



wwPDB EM Validation Summary Report ⓘ

Sep 1, 2026 – 07:46 PM EDT

PDB ID : 11YJ / pdb_000011yj
EMDB ID : EMD-76188
Title : In situ subtomogram average of the transition zone doublet microtubule in human airway cilia (composite map)
Authors : Zhou, H.; Brown, A.
Deposited on : 2026-03-18
Resolution : 7.30 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.dev133
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) : 2.50

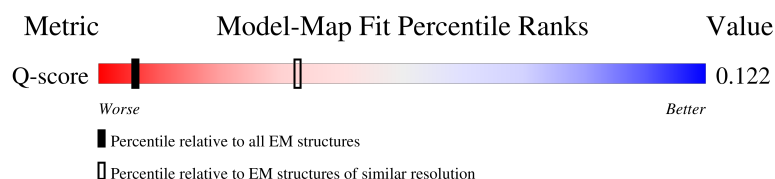
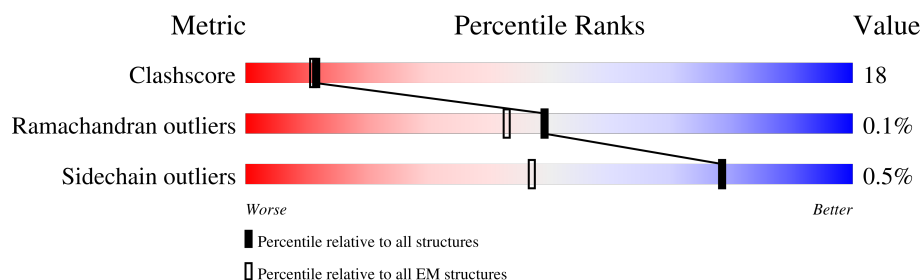
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.30 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.



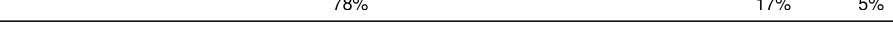
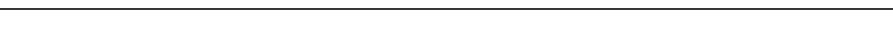
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	436 (6.80 - 7.80)

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	A0	451	
1	A2	451	
1	A4	451	
1	A6	451	

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Mol	Chain	Length	Quality of chain
1	B1	451	 83% 14% .
1	B3	451	 81% 15% .
1	B5	451	 81% 17% .
1	C1	451	 5% 82% 14% .
1	C3	451	 78% 18% .
1	C5	451	 85% 12% .
1	D1	451	 77% 18% 5%
1	D3	451	 78% 17% 5%
1	D5	451	 78% 17% 5%
1	E1	451	 77% 20% .
1	E3	451	 76% 21% .
1	E5	451	 79% 18% .
1	F1	451	 78% 17% 5%
1	F3	451	 78% 17% 5%
1	F5	451	 79% 17% 5%
1	G0	451	 76% 19% .
1	G2	451	 75% 20% 5%
1	G4	451	 81% 15% .
1	H0	451	 80% 16% .
1	H2	451	 76% 20% .
1	H4	451	 77% 18% .
1	I0	451	 83% 15% .
1	I2	451	 81% 15% .
1	I4	451	 84% 14% .
1	I6	451	 78% 18% .

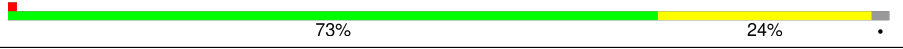
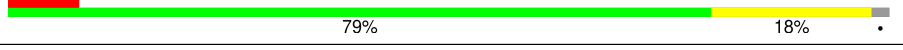
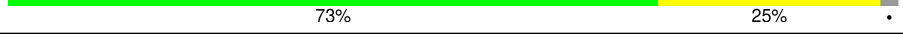
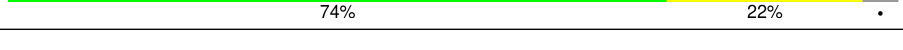
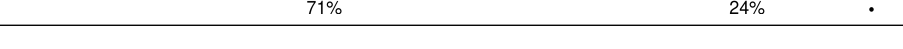
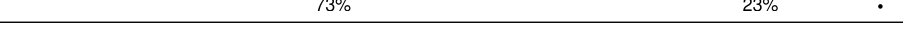
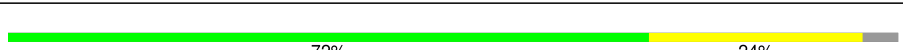
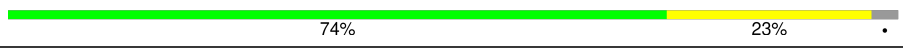
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Mol	Chain	Length	Quality of chain
1	J1	451	 81%14%5%
1	J3	451	 79%16%5%
1	J5	451	 78%17%5%
1	K0	451	 84%12%4%
1	K2	451	 83%13%4%
1	K4	451	 80%18%2%
1	L0	451	 85%11%4%
1	L2	451	 83%14%3%
1	L4	451	 85%11%4%
1	L6	451	 84%12%4%
1	M0	451	 83%13%4%
1	M2	451	 80%15%5%
1	M4	451	 82%14%4%
1	M6	451	 85%11%4%
1	N0	451	 81%16%3%
1	N2	451	 76%21%3%
1	N4	451	 74%23%3%
1	N6	451	 79%18%3%
1	O0	451	 83%15%2%
1	O2	451	 79%19%2%
1	O4	451	 78%20%2%
1	O6	451	 80%18%2%
1	P0	451	 86%12%2%
1	P2	451	 78%20%2%
1	P4	451	 77%21%2%

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Mol	Chain	Length	Quality of chain
1	P6	451	
1	Q1	451	
1	Q3	451	
1	Q5	451	
1	R1	451	
1	R3	451	
1	R5	451	
1	S1	451	
1	S3	451	
1	S5	451	
1	T1	451	
1	T3	451	
1	T5	451	
1	U1	451	
1	U3	451	
1	U5	451	
1	V0	451	
1	V2	451	
1	V4	451	
1	W0	451	
1	W2	451	
1	W4	451	
1	W6	451	
2	A1	445	
2	A3	445	

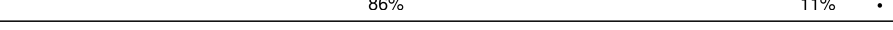
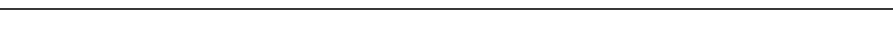
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Mol	Chain	Length	Quality of chain
2	A5	445	 78%19%.
2	B0	445	 80%16%.
2	B2	445	 80%16%.
2	B4	445	 78%18%.
2	C0	445	 79%17%.
2	C2	445	 75%20%.
2	C4	445	 74%21%.
2	D0	445	 77%18%.
2	D2	445	 77%18%.
2	D4	445	 76%20%.
2	D6	445	 79%16%.
2	E0	445	 77%18%.
2	E2	445	 77%19%.
2	E4	445	 76%19%.
2	E6	445	 76%20%.
2	F0	445	 75%20%.
2	F2	445	 76%19%.
2	F4	445	 75%20%.
2	F6	445	 76%19%.
2	G1	445	 78%18%.
2	G3	445	 74%22%.
2	G5	445	 74%22%.
2	H1	445	 83%13%.
2	H3	445	 77%19%.
2	H5	445	 74%21%.

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Mol	Chain	Length	Quality of chain
2	I1	445	 76% 20% .
2	I3	445	 80% 16% .
2	I5	445	 76% 20% .
2	J0	445	 84% 12% .
2	J2	445	 77% 19% .
2	J4	445	 80% 16% .
2	J6	445	 80% 16% .
2	K1	445	 81% 16% .
2	K3	445	 85% 12% .
2	K5	445	 78% 19% .
2	L1	445	 82% 14% .
2	L3	445	 82% 13% .
2	L5	445	 81% 15% .
2	M1	445	 86% 11% .
2	M3	445	 81% 15% .
2	M5	445	 85% 11% .
2	N1	445	 78% 18% .
2	N3	445	 72% 24% . .
2	N5	445	 68% 28% .
2	O1	445	 77% 20% .
2	O3	445	 74% 23% .
2	O5	445	 71% 25% .
2	P1	445	 76% 20% .
2	P3	445	 74% 22% . .
2	P5	445	 74% 22% .

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Mol	Chain	Length	Quality of chain
2	Q0	445	 81% 15% .
2	Q2	445	 75% 21% .
2	Q4	445	 75% 21% .
2	R0	445	 75% 21% .
2	R2	445	 67% 29% .
2	R4	445	 69% 27% .
2	R6	445	 76% 20% .
2	S0	445	 65% 30% .
2	S2	445	 63% 32% .
2	S4	445	 67% 29% .
2	S6	445	 70% 25% . .
2	T0	445	 71% 25% .
2	T2	445	 71% 24% .
2	T4	445	 70% 25% . .
2	T6	445	 76% 19% .
2	U0	445	 77% 19% .
2	U2	445	 73% 22% .
2	U4	445	 69% 27% .
2	U6	445	 80% 15% .
2	V1	445	 71% 24% .
2	V3	445	 71% 25% .
2	V5	445	 77% 19% .
2	W1	445	 72% 23% . .
2	W3	445	 73% 22% .
2	W5	445	 74% 22% .

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Mol	Chain	Length	Quality of chain
3	X0	193	
3	X1	193	
3	X2	193	
3	X3	193	
4	Y0	373	
4	Y1	373	
4	Y2	373	
5	1A	208	
5	1B	208	
5	1C	208	
5	1D	208	
5	1E	208	
5	1F	208	
5	1G	208	
5	2A	208	
5	2B	208	
5	2C	208	
5	2D	208	
5	2E	208	
5	2F	208	
5	2G	208	
5	2H	208	
5	2I	208	
5	2J	208	
5	3C	208	

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Mol	Chain	Length	Quality of chain
5	3D	208	
5	3E	208	
5	3F	208	
5	3G	208	
5	3H	208	
5	3I	208	
5	3J	208	
5	4H	208	
5	4I	208	
5	4J	208	
5	5A	208	
5	5B	208	
5	5C	208	
5	5D	208	
5	6A	208	
5	6B	208	
5	6C	208	
5	6D	208	
5	7A	208	
5	7B	208	
5	7C	208	
5	7D	208	
6	9A	647	
6	9B	647	
7	8A	346	

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Mol	Chain	Length	Quality of chain
7	8B	346	
7	8C	346	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	GTP	N4	501	-	-	X	-
8	GTP	N6	501	-	-	X	-
8	GTP	O4	501	-	-	X	-
8	GTP	O6	501	-	-	X	-
8	GTP	P0	501	-	-	X	-
8	GTP	P4	501	-	-	X	-
8	GTP	P6	501	-	-	X	-
8	GTP	Q1	501	-	-	X	-
8	GTP	Q5	501	-	-	X	-
8	GTP	R1	501	-	-	X	-
8	GTP	R5	501	-	-	X	-
8	GTP	S1	501	-	-	X	-
8	GTP	S3	501	-	-	X	-
8	GTP	S5	501	-	-	X	-
8	GTP	T3	501	-	-	X	-
8	GTP	T5	501	-	-	X	-
8	GTP	U5	501	-	-	X	-
8	GTP	V0	501	-	-	X	-
8	GTP	W6	501	-	-	X	-
9	GDP	N5	501	-	-	X	-
9	GDP	O5	501	-	-	X	-
9	GDP	P5	501	-	-	X	-
9	GDP	Q4	501	-	-	X	-
9	GDP	R2	501	-	-	X	-
9	GDP	R4	501	-	-	X	-
9	GDP	R6	501	-	-	X	-
9	GDP	S6	501	-	-	X	-
9	GDP	T4	501	-	-	X	-
9	GDP	T6	501	-	-	X	-
9	GDP	U6	501	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 607834 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 Tubulin alpha-1A chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A0	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	A2	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	A4	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	A6	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	B1	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	B3	432	Total	C	N	O	S	0	0
			3383	2143	575	643	22		
1	B5	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	C1	432	Total	C	N	O	S	0	0
			3383	2143	575	643	22		
1	C3	431	Total	C	N	O	S	0	0
			3377	2140	574	641	22		
1	C5	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	D1	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
1	D3	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
1	D5	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
1	E1	438	Total	C	N	O	S	0	0
			3423	2167	582	652	22		
1	E3	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	E5	438	Total	C	N	O	S	0	0
			3423	2167	582	652	22		
1	F1	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	F3	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
1	F5	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
1	G0	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
1	G2	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
1	G4	432	Total	C	N	O	S	0	0
			3385	2144	575	644	22		
1	H0	432	Total	C	N	O	S	0	0
			3385	2144	575	644	22		
1	H2	432	Total	C	N	O	S	0	0
			3385	2144	575	644	22		
1	H4	431	Total	C	N	O	S	0	0
			3377	2140	574	641	22		
1	I0	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	I2	432	Total	C	N	O	S	0	0
			3385	2144	575	644	22		
1	I4	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	I6	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
1	J1	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
1	J3	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
1	J5	431	Total	C	N	O	S	0	0
			3377	2140	574	641	22		
1	K0	432	Total	C	N	O	S	0	0
			3384	2145	575	642	22		
1	K2	433	Total	C	N	O	S	0	0
			3392	2149	576	645	22		
1	K4	440	Total	C	N	O	S	0	0
			3436	2175	584	655	22		
1	L0	434	Total	C	N	O	S	0	0
			3397	2150	577	648	22		
1	L2	436	Total	C	N	O	S	0	0
			3410	2158	580	650	22		
1	L4	433	Total	C	N	O	S	0	0
			3390	2148	576	644	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	L6	433	Total	C	N	O	S	0	0
			3390	2148	576	644	22		
1	M0	433	Total	C	N	O	S	0	0
			3390	2148	576	644	22		
1	M2	430	Total	C	N	O	S	0	0
			3373	2138	573	640	22		
1	M4	433	Total	C	N	O	S	0	0
			3390	2148	576	644	22		
1	M6	438	Total	C	N	O	S	0	0
			3423	2167	582	652	22		
1	N0	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	N2	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	N4	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	N6	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	O0	441	Total	C	N	O	S	0	0
			3445	2180	585	658	22		
1	O2	441	Total	C	N	O	S	0	0
			3445	2180	585	658	22		
1	O4	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	O6	441	Total	C	N	O	S	0	0
			3445	2180	585	658	22		
1	P0	441	Total	C	N	O	S	0	0
			3445	2180	585	658	22		
1	P2	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	P4	440	Total	C	N	O	S	0	0
			3436	2175	584	655	22		
1	P6	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	Q1	440	Total	C	N	O	S	0	0
			3436	2175	584	655	22		
1	Q3	440	Total	C	N	O	S	0	0
			3436	2175	584	655	22		
1	Q5	440	Total	C	N	O	S	0	0
			3436	2175	584	655	22		
1	R1	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R3	440	Total	C	N	O	S	0	0
			3436	2175	584	655	22		
1	R5	440	Total	C	N	O	S	0	0
			3436	2175	584	655	22		
1	S1	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
1	S3	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
1	S5	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
1	T1	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
1	T3	429	Total	C	N	O	S	0	0
			3365	2134	572	637	22		
1	T5	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
1	U1	432	Total	C	N	O	S	0	0
			3385	2144	575	644	22		
1	U3	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
1	U5	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
1	V0	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	V2	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		
1	V4	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	W0	438	Total	C	N	O	S	0	0
			3423	2167	582	652	22		
1	W2	430	Total	C	N	O	S	0	0
			3371	2137	573	639	22		
1	W4	439	Total	C	N	O	S	0	0
			3429	2170	583	654	22		
1	W6	431	Total	C	N	O	S	0	0
			3379	2141	574	642	22		

- Molecule 2 is a protein called Tubulin beta-4B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A1	433	Total	C	N	O	S	0	0
			3400	2134	581	659	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	A3	433	Total	C	N	O	S	0	0
			3400	2134	581	659	26		
2	A5	433	Total	C	N	O	S	0	0
			3400	2134	581	659	26		
2	B0	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
2	B2	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	B4	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
2	C0	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
2	C2	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	C4	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
2	D0	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	D2	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	D4	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	D6	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	E0	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	E2	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	E4	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	E6	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	F0	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	F2	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	F4	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	F6	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	G1	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	G3	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
2	G5	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	H1	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	H3	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
2	H5	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	I1	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	I3	429	Total	C	N	O	S	0	0
			3368	2116	577	649	26		
2	I5	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	J0	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
2	J2	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	J4	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	J6	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	K1	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
2	K3	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
2	K5	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
2	L1	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	L3	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	L5	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	M1	431	Total	C	N	O	S	0	0
			3382	2124	579	653	26		
2	M3	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	M5	431	Total	C	N	O	S	0	0
			3382	2124	579	653	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	N1	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
2	N3	429	Total	C	N	O	S	0	0
			3368	2116	577	649	26		
2	N5	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
2	O1	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
2	O3	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
2	O5	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
2	P1	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	P3	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
2	P5	429	Total	C	N	O	S	0	0
			3368	2116	577	649	26		
2	Q0	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	Q2	429	Total	C	N	O	S	0	0
			3368	2116	577	649	26		
2	Q4	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
2	R0	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	R2	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
2	R4	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	R6	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
2	S0	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	S2	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	S4	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	S6	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	T0	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	T2	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	T4	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	T6	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	U0	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	U2	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
2	U4	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	U6	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
2	V1	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
2	V3	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	V5	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
2	W1	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	W3	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
2	W5	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

- Molecule 3 is a protein called Cilia- and flagella-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	X0	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
3	X1	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
3	X2	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		
3	X3	186	Total	C	N	O	S	0	0
			1549	998	270	274	7		

- Molecule 4 is a protein called Centrosomal protein of 41 kDa.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Y0	142	Total	C	N	O	S	0	0
			1151	740	187	219	5		
4	Y1	142	Total	C	N	O	S	0	0
			1151	740	187	219	5		
4	Y2	142	Total	C	N	O	S	0	0
			1151	740	187	219	5		

- Molecule 5 is a protein called Calcyphosin-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1A	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	1B	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	1C	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	1D	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	1E	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	1F	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	2A	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	2B	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	2C	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	2D	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	2E	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	2F	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	3C	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	3D	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	3E	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	3F	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	3G	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	3H	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	3J	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	4J	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	2H	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	2I	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	3I	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	4I	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	4H	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	2J	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	7A	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	7B	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	7C	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	7D	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	6A	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	6B	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	6C	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	6D	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	5A	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	5B	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	5C	207	Total 1693	C 1069	N 296	O 318	S 10	0	0
5	5D	207	Total 1693	C 1069	N 296	O 318	S 10	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	2G	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		
5	1G	207	Total	C	N	O	S	0	0
			1693	1069	296	318	10		

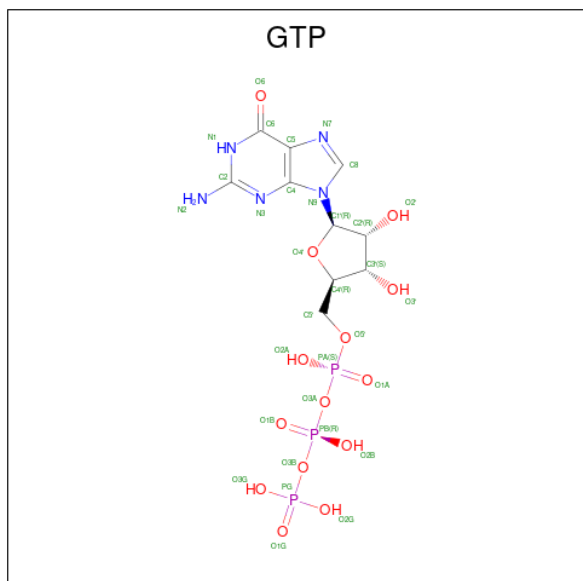
- Molecule 6 is a protein called Microtubule-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	9A	205	Total	C	N	O	S	0	0
			1773	1106	333	331	3		
6	9B	205	Total	C	N	O	S	0	0
			1773	1106	333	331	3		

- Molecule 7 is a protein called Enkurin domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	8A	68	Total	C	N	O	S	0	0
			549	344	100	103	2		
7	8C	68	Total	C	N	O	S	0	0
			549	344	100	103	2		
7	8B	68	Total	C	N	O	S	0	0
			549	344	100	103	2		

- Molecule 8 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
8	A0	1	Total 32	C 10	N 5	O 14	P 3	0
8	A2	1	Total 32	C 10	N 5	O 14	P 3	0
8	A4	1	Total 32	C 10	N 5	O 14	P 3	0
8	A6	1	Total 32	C 10	N 5	O 14	P 3	0
8	B1	1	Total 32	C 10	N 5	O 14	P 3	0
8	B3	1	Total 32	C 10	N 5	O 14	P 3	0
8	B5	1	Total 32	C 10	N 5	O 14	P 3	0
8	C1	1	Total 32	C 10	N 5	O 14	P 3	0
8	C3	1	Total 32	C 10	N 5	O 14	P 3	0
8	C5	1	Total 32	C 10	N 5	O 14	P 3	0
8	D1	1	Total 32	C 10	N 5	O 14	P 3	0
8	D3	1	Total 32	C 10	N 5	O 14	P 3	0
8	D5	1	Total 32	C 10	N 5	O 14	P 3	0
8	E1	1	Total 32	C 10	N 5	O 14	P 3	0
8	E3	1	Total 32	C 10	N 5	O 14	P 3	0
8	E5	1	Total 32	C 10	N 5	O 14	P 3	0
8	F1	1	Total 32	C 10	N 5	O 14	P 3	0
8	F3	1	Total 32	C 10	N 5	O 14	P 3	0
8	F5	1	Total 32	C 10	N 5	O 14	P 3	0
8	G0	1	Total 32	C 10	N 5	O 14	P 3	0
8	G2	1	Total 32	C 10	N 5	O 14	P 3	0
8	G4	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
8	H0	1	Total 32	C 10	N 5	O 14	P 3	0
8	H2	1	Total 32	C 10	N 5	O 14	P 3	0
8	H4	1	Total 32	C 10	N 5	O 14	P 3	0
8	I0	1	Total 32	C 10	N 5	O 14	P 3	0
8	I2	1	Total 32	C 10	N 5	O 14	P 3	0
8	I4	1	Total 32	C 10	N 5	O 14	P 3	0
8	I6	1	Total 32	C 10	N 5	O 14	P 3	0
8	J1	1	Total 32	C 10	N 5	O 14	P 3	0
8	J3	1	Total 32	C 10	N 5	O 14	P 3	0
8	J5	1	Total 32	C 10	N 5	O 14	P 3	0
8	K0	1	Total 32	C 10	N 5	O 14	P 3	0
8	K2	1	Total 32	C 10	N 5	O 14	P 3	0
8	K4	1	Total 32	C 10	N 5	O 14	P 3	0
8	L0	1	Total 32	C 10	N 5	O 14	P 3	0
8	L2	1	Total 32	C 10	N 5	O 14	P 3	0
8	L4	1	Total 32	C 10	N 5	O 14	P 3	0
8	L6	1	Total 32	C 10	N 5	O 14	P 3	0
8	M0	1	Total 32	C 10	N 5	O 14	P 3	0
8	M2	1	Total 32	C 10	N 5	O 14	P 3	0
8	M4	1	Total 32	C 10	N 5	O 14	P 3	0
8	M6	1	Total 32	C 10	N 5	O 14	P 3	0

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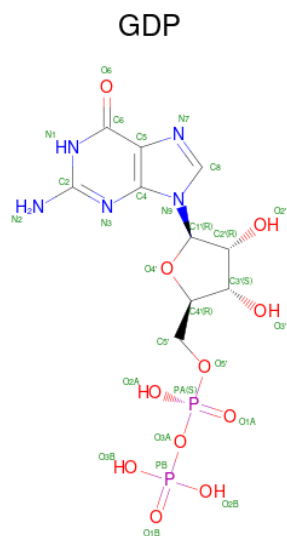
Mol	Chain	Residues	Atoms					AltConf
8	N0	1	Total 32	C 10	N 5	O 14	P 3	0
8	N2	1	Total 32	C 10	N 5	O 14	P 3	0
8	N4	1	Total 32	C 10	N 5	O 14	P 3	0
8	N6	1	Total 32	C 10	N 5	O 14	P 3	0
8	O0	1	Total 32	C 10	N 5	O 14	P 3	0
8	O2	1	Total 32	C 10	N 5	O 14	P 3	0
8	O4	1	Total 32	C 10	N 5	O 14	P 3	0
8	O6	1	Total 32	C 10	N 5	O 14	P 3	0
8	P0	1	Total 32	C 10	N 5	O 14	P 3	0
8	P1	1	Total 32	C 10	N 5	O 14	P 3	0
8	P4	1	Total 32	C 10	N 5	O 14	P 3	0
8	P6	1	Total 32	C 10	N 5	O 14	P 3	0
8	Q1	1	Total 32	C 10	N 5	O 14	P 3	0
8	Q3	1	Total 32	C 10	N 5	O 14	P 3	0
8	Q5	1	Total 32	C 10	N 5	O 14	P 3	0
8	R1	1	Total 32	C 10	N 5	O 14	P 3	0
8	R3	1	Total 32	C 10	N 5	O 14	P 3	0
8	R5	1	Total 32	C 10	N 5	O 14	P 3	0
8	S1	1	Total 32	C 10	N 5	O 14	P 3	0
8	S3	1	Total 32	C 10	N 5	O 14	P 3	0
8	S5	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
8	T1	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	T3	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	T5	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	U1	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	U3	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	U5	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	V0	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	V2	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	V4	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	W0	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	W2	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	W4	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	W6	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 9 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
9	A1	1	Total 28	C 10	N 5	O 11	P 2	0
9	A3	1	Total 28	C 10	N 5	O 11	P 2	0
9	A5	1	Total 28	C 10	N 5	O 11	P 2	0
9	B0	1	Total 28	C 10	N 5	O 11	P 2	0
9	B2	1	Total 28	C 10	N 5	O 11	P 2	0
9	B4	1	Total 28	C 10	N 5	O 11	P 2	0
9	C0	1	Total 28	C 10	N 5	O 11	P 2	0
9	C2	1	Total 28	C 10	N 5	O 11	P 2	0
9	C4	1	Total 28	C 10	N 5	O 11	P 2	0
9	D0	1	Total 28	C 10	N 5	O 11	P 2	0
9	D2	1	Total 28	C 10	N 5	O 11	P 2	0
9	D4	1	Total 28	C 10	N 5	O 11	P 2	0
9	D6	1	Total 28	C 10	N 5	O 11	P 2	0
9	E0	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
9	E2	1	Total 28	C 10	N 5	O 11	P 2	0
9	E4	1	Total 28	C 10	N 5	O 11	P 2	0
9	E6	1	Total 28	C 10	N 5	O 11	P 2	0
9	F0	1	Total 28	C 10	N 5	O 11	P 2	0
9	F2	1	Total 28	C 10	N 5	O 11	P 2	0
9	F4	1	Total 28	C 10	N 5	O 11	P 2	0
9	F6	1	Total 28	C 10	N 5	O 11	P 2	0
9	G1	1	Total 28	C 10	N 5	O 11	P 2	0
9	G3	1	Total 28	C 10	N 5	O 11	P 2	0
9	G5	1	Total 28	C 10	N 5	O 11	P 2	0
9	H1	1	Total 28	C 10	N 5	O 11	P 2	0
9	H3	1	Total 28	C 10	N 5	O 11	P 2	0
9	H5	1	Total 28	C 10	N 5	O 11	P 2	0
9	I1	1	Total 28	C 10	N 5	O 11	P 2	0
9	I3	1	Total 28	C 10	N 5	O 11	P 2	0
9	I5	1	Total 28	C 10	N 5	O 11	P 2	0
9	J0	1	Total 28	C 10	N 5	O 11	P 2	0
9	J2	1	Total 28	C 10	N 5	O 11	P 2	0
9	J4	1	Total 28	C 10	N 5	O 11	P 2	0
9	J6	1	Total 28	C 10	N 5	O 11	P 2	0
9	K1	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
9	K3	1	Total 28	C 10	N 5	O 11	P 2	0
9	K5	1	Total 28	C 10	N 5	O 11	P 2	0
9	L1	1	Total 28	C 10	N 5	O 11	P 2	0
9	L3	1	Total 28	C 10	N 5	O 11	P 2	0
9	L5	1	Total 28	C 10	N 5	O 11	P 2	0
9	M1	1	Total 28	C 10	N 5	O 11	P 2	0
9	M3	1	Total 28	C 10	N 5	O 11	P 2	0
9	M5	1	Total 28	C 10	N 5	O 11	P 2	0
9	N1	1	Total 28	C 10	N 5	O 11	P 2	0
9	N3	1	Total 28	C 10	N 5	O 11	P 2	0
9	N5	1	Total 28	C 10	N 5	O 11	P 2	0
9	O1	1	Total 28	C 10	N 5	O 11	P 2	0
9	O3	1	Total 28	C 10	N 5	O 11	P 2	0
9	O5	1	Total 28	C 10	N 5	O 11	P 2	0
9	P1	1	Total 28	C 10	N 5	O 11	P 2	0
9	P3	1	Total 28	C 10	N 5	O 11	P 2	0
9	P5	1	Total 28	C 10	N 5	O 11	P 2	0
9	Q0	1	Total 28	C 10	N 5	O 11	P 2	0
9	Q2	1	Total 28	C 10	N 5	O 11	P 2	0
9	Q4	1	Total 28	C 10	N 5	O 11	P 2	0
9	R0	1	Total 28	C 10	N 5	O 11	P 2	0

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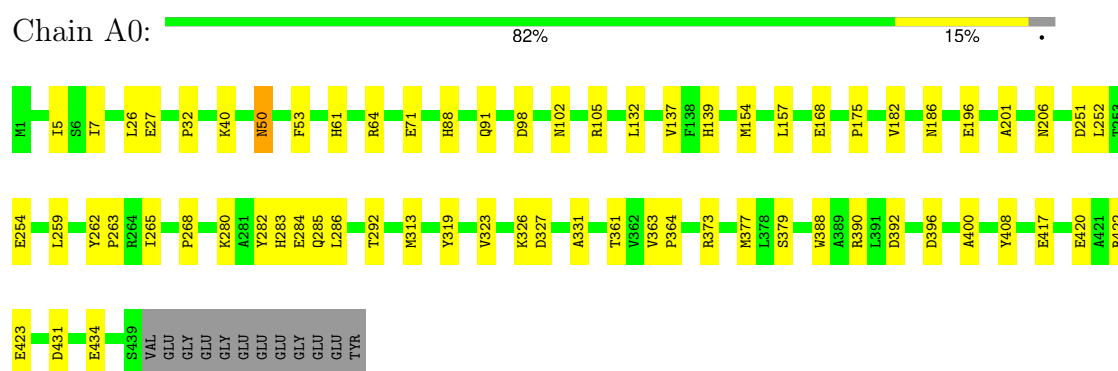
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Mol	Chain	Residues	Atoms					AltConf
9	R2	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	R4	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	R6	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	S0	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	S2	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	S4	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	S6	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	T0	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	T2	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	T4	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	T6	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	U0	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	U2	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	U4	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	U6	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	V1	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	V3	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	V5	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	W1	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	W3	1	Total	C	N	O	P	0
			28	10	5	11	2	
9	W5	1	Total	C	N	O	P	0
			28	10	5	11	2	

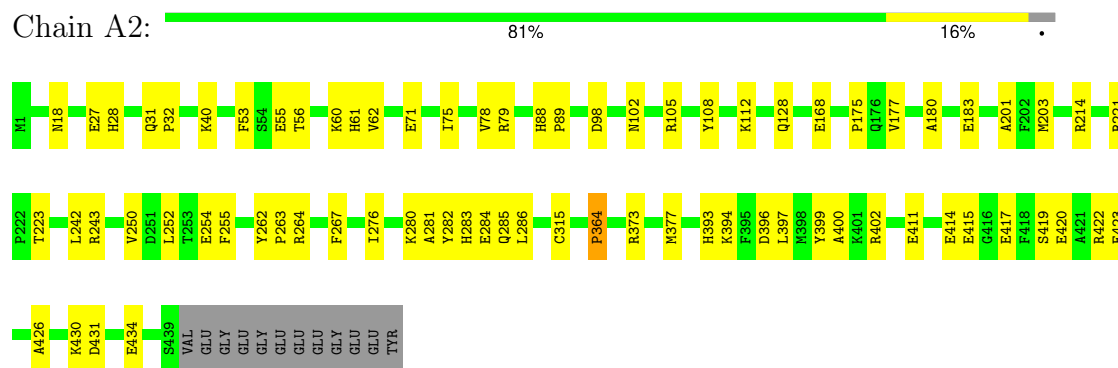
3 Residue-property plots

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

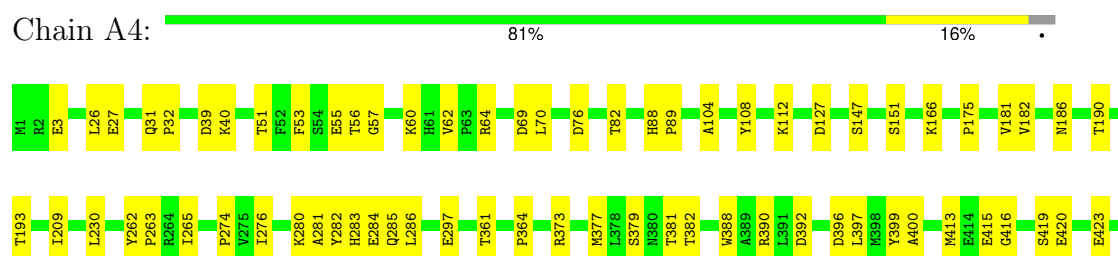
- Molecule 1: Tubulin alpha-1A chain

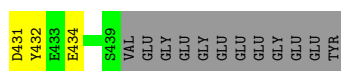


- Molecule 1: Tubulin alpha-1A chain



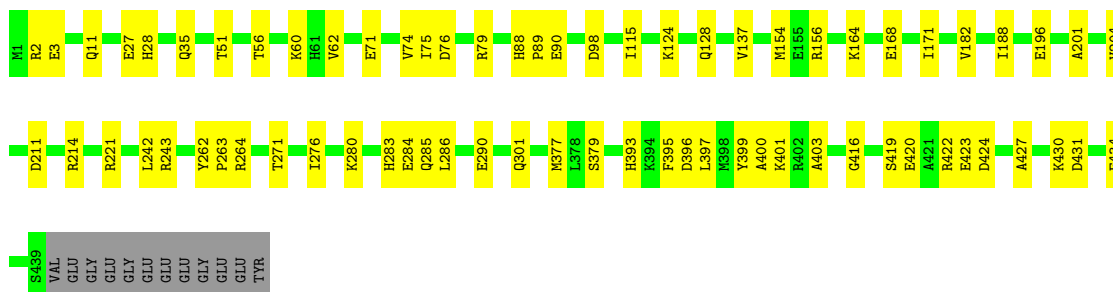
- Molecule 1: Tubulin alpha-1A chain





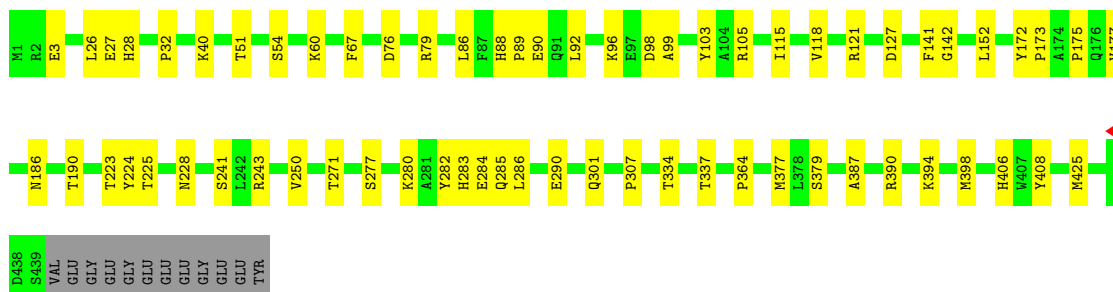
- Molecule 1: Tubulin alpha-1A chain

Chain A6: 82% 16%



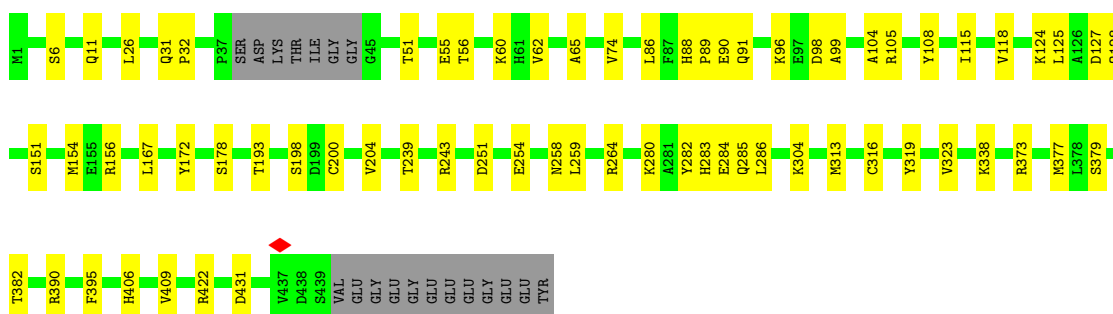
- Molecule 1: Tubulin alpha-1A chain

Chain B1: 83% 14%



- Molecule 1: Tubulin alpha-1A chain

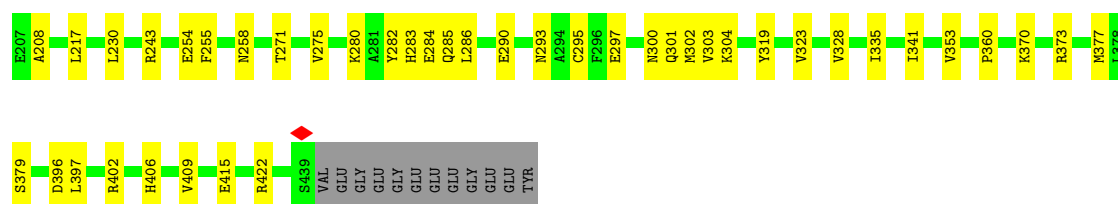
Chain B3: 81% 15%



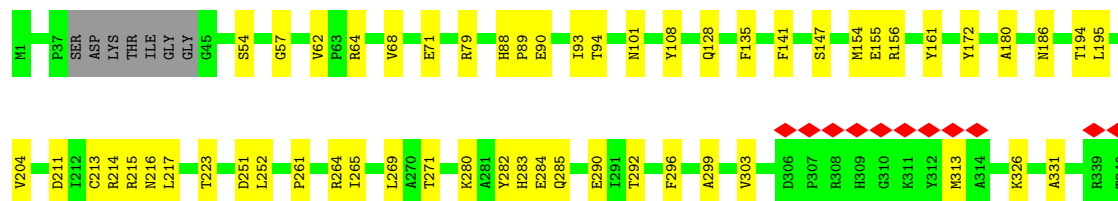
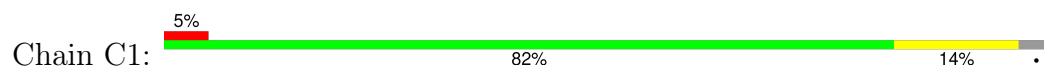
- Molecule 1: Tubulin alpha-1A chain

Chain B5: 81% 17%

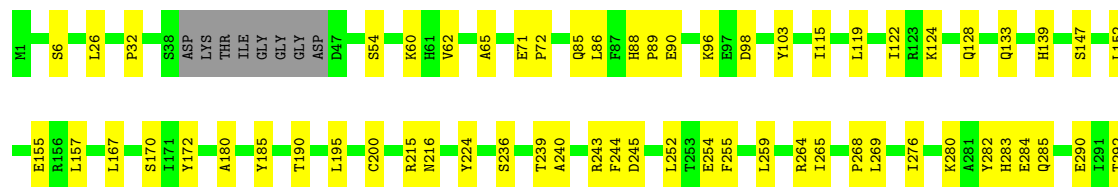
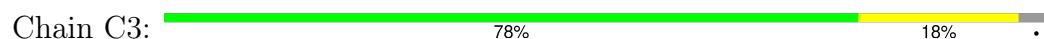




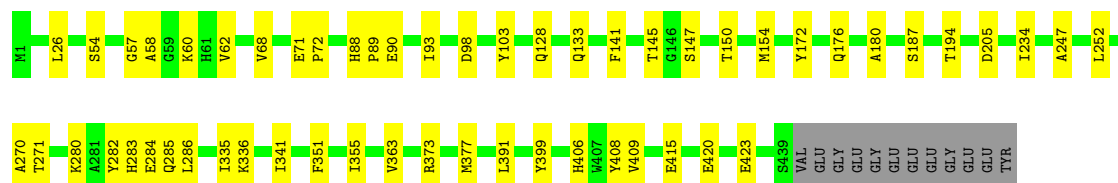
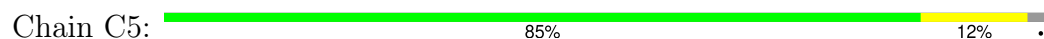
- Molecule 1: Tubulin alpha-1A chain



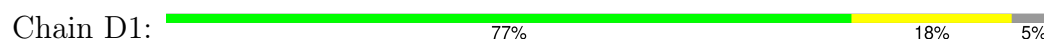
- Molecule 1: Tubulin alpha-1A chain

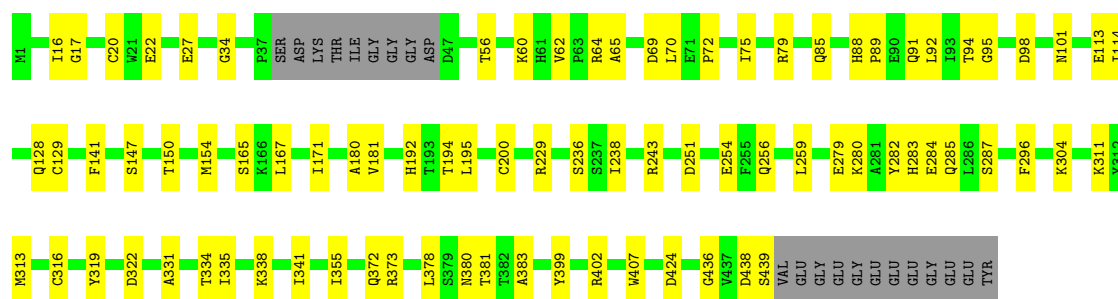


- Molecule 1: Tubulin alpha-1A chain



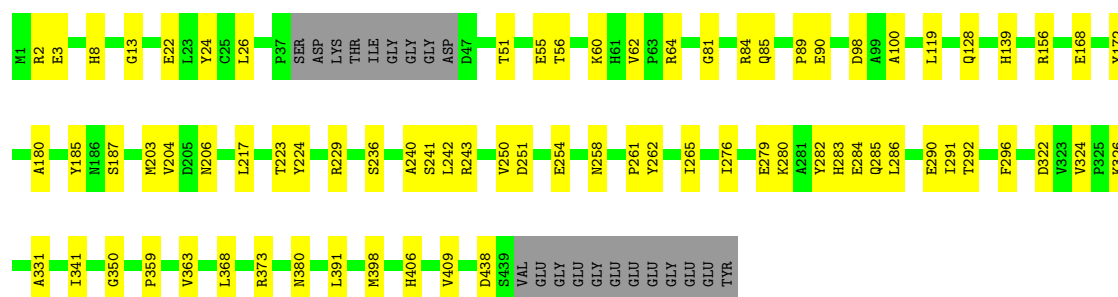
- Molecule 1: Tubulin alpha-1A chain





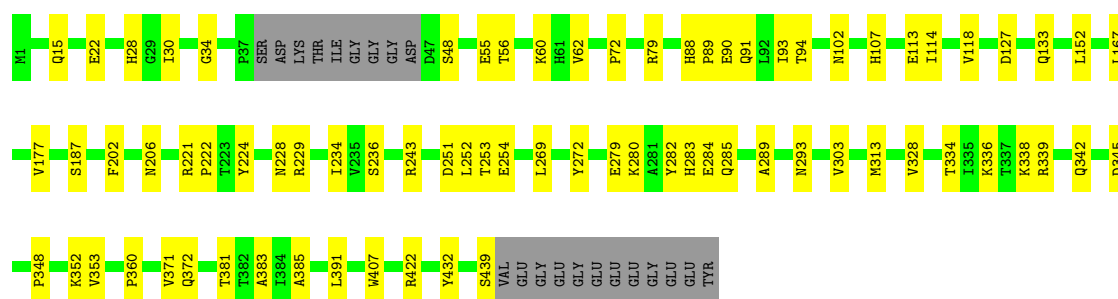
- Molecule 1: Tubulin alpha-1A chain

Chain D3: 78% 17% 5%



- Molecule 1: Tubulin alpha-1A chain

Chain D5: 78% 17% 5%



- Molecule 1: Tubulin alpha-1A chain

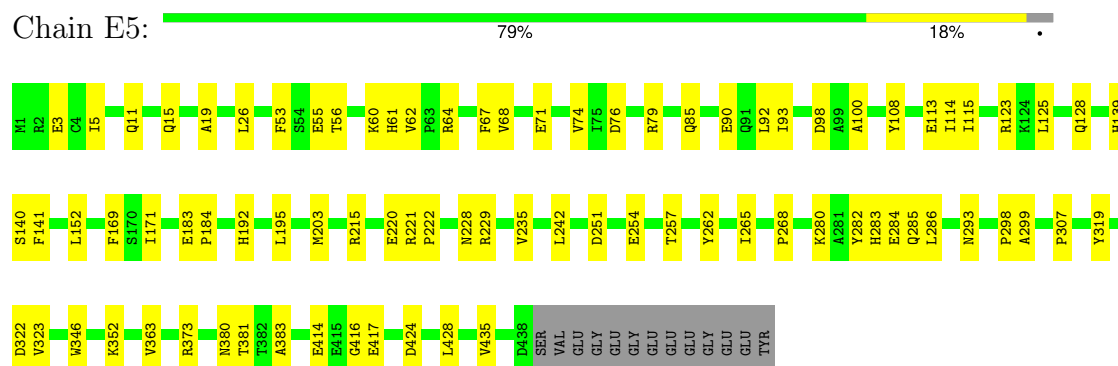
Chain E1: 77% 20% 3%



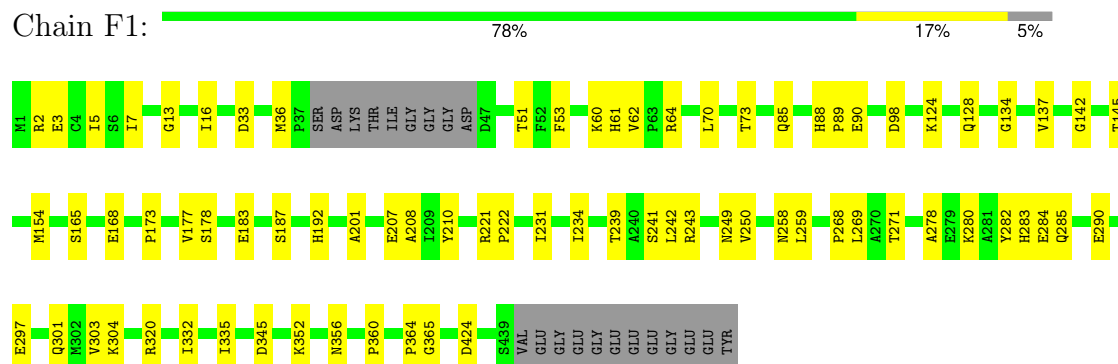
- Molecule 1: Tubulin alpha-1A chain



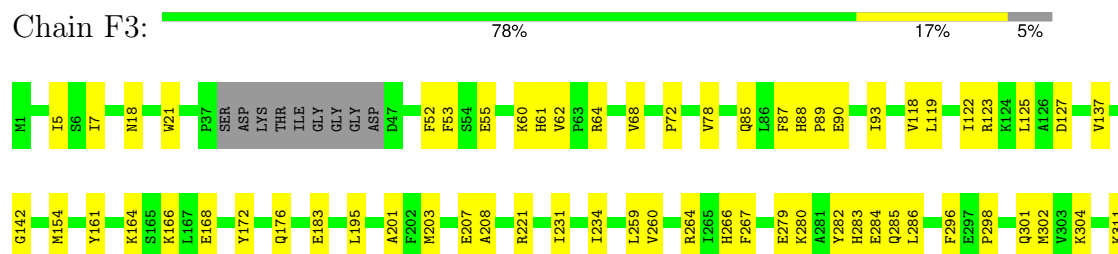
- Molecule 1: Tubulin alpha-1A chain

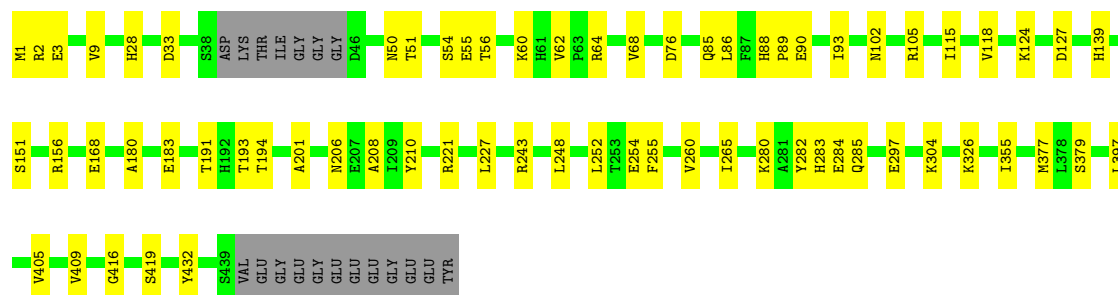


- Molecule 1: Tubulin alpha-1A chain



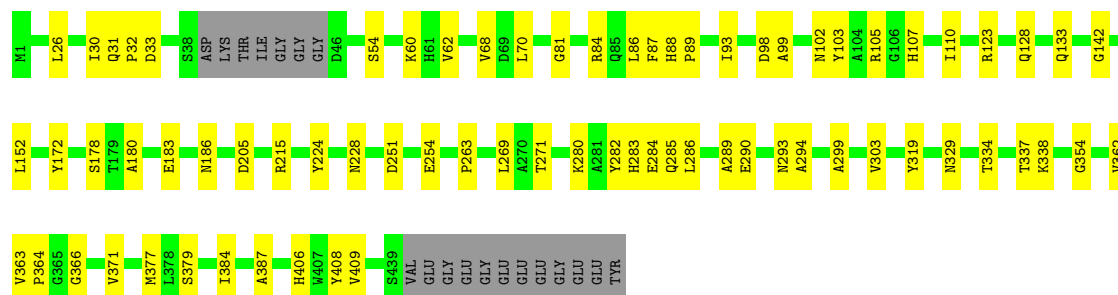
- Molecule 1: Tubulin alpha-1A chain





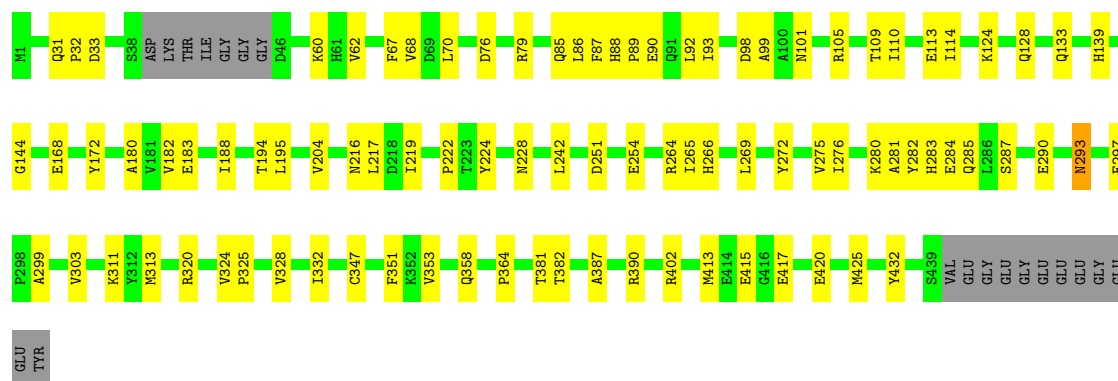
• Molecule 1: Tubulin alpha-1A chain

Chain H0: 80% 16%



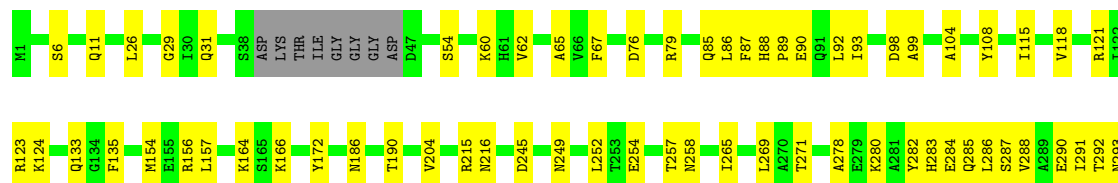
• Molecule 1: Tubulin alpha-1A chain

Chain H2: 76% 20%



• Molecule 1: Tubulin alpha-1A chain

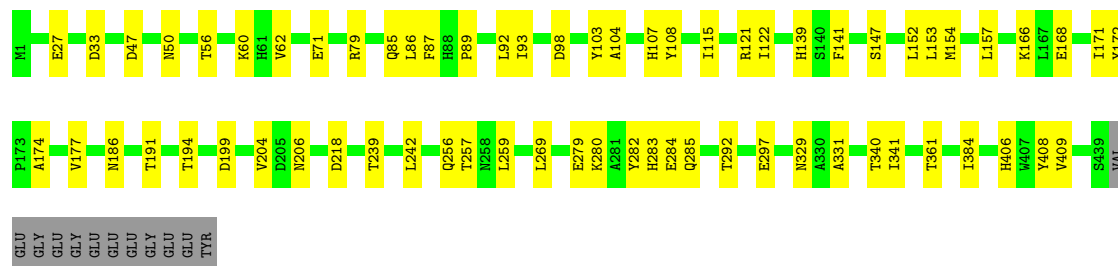
Chain H4: 77% 18%





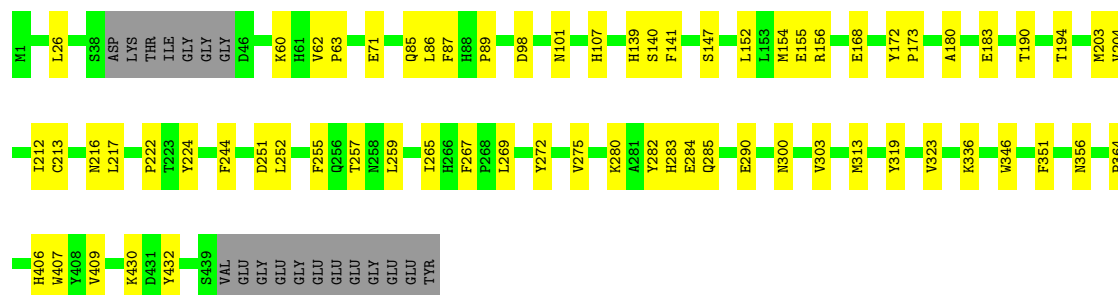
- Molecule 1: Tubulin alpha-1A chain

Chain I0: 83% 15%



- Molecule 1: Tubulin alpha-1A chain

Chain I2: 81% 15%



- Molecule 1: Tubulin alpha-1A chain

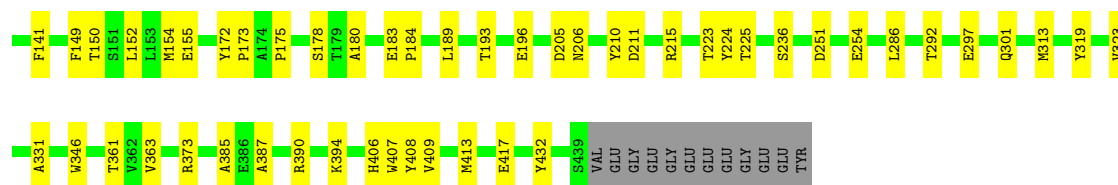
Chain I4: 84% 14%



- Molecule 1: Tubulin alpha-1A chain

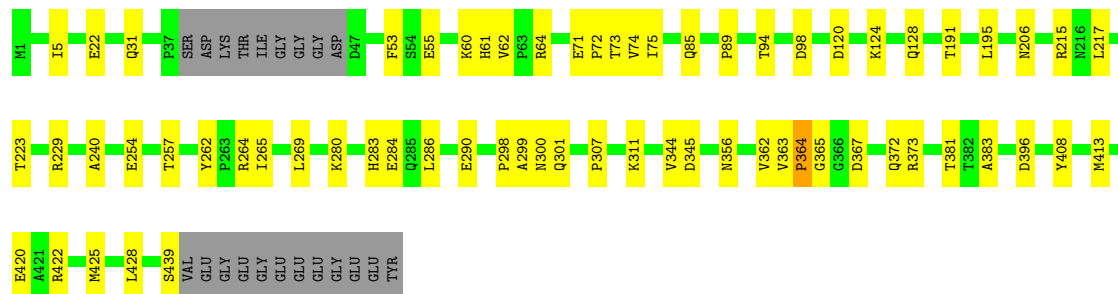
Chain I6: 78% 18%





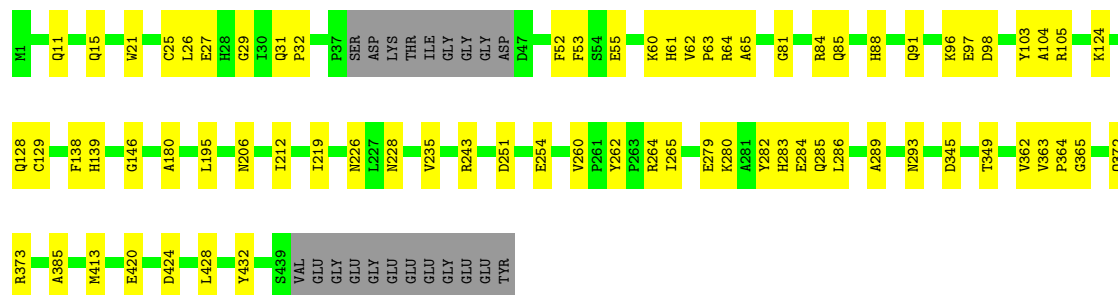
- Molecule 1: Tubulin alpha-1A chain

Chain J1: 81% 14% 5%



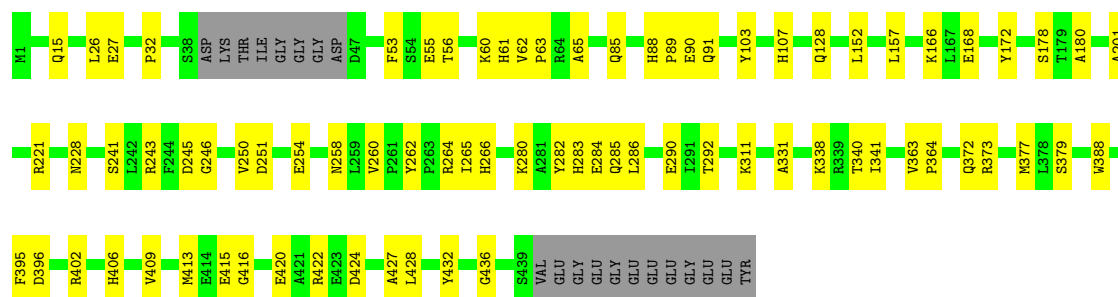
- Molecule 1: Tubulin alpha-1A chain

Chain J3: 79% 16% 5%



- Molecule 1: Tubulin alpha-1A chain

Chain J5: 78% 17% 5%



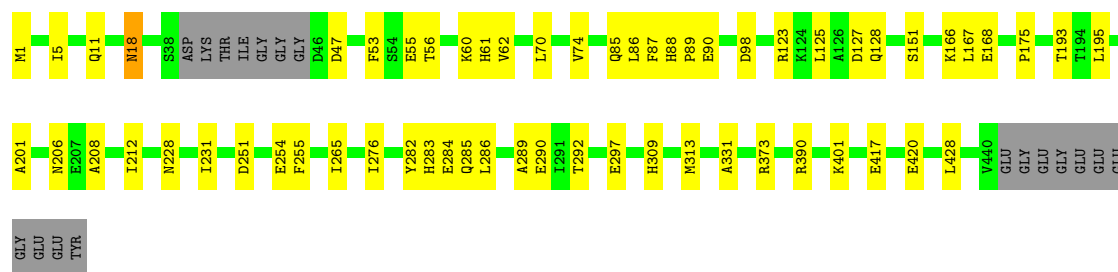
- Molecule 1: Tubulin alpha-1A chain

Chain K0: 84% 12% 4%



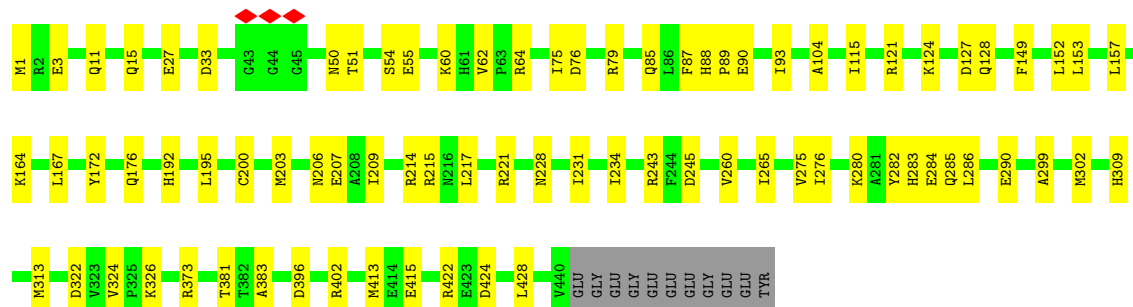
- Molecule 1: Tubulin alpha-1A chain

Chain K2: 83% 13%



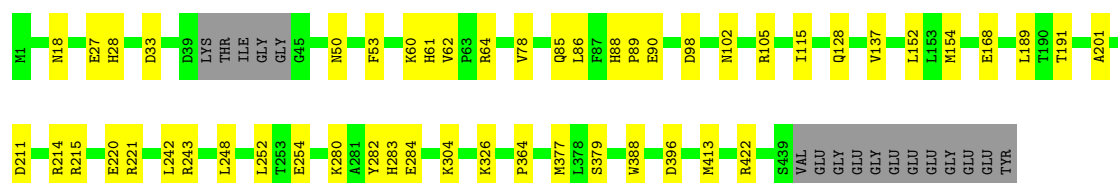
- Molecule 1: Tubulin alpha-1A chain

Chain K4: 80% 18%



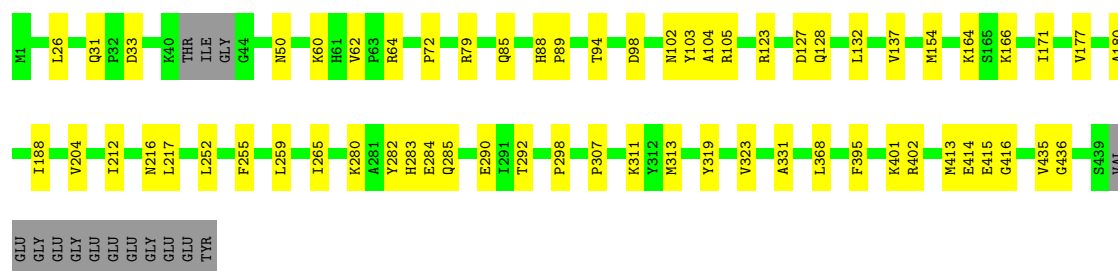
- Molecule 1: Tubulin alpha-1A chain

Chain L0: 85% 11%



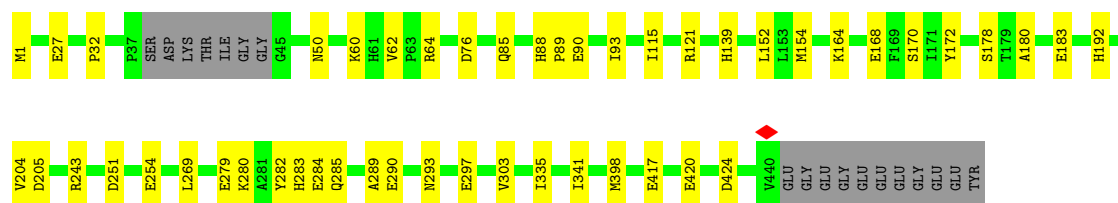
- Molecule 1: Tubulin alpha-1A chain

Chain L2: 83% 14%



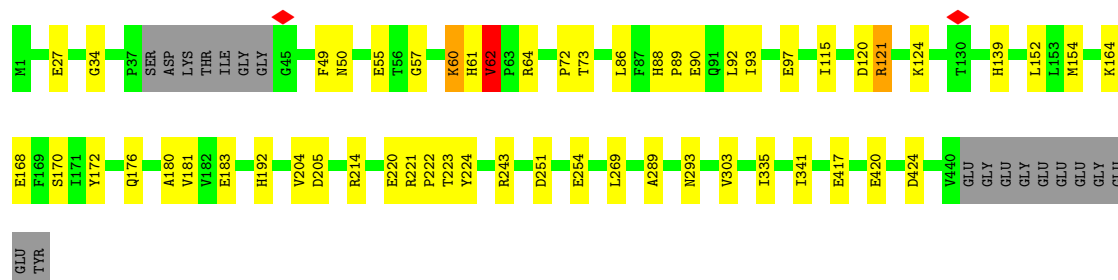
- Molecule 1: Tubulin alpha-1A chain

Chain L4: 85% 11% .



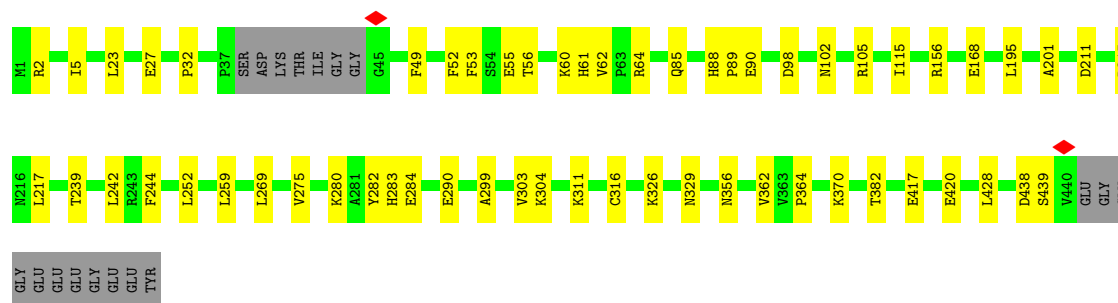
- Molecule 1: Tubulin alpha-1A chain

Chain L6: 84% 12% .



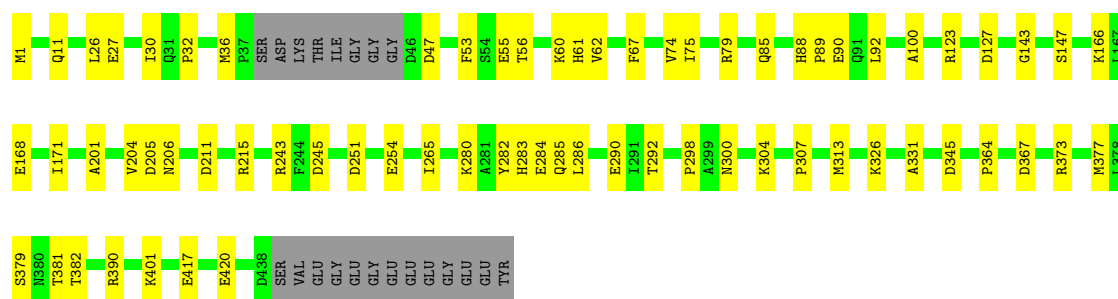
- Molecule 1: Tubulin alpha-1A chain

Chain M0: 83% 13% .



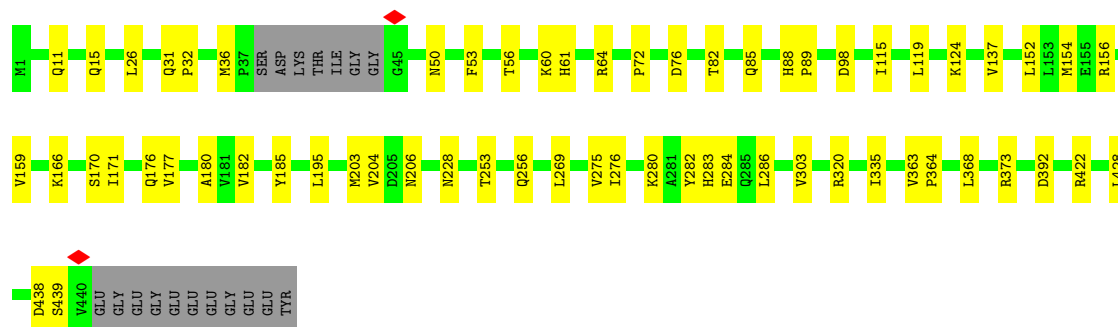
- Molecule 1: Tubulin alpha-1A chain

Chain M2: 80% 15% 5%



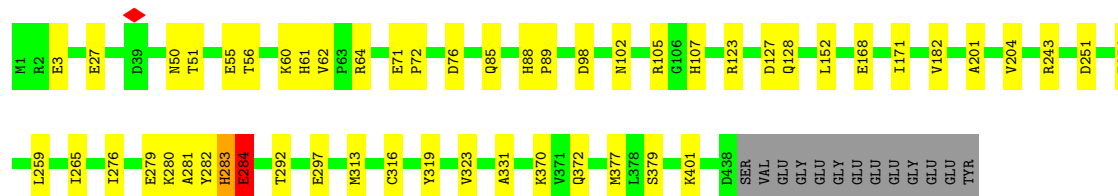
- Molecule 1: Tubulin alpha-1A chain

Chain M4: 82% 14%



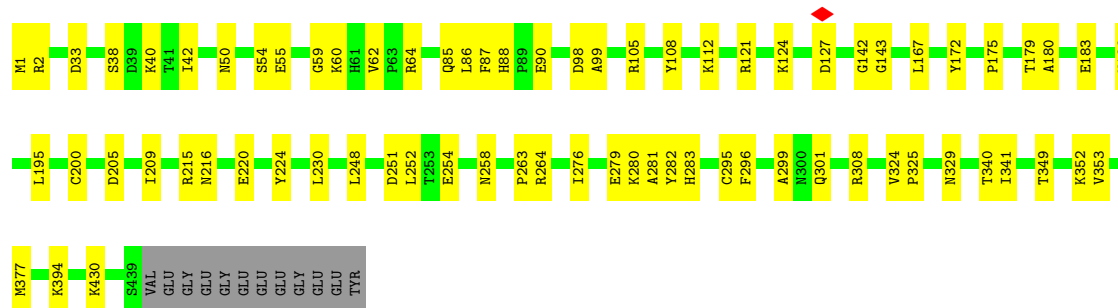
- Molecule 1: Tubulin alpha-1A chain

Chain M6: 85% 11%



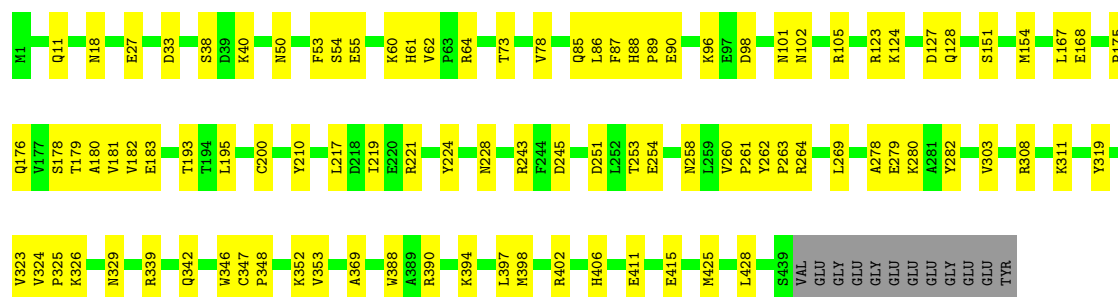
- Molecule 1: Tubulin alpha-1A chain

Chain N0: 81% 16%



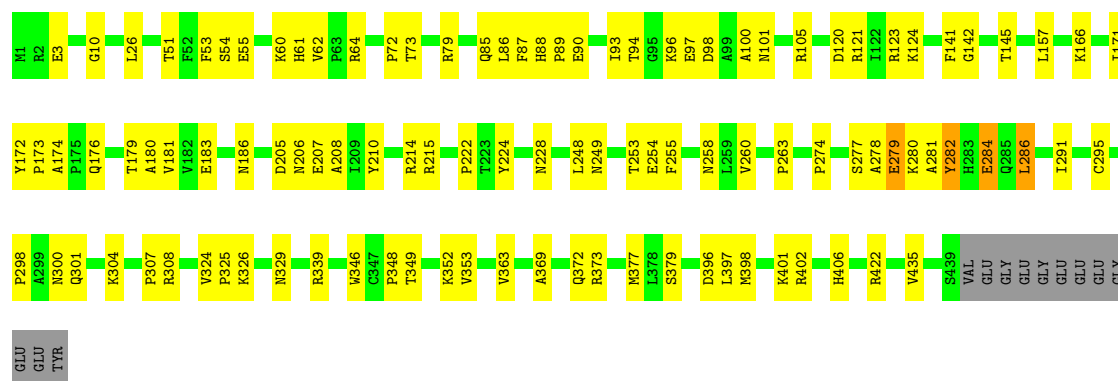
- Molecule 1: Tubulin alpha-1A chain

Chain N2:  76% 21% .



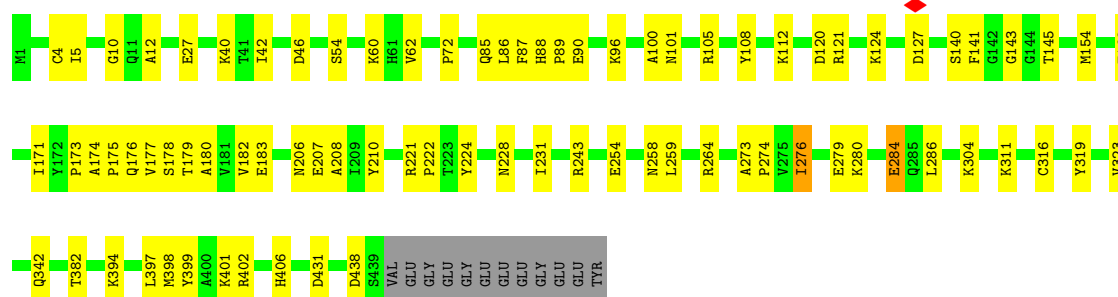
- Molecule 1: Tubulin alpha-1A chain

Chain N4:  74% 23% . .



- Molecule 1: Tubulin alpha-1A chain

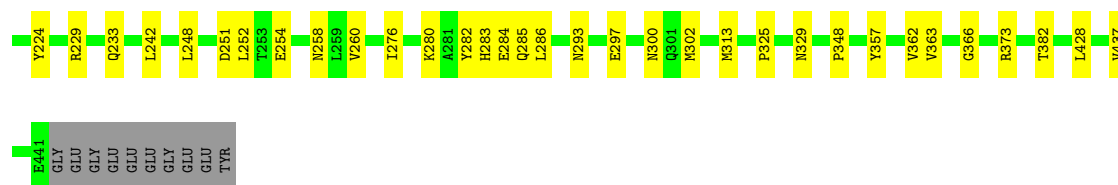
Chain N6:  79% 18% .



- Molecule 1: Tubulin alpha-1A chain

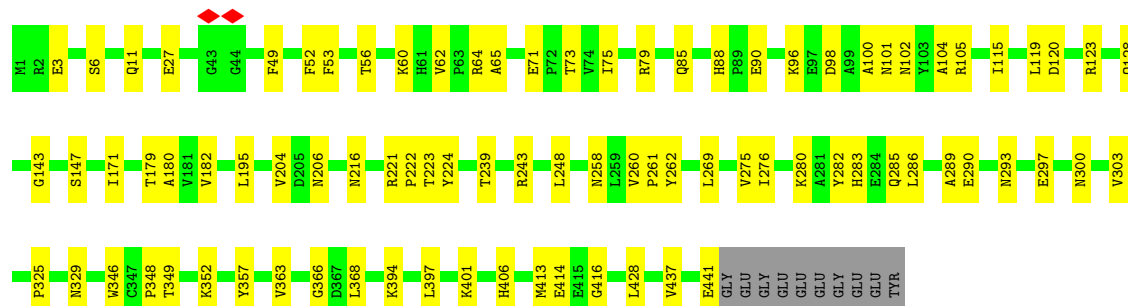
Chain O0:  83% 15% .





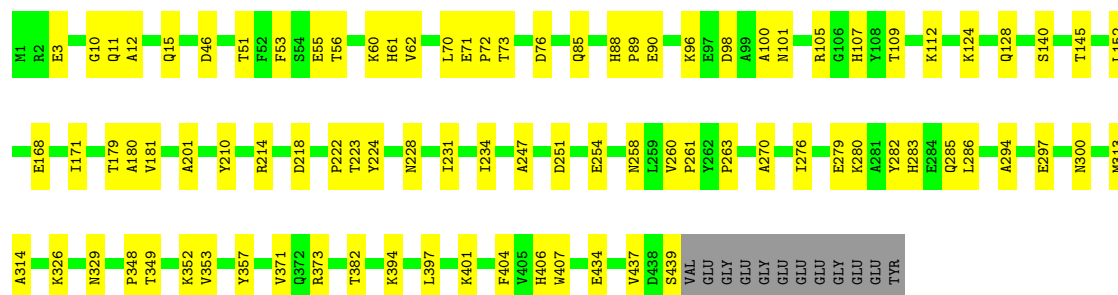
- Molecule 1: Tubulin alpha-1A chain

Chain O2: 79% 19%



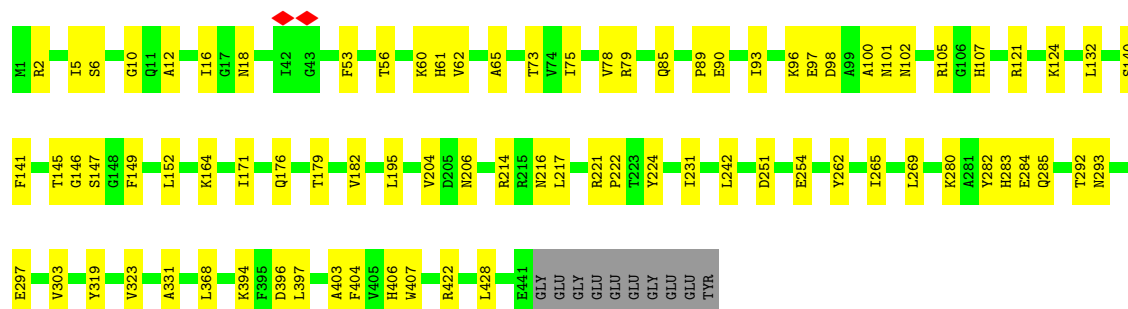
- Molecule 1: Tubulin alpha-1A chain

Chain O4: 78% 20%



- Molecule 1: Tubulin alpha-1A chain

Chain O6: 80% 18%



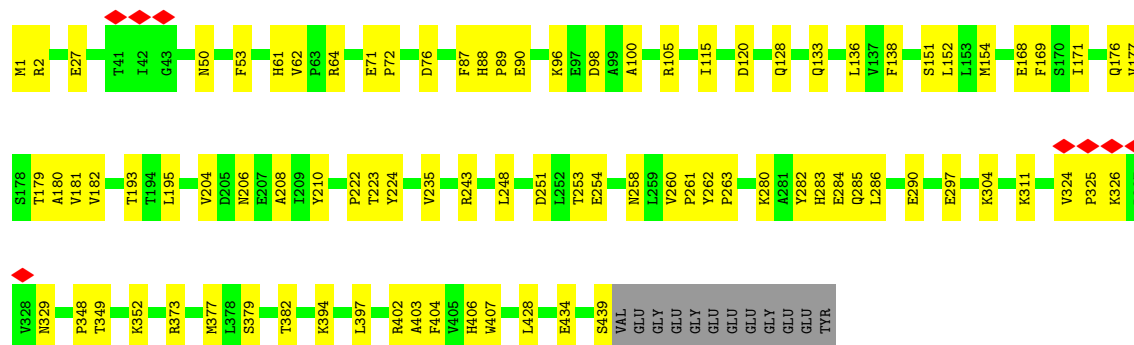
- Molecule 1: Tubulin alpha-1A chain

Chain P0: 86% 12%



- Molecule 1: Tubulin alpha-1A chain

Chain P2: 78% 20%



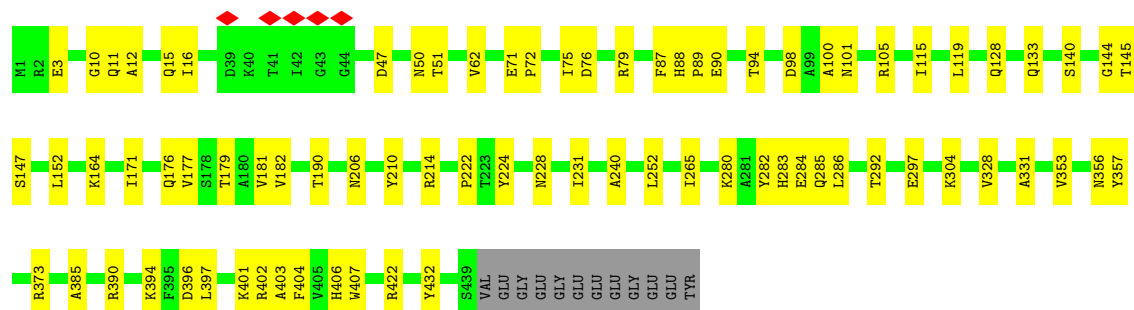
- Molecule 1: Tubulin alpha-1A chain

Chain P4: 77% 21%



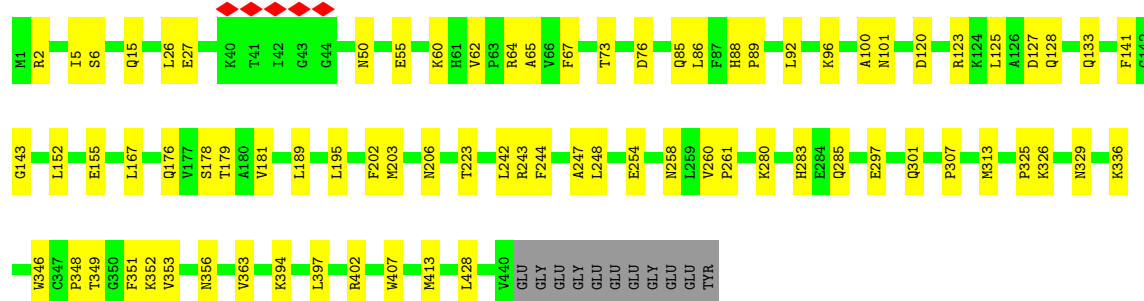
- Molecule 1: Tubulin alpha-1A chain

Chain P6: 80% 18%



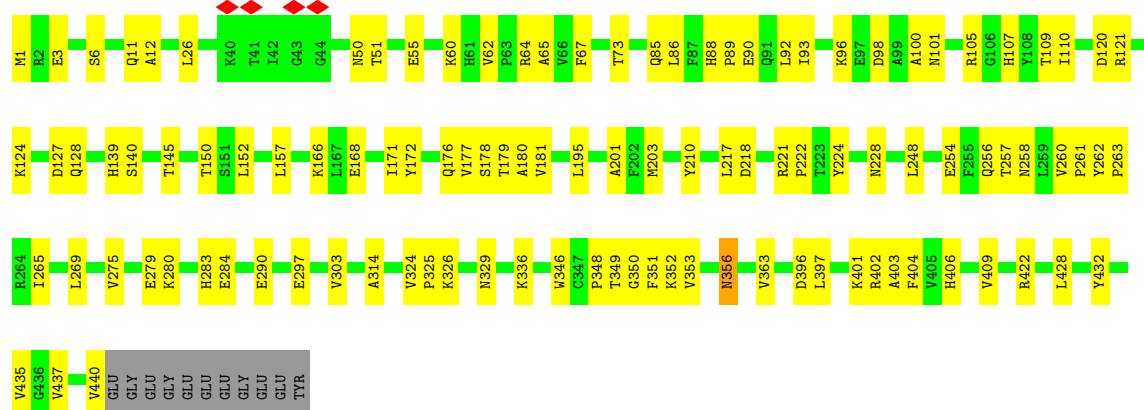
- Molecule 1: Tubulin alpha-1A chain

Chain Q1:  80% 17%



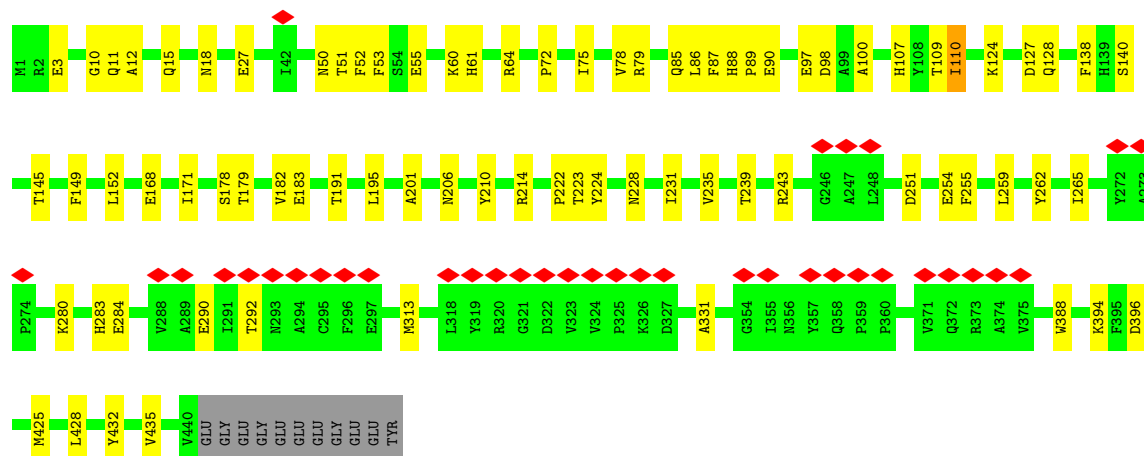
• Molecule 1: Tubulin alpha-1A chain

Chain Q3:  73% 24%

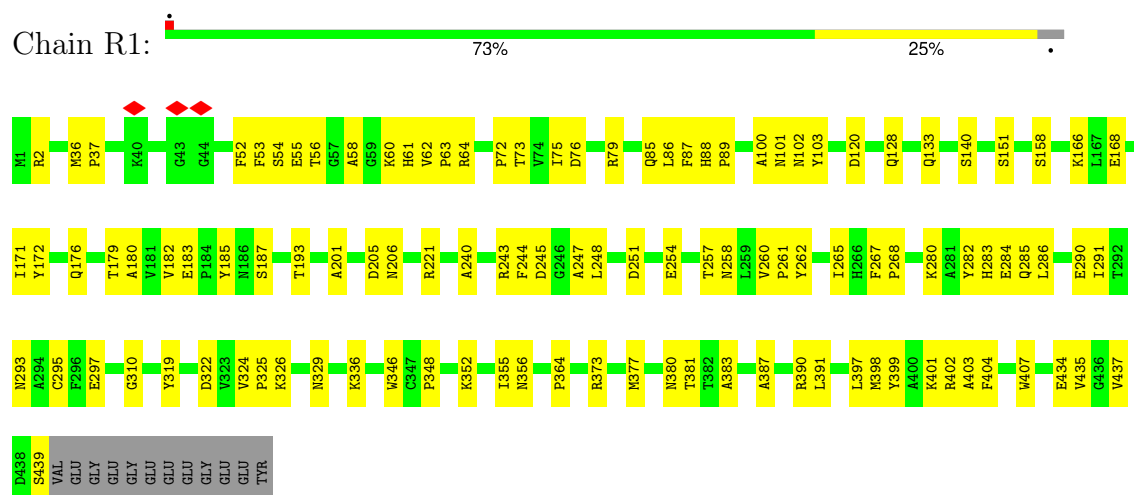


• Molecule 1: Tubulin alpha-1A chain

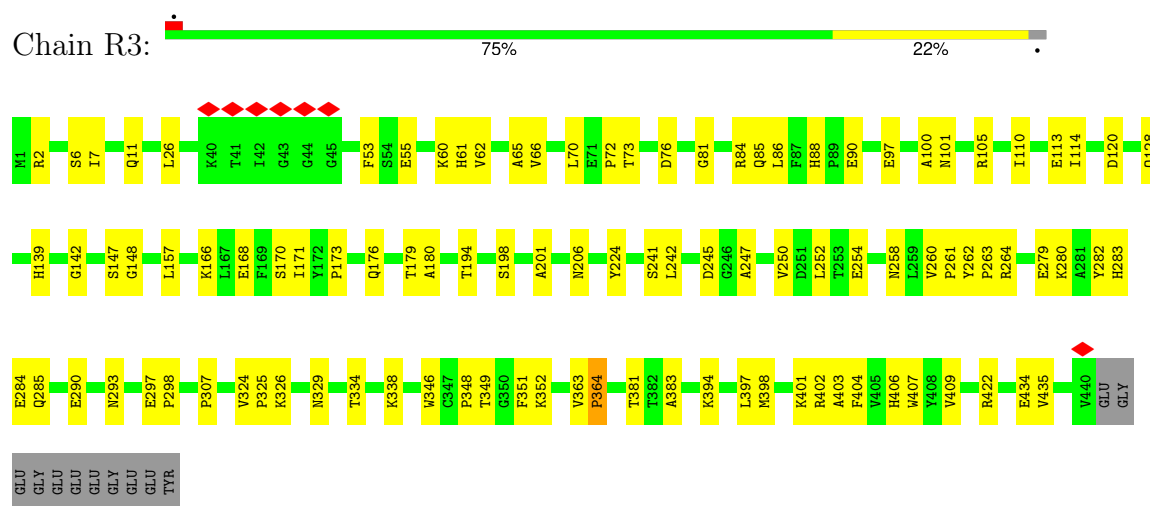
Chain Q5:  8% 79% 18%



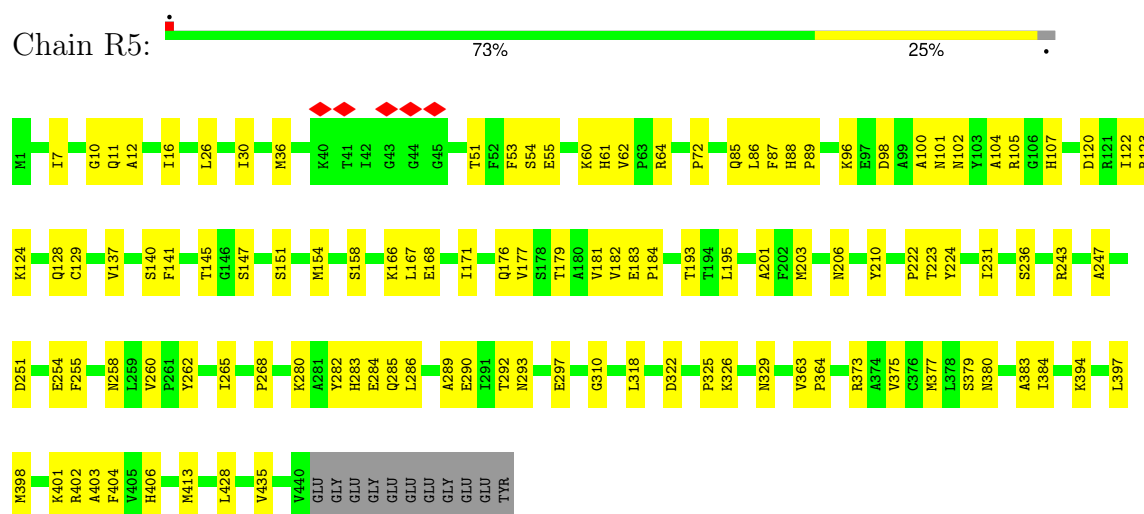
• Molecule 1: Tubulin alpha-1A chain



- Molecule 1: Tubulin alpha-1A chain

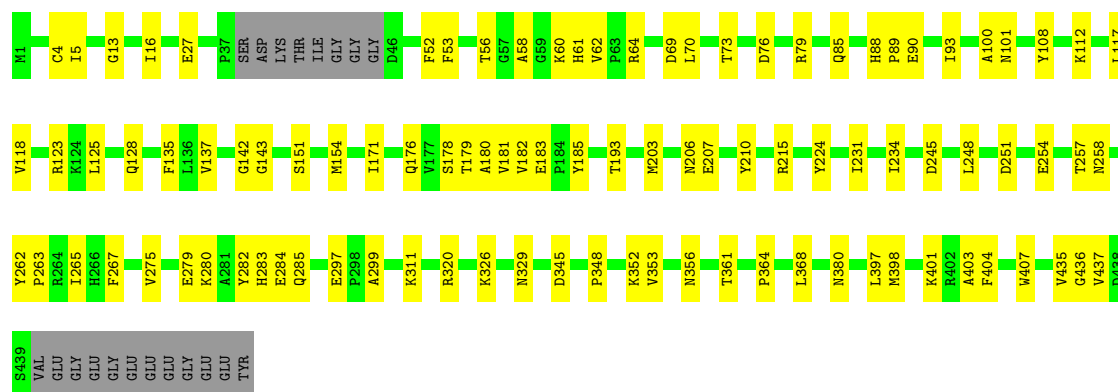


- Molecule 1: Tubulin alpha-1A chain



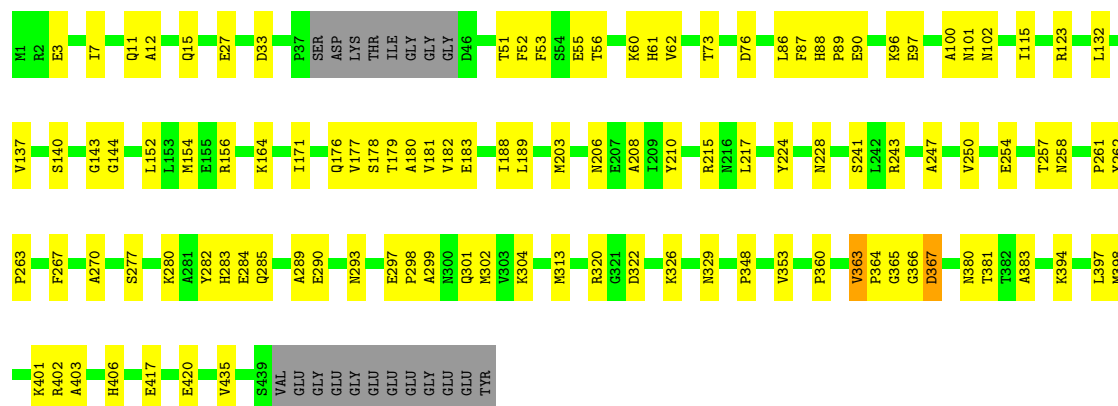
- Molecule 1: Tubulin alpha-1A chain

Chain S1:  74% 22%



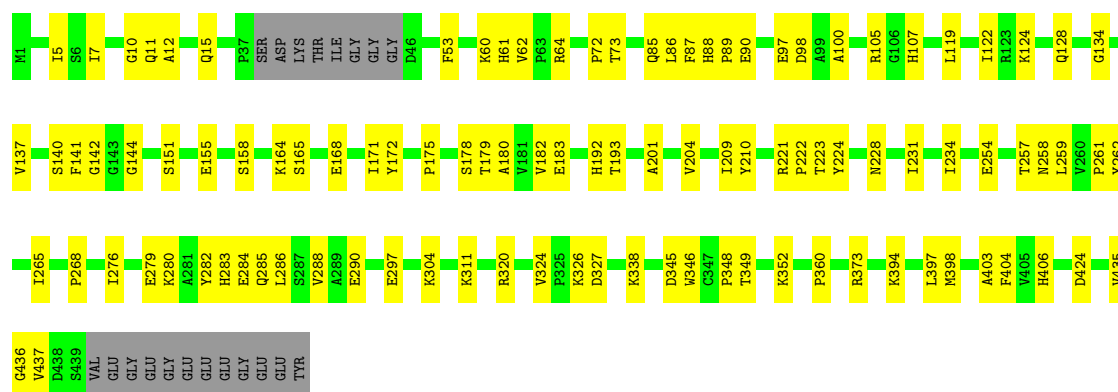
- Molecule 1: Tubulin alpha-1A chain

Chain S3:  71% 24%



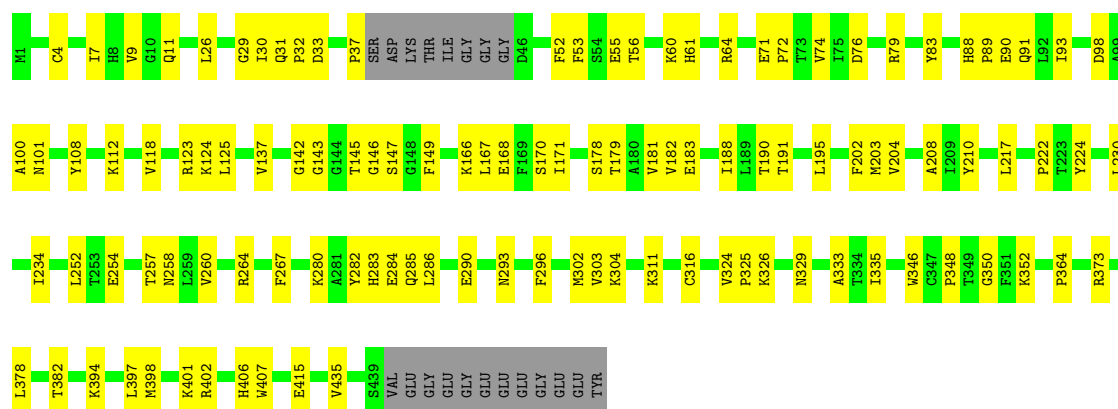
- Molecule 1: Tubulin alpha-1A chain

Chain S5:  73% 23%



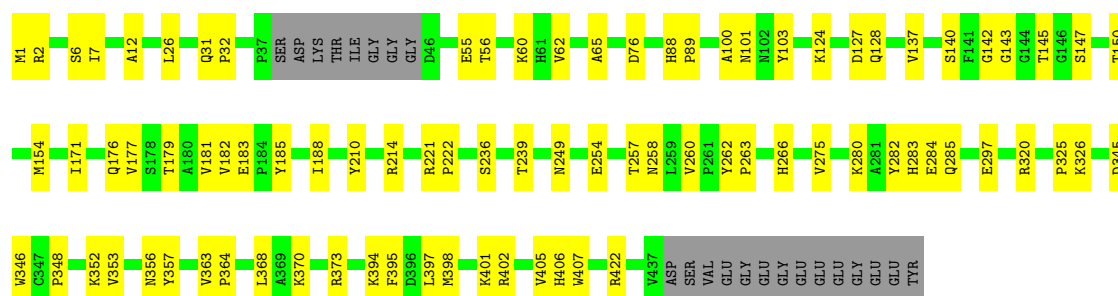
- Molecule 1: Tubulin alpha-1A chain

Chain T1:  71% 25%



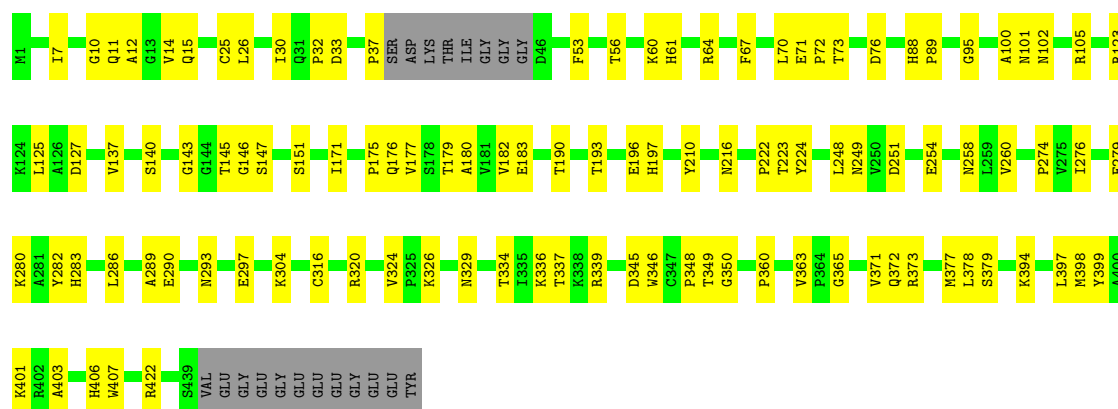
• Molecule 1: Tubulin alpha-1A chain

Chain T3: 76% 19% 5%



• Molecule 1: Tubulin alpha-1A chain

Chain T5: 72% 24% 4%

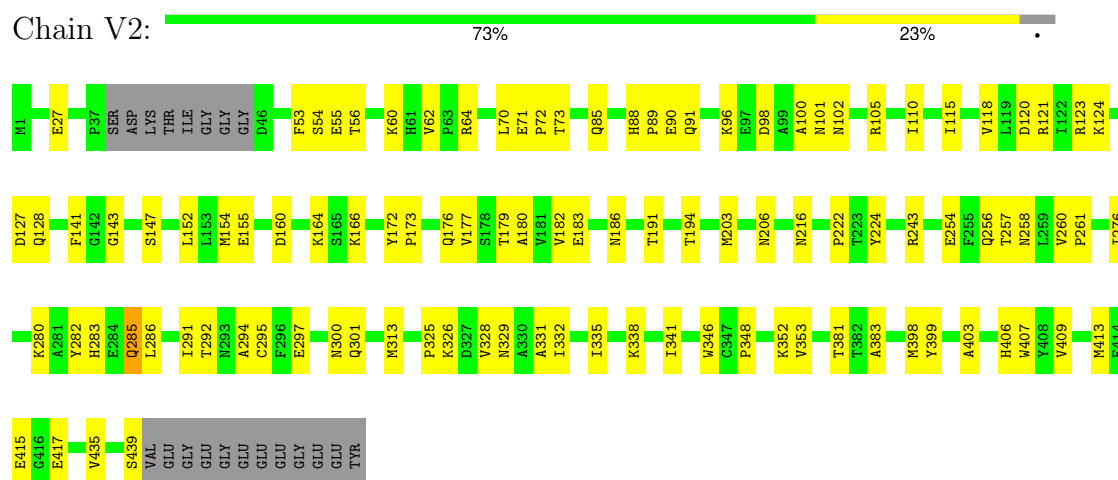


• Molecule 1: Tubulin alpha-1A chain

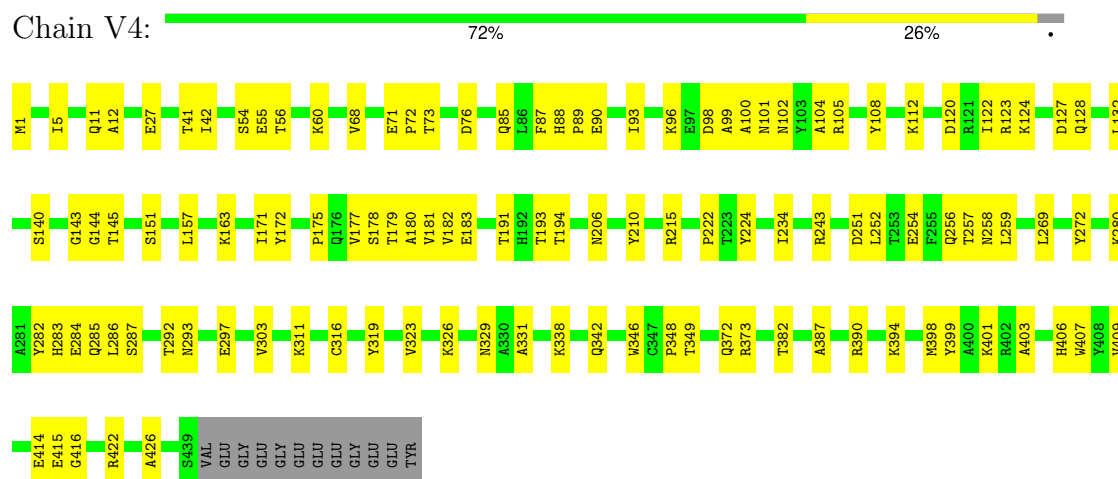
Chain U1: 80% 16% 4%



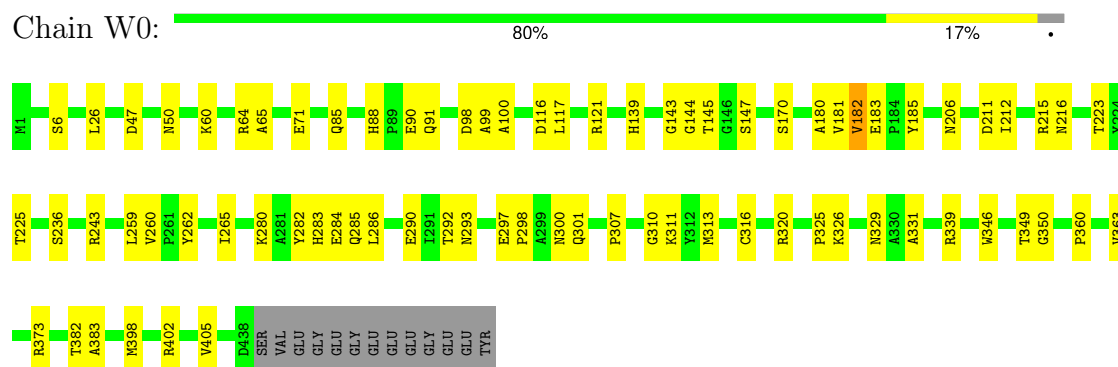
• Molecule 1: Tubulin alpha-1A chain



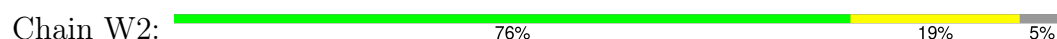
• Molecule 1: Tubulin alpha-1A chain

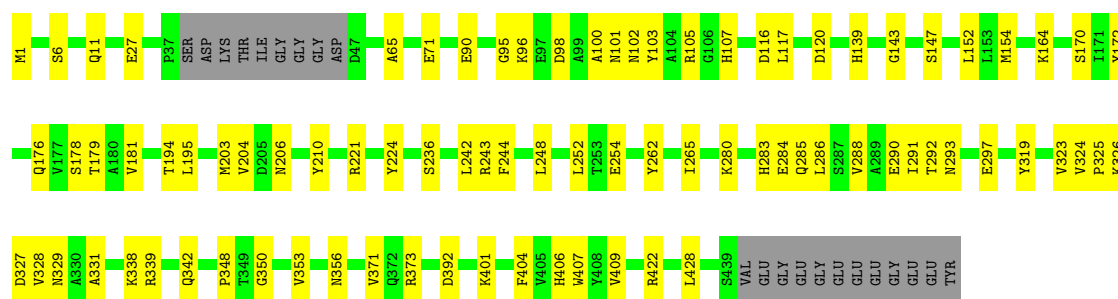


• Molecule 1: Tubulin alpha-1A chain



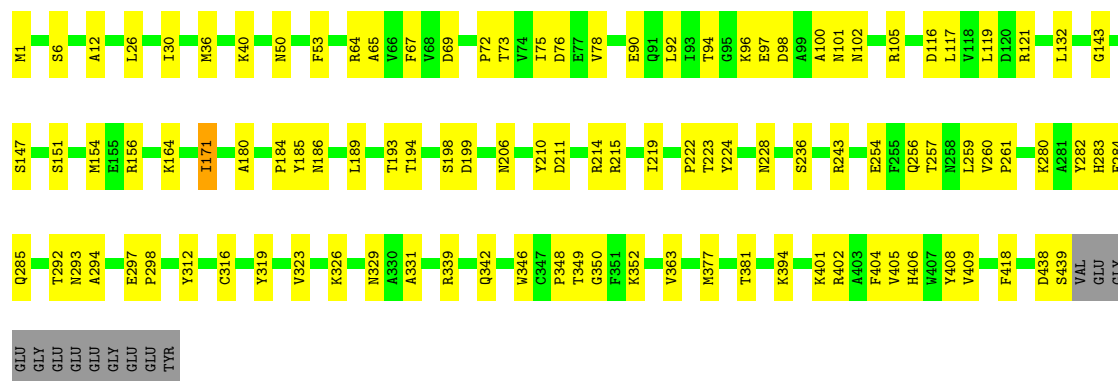
• Molecule 1: Tubulin alpha-1A chain





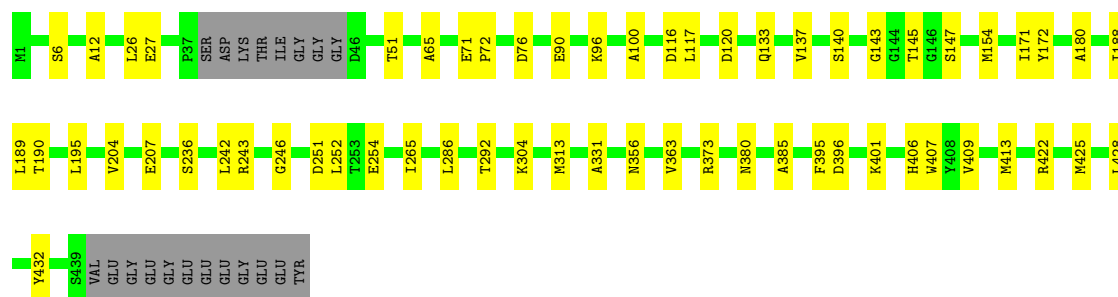
- Molecule 1: Tubulin alpha-1A chain

Chain W4: 74% 23% •



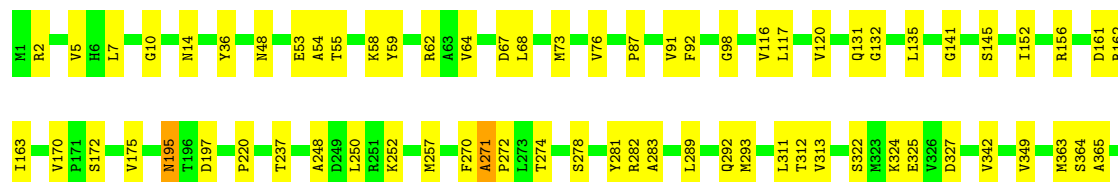
- Molecule 1: Tubulin alpha-1A chain

Chain W6: 82% 13% •



- Molecule 2: Tubulin beta-4B chain

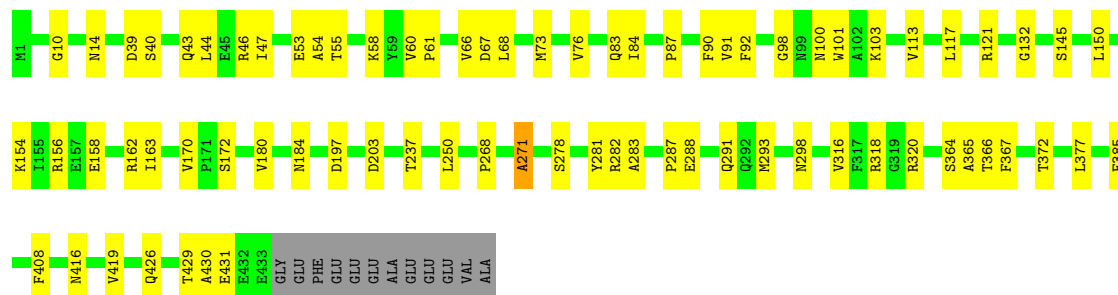
Chain A1: 80% 17% •





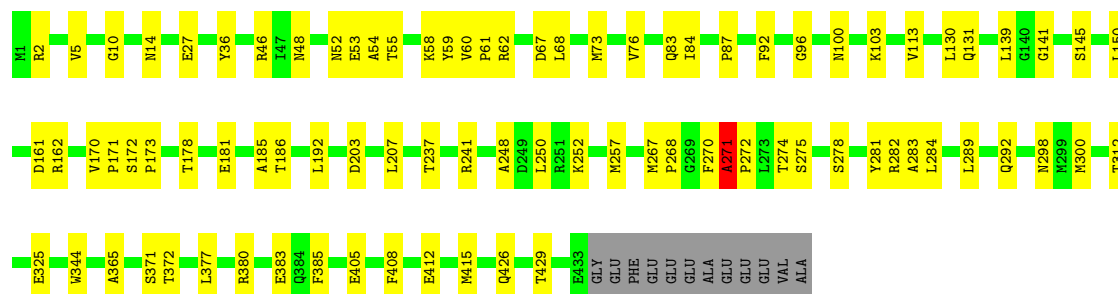
- Molecule 2: Tubulin beta-4B chain

Chain A3: 80% 17% .



