



## wwPDB EM Validation Summary Report ⓘ

Mar 20, 2025 – 08:15 AM EDT

PDB ID : 9E5C  
EMDB ID : EMD-47524  
Title : Cryo-EM structure of 96 nm repeat of microtubule doublet from *T. brucei* flagellum  
Authors : Xia, X.; Shimogawa, M.M.; Wang, H.; Liu, S.; Wijono, A.; Langousis, G.; Kassem, A.M.; Wohlschlegel, J.A.; Hill, K.; Zhou, Z.H.  
Deposited on : 2024-10-28  
Resolution : 3.20 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev117
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	<b>FAILED</b>
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

# 1 Overall quality at a glance ⓘ


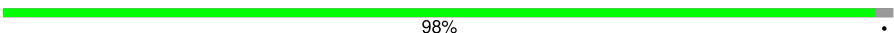
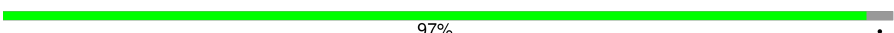

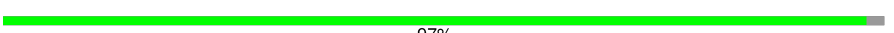





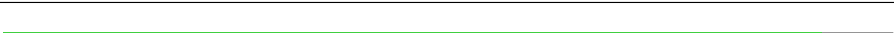

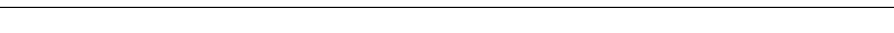
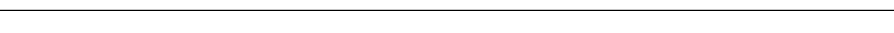
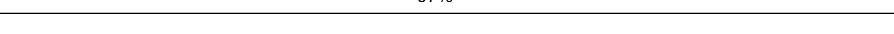
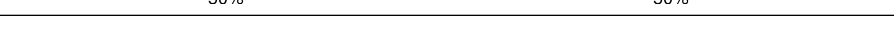
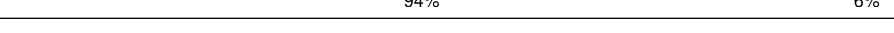
The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 Å.

There are no overall percentile quality scores available for this entry.

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  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	0A	752	 88%12%
1	0B	752	 98%.
1	0C	752	 97%.
1	0D	752	 88%12%
1	0E	752	 97%.
1	0F	752	 97%.
2	0G	779	 94%6%
2	0H	779	 94%6%
2	0I	779	 94%6%
3	0J	724	 92%8%
3	0K	724	 92%8%
3	0L	724	 92%8%
4	0M	779	 97%.
4	0N	779	 97%.
5	0O	385	 50%50%
5	0P	385	 94%6%
5	0Q	385	 91%6%

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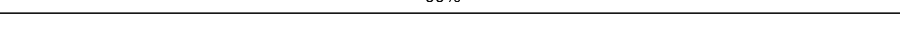
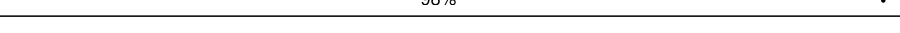
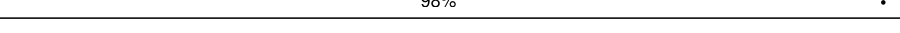
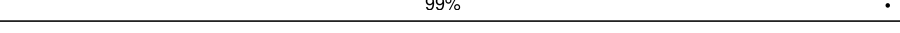
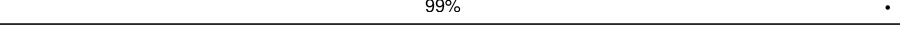
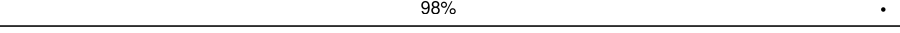
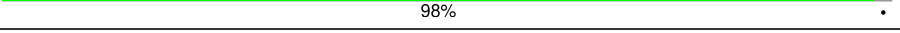





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Mol	Chain	Length	Quality of chain
5	0R	385	
5	0S	385	
5	0T	385	
6	0U	483	
6	0V	483	
6	0W	483	
6	0X	483	
7	0Y	436	
7	0Z	436	
7	1A	436	
7	1B	436	
8	0a	161	
8	0b	161	
8	0c	161	
8	0d	161	
8	0e	161	
8	0f	161	
9	0g	867	
9	0h	867	
9	0i	867	
9	0j	867	
9	0k	867	
9	0l	867	
9	0m	867	
9	0n	867	











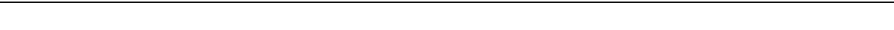

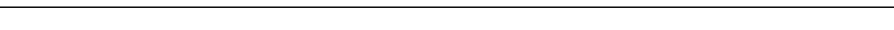
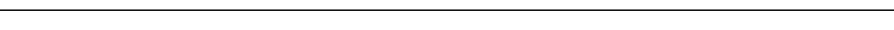






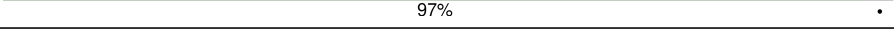




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Mol	Chain	Length	Quality of chain
9	0o	867	 8% 92%
9	0p	867	 8% 92%
10	0q	1238	 8% 92%
11	0r	476	 16% 84%
11	0s	476	 43% 57%
12	0t	759	 62% 38%
13	0u	744	 65% 35%
14	0v	856	 49% 51%
14	0w	856	 57% 43%
15	0x	872	 48% 52%
15	0y	872	 52% 47%
16	0z	302	 74% 26%
17	1C	334	 99% .
17	1D	334	 99% .
17	1G	334	 99% .
18	1E	349	 98% .
18	1F	349	 98% .
19	1H	422	 99% .
19	1I	422	 99% .
20	1J	422	 98% .
20	1K	422	 98% .
21	1L	356	 86% 14%
21	1M	356	 86% 14%
22	1N	219	 78% 22%
22	1O	219	 78% 22%

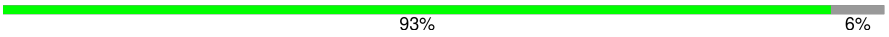

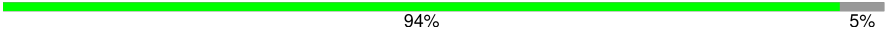

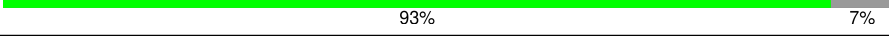
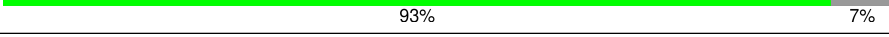


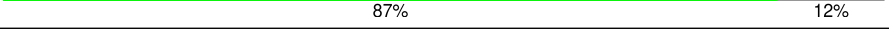

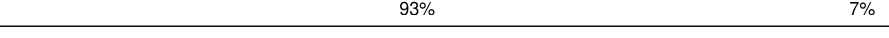
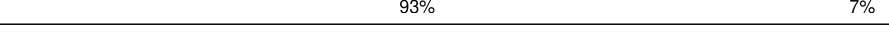
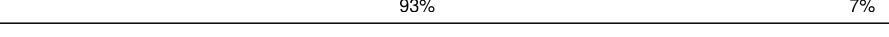
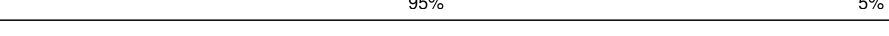
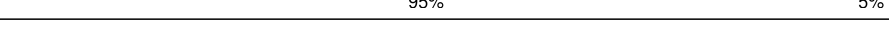
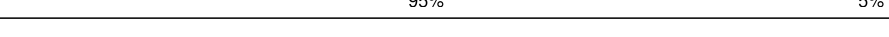
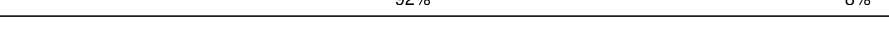
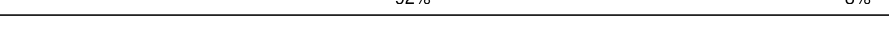
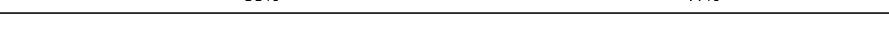






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Mol	Chain	Length	Quality of chain
23	1P	130	
23	1Q	130	
24	1R	270	
24	1S	270	
25	1T	301	
25	1U	301	
25	1V	301	
26	1W	552	
26	1X	552	
27	1Y	359	
27	1Z	359	
28	1a	848	
29	1b	1032	
30	1c	1340	
31	1d	1204	
32	1e	407	
33	1f	500	
34	1g	651	
35	1h	507	
36	1i	552	
37	1j	461	
38	1k	453	
39	1l	478	
40	1m	1403	
41	1n	568	

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Mol	Chain	Length	Quality of chain
42	1o	443	
43	1p	909	
44	1r	1460	
45	1t	1760	
46	2A	297	
46	2B	297	
46	2C	297	
47	2D	282	
47	2E	282	
47	2F	282	
48	2G	320	
48	2H	320	
48	2I	320	
49	2J	249	
49	2K	249	
49	2L	249	
50	2M	254	
50	2N	254	
50	2O	254	
51	2P	182	
51	2Q	182	
52	2R	386	
52	2S	386	
52	2T	386	
53	2U	417	


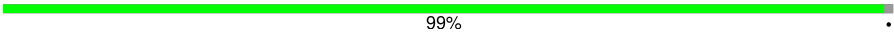
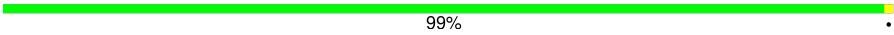


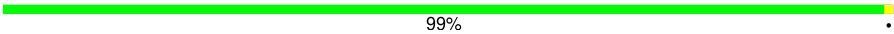



















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Mol	Chain	Length	Quality of chain
53	2V	417	
53	2W	417	
54	2X	415	
54	2Y	415	
54	2Z	415	
54	3D	415	
55	2a	322	
55	2b	322	
55	2c	322	
55	2d	322	
56	2e	518	
56	2f	518	
56	2g	518	
56	2h	518	
57	2i	332	
57	2j	332	
57	2k	332	
57	2l	332	
58	2m	585	
58	2n	585	
58	2o	585	
58	2p	585	
59	2q	548	
59	2r	548	
59	2s	548	











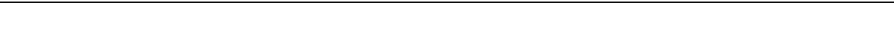

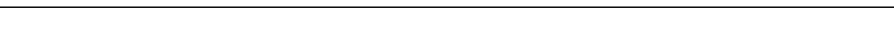
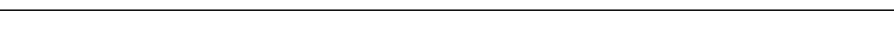











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Mol	Chain	Length	Quality of chain
59	2t	548	
60	2u	433	
61	2v	297	
61	2w	297	
61	2x	297	
61	2y	297	
62	2z	333	
62	3a	333	
62	3b	333	
62	3c	333	
63	3A	415	
63	3B	415	
63	3C	415	
64	3E	247	
64	3F	247	
64	3G	247	
64	3H	247	
64	3I	247	
65	3J	954	
65	3K	954	
65	3L	954	
66	3M	300	
66	3N	300	
66	3O	300	
66	3P	300	




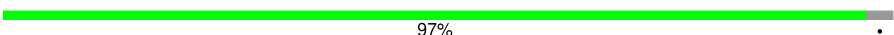
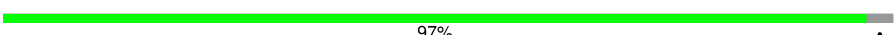

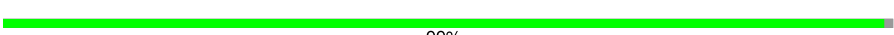




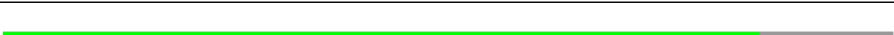

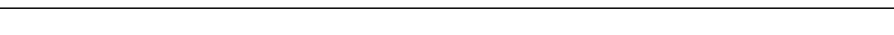
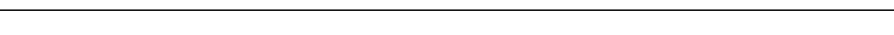
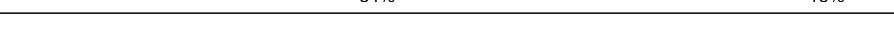
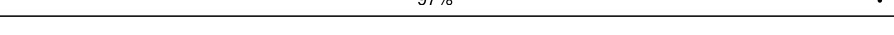
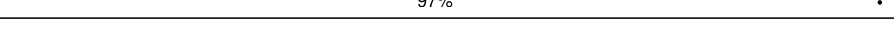
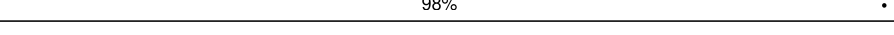
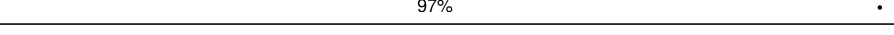
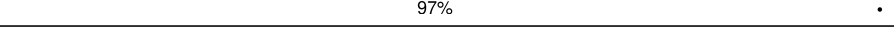
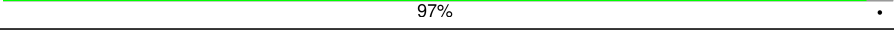
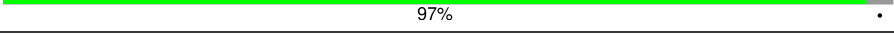
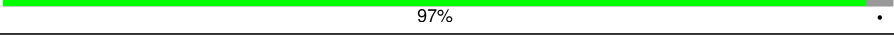
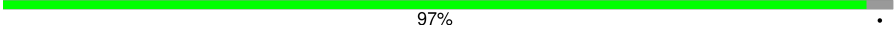
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Mol	Chain	Length	Quality of chain
66	3Q	300	 92% 8%
66	3R	300	 92% 8%
66	3S	300	 92% 8%
66	3T	300	 92% 8%
67	3U	312	 72% 28%
67	3V	312	 72% 28%
67	3W	312	 72% 28%
67	3X	312	 72% 28%
67	3Y	312	 72% 28%
68	3Z	294	 63% 37%
68	4A	294	 63% 37%
68	4B	294	 63% 37%
68	4C	294	 63% 37%
68	4D	294	 63% 37%
68	4E	294	 63% 37%
68	4F	294	 63% 37%
68	4G	294	 63% 37%
68	4H	294	 63% 37%
68	4I	294	 62% 37%
68	4J	294	 63% 37%
68	4K	294	 62% 37%
68	4L	294	 63% 37%
68	4M	294	 63% 37%
68	4N	294	 63% 37%
69	3d	823	 82% 18%

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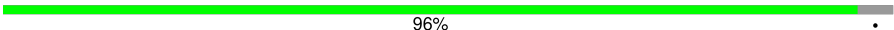
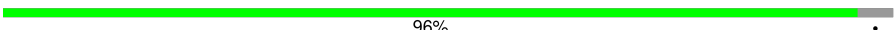
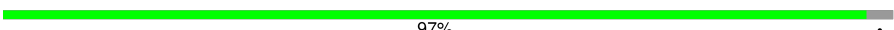
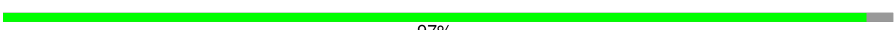






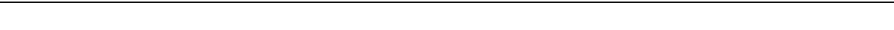

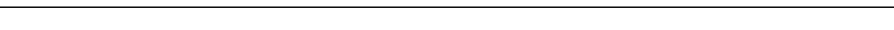
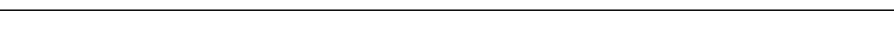

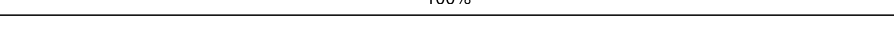
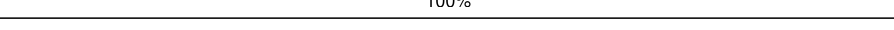
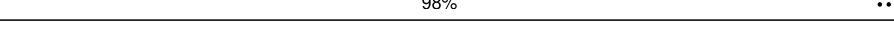

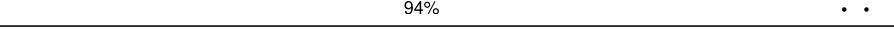
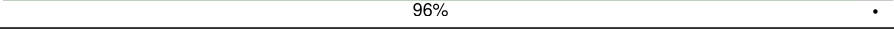
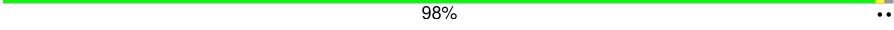



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Mol	Chain	Length	Quality of chain
69	3e	823	 82% 18%
69	3f	823	 82% 18%
69	3g	823	 82% 18%
70	3h	318	 97% .
70	3i	318	 97% .
71	3j	384	 99% .
72	3k	366	 99% .
73	3l	319	 94% . 5%
73	3m	319	 90% 9%
73	3o	319	 93% . 5%
73	3p	319	 89% . 9%
74	3q	262	 85% 15%
74	3r	262	 85% 15%
74	3s	262	 85% 15%
74	3t	262	 84% . 15%
75	3u	90	 97% .
75	3v	90	 97% .
75	3w	90	 98% .
75	3x	90	 97% .
75	3y	90	 97% .
75	3z	90	 97% .
75	4a	90	 97% .
75	4b	90	 97% .
75	4c	90	 97% .
75	4d	90	 97% .

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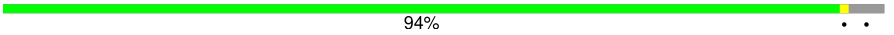
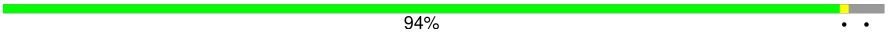
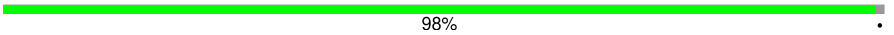
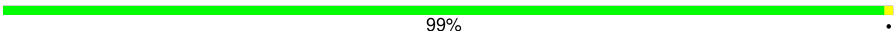
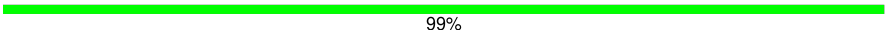
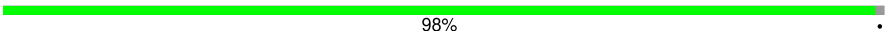
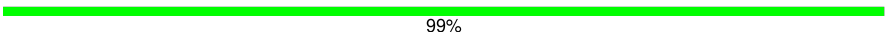
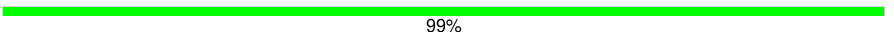
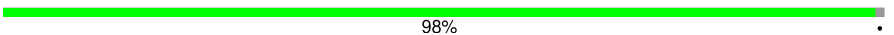





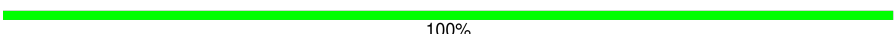
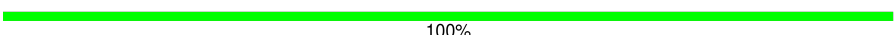
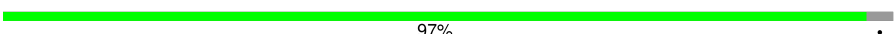
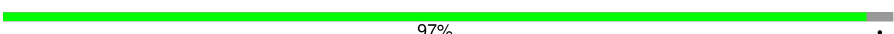
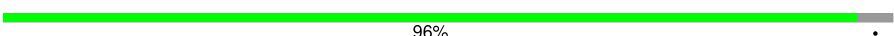
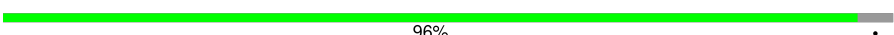






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Mol	Chain	Length	Quality of chain
75	4e	90	 96% .
75	4f	90	 96% .
75	4g	90	 97% .
75	4h	90	 97% .
75	4i	90	 96% .
75	4j	90	 96% .
75	4k	90	 96% .
75	4l	90	 96% .
75	4m	90	 94% . .
75	4n	90	 96% .
75	5s	90	 97% .
75	5t	90	 98% ..
75	5u	90	 92% . 7%
75	5v	90	 90% 6% .
75	5w	90	 100%
75	5x	90	 100%
75	7k	90	 98% ..
75	7n	90	 91% . 7%
75	7o	90	 94% . .
75	7p	90	 96% .
75	8k	90	 98% ..
75	8n	90	 92% . 7%
75	8o	90	 93% . .
75	8p	90	 94% . .
75	9k	90	 98% ..












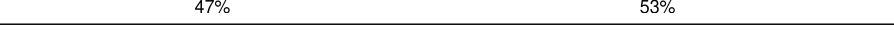


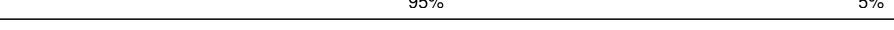
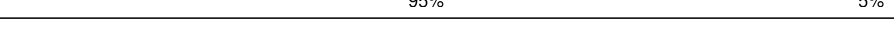

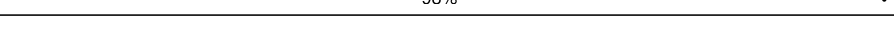

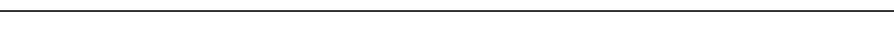

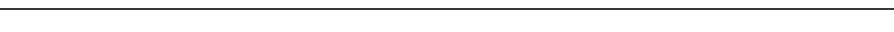
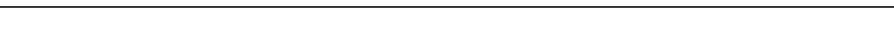


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Mol	Chain	Length	Quality of chain
75	9n	90	 91% 7%
75	9o	90	 94% . .
75	9p	90	 94% . .
76	4O	629	 98% .
76	4P	629	 99% .
76	4Q	629	 99%
76	4R	629	 98% .
76	4S	629	 99%
76	4T	629	 99%
76	4U	629	 98% .
77	4V	274	 87% 12%
77	4W	274	 88% 12%
77	4X	274	 87% 12%
77	4Y	274	 88% 12%
77	4Z	274	 87% 12%
78	4o	220	 100%
78	4p	220	 100%
79	4q	879	 97% .
79	4r	879	 97% .
80	4s	842	 96% .
80	4t	842	 96% .
81	4u	569	 88% 12%
81	4v	569	 88% 12%
82	4w	701	 73% 27%
83	4x	149	 99% .


























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Mol	Chain	Length	Quality of chain
84	4y	718	 92% 8%
85	4z	640	 82% 18%
86	5A	374	 60% 39%
86	5B	374	 60% 39%
87	5C	369	 75% 24%
87	5D	369	 74% 25%
87	5E	369	 75% 25%
87	5F	369	 75% 24%
87	5G	369	 74% 25%
87	5H	369	 75% 25%
87	5I	369	 75% 24%
87	5J	369	 47% 53%
88	5K	483	 31% 68%
88	5S	483	 34% 66%
88	5T	483	 95% 5%
88	5U	483	 95% 5%
88	5V	483	 61% 39%
88	5W	483	 98%
88	5X	483	 78% 21%
89	5L	262	 91% 9%
89	5M	262	 91% 9%
90	5N	272	 87% 12%
90	5O	272	 88% 12%
90	5P	272	 88% 12%
90	5Q	272	 88% 12%



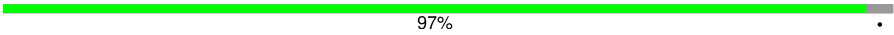
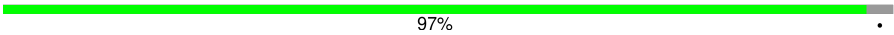
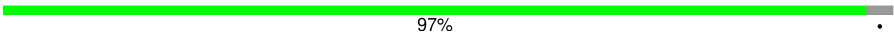
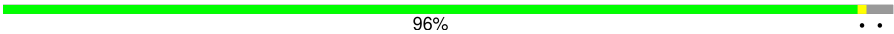









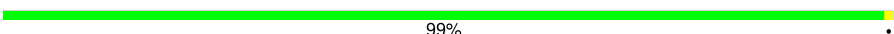


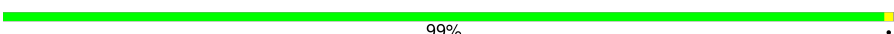


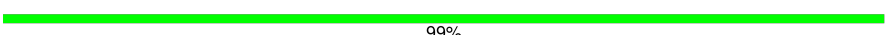
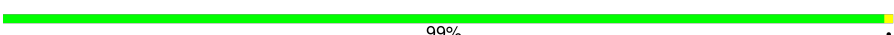


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Mol	Chain	Length	Quality of chain
90	5R	272	
91	5Y	515	
91	5Z	515	
91	6A	515	
92	5a	581	
93	5b	709	
94	5c	1027	
95	5d	1347	
96	5e	299	
97	5f	682	
98	5g	616	
99	5h	4599	
99	5i	4599	
100	5j	4674	
100	5k	4674	
101	5l	864	
102	5m	809	
103	5n	687	
104	5o	413	
105	5p	124	
105	7i	124	
105	8i	124	
105	9i	124	
106	5q	118	
106	7l	118	

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Mol	Chain	Length	Quality of chain
106	8l	118	
106	9l	118	
107	5r	98	
107	7m	98	
107	8m	98	
107	9m	98	
108	5y	116	
108	7q	116	
108	8q	116	
108	9q	116	
109	6B	348	
109	6C	348	
109	6D	348	
109	6E	348	
109	6F	348	
109	6G	348	
109	6H	348	
109	6I	348	
109	6J	348	
109	6K	348	
109	6L	348	
109	6M	348	
109	6N	348	
109	6O	348	
109	6P	348	


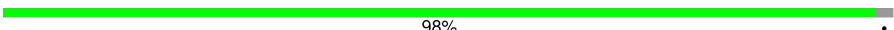
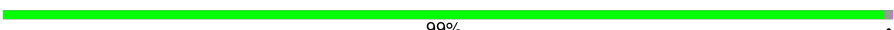
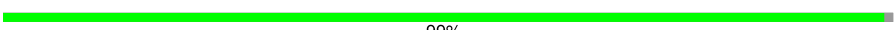






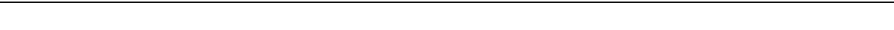

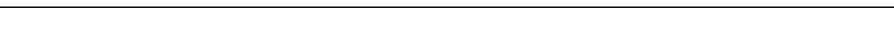
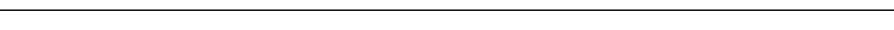
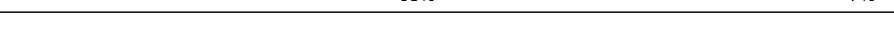


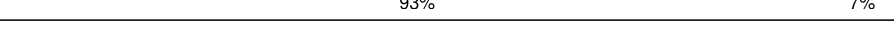







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Mol	Chain	Length	Quality of chain
109	6Q	348	
110	6R	266	
110	6S	266	
110	6T	266	
110	6U	266	
110	6V	266	
110	6W	266	
110	6X	266	
110	6Y	266	
110	6Z	266	
110	7A	266	
110	7B	266	
110	7C	266	
110	7D	266	
110	7E	266	
110	7F	266	
110	7G	266	
110	7H	266	
110	7I	266	
110	7J	266	
110	7K	266	
110	9Z	266	
111	6a	4246	
112	6b	4142	
113	6c	4112	











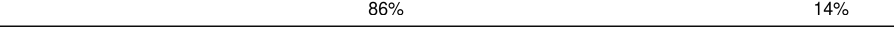
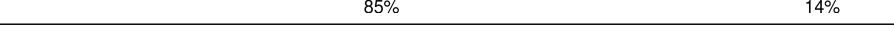
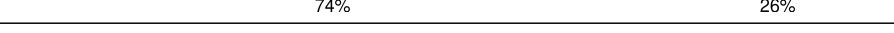
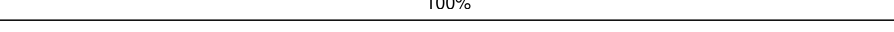
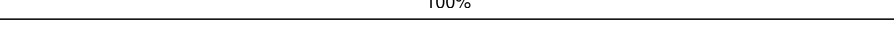
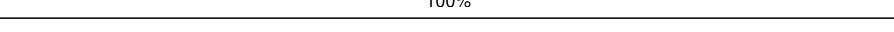

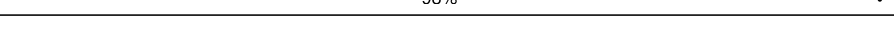
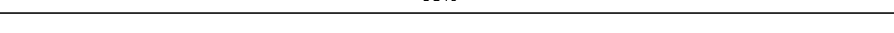






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Mol	Chain	Length	Quality of chain
114	6d	4242	 94% 6%
115	6e	4152	 98% .
116	6f	376	 99% .
116	6g	376	 99% .
117	6h	394	 100%
118	6i	421	 97% ..
119	6j	433	 90% 9%
120	6k	235	 71% 29%
120	6l	235	 90% . 9%
120	6m	235	 94% 6%
121	6n	373	 52% 48%
122	6o	274	 88% 11%
123	6p	306	 54% 46%
124	6q	363	 93% 7%
125	6r	481	 75% 24%
126	6s	470	 79% 21%
127	6t	165	 93% 7%
128	6u	186	 82% . 18%
129	7L	270	 57% 43%
129	7M	270	 57% 43%
130	7N	325	 50% 50%
130	7O	325	 50% 50%
130	7P	325	 50% 50%
131	7Q	191	 84% 16%
131	7R	191	 84% 16%

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Mol	Chain	Length	Quality of chain
131	7S	191	 84% 16%
132	7T	320	 50% 50%
132	7U	320	 93% 7%
132	8L	320	 74% 26%
133	7V	278	 86% 14%
133	7W	278	 85% 14%
133	7X	278	 83% 17%
133	7Y	278	 86% 14%
133	7Z	278	 85% 14%
133	8A	278	 83% 17%
133	8B	278	 86% 14%
133	8C	278	 85% 14%
134	7a	4639	 74% 26%
134	7e	4639	 100%
134	8e	4639	 100%
134	9e	4639	 100%
135	7b	4658	 72% 28%
135	7f	4658	 98% .
135	8f	4658	 98% .
135	9f	4658	 98% .
136	7c	570	 59% 40%
136	8c	570	 59% 40%
136	9c	570	 59% . 40%
137	7d	114	 65% . . 30%
137	8d	114	 68% . 30%

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Mol	Chain	Length	Quality of chain
137	9d	114	
138	7g	602	
138	8g	602	
138	9g	602	
139	7h	655	
139	8h	655	
139	9h	655	
140	7j	112	
140	8j	112	
140	9j	112	
141	7r	125	
141	8r	125	
141	9r	125	
142	7s	668	
142	8s	668	
142	9a	668	
142	9s	668	
143	7t	575	
143	8t	575	
143	9b	575	
143	9t	575	
144	8D	269	
144	8E	269	
144	8F	269	
144	8G	269	




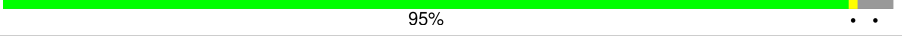




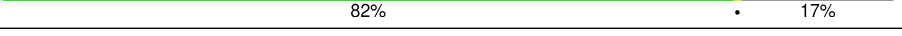

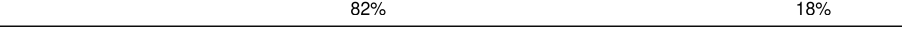
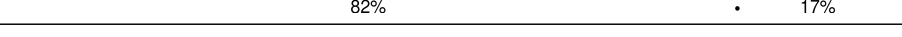

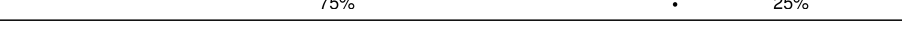


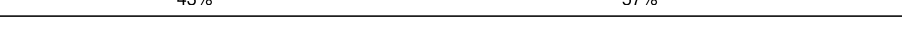

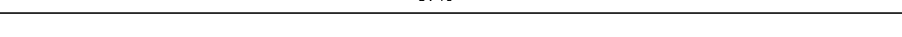






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Mol	Chain	Length	Quality of chain
144	8H	269	
144	8I	269	
144	8J	269	
144	8K	269	
145	8M	420	
145	8N	420	
145	8O	420	
145	8P	420	
145	8Q	420	
145	8R	420	
145	8S	420	
145	8T	420	
146	8U	337	
146	8V	337	
146	8W	337	
146	8X	337	
146	8Y	337	
146	8Z	337	
146	9A	337	
146	9B	337	
147	9C	329	
147	9D	329	
147	9E	329	
148	9F	350	
148	9G	350	

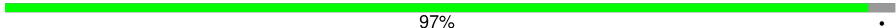
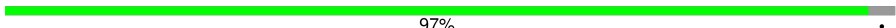
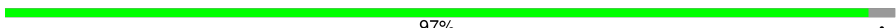
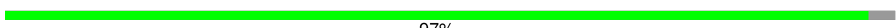









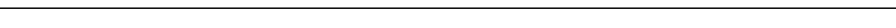

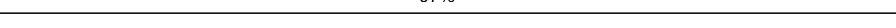
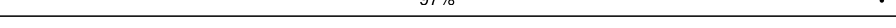
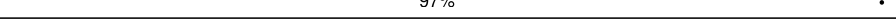
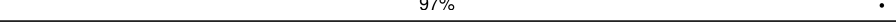
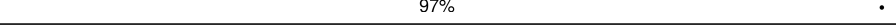
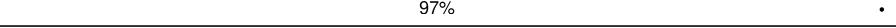
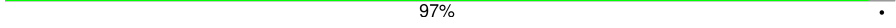
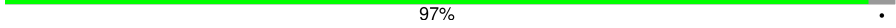
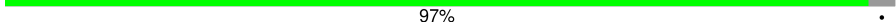
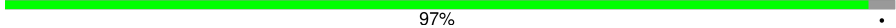
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Mol	Chain	Length	Quality of chain
148	9H	350	
148	9I	350	
149	9J	286	
149	9K	286	
149	9L	286	
150	9M	193	
150	9N	193	
150	9O	193	
150	9P	193	
150	9Q	193	
150	9R	193	
150	9S	193	
151	9T	191	
151	9U	191	
151	9V	191	
152	9W	166	
152	9X	166	
152	9Y	166	
153	AA	442	
153	AC	442	
153	AE	442	
153	AG	442	
153	AI	442	
153	AK	442	
153	AM	442	

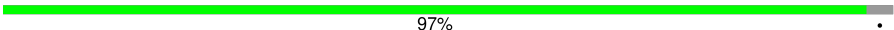
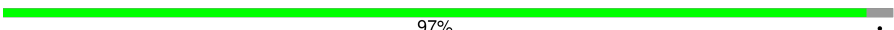
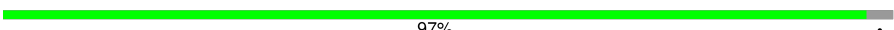
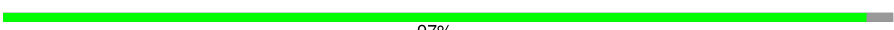






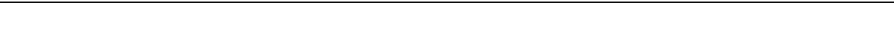

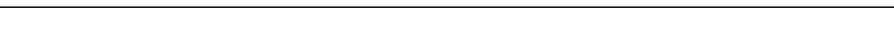
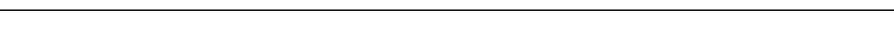
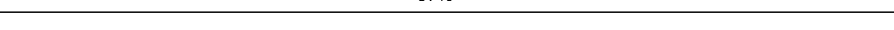
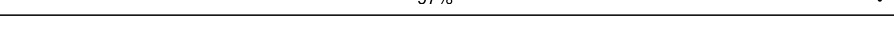
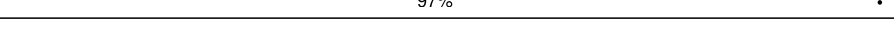
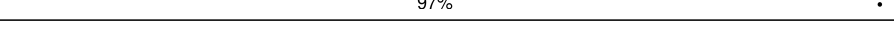
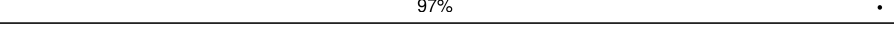
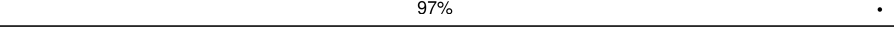
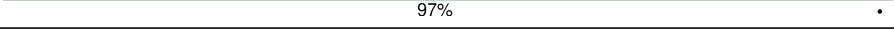
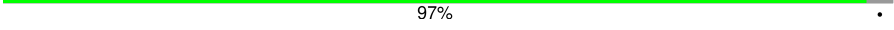
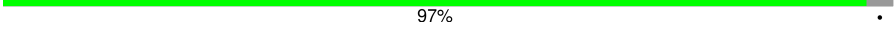
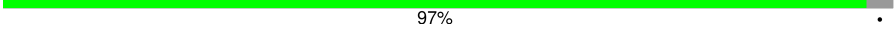
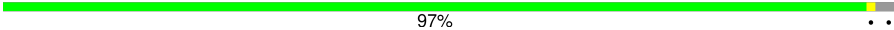
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Mol	Chain	Length	Quality of chain
153	AO	442	 97% .
153	AQ	442	 97% .
153	AS	442	 97% .
153	AU	442	 97% .
153	AW	442	 97% .
153	AY	442	 97% .
153	Aa	442	 97% .
153	Ac	442	 97% . .
153	Ae	442	 97% . .
153	Ag	442	 97% .
153	Ai	442	 97% .
153	Ak	442	 97% .
153	Am	442	 97% .
153	Ao	442	 97% . .
153	BA	442	 97% .
153	BC	442	 97% .
153	BG	442	 97% .
153	BI	442	 97% .
153	BK	442	 97% .
153	BM	442	 97% .
153	BO	442	 97% .
153	BQ	442	 97% .
153	BS	442	 97% .
153	BU	442	 97% .
153	BW	442	 97% .

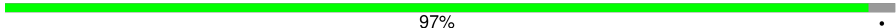
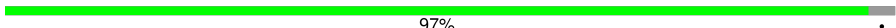
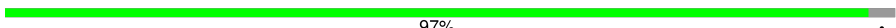
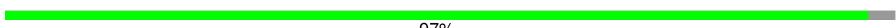









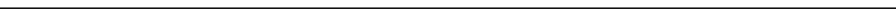

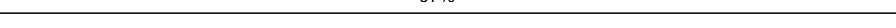
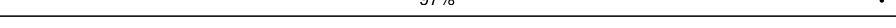
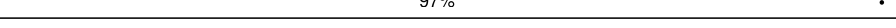
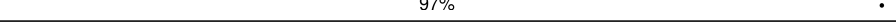
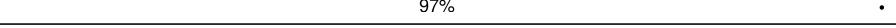
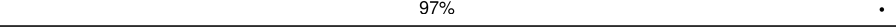
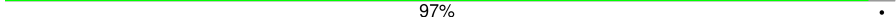
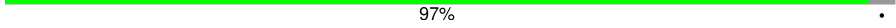
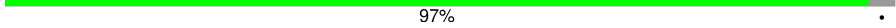
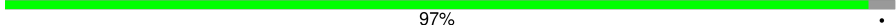
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Mol	Chain	Length	Quality of chain
153	BY	442	 97% .
153	CA	442	 97% .
153	CC	442	 97% .
153	CE	442	 97% .
153	CH	442	 97% .
153	CK	442	 96% ..
153	CM	442	 97% .
153	CO	442	 97% .
153	CQ	442	 97% .
153	CS	442	 97% ..
153	CU	442	 97% ..
153	CW	442	 96% ..
153	CY	442	 97% .
153	DA	442	 97% .
153	DC	442	 97% .
153	DE	442	 97% .
153	DG	442	 97% .
153	DI	442	 97% .
153	DK	442	 97% .
153	DN	442	 97% .
153	DP	442	 97% .
153	DR	442	 97% .
153	DT	442	 97% .
153	DV	442	 97% ..
153	DX	442	 97% .

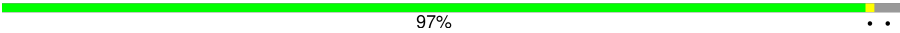
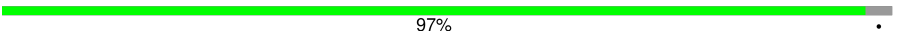
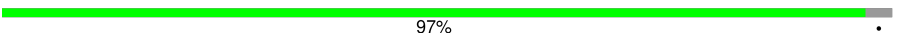
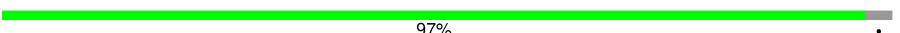

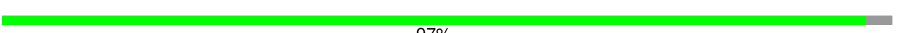









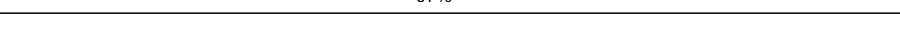
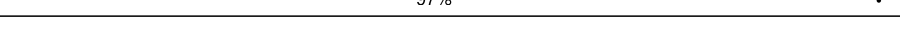
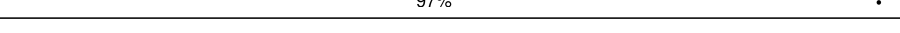
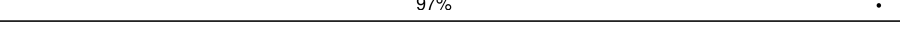
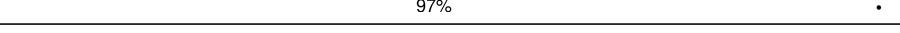
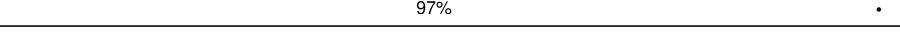
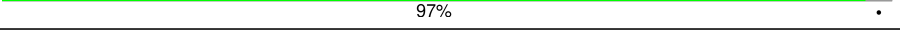
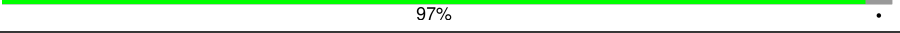
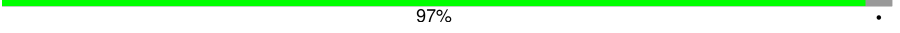
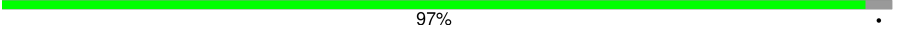
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Mol	Chain	Length	Quality of chain
153	DZ	442	 97% .
153	EB	442	 97% .
153	ED	442	 97% .
153	EF	442	 97% .
153	EH	442	 97% .
153	EJ	442	 97% .
153	EL	442	 97% .
153	EN	442	 97% .
153	ER	442	 97% .
153	ET	442	 97% .
153	EV	442	 97% .
153	EX	442	 97% .
153	EZ	442	 97% .
153	FB	442	 97% .
153	FD	442	 97% .
153	FF	442	 97% .
153	FH	442	 97% .
153	FJ	442	 97% .
153	FL	442	 97% .
153	FN	442	 97% .
153	FP	442	 97% .
153	FR	442	 97% .
153	FT	442	 97% .
153	FV	442	 97% .
153	FX	442	 96% ..

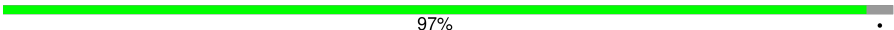
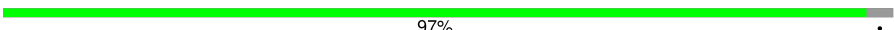
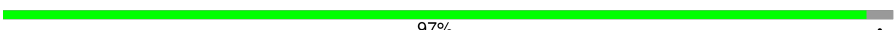
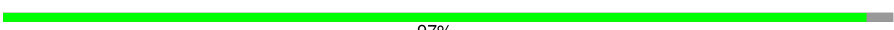






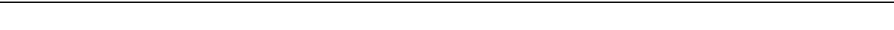

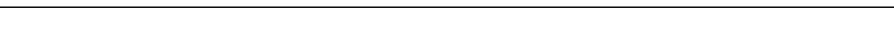
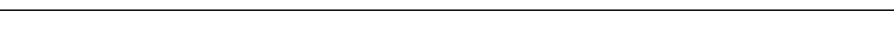
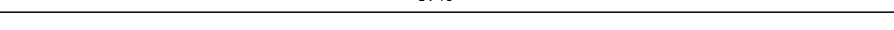
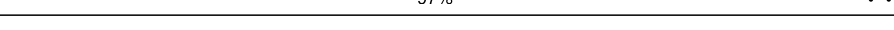
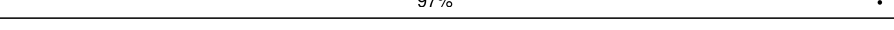
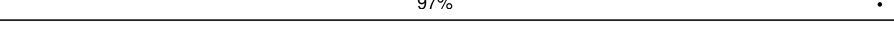
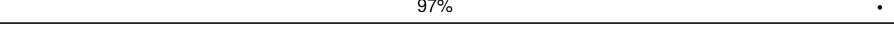
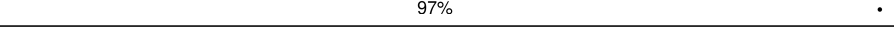
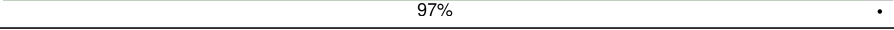
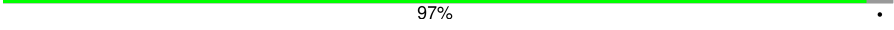
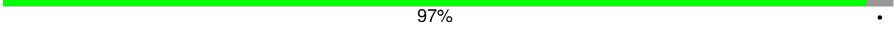
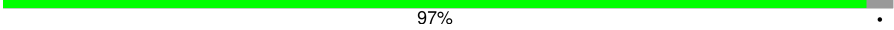
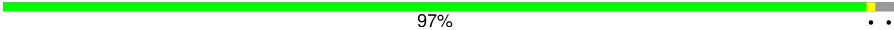
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Mol	Chain	Length	Quality of chain
153	FZ	442	 97% . .
153	GB	442	 97% .
153	GD	442	 97% .
153	GF	442	 97% .
153	GH	442	 97% .
153	GJ	442	 97% .
153	GL	442	 97% .
153	GN	442	 97% .
153	GP	442	 97% .
153	GR	442	 97% . .
153	GT	442	 97% .
153	GV	442	 97% .
153	GX	442	 97% .
153	GZ	442	 97% .
153	HB	442	 97% .
153	HD	442	 97% .
153	HF	442	 97% .
153	HH	442	 97% .
153	HJ	442	 97% .
153	HL	442	 97% .
153	HN	442	 97% .
153	HP	442	 97% .
153	HR	442	 97% .
153	HT	442	 97% .
153	HV	442	 97% .

*Continued on next page...*

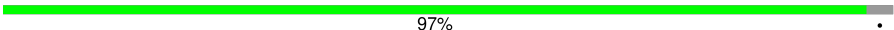
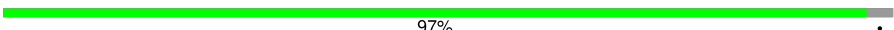
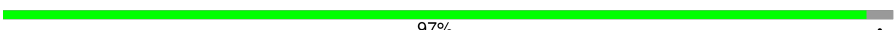
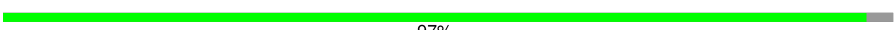






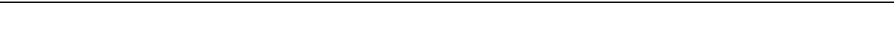

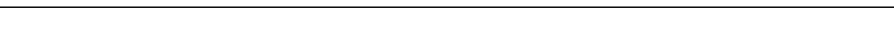
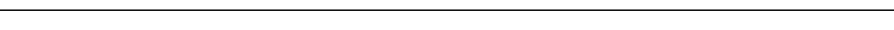
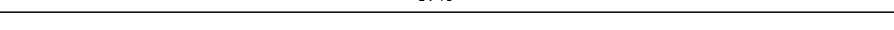
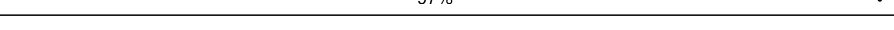
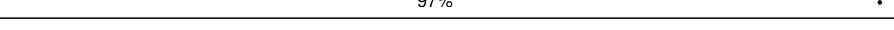
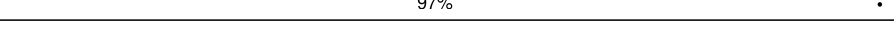
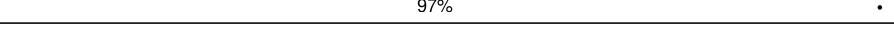
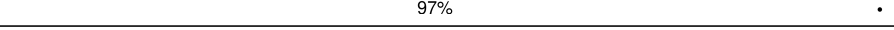
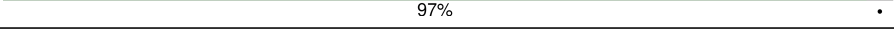
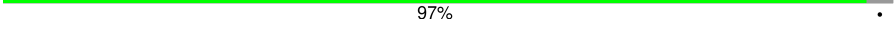
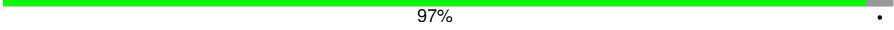
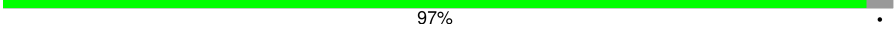
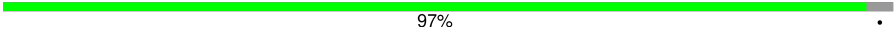
*Continued from previous page...*

Mol	Chain	Length	Quality of chain
153	HX	442	
153	HZ	442	
153	IB	442	
153	ID	442	
153	IF	442	
153	IH	442	
153	IJ	442	
153	IL	442	
153	IN	442	
153	IP	442	
153	IR	442	
153	IT	442	
153	IV	442	
153	IX	442	
153	IZ	442	
153	JB	442	
153	JD	442	
153	JF	442	
153	JG	442	
153	JI	442	
153	JK	442	
153	JM	442	
153	JO	442	
153	JQ	442	
153	JS	442	

*Continued on next page...*

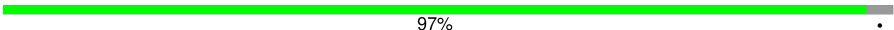
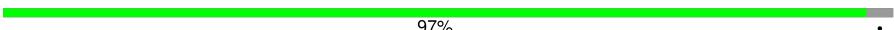
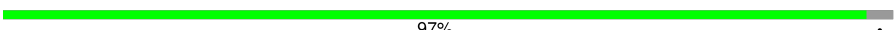
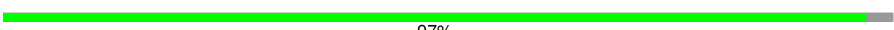






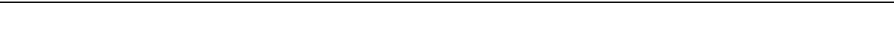

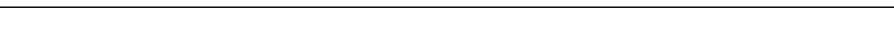
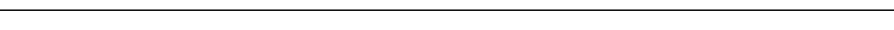
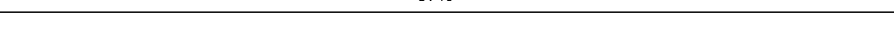
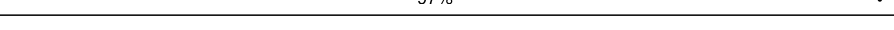
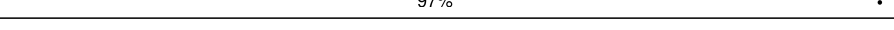
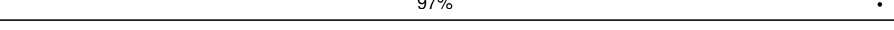
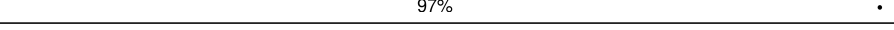
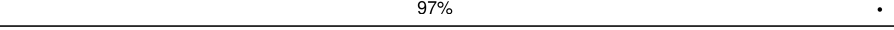
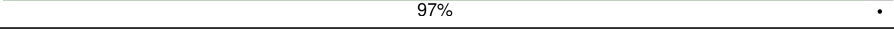
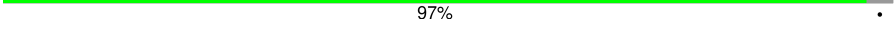
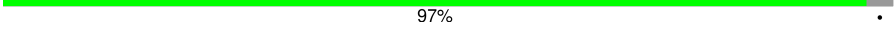
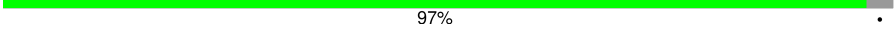
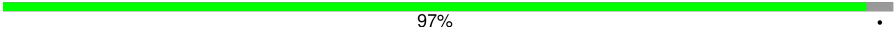


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Mol	Chain	Length	Quality of chain
153	JU	442	 97% .
153	JW	442	 97% .
153	JY	442	 97% .
153	KA	442	 97% .
153	KC	442	 97% .
153	KE	442	 97% .
153	KG	442	 97% .
153	KI	442	 97% .
153	KK	442	 97% .
153	KM	442	 97% .
153	KO	442	 97% .
153	KQ	442	 97% .
153	KS	442	 97% .
153	KU	442	 97% .
153	KW	442	 97% .
153	KY	442	 97% .
153	LA	442	 97% .
153	LC	442	 97% .
153	LE	442	 97% .
153	LG	442	 97% .
153	LI	442	 97% .
153	LK	442	 97% .
153	LM	442	 97% .
153	LO	442	 97% .
153	LQ	442	 97% .

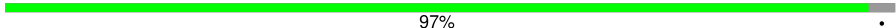
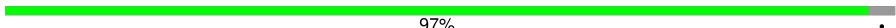
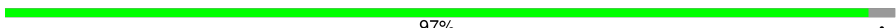
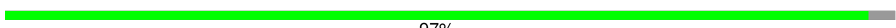









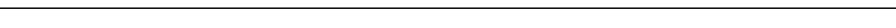

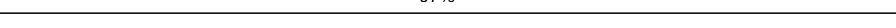
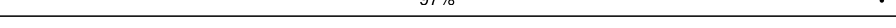
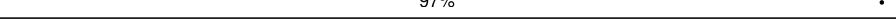
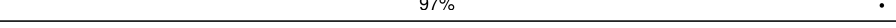
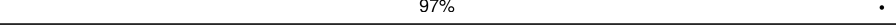
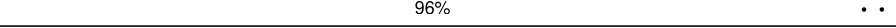
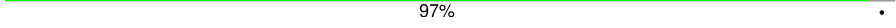
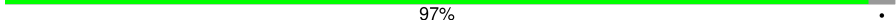
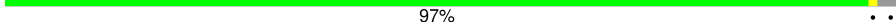
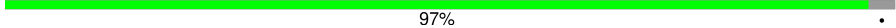
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Mol	Chain	Length	Quality of chain
153	LS	442	 97% .
153	LU	442	 97% .
153	LW	442	 97% .
153	LY	442	 97% .
153	MA	442	 97% .
153	MC	442	 97% .
153	ME	442	 97% .
153	MG	442	 97% .
153	MI	442	 97% .
153	MK	442	 97% .
153	MM	442	 97% .
153	MO	442	 97% .
153	MQ	442	 97% .
153	MU	442	 97% .
153	MW	442	 97% .
153	MY	442	 97% .
153	NA	442	 97% .
153	NC	442	 97% .
153	NE	442	 97% .
153	NG	442	 97% .
153	NI	442	 97% .
153	NK	442	 97% .
153	NM	442	 97% .
153	NO	442	 97% .
153	NQ	442	 97% .

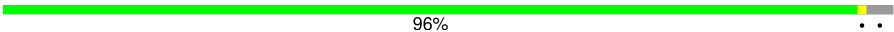
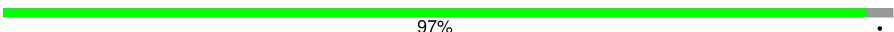
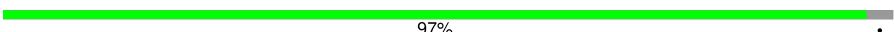

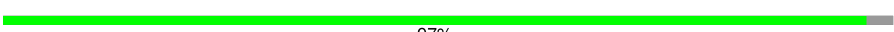







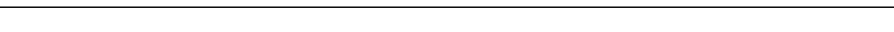

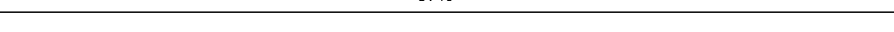
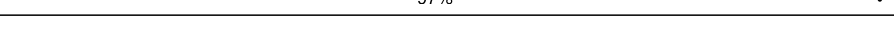
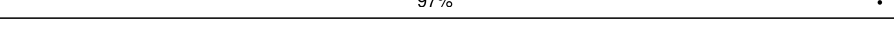
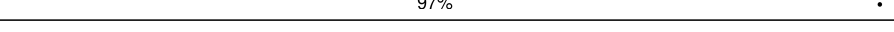
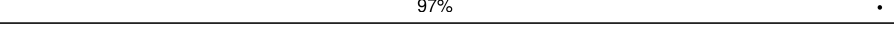
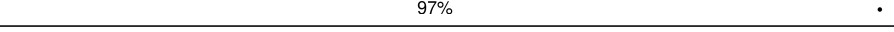
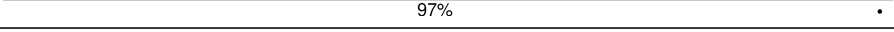
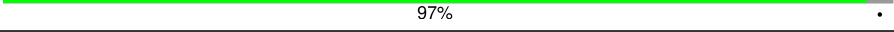
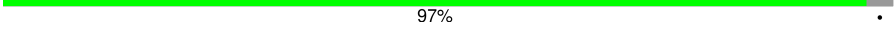
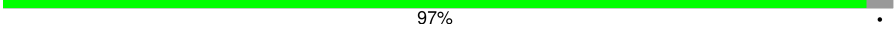
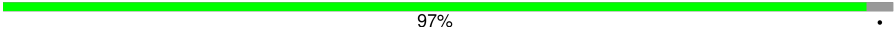
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Mol	Chain	Length	Quality of chain
153	NS	442	 97% .
153	NU	442	 97% .
153	NY	442	 97% .
153	OA	442	 97% .
153	OC	442	 97% .
153	OE	442	 97% .
153	OG	442	 97% .
153	OI	442	 97% .
153	OK	442	 97% .
153	OM	442	 97% .
153	OO	442	 97% .
153	OQ	442	 97% .
153	OS	442	 97% .
153	OU	442	 97% .
153	OW	442	 97% .
153	OY	442	 97% .
153	PA	442	 97% .
153	PD	442	 97% .
153	PF	442	 97% .
153	PH	442	 96% . .
153	PJ	442	 97% .
153	PL	442	 97% .
153	PN	442	 97% . .
153	PP	442	 97% .
153	PR	442	 97% .

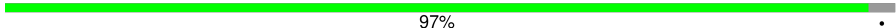
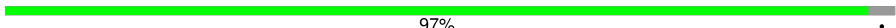
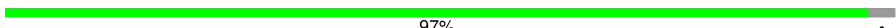
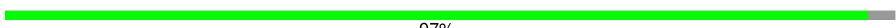









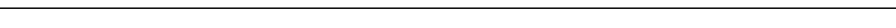

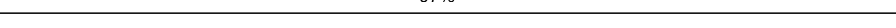
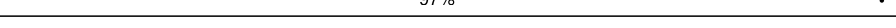
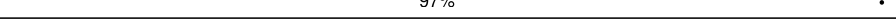
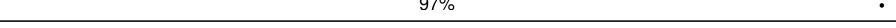
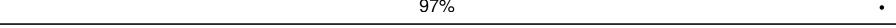
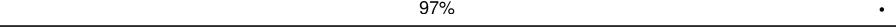
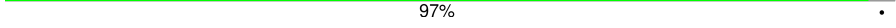
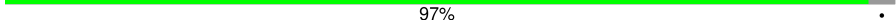
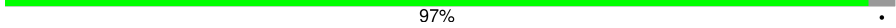
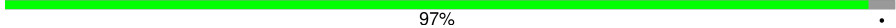
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Mol	Chain	Length	Quality of chain
153	PT	442	 96% ..
153	PV	442	 97% .
153	PX	442	 97% .
153	PZ	442	 97% ..
153	QB	442	 97% .
153	QD	442	 97% .
153	QF	442	 97% .
153	QH	442	 97% .
153	QJ	442	 97% .
153	QL	442	 97% .
153	QN	442	 97% .
153	QP	442	 97% .
153	QR	442	 97% .
153	QT	442	 97% .
153	QV	442	 97% .
153	QX	442	 97% .
153	QZ	442	 97% .
153	RB	442	 97% .
153	RD	442	 97% .
153	RF	442	 97% .
153	RH	442	 97% .
153	RJ	442	 97% .
153	RL	442	 97% .
153	RN	442	 97% .
153	RP	442	 97% .

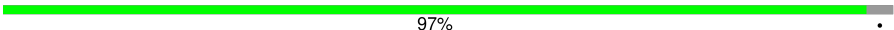
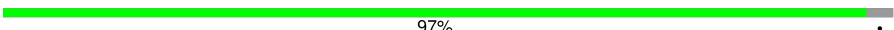
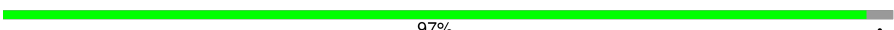
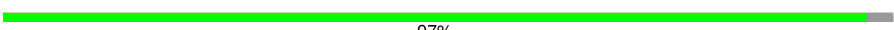






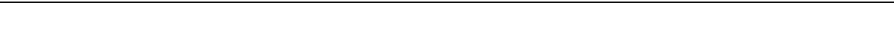

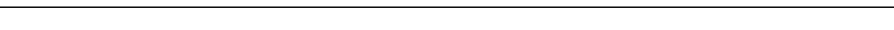
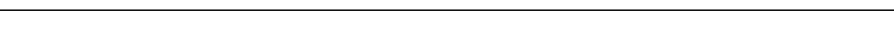
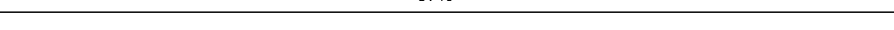
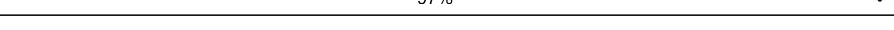
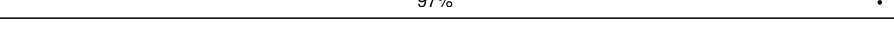
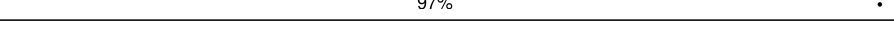
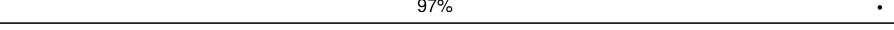
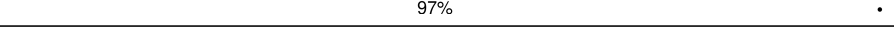
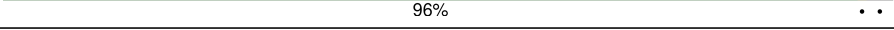
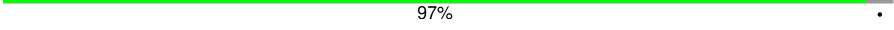
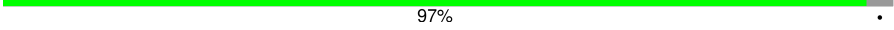
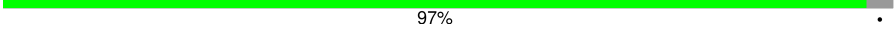
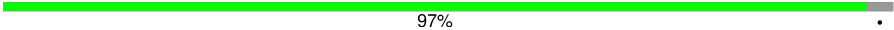
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Mol	Chain	Length	Quality of chain
153	RR	442	 97% .
153	RT	442	 97% .
153	RV	442	 97% .
153	RX	442	 97% .
153	RZ	442	 97% .
153	SB	442	 97% ..
153	SD	442	 97% .
153	SF	442	 97% .
153	SH	442	 97% .
153	SJ	442	 97% .
153	SL	442	 97% .
153	SN	442	 97% .
153	SP	442	 97% .
153	SR	442	 97% .
153	ST	442	 97% ..
153	SV	442	 97% .
153	SX	442	 97% .
153	SZ	442	 97% .
153	TB	442	 97% .
153	TD	442	 97% .
153	TF	442	 97% .
153	TH	442	 97% .
153	TJ	442	 97% .
153	TL	442	 97% .
153	TN	442	 97% .


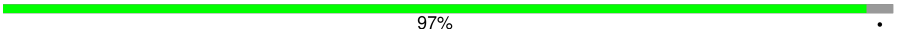
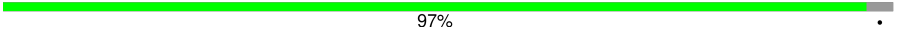
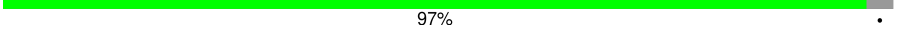
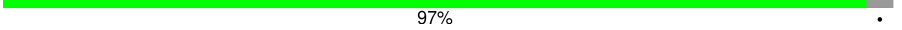
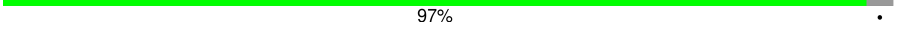
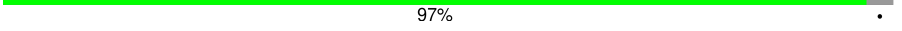
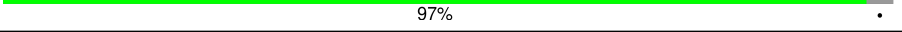
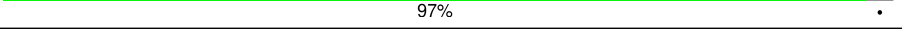
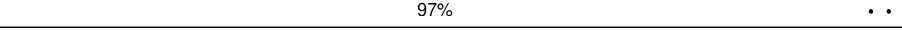
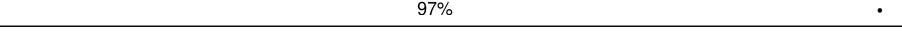
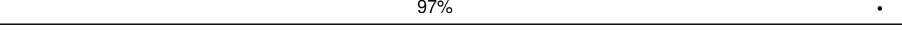
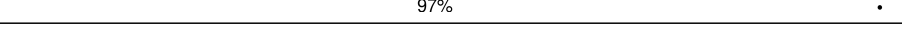
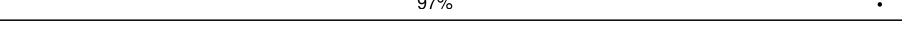
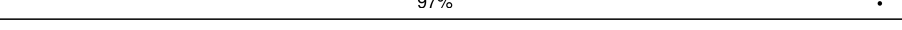
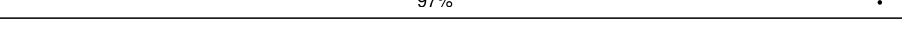
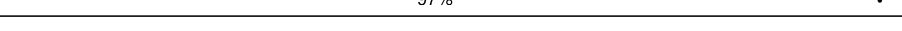
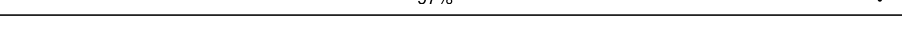
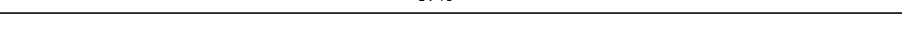
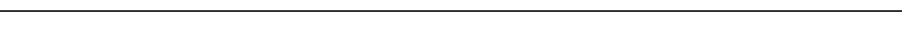

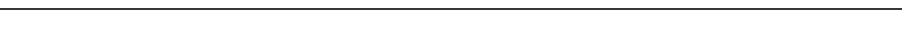
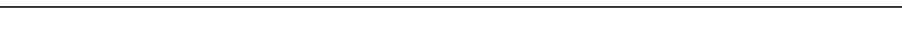


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Mol	Chain	Length	Quality of chain
153	TP	442	 97% .
153	TS	442	 97% .
153	TU	442	 97% .
153	TW	442	 97% .
153	TY	442	 97% .
153	UA	442	 97% .
153	UC	442	 97% .
153	UE	442	 97% .
153	UG	442	 97% .
153	UI	442	 97% .
153	UK	442	 97% .
153	UM	442	 97% .
153	UO	442	 97% .
153	UQ	442	 97% .
153	US	442	 97% .
153	UU	442	 97% .
153	UX	442	 97% .
153	UZ	442	 97% .
153	VB	442	 97% .
153	VD	442	 96% . .
153	VF	442	 97% .
153	VH	442	 97% .
153	VJ	442	 97% .
153	VL	442	 97% .
153	VN	442	 97% .

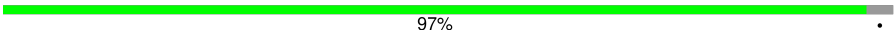
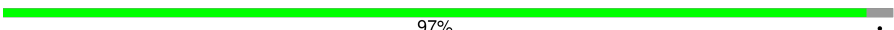
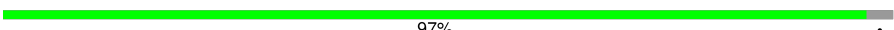
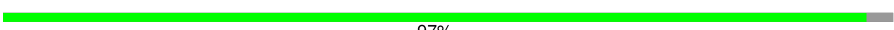






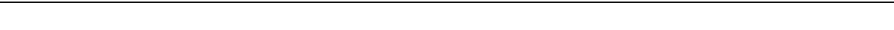

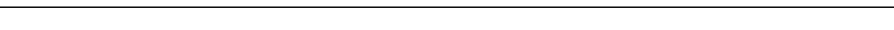
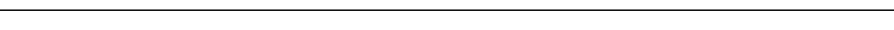
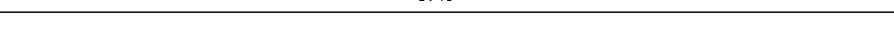
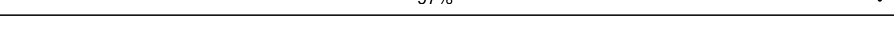
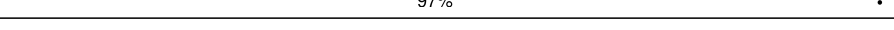
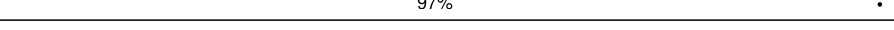
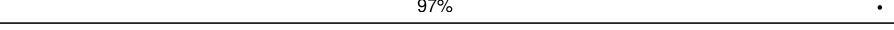
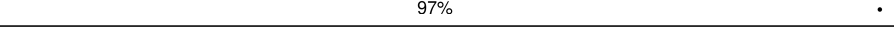
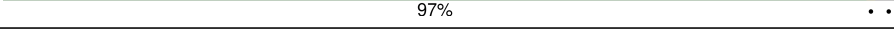
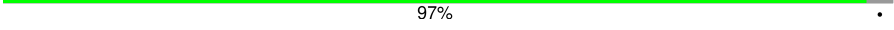
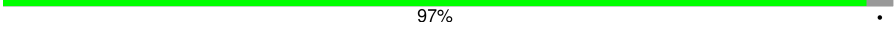
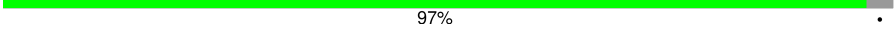
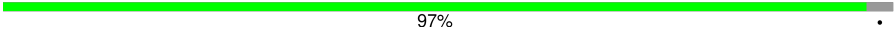
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Mol	Chain	Length	Quality of chain
153	VP	442	 96% . .
153	VR	442	 97% .
153	VT	442	 97% .
153	VV	442	 97% .
153	VX	442	 97% .
153	VZ	442	 97% .
153	WB	442	 97% .
153	WD	442	 97% .
153	WF	442	 97% .
153	WH	442	 97% . .
153	WJ	442	 97% .
153	WL	442	 97% .
153	WN	442	 97% .
153	WP	442	 97% .
153	WR	442	 97% .
153	WT	442	 97% .
153	WV	442	 97% .
153	WX	442	 97% .
153	WZ	442	 97% .
153	XB	442	 97% .
153	XD	442	 97% .
153	XF	442	 97% .
153	XH	442	 97% .
153	XJ	442	 97% . .
153	XL	442	 97% .

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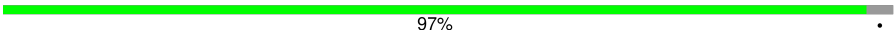
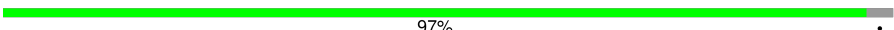
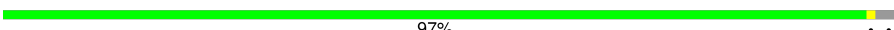
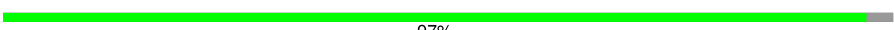






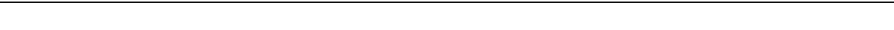

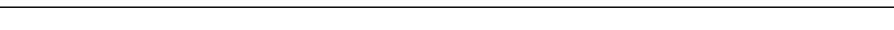
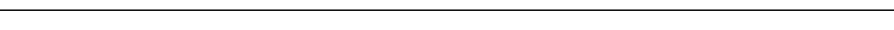
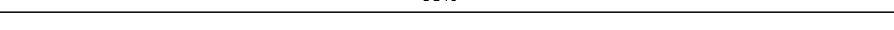
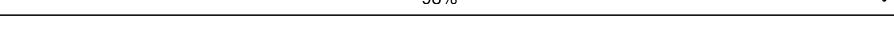
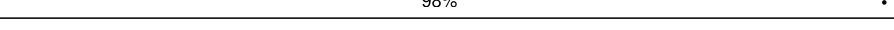
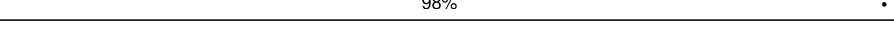
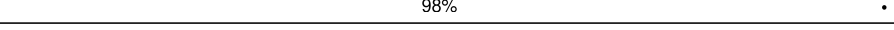
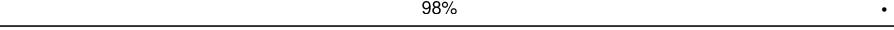
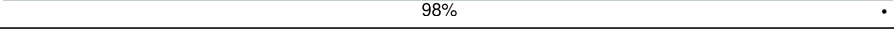
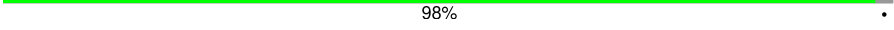
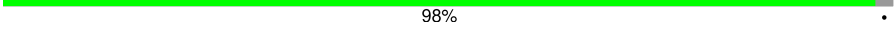
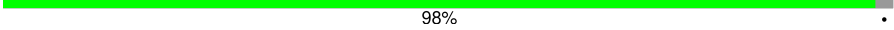
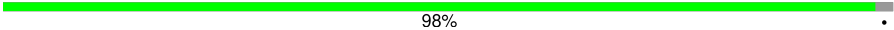
*Continued from previous page...*

Mol	Chain	Length	Quality of chain
153	XN	442	
153	XP	442	
153	XR	442	
153	XT	442	
153	XV	442	
153	XX	442	
153	XZ	442	
153	YB	442	
153	YD	442	
153	YF	442	
153	YH	442	
153	YK	442	
153	YM	442	
153	YO	442	
153	YQ	442	
153	YS	442	
153	YU	442	
153	YW	442	
153	YY	442	
153	ZA	442	
153	ZC	442	
153	ZE	442	
153	ZG	442	
153	ZI	442	
153	ZK	442	

*Continued on next page...*

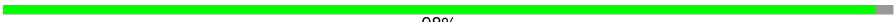













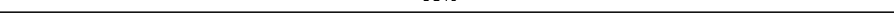
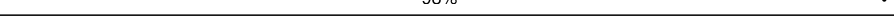
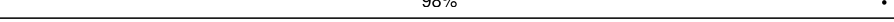
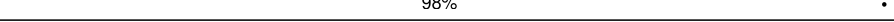
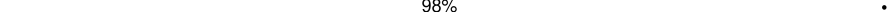
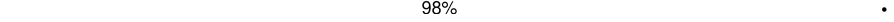
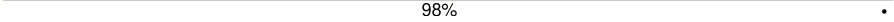
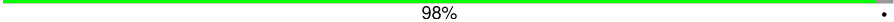
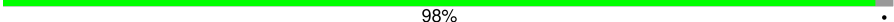
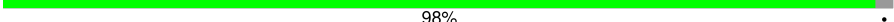
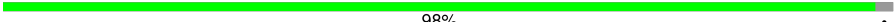


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Mol	Chain	Length	Quality of chain
153	ZM	442	 97% .
153	ZO	442	 97% .
153	ZQ	442	 97% ..
153	ZS	442	 97% .
153	ZU	442	 97% .
153	ZW	442	 97% .
153	ZY	442	 97% .
154	AB	451	 98% .
154	AD	451	 98% .
154	AF	451	 98% .
154	AH	451	 98% .
154	AJ	451	 98% .
154	AL	451	 98% .
154	AN	451	 98% .
154	AP	451	 98% .
154	AR	451	 98% .
154	AT	451	 98% .
154	AV	451	 98% .
154	AX	451	 98% .
154	AZ	451	 98% .
154	Ab	451	 98% .
154	Ad	451	 98% .
154	Af	451	 98% .
154	Ah	451	 98% .
154	Aj	451	 98% .

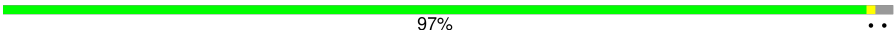
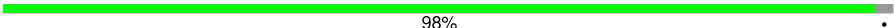
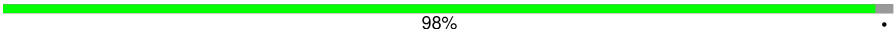
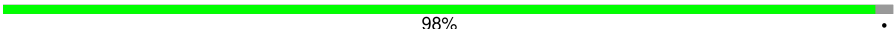


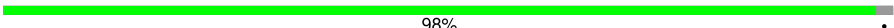
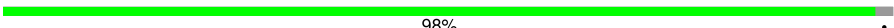
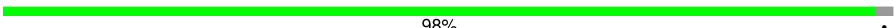
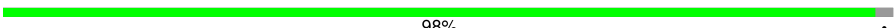
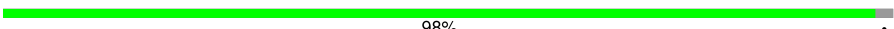

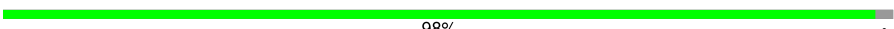


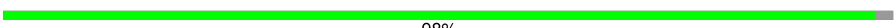
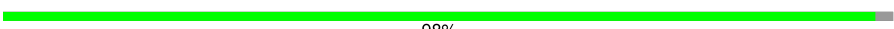
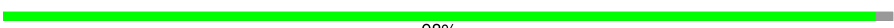
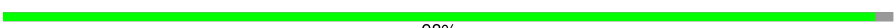
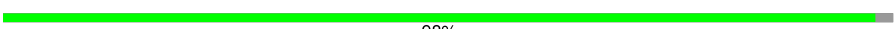
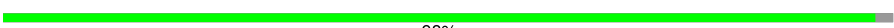

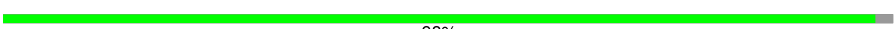


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Mol	Chain	Length	Quality of chain
154	Al	451	 98% .
154	An	451	 98% .
154	Ap	451	 98% .
154	BB	451	 98% .
154	BD	451	 98% .
154	BF	451	 98% .
154	BH	451	 98% .
154	BJ	451	 98% .
154	BL	451	 98% .
154	BN	451	 98% .
154	BP	451	 98% .
154	BR	451	 98% .
154	BT	451	 98% .
154	BV	451	 98% .
154	BX	451	 98% .
154	BZ	451	 98% .
154	CB	451	 98% .
154	CD	451	 98% .
154	CF	451	 98% .
154	CI	451	 98% .
154	CJ	451	 98% .
154	CL	451	 98% .
154	CN	451	 98% .
154	CP	451	 98% .
154	CR	451	 98% .


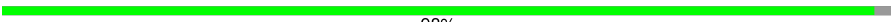













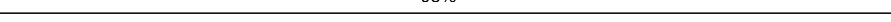
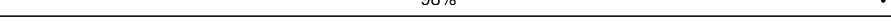
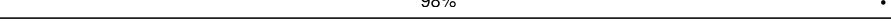
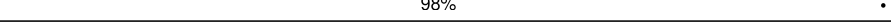
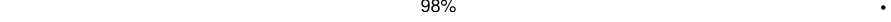
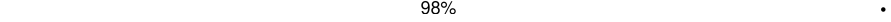
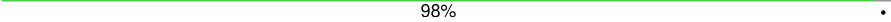
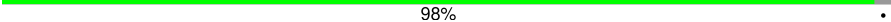
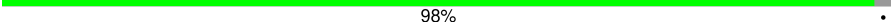
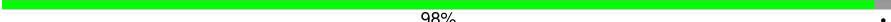
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Mol	Chain	Length	Quality of chain
154	CT	451	 97% ..
154	CV	451	 98% .
154	CX	451	 98% .
154	CZ	451	 98% .
154	DB	451	 98% .
154	DD	451	 98% .
154	DF	451	 98% .
154	DH	451	 98% .
154	DJ	451	 98% .
154	DL	451	 98% .
154	DM	451	 98% .
154	DO	451	 98% .
154	DQ	451	 98% .
154	DS	451	 98% .
154	DU	451	 98% .
154	DW	451	 98% .
154	DY	451	 98% .
154	EA	451	 98% .
154	EC	451	 98% .
154	EE	451	 98% .
154	EG	451	 98% .
154	EI	451	 98% .
154	EK	451	 98% .
154	EM	451	 98% .
154	EO	451	 98% .


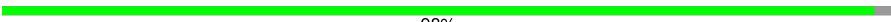













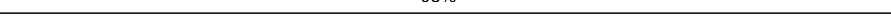
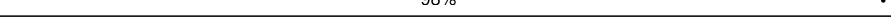
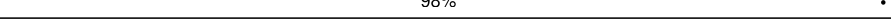
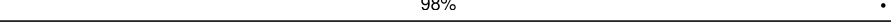
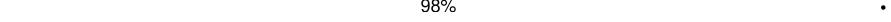
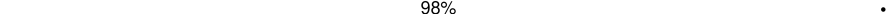
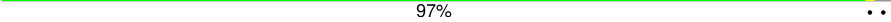
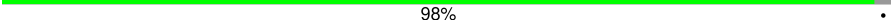
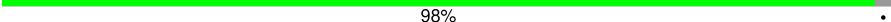
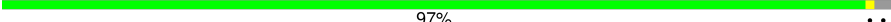
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Mol	Chain	Length	Quality of chain
154	EQ	451	 98% .
154	ES	451	 98% .
154	EU	451	 98% .
154	EW	451	 98% .
154	EY	451	 98% .
154	FA	451	 98% .
154	FC	451	 98% .
154	FE	451	 98% .
154	FG	451	 98% .
154	FI	451	 97% ..
154	FK	451	 98% .
154	FM	451	 98% .
154	FO	451	 98% .
154	FQ	451	 98% .
154	FS	451	 98% .
154	FW	451	 98% .
154	FY	451	 98% .
154	GA	451	 98% .
154	GC	451	 98% .
154	GE	451	 98% .
154	GG	451	 98% .
154	GI	451	 98% .
154	GK	451	 98% .
154	GM	451	 98% .
154	GO	451	 98% .

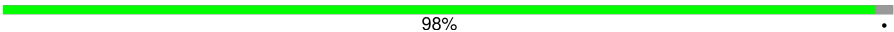
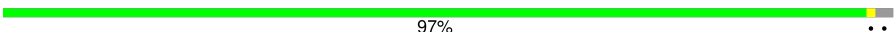
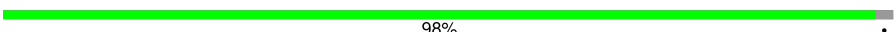

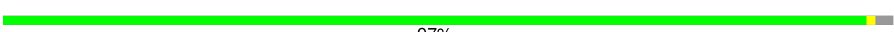







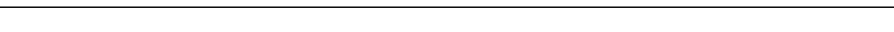

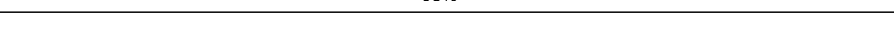
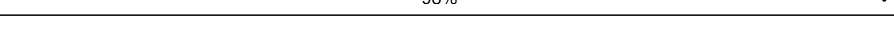
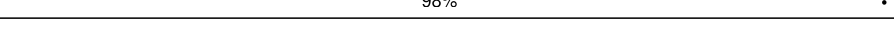
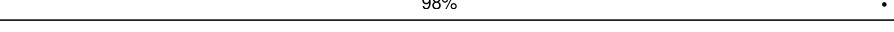
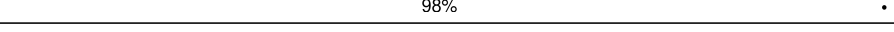
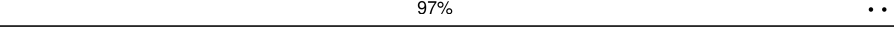
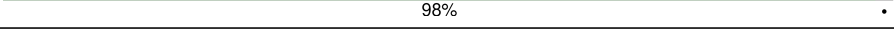
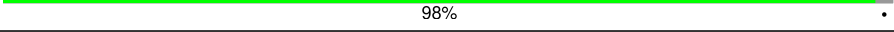
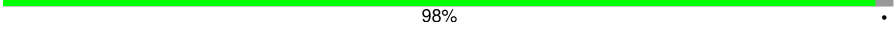
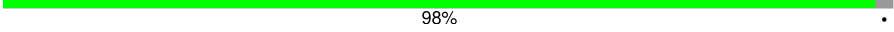
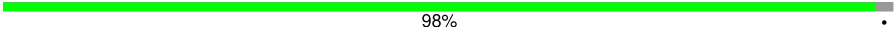
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Mol	Chain	Length	Quality of chain
154	GQ	451	 98% .
154	GS	451	 98% .
154	GU	451	 98% .
154	GW	451	 98% .
154	HA	451	 97% ..
154	HC	451	 98% .
154	HE	451	 97% .
154	HG	451	 98% .
154	HI	451	 98% .
154	HK	451	 98% .
154	HM	451	 98% .
154	HO	451	 98% .
154	HQ	451	 98% .
154	HS	451	 98% .
154	HU	451	 98% .
154	HW	451	 98% .
154	HY	451	 98% .
154	IA	451	 98% .
154	IE	451	 98% .
154	IG	451	 98% .
154	II	451	 97% ..
154	IK	451	 98% .
154	IM	451	 98% .
154	IO	451	 97% ..
154	IQ	451	 98% .


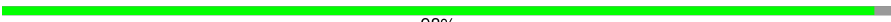













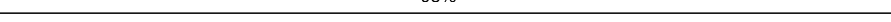
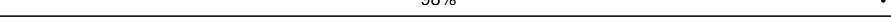
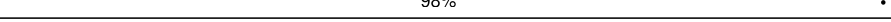
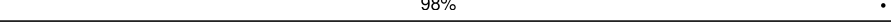
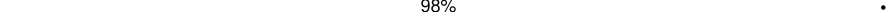
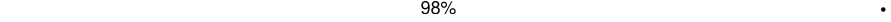
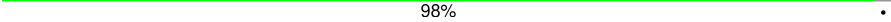
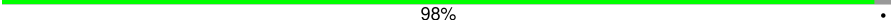
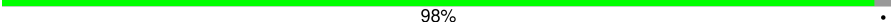
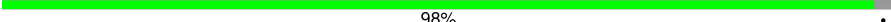
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Mol	Chain	Length	Quality of chain
154	IS	451	 98% .
154	IU	451	 97% ..
154	IW	451	 98% .
154	IY	451	 98% .
154	JA	451	 97% ..
154	JC	451	 98% .
154	JE	451	 98% .
154	JH	451	 98% .
154	JJ	451	 98% .
154	JL	451	 98% .
154	JN	451	 98% .
154	JP	451	 98% .
154	JR	451	 98% .
154	JT	451	 98% .
154	JV	451	 98% .
154	JX	451	 98% .
154	JZ	451	 98% .
154	KB	451	 98% .
154	KD	451	 97% ..
154	KF	451	 98% .
154	KH	451	 98% .
154	KJ	451	 98% .
154	KL	451	 98% .
154	KN	451	 98% .
154	KP	451	 98% .

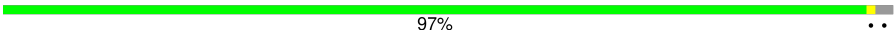
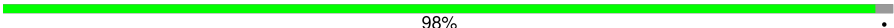
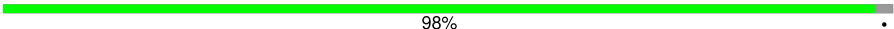
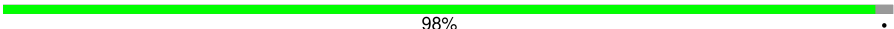


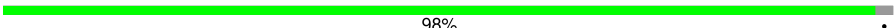
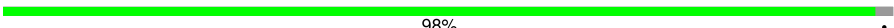
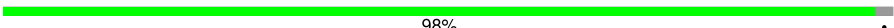
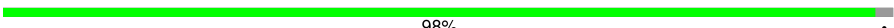
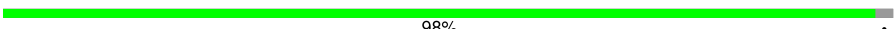

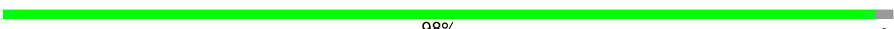


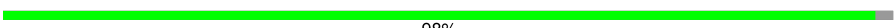
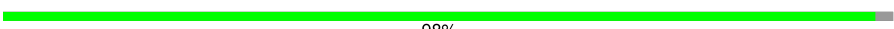
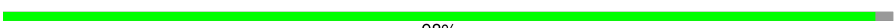
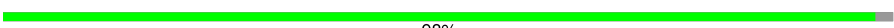
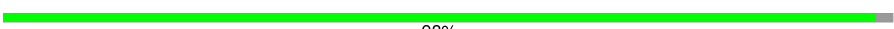
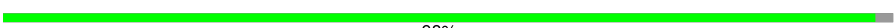

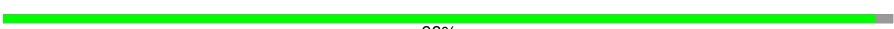


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Mol	Chain	Length	Quality of chain
154	KR	451	 98% .
154	KT	451	 98% .
154	KV	451	 98% .
154	KX	451	 98% .
154	KZ	451	 98% .
154	LB	451	 98% .
154	LD	451	 98% .
154	LF	451	 98% .
154	LH	451	 98% .
154	LJ	451	 98% .
154	LL	451	 98% .
154	LN	451	 98% .
154	LP	451	 98% .
154	LR	451	 97% ..
154	LT	451	 98% .
154	LV	451	 98% .
154	LX	451	 98% .
154	LZ	451	 98% .
154	MB	451	 98% .
154	MD	451	 98% .
154	MF	451	 98% .
154	MH	451	 98% .
154	MJ	451	 98% .
154	ML	451	 98% .
154	MN	451	 98% .

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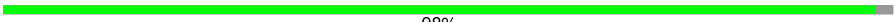













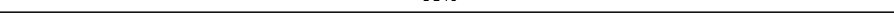
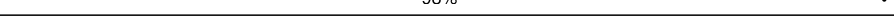
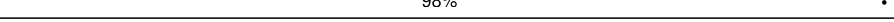
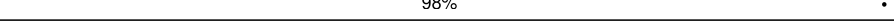
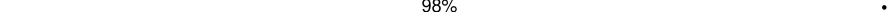
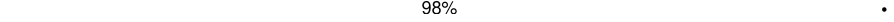
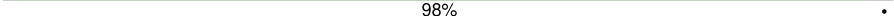
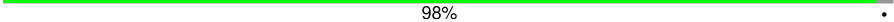
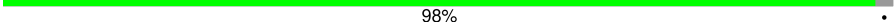
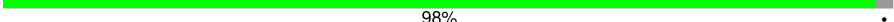
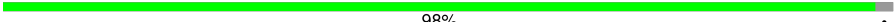
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Mol	Chain	Length	Quality of chain
154	MP	451	 97% ..
154	MR	451	 98% .
154	MT	451	 98% .
154	MV	451	 98% .
154	MX	451	 98% .
154	MZ	451	 98% .
154	NB	451	 98% .
154	ND	451	 98% .
154	NF	451	 98% .
154	NH	451	 98% .
154	NJ	451	 98% .
154	NL	451	 98% .
154	NN	451	 98% .
154	NP	451	 98% .
154	NR	451	 98% .
154	NT	451	 98% .
154	NV	451	 98% .
154	NX	451	 98% .
154	NZ	451	 98% .
154	OB	451	 98% .
154	OD	451	 98% .
154	OF	451	 98% .
154	OH	451	 98% .
154	OJ	451	 98% .
154	OL	451	 98% .

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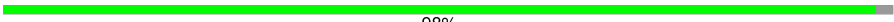













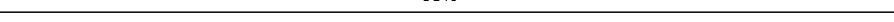
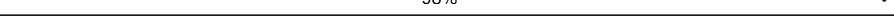
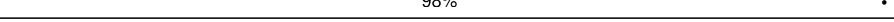
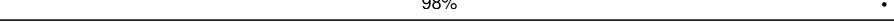
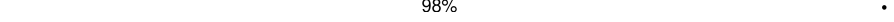
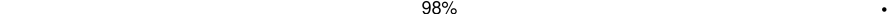
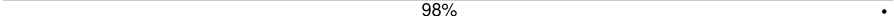
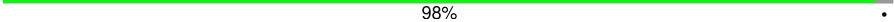
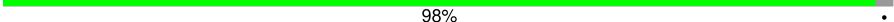
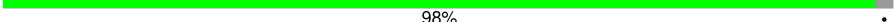
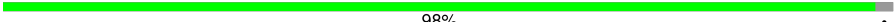


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Mol	Chain	Length	Quality of chain
154	ON	451	 98% .
154	OP	451	 98% .
154	OR	451	 98% .
154	OT	451	 98% .
154	OV	451	 98% .
154	OX	451	 98% .
154	OZ	451	 98% .
154	PC	451	 98% .
154	PE	451	 98% .
154	PG	451	 98% .
154	PI	451	 97% ..
154	PK	451	 98% .
154	PM	451	 98% .
154	PO	451	 98% .
154	PQ	451	 98% .
154	PS	451	 98% .
154	PU	451	 98% .
154	PW	451	 98% .
154	PY	451	 98% .
154	QA	451	 98% .
154	QC	451	 98% .
154	QE	451	 98% .
154	QG	451	 98% .
154	QI	451	 98% .
154	QK	451	 98% .

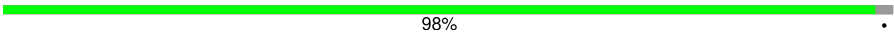
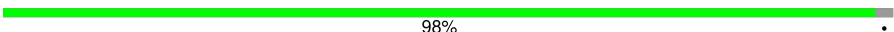
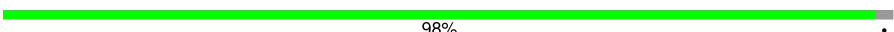

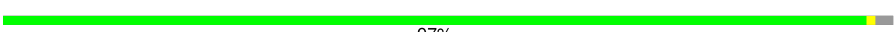







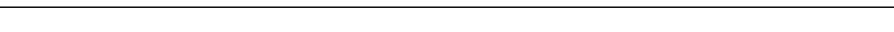

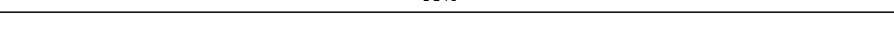
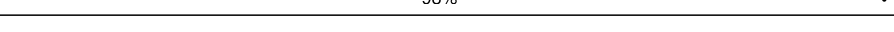
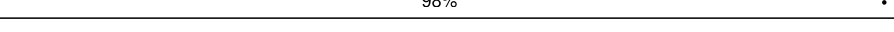
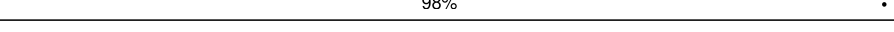
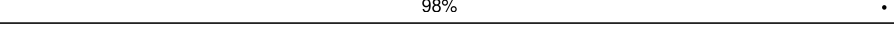
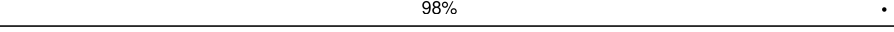
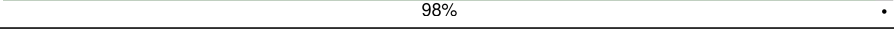
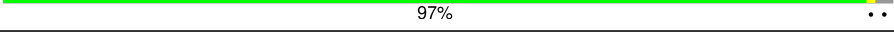
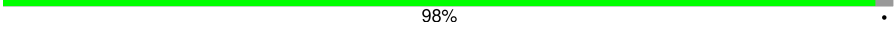
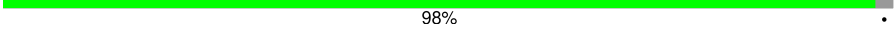
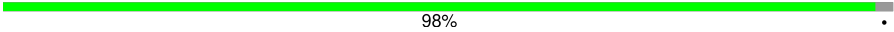
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Mol	Chain	Length	Quality of chain
154	QM	451	 98% .
154	QO	451	 98% .
154	QQ	451	 98% .
154	QS	451	 98% .
154	QU	451	 98% .
154	QW	451	 98% .
154	QY	451	 98% .
154	RA	451	 98% .
154	RC	451	 98% .
154	RE	451	 98% .
154	RG	451	 98% .
154	RI	451	 98% .
154	RK	451	 98% .
154	RM	451	 98% .
154	RO	451	 98% .
154	RQ	451	 98% .
154	RS	451	 98% .
154	RU	451	 98% .
154	RW	451	 98% .
154	RY	451	 98% .
154	SA	451	 98% .
154	SC	451	 98% .
154	SE	451	 98% .
154	SG	451	 98% .
154	SI	451	 98% .

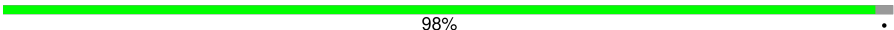
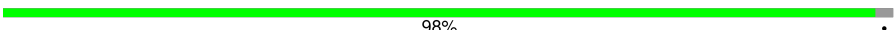
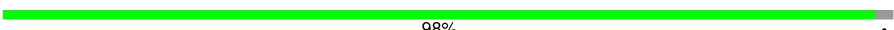
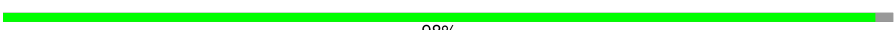






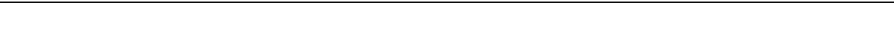

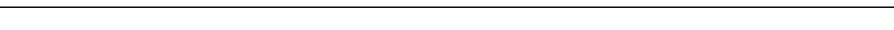
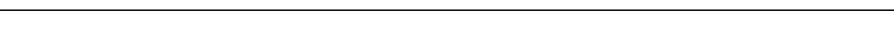
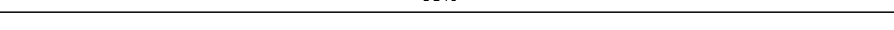
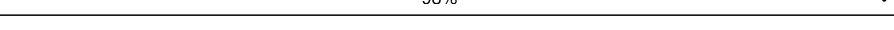
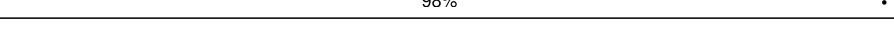
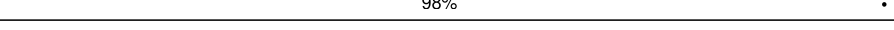
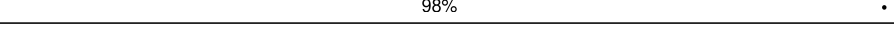
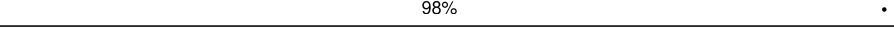
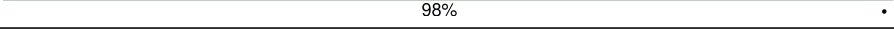
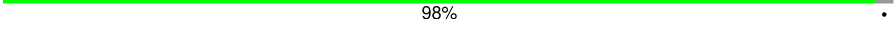
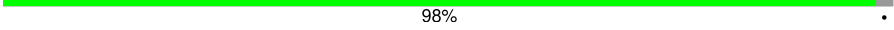
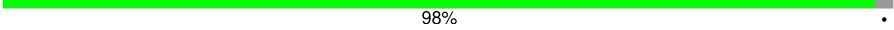
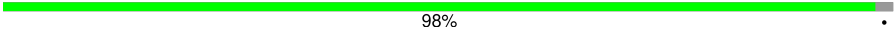
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Mol	Chain	Length	Quality of chain
154	SK	451	 98% .
154	SM	451	 98% .
154	SO	451	 98% .
154	SQ	451	 98% .
154	SS	451	 97% ..
154	SU	451	 97% ..
154	SW	451	 98% .
154	SY	451	 98% .
154	TA	451	 98% .
154	TC	451	 98% .
154	TE	451	 98% .
154	TG	451	 97% ..
154	TI	451	 98% .
154	TK	451	 98% .
154	TM	451	 98% .
154	TO	451	 98% .
154	TQ	451	 98% .
154	TR	451	 98% .
154	TT	451	 98% .
154	TV	451	 98% .
154	TX	451	 97% ..
154	TZ	451	 98% .
154	UB	451	 98% .
154	UD	451	 98% .
154	UF	451	 98% .

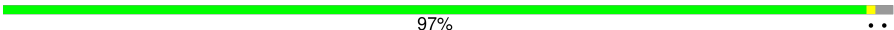
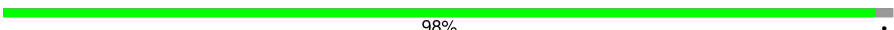
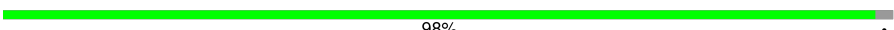
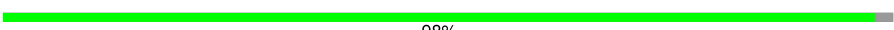






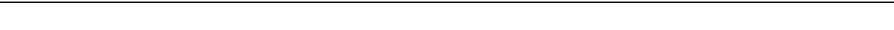

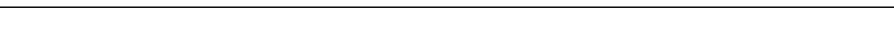
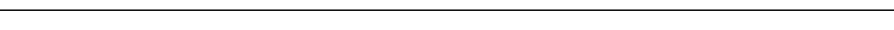
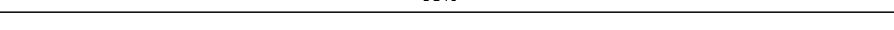
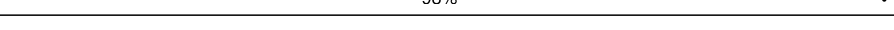
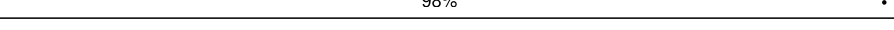
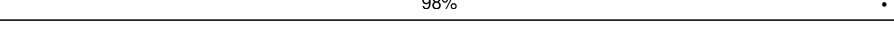
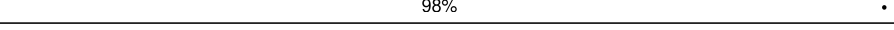
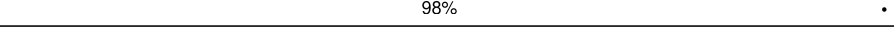
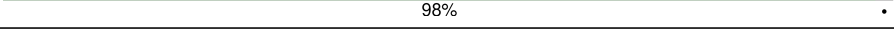
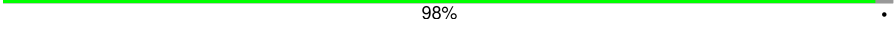
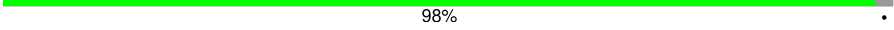
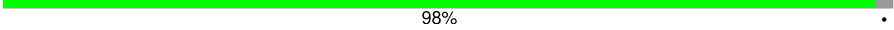
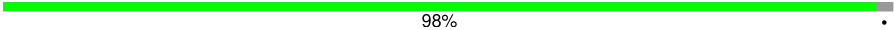
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Mol	Chain	Length	Quality of chain
154	UH	451	 98% .
154	UJ	451	 98% .
154	UL	451	 98% .
154	UN	451	 98% .
154	UP	451	 98% .
154	UR	451	 98% .
154	UT	451	 98% .
154	UW	451	 98% .
154	UY	451	 98% .
154	VA	451	 98% .
154	VC	451	 97% ..
154	VE	451	 98% .
154	VG	451	 98% .
154	VI	451	 98% .
154	VK	451	 98% .
154	VM	451	 98% .
154	VO	451	 98% .
154	VQ	451	 98% .
154	VS	451	 98% .
154	VU	451	 98% .
154	VW	451	 98% .
154	VY	451	 98% .
154	WA	451	 98% .
154	WC	451	 98% .
154	WE	451	 98% .

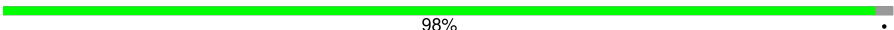
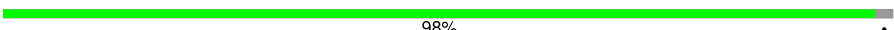

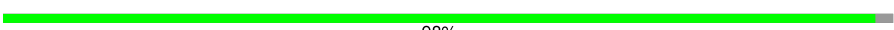








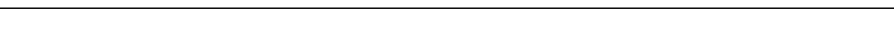
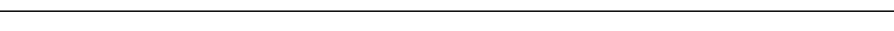
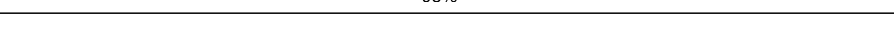
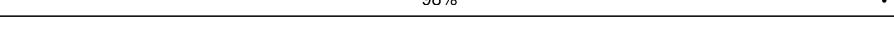
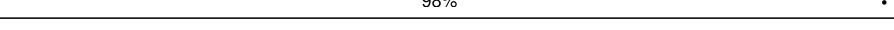
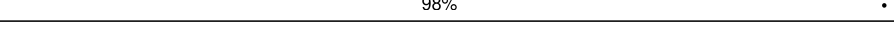
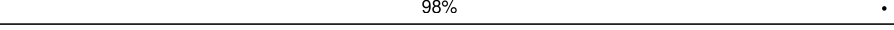
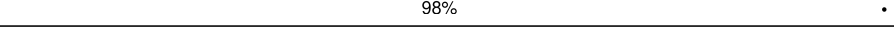
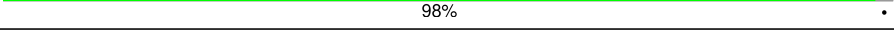
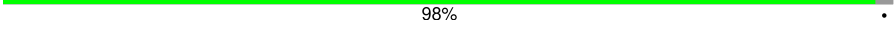
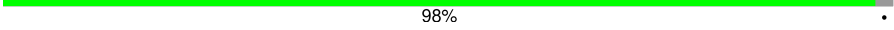
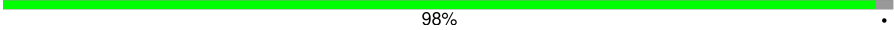
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Mol	Chain	Length	Quality of chain
154	WG	451	 97% ..
154	WI	451	 98% .
154	WK	451	 98% .
154	WM	451	 98% .
154	WO	451	 98% .
154	WQ	451	 98% .
154	WS	451	 98% .
154	WU	451	 98% .
154	WW	451	 98% .
154	WY	451	 98% .
154	XA	451	 98% .
154	XC	451	 98% .
154	XE	451	 98% .
154	XG	451	 98% .
154	XI	451	 98% .
154	XK	451	 98% .
154	XM	451	 98% .
154	XO	451	 98% .
154	XQ	451	 98% .
154	XS	451	 98% .
154	XU	451	 98% .
154	XW	451	 98% .
154	XY	451	 98% .
154	YA	451	 98% .
154	YC	451	 98% .

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Mol	Chain	Length	Quality of chain
154	YE	451	 98% .
154	YG	451	 98% .
154	YJ	451	 98% .
154	YL	451	 98% .
154	YN	451	 98% .
154	YP	451	 97% ..
154	YR	451	 98% .
154	YT	451	 98% .
154	YV	451	 98% .
154	YX	451	 98% .
154	YZ	451	 98% .
154	ZB	451	 98% .
154	ZD	451	 98% .
154	ZF	451	 98% .
154	ZH	451	 98% .
154	ZJ	451	 98% .
154	ZL	451	 98% .
154	ZN	451	 98% .
154	ZP	451	 98% .
154	ZR	451	 98% .
154	ZT	451	 98% .
154	ZV	451	 98% .
154	ZX	451	 98% .
154	ZZ	451	 98% .

## 2 Entry composition

There are 160 unique types of molecules in this entry. The entry contains 3895227 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 EF-hand domain-containing family member C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0A	662	Total	C	N	O	S	0	0
			5390	3423	929	1014	24		
1	0B	734	Total	C	N	O	S	0	0
			5972	3782	1036	1125	29		
1	0C	730	Total	C	N	O	S	0	0
			5933	3757	1026	1121	29		
1	0D	662	Total	C	N	O	S	0	0
			5390	3423	929	1014	24		
1	0E	734	Total	C	N	O	S	0	0
			5972	3782	1036	1125	29		
1	0F	730	Total	C	N	O	S	0	0
			5933	3757	1026	1121	29		

- Molecule 2 is a protein called EF-hand domain-containing family member C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0G	730	Total	C	N	O	S	0	0
			5862	3718	1025	1088	31		
2	0H	730	Total	C	N	O	S	0	0
			5862	3718	1025	1088	31		
2	0I	730	Total	C	N	O	S	0	0
			5862	3718	1025	1088	31		

- Molecule 3 is a protein called Rib72 protein-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	0J	665	Total	C	N	O	S	0	0
			5389	3412	938	1011	28		
3	0K	665	Total	C	N	O	S	0	0
			5389	3412	938	1011	28		
3	0L	665	Total	C	N	O	S	0	0
			5389	3412	938	1011	28		

- Molecule 4 is a protein called CMF34/CARP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	0M	758	Total	C	N	O	S	0	0
			6157	3875	1093	1162	27		
4	0N	758	Total	C	N	O	S	0	0
			6157	3875	1093	1162	27		

- Molecule 5 is a protein called Flagellar protofilament ribbon protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	0O	193	Total	C	N	O	S	0	0
			1673	1019	327	319	8		
5	0P	363	Total	C	N	O	S	0	0
			3131	1907	616	594	14		
5	0Q	361	Total	C	N	O	S	0	0
			3116	1899	614	591	12		
5	0R	236	Total	C	N	O	S	0	0
			2036	1237	405	386	8		
5	0S	347	Total	C	N	O	S	0	0
			3014	1834	597	569	14		
5	0T	309	Total	C	N	O	S	0	0
			2687	1635	529	513	10		

- Molecule 6 is a protein called Cilia- and flagella-associated protein 53.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	0U	32	Total	C	N	O		0	0
			277	174	55	48			
6	0V	456	Total	C	N	O	S	0	0
			3874	2350	786	723	15		
6	0W	456	Total	C	N	O	S	0	0
			3874	2350	786	723	15		
6	0X	290	Total	C	N	O	S	0	0
			2454	1478	500	465	11		

- Molecule 7 is a protein called Meiosis-specific nuclear structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	0Y	153	Total	C	N	O	S	0	0
			1299	795	251	251	2		
7	0Z	423	Total	C	N	O	S	0	0
			3586	2179	705	693	9		
7	1A	423	Total	C	N	O	S	0	0
			3586	2179	705	693	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	1B	126	Total	C	N	O	S	0	0
			1052	636	209	201	6		

- Molecule 8 is a protein called KIAA1430 homologue.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	0a	96	Total	C	N	O	S	0	0
			828	505	167	152	4		
8	0b	134	Total	C	N	O	S	0	0
			1155	706	234	210	5		
8	0c	134	Total	C	N	O	S	0	0
			1155	706	234	210	5		
8	0d	134	Total	C	N	O	S	0	0
			1155	706	234	210	5		
8	0e	134	Total	C	N	O	S	0	0
			1155	706	234	210	5		
8	0f	38	Total	C	N	O	S	0	0
			327	201	67	58	1		

- Molecule 9 is a protein called Starmaker.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	0g	72	Total	C	N	O	S	0	0
			643	395	130	116	2		
9	0h	72	Total	C	N	O	S	0	0
			643	395	130	116	2		
9	0i	72	Total	C	N	O	S	0	0
			643	395	130	116	2		
9	0j	72	Total	C	N	O	S	0	0
			643	395	130	116	2		
9	0k	72	Total	C	N	O	S	0	0
			643	395	130	116	2		
9	0l	72	Total	C	N	O	S	0	0
			643	395	130	116	2		
9	0m	72	Total	C	N	O	S	0	0
			643	395	130	116	2		
9	0n	72	Total	C	N	O	S	0	0
			643	395	130	116	2		
9	0o	72	Total	C	N	O	S	0	0
			643	395	130	116	2		
9	0p	72	Total	C	N	O	S	0	0
			643	395	130	116	2		

- Molecule 10 is a protein called LIM zinc-binding domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	0q	97	Total	C	N	O	S	0	0
			731	450	131	142	8		

- Molecule 11 is a protein called Sperm-tail PG-rich repeat.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	0r	77	Total	C	N	O	S	0	0
			613	391	114	106	2		
11	0s	207	Total	C	N	O	S	0	0
			1606	1018	292	293	3		

- Molecule 12 is a protein called MOP84A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	0t	470	Total	C	N	O	S	0	0
			3548	2199	631	697	21		

- Molecule 13 is a protein called Leucine-rich repeat protein (LRRP).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	0u	483	Total	C	N	O	S	0	0
			3730	2318	679	710	23		

- Molecule 14 is a protein called Coiled-coil domain-containing protein 39.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	0v	419	Total	C	N	O	S	0	0
			3443	2081	674	677	11		
14	0w	487	Total	C	N	O	S	0	0
			3966	2414	768	766	18		

- Molecule 15 is a protein called Coiled-coil domain-containing protein 40.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	0x	421	Total	C	N	O	S	0	0
			3425	2107	614	691	13		
15	0y	459	Total	C	N	O	S	0	0
			3706	2277	671	738	20		

- Molecule 16 is a protein called Cilia- and flagella-associated protein 299.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	0z	223	Total	C	N	O	S	0	0
			1848	1170	325	351	2		

- Molecule 17 is a protein called Nucleoside diphosphate kinase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	1C	332	Total	C	N	O	S	0	0
			2587	1637	446	484	20		
17	1D	332	Total	C	N	O	S	0	0
			2587	1637	446	484	20		
17	1G	332	Total	C	N	O	S	0	0
			2587	1637	446	484	20		

- Molecule 18 is a protein called Nucleoside diphosphate kinase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	1E	343	Total	C	N	O	S	0	0
			2685	1703	472	493	17		
18	1F	343	Total	C	N	O	S	0	0
			2685	1703	472	493	17		

- Molecule 19 is a protein called EF-hand domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1H	419	Total	C	N	O	S	0	0
			3331	2094	584	638	15		
19	1I	419	Total	C	N	O	S	0	0
			3331	2094	584	638	15		

- Molecule 20 is a protein called EF-hand domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	1J	414	Total	C	N	O	S	0	0
			3295	2050	603	624	18		
20	1K	414	Total	C	N	O	S	0	0
			3295	2050	603	624	18		

- Molecule 21 is a protein called Cyclic nucleotide-binding domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	1L	306	Total	C	N	O	S	0	0
			2446	1557	422	454	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
21	1M	306	Total	C	N	O	S	0	0
			2446	1557	422	454	13		

- Molecule 22 is a protein called TbMIP23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1N	170	Total	C	N	O	S	0	0
			1262	795	219	241	7		
22	1O	170	Total	C	N	O	S	0	0
			1262	795	219	241	7		

- Molecule 23 is a protein called FAP141.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1P	105	Total	C	N	O	S	0	0
			837	503	167	162	5		
23	1Q	105	Total	C	N	O	S	0	0
			837	503	167	162	5		

- Molecule 24 is a protein called EF-hand domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1R	181	Total	C	N	O	S	0	0
			1457	935	250	267	5		
24	1S	181	Total	C	N	O	S	0	0
			1457	935	250	267	5		

- Molecule 25 is a protein called Calpain-like cysteine peptidase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1T	269	Total	C	N	O	S	0	0
			2100	1327	366	392	15		
25	1U	269	Total	C	N	O	S	0	0
			2100	1327	366	392	15		
25	1V	269	Total	C	N	O	S	0	0
			2100	1327	366	392	15		

- Molecule 26 is a protein called EF-hand domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1W	472	Total	C	N	O	S	0	0
			3717	2352	651	692	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	1X	472	Total	C	N	O	S	0	0
			3717	2352	651	692	22		

- Molecule 27 is a protein called Calcium-binding protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1Y	357	Total	C	N	O	S	0	0
			2921	1842	511	552	16		
27	1Z	357	Total	C	N	O	S	0	0
			2921	1842	511	552	16		

- Molecule 28 is a protein called Cilia- and flagella-associated protein 58 central coiled coil domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1a	509	Total	C	N	O	S	0	0
			4224	2582	796	823	23		

- Molecule 29 is a protein called Cilia- and flagella-associated protein 58 central coiled coil domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	1b	517	Total	C	N	O	S	0	0
			4282	2632	829	803	18		

- Molecule 30 is a protein called CMF5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	1c	972	Total	C	N	O	S	0	0
			7724	4829	1382	1477	36		

- Molecule 31 is a protein called CMF6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	1d	958	Total	C	N	O	S	0	0
			7575	4739	1359	1438	39		

- Molecule 32 is a protein called CCDC113/CCDC96 coiled-coil domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1e	328	Total	C	N	O	S	0	0
			2755	1690	534	516	15		

- Molecule 33 is a protein called Cilia- and flagella-associated protein 263.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	1f	333	Total	C	N	O	S	0	0
			2738	1678	519	527	14		

- Molecule 34 is a protein called DRC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	1g	570	Total	C	N	O	S	0	0
			4747	2921	882	925	19		

- Molecule 35 is a protein called Dynein regulatory complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	1h	438	Total	C	N	O	S	0	0
			3589	2210	647	715	17		

- Molecule 36 is a protein called Dynein regulatory complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	1i	535	Total	C	N	O	S	0	0
			4420	2768	794	841	17		

- Molecule 37 is a protein called Trypanin-related protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	1j	424	Total	C	N	O	S	0	0
			3544	2189	663	675	17		

- Molecule 38 is a protein called Trypanin.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	1k	420	Total	C	N	O	S	0	0
			3534	2173	666	681	14		

- Molecule 39 is a protein called Leucine-rich repeat protein (LRRP).

Mol	Chain	Residues	Atoms					AltConf	Trace
39	1l	392	Total	C	N	O	S	0	0
			3071	1939	538	583	11		

- Molecule 40 is a protein called Transglutaminase-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	1m	484	Total	C	N	O	S	0	0
			4013	2567	710	717	19		

- Molecule 41 is a protein called DRC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	1n	410	Total	C	N	O	S	0	0
			3266	2020	609	628	9		

- Molecule 42 is a protein called Dynein regulatory complex protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	1o	416	Total	C	N	O	S	0	0
			3311	2040	579	676	16		

- Molecule 43 is a protein called ATPase AAA-type core domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	1p	553	Total	C	N	O	S	0	0
			4417	2785	782	820	30		

- Molecule 44 is a protein called Cilia- and flagella-associated protein 43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1r	1383	Total	C	N	O	S	0	0
			10942	6862	1928	2079	73		

- Molecule 45 is a protein called Cilia- and flagella-associated protein 44.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	1t	1298	Total	C	N	O	S	0	0
			10371	6524	1830	1957	60		

- Molecule 46 is a protein called EF-hand domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2A	276	Total	C	N	O	S	0	0
			2253	1422	411	409	11		
46	2B	276	Total	C	N	O	S	0	0
			2253	1422	411	409	11		
46	2C	218	Total	C	N	O	S	0	0
			1766	1113	322	322	9		

- Molecule 47 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2D	247	Total	C	N	O	S	0	0
			1908	1188	346	360	14		
47	2E	247	Total	C	N	O	S	0	0
			1908	1188	346	360	14		
47	2F	247	Total	C	N	O	S	0	0
			1908	1188	346	360	14		

- Molecule 48 is a protein called EF-hand domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	2G	298	Total	C	N	O	S	0	0
			2371	1516	415	427	13		
48	2H	298	Total	C	N	O	S	0	0
			2371	1516	415	427	13		
48	2I	298	Total	C	N	O	S	0	0
			2371	1516	415	427	13		

- Molecule 49 is a protein called FAP107/MC11.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2J	237	Total	C	N	O	S	0	0
			1880	1180	325	363	12		
49	2K	237	Total	C	N	O	S	0	0
			1880	1180	325	363	12		
49	2L	237	Total	C	N	O	S	0	0
			1880	1180	325	363	12		

- Molecule 50 is a protein called T. brucei spp.-specific protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2M	234	Total	C	N	O	S	0	0
			1862	1148	338	366	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
50	2N	234	Total	C	N	O	S	0	0
			1862	1148	338	366	10		
50	2O	149	Total	C	N	O	S	0	0
			1190	728	226	232	4		

- Molecule 51 is a protein called FAP95/MC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2P	165	Total	C	N	O	S	0	0
			1287	808	234	239	6		
51	2Q	165	Total	C	N	O	S	0	0
			1287	808	234	239	6		

- Molecule 52 is a protein called FAP129.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2R	258	Total	C	N	O	S	0	0
			2005	1242	371	379	13		
52	2S	258	Total	C	N	O	S	0	0
			2005	1242	371	379	13		
52	2T	258	Total	C	N	O	S	0	0
			2005	1242	371	379	13		

- Molecule 53 is a protein called T. brucei spp.-specific protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2U	292	Total	C	N	O	S	0	0
			2311	1433	422	450	6		
53	2V	375	Total	C	N	O	S	0	0
			2968	1848	540	572	8		
53	2W	375	Total	C	N	O	S	0	0
			2968	1848	540	572	8		

- Molecule 54 is a protein called FAP21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2X	371	Total	C	N	O	S	0	0
			2921	1801	561	536	23		
54	2Y	371	Total	C	N	O	S	0	0
			2921	1801	561	536	23		
54	2Z	127	Total	C	N	O	S	0	0
			991	597	205	182	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
54	3D	102	Total	C	N	O	S	0	0
			802	494	150	149	9		

- Molecule 55 is a protein called RSP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	2a	322	Total	C	N	O	S	0	0
			2609	1649	450	493	17		
55	2b	322	Total	C	N	O	S	0	0
			2609	1649	450	493	17		
55	2c	322	Total	C	N	O	S	0	0
			2609	1649	450	493	17		
55	2d	322	Total	C	N	O	S	0	0
			2609	1649	450	493	17		

- Molecule 56 is a protein called RSP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	2e	507	Total	C	N	O	S	0	0
			3972	2457	718	782	15		
56	2f	507	Total	C	N	O	S	0	0
			3972	2457	718	782	15		
56	2g	507	Total	C	N	O	S	0	0
			3972	2457	718	782	15		
56	2h	507	Total	C	N	O	S	0	0
			3972	2457	718	782	15		

- Molecule 57 is a protein called Radial spoke protein 3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	2i	165	Total	C	N	O	S	0	0
			1413	887	259	262	5		
57	2j	280	Total	C	N	O	S	0	0
			2352	1462	442	441	7		
57	2k	215	Total	C	N	O	S	0	0
			1815	1136	324	350	5		
57	2l	218	Total	C	N	O	S	0	0
			1835	1149	329	352	5		

- Molecule 58 is a protein called Flagellar radial spoke component, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	2m	527	Total	C	N	O	S	0	0
			4232	2656	702	854	20		
58	2n	527	Total	C	N	O	S	0	0
			4232	2656	702	854	20		
58	2o	527	Total	C	N	O	S	0	0
			4232	2656	702	854	20		
58	2p	527	Total	C	N	O	S	0	0
			4232	2656	702	854	20		

- Molecule 59 is a protein called Flagellar radial spoke protein-like, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	2q	494	Total	C	N	O	S	0	0
			3881	2454	655	760	12		
59	2r	494	Total	C	N	O	S	0	0
			3881	2454	655	760	12		
59	2s	494	Total	C	N	O	S	0	0
			3881	2454	655	760	12		
59	2t	469	Total	C	N	O	S	0	0
			3679	2330	629	708	12		

- Molecule 60 is a protein called RSP8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	2u	429	Total	C	N	O	S	0	0
			3322	2108	580	617	17		

- Molecule 61 is a protein called Radial spoke head protein 9 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	2v	297	Total	C	N	O	S	0	0
			2390	1528	408	444	10		
61	2w	297	Total	C	N	O	S	0	0
			2390	1528	408	444	10		
61	2x	297	Total	C	N	O	S	0	0
			2390	1528	408	444	10		
61	2y	297	Total	C	N	O	S	0	0
			2390	1528	408	444	10		

- Molecule 62 is a protein called Radial spoke protein RSP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	2z	310	Total	C	N	O	S	0	0
			2451	1563	411	466	11		
62	3a	279	Total	C	N	O	S	0	0
			2199	1416	376	397	10		
62	3b	310	Total	C	N	O	S	0	0
			2451	1563	411	466	11		
62	3c	272	Total	C	N	O	S	0	0
			2145	1381	368	386	10		

- Molecule 63 is a protein called Flagellar associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	3A	205	Total	C	N	O	S	0	0
			1620	1004	305	303	8		
63	3B	305	Total	C	N	O	S	0	0
			2388	1483	447	448	10		
63	3C	305	Total	C	N	O	S	0	0
			2388	1483	447	448	10		

- Molecule 64 is a protein called TbRib26b.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	3E	120	Total	C	N	O	S	0	0
			953	598	170	182	3		
64	3F	98	Total	C	N	O	S	0	0
			772	492	132	146	2		
64	3G	120	Total	C	N	O	S	0	0
			953	598	170	182	3		
64	3H	98	Total	C	N	O	S	0	0
			772	492	132	146	2		
64	3I	120	Total	C	N	O	S	0	0
			953	598	170	182	3		

- Molecule 65 is a protein called EF-hand domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	3J	650	Total	C	N	O	S	0	0
			5268	3330	951	972	15		
65	3K	556	Total	C	N	O	S	0	0
			4482	2828	816	827	11		
65	3L	94	Total	C	N	O	S	0	0
			786	502	135	145	4		

- Molecule 66 is a protein called PACRGA.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	3M	277	Total	C	N	O	S	0	0
			2223	1425	399	393	6		
66	3N	277	Total	C	N	O	S	0	0
			2223	1425	399	393	6		
66	3O	277	Total	C	N	O	S	0	0
			2223	1425	399	393	6		
66	3P	277	Total	C	N	O	S	0	0
			2223	1425	399	393	6		
66	3Q	277	Total	C	N	O	S	0	0
			2223	1425	399	393	6		
66	3R	277	Total	C	N	O	S	0	0
			2223	1425	399	393	6		
66	3S	277	Total	C	N	O	S	0	0
			2223	1425	399	393	6		
66	3T	277	Total	C	N	O	S	0	0
			2223	1425	399	393	6		

- Molecule 67 is a protein called PACRGB.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	3U	226	Total	C	N	O	S	0	0
			1819	1174	311	329	5		
67	3V	226	Total	C	N	O	S	0	0
			1819	1174	311	329	5		
67	3W	226	Total	C	N	O	S	0	0
			1819	1174	311	329	5		
67	3X	226	Total	C	N	O	S	0	0
			1819	1174	311	329	5		
67	3Y	226	Total	C	N	O	S	0	0
			1819	1174	311	329	5		

- Molecule 68 is a protein called Cilia- and flagella-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	3Z	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4A	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4B	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4C	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
68	4D	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4E	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4F	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4G	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4H	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4I	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4J	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4K	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4L	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4M	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		
68	4N	185	Total	C	N	O	S	0	0
			1537	985	271	273	8		

- Molecule 69 is a protein called Phosphatidylinositol 4-phosphate 5-kinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	3d	675	Total	C	N	O	S	0	0
			5388	3380	969	1023	16		
69	3e	675	Total	C	N	O	S	0	0
			5388	3380	969	1023	16		
69	3f	675	Total	C	N	O	S	0	0
			5388	3380	969	1023	16		
69	3g	675	Total	C	N	O	S	0	0
			5388	3380	969	1023	16		

- Molecule 70 is a protein called Cyclophilin type peptidyl-prolyl cis-trans isomerase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	3h	310	Total	C	N	O	S	0	0
			2453	1538	426	466	23		
70	3i	310	Total	C	N	O	S	0	0
			2453	1538	426	466	23		

- Molecule 71 is a protein called RSP14.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	3j	380	Total	C	N	O	S	0	0
			3009	1900	526	562	21		

- Molecule 72 is a protein called Leucine-rich repeat protein (LRRP).

Mol	Chain	Residues	Atoms					AltConf	Trace
72	3k	364	Total	C	N	O	S	0	0
			2743	1715	479	534	15		

- Molecule 73 is a protein called Chaperone protein DNAJ, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	3l	302	Total	C	N	O	S	0	0
			2354	1487	413	448	6		
73	3m	289	Total	C	N	O	S	0	0
			2252	1420	397	429	6		
73	3o	302	Total	C	N	O	S	0	0
			2354	1487	413	448	6		
73	3p	289	Total	C	N	O	S	0	0
			2252	1420	397	429	6		

- Molecule 74 is a protein called Nucleoside diphosphate kinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	3q	223	Total	C	N	O	S	0	0
			1769	1121	320	320	8		
74	3r	223	Total	C	N	O	S	0	0
			1769	1121	320	320	8		
74	3s	223	Total	C	N	O	S	0	0
			1769	1121	320	320	8		
74	3t	223	Total	C	N	O	S	0	0
			1769	1121	320	320	8		

- Molecule 75 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	3u	87	Total	C	N	O	S	0	0
			715	465	116	131	3		
75	3v	87	Total	C	N	O	S	0	0
			715	465	116	131	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
75	3w	88	Total	C	N	O	S	0	0
			722	469	117	133	3		
75	3x	87	Total	C	N	O	S	0	0
			715	465	116	131	3		
75	3y	87	Total	C	N	O	S	0	0
			715	465	116	131	3		
75	3z	87	Total	C	N	O	S	0	0
			715	465	116	131	3		
75	4a	87	Total	C	N	O	S	0	0
			715	465	116	131	3		
75	4b	87	Total	C	N	O	S	0	0
			715	465	116	131	3		
75	4c	87	Total	C	N	O	S	0	0
			717	467	116	131	3		
75	4d	87	Total	C	N	O	S	0	0
			717	467	116	131	3		
75	4e	86	Total	C	N	O	S	0	0
			710	463	115	129	3		
75	4f	86	Total	C	N	O	S	0	0
			710	463	115	129	3		
75	4g	87	Total	C	N	O	S	0	0
			717	467	116	131	3		
75	4h	87	Total	C	N	O	S	0	0
			717	467	116	131	3		
75	4i	86	Total	C	N	O	S	0	0
			710	463	115	129	3		
75	4j	86	Total	C	N	O	S	0	0
			710	463	115	129	3		
75	4k	86	Total	C	N	O	S	0	0
			710	463	115	129	3		
75	4l	86	Total	C	N	O	S	0	0
			710	463	115	129	3		
75	4m	86	Total	C	N	O	S	0	0
			710	463	115	129	3		
75	4n	86	Total	C	N	O	S	0	0
			710	463	115	129	3		
75	5s	87	Total	C	N	O	S	0	0
			715	465	116	131	3		
75	5t	89	Total	C	N	O	S	0	0
			728	472	118	135	3		
75	5u	84	Total	C	N	O	S	0	0
			687	449	109	126	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
75	5v	86	Total	C	N	O	S	0	0
			707	461	115	128	3		
75	5w	90	Total	C	N	O	S	0	0
			736	477	119	136	4		
75	5x	90	Total	C	N	O	S	0	0
			736	477	119	136	4		
75	7k	89	Total	C	N	O	S	0	0
			728	472	118	135	3		
75	7n	84	Total	C	N	O	S	0	0
			687	449	109	126	3		
75	7o	86	Total	C	N	O	S	0	0
			707	461	115	128	3		
75	7p	86	Total	C	N	O	S	0	0
			707	461	115	128	3		
75	8k	89	Total	C	N	O	S	0	0
			728	472	118	135	3		
75	8n	84	Total	C	N	O	S	0	0
			687	449	109	126	3		
75	8o	86	Total	C	N	O	S	0	0
			707	461	115	128	3		
75	8p	86	Total	C	N	O	S	0	0
			707	461	115	128	3		
75	9k	89	Total	C	N	O	S	0	0
			728	472	118	135	3		
75	9n	84	Total	C	N	O	S	0	0
			687	449	109	126	3		
75	9o	86	Total	C	N	O	S	0	0
			707	461	115	128	3		
75	9p	86	Total	C	N	O	S	0	0
			707	461	115	128	3		

- Molecule 76 is a protein called Cilia- and flagella-associated protein 52.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	4O	620	Total	C	N	O	S	0	0
			4671	2918	821	901	31		
76	4P	627	Total	C	N	O	S	0	0
			4727	2953	829	914	31		
76	4Q	627	Total	C	N	O	S	0	0
			4727	2953	829	914	31		
76	4R	620	Total	C	N	O	S	0	0
			4671	2918	821	901	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
76	4S	627	Total	C	N	O	S	0	0
			4727	2953	829	914	31		
76	4T	627	Total	C	N	O	S	0	0
			4727	2953	829	914	31		
76	4U	620	Total	C	N	O	S	0	0
			4671	2918	821	901	31		

- Molecule 77 is a protein called Enkurin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	4V	240	Total	C	N	O	S	0	0
			1867	1166	339	358	4		
77	4W	240	Total	C	N	O	S	0	0
			1867	1166	339	358	4		
77	4X	240	Total	C	N	O	S	0	0
			1867	1166	339	358	4		
77	4Y	240	Total	C	N	O	S	0	0
			1867	1166	339	358	4		
77	4Z	240	Total	C	N	O	S	0	0
			1867	1166	339	358	4		

- Molecule 78 is a protein called Cytochrome b5 domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	4o	220	Total	C	N	O	S	0	0
			1802	1139	302	352	9		
78	4p	220	Total	C	N	O	S	0	0
			1802	1139	302	352	9		

- Molecule 79 is a protein called Leucine-rich repeat protein (LRRP).

Mol	Chain	Residues	Atoms					AltConf	Trace
79	4q	852	Total	C	N	O	S	0	0
			6513	4052	1149	1276	36		
79	4r	852	Total	C	N	O	S	0	0
			6513	4052	1149	1276	36		

- Molecule 80 is a protein called VWFA domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	4s	809	Total	C	N	O	S	0	0
			6179	3905	1079	1154	41		

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Mol	Chain	Residues	Atoms					AltConf	Trace
80	4t	809	Total	C	N	O	S	0	0
			6179	3905	1079	1154	41		

- Molecule 81 is a protein called TbRSP63.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	4u	501	Total	C	N	O	S	0	0
			3934	2439	702	770	23		
81	4v	501	Total	C	N	O	S	0	0
			3934	2439	702	770	23		

- Molecule 82 is a protein called IQ and ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	4w	512	Total	C	N	O	S	0	0
			4141	2593	775	757	16		

- Molecule 83 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	4x	148	Total	C	N	O	S	0	0
			839	501	160	176	2		

- Molecule 84 is a protein called MORN repeat-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	4y	661	Total	C	N	O	S	0	0
			5306	3343	952	984	27		

- Molecule 85 is a protein called Cilia- and flagella-associated protein 206.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	4z	528	Total	C	N	O	S	0	0
			4132	2595	726	785	26		

- Molecule 86 is a protein called Enkurin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	5A	229	Total	C	N	O	S	0	0
			1905	1207	344	347	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
86	5B	229	Total	C	N	O	S	0	0
			1905	1207	344	347	7		

- Molecule 87 is a protein called MC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	5C	279	Total	C	N	O	S	0	0
			2217	1384	418	404	11		
87	5D	275	Total	C	N	O	S	0	0
			2186	1366	412	398	10		
87	5E	275	Total	C	N	O	S	0	0
			2186	1366	412	398	10		
87	5F	279	Total	C	N	O	S	0	0
			2217	1384	418	404	11		
87	5G	275	Total	C	N	O	S	0	0
			2186	1366	412	398	10		
87	5H	275	Total	C	N	O	S	0	0
			2186	1366	412	398	10		
87	5I	279	Total	C	N	O	S	0	0
			2217	1384	418	404	11		
87	5J	173	Total	C	N	O	S	0	0
			1370	849	266	247	8		

- Molecule 88 is a protein called Cilia- and flagella-associated protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	5K	153	Total	C	N	O	S	0	0
			1308	790	260	249	9		
88	5S	165	Total	C	N	O	S	0	0
			1369	821	260	275	13		
88	5T	459	Total	C	N	O	S	0	0
			3875	2336	762	753	24		
88	5U	459	Total	C	N	O	S	0	0
			3875	2336	762	753	24		
88	5V	295	Total	C	N	O	S	0	0
			2465	1490	478	482	15		
88	5W	473	Total	C	N	O	S	0	0
			3981	2402	783	772	24		
88	5X	382	Total	C	N	O	S	0	0
			3253	1966	638	632	17		

- Molecule 89 is a protein called CCDC81 HU domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	5L	239	Total	C	N	O	S	0	0
			1911	1207	342	348	14		
89	5M	239	Total	C	N	O	S	0	0
			1911	1207	342	348	14		

- Molecule 90 is a protein called MC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	5N	238	Total	C	N	O	S	0	0
			1900	1188	349	355	8		
90	5O	238	Total	C	N	O	S	0	0
			1900	1188	349	355	8		
90	5P	238	Total	C	N	O	S	0	0
			1900	1188	349	355	8		
90	5Q	238	Total	C	N	O	S	0	0
			1900	1188	349	355	8		
90	5R	238	Total	C	N	O	S	0	0
			1900	1188	349	355	8		

- Molecule 91 is a protein called Trichohyalin-plectin-homology domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	5Y	408	Total	C	N	O	S	0	0
			3422	2084	668	652	18		
91	5Z	465	Total	C	N	O	S	0	0
			3907	2378	757	751	21		
91	6A	262	Total	C	N	O	S	0	0
			2236	1357	437	429	13		

- Molecule 92 is a protein called TbRSP62.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	5a	155	Total	C	N	O	S	0	0
			1256	783	231	237	5		

- Molecule 93 is a protein called Cilia- and flagella-associated protein 91.

Mol	Chain	Residues	Atoms					AltConf	Trace
93	5b	172	Total	C	N	O	S	0	0
			1419	876	270	267	6		

- Molecule 94 is a protein called Cilia- and flagella-associated protein 251.

Mol	Chain	Residues	Atoms					AltConf	Trace
94	5c	918	Total	C	N	O	S	0	0
			7136	4531	1227	1343	35		

- Molecule 95 is a protein called Cilia- and flagella-associated protein 61 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
95	5d	1274	Total	C	N	O	S	0	0
			10191	6477	1738	1929	47		

- Molecule 96 is a protein called DUF4200 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
96	5e	225	Total	C	N	O	S	0	0
			1895	1154	373	362	6		

- Molecule 97 is a protein called DUF4200 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
97	5f	322	Total	C	N	O	S	0	0
			2649	1636	481	519	13		

- Molecule 98 is a protein called Leucine-rich repeat-containing protein 51.

Mol	Chain	Residues	Atoms					AltConf	Trace
98	5g	435	Total	C	N	O	S	0	0
			3510	2220	618	654	18		

- Molecule 99 is a protein called IDAf-alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
99	5h	1379	Total	C	N	O	S	0	0
			11265	7169	1969	2076	51		
99	5i	3336	Total	C	N	O	S	0	0
			26792	17002	4620	5021	149		

- Molecule 100 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
100	5j	1336	Total	C	N	O	S	0	0
			10917	6902	1939	2025	51		

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Mol	Chain	Residues	Atoms					AltConf	Trace
100	5k	3425	Total	C	N	O	S	0	0
			27648	17529	4783	5192	144		

- Molecule 101 is a protein called Dynein axonemal intermediate chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
101	5l	435	Total	C	N	O	S	0	0
			3410	2133	590	666	21		

- Molecule 102 is a protein called IC140.

Mol	Chain	Residues	Atoms					AltConf	Trace
102	5m	477	Total	C	N	O	S	0	0
			3788	2392	690	686	20		

- Molecule 103 is a protein called IC97/Casc1 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
103	5n	645	Total	C	N	O	S	0	0
			5223	3319	902	976	26		

- Molecule 104 is a protein called FAP120.

Mol	Chain	Residues	Atoms					AltConf	Trace
104	5o	337	Total	C	N	O	S	0	0
			2622	1621	473	512	16		

- Molecule 105 is a protein called Dynein light chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
105	5p	111	Total	C	N	O	S	0	0
			929	583	167	172	7		
105	7i	111	Total	C	N	O	S	0	0
			929	583	167	172	7		
105	8i	111	Total	C	N	O	S	0	0
			929	583	167	172	7		
105	9i	111	Total	C	N	O	S	0	0
			929	583	167	172	7		

- Molecule 106 is a protein called Dynein light chain roadblock.

Mol	Chain	Residues	Atoms					AltConf	Trace
106	5q	98	Total	C	N	O	S	0	0
			784	500	139	144	1		
106	7l	98	Total	C	N	O	S	0	0
			784	500	139	144	1		
106	8l	98	Total	C	N	O	S	0	0
			784	500	139	144	1		
106	9l	98	Total	C	N	O	S	0	0
			784	500	139	144	1		

- Molecule 107 is a protein called Dynein light chain roadblock.

Mol	Chain	Residues	Atoms					AltConf	Trace
107	5r	95	Total	C	N	O	S	0	0
			756	470	138	145	3		
107	7m	95	Total	C	N	O	S	0	0
			756	470	138	145	3		
107	8m	95	Total	C	N	O	S	0	0
			756	470	138	145	3		
107	9m	95	Total	C	N	O	S	0	0
			756	470	138	145	3		

- Molecule 108 is a protein called Dynein light chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
108	5y	102	Total	C	N	O	S	0	0
			823	533	133	153	4		
108	7q	102	Total	C	N	O	S	0	0
			823	533	133	153	4		
108	8q	102	Total	C	N	O	S	0	0
			823	533	133	153	4		
108	9q	102	Total	C	N	O	S	0	0
			823	533	133	153	4		

- Molecule 109 is a protein called Trichohyalin-plectin-homology domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
109	6B	93	Total	C	N	O	S	0	0
			786	487	155	142	2		
109	6C	318	Total	C	N	O	S	0	0
			2691	1646	523	508	14		
109	6D	318	Total	C	N	O	S	0	0
			2691	1646	523	508	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
109	6E	80	Total	C	N	O	S	0	0
			699	429	133	135	2		
109	6F	344	Total	C	N	O	S	0	0
			2892	1769	564	545	14		
109	6G	347	Total	C	N	O	S	0	0
			2912	1780	567	551	14		
109	6H	180	Total	C	N	O	S	0	0
			1538	931	303	296	8		
109	6I	239	Total	C	N	O	S	0	0
			1975	1209	384	372	10		
109	6J	346	Total	C	N	O	S	0	0
			2905	1775	566	550	14		
109	6K	285	Total	C	N	O	S	0	0
			2394	1457	467	458	12		
109	6L	141	Total	C	N	O	S	0	0
			1161	721	225	213	2		
109	6M	347	Total	C	N	O	S	0	0
			2912	1780	567	551	14		
109	6N	347	Total	C	N	O	S	0	0
			2912	1780	567	551	14		
109	6O	253	Total	C	N	O	S	0	0
			2146	1307	417	410	12		
109	6P	253	Total	C	N	O	S	0	0
			2146	1307	417	410	12		
109	6Q	163	Total	C	N	O	S	0	0
			1406	852	276	270	8		

- Molecule 110 is a protein called STOP axonemal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
110	6R	151	Total	C	N	O	S	0	0
			1199	765	212	217	5		
110	6S	228	Total	C	N	O	S	0	0
			1816	1155	318	332	11		
110	6T	177	Total	C	N	O	S	0	0
			1415	902	243	261	9		
110	6U	98	Total	C	N	O	S	0	0
			776	492	138	141	5		
110	6V	231	Total	C	N	O	S	0	0
			1846	1168	331	336	11		
110	6W	231	Total	C	N	O	S	0	0
			1846	1168	331	336	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
110	6X	51	Total 401	C 250	N 70	O 76	S 5	0	0
110	6Y	229	Total 1819	C 1152	N 322	O 334	S 11	0	0
110	6Z	229	Total 1819	C 1152	N 322	O 334	S 11	0	0
110	7A	112	Total 886	C 559	N 158	O 163	S 6	0	0
110	7B	179	Total 1430	C 912	N 251	O 262	S 5	0	0
110	7C	239	Total 1907	C 1212	N 334	O 350	S 11	0	0
110	7D	178	Total 1424	C 907	N 246	O 262	S 9	0	0
110	7E	106	Total 839	C 530	N 147	O 157	S 5	0	0
110	7F	228	Total 1814	C 1148	N 321	O 334	S 11	0	0
110	7G	228	Total 1814	C 1148	N 321	O 334	S 11	0	0
110	7H	101	Total 798	C 503	N 144	O 145	S 6	0	0
110	7I	237	Total 1884	C 1193	N 336	O 344	S 11	0	0
110	7J	237	Total 1884	C 1193	N 336	O 344	S 11	0	0
110	7K	51	Total 401	C 253	N 75	O 71	S 2	0	0
110	9Z	43	Total 337	C 213	N 64	O 59	S 1	0	0

- Molecule 111 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
111	6a	4058	Total 32697	C 20810	N 5575	O 6136	S 176	0	0

- Molecule 112 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
112	6b	4055	Total 32697	C 20834	N 5572	O 6089	S 202	0	0

- Molecule 113 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
113	6c	3929	Total	C	N	O	S	0	0
			31436	19931	5406	5916	183		

- Molecule 114 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
114	6d	4002	Total	C	N	O	S	0	0
			31959	20295	5495	6005	164		

- Molecule 115 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
115	6e	4089	Total	C	N	O	S	0	0
			32835	20894	5595	6161	185		

- Molecule 116 is a protein called Actin A.

Mol	Chain	Residues	Atoms					AltConf	Trace
116	6f	372	Total	C	N	O	S	0	0
			2905	1835	492	556	22		
116	6g	371	Total	C	N	O	S	0	0
			2896	1830	491	553	22		

- Molecule 117 is a protein called Actin-like protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
117	6h	393	Total	C	N	O	S	0	0
			3040	1901	539	578	22		

- Molecule 118 is a protein called Actin, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
118	6i	412	Total	C	N	O	S	0	0
			3215	2021	571	602	21		

- Molecule 119 is a protein called Actin, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
119	6j	392	Total	C	N	O	S	0	0
			3038	1921	525	573	19		

- Molecule 120 is a protein called Dynein arm light chain, axonemal, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
120	6k	168	Total	C	N	O	S	0	0
			1383	854	248	273	8		
120	6l	214	Total	C	N	O	S	0	0
			1770	1109	310	343	8		
120	6m	221	Total	C	N	O	S	0	0
			1825	1142	321	354	8		

- Molecule 121 is a protein called 33 kDa inner dynein arm light chain, axonemal, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
121	6n	195	Total	C	N	O	S	0	0
			1621	1004	303	308	6		

- Molecule 122 is a protein called Dynein arm light chain, axonemal, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
122	6o	243	Total	C	N	O	S	0	0
			1959	1224	365	362	8		

- Molecule 123 is a protein called Dynein arm light chain, axonemal, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
123	6p	164	Total	C	N	O	S	0	0
			1370	846	258	258	8		

- Molecule 124 is a protein called Protein TAX-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
124	6q	338	Total	C	N	O	S	0	0
			2687	1714	467	496	10		

- Molecule 125 is a protein called Tetratricopeptide repeat protein 29.

Mol	Chain	Residues	Atoms					AltConf	Trace
125	6r	364	Total	C	N	O	S	0	0
			2906	1816	517	554	19		

- Molecule 126 is a protein called Tetratricopeptide repeat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
126	6s	370	Total	C	N	O	S	0	0
			2835	1774	523	517	21		

- Molecule 127 is a protein called Centrin, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
127	6t	153	Total	C	N	O	S	0	0
			1226	772	205	244	5		

- Molecule 128 is a protein called Centrin, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
128	6u	153	Total	C	N	O	S	0	0
			1206	760	206	235	5		

- Molecule 129 is a protein called MC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
129	7L	154	Total	C	N	O	S	0	0
			1293	822	224	238	9		
129	7M	154	Total	C	N	O	S	0	0
			1293	822	224	238	9		

- Molecule 130 is a protein called MC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
130	7N	163	Total	C	N	O	S	0	0
			1338	844	232	252	10		
130	7O	163	Total	C	N	O	S	0	0
			1338	844	232	252	10		
130	7P	163	Total	C	N	O	S	0	0
			1338	844	232	252	10		

- Molecule 131 is a protein called FAP90.

Mol	Chain	Residues	Atoms					AltConf	Trace
131	7Q	161	Total	C	N	O	S	0	0
			1281	794	235	244	8		
131	7R	161	Total	C	N	O	S	0	0
			1281	794	235	244	8		
131	7S	161	Total	C	N	O	S	0	0
			1281	794	235	244	8		

- Molecule 132 is a protein called PBP36.

Mol	Chain	Residues	Atoms					AltConf	Trace
132	7T	161	Total	C	N	O	S	0	0
			1288	821	240	222	5		
132	7U	298	Total	C	N	O	S	0	0
			2408	1525	452	421	10		
132	8L	238	Total	C	N	O	S	0	0
			1938	1226	367	338	7		

- Molecule 133 is a protein called Enkurin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
133	7V	239	Total	C	N	O	S	0	0
			1920	1191	366	352	11		
133	7W	238	Total	C	N	O	S	0	0
			1906	1183	363	347	13		
133	7X	231	Total	C	N	O	S	0	0
			1844	1145	349	337	13		
133	7Y	239	Total	C	N	O	S	0	0
			1920	1191	366	352	11		
133	7Z	238	Total	C	N	O	S	0	0
			1906	1183	363	347	13		
133	8A	231	Total	C	N	O	S	0	0
			1844	1145	349	337	13		
133	8B	239	Total	C	N	O	S	0	0
			1920	1191	366	352	11		
133	8C	238	Total	C	N	O	S	0	0
			1906	1183	363	347	13		

- Molecule 134 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
134	7a	3423	Total	C	N	O	S	0	0
			27522	17521	4745	5105	151		
134	7e	4629	Total	C	N	O	S	0	0
			37310	23753	6431	6935	191		
134	8e	4629	Total	C	N	O	S	0	0
			37310	23753	6431	6935	191		
134	9e	4629	Total	C	N	O	S	0	0
			37310	23753	6431	6935	191		

- Molecule 135 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
135	7b	3366	Total	C	N	O	S	0	0
			27000	17185	4608	5047	160		
135	7f	4591	Total	C	N	O	S	0	0
			36840	23385	6285	6962	208		
135	8f	4591	Total	C	N	O	S	0	0
			36840	23385	6285	6962	208		
135	9f	4591	Total	C	N	O	S	0	0
			36840	23385	6285	6962	208		

- Molecule 136 is a protein called TbDC65.

Mol	Chain	Residues	Atoms					AltConf	Trace
136	7c	340	Total	C	N	O	S	0	0
			2790	1756	517	504	13		
136	8c	340	Total	C	N	O	S	0	0
			2790	1756	517	504	13		
136	9c	340	Total	C	N	O	S	0	0
			2790	1756	517	504	13		

- Molecule 137 is a protein called TbDC13.

Mol	Chain	Residues	Atoms					AltConf	Trace
137	7d	80	Total	C	N	O	S	0	0
			662	425	123	107	7		
137	8d	80	Total	C	N	O	S	0	0
			662	425	123	107	7		
137	9d	80	Total	C	N	O	S	0	0
			662	425	123	107	7		

- Molecule 138 is a protein called Dynein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
138	7g	533	Total	C	N	O	S	0	0
			4236	2662	743	812	19		
138	8g	533	Total	C	N	O	S	0	0
			4236	2662	743	812	19		
138	9g	533	Total	C	N	O	S	0	0
			4236	2662	743	812	19		

- Molecule 139 is a protein called Dynein intermediate chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
139	7h	609	Total	C	N	O	S	0	0
			4830	3046	835	920	29		
139	8h	609	Total	C	N	O	S	0	0
			4830	3046	835	920	29		
139	9h	609	Total	C	N	O	S	0	0
			4830	3046	835	920	29		

- Molecule 140 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
140	7j	105	Total	C	N	O	S	0	0
			855	547	139	158	11		
140	8j	105	Total	C	N	O	S	0	0
			855	547	139	158	11		
140	9j	105	Total	C	N	O	S	0	0
			855	547	139	158	11		

- Molecule 141 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
141	7r	98	Total	C	N	O	S	0	0
			776	484	140	147	5		
141	8r	98	Total	C	N	O	S	0	0
			776	484	140	147	5		
141	9r	98	Total	C	N	O	S	0	0
			776	484	140	147	5		

- Molecule 142 is a protein called Outer dynein arm docking complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
142	7s	164	Total	C	N	O	S	0	0
			1320	823	229	262	6		
142	8s	327	Total	C	N	O	S	0	0
			2670	1645	501	518	6		
142	9a	180	Total	C	N	O		0	0
			1504	916	305	283			
142	9s	344	Total	C	N	O	S	0	0
			2824	1739	534	545	6		

- Molecule 143 is a protein called ODAD1 central coiled coil region domain-containing protein.



Mol	Chain	Residues	Atoms					AltConf	Trace
143	7t	179	Total 1441	C 888	N 260	O 288	S 5	0	0
143	8t	339	Total 2727	C 1662	N 501	O 552	S 12	0	0
143	9b	181	Total 1450	C 871	N 273	O 299	S 7	0	0
143	9t	360	Total 2891	C 1759	N 533	O 587	S 12	0	0

- Molecule 144 is a protein called Enkurin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
144	8D	249	Total 2017	C 1253	N 377	O 376	S 11	0	0
144	8E	120	Total 990	C 609	N 183	O 193	S 5	0	0
144	8F	239	Total 1937	C 1202	N 360	O 364	S 11	0	0
144	8G	249	Total 2017	C 1253	N 377	O 376	S 11	0	0
144	8H	120	Total 990	C 609	N 183	O 193	S 5	0	0
144	8I	239	Total 1937	C 1202	N 360	O 364	S 11	0	0
144	8J	249	Total 2017	C 1253	N 377	O 376	S 11	0	0
144	8K	120	Total 990	C 609	N 183	O 193	S 5	0	0

- Molecule 145 is a protein called PON3.

Mol	Chain	Residues	Atoms					AltConf	Trace
145	8M	100	Total 824	C 509	N 158	O 149	S 8	0	0
145	8N	108	Total 889	C 548	N 171	O 162	S 8	0	0
145	8O	104	Total 858	C 528	N 167	O 155	S 8	0	0
145	8P	100	Total 824	C 509	N 158	O 149	S 8	0	0
145	8Q	108	Total 889	C 548	N 171	O 162	S 8	0	0
145	8R	104	Total 858	C 528	N 167	O 155	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
145	8S	100	Total	C	N	O	S	0	0
			824	509	158	149	8		
145	8T	108	Total	C	N	O	S	0	0
			889	548	171	162	8		

- Molecule 146 is a protein called PON4.

Mol	Chain	Residues	Atoms					AltConf	Trace
146	8U	40	Total	C	N	O	S	0	0
			327	199	60	67	1		
146	8V	131	Total	C	N	O	S	0	0
			1054	633	203	208	10		
146	8W	40	Total	C	N	O	S	0	0
			327	199	60	67	1		
146	8X	40	Total	C	N	O	S	0	0
			327	199	60	67	1		
146	8Y	131	Total	C	N	O	S	0	0
			1054	633	203	208	10		
146	8Z	40	Total	C	N	O	S	0	0
			327	199	60	67	1		
146	9A	40	Total	C	N	O	S	0	0
			327	199	60	67	1		
146	9B	116	Total	C	N	O	S	0	0
			942	564	181	187	10		

- Molecule 147 is a protein called MC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
147	9C	203	Total	C	N	O	S	0	0
			1642	1020	321	293	8		
147	9D	203	Total	C	N	O	S	0	0
			1642	1020	321	293	8		
147	9E	33	Total	C	N	O	S	0	0
			274	177	46	50	1		

- Molecule 148 is a protein called FAP96C/MC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
148	9F	28	Total	C	N	O	S	0	0
			223	143	39	39	2		
148	9G	155	Total	C	N	O	S	0	0
			1218	770	211	229	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
148	9H	155	Total	C	N	O	S	0	0
			1218	770	211	229	8		
148	9I	102	Total	C	N	O	S	0	0
			798	499	141	154	4		

- Molecule 149 is a protein called FAP96B.

Mol	Chain	Residues	Atoms					AltConf	Trace
149	9J	173	Total	C	N	O	S	0	0
			1432	926	252	246	8		
149	9K	275	Total	C	N	O	S	0	0
			2269	1458	402	398	11		
149	9L	253	Total	C	N	O	S	0	0
			2071	1328	364	368	11		

- Molecule 150 is a protein called MOP23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
150	9M	160	Total	C	N	O	S	0	0
			1380	847	261	270	2		
150	9N	160	Total	C	N	O	S	0	0
			1380	847	261	270	2		
150	9O	159	Total	C	N	O	S	0	0
			1373	843	260	268	2		
150	9P	160	Total	C	N	O	S	0	0
			1380	847	261	270	2		
150	9Q	160	Total	C	N	O	S	0	0
			1380	847	261	270	2		
150	9R	159	Total	C	N	O	S	0	0
			1373	843	260	268	2		
150	9S	160	Total	C	N	O	S	0	0
			1380	847	261	270	2		

- Molecule 151 is a protein called MOP23B.

Mol	Chain	Residues	Atoms					AltConf	Trace
151	9T	144	Total	C	N	O	S	0	0
			1193	730	230	229	4		
151	9U	144	Total	C	N	O	S	0	0
			1193	730	230	229	4		
151	9V	132	Total	C	N	O	S	0	0
			1091	669	210	208	4		

- Molecule 152 is a protein called MOP23C.

Mol	Chain	Residues	Atoms					AltConf	Trace
152	9W	71	Total	C	N	O	S	0	0
			583	368	100	113	2		
152	9X	71	Total	C	N	O	S	0	0
			583	368	100	113	2		
152	9Y	71	Total	C	N	O	S	0	0
			583	368	100	113	2		

- Molecule 153 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
153	AA	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AC	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AE	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AG	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AI	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AK	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AM	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AO	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AQ	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AS	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AU	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AW	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	AY	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	Aa	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	Ac	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	Ae	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	Ag	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	Ai	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	Ak	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	Am	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	Ao	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BC	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BG	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BI	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BM	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BO	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BQ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BS	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BW	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	BY	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CC	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CE	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	CK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CM	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CO	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CQ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CS	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CW	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	CY	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DC	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DE	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DG	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DI	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DR	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DT	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	DZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	EB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	ED	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	EF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	EH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	EJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	EL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	EN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	ER	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	ET	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	EV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	EX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	EZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FR	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	FT	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	FZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GR	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GT	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	GZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	HJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HR	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HT	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	HZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	ID	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IR	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IT	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	IX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	IZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JG	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JI	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JM	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JO	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JQ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JS	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JW	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	JY	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KC	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KE	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KG	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KI	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KM	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	KO	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KQ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KS	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KW	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	KY	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LC	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LE	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LG	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LI	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LM	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LO	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LQ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LS	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LW	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	LY	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MC	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	ME	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MG	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MI	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MM	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MO	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MQ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MW	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	MY	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NC	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NE	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NG	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NI	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NM	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NO	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NQ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NS	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	NU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	NY	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OC	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OE	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OG	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OI	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OM	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OO	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OQ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OS	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OW	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	OY	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	PA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	PD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	PF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	PH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	PJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	PL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	PN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	PP	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	PR	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	PT	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	PV	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	PX	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	PZ	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QB	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QD	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QF	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QH	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QJ	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QL	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QN	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QP	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QR	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QT	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QV	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QX	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	QZ	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	RB	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	RD	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	RF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	RH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	RJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	RL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	RN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	RP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	RR	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	RT	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	RV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	RX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	RZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SR	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	ST	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	SV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	SZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TS	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TW	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	TY	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UC	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UE	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UG	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UI	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	UM	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UO	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UQ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	US	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	UZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VR	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VT	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	VZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	WD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WR	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WT	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	WZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XJ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XL	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XN	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XP	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XR	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	XT	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XV	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XX	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	XZ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YB	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YD	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YF	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YH	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YK	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YM	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YO	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YQ	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YS	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YU	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YW	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	YY	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	ZA	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	ZC	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	ZE	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	ZG	430	Total 3372	C 2114	N 575	O 652	S 31	0	0
153	ZI	430	Total 3372	C 2114	N 575	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
153	ZK	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	ZM	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	ZO	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	ZQ	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	ZS	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	ZU	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	ZW	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		
153	ZY	430	Total	C	N	O	S	0	0
			3372	2114	575	652	31		

- Molecule 154 is a protein called Tubulin alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
154	AB	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		
154	AD	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		
154	AF	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		
154	AH	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		
154	AJ	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		
154	AL	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		
154	AN	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		
154	AP	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		
154	AR	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		
154	AT	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		
154	AV	442	Total	C	N	O	S	0	0
			3421	2158	582	660	21		

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	AX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	AZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	Ab	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	Ad	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	Af	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	Ah	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	Aj	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	Al	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	An	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	Ap	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BB	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BD	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BF	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BH	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BN	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	BX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	BZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CB	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CD	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CF	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CN	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	CZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DB	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DD	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DF	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DH	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	DM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	DY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ES	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	EY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	FC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	FY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	GU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	GW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	HY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	IA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	IE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	IG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	II	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	IK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	IM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	IO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	IQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	IS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	IU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	IW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	IY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JH	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JN	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	JZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KB	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KD	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	KF	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KH	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KN	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	KZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LB	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LD	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LF	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LH	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LN	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	LV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	LZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MB	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MD	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MF	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MH	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ML	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MN	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	MZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NB	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ND	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NF	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NH	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	NL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NN	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	NZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OB	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OD	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OF	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OH	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ON	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	OZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	PC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	PY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	QS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	QY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	RY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	SI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	SY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	TX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	TZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UB	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UD	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UF	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UH	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UN	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	UY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	VO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	VY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	WY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	XE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XI	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XK	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XM	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XO	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XQ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XS	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XU	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XW	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	XY	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YA	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YC	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YE	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YG	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YN	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
154	YV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	YZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZB	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZD	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZF	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZH	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZJ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZL	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZN	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZP	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZR	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZT	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZV	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZX	442	Total 3421	C 2158	N 582	O 660	S 21	0	0
154	ZZ	442	Total 3421	C 2158	N 582	O 660	S 21	0	0

- Molecule 155 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
155	0q	2	Total 2	Zn 2	0
155	5C	2	Total 2	Zn 2	0
155	5E	1	Total 1	Zn 1	0

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Mol	Chain	Residues	Atoms		AltConf
155	5F	2	Total 2	Zn 2	0
155	5H	1	Total 1	Zn 1	0
155	5I	2	Total 2	Zn 2	0
155	5L	1	Total 1	Zn 1	0
155	5M	1	Total 1	Zn 1	0
155	7V	2	Total 2	Zn 2	0
155	7W	2	Total 2	Zn 2	0
155	7X	3	Total 3	Zn 3	0
155	7Y	2	Total 2	Zn 2	0
155	7Z	2	Total 2	Zn 2	0
155	7d	1	Total 1	Zn 1	0
155	8A	3	Total 3	Zn 3	0
155	8B	2	Total 2	Zn 2	0
155	8C	3	Total 3	Zn 3	0
155	8D	3	Total 3	Zn 3	0
155	8F	1	Total 1	Zn 1	0
155	8G	1	Total 1	Zn 1	0
155	8J	2	Total 2	Zn 2	0
155	8M	1	Total 1	Zn 1	0
155	8N	1	Total 1	Zn 1	0
155	8O	1	Total 1	Zn 1	0

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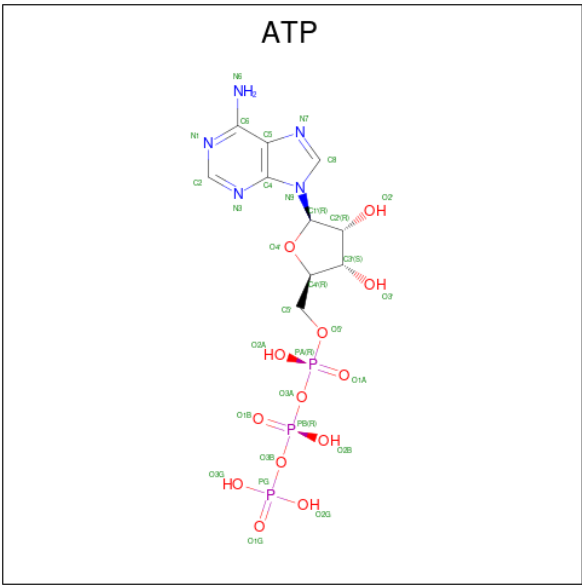
Mol	Chain	Residues	Atoms		AltConf
155	8P	1	Total 1	Zn 1	0
155	8Q	1	Total 1	Zn 1	0
155	8R	1	Total 1	Zn 1	0
155	8S	1	Total 1	Zn 1	0
155	8T	1	Total 1	Zn 1	0
155	8V	3	Total 3	Zn 3	0
155	8Y	3	Total 3	Zn 3	0
155	8d	1	Total 1	Zn 1	0
155	9B	3	Total 3	Zn 3	0
155	9d	1	Total 1	Zn 1	0
155	LP	1	Total 1	Zn 1	0
155	LV	1	Total 1	Zn 1	0
155	MB	1	Total 1	Zn 1	0
155	MD	1	Total 1	Zn 1	0
155	MN	1	Total 1	Zn 1	0
155	MV	1	Total 1	Zn 1	0
155	MX	1	Total 1	Zn 1	0
155	NF	1	Total 1	Zn 1	0
155	NH	1	Total 1	Zn 1	0
155	NJ	1	Total 1	Zn 1	0
155	NR	1	Total 1	Zn 1	0

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Mol	Chain	Residues	Atoms		AltConf
155	NV	1	Total	Zn	0
			1	1	

- Molecule 156 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
156	7a	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	7a	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	7a	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	7b	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	7b	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	7b	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	7e	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	7e	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	7e	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	7f	1	Total	C	N	O	P	0
			31	10	5	13	3	

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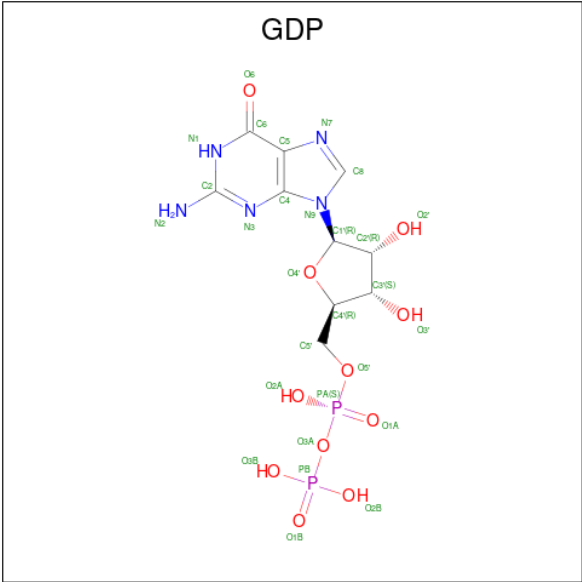
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Mol	Chain	Residues	Atoms					AltConf
156	7f	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	7f	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	8e	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	8e	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	8e	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	8f	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	8f	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	8f	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	9e	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	9e	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	9e	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	9f	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	9f	1	Total	C	N	O	P	0
			31	10	5	13	3	
156	9f	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 157 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ) (labeled as "Ligand of Interest" by depositor).







Mol	Chain	Residues	Atoms					AltConf
158	AA	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AC	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AE	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AG	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AI	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AS	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AW	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	AY	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	Aa	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
158	Ac	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	Ae	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	Ag	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	Ai	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	Ak	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	Am	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	Ao	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BA	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BC	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BG	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BI	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BS	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BW	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	BY	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	CA	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	CC	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
158	CE	1	Total 28	C 10	N 5	O 11	P 2	0
158	CH	1	Total 28	C 10	N 5	O 11	P 2	0
158	CK	1	Total 28	C 10	N 5	O 11	P 2	0
158	CM	1	Total 28	C 10	N 5	O 11	P 2	0
158	CO	1	Total 28	C 10	N 5	O 11	P 2	0
158	CQ	1	Total 28	C 10	N 5	O 11	P 2	0
158	CS	1	Total 28	C 10	N 5	O 11	P 2	0
158	CU	1	Total 28	C 10	N 5	O 11	P 2	0
158	CW	1	Total 28	C 10	N 5	O 11	P 2	0
158	CY	1	Total 28	C 10	N 5	O 11	P 2	0
158	DA	1	Total 28	C 10	N 5	O 11	P 2	0
158	DC	1	Total 28	C 10	N 5	O 11	P 2	0
158	DE	1	Total 28	C 10	N 5	O 11	P 2	0
158	DG	1	Total 28	C 10	N 5	O 11	P 2	0
158	DI	1	Total 28	C 10	N 5	O 11	P 2	0
158	DK	1	Total 28	C 10	N 5	O 11	P 2	0
158	DN	1	Total 28	C 10	N 5	O 11	P 2	0
158	DP	1	Total 28	C 10	N 5	O 11	P 2	0
158	DR	1	Total 28	C 10	N 5	O 11	P 2	0
158	DT	1	Total 28	C 10	N 5	O 11	P 2	0
158	DV	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
158	DX	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	DZ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	EB	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ED	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	EF	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	EH	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	EJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	EL	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	EN	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ER	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ET	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	EV	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	EX	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	EZ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	FB	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	FD	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	FF	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	FH	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	FJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	FL	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	FN	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
158	FP	1	Total 28	C 10	N 5	O 11	P 2	0
158	FR	1	Total 28	C 10	N 5	O 11	P 2	0
158	FT	1	Total 28	C 10	N 5	O 11	P 2	0
158	FV	1	Total 28	C 10	N 5	O 11	P 2	0
158	FX	1	Total 28	C 10	N 5	O 11	P 2	0
158	FZ	1	Total 28	C 10	N 5	O 11	P 2	0
158	GB	1	Total 28	C 10	N 5	O 11	P 2	0
158	GD	1	Total 28	C 10	N 5	O 11	P 2	0
158	GF	1	Total 28	C 10	N 5	O 11	P 2	0
158	GH	1	Total 28	C 10	N 5	O 11	P 2	0
158	GJ	1	Total 28	C 10	N 5	O 11	P 2	0
158	GL	1	Total 28	C 10	N 5	O 11	P 2	0
158	GN	1	Total 28	C 10	N 5	O 11	P 2	0
158	GP	1	Total 28	C 10	N 5	O 11	P 2	0
158	GR	1	Total 28	C 10	N 5	O 11	P 2	0
158	GT	1	Total 28	C 10	N 5	O 11	P 2	0
158	GV	1	Total 28	C 10	N 5	O 11	P 2	0
158	GX	1	Total 28	C 10	N 5	O 11	P 2	0
158	GZ	1	Total 28	C 10	N 5	O 11	P 2	0
158	HB	1	Total 28	C 10	N 5	O 11	P 2	0
158	HD	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
158	HF	1	Total 28	C 10	N 5	O 11	P 2	0
158	HH	1	Total 28	C 10	N 5	O 11	P 2	0
158	HJ	1	Total 28	C 10	N 5	O 11	P 2	0
158	HL	1	Total 28	C 10	N 5	O 11	P 2	0
158	HN	1	Total 28	C 10	N 5	O 11	P 2	0
158	HP	1	Total 28	C 10	N 5	O 11	P 2	0
158	HR	1	Total 28	C 10	N 5	O 11	P 2	0
158	HT	1	Total 28	C 10	N 5	O 11	P 2	0
158	HV	1	Total 28	C 10	N 5	O 11	P 2	0
158	HX	1	Total 28	C 10	N 5	O 11	P 2	0
158	HZ	1	Total 28	C 10	N 5	O 11	P 2	0
158	IB	1	Total 28	C 10	N 5	O 11	P 2	0
158	ID	1	Total 28	C 10	N 5	O 11	P 2	0
158	IF	1	Total 28	C 10	N 5	O 11	P 2	0
158	IH	1	Total 28	C 10	N 5	O 11	P 2	0
158	IJ	1	Total 28	C 10	N 5	O 11	P 2	0
158	IL	1	Total 28	C 10	N 5	O 11	P 2	0
158	IN	1	Total 28	C 10	N 5	O 11	P 2	0
158	IP	1	Total 28	C 10	N 5	O 11	P 2	0
158	IR	1	Total 28	C 10	N 5	O 11	P 2	0
158	IT	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
158	IV	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	IX	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	IZ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JB	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JD	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JF	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JG	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JI	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JS	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JW	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	JY	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KA	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KC	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KE	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KG	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KI	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
158	KK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KS	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KW	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	KY	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LA	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LC	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LE	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LG	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LI	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LS	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LW	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	LY	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
158	MA	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	MC	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ME	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	MG	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	MI	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	MK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	MM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	MO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	MQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	MU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	MW	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	MY	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NA	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NC	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NE	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NG	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NI	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NQ	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
158	NS	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	NY	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OA	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OC	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OE	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OG	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OI	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OS	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OW	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	OY	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	PA	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	PD	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	PF	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	PH	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	PJ	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
158	PL	1	Total 28	C 10	N 5	O 11	P 2	0
158	PN	1	Total 28	C 10	N 5	O 11	P 2	0
158	PP	1	Total 28	C 10	N 5	O 11	P 2	0
158	PR	1	Total 28	C 10	N 5	O 11	P 2	0
158	PT	1	Total 28	C 10	N 5	O 11	P 2	0
158	PV	1	Total 28	C 10	N 5	O 11	P 2	0
158	PX	1	Total 28	C 10	N 5	O 11	P 2	0
158	PZ	1	Total 28	C 10	N 5	O 11	P 2	0
158	QB	1	Total 28	C 10	N 5	O 11	P 2	0
158	QD	1	Total 28	C 10	N 5	O 11	P 2	0
158	QF	1	Total 28	C 10	N 5	O 11	P 2	0
158	QH	1	Total 28	C 10	N 5	O 11	P 2	0
158	QJ	1	Total 28	C 10	N 5	O 11	P 2	0
158	QL	1	Total 28	C 10	N 5	O 11	P 2	0
158	QN	1	Total 28	C 10	N 5	O 11	P 2	0
158	QP	1	Total 28	C 10	N 5	O 11	P 2	0
158	QR	1	Total 28	C 10	N 5	O 11	P 2	0
158	QT	1	Total 28	C 10	N 5	O 11	P 2	0
158	QV	1	Total 28	C 10	N 5	O 11	P 2	0
158	QX	1	Total 28	C 10	N 5	O 11	P 2	0
158	QZ	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
158	RB	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RD	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RF	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RH	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RL	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RN	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RP	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RR	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RT	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RV	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RX	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	RZ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	SB	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	SD	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	SF	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	SH	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	SJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	SL	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	SN	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	SP	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
158	SR	1	Total 28	C 10	N 5	O 11	P 2	0
158	ST	1	Total 28	C 10	N 5	O 11	P 2	0
158	SV	1	Total 28	C 10	N 5	O 11	P 2	0
158	SX	1	Total 28	C 10	N 5	O 11	P 2	0
158	SZ	1	Total 28	C 10	N 5	O 11	P 2	0
158	TB	1	Total 28	C 10	N 5	O 11	P 2	0
158	TD	1	Total 28	C 10	N 5	O 11	P 2	0
158	TF	1	Total 28	C 10	N 5	O 11	P 2	0
158	TH	1	Total 28	C 10	N 5	O 11	P 2	0
158	TJ	1	Total 28	C 10	N 5	O 11	P 2	0
158	TL	1	Total 28	C 10	N 5	O 11	P 2	0
158	TN	1	Total 28	C 10	N 5	O 11	P 2	0
158	TP	1	Total 28	C 10	N 5	O 11	P 2	0
158	TS	1	Total 28	C 10	N 5	O 11	P 2	0
158	TU	1	Total 28	C 10	N 5	O 11	P 2	0
158	TW	1	Total 28	C 10	N 5	O 11	P 2	0
158	TY	1	Total 28	C 10	N 5	O 11	P 2	0
158	UA	1	Total 28	C 10	N 5	O 11	P 2	0
158	UC	1	Total 28	C 10	N 5	O 11	P 2	0
158	UE	1	Total 28	C 10	N 5	O 11	P 2	0
158	UG	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
158	UI	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	UK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	UM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	UO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	UQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	US	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	UU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	UX	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	UZ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VB	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VD	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VF	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VH	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VL	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VN	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VP	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VR	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VT	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VV	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	VX	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
158	VZ	1	Total 28	C 10	N 5	O 11	P 2	0
158	WB	1	Total 28	C 10	N 5	O 11	P 2	0
158	WD	1	Total 28	C 10	N 5	O 11	P 2	0
158	WF	1	Total 28	C 10	N 5	O 11	P 2	0
158	WH	1	Total 28	C 10	N 5	O 11	P 2	0
158	WJ	1	Total 28	C 10	N 5	O 11	P 2	0
158	WL	1	Total 28	C 10	N 5	O 11	P 2	0
158	WN	1	Total 28	C 10	N 5	O 11	P 2	0
158	WP	1	Total 28	C 10	N 5	O 11	P 2	0
158	WR	1	Total 28	C 10	N 5	O 11	P 2	0
158	WT	1	Total 28	C 10	N 5	O 11	P 2	0
158	WV	1	Total 28	C 10	N 5	O 11	P 2	0
158	WX	1	Total 28	C 10	N 5	O 11	P 2	0
158	WZ	1	Total 28	C 10	N 5	O 11	P 2	0
158	XB	1	Total 28	C 10	N 5	O 11	P 2	0
158	XD	1	Total 28	C 10	N 5	O 11	P 2	0
158	XF	1	Total 28	C 10	N 5	O 11	P 2	0
158	XH	1	Total 28	C 10	N 5	O 11	P 2	0
158	XJ	1	Total 28	C 10	N 5	O 11	P 2	0
158	XL	1	Total 28	C 10	N 5	O 11	P 2	0
158	XN	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
158	XP	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	XR	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	XT	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	XV	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	XX	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	XZ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YB	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YD	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YF	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YH	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YS	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YW	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	YY	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZA	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZC	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZE	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
158	ZG	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZI	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZK	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZM	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZO	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZS	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZU	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZW	1	Total	C	N	O	P	0
			28	10	5	11	2	
158	ZY	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 159 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
159	AB	1	Total	Mg	0
			1	1	
159	AD	1	Total	Mg	0
			1	1	
159	AF	1	Total	Mg	0
			1	1	
159	AH	1	Total	Mg	0
			1	1	
159	AJ	1	Total	Mg	0
			1	1	
159	AL	1	Total	Mg	0
			1	1	
159	AN	1	Total	Mg	0
			1	1	
159	AP	1	Total	Mg	0
			1	1	
159	AR	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
159	AT	1	Total 1	Mg 1	0
159	AV	1	Total 1	Mg 1	0
159	AX	1	Total 1	Mg 1	0
159	AZ	1	Total 1	Mg 1	0
159	Ab	1	Total 1	Mg 1	0
159	Ad	1	Total 1	Mg 1	0
159	Af	1	Total 1	Mg 1	0
159	Ah	1	Total 1	Mg 1	0
159	Aj	1	Total 1	Mg 1	0
159	Al	1	Total 1	Mg 1	0
159	An	1	Total 1	Mg 1	0
159	Ap	1	Total 1	Mg 1	0
159	BB	1	Total 1	Mg 1	0
159	BD	1	Total 1	Mg 1	0
159	BF	1	Total 1	Mg 1	0
159	BH	1	Total 1	Mg 1	0
159	BJ	1	Total 1	Mg 1	0
159	BL	1	Total 1	Mg 1	0
159	BN	1	Total 1	Mg 1	0
159	BP	1	Total 1	Mg 1	0
159	BR	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	BT	1	Total 1	Mg 1	0
159	BV	1	Total 1	Mg 1	0
159	BX	1	Total 1	Mg 1	0
159	BZ	1	Total 1	Mg 1	0
159	CB	1	Total 1	Mg 1	0
159	CD	1	Total 1	Mg 1	0
159	CF	1	Total 1	Mg 1	0
159	CI	1	Total 1	Mg 1	0
159	CJ	1	Total 1	Mg 1	0
159	CL	1	Total 1	Mg 1	0
159	CN	1	Total 1	Mg 1	0
159	CP	1	Total 1	Mg 1	0
159	CR	1	Total 1	Mg 1	0
159	CT	1	Total 1	Mg 1	0
159	CV	1	Total 1	Mg 1	0
159	CX	1	Total 1	Mg 1	0
159	CZ	1	Total 1	Mg 1	0
159	DB	1	Total 1	Mg 1	0
159	DD	1	Total 1	Mg 1	0
159	DF	1	Total 1	Mg 1	0
159	DH	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	DJ	1	Total 1	Mg 1	0
159	DL	1	Total 1	Mg 1	0
159	DM	1	Total 1	Mg 1	0
159	DO	1	Total 1	Mg 1	0
159	DQ	1	Total 1	Mg 1	0
159	DS	1	Total 1	Mg 1	0
159	DU	1	Total 1	Mg 1	0
159	DW	1	Total 1	Mg 1	0
159	DY	1	Total 1	Mg 1	0
159	EA	1	Total 1	Mg 1	0
159	EC	1	Total 1	Mg 1	0
159	EE	1	Total 1	Mg 1	0
159	EG	1	Total 1	Mg 1	0
159	EI	1	Total 1	Mg 1	0
159	EK	1	Total 1	Mg 1	0
159	EM	1	Total 1	Mg 1	0
159	EO	1	Total 1	Mg 1	0
159	EQ	1	Total 1	Mg 1	0
159	ES	1	Total 1	Mg 1	0
159	EU	1	Total 1	Mg 1	0
159	EW	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	EZ	1	Total 1	Mg 1	0
159	FA	1	Total 1	Mg 1	0
159	FC	1	Total 1	Mg 1	0
159	FE	1	Total 1	Mg 1	0
159	FG	1	Total 1	Mg 1	0
159	FI	1	Total 1	Mg 1	0
159	FL	1	Total 1	Mg 1	0
159	FM	1	Total 1	Mg 1	0
159	FO	1	Total 1	Mg 1	0
159	FQ	1	Total 1	Mg 1	0
159	FS	1	Total 1	Mg 1	0
159	FW	1	Total 1	Mg 1	0
159	FY	1	Total 1	Mg 1	0
159	GA	1	Total 1	Mg 1	0
159	GC	1	Total 1	Mg 1	0
159	GE	1	Total 1	Mg 1	0
159	GG	1	Total 1	Mg 1	0
159	GI	1	Total 1	Mg 1	0
159	GK	1	Total 1	Mg 1	0
159	GM	1	Total 1	Mg 1	0
159	GO	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	GQ	1	Total 1	Mg 1	0
159	GS	1	Total 1	Mg 1	0
159	GU	1	Total 1	Mg 1	0
159	GW	1	Total 1	Mg 1	0
159	HA	1	Total 1	Mg 1	0
159	HC	1	Total 1	Mg 1	0
159	HE	1	Total 1	Mg 1	0
159	HG	1	Total 1	Mg 1	0
159	HI	1	Total 1	Mg 1	0
159	HK	1	Total 1	Mg 1	0
159	HM	1	Total 1	Mg 1	0
159	HO	1	Total 1	Mg 1	0
159	HQ	1	Total 1	Mg 1	0
159	HS	1	Total 1	Mg 1	0
159	HU	1	Total 1	Mg 1	0
159	HW	1	Total 1	Mg 1	0
159	HY	1	Total 1	Mg 1	0
159	IA	1	Total 1	Mg 1	0
159	IE	1	Total 1	Mg 1	0
159	IG	1	Total 1	Mg 1	0
159	II	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	IK	1	Total 1	Mg 1	0
159	IM	1	Total 1	Mg 1	0
159	IO	1	Total 1	Mg 1	0
159	IQ	1	Total 1	Mg 1	0
159	IS	1	Total 1	Mg 1	0
159	IU	1	Total 1	Mg 1	0
159	IW	1	Total 1	Mg 1	0
159	IY	1	Total 1	Mg 1	0
159	JA	1	Total 1	Mg 1	0
159	JC	1	Total 1	Mg 1	0
159	JE	1	Total 1	Mg 1	0
159	JH	1	Total 1	Mg 1	0
159	JJ	1	Total 1	Mg 1	0
159	JL	1	Total 1	Mg 1	0
159	JN	1	Total 1	Mg 1	0
159	JP	1	Total 1	Mg 1	0
159	JR	1	Total 1	Mg 1	0
159	JT	1	Total 1	Mg 1	0
159	JV	1	Total 1	Mg 1	0
159	JX	1	Total 1	Mg 1	0
159	JZ	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	KB	1	Total 1	Mg 1	0
159	KD	1	Total 1	Mg 1	0
159	KF	1	Total 1	Mg 1	0
159	KH	1	Total 1	Mg 1	0
159	KJ	1	Total 1	Mg 1	0
159	KL	1	Total 1	Mg 1	0
159	KN	1	Total 1	Mg 1	0
159	KP	1	Total 1	Mg 1	0
159	KR	1	Total 1	Mg 1	0
159	KT	1	Total 1	Mg 1	0
159	KV	1	Total 1	Mg 1	0
159	KX	1	Total 1	Mg 1	0
159	KZ	1	Total 1	Mg 1	0
159	LB	1	Total 1	Mg 1	0
159	LD	1	Total 1	Mg 1	0
159	LF	1	Total 1	Mg 1	0
159	LH	1	Total 1	Mg 1	0
159	LJ	1	Total 1	Mg 1	0
159	LL	1	Total 1	Mg 1	0
159	LN	1	Total 1	Mg 1	0
159	LP	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	LR	1	Total 1	Mg 1	0
159	LT	1	Total 1	Mg 1	0
159	LV	1	Total 1	Mg 1	0
159	LX	1	Total 1	Mg 1	0
159	LZ	1	Total 1	Mg 1	0
159	MB	1	Total 1	Mg 1	0
159	MD	1	Total 1	Mg 1	0
159	MF	1	Total 1	Mg 1	0
159	MH	1	Total 1	Mg 1	0
159	MJ	1	Total 1	Mg 1	0
159	ML	1	Total 1	Mg 1	0
159	MN	1	Total 1	Mg 1	0
159	MP	1	Total 1	Mg 1	0
159	MR	1	Total 1	Mg 1	0
159	MT	1	Total 1	Mg 1	0
159	MV	1	Total 1	Mg 1	0
159	MX	1	Total 1	Mg 1	0
159	MZ	1	Total 1	Mg 1	0
159	NB	1	Total 1	Mg 1	0
159	ND	1	Total 1	Mg 1	0
159	NF	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	NH	1	Total 1	Mg 1	0
159	NJ	1	Total 1	Mg 1	0
159	NL	1	Total 1	Mg 1	0
159	NN	1	Total 1	Mg 1	0
159	NP	1	Total 1	Mg 1	0
159	NR	1	Total 1	Mg 1	0
159	NT	1	Total 1	Mg 1	0
159	NV	1	Total 1	Mg 1	0
159	NX	1	Total 1	Mg 1	0
159	NZ	1	Total 1	Mg 1	0
159	OB	1	Total 1	Mg 1	0
159	OD	1	Total 1	Mg 1	0
159	OF	1	Total 1	Mg 1	0
159	OH	1	Total 1	Mg 1	0
159	OJ	1	Total 1	Mg 1	0
159	OL	1	Total 1	Mg 1	0
159	ON	1	Total 1	Mg 1	0
159	OP	1	Total 1	Mg 1	0
159	OR	1	Total 1	Mg 1	0
159	OT	1	Total 1	Mg 1	0
159	OV	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	OX	1	Total 1	Mg 1	0
159	OZ	1	Total 1	Mg 1	0
159	PC	1	Total 1	Mg 1	0
159	PE	1	Total 1	Mg 1	0
159	PG	1	Total 1	Mg 1	0
159	PI	1	Total 1	Mg 1	0
159	PK	1	Total 1	Mg 1	0
159	PM	1	Total 1	Mg 1	0
159	PO	1	Total 1	Mg 1	0
159	PQ	1	Total 1	Mg 1	0
159	PS	1	Total 1	Mg 1	0
159	PU	1	Total 1	Mg 1	0
159	PW	1	Total 1	Mg 1	0
159	PY	1	Total 1	Mg 1	0
159	QA	1	Total 1	Mg 1	0
159	QC	1	Total 1	Mg 1	0
159	QE	1	Total 1	Mg 1	0
159	QG	1	Total 1	Mg 1	0
159	QI	1	Total 1	Mg 1	0
159	QK	1	Total 1	Mg 1	0
159	QM	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	QO	1	Total 1	Mg 1	0
159	QQ	1	Total 1	Mg 1	0
159	QS	1	Total 1	Mg 1	0
159	QU	1	Total 1	Mg 1	0
159	QW	1	Total 1	Mg 1	0
159	QY	1	Total 1	Mg 1	0
159	RA	1	Total 1	Mg 1	0
159	RC	1	Total 1	Mg 1	0
159	RE	1	Total 1	Mg 1	0
159	RG	1	Total 1	Mg 1	0
159	RI	1	Total 1	Mg 1	0
159	RK	1	Total 1	Mg 1	0
159	RM	1	Total 1	Mg 1	0
159	RO	1	Total 1	Mg 1	0
159	RQ	1	Total 1	Mg 1	0
159	RS	1	Total 1	Mg 1	0
159	RU	1	Total 1	Mg 1	0
159	RW	1	Total 1	Mg 1	0
159	RY	1	Total 1	Mg 1	0
159	SA	1	Total 1	Mg 1	0
159	SC	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	SE	1	Total 1	Mg 1	0
159	SG	1	Total 1	Mg 1	0
159	SI	1	Total 1	Mg 1	0
159	SK	1	Total 1	Mg 1	0
159	SM	1	Total 1	Mg 1	0
159	SO	1	Total 1	Mg 1	0
159	SQ	1	Total 1	Mg 1	0
159	SS	1	Total 1	Mg 1	0
159	SU	1	Total 1	Mg 1	0
159	SW	1	Total 1	Mg 1	0
159	SY	1	Total 1	Mg 1	0
159	TA	1	Total 1	Mg 1	0
159	TC	1	Total 1	Mg 1	0
159	TE	1	Total 1	Mg 1	0
159	TG	1	Total 1	Mg 1	0
159	TI	1	Total 1	Mg 1	0
159	TK	1	Total 1	Mg 1	0
159	TM	1	Total 1	Mg 1	0
159	TO	1	Total 1	Mg 1	0
159	TQ	1	Total 1	Mg 1	0
159	TR	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	TT	1	Total 1	Mg 1	0
159	TV	1	Total 1	Mg 1	0
159	TX	1	Total 1	Mg 1	0
159	TZ	1	Total 1	Mg 1	0
159	UB	1	Total 1	Mg 1	0
159	UD	1	Total 1	Mg 1	0
159	UF	1	Total 1	Mg 1	0
159	UH	1	Total 1	Mg 1	0
159	UJ	1	Total 1	Mg 1	0
159	UL	1	Total 1	Mg 1	0
159	UN	1	Total 1	Mg 1	0
159	UP	1	Total 1	Mg 1	0
159	UR	1	Total 1	Mg 1	0
159	UT	1	Total 1	Mg 1	0
159	UW	1	Total 1	Mg 1	0
159	UY	1	Total 1	Mg 1	0
159	VA	1	Total 1	Mg 1	0
159	VC	1	Total 1	Mg 1	0
159	VE	1	Total 1	Mg 1	0
159	VG	1	Total 1	Mg 1	0
159	VI	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	VK	1	Total 1	Mg 1	0
159	VM	1	Total 1	Mg 1	0
159	VO	1	Total 1	Mg 1	0
159	VQ	1	Total 1	Mg 1	0
159	VS	1	Total 1	Mg 1	0
159	VU	1	Total 1	Mg 1	0
159	VW	1	Total 1	Mg 1	0
159	VY	1	Total 1	Mg 1	0
159	WA	1	Total 1	Mg 1	0
159	WC	1	Total 1	Mg 1	0
159	WE	1	Total 1	Mg 1	0
159	WG	1	Total 1	Mg 1	0
159	WI	1	Total 1	Mg 1	0
159	WK	1	Total 1	Mg 1	0
159	WM	1	Total 1	Mg 1	0
159	WO	1	Total 1	Mg 1	0
159	WQ	1	Total 1	Mg 1	0
159	WS	1	Total 1	Mg 1	0
159	WU	1	Total 1	Mg 1	0
159	WW	1	Total 1	Mg 1	0
159	WY	1	Total 1	Mg 1	0

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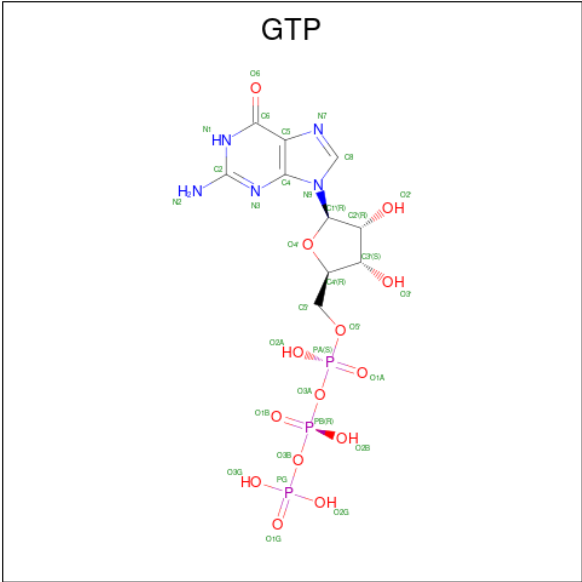
Mol	Chain	Residues	Atoms		AltConf
159	XA	1	Total 1	Mg 1	0
159	XC	1	Total 1	Mg 1	0
159	XE	1	Total 1	Mg 1	0
159	XG	1	Total 1	Mg 1	0
159	XI	1	Total 1	Mg 1	0
159	XK	1	Total 1	Mg 1	0
159	XM	1	Total 1	Mg 1	0
159	XO	1	Total 1	Mg 1	0
159	XQ	1	Total 1	Mg 1	0
159	XS	1	Total 1	Mg 1	0
159	XU	1	Total 1	Mg 1	0
159	XW	1	Total 1	Mg 1	0
159	XY	1	Total 1	Mg 1	0
159	YA	1	Total 1	Mg 1	0
159	YC	1	Total 1	Mg 1	0
159	YE	1	Total 1	Mg 1	0
159	YG	1	Total 1	Mg 1	0
159	YJ	1	Total 1	Mg 1	0
159	YL	1	Total 1	Mg 1	0
159	YN	1	Total 1	Mg 1	0
159	YP	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
159	YR	1	Total 1	Mg 1	0
159	YT	1	Total 1	Mg 1	0
159	YV	1	Total 1	Mg 1	0
159	YX	1	Total 1	Mg 1	0
159	YZ	1	Total 1	Mg 1	0
159	ZB	1	Total 1	Mg 1	0
159	ZD	1	Total 1	Mg 1	0
159	ZF	1	Total 1	Mg 1	0
159	ZH	1	Total 1	Mg 1	0
159	ZJ	1	Total 1	Mg 1	0
159	ZL	1	Total 1	Mg 1	0
159	ZN	1	Total 1	Mg 1	0
159	ZP	1	Total 1	Mg 1	0
159	ZR	1	Total 1	Mg 1	0
159	ZT	1	Total 1	Mg 1	0
159	ZV	1	Total 1	Mg 1	0
159	ZX	1	Total 1	Mg 1	0
159	ZZ	1	Total 1	Mg 1	0

- Molecule 160 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



Mol	Chain	Residues	Atoms					AltConf
160	AB	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AD	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AF	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AH	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AL	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AN	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AP	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AR	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AT	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AV	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AX	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	AZ	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	Ab	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
160	Ad	1	Total 32	C 10	N 5	O 14	P 3	0
160	Af	1	Total 32	C 10	N 5	O 14	P 3	0
160	Ah	1	Total 32	C 10	N 5	O 14	P 3	0
160	Aj	1	Total 32	C 10	N 5	O 14	P 3	0
160	Al	1	Total 32	C 10	N 5	O 14	P 3	0
160	An	1	Total 32	C 10	N 5	O 14	P 3	0
160	Ap	1	Total 32	C 10	N 5	O 14	P 3	0
160	BB	1	Total 32	C 10	N 5	O 14	P 3	0
160	BD	1	Total 32	C 10	N 5	O 14	P 3	0
160	BF	1	Total 32	C 10	N 5	O 14	P 3	0
160	BH	1	Total 32	C 10	N 5	O 14	P 3	0
160	BJ	1	Total 32	C 10	N 5	O 14	P 3	0
160	BL	1	Total 32	C 10	N 5	O 14	P 3	0
160	BN	1	Total 32	C 10	N 5	O 14	P 3	0
160	BP	1	Total 32	C 10	N 5	O 14	P 3	0
160	BR	1	Total 32	C 10	N 5	O 14	P 3	0
160	BT	1	Total 32	C 10	N 5	O 14	P 3	0
160	BV	1	Total 32	C 10	N 5	O 14	P 3	0
160	BX	1	Total 32	C 10	N 5	O 14	P 3	0
160	BZ	1	Total 32	C 10	N 5	O 14	P 3	0
160	CB	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	CD	1	Total 32	C 10	N 5	O 14	P 3	0
160	CF	1	Total 32	C 10	N 5	O 14	P 3	0
160	CI	1	Total 32	C 10	N 5	O 14	P 3	0
160	CJ	1	Total 32	C 10	N 5	O 14	P 3	0
160	CL	1	Total 32	C 10	N 5	O 14	P 3	0
160	CN	1	Total 32	C 10	N 5	O 14	P 3	0
160	CP	1	Total 32	C 10	N 5	O 14	P 3	0
160	CR	1	Total 32	C 10	N 5	O 14	P 3	0
160	CT	1	Total 32	C 10	N 5	O 14	P 3	0
160	CV	1	Total 32	C 10	N 5	O 14	P 3	0
160	CX	1	Total 32	C 10	N 5	O 14	P 3	0
160	CZ	1	Total 32	C 10	N 5	O 14	P 3	0
160	DB	1	Total 32	C 10	N 5	O 14	P 3	0
160	DD	1	Total 32	C 10	N 5	O 14	P 3	0
160	DF	1	Total 32	C 10	N 5	O 14	P 3	0
160	DH	1	Total 32	C 10	N 5	O 14	P 3	0
160	DJ	1	Total 32	C 10	N 5	O 14	P 3	0
160	DL	1	Total 32	C 10	N 5	O 14	P 3	0
160	DM	1	Total 32	C 10	N 5	O 14	P 3	0
160	DO	1	Total 32	C 10	N 5	O 14	P 3	0
160	DQ	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	DS	1	Total 32	C 10	N 5	O 14	P 3	0
160	DU	1	Total 32	C 10	N 5	O 14	P 3	0
160	DW	1	Total 32	C 10	N 5	O 14	P 3	0
160	DY	1	Total 32	C 10	N 5	O 14	P 3	0
160	EA	1	Total 32	C 10	N 5	O 14	P 3	0
160	EC	1	Total 32	C 10	N 5	O 14	P 3	0
160	EE	1	Total 32	C 10	N 5	O 14	P 3	0
160	EG	1	Total 32	C 10	N 5	O 14	P 3	0
160	EI	1	Total 32	C 10	N 5	O 14	P 3	0
160	EK	1	Total 32	C 10	N 5	O 14	P 3	0
160	EM	1	Total 32	C 10	N 5	O 14	P 3	0
160	EO	1	Total 32	C 10	N 5	O 14	P 3	0
160	EQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	ES	1	Total 32	C 10	N 5	O 14	P 3	0
160	EU	1	Total 32	C 10	N 5	O 14	P 3	0
160	EW	1	Total 32	C 10	N 5	O 14	P 3	0
160	EY	1	Total 32	C 10	N 5	O 14	P 3	0
160	FA	1	Total 32	C 10	N 5	O 14	P 3	0
160	FC	1	Total 32	C 10	N 5	O 14	P 3	0
160	FE	1	Total 32	C 10	N 5	O 14	P 3	0
160	FG	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	FI	1	Total 32	C 10	N 5	O 14	P 3	0
160	FK	1	Total 32	C 10	N 5	O 14	P 3	0
160	FM	1	Total 32	C 10	N 5	O 14	P 3	0
160	FO	1	Total 32	C 10	N 5	O 14	P 3	0
160	FQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	FS	1	Total 32	C 10	N 5	O 14	P 3	0
160	FW	1	Total 32	C 10	N 5	O 14	P 3	0
160	FY	1	Total 32	C 10	N 5	O 14	P 3	0
160	GA	1	Total 32	C 10	N 5	O 14	P 3	0
160	GC	1	Total 32	C 10	N 5	O 14	P 3	0
160	GE	1	Total 32	C 10	N 5	O 14	P 3	0
160	GG	1	Total 32	C 10	N 5	O 14	P 3	0
160	GI	1	Total 32	C 10	N 5	O 14	P 3	0
160	GK	1	Total 32	C 10	N 5	O 14	P 3	0
160	GM	1	Total 32	C 10	N 5	O 14	P 3	0
160	GO	1	Total 32	C 10	N 5	O 14	P 3	0
160	GQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	GS	1	Total 32	C 10	N 5	O 14	P 3	0
160	GU	1	Total 32	C 10	N 5	O 14	P 3	0
160	GW	1	Total 32	C 10	N 5	O 14	P 3	0
160	HA	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	HC	1	Total 32	C 10	N 5	O 14	P 3	0
160	HE	1	Total 32	C 10	N 5	O 14	P 3	0
160	HG	1	Total 32	C 10	N 5	O 14	P 3	0
160	HI	1	Total 32	C 10	N 5	O 14	P 3	0
160	HK	1	Total 32	C 10	N 5	O 14	P 3	0
160	HM	1	Total 32	C 10	N 5	O 14	P 3	0
160	HO	1	Total 32	C 10	N 5	O 14	P 3	0
160	HQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	HS	1	Total 32	C 10	N 5	O 14	P 3	0
160	HU	1	Total 32	C 10	N 5	O 14	P 3	0
160	HW	1	Total 32	C 10	N 5	O 14	P 3	0
160	HY	1	Total 32	C 10	N 5	O 14	P 3	0
160	IA	1	Total 32	C 10	N 5	O 14	P 3	0
160	IE	1	Total 32	C 10	N 5	O 14	P 3	0
160	IG	1	Total 32	C 10	N 5	O 14	P 3	0
160	II	1	Total 32	C 10	N 5	O 14	P 3	0
160	IK	1	Total 32	C 10	N 5	O 14	P 3	0
160	IM	1	Total 32	C 10	N 5	O 14	P 3	0
160	IO	1	Total 32	C 10	N 5	O 14	P 3	0
160	IQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	IS	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	IU	1	Total 32	C 10	N 5	O 14	P 3	0
160	IW	1	Total 32	C 10	N 5	O 14	P 3	0
160	IY	1	Total 32	C 10	N 5	O 14	P 3	0
160	JA	1	Total 32	C 10	N 5	O 14	P 3	0
160	JC	1	Total 32	C 10	N 5	O 14	P 3	0
160	JE	1	Total 32	C 10	N 5	O 14	P 3	0
160	JH	1	Total 32	C 10	N 5	O 14	P 3	0
160	JJ	1	Total 32	C 10	N 5	O 14	P 3	0
160	JL	1	Total 32	C 10	N 5	O 14	P 3	0
160	JN	1	Total 32	C 10	N 5	O 14	P 3	0
160	JP	1	Total 32	C 10	N 5	O 14	P 3	0
160	JR	1	Total 32	C 10	N 5	O 14	P 3	0
160	JT	1	Total 32	C 10	N 5	O 14	P 3	0
160	JV	1	Total 32	C 10	N 5	O 14	P 3	0
160	JX	1	Total 32	C 10	N 5	O 14	P 3	0
160	JZ	1	Total 32	C 10	N 5	O 14	P 3	0
160	KB	1	Total 32	C 10	N 5	O 14	P 3	0
160	KD	1	Total 32	C 10	N 5	O 14	P 3	0
160	KF	1	Total 32	C 10	N 5	O 14	P 3	0
160	KH	1	Total 32	C 10	N 5	O 14	P 3	0
160	KJ	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	KL	1	Total 32	C 10	N 5	O 14	P 3	0
160	KN	1	Total 32	C 10	N 5	O 14	P 3	0
160	KP	1	Total 32	C 10	N 5	O 14	P 3	0
160	KR	1	Total 32	C 10	N 5	O 14	P 3	0
160	KT	1	Total 32	C 10	N 5	O 14	P 3	0
160	KV	1	Total 32	C 10	N 5	O 14	P 3	0
160	KX	1	Total 32	C 10	N 5	O 14	P 3	0
160	KZ	1	Total 32	C 10	N 5	O 14	P 3	0
160	LB	1	Total 32	C 10	N 5	O 14	P 3	0
160	LD	1	Total 32	C 10	N 5	O 14	P 3	0
160	LF	1	Total 32	C 10	N 5	O 14	P 3	0
160	LH	1	Total 32	C 10	N 5	O 14	P 3	0
160	LJ	1	Total 32	C 10	N 5	O 14	P 3	0
160	LL	1	Total 32	C 10	N 5	O 14	P 3	0
160	LN	1	Total 32	C 10	N 5	O 14	P 3	0
160	LP	1	Total 32	C 10	N 5	O 14	P 3	0
160	LR	1	Total 32	C 10	N 5	O 14	P 3	0
160	LT	1	Total 32	C 10	N 5	O 14	P 3	0
160	LV	1	Total 32	C 10	N 5	O 14	P 3	0
160	LX	1	Total 32	C 10	N 5	O 14	P 3	0
160	LZ	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	MB	1	Total 32	C 10	N 5	O 14	P 3	0
160	MD	1	Total 32	C 10	N 5	O 14	P 3	0
160	MF	1	Total 32	C 10	N 5	O 14	P 3	0
160	MH	1	Total 32	C 10	N 5	O 14	P 3	0
160	MJ	1	Total 32	C 10	N 5	O 14	P 3	0
160	ML	1	Total 32	C 10	N 5	O 14	P 3	0
160	MN	1	Total 32	C 10	N 5	O 14	P 3	0
160	MP	1	Total 32	C 10	N 5	O 14	P 3	0
160	MR	1	Total 32	C 10	N 5	O 14	P 3	0
160	MT	1	Total 32	C 10	N 5	O 14	P 3	0
160	MV	1	Total 32	C 10	N 5	O 14	P 3	0
160	MX	1	Total 32	C 10	N 5	O 14	P 3	0
160	MZ	1	Total 32	C 10	N 5	O 14	P 3	0
160	NB	1	Total 32	C 10	N 5	O 14	P 3	0
160	ND	1	Total 32	C 10	N 5	O 14	P 3	0
160	NF	1	Total 32	C 10	N 5	O 14	P 3	0
160	NH	1	Total 32	C 10	N 5	O 14	P 3	0
160	NJ	1	Total 32	C 10	N 5	O 14	P 3	0
160	NL	1	Total 32	C 10	N 5	O 14	P 3	0
160	NN	1	Total 32	C 10	N 5	O 14	P 3	0
160	NP	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	NR	1	Total 32	C 10	N 5	O 14	P 3	0
160	NT	1	Total 32	C 10	N 5	O 14	P 3	0
160	NV	1	Total 32	C 10	N 5	O 14	P 3	0
160	NX	1	Total 32	C 10	N 5	O 14	P 3	0
160	NZ	1	Total 32	C 10	N 5	O 14	P 3	0
160	OB	1	Total 32	C 10	N 5	O 14	P 3	0
160	OD	1	Total 32	C 10	N 5	O 14	P 3	0
160	OF	1	Total 32	C 10	N 5	O 14	P 3	0
160	OH	1	Total 32	C 10	N 5	O 14	P 3	0
160	OJ	1	Total 32	C 10	N 5	O 14	P 3	0
160	OL	1	Total 32	C 10	N 5	O 14	P 3	0
160	ON	1	Total 32	C 10	N 5	O 14	P 3	0
160	OP	1	Total 32	C 10	N 5	O 14	P 3	0
160	OR	1	Total 32	C 10	N 5	O 14	P 3	0
160	OT	1	Total 32	C 10	N 5	O 14	P 3	0
160	OV	1	Total 32	C 10	N 5	O 14	P 3	0
160	OX	1	Total 32	C 10	N 5	O 14	P 3	0
160	OZ	1	Total 32	C 10	N 5	O 14	P 3	0
160	PC	1	Total 32	C 10	N 5	O 14	P 3	0
160	PE	1	Total 32	C 10	N 5	O 14	P 3	0
160	PG	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	PI	1	Total 32	C 10	N 5	O 14	P 3	0
160	PK	1	Total 32	C 10	N 5	O 14	P 3	0
160	PM	1	Total 32	C 10	N 5	O 14	P 3	0
160	PO	1	Total 32	C 10	N 5	O 14	P 3	0
160	PQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	PS	1	Total 32	C 10	N 5	O 14	P 3	0
160	PU	1	Total 32	C 10	N 5	O 14	P 3	0
160	PW	1	Total 32	C 10	N 5	O 14	P 3	0
160	PY	1	Total 32	C 10	N 5	O 14	P 3	0
160	QA	1	Total 32	C 10	N 5	O 14	P 3	0
160	QC	1	Total 32	C 10	N 5	O 14	P 3	0
160	QE	1	Total 32	C 10	N 5	O 14	P 3	0
160	QG	1	Total 32	C 10	N 5	O 14	P 3	0
160	QI	1	Total 32	C 10	N 5	O 14	P 3	0
160	QK	1	Total 32	C 10	N 5	O 14	P 3	0
160	QM	1	Total 32	C 10	N 5	O 14	P 3	0
160	QO	1	Total 32	C 10	N 5	O 14	P 3	0
160	QQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	QS	1	Total 32	C 10	N 5	O 14	P 3	0
160	QU	1	Total 32	C 10	N 5	O 14	P 3	0
160	QW	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	QY	1	Total 32	C 10	N 5	O 14	P 3	0
160	RA	1	Total 32	C 10	N 5	O 14	P 3	0
160	RC	1	Total 32	C 10	N 5	O 14	P 3	0
160	RE	1	Total 32	C 10	N 5	O 14	P 3	0
160	RG	1	Total 32	C 10	N 5	O 14	P 3	0
160	RI	1	Total 32	C 10	N 5	O 14	P 3	0
160	RK	1	Total 32	C 10	N 5	O 14	P 3	0
160	RM	1	Total 32	C 10	N 5	O 14	P 3	0
160	RO	1	Total 32	C 10	N 5	O 14	P 3	0
160	RQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	RS	1	Total 32	C 10	N 5	O 14	P 3	0
160	RU	1	Total 32	C 10	N 5	O 14	P 3	0
160	RW	1	Total 32	C 10	N 5	O 14	P 3	0
160	RY	1	Total 32	C 10	N 5	O 14	P 3	0
160	SA	1	Total 32	C 10	N 5	O 14	P 3	0
160	SC	1	Total 32	C 10	N 5	O 14	P 3	0
160	SE	1	Total 32	C 10	N 5	O 14	P 3	0
160	SG	1	Total 32	C 10	N 5	O 14	P 3	0
160	SI	1	Total 32	C 10	N 5	O 14	P 3	0
160	SK	1	Total 32	C 10	N 5	O 14	P 3	0
160	SM	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	SO	1	Total 32	C 10	N 5	O 14	P 3	0
160	SQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	SS	1	Total 32	C 10	N 5	O 14	P 3	0
160	SU	1	Total 32	C 10	N 5	O 14	P 3	0
160	SW	1	Total 32	C 10	N 5	O 14	P 3	0
160	SY	1	Total 32	C 10	N 5	O 14	P 3	0
160	TA	1	Total 32	C 10	N 5	O 14	P 3	0
160	TC	1	Total 32	C 10	N 5	O 14	P 3	0
160	TE	1	Total 32	C 10	N 5	O 14	P 3	0
160	TG	1	Total 32	C 10	N 5	O 14	P 3	0
160	TI	1	Total 32	C 10	N 5	O 14	P 3	0
160	TK	1	Total 32	C 10	N 5	O 14	P 3	0
160	TM	1	Total 32	C 10	N 5	O 14	P 3	0
160	TO	1	Total 32	C 10	N 5	O 14	P 3	0
160	TQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	TR	1	Total 32	C 10	N 5	O 14	P 3	0
160	TT	1	Total 32	C 10	N 5	O 14	P 3	0
160	TV	1	Total 32	C 10	N 5	O 14	P 3	0
160	TX	1	Total 32	C 10	N 5	O 14	P 3	0
160	TZ	1	Total 32	C 10	N 5	O 14	P 3	0
160	UB	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	UD	1	Total 32	C 10	N 5	O 14	P 3	0
160	UF	1	Total 32	C 10	N 5	O 14	P 3	0
160	UH	1	Total 32	C 10	N 5	O 14	P 3	0
160	UJ	1	Total 32	C 10	N 5	O 14	P 3	0
160	UL	1	Total 32	C 10	N 5	O 14	P 3	0
160	UN	1	Total 32	C 10	N 5	O 14	P 3	0
160	UP	1	Total 32	C 10	N 5	O 14	P 3	0
160	UR	1	Total 32	C 10	N 5	O 14	P 3	0
160	UT	1	Total 32	C 10	N 5	O 14	P 3	0
160	UW	1	Total 32	C 10	N 5	O 14	P 3	0
160	UY	1	Total 32	C 10	N 5	O 14	P 3	0
160	VA	1	Total 32	C 10	N 5	O 14	P 3	0
160	VC	1	Total 32	C 10	N 5	O 14	P 3	0
160	VE	1	Total 32	C 10	N 5	O 14	P 3	0
160	VG	1	Total 32	C 10	N 5	O 14	P 3	0
160	VI	1	Total 32	C 10	N 5	O 14	P 3	0
160	VK	1	Total 32	C 10	N 5	O 14	P 3	0
160	VM	1	Total 32	C 10	N 5	O 14	P 3	0
160	VO	1	Total 32	C 10	N 5	O 14	P 3	0
160	VQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	VS	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	VU	1	Total 32	C 10	N 5	O 14	P 3	0
160	VW	1	Total 32	C 10	N 5	O 14	P 3	0
160	VY	1	Total 32	C 10	N 5	O 14	P 3	0
160	WA	1	Total 32	C 10	N 5	O 14	P 3	0
160	WC	1	Total 32	C 10	N 5	O 14	P 3	0
160	WE	1	Total 32	C 10	N 5	O 14	P 3	0
160	WG	1	Total 32	C 10	N 5	O 14	P 3	0
160	WI	1	Total 32	C 10	N 5	O 14	P 3	0
160	WK	1	Total 32	C 10	N 5	O 14	P 3	0
160	WM	1	Total 32	C 10	N 5	O 14	P 3	0
160	WO	1	Total 32	C 10	N 5	O 14	P 3	0
160	WQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	WS	1	Total 32	C 10	N 5	O 14	P 3	0
160	WU	1	Total 32	C 10	N 5	O 14	P 3	0
160	WW	1	Total 32	C 10	N 5	O 14	P 3	0
160	WY	1	Total 32	C 10	N 5	O 14	P 3	0
160	XA	1	Total 32	C 10	N 5	O 14	P 3	0
160	XC	1	Total 32	C 10	N 5	O 14	P 3	0
160	XE	1	Total 32	C 10	N 5	O 14	P 3	0
160	XG	1	Total 32	C 10	N 5	O 14	P 3	0
160	XI	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
160	XK	1	Total 32	C 10	N 5	O 14	P 3	0
160	XM	1	Total 32	C 10	N 5	O 14	P 3	0
160	XO	1	Total 32	C 10	N 5	O 14	P 3	0
160	XQ	1	Total 32	C 10	N 5	O 14	P 3	0
160	XS	1	Total 32	C 10	N 5	O 14	P 3	0
160	XU	1	Total 32	C 10	N 5	O 14	P 3	0
160	XW	1	Total 32	C 10	N 5	O 14	P 3	0
160	XY	1	Total 32	C 10	N 5	O 14	P 3	0
160	YA	1	Total 32	C 10	N 5	O 14	P 3	0
160	YC	1	Total 32	C 10	N 5	O 14	P 3	0
160	YE	1	Total 32	C 10	N 5	O 14	P 3	0
160	YG	1	Total 32	C 10	N 5	O 14	P 3	0
160	YJ	1	Total 32	C 10	N 5	O 14	P 3	0
160	YL	1	Total 32	C 10	N 5	O 14	P 3	0
160	YN	1	Total 32	C 10	N 5	O 14	P 3	0
160	YP	1	Total 32	C 10	N 5	O 14	P 3	0
160	YR	1	Total 32	C 10	N 5	O 14	P 3	0
160	YT	1	Total 32	C 10	N 5	O 14	P 3	0
160	YV	1	Total 32	C 10	N 5	O 14	P 3	0
160	YX	1	Total 32	C 10	N 5	O 14	P 3	0
160	YZ	1	Total 32	C 10	N 5	O 14	P 3	0

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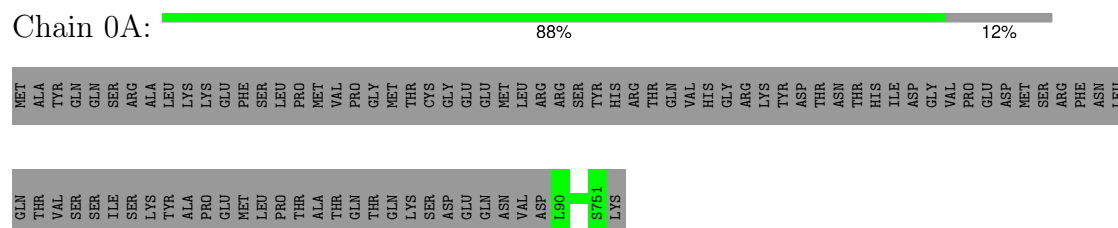
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Mol	Chain	Residues	Atoms					AltConf
160	ZB	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZD	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZF	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZH	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZJ	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZL	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZN	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZP	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZR	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZT	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZV	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZX	1	Total	C	N	O	P	0
			32	10	5	14	3	
160	ZZ	1	Total	C	N	O	P	0
			32	10	5	14	3	

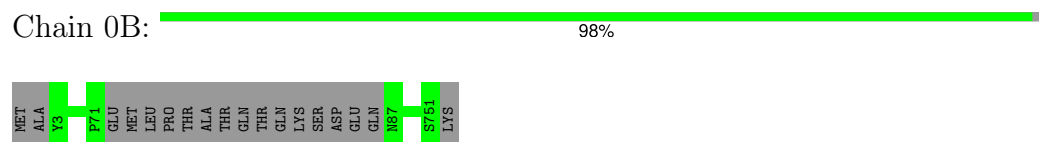
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

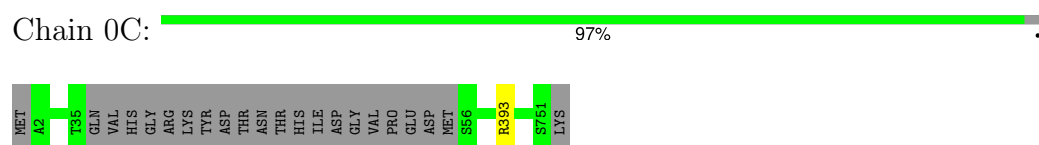
- Molecule 1: EF-hand domain-containing family member C2



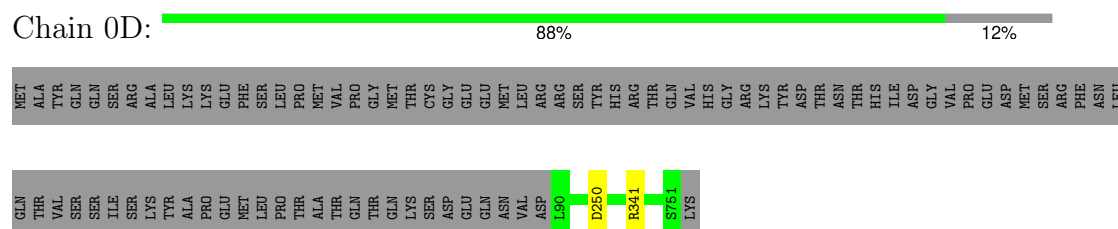
- Molecule 1: EF-hand domain-containing family member C2



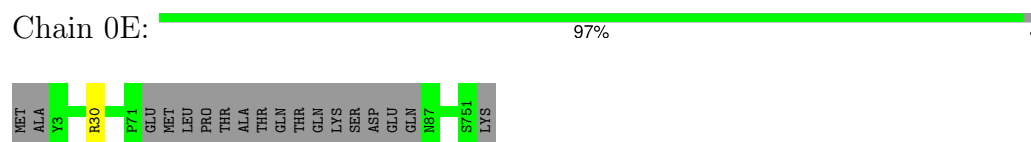
- Molecule 1: EF-hand domain-containing family member C2



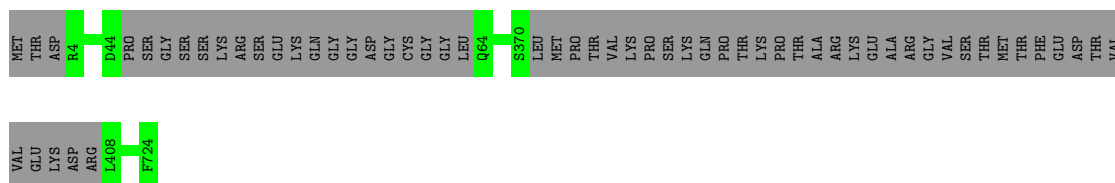
- Molecule 1: EF-hand domain-containing family member C2



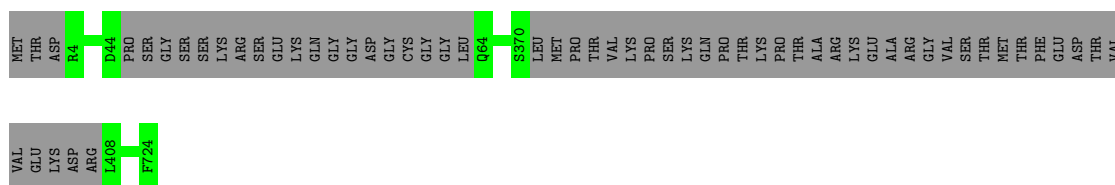
- Molecule 1: EF-hand domain-containing family member C2



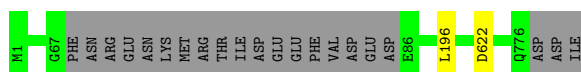
- Molecule 3: Rib72 protein-like protein



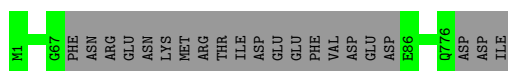
- Molecule 3: Rib72 protein-like protein



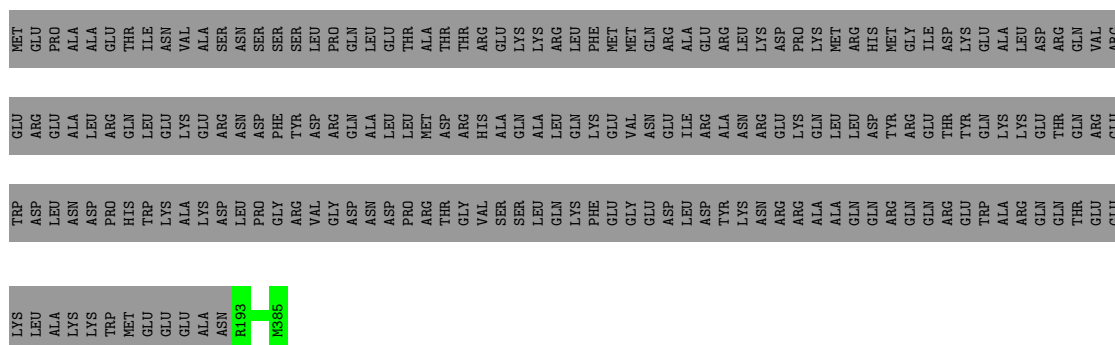
- Molecule 4: CMF34/CARP4



- Molecule 4: CMF34/CARP4



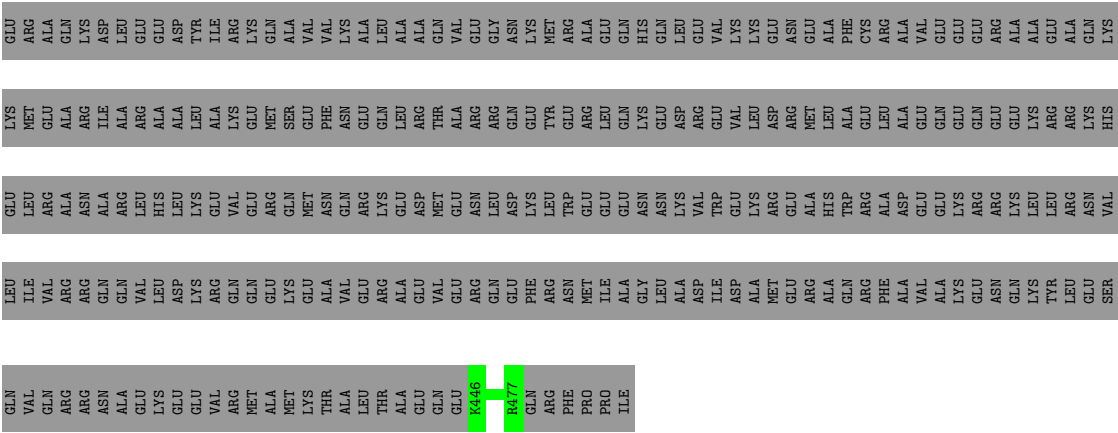
- Molecule 5: Flagellar protofilament ribbon protein, putative



- Molecule 5: Flagellar protofilament ribbon protein, putative

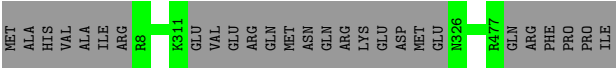






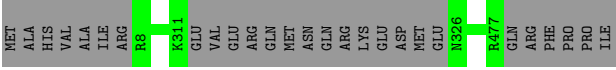
• Molecule 6: Cilia- and flagella-associated protein 53

Chain 0V: 94% 6%



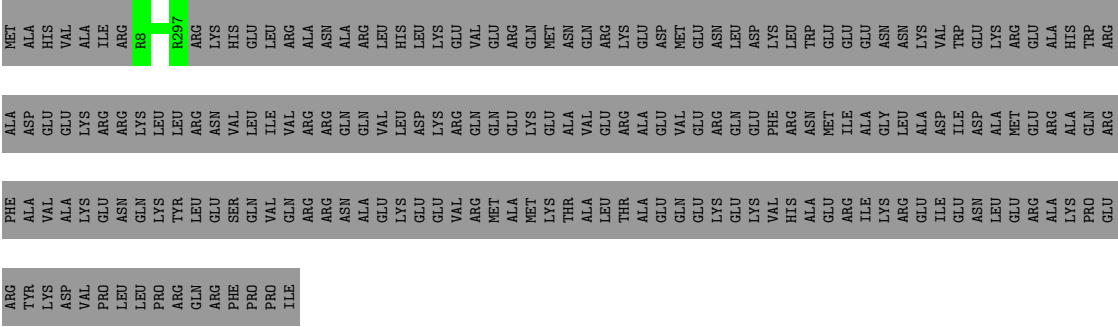
• Molecule 6: Cilia- and flagella-associated protein 53

Chain 0W: 94% 6%



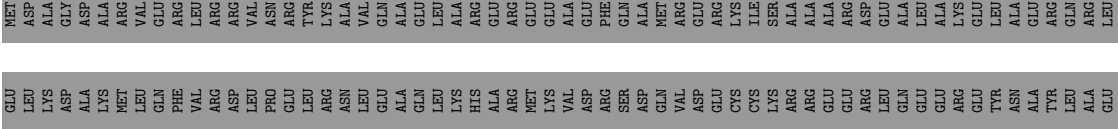
• Molecule 6: Cilia- and flagella-associated protein 53

Chain 0X: 60% 40%

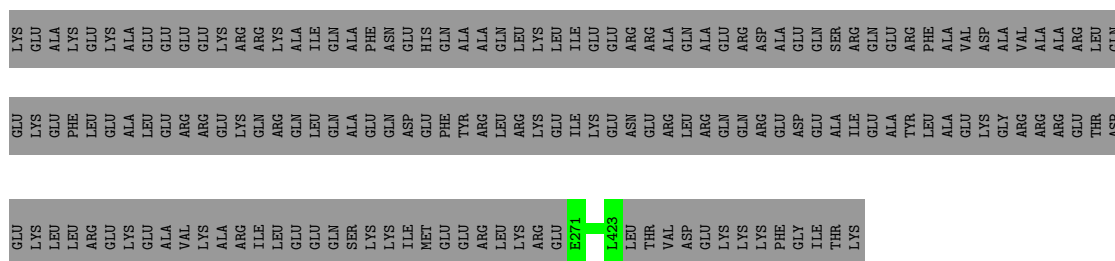


• Molecule 7: Meiosis-specific nuclear structural protein 1

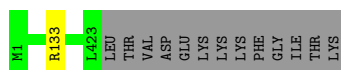
Chain 0Y: 35% 65%



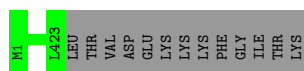




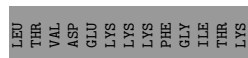
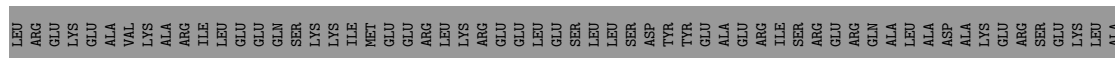
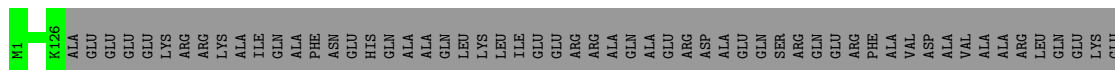
- Molecule 7: Meiosis-specific nuclear structural protein 1



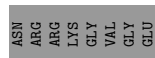
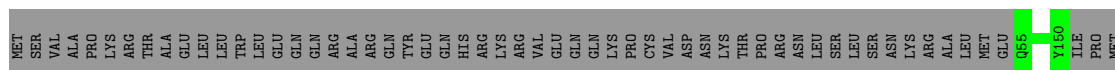
- Molecule 7: Meiosis-specific nuclear structural protein 1



- Molecule 7: Meiosis-specific nuclear structural protein 1



- Molecule 8: KIAA1430 homologue







[illegible]

ASN	ASP	VAL	VAL	ARG	ALA	SER	GLY	THR	GLY	GLU	ASP	GLU	ILE	GLU	ASP	GLU	ALA	VAL	SER	GLU	ALA	ASP	VAL	ALA	SER	GLY	ALA	SER	GLY	GLU	GLU	GLU	GLU	GLU	GLY	GLY	ASP	SER	ALA	ALA	LYS	SER	SER	SER	SER	ARG	ARG	SER	SER	SER	VAL	SER	LYS	GLY	ARG	ASN	SER	SER	SER	SER	SER	ILE	GLY	SER	GLU	LEU	GLY	SER
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- Molecule 9: Starmaker

Chain 0j:  8% 92%

[illegible]

- Molecule 9: Starmaker

Chain 0k:  8% 92%

MET	SER	LYS	SER	LEU	PRO	PRO	LEU	GLU	SER	SER	SER	ARG	GLY	GLY	ALA	ALA	ARG	VAL	GLY	VAL	TYR	ALA	SER	HIS	GLY	PRO	ALA	ALA	ALA	THR	ASN	LEU	ALA	CYS	VAL	VAL	THR	PRO	PRO	ARG	SER	SER	THR	VAL	ASN	SER	ASN	LEU	GLN	ARG	PHE	LEU	GLU	THR	GLU	LEU
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[illegible]

- Molecule 9: Starmaker

Chain 0n:  8% 92%

[illegible]

- Molecule 9: Starmaker



[illegible][illegible]

[illegible]

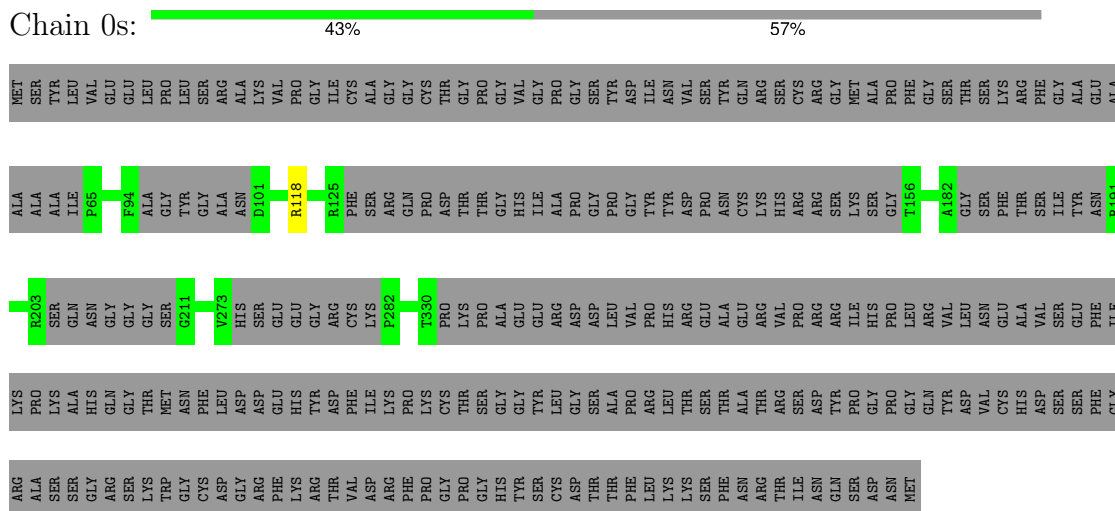
- Molecule 10: LIM zinc-binding domain-containing protein

Chain 0q:  8% 92%

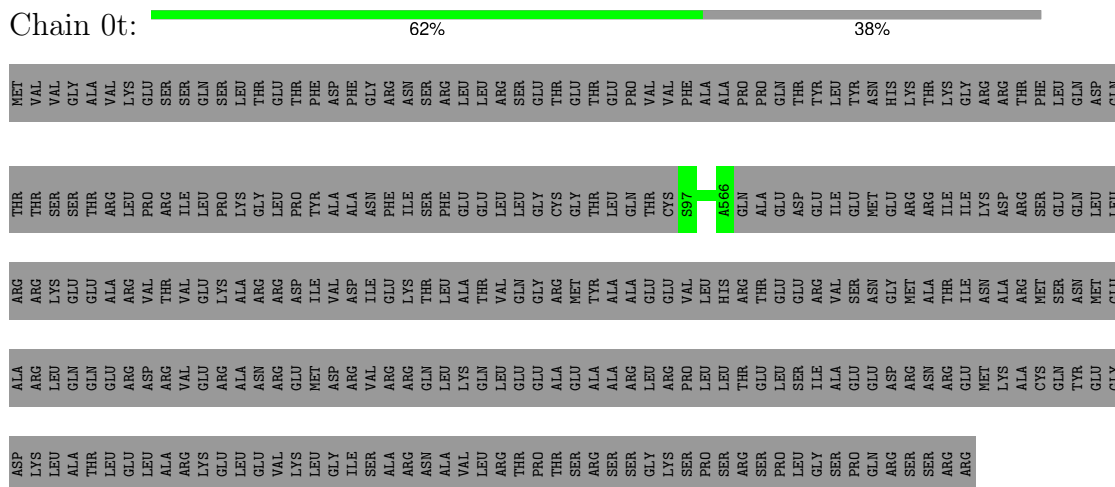
[illegible]



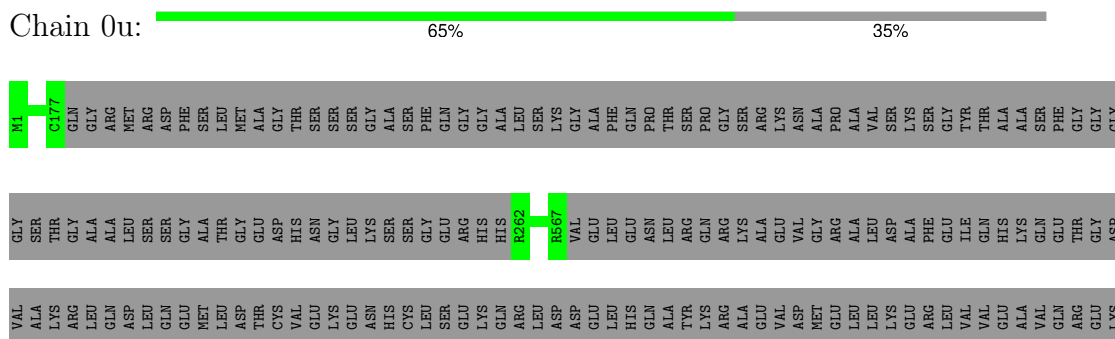
- Molecule 11: Sperm-tail PG-rich repeat



- Molecule 12: MOP84A



- Molecule 13: Leucine-rich repeat protein (LRRP)



[illegible]

- Molecule 14: Coiled-coil domain-containing protein 39

Chain 0v:  49% 51%

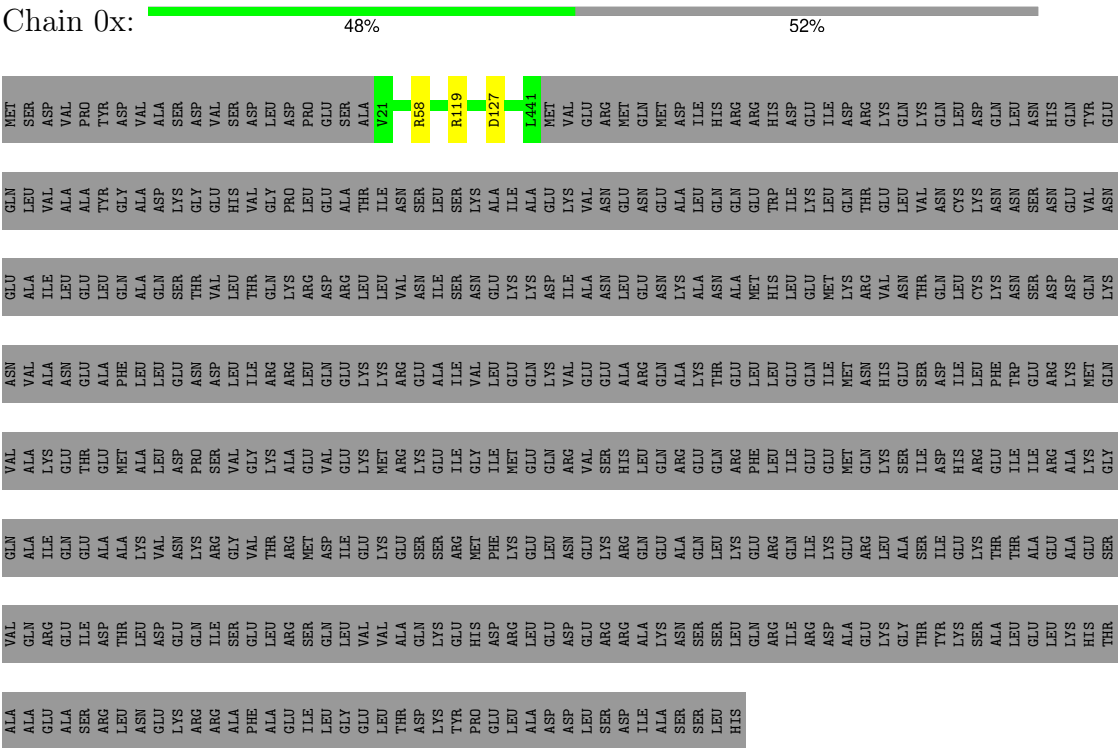
[illegible]

- Molecule 14: Coiled-coil domain-containing protein 39

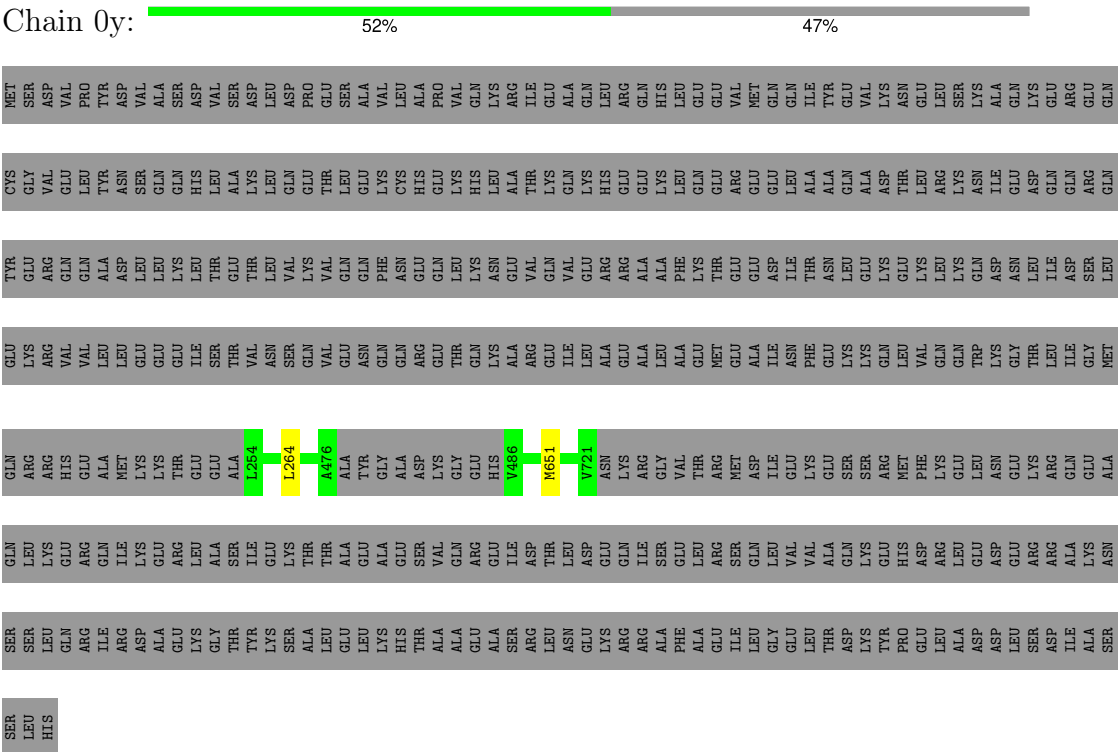
Chain 0w:  57% 43%

[illegible]

● Molecule 15: Coiled-coil domain-containing protein 40

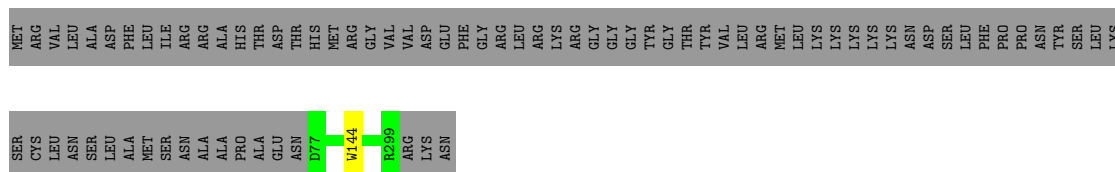


● Molecule 15: Coiled-coil domain-containing protein 40



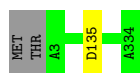
● Molecule 16: Cilia- and flagella-associated protein 299

Chain 0z:  74% 26%



- Molecule 17: Nucleoside diphosphate kinase, putative

Chain 1C:  99%



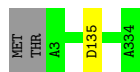
- Molecule 17: Nucleoside diphosphate kinase, putative

Chain 1D:  99%



- Molecule 17: Nucleoside diphosphate kinase, putative

Chain 1G:  99%



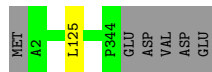
- Molecule 18: Nucleoside diphosphate kinase, putative

Chain 1E:  98%



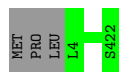
- Molecule 18: Nucleoside diphosphate kinase, putative

Chain 1F:  98%



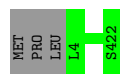
- Molecule 19: EF-hand domain-containing protein

Chain 1H:  99%



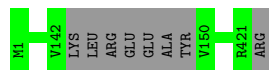
- Molecule 19: EF-hand domain-containing protein

Chain 1I:  99%



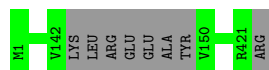
- Molecule 20: EF-hand domain-containing protein

Chain 1J:  98%





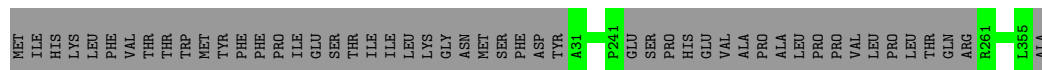
- Molecule 20: EF-hand domain-containing protein

Chain 1K:  98%



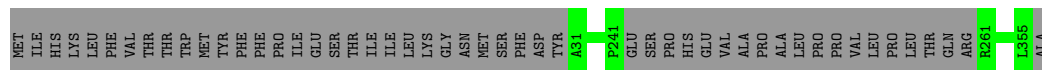
- Molecule 21: Cyclic nucleotide-binding domain-containing protein

Chain 1L:  86%  14%





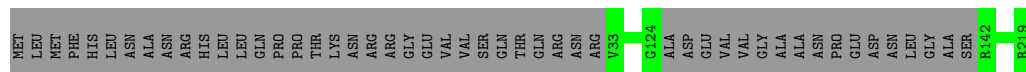
- Molecule 21: Cyclic nucleotide-binding domain-containing protein

Chain 1M:  86%  14%





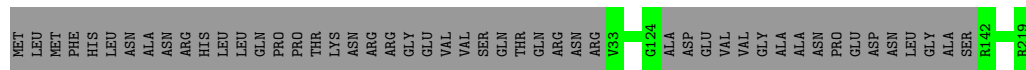
- Molecule 22: TbMIP23

Chain 1N:  78%  22%




- Molecule 22: TbMIP23

Chain 1O:  78%  22%




- Molecule 23: FAP141



Chain 1P:  81% 19%

MET ARG TYR PRO THR GLY LEU ASP ASP SER HIS ILE SER GLY VAL ARG PRO GLY GLY ALA PRO VAL 826 M130

- Molecule 23: FAP141

Chain 1Q:  81% 19%

MET ARG TYR PRO THR GLY LEU ASP ASP SER HIS ILE SER GLY VAL ARG PRO GLY GLY ALA PRO VAL 826 M130

- Molecule 24: EF-hand domain-containing protein

Chain 1R:  67% 33%

HI G51 ARG CYS GLY VAL ILE LEU ARG GLY VAL THR THR D78 P197 LYS VAL SER LEU GLU GLU ARG MET MET ALA SER ASP ILE ARG LYS SER ILE HIS THR LYS GLN HIS PRO LEU TYR GLN ALA SER SER ASP TYR GLY

LYS GLY TRP THR VAL LYS ASP GLY LYS PHE ALA CYS LYS THR THR PHE THR LYS ASN LEU GLN SER GLN CYS THR MET GLY PRO MET THR MET MET

- Molecule 24: EF-hand domain-containing protein

Chain 1S:  67% 33%

HI G51 ARG CYS GLY VAL ILE LEU ARG GLY VAL THR THR D78 P197 LYS VAL SER LEU GLU GLU ARG MET MET ALA SER ASP ILE ARG LYS SER ILE HIS THR LYS GLN HIS PRO LEU TYR GLN ALA SER SER ASP TYR GLY

LYS GLY TRP THR VAL LYS ASP GLY LYS PHE ALA CYS LYS THR THR PHE THR LYS ASN LEU GLN SER GLN CYS THR MET GLY PRO MET THR MET MET

- Molecule 25: Calpain-like cysteine peptidase, putative

Chain 1T:  89% 11%

MET P2 N270 GLY GLY ASP VAL GLU GLY GLY GLU THR THR PRO VAL ALA GLU ASN GLU VAL SER VAL MET THR SER THR ASN GLY ASP LYS LEU

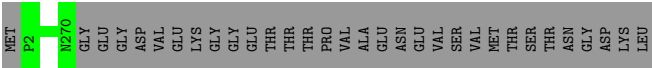
- Molecule 25: Calpain-like cysteine peptidase, putative

Chain 1U:  89% 11%

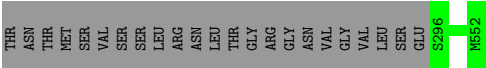
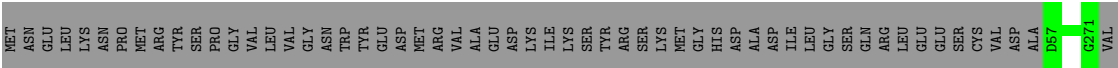
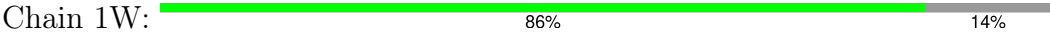
MET P2 N270 GLY GLY ASP VAL GLU GLY GLY GLU THR THR PRO VAL ALA GLU ASN GLU VAL SER VAL MET THR SER THR ASN GLY ASP LYS LEU

- Molecule 25: Calpain-like cysteine peptidase, putative

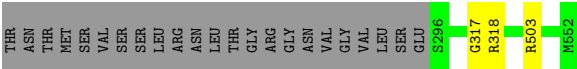
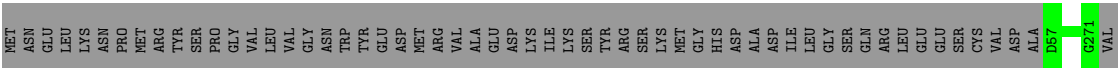
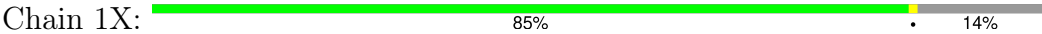
Chain 1V:  89% 11%



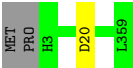
• Molecule 26: EF-hand domain-containing protein



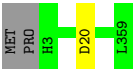
• Molecule 26: EF-hand domain-containing protein



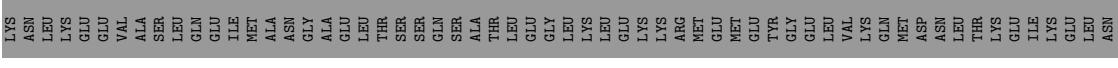
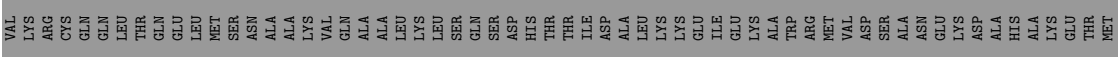
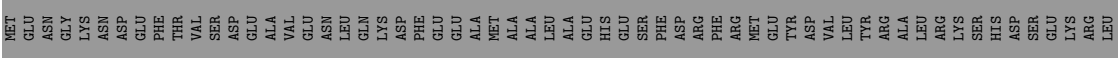
• Molecule 27: Calcium-binding protein, putative



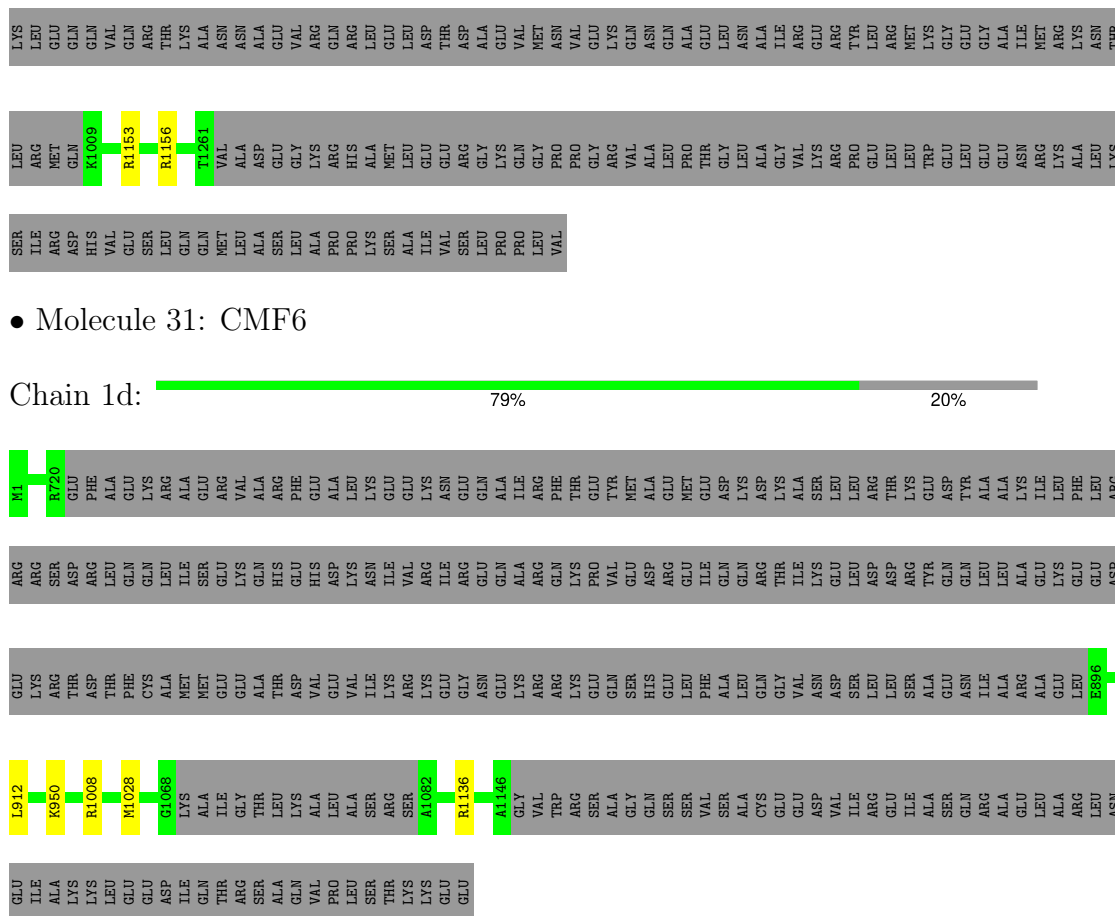
• Molecule 27: Calcium-binding protein, putative



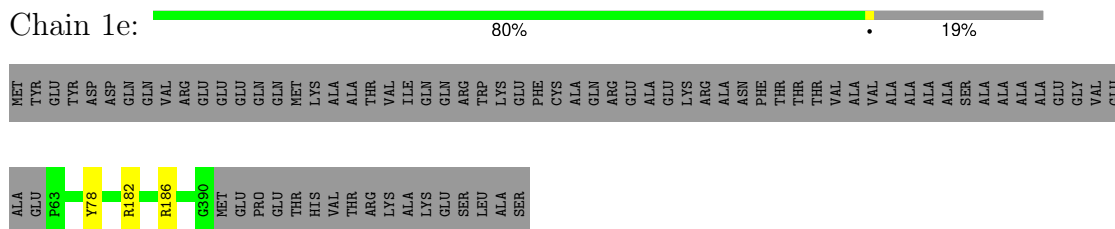
• Molecule 28: Cilia- and flagella-associated protein 58 central coiled coil domain-containing protein



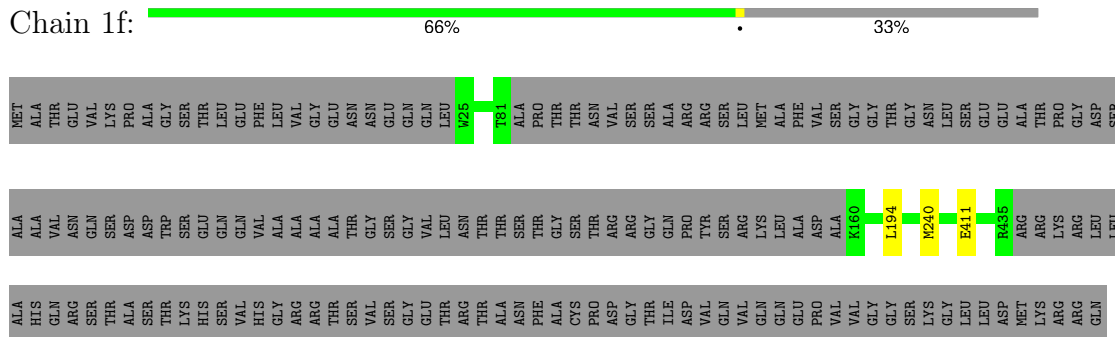




- Molecule 32: CCDC113/CCDC96 coiled-coil domain-containing protein



- Molecule 33: Cilia- and flagella-associated protein 263



- Molecule 34: DRC1

[illegible]

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

MET  
SER  
LYS  
GLY  
TYR  
THR  
VAL  
TYR  
SER  
LEU  
MET  
HIS  
GLN  
PRO  
GLN  
GLU  
THR  
V18  
R522  
C552

MET	PRO	PRO	LYS	GLU	ALA	ALA	ALA	ALA	LYS	LYS	GLY	GLY	LYS	LYS	GLY	GLY	LYS	LYS	GLN	ALA	PRO	GLU	PRO	PRO	PRO	LEU	VAL	ASP	GLY	LYS	PRO	PRO	PRO	D38	M55	L156	R256	L328	L461
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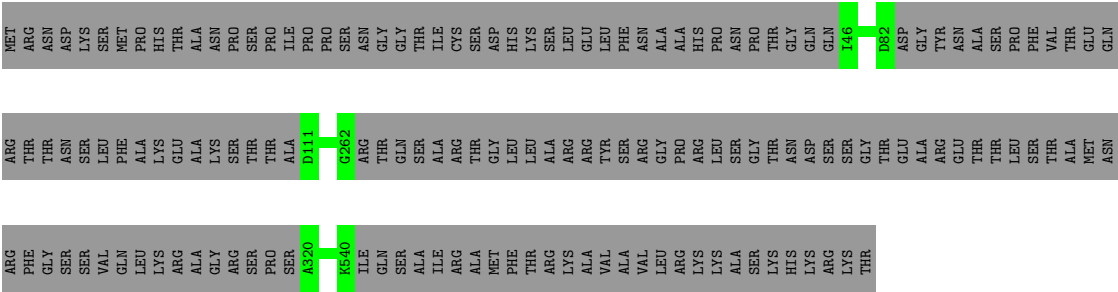
MET	PRO	PRO	ARG	THR	ALA	ALA	GLU	ARG	GLY	GLY	ARG	ARG	LYS	SER	VAL	LYS	ALA	ALA	PRO	PRO	PRO	VAL	ASP	PRO	L26	I444	ALA	SER	LEU	PRO	PRO	ARG	SER	ASN	PHE	GLU
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K448	MET	ASN	ASP	ILE	GLN	ALA	ARG	ASP	LYS	LYS	SER	ARG	GLU	ILE	ILE	HIS	ARG	GLU	VAL	GLU	GLY	LYS	LEU	SER	ASP	LEU	GLY	THR	SER	ARG	VAL	PRO	CYS	ILE	SER	PHE	PHE	VAL	PRO	SER	L57	I394	
	THR	ALA	SER	THR	VAL	PRO	ARG	LYS	GLY	ALA	GLN	ARG	SER	GLN	PHE	HIS	ARG	GLU	VAL	ALA	GLN	GLU	HIS	GLU	GLY	ASP	SER	GLU	CYS	THR	SER	ARG	VAL	PRO	CYS	ILE	SER	PHE	PHE	VAL	PRO	SER	L57

66%

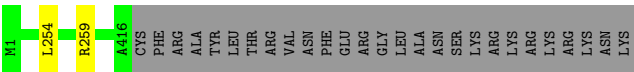
- Molecule 41: DRC9

28%



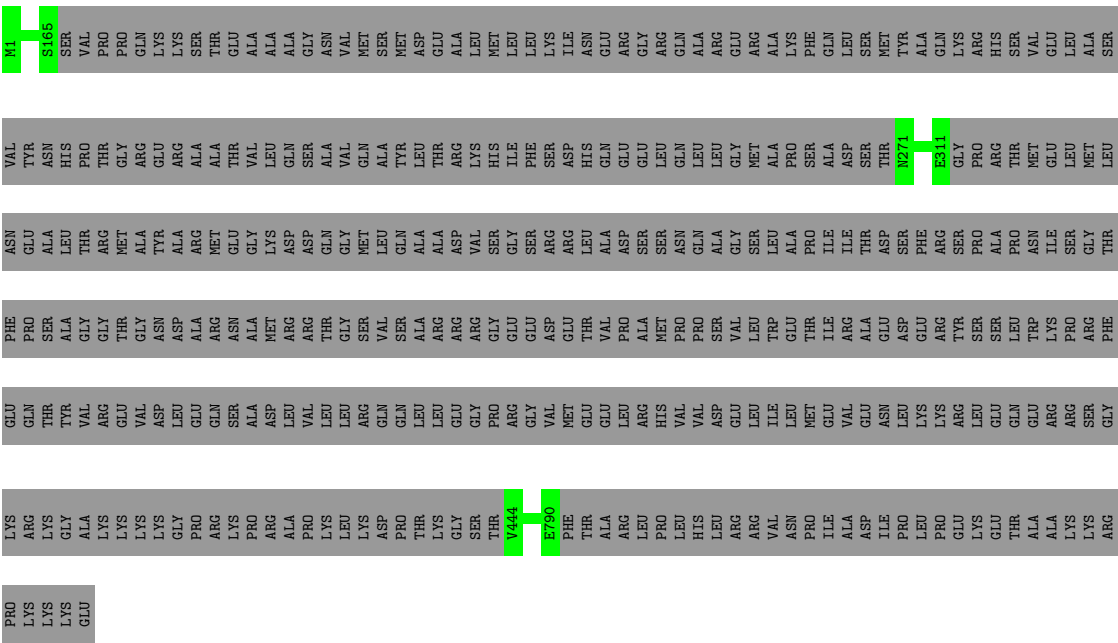
• Molecule 42: Dynein regulatory complex protein 10

Chain 1o: 93% 6%



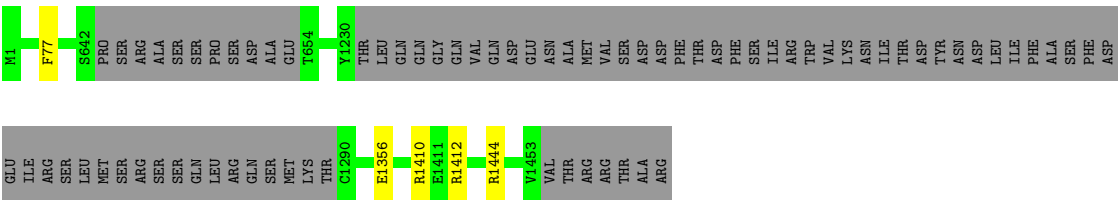
• Molecule 43: ATPase AAA-type core domain-containing protein

Chain 1p: 61% 39%



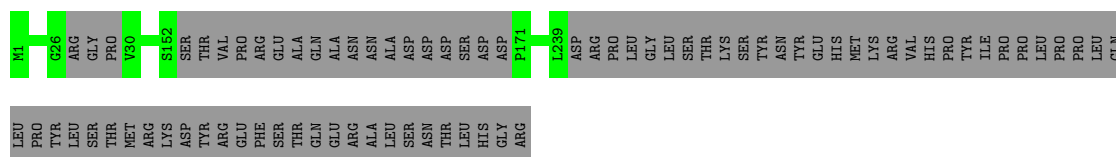
• Molecule 44: Cilia- and flagella-associated protein 43

Chain 1r: 94% 5%

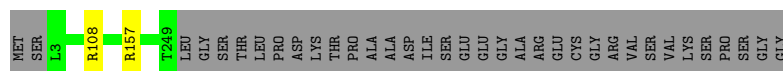
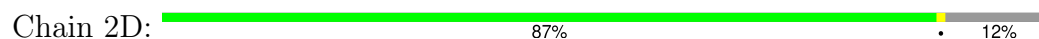




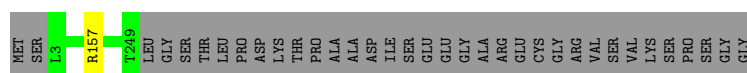




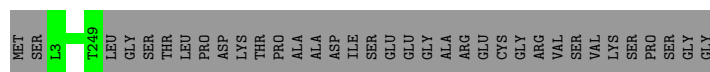
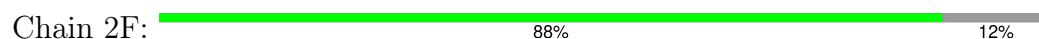
- Molecule 47: Peptidyl-prolyl cis-trans isomerase



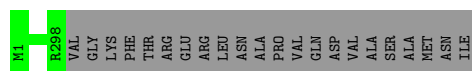
- Molecule 47: Peptidyl-prolyl cis-trans isomerase



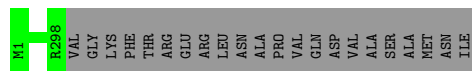
- Molecule 47: Peptidyl-prolyl cis-trans isomerase



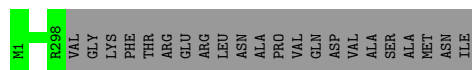
- Molecule 48: EF-hand domain-containing protein



- Molecule 48: EF-hand domain-containing protein



- Molecule 48: EF-hand domain-containing protein



- Molecule 49: FAP107/MC11

Chain 2J:  95% 5%

MET	ARG	CYS	HIS	VAL	MET	GLY	SER	PRO	GLY	H11	Y247	GLU	ASP
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- Molecule 49: FAP107/MC11

Chain 2K:  95% 5%

MET	ARG	CYS	HIS	VAL	MET	GLY	SER	PRO	GLY	H11	Y247	GLU	ASP
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- Molecule 49: FAP107/MC11

Chain 2L:  95% 5%

MET	ARG	CYS	HIS	VAL	MET	GLY	SER	PRO	GLY	H11	Y247	GLU	ASP
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- Molecule 50: T. brucei spp.-specific protein

Chain 2M:  92% 8%

MET	SER	HIS	LEU	LEU	ARG	SER	ARG	R9	V65	PRO	SER	ASP	PRO	LYS	GLN	MET	ASP	PHE	THR	SER	T78	R95	L254
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- Molecule 50: T. brucei spp.-specific protein

Chain 2N:  92% 8%

MET	SER	HIS	LEU	LEU	ARG	SER	ARG	R9	V65	PRO	SER	ASP	PRO	LYS	GLN	MET	ASP	PHE	THR	SER	T78	R95	L254
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- Molecule 50: T. brucei spp.-specific protein

Chain 2O:  58% 41%

MET	SER	HIS	LEU	LEU	ARG	SER	ARG	R9	V65	PRO	SER	ASP	PRO	LYS	GLN	MET	ASP	PHE	THR	SER	T78	R95	Q169	LEU	THR	ASN	VAL	GLY	PRO	VAL	GLU	ASP	GLY	ASN	ASN	VAL	TYR	LEU	ARG	SER	HIS	THR	GLN	LYS	VAL	HIS	CYS	LEU	PRO	GLU	LEU	PRO	VAL	VAL	ASP	SER	LEU
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CYS	ASN	ASP	TYR	LEU	LEU	ASP	GLU	PRO	ILE	THR	LEU	TYR	THR	GLY	ASN	PRO	GLU	THR	GLY	CYS	THR	MET	THR	VAL	HIS	GLY	LYS	THR	PRO	VAL	GLU	VAL	PRO	VAL	GLU	ASP	GLY	ARG	SER	ARG	PHE	THR	ARG	GLY	THR	THR	THR	ARG	LYS	TYR	CYS	LEU
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- Molecule 51: FAP95/MC6

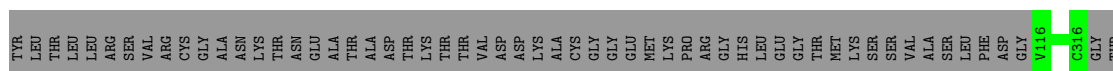
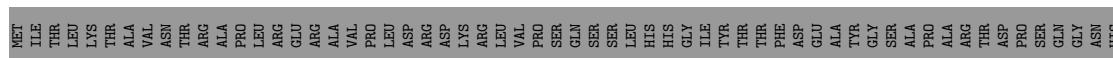
Chain 2P:  90% 9%

MET	HIS	THR	GLY	ASP	LYS	R7	D95	S171	ALA	GLY	ARG	ASN	CYS	GLY	ALA	ARG	THR	GLN	MET
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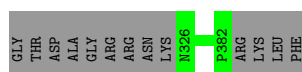
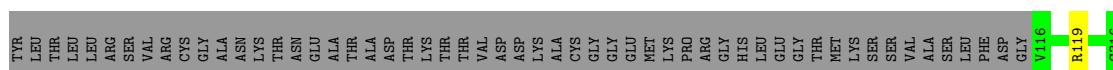
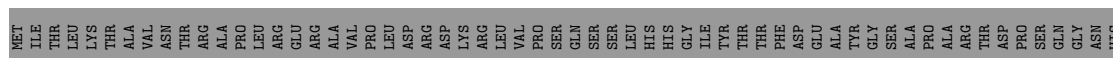
## ● Molecule 51: FAP95/MC6

Chain 2Q:  90% 9%

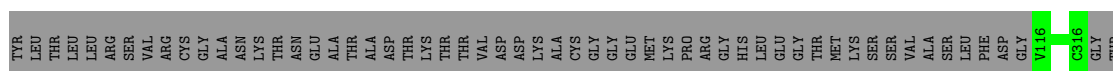
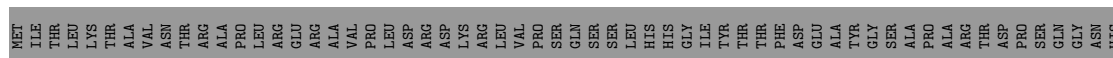
## ● Molecule 52: FAP129

Chain 2R:  67% 33%

## ● Molecule 52: FAP129

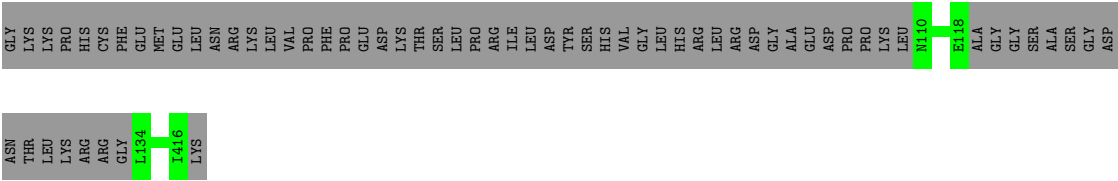
Chain 2S:  67% 33%

## ● Molecule 52: FAP129

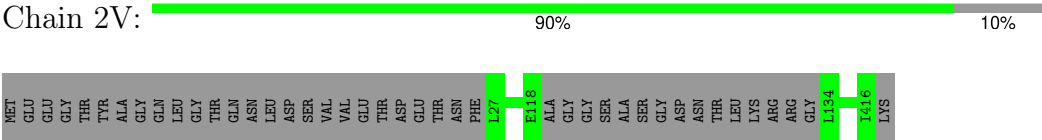
Chain 2T:  67% 33%

## ● Molecule 53: T. brucei spp.-specific protein

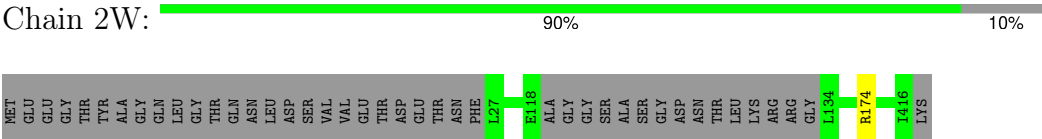
Chain 2U:  70% 30%



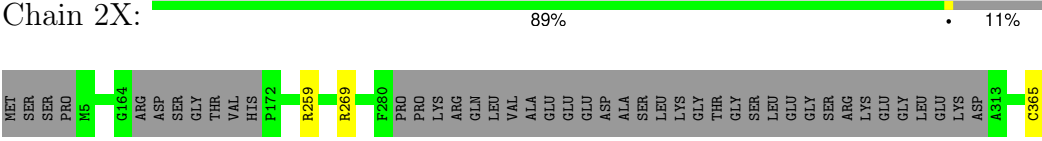
• Molecule 53: T. brucei spp.-specific protein



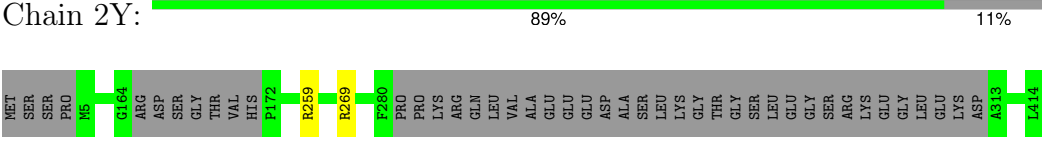
• Molecule 53: T. brucei spp.-specific protein



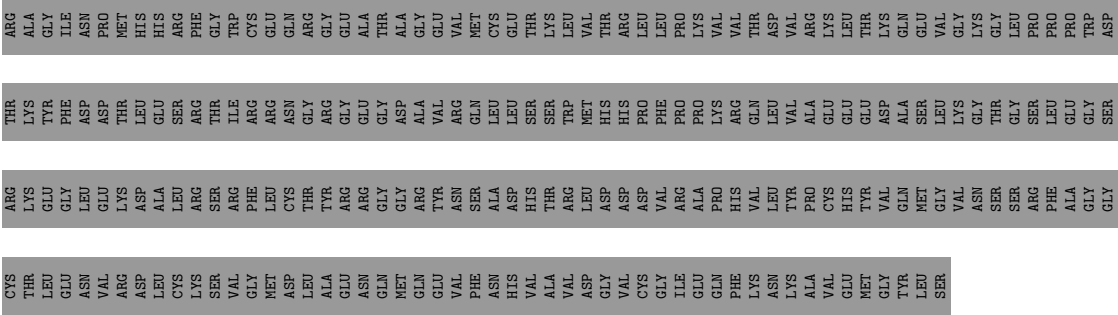
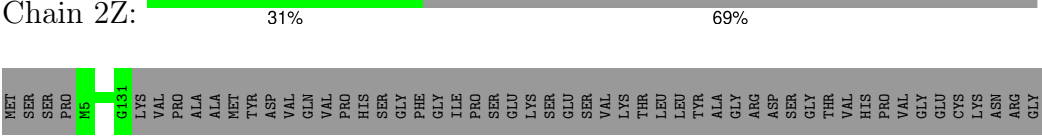
• Molecule 54: FAP21

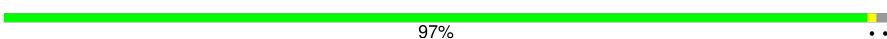


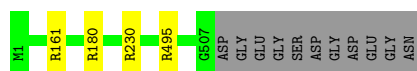
• Molecule 54: FAP21



• Molecule 54: FAP21

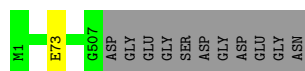






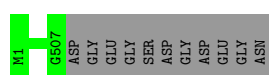
- Molecule 56: RSP2

Chain 2f: 98%



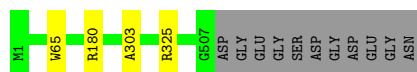
- Molecule 56: RSP2

Chain 2g: 98%



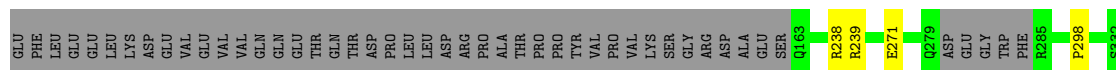
- Molecule 56: RSP2

Chain 2h: 97%



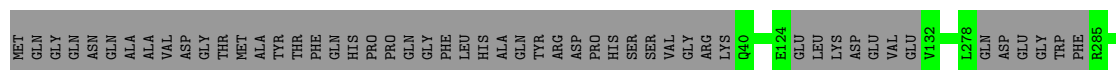
- Molecule 57: Radial spoke protein 3, putative

Chain 2i: 48%



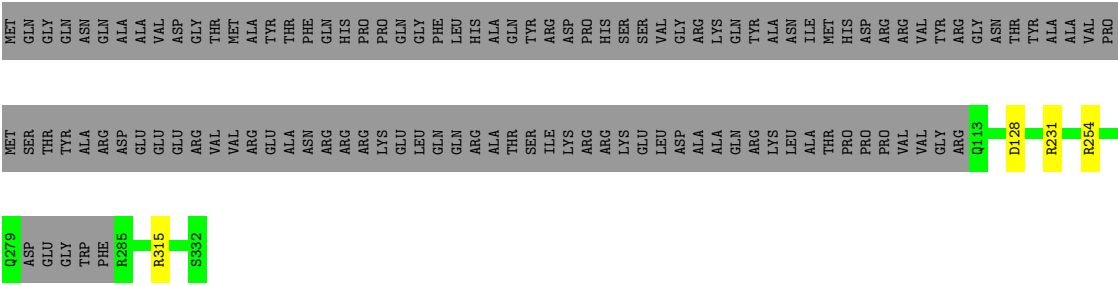
- Molecule 57: Radial spoke protein 3, putative

Chain 2j: 84%

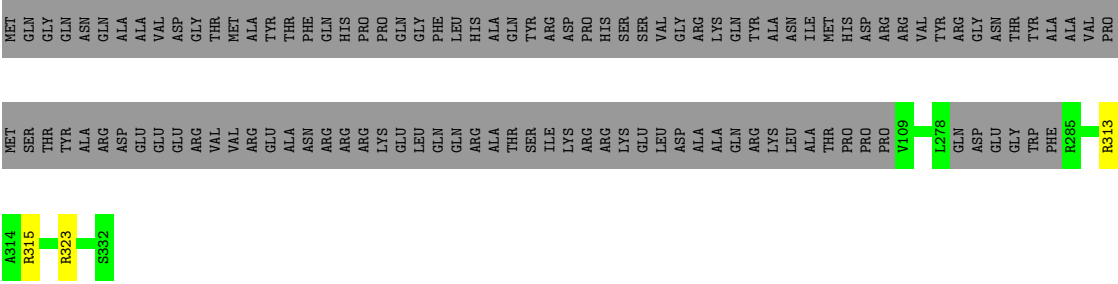


- Molecule 57: Radial spoke protein 3, putative

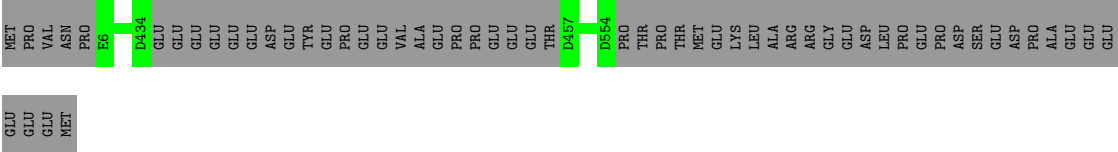
Chain 2k: 64%



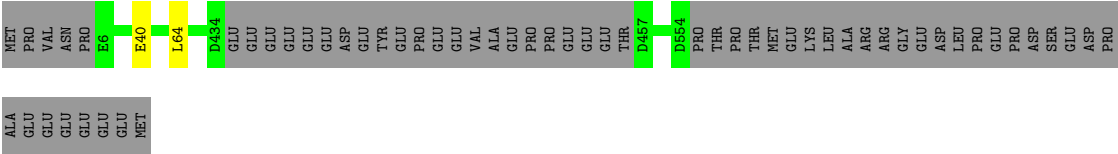
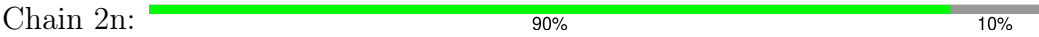
• Molecule 57: Radial spoke protein 3, putative



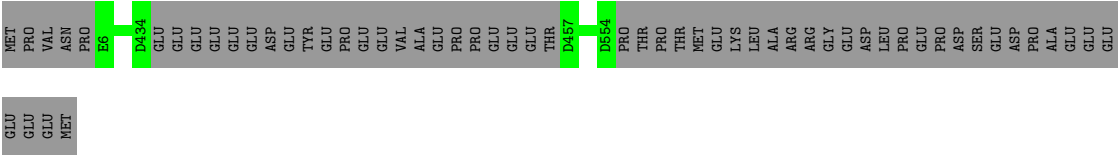
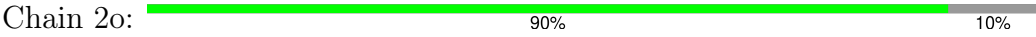
• Molecule 58: Flagellar radial spoke component, putative



• Molecule 58: Flagellar radial spoke component, putative

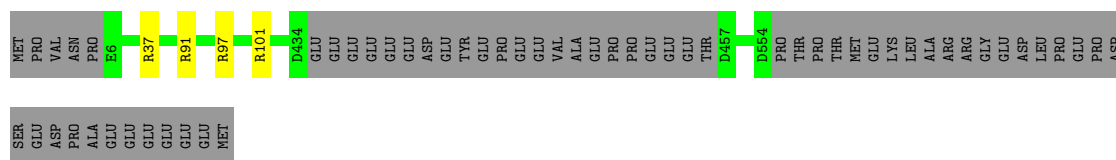


• Molecule 58: Flagellar radial spoke component, putative



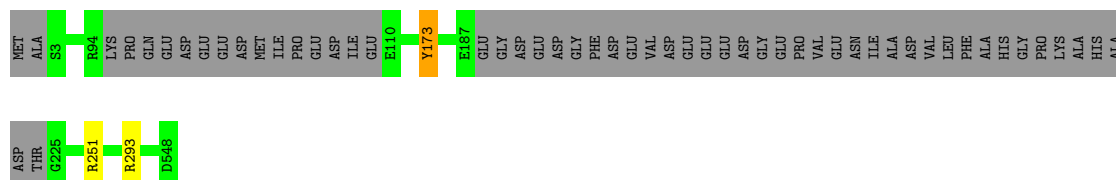
- Molecule 58: Flagellar radial spoke component, putative

Chain 2p:  89% 10%



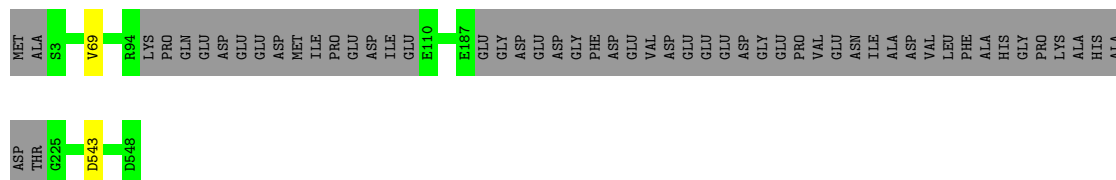
- Molecule 59: Flagellar radial spoke protein-like, putative

Chain 2q:  90% 10%



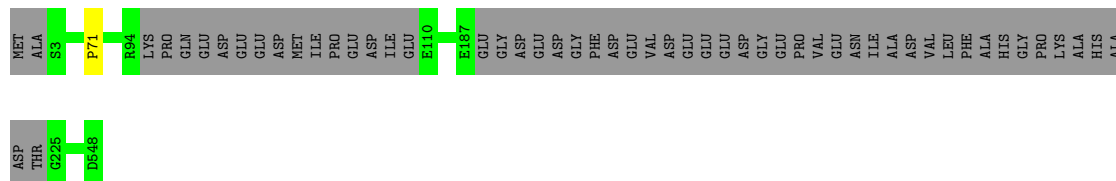
- Molecule 59: Flagellar radial spoke protein-like, putative

Chain 2r:  90% 10%




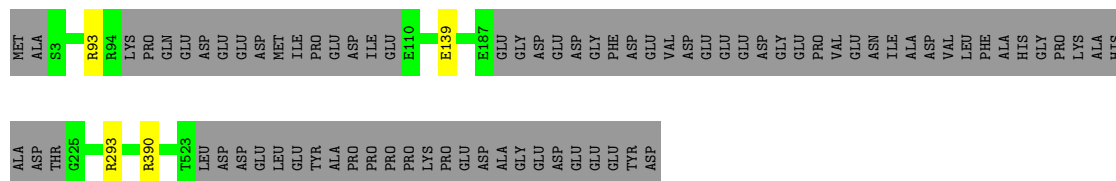
- Molecule 59: Flagellar radial spoke protein-like, putative

Chain 2s:  90% 10%



- Molecule 59: Flagellar radial spoke protein-like, putative

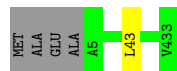
Chain 2t:  85% 14%





- Molecule 60: RSP8

Chain 2u:  99%



- Molecule 61: Radial spoke head protein 9 homolog

Chain 2v:  99%



- Molecule 61: Radial spoke head protein 9 homolog

Chain 2w:  100%

There are no outlier residues recorded for this chain.

- Molecule 61: Radial spoke head protein 9 homolog

Chain 2x:  100%

There are no outlier residues recorded for this chain.

