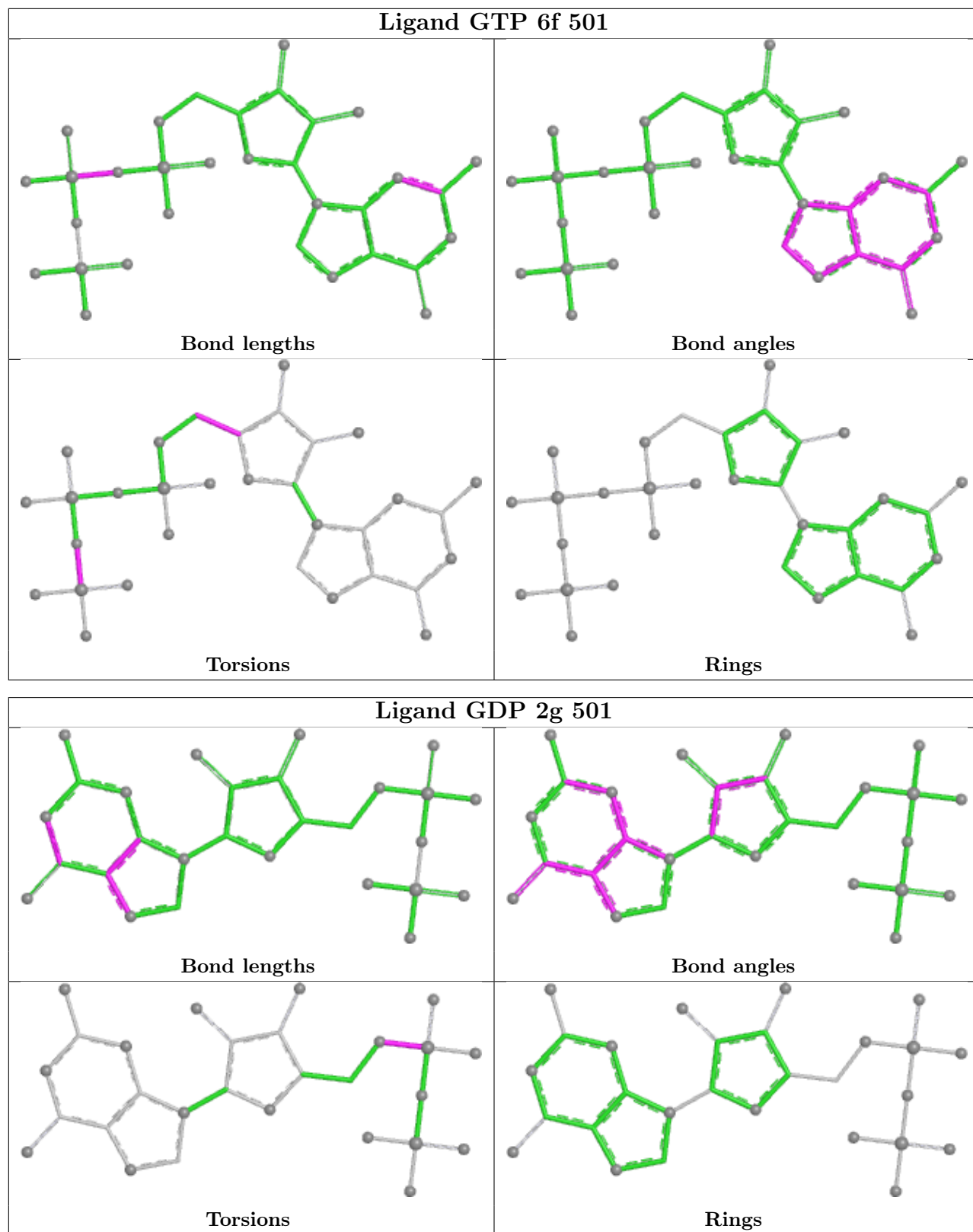


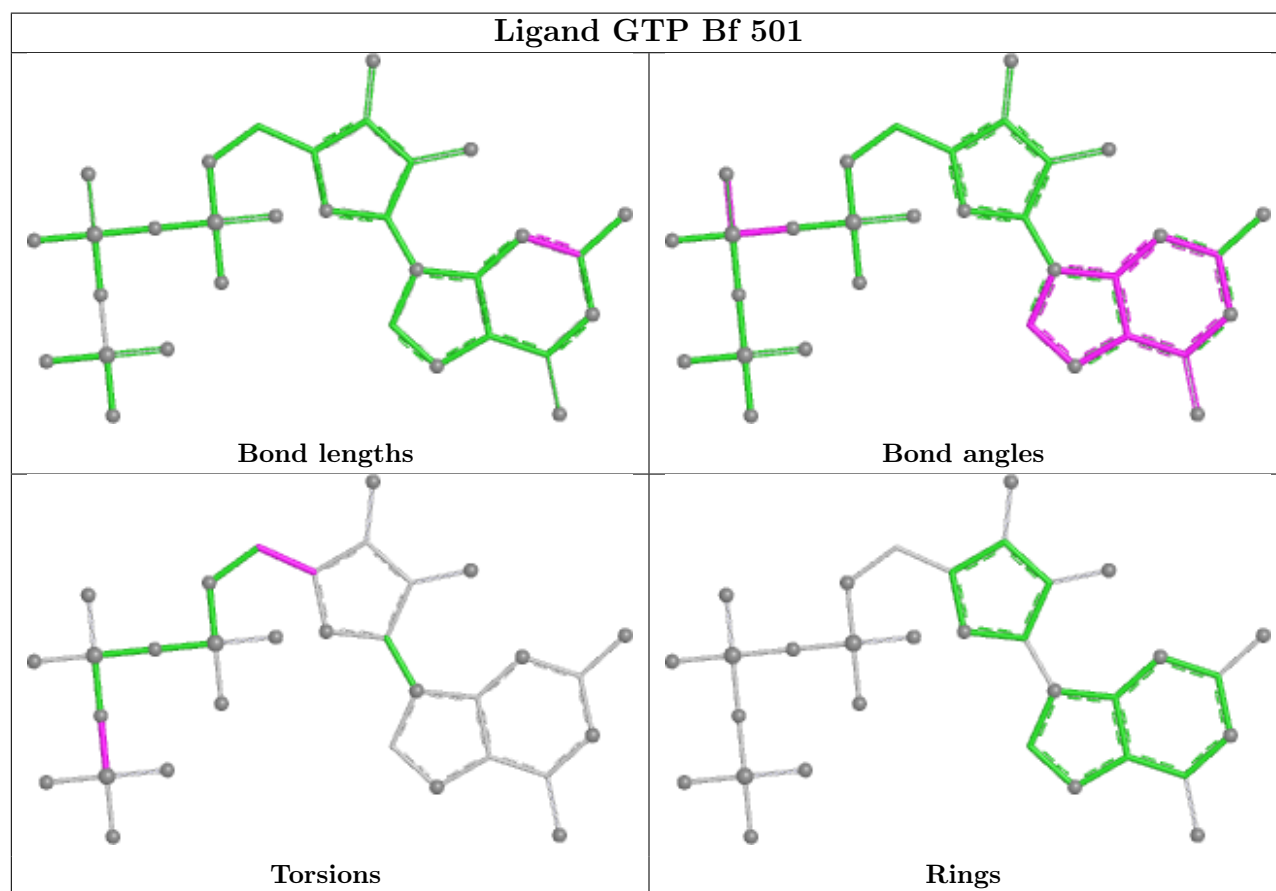
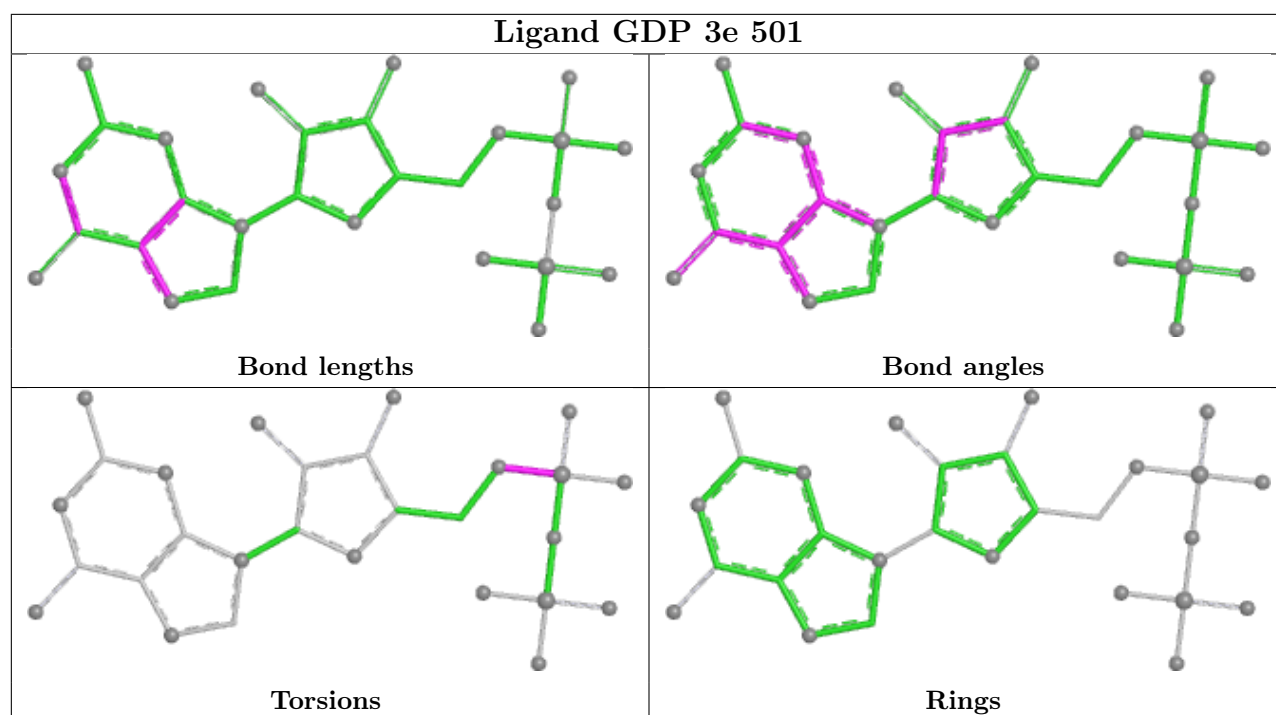


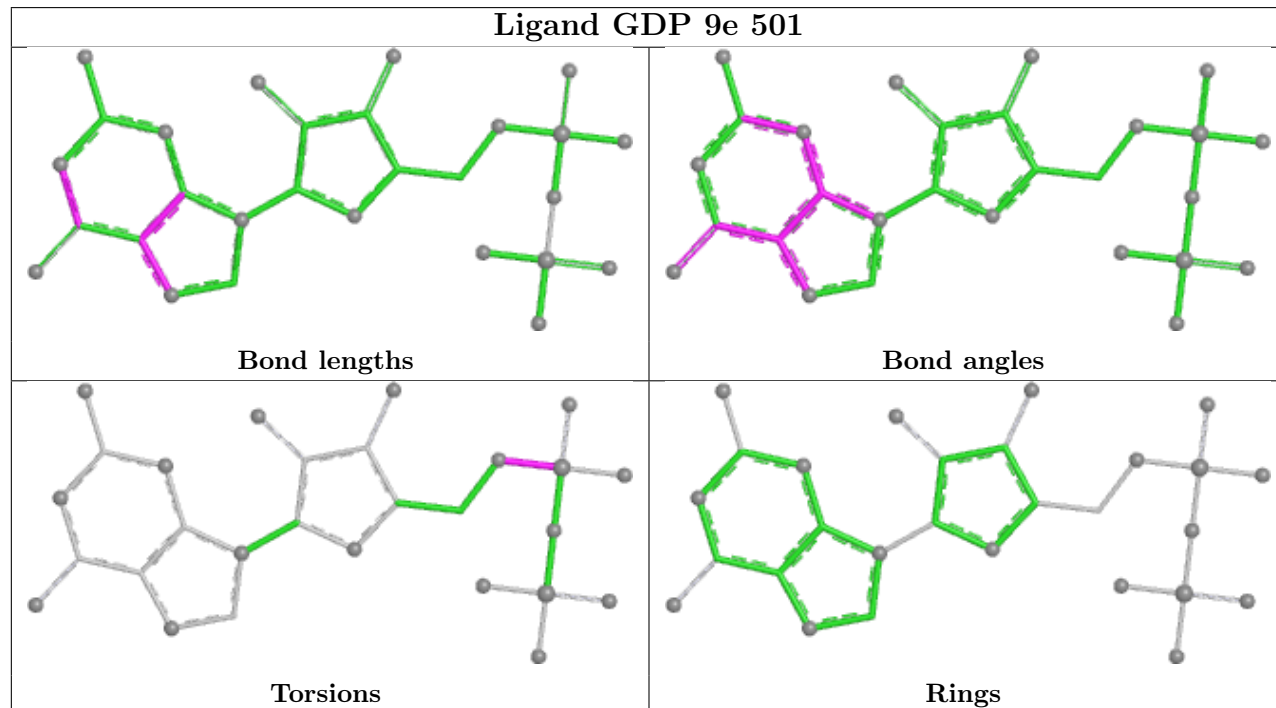
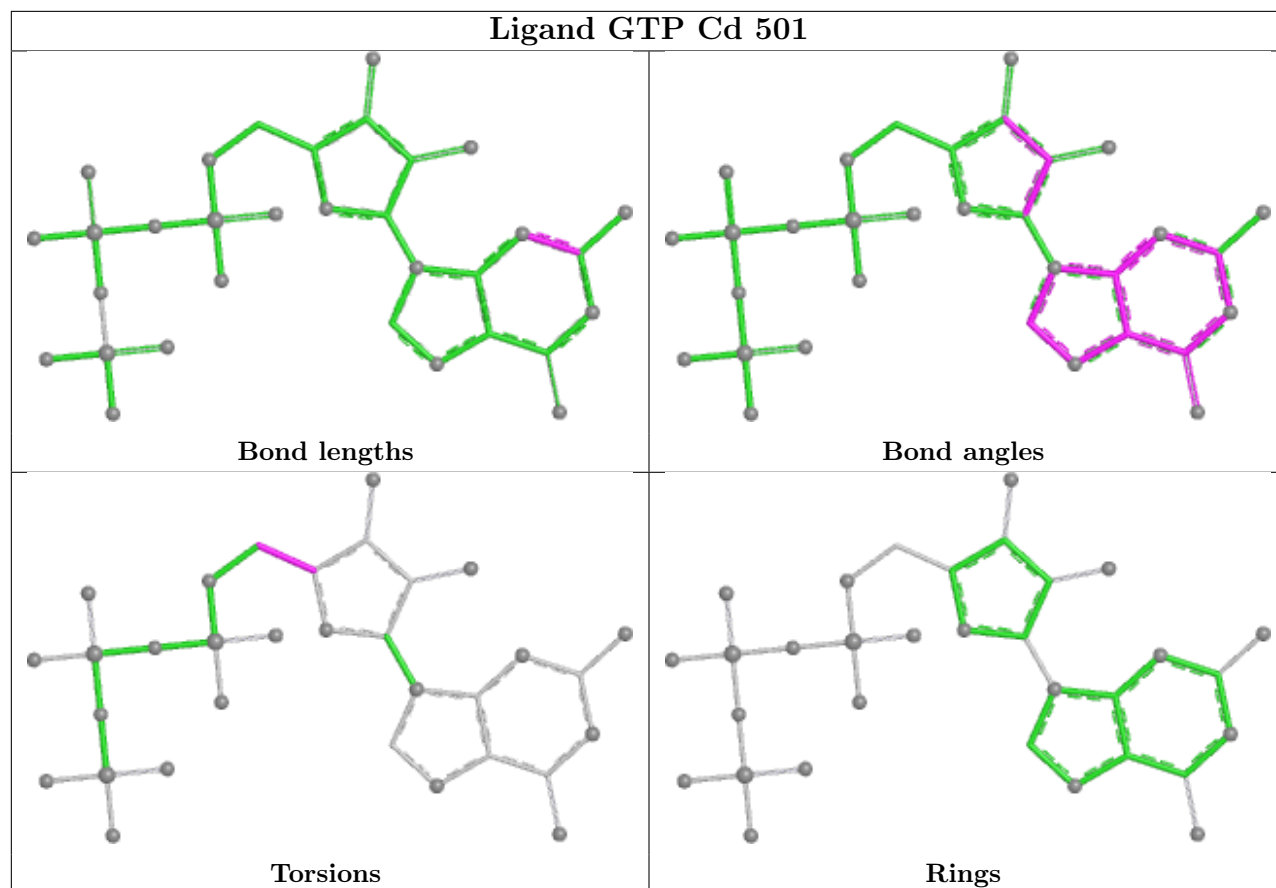