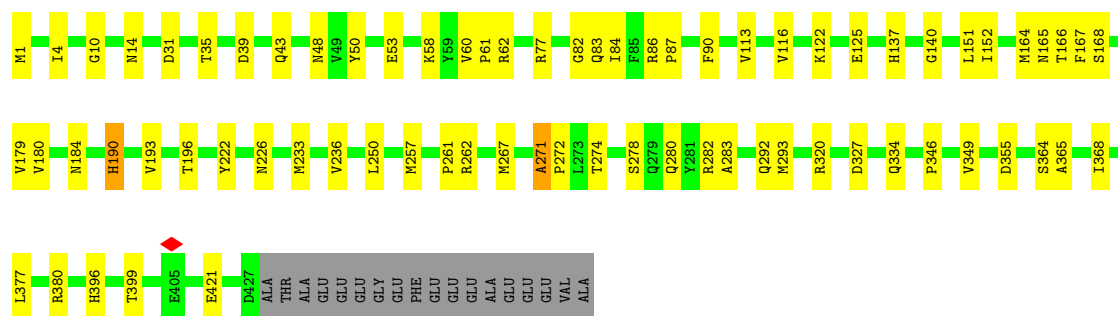
- Molecule 2: Tubulin beta-4B chain

Chain A5: 78% 19% .



- Molecule 2: Tubulin beta-4B chain

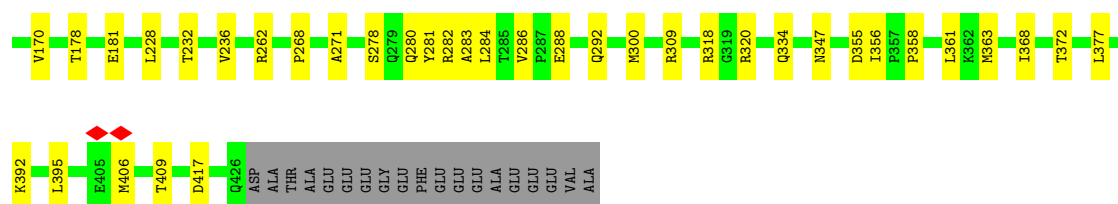
Chain B0: 80% 16% .



- Molecule 2: Tubulin beta-4B chain

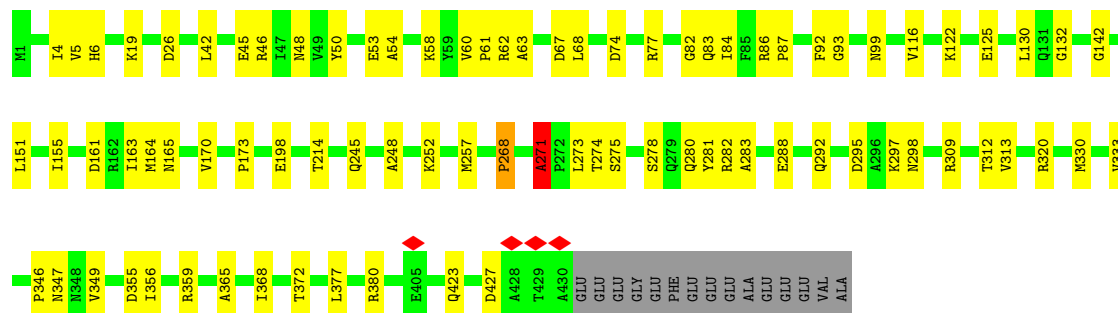
Chain B2: 80% 16% .





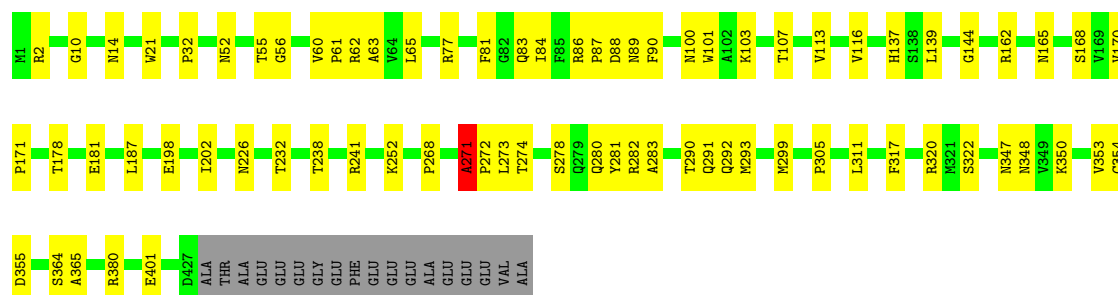
• Molecule 2: Tubulin beta-4B chain

Chain B4: 78% 18%



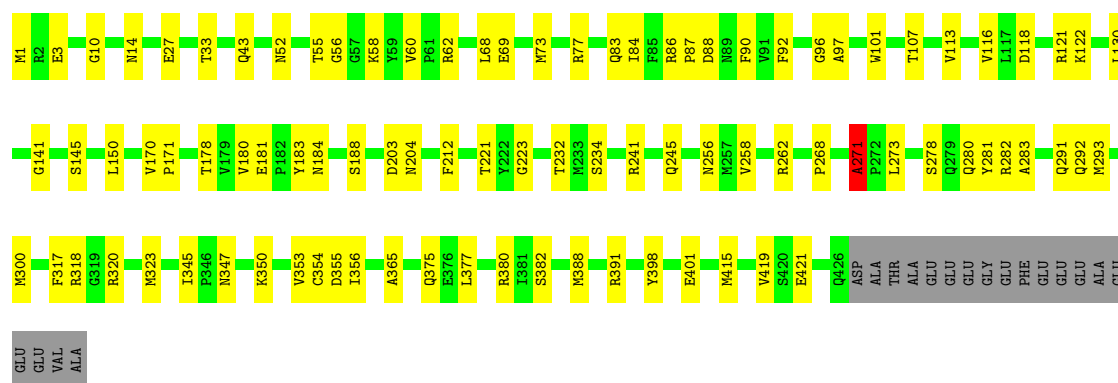
• Molecule 2: Tubulin beta-4B chain

Chain C0: 79% 17%



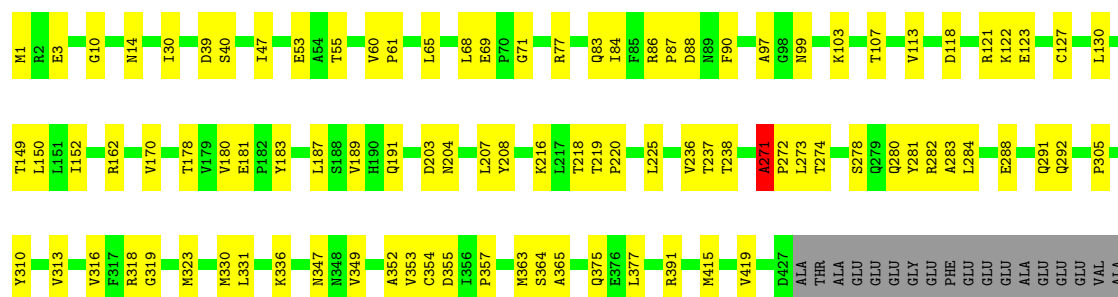
• Molecule 2: Tubulin beta-4B chain

Chain C2: 75% 20%



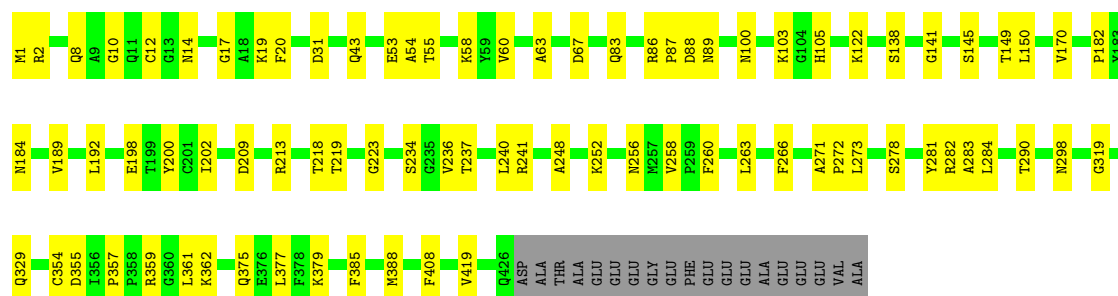
• Molecule 2: Tubulin beta-4B chain

Chain C4:  74% 21% .



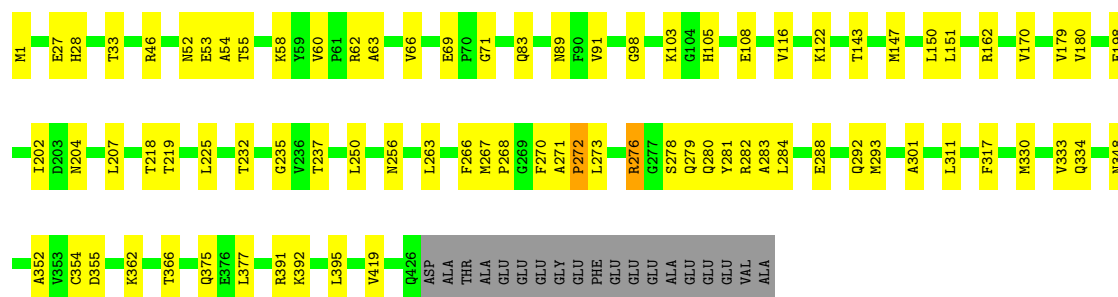
- Molecule 2: Tubulin beta-4B chain

Chain D0:  77% 18% .



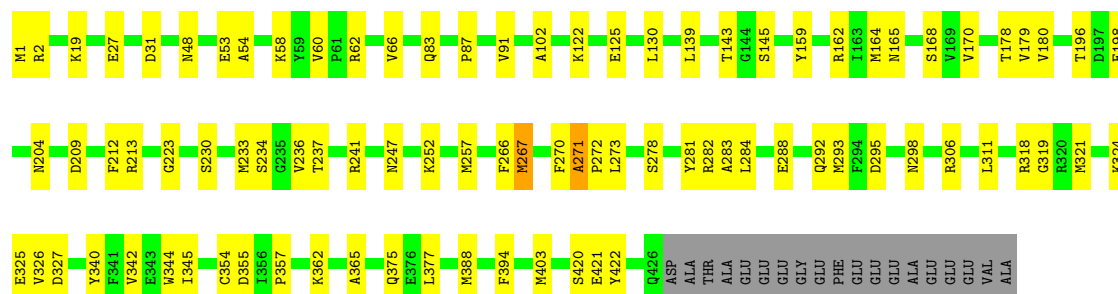
- Molecule 2: Tubulin beta-4B chain

Chain D2:  77% 18% .



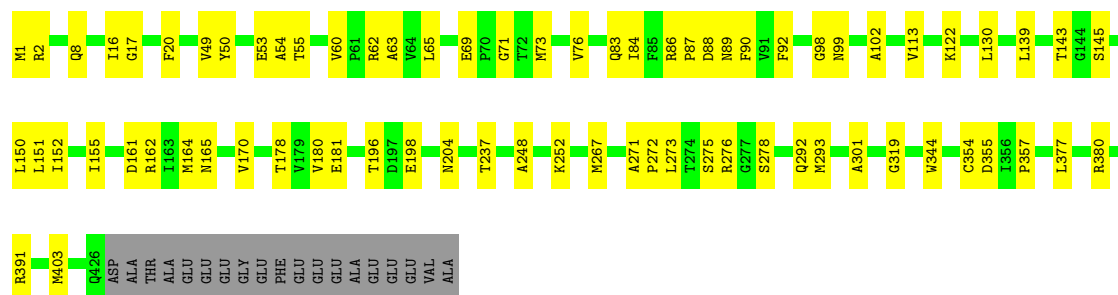
- Molecule 2: Tubulin beta-4B chain

Chain D4:  76% 20% .



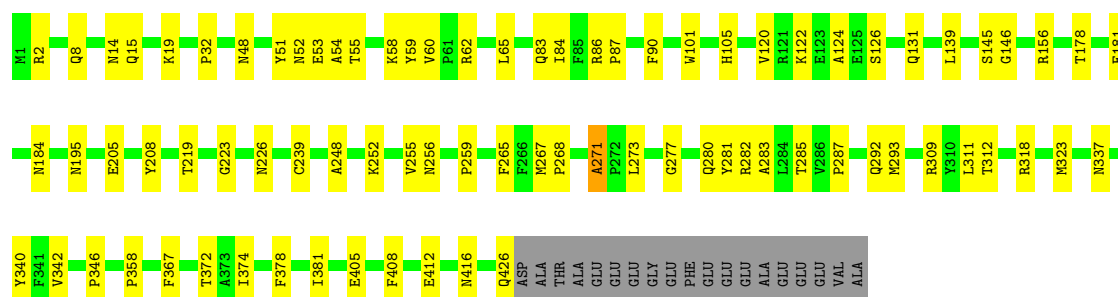
- Molecule 2: Tubulin beta-4B chain

Chain D6:  79% 16%



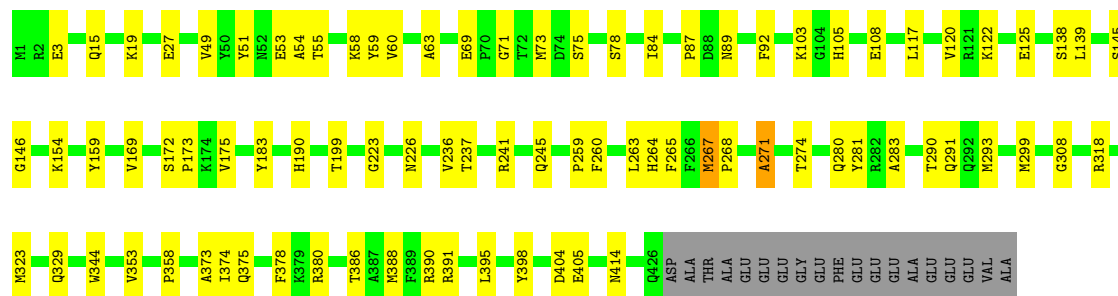
- Molecule 2: Tubulin beta-4B chain

Chain E0:  77% 18%



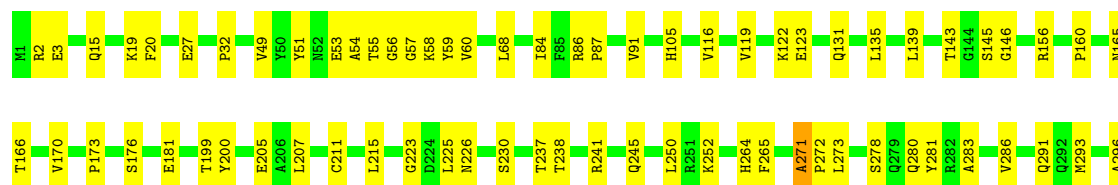
- Molecule 2: Tubulin beta-4B chain

Chain E2:  77% 19%



- Molecule 2: Tubulin beta-4B chain

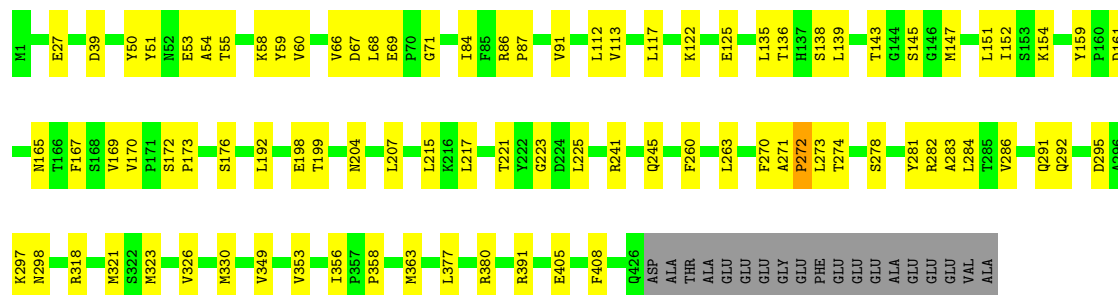
Chain E4:  76% 19%





• Molecule 2: Tubulin beta-4B chain

Chain E6: 76% 20% .



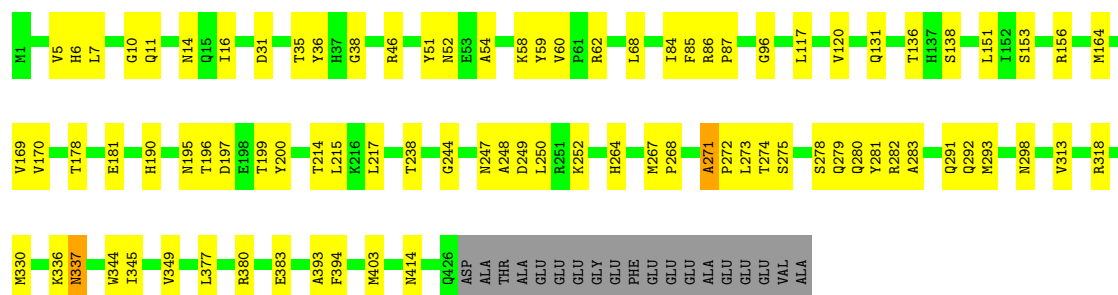
• Molecule 2: Tubulin beta-4B chain

Chain F0: 75% 20% .



• Molecule 2: Tubulin beta-4B chain

Chain F2: 76% 19% .



• Molecule 2: Tubulin beta-4B chain

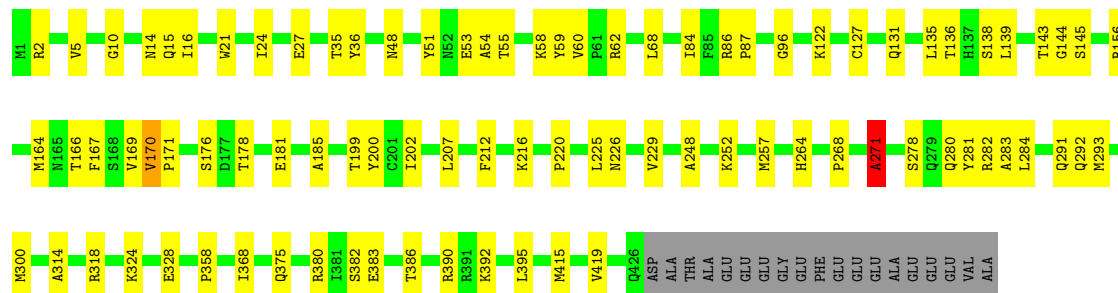
Chain F4: 75% 20% .





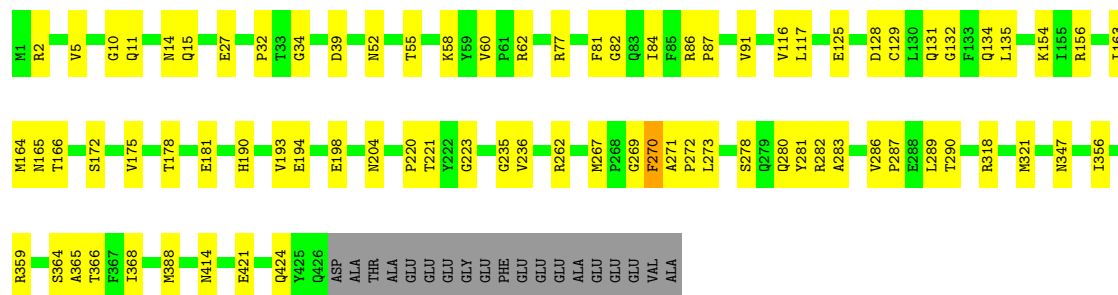
- Molecule 2: Tubulin beta-4B chain

Chain F6:



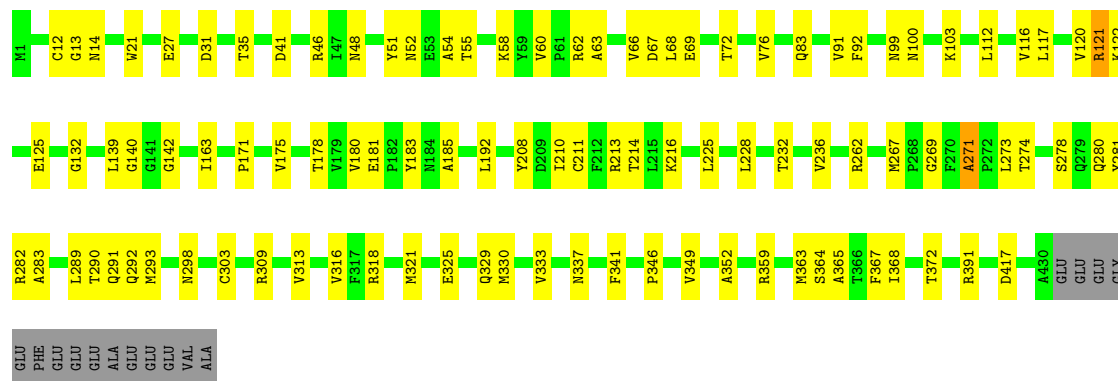
- Molecule 2: Tubulin beta-4B chain

Chain G1:



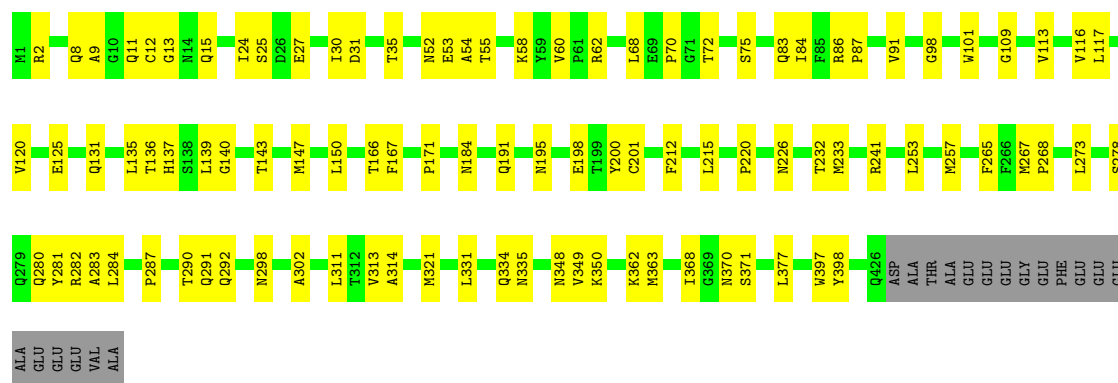
- Molecule 2: Tubulin beta-4B chain

Chain G3:



- Molecule 2: Tubulin beta-4B chain

Chain G5:  74% 22% .



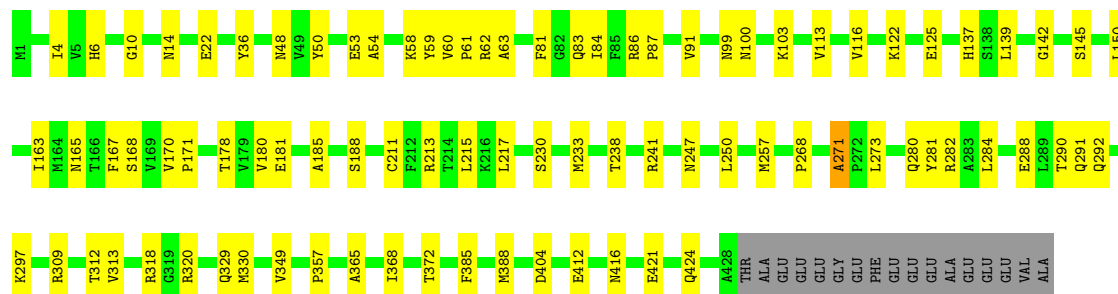
- Molecule 2: Tubulin beta-4B chain

Chain H1:  83% 13% .



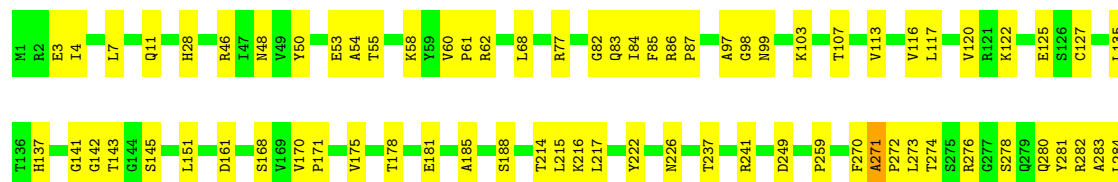
- Molecule 2: Tubulin beta-4B chain

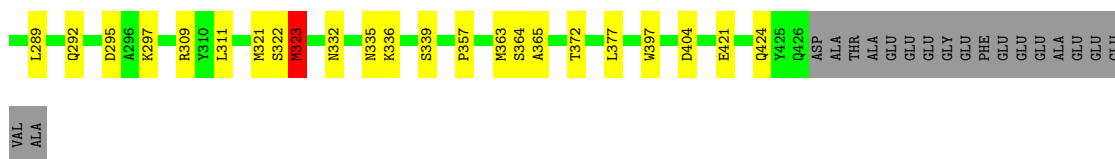
Chain H3:  77% 19% .



- Molecule 2: Tubulin beta-4B chain

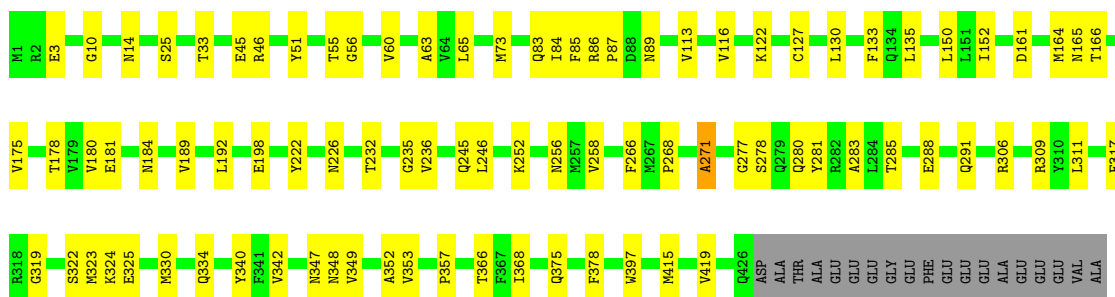
Chain H5:  74% 21% .





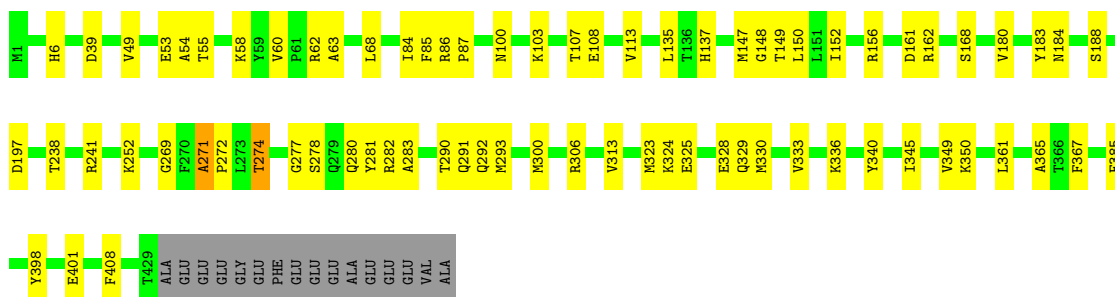
• Molecule 2: Tubulin beta-4B chain

Chain I1: 76% 20%



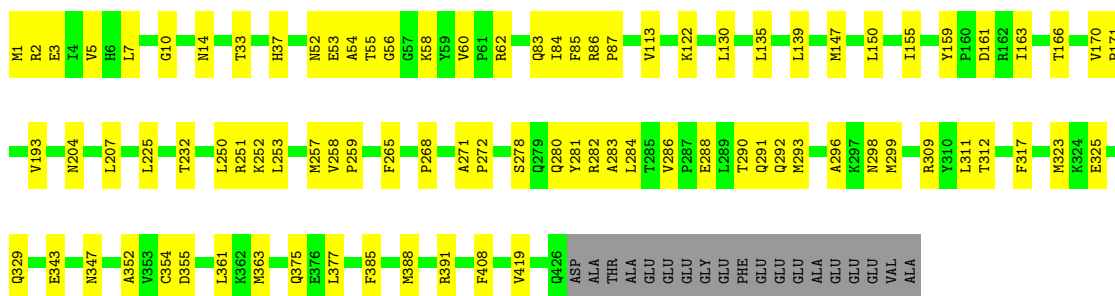
• Molecule 2: Tubulin beta-4B chain

Chain I3: 80% 16%



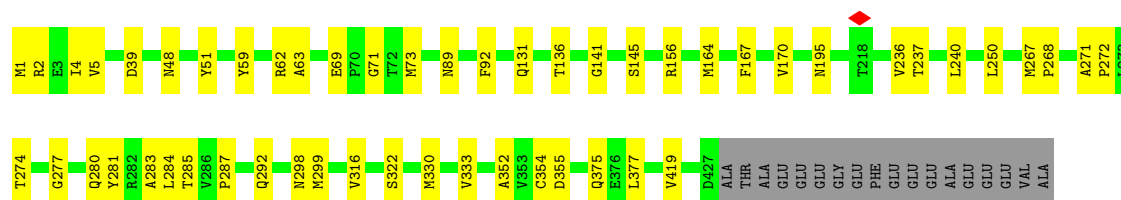
• Molecule 2: Tubulin beta-4B chain

Chain I5: 76% 20%



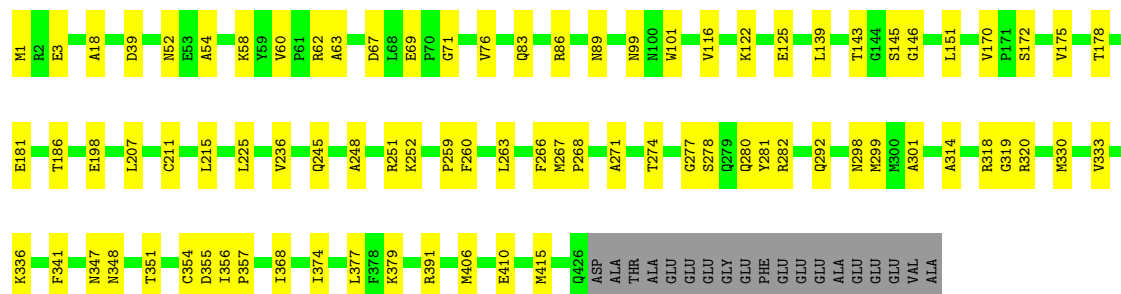
• Molecule 2: Tubulin beta-4B chain

Chain J0: 84% 12%



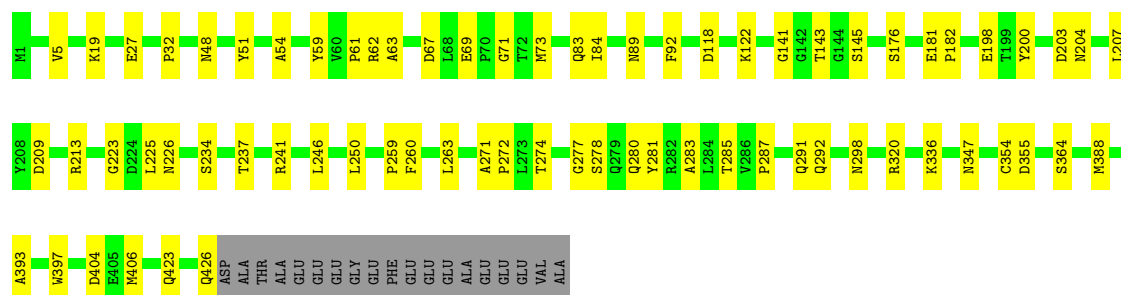
- Molecule 2: Tubulin beta-4B chain

Chain J2: 77% 19% .



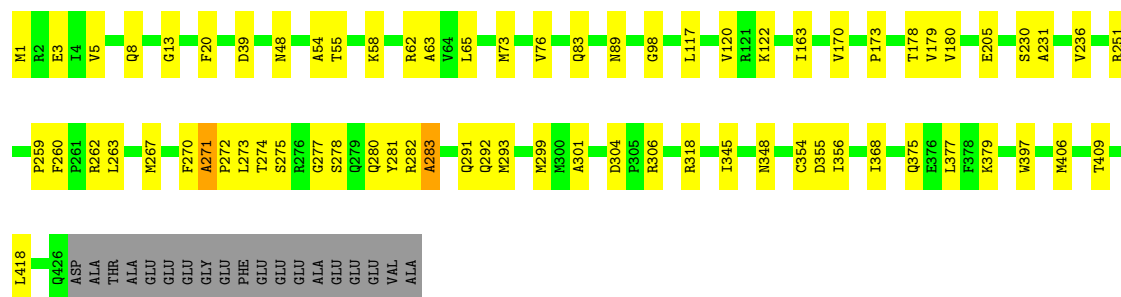
- Molecule 2: Tubulin beta-4B chain

Chain J4: 80% 16% .



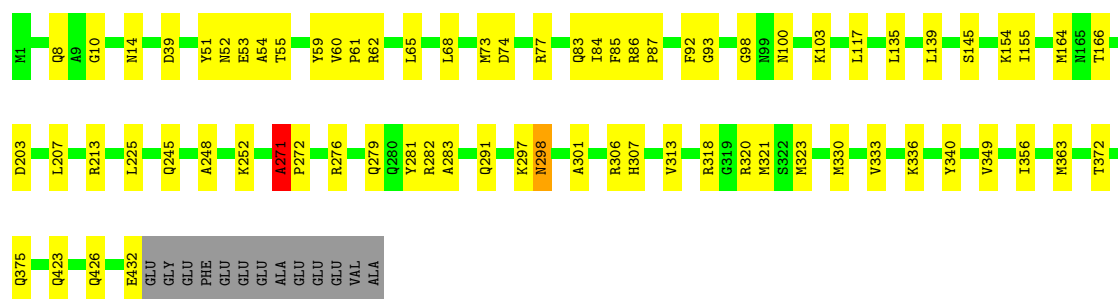
- Molecule 2: Tubulin beta-4B chain

Chain J6: 80% 16% .



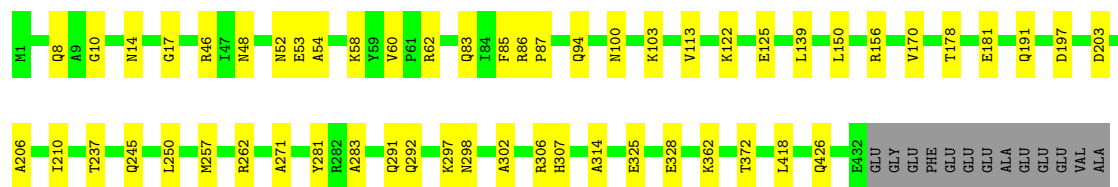
- Molecule 2: Tubulin beta-4B chain

Chain K1: 81% 16% .



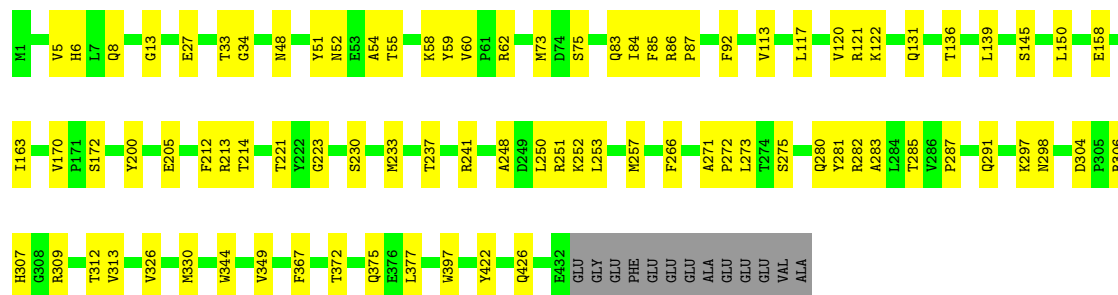
- Molecule 2: Tubulin beta-4B chain

Chain K3: 85% 12% .



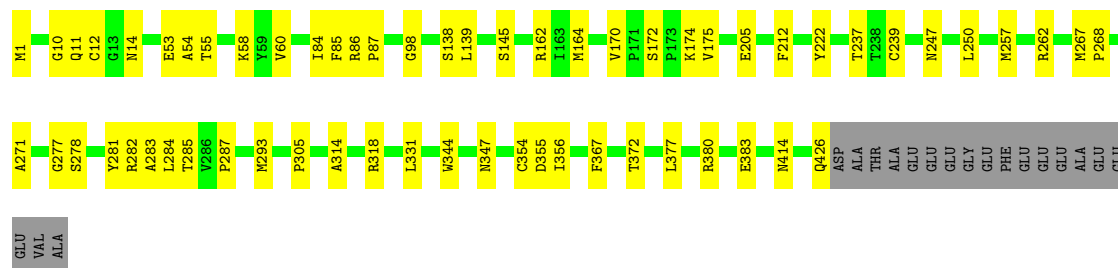
- Molecule 2: Tubulin beta-4B chain

Chain K5: 78% 19% .



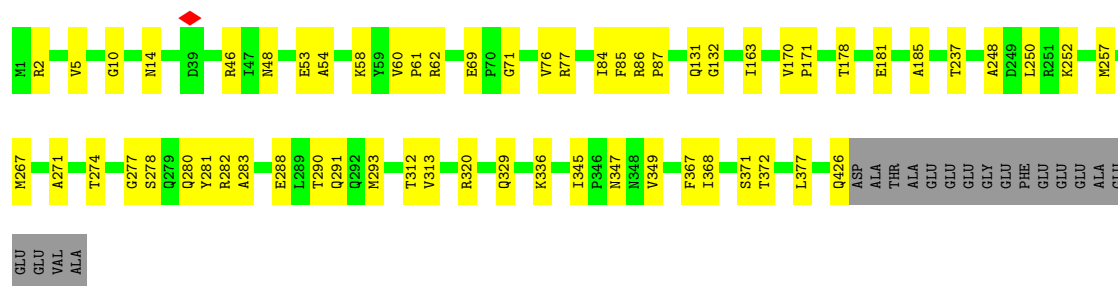
- Molecule 2: Tubulin beta-4B chain

Chain L1: 82% 14% .



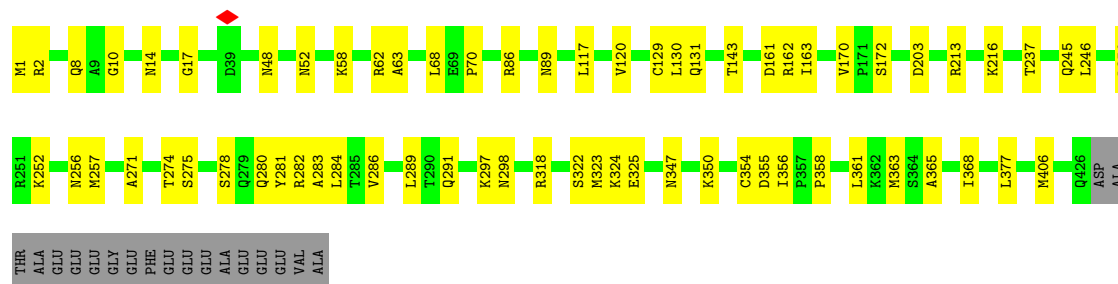
- Molecule 2: Tubulin beta-4B chain

Chain L3: 82% 13% .



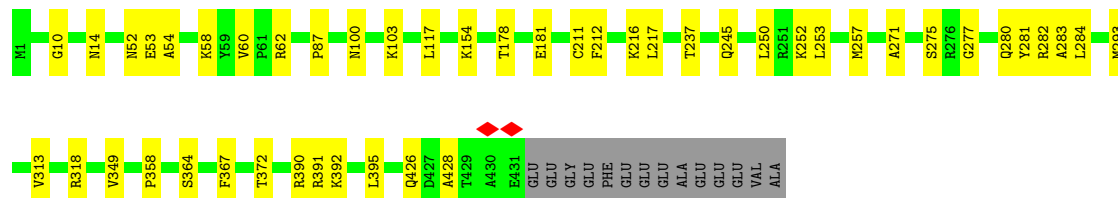
- Molecule 2: Tubulin beta-4B chain

Chain L5: 81% 15% .



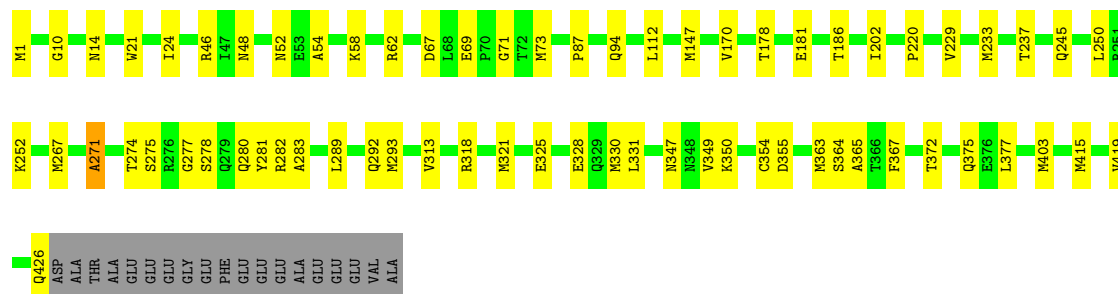
- Molecule 2: Tubulin beta-4B chain

Chain M1: 86% 11% .



- Molecule 2: Tubulin beta-4B chain

Chain M3: 81% 15% .



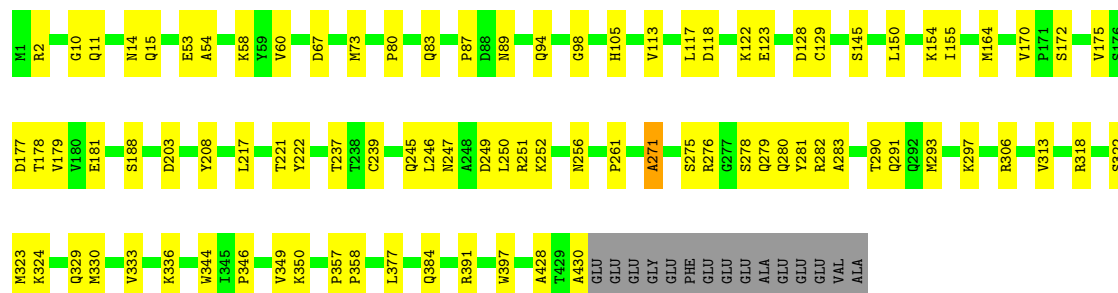
- Molecule 2: Tubulin beta-4B chain

Chain M5: 85% 11% .



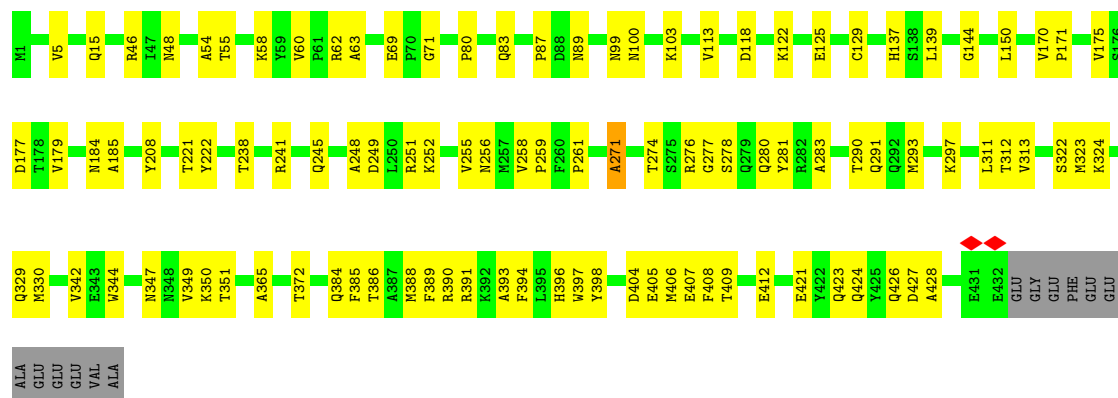
- Molecule 2: Tubulin beta-4B chain

Chain O1: 77% 20% .



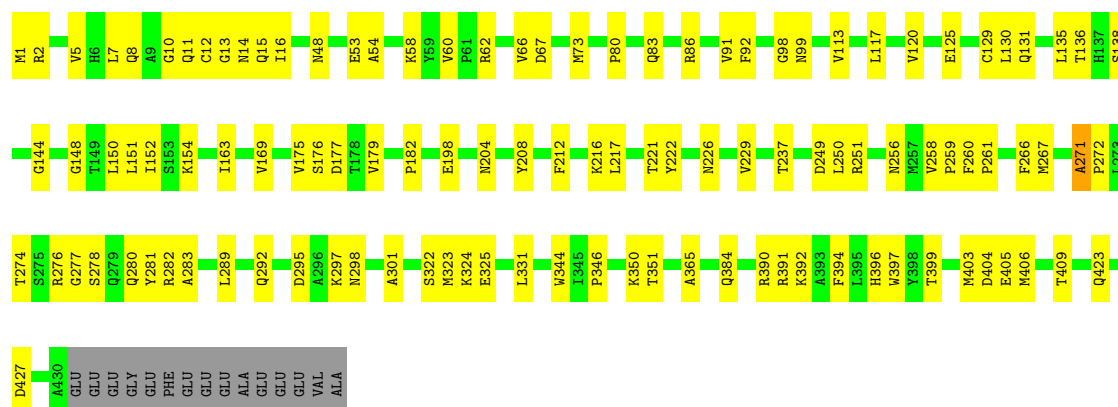
- Molecule 2: Tubulin beta-4B chain

Chain O3: 74% 23% .



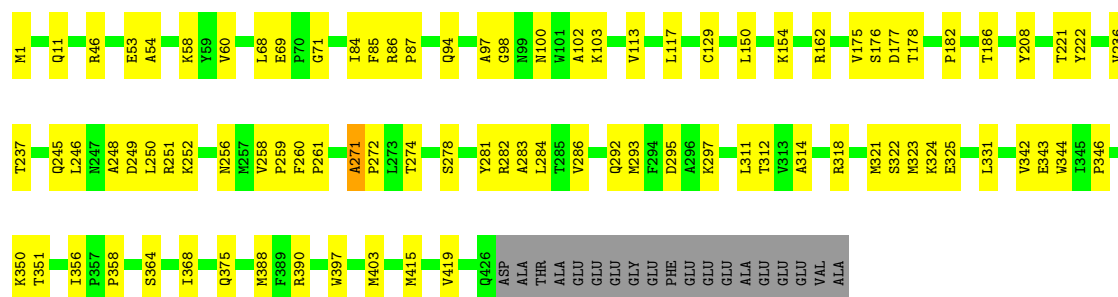
- Molecule 2: Tubulin beta-4B chain

Chain O5: 71% 25% .



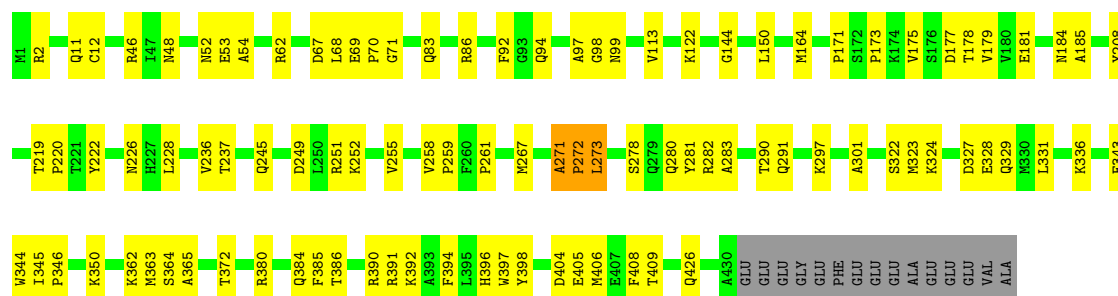
- Molecule 2: Tubulin beta-4B chain

Chain P1:  76% 20%



• Molecule 2: Tubulin beta-4B chain

Chain P3:  74% 22%



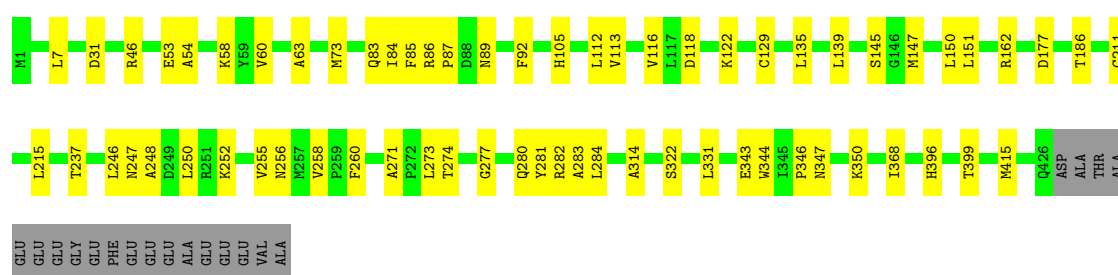
• Molecule 2: Tubulin beta-4B chain

Chain P5:  74% 22%

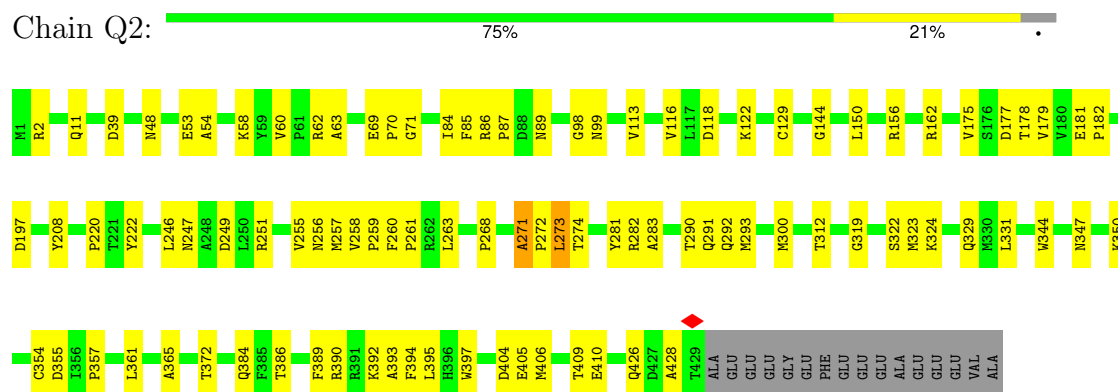


• Molecule 2: Tubulin beta-4B chain

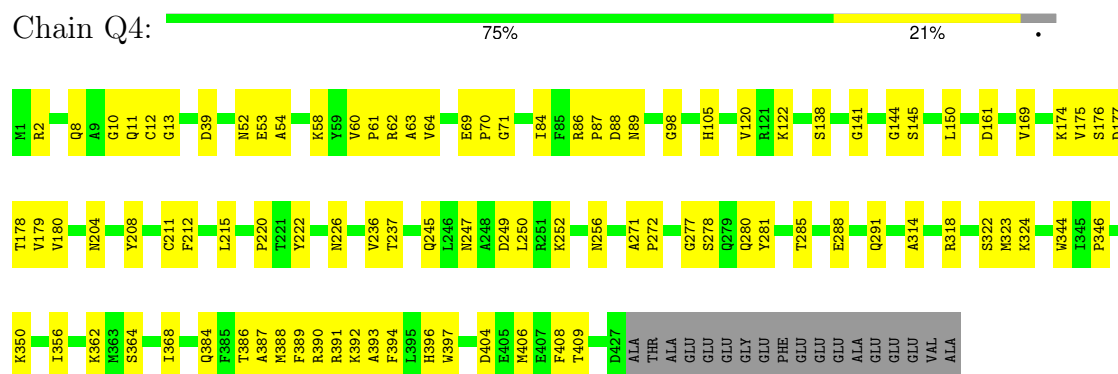
Chain Q0:  81% 15%



- Molecule 2: Tubulin beta-4B chain



- Molecule 2: Tubulin beta-4B chain

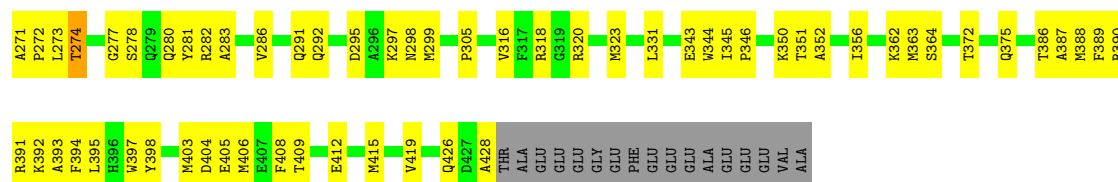


- Molecule 2: Tubulin beta-4B chain



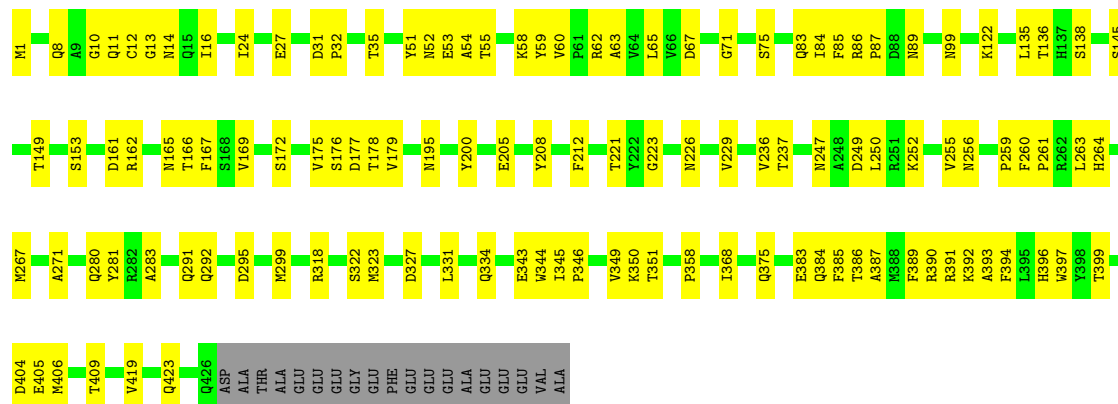
- Molecule 2: Tubulin beta-4B chain





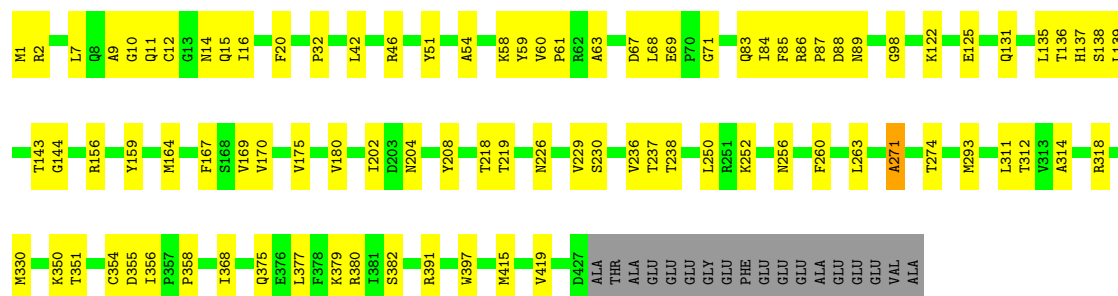
• Molecule 2: Tubulin beta-4B chain

Chain R4:



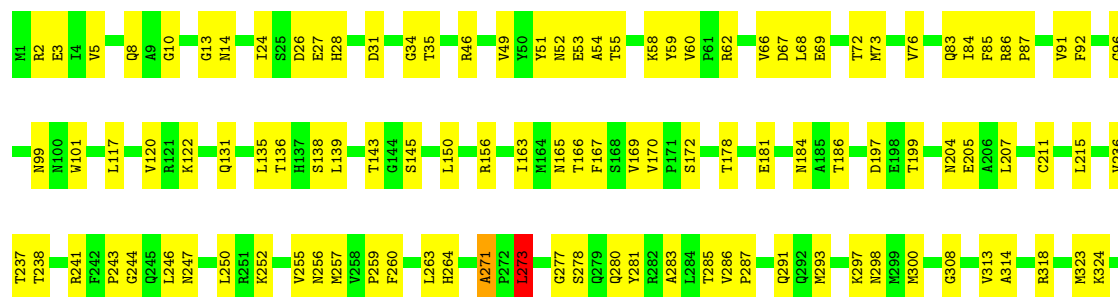
• Molecule 2: Tubulin beta-4B chain

Chain R6:



• Molecule 2: Tubulin beta-4B chain

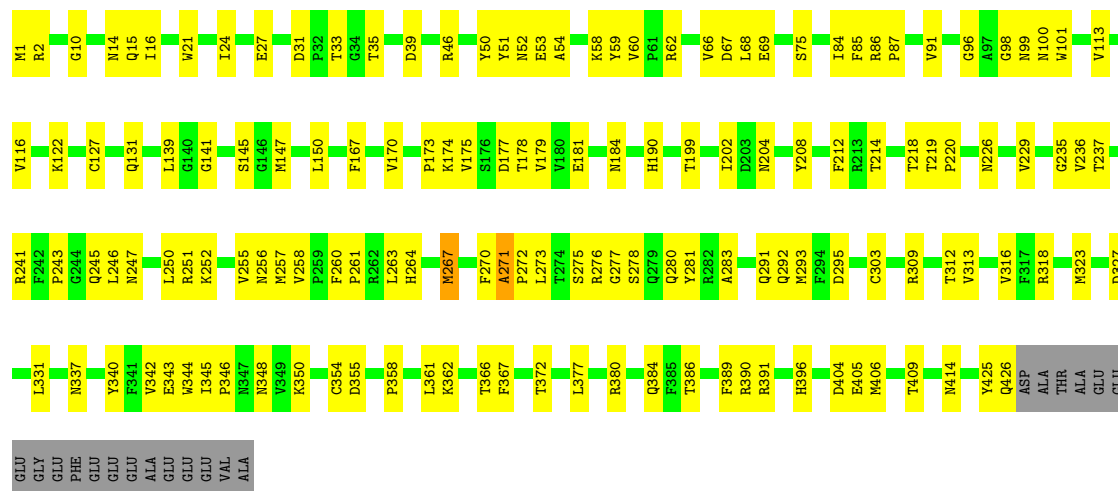
Chain S0:





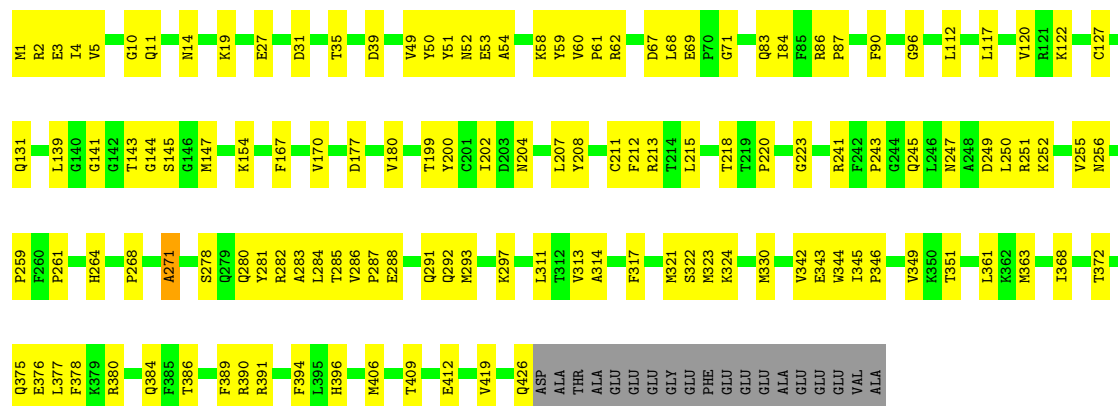
• Molecule 2: Tubulin beta-4B chain

Chain S2: 63% 32%



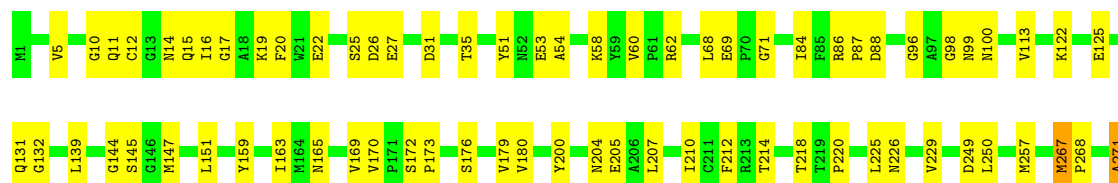
• Molecule 2: Tubulin beta-4B chain

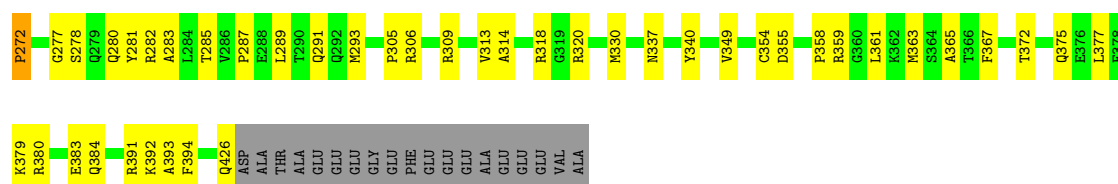
Chain S4: 67% 29%



• Molecule 2: Tubulin beta-4B chain

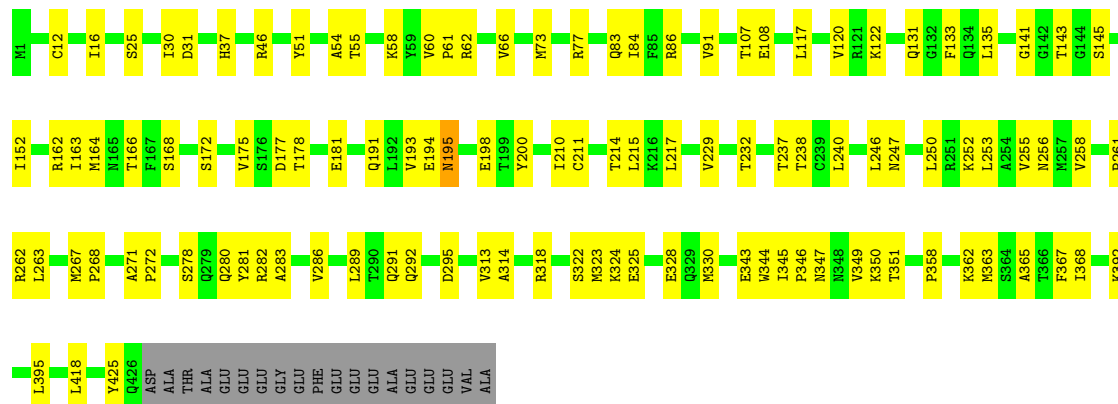
Chain S6: 70% 25%





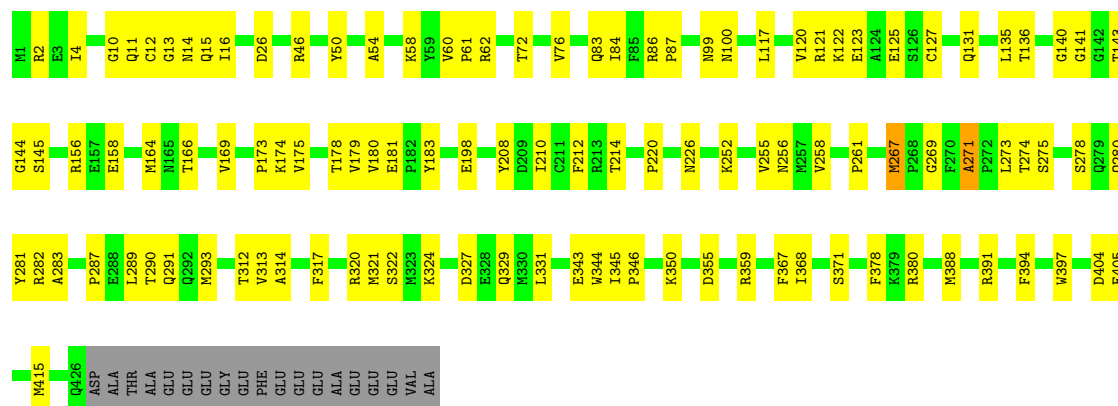
• Molecule 2: Tubulin beta-4B chain

Chain T0: 71% 25%



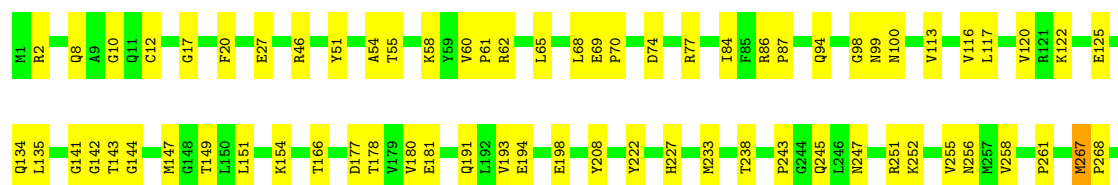
• Molecule 2: Tubulin beta-4B chain

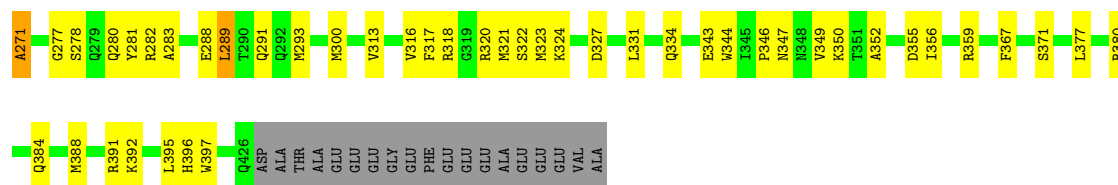
Chain T2: 71% 24%



• Molecule 2: Tubulin beta-4B chain

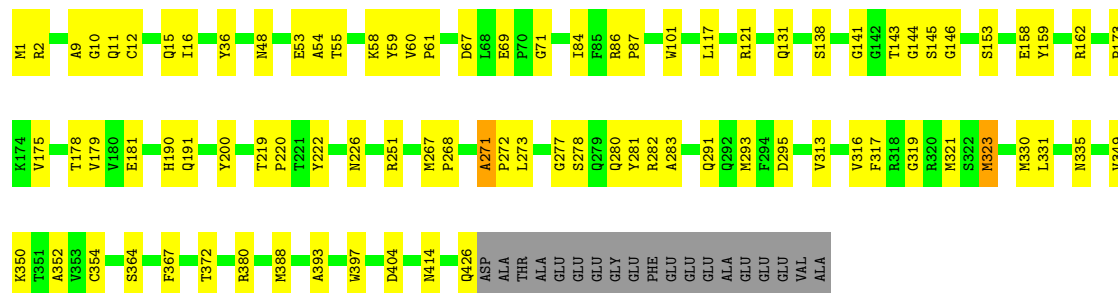
Chain T4: 70% 25%





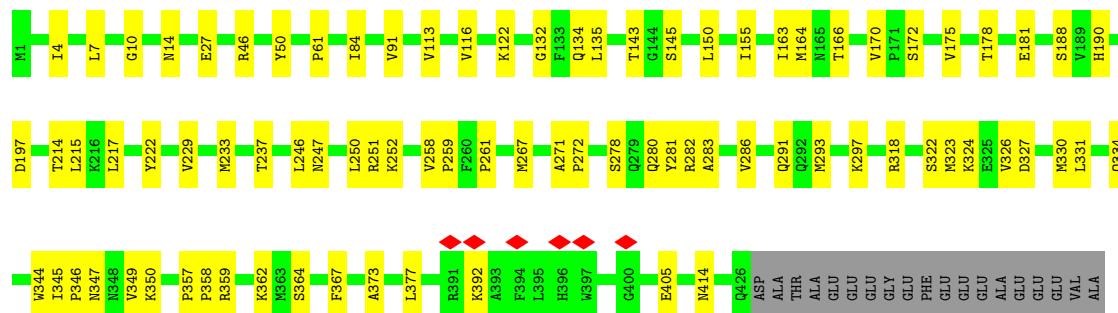
- Molecule 2: Tubulin beta-4B chain

Chain T6: 76% 19%



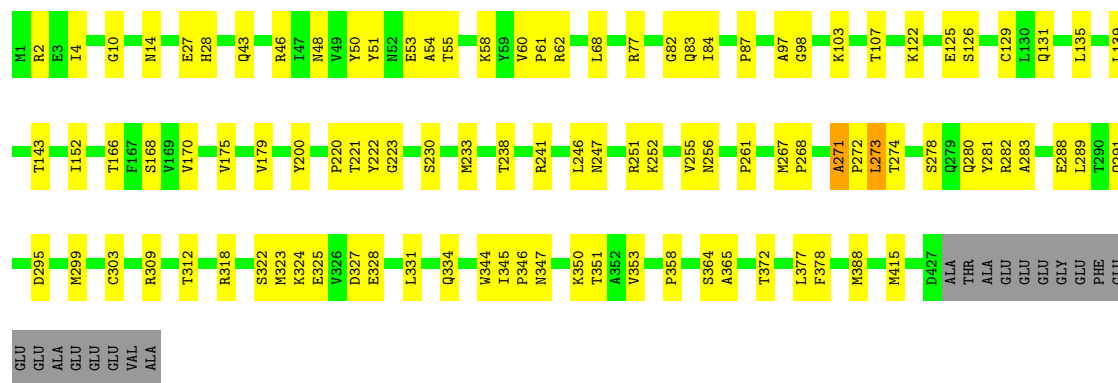
- Molecule 2: Tubulin beta-4B chain

Chain U0: 77% 19%



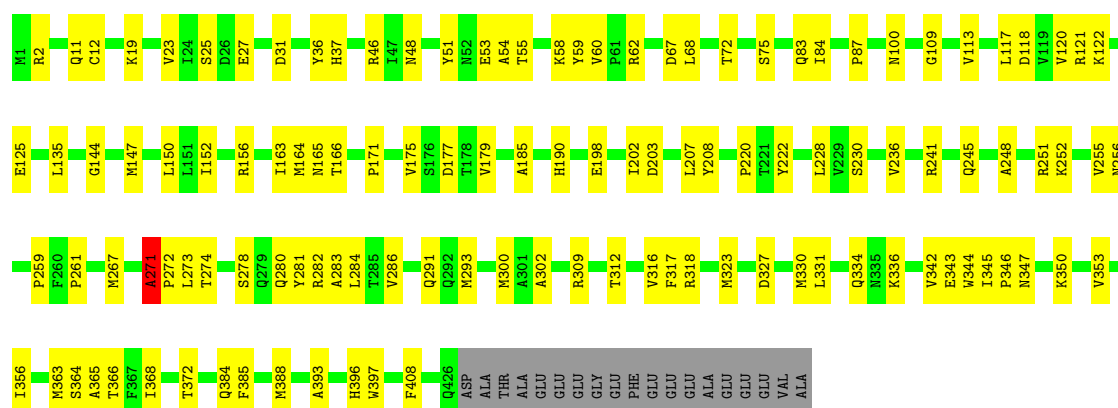
- Molecule 2: Tubulin beta-4B chain

Chain U2: 73% 22%



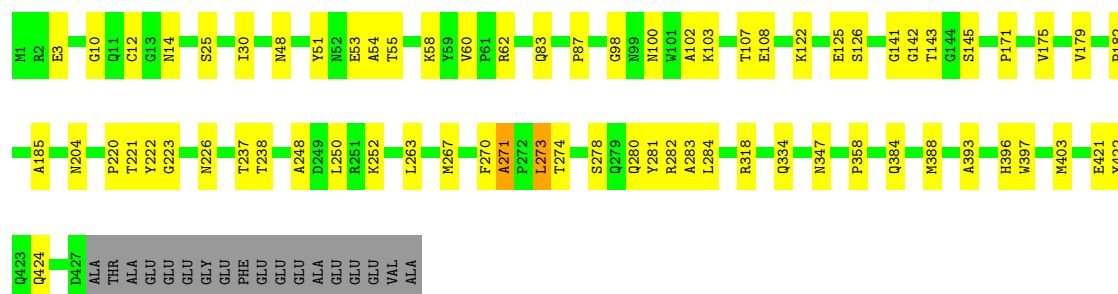
- Molecule 2: Tubulin beta-4B chain

Chain U4:  69% 27%



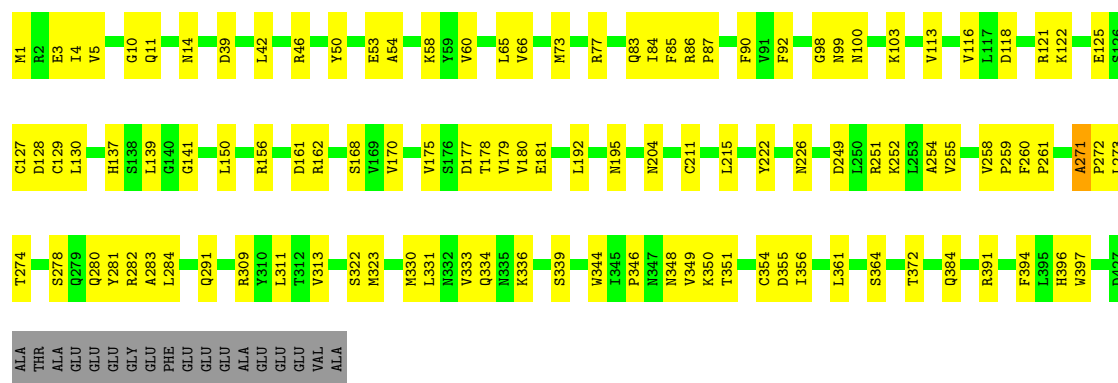
• Molecule 2: Tubulin beta-4B chain

Chain U6:  80% 15%



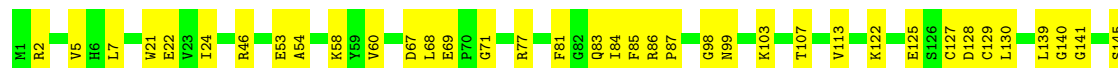
• Molecule 2: Tubulin beta-4B chain

Chain V1:  71% 24%



• Molecule 2: Tubulin beta-4B chain

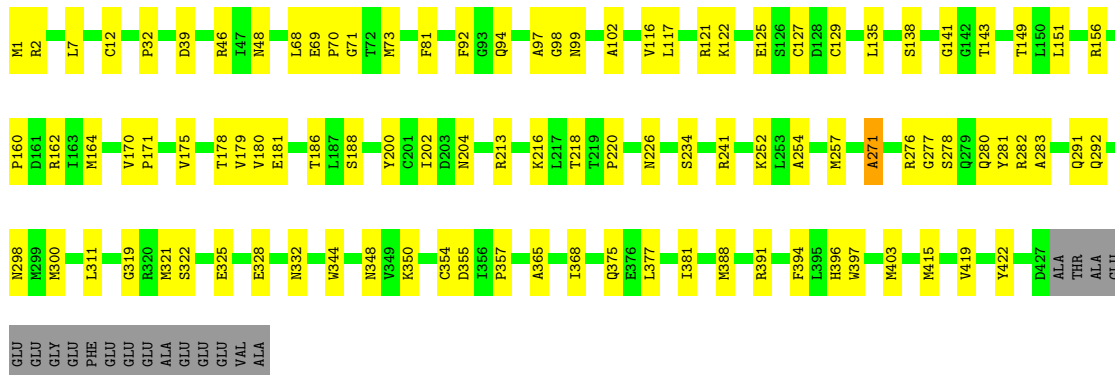
Chain V3:  71% 25%



ALA
GLU
GLU
GLU
VAL
ALA

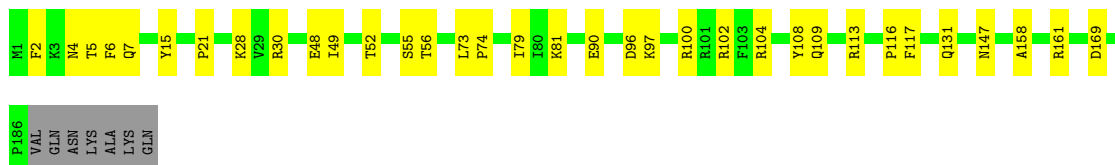
- Molecule 2: Tubulin beta-4B chain

Chain W5:  74% 22%



- Molecule 3: Cilia- and flagella-associated protein 20

Chain X0:  79% 18%



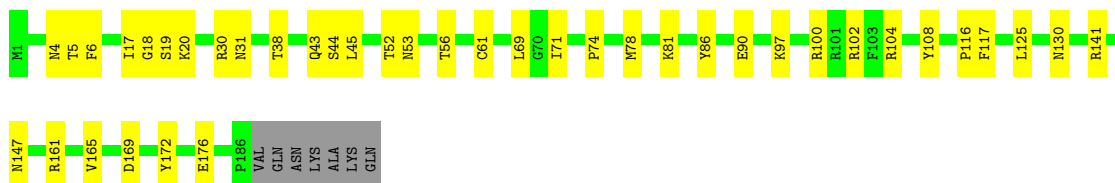
- Molecule 3: Cilia- and flagella-associated protein 20

Chain X1:  76% 20%

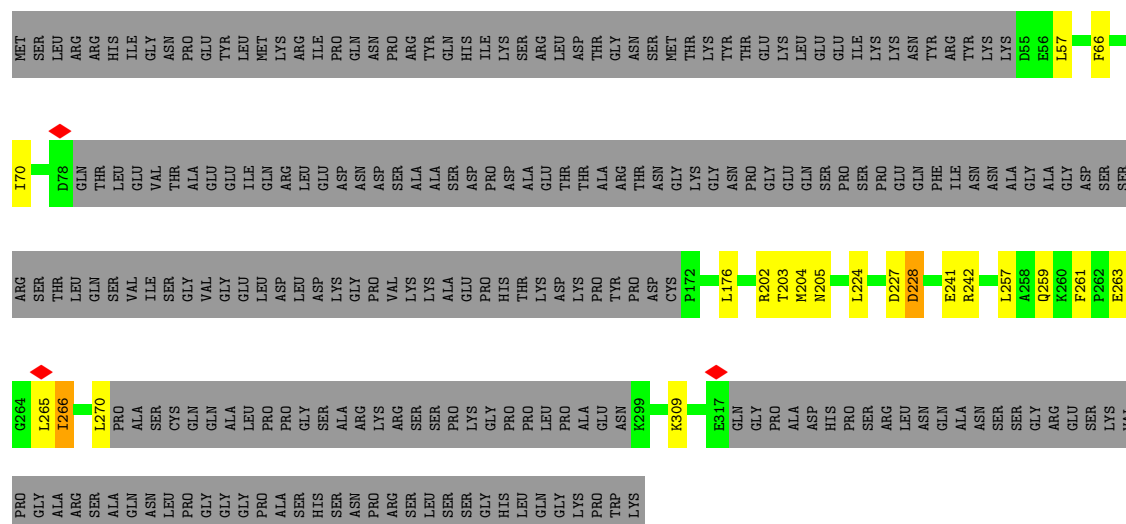


- Molecule 3: Cilia- and flagella-associated protein 20

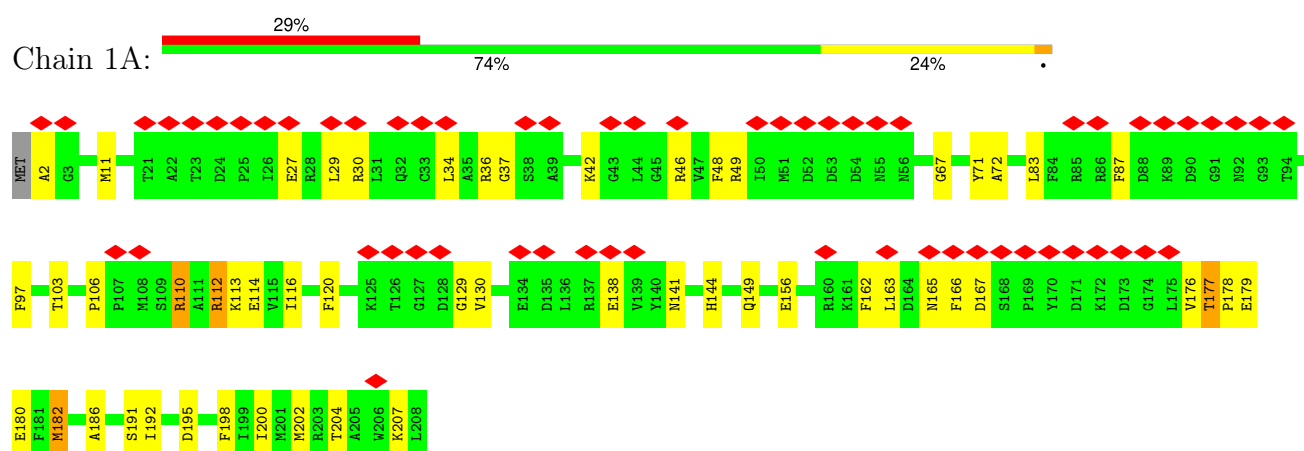
Chain X2:  76% 21%



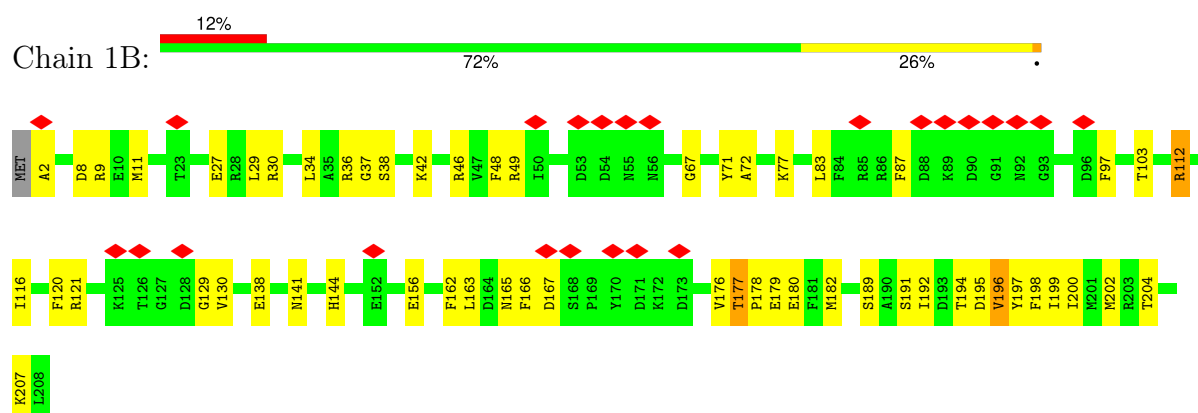
- Molecule 3: Cilia- and flagella-associated protein 20



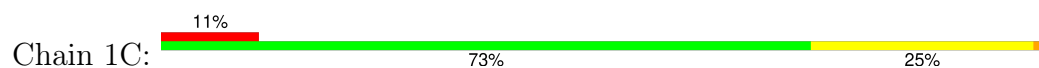
- Molecule 5: Calcyphosin-like protein

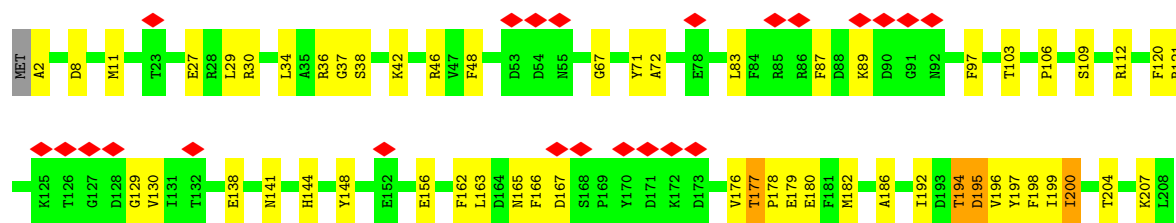


- Molecule 5: Calcyphosin-like protein

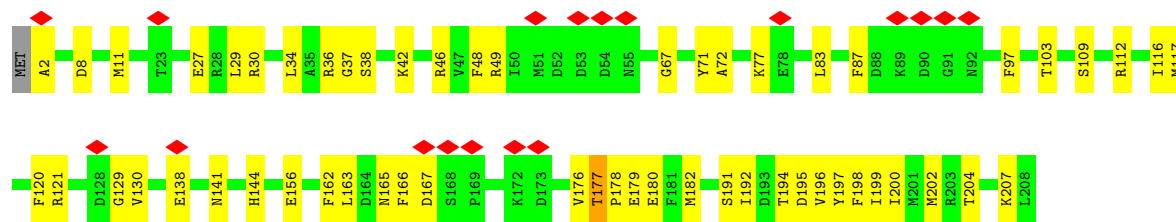
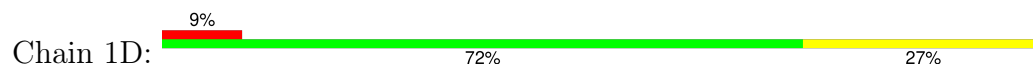


- Molecule 5: Calcyphosin-like protein

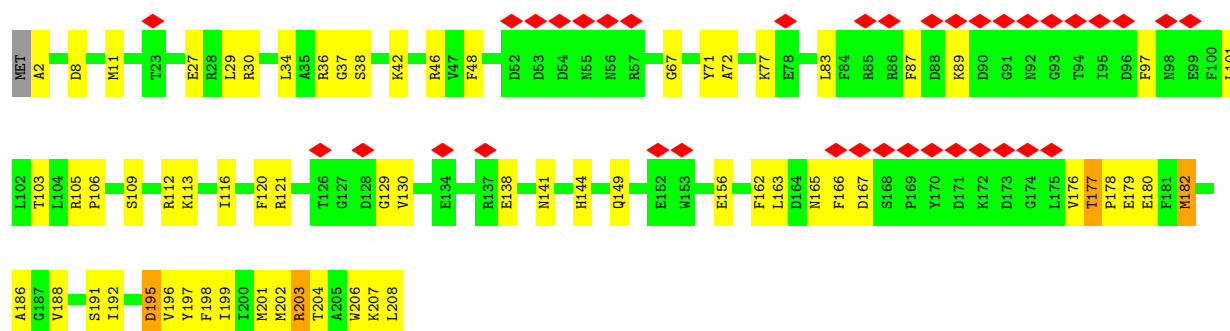




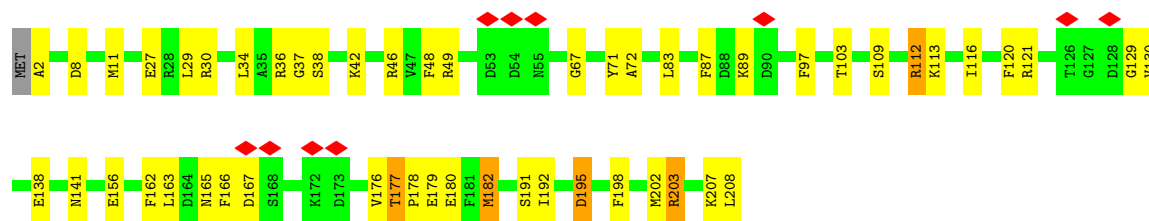
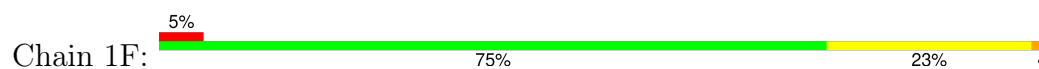
• Molecule 5: Calcyphosin-like protein



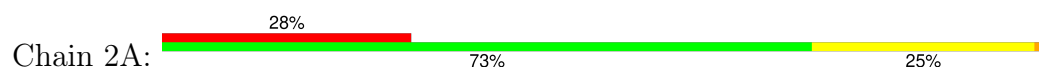
• Molecule 5: Calcyphosin-like protein

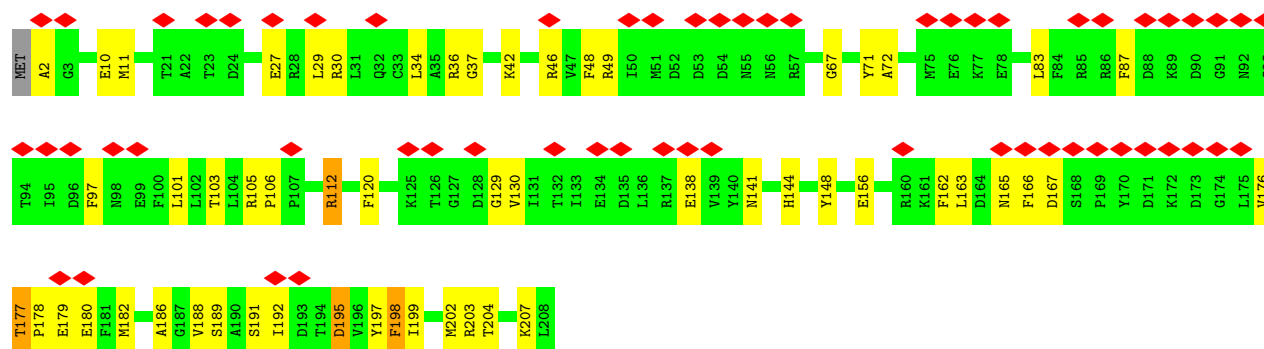


• Molecule 5: Calcyphosin-like protein

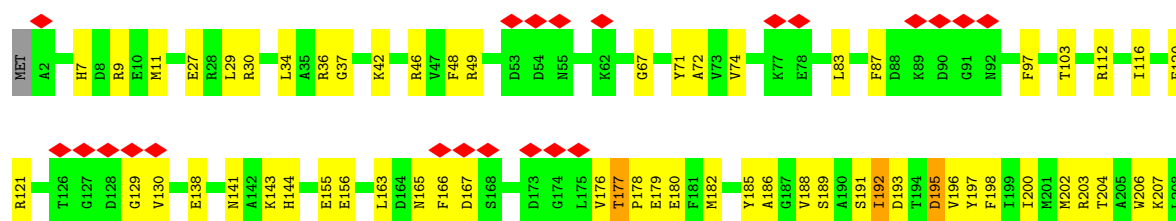


• Molecule 5: Calcyphosin-like protein

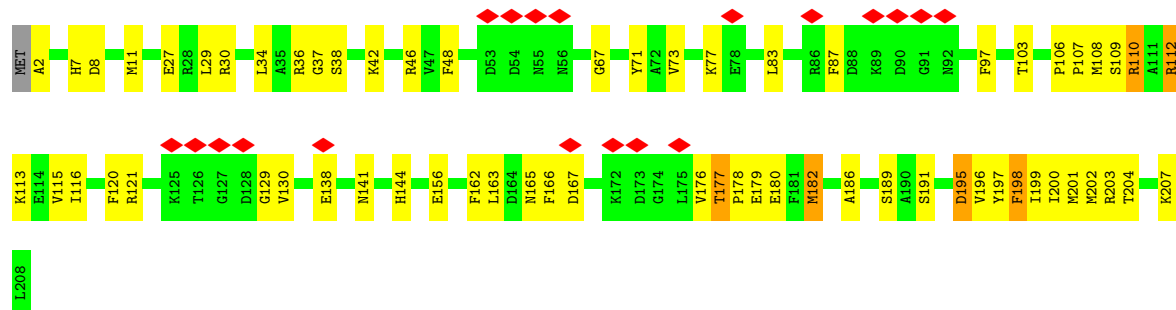




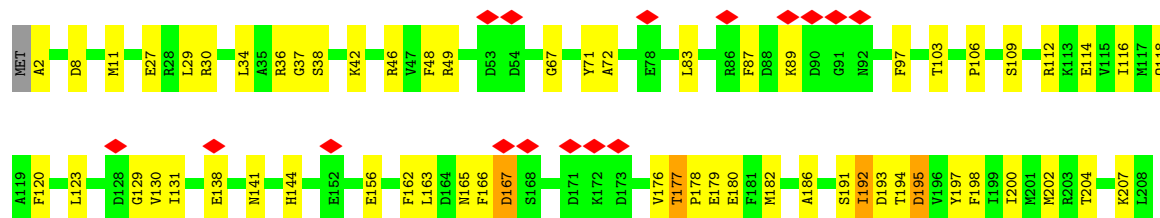
• Molecule 5: Calcyphosin-like protein



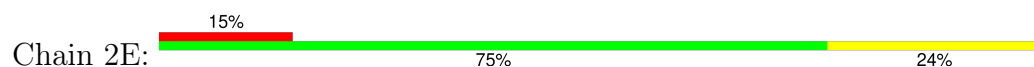
• Molecule 5: Calcyphosin-like protein

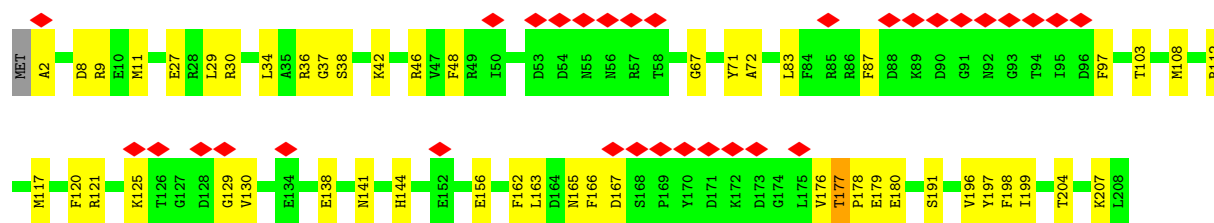


• Molecule 5: Calcyphosin-like protein

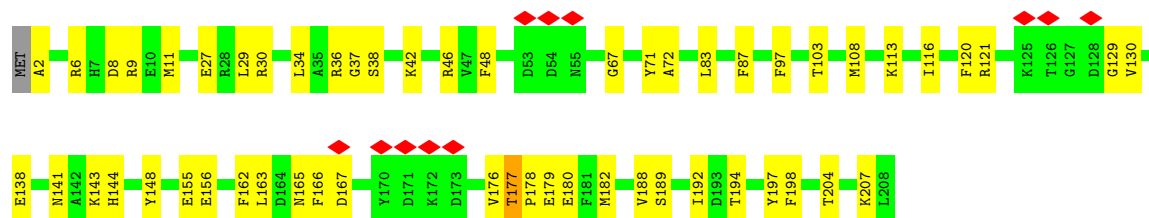
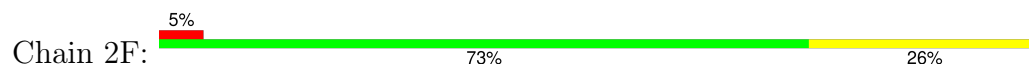


• Molecule 5: Calcyphosin-like protein

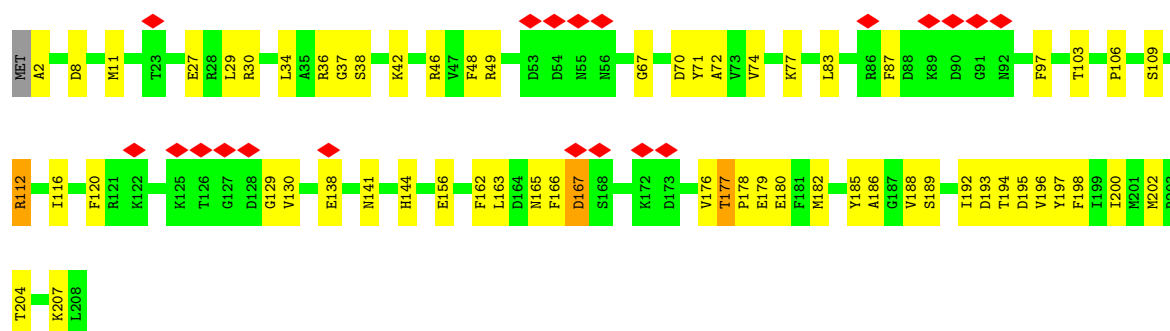




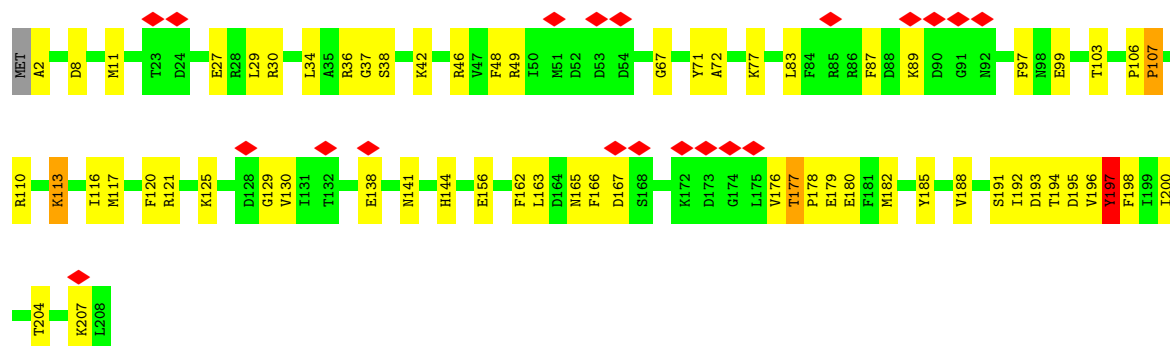
- Molecule 5: Calcyphosin-like protein



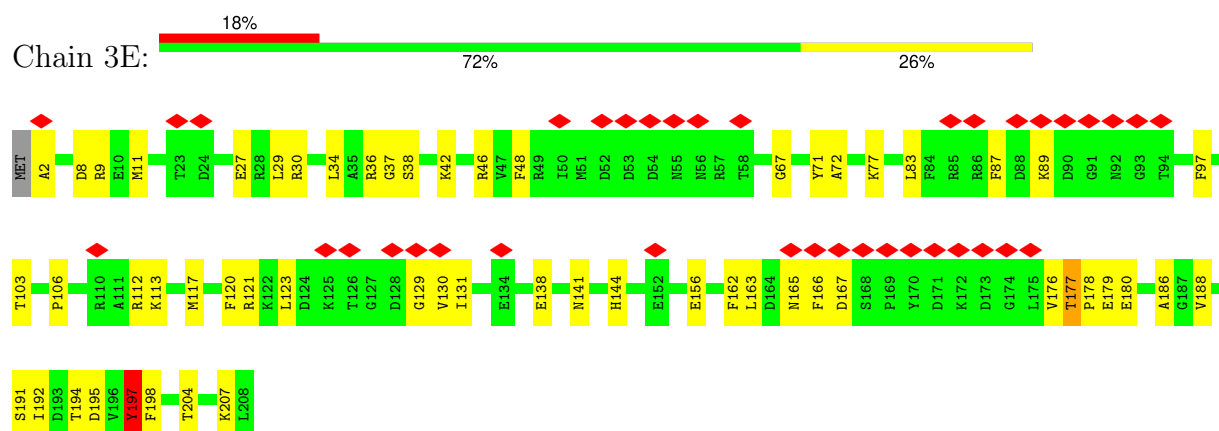
- Molecule 5: Calcyphosin-like protein



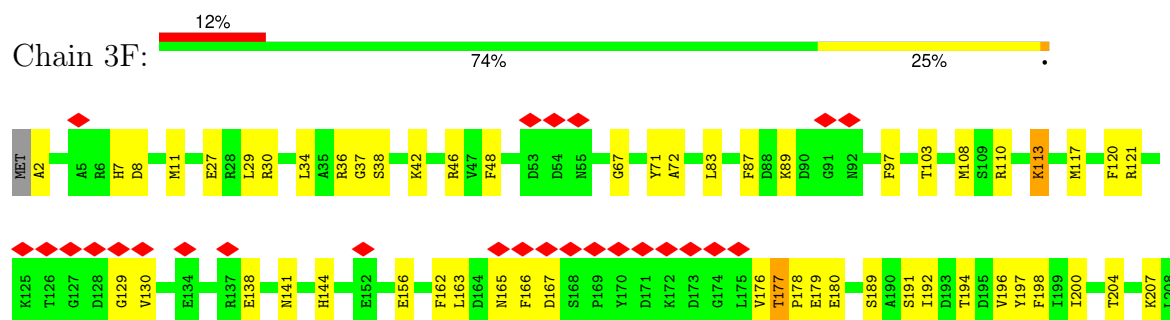
- Molecule 5: Calcyphosin-like protein



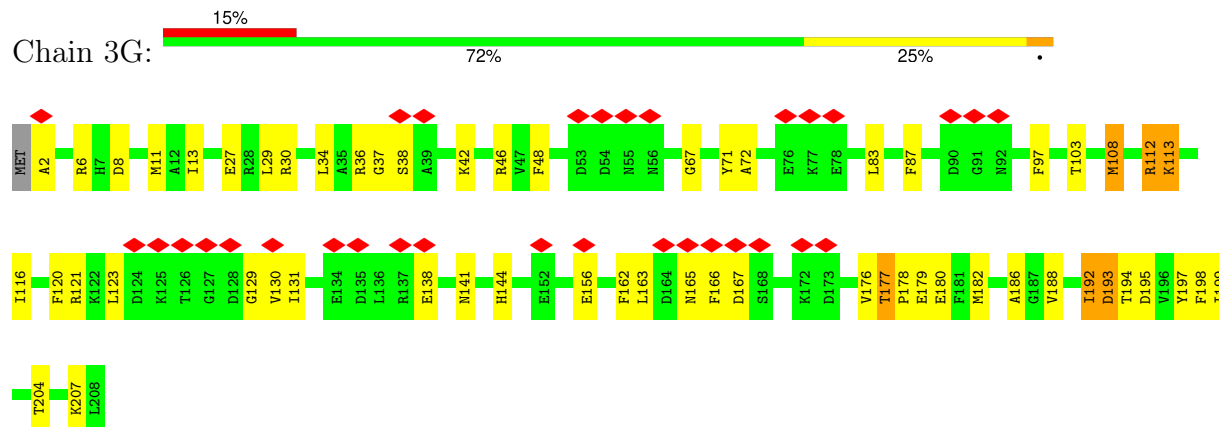
- Molecule 5: Calcyphosin-like protein



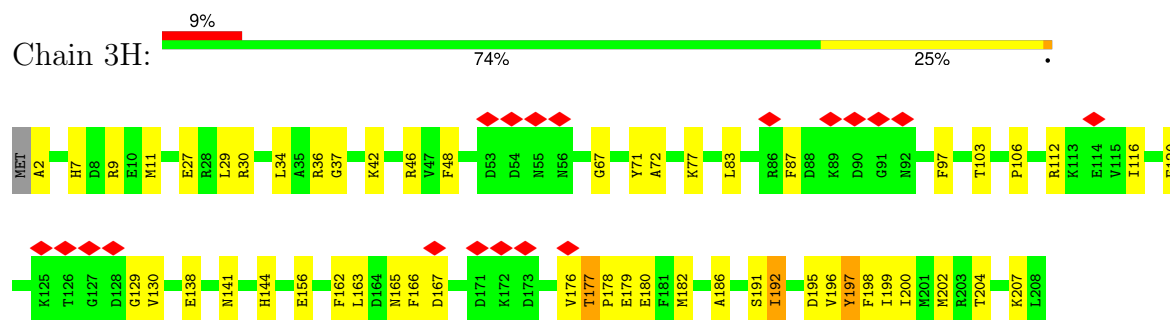
- Molecule 5: Calcyphosin-like protein



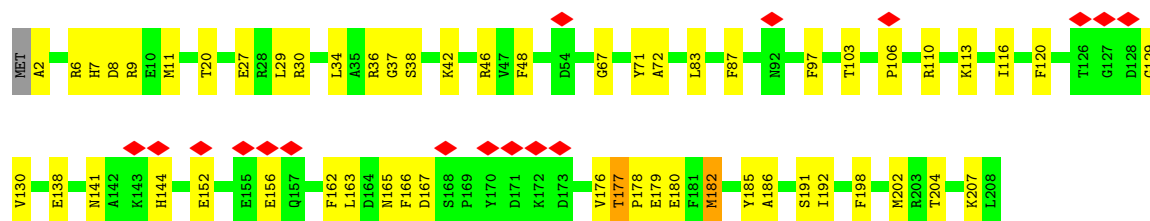
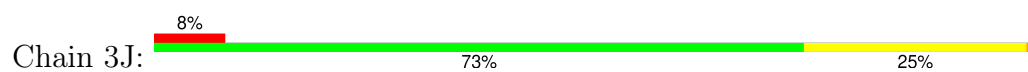
- Molecule 5: Calcyphosin-like protein