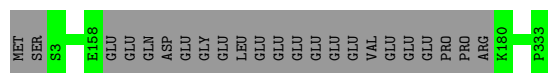
- Molecule 61: Radial spoke head protein 9 homolog

Chain 2y:  99%




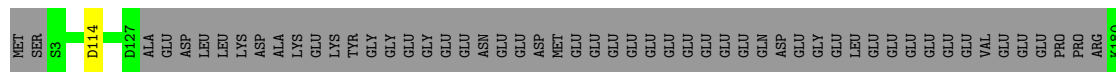
- Molecule 62: Radial spoke protein RSP9

Chain 2z:  93%



- Molecule 62: Radial spoke protein RSP9

Chain 3a:  83%



- Molecule 62: Radial spoke protein RSP9

MET
SER
S3
D75
E158
GIU
GJU
GIN
ASP
GLV
GLY
GIU
LEU
GIU
GLU
GIU
GIU
GIU
VAL
GIU
GLU
PRO
ARG

- Chain 3c:  81% . 18%

GLU	PRO	PRO	ARG	K160	R212	L228	Y259	P333
MET	S3	E120	PRO	GLU	VAL	VAL	PRO	ASP
							ALA	ALA
							GLU	GLU
							LEU	LEU
							LEU	LYS
							ASP	ASP
							ALA	ALA
							LYS	LYS
							GLU	GLU
							LYS	LYS
							TRR	TRR
							GLY	GLY
							GLY	GLY
							GLY	GLY
							GLU	GLU
							GLU	GLU
							ASN	ASN
							GLU	GLU
							GLU	GLU
							ASP	ASP
							MET	MET
							GLU	GLU
							GLU	GLU
							GLU	GLU
							GLU	GLU
							GLU	GLU
							GLU	GLU
							GLN	GLN
							ASP	ASP
							GLU	GLU
							GLY	GLY
							LEU	LEU
							GLU	GLU
							GLU	GLU
							GLU	GLU
							VAL	VAL
							GLU	GLU
							GLU	GLU

- Chain 3A:  49% 51%

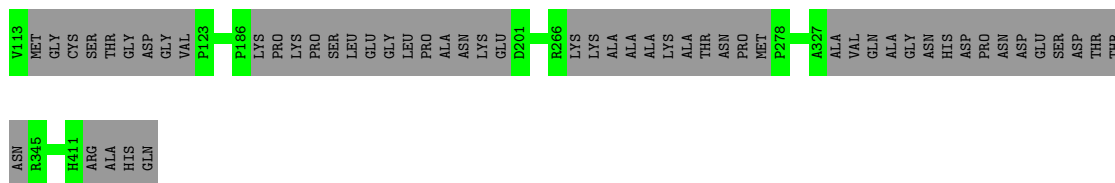
[illegible]

- Chain 3B:  73%  27%

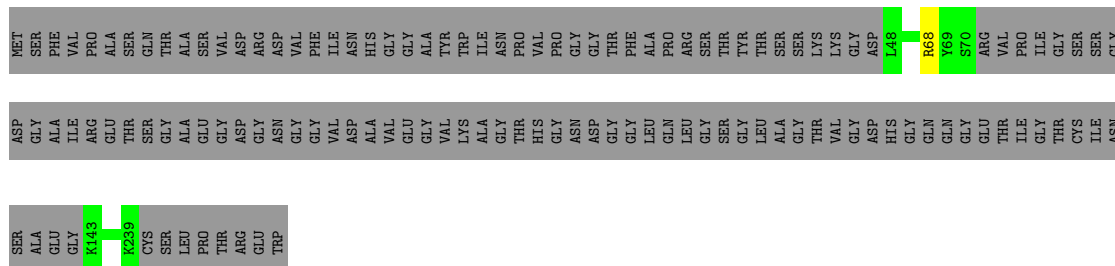
[illegible]

- Chain 3C:  73% 27%

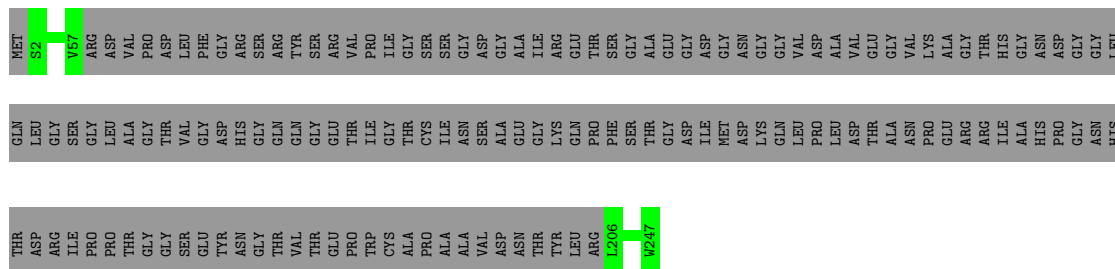
MET	PHE	GLY	GLY	SER	LYS	SER	ASP	LEU	ILE	MET	SER	PRO	PRO	PRO	HIS	PRO	LYS	ALA	ASN	MET	LEU	ASP	LEU	TYR	MET	THR	ARG	ASP	TYR	ASN	TYR	ARG	ASP	ILE	ASP	ASP	SER	GLY	GLN	GLY	GLU	LYS	LYS	SER	ASN	PHE	THR	V51	HR1	ASP	VAL	GLU	GLY	LYS	D87
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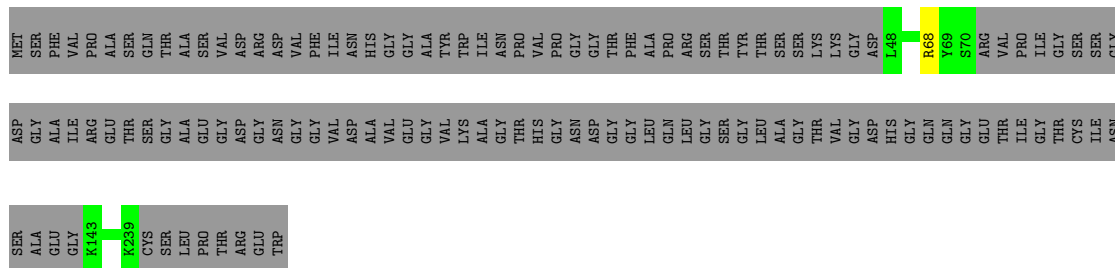
- Molecule 64: TbRib26b



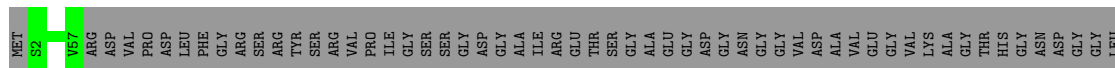
- Molecule 64: TbRib26b



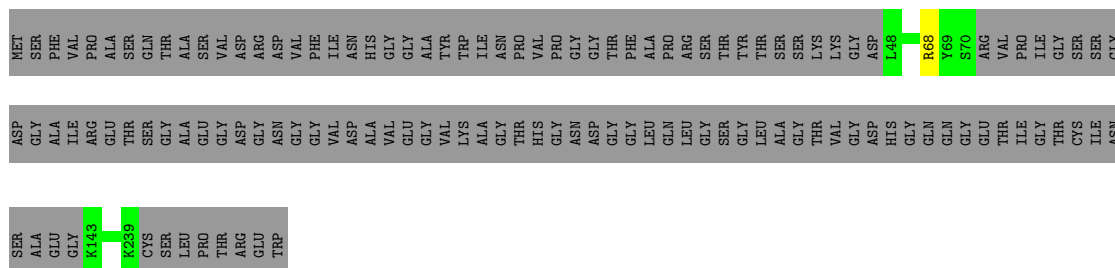
- Molecule 64: TbRib26b



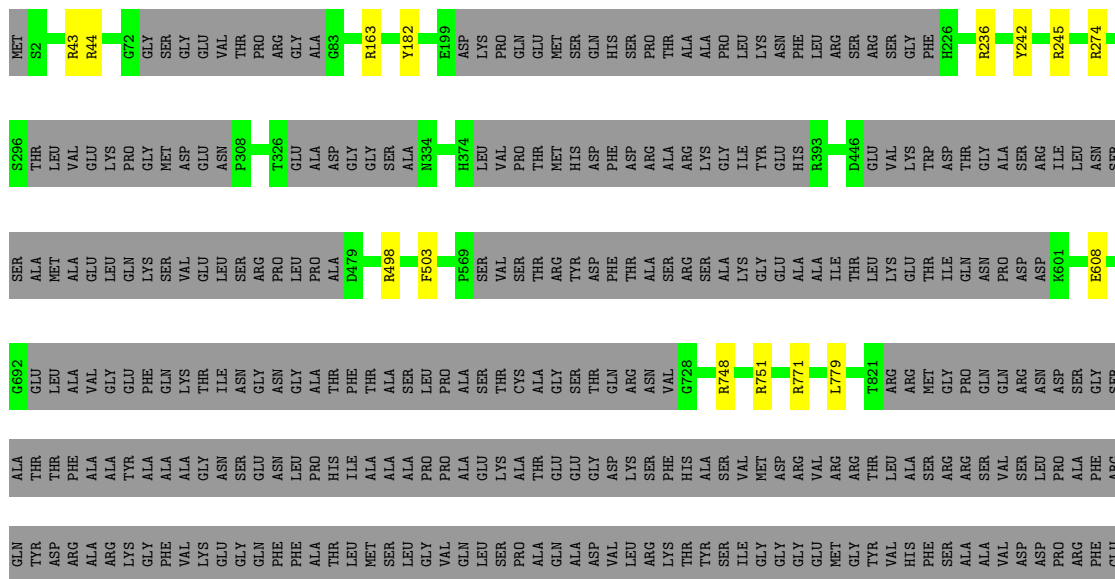
- Molecule 64: TbRib26b



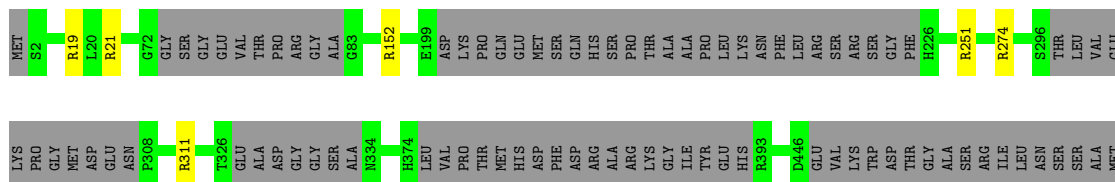
- Molecule 64: TbRib26b



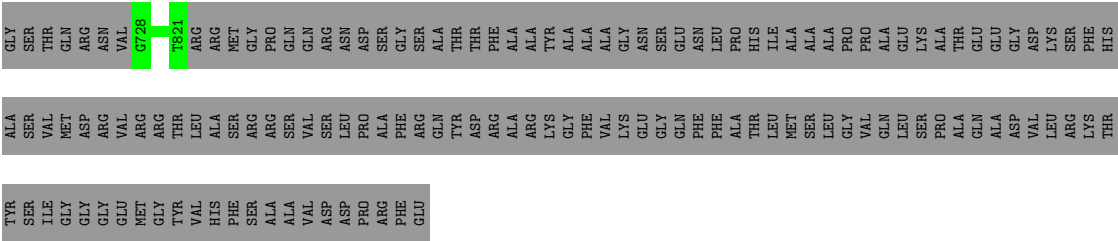
- Molecule 65: EF-hand domain-containing protein



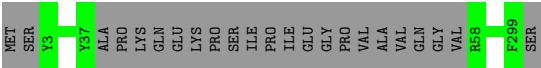
- Molecule 65: EF-hand domain-containing protein



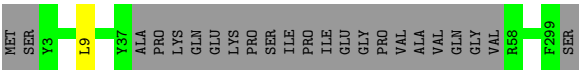




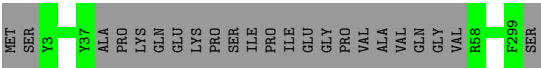
• Molecule 66: PACRGA



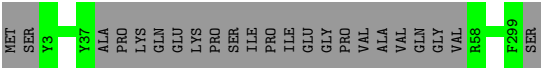
• Molecule 66: PACRGA



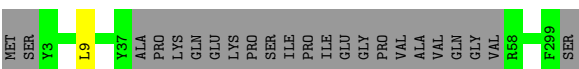
• Molecule 66: PACRGA



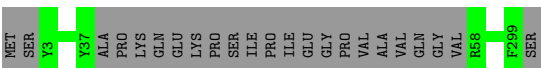
• Molecule 66: PACRGA



• Molecule 66: PACRGA



• Molecule 66: PACRGA



• Molecule 66: PACRGA

MET	SER	Y3	Y37	ALA	PRO	LYS	GLN	GLU	LYS	PRO	SER	ILE	PRO	ILE	GLU	GLY	PRO	VAL	ALA	VAL	GLN	GLY	VAL	R58	F299	SER
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- Chain 3T:  92% 8%


[illegible]

- Chain 3U:  72% 28%

VAL	GLN	LYS	ARG	GLY	LYS	GLN	ASP	THR	GLU	GLY	SER	ASP	LEU	LEU	ARG	ASP	ARG	ASP	ASP	LEU	VAL	PRO	GLN	LEU	ALA	GLU	SER	PRO	PHE	GLY	ILE	PRO	PHE	GLY	GLY	TVR	LYS	ILE	LYS	ASN	ASP	ILE	THR	VAL	THR	LYS	LYS	GLY	CYS	VAL	VAL	ARG	GLY	ASP	PRO	ALA	THR	LYS	PRO	ALA	SER	ALA																													
077	095	105	115	125	135	145	155	165	175	185	195	205	215	225	235	245	255	265	275	285	295	305	315	325	335	345	355	365	375	385	395	405	415	425	435	445	455	465	475	485	495	505	515	525	535	545	555	565	575	585	595	605	615	625	635	645	655	665	675	685	695	705	715	725	735	745	755	765	775	785	795	805	815	825	835	845	855	865	875	885	895	905	915	925	935	945	955	965	975	985	995

- Chain 3V: 

VAL	GLN	LYS	ARG	GLY	LYS	GLN	ASP	THR	GLU	SER	ASP	GLN	ARG	ASP	PRO	LYS	Q77	Q77	ASN	GLN	GLY	PHE	ARG	GLN	SER	PRO	LEU	LYS	ILE	G105	G105	L311	MET																						
MET	ALA	PHE	SER	ARG	LYS	GLU	ARG	LYS	GLN	LEU	ASP	ARG	ASP	ASP	PRO	LYS	LEU	VAL	GLN	LEU	ALA	GLU	SER	PRO	PHE	GLY	GLY	TVR	GLY	ILE	LYS	ASN	ASP	ILE	THR	VAL	THR	LYS	LYS	GLY	CYS	VAL	VAL	ARG	GLY	ASP	ASP	PRO	ALA	THR	LYS	PRO	ALA	SER	ALA

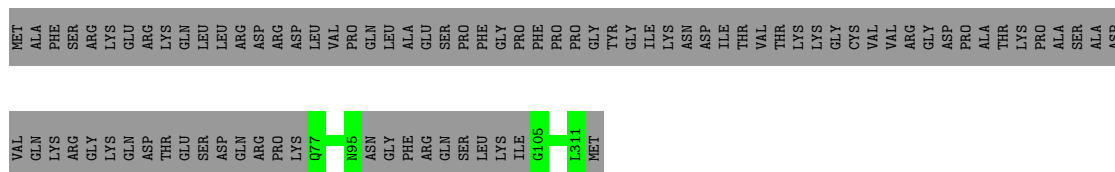
- Chain 3W:  72% 28%

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

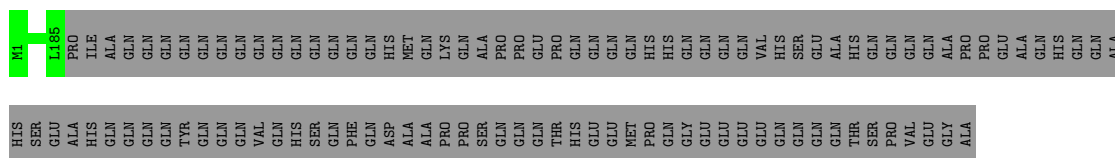
- Chain 3X:  72% 28%

[illegible]

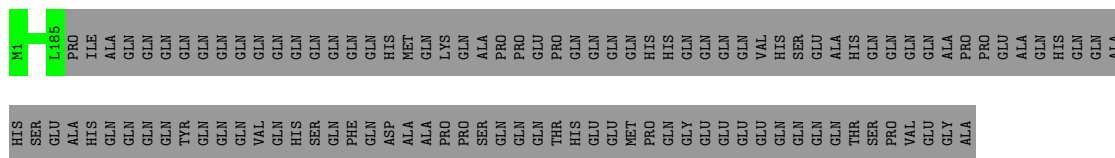
- Molecule 67: PACRGB



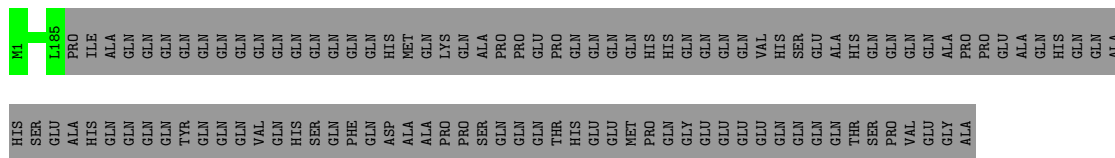
- Molecule 68: Cilia- and flagella-associated protein 20



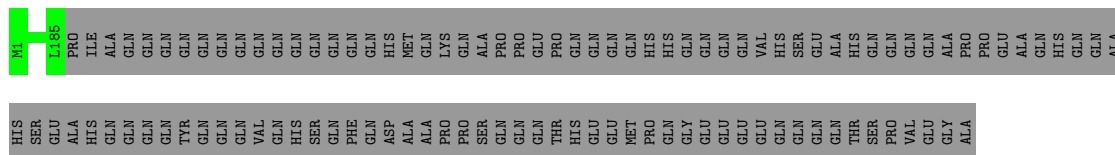
- Molecule 68: Cilia- and flagella-associated protein 20



- Molecule 68: Cilia- and flagella-associated protein 20



- Molecule 68: Cilia- and flagella-associated protein 20



- Molecule 68: Cilia- and flagella-associated protein 20







• Molecule 68: Cilia- and flagella-associated protein 20



• Molecule 68: Cilia- and flagella-associated protein 20



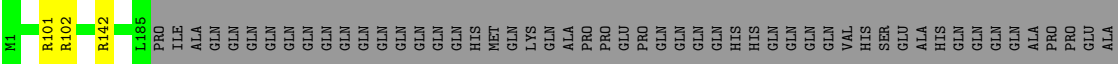
• Molecule 68: Cilia- and flagella-associated protein 20



• Molecule 68: Cilia- and flagella-associated protein 20



• Molecule 68: Cilia- and flagella-associated protein 20



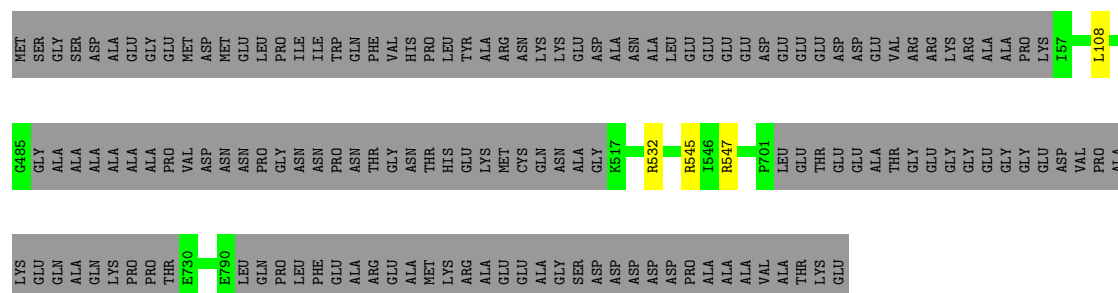
HIS	SER	GLU	ALA	HIS	GLN	GLN	GLN	GLN	TYR	GLN	GLN	GLN	VAL	GLN	HIS	SER	SER	PHE	GLN	GLN	ASP	ALA	ALA	PRO	PRO	SER	SER	GLN	GLN	GLN	THR	HIS	GLU	GLU	MET	PRO	PRO	GLY	GLY	GLU	GLU	GLU	GLU	GLN	GLN	GLN	GLN	THR	SER	SER	PRO	VAL	GLU	GLY	ALA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## ● Molecule 69: Phosphatidylinositol 4-phosphate 5-kinase

Chain 3d:

82%

18%

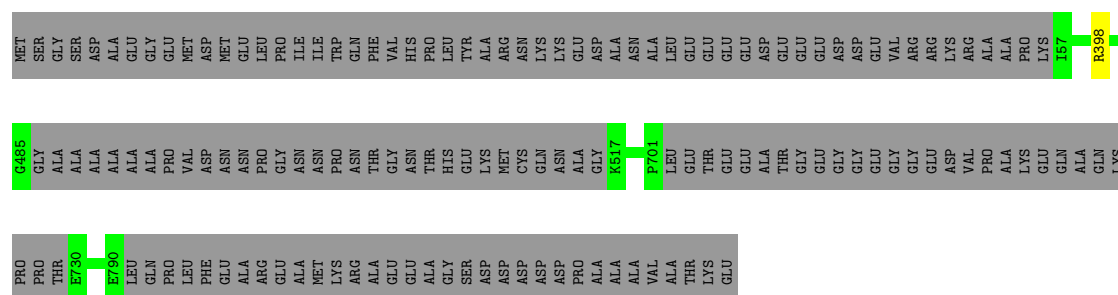


## ● Molecule 69: Phosphatidylinositol 4-phosphate 5-kinase

Chain 3e:

82%

18%

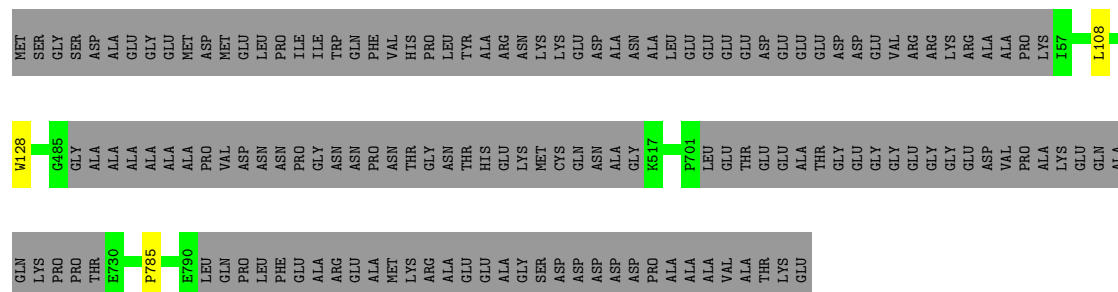


## ● Molecule 69: Phosphatidylinositol 4-phosphate 5-kinase

Chain 3f:

82%

18%

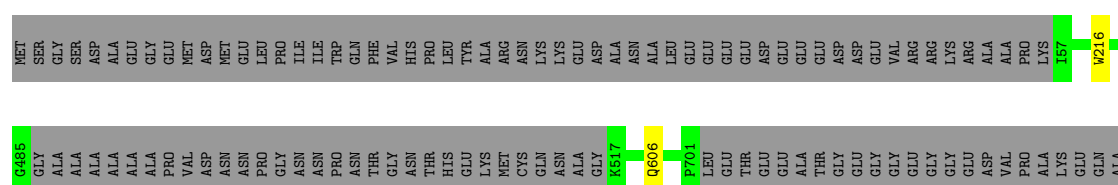


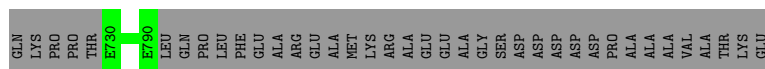
## ● Molecule 69: Phosphatidylinositol 4-phosphate 5-kinase

Chain 3g:

82%

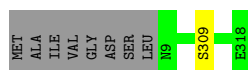
18%





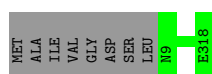
- Molecule 70: Cyclophilin type peptidyl-prolyl cis-trans isomerase, putative

Chain 3h: 97%



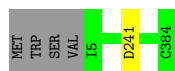
- Molecule 70: Cyclophilin type peptidyl-prolyl cis-trans isomerase, putative

Chain 3i: 97%



- Molecule 71: RSP14

Chain 3j: 99%



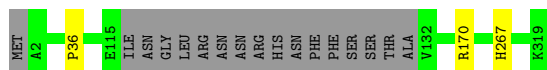
- Molecule 72: Leucine-rich repeat protein (LRRP)

Chain 3k: 99%



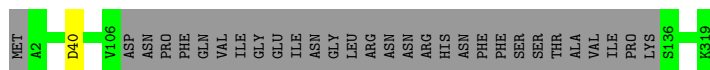
- Molecule 73: Chaperone protein DNAJ, putative

Chain 3l: 94% 5%



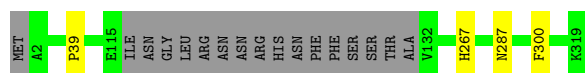
- Molecule 73: Chaperone protein DNAJ, putative

Chain 3m: 90% 9%



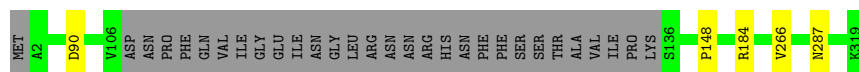
- Molecule 73: Chaperone protein DNAJ, putative

Chain 3o: 93% 5%



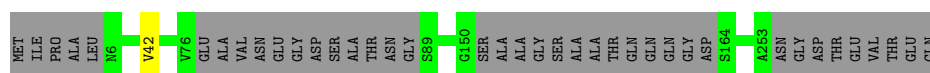
- Molecule 73: Chaperone protein DNAJ, putative

Chain 3p: 89% 9%



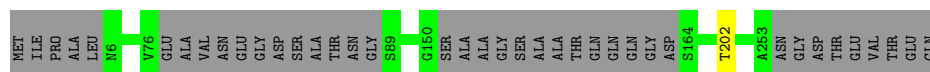
- Molecule 74: Nucleoside diphosphate kinase

Chain 3q: 85% 15%



- Molecule 74: Nucleoside diphosphate kinase

Chain 3r: 85% 15%



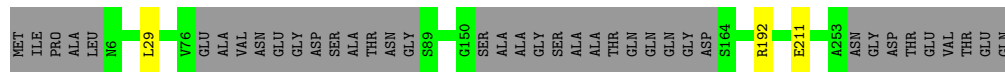
- Molecule 74: Nucleoside diphosphate kinase

Chain 3s: 85% 15%



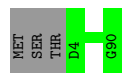
- Molecule 74: Nucleoside diphosphate kinase

Chain 3t: 84% 15%



- Molecule 75: Dynein light chain

Chain 3u: 97% .



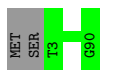
- Molecule 75: Dynein light chain

Chain 3v: 97% .



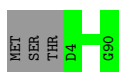
- Molecule 75: Dynein light chain

Chain 3w:  98%



- Molecule 75: Dynein light chain

Chain 3x:  97%



- Molecule 75: Dynein light chain

Chain 3y:  97%



- Molecule 75: Dynein light chain

Chain 3z:  97%



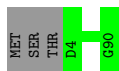
- Molecule 75: Dynein light chain

Chain 4a:  97%



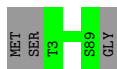
- Molecule 75: Dynein light chain

Chain 4b:  97%



- Molecule 75: Dynein light chain

Chain 4c:  97%



- Molecule 75: Dynein light chain

Chain 4d:  97%



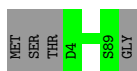
- Molecule 75: Dynein light chain

Chain 4e:  96%



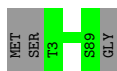
- Molecule 75: Dynein light chain

Chain 4f:  96%



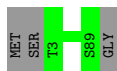
- Molecule 75: Dynein light chain

Chain 4g:  97%



- Molecule 75: Dynein light chain

Chain 4h:  97%



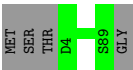
- Molecule 75: Dynein light chain

Chain 4i:  96%

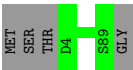


- Molecule 75: Dynein light chain

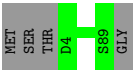
Chain 4j:  96%



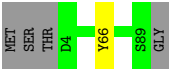
• Molecule 75: Dynein light chain



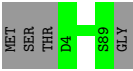
• Molecule 75: Dynein light chain



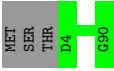
• Molecule 75: Dynein light chain



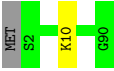
• Molecule 75: Dynein light chain



• Molecule 75: Dynein light chain



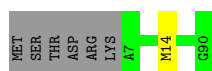
• Molecule 75: Dynein light chain



• Molecule 75: Dynein light chain







- Molecule 75: Dynein light chain



- Molecule 75: Dynein light chain



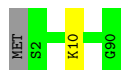
There are no outlier residues recorded for this chain.

- Molecule 75: Dynein light chain



There are no outlier residues recorded for this chain.

- Molecule 75: Dynein light chain



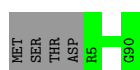
- Molecule 75: Dynein light chain



- Molecule 75: Dynein light chain



- Molecule 75: Dynein light chain



- Molecule 75: Dynein light chain

Chain 8k:  98% ..



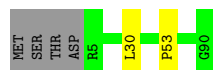
- Molecule 75: Dynein light chain

Chain 8n:  92% • 7%



- Molecule 75: Dynein light chain

Chain 8o:  93% • •



- Molecule 75: Dynein light chain

Chain 8p:  94% • •



- Molecule 75: Dynein light chain

Chain 9k:  98% ..



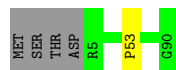
- Molecule 75: Dynein light chain

Chain 9n:  91% • 7%



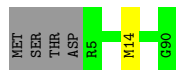
- Molecule 75: Dynein light chain

Chain 9o:  94% • •



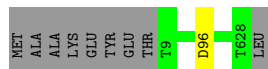
- Molecule 75: Dynein light chain

Chain 9p:  94%



- Molecule 76: Cilia- and flagella-associated protein 52

Chain 4O:  98%



- Molecule 76: Cilia- and flagella-associated protein 52

Chain 4P:  99%



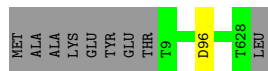
- Molecule 76: Cilia- and flagella-associated protein 52

Chain 4Q:  99%



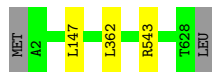
- Molecule 76: Cilia- and flagella-associated protein 52

Chain 4R:  98%



- Molecule 76: Cilia- and flagella-associated protein 52

Chain 4S:  99%



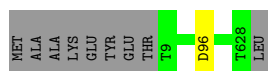
- Molecule 76: Cilia- and flagella-associated protein 52

Chain 4T:  99%



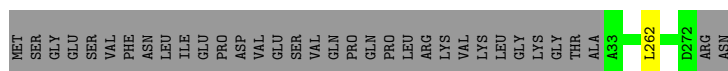
- Molecule 76: Cilia- and flagella-associated protein 52

Chain 4U:  98%



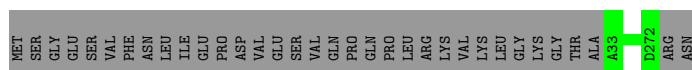
- Molecule 77: Enkurin domain-containing protein

Chain 4V:  87%




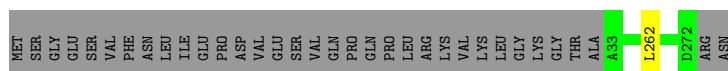
- Molecule 77: Enkurin domain-containing protein

Chain 4W:  88%



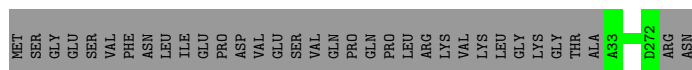
- Molecule 77: Enkurin domain-containing protein

Chain 4X:  87%




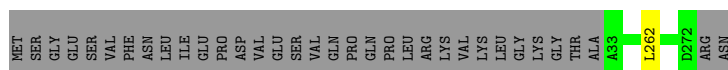
- Molecule 77: Enkurin domain-containing protein

Chain 4Y:  88%



- Molecule 77: Enkurin domain-containing protein

Chain 4Z:  87%



- Molecule 78: Cytochrome b5 domain-containing protein 1

Chain 4o:  100%

There are no outlier residues recorded for this chain.

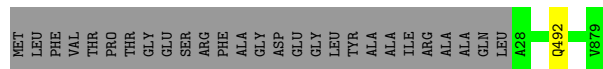
- Molecule 78: Cytochrome b5 domain-containing protein 1

Chain 4p:  100%

There are no outlier residues recorded for this chain.

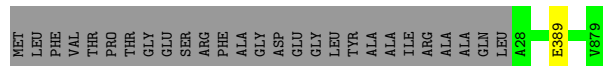
- Molecule 79: Leucine-rich repeat protein (LRRP)

Chain 4q:  97%



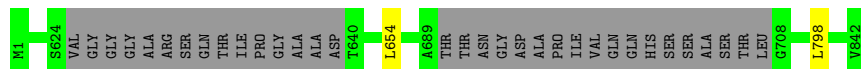
- Molecule 79: Leucine-rich repeat protein (LRRP)

Chain 4r:  97%



- Molecule 80: VWFA domain-containing protein

Chain 4s:  96%





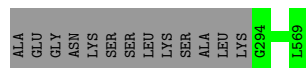
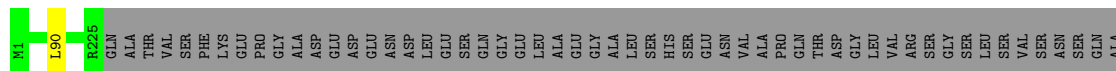
- Molecule 80: VWFA domain-containing protein

Chain 4t:  96%





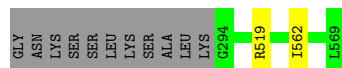
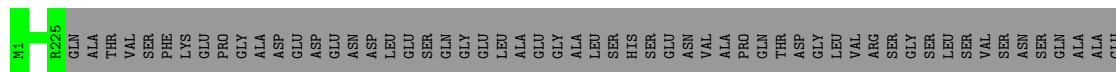
- Molecule 81: TbRSP63

Chain 4u:  88%  12%



- Molecule 81: TbRSP63

Chain 4v:  88%  12%

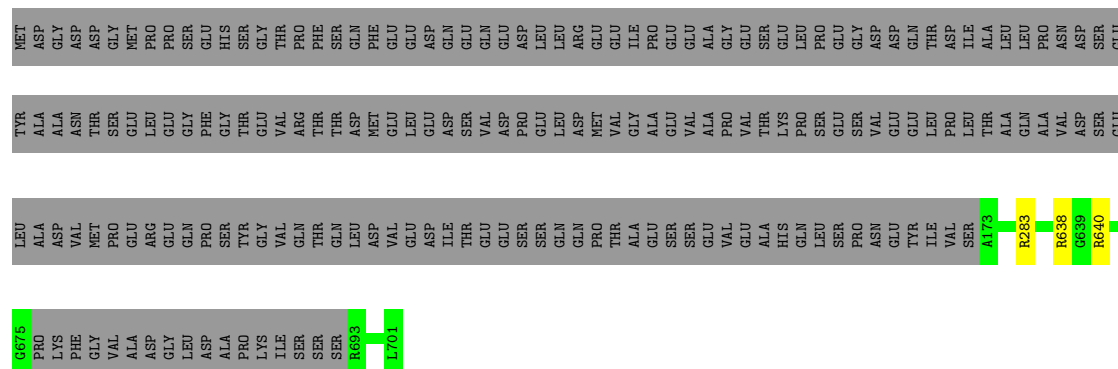


- Molecule 82: IQ and ubiquitin-like domain-containing protein

Chain 4w:

73%

27%



- Molecule 83: Calmodulin

Chain 4x:

99%

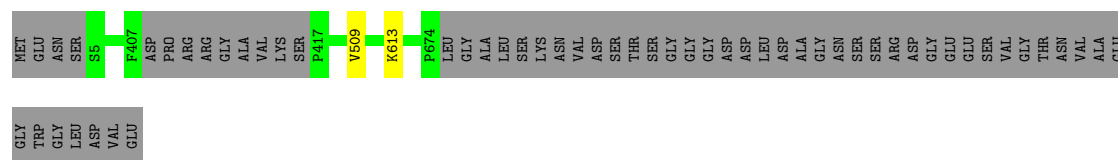


- Molecule 84: MORN repeat-containing protein 3

Chain 4y:

92%

8%

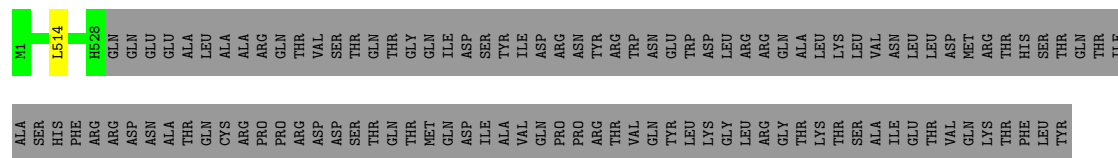


- Molecule 85: Cilia- and flagella-associated protein 206

Chain 4z:

82%

18%

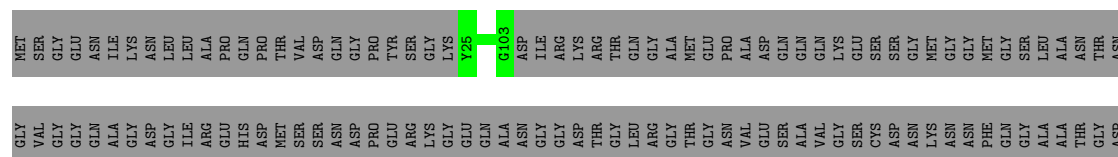


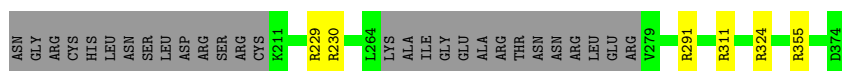
- Molecule 86: Enkurin domain-containing protein

Chain 5A:

60%

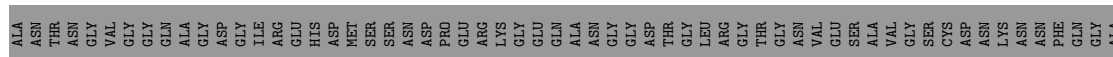
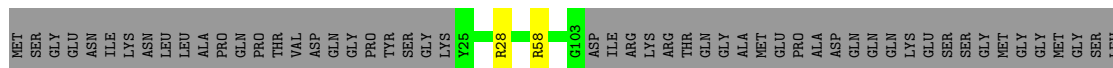
39%





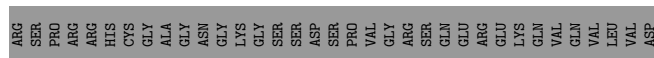
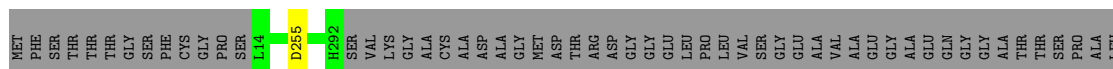
• Molecule 86: Enkurin domain-containing protein

Chain 5B: 60% 39%



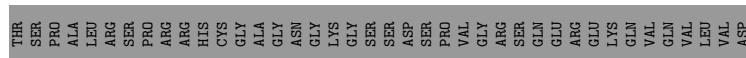
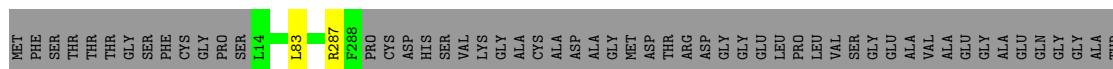
• Molecule 87: MC4

Chain 5C: 75% 24%



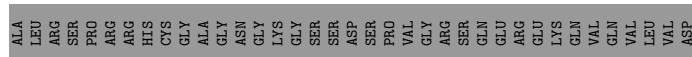
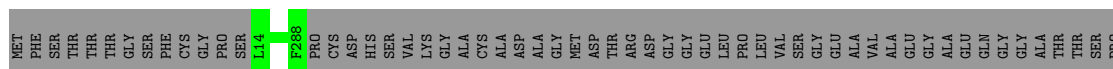
• Molecule 87: MC4

Chain 5D: 74% 25%



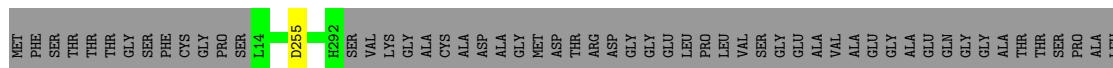
• Molecule 87: MC4

Chain 5E: 75% 25%



• Molecule 87: MC4

Chain 5F: 75% 24%



ARG SER PRO ARG ARG HIS CYS GLY ALA CYS GLY ASN LYS GLY SER SER ASP PRO VAL GLY ARG LYS GLN GLU ARG LYS GLN VAL GLN VAL LEU VAL ASP

● Molecule 87: MC4



MET PHE SER THR THR GLY SER PHE CYS GLY PRO SER L14 L83 F288 PRO CYS ASP HIS SER VAL LYS GLY ALA CYS ASP ALA GLY MET ASP THR ARG ASP GLY GLU LEU PRO LEU VAL SER SER GLY GLU LEU PRO LEU VAL ASP

SER PRO ALA LEU SER ARG PRO ARG HIS CYS GLY ALA GLY ASN LYS SER SER CYS ASP HIS VAL LYS GLY ARG CYS ALA GLU SER GLN GLU ASP MET ASP VAL GLN VAL ASP

● Molecule 87: MC4



MET PHE SER THR THR GLY SER PHE CYS GLY PRO SER L14 F288 PRO CYS ASP HIS VAL LYS GLY ALA CYS ASP MET ASP THR ARG ASP GLY GLU LEU PRO LEU VAL SER SER GLY GLU LEU VAL ASP

ALA LEU ARG SER PRO ARG ARG HIS CYS GLY ALA ASN GLY LYS GLY SER SER ASP SER PRO VAL LYS GLY ARG CYS ALA GLU SER GLN GLU ASP MET ASP VAL GLN VAL ASP

● Molecule 87: MC4



MET PHE SER THR THR GLY SER PHE CYS GLY PRO SER L14 D255 H292 SER VAL LYS GLY ALA CYS ASP MET ASP THR ARG ASP GLY GLU LEU PRO LEU VAL SER SER GLY GLU LEU VAL ASP

ARG SER PRO ARG ARG HIS CYS GLY ALA ASN LYS GLY SER SER ASP PRO VAL GLY ARG LYS GLN GLU ARG ALA GLU SER GLN GLU ASP MET ASP VAL GLN VAL ASP

● Molecule 87: MC4



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

HIS GLY ALA THR TYR ARG ASP ALA ASP ALA VAL GLU GLU ALA SER ASN THR LYS HIS TRP GLY PHE LEU SER LYS ALA ARG ILE GLN PHE GLU SER CYS GLY SER PHE VAL ARG THR ASN THR ASP ASN PRO THR THR ARG THR LYS HIS PRO LEU VAL THR TYR ASP P116 R284 F288

PRO CYS ASP HIS SER VAL LYS GLY ALA CYS GLY ASP ALA GLY MET ASP THR ARG ASP GLY GLY GLN VAL VAL ASP SER SER GLN VAL VAL ASP

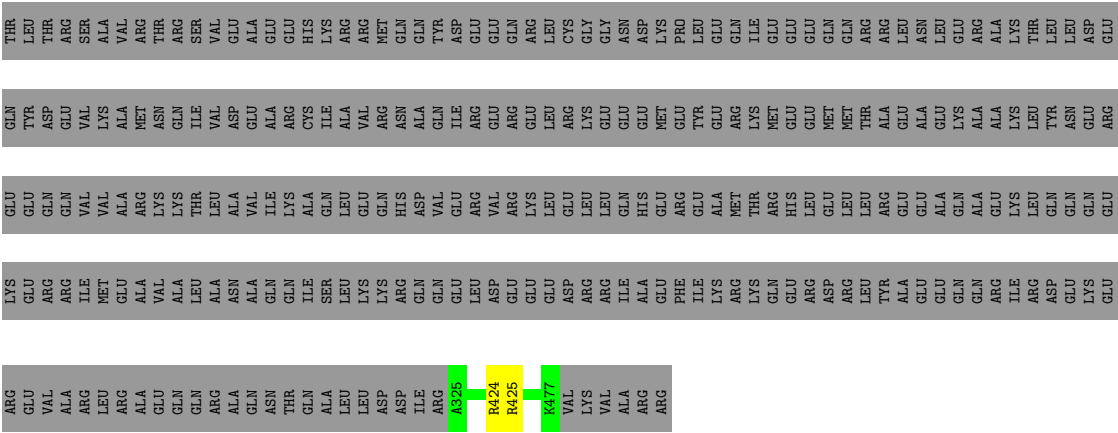
SER SER ASP SER PRO VAL GLY ARG SER GLN GLU ARG GLY LYS GLN VAL VAL ASP

● Molecule 88: Cilia- and flagella-associated protein 45

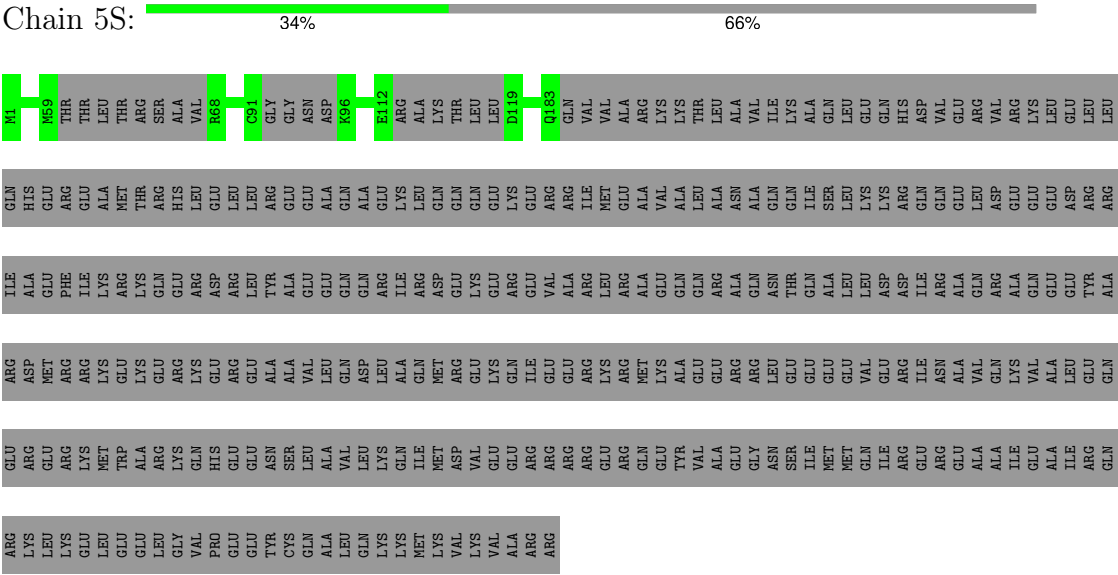


MET ILE GLY MET MET ALA ARG SER GLY ALA GLY VAL PHE PRO PRO ARG ARG PRO PRO GLY GLN THR GLY ASP ASP LEU ARG LYS GLU ASP ASN ARG ALA PRO PRO ASP SER THR ILE LEU THR ARG THR GLU LEU ASP ILE ILE THR THR ARG GLU MET ILE ILE SER GLY GLY LYS ASN ILE MET THR GLY

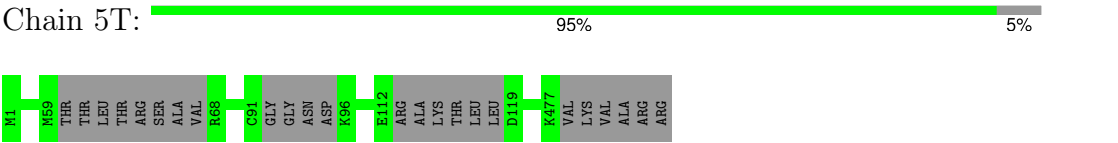




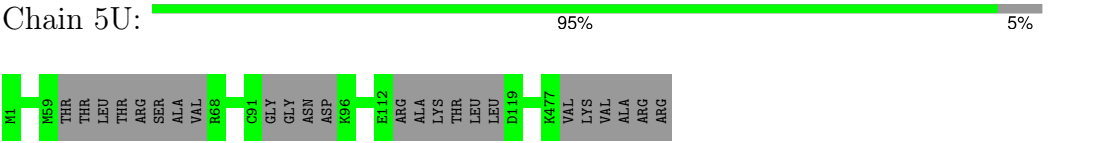
• Molecule 88: Cilia- and flagella-associated protein 45



• Molecule 88: Cilia- and flagella-associated protein 45

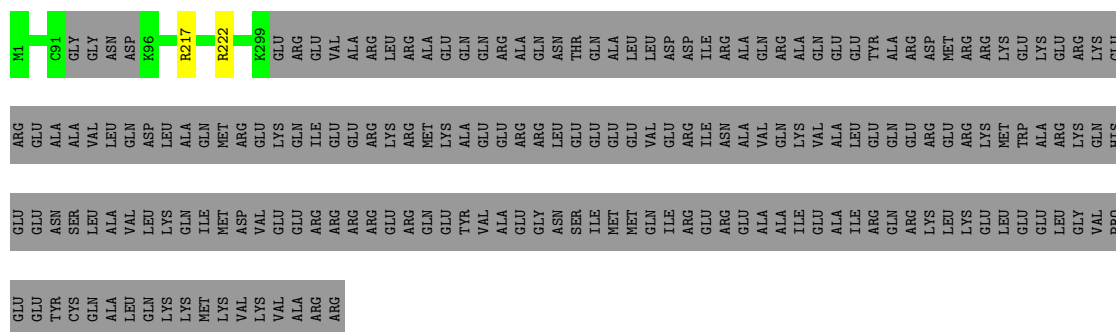


• Molecule 88: Cilia- and flagella-associated protein 45



• Molecule 88: Cilia- and flagella-associated protein 45





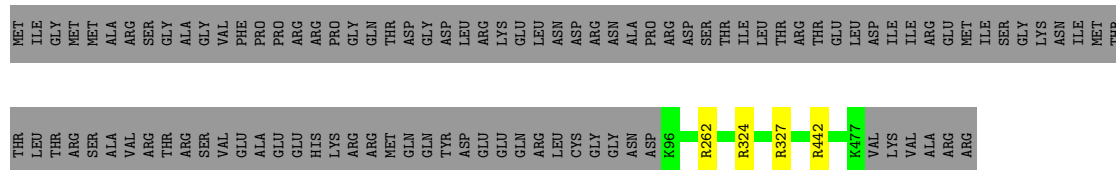
- Molecule 88: Cilia- and flagella-associated protein 45

Chain 5W: 98%



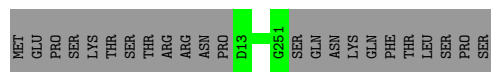
- Molecule 88: Cilia- and flagella-associated protein 45

Chain 5X: 78%



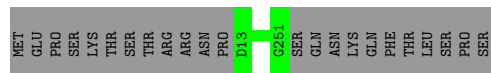
- Molecule 89: CCDC81 HU domain-containing protein

Chain 5L: 91%



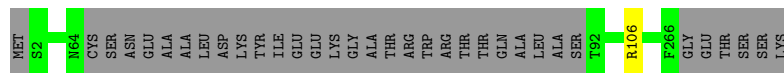
- Molecule 89: CCDC81 HU domain-containing protein

Chain 5M: 91%



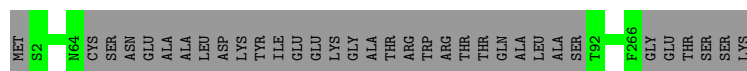
- Molecule 90: MC5

Chain 5N: 87%




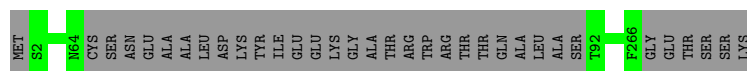
- Molecule 90: MC5

Chain 5O:  88% 12%



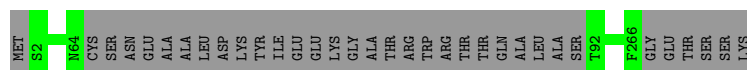
- Molecule 90: MC5

Chain 5P:  88% 12%




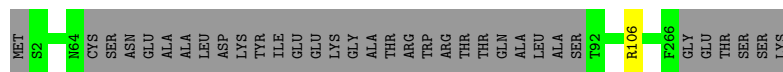
- Molecule 90: MC5

Chain 5Q:  88% 12%




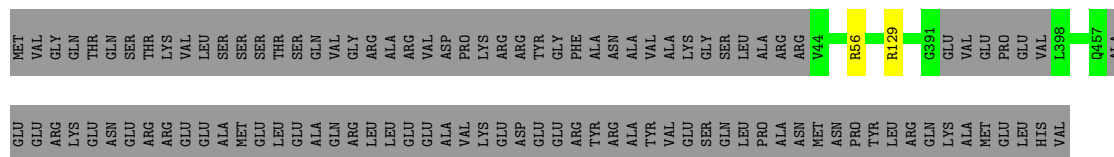
- Molecule 90: MC5

Chain 5R:  87% 12%



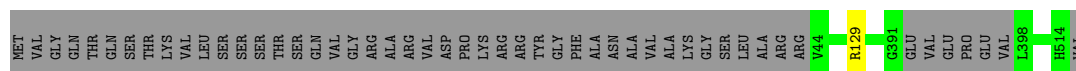
- Molecule 91: Trichohyalin-plectin-homology domain-containing protein

Chain 5Y:  79% 21%



- Molecule 91: Trichohyalin-plectin-homology domain-containing protein

Chain 5Z:  90% 10%

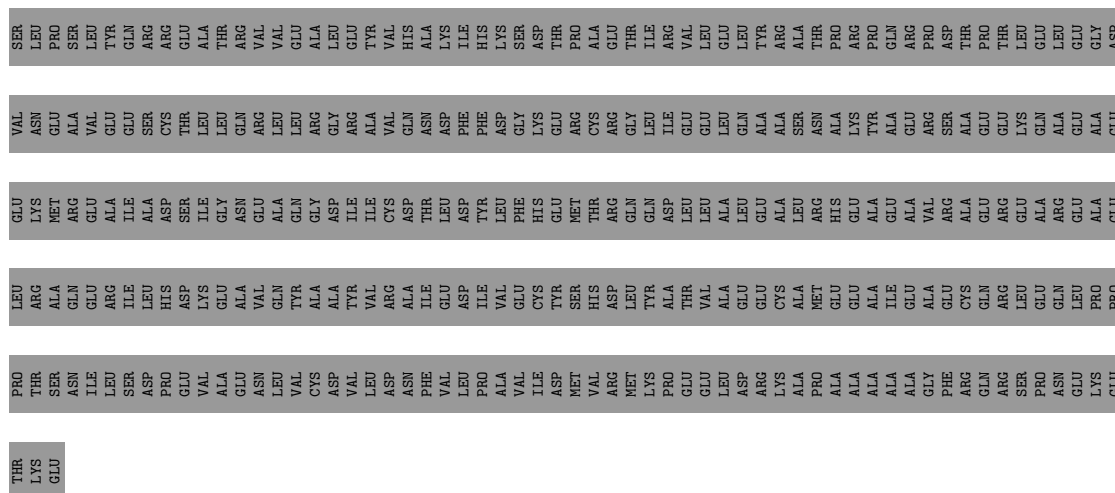


- Molecule 91: Trichohyalin-plectin-homology domain-containing protein

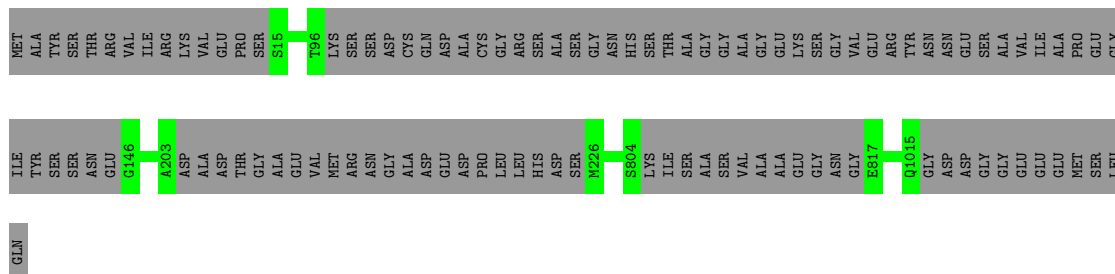
Chain 6A:  51% 49%



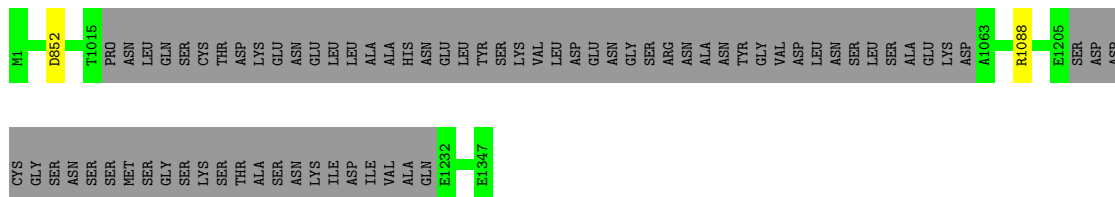




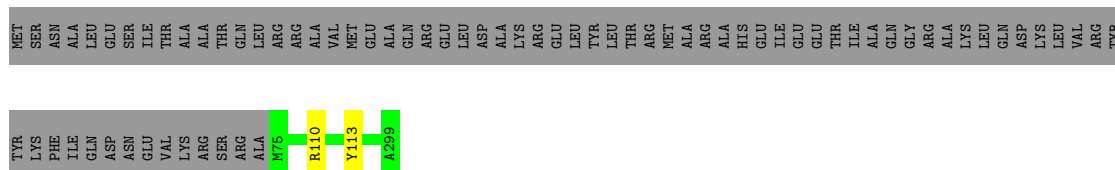
- Molecule 94: Cilia- and flagella-associated protein 251



- Molecule 95: Cilia- and flagella-associated protein 61 N-terminal domain-containing protein



- Molecule 96: DUF4200 domain-containing protein



- Molecule 97: DUF4200 domain-containing protein

Response	Percentage
Yes, the U.S. is a threat to my country's security	47%
No, the U.S. is not a threat to my country's security	53%

- Molecule 98: Leucine-rich repeat-containing protein 51

71% 29%

- Molecule 99: IDAf-alpha

Category	Percentage
Red	30%
Grey	70%









[illegible]

- Molecule 99: IDAf-alpha

Chain 5i:  72% 27%

[illegible]









- Molecule 101: Dynein axonemal intermediate chain 4

Chain 51:  50% 50%

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

LEU	ASP	ASN	GLU	ARG	TILE
MET	ASP	ASP	LEU	GLY	PRO
THR	MET	THR	VAL	ASP	SER
THR	PRO	ASN	GLU	ALA	THR
GLN	SER	ASP	ALA	LYS	GLN
ARG	ALA	GLU	ARG	ARG	GLY
ARG	THR	GLN	VAL	VAL	ALA
ARG	ASP	GLU	ASP	THR	ASN
CYS	ASP	GLY	GLU	ARG	GLN
GLU	ASN	THR	GLY	GLU	SER
ALA	LYS	ALA	THR	GLN	GLN
LEU	GLU	ASP	ARG	ARG	VAL
PHE	ALA	GLU	PHE	GLY	GLY
SER	GLU	GLU	GLN	GLU	PHE
ARG	GLN	GLU	VAL	TRP	LEU
C674	GLN	GLU	LYS	LEU	THR
T864	ASN	GLU	GLY	ALA	ALA
	ASP	VAL	SER	GLU	SER
	GLN	GLU	TRP	LYS	SER
	GLN	LEU	THR	THR	SER
	THR	VAL	PHE	THR	LEU
	ALA	GLU	ALA	VAL	THR
	GLY	ASP	PRO	VAL	SER
	VAL	SER	PRO	LEU	IIE
D495	ASP	ASP	LYS	HIS	ARG
D540	GLY	GLY	IIE	THR	THR
R627	ARG	LYS	HIS	IIE	THR
	GLN	ASP	SER	THR	GLY
	HIS	GLY	ALA	MET	GLY
	GLY	THR	GLN	LEU	GLY
	ALA	GLU	PRO	TYR	ALA
	ALA	ARG	PRO	MET	ALA
	SER	THR	SER	HIS	ALA
	GLU	THR	SER	GLN	ALA
	GLU	ASP	LYS	GLU	ALA
	SER	PRO	ASN	VAL	ALA
	ALA	SER	SER	VAL	ALA
	PHE	R342	GLY	PRO	ALA
	ALA	ALA	GLY	ASN	ALA
	ALA	R392	LEU	ASP	SER
	GLU	VAL	GLN	ARG	GLY
	SER	ARG	VAL	PRO	PRO
	SER	LYS	THR	THR	LEU
	GLY	GLU	PRO	GLU	ALA
	VAL	GLU	TRP	GLU	ASP
	LEU	ALA	MET	ASN	THR
	ASN	ALA	LEU	GLU	PRO
	GLY	THR	ARG	VAL	PRO
	LYS	SER	ASP	LEU	HIS
	LYS	GLY	ALA	GLU	THR
	ASP	LEU	PHE	ARG	SER
	GLY	MET	ALA	ASN	THR
	ALA	GLY	HIS	LYS	GLY
	PRO	PRO	PHE	ALA	GLY
	GLY	SER	GLU	TYR	HIS
	ALA	SER	GLU	ALA	GLY

- Molecule 102: IC140

Chain 5m: 

ASN	TYR	TYR	PRO	SER	ALA	GLY	MET
TYR	ALA	ASP	ASP	PRO	GLU	ALA	SER
TYR	ASP	THR	THR	THR	LEU	TYR	ARG
HIS	ASP	LEU	ASP	THR	THR	THR	LEU
HIS	ASP	PRO	MET	ASP	LYS	LYS	VAL
ASP	THR	THR	ILE	CYS	GLU	GLU	ALA
ALA	GLU	ALA	GLY	ARG	SER	GLY	LEU
PHE	ALA	ALA	THR	GLY	ASP	GLU	LEU
LEU	ALA	ARG	PRO	PRO	SER	THR	ALA
LYS	GLU	ALA	LEU	PRO	ASP	ARG	VAL
VAL	VAL	HIS	PRO	PRO	GLN	PRO	THR
GLU	ALA	GLY	VAL	GLY	ARG	LYS	ASN
ALA	PRO	LYS	MET	MET	GLY	THR	LYS
PHE	ARG	LYS	MET	ASP	VAL	THR	THR
ARG	PRO	ILE	ALA	ALA	ASN	GLU	SER
GLU	GLU	PRO	MET	MET	ALA	LEU	THR
GLU	ASP	MET	GLY	ARG	ARG	LEU	GLY
THR	THR	PRO	PHE	THR	PHE	SER	ALA
MET	MET	MET	ILE	ASN	GLY	GLU	SER
SER	SER	VAL	VAL	VAL	LYS	GLU	PRO
SER	GLU	K394	VAL	VAL	ASP	VAL	GLY
LEU	LEU	P491	PRO	PRO	GLU	ILE	VAL
ASP	ASP		ARG	ARG	ASP	GLU	SER
GLY	GLY	H739	THR	THR	ALA	ASN	SER
ASP	ASP	ALA	LEU	LEU	SER	GLY	GLY
GLY	ALA	ALA	HIS	HIS	VAL	TYR	ASP
ALA	ASP	PRO	CYS	PRO	GLN	GLN	GLY
ASP	THR	LYS	LEU	LEU	VAL	VAL	ASN
THR	THR	MET	LEU	LEU	VAL	VAL	ASN
ALA	ALA	ARG	GLN	GLN	PRO	ARG	LEU
SER	SER	ARG	TYR	TYR	VAL	PRO	PHE
PRO	PRO	ASP	GLU	GLU	MET	GLN	ARG
ILE	ILE	HIS	ILE	ILE	ASP	VAL	PHE
		THR	THR	THR	PRO	ARG	SER
		PRO	THR	THR	VAL	VAL	ALA
		ALA	ALA	ALA	GLN	ALA	THR
		ALA	ASP	ASP	SER	ARG	VAL
		ILE	THR	THR	PHE	ARG	LYS
		ALA	F231	F231	SER	ARG	VAL
		ASP	D246	D246	ARG	ASP	ALA
		SER	ASN	ASN	LYS	ILE	THR
		TRP	Q327	Q327	VAL	LEU	CYS
		GLY	A361	A361	ALA	ALA	ALA
		ASN	GLY	GLY	THR	GLN	THR
		GLU	ARG	ARG	VAL	ARG	THR
		ASP	THR	THR	GLN	LEU	ASP

- Molecule 103: IC97/Casc1 N-terminal domain-containing protein

Chain 5n:  93% • 6%

NET	PRO	PRO	LYS	THR	VAL	LYS	VAL	ILE	GLY	ARG	GLY	LYS	ASP	ASP	ASP	LYS	ASP	ASP	LYS	PRO	PRO	LYS	LYS	LEU	LYS	LYS	ALA	ALA	GLN	ILE	ILE	ILE	ASN	LYS	LYS	ALA	VAL	VAL	GLU	THR	ALA	ASP	LYS	LYS	LEU	Y43	R332	R535	H654	R652	G657
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------

- Molecule 104: FAP120

Chain 50:  82% 18%

NET	ASU	SER	GLY	THR	CYS	ILE	GLY	GLY	LEU	GLU	GLI	VAL	ASP	GLY	LYS	VAL	ARG	GLN	LYS	GLU	GLU	LEU	ASP	ARG	LEU	HIS	ARG	GLU	THR	GLU	GLU	GLU	ASP	GLU	ASP	ALA	ALA	ARG	ARG	MET	LEU	LEU	GLU	GLU	ILE	GLU	GLU	ARG	LYS	TYR	GLN	GLN
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLU GLN ARG LYS LYS ARG LEU GLU ALA ALA ALA GLU LYS ALA SER THR MET LYS LYS

- Molecule 105: Dynein light chain, putative

Chain 5p:  89% 10%


MET GLN THR ASP PHE GLY ASP ALA THR THR PHE SER LEU R14 W95 Y124

- Molecule 105: Dynein light chain, putative

Chain 7i:  90% 10%

MET GLN THR ASP PHE GLY ASP ALA THR THR PHE SER LEU R14 Y124

- Molecule 105: Dynein light chain, putative

Chain 8i:  90% 10%


MET GLN THR ASP PHE GLY ASP ALA THR THR PHE SER LEU R14 Y124

- Molecule 105: Dynein light chain, putative

Chain 9i:  90% 10%


MET GLN THR ASP PHE GLY ASP ALA THR THR PHE SER LEU R14 Y124

- Molecule 106: Dynein light chain roadblock

Chain 5q:  82% 17%


MET ALA ALA ILE GLY GLY GLY SER G9 R80 S106 GLY ASP VAL PRO ASN ALA ASN GLY VAL SER ALA

- Molecule 106: Dynein light chain roadblock

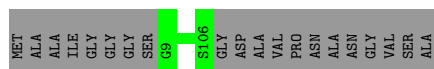
Chain 7l:  83% 17%

MET ALA ALA ILE GLY GLY GLY SER G9 S106 GLY ASP VAL PRO ASN ALA ASN GLY VAL SER ALA

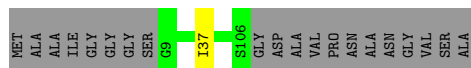
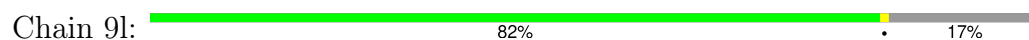
- Molecule 106: Dynein light chain roadblock

Chain 8l:  83% 17%





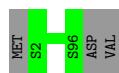
- Molecule 106: Dynein light chain roadblock



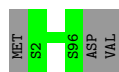
- Molecule 107: Dynein light chain roadblock



- Molecule 107: Dynein light chain roadblock



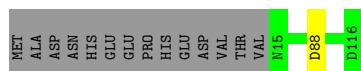
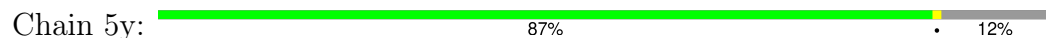
- Molecule 107: Dynein light chain roadblock



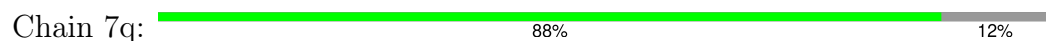
- Molecule 107: Dynein light chain roadblock



- Molecule 108: Dynein light chain, putative



- Molecule 108: Dynein light chain, putative








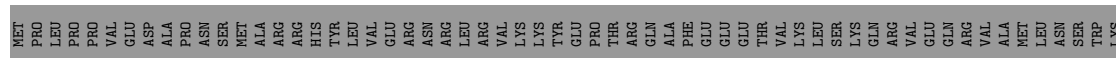
- Molecule 109: Trichohyalin-pectin-homology domain-containing protein

Chain 6J:  99%



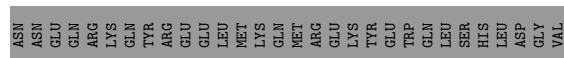
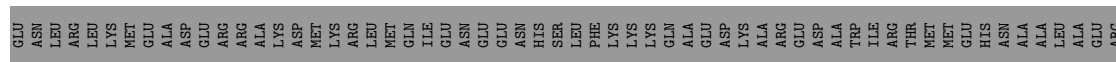
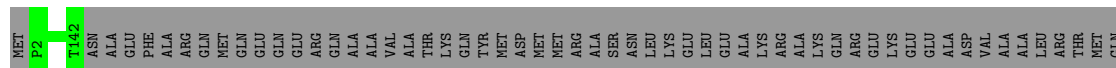
- Molecule 109: Trichohyalin-pectin-homology domain-containing protein

Chain 6K:  81% 18%



- Molecule 109: Trichohyalin-pectin-homology domain-containing protein

Chain 6L:  41% 59%



- Molecule 109: Trichohyalin-pectin-homology domain-containing protein

Chain 6M:  99%



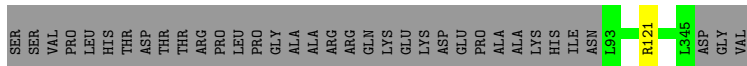
- Molecule 109: Trichohyalin-pectin-homology domain-containing protein

Chain 6N:  99%

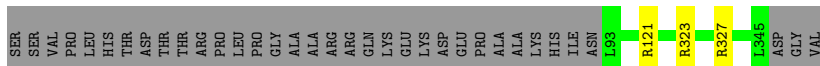


- Molecule 109: Trichohyalin-pectin-homology domain-containing protein

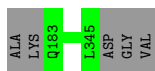
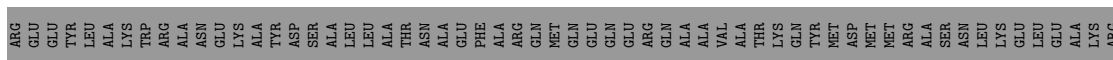
Chain 6O:  72% 27%



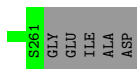
- Molecule 109: Trichohyalin-pectin-homology domain-containing protein



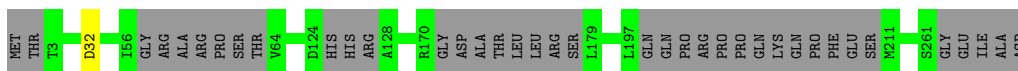
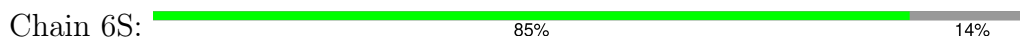
- Molecule 109: Trichohyalin-plectin-homology domain-containing protein



- Molecule 110: STOP axonemal protein

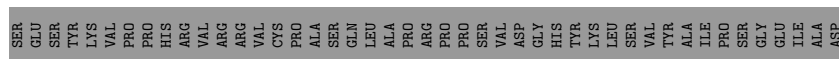


- Molecule 110: STOP axonemal protein

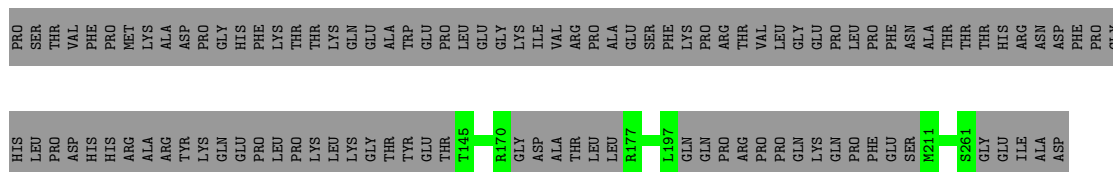


- Molecule 110: STOP axonemal protein

Response	Percentage
Doing a good job	66%
Doing a bad job	33%



- Chain 6U:



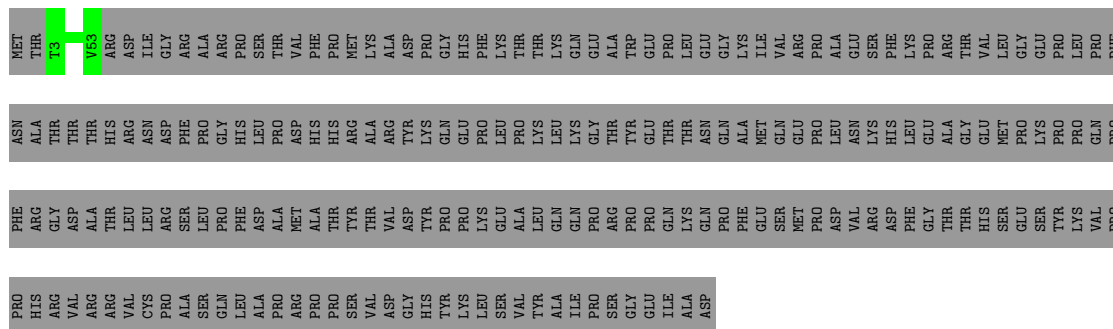
- Chain 6V:




- Chain 6W:

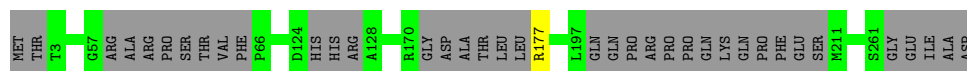


- Chain 6X:




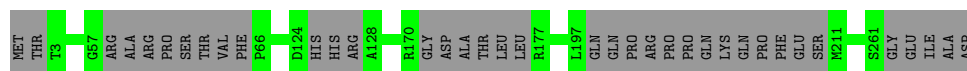
- 

Chain 6Y:  86% 14%



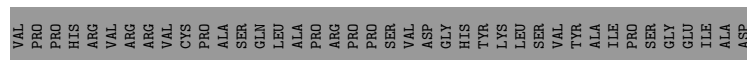
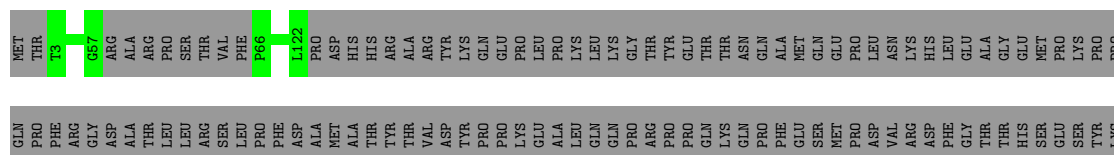
- Molecule 110: STOP axonemal protein

Chain 6Z:  86% 14%



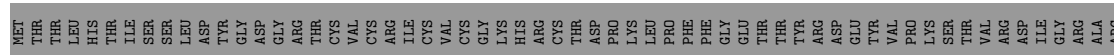
- Molecule 110: STOP axonemal protein

Chain 7A:  42% 58%



- Molecule 110: STOP axonemal protein

Chain 7B:  67% 33%



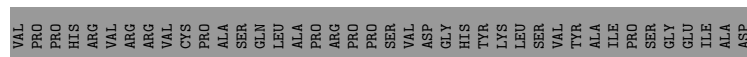
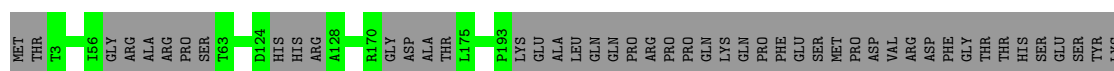
- Molecule 110: STOP axonemal protein

Chain 7C:  90% 10%



- Molecule 110: STOP axonemal protein

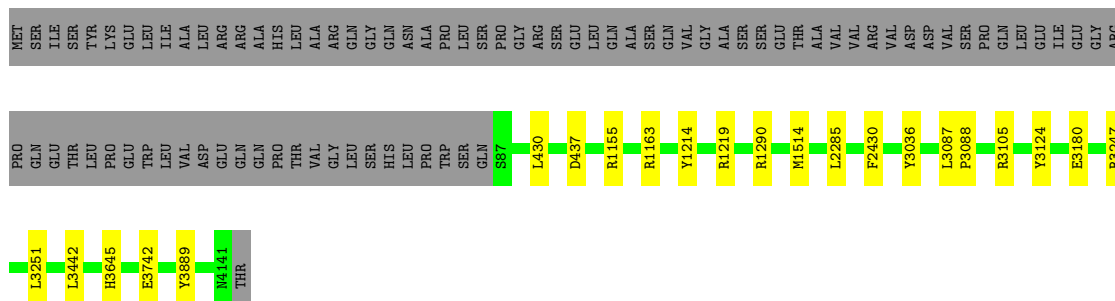
Chain 7D:  67% 33%



- Chain 7J:  89% 11%

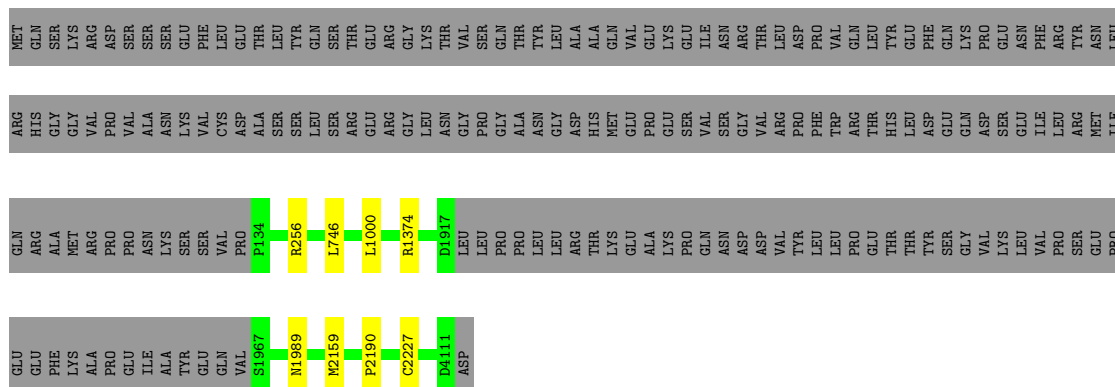






- Molecule 113: Dynein heavy chain, putative

Chain 6c:  95%



- Molecule 114: Dynein heavy chain, putative

Chain 6d:  94% 6%



- Molecule 115: Dynein heavy chain, putative

Chain 6e:  98% .





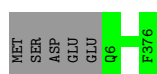
- Molecule 116: Actin A

Chain 6f: 99%



- Molecule 116: Actin A

Chain 6g: 99%



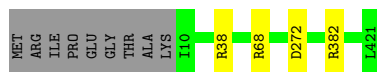
- Molecule 117: Actin-like protein, putative

Chain 6h: 100%



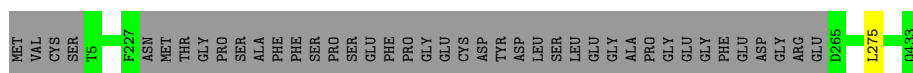
- Molecule 118: Actin, putative

Chain 6i: 97%



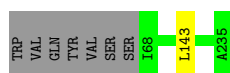
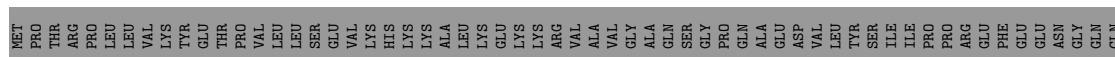
- Molecule 119: Actin, putative

Chain 6j: 90%



- Molecule 120: Dynein arm light chain, axonemal, putative

Chain 6k: 71%



- Molecule 120: Dynein arm light chain, axonemal, putative

MET  
 PRO  
 THR  
 ARG  
 PRO  
 L6  
 K29  
 ARG  
 VAL  
 ALA  
 VAL  
 GLY  
 ALA  
 GLN  
 SER  
 GLY  
 PRO  
 GLN  
 ALA  
 GLU  
 D43  
 R206  
 R216  
 A232  
 THR  
 LYS  
 ALA

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|------|
| MET  |
| PRO  |
| THR  |
| ARG  |
| PRO  |
| L6   |
| V31  |
| ALA  |
| VAL  |
| GLY  |
| ALA  |
| GLN  |
| SER  |
| GLY  |
| P39  |
| T233 |
| LYS  |
| ALA  |

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| MET | GLY | LEU | LEU | LYS | VAL | GLU | THR | HIS | VAL | ASN | ASP | ASP | VAL | GLN | VAL | VAL | ASP | ASP | VAL | LEU | SER | GLU | SER | VAL | VAL | PRO | LEU | SER | ARG | ARG | LEU | GLU | VAL | VAL | ARG | LYS | HIS | THR | SER | SER | GLY | GLN | GLY | ALA | ALA | VAL | GLU | CYS | LYS | GLU | LYS | ALA | ALA | ALA | THR | SER | GLN | MET | SER |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

SER	PRO	SER	THR	GLN	LEU	VAL	VAL	ALA	ALA	GLY	GLU	THR	THR	PRO	SER	THR	ASP	ILE	ARG	ARG	ARG	SER	LEU	MET	LYS	ALA	ALA	GLN	ARG	ARG	GLY	SER	SER	LYS	LEU	PRO	SER	CYS	THR	THR	LYS	GLU	GLU	CYS	VAL	SER	ASN	THR	THR	SER	SER	VAL	VAL	ASN	LYS	THR	THR	LEU	LEU	SER	SER	GLN	ASN	ALA	SER	SER	SER	PRO
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[illegible]

VAL  
GLU  
LEU

- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |      |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|-----|-----|-----|
| MET | GLN | PRO | TYR | GLY | MET | SER | THR | SER | ARG | THR | ARG | ASN | PRO | LEU | VAL | ALA | SER | ARG | GLY | GLY | PRO | ASN | ALA | M239 | I268 | SER | MET | PRO | SER | THR | PRO |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|-----|-----|-----|

- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| NET | ALA | THR | LEU | ASN | ALA | PRO | PRO | ASN | VAL | TYR | ASP | GLU | GLY | THR | VAL | LEU | TYR | ARG | ALA | VAL | PRO | SER | ASN | LEU | ILE | SER | ASP | ASP | GLU | PRO | THR | ILE | ALA | ALA | ALA | VAL | ASN | ALA | ALA | GLY | GLN | GLU | ALA | PRO | THR | ILE | ALA | PRO | THR | THR | ASN | ARG | GLN | LYS |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

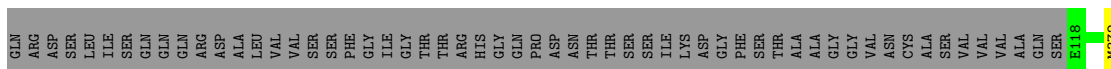
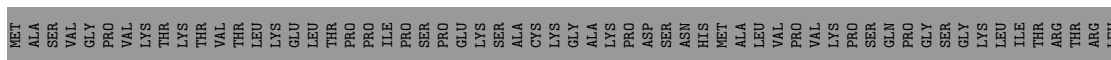
PHE	GLN	GLY	THR	GLN	SER	GLY	VAL	ALA	GLY	THR	ARG	ASP	ASP	ALA	ILE	GLN	SER	SER	GLY	GLY	PRO	VAL	VAL	ARG	LEU	LEU	THR	THR	GLN	GLU	SER	SER	LEU	LEU	THR	PRO	VAL	VAL	LYS	ASN	LEU	LEU	PHE	PRO	PRO	VAL	VAL	PRO	PRO	GLY	GLY	HIS	ASP	LYS	ASP	ASP	ARG	THR	ASN	THR	THR	ARG	GLY	GLN	GLU
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GLN	GLU	CYS	ALA	TRP	MET	LYS	ALA	ALA	ALA	VAL	ASP	HIS	THR	S135	K298	SER	SER	THR	PRO	THR	PRO	GLY	MET
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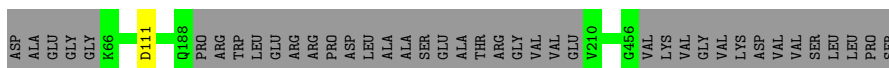
- Molecule 125: Tetratricopeptide repeat protein 29

Chain 6r:



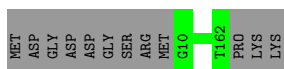
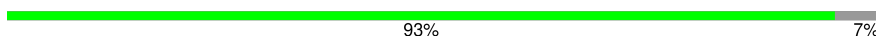
- Molecule 126: Tetratricopeptide repeat protein

Chain 6s:



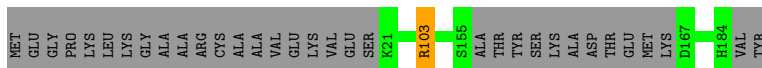
- Molecule 127: Centrin, putative

Chain 6t:



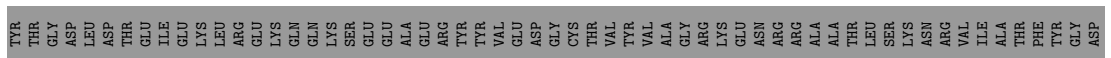
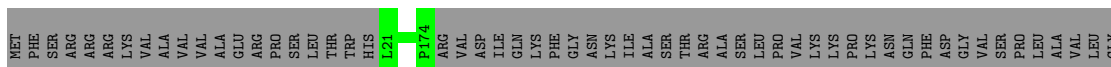
- Molecule 128: Centrin, putative

Chain 6u:



- Molecule 129: MC8

Chain 7L:

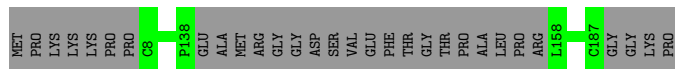


- Molecule 129: MC8



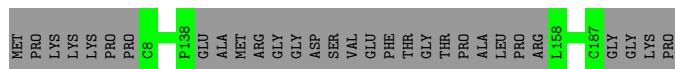
- Molecule 131: FAP90

Chain 7R:  84% 16%



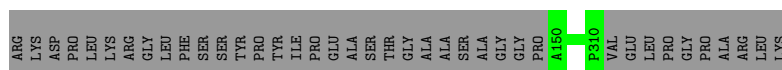
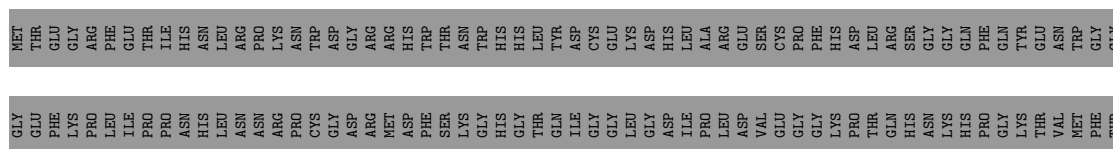
- Molecule 131: FAP90

Chain 7S: 



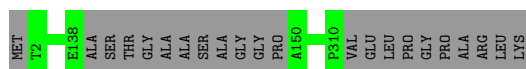
- Molecule 132: PBP36

Chain 7T:  50% 50%



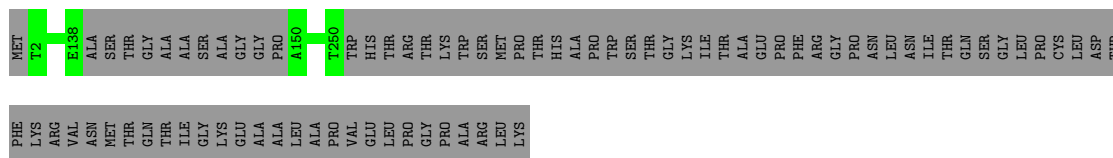
- Molecule 132: PBP36

Chain 7U:  93% 7%



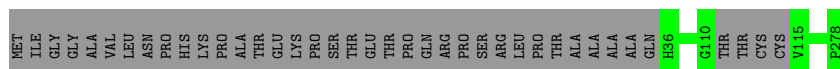
- Molecule 132: PBP36

Chain 8L:  74% 26%




- Molecule 133: Enkurin domain-containing protein

Chain 7V:  86% 14%




- Molecule 133: Enkurin domain-containing protein

Chain 7W:  85% 14%


MET ILE GLY GLY ALA VAL LEU ASN PRO HIS LYS LYS PRO ALA THR THR LYS LYS PRO SER SER THR GLU THR THR PRO PRO GLN ARG ARG SER SER ARG ARG LEU PRO PRO THR ALA ALA ALA ALA ALA ALA H36 R154 SER GLN ASP LYS ASP S150 L173 P278

- Molecule 133: Enkurin domain-containing protein

Chain 7X:  83% 17%


MET ILE GLY GLY ALA VAL LEU ASN PRO HIS LYS LYS PRO ALA THR THR LYS LYS PRO SER SER THR GLU THR THR PRO PRO GLN ARG ARG SER SER ARG ARG LEU PRO PRO THR ALA ALA ALA ALA ALA ALA H36 R154 SER GLN ASP LYS ASP S150 L173 P278

- Molecule 133: Enkurin domain-containing protein

Chain 7Y:  86% 14%


MET ILE GLY GLY ALA VAL LEU ASN PRO HIS LYS LYS PRO ALA THR THR LYS LYS PRO SER SER THR GLU THR THR PRO PRO GLN ARG ARG SER SER ARG ARG LEU PRO PRO THR ALA ALA ALA ALA ALA ALA H36 R154 SER GLN ASP LYS ASP S150 L173 P278

- Molecule 133: Enkurin domain-containing protein

Chain 7Z:  85% 14%


MET ILE GLY GLY ALA VAL LEU ASN PRO HIS LYS LYS PRO ALA THR THR LYS LYS PRO SER SER THR GLU THR THR PRO PRO GLN ARG ARG SER SER ARG ARG LEU PRO PRO THR ALA ALA ALA ALA ALA ALA H36 R154 SER GLN ASP LYS ASP S150 L173 P278

- Molecule 133: Enkurin domain-containing protein

Chain 8A:  83% 17%

MET ILE GLY GLY ALA VAL LEU ASN PRO HIS LYS LYS PRO ALA THR THR LYS LYS PRO SER SER THR GLU THR THR PRO PRO GLN ARG ARG SER SER ARG ARG LEU PRO PRO THR ALA ALA ALA ALA ALA ALA H36 R154 SER GLN ASP LYS ASP S150 L173 P278

- Molecule 133: Enkurin domain-containing protein

Chain 8B:  86% 14%

MET ILE GLY GLY ALA VAL LEU ASN PRO HIS LYS LYS PRO ALA THR THR LYS LYS PRO SER SER THR GLU THR THR PRO PRO GLN ARG ARG SER SER ARG ARG LEU PRO PRO THR ALA ALA ALA ALA ALA ALA H36 R154 SER GLN ASP LYS ASP S150 L173 P278

- Molecule 133: Enkurin domain-containing protein

Chain 8C:  85% 14%

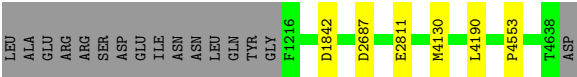
MET ILE GLY GLY ALA VAL LEU ASN PRO HIS LYS LYS PRO ALA THR THR LYS LYS PRO SER SER THR GLU THR THR PRO PRO GLN ARG ARG SER SER ARG ARG LEU PRO PRO THR ALA ALA ALA ALA ALA ALA H36 R154 SER GLN ASP LYS ASP S150 L173 P278

- Molecule 134: Dynein heavy chain, putative

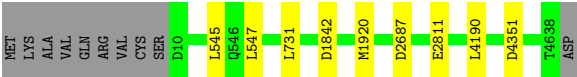


26%

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



- Molecule 134: Dynein heavy chain, putative



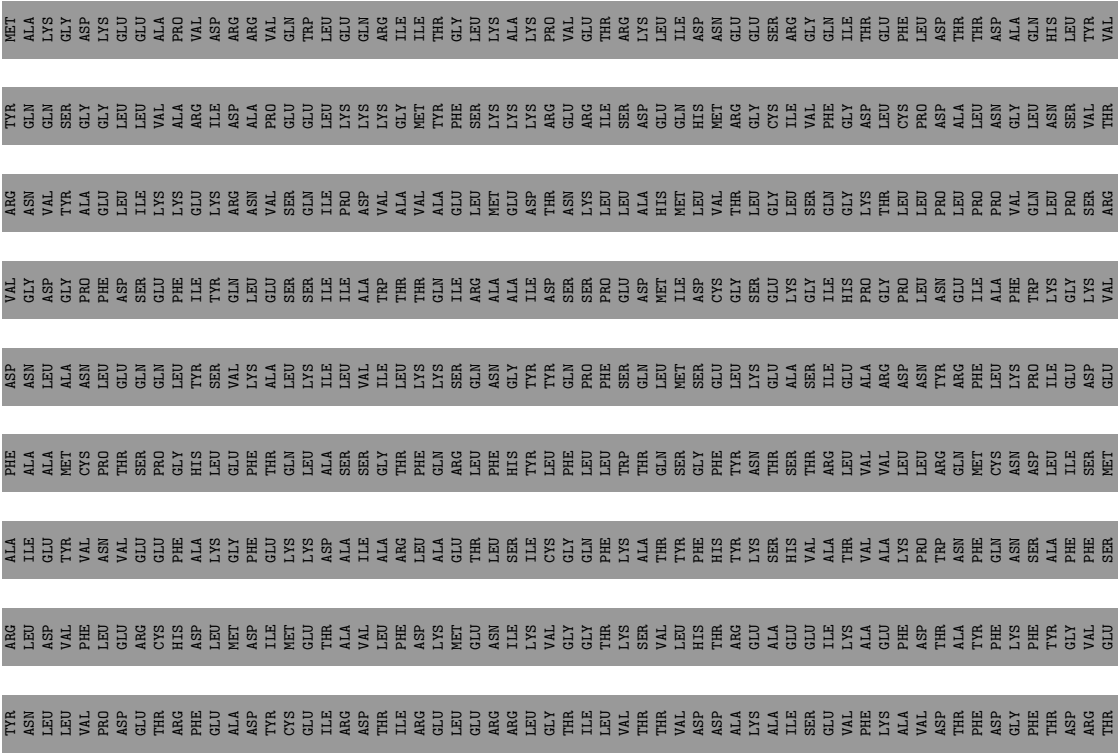
- Molecule 134: Dynein heavy chain, putative



- Molecule 134: Dynein heavy chain, putative



- Molecule 135: Dynein heavy chain, putative



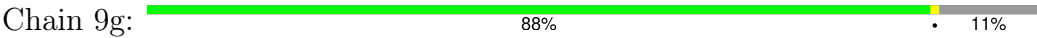






MET  
LYS  
LEU  
LEU  
GLU  
ASP  
TLE  
SER  
GLY  
GLY  
ILE  
ASP  
VAL  
ASP  
SER  
ASP

- Molecule 138: Dynein, putative



MET  
T2  
M18  
L215  
D266  
L330  
R534  
GLN  
ARG  
GLN  
ARG  
ASP  
ARG  
SER  
THR  
VAL  
LEU  
GLY  
GLU  
SER  
HIS  
LYS  
SER  
SER  
SER  
ASP  
GLU  
VAL  
THR  
GLN  
LEU  
LEU  
GLU  
LYS  
VAL  
THR  
GLU  
GLY  
TYR  
GLN  
THR  
THR  
VAL  
LYS  
SER  
GLY  
GLY  
LYS  
GLU  
ARG  
ASP  
ASP  
GLU  
GLN  
ARG  
THR  
LEU

GLU  
CYS  
ALA  
ARG  
ASN  
MET  
LYS  
LEU  
LEU  
GLU  
ASP  
ILE  
SER  
SER  
GLY  
GLY

- Molecule 139: Dynein intermediate chain, putative



MET  
ASP  
THR  
ASN  
ALA  
ARG  
ARG  
SER  
SER  
GLY  
GLY  
SER  
ALA  
ALA  
SER  
VAL  
VAL  
ASP  
ALA  
ALA  
PRO  
VAL  
VAL  
ALA  
ALA  
ALA  
PRO  
PRO  
PRO  
GLU  
ASP  
D29  
S190  
HIS  
ARG  
PRO  
THR  
THR  
LYS  
PRO  
GLU  
ASP  
LYS  
LEU  
SER  
SER  
THR  
ALA  
ASP  
GLU  
GLY  
GLY  
G208  
L364  
L485  
T584  
R554  
ALA

- Molecule 139: Dynein intermediate chain, putative



MET  
ASP  
THR  
ASN  
ALA  
ARG  
ARG  
SER  
SER  
GLY  
GLY  
SER  
ALA  
ALA  
SER  
VAL  
VAL  
ASP  
ALA  
ALA  
PRO  
VAL  
VAL  
ALA  
ALA  
ALA  
PRO  
PRO  
PRO  
GLU  
ASP  
D29  
E103  
S190  
HIS  
ARG  
PRO  
THR  
THR  
LYS  
PRO  
GLU  
ASP  
LYS  
LEU  
SER  
SER  
THR  
ALA  
ASP  
GLU  
GLY  
GLY  
G208  
W392  
M430  
L485  
G538

T584  
Q654  
ALA

- Molecule 139: Dynein intermediate chain, putative



MET  
ASP  
THR  
ASN  
ALA  
ARG  
ARG  
SER  
SER  
GLY  
GLY  
SER  
ALA  
ALA  
SER  
VAL  
VAL  
ASP  
ALA  
ALA  
PRO  
VAL  
VAL  
ALA  
ALA  
ALA  
PRO  
PRO  
PRO  
GLU  
ASP  
D29  
S190  
HIS  
ARG  
PRO  
THR  
THR  
LYS  
PRO  
GLU  
ASP  
LYS  
LEU  
SER  
SER  
THR  
ALA  
ASP  
GLU  
GLY  
GLY  
G208  
L485  
T584  
Q654  
ALA

- Molecule 140: Dynein light chain



MET  
THR  
SER  
ASN  
VAL  
LYS  
GLU  
P8  
P27  
L112

- Molecule 140: Dynein light chain



MET  
THR  
SER  
ASN  
VAL  
LYS  
GLU  
P8  
L112



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

● Molecule 142: Outer dynein arm docking complex

Chain 8s: 

48%

51%

SER	THR	VAL	SER	SER	SER	SER	GLY	GLU	HIS	GLU	ASP	THR	GLU	GLU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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● Molecule 142: Outer dynein arm docking complex

Chain 9a: 

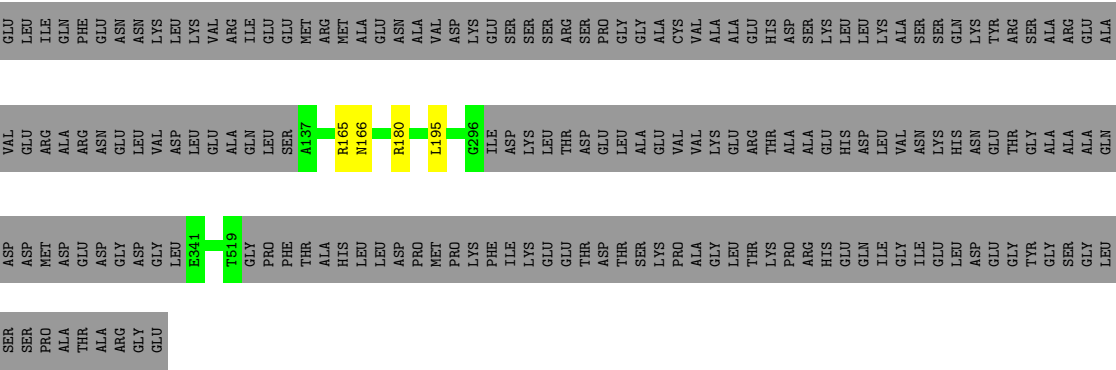
27%

73%

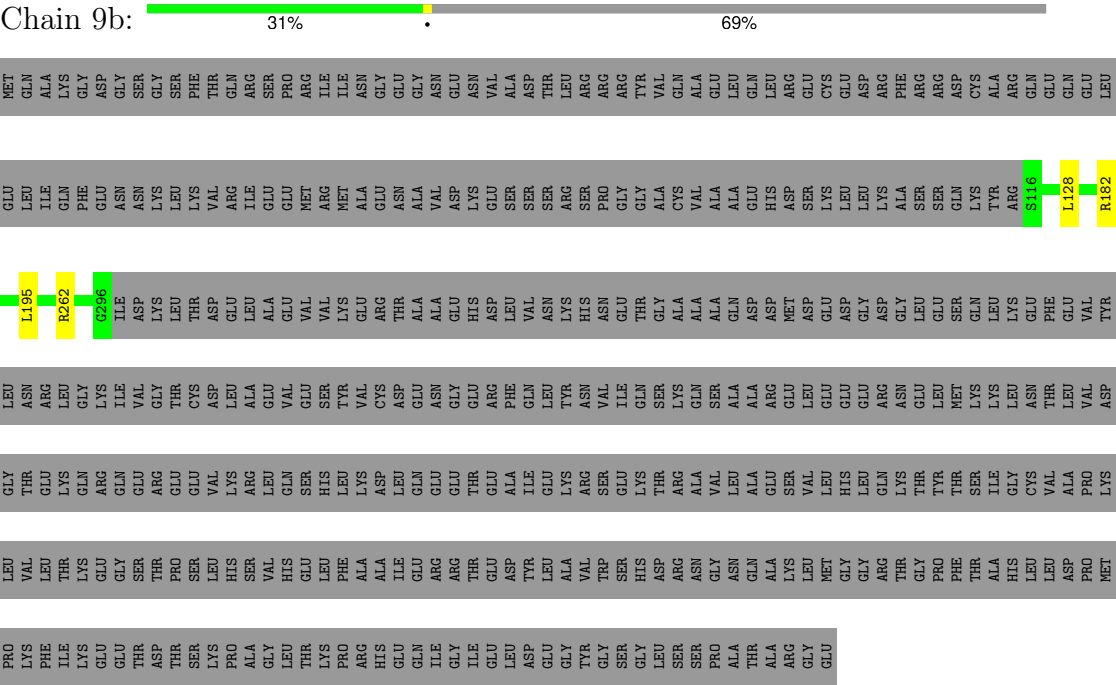
MET	THR	ARG	LEU	PRO	SER	ALA	ALA	ALA	GLY	SER	PRO	PRO	ALA	ALA	GLY	SER	SER	VAL	GLN	GLY	THR	SER	VAL	ASN	GLY	ALA	ARG	GLY	ASN	GLY	LEU	ALA
PRO	LYS	ASN	GLU	VAL	GLU	LEU	TYR	MET	GLN	ARG	ILE	ASN	GLU	ILE	SER	ALA	GLN	THR	LYS	VAL	VAL	ARG	GLU	TYR	GLN	GLN	ILE	ALA	GLY	THR	VAL	
Q252	R298	GLN	VAL	GLU	LEU	GLN	GLN	GLY	ILE	ASP	GLU	GLU	GLU	LEU	ILE	ILE	GLU	GLU	ALA	GLU	GLU	ALA	GLY	GLU	GLN	LEU	ARG	ARG	ASN	GLN	THR	
ILE	ALA	ASN	ALA	LEU	LEU	ALA	SER	GLY	SER	ALA	LYS	ASP	GLU	GLU	GLY	GLY	ARG	ALA	PHE	GLU	LYS	VAL	GLU	GLN	GLY	GLN	GLY	THR	ASP	ASP	ARG	
GLN	LYS	ARG	LEU	GLU	ASP	LEU	GLN	ASN	GLU	ALA	ARG	LEU	LYS	VAL	VAL	VAL	VAL	VAL	HIS	PRO	PRO	ALA	PRO	THR	THR	PHE	GLU	ASP	LEU	LEU	LEU	
GLU	ARG	ILE	ALA	VAL	VAL	VAL	VAL	GLN	HIS	THR	VAL	LEU	VAL	VAL	VAL	VAL	VAL	VAL	TYR	VAL	VAL	ARG	ALA	THR	ILE	GLU	ASN	ASN	GLN	THR	ALA	
PRO	CYS	VAL	ALA	SER	ILE	HIS	VAL	ASN	THR	ASP	VAL	LEU	VAL	VAL	VAL	VAL	VAL	CYS	SER	ILE	LYS	GLU	GLY	HIS	LYS	ASP	THR	ASN	THR	GLY	GLY	
SER	VAL	THR	ASN	GLY	ILE	VAL	PRO	GLY	GLY	LYS	LEU	GLY	THR	VAL	VAL	VAL	VAL	VAL	SER	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	



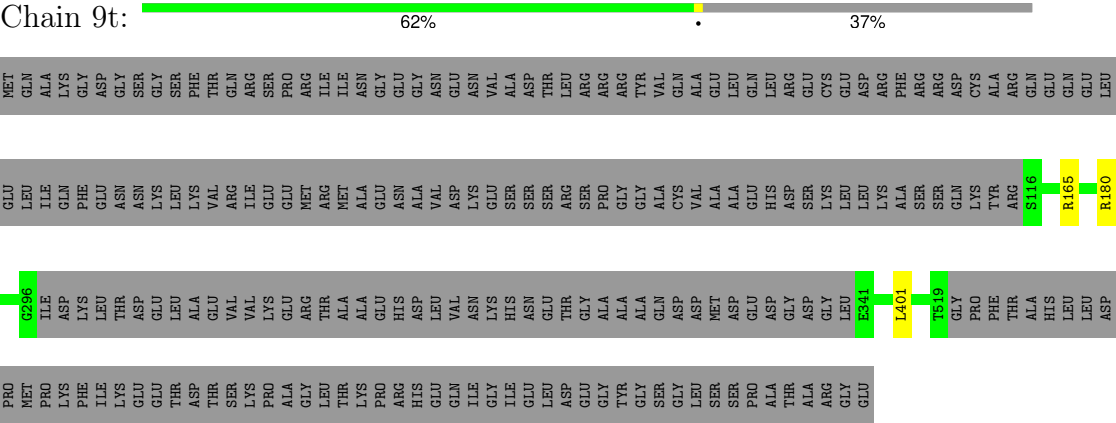




● Molecule 143: ODAD1 central coiled coil region domain-containing protein



● Molecule 143: ODAD1 central coiled coil region domain-containing protein



● Molecule 144: Enkurin domain-containing protein

MET ALA GLN THR SER ASN ASN VAL THR HIS SER D12 Y20 G21 F260 GLY SER GLN LYS THR SER GLY ARG VAL

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|
| ASN | TYR | GLY | THR | VAL | LYS | HIS | THR | PHE | PRO | ALA | ILE | GLY | GLN | PRO | ARG | ARG | LEU | T141 | GLY | P260 | GLN | LYS | THR | SER | GLY | ARG | VAL |     |
| ASN | TYR | GLN | THR | THR | CYS | SER | ASN | GLY | VAL | ASN | THR | PRO | ALA | ARG | GLY | THR | LYS | GLN  | THR | ASN  | PRO | ARG | THR | LYS | GLN | VAL | THR | CYS |

- |     |     |     |     |     |     |     |     |     |     |     |      |     |     |     |     |     |     |     |     |     |     |     |      |      |      |     |     |     |     |     |     |     |     |     |
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| MET | ALA | GLN | THR | SER | ASN | ASN | VAL | THR | HIS | DI2 | H129 | THR | PRO | PHE | ALA | ALA | ILE | GLY | GLN | PRO | ARG | ARG | L140 | R188 | F260 | GLY | SER | GLN | LYS | THR | SER | GLY | ARG | VAL |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | ALA | GLN | THR | SER | ASN | ASN | VAL | THR | HIS | SER | D12 | F260 | GLY | SER | GLN | LYS | THR | SER | GLY | ARG | VAL |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- [illegible]

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| MET | ALA | GLN | THR | SER | ASN | ASN | VAL | THR | HIS | SER | D12 | H129 | THR | PHE | PRO | ALA | ILE | GLY | GLN | PRO | ARG | ARG | L140 | R188 | F260 | GLY | SER | GLN | LYS | THR | SER | GLY | ARG | VAL |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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

[illegible]

- Molecule 145: PON3

Chain 80:  25% 75%

ALA	ALA	ASN	THR	CYS	ALA	HI
ALA	GLN	ASN	ALA	GLY	ASP	F66
VAL	GLN	GLN	LEU	HIS	GLU	
TYR	GLN	GLN	GLY	CYS	ASP	PRO
ALA	GLY	GLY	GLY	PHE	LEU	GLU
GLY	GLY	ALA	ALA	ALA	ARG	ASP
GLU	GLY	VAL	VAL	VAL	GLU	GLU
THR	THR	ASN	SER	ASN	ALA	MET
ALA	ALA	PRO	GLN	ALA	LEU	LEU
VAL	VAL	PRO	ALA	GLN	GLN	LEU
ARG	ARG	SER	SER	GLY	THR	SER
ARG	THR	THR	GLY	GLY	ILE	T75
PRO	ASN	ASN	VAL	HIS	LYS	
LYS	LYS	LEU	LEU	GLY	ASN	L112
SER	ALA	ALA	LYS	CYS	VAL	ARG
THR	SER	ASP	ASP	GLN	THR	ARG
LEU	GLU	SER	SER	VAL	GLU	GLU
PRO	SER	THR	TYR	PRO	GLY	ARG
ALA	GLY	ALA	ALA	PRO	HIS	LEU
ALA	ALA	LYS	ASN	ALA	LYS	ARG
ASN	GLN	GLN	SER	ASP	ALA	LEU
	THR	THR	ASN	VAL	SER	GLY
	LYS	ALA	ALA	LEU	GLY	LEU
GLU	GLU	GLY	GLY	ARG	GLY	THR
ASP	ASP	ALA	ALA	ASP	PRO	LEU
GLU	GLU	GLY	GLN	SER	ARG	PRO
SER	SER	GLY	GLY	LEU	PRO	ASP
ALA	ALA	ASN	VAL	LEU	GLU	GLU
ALA	ALA	VAL	VAL	PRO	SER	ASP
LEU	LEU	GLU	GLU	SER	VAL	VAL
LYS	LYS	ASN	ASP	VAL	ARG	ARG
GLY	GLY	SER	VAL	VAL	HIS	LEU
THR	THR	VAL	THR	THR	ILE	HIS
ALA	ALA	PHE	GLN	GLN	GLU	ASP
LEU	LEU	ASP	GLN	GLN	MET	GLN
TRP	ALA	ALA	ASP	GLN	LEU	SER
ARG	ARG	GLN	ALA	ARG	ARG	VAL
THR	THR	THR	ASN	PHE	LEU	GLY
THR	THR	ALA	ALA	ASN	GLU	THR
ASN	ASN	ARG	ARG	SER	VAL	ASP
GLN	GLN	SER	SER	SER	LYS	GLY
GLU	GLU	ASP	ASP	HIS	GLN	GLU
THR	THR	THR	THR	PRO	ASP	LEU
PRO	THR	MET	THR	TYR	LYS	VAL
ALA	ALA	GLN	GLY	SER	THR	GLY
ALA	ALA	MET	SER	GLY	LYS	LYS
ASN	ASN	ASN	GLY	VAL	LYS	GLY
	TYR	TYR	THR	VAL	VAL	SER
	LEU	LEU	GLY	LEU	ALA	SER
PHE	PHE	GLU	SER	PRO	GLU	ALA
LYS	LYS	GLU	GLY	LEU	CYS	GLU
LYS	LYS	THR	GLU	ASN	PRO	GLN
LEU	LEU	ALA	ALA	THR	GLU	GLU
HIS	HIS	LEU	ALA	ALA	ASP	PRO
ASP	ASP	THR	ALA	GLY	GLU	VAL
ALA	ALA	GLY	GLY	ASP	HIS	CYS
		THR	THR	ARG	LEU	SER

- Molecule 145: PON3

Chain 8P: 

PHE	LYS	GLU	LEU	CYS	GLU	HI
	LYS	GLU	ASN	PRO	GLN	K17
	LEU	THR	THR	GLU	LIN	LYS
	HIS	ALA	ALA	GLY	VAL	ARG
	ASP	GLY	ASP	ASP	CYS	SER
	ALA	GLU	ARG	LEU	SER	PHE
	PRO	THR	THR	CYS	ALA	GLY
	ALA	ASN	ALA	GLY	ASN	THR
	GLN	ALA	LEU	HIS	GLU	Q25
	VAL	GLN	LYS	CYS	ASP	F66
TYR	LYS	GLY	PHE	LEU	PRO	
ALA	GLY	GLY	ALA	ARG	GLU	
GLU	GLY	ALA	VAL	ASN	GLU	
SER	THR	SER	THR	ALA	ASP	
ALA	PRO	GLN	ALA	GLN	GLU	
VAL	PRO	ALA	GLN	THR	MET	
ARG	ARG	SER	GLY	THR	L72	
THR	THR	GLY	LYS	ILE	L112	
PRO	ASN	VAL	HIS	LYS	ARG	
ALA	LYS	LEU	CYS	VAL	GLU	
ALA	ALA	LYS	VAL	ASP	GLU	
ALA	GLN	SER	ASP	ALA	ARG	
ASN	THR	ASN	VAL	SER	GLY	
	LYS	ALA	LEU	GLY	LEU	
	GLU	GLY	ARG	GLY	THR	
	ASP	ALA	ASP	PRO	LEU	
	GLU	GLY	SER	ARG	PRO	
	SER	GLN	LEU	PRO	ASP	
	ALA	ASN	LEU	LEU	GLU	
	ALA	VAL	PRO	SER	ASP	
	LEU	GLU	SER	VAL	ASP	
	LYS	ASP	VAL	ARG	LEU	
	LYS	SER	ARG	HIS	LEU	
	GLY	ASP	GLY	ILE	HIS	
	THR	ALA	LYS	GLU	GLN	
	ALA	PHE	GLN	MET	LEU	
	LEU	ASP	GLN	LEU	SER	
	THR	GLN	ARG	VAL	THR	
	THR	ARG	SER	ARG	GLY	
	ASN	SER	SER	LYS	GLY	
	GLN	ASP	HIS	GLN	LEU	
	GLU	ASP	PRO	ASP	GLU	
	THR	THR	TYR	LYS	VAL	
	GLN	ASN	GLY	THR	GLU	
	GLY	SER	GLY	LYS	LYS	
	ASN	GLY	VAL	MET	LYS	
	ARG	SER	VAL	THR	ALA	
	TYR	THR	THR	VAL	SER	
	LEU	GLY	LEU	GLU	ALA	
	THR	SER	PRO	THR	SER	
	GLU	THR	PRO	GLU	THR	
	ASN	GLU	ASN	GLU	THR	

- Molecule 145: PON3

Chain 8Q:  26% 74%

[illegible]

- Molecule 145: PON3



ALA	ALA	ASN	THR	CYS	ALA	HI
ALA	GLN	ASN	ALA	GLY	ASP	F66
VAL	TYR	GLN	LEU	HIS	GLU	GLU
ALA	GLY	GLN	LYS	PHE	LEU	PRO
ALA	GLY	GLY	GLY	ALA	ARG	ASP
GLY	GLY	THR	ALA	VAL	GLU	GLU
THR	SER	SER	SER	ASN	ALA	MET
ALA	ALA	PRO	GLN	ALA	LEU	LEU
VAL	VAL	PRO	ALA	GLN	GLN	LEU
ARG	ARG	THR	SER	GLY	THR	SER
ARG	THR	THR	GLY	LYS	ILE	TY75
PRO	PRO	ASN	VAL	HIS	LYS	TY75
ALA	ALA	LYS	LEU	GLY	ASN	L112
SER	SER	ALA	LYS	CYS	VAL	ARG
THR	THR	ASP	ASP	GLN	THR	ARG
GLY	GLY	GLU	SER	VAL	ASP	GLU
PRO	PRO	SER	TYR	PRO	GLY	ARG
ALA	ALA	GLY	ALA	PRO	GLY	LEU
ALA	ALA	LYS	ASN	ALA	HIS	ARG
ASN	ASN	GLN	SER	ASP	ALA	LEU
		THR	ASN	VAL	SER	GLY
		LYS	ALA	LEU	GLY	LEU
		GLU	GLY	ARG	GLY	THR
		ASP	ALA	ASP	PRO	LEU
		GLU	ALA	SER	ARG	ASP
		ALA	VAL	PRO	SER	GLU
		LEU	GLU	SER	VAL	VAL
		LYS	ASP	VAL	ARG	VAL
		THR	VAL	VAL	ARG	VAL
		ASP	ASP	GLN	LEU	SER
		LEU	ASP	GLN	LEU	GLN
		LYS	VAL	ARG	ARG	VAL
		SER	VAL	ARG	GLU	VAL
		GLY	ASP	PHE	GLU	GLY
		ALA	ALA	LYS	LEU	THR
		THR	ALA	ASN	LEU	ASP
		ALA	PHE	GLN	MET	GLN
		LEU	ASP	GLN	LEU	SER
		TRP	ALA	ALA	ARG	VAL
		ARG	GLN	PHE	GLU	GLY
		THR	ASP	ASN	LEU	THR
		THR	ALA	PHE	VAL	ASP
		ASN	ARG	SER	ARG	GLY
		GLN	SER	SER	LYS	GLN
		GLU	ASP	HIS	GLN	GLU
		THR	ARG	PRO	ASP	LEU
		SER	THR	TYR	LYS	VAL
		MET	ASN	GLY	LYS	VAL
		GLN	GLY	SER	THR	GLY
		MET	SER	GLY	LYS	GLY
		ASN	GLY	VAL	LYS	LYS
		ARG	SER	VAL	MET	SER
		TYR	THR	TRP	VAL	SER
		LEU	GLY	ALA	ALA	ALA
		GLU	SER	PRO	GLU	ALA
		PHE	GLY	LEU	CYS	GLU
		LYS	GLU	ASN	PRO	GLN
		LYS	ALA	THR	GLU	GLN
		LEU	ALA	ALA	ASP	PRO
		HIS	ALA	GLY	GLU	VAL
		ASP	GLY	HIS	CYS	VAL
		ALA	THR	ARG	LEU	SER

- Molecule 145: PON3

[illegible]



- Molecule 146: PON4

Chain 8W:  12% 88%

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

- Molecule 146: PON4

Chain 8X:  12% 88%

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

- Molecule 146: PON4

Chain 8Y:  39% 61%

ASP ASP GLY ILE GLY THR SER ALA ALA LEU GLY ASN THR ASP ASN ARG ASP LEU TRP LYS ALA THR LEU LEU LYS ASN GLN PRO THR THR THR ASN







VAL	TRP	HIS	PHE	GLU	PRO	ALA	ASP	GLY	LYS	PRO	SER	LYS	ARG	LYS	LYS	ASN	LYS	GLN	GLU	ALA	PRO	THR	PHE	VAL	GLN	GLU	ARG	ALA	MET	THR	THR	PHE	VAL	TRP	THR	THR	ARG	SER	GLY	ASN	GLU	GLY	ASN	ILE	ASP	PRO	PHE	PRO	ASN	THR	THR	TRP	ILE	ASP	VAL	ALA	ALA	LEU	GLU
GLU	GLU	LYS	LYS	LYS	LYS	ASN	ARG	ARG	ARG	ARG	ARG	ALA	LYS	ALA	LYS	ASP	THR	TYR	VAL	PRO	GLY	P323	Y350																																				

- Molecule 148: FAP96C/MC15

Chain 9G: 

[illegible]

- Molecule 148: FAP96C/MC15

Chain 9H:  44% 56%

Lys	Phe	Asp	Met
Lys	Glu	Asn	Thr
Asn	Pro	Pro	His
Arg	Asp	Tyr	Leu
Arg	Glu	Asn	S5
Arg	Lys	Asp	R92
Arg	Pro	Asp	M132
Arg	Ser	Trp	Pro
Ala	Lys	Arg	Gly
Lys	Arg	Lys	Glu
Ala	Lys	His	Glu
Lys	Arg	Glu	Gly
Asp	Asn	Lys	Gly
Thr	Lys	Lys	Pro
Tyr	Lys	Leu	Pro
Val	Gln	Glu	Lys
Pro	Glu	Ala	Ser
Gly	Ala	Ala	Lys
Pro	Ala	Glu	Lys
P324	Gly	Ala	Ser
I	Pro	Lys	Lys
Y350	Arg	Lys	Arg
	Phe	Arg	Lys
	Val	Lys	Lys
	Glu	Leu	Ala
	Ala	Ala	Ser
	Thr	Pro	Ser
	Met	Pro	Ser
	Thr	Lys	Glu
	Phe	Pro	Glu
	Val	Leu	Asp
	Trp	Gly	Ser
	Thr	Pro	Lys
	Arg	Leu	Gly
	Ser	Phe	Lys
	Gly	Arg	Glu
	Asn	Thr	Leu
	Gly	Pro	Leu
	Glu	Gly	Pro
	Asn	Val	Asn
	Ile	Ile	Lys
	Asp	His	Lys
	Pro	Asp	Thr
	Phe	Tyr	Asn
	Pro	Leu	Pro
	Asn	Asp	Ser
	Thr	Glu	Lys
	Trp	Pro	Lys
	Ile	Leu	Gly
	Asp	Ala	Thr
	Val	Thr	Tyr
	Ala	Gly	Gly
	Ala	Val	Tyr
	Leu	Ser	Val
	Glu	Gly	Ile
	Glu	Val	Leu
	Glu	Tyr	Phe

- Molecule 148: FAP96C/MC15

Chain 9I:  29% 71%

[illegible]

SER  
VAL  
PHE  
GLN  
SER  
CYS  
LEU  
ARG  
ARG  
PHE  
TYR

- Molecule 149: FAP96B

Chain 9J:  60% 40%

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

THR MET ALA ARG GLN MET ASN ARG LYS ARG THR ILE THR ALA THR PHE ILE SER VAL ARG PRO LYS GLY LEU LEU GLY ASN TYR GLY LEU LEU GLN ASP GLU LEU PHE Y104 H P254 LYS SER ARG ARG LEU LYS SER GLU ASP SER I265 H L286

- Molecule 149: FAP96B

Chain 9K:  95% . .

MET Y2 R14 R22 R32 P254 LYS SER ARG LEU LYS SER SER GLU ASP I265 L286

- Molecule 149: FAP96B

Chain 9L:  88% 12%


MET Y2 R14 P254 LYS SER ARG LEU LYS SER ARG GLU ASP ILE PHE THR ARG GLY PHE ARG ARG ASP ASN PHE TYR THR SER ILE VAL PHE ARG ARG LEU

- Molecule 150: MOP23A

Chain 9M:  82% . 17%


MET ALA ASP ASN GLU VAL PRO PRO SER LEU LYS SER ARG MET T15 Q42 ARG GLN LEU ALA ARG PRO PHE CYS SER SER ARG ARG ILE LYS D58 L124 S189 ARG ARG GLY SER

- Molecule 150: MOP23A

Chain 9N:  83% 17%


MET ALA ASP ASN GLU VAL PRO PRO SER LEU LYS SER ARG MET T15 Q42 ARG GLN LEU ALA ARG PRO PHE CYS SER SER ARG ARG ILE LYS D58 S189 ARG ARG GLY SER

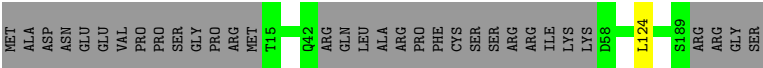
- Molecule 150: MOP23A

Chain 9O:  82% . 18%

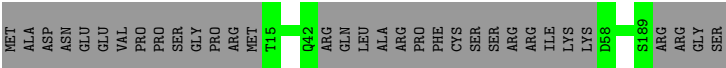
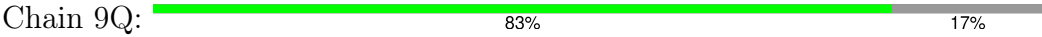
MET ALA ASP ASN GLU VAL PRO PRO SER LEU LYS SER ARG MET T15 Q42 ARG GLN LEU ALA ARG PRO PHE CYS SER SER ARG ARG ILE LYS D58 R74 S189 ARG ARG GLY SER

- Molecule 150: MOP23A

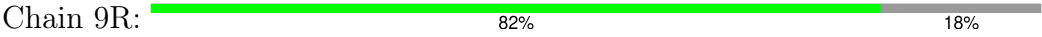
Chain 9P:  82% . 17%



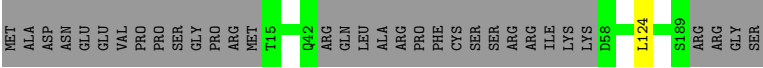
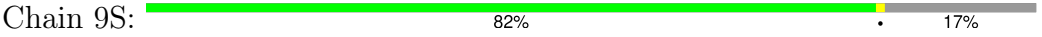
• Molecule 150: MOP23A



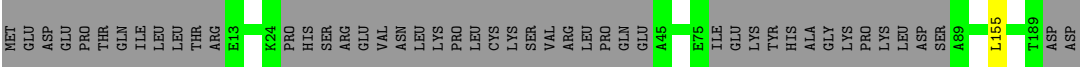
• Molecule 150: MOP23A



• Molecule 150: MOP23A



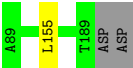
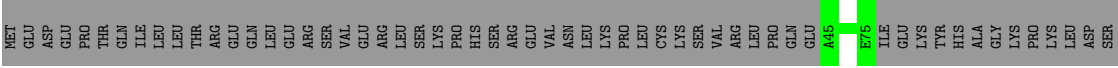
• Molecule 151: MOP23B



• Molecule 151: MOP23B

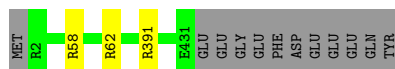


• Molecule 151: MOP23B



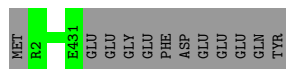
• Molecule 152: MOP23C





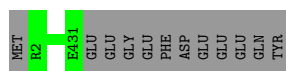
- Molecule 153: Tubulin beta chain

Chain AI:  97%



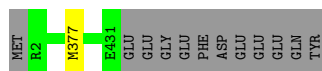
- Molecule 153: Tubulin beta chain

Chain AK:  97%



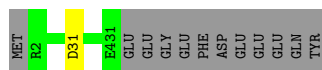
- Molecule 153: Tubulin beta chain

Chain AM:  97%



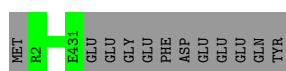
- Molecule 153: Tubulin beta chain

Chain AO:  97%



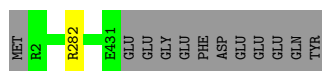
- Molecule 153: Tubulin beta chain

Chain AQ:  97%



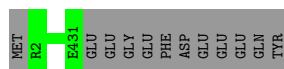
- Molecule 153: Tubulin beta chain

Chain AS:  97%



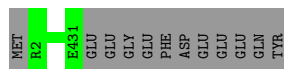
- Molecule 153: Tubulin beta chain

Chain AU:  97%



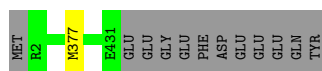
- Molecule 153: Tubulin beta chain

Chain AW: 97% .



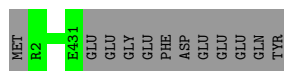
- Molecule 153: Tubulin beta chain

Chain AY: 97% .



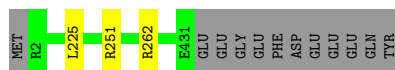
- Molecule 153: Tubulin beta chain

Chain Aa: 97% .



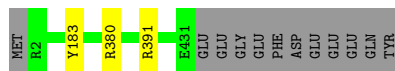
- Molecule 153: Tubulin beta chain

Chain Ac: 97% ..



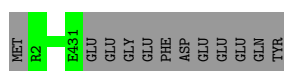
- Molecule 153: Tubulin beta chain

Chain Ae: 97% ..



- Molecule 153: Tubulin beta chain

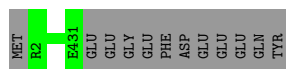
Chain Ag: 97% .



- Molecule 153: Tubulin beta chain

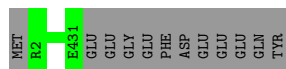
Chain Ai: 97% .





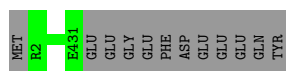
- Molecule 153: Tubulin beta chain

Chain Ak: 97% .



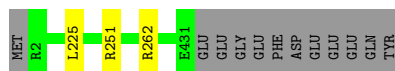
- Molecule 153: Tubulin beta chain

Chain Am: 97% .



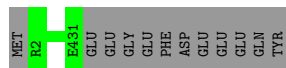
- Molecule 153: Tubulin beta chain

Chain Ao: 97% .



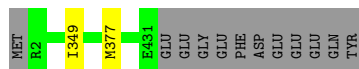
- Molecule 153: Tubulin beta chain

Chain BA: 97% .



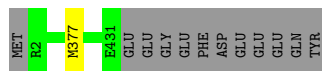
- Molecule 153: Tubulin beta chain

Chain BC: 97% .



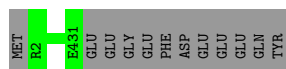
- Molecule 153: Tubulin beta chain

Chain BG: 97% .



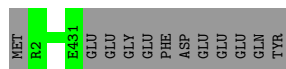
- Molecule 153: Tubulin beta chain

Chain BI: 97% .



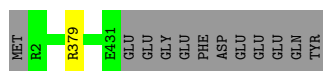
- Molecule 153: Tubulin beta chain

Chain BK: 97%



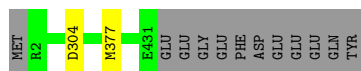
- Molecule 153: Tubulin beta chain

Chain BM: 97%



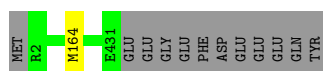
- Molecule 153: Tubulin beta chain

Chain BO: 97%



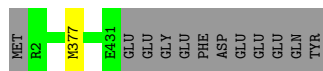
- Molecule 153: Tubulin beta chain

Chain BQ: 97%



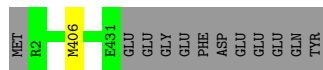
- Molecule 153: Tubulin beta chain

Chain BS: 97%



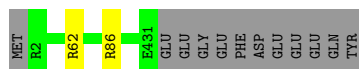
- Molecule 153: Tubulin beta chain

Chain BU: 97%



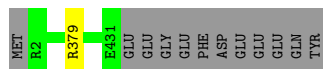
- Molecule 153: Tubulin beta chain

Chain BW: 97%



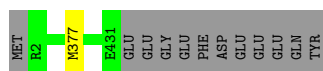
- Molecule 153: Tubulin beta chain

Chain BY: 97%



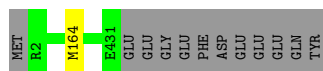
- Molecule 153: Tubulin beta chain

Chain CA: 97%



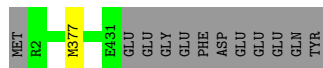
- Molecule 153: Tubulin beta chain

Chain CC: 97%



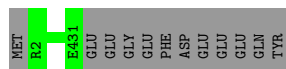
- Molecule 153: Tubulin beta chain

Chain CE: 97%



- Molecule 153: Tubulin beta chain

Chain CH: 97%



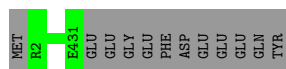
- Molecule 153: Tubulin beta chain

Chain CK: 96%



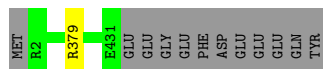
- Molecule 153: Tubulin beta chain

Chain CM: 97%



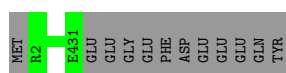
- Molecule 153: Tubulin beta chain

Chain CO: 97% .



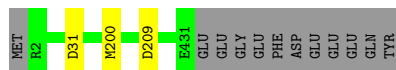
- Molecule 153: Tubulin beta chain

Chain CQ: 97% .



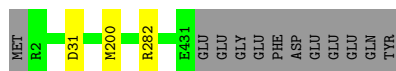
- Molecule 153: Tubulin beta chain

Chain CS: 97% ..



- Molecule 153: Tubulin beta chain

Chain CU: 97% ..



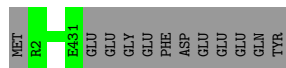
- Molecule 153: Tubulin beta chain

Chain CW: 96% ..



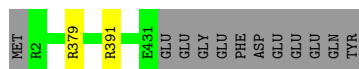
- Molecule 153: Tubulin beta chain

Chain CY: 97% .



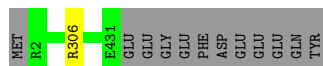
- Molecule 153: Tubulin beta chain

Chain DA: 97% .



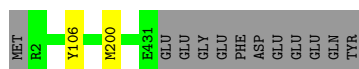
- Molecule 153: Tubulin beta chain

Chain DC:  97%



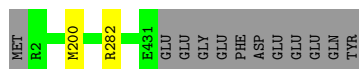
- Molecule 153: Tubulin beta chain

Chain DE:  97%



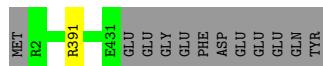
- Molecule 153: Tubulin beta chain

Chain DG:  97%



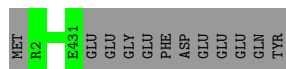
- Molecule 153: Tubulin beta chain

Chain DI:  97%



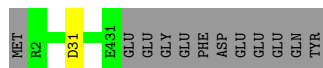
- Molecule 153: Tubulin beta chain

Chain DK:  97%



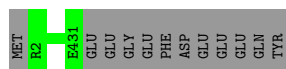
- Molecule 153: Tubulin beta chain

Chain DN:  97%



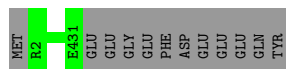
- Molecule 153: Tubulin beta chain

Chain DP:  97%



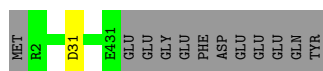
- Molecule 153: Tubulin beta chain

Chain DR: 97% .



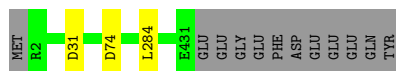
- Molecule 153: Tubulin beta chain

Chain DT: 97% .



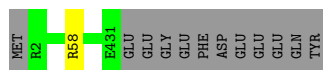
- Molecule 153: Tubulin beta chain

Chain DV: 97% . .



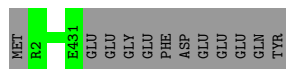
- Molecule 153: Tubulin beta chain

Chain DX: 97% .



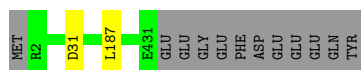
- Molecule 153: Tubulin beta chain

Chain DZ: 97% .



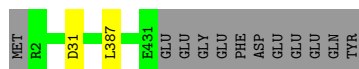
- Molecule 153: Tubulin beta chain

Chain EB: 97% .



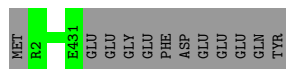
- Molecule 153: Tubulin beta chain

Chain ED: 97% .



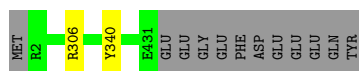
- Molecule 153: Tubulin beta chain

Chain EF: 97%



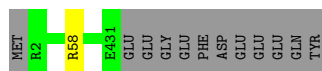
- Molecule 153: Tubulin beta chain

Chain EH: 97%



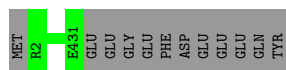
- Molecule 153: Tubulin beta chain

Chain EJ: 97%



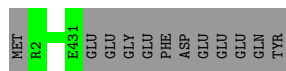
- Molecule 153: Tubulin beta chain

Chain EL: 97%



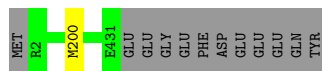
- Molecule 153: Tubulin beta chain

Chain EN: 97%



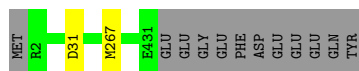
- Molecule 153: Tubulin beta chain

Chain ER: 97%



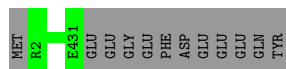
- Molecule 153: Tubulin beta chain

Chain ET: 97%



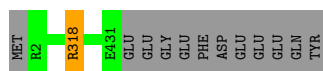
- Molecule 153: Tubulin beta chain

Chain EV:   
97%



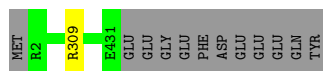
- Molecule 153: Tubulin beta chain

Chain EX:   
97%



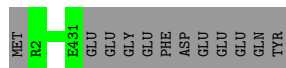
- Molecule 153: Tubulin beta chain

Chain EZ:   
97%



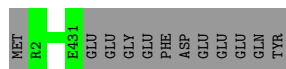
- Molecule 153: Tubulin beta chain

Chain FB:   
97%



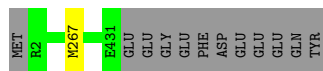
- Molecule 153: Tubulin beta chain

Chain FD:   
97%



- Molecule 153: Tubulin beta chain

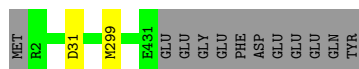
Chain FF:   
97%



- Molecule 153: Tubulin beta chain

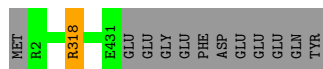
Chain FH:   
97%





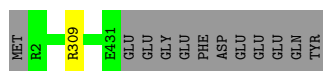
- Molecule 153: Tubulin beta chain

Chain FJ: 97% .



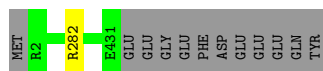
- Molecule 153: Tubulin beta chain

Chain FL: 97% .



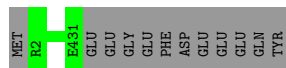
- Molecule 153: Tubulin beta chain

Chain FN: 97% .



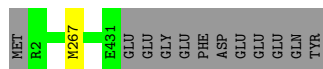
- Molecule 153: Tubulin beta chain

Chain FP: 97% .



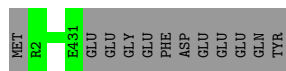
- Molecule 153: Tubulin beta chain

Chain FR: 97% .



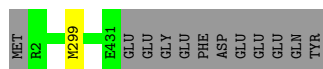
- Molecule 153: Tubulin beta chain

Chain FT: 97% .



- Molecule 153: Tubulin beta chain

Chain FV: 97% .



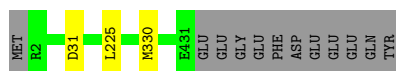
- Molecule 153: Tubulin beta chain

Chain FX:  96% 



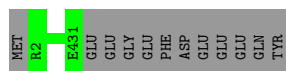
- Molecule 153: Tubulin beta chain

Chain FZ:  97% 



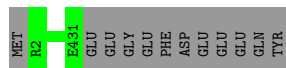
- Molecule 153: Tubulin beta chain

Chain GB:  97% 



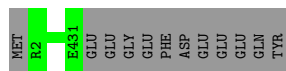
- Molecule 153: Tubulin beta chain

Chain GD:  97% 



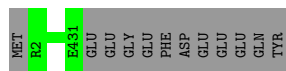
- Molecule 153: Tubulin beta chain

Chain GF:  97% 



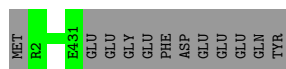
- Molecule 153: Tubulin beta chain

Chain GH:  97% 



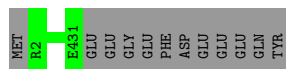
- Molecule 153: Tubulin beta chain

Chain GJ:  97% 



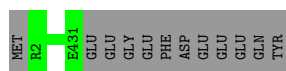
- Molecule 153: Tubulin beta chain

Chain GL: 97%



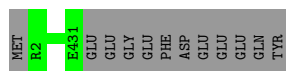
- Molecule 153: Tubulin beta chain

Chain GN: 97%



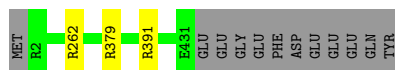
- Molecule 153: Tubulin beta chain

Chain GP: 97%



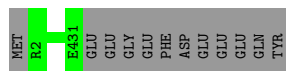
- Molecule 153: Tubulin beta chain

Chain GR: 97%



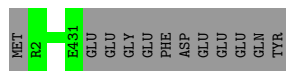
- Molecule 153: Tubulin beta chain

Chain GT: 97%



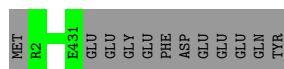
- Molecule 153: Tubulin beta chain

Chain GV: 97%



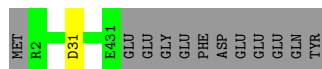
- Molecule 153: Tubulin beta chain

Chain GX: 97%



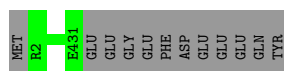
- Molecule 153: Tubulin beta chain

Chain GZ: 97% .



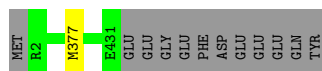
- Molecule 153: Tubulin beta chain

Chain HB: 97% .



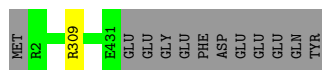
- Molecule 153: Tubulin beta chain

Chain HD: 97% .



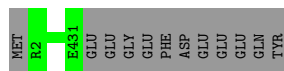
- Molecule 153: Tubulin beta chain

Chain HF: 97% .



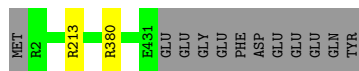
- Molecule 153: Tubulin beta chain

Chain HH: 97% .



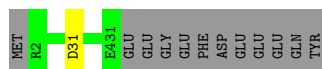
- Molecule 153: Tubulin beta chain

Chain HJ: 97% .



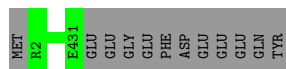
- Molecule 153: Tubulin beta chain

Chain HL: 97% .



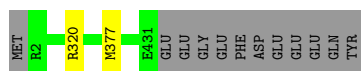
- Molecule 153: Tubulin beta chain

Chain HN:  97%



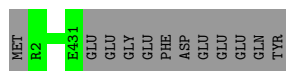
- Molecule 153: Tubulin beta chain

Chain HP:  97%



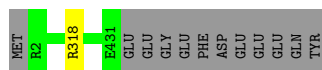
- Molecule 153: Tubulin beta chain

Chain HR:  97%



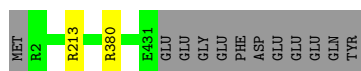
- Molecule 153: Tubulin beta chain

Chain HT:  97%



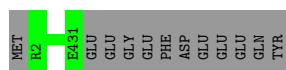
- Molecule 153: Tubulin beta chain

Chain HV:  97%



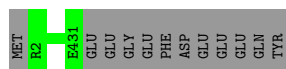
- Molecule 153: Tubulin beta chain

Chain HX:  97%



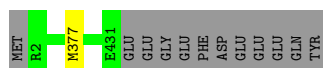
- Molecule 153: Tubulin beta chain

Chain HZ:  97%



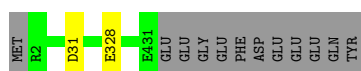
- Molecule 153: Tubulin beta chain

Chain IB: 97%



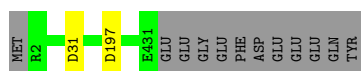
- Molecule 153: Tubulin beta chain

Chain ID: 97%



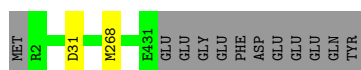
- Molecule 153: Tubulin beta chain

Chain IF: 97%



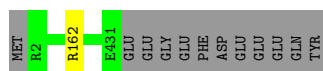
- Molecule 153: Tubulin beta chain

Chain IH: 97%



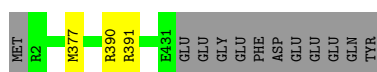
- Molecule 153: Tubulin beta chain

Chain IJ: 97%



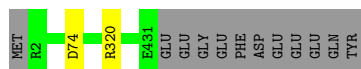
- Molecule 153: Tubulin beta chain

Chain IL: 97%



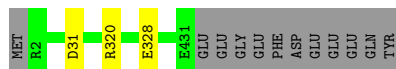
- Molecule 153: Tubulin beta chain

Chain IN: 97%



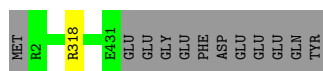
- Molecule 153: Tubulin beta chain

Chain IP: 97%



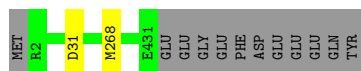
- Molecule 153: Tubulin beta chain

Chain IR: 97%



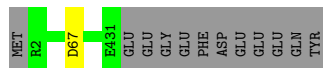
- Molecule 153: Tubulin beta chain

Chain IT: 97%



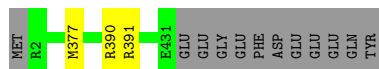
- Molecule 153: Tubulin beta chain

Chain IV: 97%



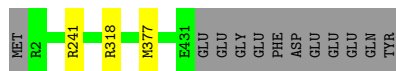
- Molecule 153: Tubulin beta chain

Chain IX: 97%



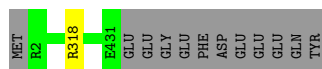
- Molecule 153: Tubulin beta chain

Chain IZ: 97%



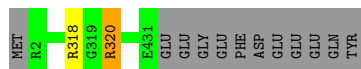
- Molecule 153: Tubulin beta chain

Chain JB: 97%



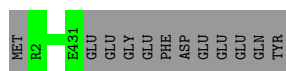
- Molecule 153: Tubulin beta chain

Chain JD:  97%



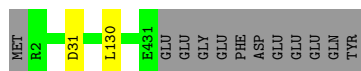
- Molecule 153: Tubulin beta chain

Chain JF:  97%



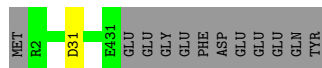
- Molecule 153: Tubulin beta chain

Chain JG:  97%



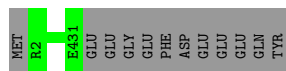
- Molecule 153: Tubulin beta chain

Chain JI:  97%



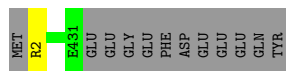
- Molecule 153: Tubulin beta chain

Chain JK:  97%



- Molecule 153: Tubulin beta chain

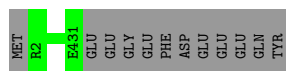
Chain JM:  97%



- Molecule 153: Tubulin beta chain

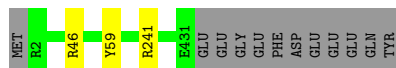
Chain JO:  97%





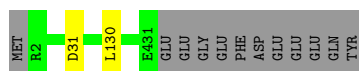
- Molecule 153: Tubulin beta chain

Chain JQ: 97% ..



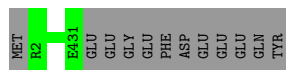
- Molecule 153: Tubulin beta chain

Chain JS: 97% .



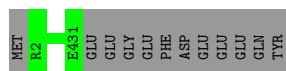
- Molecule 153: Tubulin beta chain

Chain JU: 97% .



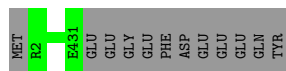
- Molecule 153: Tubulin beta chain

Chain JW: 97% .



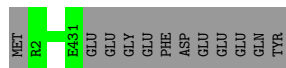
- Molecule 153: Tubulin beta chain

Chain JY: 97% .



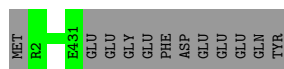
- Molecule 153: Tubulin beta chain

Chain KA: 97% .



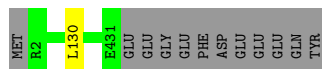
- Molecule 153: Tubulin beta chain

Chain KC: 97% .



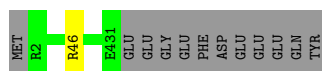
- Molecule 153: Tubulin beta chain

Chain KE:  97%



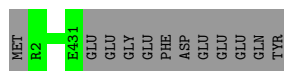
- Molecule 153: Tubulin beta chain

Chain KG:  97%



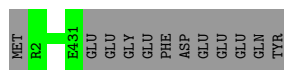
- Molecule 153: Tubulin beta chain

Chain KI:  97%



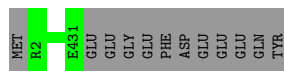
- Molecule 153: Tubulin beta chain

Chain KK:  97%



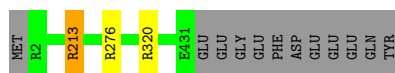
- Molecule 153: Tubulin beta chain

Chain KM:  97%



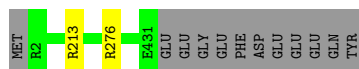
- Molecule 153: Tubulin beta chain

Chain KO:  97%



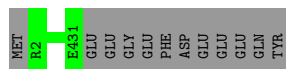
- Molecule 153: Tubulin beta chain

Chain KQ:  97%



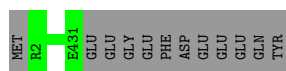
- Molecule 153: Tubulin beta chain

Chain KS: 97%



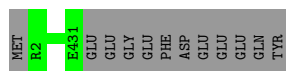
- Molecule 153: Tubulin beta chain

Chain KU: 97%



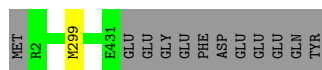
- Molecule 153: Tubulin beta chain

Chain KW: 97%



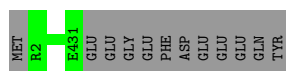
- Molecule 153: Tubulin beta chain

Chain KY: 97%



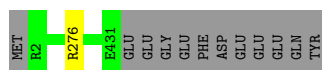
- Molecule 153: Tubulin beta chain

Chain LA: 97%



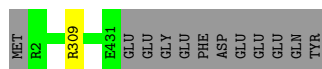
- Molecule 153: Tubulin beta chain

Chain LC: 97%



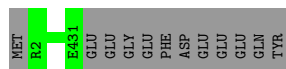
- Molecule 153: Tubulin beta chain

Chain LE: 97%



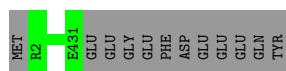
- Molecule 153: Tubulin beta chain

Chain LG: 97%



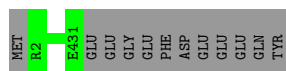
- Molecule 153: Tubulin beta chain

Chain LI: 97%



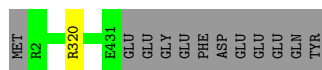
- Molecule 153: Tubulin beta chain

Chain LK: 97%



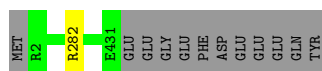
- Molecule 153: Tubulin beta chain

Chain LM: 97%



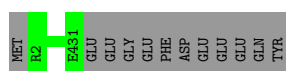
- Molecule 153: Tubulin beta chain

Chain LO: 97%



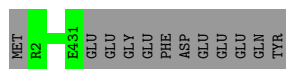
- Molecule 153: Tubulin beta chain

Chain LQ: 97%



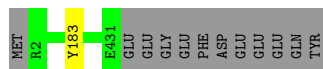
- Molecule 153: Tubulin beta chain

Chain LS: 97%



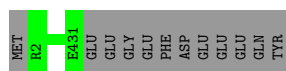
- Molecule 153: Tubulin beta chain

Chain LU: 97%



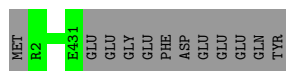
- Molecule 153: Tubulin beta chain

Chain LW: 97%



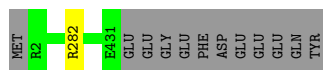
- Molecule 153: Tubulin beta chain

Chain LY: 97%



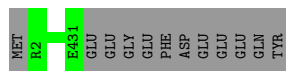
- Molecule 153: Tubulin beta chain

Chain MA: 97%



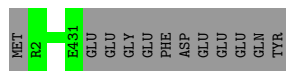
- Molecule 153: Tubulin beta chain

Chain MC: 97%



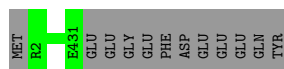
- Molecule 153: Tubulin beta chain

Chain ME: 97%



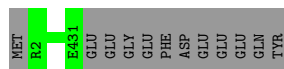
- Molecule 153: Tubulin beta chain

Chain MG: 97%



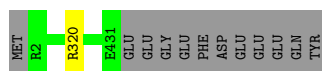
- Molecule 153: Tubulin beta chain

Chain MI: 97%



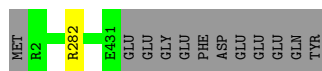
- Molecule 153: Tubulin beta chain

Chain MK: 97%



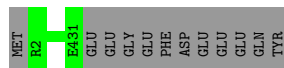
- Molecule 153: Tubulin beta chain

Chain MM: 97%



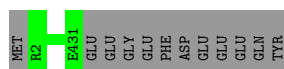
- Molecule 153: Tubulin beta chain

Chain MO: 97%



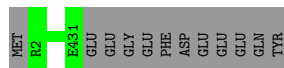
- Molecule 153: Tubulin beta chain

Chain MQ: 97%



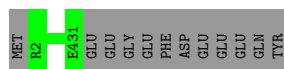
- Molecule 153: Tubulin beta chain

Chain MU: 97%



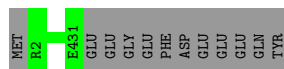
- Molecule 153: Tubulin beta chain

Chain MW: 97%



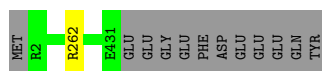
- Molecule 153: Tubulin beta chain

Chain MY: 97%



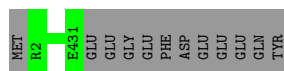
- Molecule 153: Tubulin beta chain

Chain NA: 97%



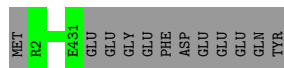
- Molecule 153: Tubulin beta chain

Chain NC: 97%



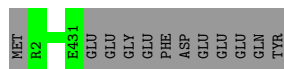
- Molecule 153: Tubulin beta chain

Chain NE: 97%



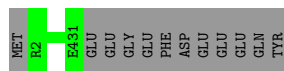
- Molecule 153: Tubulin beta chain

Chain NG: 97%



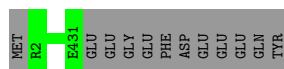
- Molecule 153: Tubulin beta chain

Chain NI: 97%



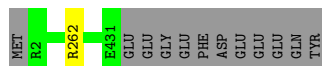
- Molecule 153: Tubulin beta chain

Chain NK: 97%



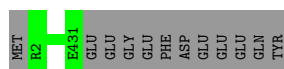
- Molecule 153: Tubulin beta chain

Chain NM: 97%



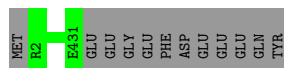
- Molecule 153: Tubulin beta chain

Chain NO: 97%



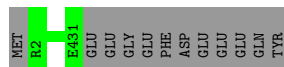
- Molecule 153: Tubulin beta chain

Chain NQ: 97%



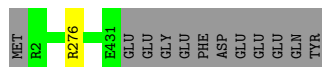
- Molecule 153: Tubulin beta chain

Chain NS: 97%



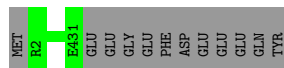
- Molecule 153: Tubulin beta chain

Chain NU: 97%



- Molecule 153: Tubulin beta chain

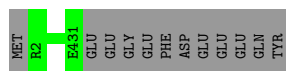
Chain NY: 97%



- Molecule 153: Tubulin beta chain

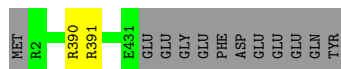
Chain OA: 97%





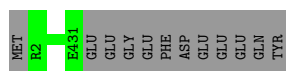
- Molecule 153: Tubulin beta chain

Chain OC:   
97%



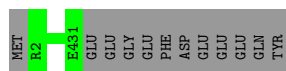
- Molecule 153: Tubulin beta chain

Chain OE:   
97%



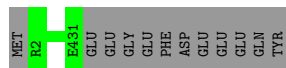
- Molecule 153: Tubulin beta chain

Chain OG:   
97%



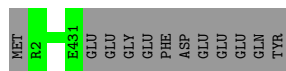
- Molecule 153: Tubulin beta chain

Chain OI:   
97%



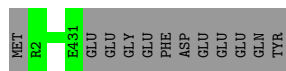
- Molecule 153: Tubulin beta chain

Chain OK:   
97%



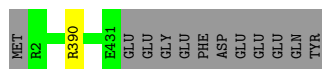
- Molecule 153: Tubulin beta chain

Chain OM:   
97%



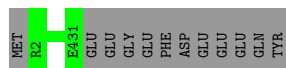
- Molecule 153: Tubulin beta chain

Chain OO:   
97%



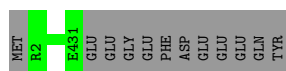
- Molecule 153: Tubulin beta chain

Chain OQ: 97% .



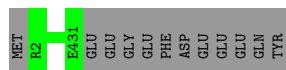
- Molecule 153: Tubulin beta chain

Chain OS: 97% .



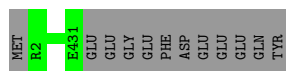
- Molecule 153: Tubulin beta chain

Chain OU: 97% .



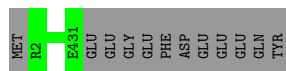
- Molecule 153: Tubulin beta chain

Chain OW: 97% .



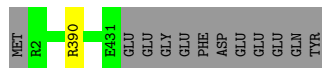
- Molecule 153: Tubulin beta chain

Chain OY: 97% .



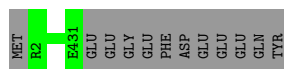
- Molecule 153: Tubulin beta chain

Chain PA: 97% .



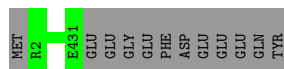
- Molecule 153: Tubulin beta chain

Chain PD: 97% .



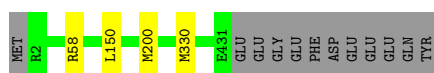
- Molecule 153: Tubulin beta chain

Chain PF: 97% .



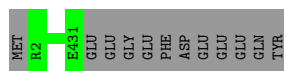
- Molecule 153: Tubulin beta chain

Chain PH: 96% ..



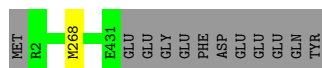
- Molecule 153: Tubulin beta chain

Chain PJ: 97% .



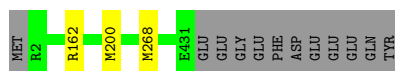
- Molecule 153: Tubulin beta chain

Chain PL: 97% .



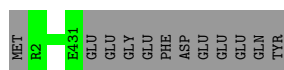
- Molecule 153: Tubulin beta chain

Chain PN: 97% ..



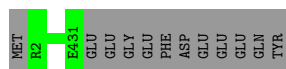
- Molecule 153: Tubulin beta chain

Chain PP: 97% .



- Molecule 153: Tubulin beta chain

Chain PR: 97% .



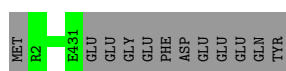
- Molecule 153: Tubulin beta chain

Chain PT: 96%



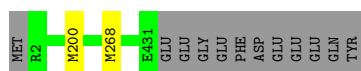
- Molecule 153: Tubulin beta chain

Chain PV: 97%



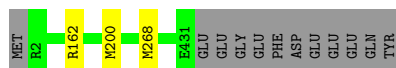
- Molecule 153: Tubulin beta chain

Chain PX: 97%



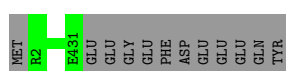
- Molecule 153: Tubulin beta chain

Chain PZ: 97%



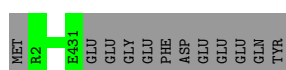
- Molecule 153: Tubulin beta chain

Chain QB: 97%



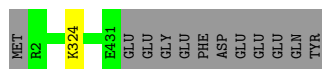
- Molecule 153: Tubulin beta chain

Chain QD: 97%



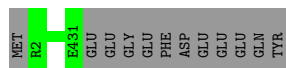
- Molecule 153: Tubulin beta chain

Chain QF: 97%



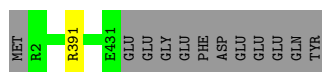
- Molecule 153: Tubulin beta chain

Chain QH:  97%



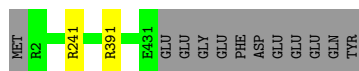
- Molecule 153: Tubulin beta chain

Chain QJ:  97%



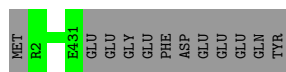
- Molecule 153: Tubulin beta chain

Chain QL:  97%



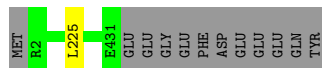
- Molecule 153: Tubulin beta chain

Chain QN:  97%



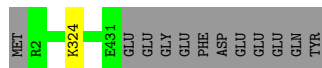
- Molecule 153: Tubulin beta chain

Chain QP:  97%



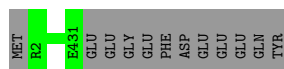
- Molecule 153: Tubulin beta chain

Chain QR:  97%



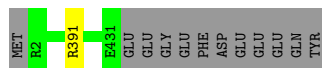
- Molecule 153: Tubulin beta chain

Chain QT:  97%



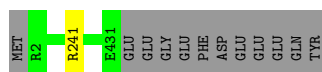
- Molecule 153: Tubulin beta chain

Chain QV:   
97%



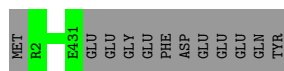
- Molecule 153: Tubulin beta chain

Chain QX:   
97%



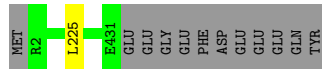
- Molecule 153: Tubulin beta chain

Chain QZ:   
97%



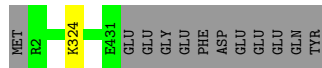
- Molecule 153: Tubulin beta chain

Chain RB:   
97%



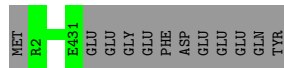
- Molecule 153: Tubulin beta chain

Chain RD:   
97%



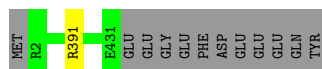
- Molecule 153: Tubulin beta chain

Chain RF:   
97%



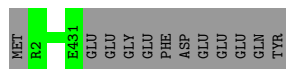
- Molecule 153: Tubulin beta chain

Chain RH:   
97%



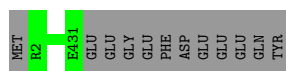
- Molecule 153: Tubulin beta chain

Chain RJ: 97%



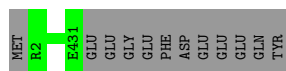
- Molecule 153: Tubulin beta chain

Chain RL: 97%



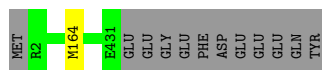
- Molecule 153: Tubulin beta chain

Chain RN: 97%



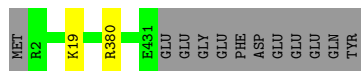
- Molecule 153: Tubulin beta chain

Chain RP: 97%



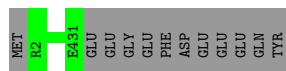
- Molecule 153: Tubulin beta chain

Chain RR: 97%



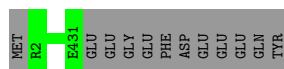
- Molecule 153: Tubulin beta chain

Chain RT: 97%



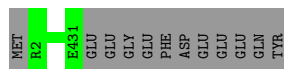
- Molecule 153: Tubulin beta chain

Chain RV: 97%



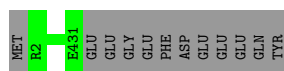
- Molecule 153: Tubulin beta chain

Chain RX: 97% .



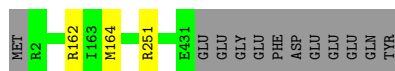
- Molecule 153: Tubulin beta chain

Chain RZ: 97% .



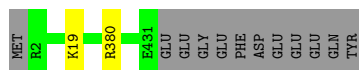
- Molecule 153: Tubulin beta chain

Chain SB: 97% .



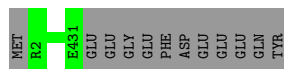
- Molecule 153: Tubulin beta chain

Chain SD: 97% .



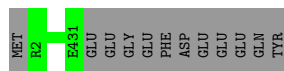
- Molecule 153: Tubulin beta chain

Chain SF: 97% .



- Molecule 153: Tubulin beta chain

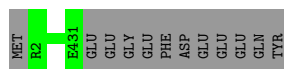
Chain SH: 97% .



- Molecule 153: Tubulin beta chain

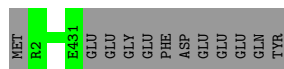
Chain SJ: 97% .





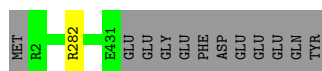
- Molecule 153: Tubulin beta chain

Chain SL: 97% .



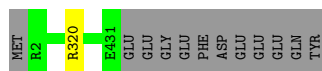
- Molecule 153: Tubulin beta chain

Chain SN: 97% .



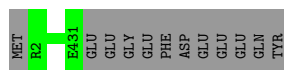
- Molecule 153: Tubulin beta chain

Chain SP: 97% .



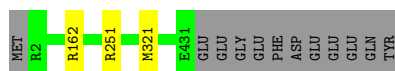
- Molecule 153: Tubulin beta chain

Chain SR: 97% .



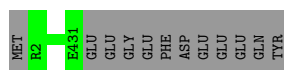
- Molecule 153: Tubulin beta chain

Chain ST: 97% ..



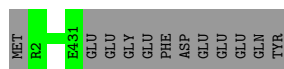
- Molecule 153: Tubulin beta chain

Chain SV: 97% .



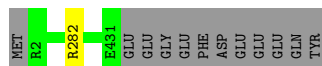
- Molecule 153: Tubulin beta chain

Chain SX: 97% .



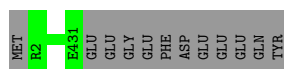
- Molecule 153: Tubulin beta chain

Chain SZ:  97%



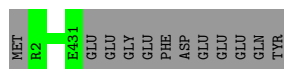
- Molecule 153: Tubulin beta chain

Chain TB:  97%



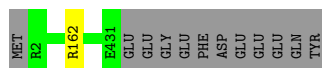
- Molecule 153: Tubulin beta chain

Chain TD:  97%



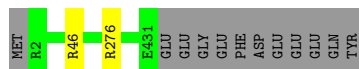
- Molecule 153: Tubulin beta chain

Chain TF:  97%



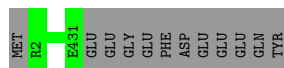
- Molecule 153: Tubulin beta chain

Chain TH:  97%



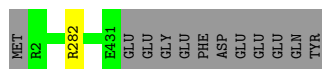
- Molecule 153: Tubulin beta chain

Chain TJ:  97%



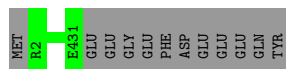
- Molecule 153: Tubulin beta chain

Chain TL:  97%



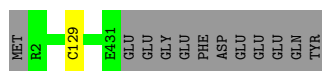
- Molecule 153: Tubulin beta chain

Chain TN: 97%



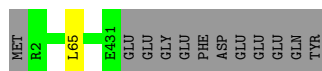
- Molecule 153: Tubulin beta chain

Chain TP: 97%



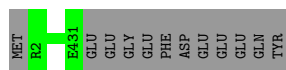
- Molecule 153: Tubulin beta chain

Chain TS: 97%



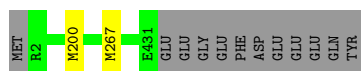
- Molecule 153: Tubulin beta chain

Chain TU: 97%



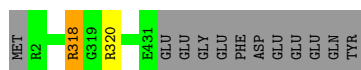
- Molecule 153: Tubulin beta chain

Chain TW: 97%



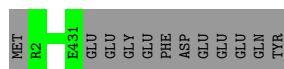
- Molecule 153: Tubulin beta chain

Chain TY: 97%



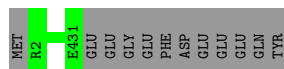
- Molecule 153: Tubulin beta chain

Chain UA: 97%



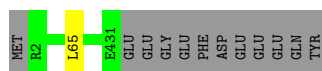
- Molecule 153: Tubulin beta chain

Chain UC: 97%



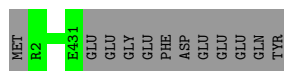
- Molecule 153: Tubulin beta chain

Chain UE: 97%



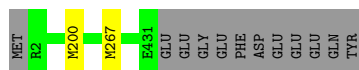
- Molecule 153: Tubulin beta chain

Chain UG: 97%



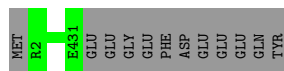
- Molecule 153: Tubulin beta chain

Chain UI: 97%



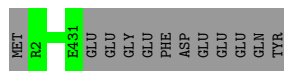
- Molecule 153: Tubulin beta chain

Chain UK: 97%



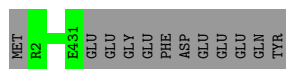
- Molecule 153: Tubulin beta chain

Chain UM: 97%



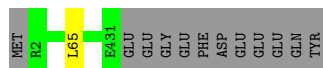
- Molecule 153: Tubulin beta chain

Chain UO: 97%



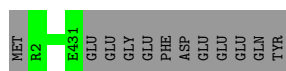
- Molecule 153: Tubulin beta chain

Chain UQ:  97%



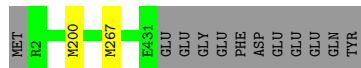
- Molecule 153: Tubulin beta chain

Chain US:  97%



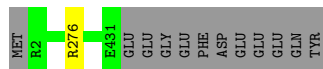
- Molecule 153: Tubulin beta chain

Chain UU:  97%



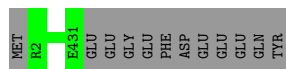
- Molecule 153: Tubulin beta chain

Chain UX:  97%



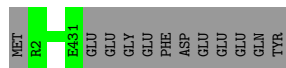
- Molecule 153: Tubulin beta chain

Chain UZ:  97%



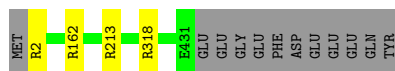
- Molecule 153: Tubulin beta chain

Chain VB:  97%



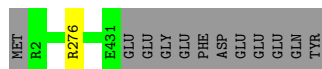
- Molecule 153: Tubulin beta chain

Chain VD:  96%



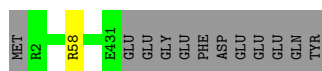
- Molecule 153: Tubulin beta chain

Chain VF: 97%



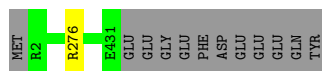
- Molecule 153: Tubulin beta chain

Chain VH: 97%



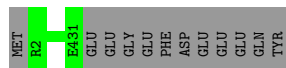
- Molecule 153: Tubulin beta chain

Chain VJ: 97%



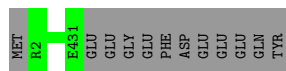
- Molecule 153: Tubulin beta chain

Chain VL: 97%



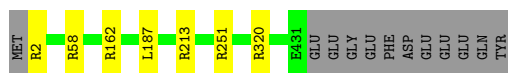
- Molecule 153: Tubulin beta chain

Chain VN: 97%



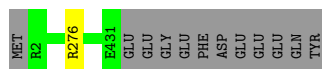
- Molecule 153: Tubulin beta chain

Chain VP: 96%



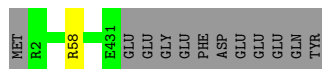
- Molecule 153: Tubulin beta chain

Chain VR: 97%



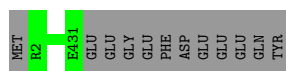
- Molecule 153: Tubulin beta chain

Chain VT:  97%



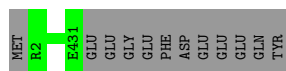
- Molecule 153: Tubulin beta chain

Chain VV:  97%



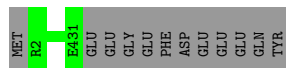
- Molecule 153: Tubulin beta chain

Chain VX:  97%



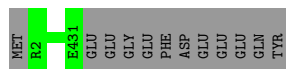
- Molecule 153: Tubulin beta chain

Chain VZ:  97%



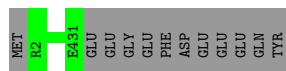
- Molecule 153: Tubulin beta chain

Chain WB:  97%



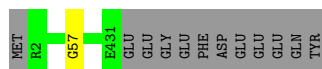
- Molecule 153: Tubulin beta chain

Chain WD:  97%



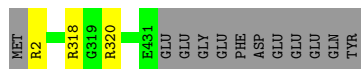
- Molecule 153: Tubulin beta chain

Chain WF:  97%



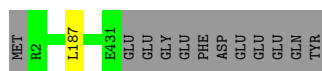
- Molecule 153: Tubulin beta chain

Chain WH: 97% ..



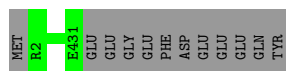
- Molecule 153: Tubulin beta chain

Chain WJ: 97% .



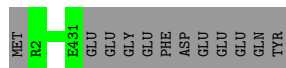
- Molecule 153: Tubulin beta chain

Chain WL: 97% .



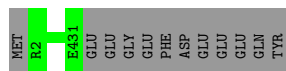
- Molecule 153: Tubulin beta chain

Chain WN: 97% .



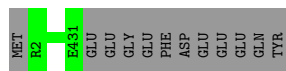
- Molecule 153: Tubulin beta chain

Chain WP: 97% .



- Molecule 153: Tubulin beta chain

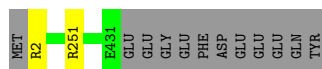
Chain WR: 97% .



- Molecule 153: Tubulin beta chain

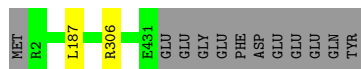
Chain WT: 97% .





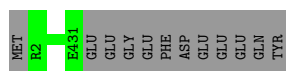
- Molecule 153: Tubulin beta chain

Chain WV: 97%



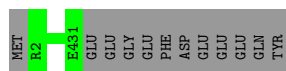
- Molecule 153: Tubulin beta chain

Chain WX: 97%



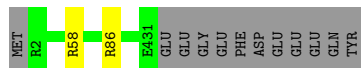
- Molecule 153: Tubulin beta chain

Chain WZ: 97%



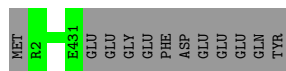
- Molecule 153: Tubulin beta chain

Chain XB: 97%



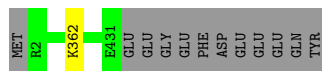
- Molecule 153: Tubulin beta chain

Chain XD: 97%



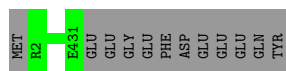
- Molecule 153: Tubulin beta chain

Chain XF: 97%



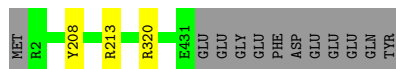
- Molecule 153: Tubulin beta chain

Chain XH: 97%



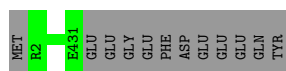
- Molecule 153: Tubulin beta chain

Chain XJ: 97%



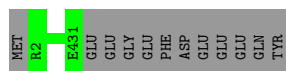
- Molecule 153: Tubulin beta chain

Chain XL: 97%



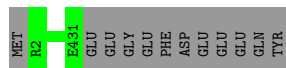
- Molecule 153: Tubulin beta chain

Chain XN: 97%



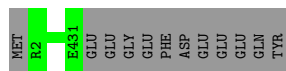
- Molecule 153: Tubulin beta chain

Chain XP: 97%



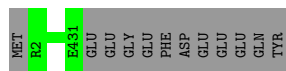
- Molecule 153: Tubulin beta chain

Chain XR: 97%



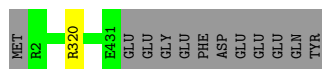
- Molecule 153: Tubulin beta chain

Chain XT: 97%



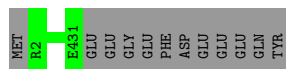
- Molecule 153: Tubulin beta chain

Chain XV: 97%



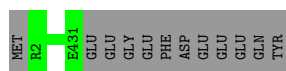
- Molecule 153: Tubulin beta chain

Chain XX:  97%



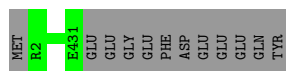
- Molecule 153: Tubulin beta chain

Chain XZ:  97%



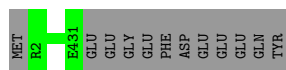
- Molecule 153: Tubulin beta chain

Chain YB:  97%



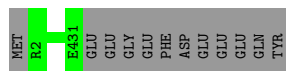
- Molecule 153: Tubulin beta chain

Chain YD:  97%



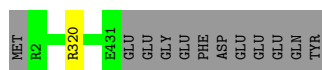
- Molecule 153: Tubulin beta chain

Chain YF:  97%



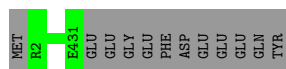
- Molecule 153: Tubulin beta chain

Chain YH:  97%



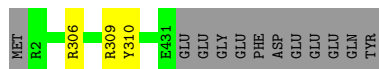
- Molecule 153: Tubulin beta chain

Chain YK:  97%



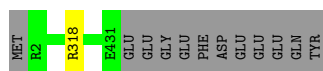
- Molecule 153: Tubulin beta chain

Chain YM:   
97%



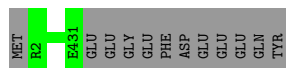
- Molecule 153: Tubulin beta chain

Chain YO:   
97%



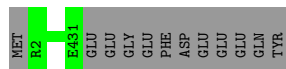
- Molecule 153: Tubulin beta chain

Chain YQ:   
97%



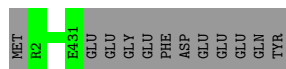
- Molecule 153: Tubulin beta chain

Chain YS:   
97%



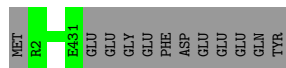
- Molecule 153: Tubulin beta chain

Chain YU:   
97%



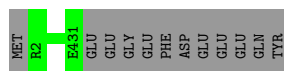
- Molecule 153: Tubulin beta chain

Chain YW:   
97%



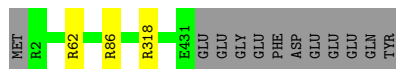
- Molecule 153: Tubulin beta chain

Chain YY:   
97%



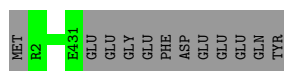
- Molecule 153: Tubulin beta chain

Chain ZA: 97%



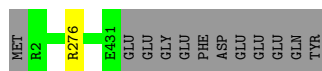
- Molecule 153: Tubulin beta chain

Chain ZC: 97%



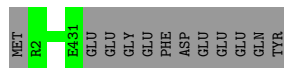
- Molecule 153: Tubulin beta chain

Chain ZE: 97%



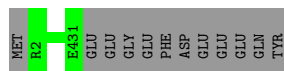
- Molecule 153: Tubulin beta chain

Chain ZG: 97%



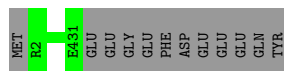
- Molecule 153: Tubulin beta chain

Chain ZI: 97%



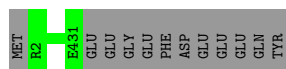
- Molecule 153: Tubulin beta chain

Chain ZK: 97%



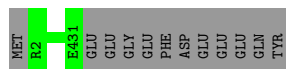
- Molecule 153: Tubulin beta chain

Chain ZM: 97%



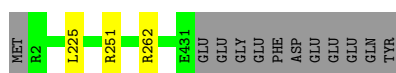
- Molecule 153: Tubulin beta chain

Chain ZO: 97% .



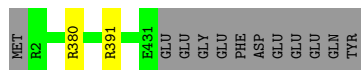
- Molecule 153: Tubulin beta chain

Chain ZQ: 97% . .



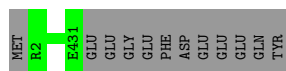
- Molecule 153: Tubulin beta chain

Chain ZS: 97% .



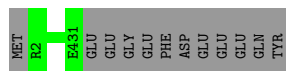
- Molecule 153: Tubulin beta chain

Chain ZU: 97% .



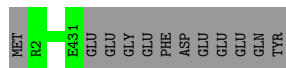
- Molecule 153: Tubulin beta chain

Chain ZW: 97% .



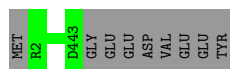
- Molecule 153: Tubulin beta chain

Chain ZY: 97% .



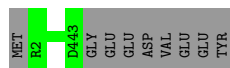
- Molecule 154: Tubulin alpha chain

Chain AB: 98% .

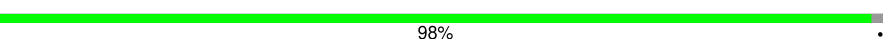


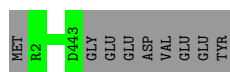
- Molecule 154: Tubulin alpha chain

Chain AD:  98%



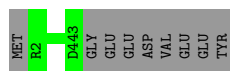
- Molecule 154: Tubulin alpha chain

Chain AF:  98%



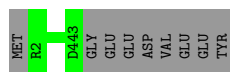
- Molecule 154: Tubulin alpha chain

Chain AH:  98%



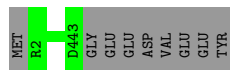
- Molecule 154: Tubulin alpha chain

Chain AJ:  98%



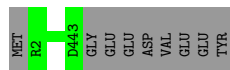
- Molecule 154: Tubulin alpha chain

Chain AL:  98%



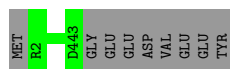
- Molecule 154: Tubulin alpha chain

Chain AN:  98%



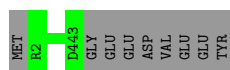
- Molecule 154: Tubulin alpha chain

Chain AP:  98%



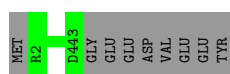
- Molecule 154: Tubulin alpha chain

Chain AR:  98%



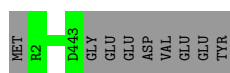
- Molecule 154: Tubulin alpha chain

Chain AT:  98%



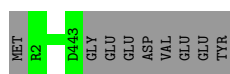
- Molecule 154: Tubulin alpha chain

Chain AV:  98%



- Molecule 154: Tubulin alpha chain

Chain AX:  98%



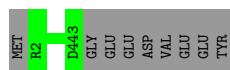
- Molecule 154: Tubulin alpha chain

Chain AZ:  98%



- Molecule 154: Tubulin alpha chain

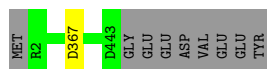
Chain Ab:  98%



- Molecule 154: Tubulin alpha chain

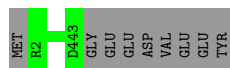
Chain Ad:  98%





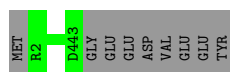
- Molecule 154: Tubulin alpha chain

Chain Af: 98% .



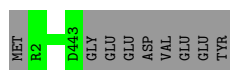
- Molecule 154: Tubulin alpha chain

Chain Ah: 98% .



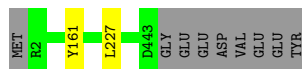
- Molecule 154: Tubulin alpha chain

Chain Aj: 98% .



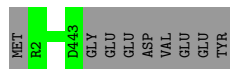
- Molecule 154: Tubulin alpha chain

Chain Al: 98% .



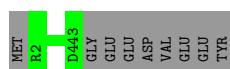
- Molecule 154: Tubulin alpha chain

Chain An: 98% .



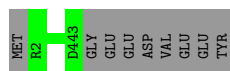
- Molecule 154: Tubulin alpha chain

Chain Ap: 98% .



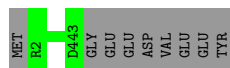
- Molecule 154: Tubulin alpha chain

Chain BB: 98% .



- Molecule 154: Tubulin alpha chain

Chain BD: 98% .



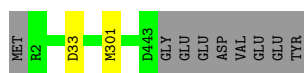
- Molecule 154: Tubulin alpha chain

Chain BF: 98% .



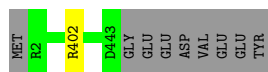
- Molecule 154: Tubulin alpha chain

Chain BH: 98% .



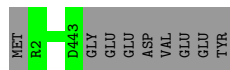
- Molecule 154: Tubulin alpha chain

Chain BJ: 98% .



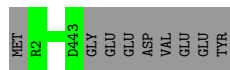
- Molecule 154: Tubulin alpha chain

Chain BL: 98% .



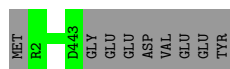
- Molecule 154: Tubulin alpha chain

Chain BN: 98% .



- Molecule 154: Tubulin alpha chain

Chain BP: 98% .



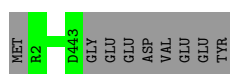
- Molecule 154: Tubulin alpha chain

Chain BR:  98%



- Molecule 154: Tubulin alpha chain

Chain BT:  98%



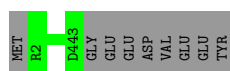
- Molecule 154: Tubulin alpha chain

Chain BV:  98%



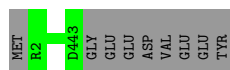
- Molecule 154: Tubulin alpha chain

Chain BX:  98%



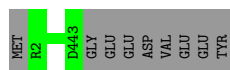
- Molecule 154: Tubulin alpha chain

Chain BZ:  98%



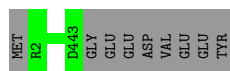
- Molecule 154: Tubulin alpha chain

Chain CB:  98%



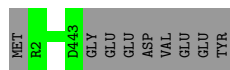
- Molecule 154: Tubulin alpha chain

Chain CD:  98%



- Molecule 154: Tubulin alpha chain

Chain CF: 98% .



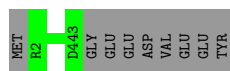
- Molecule 154: Tubulin alpha chain

Chain CI: 98% .



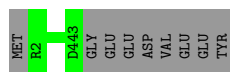
- Molecule 154: Tubulin alpha chain

Chain CJ: 98% .



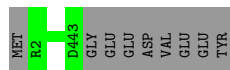
- Molecule 154: Tubulin alpha chain

Chain CL: 98% .



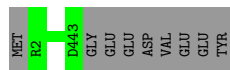
- Molecule 154: Tubulin alpha chain

Chain CN: 98% .



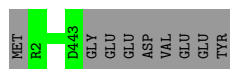
- Molecule 154: Tubulin alpha chain

Chain CP: 98% .



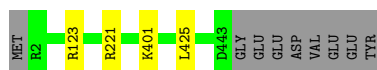
- Molecule 154: Tubulin alpha chain

Chain CR: 98% .



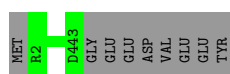
- Molecule 154: Tubulin alpha chain

Chain CT:   
97% ..



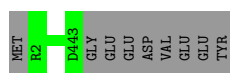
- Molecule 154: Tubulin alpha chain

Chain CV:   
98% .



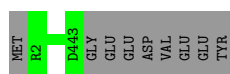
- Molecule 154: Tubulin alpha chain

Chain CX:   
98% .



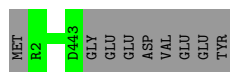
- Molecule 154: Tubulin alpha chain

Chain CZ:   
98% .



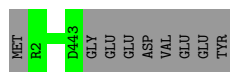
- Molecule 154: Tubulin alpha chain

Chain DB:   
98% .



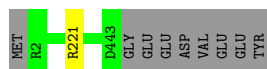
- Molecule 154: Tubulin alpha chain

Chain DD:   
98% .



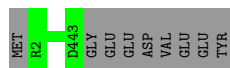
- Molecule 154: Tubulin alpha chain

Chain DF:   
98% .



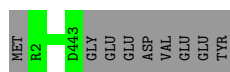
- Molecule 154: Tubulin alpha chain

Chain DH:  98% .



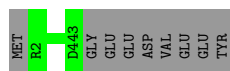
- Molecule 154: Tubulin alpha chain

Chain DJ:  98% .



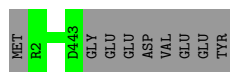
- Molecule 154: Tubulin alpha chain

Chain DL:  98% .



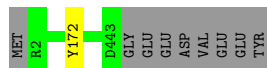
- Molecule 154: Tubulin alpha chain

Chain DM:  98% .



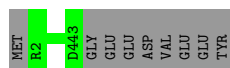
- Molecule 154: Tubulin alpha chain

Chain DO:  98% .



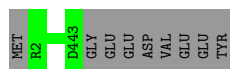
- Molecule 154: Tubulin alpha chain

Chain DQ:  98% .



- Molecule 154: Tubulin alpha chain

Chain DS:  98% .



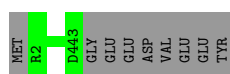
- Molecule 154: Tubulin alpha chain

Chain DU:  98% .



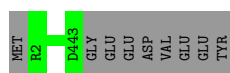
- Molecule 154: Tubulin alpha chain

Chain DW:  98% .



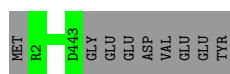
- Molecule 154: Tubulin alpha chain

Chain DY:  98% .



- Molecule 154: Tubulin alpha chain

Chain EA:  98% .



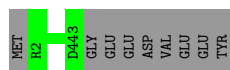
- Molecule 154: Tubulin alpha chain

Chain EC:  98% .



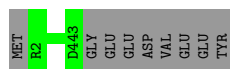
- Molecule 154: Tubulin alpha chain

Chain EE:  98% .



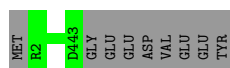
- Molecule 154: Tubulin alpha chain

Chain EG:  98% .



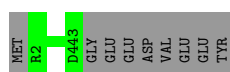
- Molecule 154: Tubulin alpha chain

Chain EI:  98%



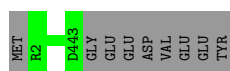
- Molecule 154: Tubulin alpha chain

Chain EK:  98%



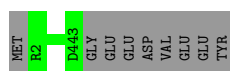
- Molecule 154: Tubulin alpha chain

Chain EM:  98%



- Molecule 154: Tubulin alpha chain

Chain EO:  98%



- Molecule 154: Tubulin alpha chain

Chain EQ:  98%



- Molecule 154: Tubulin alpha chain

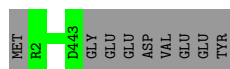
Chain ES:  98%



- Molecule 154: Tubulin alpha chain

Chain EU:  98%





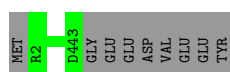
- Molecule 154: Tubulin alpha chain

Chain EW:  98%



- Molecule 154: Tubulin alpha chain

Chain EY:  98%



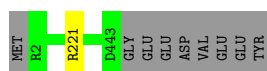
- Molecule 154: Tubulin alpha chain

Chain FA:  98%



- Molecule 154: Tubulin alpha chain

Chain FC:  98%



- Molecule 154: Tubulin alpha chain

Chain FE:  98%



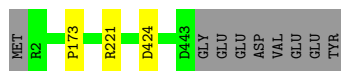
- Molecule 154: Tubulin alpha chain

Chain FG:  98%



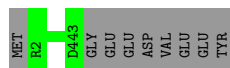
- Molecule 154: Tubulin alpha chain

Chain FI:  97%



- Molecule 154: Tubulin alpha chain

Chain FK:  98%



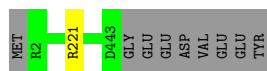
- Molecule 154: Tubulin alpha chain

Chain FM:  98%



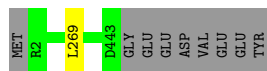
- Molecule 154: Tubulin alpha chain

Chain FO:  98%



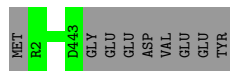
- Molecule 154: Tubulin alpha chain

Chain FQ:  98%



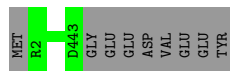
- Molecule 154: Tubulin alpha chain

Chain FS:  98%



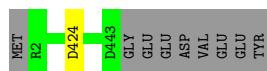
- Molecule 154: Tubulin alpha chain

Chain FW:  98%



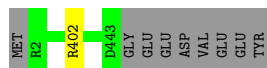
- Molecule 154: Tubulin alpha chain

Chain FY:  98%



- Molecule 154: Tubulin alpha chain

Chain GA:   
98% .



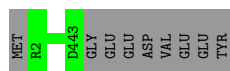
- Molecule 154: Tubulin alpha chain

Chain GC:   
98% .



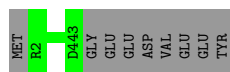
- Molecule 154: Tubulin alpha chain

Chain GE:   
98% .



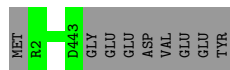
- Molecule 154: Tubulin alpha chain

Chain GG:   
98% .



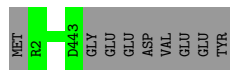
- Molecule 154: Tubulin alpha chain

Chain GI:   
98% .



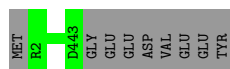
- Molecule 154: Tubulin alpha chain

Chain GK:   
98% .



- Molecule 154: Tubulin alpha chain

Chain GM:   
98% .



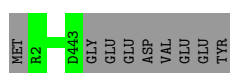
- Molecule 154: Tubulin alpha chain

Chain GO: 98%



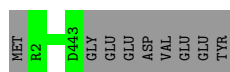
- Molecule 154: Tubulin alpha chain

Chain GQ: 98%



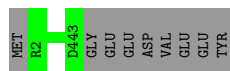
- Molecule 154: Tubulin alpha chain

Chain GS: 98%



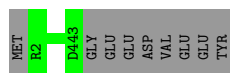
- Molecule 154: Tubulin alpha chain

Chain GU: 98%



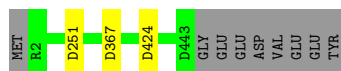
- Molecule 154: Tubulin alpha chain

Chain GW: 98%



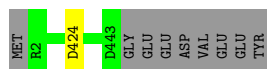
- Molecule 154: Tubulin alpha chain

Chain HA: 97%



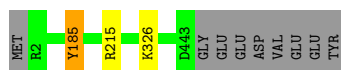
- Molecule 154: Tubulin alpha chain

Chain HC: 98%



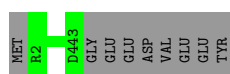
- Molecule 154: Tubulin alpha chain

Chain HE:  97%



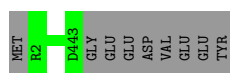
- Molecule 154: Tubulin alpha chain

Chain HG:  98%



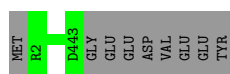
- Molecule 154: Tubulin alpha chain

Chain HI:  98%



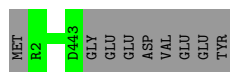
- Molecule 154: Tubulin alpha chain

Chain HK:  98%



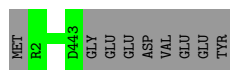
- Molecule 154: Tubulin alpha chain

Chain HM:  98%



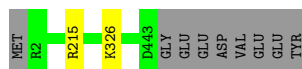
- Molecule 154: Tubulin alpha chain

Chain HO:  98%



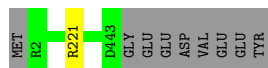
- Molecule 154: Tubulin alpha chain

Chain HQ:  98%



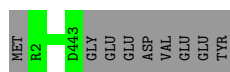
- Molecule 154: Tubulin alpha chain

Chain HS: 98%



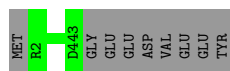
- Molecule 154: Tubulin alpha chain

Chain HU: 98%



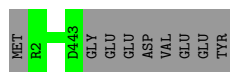
- Molecule 154: Tubulin alpha chain

Chain HW: 98%



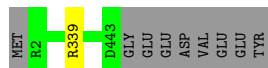
- Molecule 154: Tubulin alpha chain

Chain HY: 98%



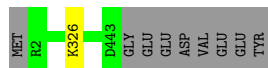
- Molecule 154: Tubulin alpha chain

Chain IA: 98%



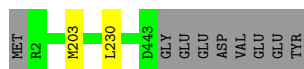
- Molecule 154: Tubulin alpha chain

Chain IE: 98%



- Molecule 154: Tubulin alpha chain

Chain IG: 98%



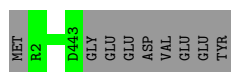
- Molecule 154: Tubulin alpha chain

Chain II: 97%



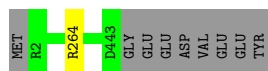
- Molecule 154: Tubulin alpha chain

Chain IK: 98%



- Molecule 154: Tubulin alpha chain

Chain IM: 98%



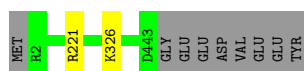
- Molecule 154: Tubulin alpha chain

Chain IO: 97%



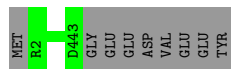
- Molecule 154: Tubulin alpha chain

Chain IQ: 98%



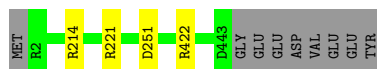
- Molecule 154: Tubulin alpha chain

Chain IS: 98%



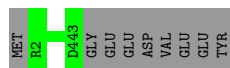
- Molecule 154: Tubulin alpha chain

Chain IU: 97%



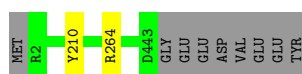
- Molecule 154: Tubulin alpha chain

Chain IW: 98% .



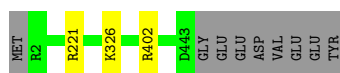
- Molecule 154: Tubulin alpha chain

Chain IY: 98% .



- Molecule 154: Tubulin alpha chain

Chain JA: 97% ..



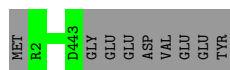
- Molecule 154: Tubulin alpha chain

Chain JC: 98% .



- Molecule 154: Tubulin alpha chain

Chain JE: 98% .



- Molecule 154: Tubulin alpha chain

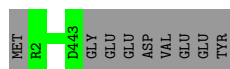
Chain JH: 98% .



- Molecule 154: Tubulin alpha chain

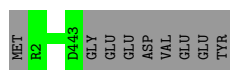
Chain JJ: 98% .





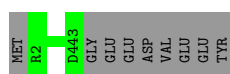
- Molecule 154: Tubulin alpha chain

Chain JL: 98% .



- Molecule 154: Tubulin alpha chain

Chain JN: 98% .



- Molecule 154: Tubulin alpha chain

Chain JP: 98% .



- Molecule 154: Tubulin alpha chain

Chain JR: 98% .



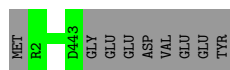
- Molecule 154: Tubulin alpha chain

Chain JT: 98% .



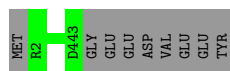
- Molecule 154: Tubulin alpha chain

Chain JV: 98% .



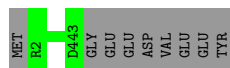
- Molecule 154: Tubulin alpha chain

Chain JX: 98% .



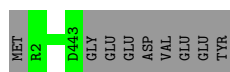
- Molecule 154: Tubulin alpha chain

Chain JZ:  98%



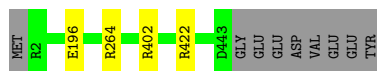
- Molecule 154: Tubulin alpha chain

Chain KB:  98%



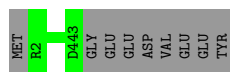
- Molecule 154: Tubulin alpha chain

Chain KD:  97%



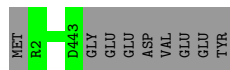
- Molecule 154: Tubulin alpha chain

Chain KF:  98%



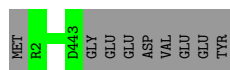
- Molecule 154: Tubulin alpha chain

Chain KH:  98%



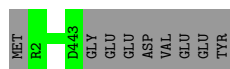
- Molecule 154: Tubulin alpha chain

Chain KJ:  98%



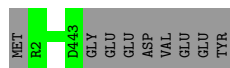
- Molecule 154: Tubulin alpha chain

Chain KL:  98%



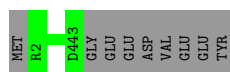
- Molecule 154: Tubulin alpha chain

Chain KN:  98% .



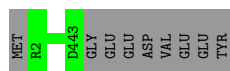
- Molecule 154: Tubulin alpha chain

Chain KP:  98% .



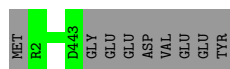
- Molecule 154: Tubulin alpha chain

Chain KR:  98% .



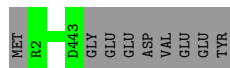
- Molecule 154: Tubulin alpha chain

Chain KT:  98% .



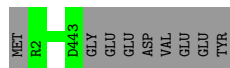
- Molecule 154: Tubulin alpha chain

Chain KV:  98% .



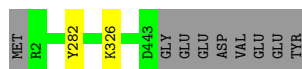
- Molecule 154: Tubulin alpha chain

Chain KX:  98% .



- Molecule 154: Tubulin alpha chain

Chain KZ:  98% .



- Molecule 154: Tubulin alpha chain

Chain LB:  98%



- Molecule 154: Tubulin alpha chain

Chain LD:  98%



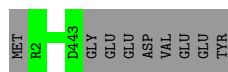
- Molecule 154: Tubulin alpha chain

Chain LF:  98%



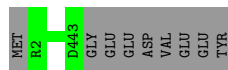
- Molecule 154: Tubulin alpha chain

Chain LH:  98%



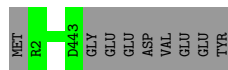
- Molecule 154: Tubulin alpha chain

Chain LJ:  98%



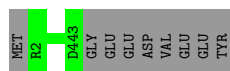
- Molecule 154: Tubulin alpha chain

Chain LL:  98%



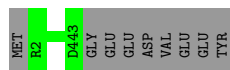
- Molecule 154: Tubulin alpha chain

Chain LN:  98%



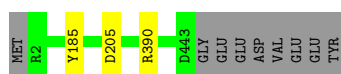
- Molecule 154: Tubulin alpha chain

Chain LP:   
98%



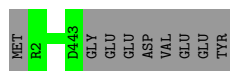
- Molecule 154: Tubulin alpha chain

Chain LR:   
97%



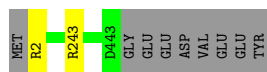
- Molecule 154: Tubulin alpha chain

Chain LT:   
98%



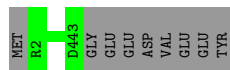
- Molecule 154: Tubulin alpha chain

Chain LV:   
98%



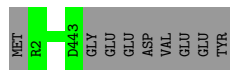
- Molecule 154: Tubulin alpha chain

Chain LX:   
98%



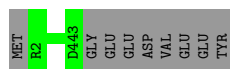
- Molecule 154: Tubulin alpha chain

Chain LZ:   
98%



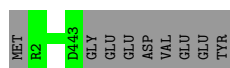
- Molecule 154: Tubulin alpha chain

Chain MB:   
98%



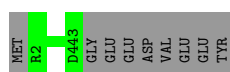
- Molecule 154: Tubulin alpha chain

Chain MD:  98% .



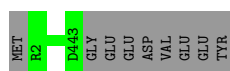
- Molecule 154: Tubulin alpha chain

Chain MF:  98% .



- Molecule 154: Tubulin alpha chain

Chain MH:  98% .



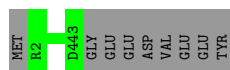
- Molecule 154: Tubulin alpha chain

Chain MJ:  98% .



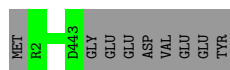
- Molecule 154: Tubulin alpha chain

Chain ML:  98% .



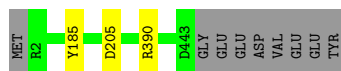
- Molecule 154: Tubulin alpha chain

Chain MN:  98% .



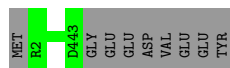
- Molecule 154: Tubulin alpha chain

Chain MP:  97% ..



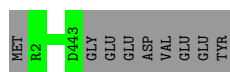
- Molecule 154: Tubulin alpha chain

Chain MR: 98% .



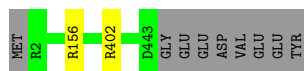
- Molecule 154: Tubulin alpha chain

Chain MT: 98% .



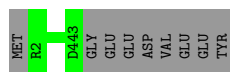
- Molecule 154: Tubulin alpha chain

Chain MV: 98% .



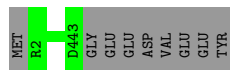
- Molecule 154: Tubulin alpha chain

Chain MX: 98% .



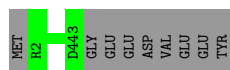
- Molecule 154: Tubulin alpha chain

Chain MZ: 98% .



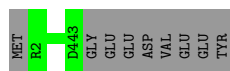
- Molecule 154: Tubulin alpha chain

Chain NB: 98% .



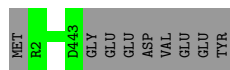
- Molecule 154: Tubulin alpha chain

Chain ND: 98% .



- Molecule 154: Tubulin alpha chain

Chain NF:  98%



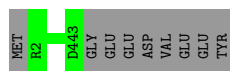
- Molecule 154: Tubulin alpha chain

Chain NH:  98%



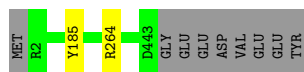
- Molecule 154: Tubulin alpha chain

Chain NJ:  98%



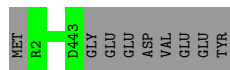
- Molecule 154: Tubulin alpha chain

Chain NL:  98%



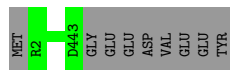
- Molecule 154: Tubulin alpha chain

Chain NN:  98%



- Molecule 154: Tubulin alpha chain

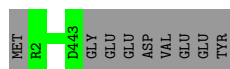
Chain NP:  98%



- Molecule 154: Tubulin alpha chain

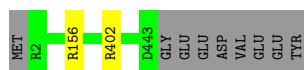
Chain NR:  98%





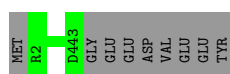
- Molecule 154: Tubulin alpha chain

Chain NT:  98%



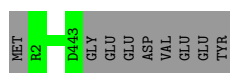
- Molecule 154: Tubulin alpha chain

Chain NV:  98%



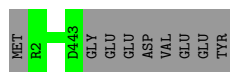
- Molecule 154: Tubulin alpha chain

Chain NX:  98%



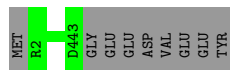
- Molecule 154: Tubulin alpha chain

Chain NZ:  98%



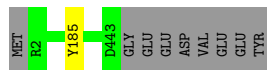
- Molecule 154: Tubulin alpha chain

Chain OB:  98%



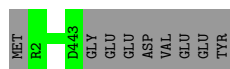
- Molecule 154: Tubulin alpha chain

Chain OD:  98%



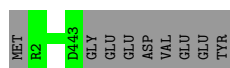
- Molecule 154: Tubulin alpha chain

Chain OF:  98%



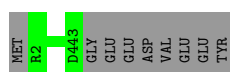
- Molecule 154: Tubulin alpha chain

Chain OH:  98% .



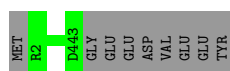
- Molecule 154: Tubulin alpha chain

Chain OJ:  98% .



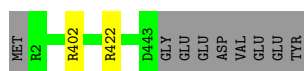
- Molecule 154: Tubulin alpha chain

Chain OL:  98% .



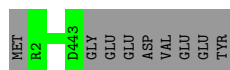
- Molecule 154: Tubulin alpha chain

Chain ON:  98% .



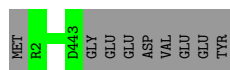
- Molecule 154: Tubulin alpha chain

Chain OP:  98% .



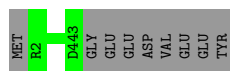
- Molecule 154: Tubulin alpha chain

Chain OR:  98% .



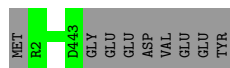
- Molecule 154: Tubulin alpha chain

Chain OT:  98% .



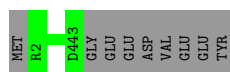
- Molecule 154: Tubulin alpha chain

Chain OV:   
98% .



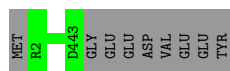
- Molecule 154: Tubulin alpha chain

Chain OX:   
98% .



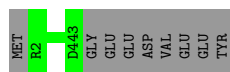
- Molecule 154: Tubulin alpha chain

Chain OZ:   
98% .



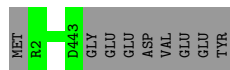
- Molecule 154: Tubulin alpha chain

Chain PC:   
98% .



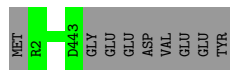
- Molecule 154: Tubulin alpha chain

Chain PE:   
98% .



- Molecule 154: Tubulin alpha chain

Chain PG:   
98% .



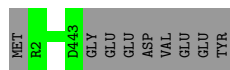
- Molecule 154: Tubulin alpha chain

Chain PI:   
97% ..



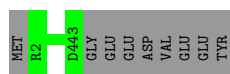
- Molecule 154: Tubulin alpha chain

Chain PK: 98% .



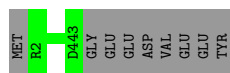
- Molecule 154: Tubulin alpha chain

Chain PM: 98% .



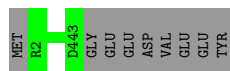
- Molecule 154: Tubulin alpha chain

Chain PO: 98% .



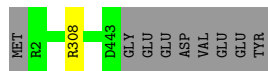
- Molecule 154: Tubulin alpha chain

Chain PQ: 98% .



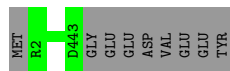
- Molecule 154: Tubulin alpha chain

Chain PS: 98% .



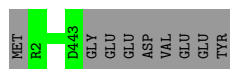
- Molecule 154: Tubulin alpha chain

Chain PU: 98% .



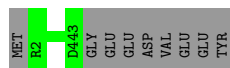
- Molecule 154: Tubulin alpha chain

Chain PW: 98% .



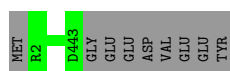
- Molecule 154: Tubulin alpha chain

Chain PY:  98%



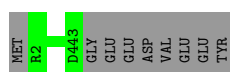
- Molecule 154: Tubulin alpha chain

Chain QA:  98%



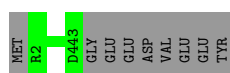
- Molecule 154: Tubulin alpha chain

Chain QC:  98%



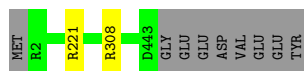
- Molecule 154: Tubulin alpha chain

Chain QE:  98%



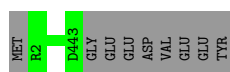
- Molecule 154: Tubulin alpha chain

Chain QG:  98%



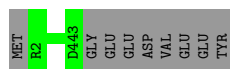
- Molecule 154: Tubulin alpha chain

Chain QI:  98%



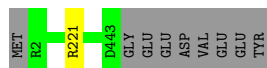
- Molecule 154: Tubulin alpha chain

Chain QK:  98%



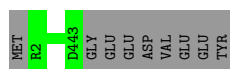
- Molecule 154: Tubulin alpha chain

Chain QM:  98%



- Molecule 154: Tubulin alpha chain

Chain QO:  98%



- Molecule 154: Tubulin alpha chain

Chain QQ:  98%



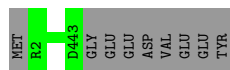
- Molecule 154: Tubulin alpha chain

Chain QS:  98%



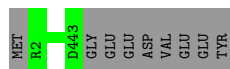
- Molecule 154: Tubulin alpha chain

Chain QU:  98%



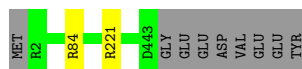
- Molecule 154: Tubulin alpha chain

Chain QW:  98%



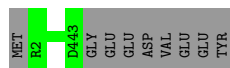
- Molecule 154: Tubulin alpha chain

Chain QY:  98%



- Molecule 154: Tubulin alpha chain

Chain RA: 98% .



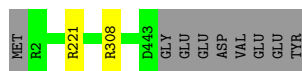
- Molecule 154: Tubulin alpha chain

Chain RC: 98% .



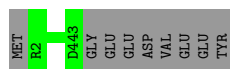
- Molecule 154: Tubulin alpha chain

Chain RE: 98% .



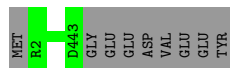
- Molecule 154: Tubulin alpha chain

Chain RG: 98% .



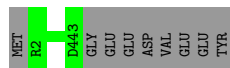
- Molecule 154: Tubulin alpha chain

Chain RI: 98% .



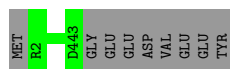
- Molecule 154: Tubulin alpha chain

Chain RK: 98% .



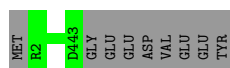
- Molecule 154: Tubulin alpha chain

Chain RM: 98% .



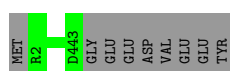
- Molecule 154: Tubulin alpha chain

Chain RO:  98%



- Molecule 154: Tubulin alpha chain

Chain RQ:  98%



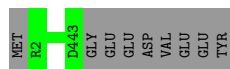
- Molecule 154: Tubulin alpha chain

Chain RS:  98%



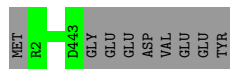
- Molecule 154: Tubulin alpha chain

Chain RU:  98%



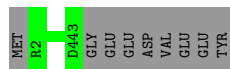
- Molecule 154: Tubulin alpha chain

Chain RW:  98%



- Molecule 154: Tubulin alpha chain

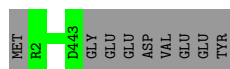
Chain RY:  98%



- Molecule 154: Tubulin alpha chain

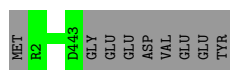
Chain SA:  98%





- Molecule 154: Tubulin alpha chain

Chain SC: 98%



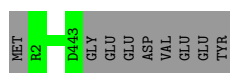
- Molecule 154: Tubulin alpha chain

Chain SE: 98%



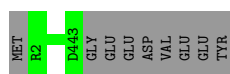
- Molecule 154: Tubulin alpha chain

Chain SG: 98%



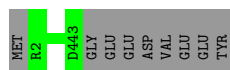
- Molecule 154: Tubulin alpha chain

Chain SI: 98%



- Molecule 154: Tubulin alpha chain

Chain SK: 98%



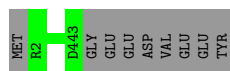
- Molecule 154: Tubulin alpha chain

Chain SM: 98%



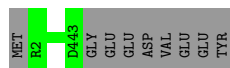
- Molecule 154: Tubulin alpha chain

Chain SO: 98%



- Molecule 154: Tubulin alpha chain

Chain SQ: 98%



- Molecule 154: Tubulin alpha chain

Chain SS: 97%



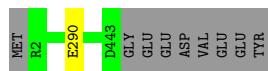
- Molecule 154: Tubulin alpha chain

Chain SU: 97%



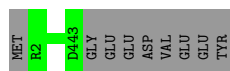
- Molecule 154: Tubulin alpha chain

Chain SW: 98%



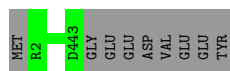
- Molecule 154: Tubulin alpha chain

Chain SY: 98%



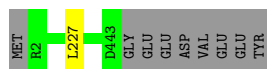
- Molecule 154: Tubulin alpha chain

Chain TA: 98%



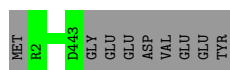
- Molecule 154: Tubulin alpha chain

Chain TC: 98%



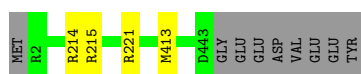
- Molecule 154: Tubulin alpha chain

Chain TE: 98%



- Molecule 154: Tubulin alpha chain

Chain TG: 97%



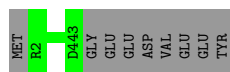
- Molecule 154: Tubulin alpha chain

Chain TI: 98%



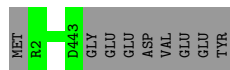
- Molecule 154: Tubulin alpha chain

Chain TK: 98%



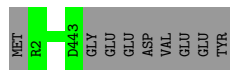
- Molecule 154: Tubulin alpha chain

Chain TM: 98%



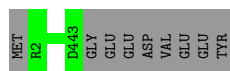
- Molecule 154: Tubulin alpha chain

Chain TO: 98%



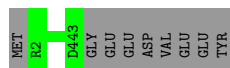
- Molecule 154: Tubulin alpha chain

Chain TQ: 98%



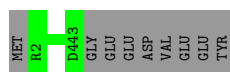
- Molecule 154: Tubulin alpha chain

Chain TR:  98% .



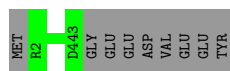
- Molecule 154: Tubulin alpha chain

Chain TT:  98% .



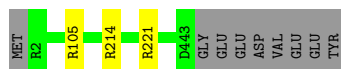
- Molecule 154: Tubulin alpha chain

Chain TV:  98% .



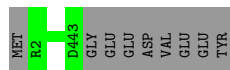
- Molecule 154: Tubulin alpha chain

Chain TX:  97% ..



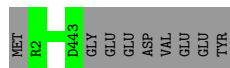
- Molecule 154: Tubulin alpha chain

Chain TZ:  98% .



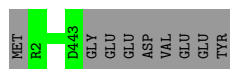
- Molecule 154: Tubulin alpha chain

Chain UB:  98% .



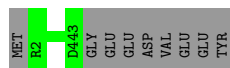
- Molecule 154: Tubulin alpha chain

Chain UD:  98% .



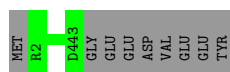
- Molecule 154: Tubulin alpha chain

Chain UF: 98% .



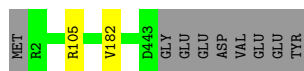
- Molecule 154: Tubulin alpha chain

Chain UH: 98% .



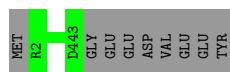
- Molecule 154: Tubulin alpha chain

Chain UJ: 98% .



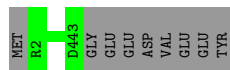
- Molecule 154: Tubulin alpha chain

Chain UL: 98% .



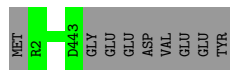
- Molecule 154: Tubulin alpha chain

Chain UN: 98% .



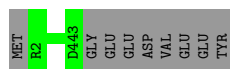
- Molecule 154: Tubulin alpha chain

Chain UP: 98% .



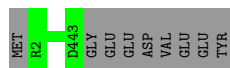
- Molecule 154: Tubulin alpha chain

Chain UR: 98% .



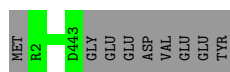
- Molecule 154: Tubulin alpha chain

Chain UT:  98% .



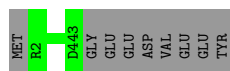
- Molecule 154: Tubulin alpha chain

Chain UW:  98% .



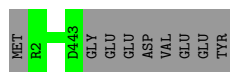
- Molecule 154: Tubulin alpha chain

Chain UY:  98% .



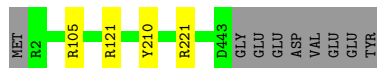
- Molecule 154: Tubulin alpha chain

Chain VA:  98% .



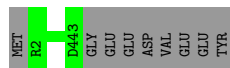
- Molecule 154: Tubulin alpha chain

Chain VC:  97% ..



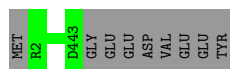
- Molecule 154: Tubulin alpha chain

Chain VE:  98% .



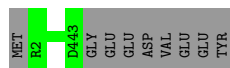
- Molecule 154: Tubulin alpha chain

Chain VG:  98% .



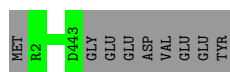
- Molecule 154: Tubulin alpha chain

Chain VI: 98%



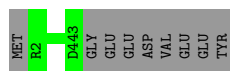
- Molecule 154: Tubulin alpha chain

Chain VK: 98%



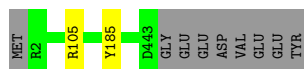
- Molecule 154: Tubulin alpha chain

Chain VM: 98%



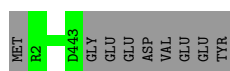
- Molecule 154: Tubulin alpha chain

Chain VO: 98%



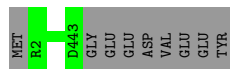
- Molecule 154: Tubulin alpha chain

Chain VQ: 98%



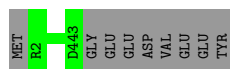
- Molecule 154: Tubulin alpha chain

Chain VS: 98%



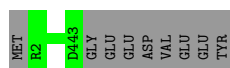
- Molecule 154: Tubulin alpha chain

Chain VU: 98%



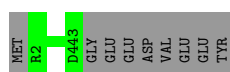
- Molecule 154: Tubulin alpha chain

Chain VW: 98%



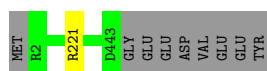
- Molecule 154: Tubulin alpha chain

Chain VY: 98%



- Molecule 154: Tubulin alpha chain

Chain WA: 98%



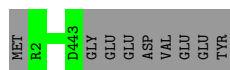
- Molecule 154: Tubulin alpha chain

Chain WC: 98%



- Molecule 154: Tubulin alpha chain

Chain WE: 98%



- Molecule 154: Tubulin alpha chain

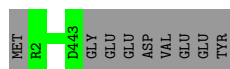
Chain WG: 97%



- Molecule 154: Tubulin alpha chain

Chain WI: 98%





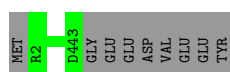
- Molecule 154: Tubulin alpha chain

Chain WK: 98%



- Molecule 154: Tubulin alpha chain

Chain WM: 98%



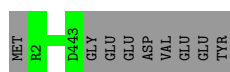
- Molecule 154: Tubulin alpha chain

Chain WO: 98%



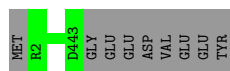
- Molecule 154: Tubulin alpha chain

Chain WQ: 98%



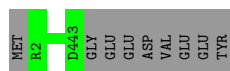
- Molecule 154: Tubulin alpha chain

Chain WS: 98%



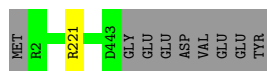
- Molecule 154: Tubulin alpha chain

Chain WU: 98%



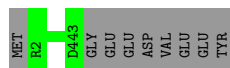
- Molecule 154: Tubulin alpha chain

Chain WW: 98%



- Molecule 154: Tubulin alpha chain

Chain WY:  98%



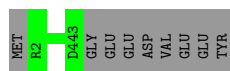
- Molecule 154: Tubulin alpha chain

Chain XA:  98%



- Molecule 154: Tubulin alpha chain

Chain XC:  98%



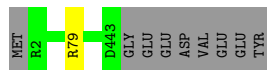
- Molecule 154: Tubulin alpha chain

Chain XE:  98%



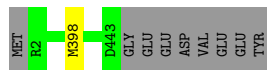
- Molecule 154: Tubulin alpha chain

Chain XG:  98%



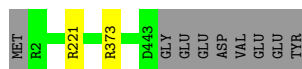
- Molecule 154: Tubulin alpha chain

Chain XI:  98%



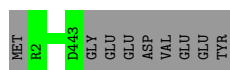
- Molecule 154: Tubulin alpha chain

Chain XK:  98%



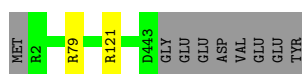
- Molecule 154: Tubulin alpha chain

Chain XM: 98%



- Molecule 154: Tubulin alpha chain

Chain XO: 98%



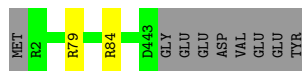
- Molecule 154: Tubulin alpha chain

Chain XQ: 98%



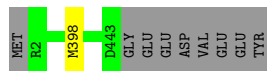
- Molecule 154: Tubulin alpha chain

Chain XS: 98%



- Molecule 154: Tubulin alpha chain

Chain XU: 98%



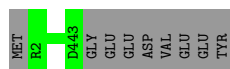
- Molecule 154: Tubulin alpha chain

Chain XW: 98%



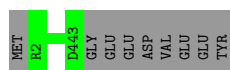
- Molecule 154: Tubulin alpha chain

Chain XY: 98%



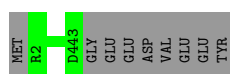
- Molecule 154: Tubulin alpha chain

Chain YA:   
98%



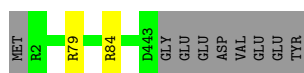
- Molecule 154: Tubulin alpha chain

Chain YC:   
98%



- Molecule 154: Tubulin alpha chain

Chain YE:   
98%



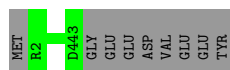
- Molecule 154: Tubulin alpha chain

Chain YG:   
98%



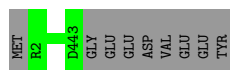
- Molecule 154: Tubulin alpha chain

Chain YJ:   
98%



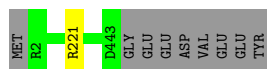
- Molecule 154: Tubulin alpha chain

Chain YL:   
98%



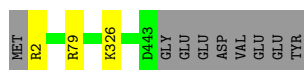
- Molecule 154: Tubulin alpha chain

Chain YN:   
98%



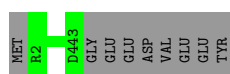
- Molecule 154: Tubulin alpha chain

Chain YP:   
97%



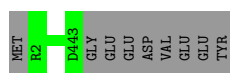
- Molecule 154: Tubulin alpha chain

Chain YR:   
98%



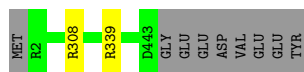
- Molecule 154: Tubulin alpha chain

Chain YT:   
98%



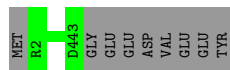
- Molecule 154: Tubulin alpha chain

Chain YV:   
98%



- Molecule 154: Tubulin alpha chain

Chain YX:   
98%



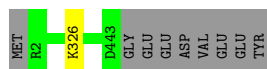
- Molecule 154: Tubulin alpha chain

Chain YZ:   
98%



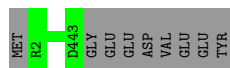
- Molecule 154: Tubulin alpha chain

Chain ZB:   
98%



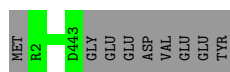
- Molecule 154: Tubulin alpha chain

Chain ZD:  98%



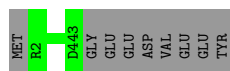
- Molecule 154: Tubulin alpha chain

Chain ZF:  98%



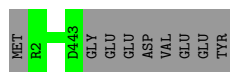
- Molecule 154: Tubulin alpha chain

Chain ZH:  98%



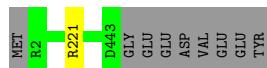
- Molecule 154: Tubulin alpha chain

Chain ZJ:  98%



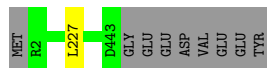
- Molecule 154: Tubulin alpha chain

Chain ZL:  98%



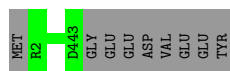
- Molecule 154: Tubulin alpha chain

Chain ZN:  98%



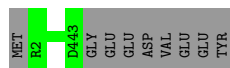
- Molecule 154: Tubulin alpha chain

Chain ZP:  98%



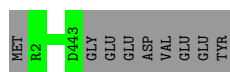
- Molecule 154: Tubulin alpha chain

Chain ZR:  98%



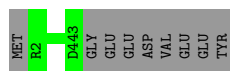
- Molecule 154: Tubulin alpha chain

Chain ZT:  98%



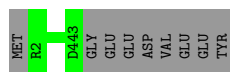
- Molecule 154: Tubulin alpha chain

Chain ZV:  98%



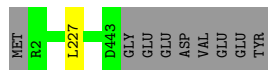
- Molecule 154: Tubulin alpha chain

Chain ZX:  98%



- Molecule 154: Tubulin alpha chain

Chain ZZ:  98%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	244497	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	0A	0.52	0/5506	0.57	0/7437
1	0B	0.52	0/6100	0.56	0/8236
1	0C	0.52	0/6058	0.55	0/8179
1	0D	0.30	0/5506	0.58	2/7437 (0.0%)
1	0E	0.52	0/6100	0.58	1/8236 (0.0%)
1	0F	0.52	0/6058	0.55	0/8179
2	0G	0.29	0/6005	0.54	1/8131 (0.0%)
2	0H	0.28	0/6005	0.54	1/8131 (0.0%)
2	0I	0.28	0/6005	0.54	1/8131 (0.0%)
3	0J	0.29	0/5505	0.55	0/7432
3	0K	0.29	0/5505	0.55	0/7432
3	0L	0.30	0/5505	0.56	0/7432
4	0M	0.27	0/6276	0.56	2/8472 (0.0%)
4	0N	0.54	0/6276	0.59	0/8472
5	0O	0.35	0/1691	0.59	0/2245
5	0P	0.35	0/3171	0.59	0/4220
5	0Q	0.38	0/3156	0.63	3/4202 (0.1%)
5	0R	0.34	0/2063	0.58	1/2747 (0.0%)
5	0S	0.53	0/3053	0.51	0/4060
5	0T	0.55	0/2723	0.55	0/3626
6	0U	0.29	0/281	0.69	0/374
6	0V	0.32	0/3905	0.60	0/5194
6	0W	0.54	0/3905	0.53	0/5194
6	0X	0.32	0/2469	0.60	0/3280
7	0Y	0.35	0/1308	0.69	0/1742
7	0Z	0.34	0/3609	0.67	0/4794
7	1A	0.35	0/3609	0.67	0/4794
7	1B	0.31	0/1058	0.63	0/1404
8	0a	0.29	0/839	0.69	0/1121
8	0b	0.27	0/1172	0.62	0/1568
8	0c	0.54	0/1172	0.72	1/1568 (0.1%)
8	0d	0.27	0/1172	0.62	0/1568

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
8	0e	0.53	0/1172	0.62	1/1568 (0.1%)
8	0f	0.28	0/333	0.56	0/447
9	0g	0.29	0/655	0.66	0/877
9	0h	0.28	0/655	0.62	0/877
9	0i	0.28	0/655	0.60	0/877
9	0j	0.29	0/655	0.62	0/877
9	0k	0.29	0/655	0.67	0/877
9	0l	0.28	0/655	0.63	0/877
9	0m	0.28	0/655	0.60	0/877
9	0n	0.29	0/655	0.63	0/877
9	0o	0.28	0/655	0.66	0/877
9	0p	0.28	0/655	0.62	0/877
10	0q	0.38	0/744	0.68	1/1009 (0.1%)
11	0r	0.37	0/634	0.66	0/856
11	0s	0.34	0/1657	0.63	0/2247
12	0t	0.29	0/3583	0.61	0/4827
13	0u	0.27	0/3775	0.61	0/5102
14	0v	0.41	0/3471	0.73	1/4642 (0.0%)
14	0w	0.38	0/3998	0.67	1/5345 (0.0%)
15	0x	0.38	0/3445	0.65	2/4606 (0.0%)
15	0y	0.38	0/3727	0.64	2/4984 (0.0%)
16	0z	0.36	1/1888 (0.1%)	0.61	0/2555
17	1C	0.31	0/2642	0.53	1/3581 (0.0%)
17	1D	0.30	0/2642	0.53	1/3581 (0.0%)
17	1G	0.31	0/2642	0.53	1/3581 (0.0%)
18	1E	0.28	0/2741	0.55	1/3718 (0.0%)
18	1F	0.28	0/2741	0.55	1/3718 (0.0%)
19	1H	0.29	0/3398	0.52	0/4607
19	1I	0.29	0/3398	0.52	0/4607
20	1J	0.29	0/3352	0.53	0/4527
20	1K	0.29	0/3352	0.53	0/4527
21	1L	0.32	0/2503	0.55	0/3389
21	1M	0.29	0/2503	0.54	0/3389
22	1N	0.27	0/1285	0.53	0/1751
22	1O	0.27	0/1285	0.53	0/1751
23	1P	0.29	0/846	0.62	0/1129
23	1Q	0.29	0/846	0.61	0/1129
24	1R	0.29	0/1489	0.54	0/2011
24	1S	0.29	0/1489	0.54	0/2011
25	1T	0.28	0/2164	0.53	0/2952
25	1U	0.28	0/2164	0.53	0/2952
25	1V	0.28	0/2164	0.53	0/2952
26	1W	0.29	0/3791	0.52	0/5129

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
26	1X	0.35	0/3791	0.62	3/5129 (0.1%)
27	1Y	0.29	0/2994	0.54	1/4043 (0.0%)
27	1Z	0.30	0/2994	0.54	1/4043 (0.0%)
28	1a	0.34	0/4250	0.67	0/5670
29	1b	0.35	0/4329	0.70	3/5808 (0.1%)
30	1c	0.39	0/7870	0.69	4/10653 (0.0%)
31	1d	0.30	0/7708	0.62	4/10404 (0.0%)
32	1e	0.37	0/2786	0.72	3/3726 (0.1%)
33	1f	0.32	0/2763	0.69	3/3699 (0.1%)
34	1g	0.35	0/4802	0.63	3/6429 (0.0%)
35	1h	0.36	1/3627 (0.0%)	0.63	3/4861 (0.1%)
36	1i	0.32	0/4482	0.64	1/6018 (0.0%)
37	1j	0.32	0/3584	0.66	4/4779 (0.1%)
38	1k	0.31	0/3573	0.63	0/4784
39	1l	0.26	0/3117	0.55	1/4216 (0.0%)
40	1m	0.28	0/4124	0.57	0/5591
41	1n	0.28	0/3294	0.58	0/4417
42	1o	0.30	0/3353	0.60	1/4531 (0.0%)
43	1p	0.25	0/4497	0.48	0/6078
44	1r	0.30	0/11128	0.60	4/15062 (0.0%)
45	1t	0.31	0/10556	0.61	3/14234 (0.0%)
46	2A	0.29	0/2308	0.56	0/3114
46	2B	0.29	0/2308	0.56	0/3114
46	2C	0.29	0/1805	0.56	0/2432
47	2D	0.29	0/1956	0.58	1/2647 (0.0%)
47	2E	0.35	0/1956	0.63	1/2647 (0.0%)
47	2F	0.28	0/1956	0.56	0/2647
48	2G	0.29	0/2432	0.57	0/3302
48	2H	0.29	0/2432	0.57	0/3302
48	2I	0.29	0/2432	0.57	0/3302
49	2J	0.28	0/1923	0.52	0/2598
49	2K	0.28	0/1923	0.52	0/2598
49	2L	0.30	0/1923	0.53	0/2598
50	2M	0.28	0/1899	0.56	0/2574
50	2N	0.28	0/1899	0.56	0/2574
50	2O	0.27	0/1210	0.57	0/1635
51	2P	0.29	0/1316	0.56	1/1786 (0.1%)
51	2Q	0.31	0/1316	0.58	2/1786 (0.1%)
52	2R	0.28	0/2045	0.57	1/2779 (0.0%)
52	2S	0.27	0/2045	0.57	1/2779 (0.0%)
52	2T	0.34	0/2045	0.64	0/2779
53	2U	0.27	0/2366	0.54	0/3218
53	2V	0.53	0/3043	0.56	0/4136

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
53	2W	0.54	0/3043	0.60	1/4136 (0.0%)
54	2X	0.56	0/2984	0.64	4/4021 (0.1%)
54	2Y	0.31	0/2984	0.61	2/4021 (0.0%)
54	2Z	0.29	0/1010	0.61	0/1358
54	3D	0.27	0/816	0.58	0/1098
55	2a	0.34	0/2678	0.62	0/3598
55	2b	0.35	0/2678	0.65	1/3598 (0.0%)
55	2c	0.32	0/2678	0.58	0/3598
55	2d	0.32	0/2678	0.63	0/3598
56	2e	0.30	0/4031	0.62	0/5452
56	2f	0.32	0/4031	0.68	1/5452 (0.0%)
56	2g	0.30	0/4031	0.59	0/5452
56	2h	0.35	0/4031	0.70	4/5452 (0.1%)
57	2i	0.36	0/1427	0.84	3/1903 (0.2%)
57	2j	0.33	0/2382	0.73	0/3195
57	2k	0.37	0/1837	0.76	3/2464 (0.1%)
57	2l	0.36	0/1857	0.74	3/2491 (0.1%)
58	2m	0.31	0/4331	0.58	0/5898
58	2n	0.31	0/4331	0.62	3/5898 (0.1%)
58	2o	0.30	0/4331	0.57	0/5898
58	2p	0.42	0/4331	0.73	4/5898 (0.1%)
59	2q	0.36	0/3984	0.64	4/5442 (0.1%)
59	2r	0.30	0/3984	0.63	1/5442 (0.0%)
59	2s	0.33	0/3984	0.61	0/5442
59	2t	0.37	0/3775	0.72	4/5155 (0.1%)
60	2u	0.30	0/3387	0.58	1/4596 (0.0%)
61	2v	0.33	0/2450	0.61	2/3315 (0.1%)
61	2w	0.30	0/2450	0.59	0/3315
61	2x	0.31	0/2450	0.55	0/3315
61	2y	0.36	0/2450	0.63	2/3315 (0.1%)
62	2z	0.32	0/2514	0.56	0/3411
62	3a	0.31	0/2261	0.61	2/3075 (0.1%)
62	3b	0.31	0/2514	0.60	1/3411 (0.0%)
62	3c	0.37	0/2205	0.70	3/2997 (0.1%)
63	3A	0.26	0/1649	0.55	1/2228 (0.0%)
63	3B	0.54	0/2437	0.57	0/3297
63	3C	0.53	0/2437	0.56	0/3297
64	3E	0.31	0/983	0.52	0/1343
64	3F	0.30	0/799	0.51	0/1091
64	3G	0.31	0/983	0.52	0/1343
64	3H	0.32	0/799	0.54	0/1091
64	3I	0.31	0/983	0.52	0/1343
65	3J	0.48	1/5367 (0.0%)	0.79	14/7239 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
65	3K	0.40	0/4563	0.71	4/6153 (0.1%)
65	3L	0.42	0/804	0.80	0/1086
66	3M	0.29	0/2279	0.54	0/3083
66	3N	0.29	0/2279	0.59	1/3083 (0.0%)
66	3O	0.30	0/2279	0.56	0/3083
66	3P	0.29	0/2279	0.54	0/3083
66	3Q	0.29	0/2279	0.59	1/3083 (0.0%)
66	3R	0.30	0/2279	0.57	0/3083
66	3S	0.39	0/2279	0.66	0/3083
66	3T	0.29	0/2279	0.59	1/3083 (0.0%)
67	3U	0.29	0/1862	0.51	0/2526
67	3V	0.29	0/1862	0.51	0/2526
67	3W	0.29	0/1862	0.52	0/2526
67	3X	0.29	0/1862	0.51	0/2526
67	3Y	0.29	0/1862	0.51	0/2526
68	3Z	0.29	0/1572	0.55	0/2124
68	4A	0.28	0/1572	0.55	0/2124
68	4B	0.29	0/1572	0.56	0/2124
68	4C	0.31	0/1572	0.56	0/2124
68	4D	0.29	0/1572	0.55	0/2124
68	4E	0.30	0/1572	0.54	0/2124
68	4F	0.29	0/1572	0.55	0/2124
68	4G	0.28	0/1572	0.55	0/2124
68	4H	0.29	0/1572	0.56	0/2124
68	4I	0.45	1/1572 (0.1%)	0.73	4/2124 (0.2%)
68	4J	0.29	0/1572	0.55	0/2124
68	4K	0.39	0/1572	0.66	2/2124 (0.1%)
68	4L	0.31	0/1572	0.57	0/2124
68	4M	0.28	0/1572	0.55	0/2124
68	4N	0.29	0/1572	0.56	0/2124
69	3d	0.36	0/5518	0.68	3/7487 (0.0%)
69	3e	0.30	0/5518	0.60	0/7487
69	3f	0.31	0/5518	0.64	2/7487 (0.0%)
69	3g	0.34	1/5518 (0.0%)	0.62	0/7487
70	3h	0.33	0/2512	0.62	0/3394
70	3i	0.31	0/2512	0.60	0/3394
71	3j	0.27	0/3058	0.60	1/4138 (0.0%)
72	3k	0.28	0/2780	0.57	0/3780
73	3l	0.36	0/2404	0.67	2/3263 (0.1%)
73	3m	0.30	0/2299	0.64	0/3119
73	3o	0.31	0/2404	0.64	1/3263 (0.0%)
73	3p	0.30	0/2299	0.68	2/3119 (0.1%)
74	3q	0.29	0/1798	0.61	0/2436

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
74	3r	0.32	0/1798	0.68	0/2436
74	3s	0.31	0/1798	0.62	0/2436
74	3t	0.40	0/1798	0.77	2/2436 (0.1%)
75	3u	0.31	0/733	0.61	0/985
75	3v	0.29	0/733	0.56	0/985
75	3w	0.32	0/740	0.58	0/995
75	3x	0.32	0/733	0.56	0/985
75	3y	0.32	0/733	0.58	0/985
75	3z	0.32	0/733	0.63	0/985
75	4a	0.30	0/733	0.52	0/985
75	4b	0.36	0/733	0.64	0/985
75	4c	0.34	0/735	0.59	0/990
75	4d	0.31	0/735	0.53	0/990
75	4e	0.33	0/728	0.57	0/980
75	4f	0.34	0/728	0.52	0/980
75	4g	0.35	0/735	0.52	0/990
75	4h	0.33	0/735	0.52	0/990
75	4i	0.32	0/728	0.60	0/980
75	4j	0.33	0/728	0.56	0/980
75	4k	0.34	0/728	0.54	0/980
75	4l	0.36	0/728	0.62	0/980
75	4m	0.39	0/728	0.64	0/980
75	4n	0.53	0/728	0.74	0/980
75	5s	0.37	0/733	0.65	0/985
75	5t	0.28	0/746	0.56	0/1003
75	5u	0.34	0/705	0.67	1/949 (0.1%)
75	5v	0.40	0/725	0.72	1/974 (0.1%)
75	5w	0.28	0/754	0.54	0/1013
75	5x	0.32	0/754	0.58	0/1013
75	7k	0.31	0/746	0.67	0/1003
75	7n	0.33	0/705	0.72	1/949 (0.1%)
75	7o	0.30	0/725	0.59	0/974
75	7p	0.28	0/725	0.54	0/974
75	8k	0.30	0/746	0.66	0/1003
75	8n	0.33	0/705	0.65	1/949 (0.1%)
75	8o	0.35	0/725	0.64	1/974 (0.1%)
75	8p	0.32	0/725	0.69	1/974 (0.1%)
75	9k	0.30	0/746	0.64	0/1003
75	9n	0.33	0/705	0.69	1/949 (0.1%)
75	9o	0.32	0/725	0.62	0/974
75	9p	0.30	0/725	0.63	1/974 (0.1%)
76	4O	0.28	0/4752	0.58	1/6445 (0.0%)
76	4P	0.33	0/4809	0.67	5/6522 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	4Q	0.28	0/4809	0.58	2/6522 (0.0%)
76	4R	0.28	0/4752	0.58	1/6445 (0.0%)
76	4S	0.32	0/4809	0.66	3/6522 (0.0%)
76	4T	0.28	0/4809	0.58	2/6522 (0.0%)
76	4U	0.30	0/4752	0.62	1/6445 (0.0%)
77	4V	0.29	0/1903	0.58	1/2566 (0.0%)
77	4W	0.29	0/1903	0.54	0/2566
77	4X	0.29	0/1903	0.58	1/2566 (0.0%)
77	4Y	0.29	0/1903	0.54	0/2566
77	4Z	0.29	0/1903	0.58	1/2566 (0.0%)
78	4o	0.33	0/1847	0.60	0/2513
78	4p	0.31	0/1847	0.58	0/2513
79	4q	0.28	0/6628	0.58	0/9023
79	4r	0.29	0/6628	0.59	0/9023
80	4s	0.31	0/6306	0.61	2/8582 (0.0%)
80	4t	0.32	0/6306	0.63	3/8582 (0.0%)
81	4u	0.31	0/3991	0.63	1/5386 (0.0%)
81	4v	0.33	0/3991	0.66	2/5386 (0.0%)
82	4w	0.35	0/4215	0.69	3/5684 (0.1%)
83	4x	0.24	0/841	0.46	0/1151
84	4y	0.29	0/5414	0.61	0/7288
85	4z	0.30	0/4196	0.58	1/5668 (0.0%)
86	5A	0.52	1/1943 (0.1%)	0.83	3/2602 (0.1%)
86	5B	0.40	0/1943	0.72	2/2602 (0.1%)
87	5C	0.29	0/2276	0.56	1/3084 (0.0%)
87	5D	0.31	0/2243	0.60	2/3038 (0.1%)
87	5E	0.27	0/2243	0.55	0/3038
87	5F	0.29	0/2276	0.57	1/3084 (0.0%)
87	5G	0.31	0/2243	0.59	1/3038 (0.0%)
87	5H	0.27	0/2243	0.56	0/3038
87	5I	0.29	0/2276	0.56	1/3084 (0.0%)
87	5J	0.34	0/1405	0.61	1/1898 (0.1%)
88	5K	0.45	0/1314	0.71	2/1737 (0.1%)
88	5S	0.32	0/1376	0.59	0/1828
88	5T	0.56	0/3894	0.52	0/5170
88	5U	0.56	0/3894	0.52	0/5170
88	5V	0.36	0/2479	0.66	2/3301 (0.1%)
88	5W	0.55	0/4002	0.56	0/5320
88	5X	0.57	0/3268	0.56	0/4339
89	5L	0.30	0/1951	0.54	0/2639
89	5M	0.30	0/1951	0.54	0/2639
90	5N	0.31	0/1944	0.58	1/2631 (0.0%)
90	5O	0.28	0/1944	0.52	0/2631

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
90	5P	0.28	0/1944	0.52	0/2631
90	5Q	0.31	0/1944	0.58	0/2631
90	5R	0.31	0/1944	0.58	1/2631 (0.0%)
91	5Y	0.54	0/3460	0.60	1/4601 (0.0%)
91	5Z	0.59	0/3951	0.57	0/5258
91	6A	0.53	0/2262	0.56	0/3005
92	5a	0.35	0/1281	0.71	2/1726 (0.1%)
93	5b	0.36	0/1436	0.70	0/1918
94	5c	0.27	0/7291	0.56	0/9891
95	5d	0.28	0/10413	0.55	1/14150 (0.0%)
96	5e	0.42	0/1917	0.72	1/2568 (0.0%)
97	5f	0.34	0/2677	0.67	3/3587 (0.1%)
98	5g	0.28	0/3570	0.62	0/4836
99	5h	0.32	0/11494	0.62	6/15540 (0.0%)
99	5i	0.29	0/27334	0.60	2/36978 (0.0%)
100	5j	0.31	0/11128	0.61	4/15019 (0.0%)
100	5k	0.28	0/28204	0.57	9/38163 (0.0%)
101	5l	0.37	0/3481	0.67	1/4731 (0.0%)
102	5m	0.30	0/3882	0.62	1/5269 (0.0%)
103	5n	0.33	0/5346	0.67	3/7240 (0.0%)
104	5o	0.28	0/2661	0.58	0/3594
105	5p	0.25	0/947	0.58	0/1269
105	7i	0.27	0/947	0.64	0/1269
105	8i	0.29	0/947	0.68	0/1269
105	9i	0.27	0/947	0.62	0/1269
106	5q	0.26	0/795	0.59	0/1077
106	7l	0.31	0/795	0.65	0/1077
106	8l	0.30	0/795	0.63	0/1077
106	9l	0.30	0/795	0.64	0/1077
107	5r	0.28	0/766	0.65	0/1037
107	7m	0.27	0/766	0.62	0/1037
107	8m	0.28	0/766	0.62	0/1037
107	9m	0.30	0/766	0.61	0/1037
108	5y	0.26	0/842	0.54	0/1144
108	7q	0.30	0/842	0.55	0/1144
108	8q	0.29	0/842	0.58	0/1144
108	9q	0.31	0/842	0.60	0/1144
109	6B	0.28	0/796	0.57	0/1065
109	6C	0.54	0/2723	0.55	0/3628
109	6D	0.54	0/2723	0.54	0/3628
109	6E	0.31	0/709	0.61	0/943
109	6F	0.61	0/2930	0.57	0/3912
109	6G	0.53	0/2950	0.53	0/3938



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
109	6H	0.31	0/1553	0.60	0/2059
109	6I	0.32	0/1998	0.64	2/2669 (0.1%)
109	6J	0.72	0/2942	0.68	1/3927 (0.0%)
109	6K	0.73	0/2421	0.73	2/3224 (0.1%)
109	6L	0.30	0/1181	0.59	0/1590
109	6M	0.55	0/2950	0.59	0/3938
109	6N	0.55	0/2950	0.56	0/3938
109	6O	0.35	0/2167	0.65	0/2881
109	6P	0.40	0/2167	0.69	2/2881 (0.1%)
109	6Q	0.32	0/1421	0.64	0/1886
110	6R	0.28	0/1238	0.57	0/1686
110	6S	0.54	0/1872	0.63	1/2545 (0.0%)
110	6T	0.53	0/1457	0.61	2/1978 (0.1%)
110	6U	0.29	0/801	0.53	0/1091
110	6V	0.53	0/1904	0.57	0/2587
110	6W	0.53	0/1904	0.57	0/2587
110	6X	0.29	0/410	0.55	0/555
110	6Y	0.54	0/1874	0.60	0/2545
110	6Z	0.54	0/1874	0.61	0/2545
110	7A	0.41	0/911	0.65	0/1234
110	7B	0.29	0/1477	0.57	1/2011 (0.0%)
110	7C	0.54	0/1965	0.58	0/2671
110	7D	0.54	0/1466	0.59	0/1991
110	7E	0.32	0/865	0.57	1/1177 (0.1%)
110	7F	0.54	0/1869	0.59	0/2538
110	7G	0.53	0/1869	0.59	0/2538
110	7H	0.30	0/819	0.54	0/1108
110	7I	0.29	0/1942	0.52	0/2640
110	7J	0.29	0/1942	0.52	0/2640
110	7K	0.27	0/415	0.51	0/567
110	9Z	0.26	0/349	0.54	0/478
111	6a	0.28	0/33393	0.54	4/45239 (0.0%)
112	6b	0.31	0/33415	0.60	11/45256 (0.0%)
113	6c	0.29	0/32078	0.57	5/43456 (0.0%)
114	6d	0.26	0/32635	0.53	3/44198 (0.0%)
115	6e	0.27	0/33541	0.55	2/45416 (0.0%)
116	6f	0.30	0/2969	0.57	0/4015
116	6g	0.30	0/2960	0.60	0/4003
117	6h	0.30	0/3102	0.60	0/4204
118	6i	0.33	0/3290	0.66	4/4468 (0.1%)
119	6j	0.31	0/3111	0.60	1/4224 (0.0%)
120	6k	0.44	0/1395	0.74	1/1870 (0.1%)
120	6l	0.37	0/1791	0.68	2/2406 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
120	6m	0.33	0/1847	0.63	0/2482
121	6n	0.30	0/1639	0.69	1/2210 (0.0%)
122	6o	0.32	0/1993	0.62	1/2685 (0.0%)
123	6p	0.34	0/1387	0.68	0/1856
124	6q	0.29	0/2744	0.57	0/3715
125	6r	0.31	0/2956	0.63	0/3982
126	6s	0.29	0/2880	0.65	1/3891 (0.0%)
127	6t	0.29	0/1244	0.59	0/1681
128	6u	0.41	0/1223	1.32	2/1646 (0.1%)
129	7L	0.27	0/1329	0.53	0/1791
129	7M	0.27	0/1329	0.53	0/1791
130	7N	0.33	0/1370	0.60	0/1856
130	7O	0.32	0/1370	0.57	0/1856
130	7P	0.36	0/1370	0.62	1/1856 (0.1%)
131	7Q	0.29	0/1304	0.54	0/1756
131	7R	0.31	0/1304	0.57	0/1756
131	7S	0.29	0/1304	0.54	0/1756
132	7T	0.28	0/1329	0.54	0/1804
132	7U	0.53	0/2489	0.56	0/3372
132	8L	0.53	0/2003	0.56	0/2707
133	7V	0.29	0/1962	0.55	0/2639
133	7W	0.28	0/1948	0.59	1/2622 (0.0%)
133	7X	0.33	0/1884	0.64	0/2536
133	7Y	0.29	0/1962	0.55	0/2639
133	7Z	0.29	0/1948	0.60	1/2622 (0.0%)
133	8A	0.30	0/1884	0.61	0/2536
133	8B	0.29	0/1962	0.55	0/2639
133	8C	0.29	0/1948	0.59	1/2622 (0.0%)
134	7a	0.29	0/28099	0.57	4/38007 (0.0%)
134	7e	0.28	0/38074	0.57	8/51496 (0.0%)
134	8e	0.29	0/38074	0.58	8/51496 (0.0%)
134	9e	0.29	0/38074	0.57	5/51496 (0.0%)
135	7b	0.28	0/27552	0.57	6/37271 (0.0%)
135	7f	0.29	0/37575	0.58	8/50802 (0.0%)
135	8f	0.28	0/37575	0.58	9/50802 (0.0%)
135	9f	0.29	0/37575	0.59	15/50802 (0.0%)
136	7c	0.32	0/2856	0.69	1/3860 (0.0%)
136	8c	0.30	0/2856	0.71	1/3860 (0.0%)
136	9c	0.30	0/2856	0.69	2/3860 (0.1%)
137	7d	0.55	0/677	0.99	4/906 (0.4%)
137	8d	0.67	0/677	1.08	2/906 (0.2%)
137	9d	0.55	0/677	1.05	3/906 (0.3%)
138	7g	0.29	0/4346	0.62	2/5902 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
138	8g	0.30	0/4346	0.61	1/5902 (0.0%)
138	9g	0.29	0/4346	0.62	4/5902 (0.1%)
139	7h	0.28	0/4938	0.59	2/6692 (0.0%)
139	8h	0.29	0/4938	0.61	4/6692 (0.1%)
139	9h	0.28	0/4938	0.59	1/6692 (0.0%)
140	7j	0.34	0/877	0.67	1/1176 (0.1%)
140	8j	0.31	0/877	0.63	0/1176
140	9j	0.34	0/877	0.69	0/1176
141	7r	0.29	0/789	0.63	0/1068
141	8r	0.31	0/789	0.71	1/1068 (0.1%)
141	9r	0.30	0/789	0.66	2/1068 (0.2%)
142	7s	0.39	0/1334	0.73	2/1796 (0.1%)
142	8s	0.36	0/2698	0.73	4/3622 (0.1%)
142	9a	0.33	0/1519	0.76	1/2032 (0.0%)
142	9s	0.31	0/2853	0.67	1/3828 (0.0%)
143	7t	0.29	0/1457	0.61	0/1956
143	8t	0.35	0/2751	0.70	2/3689 (0.1%)
143	9b	0.38	0/1458	0.87	4/1954 (0.2%)
143	9t	0.33	0/2915	0.67	2/3910 (0.1%)
144	8D	0.39	0/2061	0.71	2/2778 (0.1%)
144	8E	0.29	0/1004	0.64	0/1344
144	8F	0.36	0/1977	0.67	0/2662
144	8G	0.31	0/2061	0.59	0/2778
144	8H	0.30	0/1004	0.64	0/1344
144	8I	0.29	0/1977	0.59	0/2662
144	8J	0.33	0/2061	0.62	0/2778
144	8K	0.29	0/1004	0.63	0/1344
145	8M	0.27	0/832	0.52	0/1109
145	8N	0.27	0/899	0.54	0/1199
145	8O	0.26	0/868	0.54	0/1157
145	8P	0.28	0/832	0.53	0/1109
145	8Q	0.27	0/899	0.53	0/1199
145	8R	0.25	0/868	0.54	0/1157
145	8S	0.28	0/832	0.53	0/1109
145	8T	0.28	0/899	0.54	0/1199
146	8U	0.26	0/328	0.68	0/437
146	8V	0.26	0/1071	0.50	0/1439
146	8W	0.26	0/328	0.64	0/437
146	8X	0.26	0/328	0.68	0/437
146	8Y	0.26	0/1071	0.49	0/1439
146	8Z	0.26	0/328	0.64	0/437
146	9A	0.27	0/328	0.68	0/437
146	9B	0.26	0/955	0.56	0/1281

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
147	9C	0.31	0/1686	0.54	0/2272
147	9D	0.31	0/1686	0.54	0/2272
147	9E	0.26	0/288	0.37	0/394
148	9F	0.40	0/230	0.54	0/310
148	9G	0.32	0/1252	0.52	0/1685
148	9H	0.53	0/1252	0.80	1/1685 (0.1%)
148	9I	0.28	0/817	0.52	0/1099
149	9J	0.32	0/1484	0.57	0/2015
149	9K	0.55	0/2344	0.64	2/3175 (0.1%)
149	9L	0.55	0/2141	0.61	0/2907
150	9M	0.26	0/1396	0.63	1/1865 (0.1%)
150	9N	0.25	0/1396	0.57	0/1865
150	9O	0.25	0/1389	0.55	0/1855
150	9P	0.27	0/1396	0.63	1/1865 (0.1%)
150	9Q	0.25	0/1396	0.57	0/1865
150	9R	0.25	0/1389	0.56	0/1855
150	9S	0.27	0/1396	0.63	1/1865 (0.1%)
151	9T	0.27	0/1205	0.59	1/1602 (0.1%)
151	9U	0.27	0/1205	0.58	1/1602 (0.1%)
151	9V	0.27	0/1104	0.59	1/1470 (0.1%)
152	9W	0.26	0/590	0.56	0/788
152	9X	0.27	0/590	0.56	0/788
152	9Y	0.27	0/590	0.56	0/788
153	AA	0.55	0/3443	0.66	2/4657 (0.0%)
153	AC	0.30	0/3443	0.60	1/4657 (0.0%)
153	AE	0.54	0/3443	0.63	0/4657
153	AG	0.58	0/3443	0.73	3/4657 (0.1%)
153	AI	0.55	0/3443	0.62	0/4657
153	AK	0.55	0/3443	0.63	0/4657
153	AM	0.55	0/3443	0.66	2/4657 (0.0%)
153	AO	0.30	0/3443	0.60	1/4657 (0.0%)
153	AQ	0.55	0/3443	0.62	0/4657
153	AS	0.58	0/3443	0.73	1/4657 (0.0%)
153	AU	0.55	0/3443	0.63	0/4657
153	AW	0.55	0/3443	0.63	0/4657
153	AY	0.56	0/3443	0.66	2/4657 (0.0%)
153	Aa	0.55	0/3443	0.64	0/4657
153	Ac	0.55	0/3443	0.64	1/4657 (0.0%)
153	Ae	0.58	0/3443	0.71	2/4657 (0.0%)
153	Ag	0.55	0/3443	0.64	0/4657
153	Ai	0.55	0/3443	0.63	0/4657
153	Ak	0.55	0/3443	0.62	0/4657
153	Am	0.55	0/3443	0.64	0/4657

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
153	Ao	0.55	0/3443	0.65	1/4657 (0.0%)
153	BA	0.55	0/3443	0.62	0/4657
153	BC	0.31	0/3443	0.62	2/4657 (0.0%)
153	BG	0.55	0/3443	0.65	1/4657 (0.0%)
153	BI	0.55	0/3443	0.64	0/4657
153	BK	0.57	0/3443	0.69	0/4657
153	BM	0.55	0/3443	0.64	0/4657
153	BO	0.33	0/3443	0.66	3/4657 (0.1%)
153	BQ	0.56	0/3443	0.65	1/4657 (0.0%)
153	BS	0.55	0/3443	0.64	1/4657 (0.0%)
153	BU	0.33	0/3443	0.64	1/4657 (0.0%)
153	BW	0.58	0/3443	0.73	2/4657 (0.0%)
153	BY	0.56	0/3443	0.65	0/4657
153	CA	0.56	0/3443	0.65	1/4657 (0.0%)
153	CC	0.56	0/3443	0.65	1/4657 (0.0%)
153	CE	0.55	0/3443	0.65	1/4657 (0.0%)
153	CH	0.55	0/3443	0.64	0/4657
153	CK	0.33	0/3443	0.66	4/4657 (0.1%)
153	CM	0.55	0/3443	0.64	0/4657
153	CO	0.56	0/3443	0.67	0/4657
153	CQ	0.55	0/3443	0.65	0/4657
153	CS	0.31	0/3443	0.62	4/4657 (0.1%)
153	CU	0.34	0/3443	0.68	2/4657 (0.0%)
153	CW	0.33	0/3443	0.66	4/4657 (0.1%)
153	CY	0.56	0/3443	0.66	0/4657
153	DA	0.58	0/3443	0.71	1/4657 (0.0%)
153	DC	0.56	0/3443	0.69	1/4657 (0.0%)
153	DE	0.55	0/3443	0.68	2/4657 (0.0%)
153	DG	0.55	0/3443	0.67	1/4657 (0.0%)
153	DI	0.55	0/3443	0.66	0/4657
153	DK	0.56	0/3443	0.65	0/4657
153	DN	0.34	0/3443	0.66	1/4657 (0.0%)
153	DP	0.55	0/3443	0.63	0/4657
153	DR	0.55	0/3443	0.65	0/4657
153	DT	0.32	0/3443	0.67	1/4657 (0.0%)
153	DV	0.31	0/3443	0.62	3/4657 (0.1%)
153	DX	0.55	0/3443	0.65	0/4657
153	DZ	0.56	0/3443	0.66	0/4657
153	EB	0.33	0/3443	0.63	2/4657 (0.0%)
153	ED	0.34	0/3443	0.65	2/4657 (0.0%)
153	EF	0.55	0/3443	0.66	0/4657
153	EH	0.57	0/3443	0.69	2/4657 (0.0%)
153	EJ	0.56	0/3443	0.65	0/4657

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
153	EL	0.56	0/3443	0.66	0/4657
153	EN	0.55	0/3443	0.63	0/4657
153	ER	0.33	0/3443	0.65	1/4657 (0.0%)
153	ET	0.33	0/3443	0.67	3/4657 (0.1%)
153	EV	0.55	0/3443	0.68	0/4657
153	EX	0.55	0/3443	0.66	1/4657 (0.0%)
153	EZ	0.55	0/3443	0.63	0/4657
153	FB	0.55	0/3443	0.67	0/4657
153	FD	0.55	0/3443	0.65	0/4657
153	FF	0.56	0/3443	0.67	2/4657 (0.0%)
153	FH	0.34	0/3443	0.70	2/4657 (0.0%)
153	FJ	0.55	0/3443	0.66	1/4657 (0.0%)
153	FL	0.56	0/3443	0.63	0/4657
153	FN	0.56	0/3443	0.70	1/4657 (0.0%)
153	FP	0.56	0/3443	0.65	0/4657
153	FR	0.56	0/3443	0.67	2/4657 (0.0%)
153	FT	0.55	0/3443	0.68	0/4657
153	FV	0.35	0/3443	0.66	1/4657 (0.0%)
153	FX	0.32	0/3443	0.66	5/4657 (0.1%)
153	FZ	0.32	0/3443	0.67	3/4657 (0.1%)
153	GB	0.57	0/3443	0.71	0/4657
153	GD	0.55	0/3443	0.64	0/4657
153	GF	0.55	0/3443	0.65	0/4657
153	GH	0.55	0/3443	0.66	0/4657
153	GJ	0.55	0/3443	0.66	0/4657
153	GL	0.55	0/3443	0.65	0/4657
153	GN	0.55	0/3443	0.63	0/4657
153	GP	0.55	0/3443	0.64	0/4657
153	GR	0.58	0/3443	0.73	3/4657 (0.1%)
153	GT	0.56	0/3443	0.66	0/4657
153	GV	0.55	0/3443	0.66	0/4657
153	GX	0.55	0/3443	0.66	0/4657
153	GZ	0.31	0/3443	0.64	1/4657 (0.0%)
153	HB	0.32	0/3443	0.62	0/4657
153	HD	0.32	0/3443	0.63	1/4657 (0.0%)
153	HF	0.57	0/3443	0.66	1/4657 (0.0%)
153	HH	0.56	0/3443	0.63	0/4657
153	HJ	0.56	0/3443	0.62	0/4657
153	HL	0.31	0/3443	0.64	1/4657 (0.0%)
153	HN	0.55	0/3443	0.63	0/4657
153	HP	0.55	0/3443	0.63	1/4657 (0.0%)
153	HR	0.56	0/3443	0.63	0/4657
153	HT	0.56	0/3443	0.66	1/4657 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
153	HV	0.56	0/3443	0.62	0/4657
153	HX	0.55	0/3443	0.64	0/4657
153	HZ	0.55	0/3443	0.63	0/4657
153	IB	0.55	0/3443	0.63	1/4657 (0.0%)
153	ID	0.34	0/3443	0.65	3/4657 (0.1%)
153	IF	0.32	0/3443	0.66	2/4657 (0.0%)
153	IH	0.32	0/3443	0.62	2/4657 (0.0%)
153	IJ	0.56	0/3443	0.69	1/4657 (0.0%)
153	IL	0.33	0/3443	0.63	2/4657 (0.0%)
153	IN	0.32	0/3443	0.65	1/4657 (0.0%)
153	IP	0.35	0/3443	0.66	4/4657 (0.1%)
153	IR	0.56	0/3443	0.69	1/4657 (0.0%)
153	IT	0.32	0/3443	0.62	2/4657 (0.0%)
153	IV	0.38	0/3443	0.68	1/4657 (0.0%)
153	IX	0.56	0/3443	0.65	2/4657 (0.0%)
153	IZ	0.55	0/3443	0.69	3/4657 (0.1%)
153	JB	0.56	0/3443	0.69	1/4657 (0.0%)
153	JD	0.57	0/3443	0.69	2/4657 (0.0%)
153	JF	0.55	0/3443	0.63	0/4657
153	JG	0.32	0/3443	0.63	2/4657 (0.0%)
153	JI	0.34	0/3443	0.63	1/4657 (0.0%)
153	JK	0.33	0/3443	0.60	0/4657
153	JM	0.55	0/3443	0.67	1/4657 (0.0%)
153	JO	0.56	0/3443	0.62	0/4657
153	JQ	0.58	0/3443	0.72	2/4657 (0.0%)
153	JS	0.32	0/3443	0.64	2/4657 (0.0%)
153	JU	0.56	0/3443	0.64	0/4657
153	JW	0.32	0/3443	0.60	0/4657
153	JY	0.33	0/3443	0.62	0/4657
153	KA	0.56	0/3443	0.62	0/4657
153	KC	0.55	0/3443	0.65	0/4657
153	KE	0.55	0/3443	0.64	1/4657 (0.0%)
153	KG	0.57	0/3443	0.66	1/4657 (0.0%)
153	KI	0.55	0/3443	0.62	0/4657
153	KK	0.55	0/3443	0.61	0/4657
153	KM	0.55	0/3443	0.64	0/4657
153	KO	0.55	0/3443	0.66	2/4657 (0.0%)
153	KQ	0.56	0/3443	0.67	2/4657 (0.0%)
153	KS	0.55	0/3443	0.63	0/4657
153	KU	0.55	0/3443	0.63	0/4657
153	KW	0.55	0/3443	0.61	0/4657
153	KY	0.55	0/3443	0.64	1/4657 (0.0%)
153	LA	0.54	0/3443	0.62	0/4657

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
153	LC	0.56	0/3443	0.68	1/4657 (0.0%)
153	LE	0.56	0/3443	0.66	1/4657 (0.0%)
153	LG	0.55	0/3443	0.64	0/4657
153	LI	0.55	0/3443	0.61	0/4657
153	LK	0.55	0/3443	0.64	0/4657
153	LM	0.54	0/3443	0.62	0/4657
153	LO	0.54	0/3443	0.59	0/4657
153	LQ	0.55	0/3443	0.61	0/4657
153	LS	0.55	0/3443	0.59	0/4657
153	LU	0.57	0/3443	0.66	1/4657 (0.0%)
153	LW	0.55	0/3443	0.64	0/4657
153	LY	0.54	0/3443	0.62	0/4657
153	MA	0.54	0/3443	0.59	0/4657
153	MC	0.55	0/3443	0.61	0/4657
153	ME	0.54	0/3443	0.58	0/4657
153	MG	0.56	0/3443	0.66	0/4657
153	MI	0.54	0/3443	0.62	0/4657
153	MK	0.55	0/3443	0.62	1/4657 (0.0%)
153	MM	0.54	0/3443	0.59	0/4657
153	MO	0.55	0/3443	0.61	0/4657
153	MQ	0.31	0/3443	0.57	0/4657
153	MU	0.55	0/3443	0.63	0/4657
153	MW	0.55	0/3443	0.64	0/4657
153	MY	0.55	0/3443	0.62	0/4657
153	NA	0.56	0/3443	0.62	0/4657
153	NC	0.55	0/3443	0.61	0/4657
153	NE	0.54	0/3443	0.60	0/4657
153	NG	0.55	0/3443	0.63	0/4657
153	NI	0.55	0/3443	0.64	0/4657
153	NK	0.54	0/3443	0.62	0/4657
153	NM	0.56	0/3443	0.63	0/4657
153	NO	0.55	0/3443	0.61	0/4657
153	NQ	0.54	0/3443	0.60	0/4657
153	NS	0.55	0/3443	0.63	0/4657
153	NU	0.55	0/3443	0.64	0/4657
153	NY	0.55	0/3443	0.63	0/4657
153	OA	0.55	0/3443	0.64	0/4657
153	OC	0.55	0/3443	0.65	0/4657
153	OE	0.56	0/3443	0.67	0/4657
153	OG	0.55	0/3443	0.61	0/4657
153	OI	0.55	0/3443	0.64	0/4657
153	OK	0.54	0/3443	0.63	0/4657
153	OM	0.55	0/3443	0.64	0/4657



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
153	OO	0.55	0/3443	0.64	0/4657
153	OQ	0.55	0/3443	0.62	0/4657
153	OS	0.55	0/3443	0.62	0/4657
153	OU	0.55	0/3443	0.65	0/4657
153	OW	0.54	0/3443	0.63	0/4657
153	OY	0.55	0/3443	0.64	0/4657
153	PA	0.55	0/3443	0.65	0/4657
153	PD	0.55	0/3443	0.65	0/4657
153	PF	0.55	0/3443	0.67	0/4657
153	PH	0.55	0/3443	0.70	5/4657 (0.1%)
153	PJ	0.55	0/3443	0.62	0/4657
153	PL	0.55	0/3443	0.66	1/4657 (0.0%)
153	PN	0.55	0/3443	0.68	4/4657 (0.1%)
153	PP	0.54	0/3443	0.65	0/4657
153	PR	0.55	0/3443	0.67	0/4657
153	PT	0.55	0/3443	0.70	5/4657 (0.1%)
153	PV	0.55	0/3443	0.63	0/4657
153	PX	0.55	0/3443	0.66	2/4657 (0.0%)
153	PZ	0.55	0/3443	0.68	4/4657 (0.1%)
153	QB	0.55	0/3443	0.65	0/4657
153	QD	0.55	0/3443	0.67	0/4657
153	QF	0.55	0/3443	0.66	2/4657 (0.0%)
153	QH	0.55	0/3443	0.65	0/4657
153	QJ	0.55	0/3443	0.67	0/4657
153	QL	0.58	0/3443	0.70	1/4657 (0.0%)
153	QN	0.56	0/3443	0.65	0/4657
153	QP	0.55	0/3443	0.63	1/4657 (0.0%)
153	QR	0.55	0/3443	0.66	2/4657 (0.0%)
153	QT	0.55	0/3443	0.65	0/4657
153	QV	0.55	0/3443	0.66	0/4657
153	QX	0.55	0/3443	0.66	0/4657
153	QZ	0.56	0/3443	0.67	0/4657
153	RB	0.55	0/3443	0.64	1/4657 (0.0%)
153	RD	0.55	0/3443	0.66	2/4657 (0.0%)
153	RF	0.55	0/3443	0.65	0/4657
153	RH	0.55	0/3443	0.66	0/4657
153	RJ	0.55	0/3443	0.66	0/4657
153	RL	0.55	0/3443	0.66	0/4657
153	RN	0.55	0/3443	0.64	0/4657
153	RP	0.55	0/3443	0.67	1/4657 (0.0%)
153	RR	0.55	0/3443	0.66	2/4657 (0.0%)
153	RT	0.55	0/3443	0.65	0/4657
153	RV	0.55	0/3443	0.67	0/4657

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
153	RX	0.55	0/3443	0.66	0/4657
153	RZ	0.55	0/3443	0.63	0/4657
153	SB	0.55	0/3443	0.70	3/4657 (0.1%)
153	SD	0.55	0/3443	0.67	2/4657 (0.0%)
153	SF	0.55	0/3443	0.65	0/4657
153	SH	0.55	0/3443	0.66	0/4657
153	SJ	0.55	0/3443	0.66	0/4657
153	SL	0.55	0/3443	0.64	0/4657
153	SN	0.56	0/3443	0.67	0/4657
153	SP	0.55	0/3443	0.67	1/4657 (0.0%)
153	SR	0.55	0/3443	0.65	0/4657
153	ST	0.55	0/3443	0.71	2/4657 (0.0%)
153	SV	0.55	0/3443	0.63	0/4657
153	SX	0.55	0/3443	0.63	0/4657
153	SZ	0.55	0/3443	0.67	0/4657
153	TB	0.55	0/3443	0.64	0/4657
153	TD	0.56	0/3443	0.65	0/4657
153	TF	0.55	0/3443	0.67	0/4657
153	TH	0.55	0/3443	0.67	1/4657 (0.0%)
153	TJ	0.55	0/3443	0.63	0/4657
153	TL	0.56	0/3443	0.67	0/4657
153	TN	0.55	0/3443	0.64	0/4657
153	TP	0.56	0/3443	0.73	2/4657 (0.0%)
153	TS	0.55	0/3443	0.64	1/4657 (0.0%)
153	TU	0.55	0/3443	0.65	0/4657
153	TW	0.56	0/3443	0.69	2/4657 (0.0%)
153	TY	0.56	0/3443	0.73	2/4657 (0.0%)
153	UA	0.55	0/3443	0.67	0/4657
153	UC	0.55	0/3443	0.62	0/4657
153	UE	0.54	0/3443	0.64	1/4657 (0.0%)
153	UG	0.55	0/3443	0.65	0/4657
153	UI	0.57	0/3443	0.68	3/4657 (0.1%)
153	UK	0.56	0/3443	0.69	0/4657
153	UM	0.55	0/3443	0.68	0/4657
153	UO	0.55	0/3443	0.62	0/4657
153	UQ	0.55	0/3443	0.64	1/4657 (0.0%)
153	US	0.55	0/3443	0.65	0/4657
153	UU	0.56	0/3443	0.68	3/4657 (0.1%)
153	UX	0.56	0/3443	0.68	0/4657
153	UZ	0.55	0/3443	0.65	0/4657
153	VB	0.56	0/3443	0.69	0/4657
153	VD	0.57	0/3443	0.77	3/4657 (0.1%)
153	VF	0.55	0/3443	0.65	0/4657

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
153	VH	0.54	0/3443	0.65	0/4657
153	VJ	0.55	0/3443	0.68	0/4657
153	VL	0.55	0/3443	0.64	0/4657
153	VN	0.55	0/3443	0.68	0/4657
153	VP	0.56	0/3443	0.77	5/4657 (0.1%)
153	VR	0.55	0/3443	0.66	0/4657
153	VT	0.55	0/3443	0.65	0/4657
153	VV	0.55	0/3443	0.68	0/4657
153	VX	0.55	0/3443	0.65	0/4657
153	VZ	0.55	0/3443	0.68	0/4657
153	WB	0.55	0/3443	0.66	0/4657
153	WD	0.31	0/3443	0.64	0/4657
153	WF	0.32	0/3443	0.62	0/4657
153	WH	0.57	0/3443	0.77	4/4657 (0.1%)
153	WJ	0.55	0/3443	0.66	1/4657 (0.0%)
153	WL	0.31	0/3443	0.65	0/4657
153	WN	0.54	0/3443	0.66	0/4657
153	WP	0.55	0/3443	0.65	0/4657
153	WR	0.55	0/3443	0.63	0/4657
153	WT	0.55	0/3443	0.74	2/4657 (0.0%)
153	WV	0.56	0/3443	0.71	2/4657 (0.0%)
153	WX	0.31	0/3443	0.65	0/4657
153	WZ	0.55	0/3443	0.66	0/4657
153	XB	0.57	0/3443	0.72	2/4657 (0.0%)
153	XD	0.55	0/3443	0.63	0/4657
153	XF	0.32	0/3443	0.64	1/4657 (0.0%)
153	XH	0.56	0/3443	0.67	0/4657
153	XJ	0.56	0/3443	0.72	2/4657 (0.0%)
153	XL	0.55	0/3443	0.64	0/4657
153	XN	0.55	0/3443	0.65	0/4657
153	XP	0.55	0/3443	0.64	0/4657
153	XR	0.55	0/3443	0.65	0/4657
153	XT	0.55	0/3443	0.65	0/4657
153	XV	0.55	0/3443	0.67	0/4657
153	XX	0.55	0/3443	0.64	0/4657
153	XZ	0.55	0/3443	0.65	0/4657
153	YB	0.55	0/3443	0.64	0/4657
153	YD	0.55	0/3443	0.65	0/4657
153	YF	0.56	0/3443	0.65	0/4657
153	YH	0.55	0/3443	0.67	0/4657
153	YK	0.55	0/3443	0.61	0/4657
153	YM	0.57	0/3443	0.68	2/4657 (0.0%)
153	YO	0.55	0/3443	0.66	0/4657

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
153	YQ	0.54	0/3443	0.63	0/4657
153	YS	0.55	0/3443	0.63	0/4657
153	YU	0.54	0/3443	0.63	0/4657
153	YW	0.55	0/3443	0.65	0/4657
153	YY	0.55	0/3443	0.63	0/4657
153	ZA	0.56	0/3443	0.71	2/4657 (0.0%)
153	ZC	0.54	0/3443	0.63	0/4657
153	ZE	0.55	0/3443	0.63	0/4657
153	ZG	0.55	0/3443	0.63	0/4657
153	ZI	0.55	0/3443	0.61	0/4657
153	ZK	0.55	0/3443	0.64	0/4657
153	ZM	0.55	0/3443	0.62	0/4657
153	ZO	0.55	0/3443	0.64	0/4657
153	ZQ	0.55	0/3443	0.65	1/4657 (0.0%)
153	ZS	0.56	0/3443	0.67	1/4657 (0.0%)
153	ZU	0.55	0/3443	0.63	0/4657
153	ZW	0.55	0/3443	0.63	0/4657
153	ZY	0.55	0/3443	0.62	0/4657
154	AB	0.34	0/3494	0.61	0/4744
154	AD	0.32	0/3494	0.61	0/4744
154	AF	0.55	0/3494	0.63	0/4744
154	AH	0.57	0/3494	0.66	0/4744
154	AJ	0.56	0/3494	0.63	0/4744
154	AL	0.56	0/3494	0.64	0/4744
154	AN	0.56	0/3494	0.62	0/4744
154	AP	0.55	0/3494	0.63	0/4744
154	AR	0.56	0/3494	0.62	0/4744
154	AT	0.57	0/3494	0.67	0/4744
154	AV	0.56	0/3494	0.63	0/4744
154	AX	0.56	0/3494	0.64	0/4744
154	AZ	0.56	0/3494	0.63	0/4744
154	Ab	0.55	0/3494	0.62	0/4744
154	Ad	0.32	0/3494	0.62	1/4744 (0.0%)
154	Af	0.55	0/3494	0.66	0/4744
154	Ah	0.55	0/3494	0.63	0/4744
154	Aj	0.56	0/3494	0.63	0/4744
154	Al	0.56	0/3494	0.67	1/4744 (0.0%)
154	An	0.55	0/3494	0.63	0/4744
154	Ap	0.55	0/3494	0.63	0/4744
154	BB	0.56	0/3494	0.63	0/4744
154	BD	0.56	0/3494	0.63	0/4744
154	BF	0.34	0/3494	0.66	1/4744 (0.0%)
154	BH	0.33	0/3494	0.66	2/4744 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
154	BJ	0.56	0/3494	0.63	0/4744
154	BL	0.57	0/3494	0.68	0/4744
154	BN	0.34	0/3494	0.65	0/4744
154	BP	0.56	0/3494	0.64	0/4744
154	BR	0.34	0/3494	0.66	1/4744 (0.0%)
154	BT	0.56	0/3494	0.65	0/4744
154	BV	0.55	0/3494	0.63	0/4744
154	BX	0.57	0/3494	0.69	0/4744
154	BZ	0.56	0/3494	0.66	0/4744
154	CB	0.57	0/3494	0.65	0/4744
154	CD	0.56	0/3494	0.65	0/4744
154	CF	0.56	0/3494	0.65	0/4744
154	CI	0.56	0/3494	0.63	0/4744
154	CJ	0.56	0/3494	0.64	0/4744
154	CL	0.34	0/3494	0.62	0/4744
154	CN	0.56	0/3494	0.67	0/4744
154	CP	0.56	0/3494	0.64	0/4744
154	CR	0.55	0/3494	0.62	0/4744
154	CT	0.33	0/3494	0.66	3/4744 (0.1%)
154	CV	0.33	0/3494	0.62	0/4744
154	CX	0.34	0/3494	0.62	0/4744
154	CZ	0.56	0/3494	0.67	0/4744
154	DB	0.57	0/3494	0.67	0/4744
154	DD	0.55	0/3494	0.63	0/4744
154	DF	0.56	0/3494	0.66	0/4744
154	DH	0.56	0/3494	0.64	0/4744
154	DJ	0.56	0/3494	0.64	0/4744
154	DL	0.56	0/3494	0.67	0/4744
154	DM	0.56	0/3494	0.64	0/4744
154	DO	0.35	0/3494	0.63	1/4744 (0.0%)
154	DQ	0.56	0/3494	0.65	0/4744
154	DS	0.32	0/3494	0.63	0/4744
154	DU	0.32	0/3494	0.63	1/4744 (0.0%)
154	DW	0.33	0/3494	0.60	0/4744
154	DY	0.56	0/3494	0.64	0/4744
154	EA	0.56	0/3494	0.65	0/4744
154	EC	0.37	0/3494	0.64	1/4744 (0.0%)
154	EE	0.56	0/3494	0.66	0/4744
154	EG	0.55	0/3494	0.65	0/4744
154	EI	0.56	0/3494	0.62	0/4744
154	EK	0.55	0/3494	0.64	0/4744
154	EM	0.56	0/3494	0.65	0/4744
154	EO	0.56	0/3494	0.65	0/4744

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
154	EQ	0.56	0/3494	0.65	0/4744
154	ES	0.32	0/3494	0.63	1/4744 (0.0%)
154	EU	0.55	0/3494	0.65	0/4744
154	EW	0.56	0/3494	0.70	0/4744
154	EY	0.55	0/3494	0.64	0/4744
154	FA	0.55	0/3494	0.63	0/4744
154	FC	0.56	0/3494	0.67	0/4744
154	FE	0.55	0/3494	0.65	1/4744 (0.0%)
154	FG	0.37	0/3494	0.66	1/4744 (0.0%)
154	FI	0.37	0/3494	0.71	3/4744 (0.1%)
154	FK	0.55	0/3494	0.64	0/4744
154	FM	0.57	0/3494	0.67	0/4744
154	FO	0.56	0/3494	0.65	0/4744
154	FQ	0.56	0/3494	0.65	1/4744 (0.0%)
154	FS	0.55	0/3494	0.65	0/4744
154	FW	0.31	0/3494	0.64	0/4744
154	FY	0.33	0/3494	0.63	1/4744 (0.0%)
154	GA	0.36	0/3494	0.66	1/4744 (0.0%)
154	GC	0.56	0/3494	0.64	0/4744
154	GE	0.55	0/3494	0.63	0/4744
154	GG	0.55	0/3494	0.64	0/4744
154	GI	0.55	0/3494	0.64	0/4744
154	GK	0.55	0/3494	0.65	0/4744
154	GM	0.55	0/3494	0.63	0/4744
154	GO	0.56	0/3494	0.64	1/4744 (0.0%)
154	GQ	0.55	0/3494	0.64	0/4744
154	GS	0.57	0/3494	0.66	0/4744
154	GU	0.55	0/3494	0.64	0/4744
154	GW	0.56	0/3494	0.65	0/4744
154	HA	0.34	0/3494	0.65	3/4744 (0.1%)
154	HC	0.35	0/3494	0.62	1/4744 (0.0%)
154	HE	0.38	0/3494	0.68	3/4744 (0.1%)
154	HG	0.56	0/3494	0.63	0/4744
154	HI	0.55	0/3494	0.63	0/4744
154	HK	0.55	0/3494	0.62	0/4744
154	HM	0.56	0/3494	0.65	0/4744
154	HO	0.56	0/3494	0.62	0/4744
154	HQ	0.55	0/3494	0.64	2/4744 (0.0%)
154	HS	0.56	0/3494	0.64	1/4744 (0.0%)
154	HU	0.55	0/3494	0.63	0/4744
154	HW	0.55	0/3494	0.62	0/4744
154	HY	0.56	0/3494	0.65	0/4744
154	IA	0.58	1/3494 (0.0%)	0.65	1/4744 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
154	IE	0.32	0/3494	0.61	1/4744 (0.0%)
154	IG	0.33	0/3494	0.64	2/4744 (0.0%)
154	II	0.37	0/3494	0.66	2/4744 (0.0%)
154	IK	0.33	0/3494	0.62	0/4744
154	IM	0.56	0/3494	0.64	0/4744
154	IO	0.38	0/3494	0.71	8/4744 (0.2%)
154	IQ	0.35	0/3494	0.65	2/4744 (0.0%)
154	IS	0.55	0/3494	0.66	0/4744
154	IU	0.33	0/3494	0.60	1/4744 (0.0%)
154	IW	0.56	0/3494	0.66	0/4744
154	IY	0.57	0/3494	0.65	0/4744
154	JA	0.58	0/3494	0.69	3/4744 (0.1%)
154	JC	0.56	0/3494	0.63	0/4744
154	JE	0.56	0/3494	0.64	0/4744
154	JH	0.33	0/3494	0.60	1/4744 (0.0%)
154	JJ	0.32	0/3494	0.60	0/4744
154	JL	0.34	0/3494	0.61	0/4744
154	JN	0.56	0/3494	0.62	0/4744
154	JP	0.34	0/3494	0.60	1/4744 (0.0%)
154	JR	0.33	0/3494	0.61	1/4744 (0.0%)
154	JT	0.57	0/3494	0.65	1/4744 (0.0%)
154	JV	0.33	0/3494	0.62	0/4744
154	JX	0.31	0/3494	0.58	0/4744
154	JZ	0.55	0/3494	0.62	0/4744
154	KB	0.56	0/3494	0.61	0/4744
154	KD	0.60	2/3494 (0.1%)	0.66	3/4744 (0.1%)
154	KF	0.56	0/3494	0.62	0/4744
154	KH	0.56	0/3494	0.62	0/4744
154	KJ	0.55	0/3494	0.61	0/4744
154	KL	0.55	0/3494	0.63	0/4744
154	KN	0.55	0/3494	0.64	0/4744
154	KP	0.55	0/3494	0.63	0/4744
154	KR	0.56	0/3494	0.67	0/4744
154	KT	0.56	0/3494	0.64	0/4744
154	KV	0.55	0/3494	0.62	0/4744
154	KX	0.56	0/3494	0.63	0/4744
154	KZ	0.32	0/3494	0.63	2/4744 (0.0%)
154	LB	0.57	0/3494	0.68	2/4744 (0.0%)
154	LD	0.56	0/3494	0.66	1/4744 (0.0%)
154	LF	0.57	1/3494 (0.0%)	0.64	0/4744
154	LH	0.55	0/3494	0.63	0/4744
154	LJ	0.55	0/3494	0.63	0/4744
154	LL	0.55	0/3494	0.64	0/4744

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
154	LN	0.55	0/3494	0.63	0/4744
154	LP	0.55	0/3494	0.61	0/4744
154	LR	0.57	0/3494	0.68	3/4744 (0.1%)
154	LT	0.55	0/3494	0.60	0/4744
154	LV	0.57	0/3494	0.72	2/4744 (0.0%)
154	LX	0.55	0/3494	0.61	0/4744
154	LZ	0.55	0/3494	0.62	0/4744
154	MB	0.55	0/3494	0.61	0/4744
154	MD	0.56	0/3494	0.64	0/4744
154	MF	0.55	0/3494	0.60	0/4744
154	MH	0.56	0/3494	0.64	0/4744
154	MJ	0.55	0/3494	0.65	1/4744 (0.0%)
154	ML	0.56	0/3494	0.63	0/4744
154	MN	0.55	0/3494	0.61	0/4744
154	MP	0.57	0/3494	0.68	3/4744 (0.1%)
154	MR	0.55	0/3494	0.60	0/4744
154	MT	0.56	0/3494	0.63	0/4744
154	MV	0.56	0/3494	0.62	0/4744
154	MX	0.55	0/3494	0.62	0/4744
154	MZ	0.55	0/3494	0.63	0/4744
154	NB	0.55	0/3494	0.61	0/4744
154	ND	0.55	0/3494	0.61	0/4744
154	NF	0.55	0/3494	0.63	0/4744
154	NH	0.56	0/3494	0.62	0/4744
154	NJ	0.55	0/3494	0.61	0/4744
154	NL	0.57	0/3494	0.66	2/4744 (0.0%)
154	NN	0.55	0/3494	0.61	0/4744
154	NP	0.55	0/3494	0.62	0/4744
154	NR	0.55	0/3494	0.63	0/4744
154	NT	0.57	0/3494	0.66	0/4744
154	NV	0.55	0/3494	0.62	0/4744
154	NX	0.55	0/3494	0.62	0/4744
154	NZ	0.56	0/3494	0.62	0/4744
154	OB	0.55	0/3494	0.62	0/4744
154	OD	0.58	0/3494	0.68	0/4744
154	OF	0.55	0/3494	0.61	0/4744
154	OH	0.55	0/3494	0.63	0/4744
154	OJ	0.55	0/3494	0.62	0/4744
154	OL	0.56	0/3494	0.61	0/4744
154	ON	0.56	0/3494	0.64	2/4744 (0.0%)
154	OP	0.55	0/3494	0.64	0/4744
154	OR	0.55	0/3494	0.62	0/4744
154	OT	0.56	0/3494	0.63	0/4744



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
154	OV	0.55	0/3494	0.63	0/4744
154	OX	0.56	0/3494	0.62	0/4744
154	OZ	0.55	0/3494	0.62	0/4744
154	PC	0.33	0/3494	0.65	0/4744
154	PE	0.56	0/3494	0.67	0/4744
154	PG	0.55	0/3494	0.64	0/4744
154	PI	0.57	0/3494	0.72	4/4744 (0.1%)
154	PK	0.56	0/3494	0.63	0/4744
154	PM	0.56	0/3494	0.65	0/4744
154	PO	0.55	0/3494	0.65	0/4744
154	PQ	0.56	0/3494	0.66	0/4744
154	PS	0.56	0/3494	0.68	1/4744 (0.0%)
154	PU	0.56	0/3494	0.64	0/4744
154	PW	0.55	0/3494	0.64	0/4744
154	PY	0.56	0/3494	0.65	0/4744
154	QA	0.56	0/3494	0.65	0/4744
154	QC	0.56	0/3494	0.67	0/4744
154	QE	0.55	0/3494	0.64	0/4744
154	QG	0.56	0/3494	0.65	0/4744
154	QI	0.35	0/3494	0.64	0/4744
154	QK	0.56	0/3494	0.68	0/4744
154	QM	0.56	0/3494	0.68	0/4744
154	QO	0.56	0/3494	0.63	0/4744
154	QQ	0.55	0/3494	0.67	0/4744
154	QS	0.56	0/3494	0.65	0/4744
154	QU	0.56	0/3494	0.64	0/4744
154	QW	0.56	0/3494	0.68	0/4744
154	QY	0.56	0/3494	0.68	1/4744 (0.0%)
154	RA	0.56	0/3494	0.64	0/4744
154	RC	0.56	0/3494	0.67	0/4744
154	RE	0.56	0/3494	0.66	0/4744
154	RG	0.56	0/3494	0.65	0/4744
154	RI	0.56	0/3494	0.68	0/4744
154	RK	0.56	0/3494	0.66	0/4744
154	RM	0.56	0/3494	0.64	0/4744
154	RO	0.56	0/3494	0.67	0/4744
154	RQ	0.56	0/3494	0.64	0/4744
154	RS	0.56	0/3494	0.67	1/4744 (0.0%)
154	RU	0.56	0/3494	0.65	0/4744
154	RW	0.56	0/3494	0.66	0/4744
154	RY	0.56	0/3494	0.63	0/4744
154	SA	0.58	0/3494	0.71	0/4744
154	SC	0.56	0/3494	0.66	0/4744

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
154	SE	0.56	0/3494	0.67	2/4744 (0.0%)
154	SG	0.56	0/3494	0.64	0/4744
154	SI	0.56	0/3494	0.66	0/4744
154	SK	0.56	0/3494	0.64	0/4744
154	SM	0.56	0/3494	0.67	0/4744
154	SO	0.57	0/3494	0.67	0/4744
154	SQ	0.56	0/3494	0.66	0/4744
154	SS	0.58	0/3494	0.75	5/4744 (0.1%)
154	SU	0.56	0/3494	0.70	2/4744 (0.0%)
154	SW	0.55	1/3494 (0.0%)	0.65	0/4744
154	SY	0.56	0/3494	0.64	0/4744
154	TA	0.56	0/3494	0.65	0/4744
154	TC	0.56	0/3494	0.66	1/4744 (0.0%)
154	TE	0.56	0/3494	0.65	0/4744
154	TG	0.57	0/3494	0.70	1/4744 (0.0%)
154	TI	0.55	0/3494	0.66	1/4744 (0.0%)
154	TK	0.56	0/3494	0.64	0/4744
154	TM	0.56	0/3494	0.65	0/4744
154	TO	0.56	0/3494	0.66	0/4744
154	TQ	0.56	0/3494	0.65	0/4744
154	TR	0.56	0/3494	0.66	0/4744
154	TT	0.56	0/3494	0.65	0/4744
154	TV	0.55	0/3494	0.65	0/4744
154	TX	0.58	0/3494	0.76	3/4744 (0.1%)
154	TZ	0.56	0/3494	0.66	0/4744
154	UB	0.56	0/3494	0.65	0/4744
154	UD	0.55	0/3494	0.66	0/4744
154	UF	0.56	0/3494	0.65	0/4744
154	UH	0.55	0/3494	0.64	0/4744
154	UJ	0.57	0/3494	0.71	2/4744 (0.0%)
154	UL	0.56	0/3494	0.68	0/4744
154	UN	0.56	0/3494	0.65	0/4744
154	UP	0.55	0/3494	0.65	0/4744
154	UR	0.56	0/3494	0.66	0/4744
154	UT	0.55	0/3494	0.65	0/4744
154	UW	0.55	0/3494	0.66	0/4744
154	UY	0.55	0/3494	0.67	0/4744
154	VA	0.55	0/3494	0.64	0/4744
154	VC	0.59	0/3494	0.80	5/4744 (0.1%)
154	VE	0.56	0/3494	0.64	0/4744
154	VG	0.56	0/3494	0.64	0/4744
154	VI	0.55	0/3494	0.66	0/4744
154	VK	0.55	0/3494	0.67	0/4744

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
154	VM	0.55	0/3494	0.63	0/4744
154	VO	0.57	0/3494	0.71	2/4744 (0.0%)
154	VQ	0.55	0/3494	0.65	0/4744
154	VS	0.56	0/3494	0.65	0/4744
154	VU	0.55	0/3494	0.66	0/4744
154	VW	0.55	0/3494	0.67	0/4744
154	VY	0.55	0/3494	0.63	0/4744
154	WA	0.35	0/3494	0.66	1/4744 (0.0%)
154	WC	0.56	0/3494	0.65	0/4744
154	WE	0.34	0/3494	0.63	0/4744
154	WG	0.43	0/3494	0.73	6/4744 (0.1%)
154	WI	0.56	0/3494	0.64	0/4744
154	WK	0.56	0/3494	0.65	0/4744
154	WM	0.56	0/3494	0.67	0/4744
154	WO	0.56	0/3494	0.65	0/4744
154	WQ	0.56	0/3494	0.64	0/4744
154	WS	0.57	0/3494	0.68	0/4744
154	WU	0.55	0/3494	0.64	0/4744
154	WW	0.56	0/3494	0.65	0/4744
154	WY	0.56	0/3494	0.66	0/4744
154	XA	0.56	0/3494	0.65	0/4744
154	XC	0.56	0/3494	0.64	0/4744
154	XE	0.33	0/3494	0.66	1/4744 (0.0%)
154	XG	0.56	0/3494	0.66	0/4744
154	XI	0.56	0/3494	0.68	1/4744 (0.0%)
154	XK	0.56	0/3494	0.70	1/4744 (0.0%)
154	XM	0.57	0/3494	0.66	0/4744
154	XO	0.34	0/3494	0.67	2/4744 (0.0%)
154	XQ	0.56	0/3494	0.67	1/4744 (0.0%)
154	XS	0.34	0/3494	0.65	0/4744
154	XU	0.56	0/3494	0.67	1/4744 (0.0%)
154	XW	0.56	0/3494	0.66	0/4744
154	XY	0.56	0/3494	0.66	0/4744
154	YA	0.56	0/3494	0.65	0/4744
154	YC	0.56	0/3494	0.65	0/4744
154	YE	0.56	0/3494	0.65	0/4744
154	YG	0.56	0/3494	0.68	1/4744 (0.0%)
154	YJ	0.56	0/3494	0.64	0/4744
154	YL	0.55	0/3494	0.63	0/4744
154	YN	0.56	0/3494	0.64	0/4744
154	YP	0.58	0/3494	0.74	3/4744 (0.1%)
154	YR	0.55	0/3494	0.62	0/4744
154	YT	0.56	0/3494	0.66	0/4744

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
154	YV	0.56	0/3494	0.66	1/4744 (0.0%)
154	YX	0.55	0/3494	0.63	0/4744
154	YZ	0.56	0/3494	0.63	0/4744
154	ZB	0.57	0/3494	0.70	1/4744 (0.0%)
154	ZD	0.55	0/3494	0.63	0/4744
154	ZF	0.56	0/3494	0.63	0/4744
154	ZH	0.56	0/3494	0.64	0/4744
154	ZJ	0.55	0/3494	0.63	0/4744
154	ZL	0.55	0/3494	0.64	0/4744
154	ZN	0.56	0/3494	0.65	1/4744 (0.0%)
154	ZP	0.55	0/3494	0.63	0/4744
154	ZR	0.55	0/3494	0.63	0/4744
154	ZT	0.55	0/3494	0.66	0/4744
154	ZV	0.55	0/3494	0.62	0/4744
154	ZX	0.56	0/3494	0.63	0/4744
154	ZZ	0.55	0/3494	0.65	1/4744 (0.0%)
All	All	0.46	11/3953396 (0.0%)	0.63	783/5350391 (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	0C	0	1
5	0Q	0	8
5	0T	0	1
7	0Z	0	1
8	0c	0	3
11	0r	0	1
11	0s	0	1
14	0w	0	1
15	0x	0	1
30	1c	0	1
31	1d	0	1
40	1m	0	1
42	1o	0	1
44	1r	0	1
45	1t	0	5
47	2D	0	1
50	2M	0	1
50	2N	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
50	2O	0	1
55	2a	0	1
55	2c	0	1
56	2e	0	4
57	2i	0	1
57	2k	0	1
59	2q	0	1
59	2r	0	1
59	2s	0	1
61	2y	0	1
64	3E	0	1
64	3G	0	1
64	3I	0	1
65	3J	0	2
65	3K	0	2
69	3d	0	1
69	3e	0	1
69	3f	0	1
69	3g	0	1
70	3h	0	1
73	3l	0	1
73	3m	0	1
73	3o	0	3
73	3p	0	3
74	3q	0	1
74	3r	0	1
74	3s	0	1
74	3t	0	1
75	4m	0	1
75	5t	0	1
75	5v	0	4
75	7k	0	1
75	7n	0	1
75	7o	0	1
75	8k	0	1
75	8o	0	1
75	9k	0	1
75	9n	0	1
75	9o	0	1
76	4P	0	1
79	4q	0	1
79	4r	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
84	4y	0	2
86	5A	0	2
86	5B	0	3
88	5W	0	2
88	5X	0	4
91	5Y	0	1
91	5Z	0	1
92	5a	0	1
95	5d	0	1
96	5e	0	1
99	5i	0	8
100	5k	0	4
102	5m	0	2
103	5n	0	1
105	5p	0	1
106	5q	0	1
106	9l	0	1
107	9m	0	1
108	5y	0	1
109	6C	0	1
109	6F	0	3
109	6G	0	3
109	6J	0	2
109	6M	0	1
109	6N	0	2
109	6O	0	1
109	6P	0	1
110	6Y	0	1
110	7E	0	1
111	6a	0	7
112	6b	0	11
113	6c	0	3
114	6d	0	3
115	6e	0	2
125	6r	0	1
128	6u	0	1
134	7a	0	2
134	7e	0	1
134	8e	0	3
134	9e	0	2
135	7b	0	3
135	7f	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
135	8f	0	1
135	9f	0	2
136	7c	0	1
136	8c	0	1
136	9c	0	1
137	7d	0	3
137	9d	0	1
138	7g	0	2
138	8g	0	1
139	7h	0	1
139	8h	0	3
139	9h	0	1
141	7r	0	1
141	8r	0	1
141	9r	0	1
142	8s	0	1
143	8t	0	2
143	9t	0	1
144	8F	0	1
144	8I	0	1
146	9B	0	1
148	9H	0	1
149	9K	0	2
149	9L	0	1
150	9O	0	1
153	Ac	0	2
153	Ae	0	1
153	Ao	0	2
153	BM	0	1
153	BY	0	1
153	CK	0	1
153	CO	0	1
153	CU	0	1
153	CW	0	1
153	DA	0	1
153	DG	0	1
153	DI	0	1
153	DX	0	1
153	EJ	0	1
153	EX	0	1
153	EZ	0	1
153	FJ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
153	FL	0	1
153	HJ	0	2
153	HP	0	1
153	HV	0	2
153	IL	0	2
153	IN	0	1
153	IX	0	2
153	JD	0	1
153	JQ	0	1
153	KO	0	2
153	LM	0	1
153	LO	0	1
153	MA	0	1
153	MM	0	1
153	NA	0	1
153	NM	0	1
153	NU	0	1
153	OC	0	2
153	OO	0	1
153	PA	0	1
153	QJ	0	1
153	QL	0	1
153	QV	0	1
153	QX	0	1
153	RH	0	1
153	SN	0	1
153	ST	0	1
153	SZ	0	1
153	TF	0	1
153	TH	0	1
153	TL	0	1
153	TY	0	1
153	UX	0	1
153	VD	0	1
153	VF	0	1
153	VH	0	1
153	VJ	0	1
153	VP	0	2
153	VR	0	1
153	VT	0	1
153	WF	0	1
153	XJ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
153	XV	0	1
153	YH	0	1
153	YM	0	1
153	YO	0	1
153	ZA	0	1
153	ZE	0	1
153	ZQ	0	2
153	ZS	0	1
154	AZ	0	1
154	AI	0	1
154	BJ	0	1
154	BV	0	1
154	CI	0	1
154	CT	0	1
154	DF	0	1
154	EQ	0	1
154	EW	0	1
154	FA	0	1
154	FC	0	1
154	FM	0	1
154	FO	0	1
154	GC	0	1
154	HE	0	1
154	II	0	3
154	IM	0	1
154	IU	0	3
154	IY	0	2
154	JC	0	1
154	MV	0	2
154	NH	0	2
154	NT	0	2
154	OD	0	1
154	PI	0	1
154	QG	0	2
154	QM	0	1
154	QQ	0	2
154	QS	0	2
154	QY	0	1
154	RC	0	2
154	RE	0	2
154	SM	0	1
154	SS	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
154	SU	0	3
154	TG	0	3
154	VC	0	1
154	WC	0	1
154	WG	0	1
154	WK	0	1
154	WO	0	1
154	WW	0	1
154	XA	0	1
154	XG	0	1
154	XK	0	1
154	XS	0	2
154	XW	0	1
154	YE	0	2
154	YN	0	1
154	YV	0	1
154	YZ	0	1
154	ZL	0	1
All	All	0	361

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
154	KD	196	GLU	CD-OE2	-12.32	1.12	1.25
35	1h	456	SER	CB-OG	-10.54	1.28	1.42
65	3J	751	ARG	CB-CG	-7.33	1.32	1.52
154	IA	339	ARG	CZ-NH2	-6.69	1.24	1.33
16	0z	144	TRP	CD2-CE2	-6.60	1.33	1.41

The worst 5 of 783 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
128	6u	103	ARG	O-C-N	-44.06	52.20	122.70
153	TP	129	CYS	N-CA-CB	-17.95	78.29	110.60
153	TP	129	CYS	CB-CA-C	-11.12	88.17	110.40
154	VC	121	ARG	NE-CZ-NH2	10.31	125.45	120.30
65	3J	751	ARG	CA-CB-CG	10.21	135.85	113.40

There are no chirality outliers.