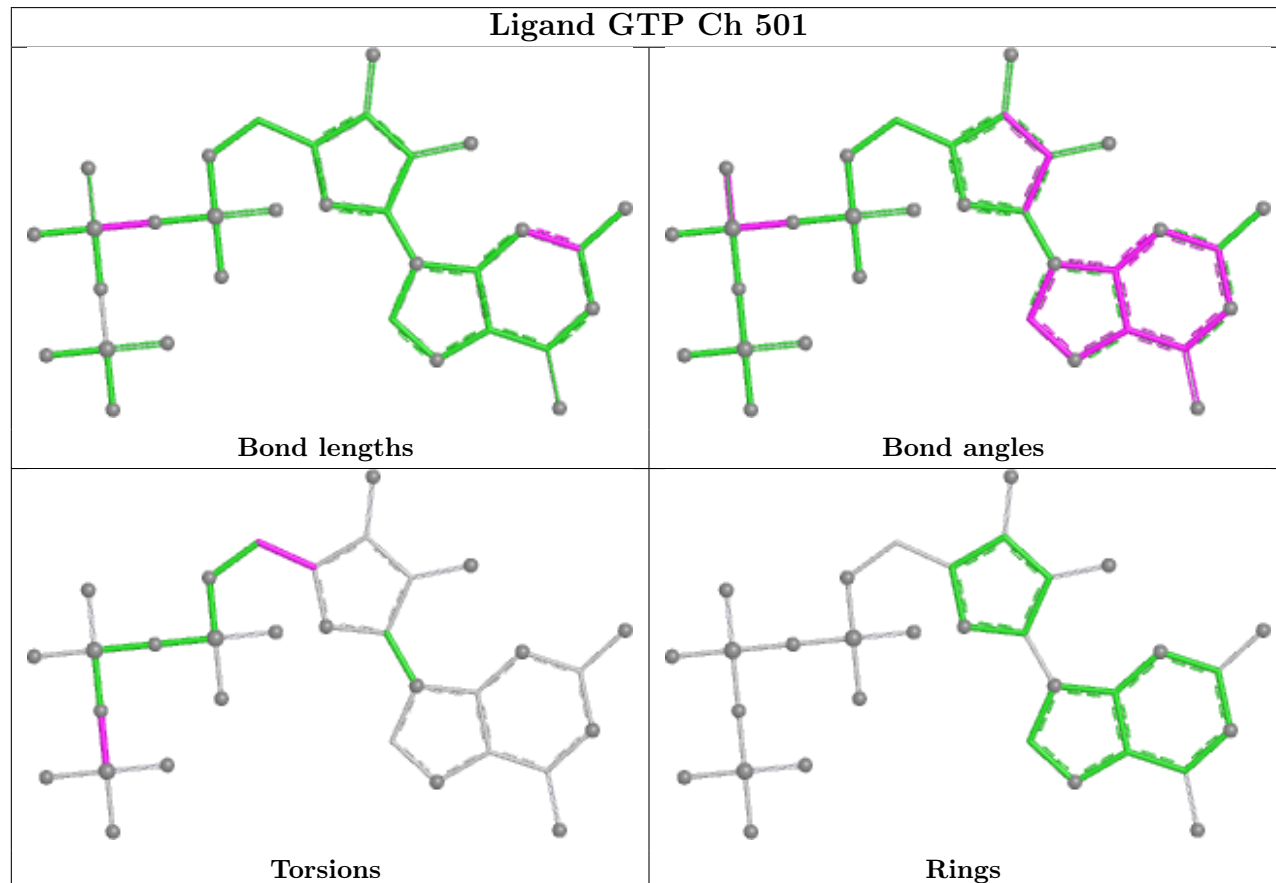
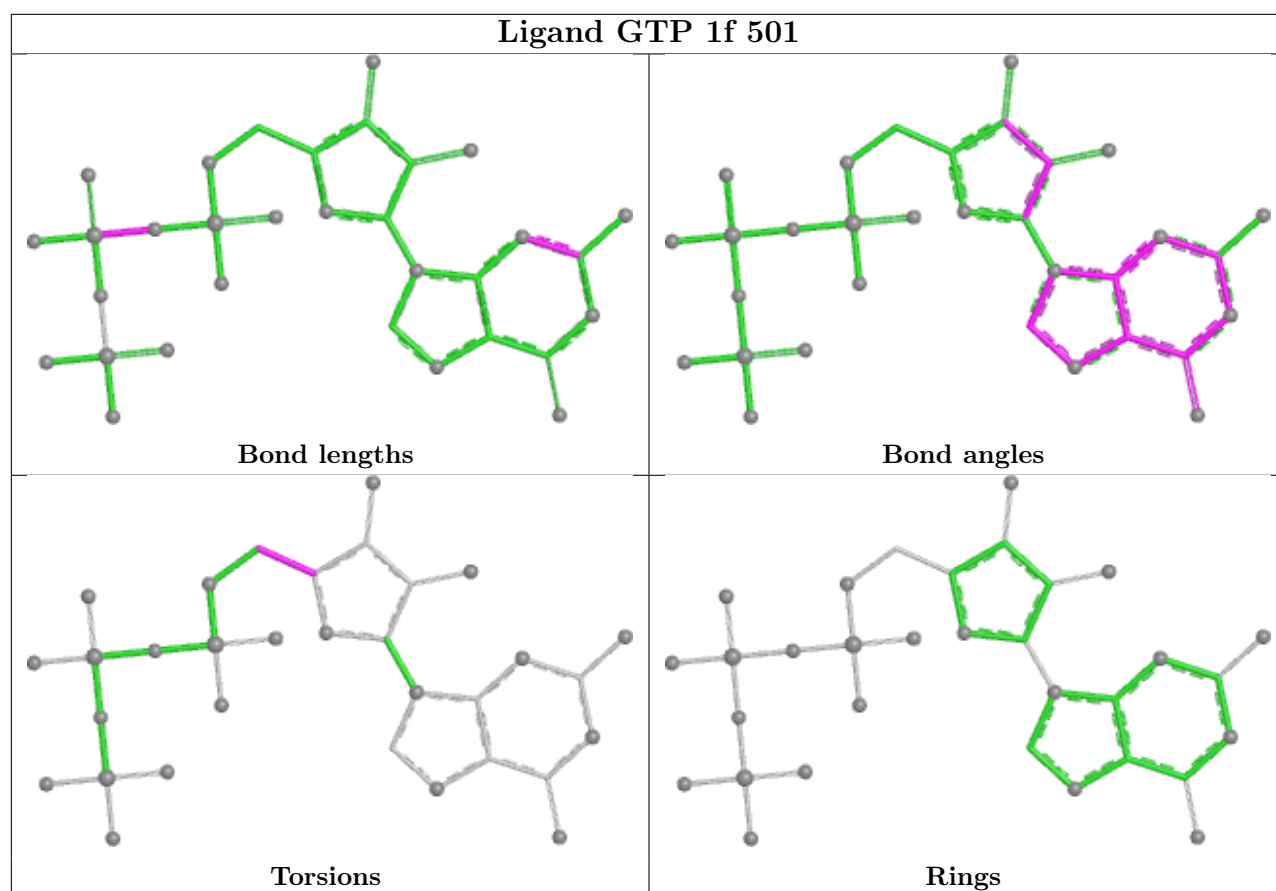


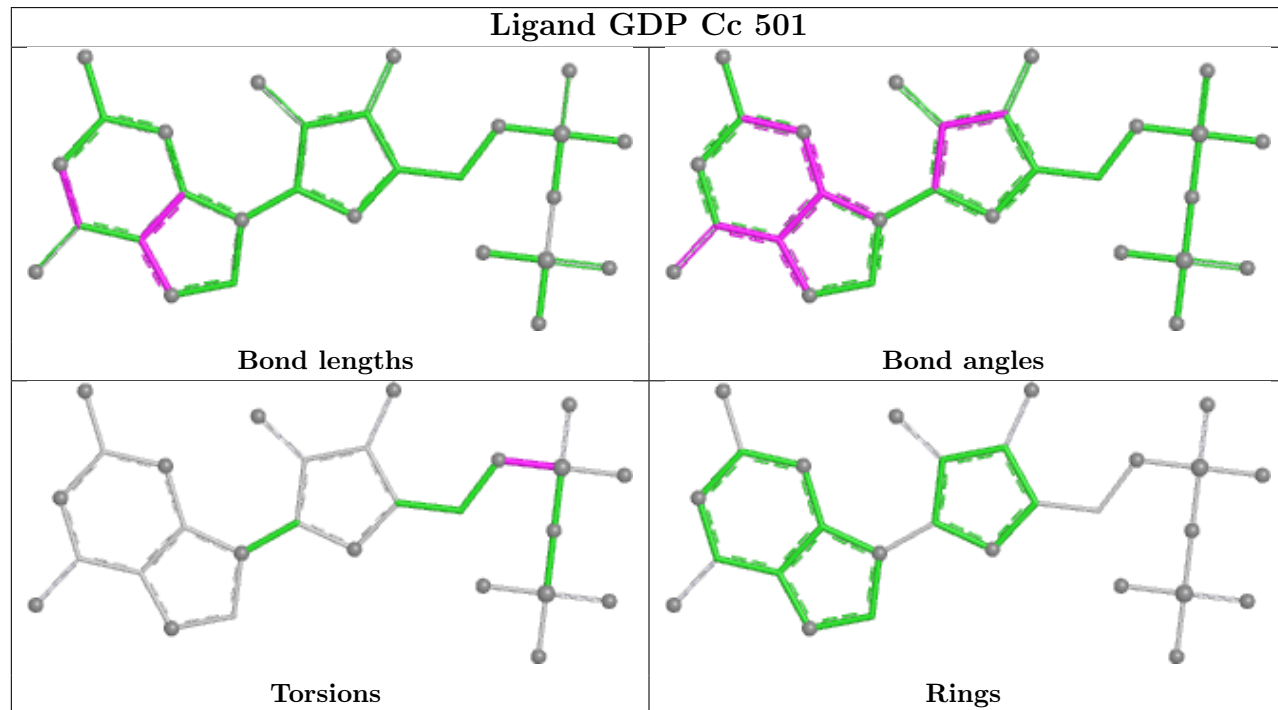
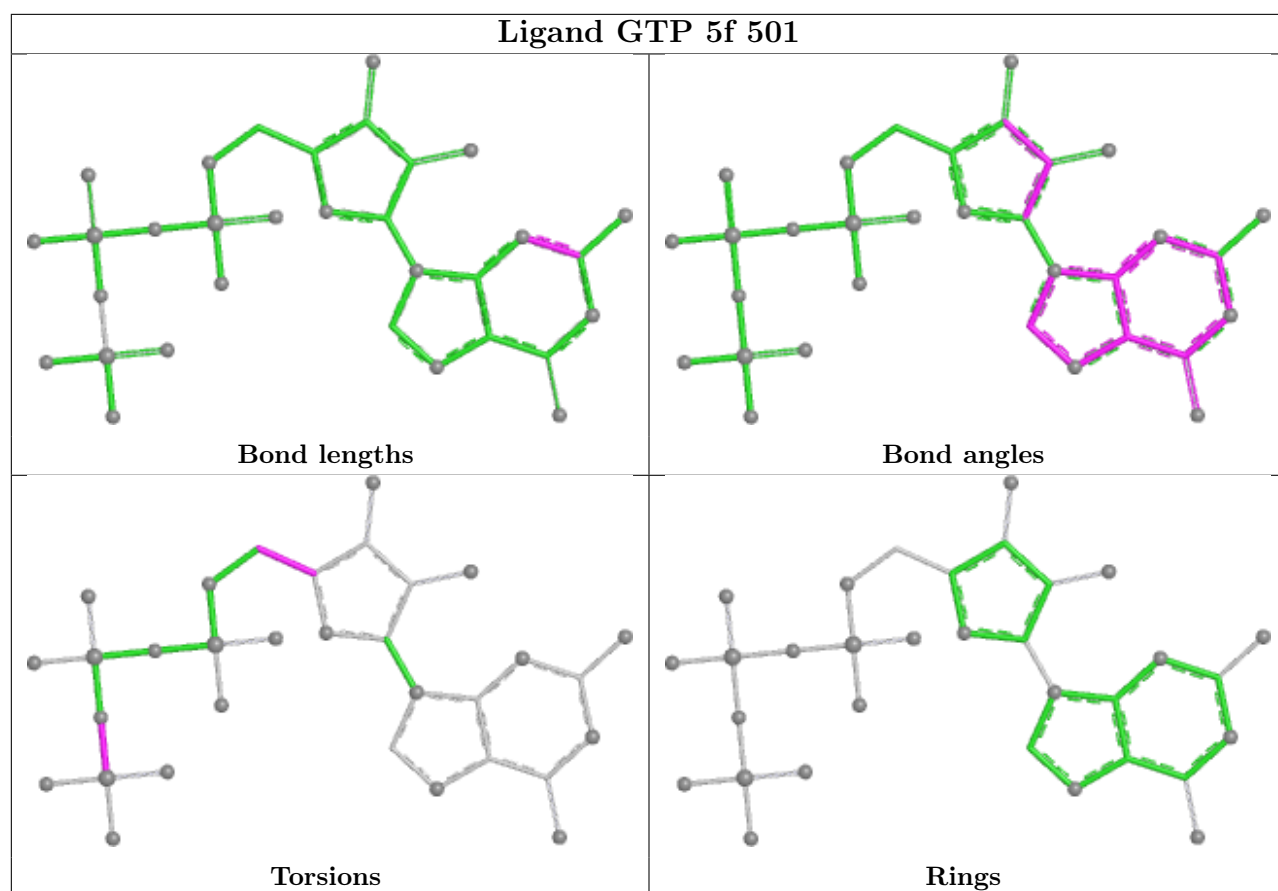


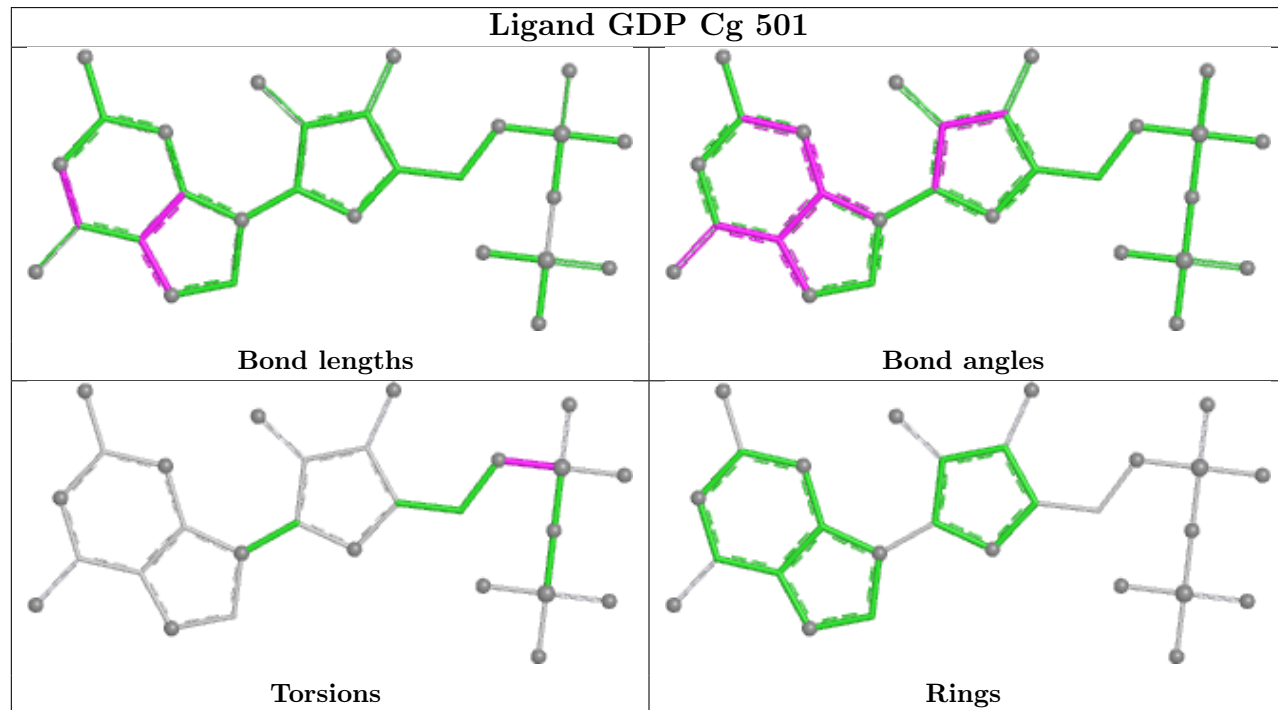
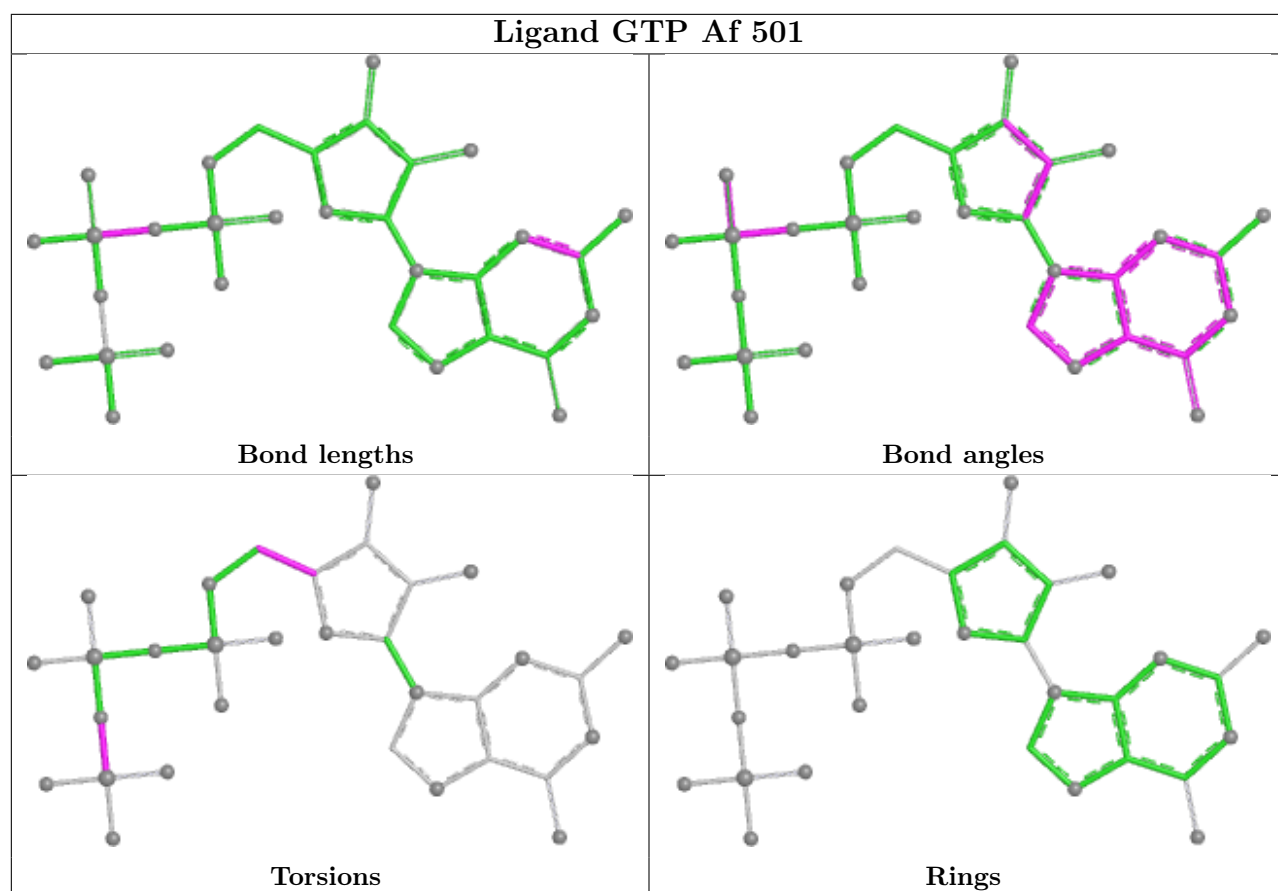