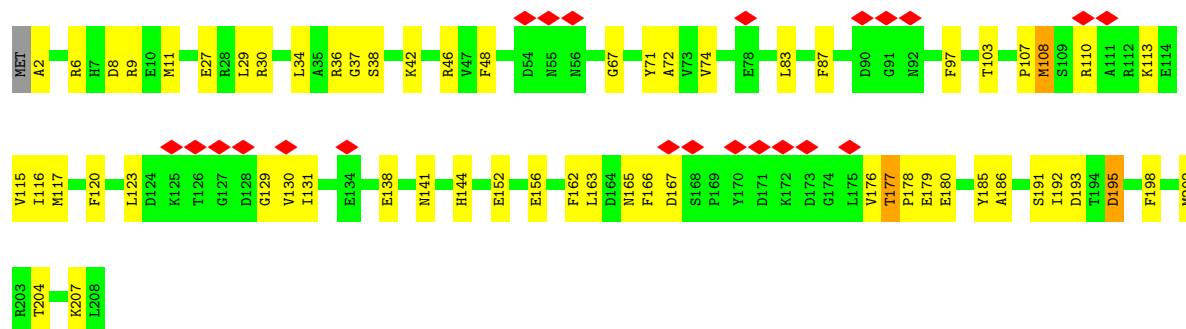
- Molecule 5: Calcyphosin-like protein



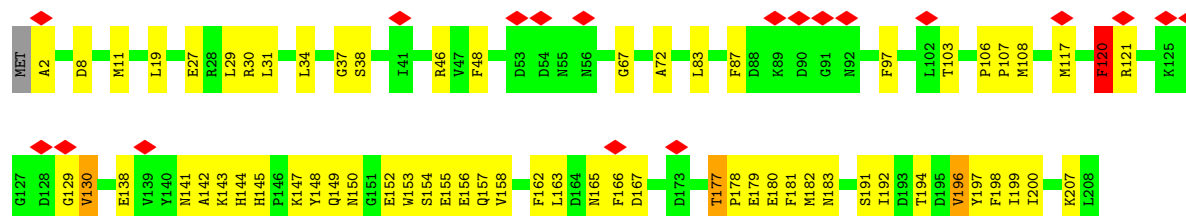
- Molecule 5: Calcyphosin-like protein



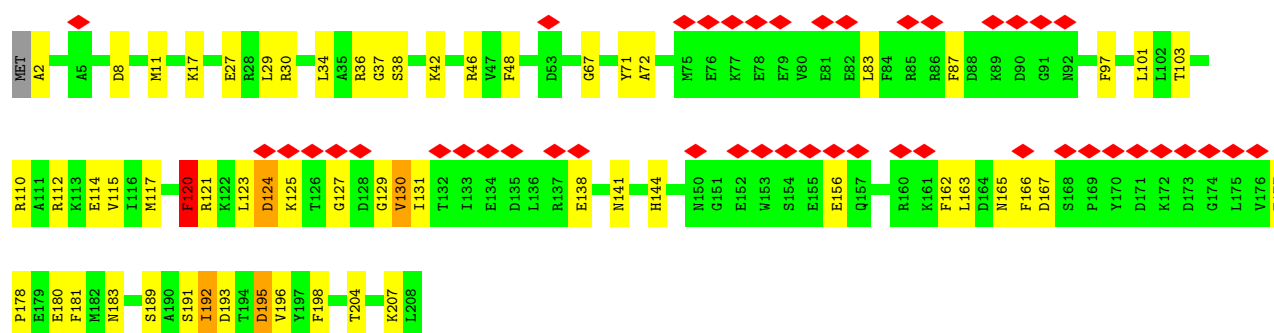
• Molecule 5: Calcyphosin-like protein



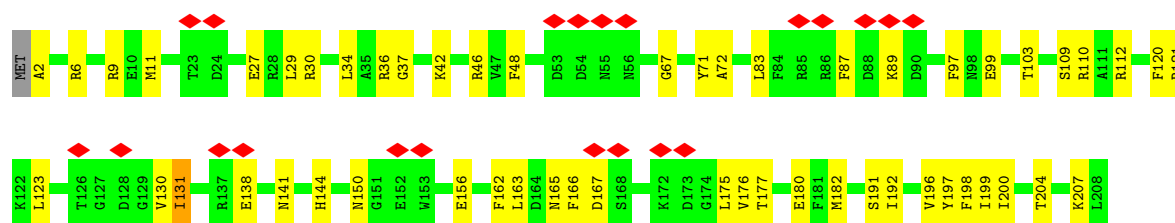
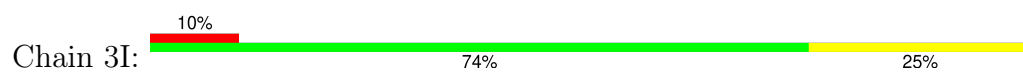
• Molecule 5: Calcyphosin-like protein



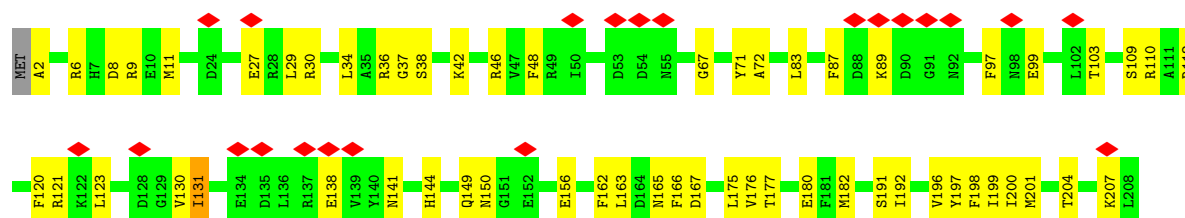
• Molecule 5: Calcyphosin-like protein



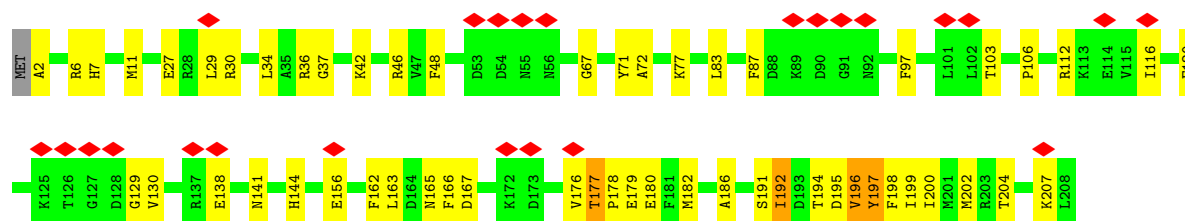
• Molecule 5: Calcyphosin-like protein



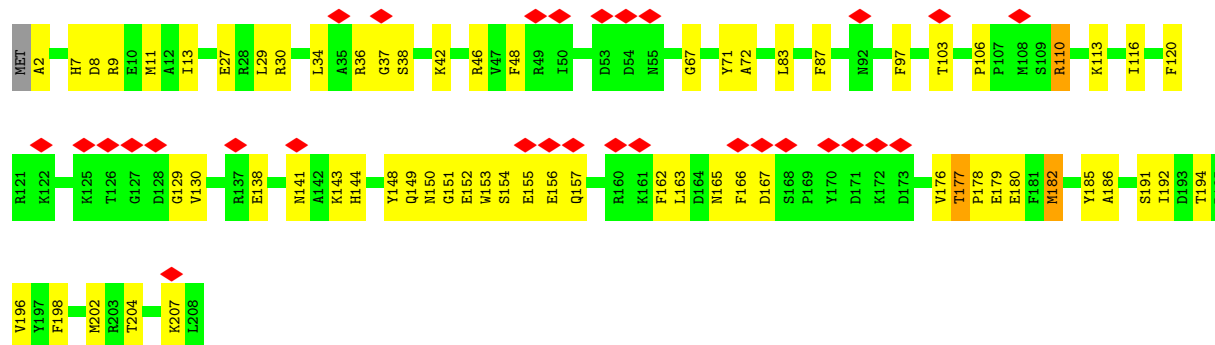
• Molecule 5: Calcyphosin-like protein



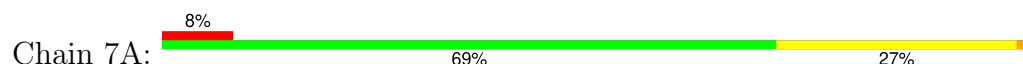
• Molecule 5: Calcyphosin-like protein

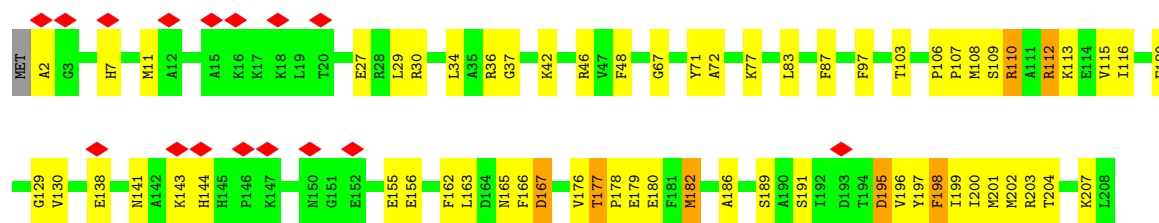


• Molecule 5: Calcyphosin-like protein

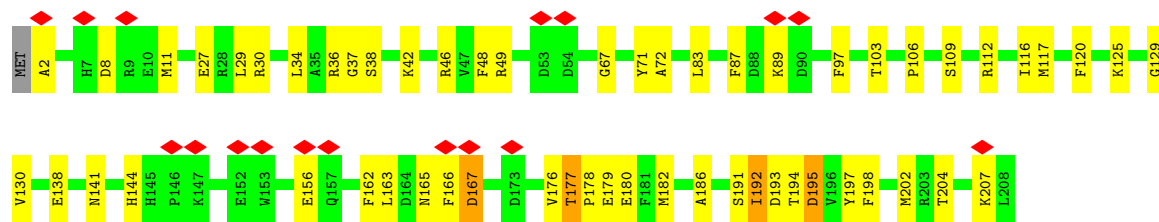
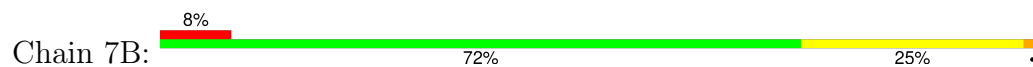


• Molecule 5: Calcyphosin-like protein

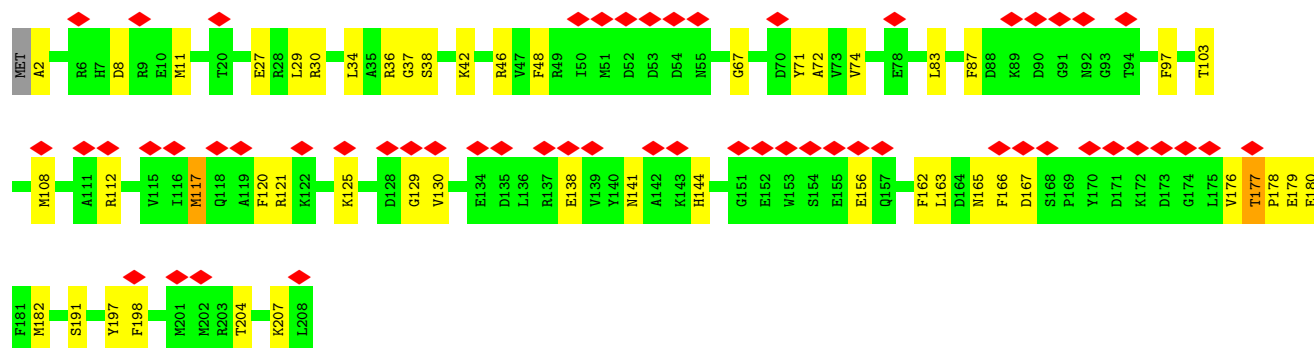
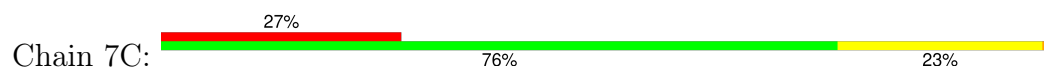




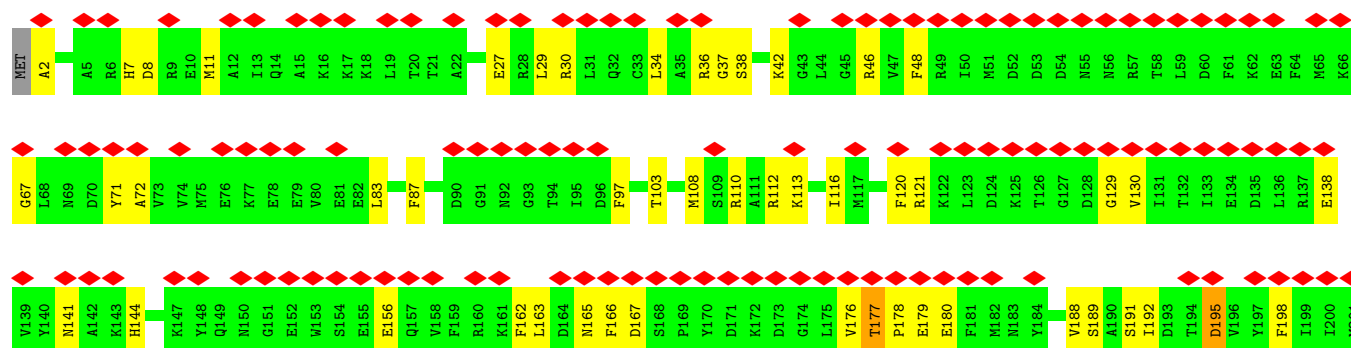
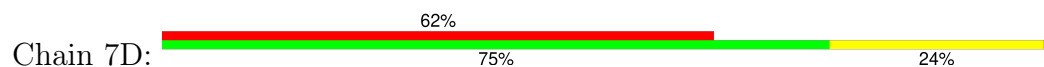
• Molecule 5: Calcyphosin-like protein

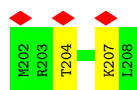


• Molecule 5: Calcyphosin-like protein

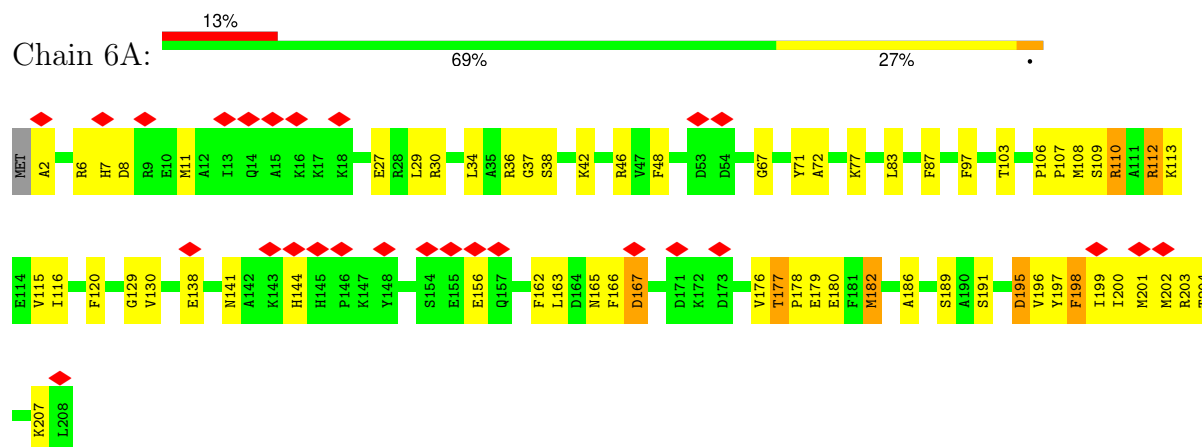


• Molecule 5: Calcyphosin-like protein

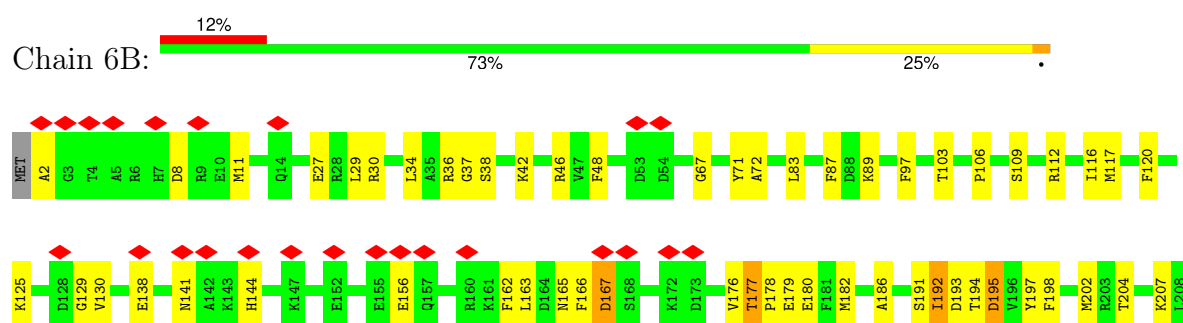




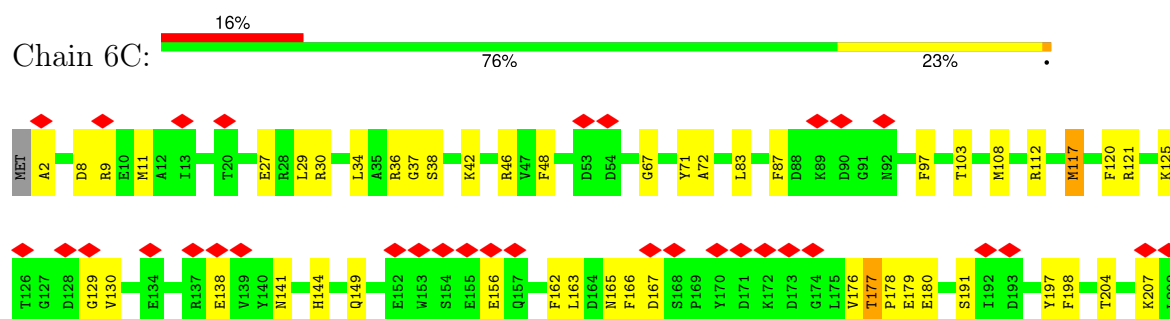
- Molecule 5: Calcyphosin-like protein



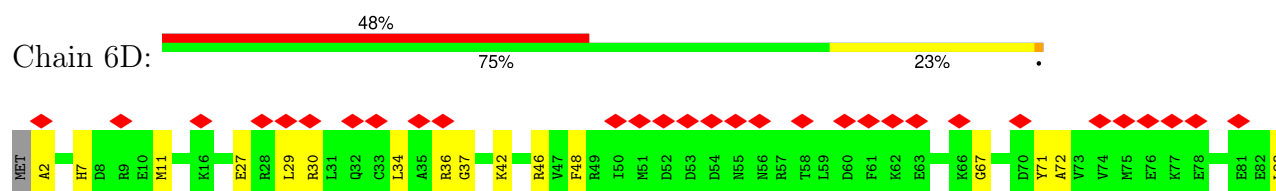
- Molecule 5: Calcyphosin-like protein

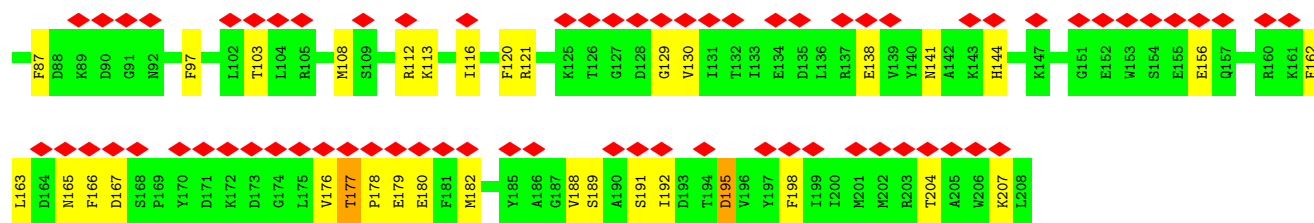


- Molecule 5: Calcyphosin-like protein

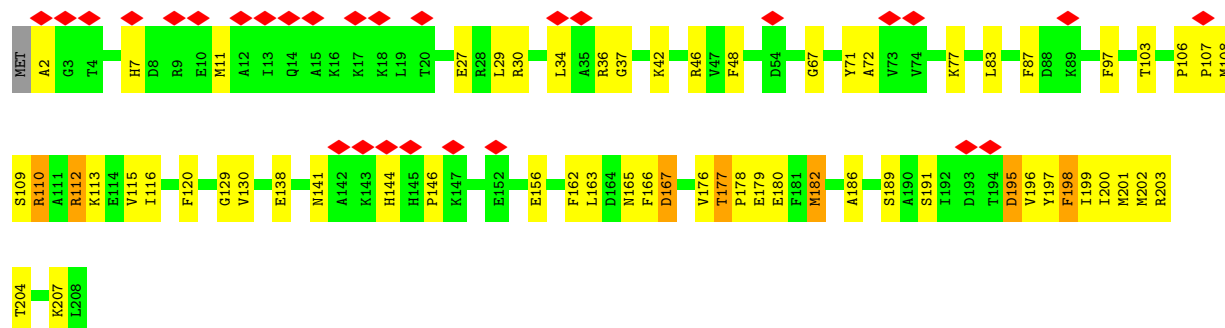
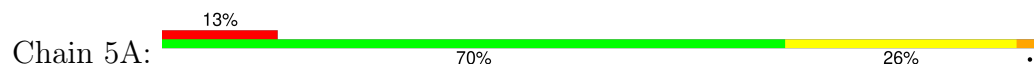


- Molecule 5: Calcyphosin-like protein

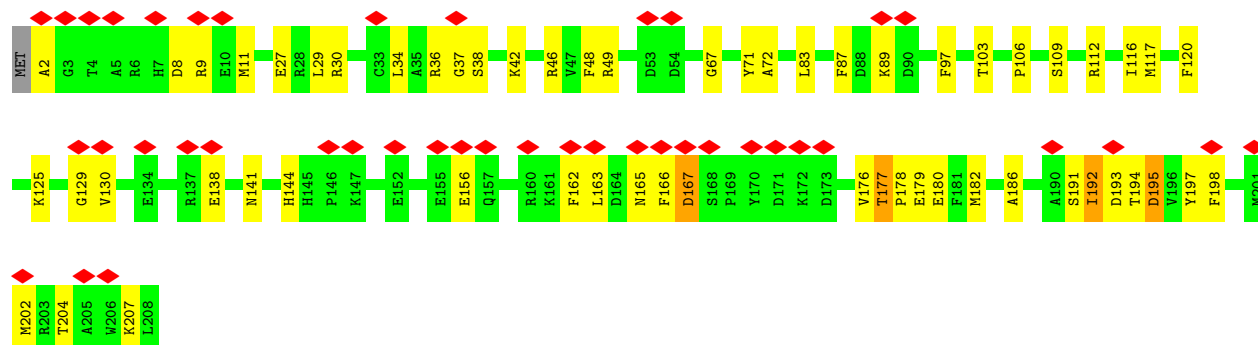




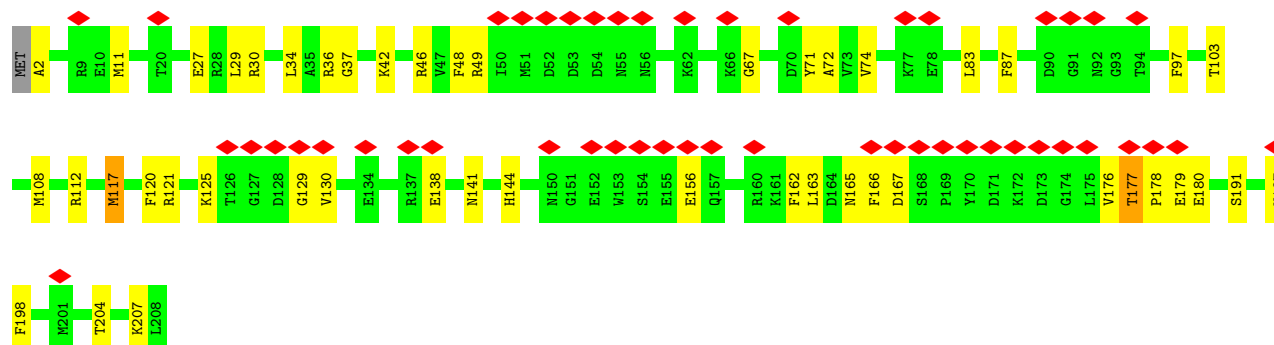
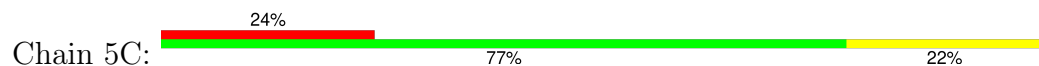
• Molecule 5: Calcyphosin-like protein



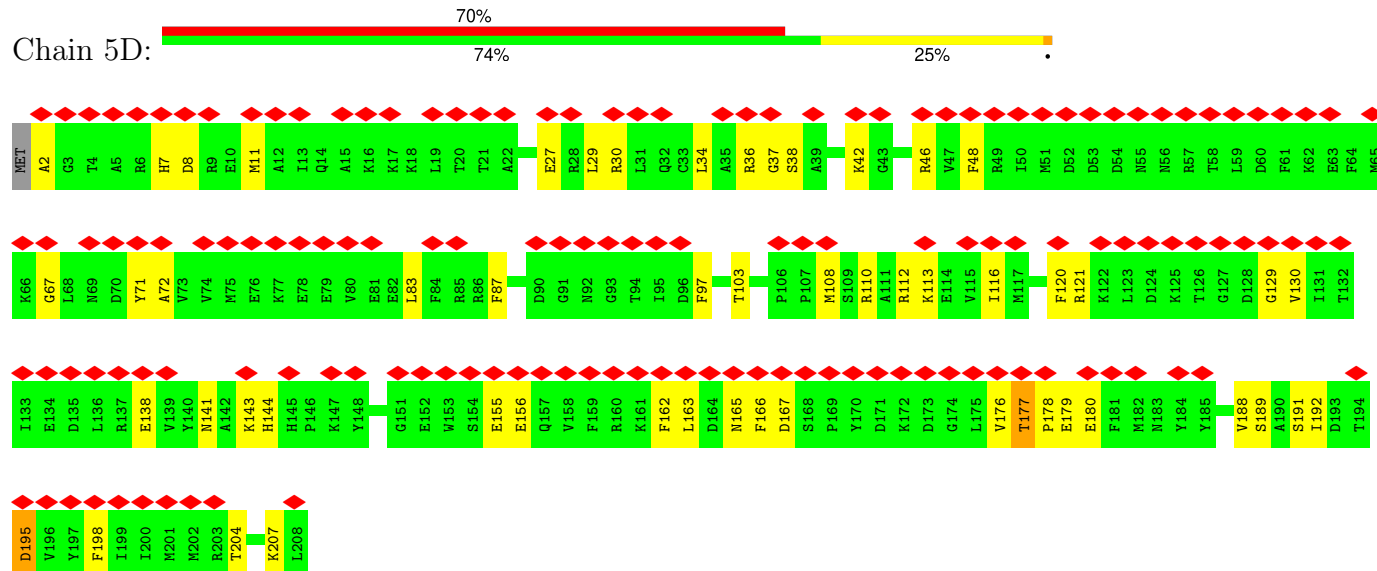
• Molecule 5: Calcyphosin-like protein



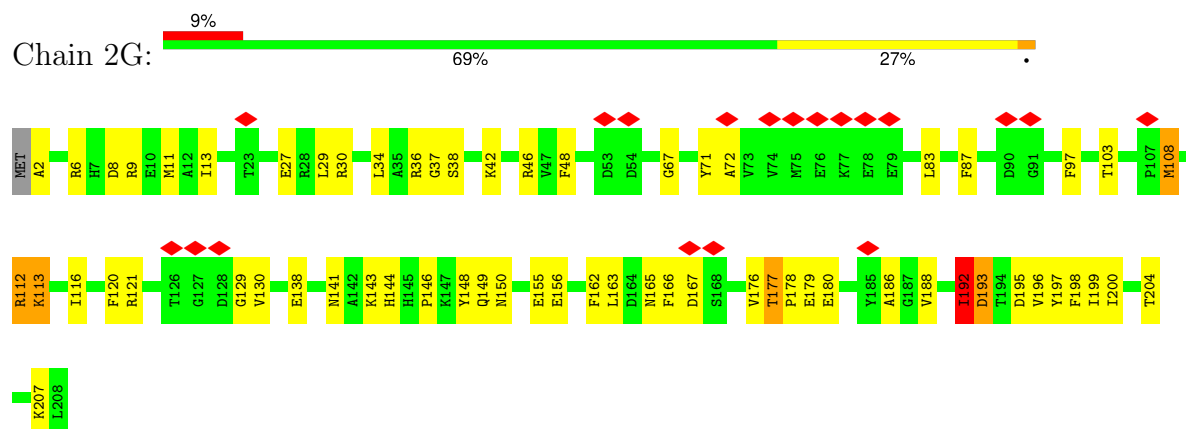
• Molecule 5: Calcyphosin-like protein



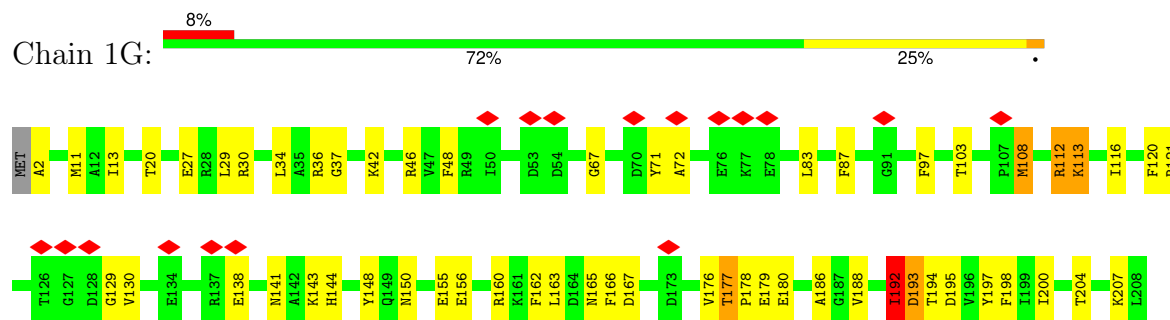
- Molecule 5: Calcyphosin-like protein



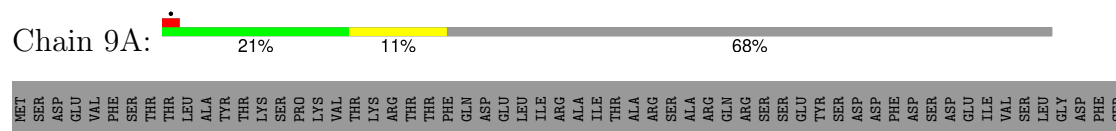
- Molecule 5: Calcyphosin-like protein



- Molecule 5: Calcyphosin-like protein

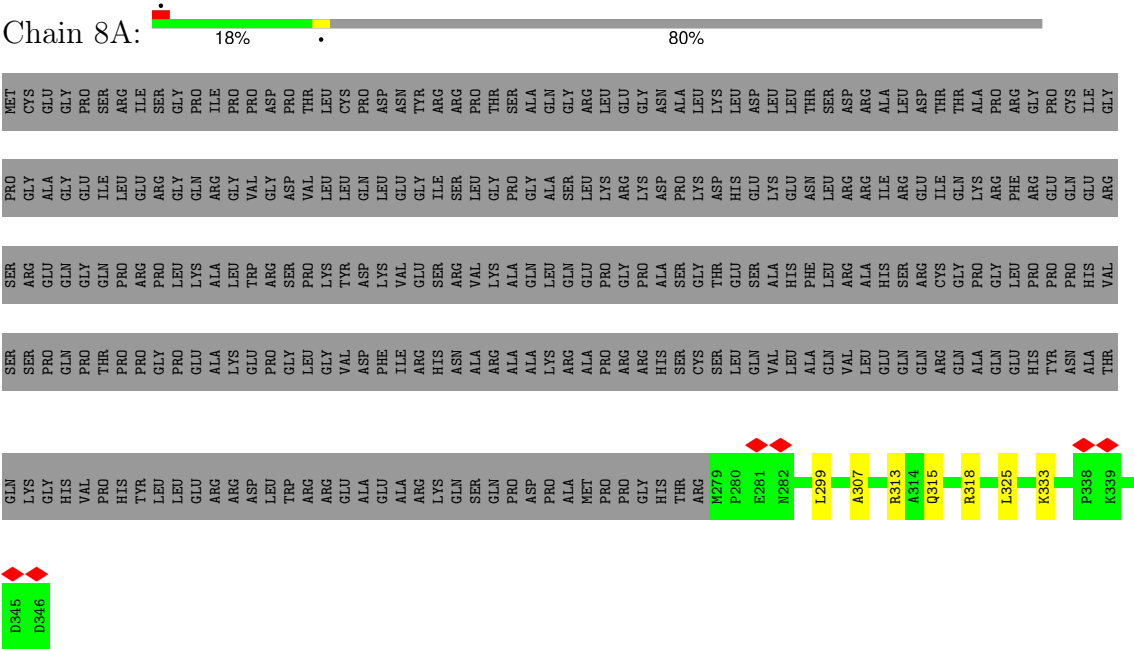


- Molecule 6: Microtubule-associated protein 9

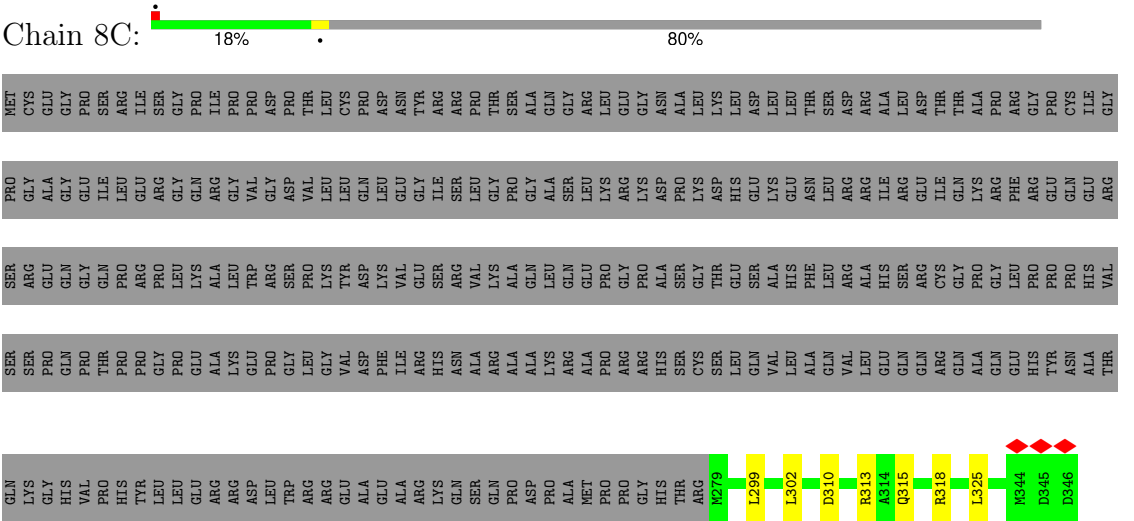




• Molecule 7: Enkurin domain-containing protein 1



• Molecule 7: Enkurin domain-containing protein 1



• Molecule 7: Enkurin domain-containing protein 1

Response	Percentage
Doing a good job	19%
Not doing a good job	80%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, Not provided	
Number of subtomograms used	33196	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	154.44	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	0.000	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.001	Depositor
Map size (Å)	669.552, 554.112, 461.76	wwPDB
Map dimensions	348, 288, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.924, 1.924, 1.924	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A0	0.19	0/3507	0.42	1/4761 (0.0%)
1	A2	0.20	0/3507	0.40	1/4761 (0.0%)
1	A4	0.19	0/3507	0.43	2/4761 (0.0%)
1	A6	0.19	0/3507	0.42	1/4761 (0.0%)
1	B1	0.20	0/3507	0.41	0/4761
1	B3	0.20	0/3460	0.43	0/4697
1	B5	0.18	0/3507	0.40	0/4761
1	C1	0.17	0/3460	0.40	1/4697 (0.0%)
1	C3	0.19	0/3454	0.43	0/4689
1	C5	0.18	0/3507	0.41	0/4761
1	D1	0.18	0/3448	0.42	0/4681
1	D3	0.18	0/3448	0.42	1/4681 (0.0%)
1	D5	0.22	0/3448	0.45	0/4681
1	E1	0.18	0/3501	0.44	0/4753
1	E3	0.18	0/3507	0.44	0/4761
1	E5	0.17	0/3501	0.42	0/4753
1	F1	0.19	0/3448	0.42	0/4681
1	F3	0.18	0/3448	0.44	0/4681
1	F5	0.18	0/3448	0.41	0/4681
1	G0	0.23	0/3456	0.43	0/4692
1	G2	0.17	0/3448	0.43	0/4681
1	G4	0.17	0/3462	0.39	0/4700
1	H0	0.18	0/3462	0.43	0/4700
1	H2	0.17	0/3462	0.41	1/4700 (0.0%)
1	H4	0.19	0/3454	0.44	0/4689
1	I0	0.16	0/3507	0.39	0/4761
1	I2	0.17	0/3462	0.39	0/4700
1	I4	0.15	0/3507	0.38	1/4761 (0.0%)
1	I6	0.23	0/3456	0.46	1/4692 (0.0%)
1	J1	0.19	0/3448	0.42	3/4681 (0.1%)
1	J3	0.17	0/3448	0.40	0/4681
1	J5	0.19	0/3454	0.46	0/4689

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	K0	0.19	0/3461	0.42	0/4699
1	K2	0.21	0/3469	0.42	0/4710
1	K4	0.20	0/3514	0.44	0/4771
1	L0	0.21	0/3474	0.43	0/4716
1	L2	0.20	0/3487	0.41	0/4732
1	L4	0.22	0/3467	0.44	0/4707
1	L6	0.30	0/3467	0.51	0/4707
1	M0	0.21	0/3467	0.45	0/4707
1	M2	0.21	0/3450	0.42	0/4684
1	M4	0.21	0/3467	0.44	0/4707
1	M6	0.24	0/3501	0.62	3/4753 (0.1%)
1	N0	0.20	0/3507	0.48	4/4761 (0.1%)
1	N2	0.20	0/3507	0.45	3/4761 (0.1%)
1	N4	0.19	0/3507	0.47	5/4761 (0.1%)
1	N6	0.19	0/3507	0.43	3/4761 (0.1%)
1	O0	0.19	0/3523	0.40	0/4783
1	O2	0.19	0/3523	0.41	0/4783
1	O4	0.16	0/3507	0.37	0/4761
1	O6	0.19	0/3523	0.40	0/4783
1	P0	0.18	0/3523	0.40	0/4783
1	P2	0.17	0/3507	0.38	0/4761
1	P4	0.19	0/3514	0.43	0/4771
1	P6	0.17	0/3507	0.35	0/4761
1	Q1	0.19	0/3514	0.42	0/4771
1	Q3	0.17	0/3514	0.40	0/4771
1	Q5	0.19	0/3514	0.44	1/4771 (0.0%)
1	R1	0.17	0/3507	0.41	0/4761
1	R3	0.20	0/3514	0.48	2/4771 (0.0%)
1	R5	0.20	0/3514	0.44	0/4771
1	S1	0.18	0/3456	0.43	0/4692
1	S3	0.18	0/3456	0.42	1/4692 (0.0%)
1	S5	0.19	0/3456	0.44	0/4692
1	T1	0.17	0/3456	0.40	0/4692
1	T3	0.18	0/3442	0.41	0/4673
1	T5	0.16	0/3456	0.38	0/4692
1	U1	0.19	0/3462	0.44	1/4700 (0.0%)
1	U3	0.19	0/3456	0.40	1/4692 (0.0%)
1	U5	0.16	0/3456	0.40	1/4692 (0.0%)
1	V0	0.16	0/3507	0.39	0/4761
1	V2	0.25	0/3456	0.46	0/4692
1	V4	0.16	0/3507	0.42	1/4761 (0.0%)
1	W0	0.19	0/3501	0.46	1/4753 (0.0%)
1	W2	0.20	0/3448	0.43	0/4681

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	W4	0.19	0/3507	0.48	2/4761 (0.0%)
1	W6	0.19	0/3456	0.44	0/4692
2	A1	0.27	0/3475	0.50	2/4709 (0.0%)
2	A3	0.25	0/3475	0.50	3/4709 (0.1%)
2	A5	0.25	0/3475	0.49	3/4709 (0.1%)
2	B0	0.23	0/3431	0.46	3/4649 (0.1%)
2	B2	0.22	0/3423	0.46	1/4638 (0.0%)
2	B4	0.25	0/3448	0.50	2/4673 (0.0%)
2	C0	0.21	0/3431	0.47	1/4649 (0.0%)
2	C2	0.21	0/3423	0.46	3/4638 (0.1%)
2	C4	0.20	0/3431	0.45	1/4649 (0.0%)
2	D0	0.24	0/3423	0.45	0/4638
2	D2	0.25	0/3423	0.49	0/4638
2	D4	0.20	0/3423	0.53	6/4638 (0.1%)
2	D6	0.25	0/3423	0.45	0/4638
2	E0	0.23	0/3423	0.47	4/4638 (0.1%)
2	E2	0.25	0/3423	0.51	3/4638 (0.1%)
2	E4	0.20	0/3423	0.48	3/4638 (0.1%)
2	E6	0.18	0/3423	0.41	0/4638
2	F0	0.21	0/3423	0.48	6/4638 (0.1%)
2	F2	0.23	0/3423	0.51	5/4638 (0.1%)
2	F4	0.20	0/3423	0.49	4/4638 (0.1%)
2	F6	0.22	0/3423	0.50	1/4638 (0.0%)
2	G1	0.20	0/3423	0.48	5/4638 (0.1%)
2	G3	0.22	0/3448	0.54	5/4673 (0.1%)
2	G5	0.19	0/3423	0.44	0/4638
2	H1	0.20	0/3423	0.44	1/4638 (0.0%)
2	H3	0.22	0/3436	0.51	2/4656 (0.0%)
2	H5	0.23	0/3423	0.48	3/4638 (0.1%)
2	I1	0.23	0/3423	0.48	1/4638 (0.0%)
2	I3	0.21	0/3443	0.46	1/4666 (0.0%)
2	I5	0.20	0/3423	0.43	1/4638 (0.0%)
2	J0	0.20	0/3431	0.47	2/4649 (0.0%)
2	J2	0.22	0/3423	0.46	2/4638 (0.0%)
2	J4	0.19	0/3423	0.44	1/4638 (0.0%)
2	J6	0.28	0/3423	0.49	2/4638 (0.0%)
2	K1	0.24	0/3466	0.48	3/4697 (0.1%)
2	K3	0.21	0/3466	0.45	1/4697 (0.0%)
2	K5	0.24	0/3466	0.53	3/4697 (0.1%)
2	L1	0.23	0/3423	0.43	2/4638 (0.0%)
2	L3	0.24	0/3423	0.46	1/4638 (0.0%)
2	L5	0.23	0/3423	0.46	1/4638 (0.0%)
2	M1	0.27	0/3457	0.48	1/4685 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	M3	0.22	0/3423	0.46	3/4638 (0.1%)
2	M5	0.26	0/3457	0.51	3/4685 (0.1%)
2	N1	0.23	0/3436	0.51	2/4656 (0.0%)
2	N3	0.24	0/3443	0.56	7/4666 (0.2%)
2	N5	0.25	0/3436	0.62	8/4656 (0.2%)
2	O1	0.26	0/3448	0.49	3/4673 (0.1%)
2	O3	0.26	0/3466	0.48	3/4697 (0.1%)
2	O5	0.22	0/3448	0.46	1/4673 (0.0%)
2	P1	0.22	0/3423	0.41	1/4638 (0.0%)
2	P3	0.21	0/3448	0.46	1/4673 (0.0%)
2	P5	0.22	0/3443	0.46	3/4666 (0.1%)
2	Q0	0.21	0/3423	0.42	1/4638 (0.0%)
2	Q2	0.21	0/3443	0.45	1/4666 (0.0%)
2	Q4	0.20	0/3431	0.45	1/4649 (0.0%)
2	R0	0.20	0/3423	0.41	1/4638 (0.0%)
2	R2	0.21	0/3436	0.54	4/4656 (0.1%)
2	R4	0.17	0/3423	0.43	0/4638
2	R6	0.20	0/3431	0.47	1/4649 (0.0%)
2	S0	0.22	0/3423	0.49	2/4638 (0.0%)
2	S2	0.21	0/3423	0.52	7/4638 (0.2%)
2	S4	0.24	0/3423	0.49	2/4638 (0.0%)
2	S6	0.24	0/3423	0.51	5/4638 (0.1%)
2	T0	0.20	0/3423	0.48	5/4638 (0.1%)
2	T2	0.19	0/3423	0.48	6/4638 (0.1%)
2	T4	0.22	0/3423	0.52	4/4638 (0.1%)
2	T6	0.21	0/3423	0.48	3/4638 (0.1%)
2	U0	0.18	0/3423	0.40	1/4638 (0.0%)
2	U2	0.20	0/3431	0.46	6/4649 (0.1%)
2	U4	0.20	0/3423	0.46	3/4638 (0.1%)
2	U6	0.19	0/3431	0.44	5/4649 (0.1%)
2	V1	0.20	0/3431	0.46	3/4649 (0.1%)
2	V3	0.19	0/3423	0.44	1/4638 (0.0%)
2	V5	0.21	0/3431	0.47	3/4649 (0.1%)
2	W1	0.24	0/3423	0.45	3/4638 (0.1%)
2	W3	0.23	0/3423	0.50	1/4638 (0.0%)
2	W5	0.21	0/3431	0.45	1/4649 (0.0%)
3	X0	0.16	0/1583	0.37	0/2137
3	X1	0.26	0/1583	0.43	0/2137
3	X2	0.26	0/1583	0.42	0/2137
3	X3	0.27	0/1583	0.42	0/2137
4	Y0	0.70	0/1172	1.12	1/1579 (0.1%)
4	Y1	0.69	0/1172	1.12	1/1579 (0.1%)
4	Y2	0.72	0/1172	1.28	5/1579 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	1A	0.73	0/1725	1.00	0/2316
5	1B	0.72	0/1725	0.98	0/2316
5	1C	0.74	0/1725	1.00	0/2316
5	1D	0.72	0/1725	0.98	0/2316
5	1E	0.75	0/1725	1.01	0/2316
5	1F	0.74	0/1725	1.00	0/2316
5	1G	0.72	0/1725	0.97	0/2316
5	2A	0.74	0/1725	1.00	0/2316
5	2B	0.74	0/1725	1.01	0/2316
5	2C	0.74	0/1725	0.99	0/2316
5	2D	0.73	0/1725	0.97	0/2316
5	2E	0.73	0/1725	0.99	0/2316
5	2F	0.74	0/1725	0.99	0/2316
5	2G	0.72	0/1725	0.97	0/2316
5	2H	0.74	0/1725	0.97	1/2316 (0.0%)
5	2I	0.73	0/1725	0.97	1/2316 (0.0%)
5	2J	0.73	0/1725	0.99	0/2316
5	3C	0.74	0/1725	1.01	0/2316
5	3D	0.73	0/1725	0.99	2/2316 (0.1%)
5	3E	0.73	0/1725	1.00	1/2316 (0.0%)
5	3F	0.73	0/1725	0.99	0/2316
5	3G	0.74	0/1725	1.00	0/2316
5	3H	0.73	0/1725	0.99	0/2316
5	3I	0.73	0/1725	0.96	0/2316
5	3J	0.73	0/1725	0.99	0/2316
5	4H	0.73	0/1725	0.99	0/2316
5	4I	0.74	0/1725	0.96	0/2316
5	4J	0.73	0/1725	0.98	0/2316
5	5A	0.73	0/1725	0.98	0/2316
5	5B	0.73	0/1725	0.99	0/2316
5	5C	0.73	0/1725	0.99	0/2316
5	5D	0.72	0/1725	0.96	0/2316
5	6A	0.73	0/1725	0.98	0/2316
5	6B	0.73	0/1725	0.99	0/2316
5	6C	0.73	0/1725	0.99	0/2316
5	6D	0.72	0/1725	0.97	0/2316
5	7A	0.73	0/1725	0.98	0/2316
5	7B	0.73	0/1725	0.99	0/2316
5	7C	0.73	0/1725	0.99	0/2316
5	7D	0.72	0/1725	0.97	0/2316
6	9A	0.76	0/1794	1.05	0/2363
6	9B	0.93	0/1794	1.22	0/2363
7	8A	0.68	0/554	1.19	0/742

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	8B	0.68	0/554	1.19	0/742
7	8C	0.68	0/554	1.19	0/742
All	All	0.33	0/616490	0.55	248/834973 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L6	0	1
2	D2	0	1
2	D6	0	1
5	1A	0	1
5	1B	0	1
5	1E	0	1
5	1F	0	2
5	1G	0	2
5	2B	0	2
5	2C	0	2
5	2D	0	1
5	2E	0	1
5	2F	0	1
5	2G	0	2
5	2J	0	1
5	3C	0	1
5	3G	0	3
5	3I	0	1
5	3J	0	1
5	4I	0	1
5	5A	0	1
5	5B	0	1
5	5C	0	1
5	6A	0	1
5	6B	0	1
5	6C	0	1
5	7A	0	1
5	7B	0	1
5	7C	0	1
All	All	0	36

There are no bond length outliers.

The worst 5 of 248 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M6	284	GLU	CG-CD-OE2	-21.22	69.60	118.40
1	M6	284	GLU	CG-CD-OE1	-20.11	72.15	118.40
2	N5	277	GLY	N-CA-C	16.66	132.72	112.73
4	Y2	228	ASP	N-CA-C	14.74	142.20	110.80
2	D4	271	ALA	N-CA-C	13.40	128.05	108.76

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	1A	110	ARG	Sidechain
5	1B	112	ARG	Sidechain
2	D2	276	ARG	Sidechain
2	D6	276	ARG	Sidechain
1	L6	121	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	A0	3429	0	3340	108	0
1	A2	3429	0	3338	215	0
1	A4	3429	0	3340	222	0
1	A6	3429	0	3338	307	0
1	B1	3429	0	3339	157	0
1	B3	3383	0	3293	208	0
1	B5	3429	0	3340	165	0
1	C1	3383	0	3291	140	0
1	C3	3377	0	3289	206	0
1	C5	3429	0	3335	148	0
1	D1	3371	0	3282	123	0
1	D3	3371	0	3286	142	0
1	D5	3371	0	3285	128	0
1	E1	3423	0	3332	160	0
1	E3	3429	0	3340	138	0
1	E5	3423	0	3334	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F1	3371	0	3286	177	0
1	F3	3371	0	3286	144	0
1	F5	3371	0	3285	124	0
1	G0	3379	0	3290	236	0
1	G2	3371	0	3282	144	0
1	G4	3385	0	3292	146	0
1	H0	3385	0	3292	264	0
1	H2	3385	0	3292	164	0
1	H4	3377	0	3289	175	0
1	I0	3429	0	3340	128	0
1	I2	3385	0	3295	150	0
1	I4	3429	0	3340	133	0
1	I6	3379	0	3290	99	0
1	J1	3371	0	3283	133	0
1	J3	3371	0	3285	220	0
1	J5	3377	0	3290	173	0
1	K0	3384	0	3300	117	0
1	K2	3392	0	3304	119	0
1	K4	3436	0	3347	176	0
1	L0	3397	0	3300	154	0
1	L2	3410	0	3316	144	0
1	L4	3390	0	3299	163	0
1	L6	3390	0	3300	116	0
1	M0	3390	0	3300	157	0
1	M2	3373	0	3280	125	0
1	M4	3390	0	3299	107	0
1	M6	3423	0	3333	78	0
1	N0	3429	0	3333	166	0
1	N2	3429	0	3336	236	0
1	N4	3429	0	3336	251	0
1	N6	3429	0	3338	199	0
1	O0	3445	0	3353	132	0
1	O2	3445	0	3355	234	0
1	O4	3429	0	3339	255	0
1	O6	3445	0	3355	243	0
1	P0	3445	0	3354	88	0
1	P2	3429	0	3339	196	0
1	P4	3436	0	3349	186	0
1	P6	3429	0	3338	225	0
1	Q1	3436	0	3347	170	0
1	Q3	3436	0	3345	281	0
1	Q5	3436	0	3349	201	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R1	3429	0	3333	255	0
1	R3	3436	0	3349	258	0
1	R5	3436	0	3347	267	0
1	S1	3379	0	3290	251	0
1	S3	3379	0	3288	254	0
1	S5	3379	0	3287	279	0
1	T1	3379	0	3290	301	0
1	T3	3365	0	3281	294	0
1	T5	3379	0	3287	305	0
1	U1	3385	0	3291	227	0
1	U3	3379	0	3290	202	0
1	U5	3379	0	3290	295	0
1	V0	3429	0	3340	257	0
1	V2	3379	0	3290	233	0
1	V4	3429	0	3338	301	0
1	W0	3423	0	3335	169	0
1	W2	3371	0	3286	200	0
1	W4	3429	0	3340	199	0
1	W6	3379	0	3290	79	0
2	A1	3400	0	3275	101	0
2	A3	3400	0	3275	106	0
2	A5	3400	0	3275	113	0
2	B0	3356	0	3239	100	0
2	B2	3348	0	3236	112	0
2	B4	3373	0	3257	150	0
2	C0	3356	0	3238	135	0
2	C2	3348	0	3235	156	0
2	C4	3356	0	3237	170	0
2	D0	3348	0	3235	152	0
2	D2	3348	0	3236	148	0
2	D4	3348	0	3236	132	0
2	D6	3348	0	3235	92	0
2	E0	3348	0	3234	143	0
2	E2	3348	0	3236	138	0
2	E4	3348	0	3234	133	0
2	E6	3348	0	3234	158	0
2	F0	3348	0	3236	115	0
2	F2	3348	0	3235	117	0
2	F4	3348	0	3232	137	0
2	F6	3348	0	3235	148	0
2	G1	3348	0	3234	92	0
2	G3	3373	0	3257	147	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G5	3348	0	3235	159	0
2	H1	3348	0	3234	100	0
2	H3	3361	0	3244	146	0
2	H5	3348	0	3236	168	0
2	I1	3348	0	3235	163	0
2	I3	3368	0	3249	172	0
2	I5	3348	0	3235	180	0
2	J0	3356	0	3240	64	0
2	J2	3348	0	3236	118	0
2	J4	3348	0	3234	166	0
2	J6	3348	0	3234	128	0
2	K1	3391	0	3269	132	0
2	K3	3391	0	3268	134	0
2	K5	3391	0	3265	168	0
2	L1	3348	0	3234	157	0
2	L3	3348	0	3236	190	0
2	L5	3348	0	3227	238	0
2	M1	3382	0	3262	119	0
2	M3	3348	0	3234	118	0
2	M5	3382	0	3262	74	0
2	N1	3361	0	3243	182	0
2	N3	3368	0	3251	207	0
2	N5	3361	0	3239	269	0
2	O1	3373	0	3254	178	0
2	O3	3391	0	3267	307	0
2	O5	3373	0	3251	336	0
2	P1	3348	0	3236	171	0
2	P3	3373	0	3256	248	0
2	P5	3368	0	3251	253	0
2	Q0	3348	0	3236	199	0
2	Q2	3368	0	3248	364	0
2	Q4	3356	0	3236	307	0
2	R0	3348	0	3236	247	0
2	R2	3361	0	3241	363	0
2	R4	3348	0	3233	394	0
2	R6	3356	0	3239	152	0
2	S0	3348	0	3235	235	0
2	S2	3348	0	3233	355	0
2	S4	3348	0	3233	313	0
2	S6	3348	0	3235	314	0
2	T0	3348	0	3234	257	0
2	T2	3348	0	3235	218	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	T4	3348	0	3235	251	0
2	T6	3348	0	3233	240	0
2	U0	3348	0	3234	161	0
2	U2	3356	0	3237	231	0
2	U4	3348	0	3235	247	0
2	U6	3356	0	3234	136	0
2	V1	3356	0	3240	308	0
2	V3	3348	0	3234	285	0
2	V5	3356	0	3238	167	0
2	W1	3348	0	3233	243	0
2	W3	3348	0	3230	230	0
2	W5	3356	0	3237	245	0
3	X0	1549	0	1577	75	0
3	X1	1549	0	1580	178	0
3	X2	1549	0	1581	177	0
3	X3	1549	0	1577	264	0
4	Y0	1151	0	1144	44	0
4	Y1	1151	0	1142	76	0
4	Y2	1151	0	1143	51	0
5	1A	1693	0	1667	66	0
5	1B	1693	0	1665	89	0
5	1C	1693	0	1664	99	0
5	1D	1693	0	1663	96	0
5	1E	1693	0	1665	92	0
5	1F	1693	0	1664	72	0
5	1G	1693	0	1661	123	0
5	2A	1693	0	1667	69	0
5	2B	1693	0	1666	91	0
5	2C	1693	0	1665	92	0
5	2D	1693	0	1665	75	0
5	2E	1693	0	1663	66	0
5	2F	1693	0	1664	67	0
5	2G	1693	0	1662	135	0
5	2H	1693	0	1667	76	0
5	2I	1693	0	1665	58	0
5	2J	1693	0	1667	94	0
5	3C	1693	0	1666	92	0
5	3D	1693	0	1665	118	0
5	3E	1693	0	1665	86	0
5	3F	1693	0	1663	66	0
5	3G	1693	0	1663	61	0
5	3H	1693	0	1667	90	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	3I	1693	0	1661	92	0
5	3J	1693	0	1667	72	0
5	4H	1693	0	1666	150	0
5	4I	1693	0	1663	124	0
5	4J	1693	0	1667	88	0
5	5A	1693	0	1664	108	0
5	5B	1693	0	1662	75	0
5	5C	1693	0	1663	63	0
5	5D	1693	0	1666	58	0
5	6A	1693	0	1665	103	0
5	6B	1693	0	1662	78	0
5	6C	1693	0	1663	81	0
5	6D	1693	0	1666	57	0
5	7A	1693	0	1664	125	0
5	7B	1693	0	1662	84	0
5	7C	1693	0	1663	67	0
5	7D	1693	0	1666	57	0
6	9A	1773	0	1833	394	0
6	9B	1773	0	1823	422	0
7	8A	549	0	577	31	0
7	8B	549	0	578	6	0
7	8C	549	0	576	35	0
8	A0	32	0	12	1	0
8	A2	32	0	12	0	0
8	A4	32	0	12	0	0
8	A6	32	0	12	0	0
8	B1	32	0	12	0	0
8	B3	32	0	12	0	0
8	B5	32	0	12	1	0
8	C1	32	0	12	0	0
8	C3	32	0	12	0	0
8	C5	32	0	12	1	0
8	D1	32	0	12	0	0
8	D3	32	0	12	2	0
8	D5	32	0	12	1	0
8	E1	32	0	12	1	0
8	E3	32	0	12	0	0
8	E5	32	0	12	0	0
8	F1	32	0	12	1	0
8	F3	32	0	12	0	0
8	F5	32	0	12	1	0
8	G0	32	0	12	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	G2	32	0	12	1	0
8	G4	32	0	12	1	0
8	H0	32	0	12	0	0
8	H2	32	0	12	0	0
8	H4	32	0	12	0	0
8	I0	32	0	12	1	0
8	I2	32	0	12	1	0
8	I4	32	0	12	0	0
8	I6	32	0	12	1	0
8	J1	32	0	12	1	0
8	J3	32	0	12	1	0
8	J5	32	0	12	1	0
8	K0	32	0	12	2	0
8	K2	32	0	12	1	0
8	K4	32	0	12	1	0
8	L0	32	0	12	0	0
8	L2	32	0	12	0	0
8	L4	32	0	12	0	0
8	L6	32	0	12	0	0
8	M0	32	0	12	0	0
8	M2	32	0	12	1	0
8	M4	32	0	12	1	0
8	M6	32	0	12	0	0
8	N0	32	0	12	8	0
8	N2	32	0	12	0	0
8	N4	32	0	12	15	0
8	N6	32	0	11	53	0
8	O0	32	0	12	8	0
8	O2	32	0	12	5	0
8	O4	32	0	12	23	0
8	O6	32	0	11	55	0
8	P0	32	0	11	9	0
8	P1	32	0	12	6	0
8	P4	32	0	12	24	0
8	P6	32	0	12	74	0
8	Q1	32	0	12	16	0
8	Q3	32	0	12	8	0
8	Q5	32	0	12	58	0
8	R1	32	0	12	21	0
8	R3	32	0	12	2	0
8	R5	32	0	12	41	0
8	S1	32	0	12	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	S3	32	0	12	11	0
8	S5	32	0	12	38	0
8	T1	32	0	12	7	0
8	T3	32	0	12	13	0
8	T5	32	0	12	45	0
8	U1	32	0	12	8	0
8	U3	32	0	12	7	0
8	U5	32	0	12	37	0
8	V0	32	0	12	9	0
8	V2	32	0	12	5	0
8	V4	32	0	12	8	0
8	W0	32	0	12	8	0
8	W2	32	0	12	6	0
8	W4	32	0	12	7	0
8	W6	32	0	12	20	0
9	A1	28	0	12	0	0
9	A3	28	0	12	0	0
9	A5	28	0	12	0	0
9	B0	28	0	12	0	0
9	B2	28	0	12	0	0
9	B4	28	0	12	0	0
9	C0	28	0	12	1	0
9	C2	28	0	12	0	0
9	C4	28	0	12	1	0
9	D0	28	0	12	0	0
9	D2	28	0	12	2	0
9	D4	28	0	12	2	0
9	D6	28	0	12	2	0
9	E0	28	0	12	0	0
9	E2	28	0	12	0	0
9	E4	28	0	12	0	0
9	E6	28	0	12	1	0
9	F0	28	0	12	1	0
9	F2	28	0	12	0	0
9	F4	28	0	12	3	0
9	F6	28	0	12	1	0
9	G1	28	0	12	2	0
9	G3	28	0	12	0	0
9	G5	28	0	12	0	0
9	H1	28	0	12	0	0
9	H3	28	0	12	0	0
9	H5	28	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	I1	28	0	12	0	0
9	I3	28	0	12	0	0
9	I5	28	0	12	0	0
9	J0	28	0	12	0	0
9	J2	28	0	12	0	0
9	J4	28	0	12	1	0
9	J6	28	0	12	0	0
9	K1	28	0	12	0	0
9	K3	28	0	12	0	0
9	K5	28	0	12	0	0
9	L1	28	0	12	1	0
9	L3	28	0	12	0	0
9	L5	28	0	12	0	0
9	M1	28	0	12	0	0
9	M3	28	0	12	0	0
9	M5	28	0	12	0	0
9	N1	28	0	12	2	0
9	N3	28	0	12	6	0
9	N5	28	0	11	29	0
9	O1	28	0	12	3	0
9	O3	28	0	12	1	0
9	O5	28	0	12	36	0
9	P1	28	0	12	3	0
9	P3	28	0	12	3	0
9	P5	28	0	12	23	0
9	Q0	28	0	12	4	0
9	Q2	28	0	12	1	0
9	Q4	28	0	12	23	0
9	R0	28	0	11	5	0
9	R2	28	0	12	9	0
9	R4	28	0	12	19	0
9	R6	28	0	11	28	0
9	S0	28	0	11	4	0
9	S2	28	0	12	8	0
9	S4	28	0	12	5	0
9	S6	28	0	12	52	0
9	T0	28	0	12	8	0
9	T2	28	0	12	8	0
9	T4	28	0	12	13	0
9	T6	28	0	12	41	0
9	U0	28	0	12	3	0
9	U2	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	U4	28	0	12	4	0
9	U6	28	0	12	9	0
9	V1	28	0	12	8	0
9	V3	28	0	12	3	0
9	V5	28	0	12	5	0
9	W1	28	0	12	6	0
9	W3	28	0	12	0	0
9	W5	28	0	12	8	0
All	All	607834	0	588343	21159	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 18.

The worst 5 of 21159 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)
1:H2:60:LYS:CE	1:I2:282:TYR:CZ	1.75	1.68
2:L5:86:ARG:HD2	2:M5:281:TYR:CB	1.20	1.67
1:T1:89:PRO:CG	1:U1:280:LYS:HD3	1.25	1.66
1:K4:60:LYS:HE2	1:L4:282:TYR:CE2	1.29	1.66
1:J3:29:GLY:CA	5:2G:196:VAL:HG21	1.27	1.65

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	A0	437/451 (97%)	426 (98%)	11 (2%)	0	100	100
1	A2	437/451 (97%)	425 (97%)	12 (3%)	0	100	100
1	A4	437/451 (97%)	425 (97%)	11 (2%)	1 (0%)	43	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A6	437/451 (97%)	428 (98%)	9 (2%)	0	100	100
1	B1	437/451 (97%)	420 (96%)	17 (4%)	0	100	100
1	B3	428/451 (95%)	415 (97%)	13 (3%)	0	100	100
1	B5	437/451 (97%)	420 (96%)	17 (4%)	0	100	100
1	C1	428/451 (95%)	412 (96%)	16 (4%)	0	100	100
1	C3	427/451 (95%)	412 (96%)	15 (4%)	0	100	100
1	C5	437/451 (97%)	424 (97%)	13 (3%)	0	100	100
1	D1	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
1	D3	426/451 (94%)	411 (96%)	15 (4%)	0	100	100
1	D5	426/451 (94%)	409 (96%)	17 (4%)	0	100	100
1	E1	436/451 (97%)	412 (94%)	24 (6%)	0	100	100
1	E3	437/451 (97%)	418 (96%)	19 (4%)	0	100	100
1	E5	436/451 (97%)	421 (97%)	15 (3%)	0	100	100
1	F1	426/451 (94%)	410 (96%)	16 (4%)	0	100	100
1	F3	426/451 (94%)	412 (97%)	14 (3%)	0	100	100
1	F5	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
1	G0	427/451 (95%)	412 (96%)	15 (4%)	0	100	100
1	G2	426/451 (94%)	419 (98%)	7 (2%)	0	100	100
1	G4	428/451 (95%)	422 (99%)	6 (1%)	0	100	100
1	H0	428/451 (95%)	414 (97%)	14 (3%)	0	100	100
1	H2	428/451 (95%)	420 (98%)	8 (2%)	0	100	100
1	H4	427/451 (95%)	416 (97%)	11 (3%)	0	100	100
1	I0	437/451 (97%)	424 (97%)	13 (3%)	0	100	100
1	I2	428/451 (95%)	416 (97%)	12 (3%)	0	100	100
1	I4	437/451 (97%)	427 (98%)	10 (2%)	0	100	100
1	I6	427/451 (95%)	414 (97%)	13 (3%)	0	100	100
1	J1	426/451 (94%)	415 (97%)	11 (3%)	0	100	100
1	J3	426/451 (94%)	410 (96%)	16 (4%)	0	100	100
1	J5	427/451 (95%)	411 (96%)	16 (4%)	0	100	100
1	K0	428/451 (95%)	417 (97%)	11 (3%)	0	100	100
1	K2	429/451 (95%)	418 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K4	438/451 (97%)	428 (98%)	10 (2%)	0	100	100
1	L0	430/451 (95%)	417 (97%)	13 (3%)	0	100	100
1	L2	432/451 (96%)	419 (97%)	13 (3%)	0	100	100
1	L4	429/451 (95%)	420 (98%)	9 (2%)	0	100	100
1	L6	429/451 (95%)	418 (97%)	10 (2%)	1 (0%)	43	78
1	M0	429/451 (95%)	417 (97%)	12 (3%)	0	100	100
1	M2	426/451 (94%)	411 (96%)	15 (4%)	0	100	100
1	M4	429/451 (95%)	418 (97%)	11 (3%)	0	100	100
1	M6	436/451 (97%)	419 (96%)	17 (4%)	0	100	100
1	N0	437/451 (97%)	424 (97%)	12 (3%)	1 (0%)	43	78
1	N2	437/451 (97%)	427 (98%)	10 (2%)	0	100	100
1	N4	437/451 (97%)	429 (98%)	8 (2%)	0	100	100
1	N6	437/451 (97%)	424 (97%)	13 (3%)	0	100	100
1	O0	439/451 (97%)	424 (97%)	15 (3%)	0	100	100
1	O2	439/451 (97%)	429 (98%)	10 (2%)	0	100	100
1	O4	437/451 (97%)	429 (98%)	8 (2%)	0	100	100
1	O6	439/451 (97%)	424 (97%)	15 (3%)	0	100	100
1	P0	439/451 (97%)	420 (96%)	19 (4%)	0	100	100
1	P2	437/451 (97%)	425 (97%)	12 (3%)	0	100	100
1	P4	438/451 (97%)	426 (97%)	12 (3%)	0	100	100
1	P6	437/451 (97%)	423 (97%)	14 (3%)	0	100	100
1	Q1	438/451 (97%)	423 (97%)	15 (3%)	0	100	100
1	Q3	438/451 (97%)	425 (97%)	13 (3%)	0	100	100
1	Q5	438/451 (97%)	425 (97%)	13 (3%)	0	100	100
1	R1	437/451 (97%)	418 (96%)	19 (4%)	0	100	100
1	R3	438/451 (97%)	427 (98%)	11 (2%)	0	100	100
1	R5	438/451 (97%)	420 (96%)	18 (4%)	0	100	100
1	S1	427/451 (95%)	409 (96%)	18 (4%)	0	100	100
1	S3	427/451 (95%)	417 (98%)	10 (2%)	0	100	100
1	S5	427/451 (95%)	413 (97%)	14 (3%)	0	100	100
1	T1	427/451 (95%)	417 (98%)	10 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T3	425/451 (94%)	412 (97%)	13 (3%)	0	100	100
1	T5	427/451 (95%)	413 (97%)	14 (3%)	0	100	100
1	U1	428/451 (95%)	415 (97%)	13 (3%)	0	100	100
1	U3	427/451 (95%)	418 (98%)	9 (2%)	0	100	100
1	U5	427/451 (95%)	417 (98%)	10 (2%)	0	100	100
1	V0	437/451 (97%)	422 (97%)	14 (3%)	1 (0%)	43	78
1	V2	427/451 (95%)	416 (97%)	11 (3%)	0	100	100
1	V4	437/451 (97%)	428 (98%)	9 (2%)	0	100	100
1	W0	436/451 (97%)	420 (96%)	16 (4%)	0	100	100
1	W2	426/451 (94%)	414 (97%)	12 (3%)	0	100	100
1	W4	437/451 (97%)	415 (95%)	22 (5%)	0	100	100
1	W6	427/451 (95%)	408 (96%)	19 (4%)	0	100	100
2	A1	431/445 (97%)	411 (95%)	20 (5%)	0	100	100
2	A3	431/445 (97%)	413 (96%)	17 (4%)	1 (0%)	43	78
2	A5	431/445 (97%)	415 (96%)	15 (4%)	1 (0%)	43	78
2	B0	425/445 (96%)	409 (96%)	16 (4%)	0	100	100
2	B2	424/445 (95%)	404 (95%)	20 (5%)	0	100	100
2	B4	428/445 (96%)	413 (96%)	13 (3%)	2 (0%)	24	63
2	C0	425/445 (96%)	411 (97%)	13 (3%)	1 (0%)	43	78
2	C2	424/445 (95%)	406 (96%)	17 (4%)	1 (0%)	43	78
2	C4	425/445 (96%)	407 (96%)	16 (4%)	2 (0%)	24	63
2	D0	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
2	D2	424/445 (95%)	397 (94%)	26 (6%)	1 (0%)	43	78
2	D4	424/445 (95%)	404 (95%)	19 (4%)	1 (0%)	43	78
2	D6	424/445 (95%)	399 (94%)	25 (6%)	0	100	100
2	E0	424/445 (95%)	404 (95%)	20 (5%)	0	100	100
2	E2	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
2	E4	424/445 (95%)	405 (96%)	19 (4%)	0	100	100
2	E6	424/445 (95%)	410 (97%)	13 (3%)	1 (0%)	43	78
2	F0	424/445 (95%)	410 (97%)	13 (3%)	1 (0%)	43	78
2	F2	424/445 (95%)	407 (96%)	17 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F4	424/445 (95%)	409 (96%)	15 (4%)	0	100	100
2	F6	424/445 (95%)	405 (96%)	17 (4%)	2 (0%)	24	63
2	G1	424/445 (95%)	406 (96%)	18 (4%)	0	100	100
2	G3	428/445 (96%)	408 (95%)	19 (4%)	1 (0%)	43	78
2	G5	424/445 (95%)	404 (95%)	20 (5%)	0	100	100
2	H1	424/445 (95%)	406 (96%)	17 (4%)	1 (0%)	43	78
2	H3	426/445 (96%)	412 (97%)	13 (3%)	1 (0%)	43	78
2	H5	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
2	I1	424/445 (95%)	406 (96%)	17 (4%)	1 (0%)	43	78
2	I3	427/445 (96%)	410 (96%)	17 (4%)	0	100	100
2	I5	424/445 (95%)	403 (95%)	21 (5%)	0	100	100
2	J0	425/445 (96%)	408 (96%)	16 (4%)	1 (0%)	43	78
2	J2	424/445 (95%)	402 (95%)	22 (5%)	0	100	100
2	J4	424/445 (95%)	407 (96%)	17 (4%)	0	100	100
2	J6	424/445 (95%)	399 (94%)	24 (6%)	1 (0%)	43	78
2	K1	430/445 (97%)	416 (97%)	13 (3%)	1 (0%)	43	78
2	K3	430/445 (97%)	417 (97%)	13 (3%)	0	100	100
2	K5	430/445 (97%)	414 (96%)	15 (4%)	1 (0%)	43	78
2	L1	424/445 (95%)	403 (95%)	21 (5%)	0	100	100
2	L3	424/445 (95%)	410 (97%)	14 (3%)	0	100	100
2	L5	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
2	M1	429/445 (96%)	416 (97%)	13 (3%)	0	100	100
2	M3	424/445 (95%)	410 (97%)	14 (3%)	0	100	100
2	M5	429/445 (96%)	410 (96%)	18 (4%)	1 (0%)	43	78
2	N1	426/445 (96%)	404 (95%)	21 (5%)	1 (0%)	43	78
2	N3	427/445 (96%)	409 (96%)	18 (4%)	0	100	100
2	N5	426/445 (96%)	404 (95%)	22 (5%)	0	100	100
2	O1	428/445 (96%)	409 (96%)	19 (4%)	0	100	100
2	O3	430/445 (97%)	417 (97%)	13 (3%)	0	100	100
2	O5	428/445 (96%)	408 (95%)	18 (4%)	2 (0%)	24	63
2	P1	424/445 (95%)	404 (95%)	20 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	P3	428/445 (96%)	413 (96%)	14 (3%)	1 (0%)	43	78
2	P5	427/445 (96%)	406 (95%)	21 (5%)	0	100	100
2	Q0	424/445 (95%)	409 (96%)	15 (4%)	0	100	100
2	Q2	427/445 (96%)	408 (96%)	19 (4%)	0	100	100
2	Q4	425/445 (96%)	414 (97%)	11 (3%)	0	100	100
2	R0	424/445 (95%)	406 (96%)	17 (4%)	1 (0%)	43	78
2	R2	426/445 (96%)	408 (96%)	17 (4%)	1 (0%)	43	78
2	R4	424/445 (95%)	407 (96%)	17 (4%)	0	100	100
2	R6	425/445 (96%)	410 (96%)	15 (4%)	0	100	100
2	S0	424/445 (95%)	412 (97%)	12 (3%)	0	100	100
2	S2	424/445 (95%)	404 (95%)	20 (5%)	0	100	100
2	S4	424/445 (95%)	408 (96%)	16 (4%)	0	100	100
2	S6	424/445 (95%)	409 (96%)	14 (3%)	1 (0%)	43	78
2	T0	424/445 (95%)	407 (96%)	17 (4%)	0	100	100
2	T2	424/445 (95%)	407 (96%)	17 (4%)	0	100	100
2	T4	424/445 (95%)	400 (94%)	24 (6%)	0	100	100
2	T6	424/445 (95%)	403 (95%)	21 (5%)	0	100	100
2	U0	424/445 (95%)	413 (97%)	11 (3%)	0	100	100
2	U2	425/445 (96%)	406 (96%)	19 (4%)	0	100	100
2	U4	424/445 (95%)	411 (97%)	12 (3%)	1 (0%)	43	78
2	U6	425/445 (96%)	407 (96%)	17 (4%)	1 (0%)	43	78
2	V1	425/445 (96%)	408 (96%)	16 (4%)	1 (0%)	43	78
2	V3	424/445 (95%)	408 (96%)	15 (4%)	1 (0%)	43	78
2	V5	425/445 (96%)	406 (96%)	18 (4%)	1 (0%)	43	78
2	W1	424/445 (95%)	401 (95%)	23 (5%)	0	100	100
2	W3	424/445 (95%)	404 (95%)	20 (5%)	0	100	100
2	W5	425/445 (96%)	401 (94%)	24 (6%)	0	100	100
3	X0	184/193 (95%)	178 (97%)	6 (3%)	0	100	100
3	X1	184/193 (95%)	177 (96%)	7 (4%)	0	100	100
3	X2	184/193 (95%)	176 (96%)	8 (4%)	0	100	100
3	X3	184/193 (95%)	175 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Y0	136/373 (36%)	132 (97%)	4 (3%)	0	100	100
4	Y1	136/373 (36%)	132 (97%)	4 (3%)	0	100	100
4	Y2	136/373 (36%)	131 (96%)	5 (4%)	0	100	100
5	1A	205/208 (99%)	200 (98%)	4 (2%)	1 (0%)	24	63
5	1B	205/208 (99%)	200 (98%)	4 (2%)	1 (0%)	24	63
5	1C	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	1D	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	1E	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	1F	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	1G	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	2A	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	2B	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	2C	205/208 (99%)	194 (95%)	9 (4%)	2 (1%)	12	48
5	2D	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	2E	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	2F	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	2G	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	2H	205/208 (99%)	198 (97%)	4 (2%)	3 (2%)	8	40
5	2I	205/208 (99%)	196 (96%)	7 (3%)	2 (1%)	12	48
5	2J	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	3C	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	3D	205/208 (99%)	198 (97%)	5 (2%)	2 (1%)	12	48
5	3E	205/208 (99%)	200 (98%)	4 (2%)	1 (0%)	24	63
5	3F	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	3G	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	3H	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	3I	205/208 (99%)	200 (98%)	4 (2%)	1 (0%)	24	63
5	3J	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	4H	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	4I	205/208 (99%)	200 (98%)	4 (2%)	1 (0%)	24	63
5	4J	205/208 (99%)	199 (97%)	4 (2%)	2 (1%)	12	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	5A	205/208 (99%)	194 (95%)	9 (4%)	2 (1%)	12	48
5	5B	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	5C	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	5D	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	6A	205/208 (99%)	194 (95%)	9 (4%)	2 (1%)	12	48
5	6B	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	6C	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	6D	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	7A	205/208 (99%)	194 (95%)	9 (4%)	2 (1%)	12	48
5	7B	205/208 (99%)	198 (97%)	6 (3%)	1 (0%)	24	63
5	7C	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
5	7D	205/208 (99%)	199 (97%)	5 (2%)	1 (0%)	24	63
6	9A	203/647 (31%)	203 (100%)	0	0	100	100
6	9B	203/647 (31%)	203 (100%)	0	0	100	100
7	8A	66/346 (19%)	64 (97%)	2 (3%)	0	100	100
7	8B	66/346 (19%)	64 (97%)	2 (3%)	0	100	100
7	8C	66/346 (19%)	64 (97%)	2 (3%)	0	100	100
All	All	75965/81535 (93%)	73259 (96%)	2618 (3%)	88 (0%)	49	83

5 of 88 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E6	272	PRO
1	A4	40	LYS
2	A5	271	ALA
2	F6	176	SER
1	L6	62	VAL

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	A0	369/378 (98%)	368 (100%)	1 (0%)	86	86
1	A2	369/378 (98%)	368 (100%)	1 (0%)	86	86
1	A4	369/378 (98%)	369 (100%)	0	100	100
1	A6	369/378 (98%)	369 (100%)	0	100	100
1	B1	369/378 (98%)	369 (100%)	0	100	100
1	B3	364/378 (96%)	364 (100%)	0	100	100
1	B5	369/378 (98%)	369 (100%)	0	100	100
1	C1	364/378 (96%)	364 (100%)	0	100	100
1	C3	364/378 (96%)	364 (100%)	0	100	100
1	C5	369/378 (98%)	369 (100%)	0	100	100
1	D1	363/378 (96%)	363 (100%)	0	100	100
1	D3	363/378 (96%)	363 (100%)	0	100	100
1	D5	363/378 (96%)	363 (100%)	0	100	100
1	E1	368/378 (97%)	368 (100%)	0	100	100
1	E3	369/378 (98%)	369 (100%)	0	100	100
1	E5	368/378 (97%)	368 (100%)	0	100	100
1	F1	363/378 (96%)	363 (100%)	0	100	100
1	F3	363/378 (96%)	363 (100%)	0	100	100
1	F5	363/378 (96%)	363 (100%)	0	100	100
1	G0	364/378 (96%)	361 (99%)	3 (1%)	73	80
1	G2	363/378 (96%)	363 (100%)	0	100	100
1	G4	365/378 (97%)	365 (100%)	0	100	100
1	H0	365/378 (97%)	365 (100%)	0	100	100
1	H2	365/378 (97%)	364 (100%)	1 (0%)	86	86
1	H4	364/378 (96%)	364 (100%)	0	100	100
1	I0	369/378 (98%)	369 (100%)	0	100	100
1	I2	365/378 (97%)	365 (100%)	0	100	100
1	I4	369/378 (98%)	369 (100%)	0	100	100
1	I6	364/378 (96%)	364 (100%)	0	100	100
1	J1	363/378 (96%)	361 (99%)	2 (1%)	78	83
1	J3	363/378 (96%)	363 (100%)	0	100	100
1	J5	364/378 (96%)	364 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K0	365/378 (97%)	364 (100%)	1 (0%)	86	86
1	K2	366/378 (97%)	365 (100%)	1 (0%)	86	86
1	K4	370/378 (98%)	370 (100%)	0	100	100
1	L0	366/378 (97%)	366 (100%)	0	100	100
1	L2	367/378 (97%)	367 (100%)	0	100	100
1	L4	365/378 (97%)	365 (100%)	0	100	100
1	L6	365/378 (97%)	362 (99%)	3 (1%)	73	80
1	M0	365/378 (97%)	365 (100%)	0	100	100
1	M2	363/378 (96%)	363 (100%)	0	100	100
1	M4	365/378 (97%)	365 (100%)	0	100	100
1	M6	368/378 (97%)	366 (100%)	2 (0%)	81	83
1	N0	369/378 (98%)	369 (100%)	0	100	100
1	N2	369/378 (98%)	369 (100%)	0	100	100
1	N4	369/378 (98%)	365 (99%)	4 (1%)	65	76
1	N6	369/378 (98%)	366 (99%)	3 (1%)	73	80
1	O0	371/378 (98%)	371 (100%)	0	100	100
1	O2	371/378 (98%)	370 (100%)	1 (0%)	86	86
1	O4	369/378 (98%)	369 (100%)	0	100	100
1	O6	371/378 (98%)	371 (100%)	0	100	100
1	P0	371/378 (98%)	370 (100%)	1 (0%)	86	86
1	P2	369/378 (98%)	369 (100%)	0	100	100
1	P4	370/378 (98%)	370 (100%)	0	100	100
1	P6	369/378 (98%)	369 (100%)	0	100	100
1	Q1	370/378 (98%)	370 (100%)	0	100	100
1	Q3	370/378 (98%)	369 (100%)	1 (0%)	86	86
1	Q5	370/378 (98%)	370 (100%)	0	100	100
1	R1	369/378 (98%)	369 (100%)	0	100	100
1	R3	370/378 (98%)	370 (100%)	0	100	100
1	R5	370/378 (98%)	370 (100%)	0	100	100
1	S1	364/378 (96%)	364 (100%)	0	100	100
1	S3	364/378 (96%)	362 (100%)	2 (0%)	81	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S5	364/378 (96%)	364 (100%)	0	100	100
1	T1	364/378 (96%)	364 (100%)	0	100	100
1	T3	362/378 (96%)	362 (100%)	0	100	100
1	T5	364/378 (96%)	364 (100%)	0	100	100
1	U1	365/378 (97%)	365 (100%)	0	100	100
1	U3	364/378 (96%)	364 (100%)	0	100	100
1	U5	364/378 (96%)	364 (100%)	0	100	100
1	V0	369/378 (98%)	369 (100%)	0	100	100
1	V2	364/378 (96%)	362 (100%)	2 (0%)	81	83
1	V4	369/378 (98%)	369 (100%)	0	100	100
1	W0	368/378 (97%)	368 (100%)	0	100	100
1	W2	363/378 (96%)	363 (100%)	0	100	100
1	W4	369/378 (98%)	369 (100%)	0	100	100
1	W6	364/378 (96%)	364 (100%)	0	100	100
2	A1	371/380 (98%)	369 (100%)	2 (0%)	81	83
2	A3	371/380 (98%)	370 (100%)	1 (0%)	86	86
2	A5	371/380 (98%)	369 (100%)	2 (0%)	81	83
2	B0	367/380 (97%)	365 (100%)	2 (0%)	81	83
2	B2	366/380 (96%)	366 (100%)	0	100	100
2	B4	368/380 (97%)	367 (100%)	1 (0%)	86	86
2	C0	367/380 (97%)	366 (100%)	1 (0%)	86	86
2	C2	366/380 (96%)	366 (100%)	0	100	100
2	C4	367/380 (97%)	366 (100%)	1 (0%)	86	86
2	D0	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	D2	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	D4	366/380 (96%)	366 (100%)	0	100	100
2	D6	366/380 (96%)	366 (100%)	0	100	100
2	E0	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	E2	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	E4	366/380 (96%)	366 (100%)	0	100	100
2	E6	366/380 (96%)	366 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F0	366/380 (96%)	366 (100%)	0	100	100
2	F2	366/380 (96%)	364 (100%)	2 (0%)	81	83
2	F4	366/380 (96%)	366 (100%)	0	100	100
2	F6	366/380 (96%)	364 (100%)	2 (0%)	81	83
2	G1	366/380 (96%)	366 (100%)	0	100	100
2	G3	368/380 (97%)	366 (100%)	2 (0%)	81	83
2	G5	366/380 (96%)	366 (100%)	0	100	100
2	H1	366/380 (96%)	366 (100%)	0	100	100
2	H3	367/380 (97%)	366 (100%)	1 (0%)	86	86
2	H5	366/380 (96%)	363 (99%)	3 (1%)	73	80
2	I1	366/380 (96%)	366 (100%)	0	100	100
2	I3	368/380 (97%)	367 (100%)	1 (0%)	86	86
2	I5	366/380 (96%)	366 (100%)	0	100	100
2	J0	367/380 (97%)	366 (100%)	1 (0%)	86	86
2	J2	366/380 (96%)	366 (100%)	0	100	100
2	J4	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	J6	366/380 (96%)	366 (100%)	0	100	100
2	K1	370/380 (97%)	369 (100%)	1 (0%)	86	86
2	K3	370/380 (97%)	370 (100%)	0	100	100
2	K5	370/380 (97%)	368 (100%)	2 (0%)	81	83
2	L1	366/380 (96%)	366 (100%)	0	100	100
2	L3	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	L5	366/380 (96%)	364 (100%)	2 (0%)	81	83
2	M1	369/380 (97%)	369 (100%)	0	100	100
2	M3	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	M5	369/380 (97%)	368 (100%)	1 (0%)	86	86
2	N1	367/380 (97%)	367 (100%)	0	100	100
2	N3	368/380 (97%)	366 (100%)	2 (0%)	81	83
2	N5	367/380 (97%)	367 (100%)	0	100	100
2	O1	368/380 (97%)	368 (100%)	0	100	100
2	O3	370/380 (97%)	369 (100%)	1 (0%)	86	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	O5	368/380 (97%)	367 (100%)	1 (0%)	86	86
2	P1	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	P3	368/380 (97%)	367 (100%)	1 (0%)	86	86
2	P5	368/380 (97%)	368 (100%)	0	100	100
2	Q0	366/380 (96%)	366 (100%)	0	100	100
2	Q2	368/380 (97%)	366 (100%)	2 (0%)	81	83
2	Q4	367/380 (97%)	367 (100%)	0	100	100
2	R0	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	R2	367/380 (97%)	366 (100%)	1 (0%)	86	86
2	R4	366/380 (96%)	366 (100%)	0	100	100
2	R6	367/380 (97%)	366 (100%)	1 (0%)	86	86
2	S0	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	S2	366/380 (96%)	366 (100%)	0	100	100
2	S4	366/380 (96%)	366 (100%)	0	100	100
2	S6	366/380 (96%)	366 (100%)	0	100	100
2	T0	366/380 (96%)	365 (100%)	1 (0%)	86	86
2	T2	366/380 (96%)	364 (100%)	2 (0%)	81	83
2	T4	366/380 (96%)	363 (99%)	3 (1%)	73	80
2	T6	366/380 (96%)	364 (100%)	2 (0%)	81	83
2	U0	366/380 (96%)	366 (100%)	0	100	100
2	U2	367/380 (97%)	366 (100%)	1 (0%)	86	86
2	U4	366/380 (96%)	363 (99%)	3 (1%)	73	80
2	U6	367/380 (97%)	365 (100%)	2 (0%)	81	83
2	V1	367/380 (97%)	365 (100%)	2 (0%)	81	83
2	V3	366/380 (96%)	366 (100%)	0	100	100
2	V5	367/380 (97%)	366 (100%)	1 (0%)	86	86
2	W1	366/380 (96%)	364 (100%)	2 (0%)	81	83
2	W3	366/380 (96%)	364 (100%)	2 (0%)	81	83
2	W5	367/380 (97%)	367 (100%)	0	100	100
3	X0	174/180 (97%)	174 (100%)	0	100	100
3	X1	174/180 (97%)	172 (99%)	2 (1%)	65	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	X2	174/180 (97%)	174 (100%)	0	100	100
3	X3	174/180 (97%)	174 (100%)	0	100	100
4	Y0	126/320 (39%)	126 (100%)	0	100	100
4	Y1	126/320 (39%)	126 (100%)	0	100	100
4	Y2	126/320 (39%)	124 (98%)	2 (2%)	55	70
5	1A	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	1B	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	1C	180/181 (99%)	173 (96%)	7 (4%)	28	49
5	1D	180/181 (99%)	177 (98%)	3 (2%)	53	69
5	1E	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	1F	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	1G	180/181 (99%)	174 (97%)	6 (3%)	33	55
5	2A	180/181 (99%)	173 (96%)	7 (4%)	28	49
5	2B	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	2C	180/181 (99%)	173 (96%)	7 (4%)	28	49
5	2D	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	2E	180/181 (99%)	175 (97%)	5 (3%)	38	59
5	2F	180/181 (99%)	177 (98%)	3 (2%)	53	69
5	2G	180/181 (99%)	174 (97%)	6 (3%)	33	55
5	2H	180/181 (99%)	174 (97%)	6 (3%)	33	55
5	2I	180/181 (99%)	172 (96%)	8 (4%)	25	47
5	2J	180/181 (99%)	177 (98%)	3 (2%)	53	69
5	3C	180/181 (99%)	175 (97%)	5 (3%)	38	59
5	3D	180/181 (99%)	173 (96%)	7 (4%)	28	49
5	3E	180/181 (99%)	175 (97%)	5 (3%)	38	59
5	3F	180/181 (99%)	174 (97%)	6 (3%)	33	55
5	3G	180/181 (99%)	175 (97%)	5 (3%)	38	59
5	3H	180/181 (99%)	174 (97%)	6 (3%)	33	55
5	3I	180/181 (99%)	175 (97%)	5 (3%)	38	59
5	3J	180/181 (99%)	177 (98%)	3 (2%)	53	69
5	4H	180/181 (99%)	174 (97%)	6 (3%)	33	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	4I	180/181 (99%)	175 (97%)	5 (3%)	38	59
5	4J	180/181 (99%)	173 (96%)	7 (4%)	28	49
5	5A	180/181 (99%)	173 (96%)	7 (4%)	28	49
5	5B	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	5C	180/181 (99%)	175 (97%)	5 (3%)	38	59
5	5D	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	6A	180/181 (99%)	173 (96%)	7 (4%)	28	49
5	6B	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	6C	180/181 (99%)	175 (97%)	5 (3%)	38	59
5	6D	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	7A	180/181 (99%)	173 (96%)	7 (4%)	28	49
5	7B	180/181 (99%)	176 (98%)	4 (2%)	45	64
5	7C	180/181 (99%)	175 (97%)	5 (3%)	38	59
5	7D	180/181 (99%)	176 (98%)	4 (2%)	45	64
6	9A	182/588 (31%)	182 (100%)	0	100	100
6	9B	182/588 (31%)	182 (100%)	0	100	100
7	8A	62/294 (21%)	62 (100%)	0	100	100
7	8B	62/294 (21%)	62 (100%)	0	100	100
7	8C	62/294 (21%)	62 (100%)	0	100	100
All	All	65299/69344 (94%)	64993 (100%)	306 (0%)	78	83

5 of 306 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	2J	167	ASP
5	5C	117	MET
5	7A	182	MET
5	6A	198	PHE
5	1G	108	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 924 such sidechains are listed below:

Mol	Chain	Res	Type
1	M6	293	ASN

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Mol	Chain	Res	Type
1	W4	258	ASN
2	P3	256	ASN
2	W3	165	ASN
1	U3	300	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

154 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
8	GTP	H4	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.59	9 (18%)
9	GDP	C4	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
8	GTP	K2	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.61	8 (16%)
8	GTP	U5	501	-	33,34,34	0.94	2 (6%)	50,54,54	1.60	8 (16%)
8	GTP	T5	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.55	9 (18%)
9	GDP	H1	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
8	GTP	K4	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.59	8 (16%)
8	GTP	L0	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.60	9 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	GTP	E5	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.59	9 (18%)
8	GTP	D5	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.60	10 (20%)
9	GDP	Q4	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
8	GTP	M0	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.63	9 (18%)
8	GTP	P0	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.61	9 (18%)
8	GTP	L2	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.64	9 (18%)
8	GTP	S3	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.60	10 (20%)
9	GDP	H5	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.77	7 (15%)
8	GTP	W6	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.60	8 (16%)
8	GTP	I2	501	-	33,34,34	0.89	1 (3%)	50,54,54	1.62	9 (18%)
9	GDP	Q0	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	6 (13%)
8	GTP	Q5	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.59	8 (16%)
8	GTP	N4	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.58	8 (16%)
9	GDP	B2	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.76	7 (15%)
8	GTP	K0	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.60	8 (16%)
9	GDP	P3	501	-	29,30,30	1.12	3 (10%)	45,47,47	1.75	7 (15%)
8	GTP	A2	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.59	8 (16%)
8	GTP	O2	501	-	33,34,34	0.89	2 (6%)	50,54,54	1.62	9 (18%)
9	GDP	F4	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
8	GTP	G0	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.56	9 (18%)
8	GTP	B3	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.60	10 (20%)
8	GTP	D3	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.59	9 (18%)
8	GTP	M2	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.66	8 (16%)
9	GDP	D0	501	-	29,30,30	1.17	2 (6%)	45,47,47	1.78	7 (15%)
8	GTP	I6	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.57	9 (18%)
9	GDP	F0	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
9	GDP	R6	501	-	29,30,30	1.18	3 (10%)	45,47,47	1.79	7 (15%)
9	GDP	M3	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.79	7 (15%)
9	GDP	V5	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
8	GTP	D1	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.61	9 (18%)
9	GDP	R0	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
9	GDP	K1	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	6 (13%)
8	GTP	J3	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.61	9 (18%)
8	GTP	P4	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.59	9 (18%)
9	GDP	K3	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.79	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	GDP	N3	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
8	GTP	B5	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.58	8 (16%)
8	GTP	F5	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.53	8 (16%)
9	GDP	J6	501	-	29,30,30	1.17	3 (10%)	45,47,47	1.78	6 (13%)
9	GDP	W5	501	-	29,30,30	1.15	2 (6%)	45,47,47	1.76	5 (11%)
8	GTP	V4	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.62	10 (20%)
8	GTP	F1	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.58	8 (16%)
9	GDP	J4	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
8	GTP	U1	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.58	9 (18%)
9	GDP	W1	501	-	29,30,30	1.14	2 (6%)	45,47,47	1.77	5 (11%)
9	GDP	T2	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
8	GTP	C5	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.66	9 (18%)
9	GDP	B4	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
9	GDP	C0	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
8	GTP	G2	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.55	8 (16%)
9	GDP	S0	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.73	6 (13%)
8	GTP	P1	502	-	33,34,34	0.92	1 (3%)	50,54,54	1.62	10 (20%)
9	GDP	O1	501	-	29,30,30	1.12	3 (10%)	45,47,47	1.79	6 (13%)
8	GTP	T1	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.54	8 (16%)
9	GDP	M1	501	-	29,30,30	1.15	2 (6%)	45,47,47	1.79	6 (13%)
8	GTP	R5	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.61	8 (16%)
9	GDP	A5	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.79	7 (15%)
9	GDP	E4	501	-	29,30,30	1.15	2 (6%)	45,47,47	1.74	6 (13%)
8	GTP	I0	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.63	9 (18%)
8	GTP	V2	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.64	9 (18%)
9	GDP	N5	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
9	GDP	T6	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	6 (13%)
8	GTP	I4	501	-	33,34,34	0.88	1 (3%)	50,54,54	1.63	9 (18%)
8	GTP	J5	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.63	9 (18%)
9	GDP	R4	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
8	GTP	M6	501	-	33,34,34	0.90	2 (6%)	50,54,54	1.65	8 (16%)
8	GTP	W0	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.61	9 (18%)
9	GDP	D2	501	-	29,30,30	1.17	3 (10%)	45,47,47	1.78	5 (11%)
9	GDP	I1	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.81	7 (15%)
9	GDP	J0	501	-	29,30,30	1.15	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
8	GTP	O0	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.60	9 (18%)
8	GTP	M4	501	-	33,34,34	0.93	2 (6%)	50,54,54	1.62	9 (18%)
9	GDP	H3	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	6 (13%)
8	GTP	H2	501	-	33,34,34	0.89	1 (3%)	50,54,54	1.60	9 (18%)
8	GTP	U3	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.57	8 (16%)
9	GDP	F2	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
9	GDP	S6	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
9	GDP	I5	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	7 (15%)
9	GDP	E6	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.74	6 (13%)
8	GTP	C1	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.61	8 (16%)
9	GDP	W3	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	6 (13%)
9	GDP	P5	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
8	GTP	N2	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.56	8 (16%)
9	GDP	O3	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.76	6 (13%)
9	GDP	B0	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.79	7 (15%)
9	GDP	A1	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.75	7 (15%)
8	GTP	N6	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.58	8 (16%)
9	GDP	D6	501	-	29,30,30	1.17	3 (10%)	45,47,47	1.80	7 (15%)
9	GDP	L5	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
8	GTP	T3	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.57	8 (16%)
9	GDP	U0	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
8	GTP	C3	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.58	8 (16%)
9	GDP	E2	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	6 (13%)
8	GTP	O6	501	-	33,34,34	0.91	2 (6%)	50,54,54	1.62	8 (16%)
9	GDP	G5	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
9	GDP	G3	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	8 (17%)
8	GTP	Q3	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.65	8 (16%)
8	GTP	L4	501	-	33,34,34	0.89	1 (3%)	50,54,54	1.64	8 (16%)
8	GTP	Q1	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.60	8 (16%)
9	GDP	M5	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	6 (13%)
9	GDP	J2	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	6 (13%)
9	GDP	F6	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.72	6 (13%)
9	GDP	V1	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	7 (15%)
9	GDP	L3	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.81	7 (15%)
9	GDP	P1	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	6 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	GTP	S1	501	-	33,34,34	1.00	1 (3%)	50,54,54	1.59	9 (18%)
9	GDP	U6	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.76	7 (15%)
9	GDP	O5	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	6 (13%)
8	GTP	H0	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.60	8 (16%)
8	GTP	B1	501	-	33,34,34	0.93	2 (6%)	50,54,54	1.54	9 (18%)
8	GTP	P6	501	-	33,34,34	0.89	1 (3%)	50,54,54	1.60	8 (16%)
8	GTP	N0	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.61	10 (20%)
9	GDP	L1	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.79	7 (15%)
8	GTP	L6	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.64	8 (16%)
9	GDP	I3	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.79	7 (15%)
9	GDP	G1	501	-	29,30,30	1.15	2 (6%)	45,47,47	1.76	7 (15%)
9	GDP	T0	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
9	GDP	U4	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
9	GDP	Q2	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
9	GDP	S2	501	-	29,30,30	1.17	3 (10%)	45,47,47	1.78	7 (15%)
9	GDP	E0	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.79	7 (15%)
8	GTP	J1	501	-	33,34,34	0.91	0	50,54,54	1.62	9 (18%)
8	GTP	E1	501	-	33,34,34	0.99	3 (9%)	50,54,54	1.64	10 (20%)
9	GDP	S4	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.74	7 (15%)
9	GDP	U2	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	6 (13%)
8	GTP	E3	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.60	8 (16%)
9	GDP	T4	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
8	GTP	V0	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.61	8 (16%)
8	GTP	O4	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.62	9 (18%)
9	GDP	A3	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.79	7 (15%)
8	GTP	G4	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.56	8 (16%)
8	GTP	R3	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.62	8 (16%)
8	GTP	S5	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.57	8 (16%)
8	GTP	W4	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.63	8 (16%)
8	GTP	A4	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.58	8 (16%)
9	GDP	C2	501	-	29,30,30	1.13	2 (6%)	45,47,47	1.78	5 (11%)
8	GTP	A6	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.58	8 (16%)
8	GTP	A0	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.58	8 (16%)
8	GTP	R1	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.61	8 (16%)
8	GTP	W2	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.59	9 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	GDP	K5	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	6 (13%)
9	GDP	R2	501	-	29,30,30	1.20	3 (10%)	45,47,47	1.78	7 (15%)
9	GDP	V3	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.76	7 (15%)
8	GTP	F3	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.59	10 (20%)
9	GDP	D4	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	6 (13%)
9	GDP	N1	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)

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
8	GTP	H4	501	-	-	4/22/38/38	0/3/3/3
9	GDP	C4	501	-	-	1/16/32/32	0/3/3/3
8	GTP	K2	501	-	-	5/22/38/38	0/3/3/3
8	GTP	U5	501	-	-	8/22/38/38	0/3/3/3
8	GTP	T5	501	-	-	4/22/38/38	0/3/3/3
9	GDP	H1	501	-	-	0/16/32/32	0/3/3/3
8	GTP	K4	501	-	-	5/22/38/38	0/3/3/3
8	GTP	L0	501	-	-	6/22/38/38	0/3/3/3
8	GTP	E5	501	-	-	6/22/38/38	0/3/3/3
8	GTP	D5	501	-	-	3/22/38/38	0/3/3/3
9	GDP	Q4	501	-	-	3/16/32/32	0/3/3/3
8	GTP	M0	501	-	-	6/22/38/38	0/3/3/3
8	GTP	P0	501	-	-	8/22/38/38	0/3/3/3
8	GTP	L2	501	-	-	6/22/38/38	0/3/3/3
8	GTP	S3	501	-	-	6/22/38/38	0/3/3/3
9	GDP	H5	501	-	-	1/16/32/32	0/3/3/3
8	GTP	W6	501	-	-	3/22/38/38	0/3/3/3
8	GTP	I2	501	-	-	5/22/38/38	0/3/3/3
9	GDP	Q0	501	-	-	4/16/32/32	0/3/3/3
8	GTP	Q5	501	-	-	8/22/38/38	0/3/3/3
8	GTP	N4	501	-	-	5/22/38/38	0/3/3/3
9	GDP	B2	501	-	-	2/16/32/32	0/3/3/3
8	GTP	K0	501	-	-	5/22/38/38	0/3/3/3
9	GDP	P3	501	-	-	1/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	GTP	A2	501	-	-	5/22/38/38	0/3/3/3
8	GTP	O2	501	-	-	3/22/38/38	0/3/3/3
9	GDP	F4	501	-	-	1/16/32/32	0/3/3/3
8	GTP	G0	501	-	-	3/22/38/38	0/3/3/3
8	GTP	B3	501	-	-	4/22/38/38	0/3/3/3
8	GTP	D3	501	-	-	3/22/38/38	0/3/3/3
8	GTP	M2	501	-	-	6/22/38/38	0/3/3/3
9	GDP	D0	501	-	-	1/16/32/32	0/3/3/3
8	GTP	I6	501	-	-	8/22/38/38	0/3/3/3
9	GDP	F0	501	-	-	3/16/32/32	0/3/3/3
9	GDP	R6	501	-	-	1/16/32/32	0/3/3/3
9	GDP	M3	501	-	-	3/16/32/32	0/3/3/3
9	GDP	V5	501	-	-	2/16/32/32	0/3/3/3
8	GTP	D1	501	-	-	8/22/38/38	0/3/3/3
9	GDP	R0	501	-	-	0/16/32/32	0/3/3/3
9	GDP	K1	501	-	-	1/16/32/32	0/3/3/3
8	GTP	J3	501	-	-	2/22/38/38	0/3/3/3
8	GTP	P4	501	-	-	6/22/38/38	0/3/3/3
9	GDP	K3	501	-	-	3/16/32/32	0/3/3/3
9	GDP	N3	501	-	-	1/16/32/32	0/3/3/3
8	GTP	B5	501	-	-	5/22/38/38	0/3/3/3
8	GTP	F5	501	-	-	6/22/38/38	0/3/3/3
9	GDP	J6	501	-	-	1/16/32/32	0/3/3/3
9	GDP	W5	501	-	-	3/16/32/32	0/3/3/3
8	GTP	V4	501	-	-	7/22/38/38	0/3/3/3
8	GTP	F1	501	-	-	5/22/38/38	0/3/3/3
9	GDP	J4	501	-	-	1/16/32/32	0/3/3/3
8	GTP	U1	501	-	-	4/22/38/38	0/3/3/3
9	GDP	W1	501	-	-	2/16/32/32	0/3/3/3
9	GDP	T2	501	-	-	3/16/32/32	0/3/3/3
8	GTP	C5	501	-	-	11/22/38/38	0/3/3/3
9	GDP	B4	501	-	-	3/16/32/32	0/3/3/3
9	GDP	C0	501	-	-	2/16/32/32	0/3/3/3
8	GTP	G2	501	-	-	4/22/38/38	0/3/3/3
9	GDP	S0	501	-	-	3/16/32/32	0/3/3/3
8	GTP	P1	502	-	-	3/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	GDP	O1	501	-	-	2/16/32/32	0/3/3/3
8	GTP	T1	501	-	-	3/22/38/38	0/3/3/3
9	GDP	M1	501	-	-	0/16/32/32	0/3/3/3
8	GTP	R5	501	-	-	6/22/38/38	0/3/3/3
9	GDP	A5	501	-	-	2/16/32/32	0/3/3/3
9	GDP	E4	501	-	-	1/16/32/32	0/3/3/3
8	GTP	I0	501	-	-	7/22/38/38	0/3/3/3
8	GTP	V2	501	-	-	5/22/38/38	0/3/3/3
9	GDP	N5	501	-	-	1/16/32/32	0/3/3/3
9	GDP	T6	501	-	-	4/16/32/32	0/3/3/3
8	GTP	I4	501	-	-	5/22/38/38	0/3/3/3
8	GTP	J5	501	-	-	5/22/38/38	0/3/3/3
9	GDP	R4	501	-	-	0/16/32/32	0/3/3/3
8	GTP	M6	501	-	-	6/22/38/38	0/3/3/3
8	GTP	W0	501	-	-	3/22/38/38	0/3/3/3
9	GDP	D2	501	-	-	1/16/32/32	0/3/3/3
9	GDP	I1	501	-	-	2/16/32/32	0/3/3/3
9	GDP	J0	501	-	-	1/16/32/32	0/3/3/3
8	GTP	O0	501	-	-	5/22/38/38	0/3/3/3
8	GTP	M4	501	-	-	8/22/38/38	0/3/3/3
9	GDP	H3	501	-	-	1/16/32/32	0/3/3/3
8	GTP	H2	501	-	-	8/22/38/38	0/3/3/3
8	GTP	U3	501	-	-	3/22/38/38	0/3/3/3
9	GDP	F2	501	-	-	3/16/32/32	0/3/3/3
9	GDP	S6	501	-	-	3/16/32/32	0/3/3/3
9	GDP	I5	501	-	-	1/16/32/32	0/3/3/3
9	GDP	E6	501	-	-	2/16/32/32	0/3/3/3
8	GTP	C1	501	-	-	6/22/38/38	0/3/3/3
9	GDP	W3	501	-	-	1/16/32/32	0/3/3/3
9	GDP	P5	501	-	-	2/16/32/32	0/3/3/3
8	GTP	N2	501	-	-	3/22/38/38	0/3/3/3
9	GDP	O3	501	-	-	3/16/32/32	0/3/3/3
9	GDP	B0	501	-	-	2/16/32/32	0/3/3/3
9	GDP	A1	501	-	-	2/16/32/32	0/3/3/3
8	GTP	N6	501	-	-	5/22/38/38	0/3/3/3
9	GDP	D6	501	-	-	1/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	GDP	L5	501	-	-	3/16/32/32	0/3/3/3
8	GTP	T3	501	-	-	5/22/38/38	0/3/3/3
9	GDP	U0	501	-	-	1/16/32/32	0/3/3/3
8	GTP	C3	501	-	-	8/22/38/38	0/3/3/3
9	GDP	E2	501	-	-	2/16/32/32	0/3/3/3
8	GTP	O6	501	-	-	7/22/38/38	0/3/3/3
9	GDP	G5	501	-	-	0/16/32/32	0/3/3/3
9	GDP	G3	501	-	-	3/16/32/32	0/3/3/3
8	GTP	Q3	501	-	-	9/22/38/38	0/3/3/3
8	GTP	L4	501	-	-	6/22/38/38	0/3/3/3
8	GTP	Q1	501	-	-	6/22/38/38	0/3/3/3
9	GDP	M5	501	-	-	1/16/32/32	0/3/3/3
9	GDP	J2	501	-	-	1/16/32/32	0/3/3/3
9	GDP	F6	501	-	-	3/16/32/32	0/3/3/3
9	GDP	V1	501	-	-	2/16/32/32	0/3/3/3
9	GDP	L3	501	-	-	3/16/32/32	0/3/3/3
9	GDP	P1	501	-	-	3/16/32/32	0/3/3/3
8	GTP	S1	501	-	-	5/22/38/38	0/3/3/3
9	GDP	U6	501	-	-	1/16/32/32	0/3/3/3
9	GDP	O5	501	-	-	4/16/32/32	0/3/3/3
8	GTP	H0	501	-	-	4/22/38/38	0/3/3/3
8	GTP	B1	501	-	-	5/22/38/38	0/3/3/3
8	GTP	P6	501	-	-	8/22/38/38	0/3/3/3
8	GTP	N0	501	-	-	5/22/38/38	0/3/3/3
9	GDP	L1	501	-	-	4/16/32/32	0/3/3/3
8	GTP	L6	501	-	-	6/22/38/38	0/3/3/3
9	GDP	I3	501	-	-	1/16/32/32	0/3/3/3
9	GDP	G1	501	-	-	1/16/32/32	0/3/3/3
9	GDP	T0	501	-	-	4/16/32/32	0/3/3/3
9	GDP	U4	501	-	-	1/16/32/32	0/3/3/3
9	GDP	Q2	501	-	-	1/16/32/32	0/3/3/3
9	GDP	S2	501	-	-	0/16/32/32	0/3/3/3
9	GDP	E0	501	-	-	0/16/32/32	0/3/3/3
8	GTP	J1	501	-	-	1/22/38/38	0/3/3/3
8	GTP	E1	501	-	-	5/22/38/38	0/3/3/3
9	GDP	S4	501	-	-	0/16/32/32	0/3/3/3
9	GDP	U2	501	-	-	3/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	GTP	E3	501	-	-	6/22/38/38	0/3/3/3
9	GDP	T4	501	-	-	4/16/32/32	0/3/3/3
8	GTP	V0	501	-	-	6/22/38/38	0/3/3/3
8	GTP	O4	501	-	-	5/22/38/38	0/3/3/3
9	GDP	A3	501	-	-	1/16/32/32	0/3/3/3
8	GTP	G4	501	-	-	5/22/38/38	0/3/3/3
8	GTP	R3	501	-	-	3/22/38/38	0/3/3/3
8	GTP	S5	501	-	-	5/22/38/38	0/3/3/3
8	GTP	W4	501	-	-	7/22/38/38	0/3/3/3
8	GTP	A4	501	-	-	4/22/38/38	0/3/3/3
9	GDP	C2	501	-	-	1/16/32/32	0/3/3/3
8	GTP	A6	501	-	-	4/22/38/38	0/3/3/3
8	GTP	A0	501	-	-	3/22/38/38	0/3/3/3
8	GTP	R1	501	-	-	3/22/38/38	0/3/3/3
8	GTP	W2	501	-	-	6/22/38/38	0/3/3/3
9	GDP	K5	501	-	-	4/16/32/32	0/3/3/3
9	GDP	R2	501	-	-	1/16/32/32	0/3/3/3
9	GDP	V3	501	-	-	1/16/32/32	0/3/3/3
8	GTP	F3	501	-	-	6/22/38/38	0/3/3/3
9	GDP	D4	501	-	-	1/16/32/32	0/3/3/3
9	GDP	N1	501	-	-	1/16/32/32	0/3/3/3

The worst 5 of 319 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	G5	501	GDP	C5-C4	3.19	1.47	1.38
9	T4	501	GDP	C5-C4	3.17	1.47	1.38
9	I1	501	GDP	C5-C4	3.17	1.47	1.38
9	D6	501	GDP	C5-C4	3.16	1.47	1.38
9	T0	501	GDP	C5-C4	3.14	1.47	1.38

The worst 5 of 1173 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	D6	501	GDP	C5-C4-N3	-6.36	118.27	128.39
9	D2	501	GDP	C5-C4-N3	-6.35	118.29	128.39
9	I1	501	GDP	C5-C4-N3	-6.34	118.30	128.39
9	C4	501	GDP	C5-C4-N3	-6.28	118.40	128.39
9	L3	501	GDP	C5-C4-N3	-6.27	118.42	128.39

There are no chirality outliers.