5 of 361 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0C	393	ARG	Sidechain
5	0Q	119	ARG	Sidechain
5	0Q	297	ARG	Sidechain
5	0Q	299	ARG	Sidechain
5	0Q	301	ARG	Sidechain

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 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](#)

Of 1125 ligands modelled in this entry, 412 are monoatomic - leaving 713 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
156	ATP	7e	4704	-	28,33,33	0.75	0	34,52,52	0.69	1 (2%)
156	ATP	7e	4702	-	28,33,33	0.71	0	34,52,52	0.62	1 (2%)
160	GTP	ES	501	159	29,34,34	1.20	1 (3%)	35,54,54	1.30	5 (14%)
158	GDP	ZC	501	-	25,30,30	0.84	0	30,47,47	0.81	0
158	GDP	VP	501	-	25,30,30	0.84	0	30,47,47	0.85	1 (3%)
160	GTP	UY	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	Ad	602	159	29,34,34	1.19	2 (6%)	35,54,54	1.35	5 (14%)
157	ADP	8f	4701	-	24,29,29	0.82	0	29,45,45	1.33	4 (13%)
158	GDP	ZU	501	-	25,30,30	0.85	0	30,47,47	0.85	2 (6%)
160	GTP	XQ	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	UK	501	-	25,30,30	0.86	0	30,47,47	0.87	2 (6%)
157	ADP	7e	4701	-	24,29,29	0.89	0	29,45,45	1.19	2 (6%)
158	GDP	Ac	501	-	25,30,30	0.83	0	30,47,47	0.83	1 (3%)
158	GDP	MO	501	-	25,30,30	0.83	0	30,47,47	0.82	1 (3%)
160	GTP	CJ	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	EC	501	159	29,34,34	1.21	1 (3%)	35,54,54	1.35	4 (11%)
158	GDP	IH	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.12	3 (10%)
158	GDP	ER	501	-	25,30,30	0.96	1 (4%)	30,47,47	1.06	3 (10%)
160	GTP	Ap	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.87	2 (5%)
160	GTP	HQ	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.88	1 (2%)
160	GTP	DL	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	SQ	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	KW	501	-	25,30,30	0.82	0	30,47,47	0.82	0
160	GTP	UN	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	BV	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	CQ	501	-	25,30,30	0.84	0	30,47,47	0.83	1 (3%)
158	GDP	OS	501	-	25,30,30	0.84	0	30,47,47	0.84	0
160	GTP	KL	602	159	29,34,34	1.16	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	XN	501	-	25,30,30	0.85	0	30,47,47	0.88	2 (6%)
160	GTP	TQ	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.91	2 (5%)
160	GTP	AN	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	LG	501	-	25,30,30	0.86	0	30,47,47	0.86	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
158	GDP	Am	501	-	25,30,30	0.84	0	30,47,47	0.84	1 (3%)
158	GDP	KA	501	-	25,30,30	0.85	0	30,47,47	0.82	0
160	GTP	NZ	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	QK	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	BP	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.91	2 (5%)
160	GTP	HC	602	159	29,34,34	1.19	2 (6%)	35,54,54	1.38	4 (11%)
158	GDP	ZW	501	-	25,30,30	0.82	0	30,47,47	0.91	2 (6%)
158	GDP	NI	501	-	25,30,30	0.84	0	30,47,47	0.84	1 (3%)
160	GTP	XE	501	159	29,34,34	1.21	2 (6%)	35,54,54	1.37	5 (14%)
160	GTP	UJ	501	159	29,34,34	1.40	6 (20%)	35,54,54	1.24	5 (14%)
160	GTP	RG	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.83	1 (2%)
157	ADP	9f	4702	-	24,29,29	0.83	0	29,45,45	1.35	4 (13%)
158	GDP	NS	501	-	25,30,30	0.84	0	30,47,47	0.85	2 (6%)
156	ATP	9e	5004	-	28,33,33	0.74	1 (3%)	34,52,52	0.85	2 (5%)
158	GDP	TS	501	-	25,30,30	0.85	0	30,47,47	0.90	1 (3%)
158	GDP	XT	501	-	25,30,30	0.86	0	30,47,47	0.79	0
160	GTP	AX	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	AT	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.88	1 (2%)
160	GTP	PE	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	EQ	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	XB	501	-	25,30,30	0.83	0	30,47,47	0.80	0
158	GDP	PJ	501	-	25,30,30	0.84	0	30,47,47	0.80	0
157	ADP	8e	4701	-	24,29,29	0.89	0	29,45,45	1.18	2 (6%)
158	GDP	HD	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.21	3 (10%)
160	GTP	UP	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.90	2 (5%)
156	ATP	7a	4702	-	28,33,33	0.72	0	34,52,52	0.84	2 (5%)
160	GTP	ND	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.85	2 (5%)
158	GDP	NY	501	-	25,30,30	0.80	0	30,47,47	0.90	2 (6%)
158	GDP	NO	501	-	25,30,30	0.84	0	30,47,47	0.81	0
160	GTP	FE	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.82	1 (2%)
158	GDP	NC	501	-	25,30,30	0.85	0	30,47,47	0.82	0
160	GTP	BJ	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	QN	501	-	25,30,30	0.83	0	30,47,47	0.82	0
158	GDP	Ak	501	-	25,30,30	0.81	0	30,47,47	0.90	3 (10%)
160	GTP	WK	602	159	29,34,34	1.09	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	TH	501	-	25,30,30	0.87	0	30,47,47	0.84	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
158	GDP	EV	501	-	25,30,30	0.86	0	30,47,47	0.83	1 (3%)
160	GTP	LB	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	CI	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	HF	501	-	25,30,30	0.83	0	30,47,47	0.88	2 (6%)
158	GDP	PA	501	-	25,30,30	0.84	0	30,47,47	0.88	1 (3%)
160	GTP	JE	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	FS	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.87	2 (5%)
158	GDP	Ai	501	-	25,30,30	0.82	0	30,47,47	0.90	2 (6%)
160	GTP	GG	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.87	2 (5%)
158	GDP	PH	501	-	25,30,30	0.86	0	30,47,47	0.79	0
158	GDP	LY	501	-	25,30,30	0.82	0	30,47,47	0.84	1 (3%)
158	GDP	WF	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.17	3 (10%)
156	ATP	8e	4702	-	28,33,33	0.68	0	34,52,52	0.87	2 (5%)
160	GTP	NR	502	159	29,34,34	1.14	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	SM	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	SK	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.93	2 (5%)
158	GDP	CW	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.09	3 (10%)
160	GTP	GO	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	TK	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	TC	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	FN	501	-	25,30,30	0.84	0	30,47,47	0.83	0
158	GDP	WR	501	-	25,30,30	0.87	0	30,47,47	0.86	0
160	GTP	KN	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	EJ	501	-	25,30,30	0.82	0	30,47,47	0.84	0
160	GTP	OR	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.88	1 (2%)
160	GTP	RK	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.86	2 (5%)
160	GTP	DM	501	159	29,34,34	1.10	2 (6%)	35,54,54	0.84	1 (2%)
156	ATP	9f	4703	-	28,33,33	0.74	0	34,52,52	0.61	1 (2%)
160	GTP	YG	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	AQ	501	-	25,30,30	0.83	0	30,47,47	0.85	1 (3%)
158	GDP	SB	501	-	25,30,30	0.82	0	30,47,47	0.89	2 (6%)
158	GDP	RF	501	-	25,30,30	0.84	0	30,47,47	0.83	0
160	GTP	TT	602	159	29,34,34	1.15	2 (6%)	35,54,54	0.85	1 (2%)
156	ATP	7a	4704	-	28,33,33	0.73	0	34,52,52	0.68	1 (2%)
160	GTP	KF	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	RB	501	-	25,30,30	0.84	0	30,47,47	0.82	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
158	GDP	EH	501	-	25,30,30	0.80	0	30,47,47	0.81	1 (3%)
160	GTP	RC	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	GL	501	-	25,30,30	0.83	0	30,47,47	0.87	1 (3%)
158	GDP	HB	501	-	25,30,30	1.03	3 (12%)	30,47,47	0.78	0
157	ADP	7b	4704	-	24,29,29	0.85	0	29,45,45	1.38	4 (13%)
160	GTP	PI	602	159	29,34,34	1.15	2 (6%)	35,54,54	0.82	1 (2%)
156	ATP	8f	4703	-	28,33,33	0.98	1 (3%)	34,52,52	0.63	1 (2%)
160	GTP	MZ	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	Ab	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	VW	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	QH	501	-	25,30,30	0.86	0	30,47,47	0.83	1 (3%)
160	GTP	MP	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	HV	501	-	25,30,30	0.80	0	30,47,47	0.89	1 (3%)
158	GDP	WD	501	-	25,30,30	0.98	2 (8%)	30,47,47	1.14	3 (10%)
158	GDP	EL	501	-	25,30,30	0.84	0	30,47,47	0.81	1 (3%)
160	GTP	WE	602	159	29,34,34	1.24	1 (3%)	35,54,54	1.31	5 (14%)
158	GDP	LC	501	-	25,30,30	0.86	0	30,47,47	0.88	1 (3%)
160	GTP	RY	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.93	2 (5%)
158	GDP	EZ	602	-	25,30,30	0.86	0	30,47,47	0.85	1 (3%)
158	GDP	ZE	501	-	25,30,30	0.86	0	30,47,47	0.82	1 (3%)
158	GDP	DE	501	-	25,30,30	0.84	0	30,47,47	0.81	1 (3%)
160	GTP	FQ	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	RZ	501	-	25,30,30	0.80	0	30,47,47	0.92	2 (6%)
158	GDP	AM	501	-	25,30,30	0.85	0	30,47,47	0.89	1 (3%)
156	ATP	8e	4704	-	28,33,33	0.77	1 (3%)	34,52,52	0.65	1 (2%)
160	GTP	OJ	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.91	1 (2%)
160	GTP	OB	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.89	2 (5%)
160	GTP	VC	501	159	29,34,34	1.36	6 (20%)	35,54,54	1.34	6 (17%)
158	GDP	BM	501	-	25,30,30	0.86	0	30,47,47	0.82	0
158	GDP	IV	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.16	3 (10%)
160	GTP	IM	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	PS	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.83	1 (2%)
160	GTP	UD	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.91	2 (5%)
158	GDP	WN	501	-	25,30,30	0.84	0	30,47,47	0.86	0
160	GTP	LD	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.84	1 (2%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	SW	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	IE	501	159	29,34,34	1.22	2 (6%)	35,54,54	1.39	5 (14%)
160	GTP	XM	602	159	29,34,34	0.99	3 (10%)	35,54,54	0.78	0
160	GTP	JP	602	159	29,34,34	1.22	2 (6%)	35,54,54	1.29	6 (17%)
158	GDP	BY	501	-	25,30,30	0.84	0	30,47,47	0.80	0
160	GTP	YZ	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	VK	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.82	1 (2%)
160	GTP	YV	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.89	2 (5%)
158	GDP	CY	501	-	25,30,30	0.86	0	30,47,47	0.83	0
158	GDP	CO	501	-	25,30,30	0.83	0	30,47,47	0.82	0
160	GTP	BD	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	UU	501	-	25,30,30	0.84	0	30,47,47	0.84	0
158	GDP	LW	501	-	25,30,30	0.82	0	30,47,47	0.79	0
156	ATP	7b	4702	-	28,33,33	0.72	0	34,52,52	0.61	1 (2%)
160	GTP	AL	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	JA	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	EF	501	-	25,30,30	0.82	0	30,47,47	0.79	0
160	GTP	WA	602	159	29,34,34	1.21	1 (3%)	35,54,54	1.35	5 (14%)
158	GDP	FV	501	-	25,30,30	1.02	2 (8%)	30,47,47	1.16	3 (10%)
158	GDP	YM	501	-	25,30,30	0.83	0	30,47,47	0.82	0
158	GDP	BS	501	-	25,30,30	0.83	0	30,47,47	0.84	1 (3%)
160	GTP	KT	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	VN	501	-	25,30,30	0.84	0	30,47,47	0.81	0
158	GDP	KK	501	-	25,30,30	0.81	0	30,47,47	0.85	1 (3%)
160	GTP	LN	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	XD	501	-	25,30,30	0.87	0	30,47,47	0.86	1 (3%)
160	GTP	MX	502	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	RU	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	YK	501	-	25,30,30	0.84	0	30,47,47	0.88	2 (6%)
158	GDP	IJ	501	-	25,30,30	0.85	0	30,47,47	0.84	1 (3%)
158	GDP	DN	501	-	25,30,30	0.95	1 (4%)	30,47,47	1.05	2 (6%)
158	GDP	SJ	501	-	25,30,30	0.81	0	30,47,47	0.91	3 (10%)
158	GDP	VB	501	-	25,30,30	0.82	0	30,47,47	0.83	1 (3%)
158	GDP	ET	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.12	3 (10%)
160	GTP	RO	602	159	29,34,34	1.10	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	YF	501	-	25,30,30	0.86	0	30,47,47	0.80	1 (3%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	BB	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	IF	501	-	25,30,30	0.98	2 (8%)	30,47,47	1.11	3 (10%)
160	GTP	JX	501	159	29,34,34	1.17	1 (3%)	35,54,54	1.32	5 (14%)
158	GDP	YY	501	-	25,30,30	0.82	0	30,47,47	0.83	0
160	GTP	VA	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	FT	501	-	25,30,30	0.86	0	30,47,47	0.82	1 (3%)
158	GDP	CS	501	-	25,30,30	0.97	2 (8%)	30,47,47	1.11	3 (10%)
160	GTP	IS	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	AO	501	-	25,30,30	0.98	2 (8%)	30,47,47	1.10	3 (10%)
160	GTP	DU	501	159	29,34,34	1.22	1 (3%)	35,54,54	1.32	5 (14%)
160	GTP	EK	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	LJ	501	159	29,34,34	1.16	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	PF	501	-	25,30,30	0.84	0	30,47,47	0.80	0
158	GDP	AC	501	-	25,30,30	0.96	1 (4%)	30,47,47	1.10	3 (10%)
158	GDP	WZ	501	-	25,30,30	0.82	0	30,47,47	0.85	0
160	GTP	EE	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	DW	602	159	29,34,34	1.19	1 (3%)	35,54,54	1.33	5 (14%)
160	GTP	FC	501	159	29,34,34	1.09	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	KG	501	-	25,30,30	0.84	0	30,47,47	0.83	0
160	GTP	HY	501	159	29,34,34	1.10	2 (6%)	35,54,54	0.91	2 (5%)
160	GTP	VM	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.84	2 (5%)
160	GTP	ON	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	QZ	501	-	25,30,30	0.85	0	30,47,47	0.79	0
160	GTP	PG	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.83	1 (2%)
160	GTP	YX	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	KD	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	KU	501	-	25,30,30	0.85	0	30,47,47	0.84	0
160	GTP	MR	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	2 (5%)
160	GTP	TG	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	2 (5%)
160	GTP	FI	602	159	29,34,34	1.24	2 (6%)	35,54,54	1.34	5 (14%)
158	GDP	OY	501	-	25,30,30	0.83	0	30,47,47	0.84	0
158	GDP	HL	501	-	25,30,30	0.99	2 (8%)	30,47,47	1.15	3 (10%)
158	GDP	PL	501	-	25,30,30	0.82	0	30,47,47	0.82	0
158	GDP	SN	501	-	25,30,30	0.83	0	30,47,47	0.91	3 (10%)
157	ADP	9e	5002	-	24,29,29	0.88	0	29,45,45	1.16	2 (6%)
160	GTP	HA	501	159	29,34,34	1.18	2 (6%)	35,54,54	1.42	4 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	ZP	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	HN	501	-	25,30,30	1.02	3 (12%)	30,47,47	0.77	0
158	GDP	JD	501	-	25,30,30	0.86	0	30,47,47	0.81	0
158	GDP	RV	501	-	25,30,30	0.83	0	30,47,47	0.85	1 (3%)
160	GTP	AZ	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	YT	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	MI	501	-	25,30,30	0.84	0	30,47,47	0.80	0
160	GTP	JV	501	159	29,34,34	1.21	2 (6%)	35,54,54	1.30	5 (14%)
158	GDP	JS	501	-	25,30,30	0.99	2 (8%)	30,47,47	1.11	3 (10%)
160	GTP	GU	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	IZ	501	-	25,30,30	0.85	0	30,47,47	0.86	0
158	GDP	HP	501	-	25,30,30	0.83	0	30,47,47	0.90	2 (6%)
158	GDP	VL	501	-	25,30,30	0.82	0	30,47,47	0.83	1 (3%)
160	GTP	XG	602	159	29,34,34	1.15	2 (6%)	35,54,54	0.86	2 (5%)
158	GDP	TL	501	-	25,30,30	0.84	0	30,47,47	0.92	3 (10%)
158	GDP	GZ	501	-	25,30,30	1.01	2 (8%)	30,47,47	1.14	3 (10%)
160	GTP	VS	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.81	1 (2%)
160	GTP	IW	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	2 (5%)
158	GDP	KM	501	-	25,30,30	0.87	0	30,47,47	0.93	1 (3%)
158	GDP	DV	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.08	3 (10%)
158	GDP	BC	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.11	3 (10%)
158	GDP	TB	501	-	25,30,30	0.82	0	30,47,47	0.85	1 (3%)
160	GTP	TE	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.91	2 (5%)
158	GDP	QJ	501	-	25,30,30	0.87	0	30,47,47	0.87	1 (3%)
160	GTP	NH	502	159	29,34,34	1.14	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	ZM	501	-	25,30,30	0.81	0	30,47,47	0.91	3 (10%)
158	GDP	XF	501	-	25,30,30	0.99	2 (8%)	30,47,47	1.13	3 (10%)
158	GDP	QV	501	-	25,30,30	0.86	0	30,47,47	0.88	1 (3%)
158	GDP	LM	501	-	25,30,30	0.84	0	30,47,47	0.81	0
160	GTP	LH	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	IN	501	-	25,30,30	0.98	2 (8%)	30,47,47	1.11	3 (10%)
160	GTP	BX	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	2 (5%)
158	GDP	OC	501	-	25,30,30	0.82	0	30,47,47	0.86	1 (3%)
160	GTP	HE	602	159	29,34,34	1.21	2 (6%)	35,54,54	1.30	6 (17%)
156	ATP	7b	4701	-	28,33,33	0.72	0	34,52,52	0.61	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	LT	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	VH	501	-	25,30,30	0.82	0	30,47,47	0.84	1 (3%)
158	GDP	AW	501	-	25,30,30	0.85	0	30,47,47	0.80	0
158	GDP	VV	501	-	25,30,30	0.84	0	30,47,47	0.84	0
160	GTP	AF	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	WG	501	159	29,34,34	1.27	4 (13%)	35,54,54	1.23	5 (14%)
158	GDP	ST	501	-	25,30,30	0.82	0	30,47,47	0.88	1 (3%)
160	GTP	PK	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	VG	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.82	1 (2%)
160	GTP	Al	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	Aa	501	-	25,30,30	0.83	0	30,47,47	0.86	1 (3%)
158	GDP	WH	501	-	25,30,30	0.87	0	30,47,47	0.83	0
158	GDP	UM	501	-	25,30,30	0.87	0	30,47,47	0.78	0
160	GTP	TM	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.86	2 (5%)
158	GDP	QL	501	-	25,30,30	0.85	0	30,47,47	0.82	1 (3%)
158	GDP	HJ	501	-	25,30,30	0.80	0	30,47,47	0.89	2 (6%)
160	GTP	EA	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	GS	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	KV	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	RD	501	-	25,30,30	0.88	0	30,47,47	0.83	2 (6%)
156	ATP	7b	4703	-	28,33,33	0.73	0	34,52,52	0.59	1 (2%)
160	GTP	GM	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	PT	501	-	25,30,30	0.86	0	30,47,47	0.78	0
160	GTP	CV	501	159	29,34,34	1.20	2 (6%)	35,54,54	1.35	5 (14%)
160	GTP	AR	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	GA	602	159	29,34,34	1.21	1 (3%)	35,54,54	1.30	5 (14%)
158	GDP	CC	501	-	25,30,30	0.87	0	30,47,47	0.84	0
160	GTP	HW	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	LQ	501	-	25,30,30	0.83	0	30,47,47	0.81	0
160	GTP	KP	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.84	1 (2%)
156	ATP	7e	4703	-	28,33,33	0.73	0	34,52,52	0.89	2 (5%)
158	GDP	GF	501	-	25,30,30	0.80	0	30,47,47	0.95	3 (10%)
158	GDP	JO	501	-	25,30,30	0.86	0	30,47,47	0.81	0
158	GDP	MW	501	-	25,30,30	0.84	0	30,47,47	0.83	0
160	GTP	GE	602	159	29,34,34	1.09	2 (6%)	35,54,54	0.87	2 (5%)
160	GTP	CZ	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.86	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	CB	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.89	2 (5%)
160	GTP	WO	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.82	1 (2%)
158	GDP	ME	501	-	25,30,30	0.83	0	30,47,47	0.82	1 (3%)
158	GDP	JI	501	-	25,30,30	0.96	1 (4%)	30,47,47	1.09	3 (10%)
158	GDP	BG	501	-	25,30,30	0.83	0	30,47,47	0.84	1 (3%)
158	GDP	TF	501	-	25,30,30	0.82	0	30,47,47	0.87	1 (3%)
158	GDP	AE	501	-	25,30,30	0.83	0	30,47,47	0.83	0
160	GTP	NP	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.84	2 (5%)
158	GDP	GX	501	-	25,30,30	0.84	0	30,47,47	0.88	1 (3%)
158	GDP	MY	501	-	25,30,30	0.84	0	30,47,47	0.88	1 (3%)
158	GDP	IX	501	-	25,30,30	0.86	0	30,47,47	0.82	0
158	GDP	KS	501	-	25,30,30	0.83	0	30,47,47	0.84	2 (6%)
160	GTP	XS	501	159	29,34,34	1.21	3 (10%)	35,54,54	1.36	5 (14%)
158	GDP	OW	501	-	25,30,30	0.81	0	30,47,47	0.90	3 (10%)
158	GDP	FX	501	-	25,30,30	0.98	2 (8%)	30,47,47	1.10	3 (10%)
160	GTP	MB	502	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	US	501	-	25,30,30	0.81	0	30,47,47	0.83	1 (3%)
158	GDP	EX	501	-	25,30,30	0.85	0	30,47,47	0.85	1 (3%)
158	GDP	FF	501	-	25,30,30	0.85	0	30,47,47	0.81	1 (3%)
158	GDP	TN	501	-	25,30,30	0.84	0	30,47,47	0.84	1 (3%)
160	GTP	CT	602	159	29,34,34	1.19	2 (6%)	35,54,54	1.34	5 (14%)
160	GTP	QG	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	QP	501	-	25,30,30	0.85	0	30,47,47	0.80	0
158	GDP	XR	501	-	25,30,30	0.85	0	30,47,47	0.85	1 (3%)
160	GTP	SG	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	UX	501	-	25,30,30	0.85	0	30,47,47	0.85	0
160	GTP	DY	501	159	29,34,34	1.10	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	OX	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	ZS	501	-	25,30,30	1.14	2 (8%)	30,47,47	1.19	2 (6%)
160	GTP	FK	501	159	29,34,34	1.10	2 (6%)	35,54,54	0.88	2 (5%)
160	GTP	GW	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.89	2 (5%)
160	GTP	CD	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	2 (5%)
160	GTP	ZZ	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	UO	501	-	25,30,30	0.84	0	30,47,47	0.85	0
160	GTP	II	501	159	29,34,34	1.22	5 (17%)	35,54,54	1.23	4 (11%)
160	GTP	NV	503	159	29,34,34	1.11	2 (6%)	35,54,54	0.86	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
158	GDP	AS	501	-	25,30,30	1.14	2 (8%)	30,47,47	1.27	3 (10%)
156	ATP	7f	4703	-	28,33,33	0.72	0	34,52,52	0.62	1 (2%)
158	GDP	NQ	501	-	25,30,30	0.86	0	30,47,47	0.82	0
160	GTP	JJ	501	159	29,34,34	1.19	1 (3%)	35,54,54	1.30	5 (14%)
156	ATP	8e	4703	-	28,33,33	0.70	0	34,52,52	0.62	1 (2%)
160	GTP	XK	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.88	2 (5%)
160	GTP	XW	602	159	29,34,34	1.16	2 (6%)	35,54,54	0.89	2 (5%)
158	GDP	XZ	501	-	25,30,30	0.86	0	30,47,47	0.87	1 (3%)
160	GTP	NN	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	SH	501	-	25,30,30	0.84	0	30,47,47	0.85	1 (3%)
160	GTP	LX	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	UZ	501	-	25,30,30	0.81	0	30,47,47	0.83	0
158	GDP	DC	501	-	25,30,30	0.83	0	30,47,47	0.83	1 (3%)
160	GTP	YA	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	BI	501	-	25,30,30	0.85	0	30,47,47	0.85	1 (3%)
158	GDP	RR	501	-	25,30,30	0.82	0	30,47,47	0.90	2 (6%)
158	GDP	KI	501	-	25,30,30	0.83	0	30,47,47	0.83	0
160	GTP	JC	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	VJ	501	-	25,30,30	0.86	0	30,47,47	0.84	0
160	GTP	KZ	602	159	29,34,34	1.22	2 (6%)	35,54,54	1.33	5 (14%)
158	GDP	XX	501	-	25,30,30	0.83	0	30,47,47	0.82	0
160	GTP	KX	501	159	29,34,34	1.17	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	OI	501	-	25,30,30	0.82	0	30,47,47	0.87	1 (3%)
158	GDP	PN	501	-	25,30,30	0.85	0	30,47,47	0.84	1 (3%)
160	GTP	CR	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	HS	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	QT	501	-	25,30,30	0.85	0	30,47,47	0.84	1 (3%)
158	GDP	KY	501	-	25,30,30	0.87	0	30,47,47	0.89	0
160	GTP	BF	602	159	29,34,34	1.17	1 (3%)	35,54,54	1.38	5 (14%)
160	GTP	AH	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	UF	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	IP	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.15	3 (10%)
156	ATP	9f	4704	-	28,33,33	0.70	0	34,52,52	0.66	1 (2%)
158	GDP	BU	501	-	25,30,30	1.03	2 (8%)	30,47,47	1.17	3 (10%)
160	GTP	GI	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	FJ	501	-	25,30,30	0.84	0	30,47,47	0.85	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	DD	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.82	1 (2%)
158	GDP	LU	501	-	25,30,30	0.85	0	30,47,47	0.88	1 (3%)
160	GTP	BT	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	Ao	501	-	25,30,30	0.83	0	30,47,47	0.83	1 (3%)
160	GTP	ZX	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	PV	501	-	25,30,30	0.85	0	30,47,47	0.81	0
160	GTP	VY	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	HI	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	HZ	501	-	25,30,30	1.01	3 (12%)	30,47,47	0.79	0
160	GTP	EW	501	159	29,34,34	1.20	3 (10%)	35,54,54	1.32	3 (8%)
160	GTP	DB	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.82	1 (2%)
158	GDP	IT	501	-	25,30,30	1.01	2 (8%)	30,47,47	1.12	3 (10%)
158	GDP	AK	501	-	25,30,30	0.85	0	30,47,47	0.80	0
158	GDP	RL	501	-	25,30,30	0.81	0	30,47,47	0.90	2 (6%)
158	GDP	KQ	501	-	25,30,30	0.84	0	30,47,47	0.87	0
158	GDP	MK	501	-	25,30,30	0.82	0	30,47,47	0.84	1 (3%)
160	GTP	NF	502	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	WX	501	-	25,30,30	0.96	1 (4%)	30,47,47	1.08	3 (10%)
158	GDP	KE	501	-	25,30,30	0.84	0	30,47,47	0.79	0
158	GDP	YH	501	-	25,30,30	0.85	0	30,47,47	0.83	1 (3%)
160	GTP	BR	501	159	29,34,34	1.18	1 (3%)	35,54,54	1.38	5 (14%)
160	GTP	UT	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	HT	501	-	25,30,30	0.81	0	30,47,47	0.91	3 (10%)
160	GTP	AV	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	An	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	HR	501	-	25,30,30	0.83	0	30,47,47	0.89	2 (6%)
160	GTP	GK	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	KO	501	-	25,30,30	0.85	0	30,47,47	0.80	0
158	GDP	RT	501	-	25,30,30	0.81	0	30,47,47	0.88	2 (6%)
158	GDP	WV	501	-	25,30,30	0.83	0	30,47,47	0.81	1 (3%)
160	GTP	ZL	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	YL	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.86	2 (5%)
158	GDP	TU	501	-	25,30,30	0.82	0	30,47,47	0.83	1 (3%)
158	GDP	OQ	501	-	25,30,30	0.84	0	30,47,47	0.84	0
160	GTP	JT	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	LR	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.84	1 (2%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
158	GDP	LA	501	-	25,30,30	0.84	0	30,47,47	0.78	0
160	GTP	NL	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	TX	602	159	29,34,34	1.26	6 (20%)	35,54,54	1.32	5 (14%)
160	GTP	VE	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.82	1 (2%)
160	GTP	LZ	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	OO	501	-	25,30,30	0.82	0	30,47,47	0.87	1 (3%)
160	GTP	SY	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	MM	501	-	25,30,30	0.82	0	30,47,47	0.80	0
160	GTP	CX	602	159	29,34,34	1.19	2 (6%)	35,54,54	1.33	5 (14%)
160	GTP	QA	602	159	29,34,34	1.16	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	WP	501	-	25,30,30	0.84	0	30,47,47	0.81	0
158	GDP	GD	501	-	25,30,30	0.82	0	30,47,47	0.88	2 (6%)
158	GDP	YB	501	-	25,30,30	0.86	0	30,47,47	0.83	0
160	GTP	OD	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.88	1 (2%)
160	GTP	RQ	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	VT	501	-	25,30,30	0.82	0	30,47,47	0.83	0
160	GTP	YE	602	159	29,34,34	1.15	2 (6%)	35,54,54	0.86	2 (5%)
158	GDP	NU	501	-	25,30,30	0.84	0	30,47,47	0.83	0
158	GDP	SZ	501	-	25,30,30	0.83	0	30,47,47	0.92	3 (10%)
160	GTP	ZJ	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	2 (5%)
160	GTP	IY	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	QQ	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	JZ	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	UG	501	-	25,30,30	0.81	0	30,47,47	0.81	0
160	GTP	DS	602	159	29,34,34	1.21	1 (3%)	35,54,54	1.32	4 (11%)
158	GDP	HH	501	-	25,30,30	0.81	0	30,47,47	0.88	2 (6%)
158	GDP	SD	501	-	25,30,30	0.84	0	30,47,47	0.90	2 (6%)
160	GTP	NT	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	FP	501	-	25,30,30	0.83	0	30,47,47	0.80	0
158	GDP	GT	501	-	25,30,30	0.82	0	30,47,47	0.90	1 (3%)
160	GTP	LF	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	UR	501	159	29,34,34	1.16	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	PZ	501	-	25,30,30	0.85	0	30,47,47	0.83	0
158	GDP	MC	501	-	25,30,30	0.83	0	30,47,47	0.82	1 (3%)
158	GDP	FB	501	-	25,30,30	0.84	0	30,47,47	0.84	1 (3%)
158	GDP	FZ	501	-	25,30,30	1.01	2 (8%)	30,47,47	1.15	3 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	WW	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	VX	501	-	25,30,30	0.82	0	30,47,47	0.83	0
160	GTP	PW	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	ZR	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.86	2 (5%)
160	GTP	XA	501	159	29,34,34	1.10	2 (6%)	35,54,54	0.84	1 (2%)
156	ATP	9e	5001	-	28,33,33	0.75	0	34,52,52	0.64	1 (2%)
158	GDP	CE	501	-	25,30,30	0.83	0	30,47,47	0.84	1 (3%)
160	GTP	TZ	602	159	29,34,34	1.16	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	AU	501	-	25,30,30	0.83	0	30,47,47	0.85	1 (3%)
160	GTP	ML	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	YO	501	-	25,30,30	0.85	0	30,47,47	0.81	0
160	GTP	SO	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	ZT	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	CK	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.09	3 (10%)
160	GTP	ZV	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	2 (5%)
158	GDP	DA	501	-	25,30,30	0.82	0	30,47,47	0.83	0
158	GDP	WT	501	-	25,30,30	0.87	0	30,47,47	0.81	0
158	GDP	XL	501	-	25,30,30	0.84	0	30,47,47	0.82	0
160	GTP	GC	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.85	2 (5%)
158	GDP	FL	602	-	25,30,30	0.85	0	30,47,47	0.84	1 (3%)
160	GTP	IK	602	159	29,34,34	1.19	2 (6%)	35,54,54	1.38	5 (14%)
158	GDP	AI	501	-	25,30,30	0.84	0	30,47,47	0.86	1 (3%)
158	GDP	LS	501	-	25,30,30	0.84	0	30,47,47	0.83	0
160	GTP	LV	502	159	29,34,34	1.11	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	VR	501	-	25,30,30	0.81	0	30,47,47	0.83	0
160	GTP	VO	501	159	29,34,34	1.30	5 (17%)	35,54,54	1.19	5 (14%)
158	GDP	RN	501	-	25,30,30	0.82	0	30,47,47	0.91	2 (6%)
160	GTP	TI	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	DO	501	159	29,34,34	1.21	1 (3%)	35,54,54	1.34	4 (11%)
158	GDP	LI	501	-	25,30,30	0.82	0	30,47,47	0.86	1 (3%)
160	GTP	UL	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	OE	501	-	25,30,30	0.85	0	30,47,47	0.83	0
158	GDP	DR	501	-	25,30,30	0.85	0	30,47,47	0.84	1 (3%)
158	GDP	ZG	501	-	25,30,30	0.83	0	30,47,47	0.84	1 (3%)
158	GDP	UC	501	-	25,30,30	0.83	0	30,47,47	0.85	0
160	GTP	WM	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.83	1 (2%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	AJ	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
156	ATP	8f	4702	-	28,33,33	0.78	0	34,52,52	0.64	1 (2%)
158	GDP	TP	501	-	25,30,30	0.79	0	30,47,47	0.98	3 (10%)
158	GDP	UQ	501	-	25,30,30	0.84	0	30,47,47	0.90	1 (3%)
158	GDP	JF	501	-	25,30,30	0.84	0	30,47,47	0.82	0
158	GDP	JK	501	-	25,30,30	0.97	2 (8%)	30,47,47	1.12	3 (10%)
158	GDP	BQ	501	-	25,30,30	0.86	0	30,47,47	0.84	0
158	GDP	DT	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.08	3 (10%)
158	GDP	PX	501	-	25,30,30	0.82	0	30,47,47	0.81	0
158	GDP	DG	501	-	25,30,30	0.81	0	30,47,47	0.86	1 (3%)
160	GTP	FA	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	GP	501	-	25,30,30	0.82	0	30,47,47	0.87	0
160	GTP	RI	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	UW	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	CH	501	-	25,30,30	0.86	0	30,47,47	0.85	2 (6%)
160	GTP	XY	501	159	29,34,34	1.00	3 (10%)	35,54,54	0.79	1 (2%)
158	GDP	WJ	501	-	25,30,30	0.84	0	30,47,47	0.79	1 (3%)
160	GTP	TA	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	AG	501	-	25,30,30	1.10	2 (8%)	30,47,47	1.20	2 (6%)
157	ADP	7a	4703	-	24,29,29	0.87	0	29,45,45	1.18	2 (6%)
160	GTP	EI	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	FG	501	159	29,34,34	1.22	2 (6%)	35,54,54	1.34	4 (11%)
160	GTP	FW	602	159	29,34,34	1.22	2 (6%)	35,54,54	1.36	5 (14%)
160	GTP	XI	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	ZK	501	-	25,30,30	0.83	0	30,47,47	0.82	0
160	GTP	FO	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	NE	501	-	25,30,30	0.86	0	30,47,47	0.84	1 (3%)
160	GTP	ZD	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.86	1 (2%)
157	ADP	7f	4701	-	24,29,29	0.83	0	29,45,45	1.35	4 (13%)
160	GTP	JL	501	159	29,34,34	1.21	4 (13%)	35,54,54	1.18	2 (5%)
158	GDP	YD	501	-	25,30,30	0.85	0	30,47,47	0.86	1 (3%)
160	GTP	RM	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.93	2 (5%)
160	GTP	OP	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	SR	501	-	25,30,30	0.79	0	30,47,47	0.99	3 (10%)
158	GDP	RJ	501	-	25,30,30	0.84	0	30,47,47	0.86	1 (3%)
160	GTP	NX	501	159	29,34,34	1.10	2 (6%)	35,54,54	0.90	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
158	GDP	BK	501	-	25,30,30	0.84	0	30,47,47	0.80	0
160	GTP	QO	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	OV	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.90	1 (2%)
160	GTP	LP	502	159	29,34,34	1.14	2 (6%)	35,54,54	0.86	1 (2%)
156	ATP	8f	4704	-	28,33,33	0.82	1 (3%)	34,52,52	0.60	1 (2%)
158	GDP	FR	501	-	25,30,30	0.85	0	30,47,47	0.82	0
160	GTP	QI	602	159	29,34,34	1.18	2 (6%)	35,54,54	1.34	5 (14%)
160	GTP	FY	501	159	29,34,34	1.19	1 (3%)	35,54,54	1.36	4 (11%)
160	GTP	GQ	602	159	29,34,34	1.08	2 (6%)	35,54,54	0.86	2 (5%)
160	GTP	CL	501	159	29,34,34	1.19	2 (6%)	35,54,54	1.34	5 (14%)
160	GTP	PU	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	NA	501	-	25,30,30	0.82	0	30,47,47	0.84	1 (3%)
160	GTP	SC	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.88	1 (2%)
160	GTP	QY	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	MJ	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	RS	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	2 (5%)
160	GTP	YP	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.82	1 (2%)
158	GDP	XJ	501	-	25,30,30	1.12	2 (8%)	30,47,47	1.15	2 (6%)
158	GDP	ZY	501	-	25,30,30	0.82	0	30,47,47	0.91	3 (10%)
158	GDP	EN	501	-	25,30,30	0.85	0	30,47,47	0.81	1 (3%)
160	GTP	MD	502	159	29,34,34	1.15	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	MQ	501	-	25,30,30	0.96	2 (8%)	30,47,47	1.10	3 (10%)
158	GDP	YW	501	-	25,30,30	0.85	0	30,47,47	0.89	2 (6%)
160	GTP	YC	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	GH	501	-	25,30,30	0.83	0	30,47,47	0.91	2 (6%)
160	GTP	HU	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	QC	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	JU	501	-	25,30,30	0.84	0	30,47,47	0.81	0
158	GDP	MA	501	-	25,30,30	0.80	0	30,47,47	0.79	0
156	ATP	7f	4702	-	28,33,33	0.74	0	34,52,52	0.60	1 (2%)
158	GDP	NG	501	-	25,30,30	0.84	0	30,47,47	0.84	0
160	GTP	WS	501	159	29,34,34	1.23	4 (13%)	35,54,54	1.24	4 (11%)
160	GTP	WY	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.83	1 (2%)
160	GTP	Ah	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.83	1 (2%)
160	GTP	IA	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.89	1 (2%)
158	GDP	FH	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.10	3 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
158	GDP	PP	501	-	25,30,30	0.86	0	30,47,47	0.86	1 (3%)
160	GTP	TR	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.90	2 (5%)
158	GDP	KC	501	-	25,30,30	0.85	0	30,47,47	0.83	1 (3%)
158	GDP	GV	501	-	25,30,30	0.81	0	30,47,47	0.88	2 (6%)
160	GTP	HO	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	Ag	501	-	25,30,30	0.84	0	30,47,47	0.86	2 (6%)
160	GTP	DH	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	BA	501	-	25,30,30	0.84	0	30,47,47	0.83	0
158	GDP	MG	501	-	25,30,30	0.85	0	30,47,47	0.87	1 (3%)
160	GTP	JN	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.81	1 (2%)
160	GTP	MV	502	159	29,34,34	1.14	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	AD	501	159	29,34,34	1.18	2 (6%)	35,54,54	1.33	4 (11%)
158	GDP	BW	501	-	25,30,30	0.84	0	30,47,47	0.81	1 (3%)
160	GTP	XO	602	159	29,34,34	1.20	2 (6%)	35,54,54	1.38	5 (14%)
158	GDP	MU	501	-	25,30,30	0.85	0	30,47,47	0.85	1 (3%)
160	GTP	SU	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.85	2 (5%)
160	GTP	KB	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	VU	501	159	29,34,34	1.10	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	DP	501	-	25,30,30	0.84	0	30,47,47	0.80	1 (3%)
158	GDP	JB	501	-	25,30,30	0.86	0	30,47,47	0.81	0
160	GTP	KH	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.81	1 (2%)
158	GDP	VZ	501	-	25,30,30	0.82	0	30,47,47	0.81	1 (3%)
160	GTP	IG	501	159	29,34,34	1.21	1 (3%)	35,54,54	1.36	5 (14%)
158	GDP	FD	501	-	25,30,30	0.84	0	30,47,47	0.79	0
158	GDP	SX	501	-	25,30,30	0.81	0	30,47,47	0.85	0
160	GTP	YR	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	LK	501	-	25,30,30	0.85	0	30,47,47	0.92	1 (3%)
160	GTP	RW	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.86	2 (5%)
158	GDP	DX	501	-	25,30,30	0.84	0	30,47,47	0.84	1 (3%)
160	GTP	IU	501	159	29,34,34	1.21	2 (6%)	35,54,54	1.36	5 (14%)
158	GDP	IB	501	-	25,30,30	0.83	0	30,47,47	0.92	2 (6%)
158	GDP	SF	501	-	25,30,30	0.80	0	30,47,47	0.88	2 (6%)
160	GTP	ZN	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	HX	501	-	25,30,30	0.82	0	30,47,47	0.84	1 (3%)
160	GTP	FM	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.83	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	QU	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	DZ	501	-	25,30,30	0.84	0	30,47,47	0.79	1 (3%)
158	GDP	SP	501	-	25,30,30	0.84	0	30,47,47	0.84	0
160	GTP	WI	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.81	1 (2%)
160	GTP	MN	502	159	29,34,34	1.14	2 (6%)	35,54,54	0.87	2 (5%)
158	GDP	UA	501	-	25,30,30	0.85	0	30,47,47	0.79	1 (3%)
158	GDP	Ae	501	-	25,30,30	1.13	2 (8%)	30,47,47	1.21	3 (10%)
158	GDP	OK	501	-	25,30,30	0.81	0	30,47,47	0.89	2 (6%)
160	GTP	RE	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	VI	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	Aj	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	ID	501	-	25,30,30	0.99	2 (8%)	30,47,47	1.16	3 (10%)
156	ATP	7f	4704	-	28,33,33	0.74	0	34,52,52	0.60	1 (2%)
160	GTP	ZH	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.89	2 (5%)
158	GDP	OU	501	-	25,30,30	0.83	0	30,47,47	0.87	1 (3%)
158	GDP	LO	501	-	25,30,30	0.81	0	30,47,47	0.79	0
160	GTP	IQ	501	159	29,34,34	1.21	1 (3%)	35,54,54	1.34	6 (17%)
158	GDP	ZO	501	-	25,30,30	0.84	0	30,47,47	0.86	1 (3%)
158	GDP	QR	501	-	25,30,30	0.88	0	30,47,47	0.82	2 (6%)
158	GDP	WB	501	-	25,30,30	0.83	0	30,47,47	0.85	0
158	GDP	VD	501	-	25,30,30	0.85	0	30,47,47	0.84	1 (3%)
160	GTP	QM	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	OF	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	DJ	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	JH	602	159	29,34,34	1.20	1 (3%)	35,54,54	1.31	5 (14%)
158	GDP	DK	501	-	25,30,30	0.83	0	30,47,47	0.84	1 (3%)
158	GDP	NK	501	-	25,30,30	0.83	0	30,47,47	0.88	1 (3%)
158	GDP	PR	501	-	25,30,30	0.85	0	30,47,47	0.79	0
158	GDP	RP	501	-	25,30,30	0.82	0	30,47,47	0.89	2 (6%)
160	GTP	NJ	503	159	29,34,34	1.10	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	XC	602	159	29,34,34	1.16	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	WL	501	-	25,30,30	0.95	1 (4%)	30,47,47	1.08	3 (10%)
160	GTP	Af	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	PD	501	-	25,30,30	0.85	0	30,47,47	0.84	0
160	GTP	AB	602	159	29,34,34	1.20	2 (6%)	35,54,54	1.36	5 (14%)
160	GTP	AP	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.84	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	CN	602	159	29,34,34	1.15	2 (6%)	35,54,54	0.88	1 (2%)
160	GTP	EY	501	159	29,34,34	1.09	2 (6%)	35,54,54	0.87	2 (5%)
158	GDP	OG	501	-	25,30,30	0.83	0	30,47,47	0.85	0
160	GTP	BL	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.87	2 (5%)
160	GTP	OL	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	PY	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	IO	501	159	29,34,34	1.19	4 (13%)	35,54,54	1.27	3 (8%)
160	GTP	WC	501	159	29,34,34	1.10	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	OA	501	-	25,30,30	0.83	0	30,47,47	0.85	1 (3%)
160	GTP	BH	602	159	29,34,34	1.20	2 (6%)	35,54,54	1.35	5 (14%)
160	GTP	OZ	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.88	2 (5%)
158	GDP	GN	501	-	25,30,30	0.80	0	30,47,47	0.88	1 (3%)
158	GDP	JQ	501	-	25,30,30	0.86	0	30,47,47	0.81	0
158	GDP	JY	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.10	3 (10%)
158	GDP	CM	501	-	25,30,30	0.83	0	30,47,47	0.83	1 (3%)
158	GDP	IR	501	-	25,30,30	0.85	0	30,47,47	0.82	0
156	ATP	7a	4701	-	28,33,33	0.73	0	34,52,52	0.63	1 (2%)
158	GDP	YS	501	-	25,30,30	0.86	0	30,47,47	0.83	1 (3%)
160	GTP	MH	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.83	1 (2%)
160	GTP	EG	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.83	1 (2%)
160	GTP	PO	602	159	29,34,34	1.16	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	WU	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.82	1 (2%)
160	GTP	OT	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.88	1 (2%)
160	GTP	XU	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	2 (5%)
160	GTP	QS	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	JM	501	-	25,30,30	0.84	0	30,47,47	0.81	0
160	GTP	NB	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	UE	501	-	25,30,30	0.85	0	30,47,47	0.88	1 (3%)
158	GDP	IL	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.10	3 (10%)
158	GDP	XP	501	-	25,30,30	0.87	0	30,47,47	0.84	0
158	GDP	ZQ	501	-	25,30,30	0.83	0	30,47,47	0.84	1 (3%)
158	GDP	TY	501	-	25,30,30	0.83	0	30,47,47	0.85	1 (3%)
158	GDP	GJ	501	-	25,30,30	0.82	0	30,47,47	0.89	2 (6%)
160	GTP	TO	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
158	GDP	XV	501	-	25,30,30	0.85	0	30,47,47	0.84	1 (3%)
160	GTP	HG	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.88	2 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	KJ	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.82	1 (2%)
160	GTP	PM	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	CA	501	-	25,30,30	0.82	0	30,47,47	0.93	2 (6%)
158	GDP	QD	501	-	25,30,30	0.85	0	30,47,47	0.81	0
160	GTP	CF	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	AA	501	-	25,30,30	0.84	0	30,47,47	0.89	1 (3%)
156	ATP	9e	5003	-	28,33,33	0.74	0	34,52,52	0.61	1 (2%)
158	GDP	EB	501	-	25,30,30	0.95	1 (4%)	30,47,47	1.09	3 (10%)
158	GDP	LE	501	-	25,30,30	0.84	0	30,47,47	0.87	2 (6%)
158	GDP	QF	501	-	25,30,30	0.86	0	30,47,47	0.81	0
158	GDP	NM	501	-	25,30,30	0.82	0	30,47,47	0.83	1 (3%)
156	ATP	9f	4701	-	28,33,33	0.78	1 (3%)	34,52,52	0.60	1 (2%)
160	GTP	SI	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	2 (5%)
160	GTP	SE	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	AY	501	-	25,30,30	0.86	0	30,47,47	0.90	2 (6%)
158	GDP	ED	501	-	25,30,30	1.09	1 (4%)	30,47,47	1.07	2 (6%)
158	GDP	JW	501	-	25,30,30	0.97	2 (8%)	30,47,47	1.12	3 (10%)
158	GDP	QX	501	-	25,30,30	0.85	0	30,47,47	0.83	2 (6%)
158	GDP	JG	501	-	25,30,30	0.99	2 (8%)	30,47,47	1.11	3 (10%)
158	GDP	OM	501	-	25,30,30	0.83	0	30,47,47	0.84	0
158	GDP	RX	501	-	25,30,30	0.79	0	30,47,47	0.91	3 (10%)
160	GTP	RA	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	YU	501	-	25,30,30	0.83	0	30,47,47	0.86	2 (6%)
160	GTP	YJ	602	159	29,34,34	1.12	2 (6%)	35,54,54	0.89	2 (5%)
158	GDP	SL	501	-	25,30,30	0.81	0	30,47,47	0.89	1 (3%)
160	GTP	YN	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	KR	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.84	1 (2%)
158	GDP	CU	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.13	3 (10%)
160	GTP	HK	501	159	29,34,34	1.10	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	ZI	501	-	25,30,30	0.84	0	30,47,47	0.88	2 (6%)
160	GTP	MF	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	2 (5%)
160	GTP	EM	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	ZB	501	159	29,34,34	1.16	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	BN	602	159	29,34,34	1.20	2 (6%)	35,54,54	1.39	5 (14%)
160	GTP	DF	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.85	1 (2%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
158	GDP	BO	501	-	25,30,30	1.03	2 (8%)	30,47,47	1.21	3 (10%)
160	GTP	HM	602	159	29,34,34	1.11	2 (6%)	35,54,54	0.90	2 (5%)
160	GTP	LL	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
158	GDP	VF	501	-	25,30,30	0.83	0	30,47,47	0.81	0
158	GDP	XH	501	-	25,30,30	0.85	0	30,47,47	0.78	1 (3%)
158	GDP	GR	501	-	25,30,30	0.80	0	30,47,47	0.94	3 (10%)
160	GTP	QE	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	QW	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	WQ	602	159	29,34,34	1.14	2 (6%)	35,54,54	0.83	1 (2%)
160	GTP	TV	501	159	29,34,34	1.16	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	EO	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.83	1 (2%)
158	GDP	RH	501	-	25,30,30	0.87	0	30,47,47	0.88	1 (3%)
160	GTP	OH	501	159	29,34,34	1.11	2 (6%)	35,54,54	0.88	1 (2%)
158	GDP	YQ	501	-	25,30,30	0.85	0	30,47,47	0.82	0
158	GDP	TJ	501	-	25,30,30	0.81	0	30,47,47	0.85	0
158	GDP	UI	501	-	25,30,30	0.84	0	30,47,47	0.84	0
160	GTP	DQ	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	SS	602	159	29,34,34	1.20	4 (13%)	35,54,54	1.44	5 (14%)
158	GDP	QB	501	-	25,30,30	0.86	0	30,47,47	0.84	0
158	GDP	DI	501	-	25,30,30	0.83	0	30,47,47	0.82	1 (3%)
158	GDP	SV	501	-	25,30,30	0.84	0	30,47,47	0.85	1 (3%)
160	GTP	ZF	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.87	1 (2%)
160	GTP	VQ	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	MT	501	159	29,34,34	1.14	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	BZ	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.86	1 (2%)
158	GDP	GB	501	-	25,30,30	0.81	0	30,47,47	0.89	2 (6%)
158	GDP	TW	501	-	25,30,30	0.83	0	30,47,47	0.86	1 (3%)
160	GTP	UH	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.84	1 (2%)
160	GTP	PC	602	159	29,34,34	1.23	1 (3%)	35,54,54	1.39	5 (14%)
160	GTP	EU	501	159	29,34,34	1.12	2 (6%)	35,54,54	0.86	2 (5%)
160	GTP	PQ	501	159	29,34,34	1.13	2 (6%)	35,54,54	0.86	1 (2%)
160	GTP	UB	501	159	29,34,34	1.15	2 (6%)	35,54,54	0.86	2 (5%)
158	GDP	TD	501	-	25,30,30	0.80	0	30,47,47	0.97	3 (10%)
158	GDP	ZA	501	-	25,30,30	0.85	0	30,47,47	0.81	1 (3%)
160	GTP	CP	602	159	29,34,34	1.13	2 (6%)	35,54,54	0.85	1 (2%)
160	GTP	JR	602	159	29,34,34	1.20	1 (3%)	35,54,54	1.32	5 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
160	GTP	SA	501	159	29,34,34	1.28	4 (13%)	35,54,54	1.45	6 (17%)

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
156	ATP	7e	4704	-	-	5/18/38/38	0/3/3/3
156	ATP	7e	4702	-	-	5/18/38/38	0/3/3/3
160	GTP	ES	501	159	-	5/18/38/38	0/3/3/3
158	GDP	ZC	501	-	-	2/12/32/32	0/3/3/3
158	GDP	VP	501	-	-	2/12/32/32	0/3/3/3
160	GTP	UY	602	159	-	5/18/38/38	0/3/3/3
160	GTP	Ad	602	159	-	5/18/38/38	0/3/3/3
157	ADP	8f	4701	-	-	5/12/32/32	0/3/3/3
158	GDP	ZU	501	-	-	2/12/32/32	0/3/3/3
160	GTP	XQ	501	159	-	5/18/38/38	0/3/3/3
158	GDP	UK	501	-	-	2/12/32/32	0/3/3/3
157	ADP	7e	4701	-	-	4/12/32/32	0/3/3/3
158	GDP	Ac	501	-	-	2/12/32/32	0/3/3/3
158	GDP	MO	501	-	-	2/12/32/32	0/3/3/3
160	GTP	CJ	501	159	-	5/18/38/38	0/3/3/3
160	GTP	EC	501	159	-	5/18/38/38	0/3/3/3
158	GDP	IH	501	-	-	2/12/32/32	0/3/3/3
158	GDP	ER	501	-	-	2/12/32/32	0/3/3/3
160	GTP	Ap	501	159	-	5/18/38/38	0/3/3/3
160	GTP	HQ	602	159	-	5/18/38/38	0/3/3/3
160	GTP	DL	501	159	-	5/18/38/38	0/3/3/3
160	GTP	SQ	602	159	-	5/18/38/38	0/3/3/3
158	GDP	KW	501	-	-	2/12/32/32	0/3/3/3
160	GTP	UN	602	159	-	5/18/38/38	0/3/3/3
160	GTP	BV	602	159	-	5/18/38/38	0/3/3/3
158	GDP	CQ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	OS	501	-	-	2/12/32/32	0/3/3/3
160	GTP	KL	602	159	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	XN	501	-	-	2/12/32/32	0/3/3/3
160	GTP	TQ	602	159	-	5/18/38/38	0/3/3/3
160	GTP	AN	501	159	-	5/18/38/38	0/3/3/3
158	GDP	LG	501	-	-	2/12/32/32	0/3/3/3
158	GDP	Am	501	-	-	2/12/32/32	0/3/3/3
158	GDP	KA	501	-	-	2/12/32/32	0/3/3/3
160	GTP	NZ	602	159	-	5/18/38/38	0/3/3/3
160	GTP	QK	602	159	-	5/18/38/38	0/3/3/3
160	GTP	BP	501	159	-	5/18/38/38	0/3/3/3
160	GTP	HC	602	159	-	5/18/38/38	0/3/3/3
158	GDP	ZW	501	-	-	2/12/32/32	0/3/3/3
158	GDP	NI	501	-	-	2/12/32/32	0/3/3/3
160	GTP	XE	501	159	-	5/18/38/38	0/3/3/3
160	GTP	UJ	501	159	-	4/18/38/38	0/3/3/3
160	GTP	RG	501	159	-	5/18/38/38	0/3/3/3
157	ADP	9f	4702	-	-	4/12/32/32	0/3/3/3
158	GDP	NS	501	-	-	2/12/32/32	0/3/3/3
156	ATP	9e	5004	-	-	8/18/38/38	0/3/3/3
158	GDP	TS	501	-	-	2/12/32/32	0/3/3/3
158	GDP	XT	501	-	-	2/12/32/32	0/3/3/3
160	GTP	AX	501	159	-	5/18/38/38	0/3/3/3
160	GTP	AT	501	159	-	5/18/38/38	0/3/3/3
160	GTP	PE	602	159	-	5/18/38/38	0/3/3/3
160	GTP	EQ	602	159	-	5/18/38/38	0/3/3/3
158	GDP	XB	501	-	-	2/12/32/32	0/3/3/3
158	GDP	PJ	501	-	-	2/12/32/32	0/3/3/3
157	ADP	8e	4701	-	-	4/12/32/32	0/3/3/3
158	GDP	HD	501	-	-	2/12/32/32	0/3/3/3
160	GTP	UP	501	159	-	5/18/38/38	0/3/3/3
156	ATP	7a	4702	-	-	8/18/38/38	0/3/3/3
160	GTP	ND	501	159	-	5/18/38/38	0/3/3/3
158	GDP	NY	501	-	-	2/12/32/32	0/3/3/3
158	GDP	NO	501	-	-	2/12/32/32	0/3/3/3
160	GTP	FE	501	159	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	NC	501	-	-	2/12/32/32	0/3/3/3
160	GTP	BJ	602	159	-	5/18/38/38	0/3/3/3
158	GDP	QN	501	-	-	2/12/32/32	0/3/3/3
158	GDP	Ak	501	-	-	2/12/32/32	0/3/3/3
160	GTP	WK	602	159	-	5/18/38/38	0/3/3/3
158	GDP	TH	501	-	-	2/12/32/32	0/3/3/3
158	GDP	EV	501	-	-	2/12/32/32	0/3/3/3
160	GTP	LB	501	159	-	5/18/38/38	0/3/3/3
160	GTP	CI	501	159	-	5/18/38/38	0/3/3/3
158	GDP	HF	501	-	-	2/12/32/32	0/3/3/3
158	GDP	PA	501	-	-	2/12/32/32	0/3/3/3
160	GTP	JE	501	159	-	5/18/38/38	0/3/3/3
160	GTP	FS	602	159	-	5/18/38/38	0/3/3/3
158	GDP	Ai	501	-	-	2/12/32/32	0/3/3/3
160	GTP	GG	501	159	-	5/18/38/38	0/3/3/3
158	GDP	PH	501	-	-	2/12/32/32	0/3/3/3
158	GDP	LY	501	-	-	2/12/32/32	0/3/3/3
158	GDP	WF	501	-	-	2/12/32/32	0/3/3/3
156	ATP	8e	4702	-	-	8/18/38/38	0/3/3/3
160	GTP	NR	502	159	-	5/18/38/38	0/3/3/3
160	GTP	SM	501	159	-	5/18/38/38	0/3/3/3
160	GTP	SK	602	159	-	5/18/38/38	0/3/3/3
158	GDP	CW	501	-	-	2/12/32/32	0/3/3/3
160	GTP	GO	501	159	-	5/18/38/38	0/3/3/3
160	GTP	TK	501	159	-	5/18/38/38	0/3/3/3
160	GTP	TC	501	159	-	5/18/38/38	0/3/3/3
158	GDP	FN	501	-	-	2/12/32/32	0/3/3/3
158	GDP	WR	501	-	-	2/12/32/32	0/3/3/3
160	GTP	KN	602	159	-	5/18/38/38	0/3/3/3
158	GDP	EJ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	OR	602	159	-	5/18/38/38	0/3/3/3
160	GTP	RK	602	159	-	5/18/38/38	0/3/3/3
160	GTP	DM	501	159	-	5/18/38/38	0/3/3/3
156	ATP	9f	4703	-	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
160	GTP	YG	602	159	-	5/18/38/38	0/3/3/3
158	GDP	AQ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	SB	501	-	-	2/12/32/32	0/3/3/3
158	GDP	RF	501	-	-	2/12/32/32	0/3/3/3
160	GTP	TT	602	159	-	5/18/38/38	0/3/3/3
156	ATP	7a	4704	-	-	4/18/38/38	0/3/3/3
160	GTP	KF	602	159	-	5/18/38/38	0/3/3/3
158	GDP	RB	501	-	-	2/12/32/32	0/3/3/3
158	GDP	EH	501	-	-	2/12/32/32	0/3/3/3
160	GTP	RC	501	159	-	5/18/38/38	0/3/3/3
158	GDP	GL	501	-	-	2/12/32/32	0/3/3/3
158	GDP	HB	501	-	-	3/12/32/32	0/3/3/3
157	ADP	7b	4704	-	-	4/12/32/32	0/3/3/3
160	GTP	PI	602	159	-	5/18/38/38	0/3/3/3
156	ATP	8f	4703	-	-	6/18/38/38	0/3/3/3
160	GTP	MZ	602	159	-	5/18/38/38	0/3/3/3
160	GTP	Ab	501	159	-	5/18/38/38	0/3/3/3
160	GTP	VW	501	159	-	5/18/38/38	0/3/3/3
158	GDP	QH	501	-	-	2/12/32/32	0/3/3/3
160	GTP	MP	501	159	-	5/18/38/38	0/3/3/3
158	GDP	HV	501	-	-	2/12/32/32	0/3/3/3
158	GDP	WD	501	-	-	2/12/32/32	0/3/3/3
158	GDP	EL	501	-	-	2/12/32/32	0/3/3/3
160	GTP	WE	602	159	-	5/18/38/38	0/3/3/3
158	GDP	LC	501	-	-	2/12/32/32	0/3/3/3
160	GTP	RY	602	159	-	5/18/38/38	0/3/3/3
158	GDP	EZ	602	-	-	2/12/32/32	0/3/3/3
158	GDP	ZE	501	-	-	2/12/32/32	0/3/3/3
158	GDP	DE	501	-	-	2/12/32/32	0/3/3/3
160	GTP	FQ	501	159	-	5/18/38/38	0/3/3/3
158	GDP	RZ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	AM	501	-	-	2/12/32/32	0/3/3/3
156	ATP	8e	4704	-	-	7/18/38/38	0/3/3/3
160	GTP	OJ	602	159	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
160	GTP	OB	501	159	-	5/18/38/38	0/3/3/3
160	GTP	VC	501	159	-	2/18/38/38	0/3/3/3
158	GDP	BM	501	-	-	2/12/32/32	0/3/3/3
158	GDP	IV	501	-	-	2/12/32/32	0/3/3/3
160	GTP	IM	602	159	-	5/18/38/38	0/3/3/3
160	GTP	PS	501	159	-	5/18/38/38	0/3/3/3
160	GTP	UD	501	159	-	5/18/38/38	0/3/3/3
158	GDP	WN	501	-	-	2/12/32/32	0/3/3/3
160	GTP	LD	602	159	-	5/18/38/38	0/3/3/3
160	GTP	SW	501	159	-	5/18/38/38	0/3/3/3
160	GTP	IE	501	159	-	5/18/38/38	0/3/3/3
160	GTP	XM	602	159	-	5/18/38/38	0/3/3/3
160	GTP	JP	602	159	-	5/18/38/38	0/3/3/3
158	GDP	BY	501	-	-	2/12/32/32	0/3/3/3
160	GTP	YZ	602	159	-	5/18/38/38	0/3/3/3
160	GTP	VK	501	159	-	5/18/38/38	0/3/3/3
160	GTP	YV	602	159	-	5/18/38/38	0/3/3/3
158	GDP	CY	501	-	-	2/12/32/32	0/3/3/3
158	GDP	CO	501	-	-	2/12/32/32	0/3/3/3
160	GTP	BD	602	159	-	5/18/38/38	0/3/3/3
158	GDP	UU	501	-	-	2/12/32/32	0/3/3/3
158	GDP	LW	501	-	-	2/12/32/32	0/3/3/3
156	ATP	7b	4702	-	-	5/18/38/38	0/3/3/3
160	GTP	AL	602	159	-	5/18/38/38	0/3/3/3
160	GTP	JA	501	159	-	5/18/38/38	0/3/3/3
158	GDP	EF	501	-	-	2/12/32/32	0/3/3/3
160	GTP	WA	602	159	-	5/18/38/38	0/3/3/3
158	GDP	FV	501	-	-	2/12/32/32	0/3/3/3
158	GDP	YM	501	-	-	2/12/32/32	0/3/3/3
158	GDP	BS	501	-	-	2/12/32/32	0/3/3/3
160	GTP	KT	501	159	-	5/18/38/38	0/3/3/3
158	GDP	VN	501	-	-	2/12/32/32	0/3/3/3
158	GDP	KK	501	-	-	2/12/32/32	0/3/3/3
160	GTP	LN	501	159	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	XD	501	-	-	2/12/32/32	0/3/3/3
160	GTP	MX	502	159	-	5/18/38/38	0/3/3/3
160	GTP	RU	501	159	-	5/18/38/38	0/3/3/3
158	GDP	YK	501	-	-	2/12/32/32	0/3/3/3
158	GDP	IJ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	DN	501	-	-	2/12/32/32	0/3/3/3
158	GDP	SJ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	VB	501	-	-	2/12/32/32	0/3/3/3
158	GDP	ET	501	-	-	2/12/32/32	0/3/3/3
160	GTP	RO	602	159	-	5/18/38/38	0/3/3/3
158	GDP	YF	501	-	-	2/12/32/32	0/3/3/3
160	GTP	BB	501	159	-	5/18/38/38	0/3/3/3
158	GDP	IF	501	-	-	2/12/32/32	0/3/3/3
160	GTP	JX	501	159	-	5/18/38/38	0/3/3/3
158	GDP	YY	501	-	-	2/12/32/32	0/3/3/3
160	GTP	VA	501	159	-	5/18/38/38	0/3/3/3
158	GDP	FT	501	-	-	2/12/32/32	0/3/3/3
158	GDP	CS	501	-	-	2/12/32/32	0/3/3/3
160	GTP	IS	501	159	-	5/18/38/38	0/3/3/3
158	GDP	AO	501	-	-	2/12/32/32	0/3/3/3
160	GTP	DU	501	159	-	5/18/38/38	0/3/3/3
160	GTP	EK	602	159	-	5/18/38/38	0/3/3/3
160	GTP	LJ	501	159	-	5/18/38/38	0/3/3/3
158	GDP	PF	501	-	-	2/12/32/32	0/3/3/3
158	GDP	AC	501	-	-	2/12/32/32	0/3/3/3
158	GDP	WZ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	EE	501	159	-	5/18/38/38	0/3/3/3
160	GTP	DW	602	159	-	5/18/38/38	0/3/3/3
160	GTP	FC	501	159	-	5/18/38/38	0/3/3/3
158	GDP	KG	501	-	-	2/12/32/32	0/3/3/3
160	GTP	HY	501	159	-	5/18/38/38	0/3/3/3
160	GTP	VM	602	159	-	5/18/38/38	0/3/3/3
160	GTP	ON	501	159	-	5/18/38/38	0/3/3/3
158	GDP	QZ	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
160	GTP	PG	501	159	-	5/18/38/38	0/3/3/3
160	GTP	YX	602	159	-	5/18/38/38	0/3/3/3
160	GTP	KD	501	159	-	5/18/38/38	0/3/3/3
158	GDP	KU	501	-	-	2/12/32/32	0/3/3/3
160	GTP	MR	602	159	-	5/18/38/38	0/3/3/3
160	GTP	TG	501	159	-	5/18/38/38	0/3/3/3
160	GTP	FI	602	159	-	5/18/38/38	0/3/3/3
158	GDP	OY	501	-	-	2/12/32/32	0/3/3/3
158	GDP	HL	501	-	-	2/12/32/32	0/3/3/3
158	GDP	PL	501	-	-	2/12/32/32	0/3/3/3
158	GDP	SN	501	-	-	2/12/32/32	0/3/3/3
157	ADP	9e	5002	-	-	4/12/32/32	0/3/3/3
160	GTP	HA	501	159	-	5/18/38/38	0/3/3/3
160	GTP	ZP	501	159	-	5/18/38/38	0/3/3/3
158	GDP	HN	501	-	-	3/12/32/32	0/3/3/3
158	GDP	JD	501	-	-	2/12/32/32	0/3/3/3
158	GDP	RV	501	-	-	2/12/32/32	0/3/3/3
160	GTP	AZ	501	159	-	5/18/38/38	0/3/3/3
160	GTP	YT	602	159	-	5/18/38/38	0/3/3/3
158	GDP	MI	501	-	-	2/12/32/32	0/3/3/3
160	GTP	JV	501	159	-	5/18/38/38	0/3/3/3
158	GDP	JS	501	-	-	2/12/32/32	0/3/3/3
160	GTP	GU	602	159	-	5/18/38/38	0/3/3/3
158	GDP	IZ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	HP	501	-	-	2/12/32/32	0/3/3/3
158	GDP	VL	501	-	-	2/12/32/32	0/3/3/3
160	GTP	XG	602	159	-	5/18/38/38	0/3/3/3
158	GDP	TL	501	-	-	2/12/32/32	0/3/3/3
158	GDP	GZ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	VS	501	159	-	5/18/38/38	0/3/3/3
160	GTP	IW	501	159	-	5/18/38/38	0/3/3/3
158	GDP	KM	501	-	-	2/12/32/32	0/3/3/3
158	GDP	DV	501	-	-	2/12/32/32	0/3/3/3
158	GDP	BC	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	TB	501	-	-	2/12/32/32	0/3/3/3
160	GTP	TE	501	159	-	5/18/38/38	0/3/3/3
158	GDP	QJ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	NH	502	159	-	5/18/38/38	0/3/3/3
158	GDP	ZM	501	-	-	2/12/32/32	0/3/3/3
158	GDP	XF	501	-	-	2/12/32/32	0/3/3/3
158	GDP	QV	501	-	-	2/12/32/32	0/3/3/3
158	GDP	LM	501	-	-	2/12/32/32	0/3/3/3
160	GTP	LH	501	159	-	5/18/38/38	0/3/3/3
158	GDP	IN	501	-	-	2/12/32/32	0/3/3/3
160	GTP	BX	602	159	-	5/18/38/38	0/3/3/3
158	GDP	OC	501	-	-	2/12/32/32	0/3/3/3
160	GTP	HE	602	159	-	5/18/38/38	0/3/3/3
156	ATP	7b	4701	-	-	4/18/38/38	0/3/3/3
160	GTP	LT	602	159	-	5/18/38/38	0/3/3/3
158	GDP	VH	501	-	-	2/12/32/32	0/3/3/3
158	GDP	AW	501	-	-	2/12/32/32	0/3/3/3
158	GDP	VV	501	-	-	2/12/32/32	0/3/3/3
160	GTP	AF	501	159	-	5/18/38/38	0/3/3/3
160	GTP	WG	501	159	-	2/18/38/38	0/3/3/3
158	GDP	ST	501	-	-	2/12/32/32	0/3/3/3
160	GTP	PK	501	159	-	5/18/38/38	0/3/3/3
160	GTP	VG	501	159	-	5/18/38/38	0/3/3/3
160	GTP	Al	602	159	-	5/18/38/38	0/3/3/3
158	GDP	Aa	501	-	-	2/12/32/32	0/3/3/3
158	GDP	WH	501	-	-	2/12/32/32	0/3/3/3
158	GDP	UM	501	-	-	2/12/32/32	0/3/3/3
160	GTP	TM	501	159	-	5/18/38/38	0/3/3/3
158	GDP	QL	501	-	-	2/12/32/32	0/3/3/3
158	GDP	HJ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	EA	501	159	-	5/18/38/38	0/3/3/3
160	GTP	GS	602	159	-	5/18/38/38	0/3/3/3
160	GTP	KV	602	159	-	5/18/38/38	0/3/3/3
158	GDP	RD	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
156	ATP	7b	4703	-	-	9/18/38/38	0/3/3/3
160	GTP	GM	501	159	-	5/18/38/38	0/3/3/3
158	GDP	PT	501	-	-	2/12/32/32	0/3/3/3
160	GTP	CV	501	159	-	5/18/38/38	0/3/3/3
160	GTP	AR	602	159	-	5/18/38/38	0/3/3/3
160	GTP	GA	602	159	-	5/18/38/38	0/3/3/3
158	GDP	CC	501	-	-	2/12/32/32	0/3/3/3
160	GTP	HW	501	159	-	5/18/38/38	0/3/3/3
158	GDP	LQ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	KP	602	159	-	5/18/38/38	0/3/3/3
156	ATP	7e	4703	-	-	8/18/38/38	0/3/3/3
158	GDP	GF	501	-	-	2/12/32/32	0/3/3/3
158	GDP	JO	501	-	-	2/12/32/32	0/3/3/3
158	GDP	MW	501	-	-	2/12/32/32	0/3/3/3
160	GTP	GE	602	159	-	5/18/38/38	0/3/3/3
160	GTP	CZ	501	159	-	5/18/38/38	0/3/3/3
160	GTP	CB	501	159	-	5/18/38/38	0/3/3/3
160	GTP	WO	501	159	-	5/18/38/38	0/3/3/3
158	GDP	ME	501	-	-	2/12/32/32	0/3/3/3
158	GDP	JI	501	-	-	2/12/32/32	0/3/3/3
158	GDP	BG	501	-	-	2/12/32/32	0/3/3/3
158	GDP	TF	501	-	-	2/12/32/32	0/3/3/3
158	GDP	AE	501	-	-	2/12/32/32	0/3/3/3
160	GTP	NP	501	159	-	5/18/38/38	0/3/3/3
158	GDP	GX	501	-	-	2/12/32/32	0/3/3/3
158	GDP	MY	501	-	-	2/12/32/32	0/3/3/3
158	GDP	IX	501	-	-	2/12/32/32	0/3/3/3
158	GDP	KS	501	-	-	2/12/32/32	0/3/3/3
160	GTP	XS	501	159	-	5/18/38/38	0/3/3/3
158	GDP	OW	501	-	-	2/12/32/32	0/3/3/3
158	GDP	FX	501	-	-	2/12/32/32	0/3/3/3
160	GTP	MB	502	159	-	5/18/38/38	0/3/3/3
158	GDP	US	501	-	-	2/12/32/32	0/3/3/3
158	GDP	EX	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	FF	501	-	-	2/12/32/32	0/3/3/3
158	GDP	TN	501	-	-	2/12/32/32	0/3/3/3
160	GTP	CT	602	159	-	5/18/38/38	0/3/3/3
160	GTP	QG	602	159	-	5/18/38/38	0/3/3/3
158	GDP	QP	501	-	-	2/12/32/32	0/3/3/3
158	GDP	XR	501	-	-	2/12/32/32	0/3/3/3
160	GTP	SG	501	159	-	5/18/38/38	0/3/3/3
158	GDP	UX	501	-	-	2/12/32/32	0/3/3/3
160	GTP	DY	501	159	-	5/18/38/38	0/3/3/3
160	GTP	OX	602	159	-	5/18/38/38	0/3/3/3
158	GDP	ZS	501	-	-	4/12/32/32	0/3/3/3
160	GTP	FK	501	159	-	5/18/38/38	0/3/3/3
160	GTP	GW	501	159	-	5/18/38/38	0/3/3/3
160	GTP	CD	602	159	-	5/18/38/38	0/3/3/3
160	GTP	ZZ	501	159	-	5/18/38/38	0/3/3/3
158	GDP	UO	501	-	-	2/12/32/32	0/3/3/3
160	GTP	II	501	159	-	3/18/38/38	0/3/3/3
160	GTP	NV	503	159	-	5/18/38/38	0/3/3/3
158	GDP	AS	501	-	-	2/12/32/32	0/3/3/3
156	ATP	7f	4703	-	-	9/18/38/38	0/3/3/3
158	GDP	NQ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	JJ	501	159	-	5/18/38/38	0/3/3/3
156	ATP	8e	4703	-	-	5/18/38/38	0/3/3/3
160	GTP	XK	501	159	-	5/18/38/38	0/3/3/3
160	GTP	XW	602	159	-	5/18/38/38	0/3/3/3
158	GDP	XZ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	NN	501	159	-	5/18/38/38	0/3/3/3
158	GDP	SH	501	-	-	2/12/32/32	0/3/3/3
160	GTP	LX	501	159	-	5/18/38/38	0/3/3/3
158	GDP	UZ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	DC	501	-	-	2/12/32/32	0/3/3/3
160	GTP	YA	602	159	-	5/18/38/38	0/3/3/3
158	GDP	BI	501	-	-	2/12/32/32	0/3/3/3
158	GDP	RR	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	KI	501	-	-	2/12/32/32	0/3/3/3
160	GTP	JC	501	159	-	5/18/38/38	0/3/3/3
158	GDP	VJ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	KZ	602	159	-	5/18/38/38	0/3/3/3
158	GDP	XX	501	-	-	2/12/32/32	0/3/3/3
160	GTP	KX	501	159	-	5/18/38/38	0/3/3/3
158	GDP	OI	501	-	-	2/12/32/32	0/3/3/3
158	GDP	PN	501	-	-	2/12/32/32	0/3/3/3
160	GTP	CR	501	159	-	5/18/38/38	0/3/3/3
160	GTP	HS	501	159	-	5/18/38/38	0/3/3/3
158	GDP	QT	501	-	-	2/12/32/32	0/3/3/3
158	GDP	KY	501	-	-	2/12/32/32	0/3/3/3
160	GTP	BF	602	159	-	5/18/38/38	0/3/3/3
160	GTP	AH	501	159	-	5/18/38/38	0/3/3/3
160	GTP	UF	501	159	-	5/18/38/38	0/3/3/3
158	GDP	IP	501	-	-	2/12/32/32	0/3/3/3
156	ATP	9f	4704	-	-	8/18/38/38	0/3/3/3
158	GDP	BU	501	-	-	2/12/32/32	0/3/3/3
160	GTP	GI	501	159	-	5/18/38/38	0/3/3/3
158	GDP	FJ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	DD	501	159	-	5/18/38/38	0/3/3/3
158	GDP	LU	501	-	-	2/12/32/32	0/3/3/3
160	GTP	BT	602	159	-	5/18/38/38	0/3/3/3
158	GDP	Ao	501	-	-	2/12/32/32	0/3/3/3
160	GTP	ZX	501	159	-	5/18/38/38	0/3/3/3
158	GDP	PV	501	-	-	2/12/32/32	0/3/3/3
160	GTP	VY	501	159	-	5/18/38/38	0/3/3/3
160	GTP	HI	602	159	-	5/18/38/38	0/3/3/3
158	GDP	HZ	501	-	-	3/12/32/32	0/3/3/3
160	GTP	EW	501	159	-	5/18/38/38	0/3/3/3
160	GTP	DB	501	159	-	5/18/38/38	0/3/3/3
158	GDP	IT	501	-	-	2/12/32/32	0/3/3/3
158	GDP	AK	501	-	-	2/12/32/32	0/3/3/3
158	GDP	RL	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	KQ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	MK	501	-	-	2/12/32/32	0/3/3/3
160	GTP	NF	502	159	-	5/18/38/38	0/3/3/3
158	GDP	WX	501	-	-	2/12/32/32	0/3/3/3
158	GDP	KE	501	-	-	2/12/32/32	0/3/3/3
158	GDP	YH	501	-	-	2/12/32/32	0/3/3/3
160	GTP	BR	501	159	-	5/18/38/38	0/3/3/3
160	GTP	UT	501	159	-	5/18/38/38	0/3/3/3
158	GDP	HT	501	-	-	2/12/32/32	0/3/3/3
160	GTP	AV	501	159	-	5/18/38/38	0/3/3/3
160	GTP	An	602	159	-	5/18/38/38	0/3/3/3
158	GDP	HR	501	-	-	2/12/32/32	0/3/3/3
160	GTP	GK	602	159	-	5/18/38/38	0/3/3/3
158	GDP	KO	501	-	-	2/12/32/32	0/3/3/3
158	GDP	RT	501	-	-	2/12/32/32	0/3/3/3
158	GDP	WV	501	-	-	2/12/32/32	0/3/3/3
160	GTP	ZL	602	159	-	5/18/38/38	0/3/3/3
160	GTP	YL	602	159	-	5/18/38/38	0/3/3/3
158	GDP	TU	501	-	-	2/12/32/32	0/3/3/3
158	GDP	OQ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	JT	501	159	-	5/18/38/38	0/3/3/3
160	GTP	LR	501	159	-	5/18/38/38	0/3/3/3
158	GDP	LA	501	-	-	2/12/32/32	0/3/3/3
160	GTP	NL	602	159	-	5/18/38/38	0/3/3/3
160	GTP	TX	602	159	-	4/18/38/38	0/3/3/3
160	GTP	VE	501	159	-	5/18/38/38	0/3/3/3
160	GTP	LZ	501	159	-	5/18/38/38	0/3/3/3
158	GDP	OO	501	-	-	2/12/32/32	0/3/3/3
160	GTP	SY	602	159	-	5/18/38/38	0/3/3/3
158	GDP	MM	501	-	-	2/12/32/32	0/3/3/3
160	GTP	CX	602	159	-	5/18/38/38	0/3/3/3
160	GTP	QA	602	159	-	5/18/38/38	0/3/3/3
158	GDP	WP	501	-	-	2/12/32/32	0/3/3/3
158	GDP	GD	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	YB	501	-	-	2/12/32/32	0/3/3/3
160	GTP	OD	602	159	-	5/18/38/38	0/3/3/3
160	GTP	RQ	501	159	-	5/18/38/38	0/3/3/3
158	GDP	VT	501	-	-	2/12/32/32	0/3/3/3
160	GTP	YE	602	159	-	5/18/38/38	0/3/3/3
158	GDP	NU	501	-	-	2/12/32/32	0/3/3/3
158	GDP	SZ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	ZJ	501	159	-	5/18/38/38	0/3/3/3
160	GTP	IY	501	159	-	5/18/38/38	0/3/3/3
160	GTP	QQ	501	159	-	5/18/38/38	0/3/3/3
160	GTP	JZ	501	159	-	5/18/38/38	0/3/3/3
158	GDP	UG	501	-	-	2/12/32/32	0/3/3/3
160	GTP	DS	602	159	-	5/18/38/38	0/3/3/3
158	GDP	HH	501	-	-	2/12/32/32	0/3/3/3
158	GDP	SD	501	-	-	2/12/32/32	0/3/3/3
160	GTP	NT	602	159	-	5/18/38/38	0/3/3/3
158	GDP	FP	501	-	-	2/12/32/32	0/3/3/3
158	GDP	GT	501	-	-	2/12/32/32	0/3/3/3
160	GTP	LF	602	159	-	5/18/38/38	0/3/3/3
160	GTP	UR	501	159	-	5/18/38/38	0/3/3/3
158	GDP	PZ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	MC	501	-	-	2/12/32/32	0/3/3/3
158	GDP	FB	501	-	-	2/12/32/32	0/3/3/3
158	GDP	FZ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	WW	501	159	-	5/18/38/38	0/3/3/3
158	GDP	VX	501	-	-	2/12/32/32	0/3/3/3
160	GTP	PW	501	159	-	5/18/38/38	0/3/3/3
160	GTP	ZR	602	159	-	5/18/38/38	0/3/3/3
160	GTP	XA	501	159	-	5/18/38/38	0/3/3/3
156	ATP	9e	5001	-	-	6/18/38/38	0/3/3/3
158	GDP	CE	501	-	-	2/12/32/32	0/3/3/3
160	GTP	TZ	602	159	-	5/18/38/38	0/3/3/3
158	GDP	AU	501	-	-	2/12/32/32	0/3/3/3
160	GTP	ML	602	159	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	YO	501	-	-	2/12/32/32	0/3/3/3
160	GTP	SO	501	159	-	5/18/38/38	0/3/3/3
160	GTP	ZT	602	159	-	5/18/38/38	0/3/3/3
158	GDP	CK	501	-	-	2/12/32/32	0/3/3/3
160	GTP	ZV	602	159	-	5/18/38/38	0/3/3/3
158	GDP	DA	501	-	-	2/12/32/32	0/3/3/3
158	GDP	WT	501	-	-	2/12/32/32	0/3/3/3
158	GDP	XL	501	-	-	2/12/32/32	0/3/3/3
160	GTP	GC	602	159	-	5/18/38/38	0/3/3/3
158	GDP	FL	602	-	-	2/12/32/32	0/3/3/3
160	GTP	IK	602	159	-	5/18/38/38	0/3/3/3
158	GDP	AI	501	-	-	2/12/32/32	0/3/3/3
158	GDP	LS	501	-	-	2/12/32/32	0/3/3/3
160	GTP	LV	502	159	-	5/18/38/38	0/3/3/3
158	GDP	VR	501	-	-	2/12/32/32	0/3/3/3
160	GTP	VO	501	159	-	5/18/38/38	0/3/3/3
158	GDP	RN	501	-	-	2/12/32/32	0/3/3/3
160	GTP	TI	501	159	-	5/18/38/38	0/3/3/3
160	GTP	DO	501	159	-	5/18/38/38	0/3/3/3
158	GDP	LI	501	-	-	2/12/32/32	0/3/3/3
160	GTP	UL	602	159	-	5/18/38/38	0/3/3/3
158	GDP	OE	501	-	-	2/12/32/32	0/3/3/3
158	GDP	DR	501	-	-	2/12/32/32	0/3/3/3
158	GDP	ZG	501	-	-	2/12/32/32	0/3/3/3
158	GDP	UC	501	-	-	2/12/32/32	0/3/3/3
160	GTP	WM	602	159	-	5/18/38/38	0/3/3/3
160	GTP	AJ	501	159	-	5/18/38/38	0/3/3/3
156	ATP	8f	4702	-	-	8/18/38/38	0/3/3/3
158	GDP	TP	501	-	-	2/12/32/32	0/3/3/3
158	GDP	UQ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	JF	501	-	-	2/12/32/32	0/3/3/3
158	GDP	JK	501	-	-	2/12/32/32	0/3/3/3
158	GDP	BQ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	DT	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	PX	501	-	-	2/12/32/32	0/3/3/3
158	GDP	DG	501	-	-	2/12/32/32	0/3/3/3
160	GTP	FA	602	159	-	5/18/38/38	0/3/3/3
158	GDP	GP	501	-	-	2/12/32/32	0/3/3/3
160	GTP	RI	501	159	-	5/18/38/38	0/3/3/3
160	GTP	UW	602	159	-	5/18/38/38	0/3/3/3
158	GDP	CH	501	-	-	2/12/32/32	0/3/3/3
160	GTP	XY	501	159	-	5/18/38/38	0/3/3/3
158	GDP	WJ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	TA	602	159	-	5/18/38/38	0/3/3/3
158	GDP	AG	501	-	-	4/12/32/32	0/3/3/3
157	ADP	7a	4703	-	-	4/12/32/32	0/3/3/3
160	GTP	EI	501	159	-	5/18/38/38	0/3/3/3
160	GTP	FG	501	159	-	5/18/38/38	0/3/3/3
160	GTP	FW	602	159	-	5/18/38/38	0/3/3/3
160	GTP	XI	602	159	-	5/18/38/38	0/3/3/3
158	GDP	ZK	501	-	-	2/12/32/32	0/3/3/3
160	GTP	FO	602	159	-	5/18/38/38	0/3/3/3
158	GDP	NE	501	-	-	2/12/32/32	0/3/3/3
160	GTP	ZD	501	159	-	5/18/38/38	0/3/3/3
157	ADP	7f	4701	-	-	5/12/32/32	0/3/3/3
160	GTP	JL	501	159	-	6/18/38/38	0/3/3/3
158	GDP	YD	501	-	-	2/12/32/32	0/3/3/3
160	GTP	RM	501	159	-	5/18/38/38	0/3/3/3
160	GTP	OP	501	159	-	5/18/38/38	0/3/3/3
158	GDP	SR	501	-	-	2/12/32/32	0/3/3/3
158	GDP	RJ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	NX	501	159	-	5/18/38/38	0/3/3/3
158	GDP	BK	501	-	-	2/12/32/32	0/3/3/3
160	GTP	QO	602	159	-	5/18/38/38	0/3/3/3
160	GTP	OV	501	159	-	5/18/38/38	0/3/3/3
160	GTP	LP	502	159	-	5/18/38/38	0/3/3/3
156	ATP	8f	4704	-	-	8/18/38/38	0/3/3/3
158	GDP	FR	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
160	GTP	QI	602	159	-	5/18/38/38	0/3/3/3
160	GTP	FY	501	159	-	5/18/38/38	0/3/3/3
160	GTP	GQ	602	159	-	5/18/38/38	0/3/3/3
160	GTP	CL	501	159	-	5/18/38/38	0/3/3/3
160	GTP	PU	602	159	-	5/18/38/38	0/3/3/3
158	GDP	NA	501	-	-	2/12/32/32	0/3/3/3
160	GTP	SC	602	159	-	5/18/38/38	0/3/3/3
160	GTP	QY	501	159	-	5/18/38/38	0/3/3/3
160	GTP	MJ	602	159	-	5/18/38/38	0/3/3/3
160	GTP	RS	501	159	-	5/18/38/38	0/3/3/3
160	GTP	YP	602	159	-	5/18/38/38	0/3/3/3
158	GDP	XJ	501	-	-	3/12/32/32	0/3/3/3
158	GDP	ZY	501	-	-	2/12/32/32	0/3/3/3
158	GDP	EN	501	-	-	2/12/32/32	0/3/3/3
160	GTP	MD	502	159	-	5/18/38/38	0/3/3/3
158	GDP	MQ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	YW	501	-	-	2/12/32/32	0/3/3/3
160	GTP	YC	501	159	-	5/18/38/38	0/3/3/3
158	GDP	GH	501	-	-	2/12/32/32	0/3/3/3
160	GTP	HU	602	159	-	5/18/38/38	0/3/3/3
160	GTP	QC	501	159	-	5/18/38/38	0/3/3/3
158	GDP	JU	501	-	-	2/12/32/32	0/3/3/3
158	GDP	MA	501	-	-	2/12/32/32	0/3/3/3
156	ATP	7f	4702	-	-	7/18/38/38	0/3/3/3
158	GDP	NG	501	-	-	2/12/32/32	0/3/3/3
160	GTP	WS	501	159	-	5/18/38/38	0/3/3/3
160	GTP	WY	602	159	-	5/18/38/38	0/3/3/3
160	GTP	Ah	501	159	-	5/18/38/38	0/3/3/3
160	GTP	IA	501	159	-	5/18/38/38	0/3/3/3
158	GDP	FH	501	-	-	2/12/32/32	0/3/3/3
158	GDP	PP	501	-	-	2/12/32/32	0/3/3/3
160	GTP	TR	501	159	-	5/18/38/38	0/3/3/3
158	GDP	KC	501	-	-	2/12/32/32	0/3/3/3
158	GDP	GV	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
160	GTP	HO	501	159	-	5/18/38/38	0/3/3/3
158	GDP	Ag	501	-	-	2/12/32/32	0/3/3/3
160	GTP	DH	501	159	-	5/18/38/38	0/3/3/3
158	GDP	BA	501	-	-	2/12/32/32	0/3/3/3
158	GDP	MG	501	-	-	2/12/32/32	0/3/3/3
160	GTP	JN	501	159	-	5/18/38/38	0/3/3/3
160	GTP	MV	502	159	-	5/18/38/38	0/3/3/3
160	GTP	AD	501	159	-	5/18/38/38	0/3/3/3
158	GDP	BW	501	-	-	2/12/32/32	0/3/3/3
160	GTP	XO	602	159	-	5/18/38/38	0/3/3/3
158	GDP	MU	501	-	-	2/12/32/32	0/3/3/3
160	GTP	SU	501	159	-	5/18/38/38	0/3/3/3
160	GTP	KB	501	159	-	5/18/38/38	0/3/3/3
160	GTP	VU	501	159	-	5/18/38/38	0/3/3/3
158	GDP	DP	501	-	-	2/12/32/32	0/3/3/3
158	GDP	JB	501	-	-	2/12/32/32	0/3/3/3
160	GTP	KH	501	159	-	5/18/38/38	0/3/3/3
158	GDP	VZ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	IG	501	159	-	5/18/38/38	0/3/3/3
158	GDP	FD	501	-	-	2/12/32/32	0/3/3/3
158	GDP	SX	501	-	-	2/12/32/32	0/3/3/3
160	GTP	YR	501	159	-	5/18/38/38	0/3/3/3
158	GDP	LK	501	-	-	2/12/32/32	0/3/3/3
160	GTP	RW	501	159	-	5/18/38/38	0/3/3/3
158	GDP	DX	501	-	-	2/12/32/32	0/3/3/3
160	GTP	IU	501	159	-	5/18/38/38	0/3/3/3
158	GDP	IB	501	-	-	2/12/32/32	0/3/3/3
158	GDP	SF	501	-	-	2/12/32/32	0/3/3/3
160	GTP	ZN	602	159	-	5/18/38/38	0/3/3/3
158	GDP	HX	501	-	-	2/12/32/32	0/3/3/3
160	GTP	FM	501	159	-	5/18/38/38	0/3/3/3
160	GTP	QU	602	159	-	5/18/38/38	0/3/3/3
158	GDP	DZ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	SP	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
160	GTP	WI	602	159	-	5/18/38/38	0/3/3/3
160	GTP	MN	502	159	-	5/18/38/38	0/3/3/3
158	GDP	UA	501	-	-	2/12/32/32	0/3/3/3
158	GDP	Ae	501	-	-	4/12/32/32	0/3/3/3
158	GDP	OK	501	-	-	2/12/32/32	0/3/3/3
160	GTP	RE	501	159	-	5/18/38/38	0/3/3/3
160	GTP	VI	501	159	-	5/18/38/38	0/3/3/3
160	GTP	Aj	501	159	-	5/18/38/38	0/3/3/3
158	GDP	ID	501	-	-	2/12/32/32	0/3/3/3
156	ATP	7f	4704	-	-	4/18/38/38	0/3/3/3
160	GTP	ZH	501	159	-	5/18/38/38	0/3/3/3
158	GDP	OU	501	-	-	2/12/32/32	0/3/3/3
158	GDP	LO	501	-	-	2/12/32/32	0/3/3/3
160	GTP	IQ	501	159	-	5/18/38/38	0/3/3/3
158	GDP	ZO	501	-	-	2/12/32/32	0/3/3/3
158	GDP	QR	501	-	-	2/12/32/32	0/3/3/3
158	GDP	WB	501	-	-	2/12/32/32	0/3/3/3
158	GDP	VD	501	-	-	2/12/32/32	0/3/3/3
160	GTP	QM	501	159	-	5/18/38/38	0/3/3/3
160	GTP	OF	501	159	-	5/18/38/38	0/3/3/3
160	GTP	DJ	501	159	-	5/18/38/38	0/3/3/3
160	GTP	JH	602	159	-	5/18/38/38	0/3/3/3
158	GDP	DK	501	-	-	2/12/32/32	0/3/3/3
158	GDP	NK	501	-	-	2/12/32/32	0/3/3/3
158	GDP	PR	501	-	-	2/12/32/32	0/3/3/3
158	GDP	RP	501	-	-	2/12/32/32	0/3/3/3
160	GTP	NJ	503	159	-	5/18/38/38	0/3/3/3
160	GTP	XC	602	159	-	5/18/38/38	0/3/3/3
158	GDP	WL	501	-	-	2/12/32/32	0/3/3/3
160	GTP	Af	501	159	-	5/18/38/38	0/3/3/3
158	GDP	PD	501	-	-	2/12/32/32	0/3/3/3
160	GTP	AB	602	159	-	5/18/38/38	0/3/3/3
160	GTP	AP	602	159	-	5/18/38/38	0/3/3/3
160	GTP	CN	602	159	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
160	GTP	EY	501	159	-	5/18/38/38	0/3/3/3
158	GDP	OG	501	-	-	2/12/32/32	0/3/3/3
160	GTP	BL	501	159	-	5/18/38/38	0/3/3/3
160	GTP	OL	602	159	-	5/18/38/38	0/3/3/3
160	GTP	PY	602	159	-	5/18/38/38	0/3/3/3
160	GTP	IO	501	159	-	3/18/38/38	0/3/3/3
160	GTP	WC	501	159	-	5/18/38/38	0/3/3/3
158	GDP	OA	501	-	-	2/12/32/32	0/3/3/3
160	GTP	BH	602	159	-	5/18/38/38	0/3/3/3
160	GTP	OZ	501	159	-	5/18/38/38	0/3/3/3
158	GDP	GN	501	-	-	2/12/32/32	0/3/3/3
158	GDP	JQ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	JY	501	-	-	2/12/32/32	0/3/3/3
158	GDP	CM	501	-	-	2/12/32/32	0/3/3/3
158	GDP	IR	501	-	-	2/12/32/32	0/3/3/3
156	ATP	7a	4701	-	-	5/18/38/38	0/3/3/3
158	GDP	YS	501	-	-	2/12/32/32	0/3/3/3
160	GTP	MH	501	159	-	5/18/38/38	0/3/3/3
160	GTP	EG	501	159	-	5/18/38/38	0/3/3/3
160	GTP	PO	602	159	-	5/18/38/38	0/3/3/3
160	GTP	WU	501	159	-	5/18/38/38	0/3/3/3
160	GTP	OT	602	159	-	5/18/38/38	0/3/3/3
160	GTP	XU	501	159	-	5/18/38/38	0/3/3/3
160	GTP	QS	501	159	-	5/18/38/38	0/3/3/3
158	GDP	JM	501	-	-	2/12/32/32	0/3/3/3
160	GTP	NB	501	159	-	5/18/38/38	0/3/3/3
158	GDP	UE	501	-	-	2/12/32/32	0/3/3/3
158	GDP	IL	501	-	-	2/12/32/32	0/3/3/3
158	GDP	XP	501	-	-	2/12/32/32	0/3/3/3
158	GDP	ZQ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	TY	501	-	-	2/12/32/32	0/3/3/3
158	GDP	GJ	501	-	-	2/12/32/32	0/3/3/3
160	GTP	TO	501	159	-	5/18/38/38	0/3/3/3
158	GDP	XV	501	-	-	2/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
160	GTP	HG	501	159	-	5/18/38/38	0/3/3/3
160	GTP	KJ	602	159	-	5/18/38/38	0/3/3/3
160	GTP	PM	602	159	-	5/18/38/38	0/3/3/3
158	GDP	CA	501	-	-	2/12/32/32	0/3/3/3
158	GDP	QD	501	-	-	2/12/32/32	0/3/3/3
160	GTP	CF	501	159	-	5/18/38/38	0/3/3/3
158	GDP	AA	501	-	-	2/12/32/32	0/3/3/3
156	ATP	9e	5003	-	-	5/18/38/38	0/3/3/3
158	GDP	EB	501	-	-	2/12/32/32	0/3/3/3
158	GDP	LE	501	-	-	2/12/32/32	0/3/3/3
158	GDP	QF	501	-	-	2/12/32/32	0/3/3/3
158	GDP	NM	501	-	-	2/12/32/32	0/3/3/3
156	ATP	9f	4701	-	-	9/18/38/38	0/3/3/3
160	GTP	SI	501	159	-	5/18/38/38	0/3/3/3
160	GTP	SE	501	159	-	5/18/38/38	0/3/3/3
158	GDP	AY	501	-	-	2/12/32/32	0/3/3/3
158	GDP	ED	501	-	-	2/12/32/32	0/3/3/3
158	GDP	JW	501	-	-	2/12/32/32	0/3/3/3
158	GDP	QX	501	-	-	2/12/32/32	0/3/3/3
158	GDP	JG	501	-	-	2/12/32/32	0/3/3/3
158	GDP	OM	501	-	-	2/12/32/32	0/3/3/3
158	GDP	RX	501	-	-	2/12/32/32	0/3/3/3
160	GTP	RA	602	159	-	5/18/38/38	0/3/3/3
158	GDP	YU	501	-	-	2/12/32/32	0/3/3/3
160	GTP	YJ	602	159	-	5/18/38/38	0/3/3/3
158	GDP	SL	501	-	-	2/12/32/32	0/3/3/3
160	GTP	YN	501	159	-	5/18/38/38	0/3/3/3
160	GTP	KR	602	159	-	5/18/38/38	0/3/3/3
158	GDP	CU	501	-	-	2/12/32/32	0/3/3/3
160	GTP	HK	501	159	-	5/18/38/38	0/3/3/3
158	GDP	ZI	501	-	-	2/12/32/32	0/3/3/3
160	GTP	MF	602	159	-	5/18/38/38	0/3/3/3
160	GTP	EM	501	159	-	5/18/38/38	0/3/3/3
160	GTP	ZB	501	159	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
160	GTP	BN	602	159	-	5/18/38/38	0/3/3/3
160	GTP	DF	501	159	-	5/18/38/38	0/3/3/3
158	GDP	BO	501	-	-	2/12/32/32	0/3/3/3
160	GTP	HM	602	159	-	5/18/38/38	0/3/3/3
160	GTP	LL	501	159	-	5/18/38/38	0/3/3/3
158	GDP	VF	501	-	-	2/12/32/32	0/3/3/3
158	GDP	XH	501	-	-	2/12/32/32	0/3/3/3
158	GDP	GR	501	-	-	2/12/32/32	0/3/3/3
160	GTP	QE	501	159	-	5/18/38/38	0/3/3/3
160	GTP	QW	501	159	-	5/18/38/38	0/3/3/3
160	GTP	WQ	602	159	-	5/18/38/38	0/3/3/3
160	GTP	TV	501	159	-	5/18/38/38	0/3/3/3
160	GTP	EO	501	159	-	5/18/38/38	0/3/3/3
158	GDP	RH	501	-	-	2/12/32/32	0/3/3/3
160	GTP	OH	501	159	-	5/18/38/38	0/3/3/3
158	GDP	YQ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	TJ	501	-	-	2/12/32/32	0/3/3/3
158	GDP	UI	501	-	-	2/12/32/32	0/3/3/3
160	GTP	DQ	501	159	-	5/18/38/38	0/3/3/3
160	GTP	SS	602	159	-	2/18/38/38	0/3/3/3
158	GDP	QB	501	-	-	2/12/32/32	0/3/3/3
158	GDP	DI	501	-	-	2/12/32/32	0/3/3/3
158	GDP	SV	501	-	-	2/12/32/32	0/3/3/3
160	GTP	ZF	602	159	-	5/18/38/38	0/3/3/3
160	GTP	VQ	501	159	-	5/18/38/38	0/3/3/3
160	GTP	MT	501	159	-	5/18/38/38	0/3/3/3
160	GTP	BZ	501	159	-	5/18/38/38	0/3/3/3
158	GDP	GB	501	-	-	2/12/32/32	0/3/3/3
158	GDP	TW	501	-	-	2/12/32/32	0/3/3/3
160	GTP	UH	501	159	-	5/18/38/38	0/3/3/3
160	GTP	PC	602	159	-	5/18/38/38	0/3/3/3
160	GTP	EU	501	159	-	5/18/38/38	0/3/3/3
160	GTP	PQ	501	159	-	5/18/38/38	0/3/3/3
160	GTP	UB	501	159	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
158	GDP	TD	501	-	-	2/12/32/32	0/3/3/3
158	GDP	ZA	501	-	-	2/12/32/32	0/3/3/3
160	GTP	CP	602	159	-	5/18/38/38	0/3/3/3
160	GTP	JR	602	159	-	5/18/38/38	0/3/3/3
160	GTP	SA	501	159	-	4/18/38/38	0/3/3/3

The worst 5 of 794 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
160	EC	501	GTP	C5-C6	-4.59	1.38	1.47
160	JP	602	GTP	C5-C6	-4.55	1.38	1.47
160	WA	602	GTP	C5-C6	-4.52	1.38	1.47
160	IE	501	GTP	C5-C6	-4.52	1.38	1.47
160	JR	602	GTP	C5-C6	-4.51	1.38	1.47

The worst 5 of 1054 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
160	EW	501	GTP	O6-C6-N1	-4.11	115.75	120.62
160	SA	501	GTP	O6-C6-N1	-4.07	115.79	120.62
160	SS	602	GTP	O6-C6-N1	-3.92	115.96	120.62
160	IO	501	GTP	O6-C6-N1	-3.84	116.06	120.62
158	AS	501	GDP	O6-C6-N1	-3.83	116.08	120.62

There are no chirality outliers.

5 of 2573 torsion outliers are listed below:

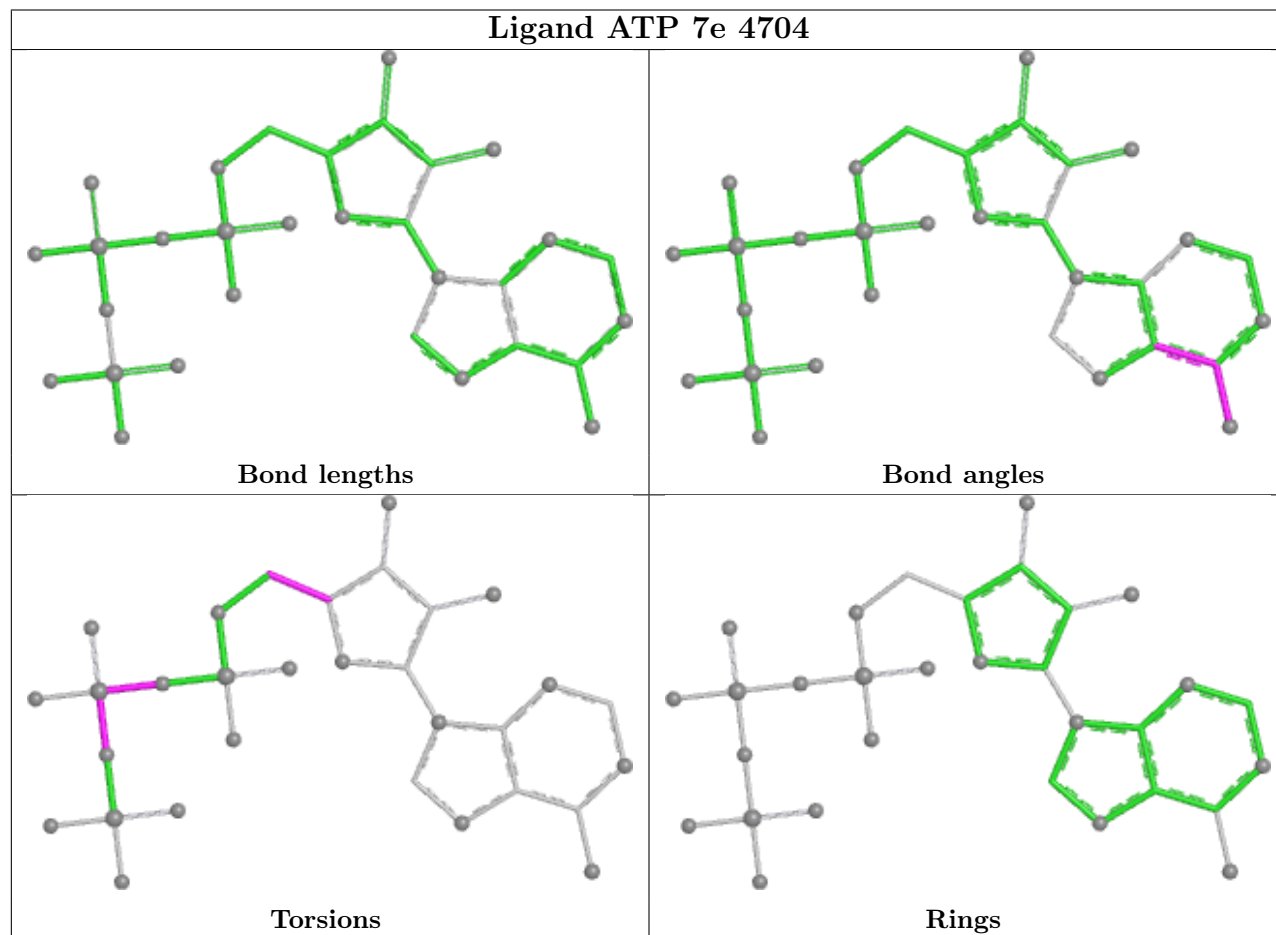
Mol	Chain	Res	Type	Atoms
156	7a	4701	ATP	C5'-O5'-PA-O3A
156	7a	4701	ATP	C4'-C5'-O5'-PA
156	7a	4702	ATP	PB-O3B-PG-O2G
156	7a	4702	ATP	C5'-O5'-PA-O2A
156	7a	4702	ATP	C5'-O5'-PA-O3A

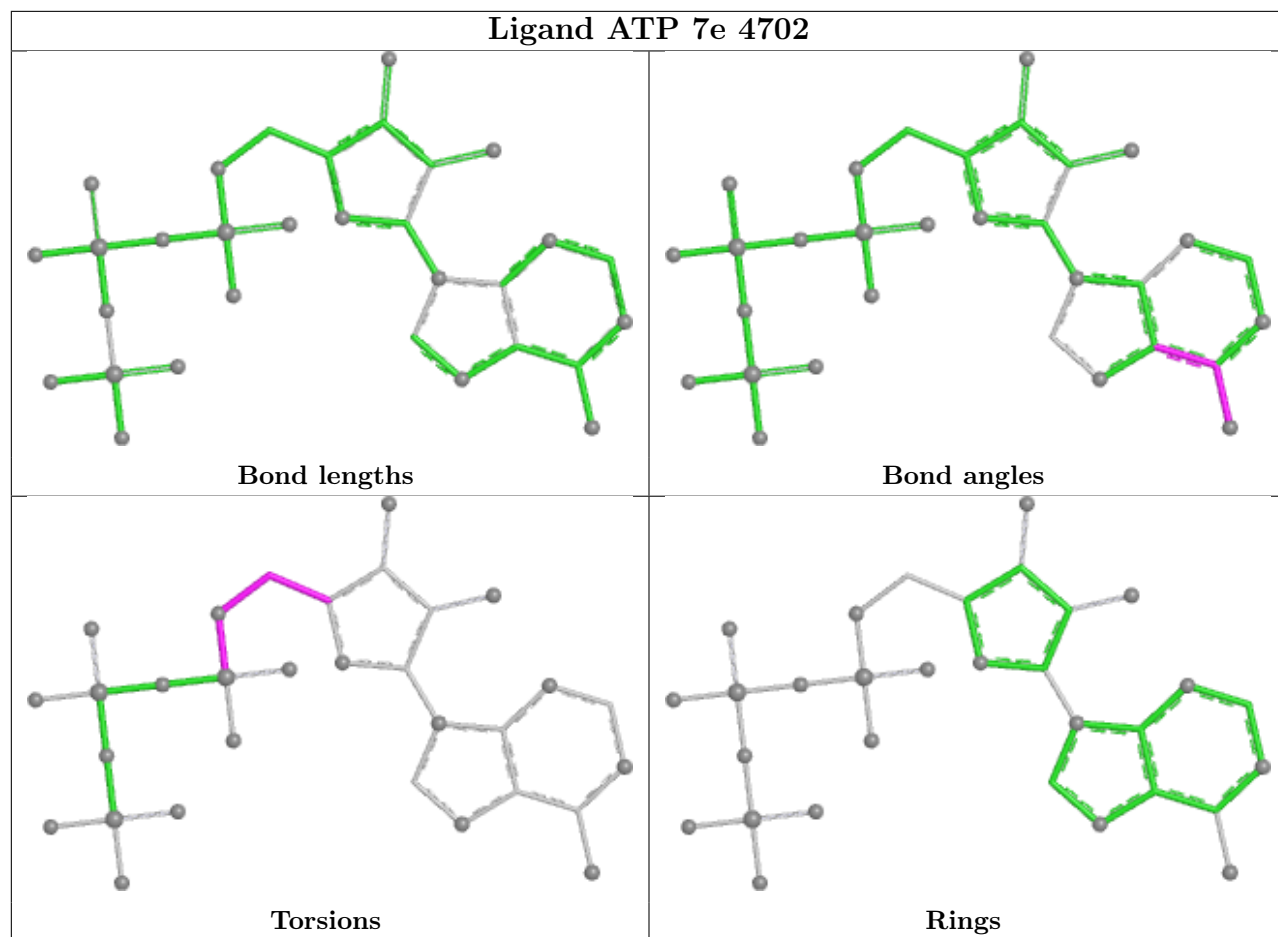
There are no ring outliers.

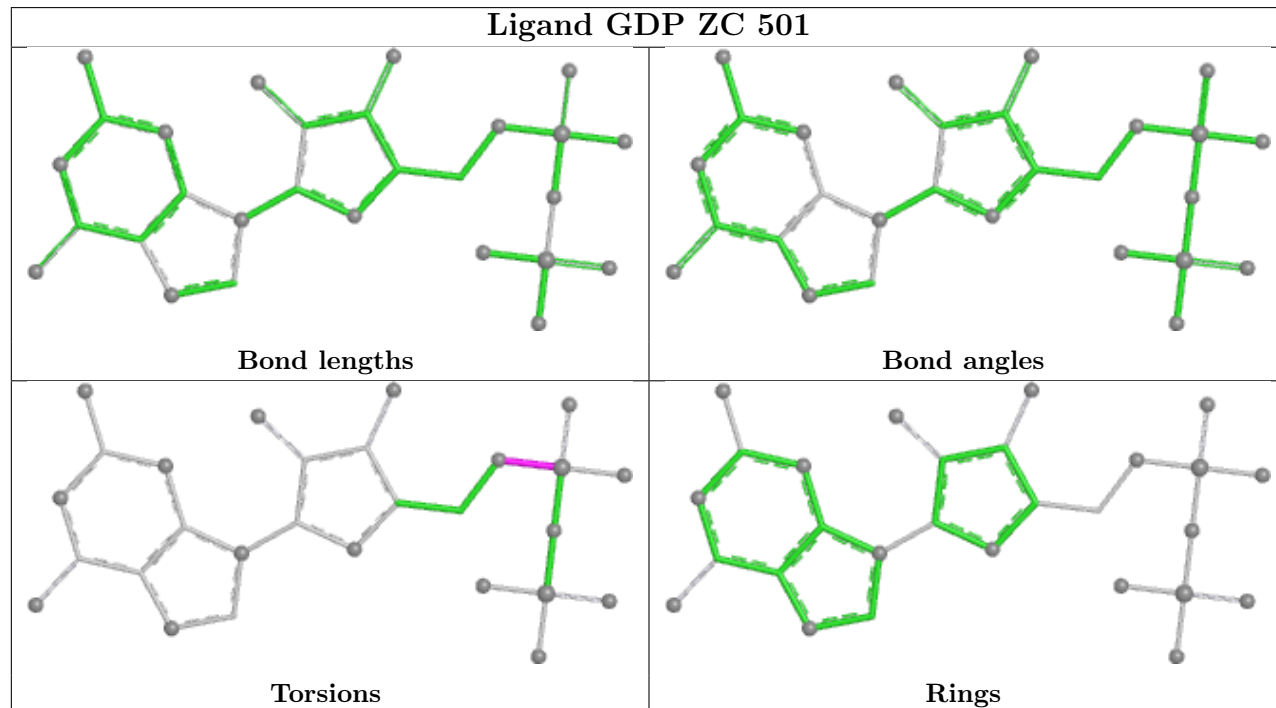
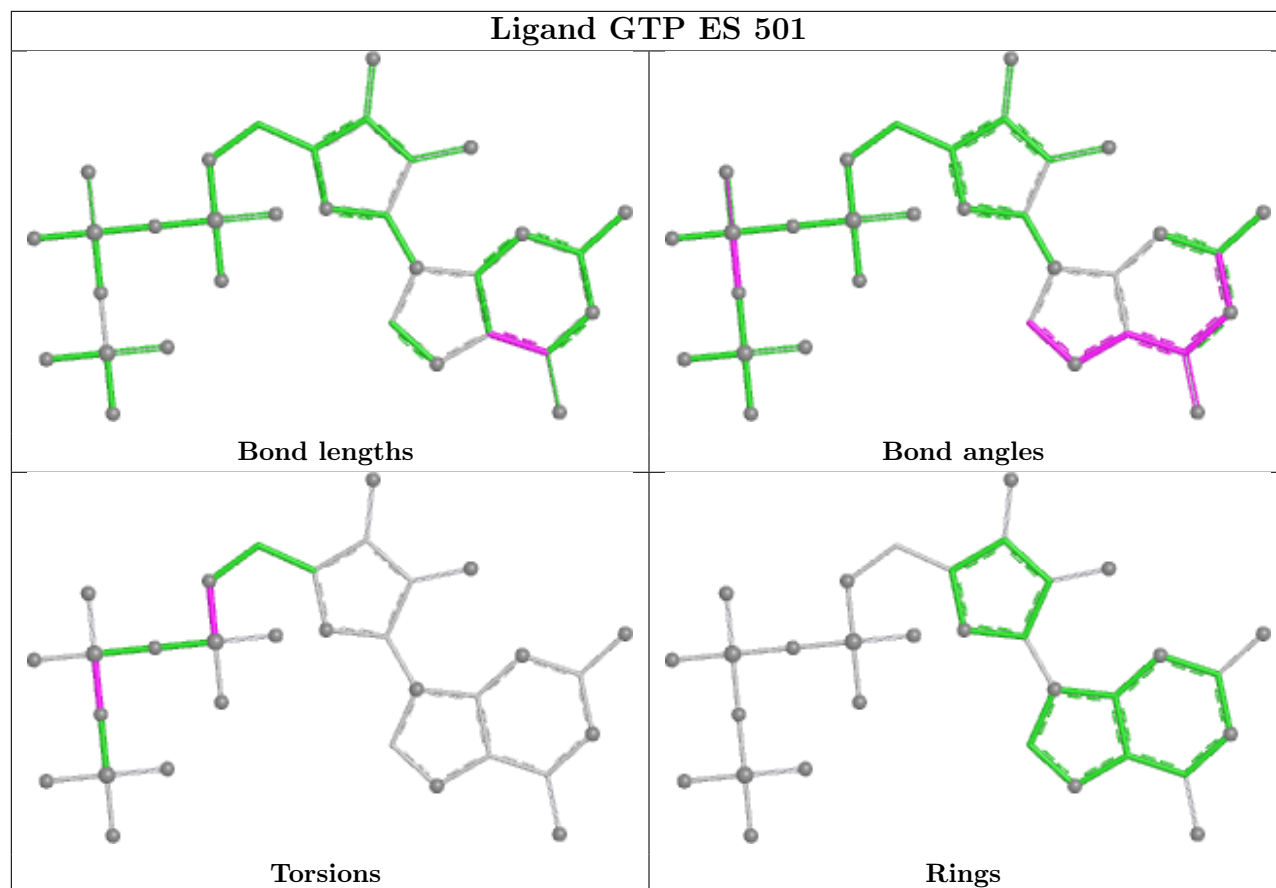
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

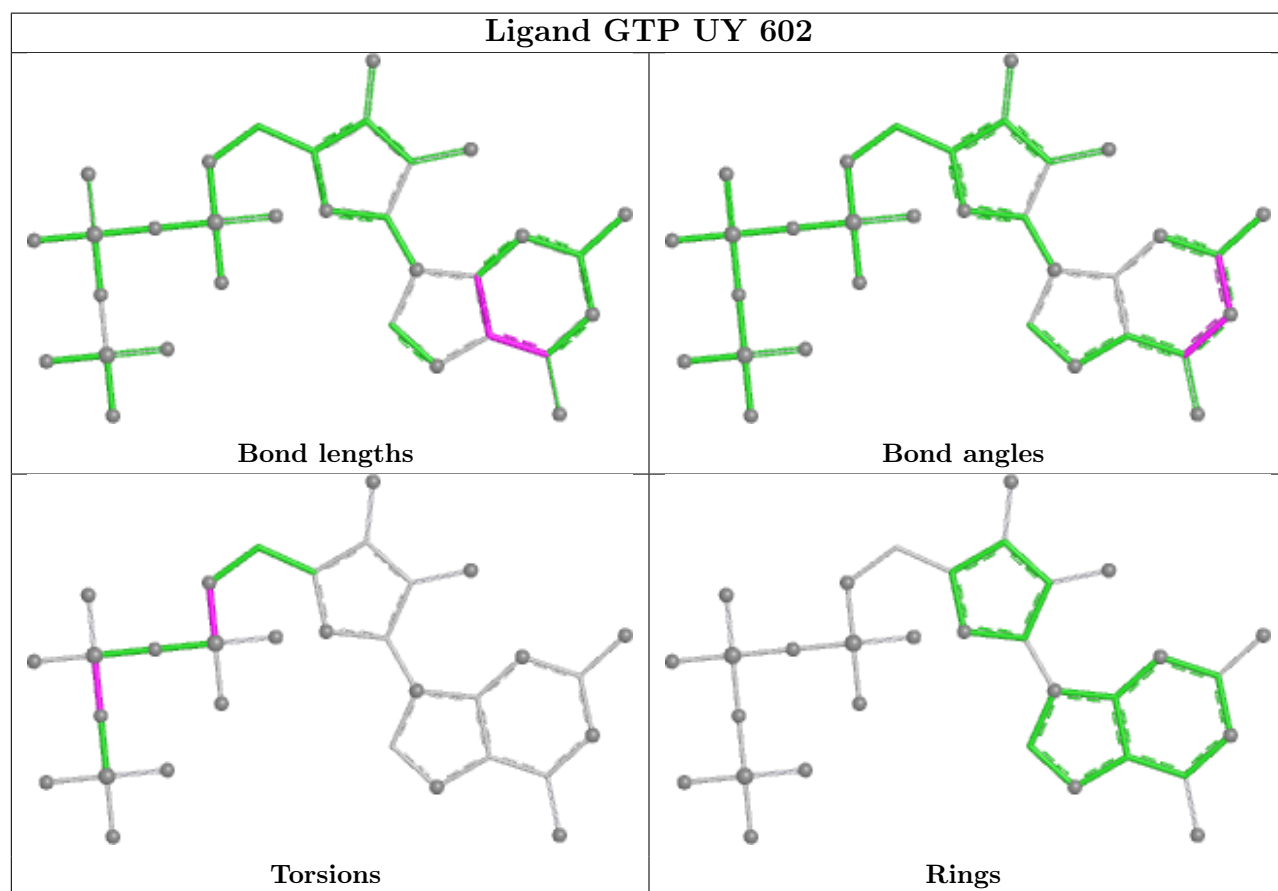
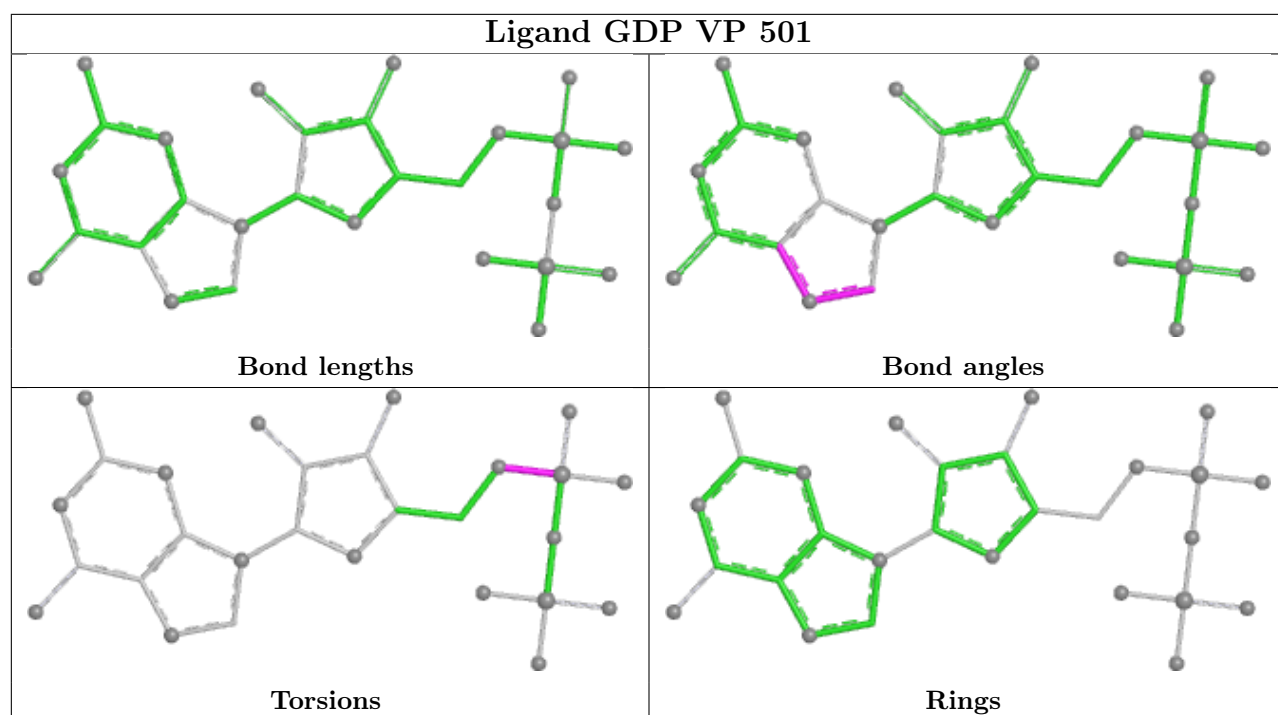
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

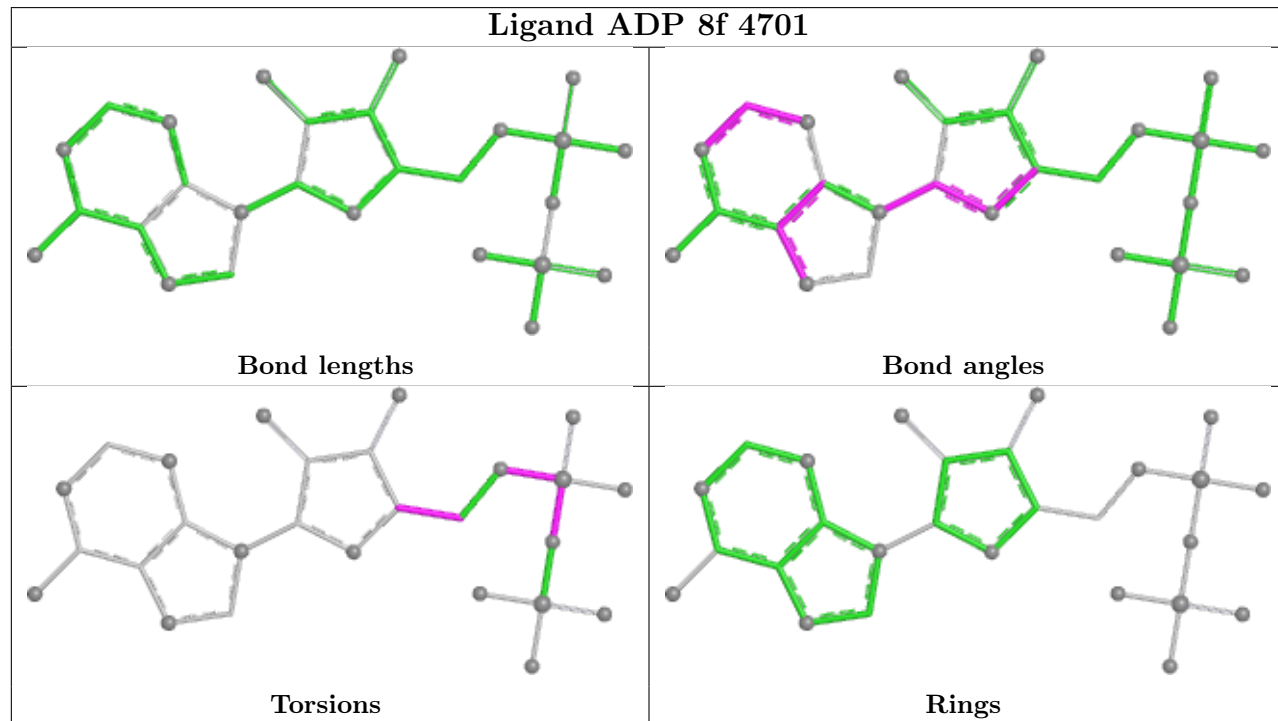
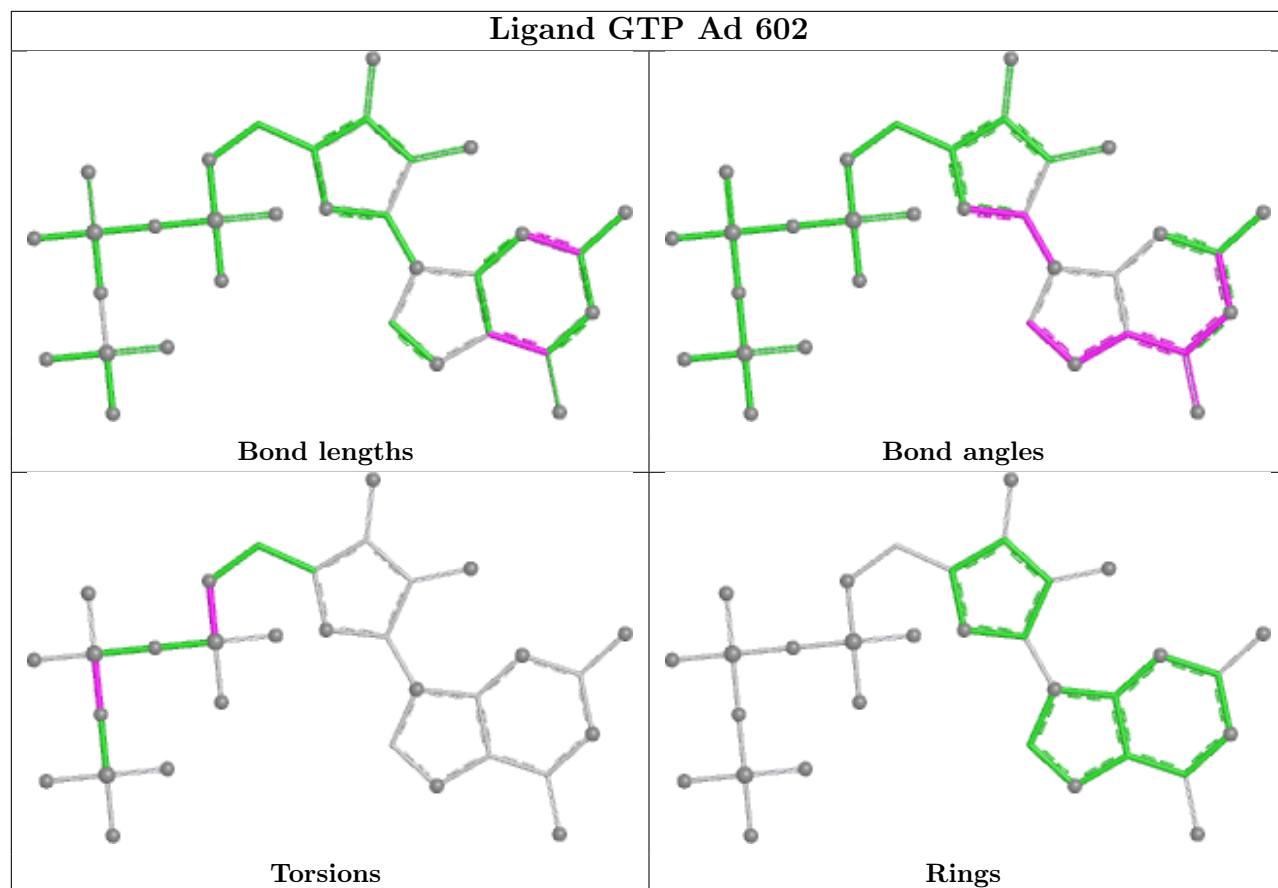


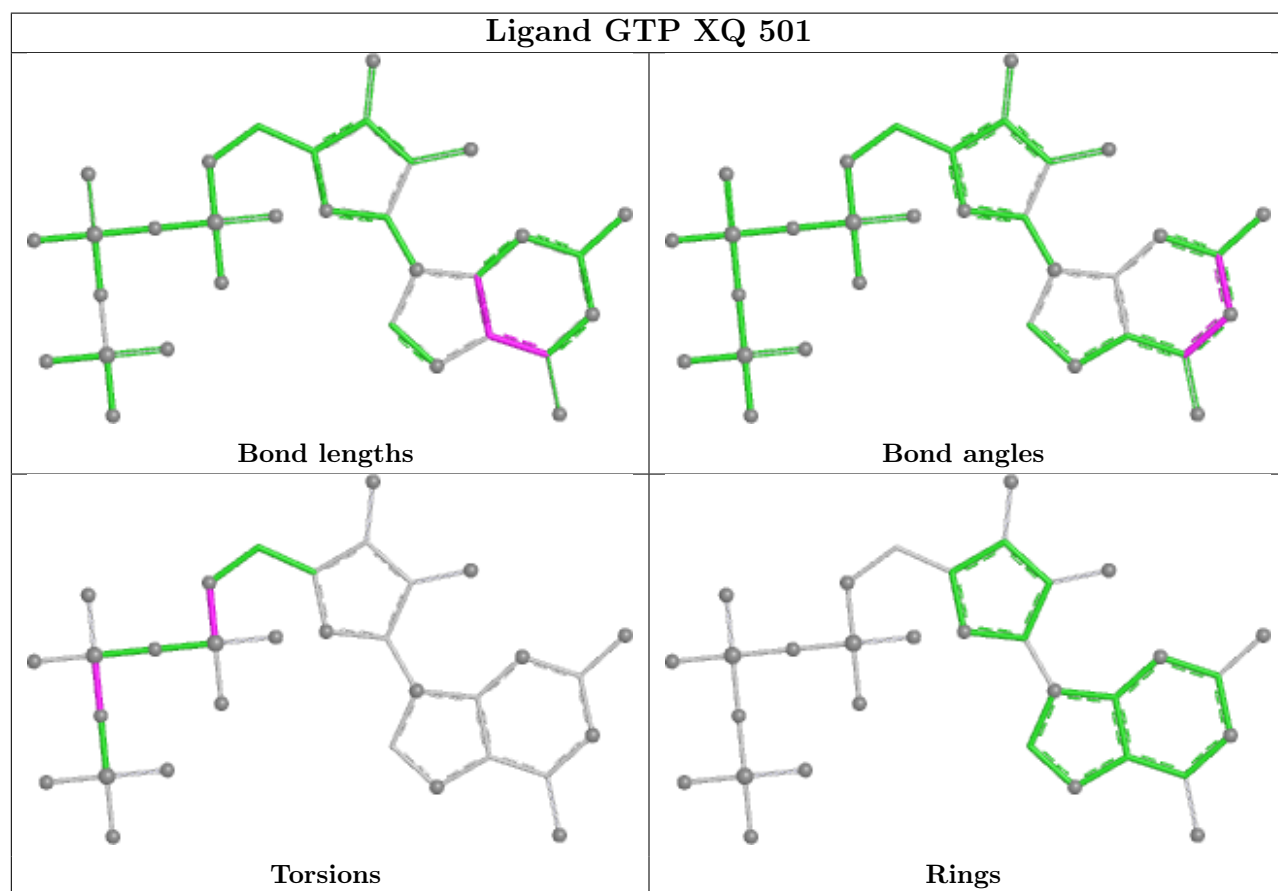
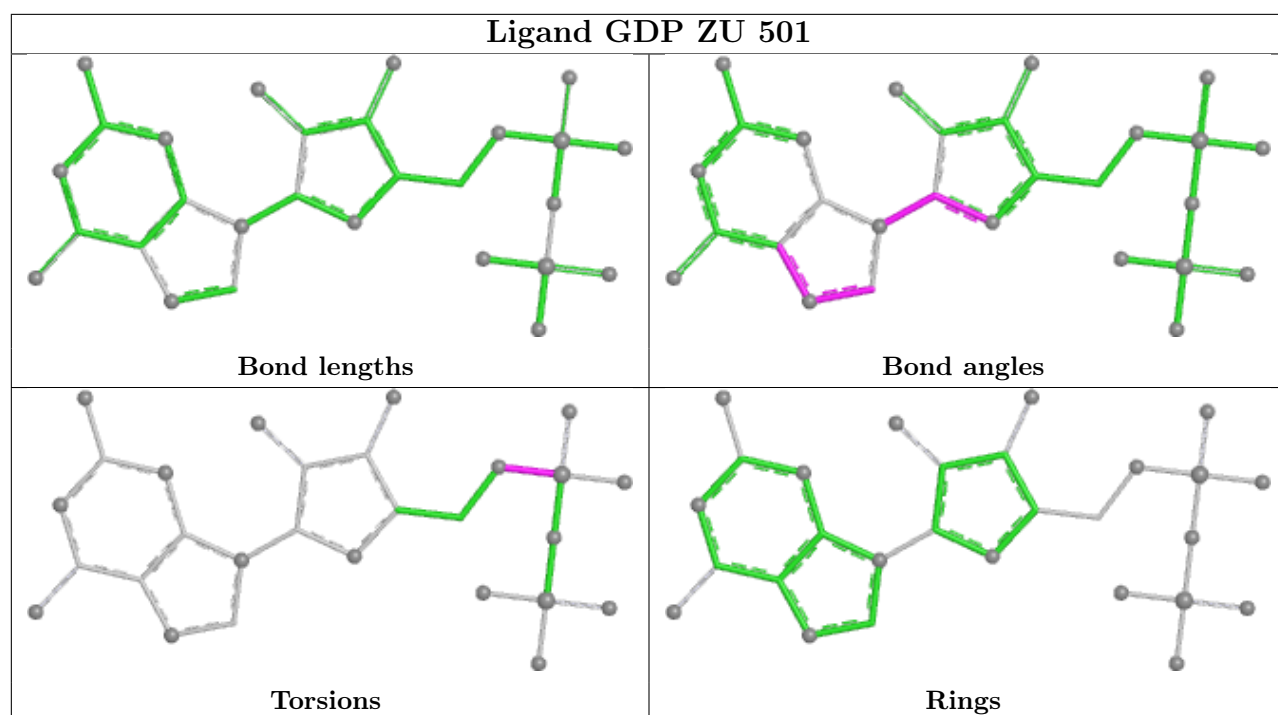




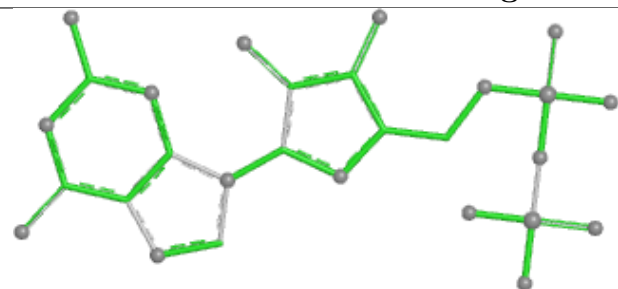




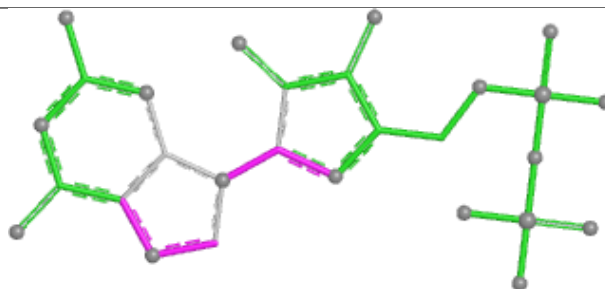




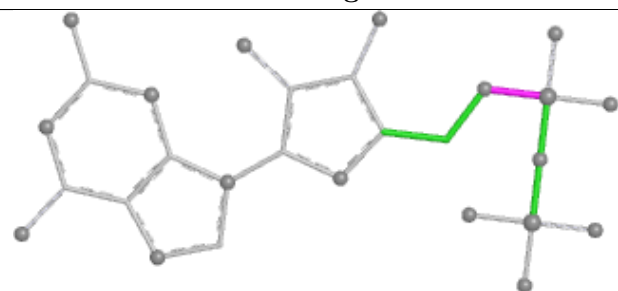
## Ligand GDP UK 501



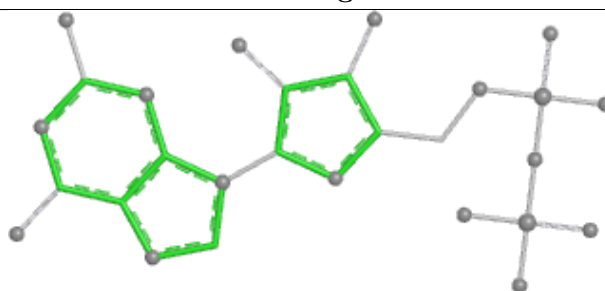
Bond lengths



Bond angles

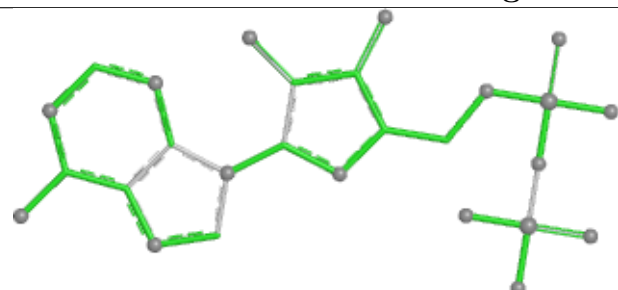


Torsions

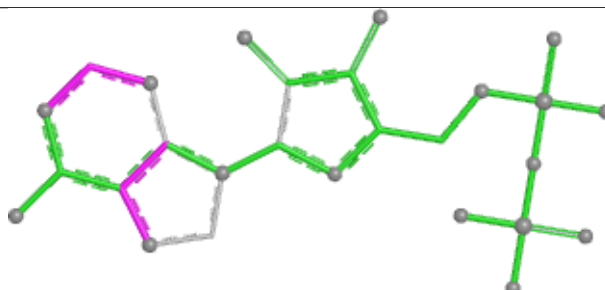


Rings

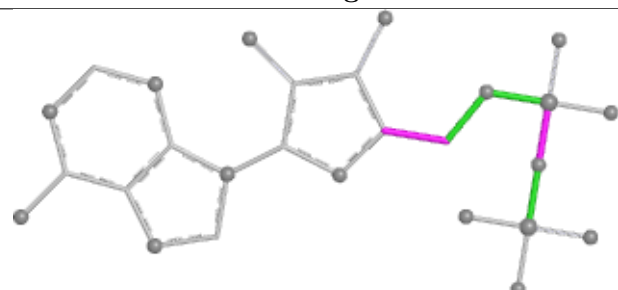
## Ligand ADP 7e 4701



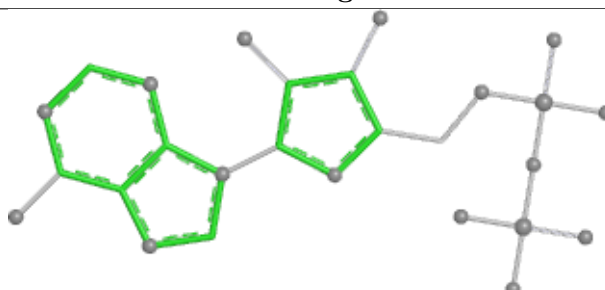
Bond lengths



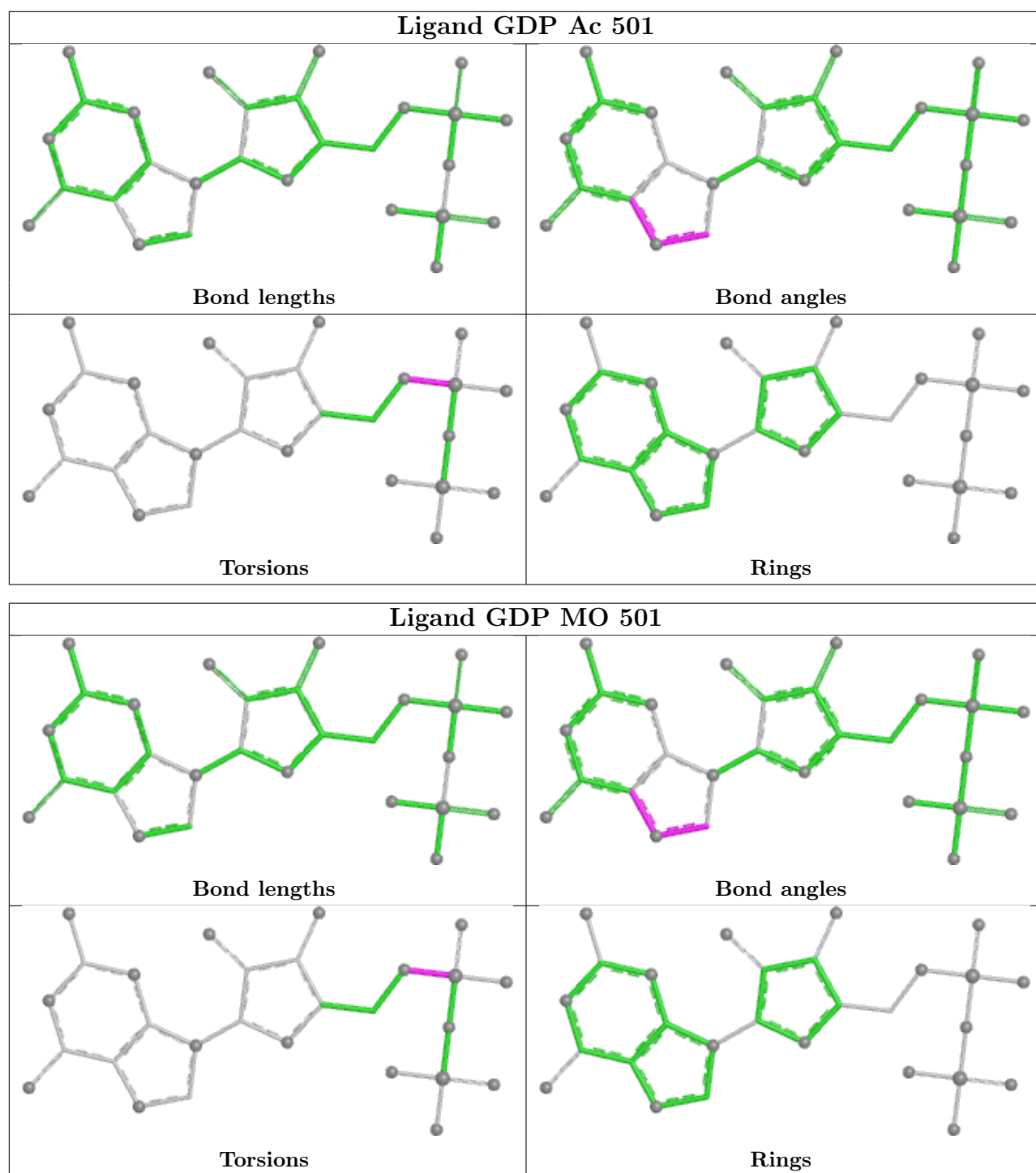
Bond angles



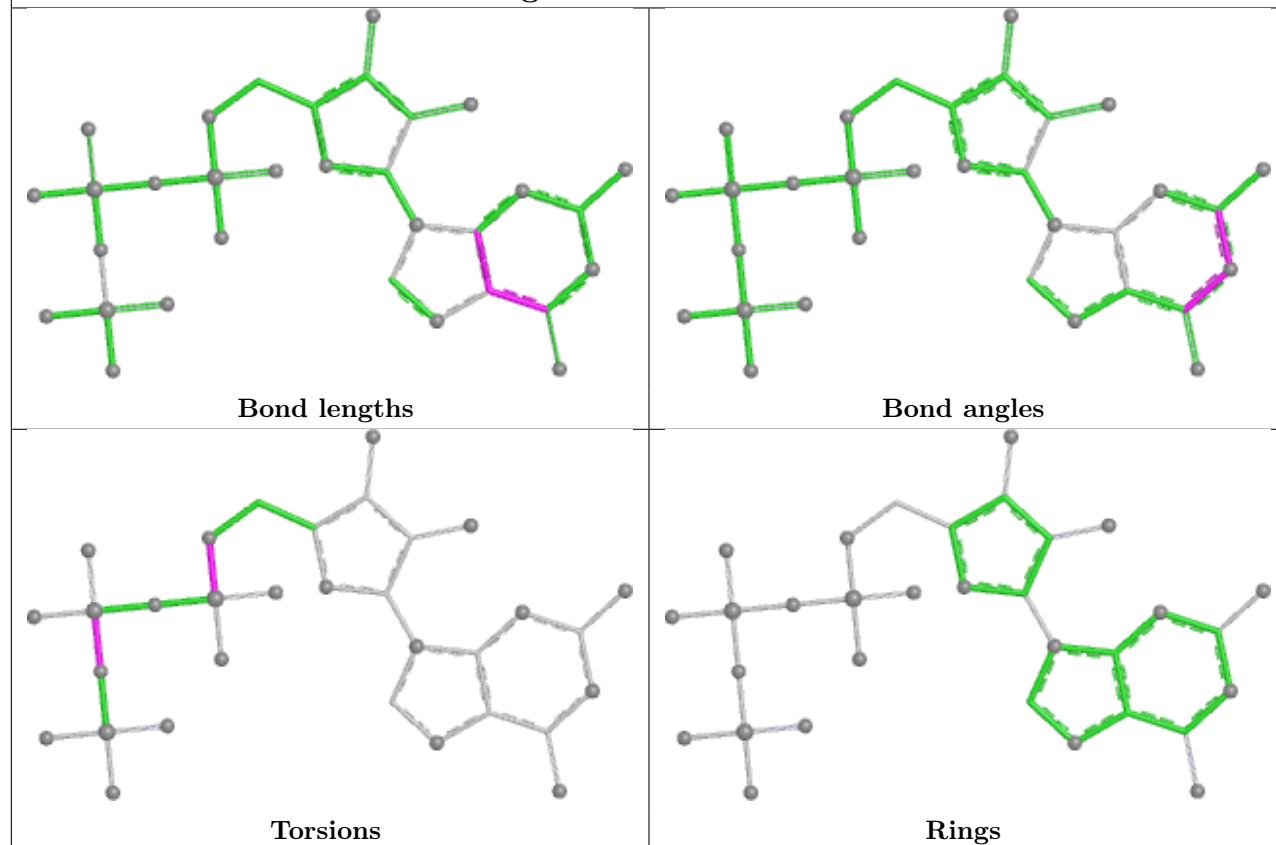
Torsions



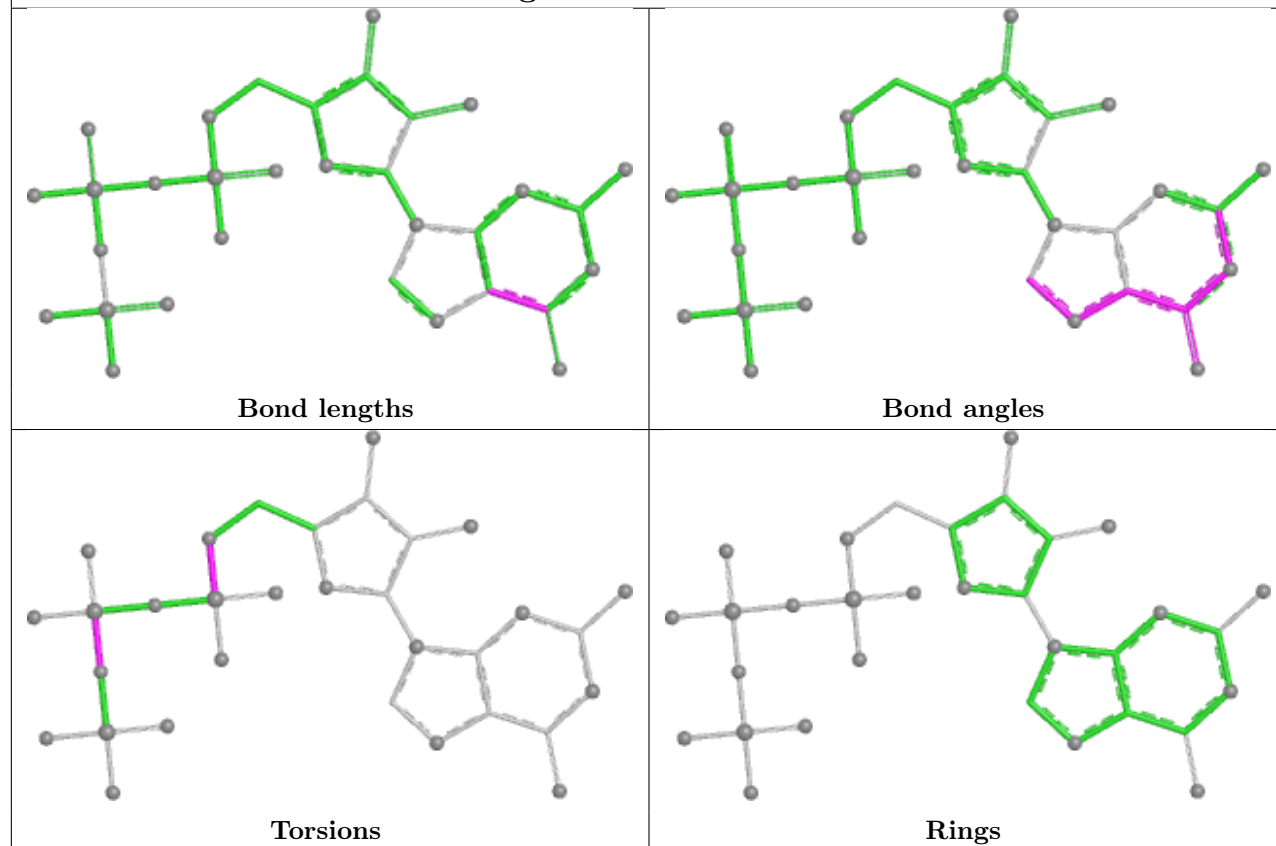
Rings

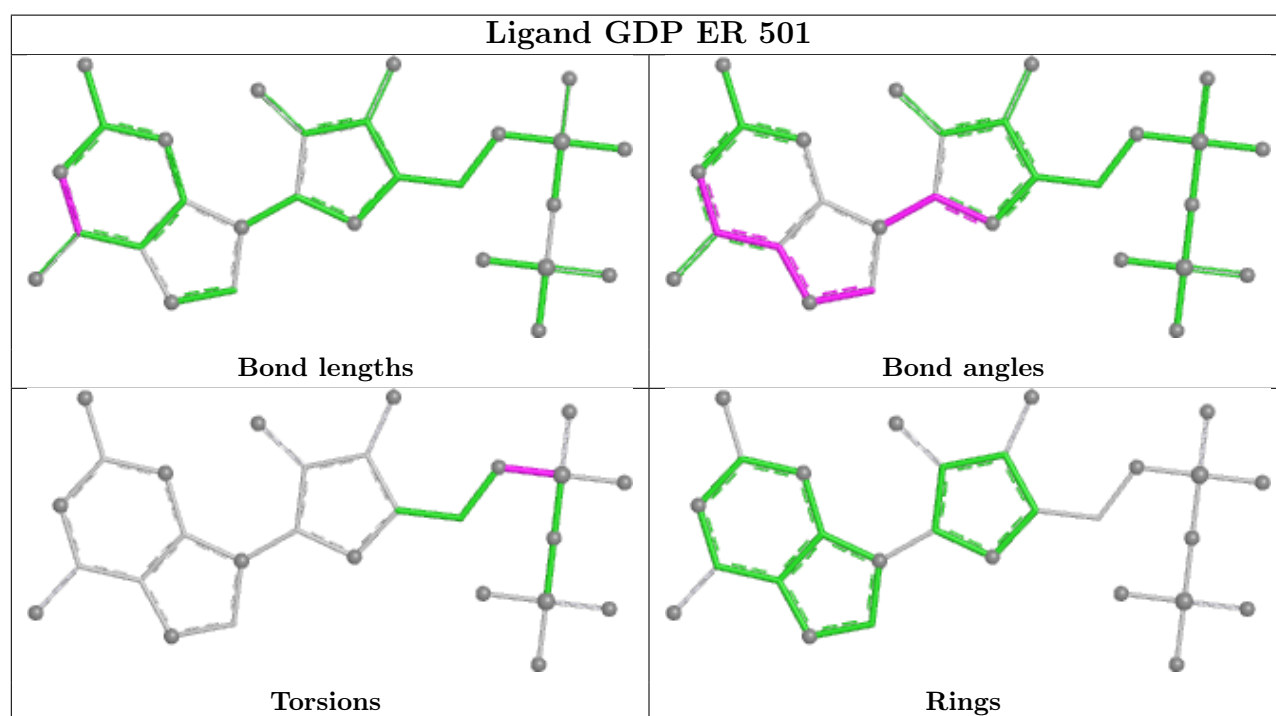
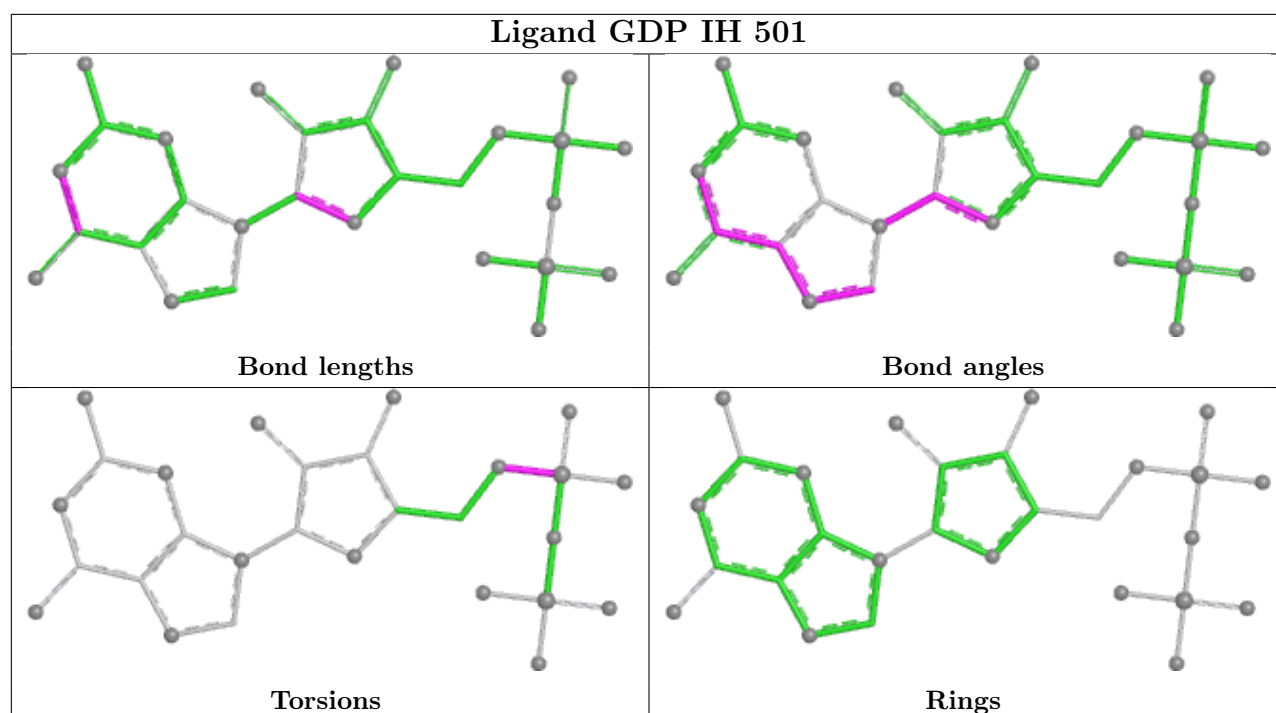


## Ligand GTP CJ 501

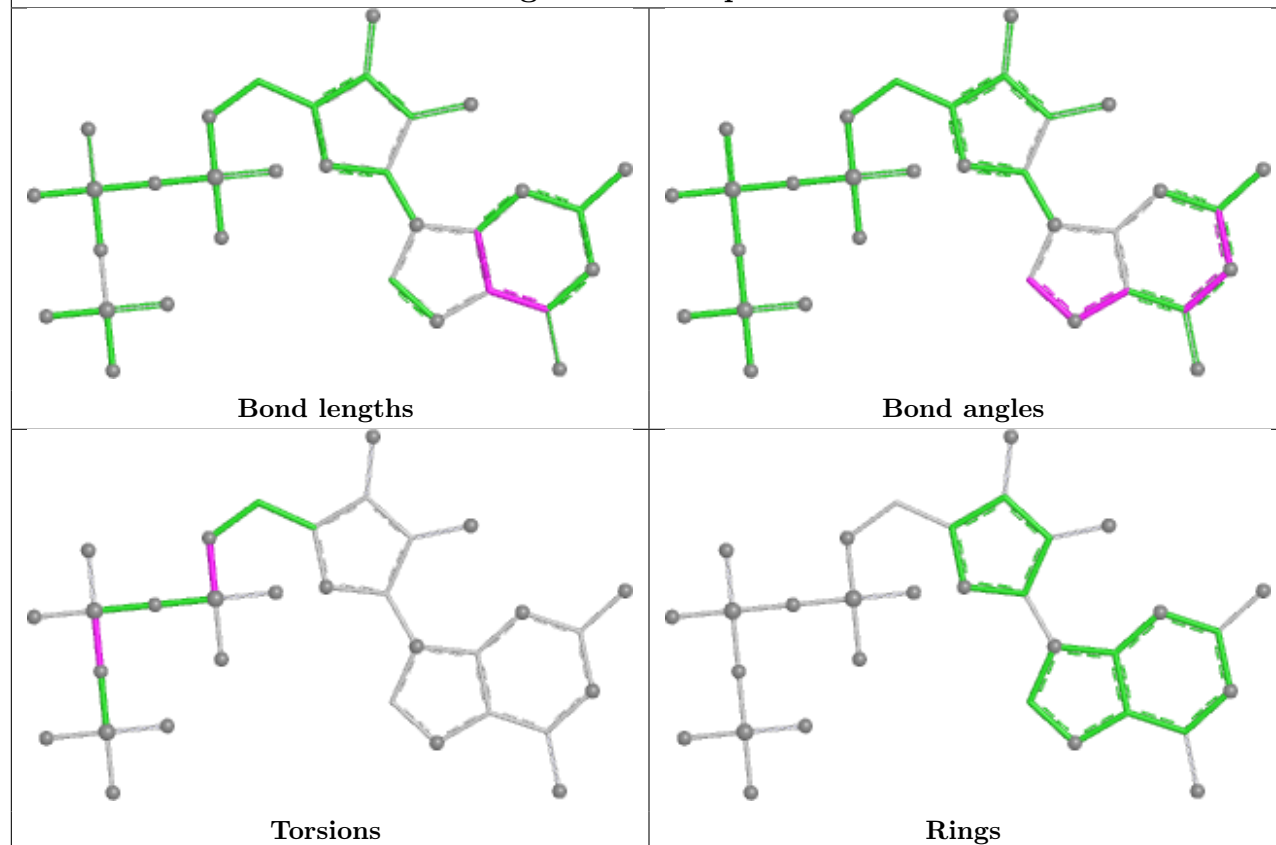


## Ligand GTP EC 501

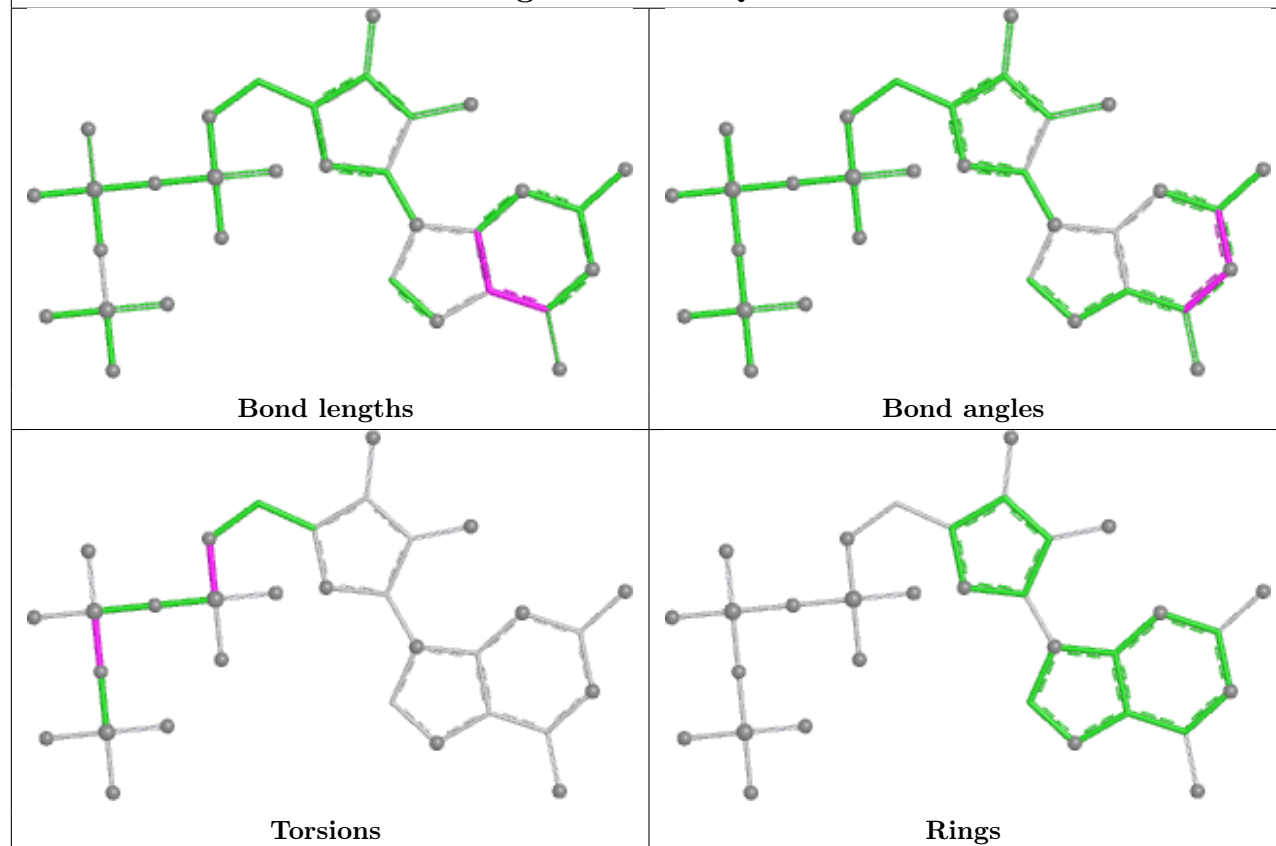




## Ligand GTP Ap 501

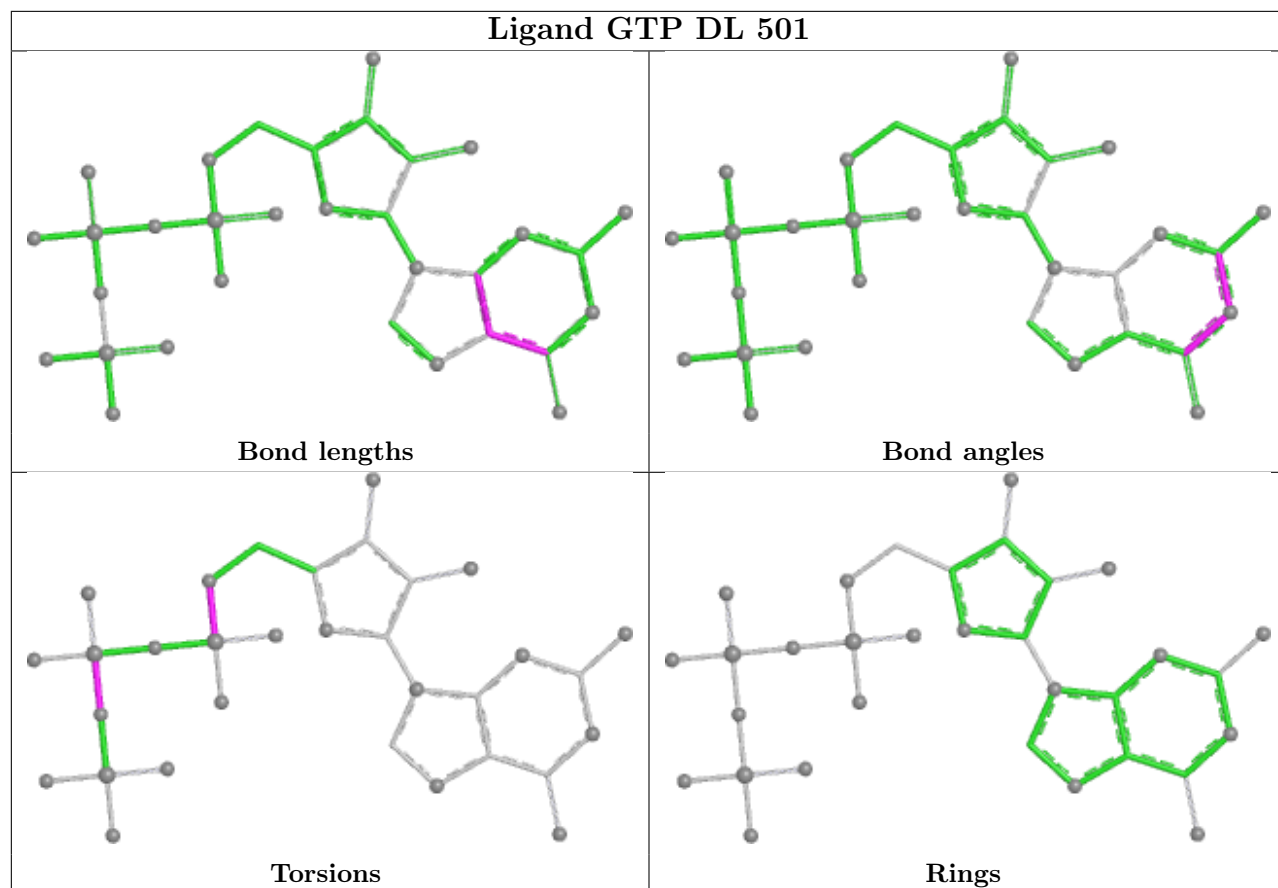


## Ligand GTP HQ 602

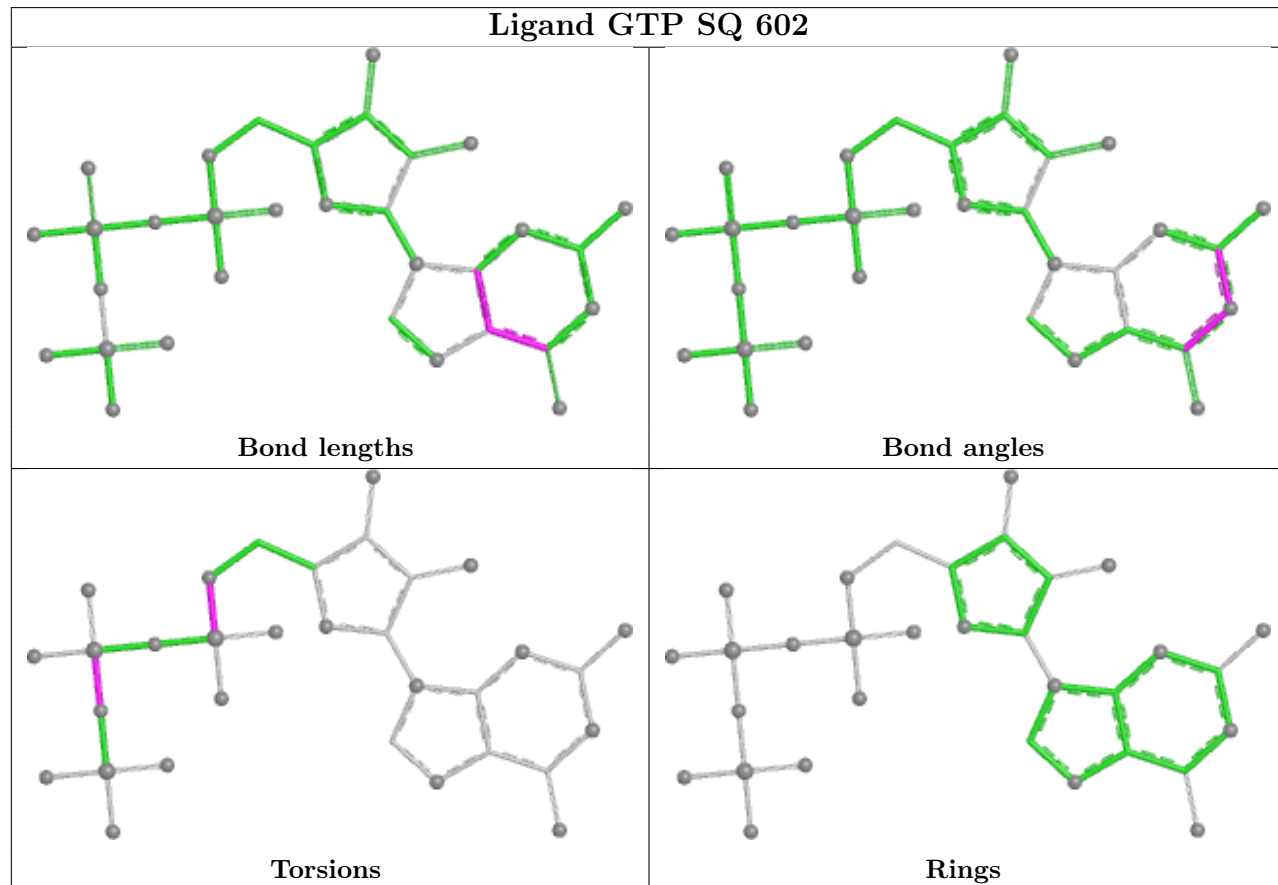




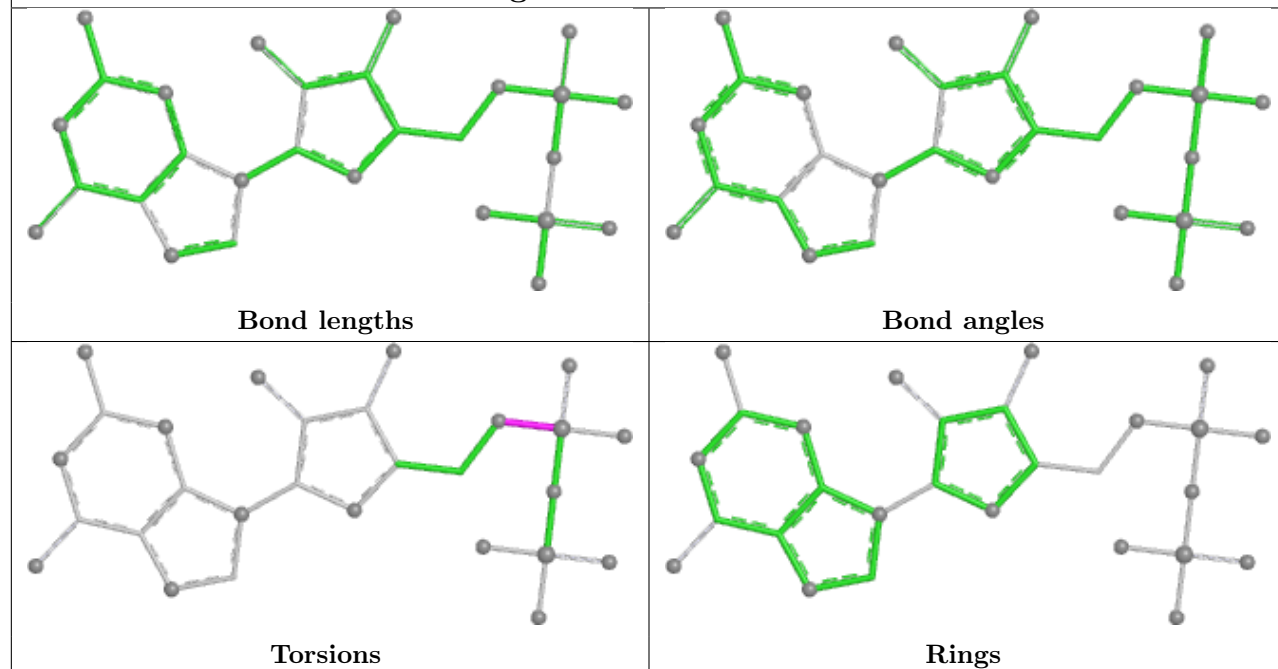
## Ligand GTP DL 501



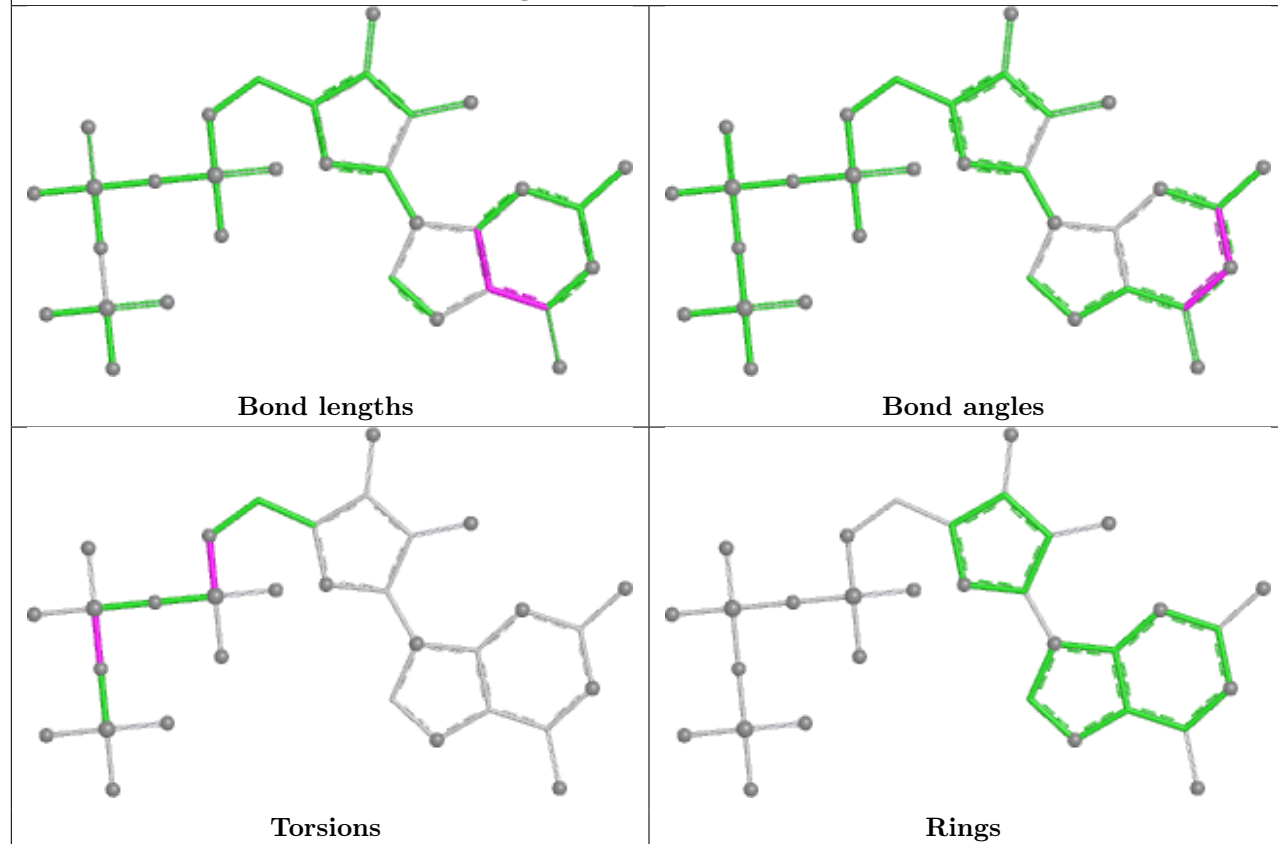
## Ligand GTP SQ 602



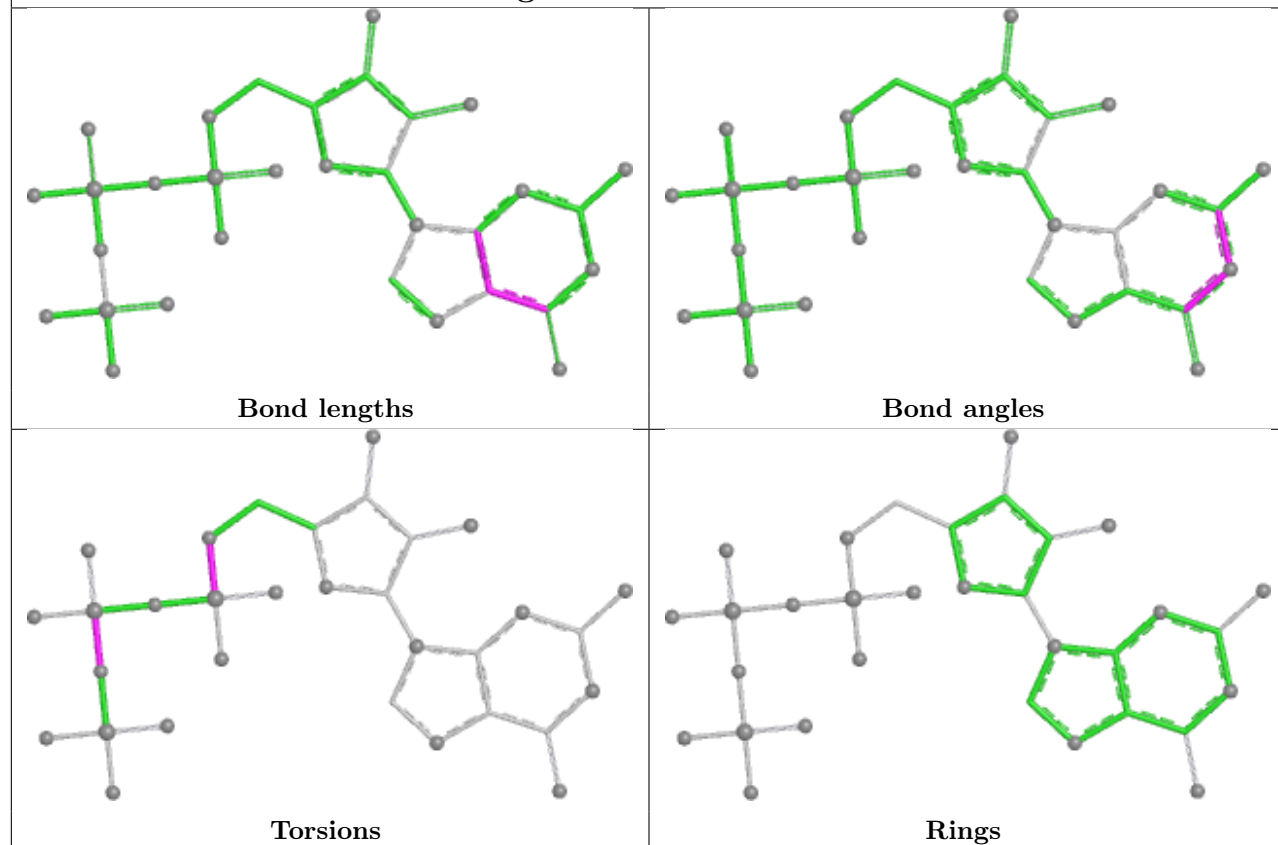
## Ligand GDP KW 501



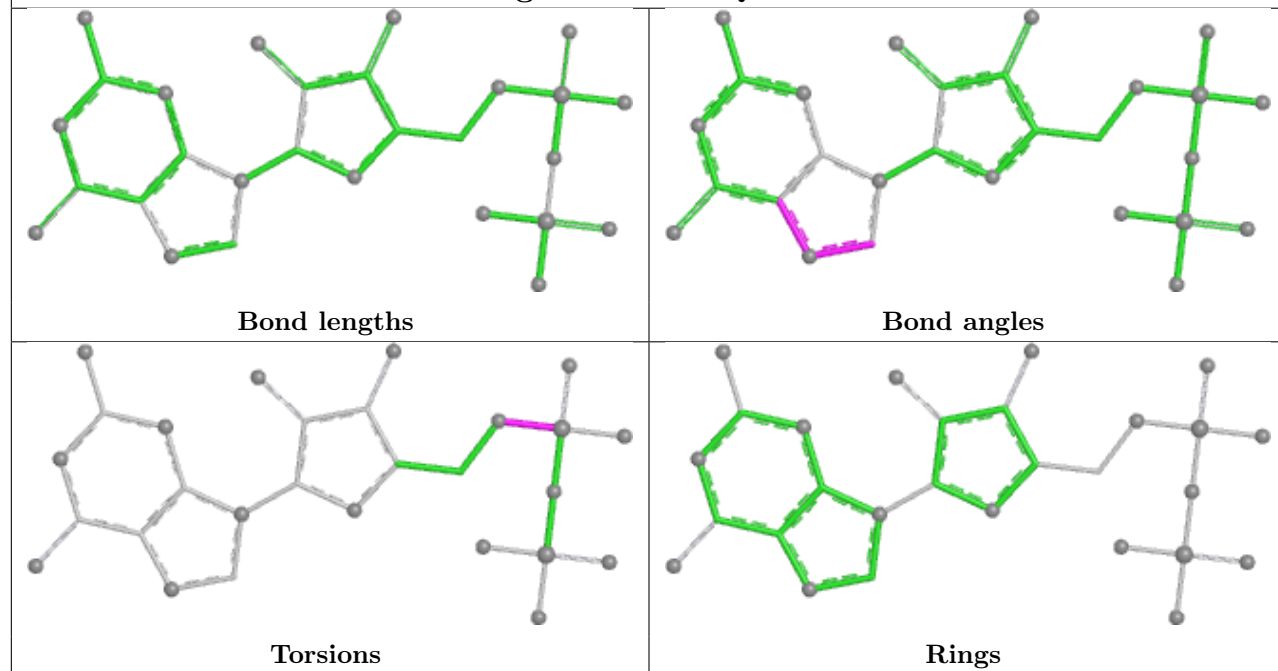
## Ligand GTP UN 602

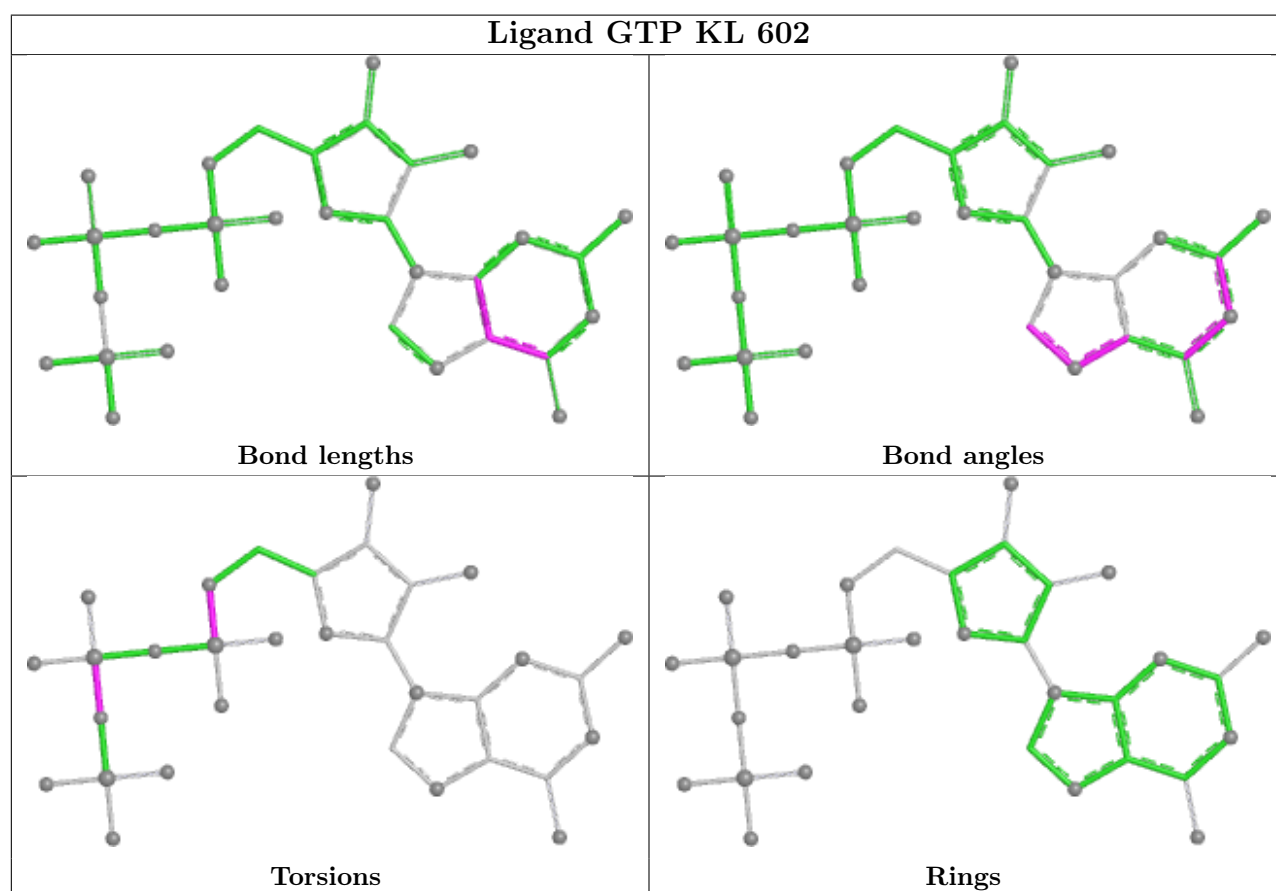
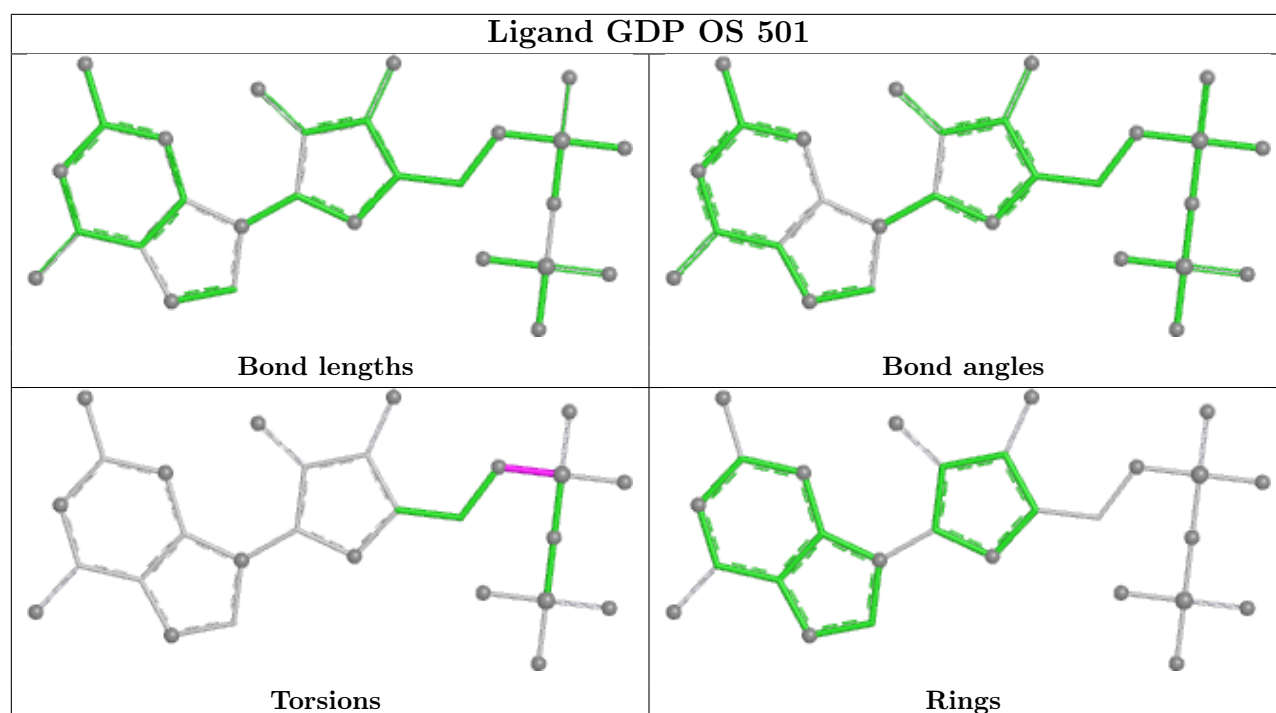


## Ligand GTP BV 602

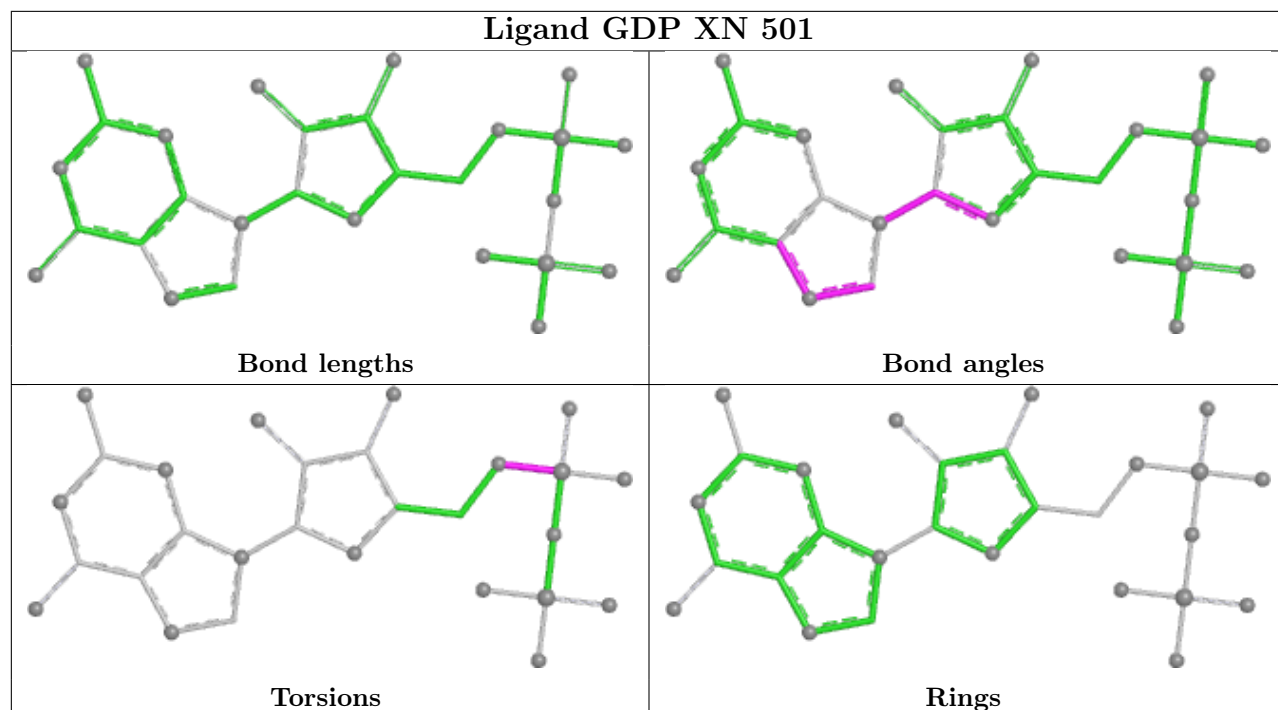


## Ligand GDP CQ 501

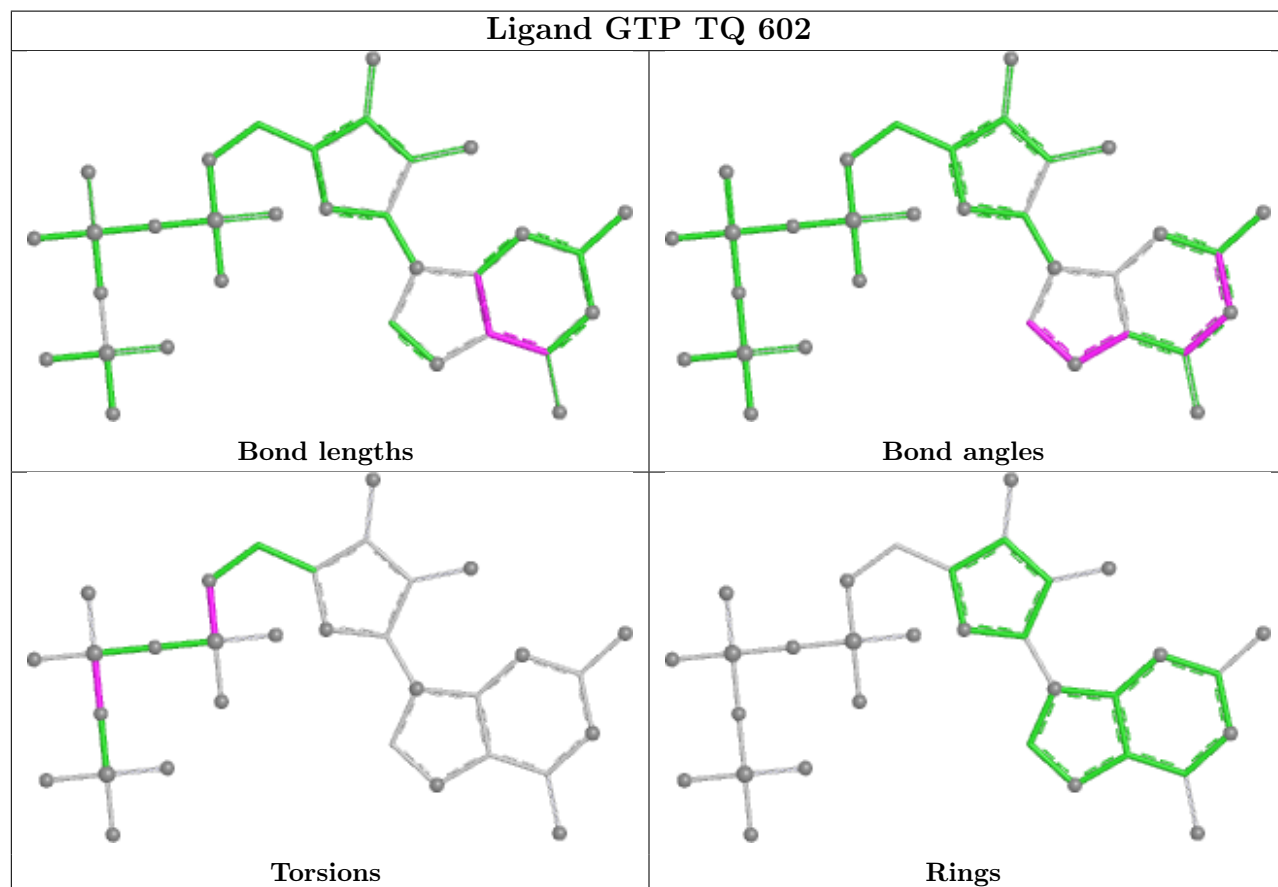




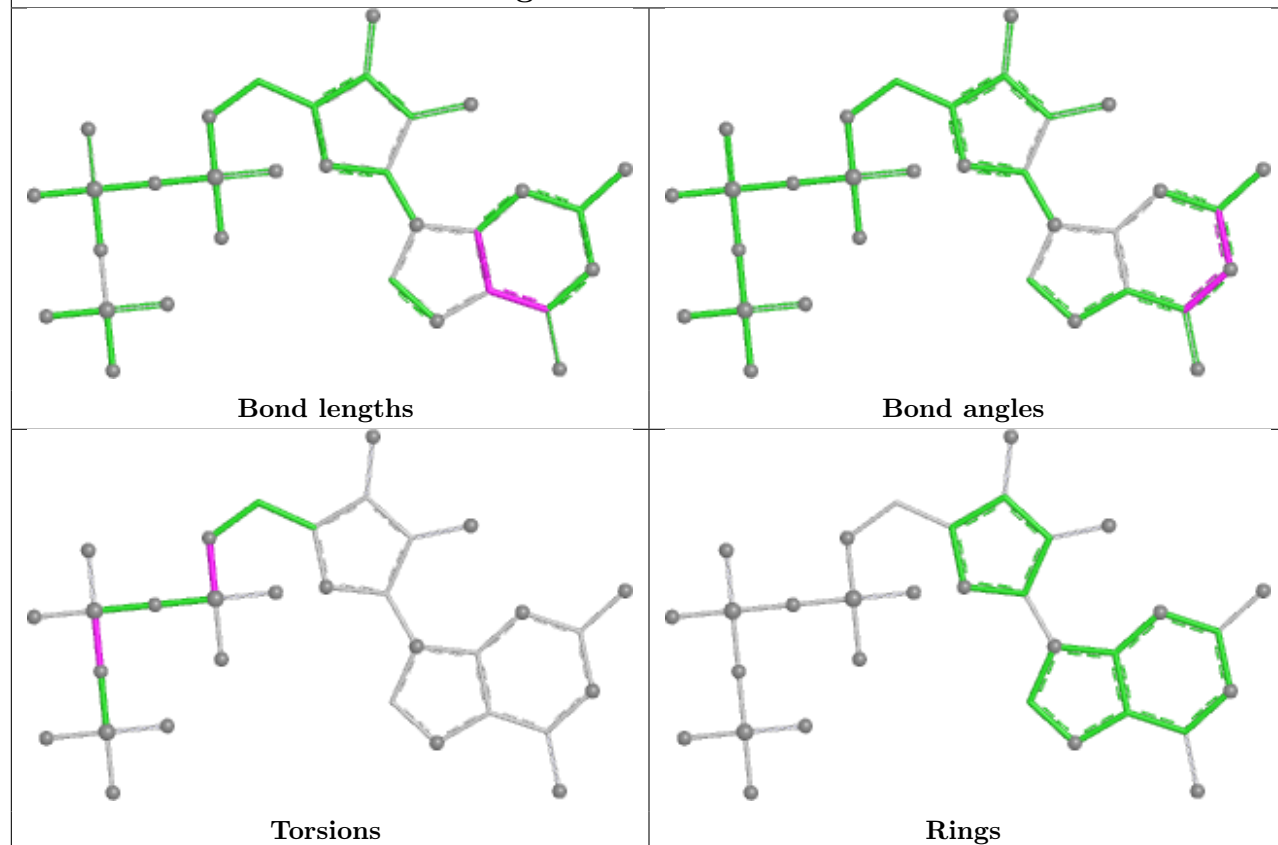
## Ligand GDP XN 501



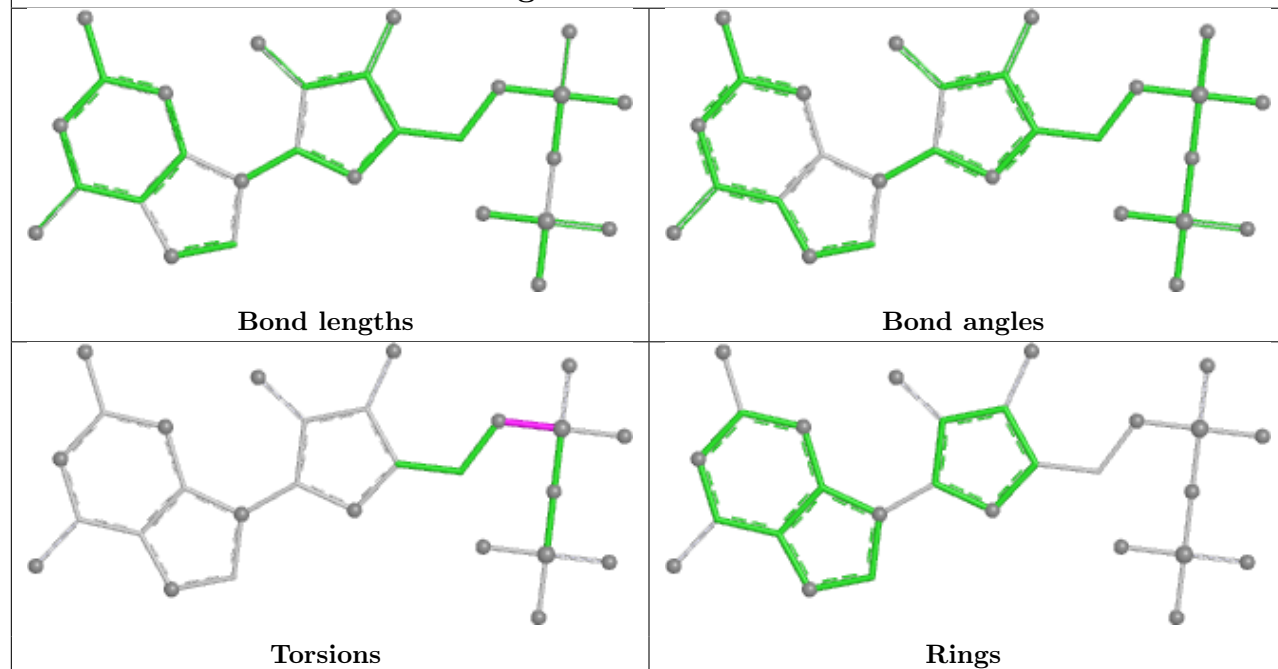
## Ligand GTP TQ 602

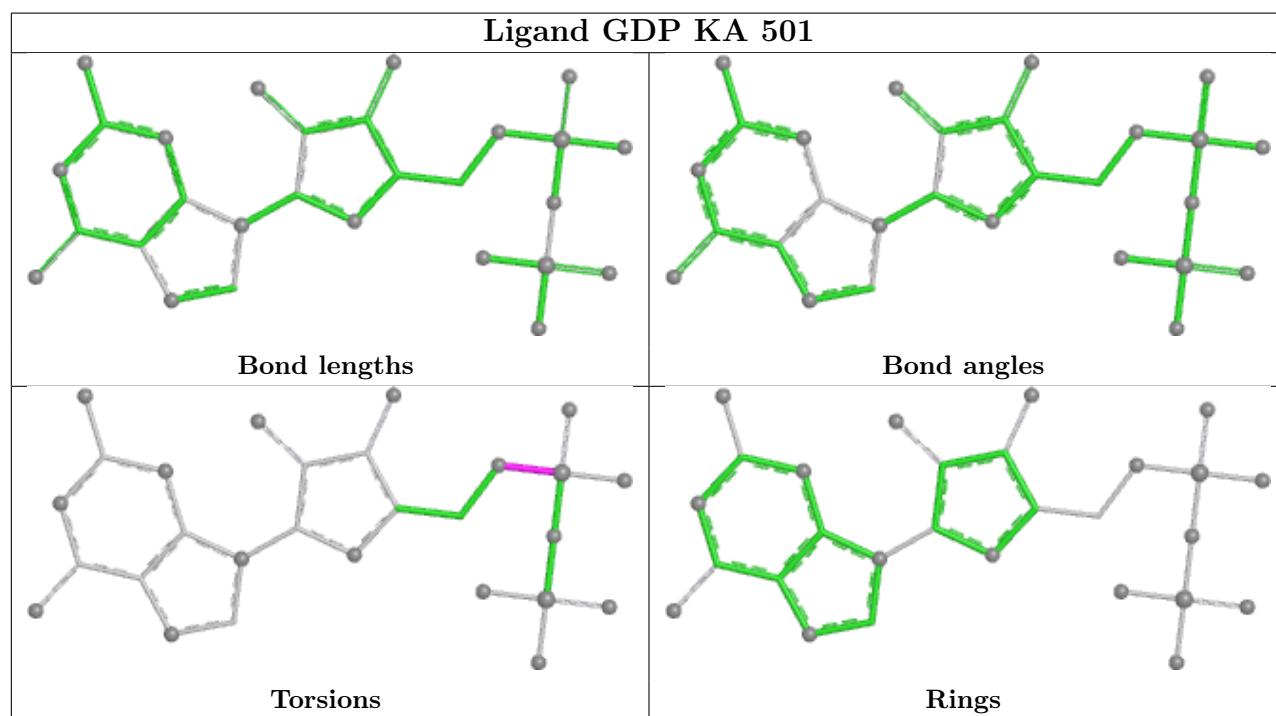
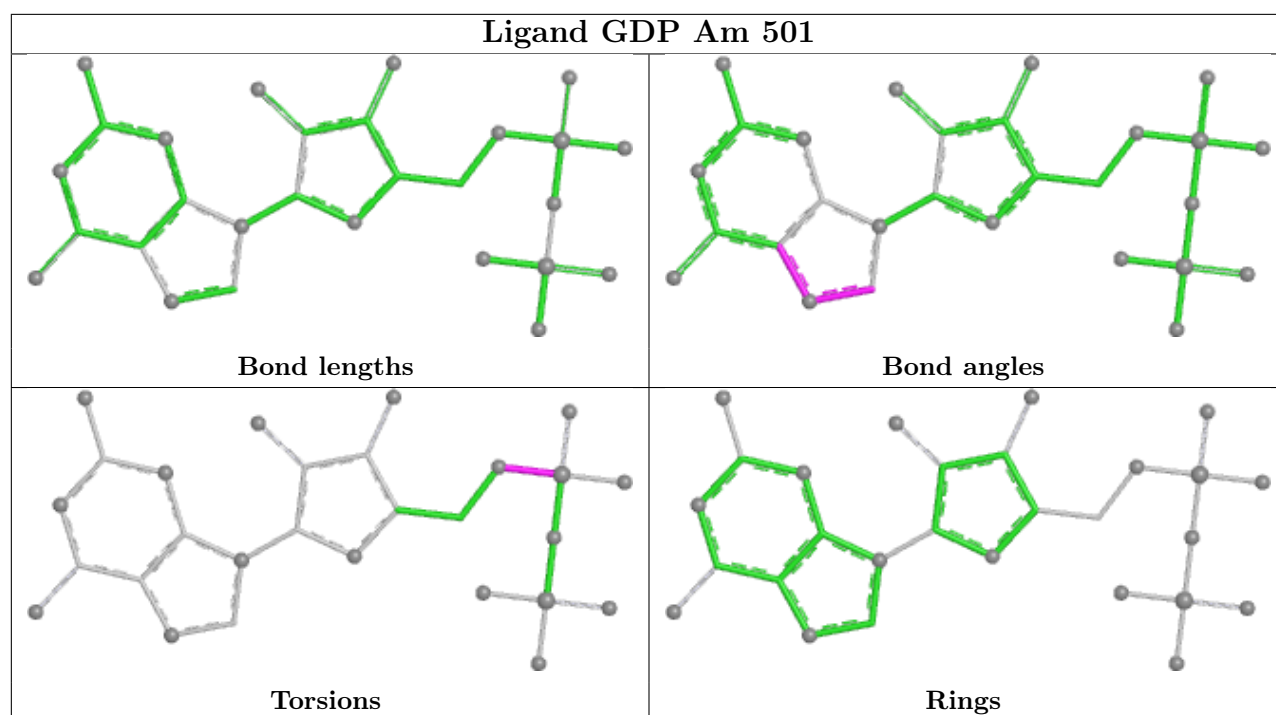


## Ligand GTP AN 501

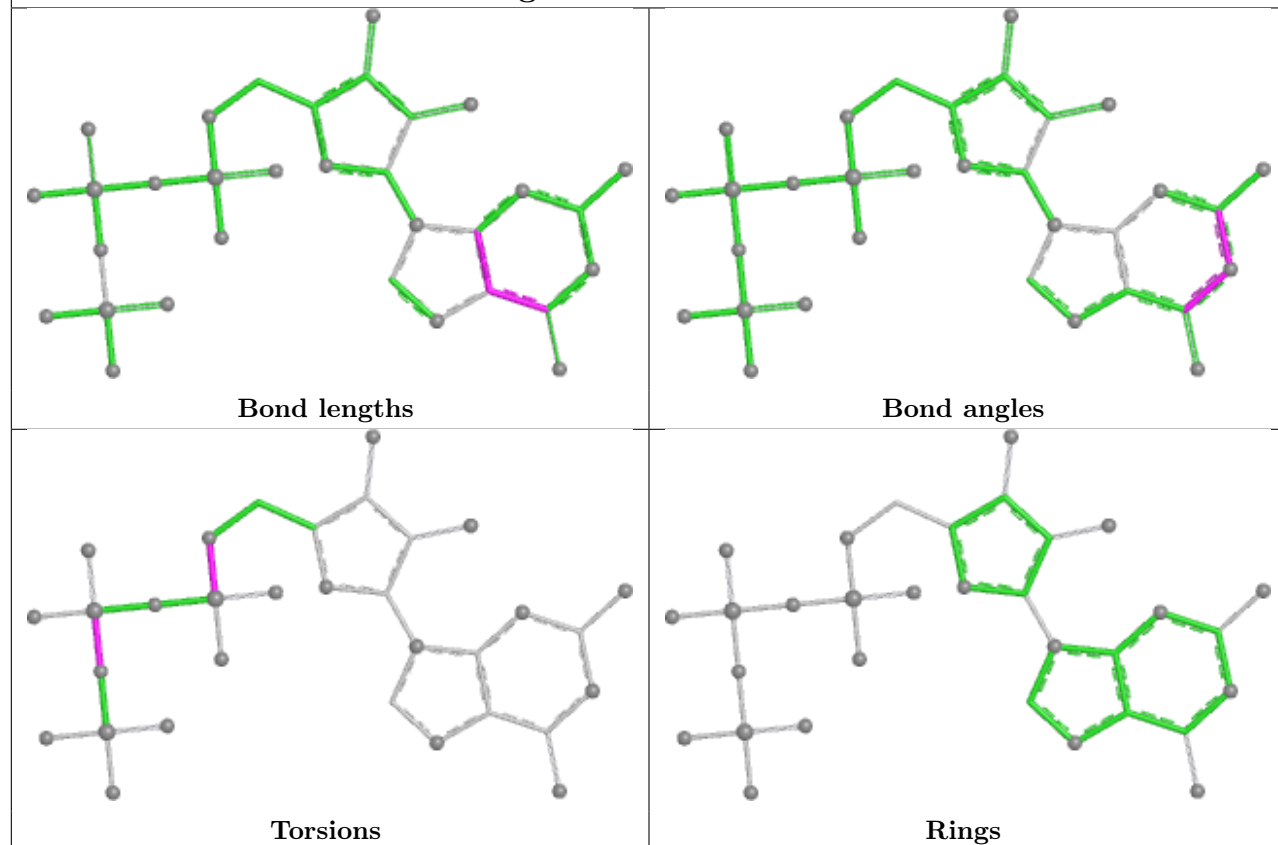


## Ligand GDP LG 501

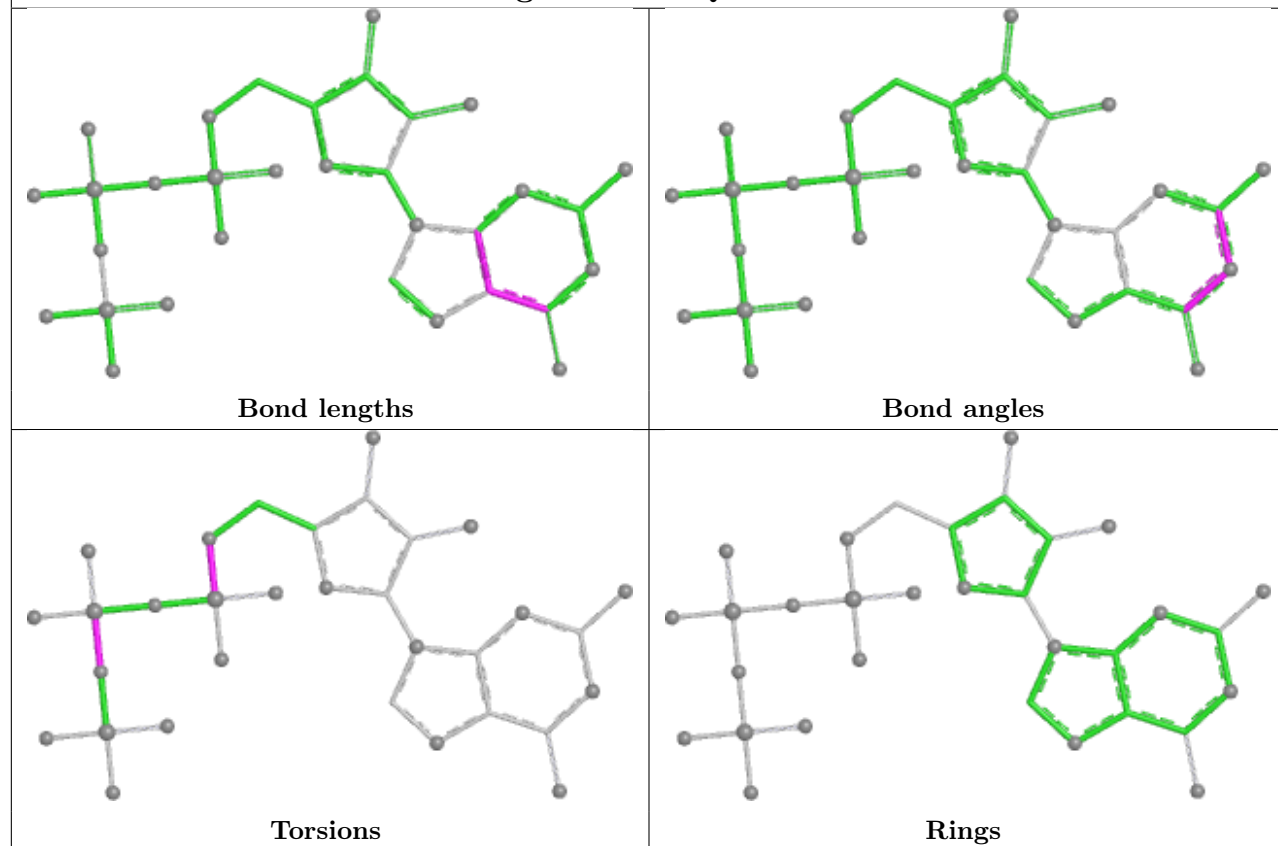




## Ligand GTP NZ 602

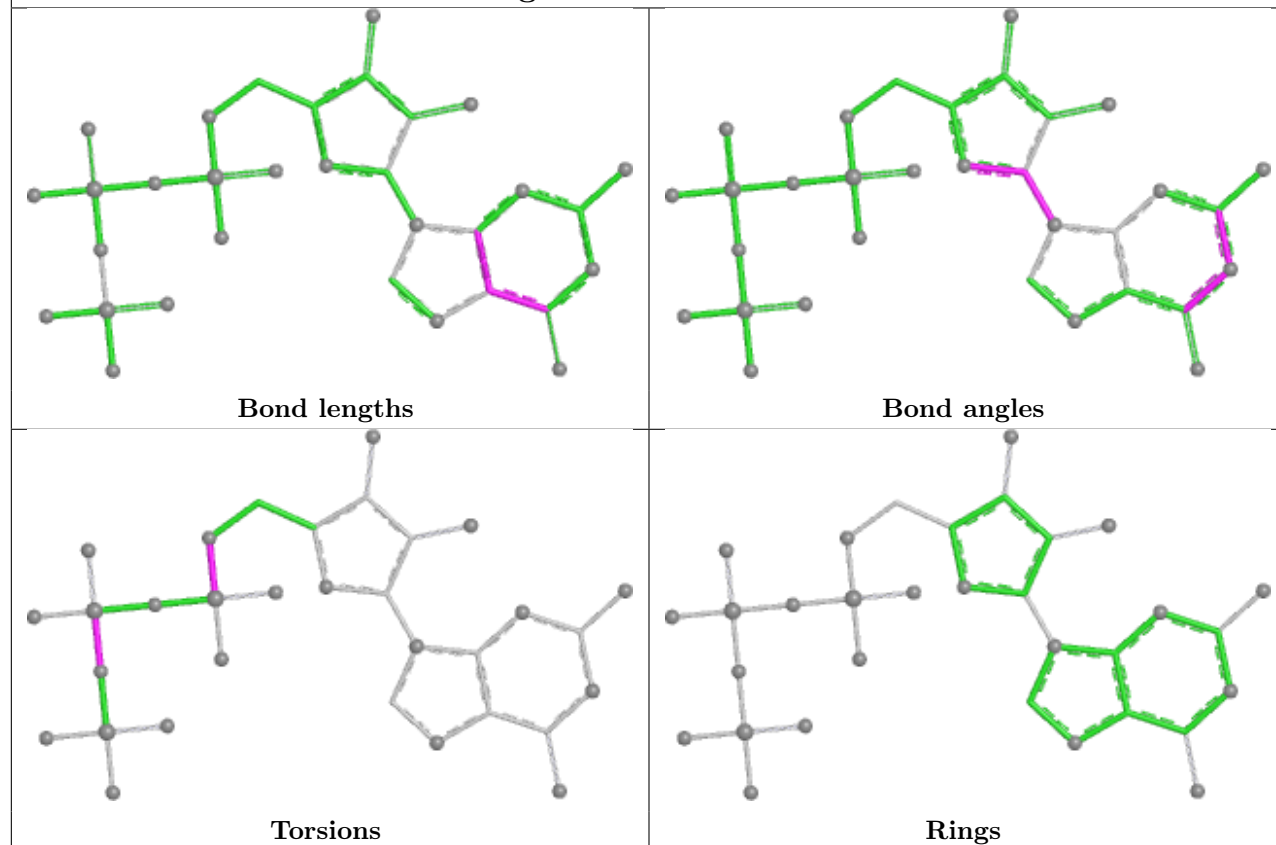


## Ligand GTP QK 602

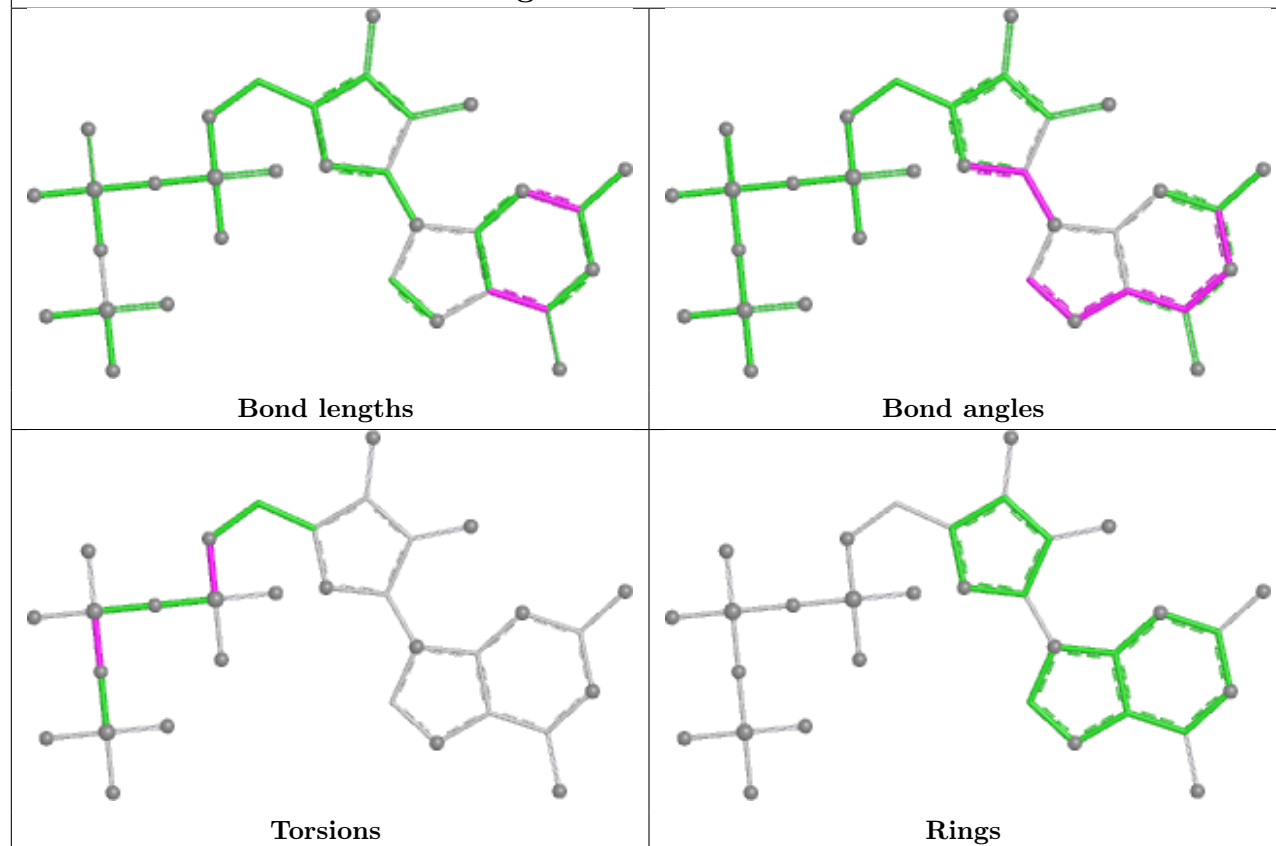


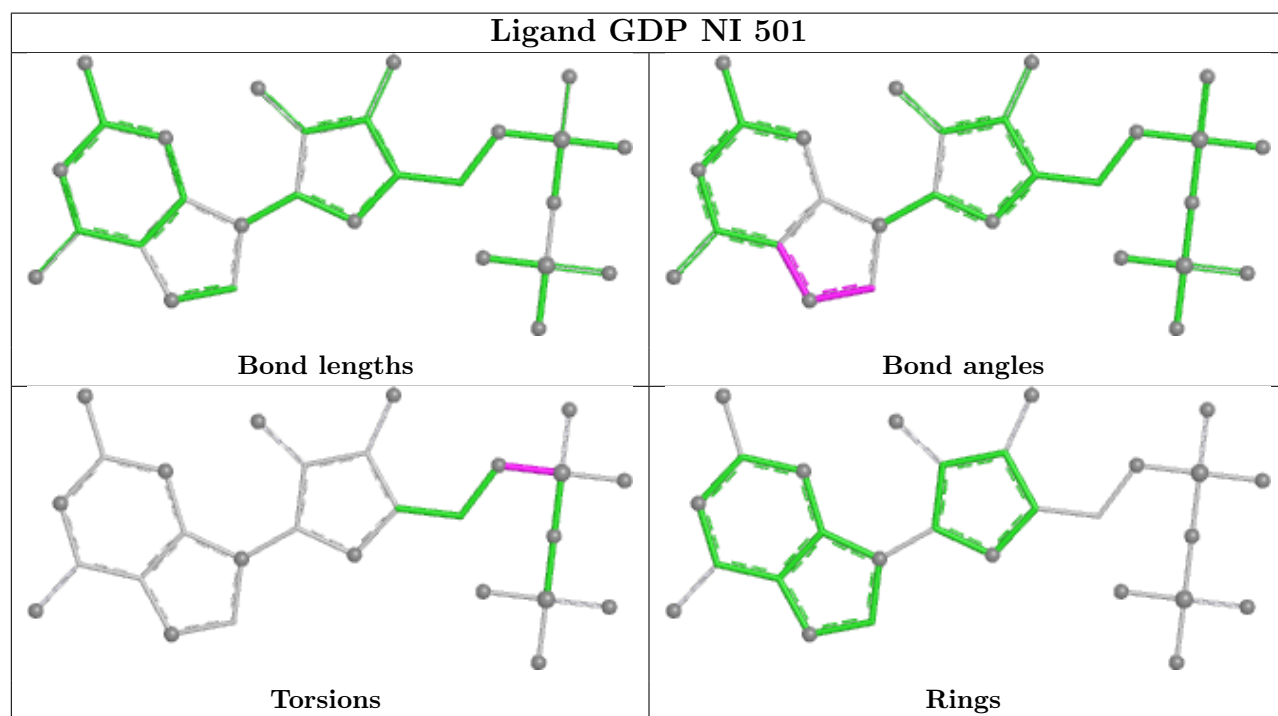
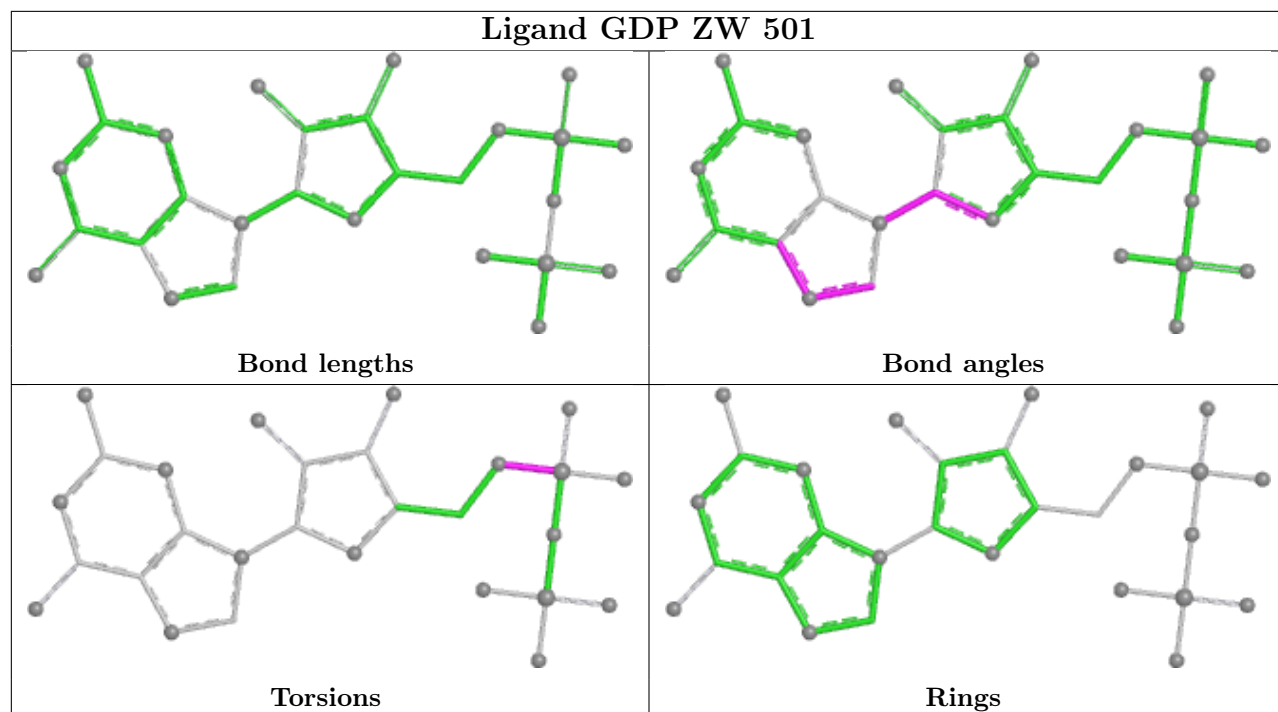


## Ligand GTP BP 501

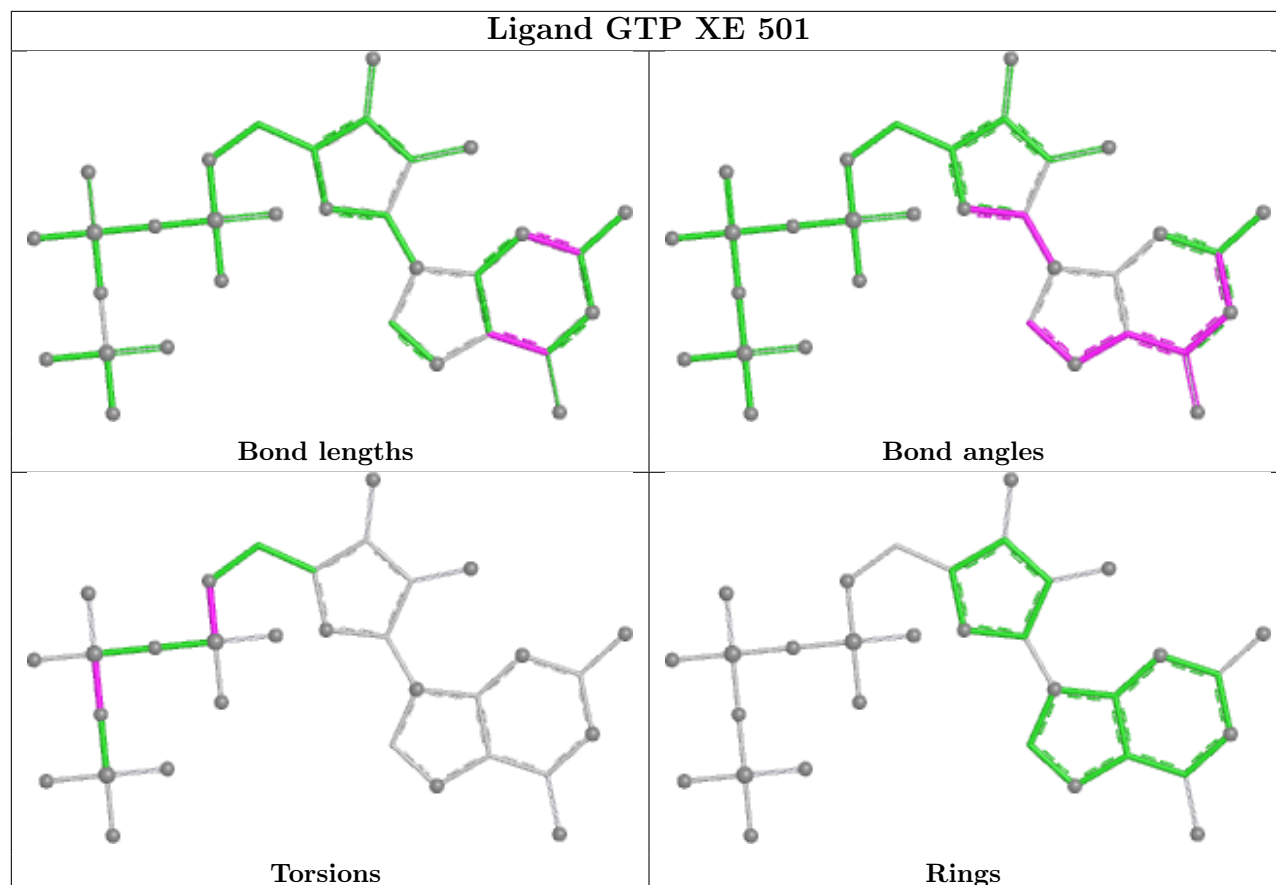


## Ligand GTP HC 602

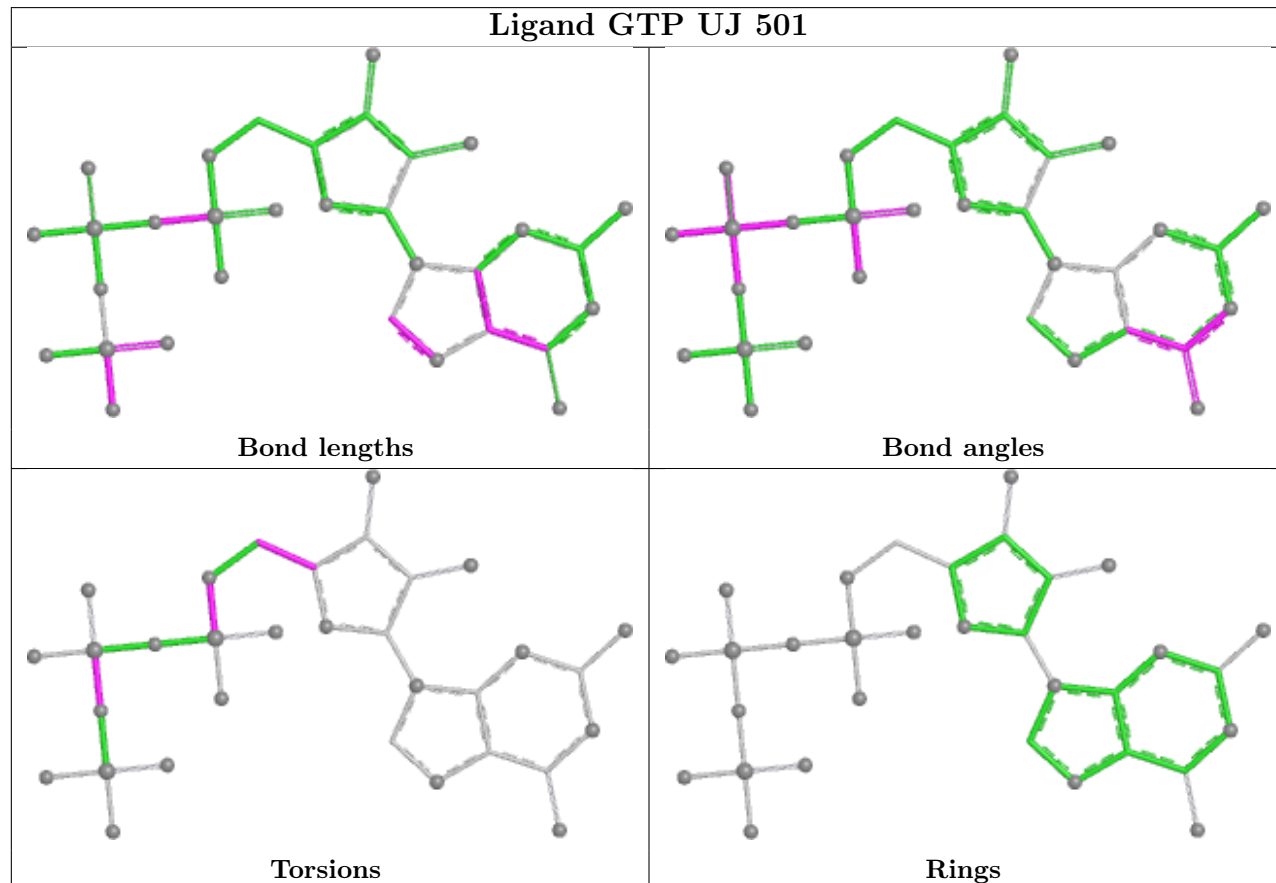




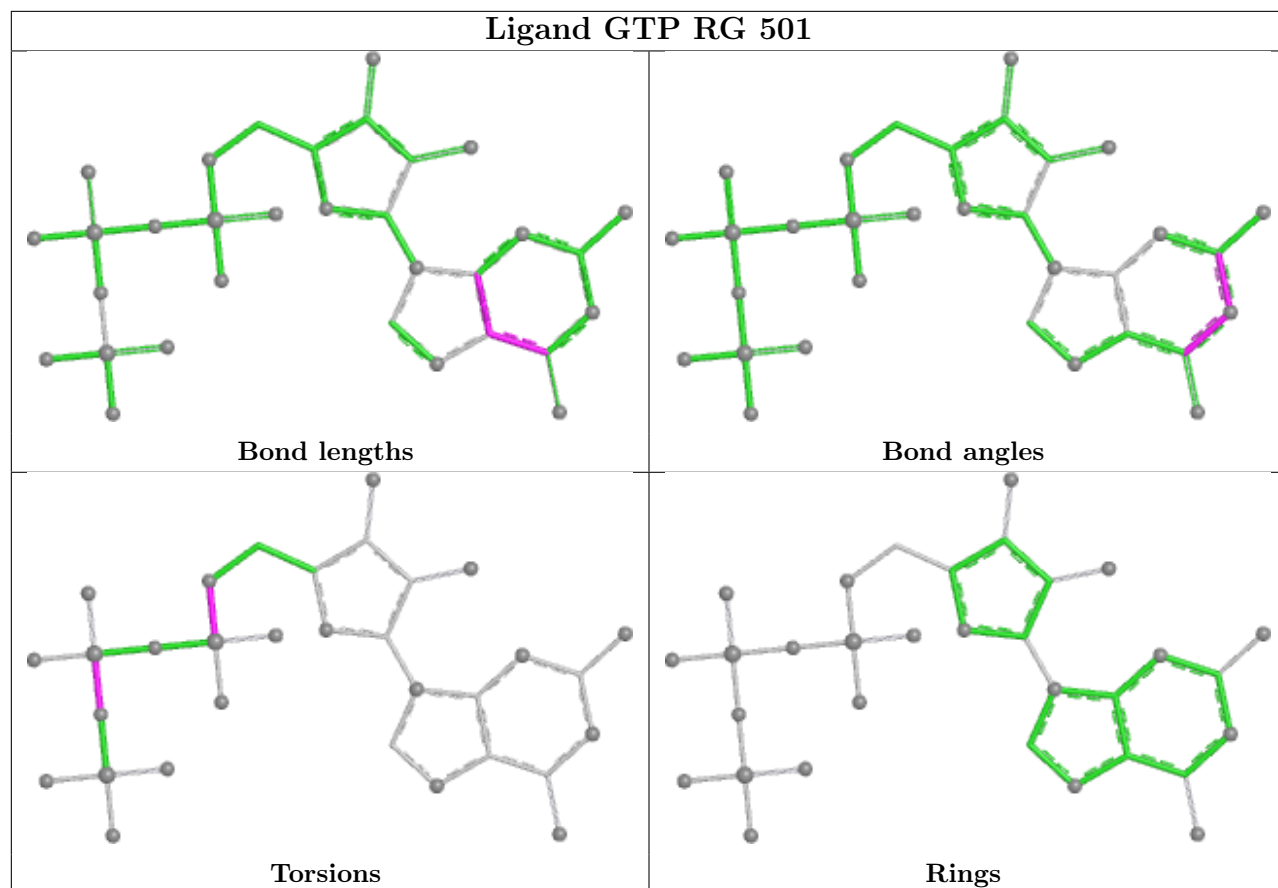
## Ligand GTP XE 501



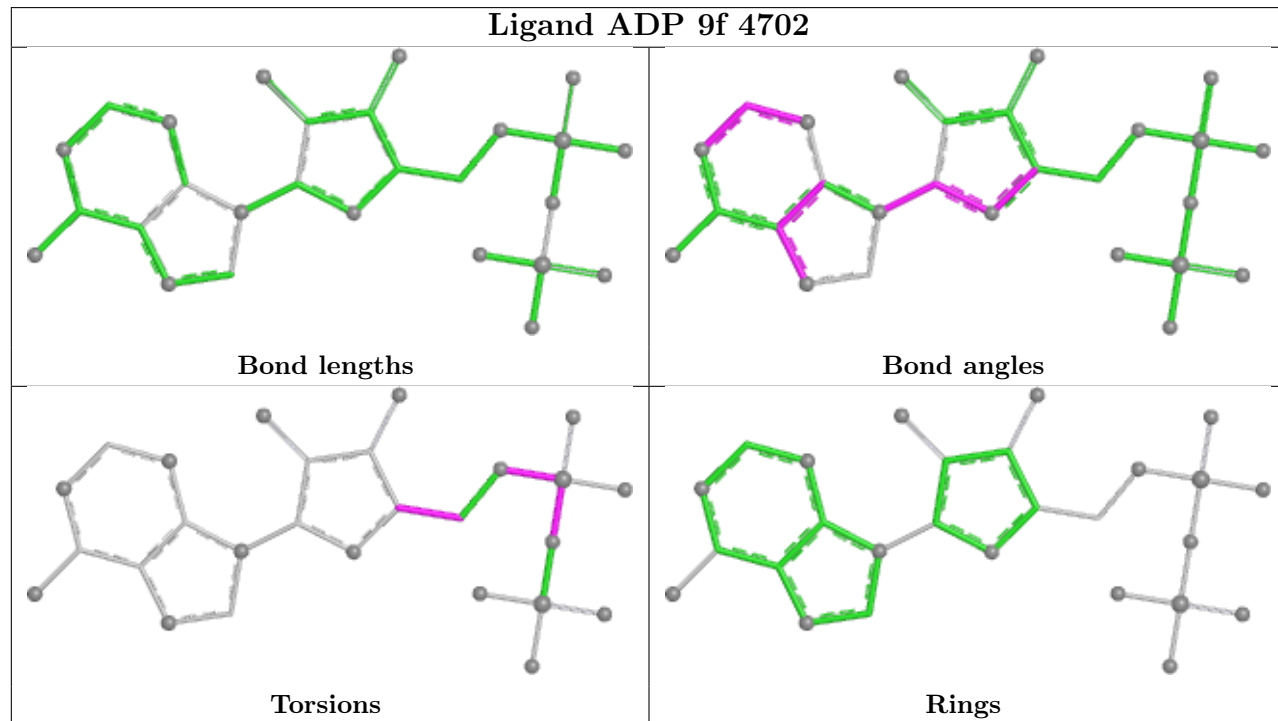
## Ligand GTP UJ 501

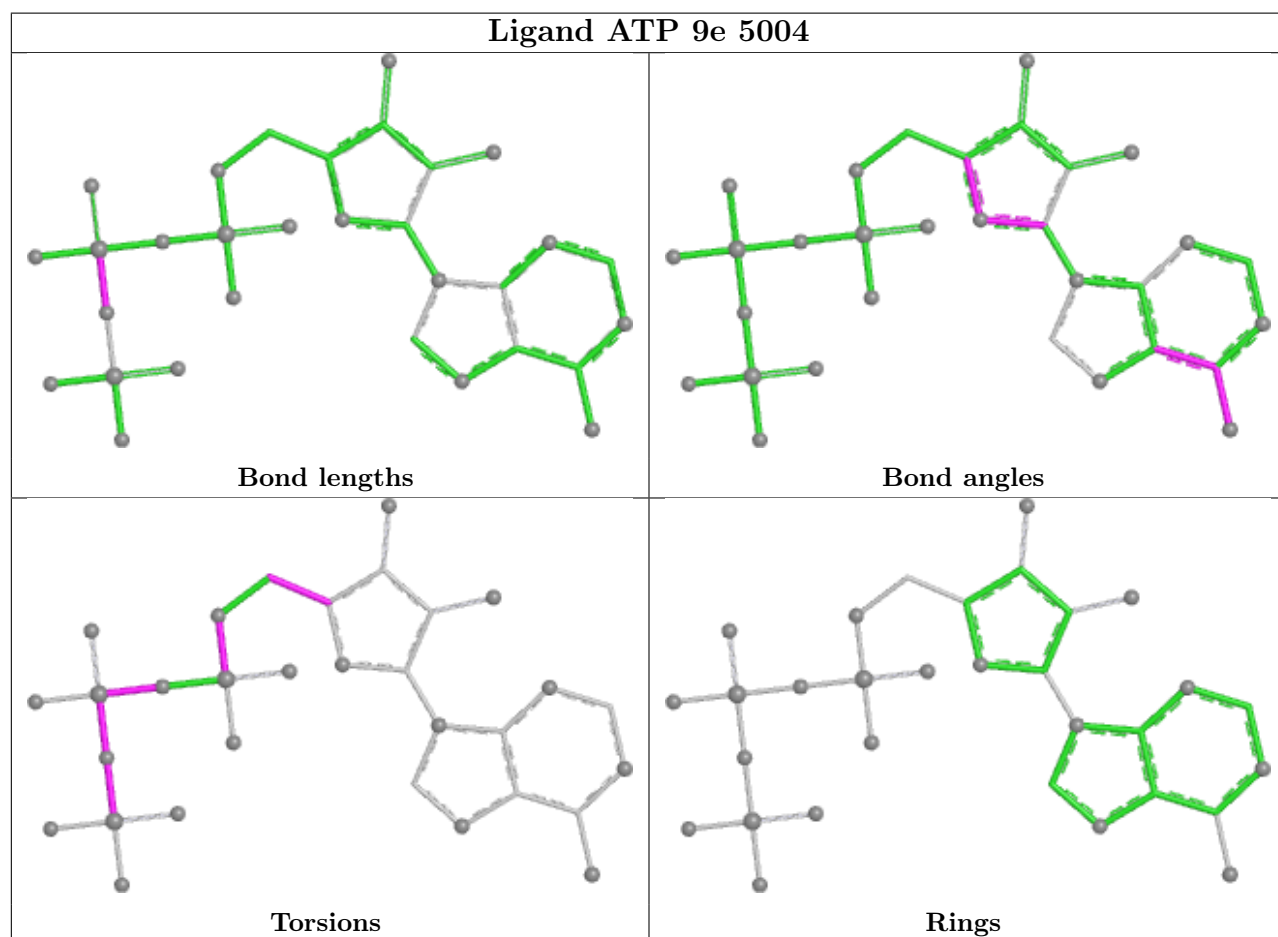
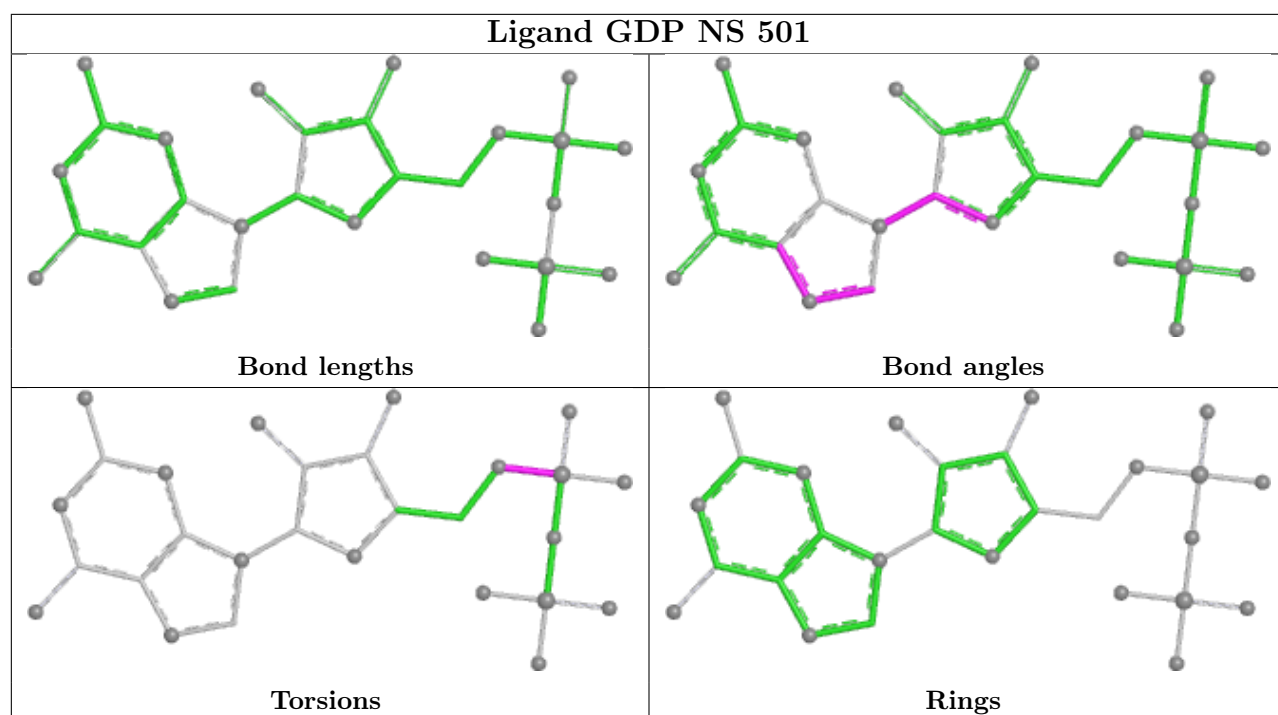


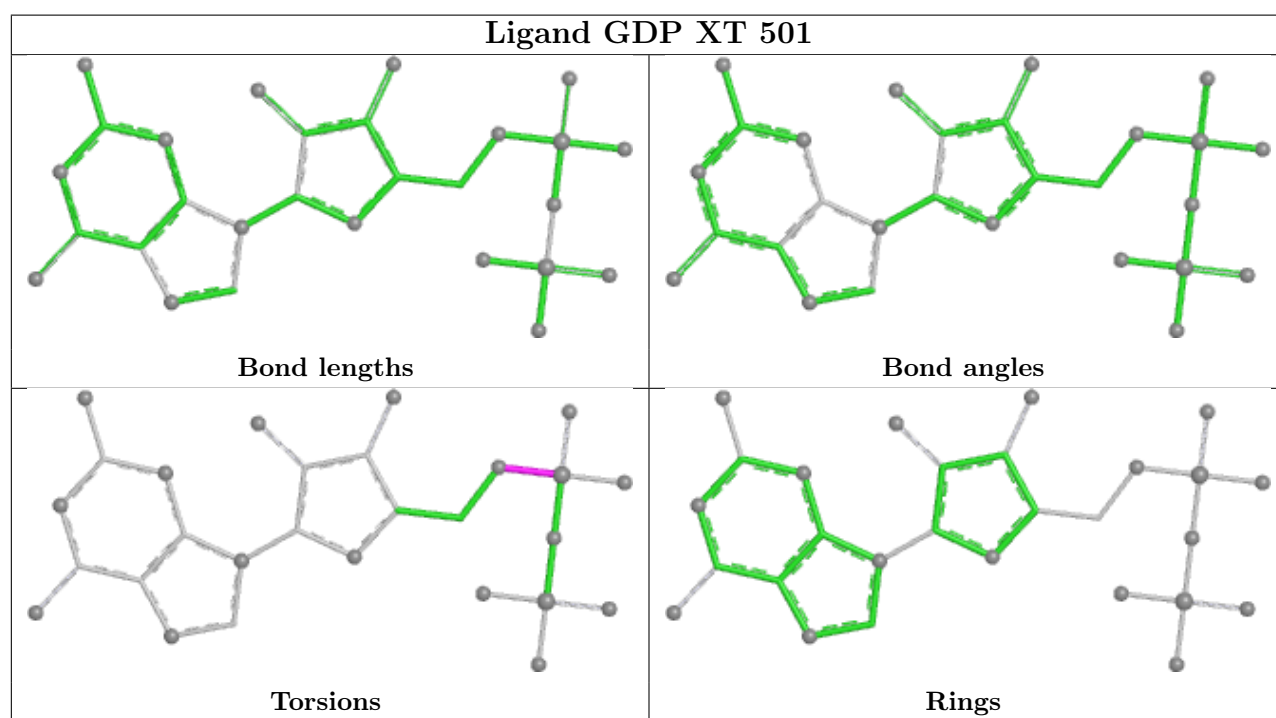
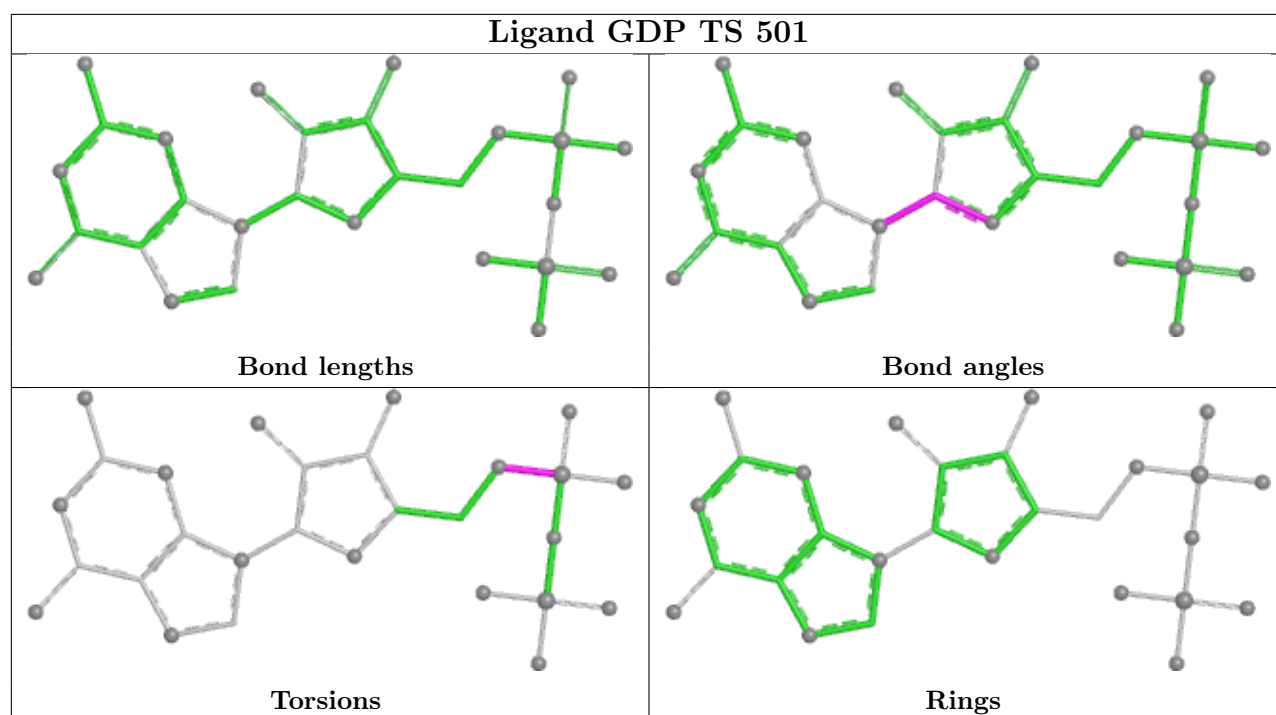
## Ligand GTP RG 501



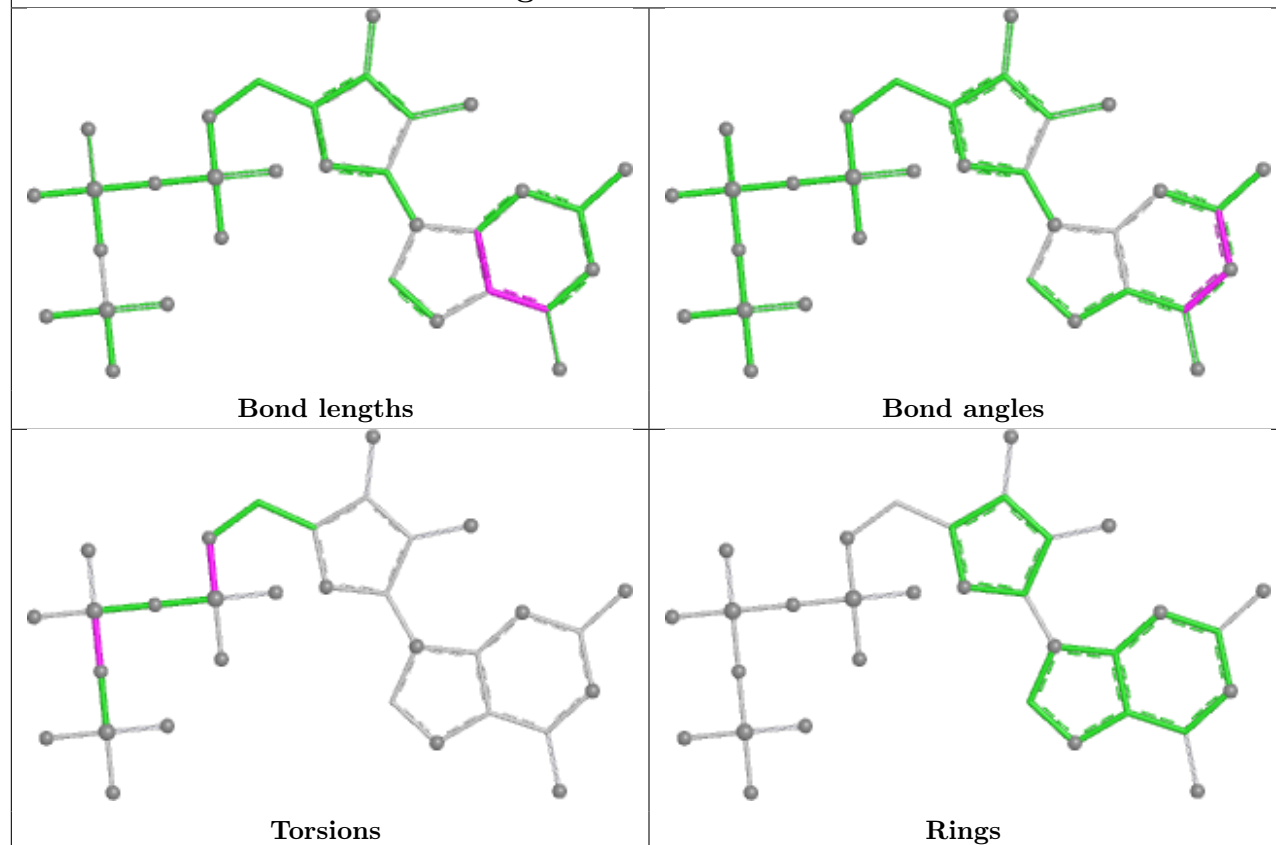
## Ligand ADP 9f 4702



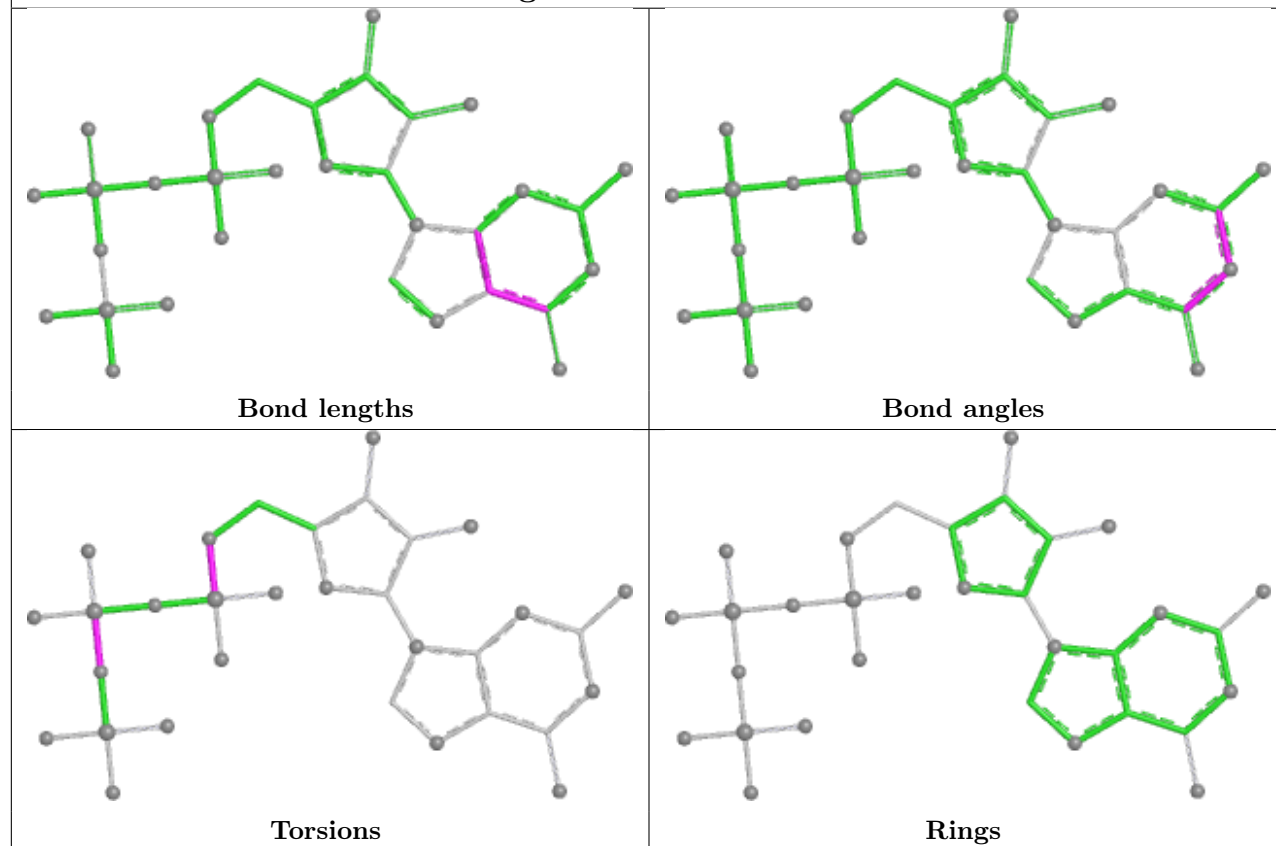




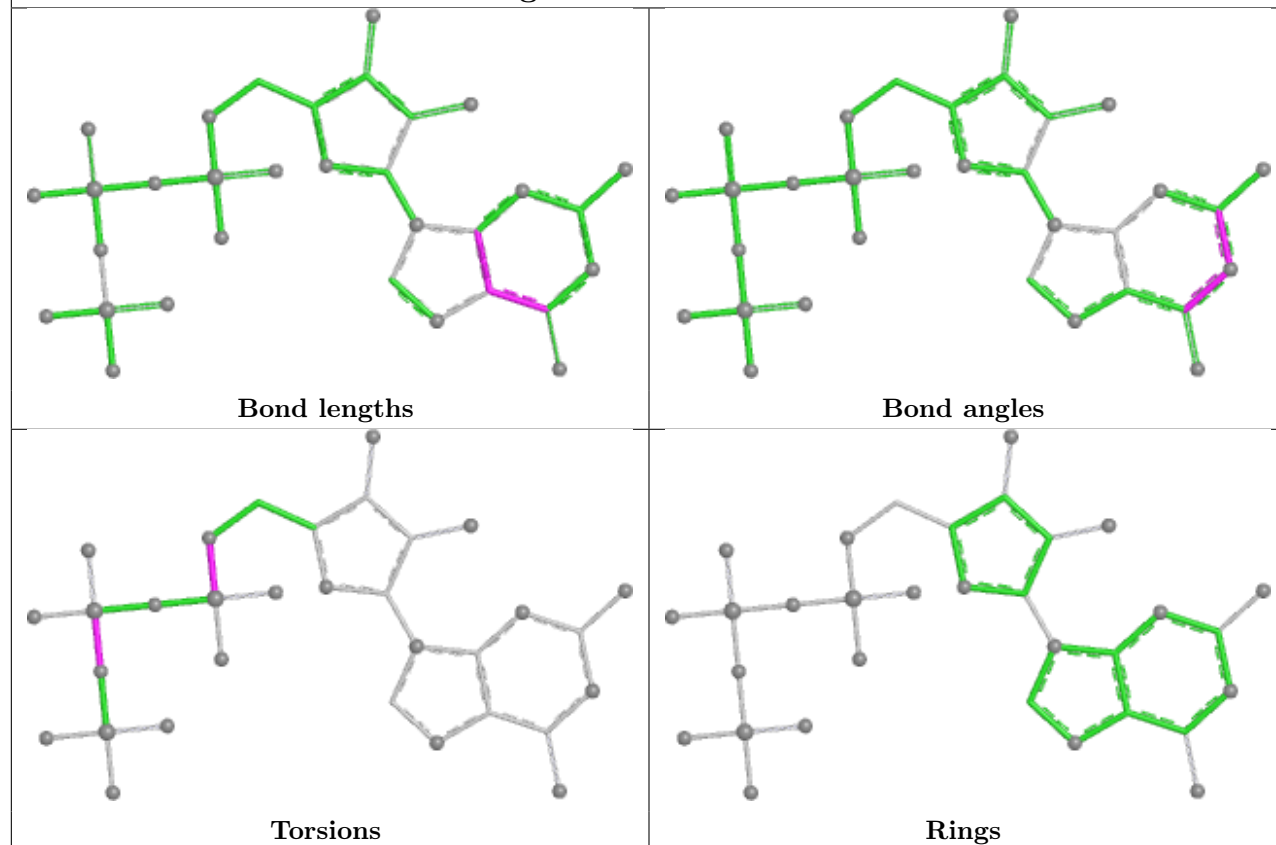
## Ligand GTP AX 501



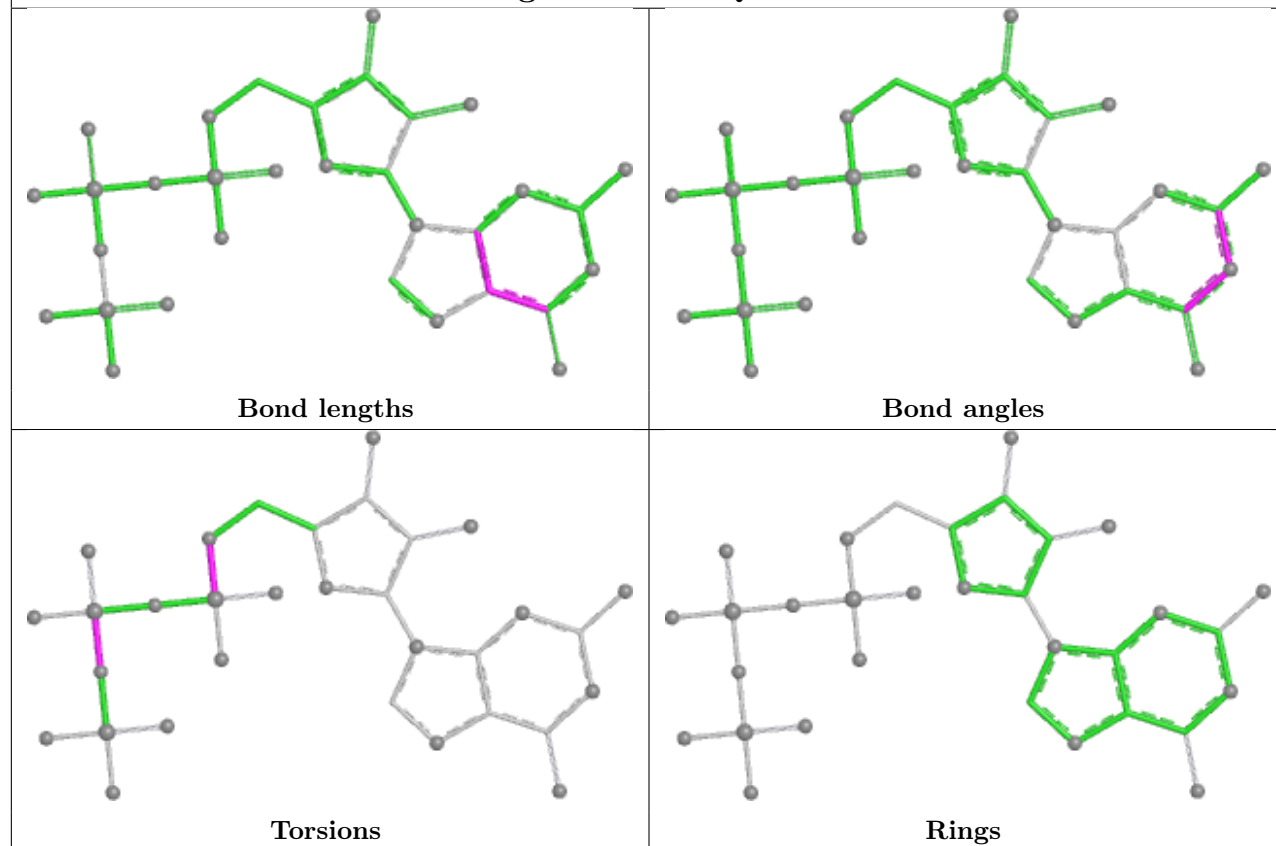
## Ligand GTP AT 501



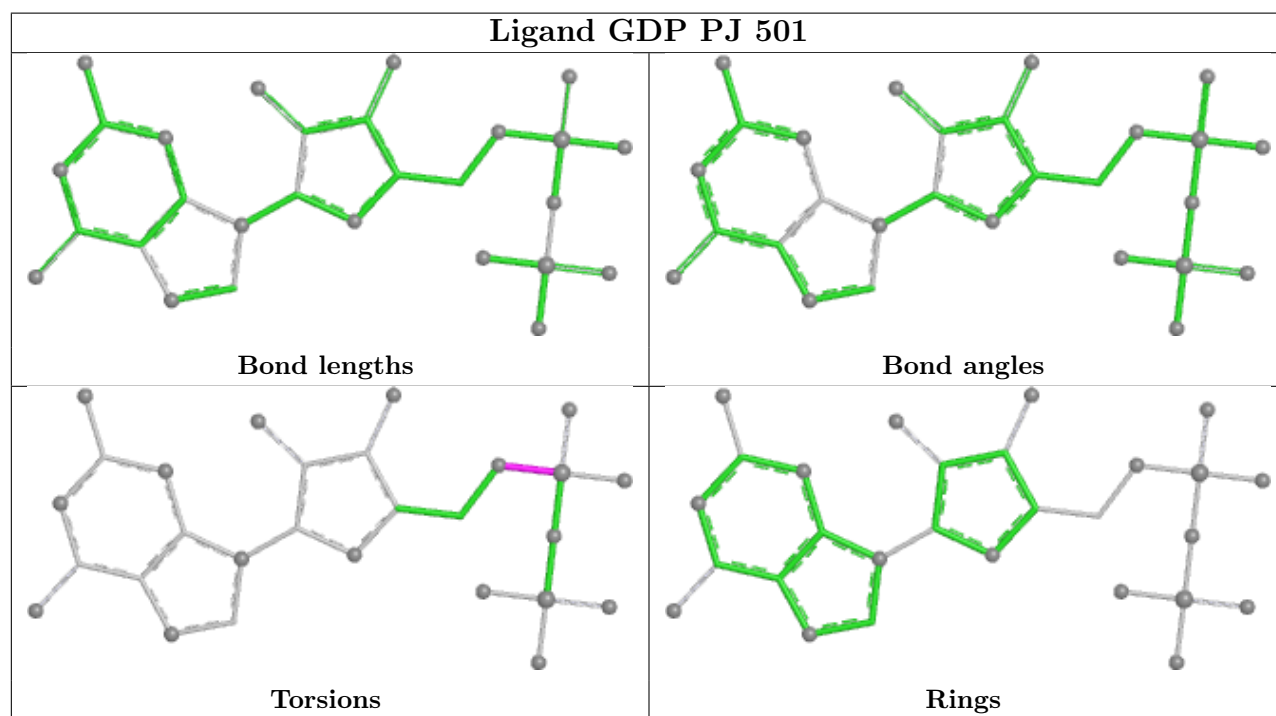
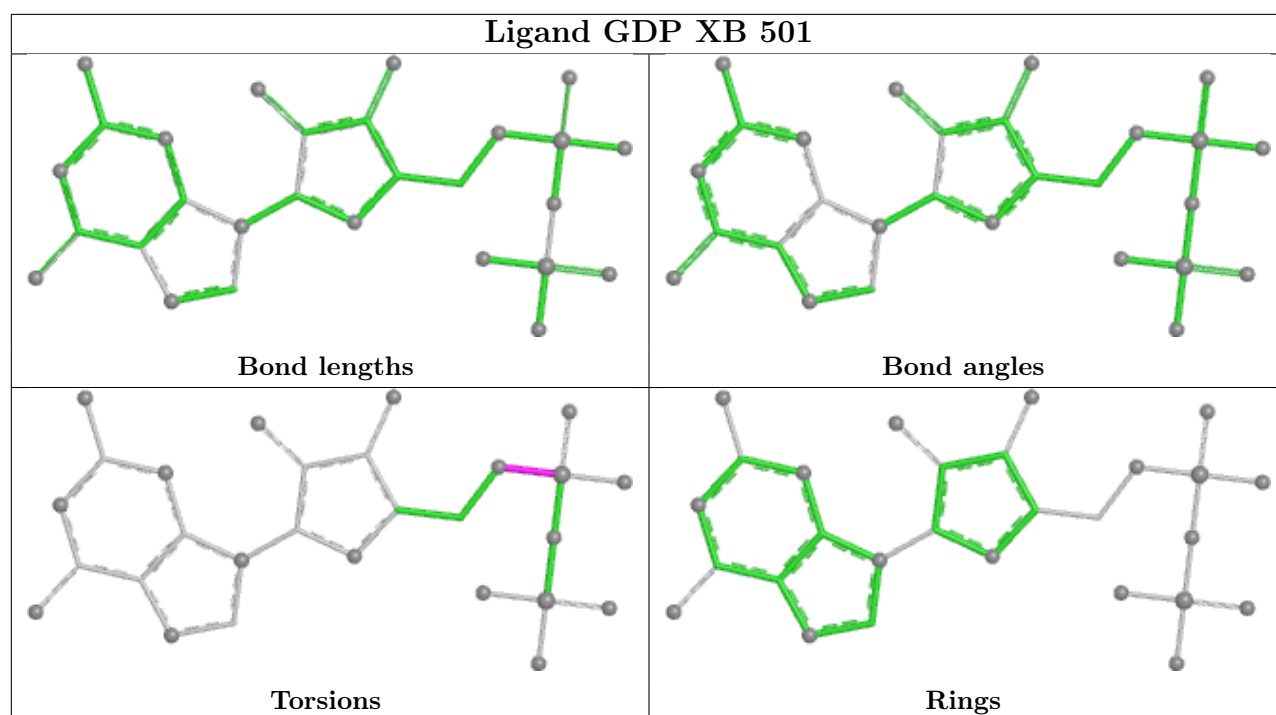
## Ligand GTP PE 602