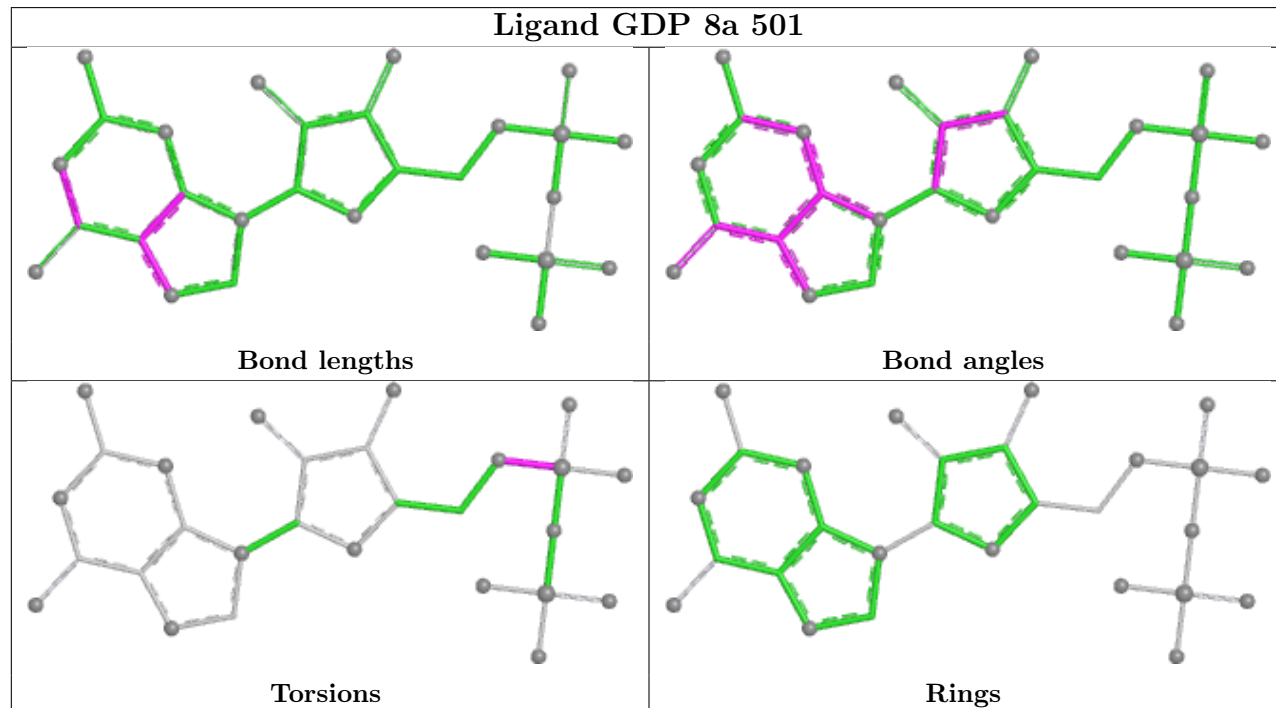
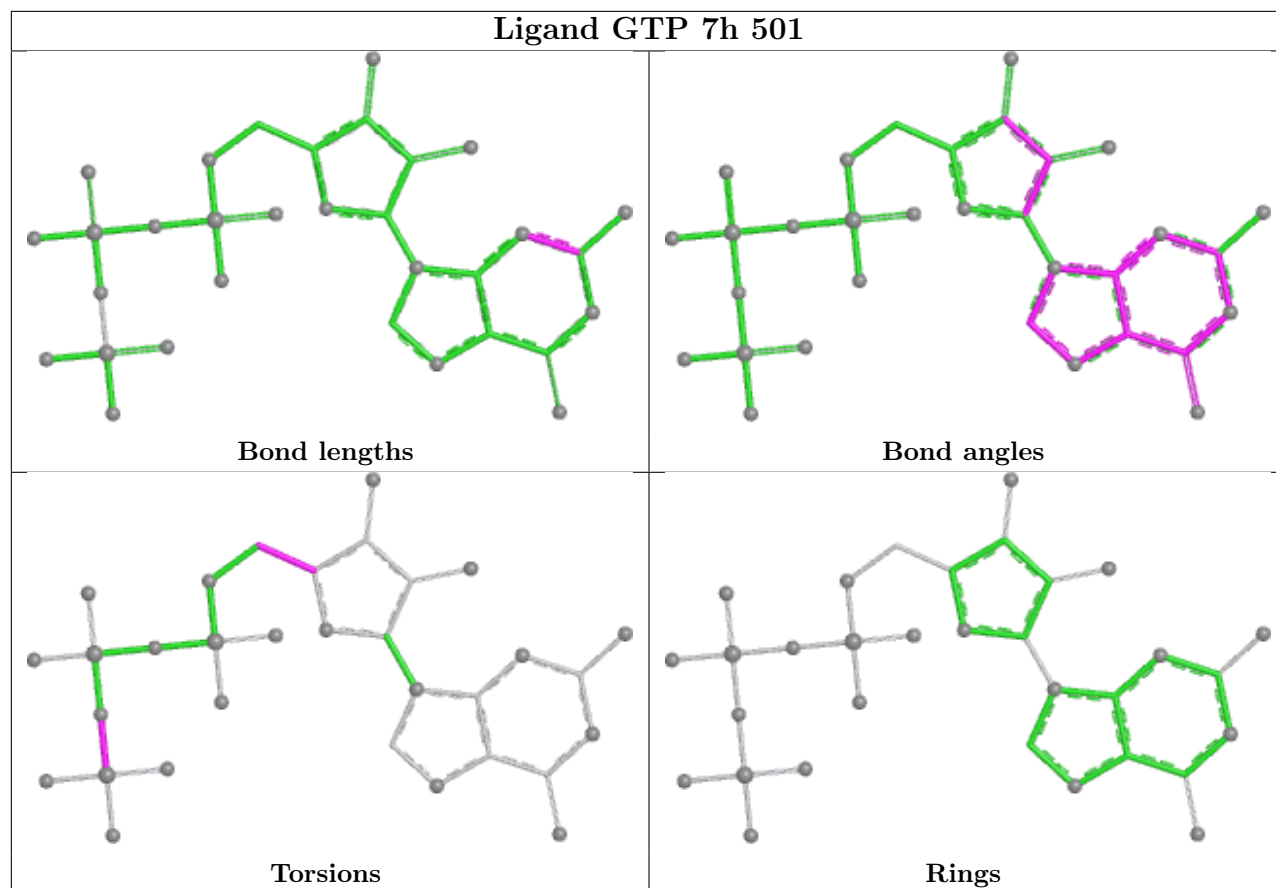


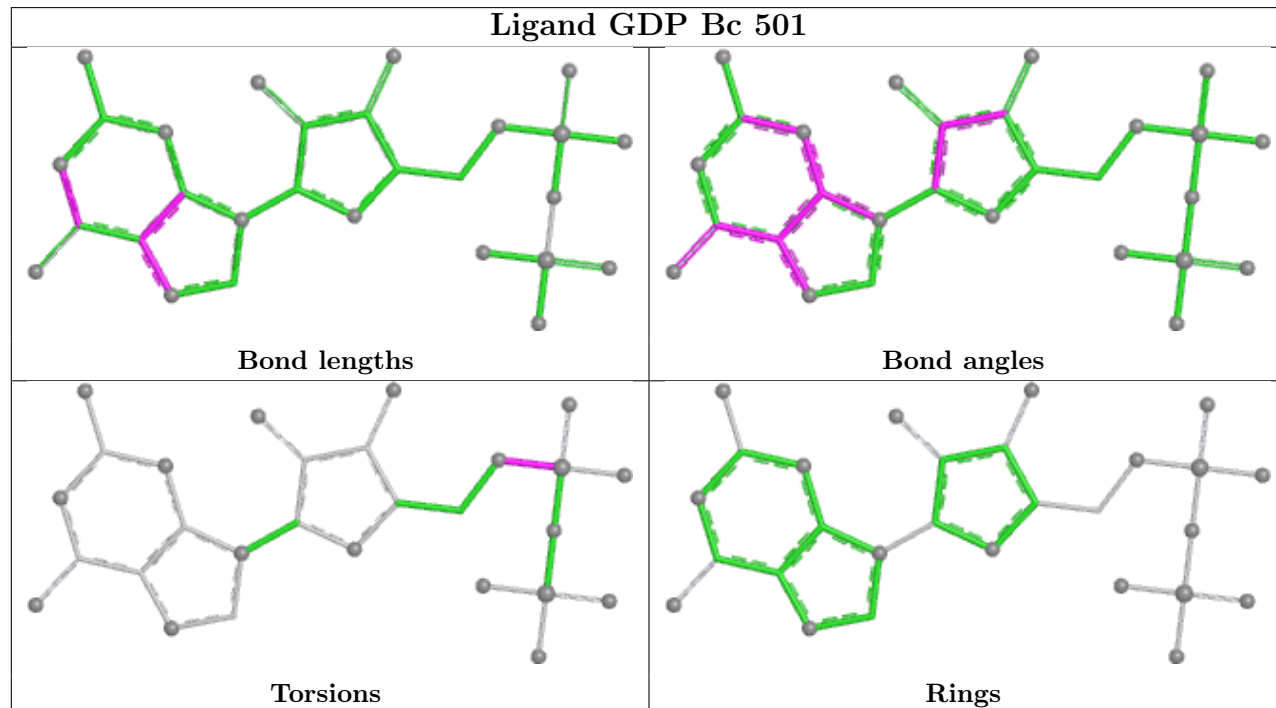
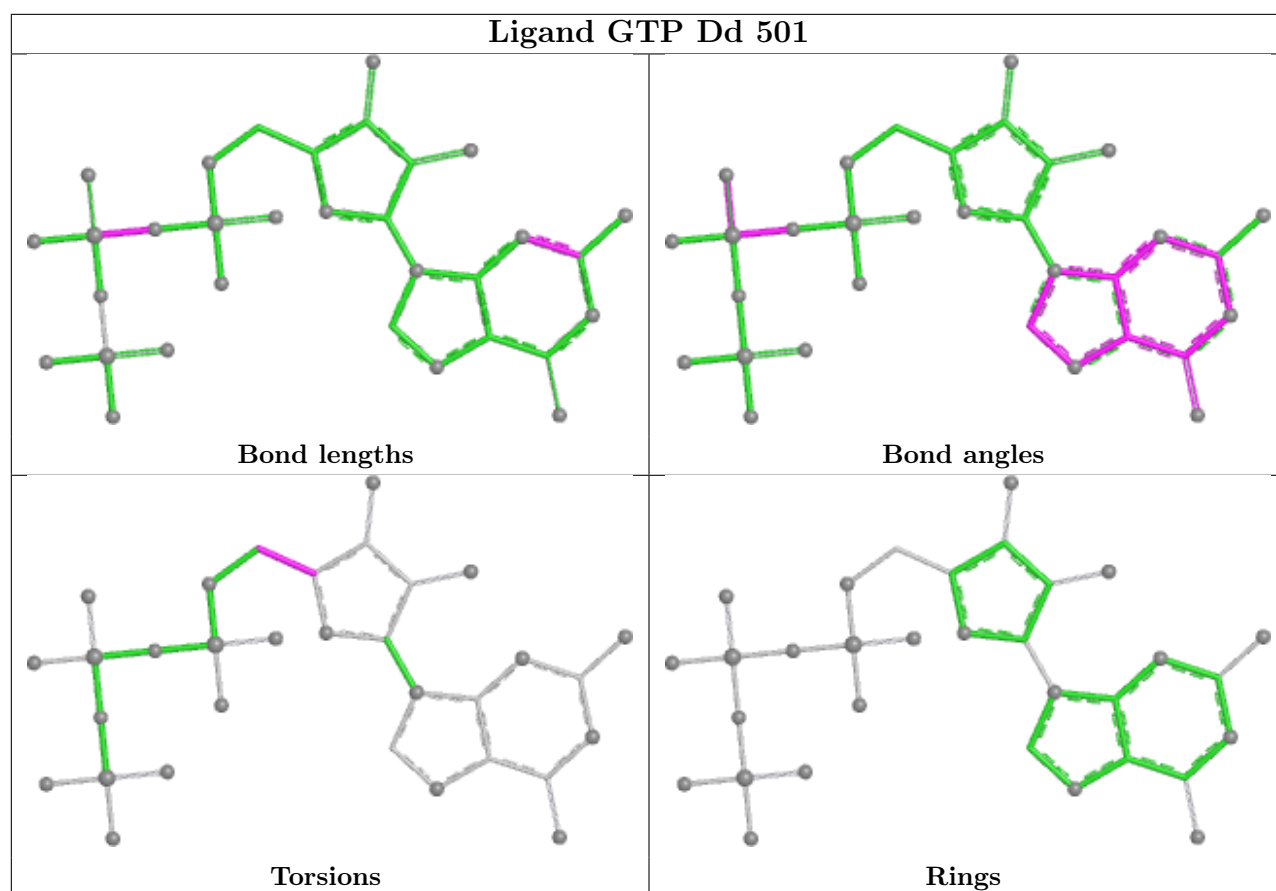


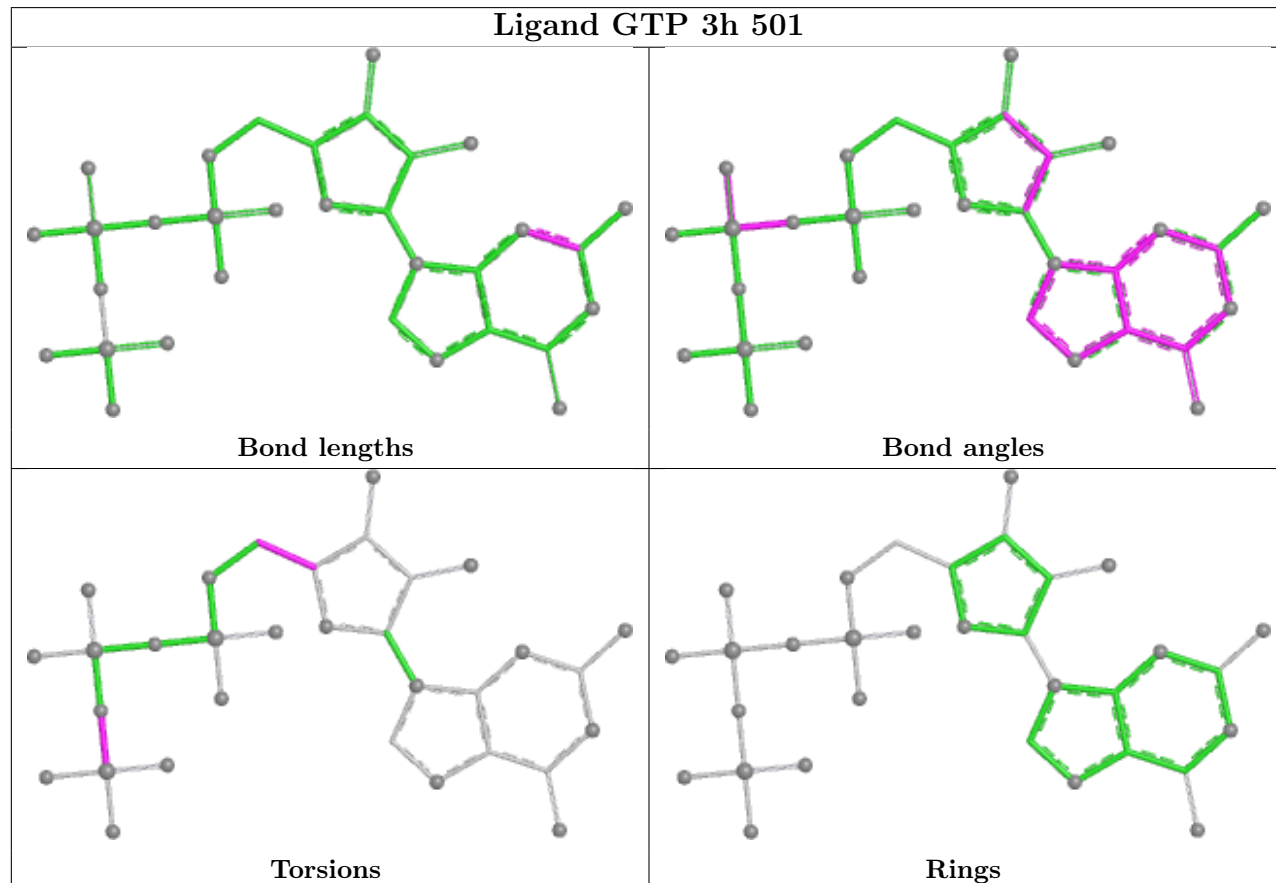
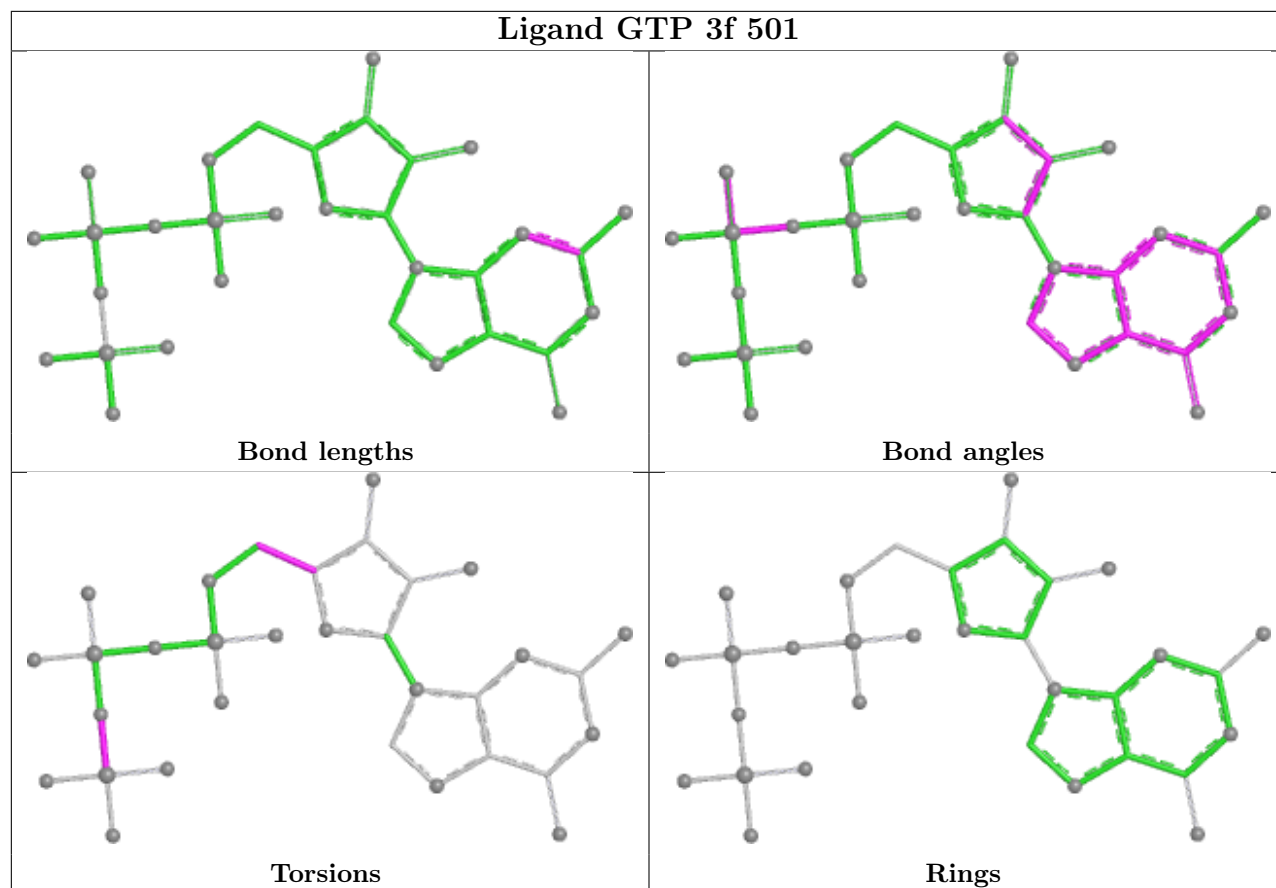