5 of 544 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A0	501	GTP	PB-O3A-PA-O5'
8	A2	501	GTP	C5'-O5'-PA-O1A
8	A6	501	GTP	C5'-O5'-PA-O3A
8	A6	501	GTP	C5'-O5'-PA-O1A
8	B1	501	GTP	PB-O3A-PA-O5'

There are no ring outliers.

100 monomers are involved in 1102 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	C4	501	GDP	1	0
8	K2	501	GTP	1	0
8	U5	501	GTP	37	0
8	T5	501	GTP	45	0
8	K4	501	GTP	1	0
8	D5	501	GTP	1	0
9	Q4	501	GDP	23	0
8	P0	501	GTP	9	0
8	S3	501	GTP	11	0
8	W6	501	GTP	20	0
8	I2	501	GTP	1	0
9	Q0	501	GDP	4	0
8	Q5	501	GTP	58	0
8	N4	501	GTP	15	0
8	K0	501	GTP	2	0
9	P3	501	GDP	3	0
8	O2	501	GTP	5	0
9	F4	501	GDP	3	0
8	G0	501	GTP	2	0
8	D3	501	GTP	2	0
8	M2	501	GTP	1	0
8	I6	501	GTP	1	0
9	F0	501	GDP	1	0
9	R6	501	GDP	28	0
9	V5	501	GDP	5	0
9	R0	501	GDP	5	0
8	J3	501	GTP	1	0
8	P4	501	GTP	24	0
9	N3	501	GDP	6	0
8	B5	501	GTP	1	0

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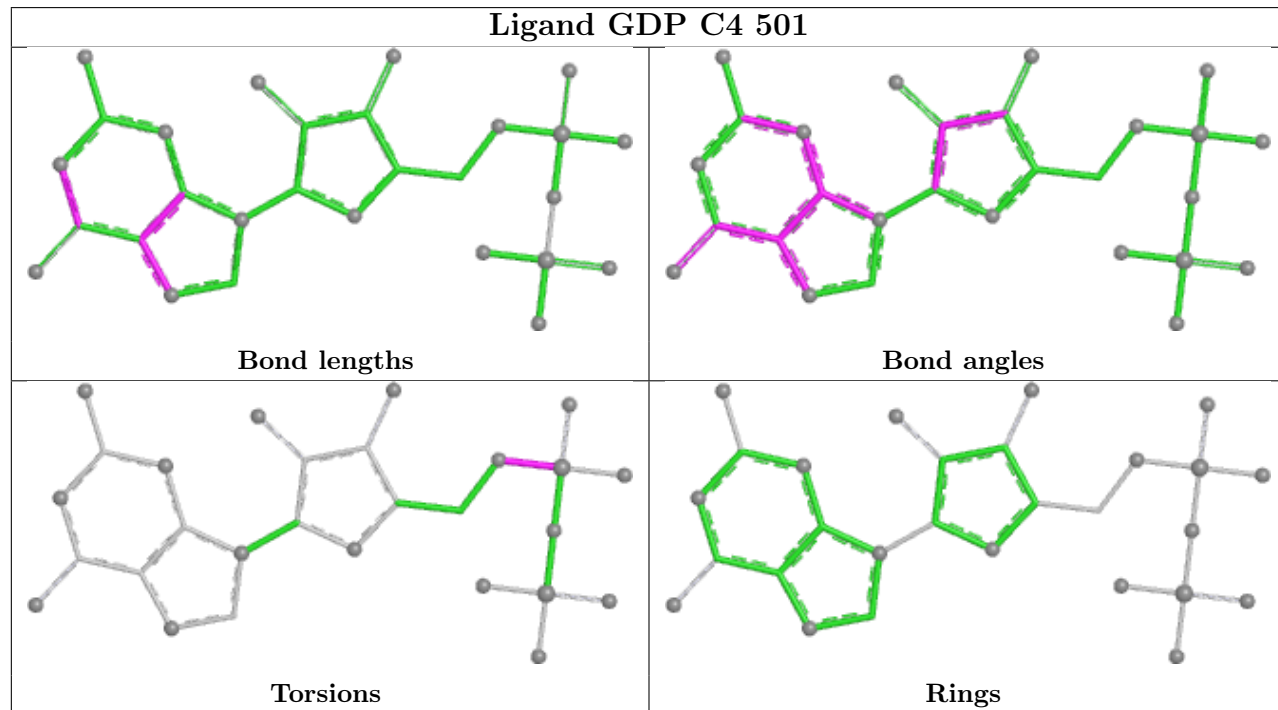
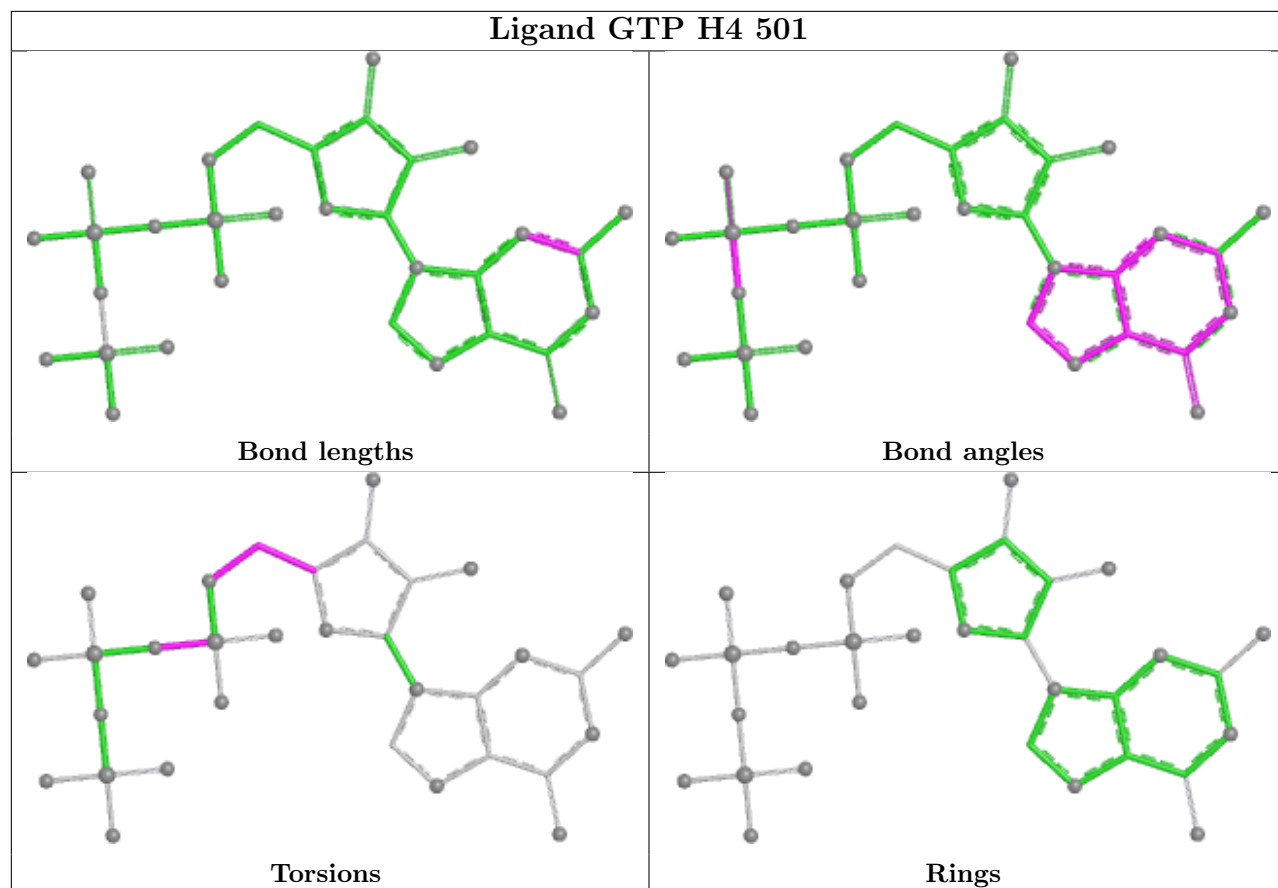
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	F5	501	GTP	1	0
9	W5	501	GDP	8	0
8	V4	501	GTP	8	0
8	F1	501	GTP	1	0
9	J4	501	GDP	1	0
8	U1	501	GTP	8	0
9	W1	501	GDP	6	0
9	T2	501	GDP	8	0
8	C5	501	GTP	1	0
9	C0	501	GDP	1	0
8	G2	501	GTP	1	0
9	S0	501	GDP	4	0
8	P1	502	GTP	6	0
9	O1	501	GDP	3	0
8	T1	501	GTP	7	0
8	R5	501	GTP	41	0
8	I0	501	GTP	1	0
8	V2	501	GTP	5	0
9	N5	501	GDP	29	0
9	T6	501	GDP	41	0
8	J5	501	GTP	1	0
9	R4	501	GDP	19	0
8	W0	501	GTP	8	0
9	D2	501	GDP	2	0
8	O0	501	GTP	8	0
8	M4	501	GTP	1	0
8	U3	501	GTP	7	0
9	S6	501	GDP	52	0
9	E6	501	GDP	1	0
9	P5	501	GDP	23	0
9	O3	501	GDP	1	0
8	N6	501	GTP	53	0
9	D6	501	GDP	2	0
8	T3	501	GTP	13	0
9	U0	501	GDP	3	0
8	O6	501	GTP	55	0
8	Q3	501	GTP	8	0
8	Q1	501	GTP	16	0
9	F6	501	GDP	1	0
9	V1	501	GDP	8	0
9	P1	501	GDP	3	0
8	S1	501	GTP	23	0

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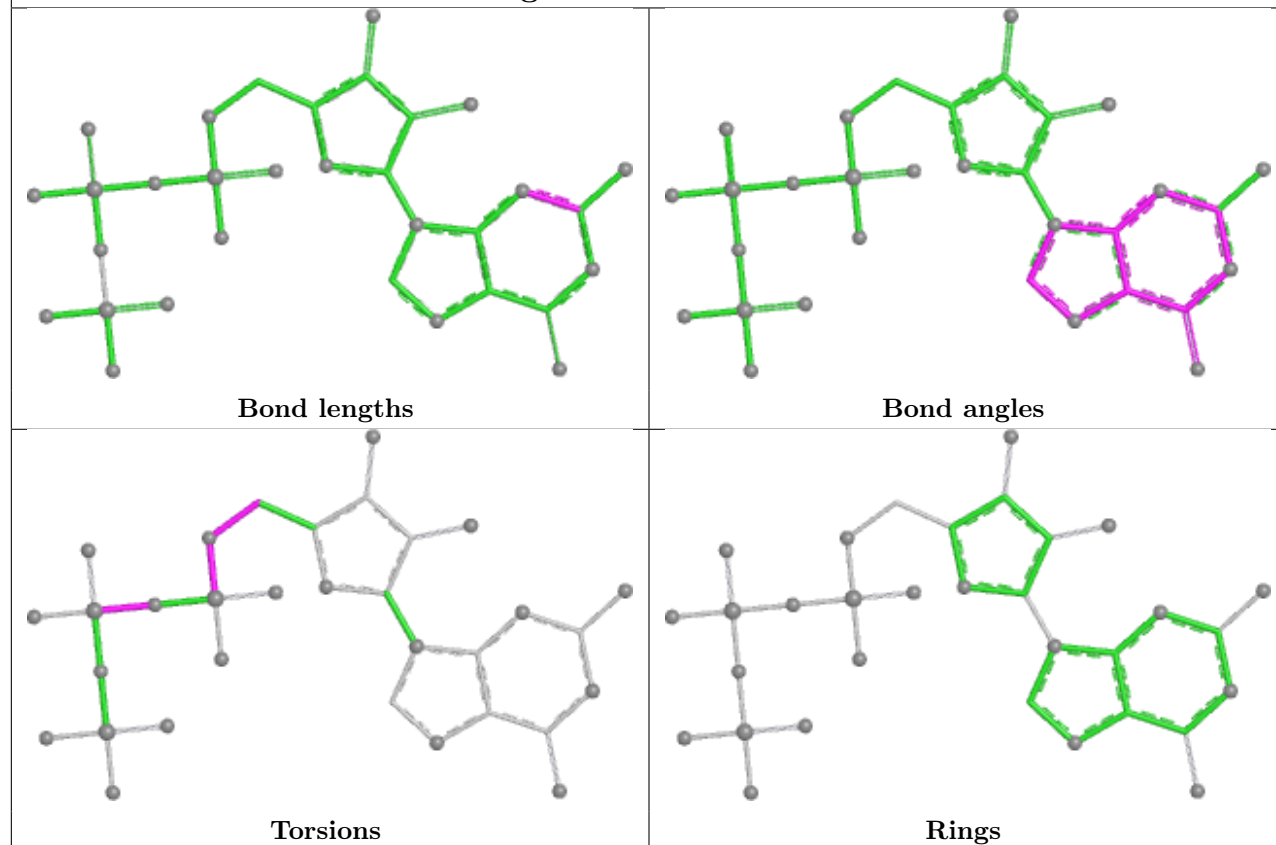
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	U6	501	GDP	9	0
9	O5	501	GDP	36	0
8	P6	501	GTP	74	0
8	N0	501	GTP	8	0
9	L1	501	GDP	1	0
9	G1	501	GDP	2	0
9	T0	501	GDP	8	0
9	U4	501	GDP	4	0
9	Q2	501	GDP	1	0
9	S2	501	GDP	8	0
8	J1	501	GTP	1	0
8	E1	501	GTP	1	0
9	S4	501	GDP	5	0
9	U2	501	GDP	1	0
9	T4	501	GDP	13	0
8	V0	501	GTP	9	0
8	O4	501	GTP	23	0
8	G4	501	GTP	1	0
8	R3	501	GTP	2	0
8	S5	501	GTP	38	0
8	W4	501	GTP	7	0
8	A0	501	GTP	1	0
8	R1	501	GTP	21	0
8	W2	501	GTP	6	0
9	R2	501	GDP	9	0
9	V3	501	GDP	3	0
9	D4	501	GDP	2	0
9	N1	501	GDP	2	0

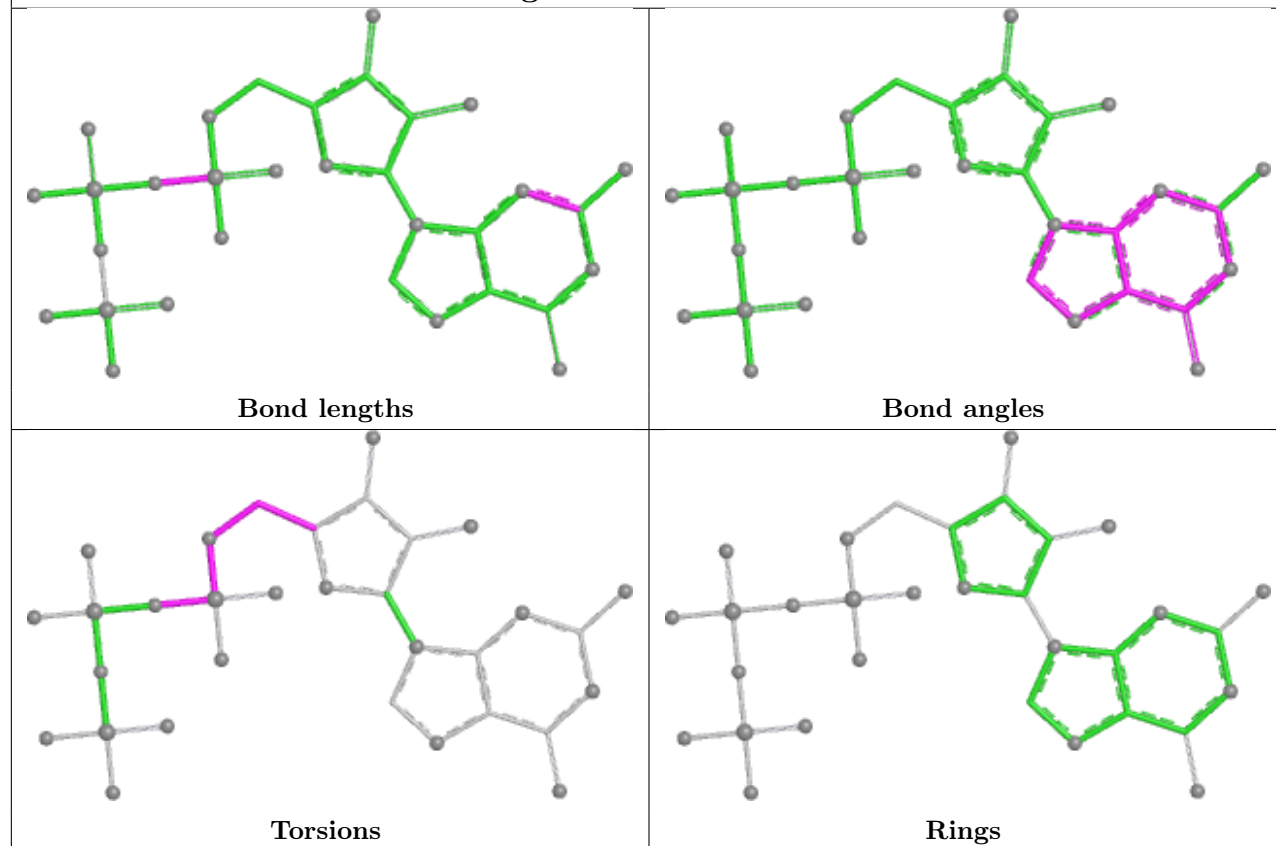
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

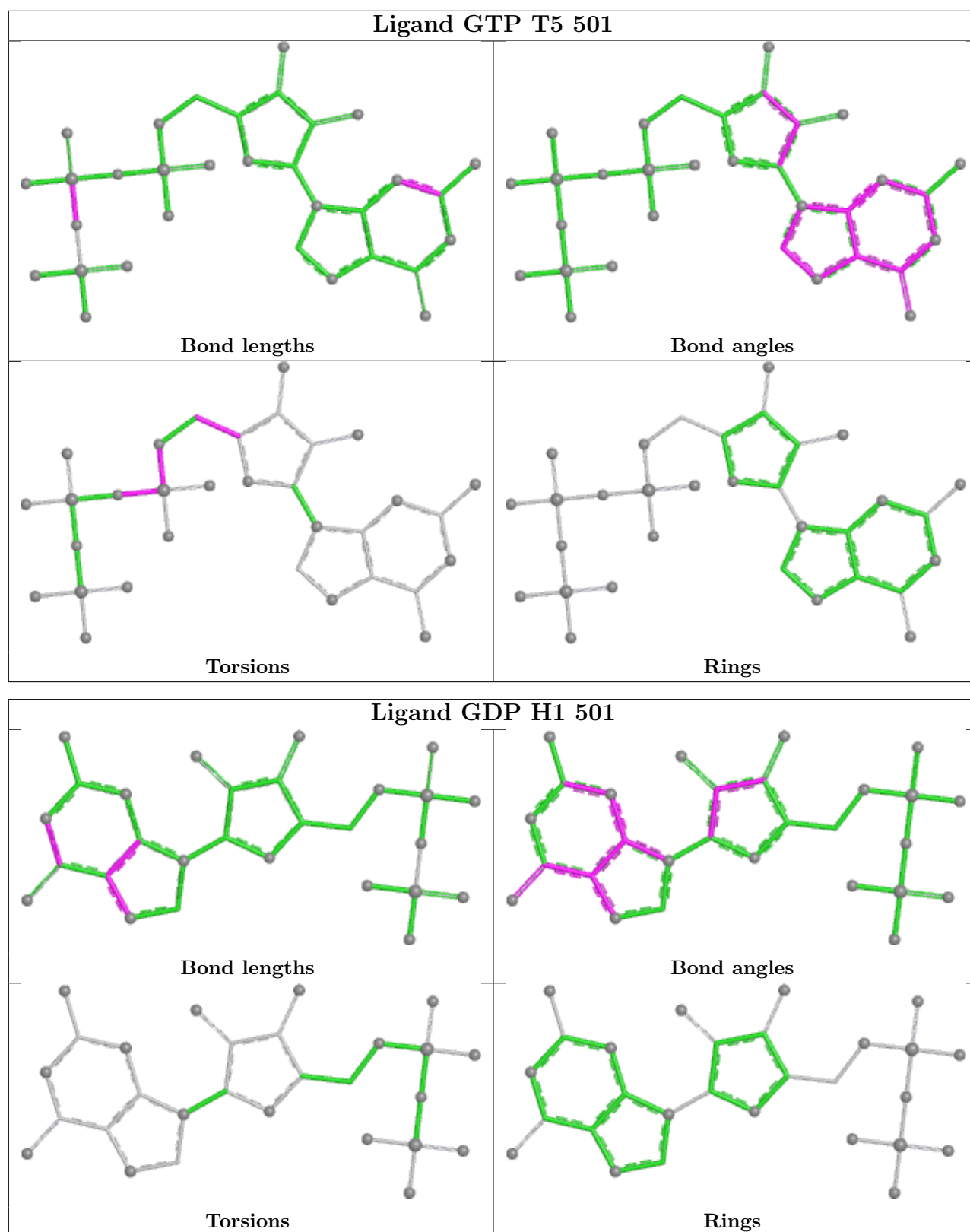


Ligand GTP K2 501

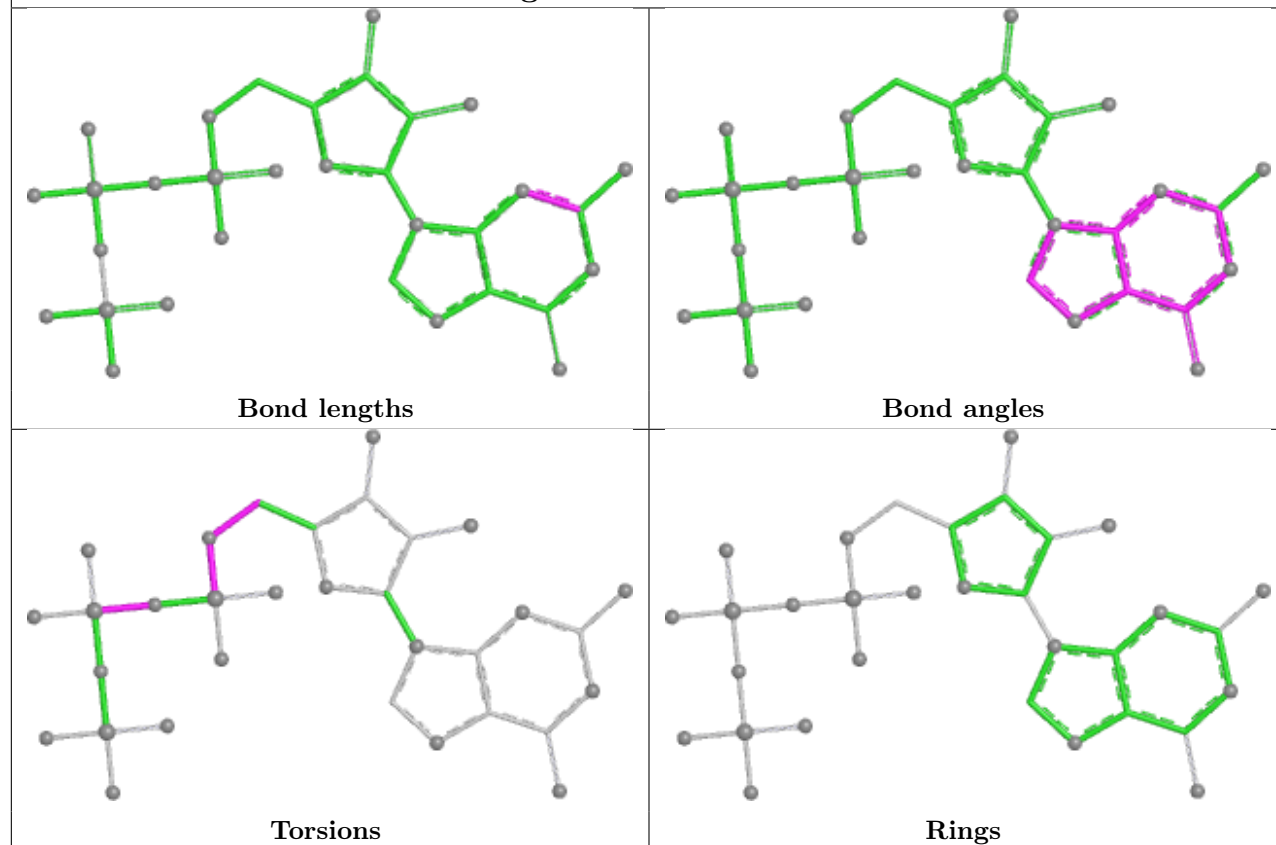


Ligand GTP U5 501

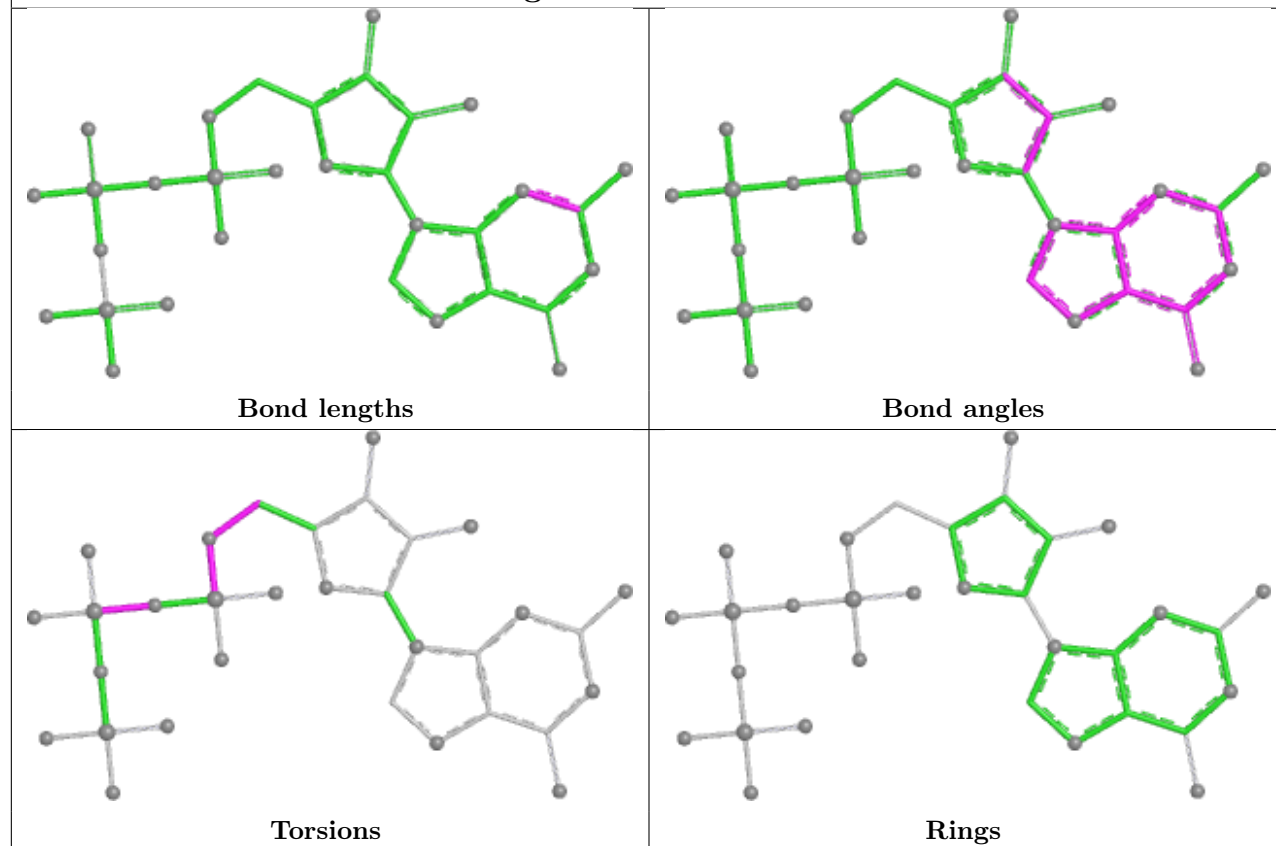


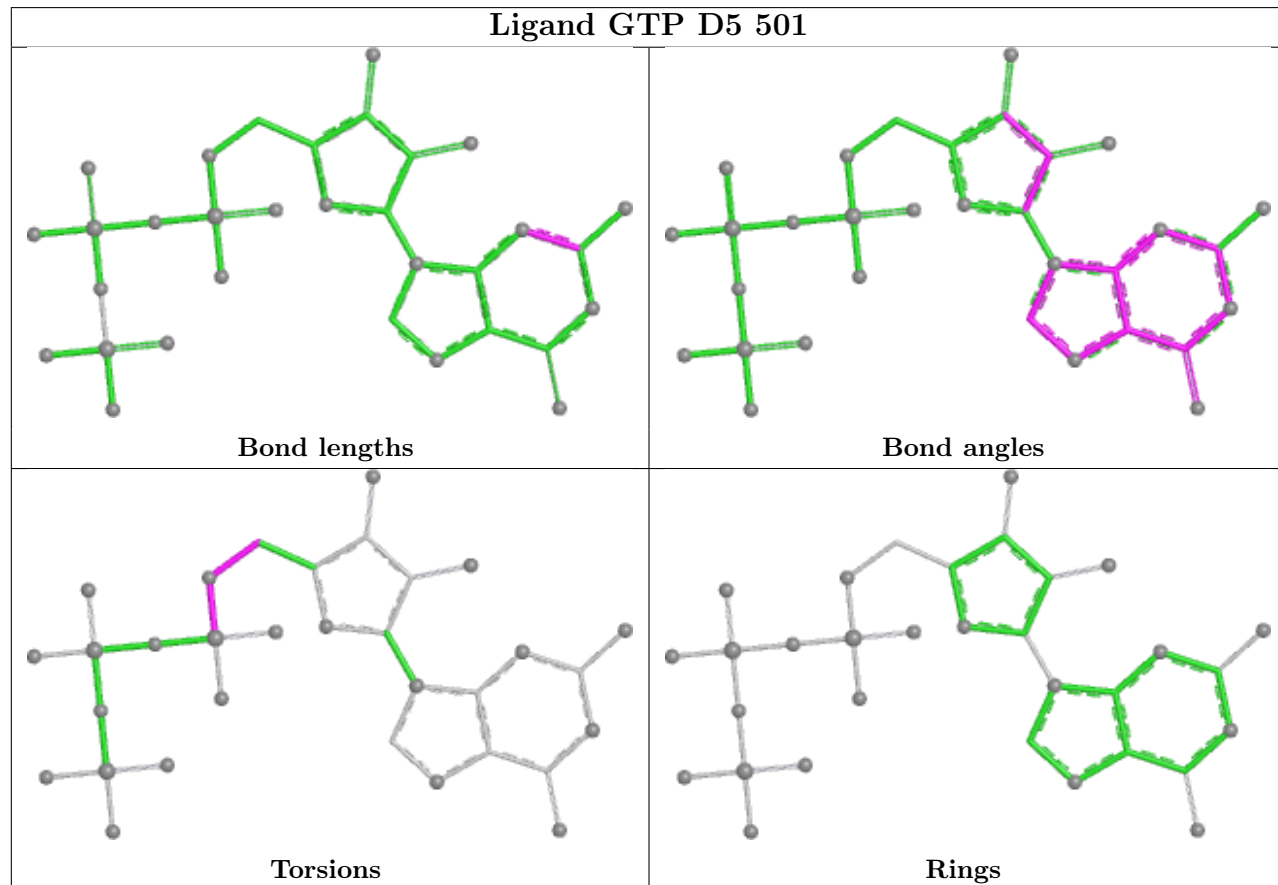
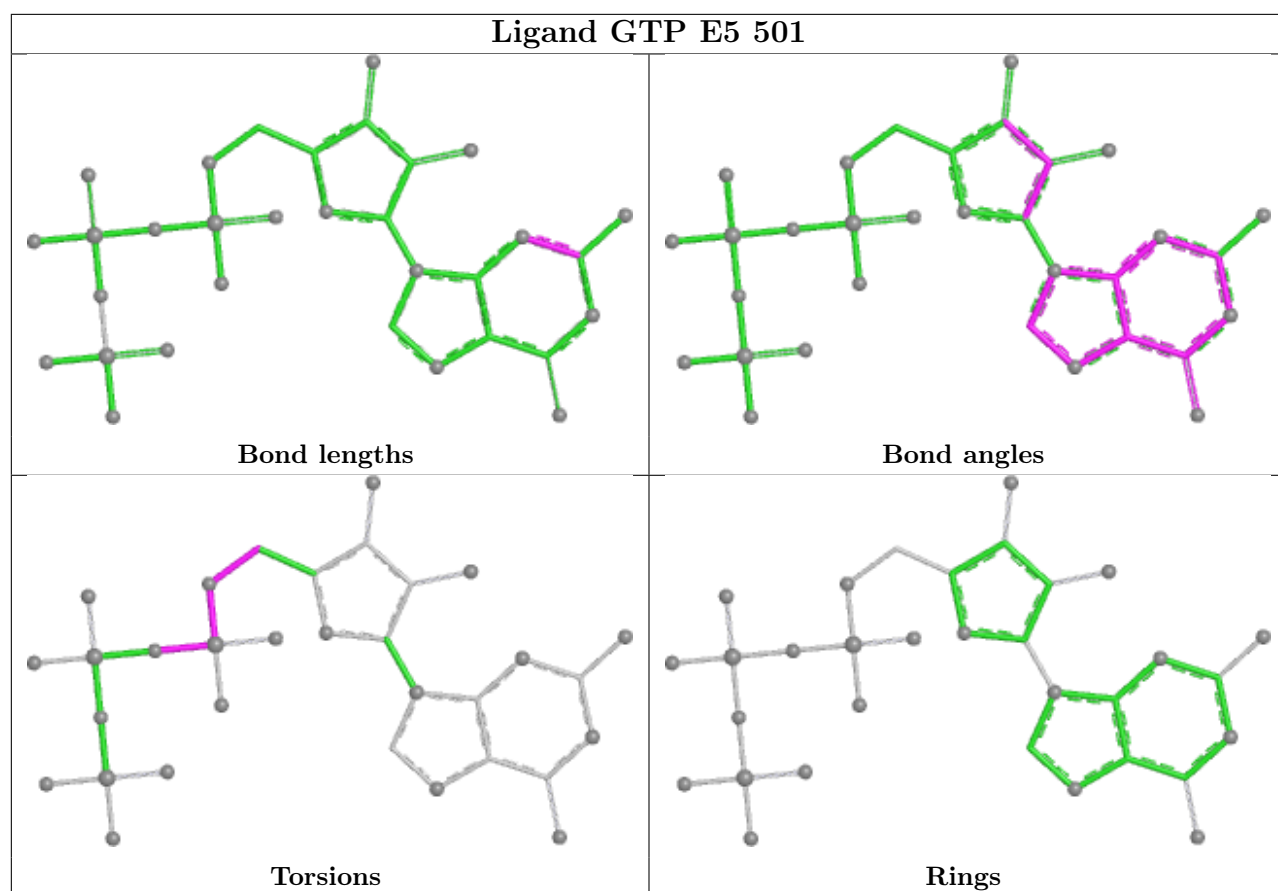


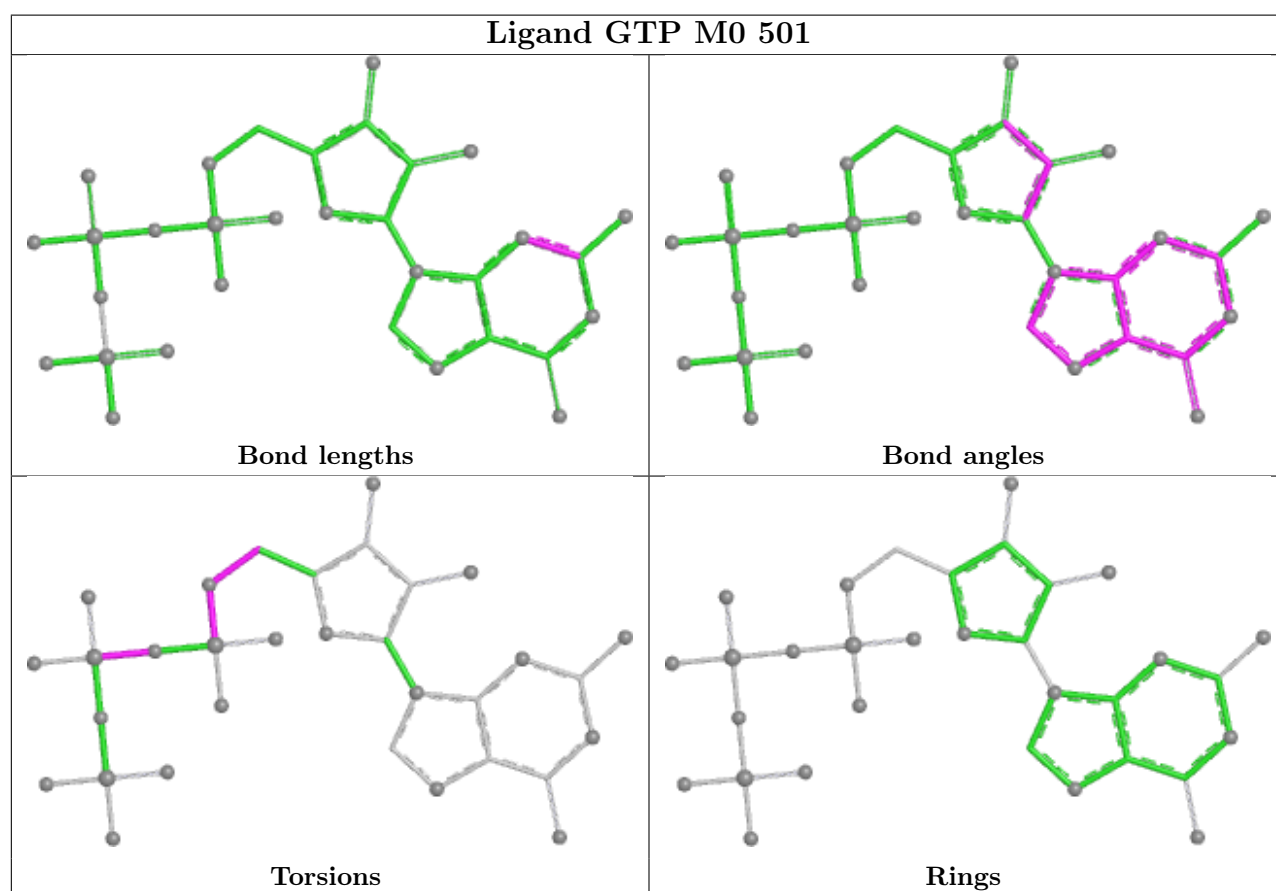
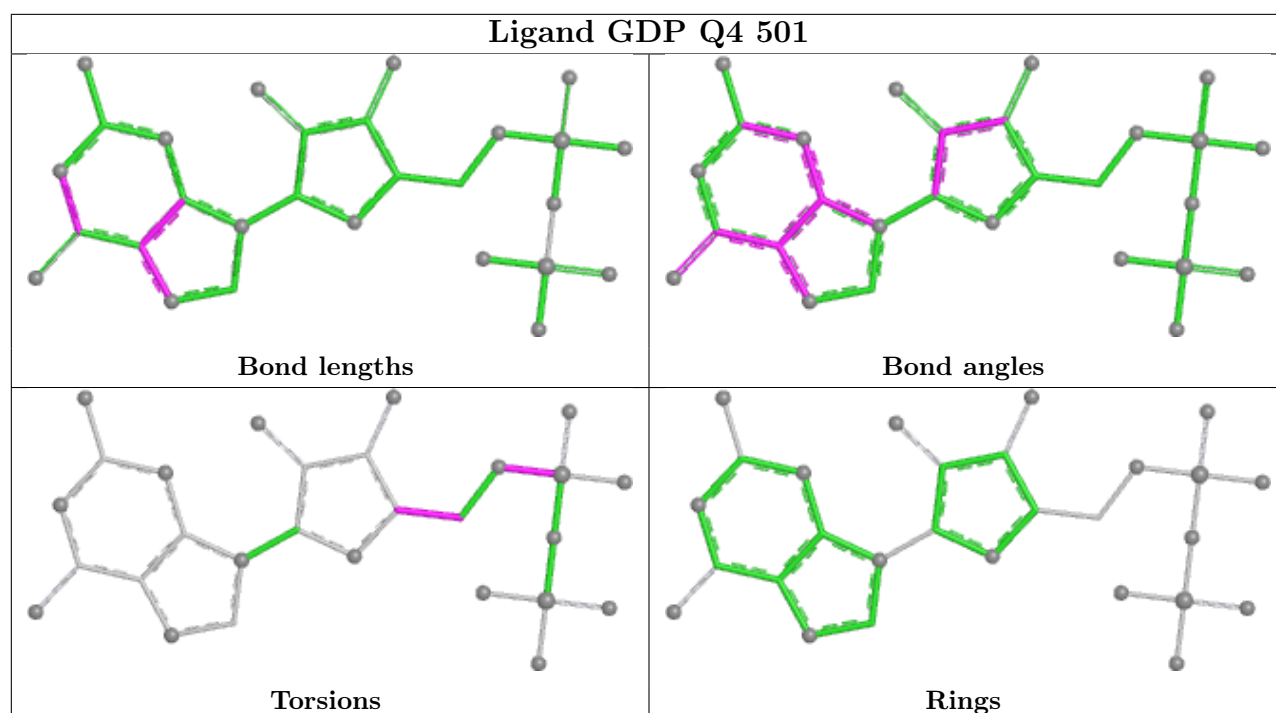
Ligand GTP K4 501



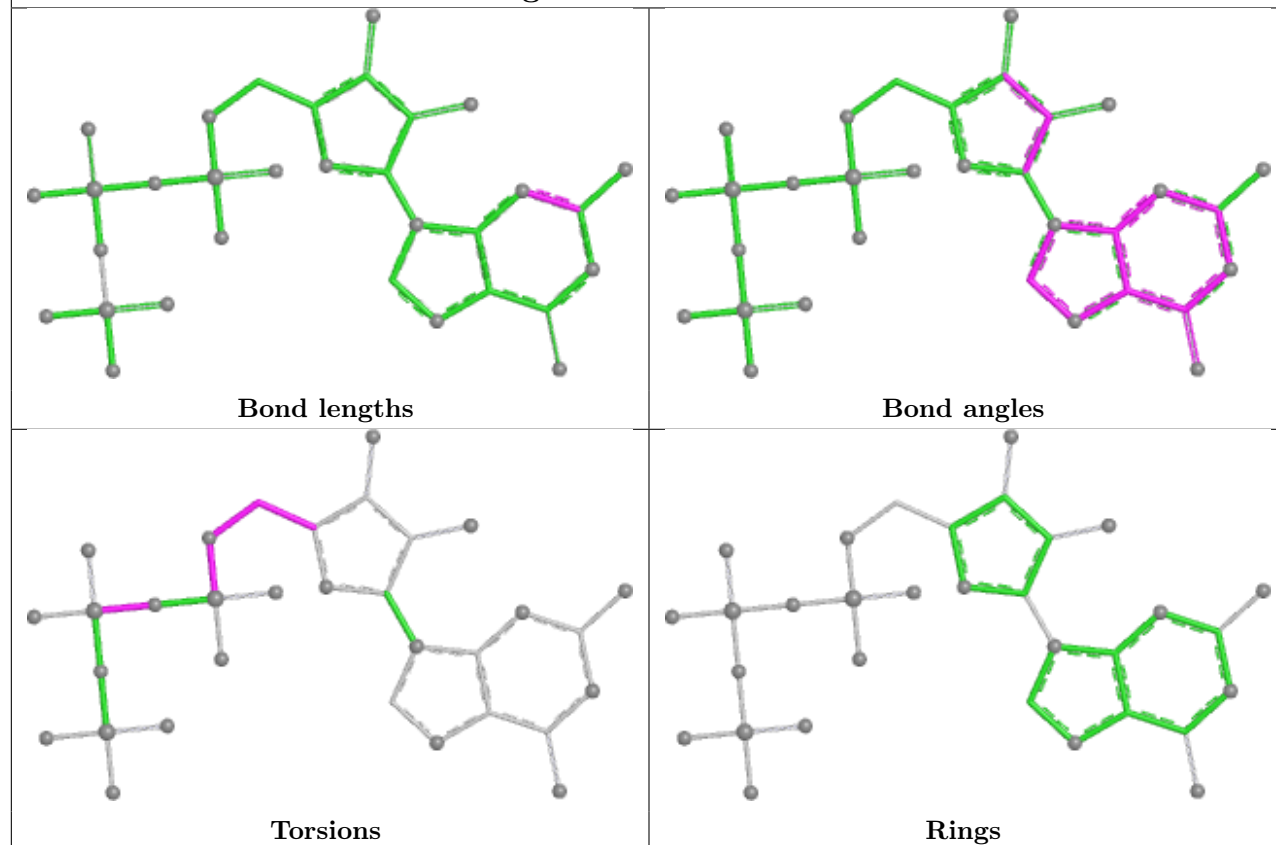
Ligand GTP L0 501



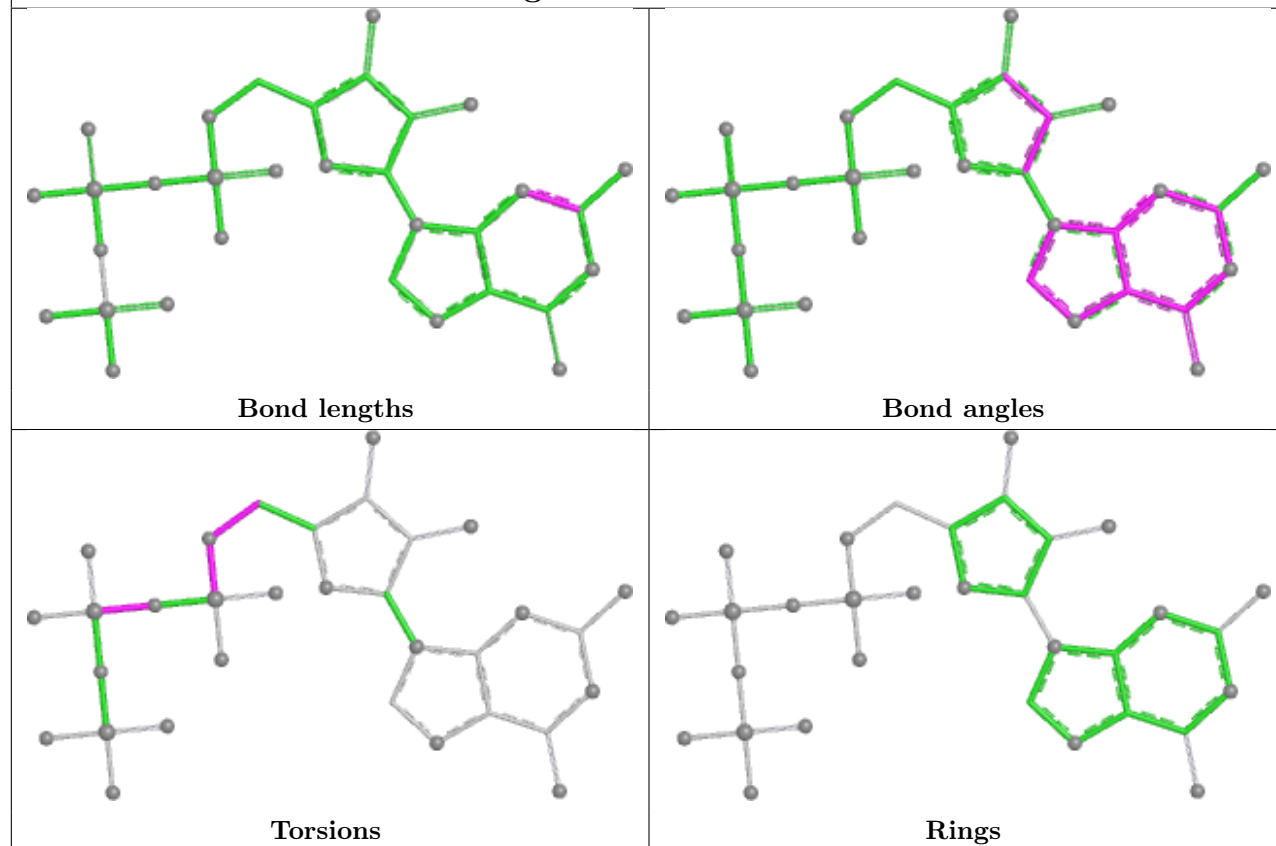


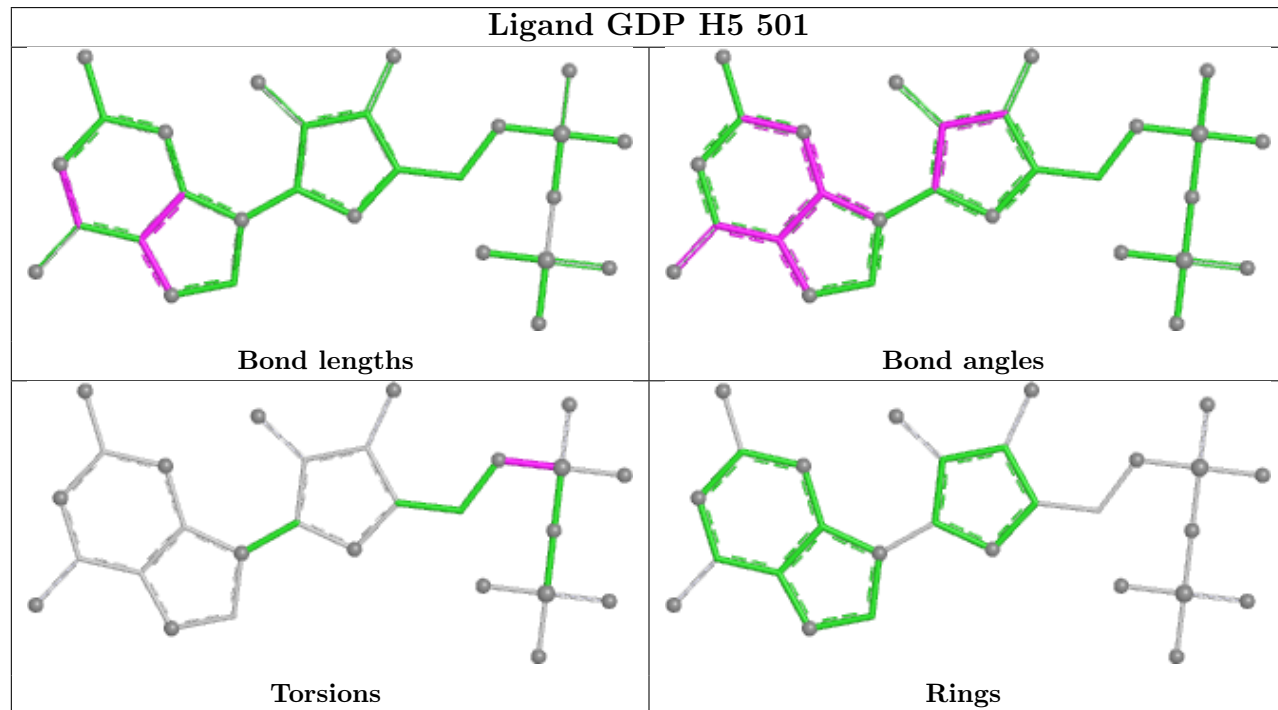
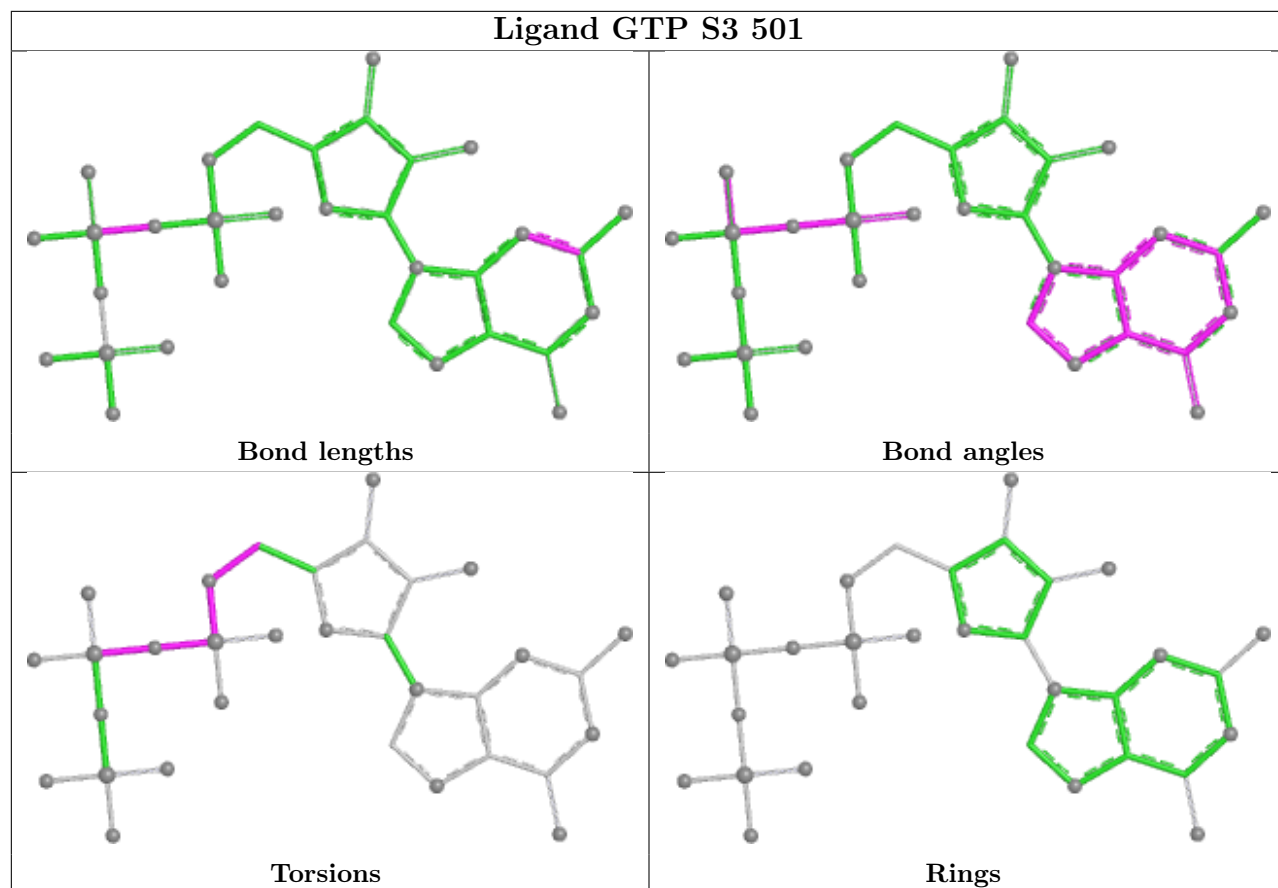


Ligand GTP P0 501

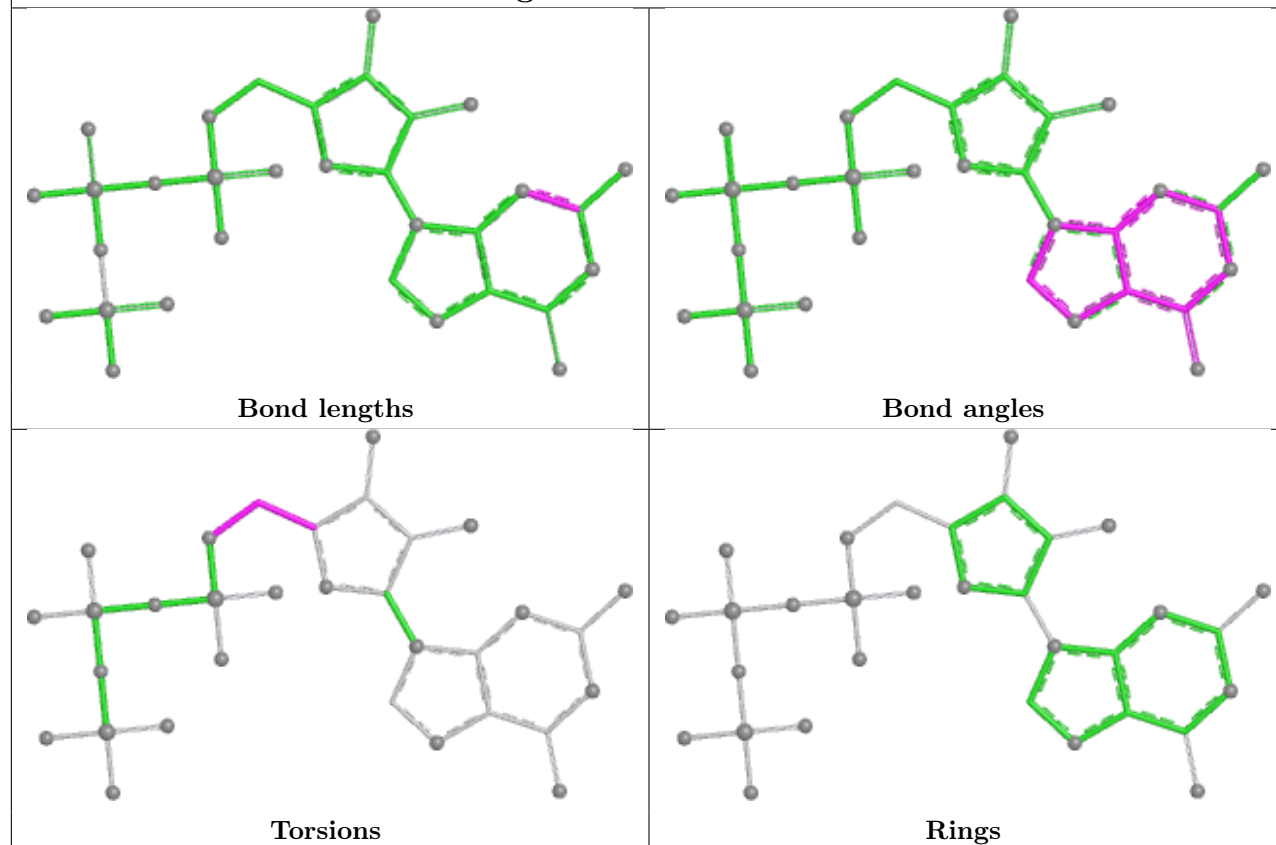


Ligand GTP L2 501

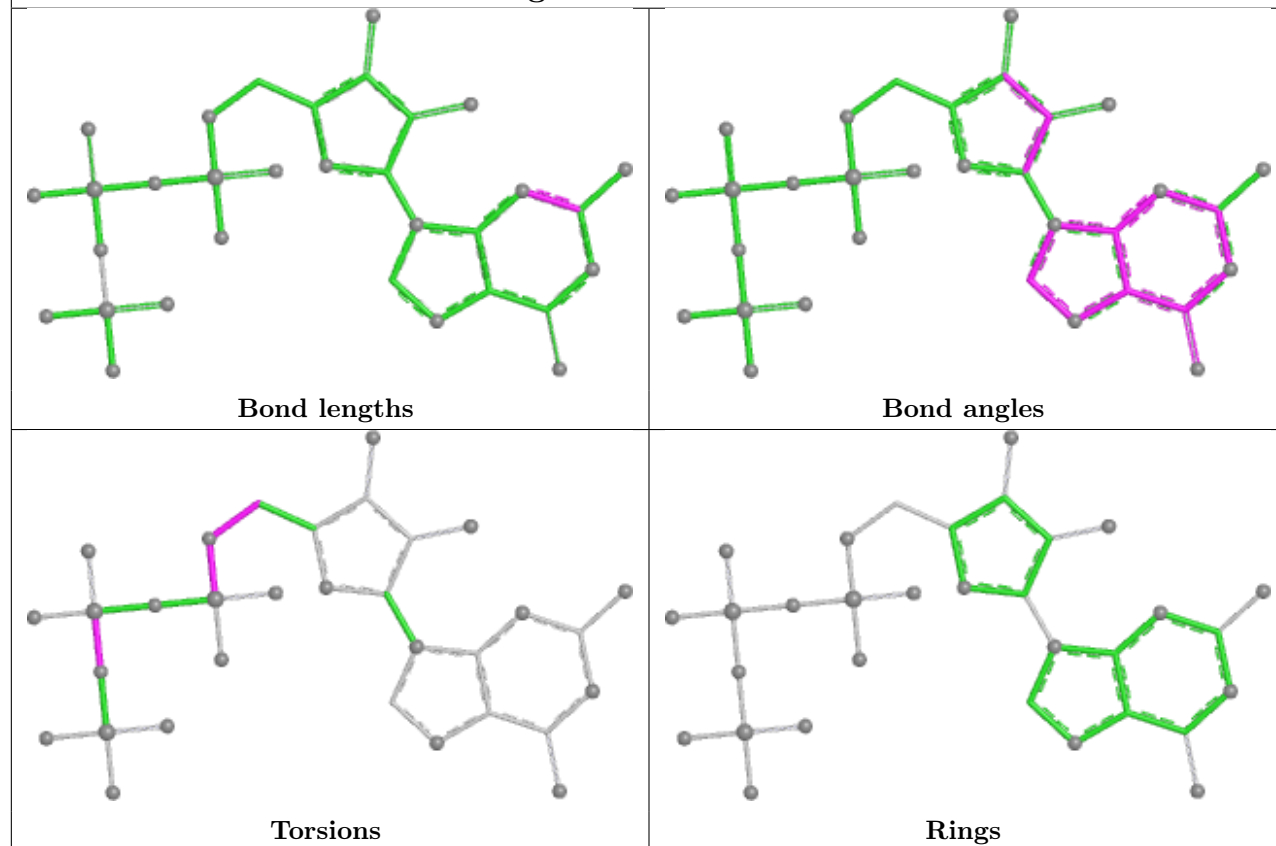


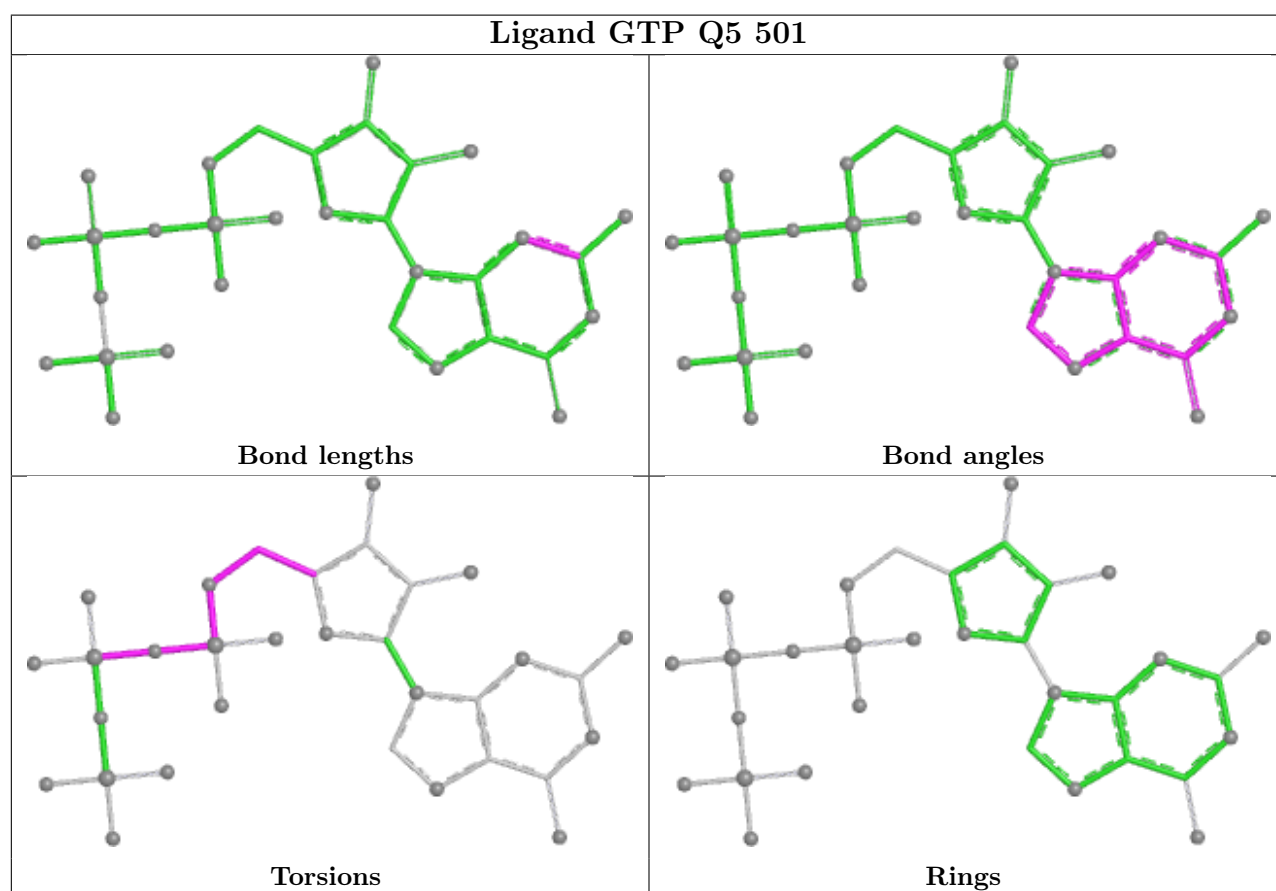
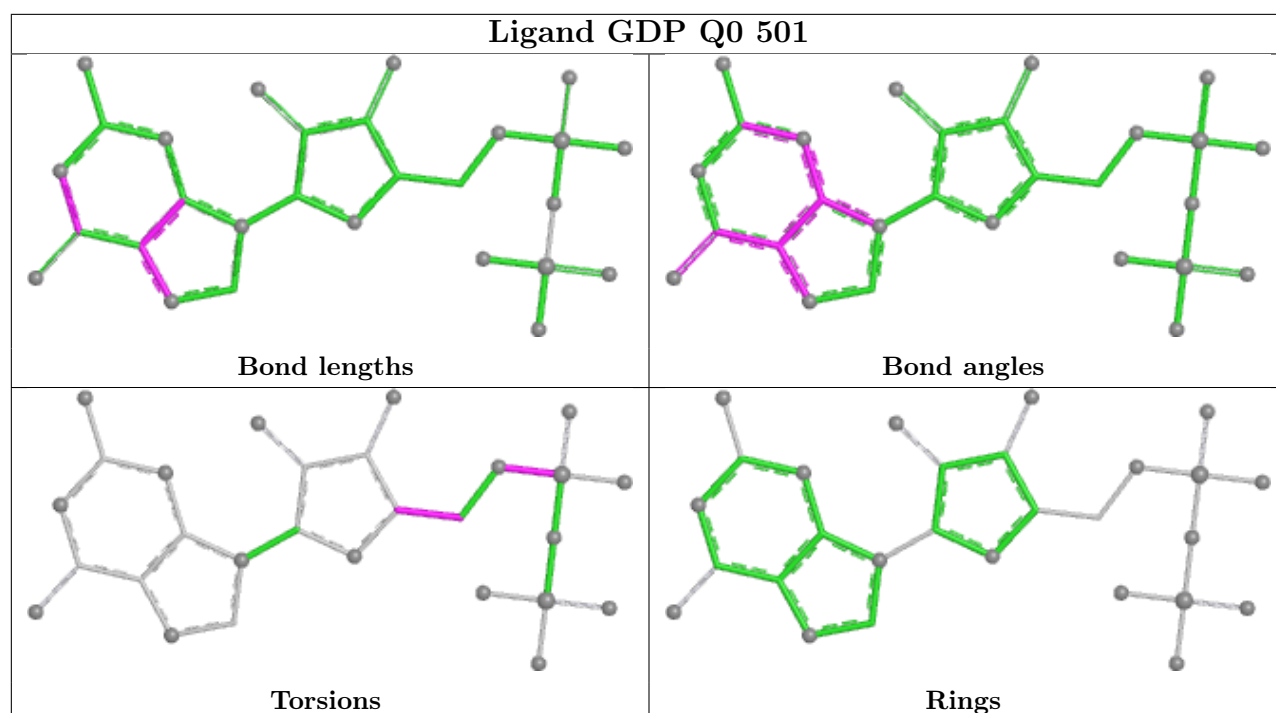


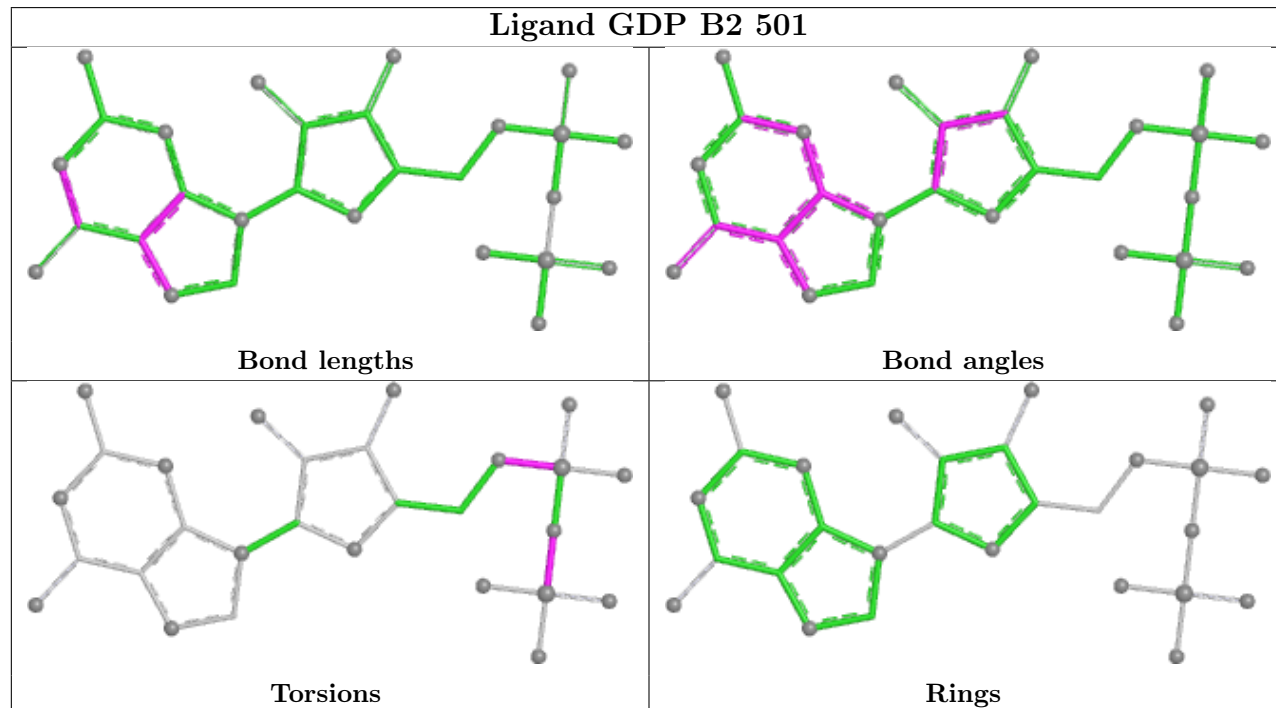
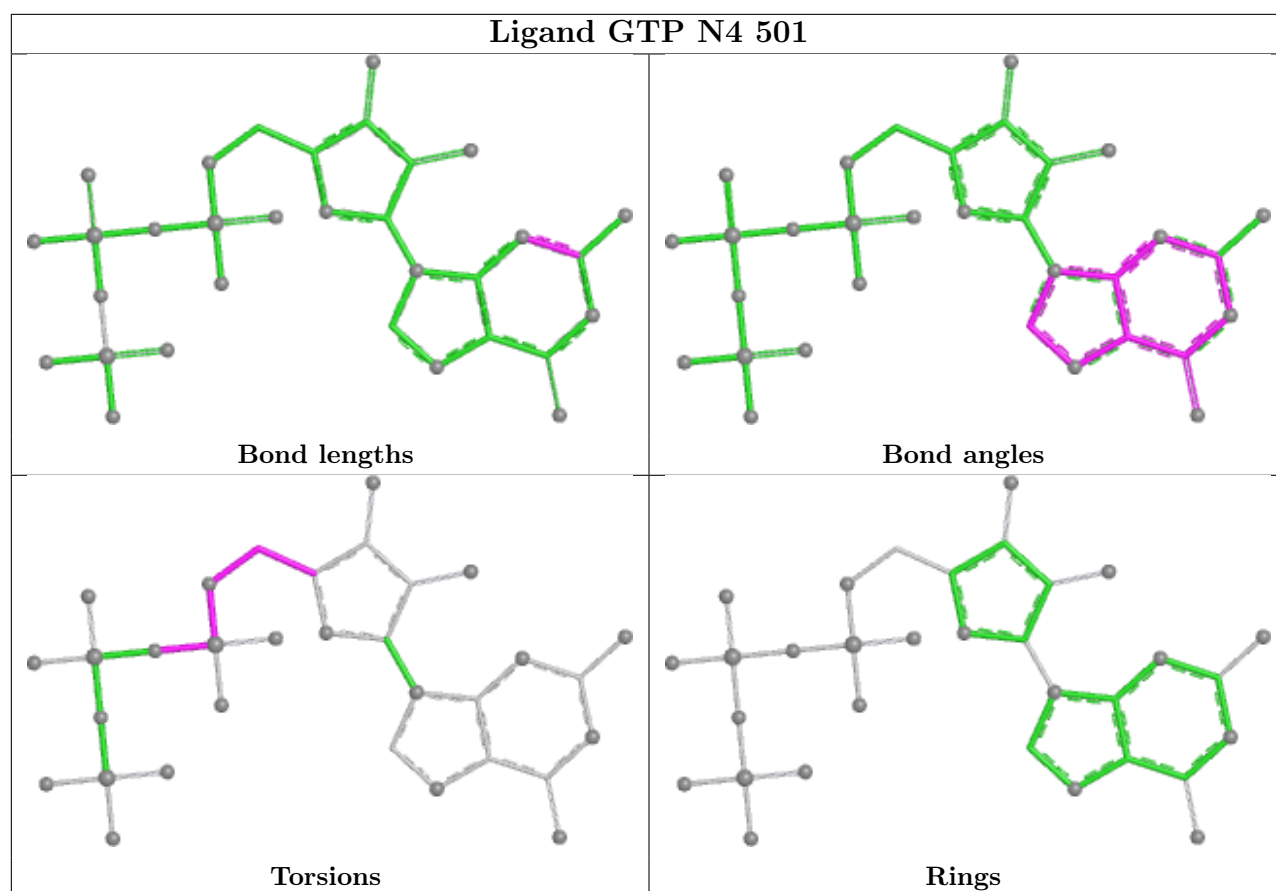
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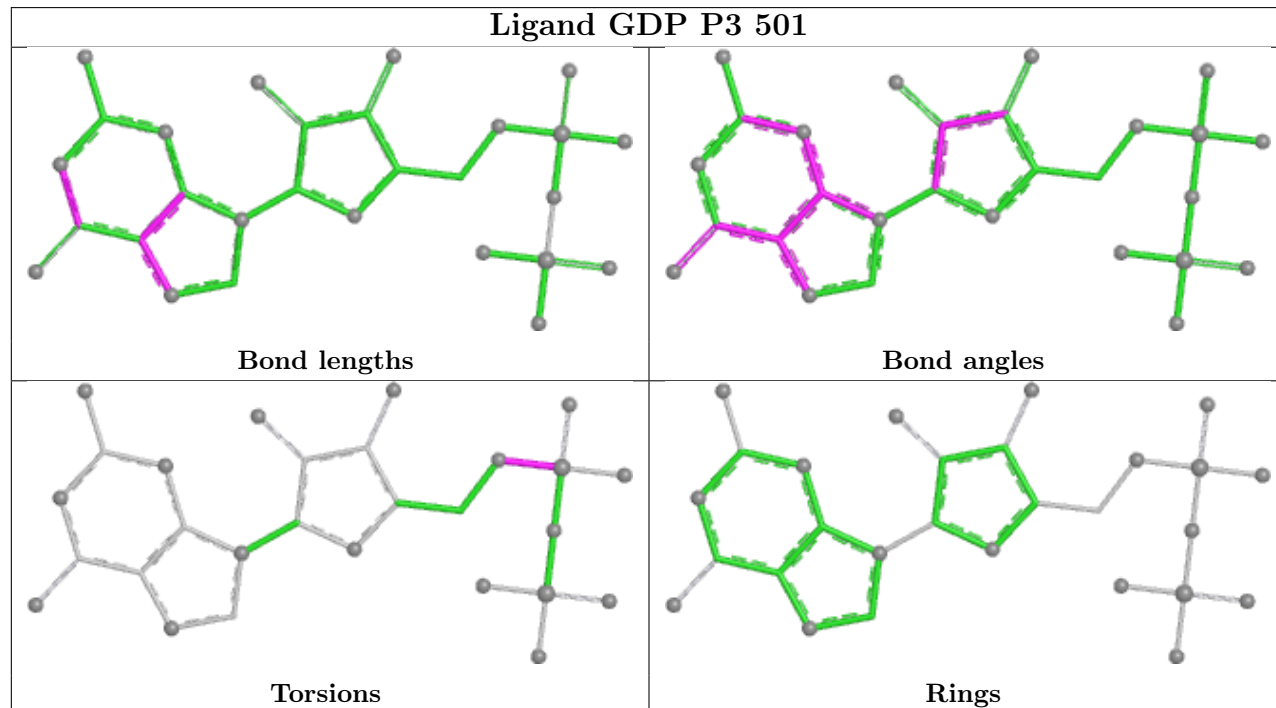
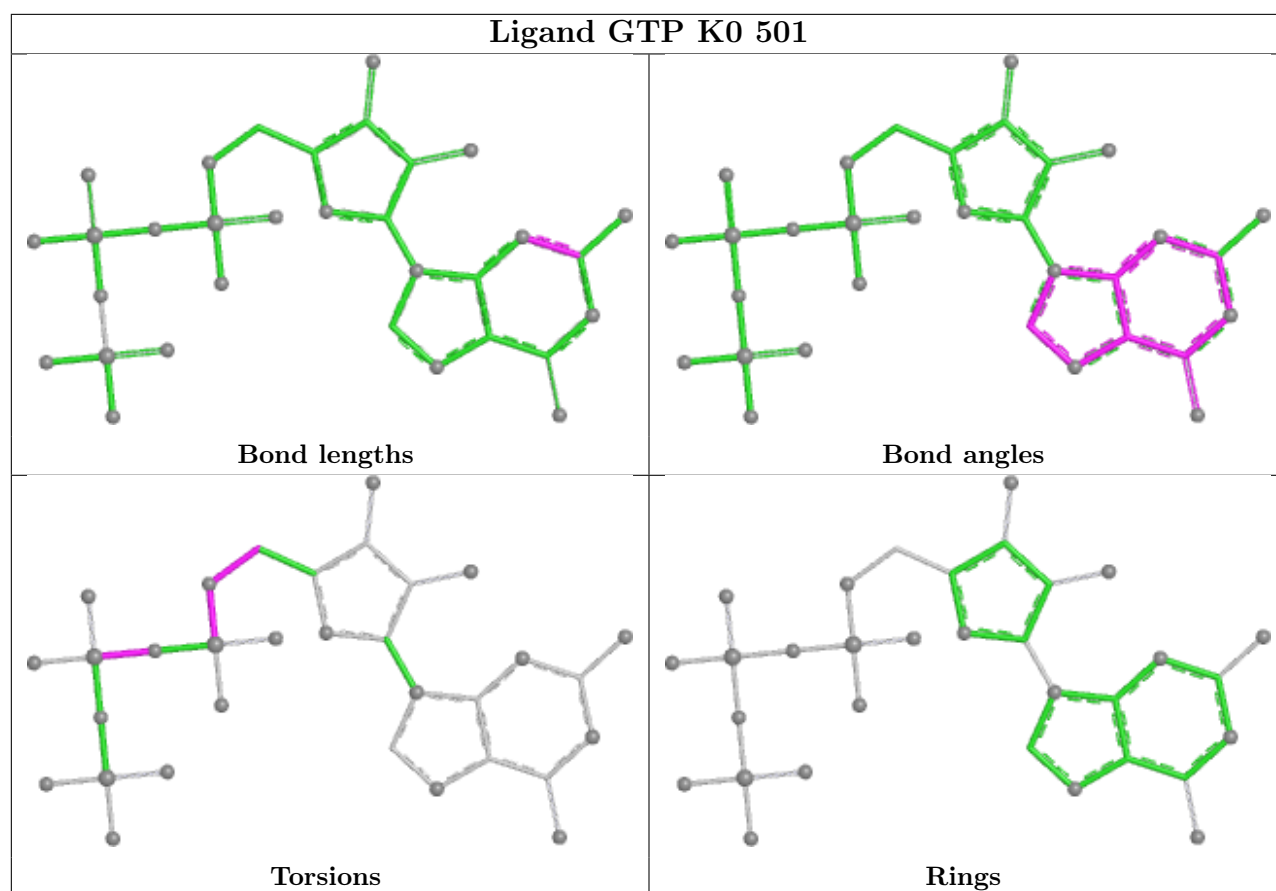


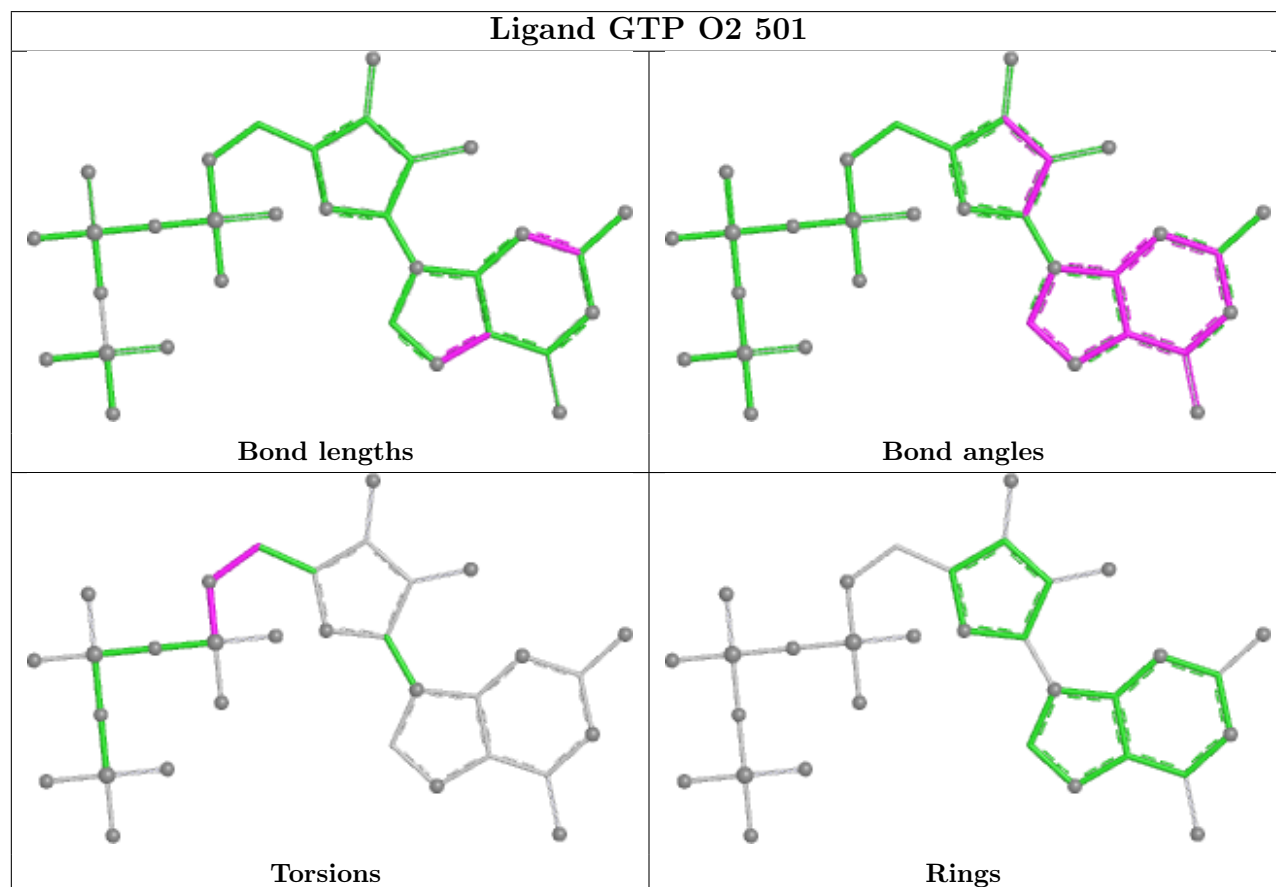
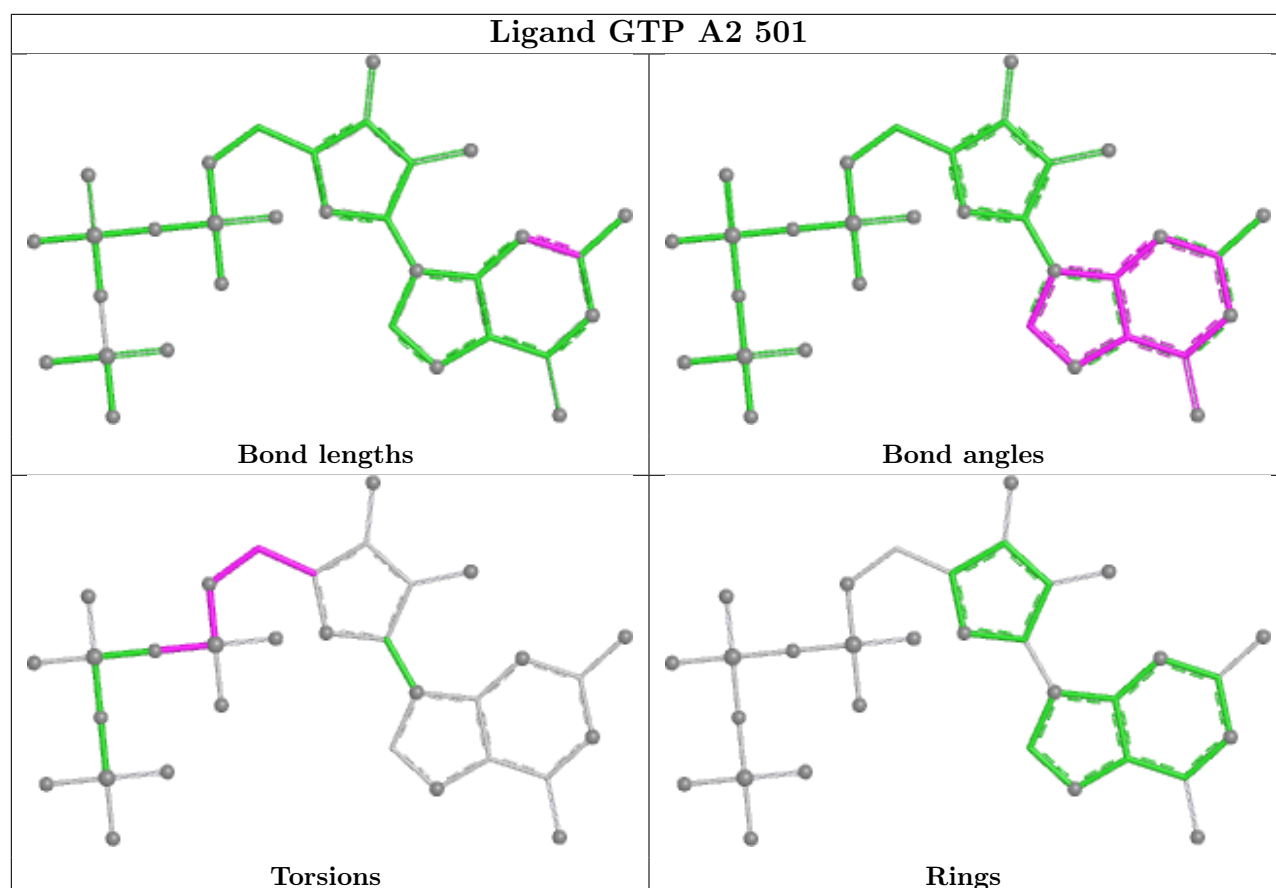
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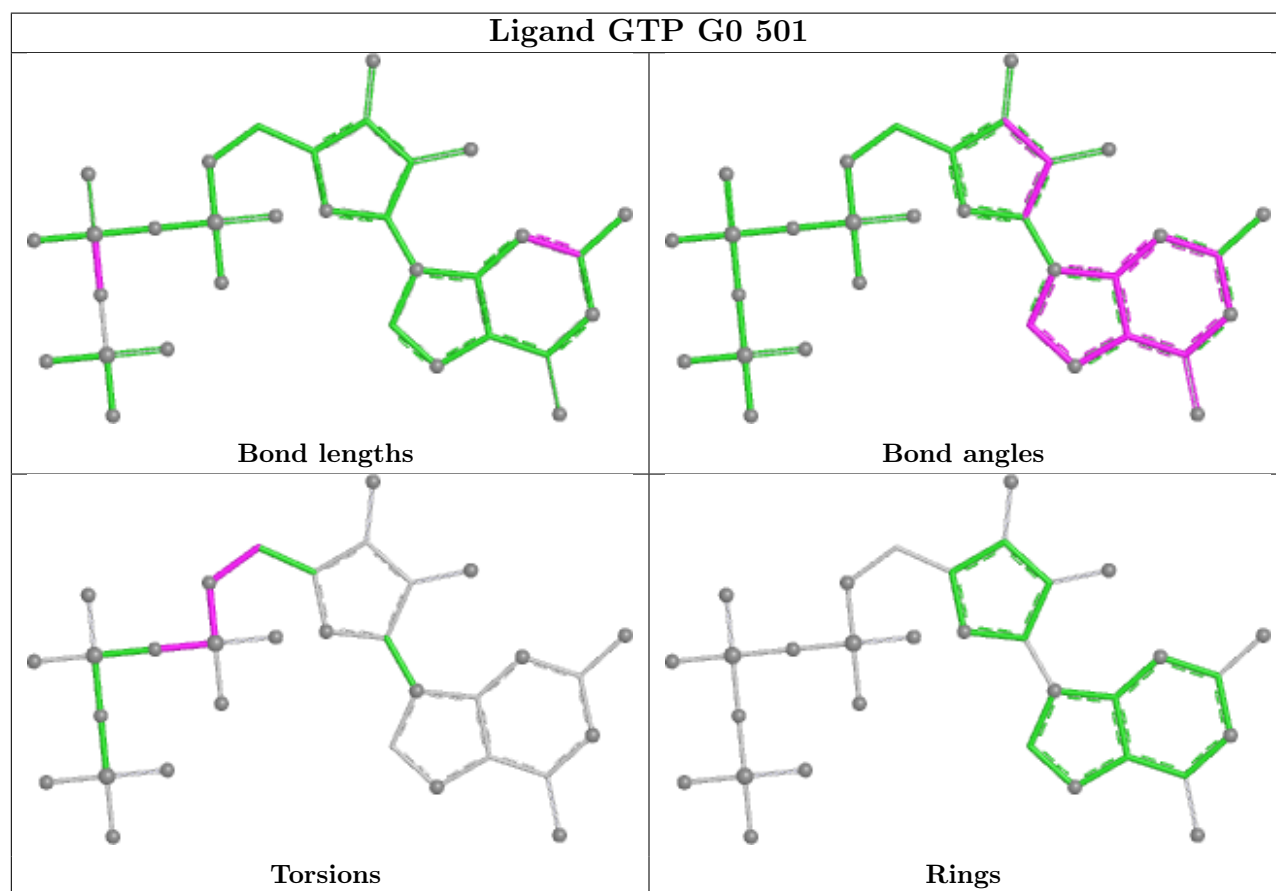
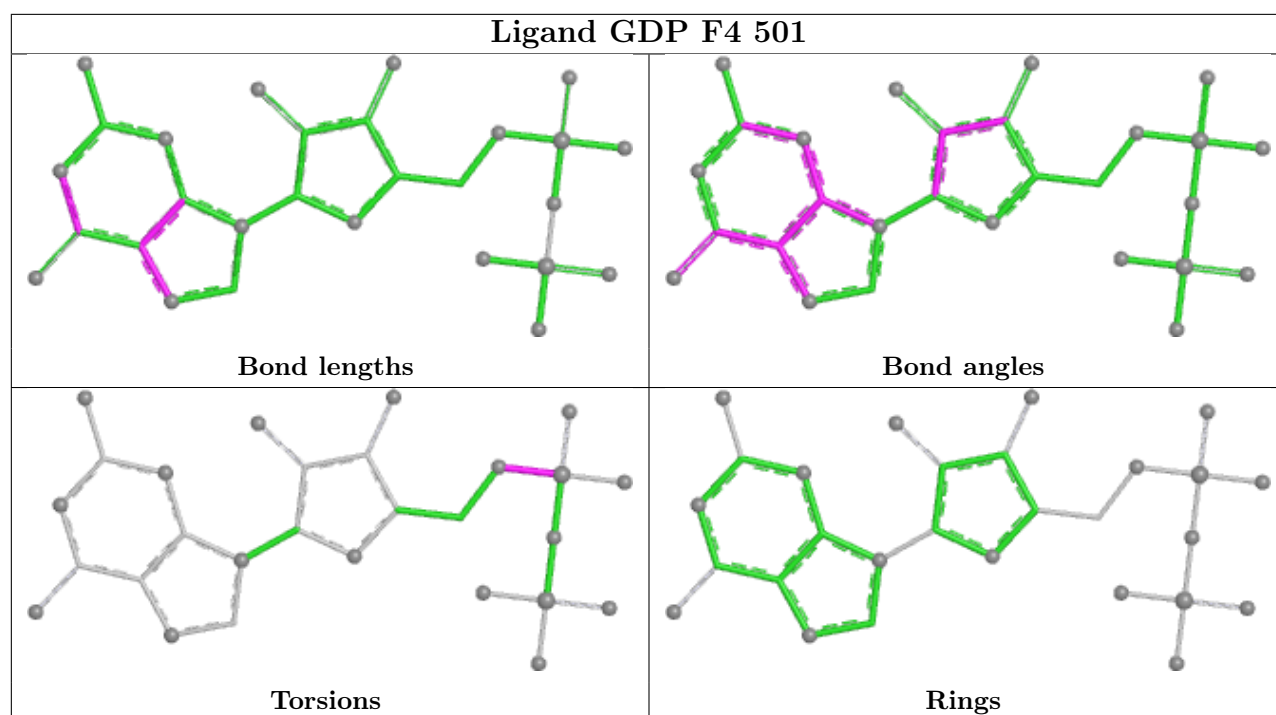