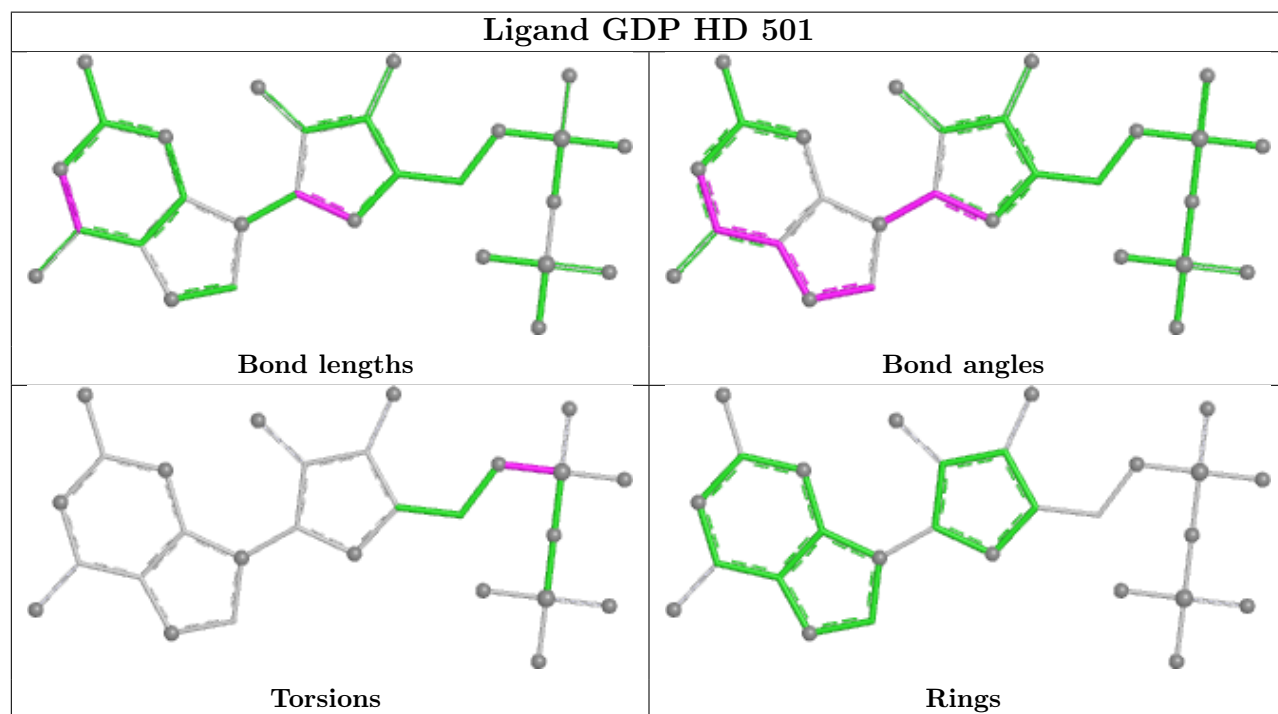
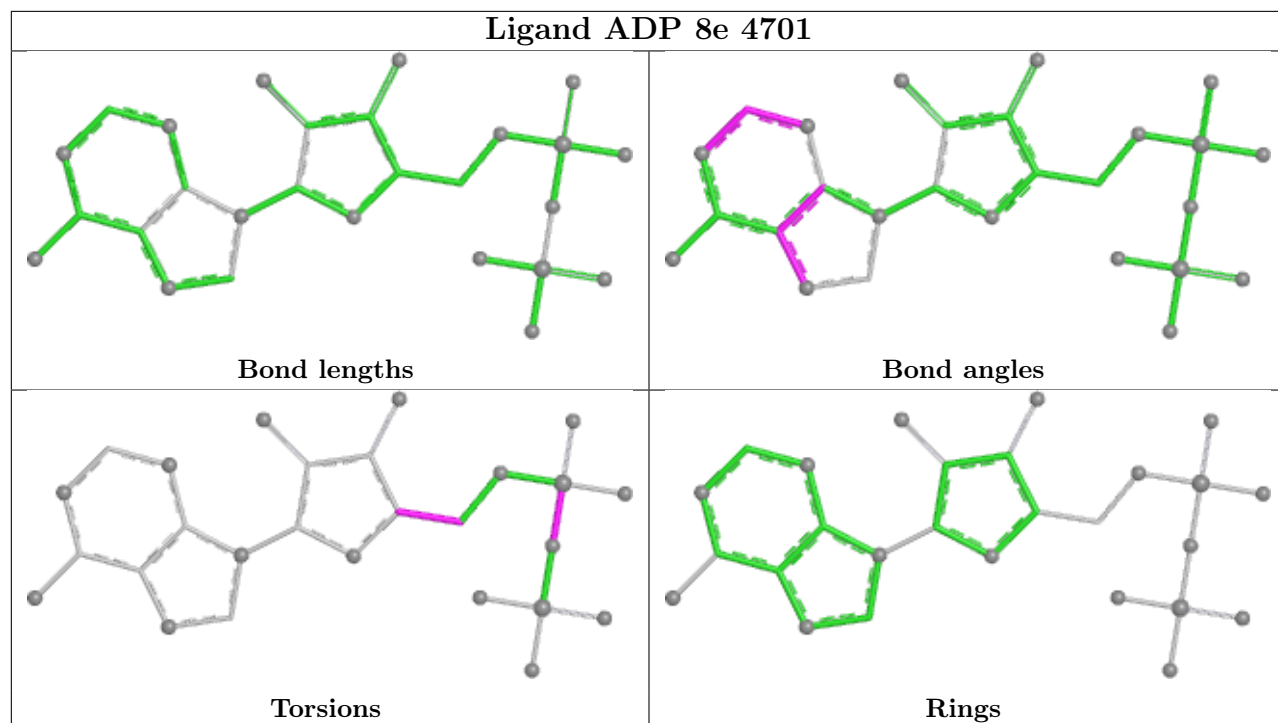


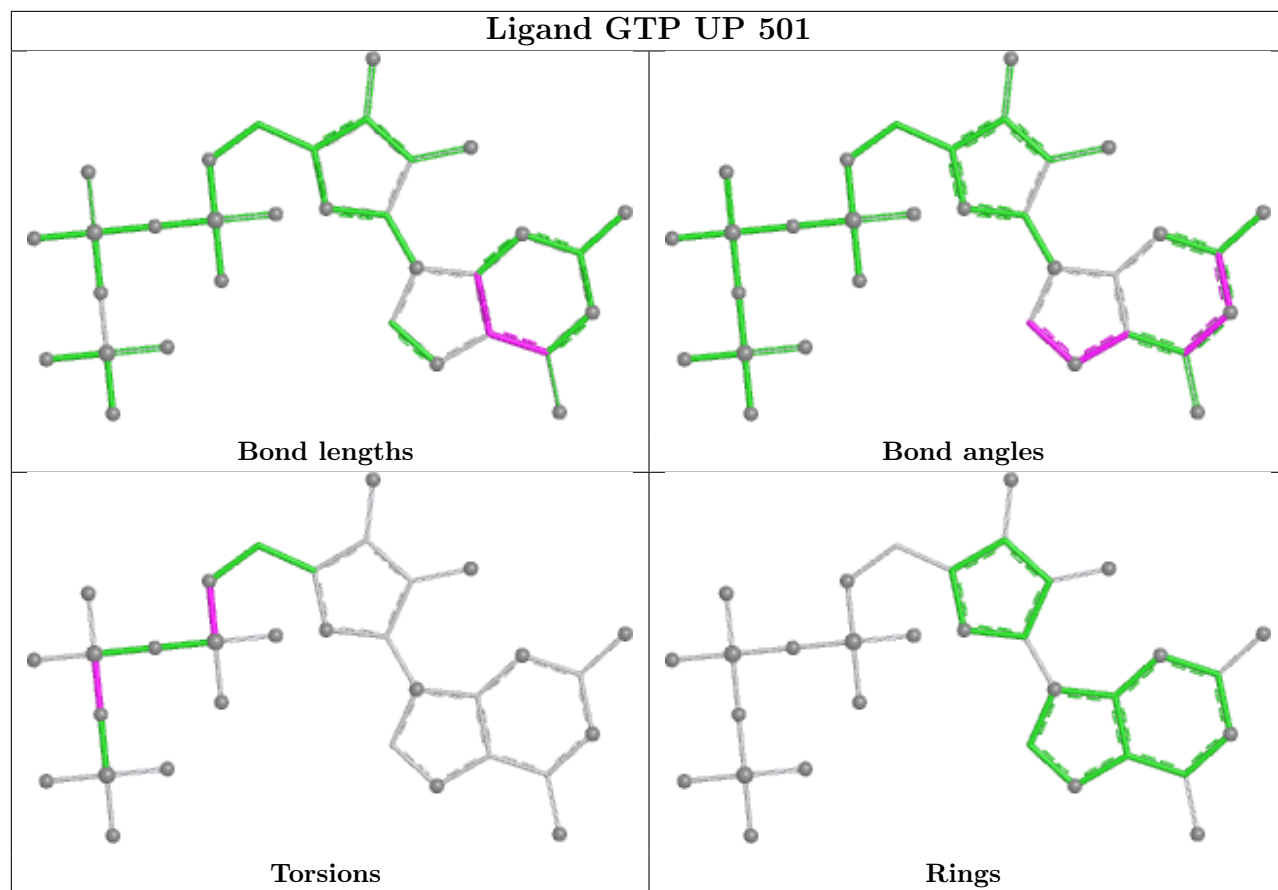
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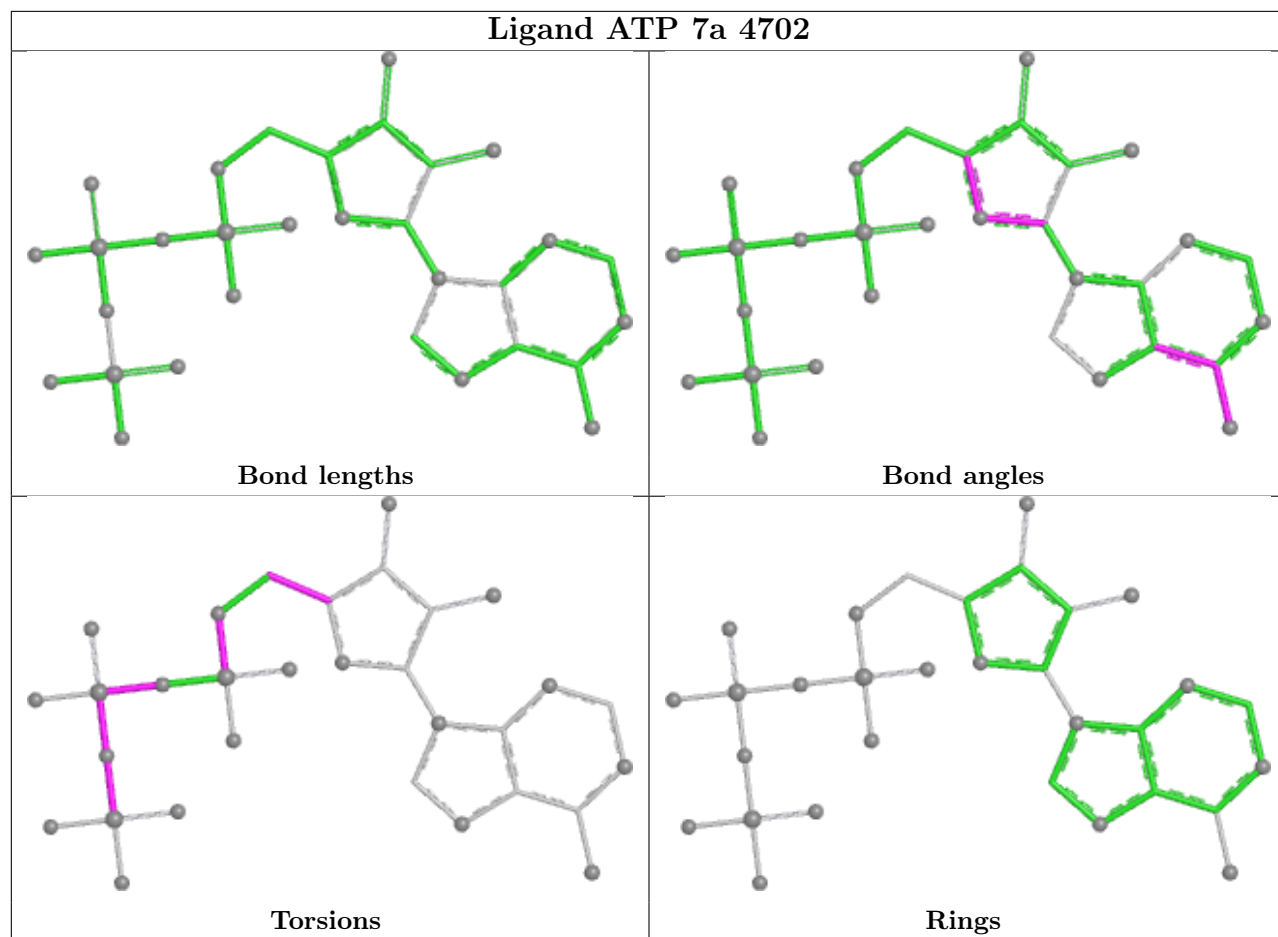




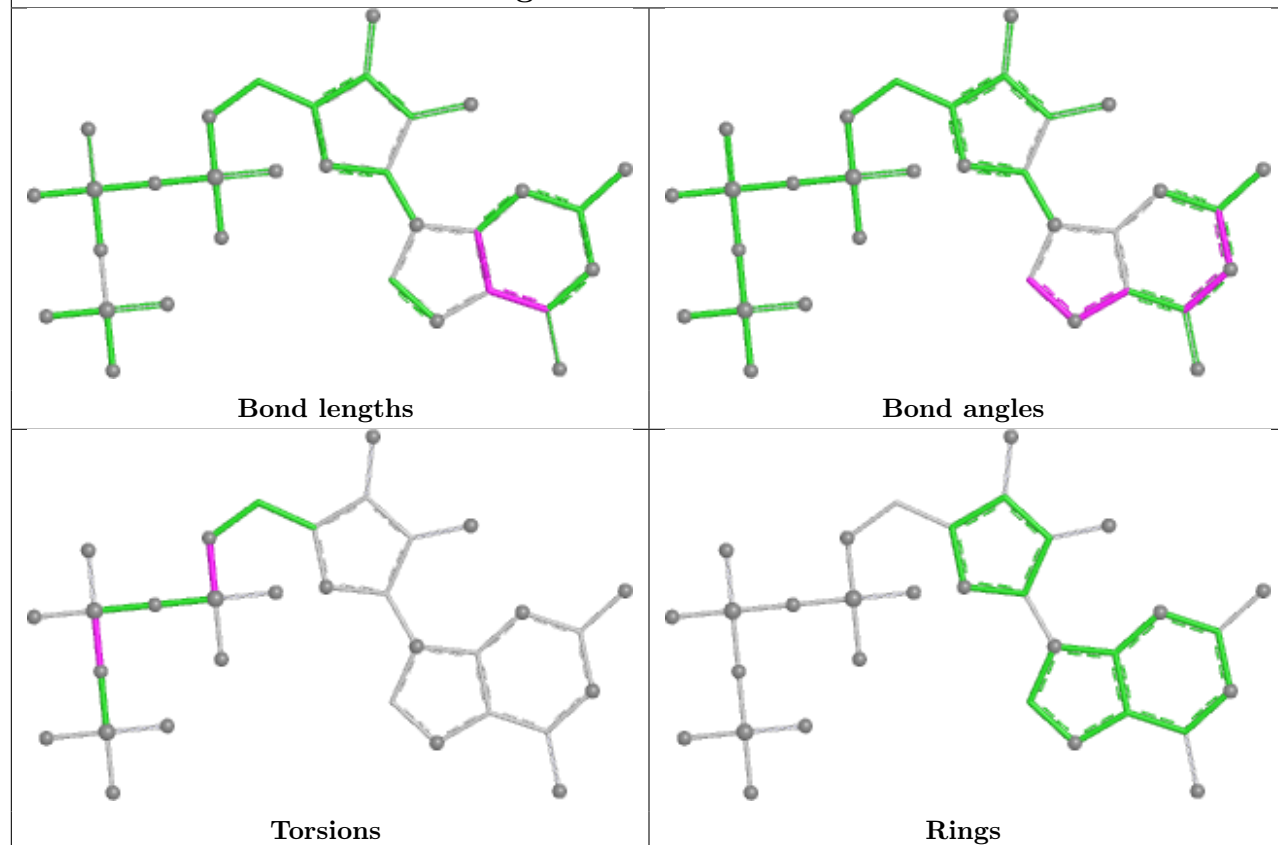




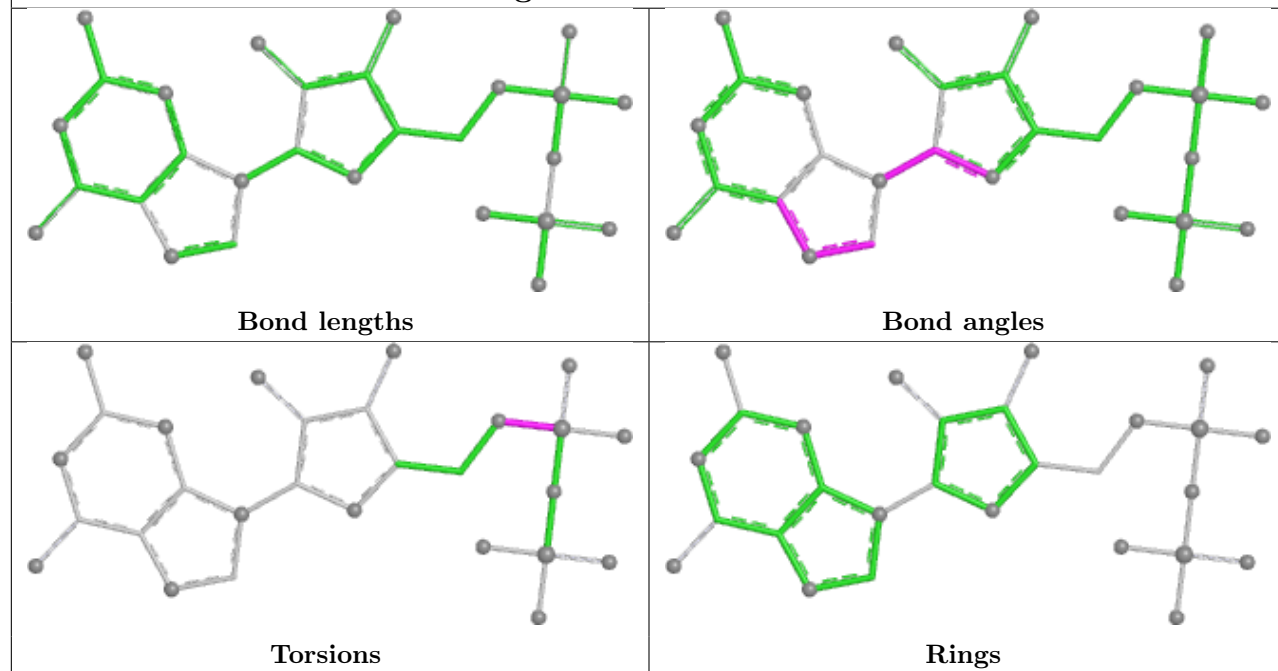




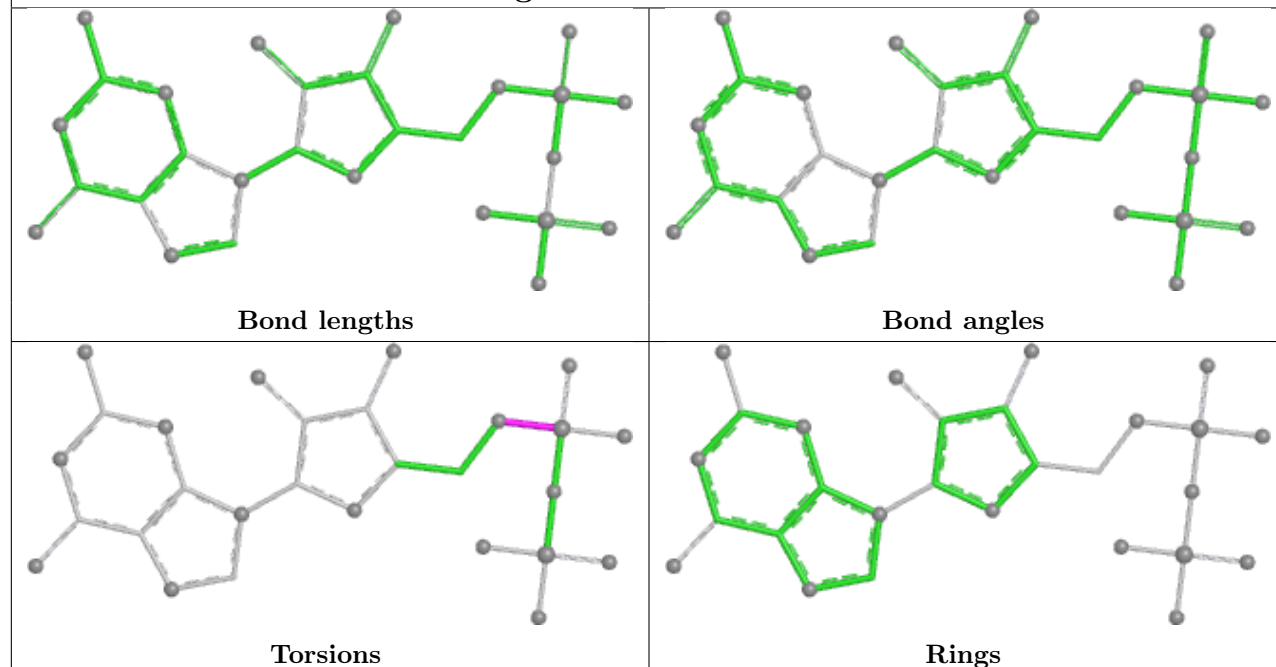
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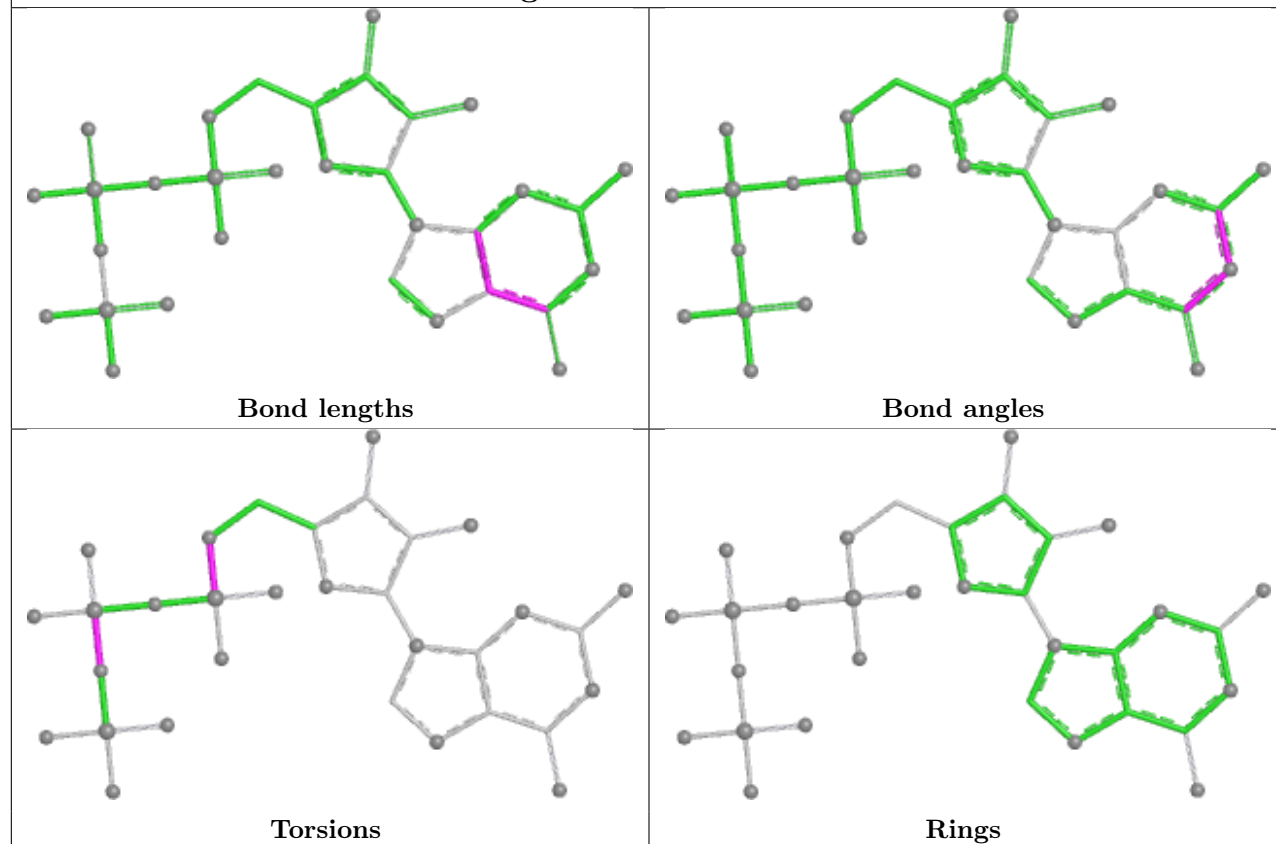
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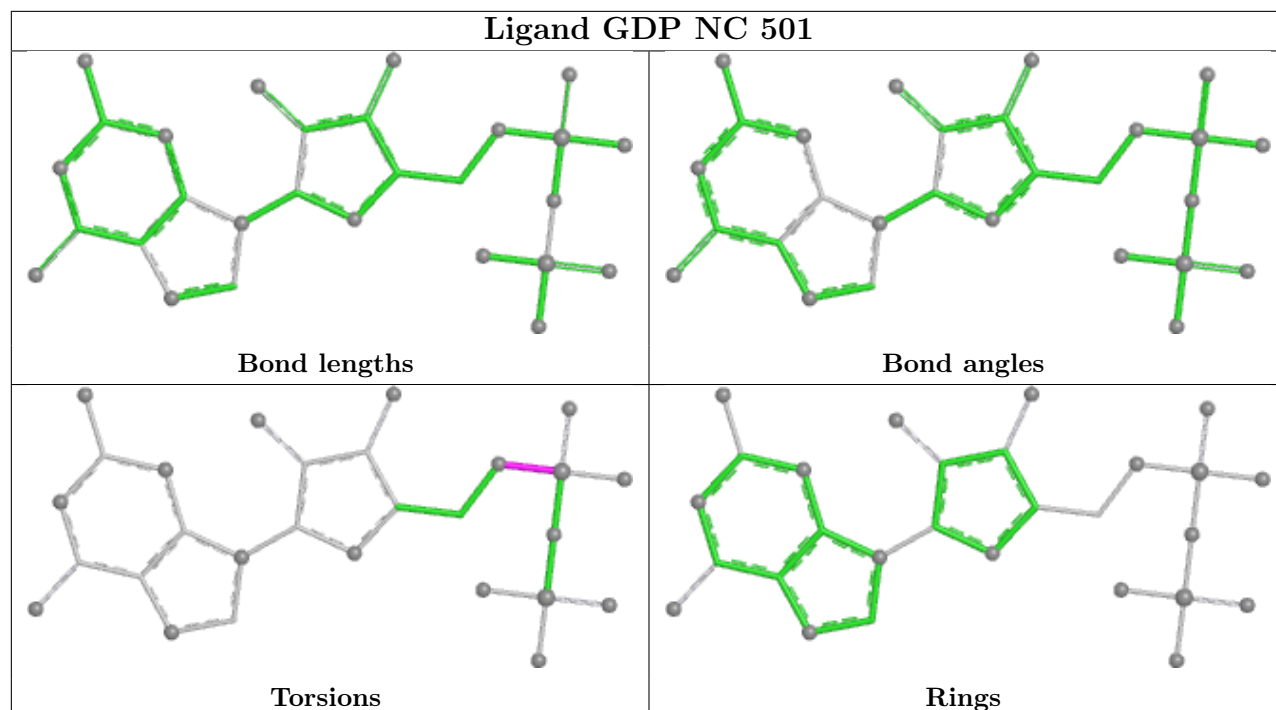
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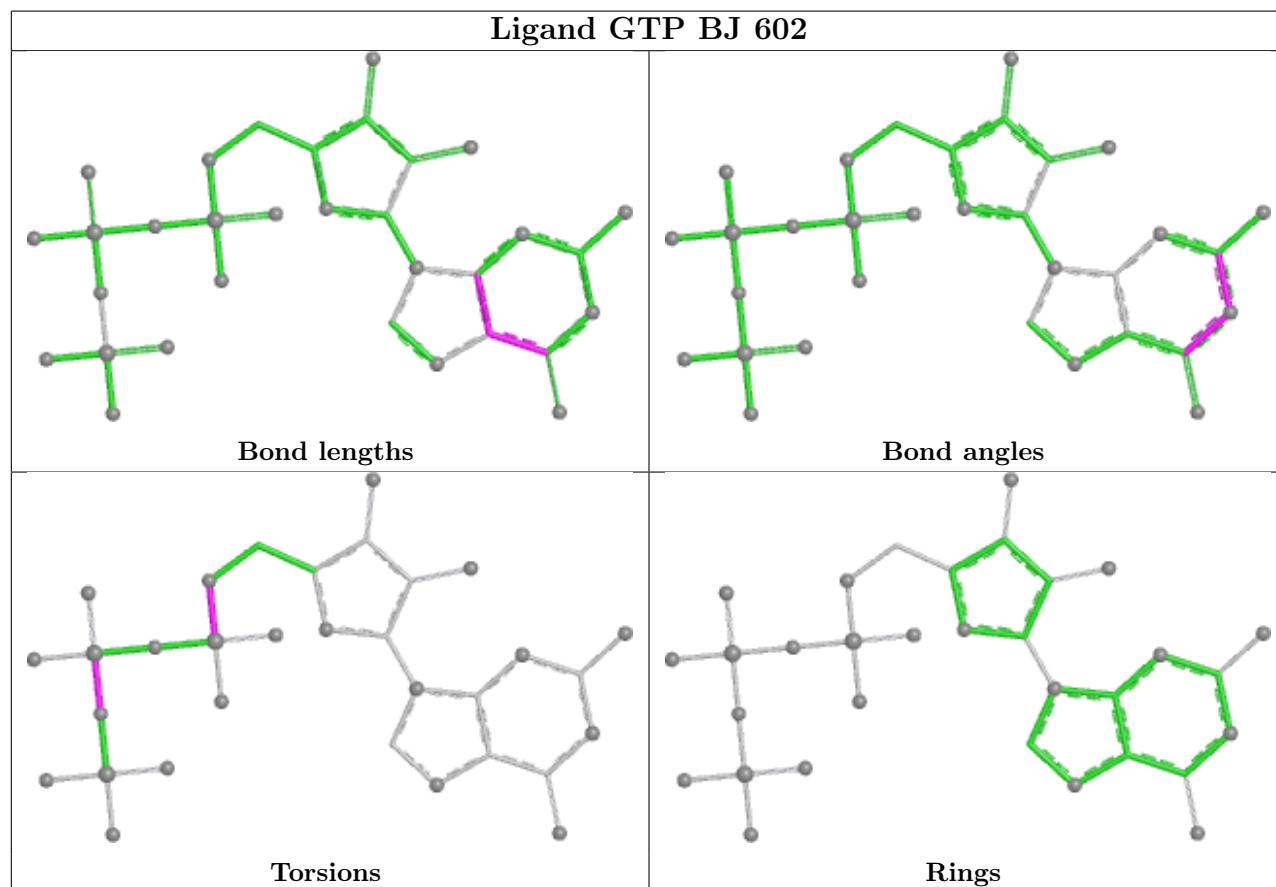
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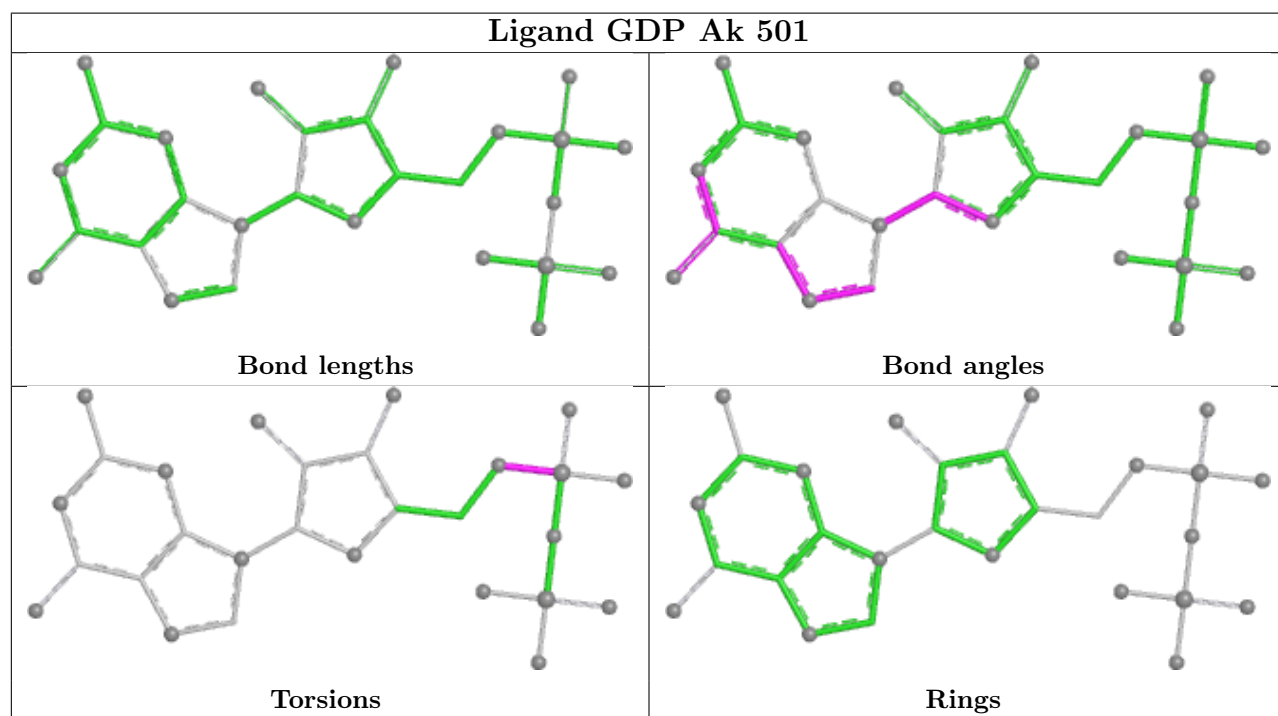
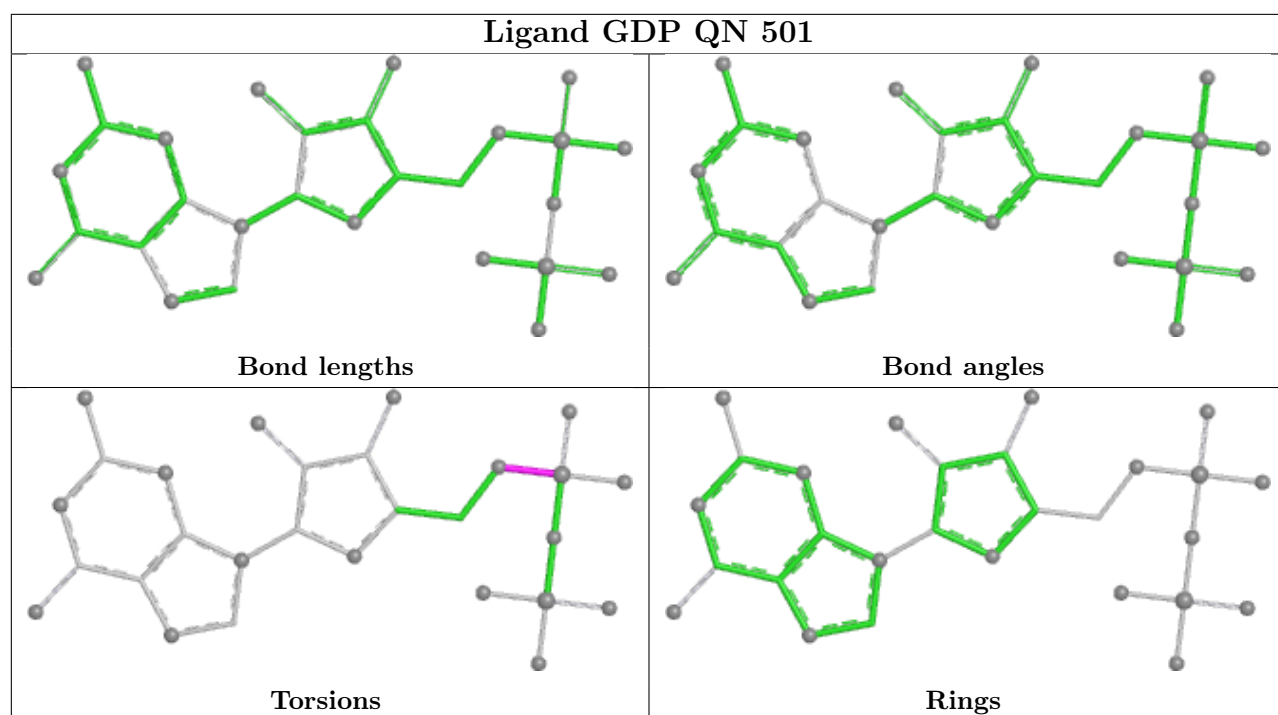


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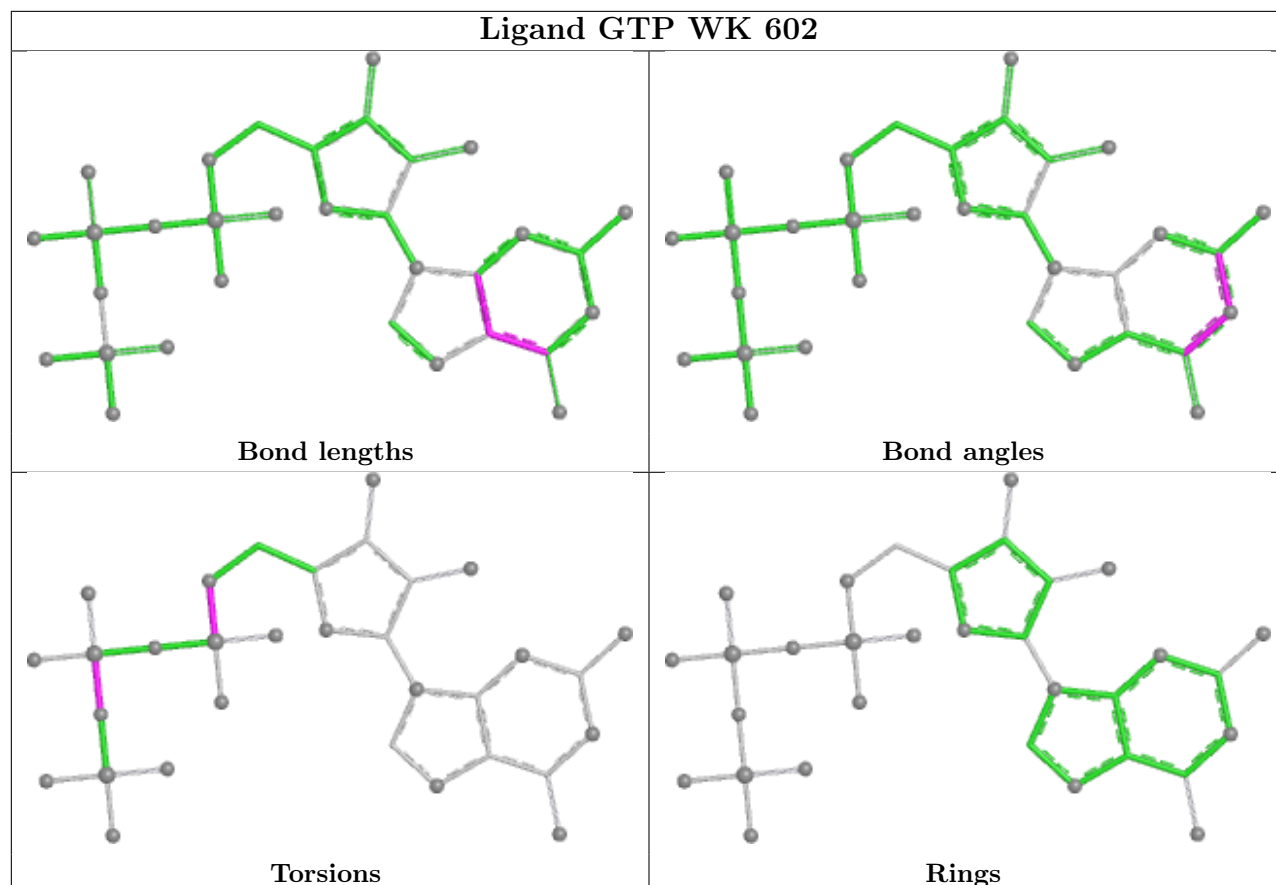
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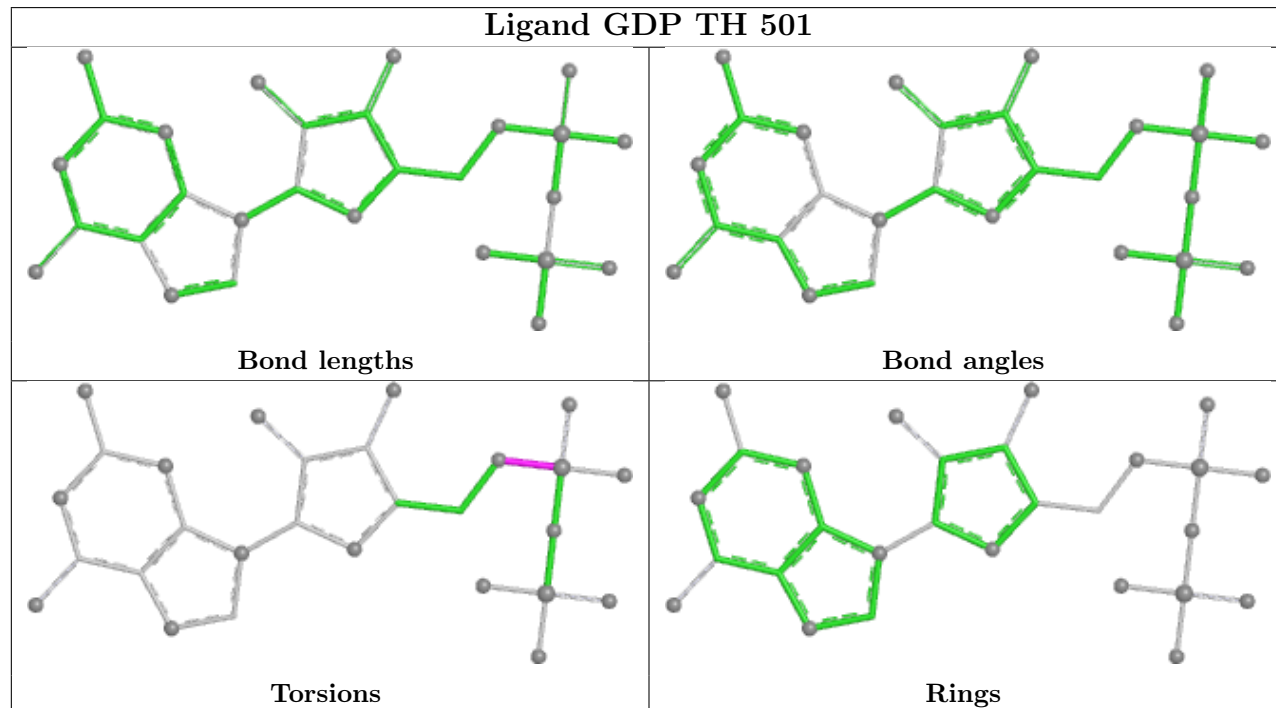


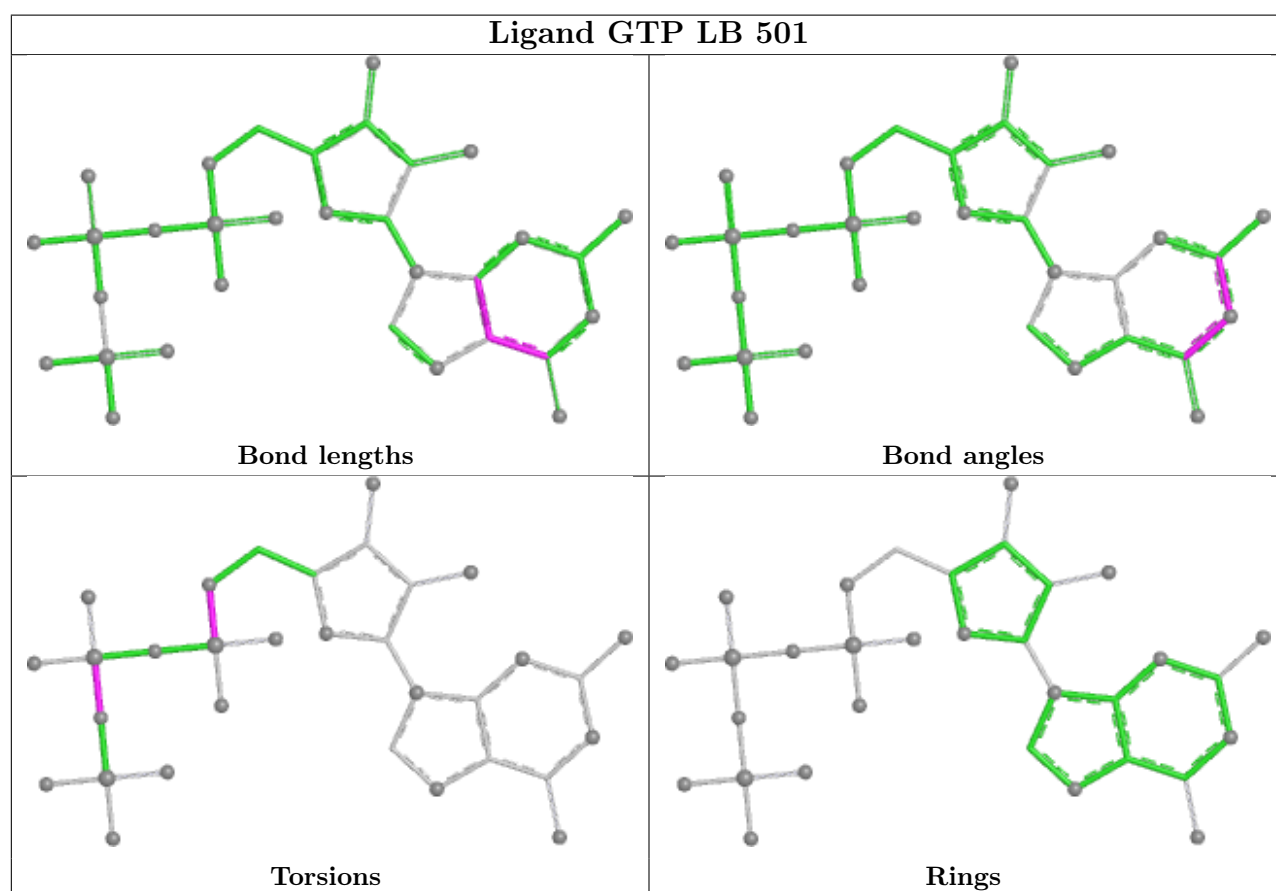
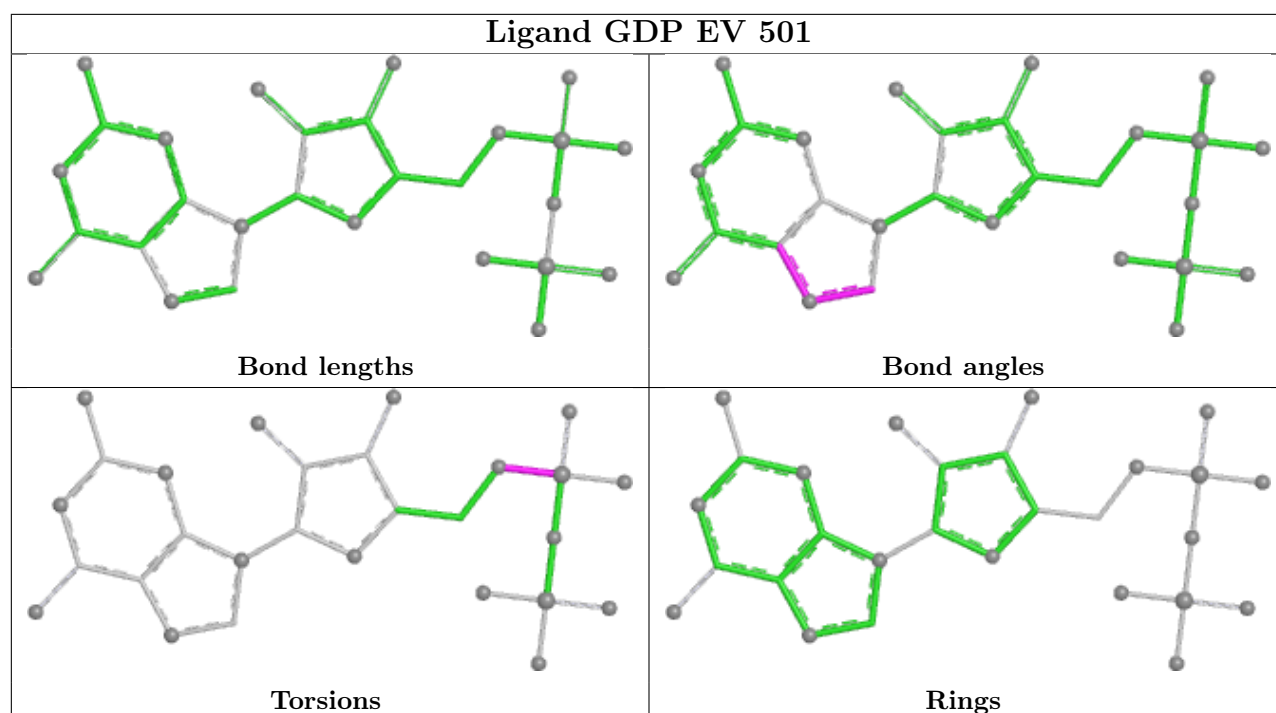


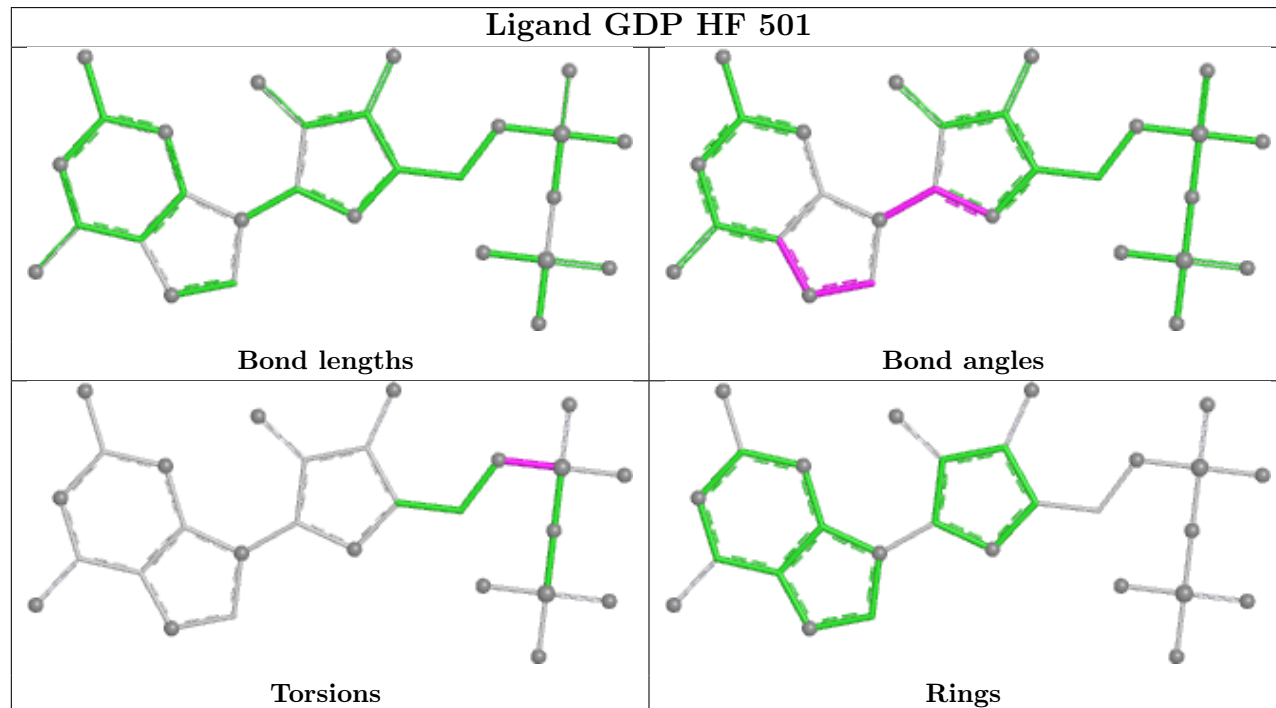
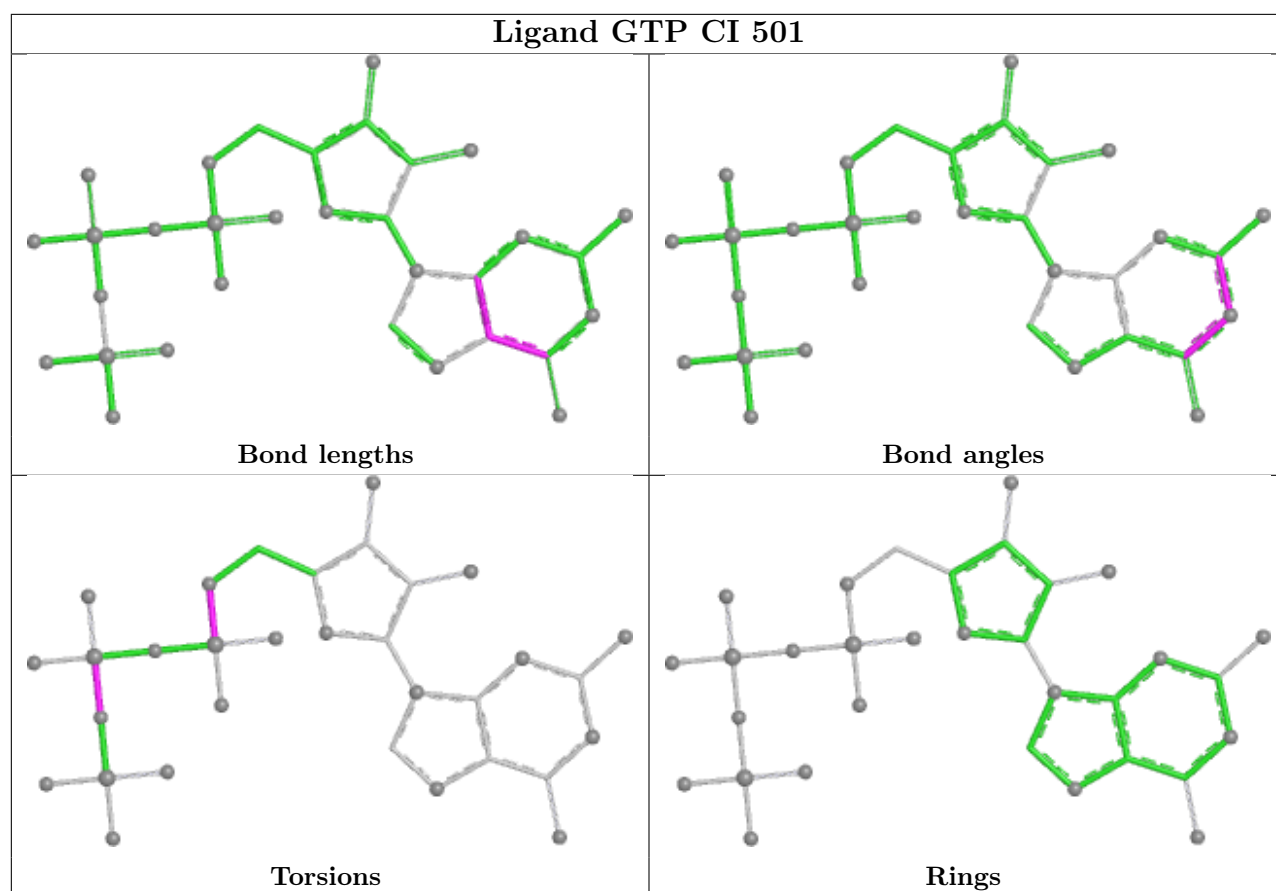
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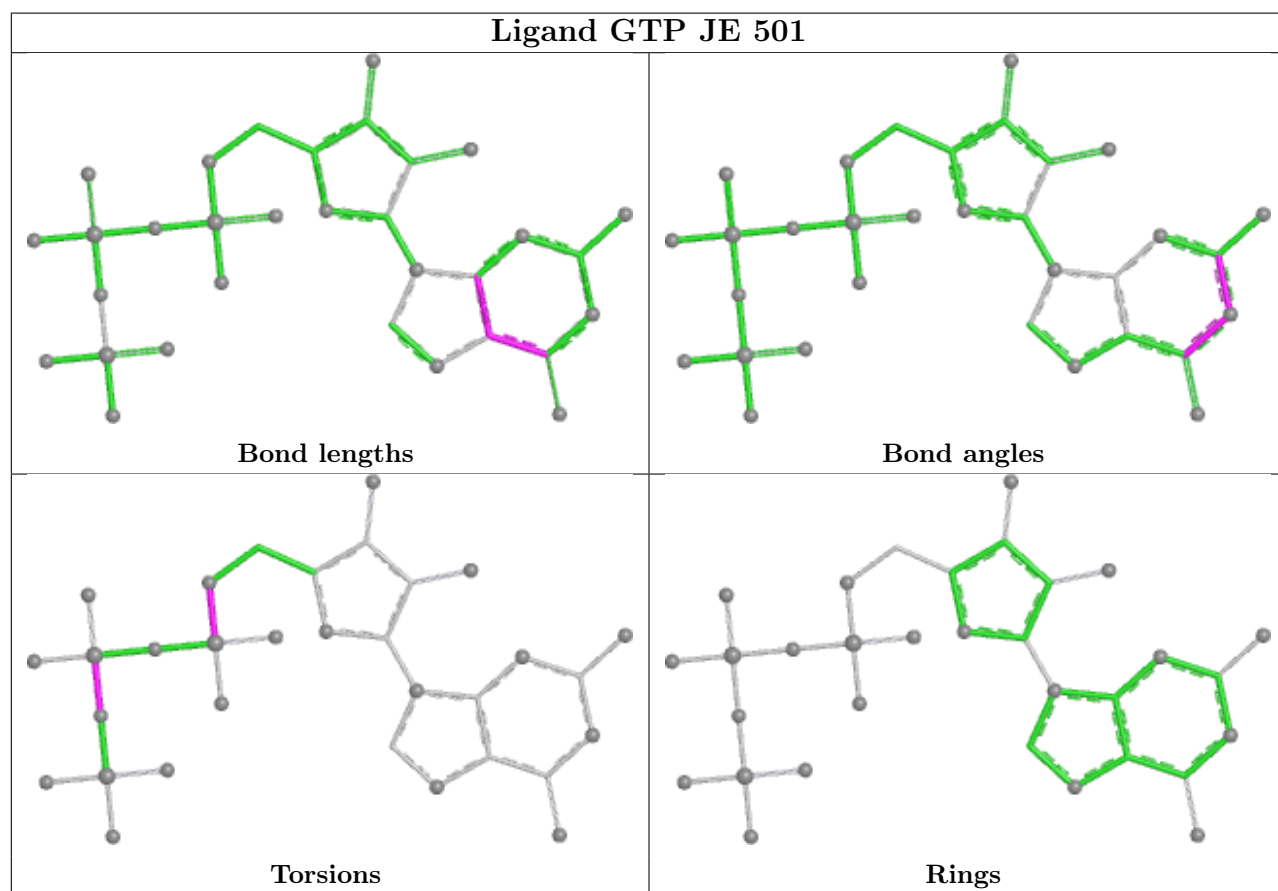
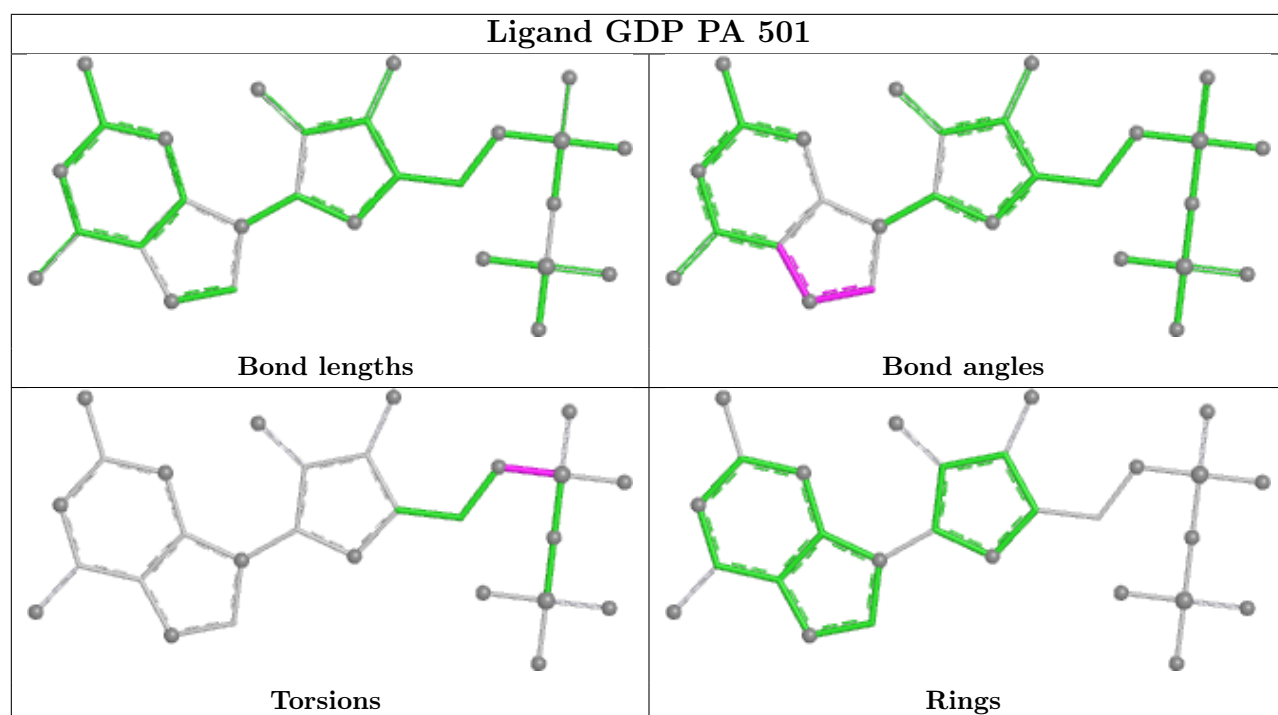


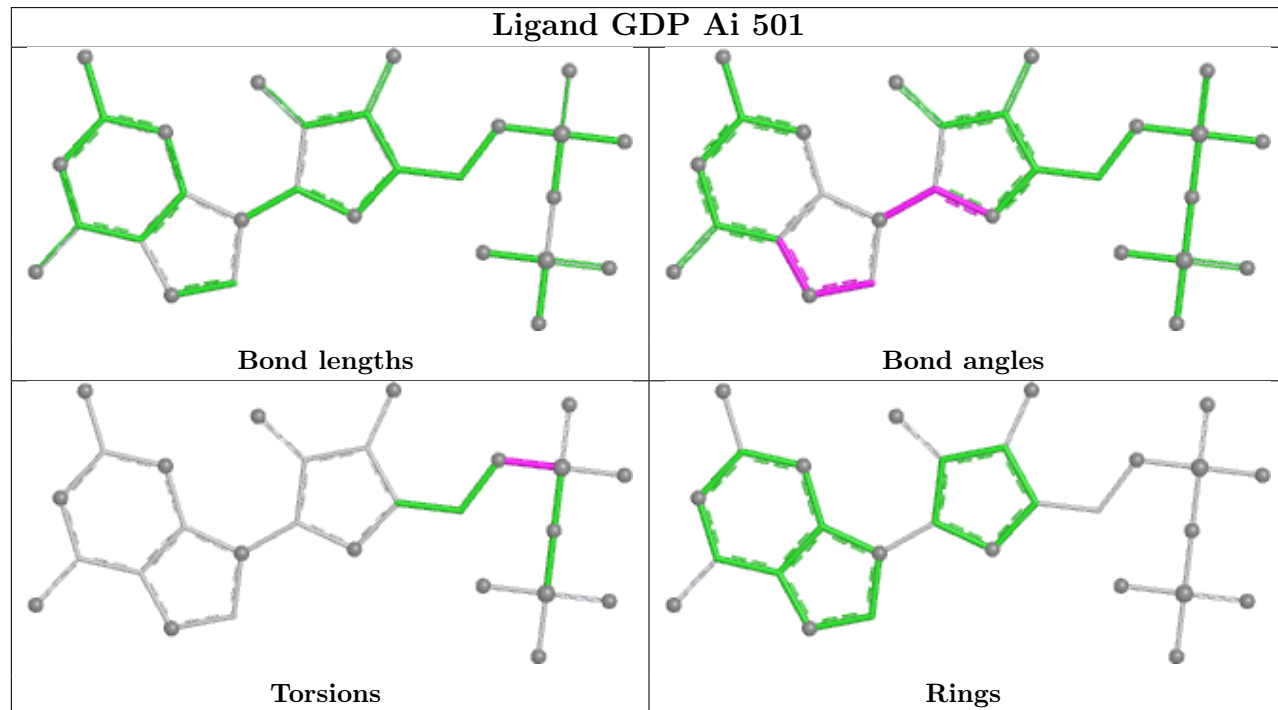
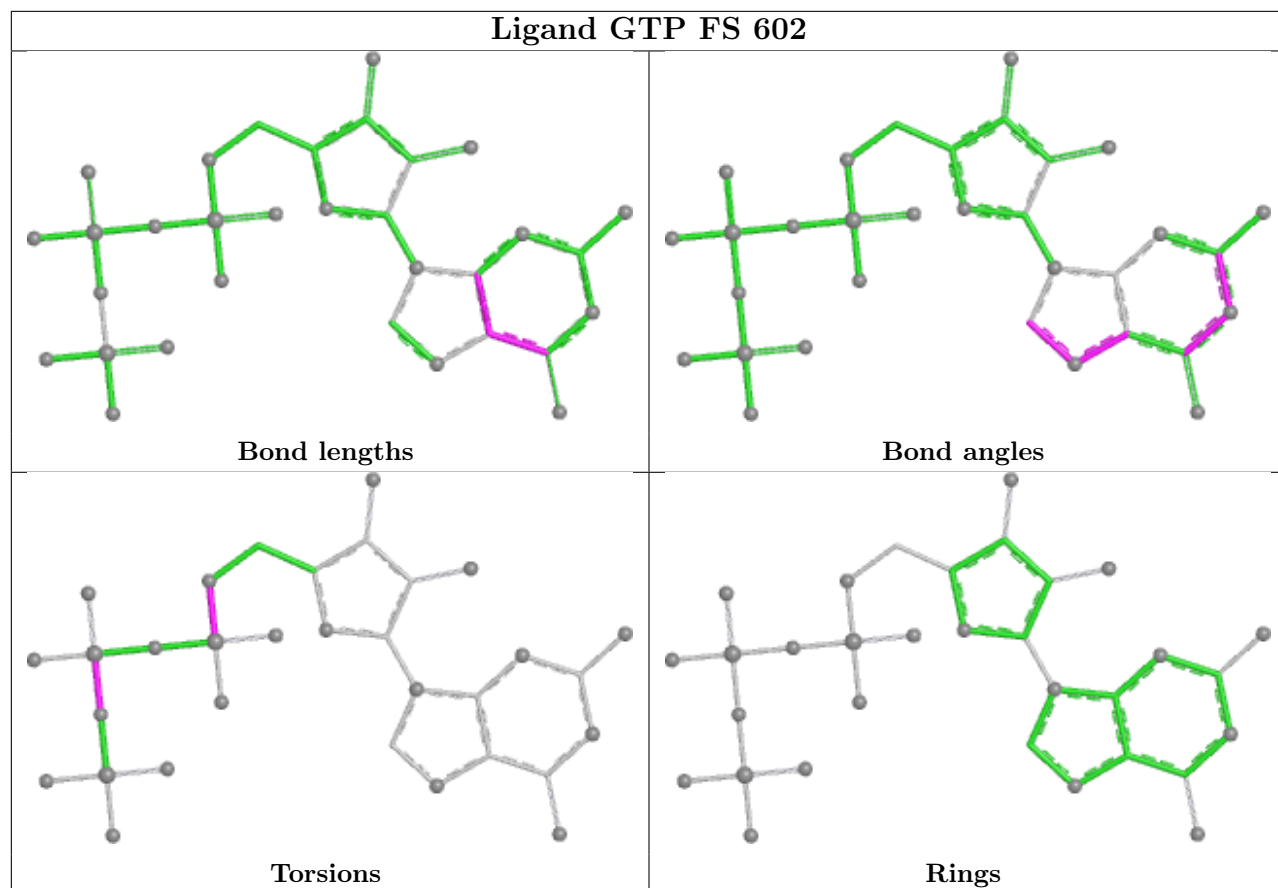
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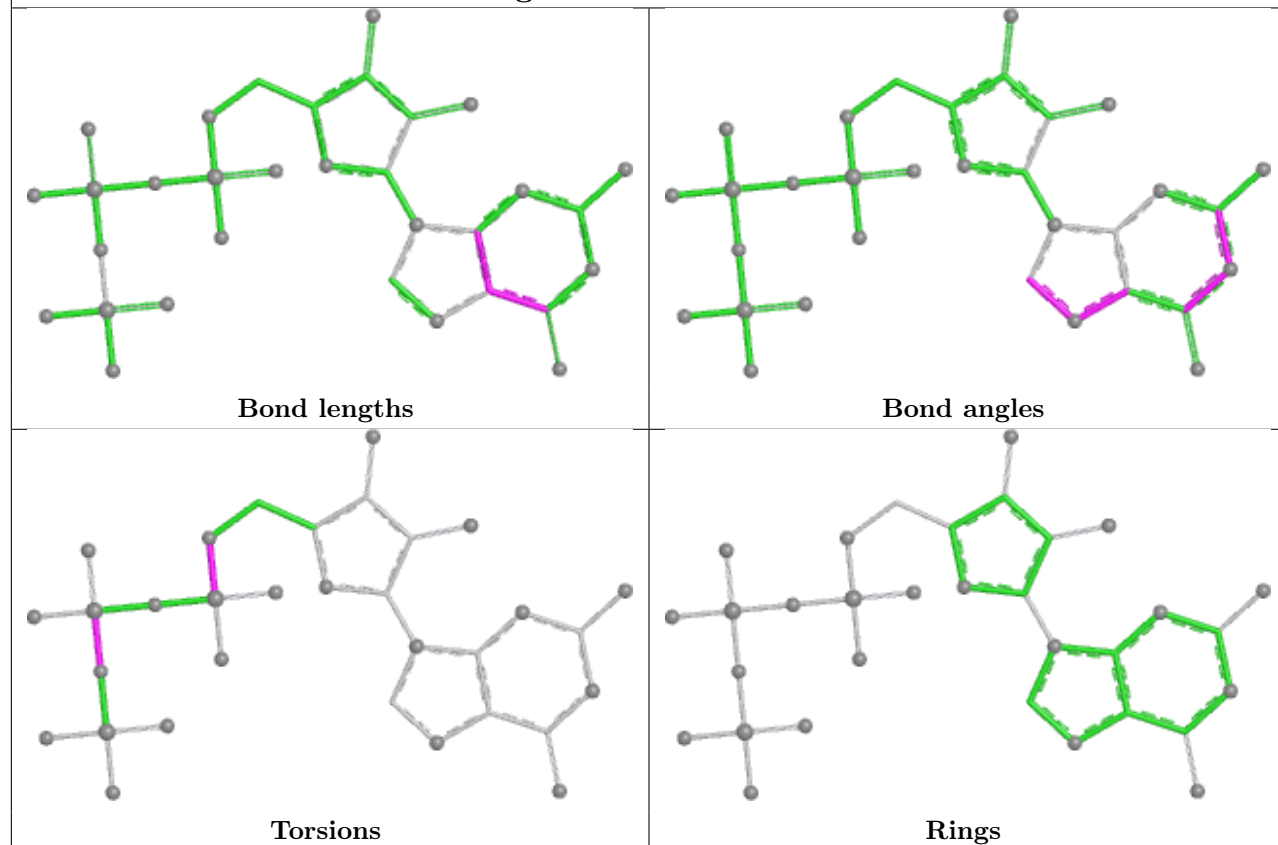




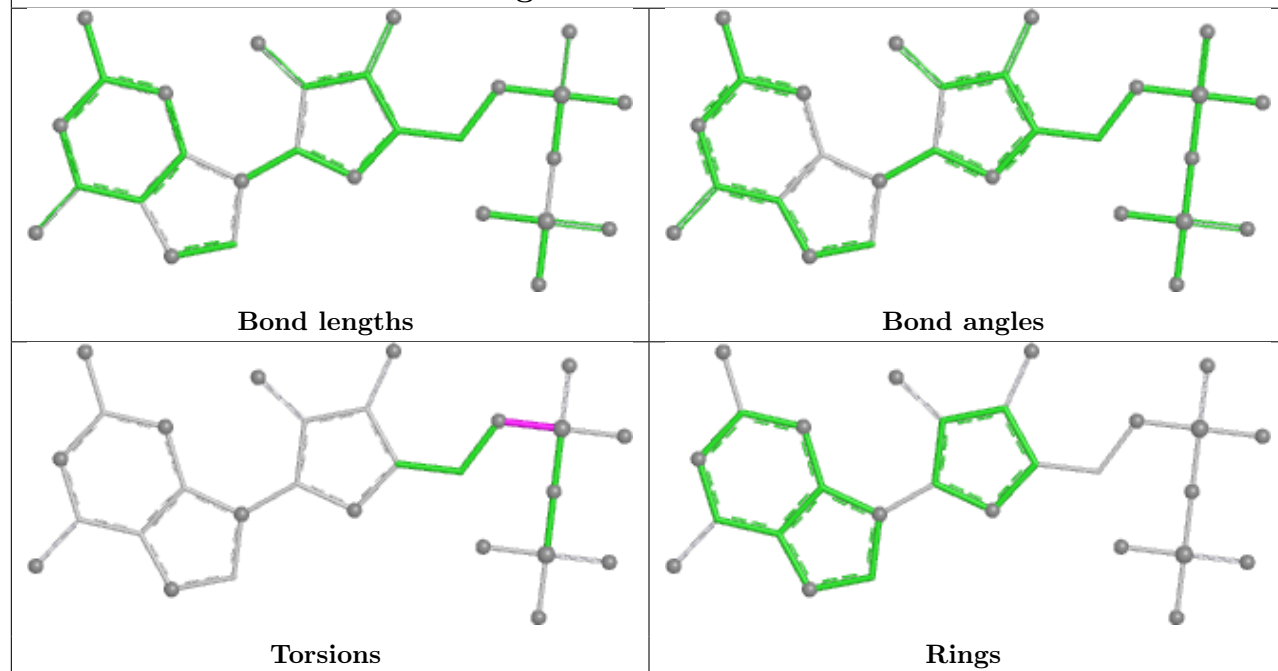


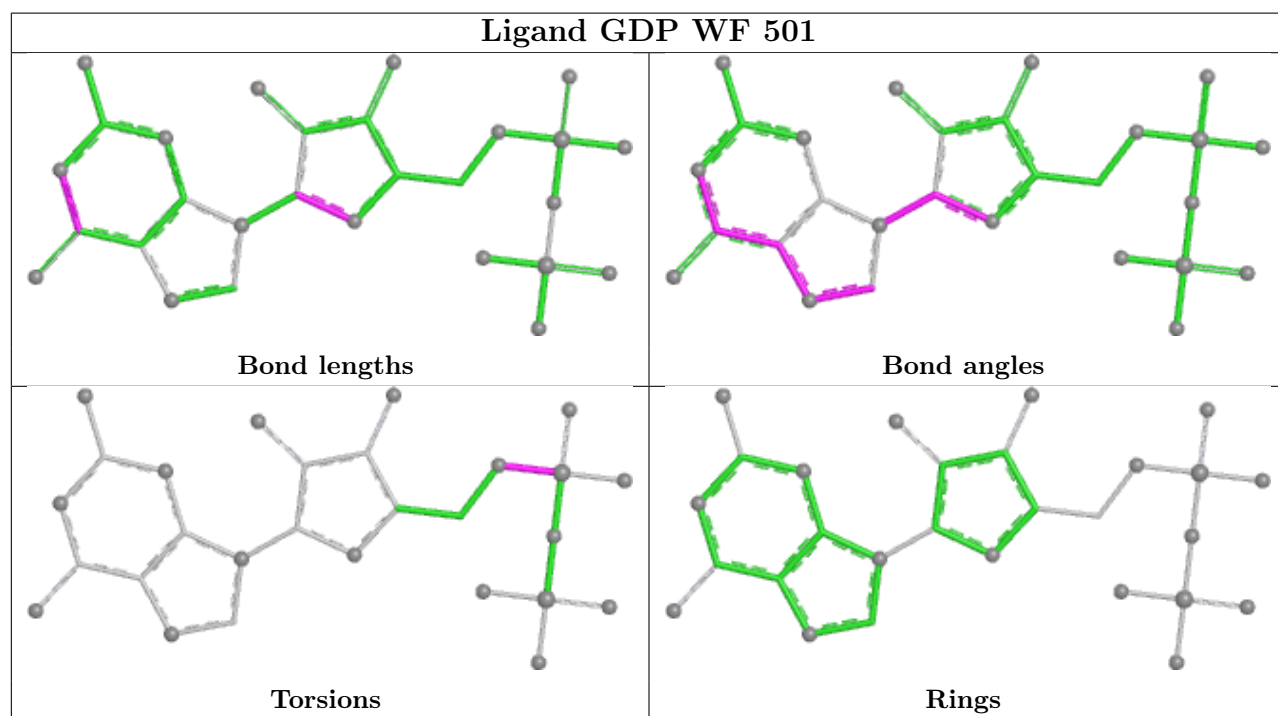
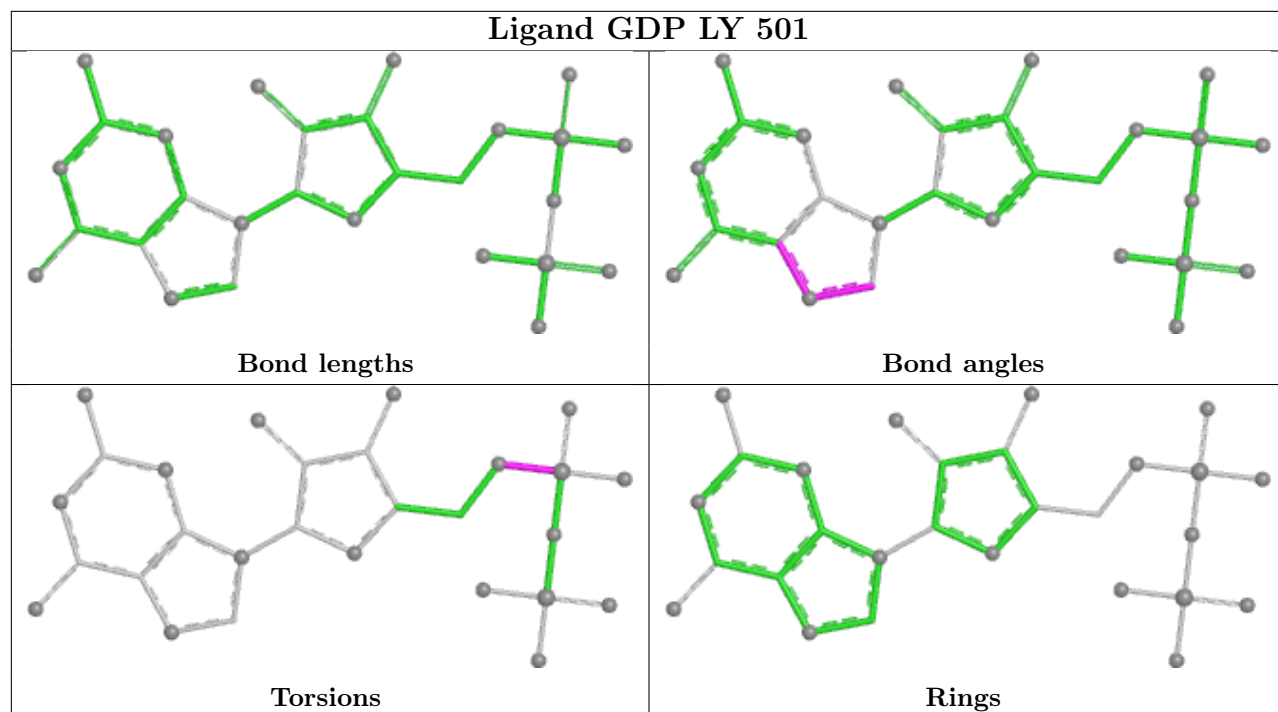


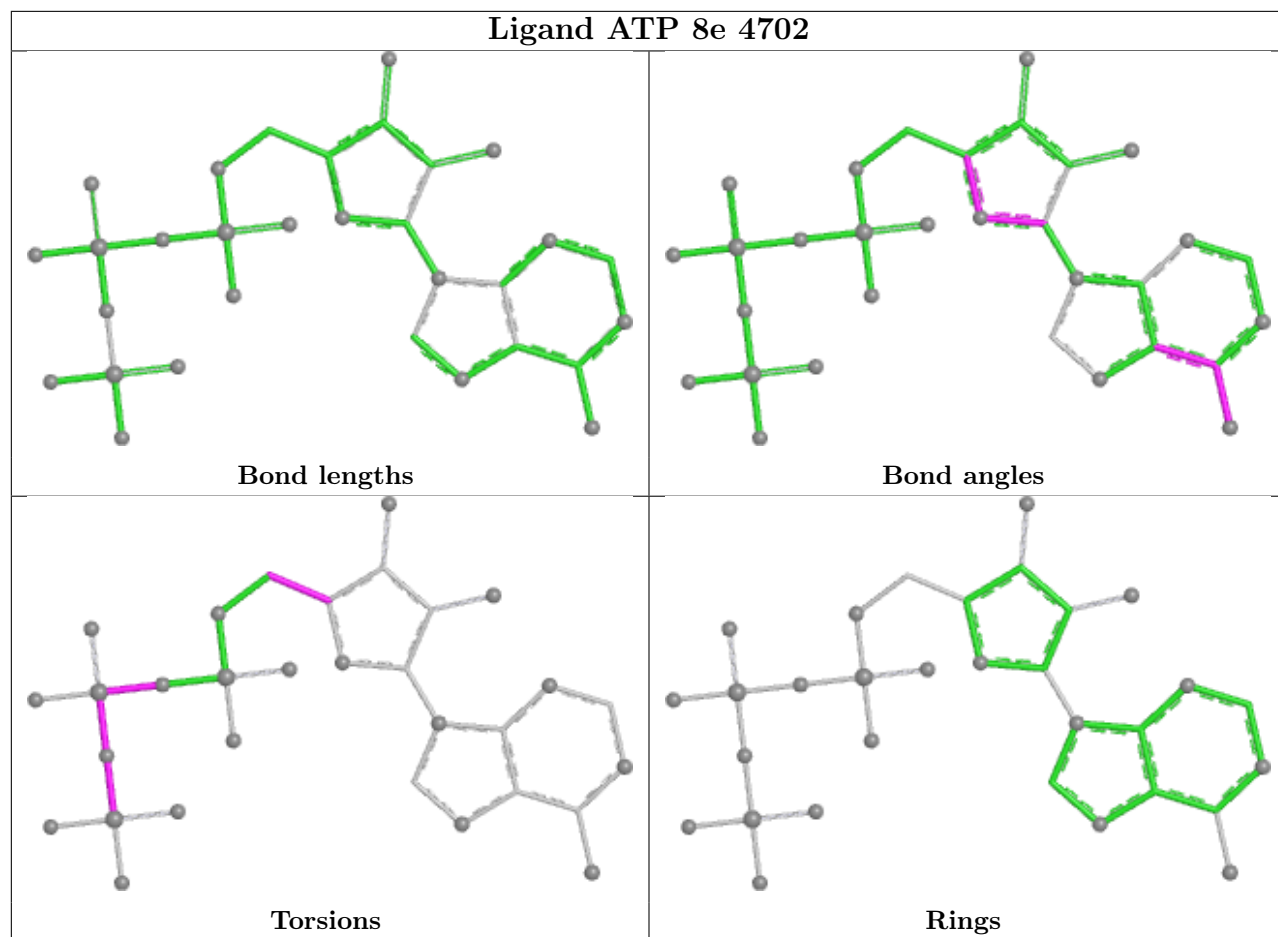
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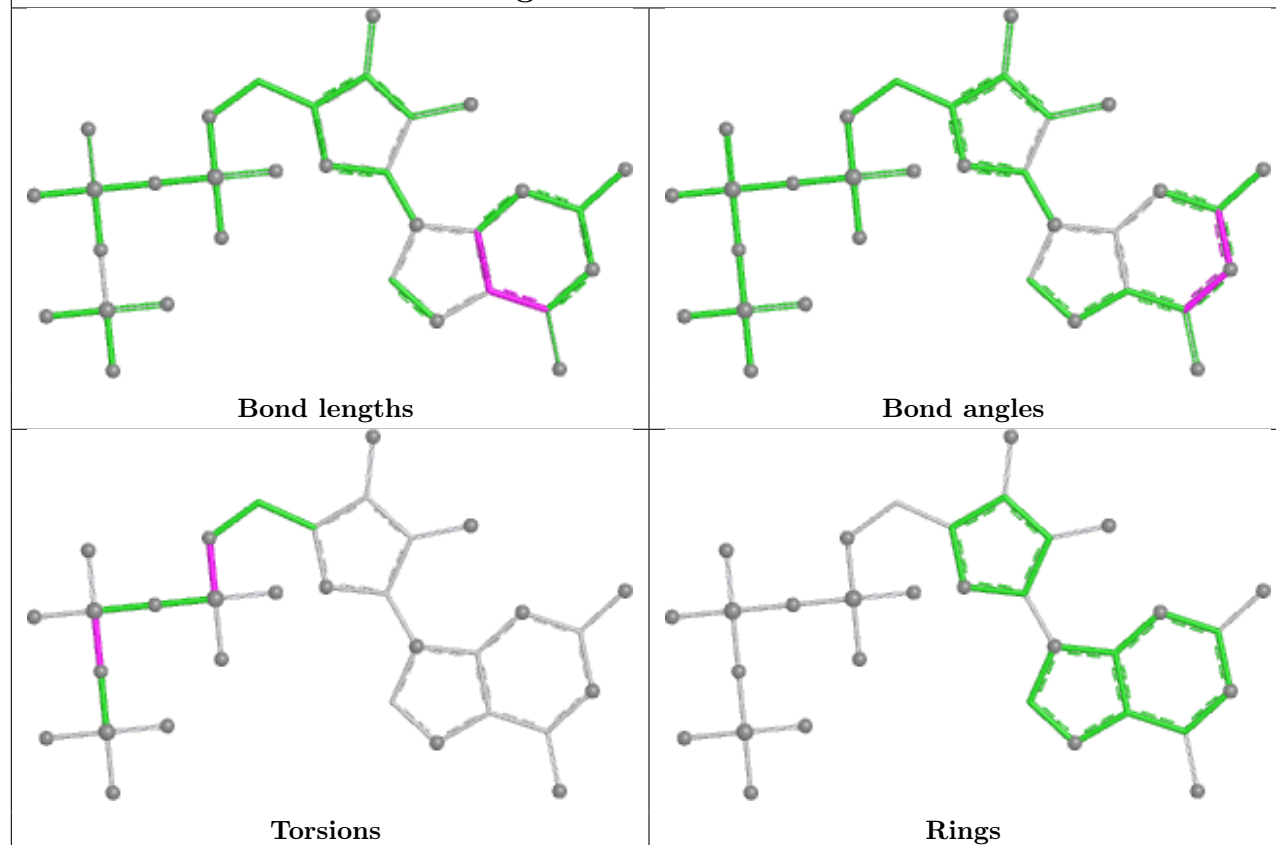




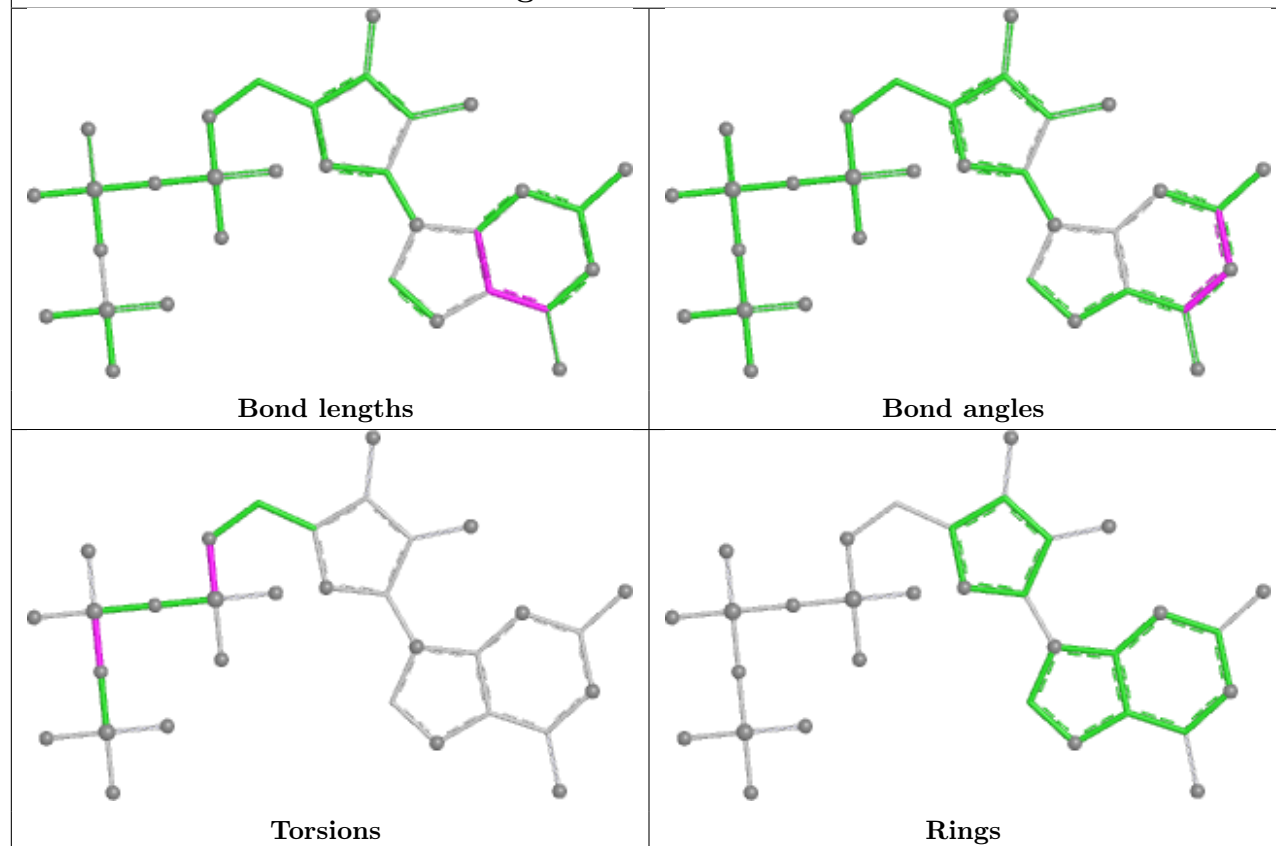




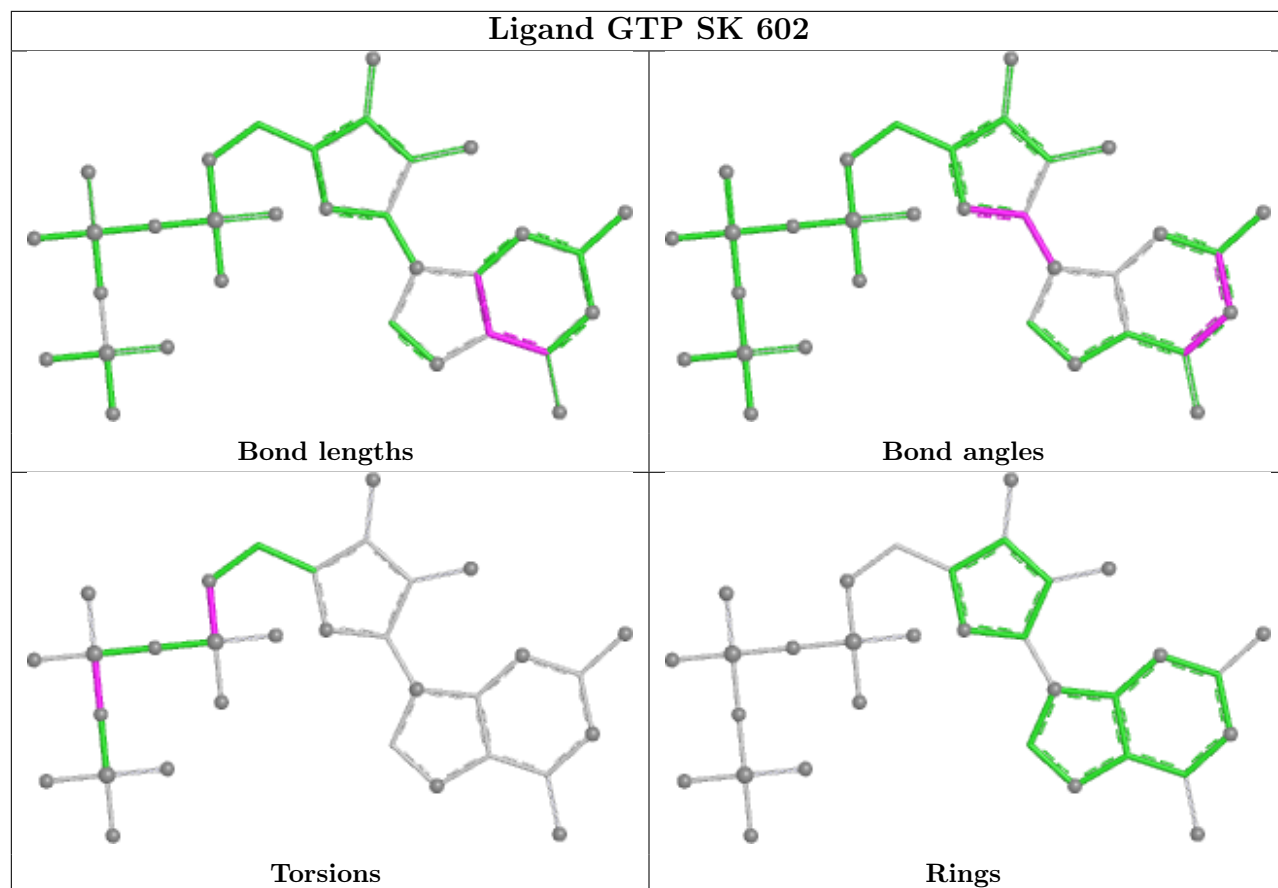
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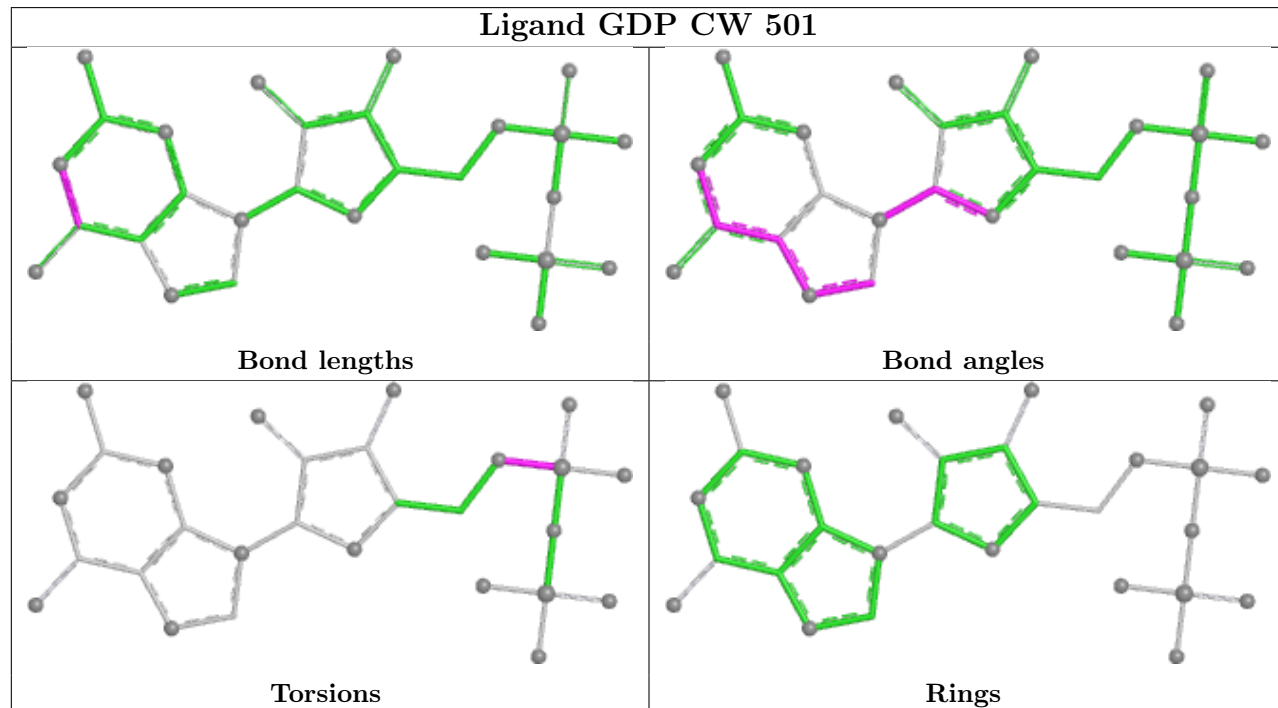
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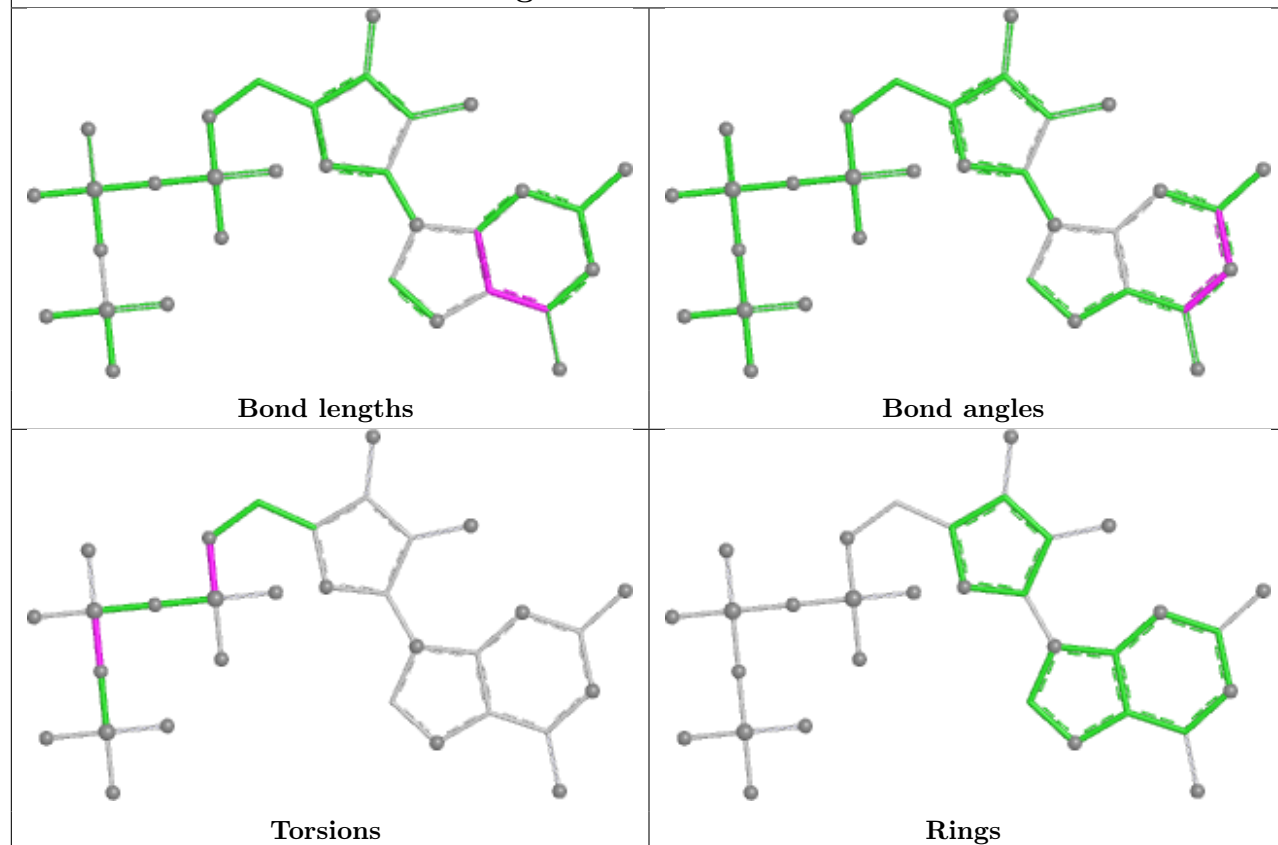
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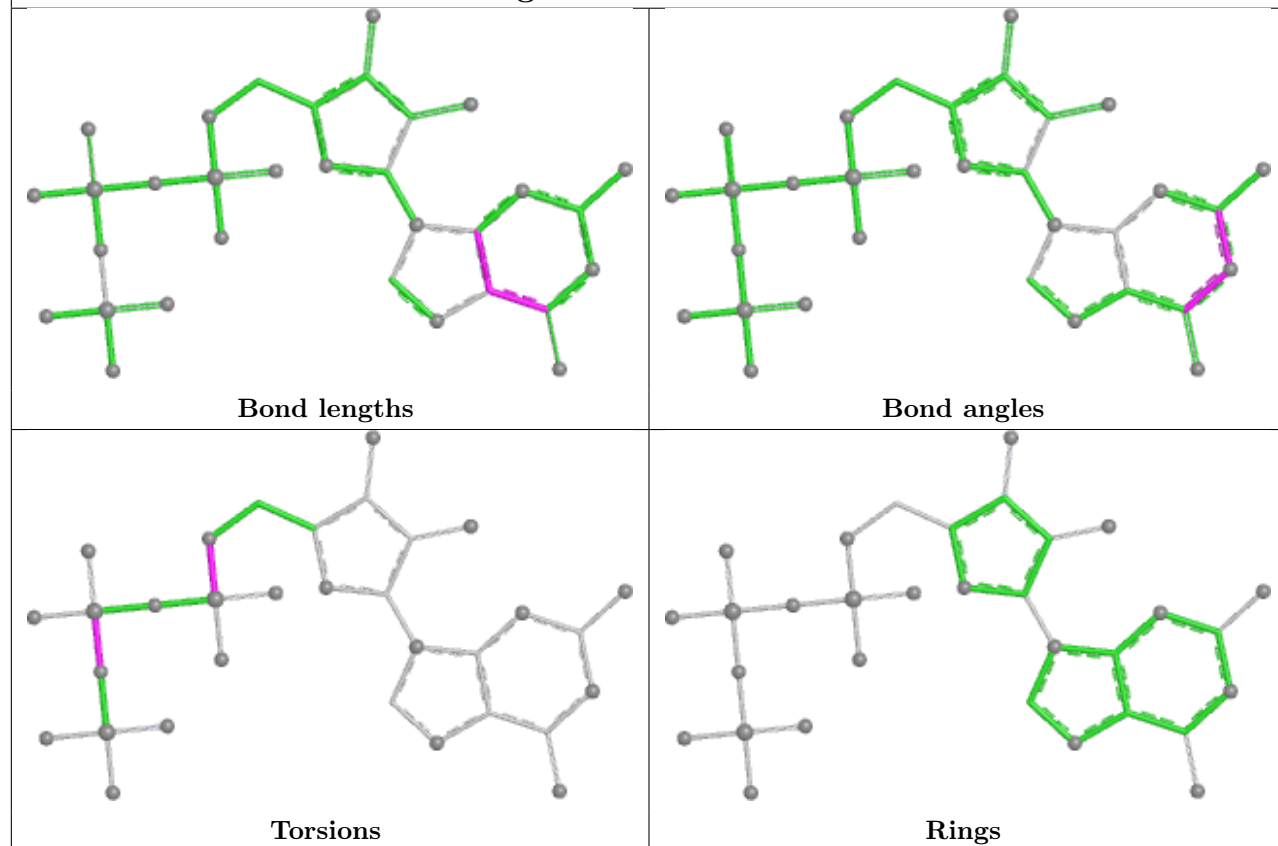
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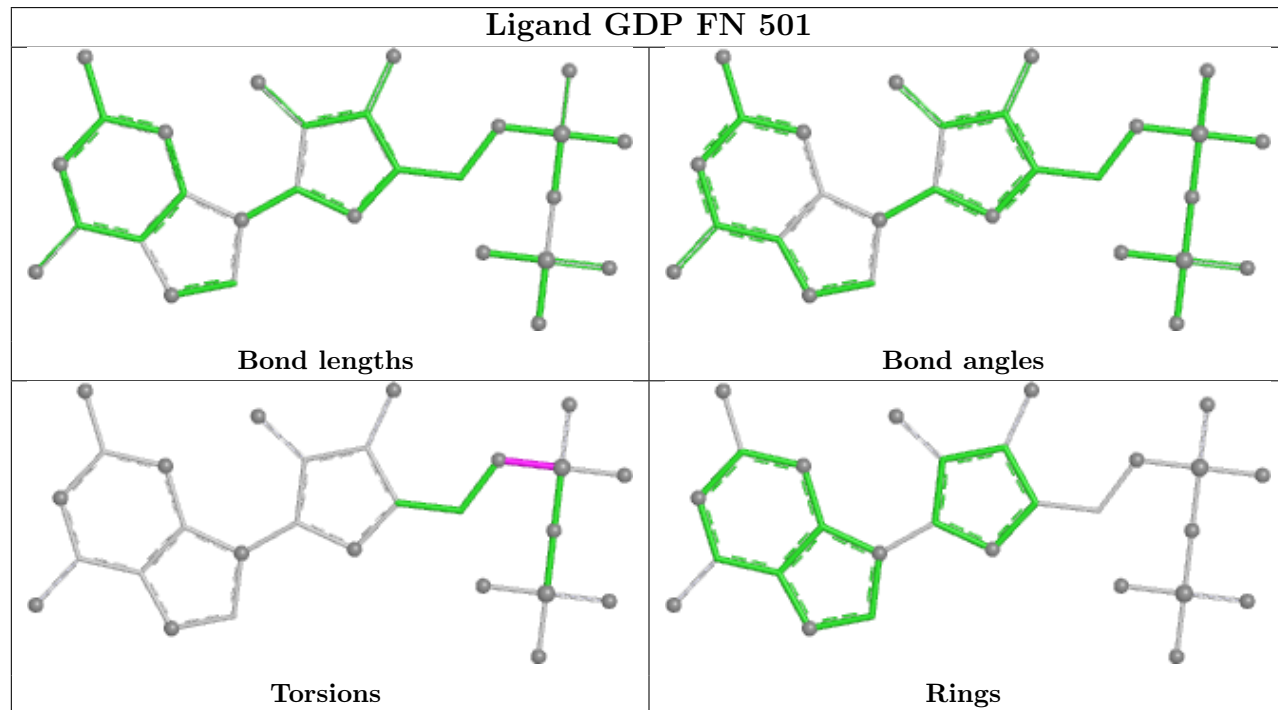
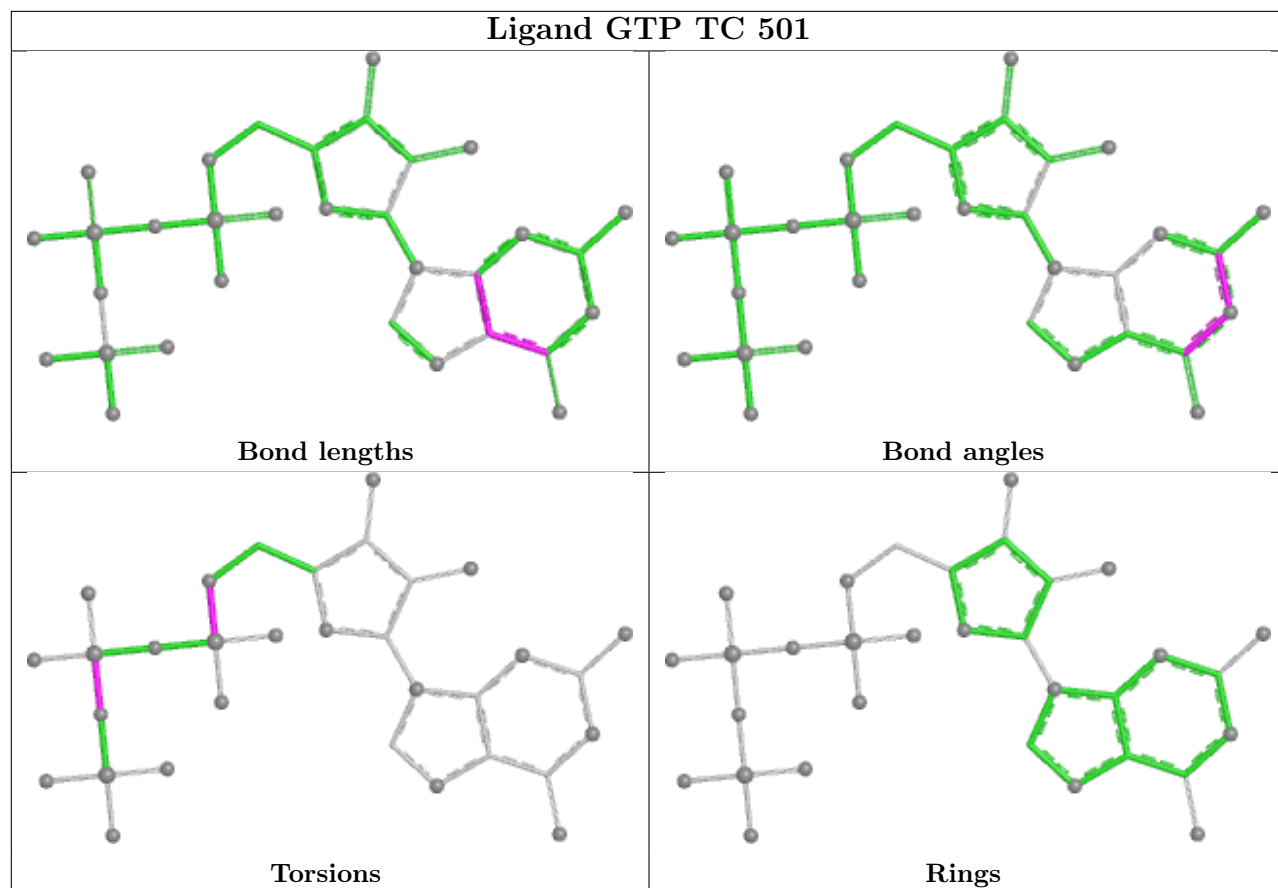


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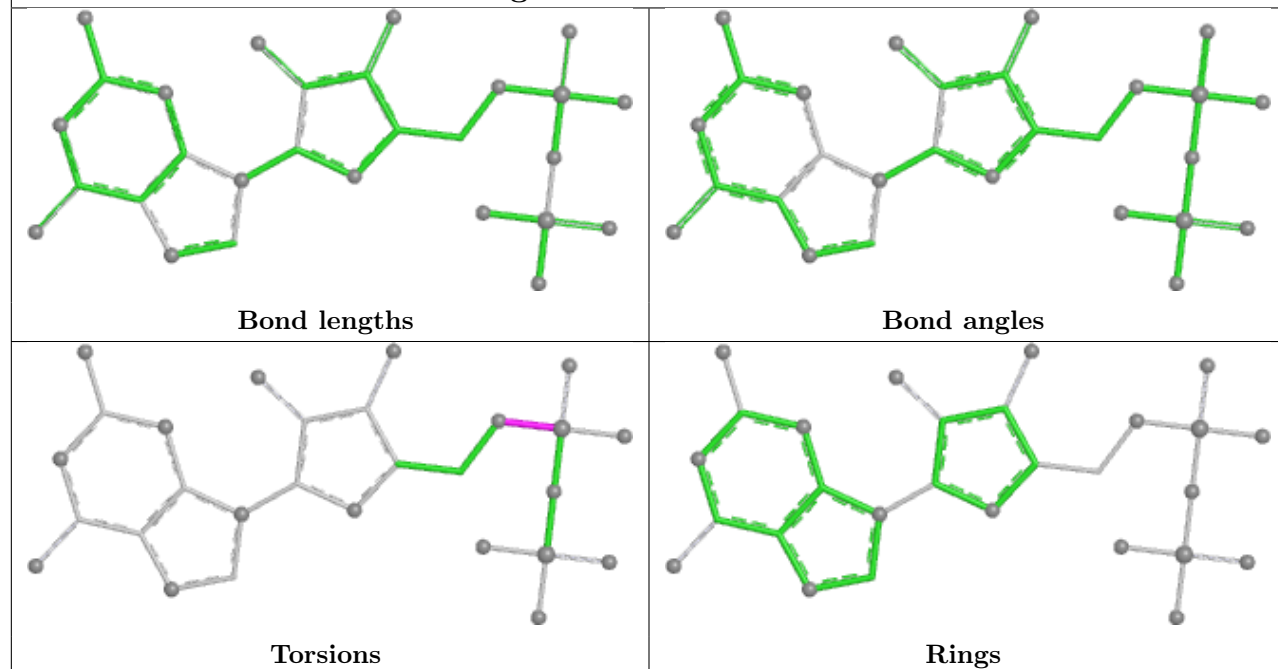


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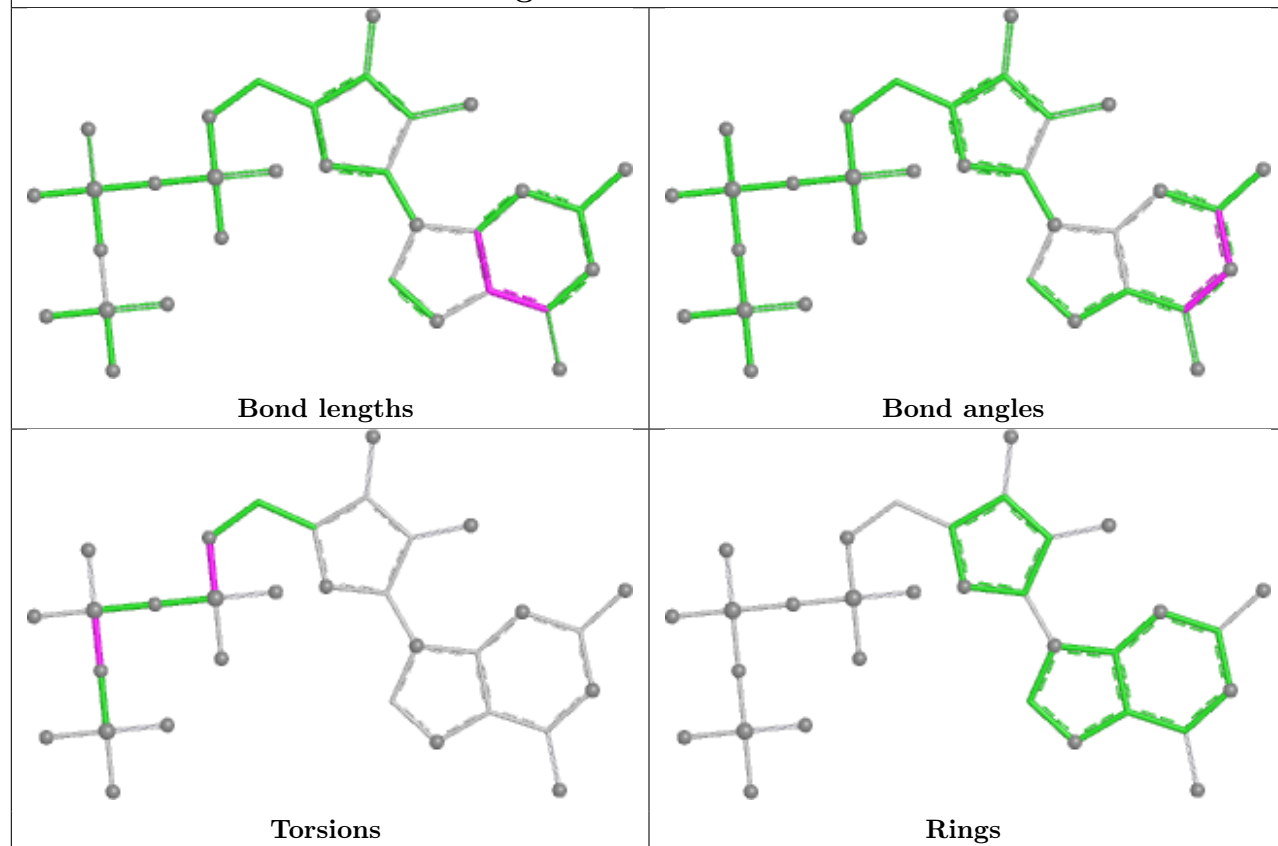


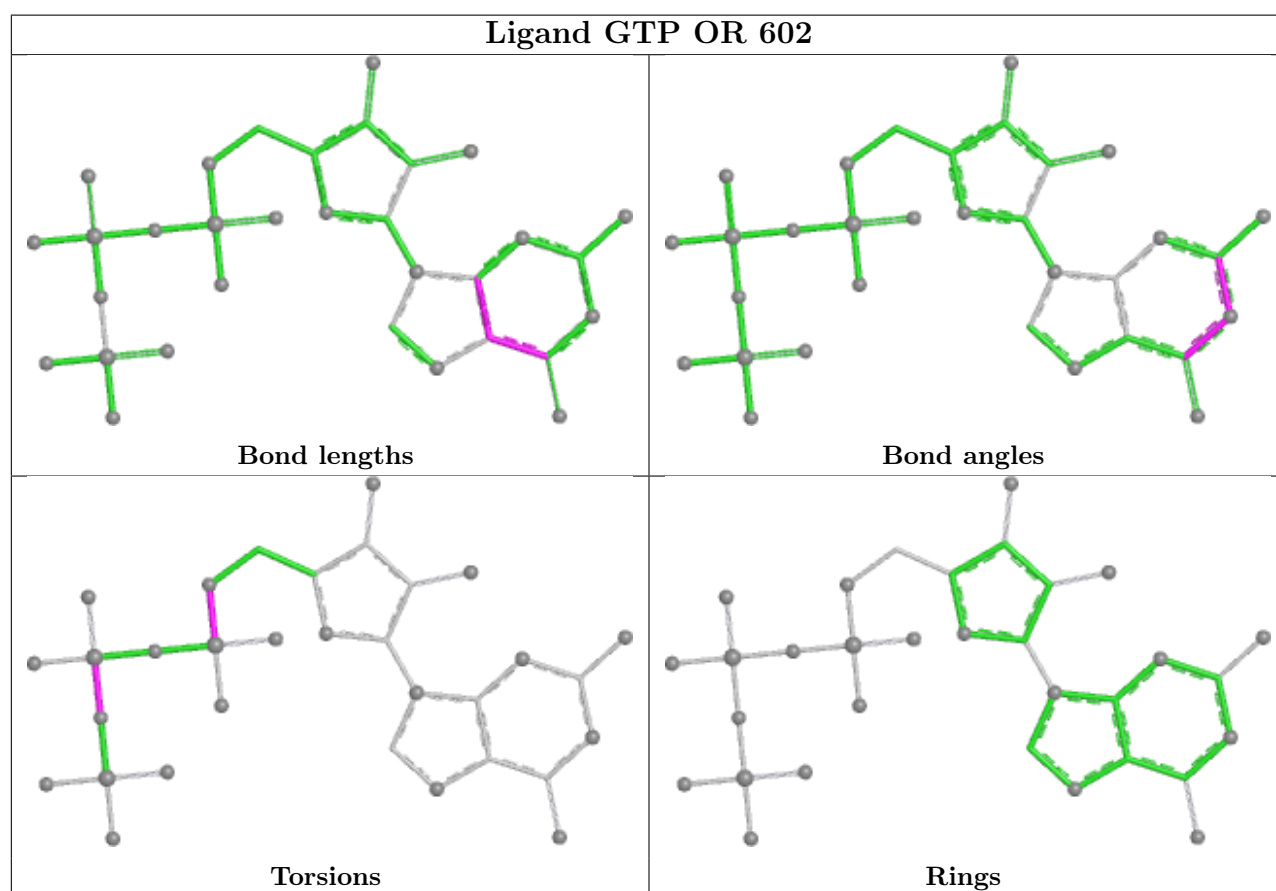
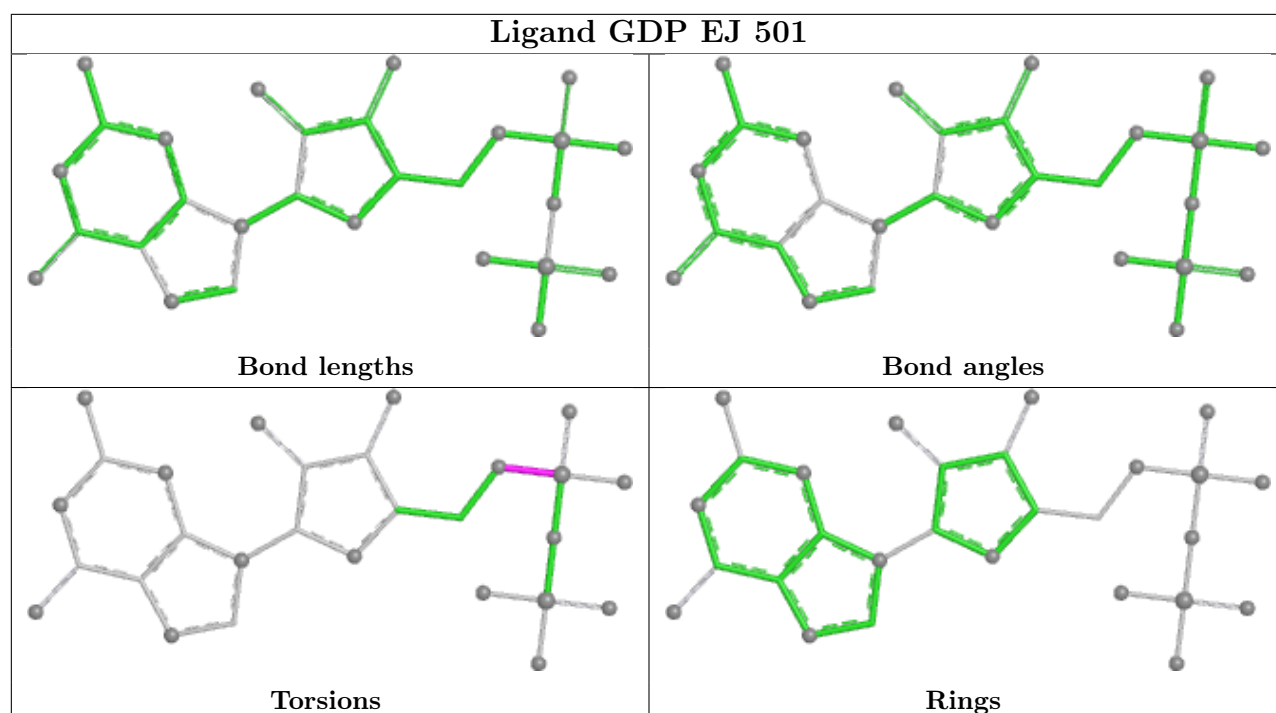


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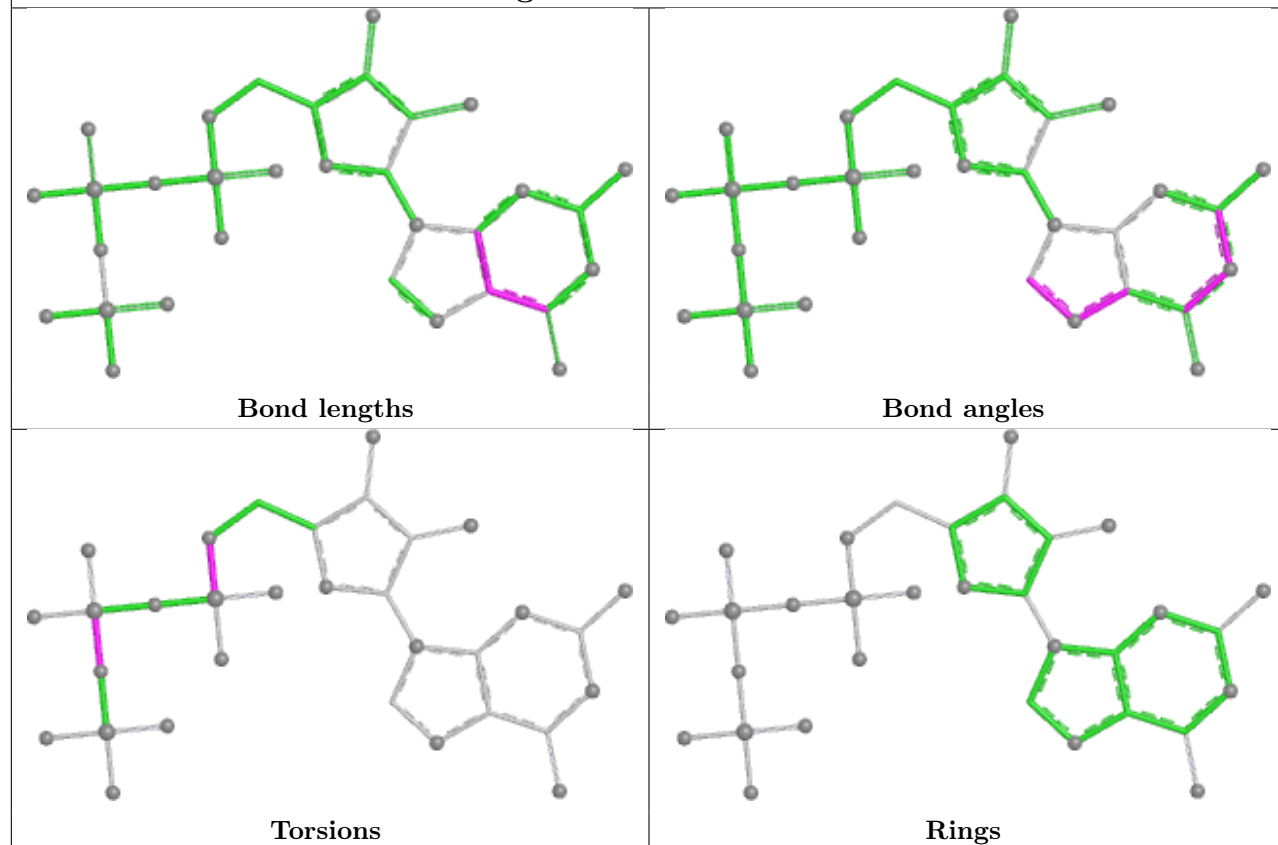


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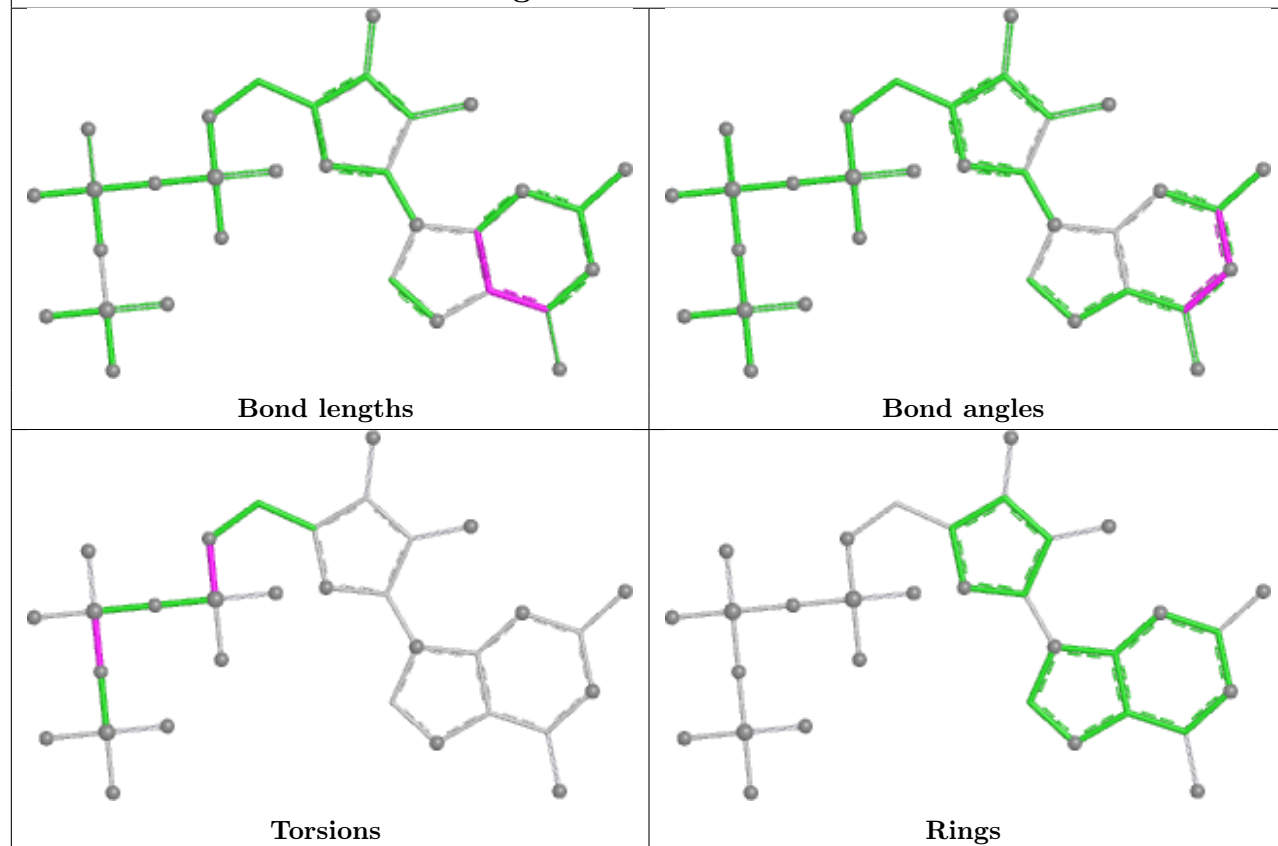


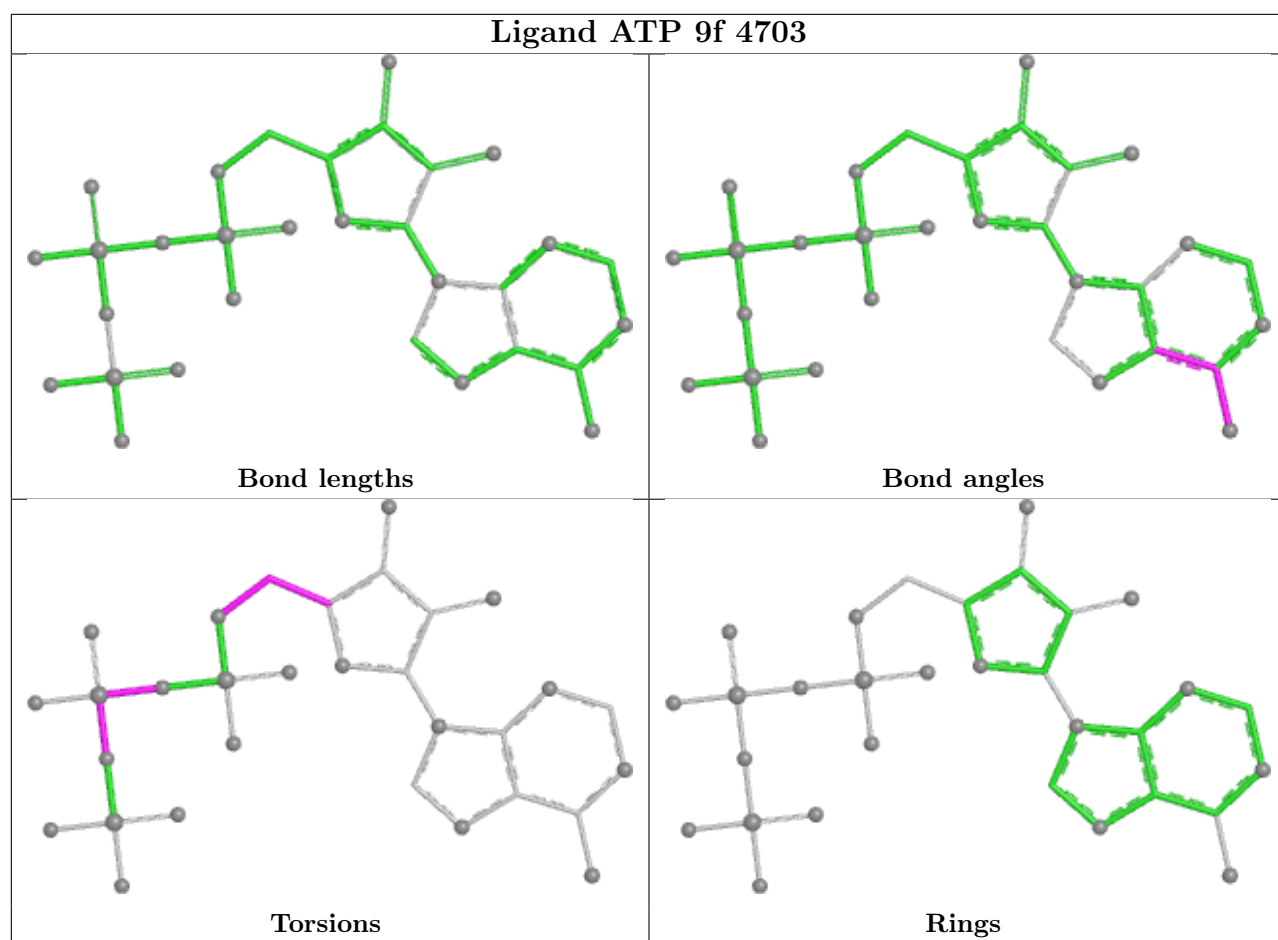


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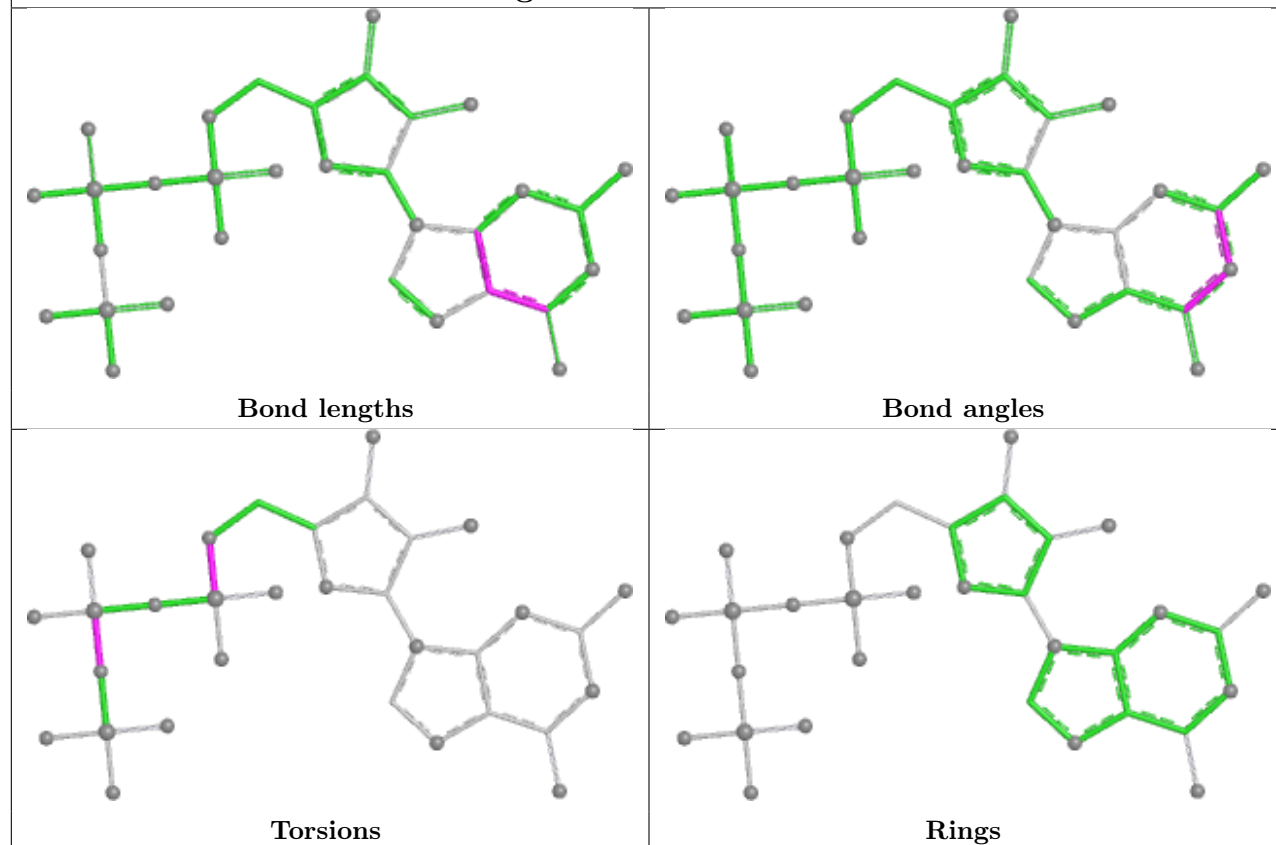
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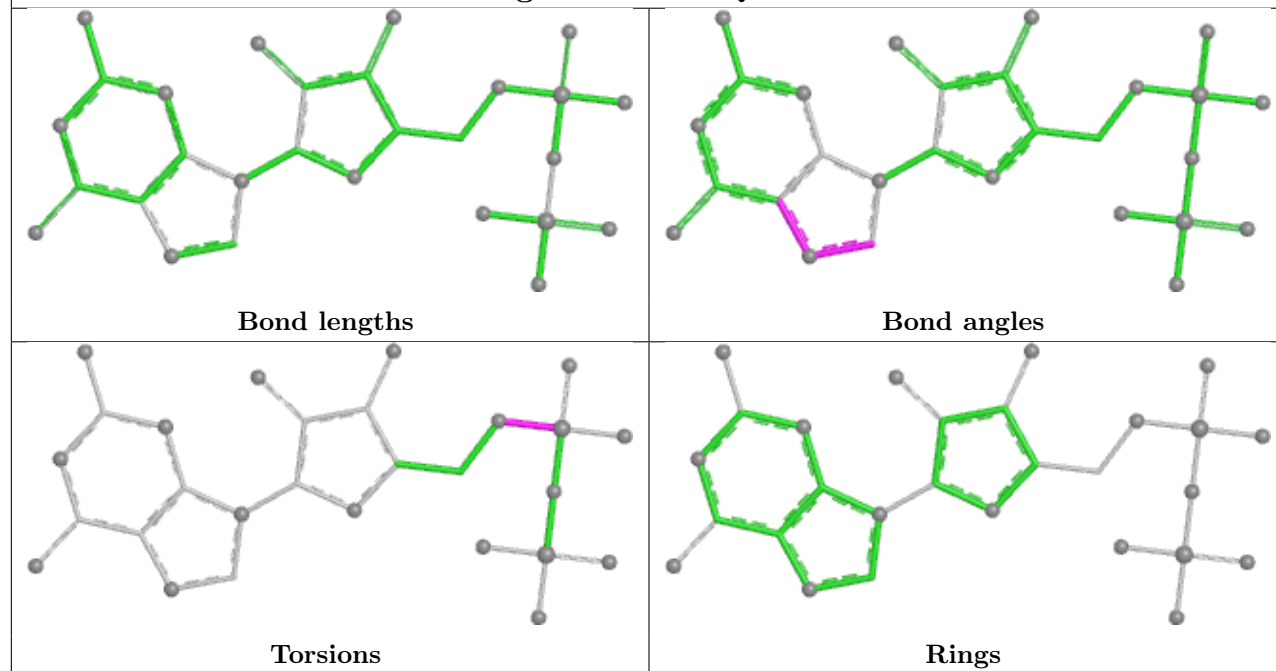


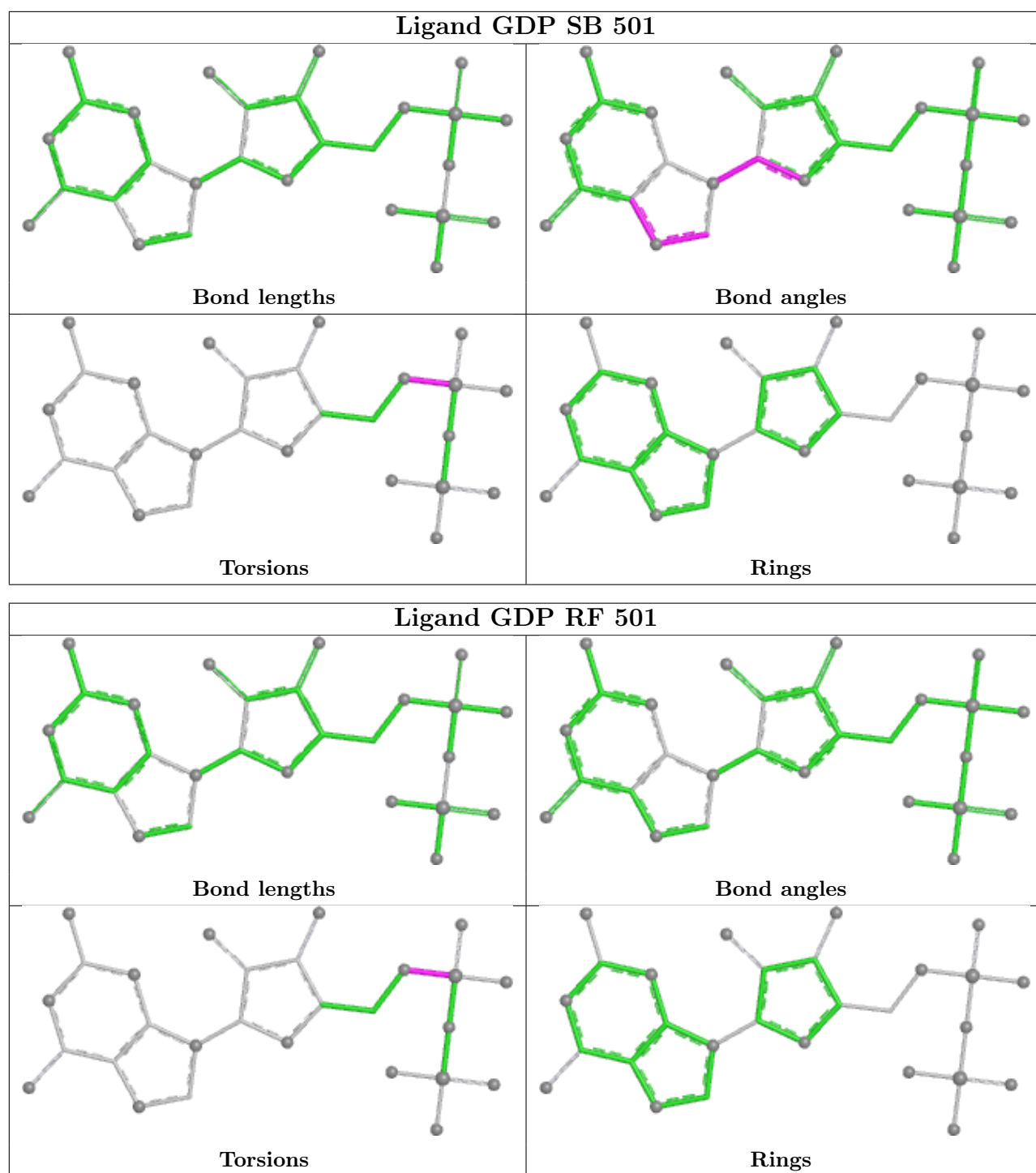


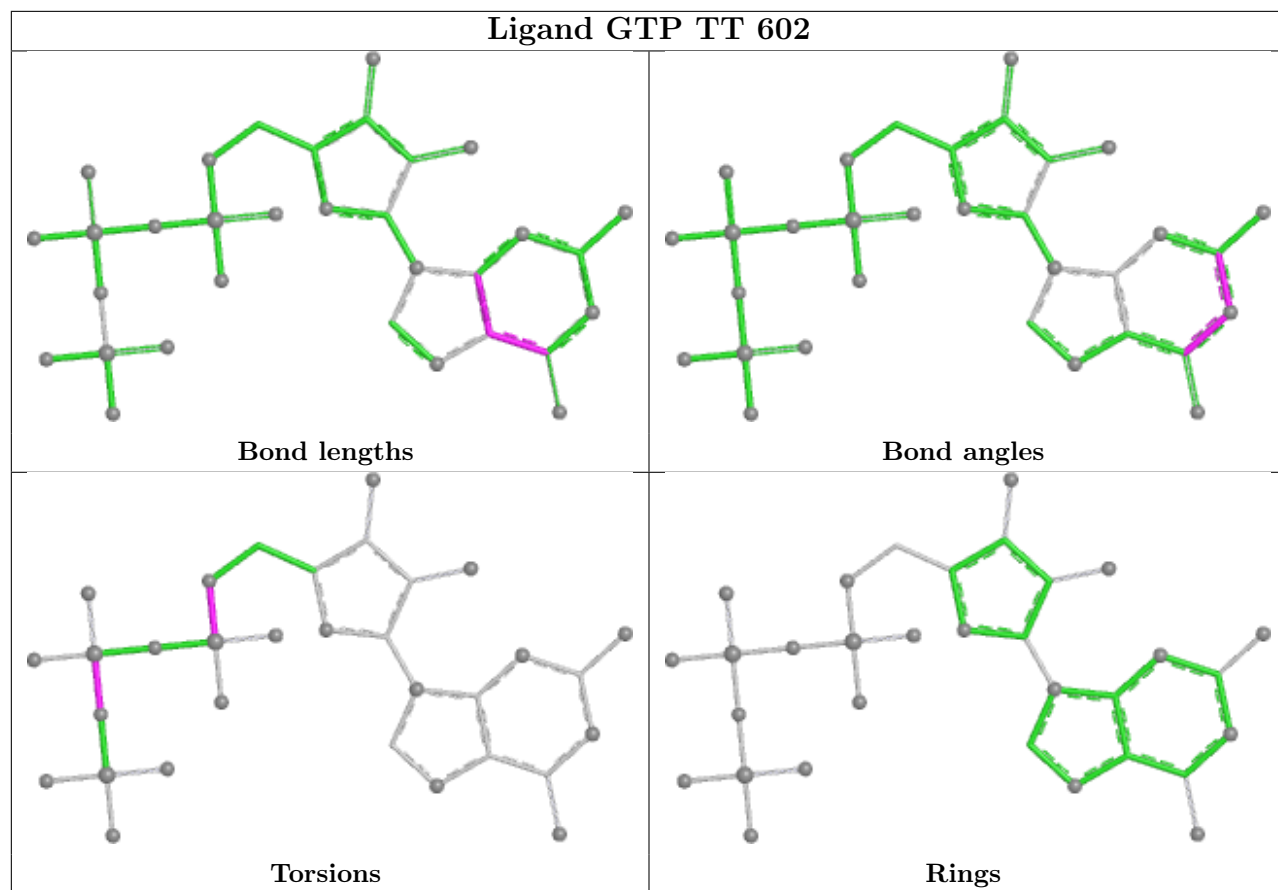
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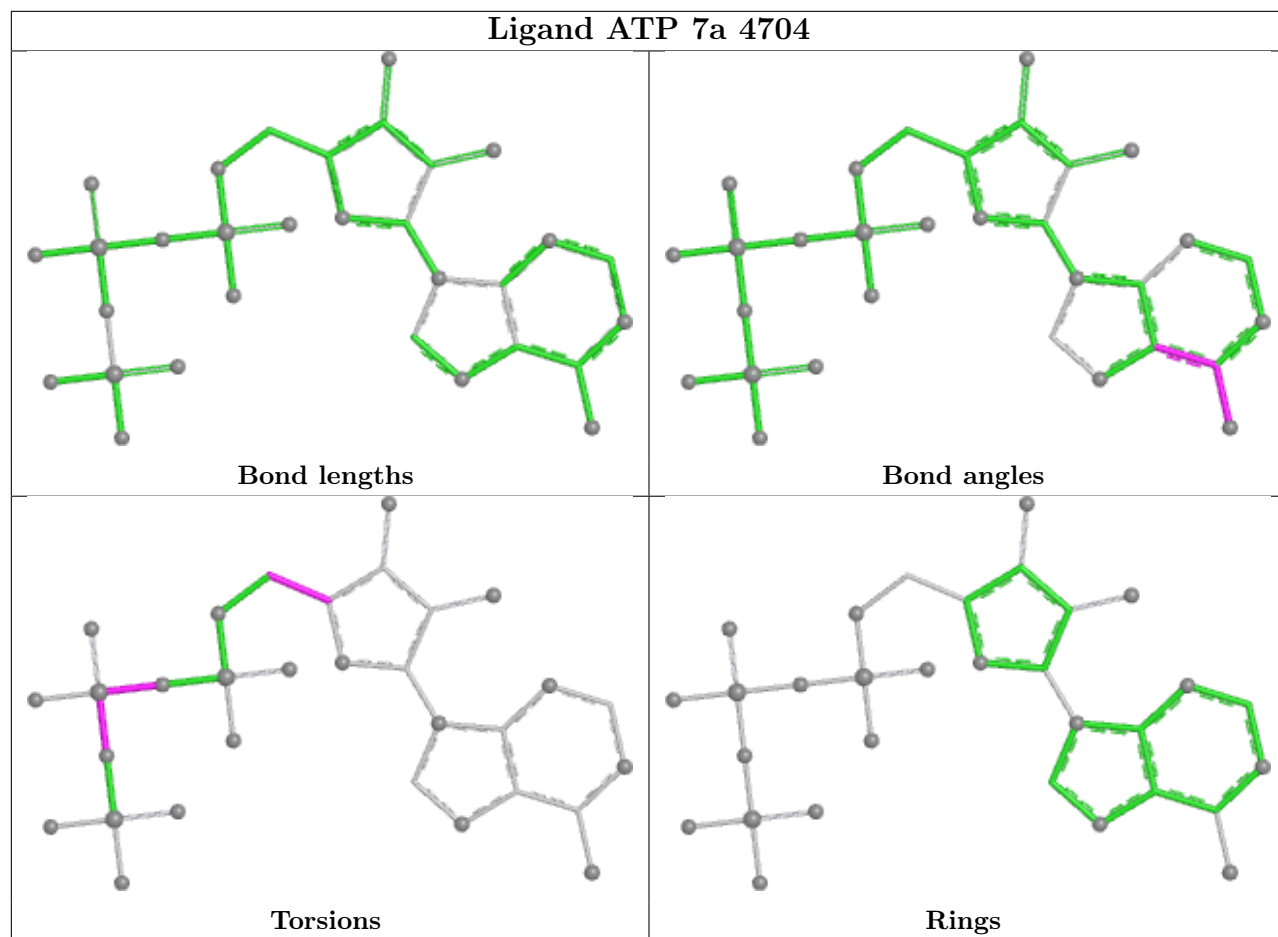


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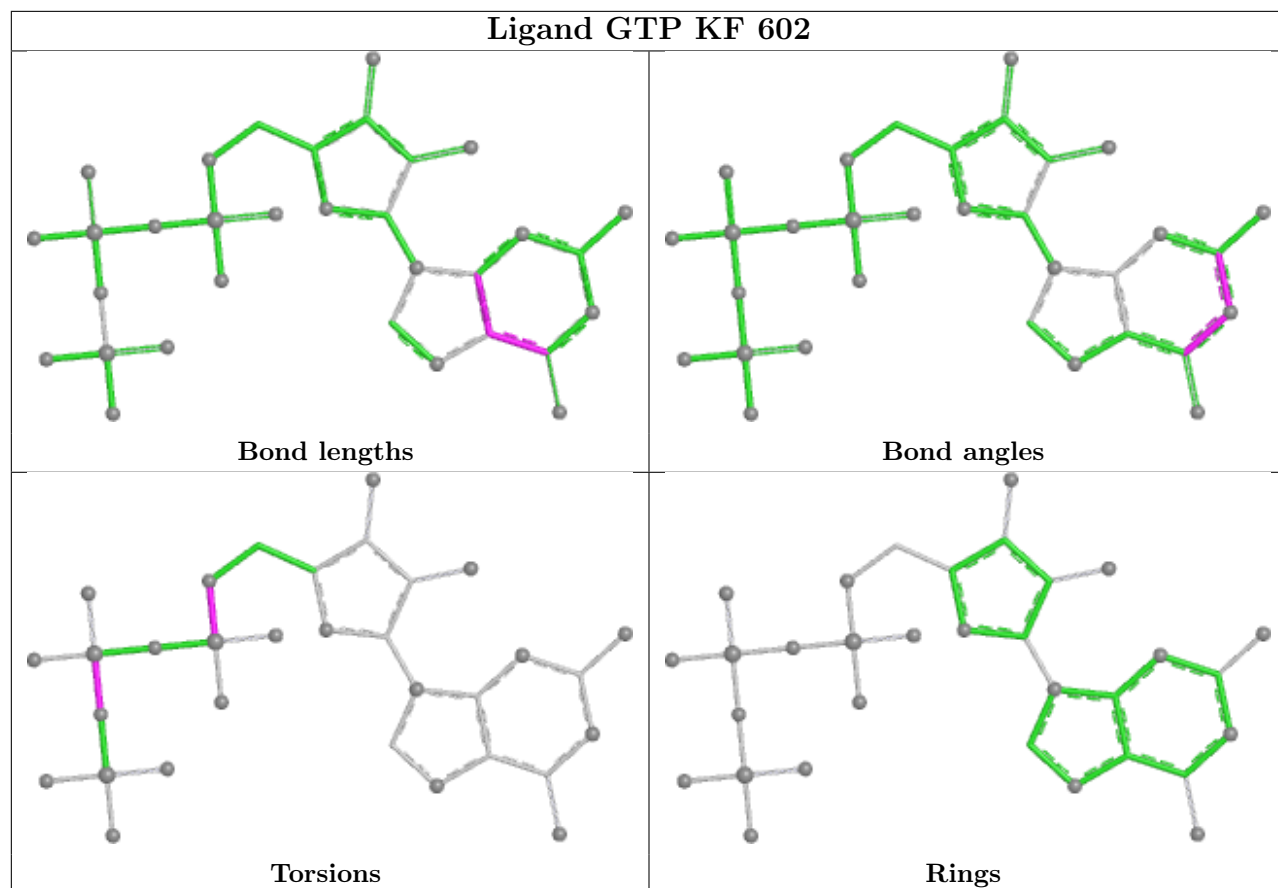




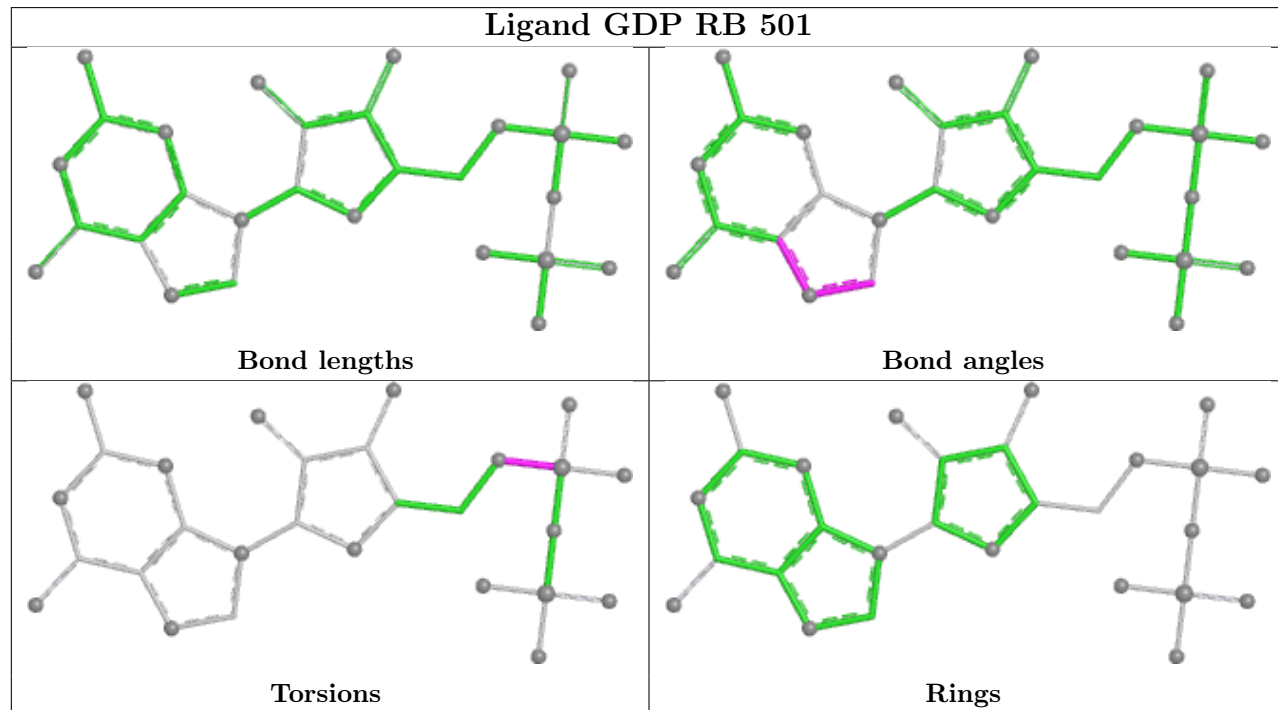


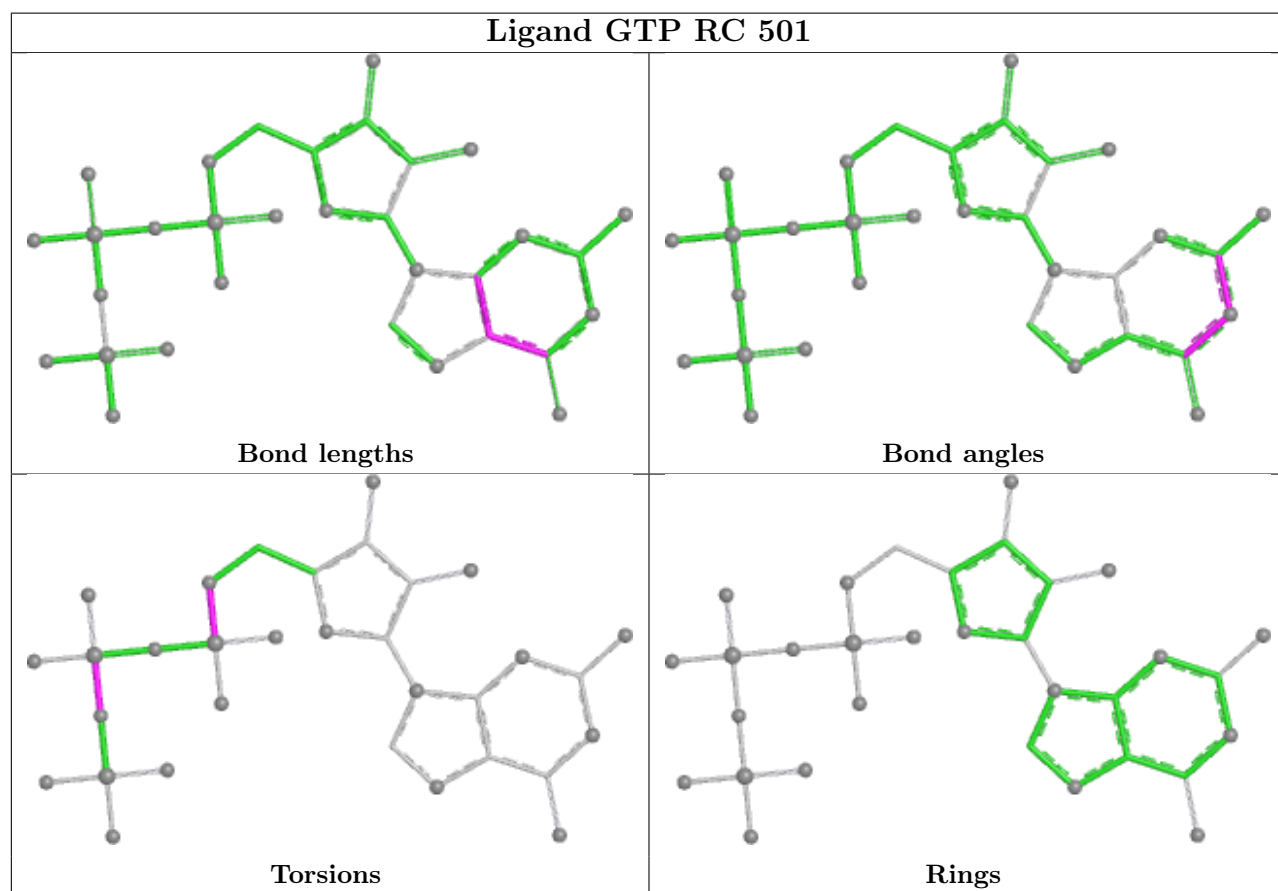
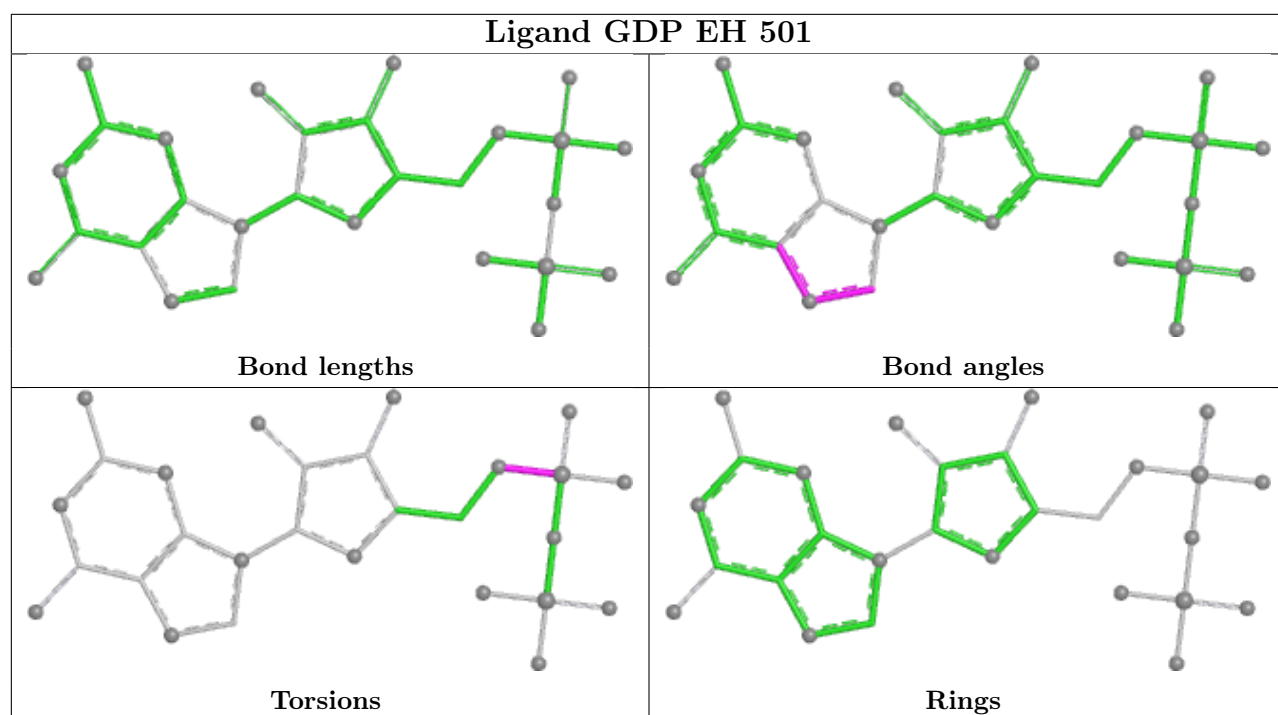


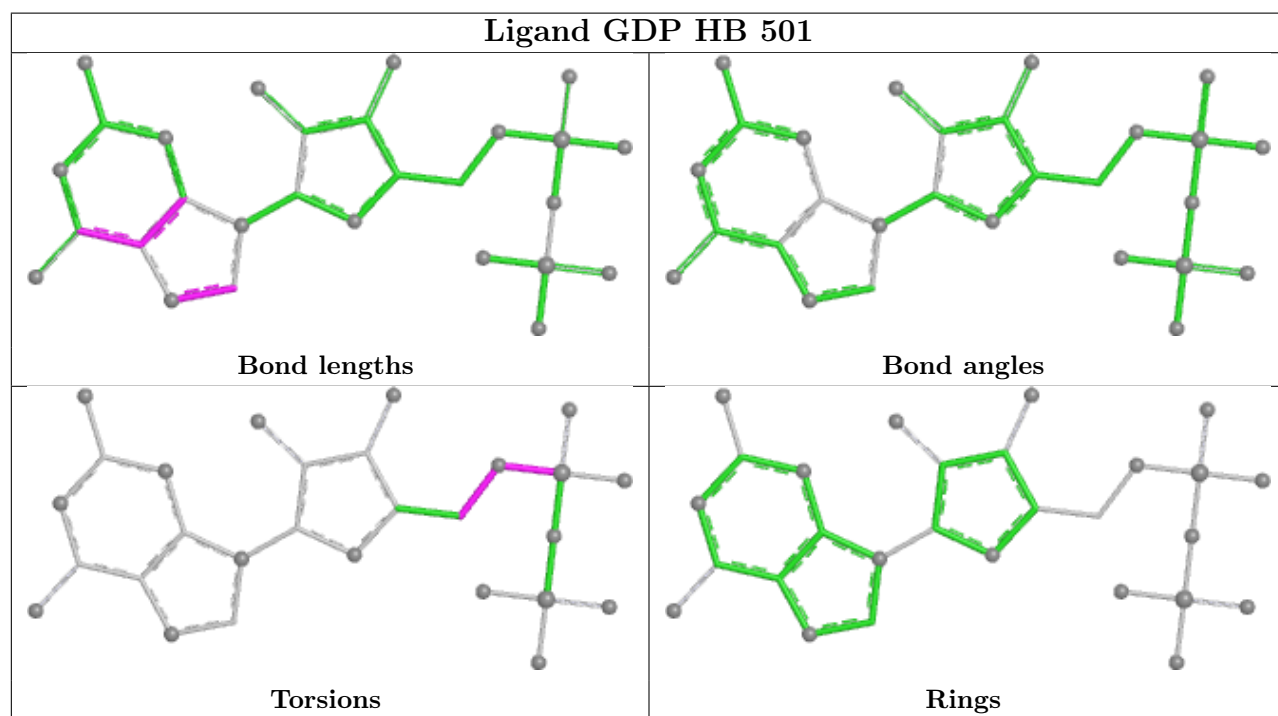
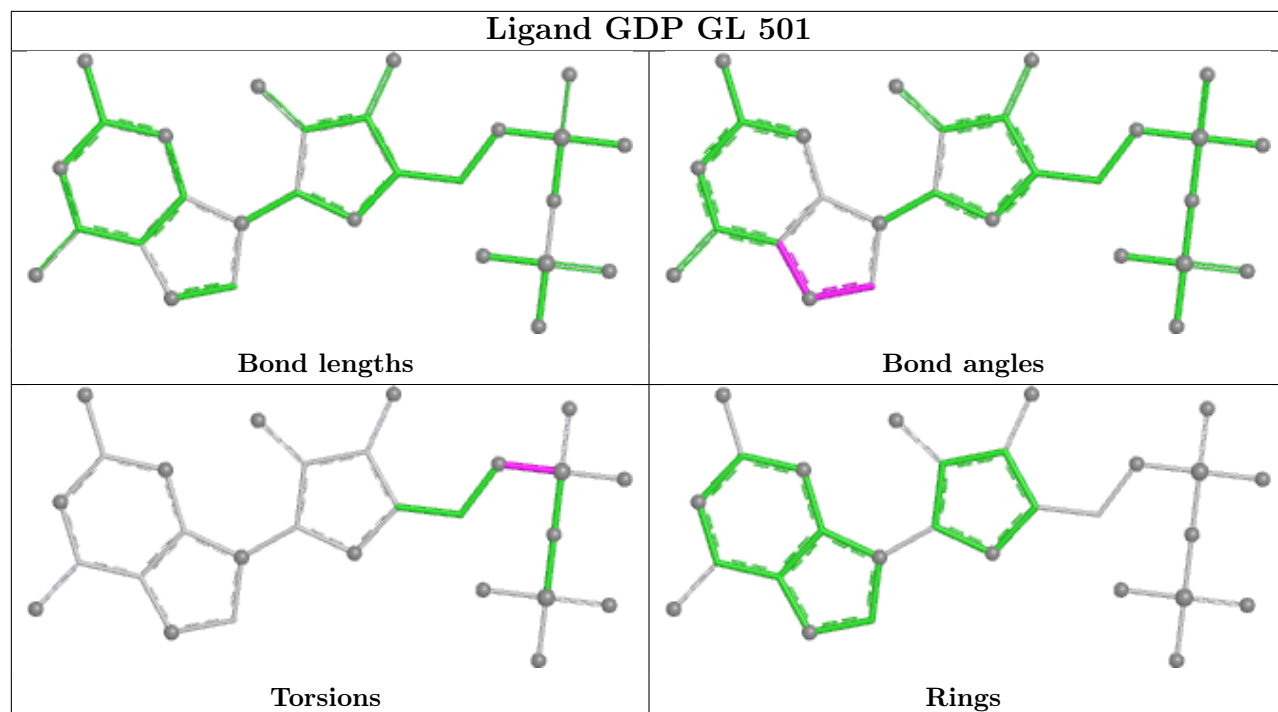
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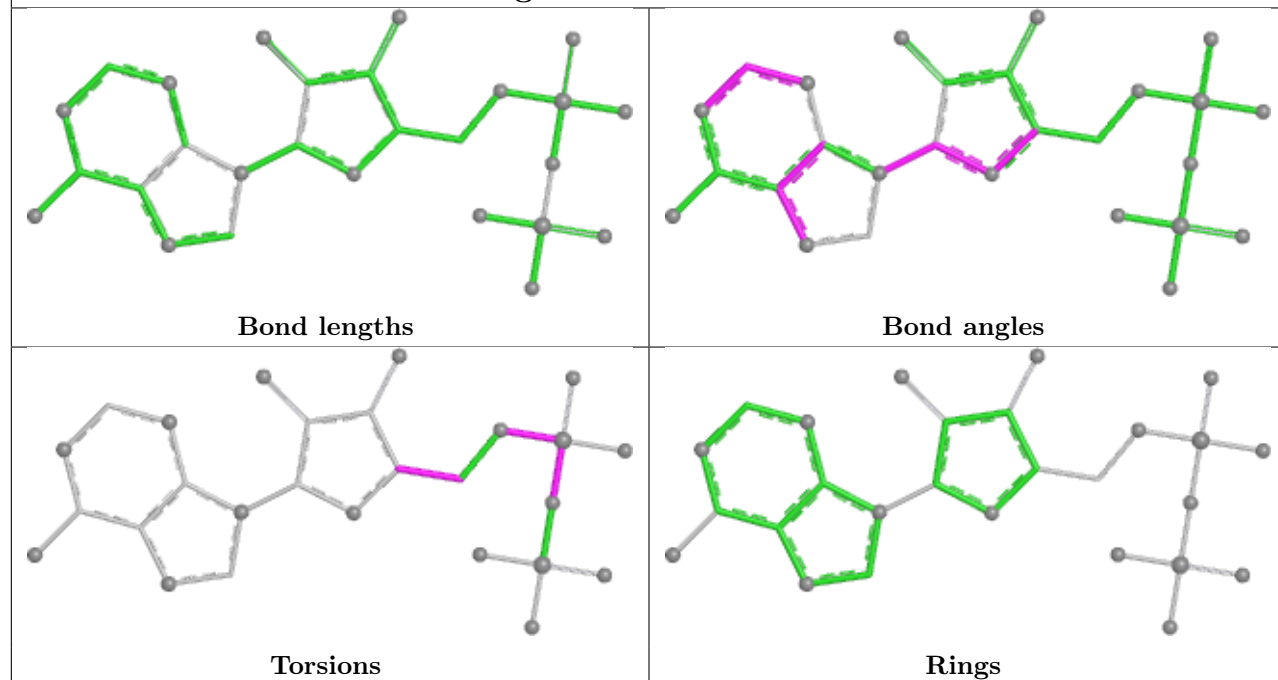
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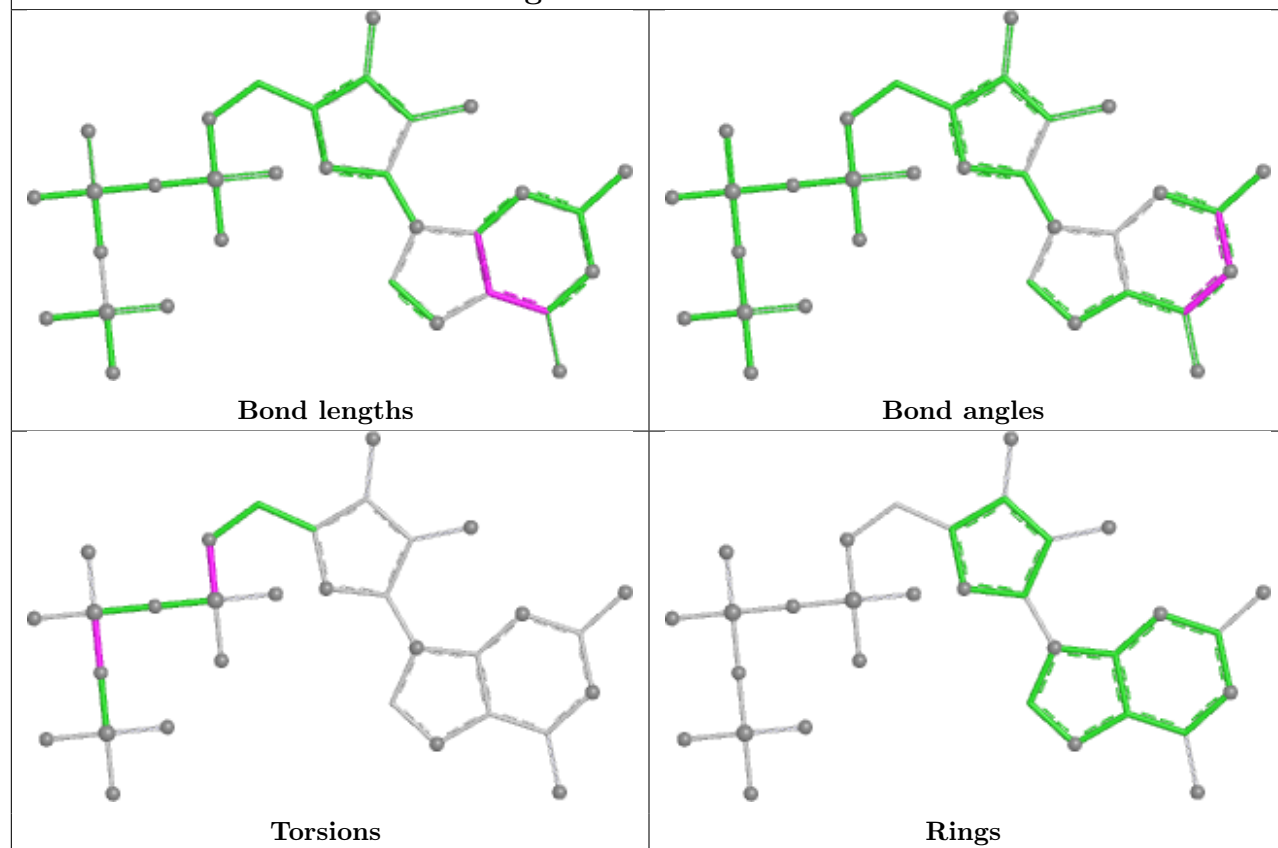




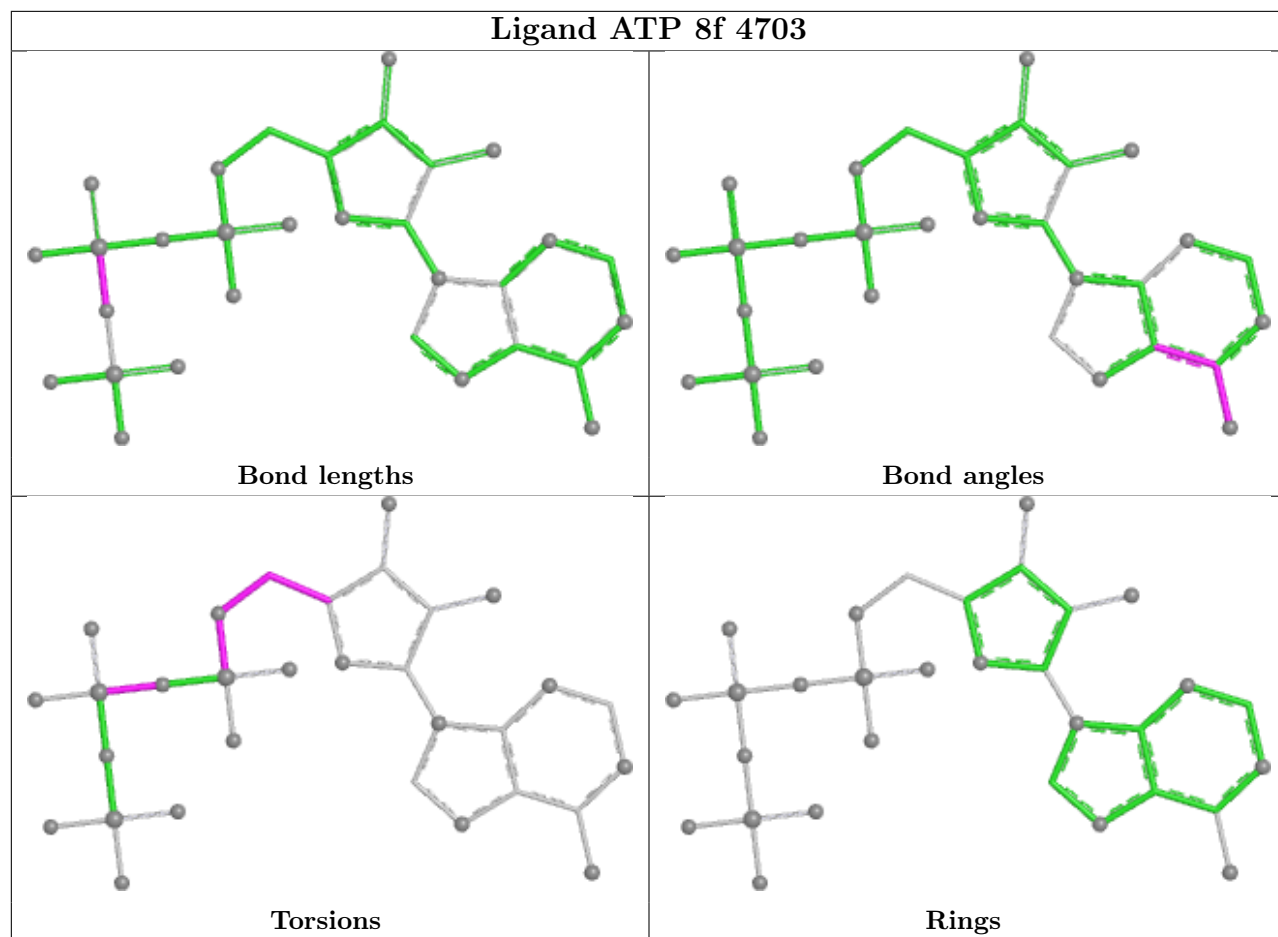
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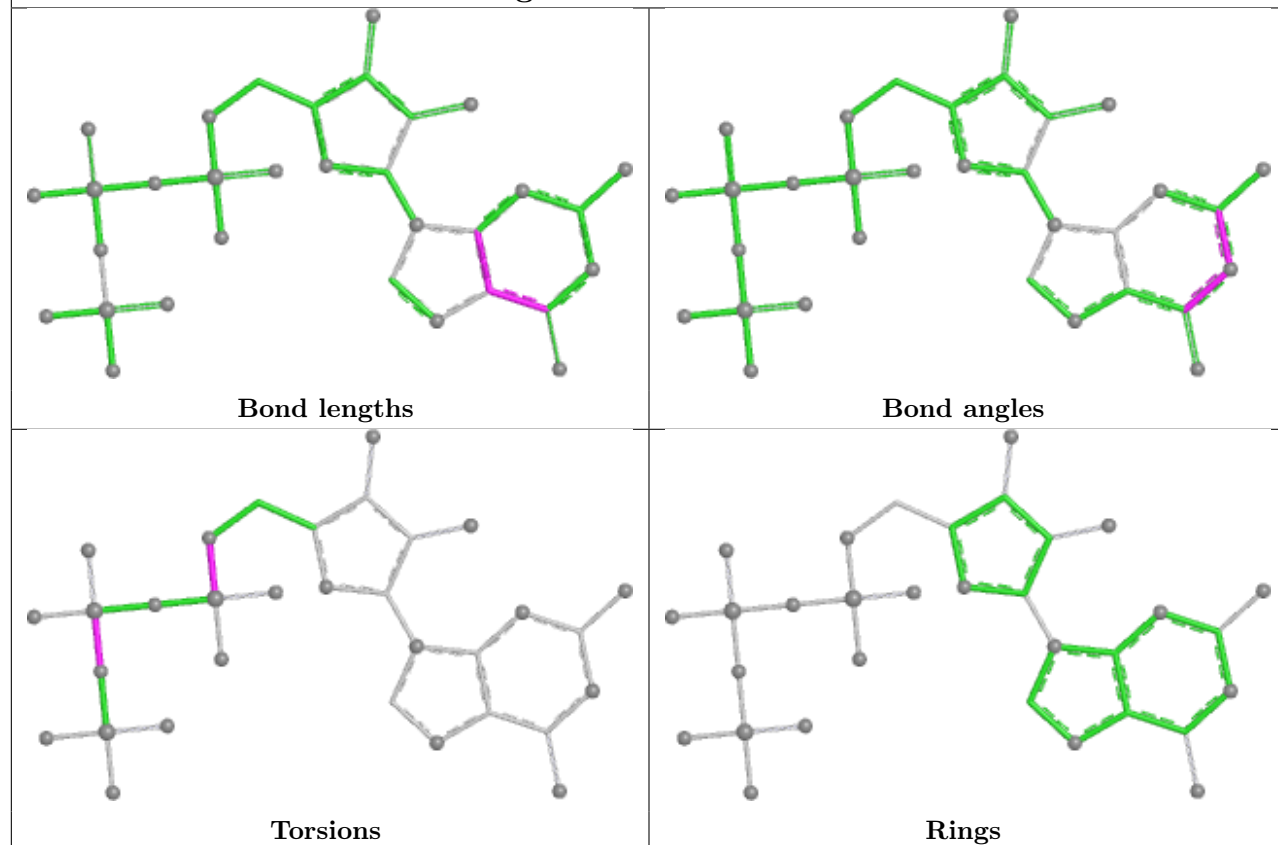
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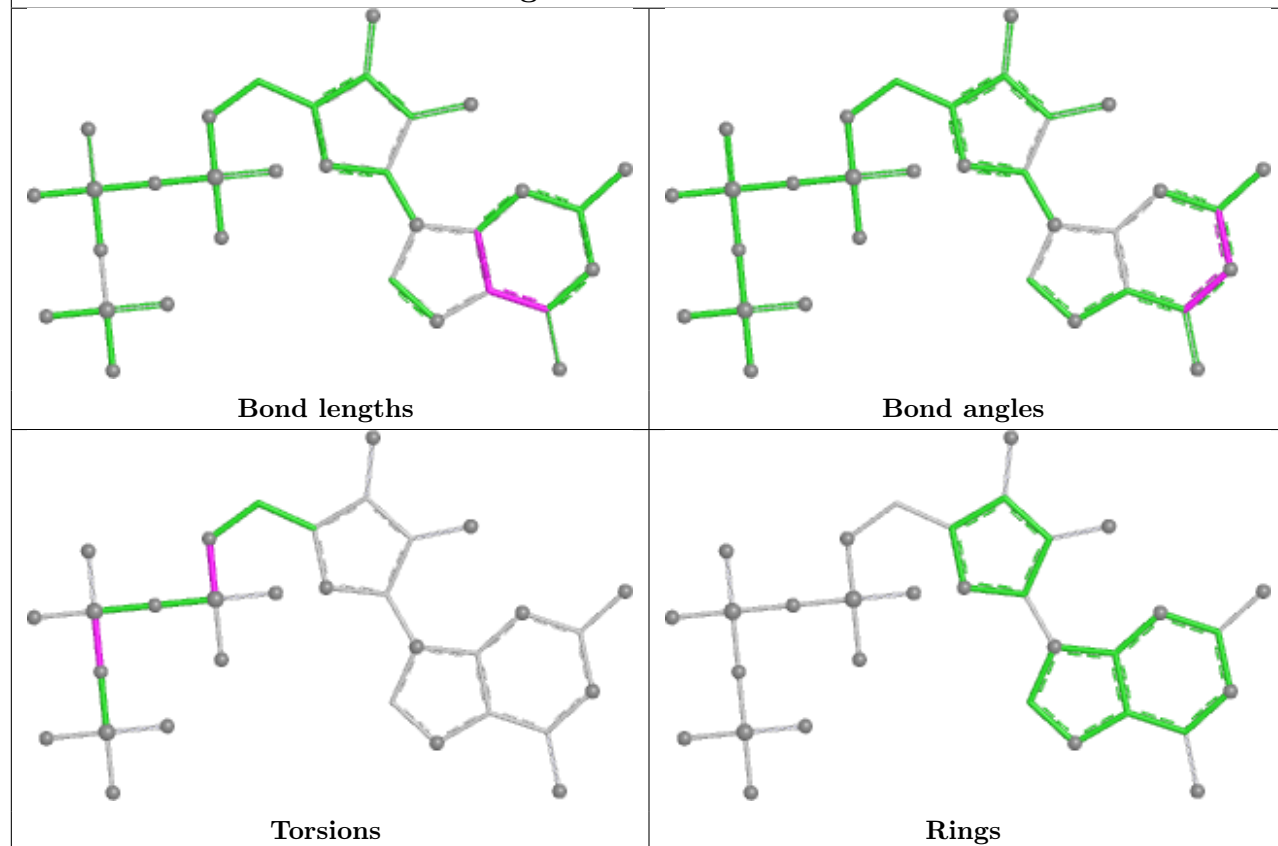




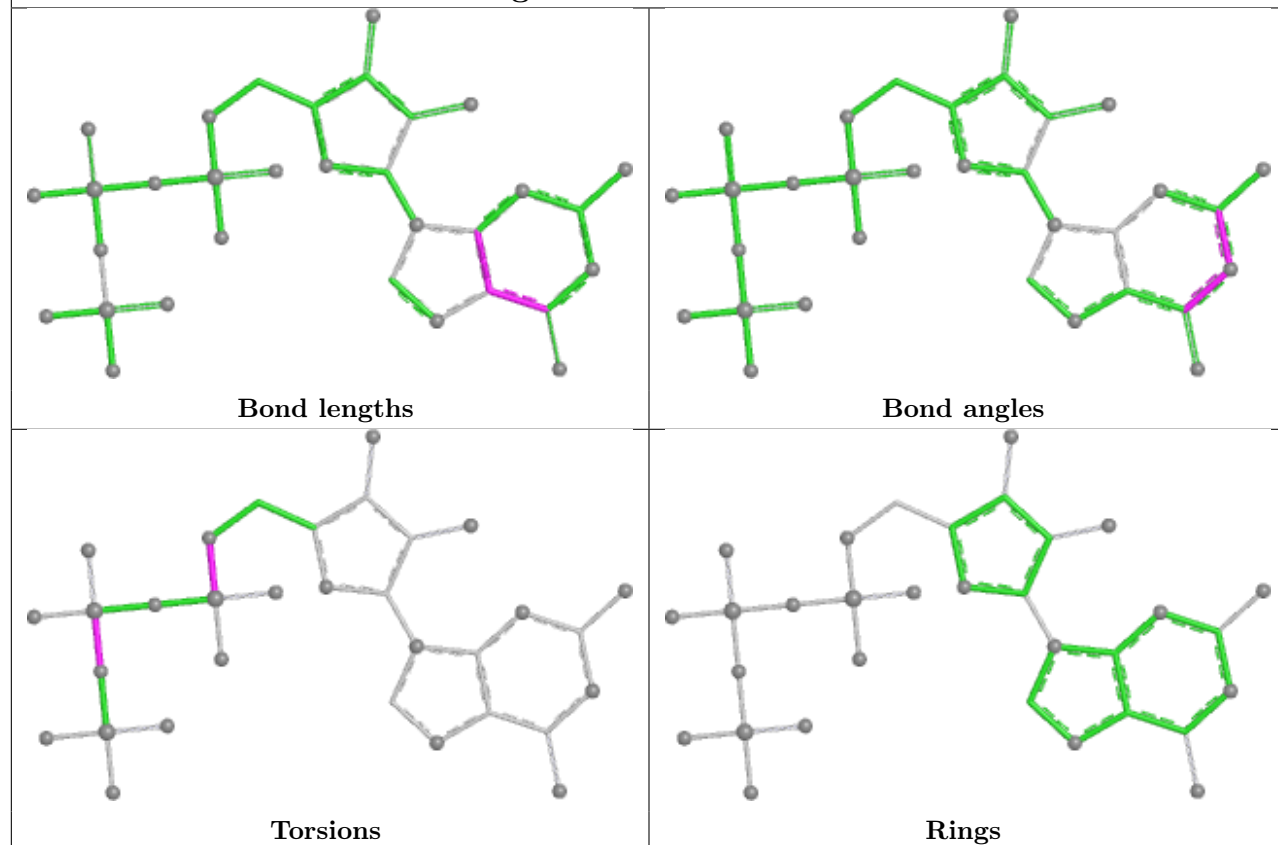
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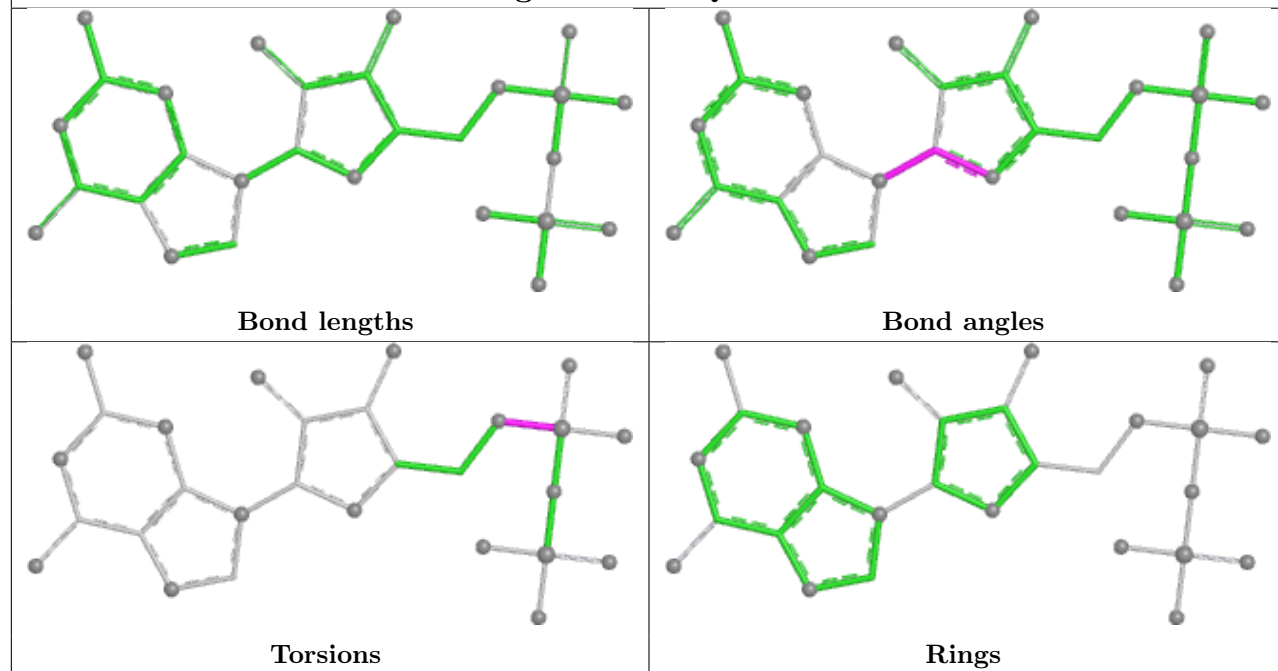
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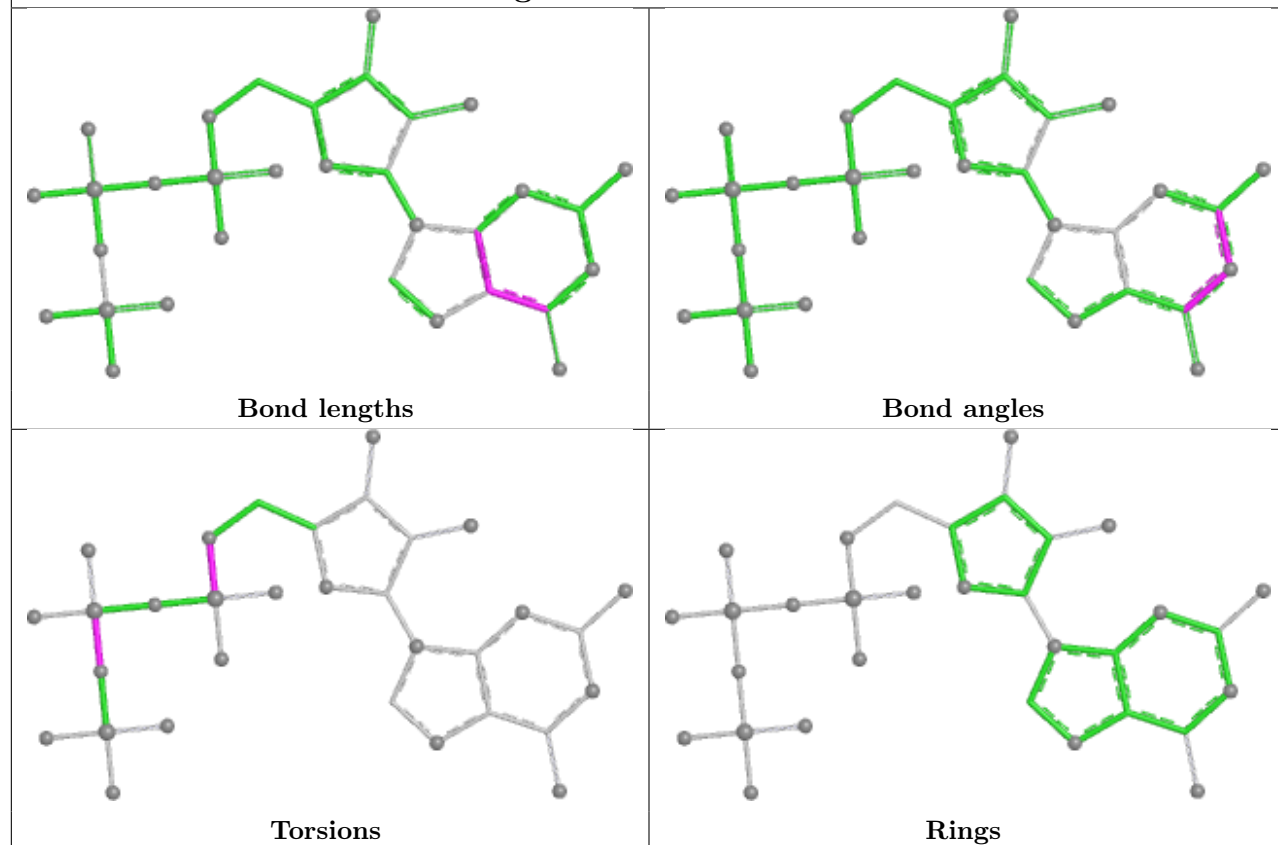
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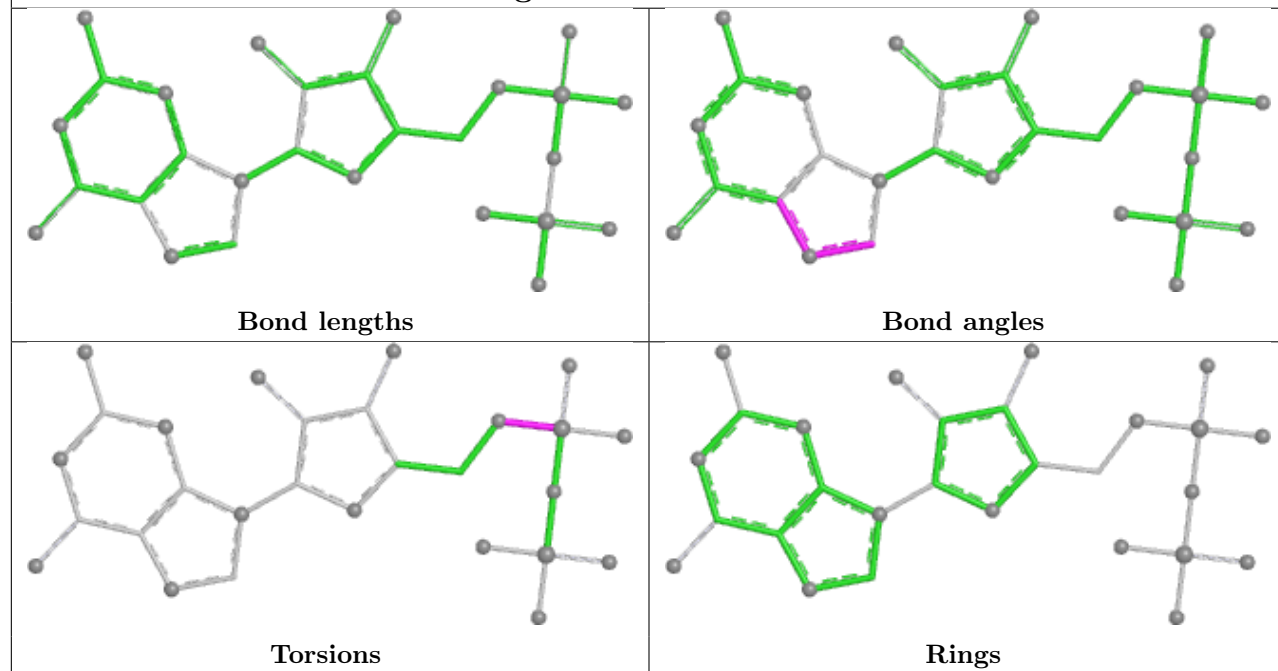
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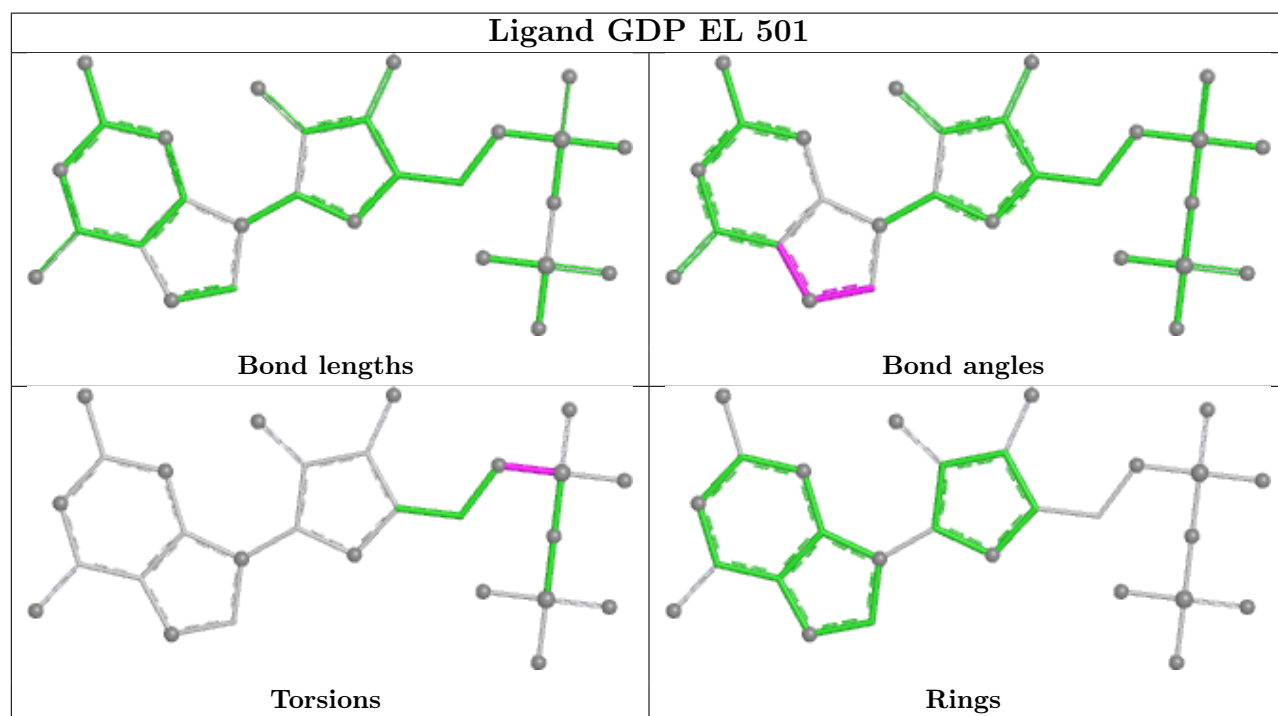
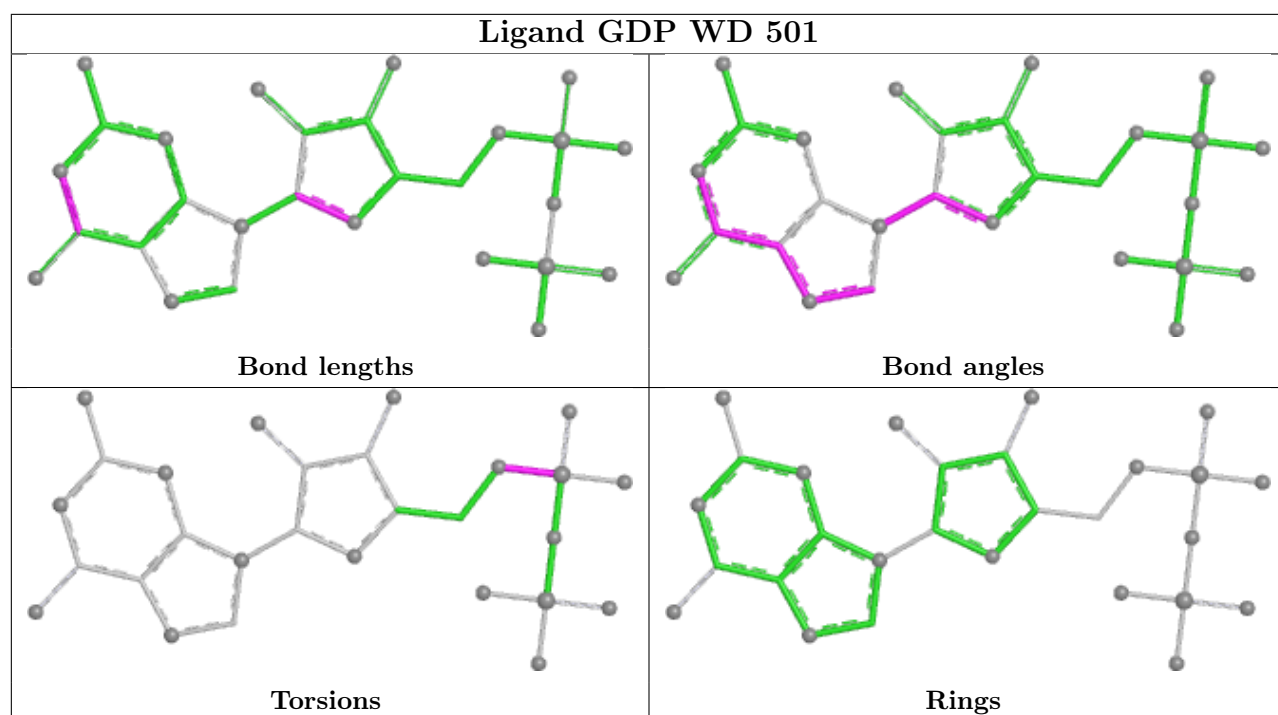


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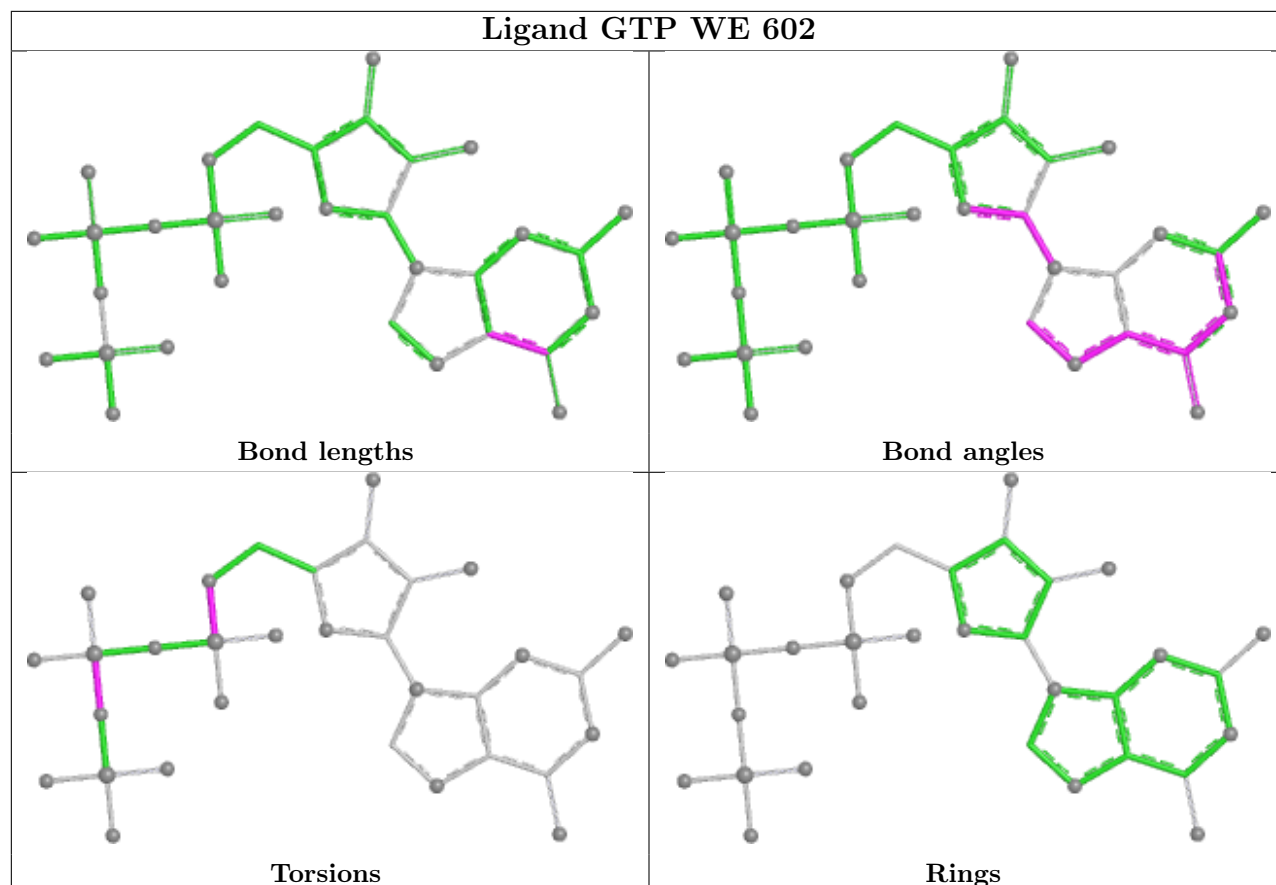


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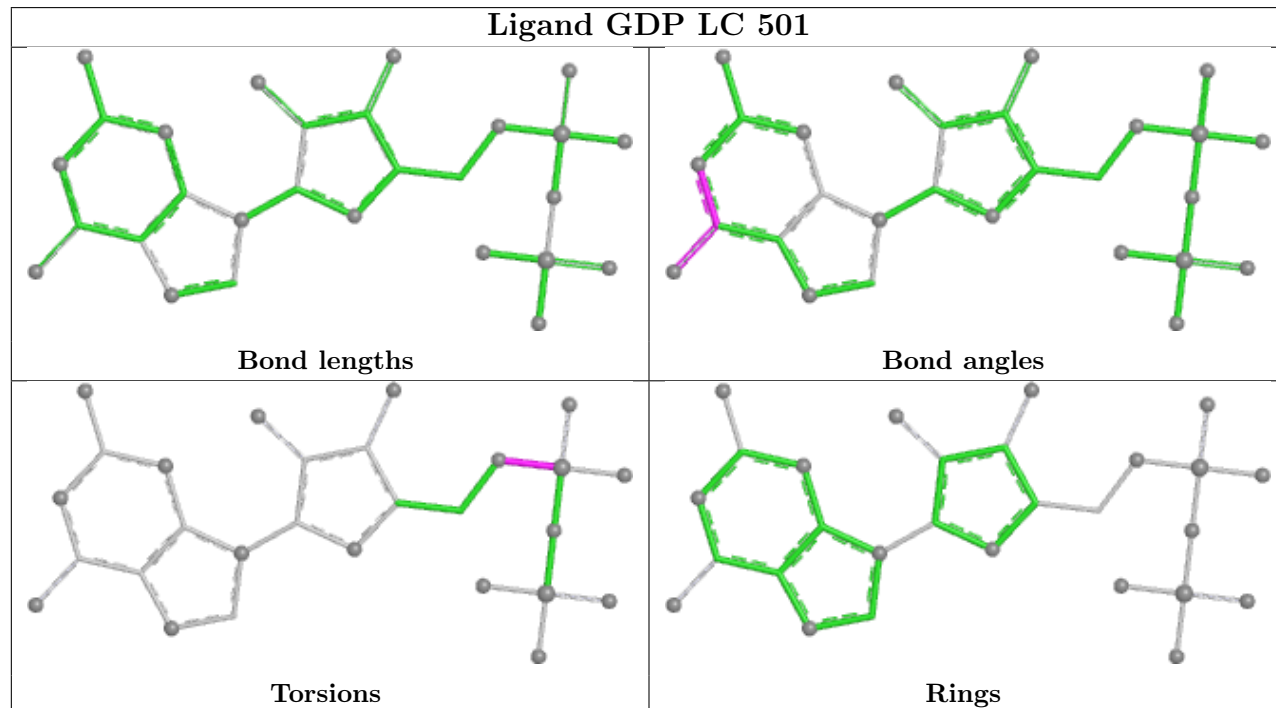


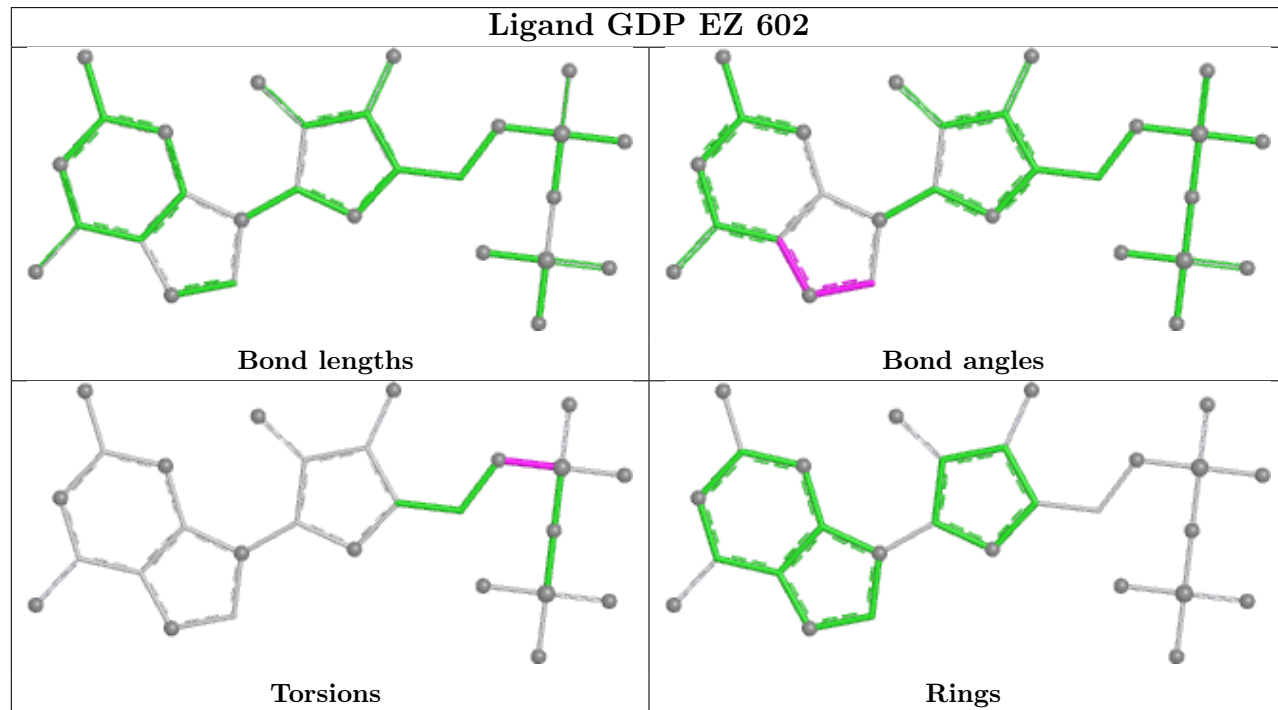
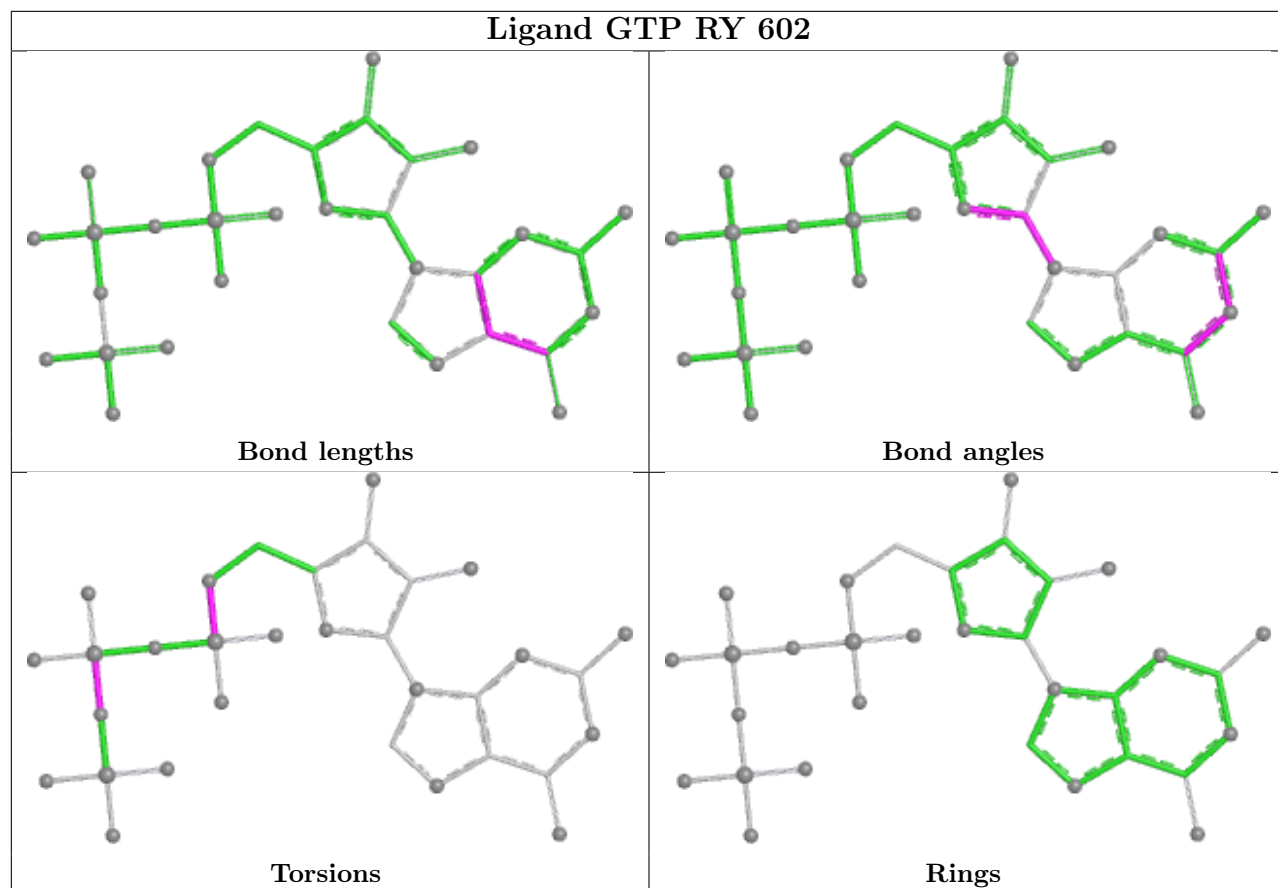


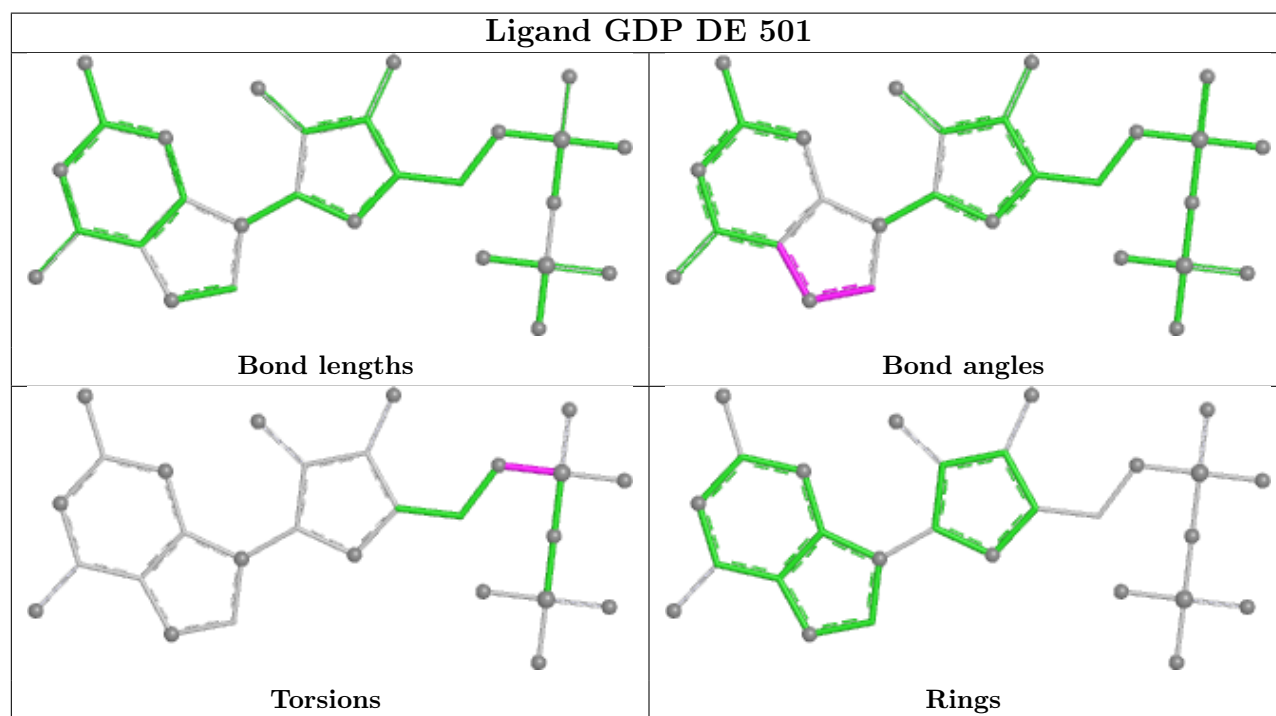
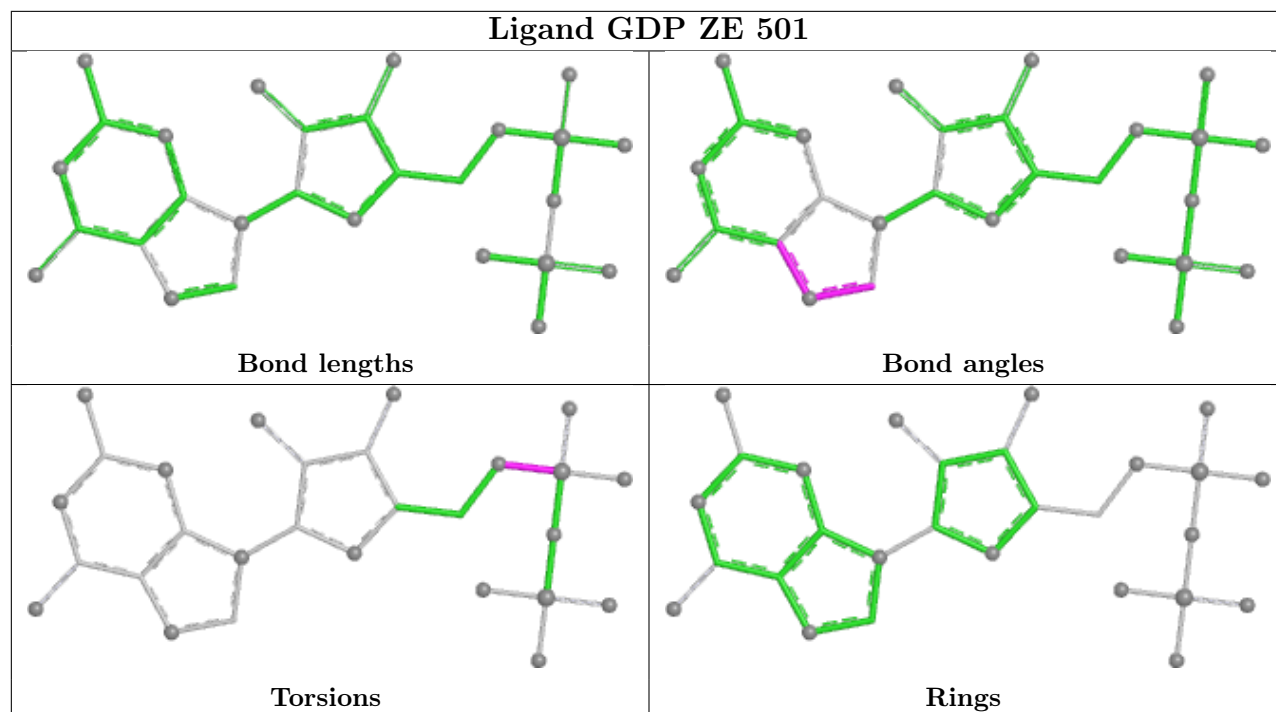
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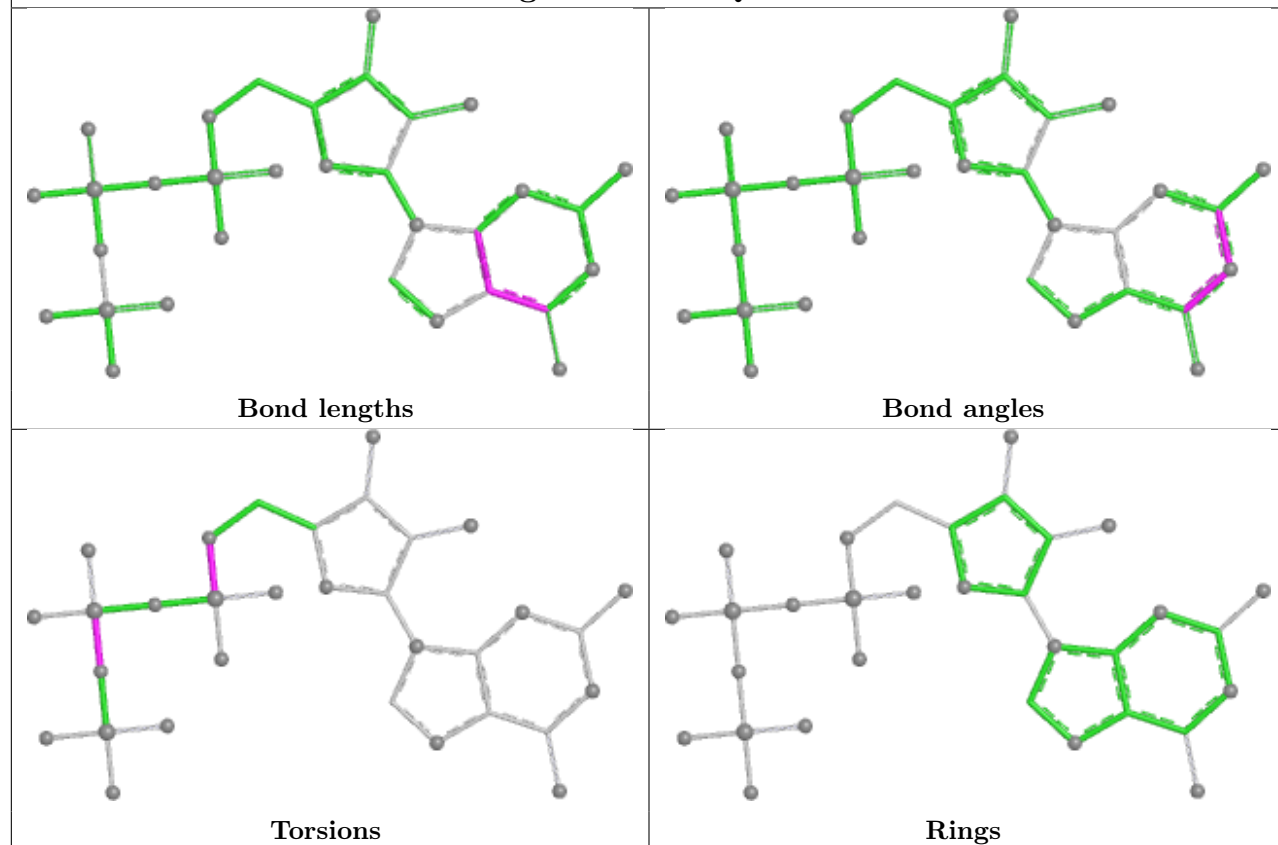




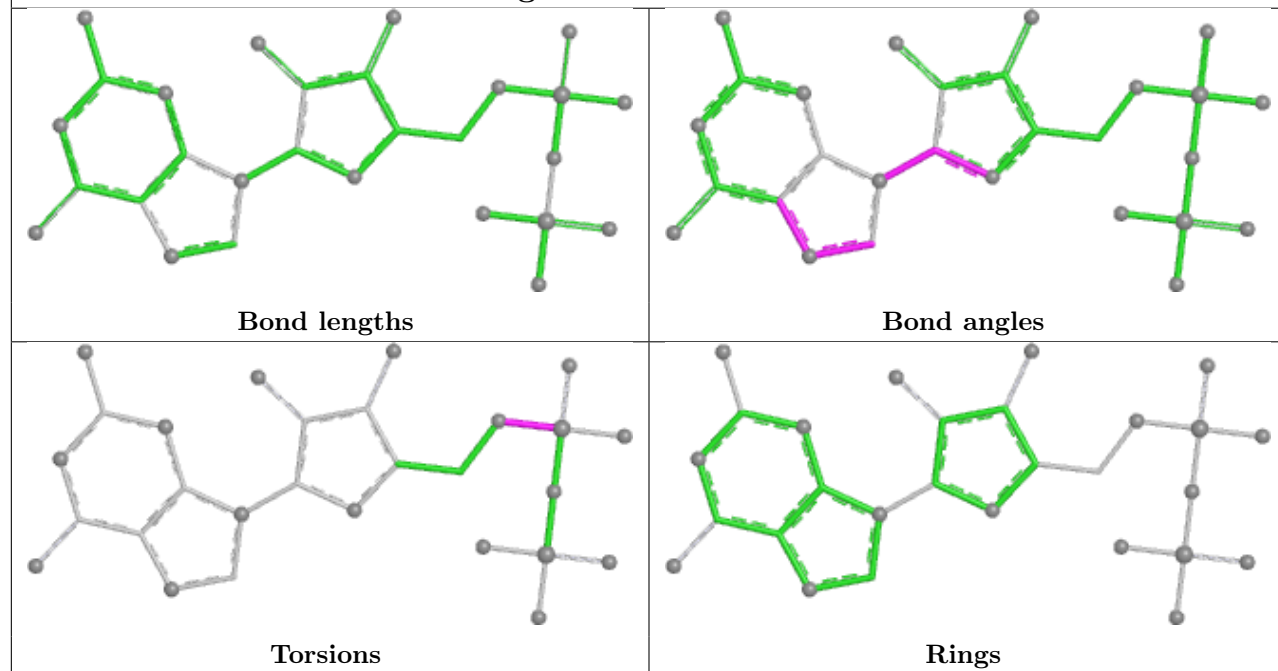


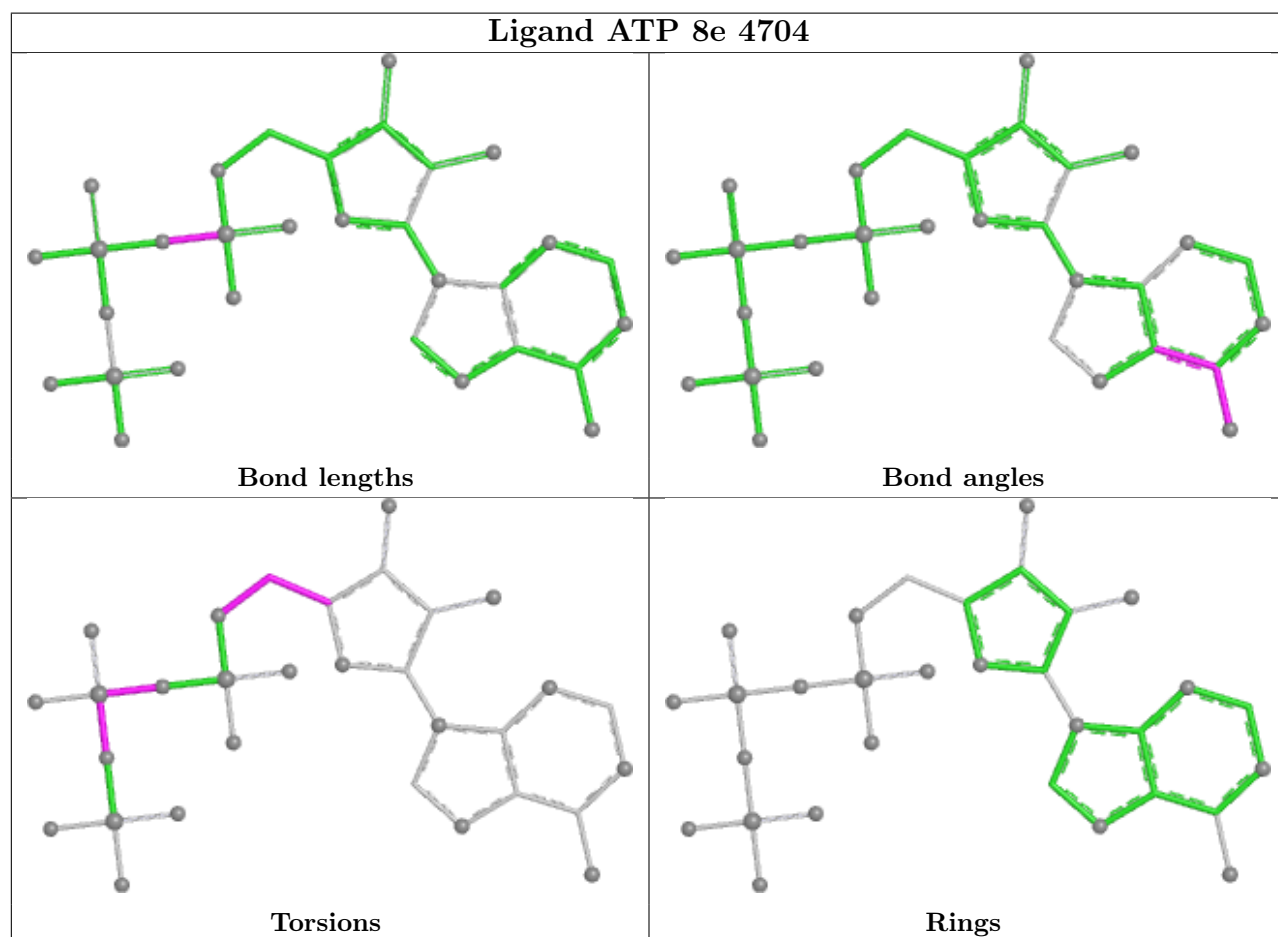
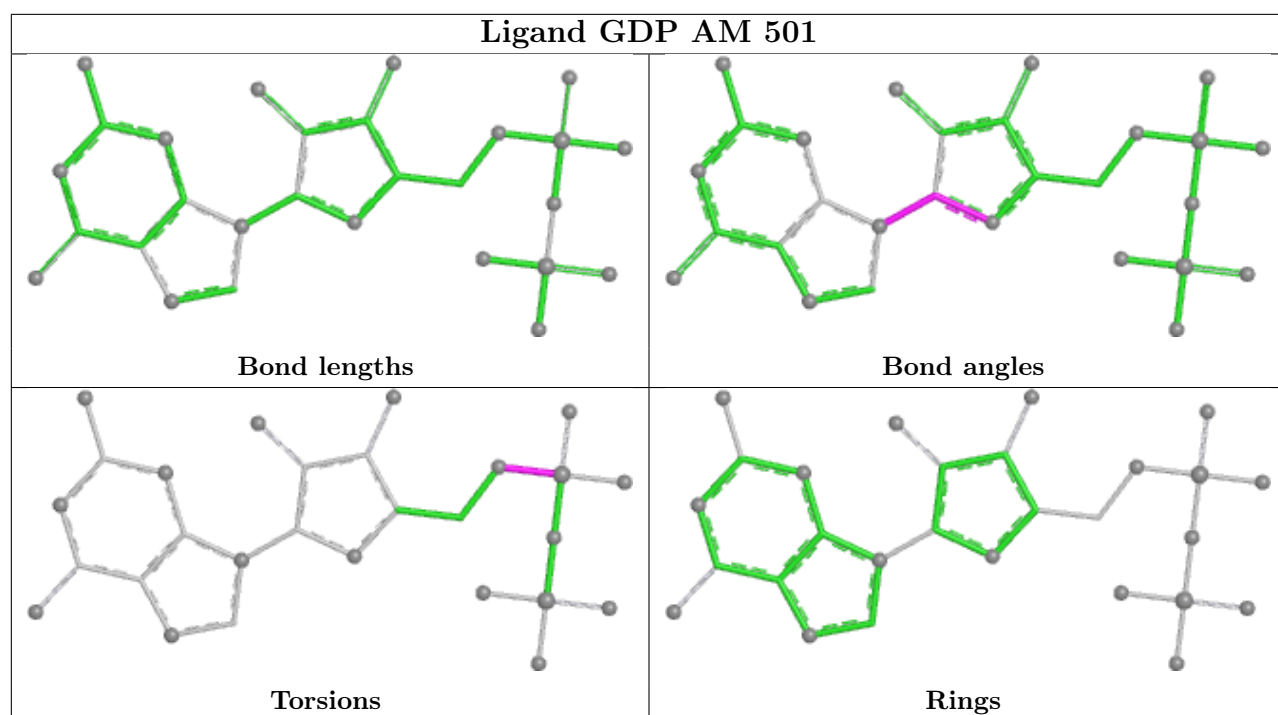


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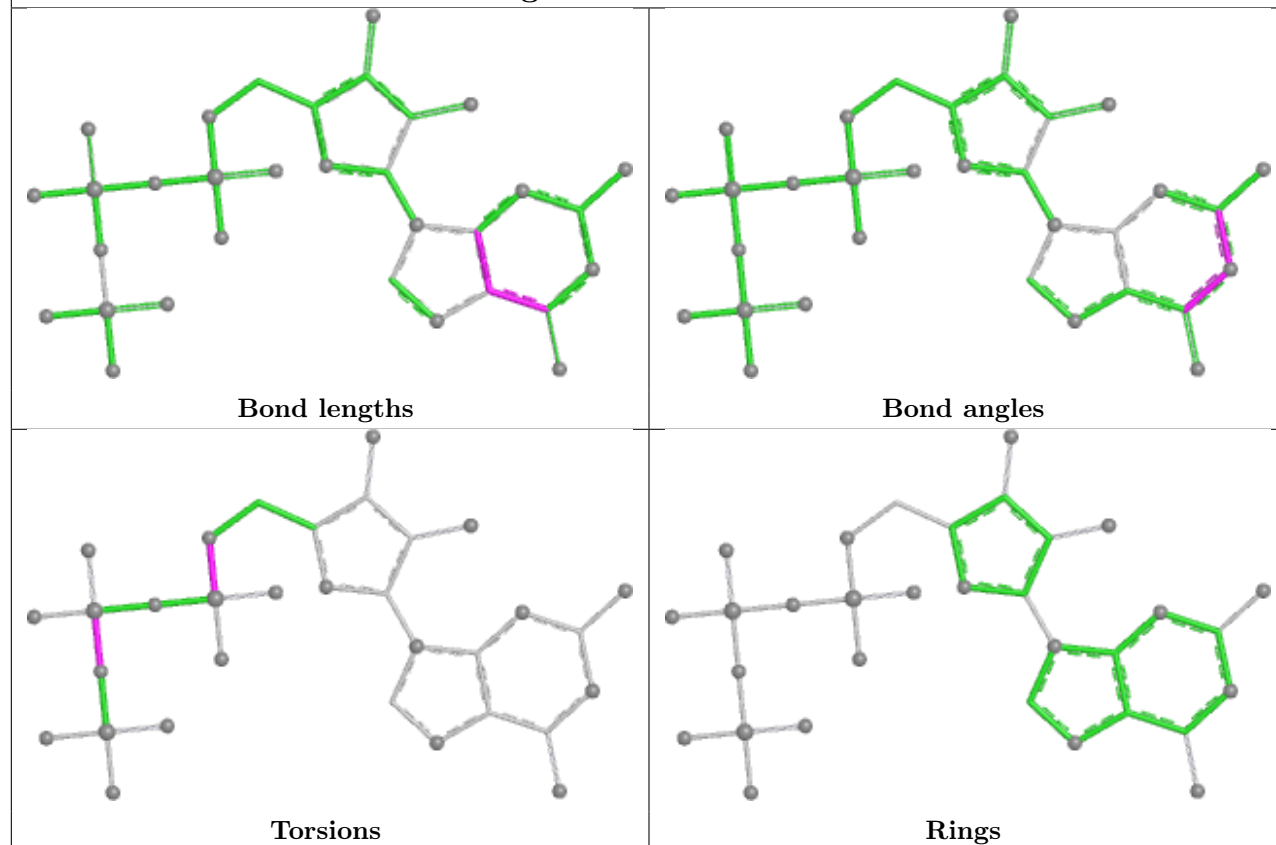


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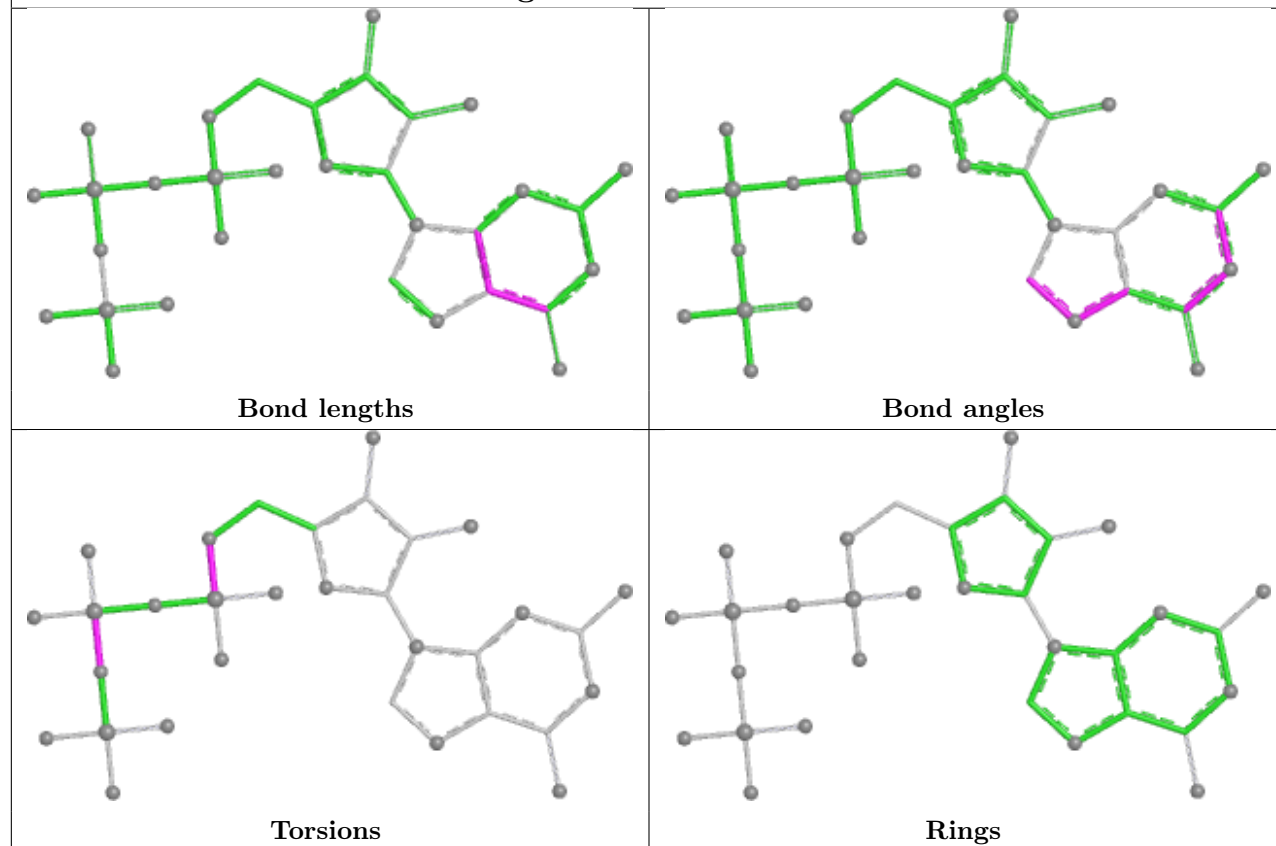




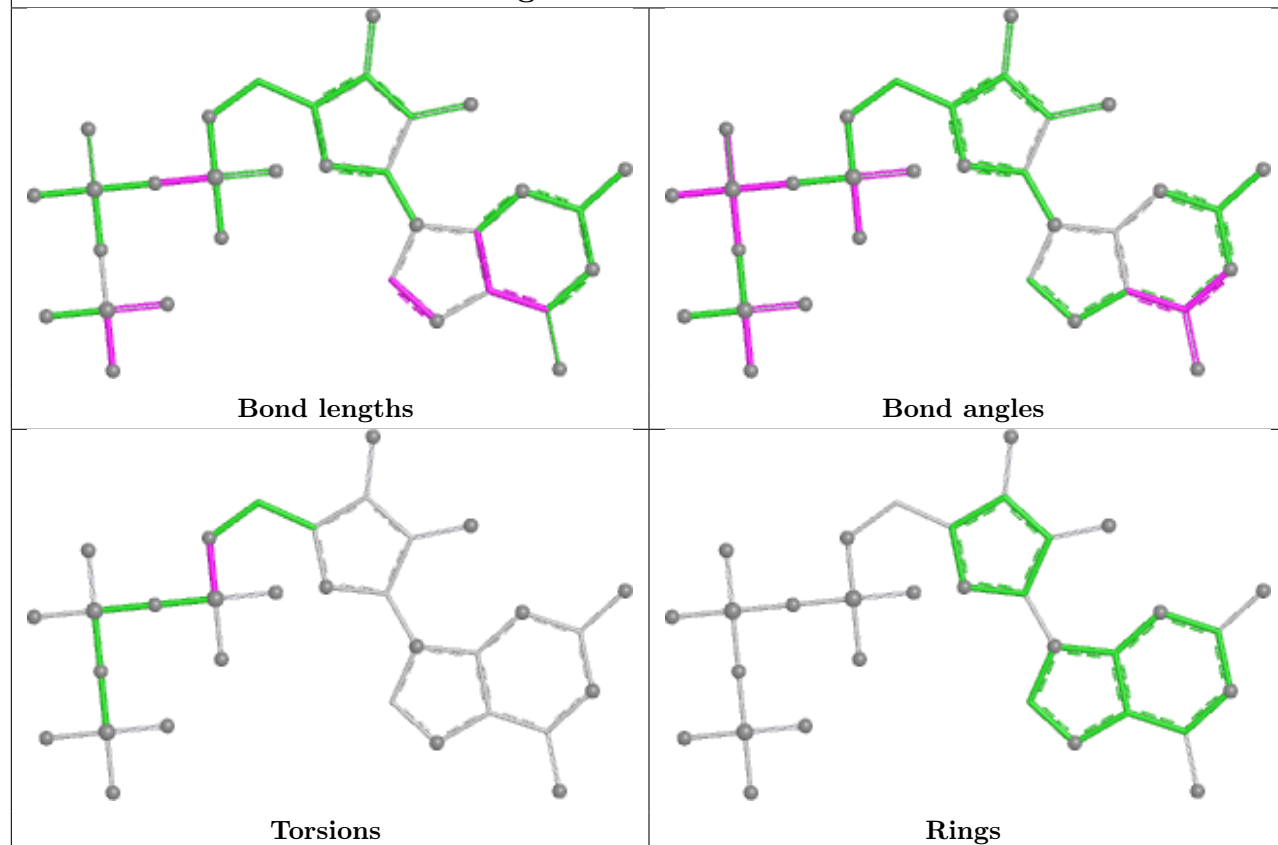
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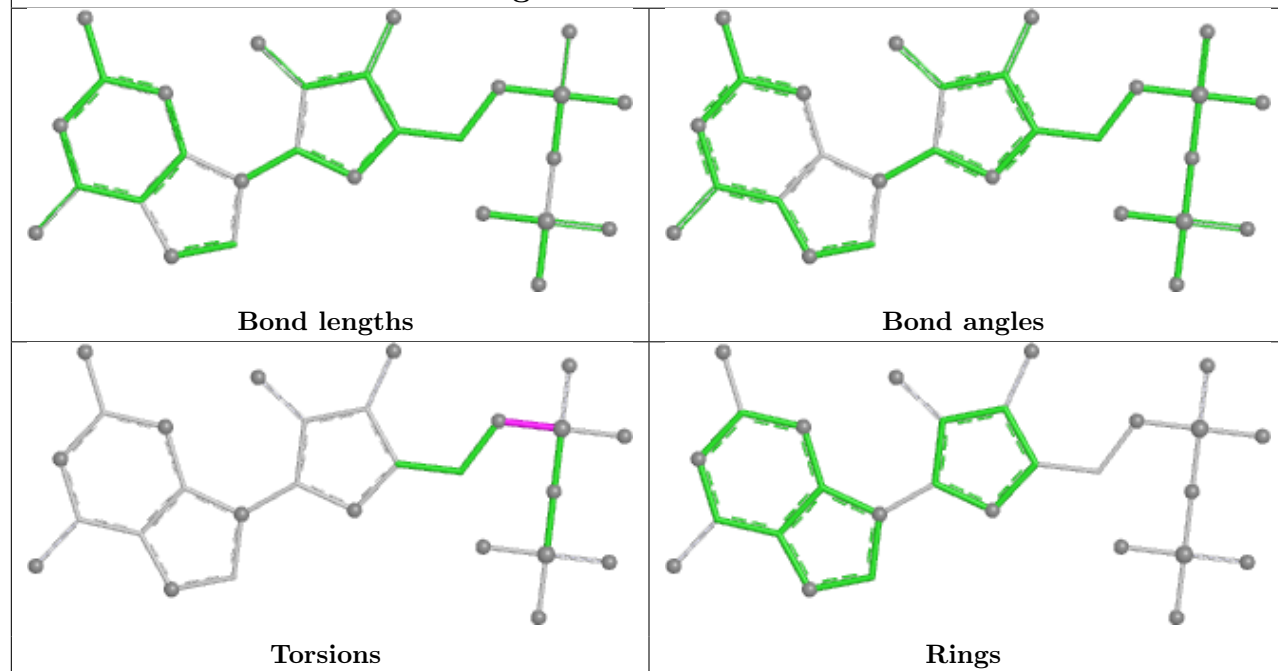
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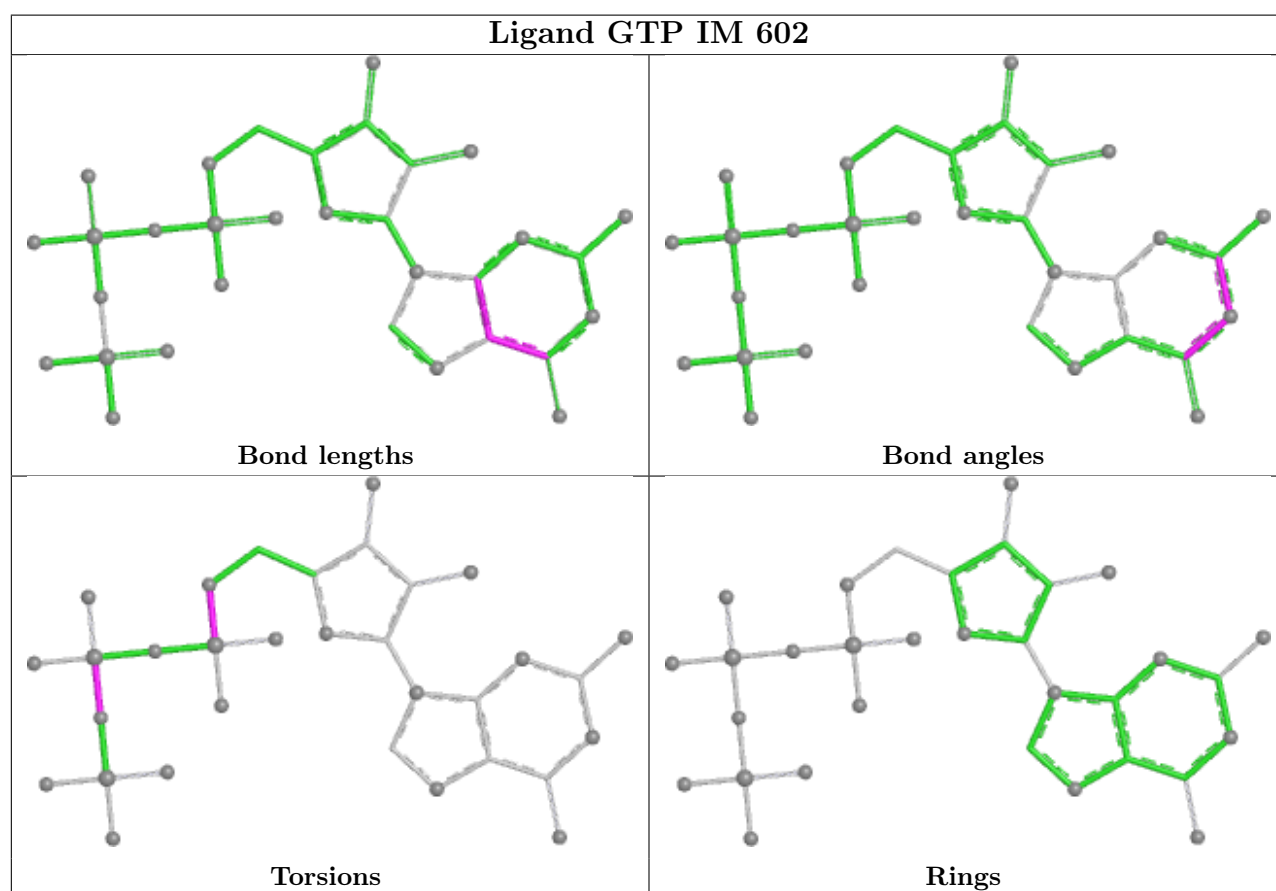
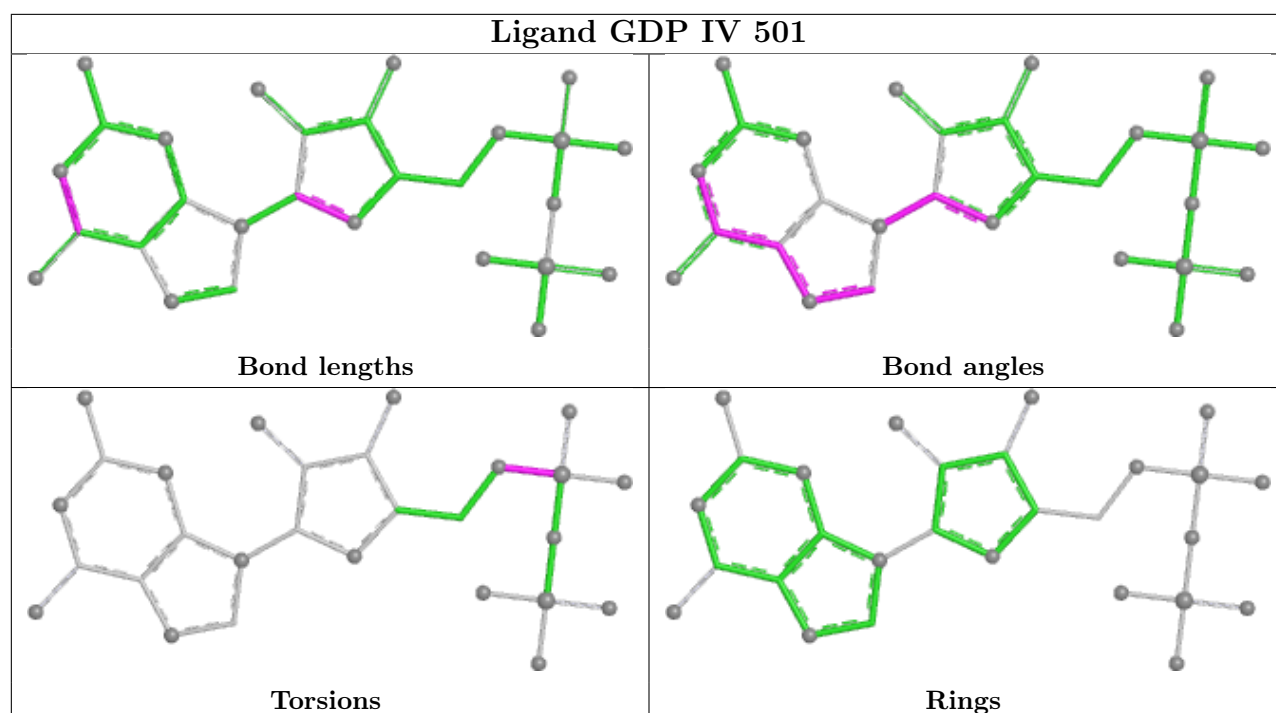


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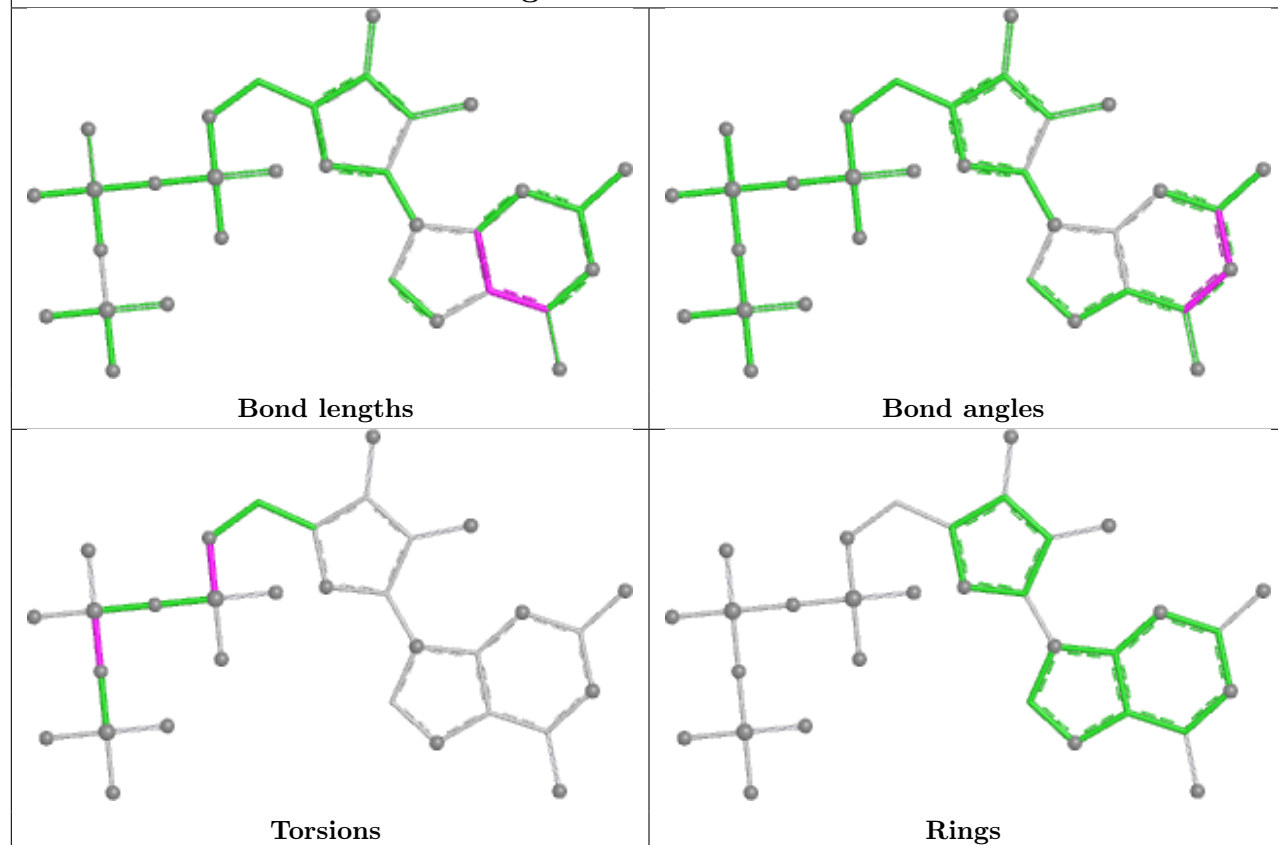


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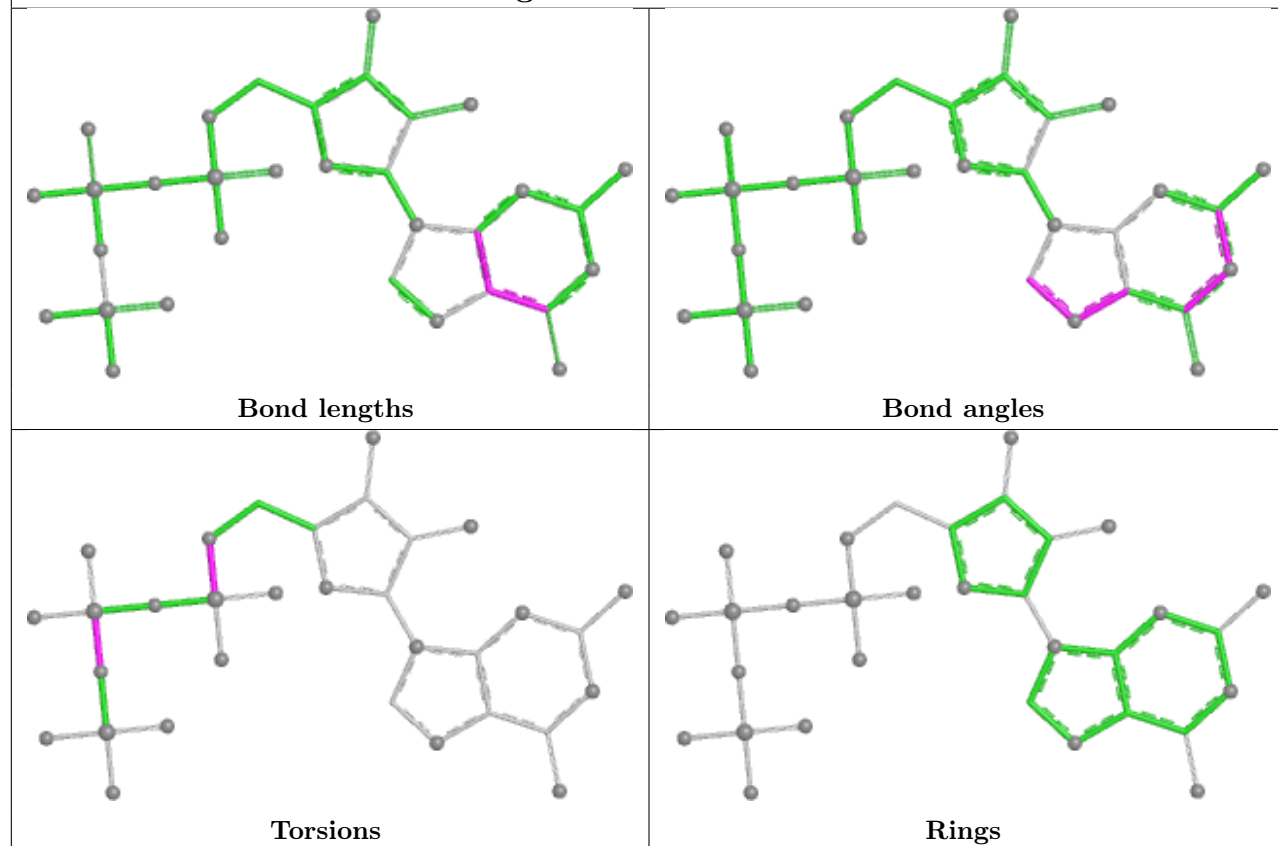




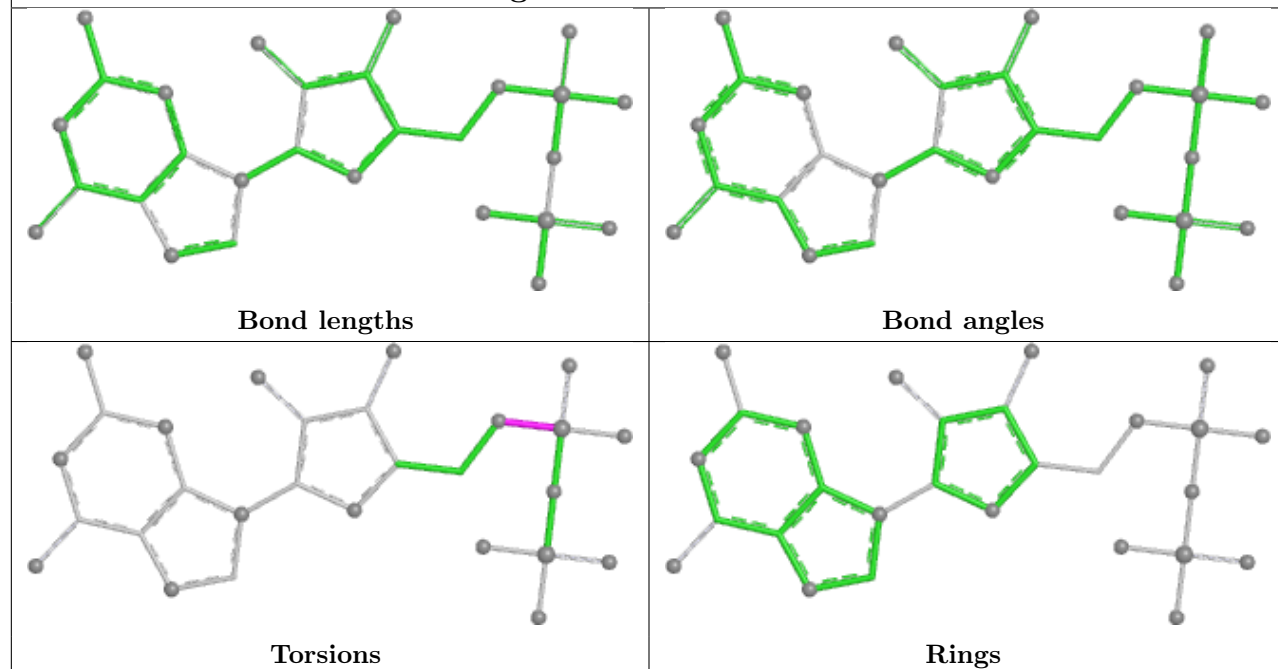
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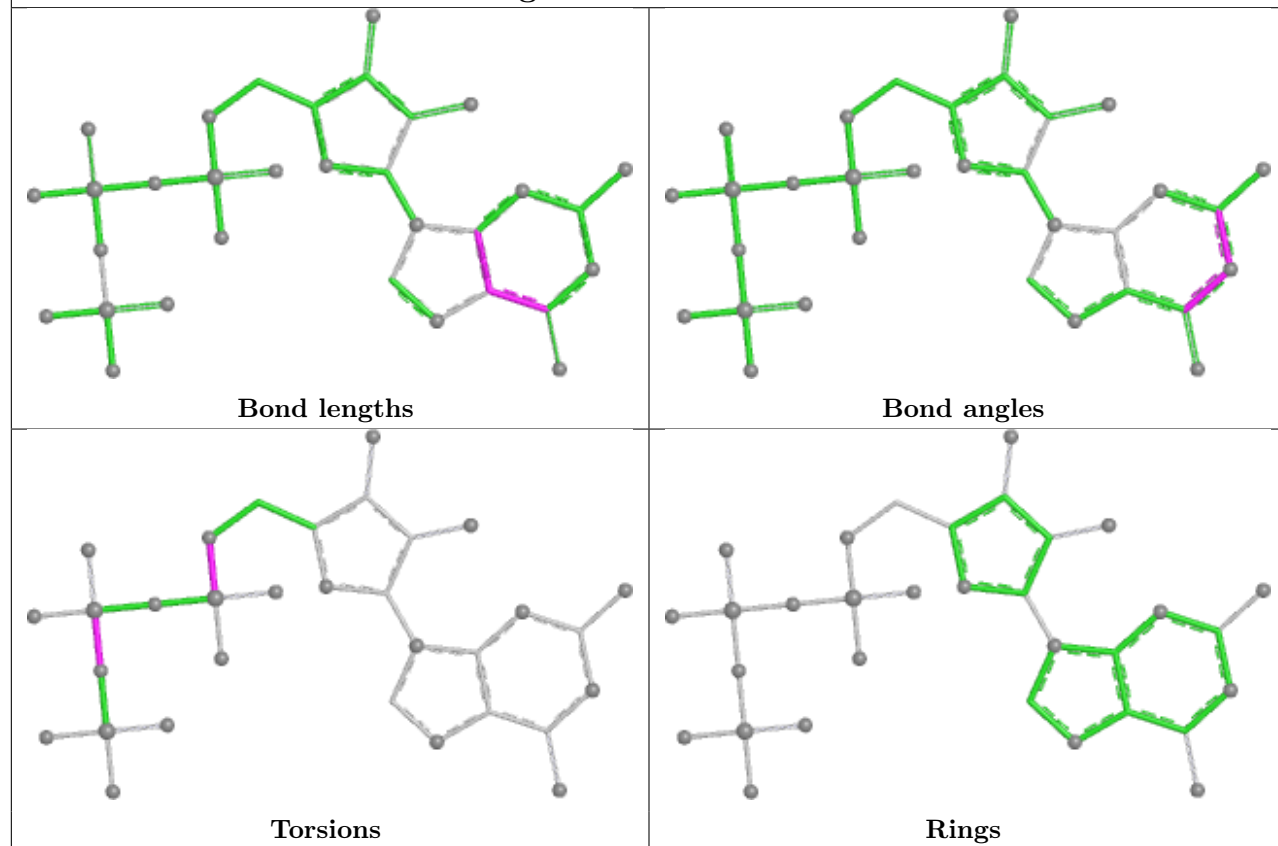
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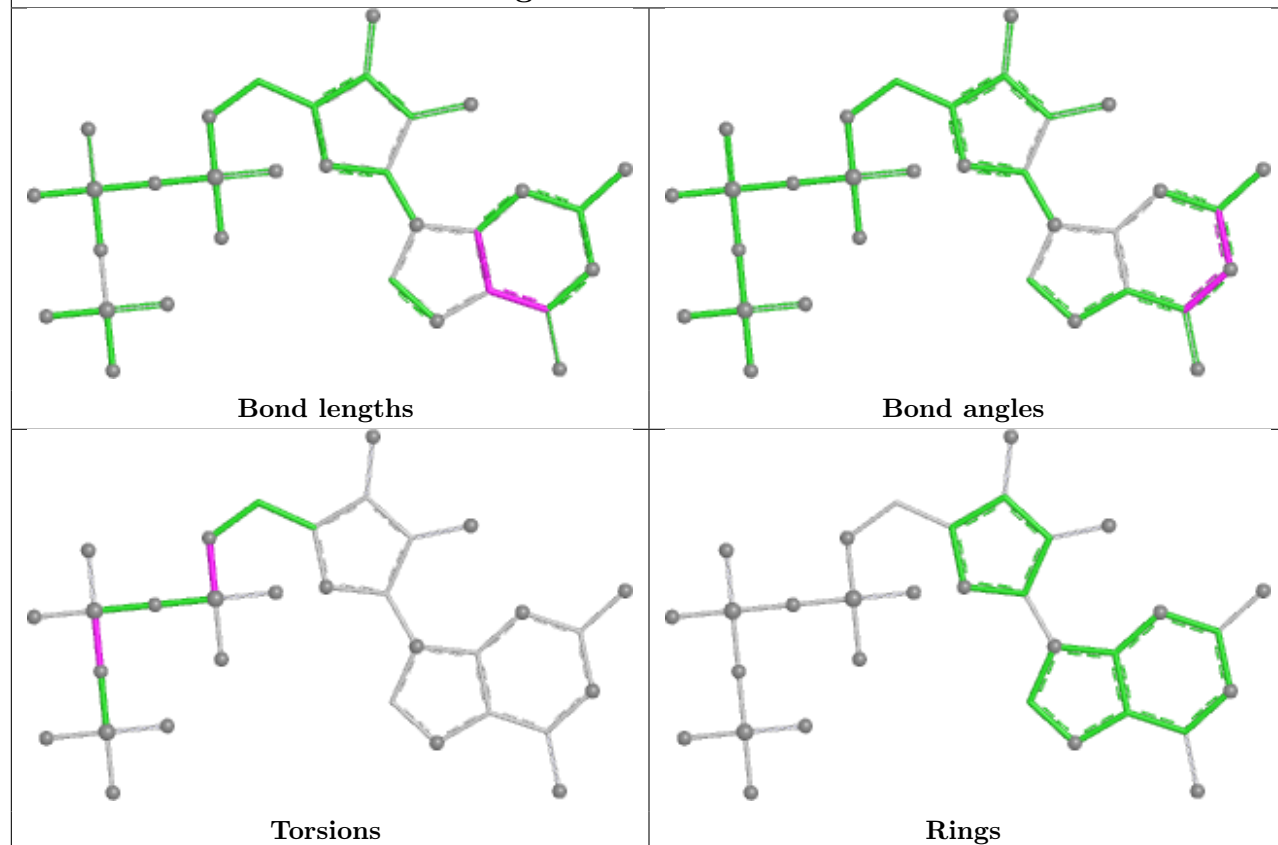
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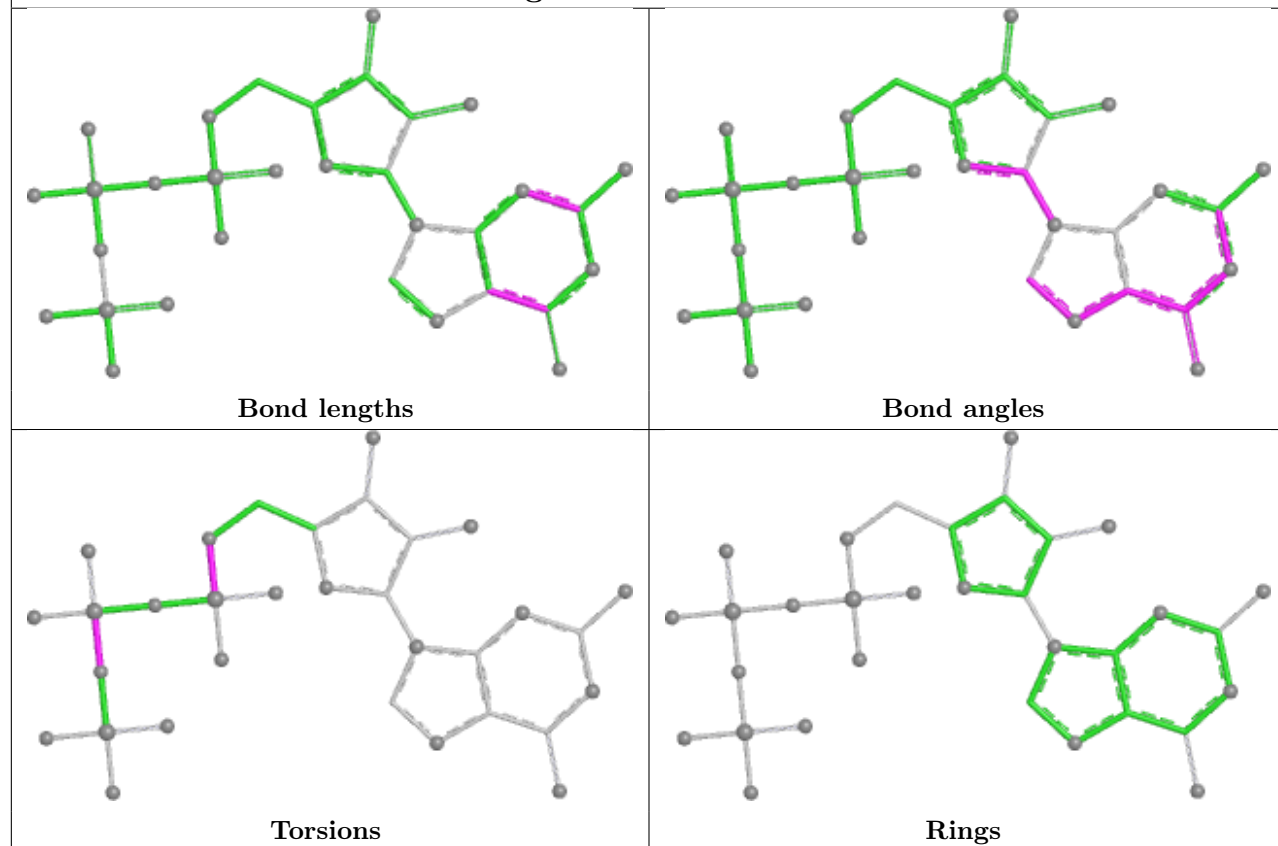
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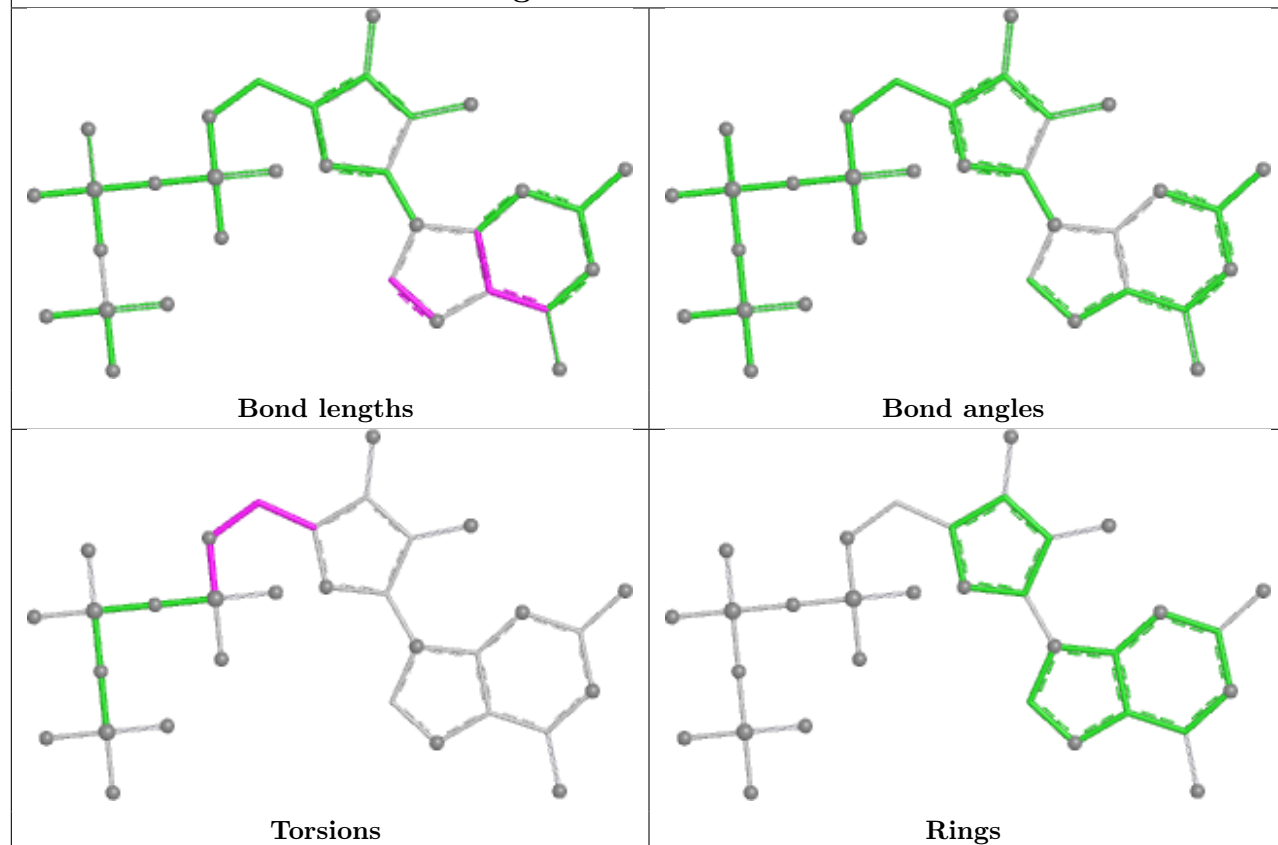


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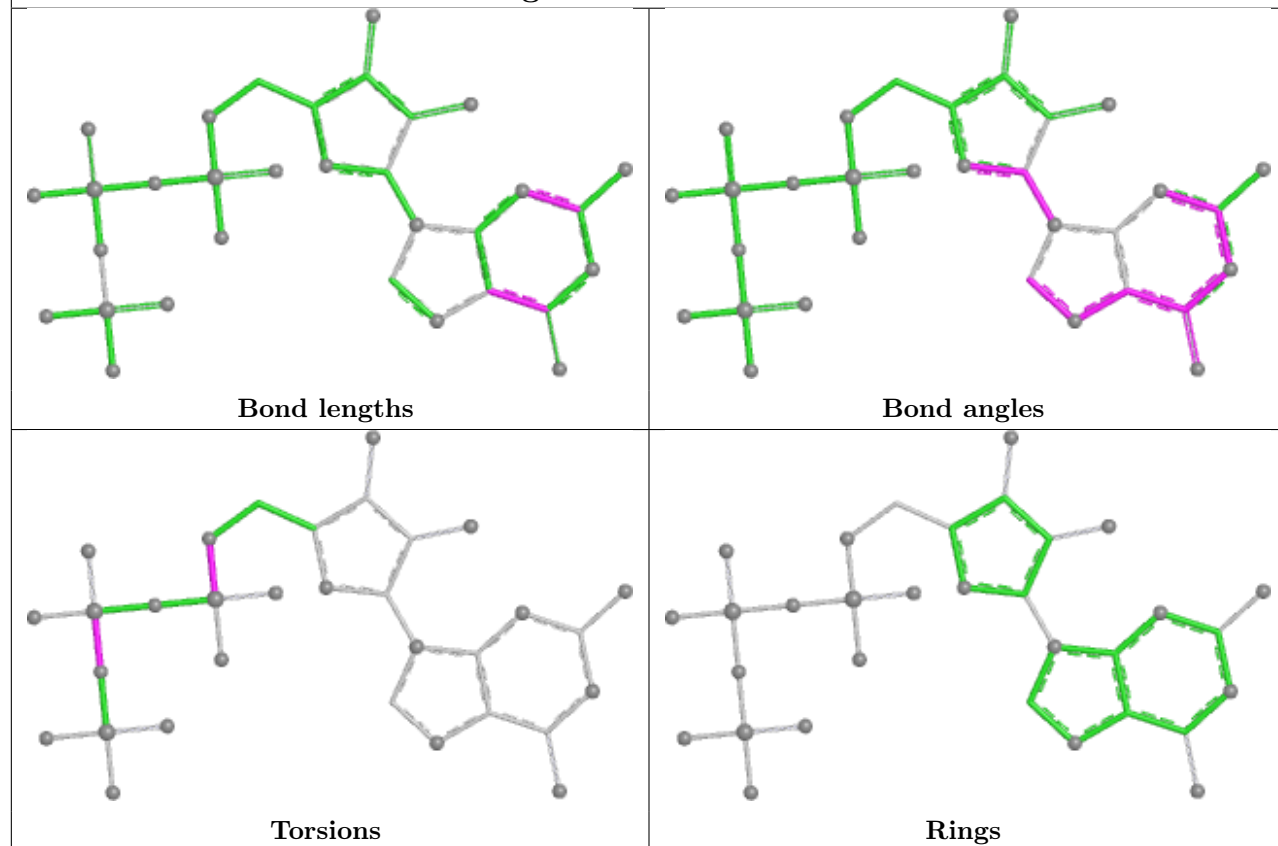