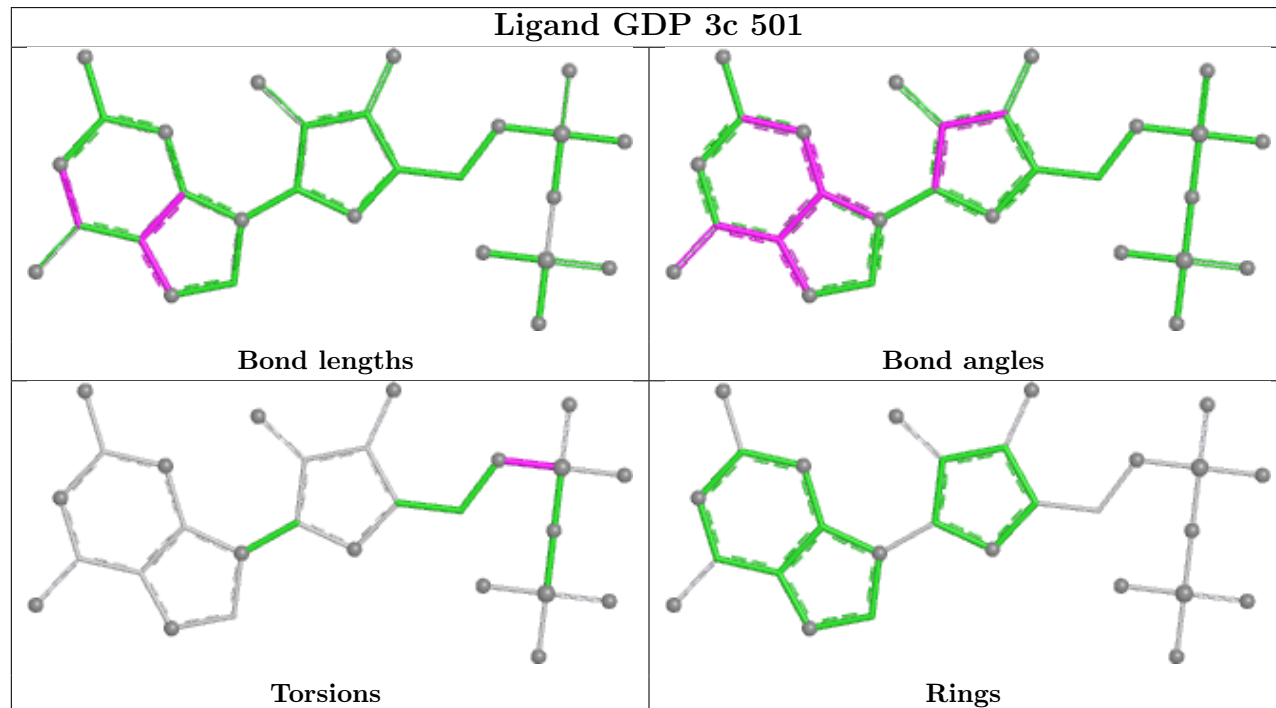
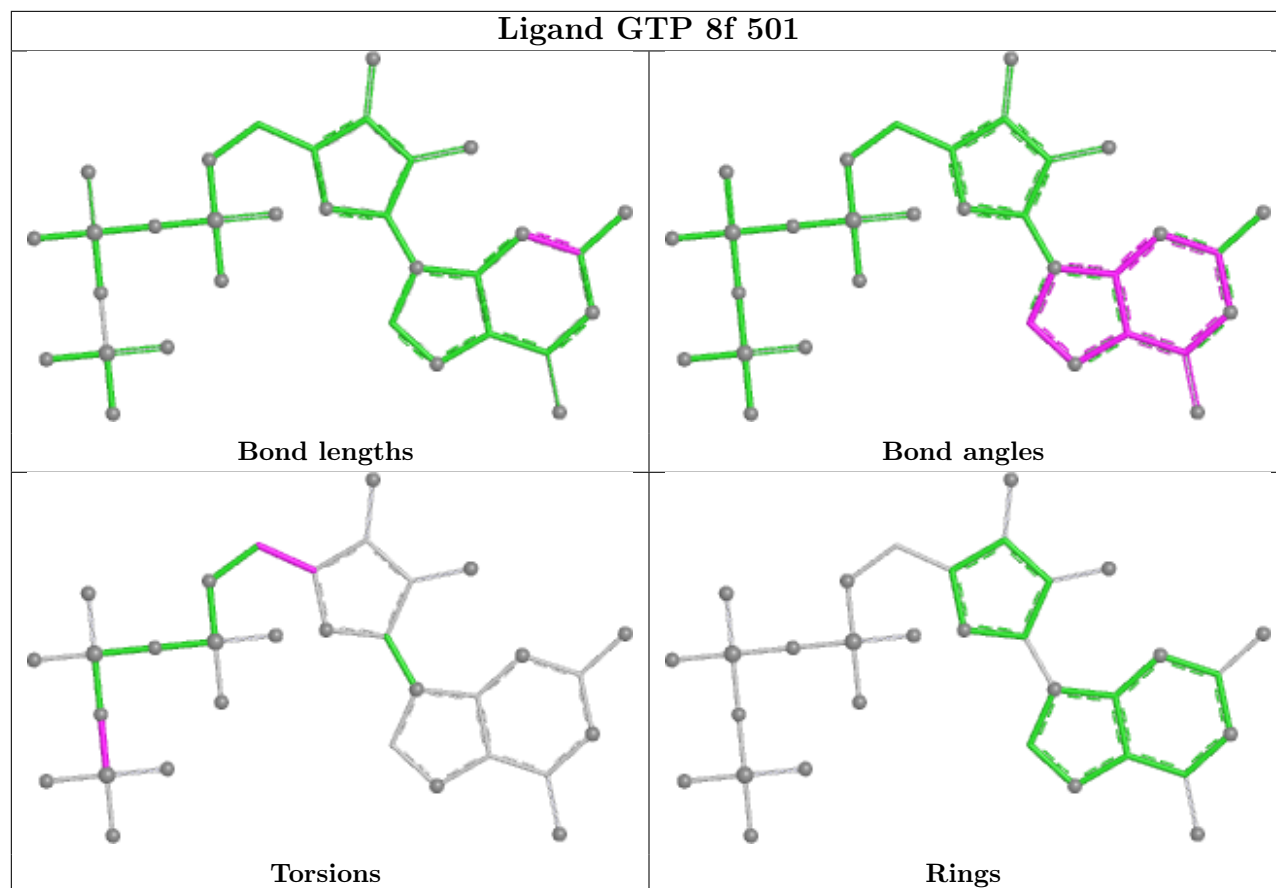


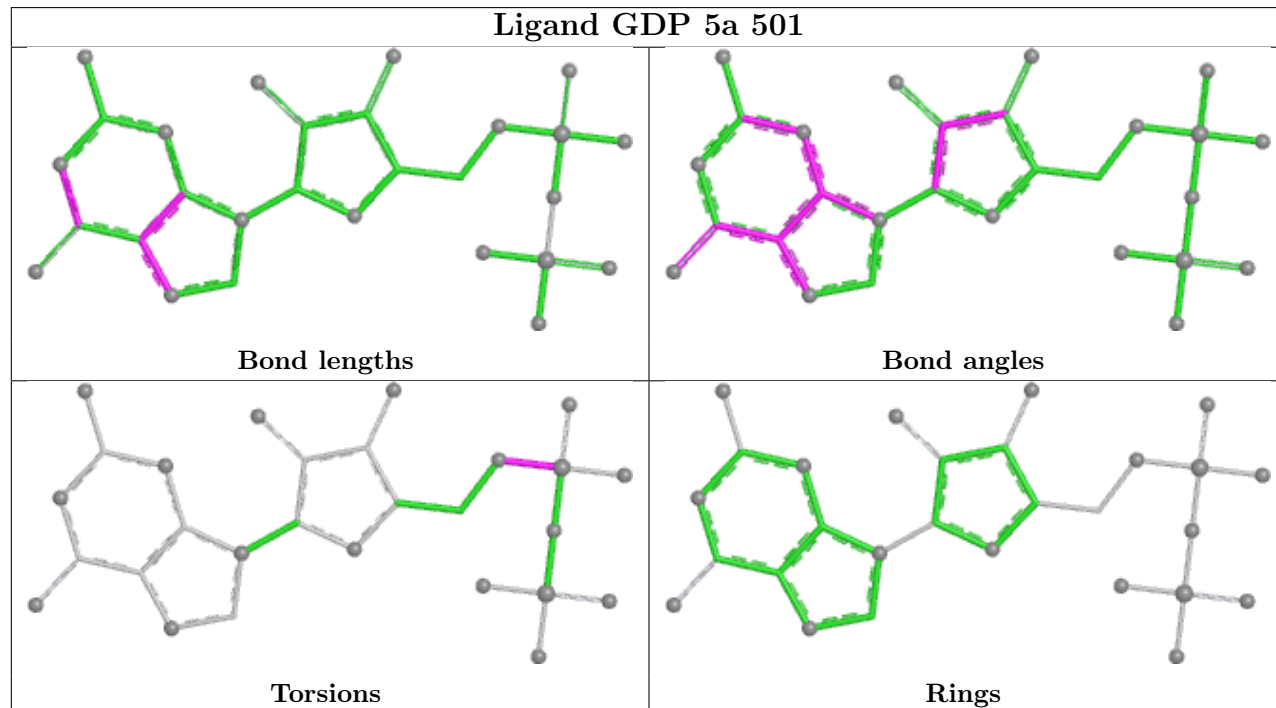
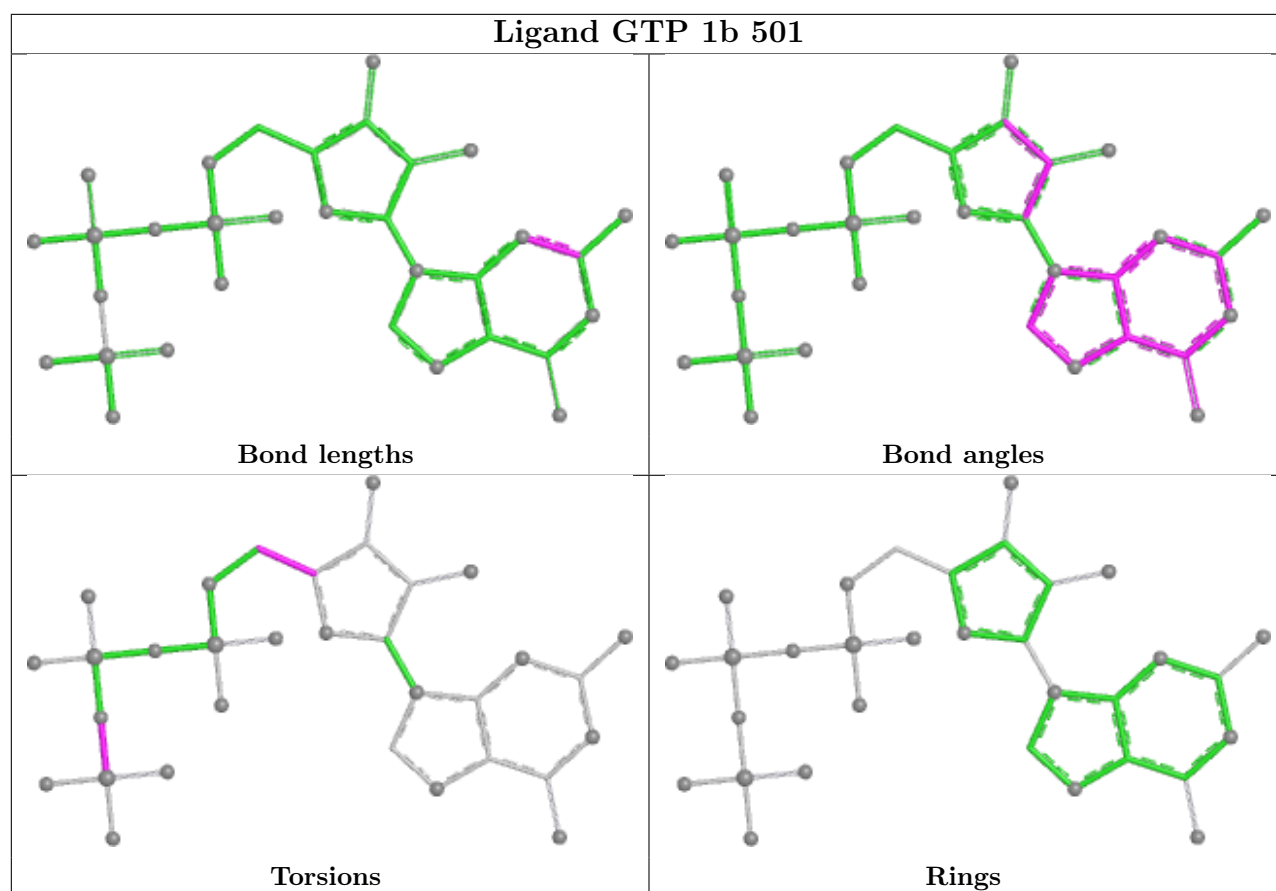


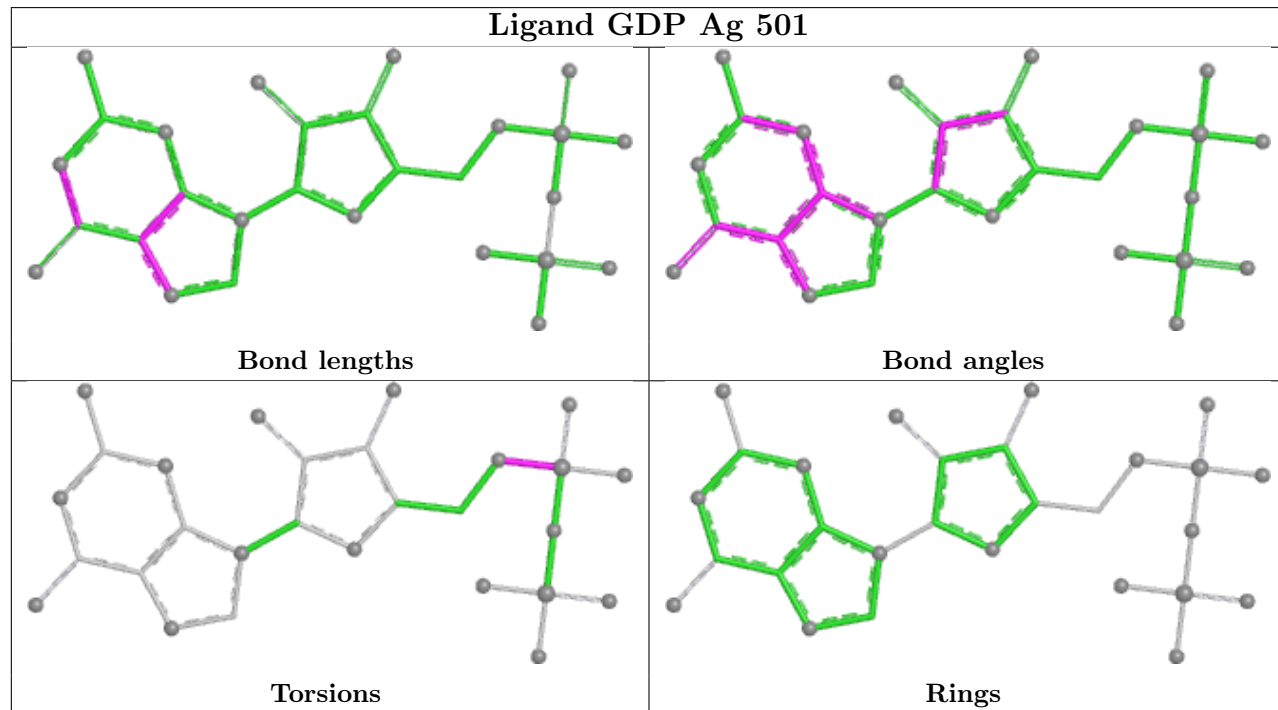
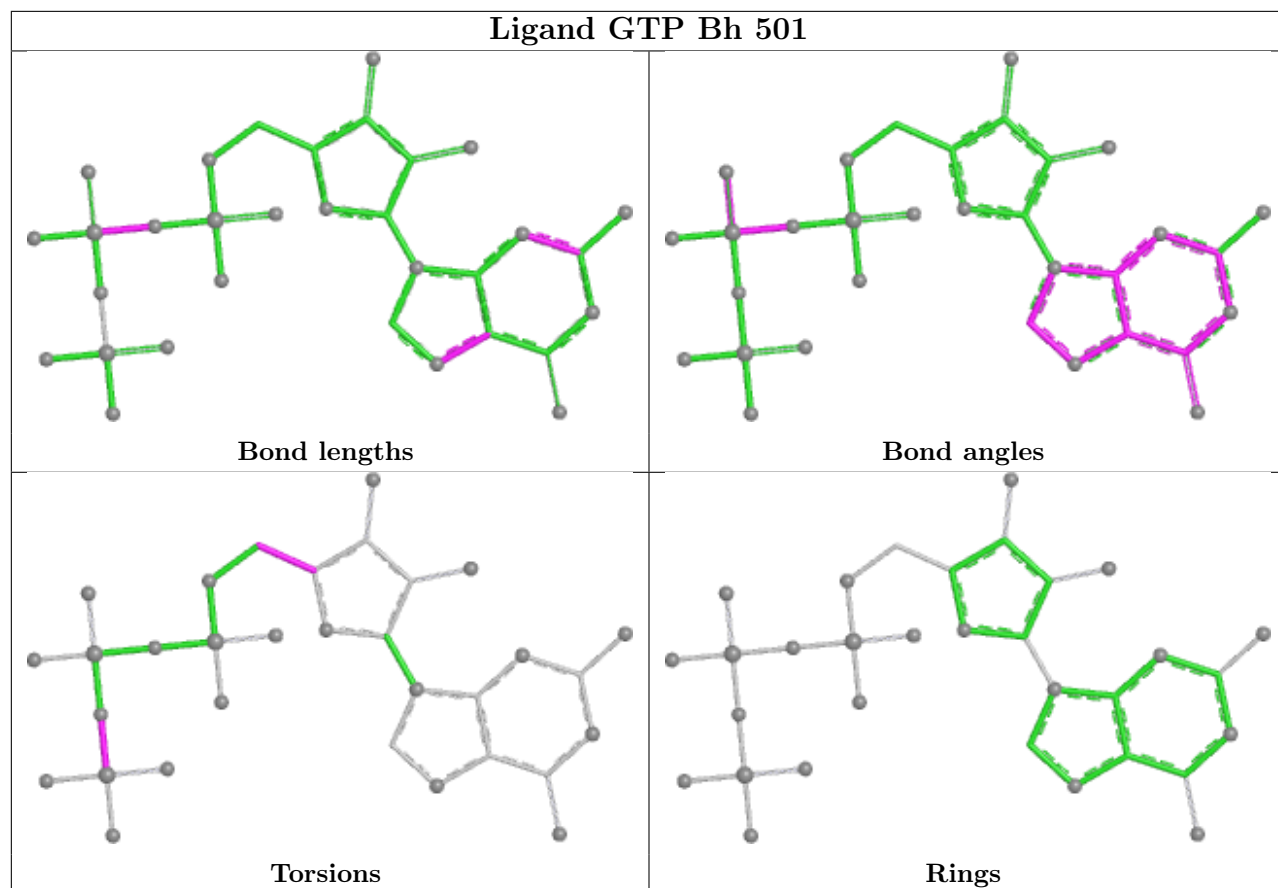