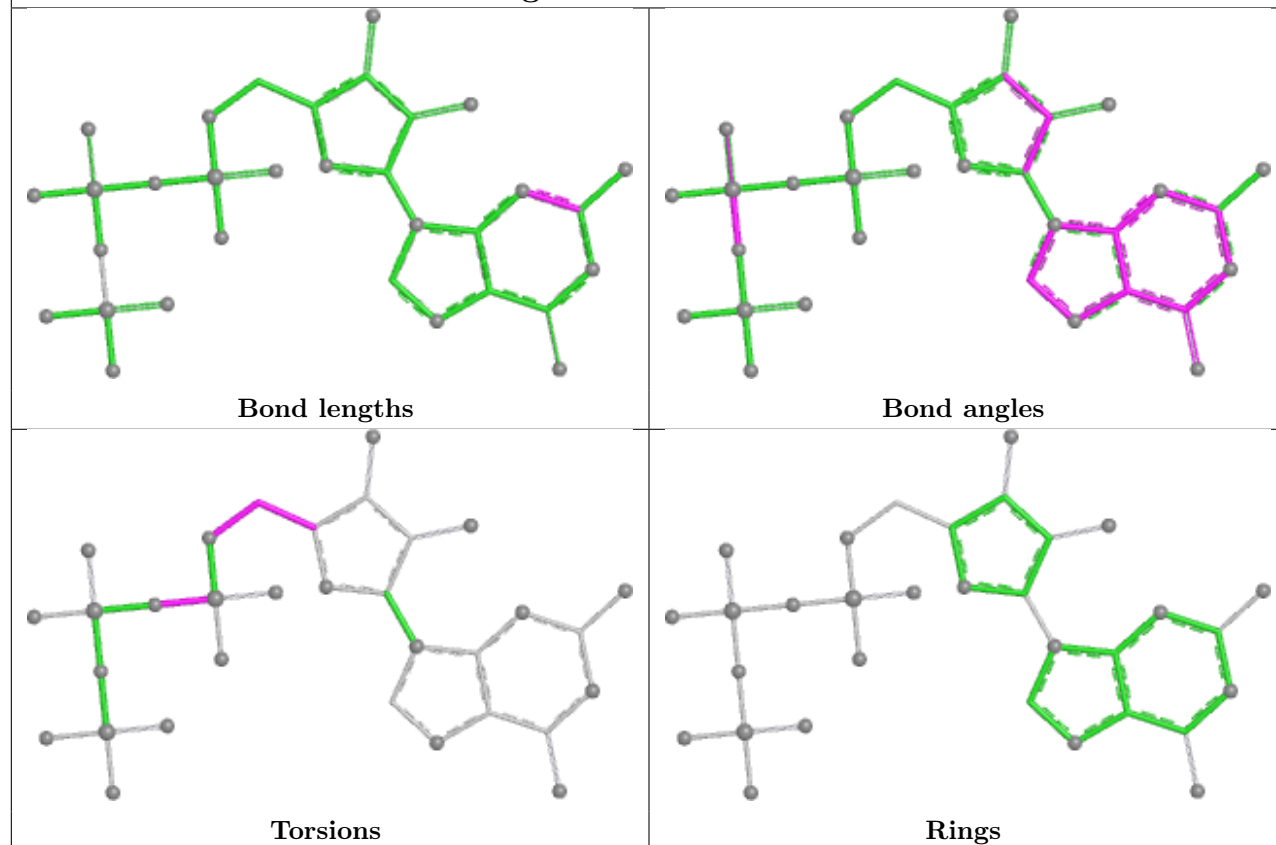




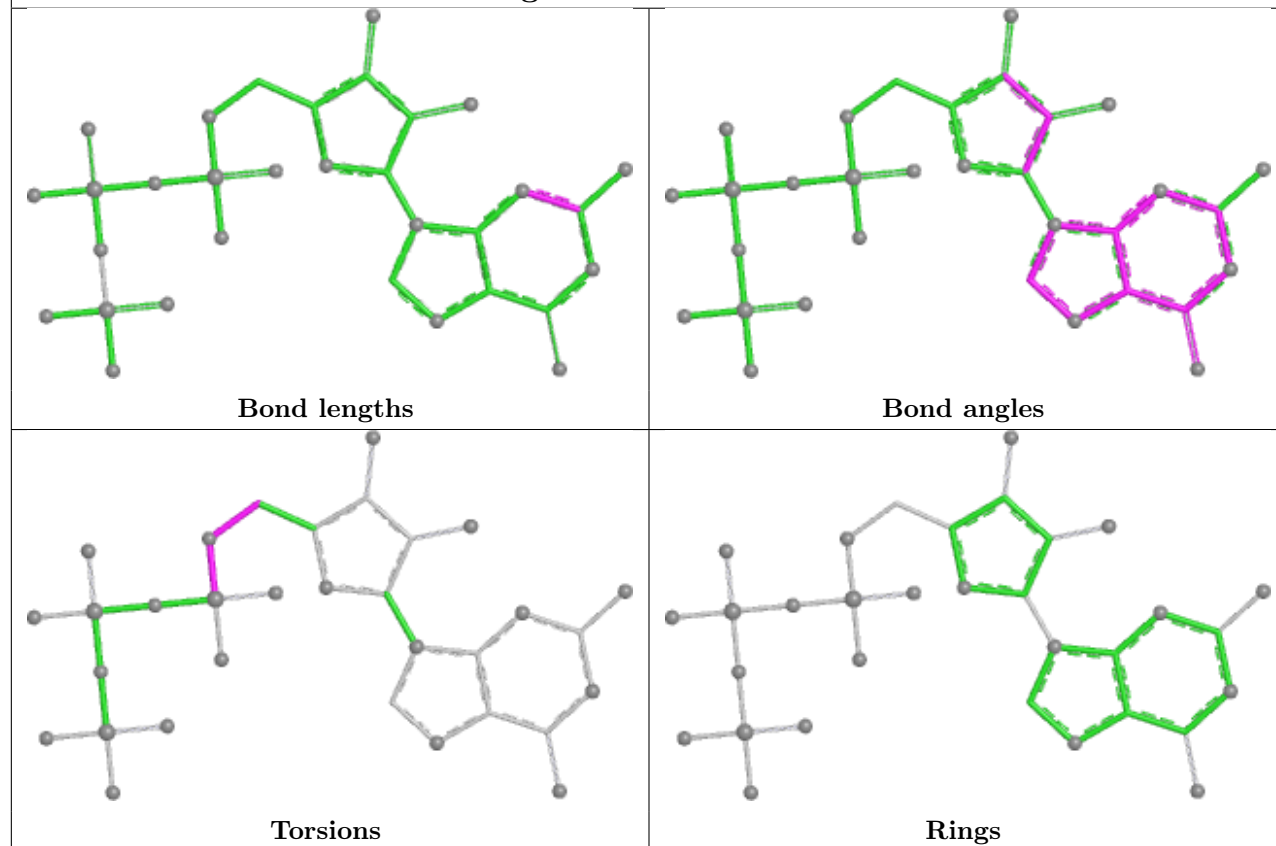


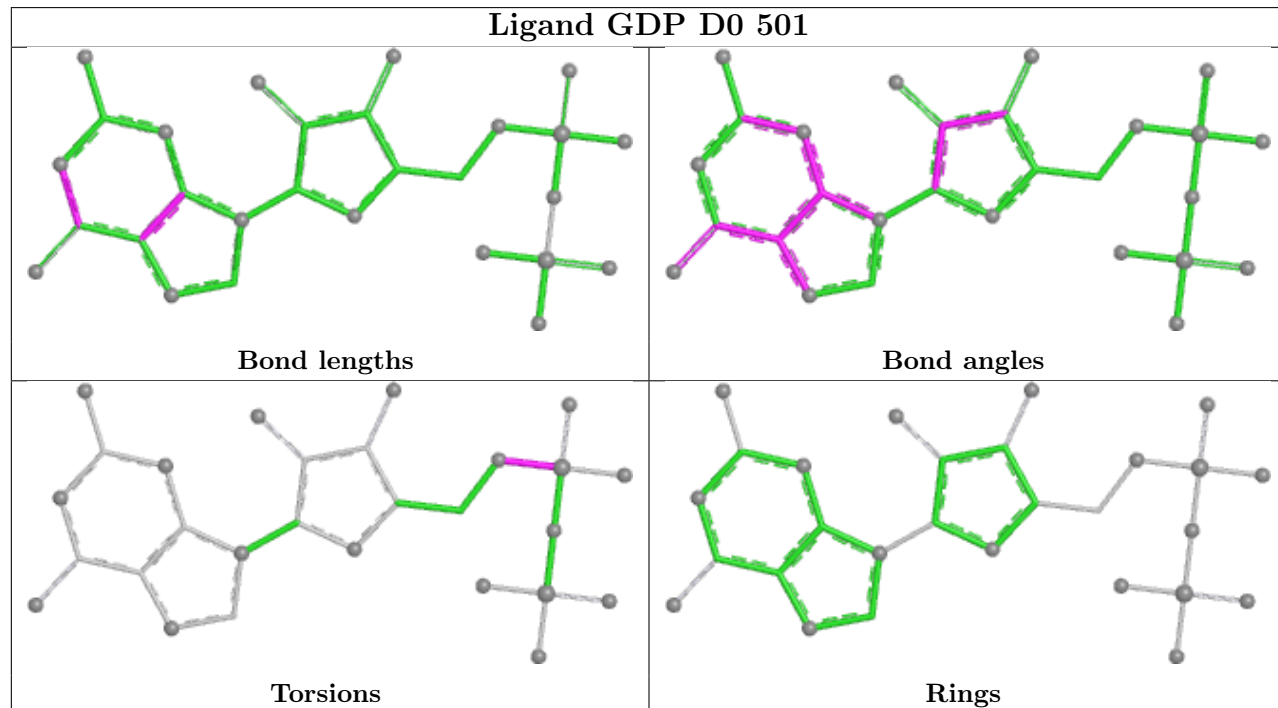
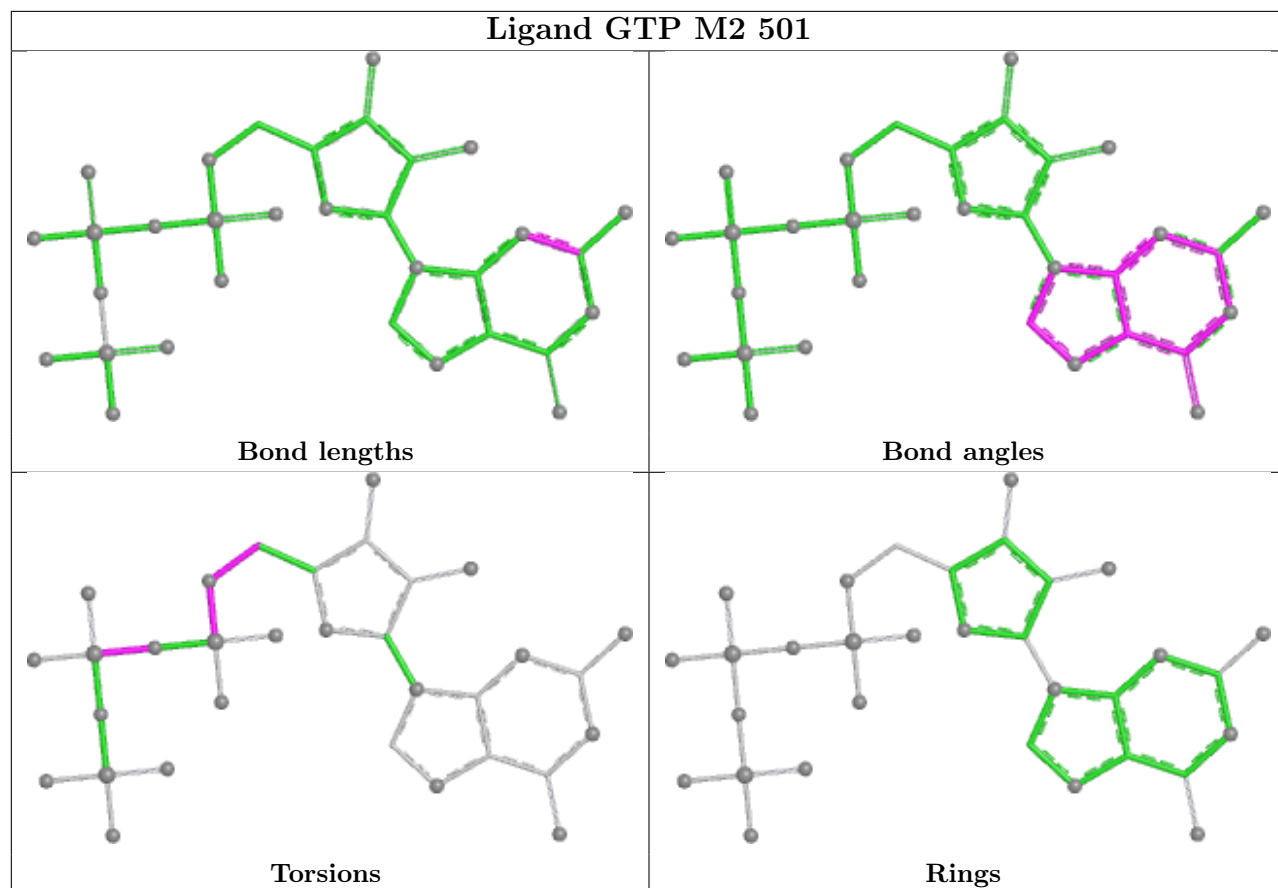


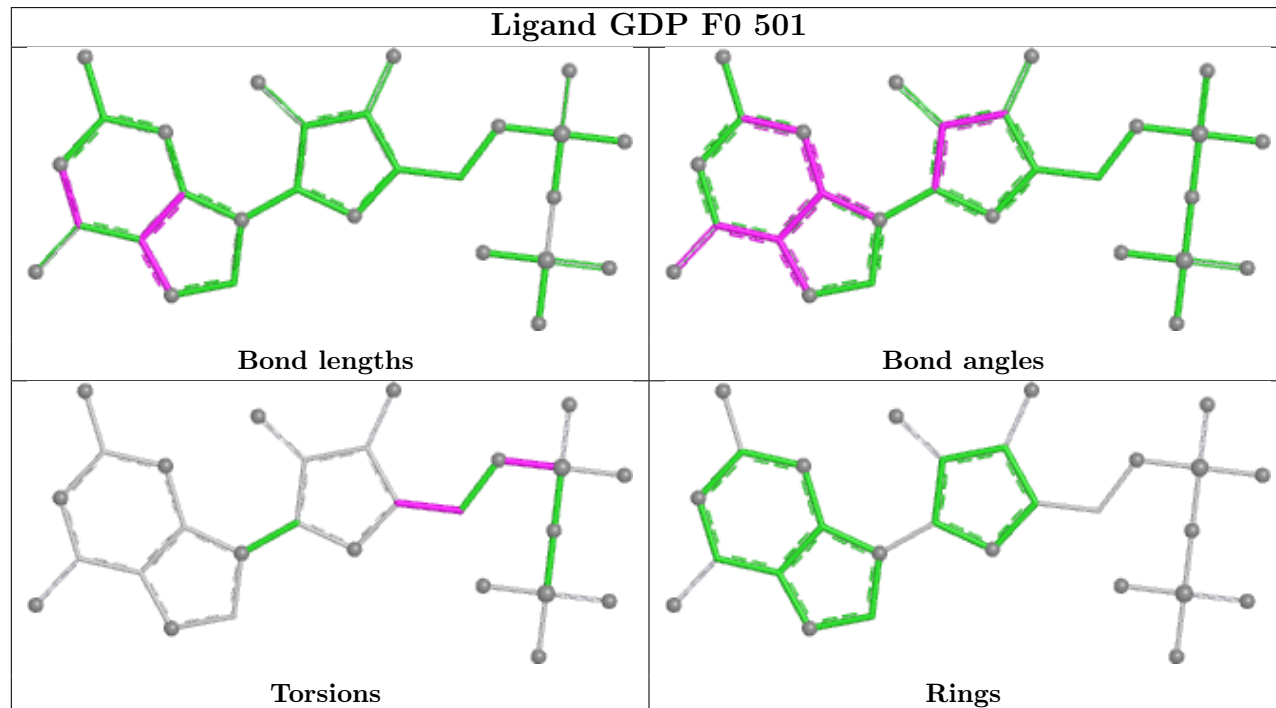
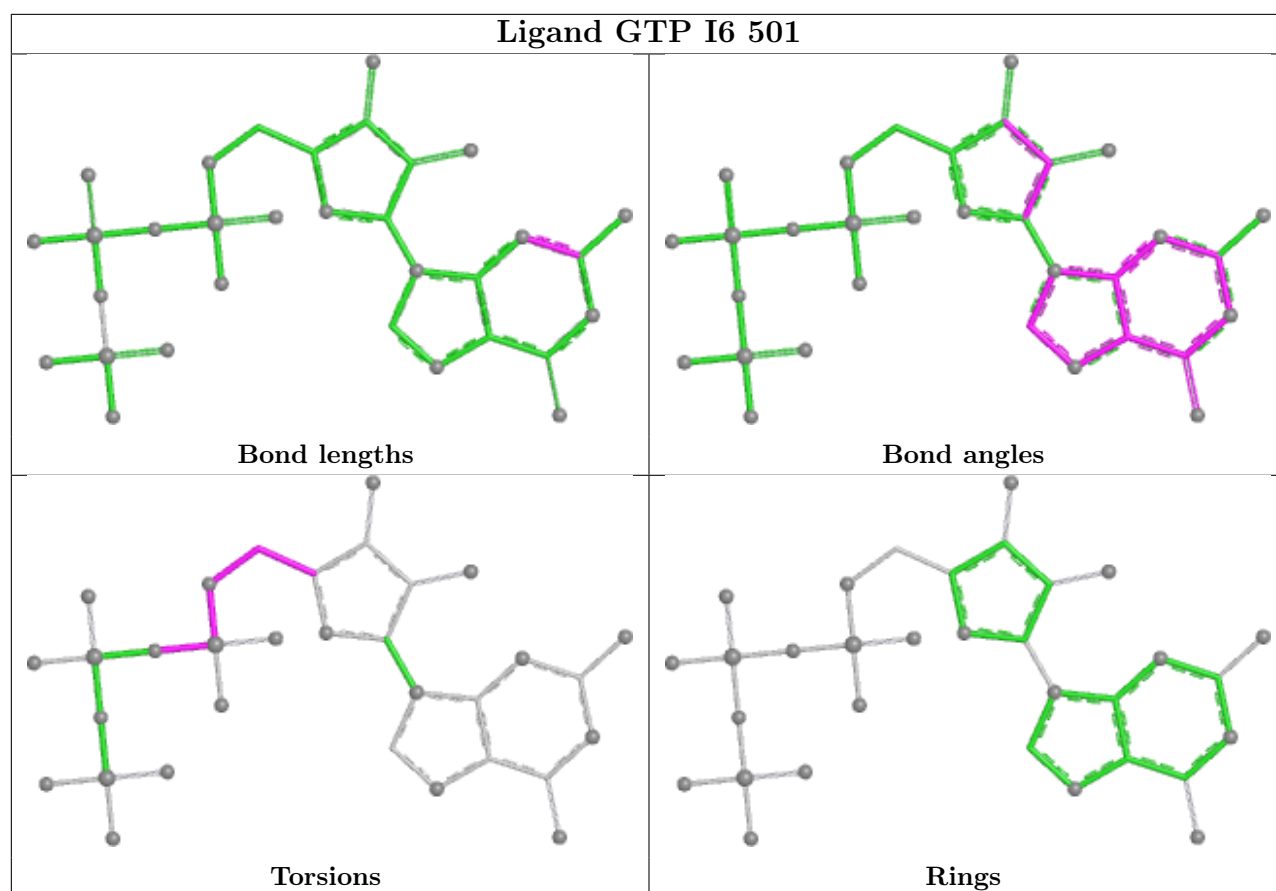
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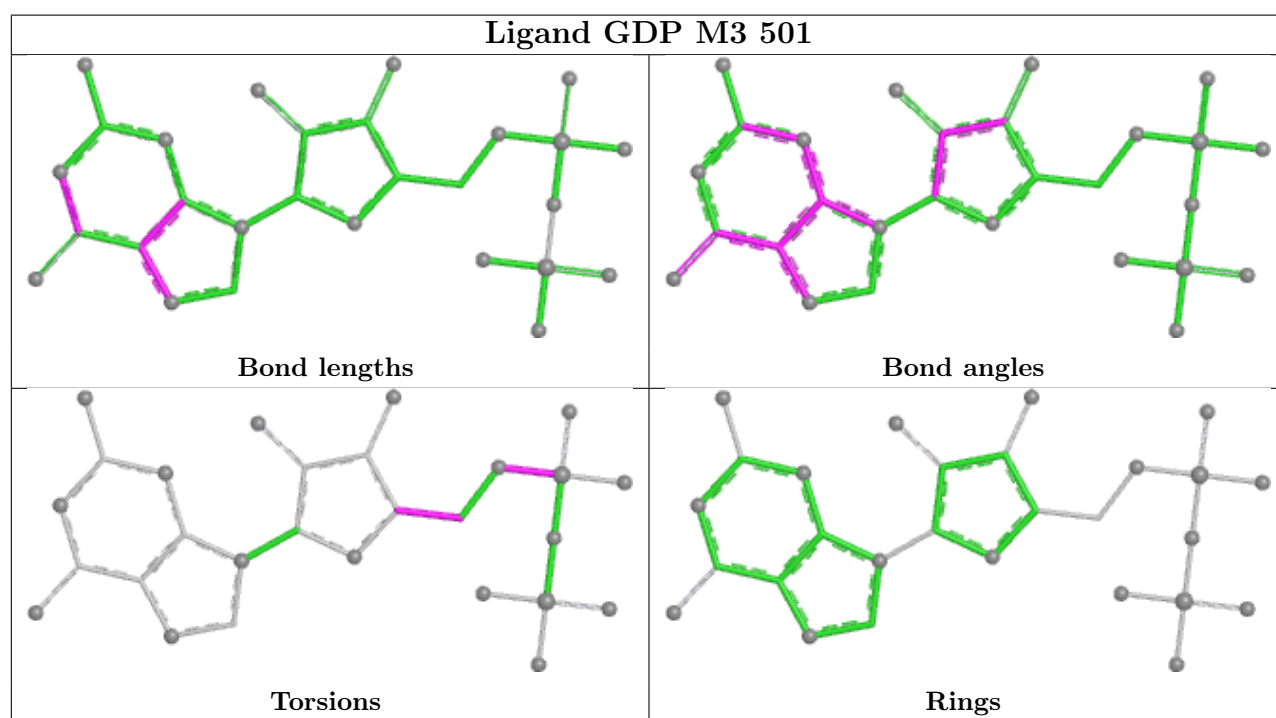
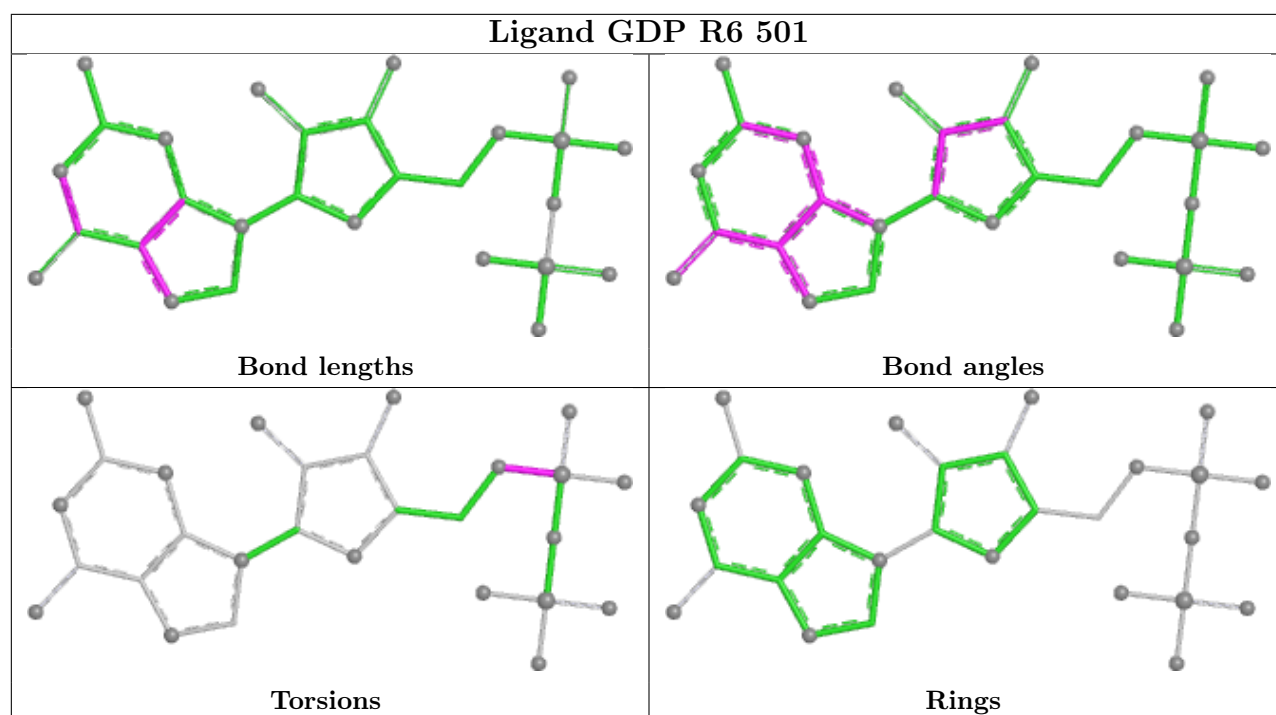


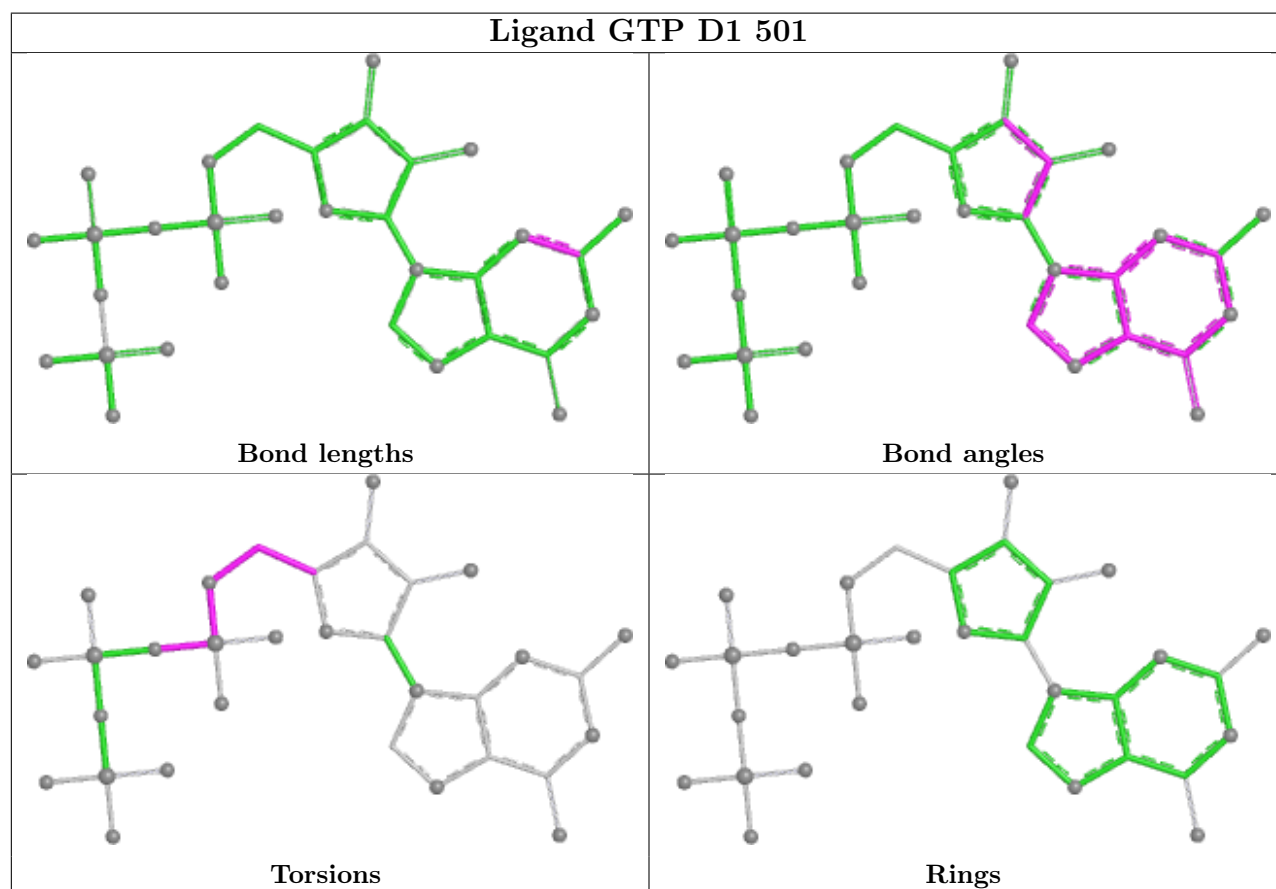
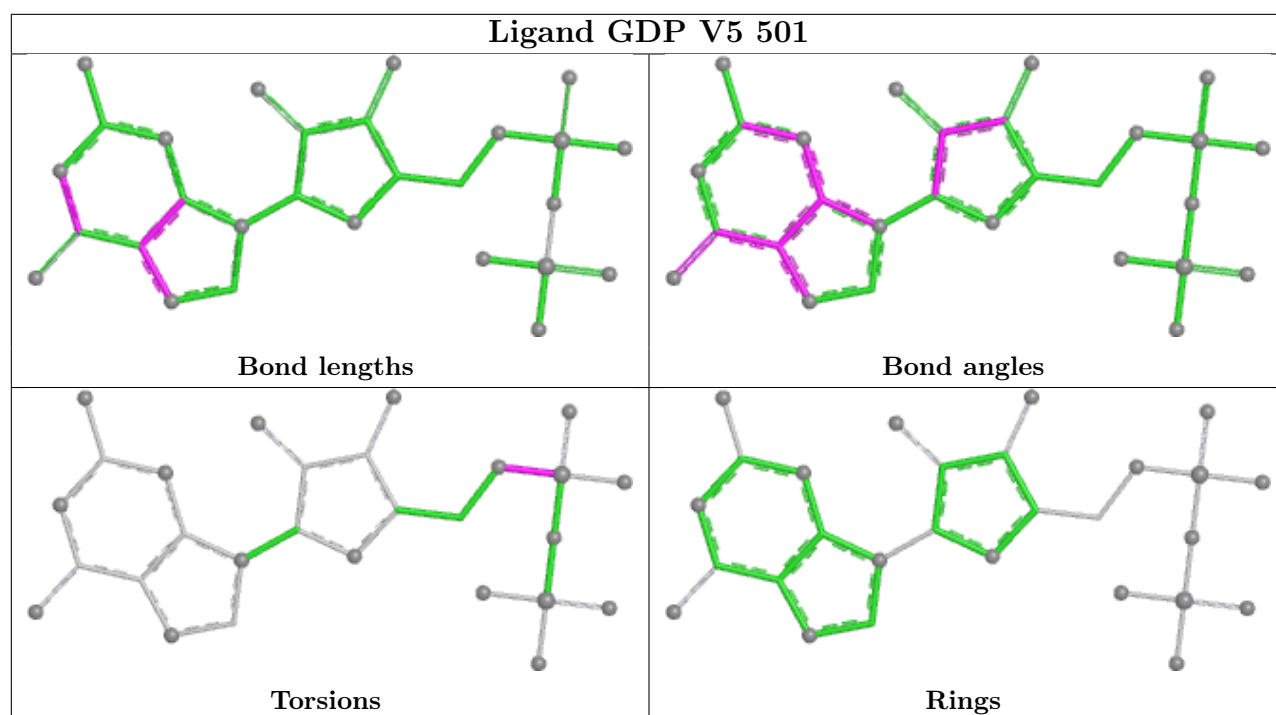
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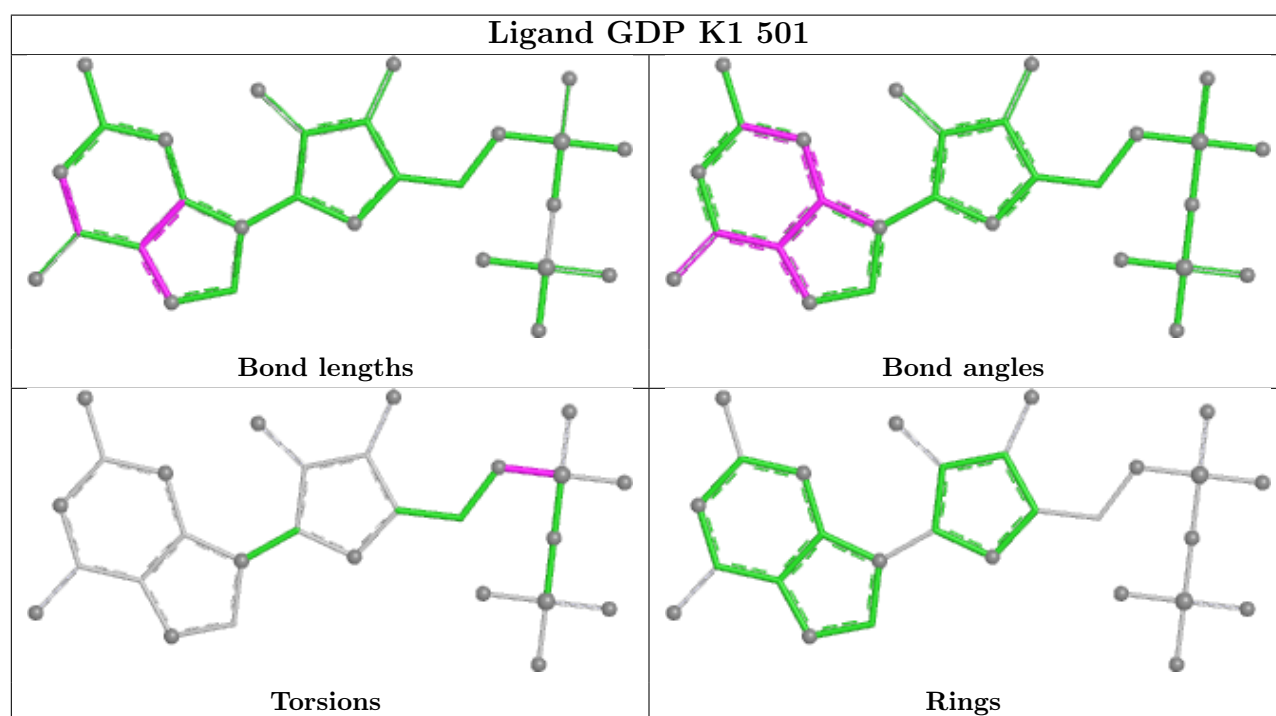
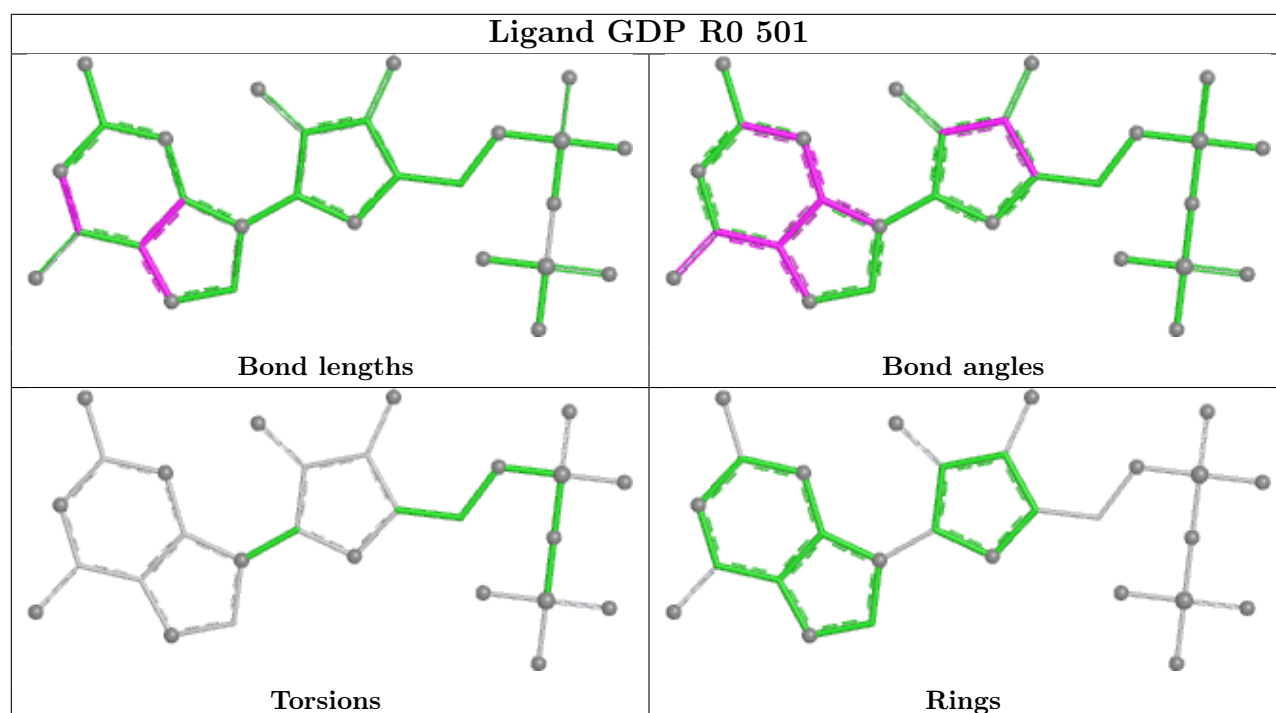


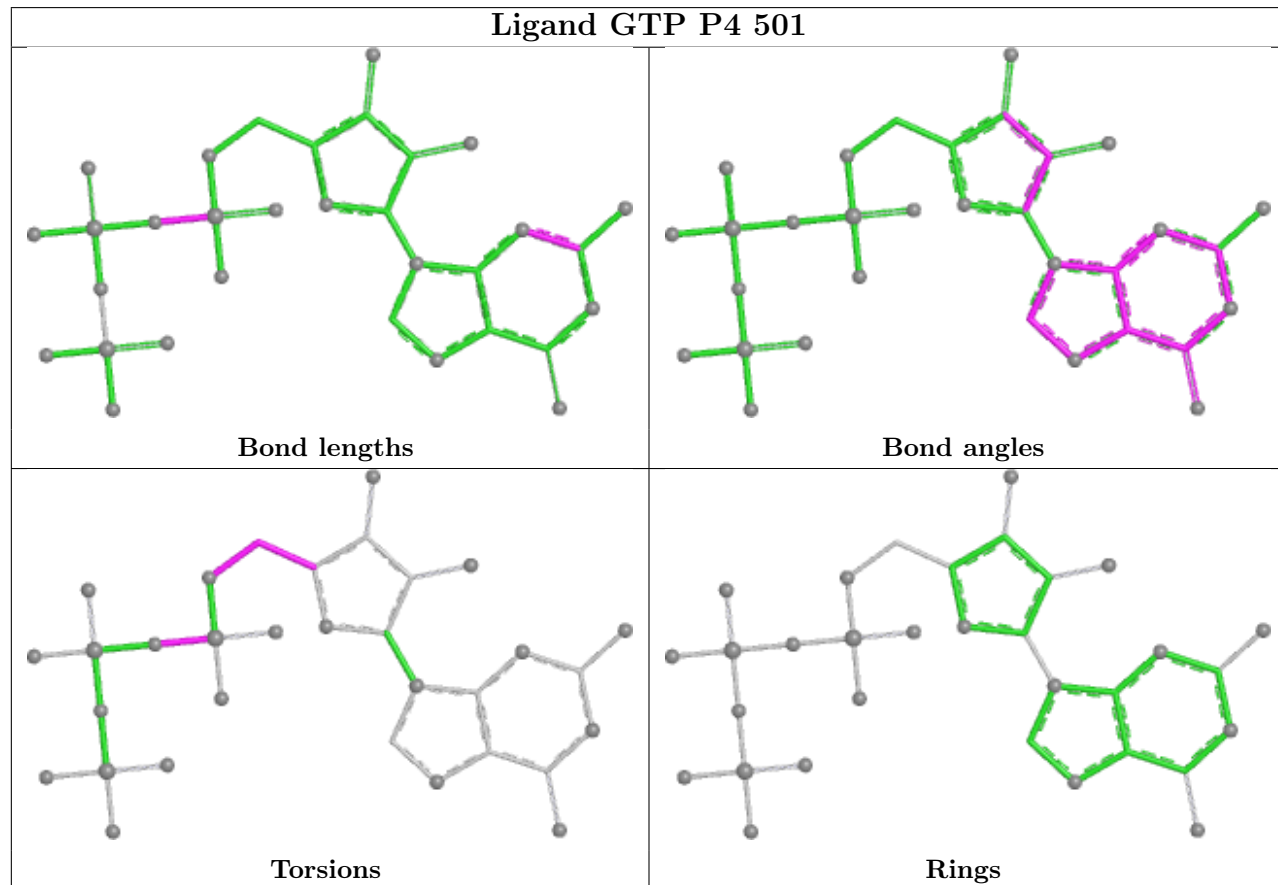
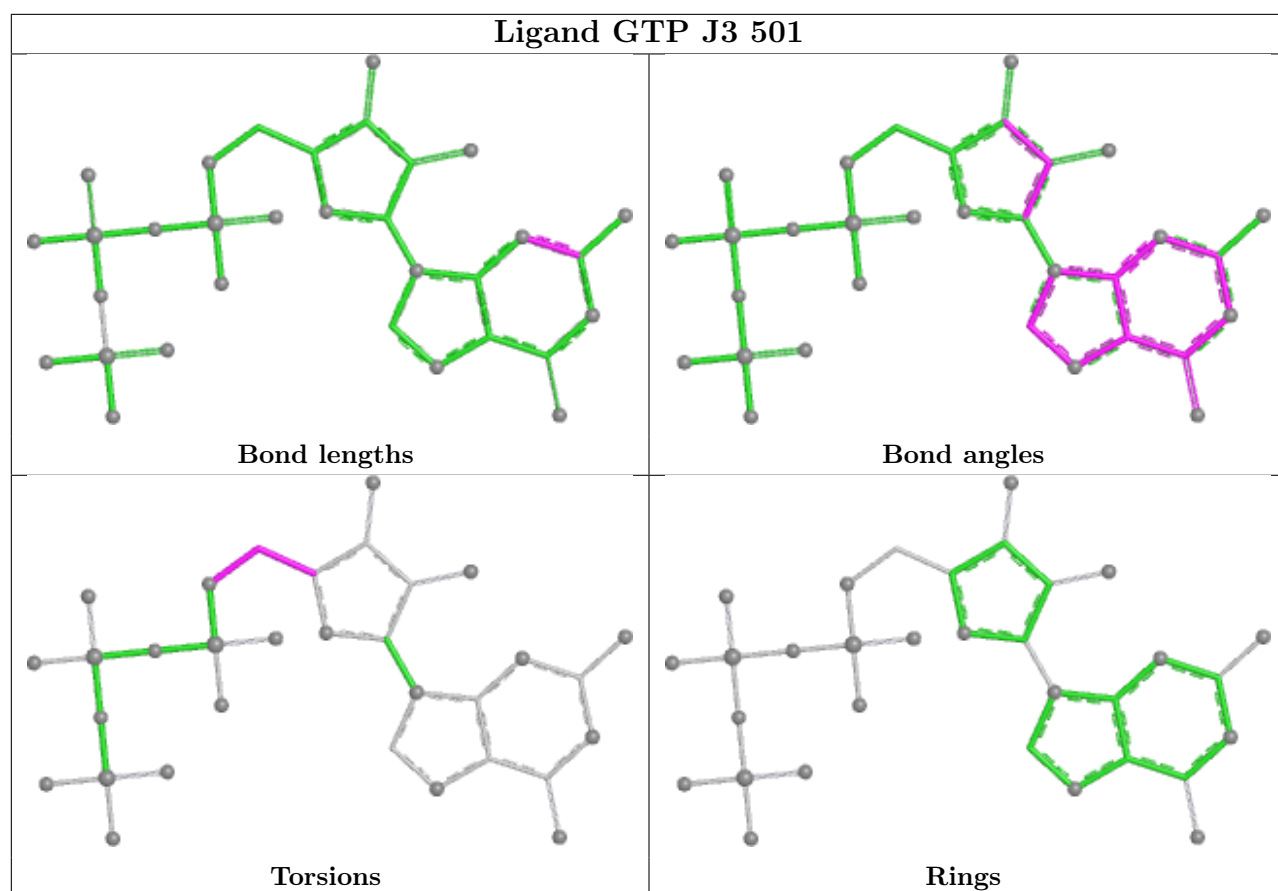


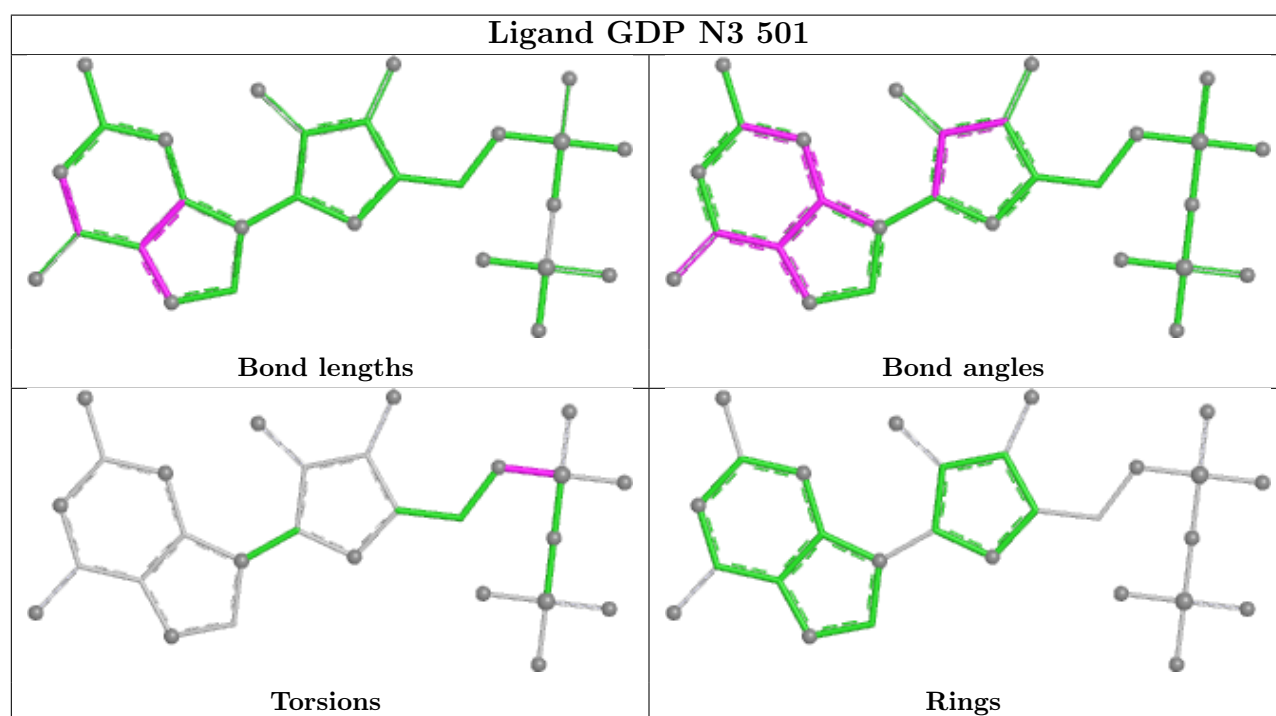
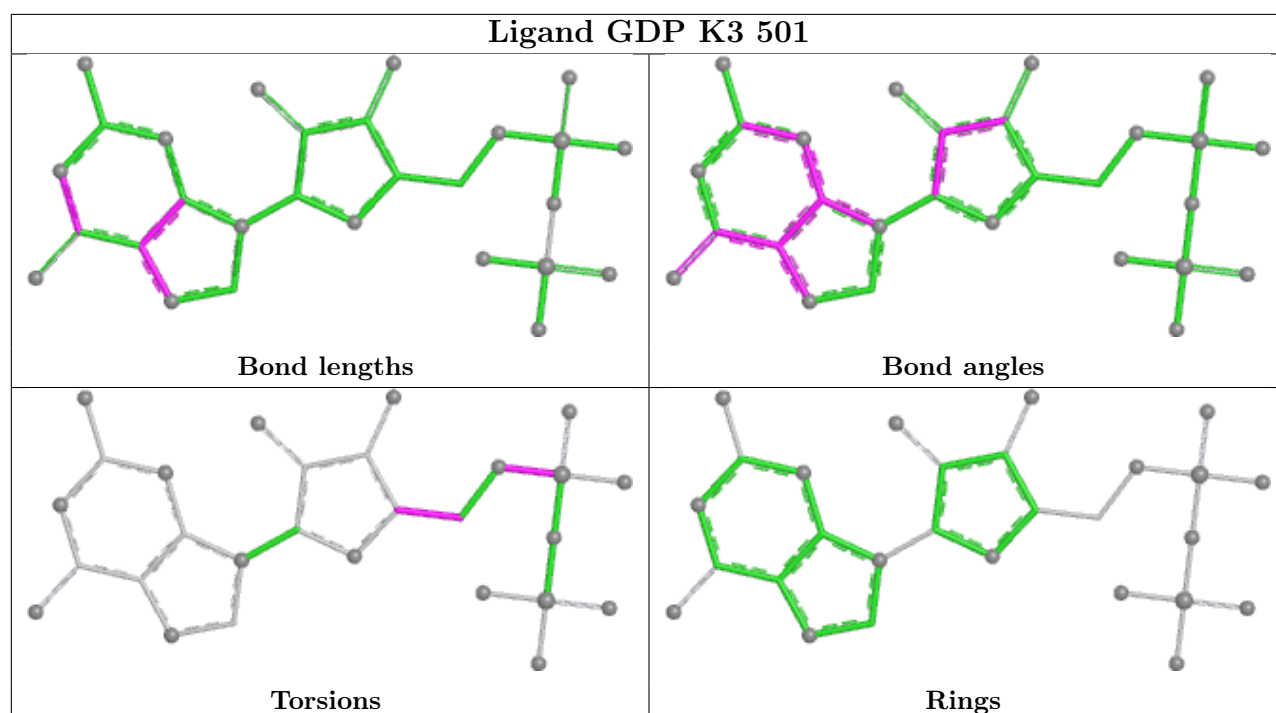




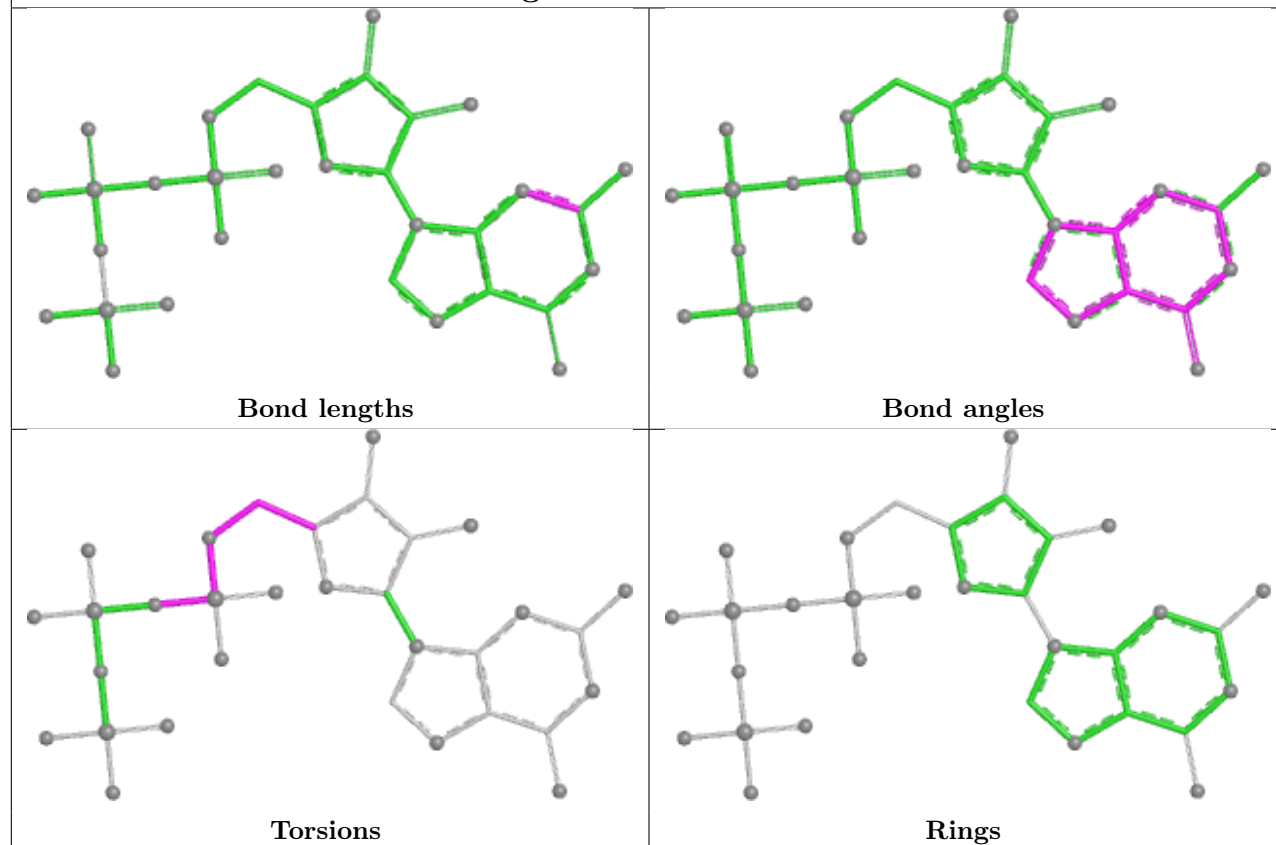




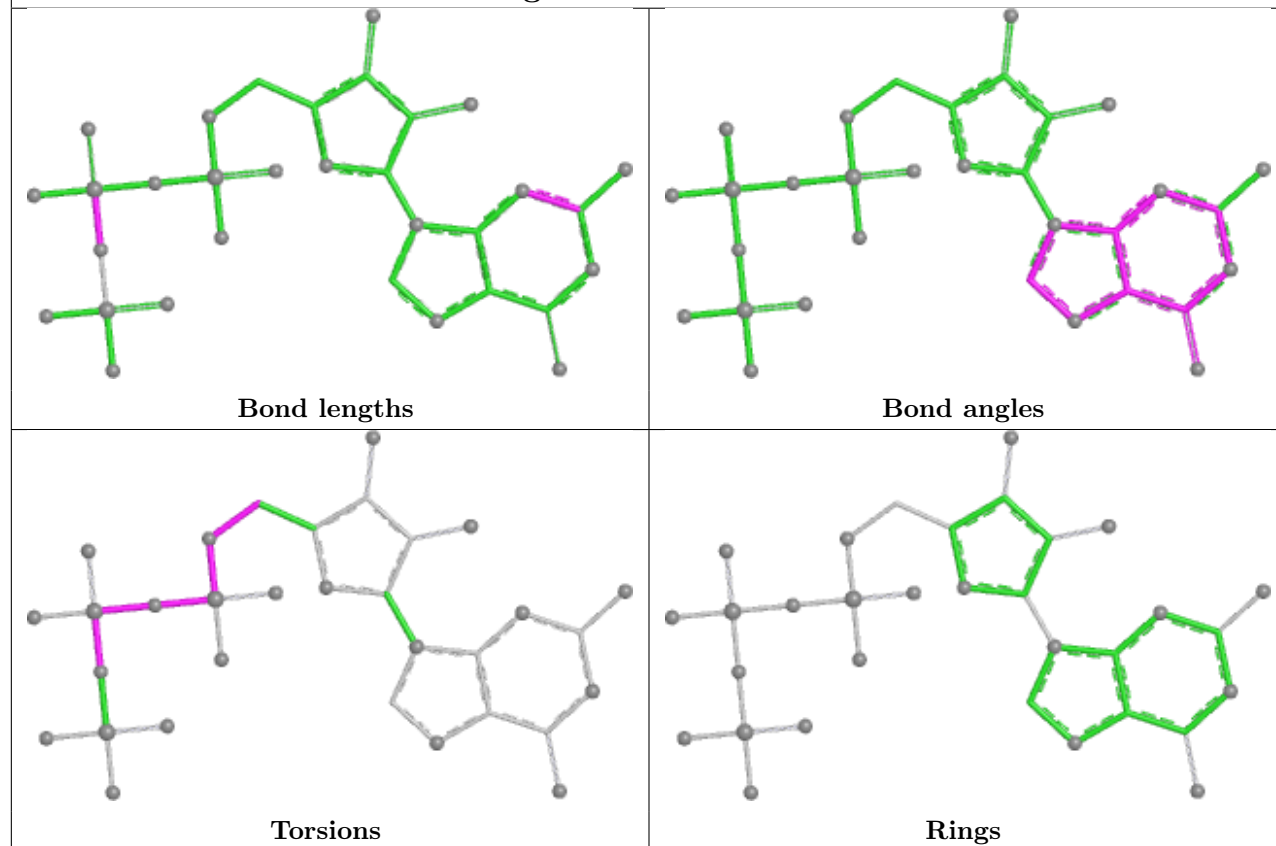


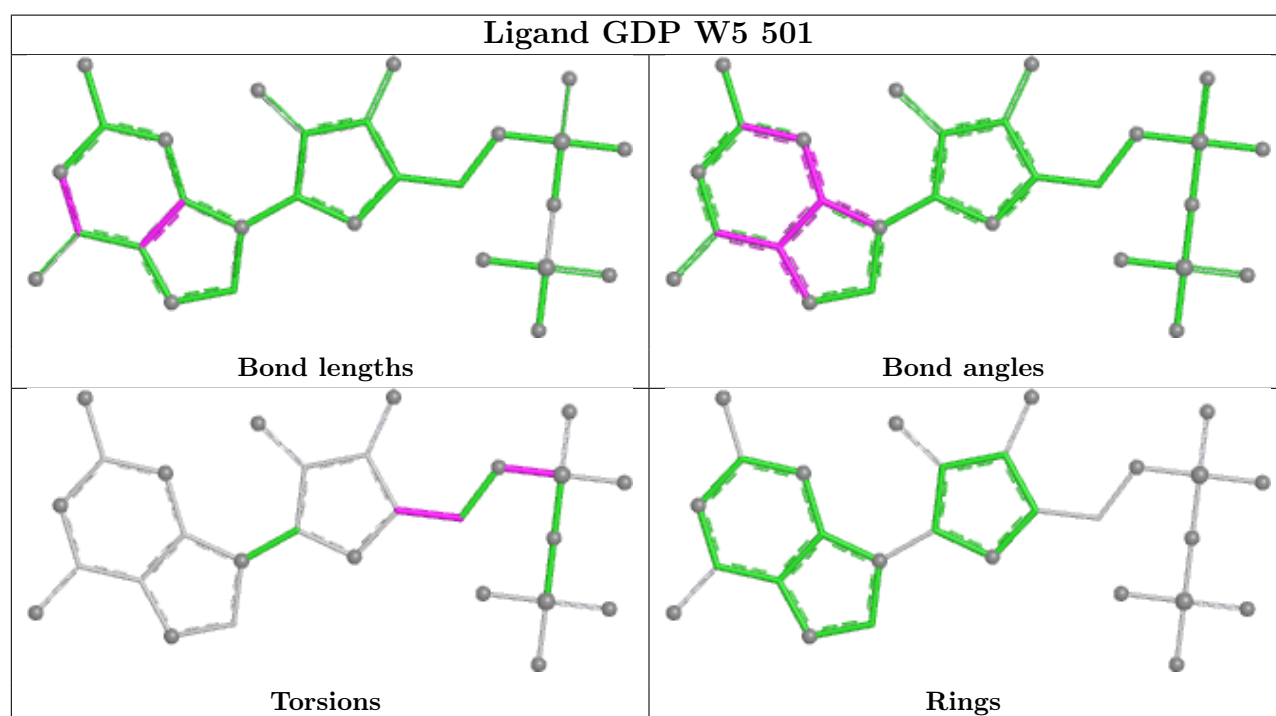
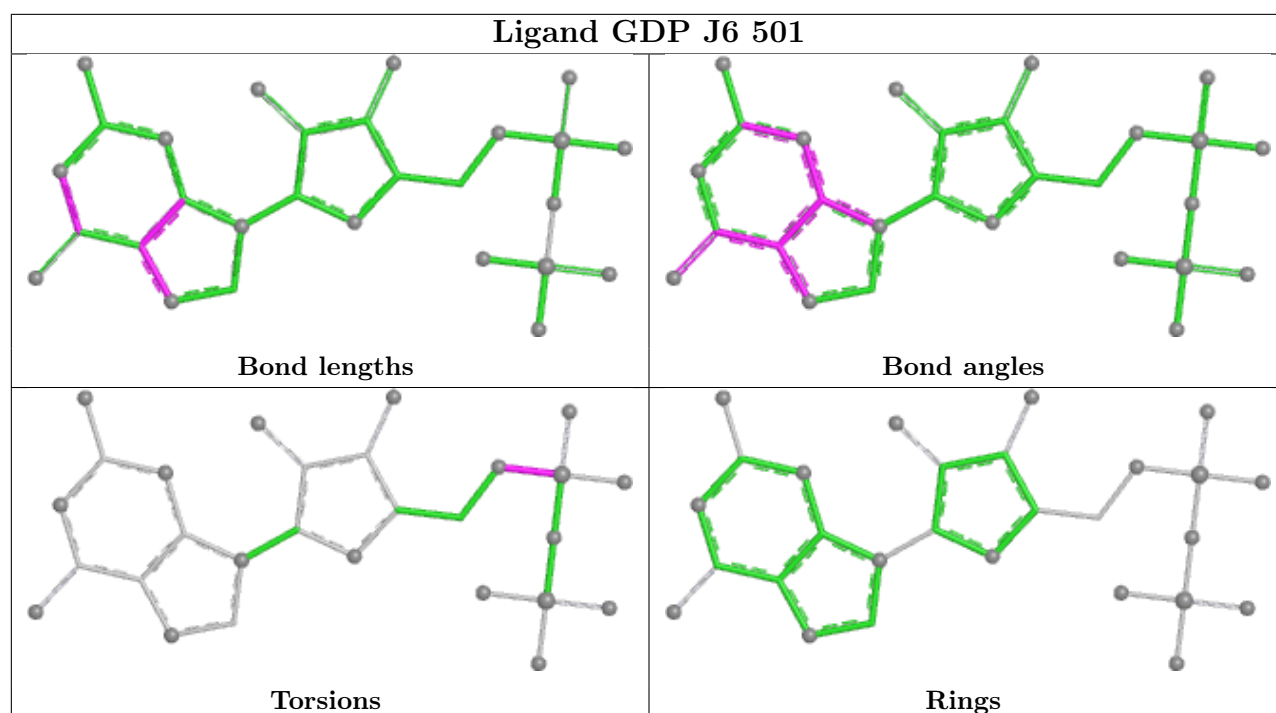


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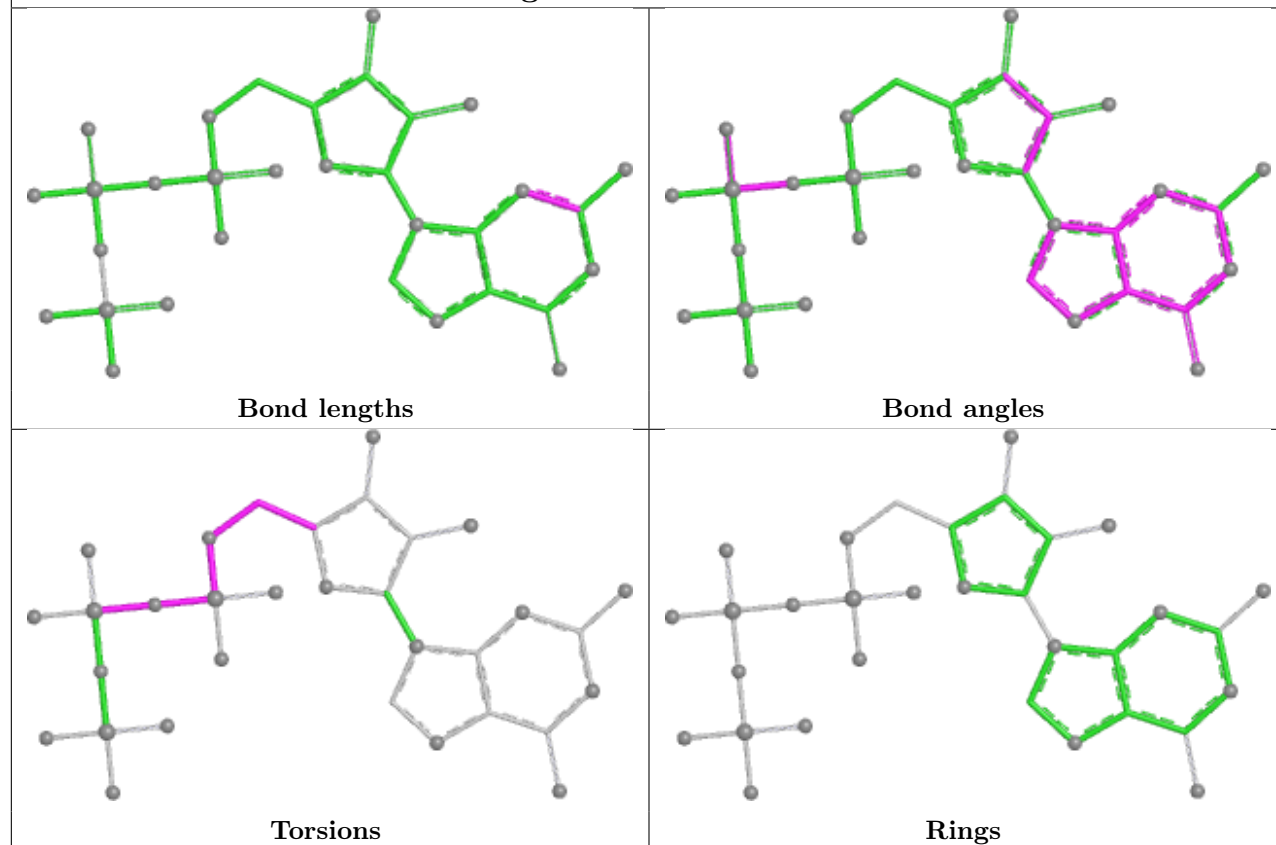


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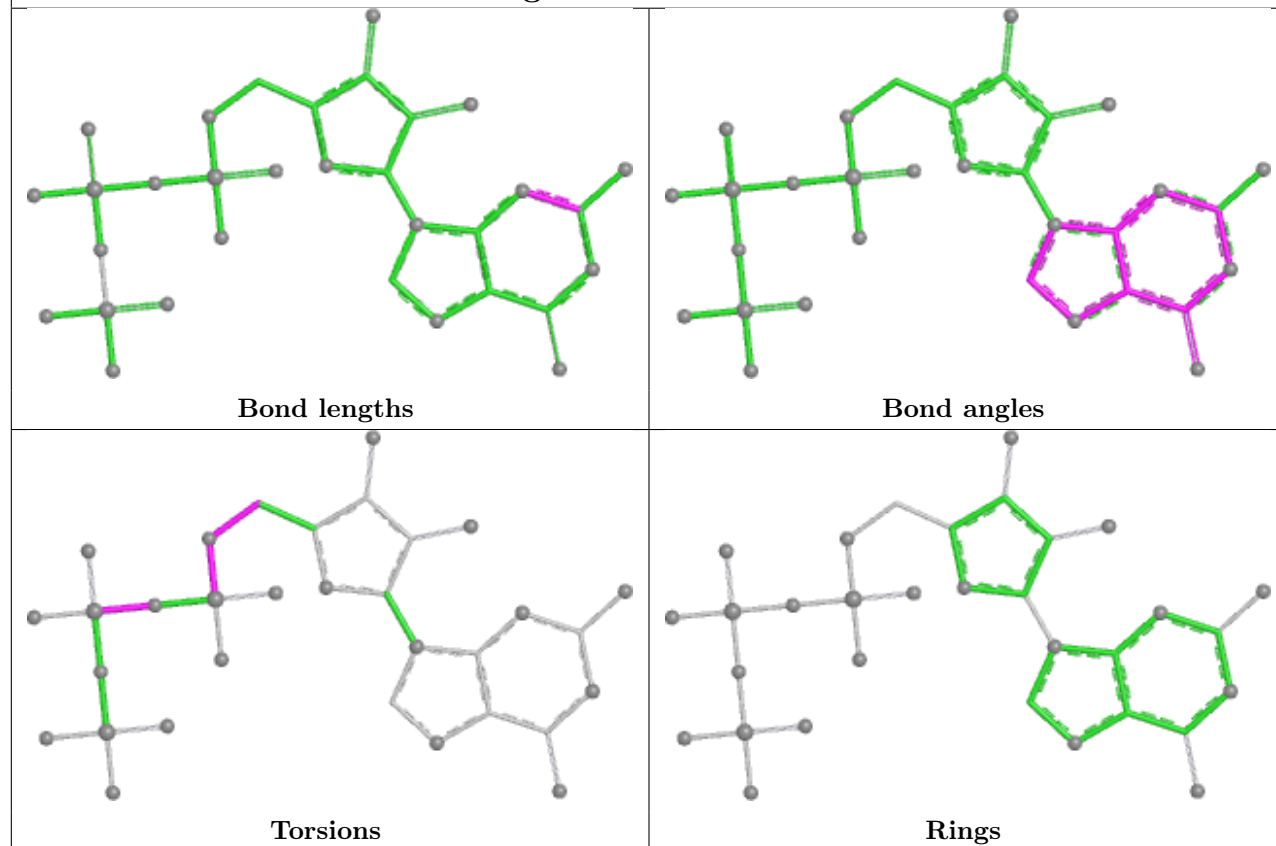


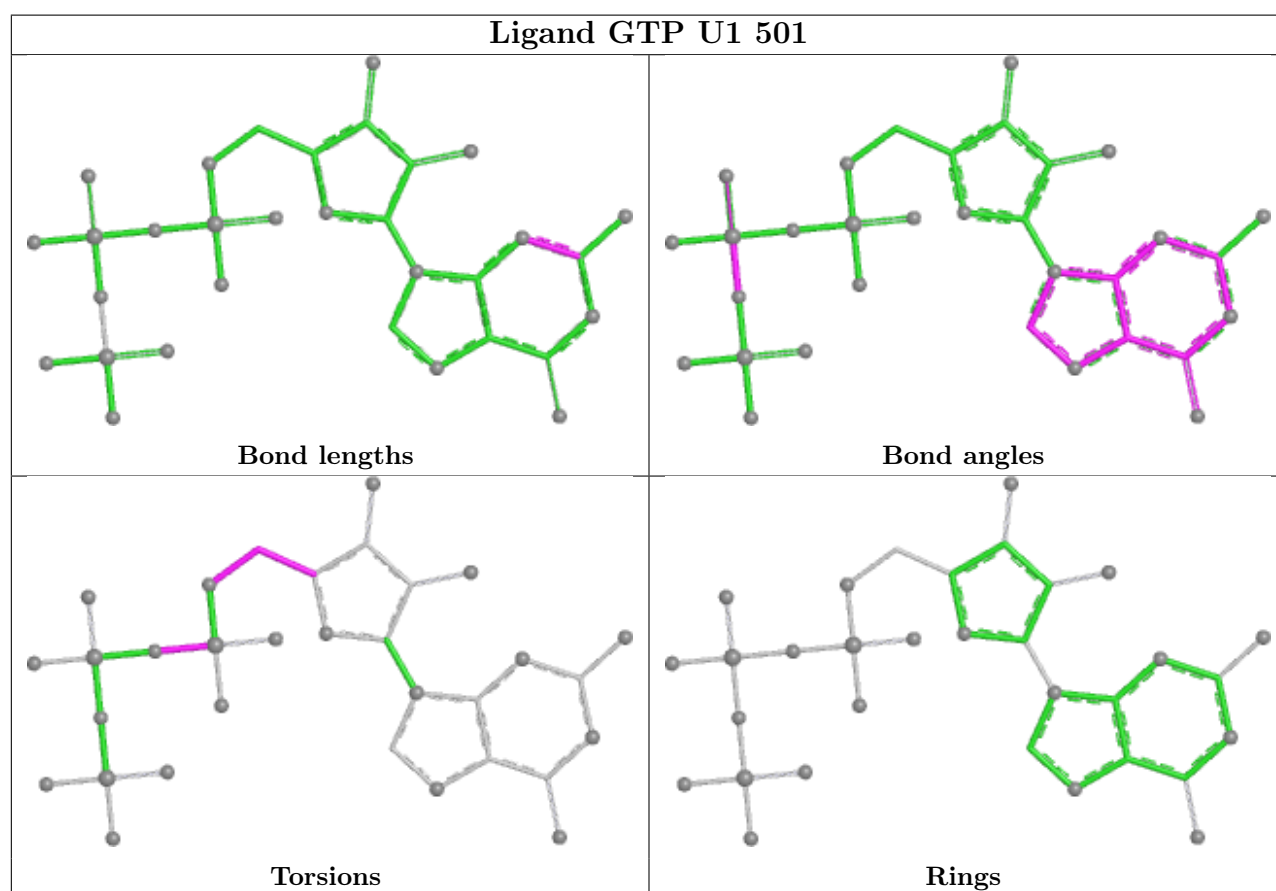
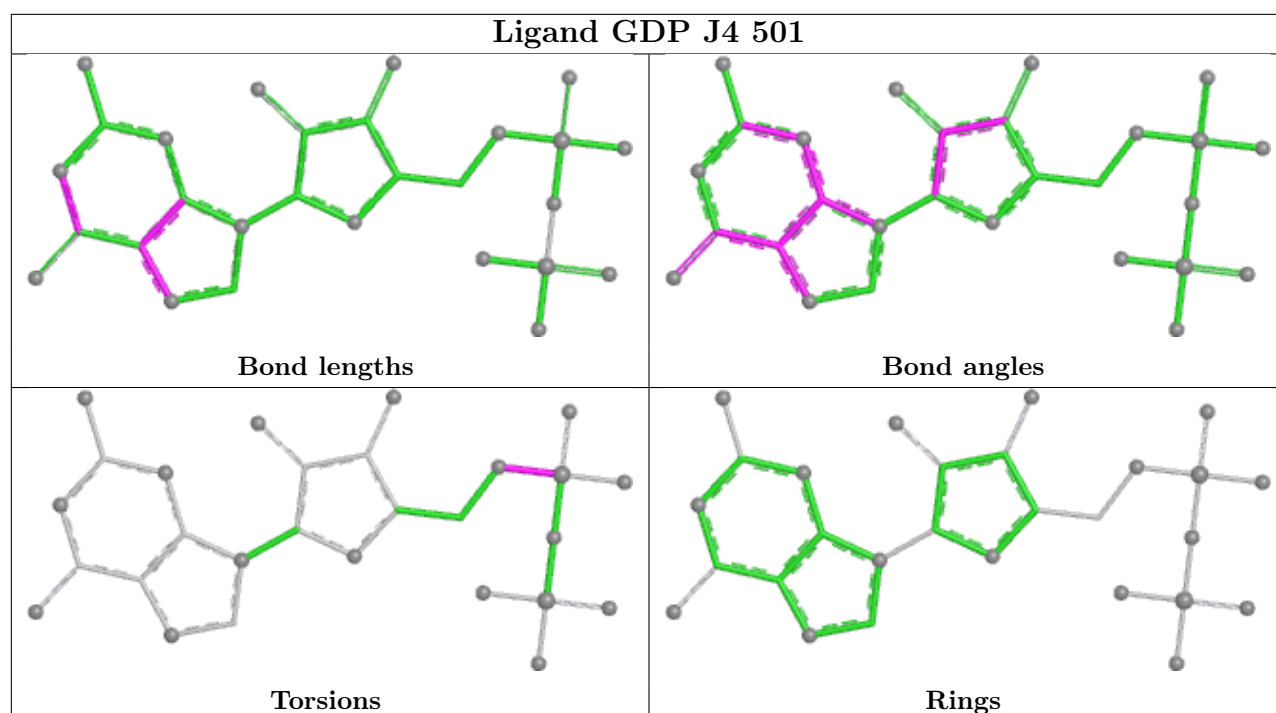


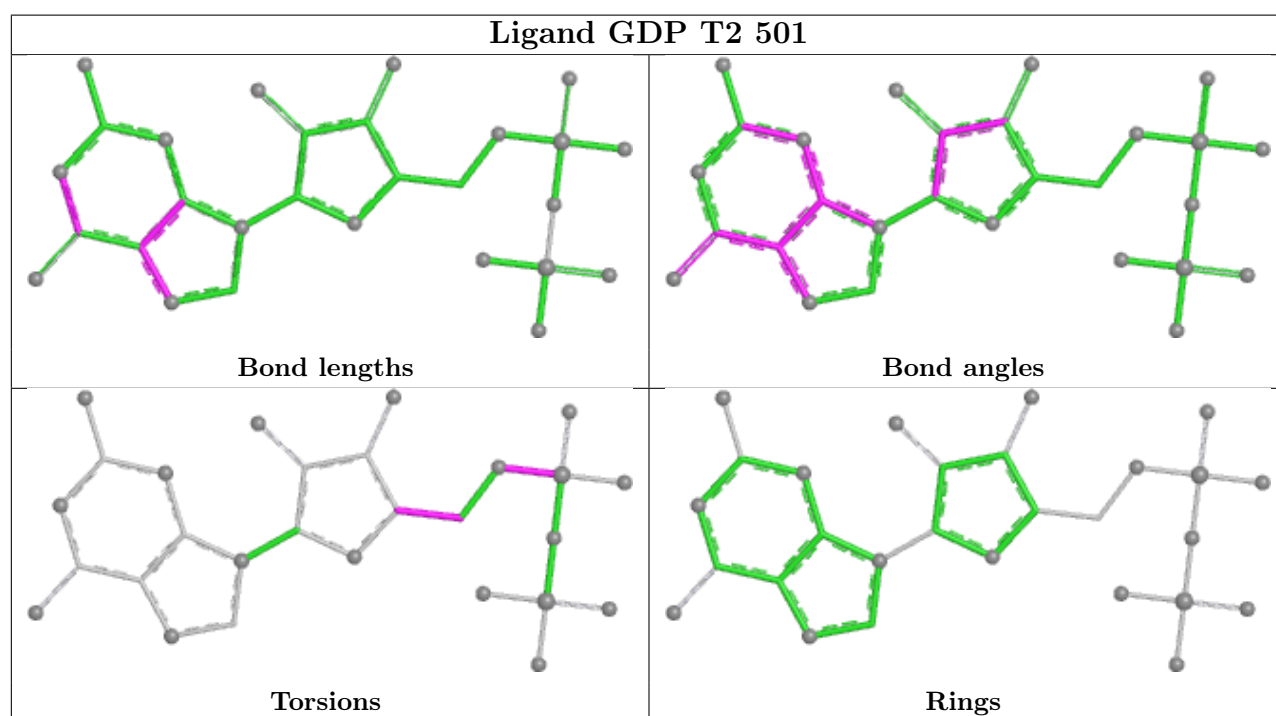
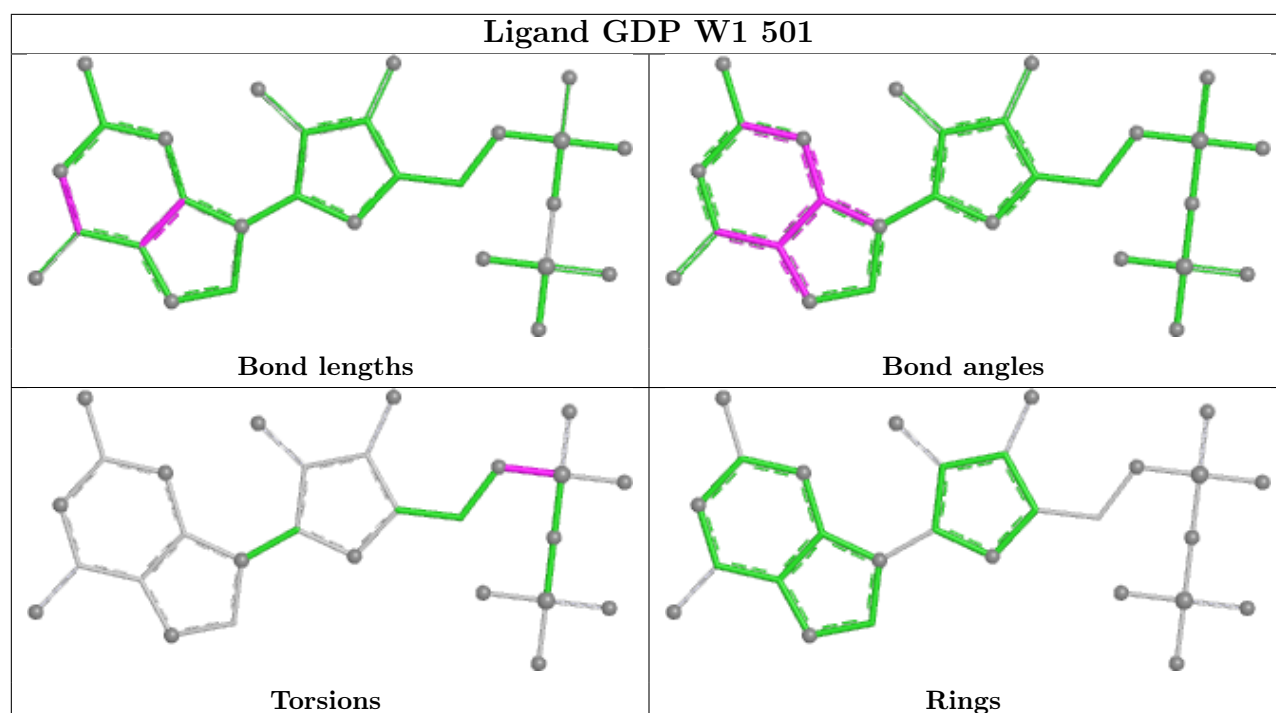
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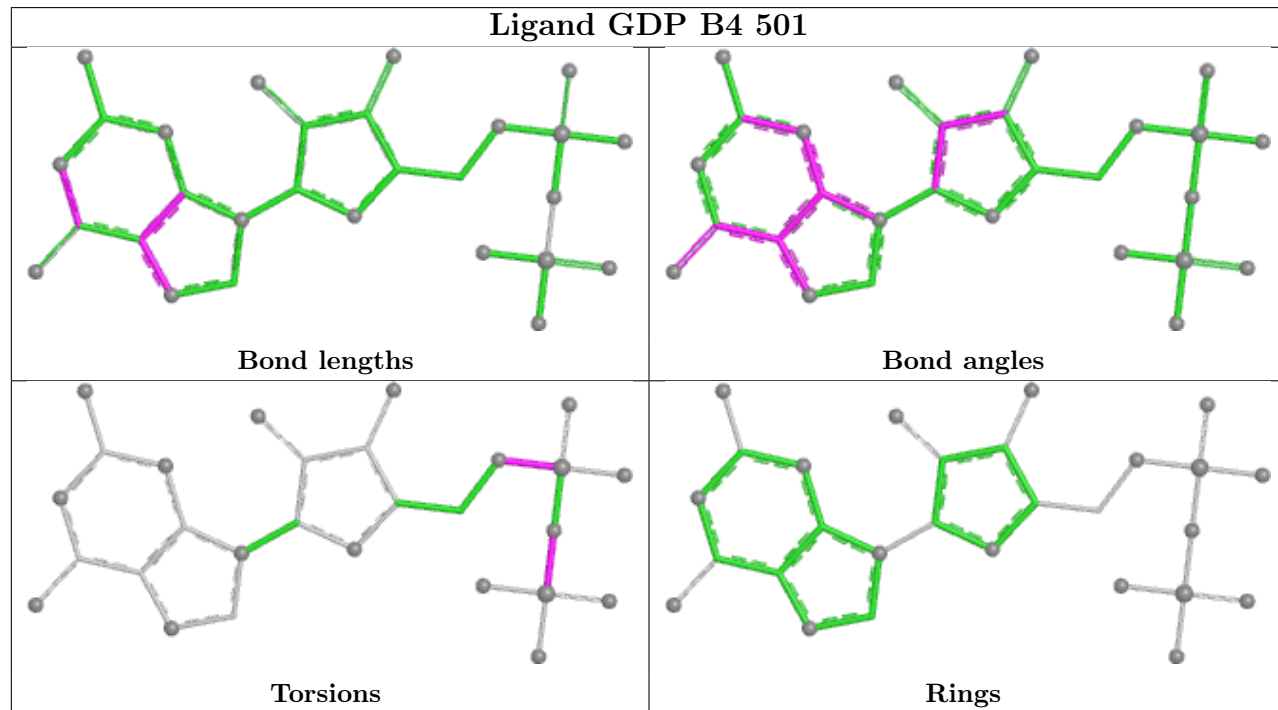
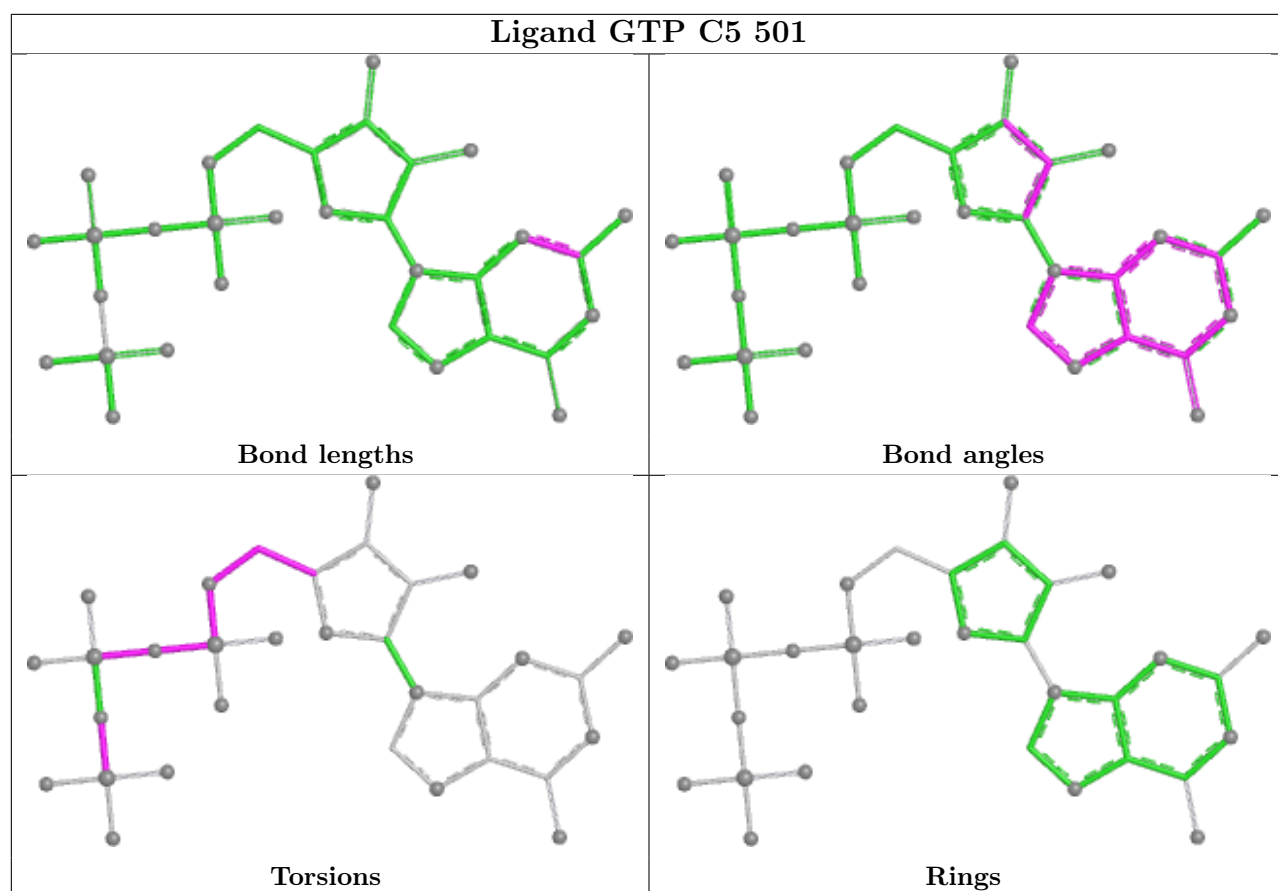


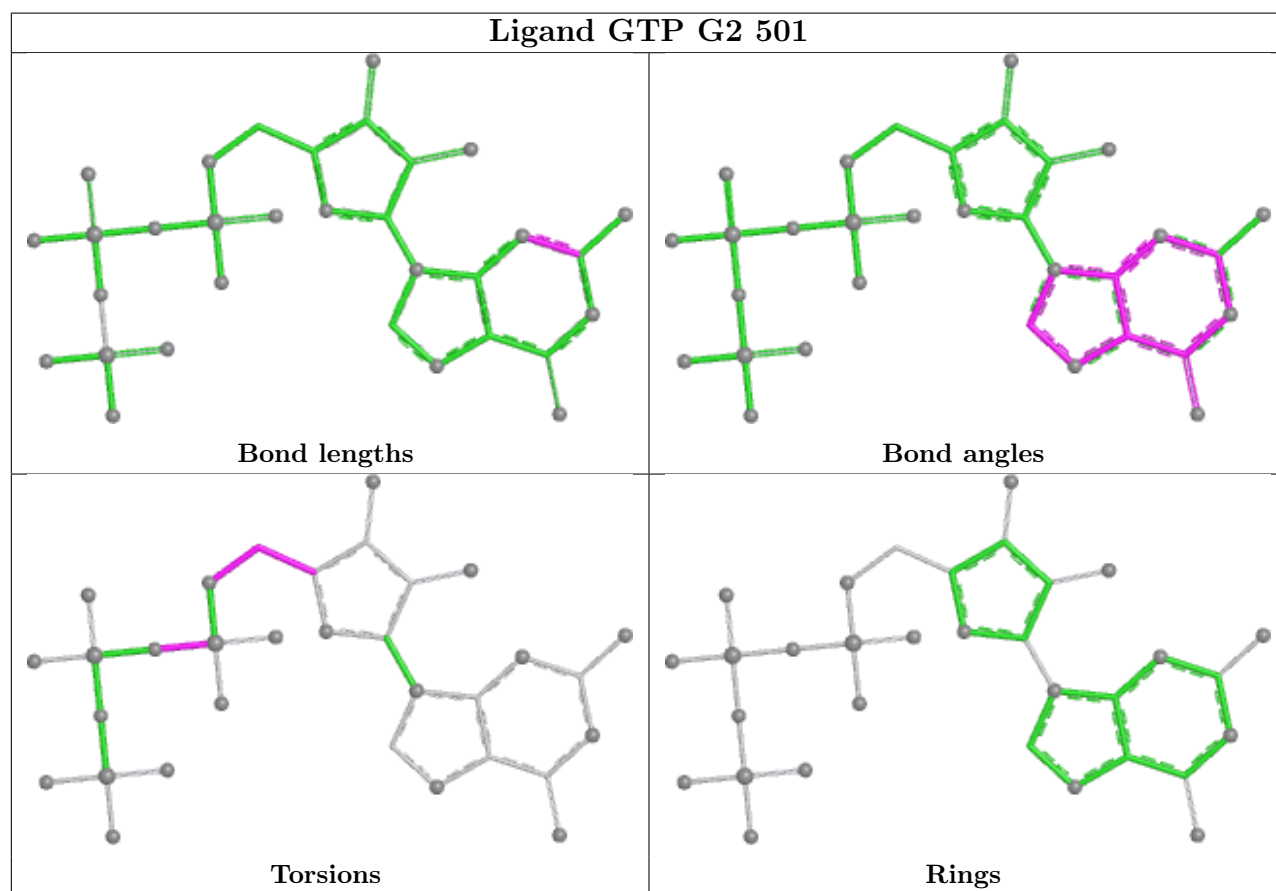
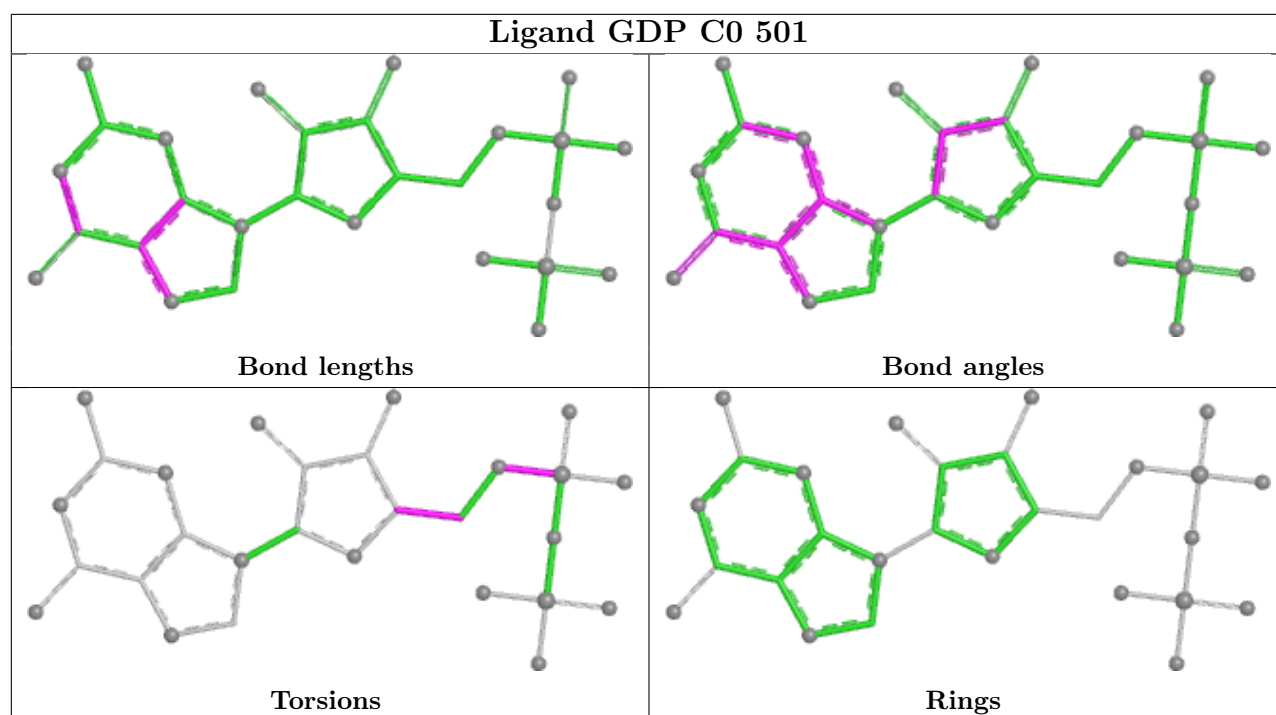
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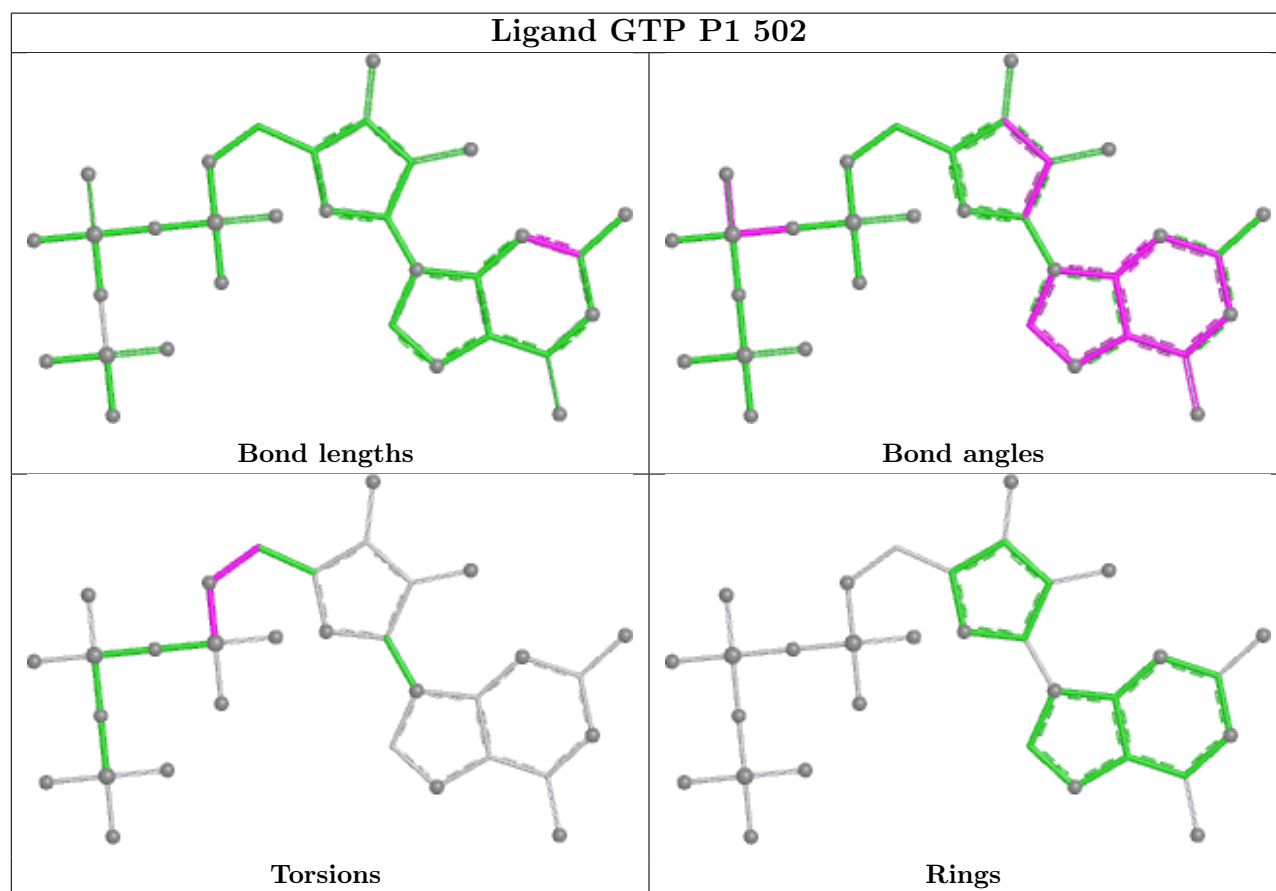
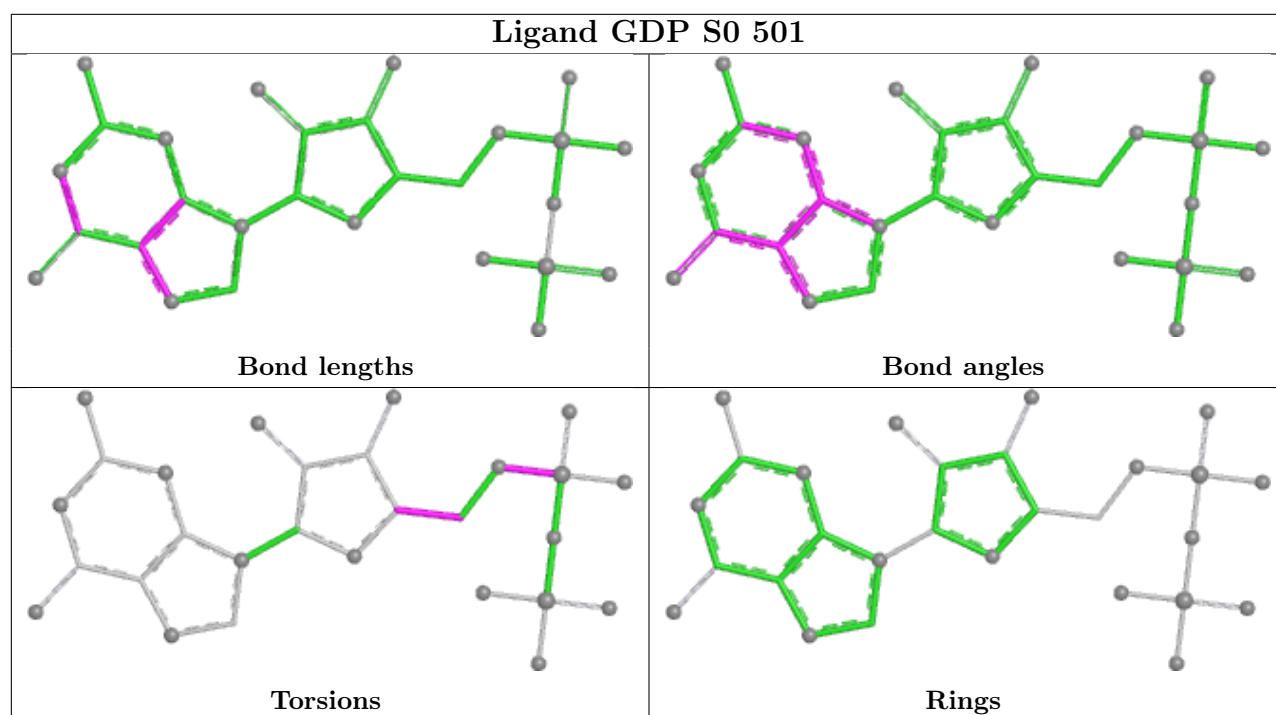


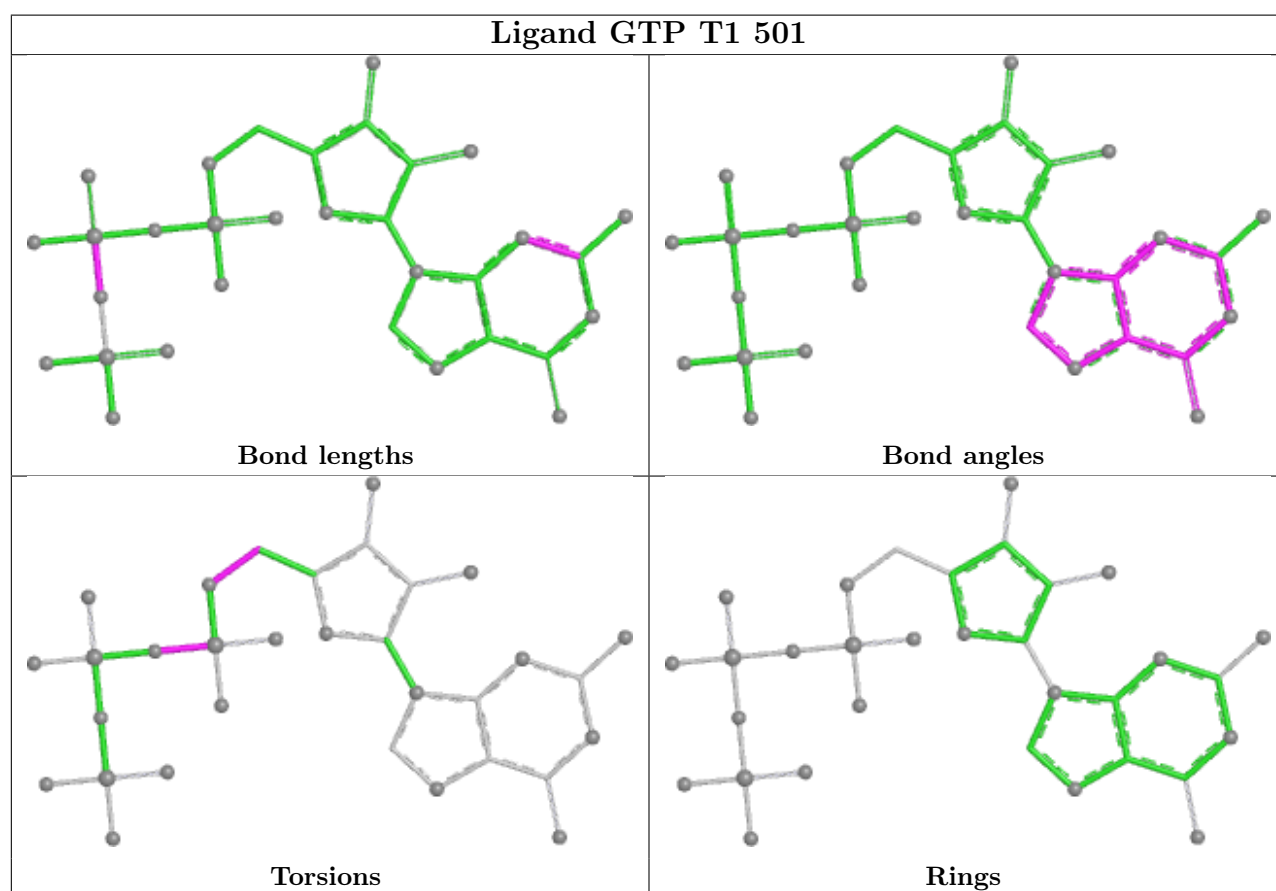
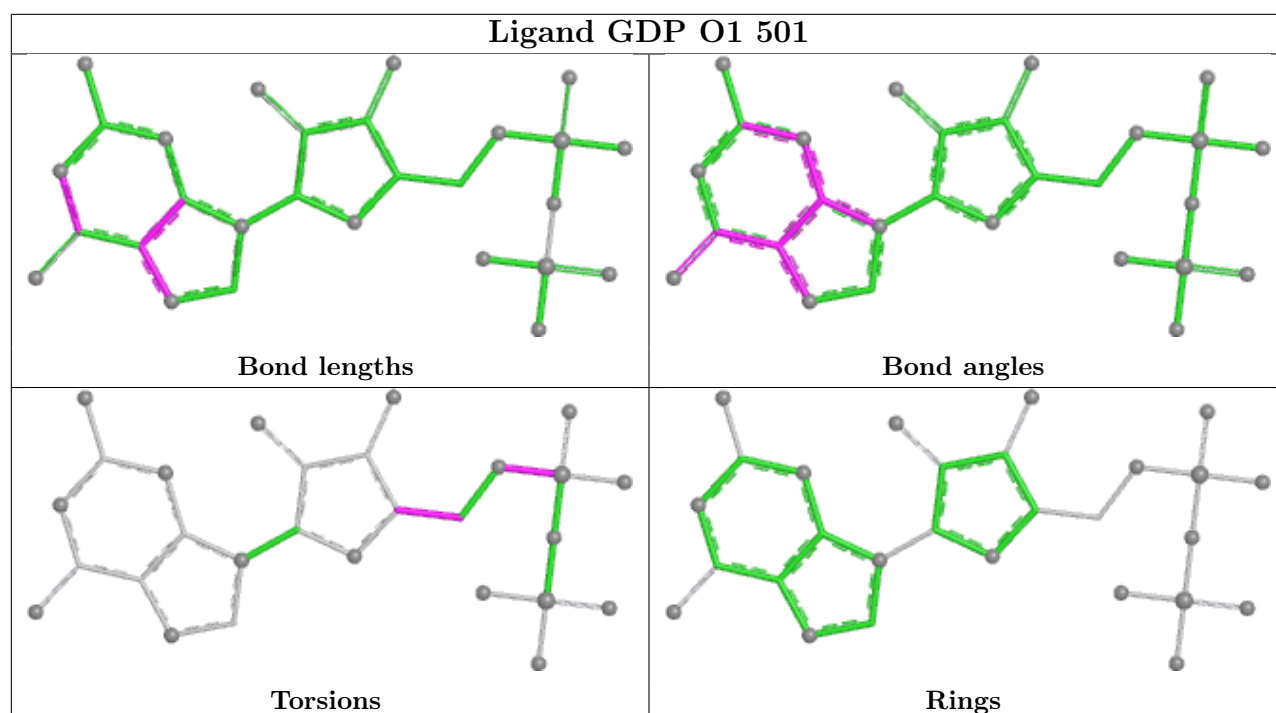