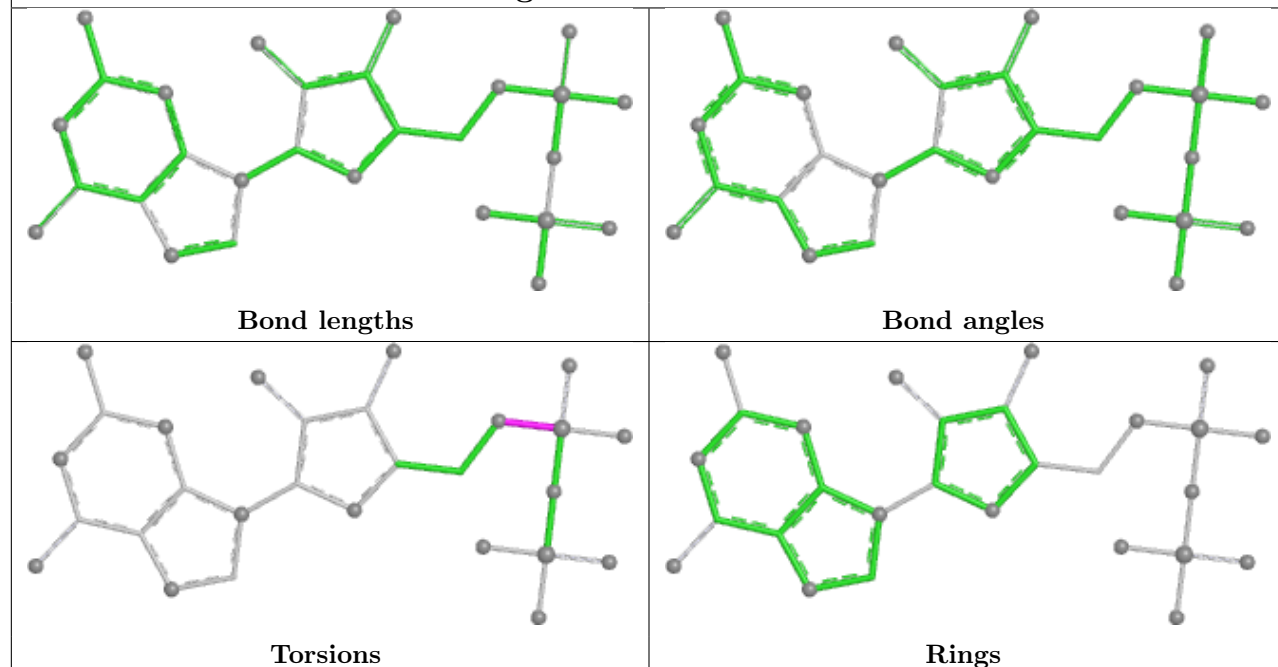
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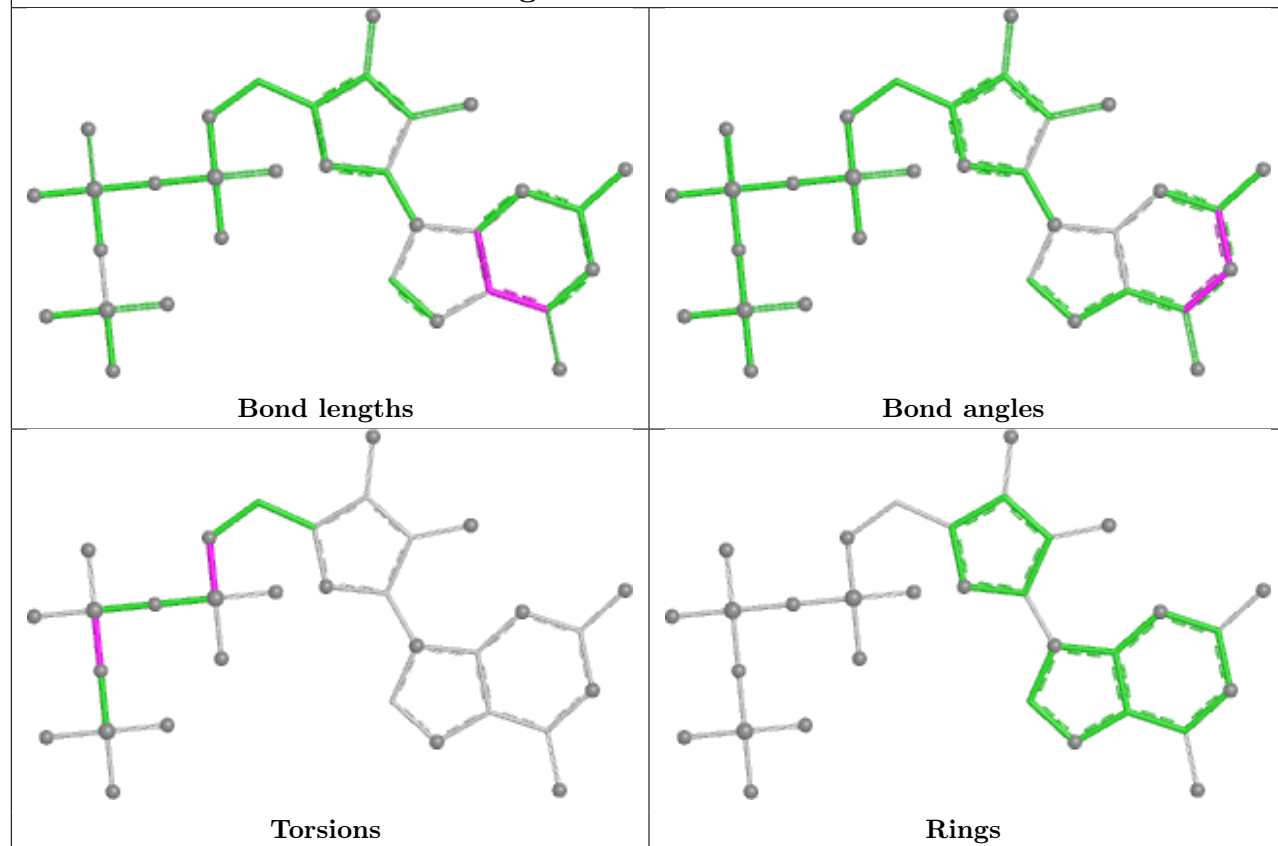
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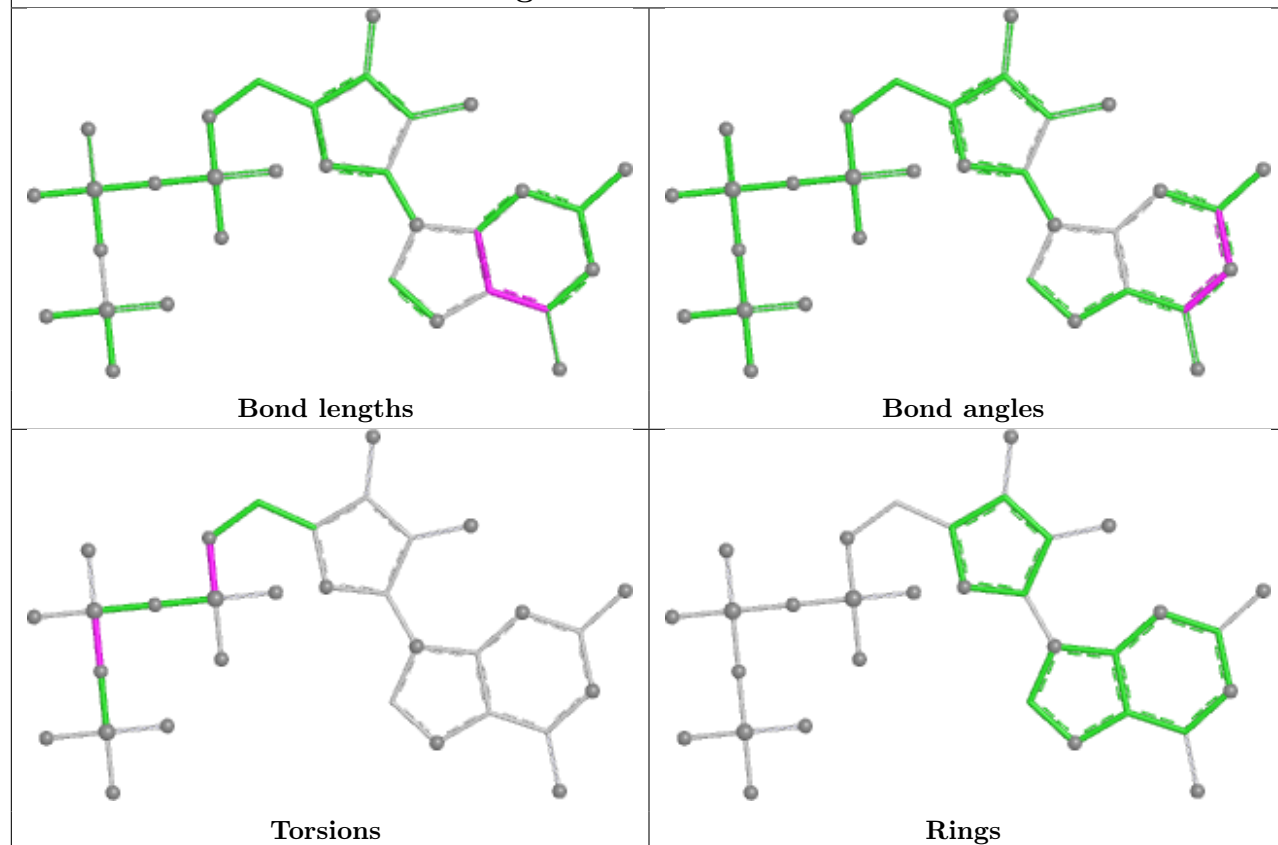
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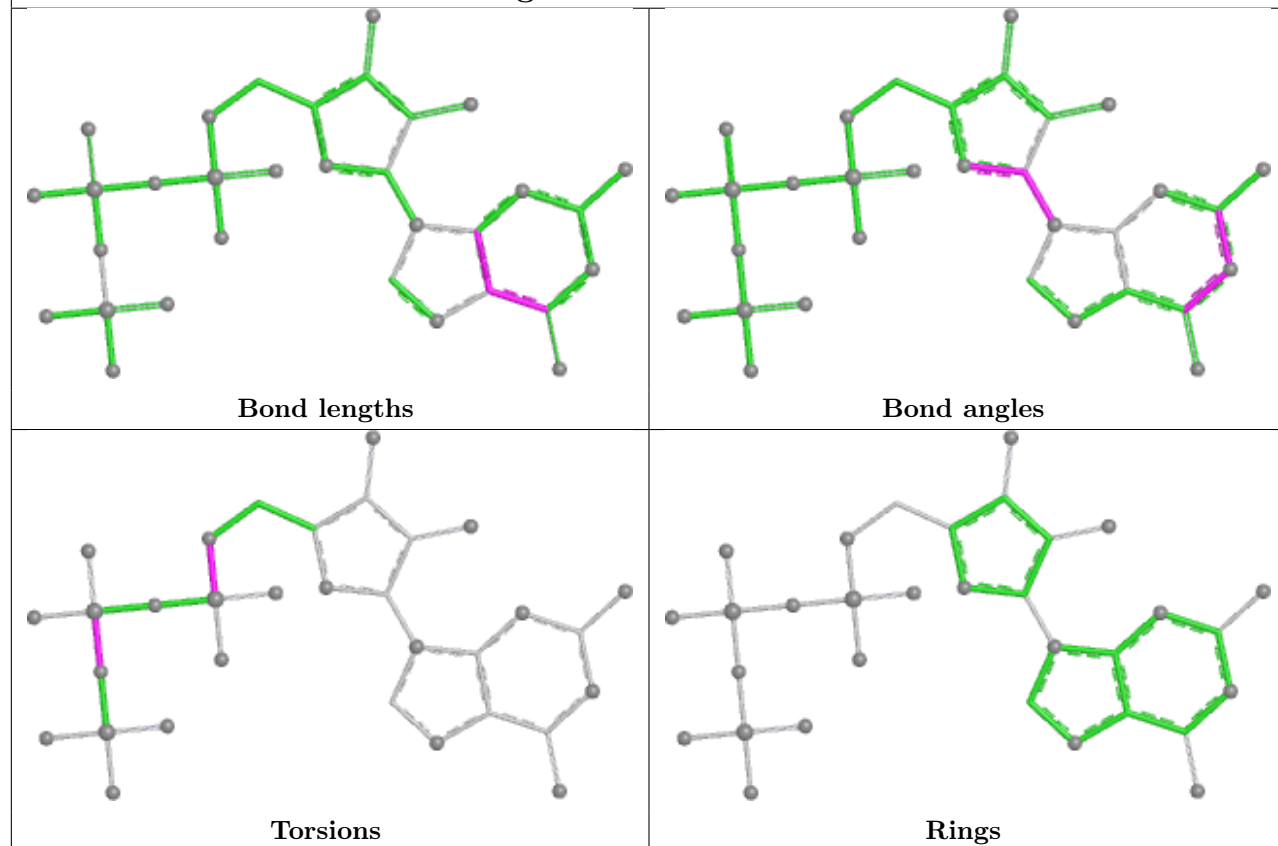
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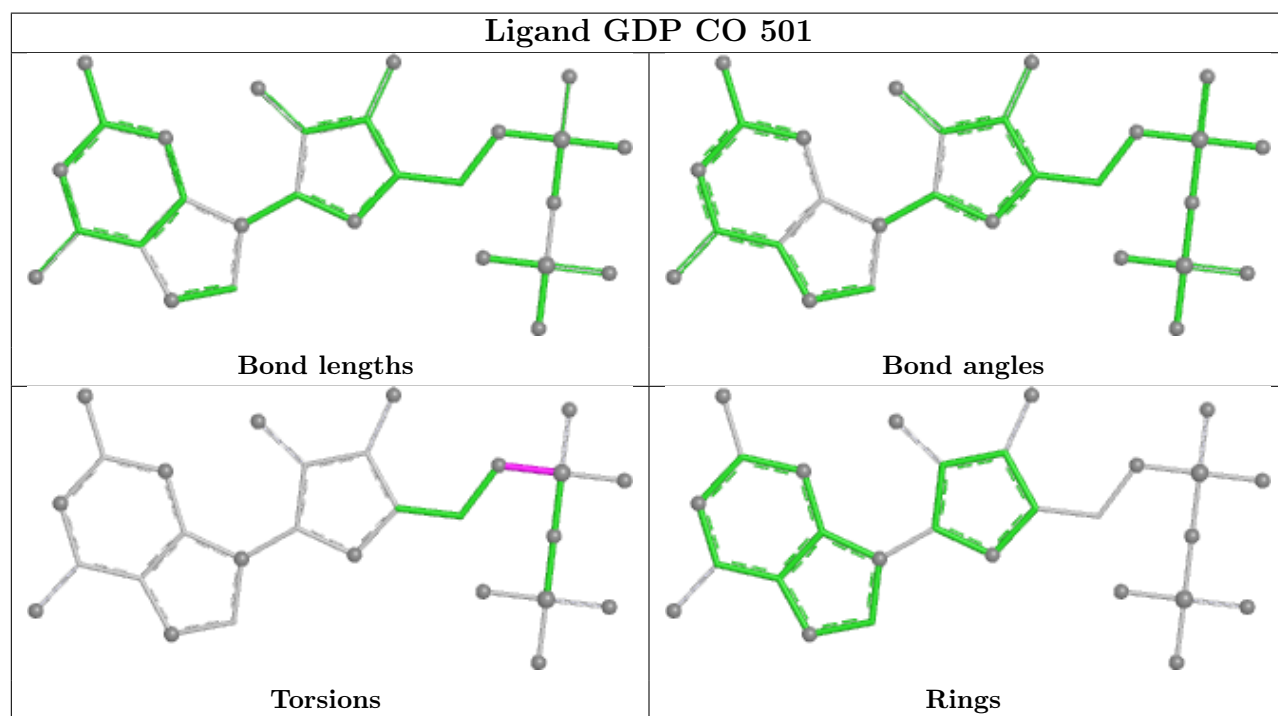
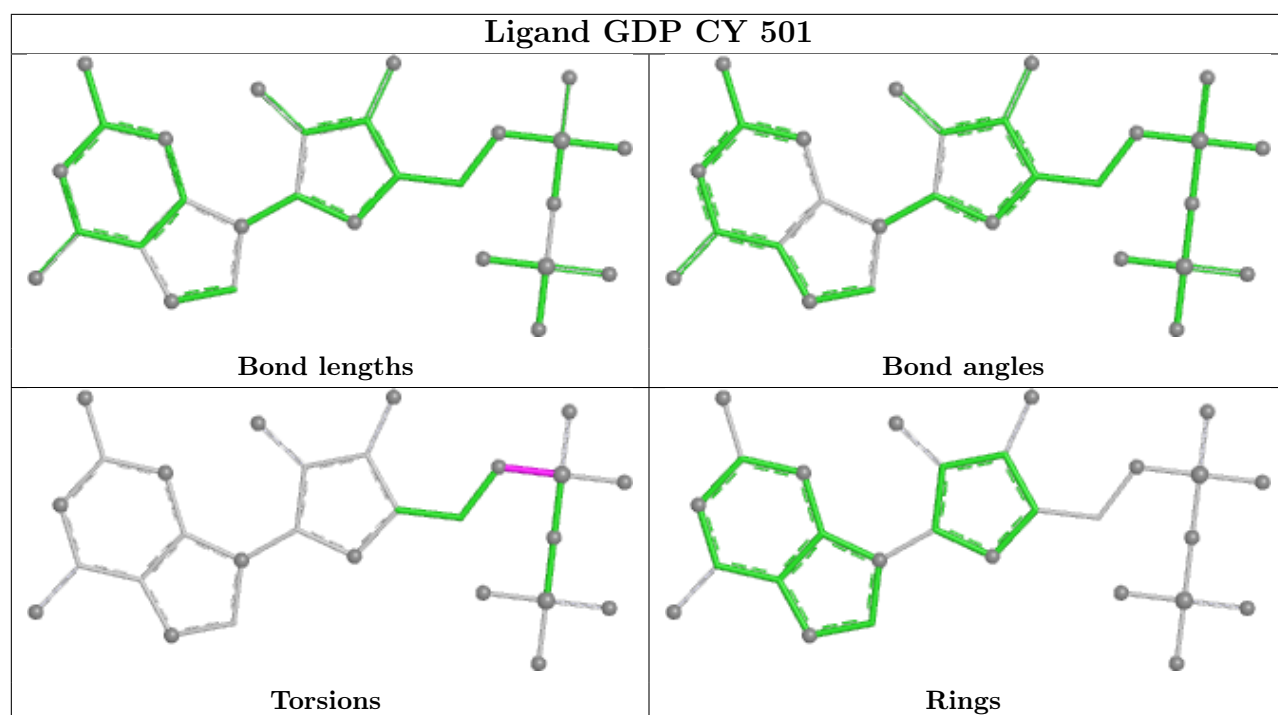


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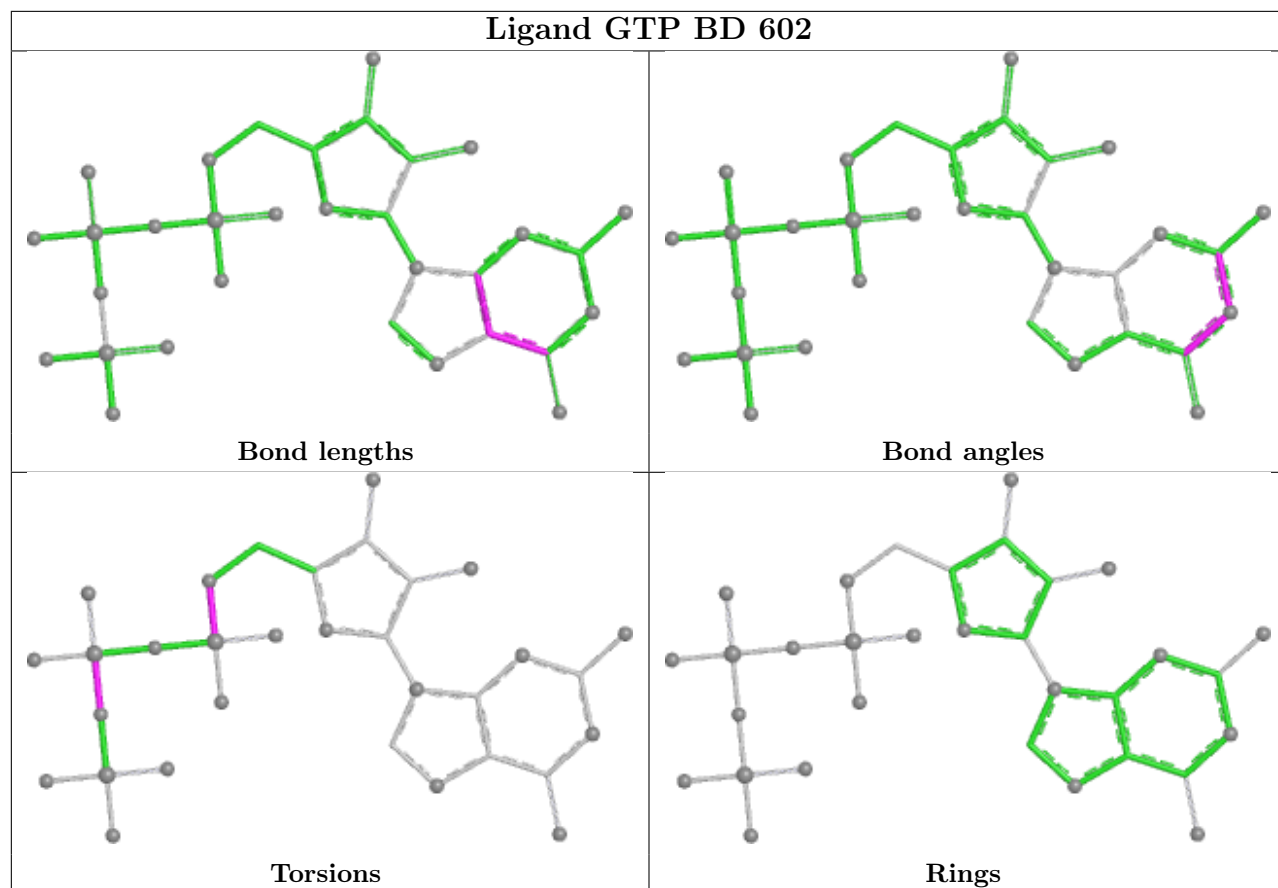


## Ligand GTP YV 602

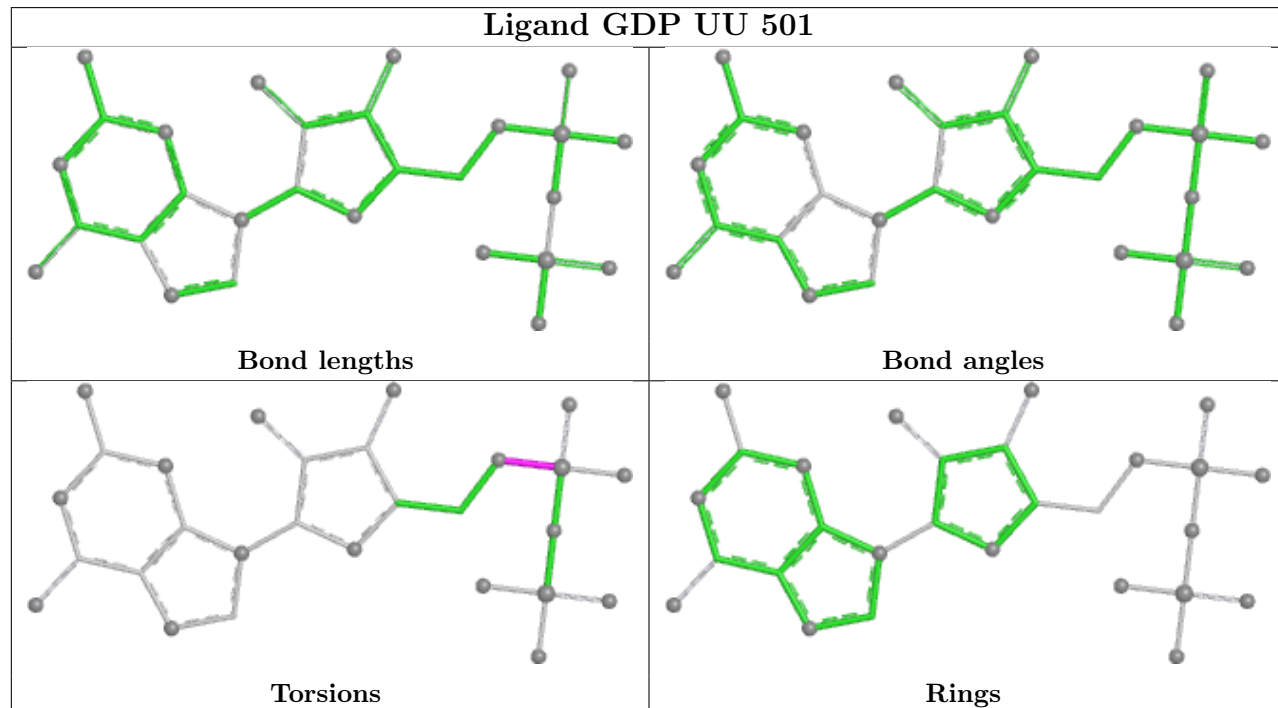


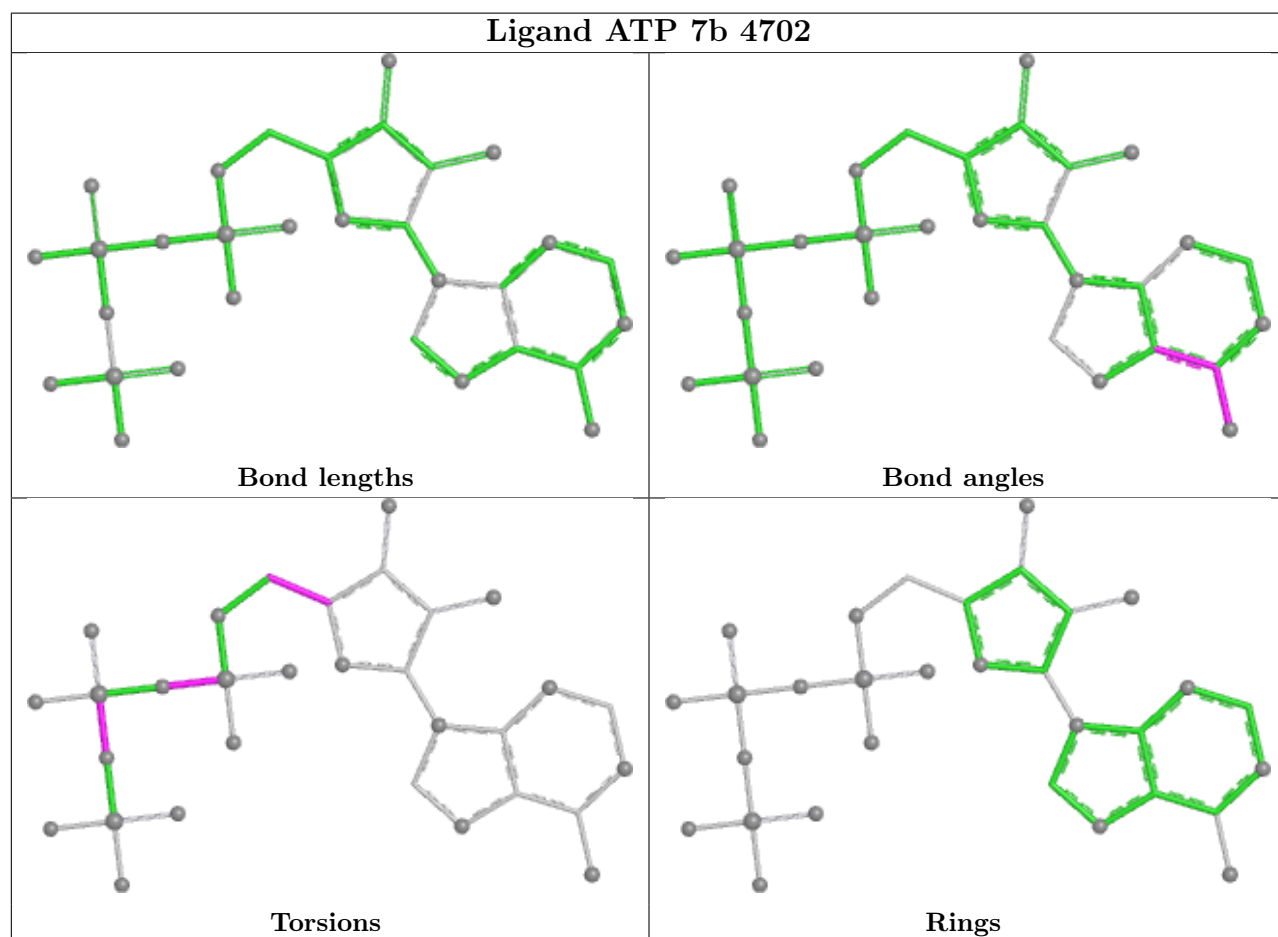
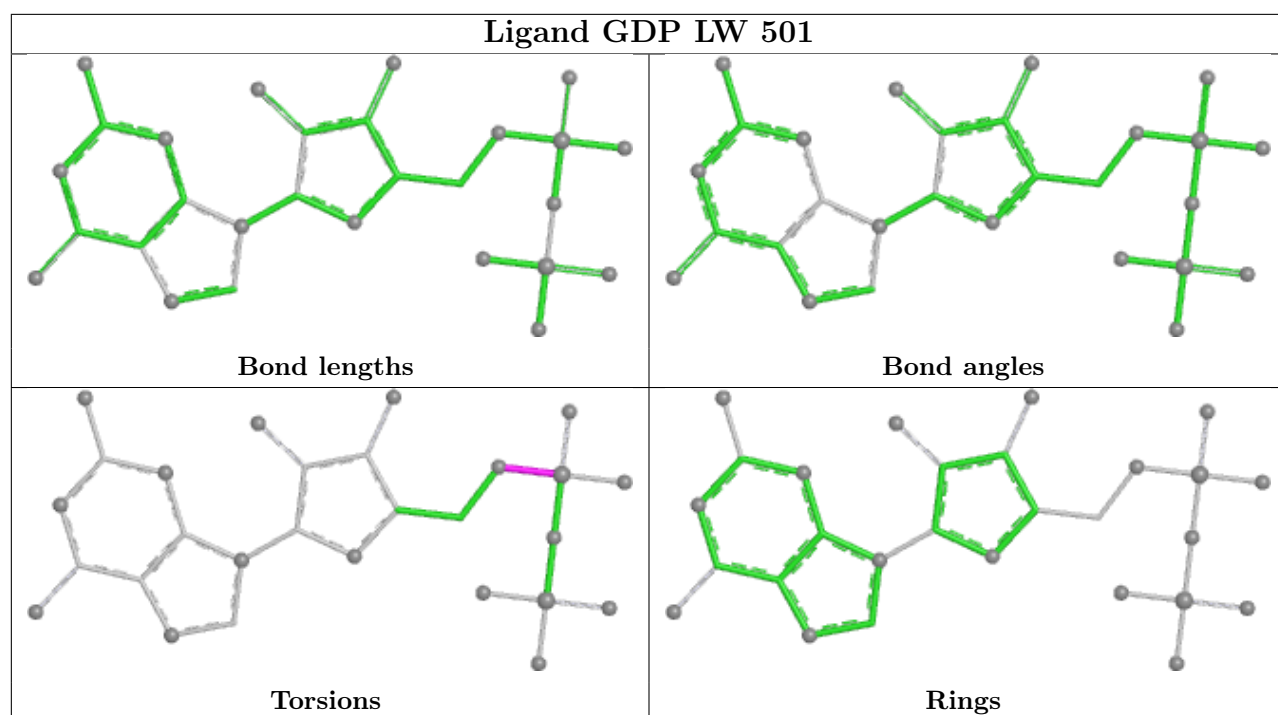


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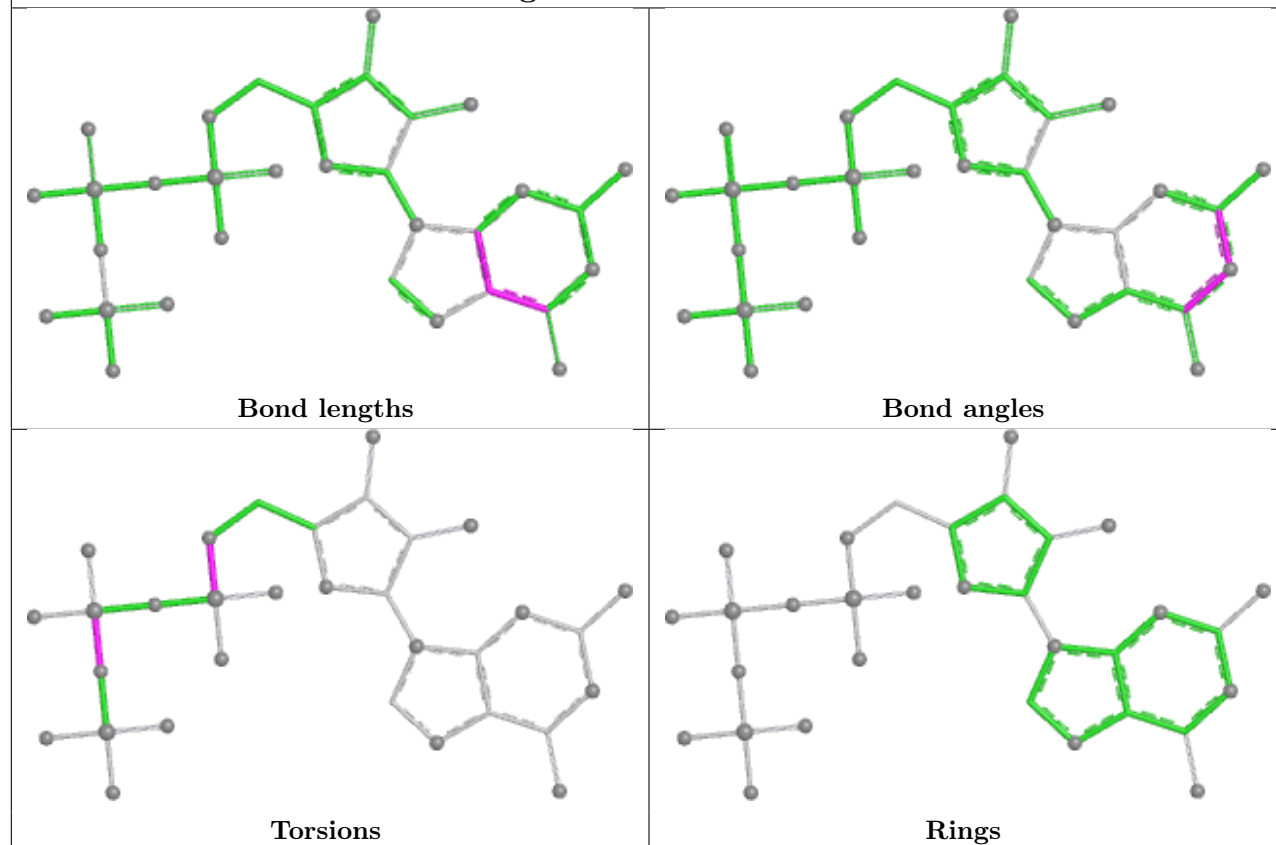


## Ligand GDP UU 501

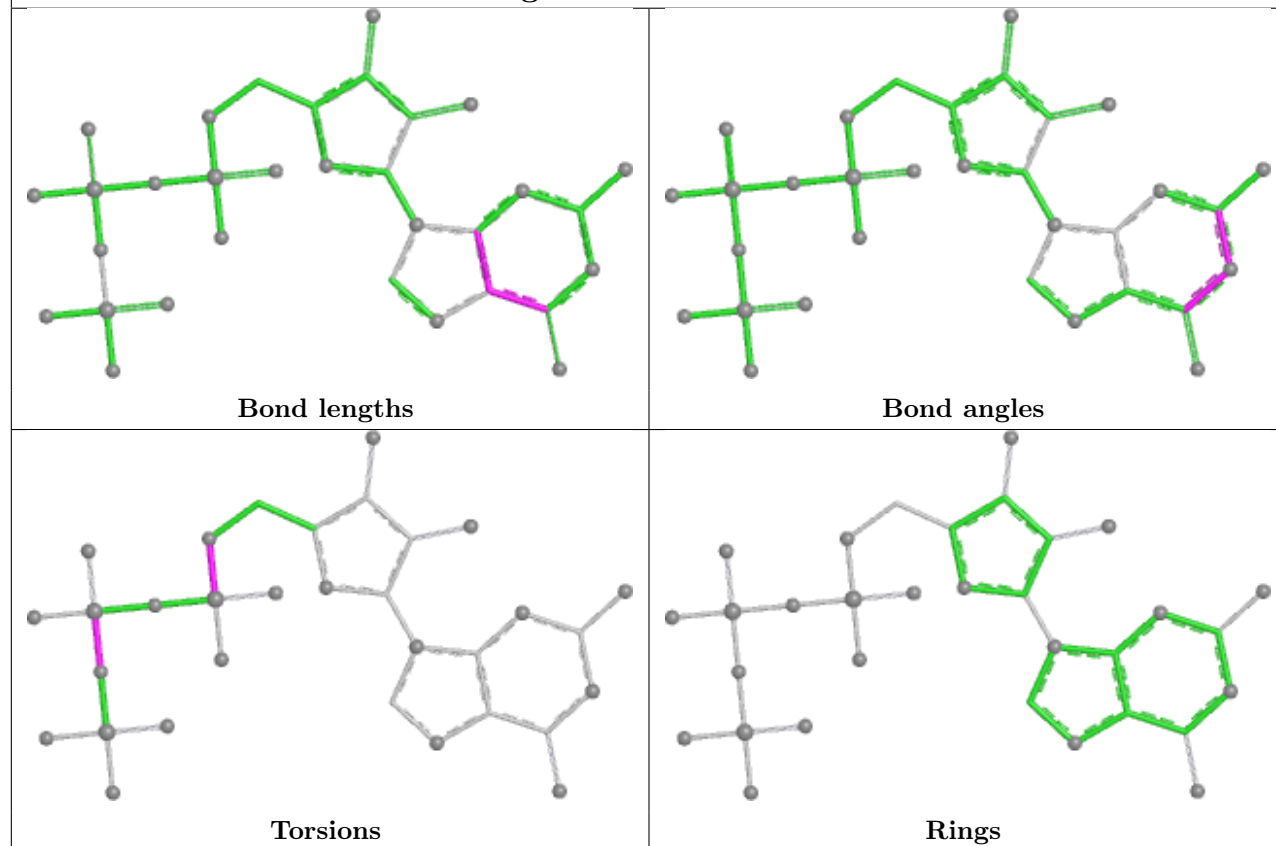


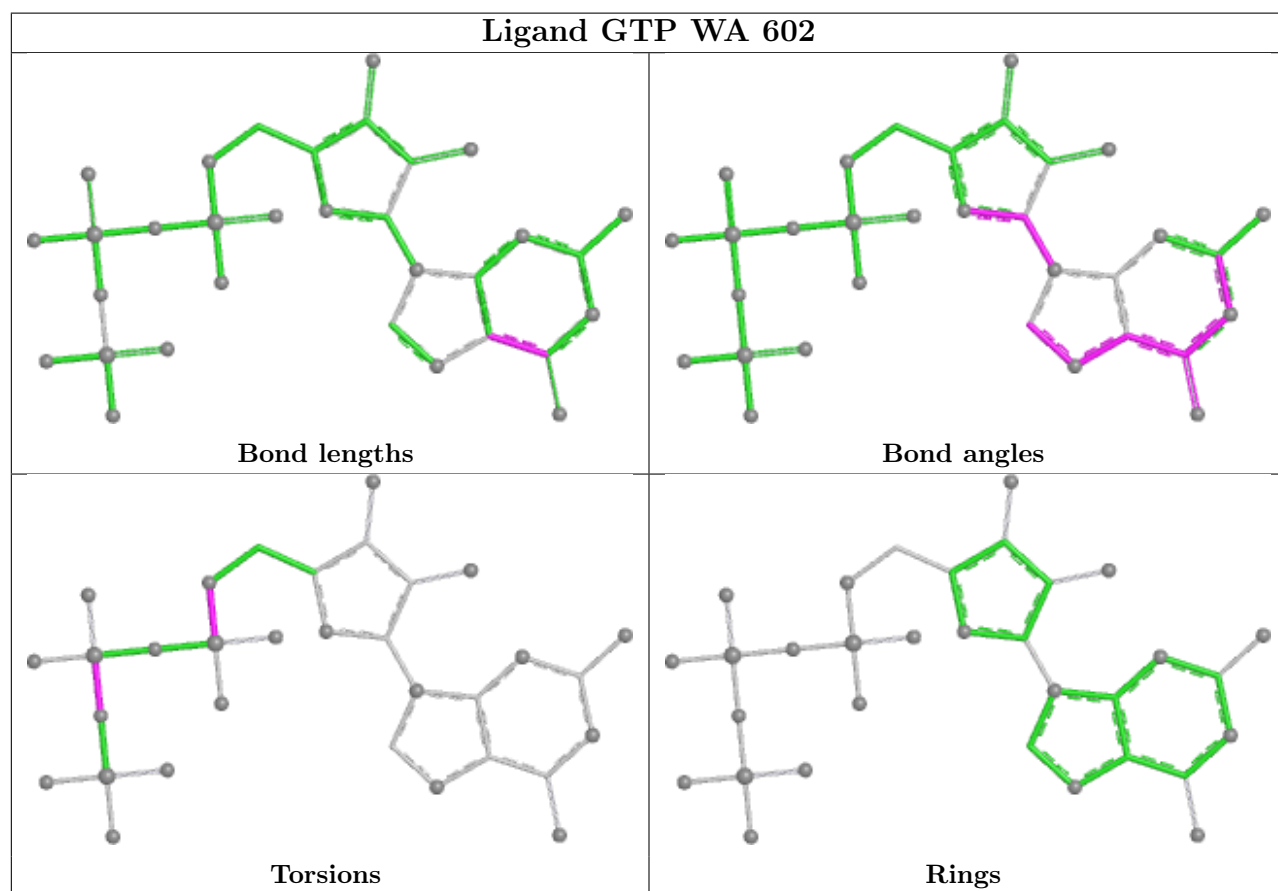
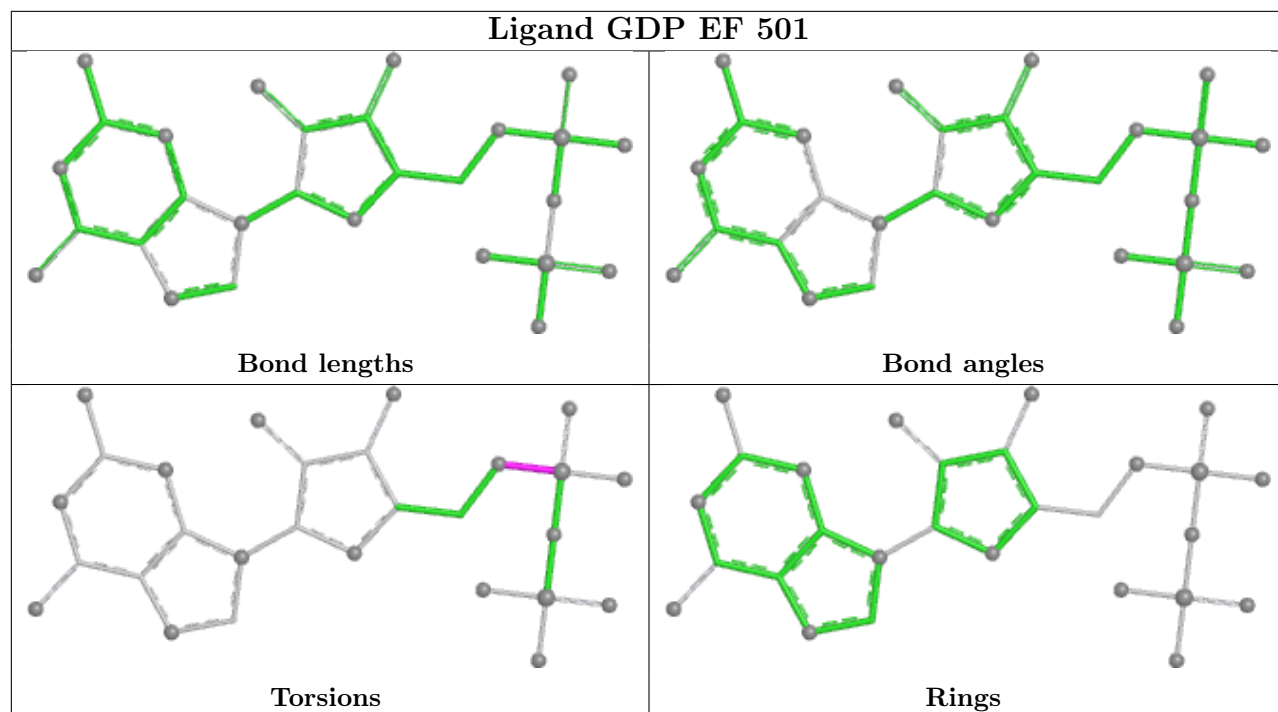


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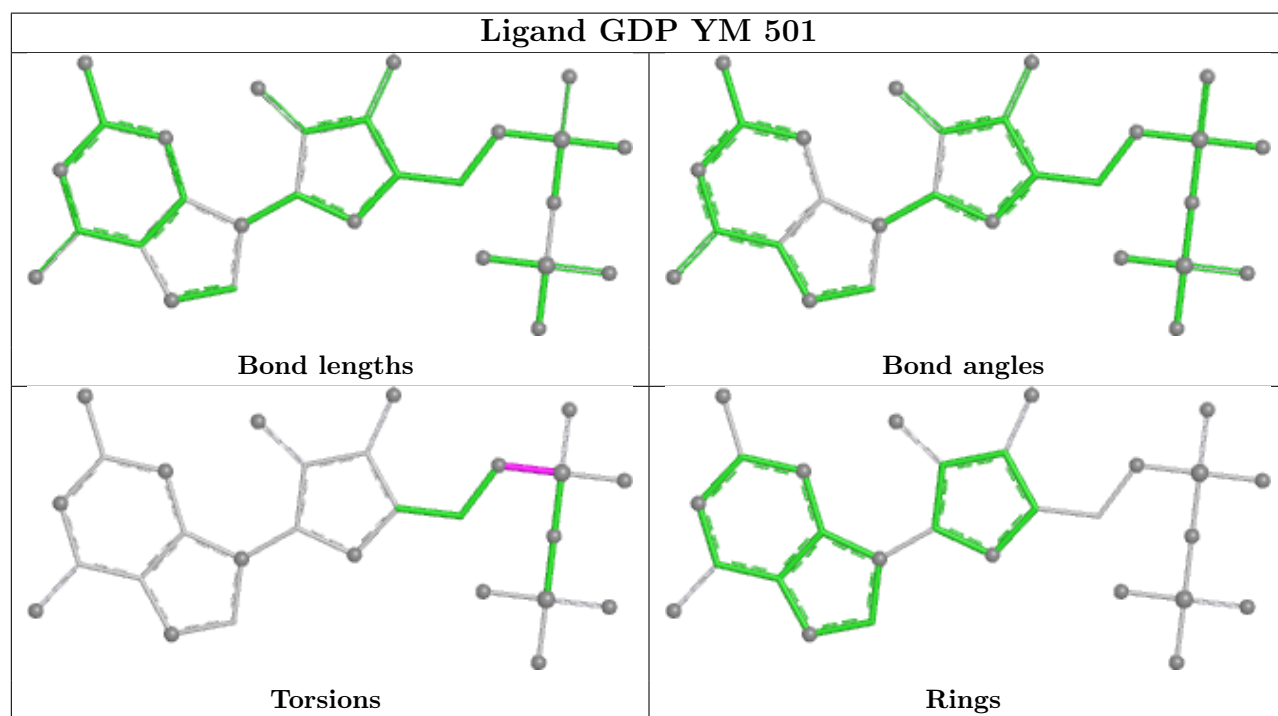
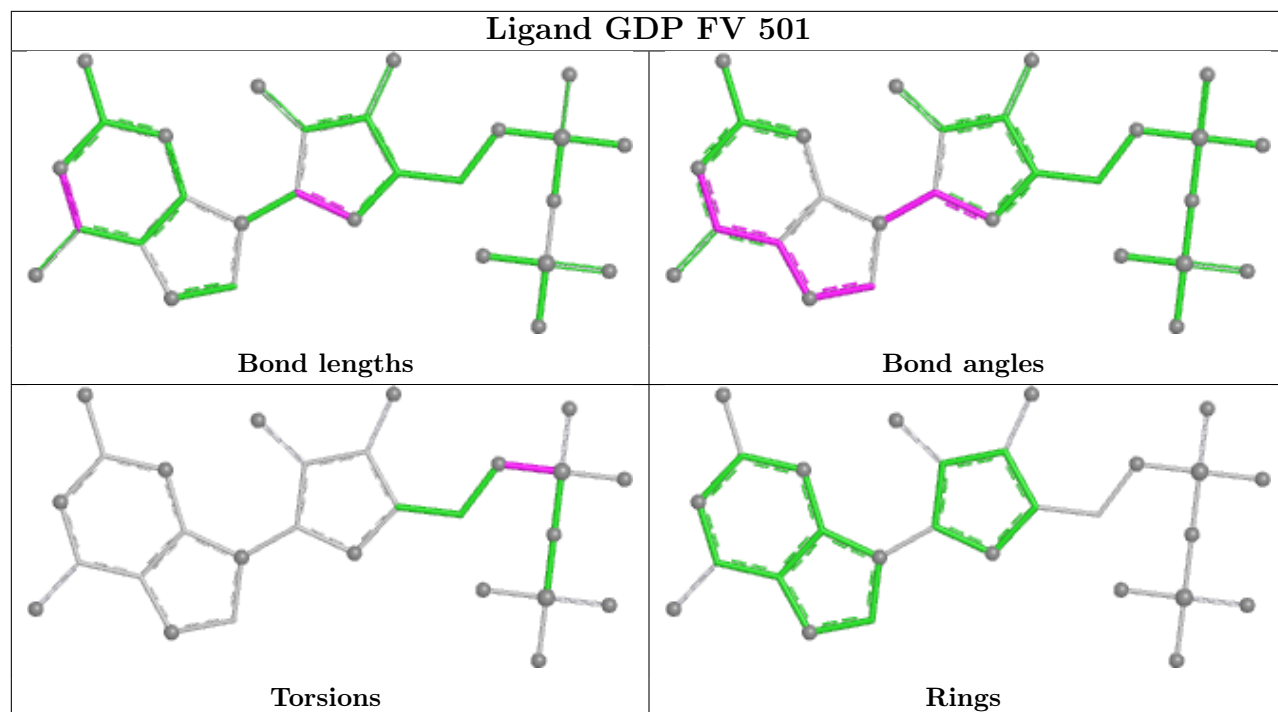


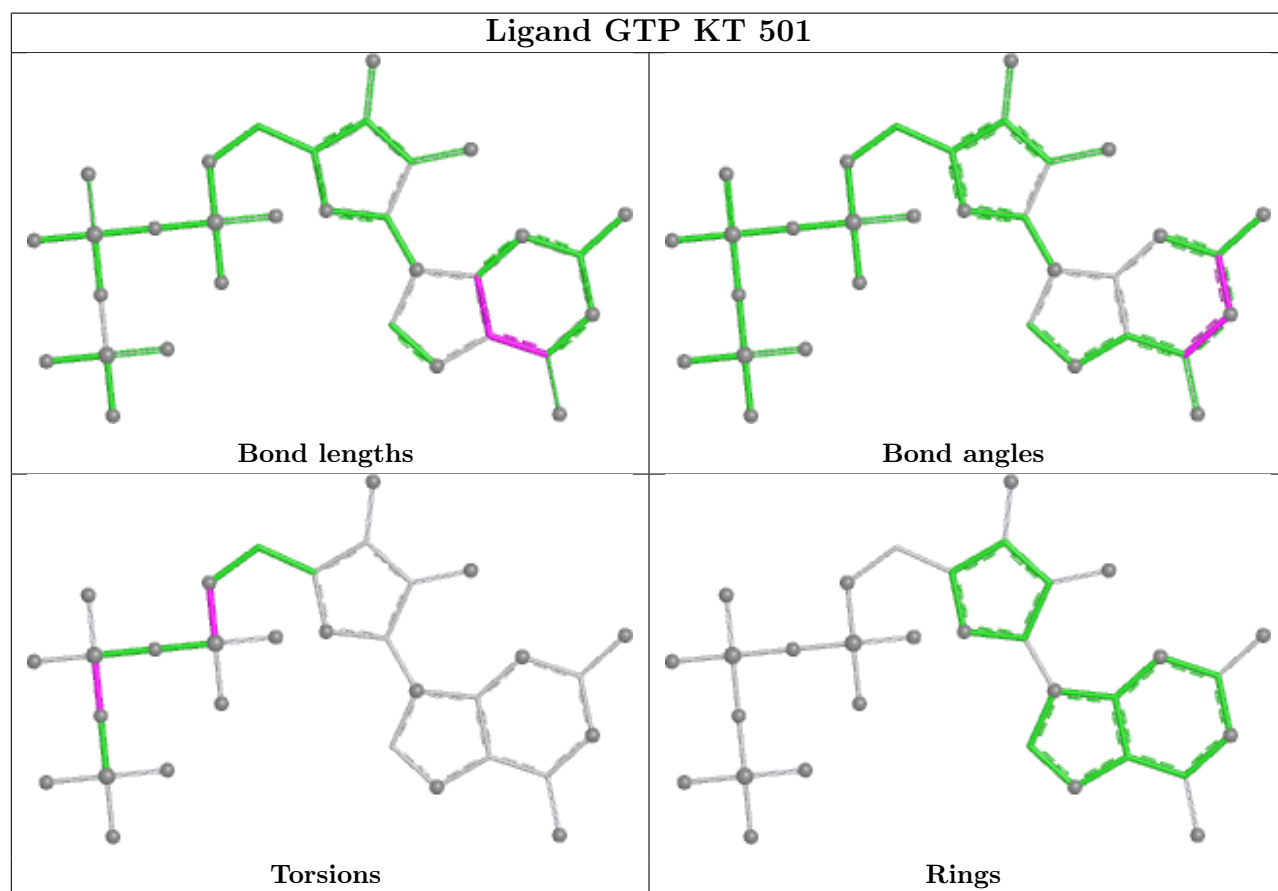
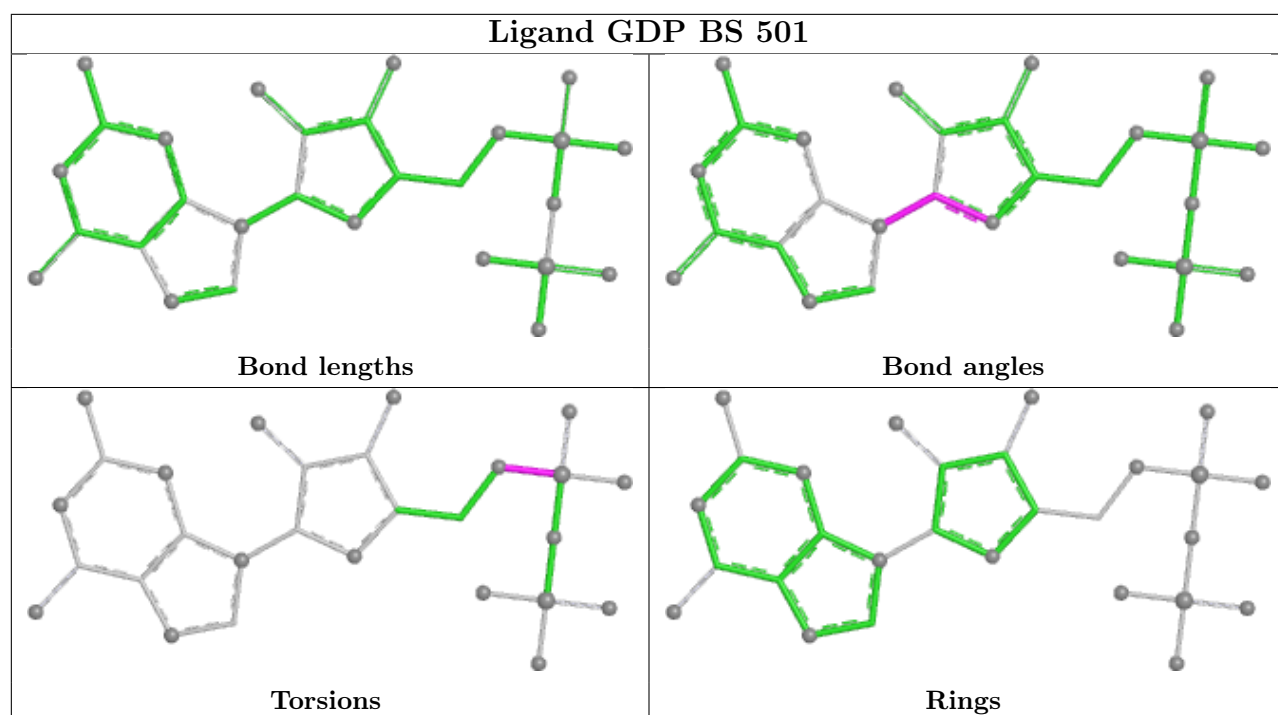
## Ligand GTP JA 501

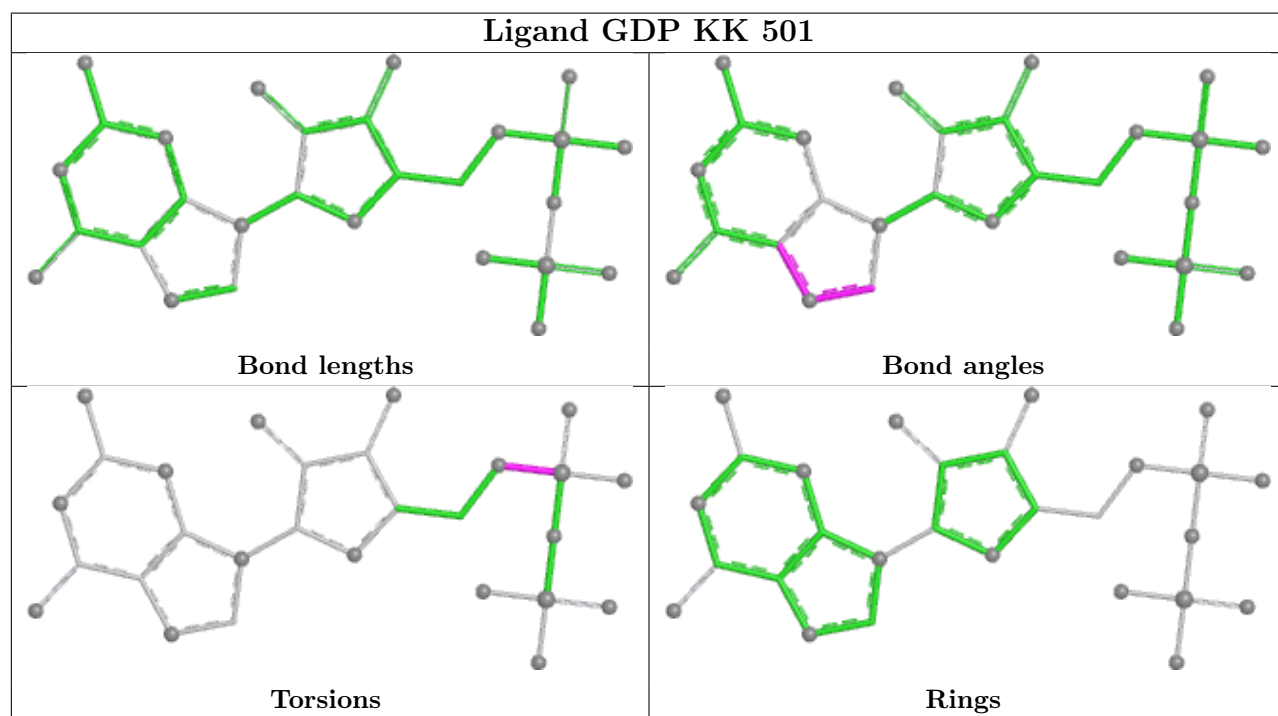
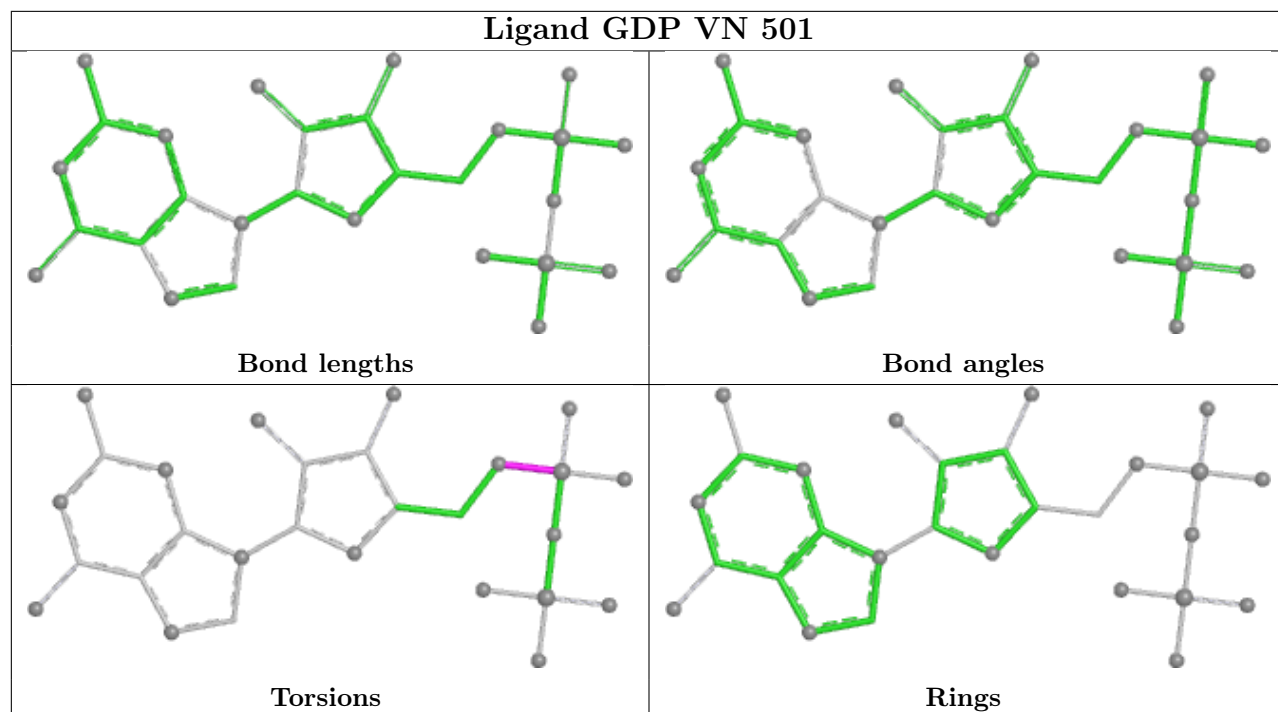




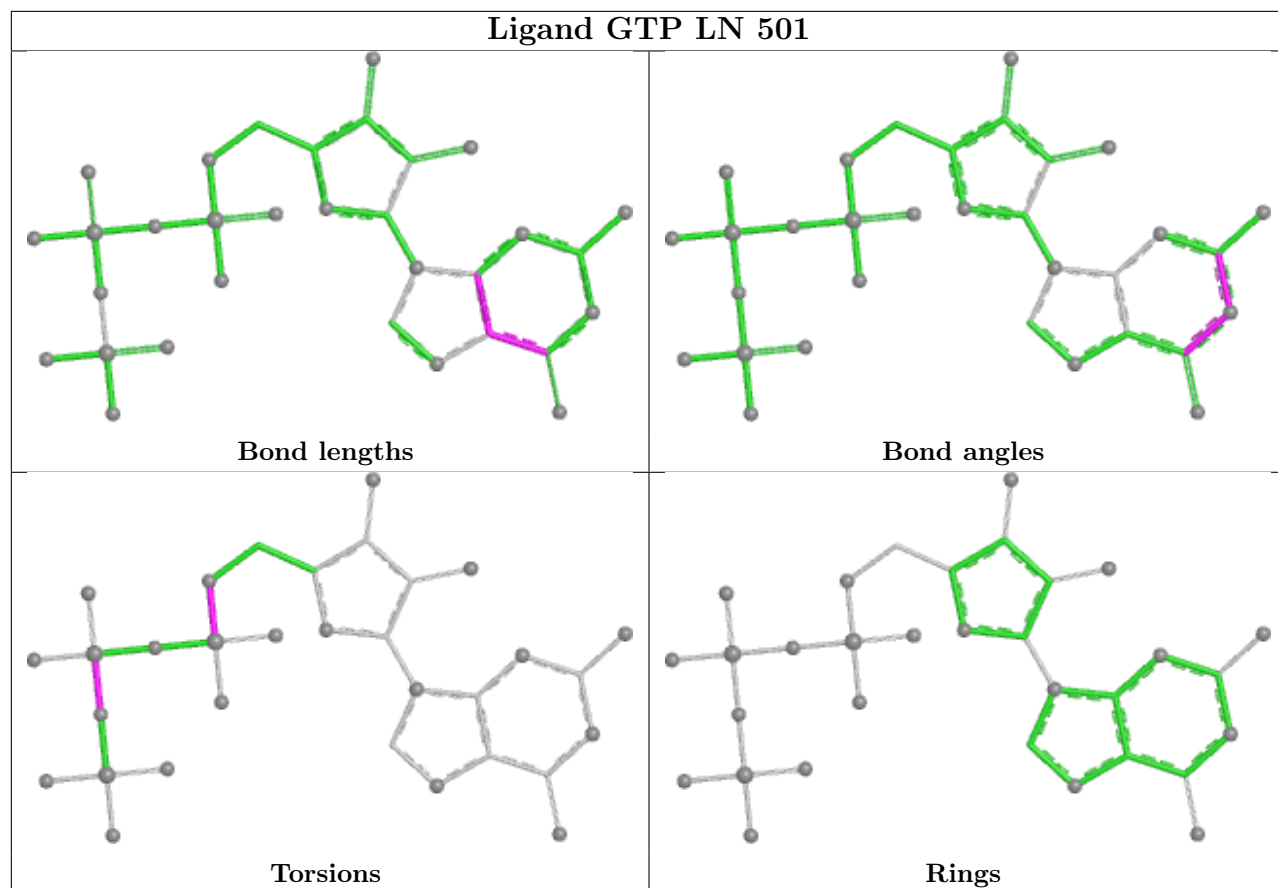




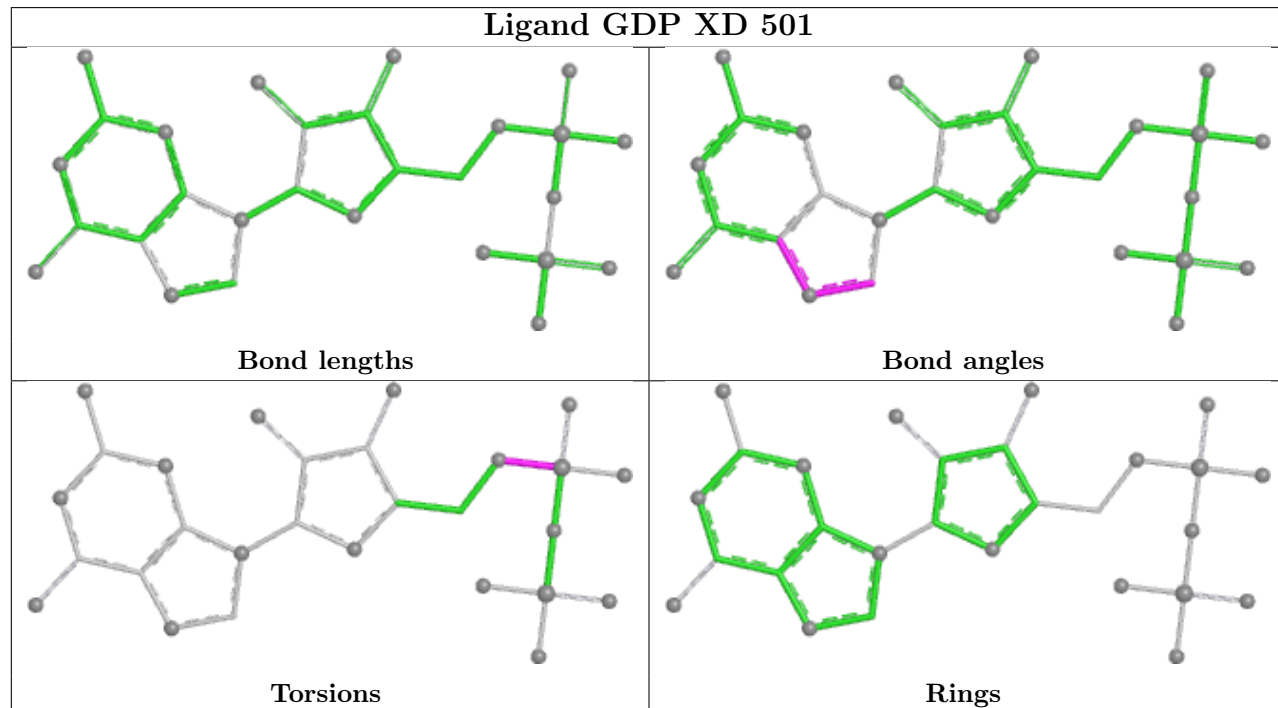




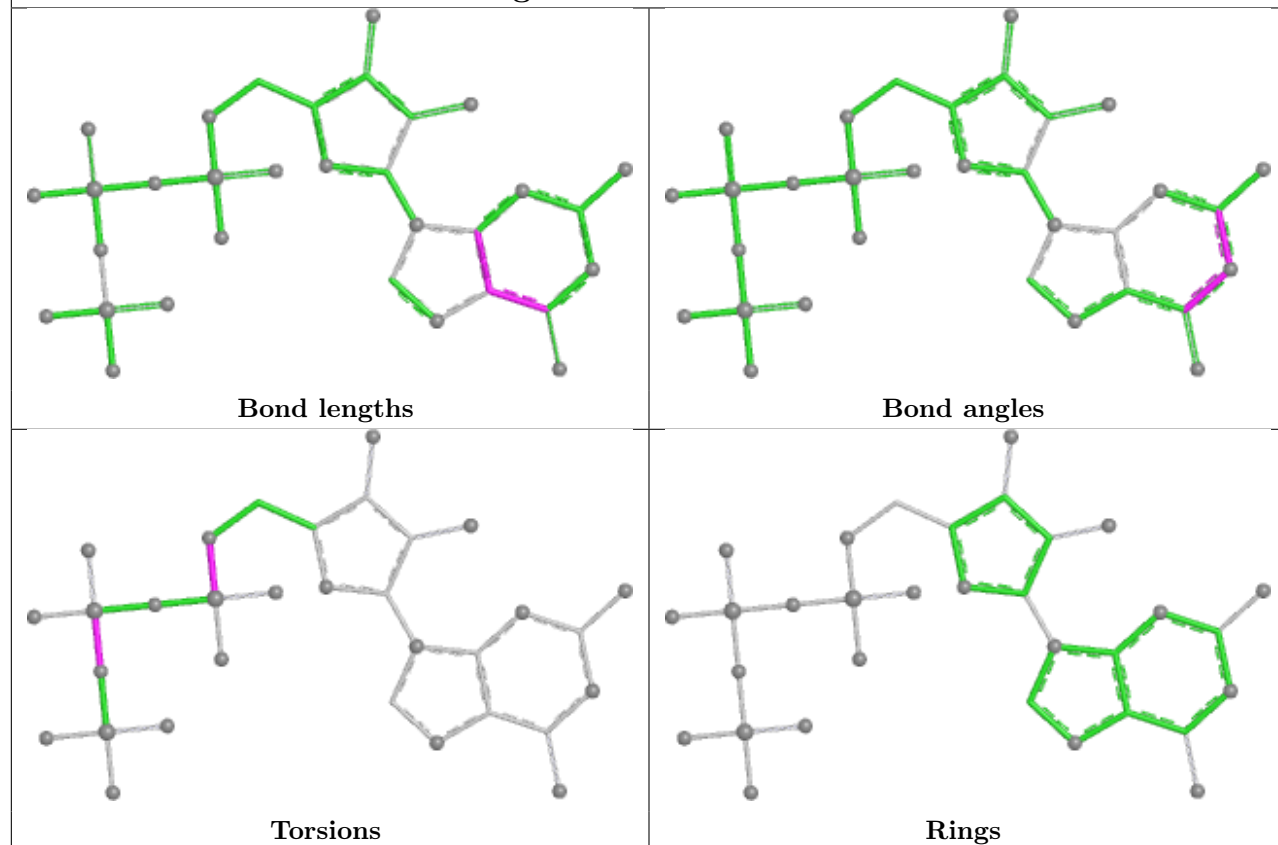
## Ligand GTP LN 501



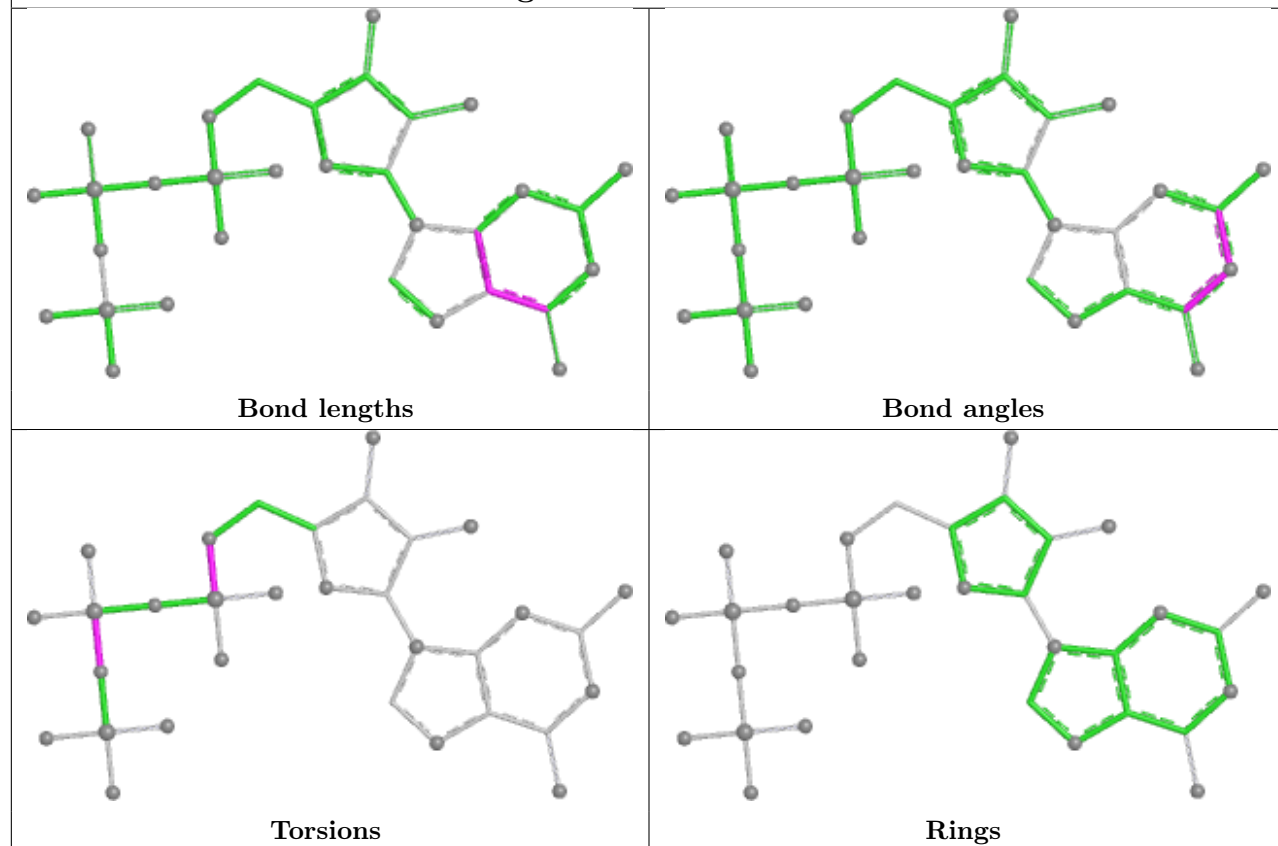
## Ligand GDP XD 501

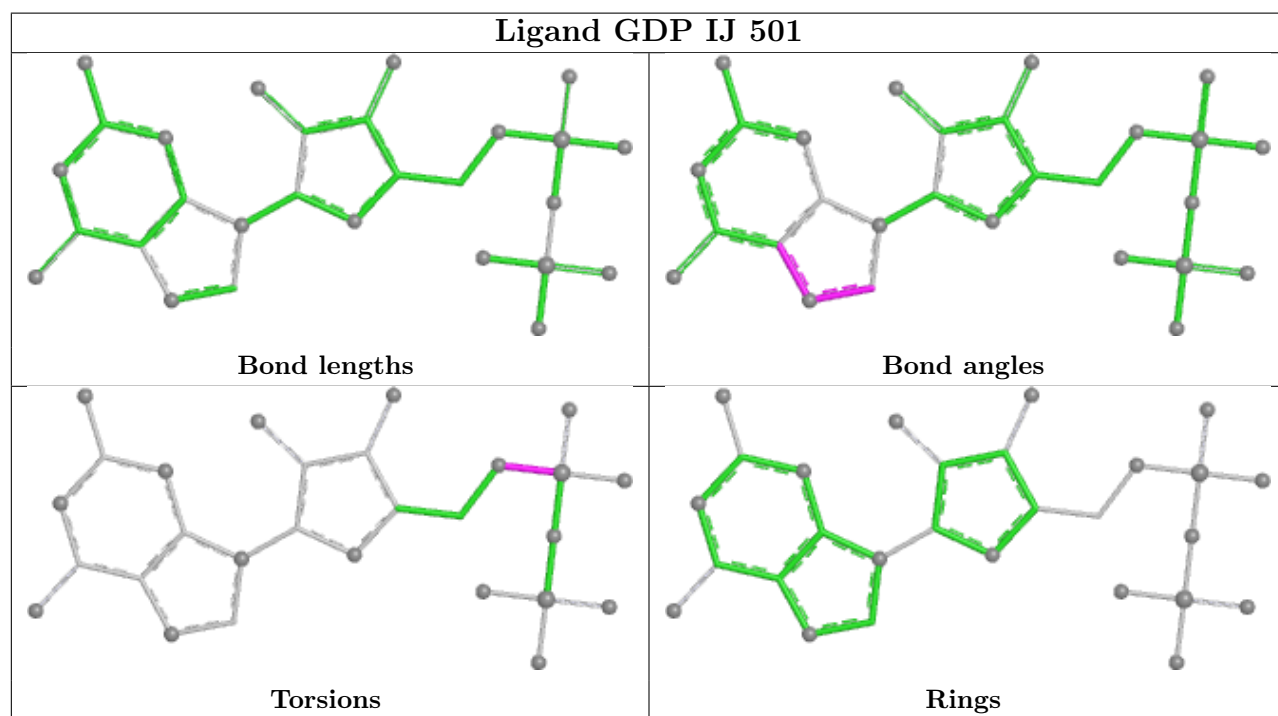
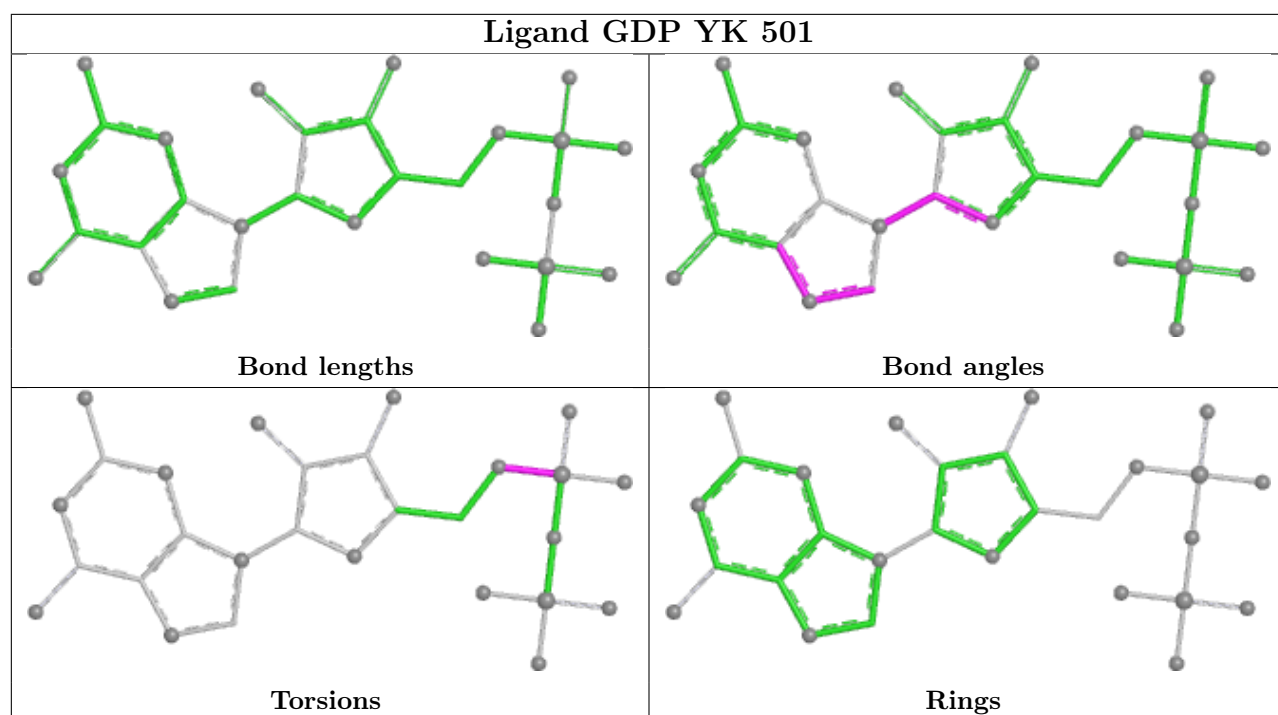


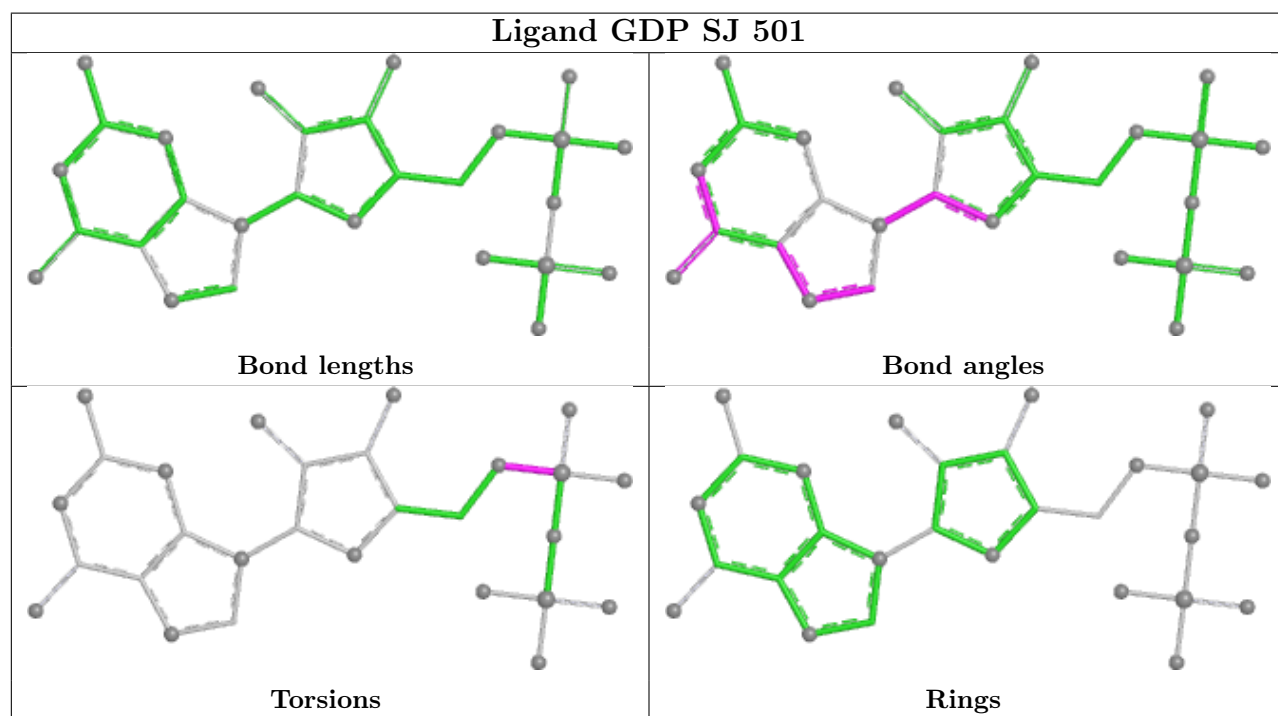
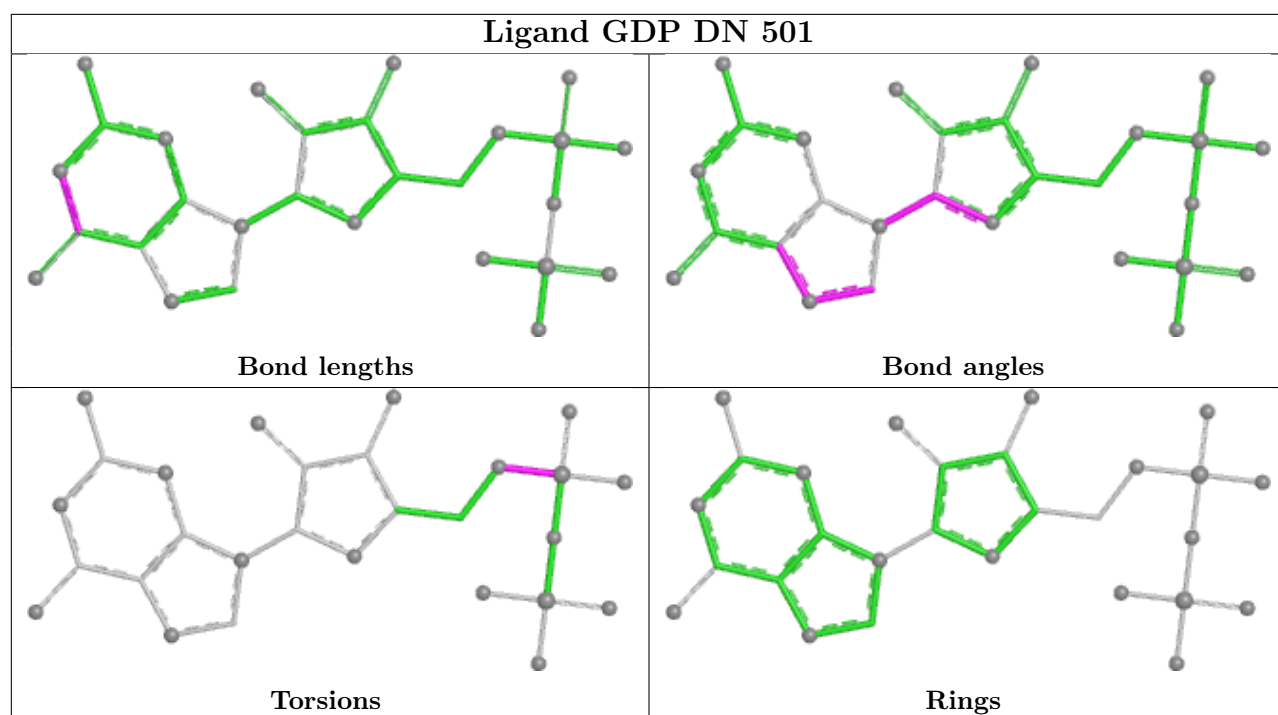
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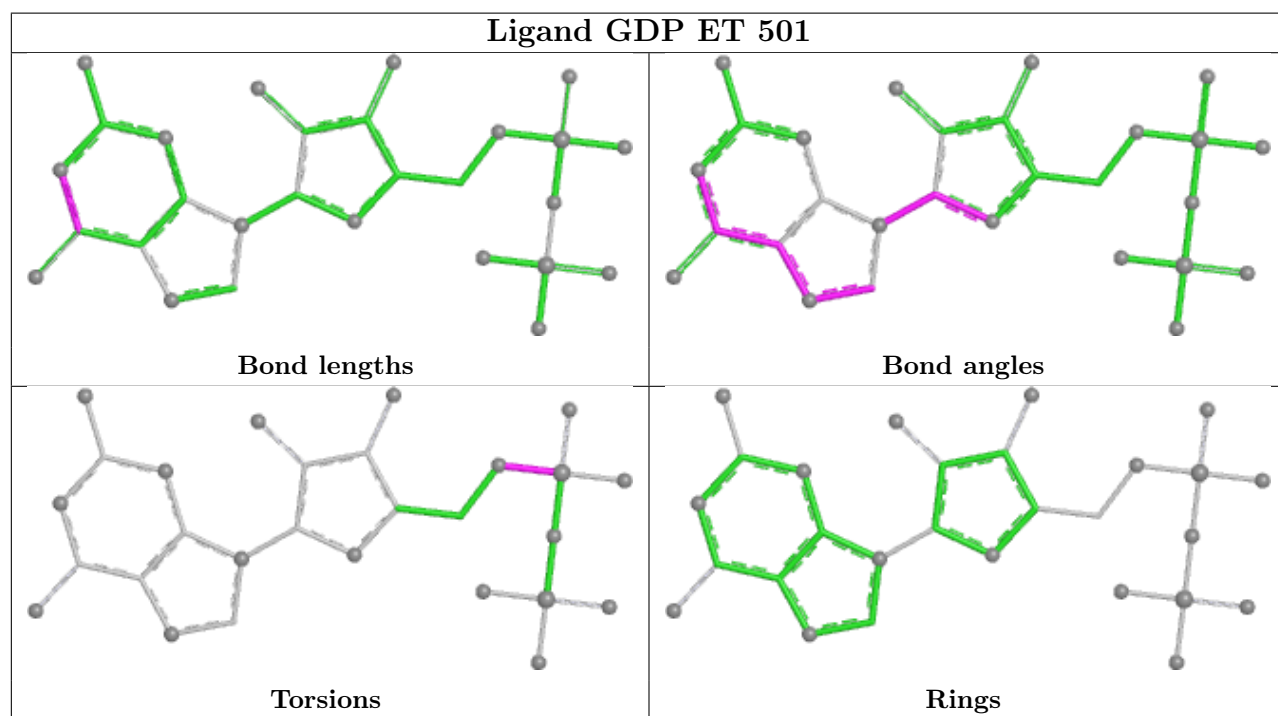
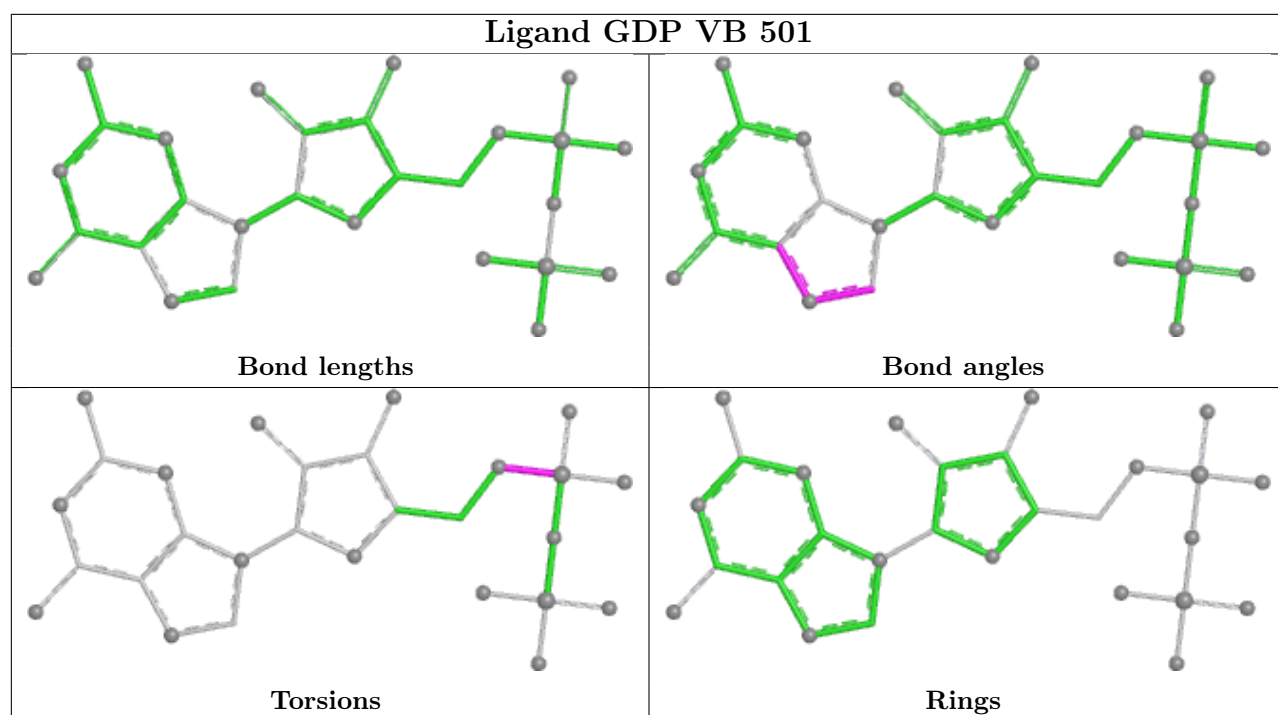


## Ligand GTP RU 501



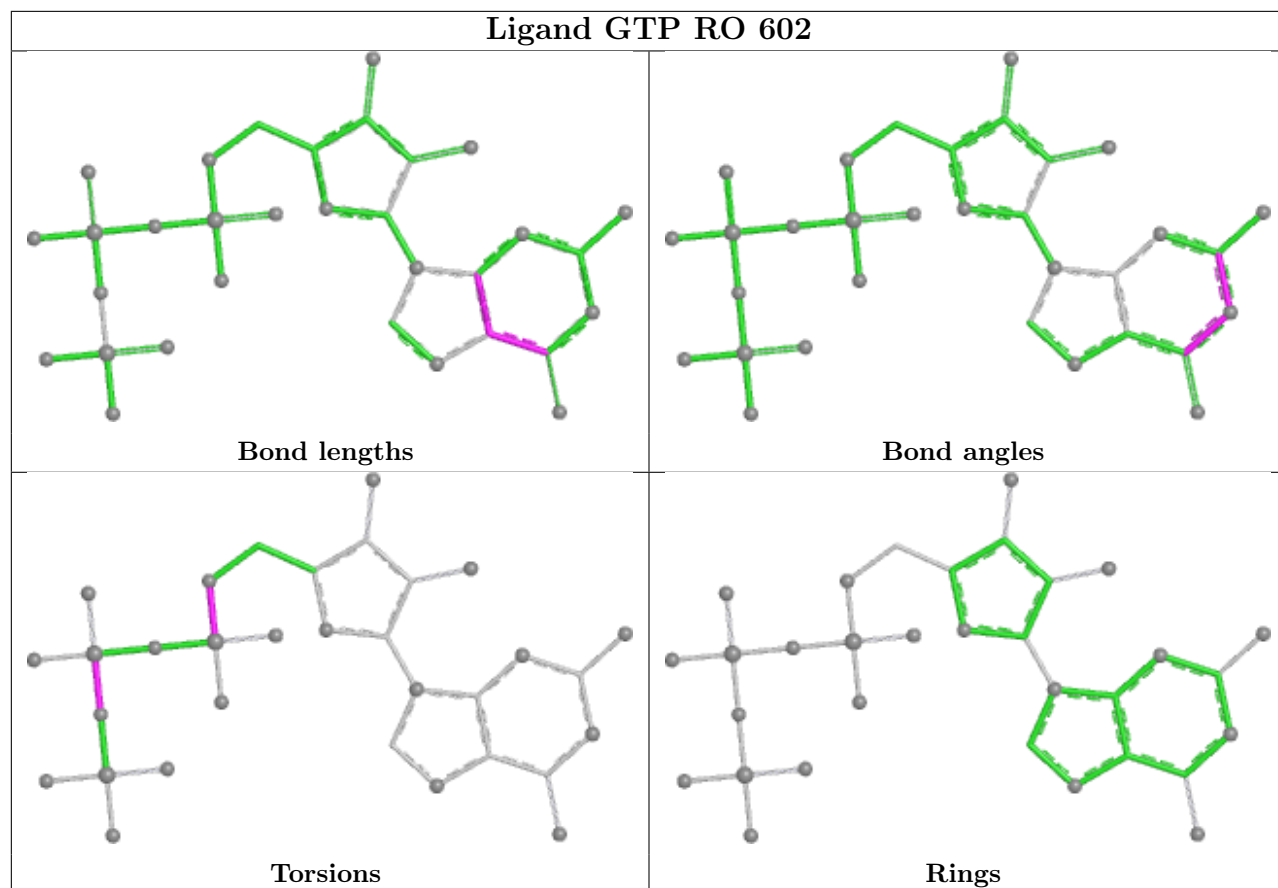




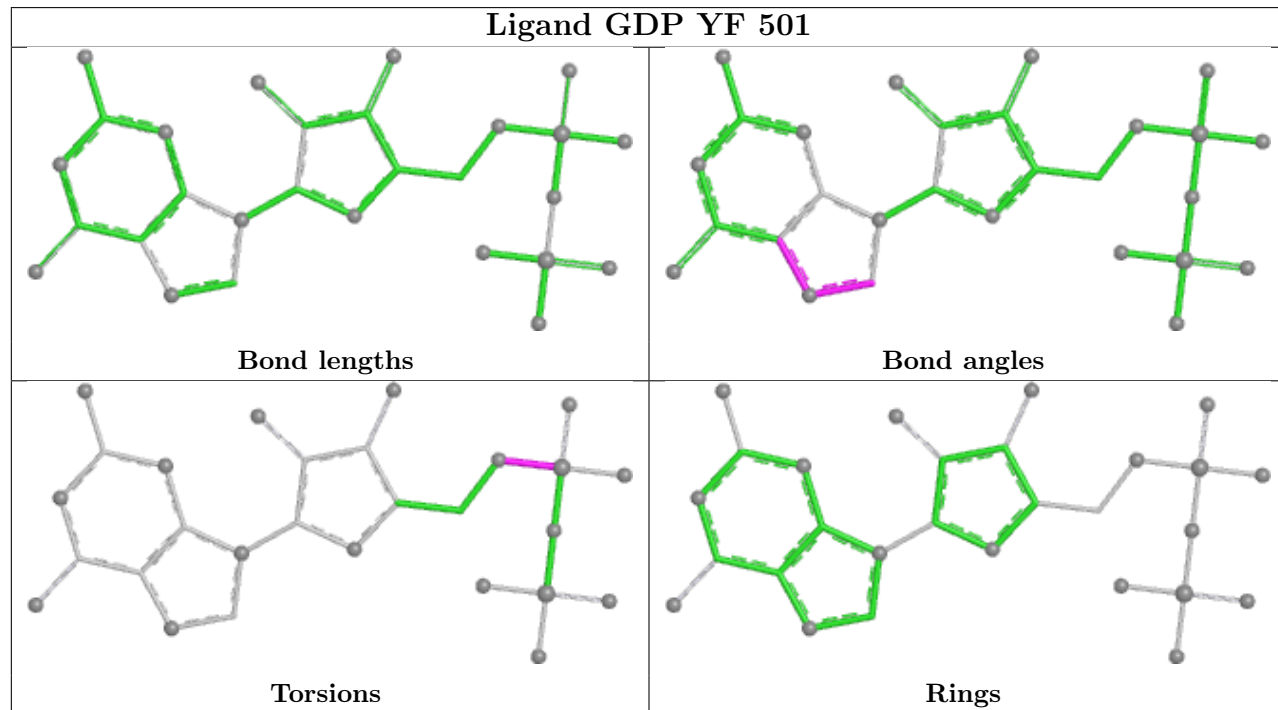




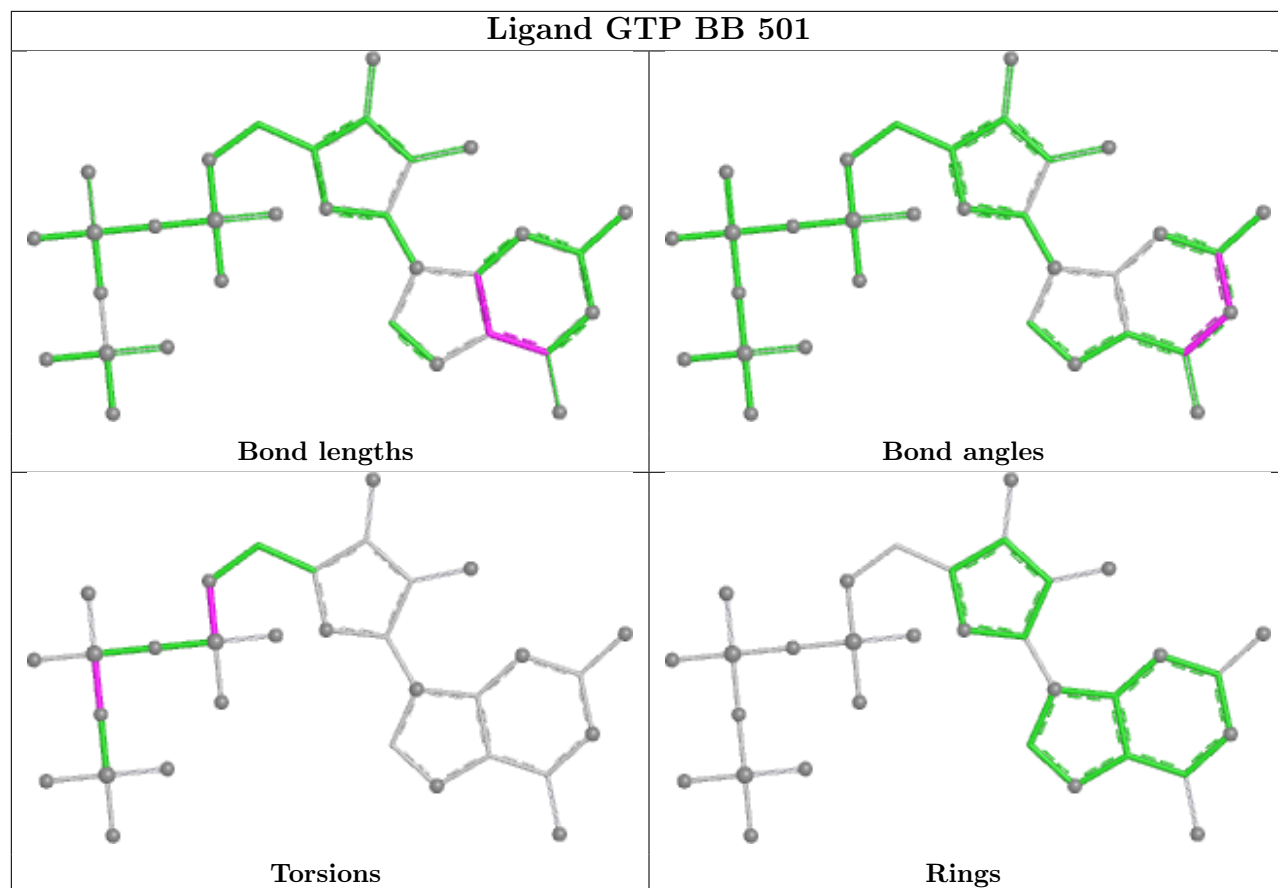
## Ligand GTP RO 602



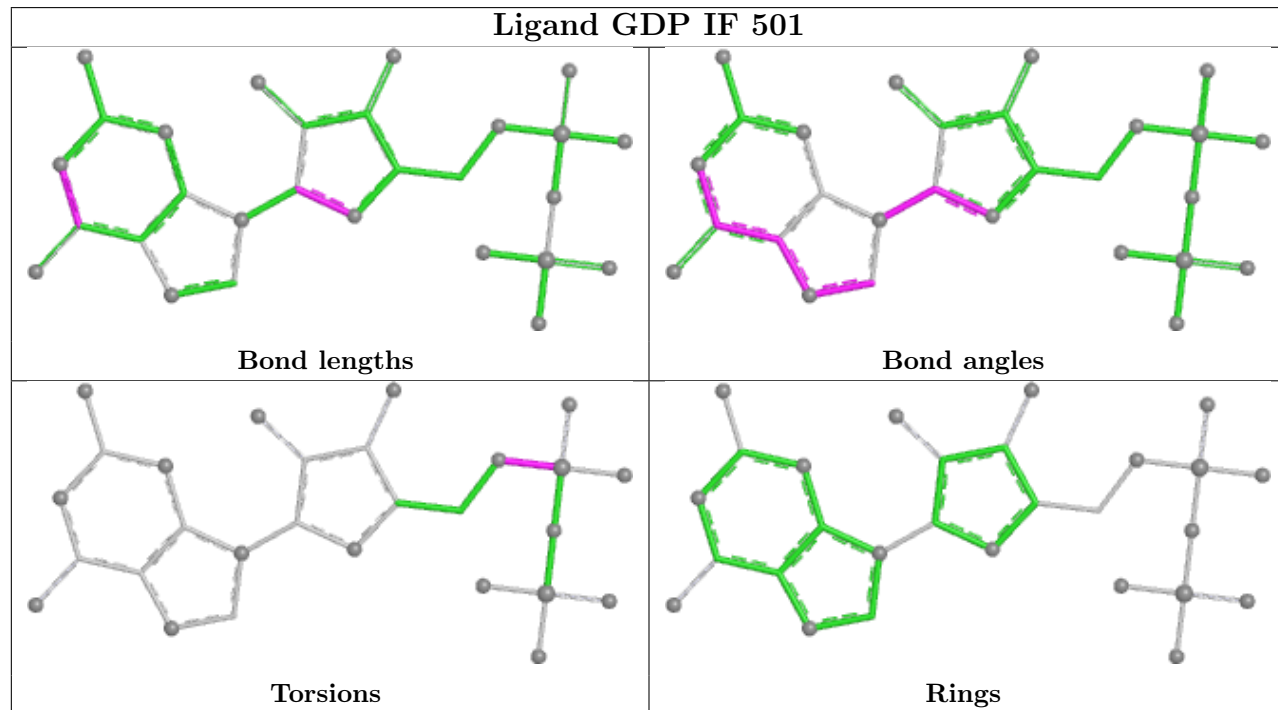
## Ligand GDP YF 501

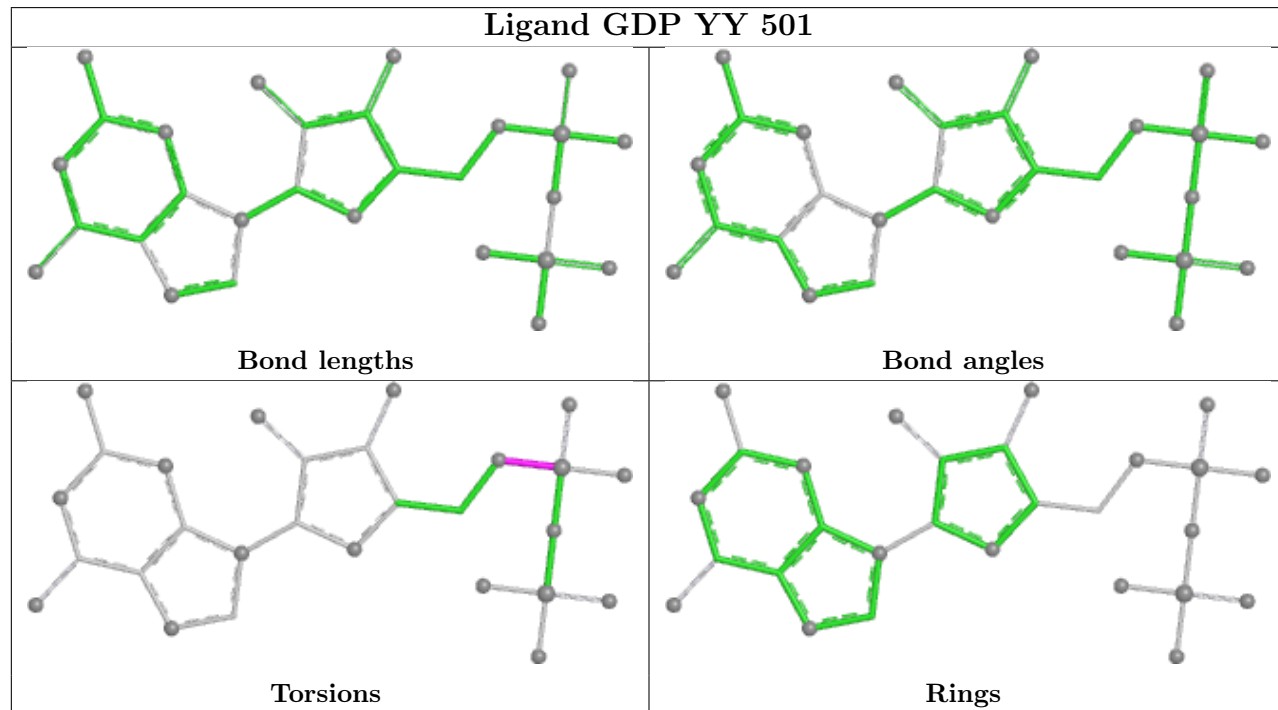
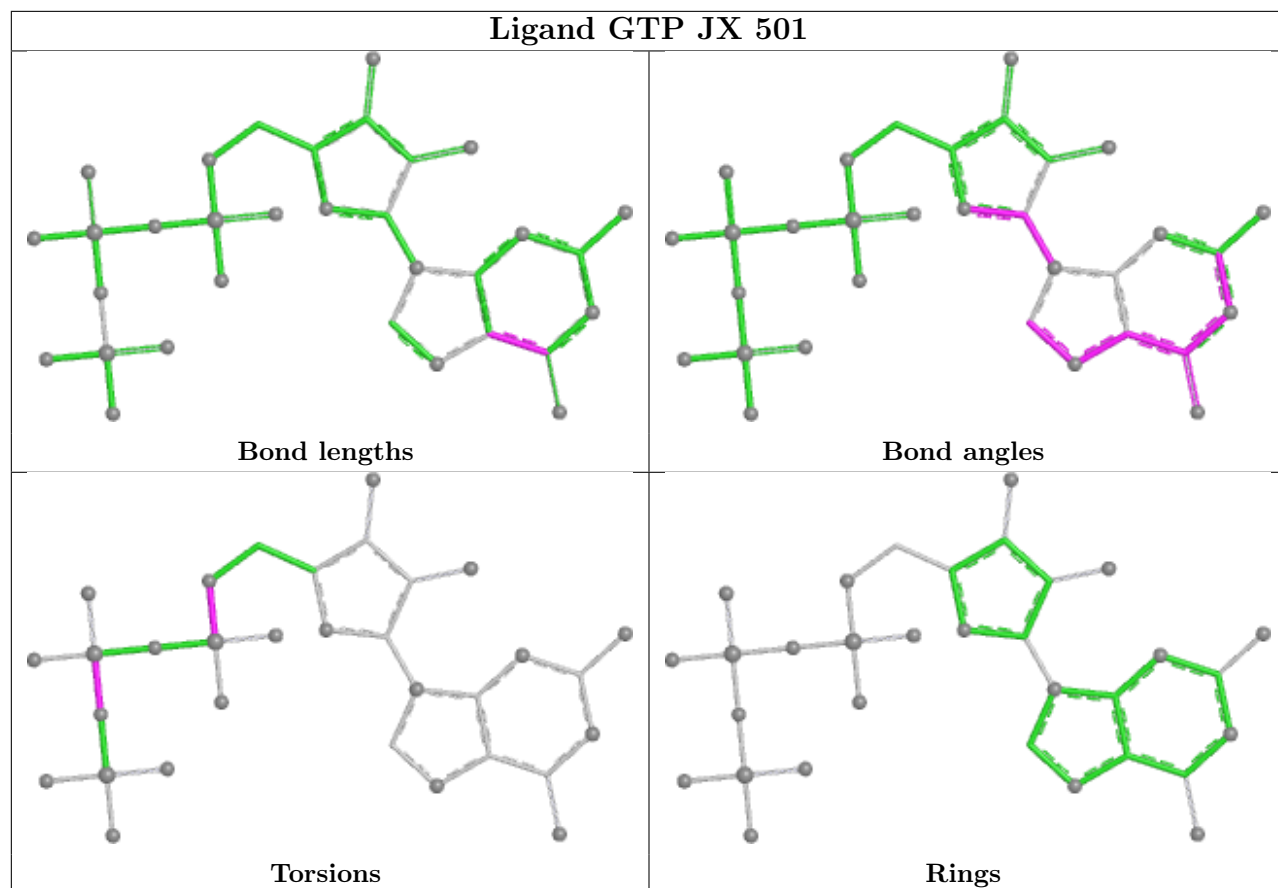


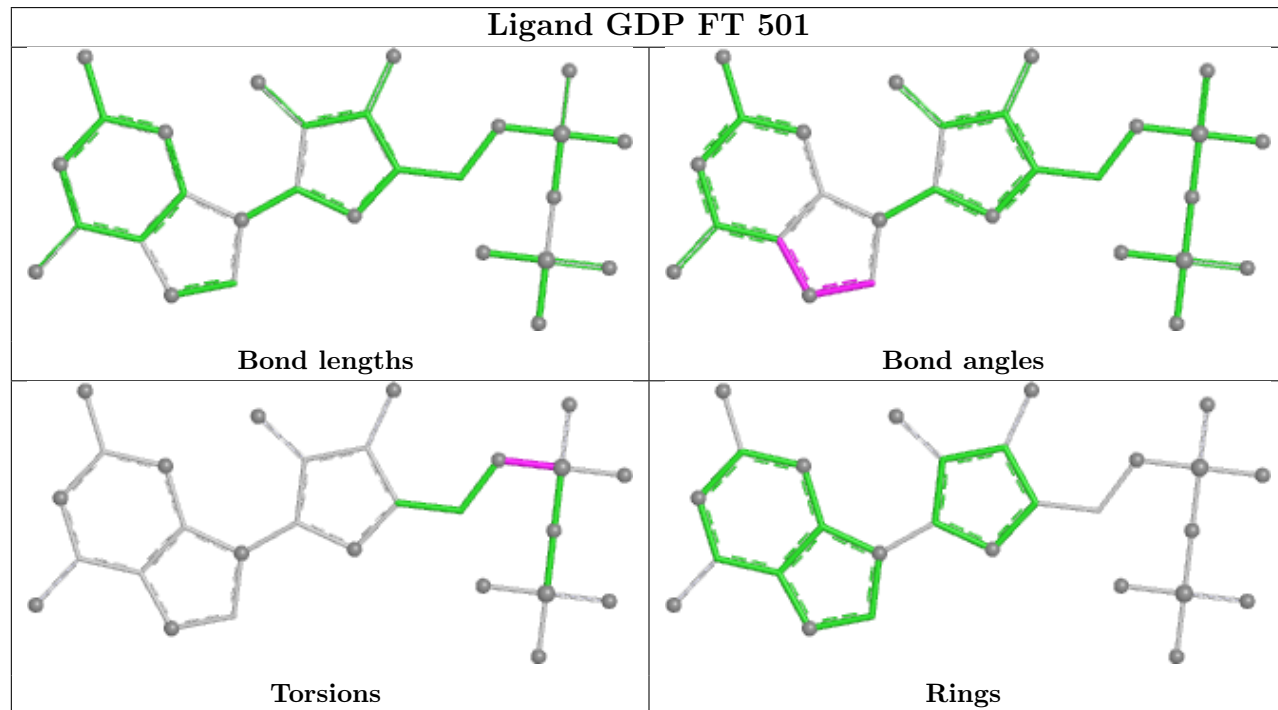
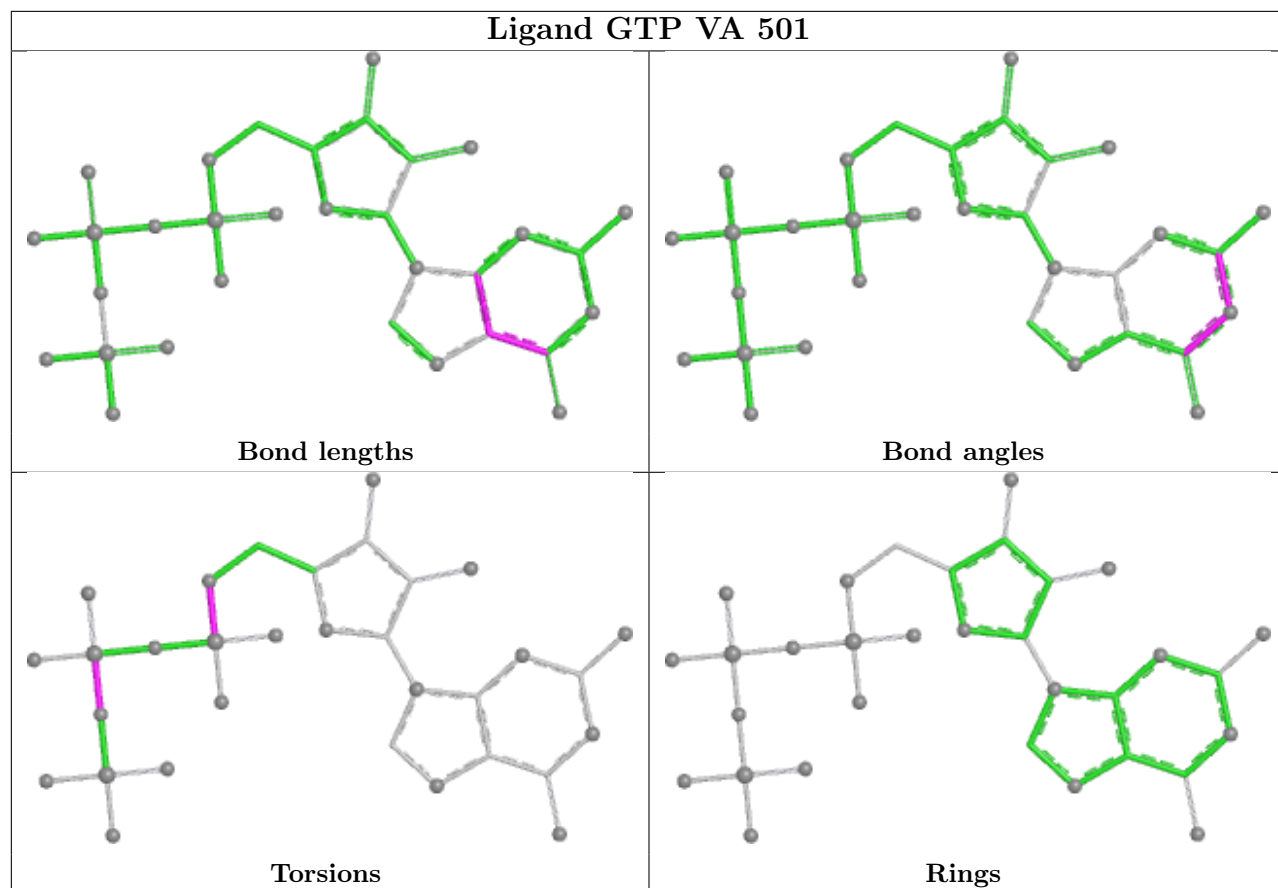
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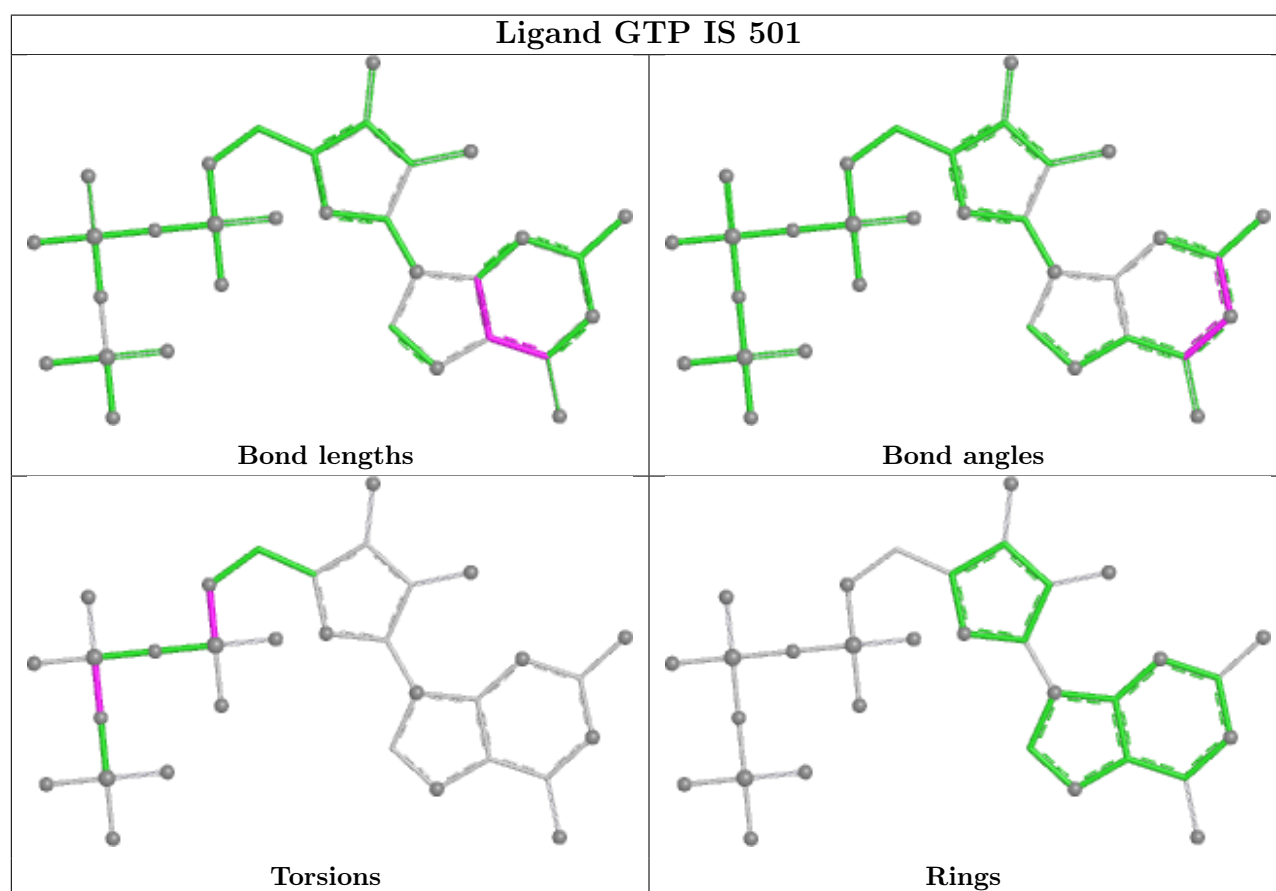
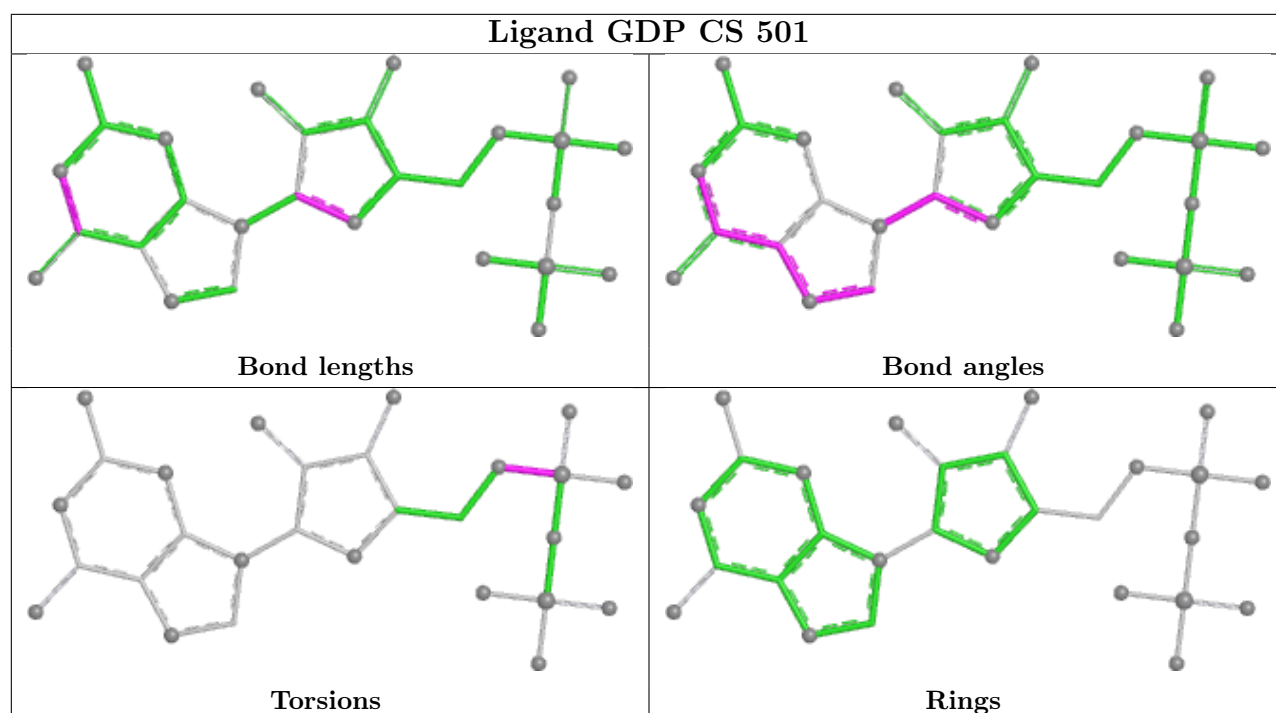


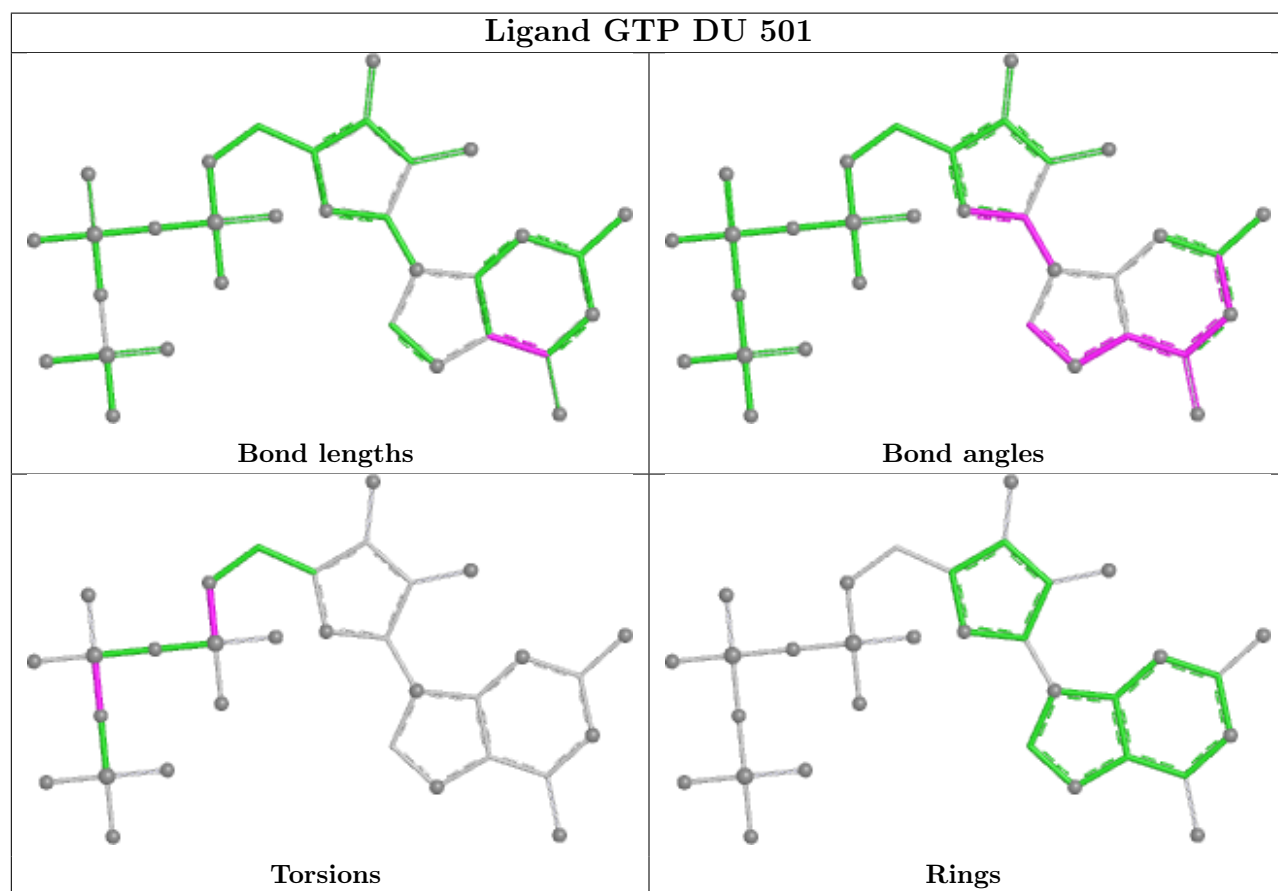
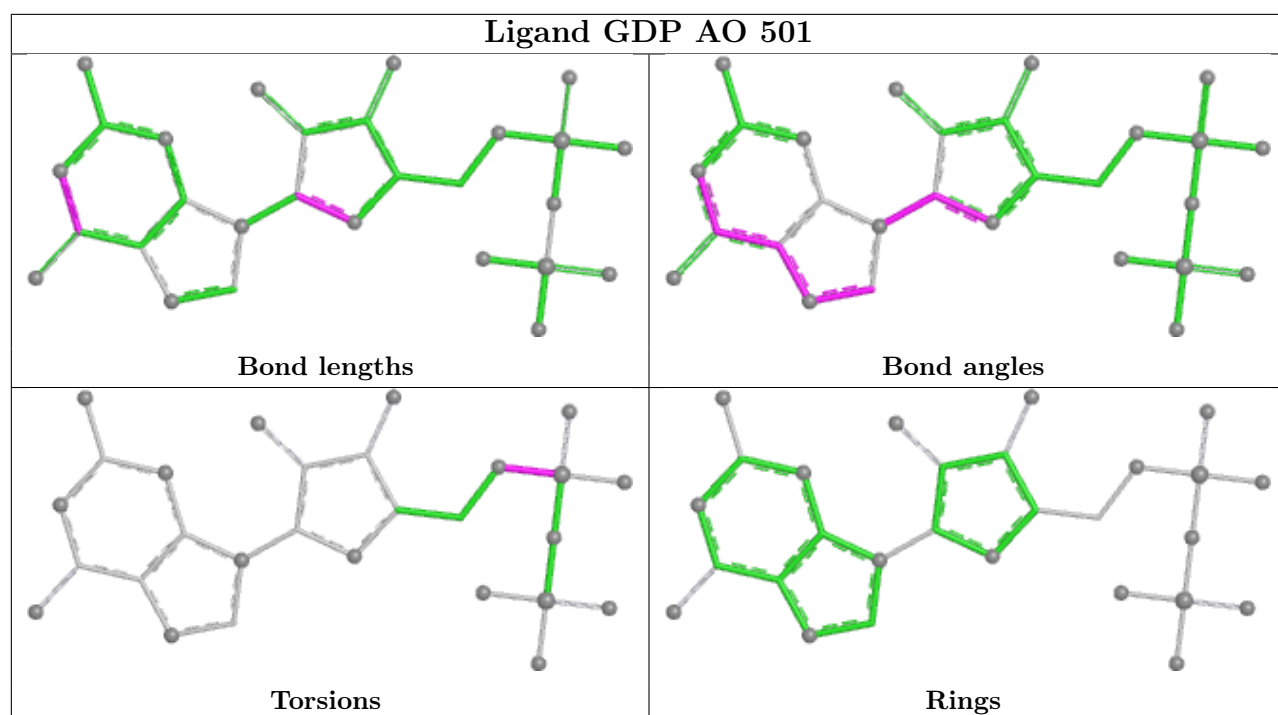
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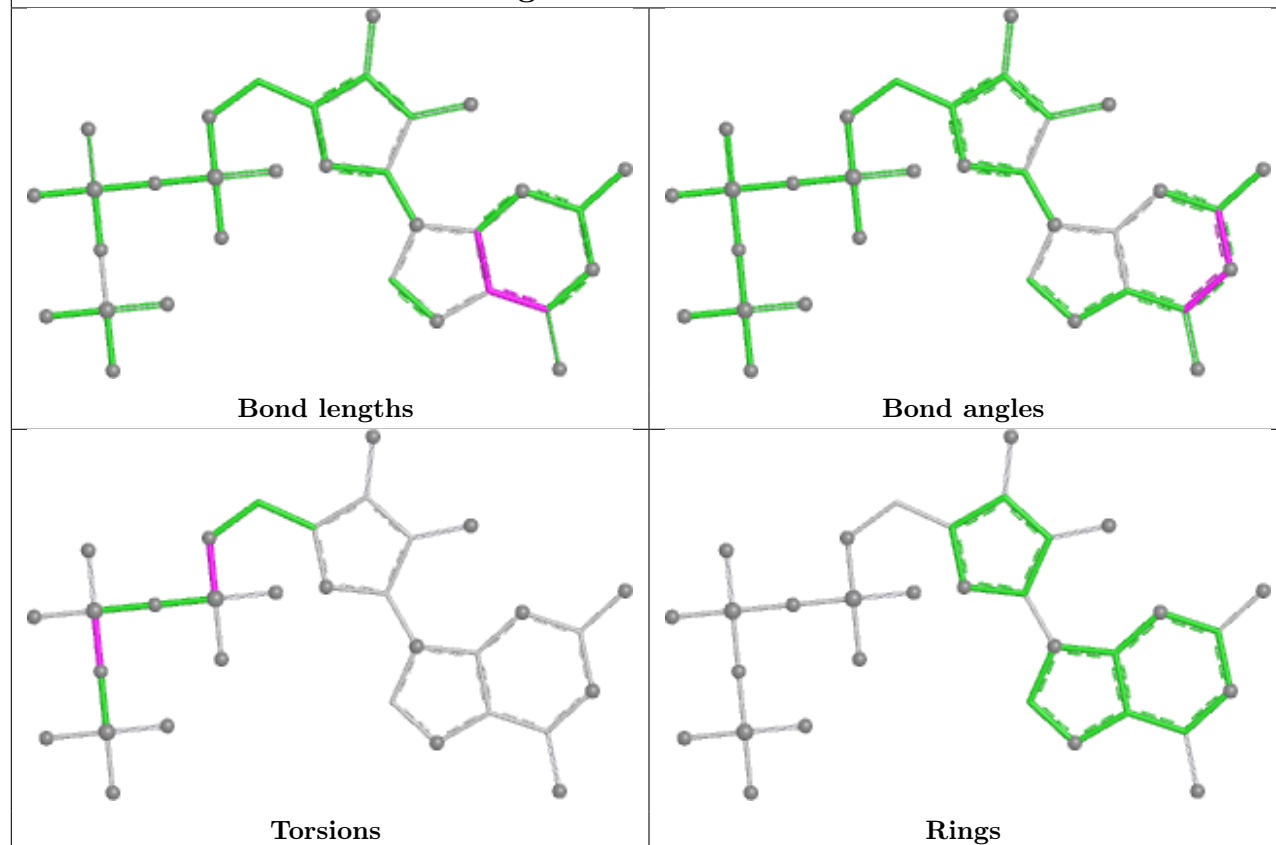




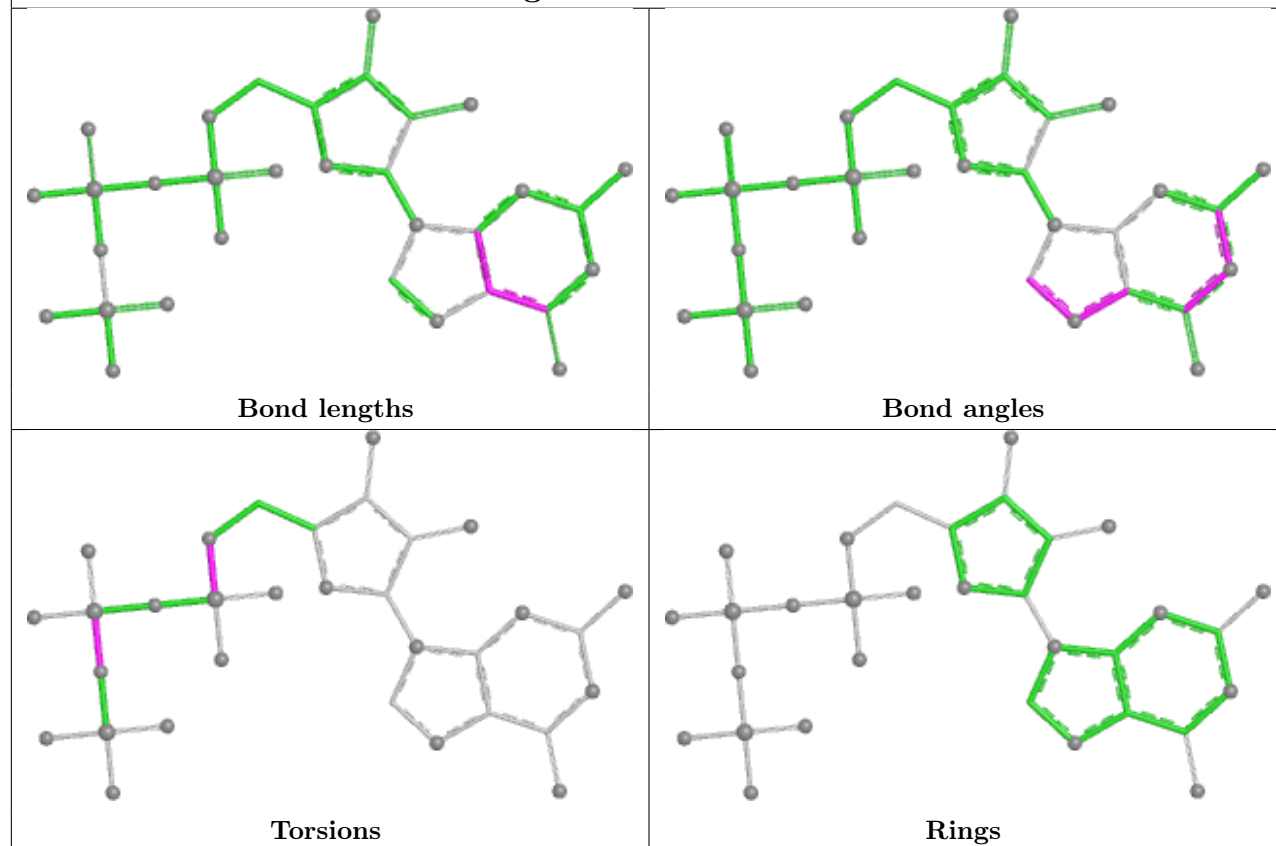


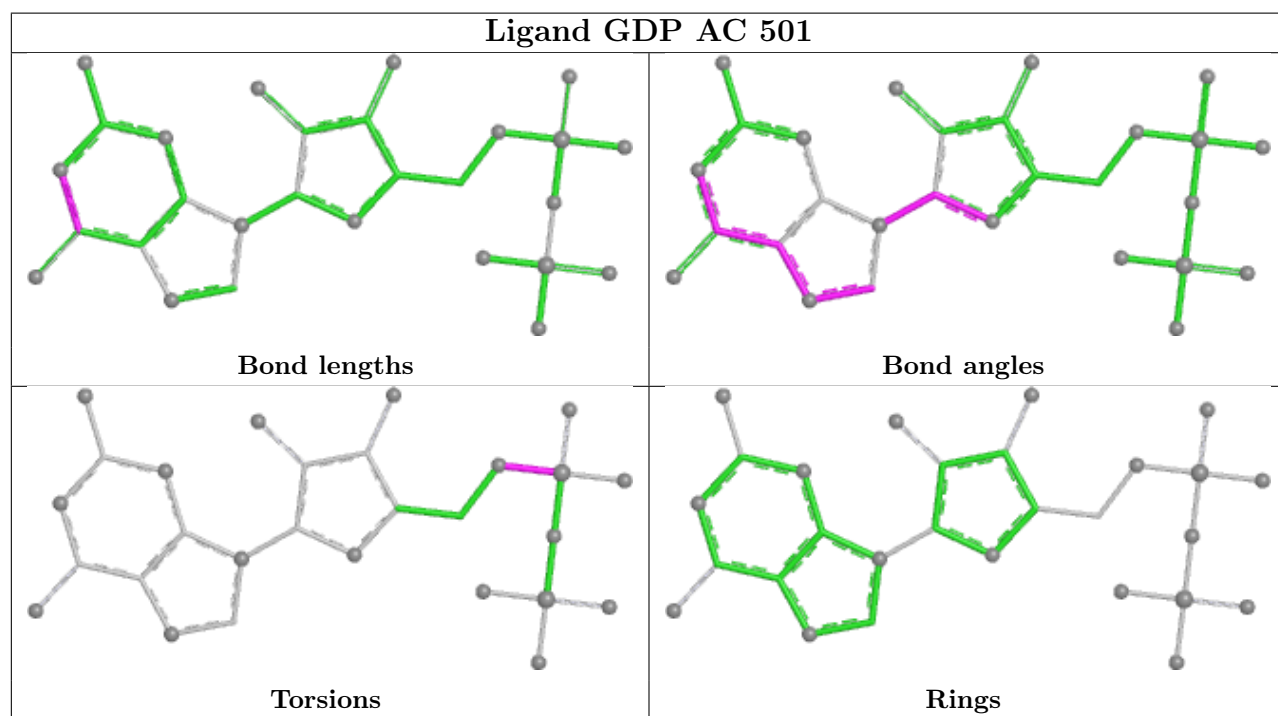
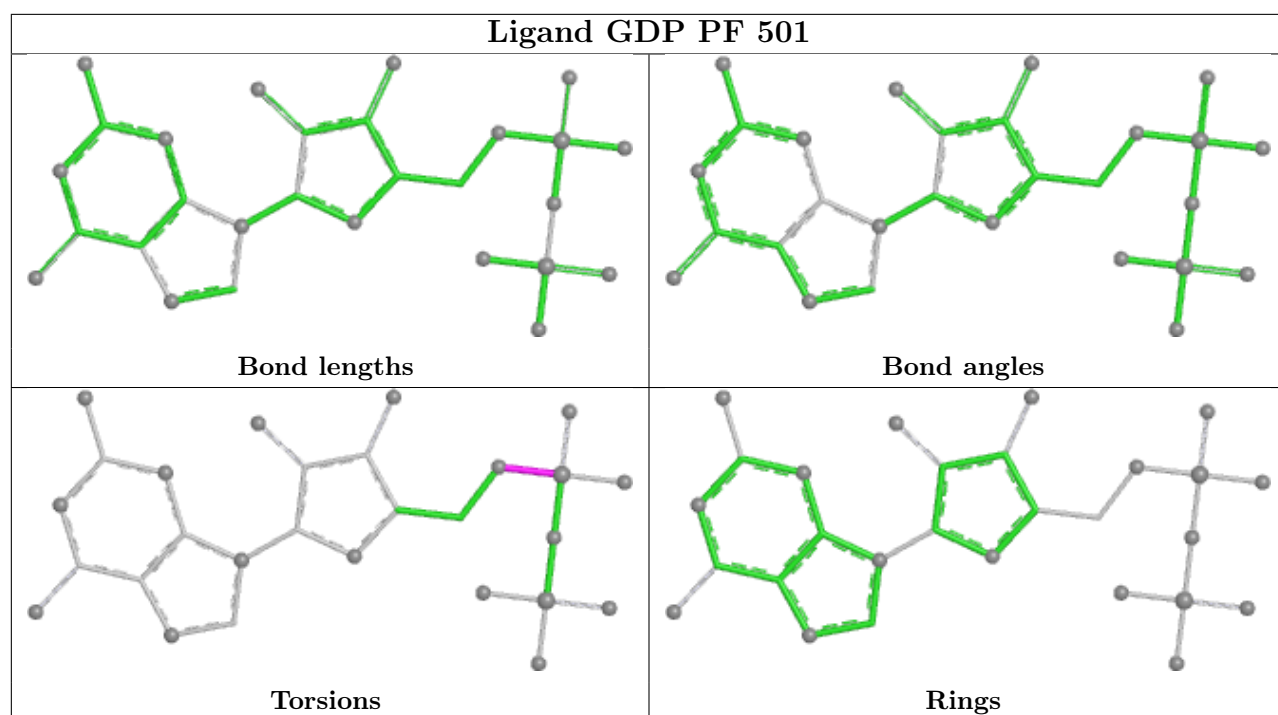


## Ligand GTP EK 602



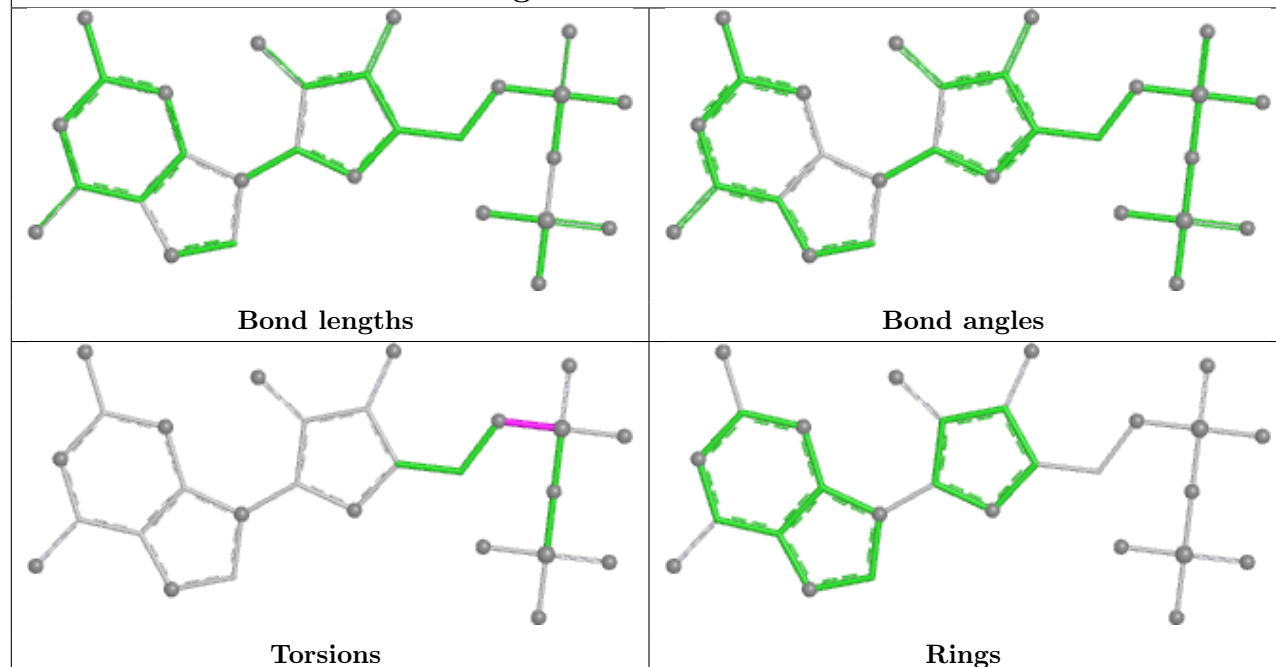
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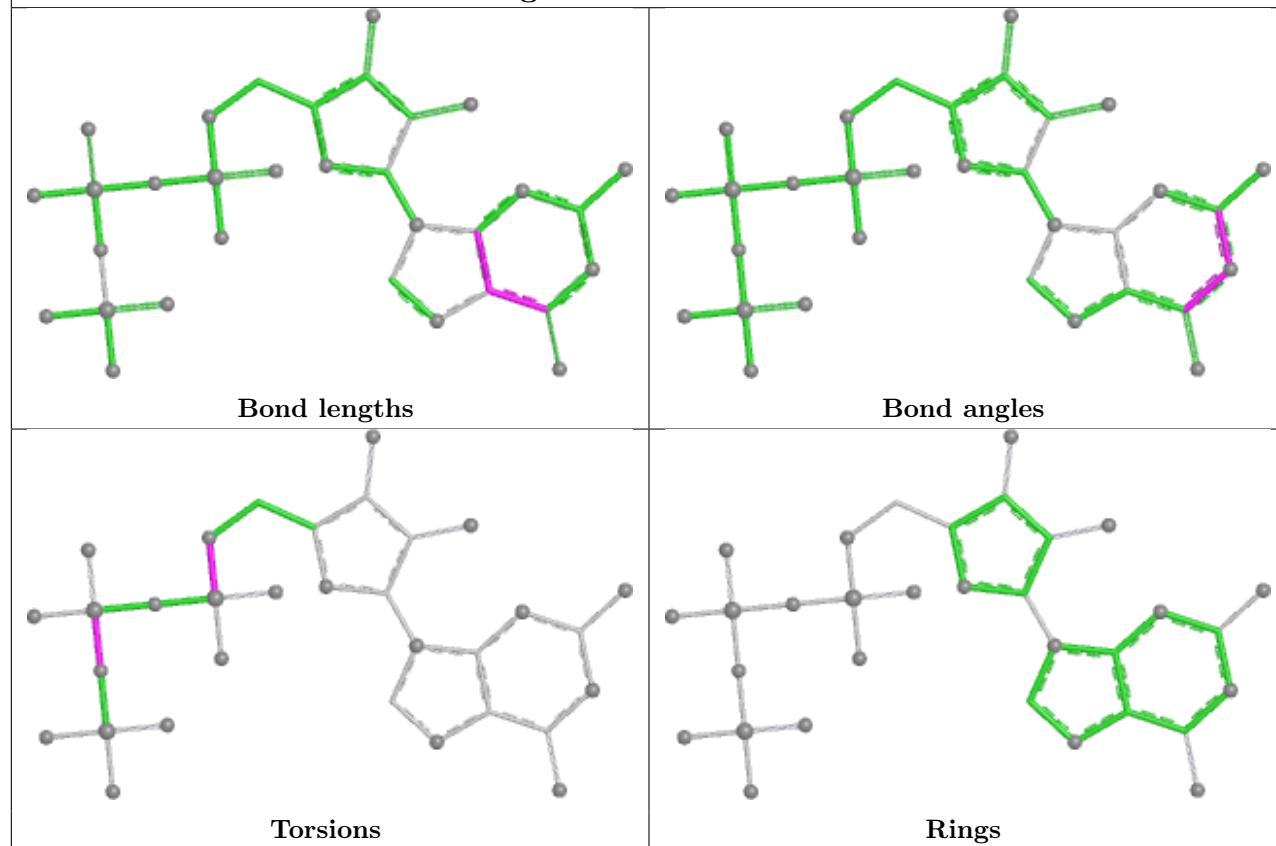




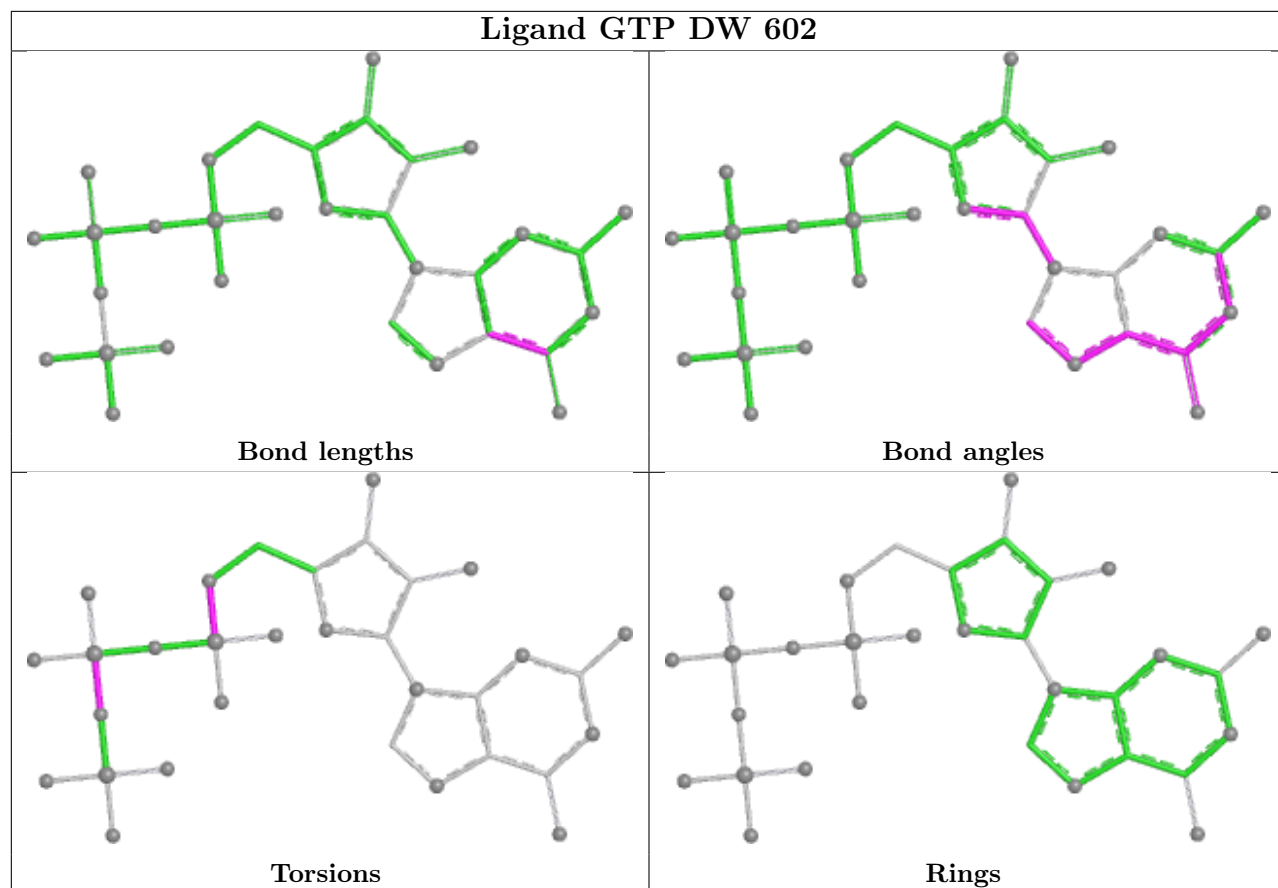
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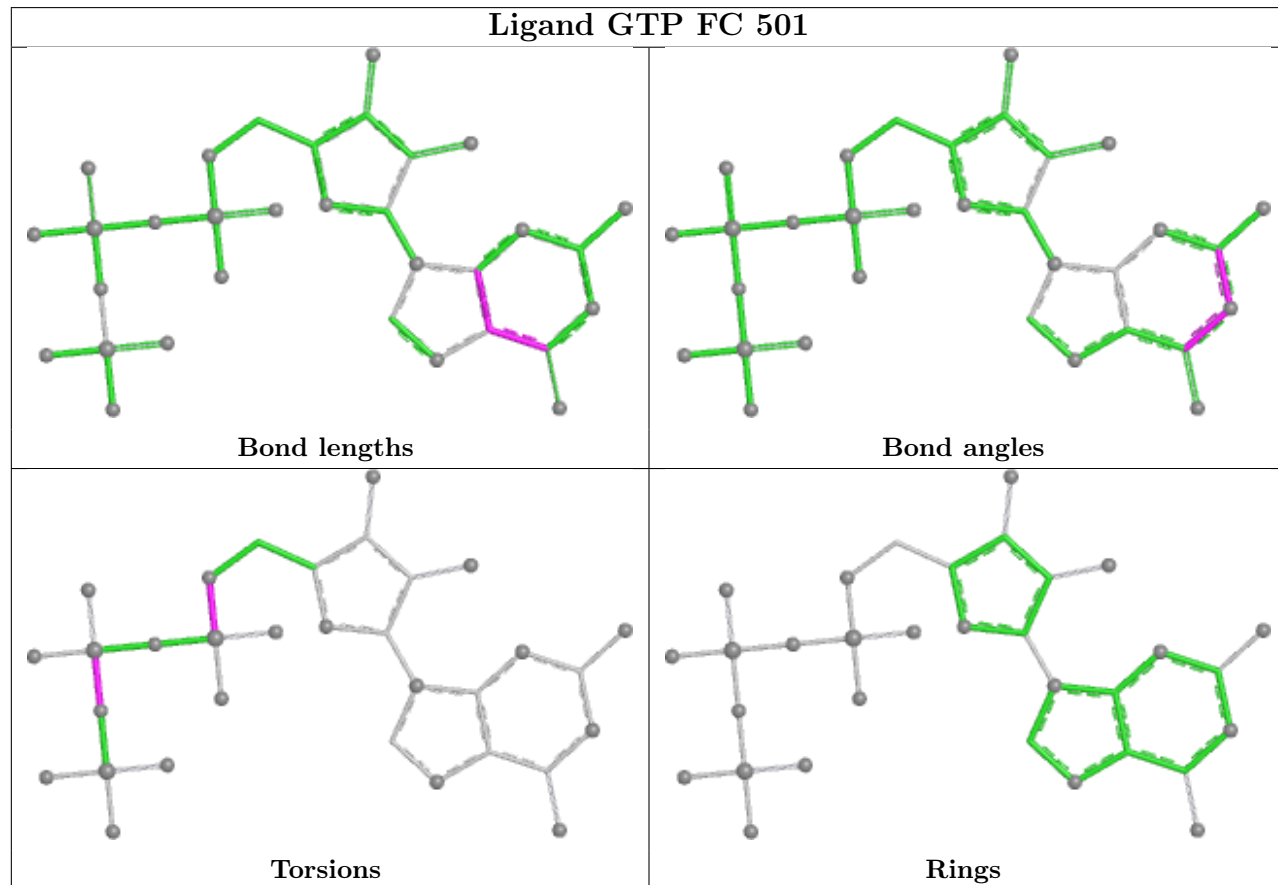
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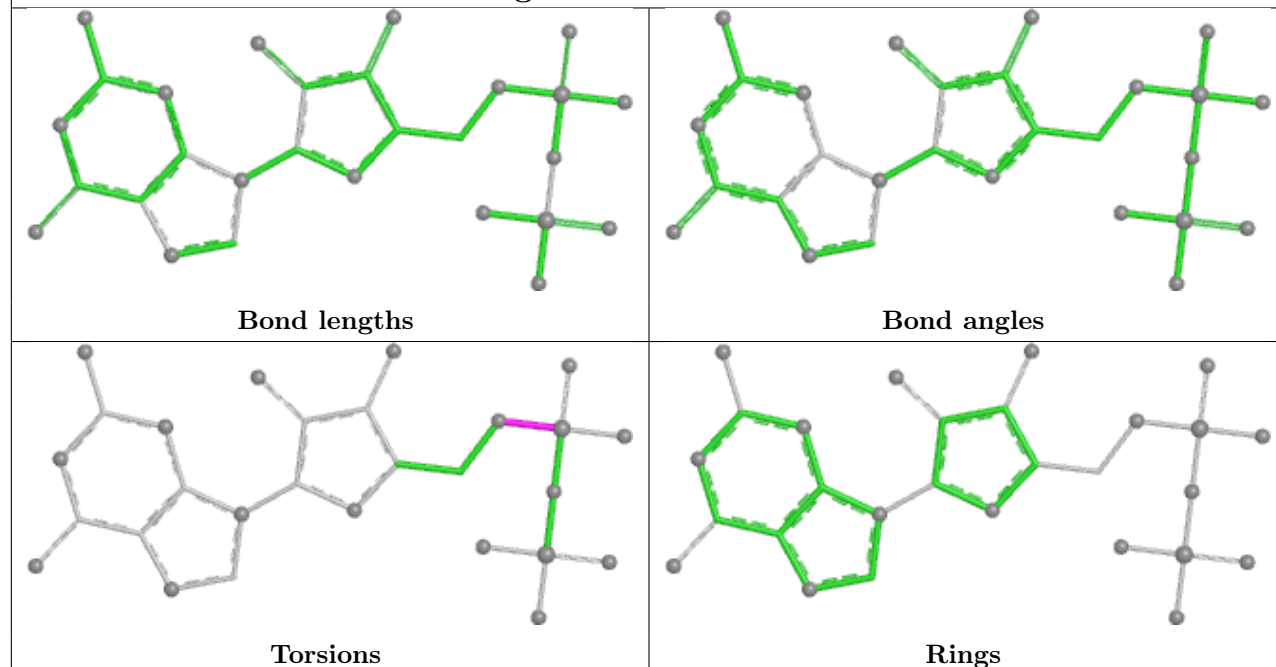
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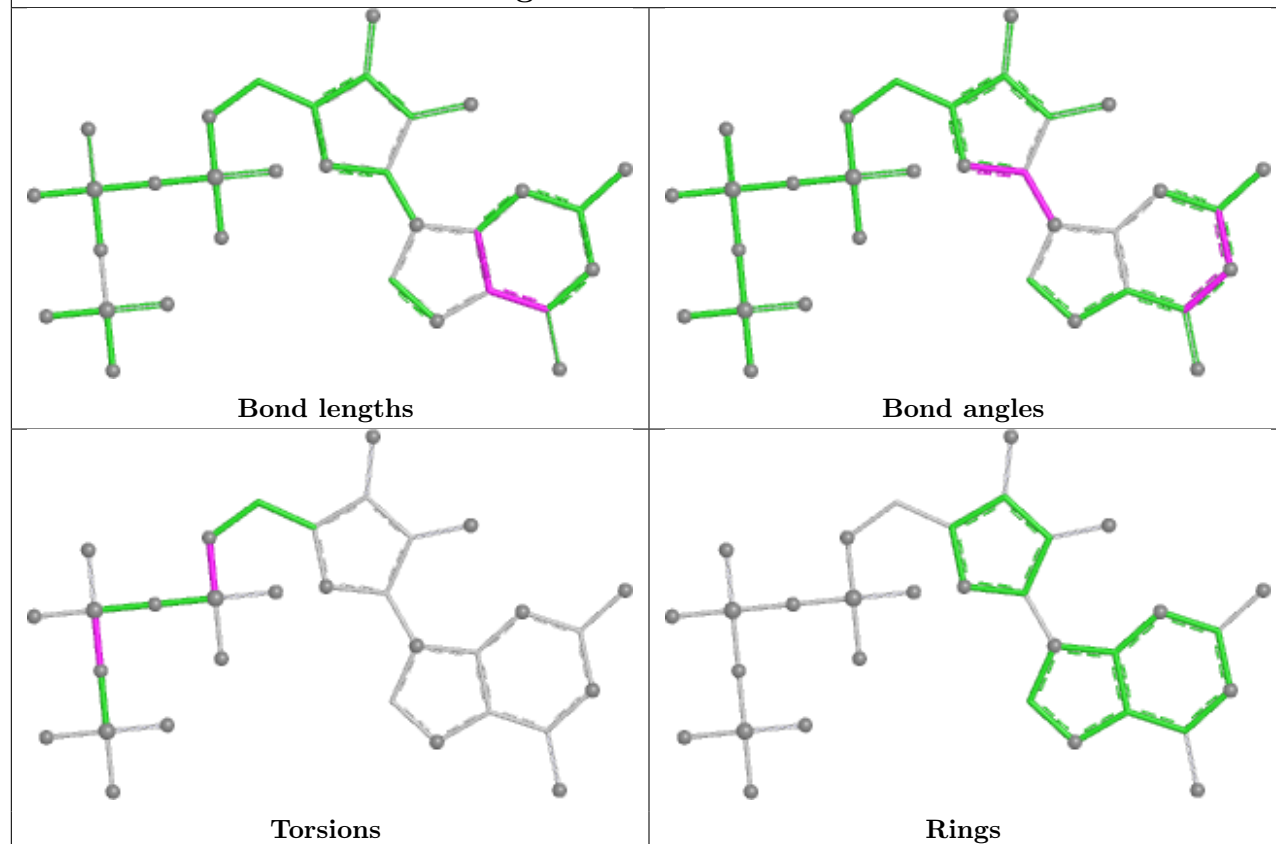
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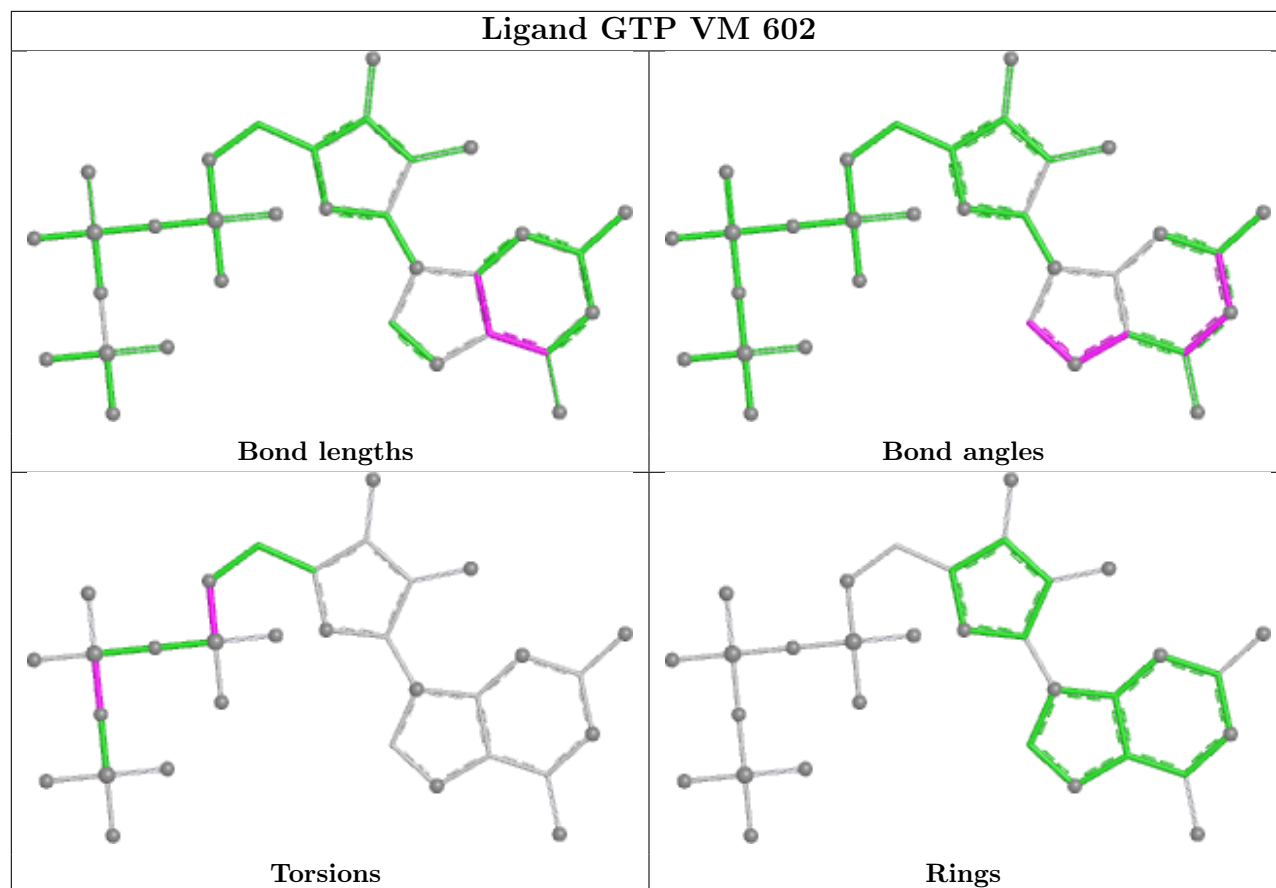
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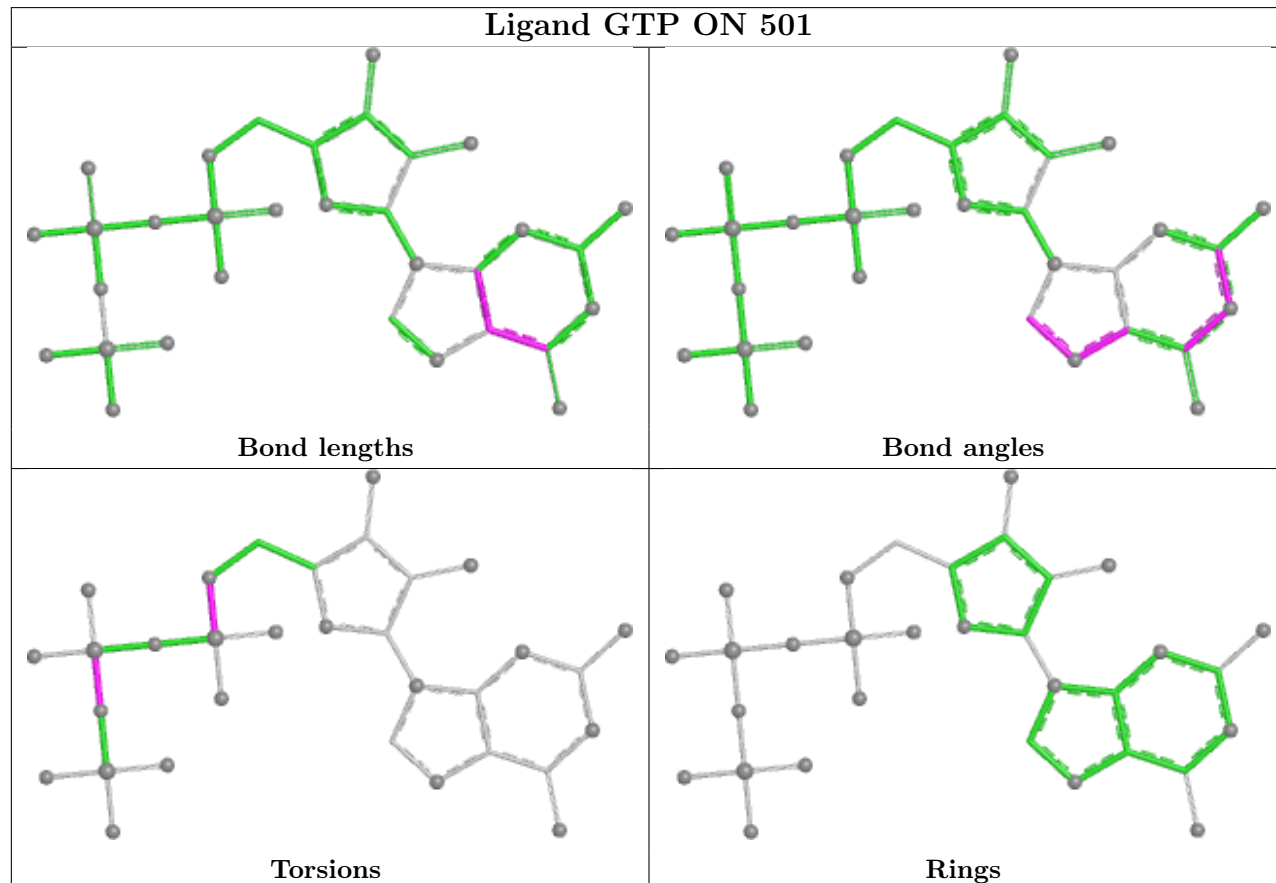
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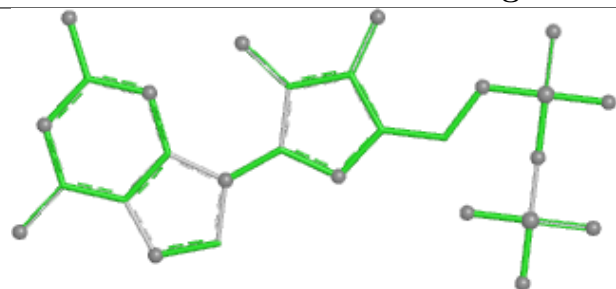
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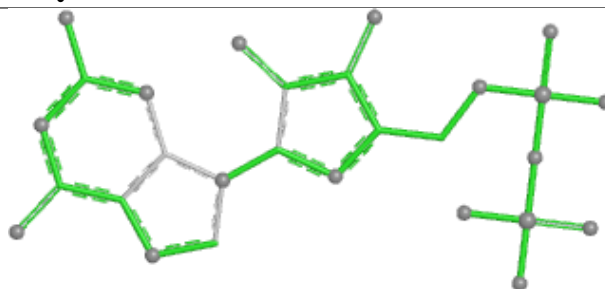
## Ligand GTP ON 501



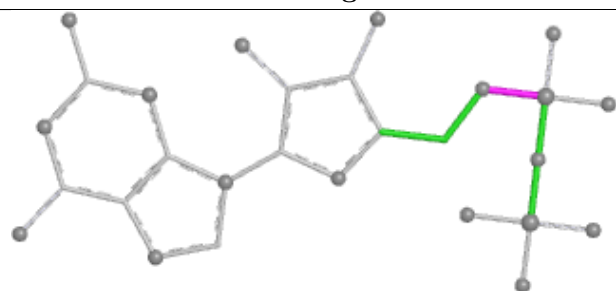
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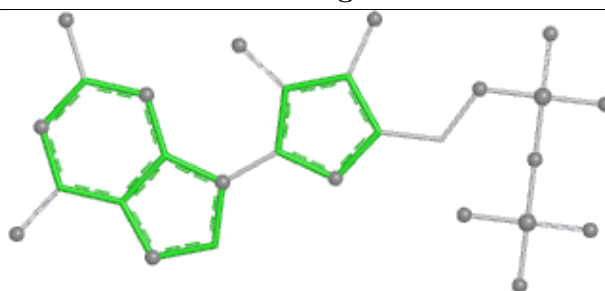
Bond lengths



Bond angles

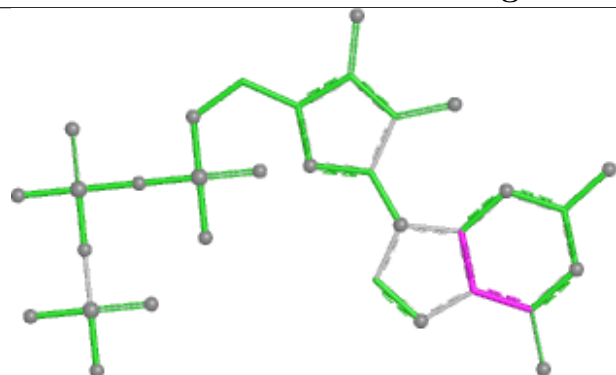


Torsions

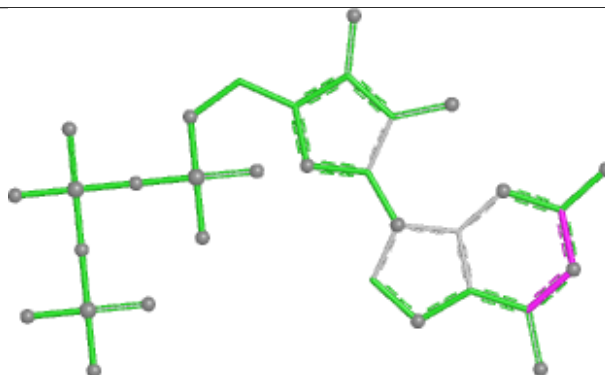


Rings

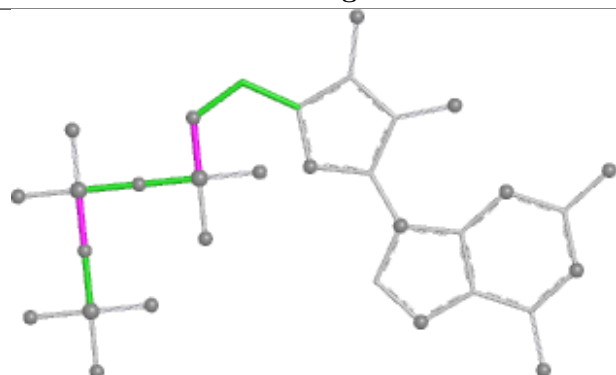
## Ligand GTP PG 501



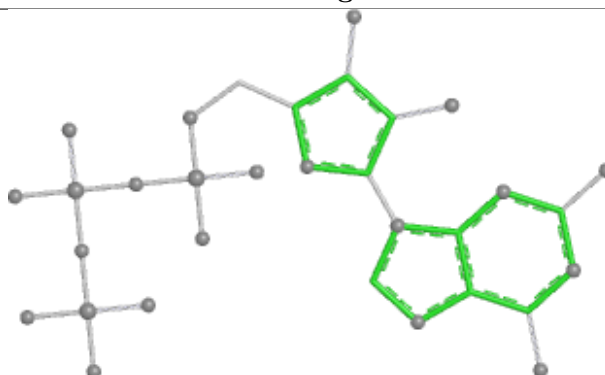
Bond lengths



Bond angles

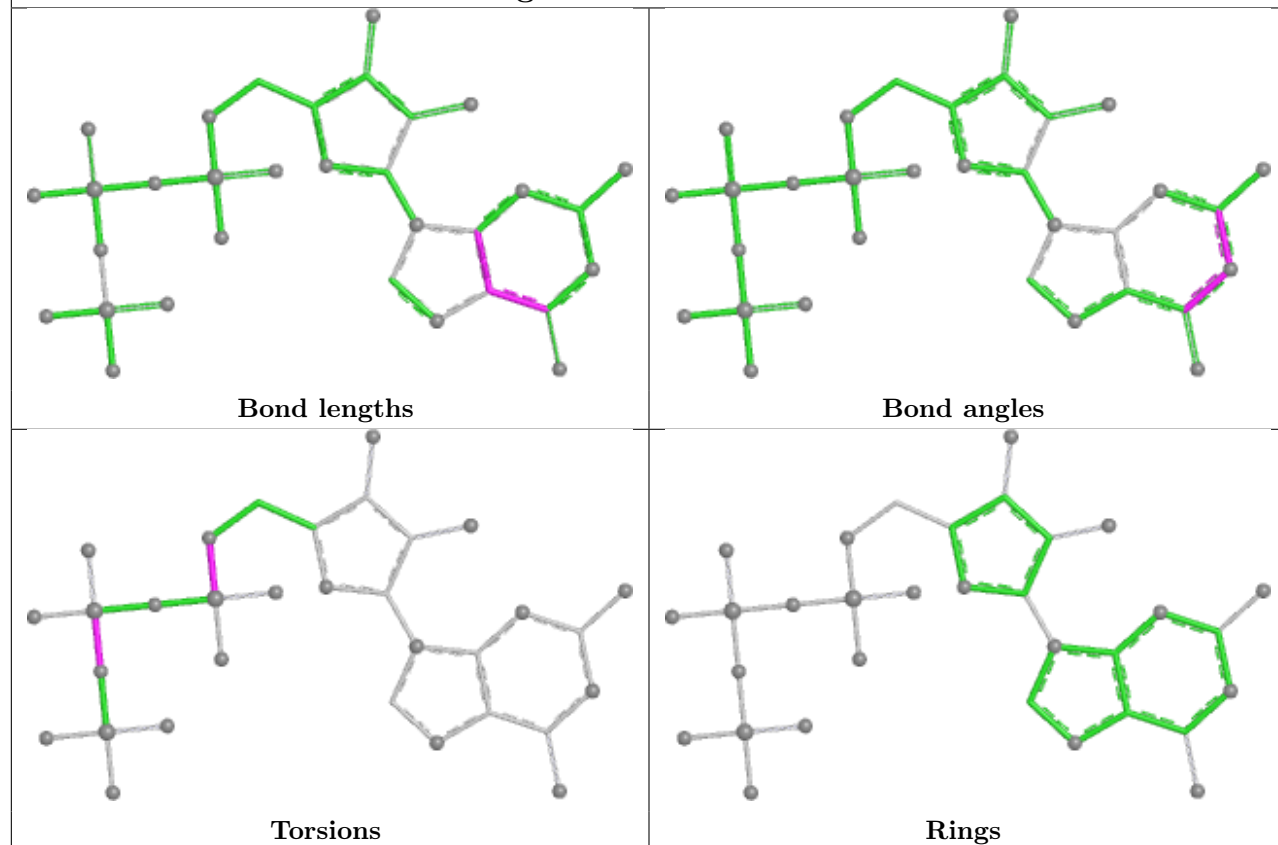


Torsions

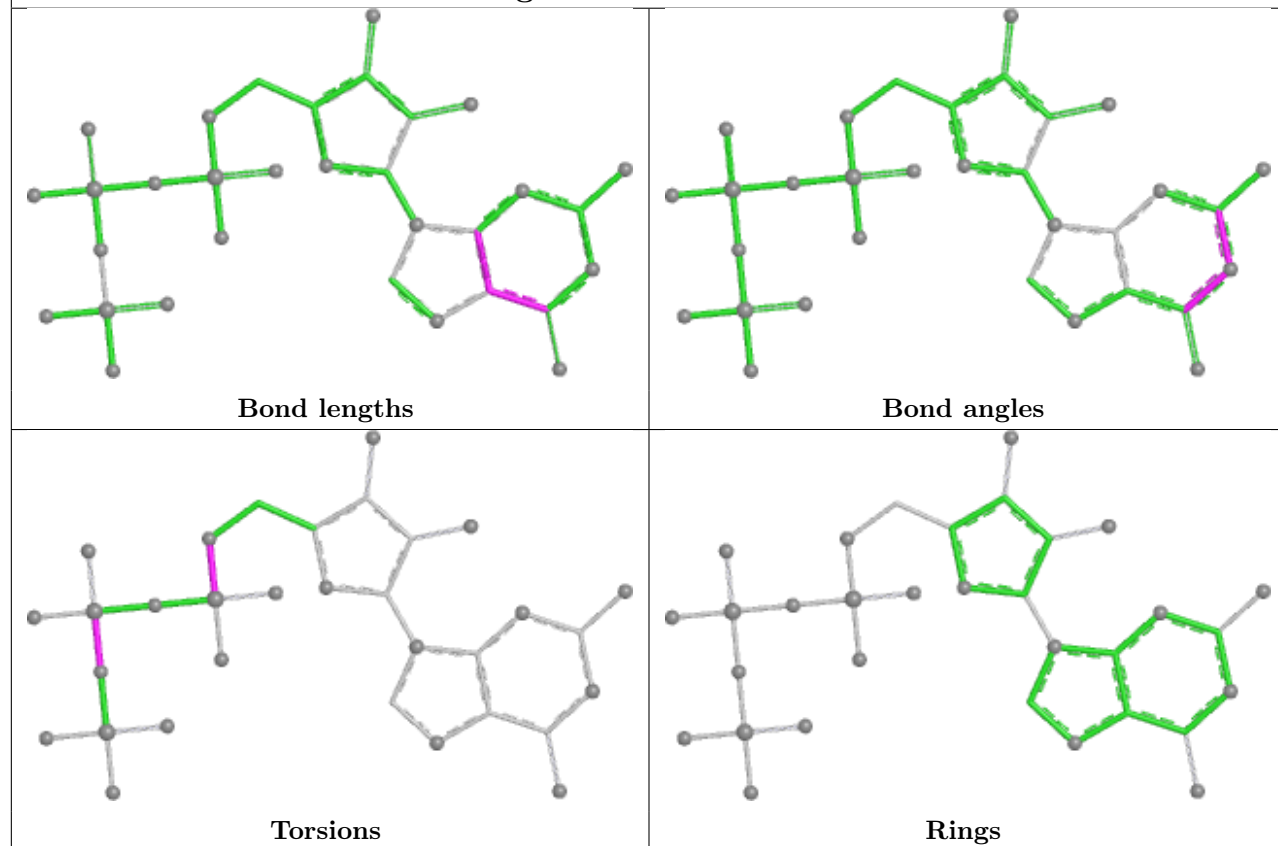


Rings

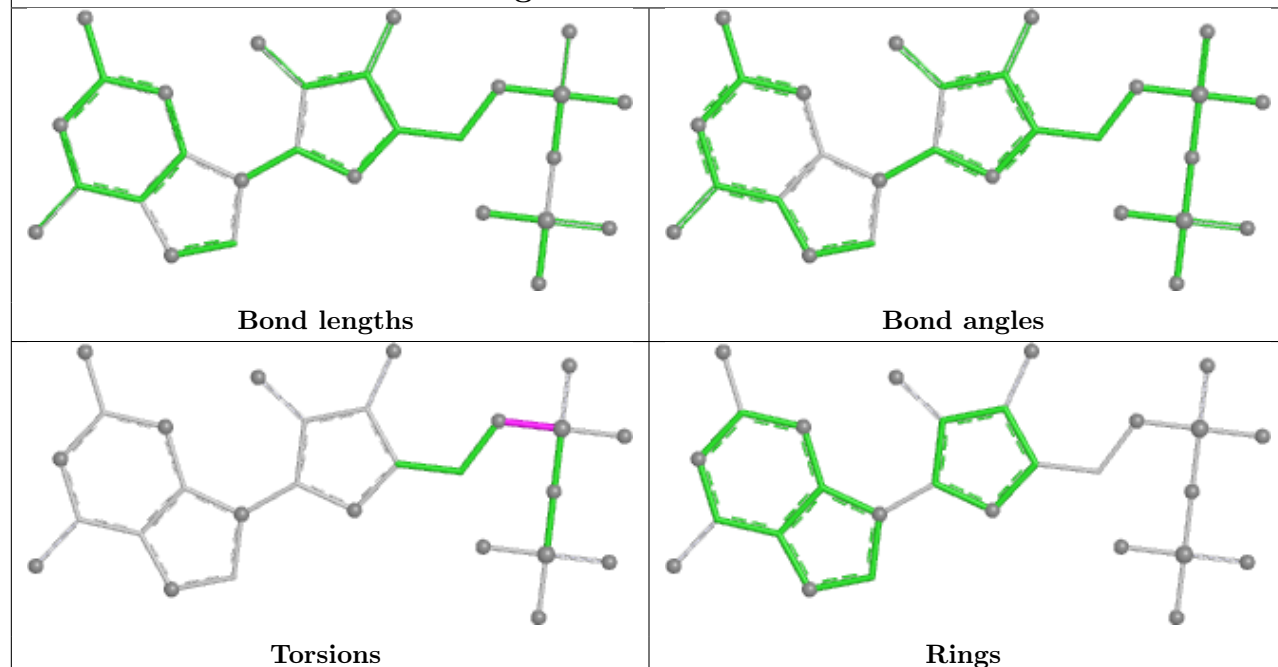
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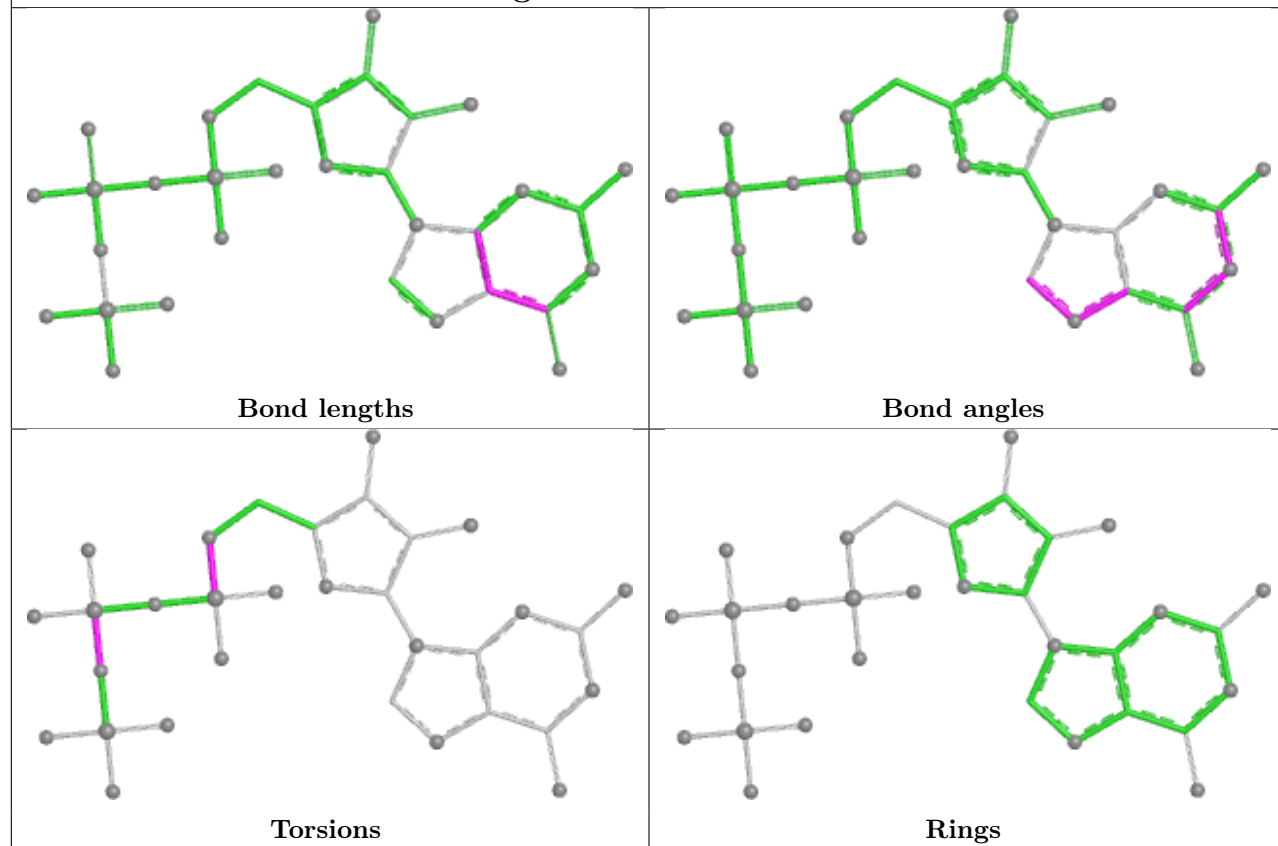
## Ligand GTP KD 501



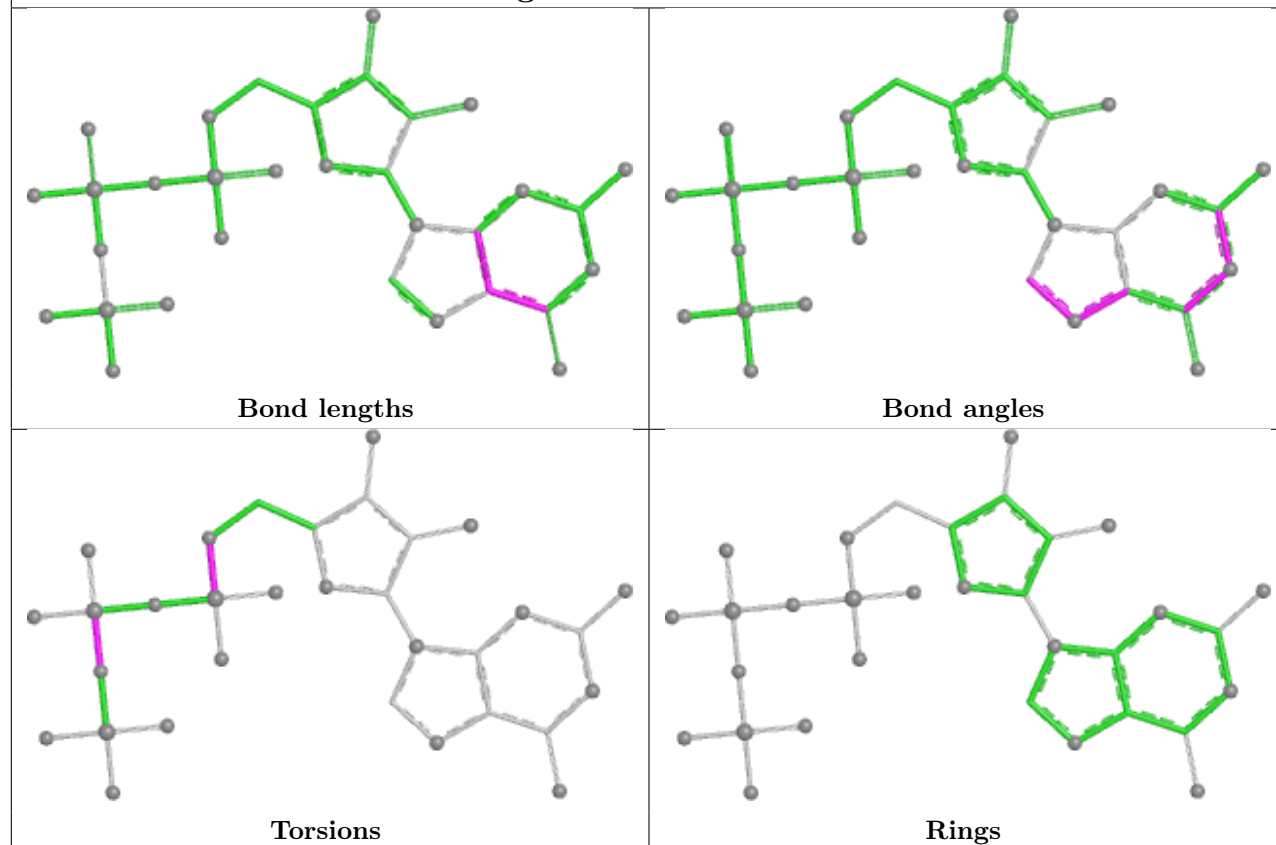
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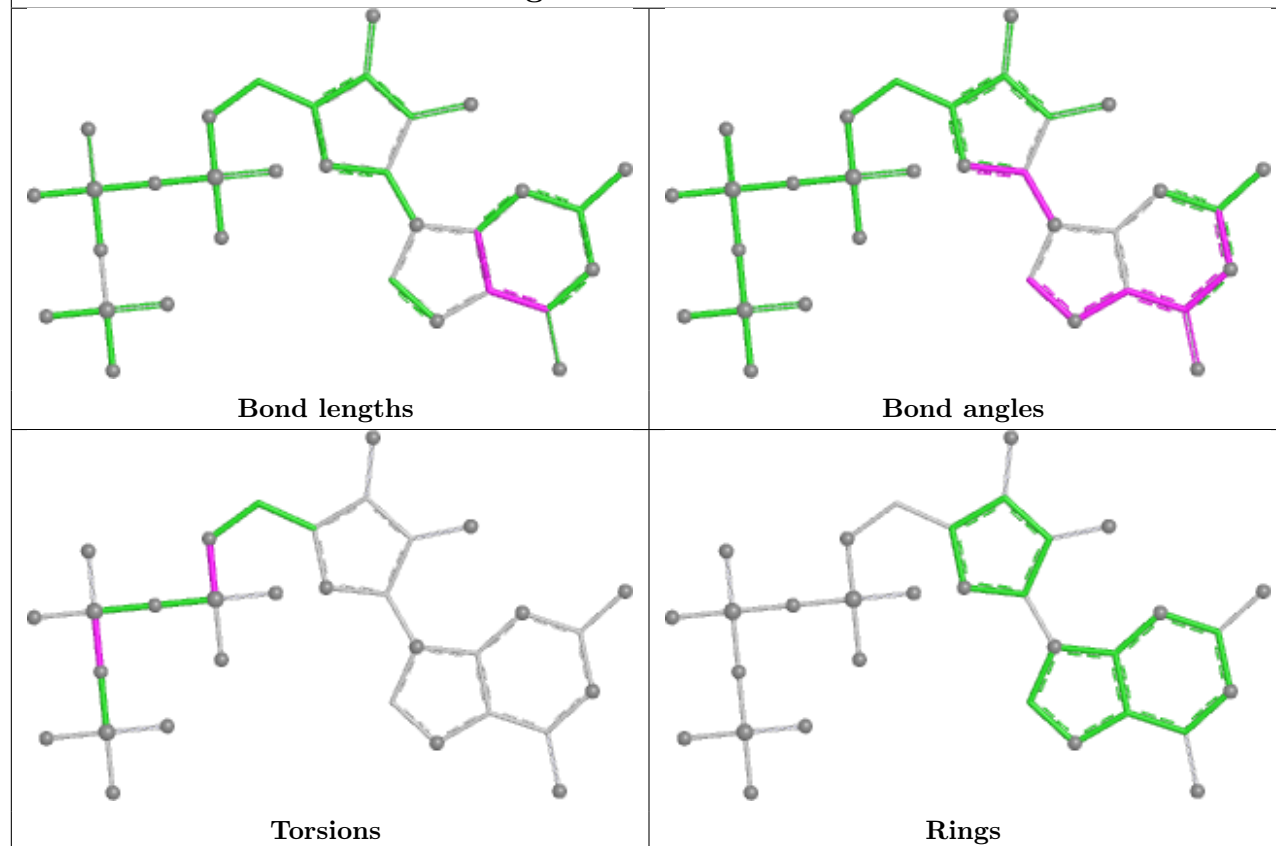
## Ligand GTP MR 602



## Ligand GTP TG 501

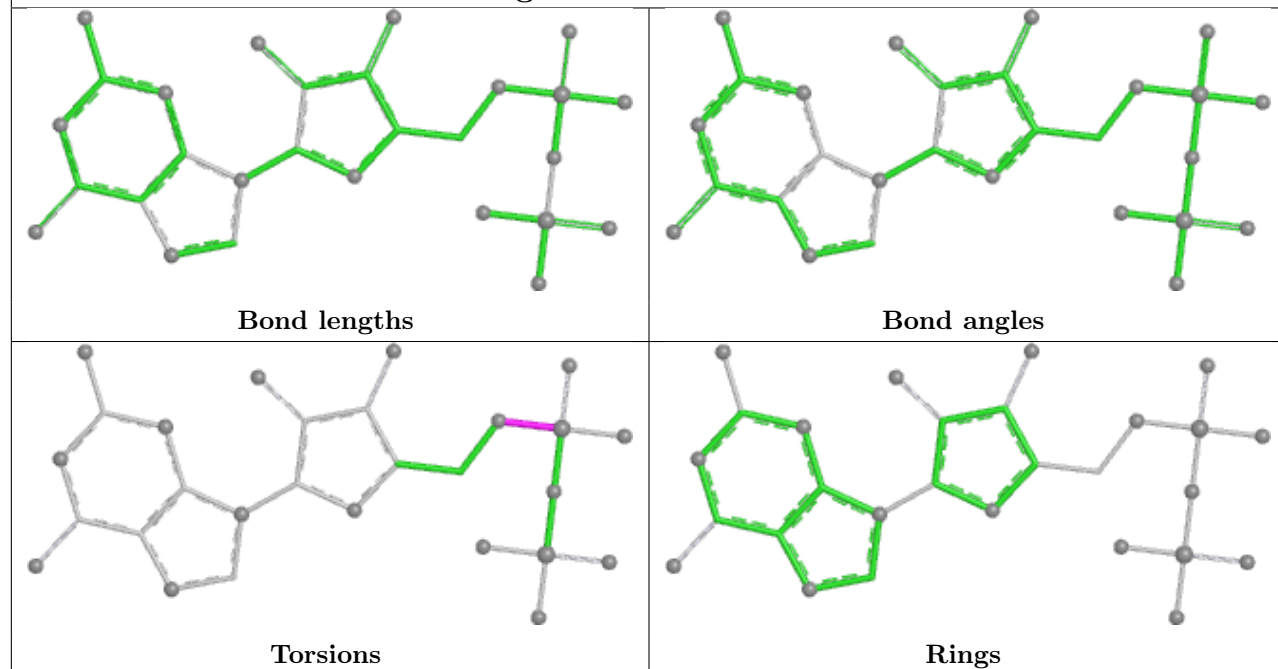


## Ligand GTP FI 602

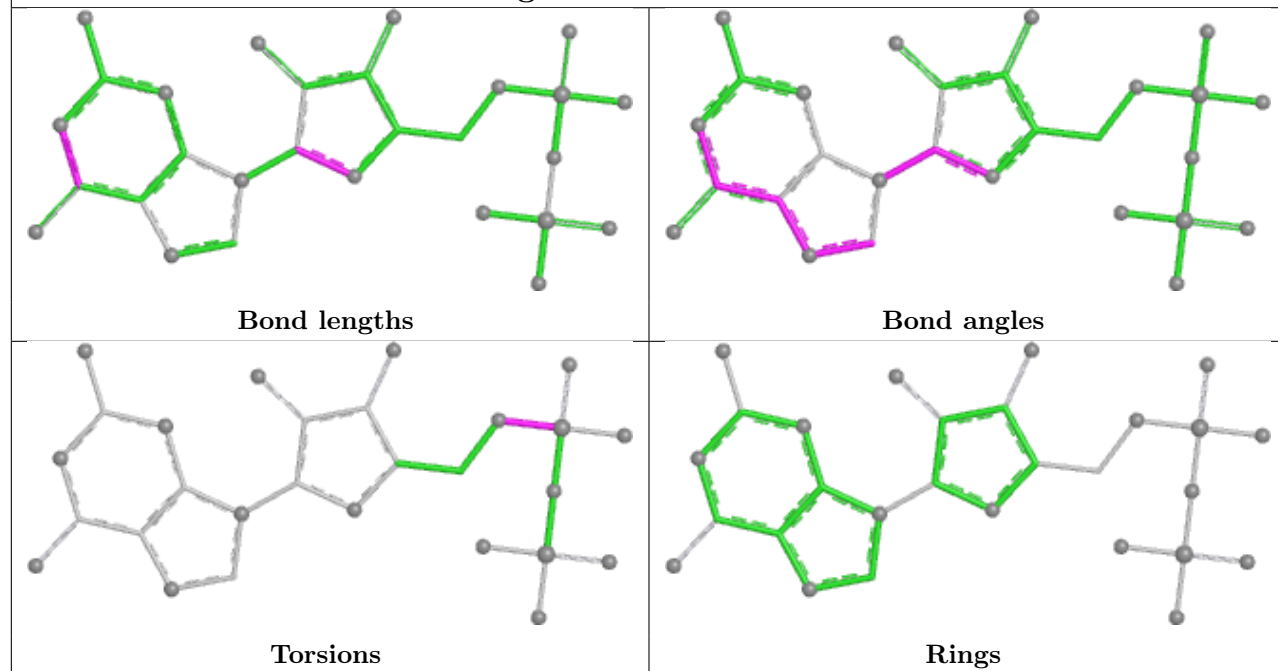


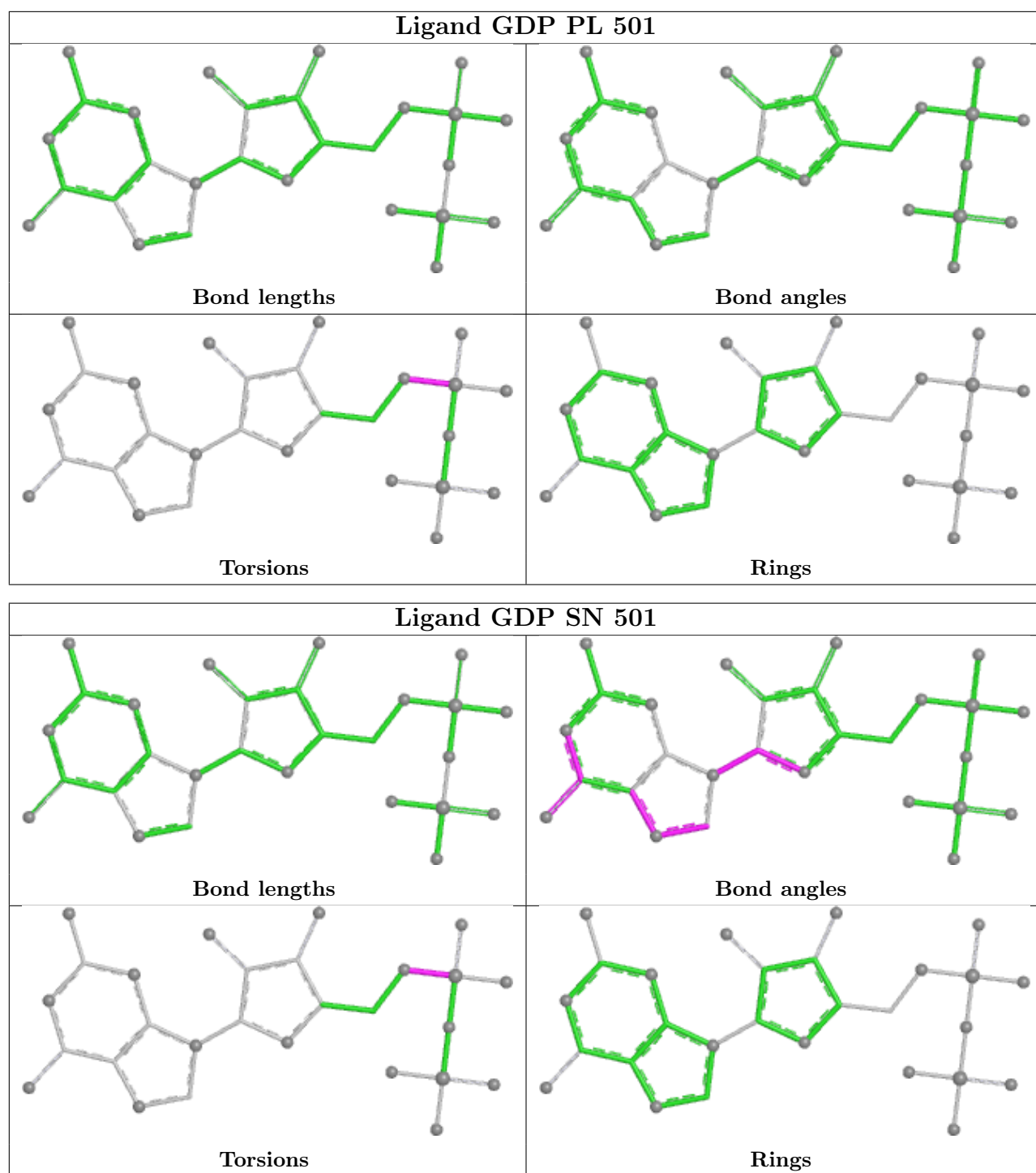


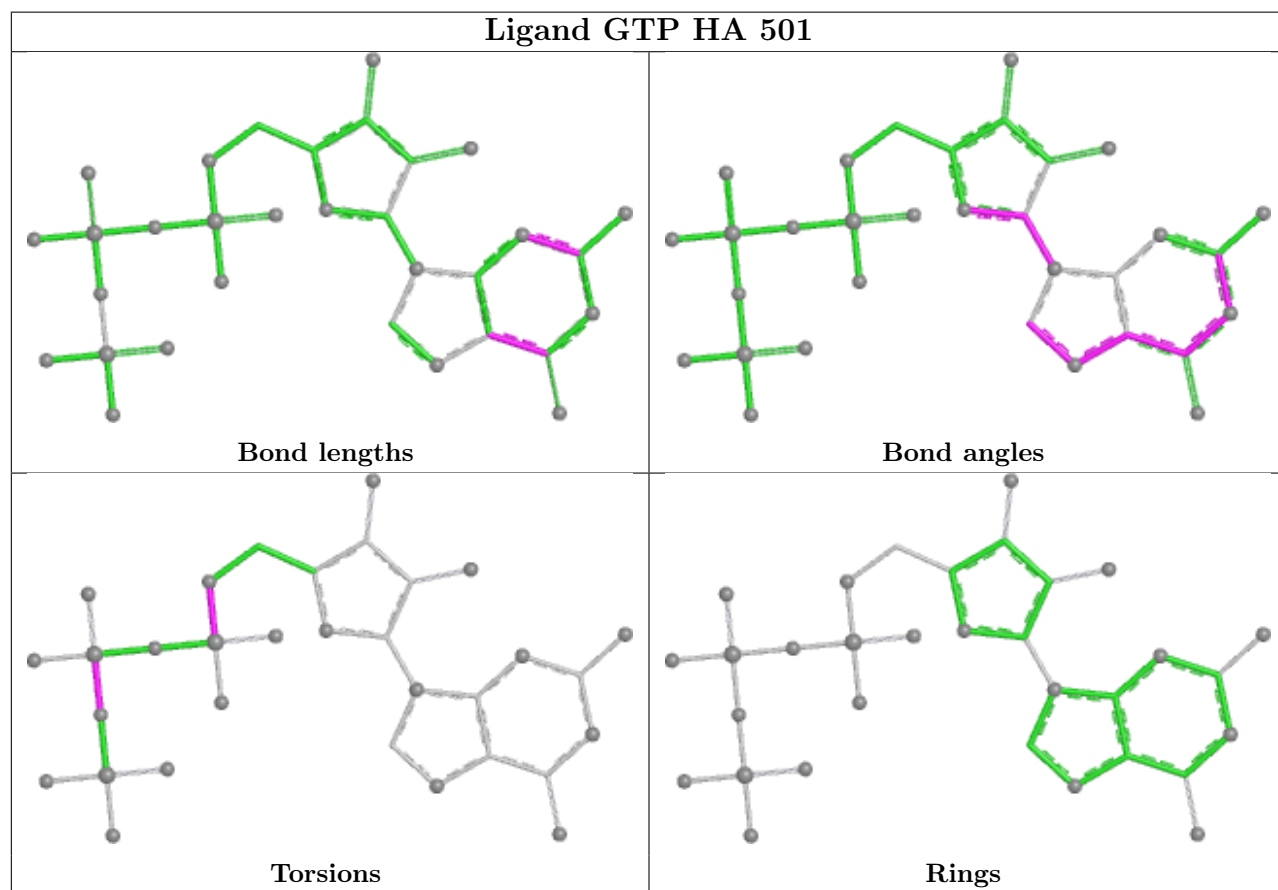
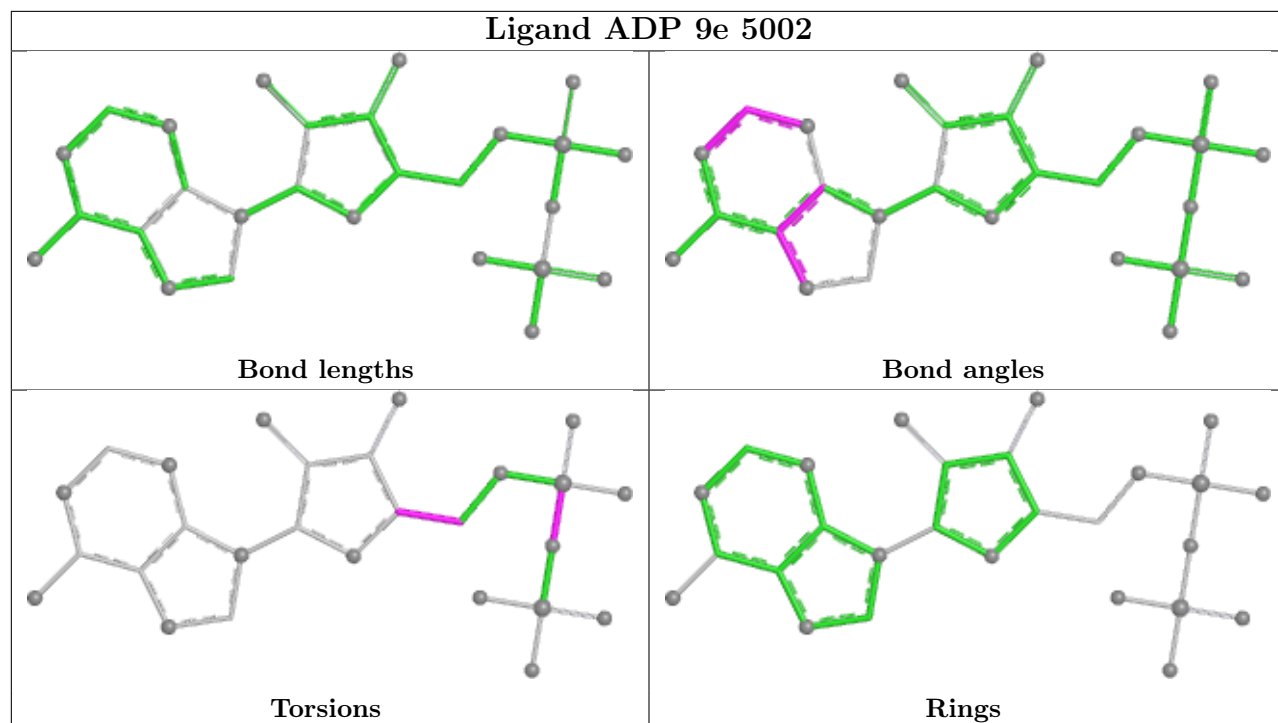
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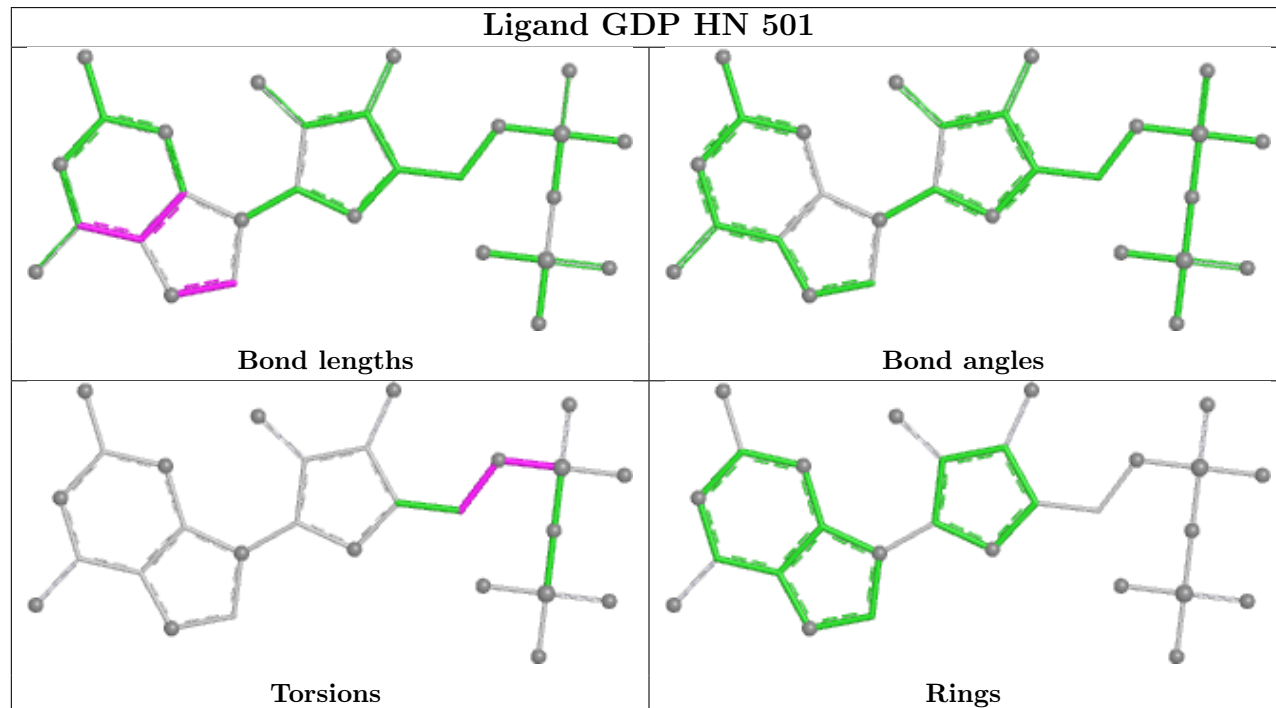
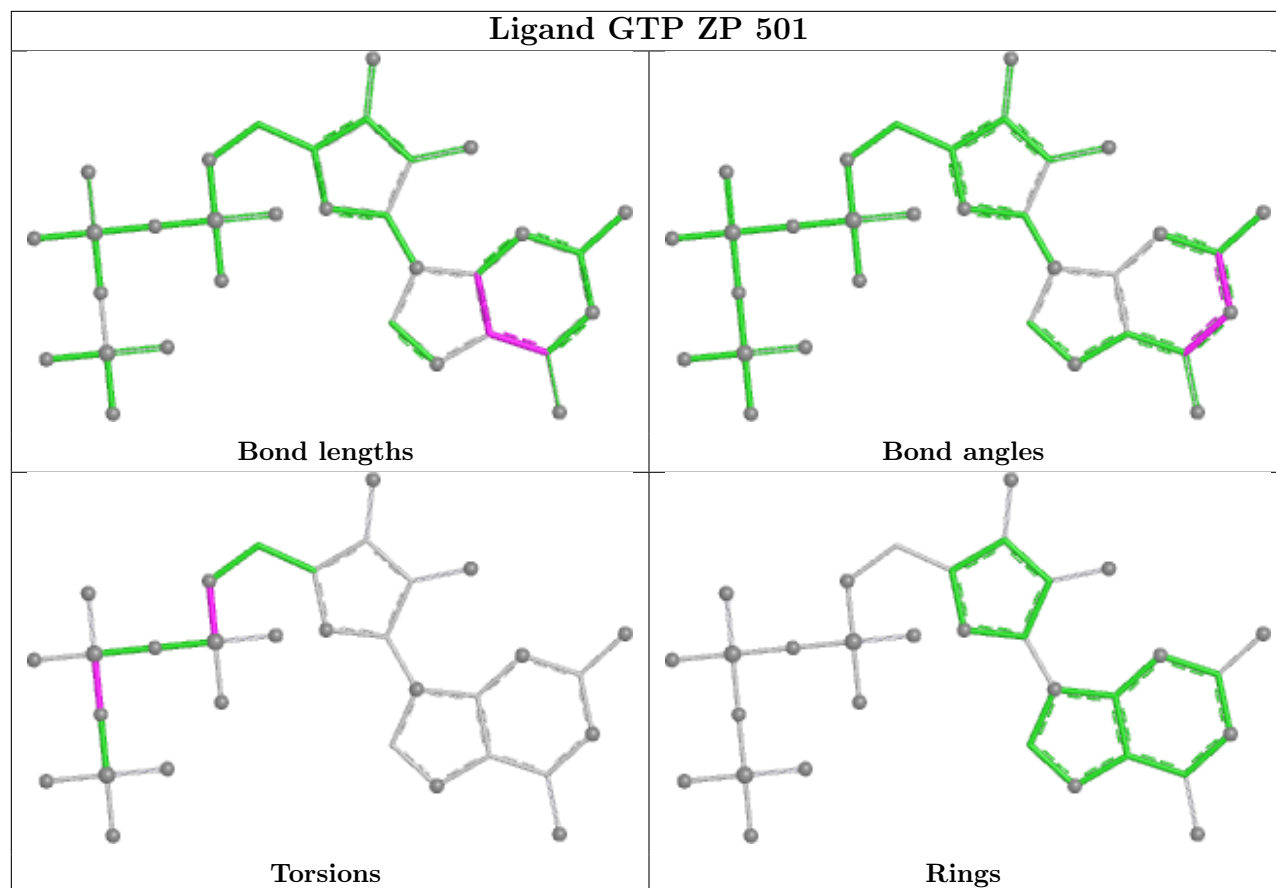


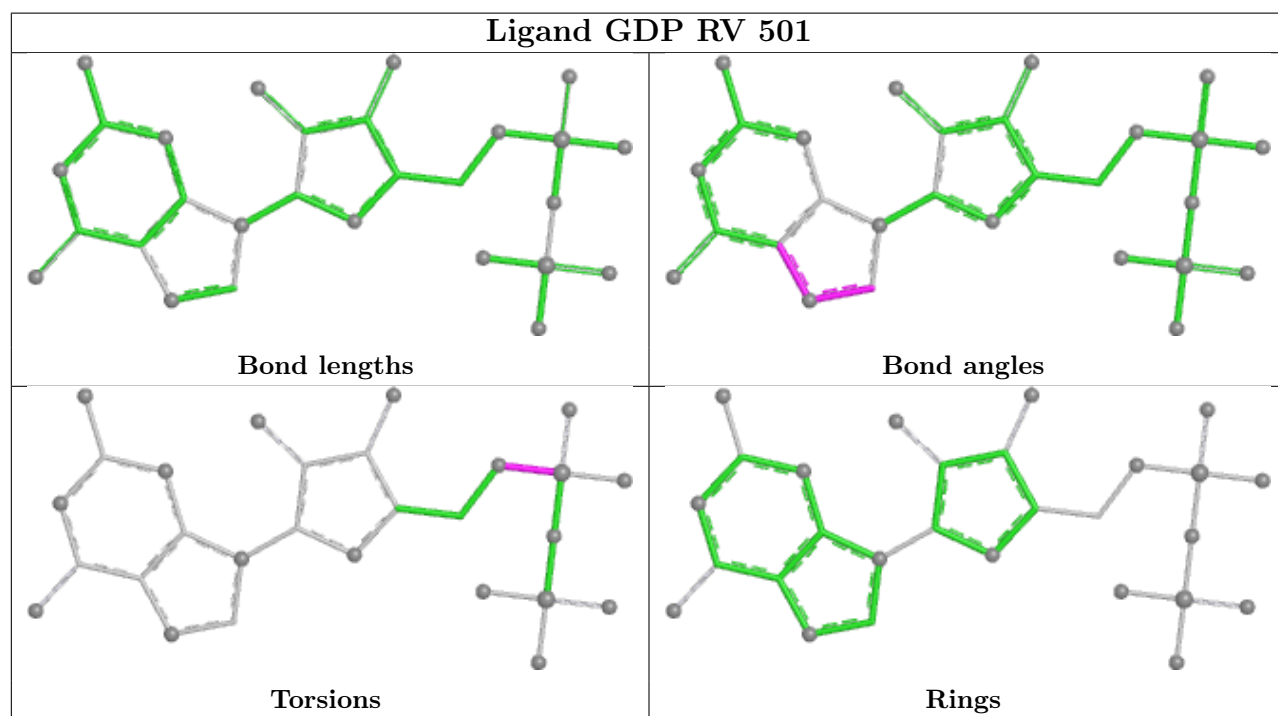
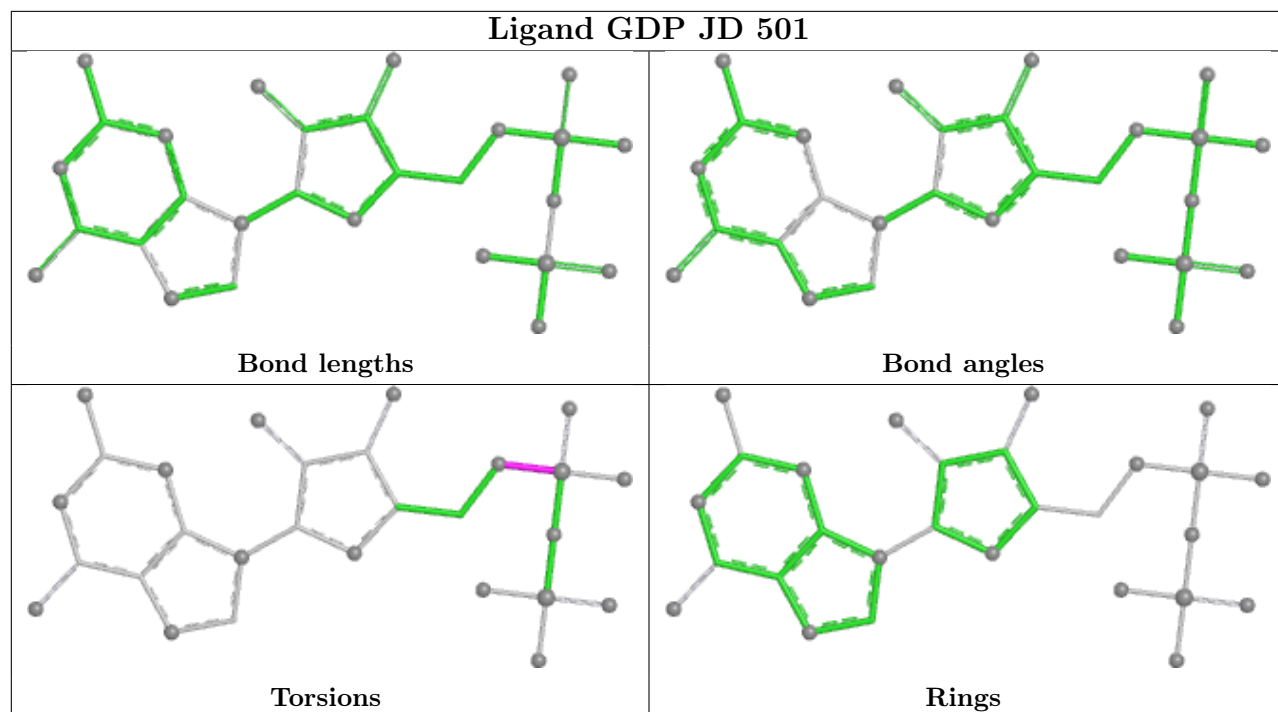
## Ligand GDP HL 501



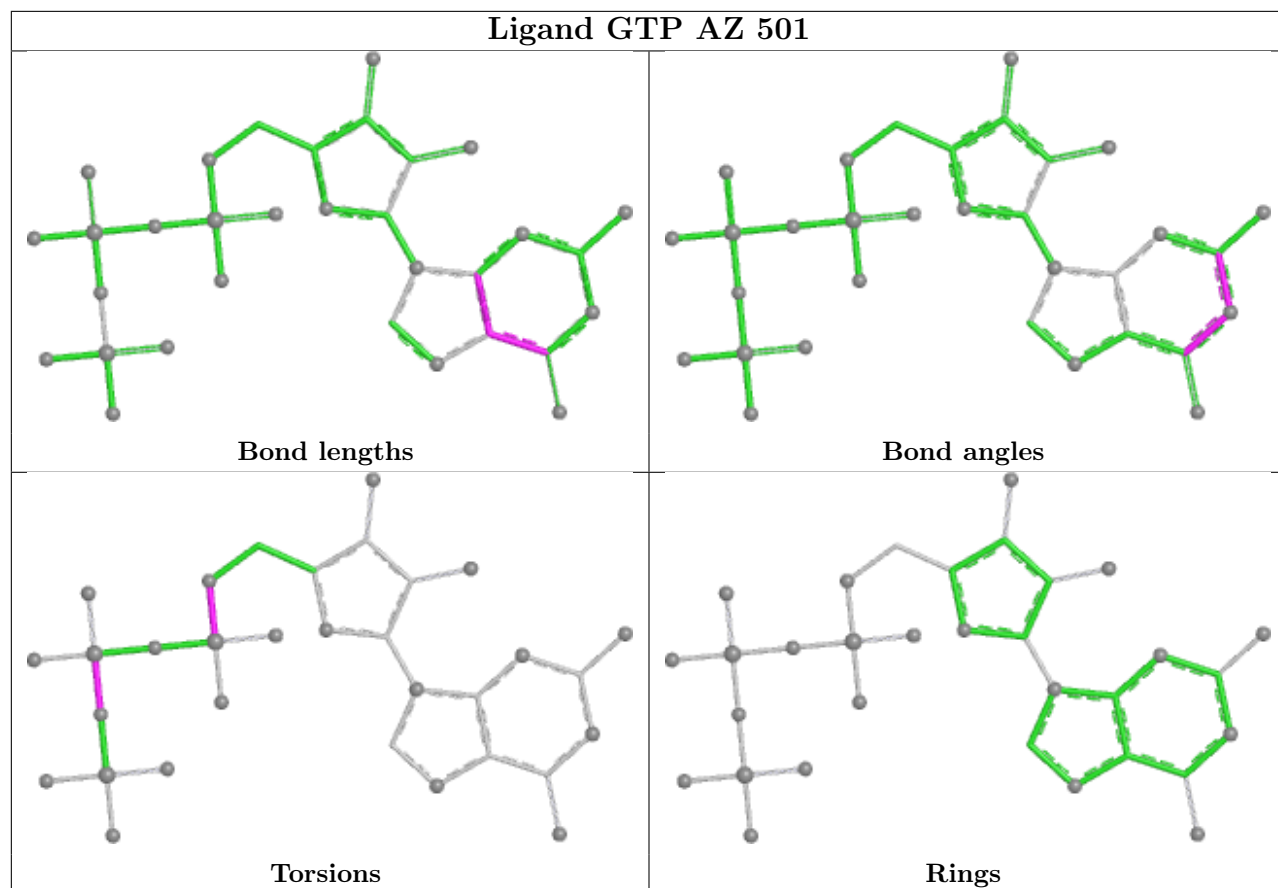




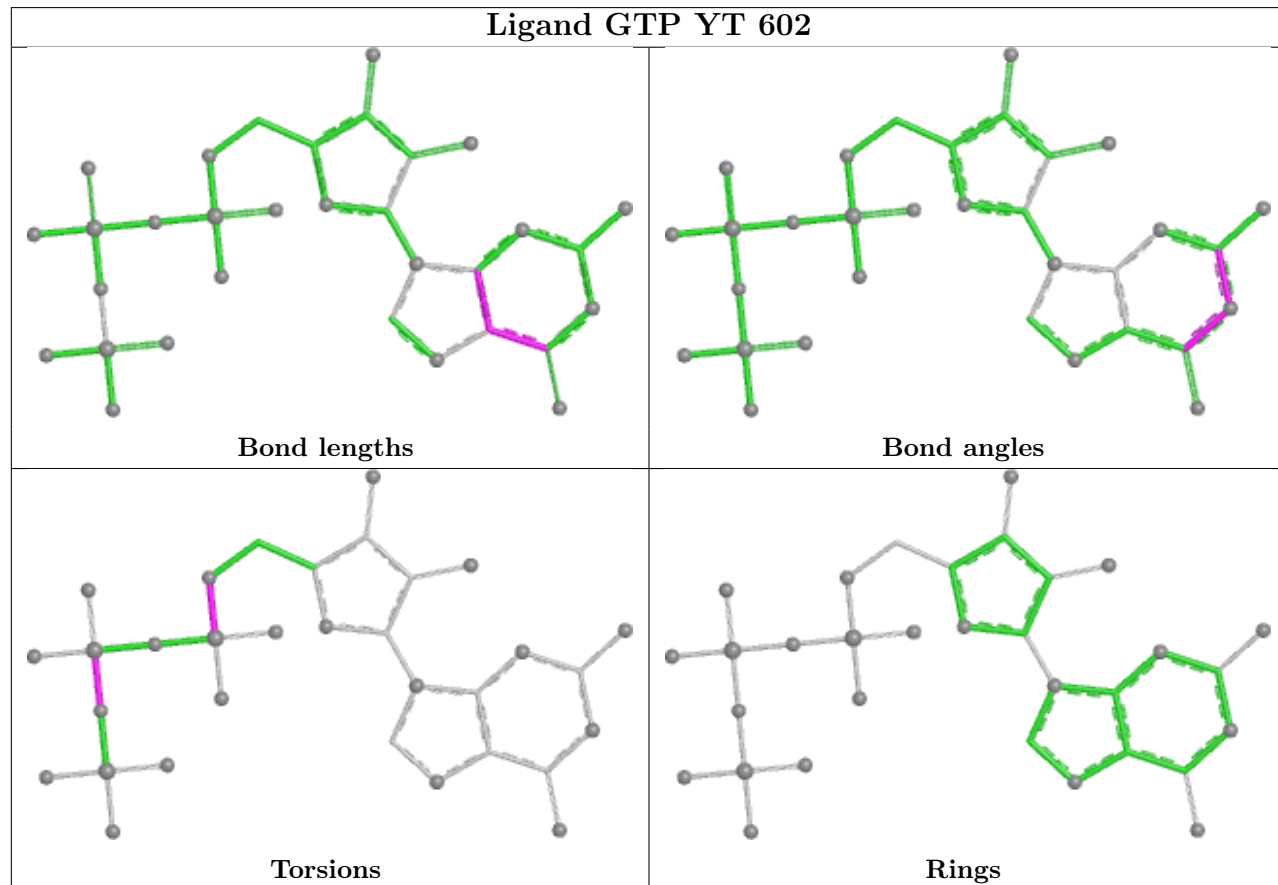


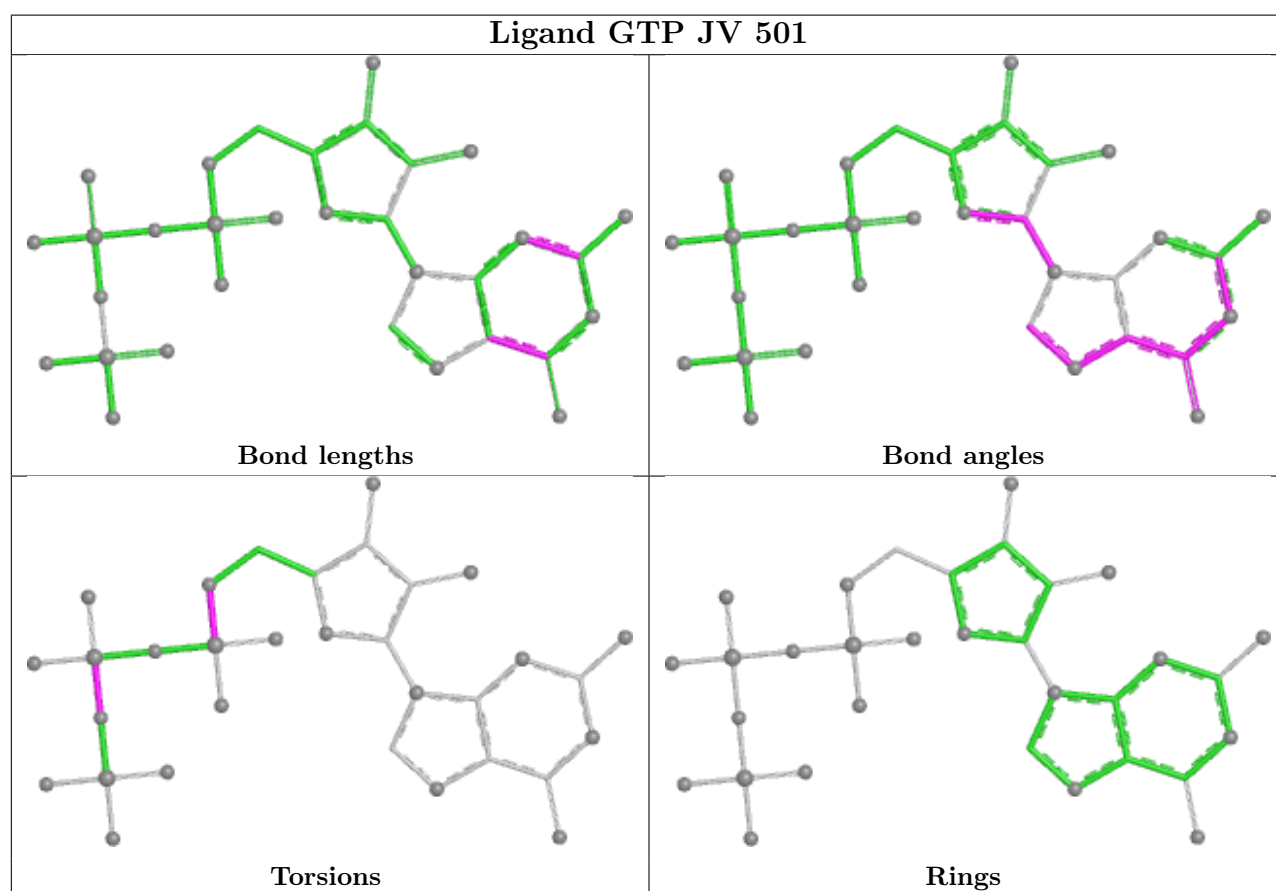
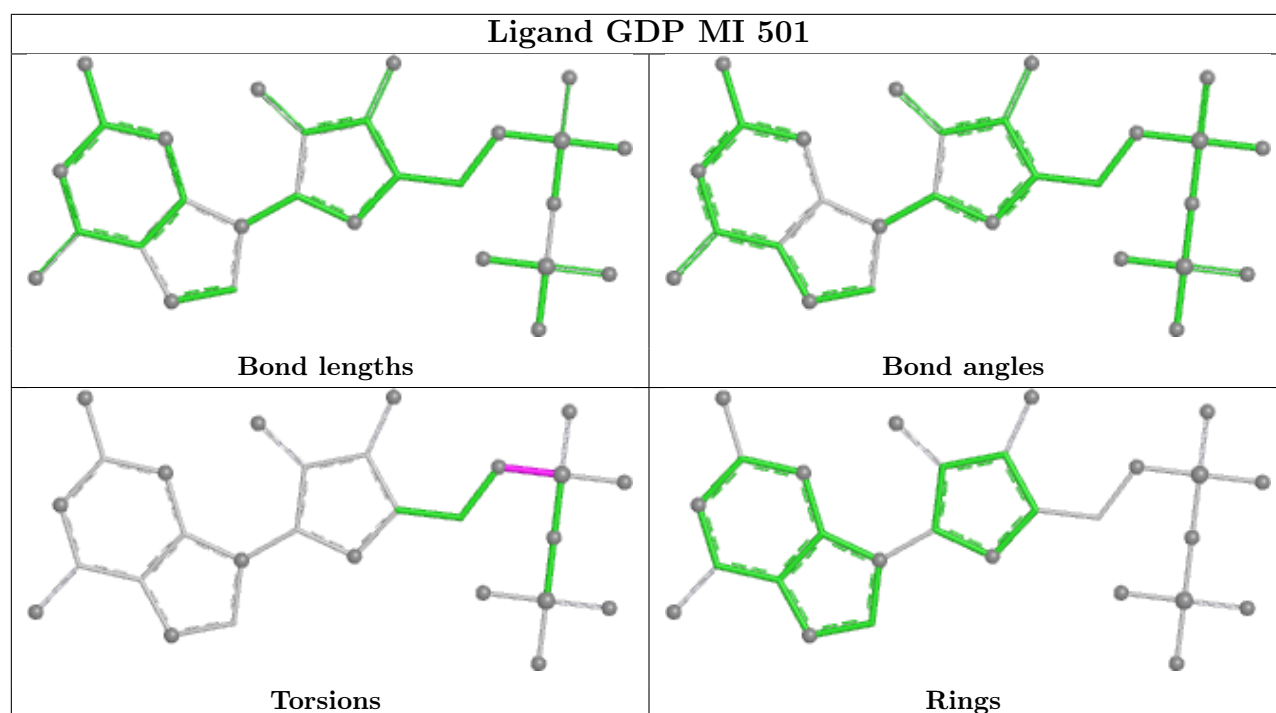


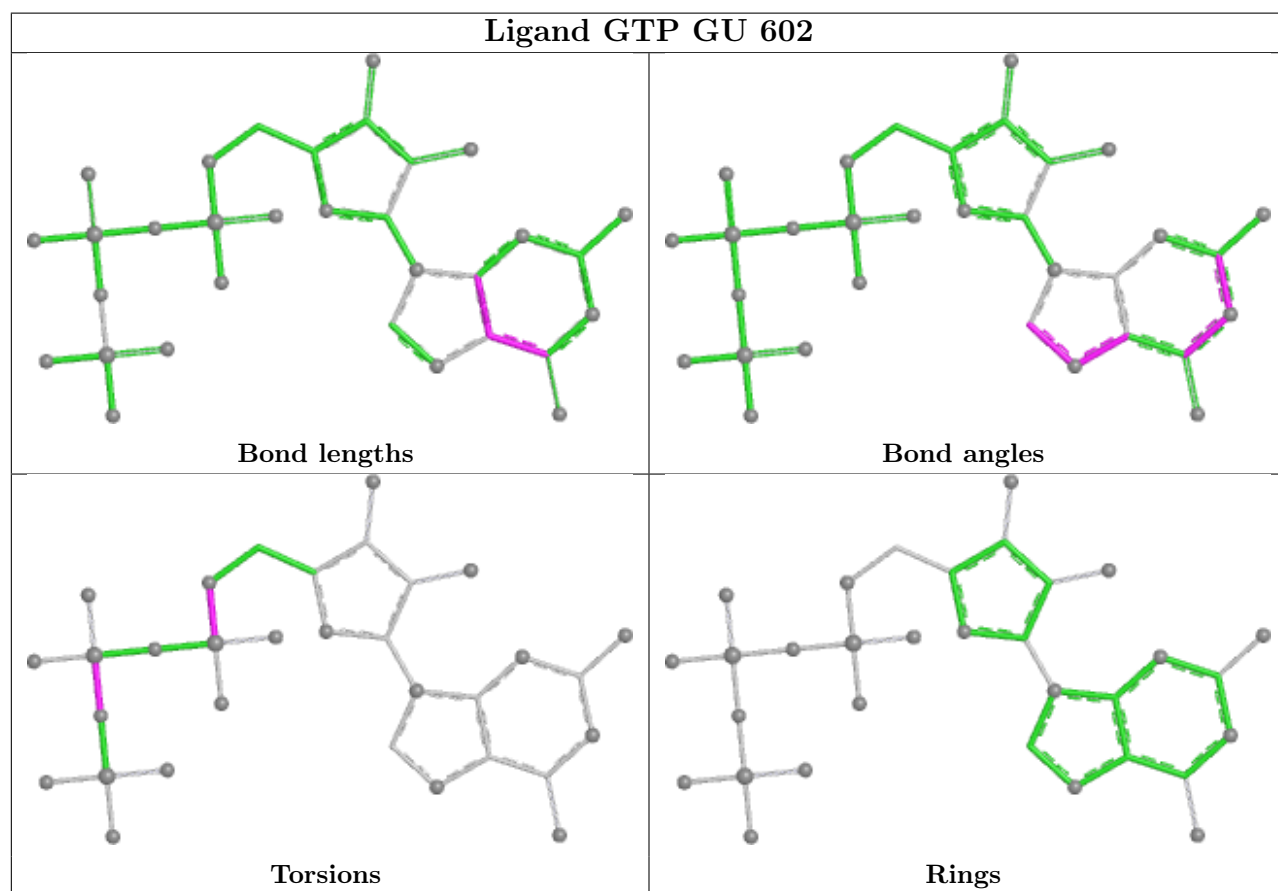
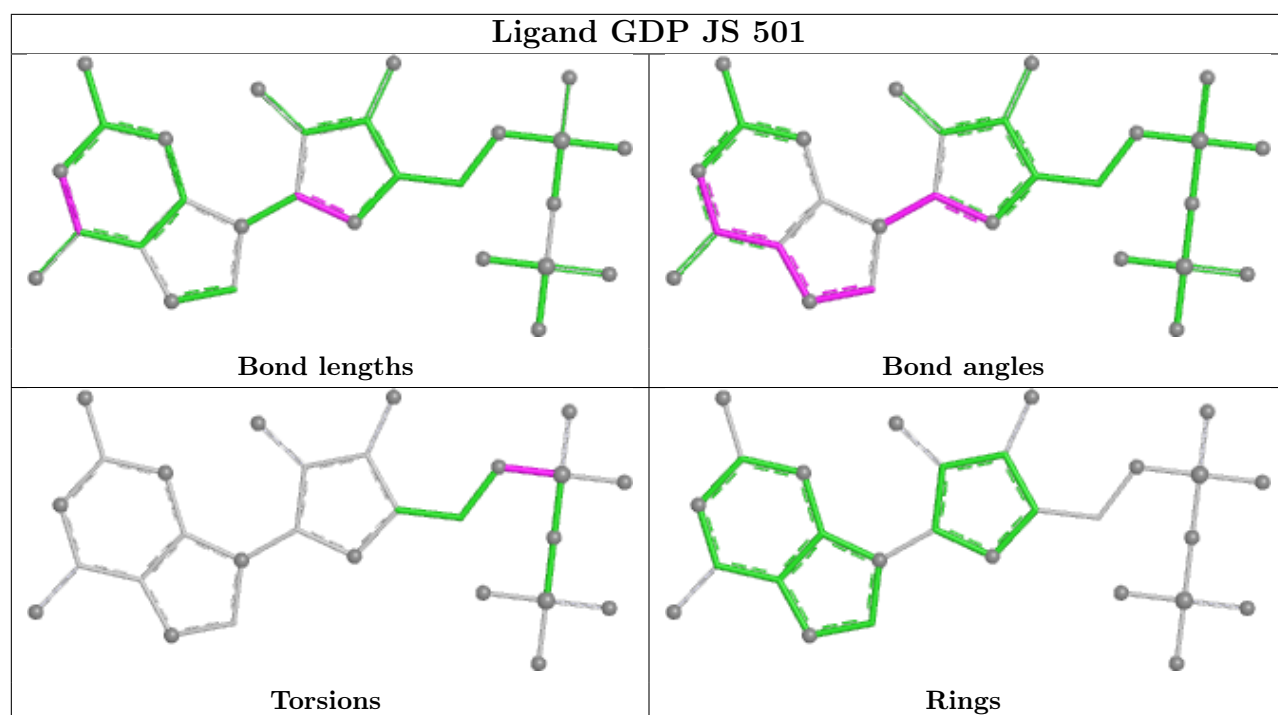
## Ligand GTP AZ 501



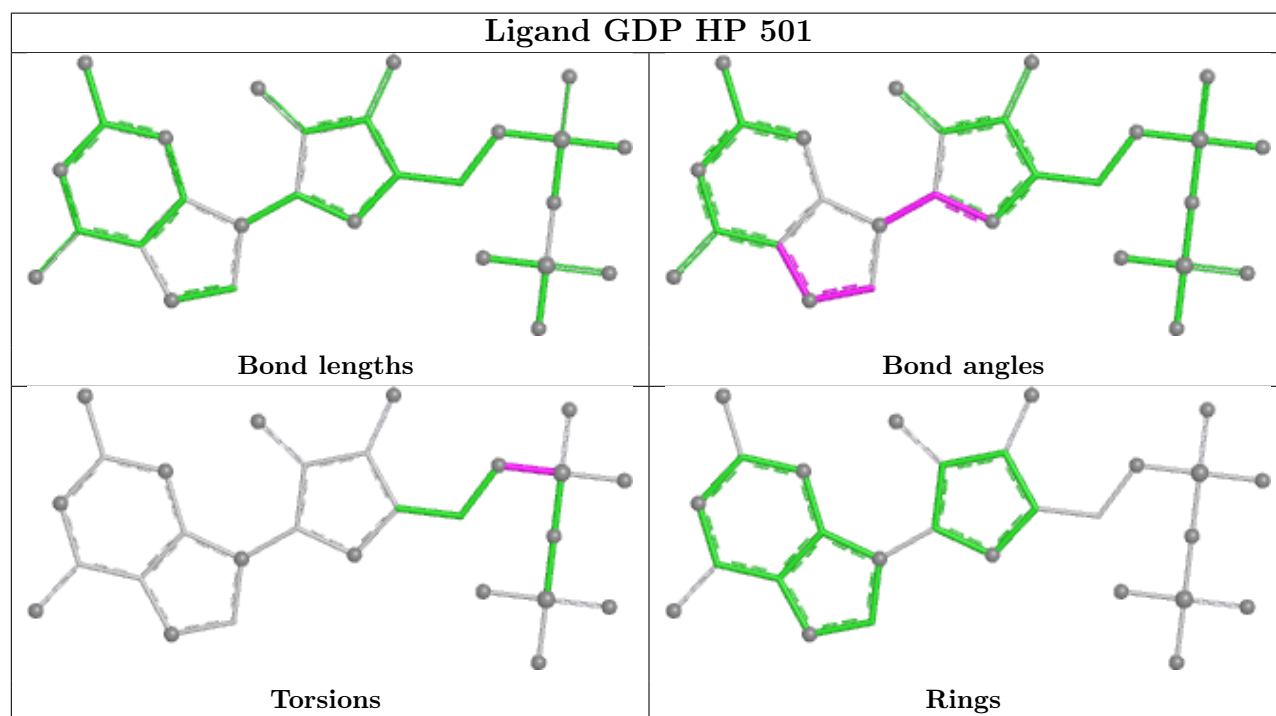
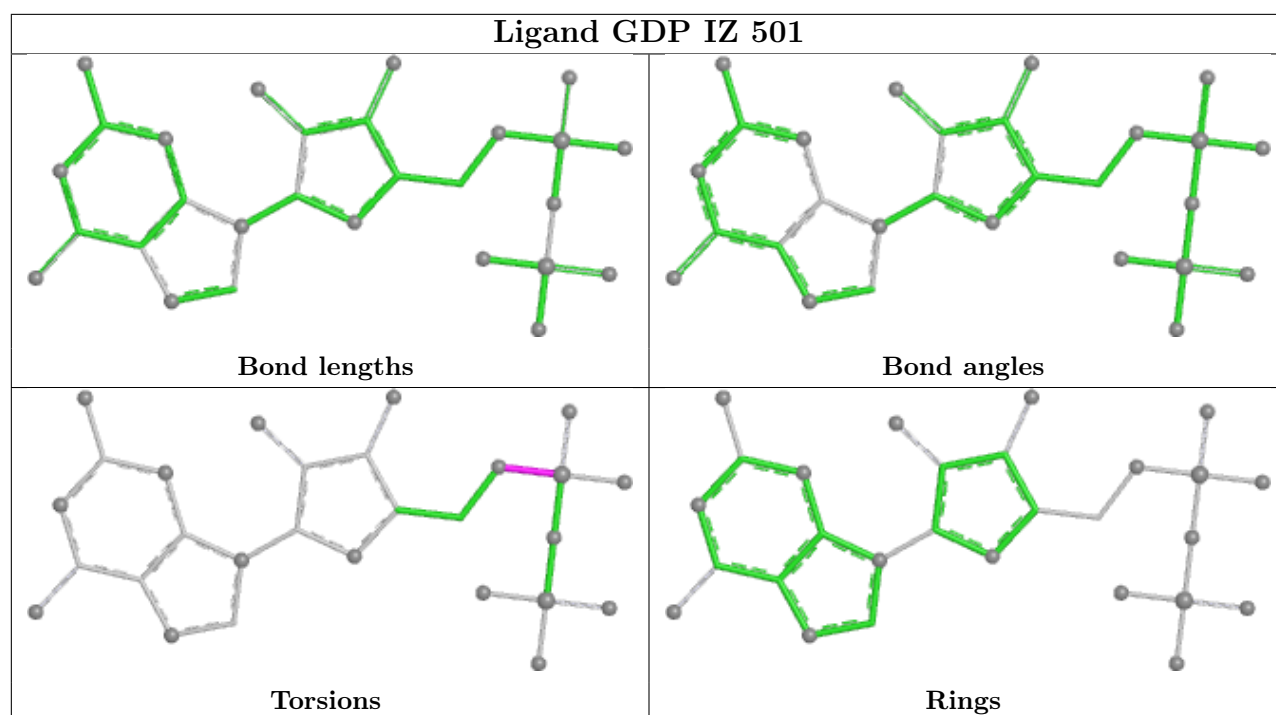
## Ligand GTP YT 602



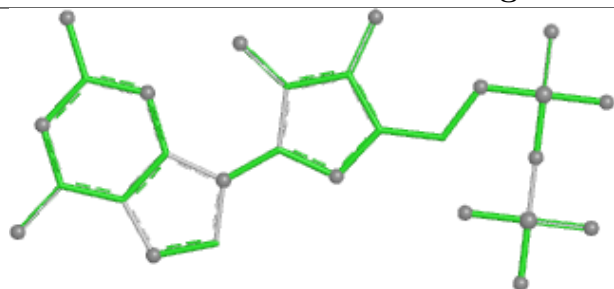




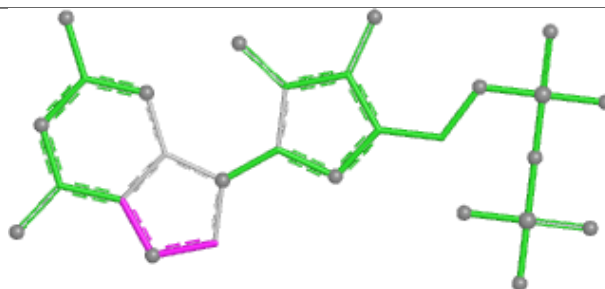




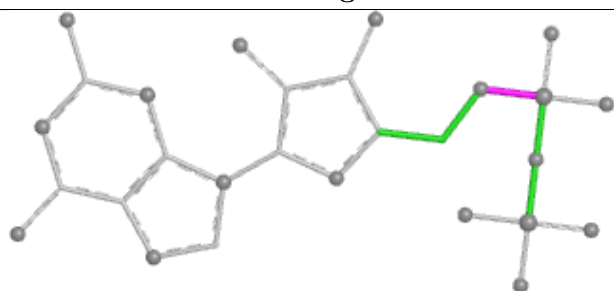
## Ligand GDP VL 501



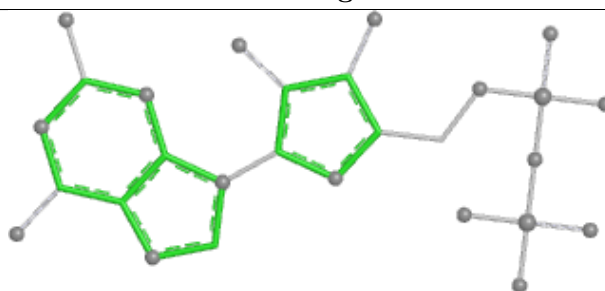
Bond lengths



Bond angles

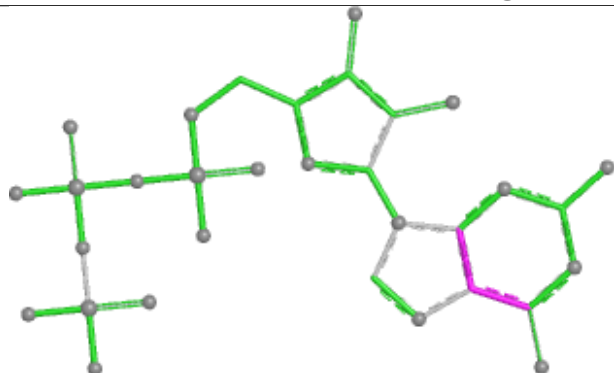


Torsions

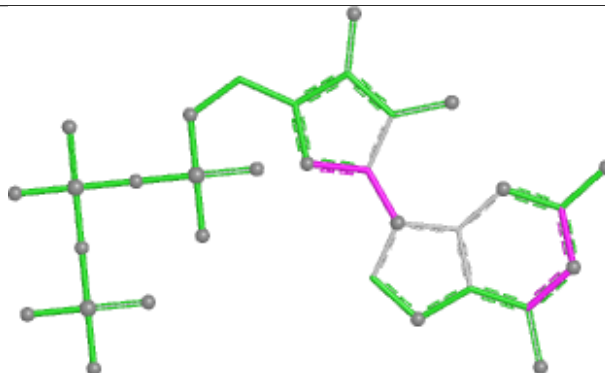


Rings

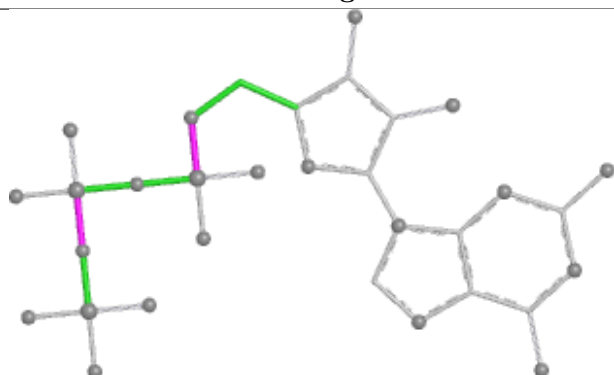
## Ligand GTP XG 602



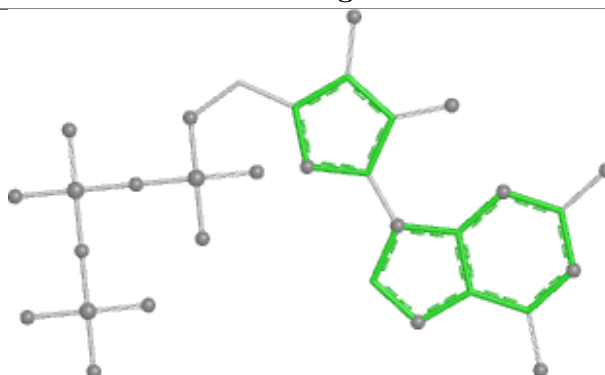
Bond lengths



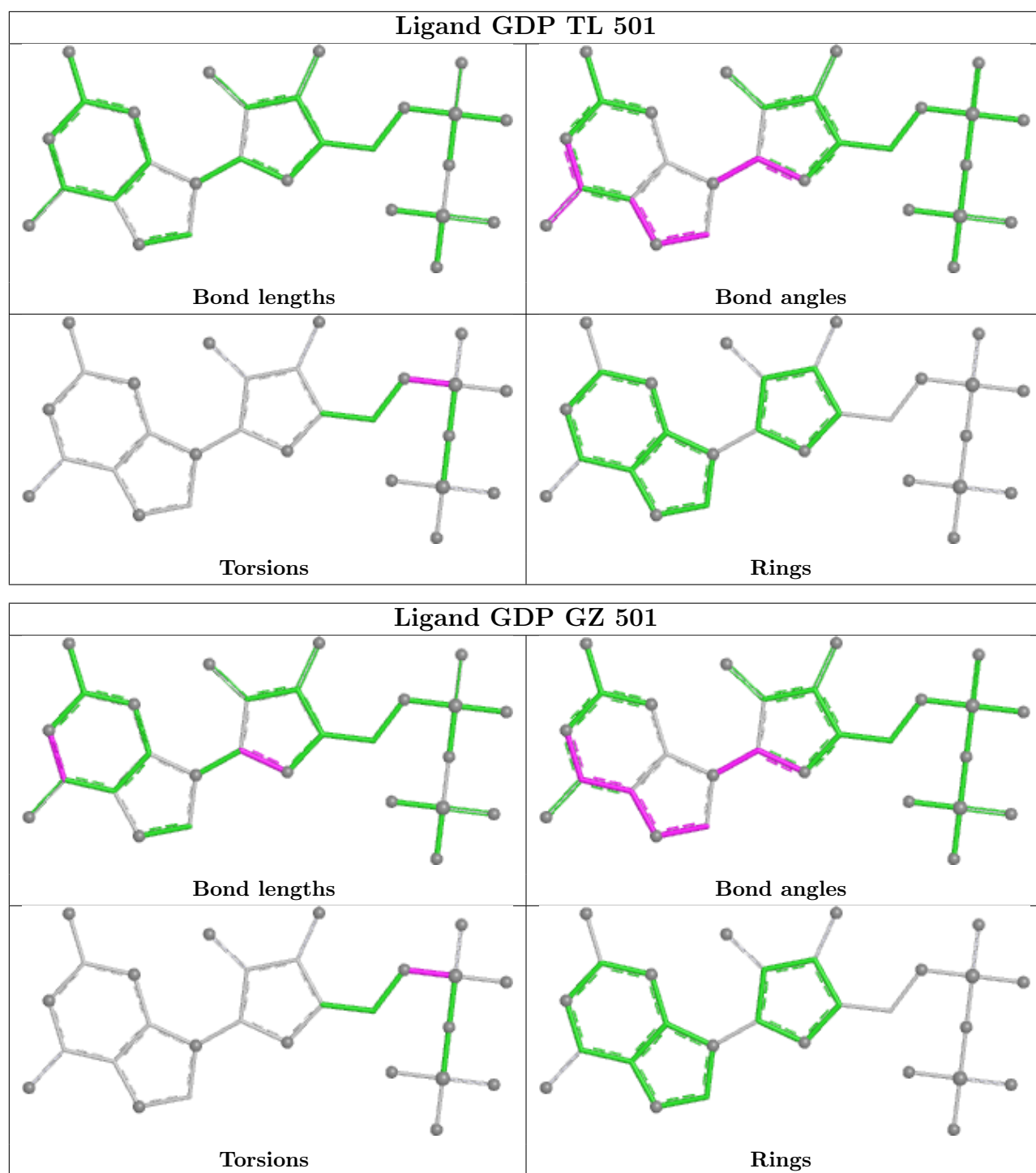
Bond angles



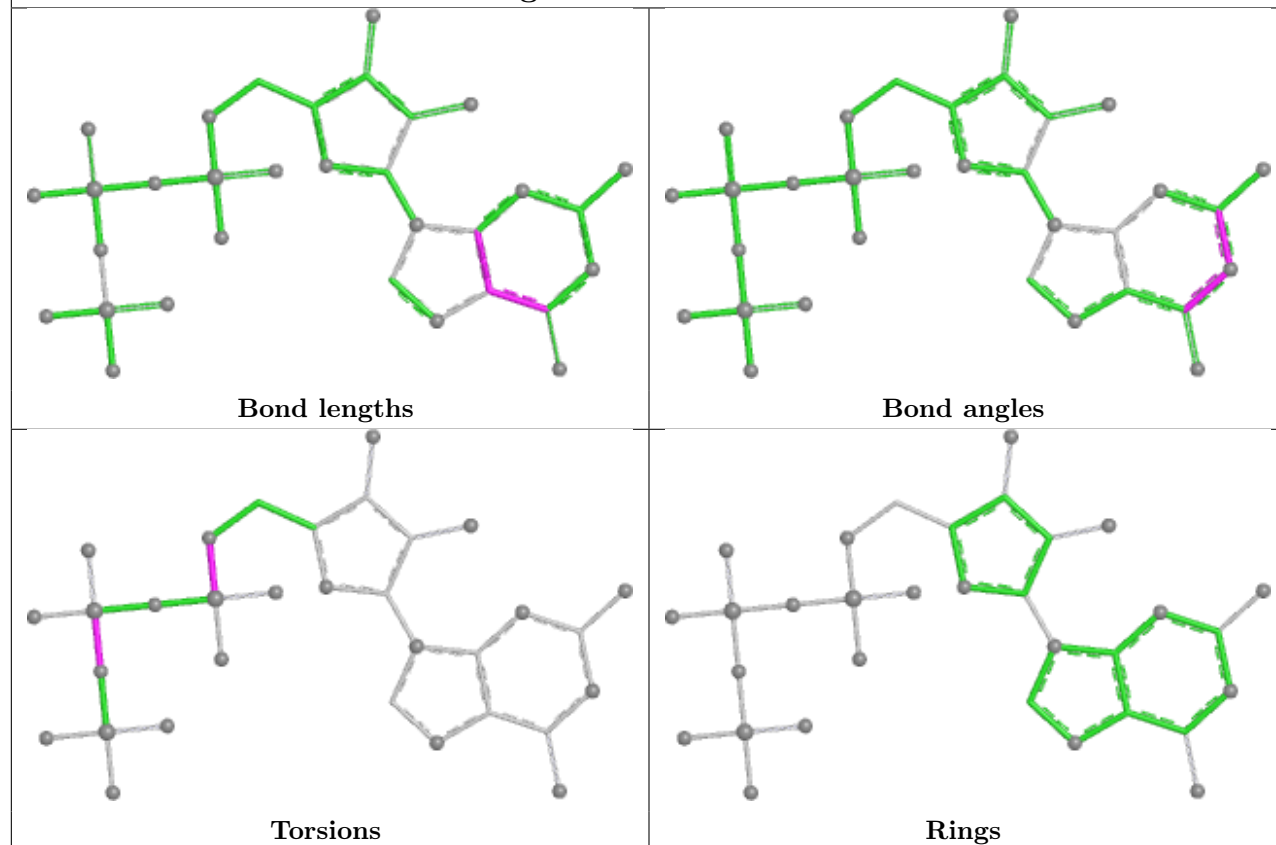
Torsions



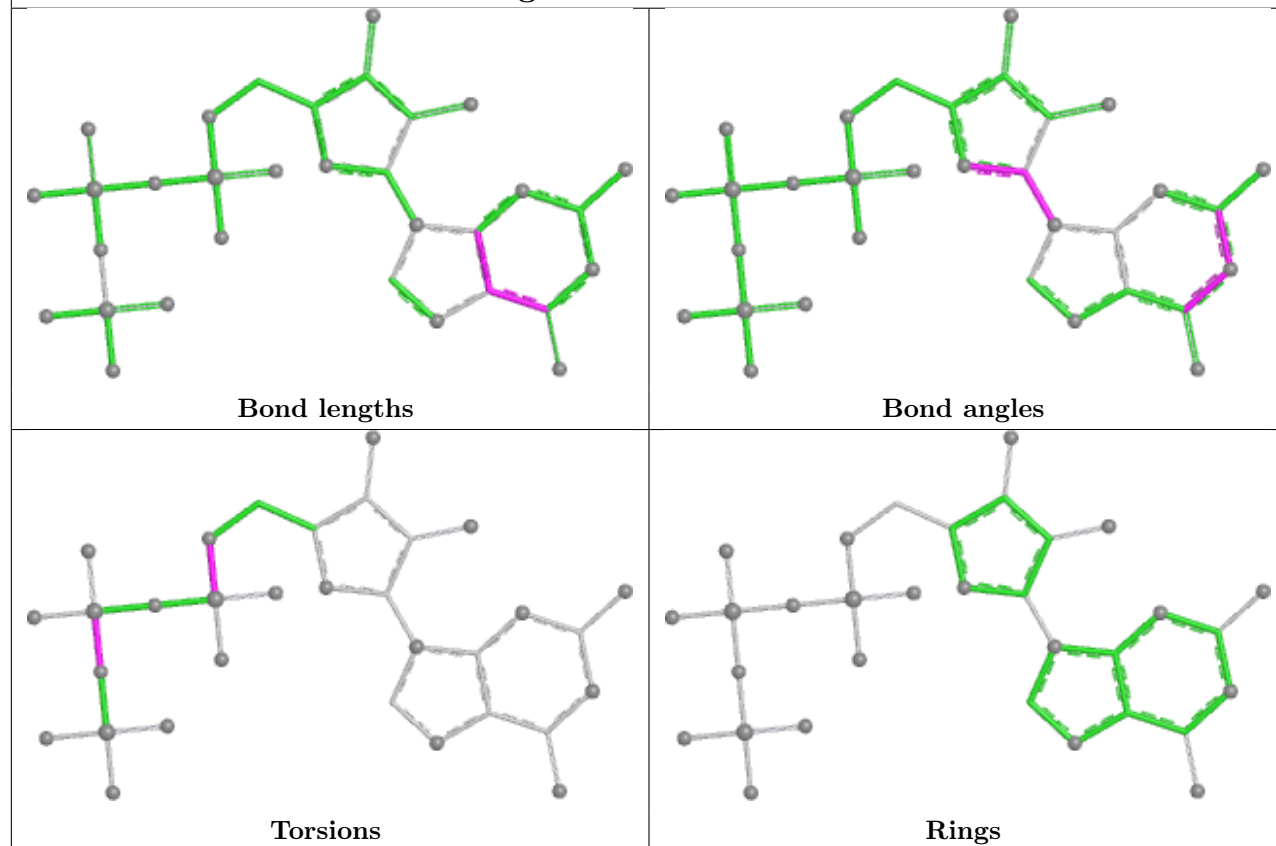
Rings



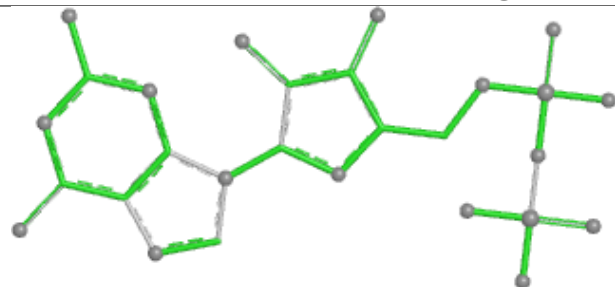
## Ligand GTP VS 501



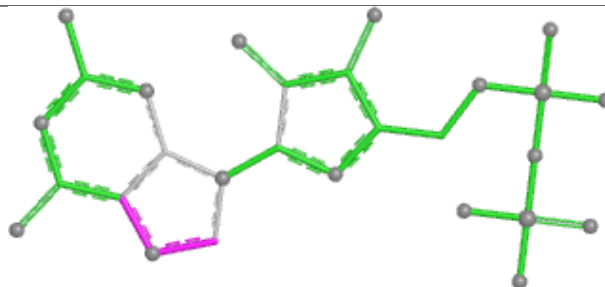
## Ligand GTP IW 501



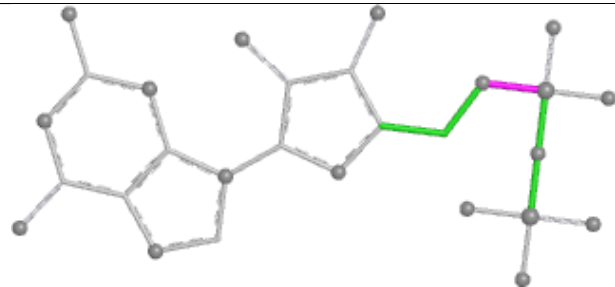
## Ligand GDP KM 501



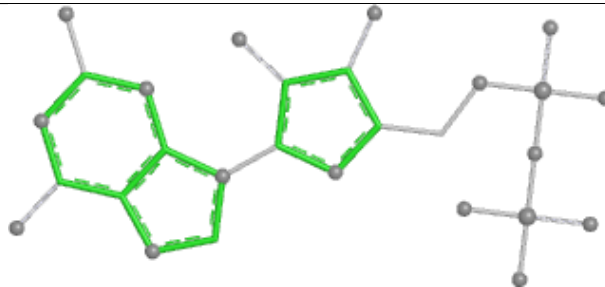
Bond lengths



Bond angles

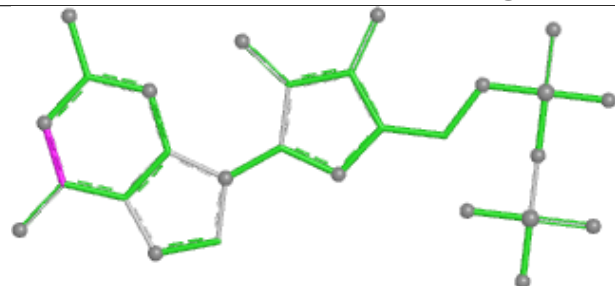


Torsions

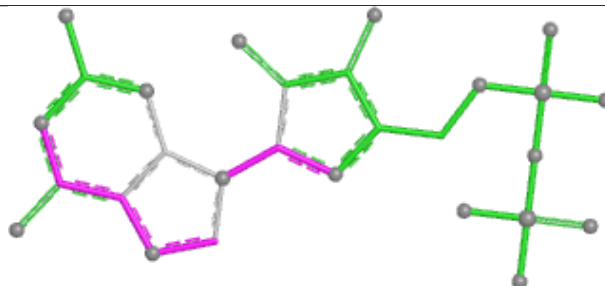


Rings

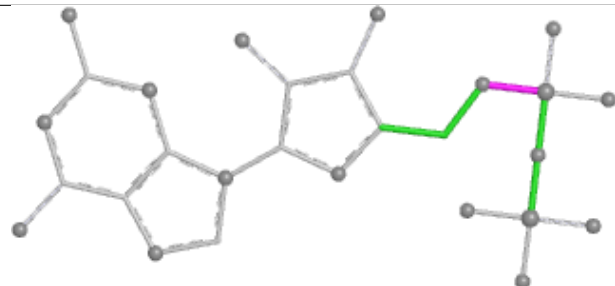
## Ligand GDP DV 501



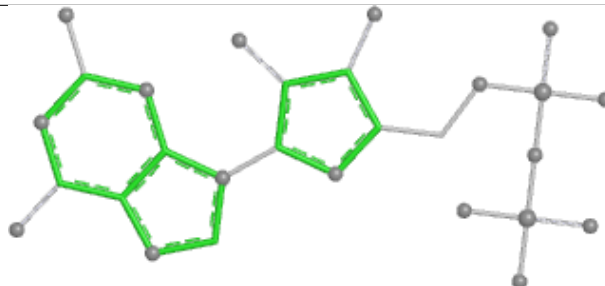
Bond lengths



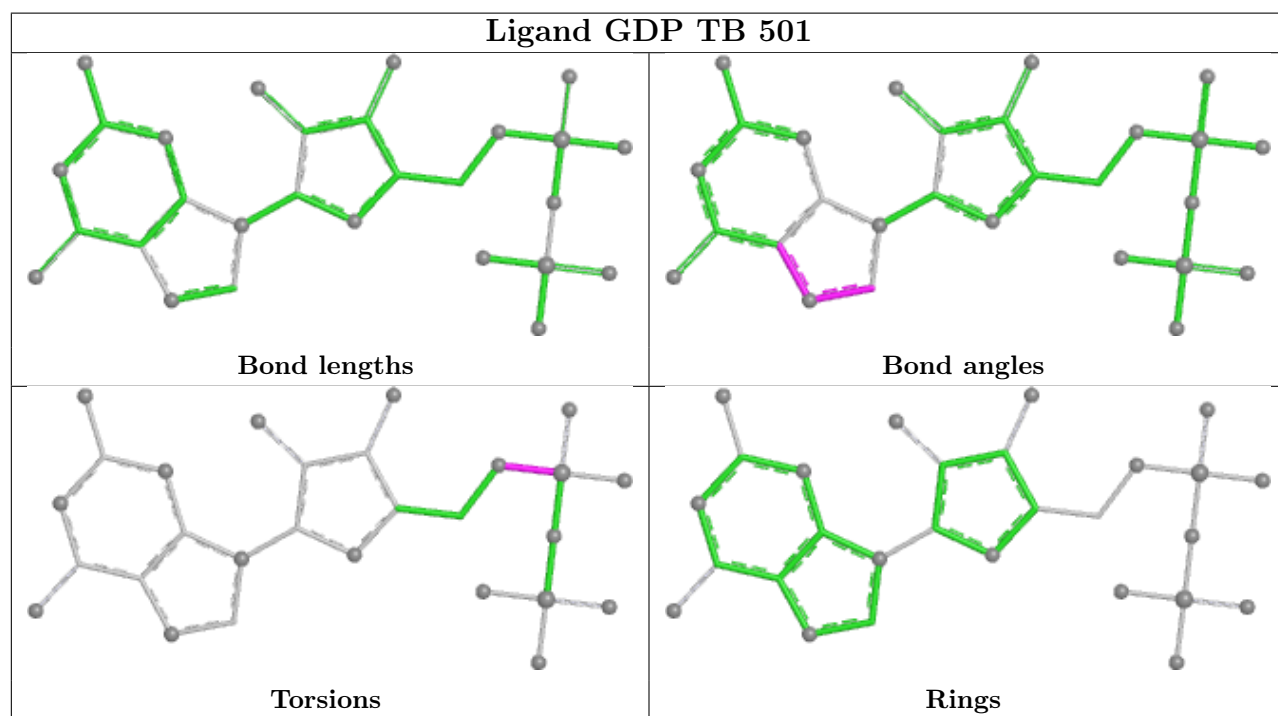
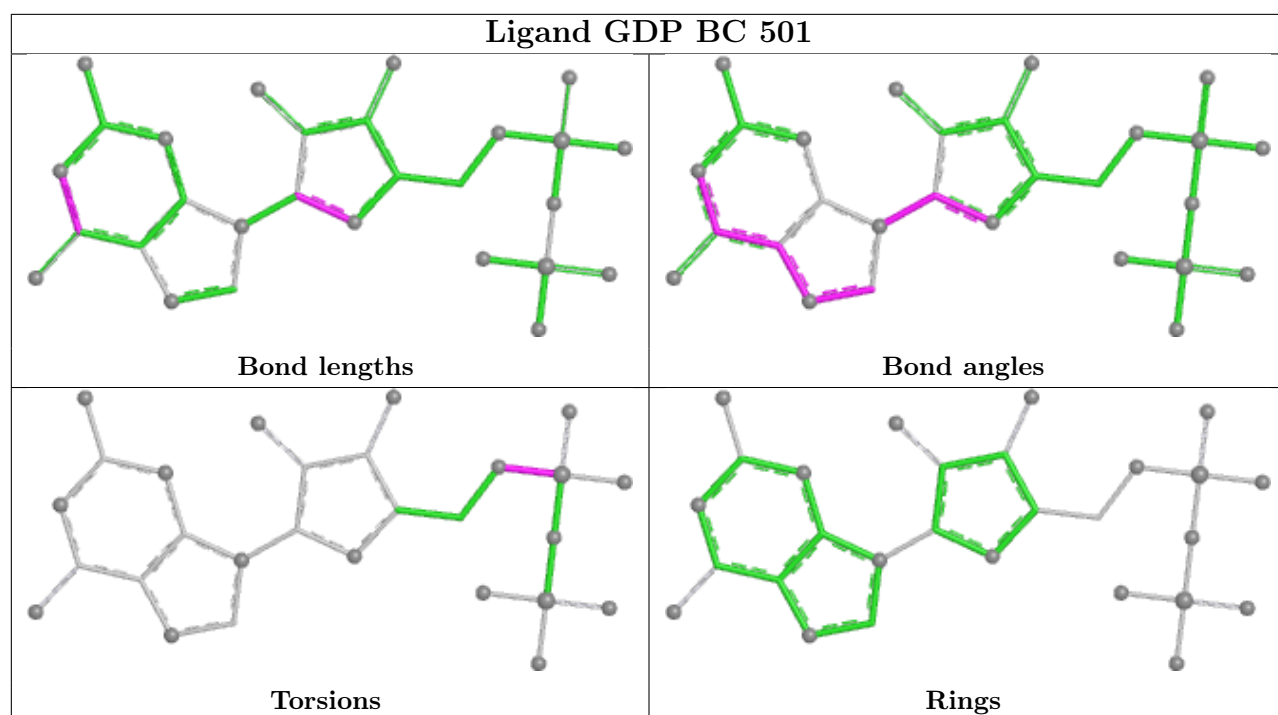
Bond angles

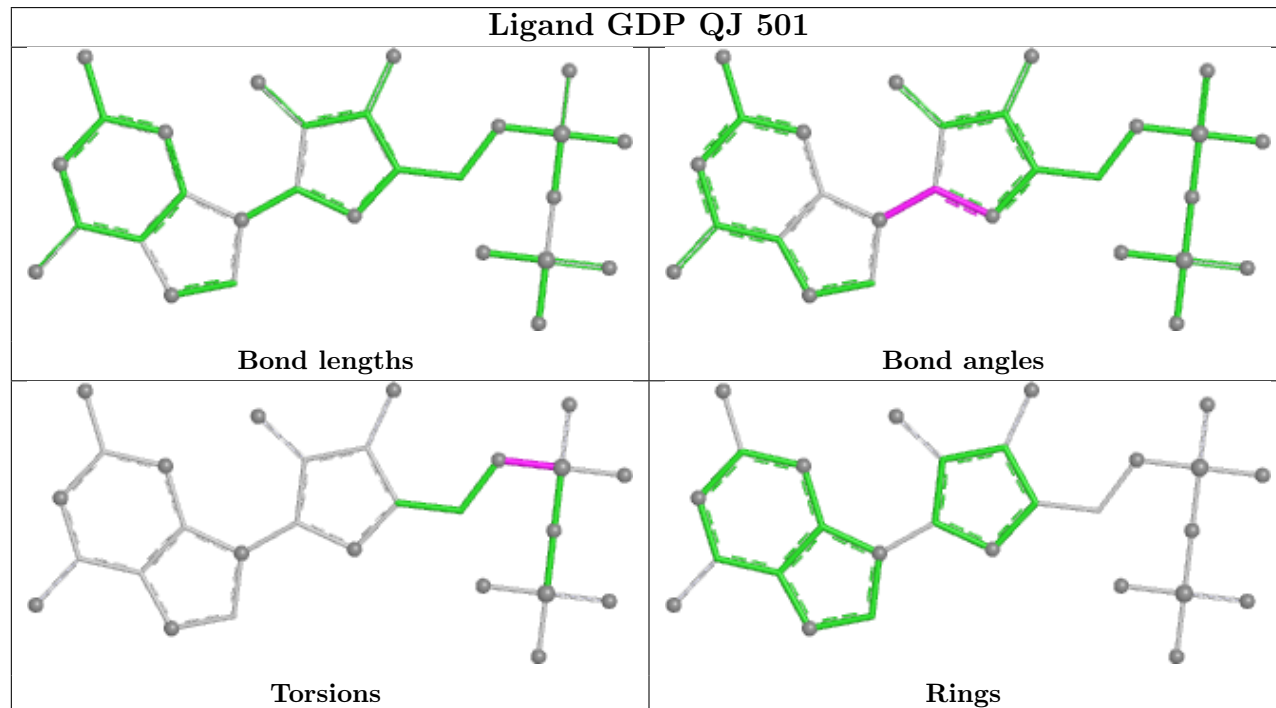
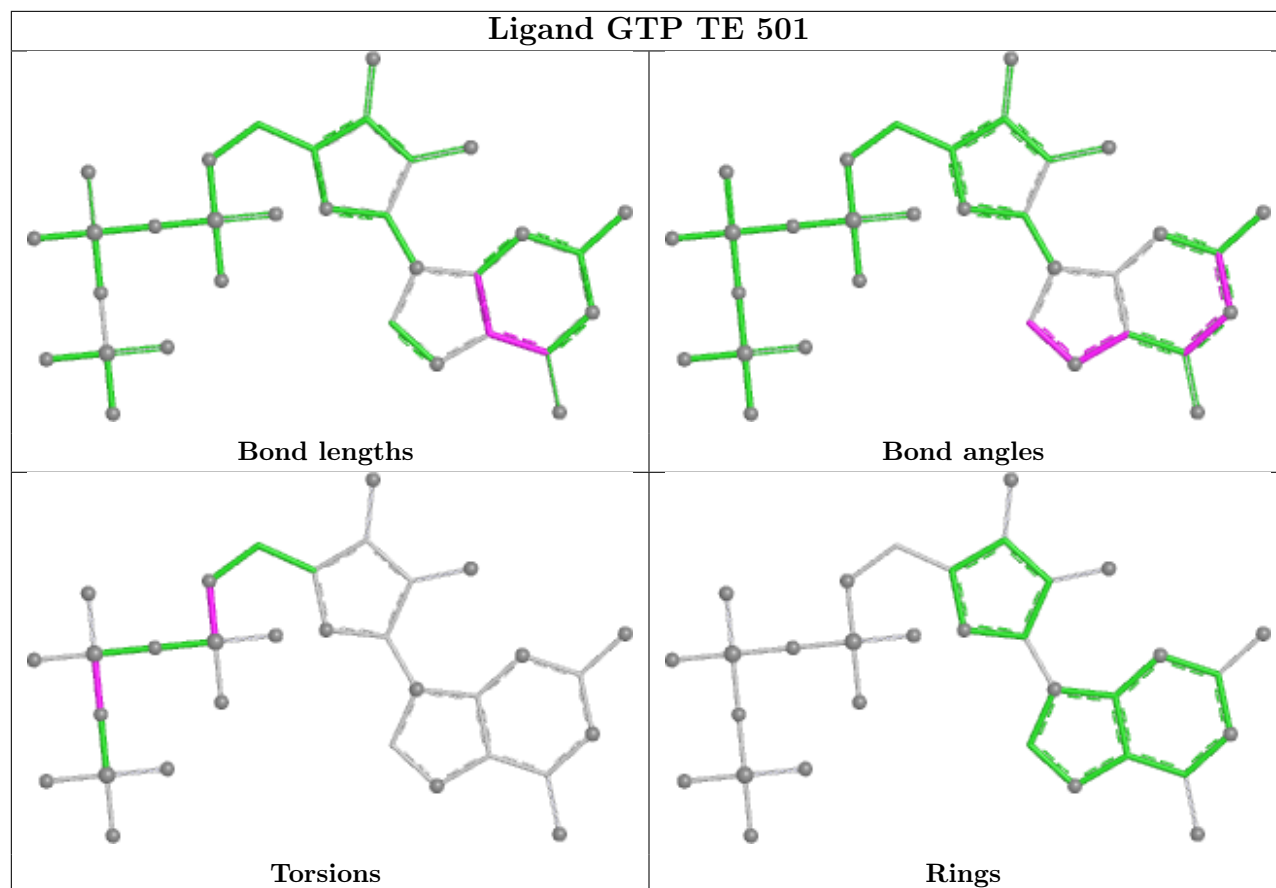


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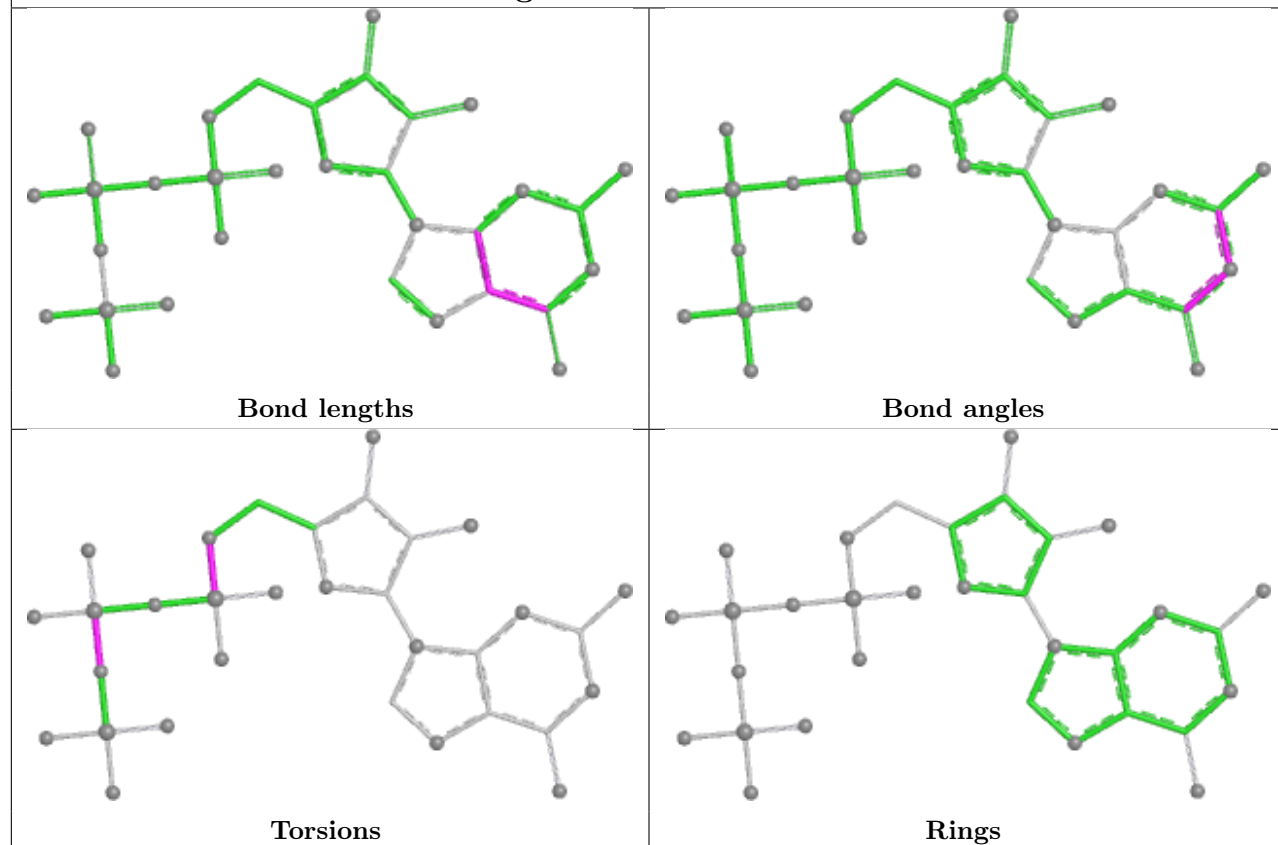


Rings

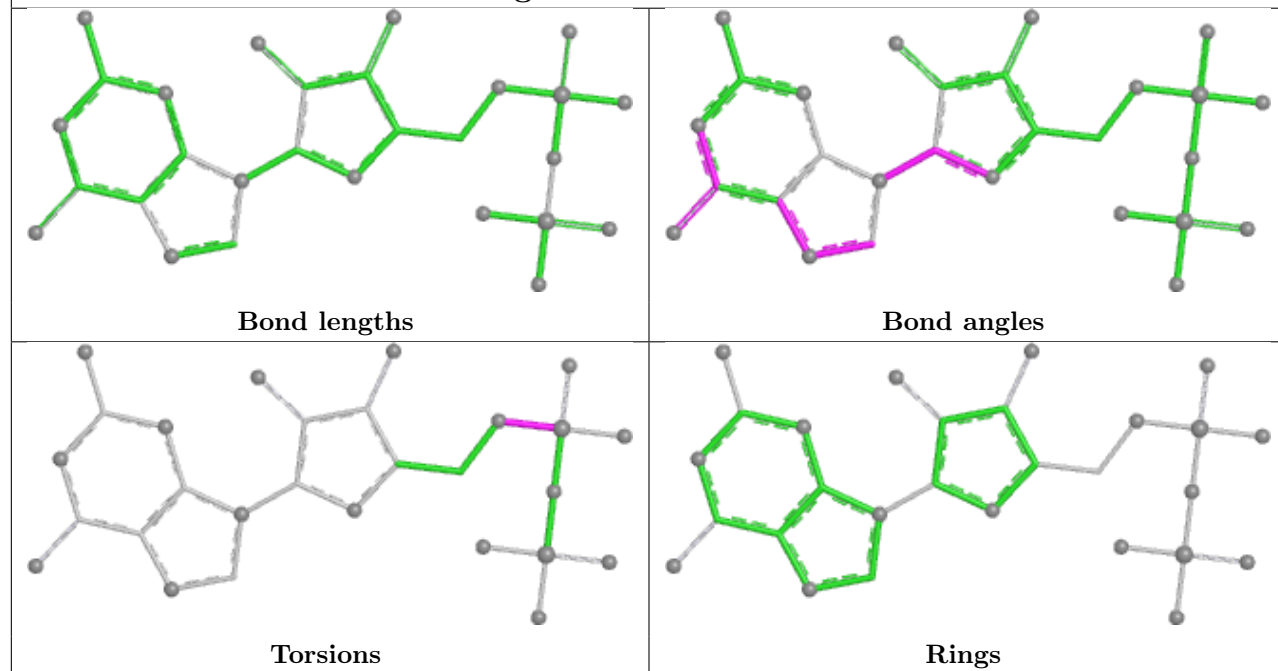




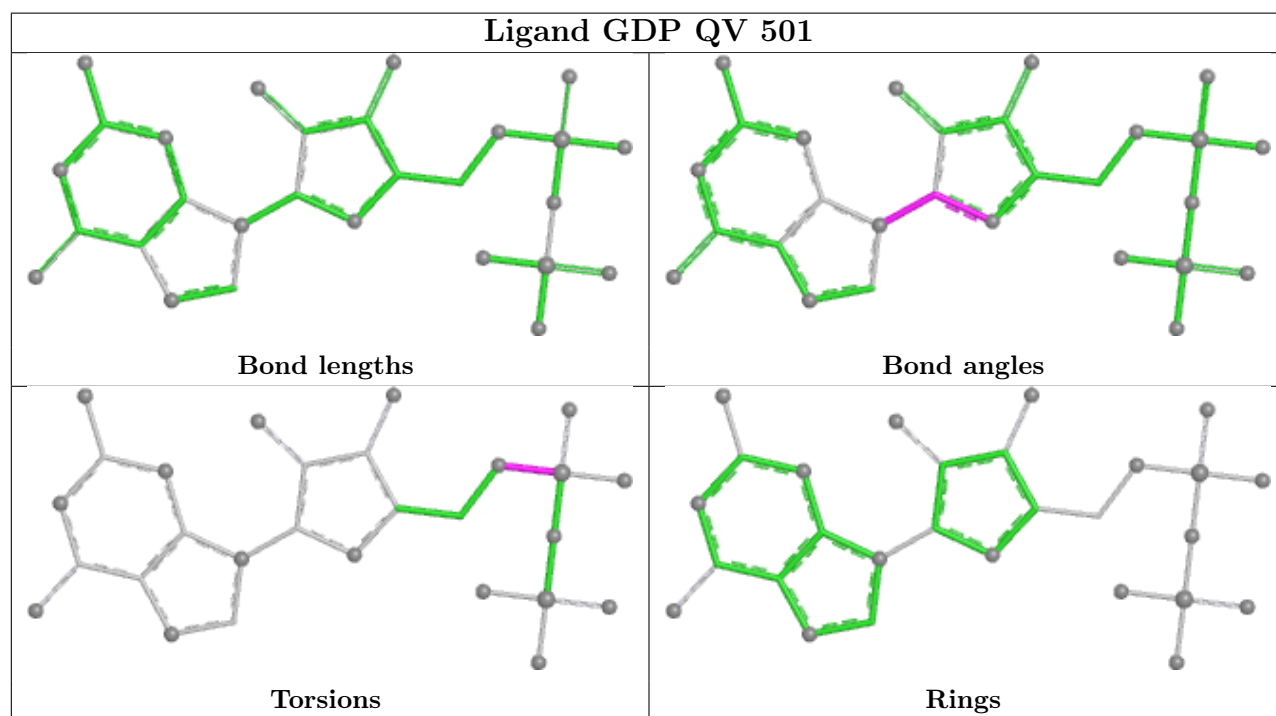
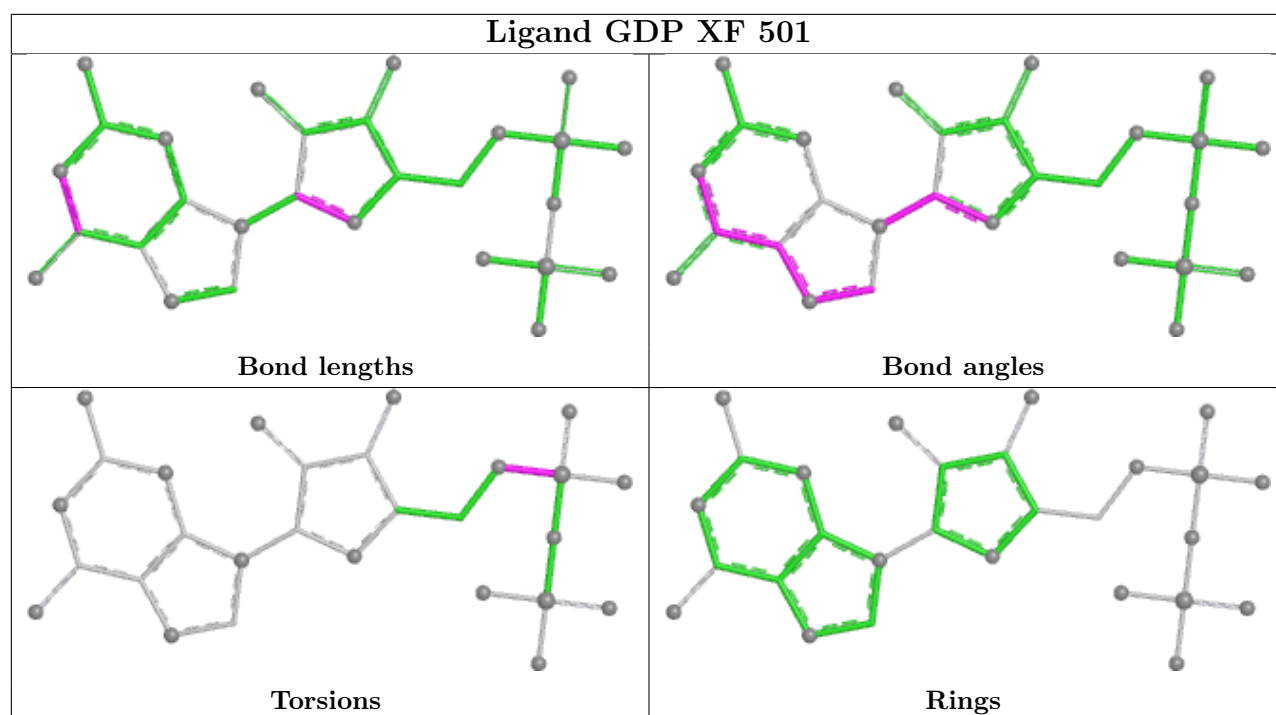
## Ligand GTP NH 502