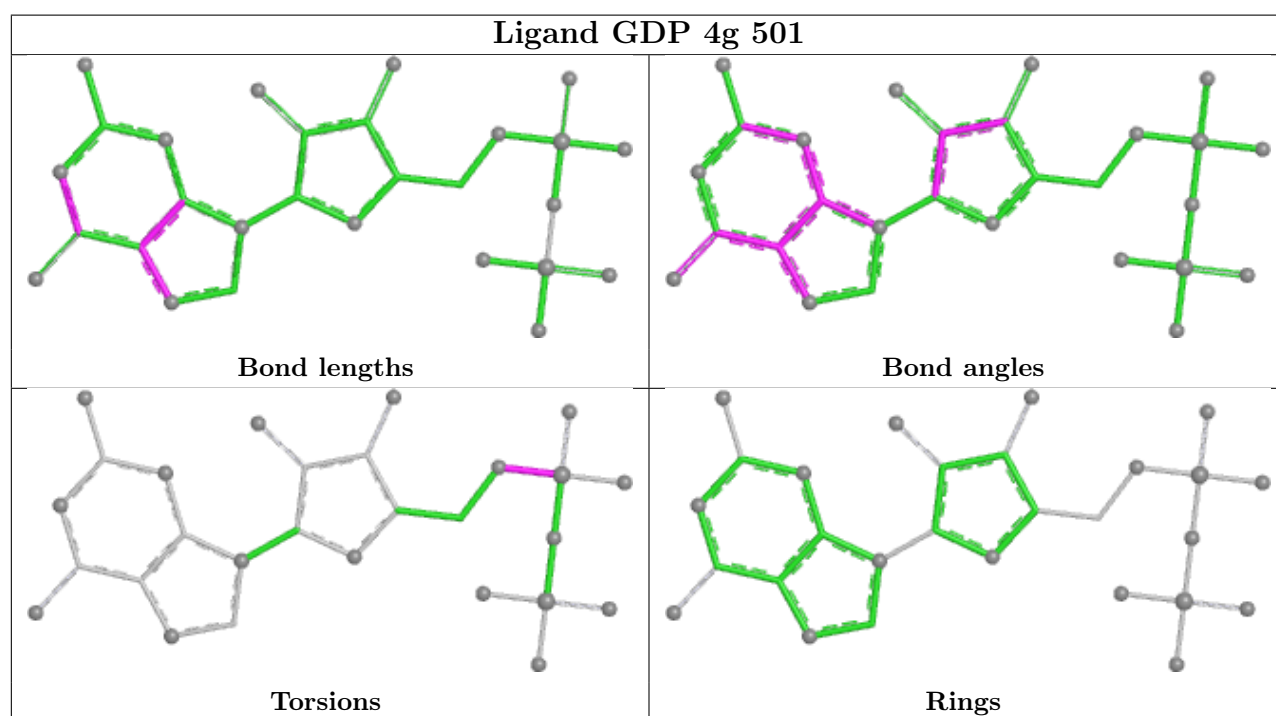
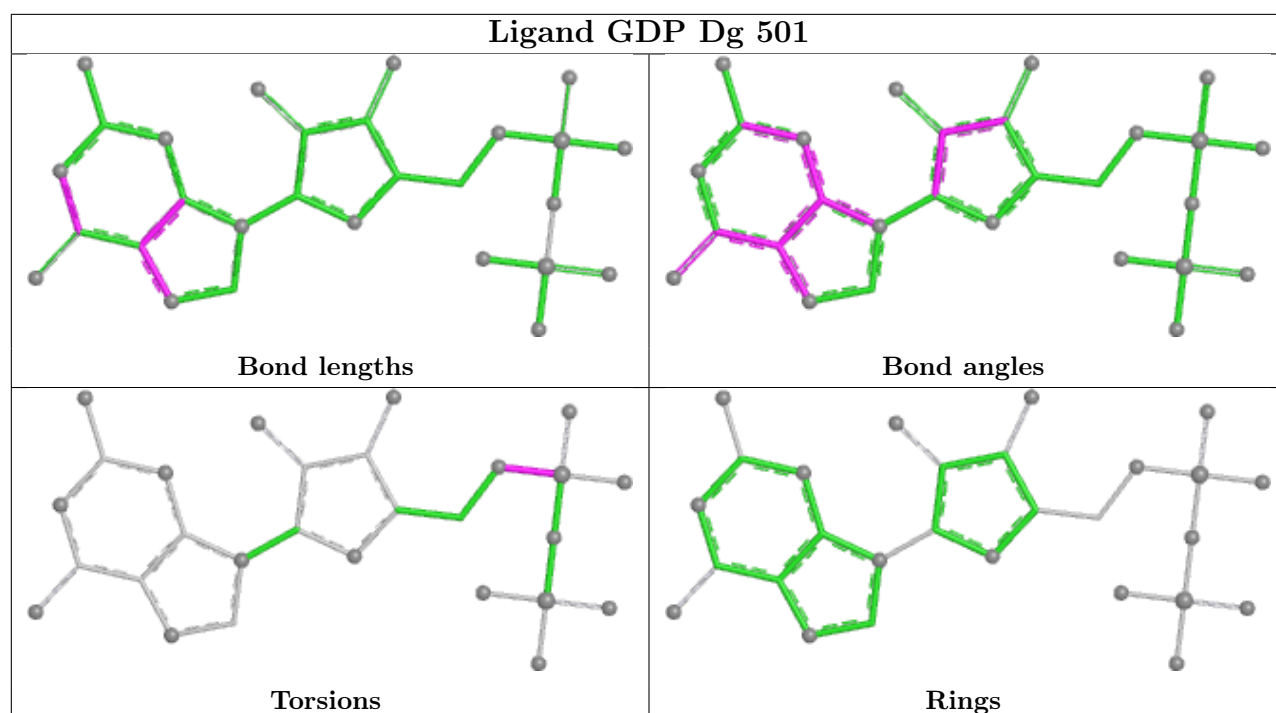




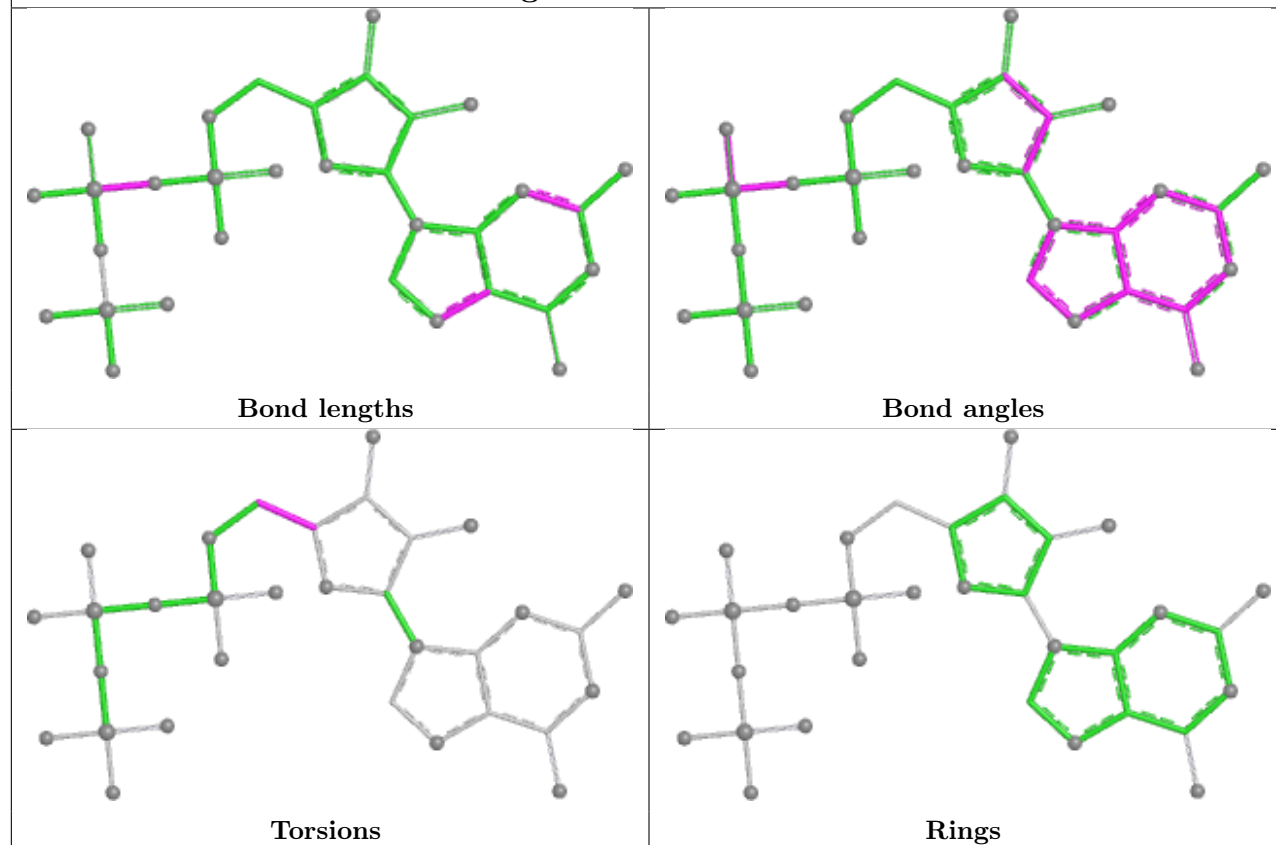




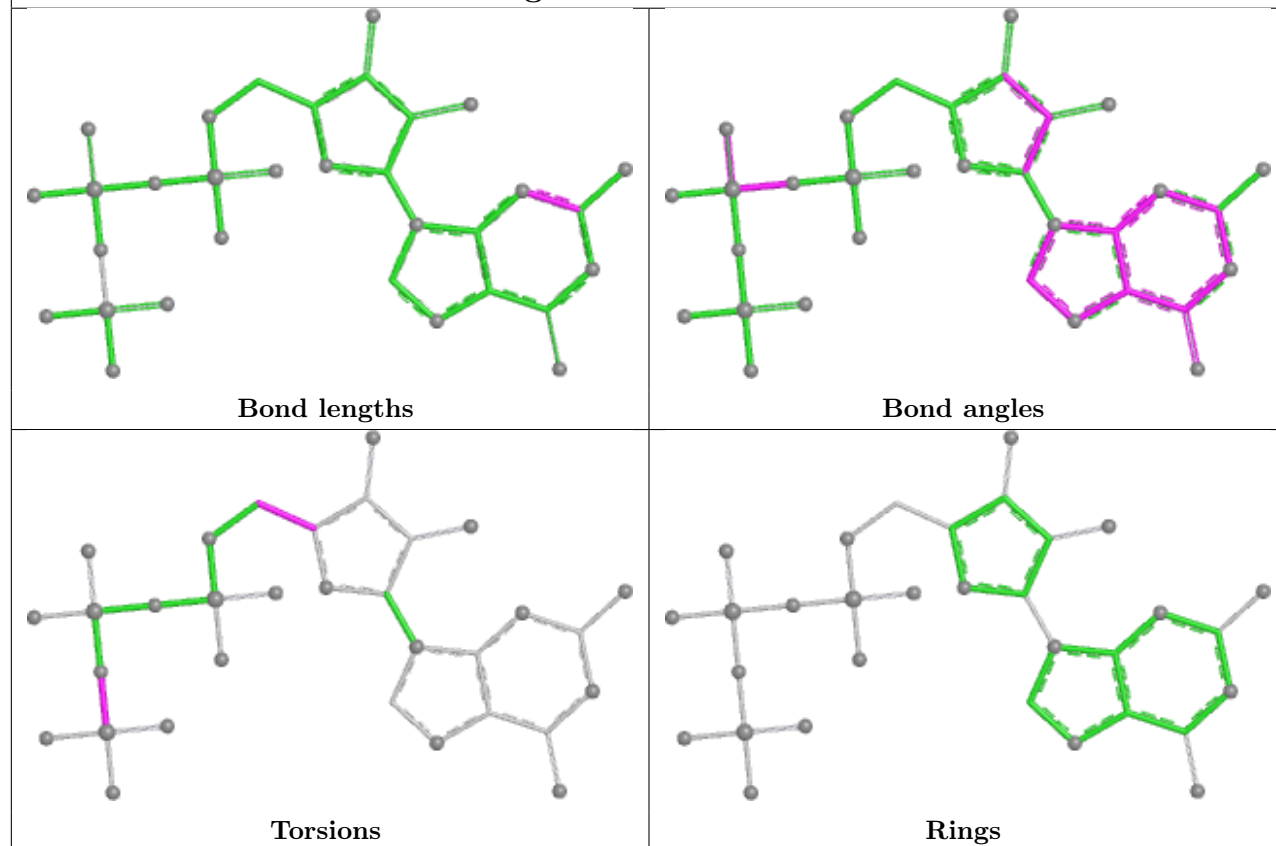


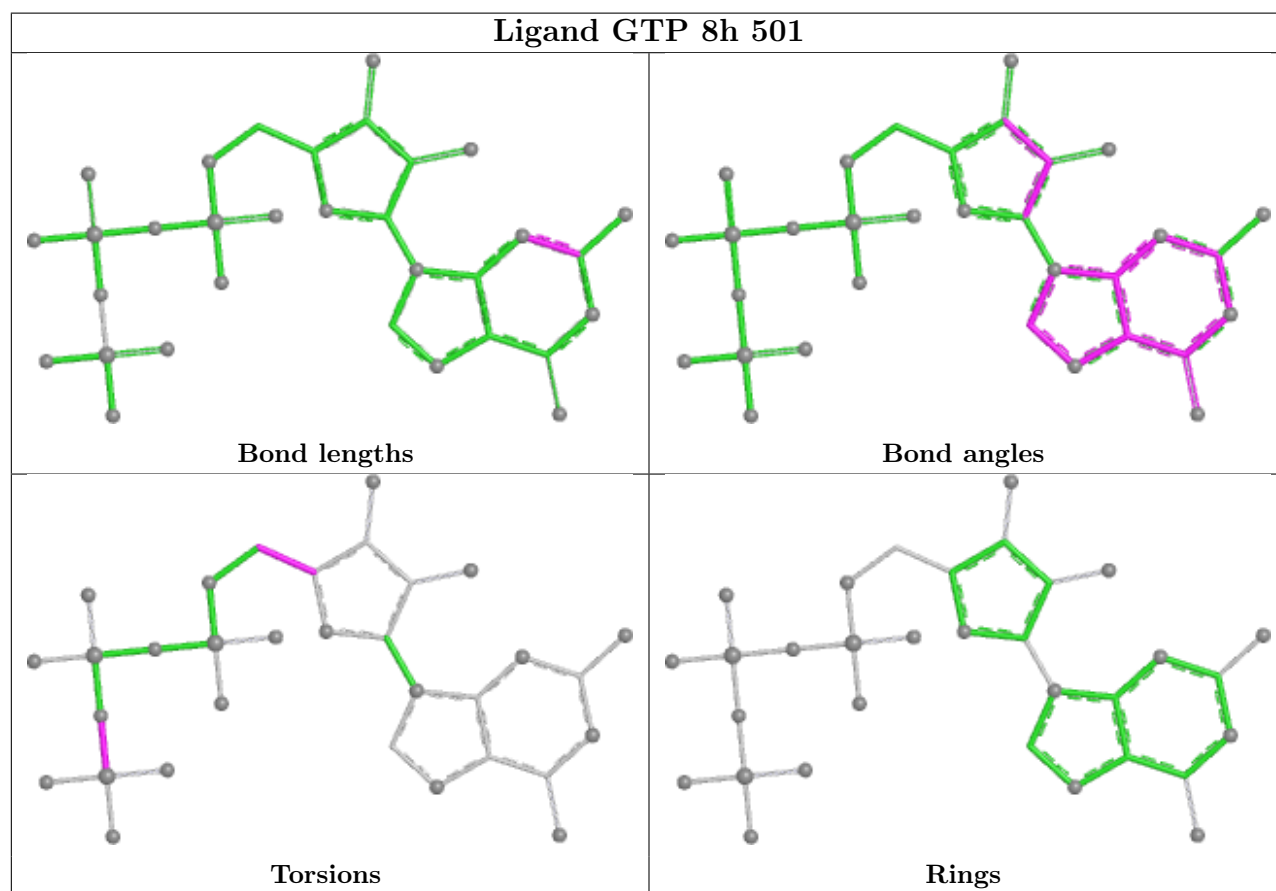
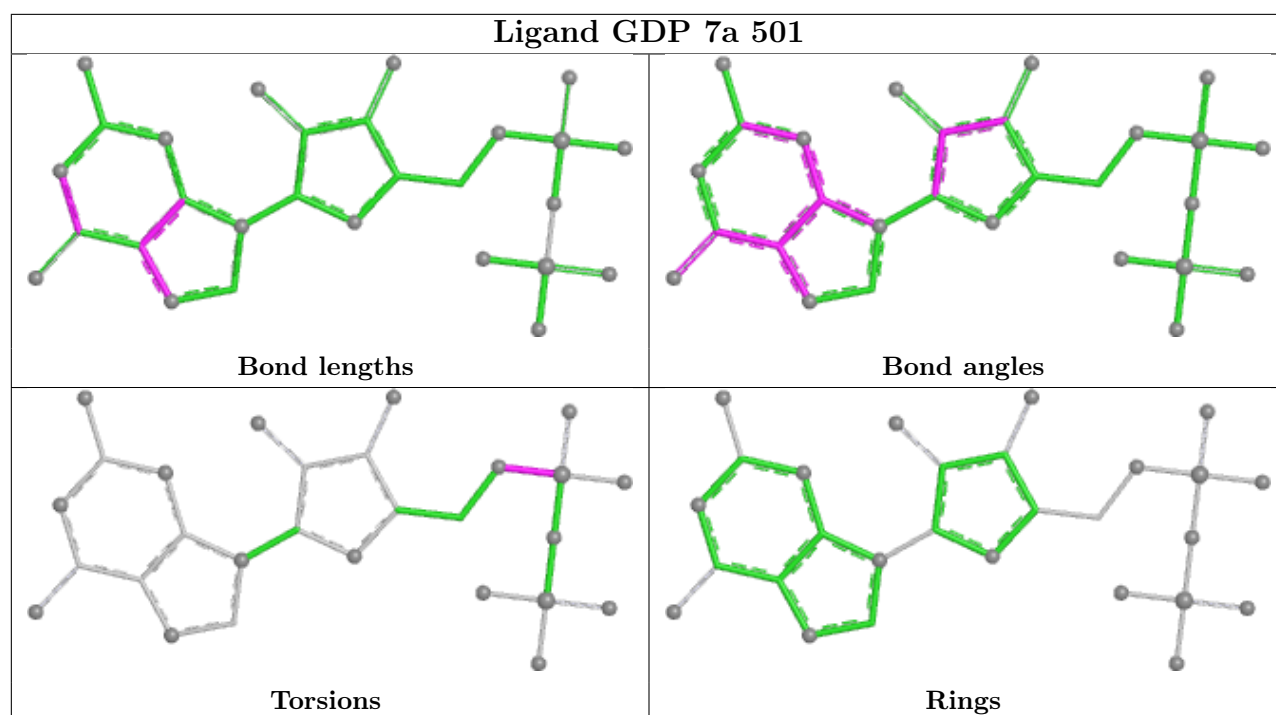