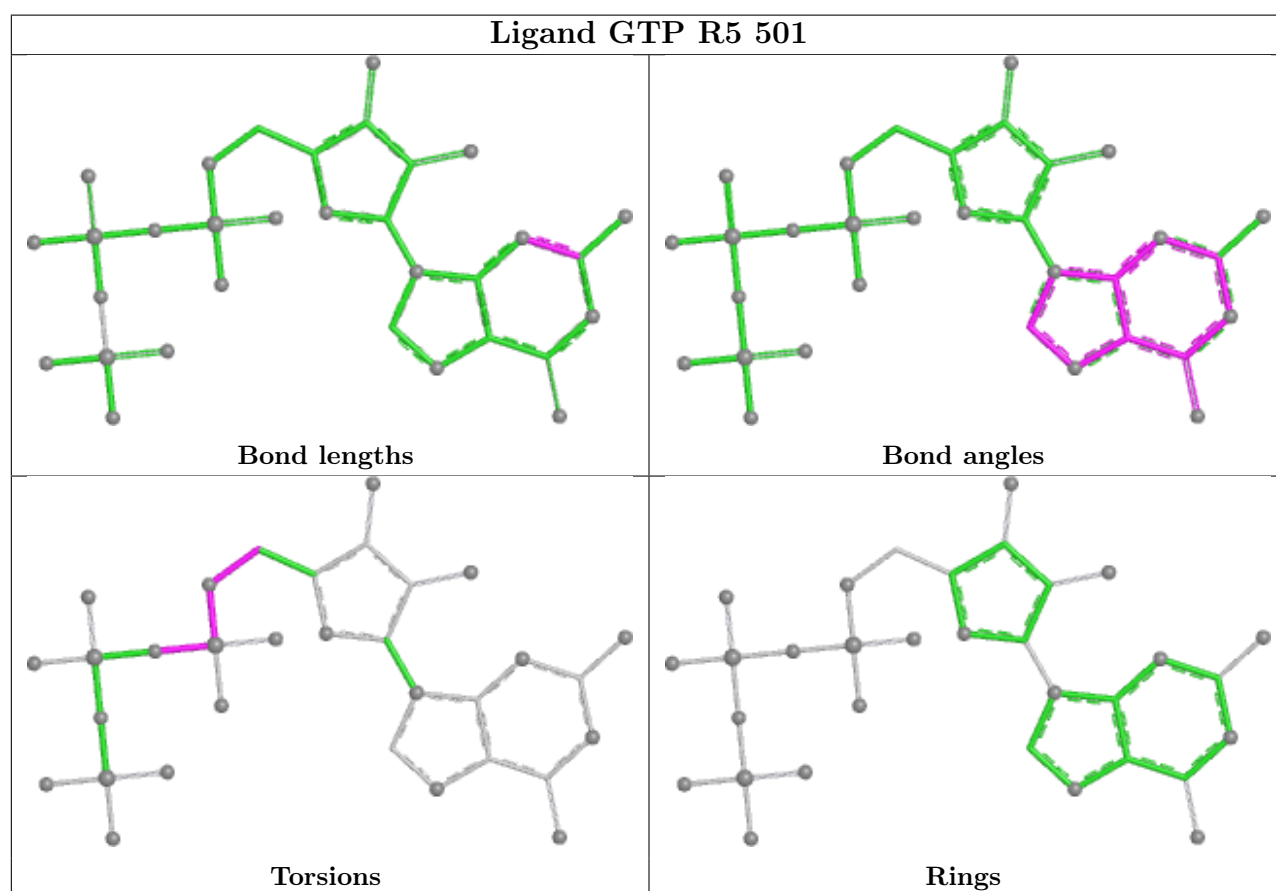
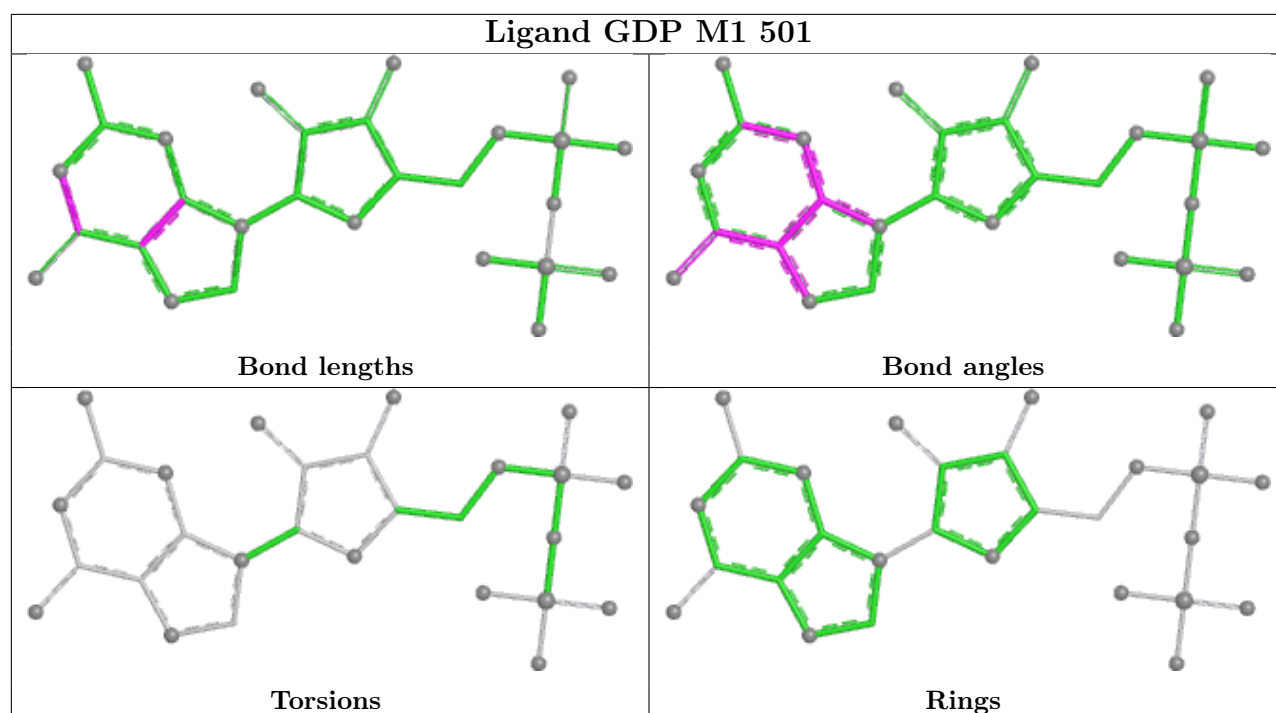


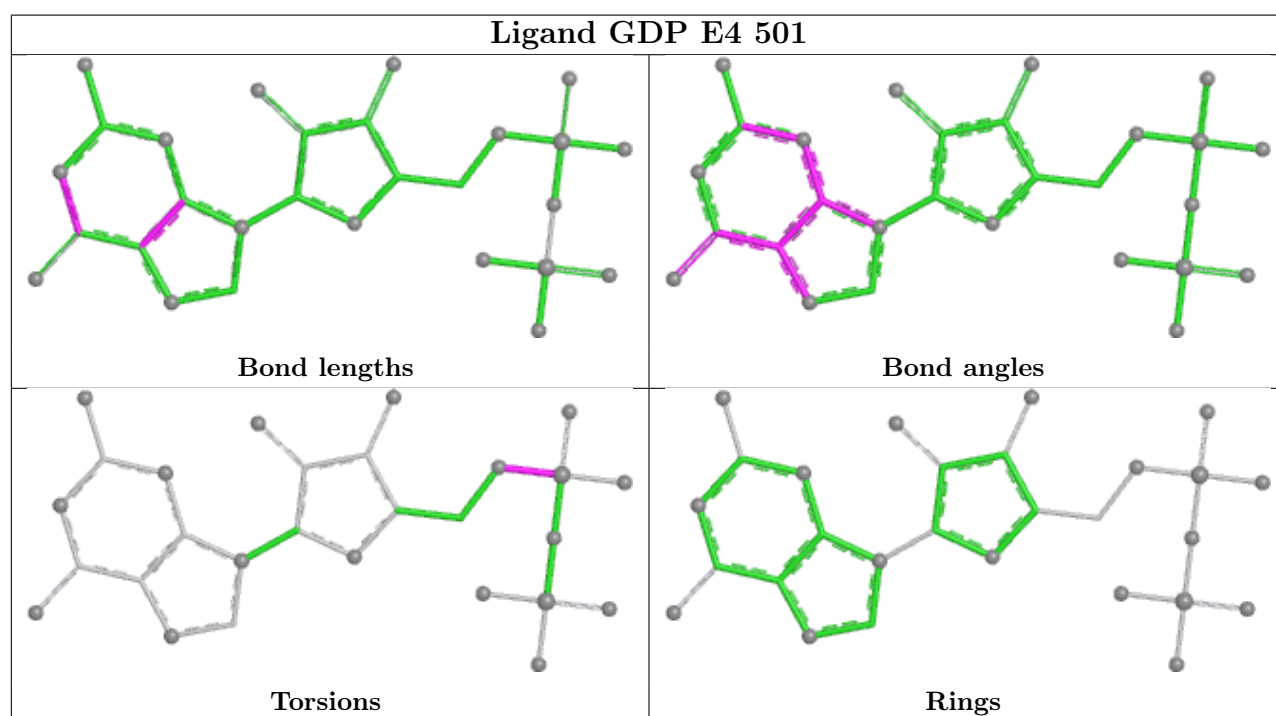
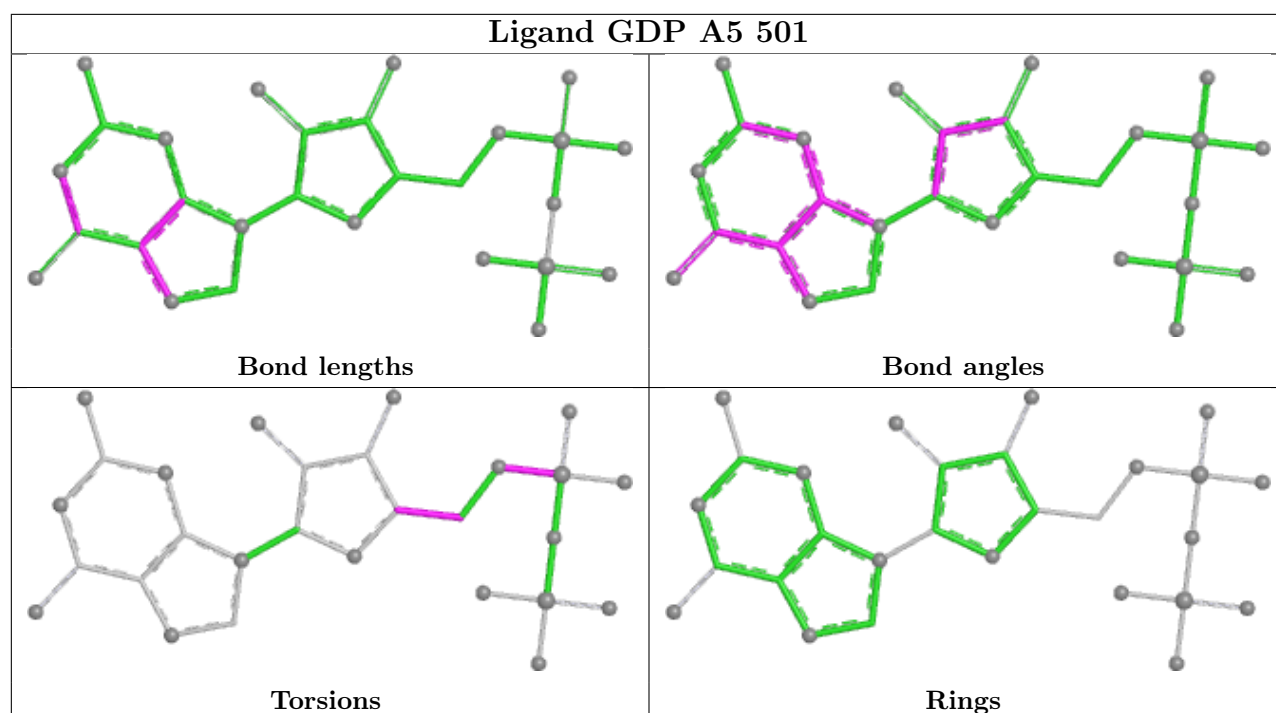


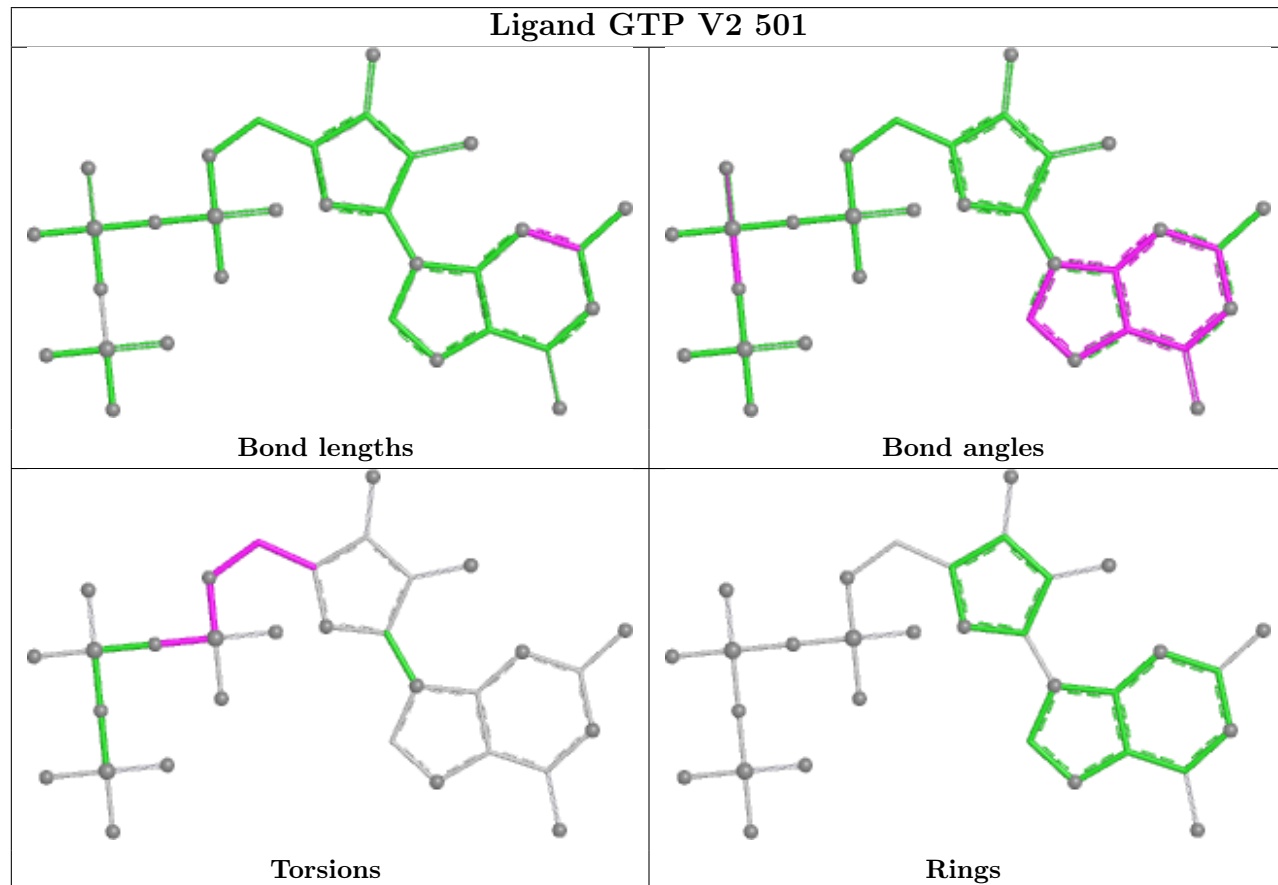
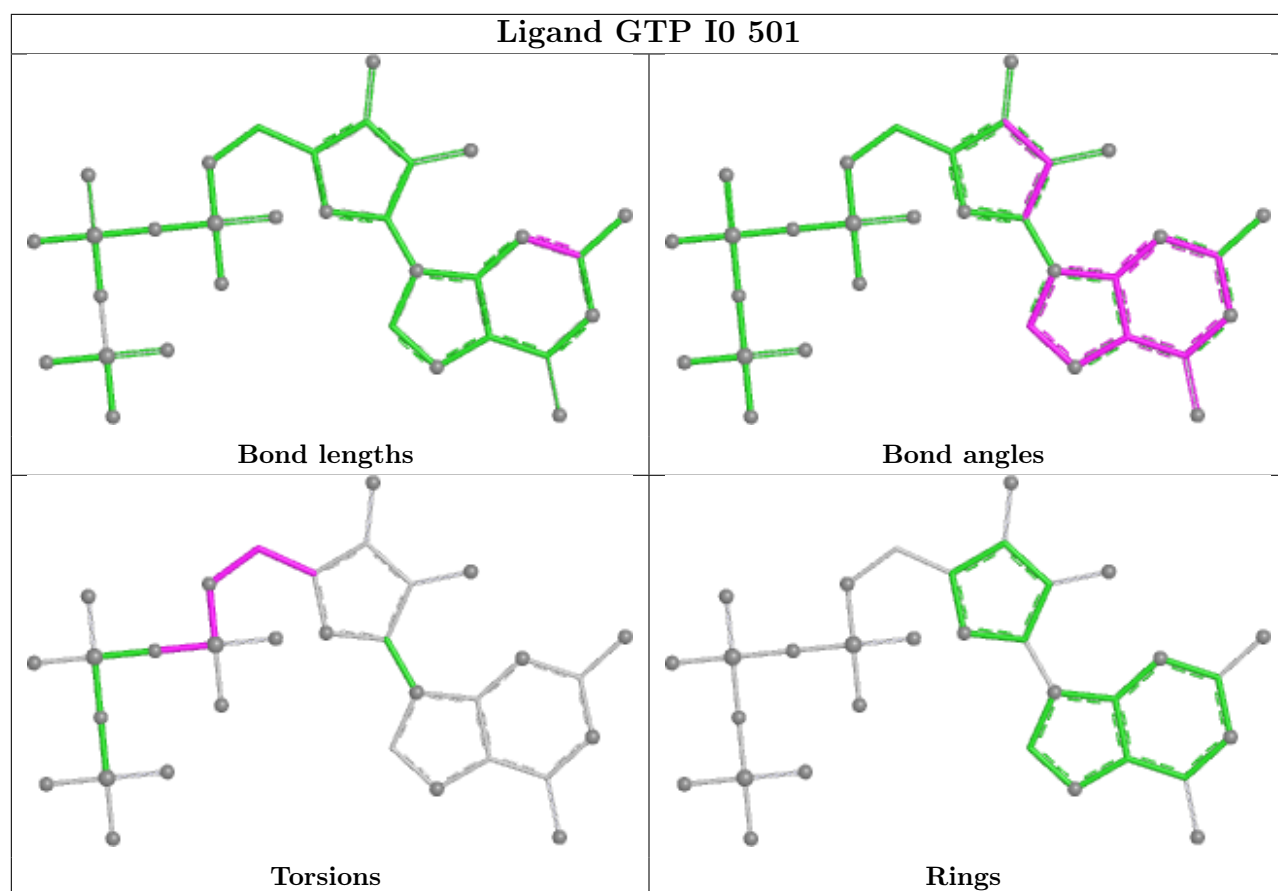


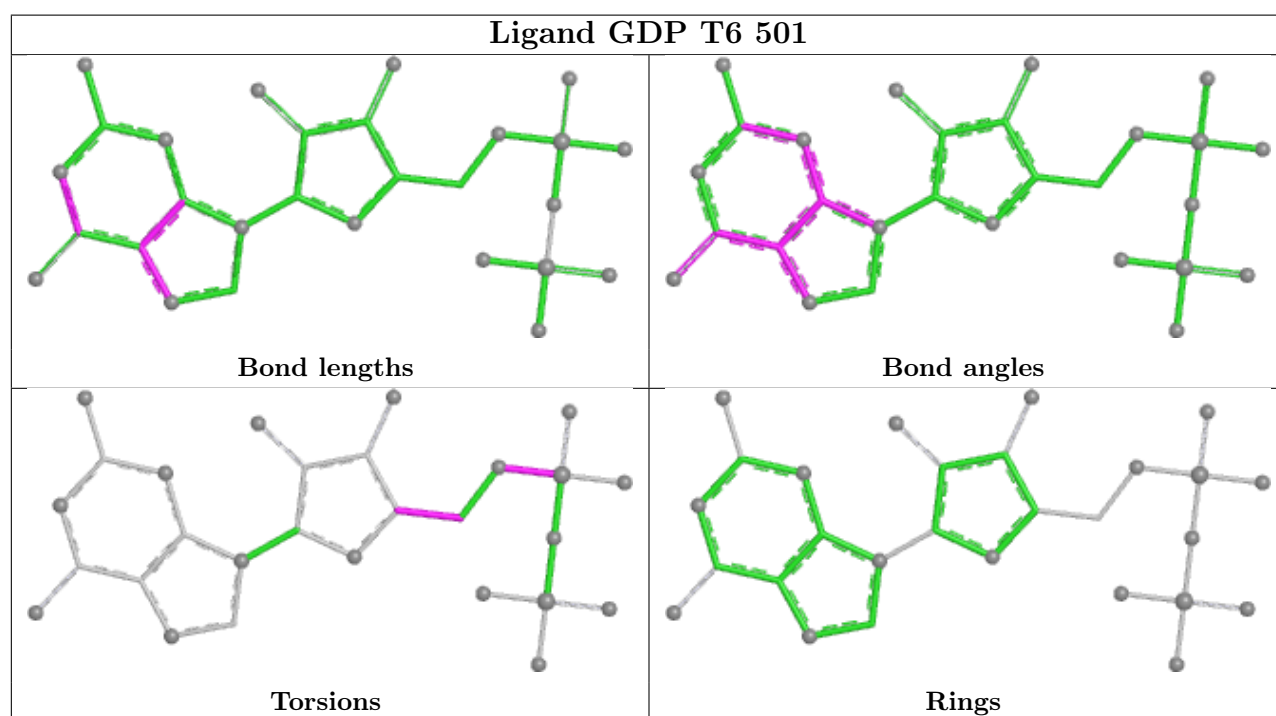
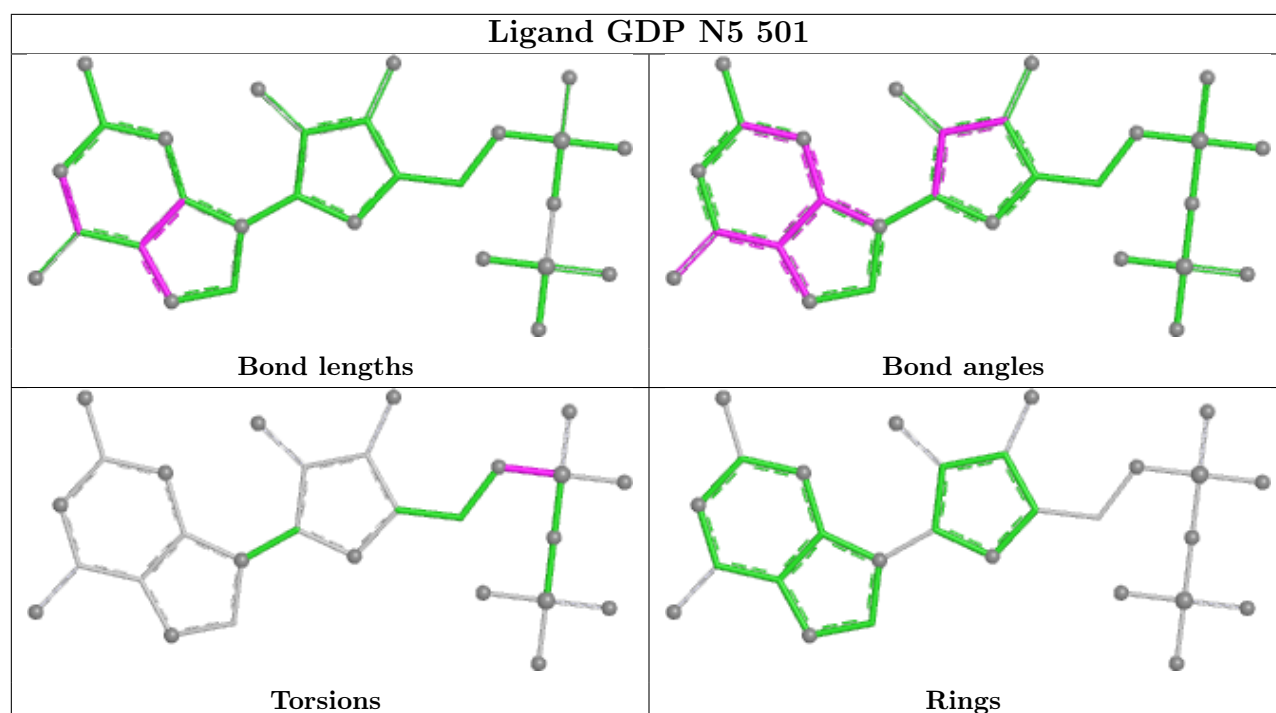


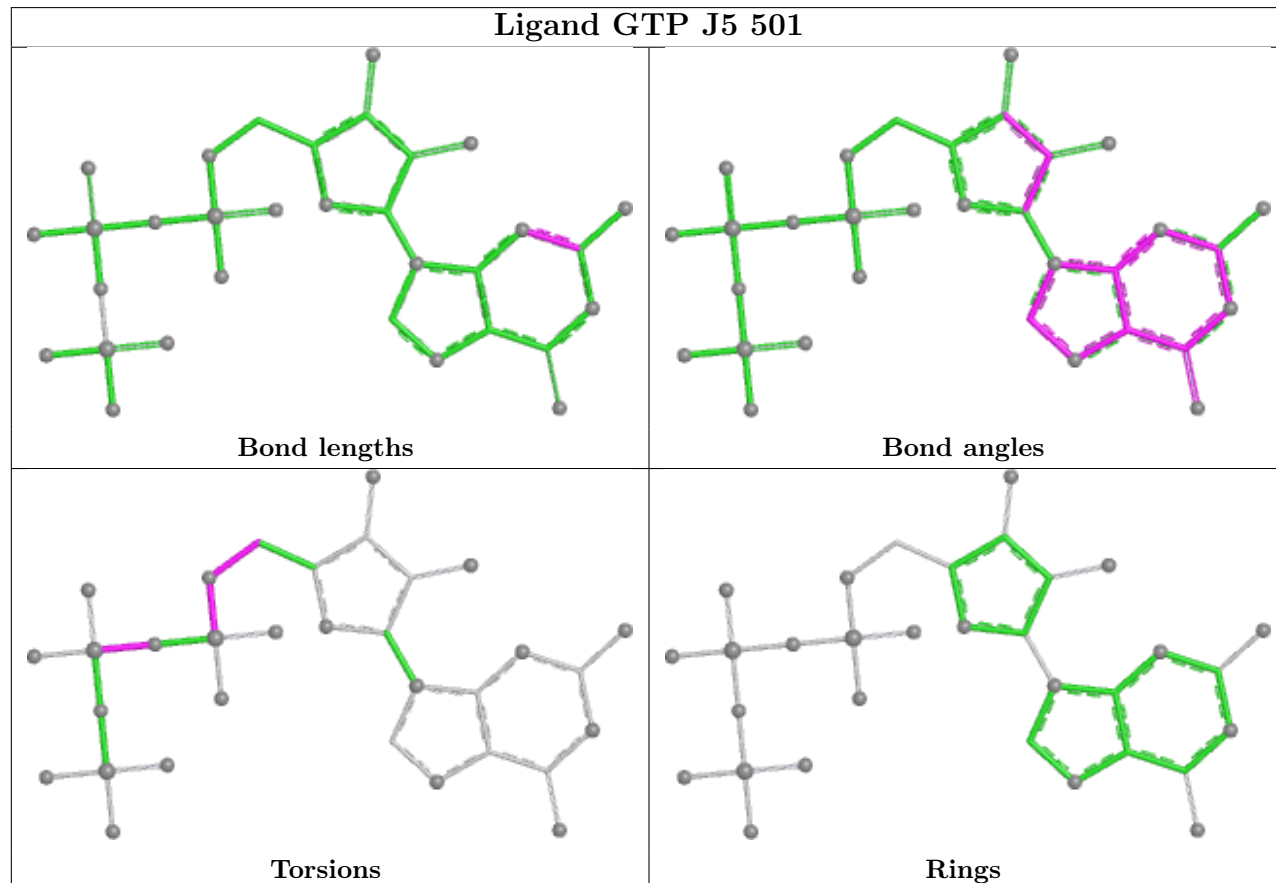
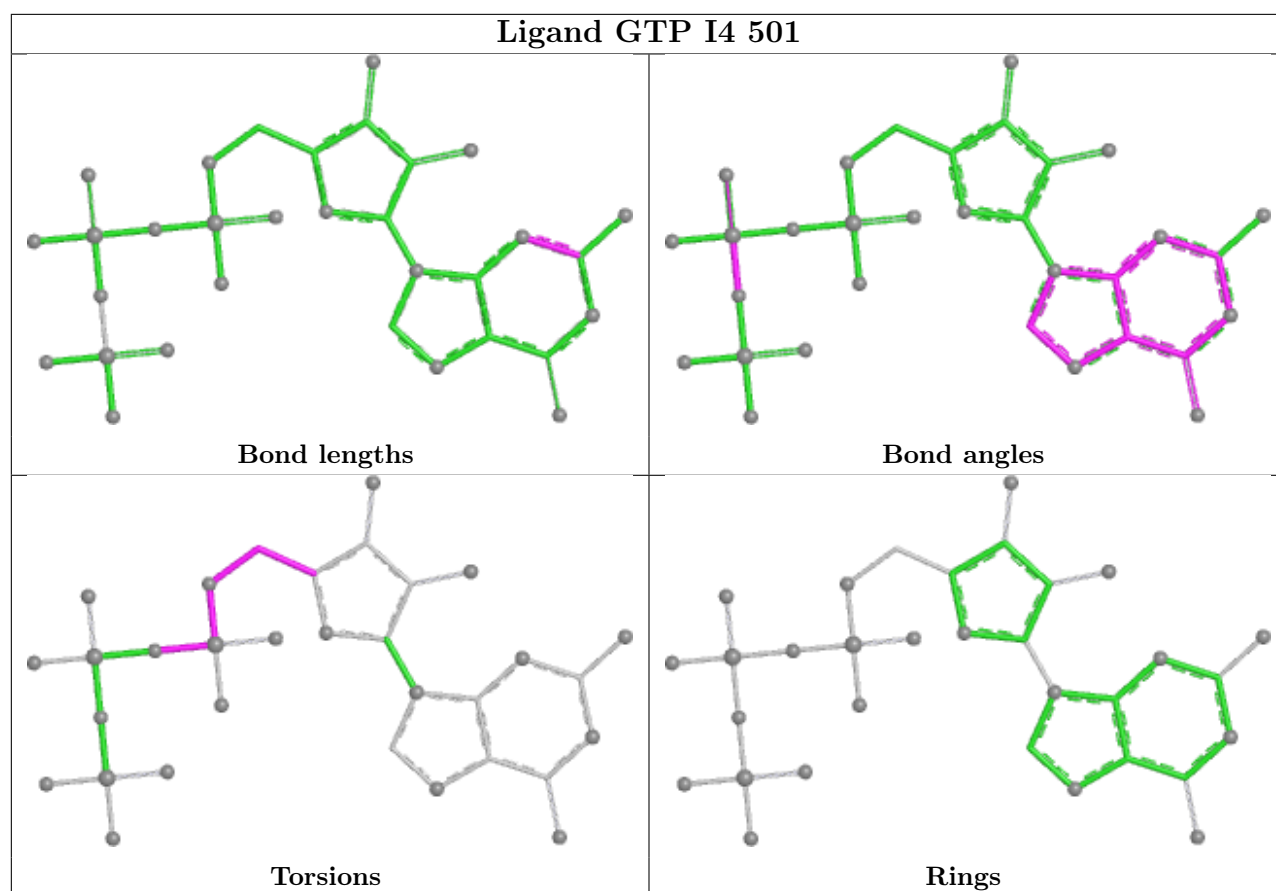


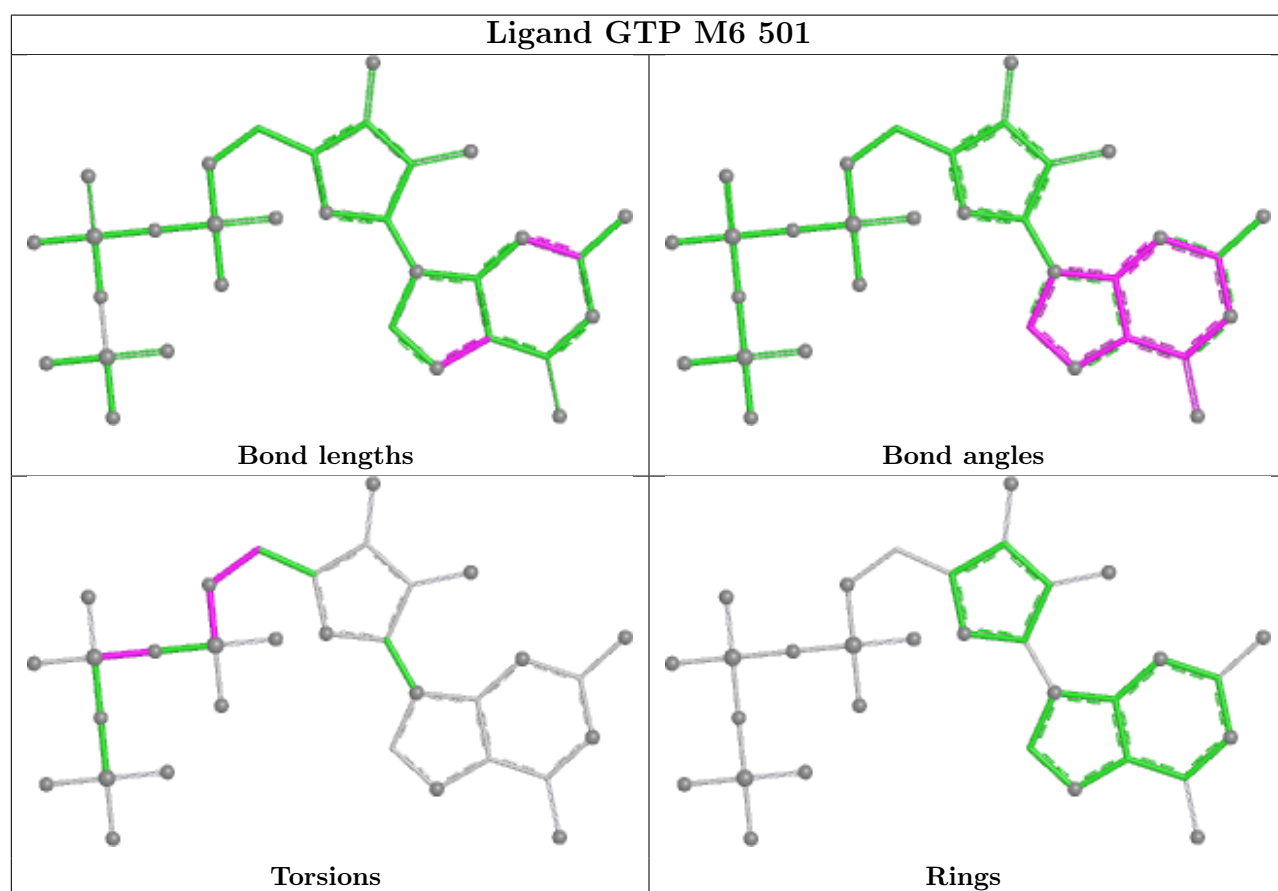
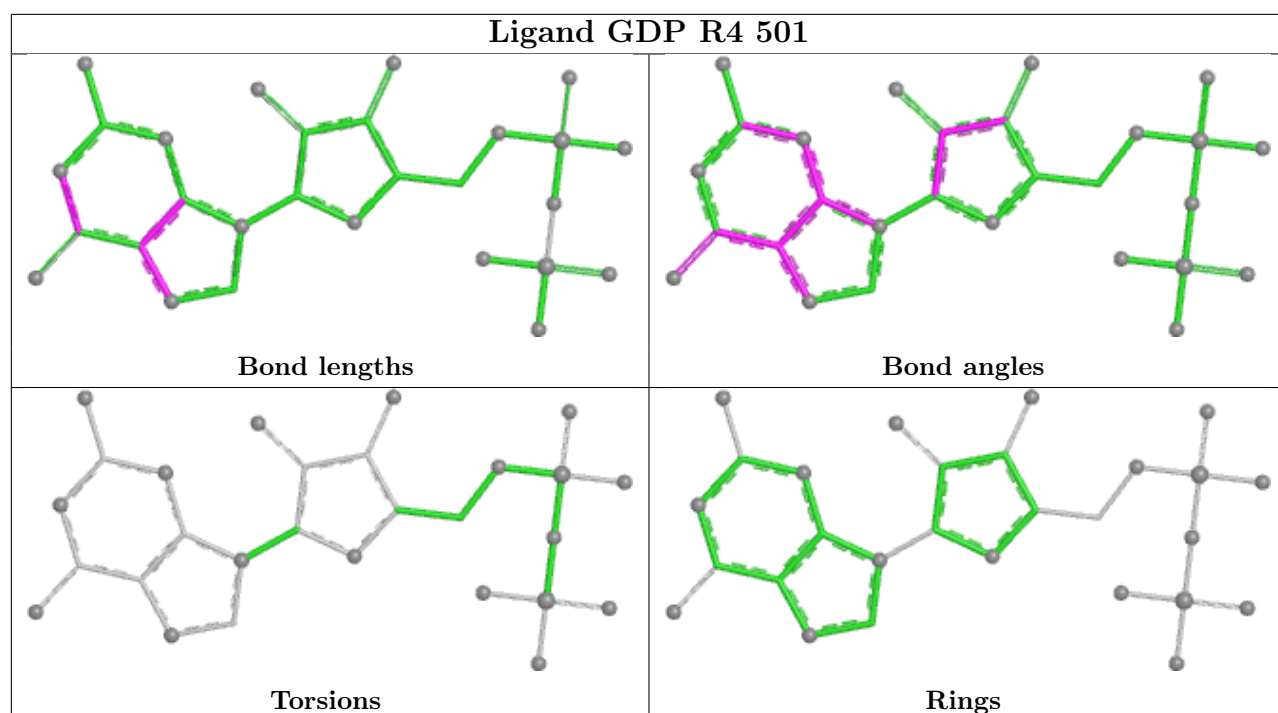




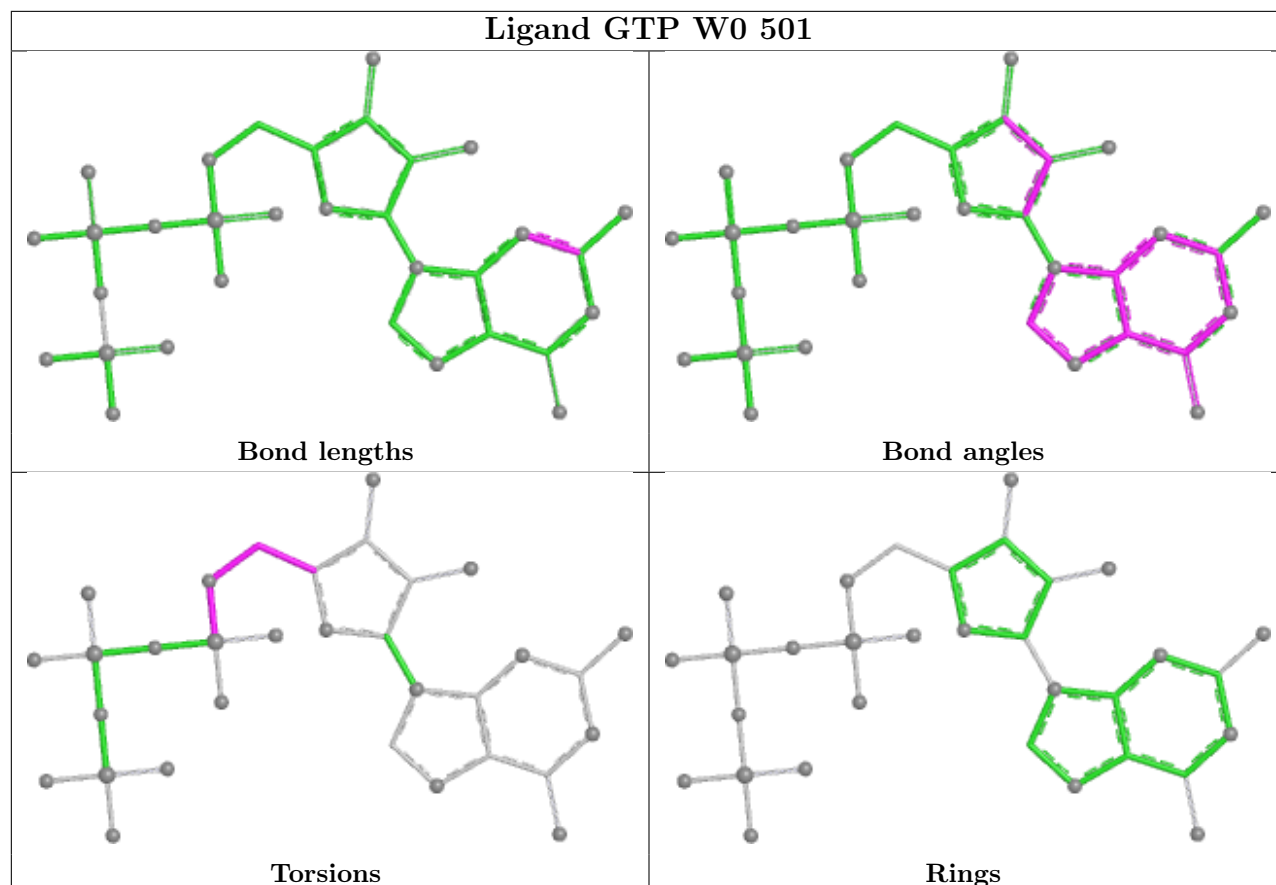




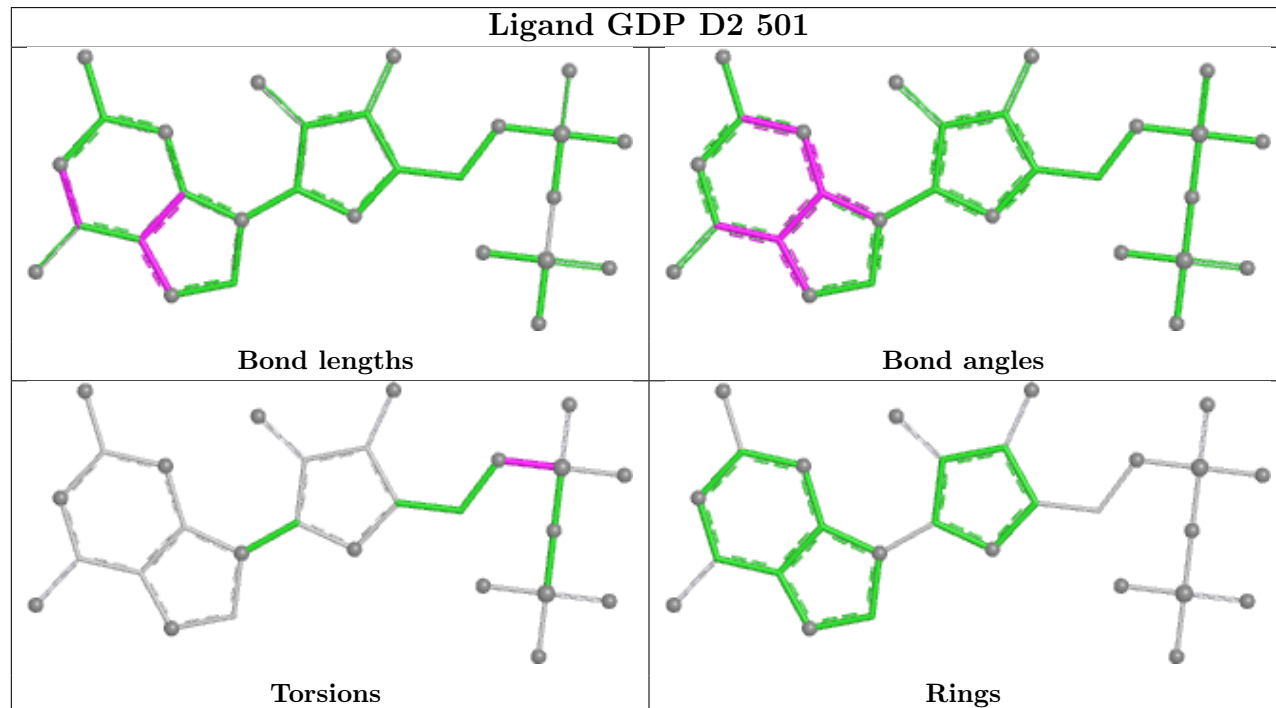


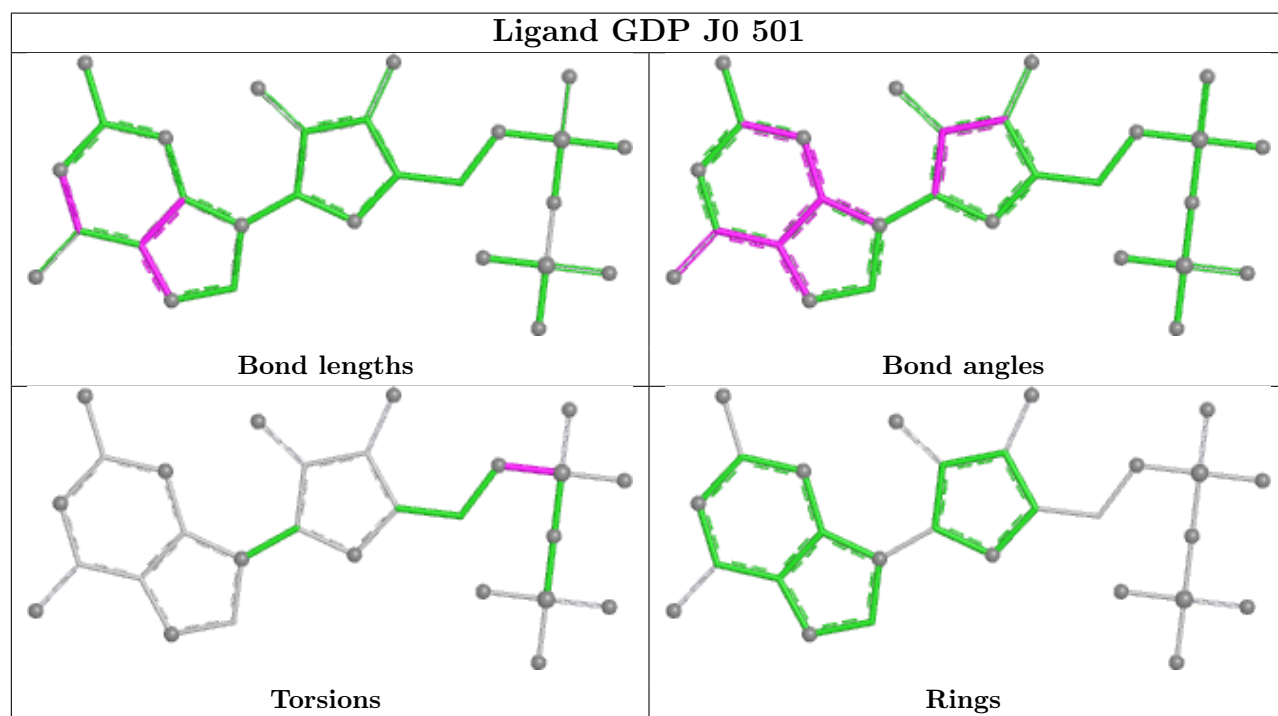
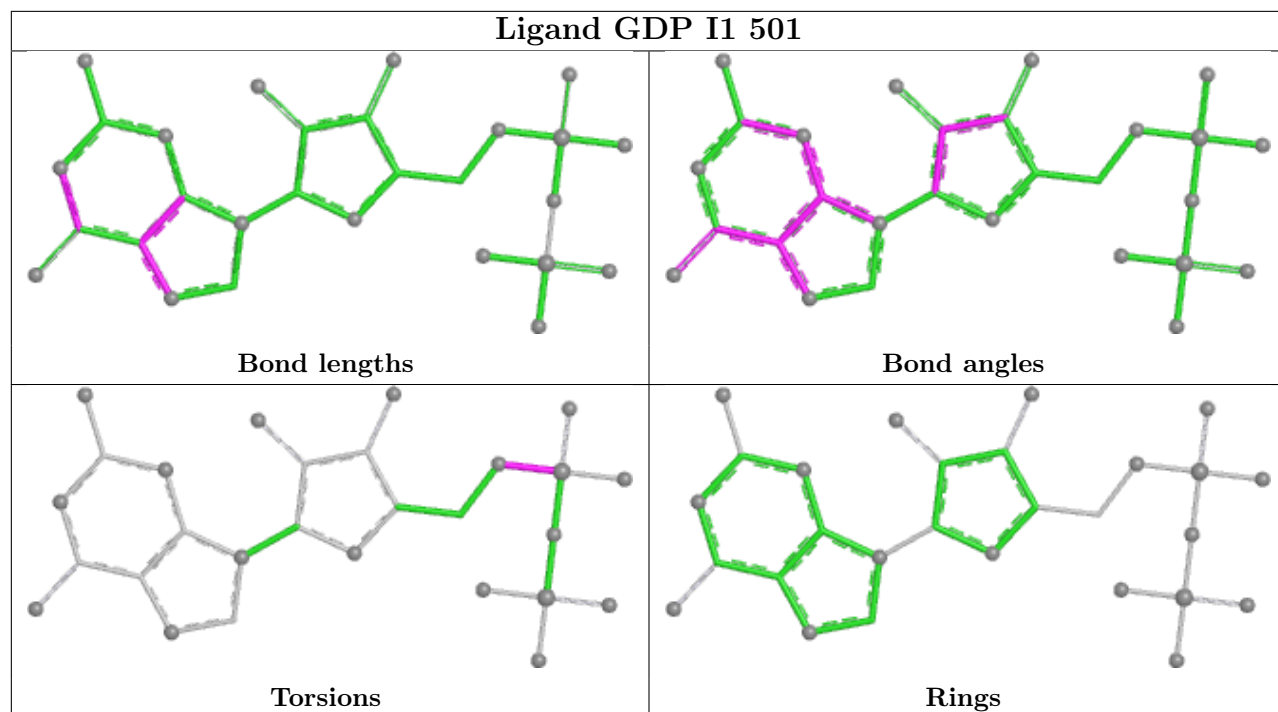


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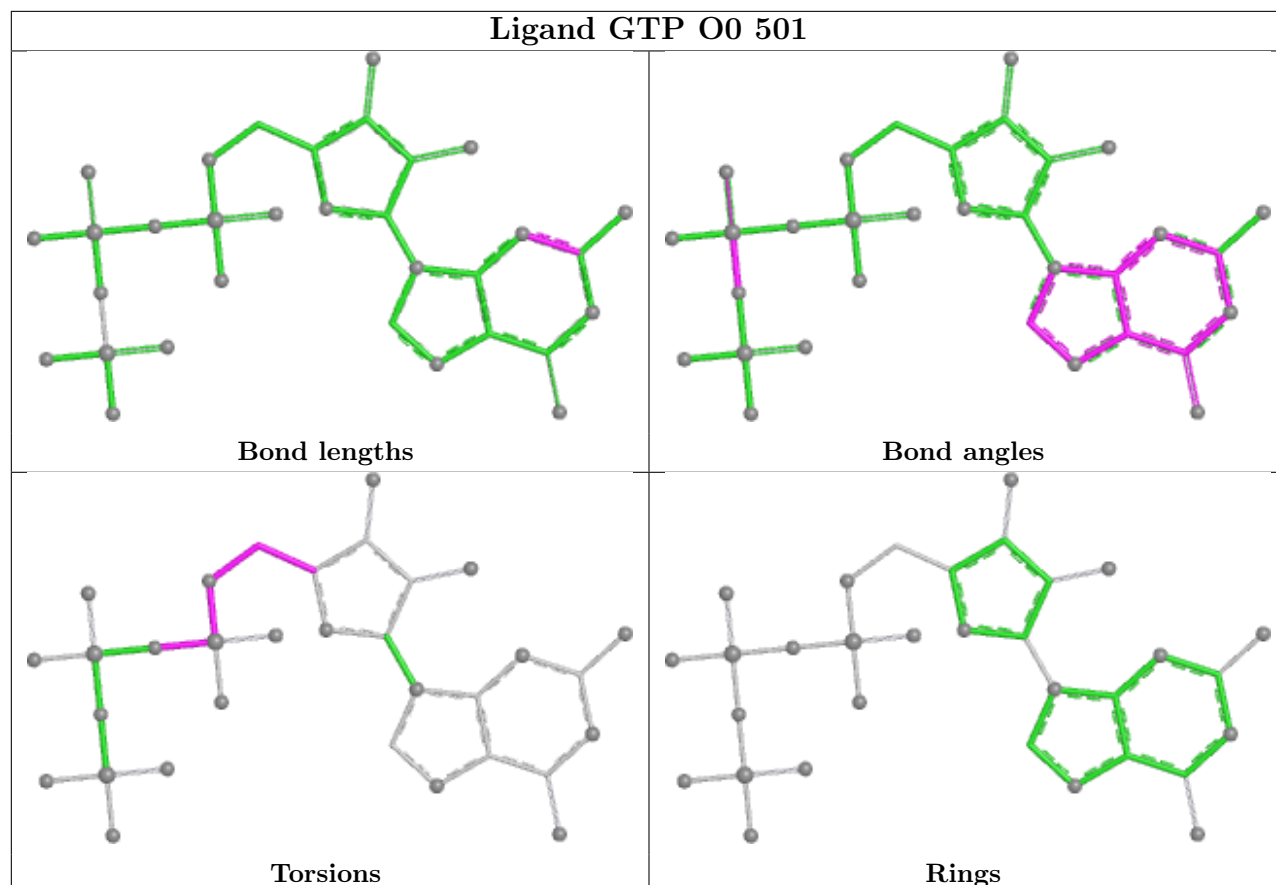


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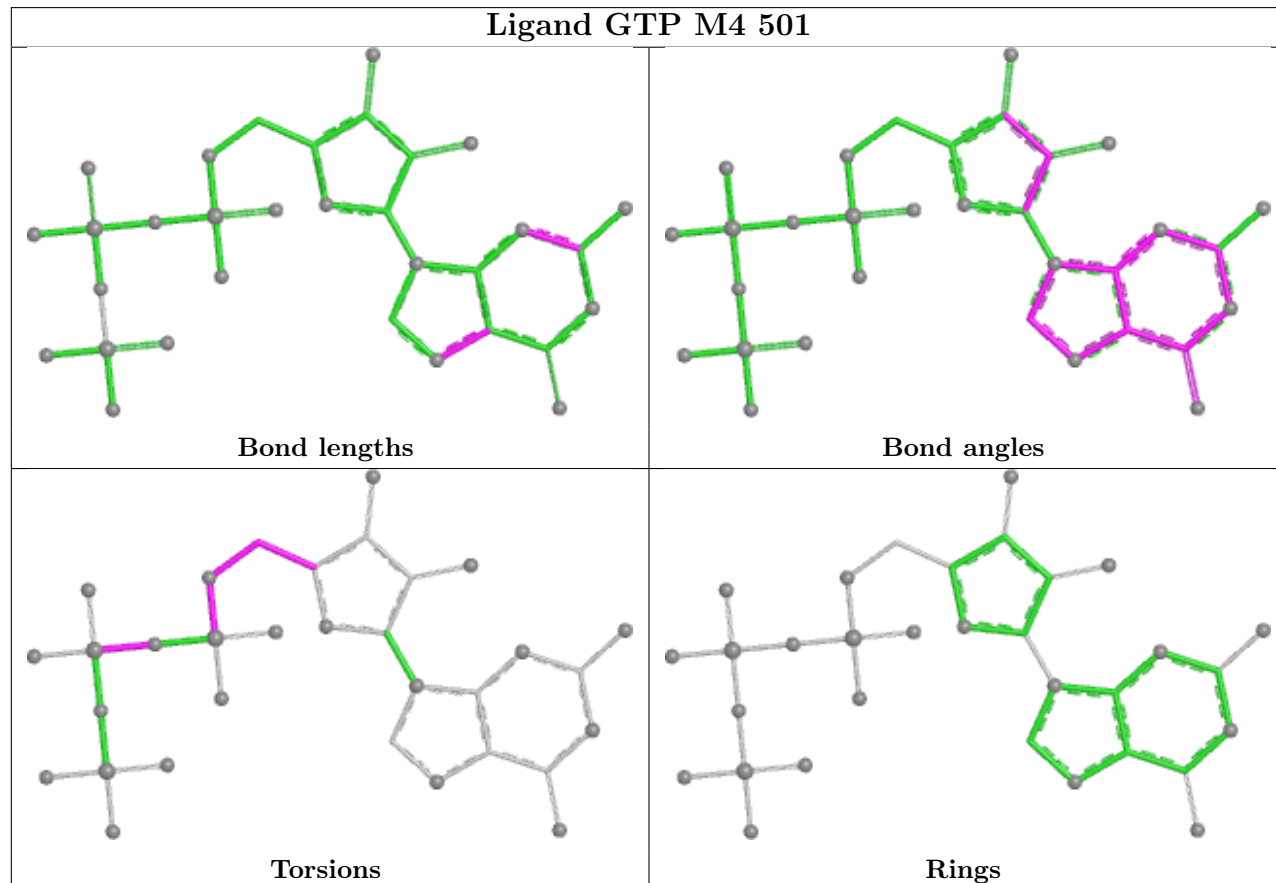


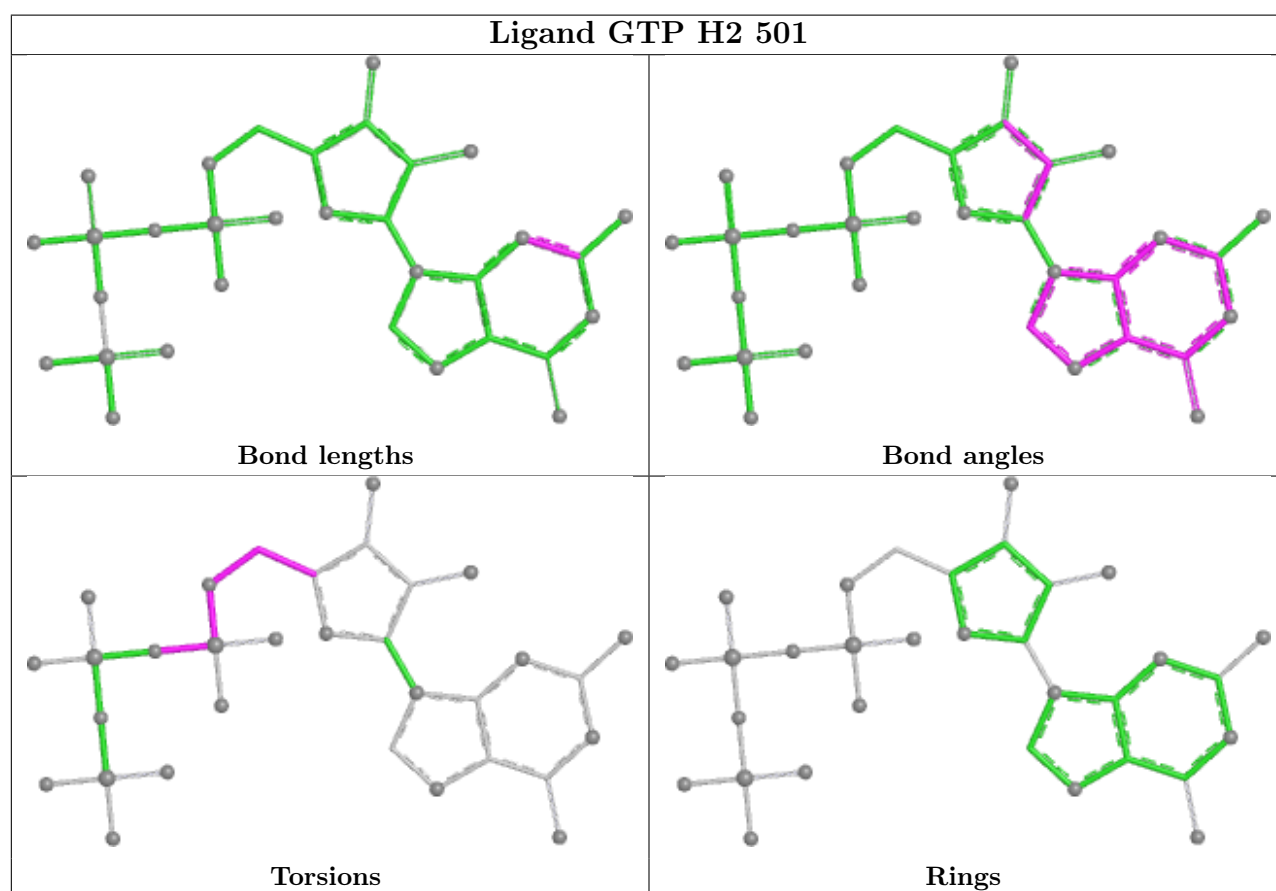
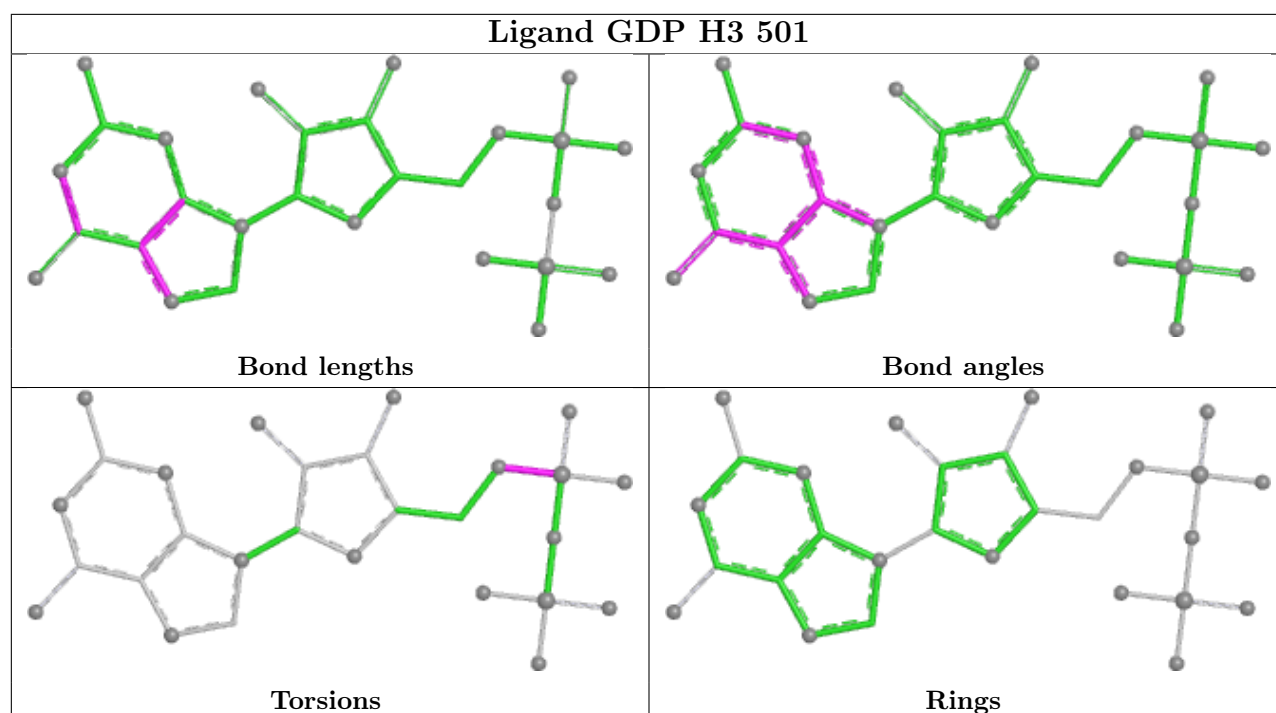


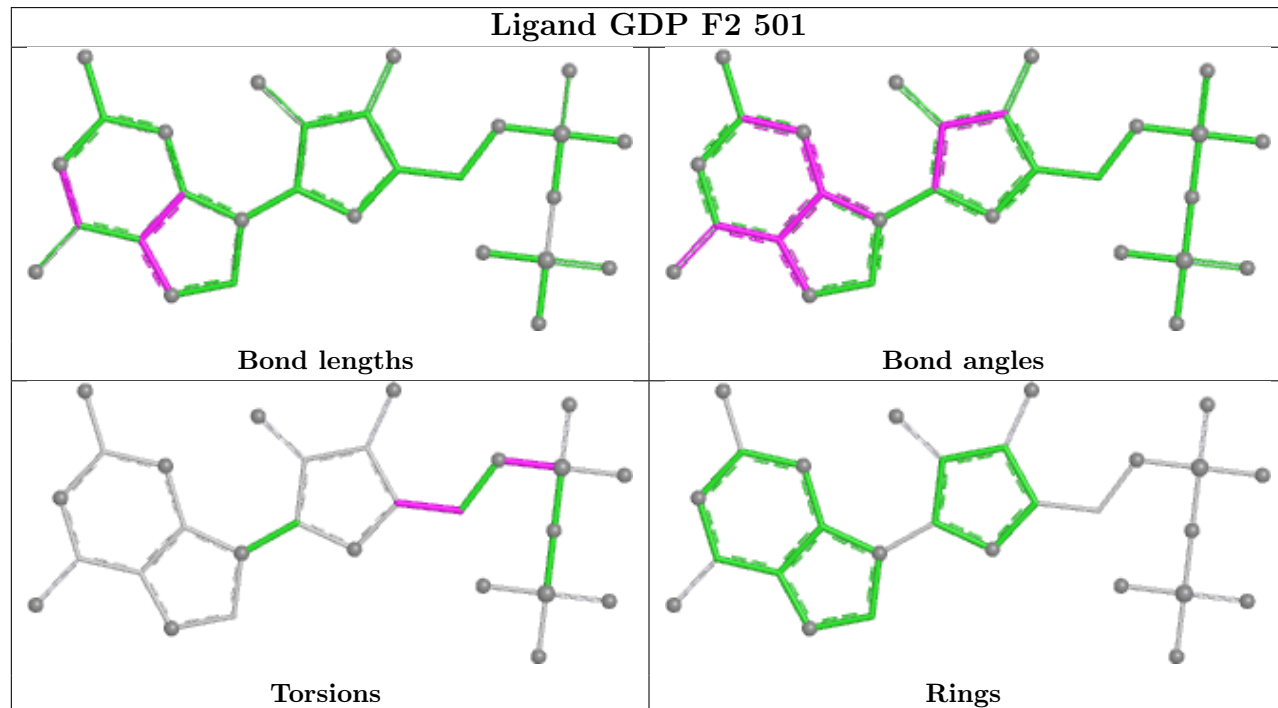
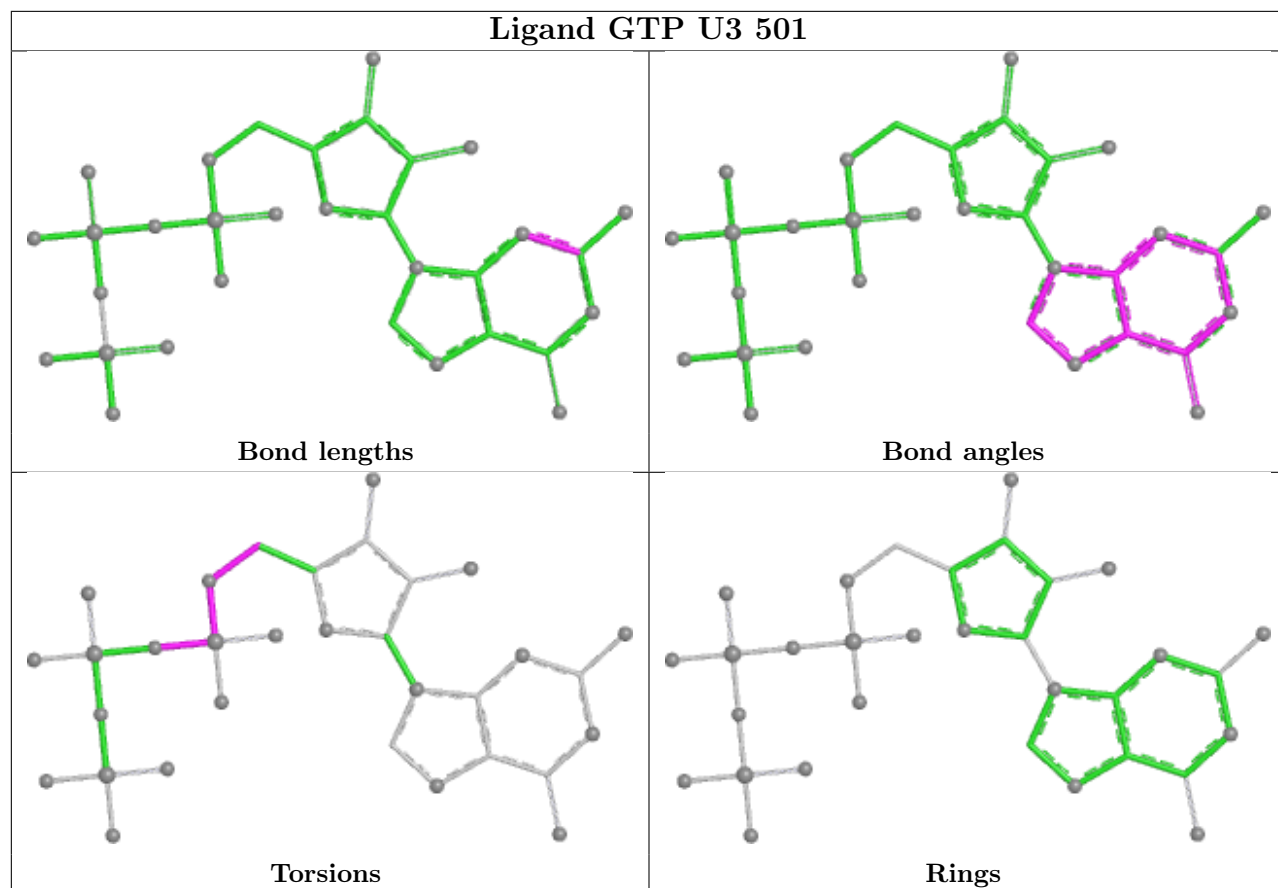
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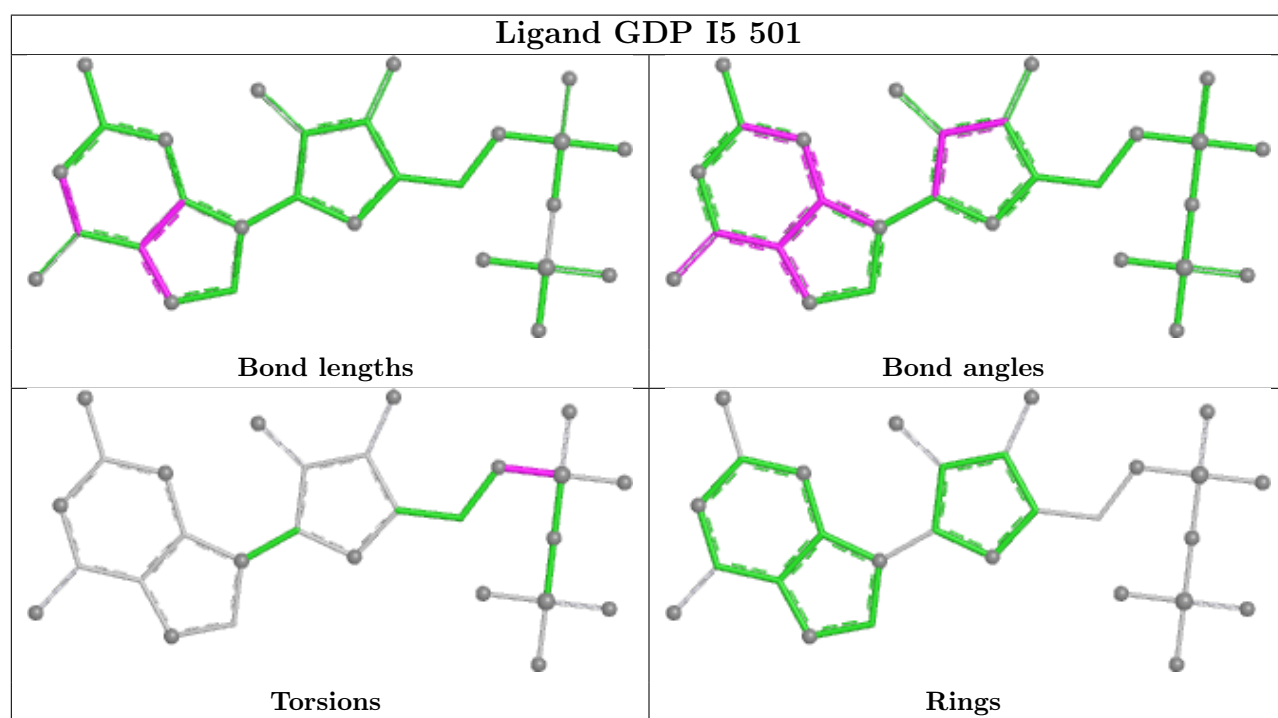
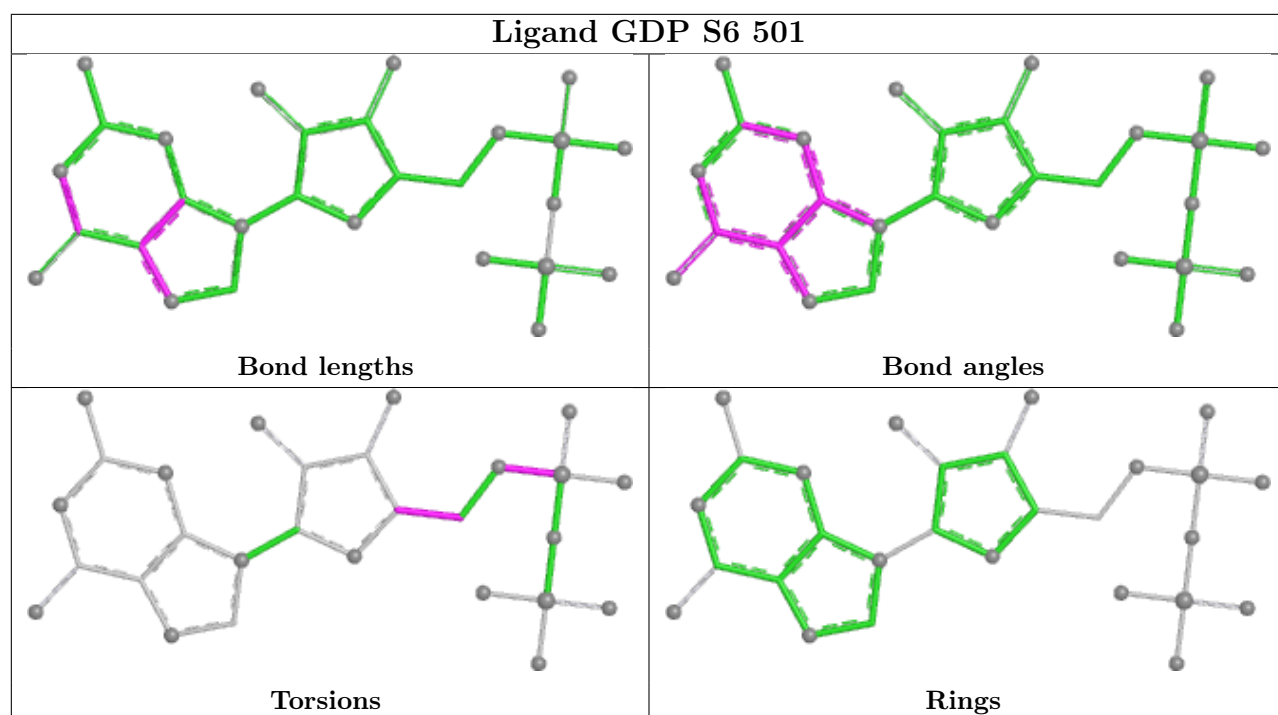


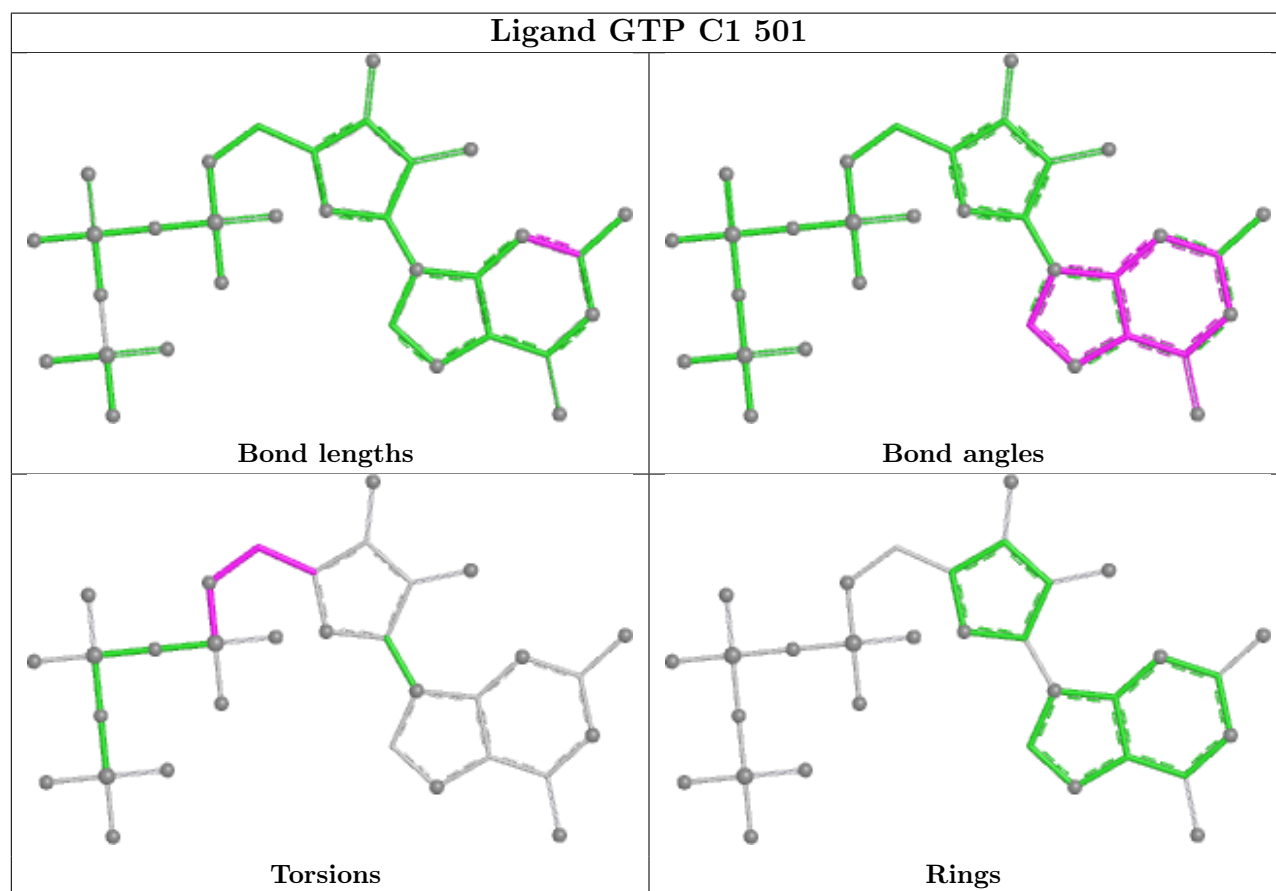
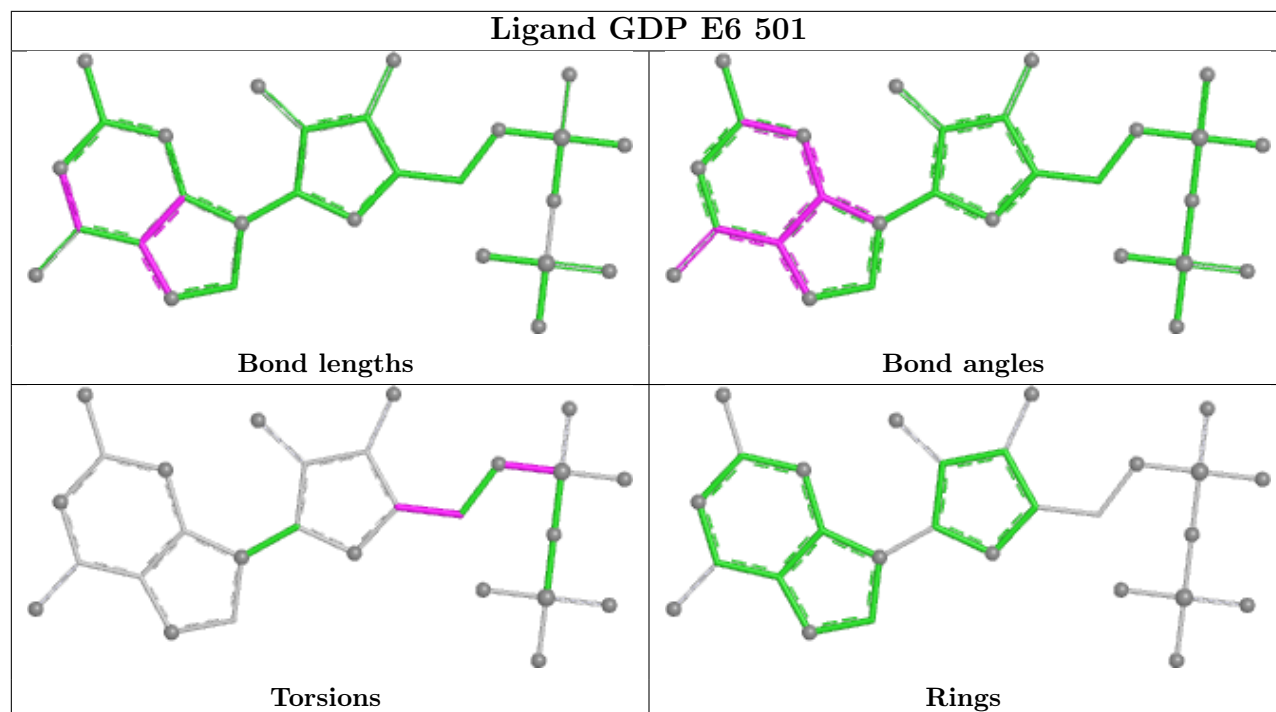
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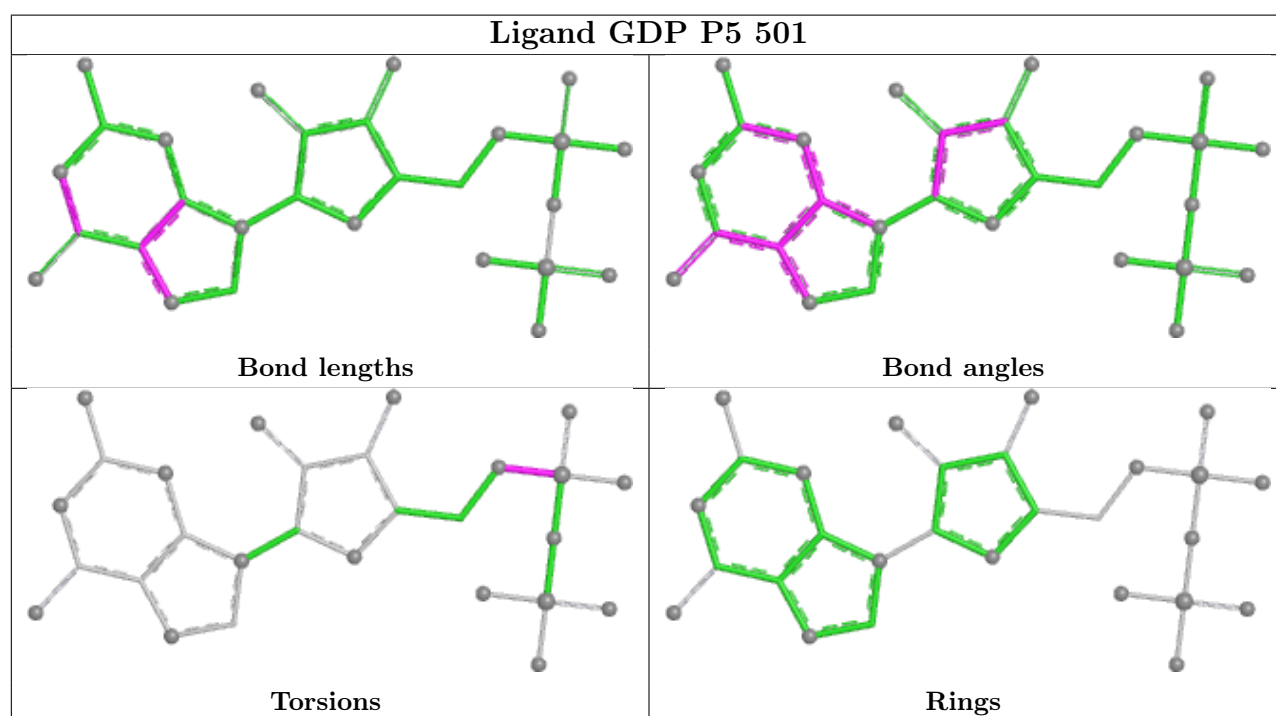
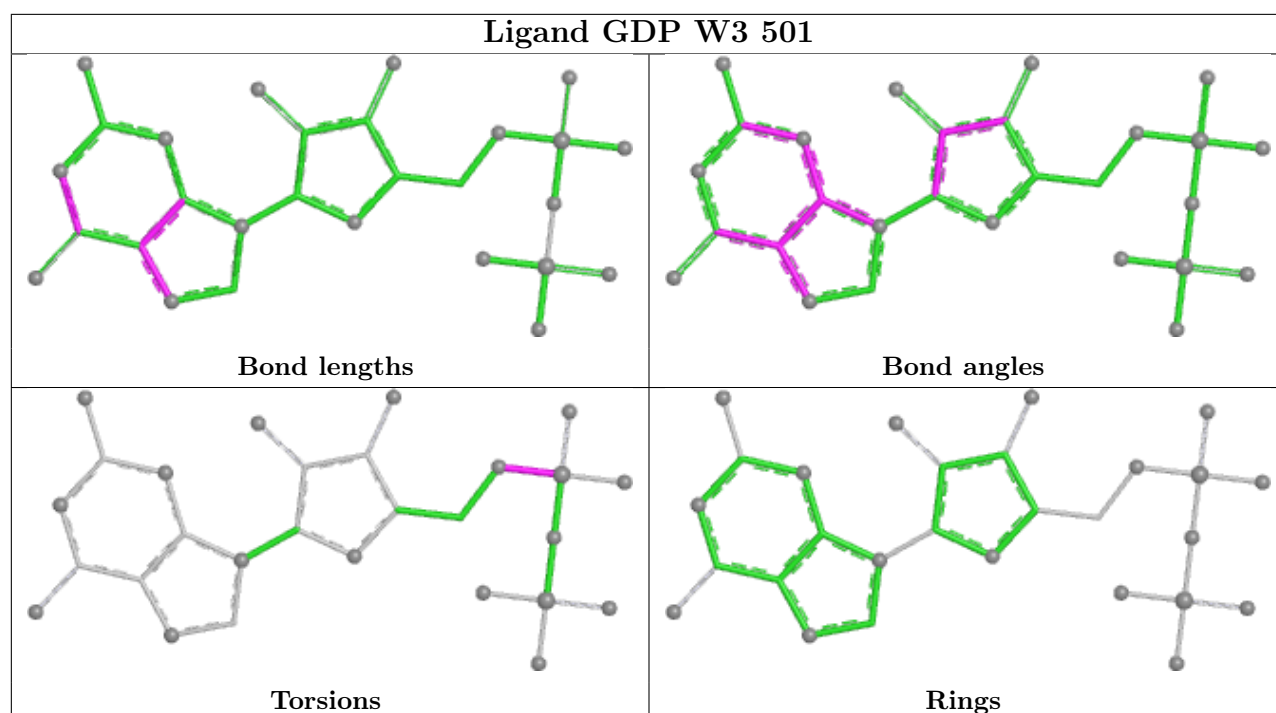


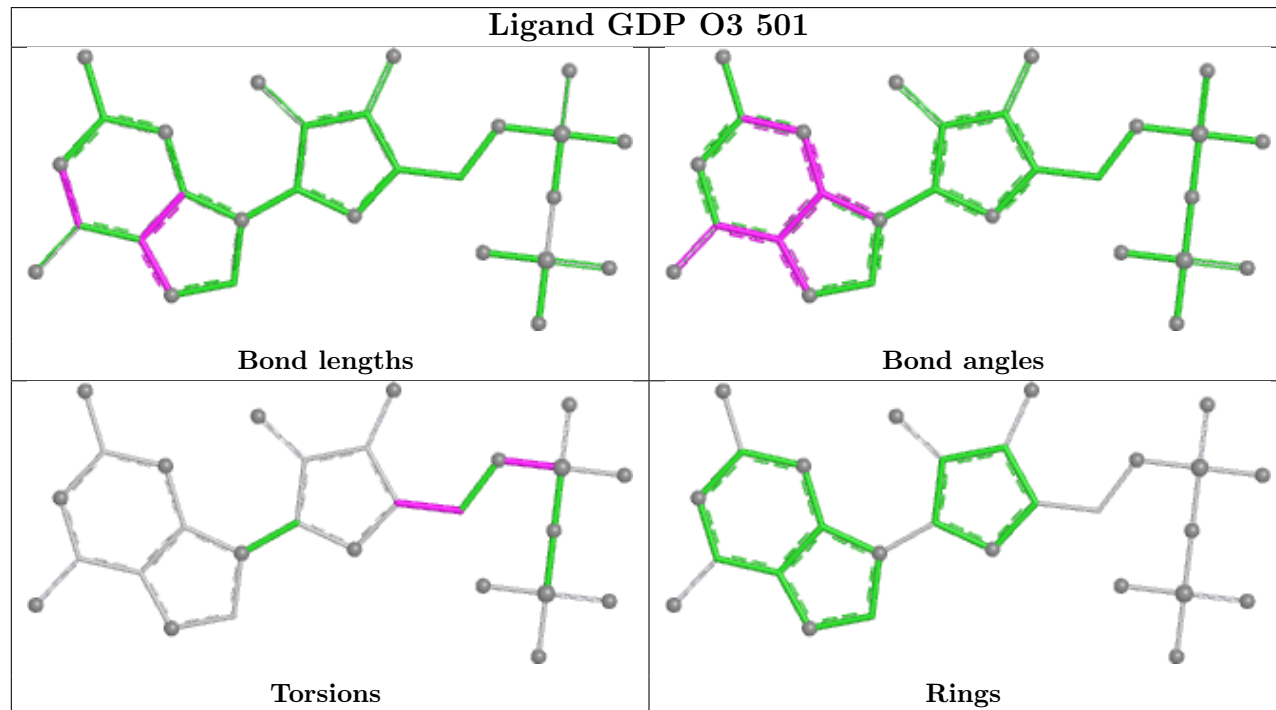
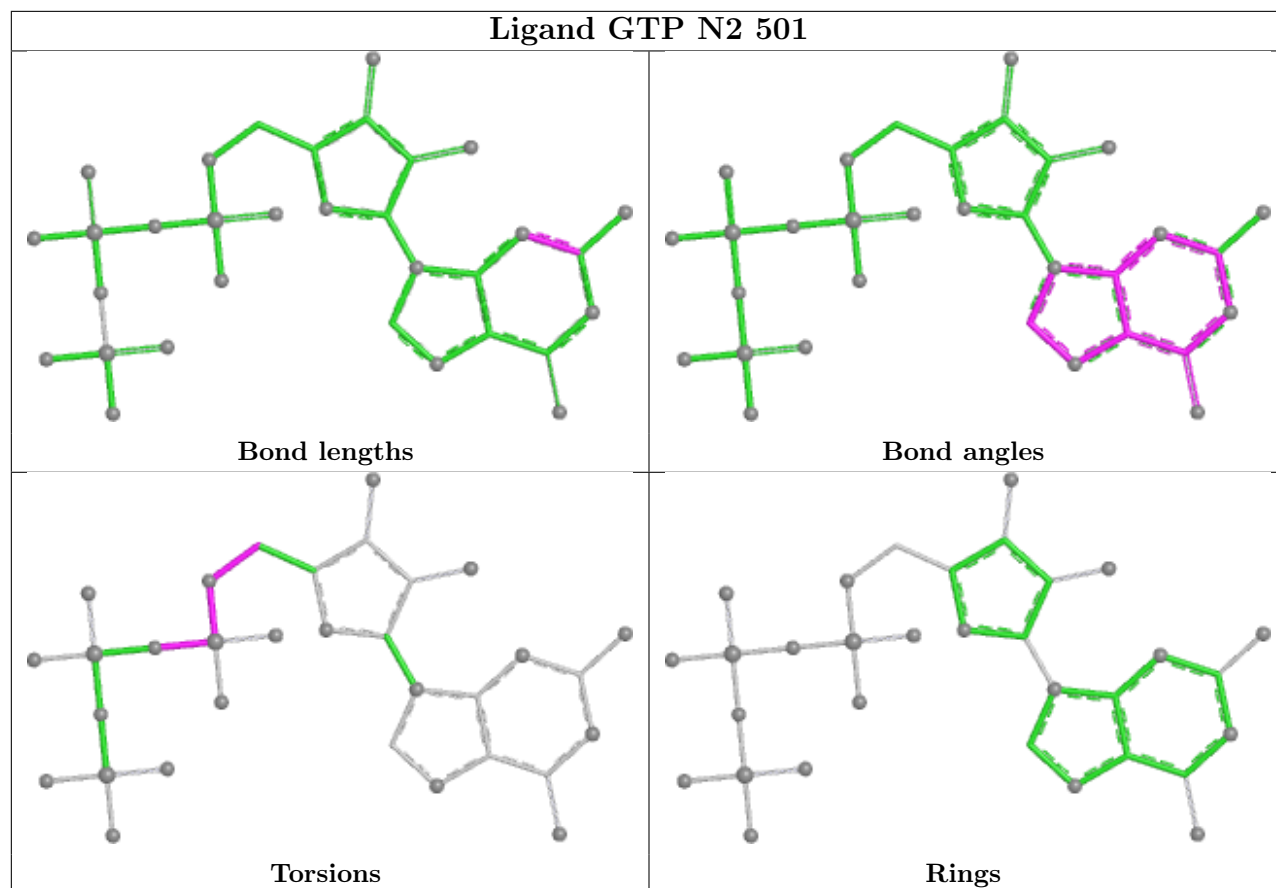


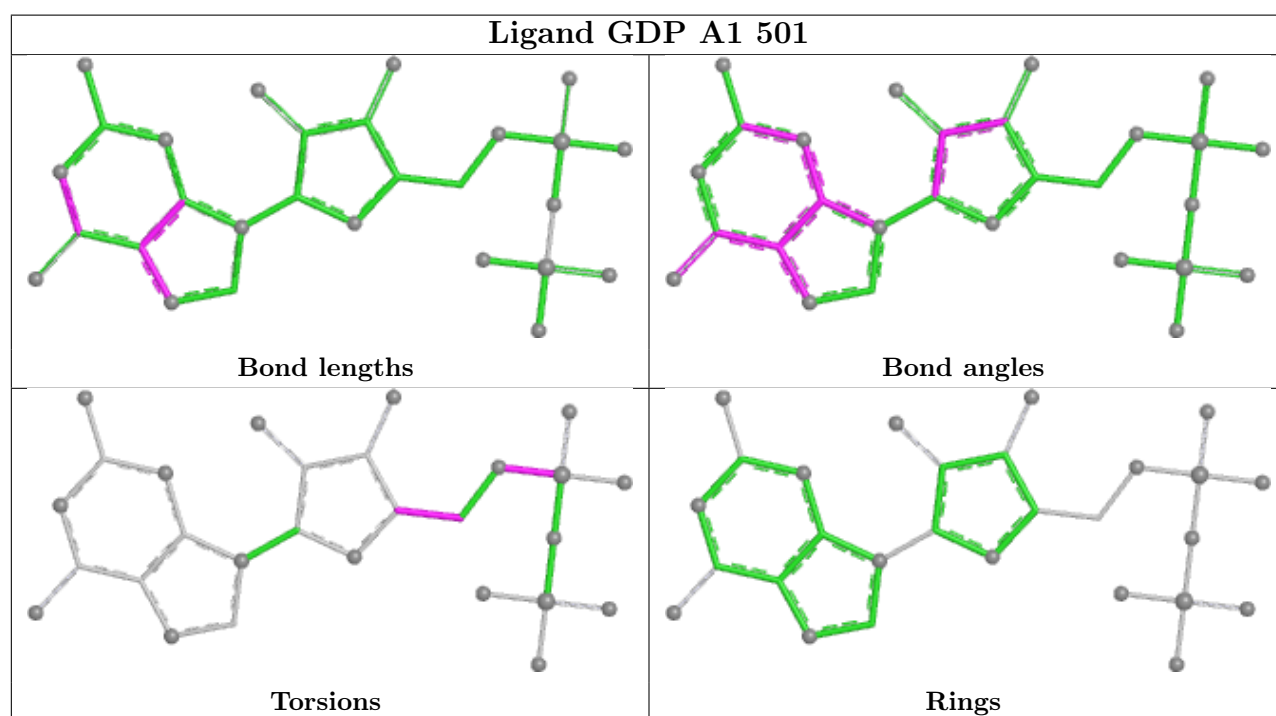
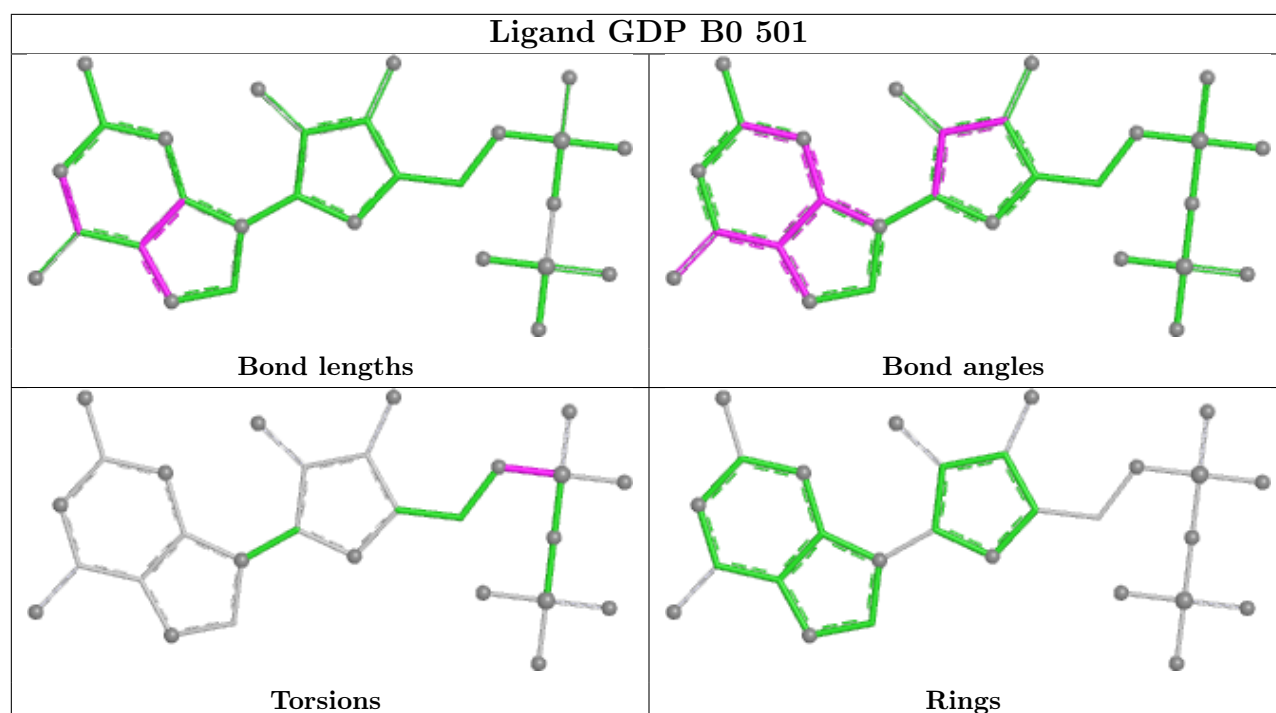


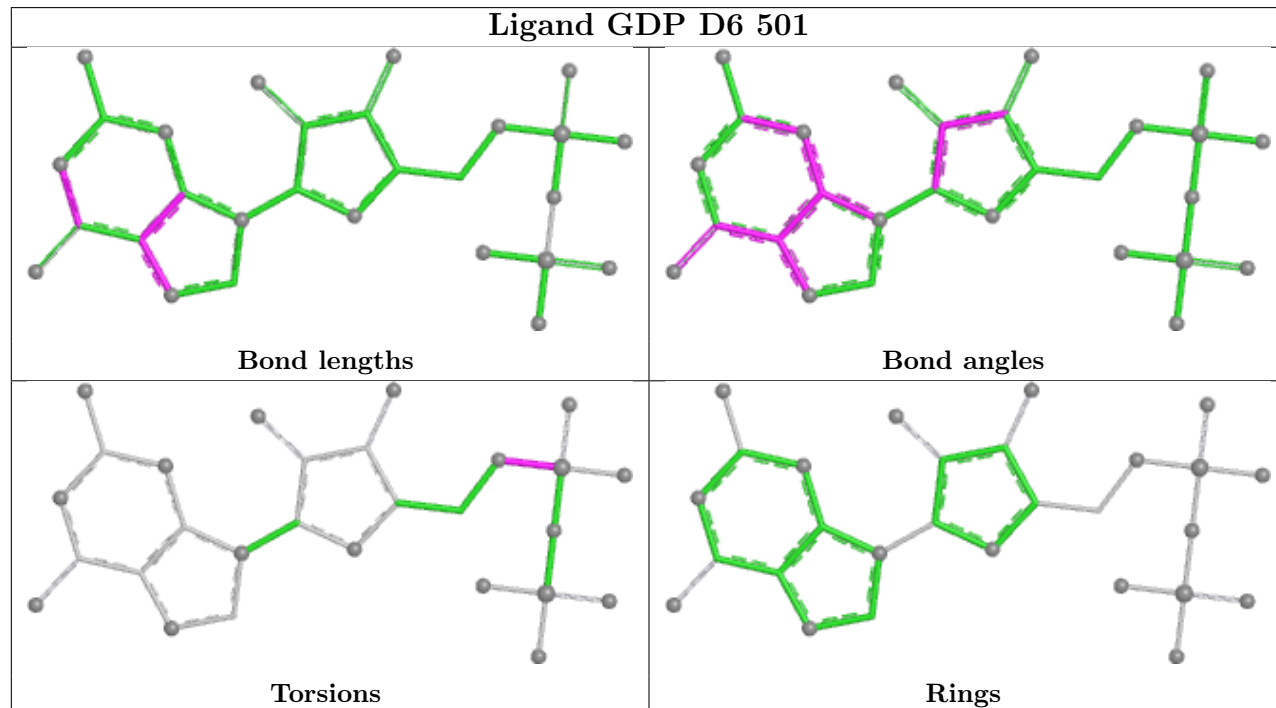
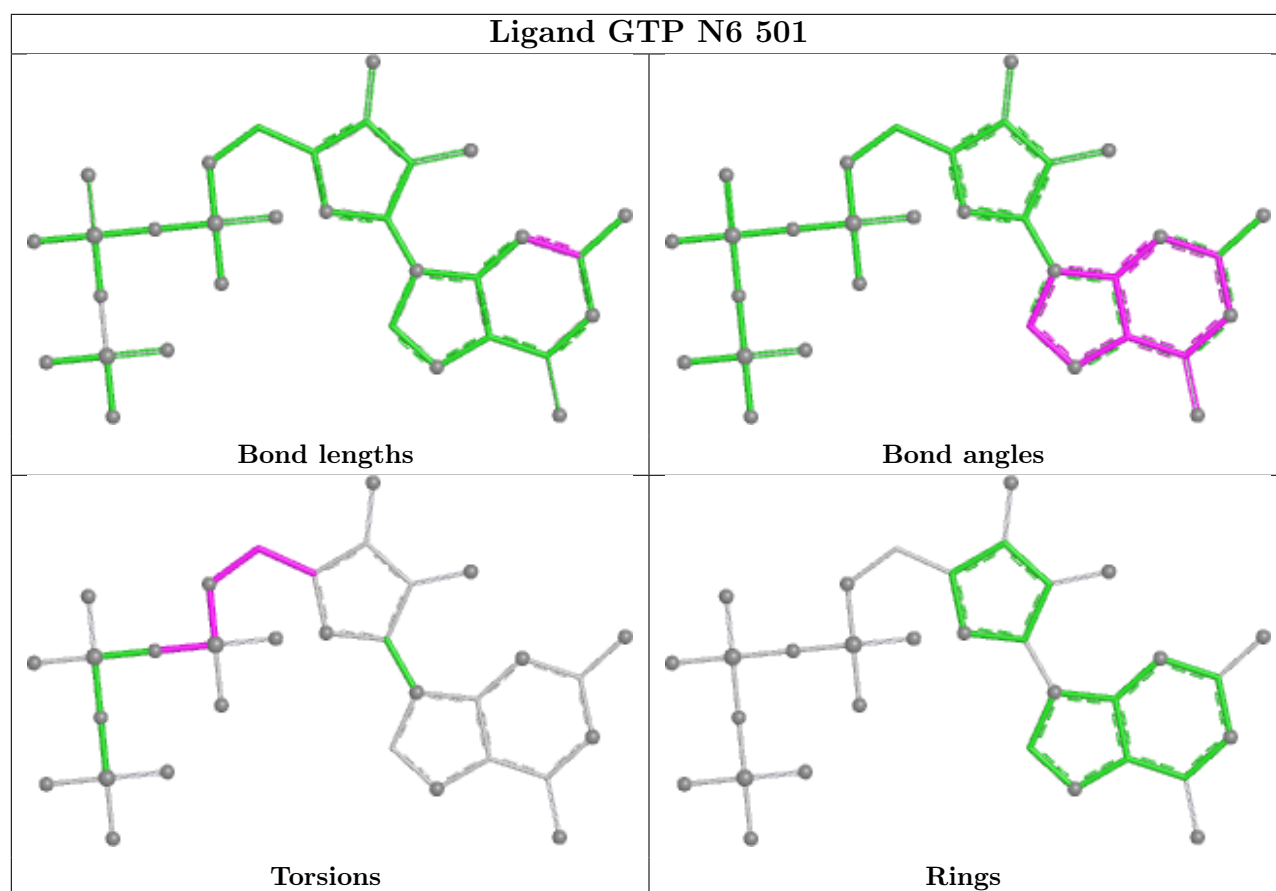