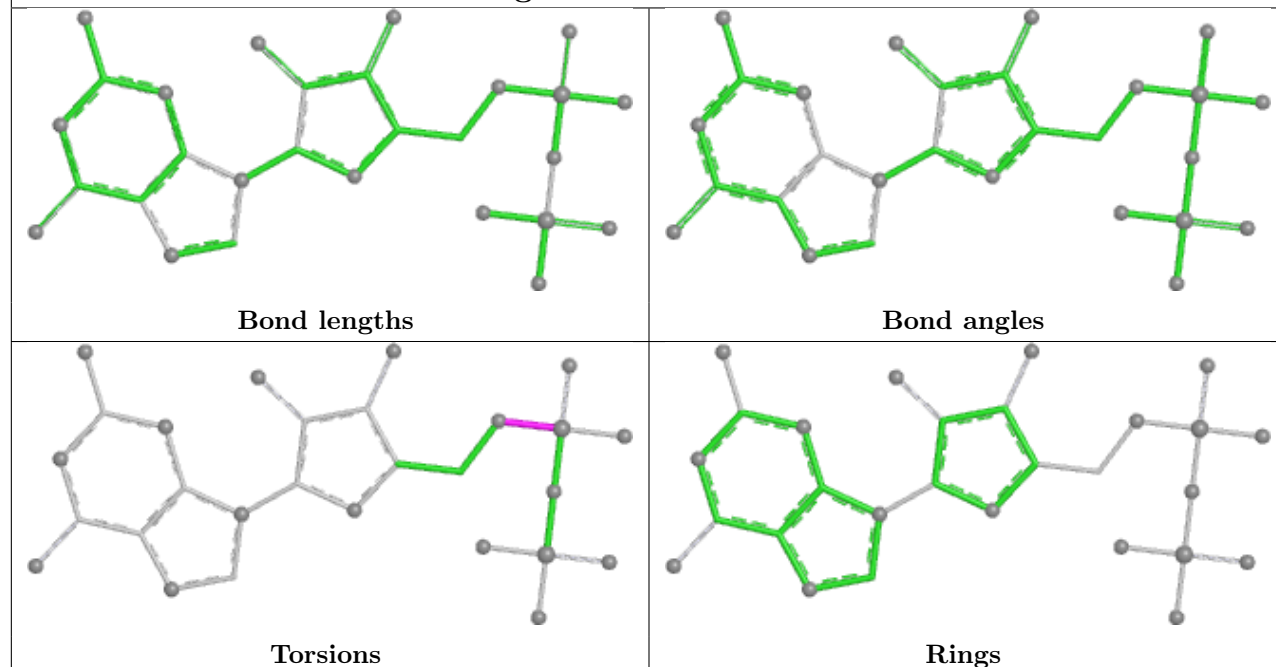
## Ligand GDP ZM 501



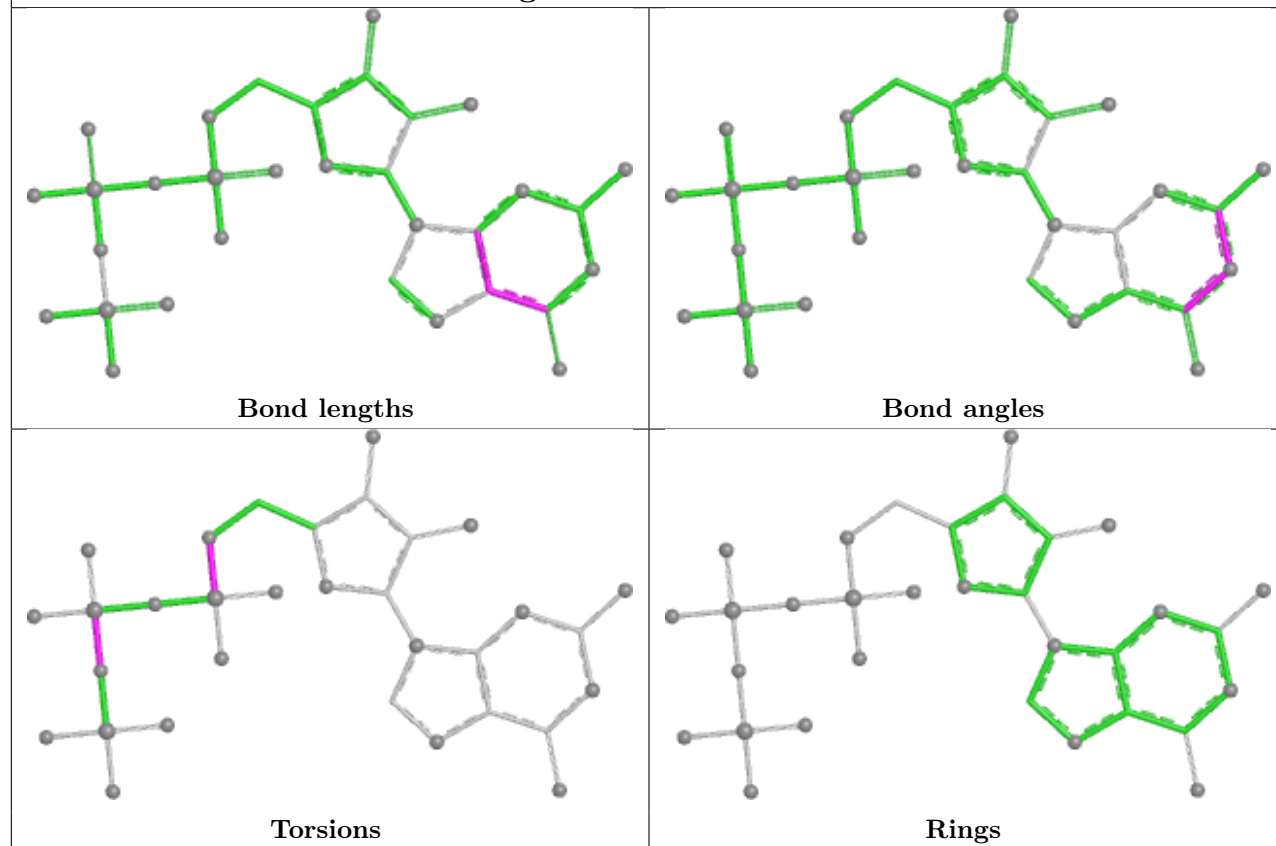


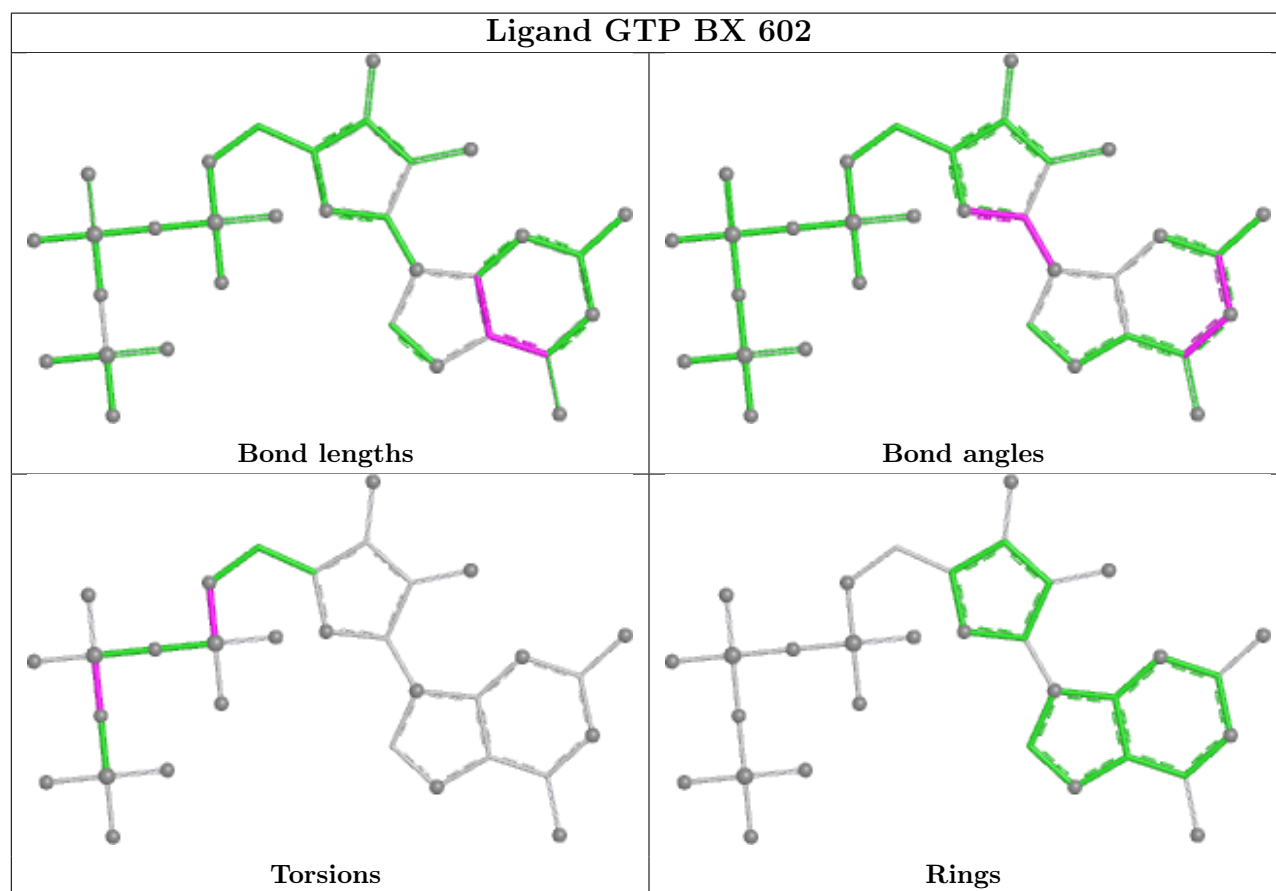
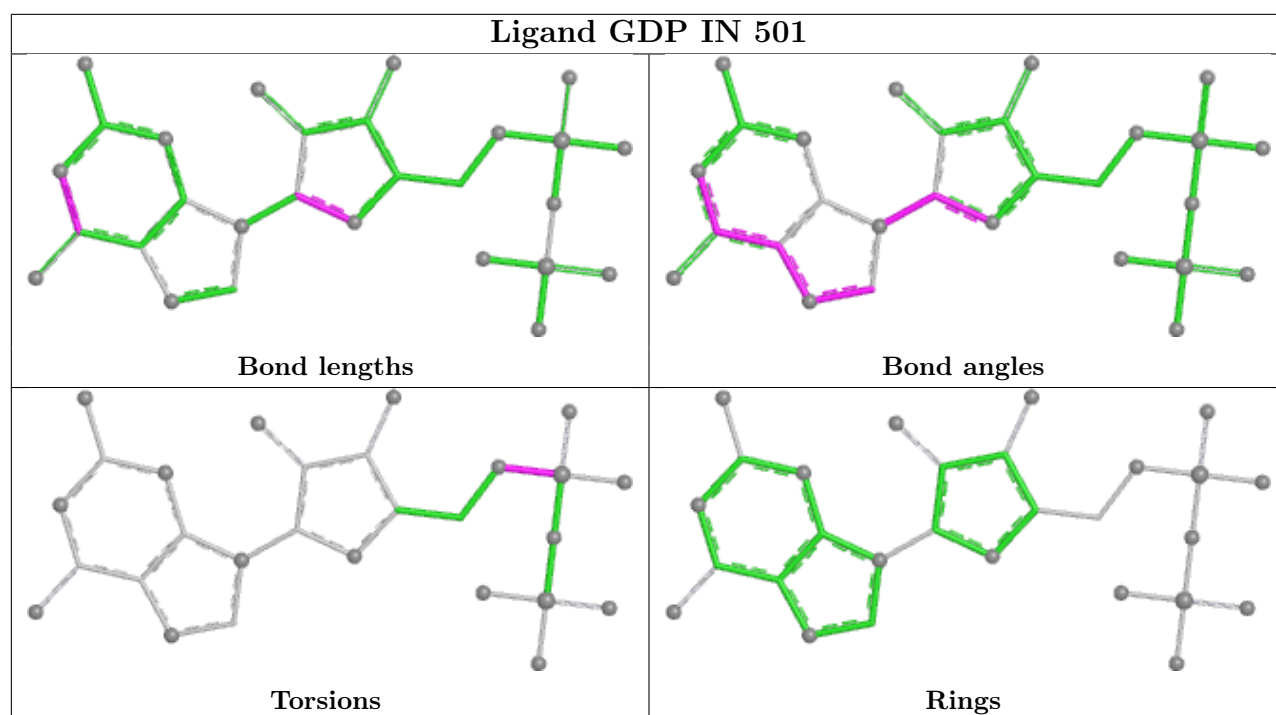


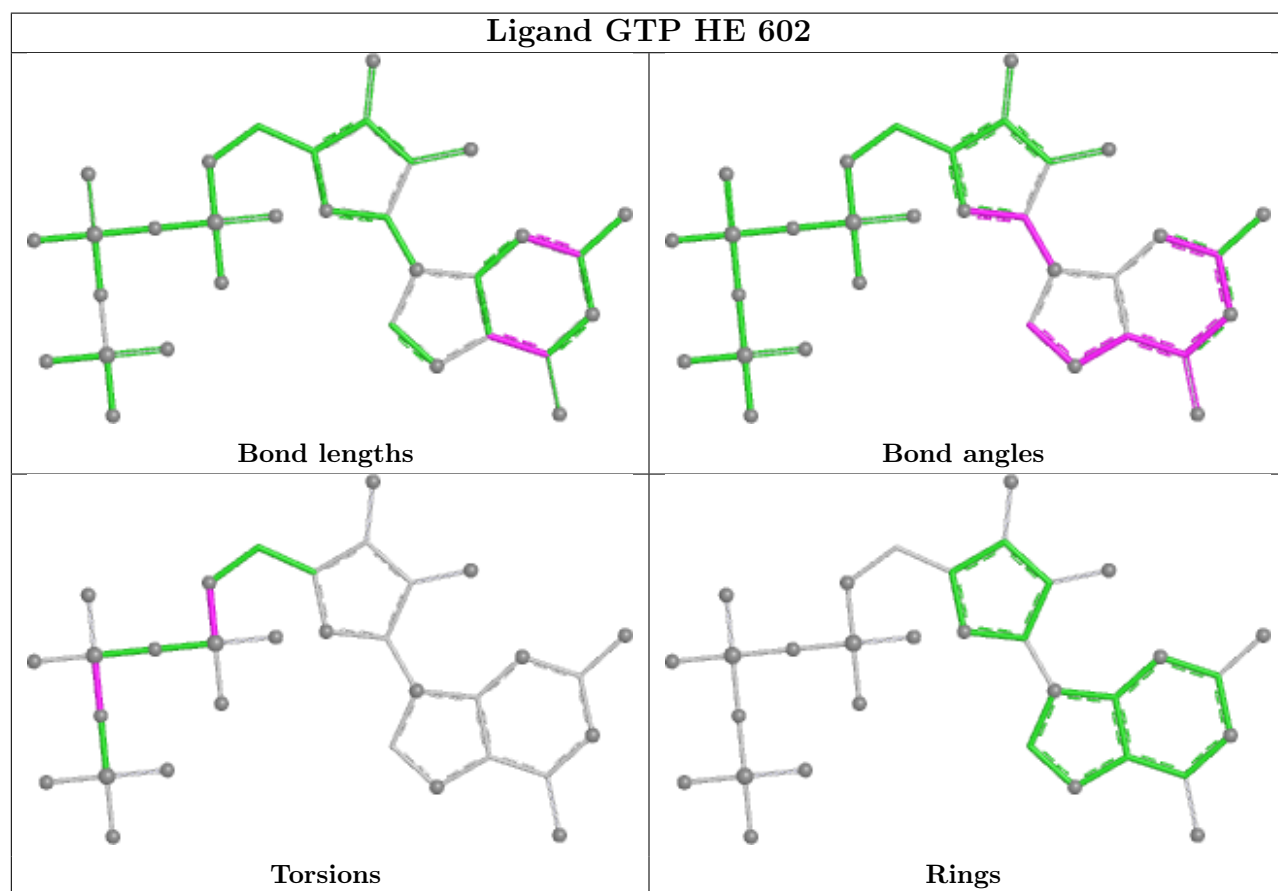
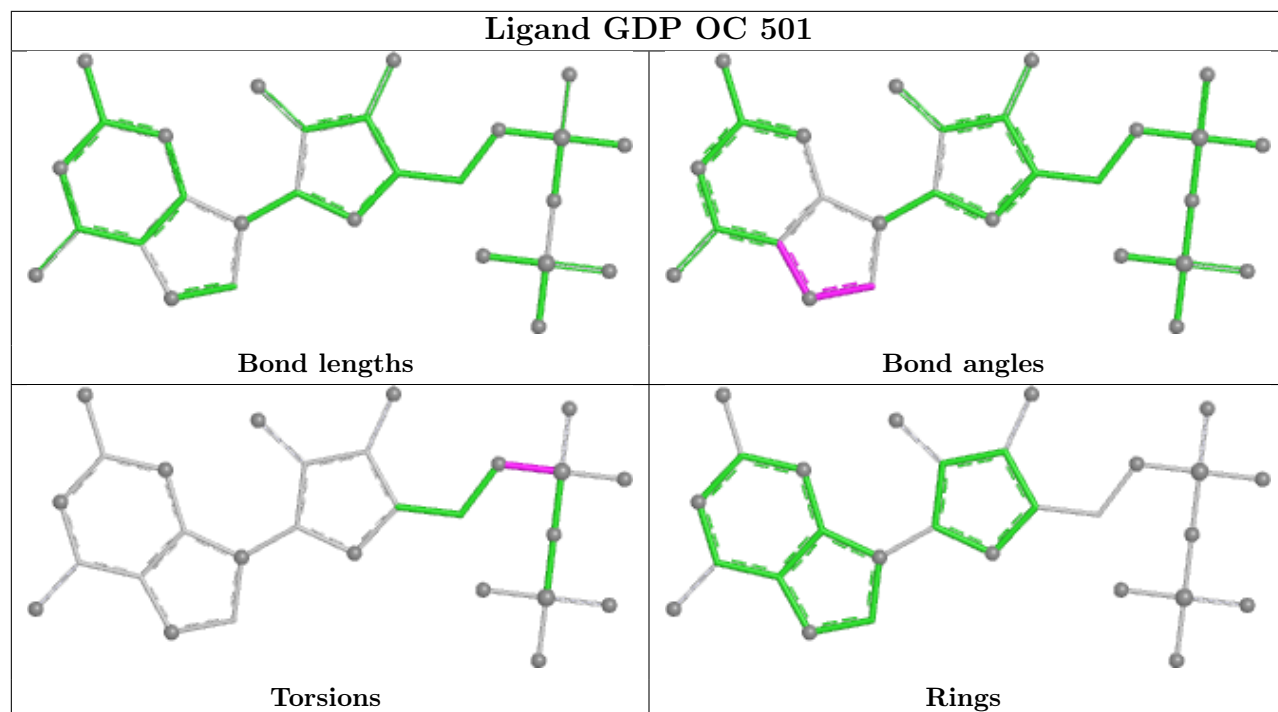
## Ligand GDP LM 501

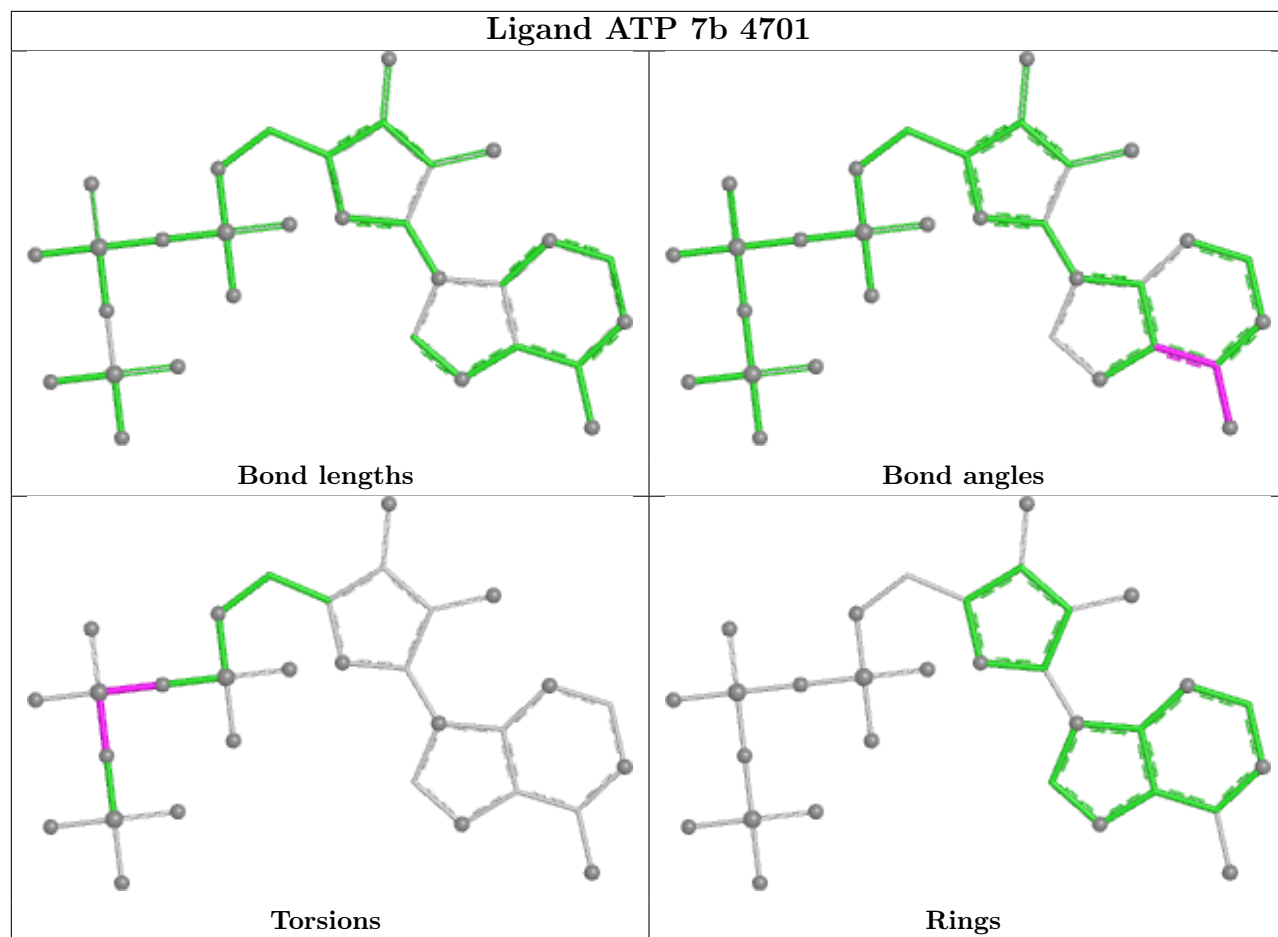


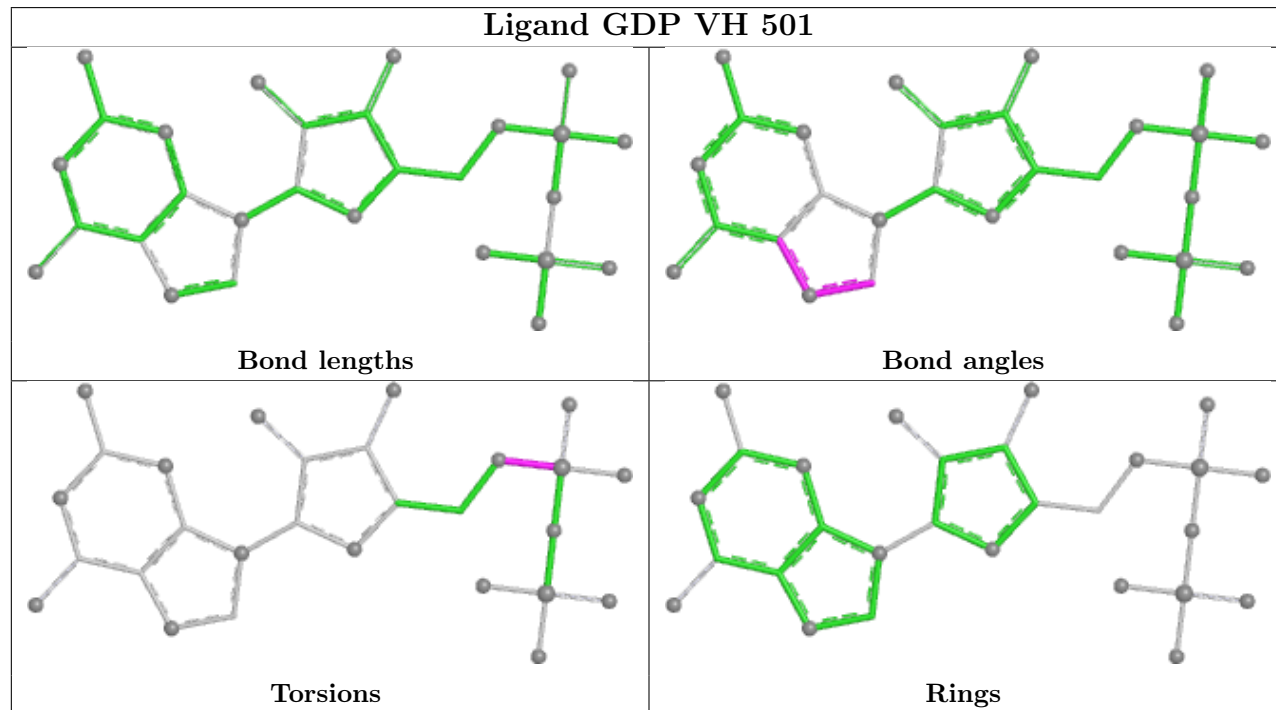
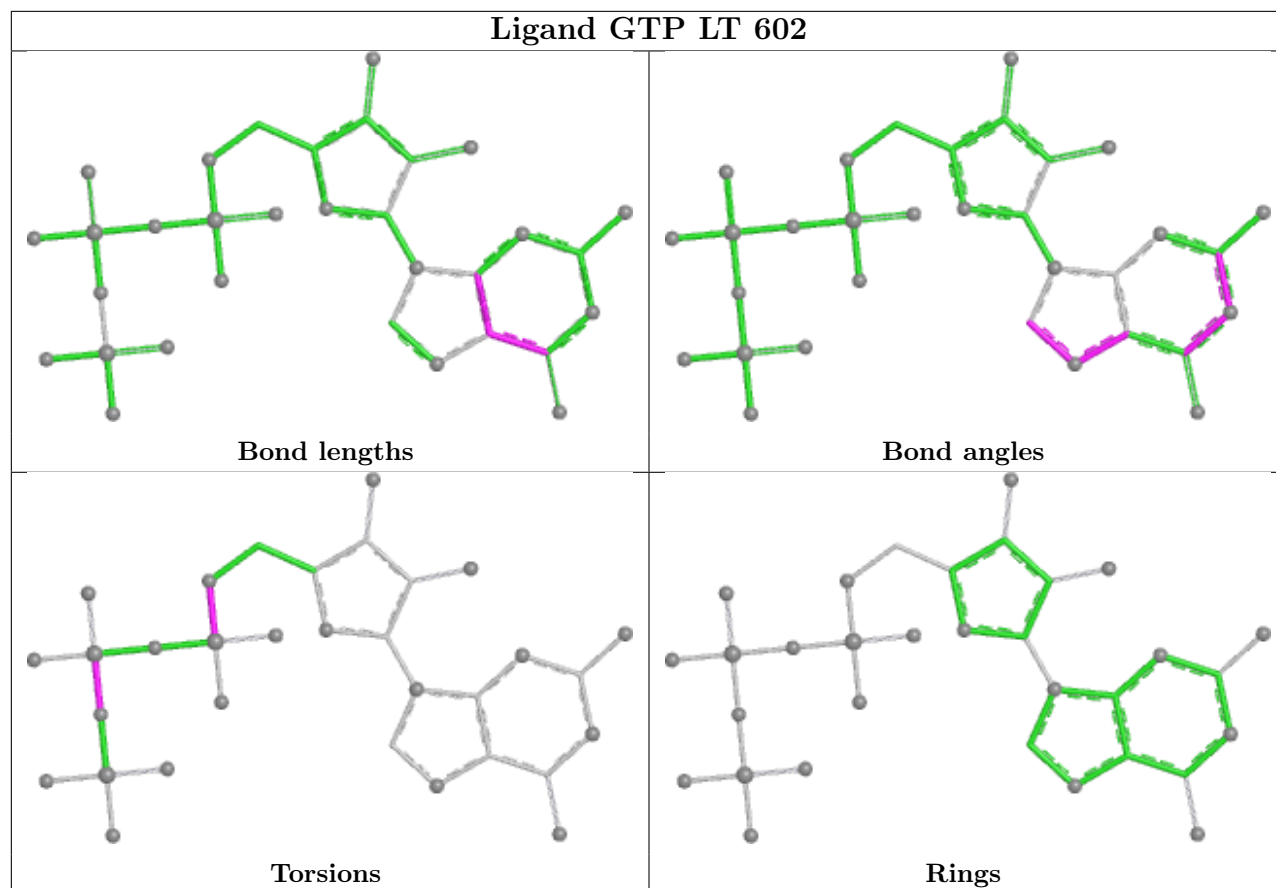
## Ligand GTP LH 501



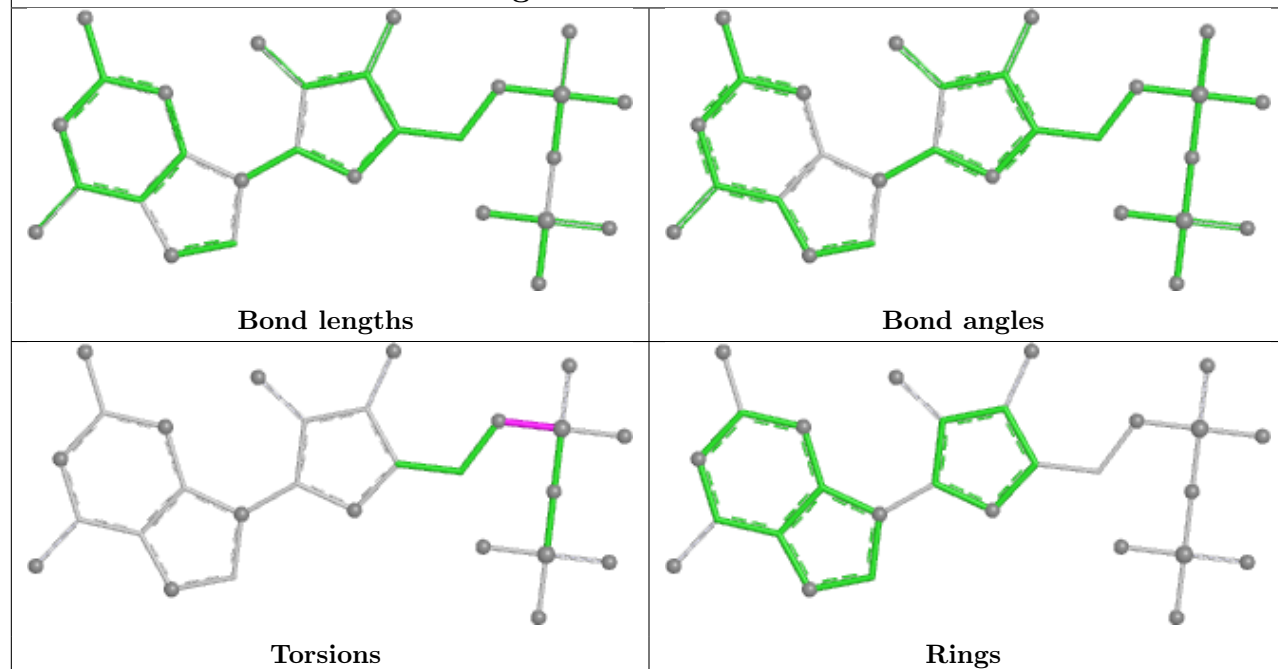




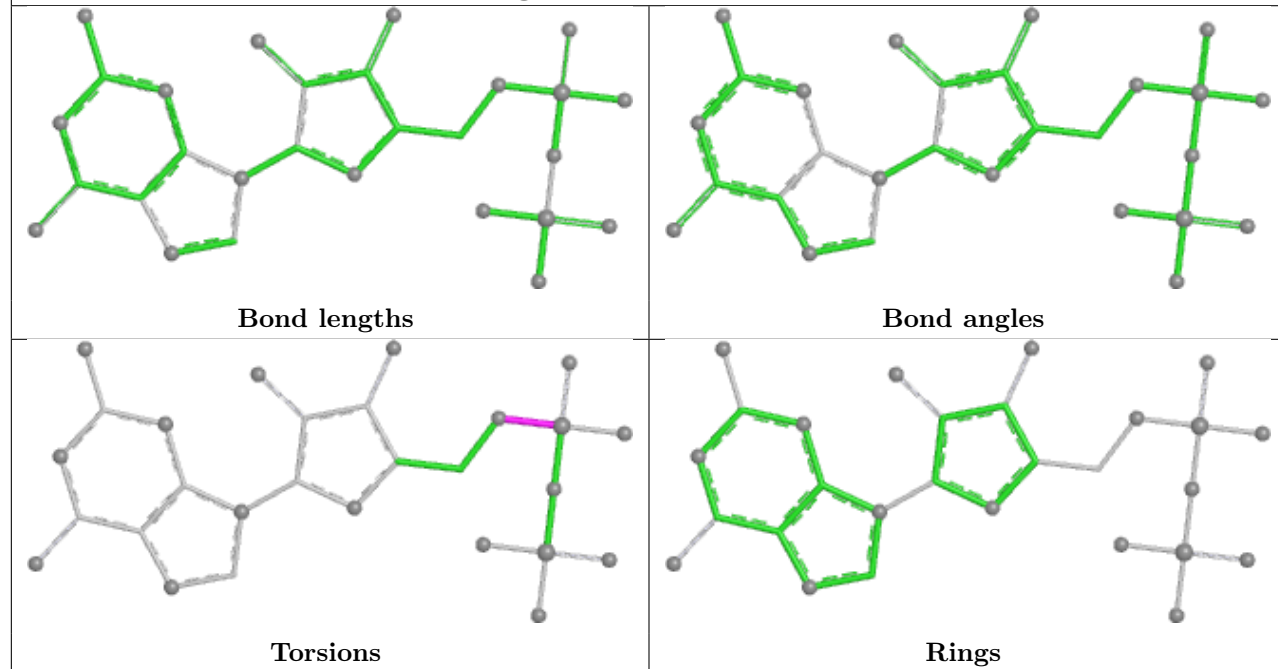




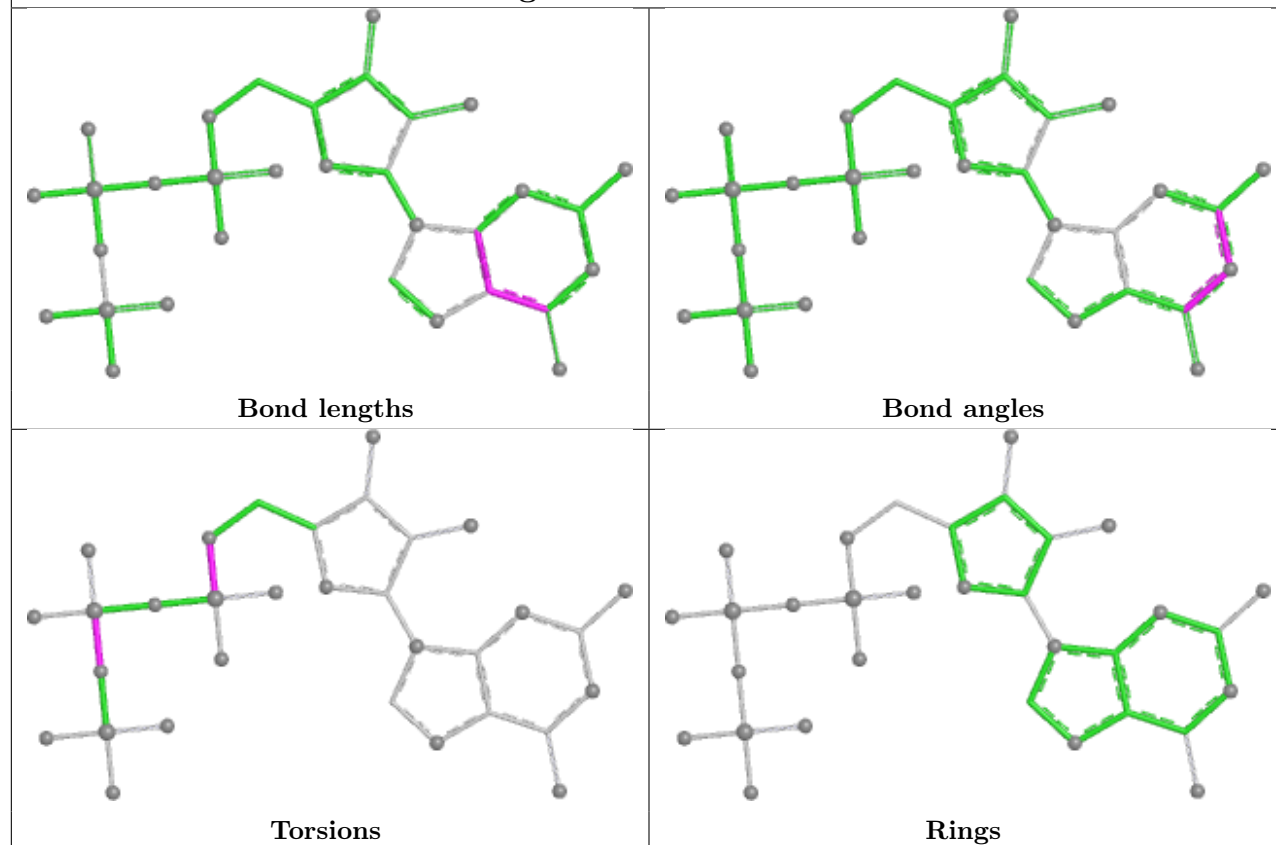
## Ligand GDP AW 501



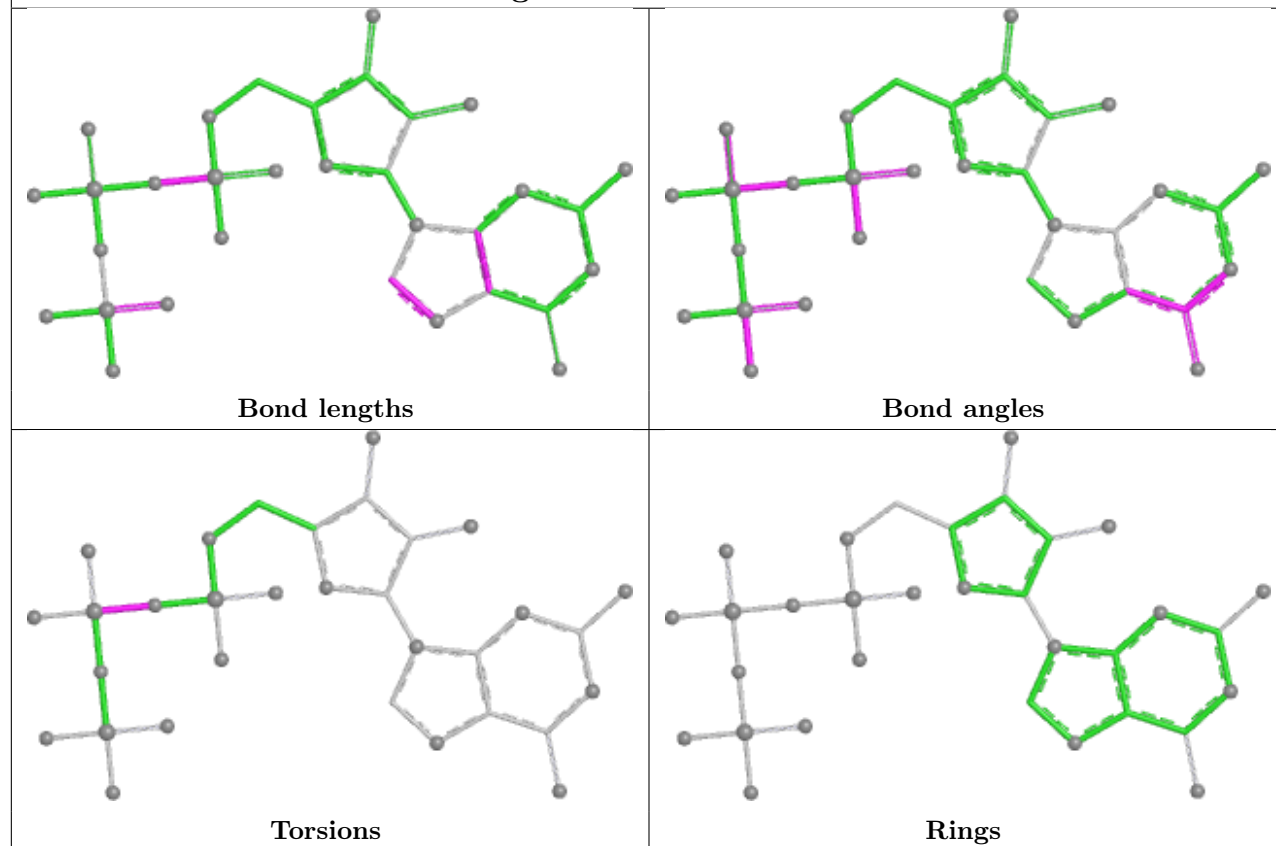
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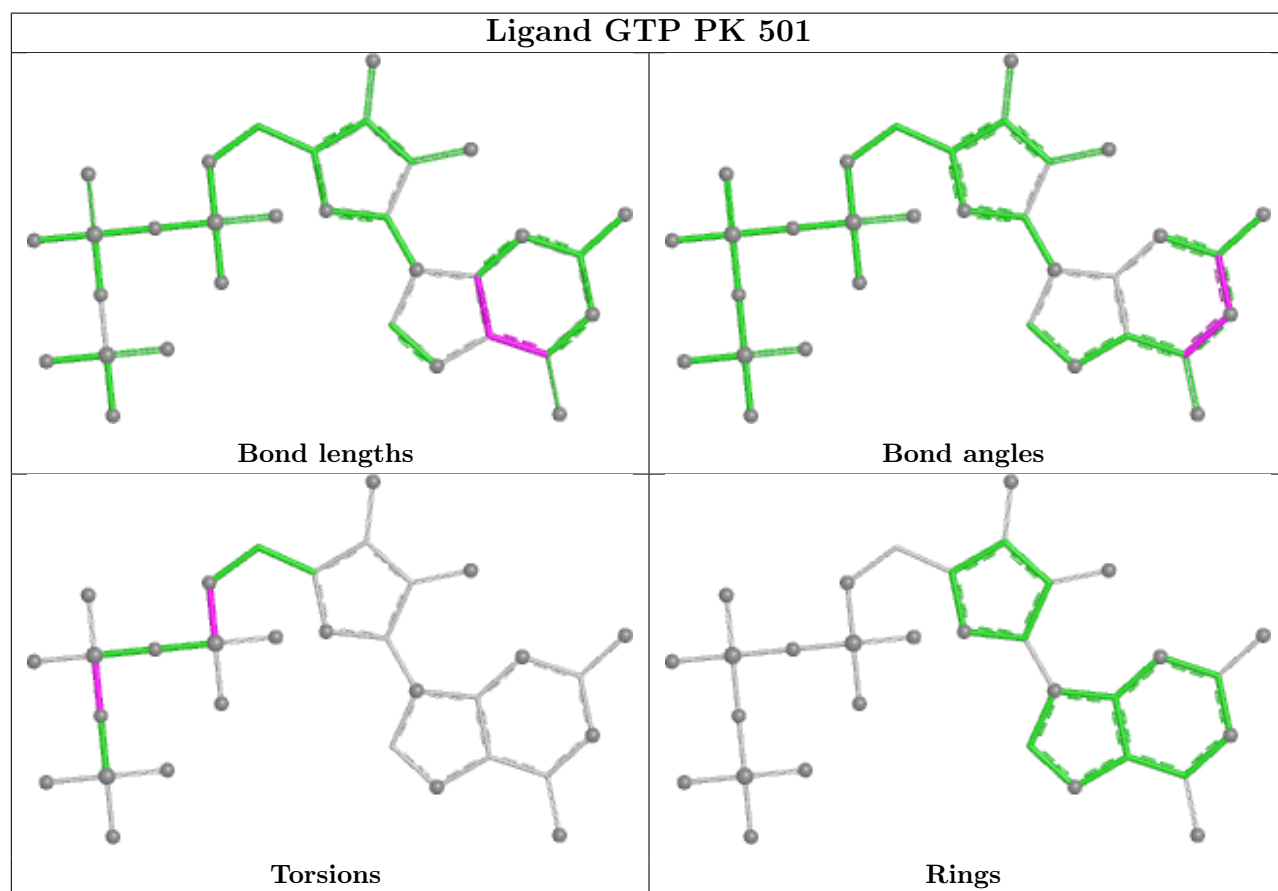
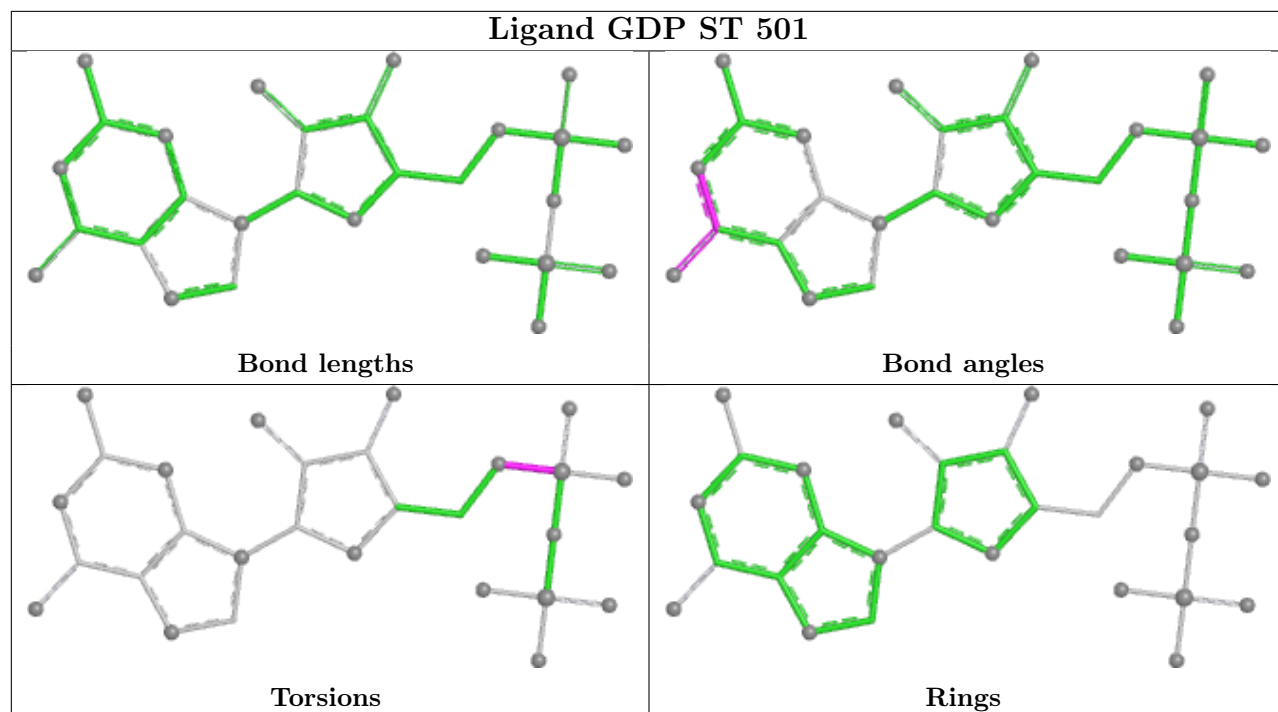
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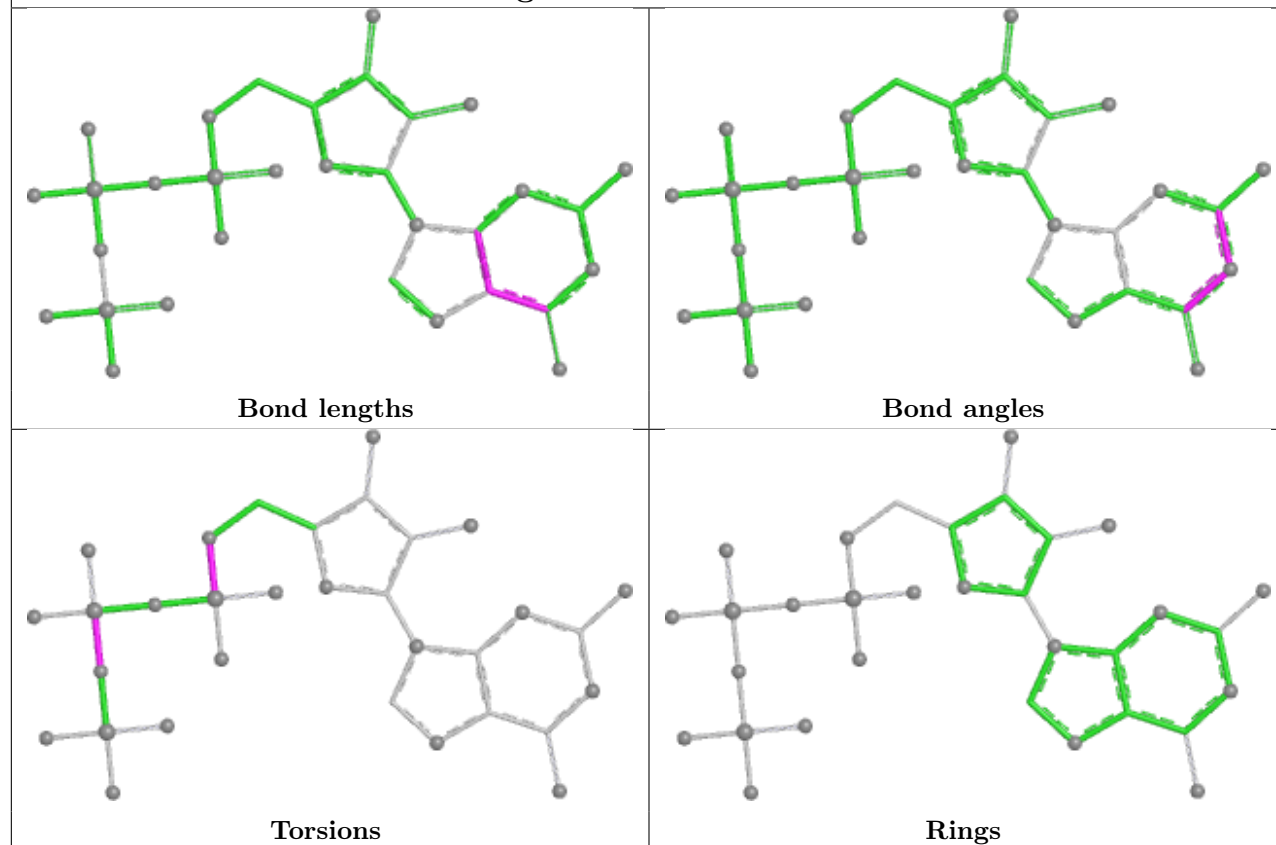
## Ligand GTP WG 501



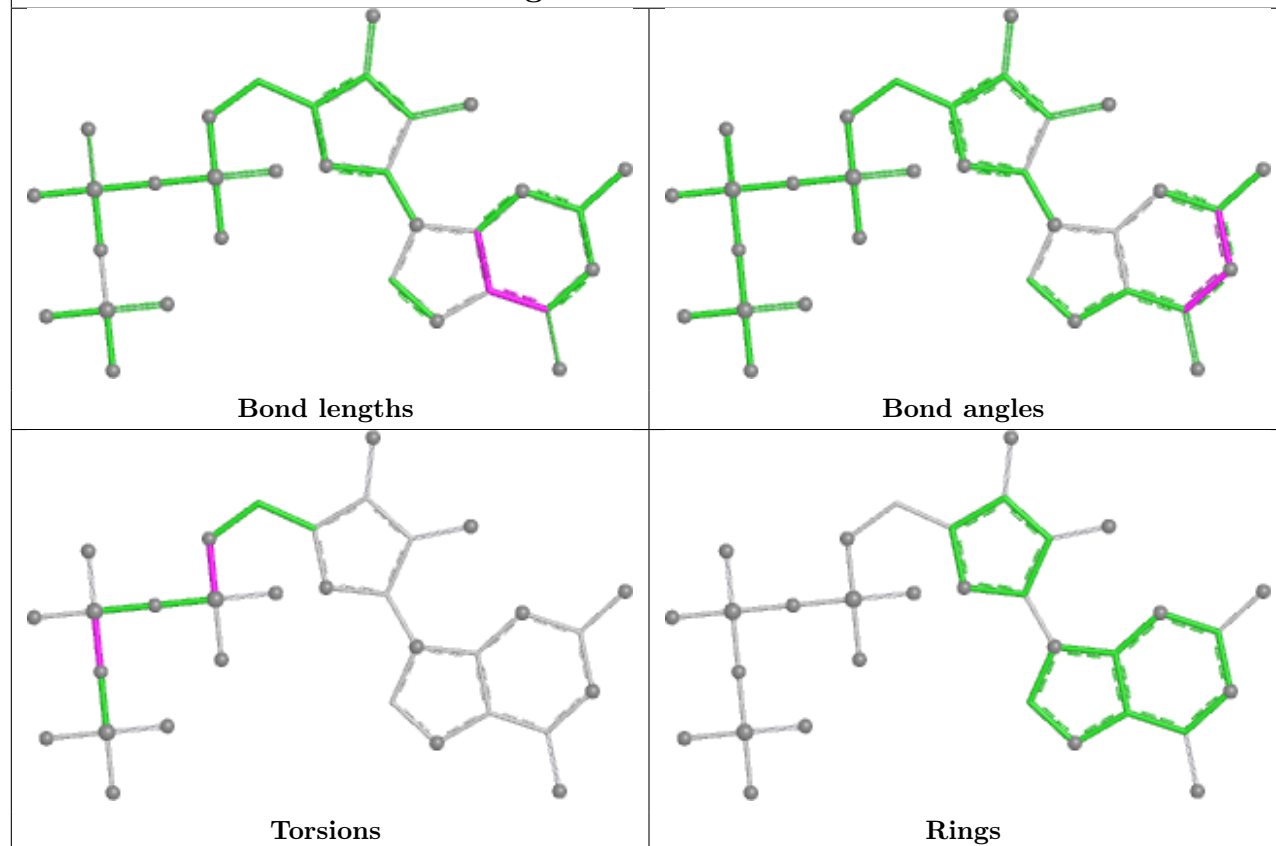


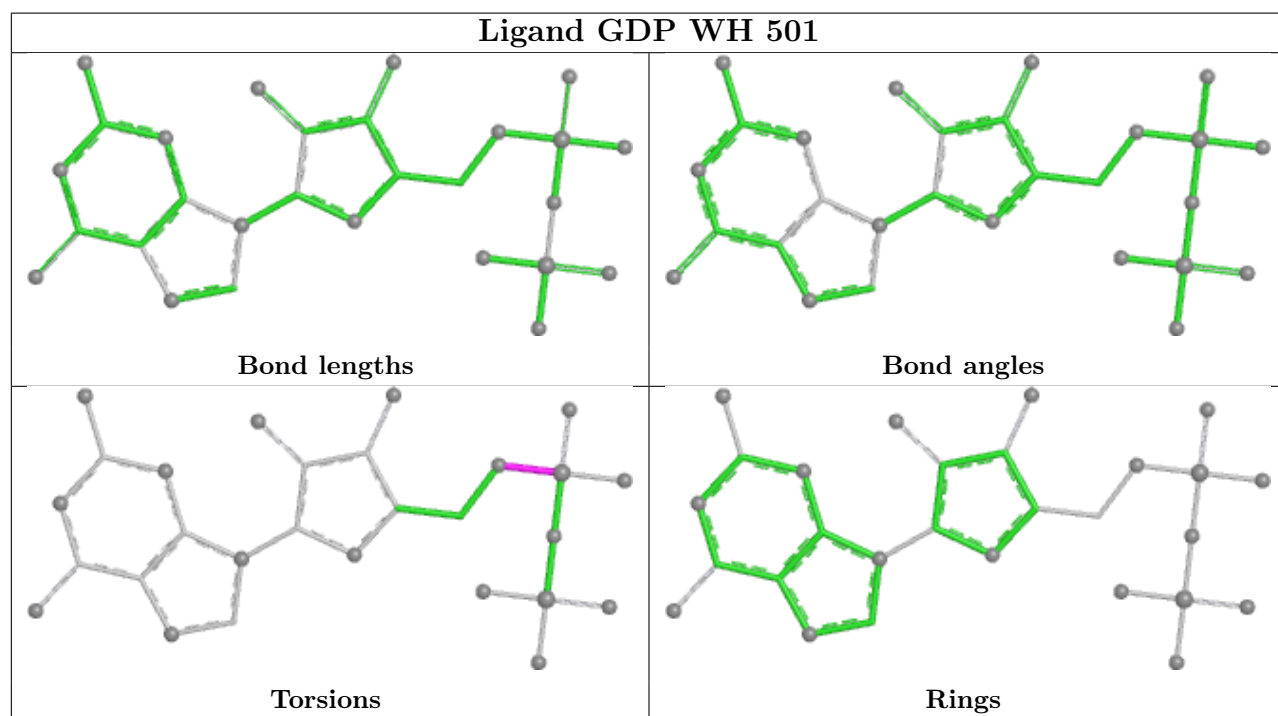
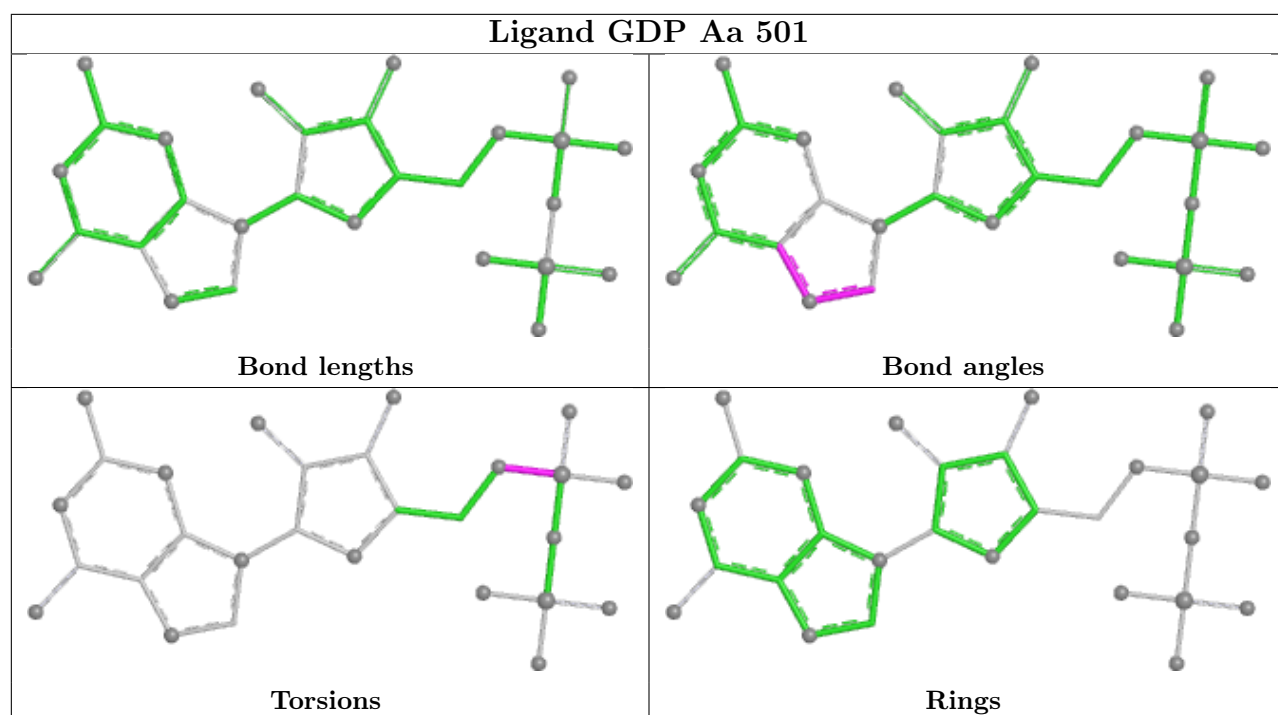


## Ligand GTP VG 501

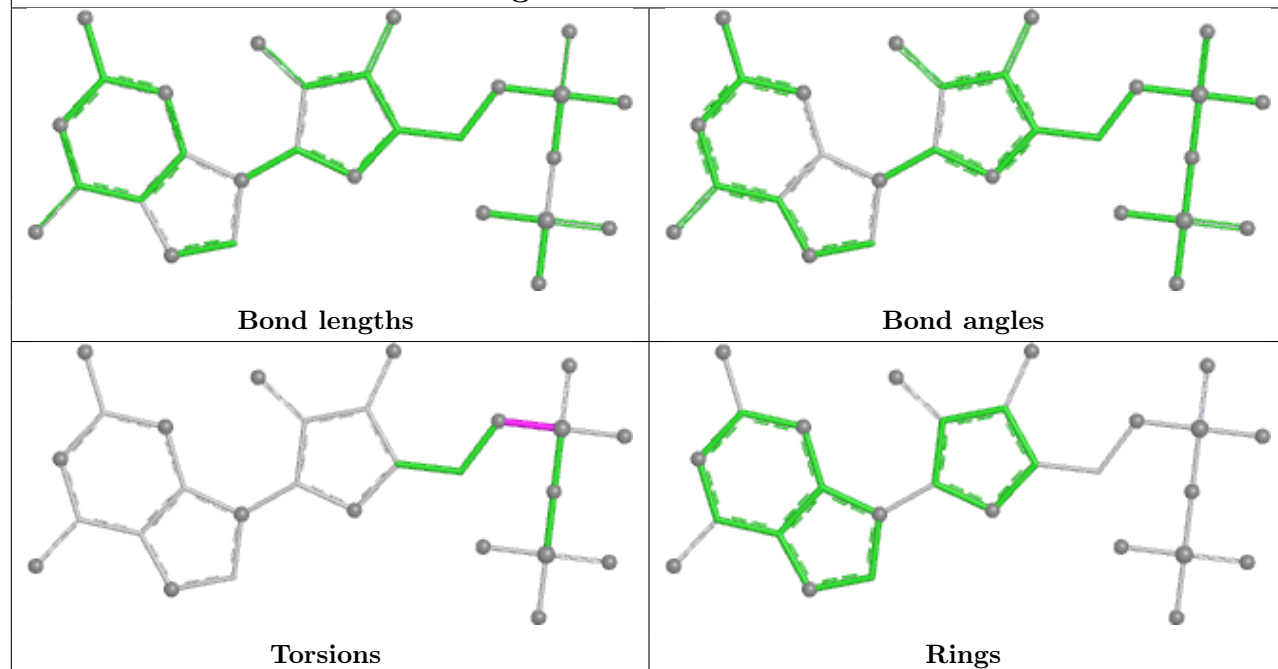


## Ligand GTP AI 602

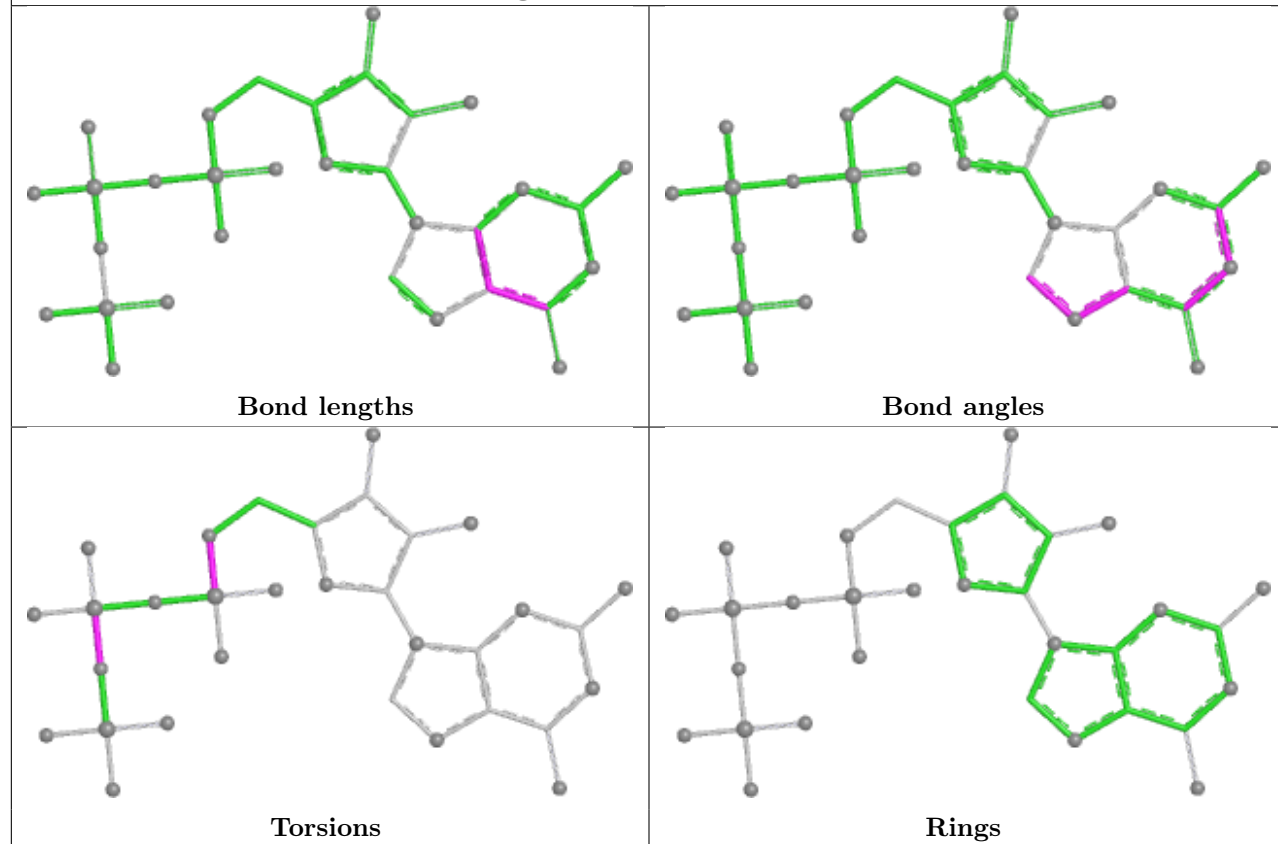


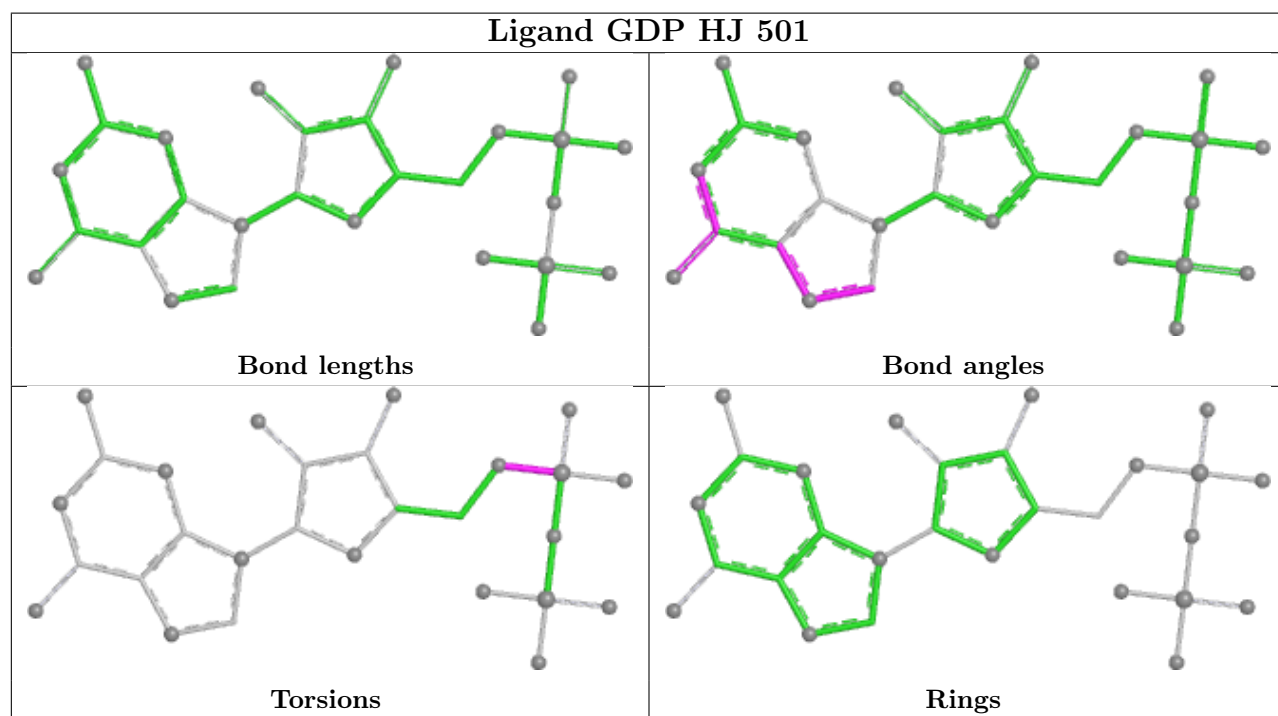
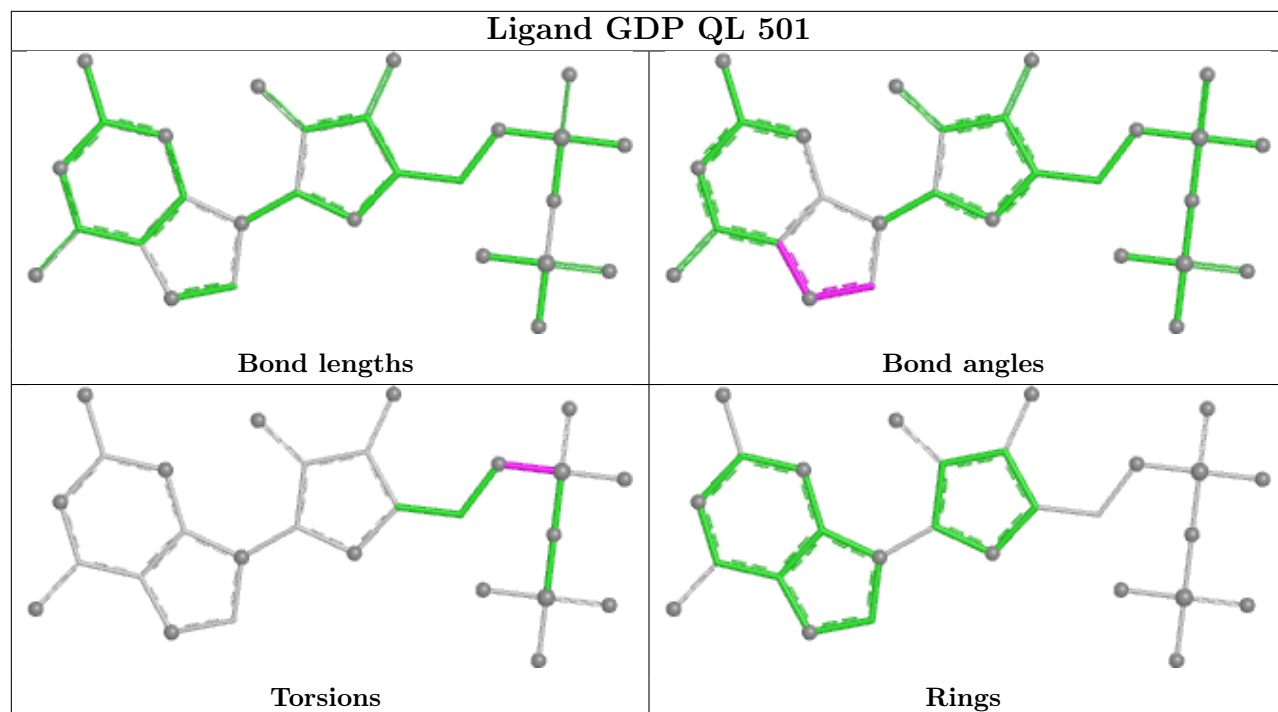


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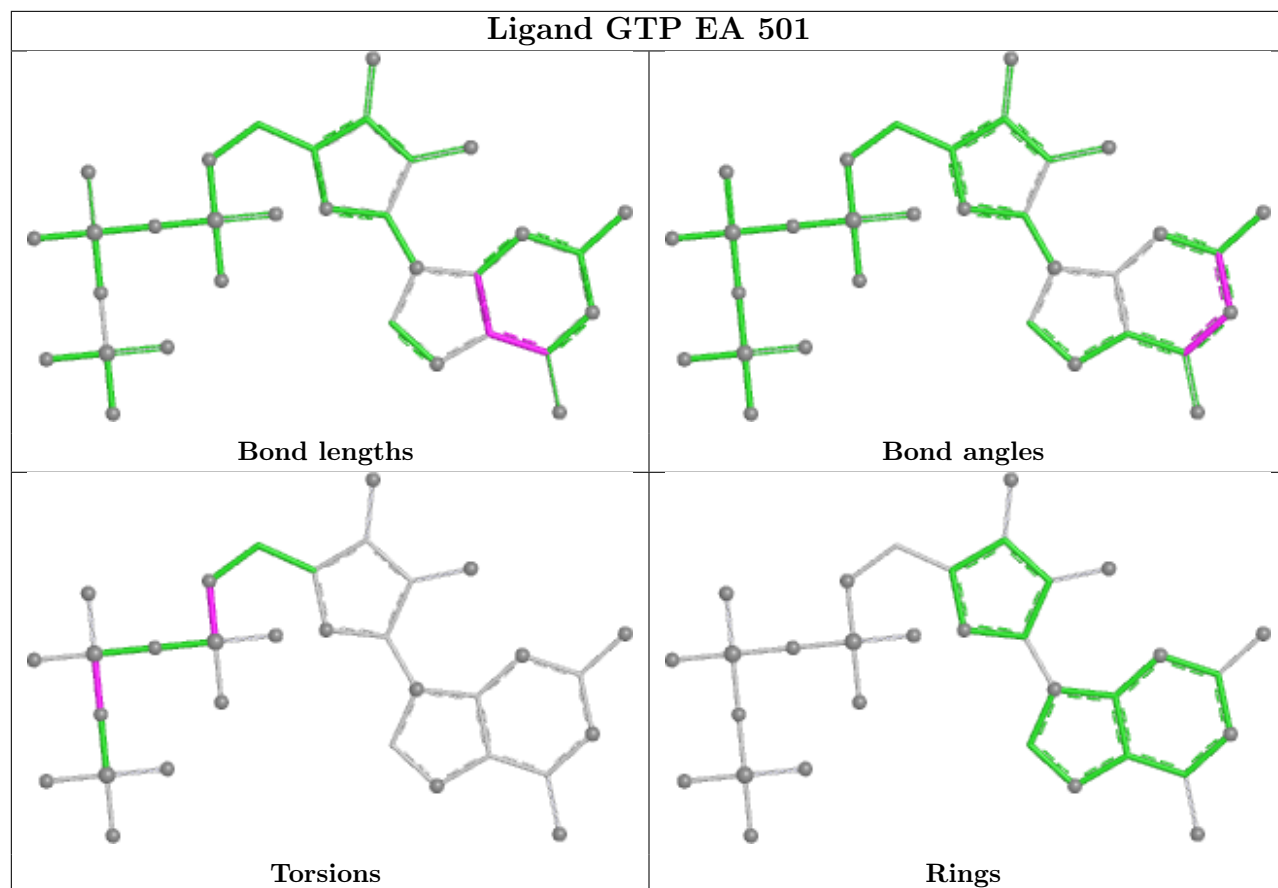


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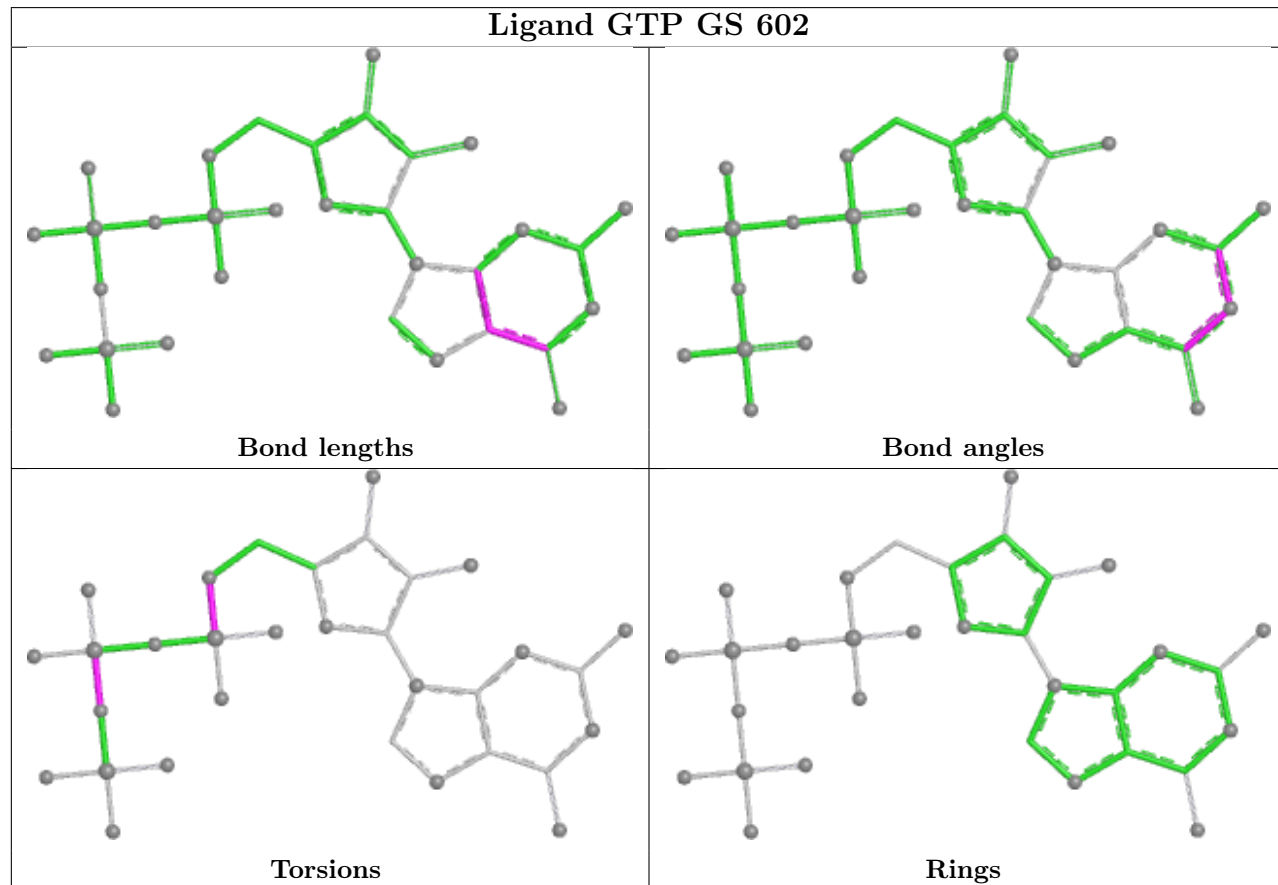




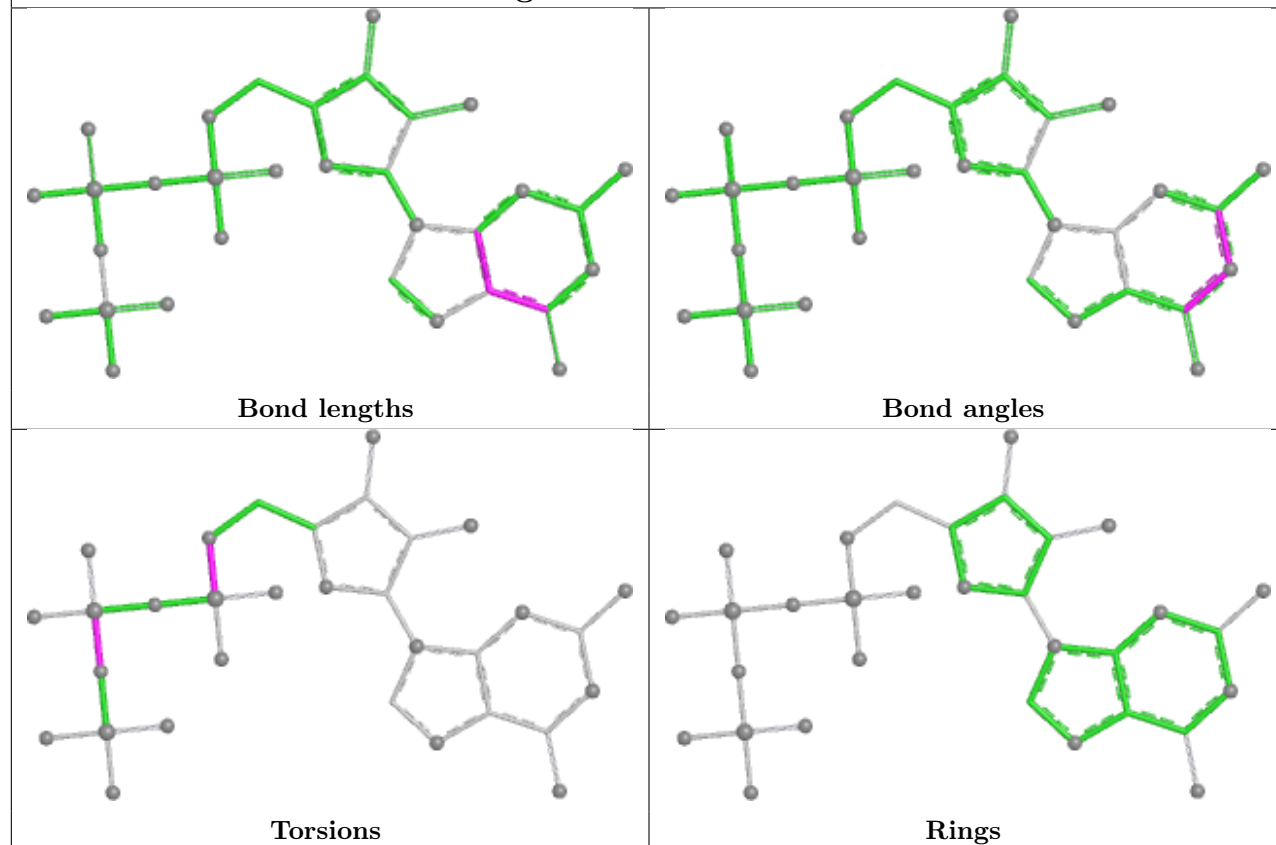
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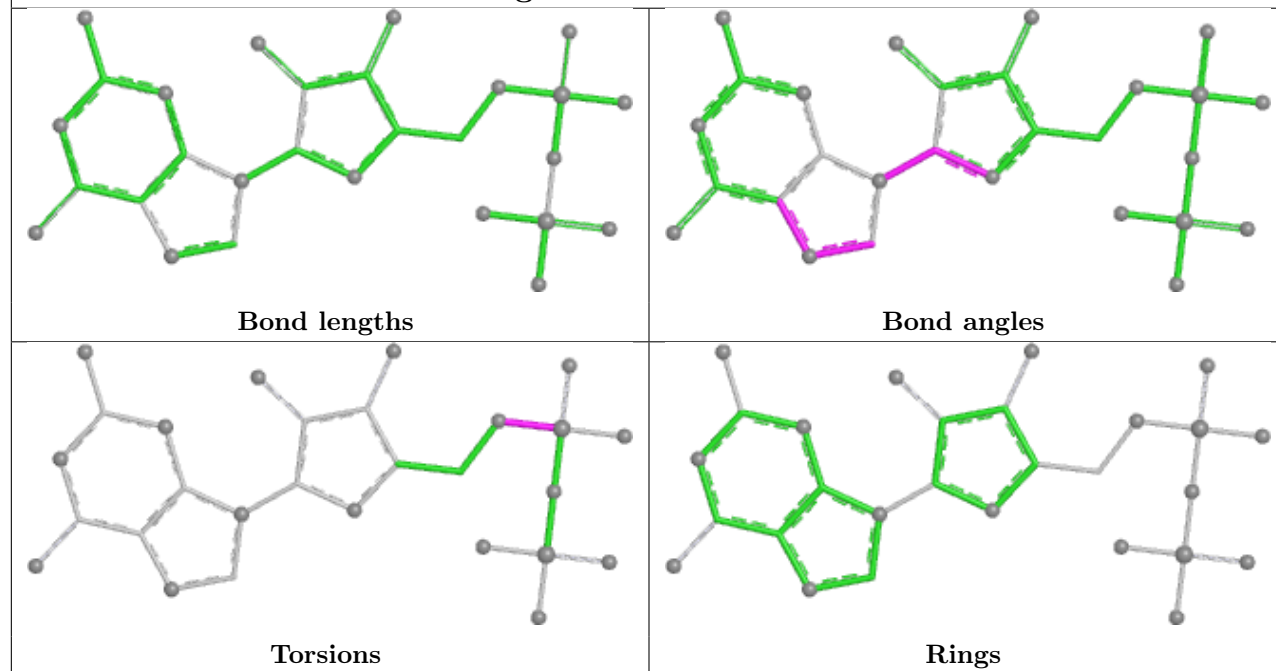
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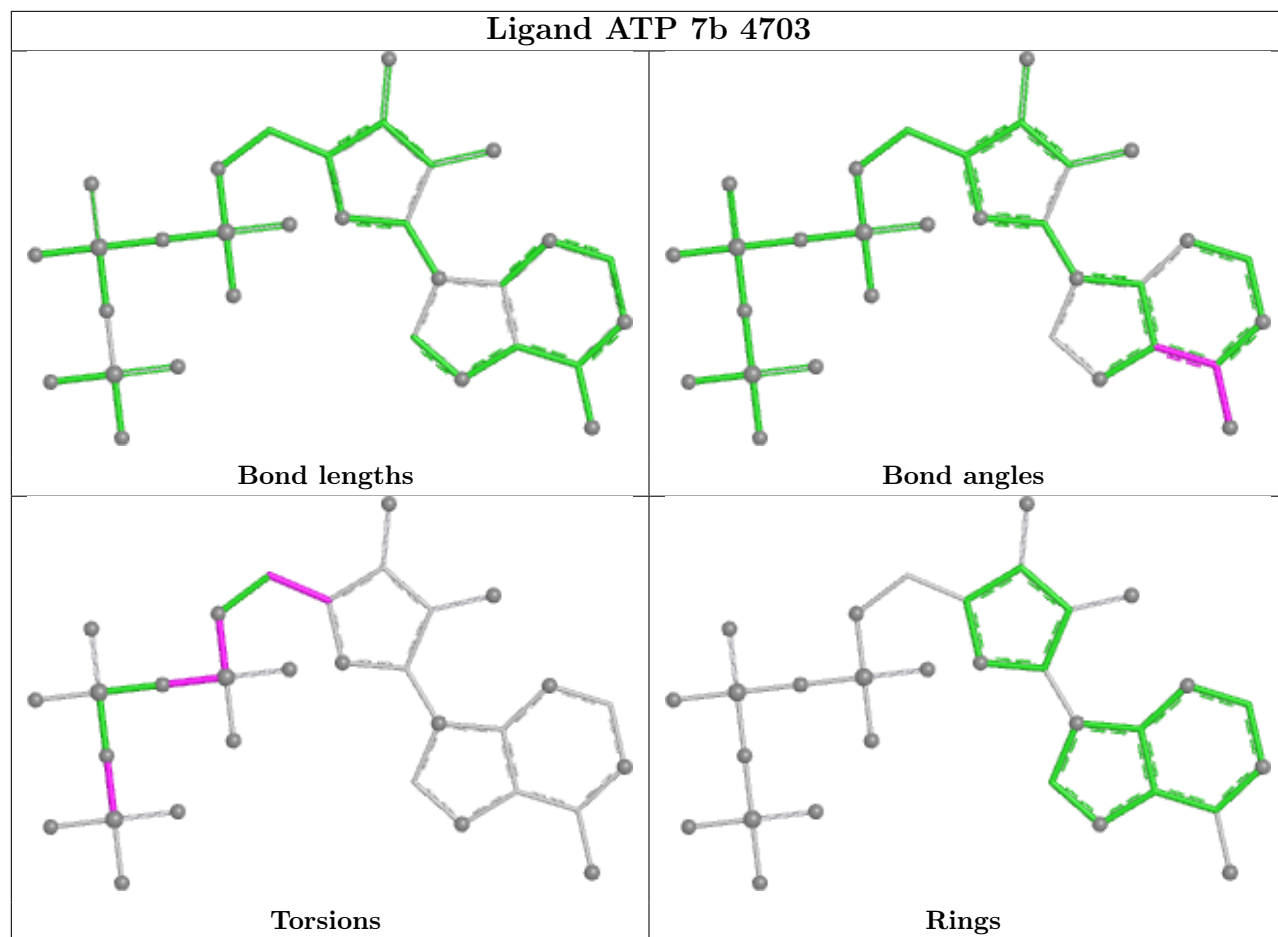


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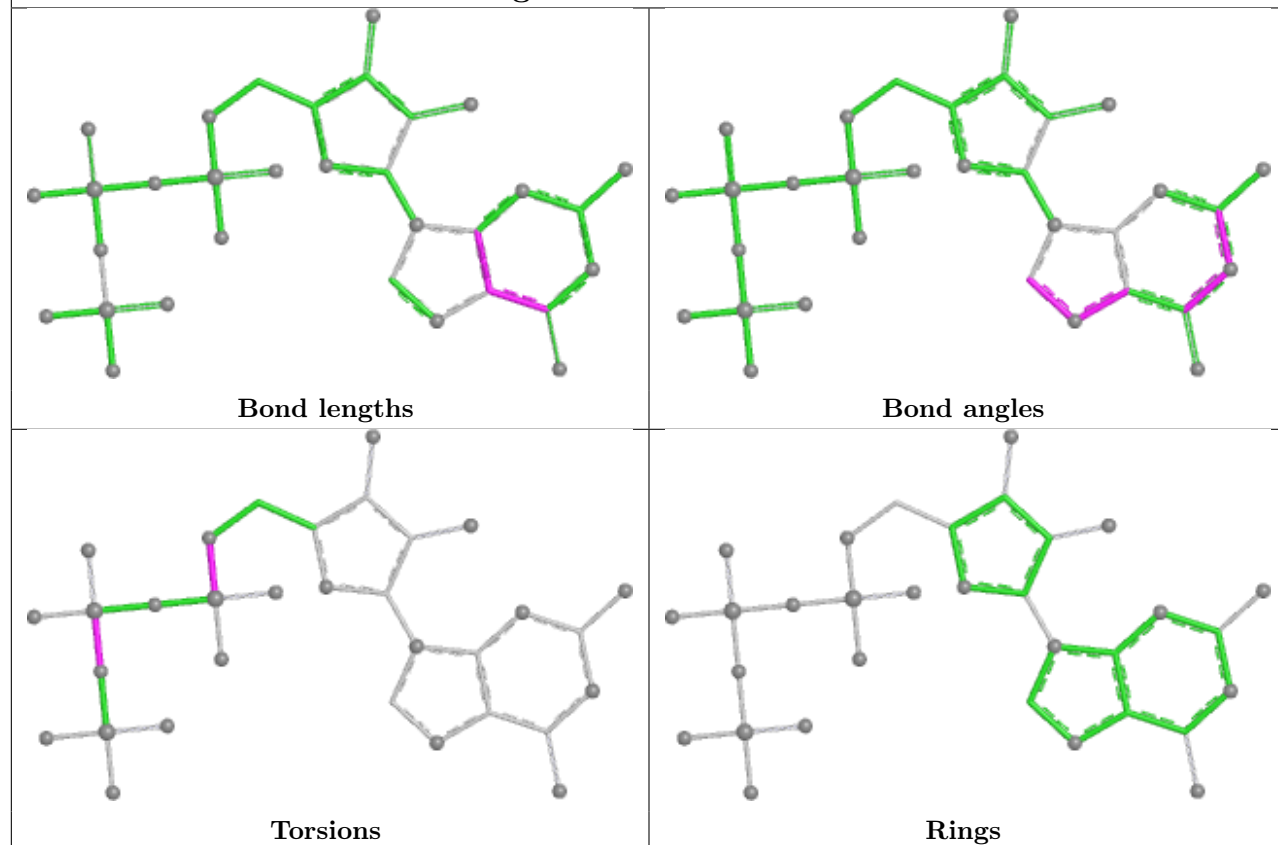
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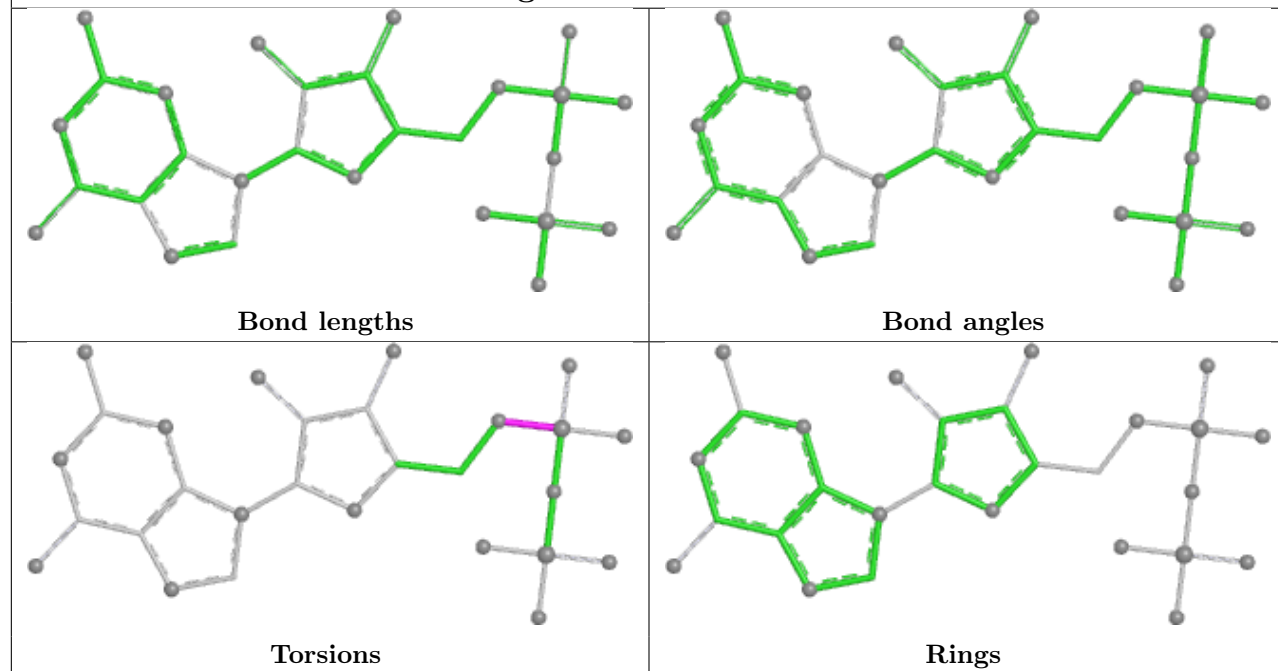




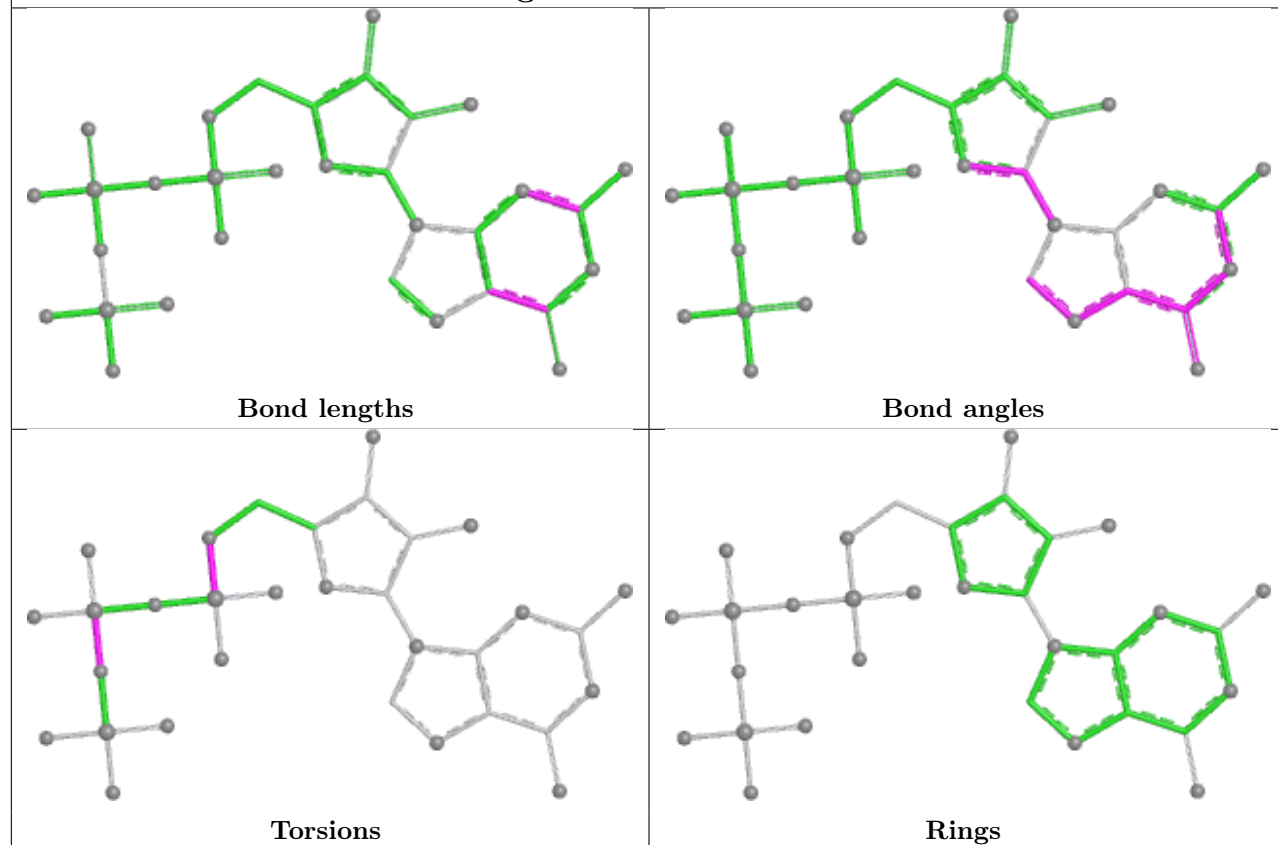
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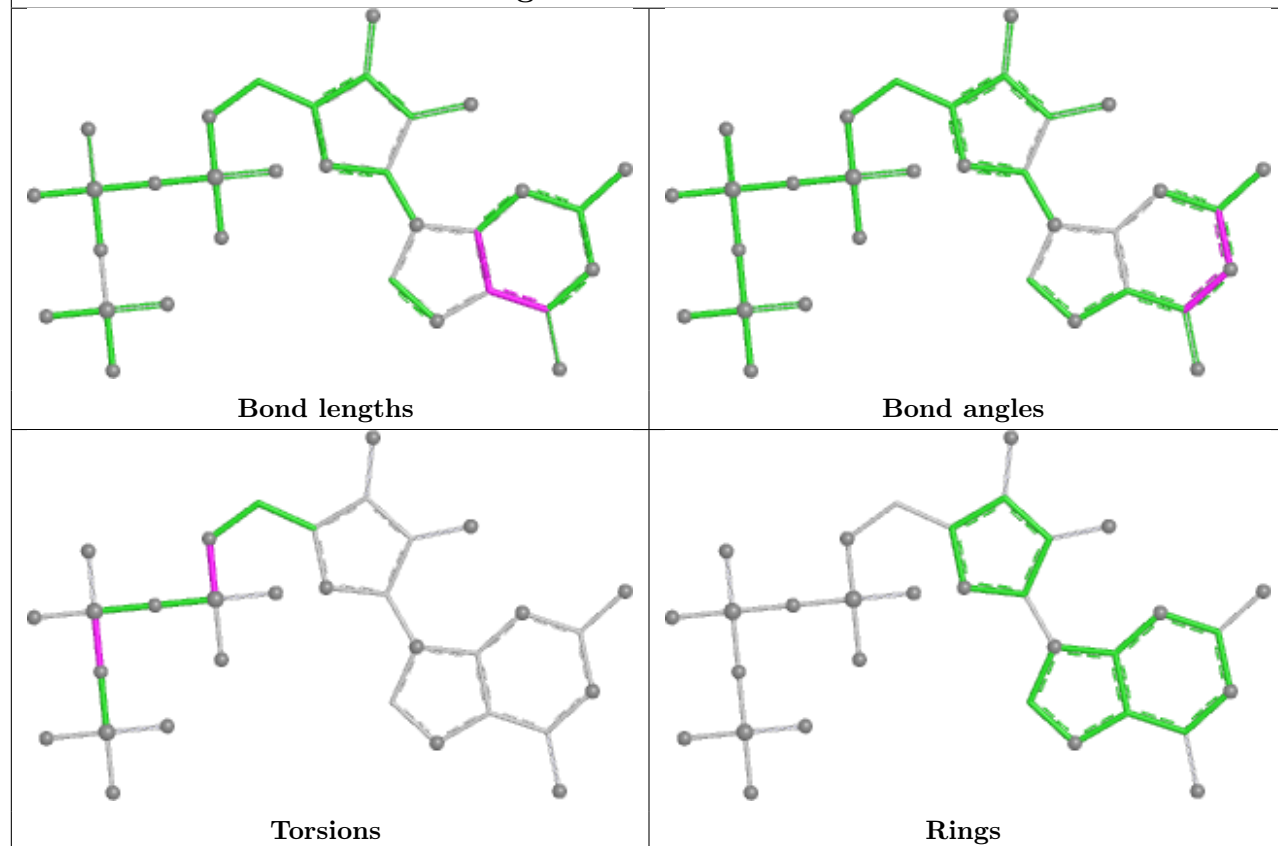
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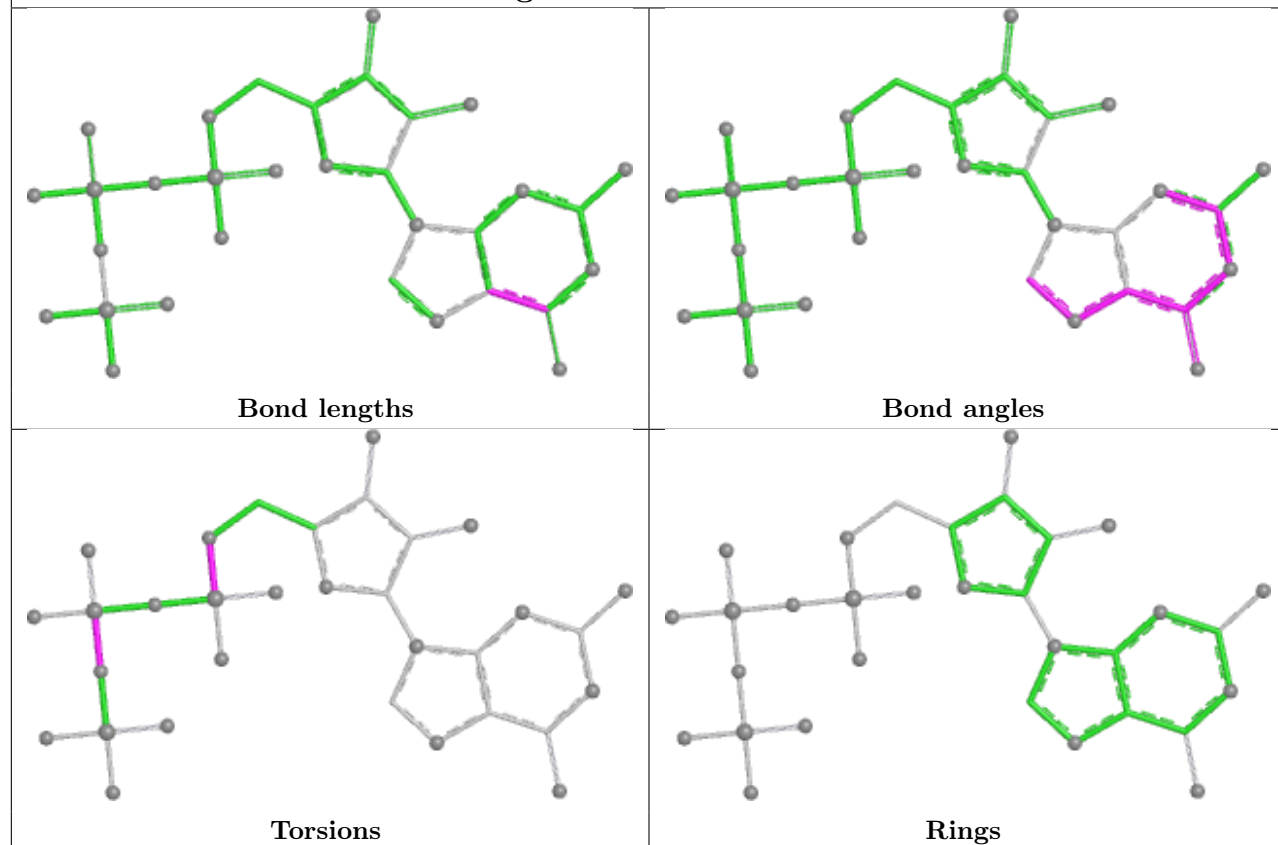
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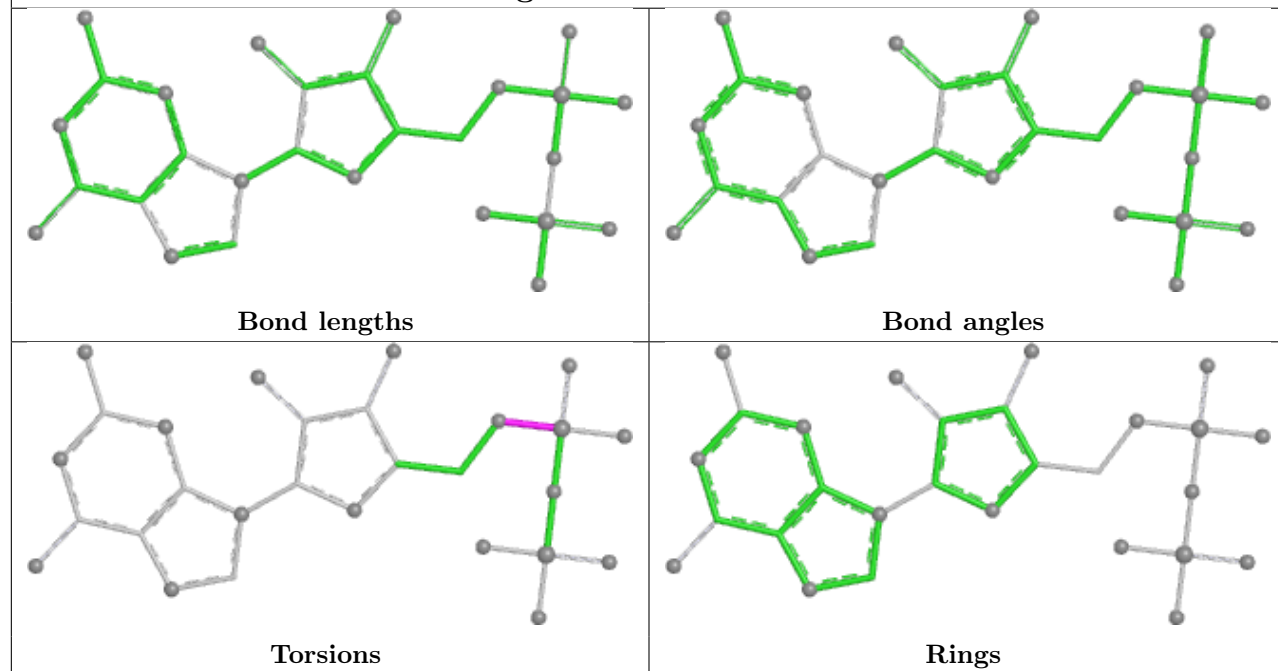
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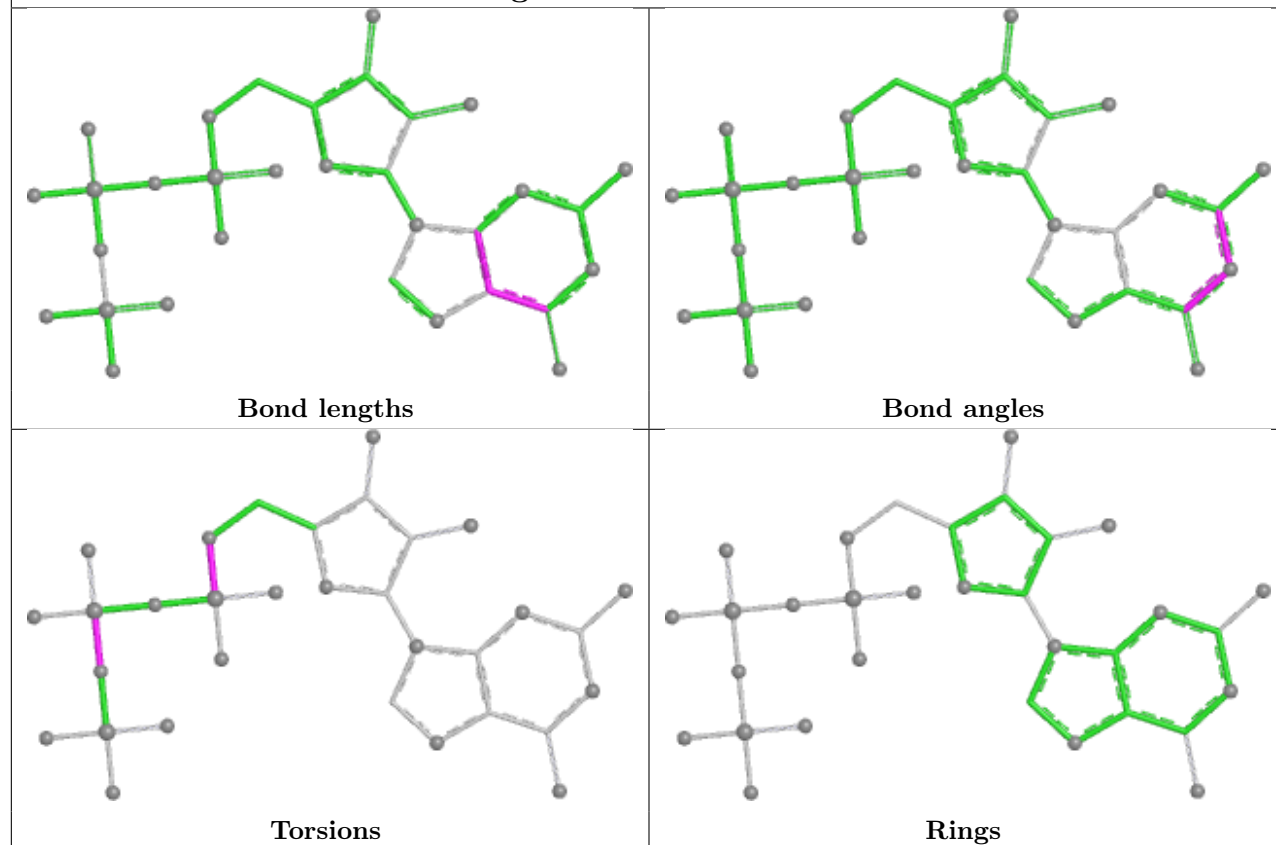
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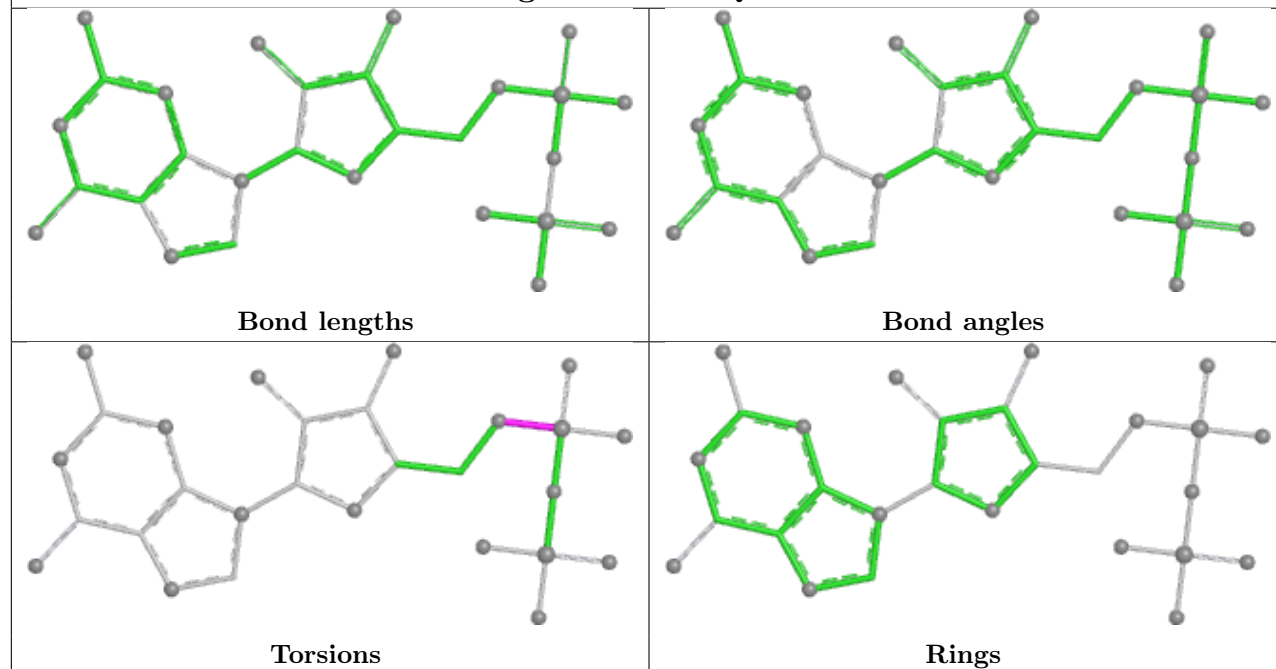
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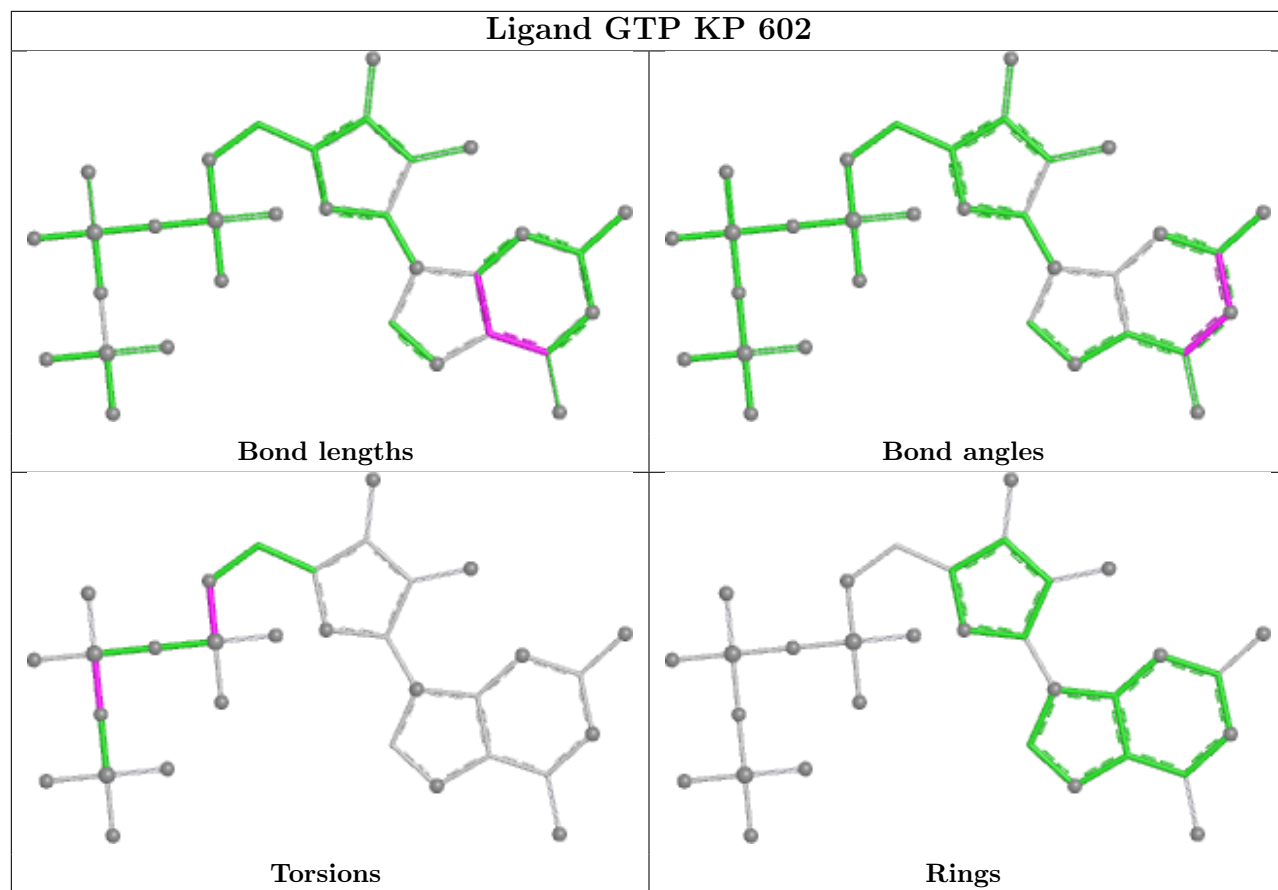


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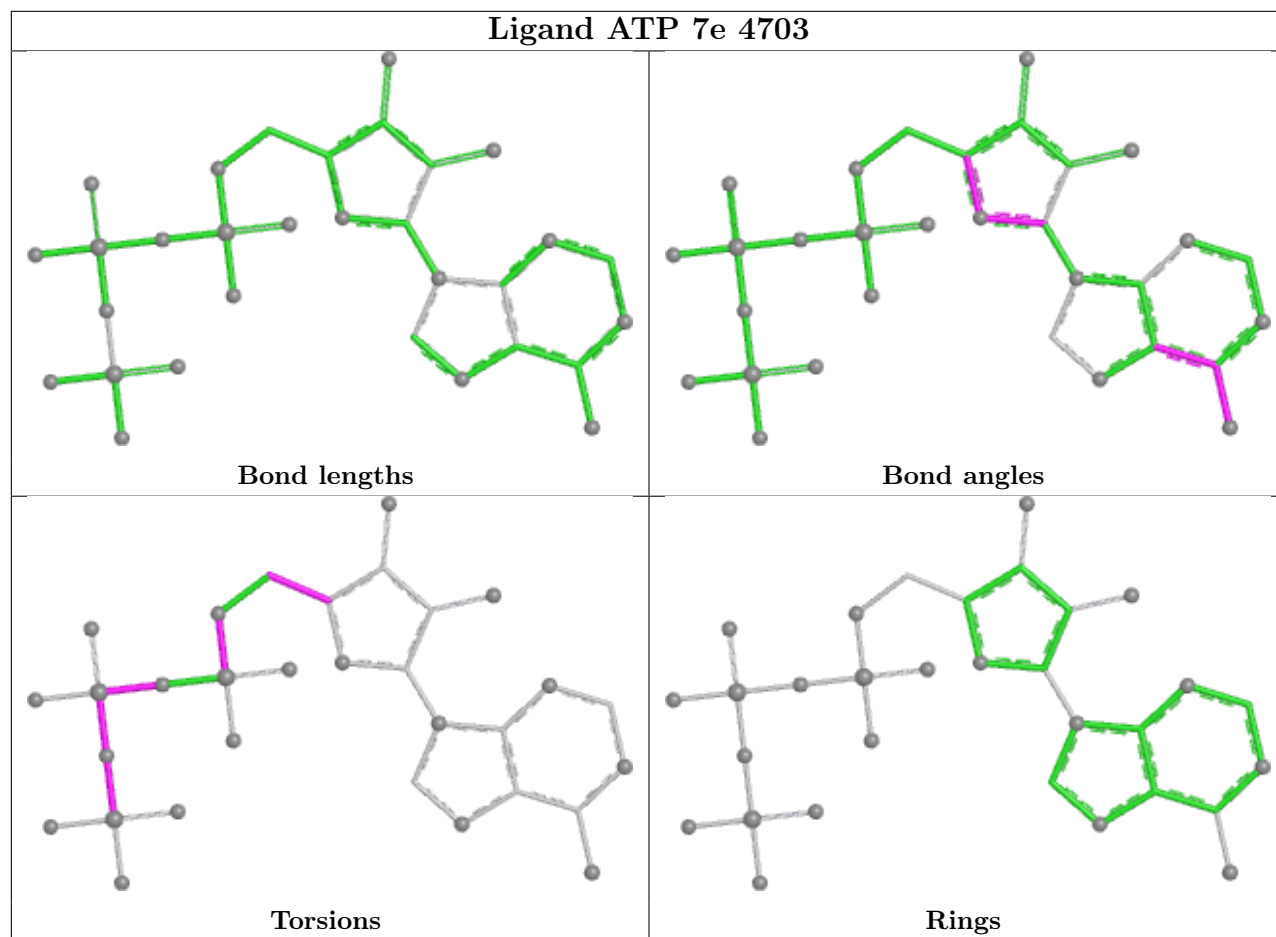


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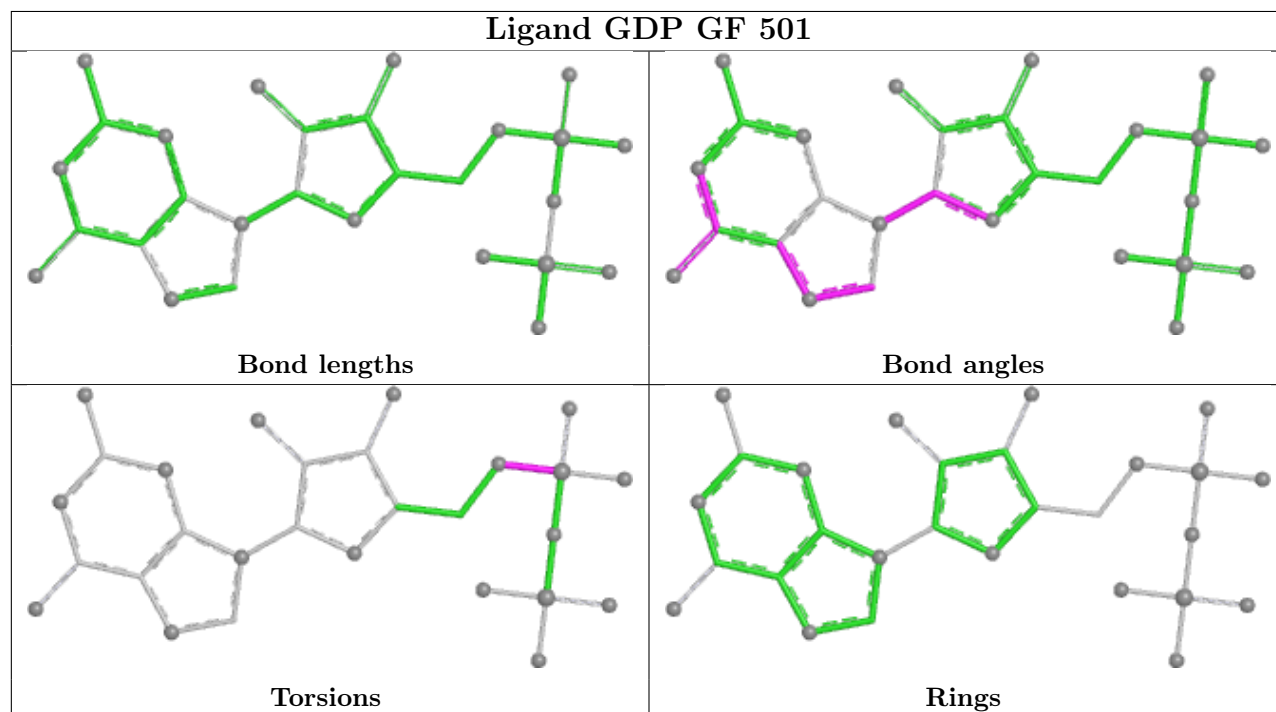


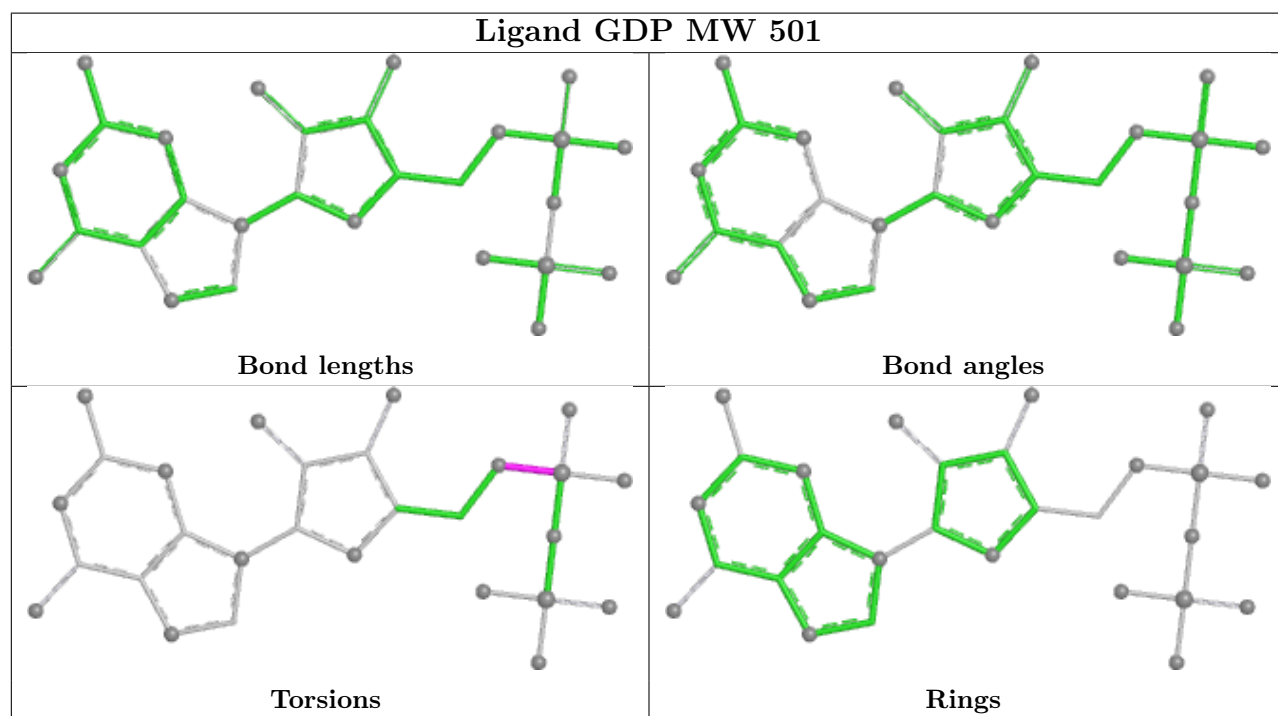
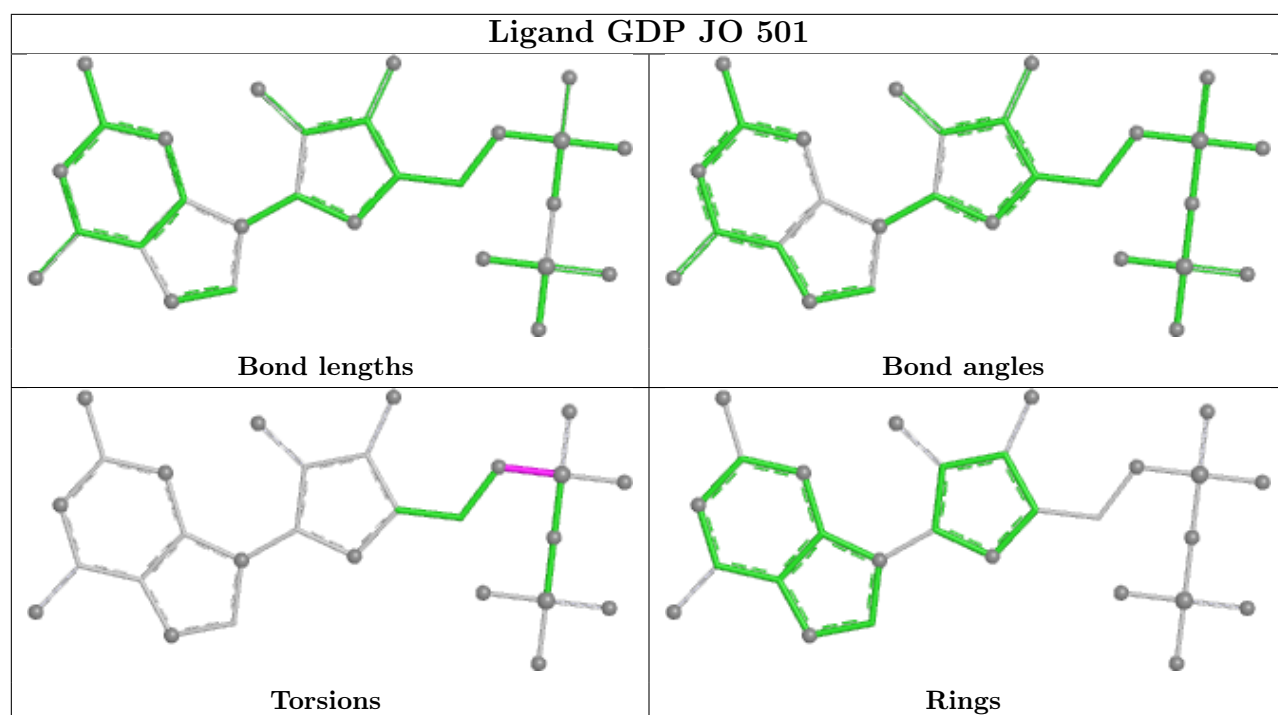


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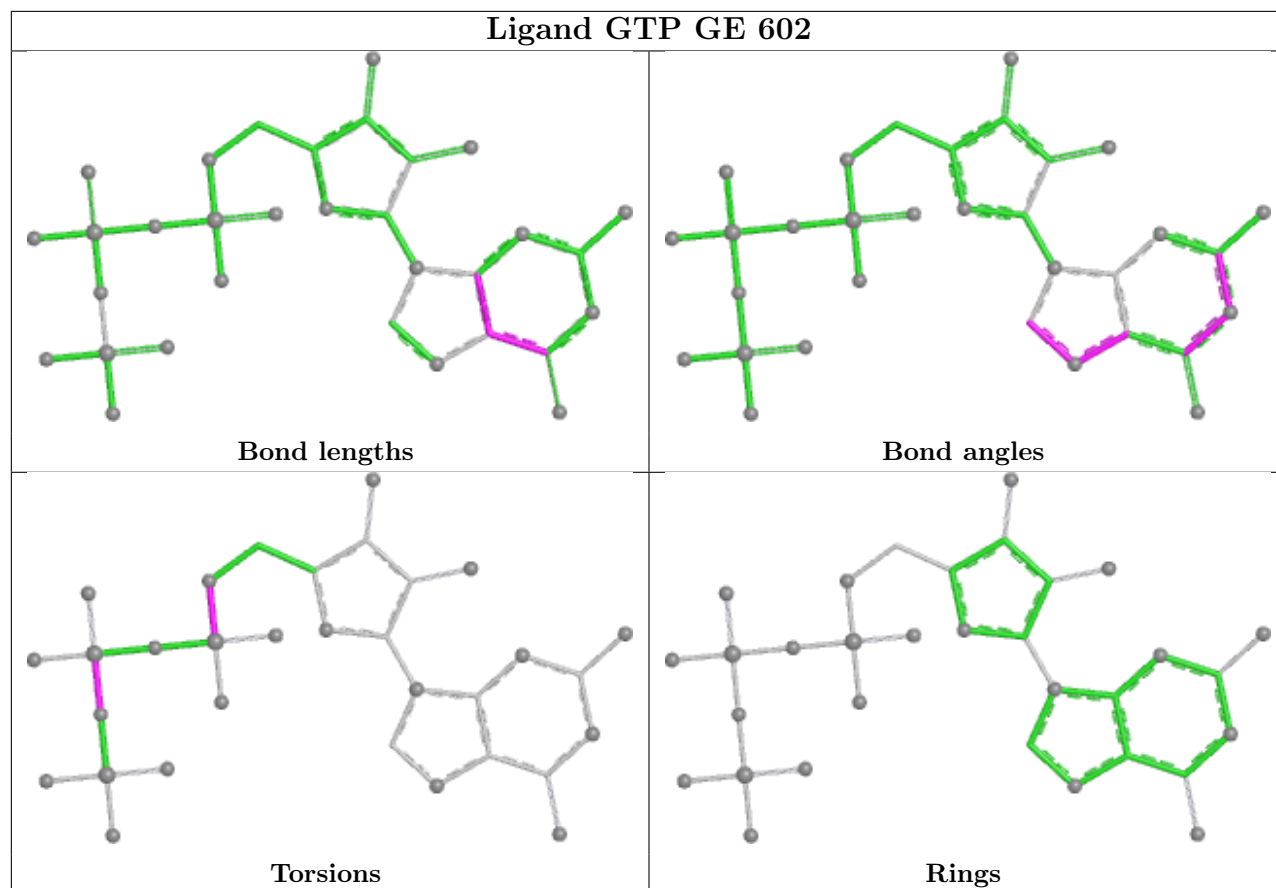


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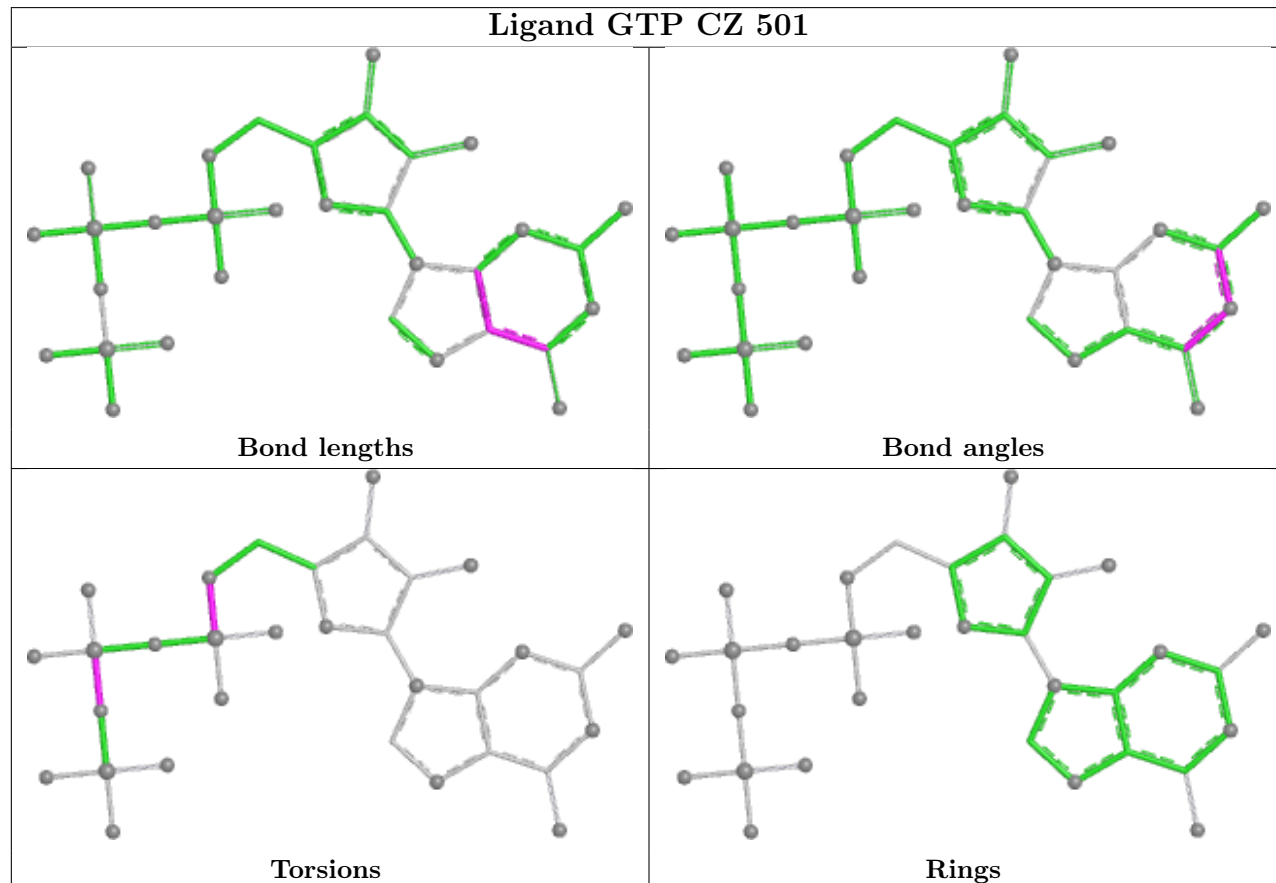




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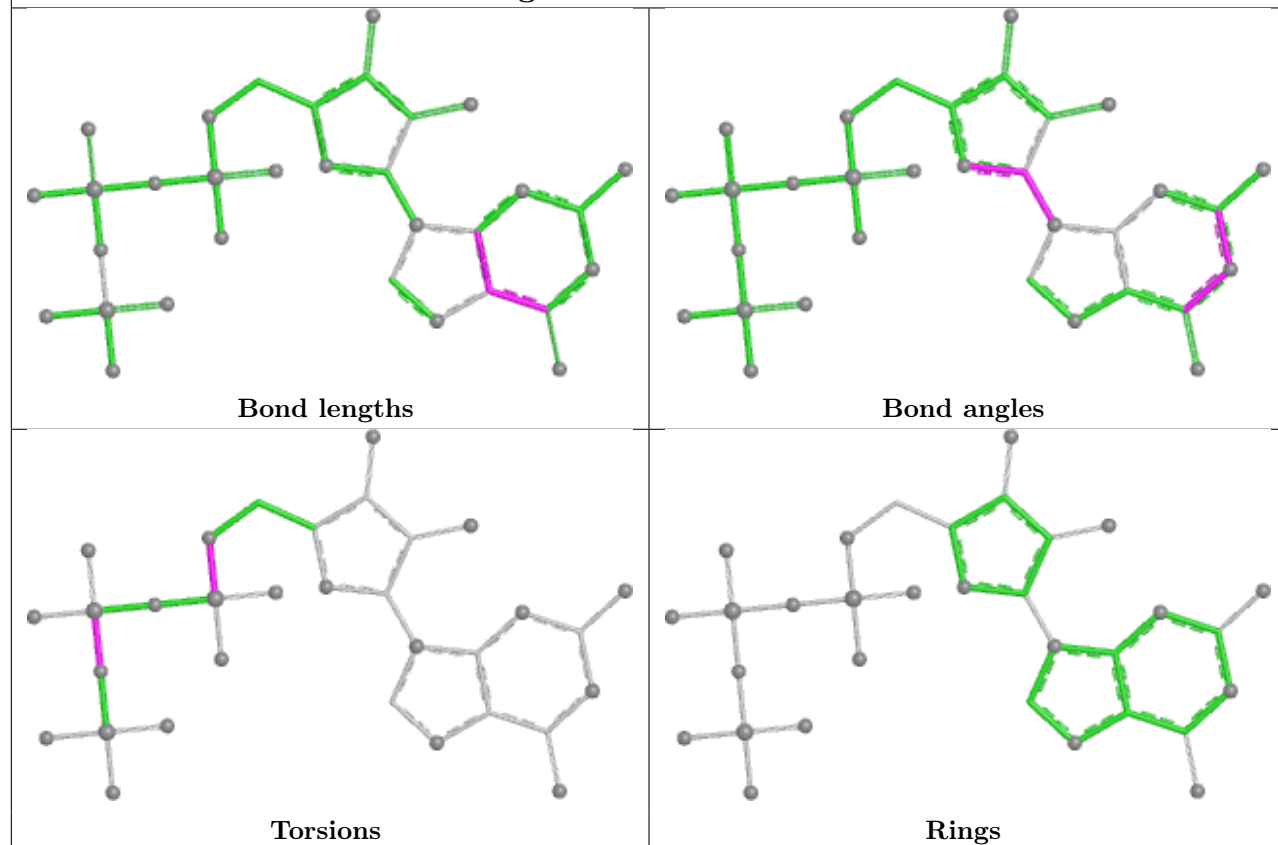


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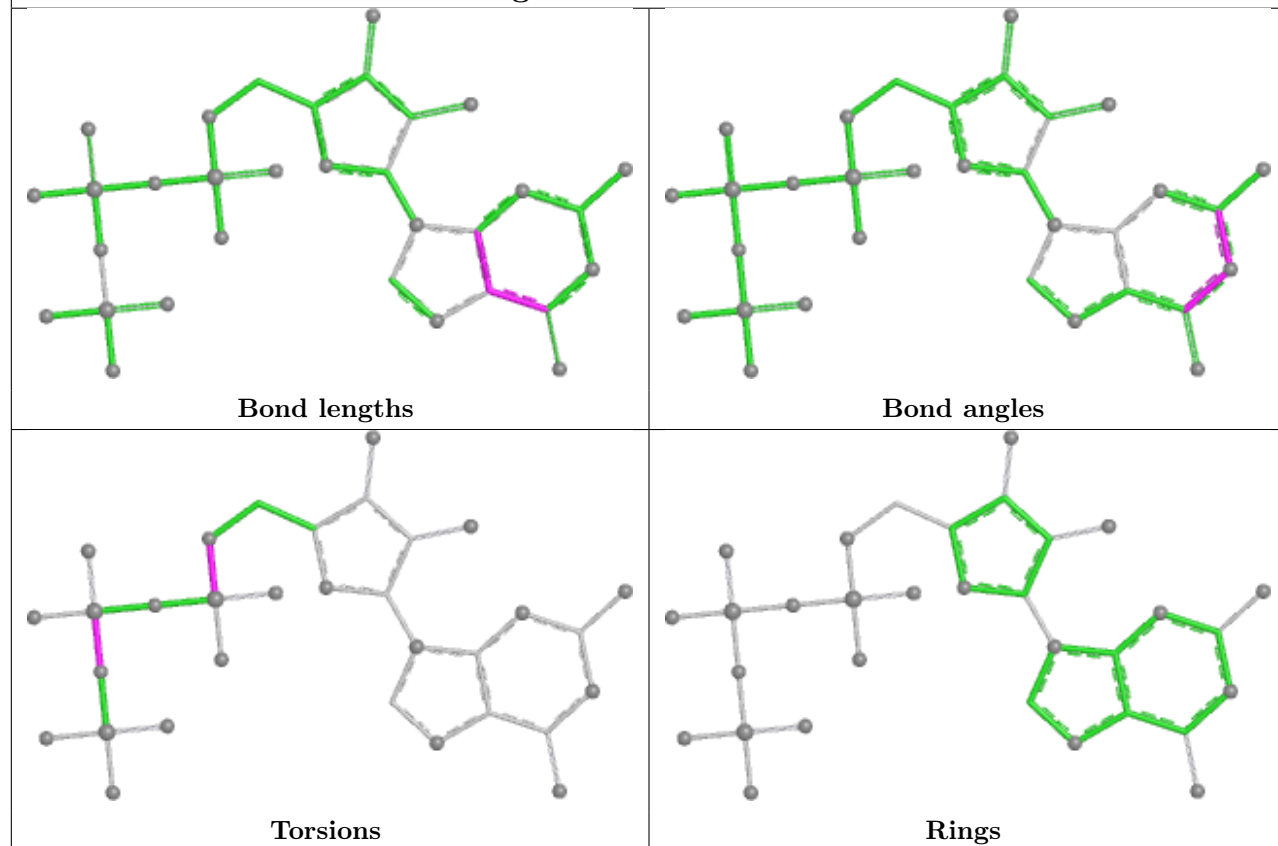


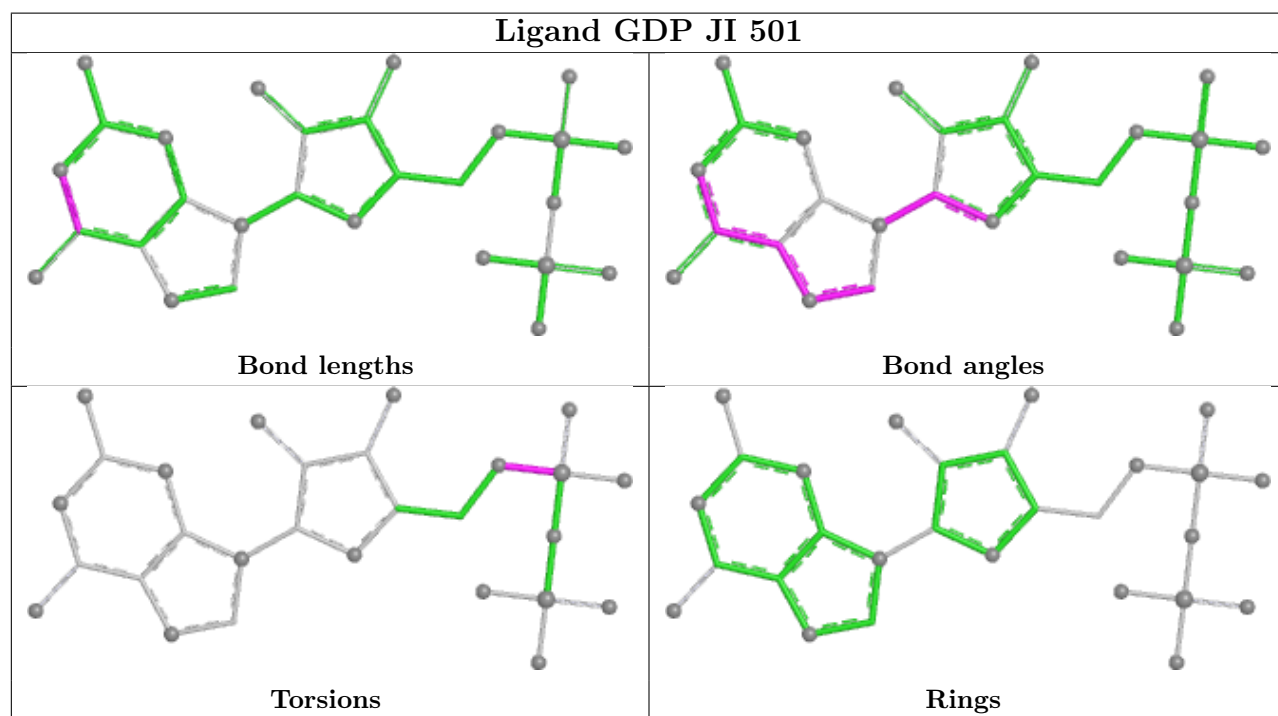
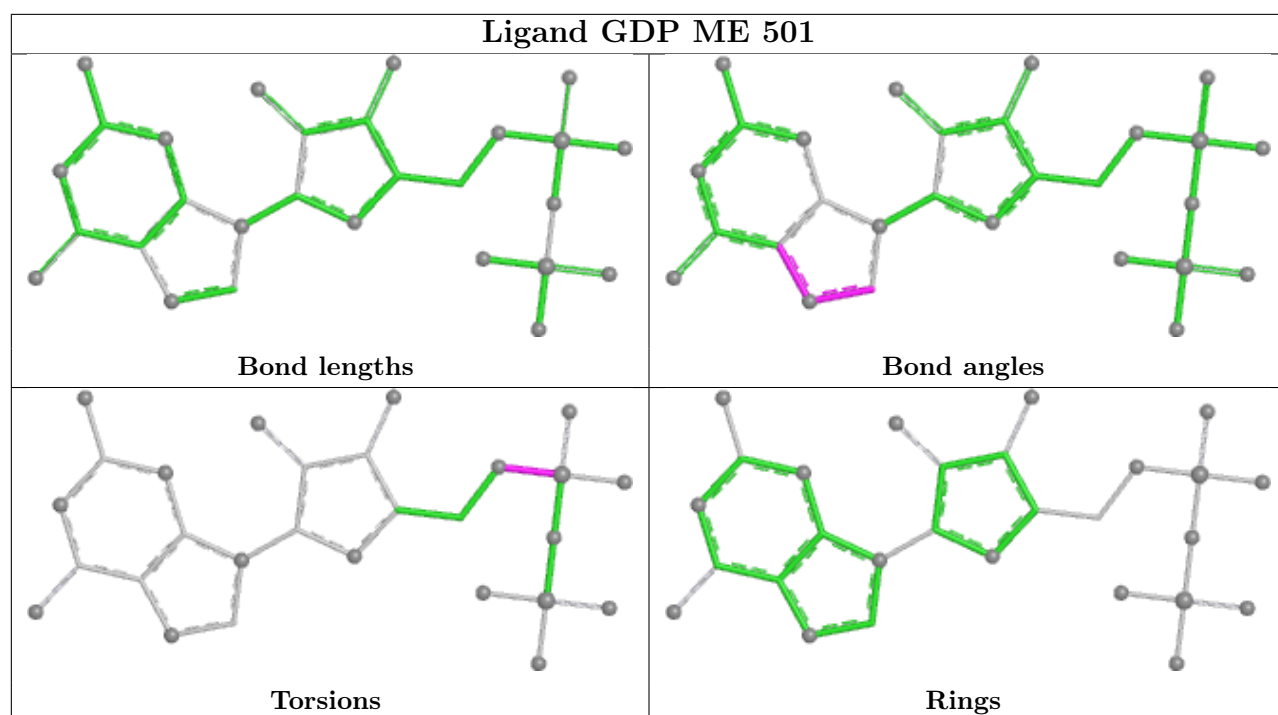


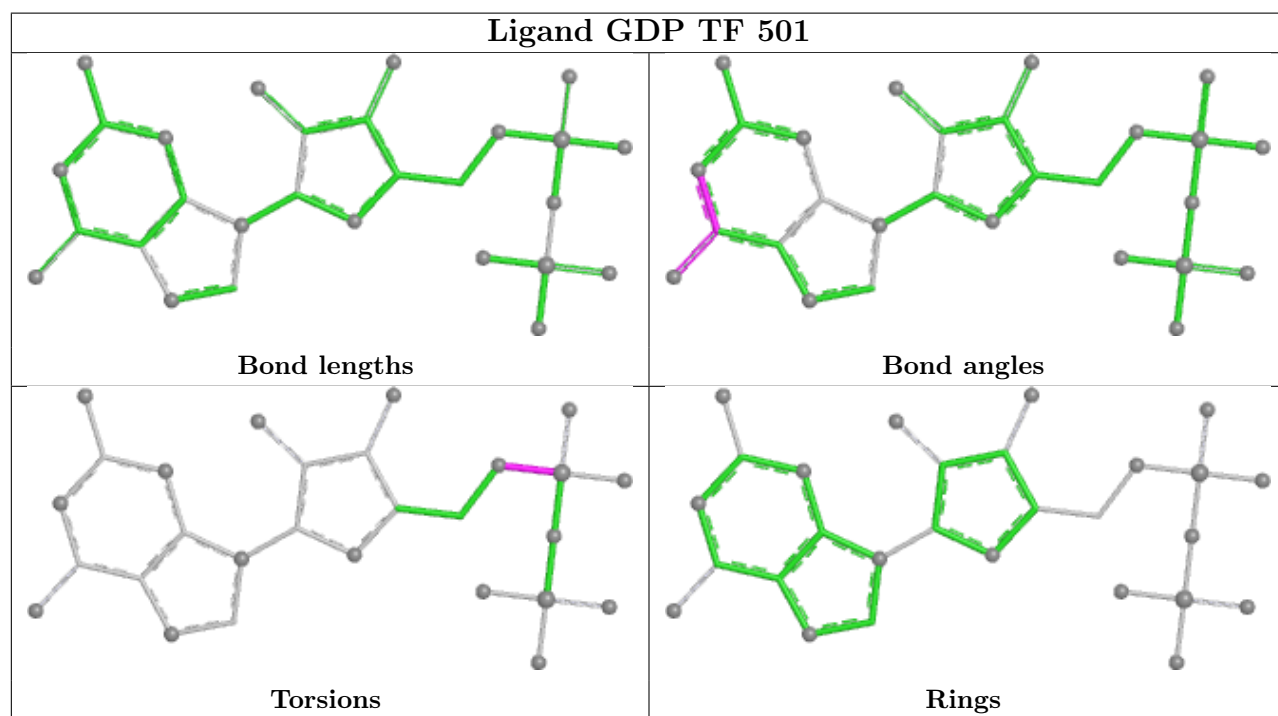
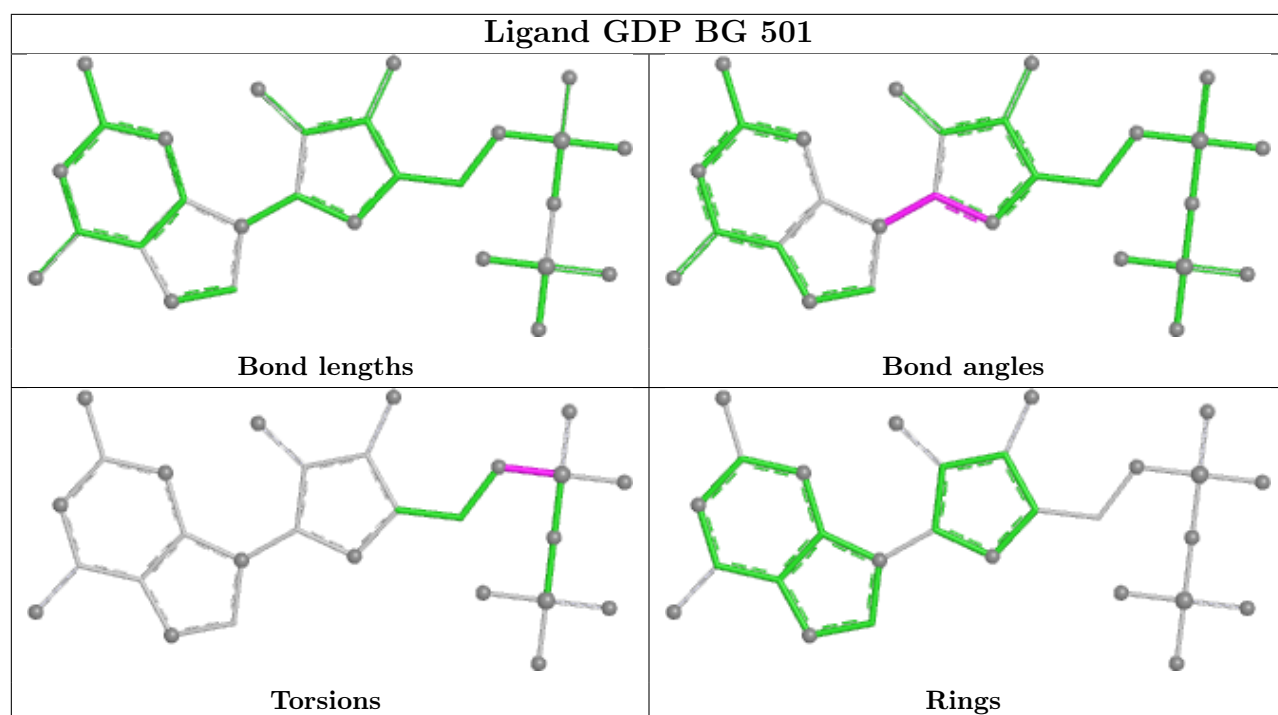
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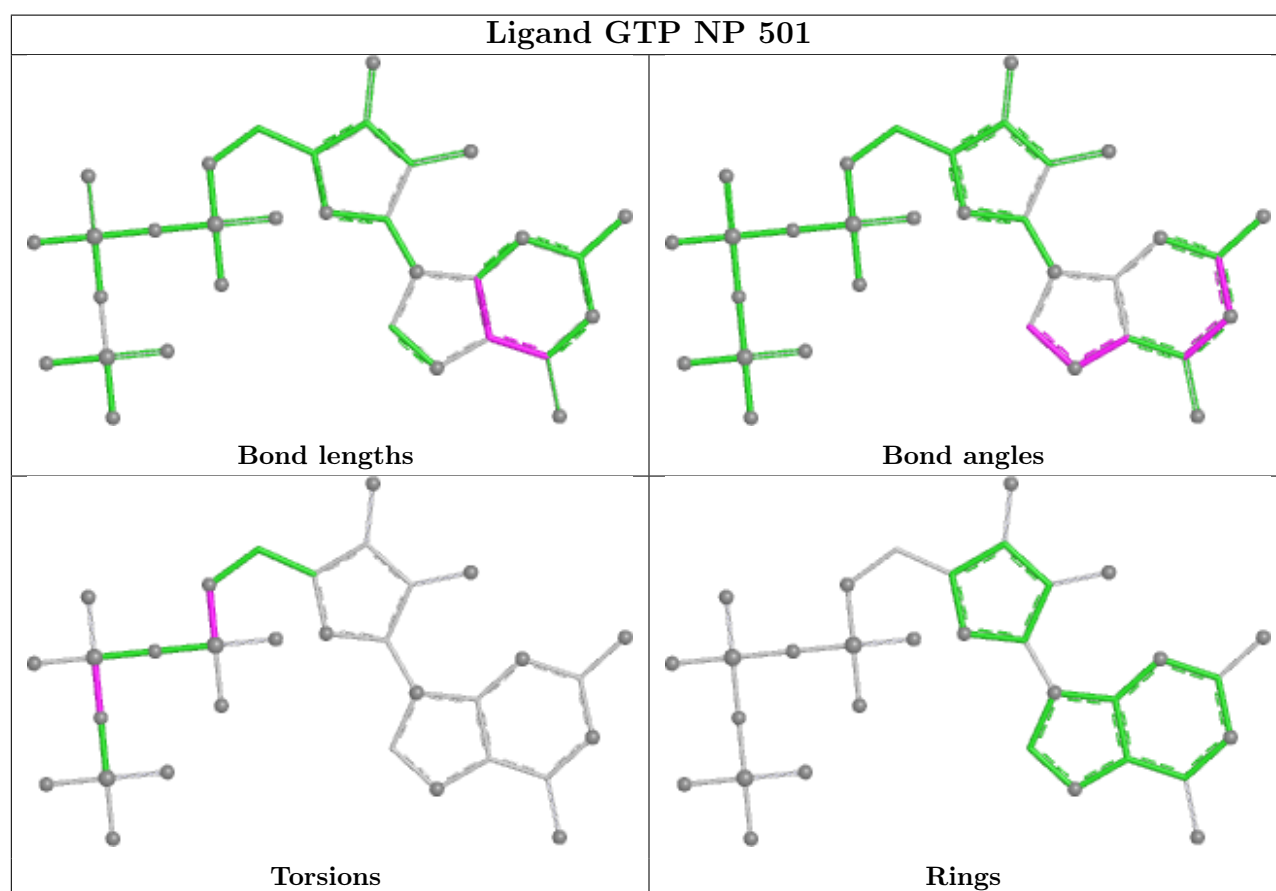
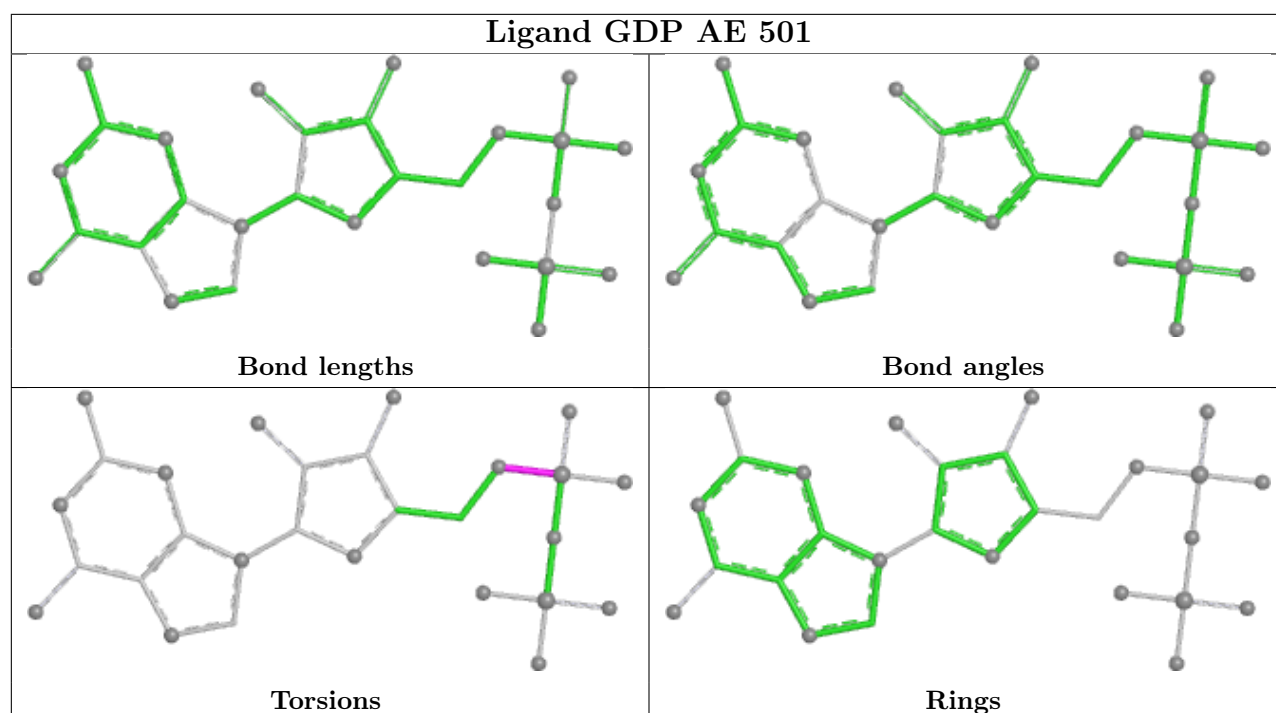


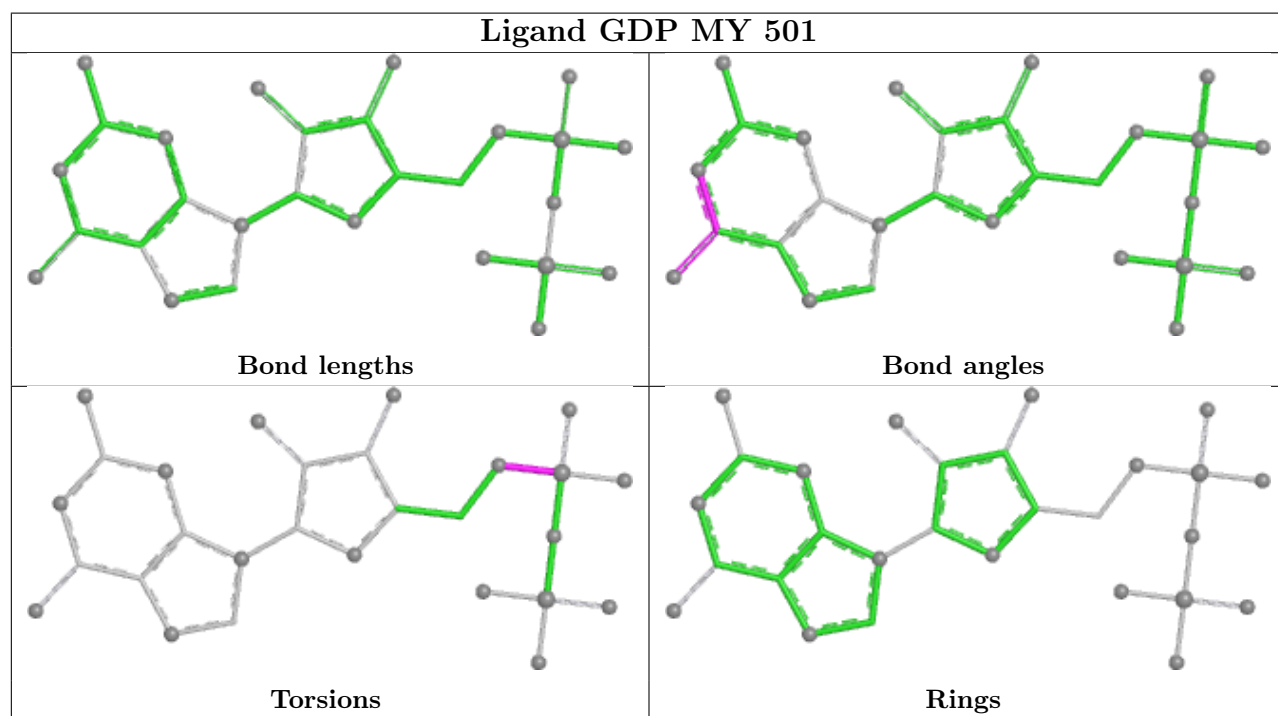
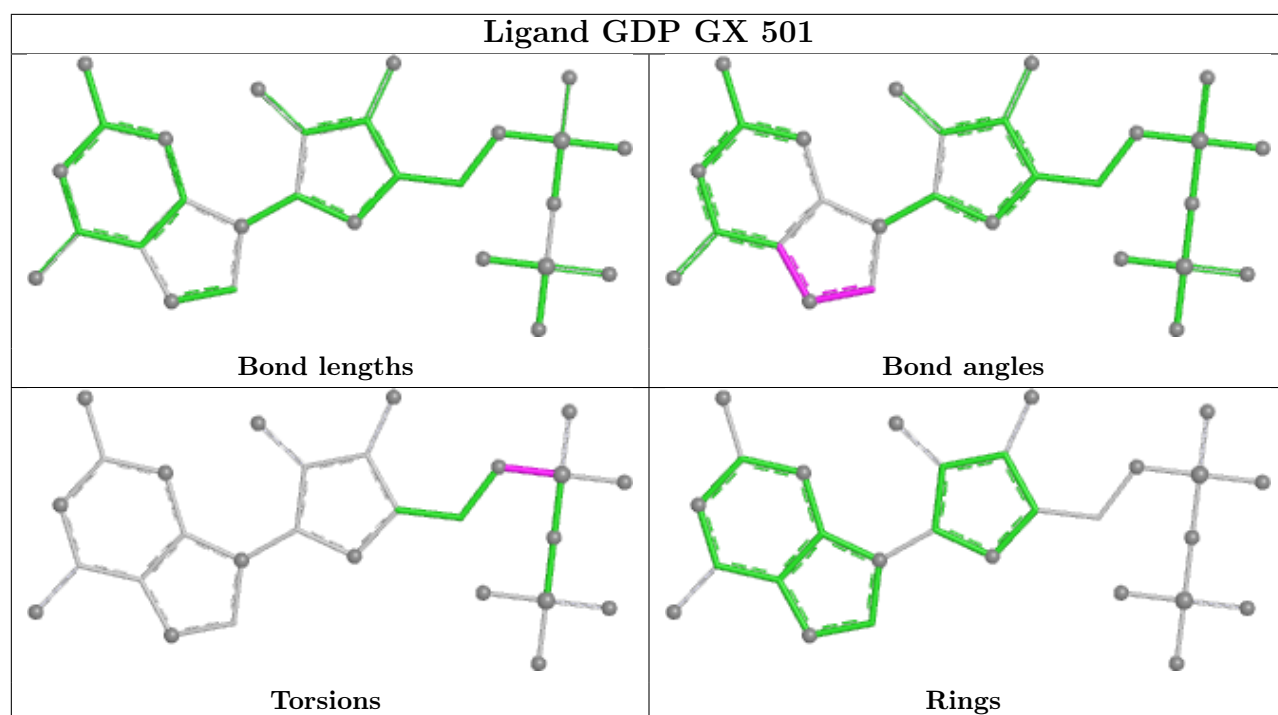
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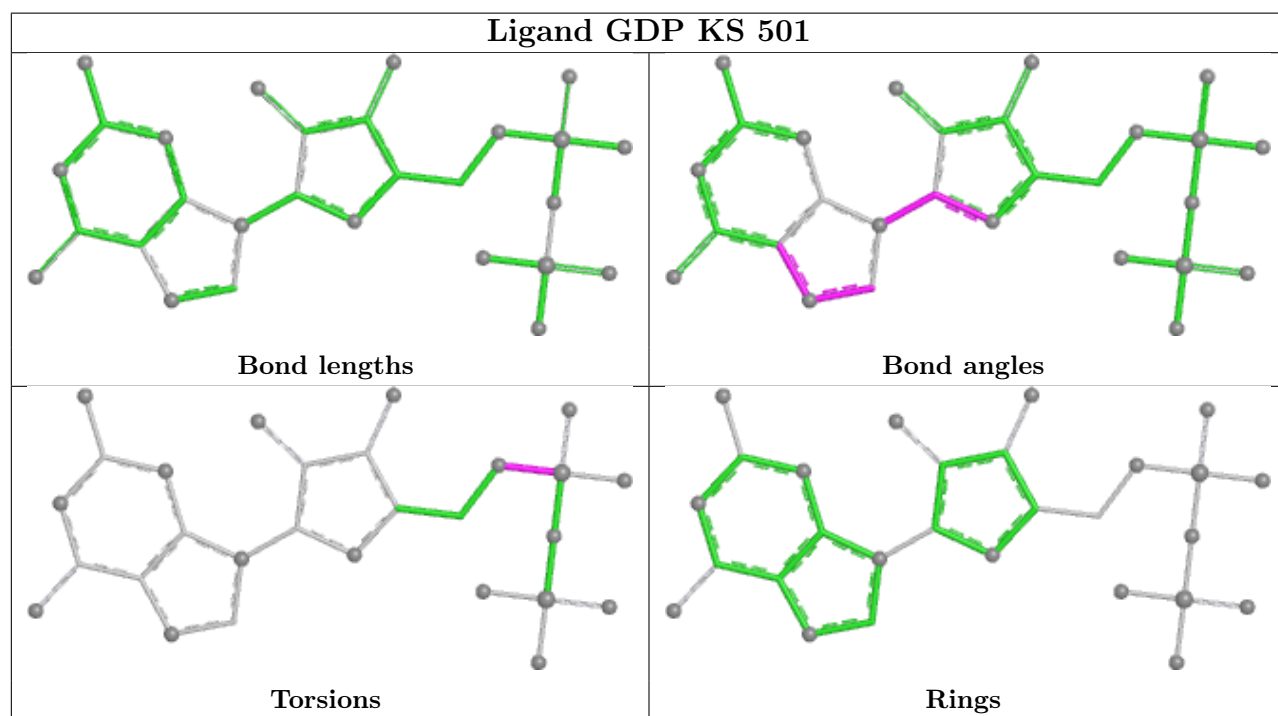
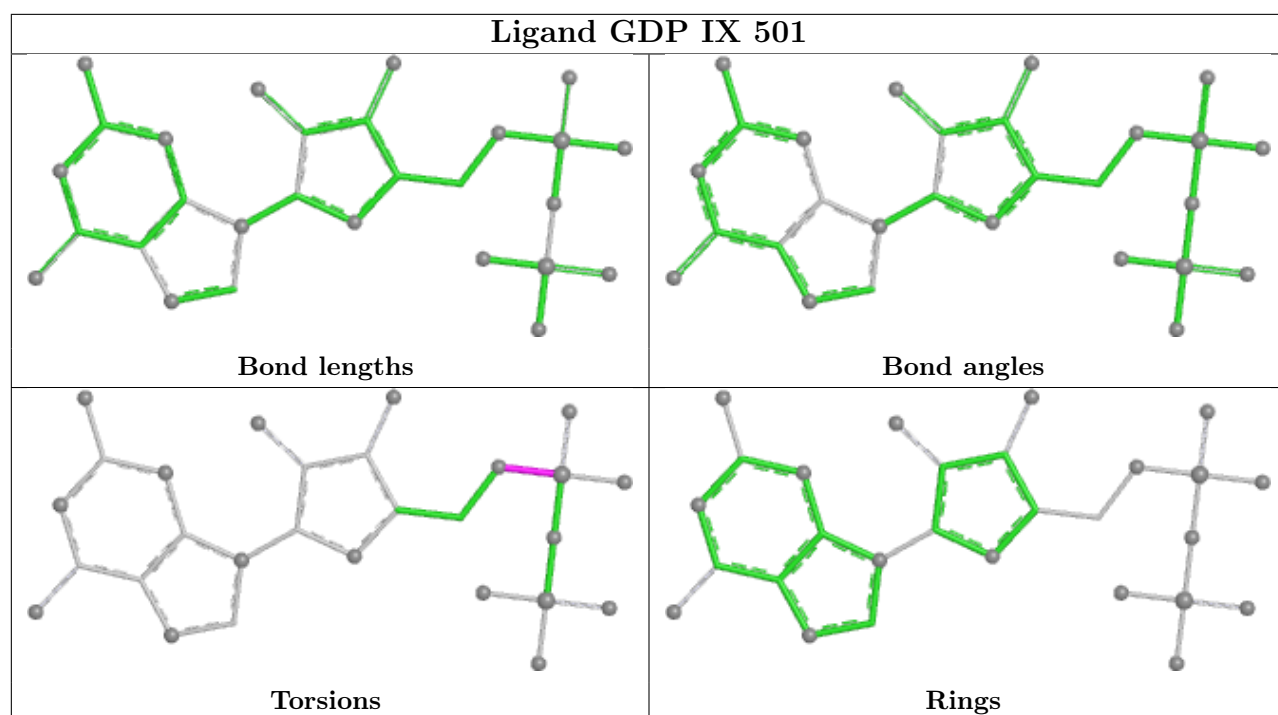


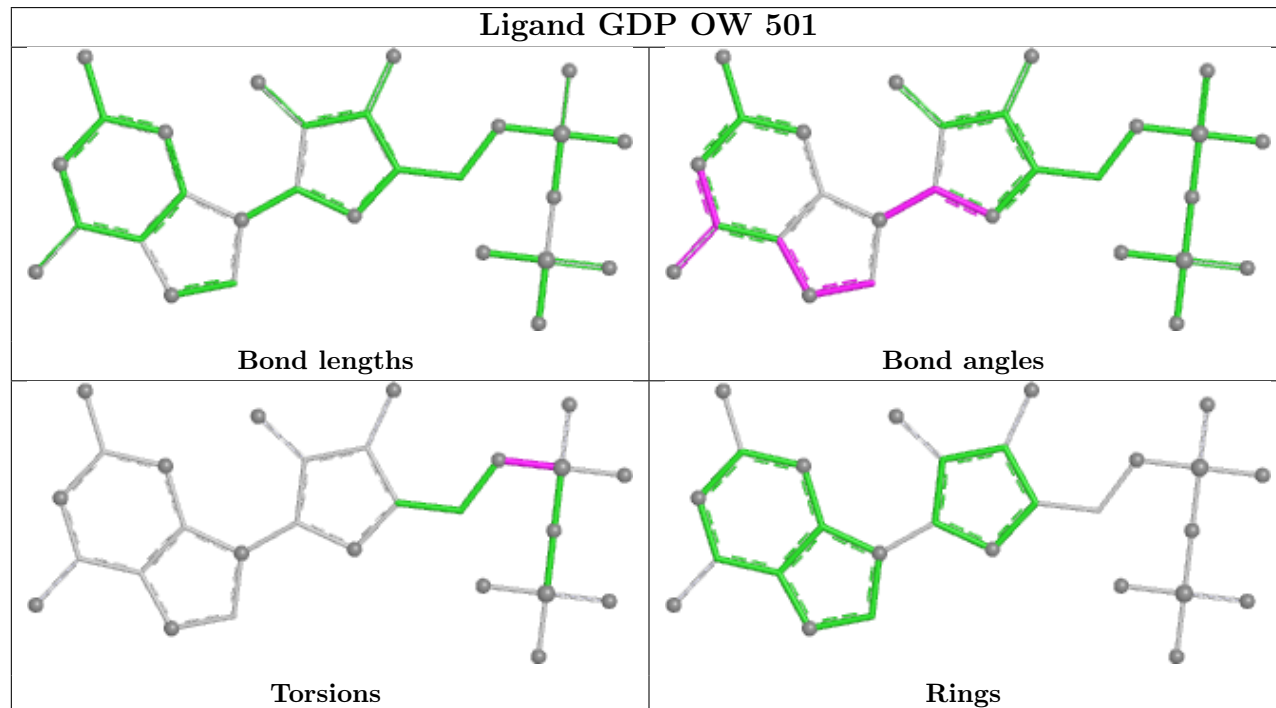
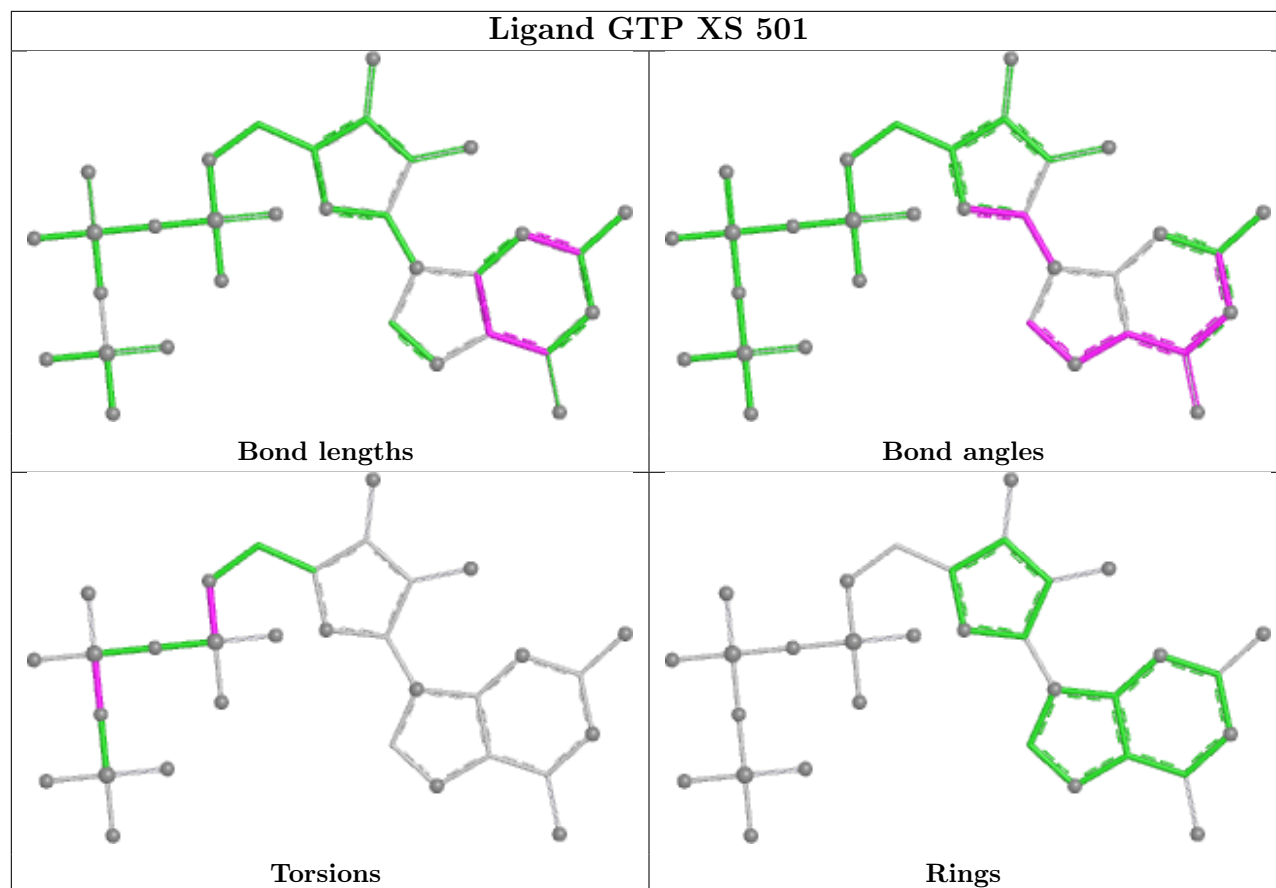




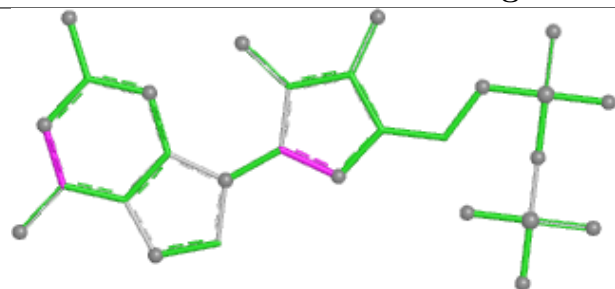




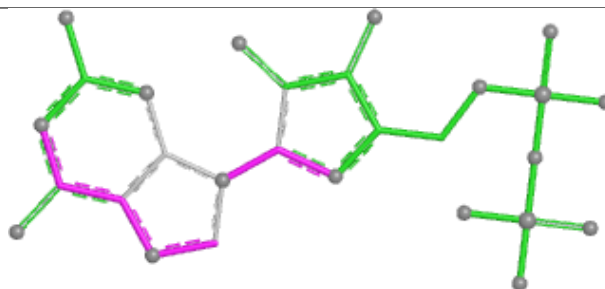




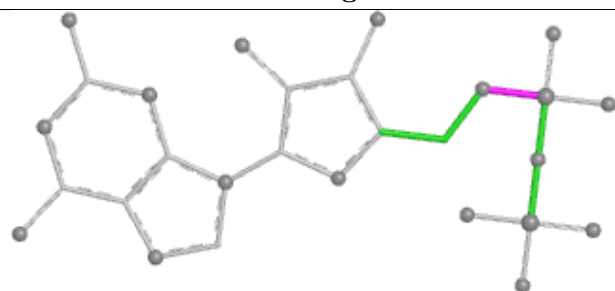
## Ligand GDP FX 501



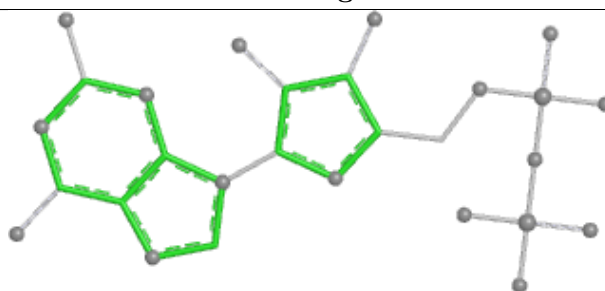
Bond lengths



Bond angles

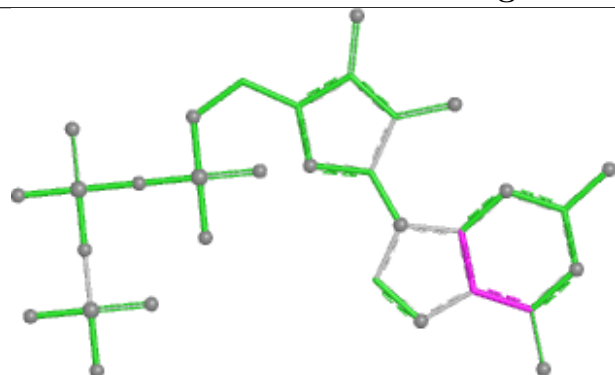


Torsions

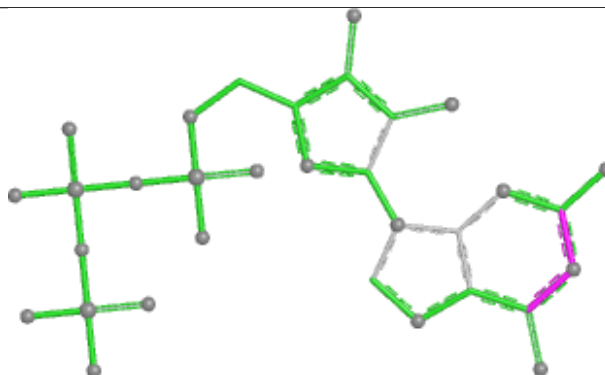


Rings

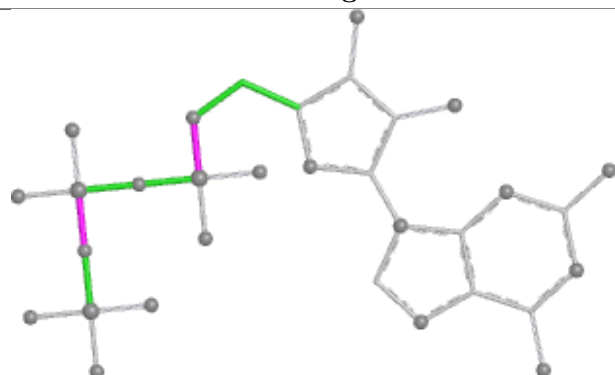
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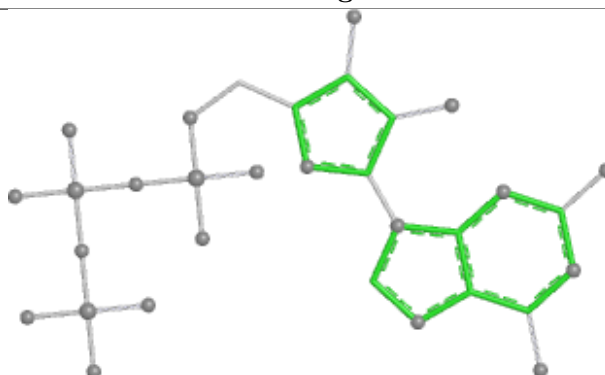
Bond lengths



Bond angles

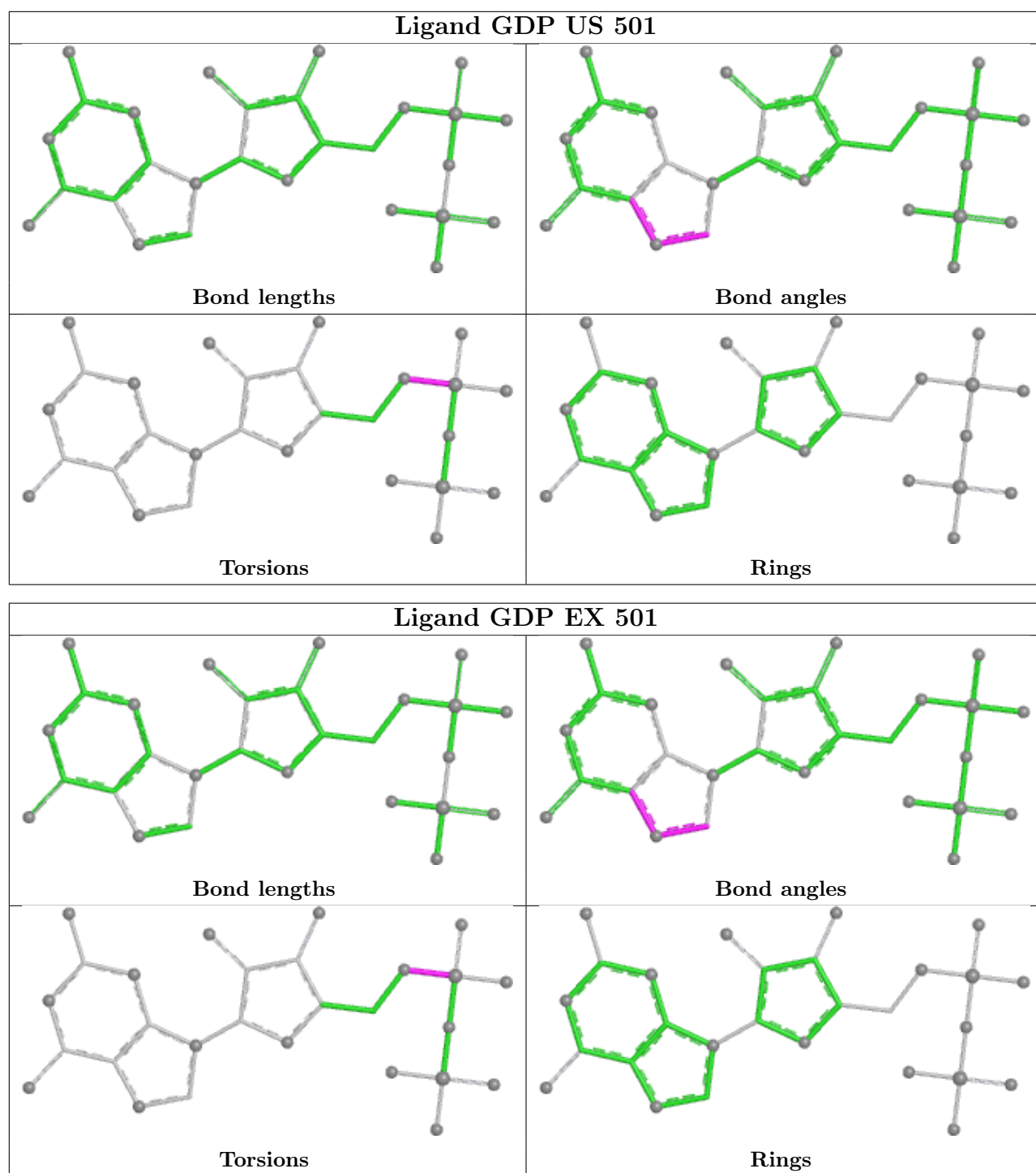


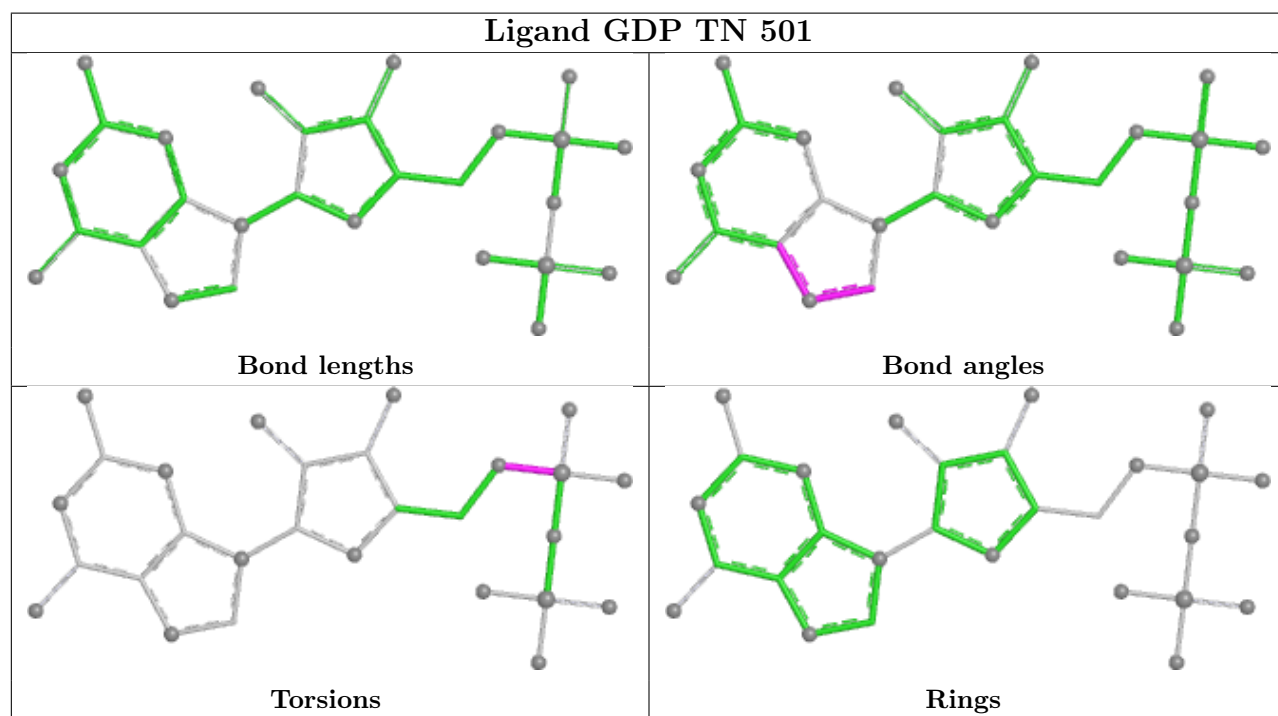
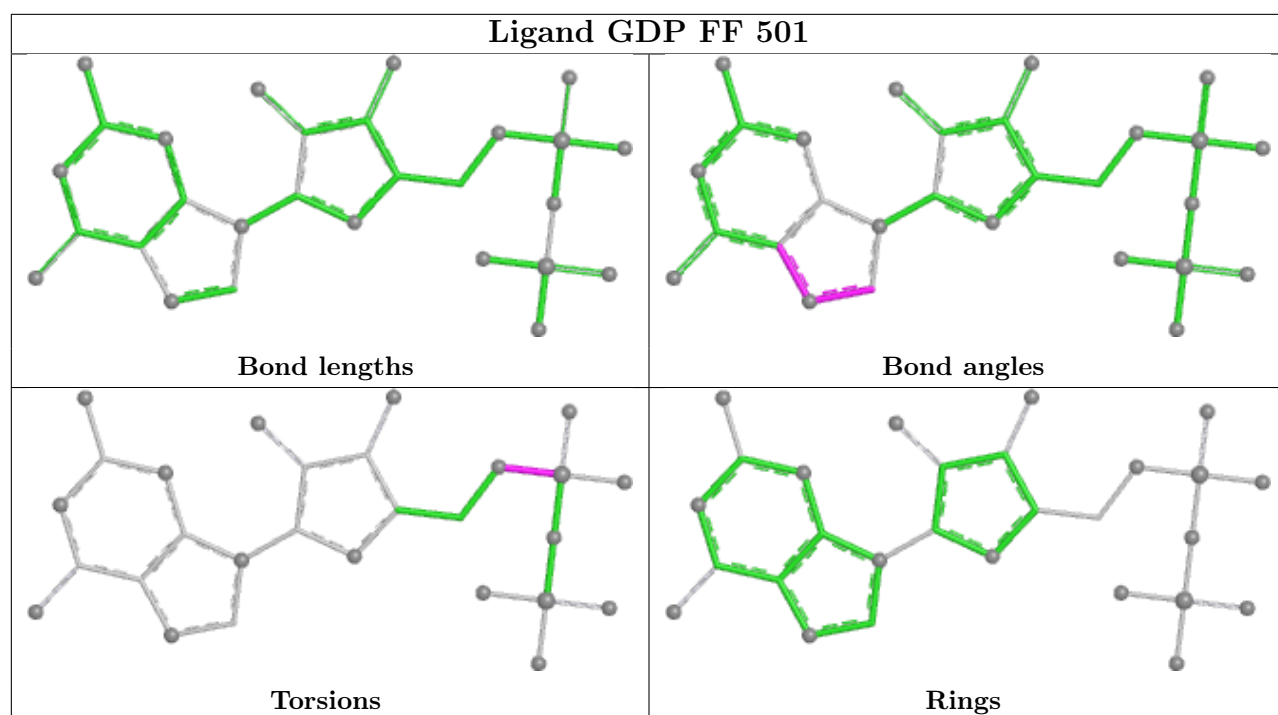
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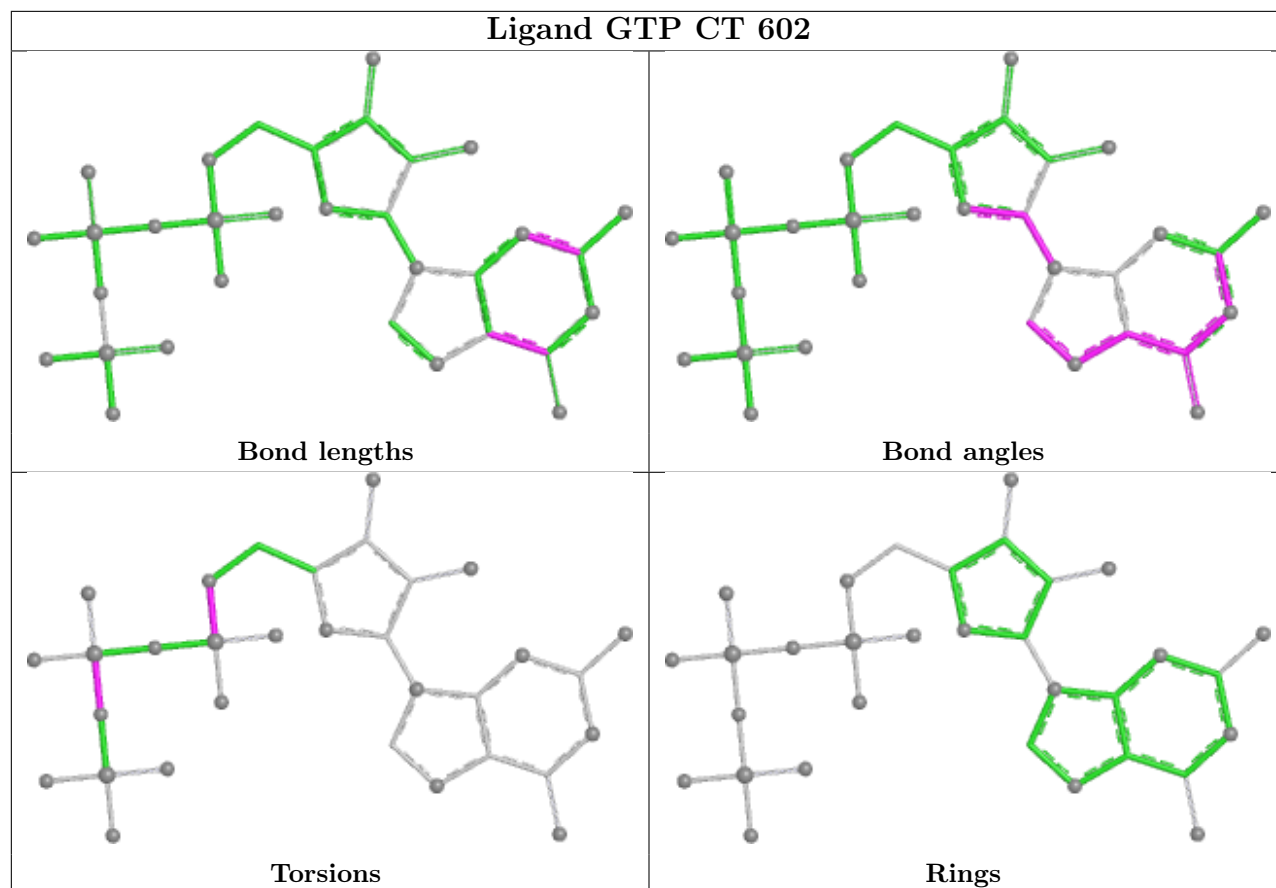
Rings



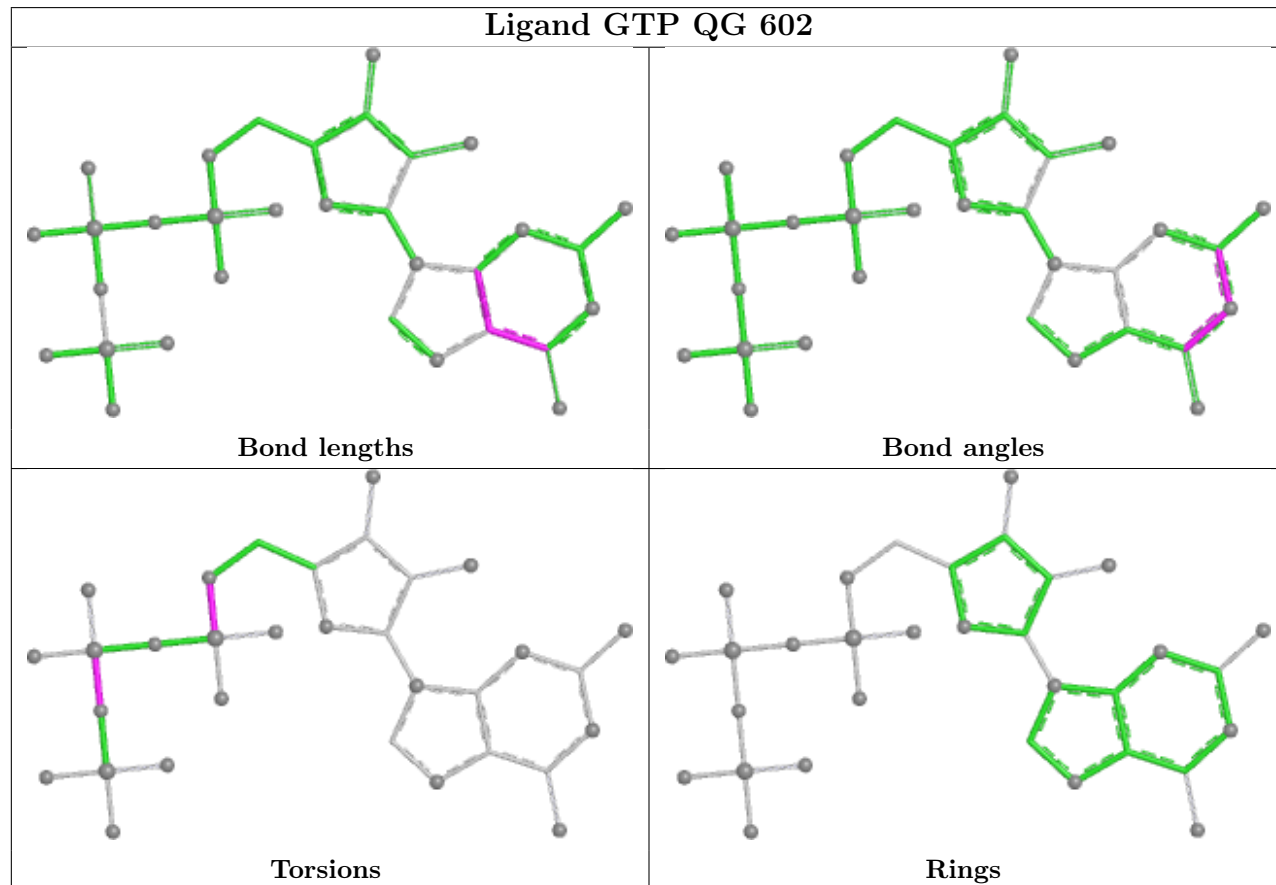


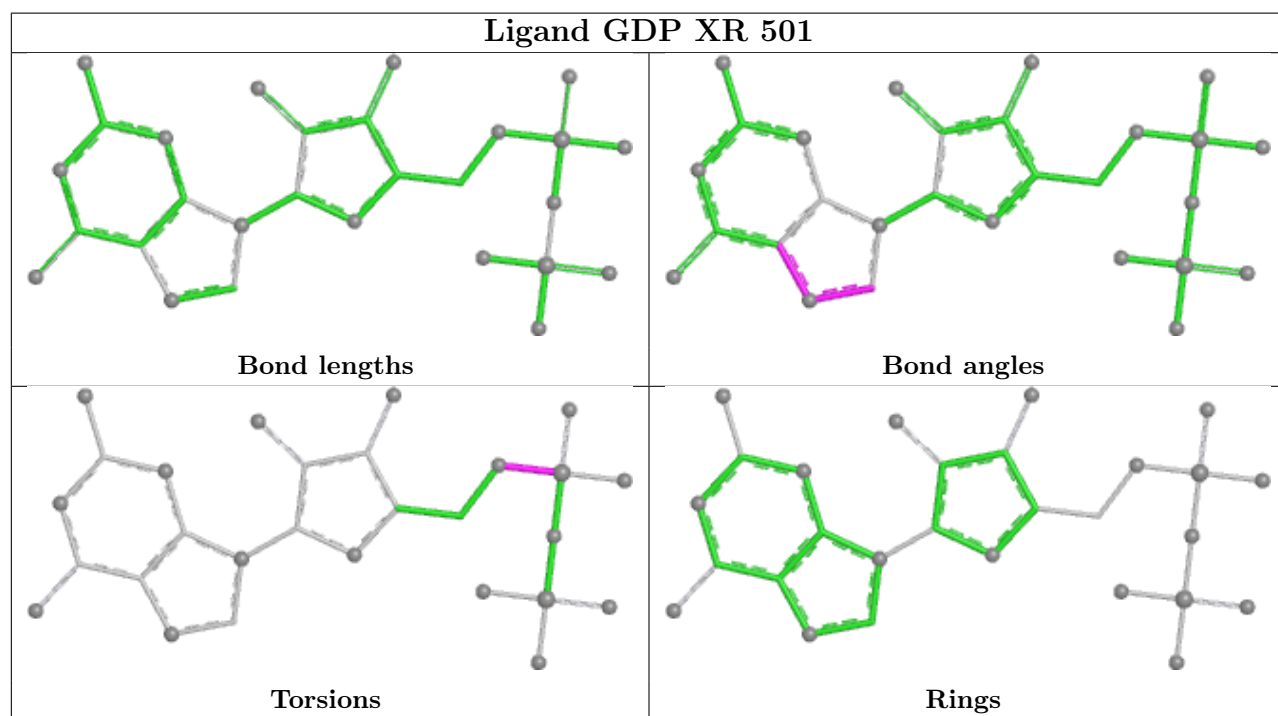
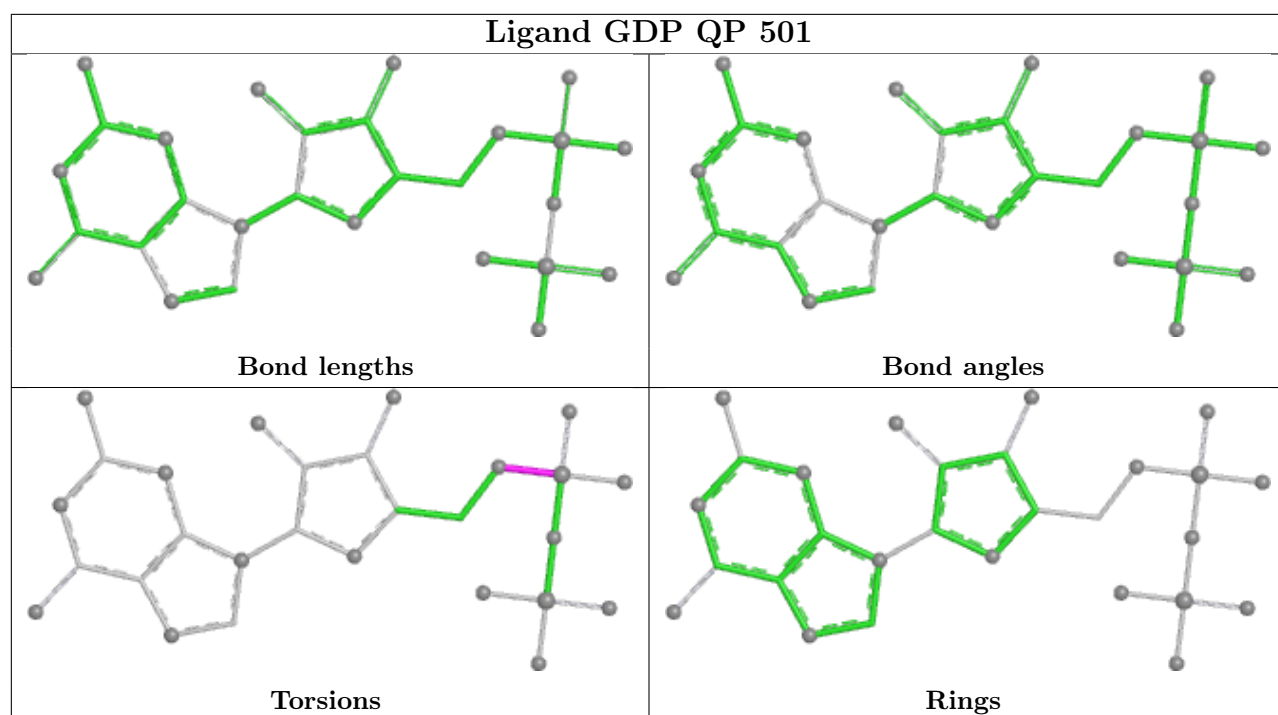


## Ligand GTP CT 602

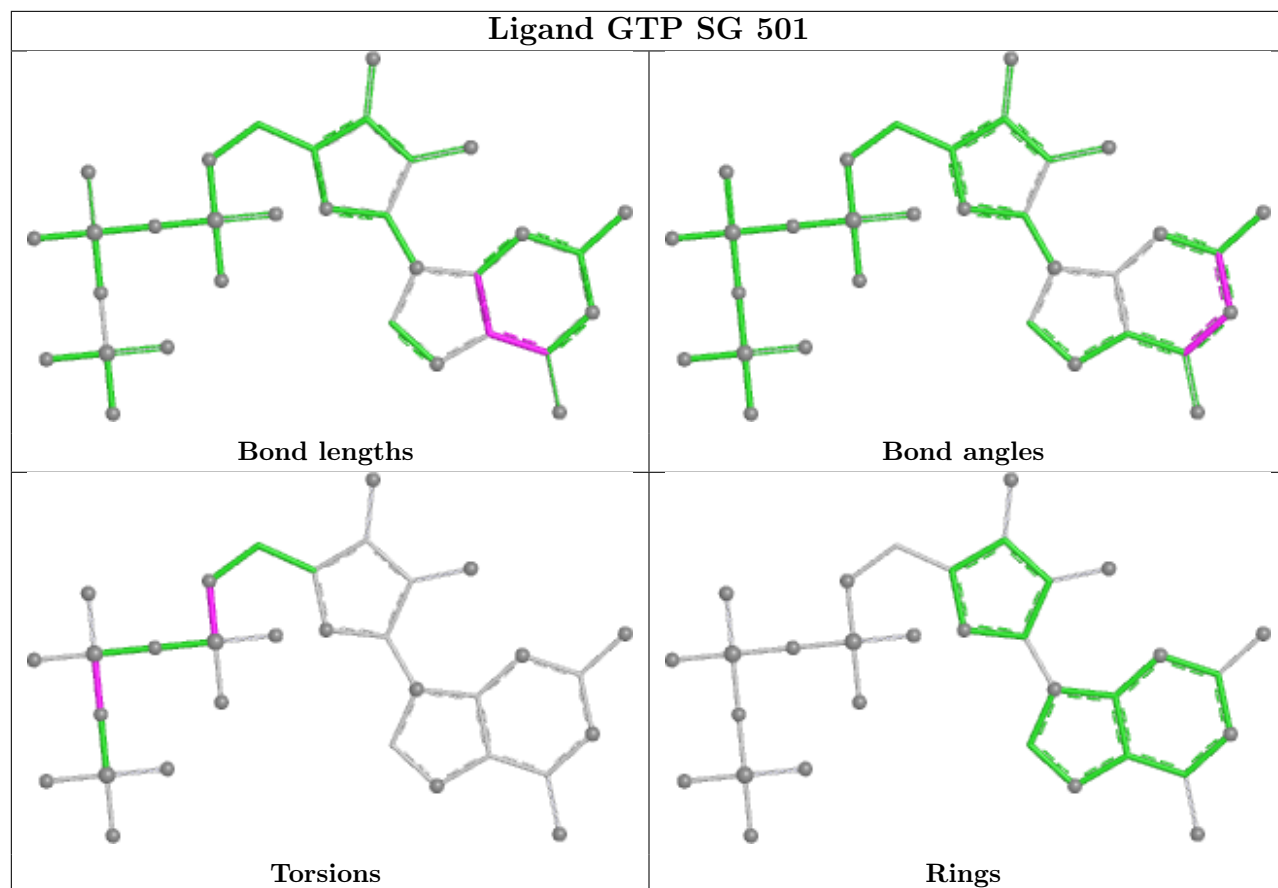


## Ligand GTP QG 602

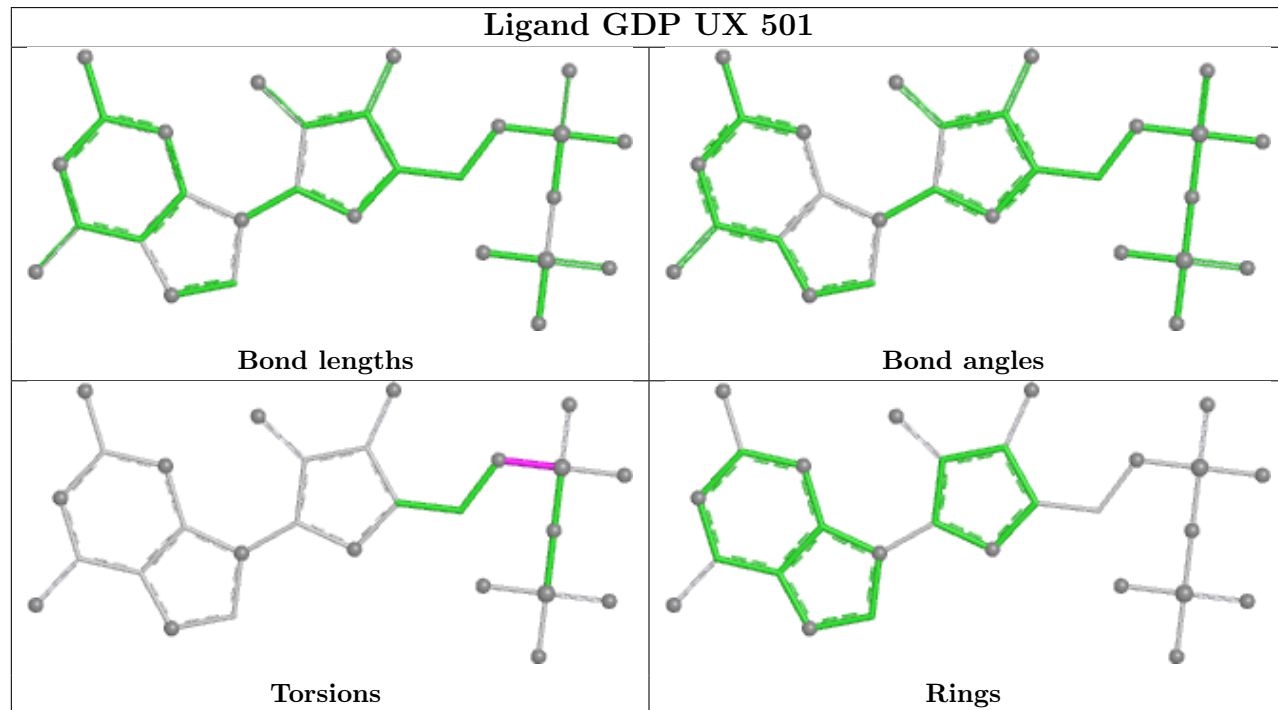




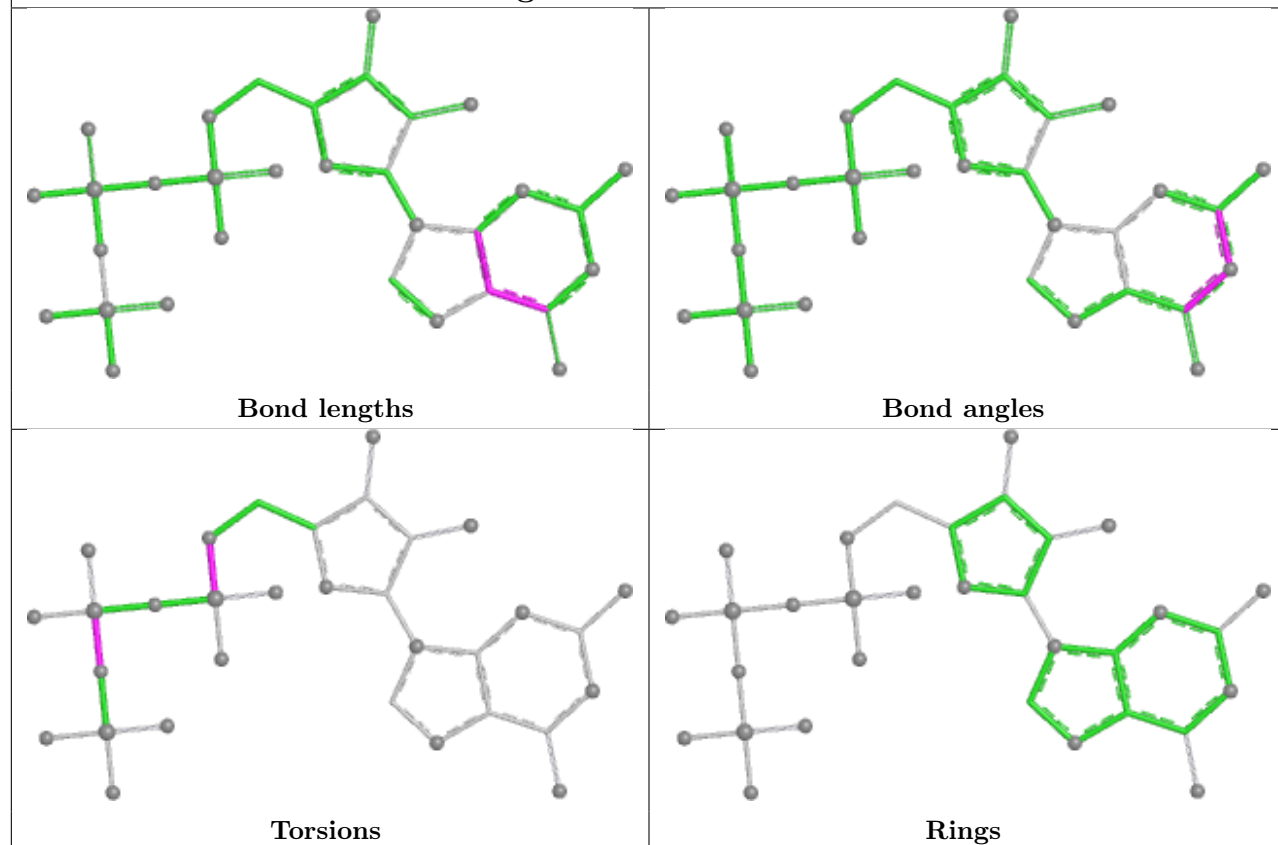
## Ligand GTP SG 501



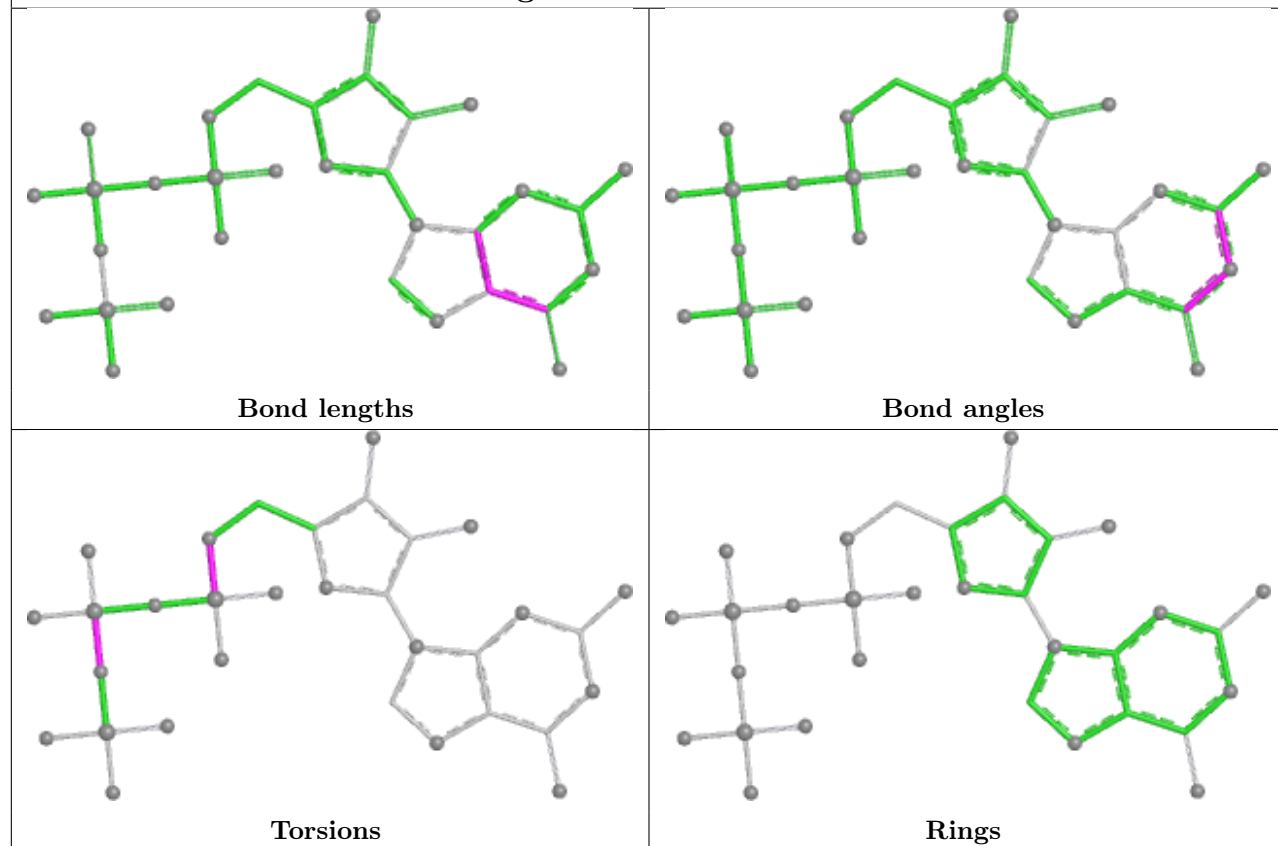
## Ligand GDP UX 501

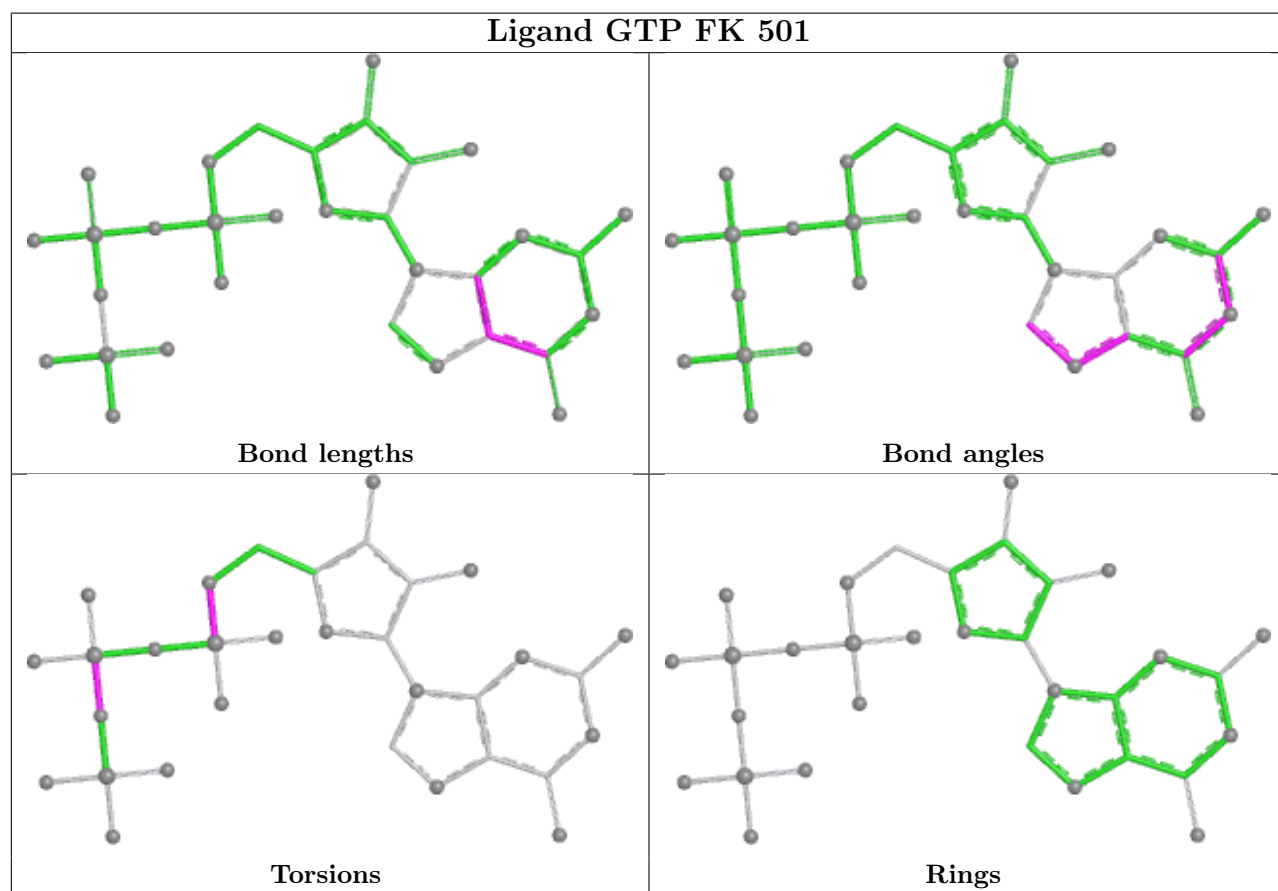
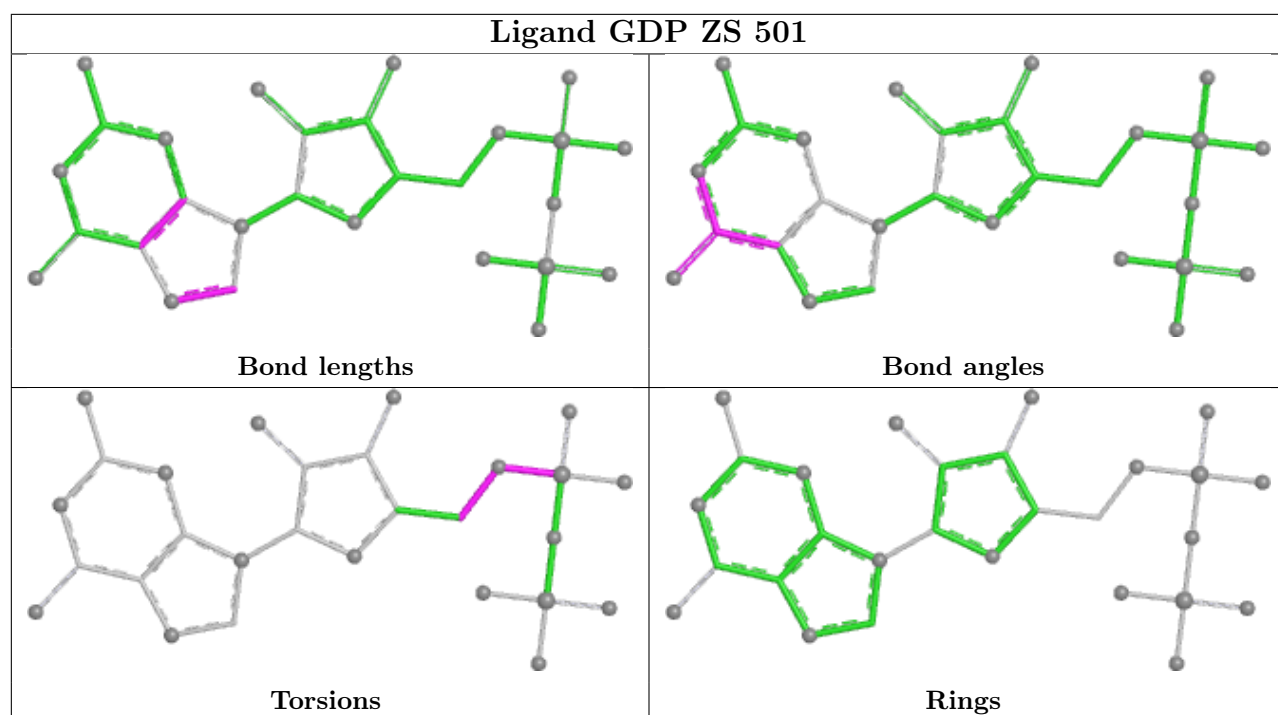


## Ligand GTP DY 501

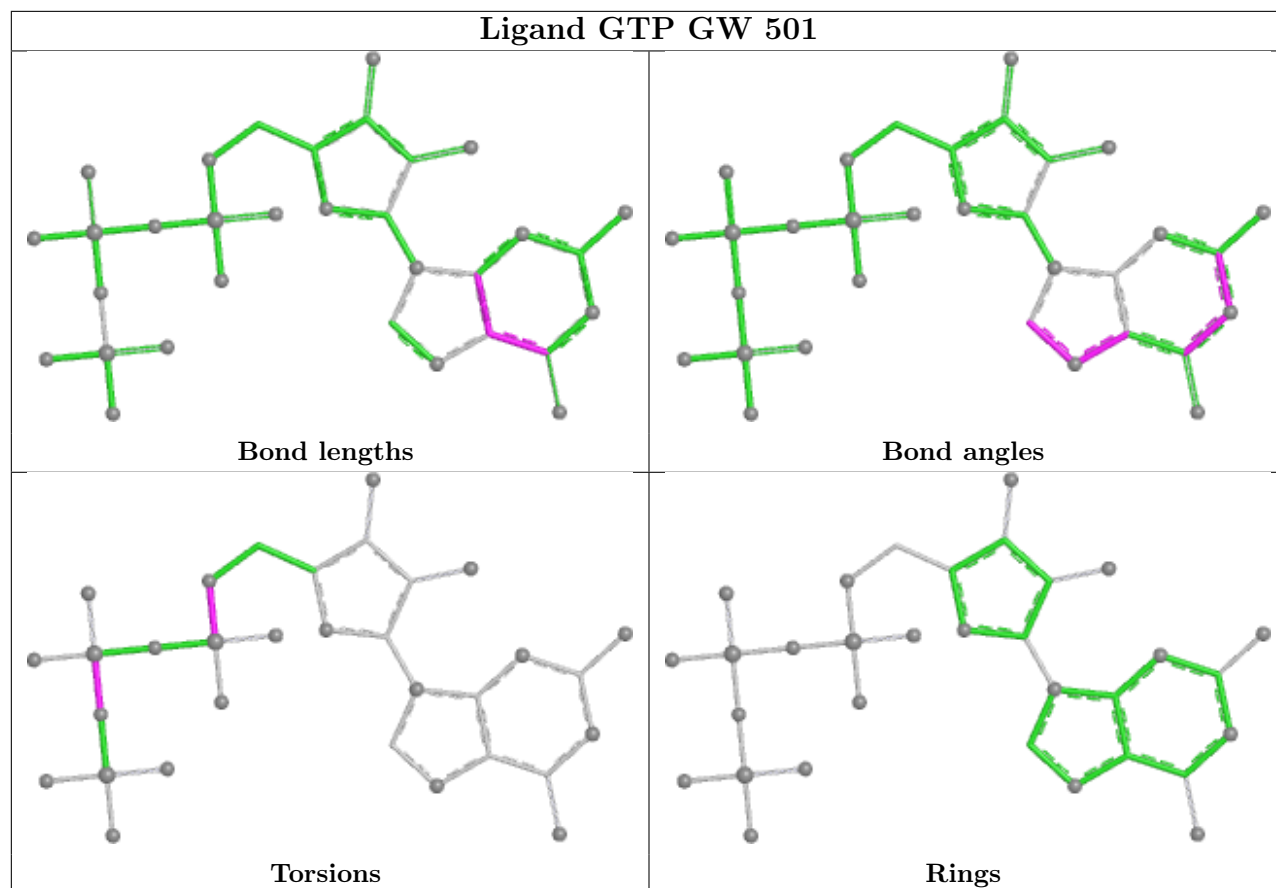


## Ligand GTP OX 602

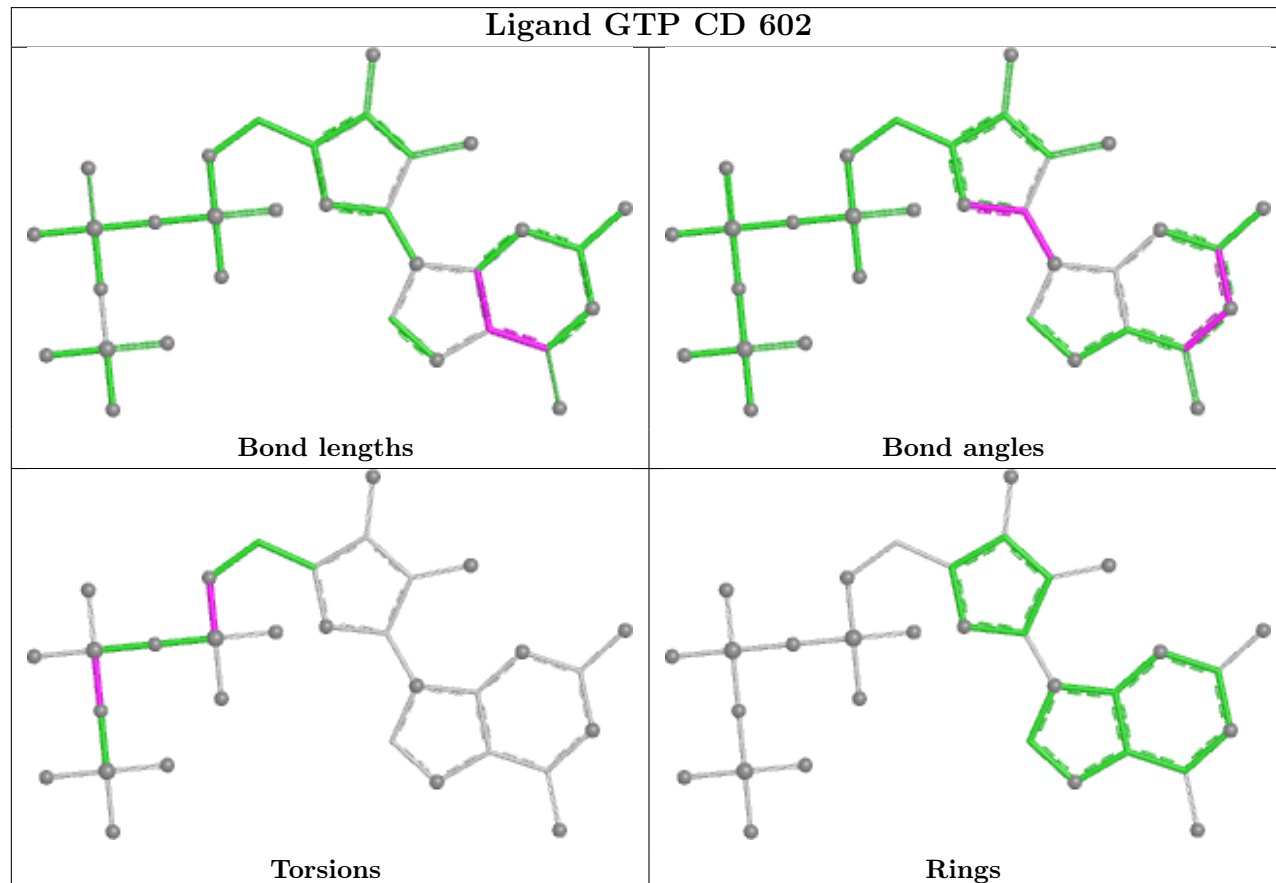




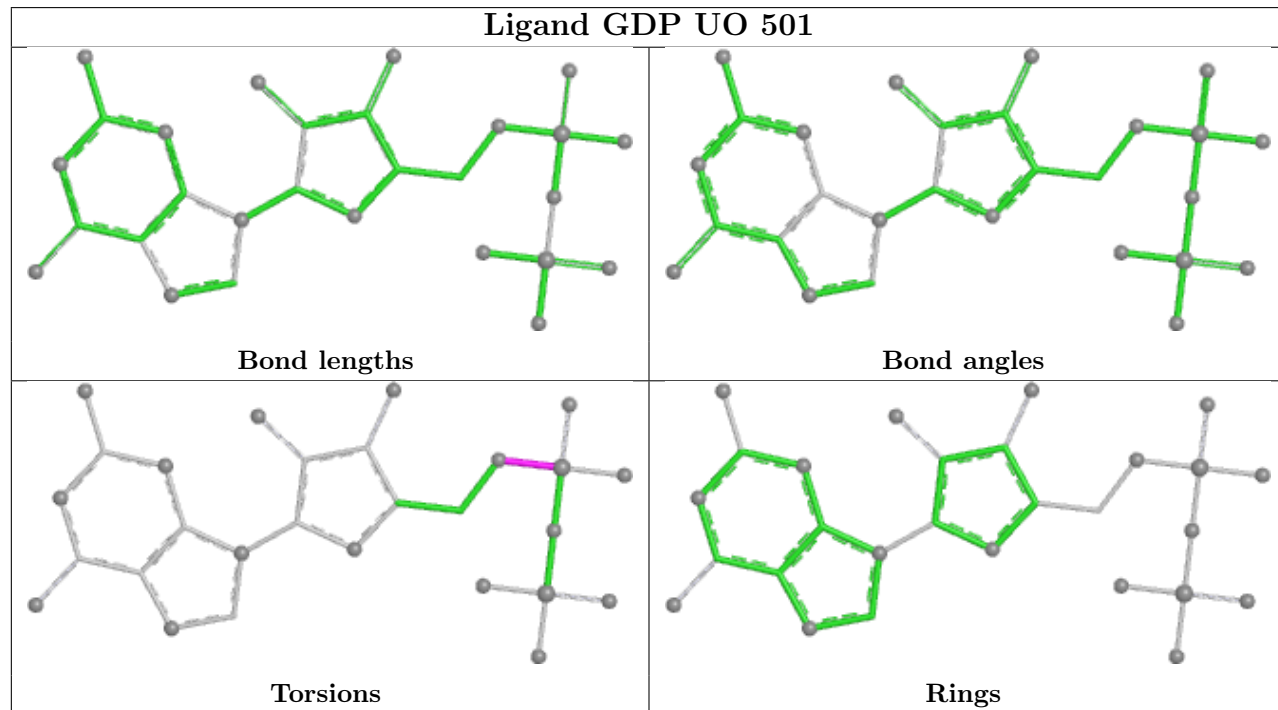
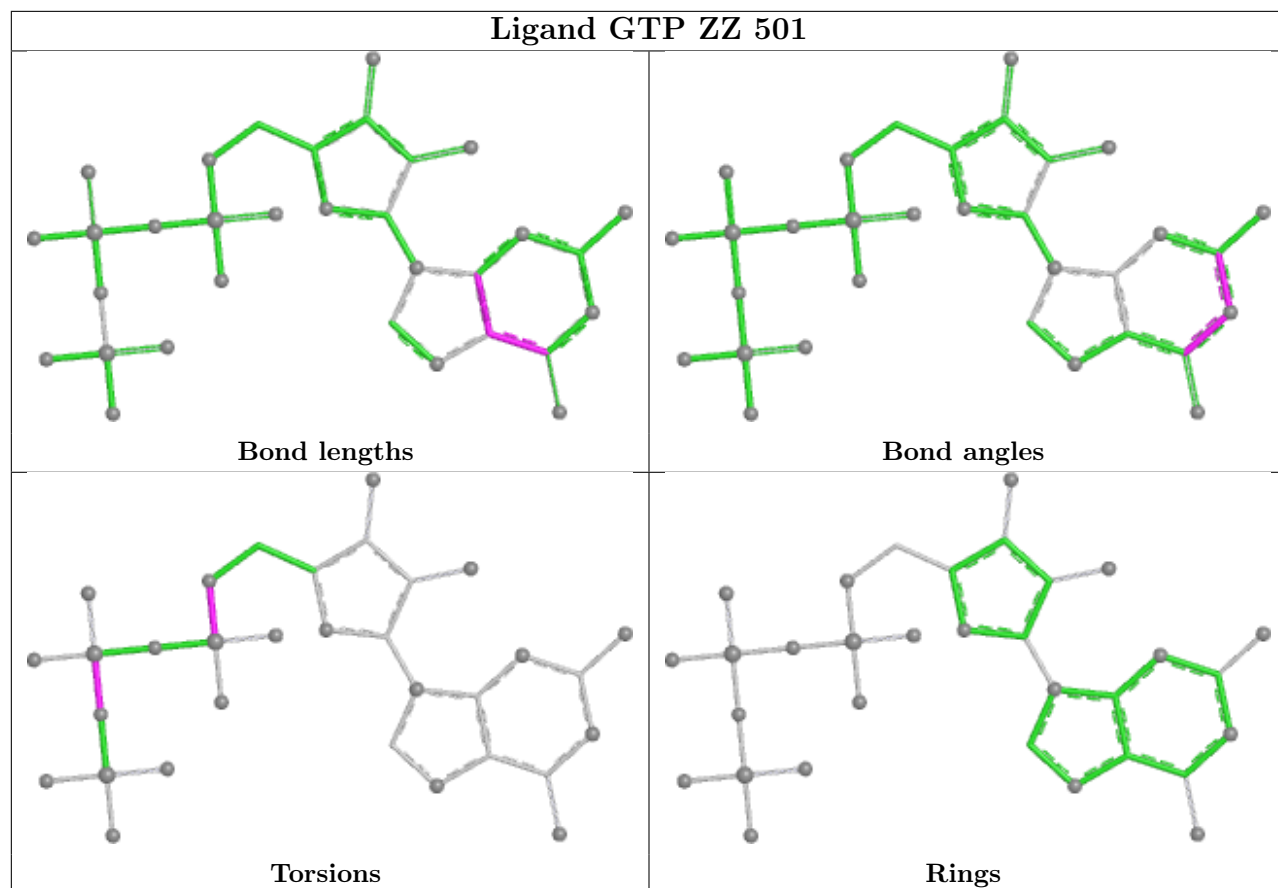
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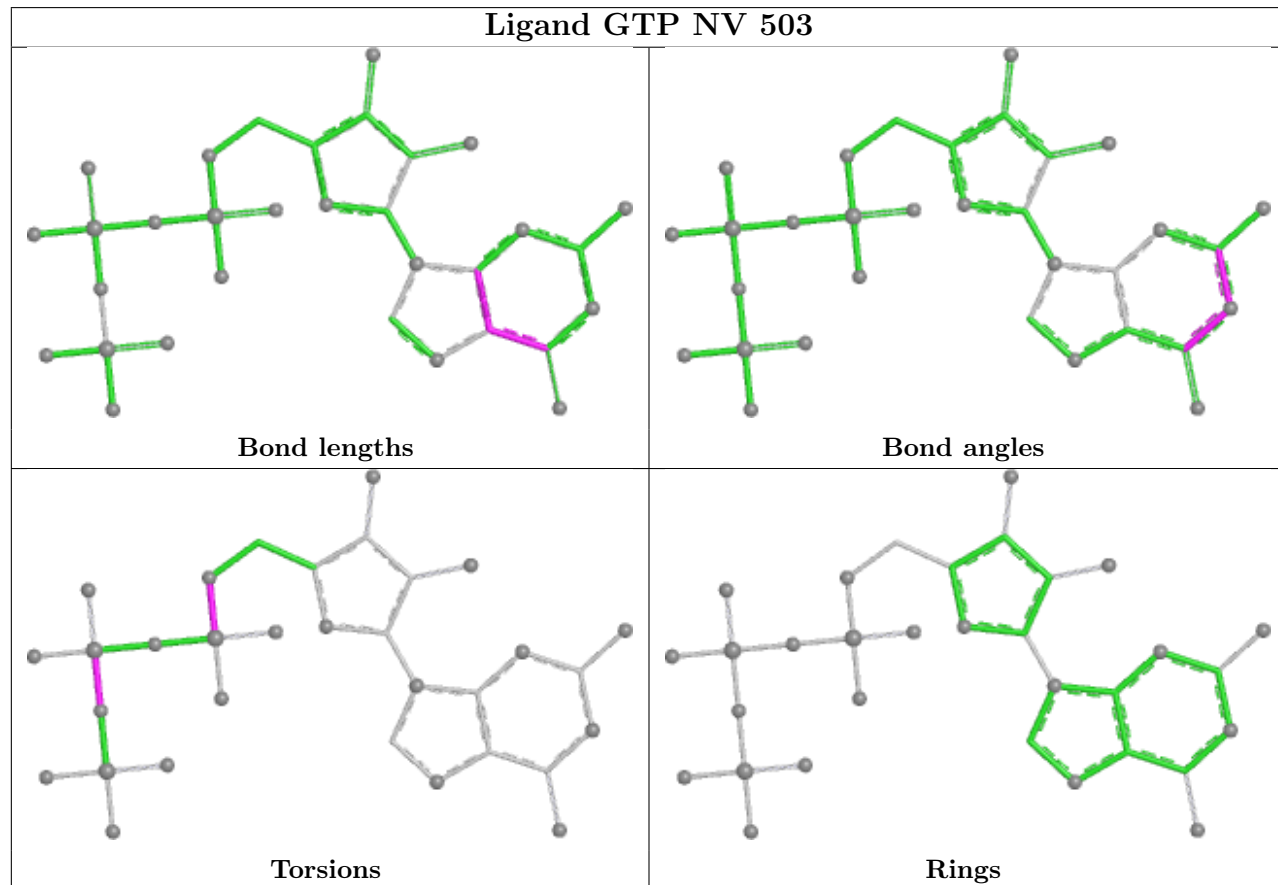
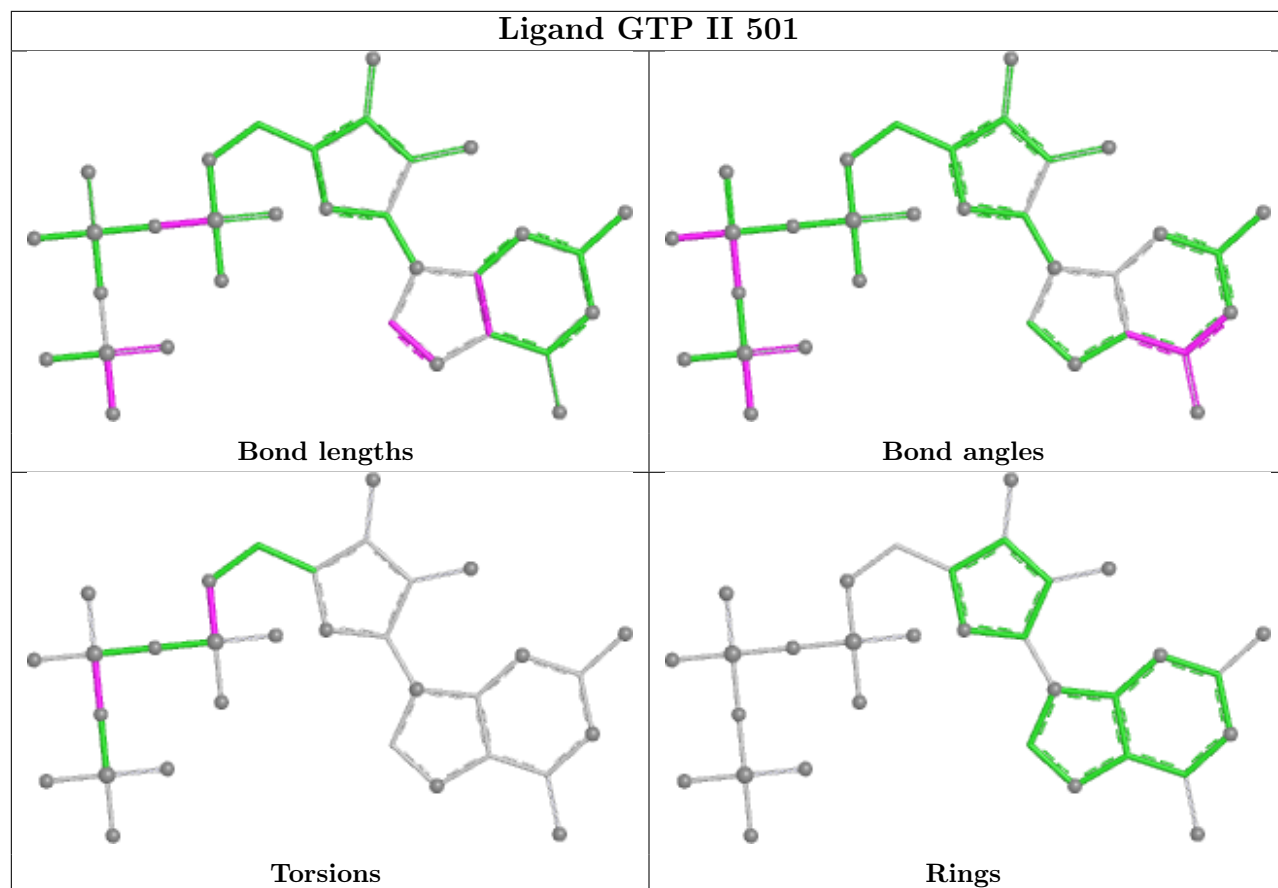


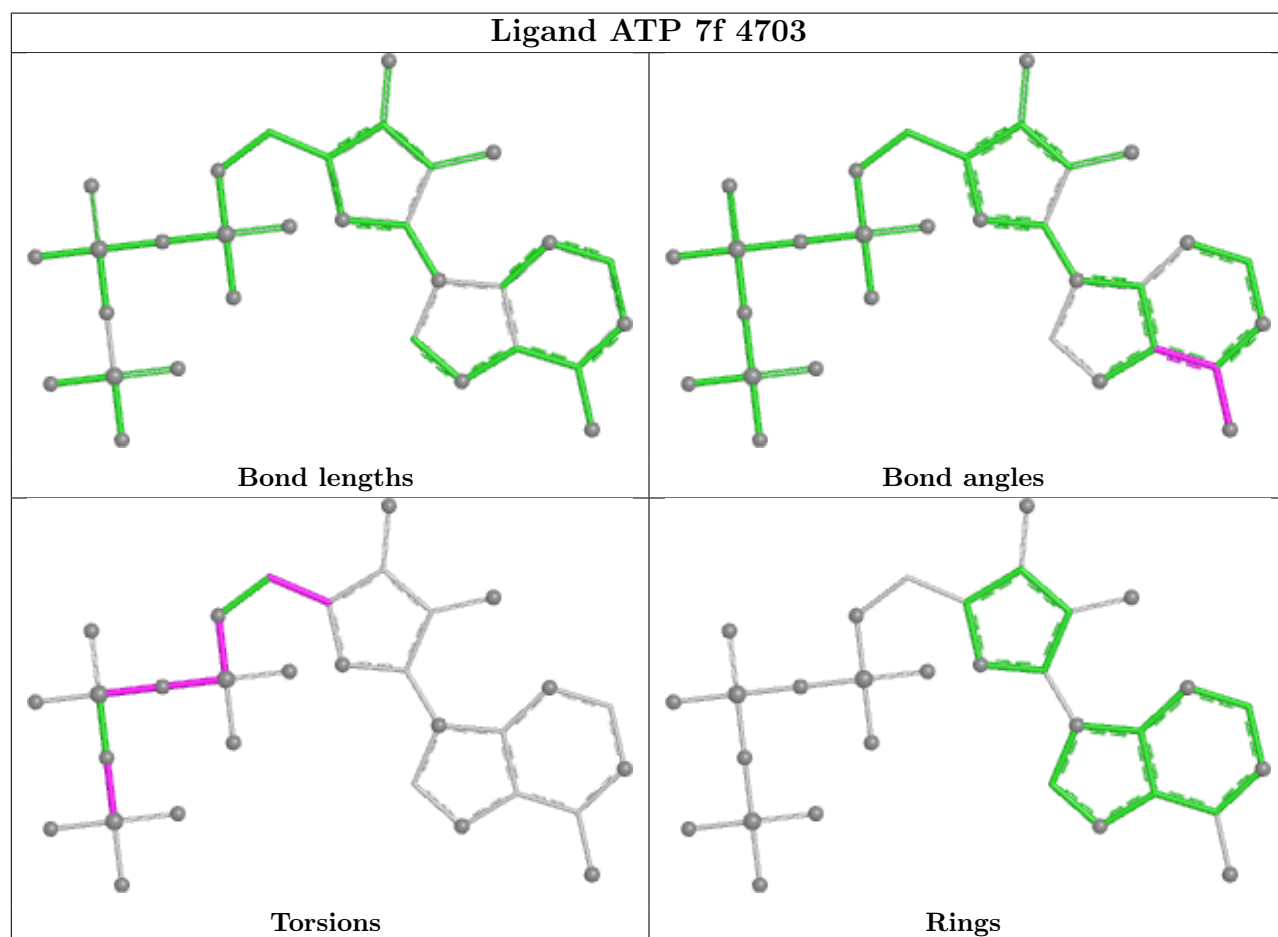
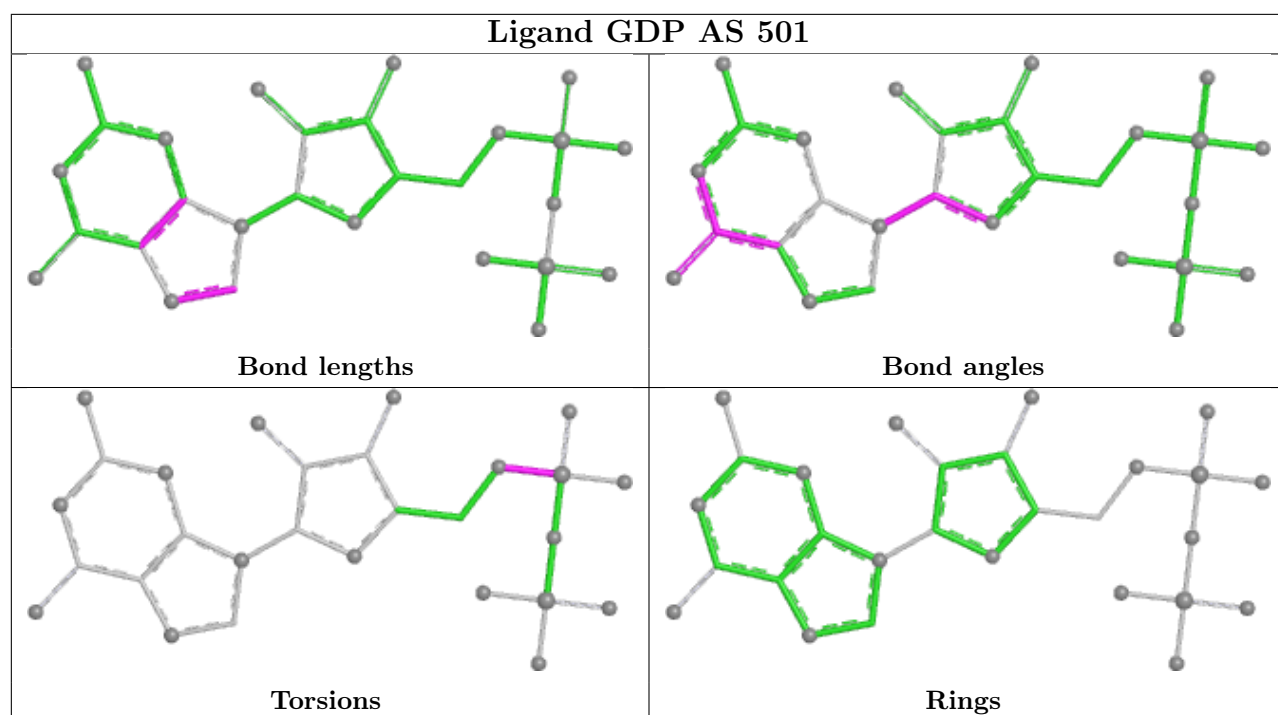
## Ligand GTP CD 602

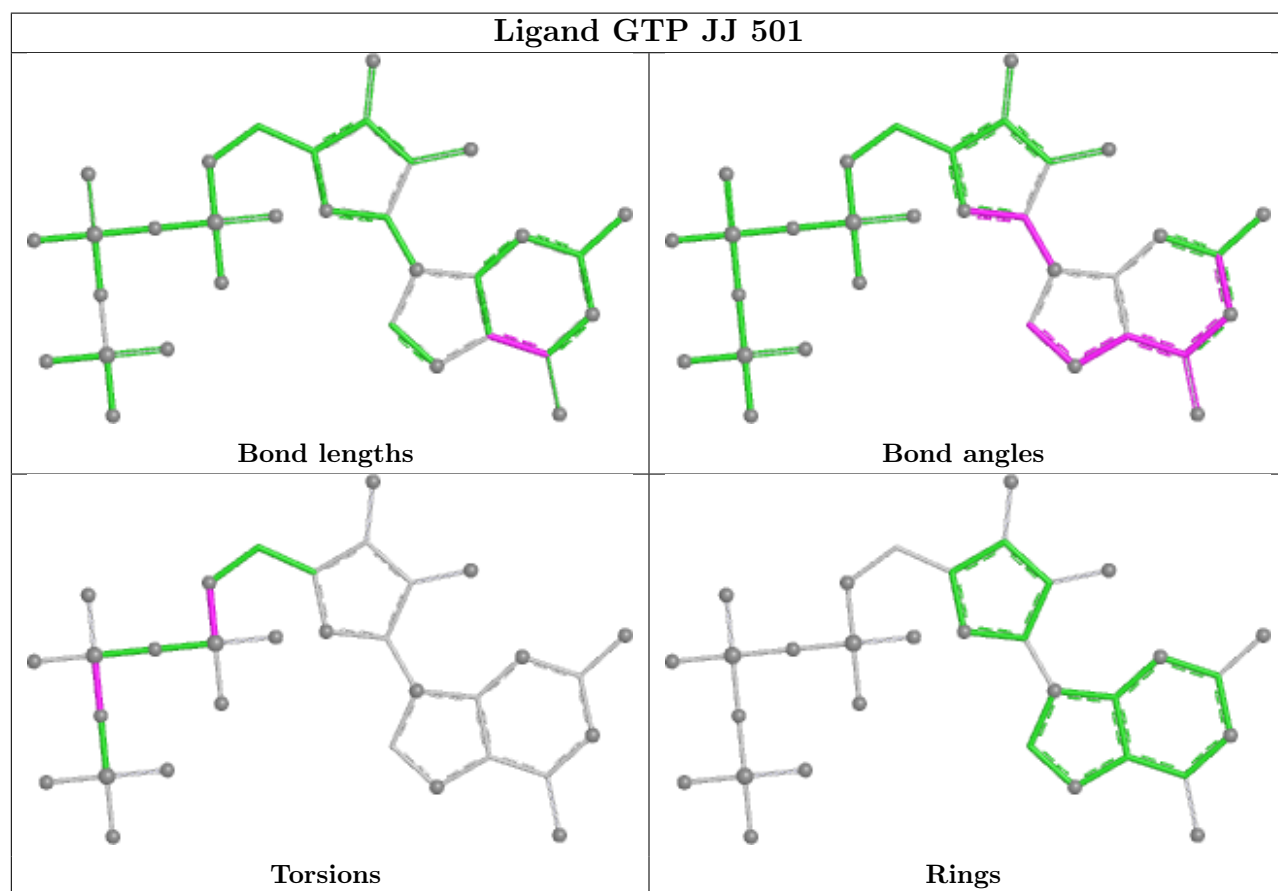
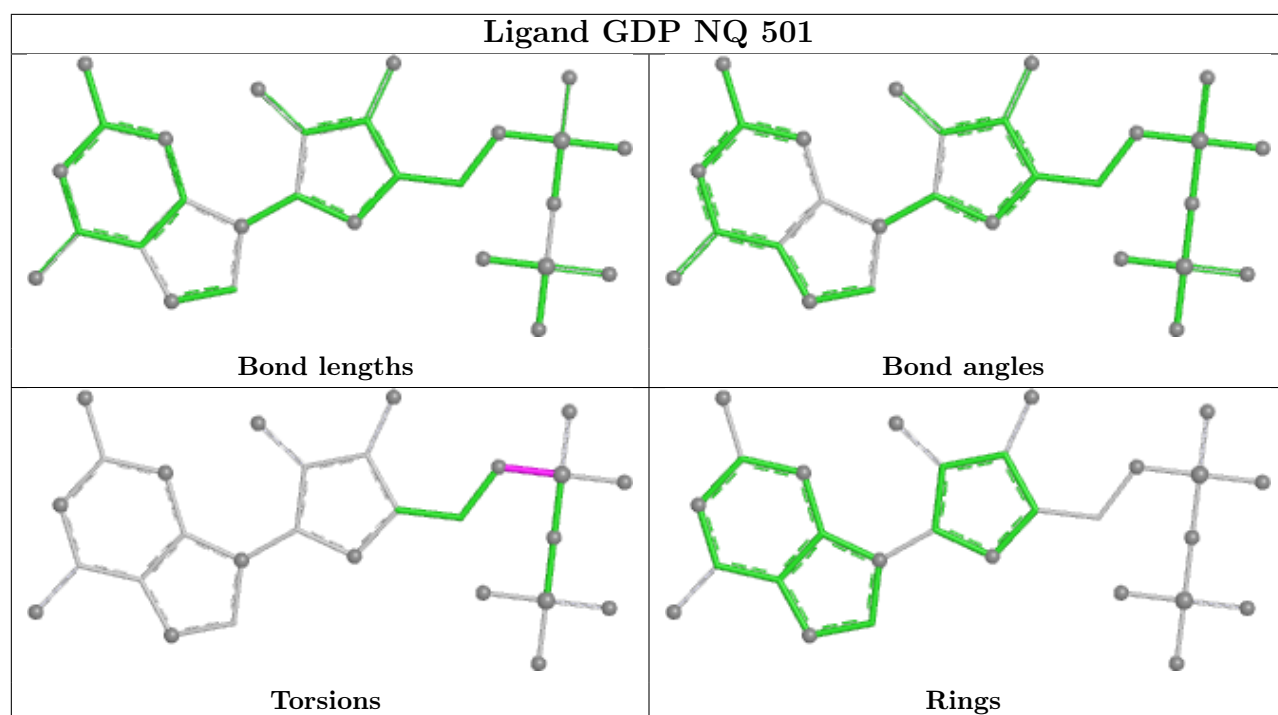


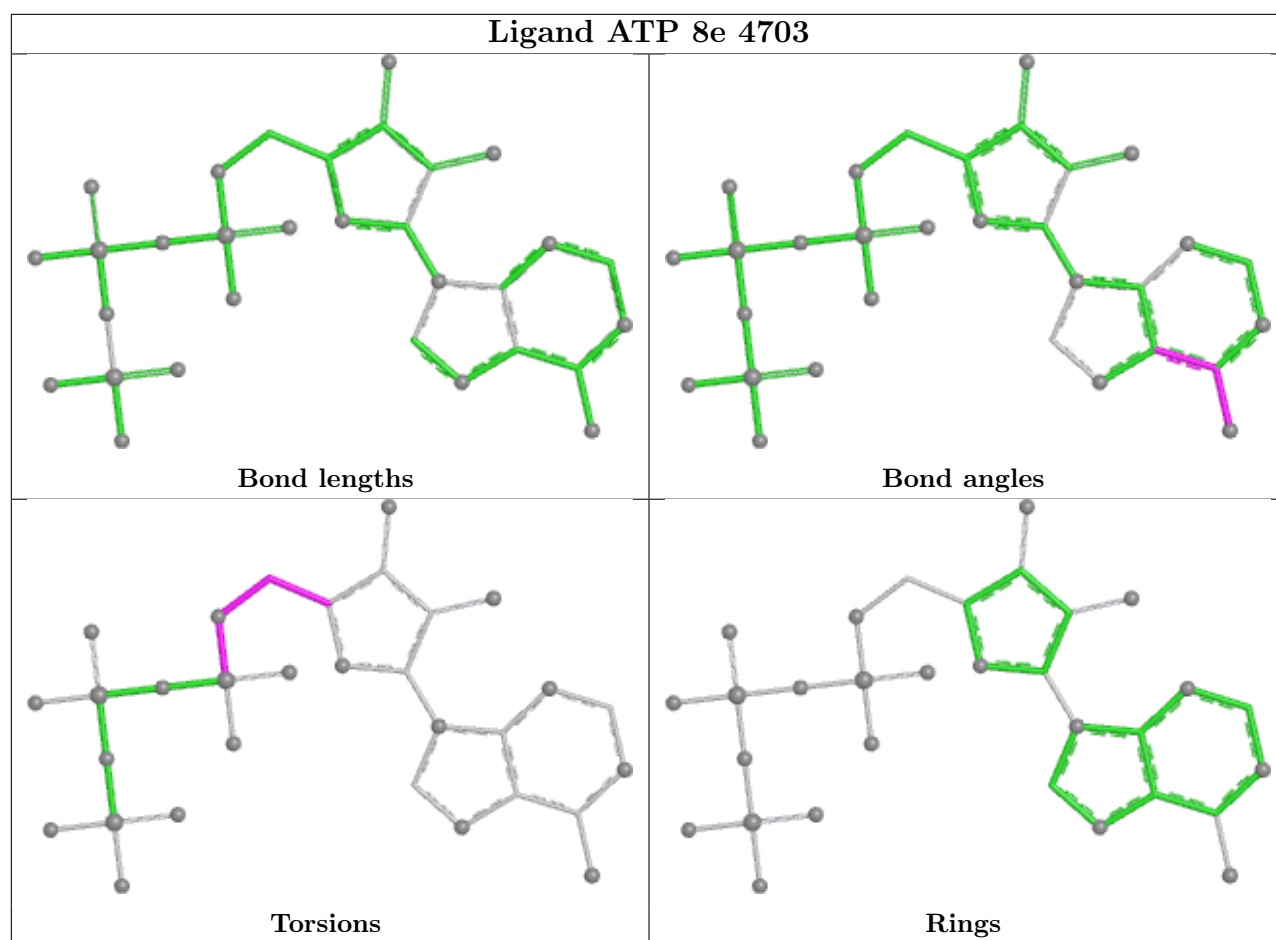




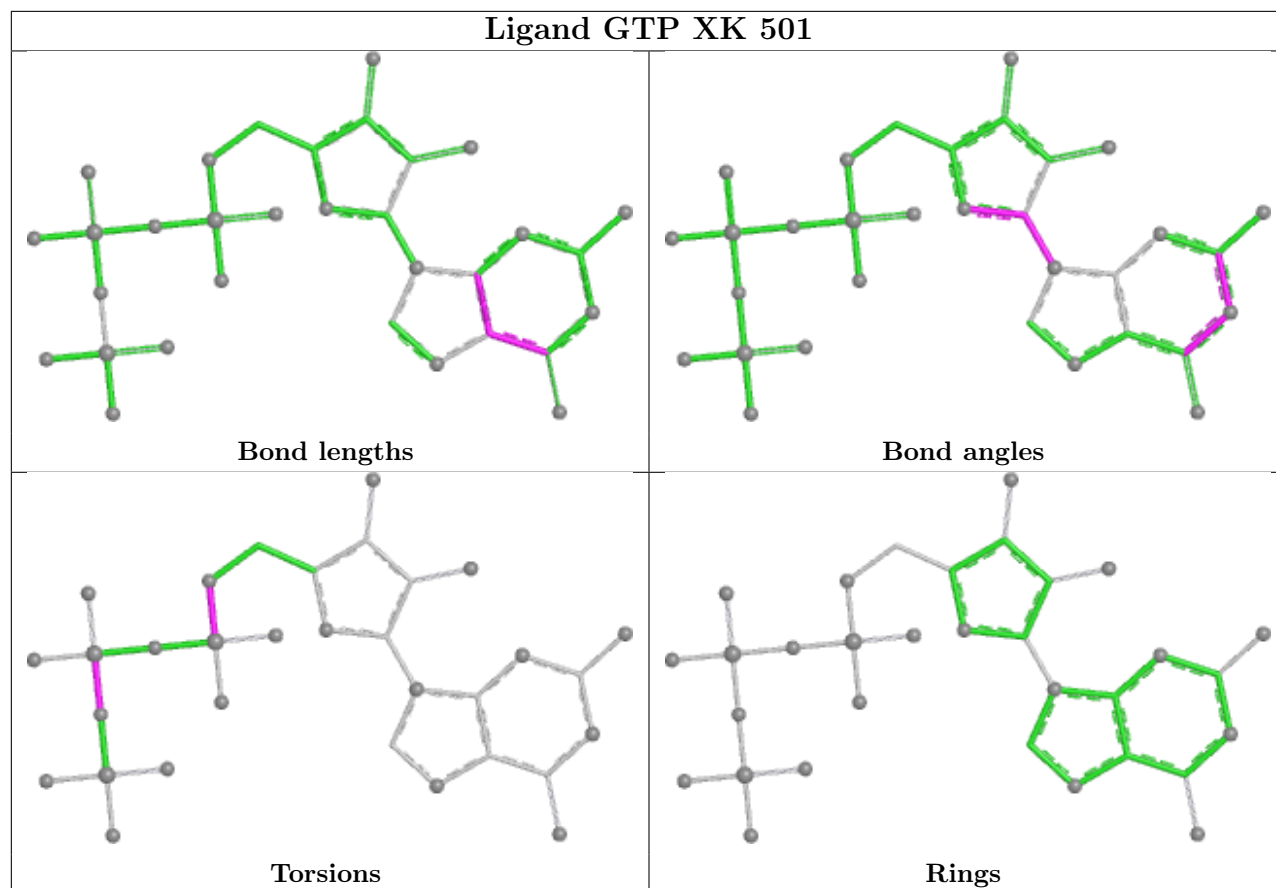




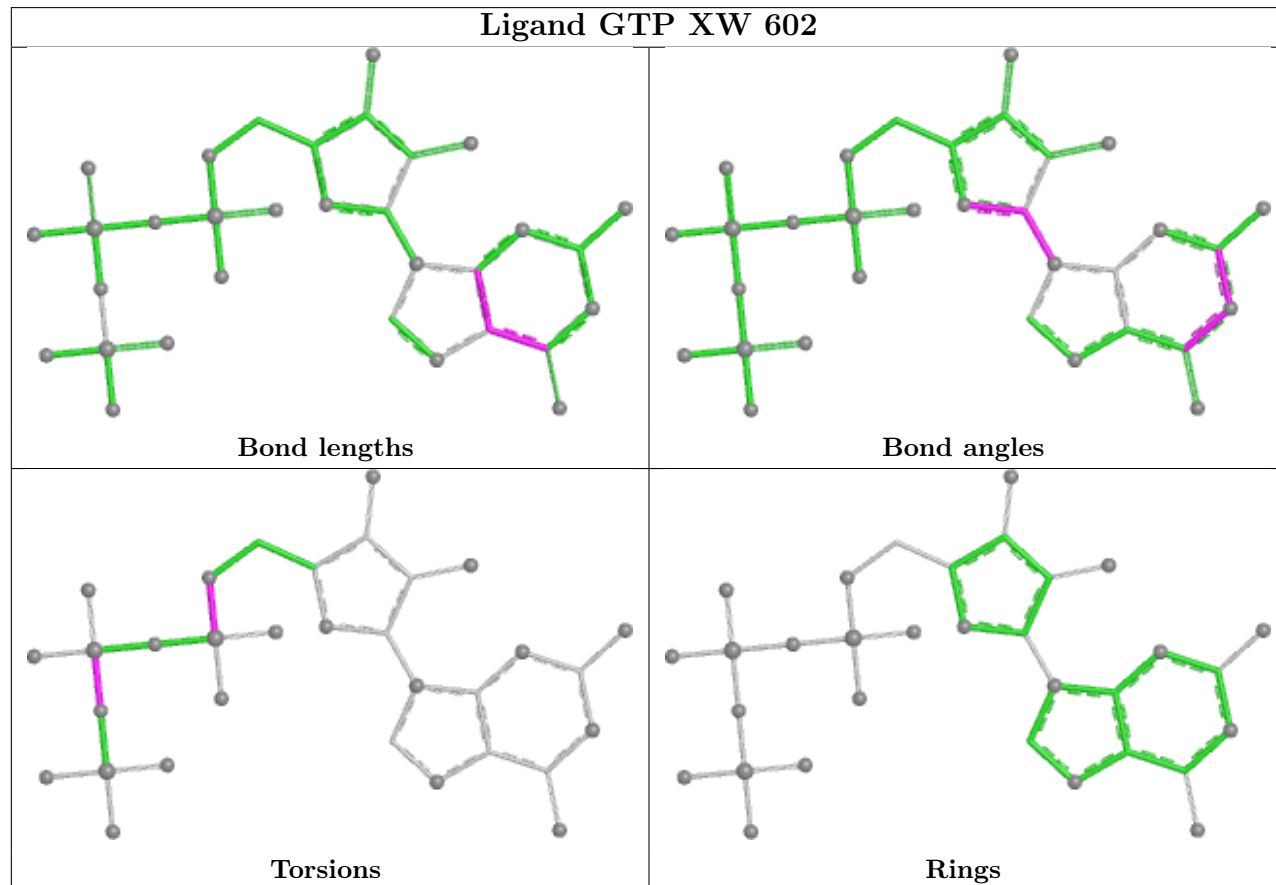


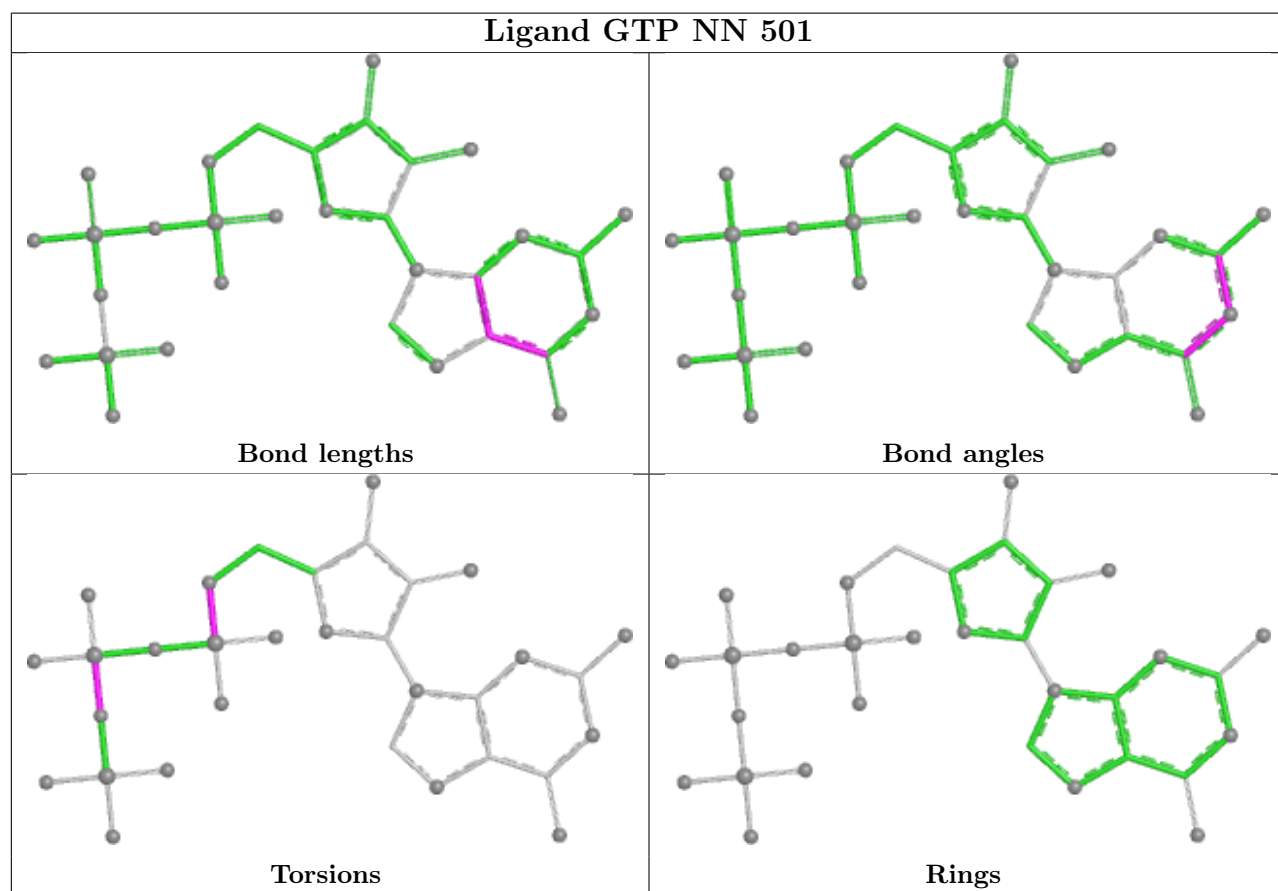
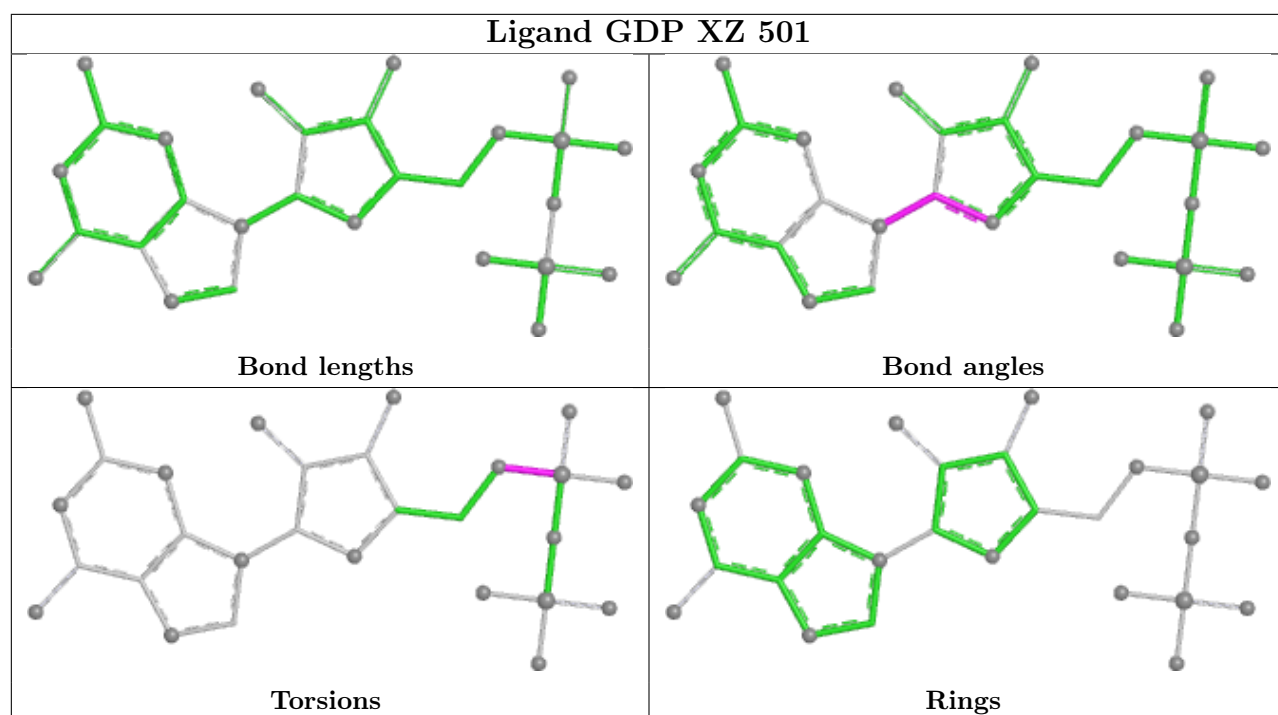


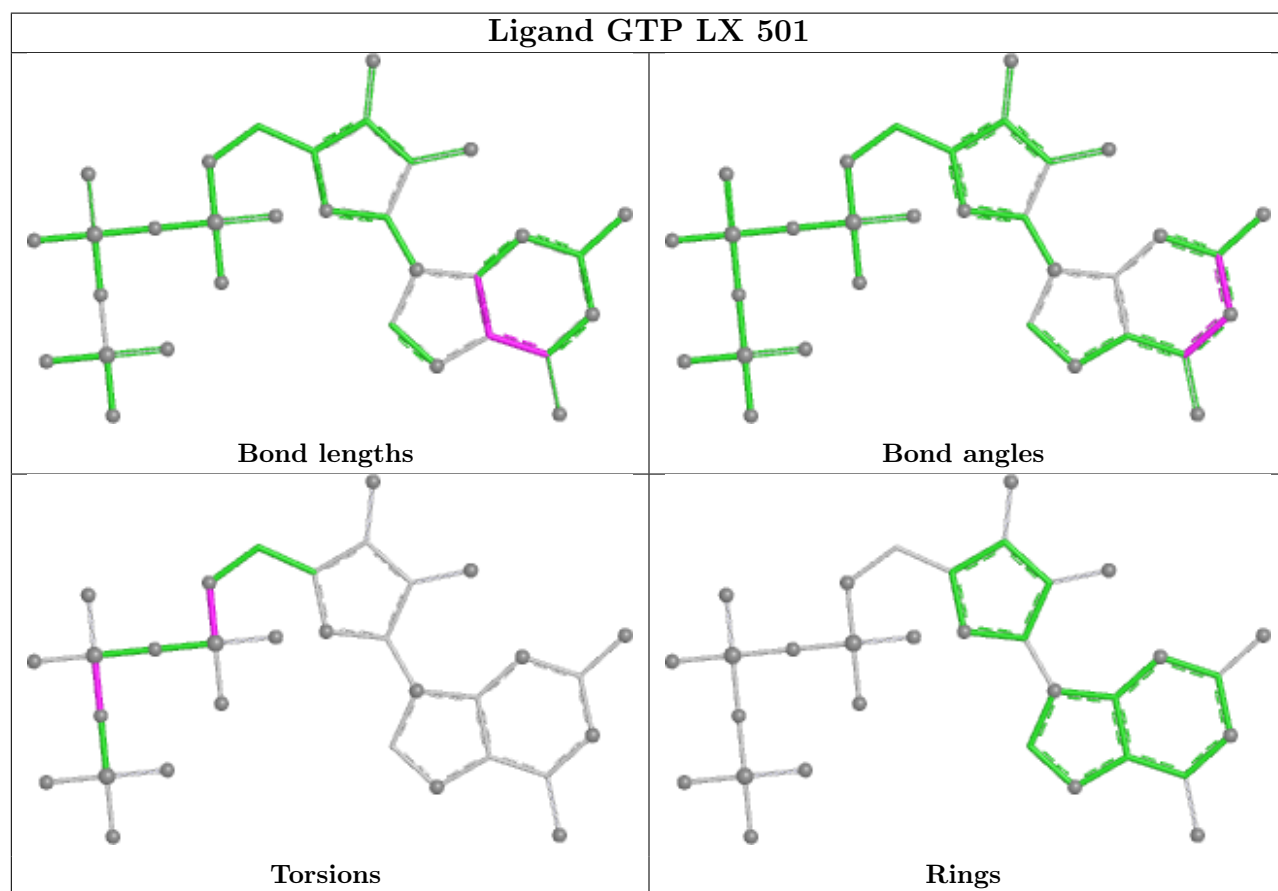
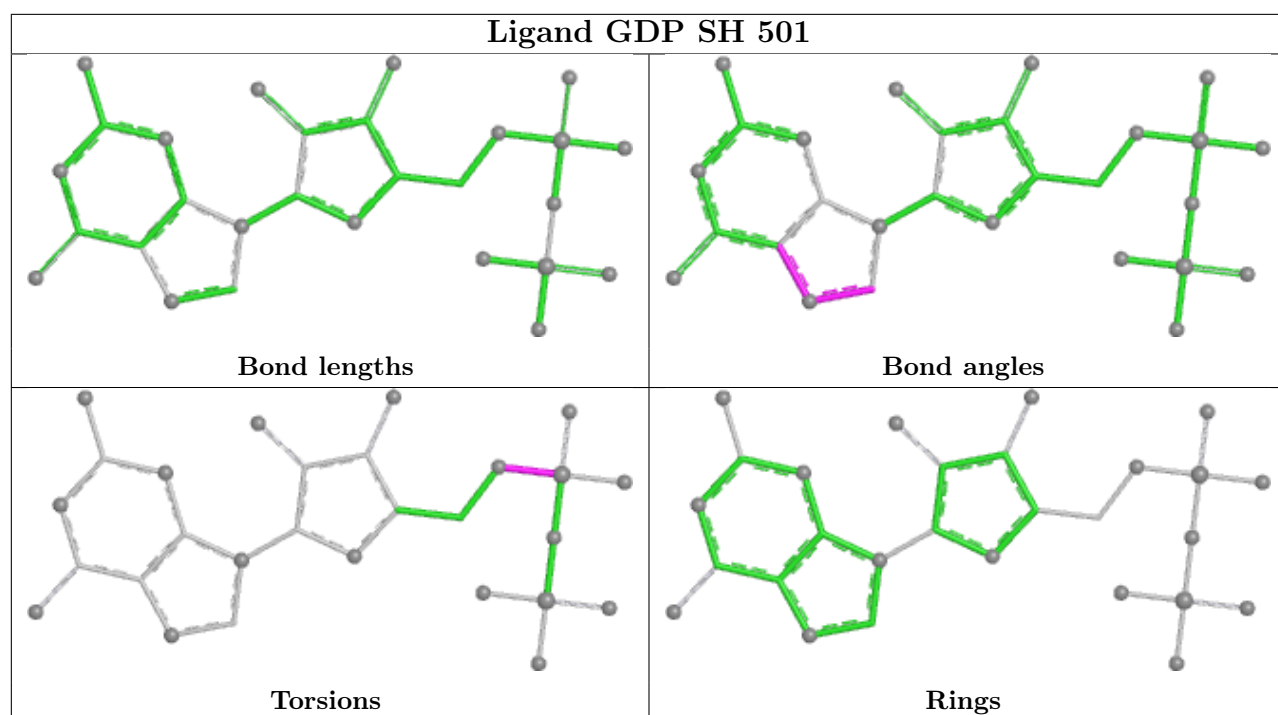
## Ligand GTP XK 501