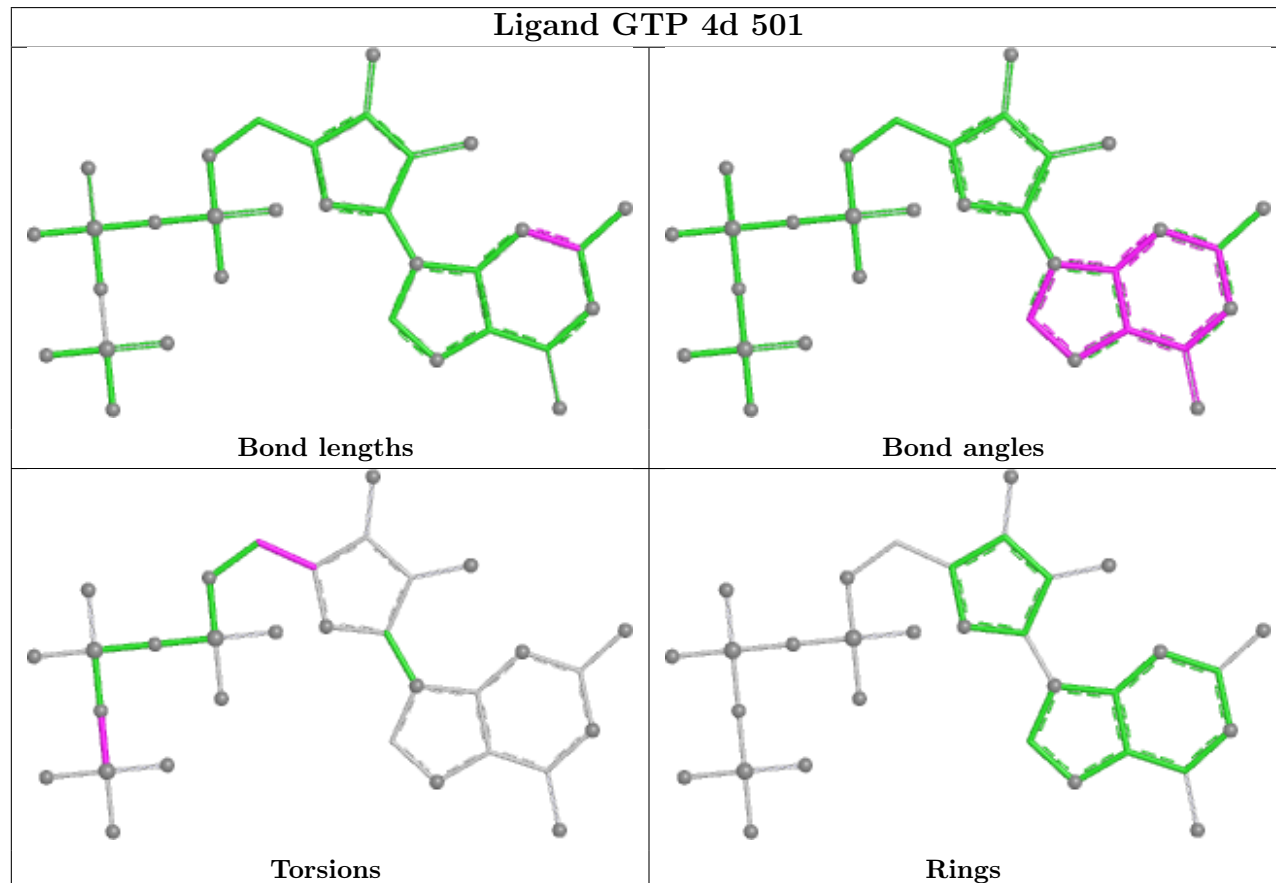
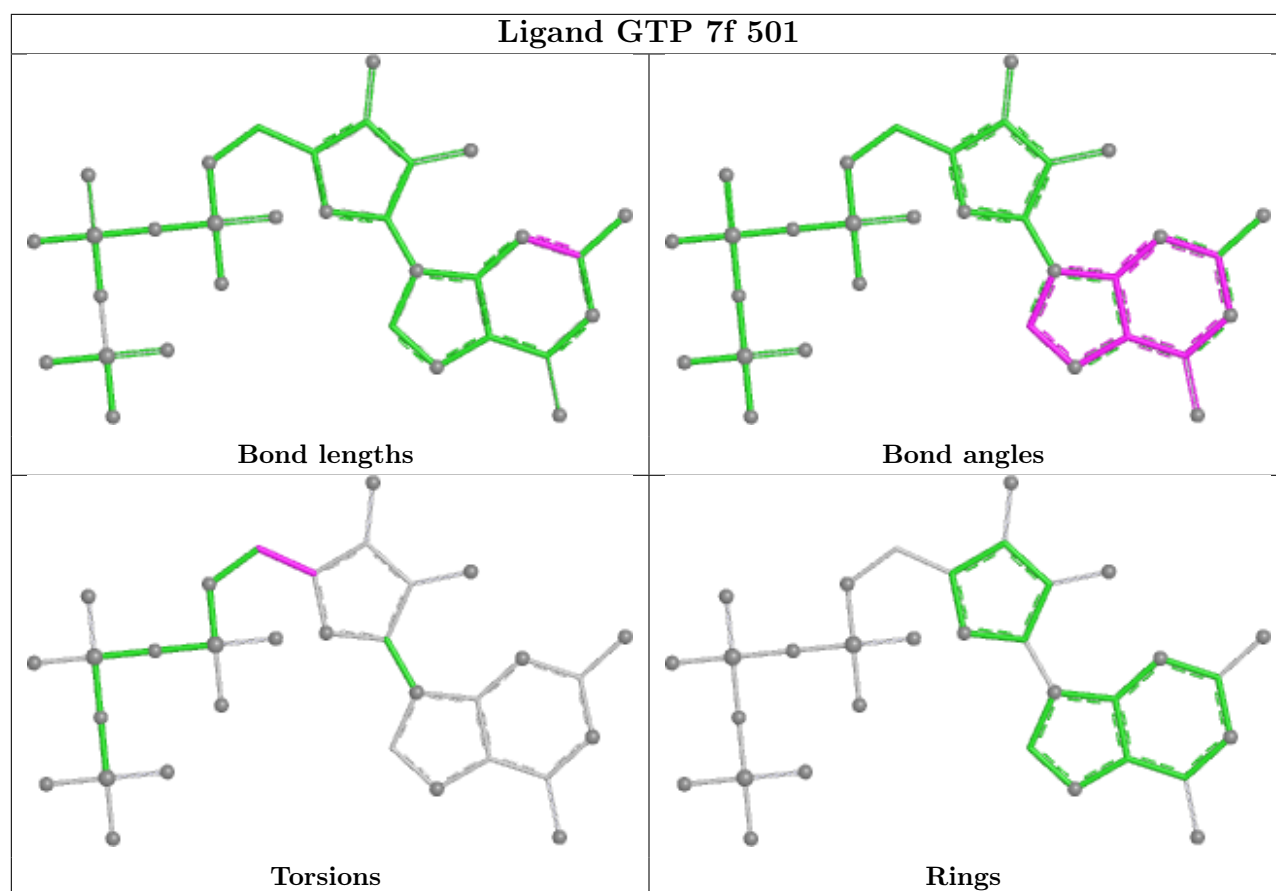
Ligand GTP Bd 501

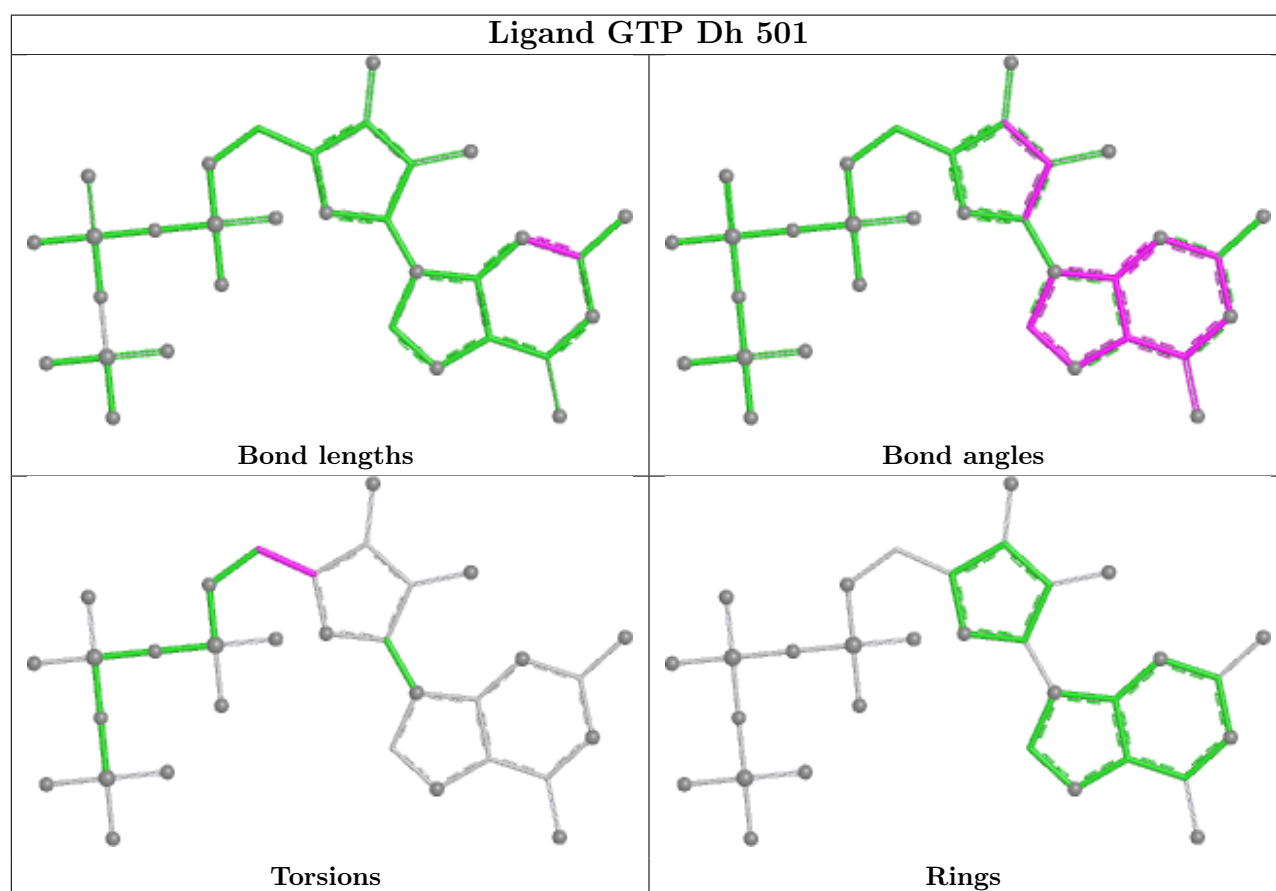
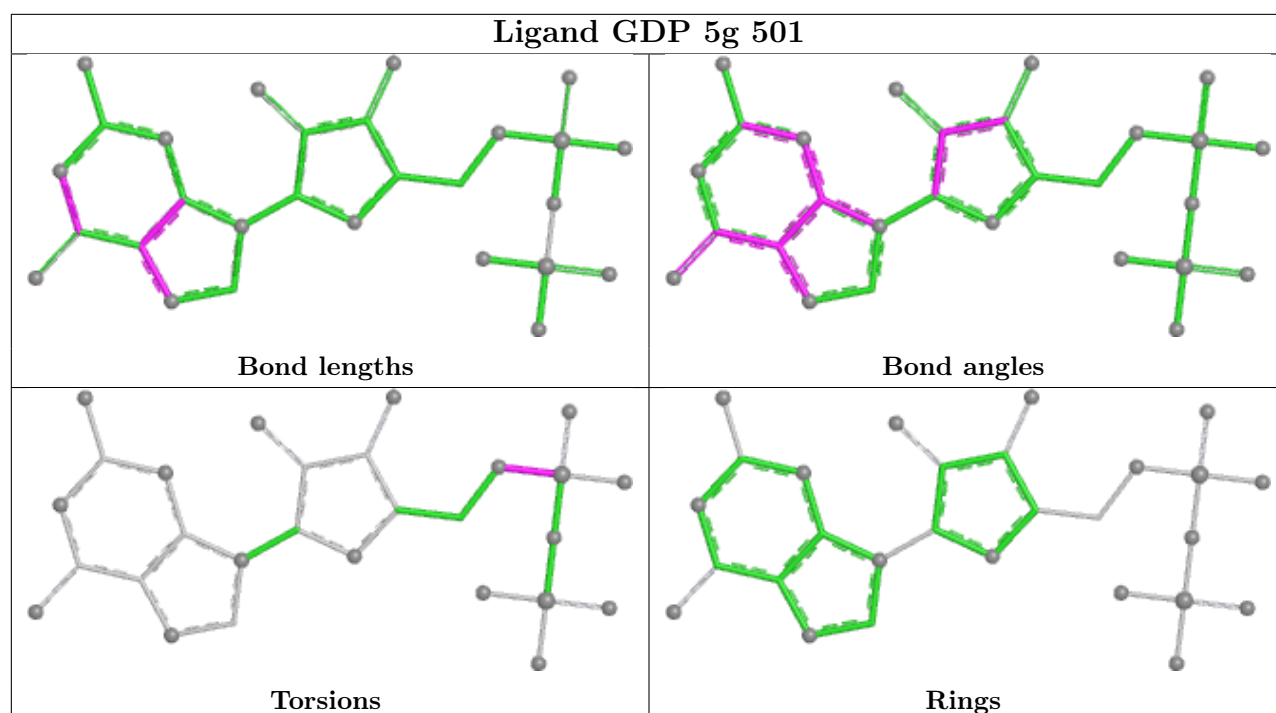