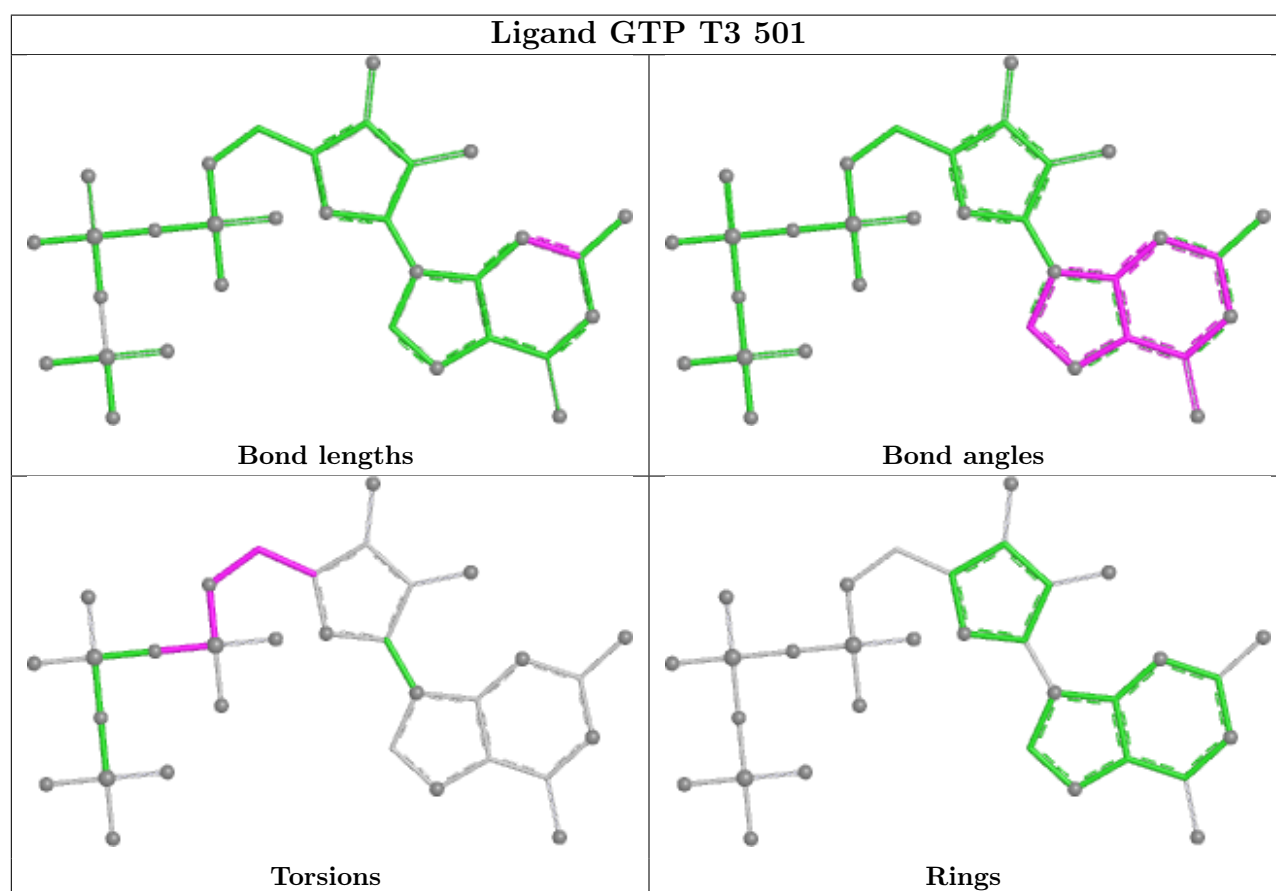
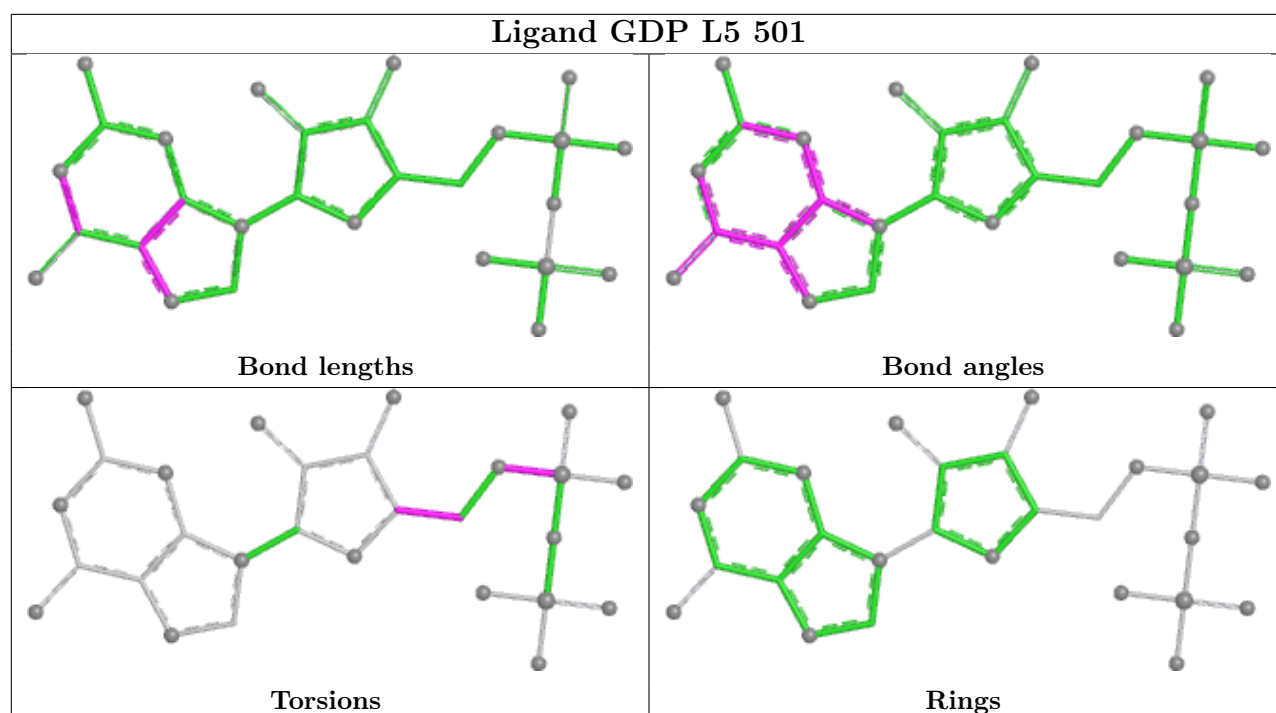


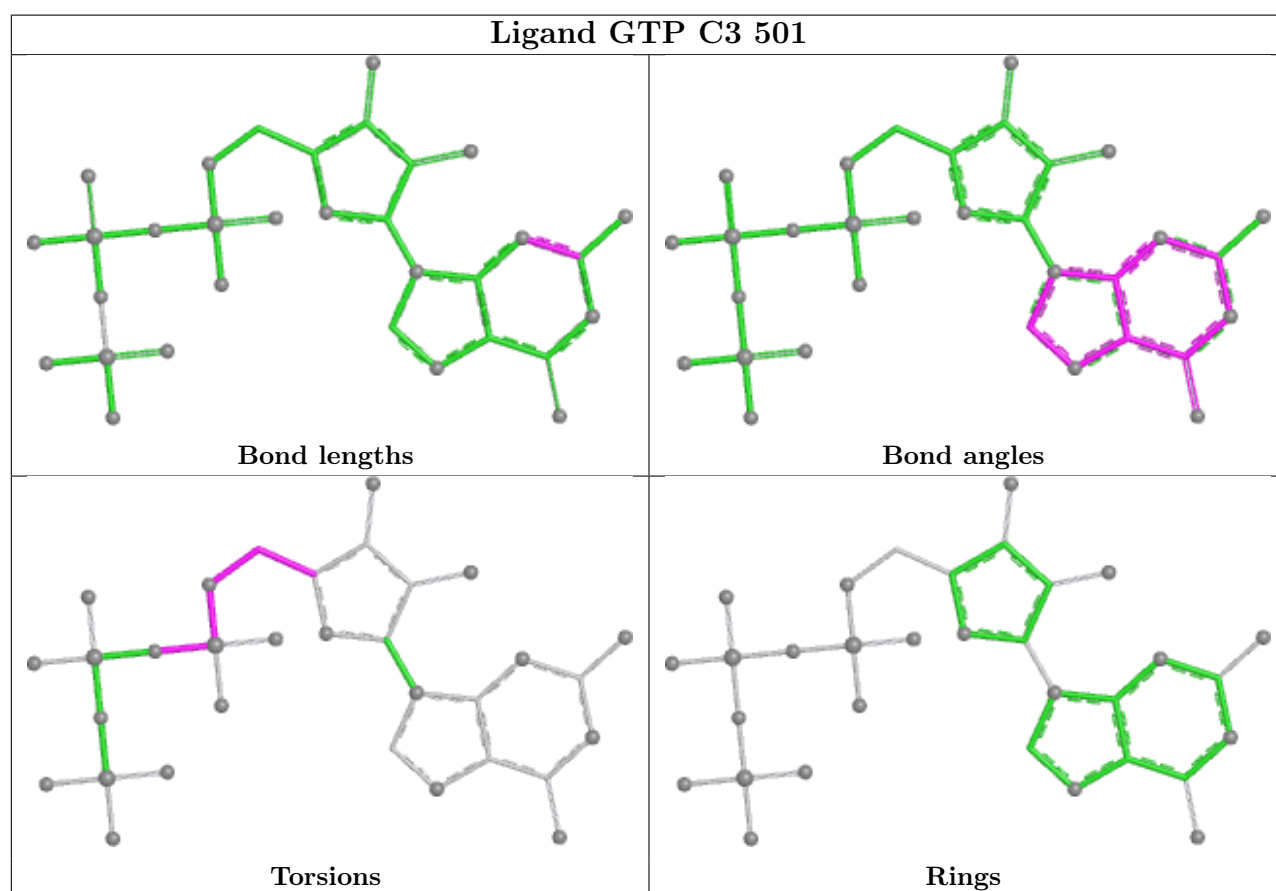
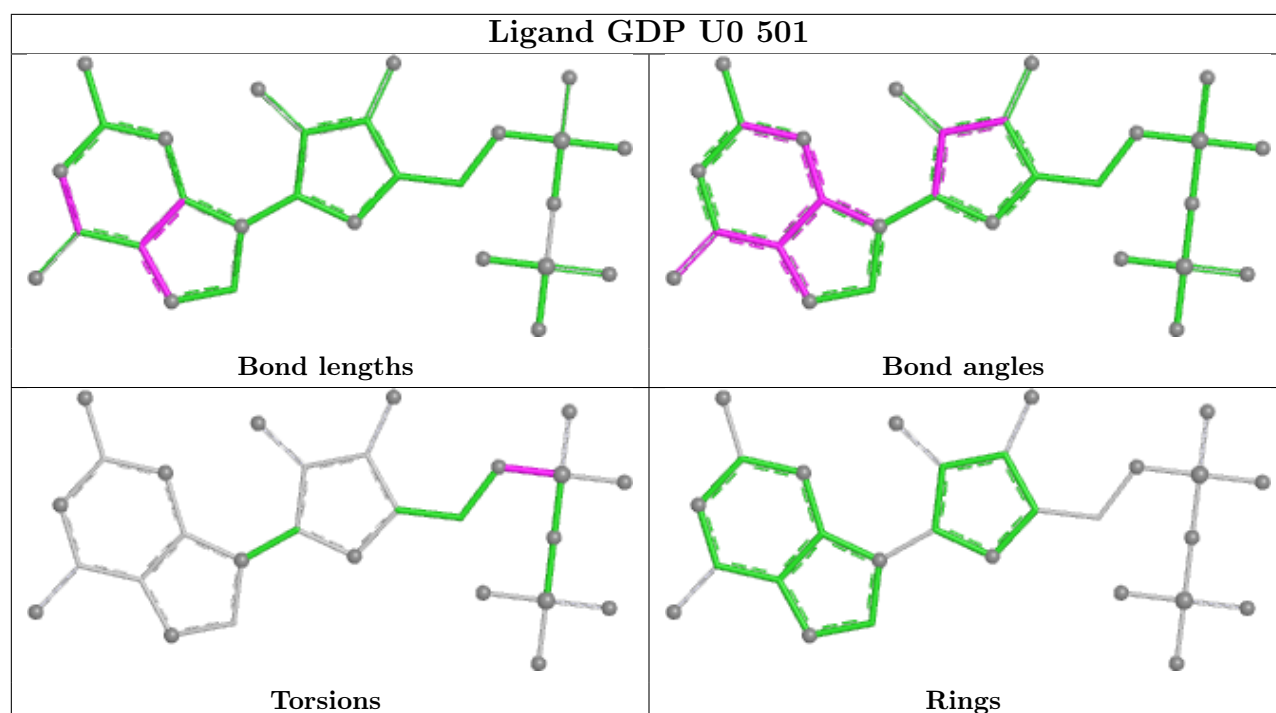


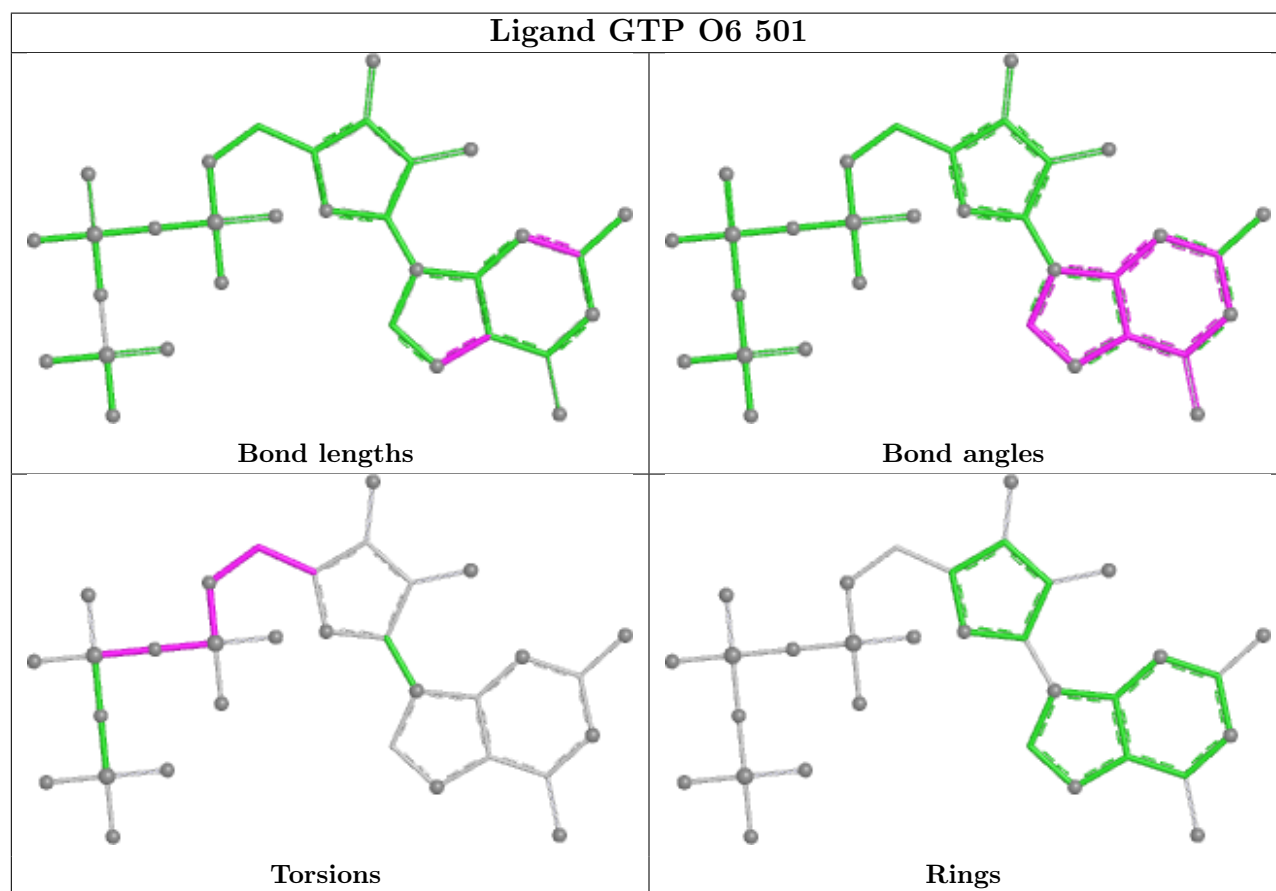
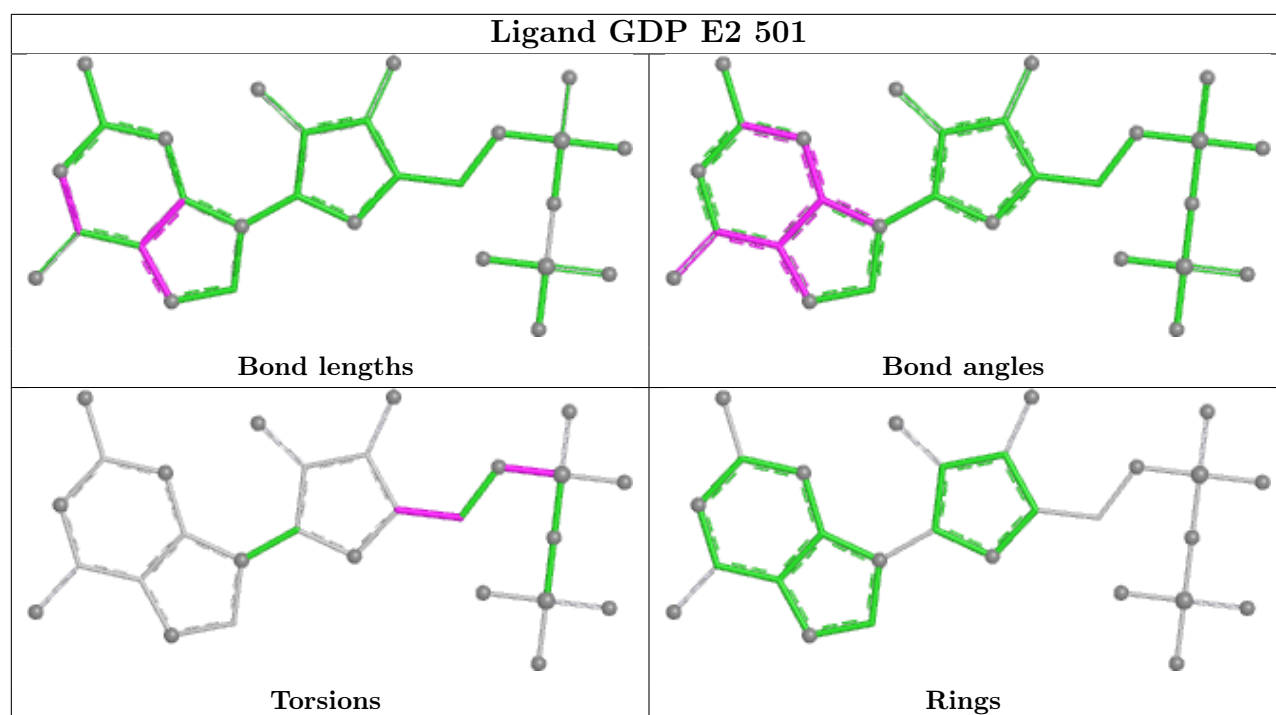


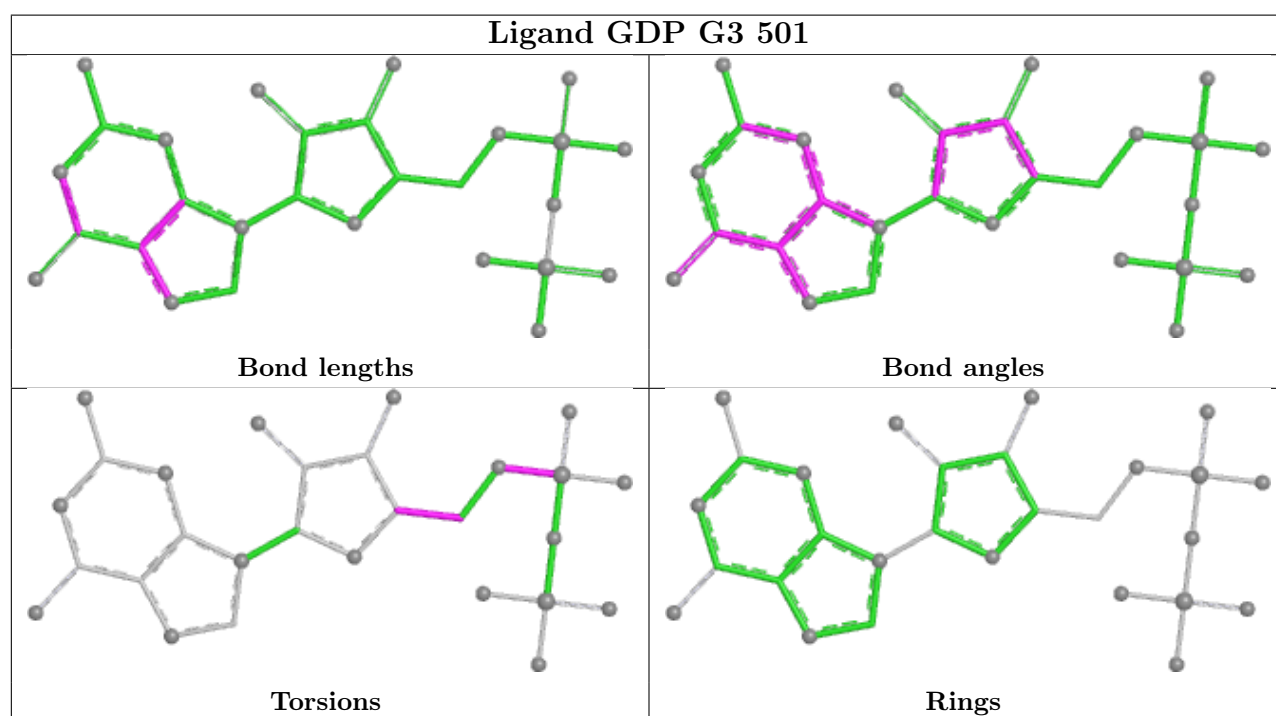
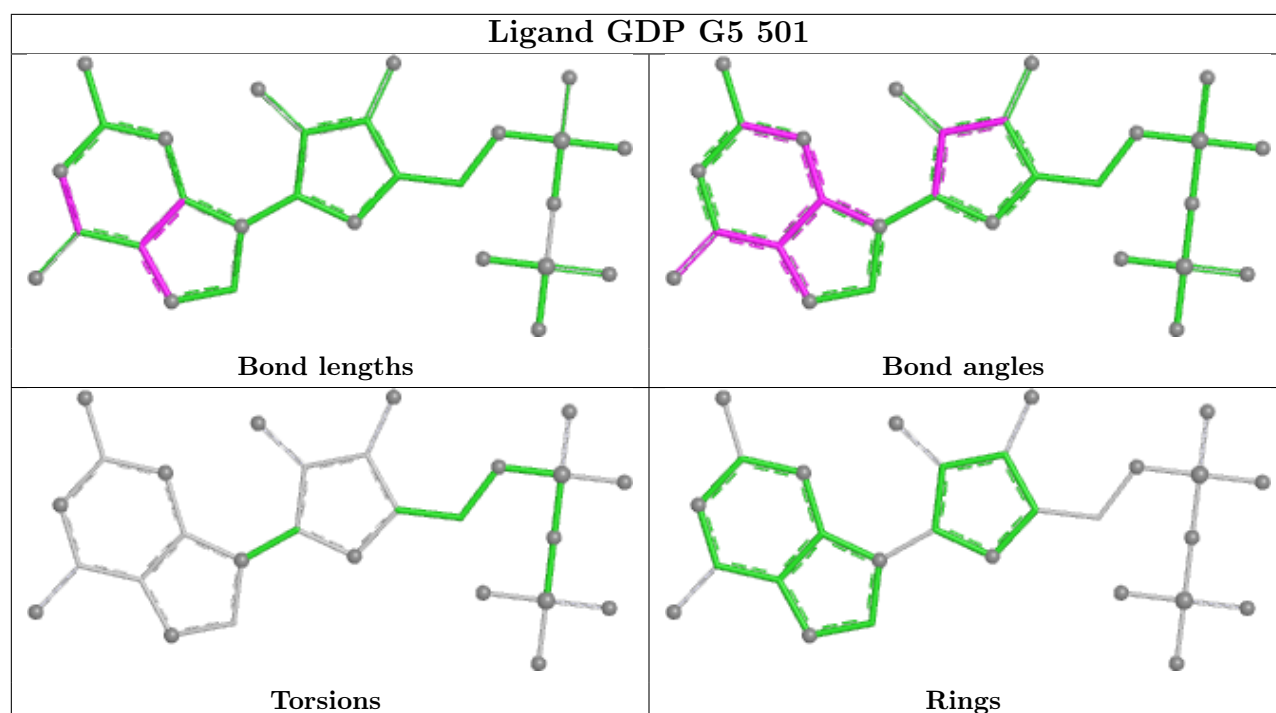




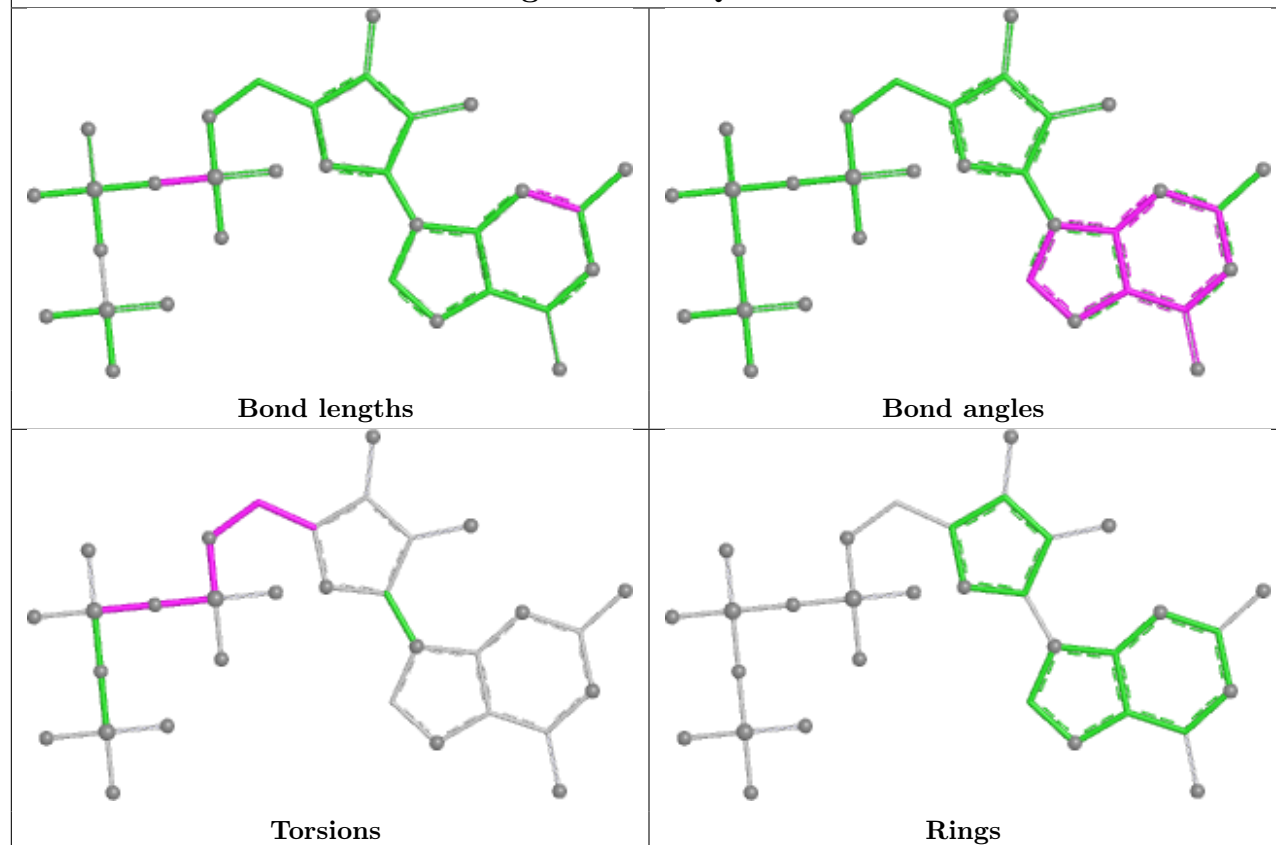




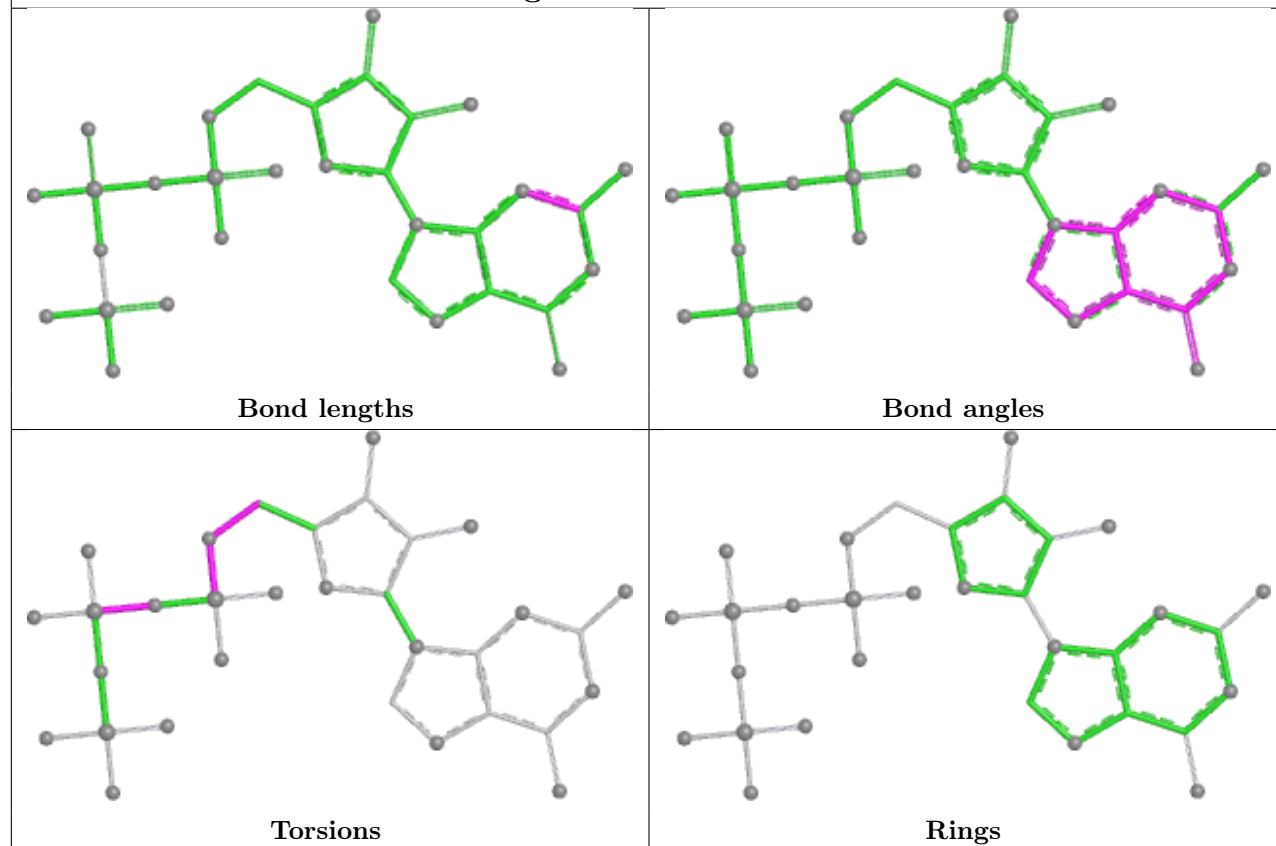


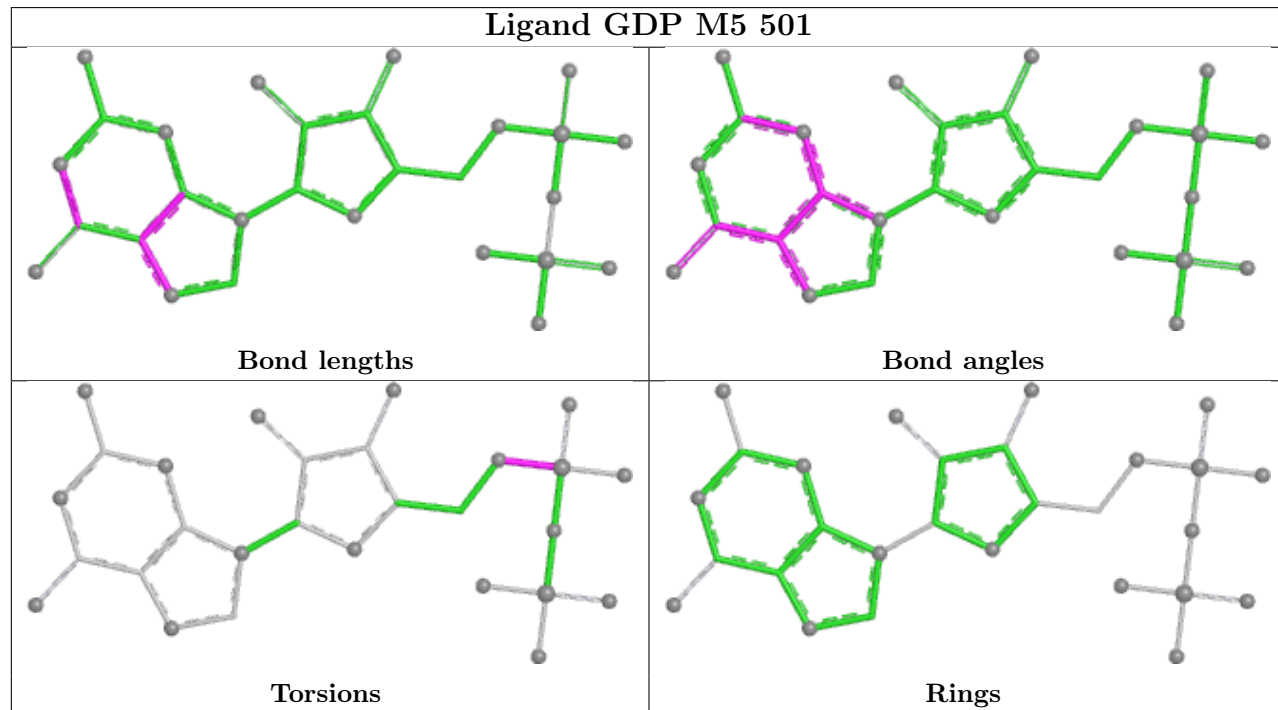
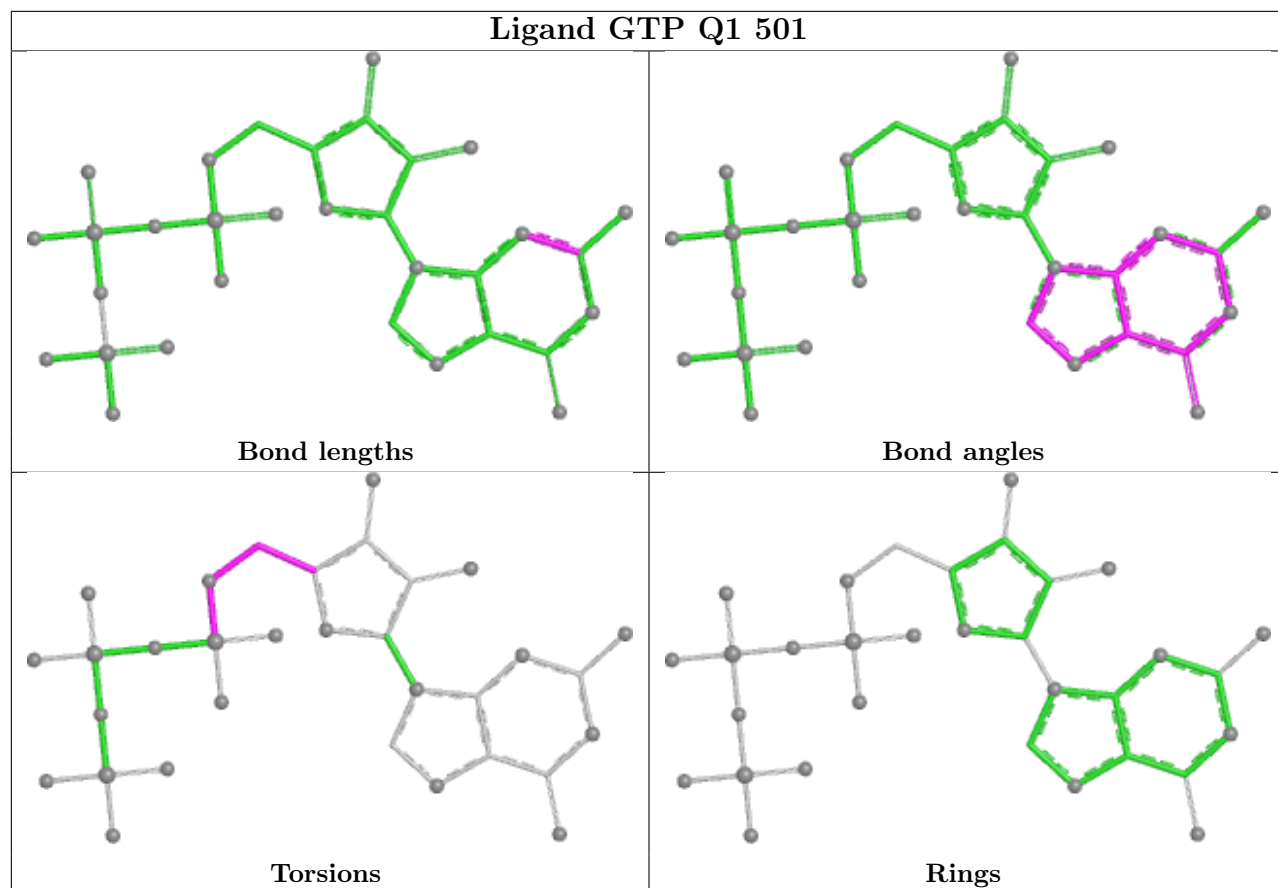


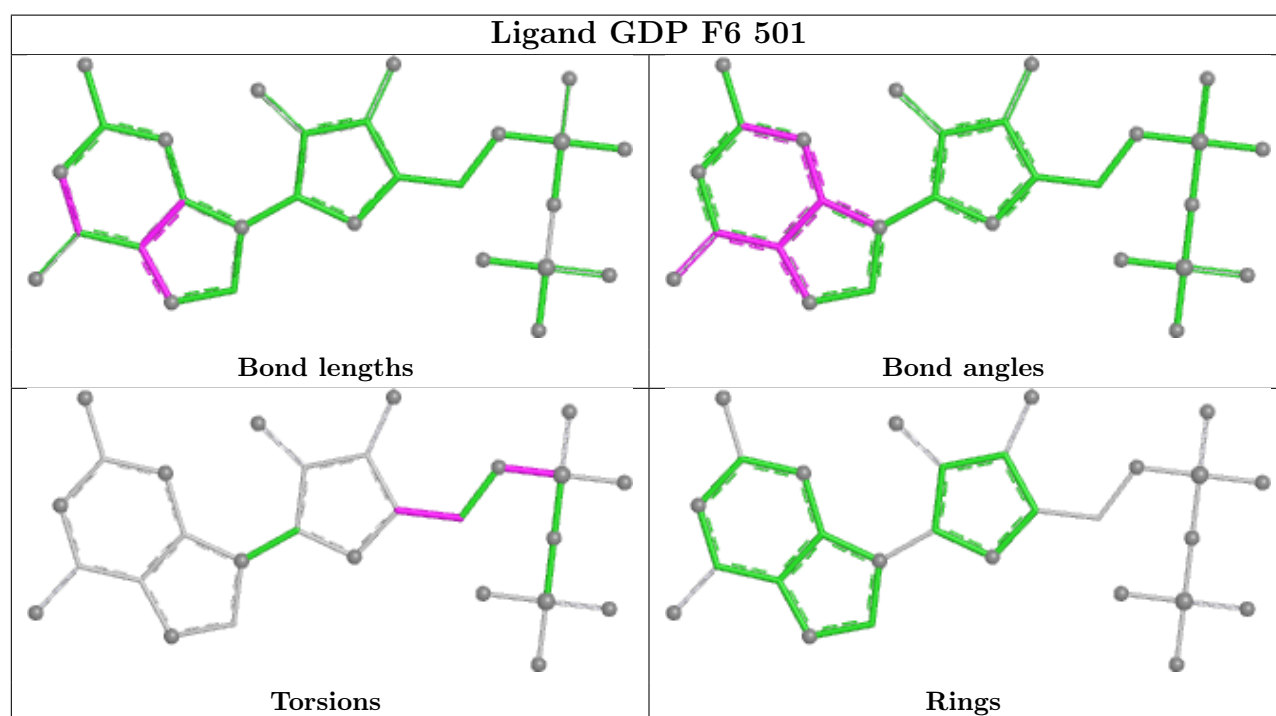
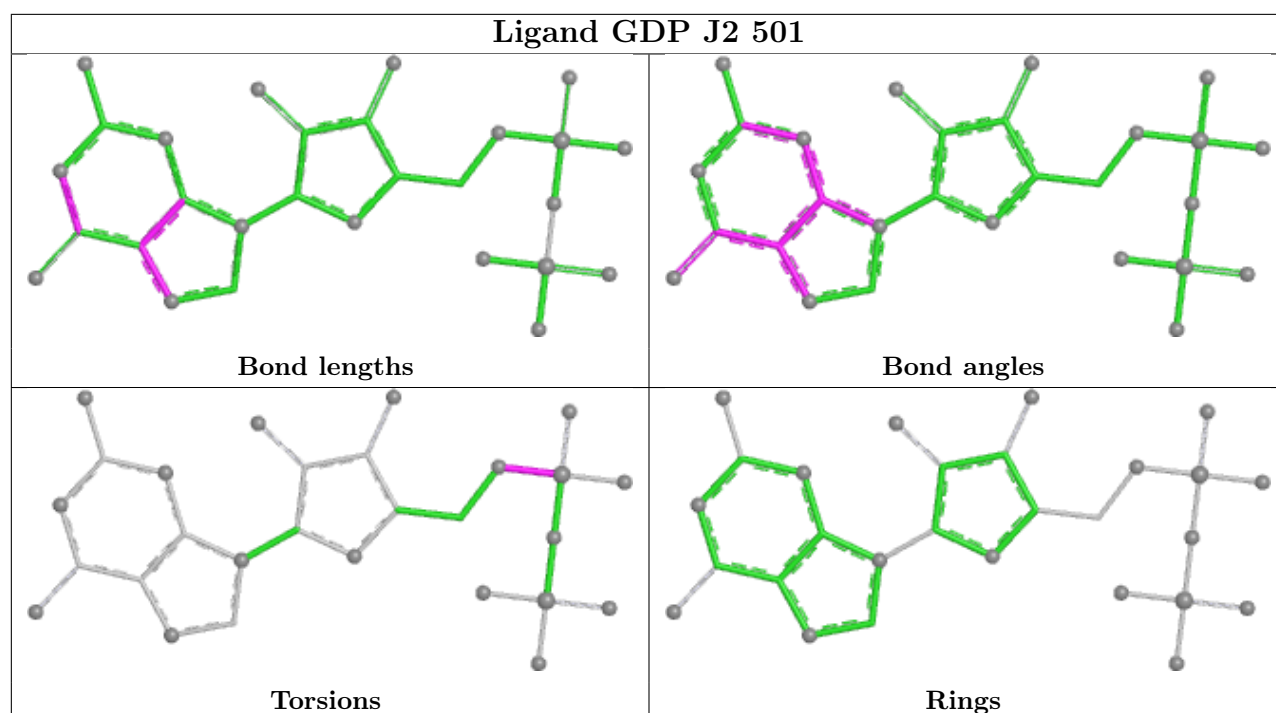
Ligand GTP Q3 501

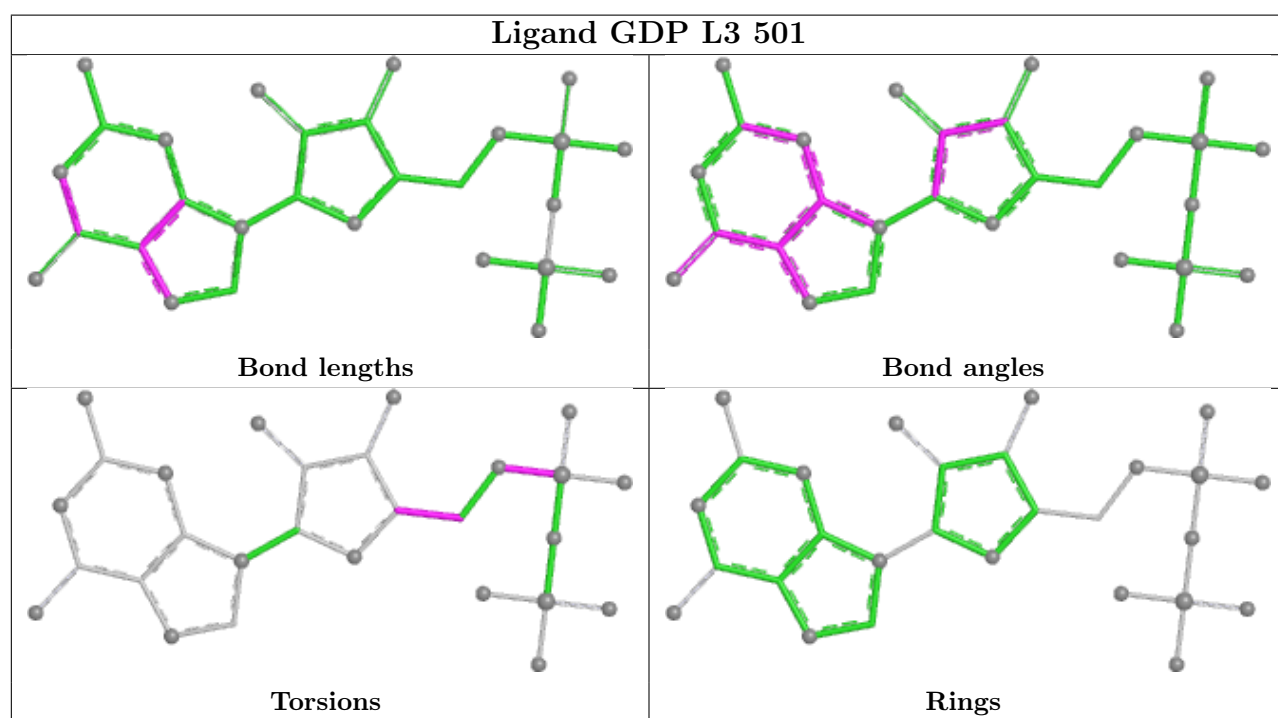
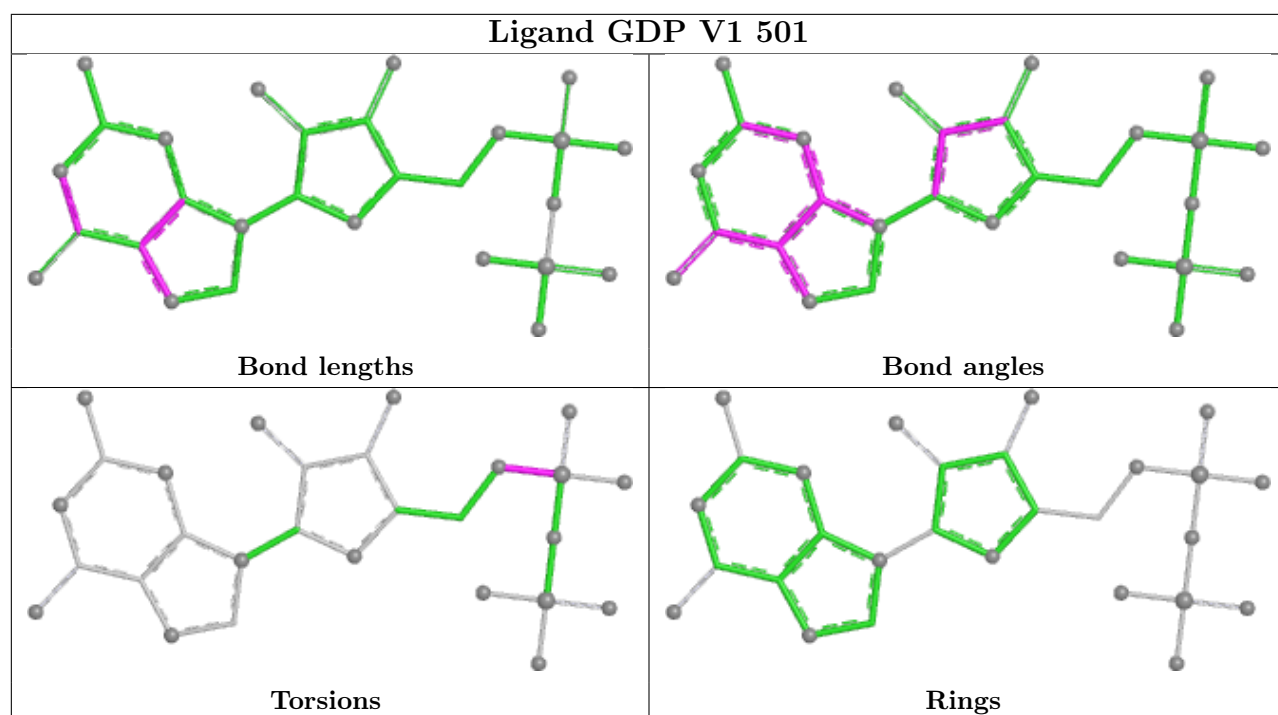


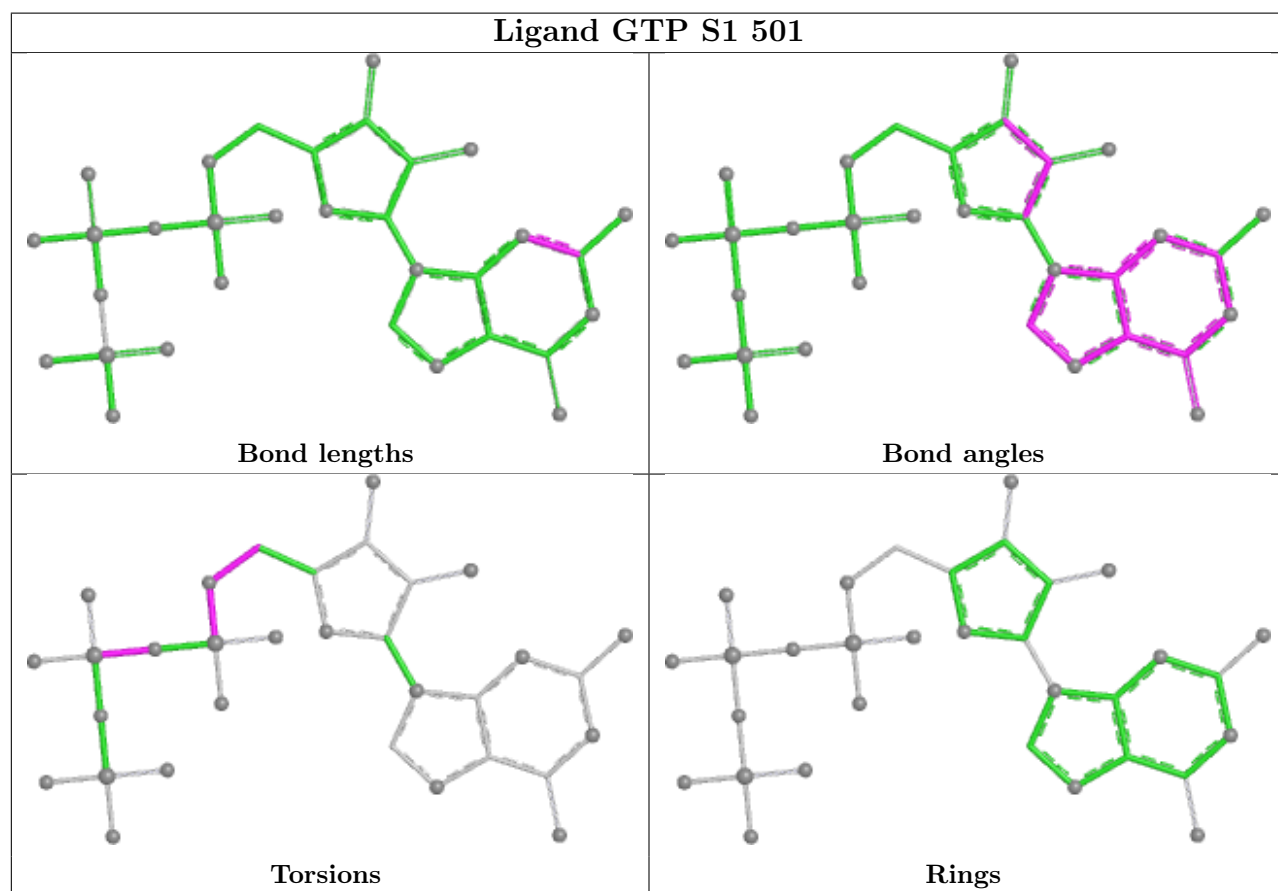
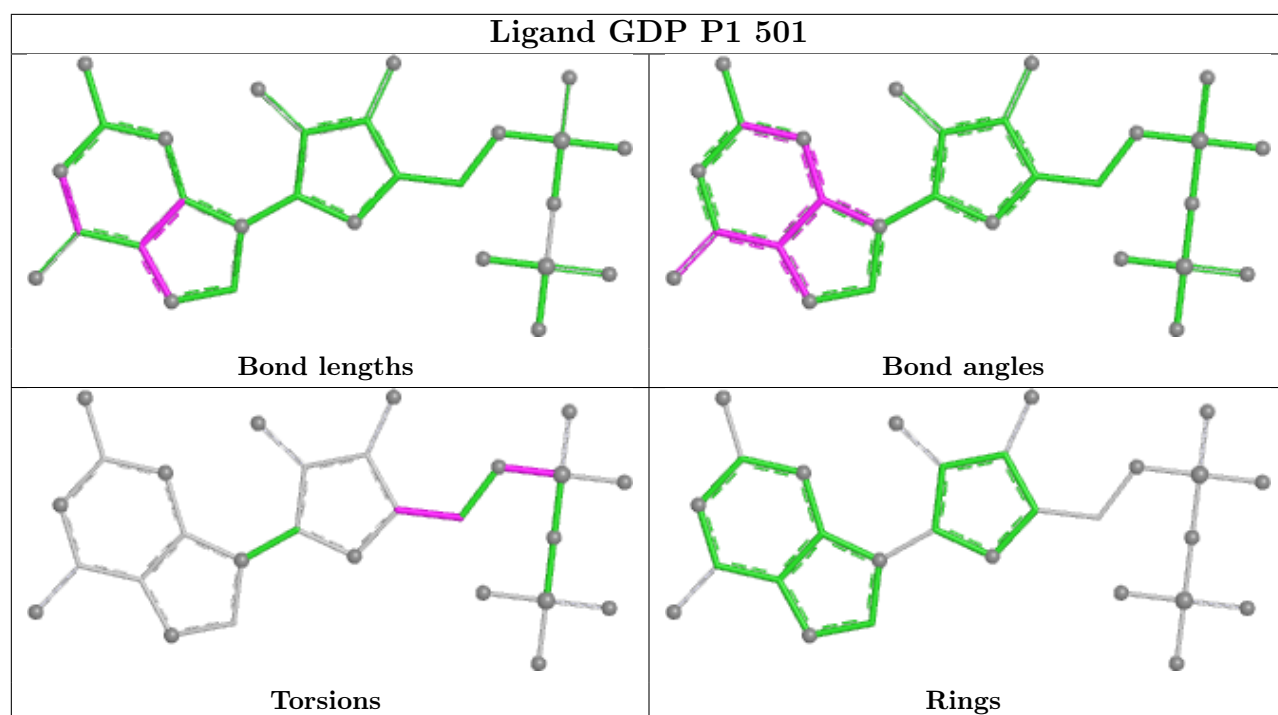
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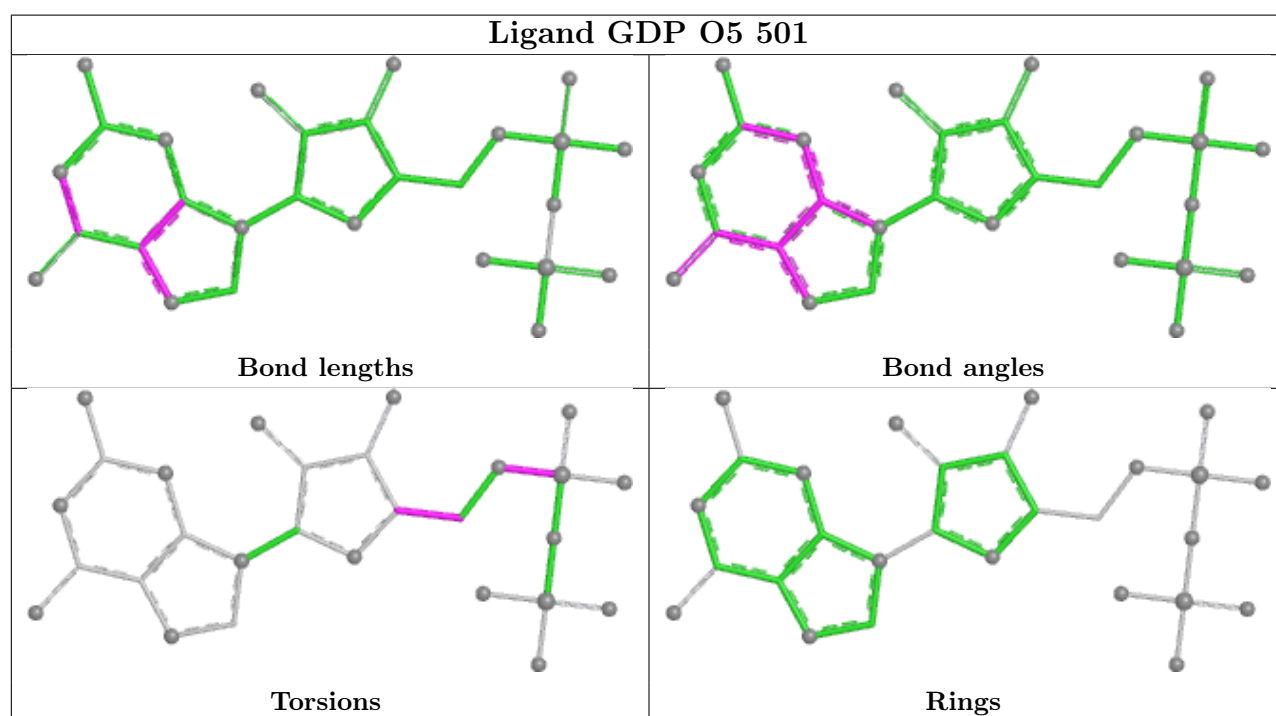
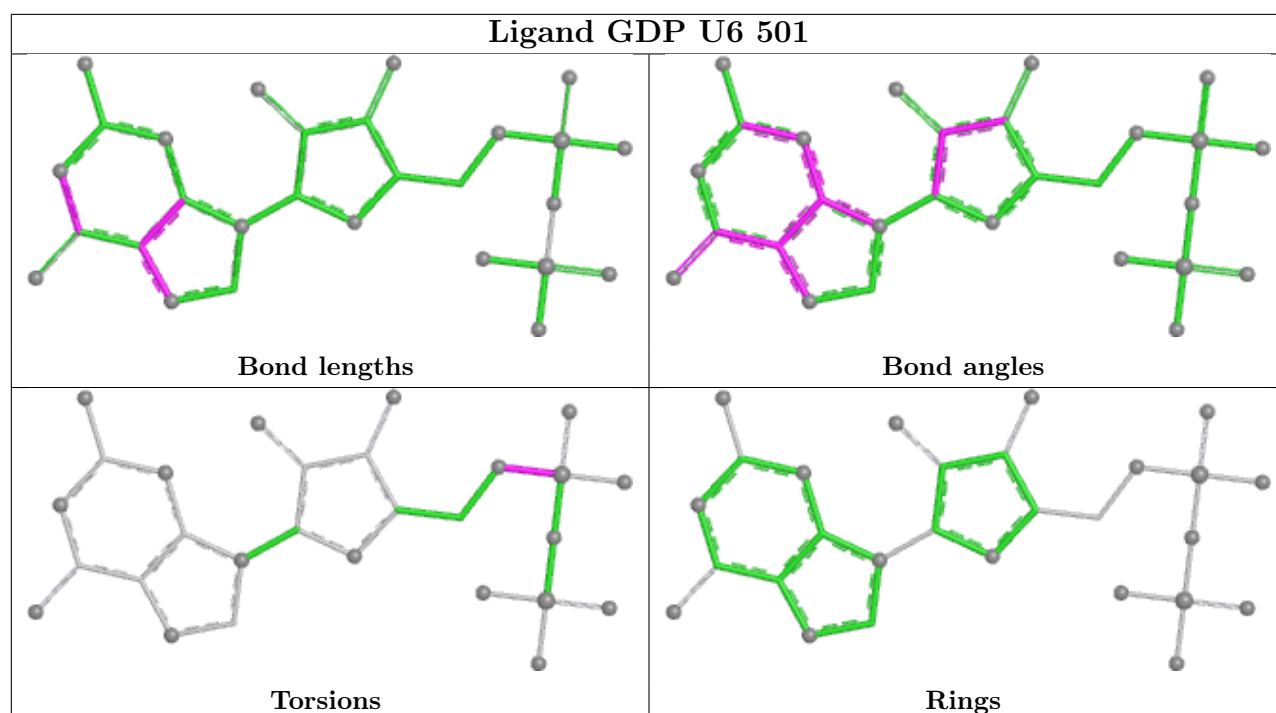




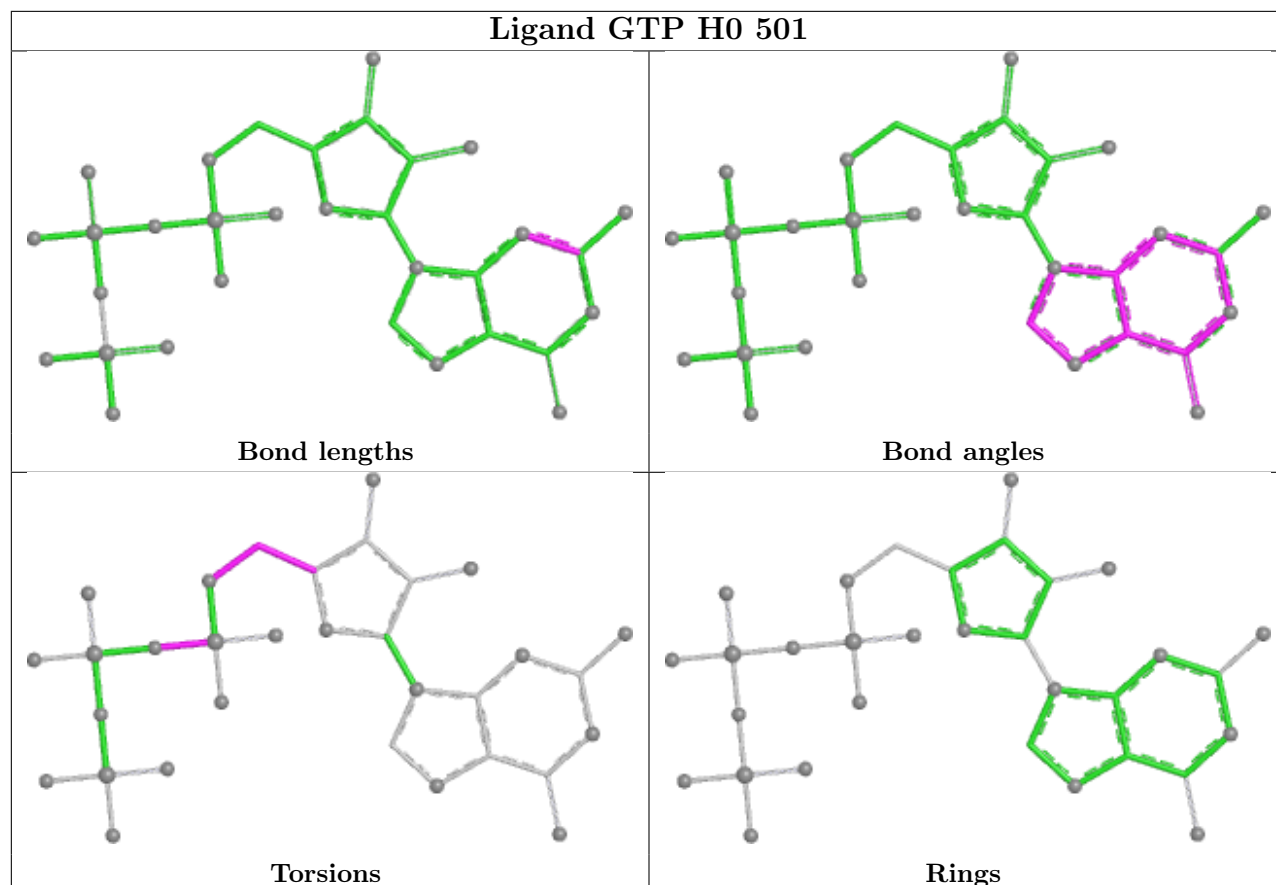




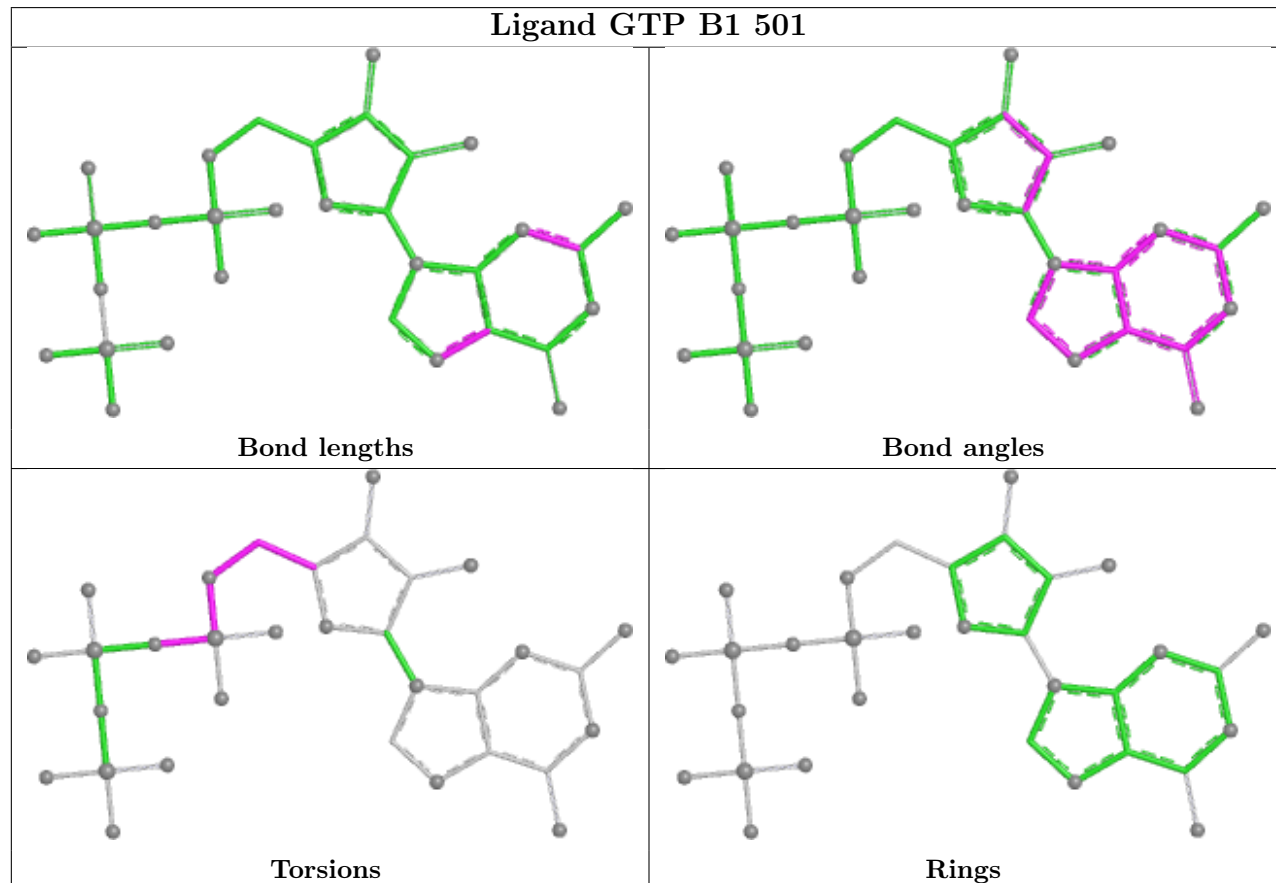




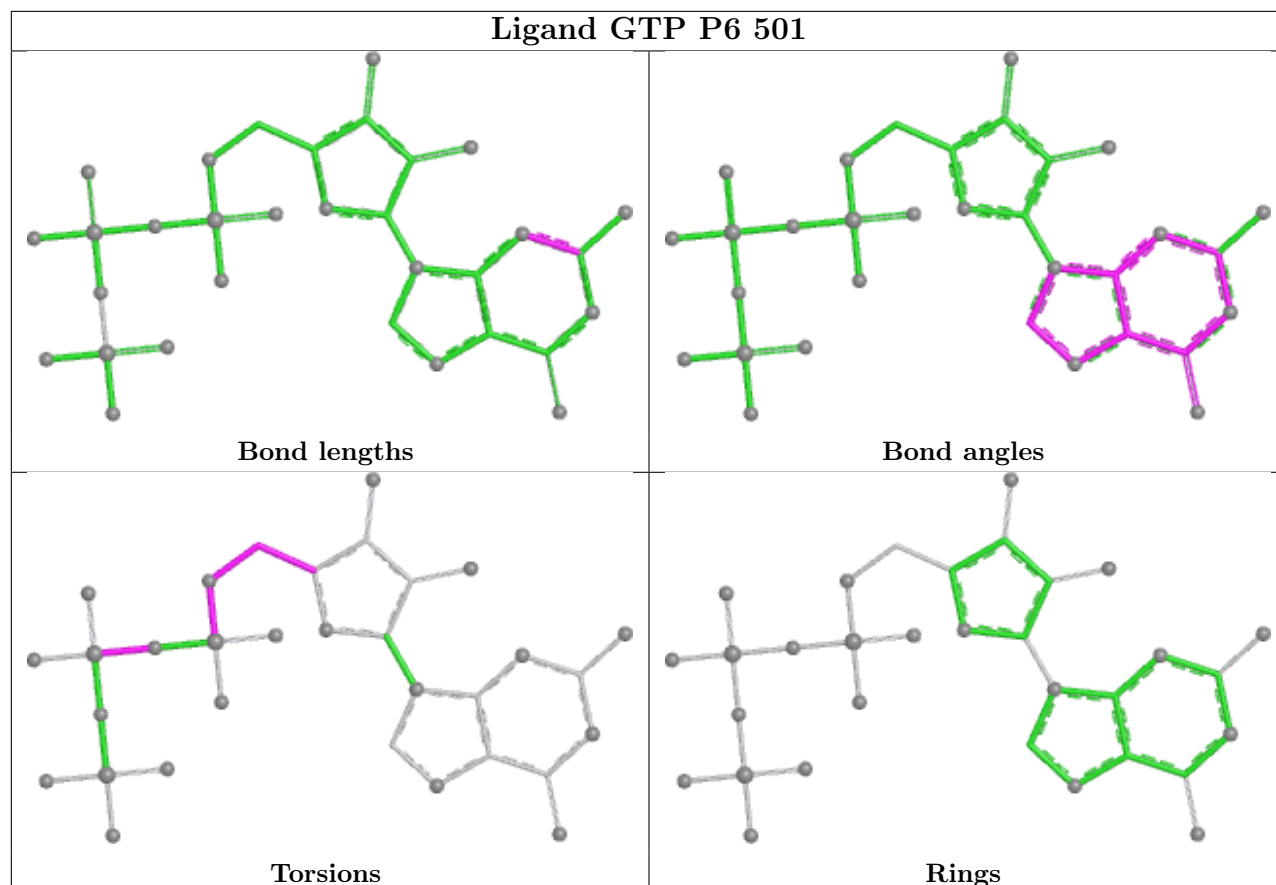
Ligand GTP H0 501



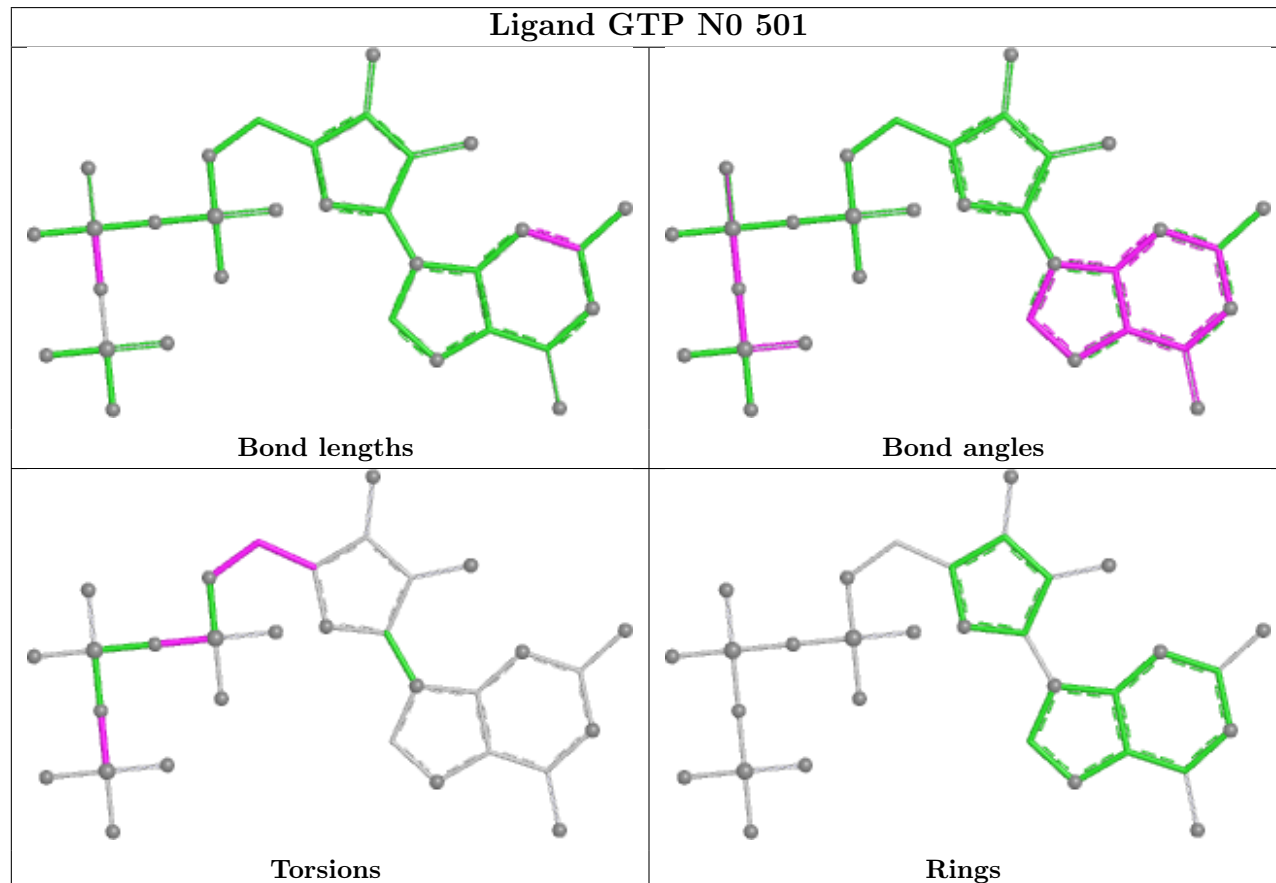
Ligand GTP B1 501

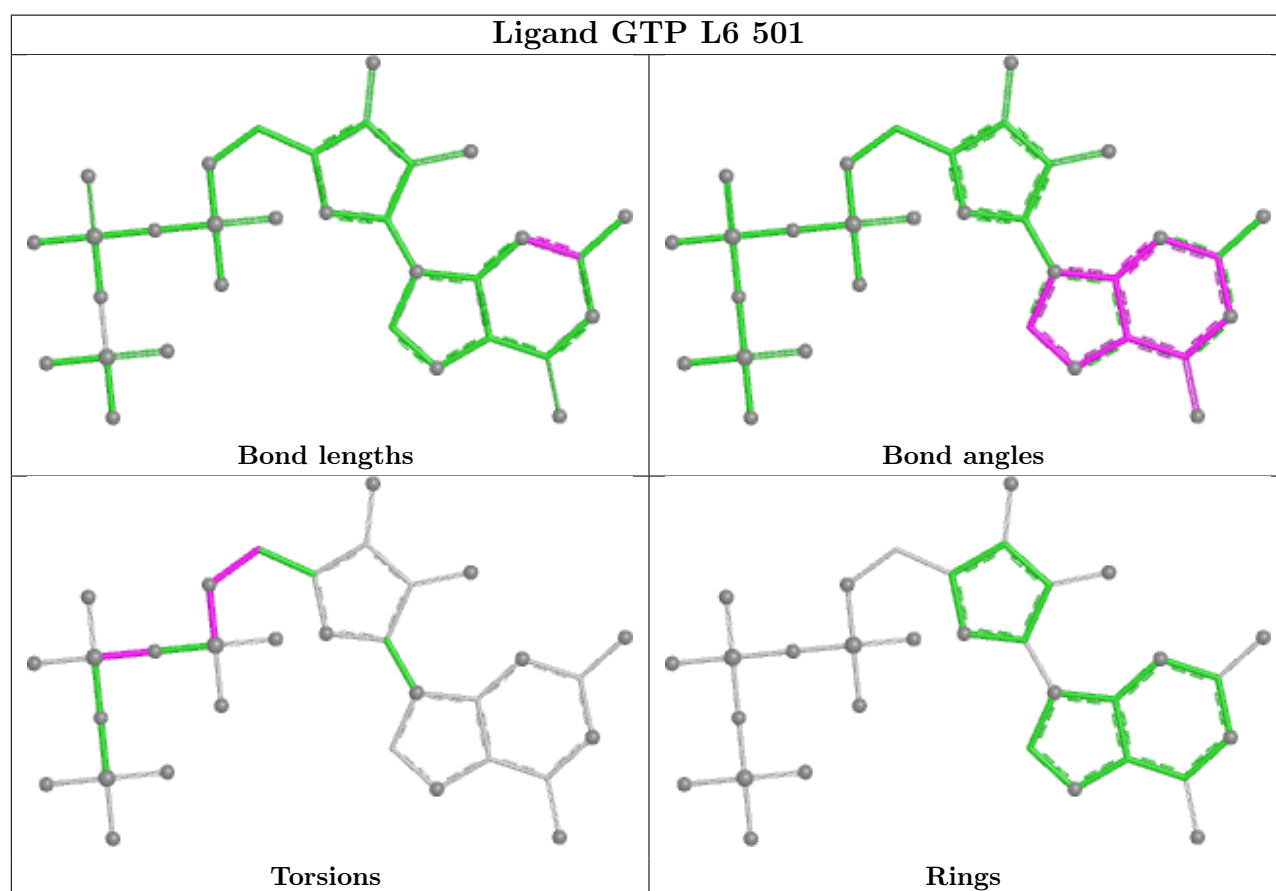
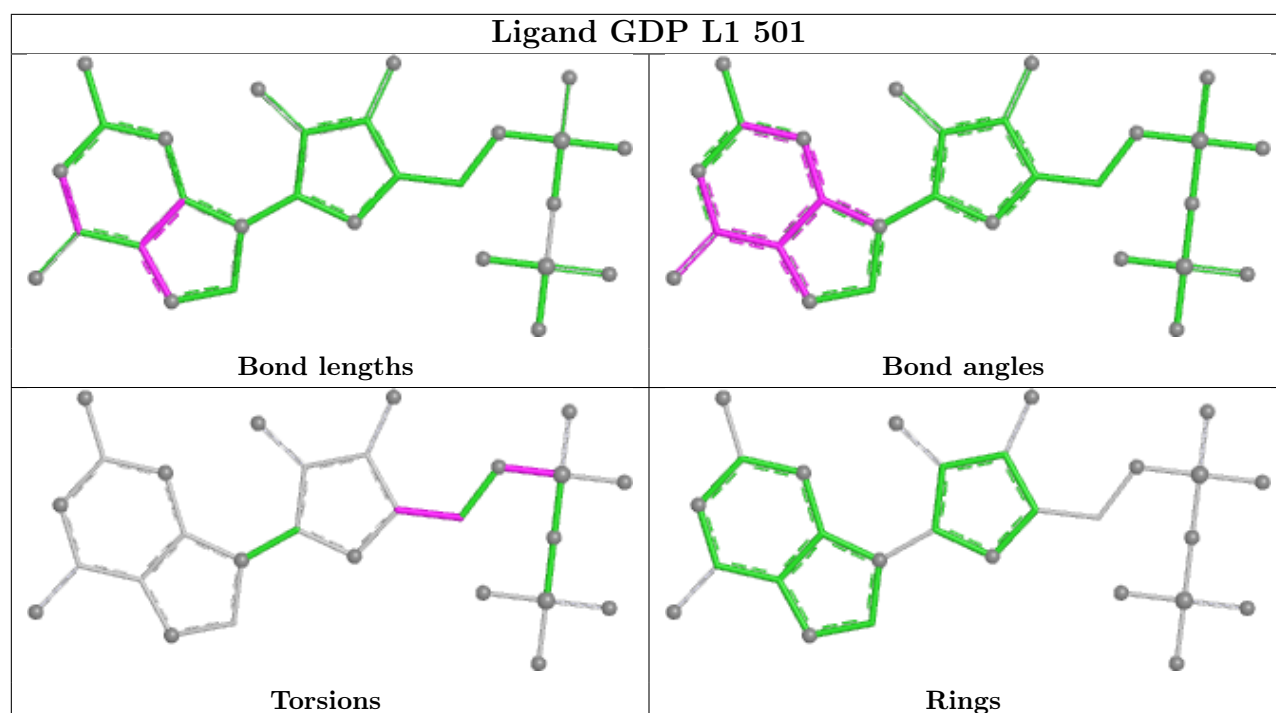


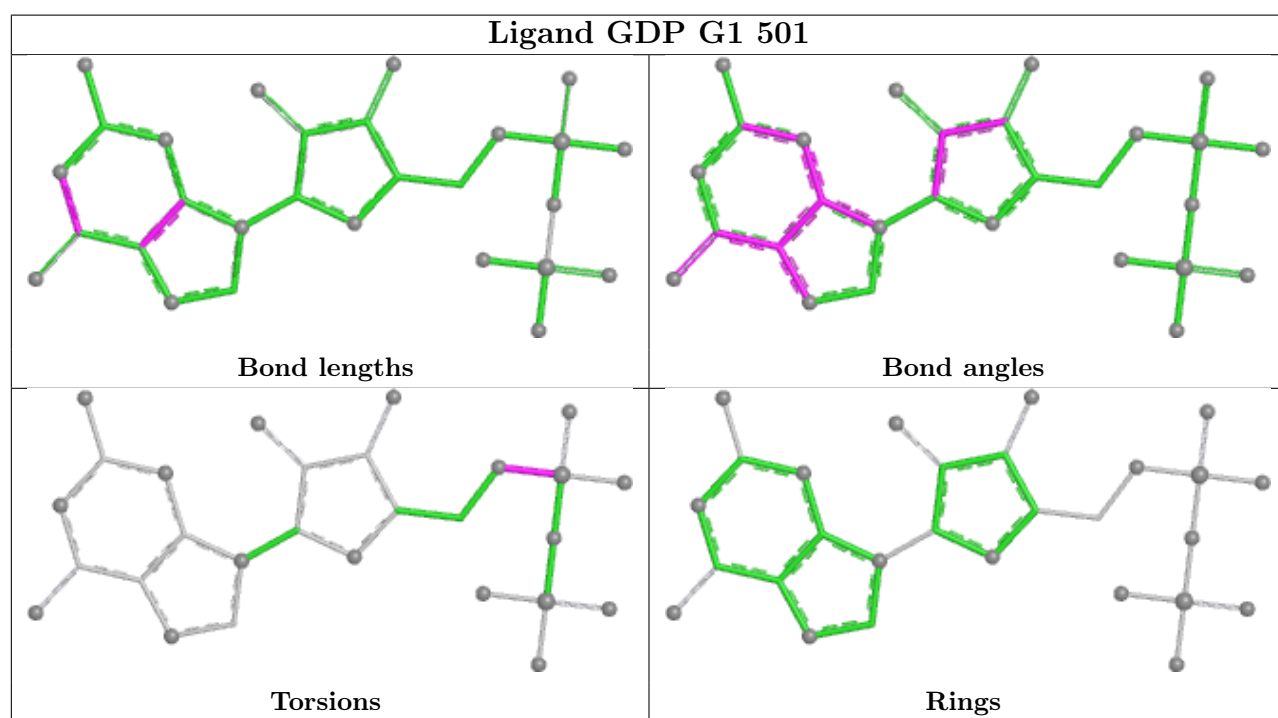
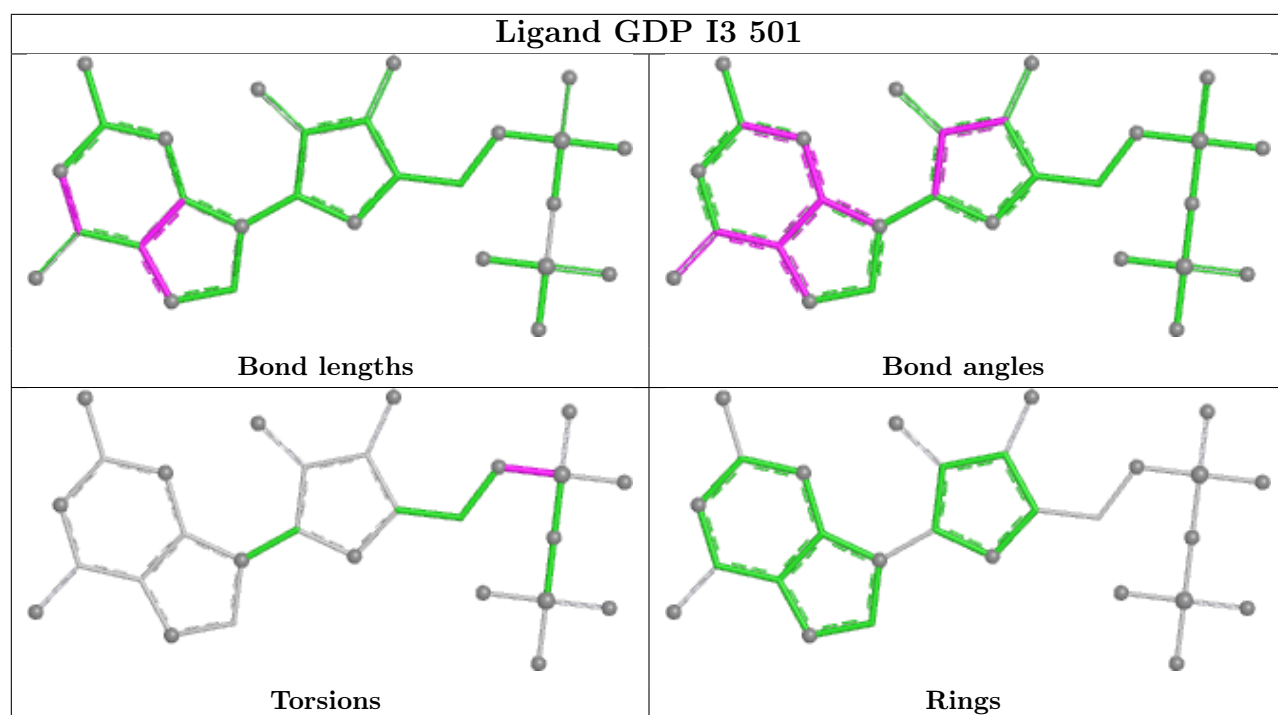
Ligand GTP P6 501

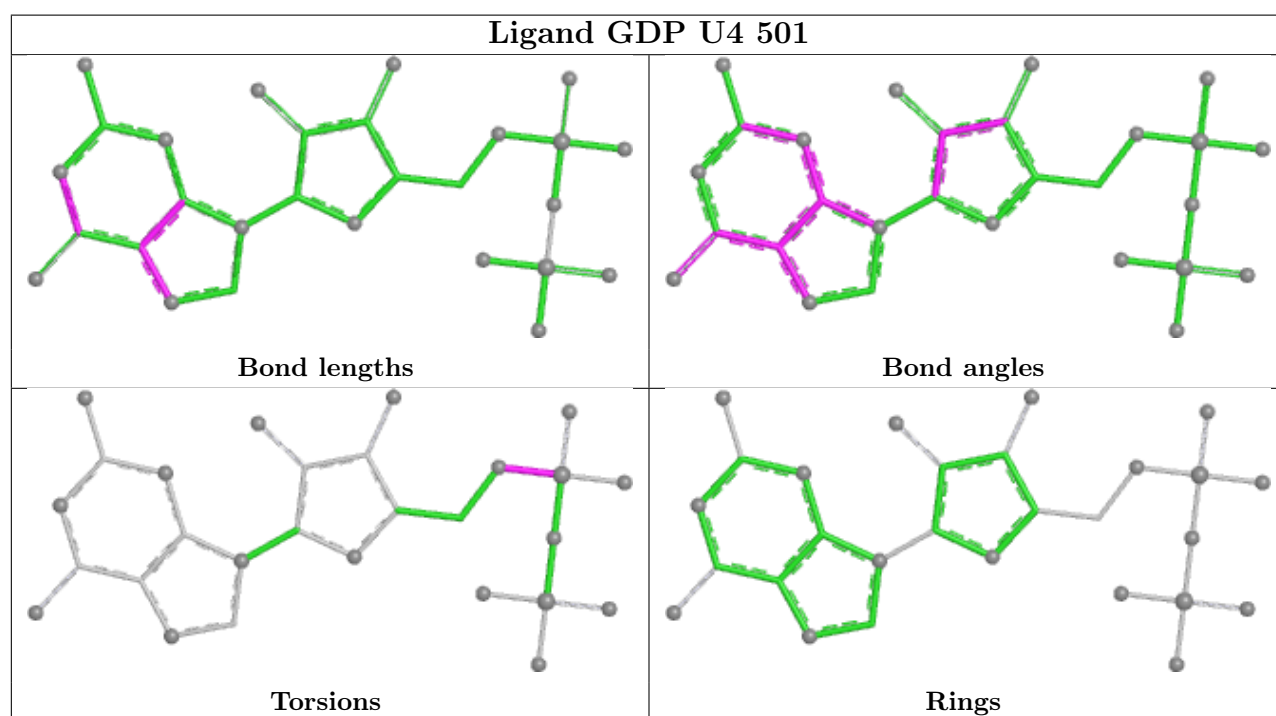
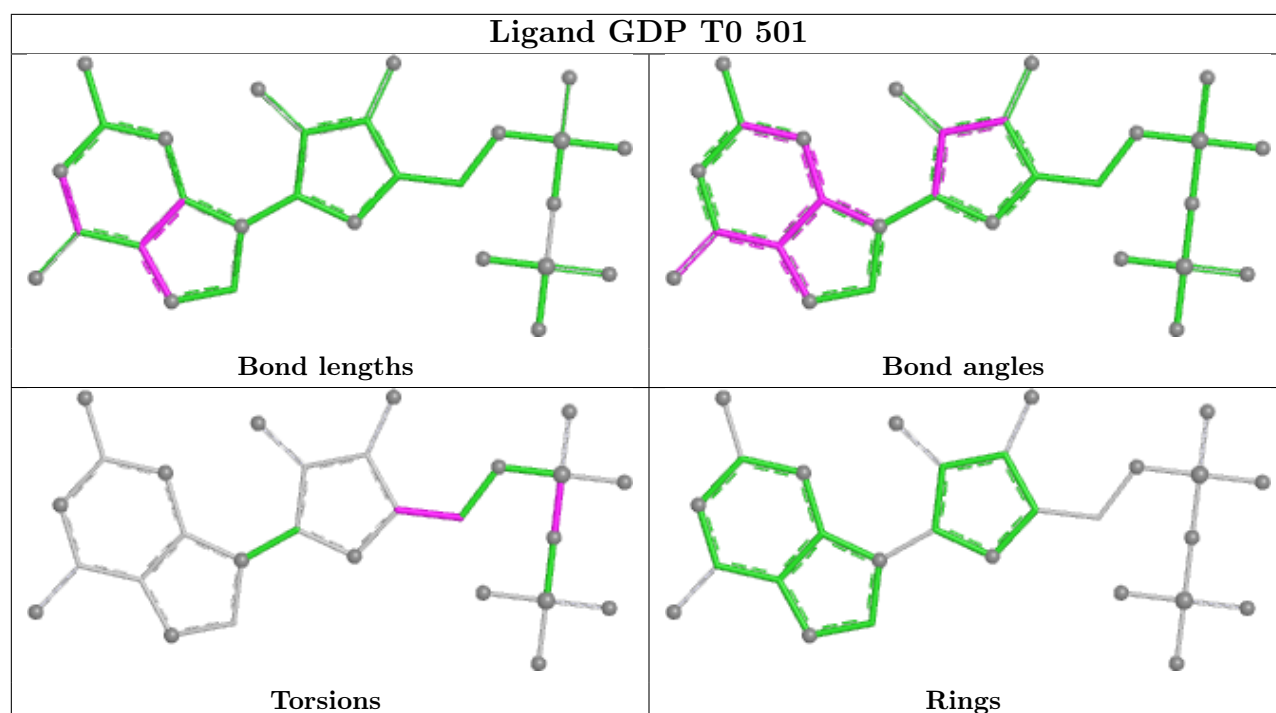


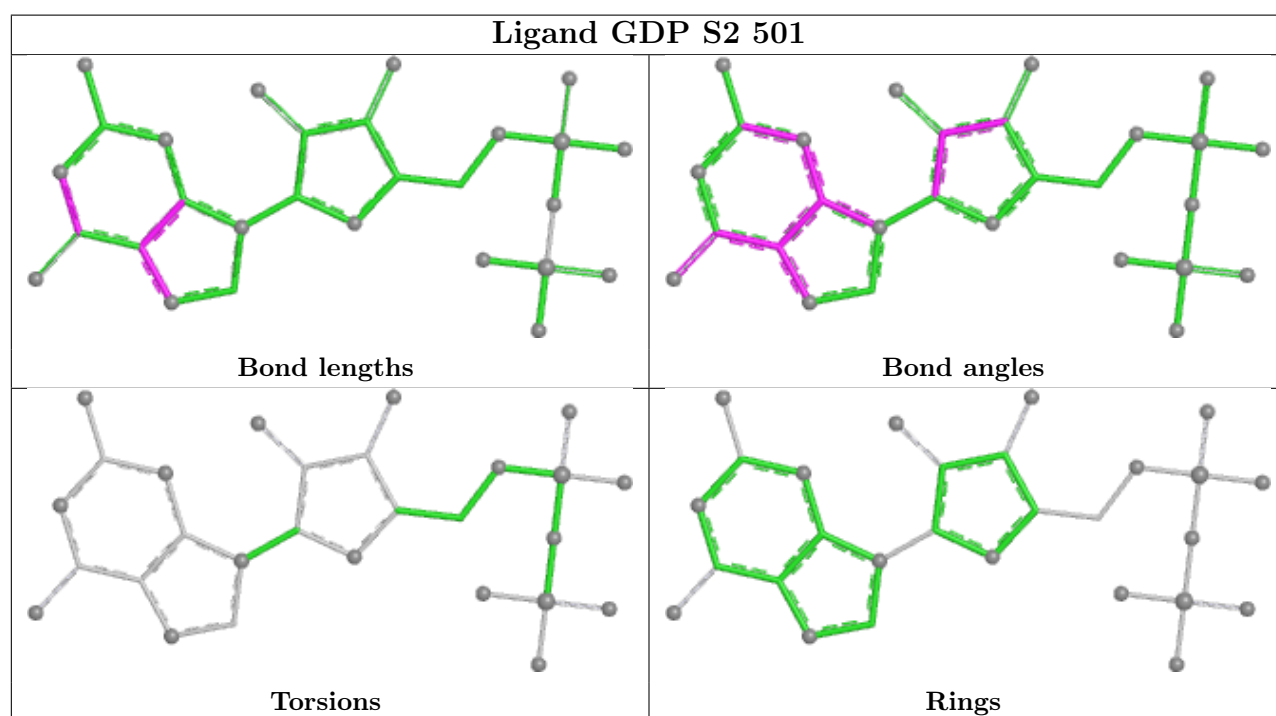
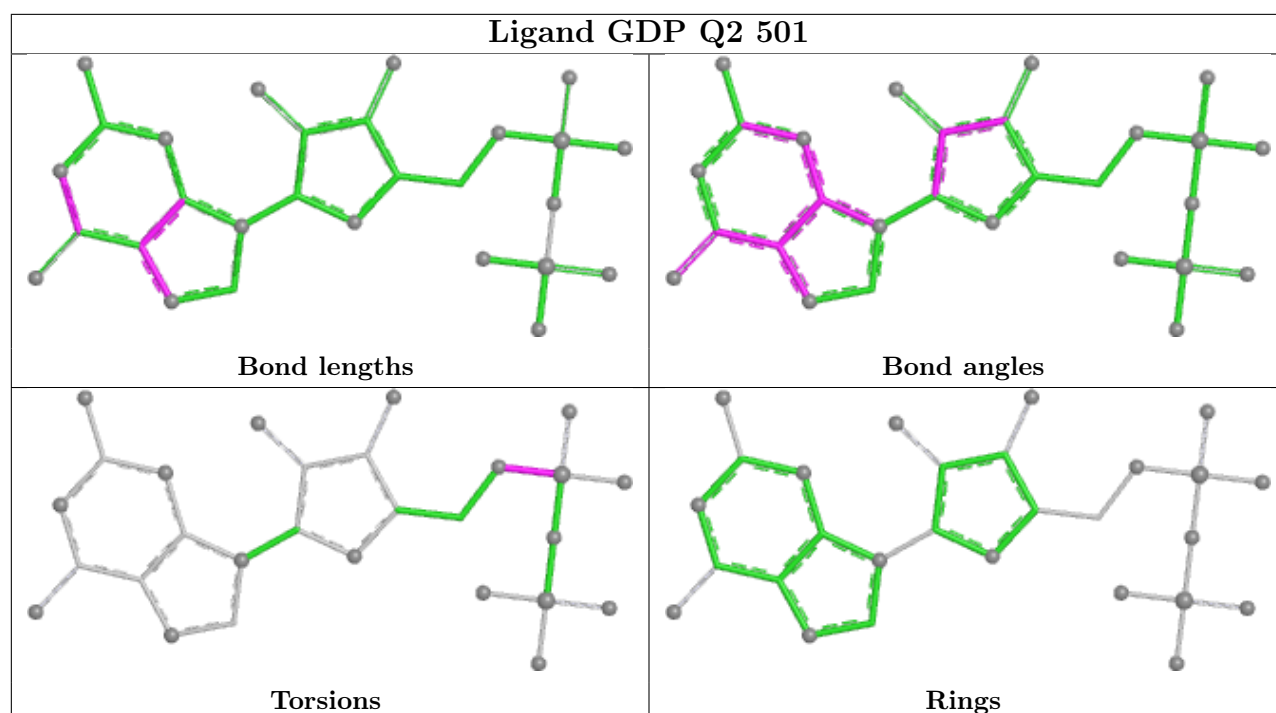
Ligand GTP N0 501

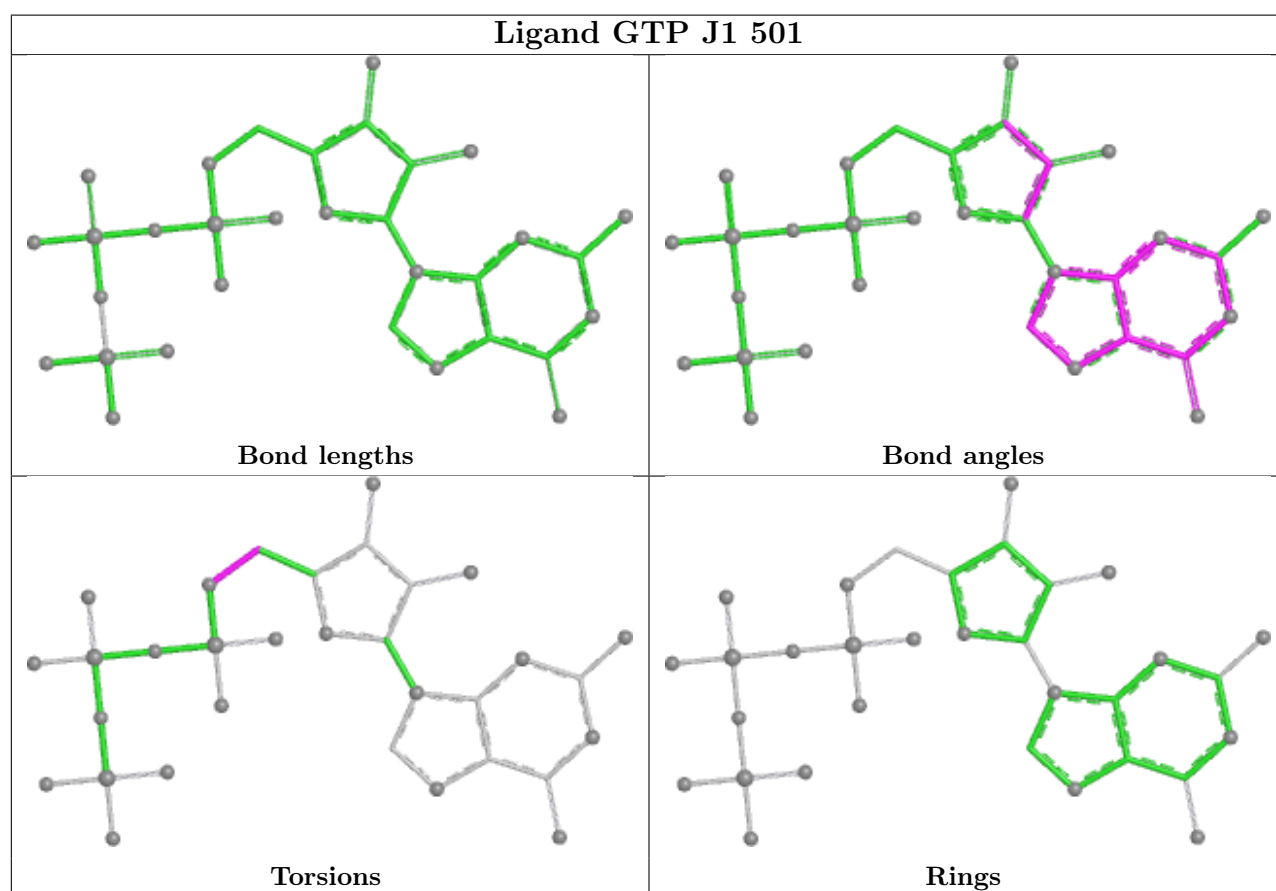
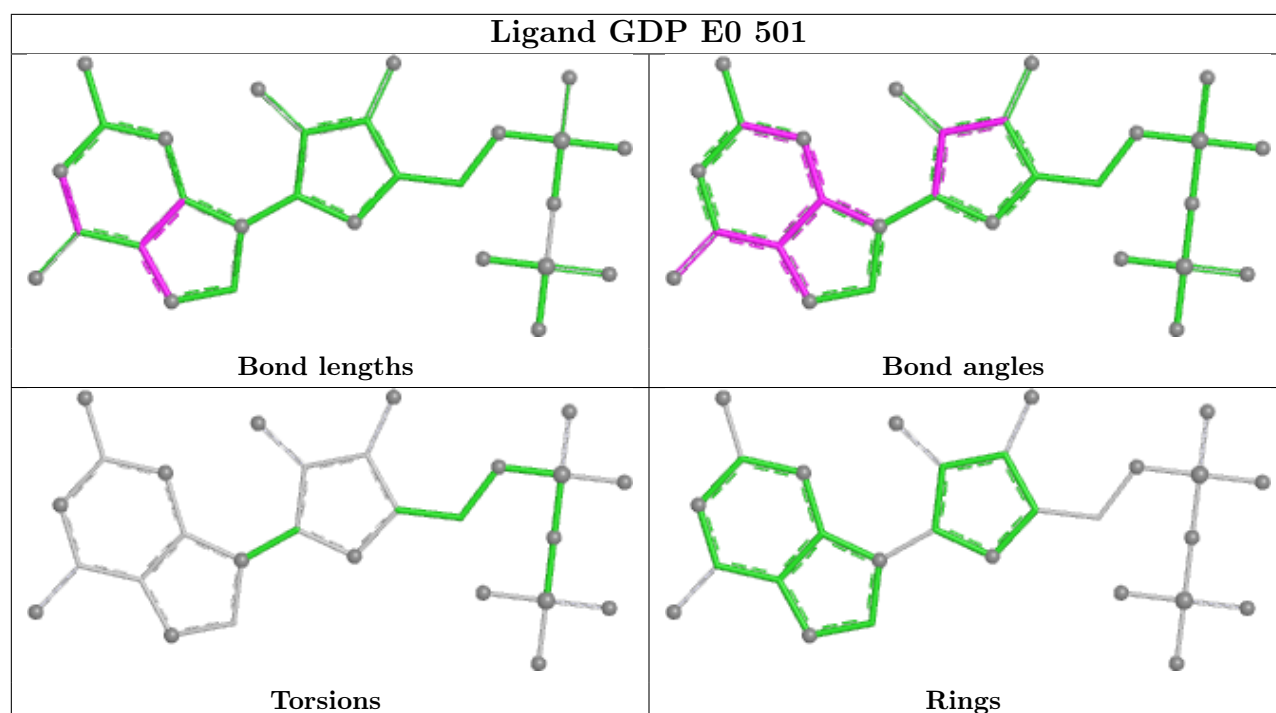