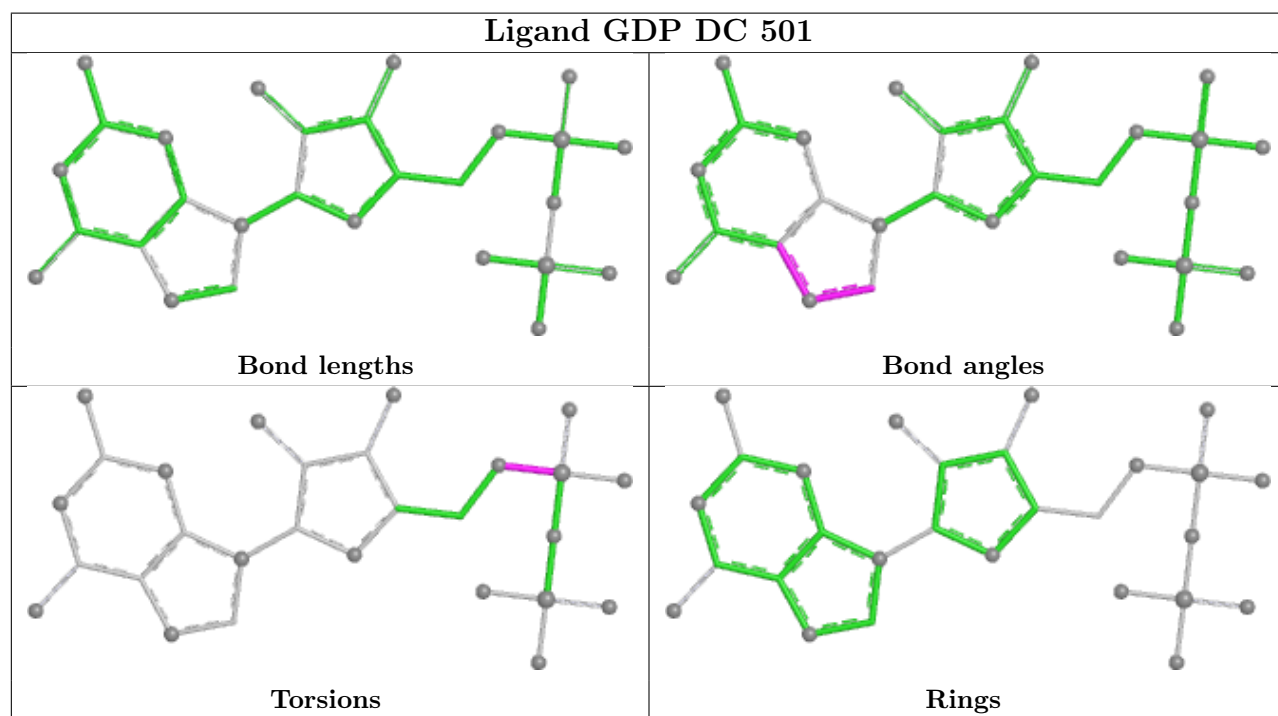
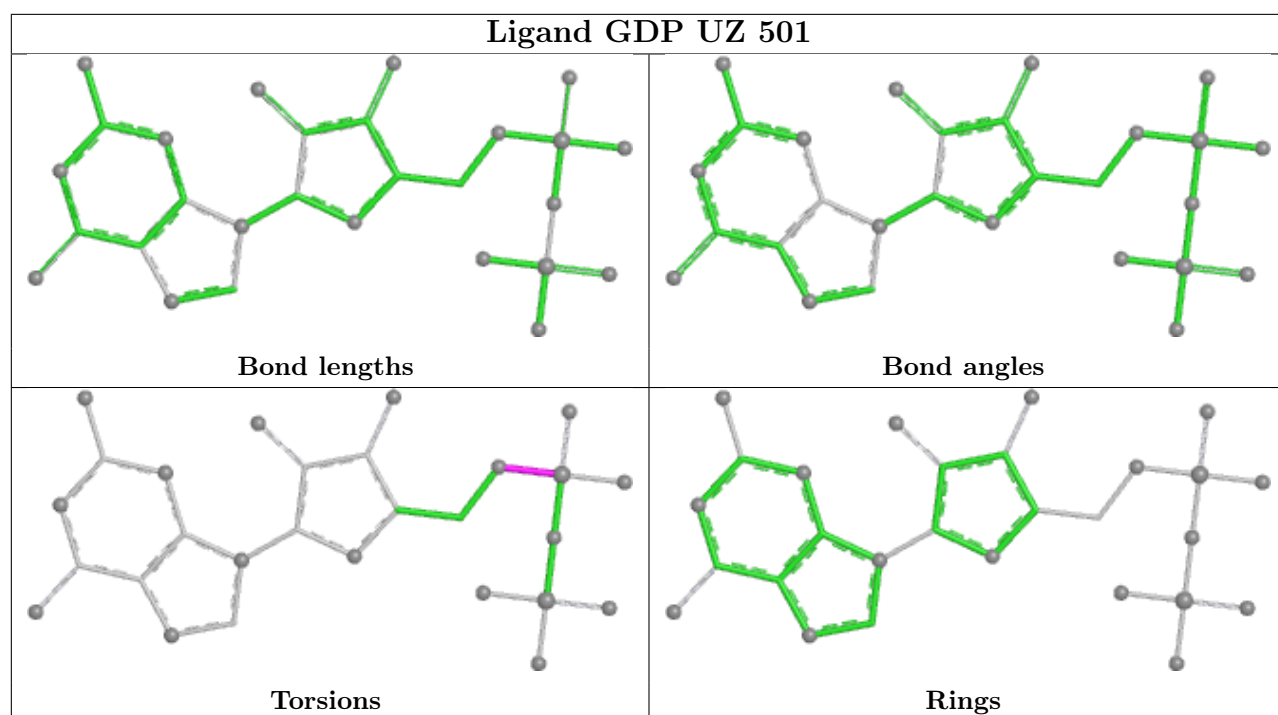
## Ligand GTP XW 602



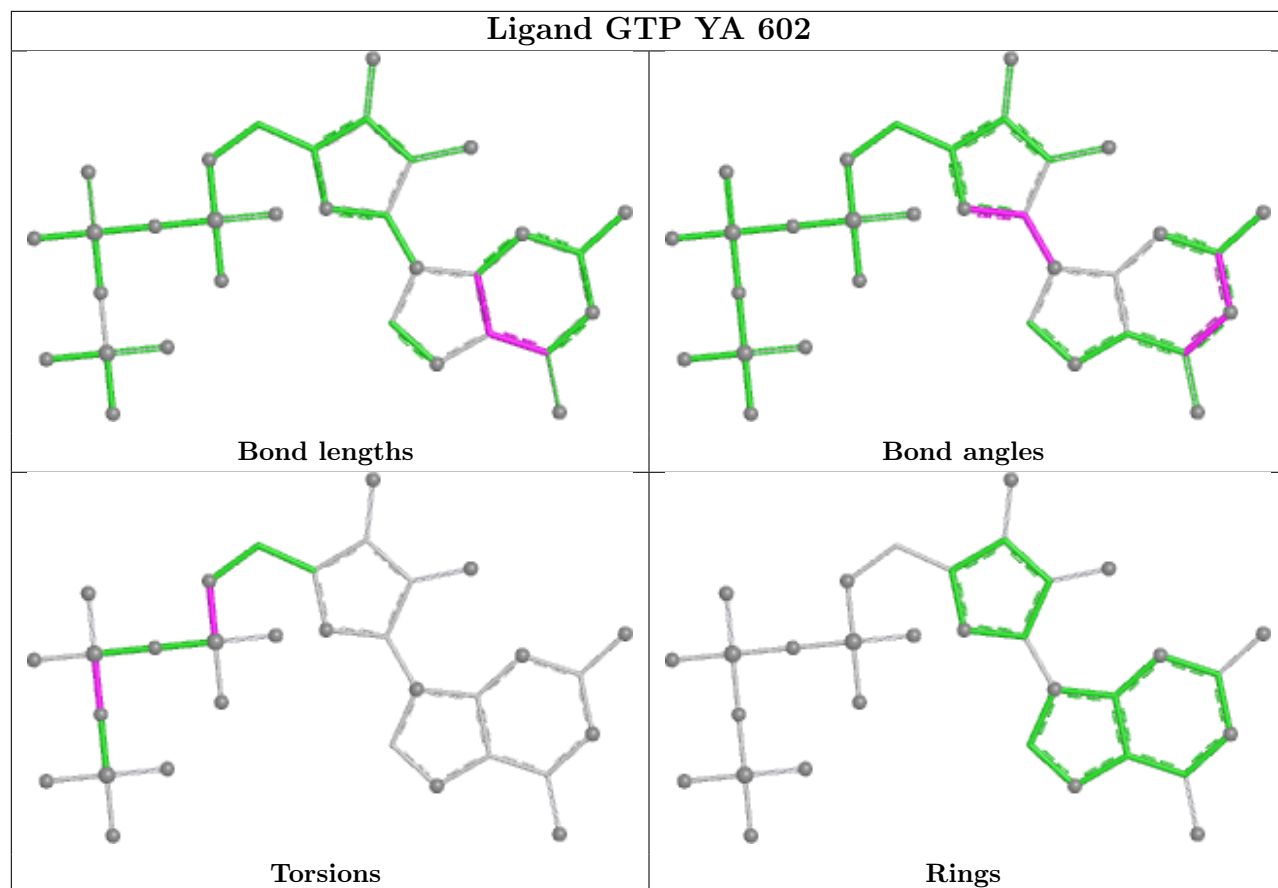




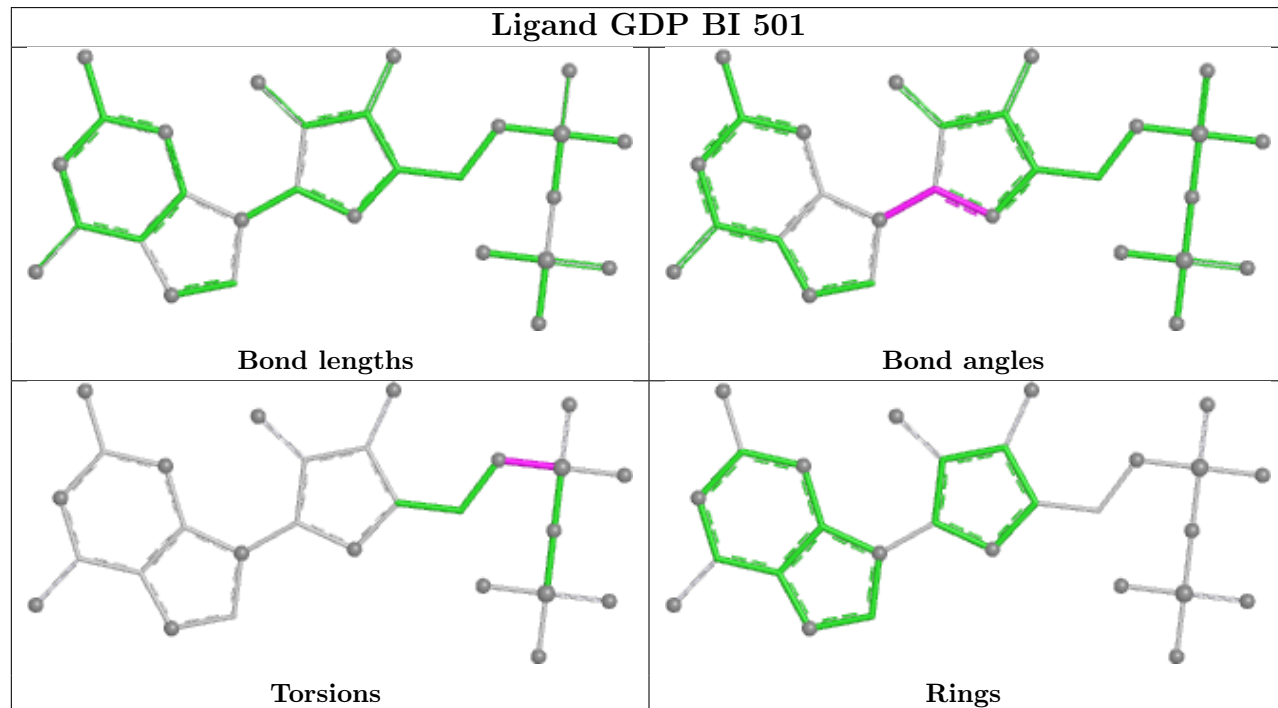


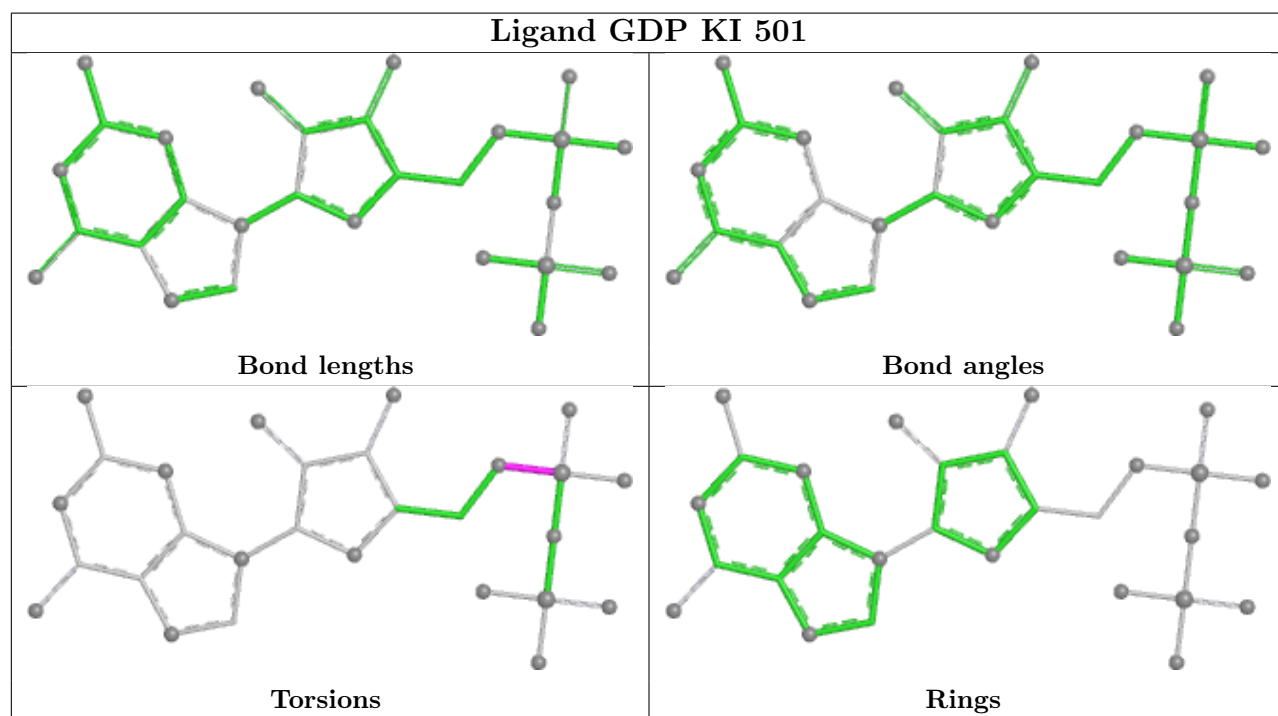
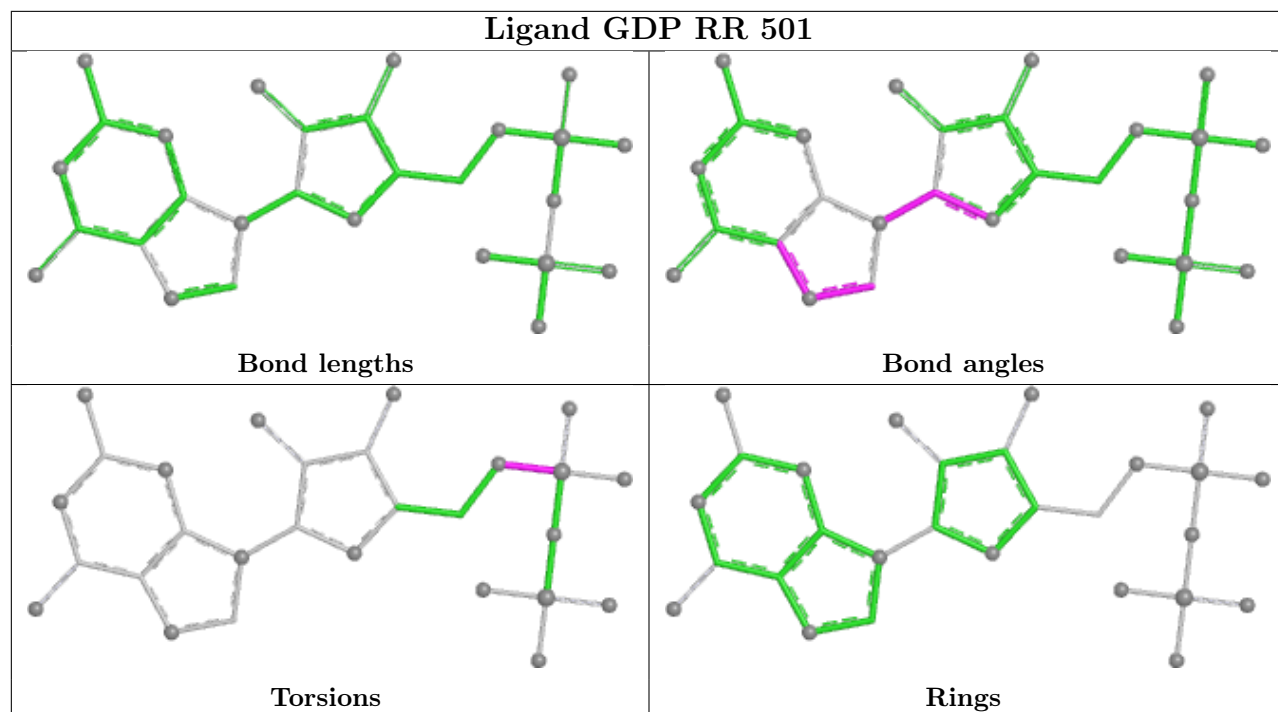


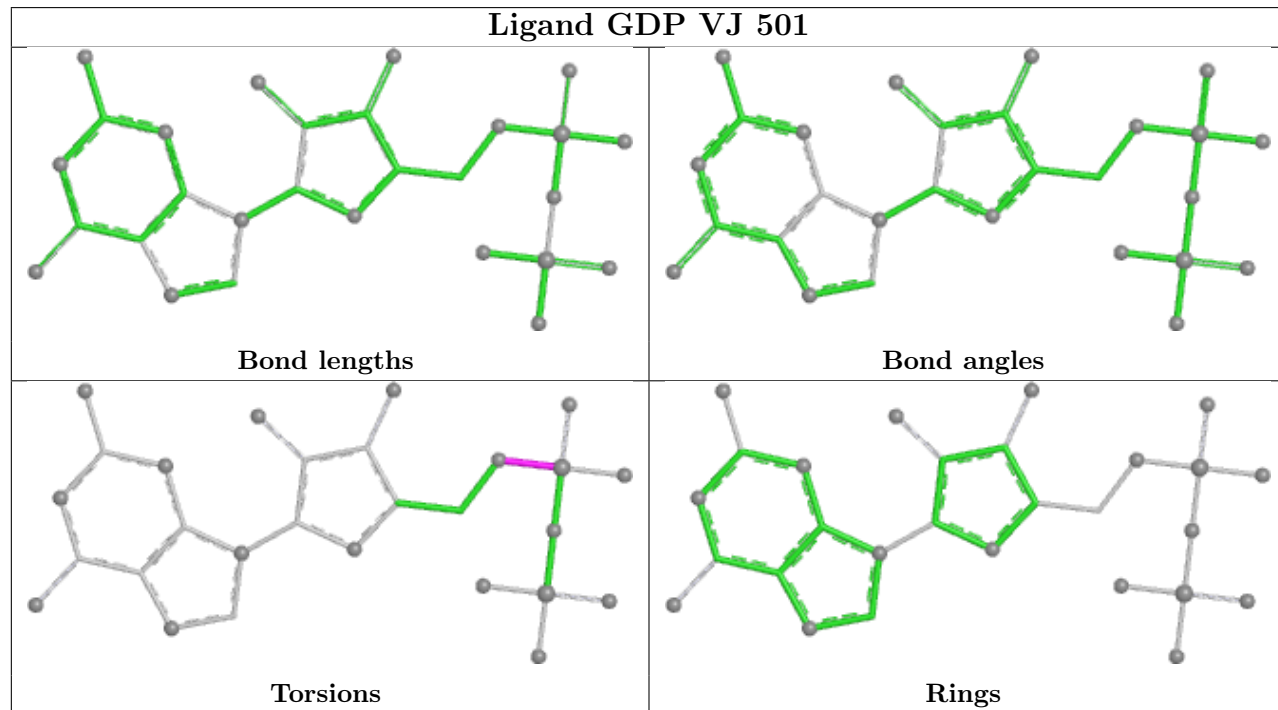
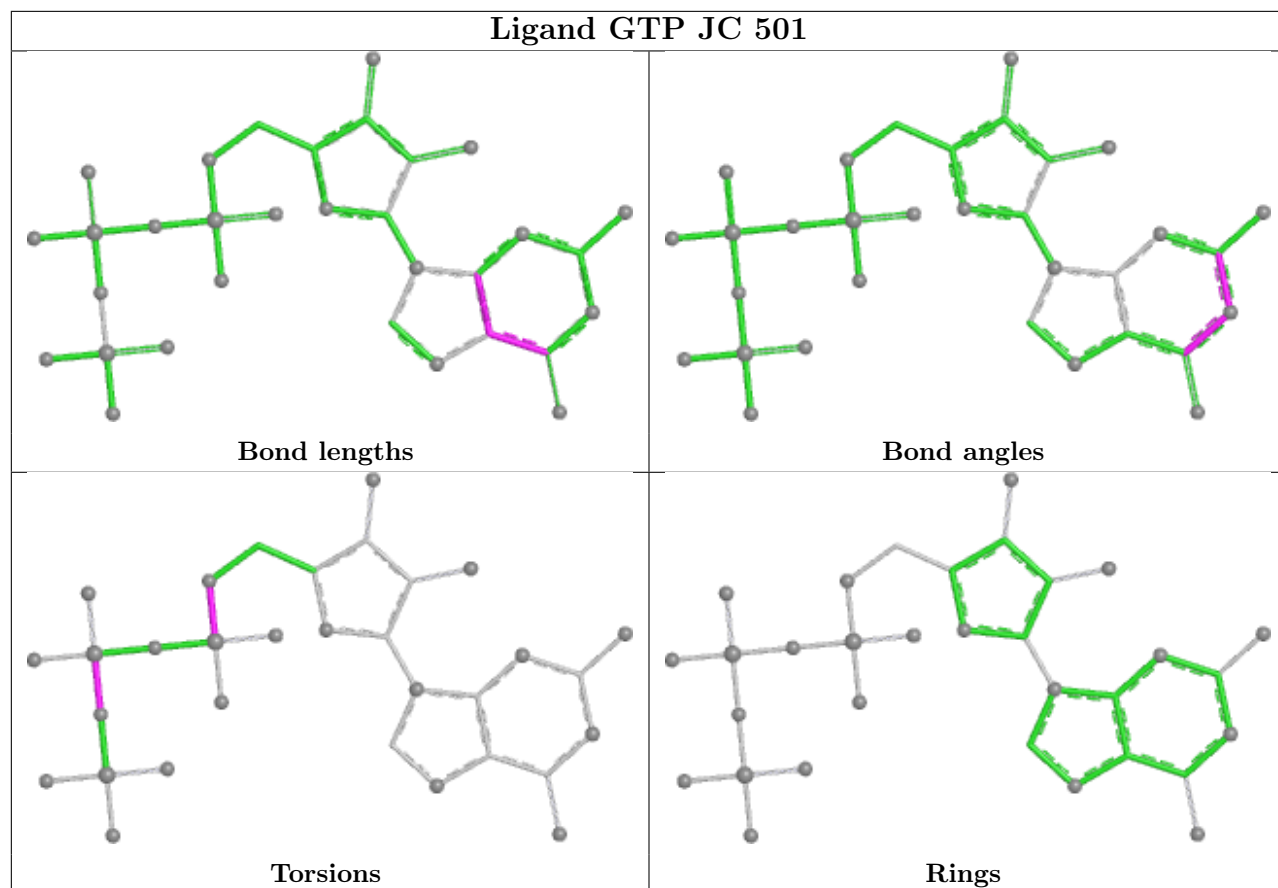
## Ligand GTP YA 602



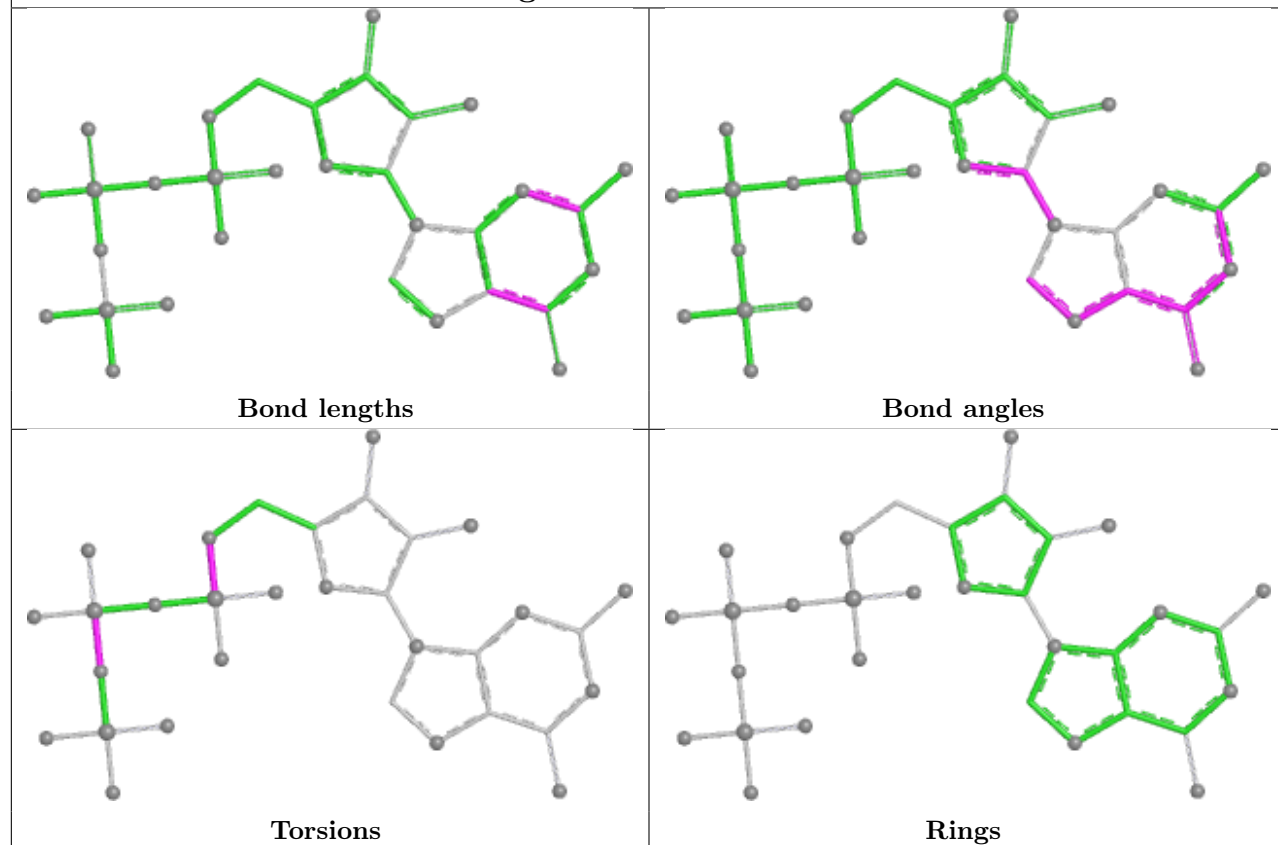
## Ligand GDP BI 501



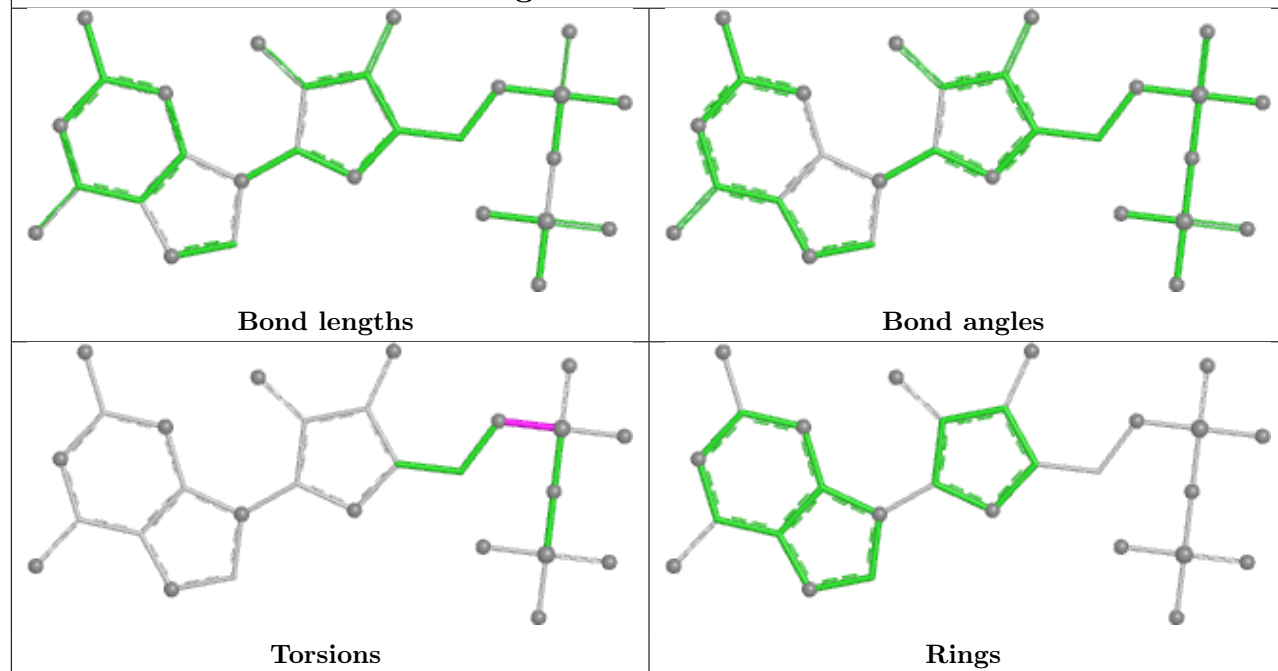




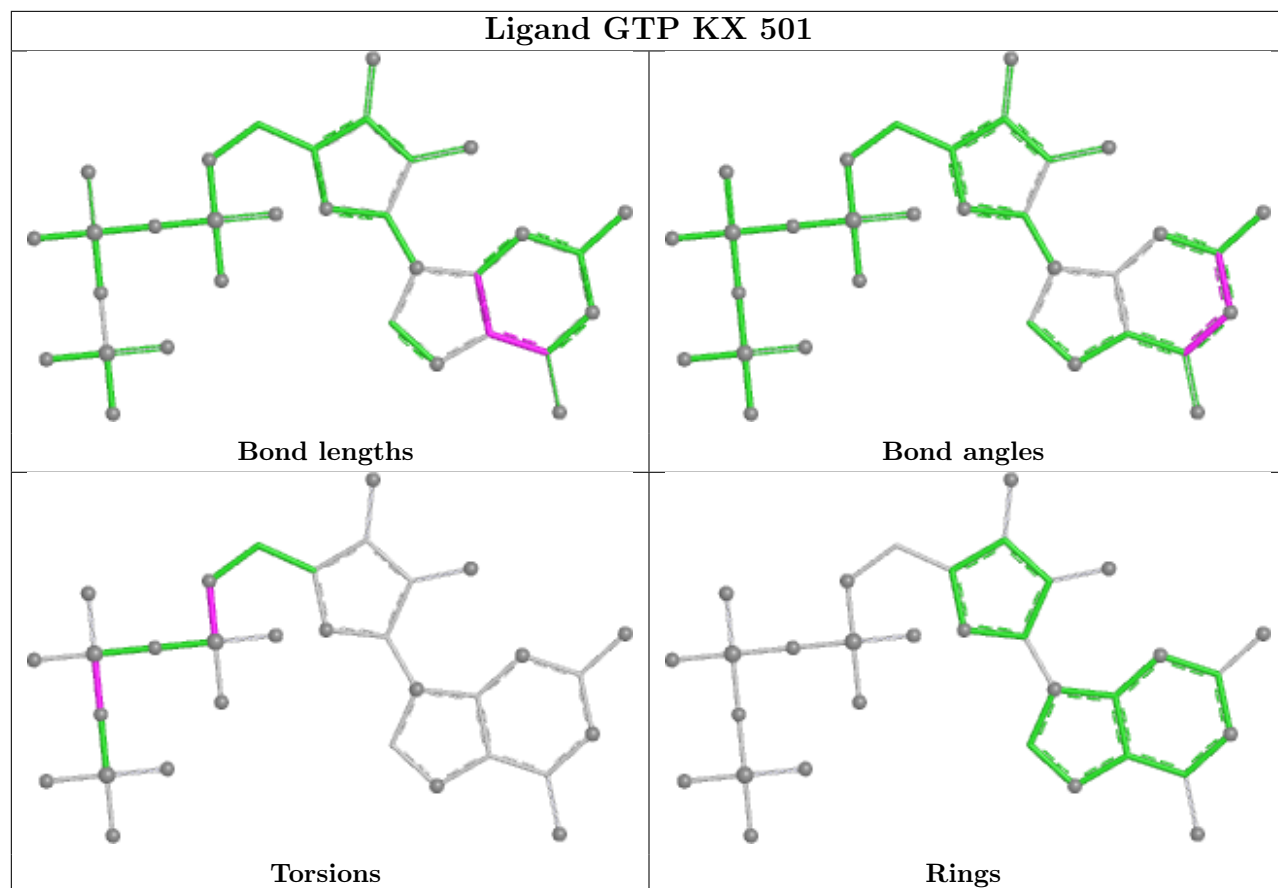
## Ligand GTP KZ 602



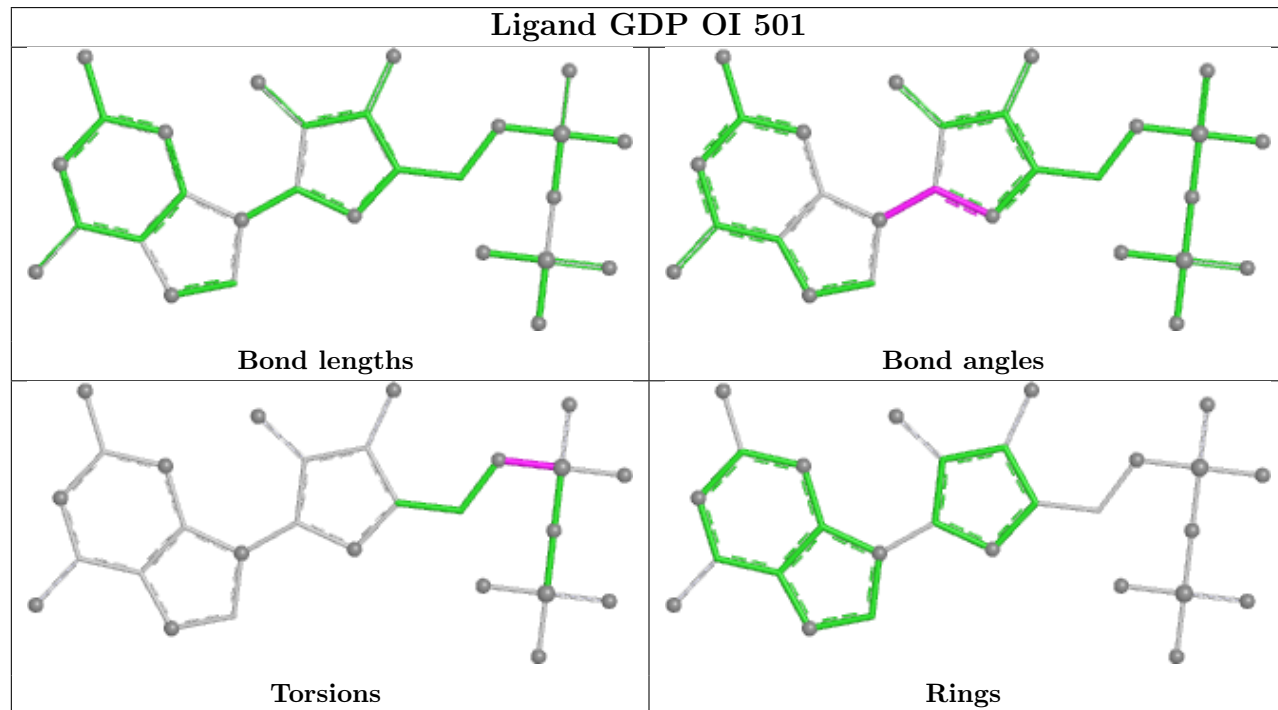
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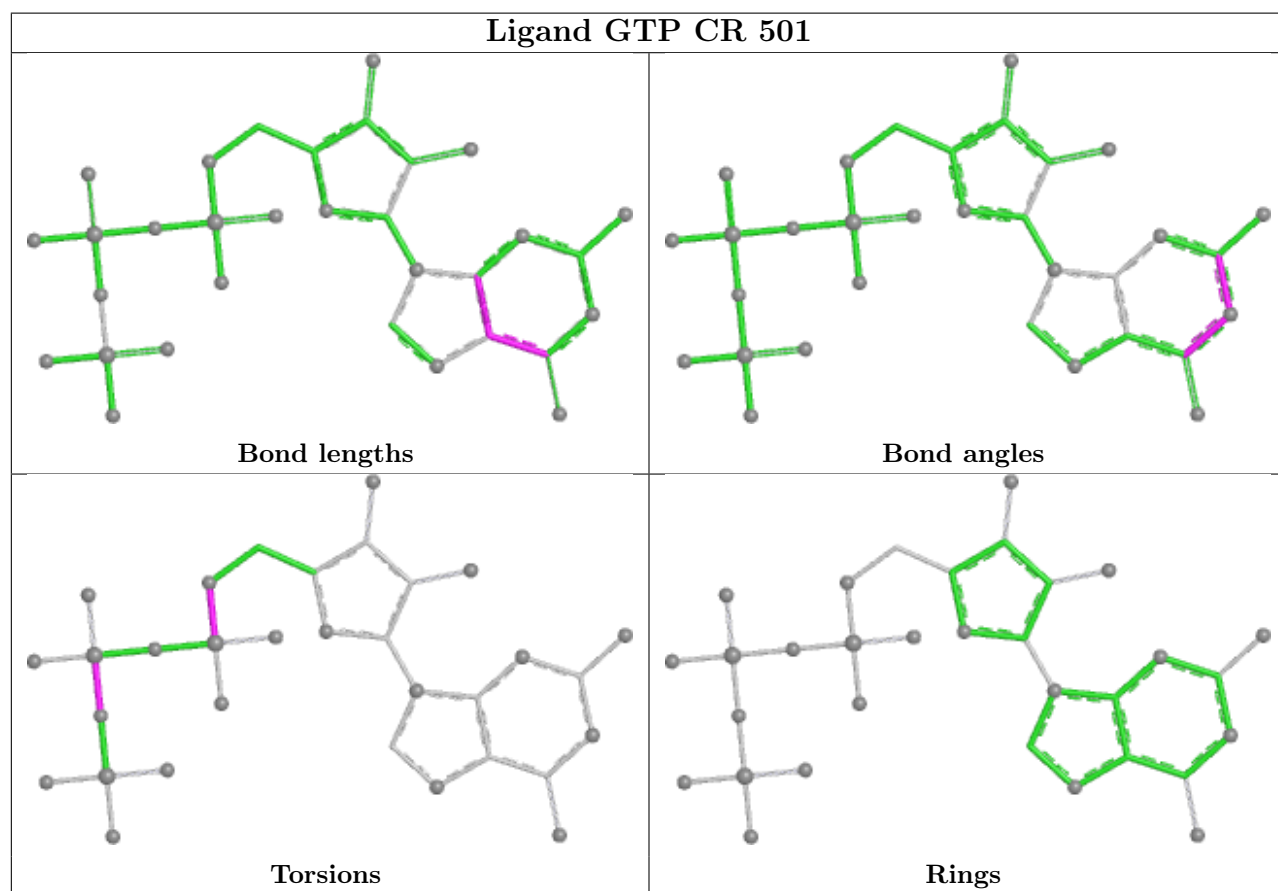
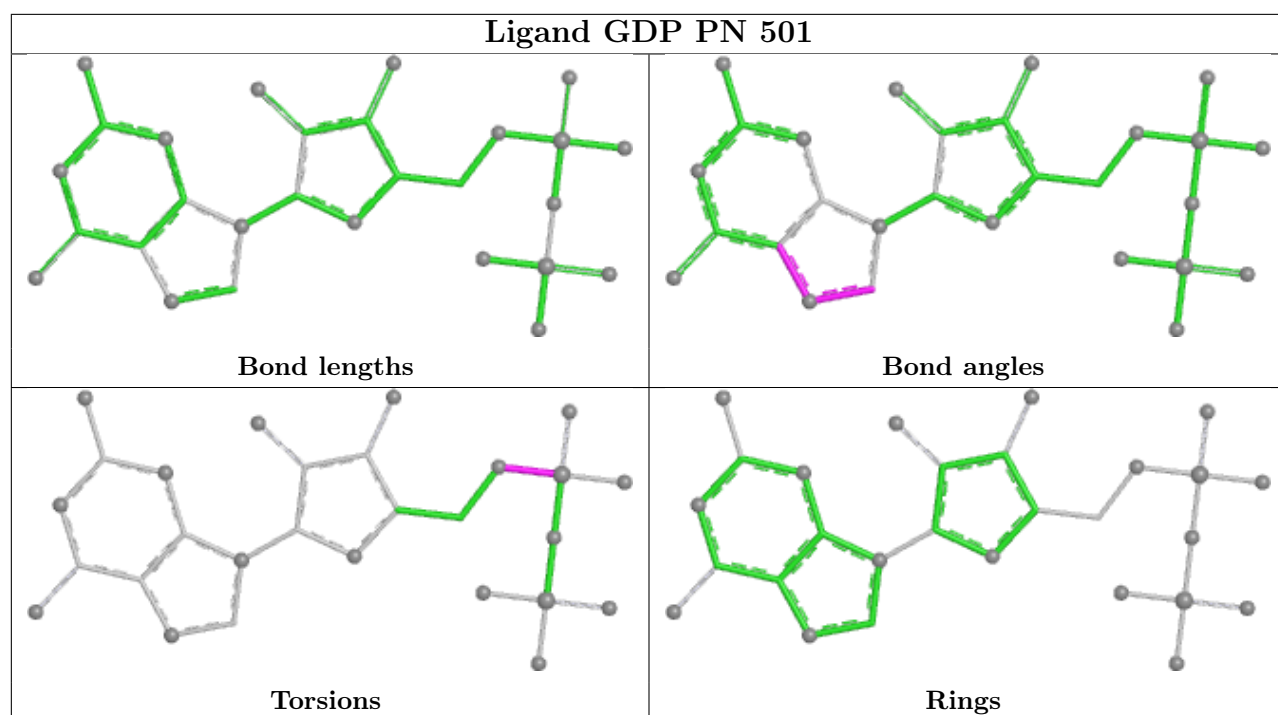


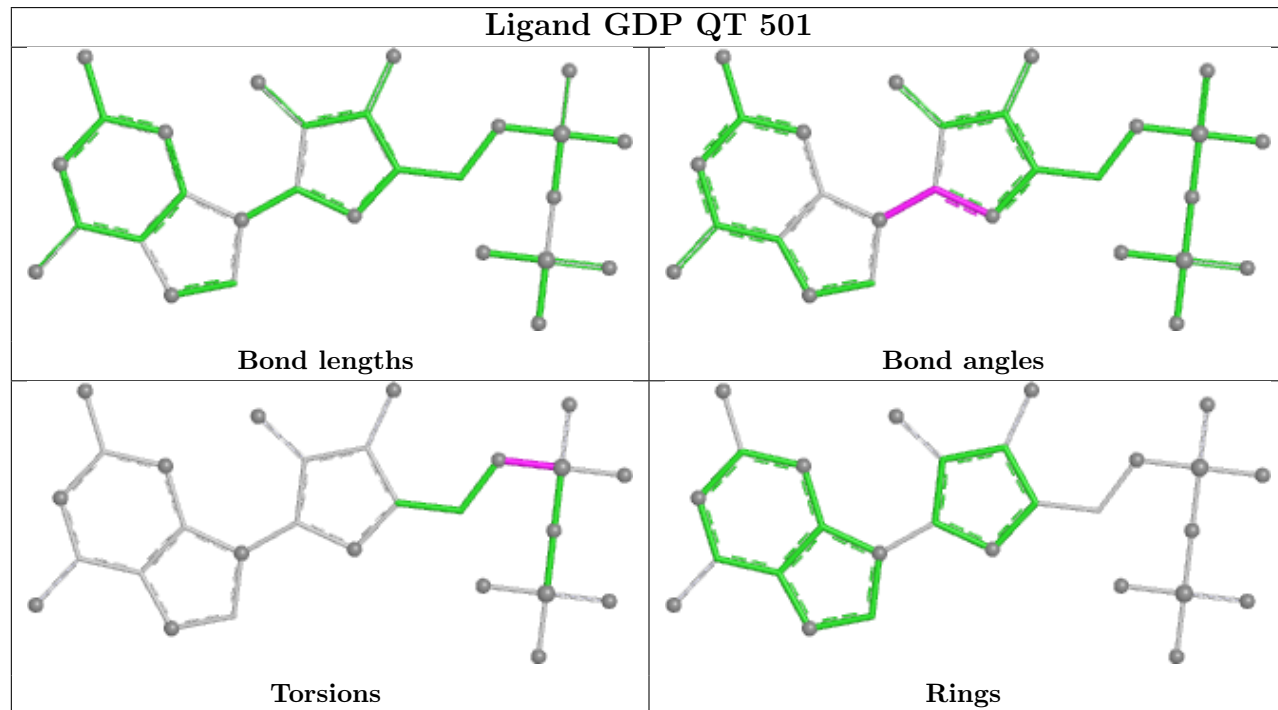
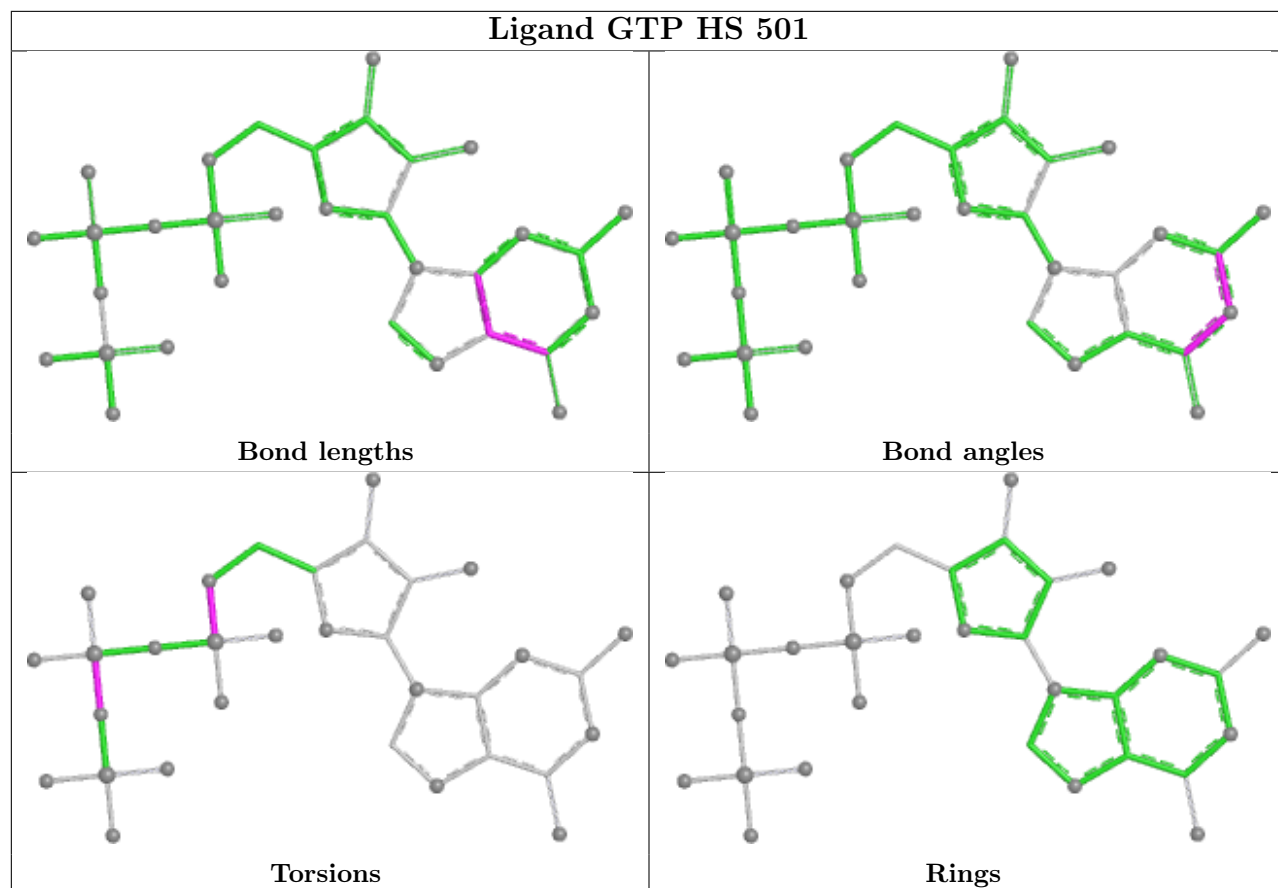
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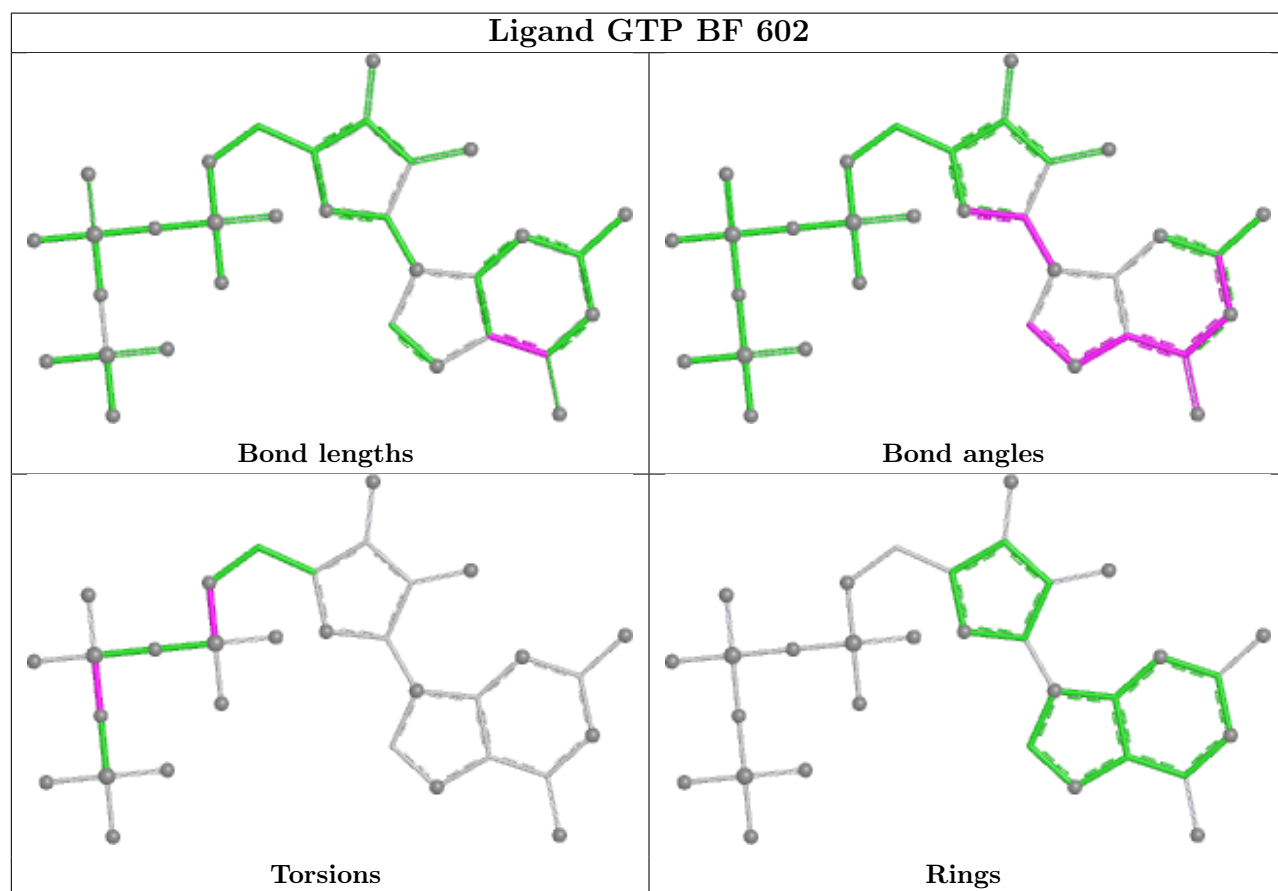
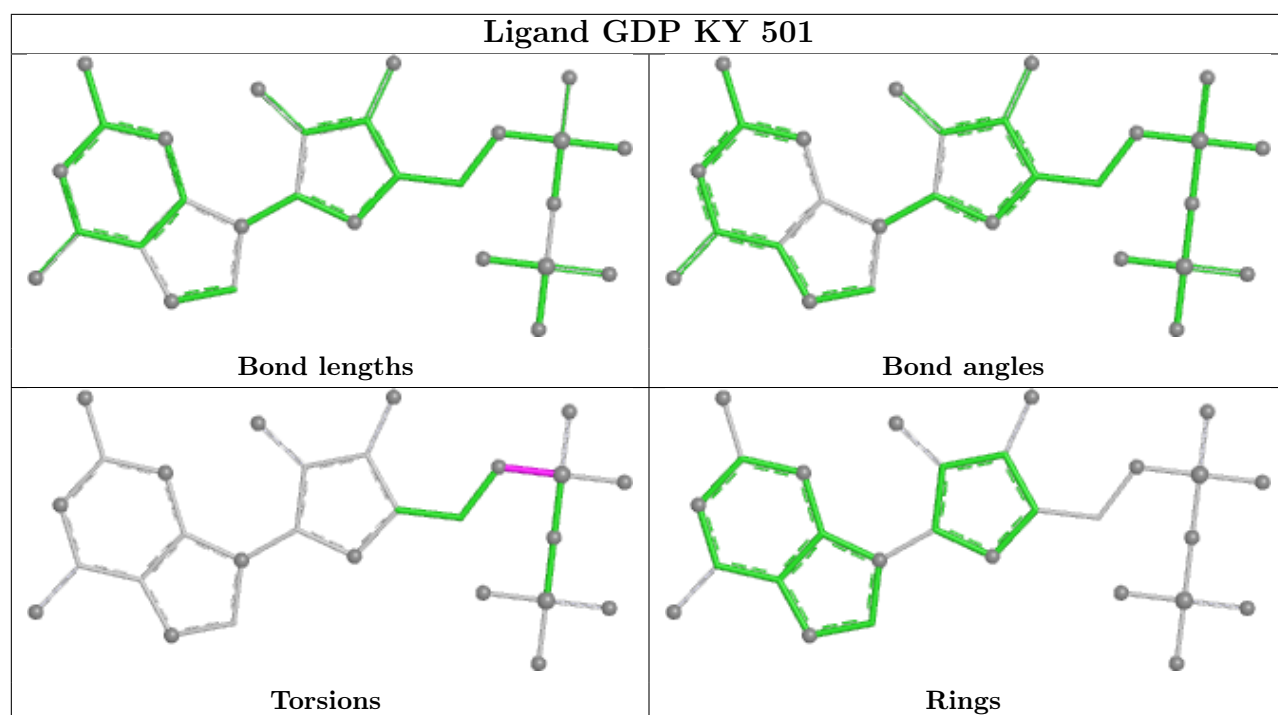
## Ligand GDP OI 501



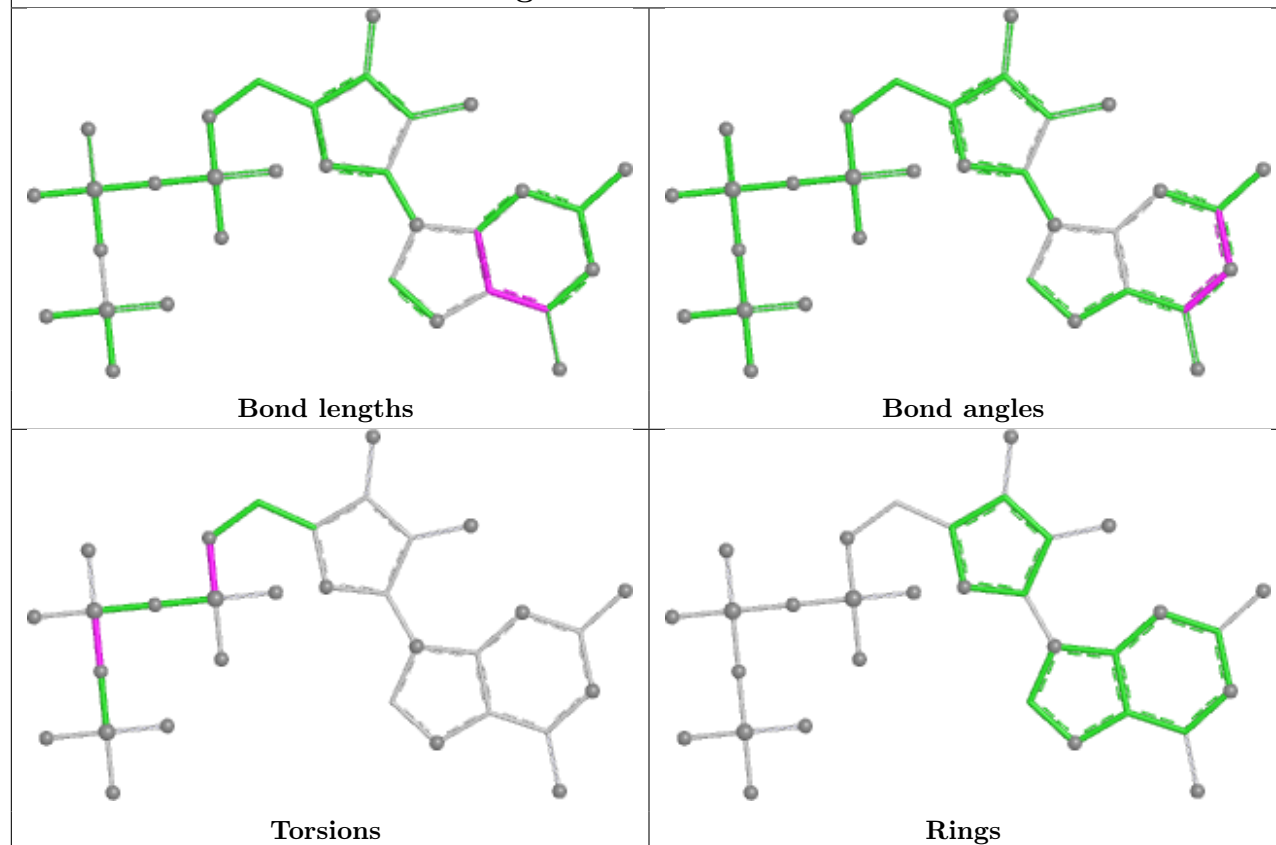




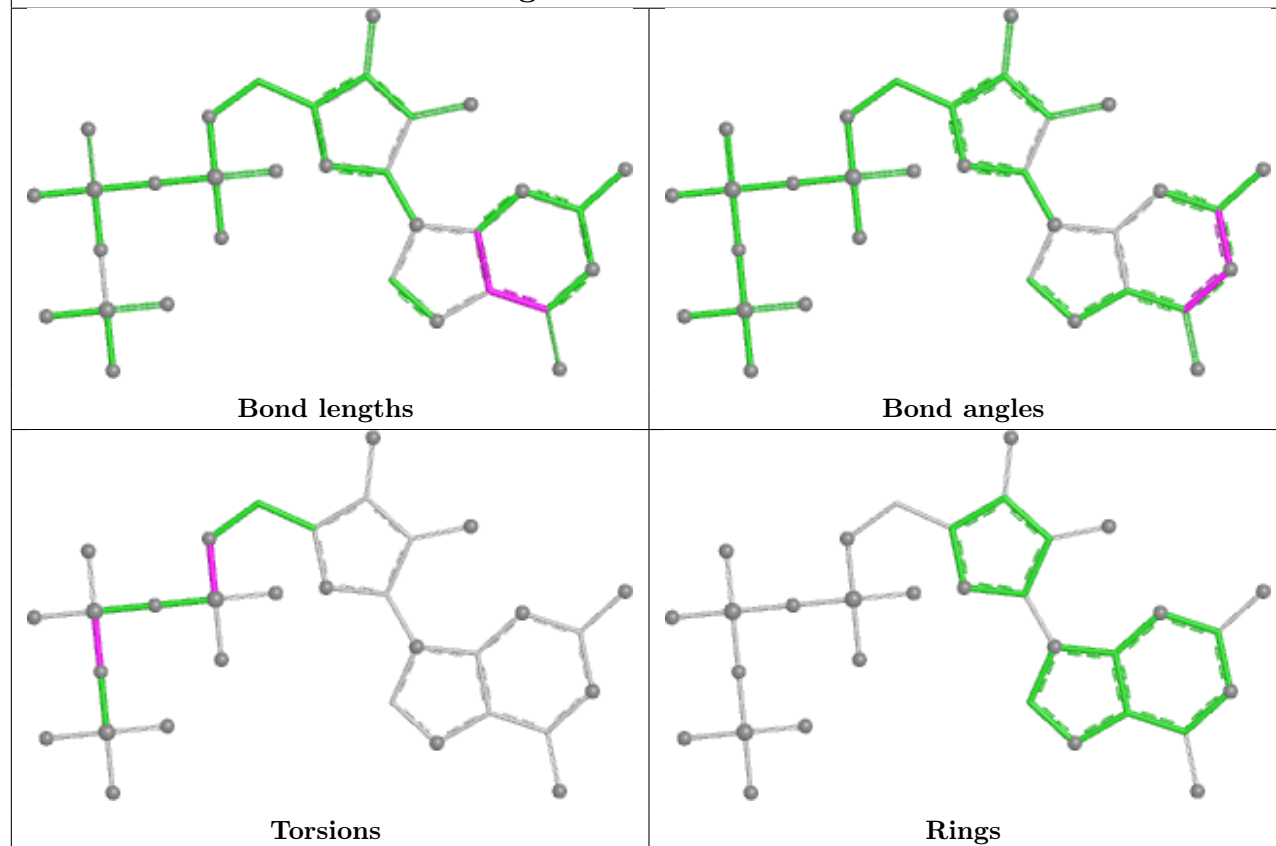


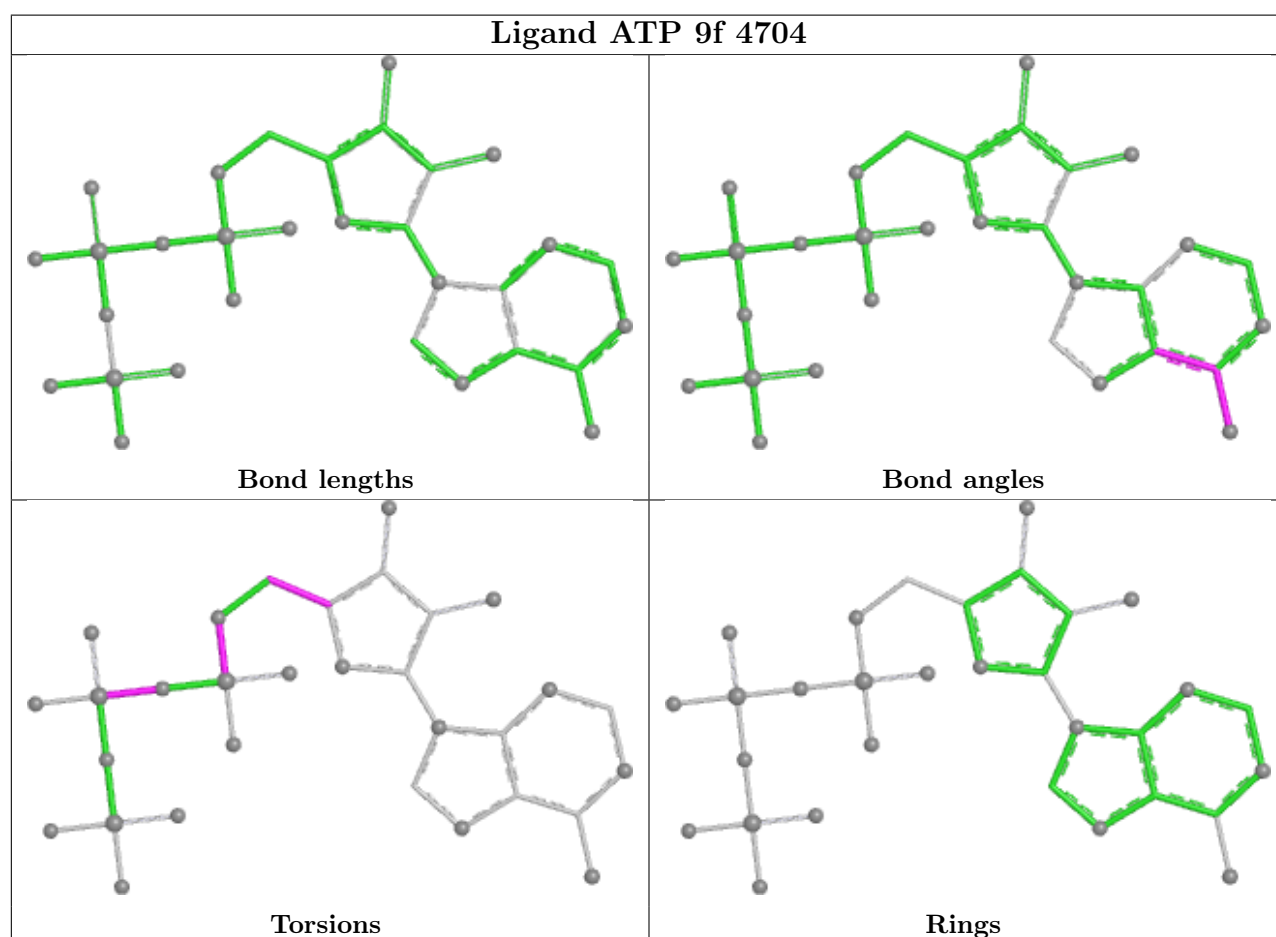
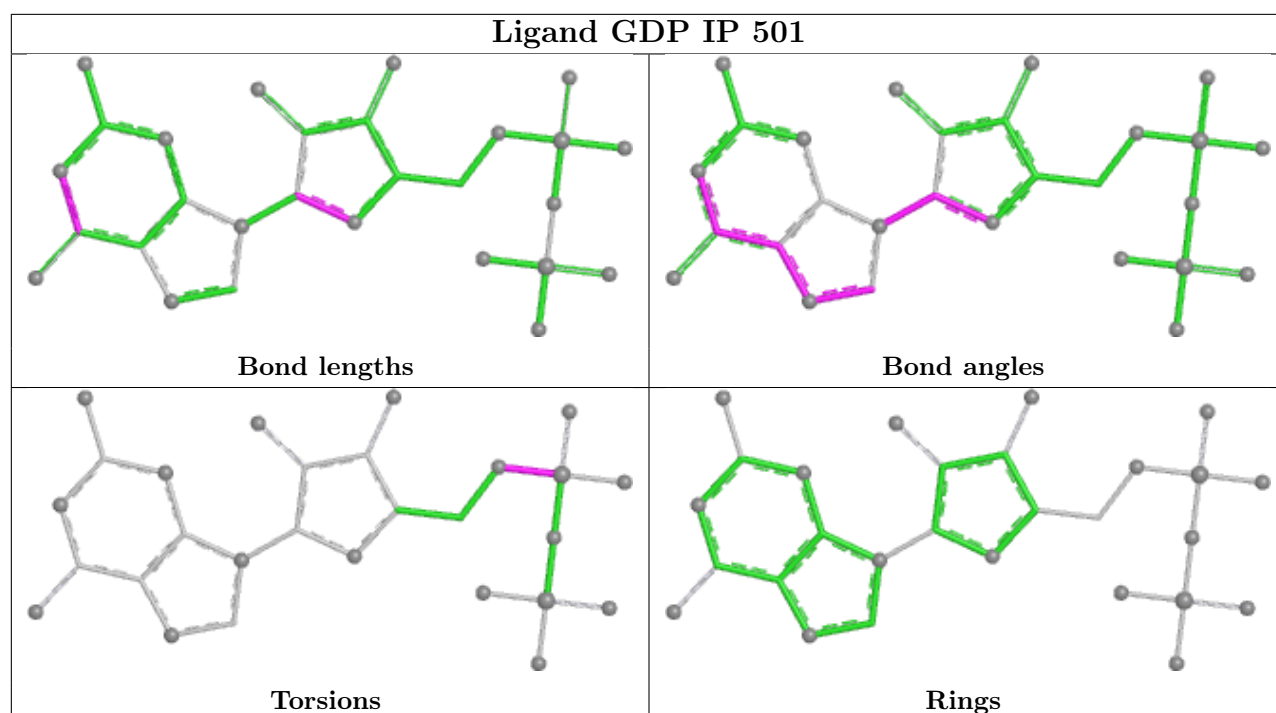


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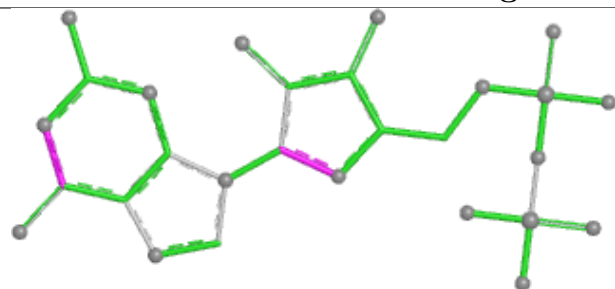


## Ligand GTP UF 501

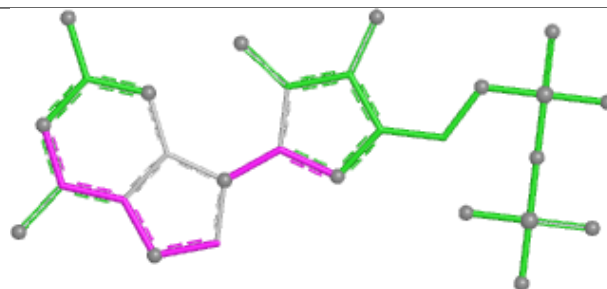




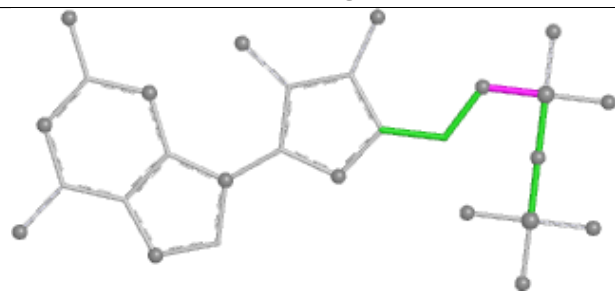
## Ligand GDP BU 501



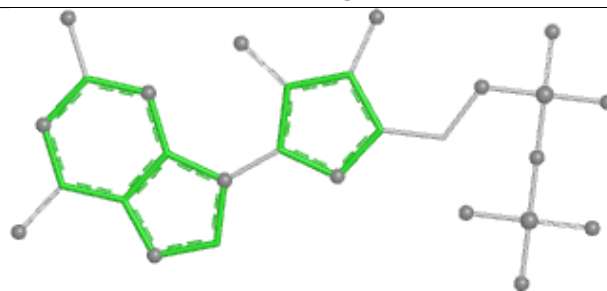
Bond lengths



Bond angles

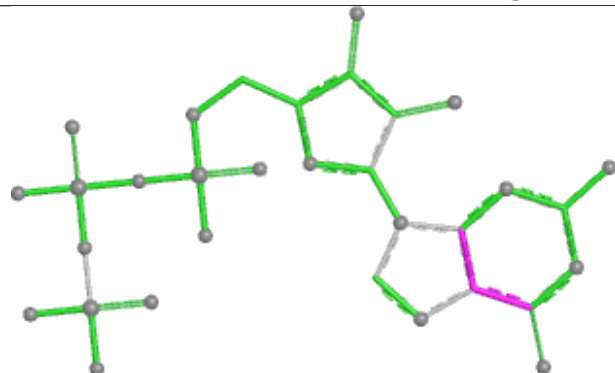


Torsions

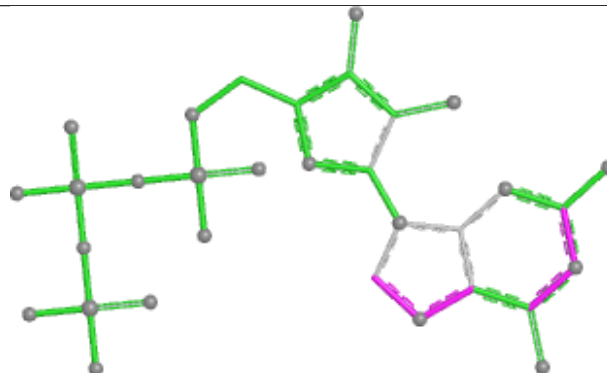


Rings

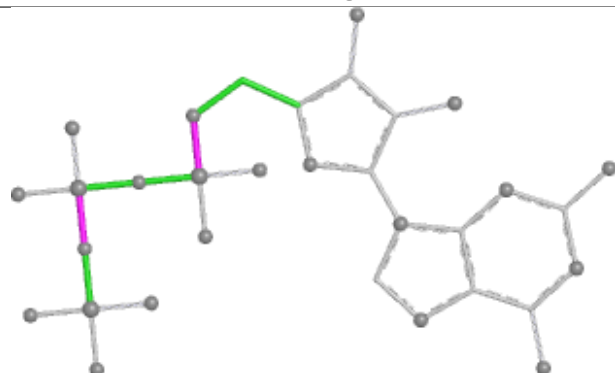
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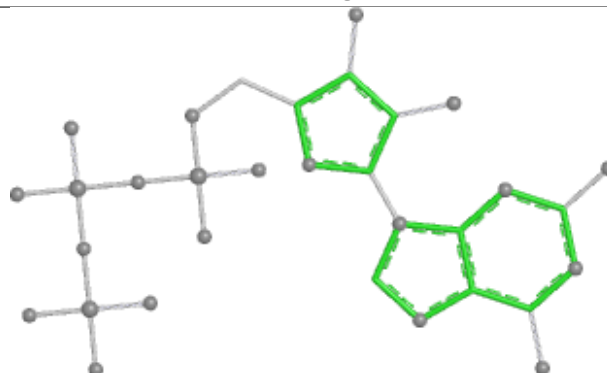
Bond lengths



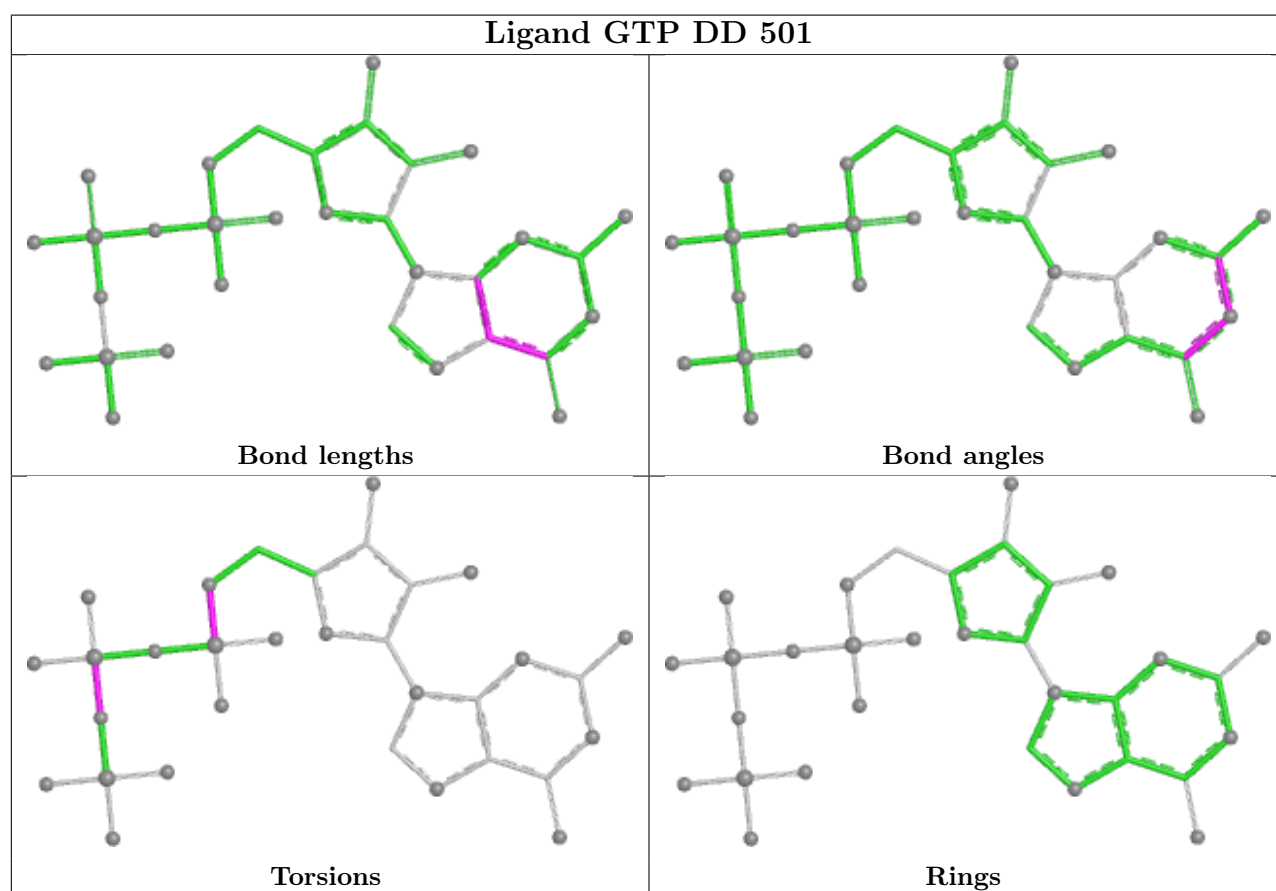
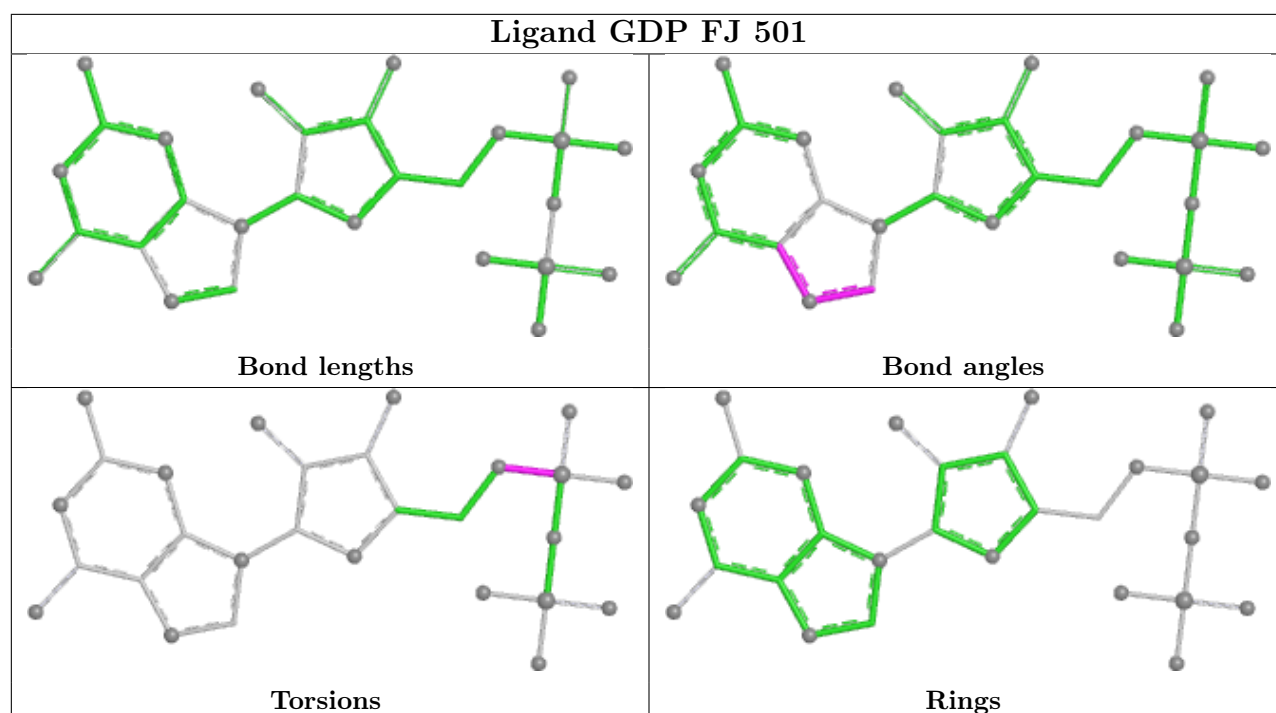
Bond angles



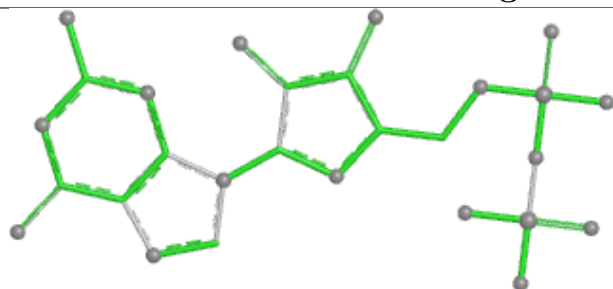
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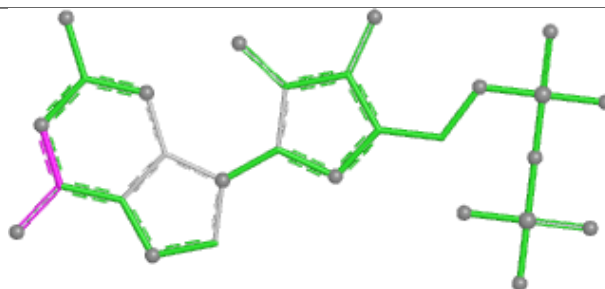
Rings



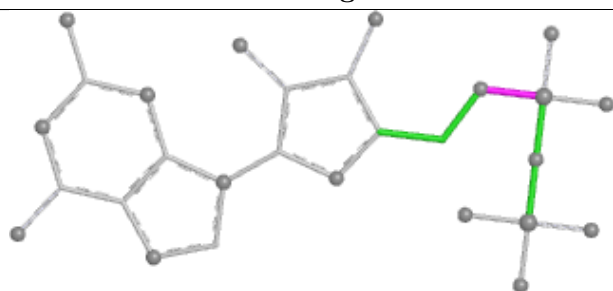
## Ligand GDP LU 501



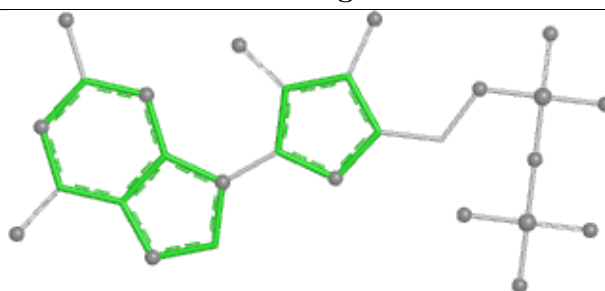
Bond lengths



Bond angles

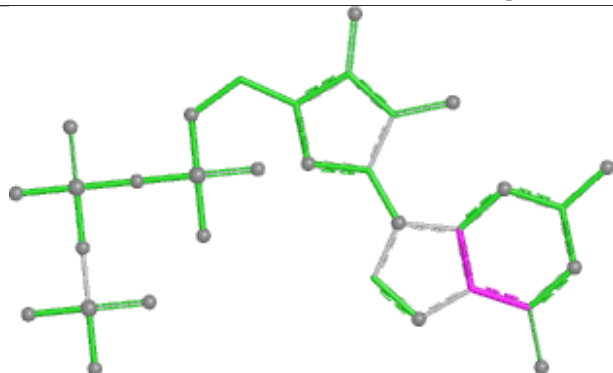


Torsions

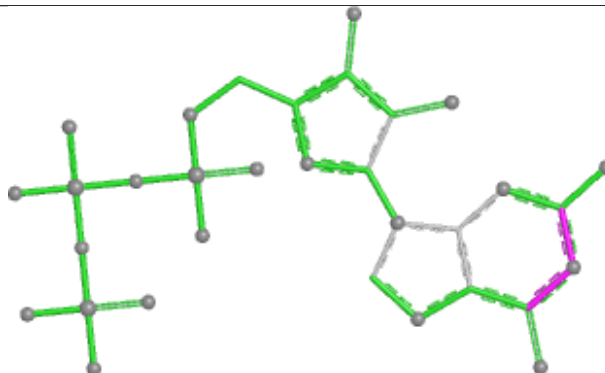


Rings

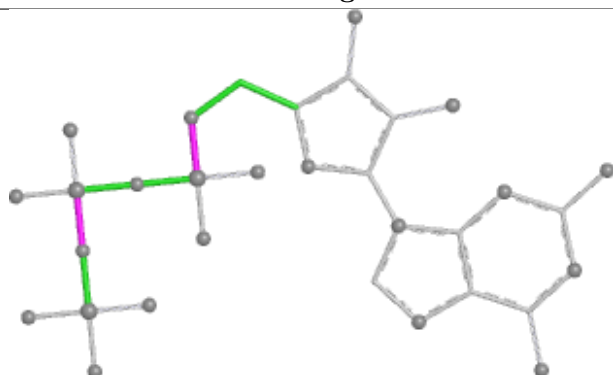
## Ligand GTP BT 602



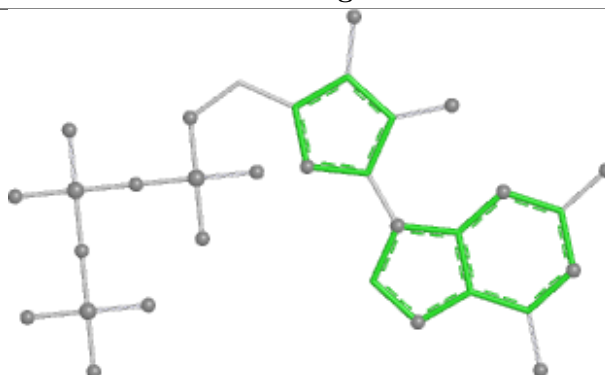
Bond lengths



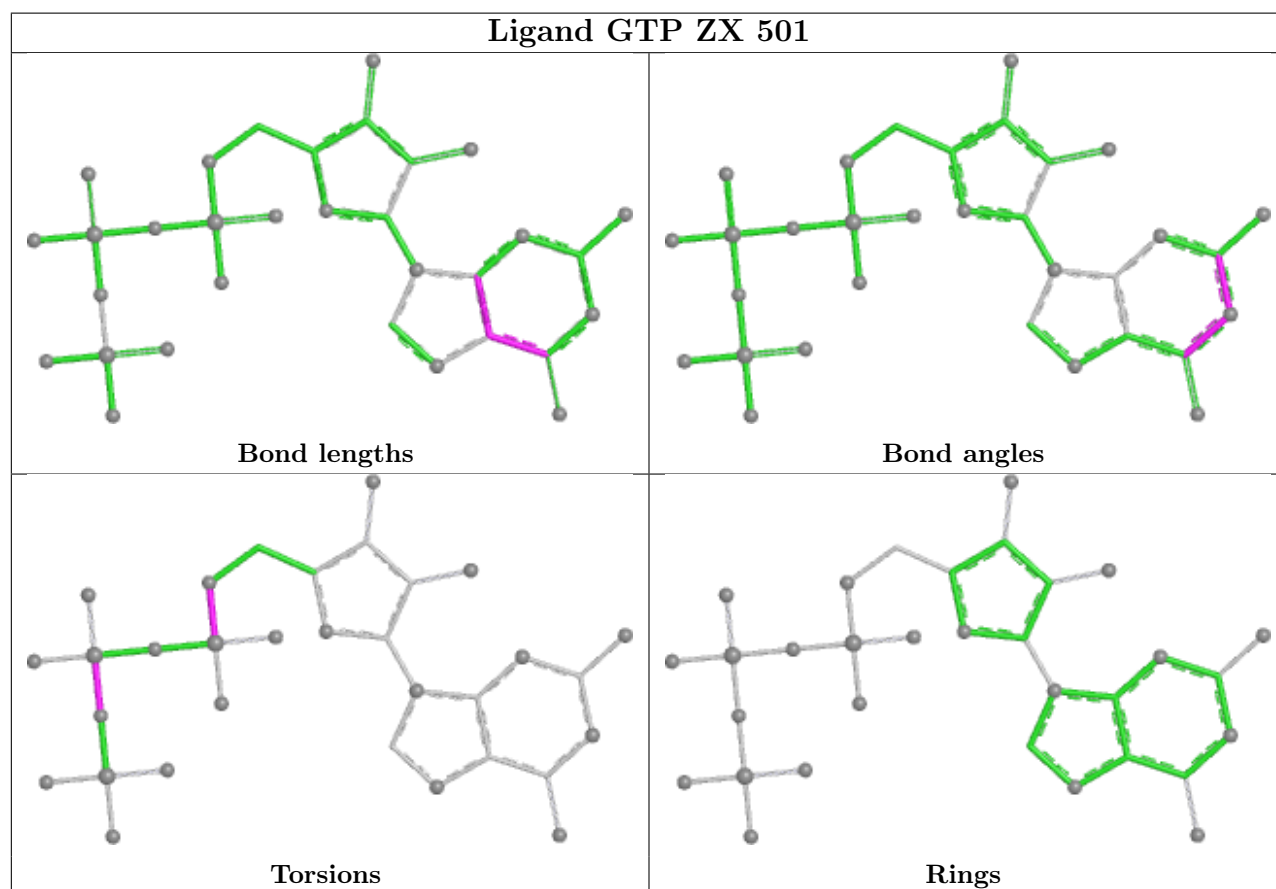
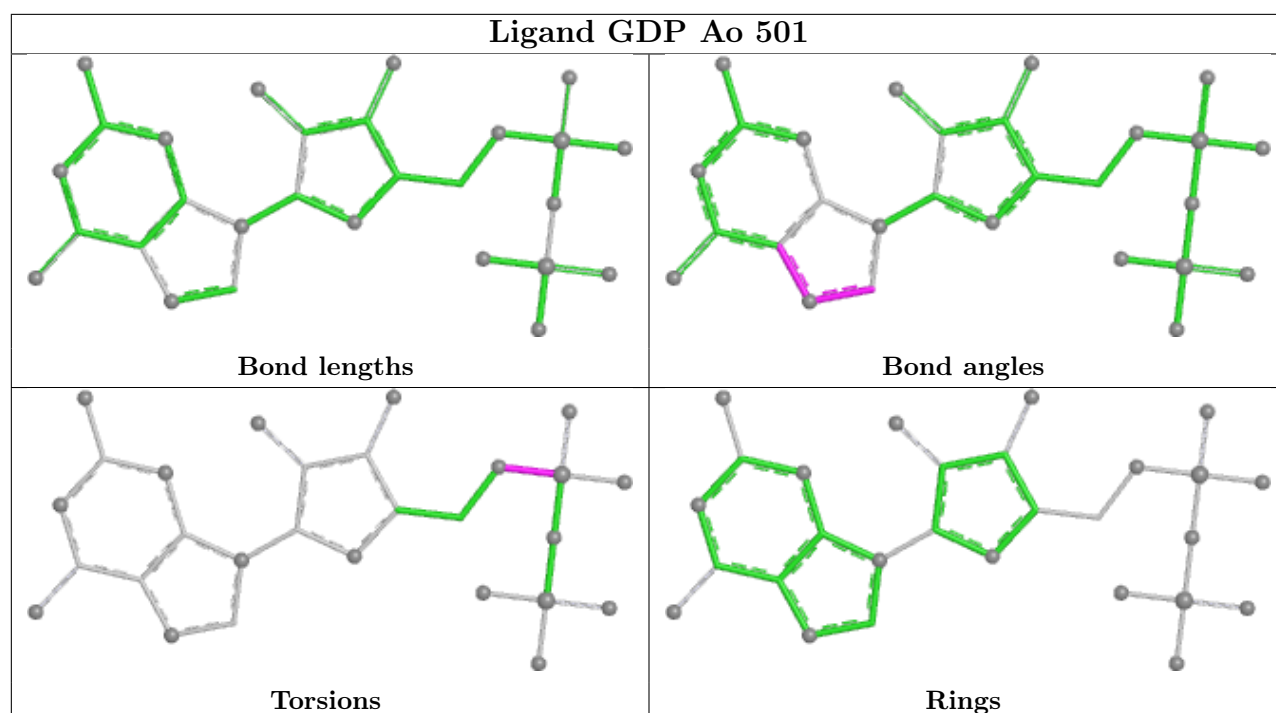
Bond angles

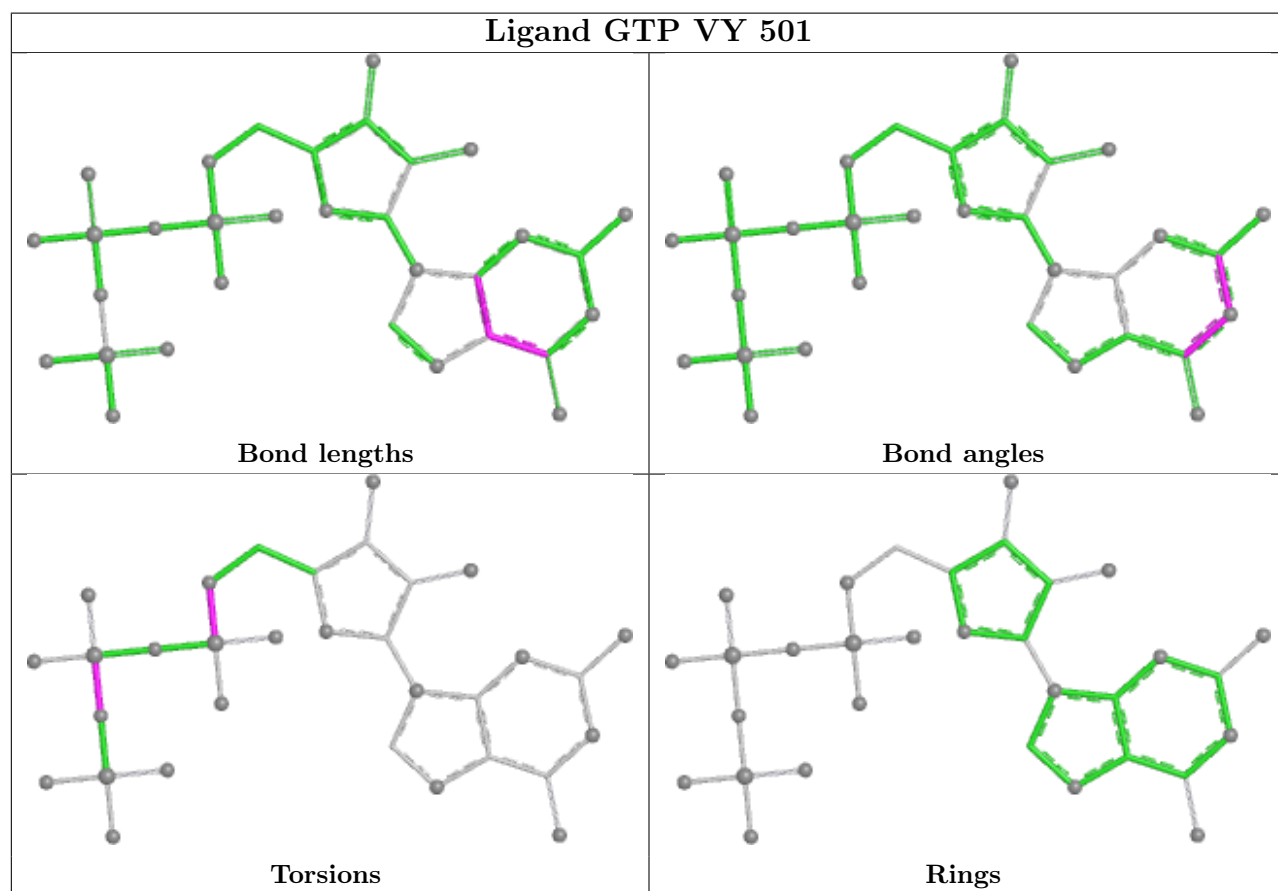
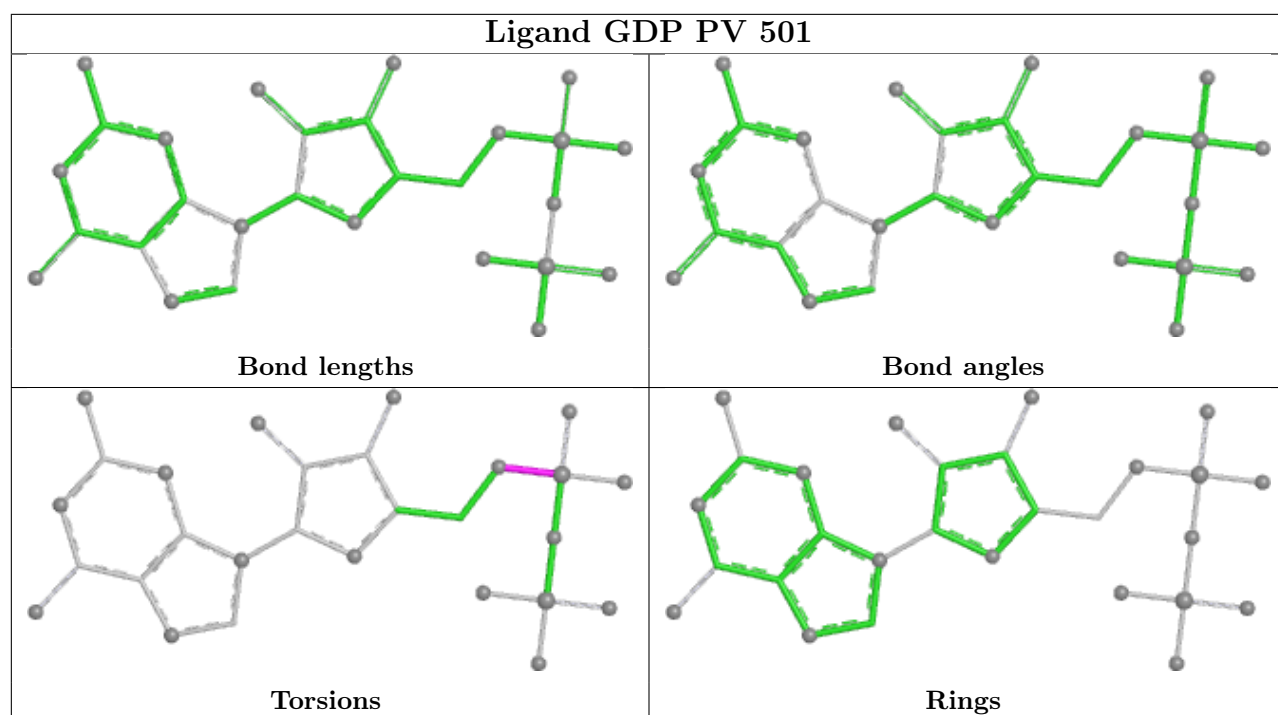


Torsions

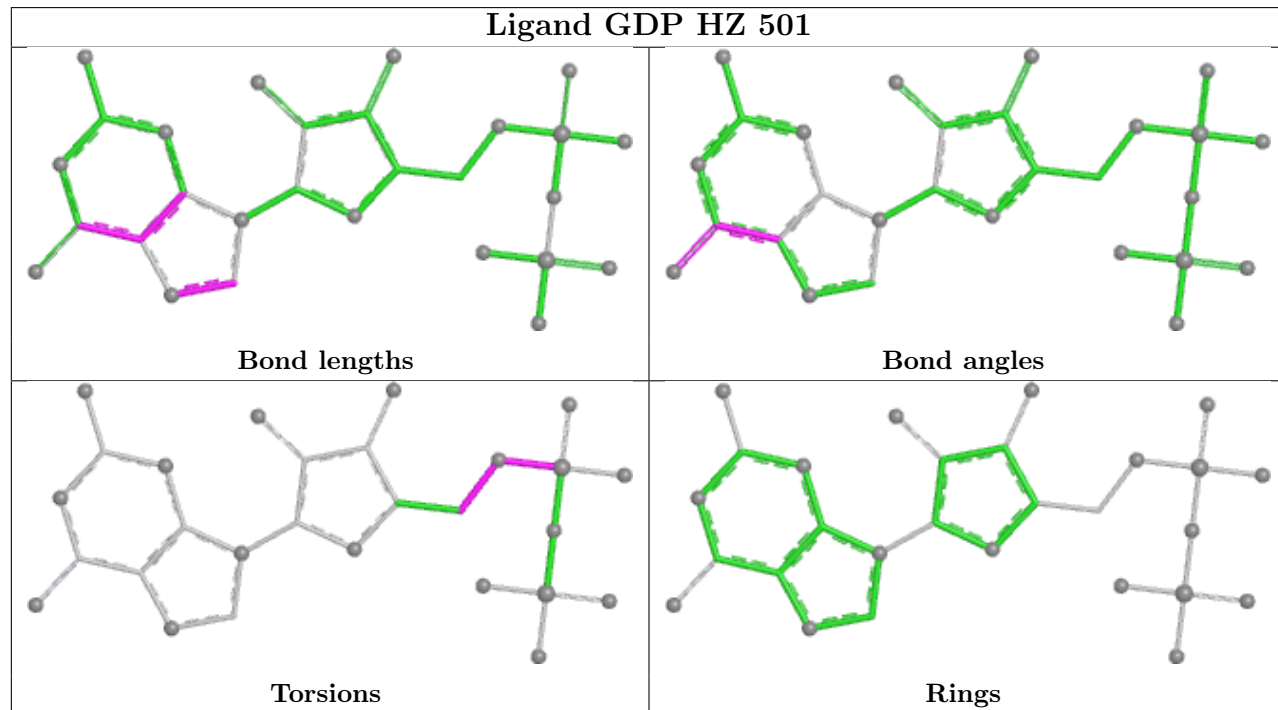
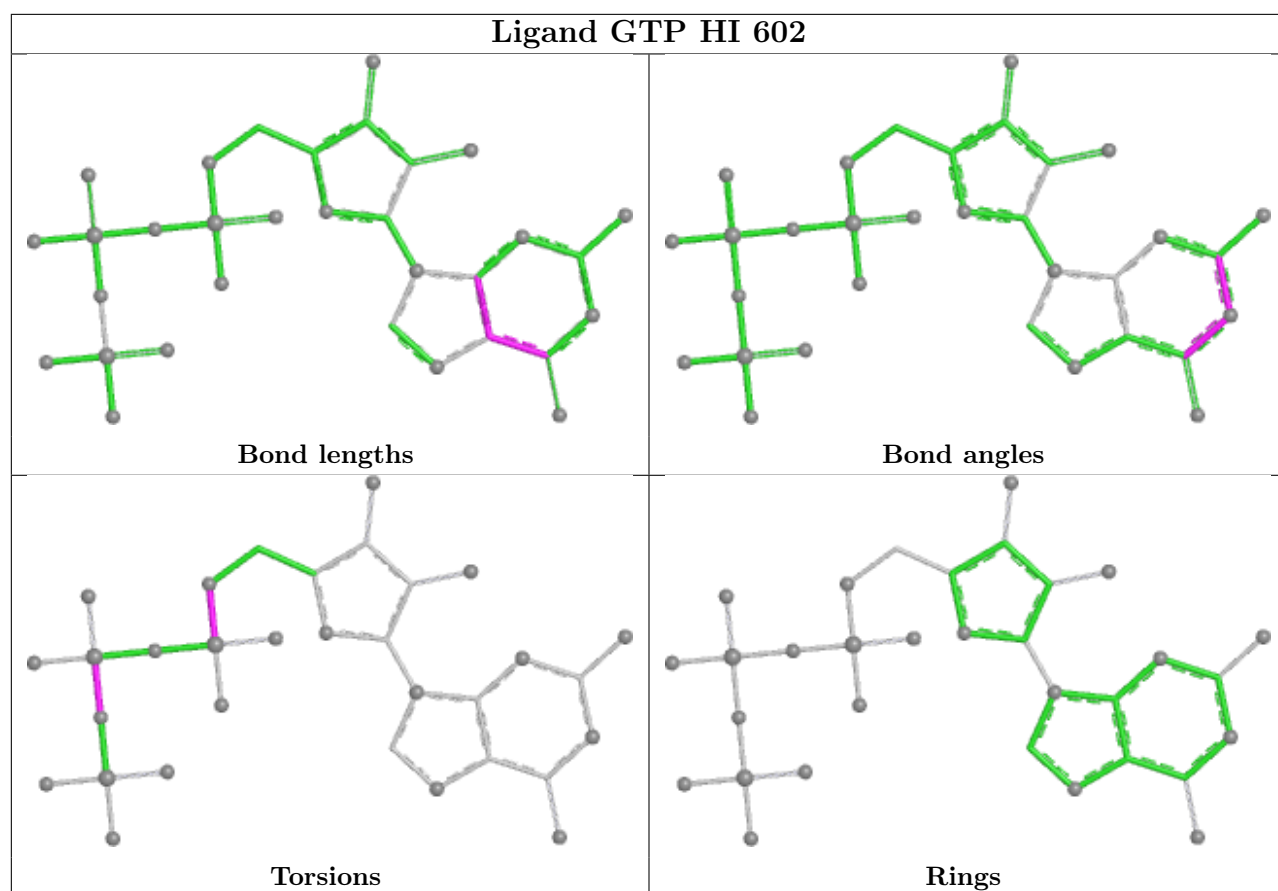


Rings

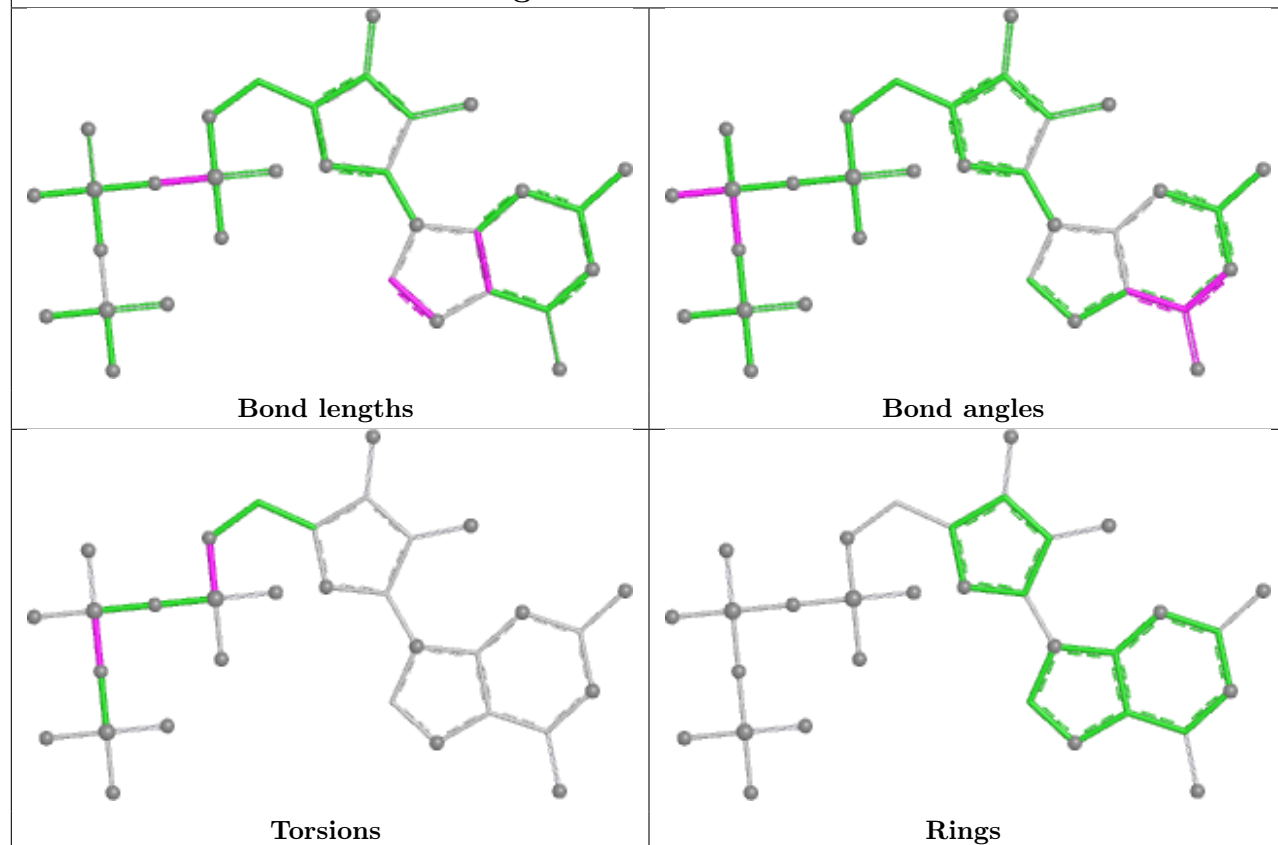




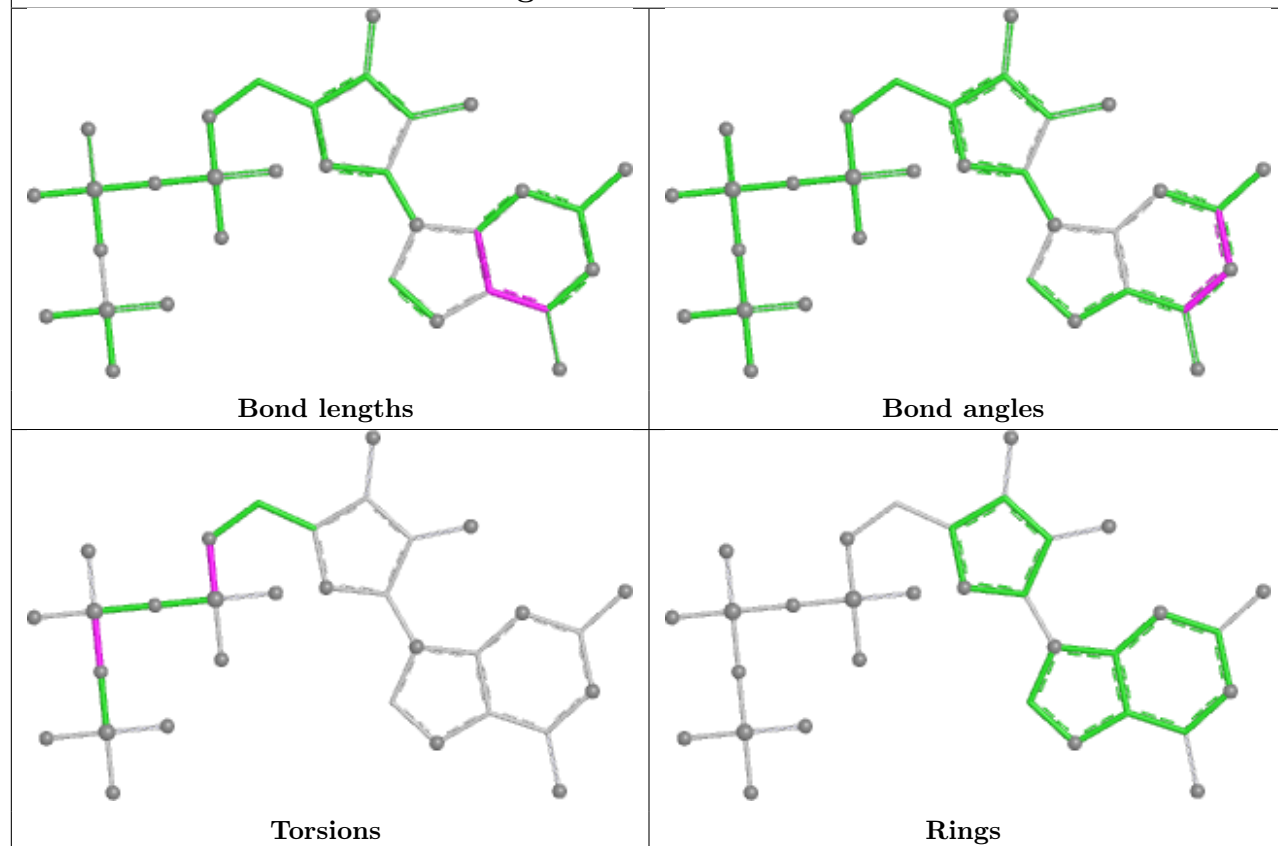


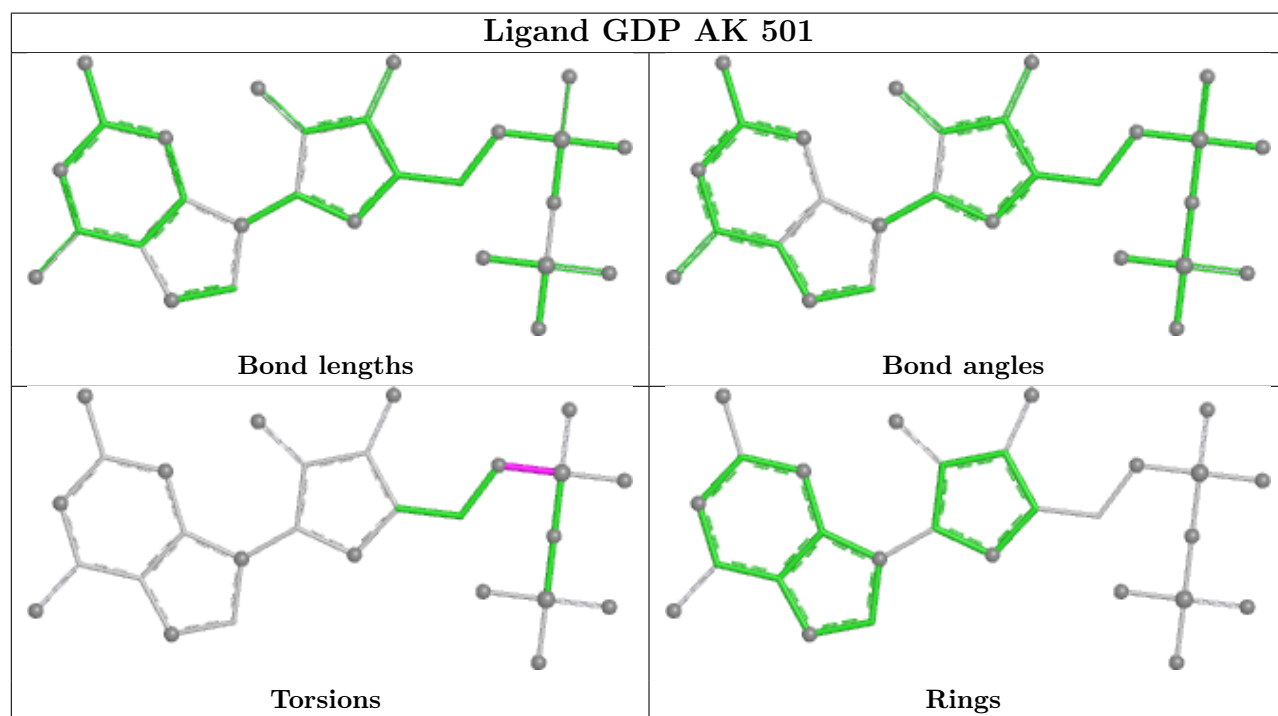
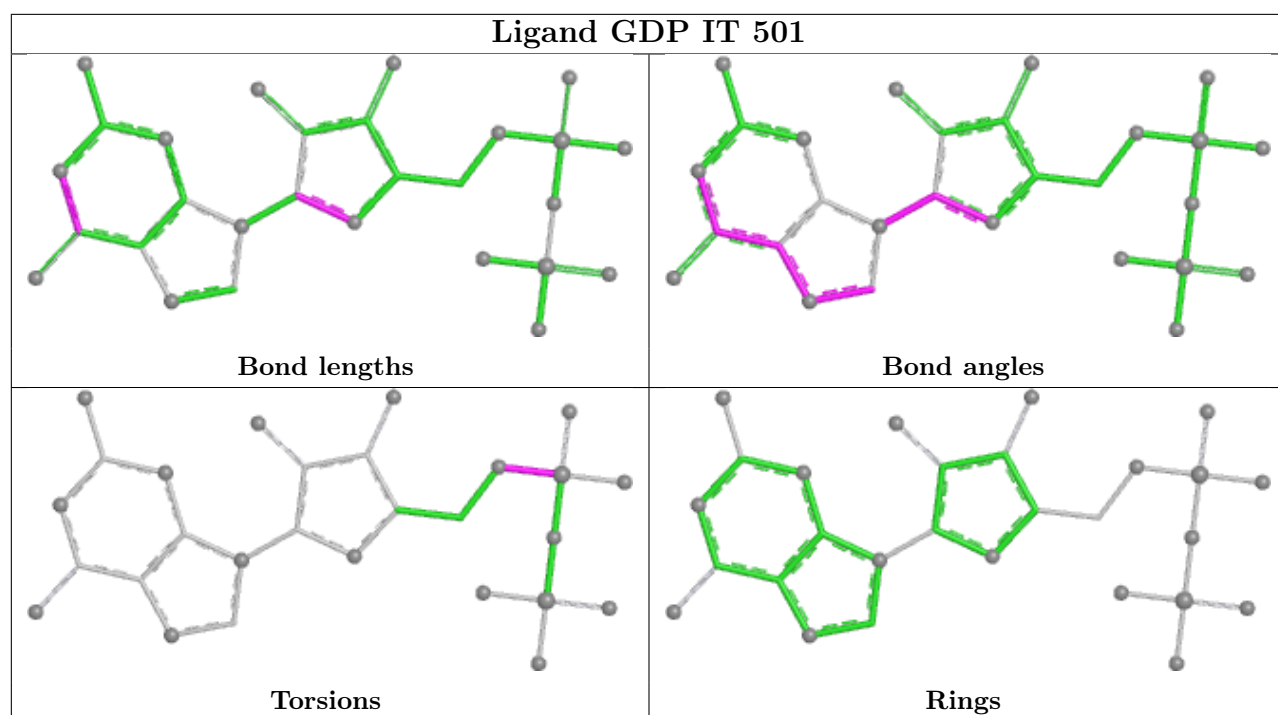


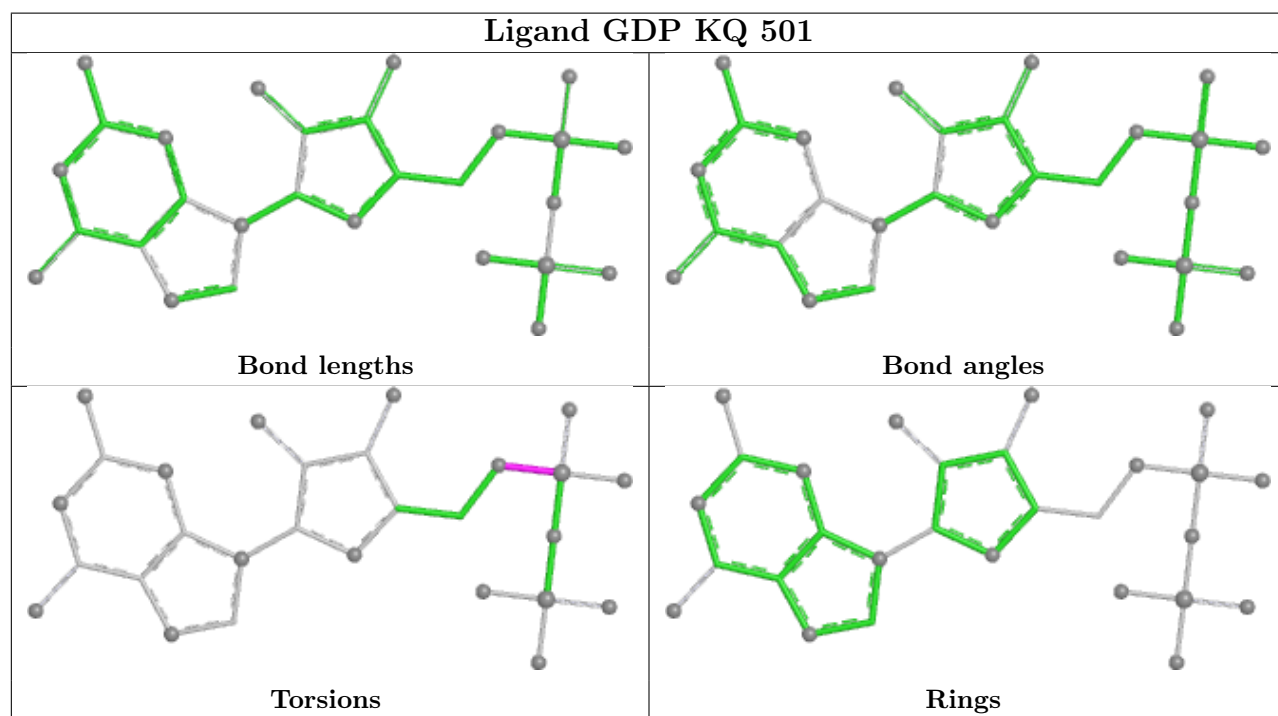
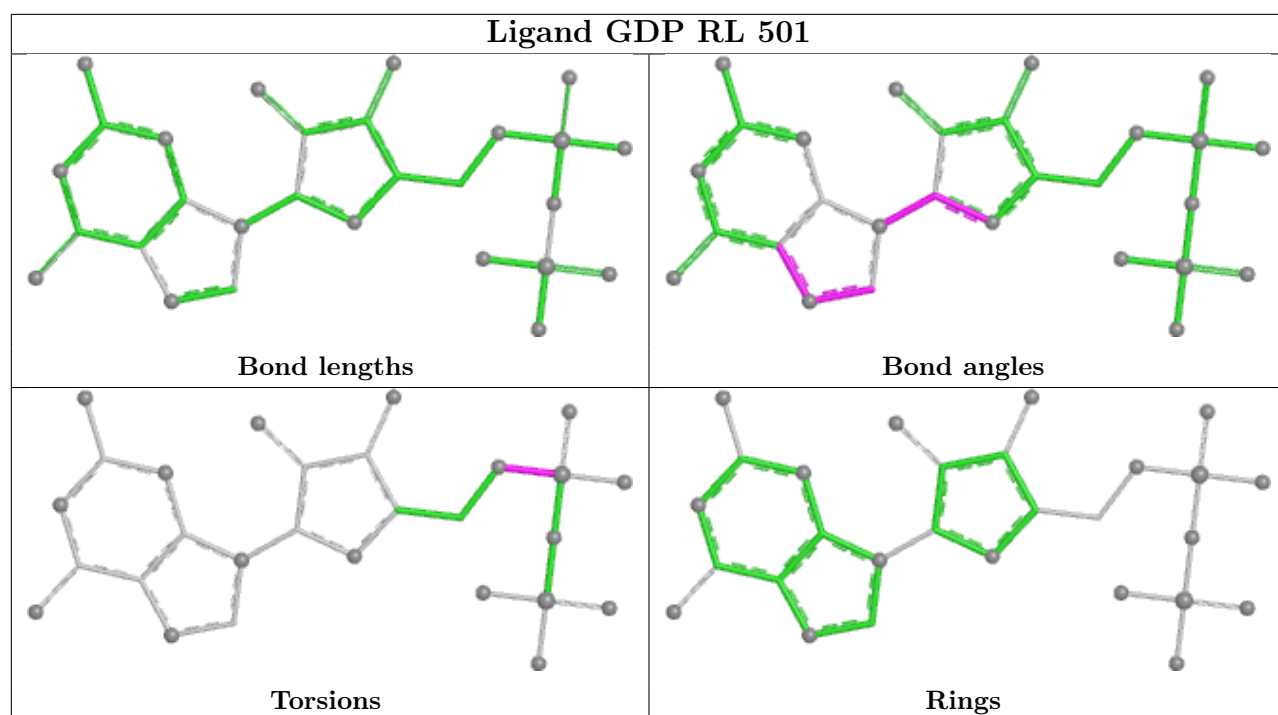
## Ligand GTP EW 501

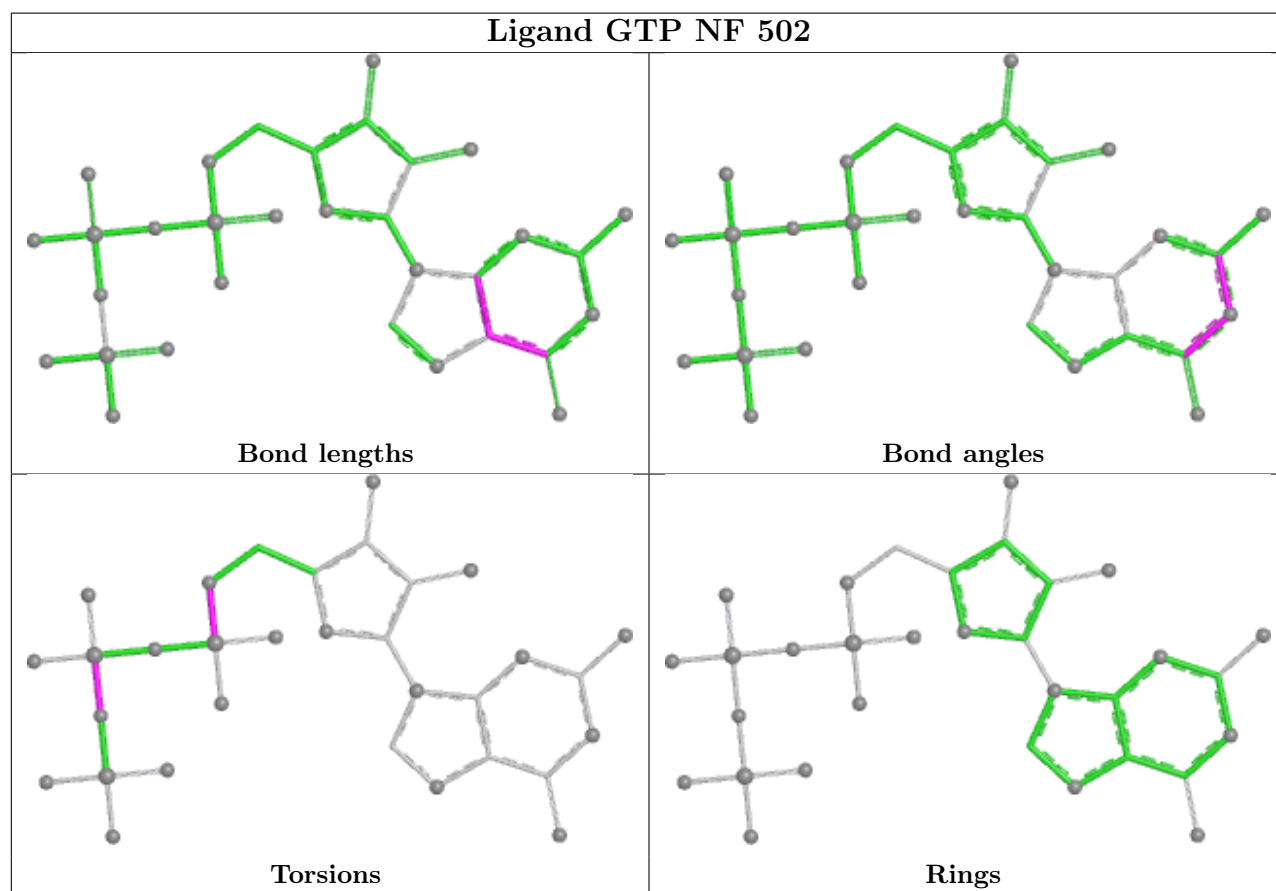
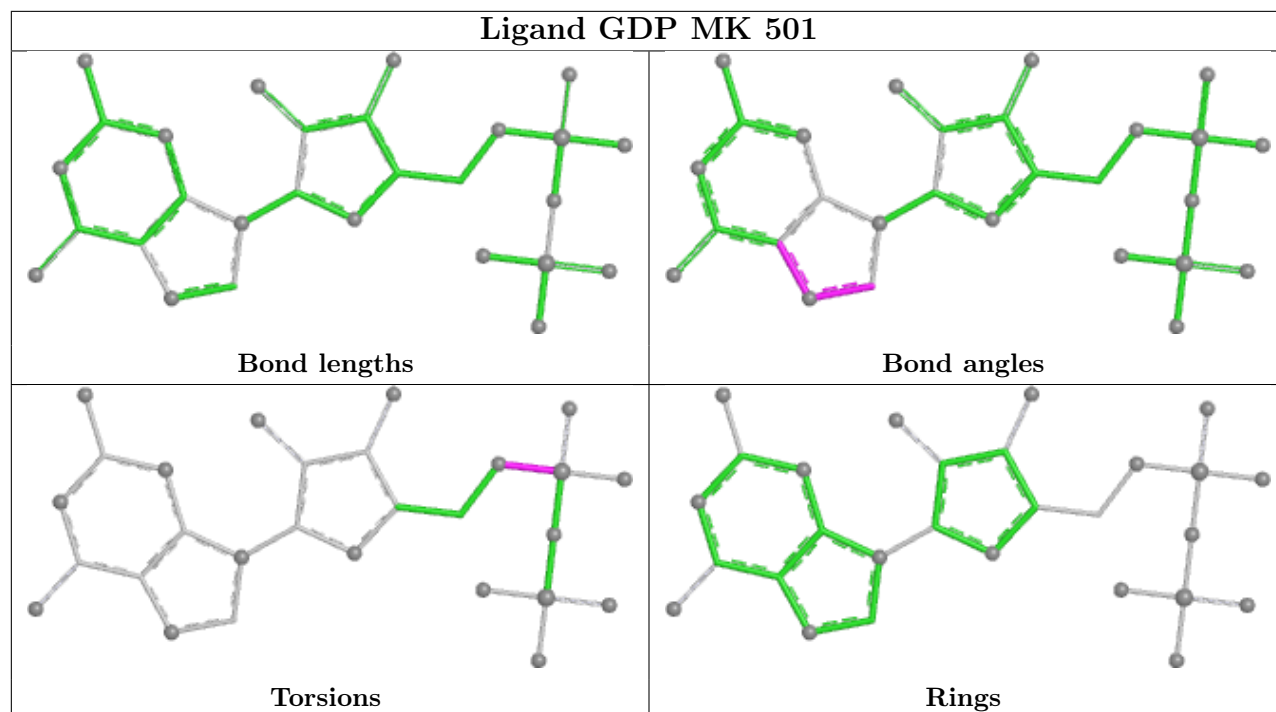


## Ligand GTP DB 501

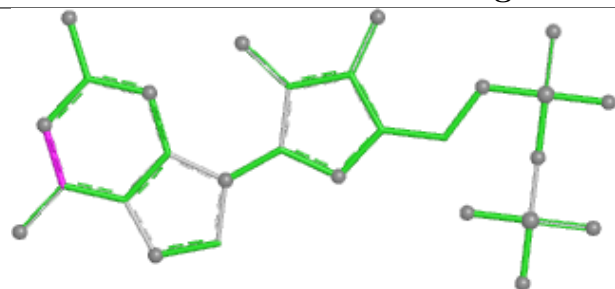




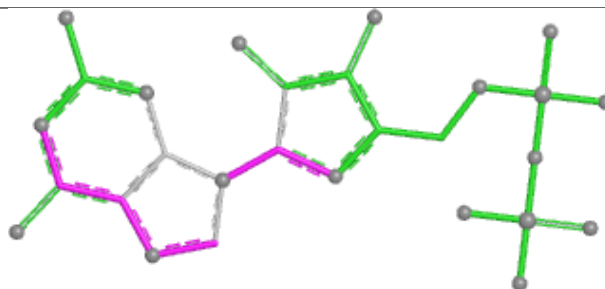




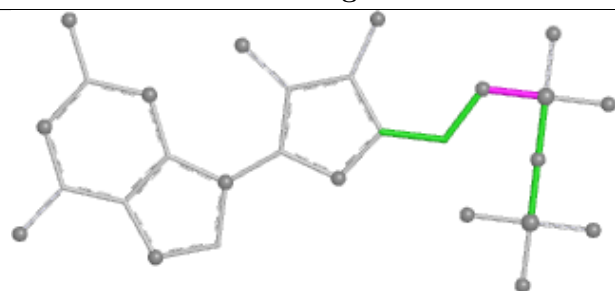
## Ligand GDP WX 501



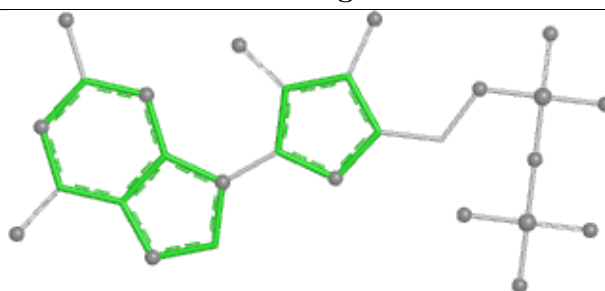
Bond lengths



Bond angles

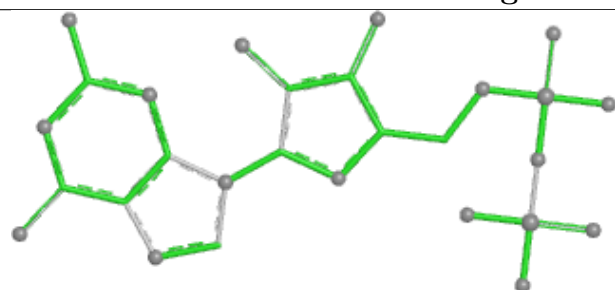


Torsions

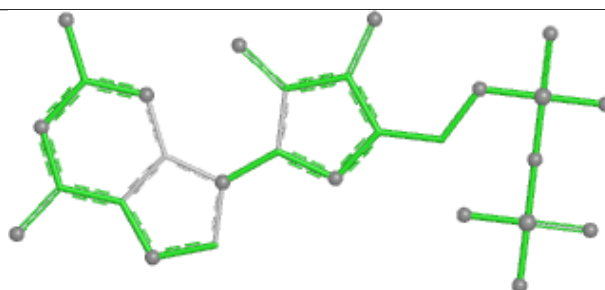


Rings

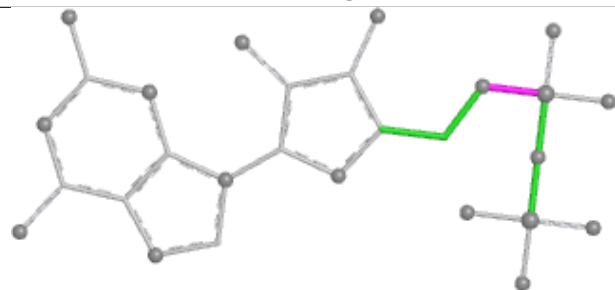
## Ligand GDP KE 501



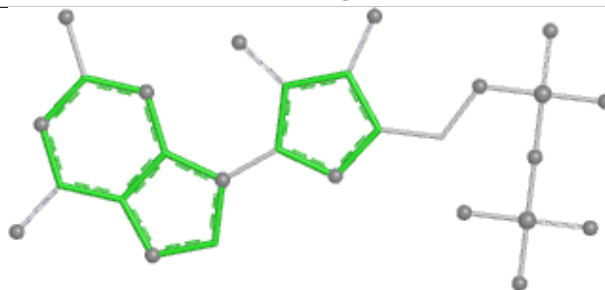
Bond lengths



Bond angles

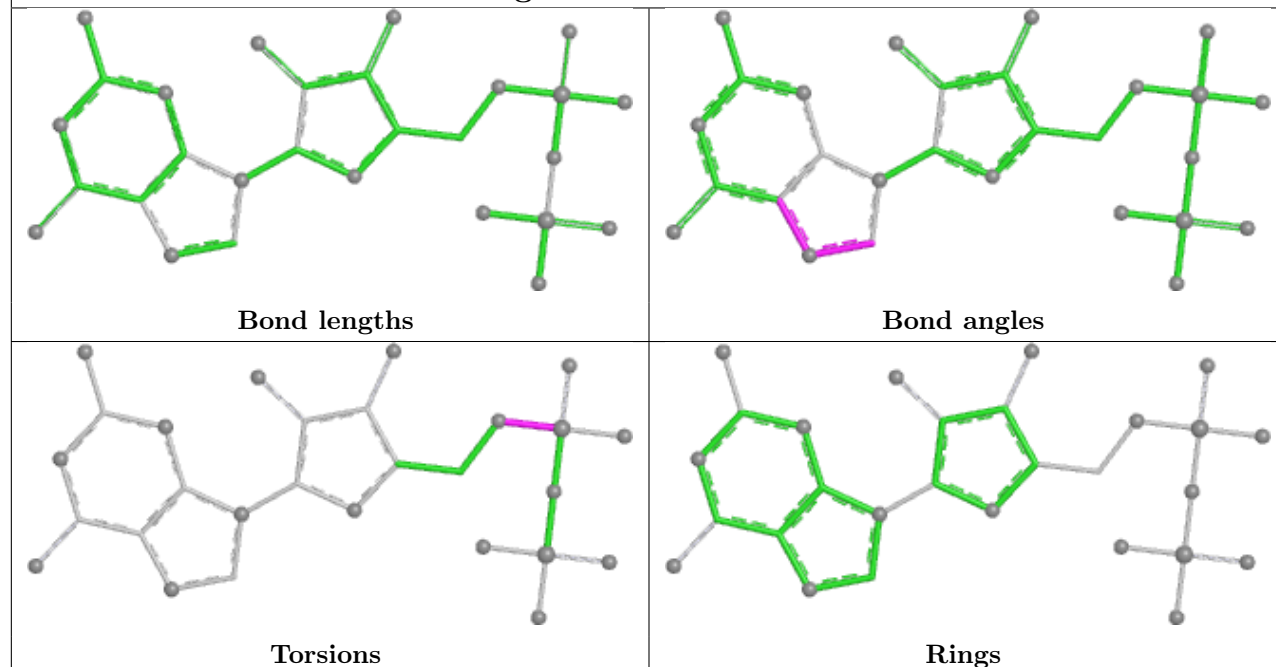


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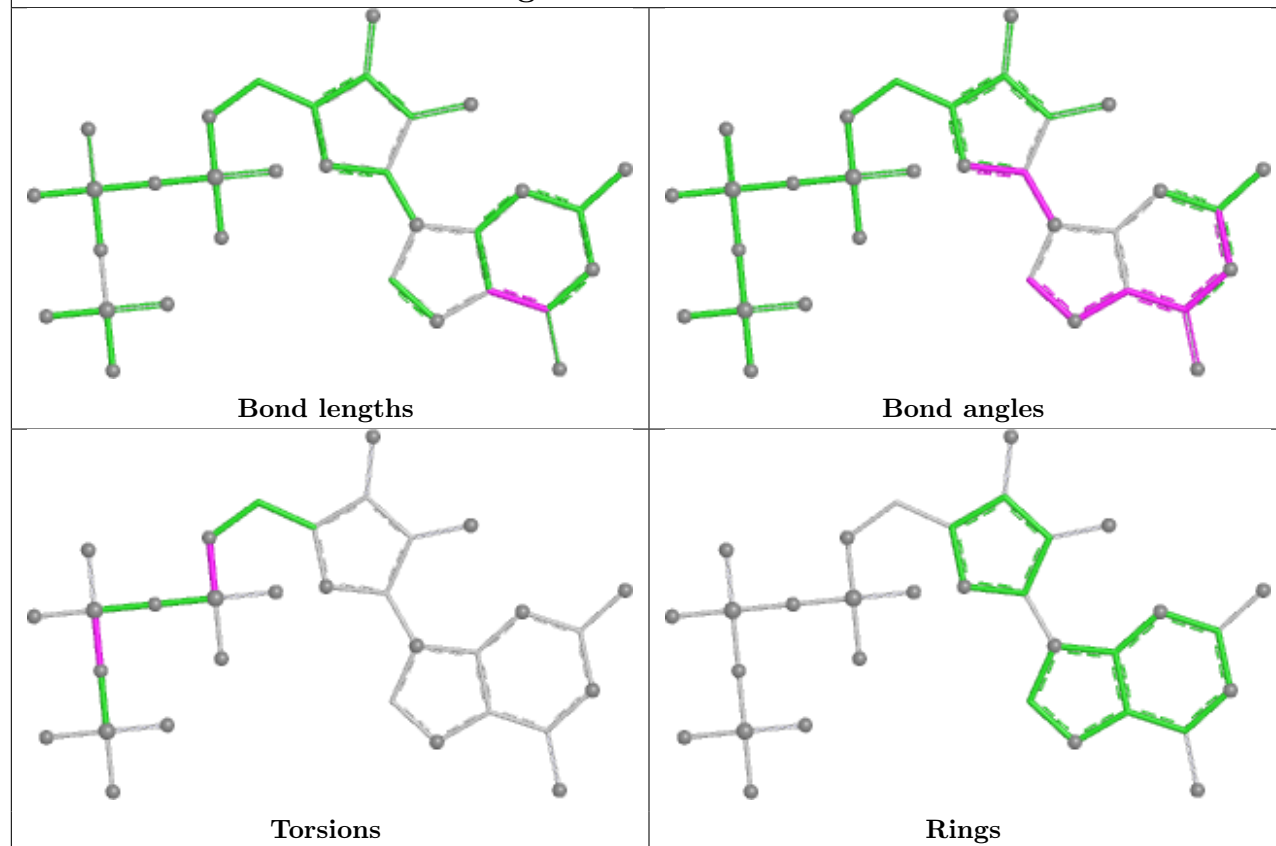


Rings

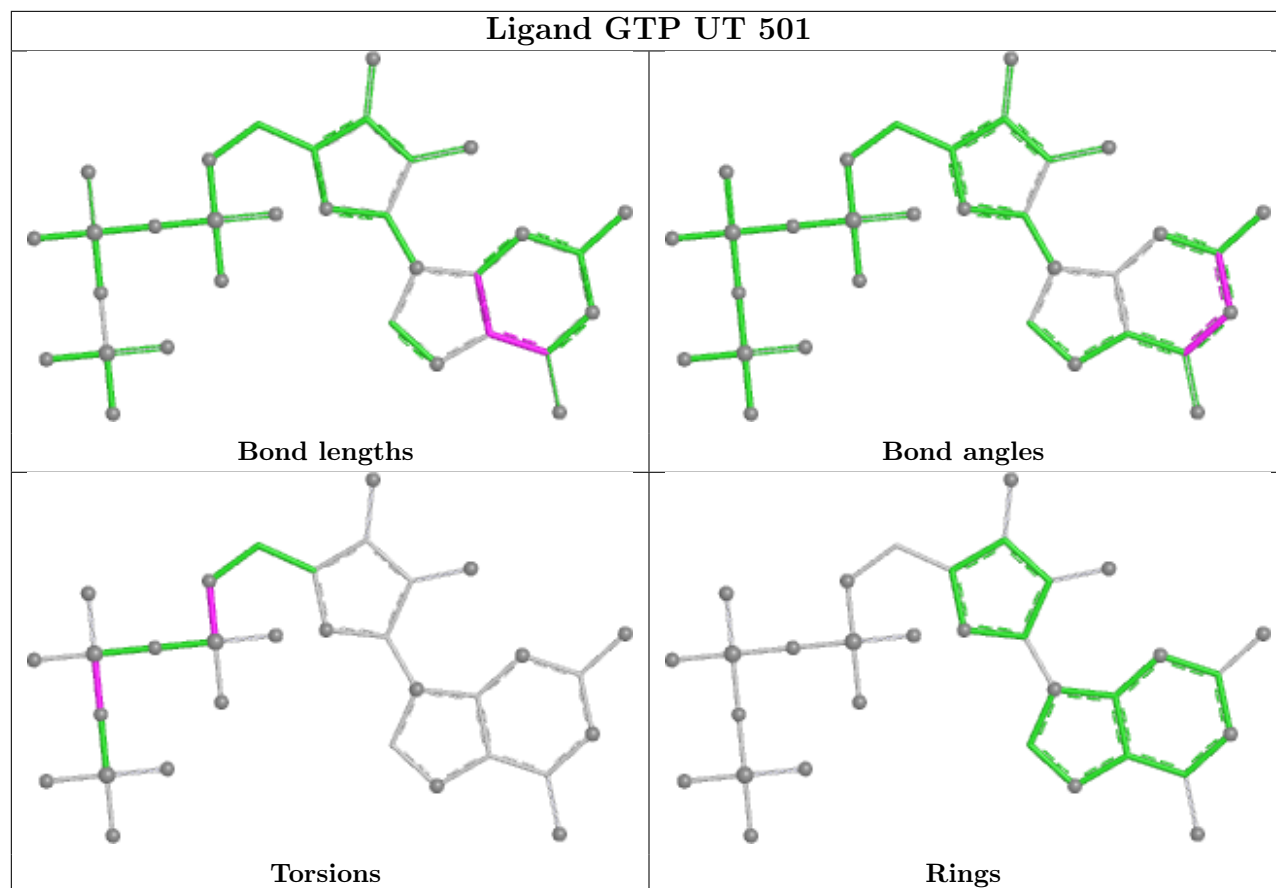
## Ligand GDP YH 501



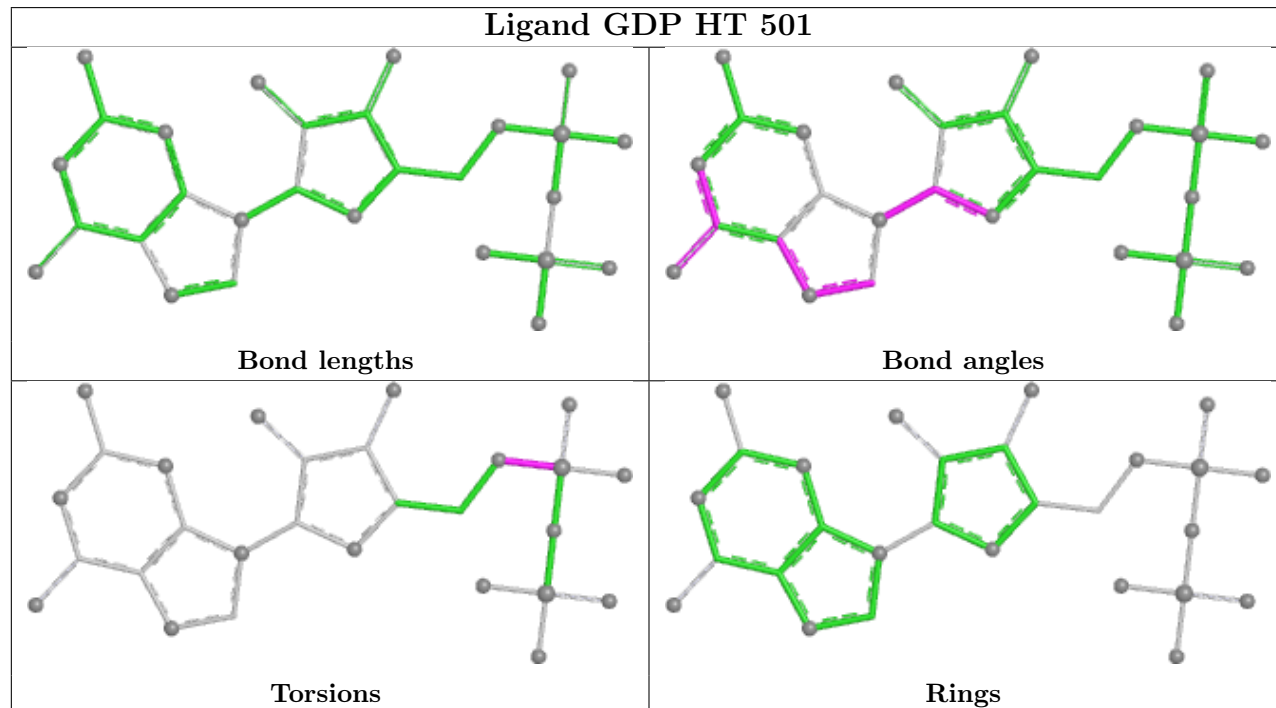
## Ligand GTP BR 501



## Ligand GTP UT 501

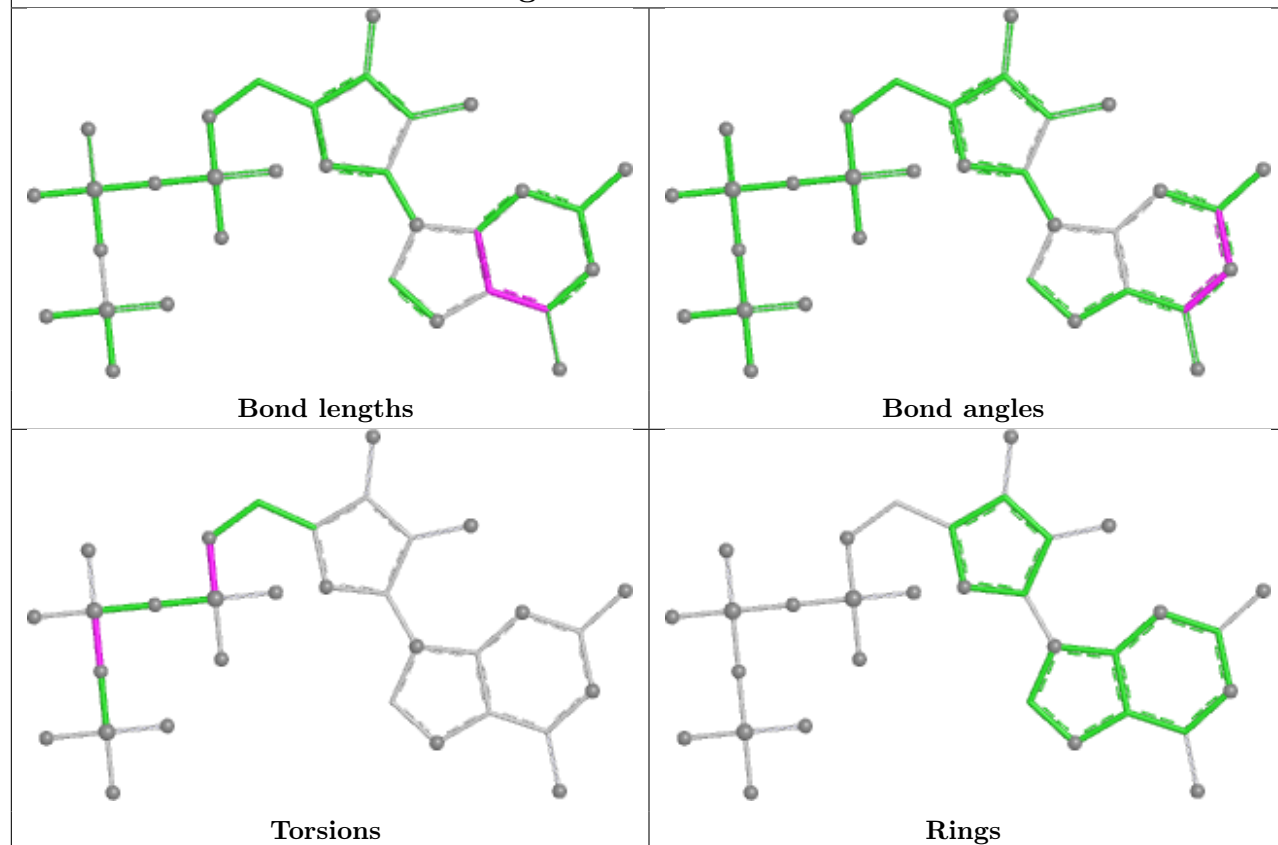


## Ligand GDP HT 501

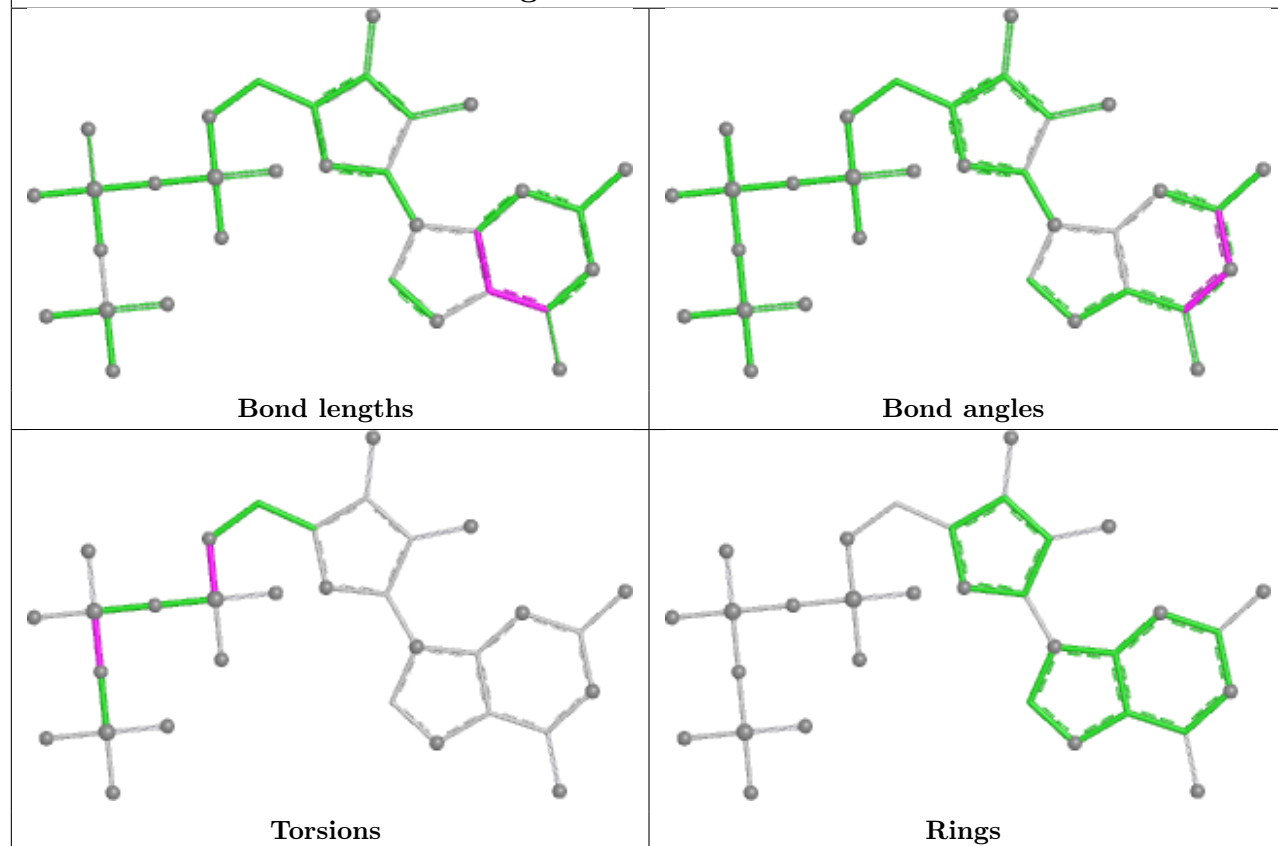


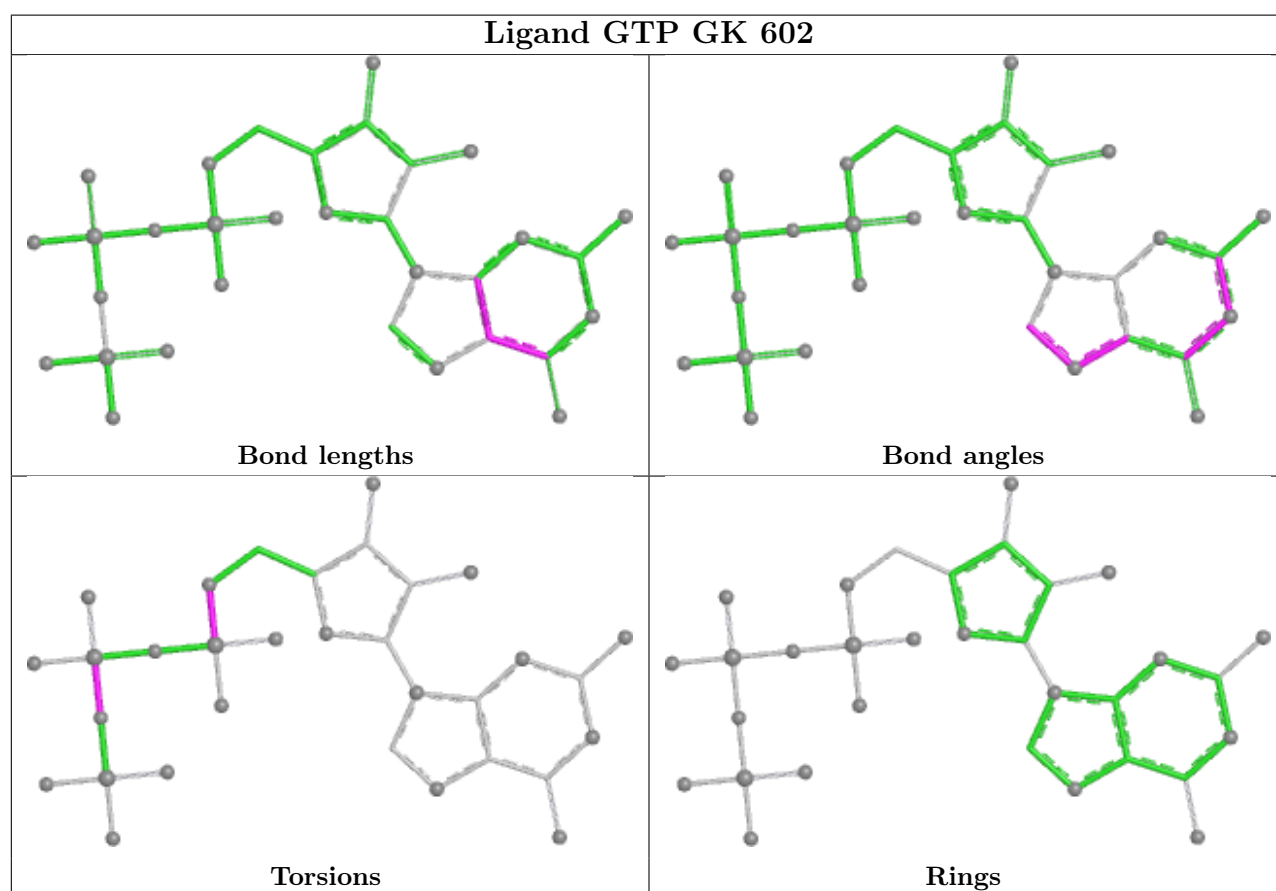
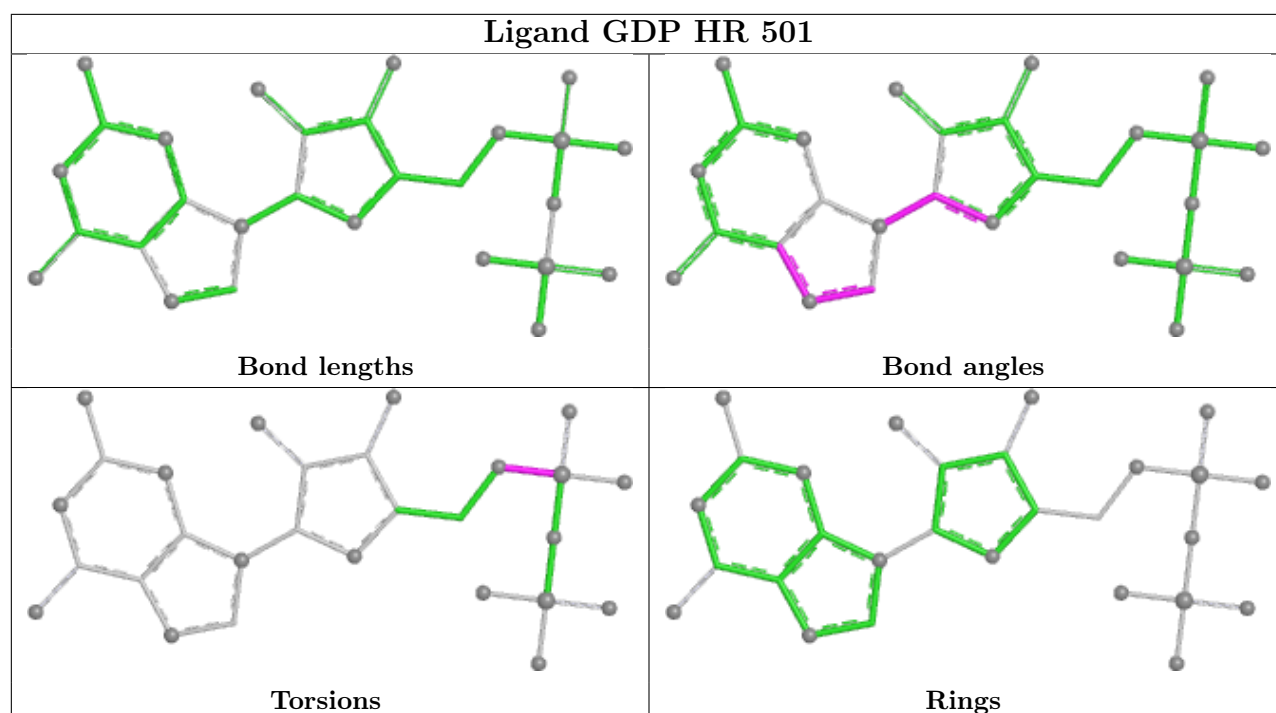


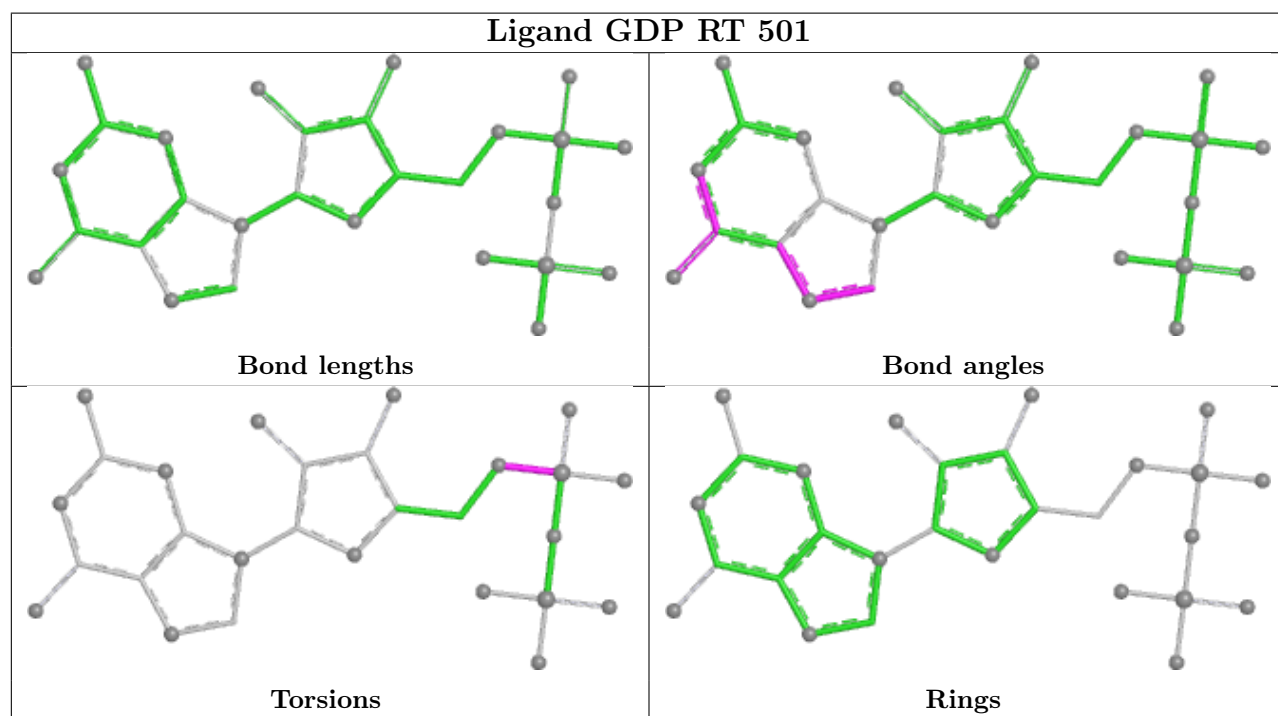
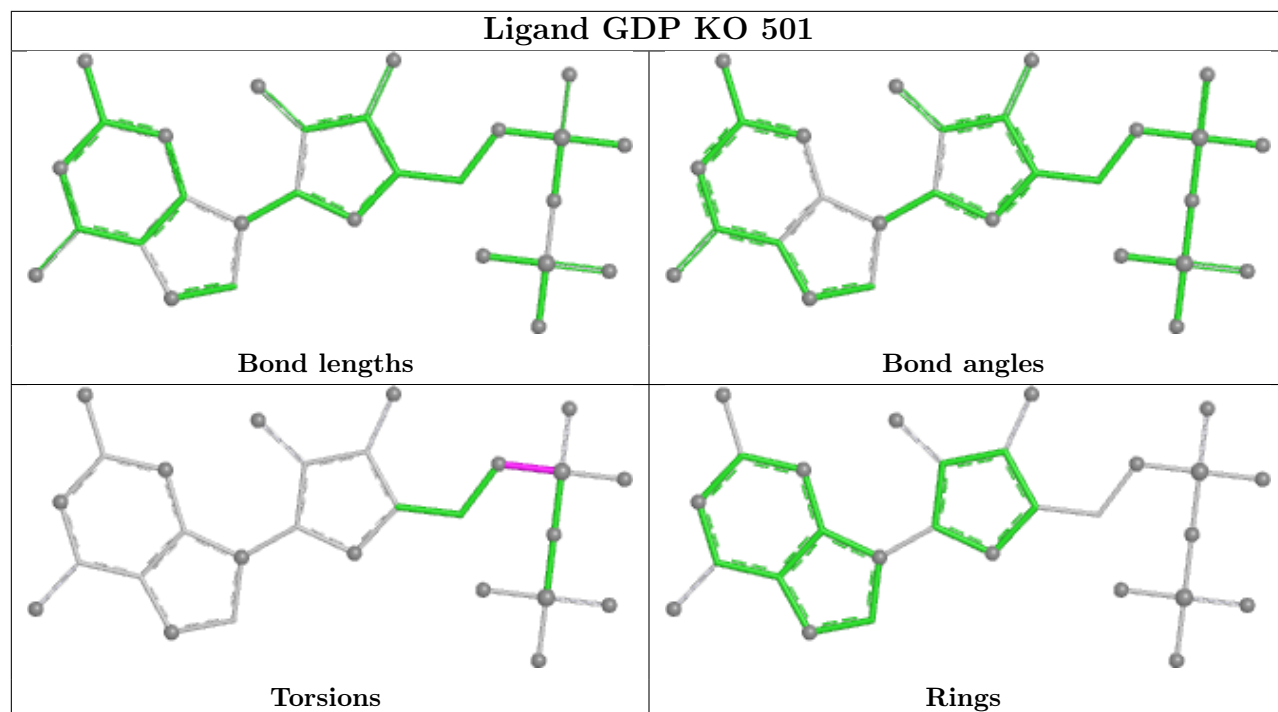
## Ligand GTP AV 501

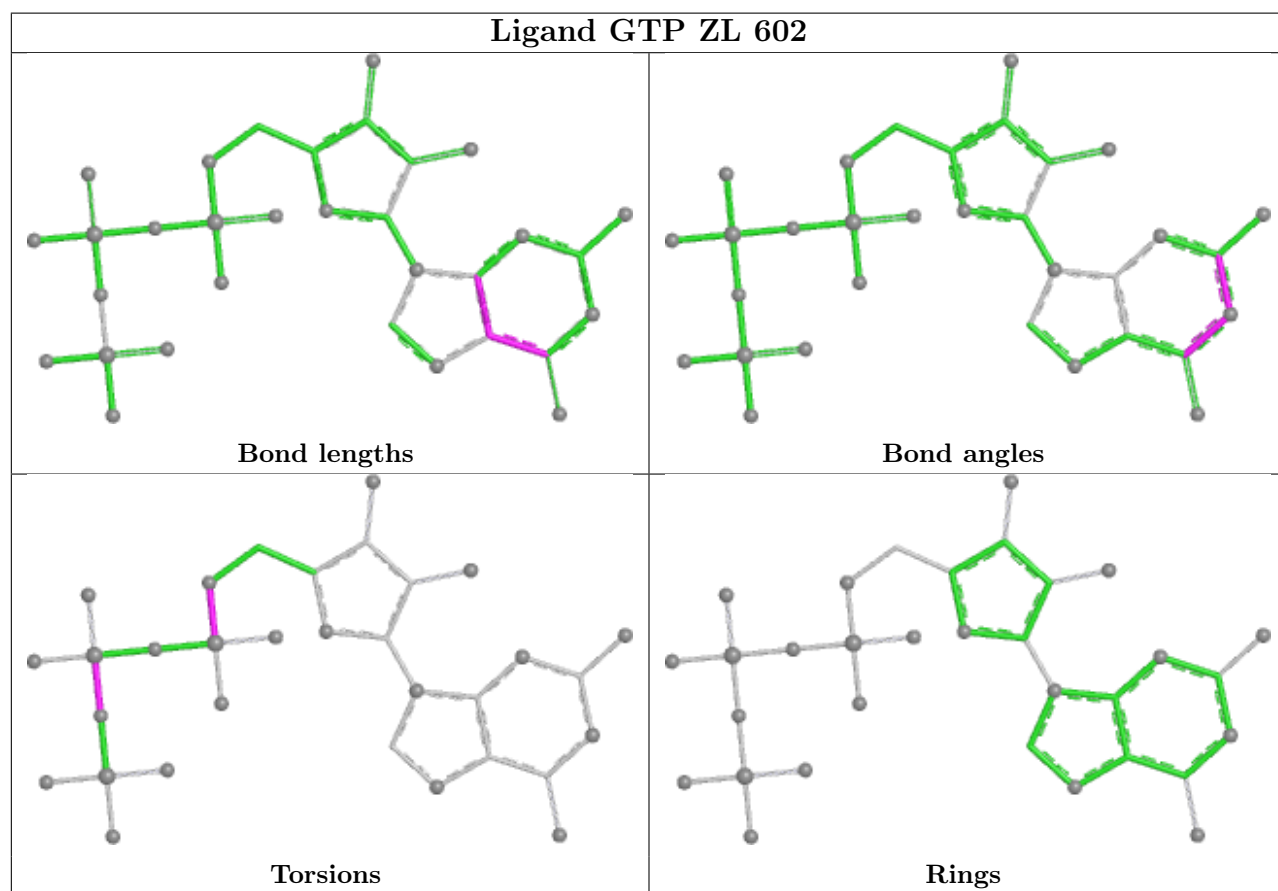
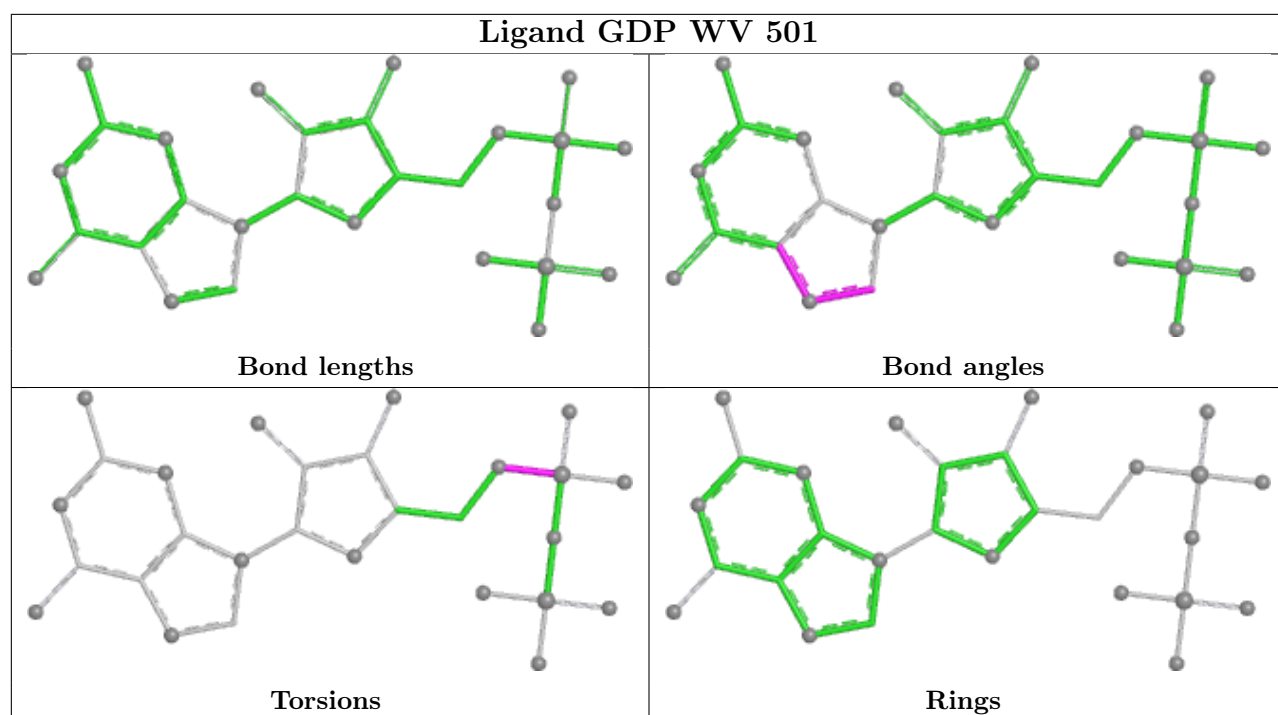


## Ligand GTP An 602

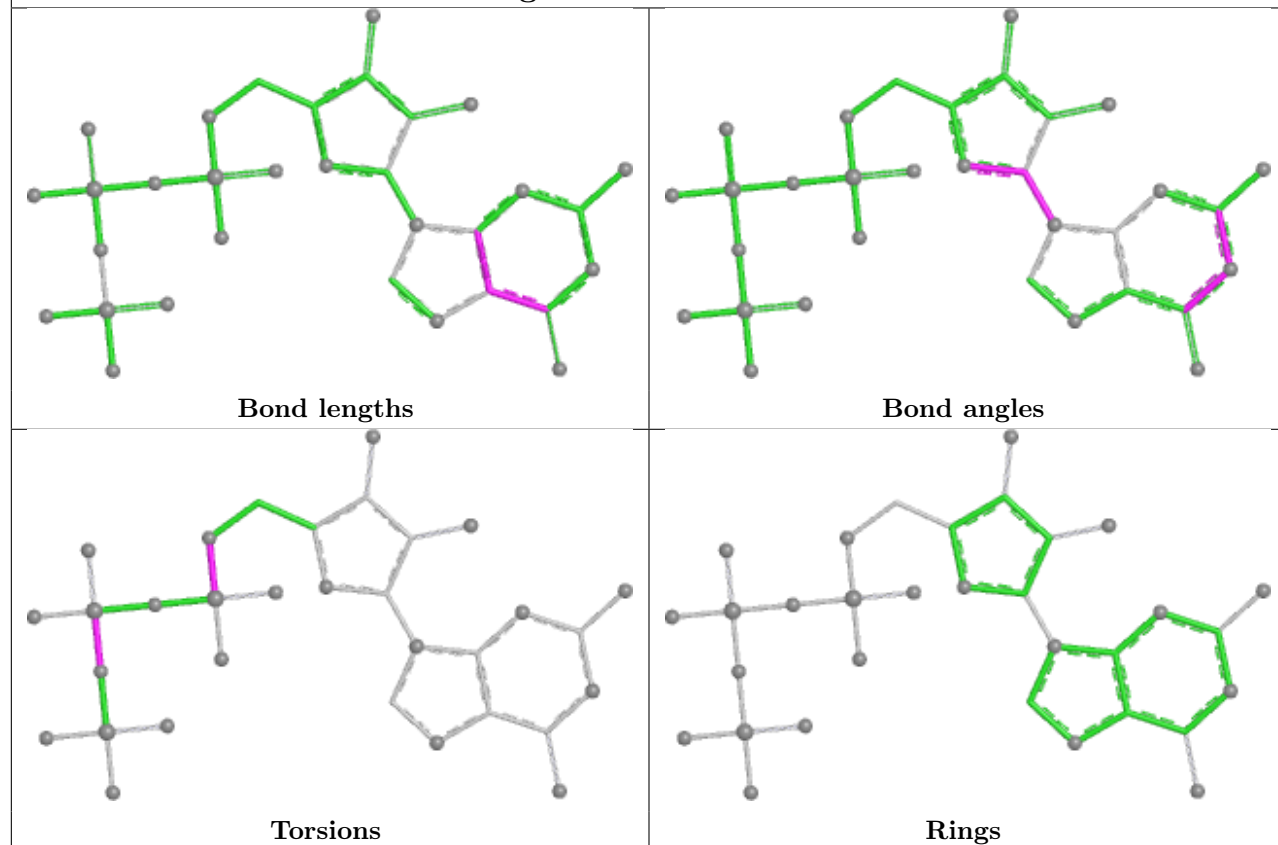




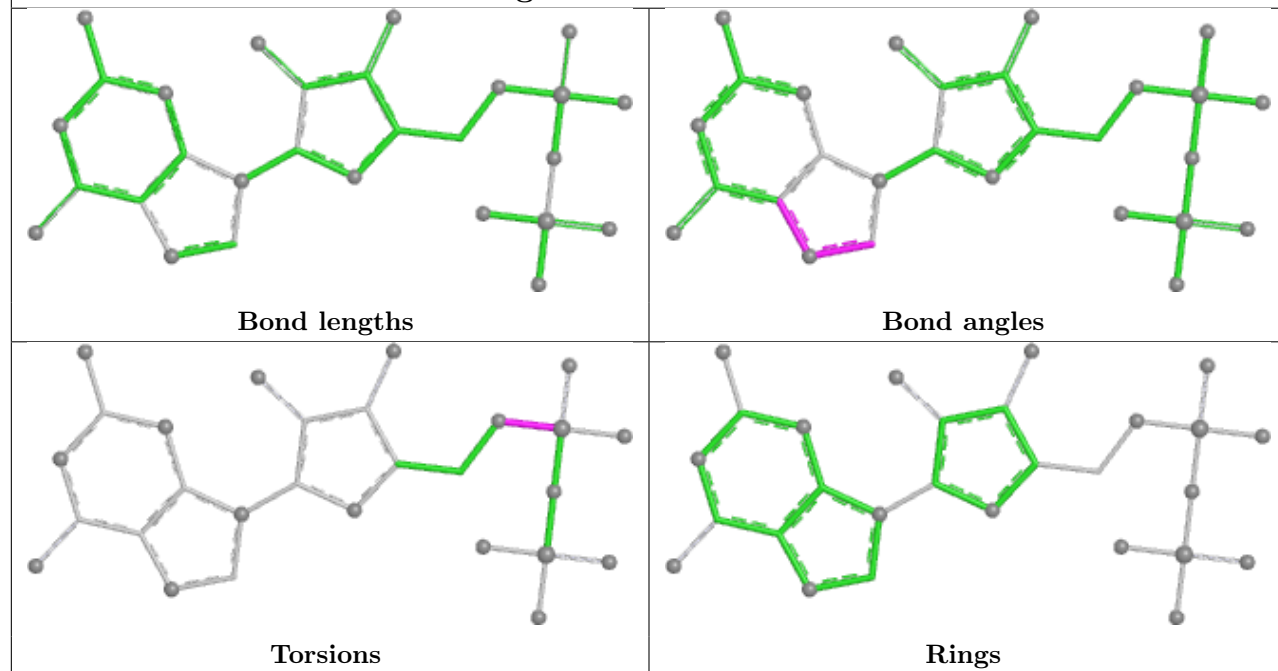




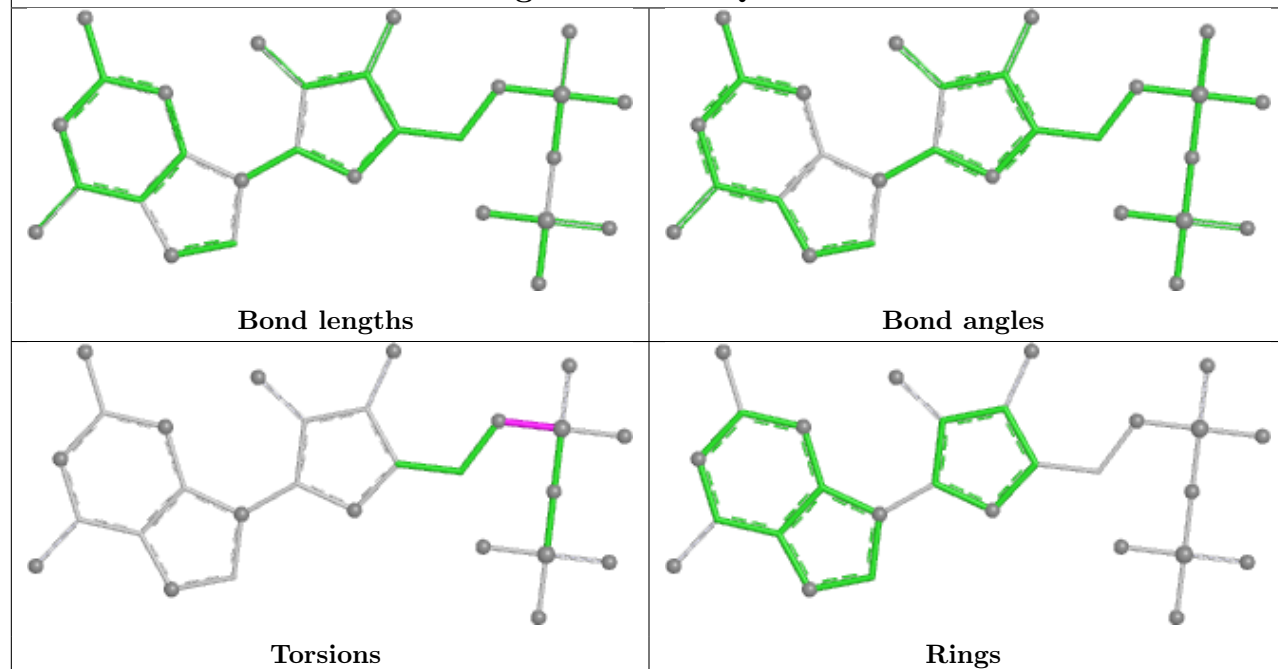
## Ligand GTP YL 602



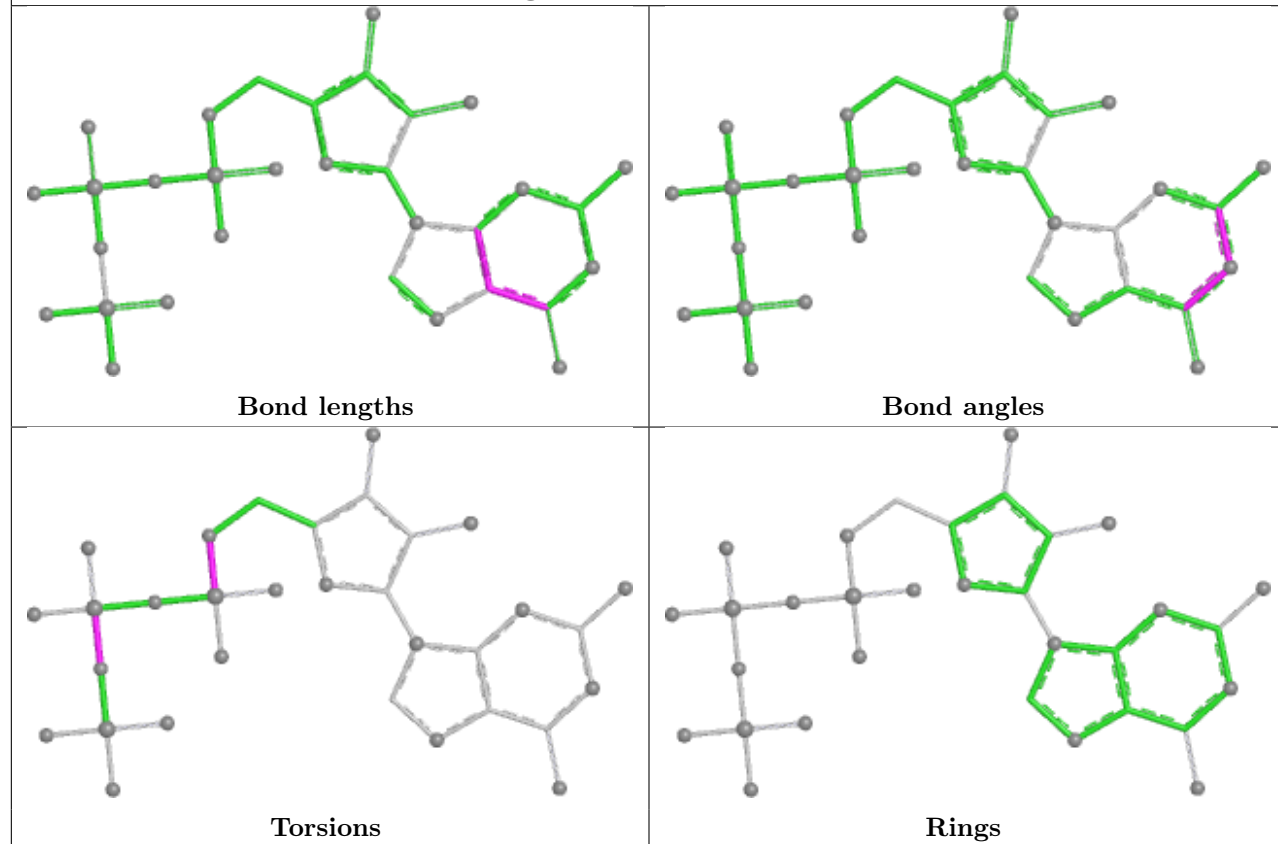
## Ligand GDP TU 501



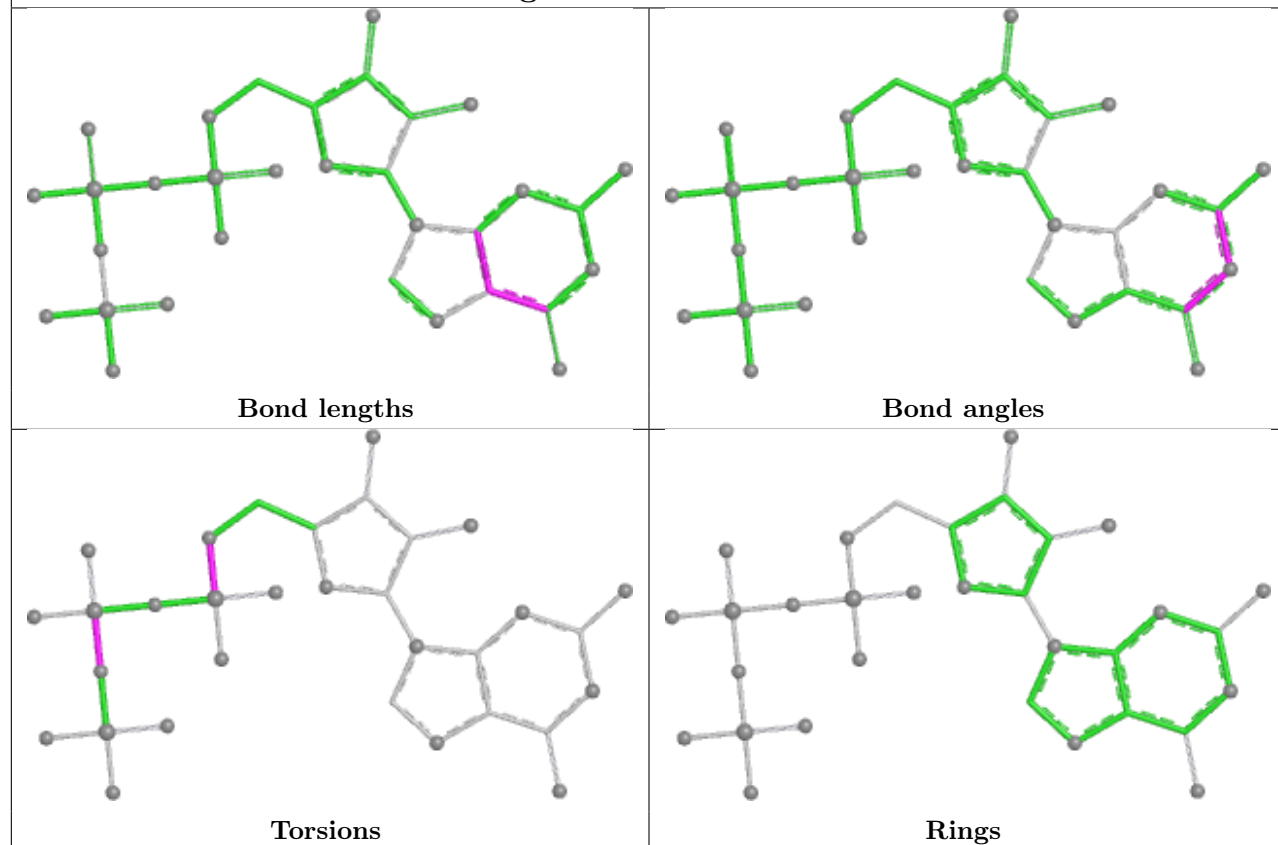
## Ligand GDP OQ 501



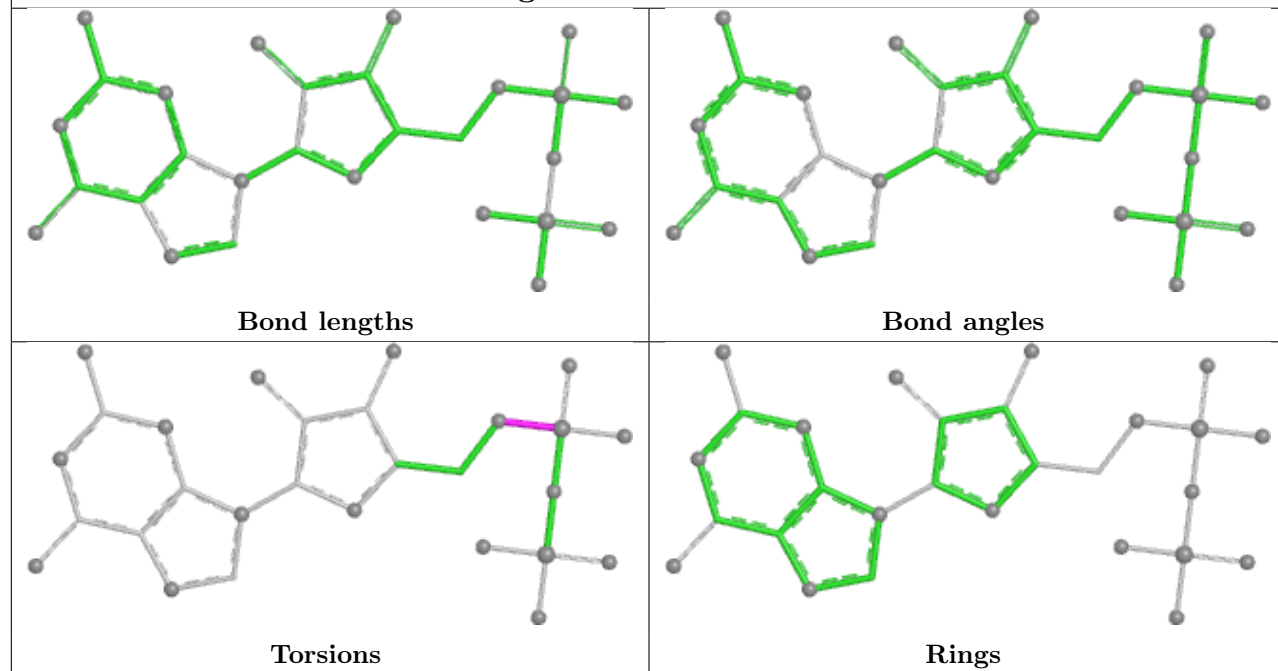
## Ligand GTP JT 501



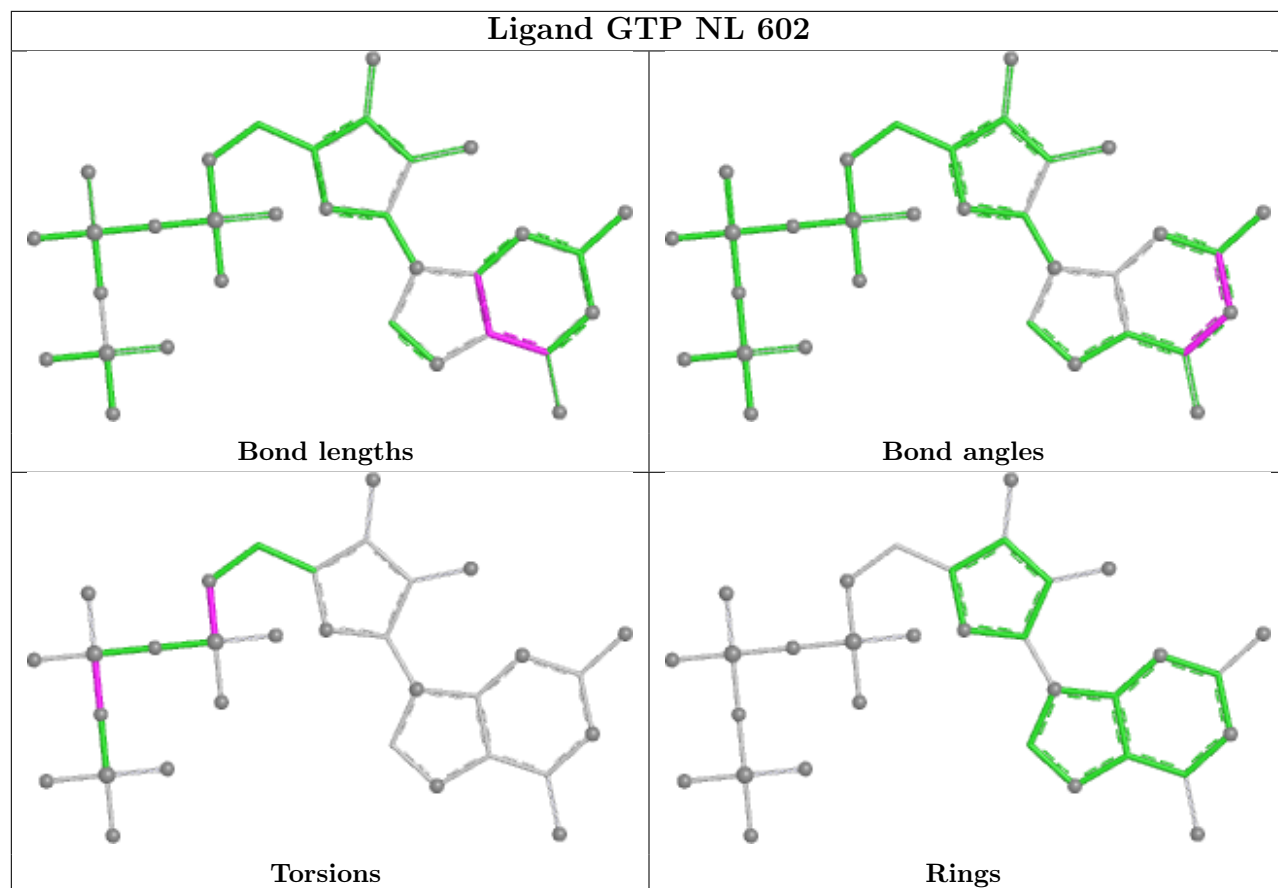
## Ligand GTP LR 501



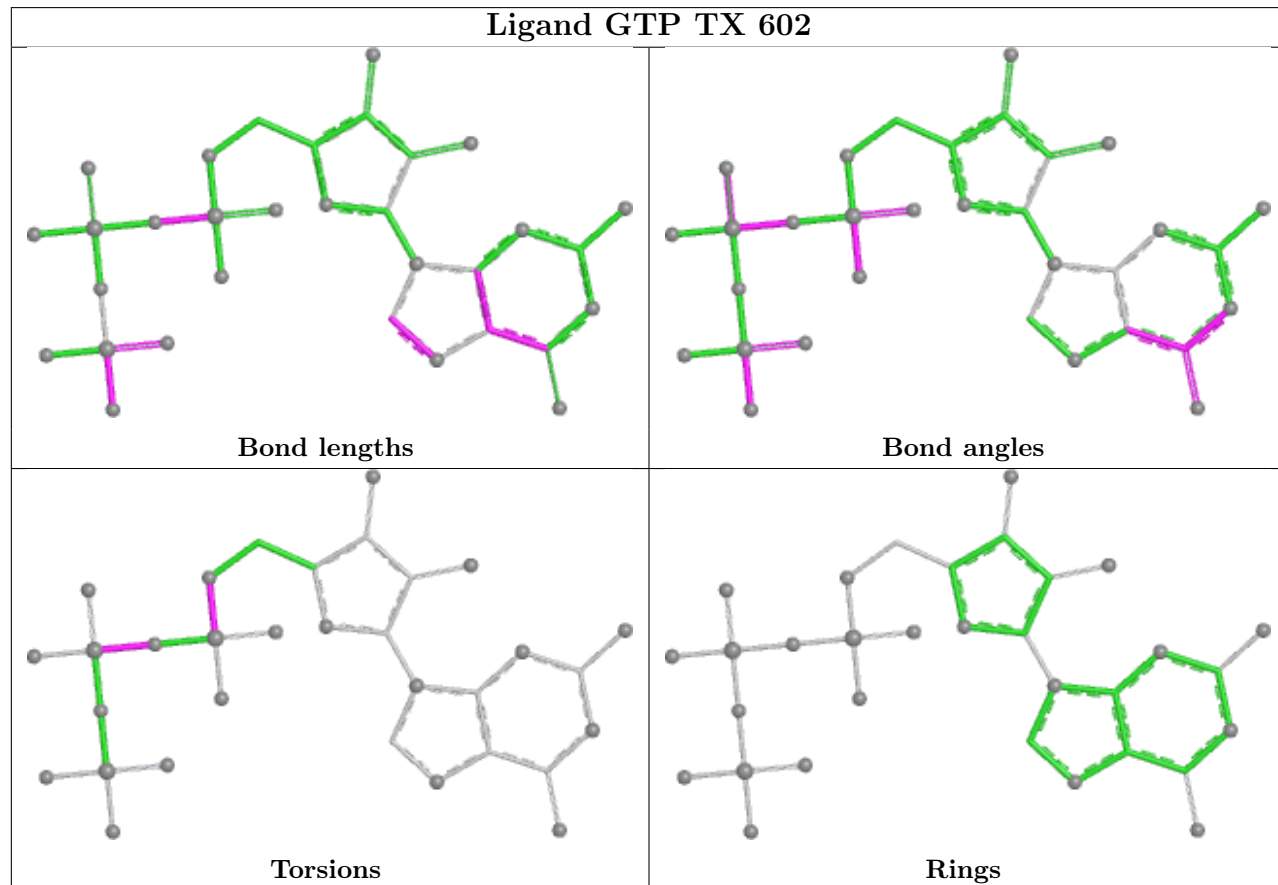
## Ligand GDP LA 501



## Ligand GTP NL 602

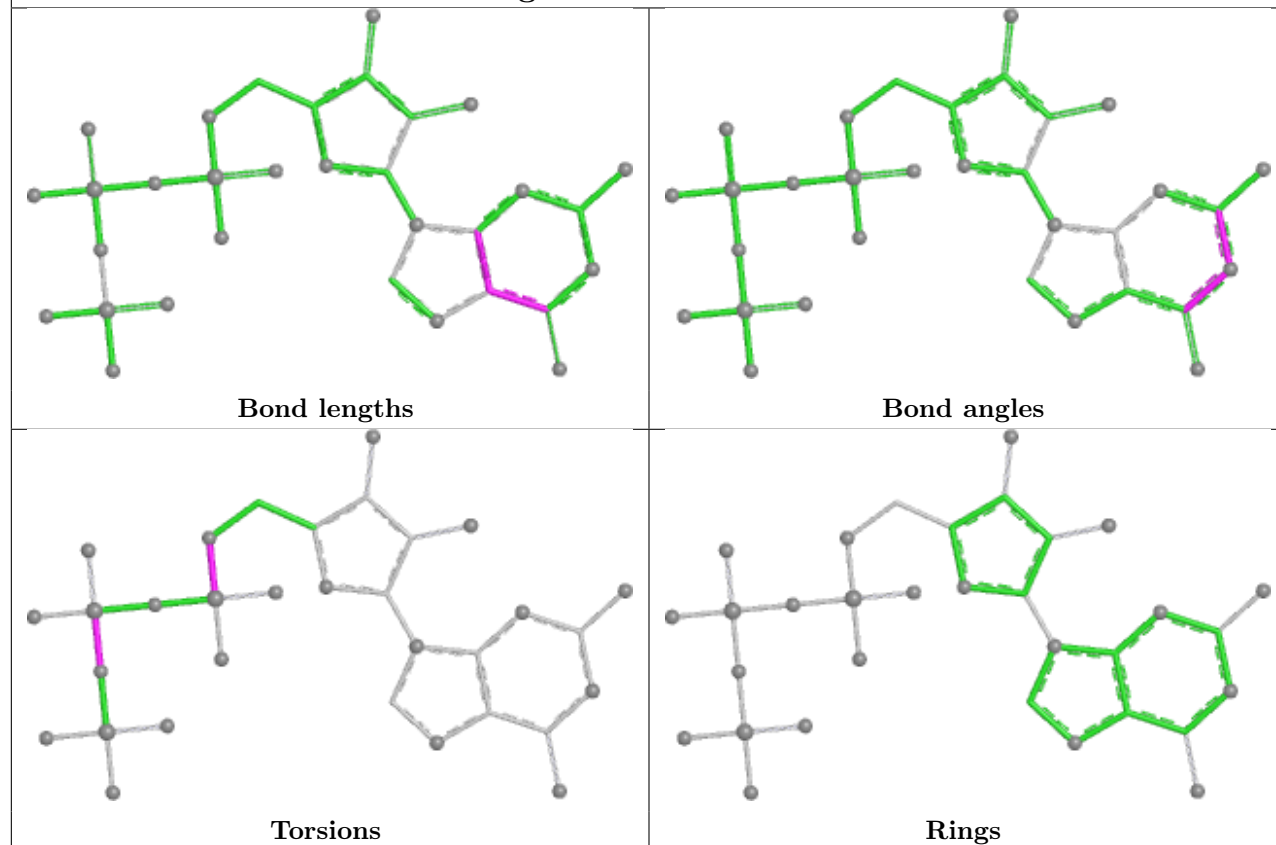


## Ligand GTP TX 602

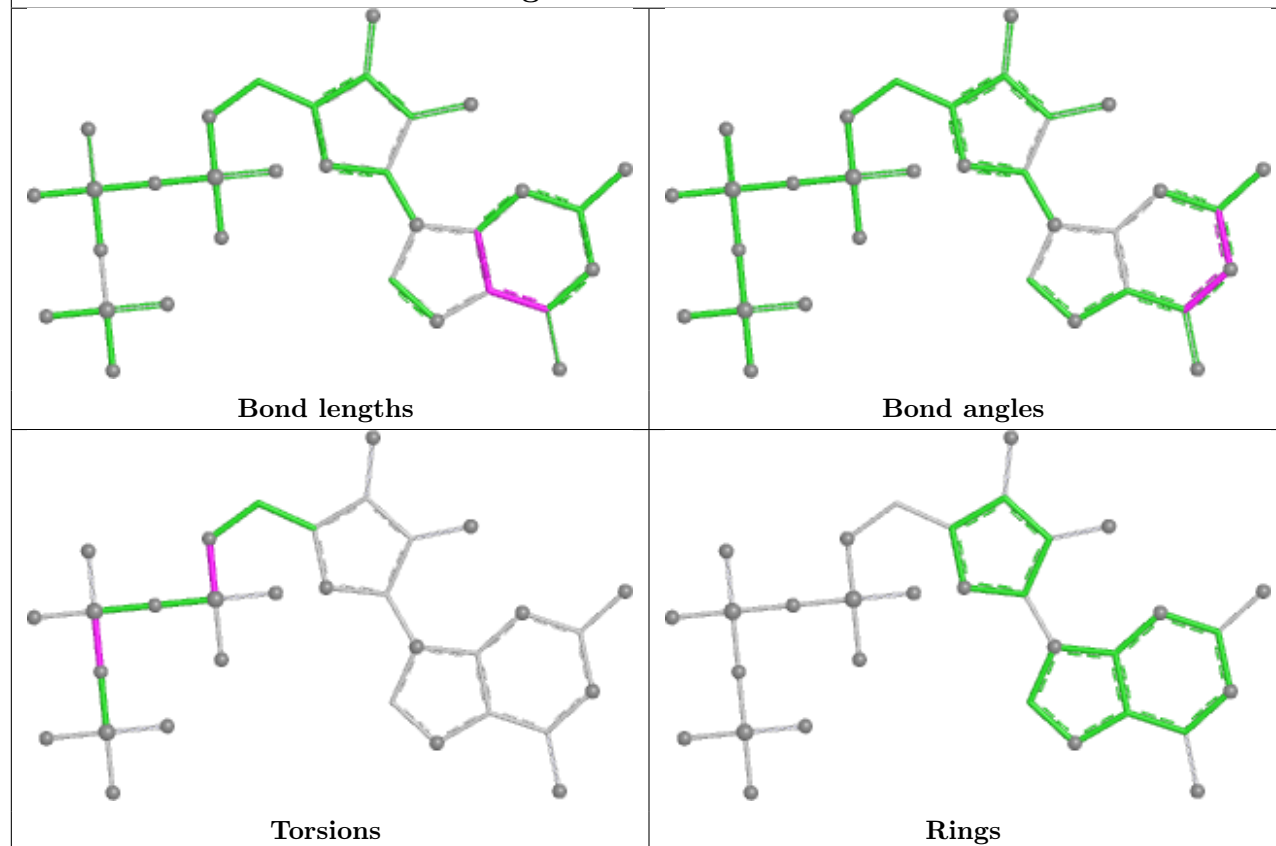




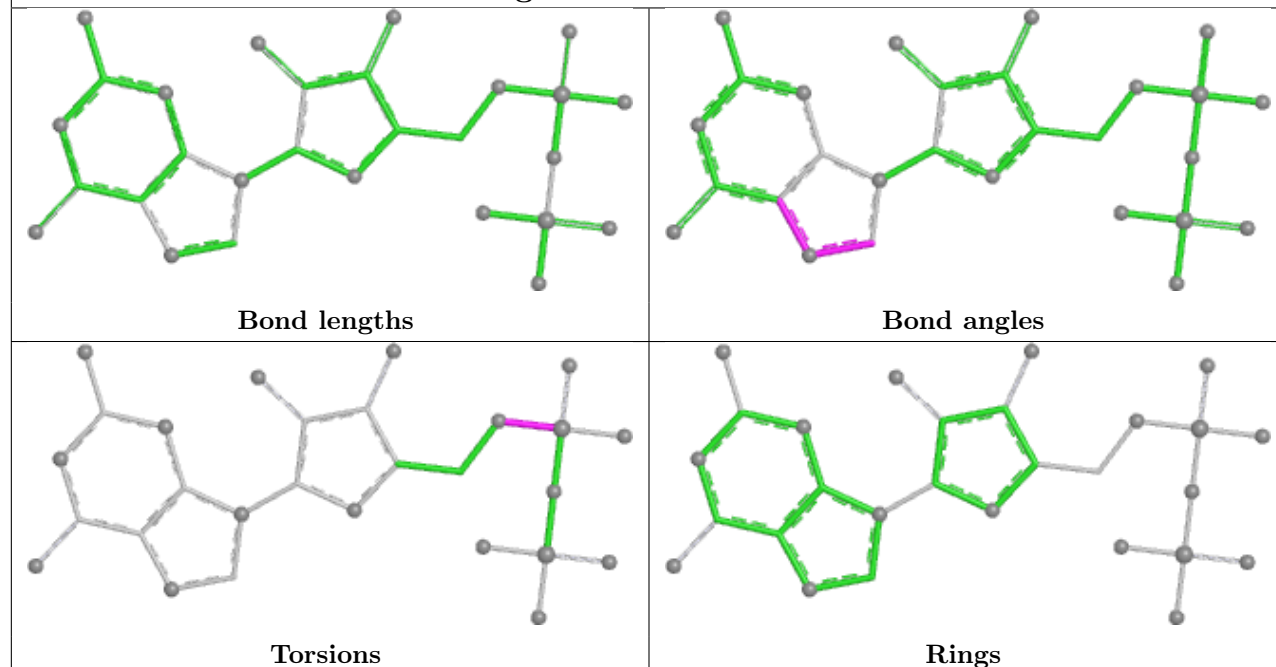
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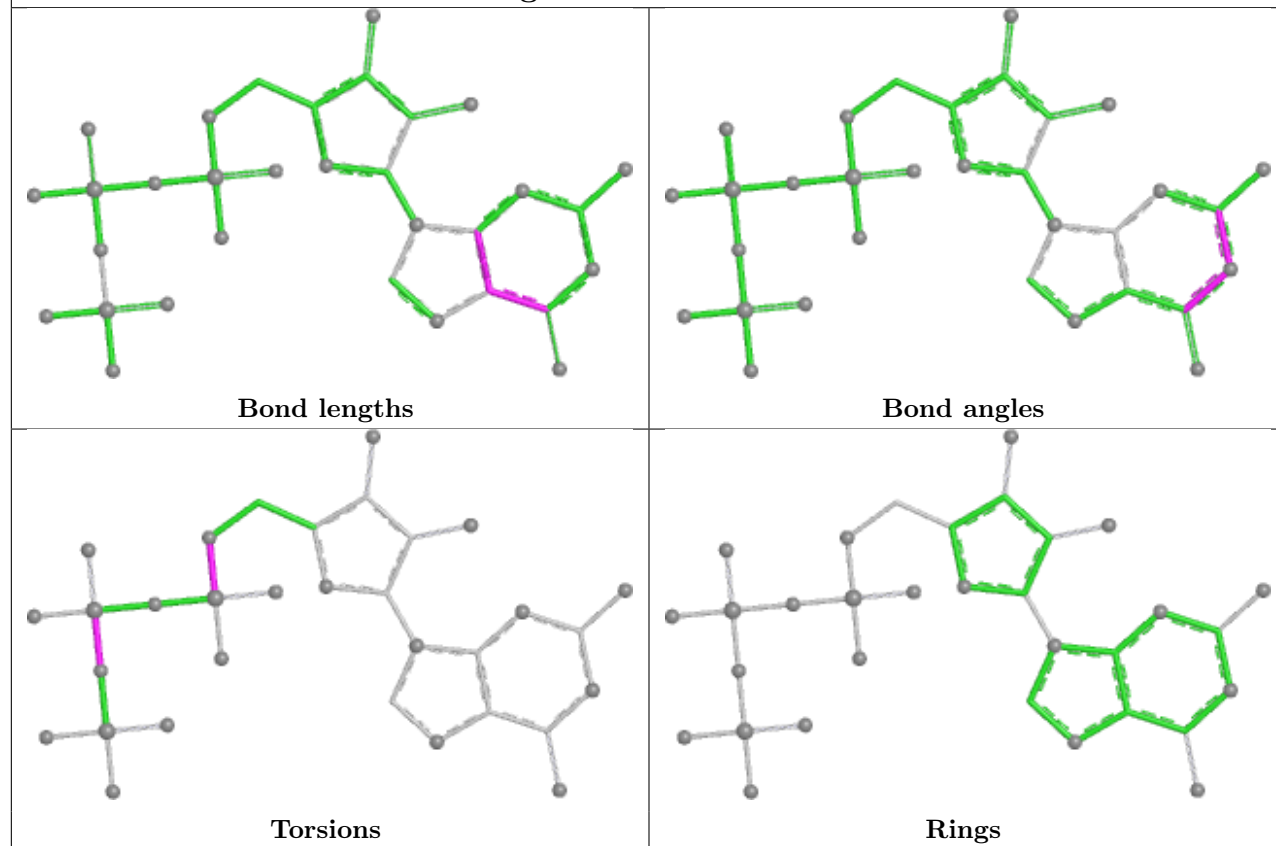
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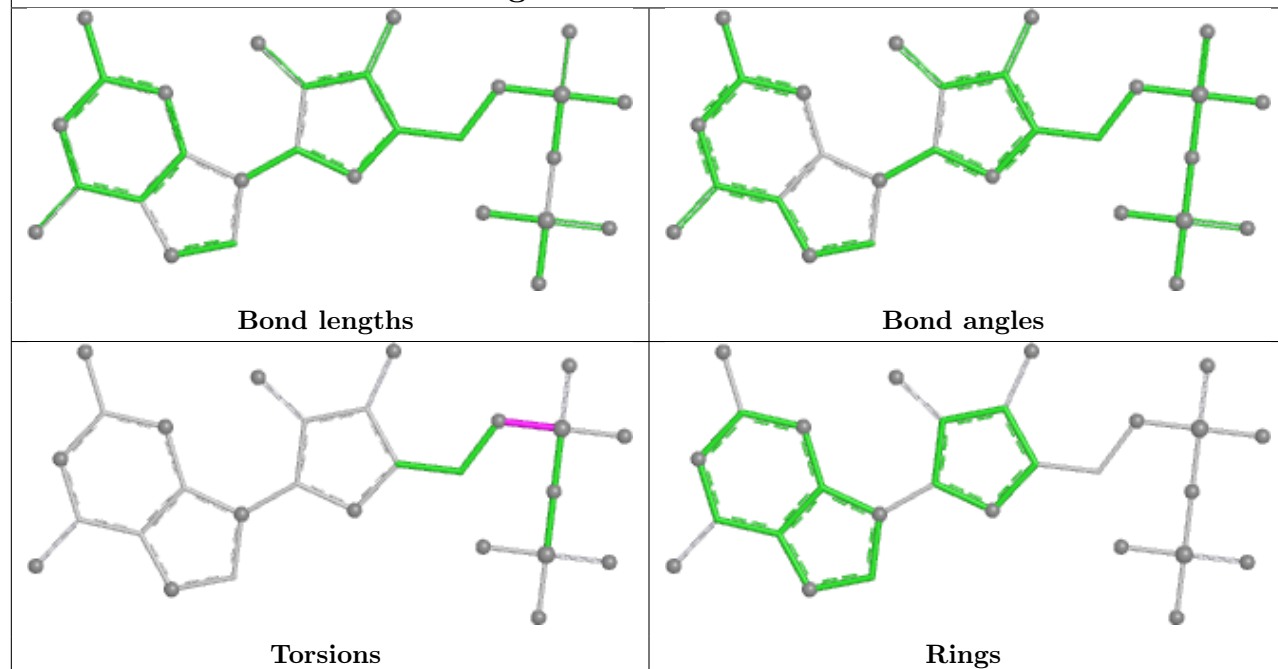
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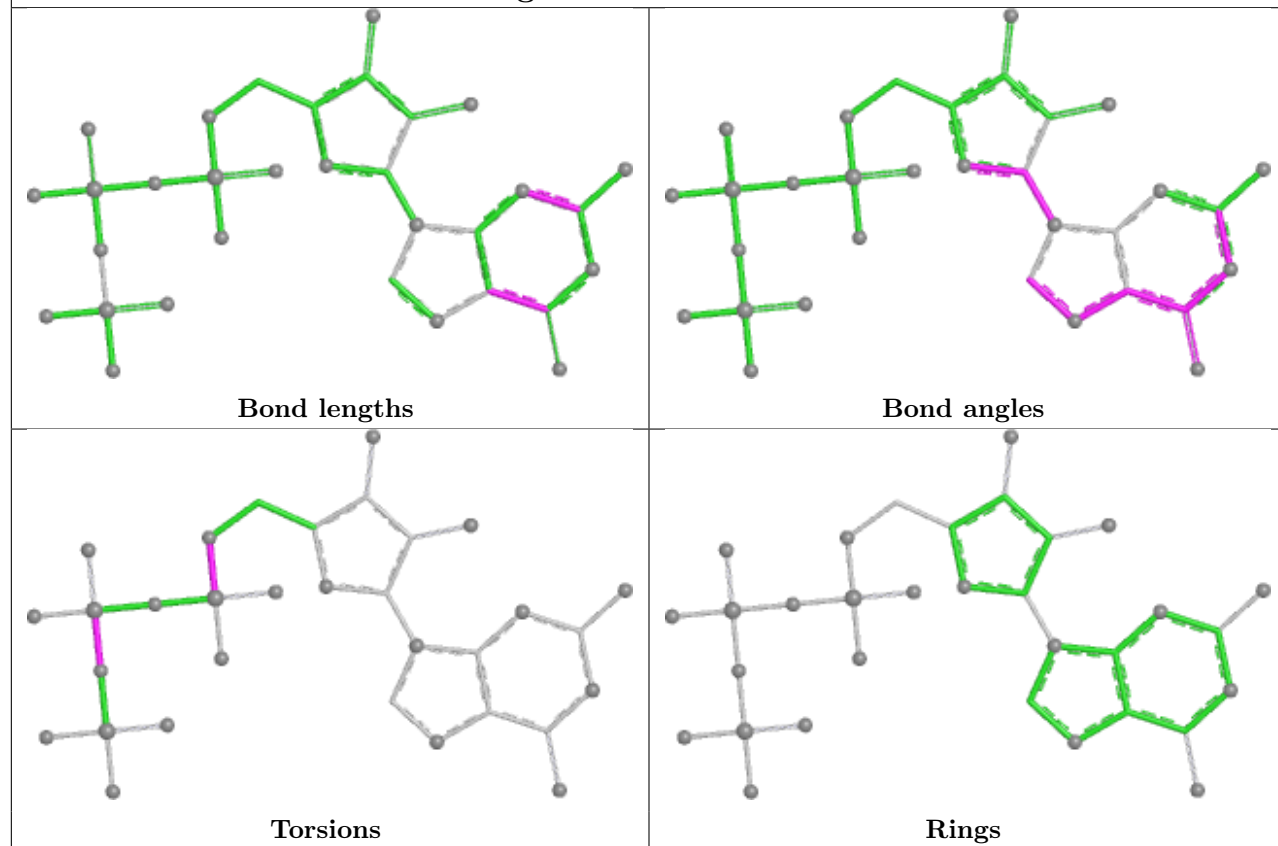
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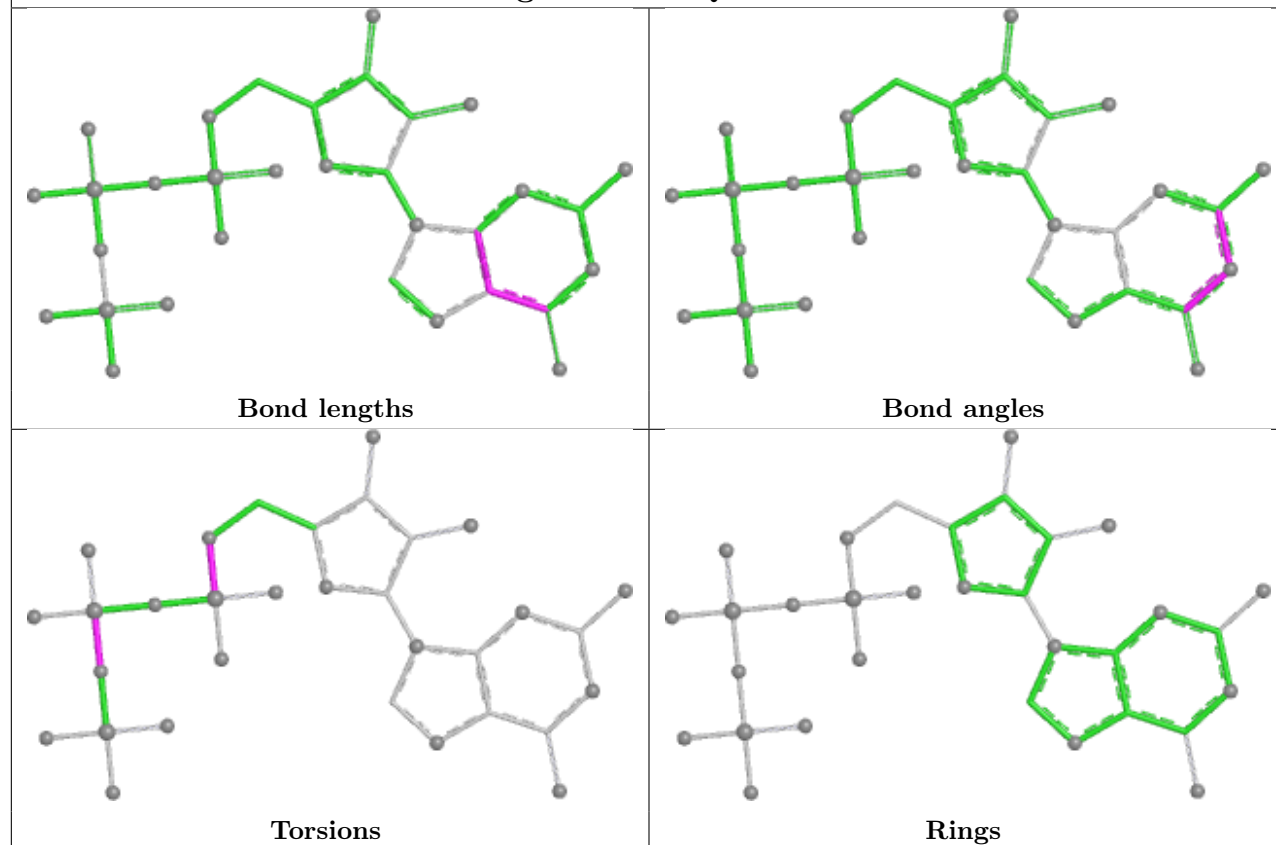
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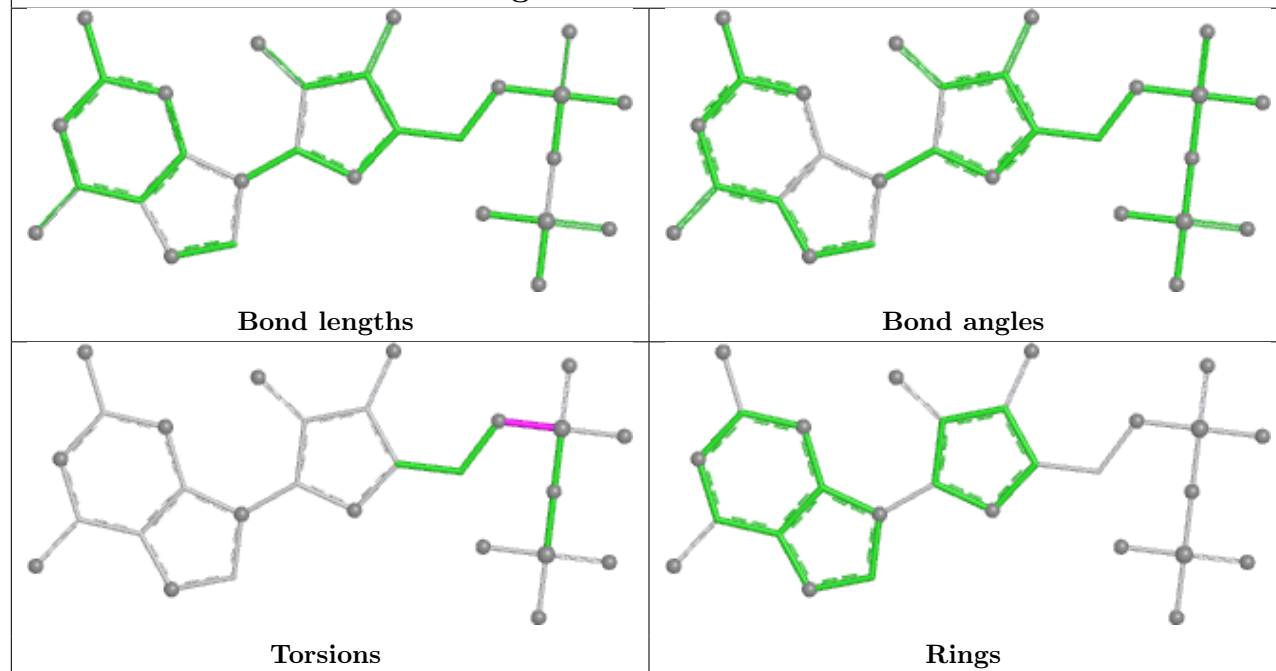
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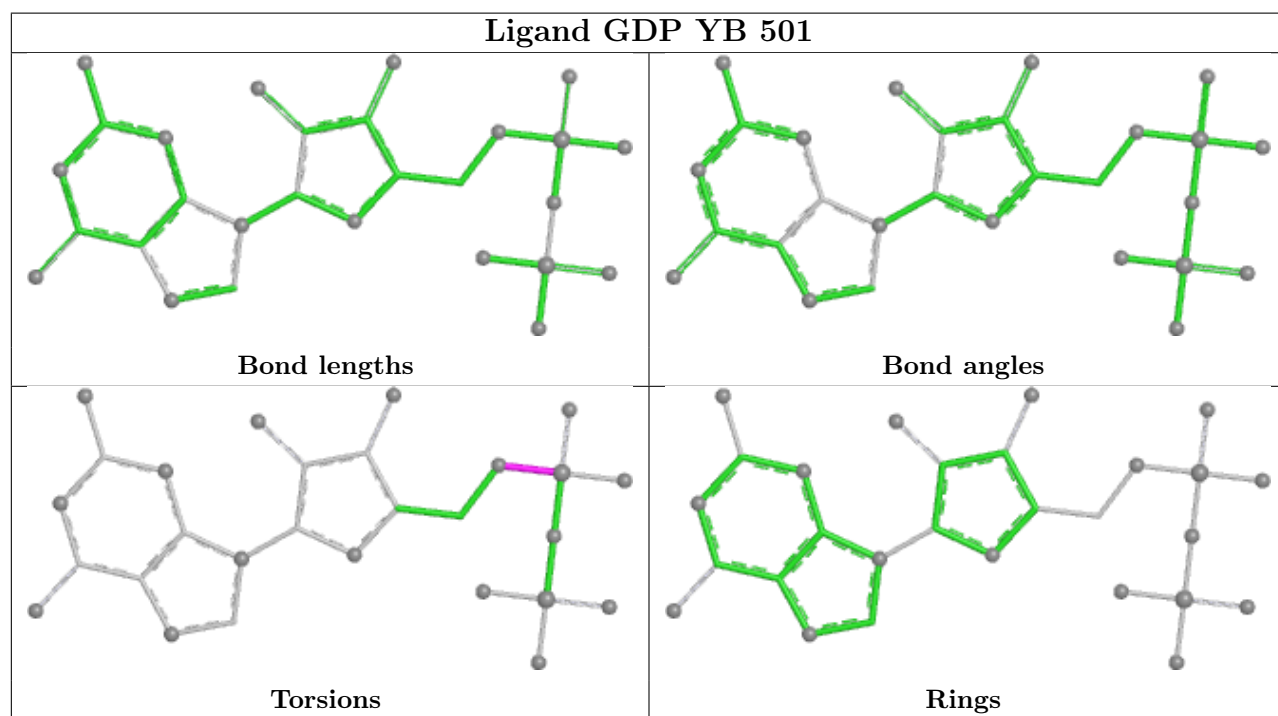
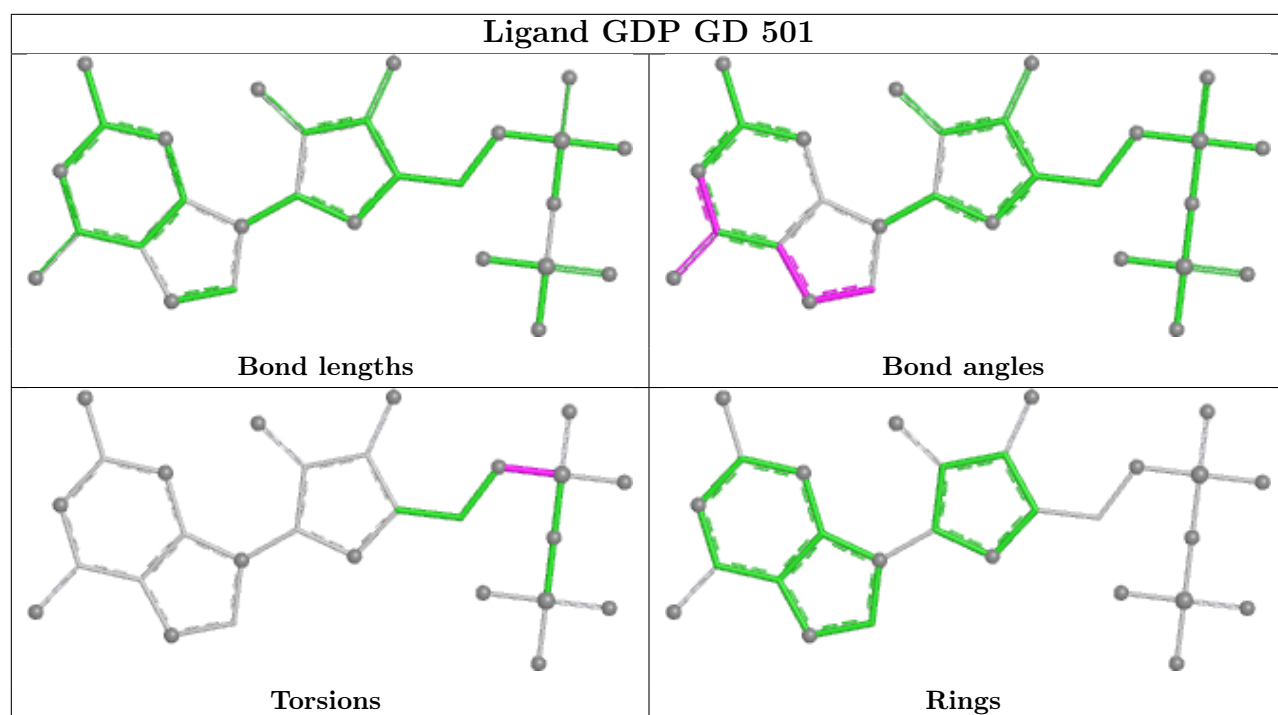


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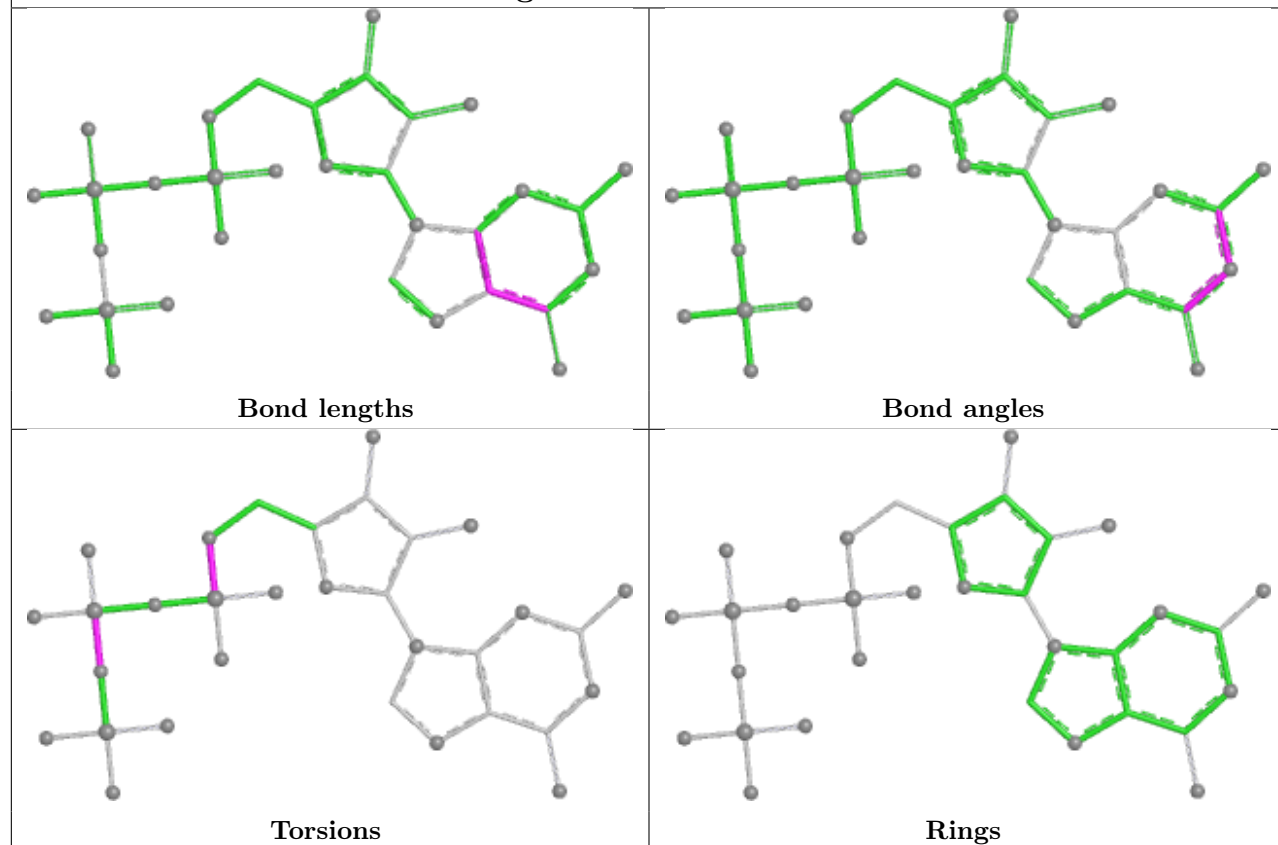


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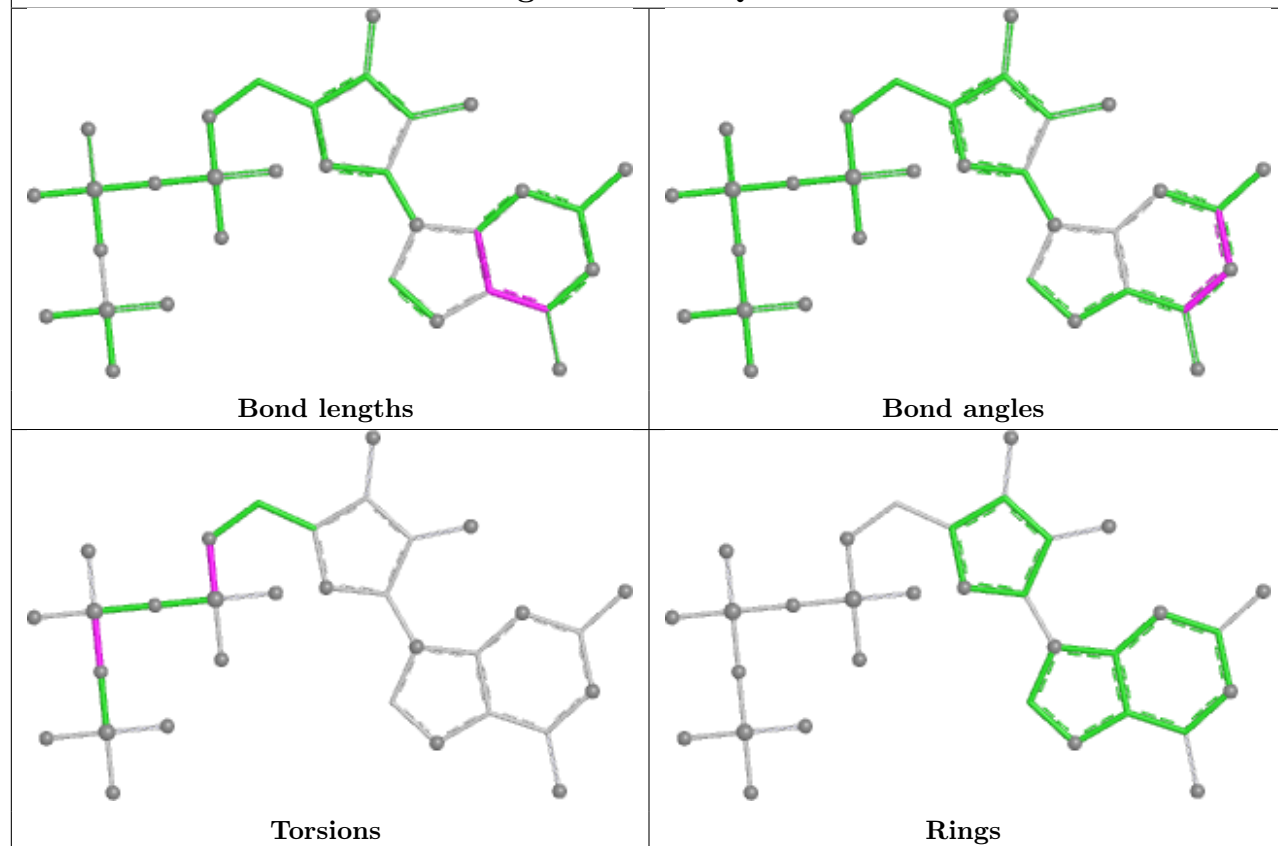




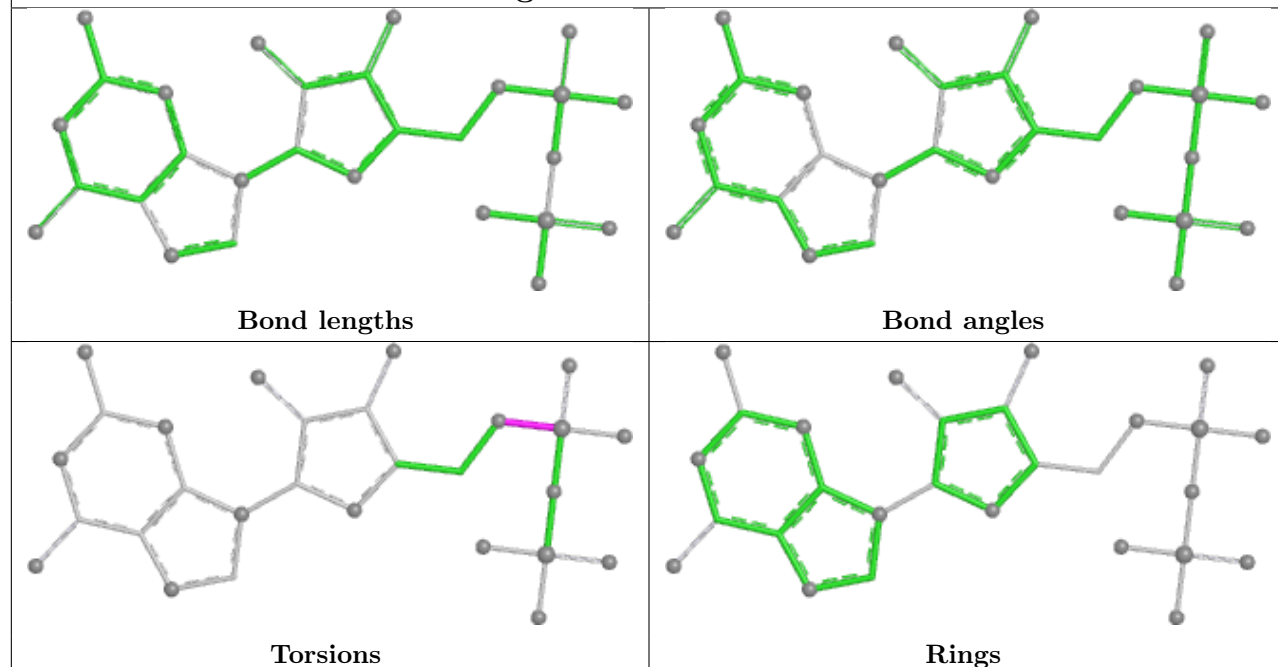
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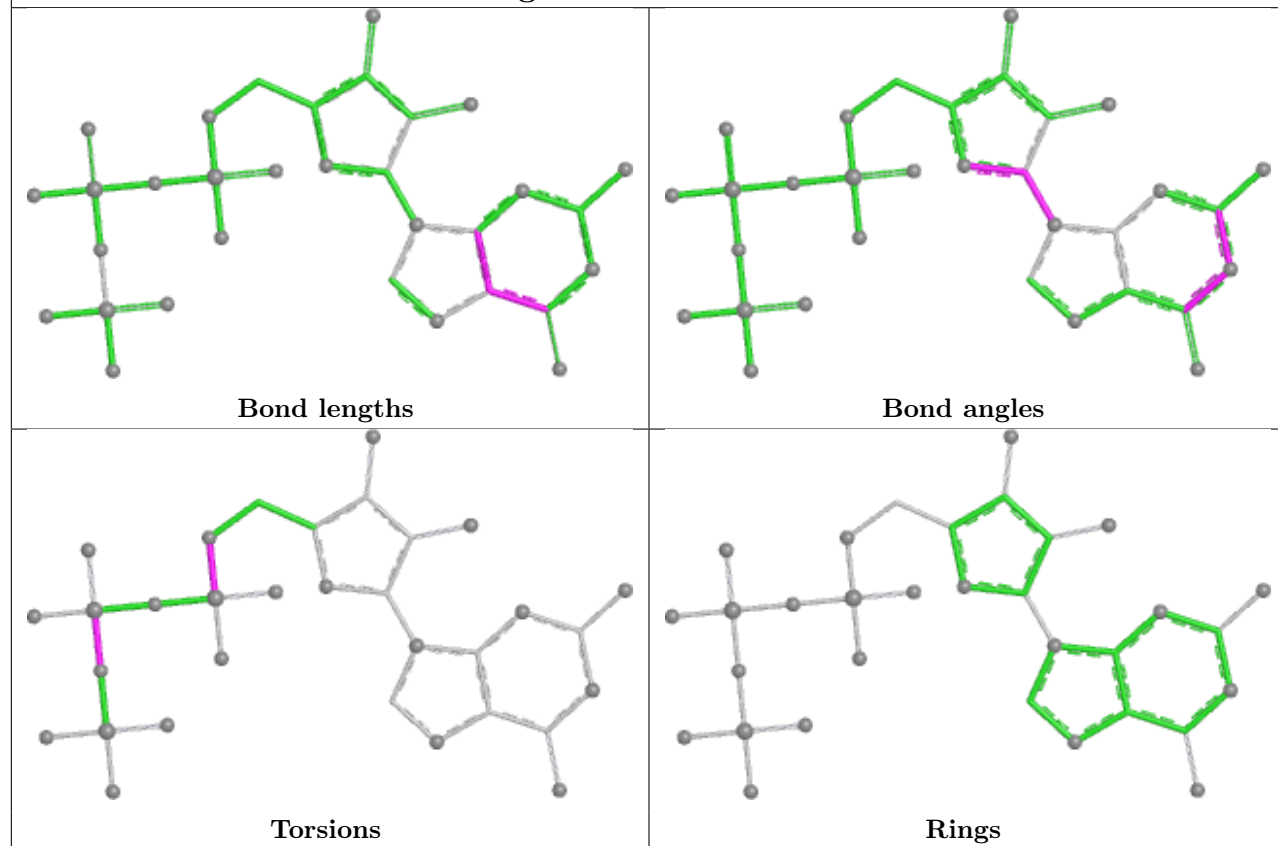
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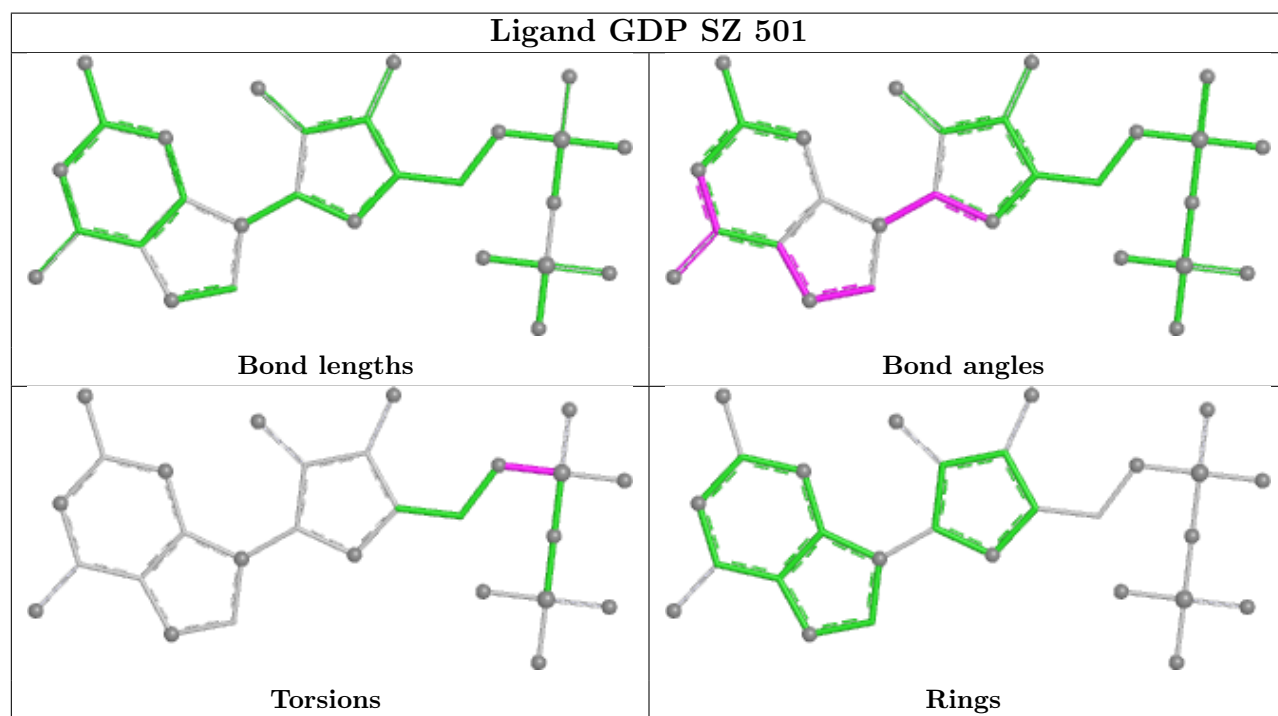
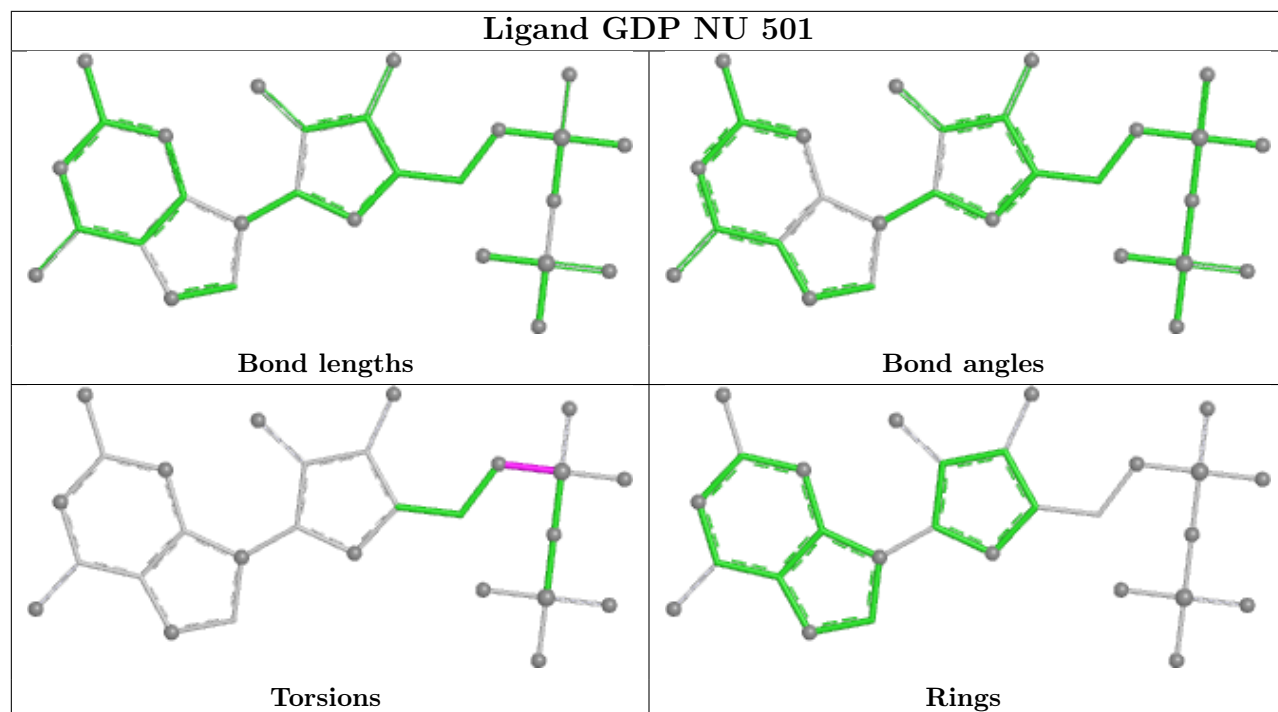


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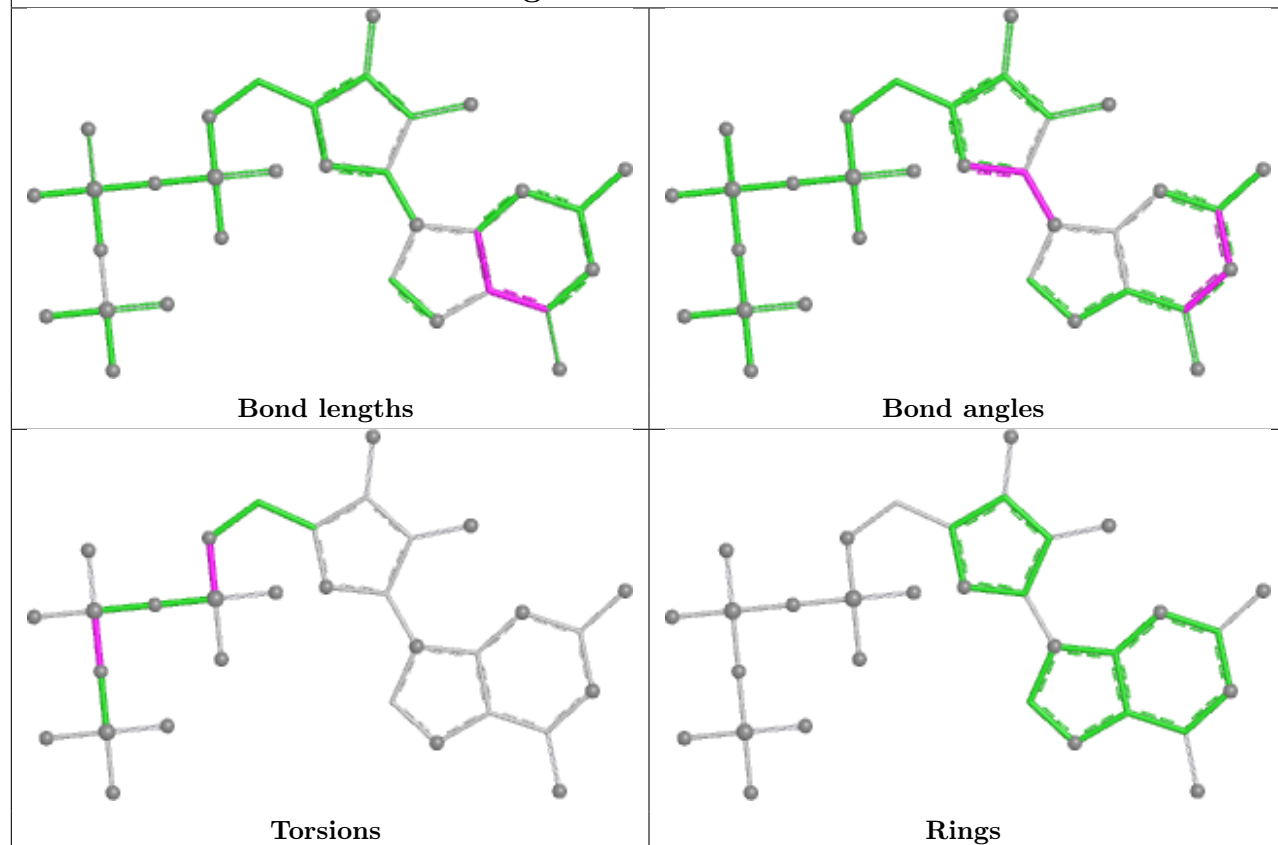
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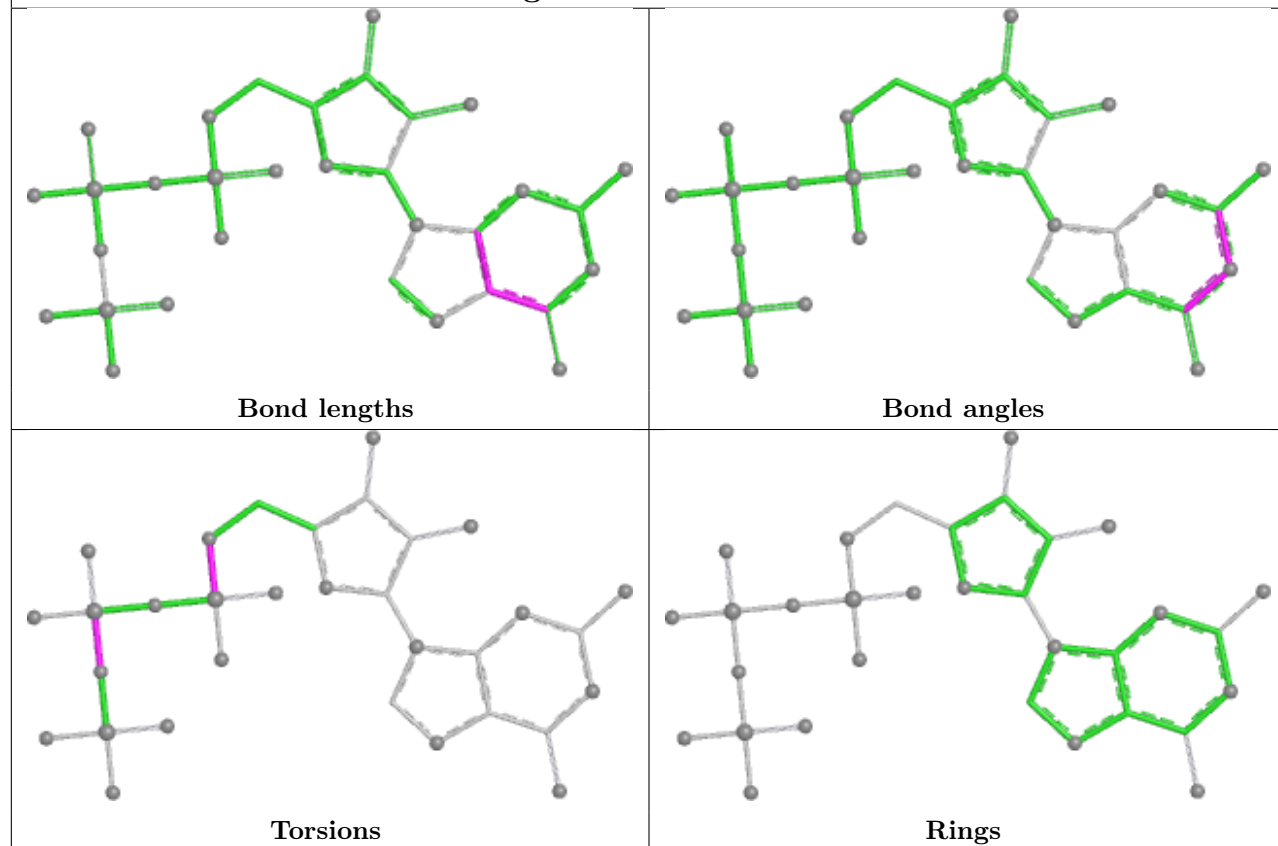




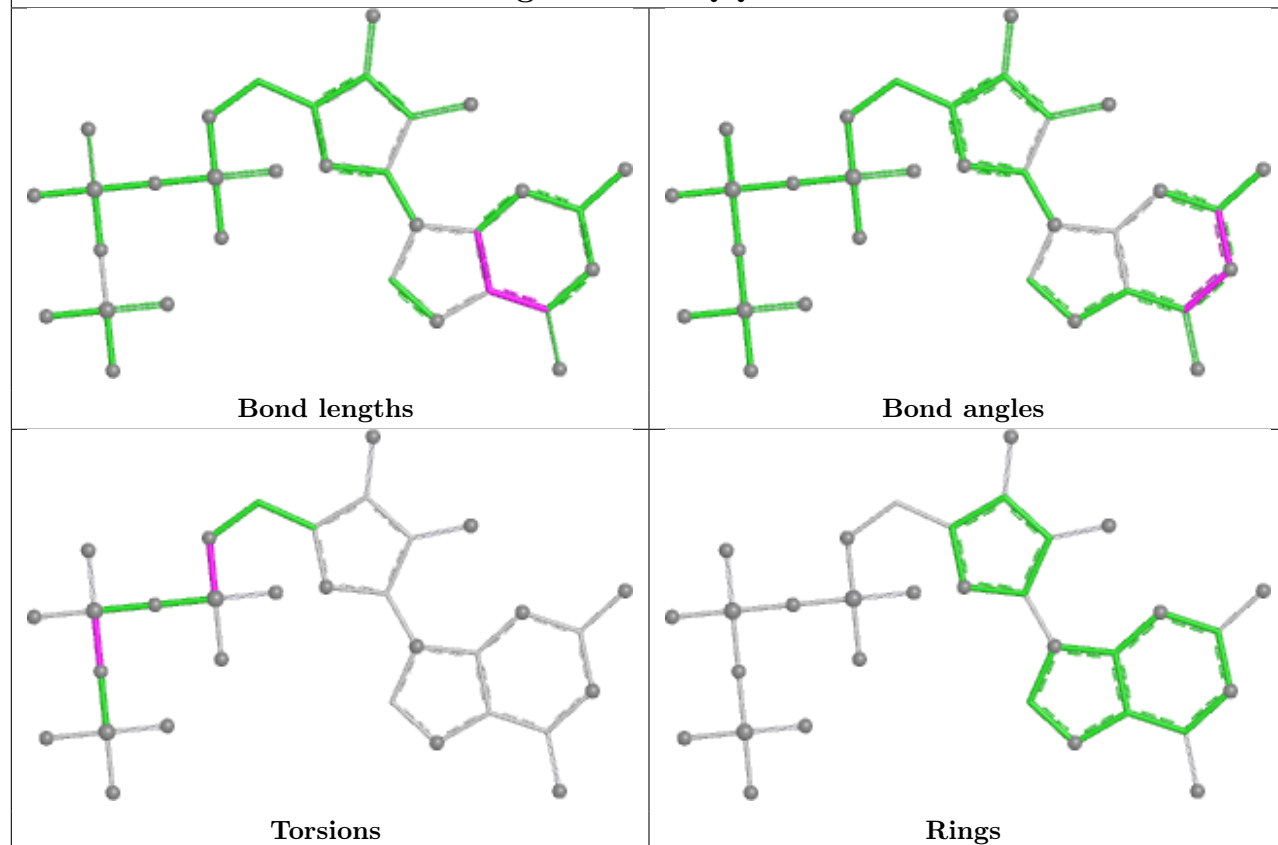
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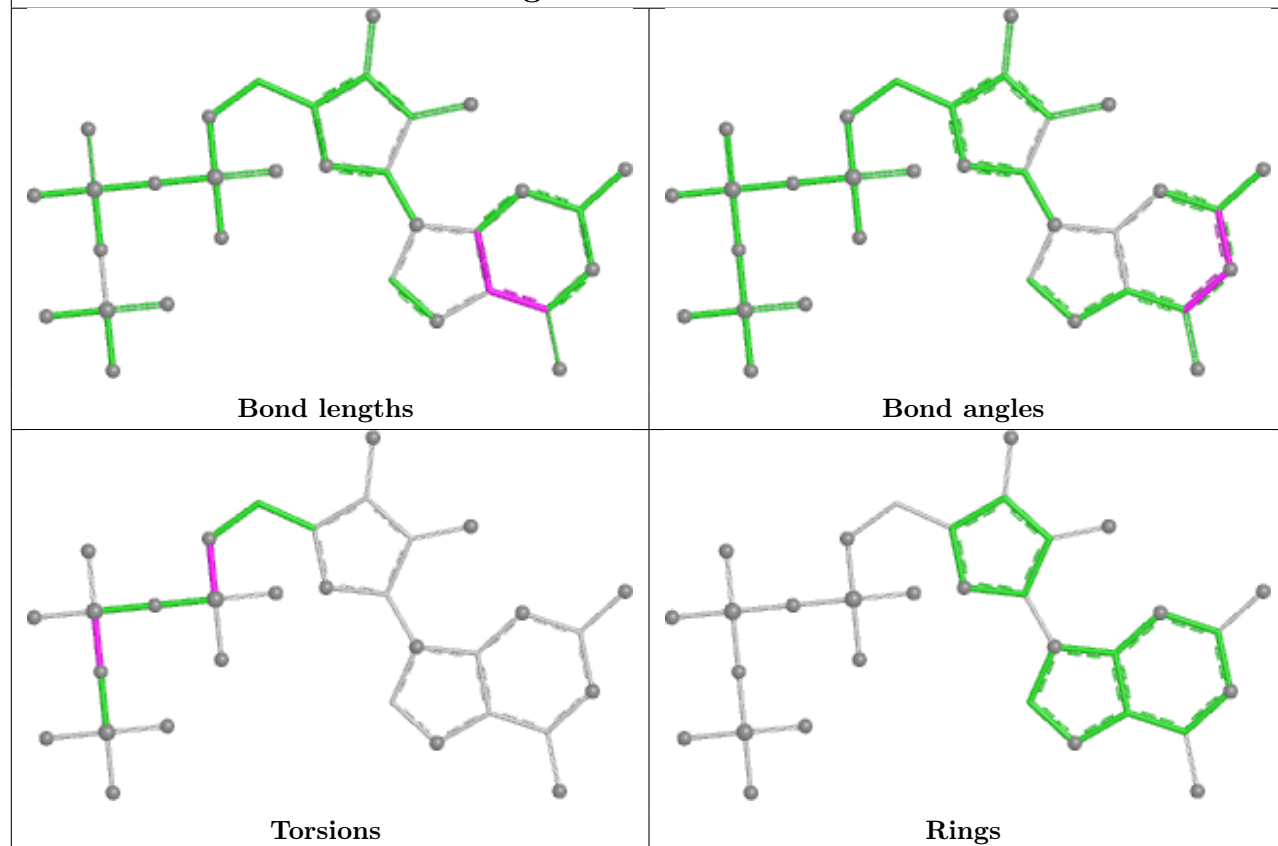
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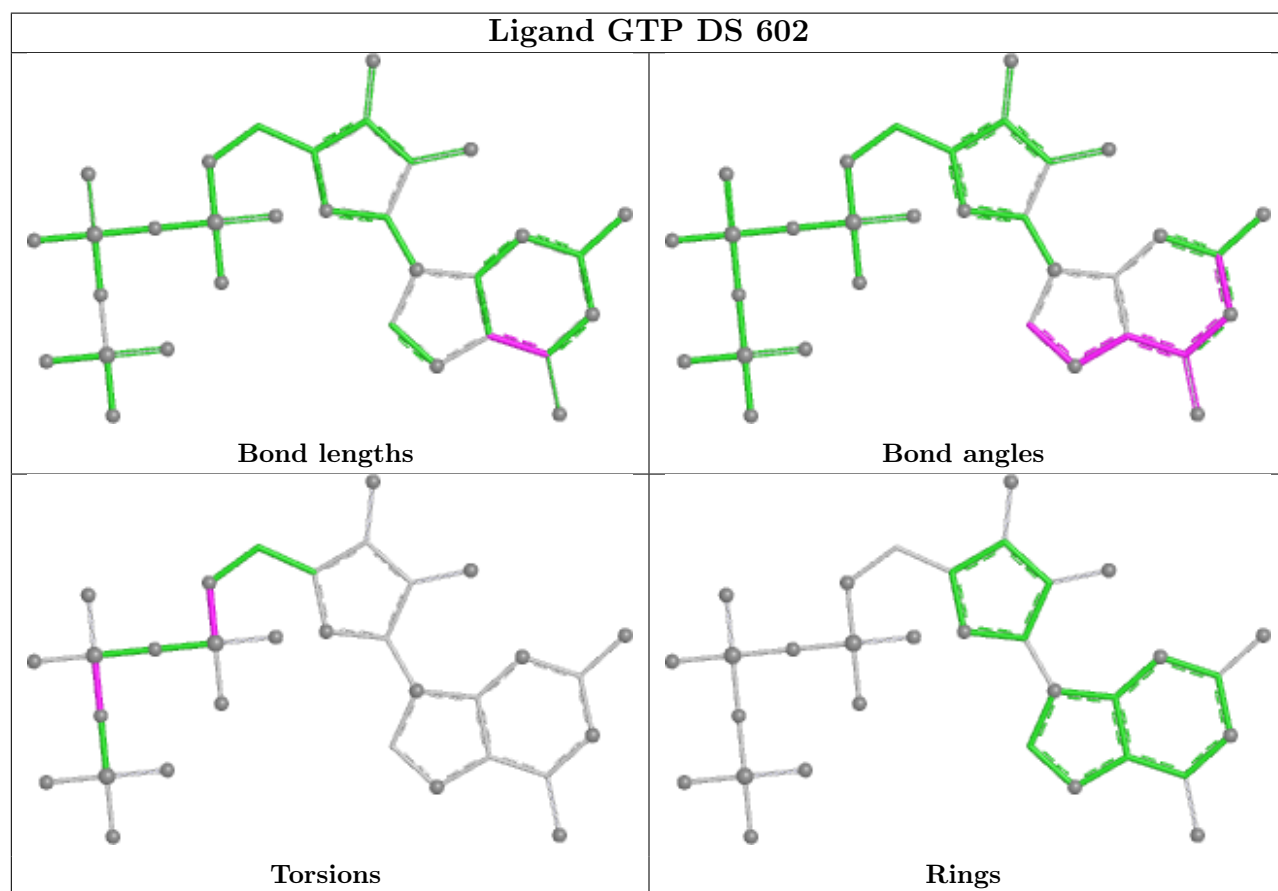
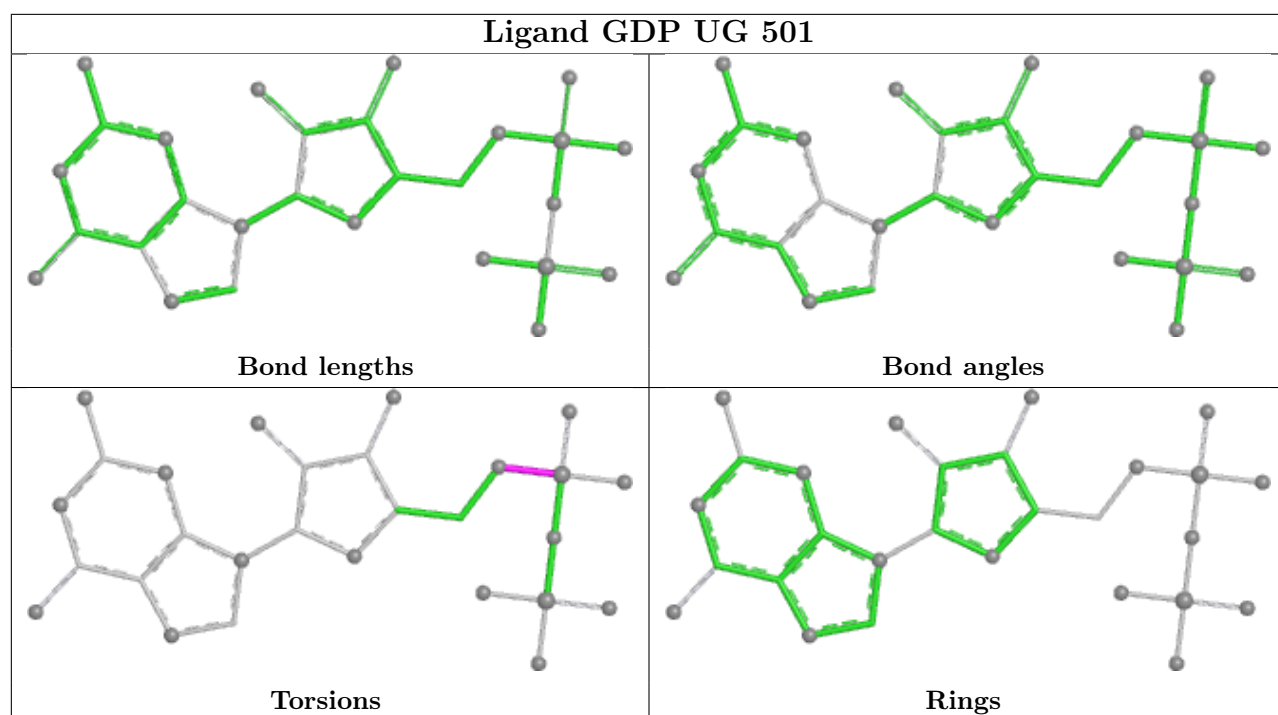


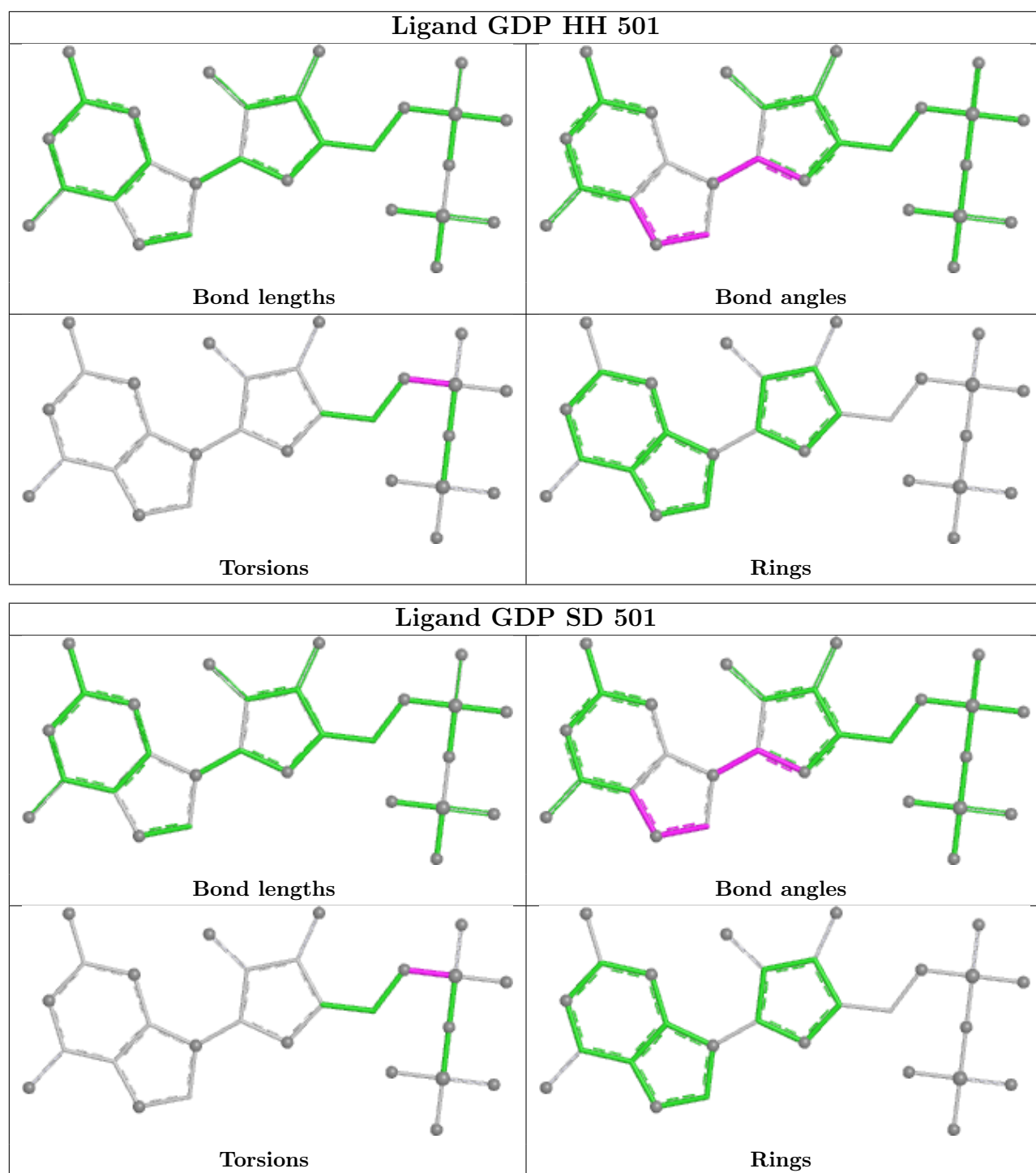
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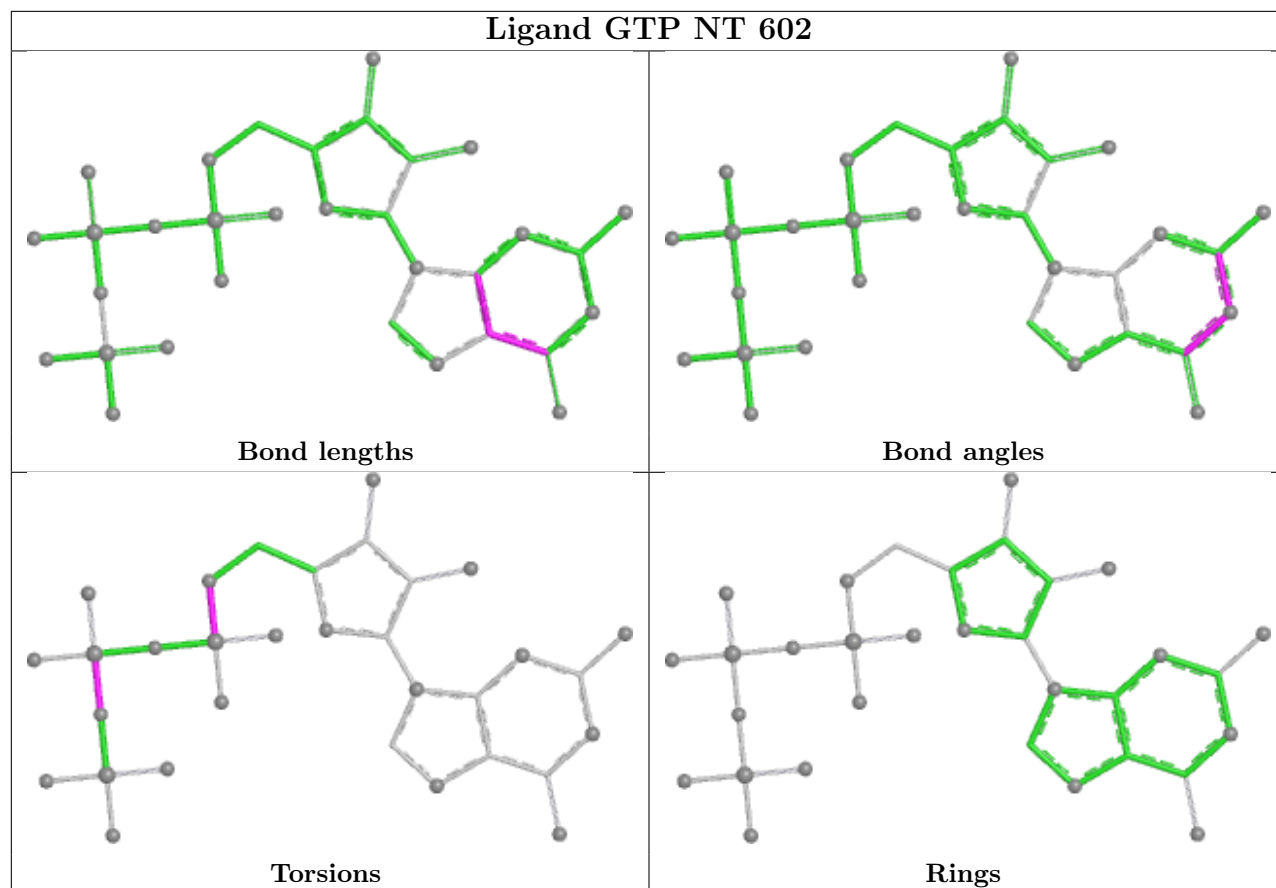
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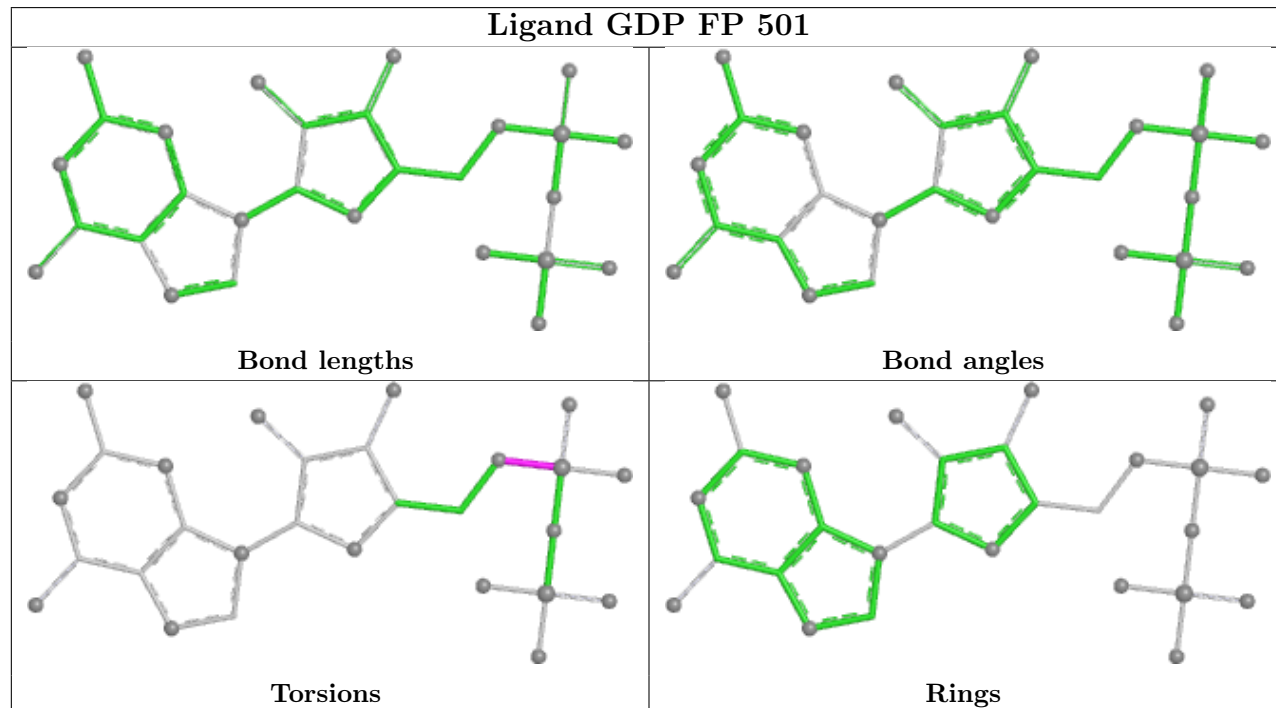