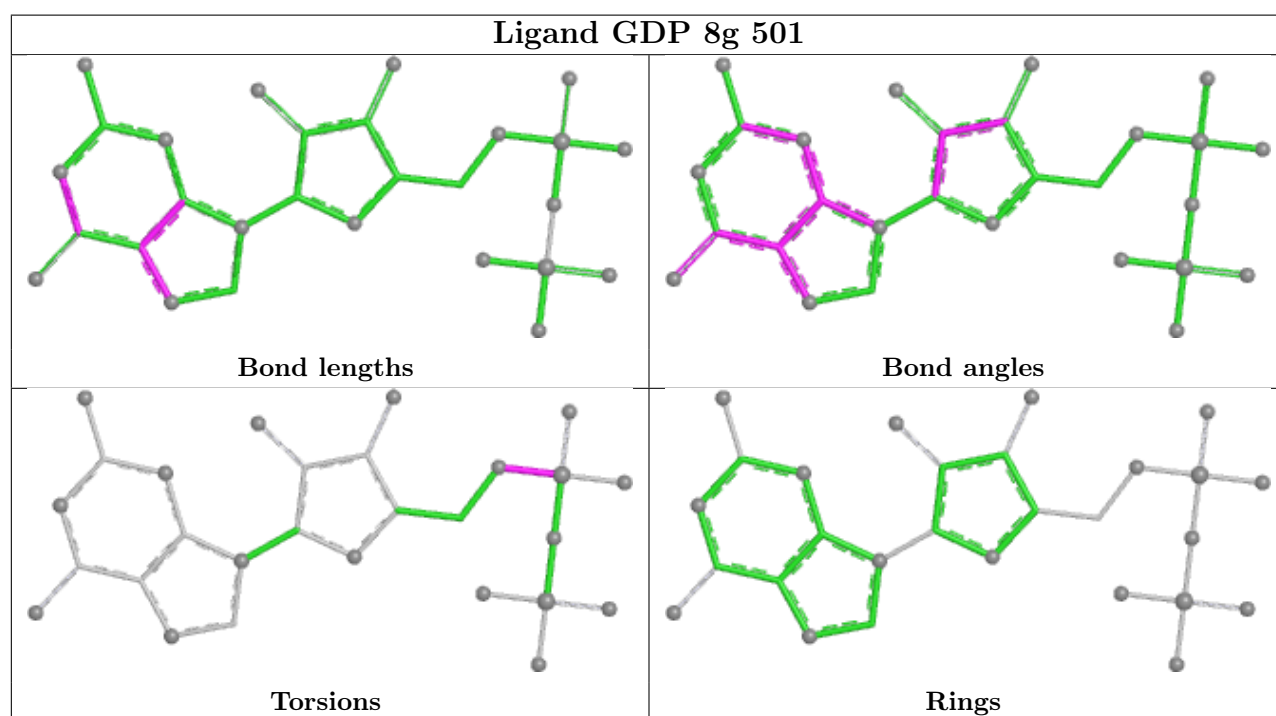
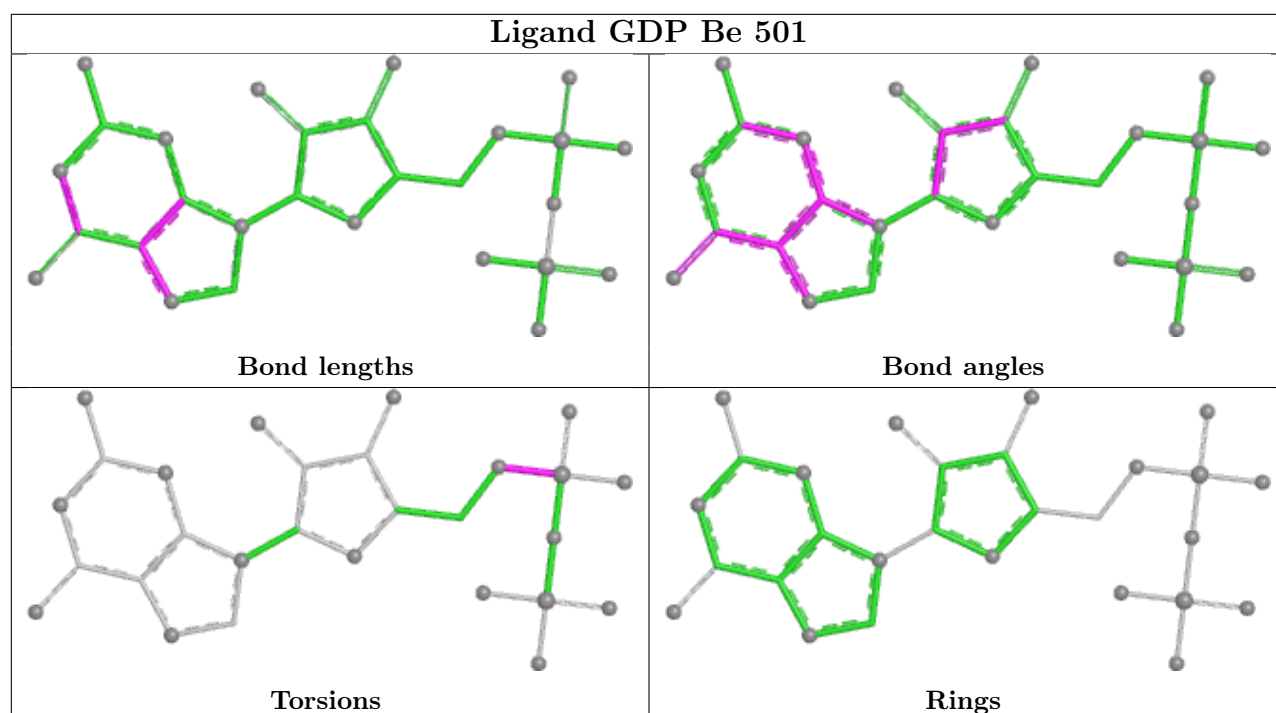
Ligand GTP 8b 501

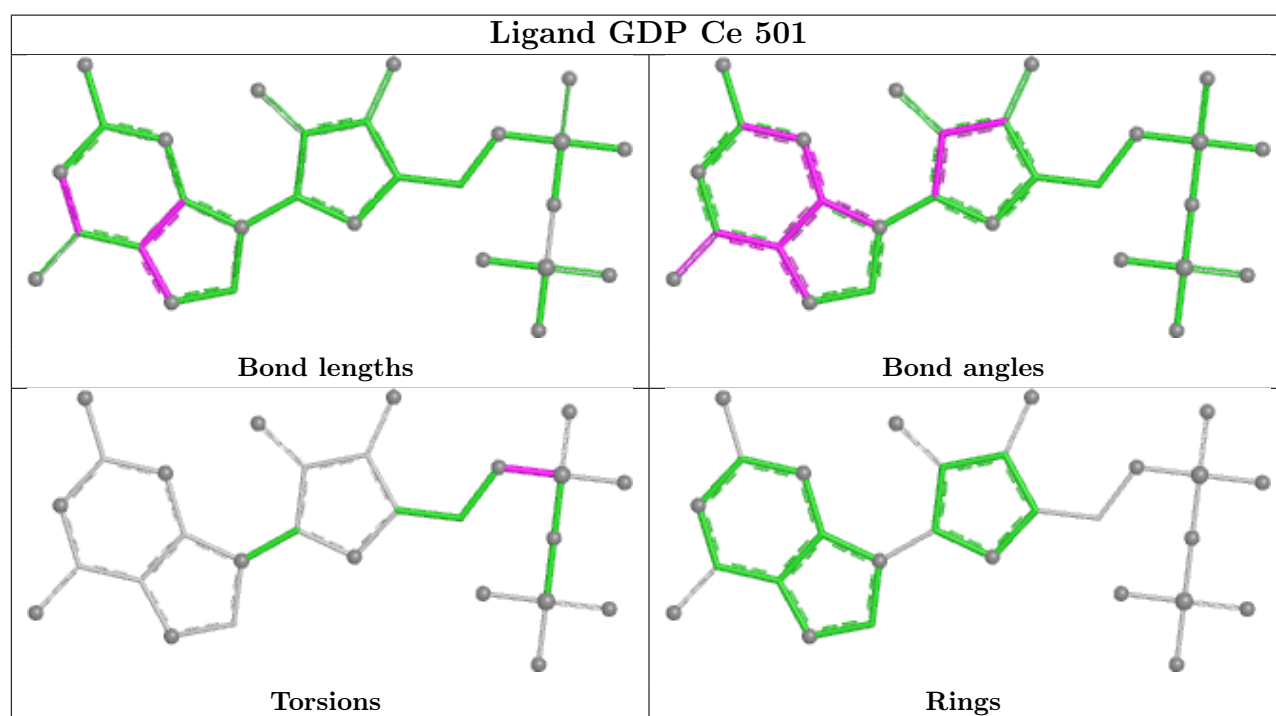
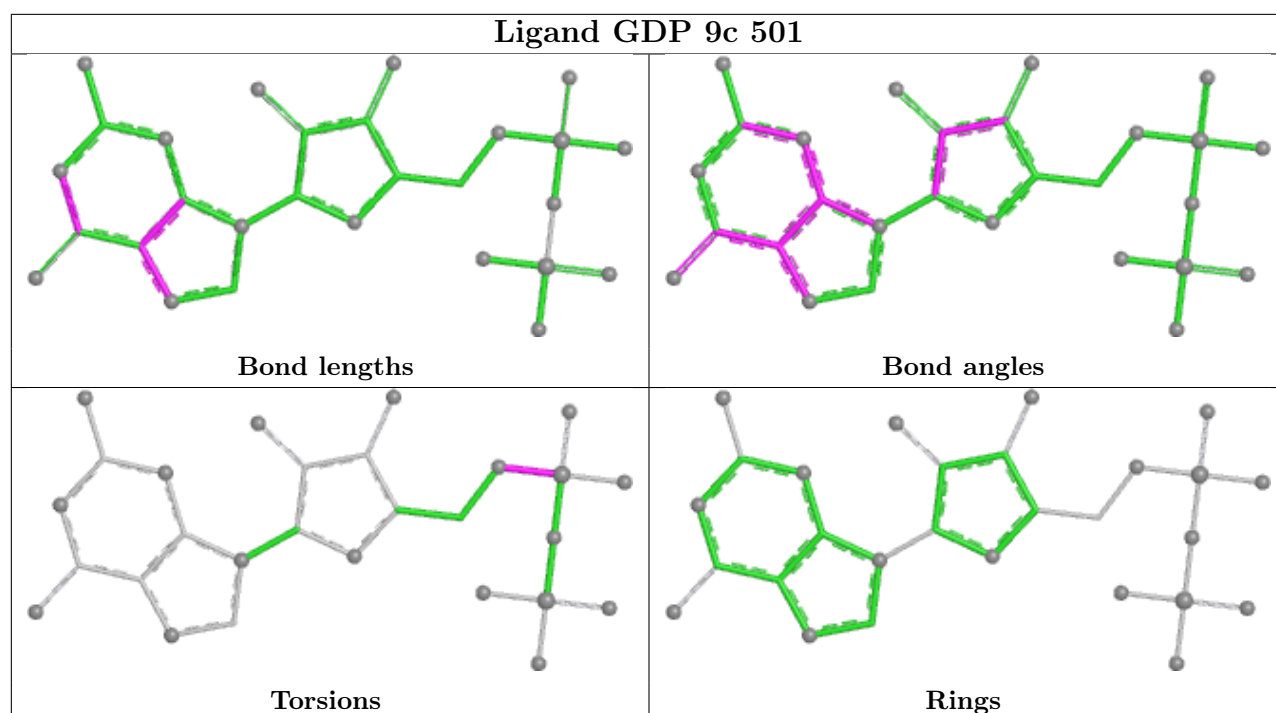


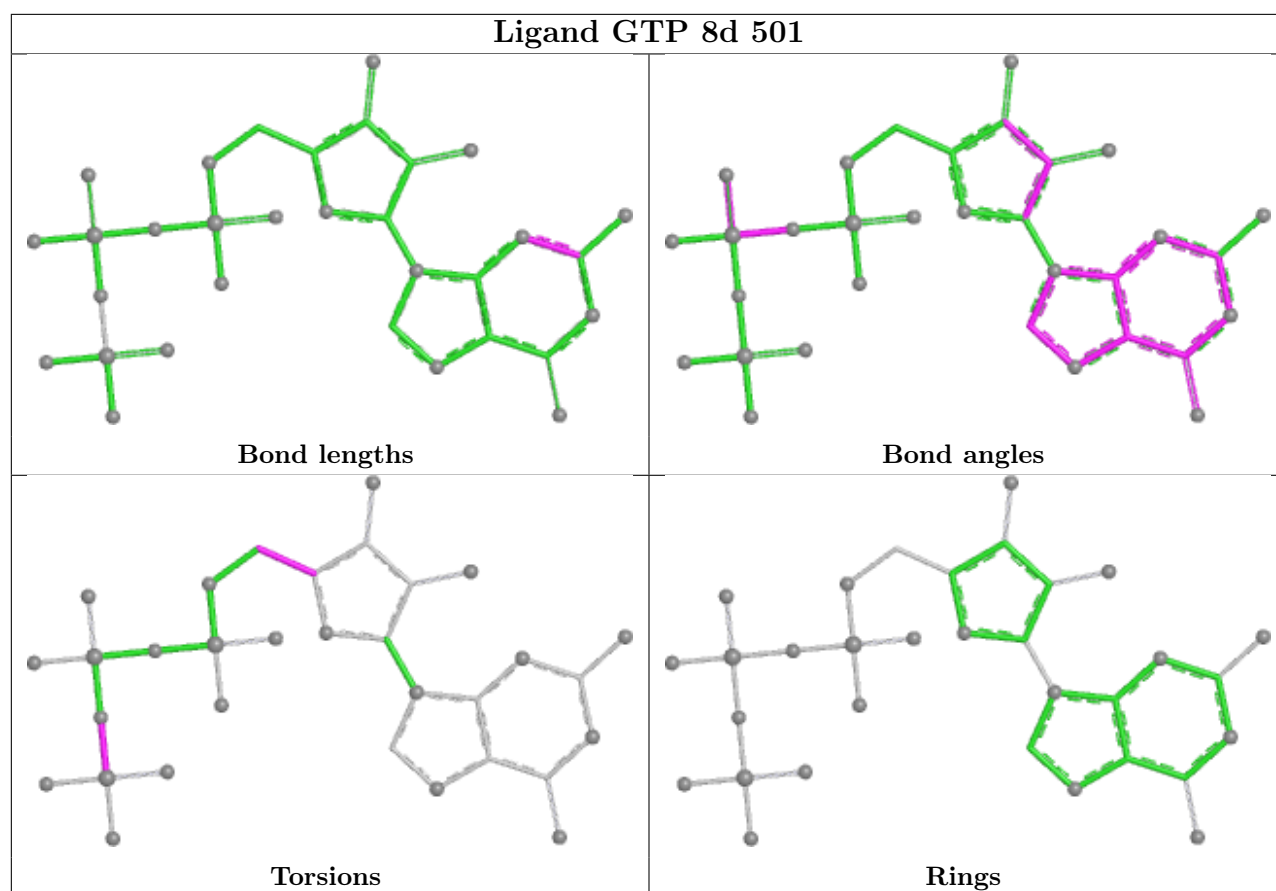












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

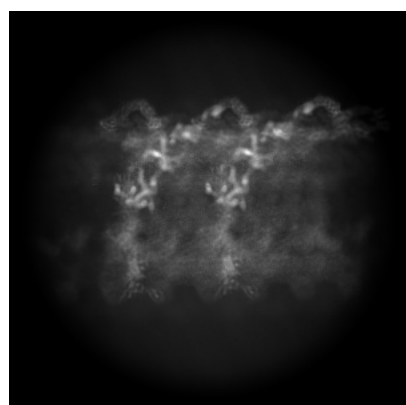
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24191. These allow visual inspection of the internal detail of the map and identification of artifacts.

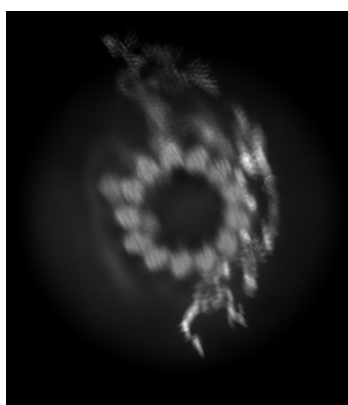
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

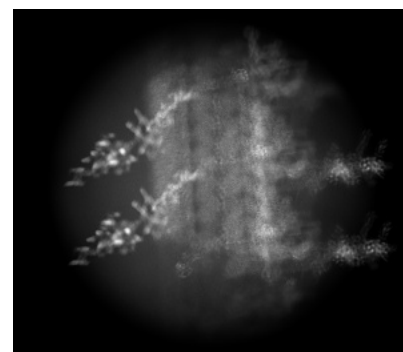
6.1.1 Primary map



X



Y

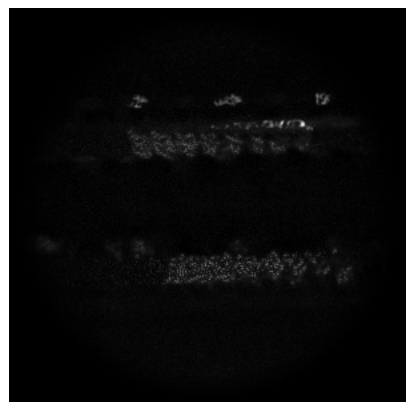


Z

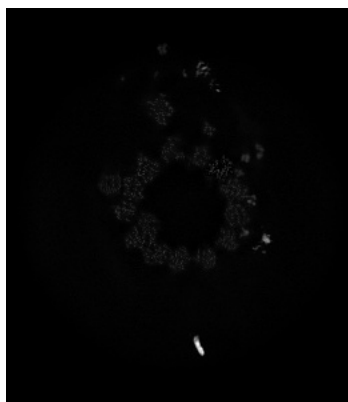
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

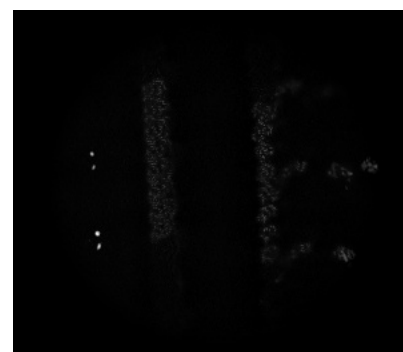
6.2.1 Primary map



X Index: 303



Y Index: 263



Z Index: 263

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

6.3 Largest variance slices [i](#)

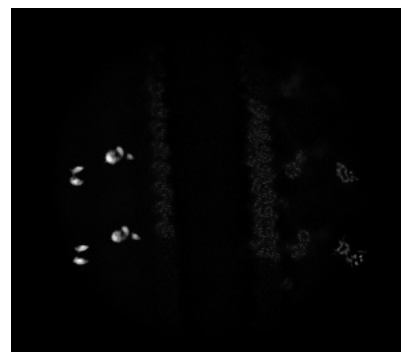
6.3.1 Primary map



X Index: 147



Y Index: 294

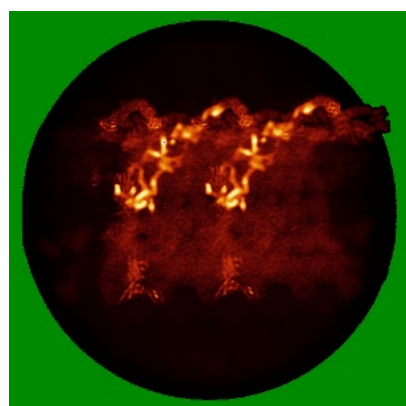


Z Index: 288

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

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

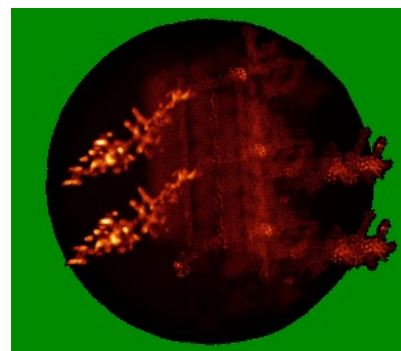
6.4.1 Primary map



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

This section was not generated.