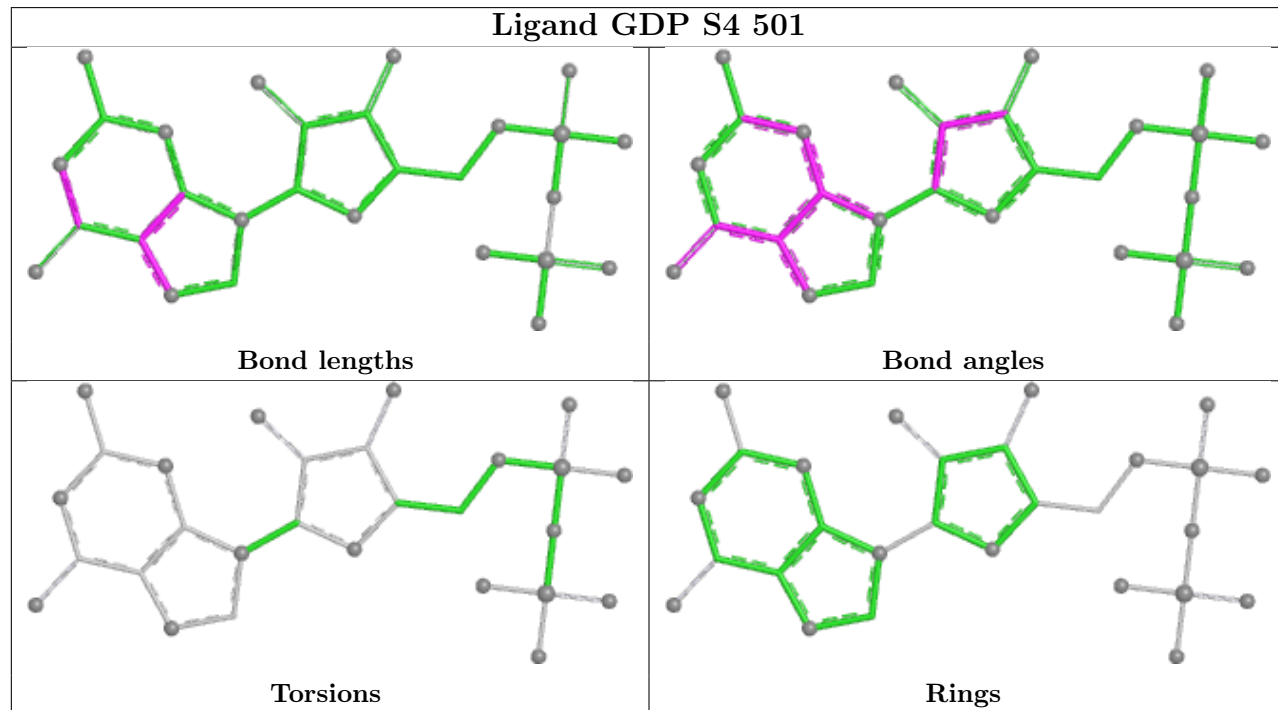
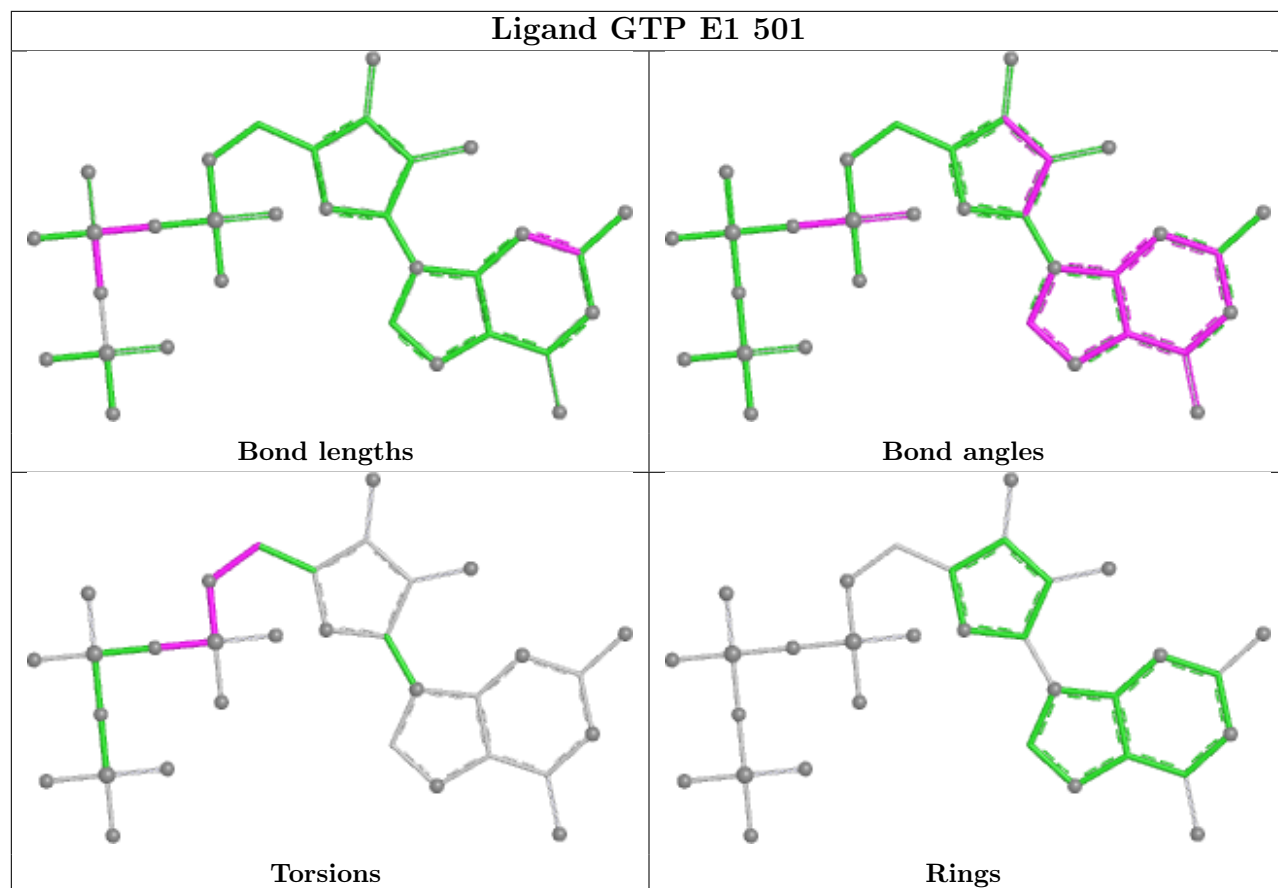


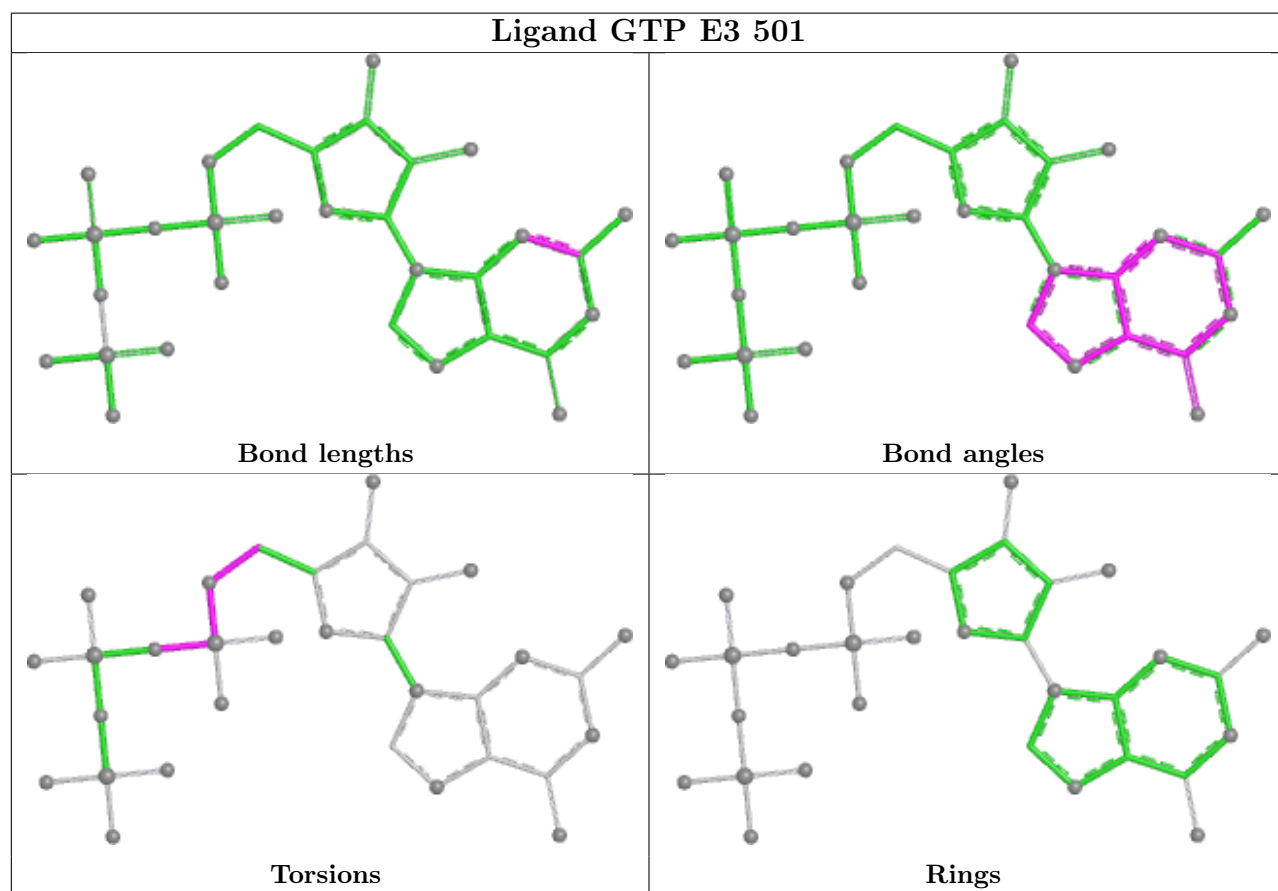
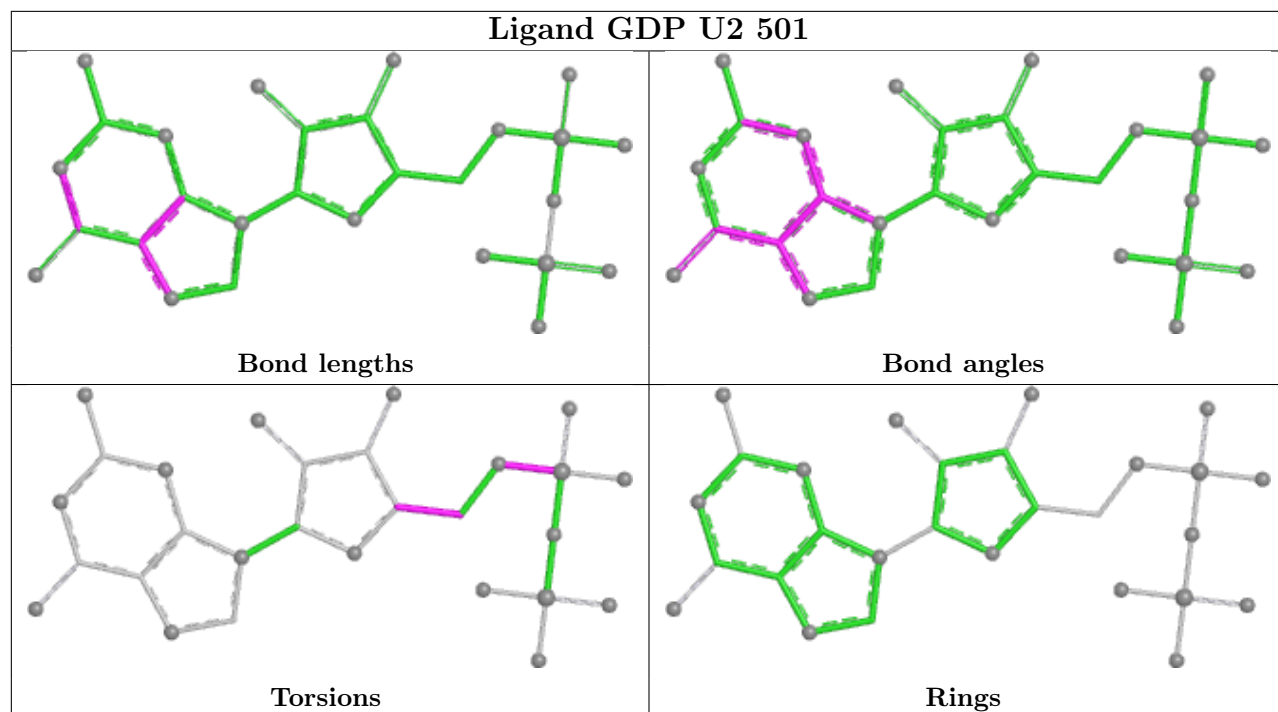


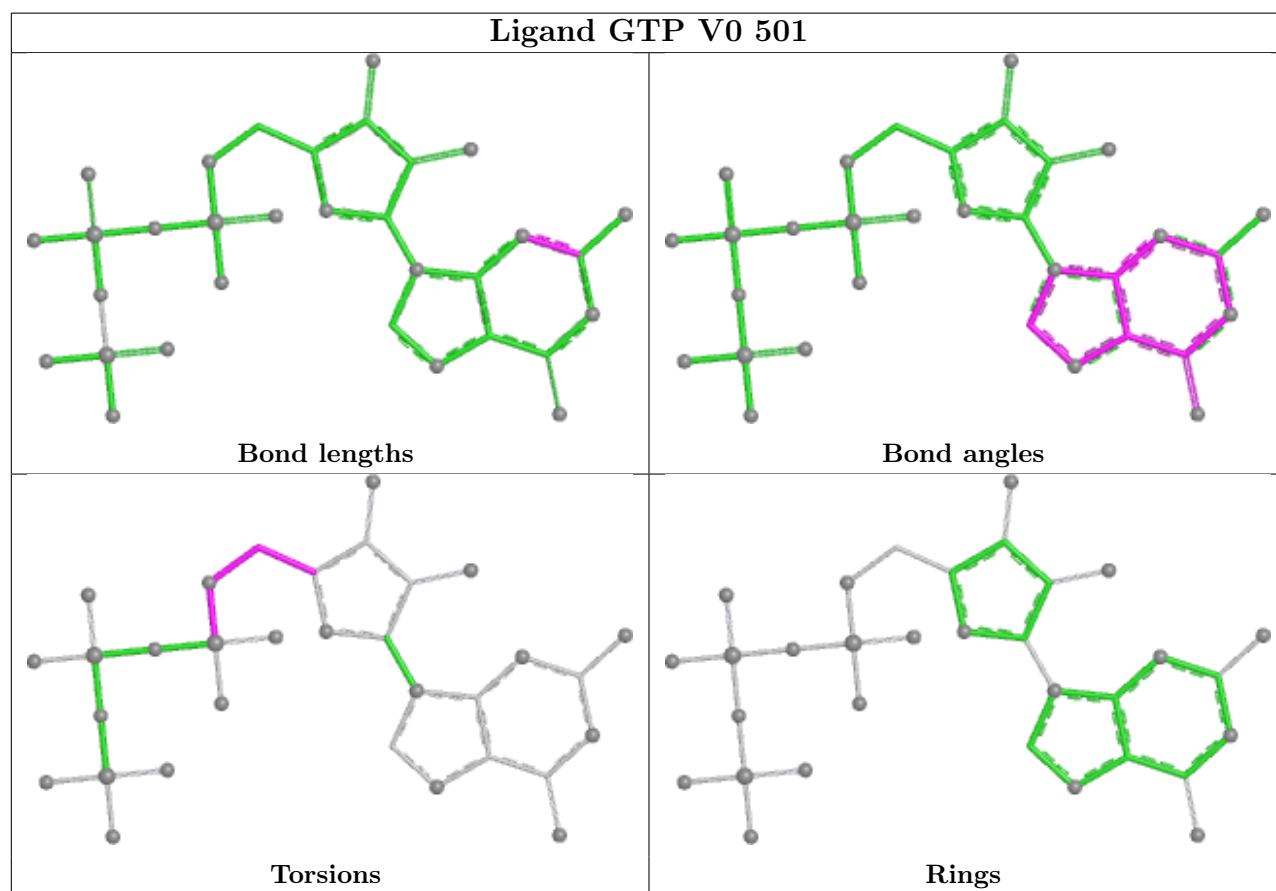
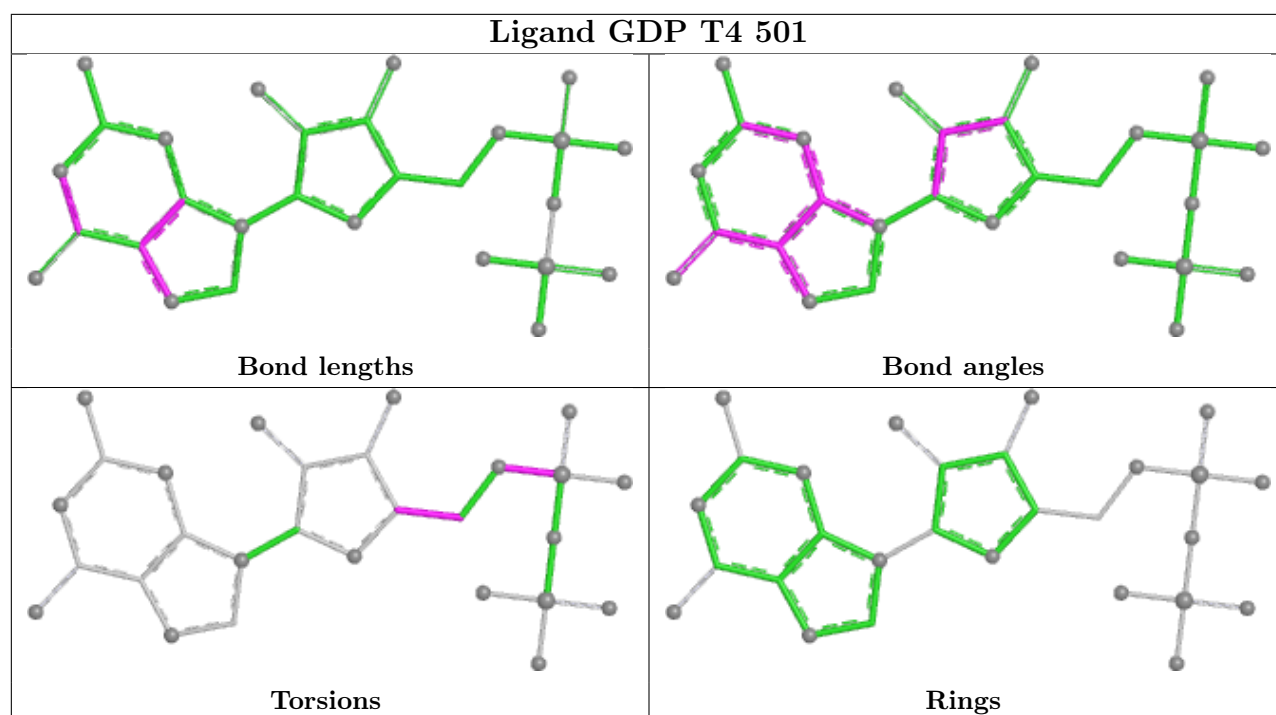


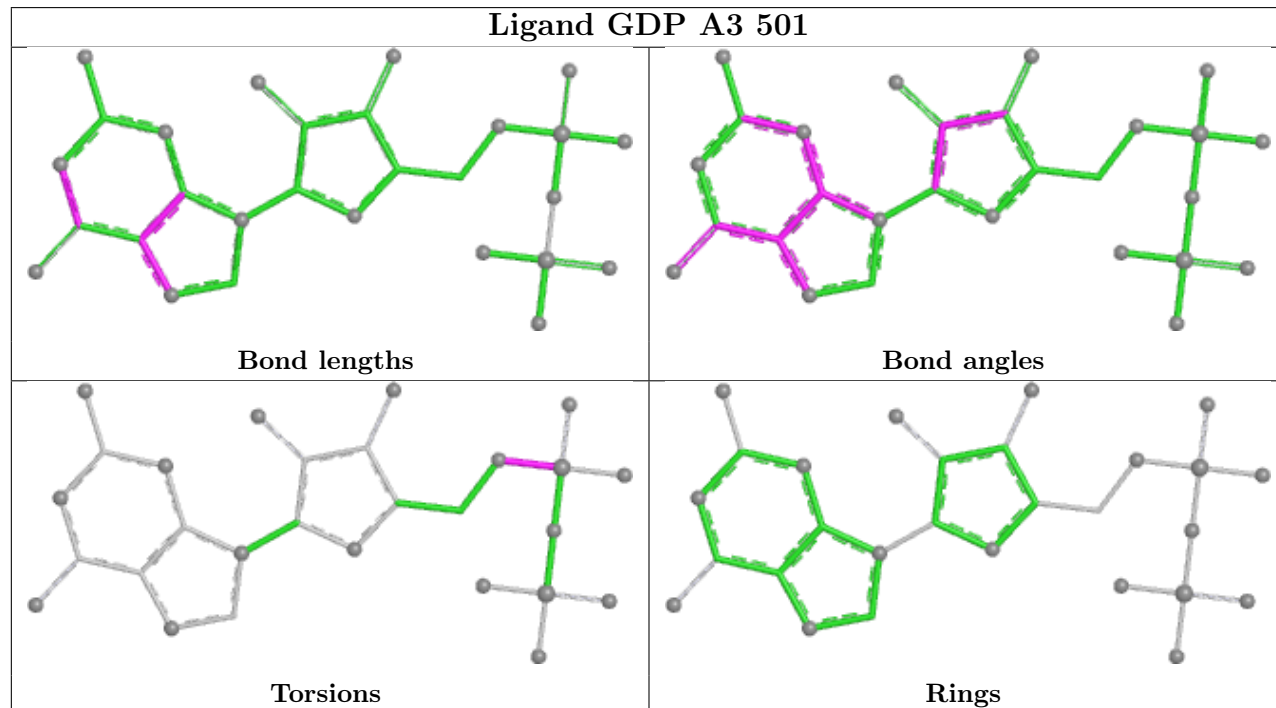
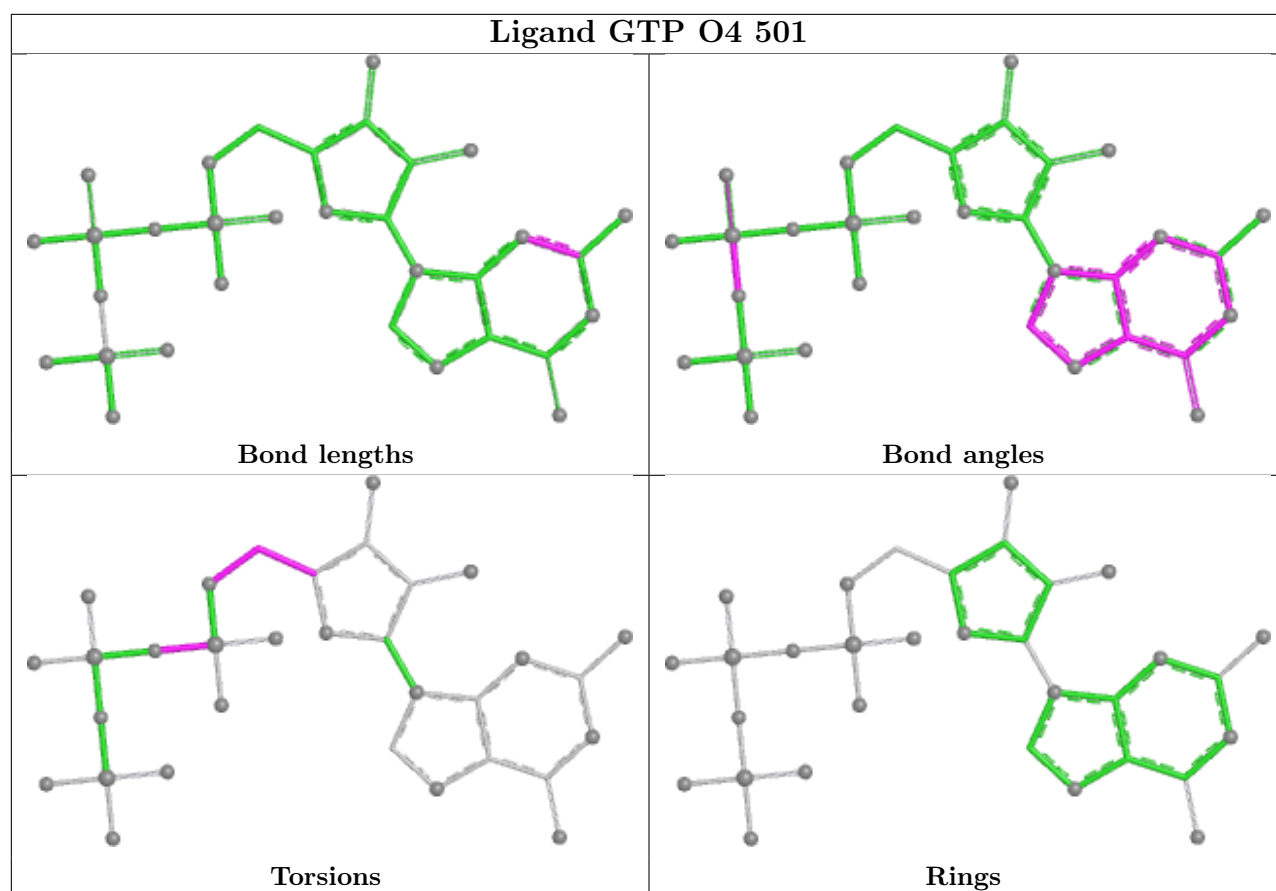




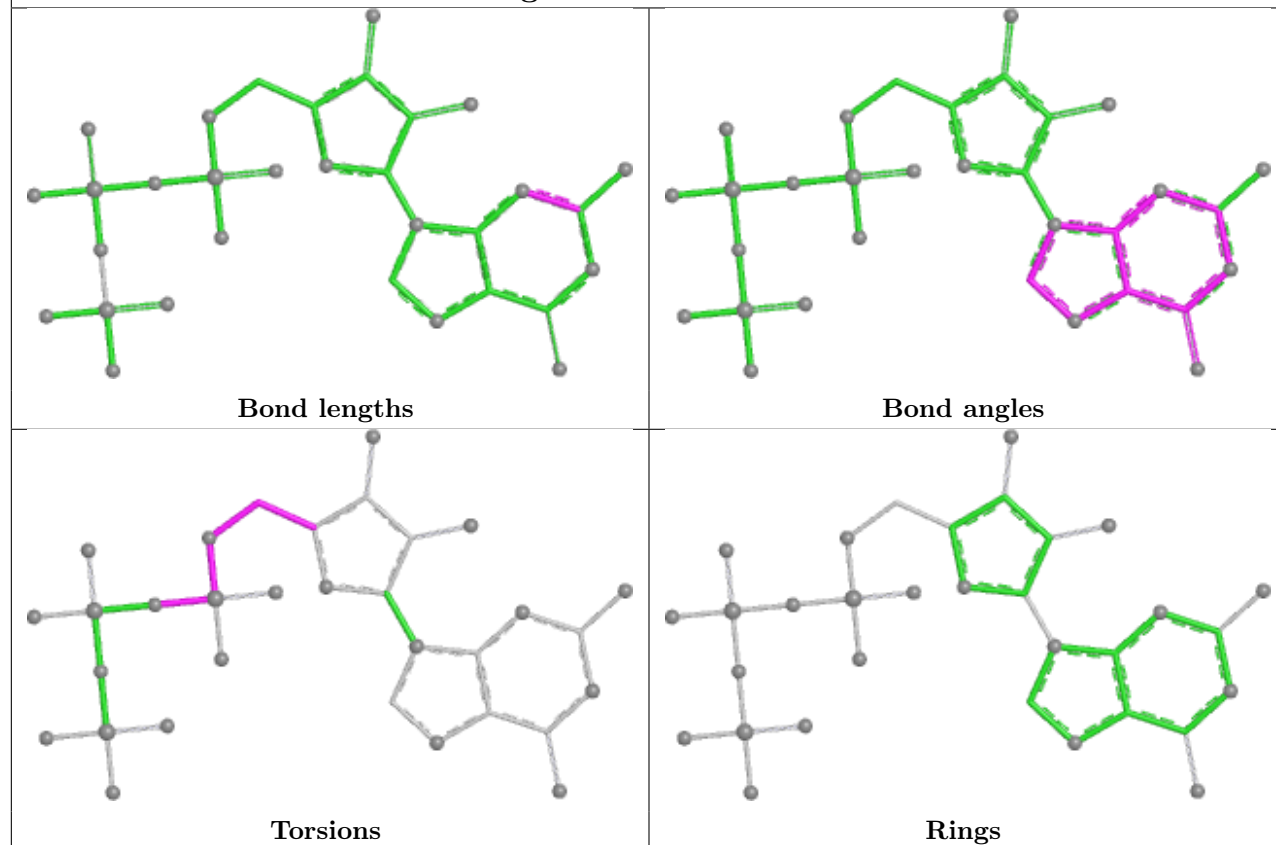




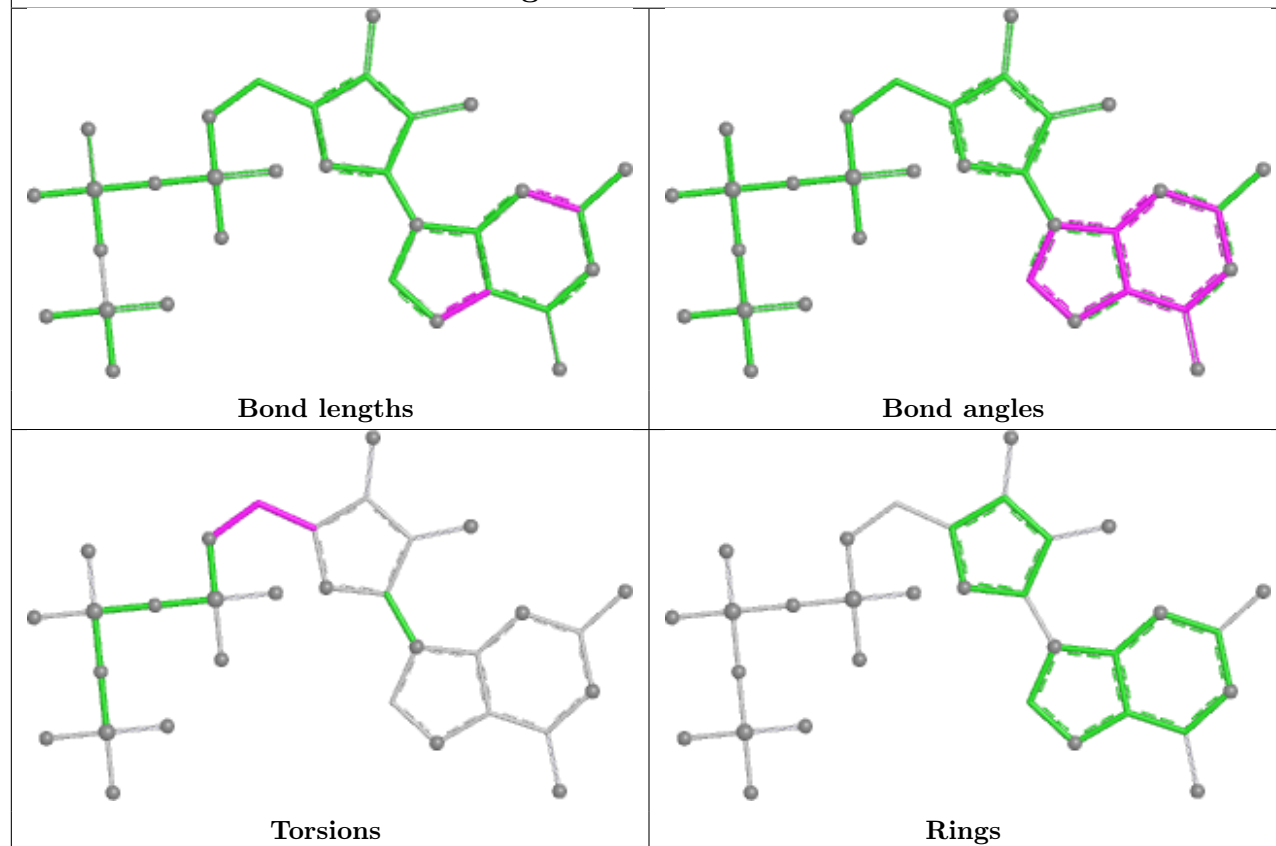


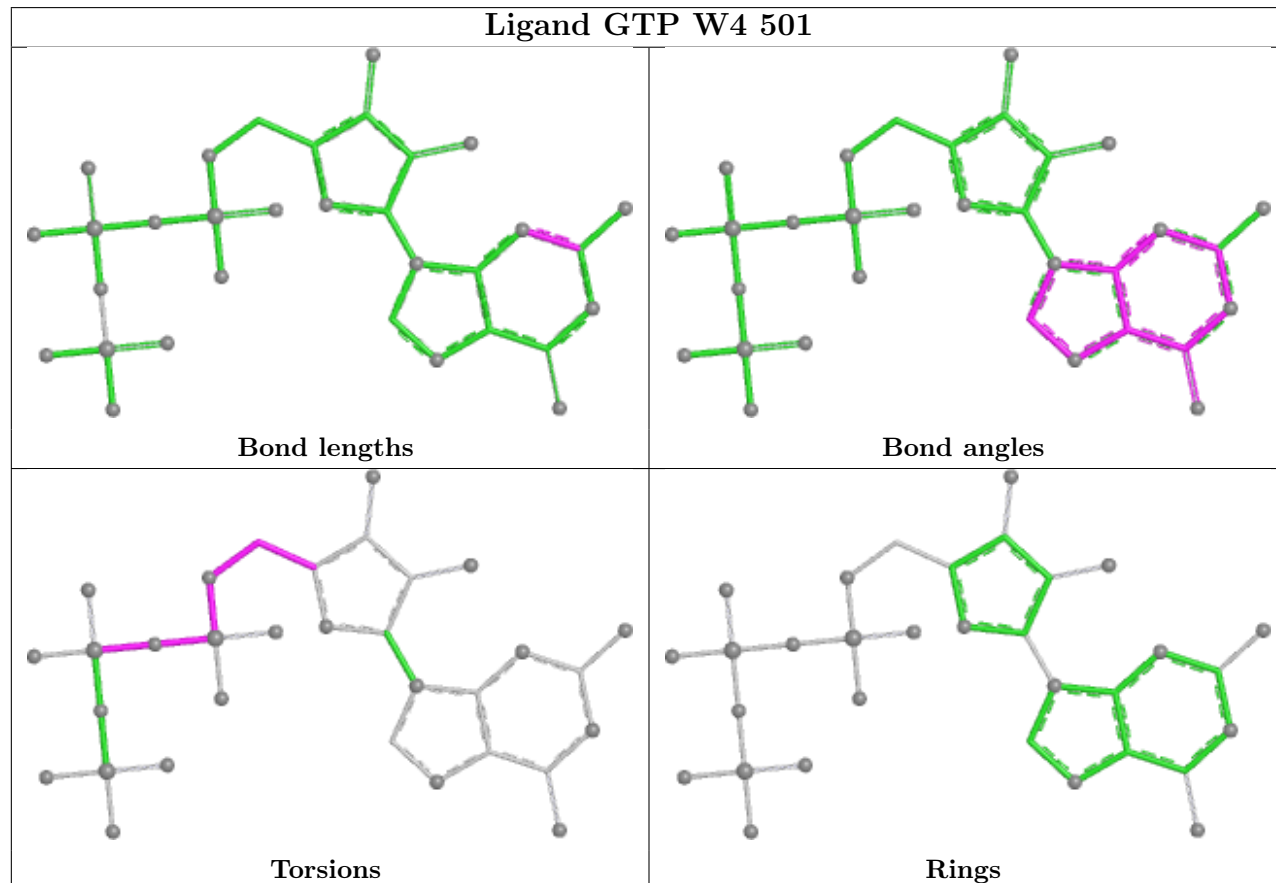
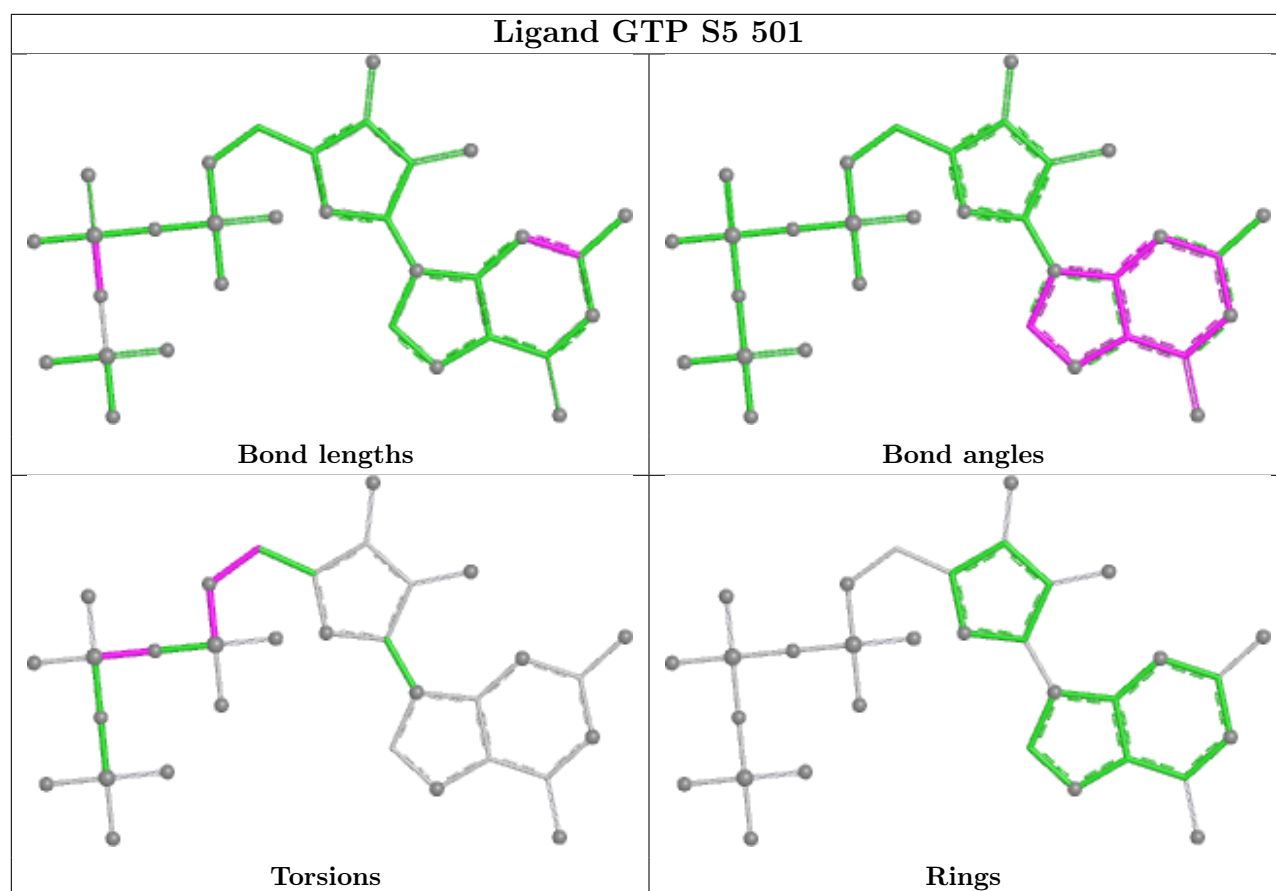


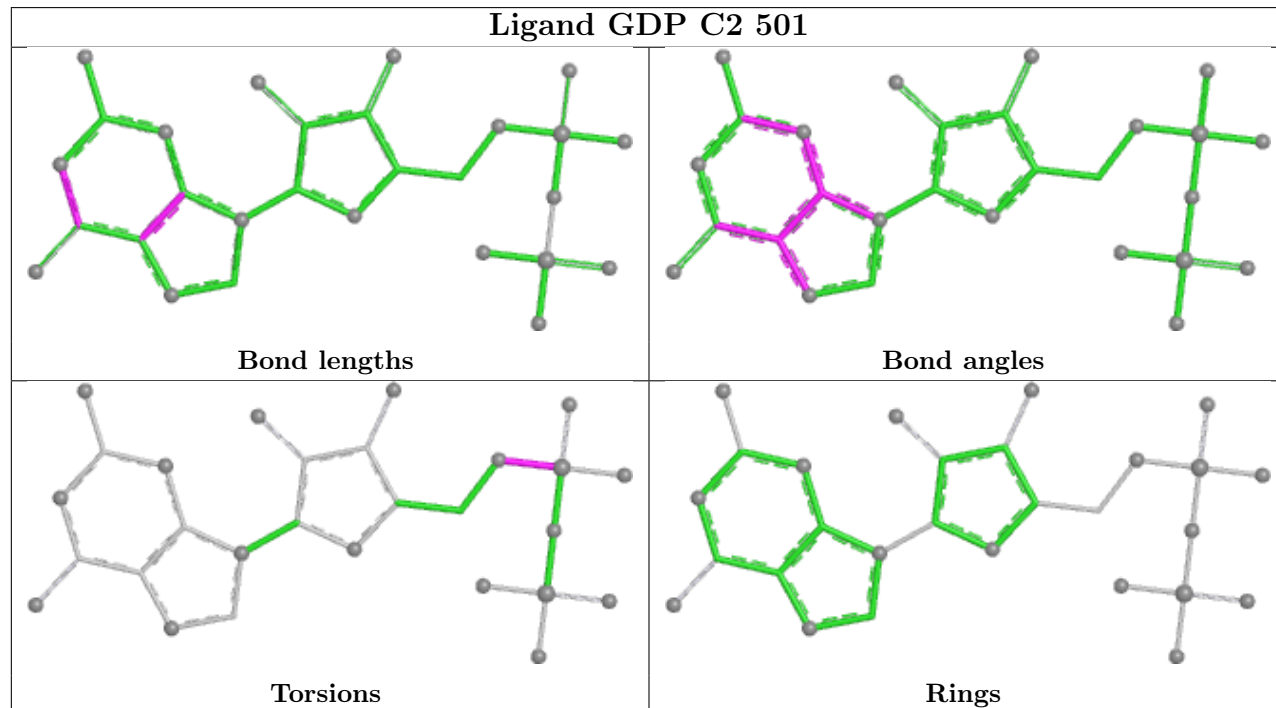
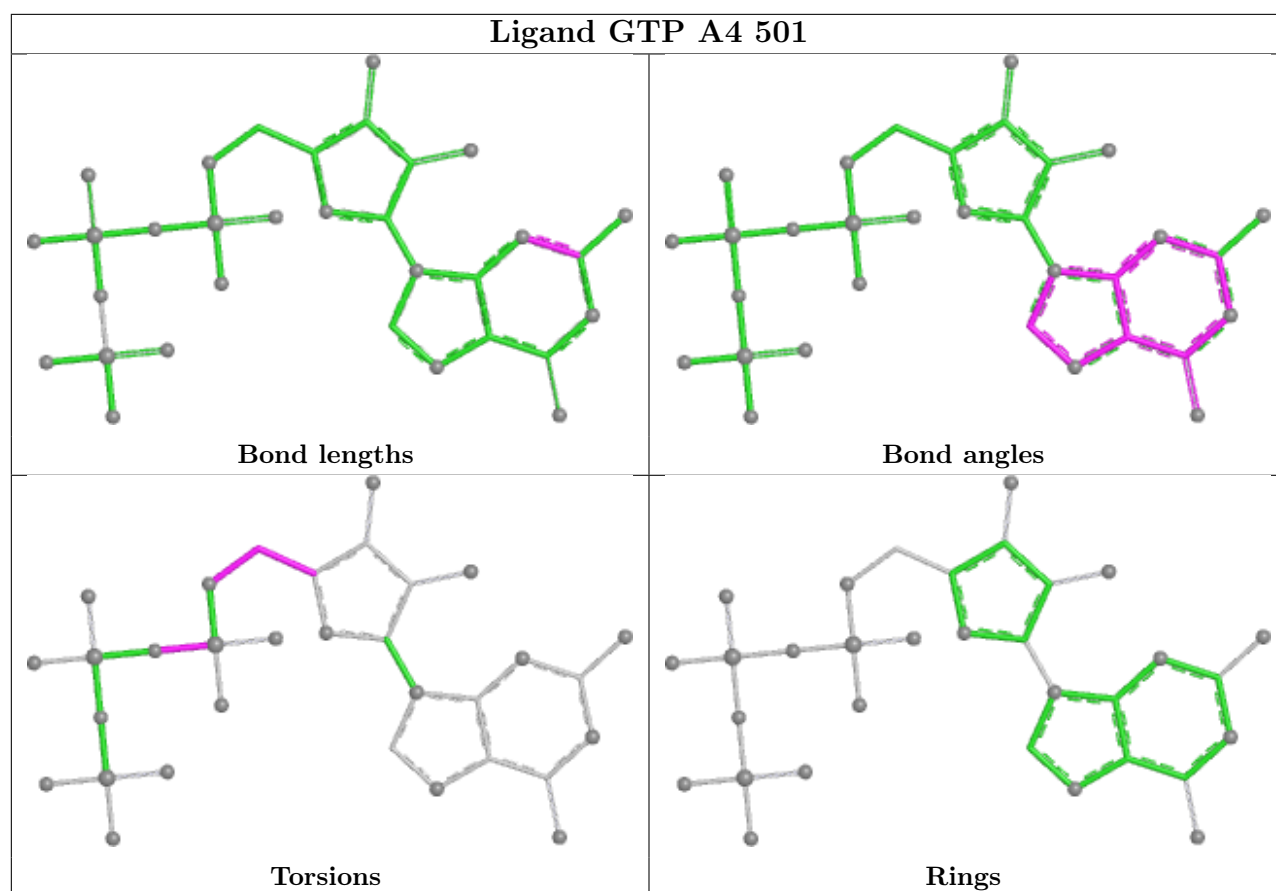
Ligand GTP G4 501



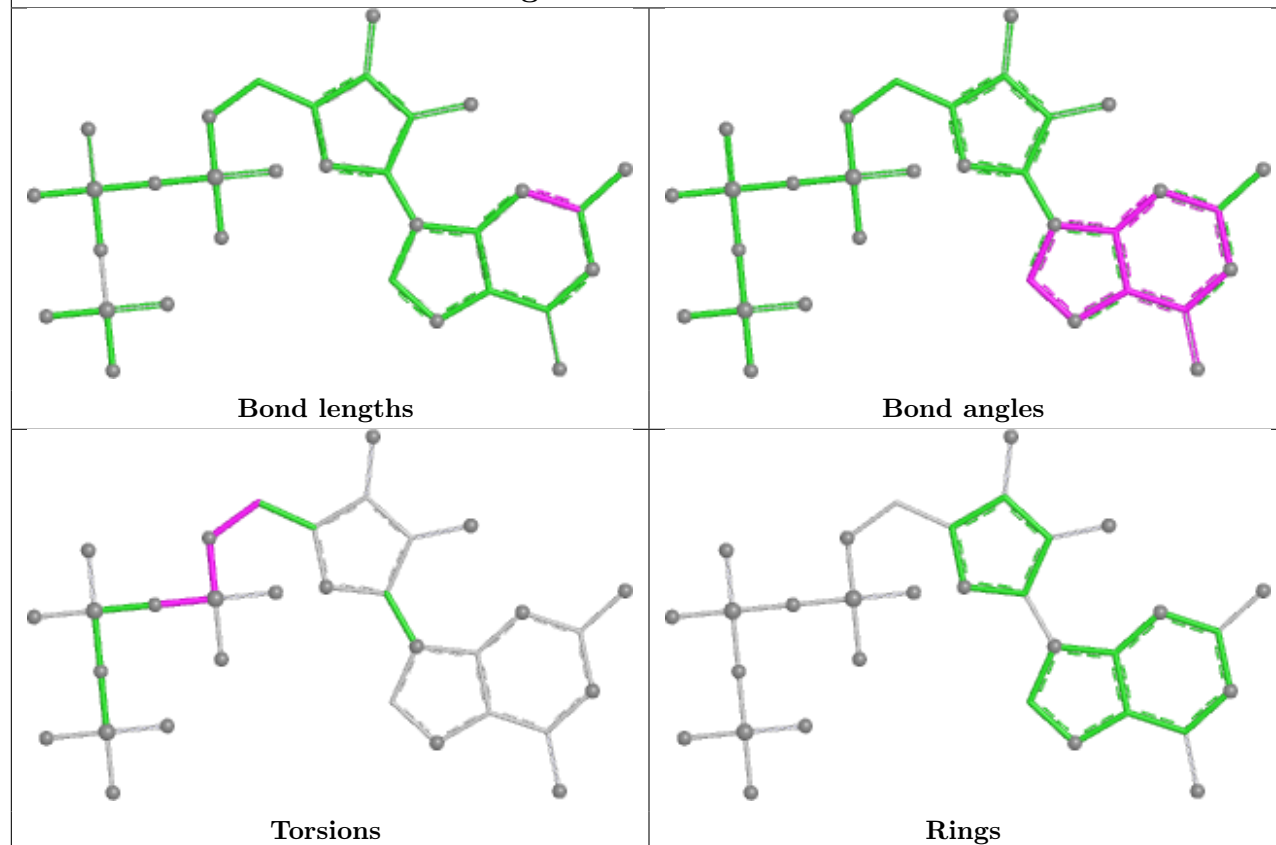
Ligand GTP R3 501



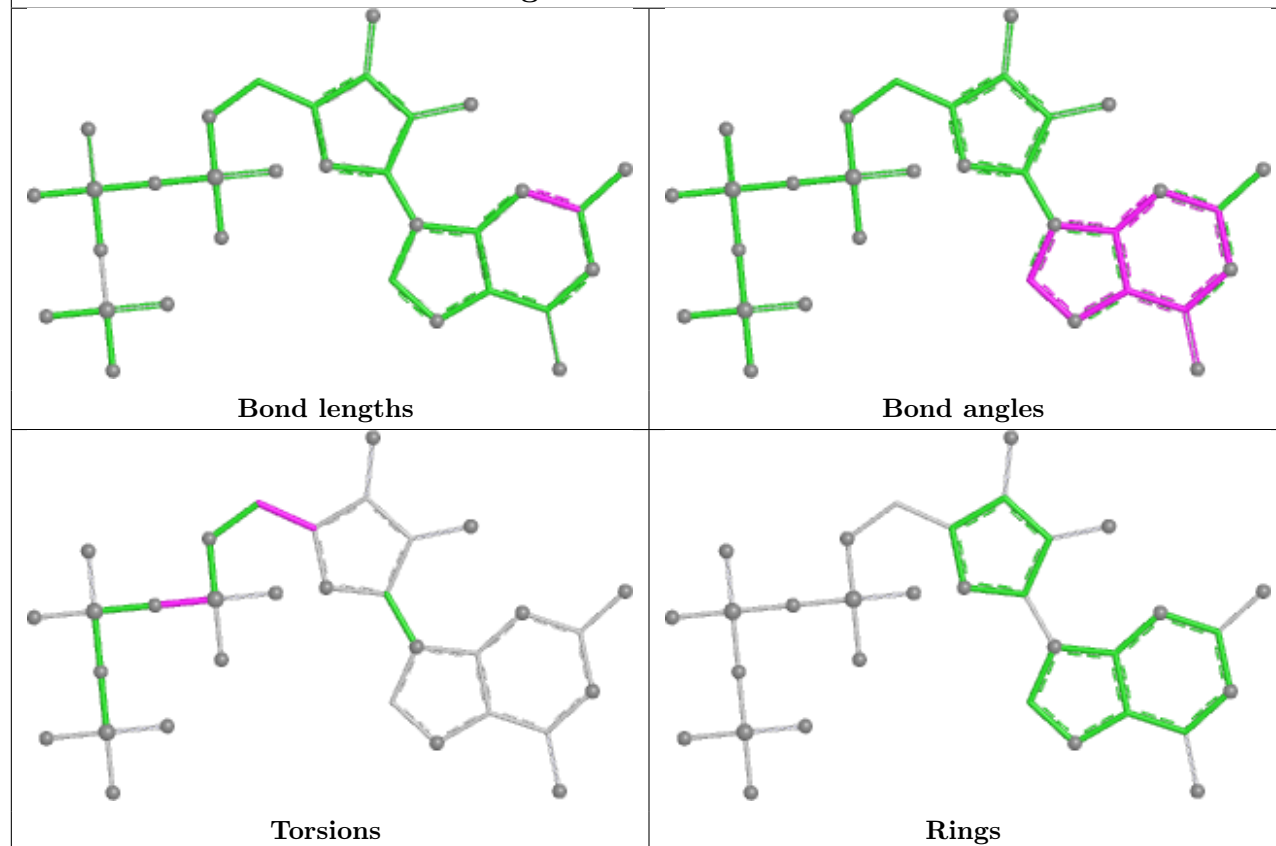




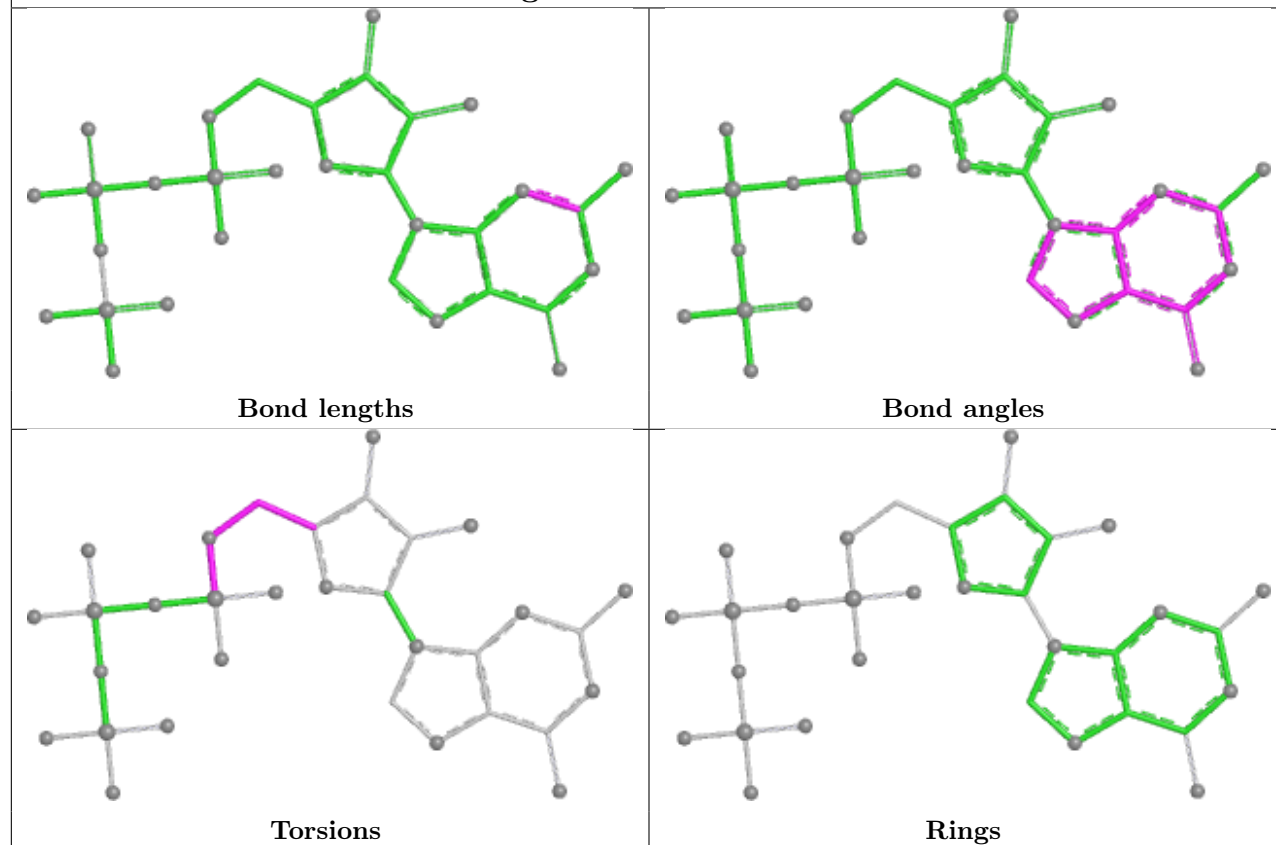
Ligand GTP A6 501



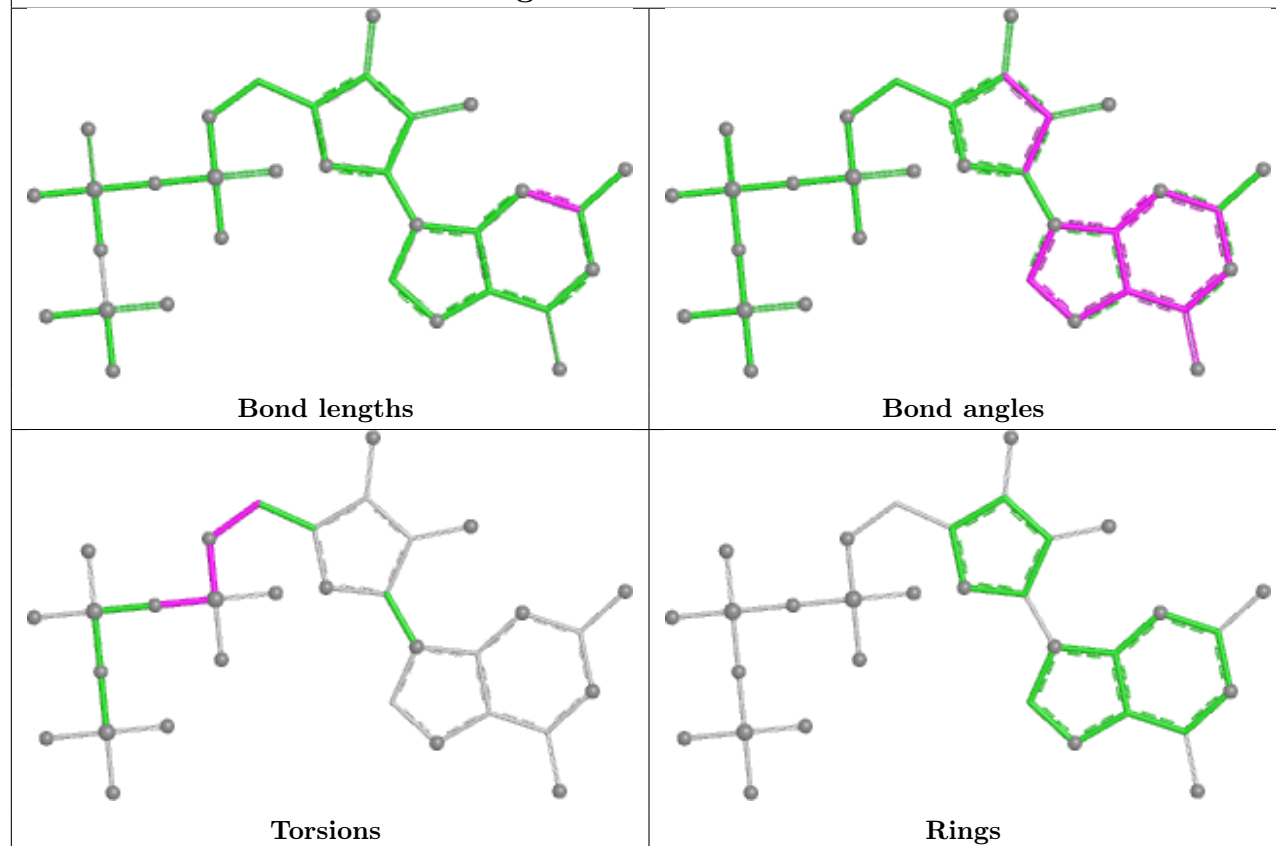
Ligand GTP A0 501

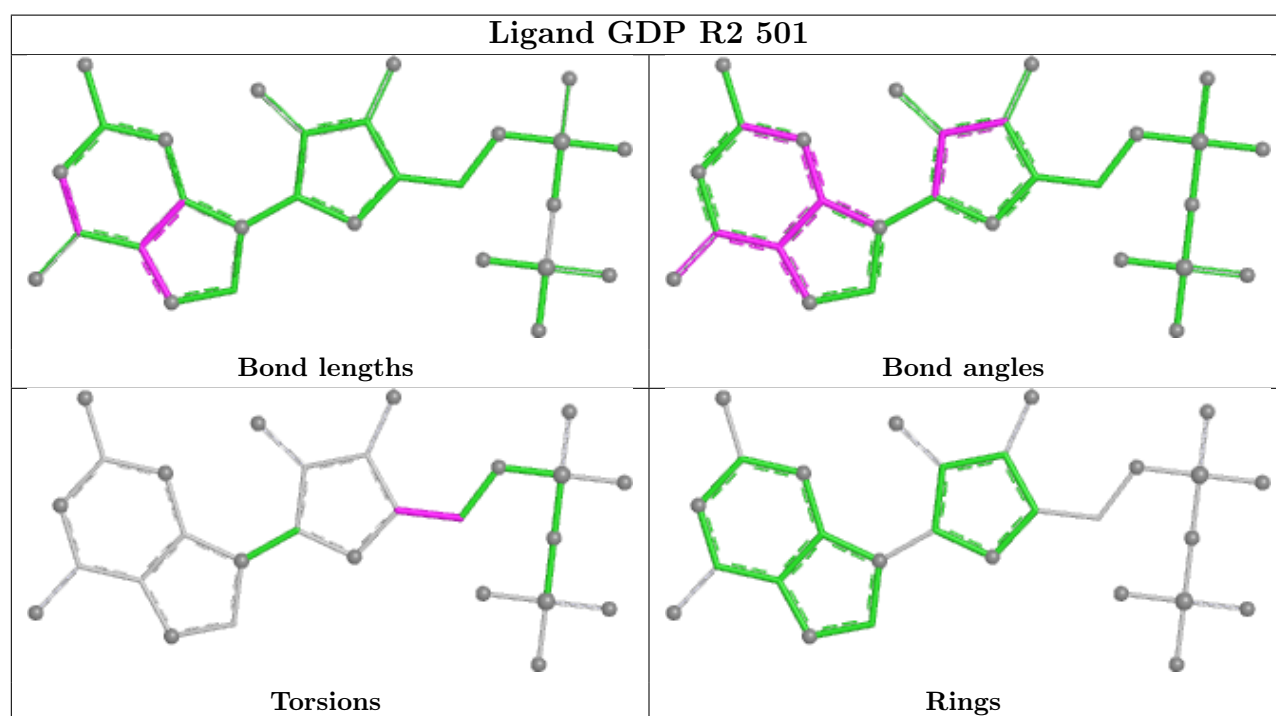
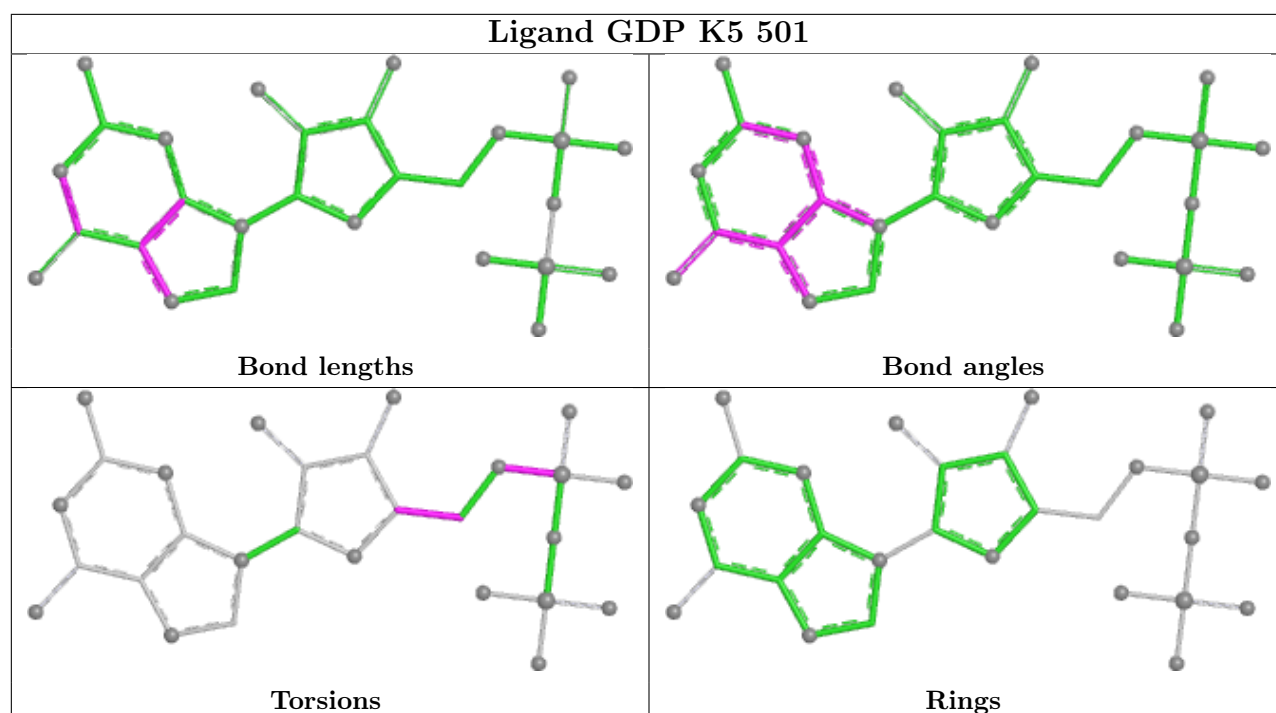


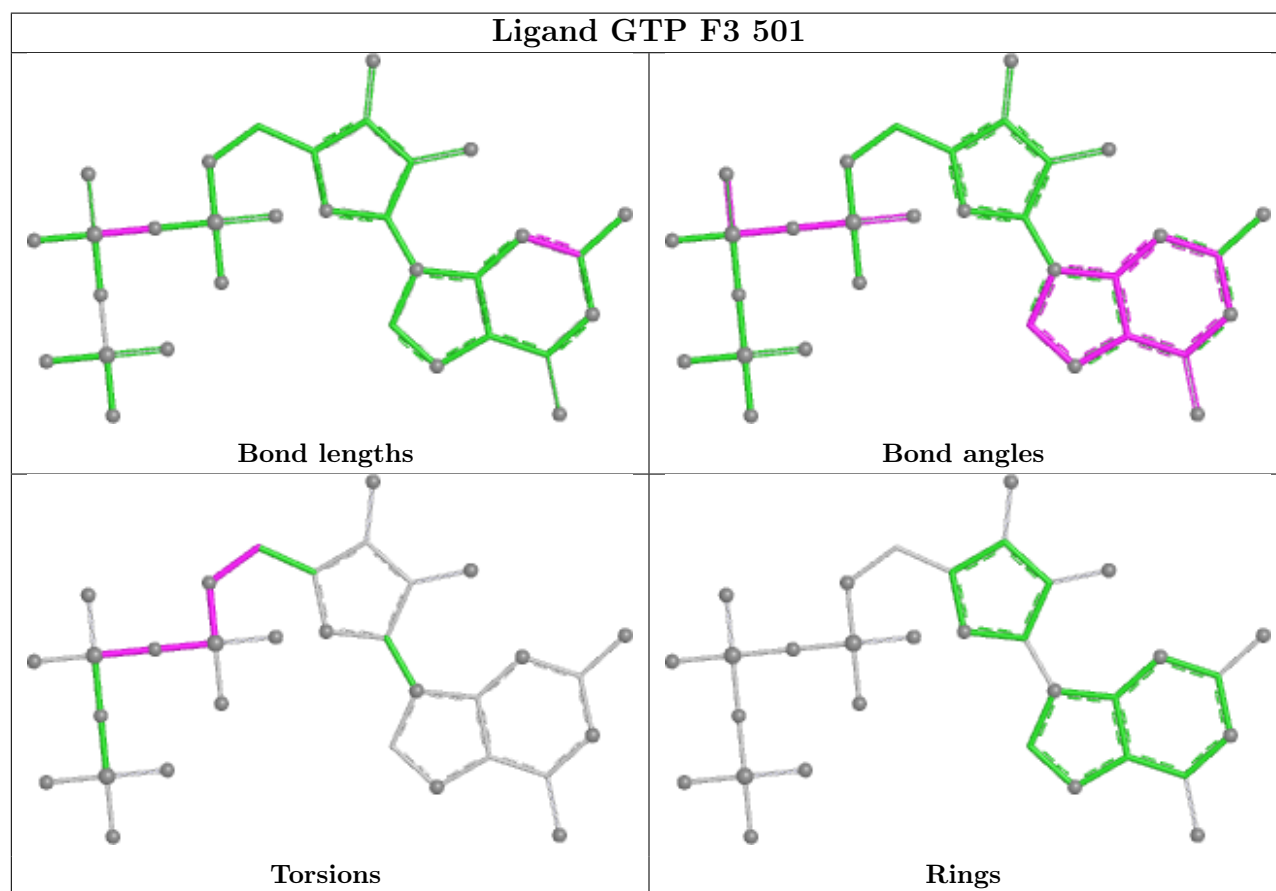
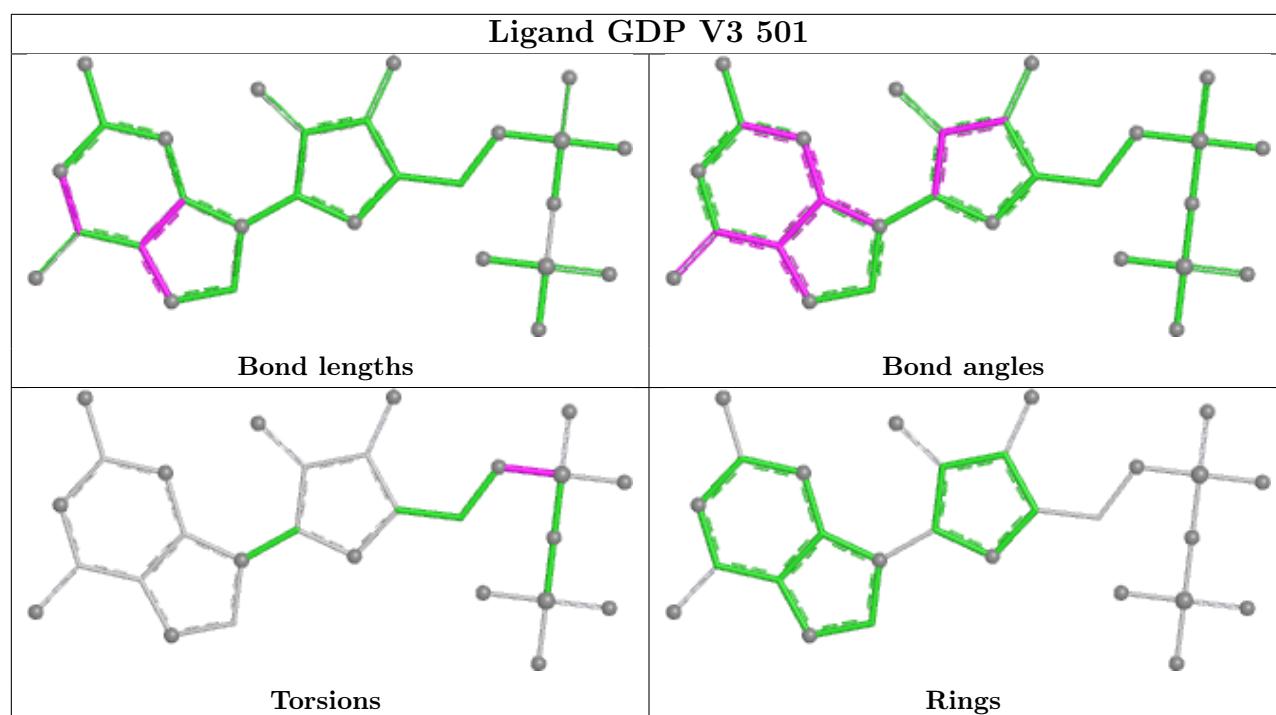
Ligand GTP R1 501

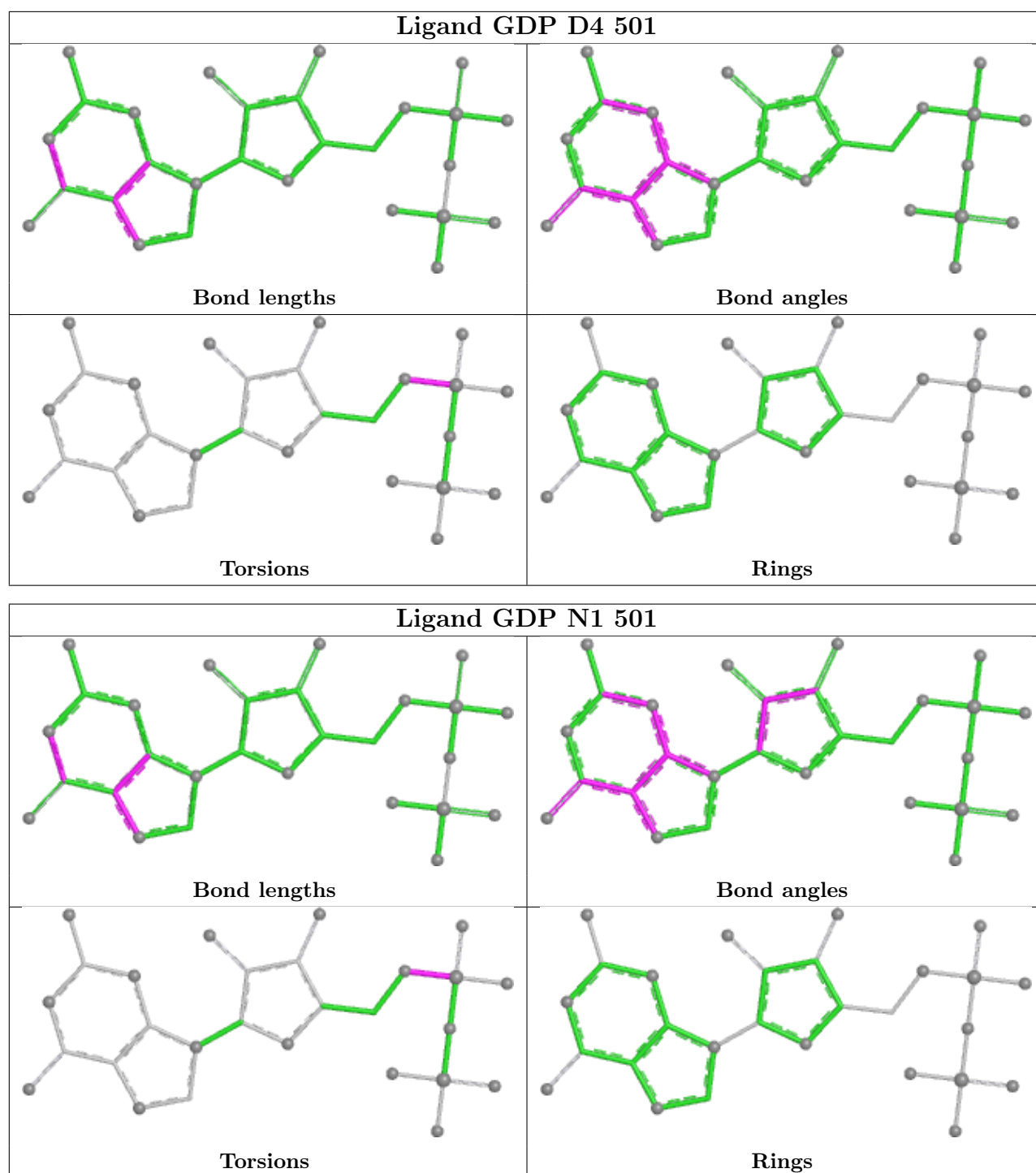


Ligand GTP W2 501









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.

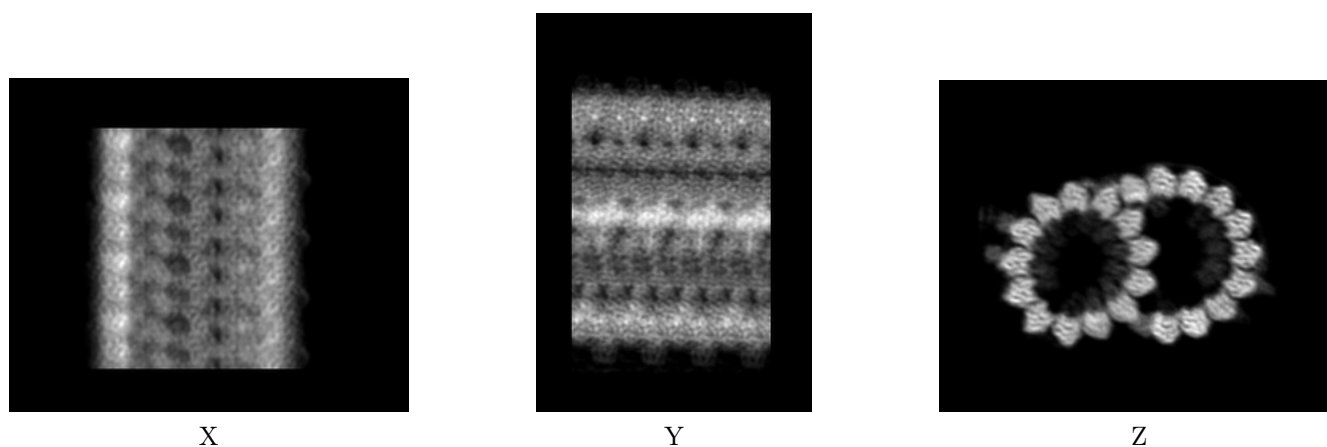
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-76188. 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](#)

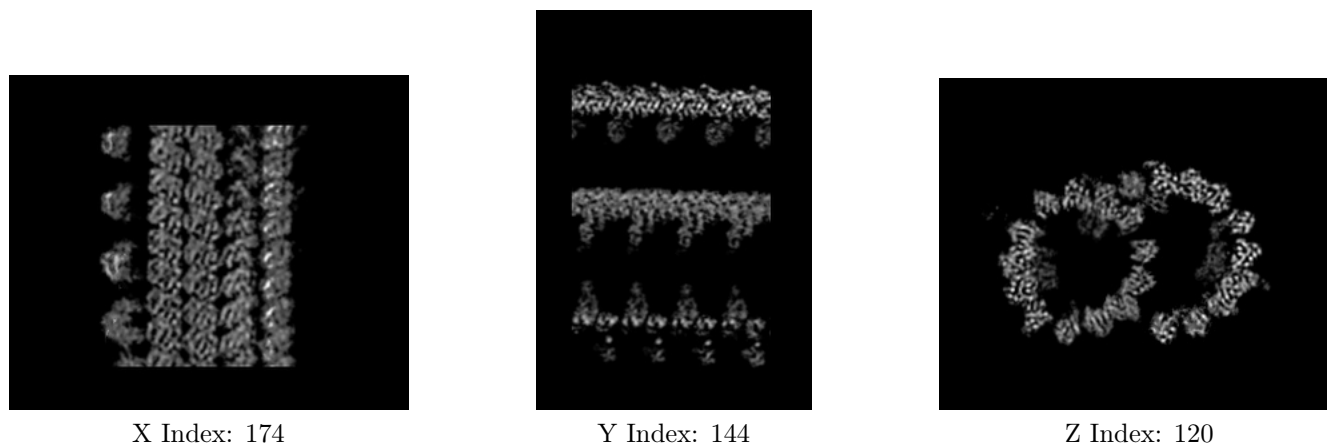
6.1.1 Primary map



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

6.2 Central slices [i](#)

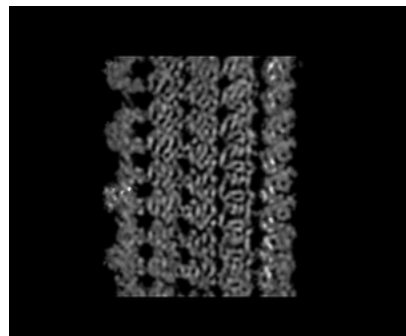
6.2.1 Primary map



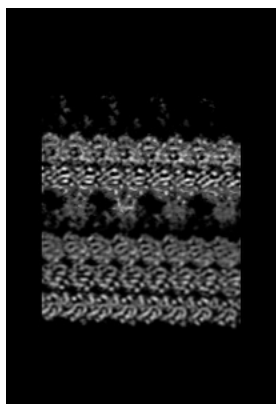
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 170



Y Index: 77

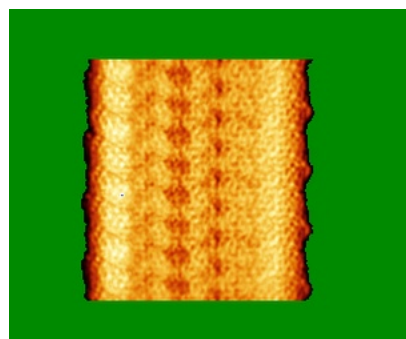


Z Index: 104

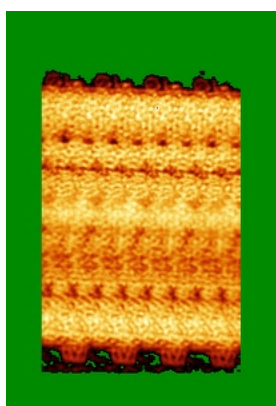
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

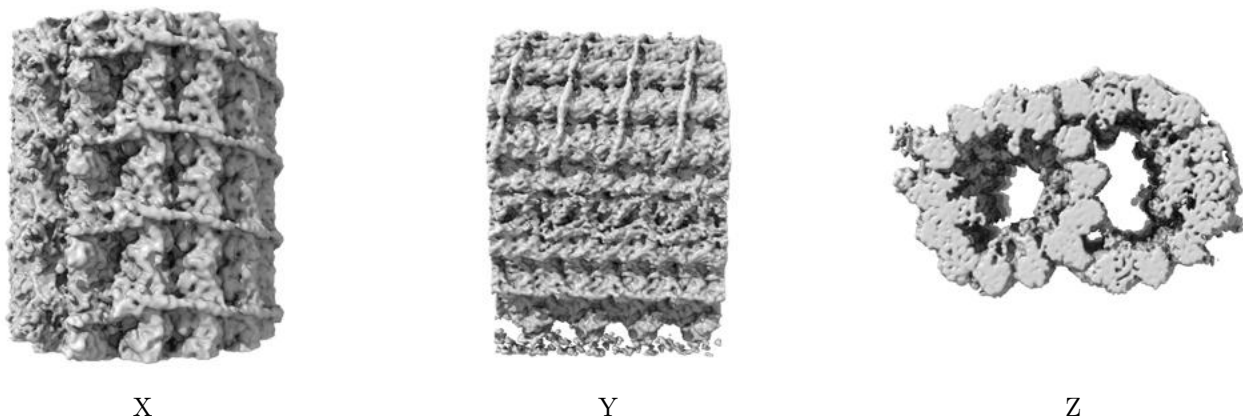


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.001. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

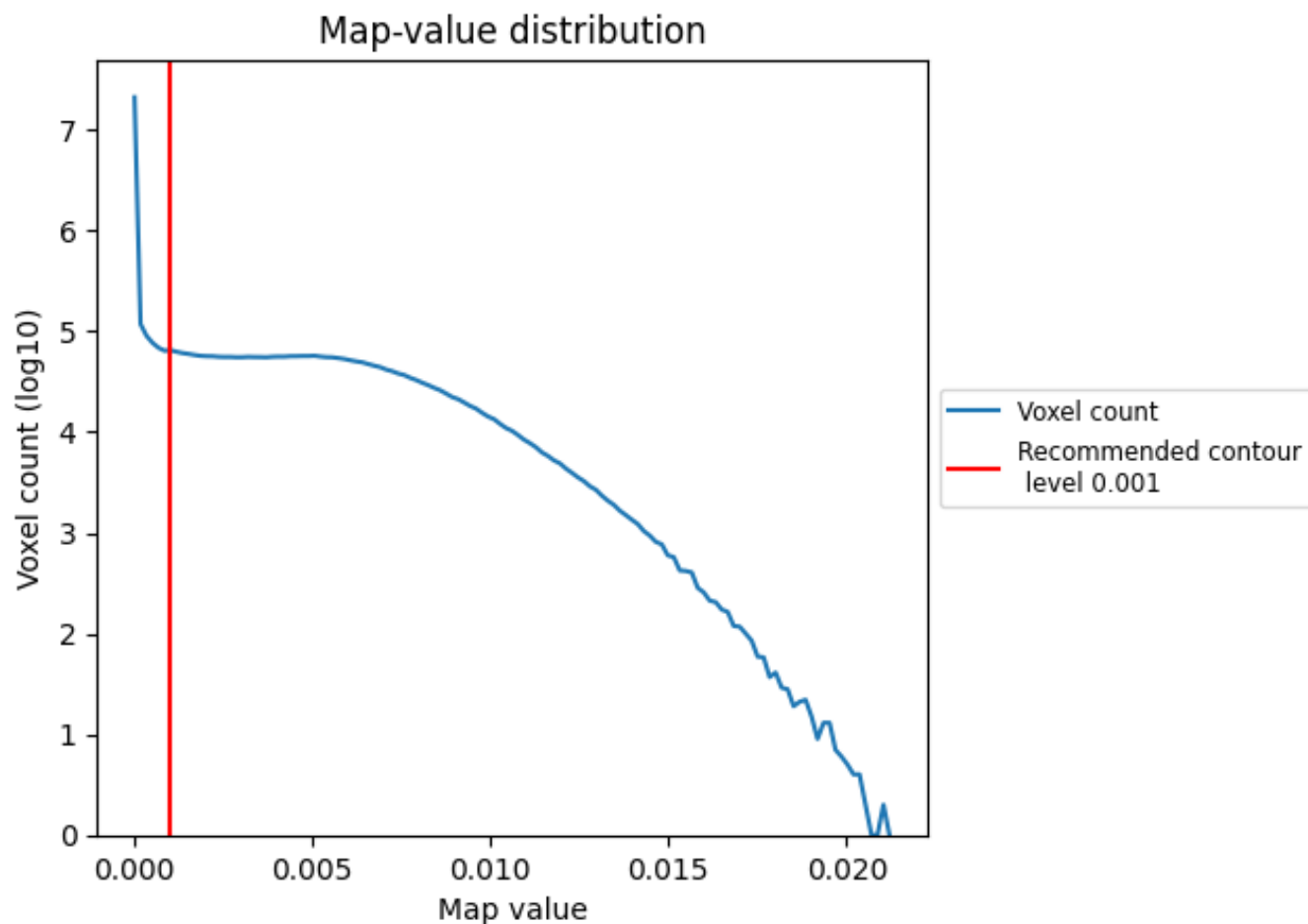
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

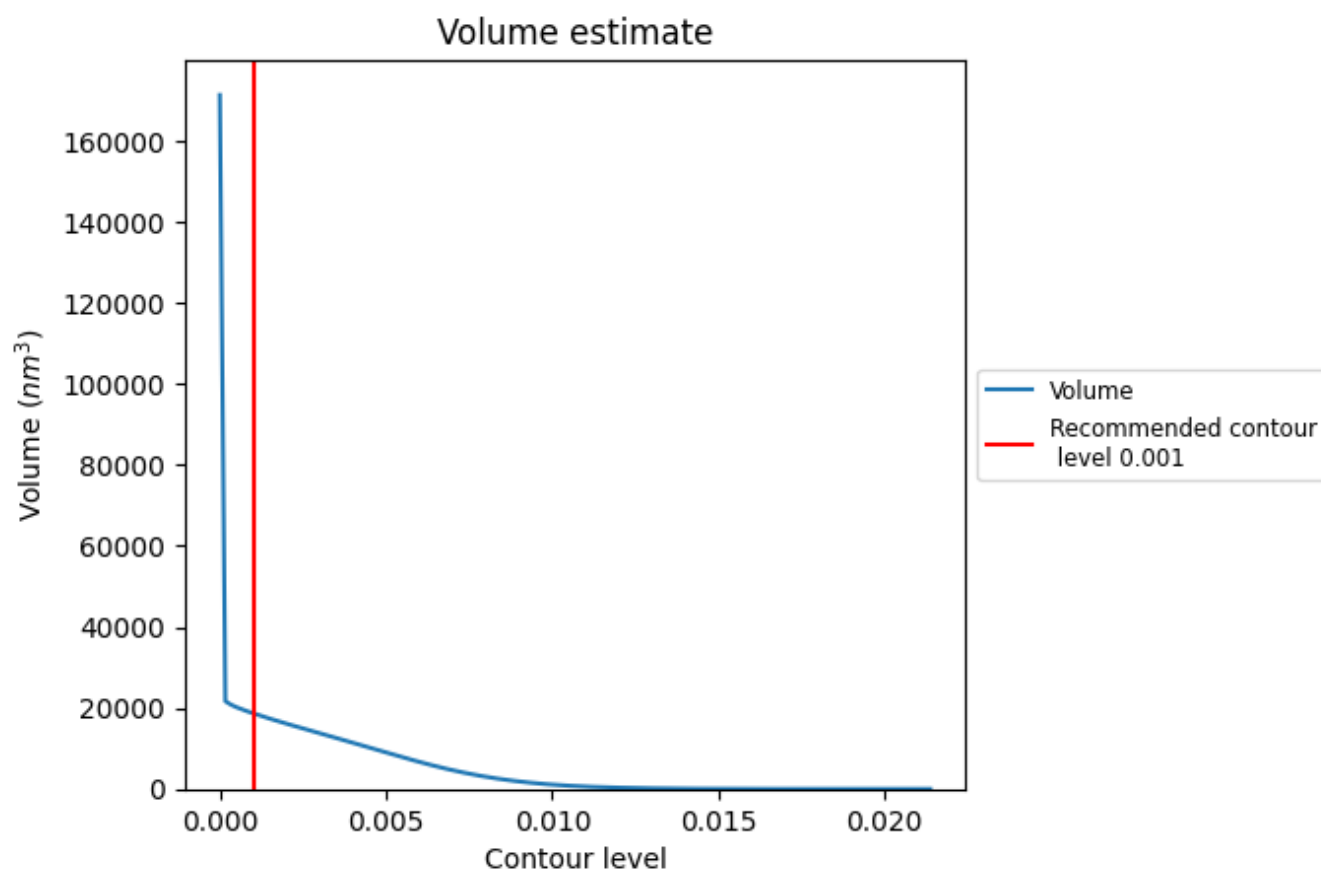
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 18698 nm³; this corresponds to an approximate mass of 16891 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.

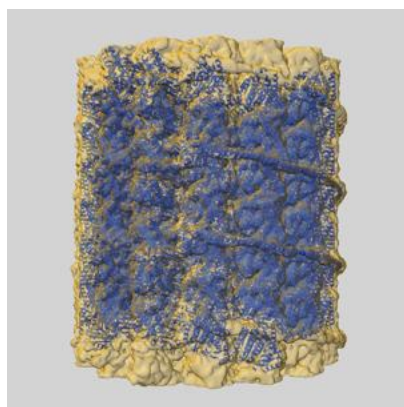
8 Fourier-Shell correlation

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

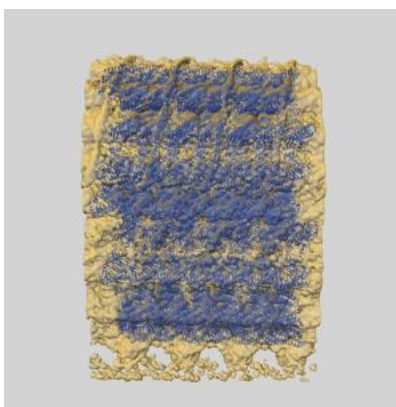
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-76188 and PDB model 11YJ. Per-residue inclusion information can be found in section [3](#) on page [31](#).

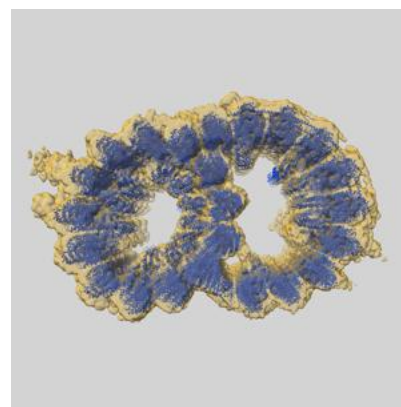
9.1 Map-model overlay [i](#)



X



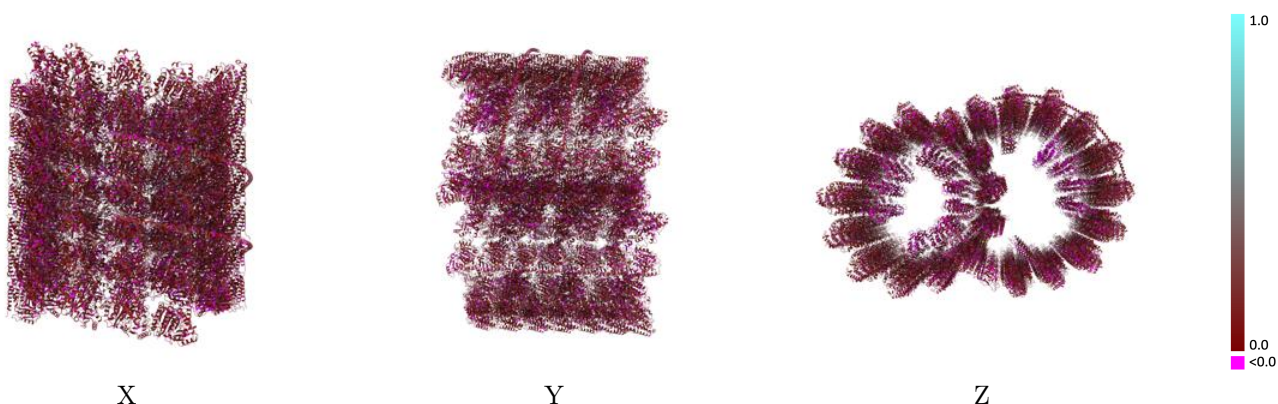
Y



Z

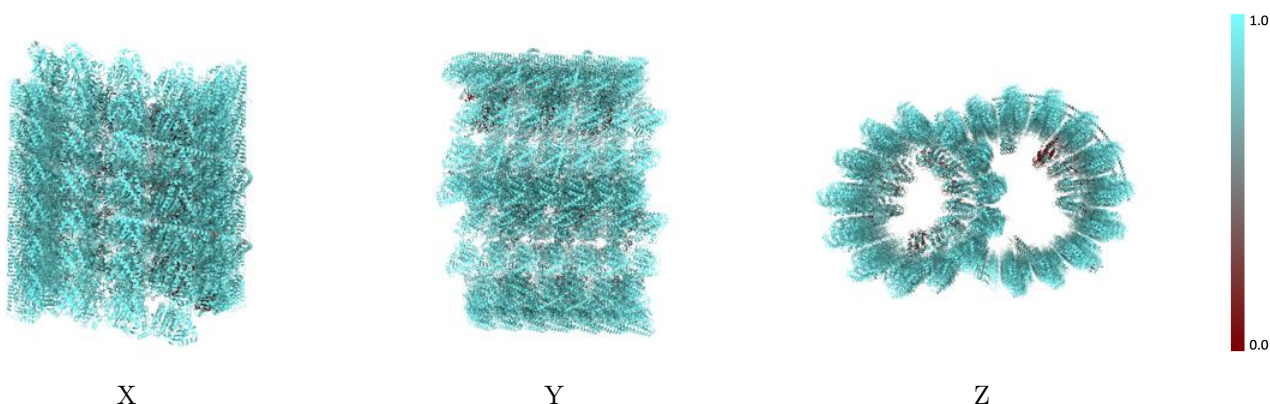
The images above show the 3D surface view of the map at the recommended contour level 0.001 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



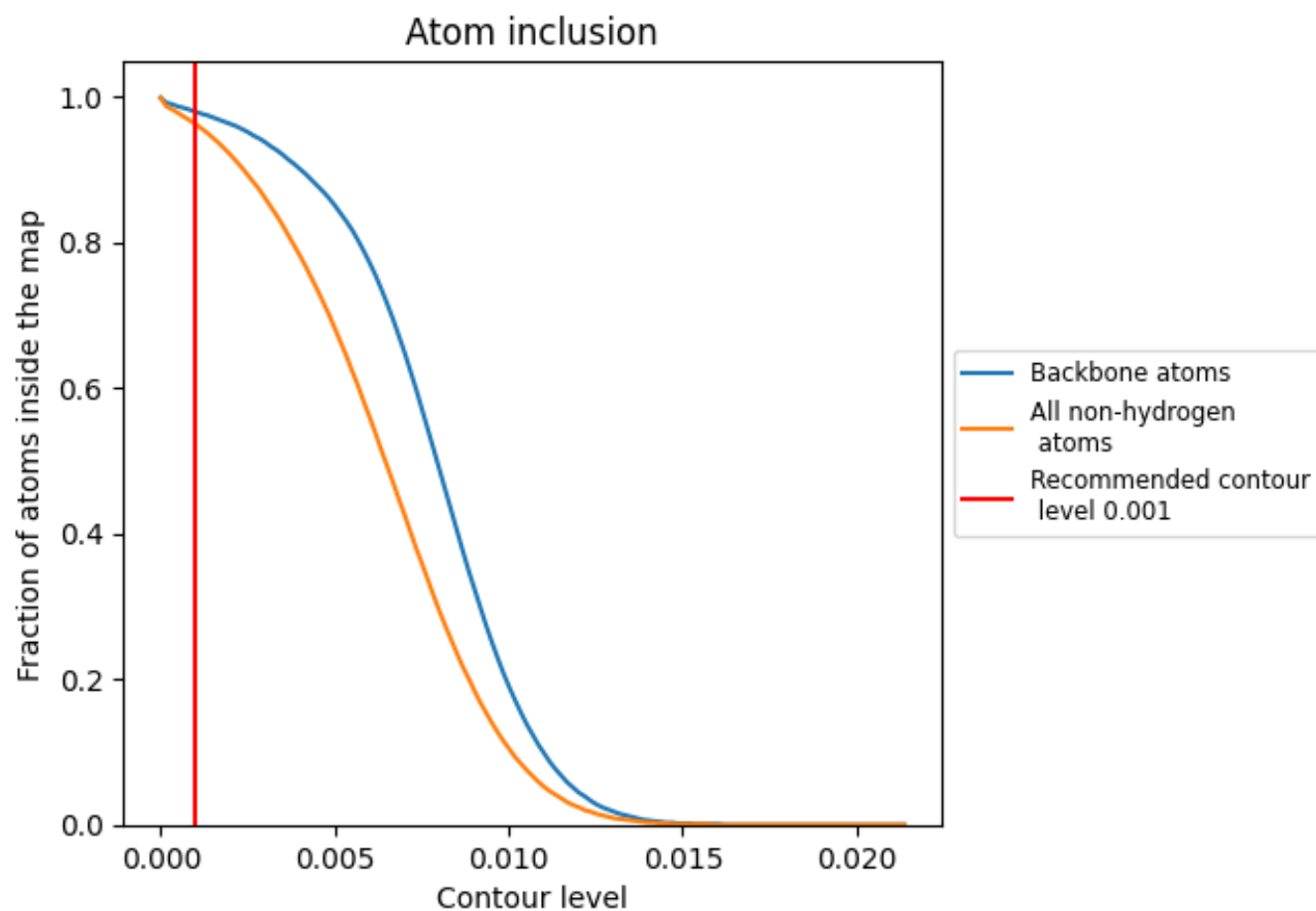
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.001).

9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.001) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9620	 0.1220
1A	 0.6330	 0.0340
1B	 0.8270	 0.0670
1C	 0.8390	 0.0780
1D	 0.8590	 0.0910
1E	 0.7730	 0.0650
1F	 0.8920	 0.1060
1G	 0.8590	 0.0960
2A	 0.6310	 0.0290
2B	 0.8360	 0.0770
2C	 0.8380	 0.0740
2D	 0.8690	 0.0920
2E	 0.7790	 0.0700
2F	 0.8900	 0.1020
2G	 0.8420	 0.0850
2H	 0.8360	 0.0720
2I	 0.7130	 0.0130
2J	 0.8010	 0.0090
3C	 0.8500	 0.0670
3D	 0.8350	 0.0790
3E	 0.7780	 0.0600
3F	 0.8180	 0.0730
3G	 0.7510	 0.0580
3H	 0.8250	 0.0790
3I	 0.8190	 0.0610
3J	 0.8610	 0.0650
4H	 0.8000	 0.0620
4I	 0.8330	 0.0630
4J	 0.8480	 0.0290
5A	 0.8080	 0.0420
5B	 0.7500	 0.0310
5C	 0.7100	 -0.0120
5D	 0.2820	 -0.0570
6A	 0.8240	 0.0360
6B	 0.8330	 0.0480



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Chain	Atom inclusion	Q-score
6C	 0.7700	 0.0330
6D	 0.4520	 -0.0370
7A	 0.8560	 0.0510
7B	 0.8530	 0.0420
7C	 0.6640	 -0.0100
7D	 0.3330	 -0.0550
8A	 0.8270	 0.0480
8B	 0.8120	 0.0550
8C	 0.8470	 0.0410
9A	 0.8300	 0.1180
9B	 0.8700	 0.1250
A0	 0.9940	 0.1110
A1	 0.9900	 0.1190
A2	 0.9940	 0.1190
A3	 0.9880	 0.1200
A4	 0.9940	 0.1210
A5	 0.9870	 0.1220
A6	 0.9930	 0.1060
B0	 0.9820	 0.1190
B1	 0.9830	 0.1060
B2	 0.9830	 0.1090
B3	 0.9850	 0.1060
B4	 0.9810	 0.1110
B5	 0.9810	 0.1060
C0	 0.9940	 0.1430
C1	 0.9430	 0.1190
C2	 0.9930	 0.1430
C3	 0.9940	 0.1480
C4	 0.9940	 0.1480
C5	 0.9920	 0.1410
D0	 0.9970	 0.1350
D1	 0.9940	 0.1410
D2	 0.9970	 0.1400
D3	 0.9950	 0.1450
D4	 0.9940	 0.1450
D5	 0.9960	 0.1450
D6	 0.9950	 0.1420
E0	 0.9870	 0.1440
E1	 0.9900	 0.1430
E2	 0.9920	 0.1480
E3	 0.9920	 0.1460
E4	 0.9930	 0.1460

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Chain	Atom inclusion	Q-score
E5	 0.9910	 0.1440
E6	 0.9960	 0.1440
F0	 0.9920	 0.1460
F1	 0.9930	 0.1450
F2	 0.9890	 0.1480
F3	 0.9930	 0.1510
F4	 0.9920	 0.1530
F5	 0.9950	 0.1460
F6	 0.9920	 0.1360
G0	 0.9900	 0.1290
G1	 0.9910	 0.1370
G2	 0.9930	 0.1510
G3	 0.9920	 0.1460
G4	 0.9920	 0.1520
G5	 0.9930	 0.1330
H0	 0.9910	 0.1280
H1	 0.9940	 0.1440
H2	 0.9940	 0.1380
H3	 0.9920	 0.1480
H4	 0.9960	 0.1430
H5	 0.9930	 0.1270
I0	 0.9870	 0.1140
I1	 0.9850	 0.1280
I2	 0.9910	 0.1460
I3	 0.9900	 0.1430
I4	 0.9930	 0.1440
I5	 0.9900	 0.1290
I6	 0.9880	 0.1190
J0	 0.9870	 0.1060
J1	 0.9940	 0.1280
J2	 0.9910	 0.1350
J3	 0.9940	 0.1400
J4	 0.9920	 0.1320
J5	 0.9910	 0.1280
J6	 0.9870	 0.1070
K0	 0.9900	 0.1210
K1	 0.9890	 0.1250
K2	 0.9940	 0.1330
K3	 0.9910	 0.1370
K4	 0.9840	 0.1310
K5	 0.9910	 0.1220
L0	 0.9940	 0.1230

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Chain	Atom inclusion	Q-score
L1	 0.9880	 0.1130
L2	 0.9930	 0.1390
L3	 0.9920	 0.1290
L4	 0.9890	 0.1150
L5	 0.9890	 0.1160
L6	 0.9800	 0.0770
M0	 0.9900	 0.1290
M1	 0.9840	 0.1150
M2	 0.9920	 0.1330
M3	 0.9870	 0.1240
M4	 0.9850	 0.1300
M5	 0.9860	 0.1270
M6	 0.9910	 0.1160
N0	 0.9930	 0.1040
N1	 0.9960	 0.1300
N2	 0.9970	 0.1230
N3	 0.9960	 0.1280
N4	 0.9940	 0.1220
N5	 0.9970	 0.1180
N6	 0.9890	 0.1000
O0	 0.9880	 0.1320
O1	 0.9920	 0.1370
O2	 0.9880	 0.1440
O3	 0.9850	 0.1400
O4	 0.9870	 0.1410
O5	 0.9870	 0.1360
O6	 0.9900	 0.1300
P0	 0.9860	 0.1260
P1	 0.9930	 0.1250
P2	 0.9760	 0.1300
P3	 0.9890	 0.1340
P4	 0.9860	 0.1400
P5	 0.9840	 0.1310
P6	 0.9830	 0.1240
Q0	 0.9800	 0.1360
Q1	 0.9750	 0.1440
Q2	 0.9800	 0.1460
Q3	 0.9790	 0.1500
Q4	 0.9800	 0.1400
Q5	 0.8920	 0.1060
R0	 0.9860	 0.1480
R1	 0.9810	 0.1480

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Chain	Atom inclusion	Q-score
R2	 0.9900	 0.1510
R3	 0.9730	 0.1530
R4	 0.9830	 0.1420
R5	 0.9750	 0.1460
R6	 0.9800	 0.1230
S0	 0.9850	 0.1480
S1	 0.9870	 0.1550
S2	 0.9860	 0.1510
S3	 0.9900	 0.1570
S4	 0.9850	 0.1510
S5	 0.9900	 0.1500
S6	 0.9910	 0.1380
T0	 0.9820	 0.1360
T1	 0.9840	 0.1400
T2	 0.9790	 0.1410
T3	 0.9870	 0.1470
T4	 0.9890	 0.1440
T5	 0.9910	 0.1390
T6	 0.9910	 0.1370
U0	 0.9710	 0.1100
U1	 0.9910	 0.1300
U2	 0.9860	 0.1260
U3	 0.9870	 0.1250
U4	 0.9880	 0.1330
U5	 0.9900	 0.1200
U6	 0.9930	 0.1180
V0	 0.9850	 0.1110
V1	 0.9890	 0.1110
V2	 0.9880	 0.1220
V3	 0.9890	 0.1150
V4	 0.9860	 0.1170
V5	 0.9880	 0.1090
W0	 0.9840	 0.1360
W1	 0.9860	 0.1290
W2	 0.9830	 0.1350
W3	 0.9830	 0.1320
W4	 0.9810	 0.1410
W5	 0.9800	 0.1280
W6	 0.9810	 0.1290
X0	 0.9890	 0.0930
X1	 0.9930	 0.1000
X2	 0.9960	 0.1180

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Chain	Atom inclusion	Q-score
X3	 0.9910	 0.0870
Y0	 0.8790	 0.1110
Y1	 0.9130	 0.1150
Y2	 0.8910	 0.1090