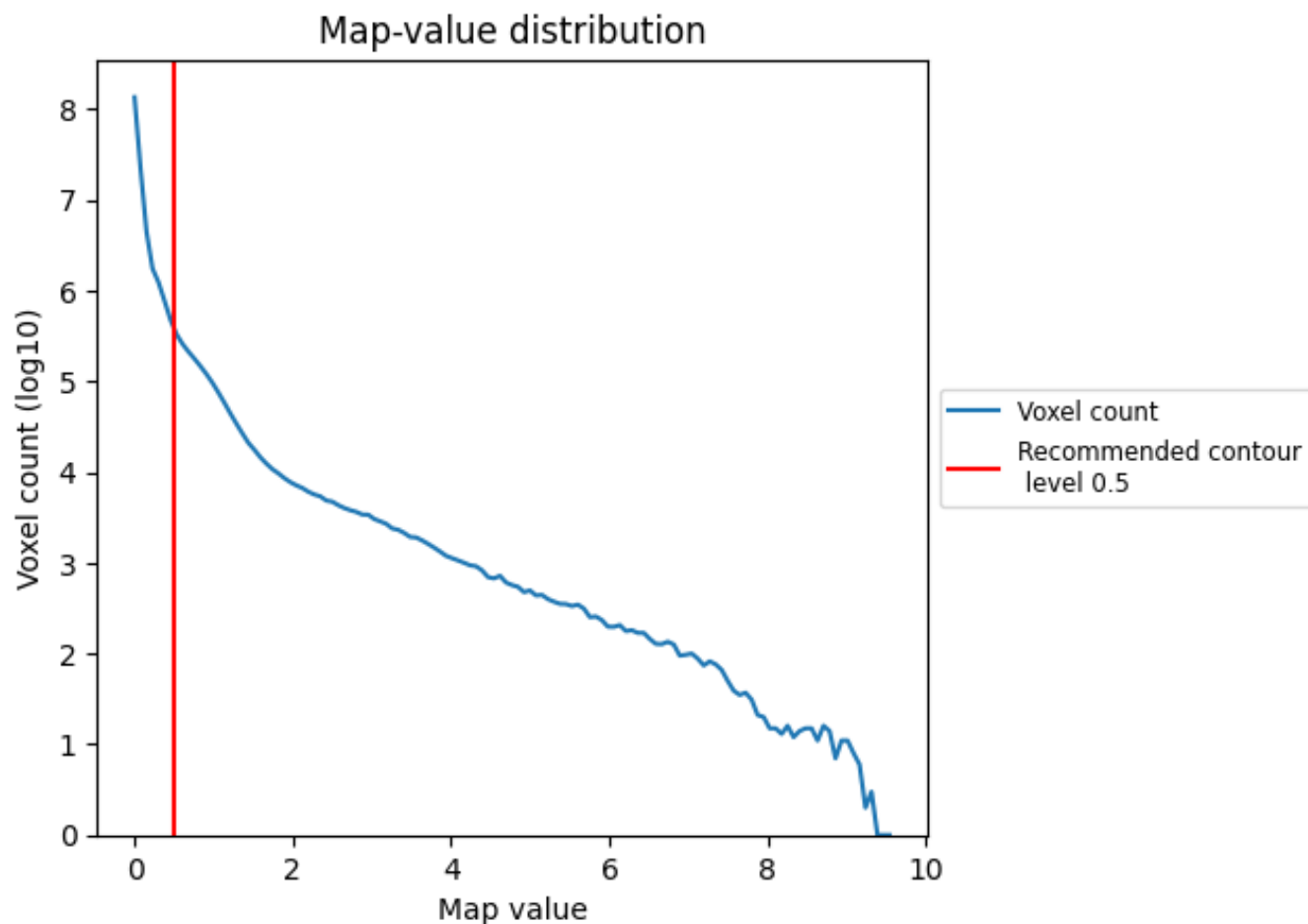
6.6 Mask visualisation

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

7 Map analysis [i](#)

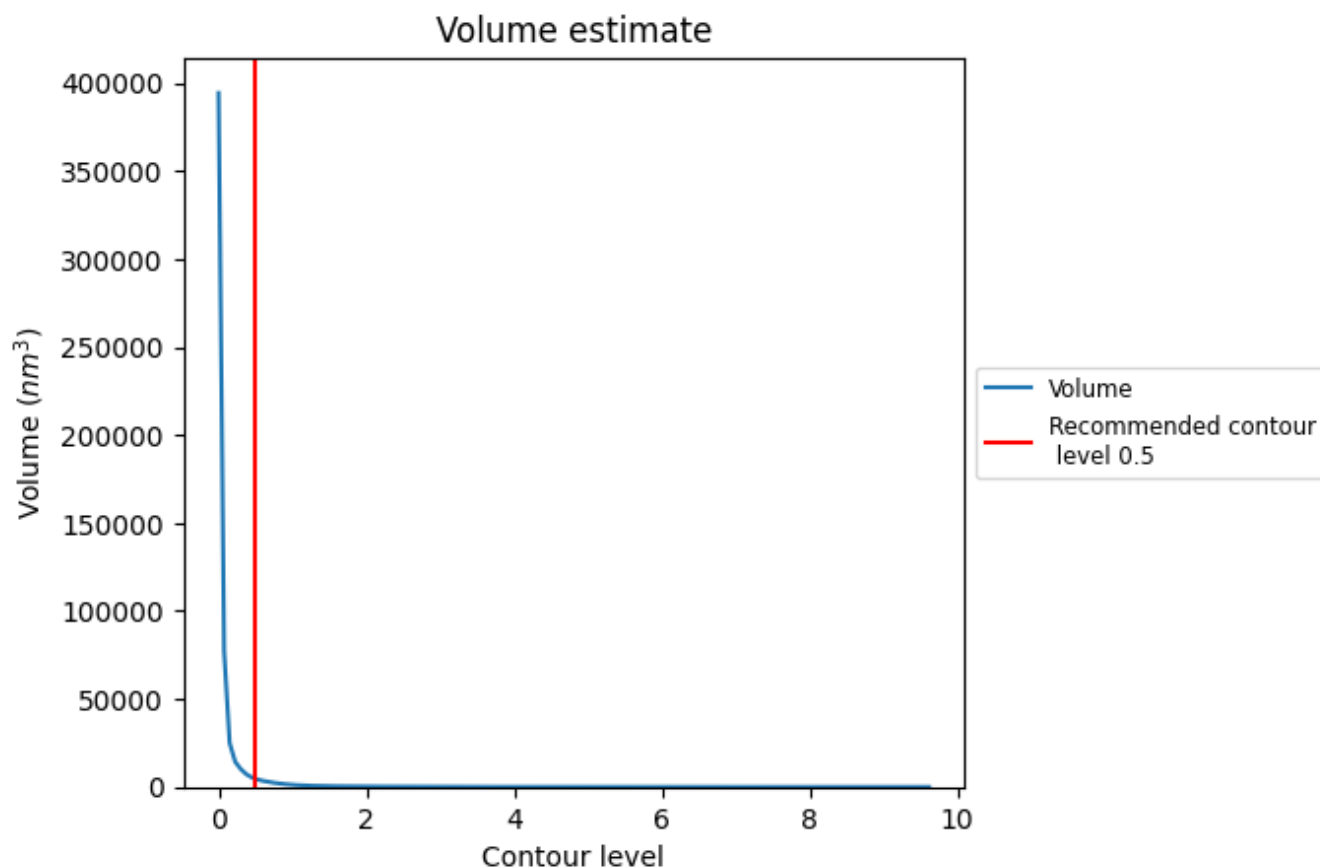
This section contains the results of statistical analysis of the map.

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 4655 nm³; this corresponds to an approximate mass of 4205 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.

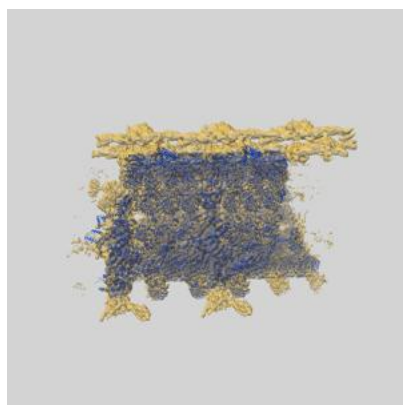
8 Fourier-Shell correlation

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

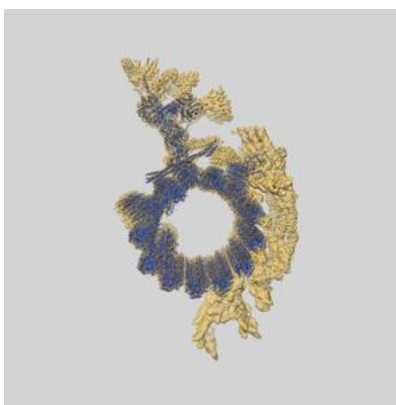
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24191 and PDB model 7N61. Per-residue inclusion information can be found in section [3](#) on page [24](#).

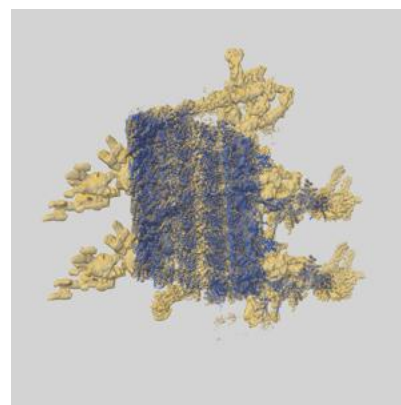
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 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](#)

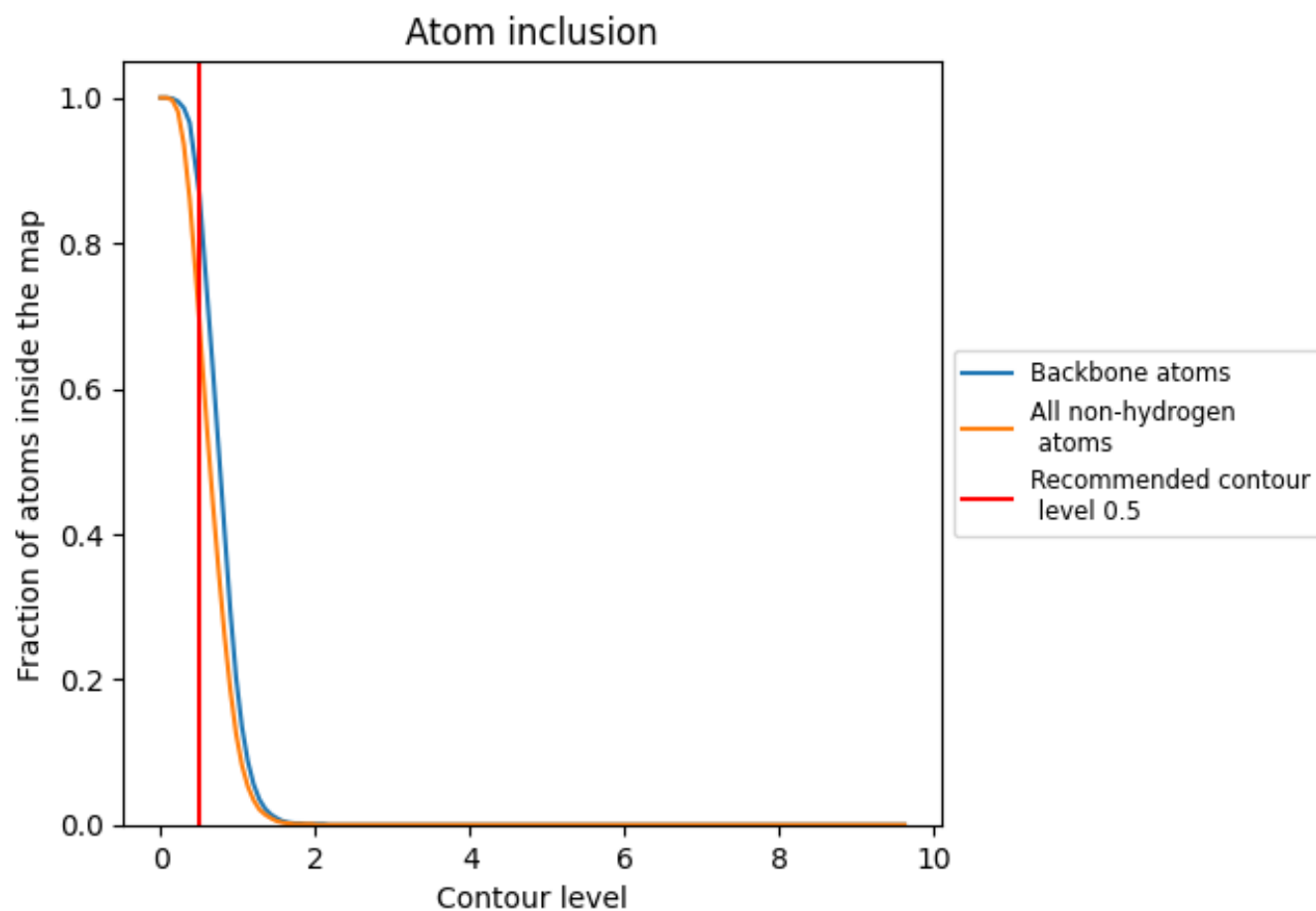


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

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	 0.6950	 0.4050
0A	 0.5700	 0.3440
0B	 0.6230	 0.3750
0C	 0.5950	 0.3680
0D	 0.4350	 0.3010
0E	 0.6710	 0.4680
0F	 0.7080	 0.4710
0G	 0.4120	 0.3520
0H	 0.6160	 0.4340
0I	 0.7720	 0.3700
0J	 0.7870	 0.3700
0K	 0.5770	 0.3620
0L	 0.3180	 0.2630
0M	 0.5730	 0.4280
0N	 0.4340	 0.3900
0O	 0.4650	 0.3740
0P	 0.6640	 0.4190
0Q	 0.6920	 0.4490
0S	 0.6390	 0.4290
0T	 0.6710	 0.4930
0U	 0.5750	 0.4690
0V	 0.6030	 0.4890
0W	 0.8360	 0.4680
0X	 0.5370	 0.4480
0Y	 0.4750	 0.4020
0Z	 0.5290	 0.4490
1A	 0.4610	 0.4040
1B	 0.7520	 0.3620
1C	 0.6740	 0.3370
1D	 0.7460	 0.2730
1E	 0.7550	 0.2830
1F	 0.7520	 0.2980
1G	 0.7550	 0.3060
1H	 0.7430	 0.4800
1L	 0.9580	 0.4980



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Chain	Atom inclusion	Q-score
1M	 0.9600	 0.4900
1a	 0.7160	 0.4460
1b	 0.5890	 0.3780
1c	 0.7430	 0.4320
1d	 0.7750	 0.4650
1e	 0.8190	 0.4800
1f	 0.8030	 0.4700
1g	 0.8120	 0.4690
1h	 0.7790	 0.4610
2a	 0.6370	 0.4260
2b	 0.5930	 0.3910
2c	 0.7010	 0.4230
2d	 0.7290	 0.4460
2e	 0.7050	 0.4370
2f	 0.6960	 0.4390
2g	 0.7460	 0.4500
2h	 0.6950	 0.4330
3a	 0.6250	 0.4080
3b	 0.6710	 0.4280
3c	 0.7430	 0.4390
3d	 0.7500	 0.4490
3e	 0.7170	 0.4340
3f	 0.6620	 0.4190
3g	 0.7230	 0.4290
3h	 0.6850	 0.4220
4a	 0.5430	 0.3810
4b	 0.6330	 0.4040
4c	 0.6700	 0.4010
4d	 0.6920	 0.4170
4e	 0.6960	 0.4160
4f	 0.6750	 0.4090
4g	 0.7270	 0.4230
4h	 0.6780	 0.4000
5a	 0.5660	 0.3480
5b	 0.5980	 0.3720
5c	 0.6590	 0.3680
5d	 0.6490	 0.3590
5e	 0.6920	 0.3760
5f	 0.6580	 0.3600
5g	 0.6980	 0.3820
5h	 0.6850	 0.3680
6a	 0.4780	 0.2610

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Chain	Atom inclusion	Q-score
6b	 0.5190	 0.3180
6c	 0.5830	 0.3060
6d	 0.6120	 0.3220
6e	 0.6390	 0.3150
6f	 0.5940	 0.3040
6g	 0.6100	 0.3000
6h	 0.5990	 0.2920
7a	 0.6030	 0.3430
7b	 0.5940	 0.3630
7c	 0.7040	 0.3780
7d	 0.7040	 0.3810
7e	 0.7070	 0.3680
7f	 0.7060	 0.3670
7g	 0.7080	 0.3580
7h	 0.6850	 0.3530
8a	 0.6170	 0.3630
8b	 0.6490	 0.3800
8c	 0.7590	 0.3980
8d	 0.7880	 0.4150
8e	 0.7750	 0.4090
8f	 0.7590	 0.3890
8g	 0.7790	 0.3900
8h	 0.7380	 0.3870
9a	 0.7940	 0.4710
9b	 0.8250	 0.5090
9c	 0.8380	 0.5110
9d	 0.8180	 0.4800
9e	 0.7850	 0.4580
9f	 0.8260	 0.5090
9g	 0.8310	 0.5060
9h	 0.8120	 0.4790
Aa	 0.6880	 0.4040
Ab	 0.6060	 0.3800
Ac	 0.6910	 0.3760
Ad	 0.7370	 0.4000
Ae	 0.7450	 0.3950
Af	 0.7370	 0.4100
Ag	 0.7500	 0.4030
Ah	 0.7380	 0.4120
Ba	 0.5970	 0.3670
Bb	 0.6530	 0.3960
Bc	 0.8280	 0.4370

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Chain	Atom inclusion	Q-score
Bd	 0.8070	 0.4330
Be	 0.7300	 0.4110
Bf	 0.7520	 0.4220
Bg	 0.8240	 0.4410
Bh	 0.7980	 0.4220
Ca	 0.6550	 0.4240
Cb	 0.6950	 0.4330
Cc	 0.7850	 0.4510
Cd	 0.7930	 0.4650
Ce	 0.8140	 0.4710
Cf	 0.7770	 0.4600
Cg	 0.7700	 0.4540
Ch	 0.7640	 0.4510
Da	 0.6700	 0.4300
Db	 0.7180	 0.4480
Dc	 0.7890	 0.4780
Dd	 0.8060	 0.4770
De	 0.8170	 0.4830
Df	 0.7750	 0.4630
Dg	 0.7590	 0.4680
Dh	 0.7190	 0.4500