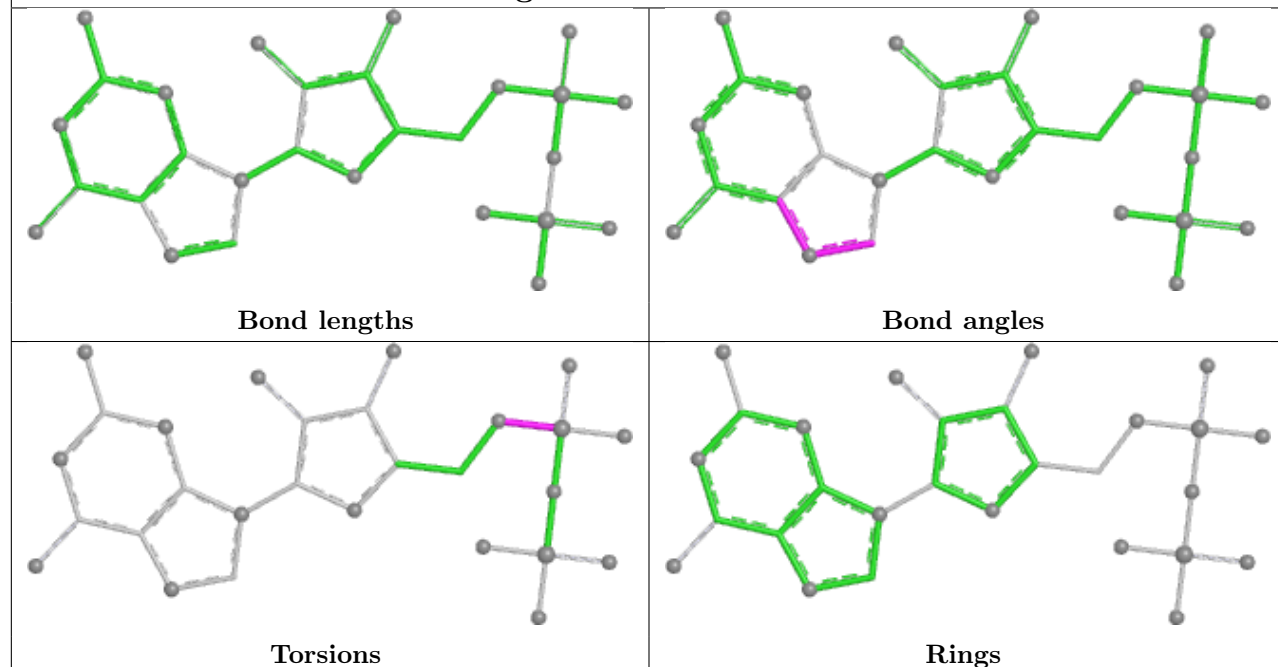
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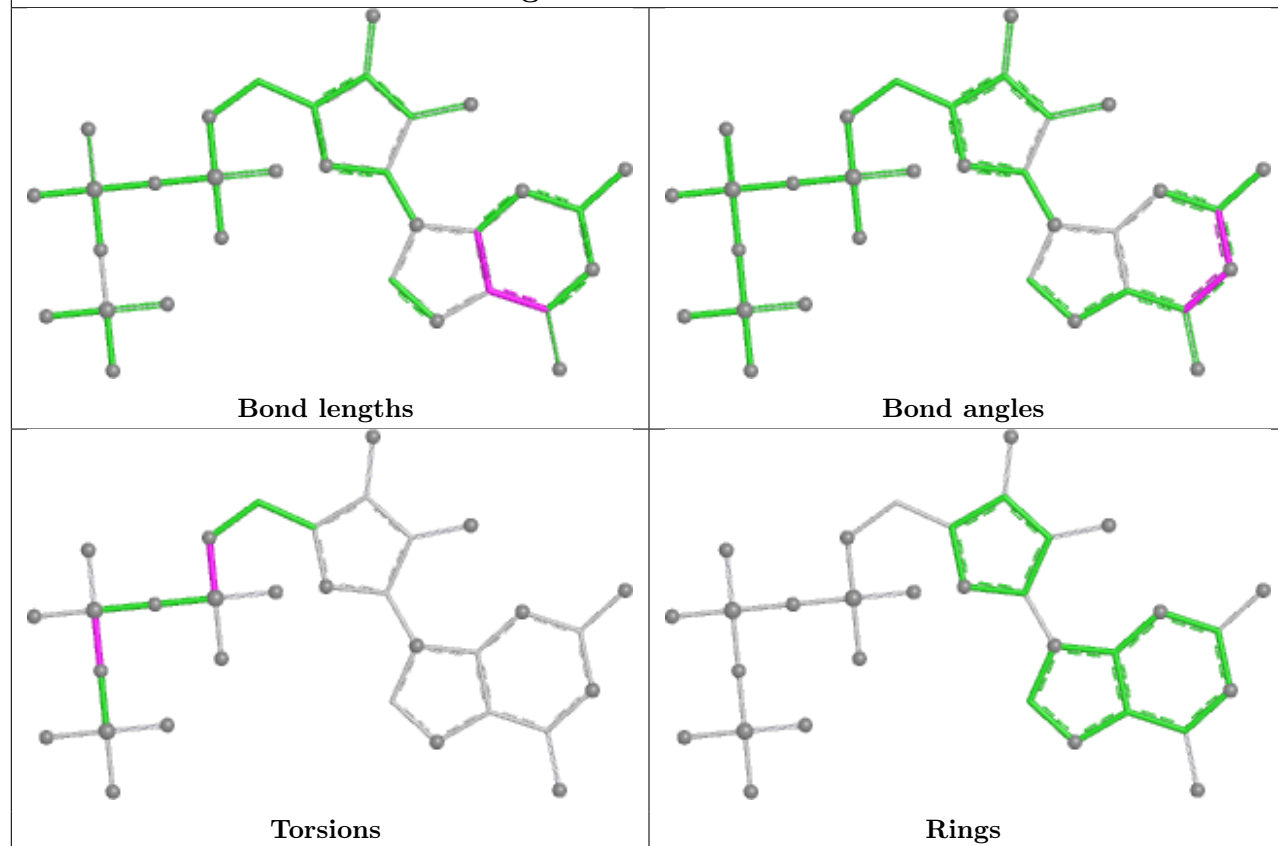
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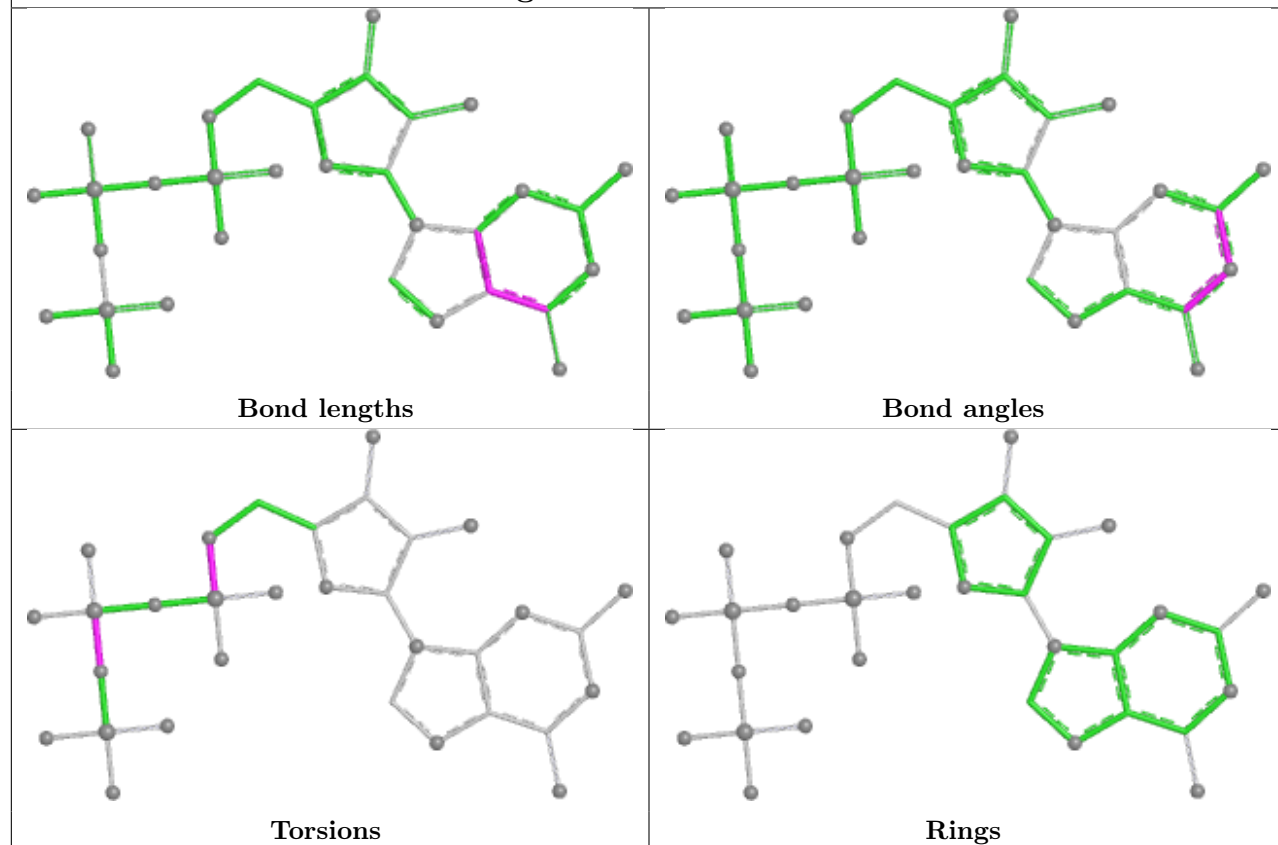
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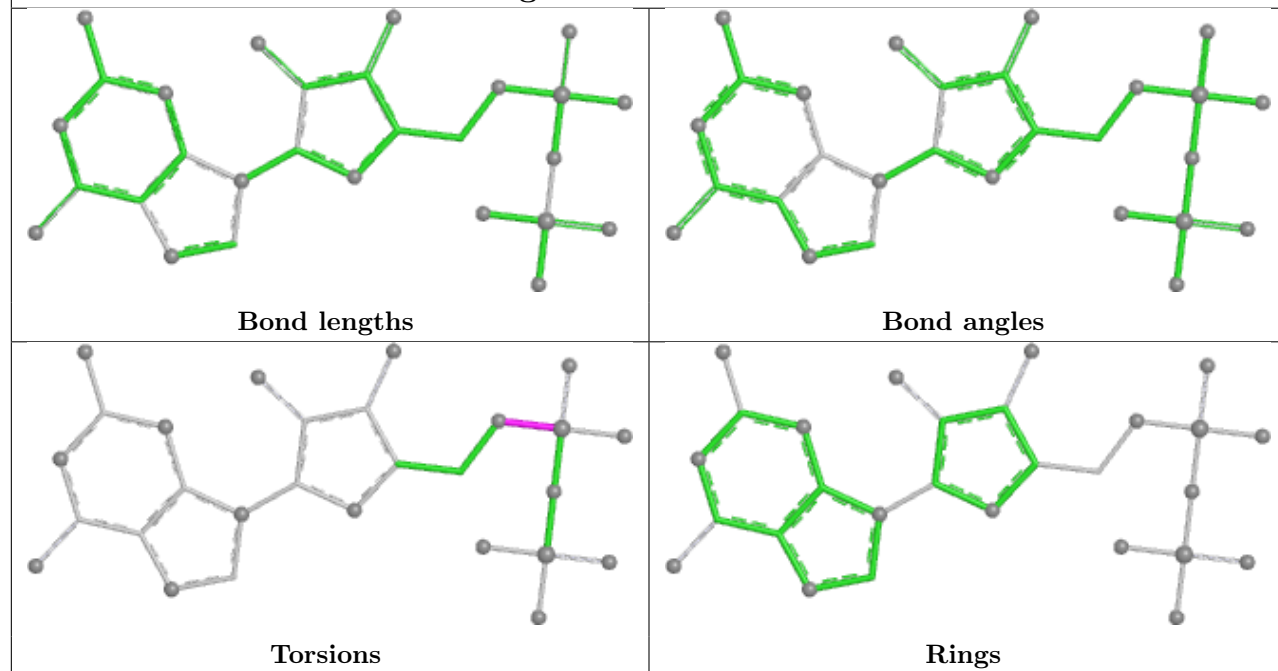
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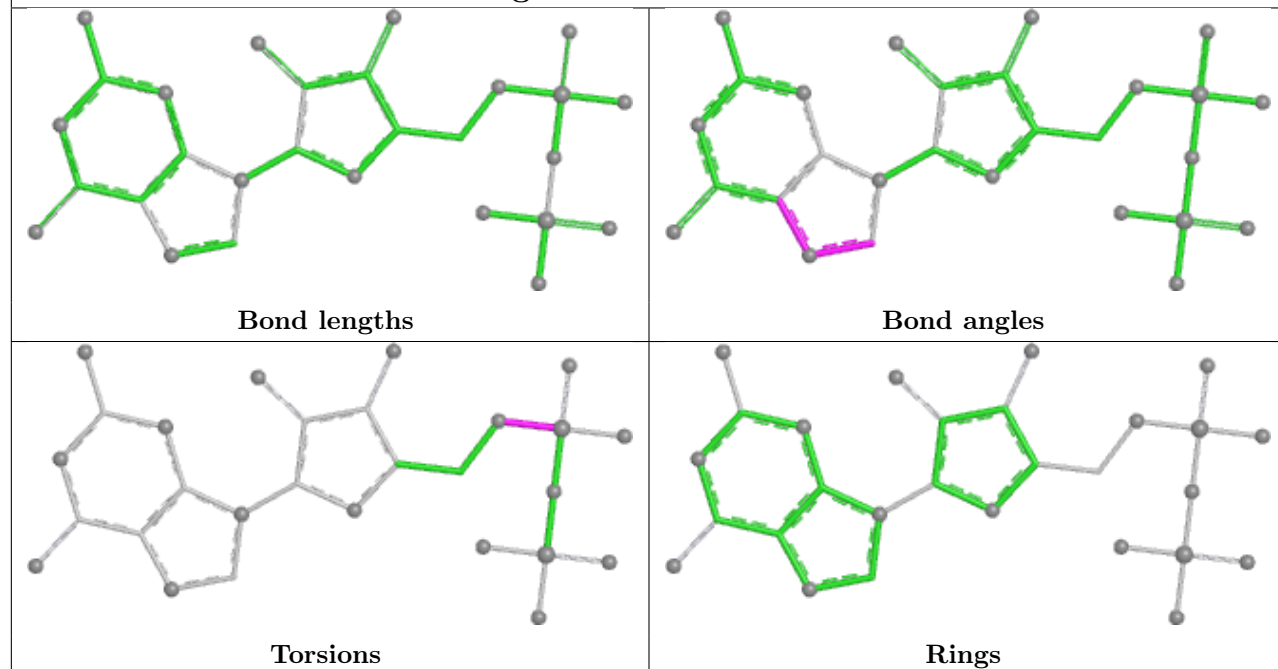
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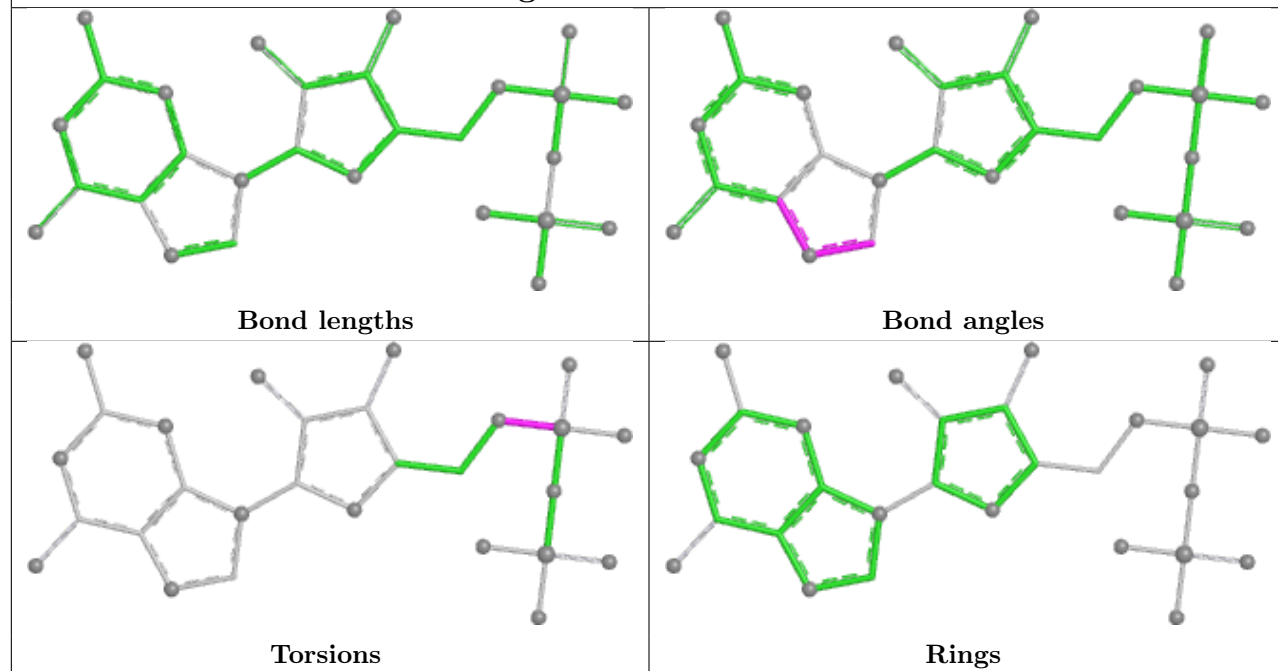
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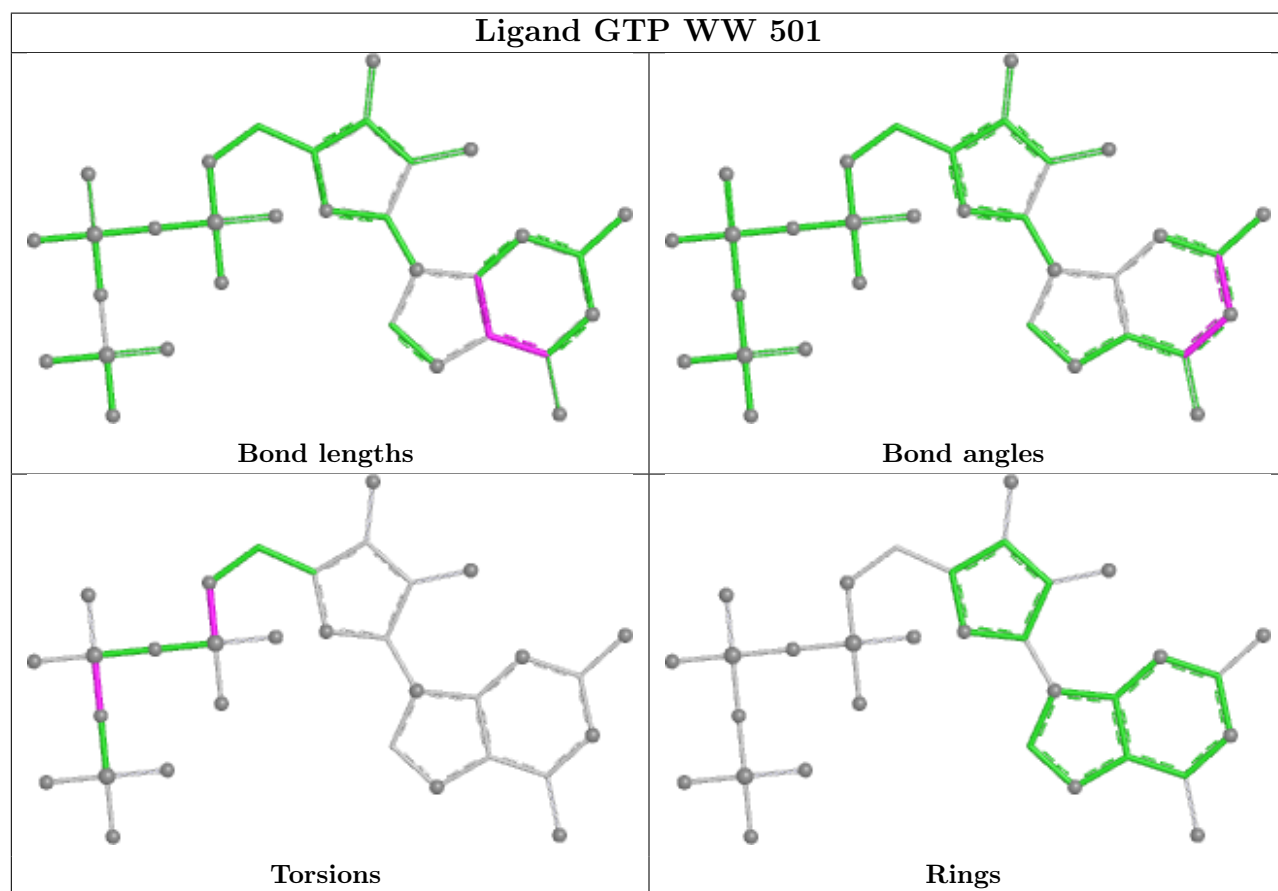
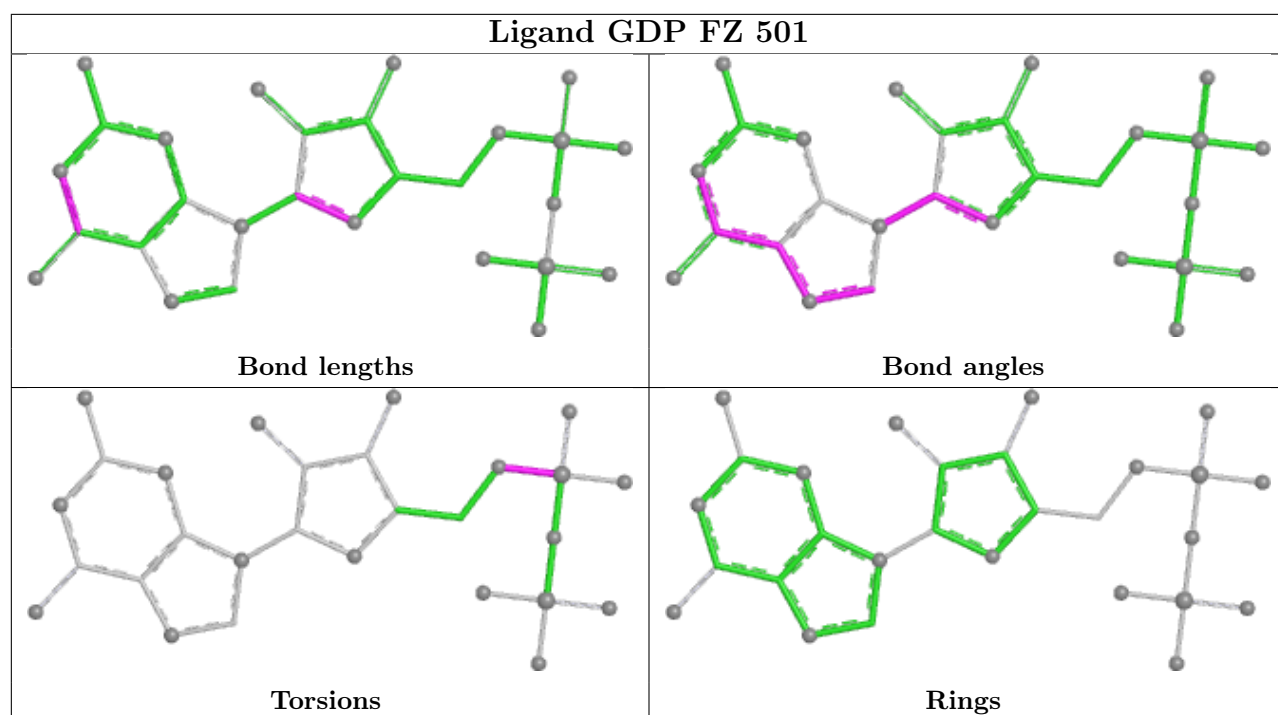
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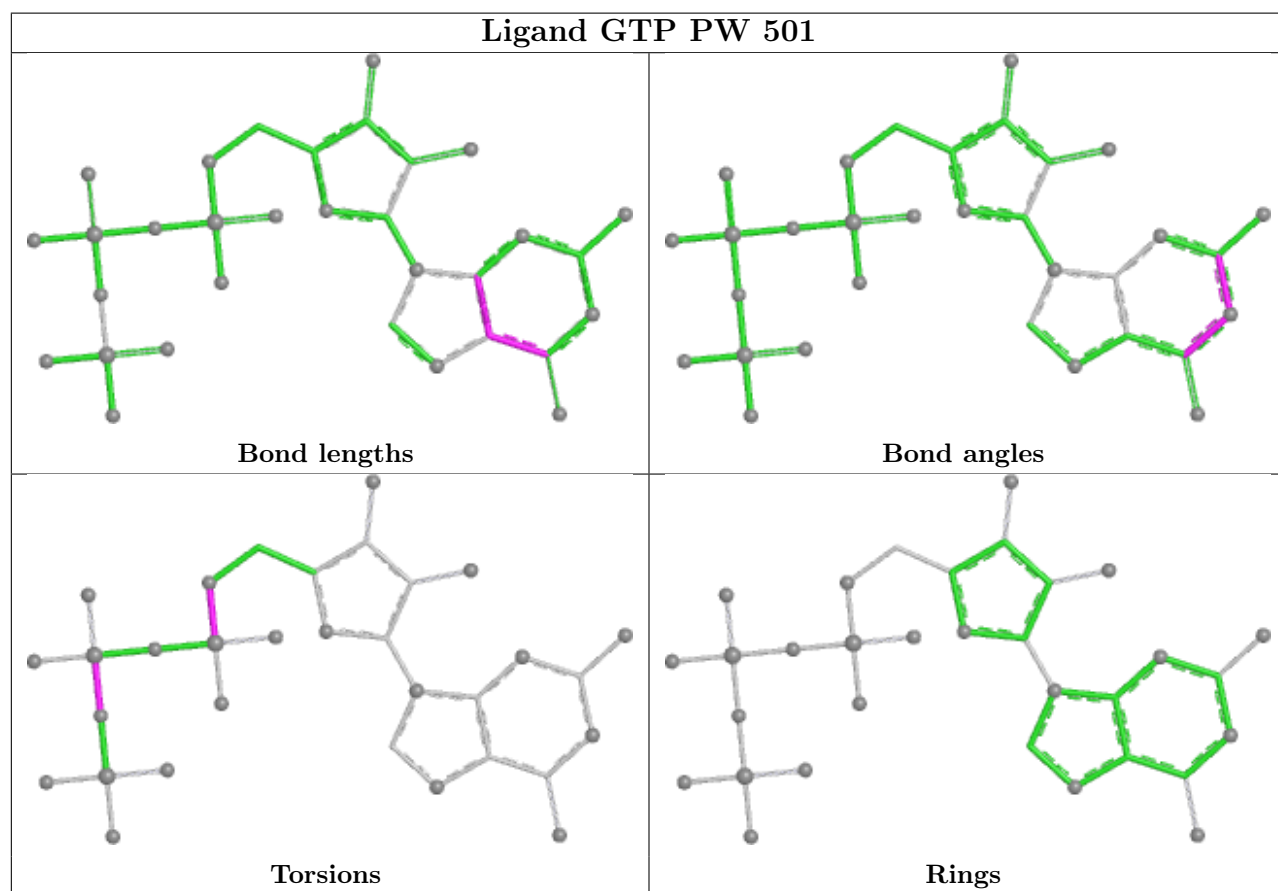
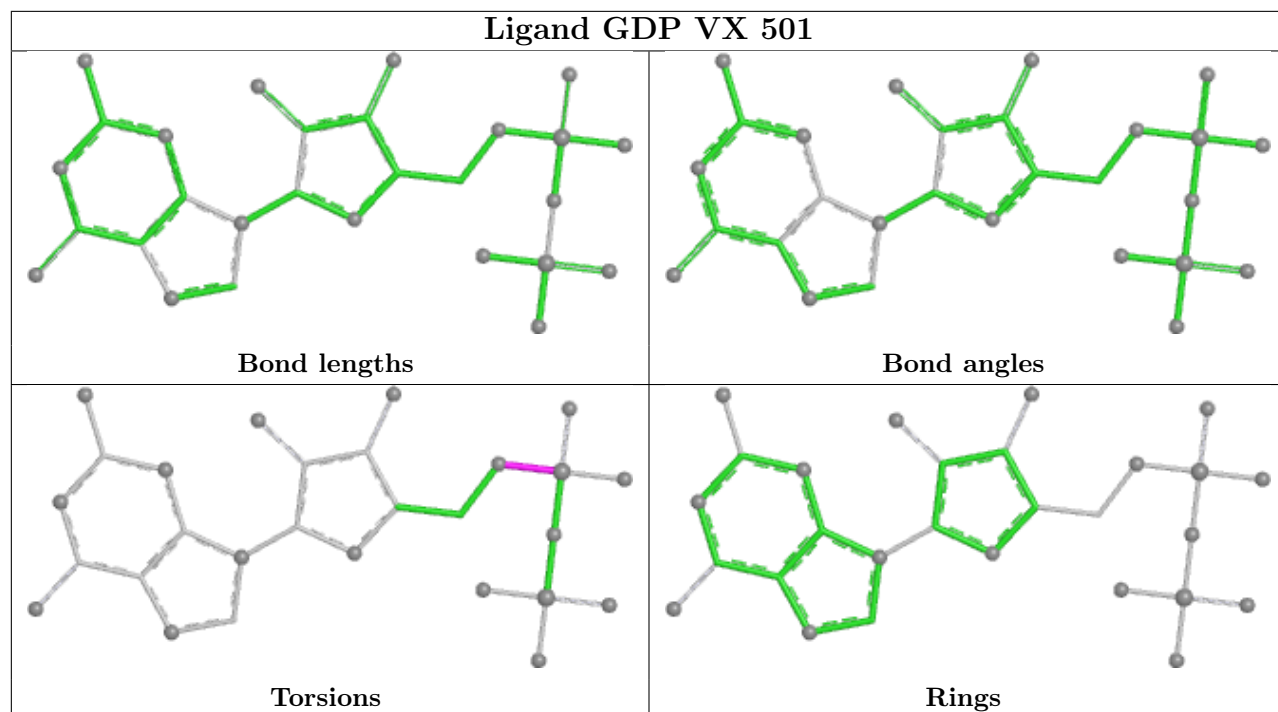


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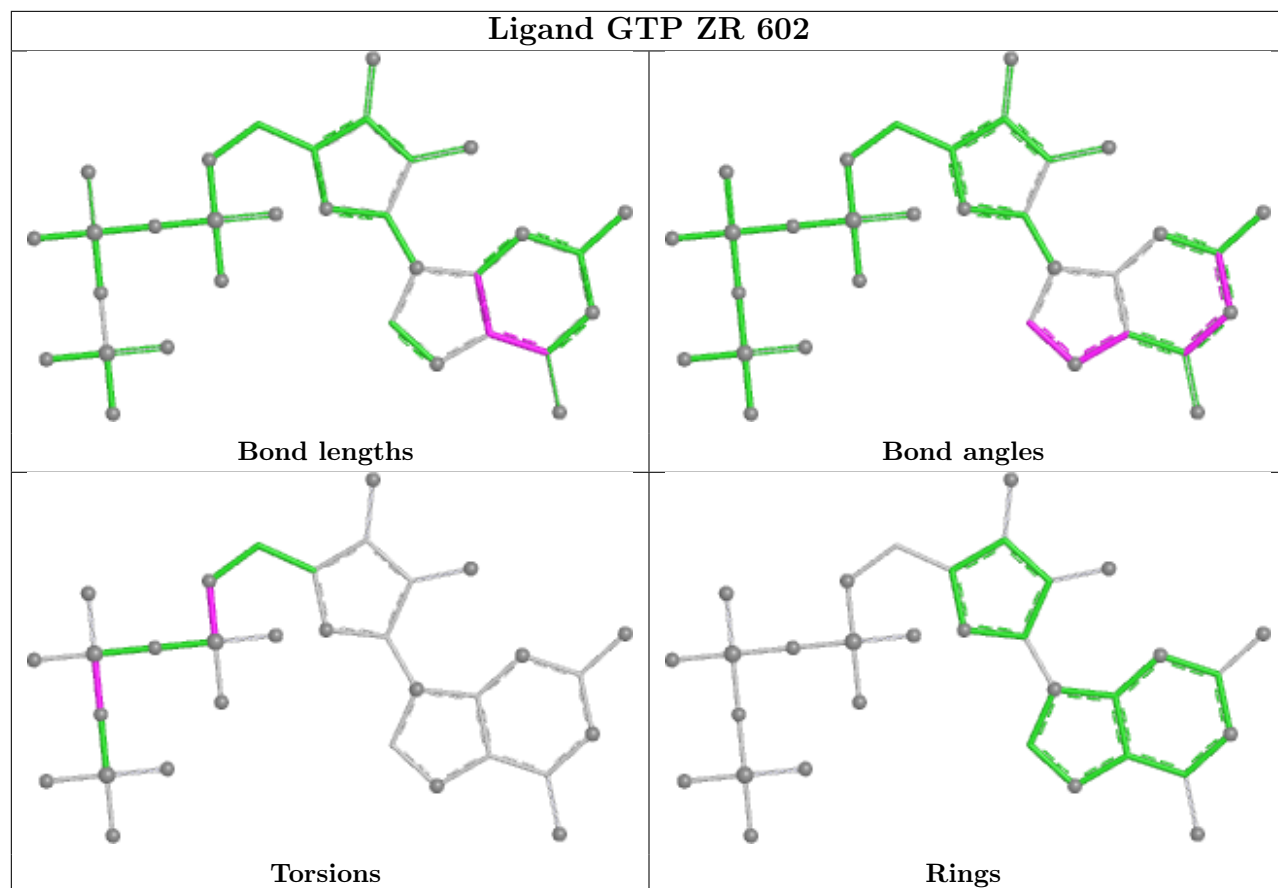




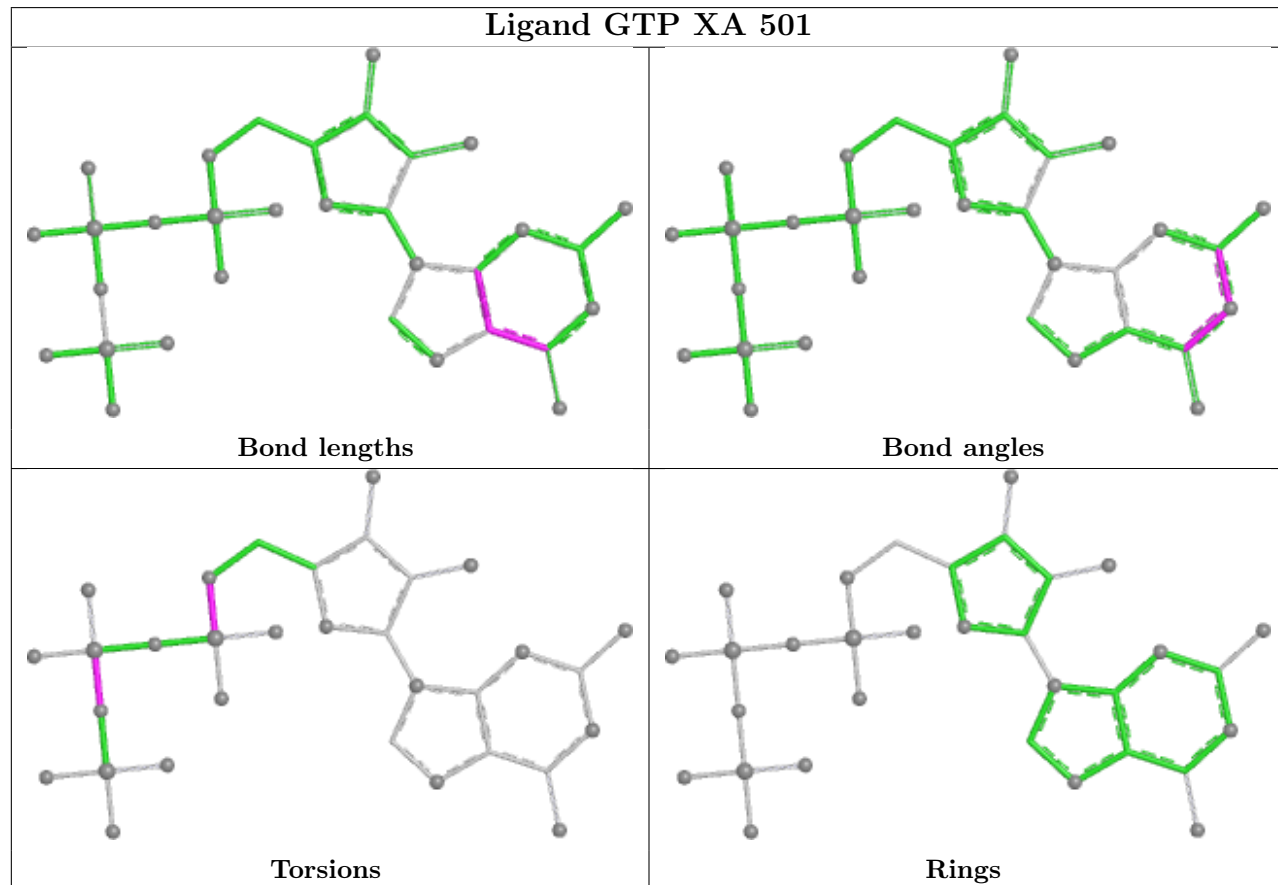




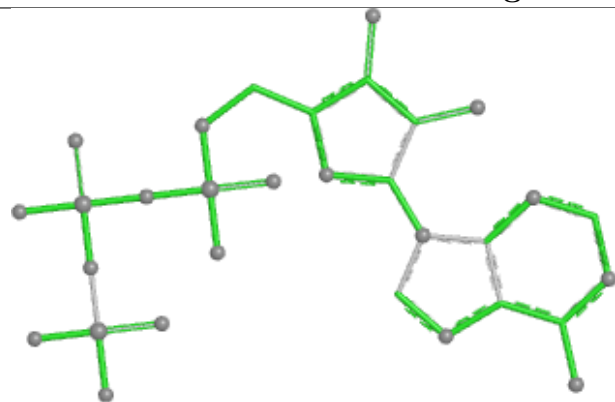
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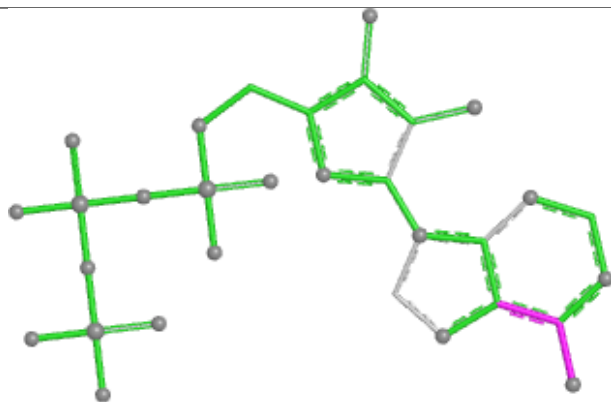
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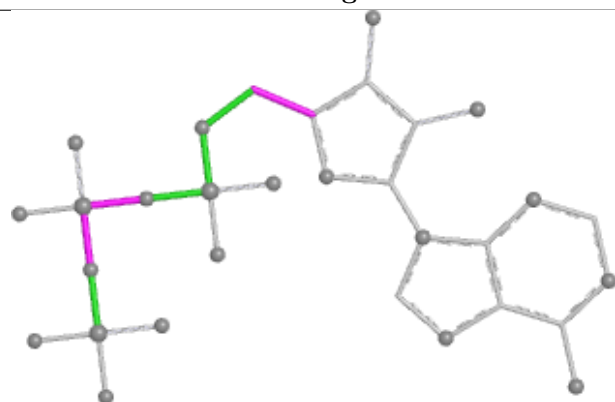
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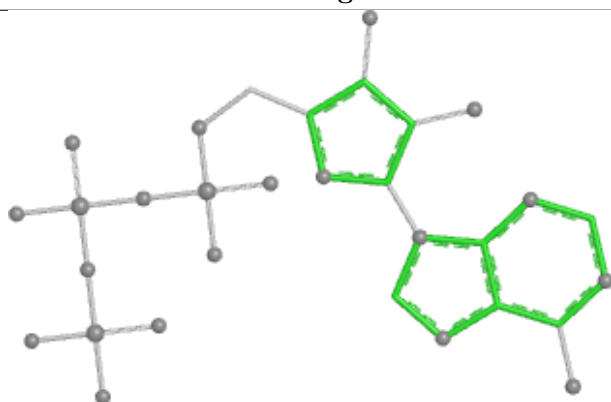
Bond lengths



Bond angles

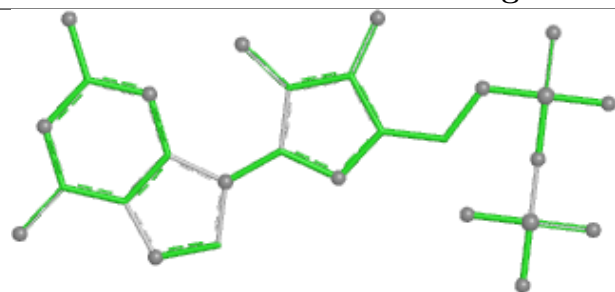


Torsions

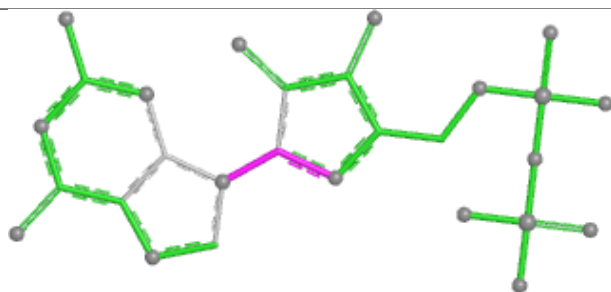


Rings

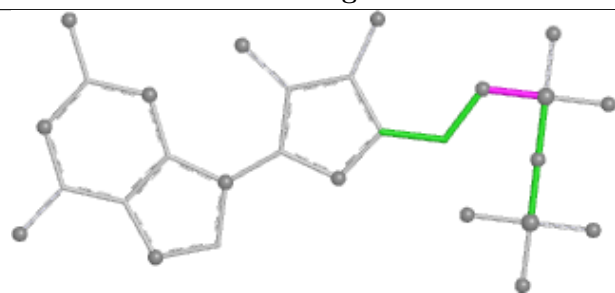
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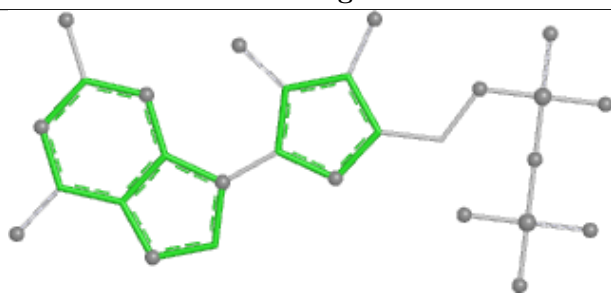
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Bond angles

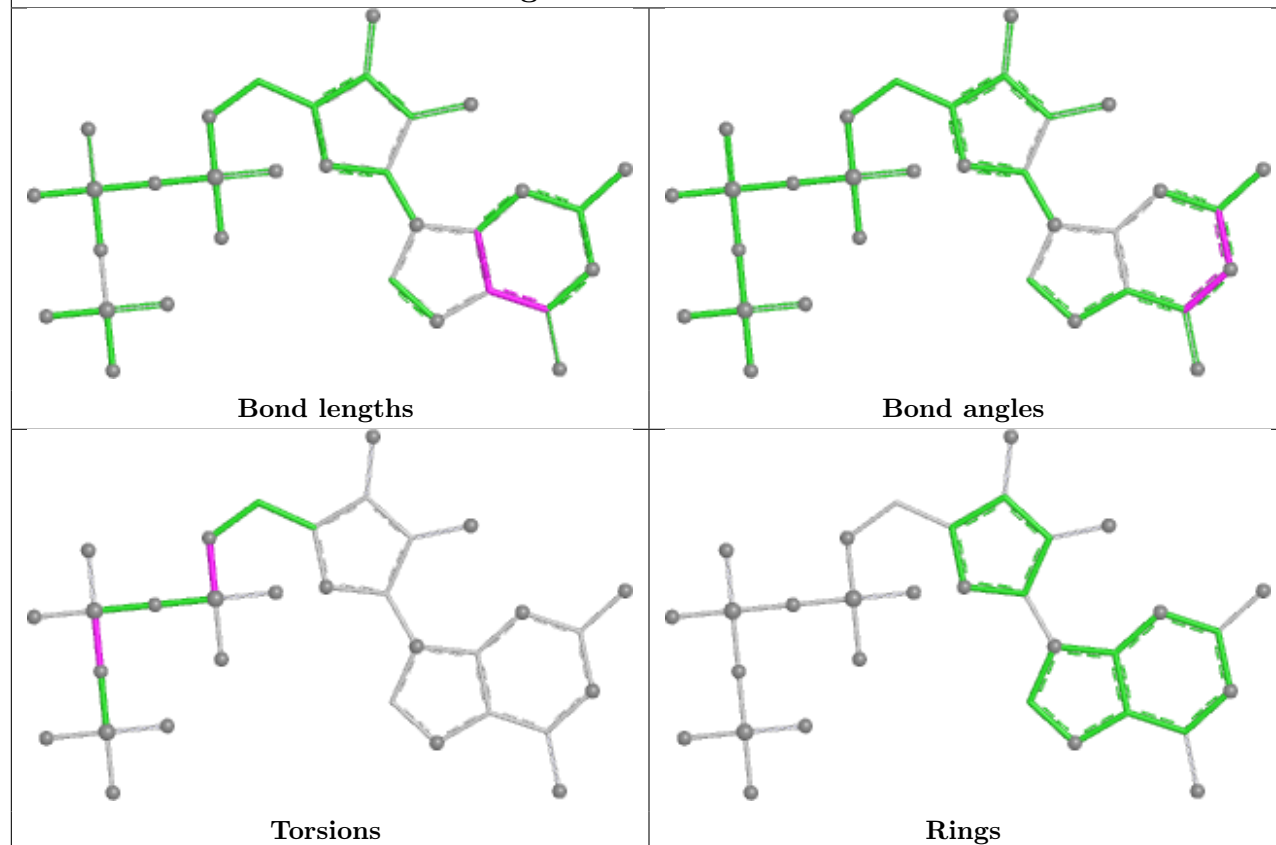


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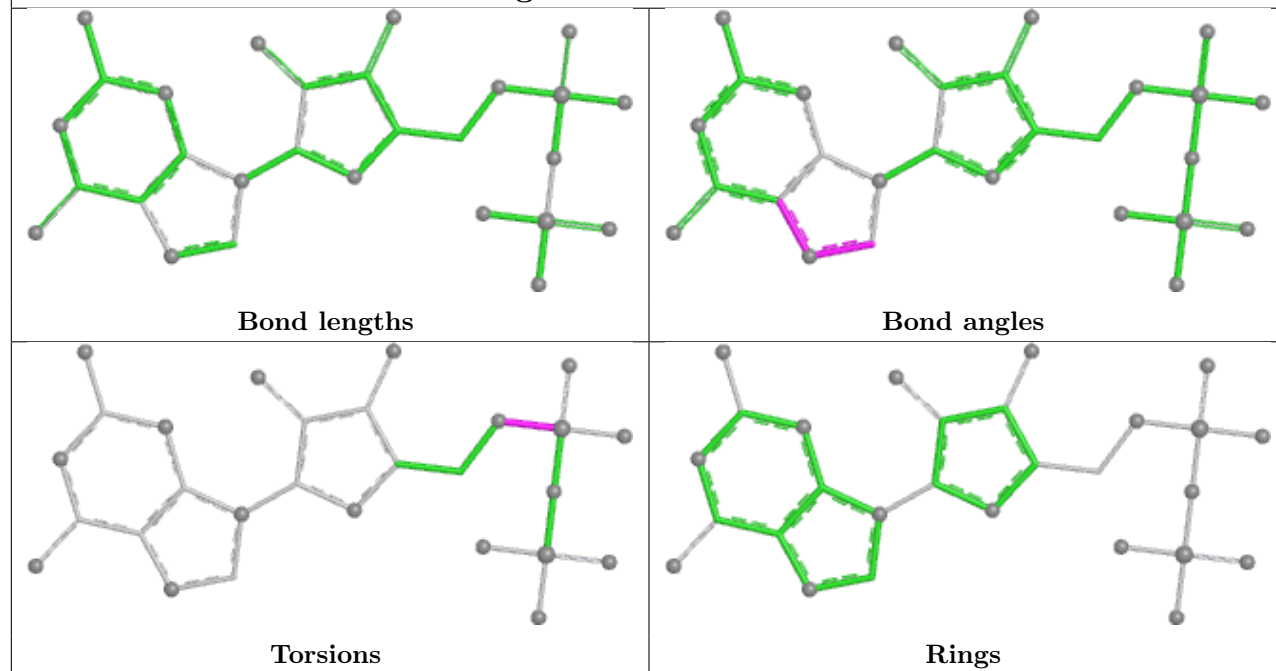


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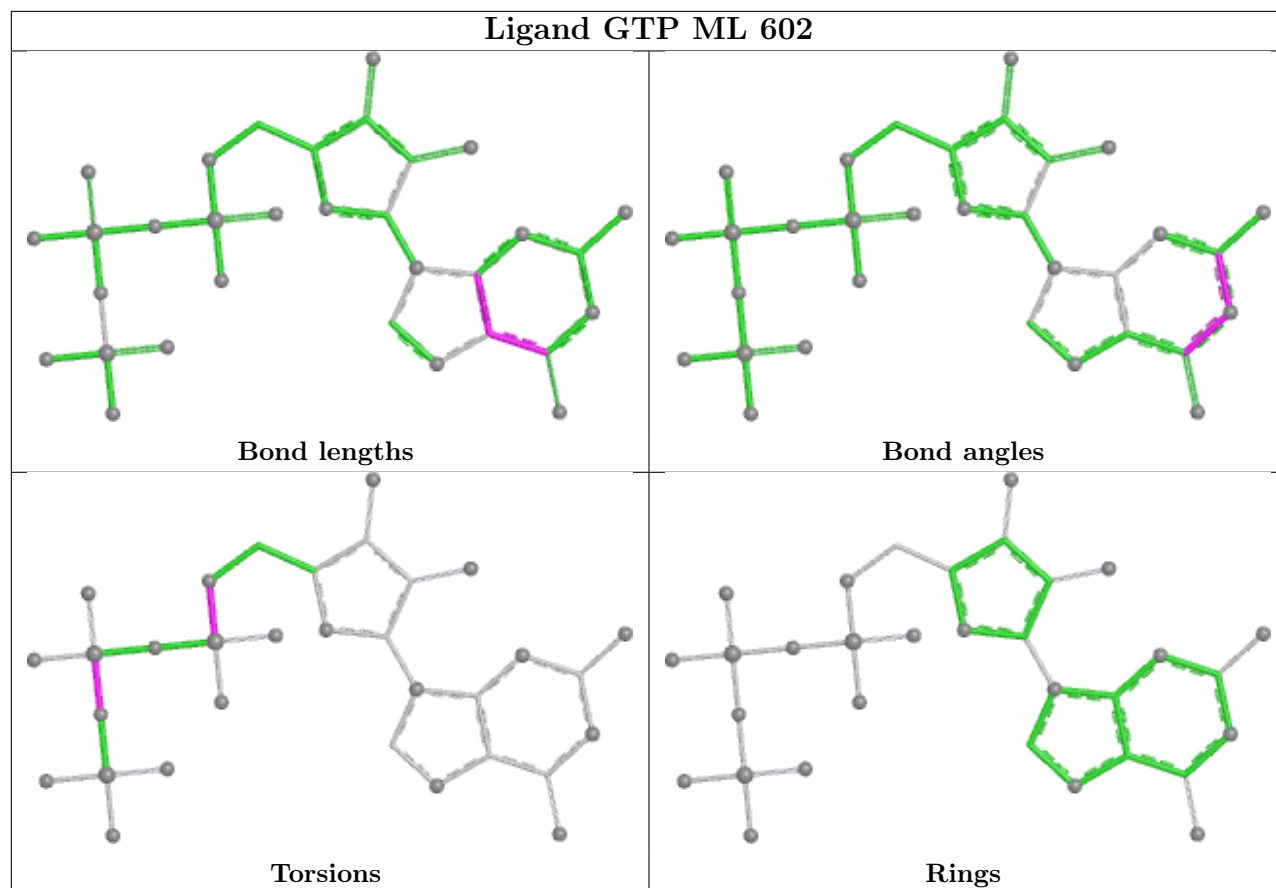
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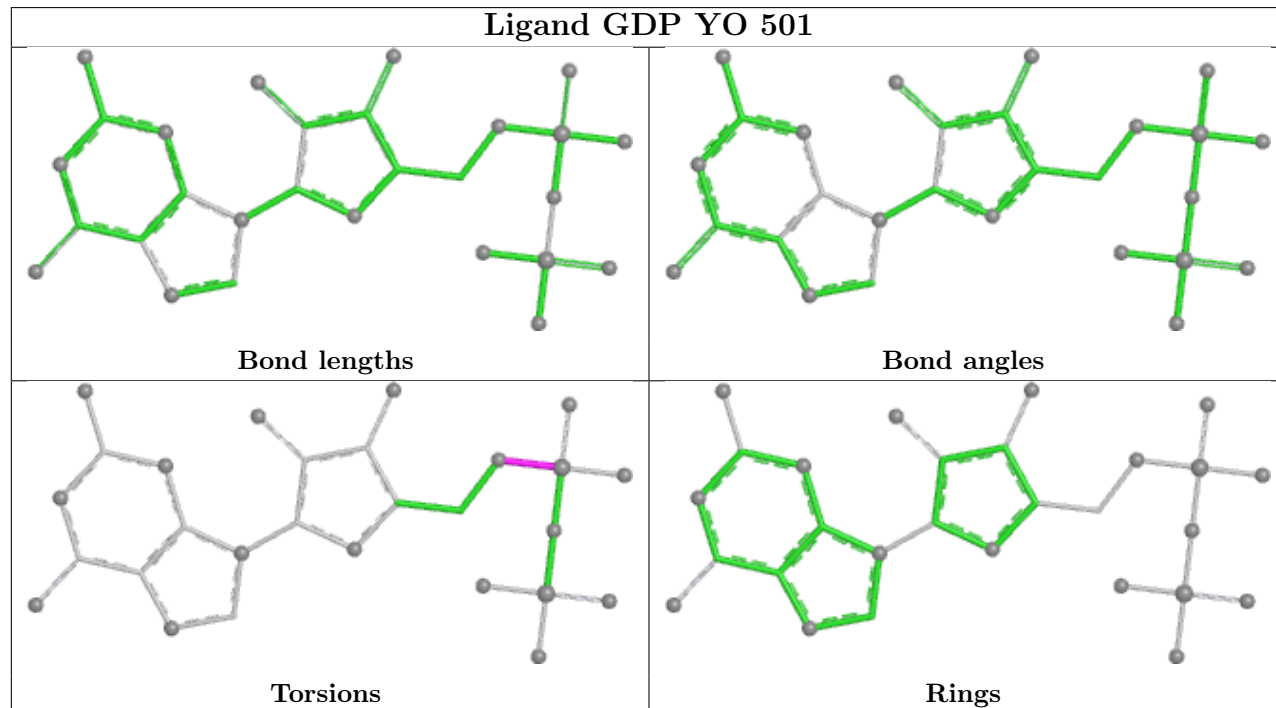
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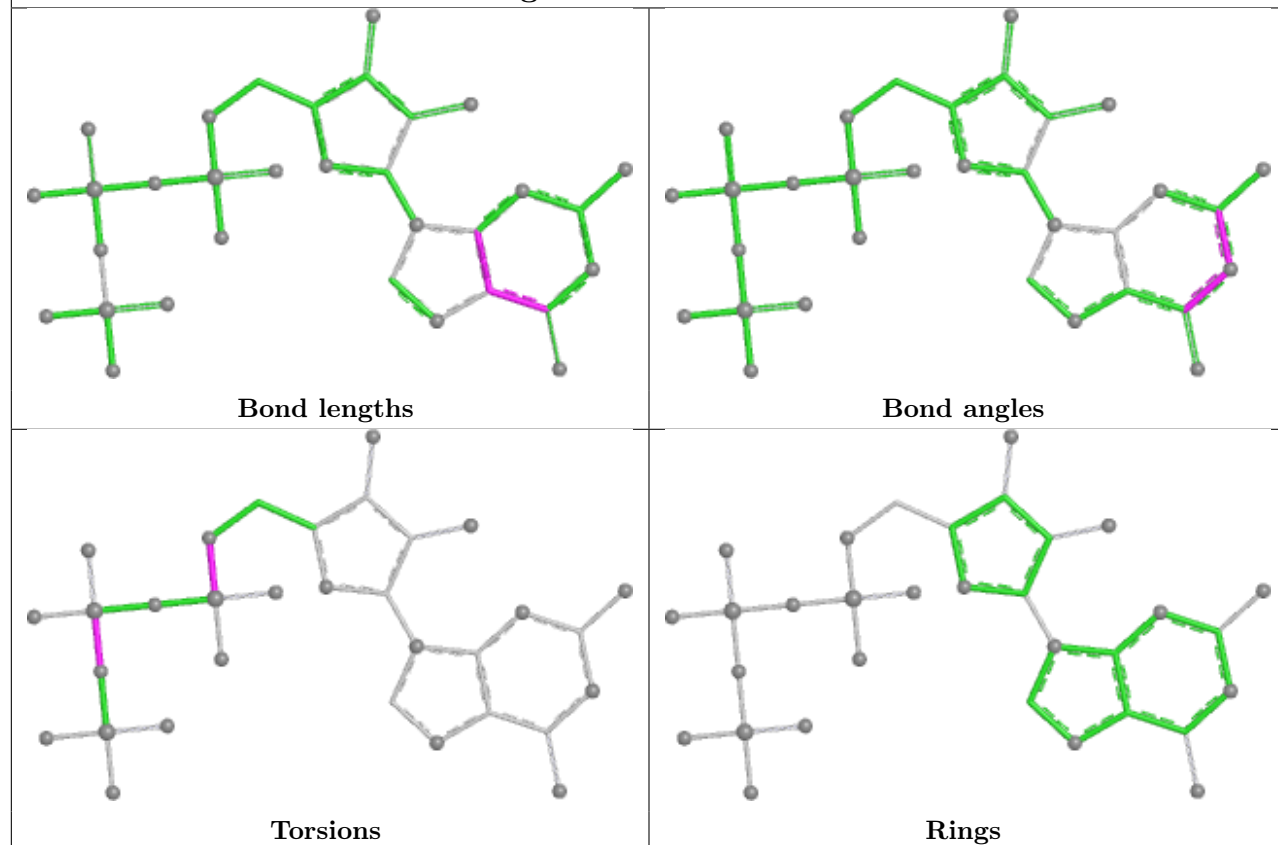
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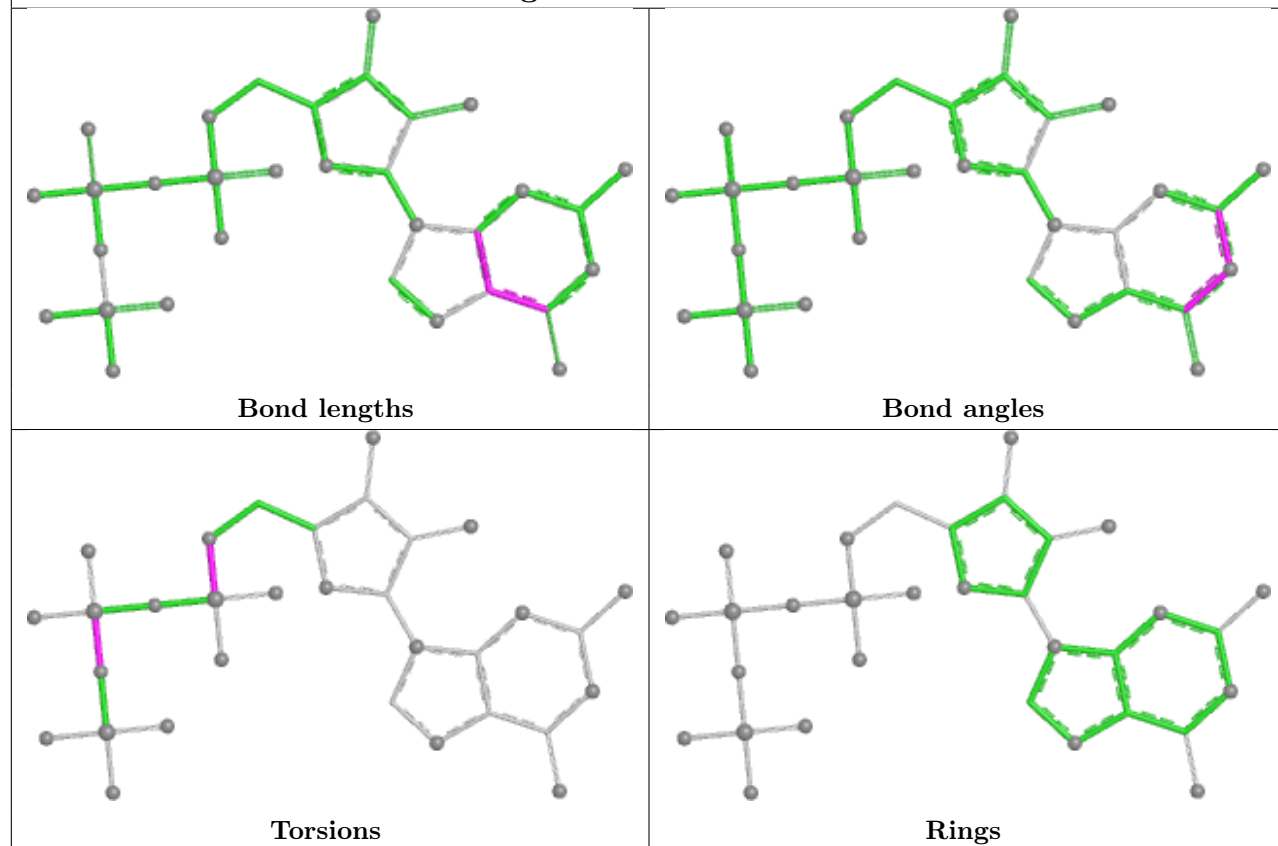
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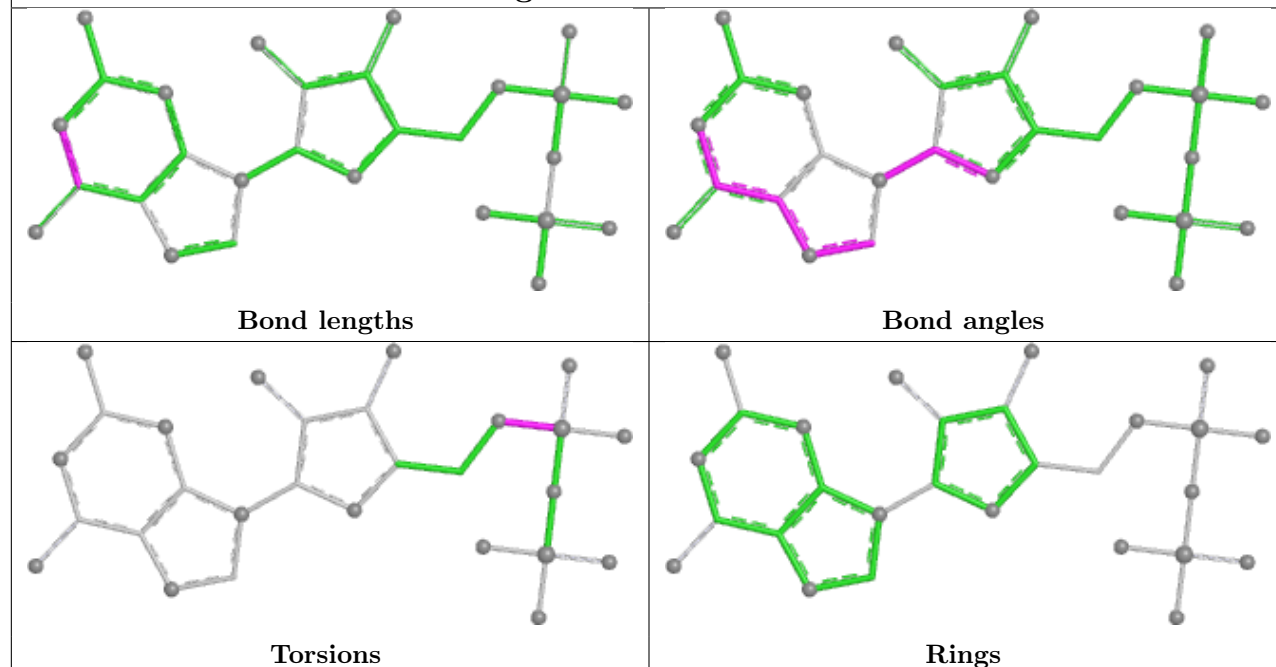
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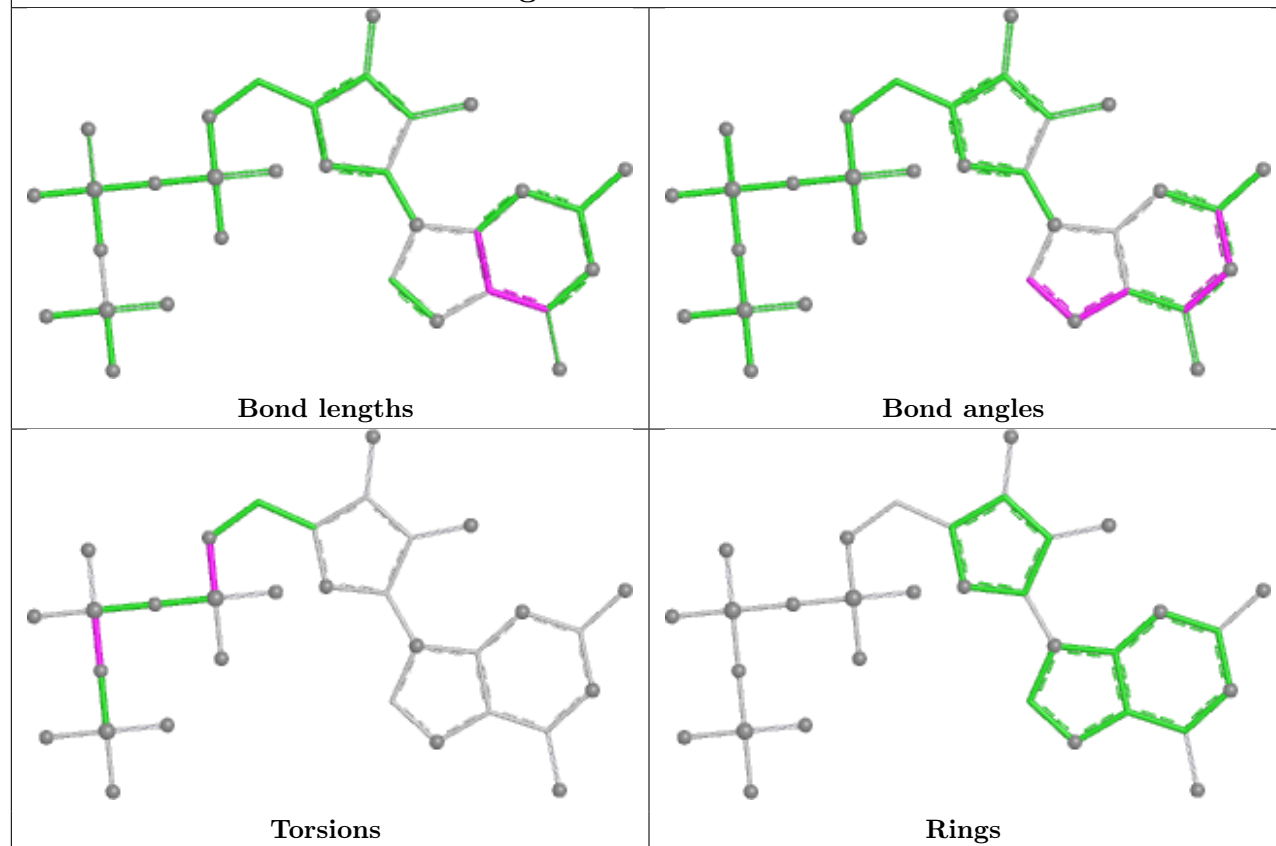
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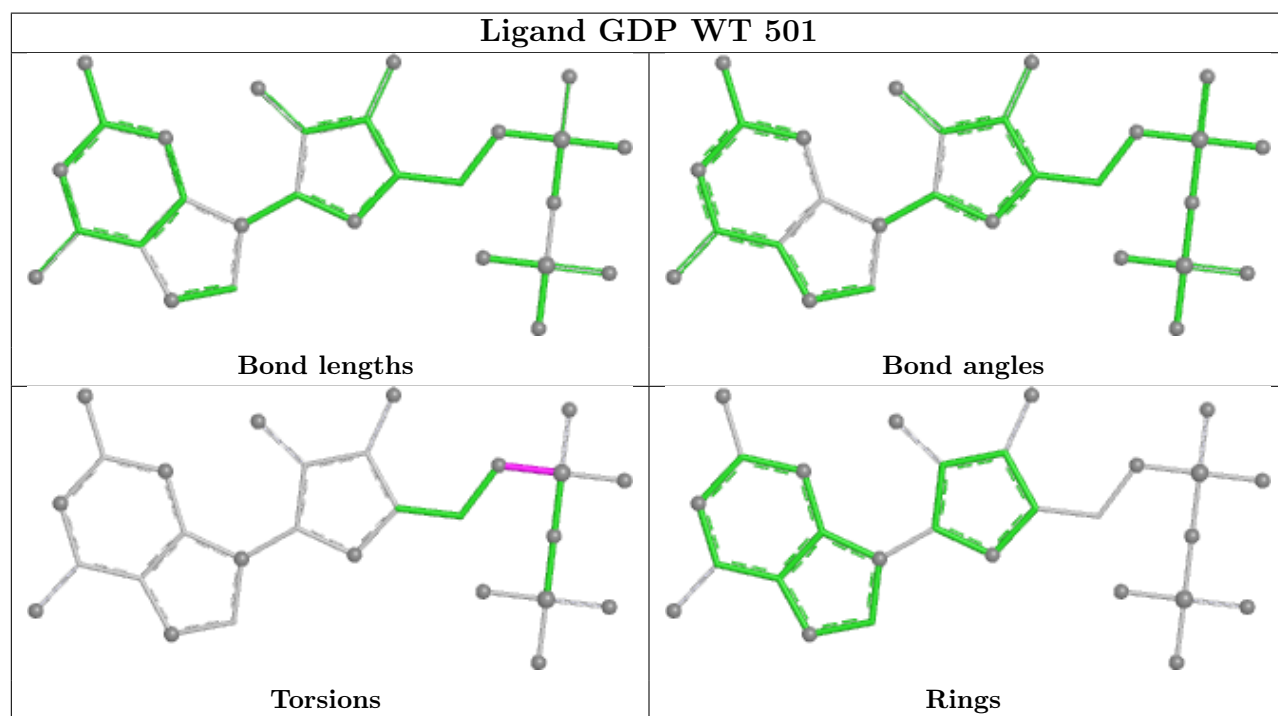
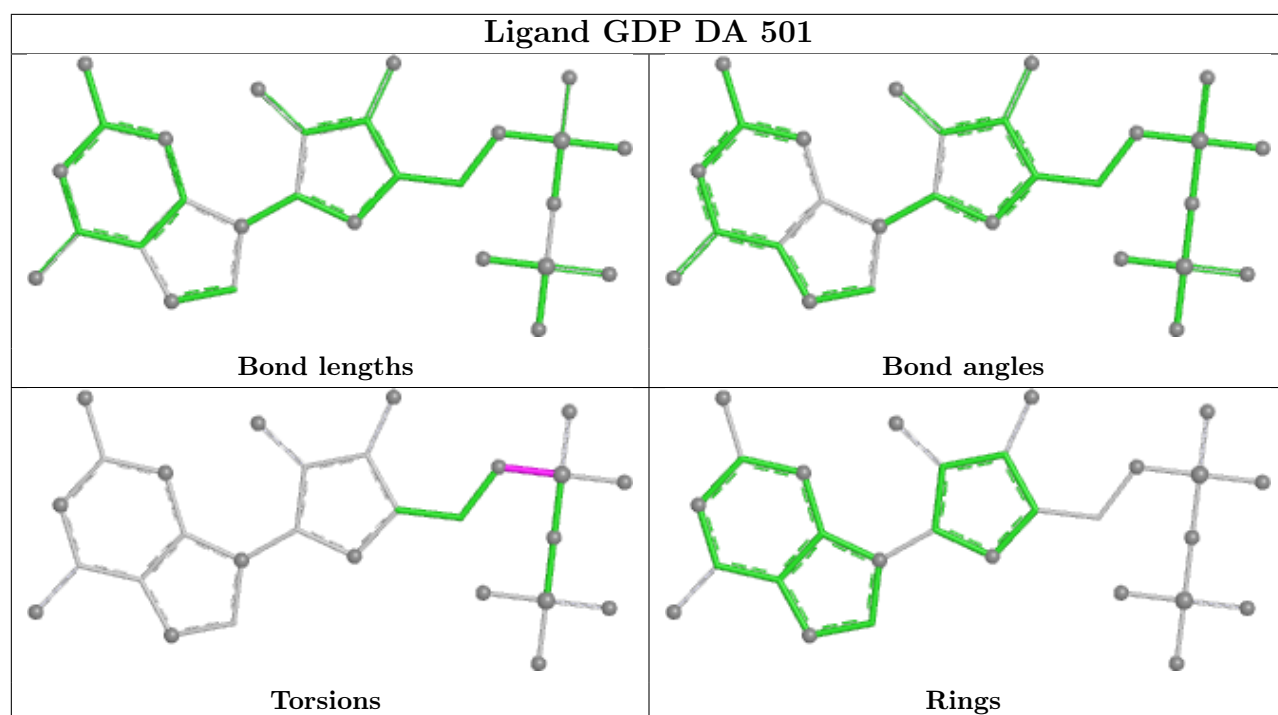
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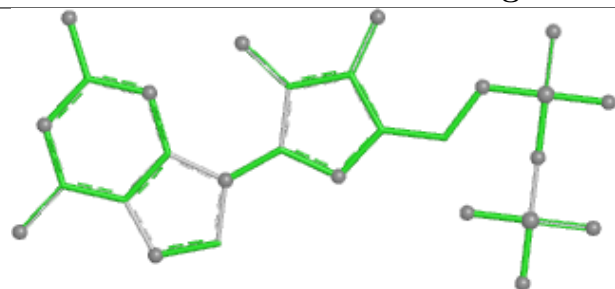
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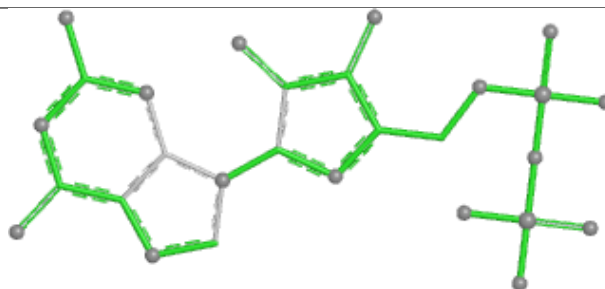




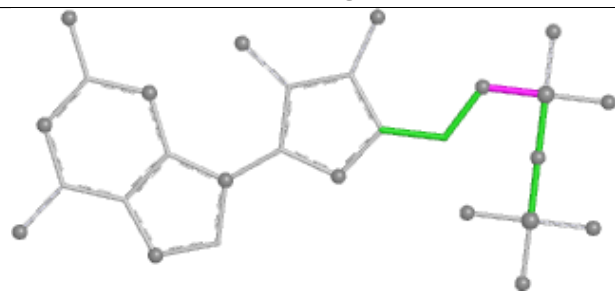
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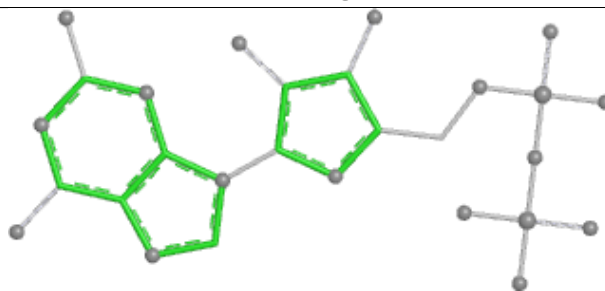
Bond lengths



Bond angles

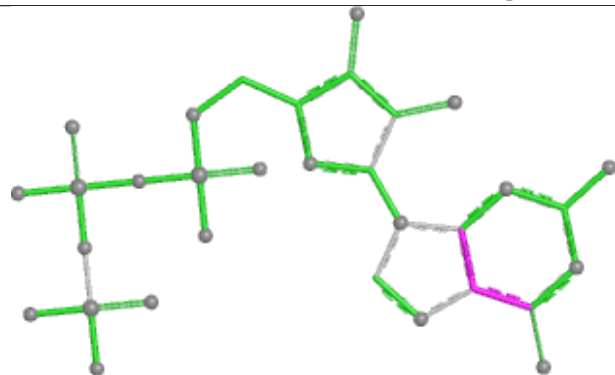


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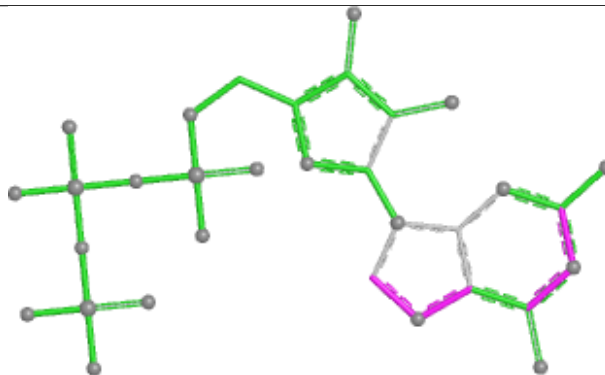


Rings

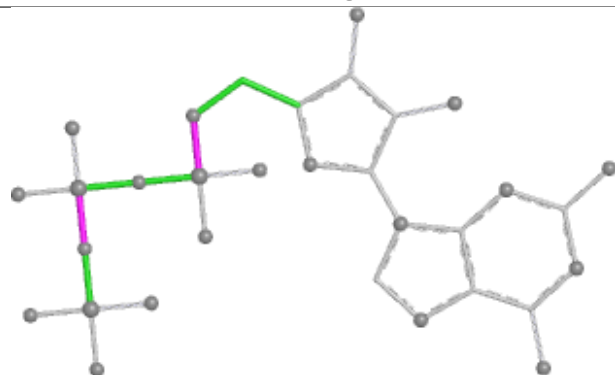
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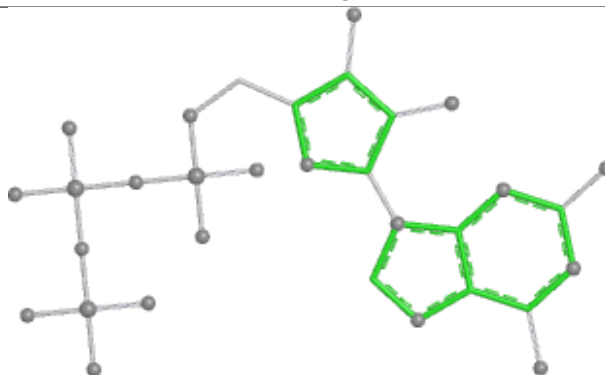
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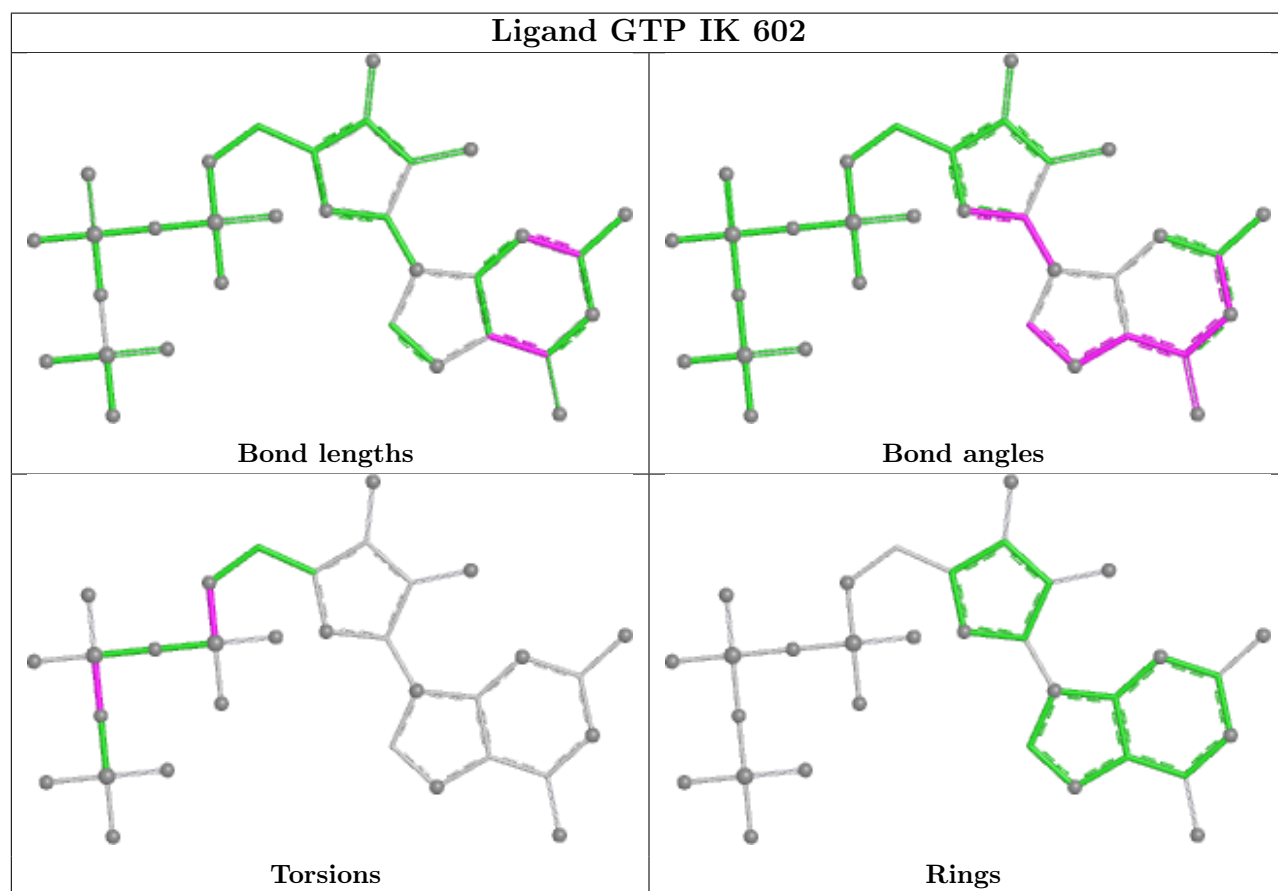
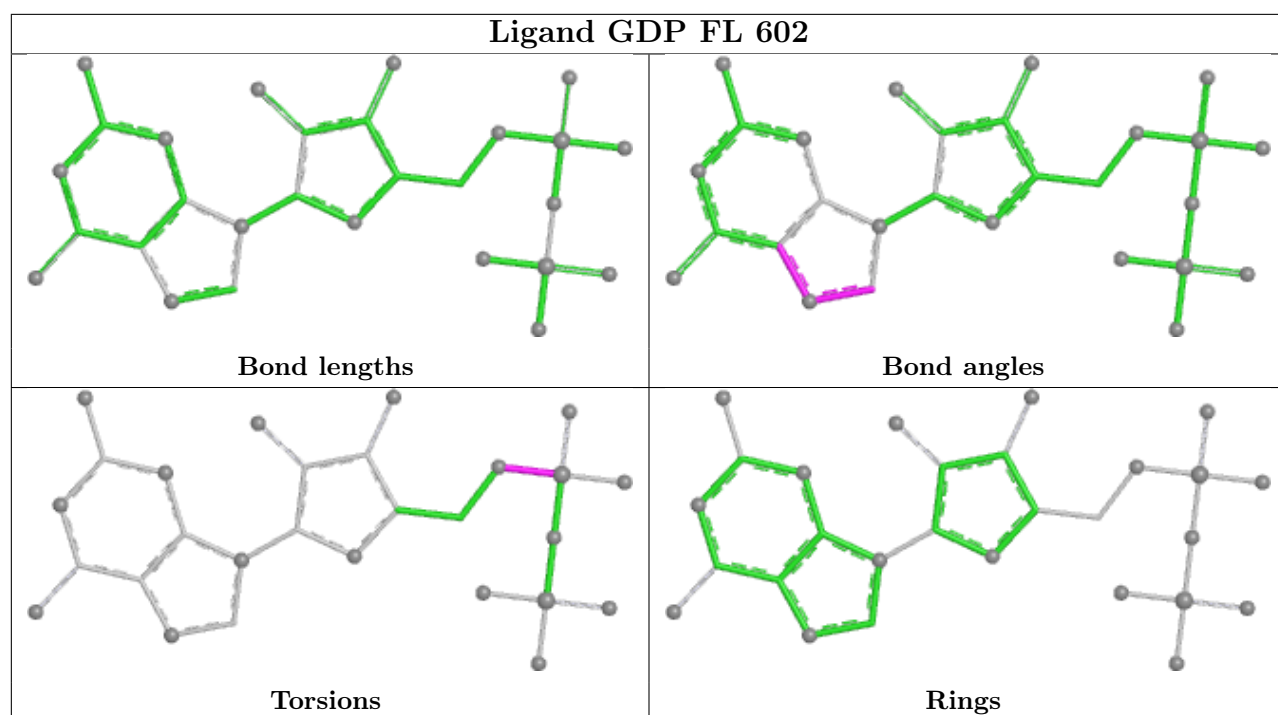
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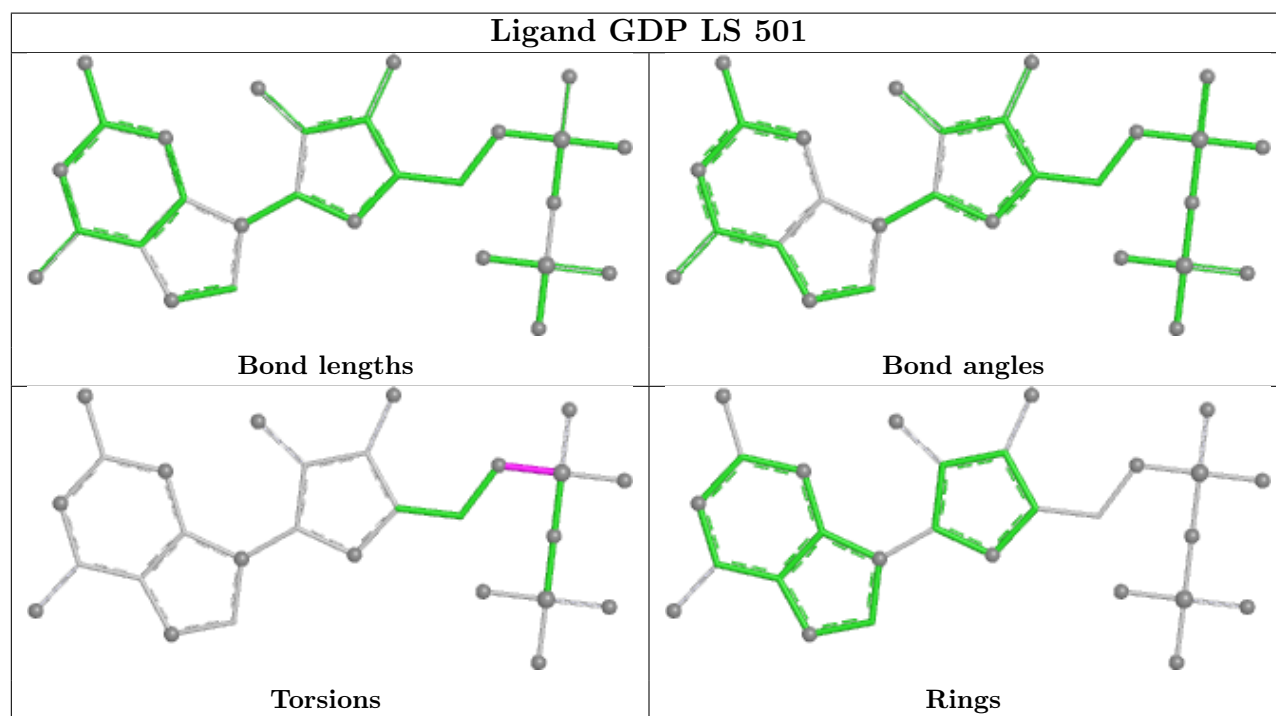
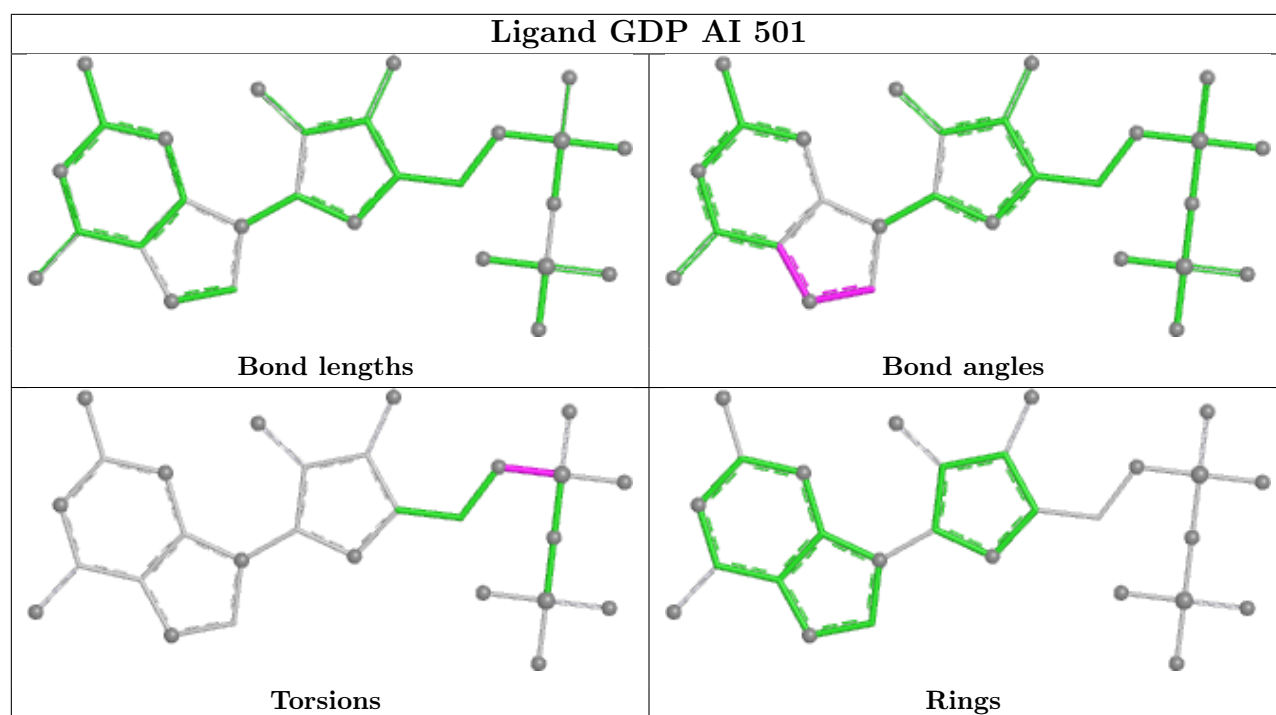


Torsions

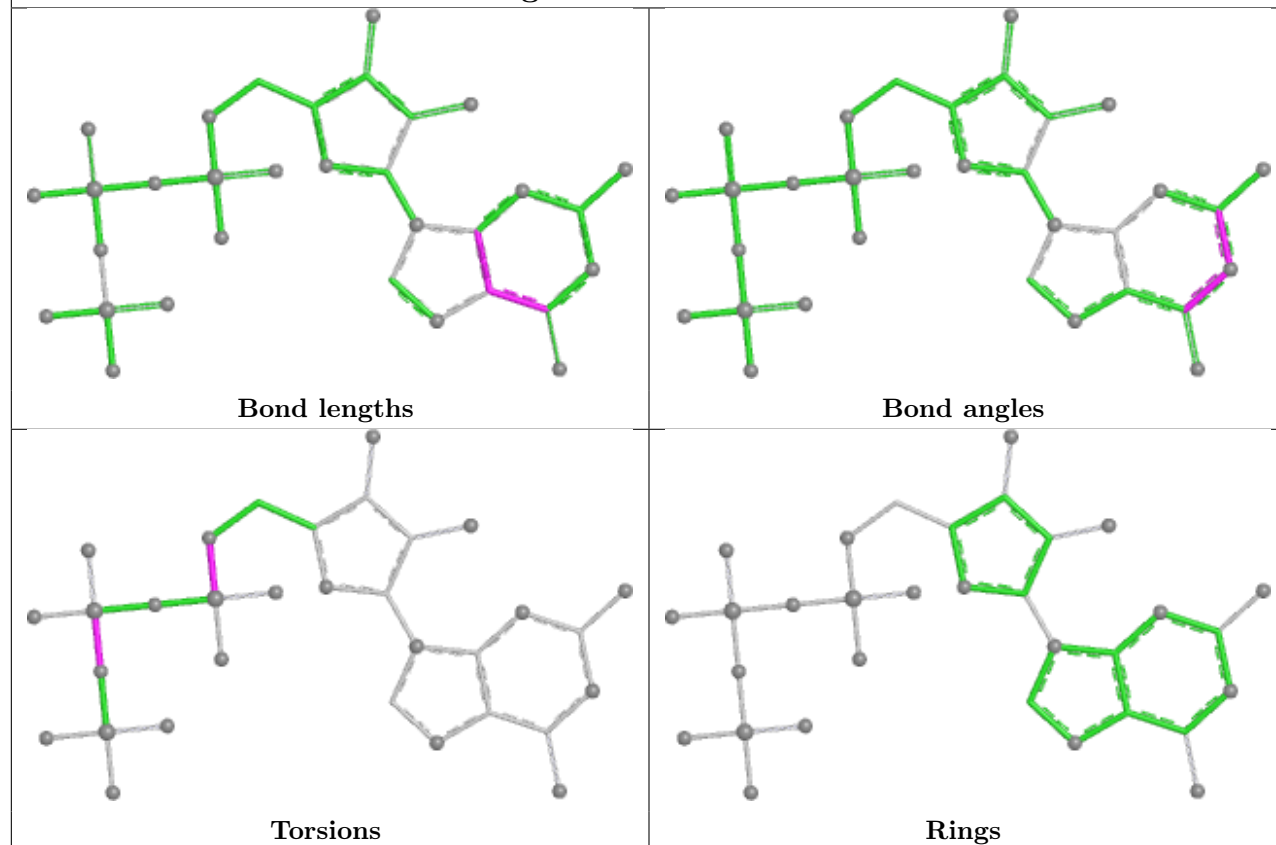


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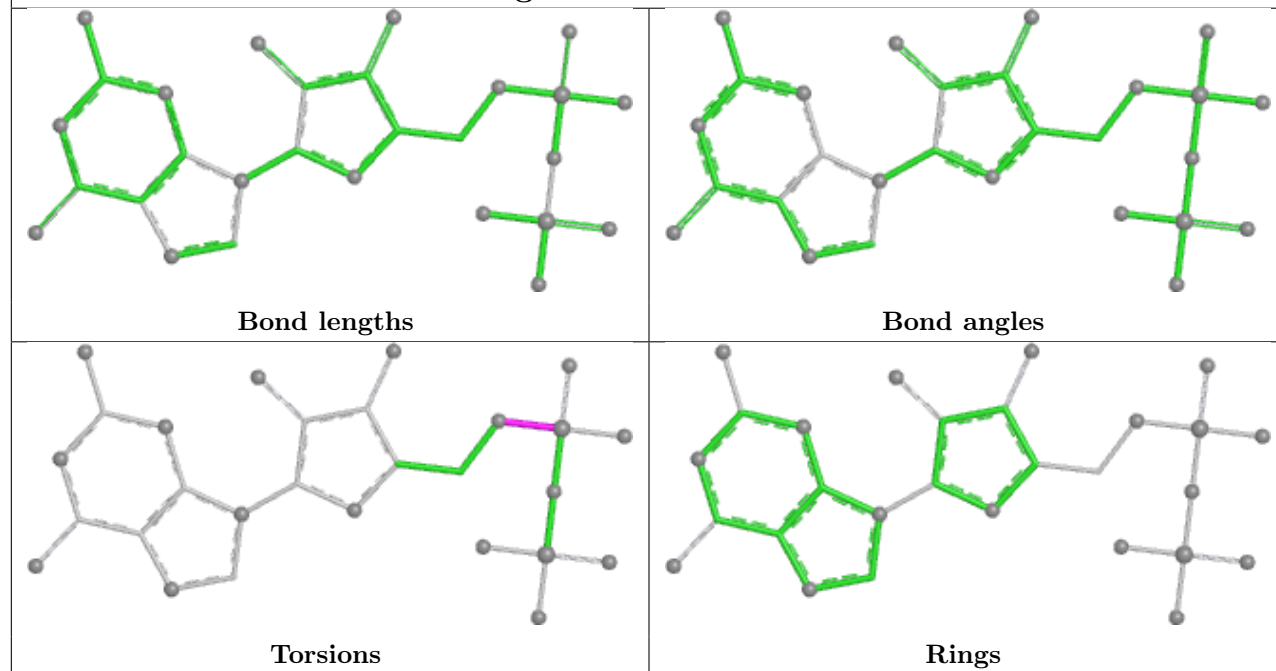




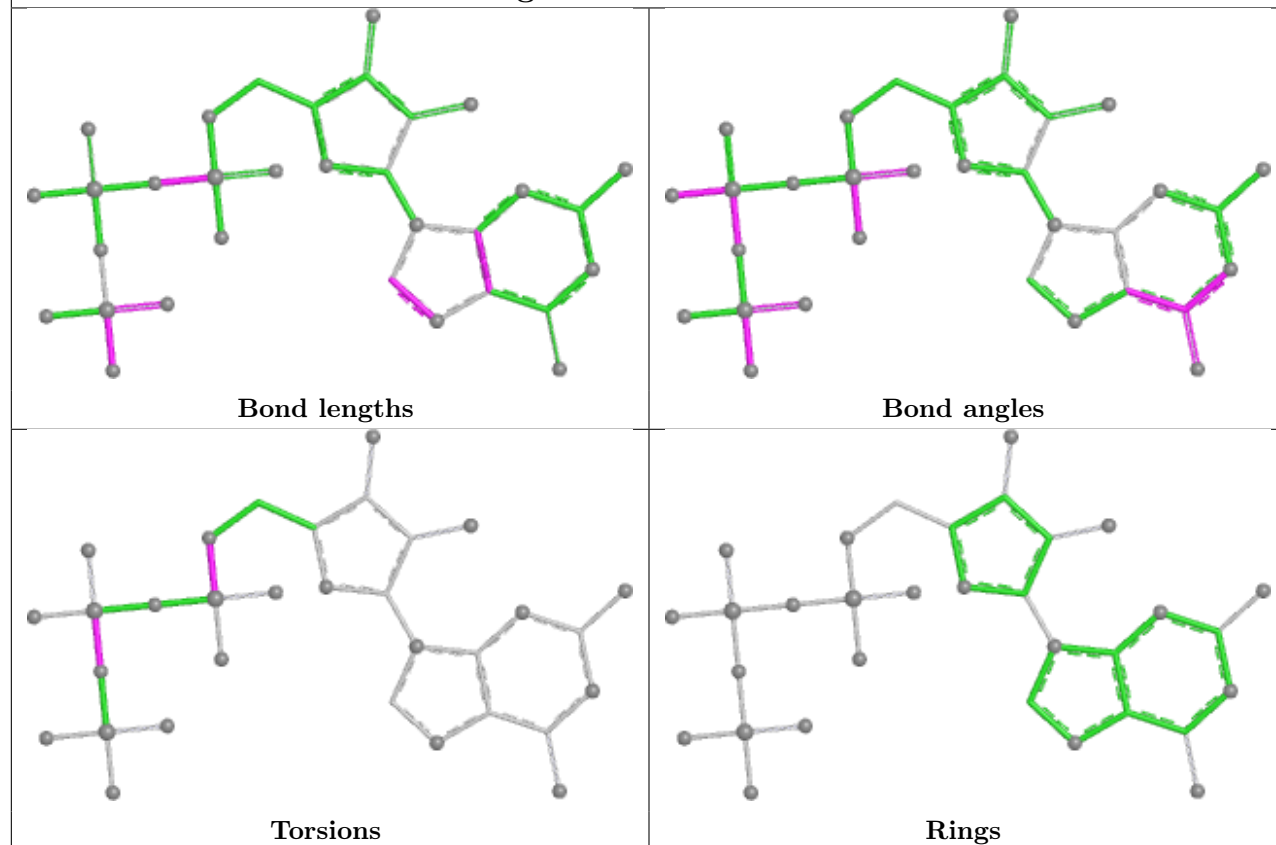
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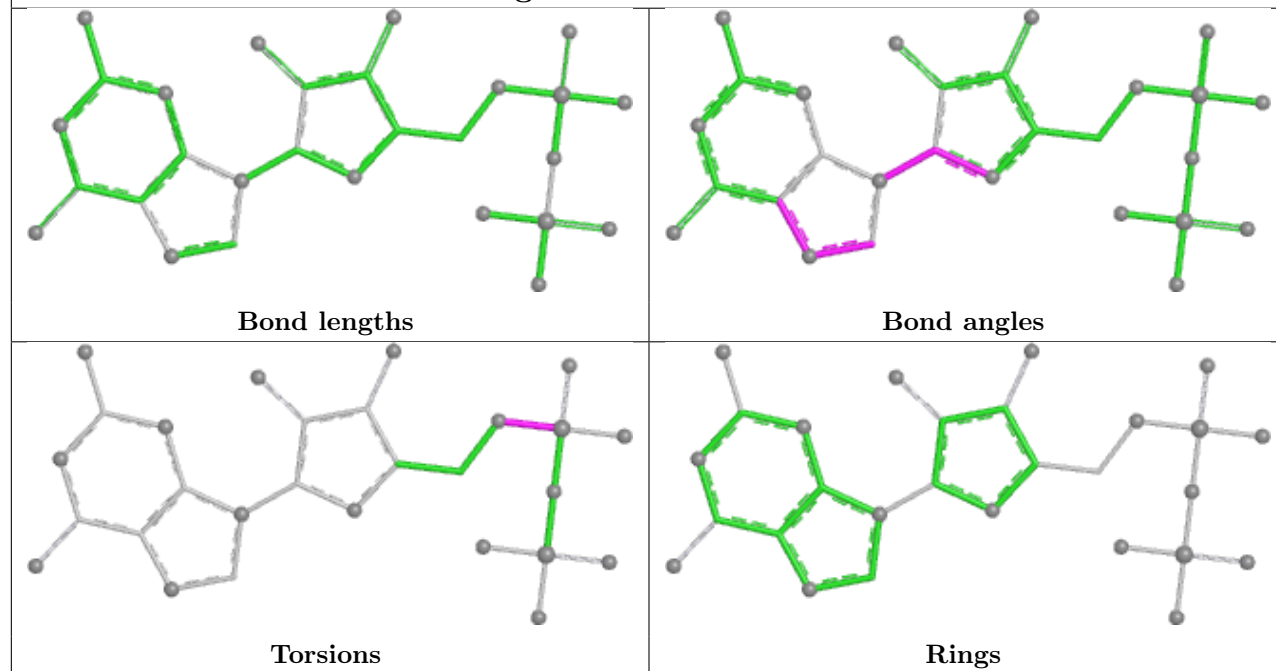
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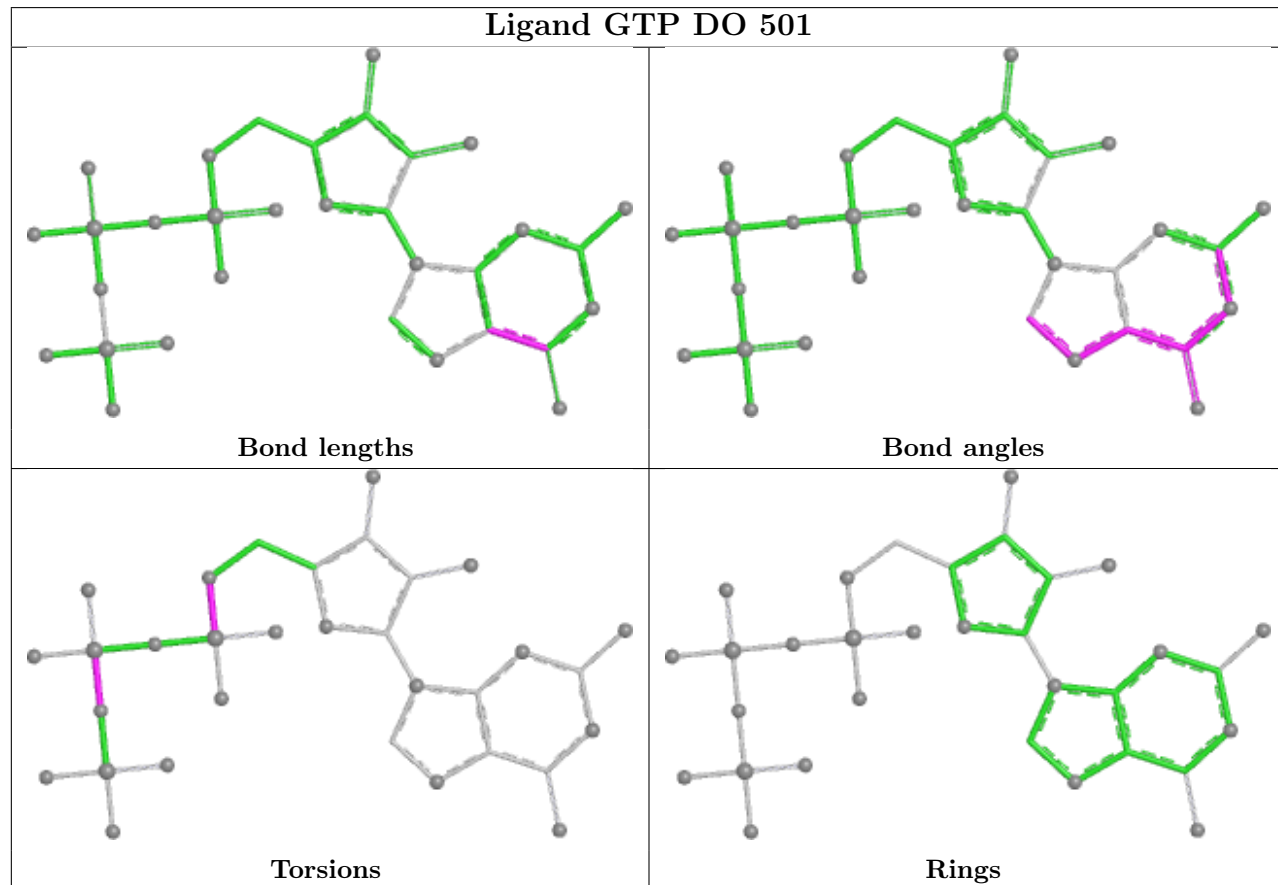
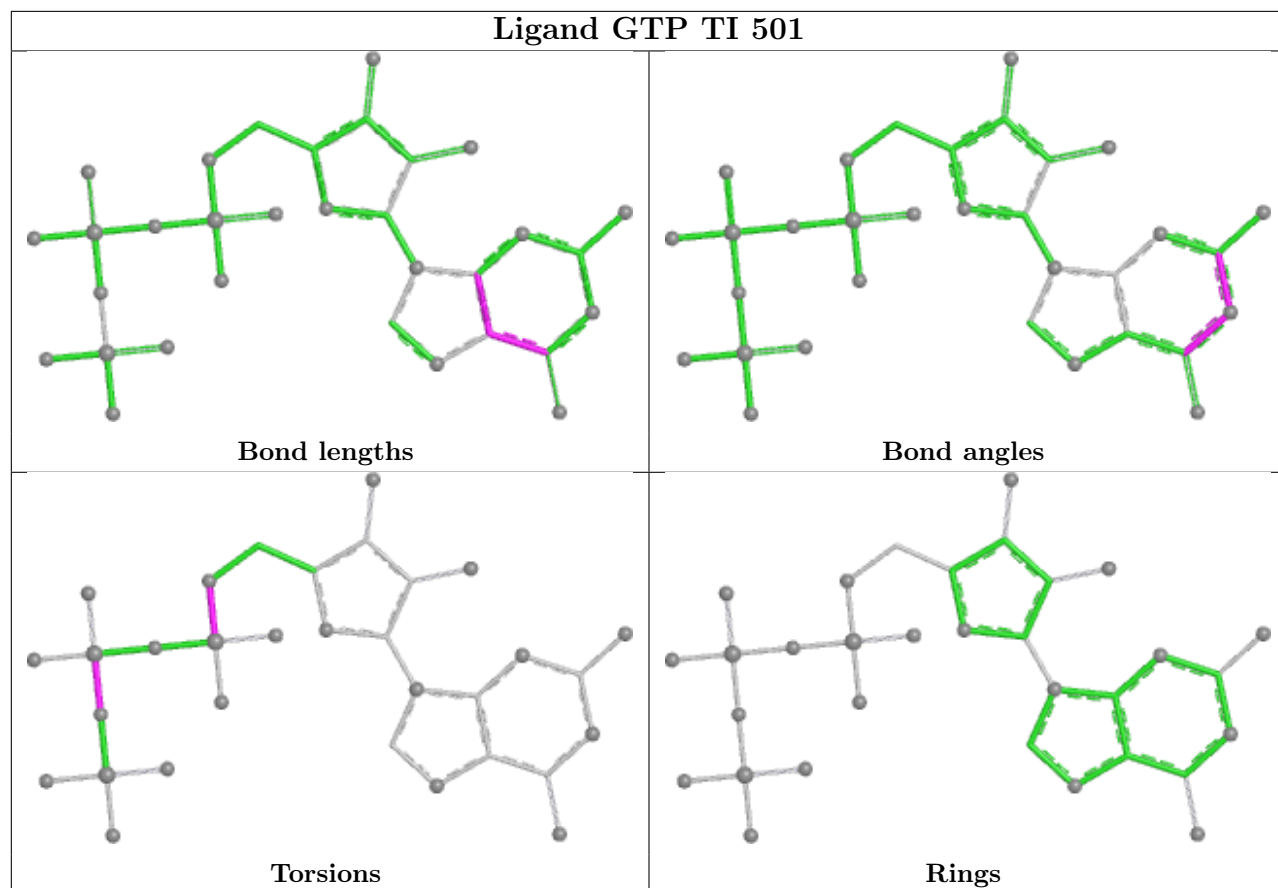


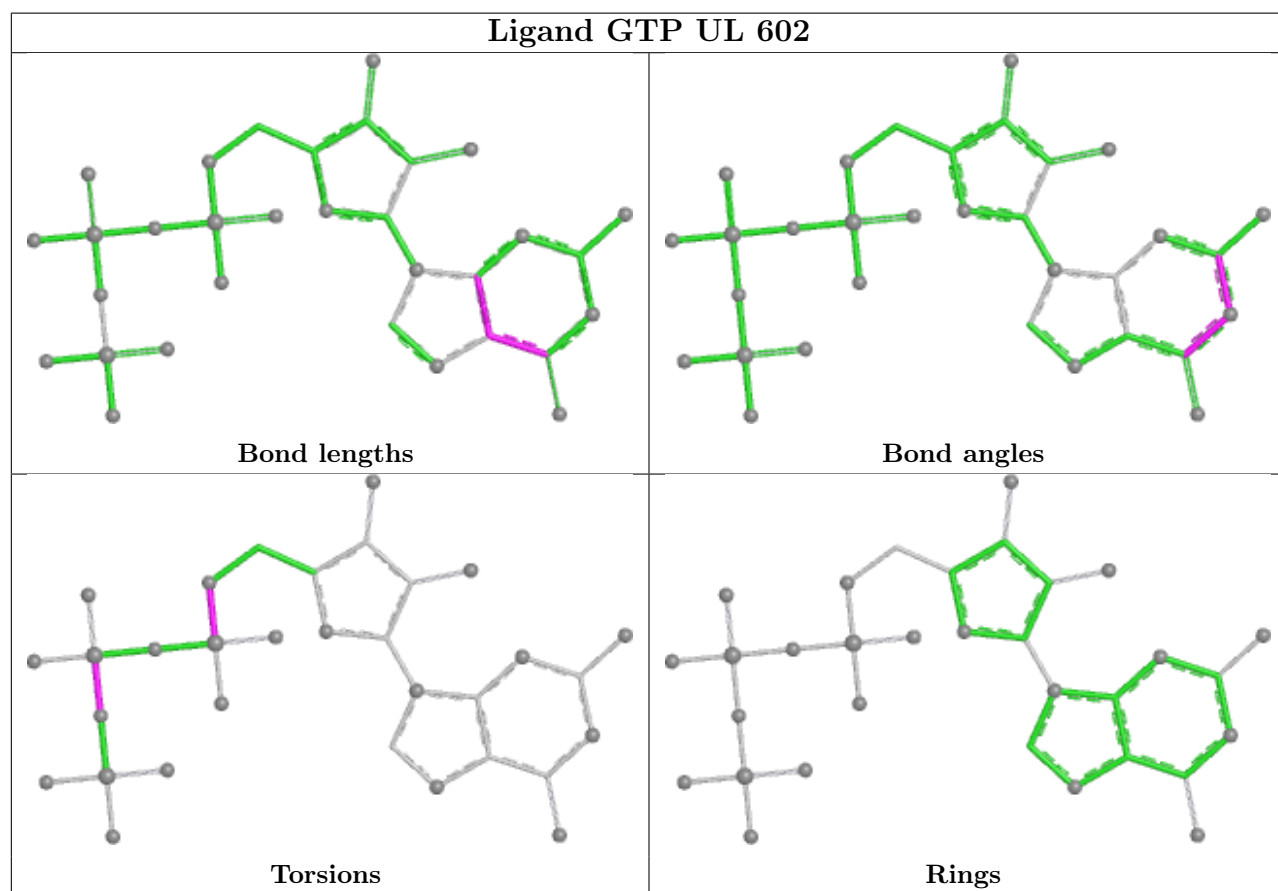
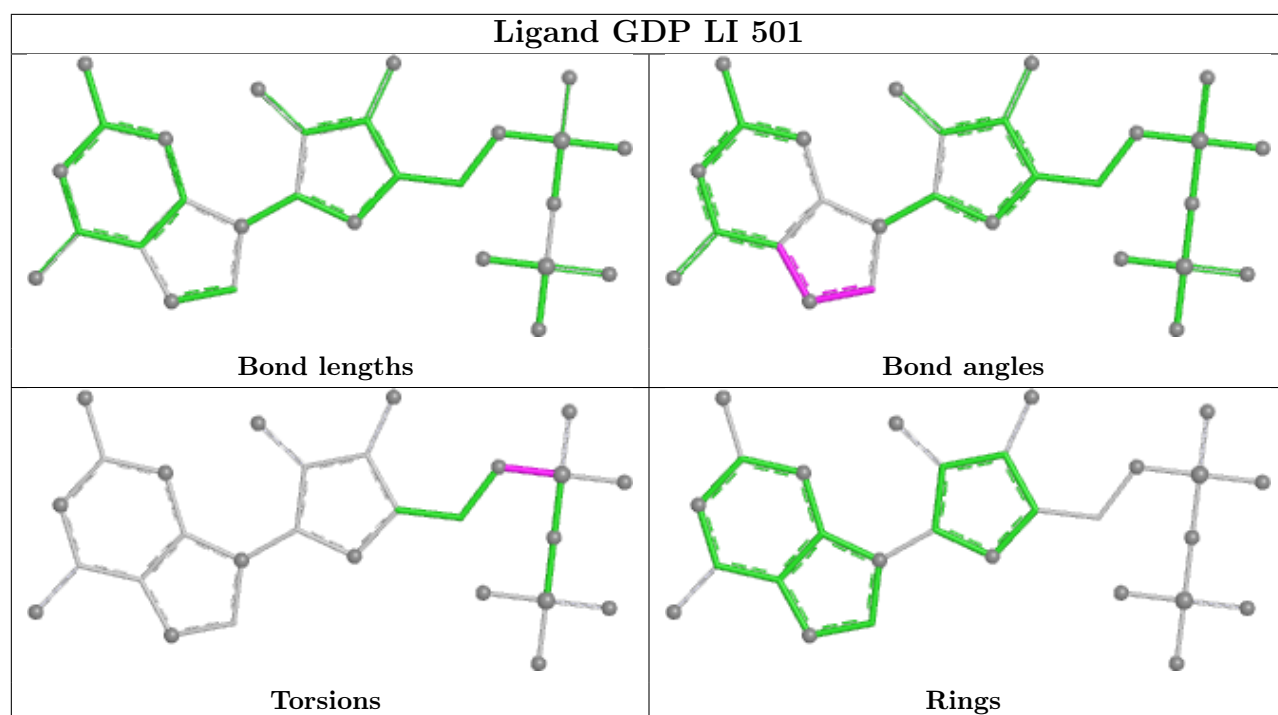
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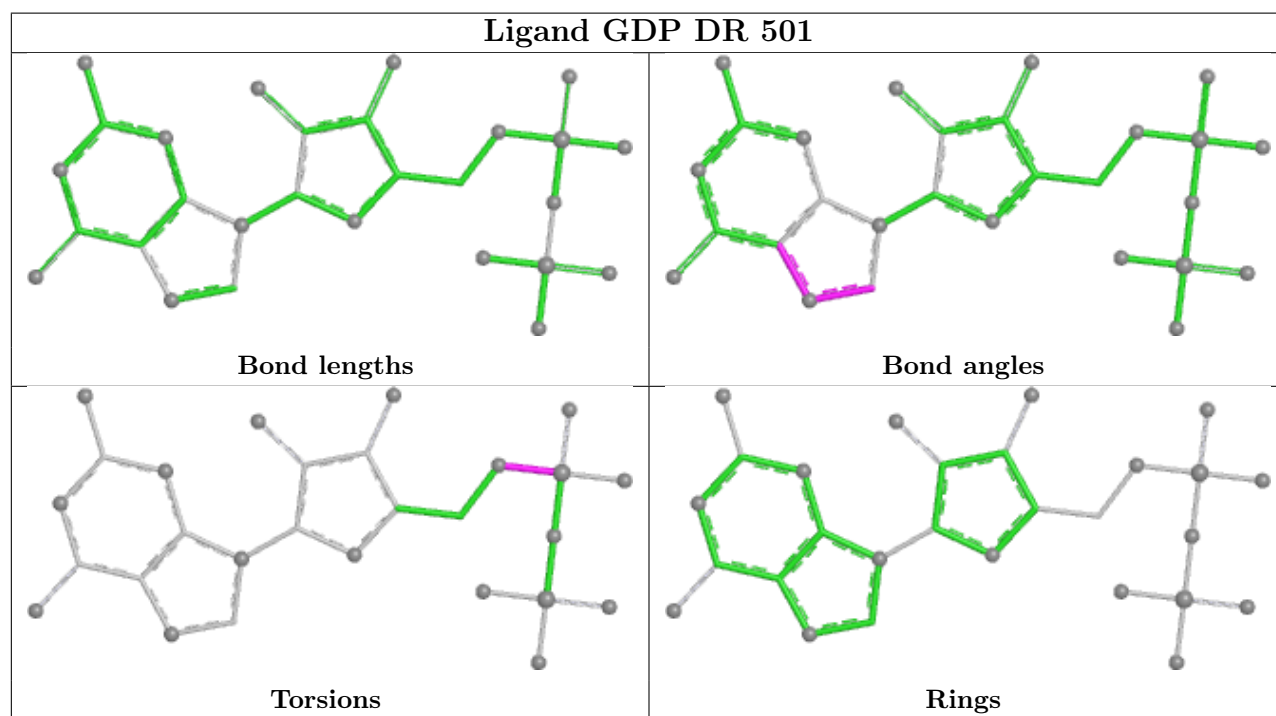
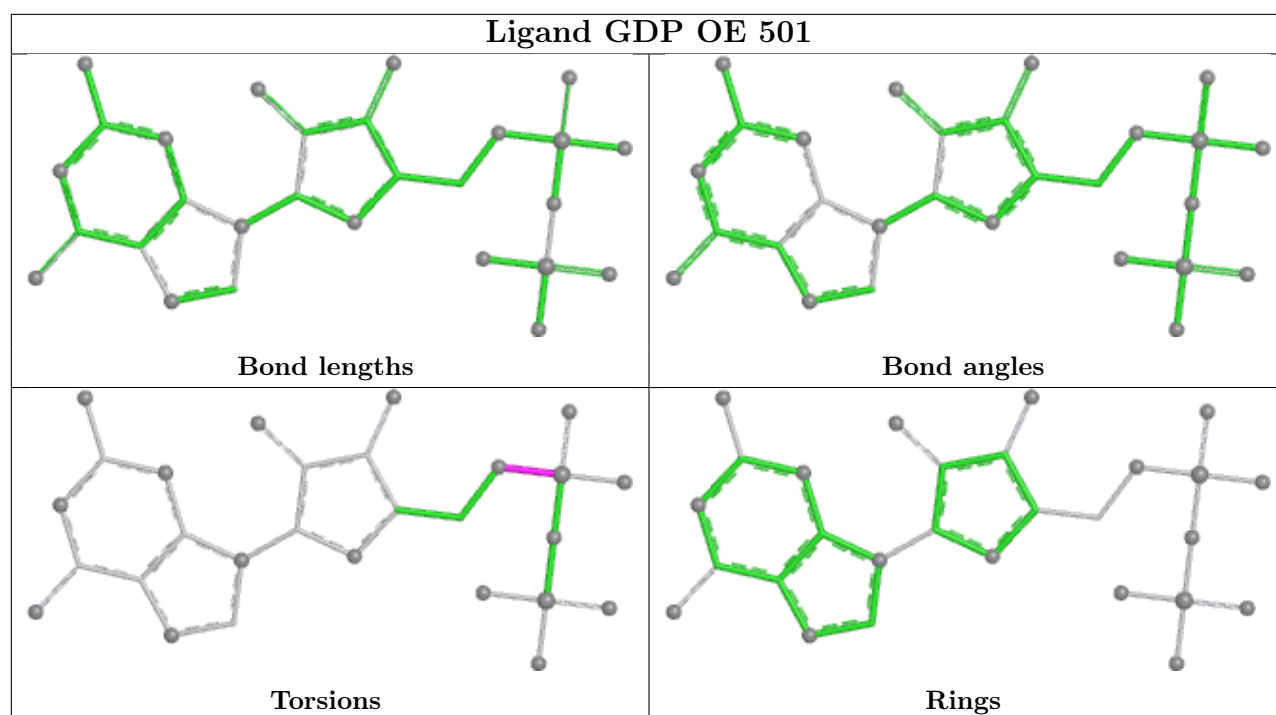
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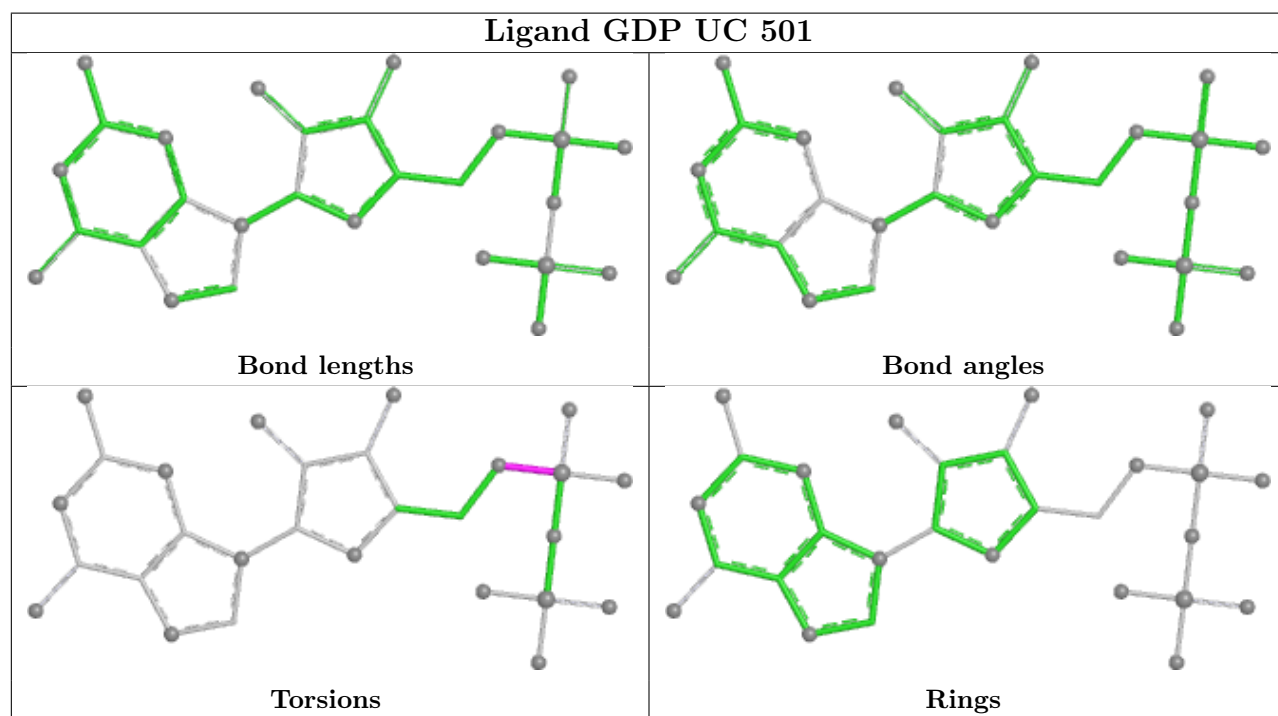
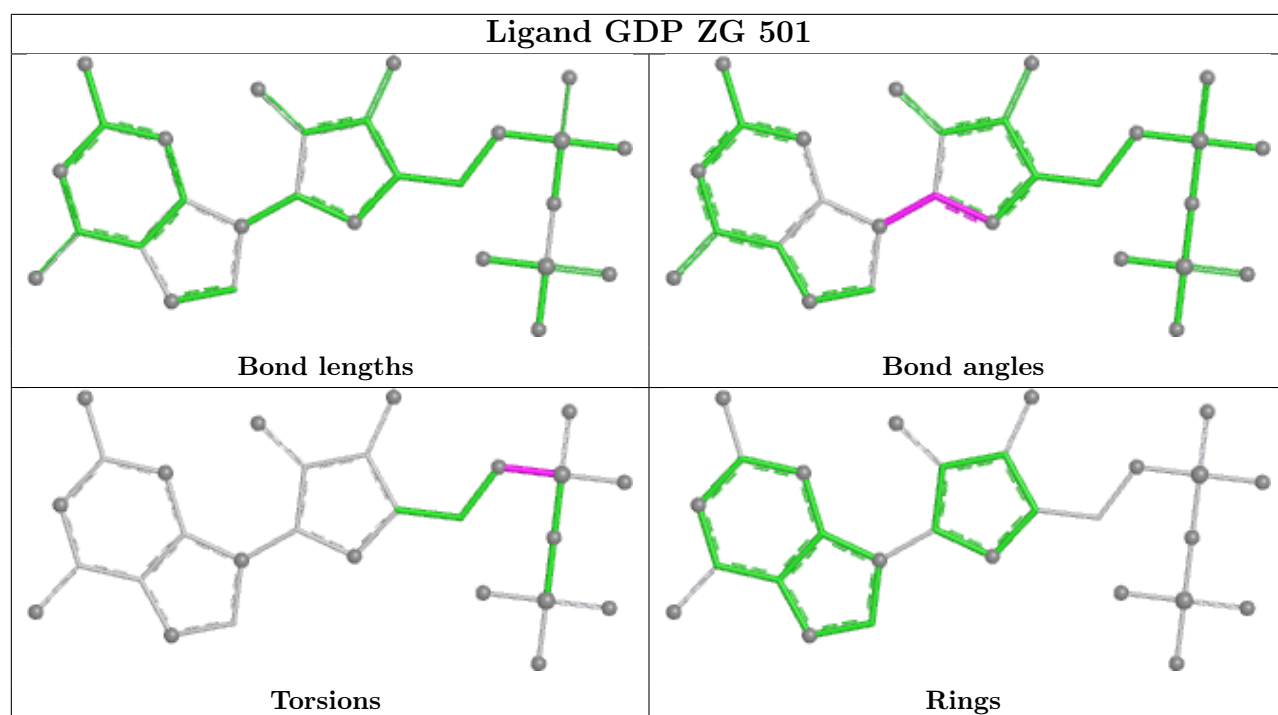




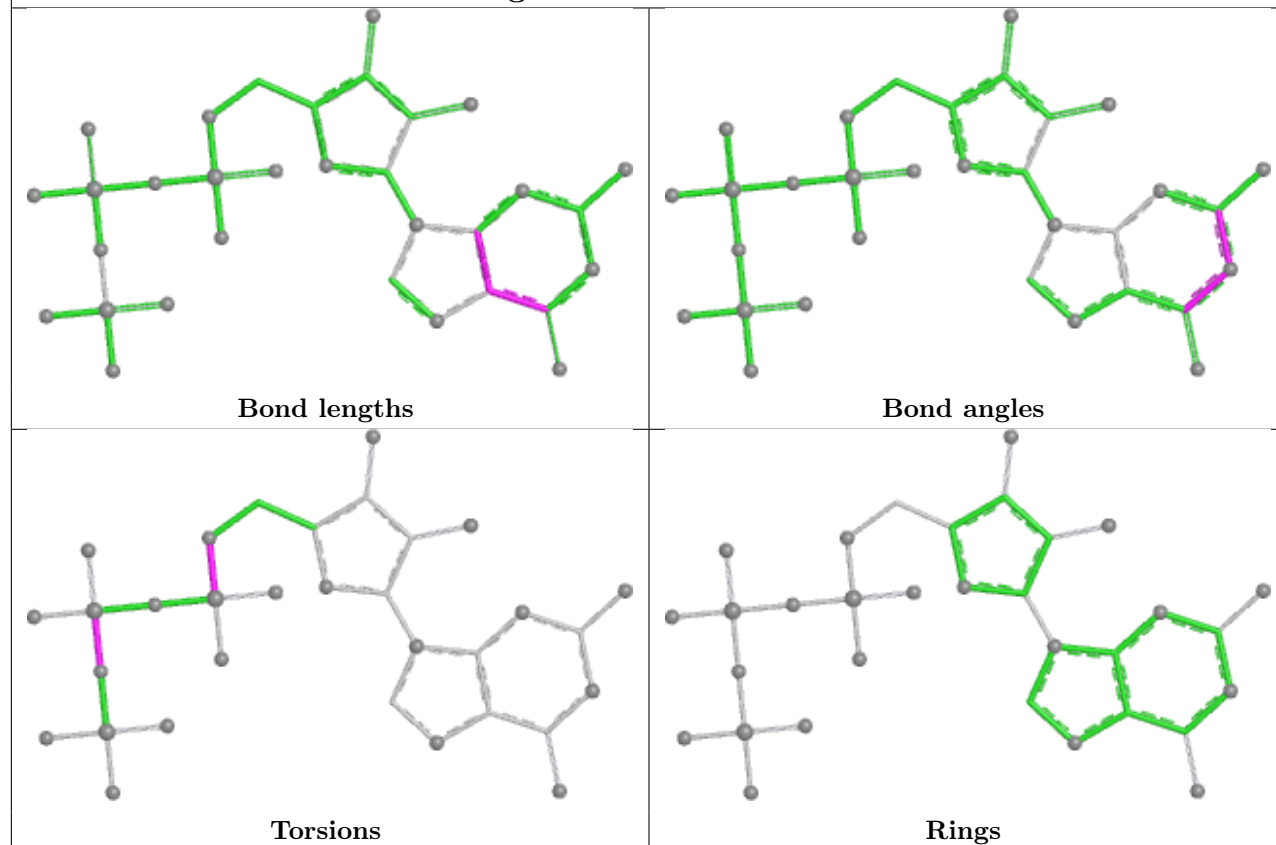




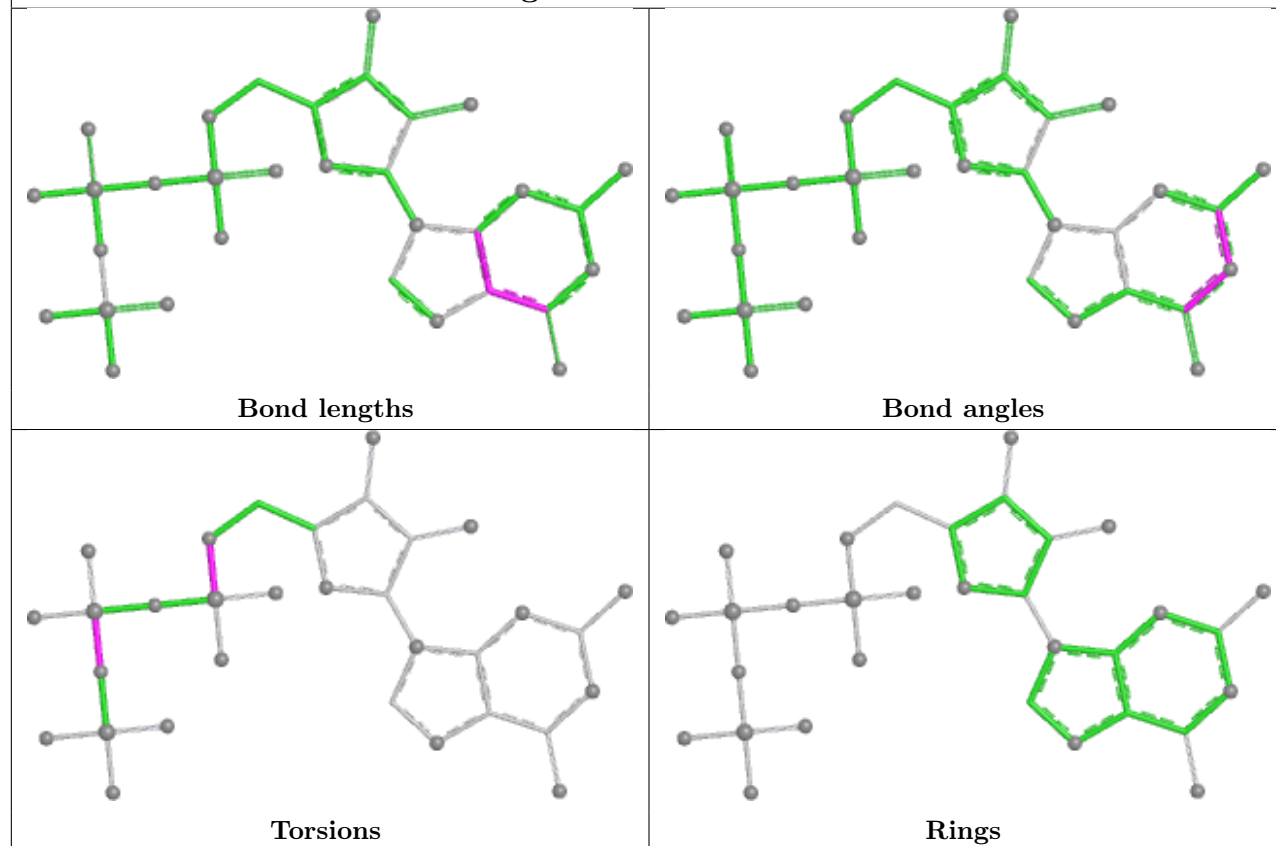




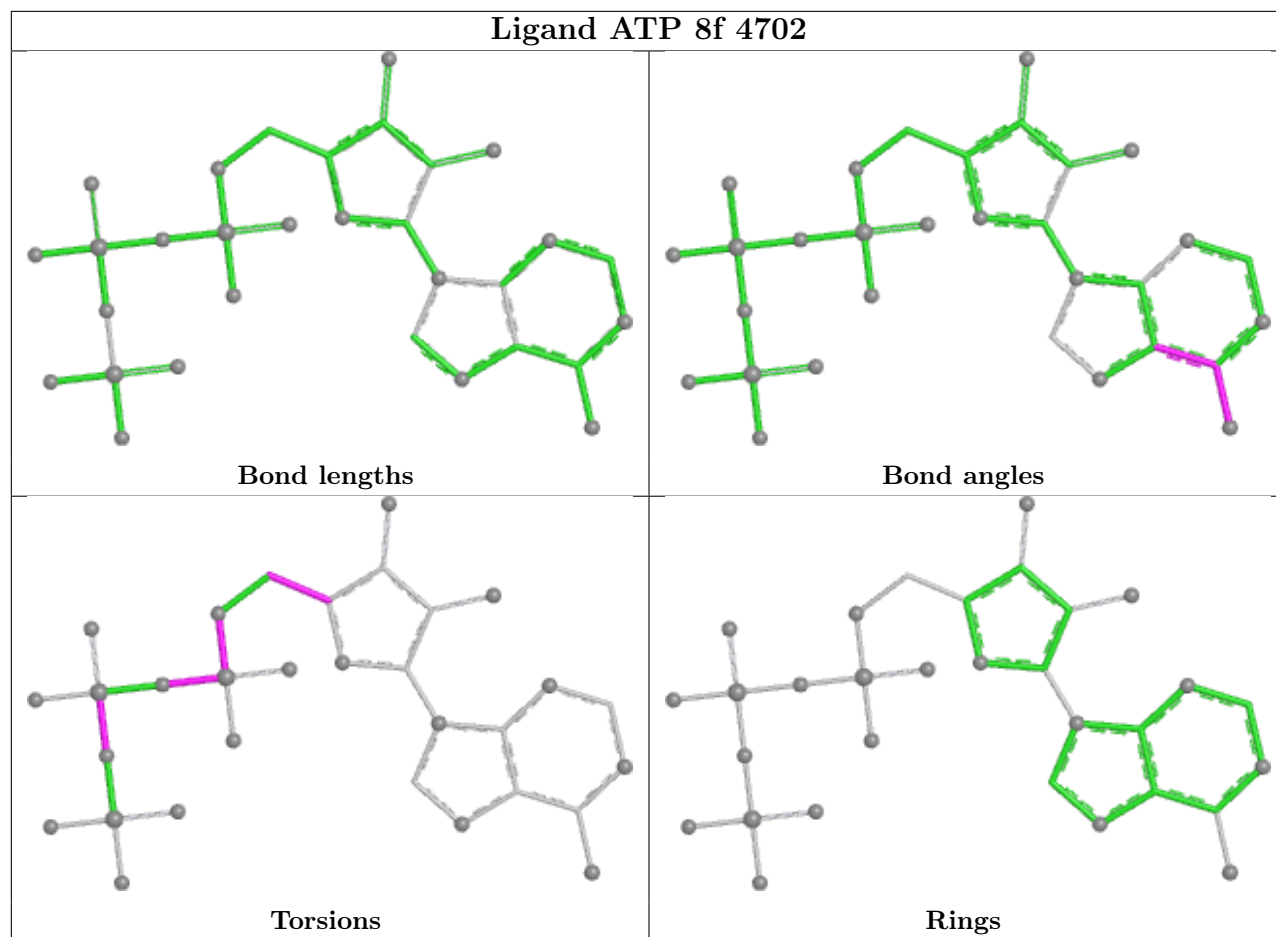
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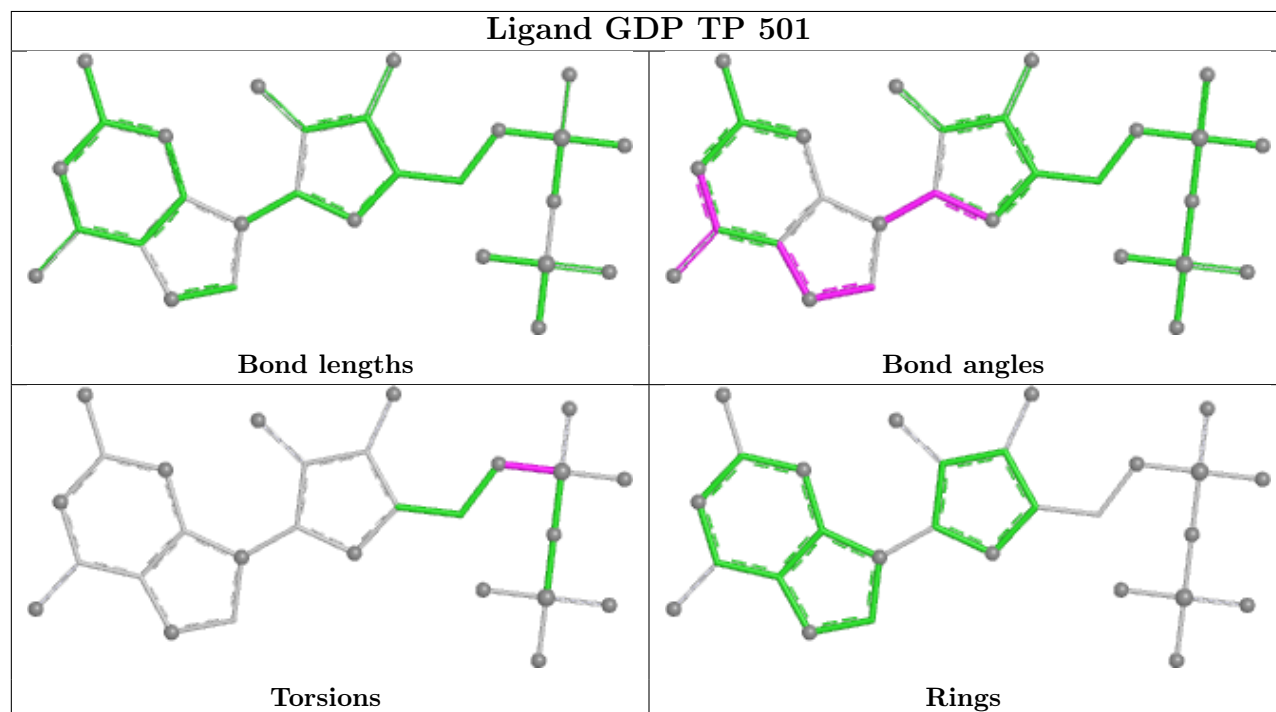
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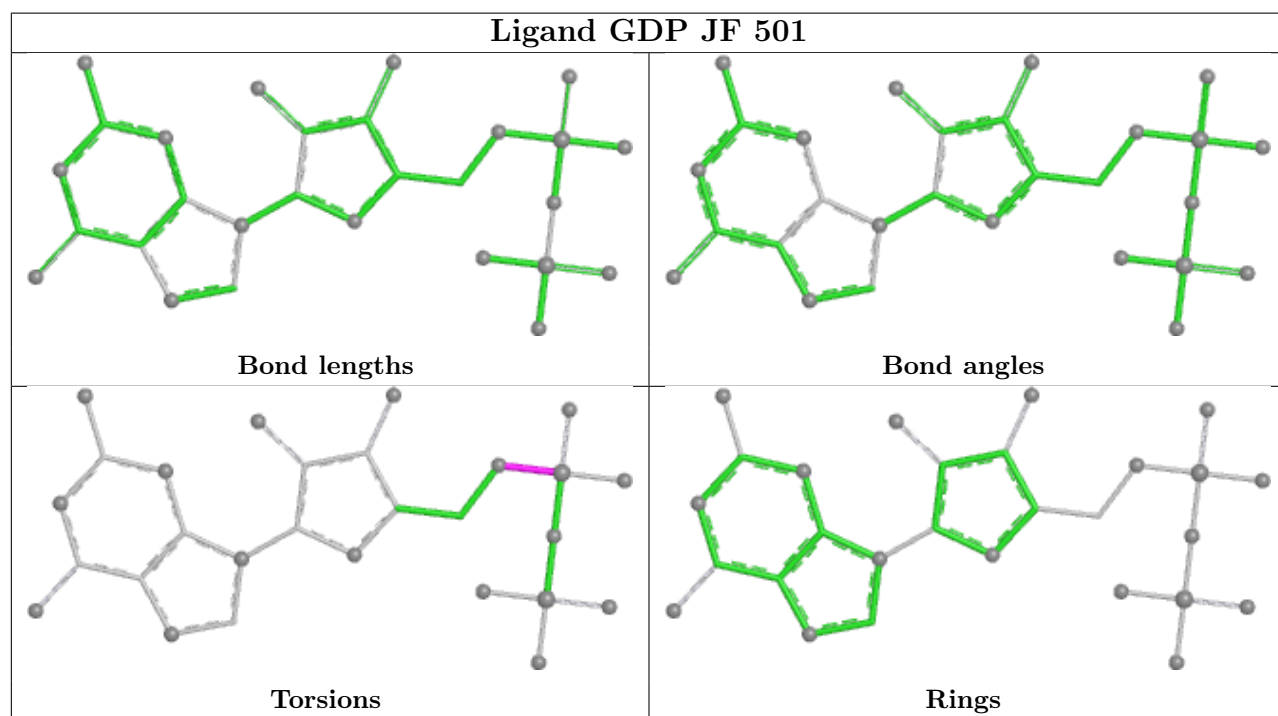
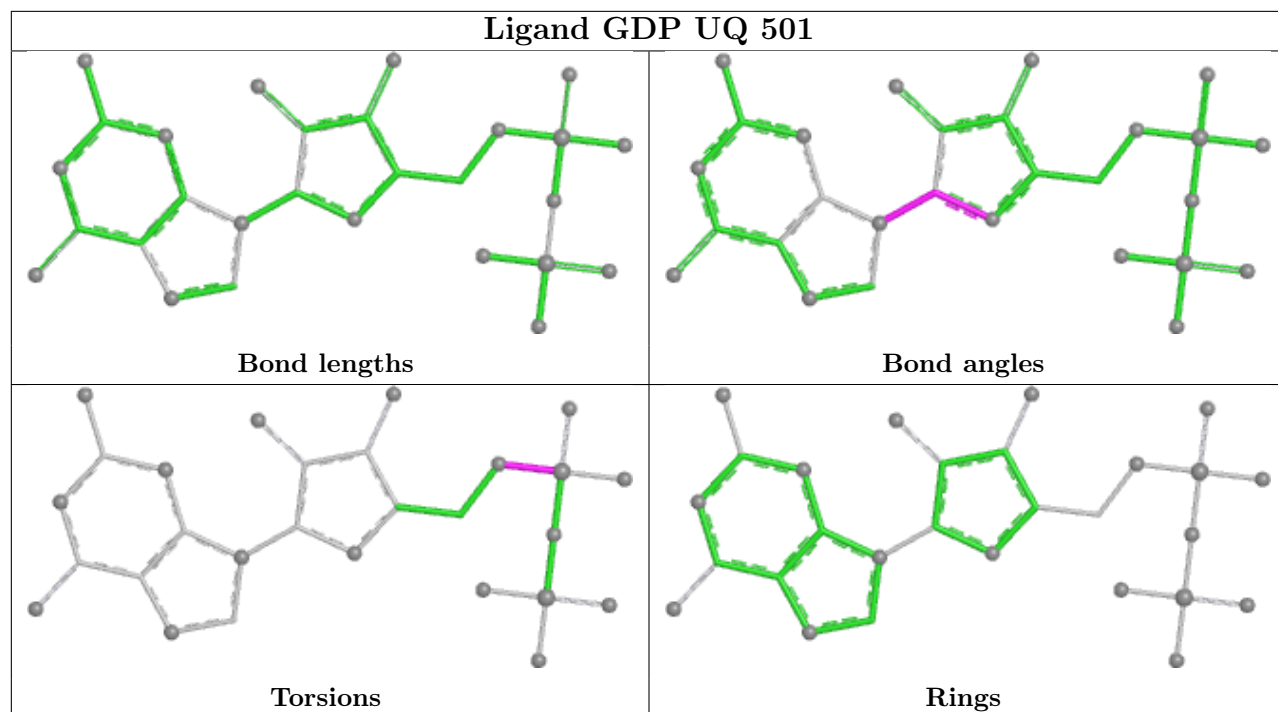


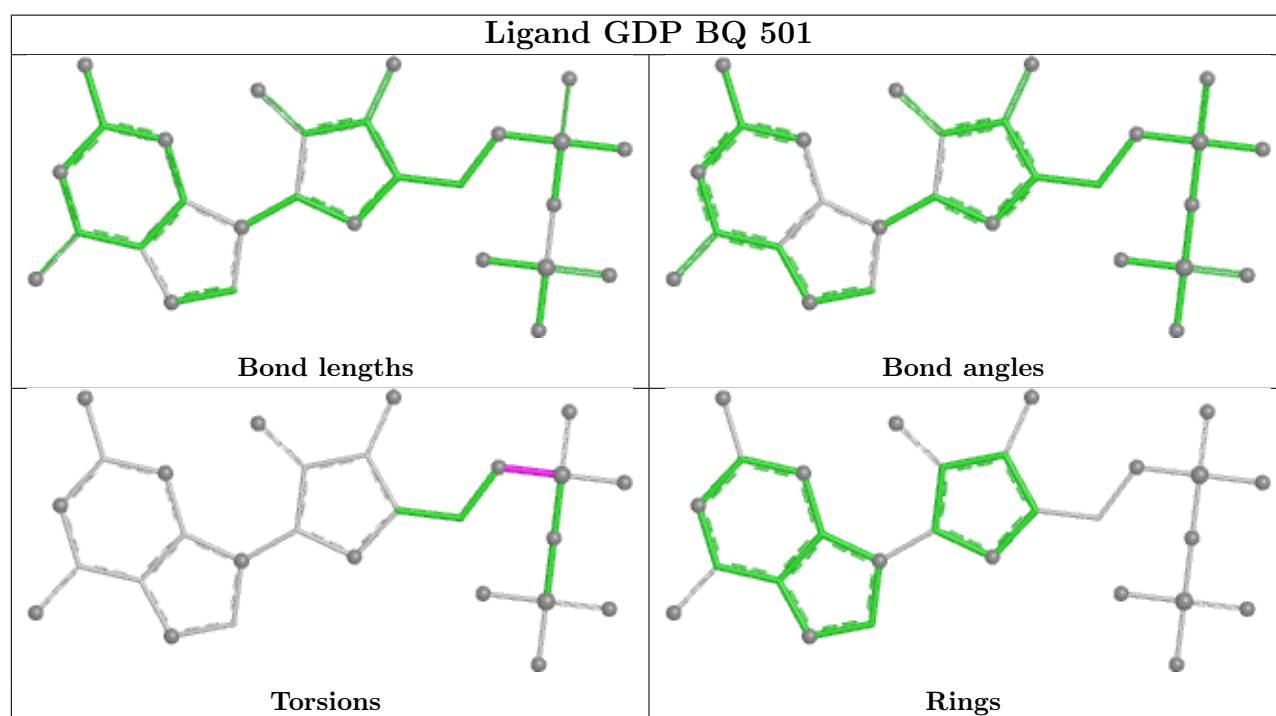
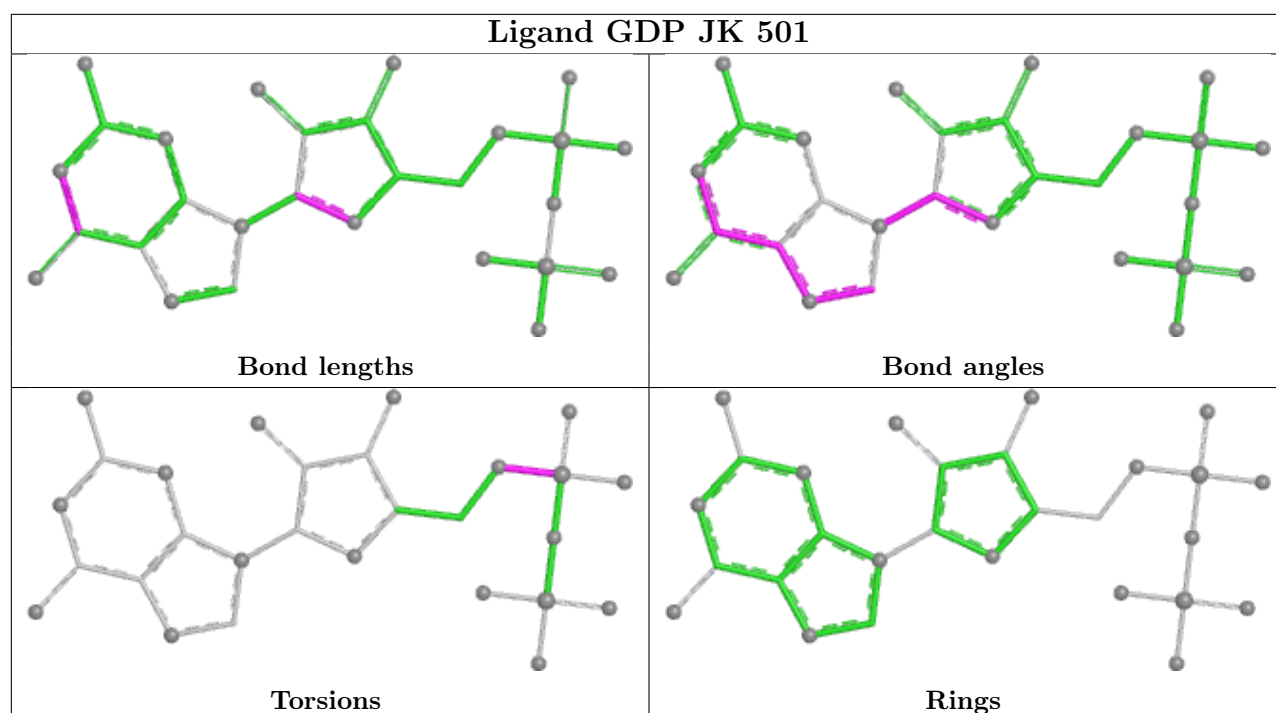
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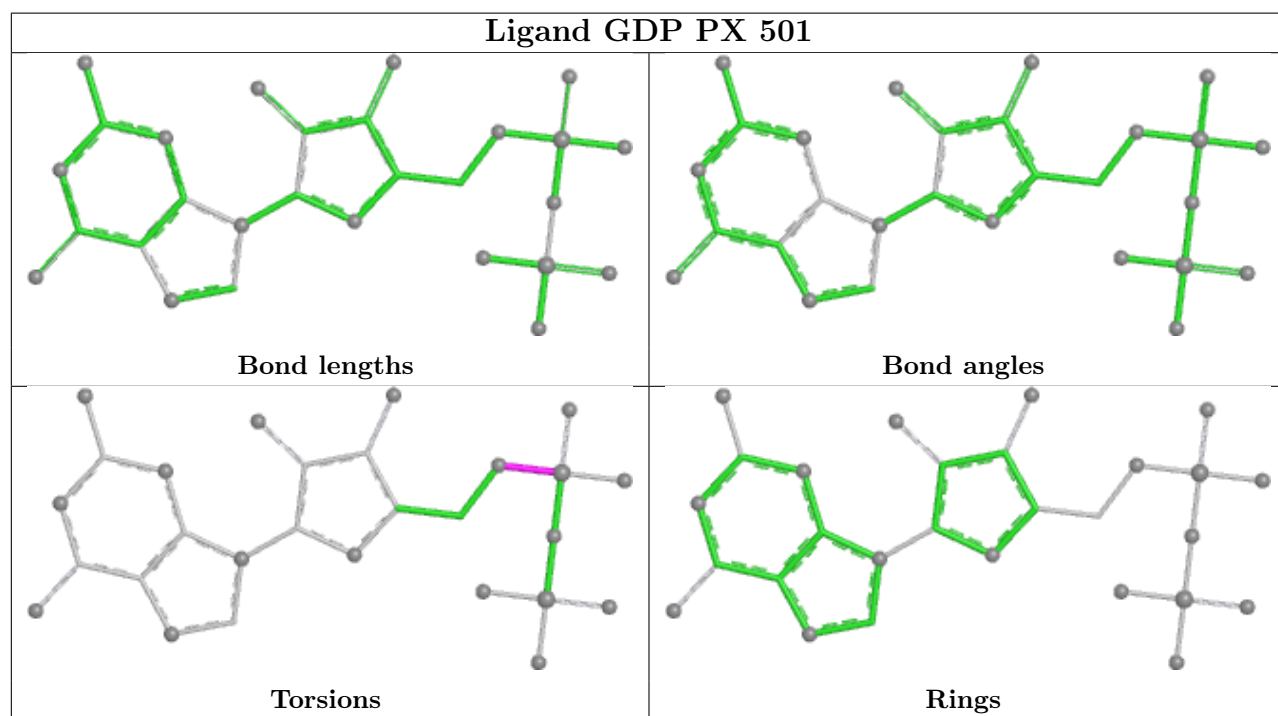
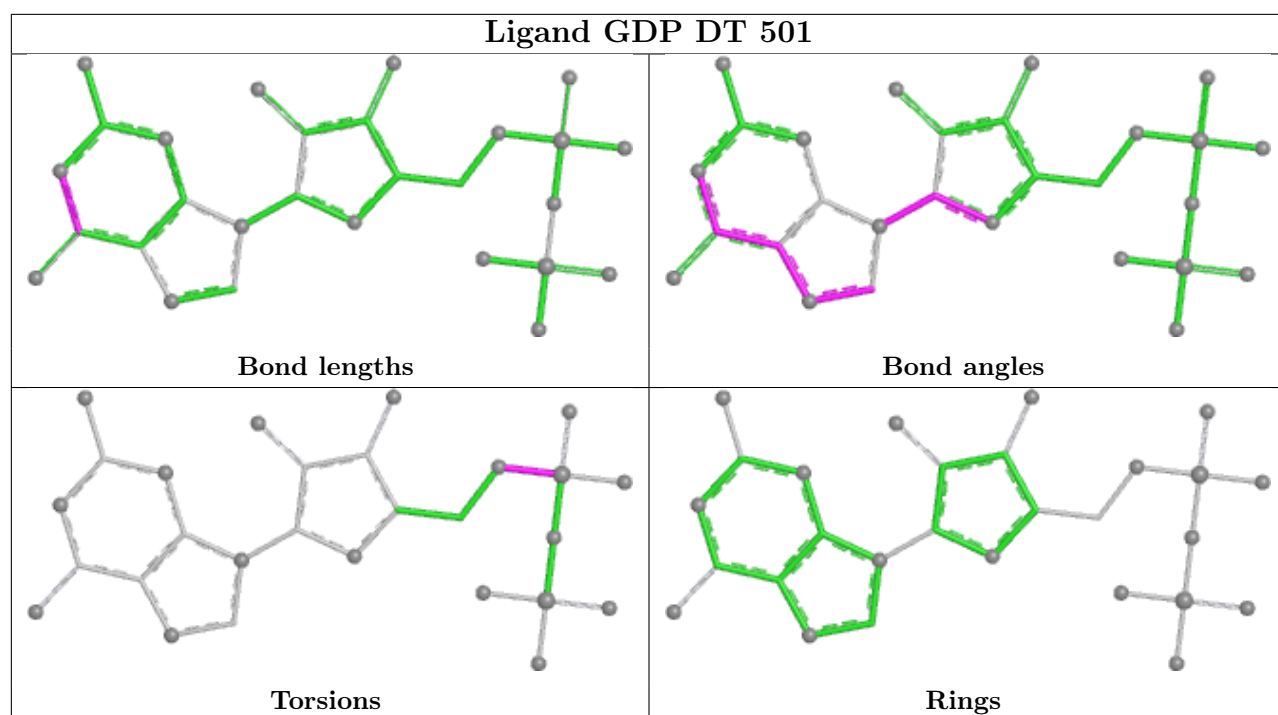


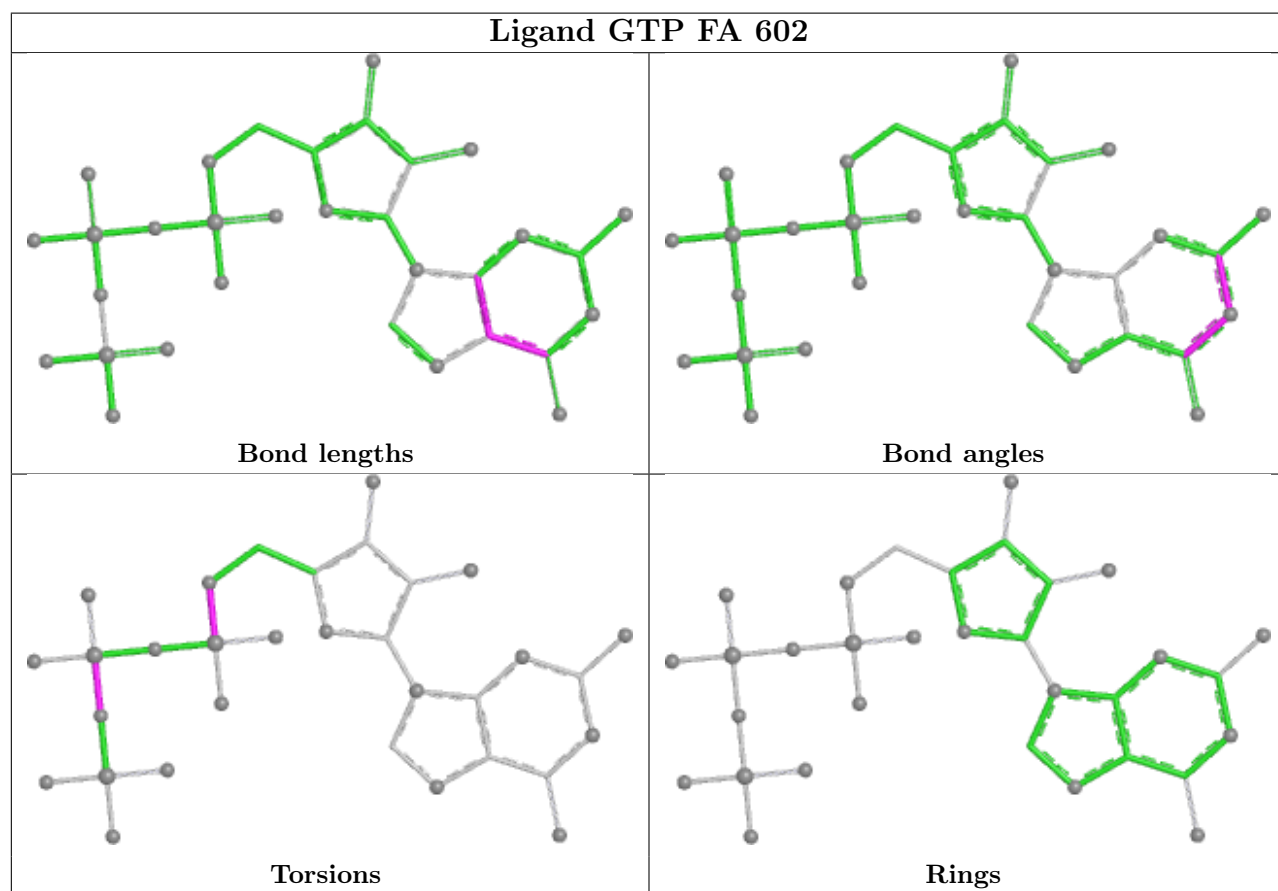
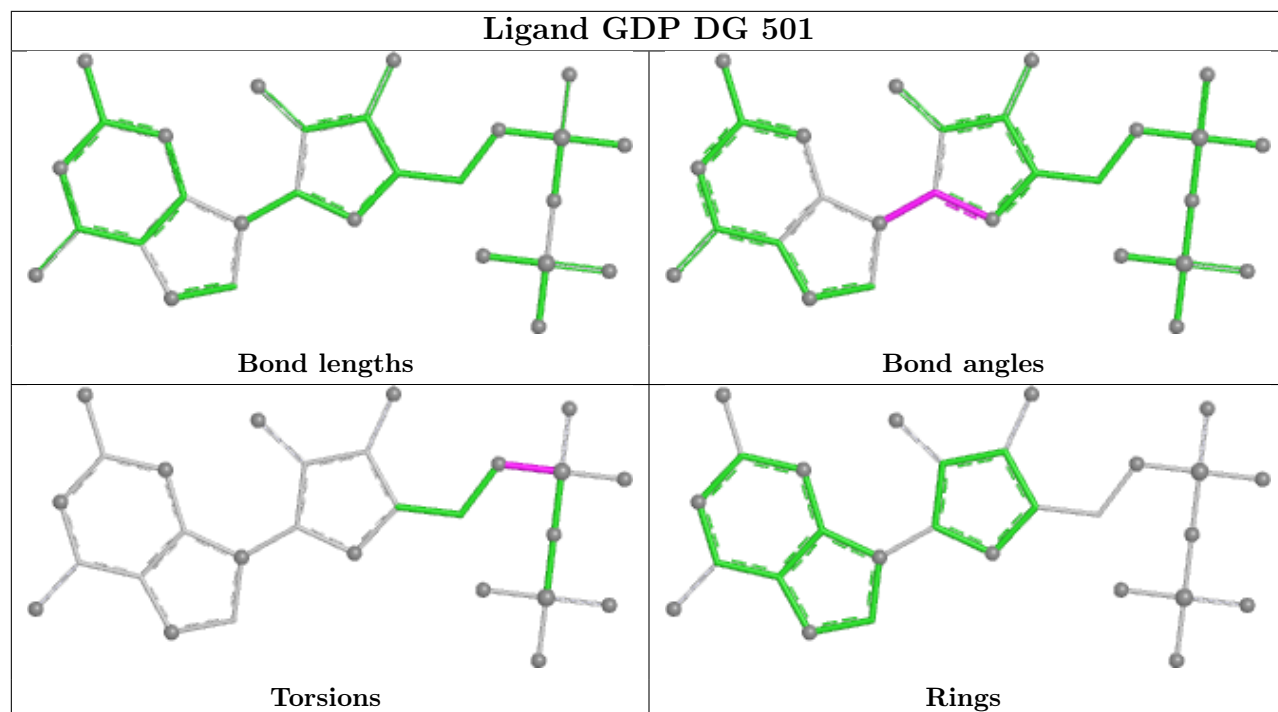
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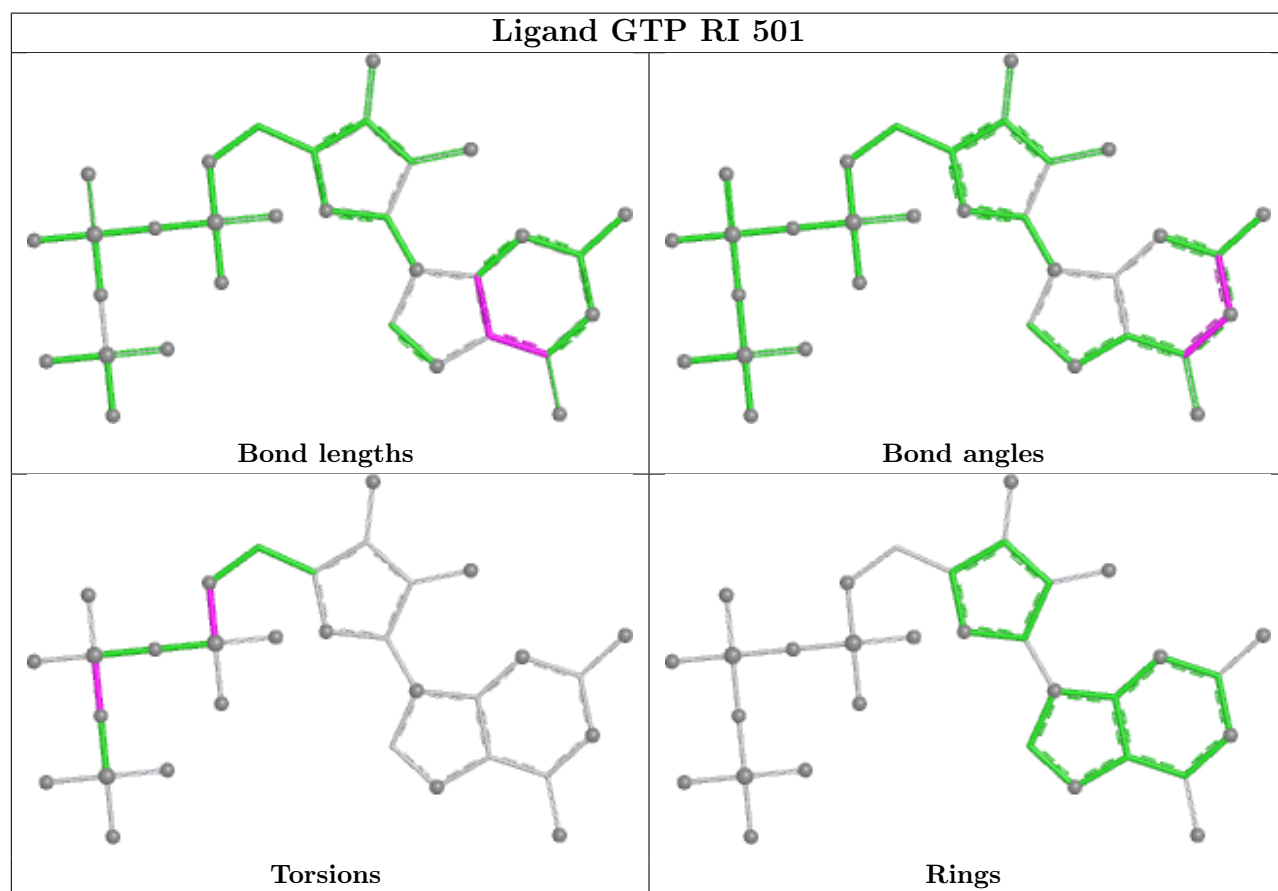
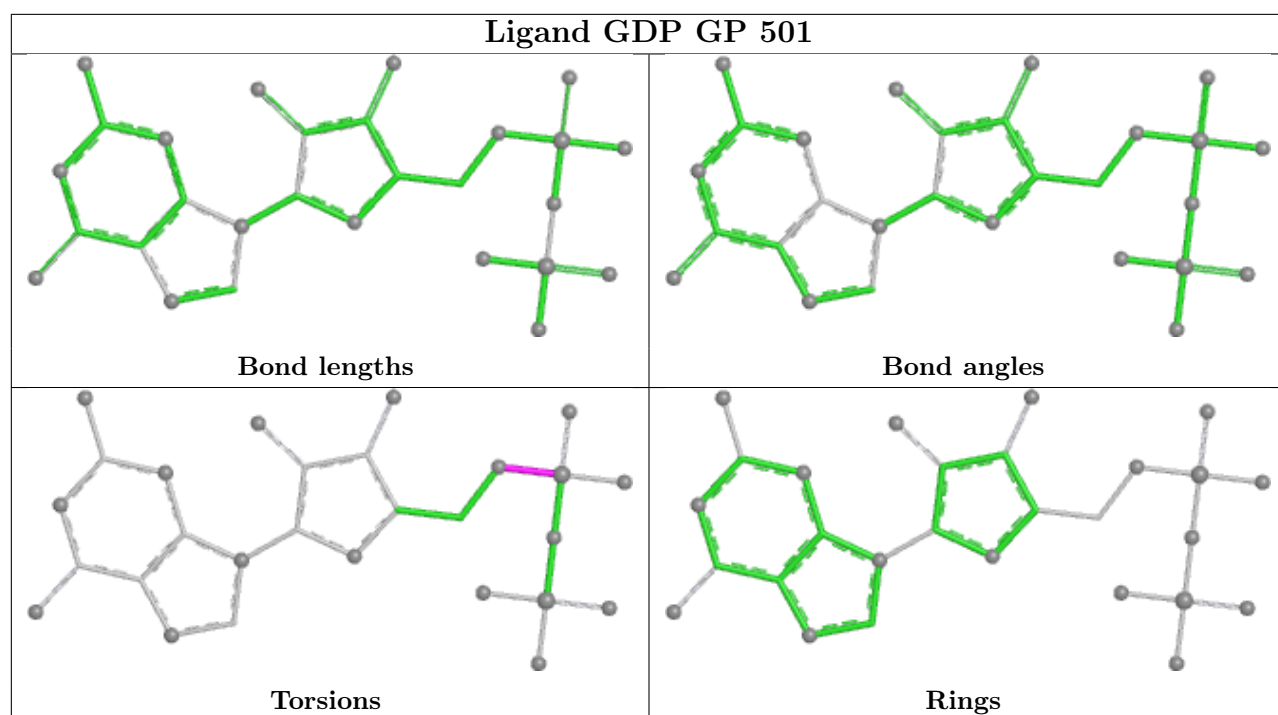




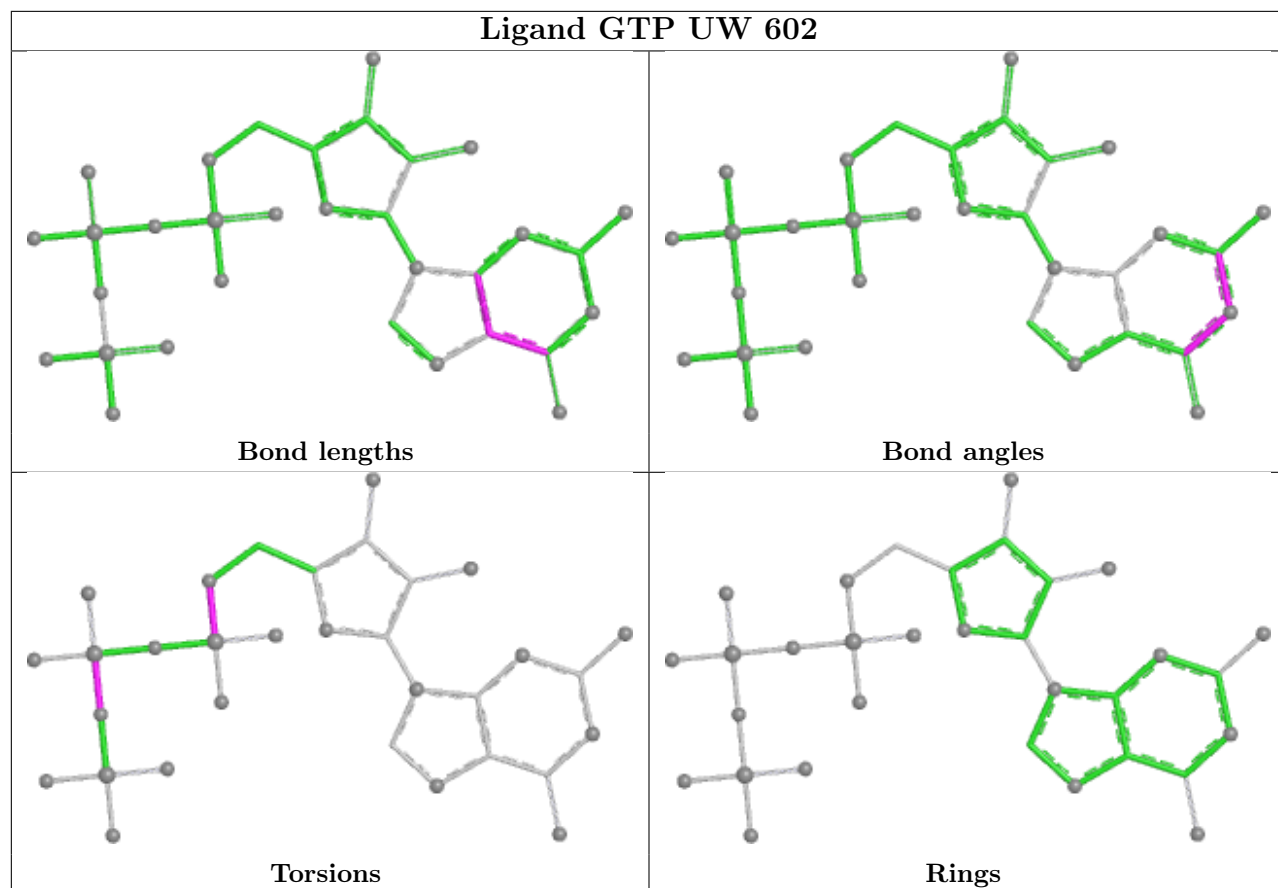




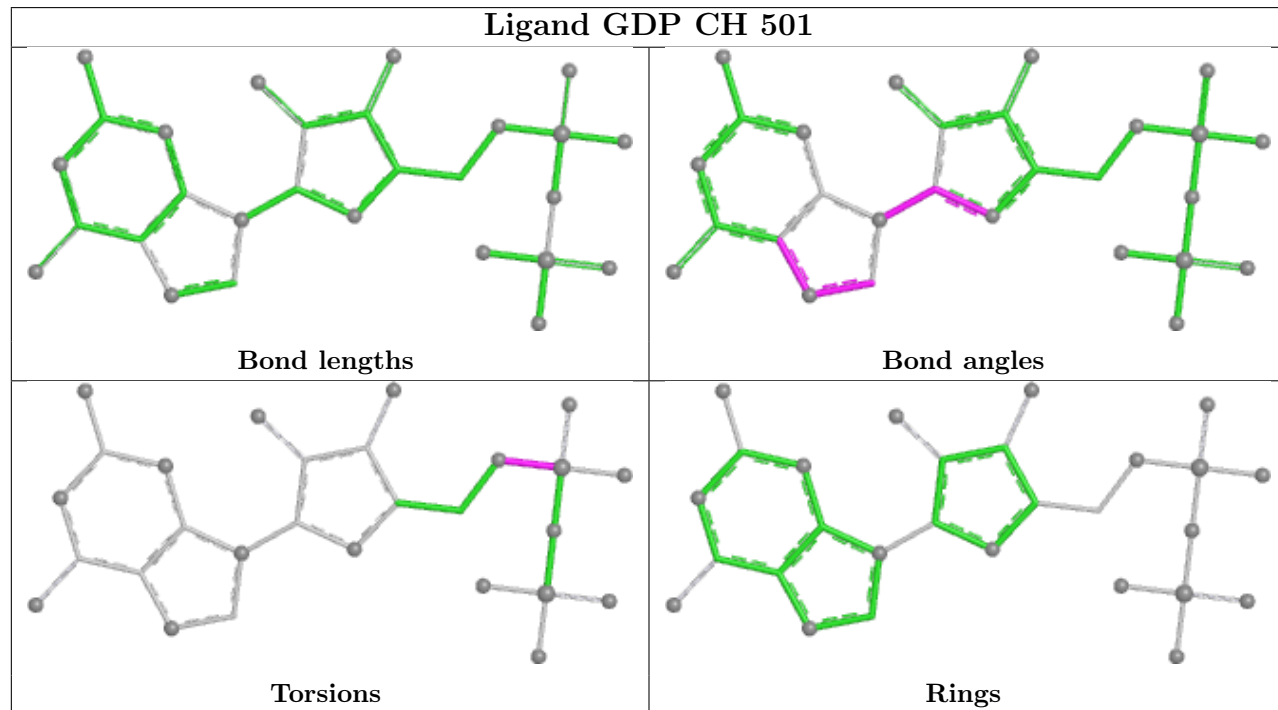




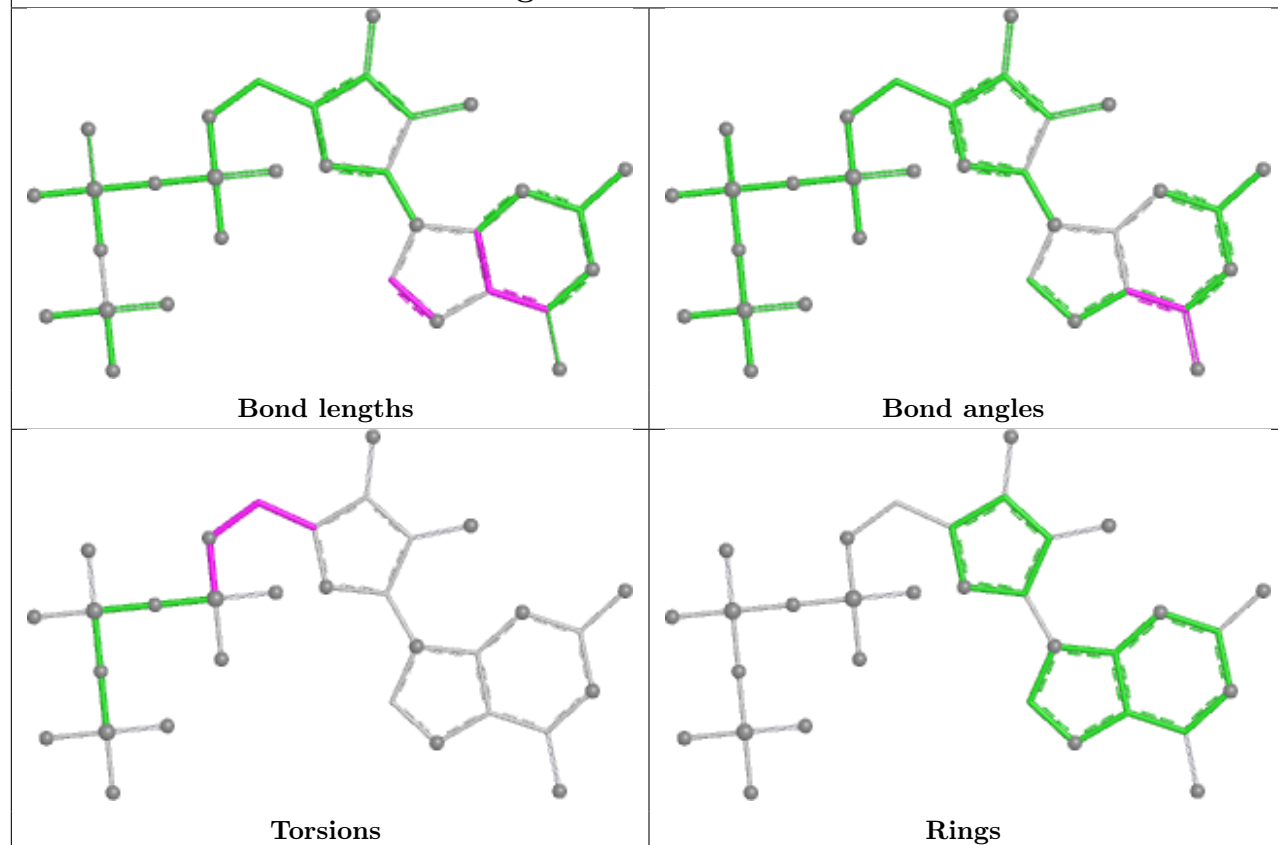
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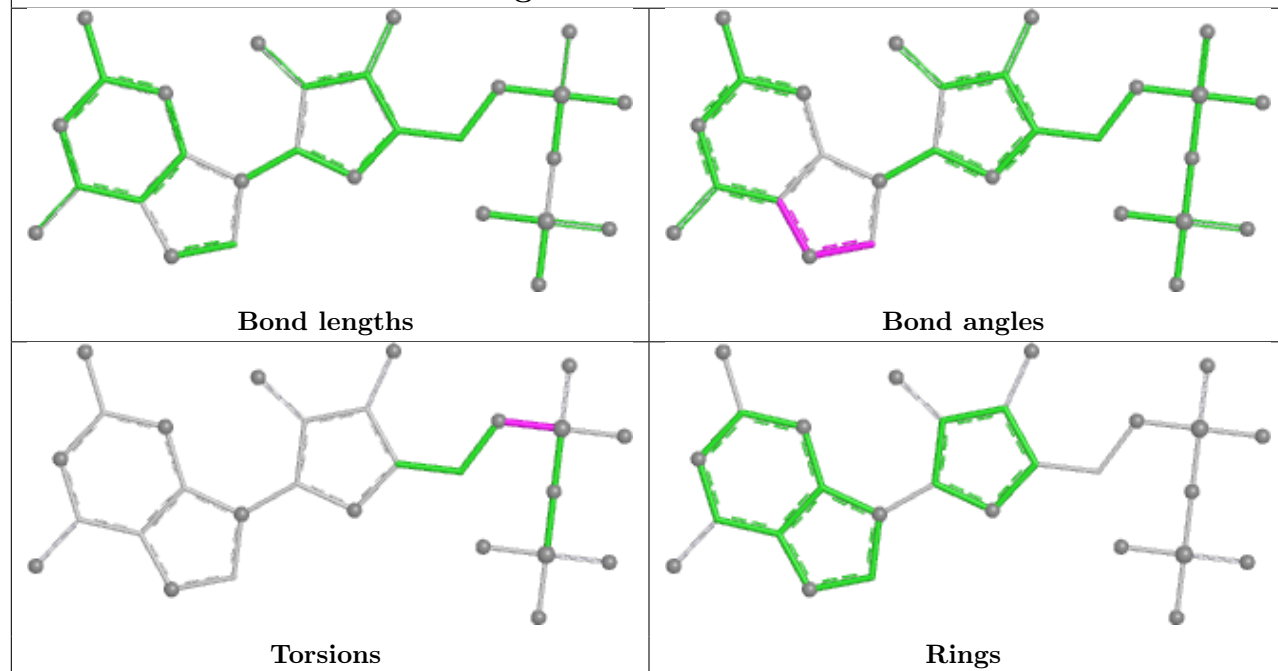
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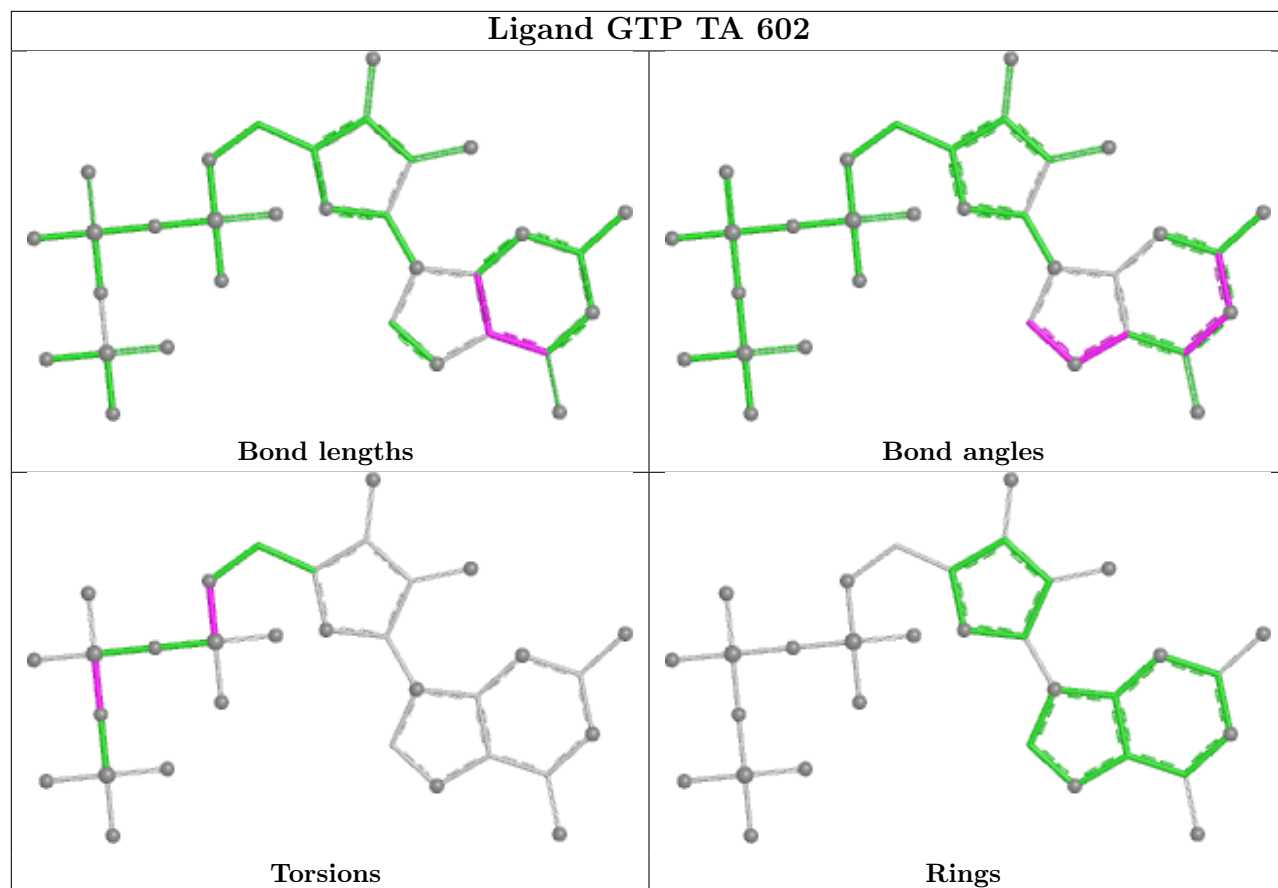
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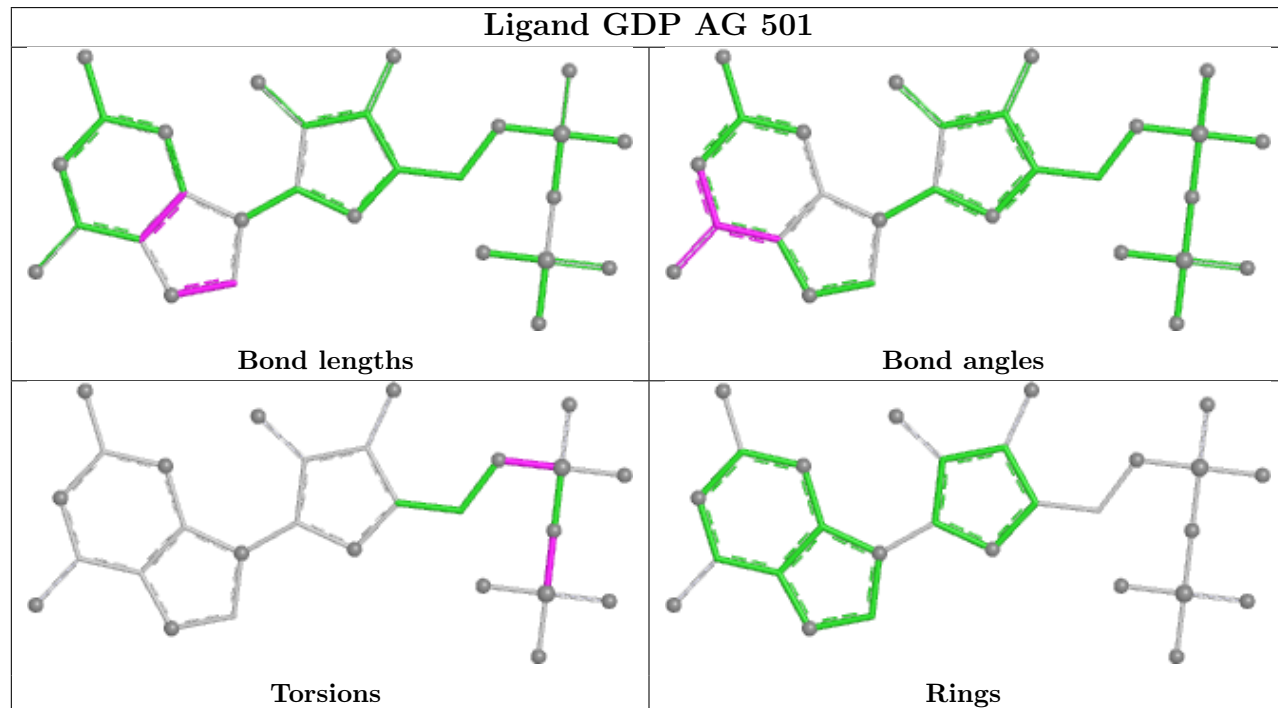
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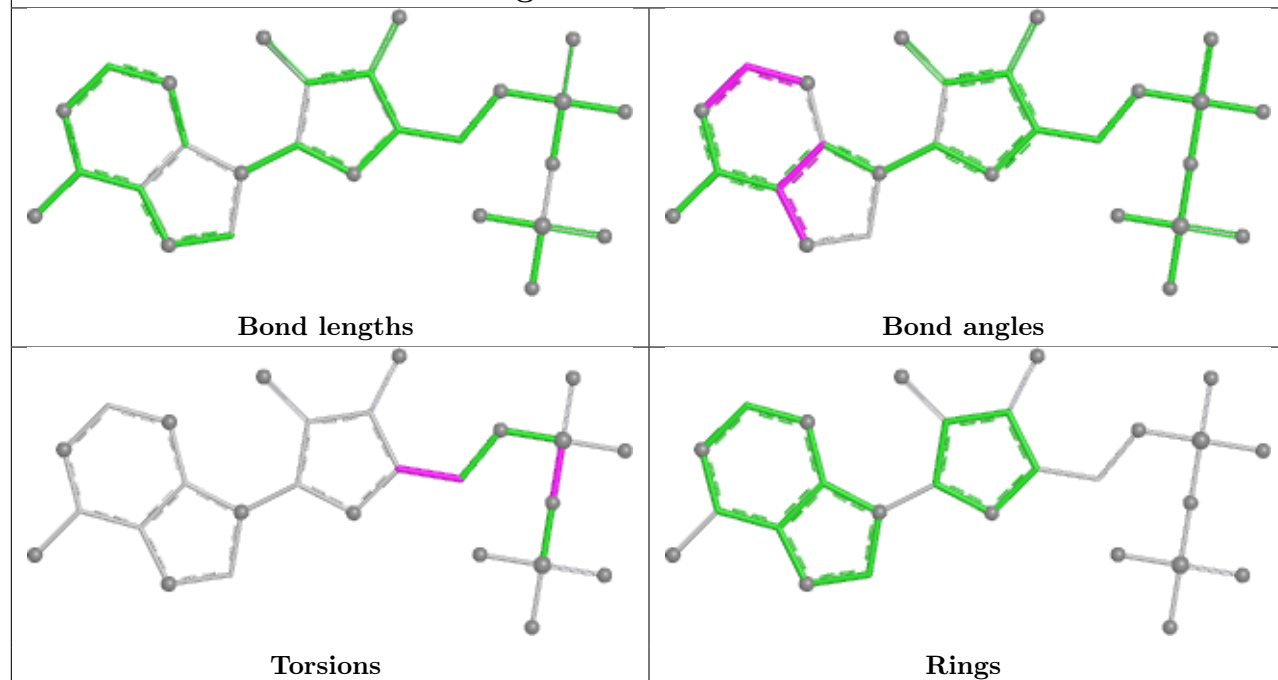
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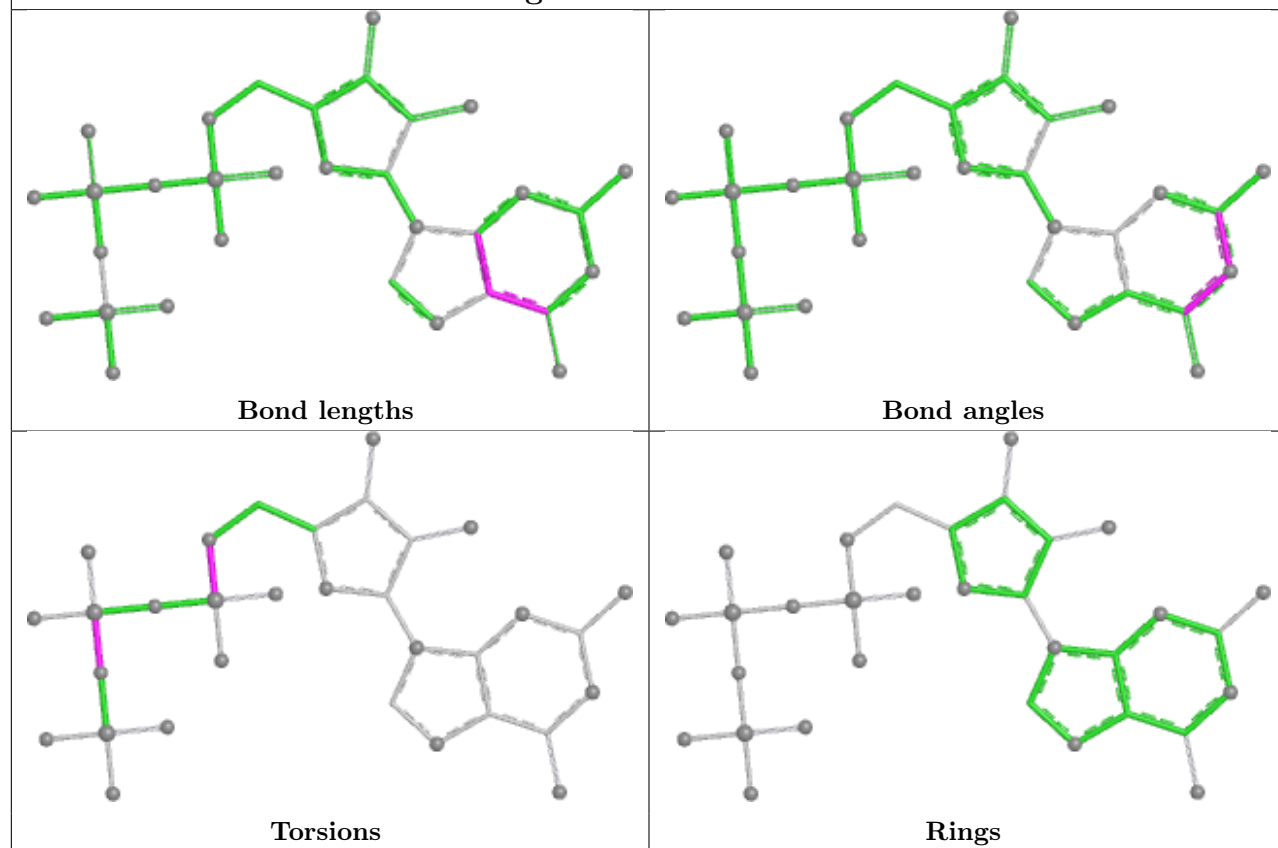
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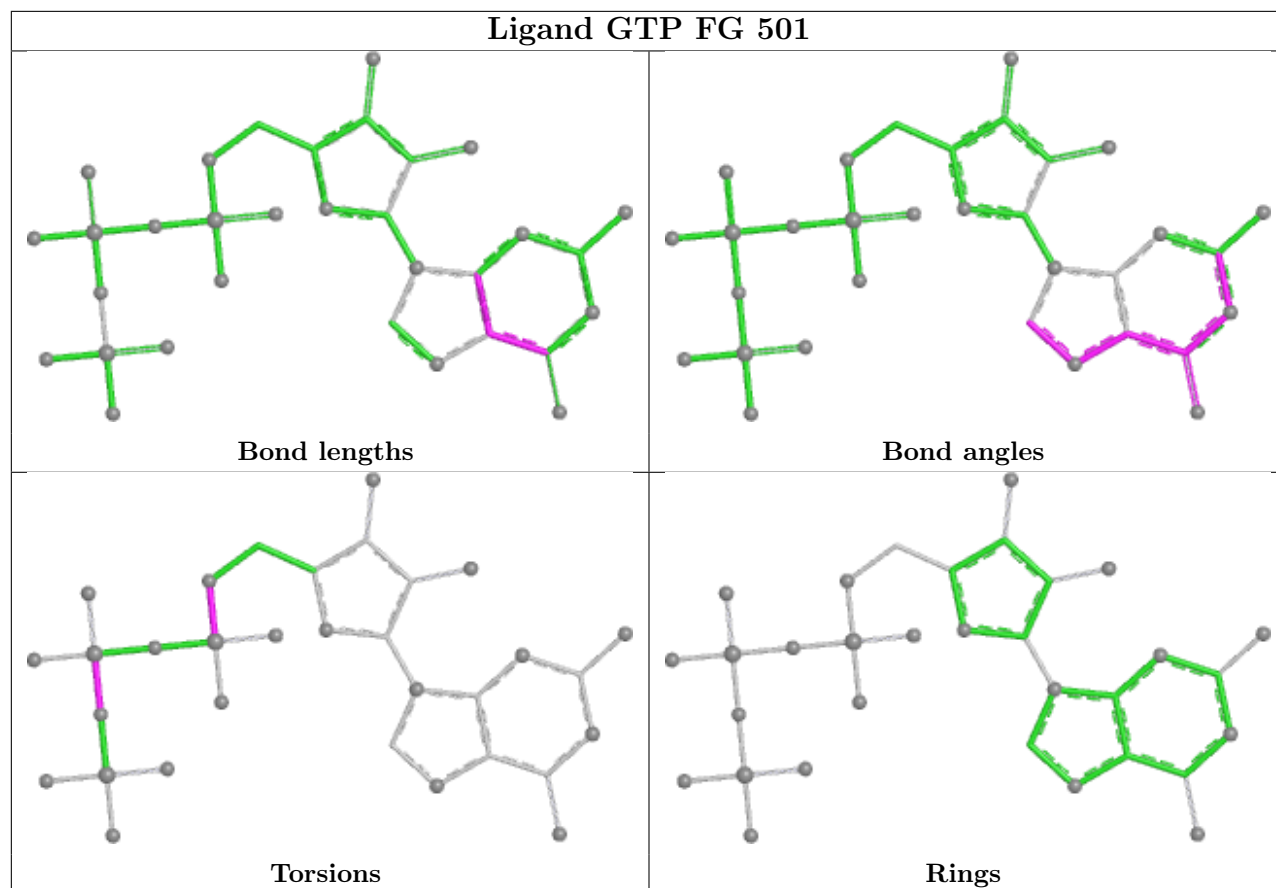
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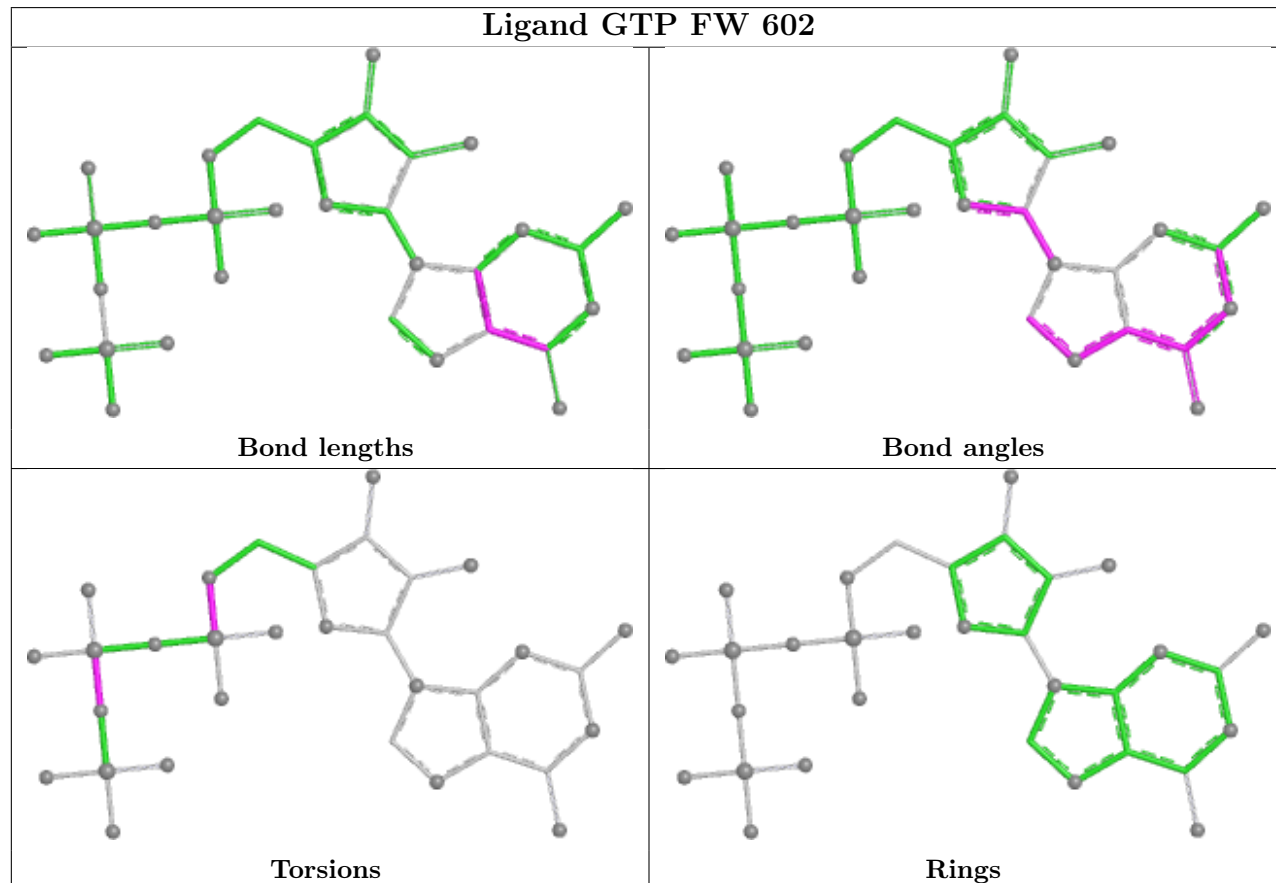
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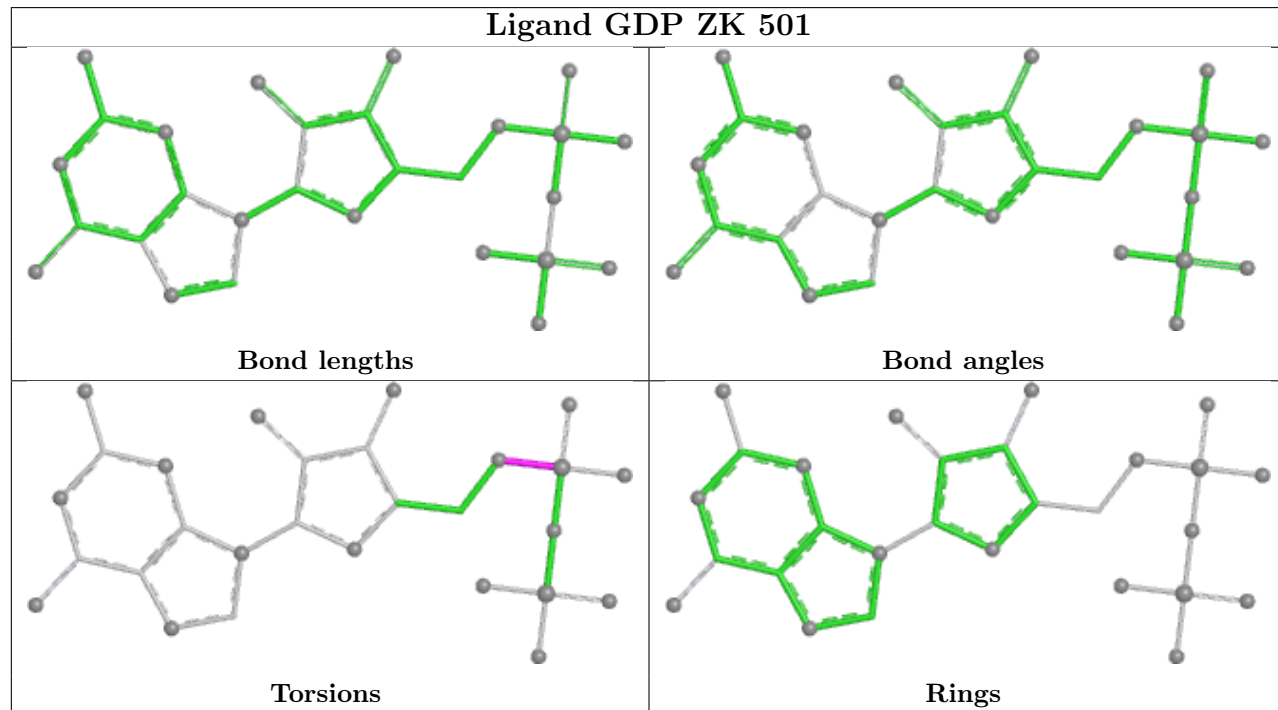
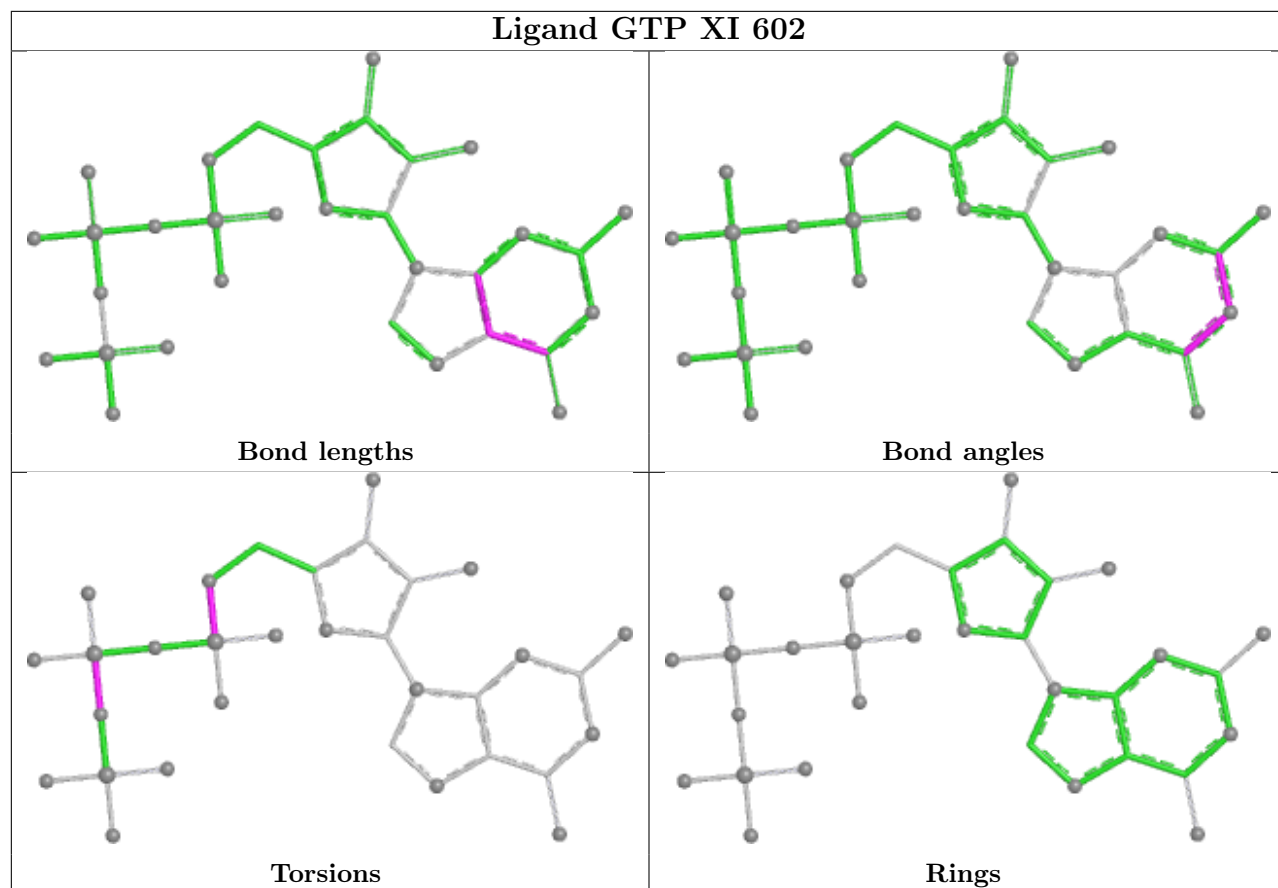


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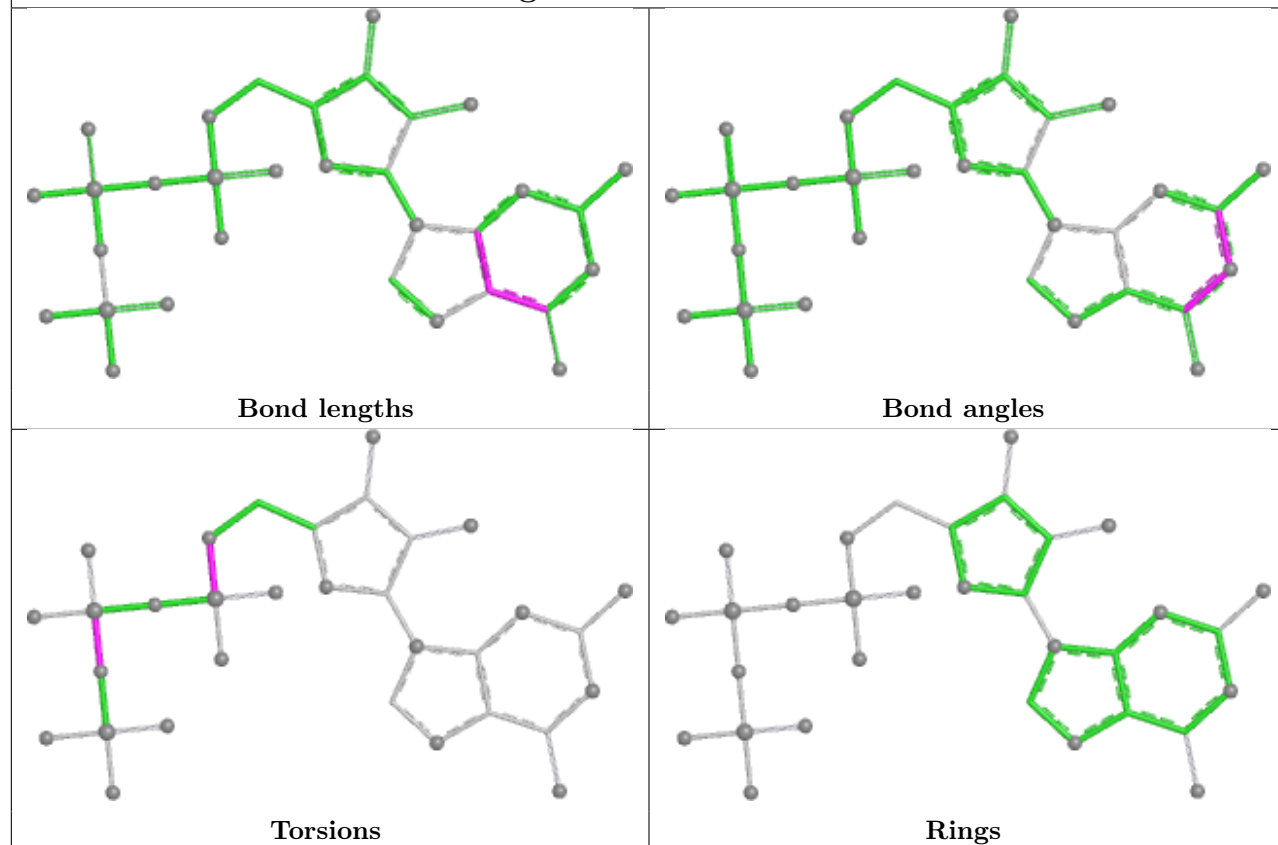


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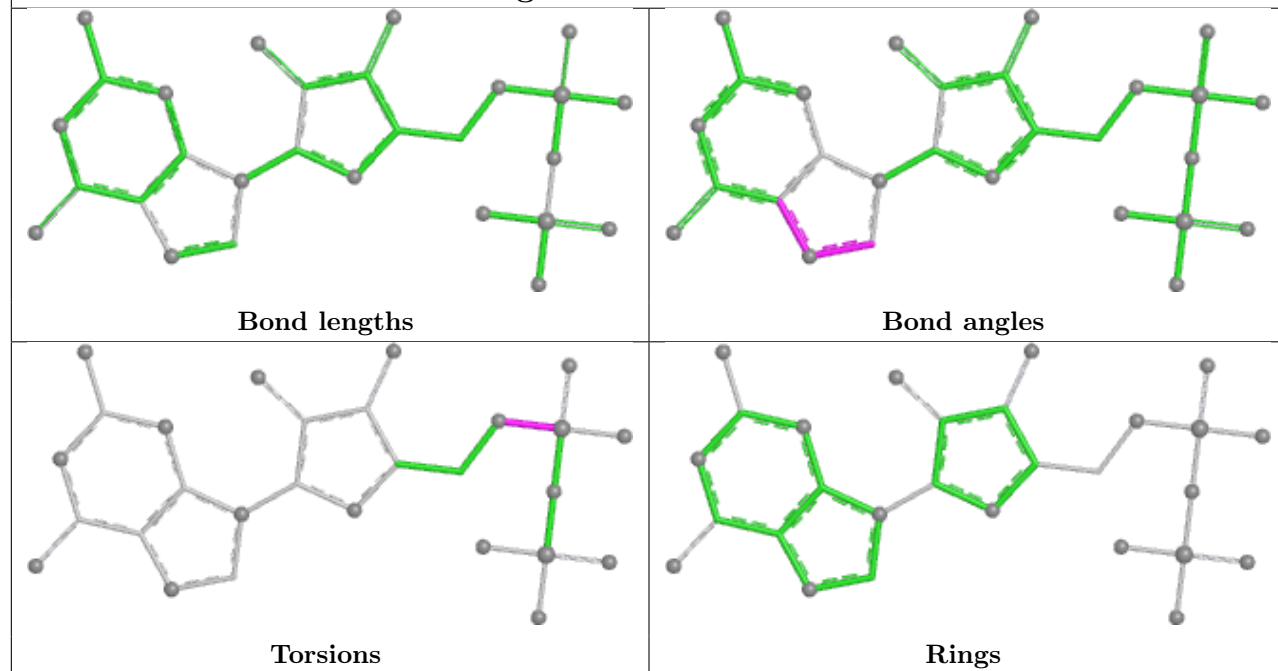




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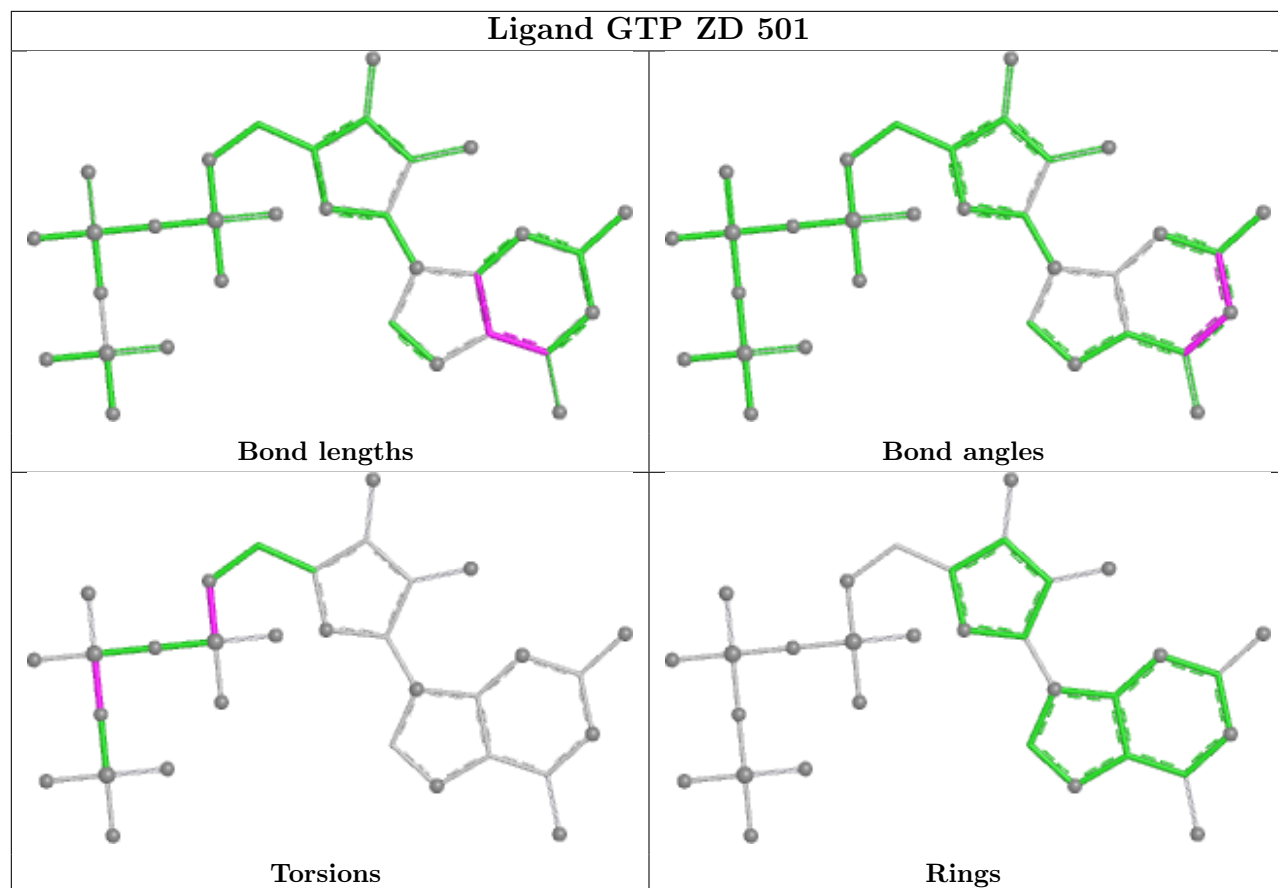


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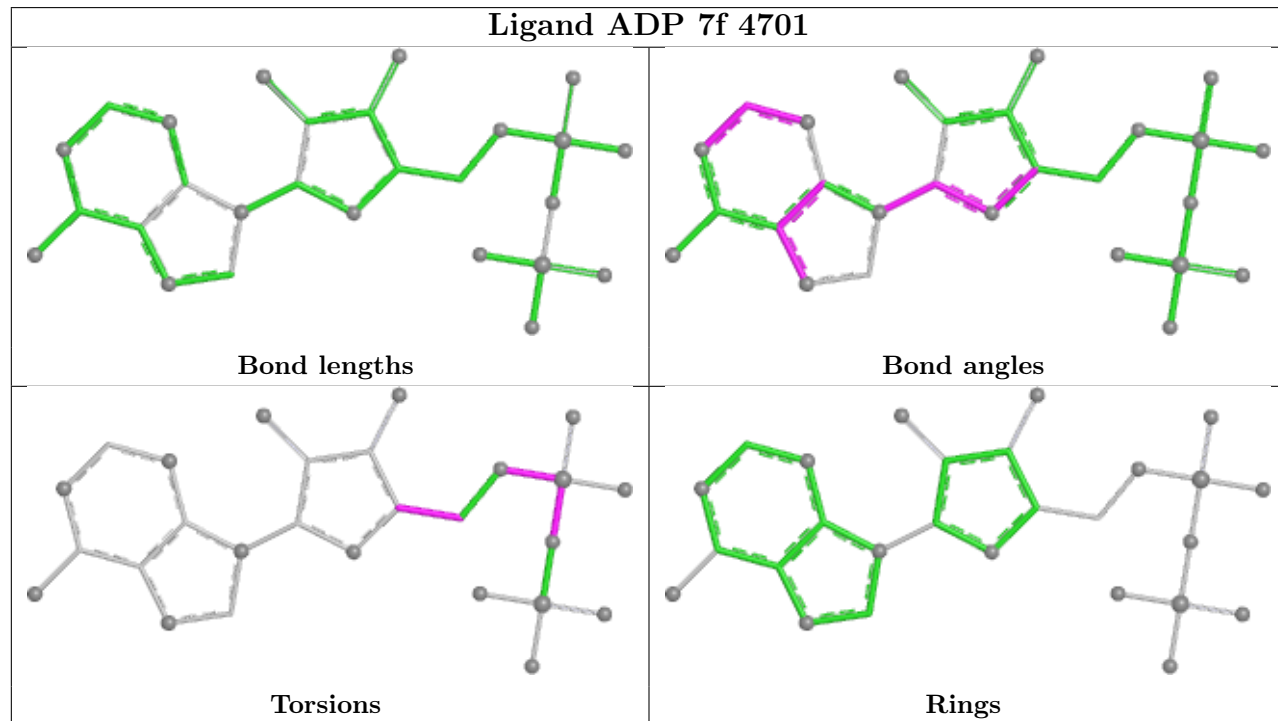


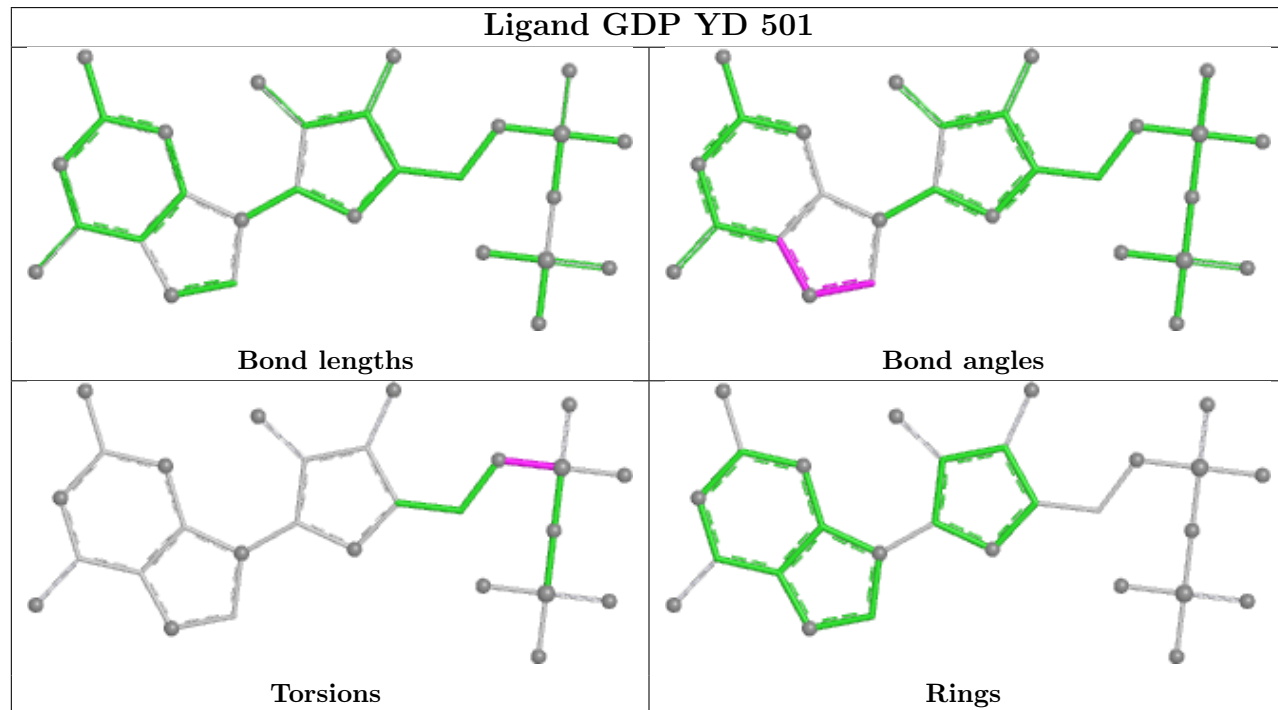
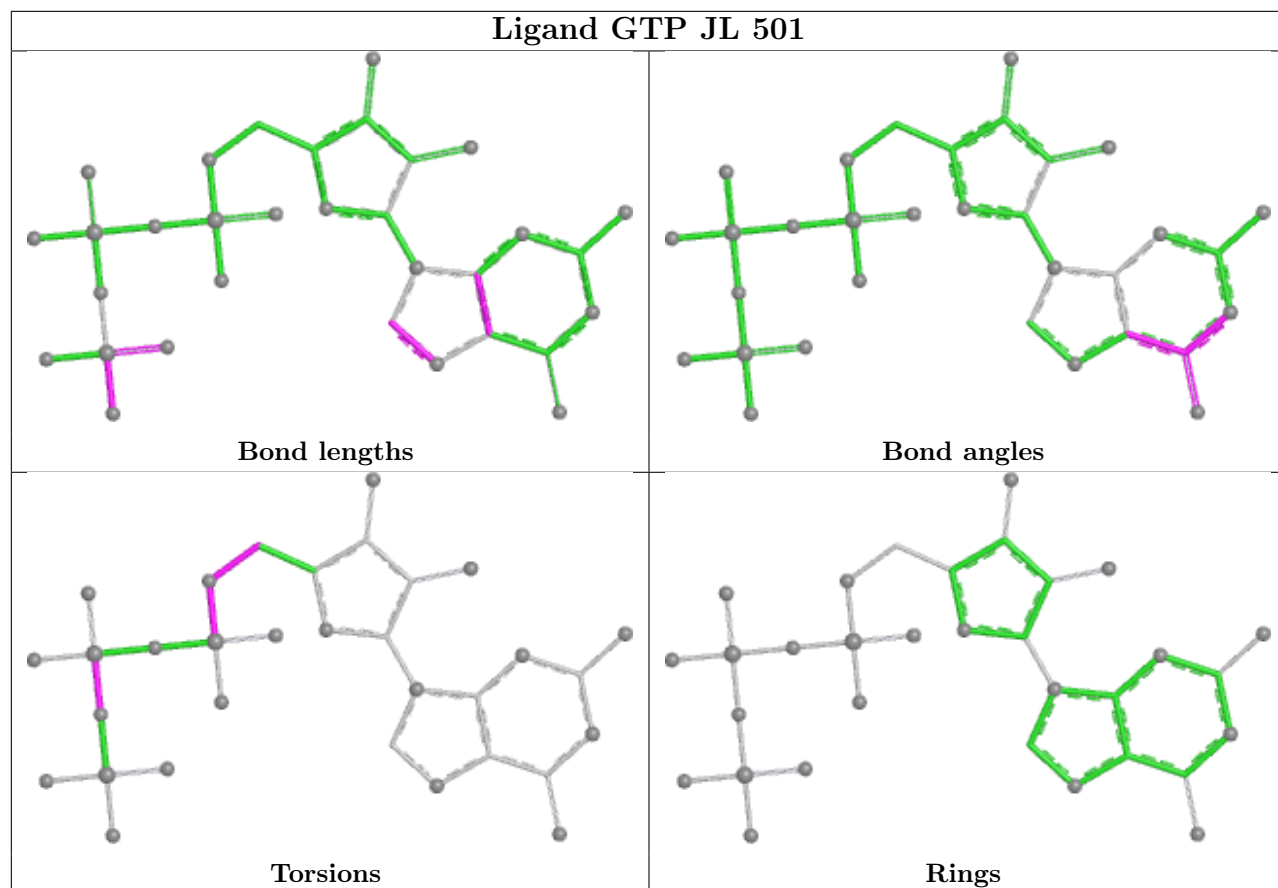


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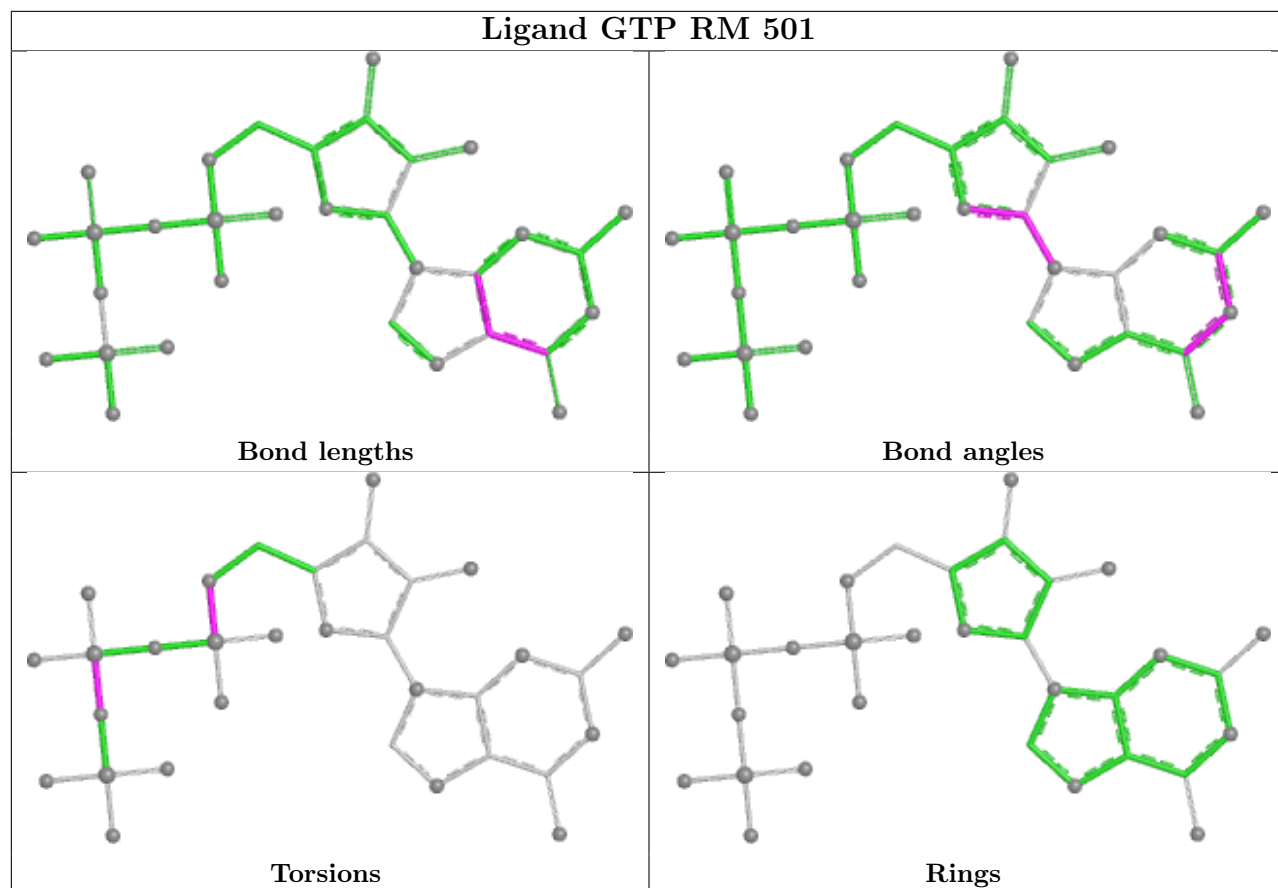


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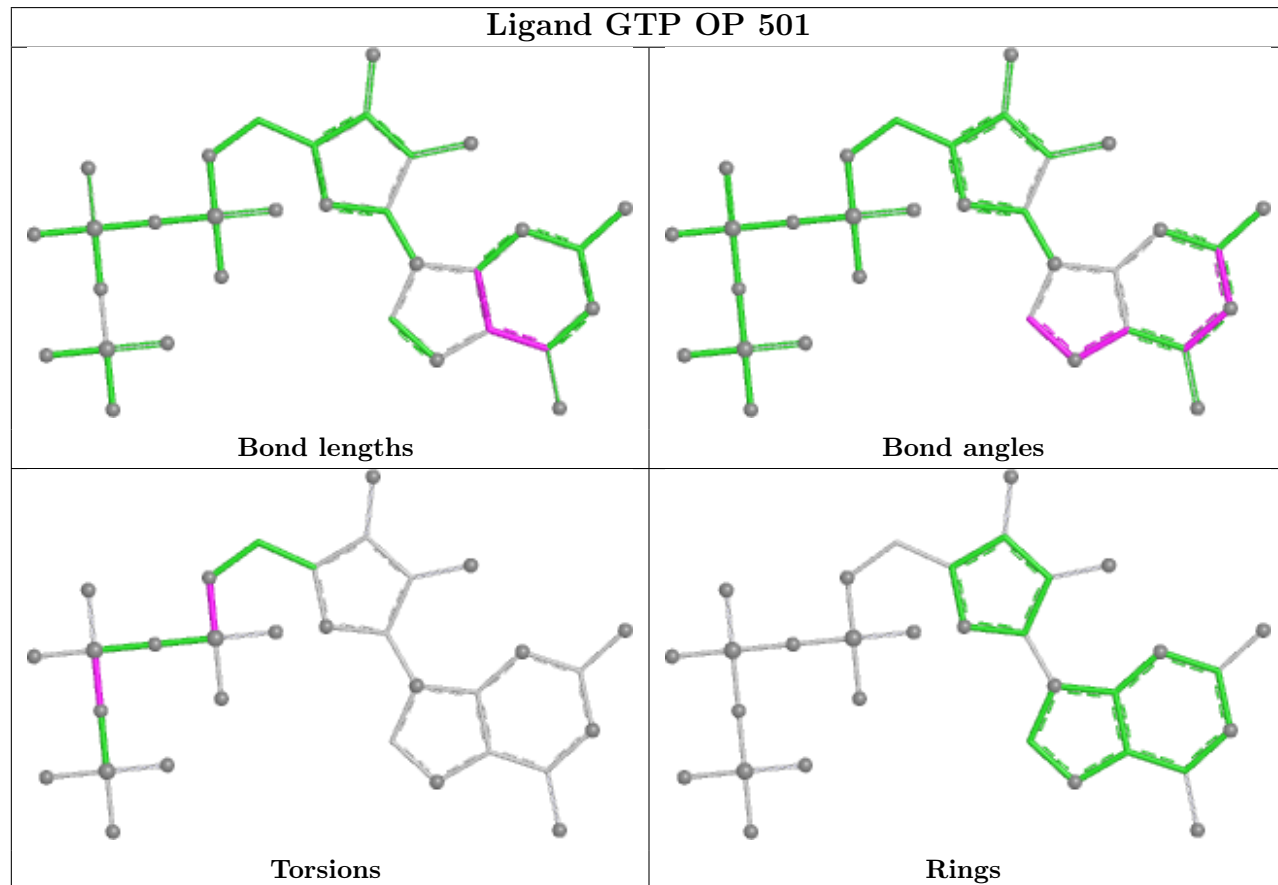


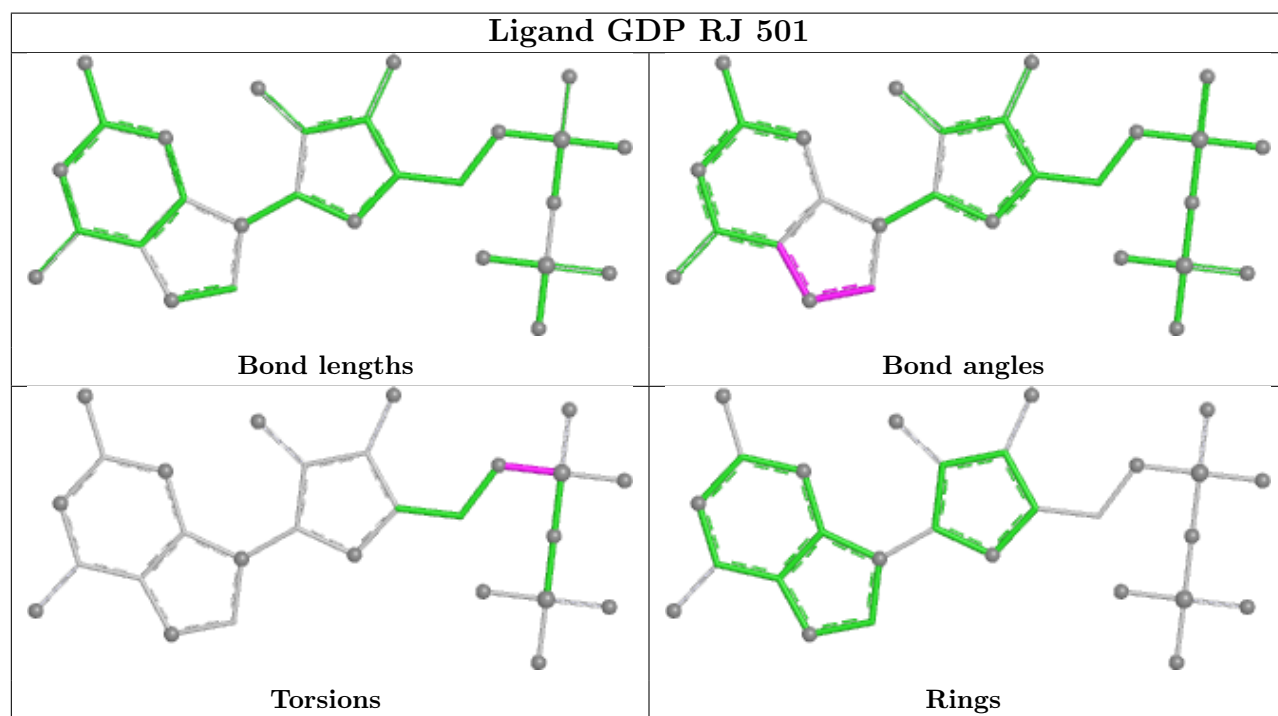
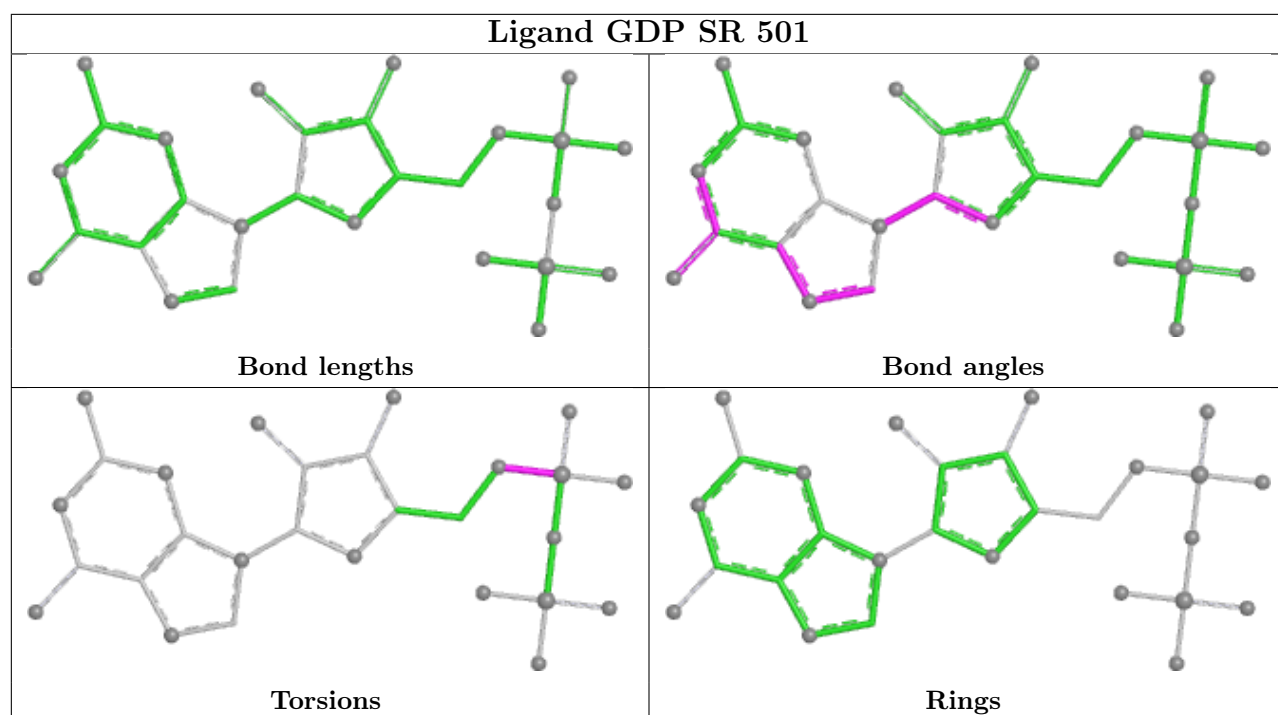


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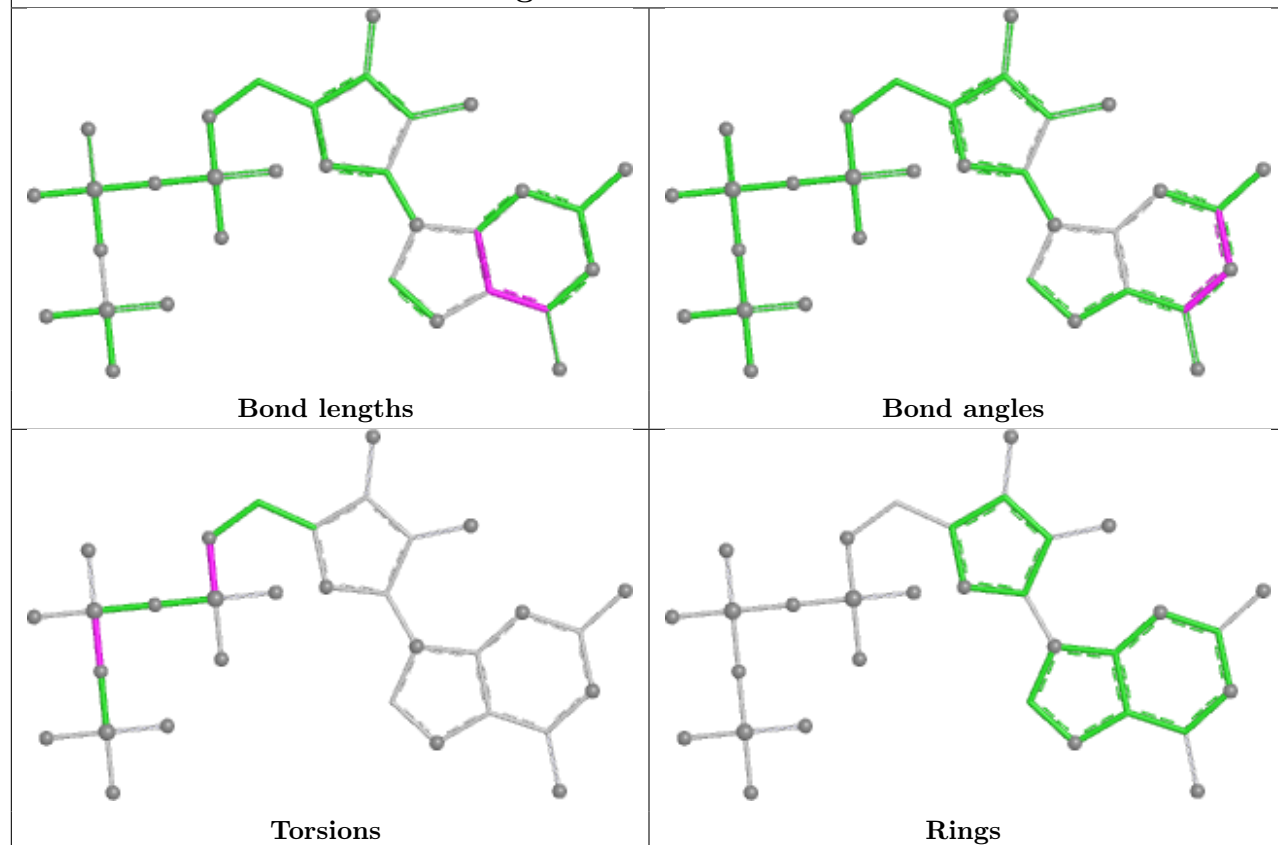


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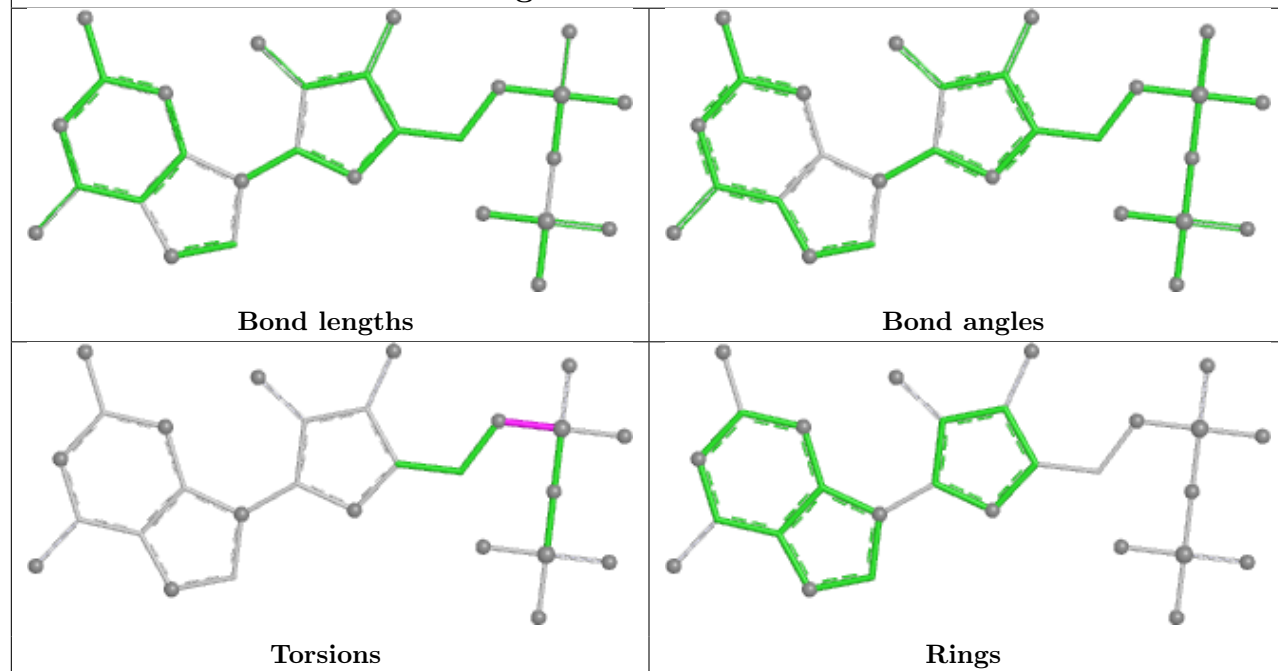




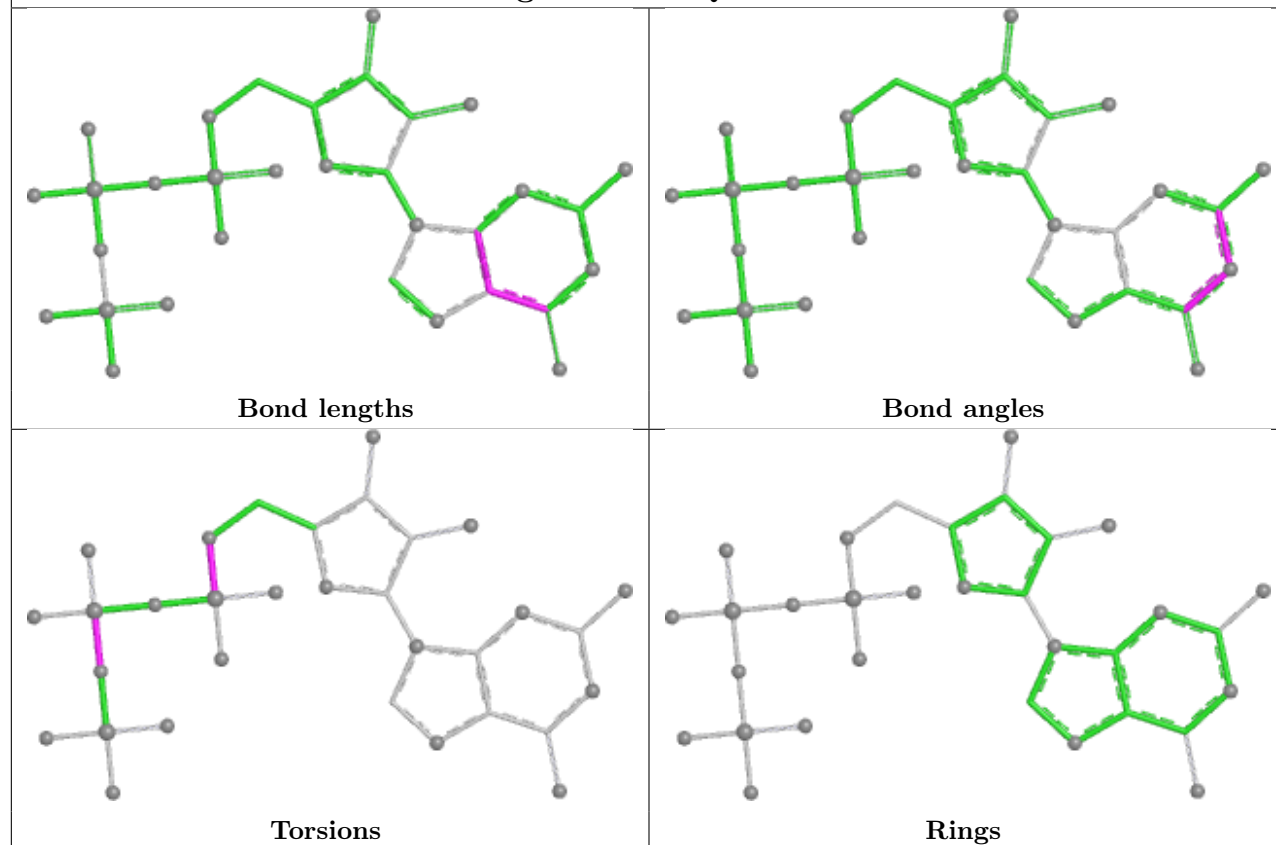
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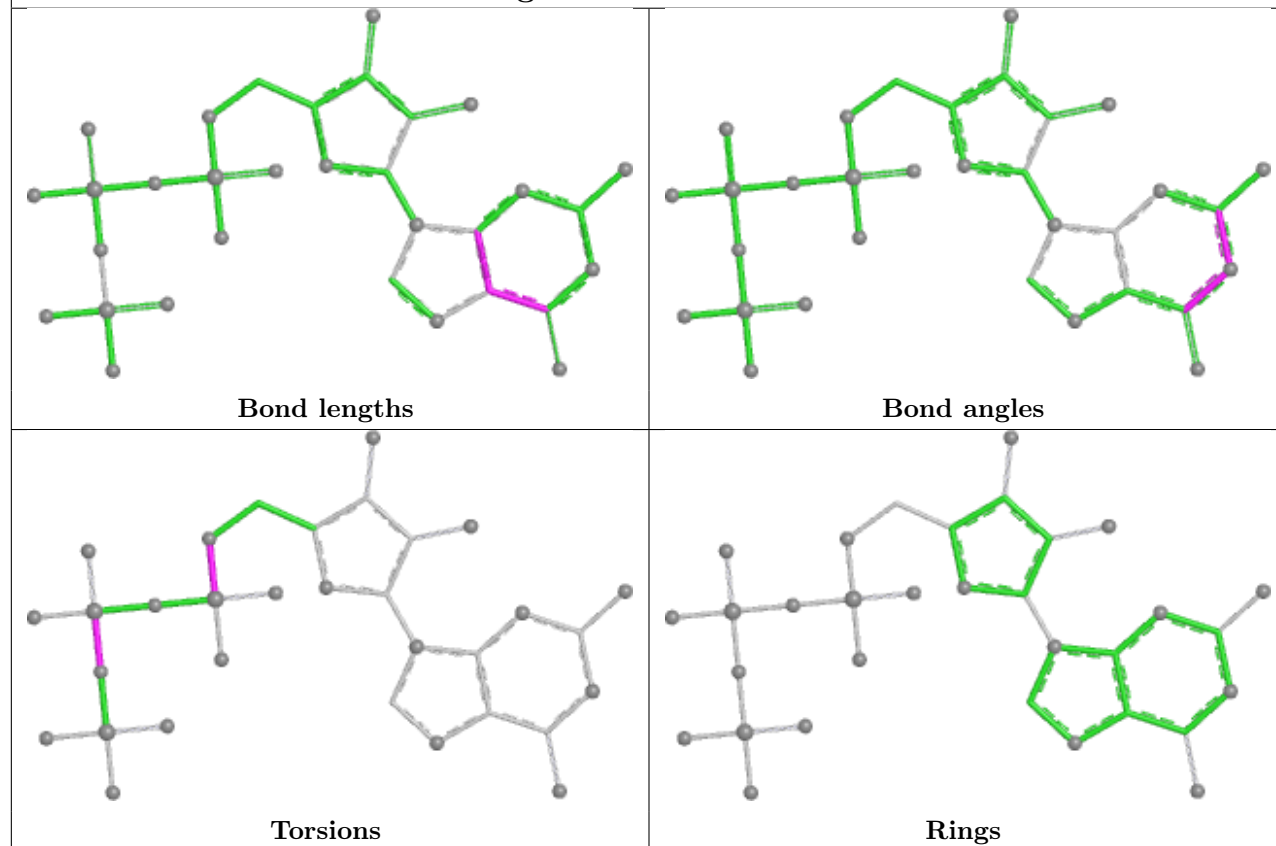
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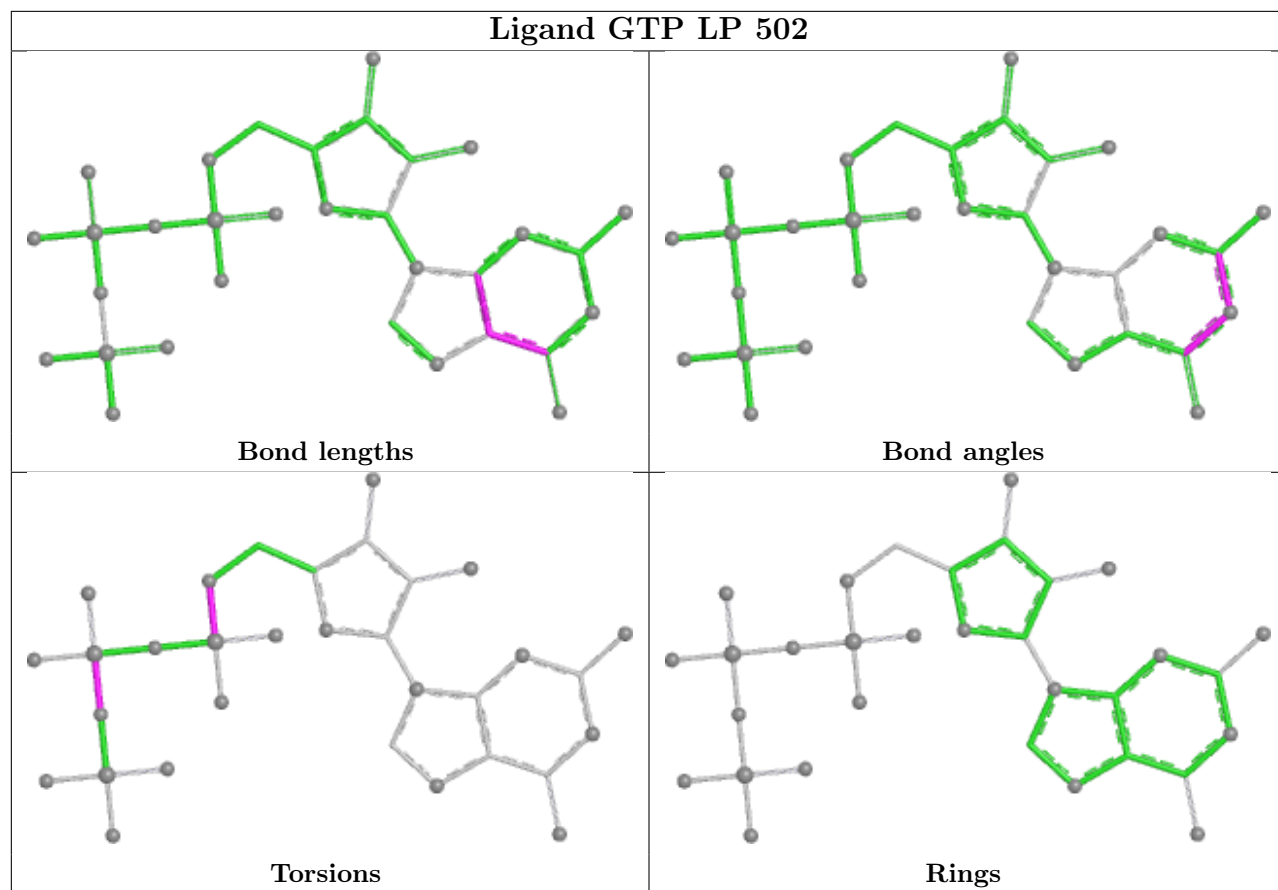


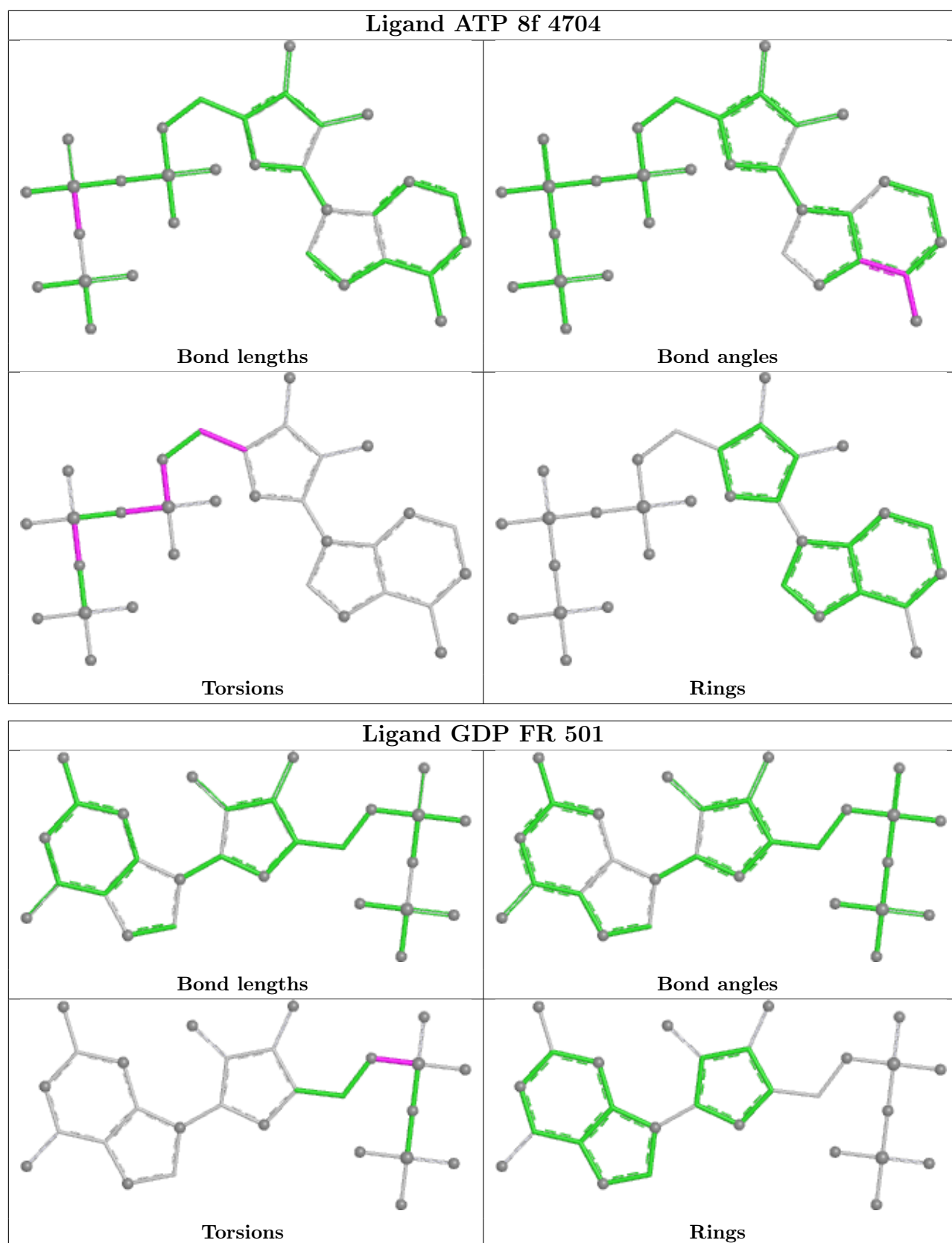
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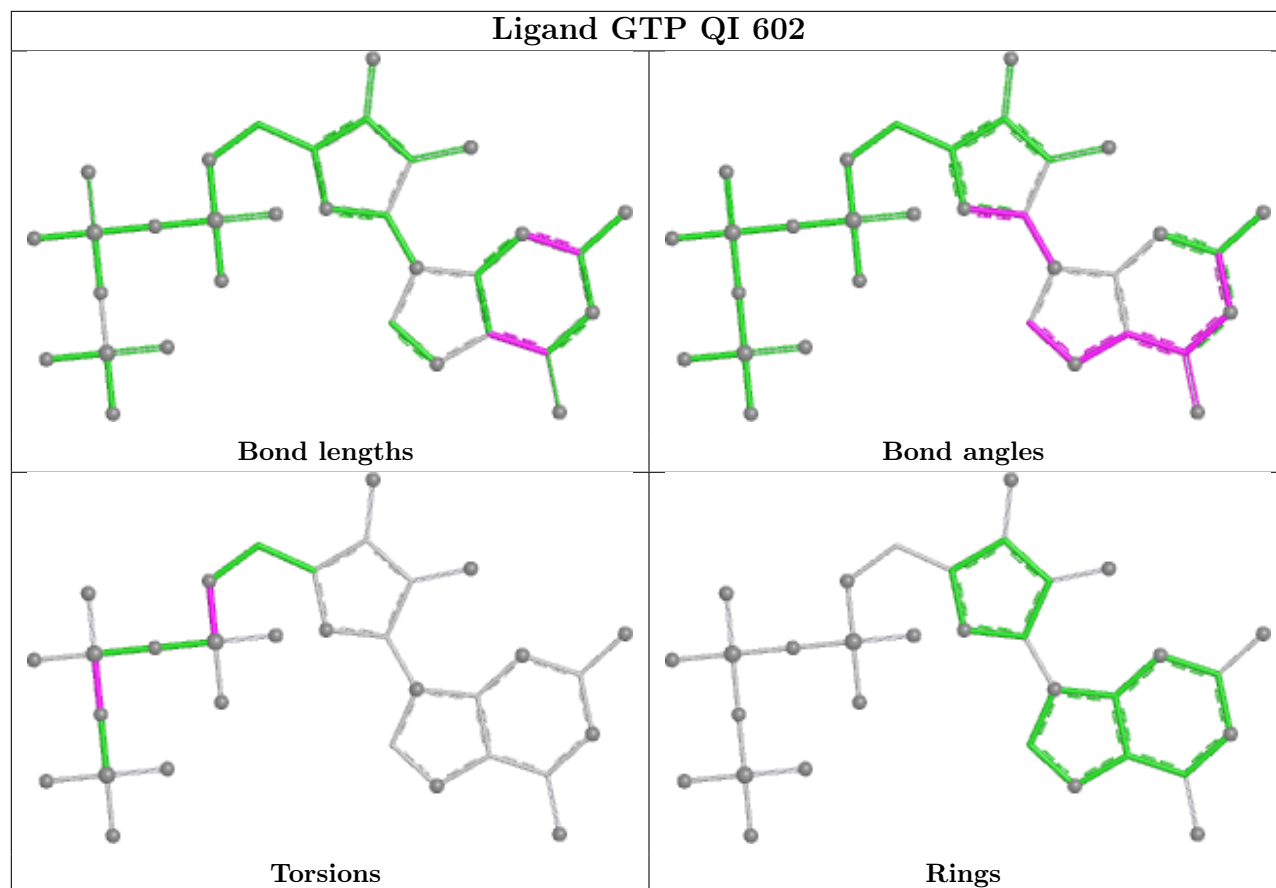




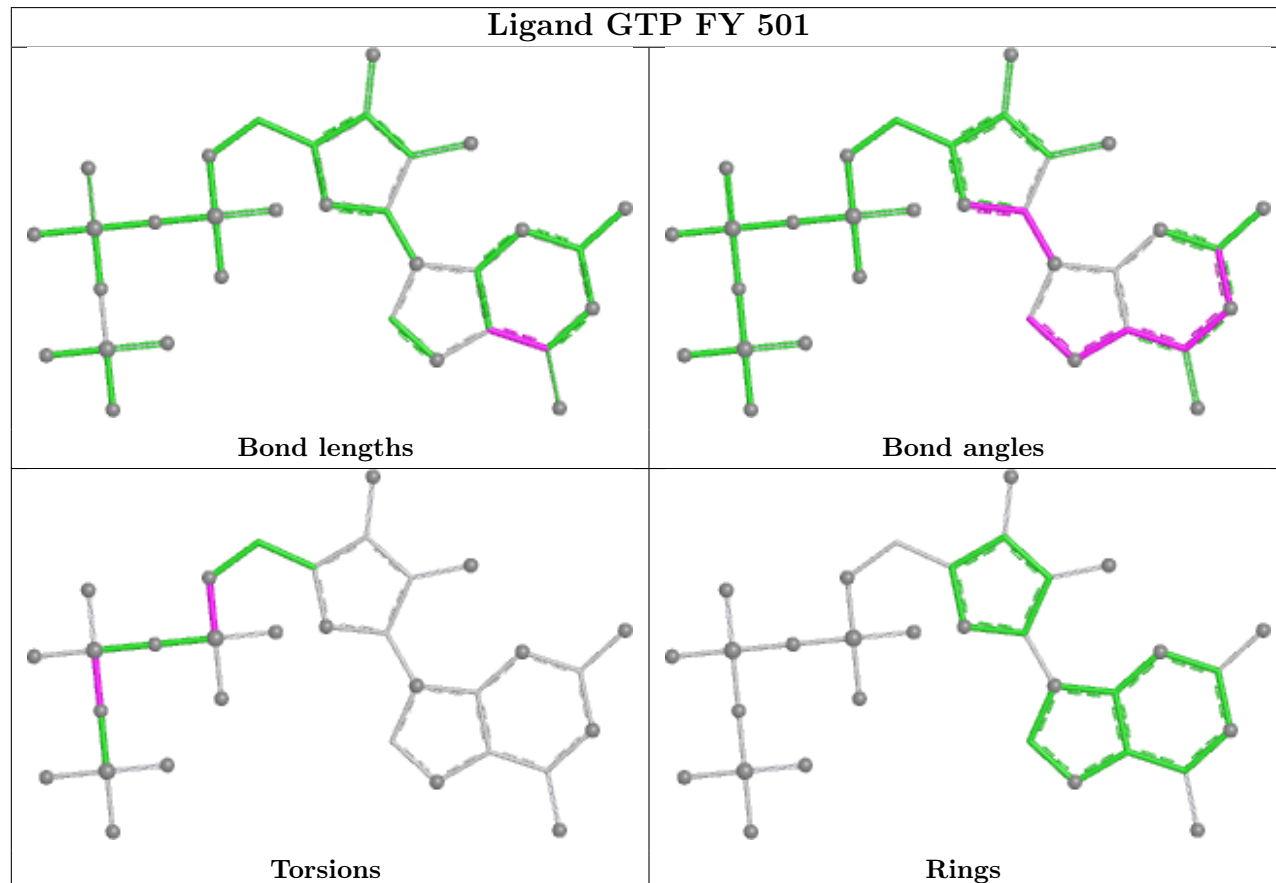




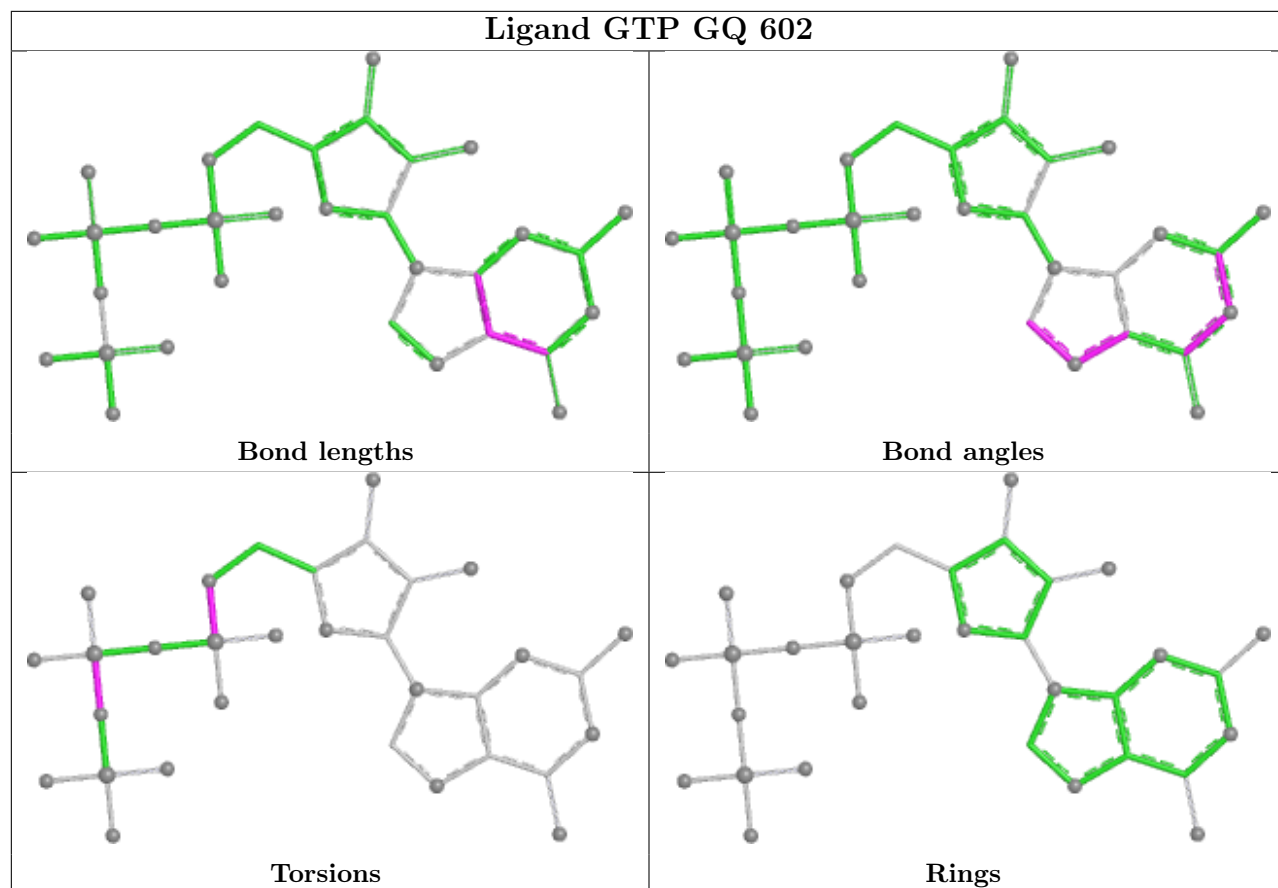
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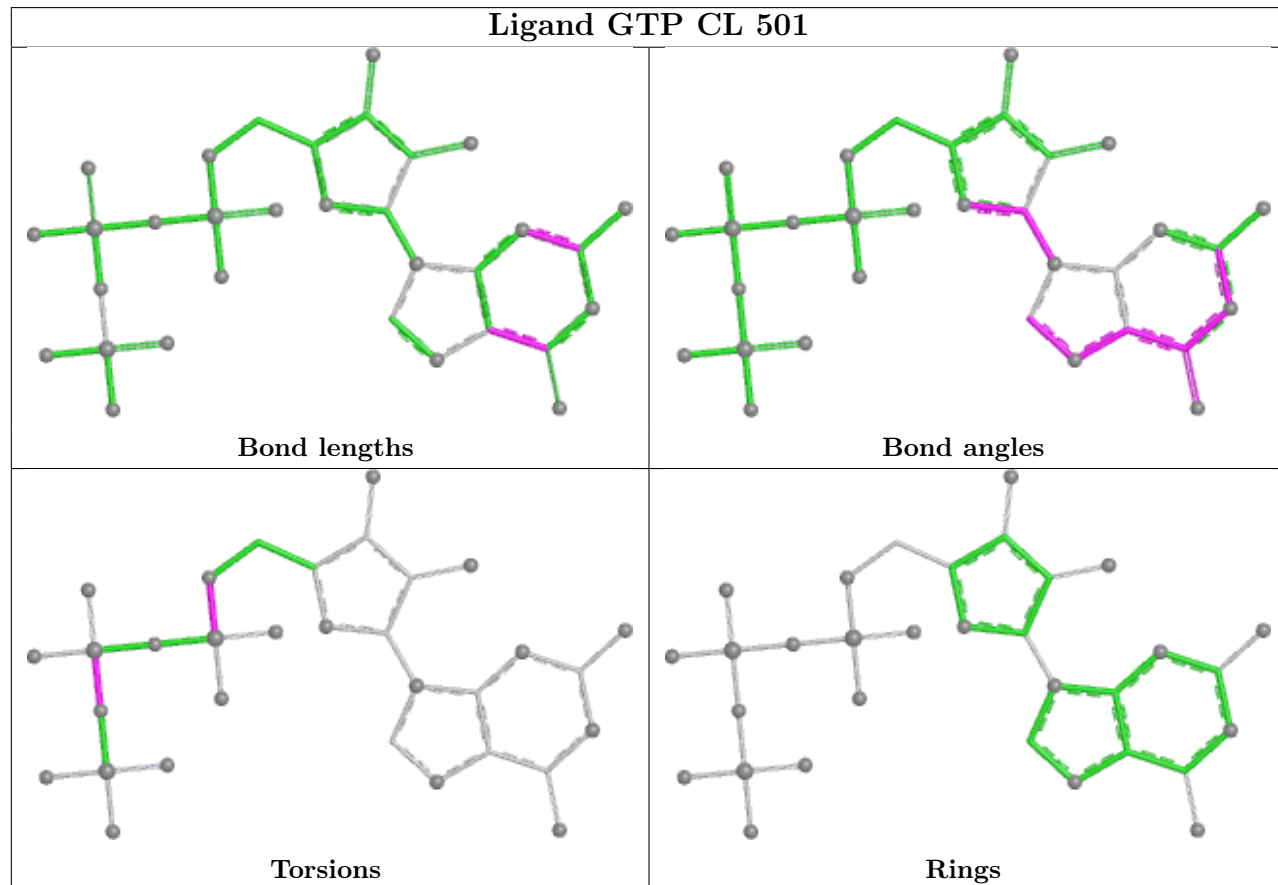
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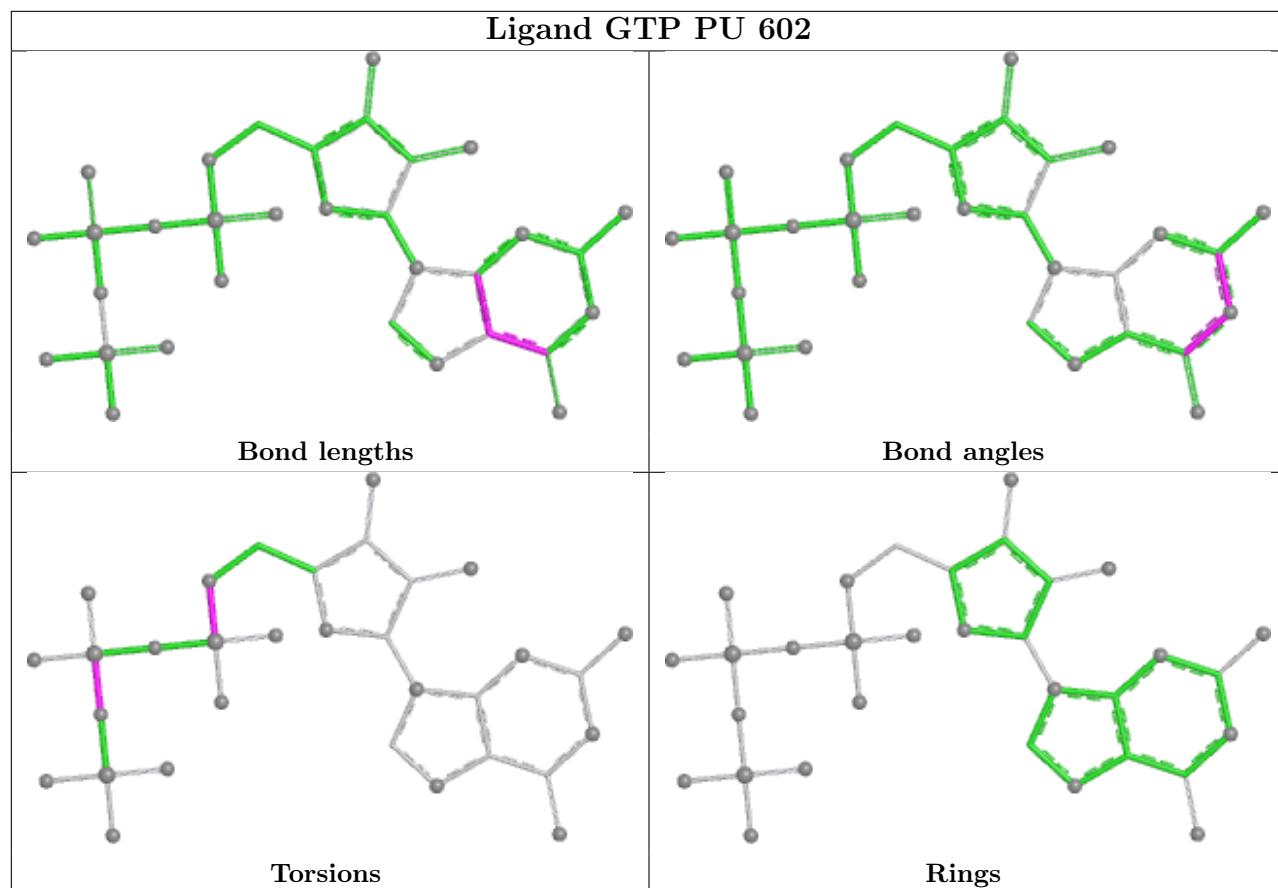
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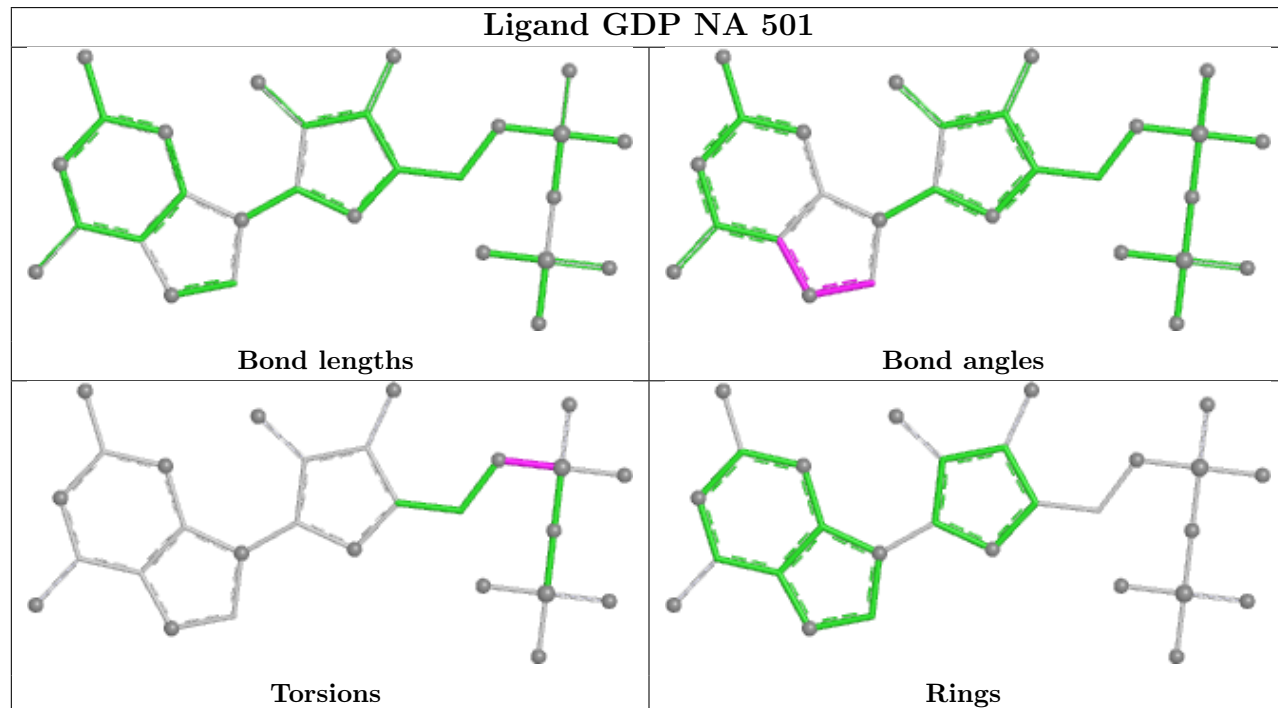
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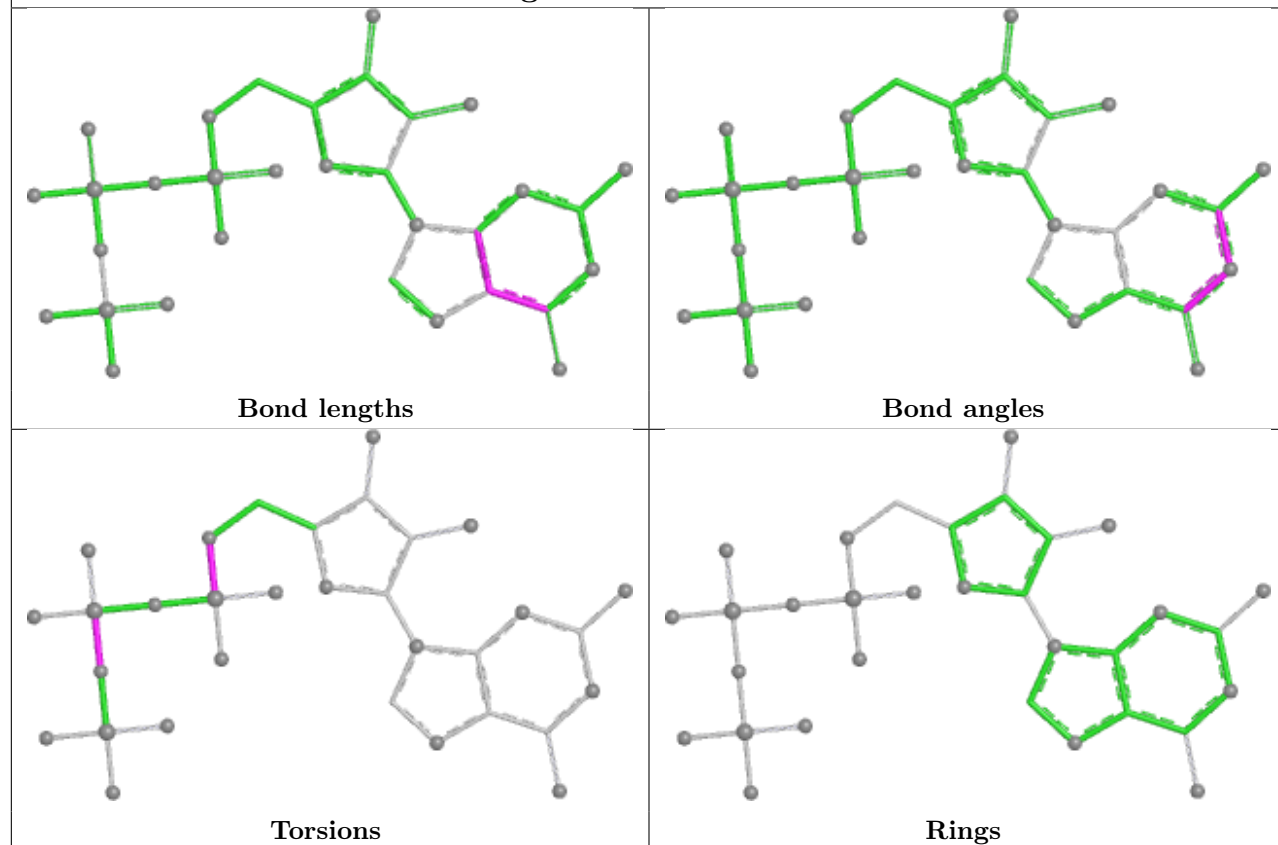
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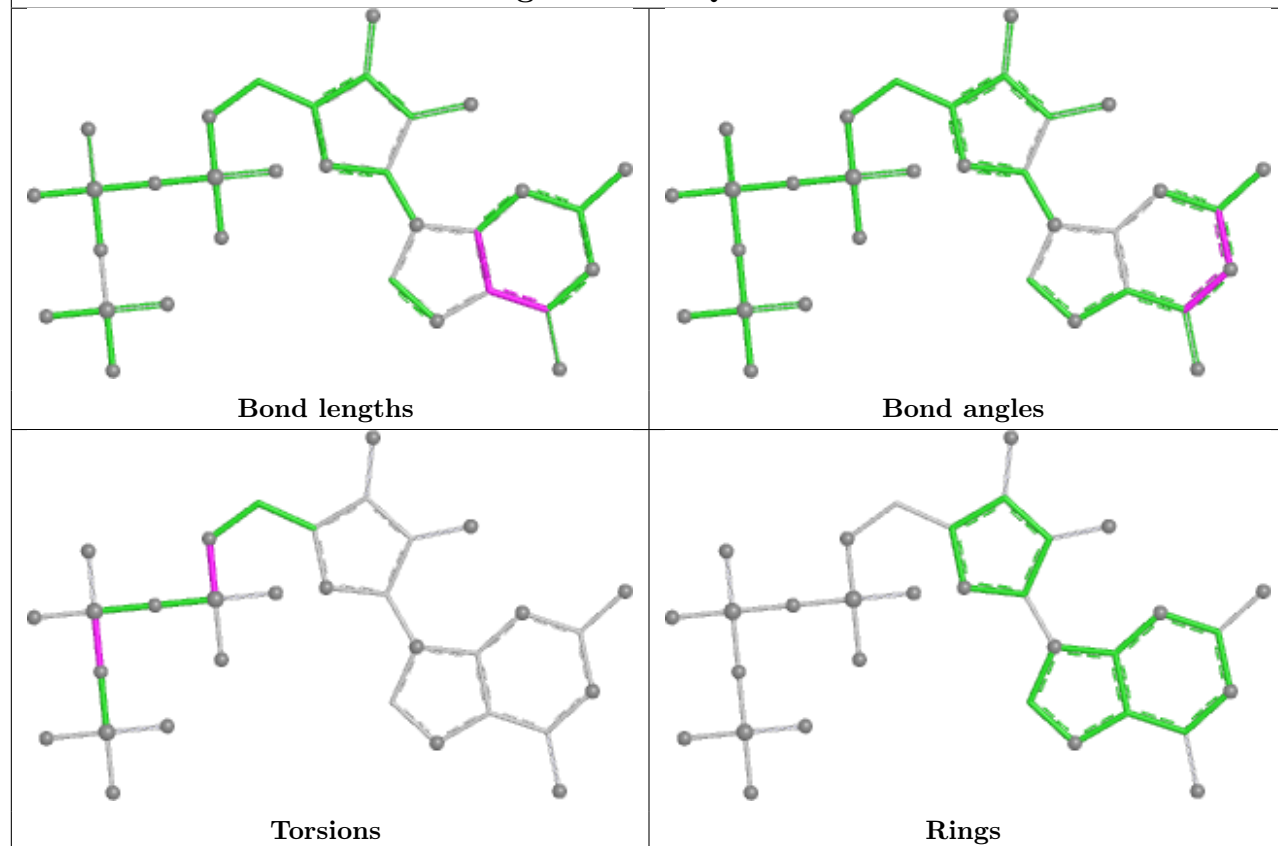
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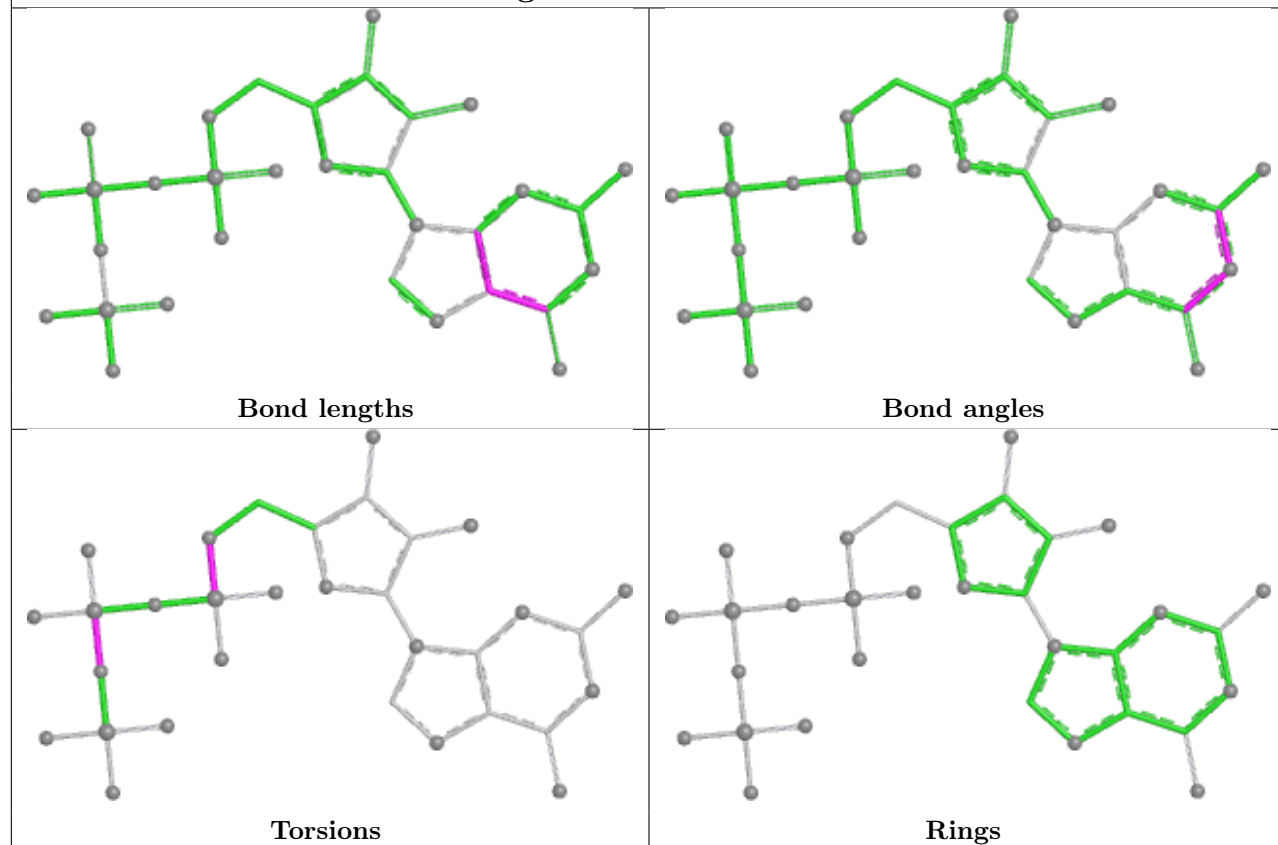
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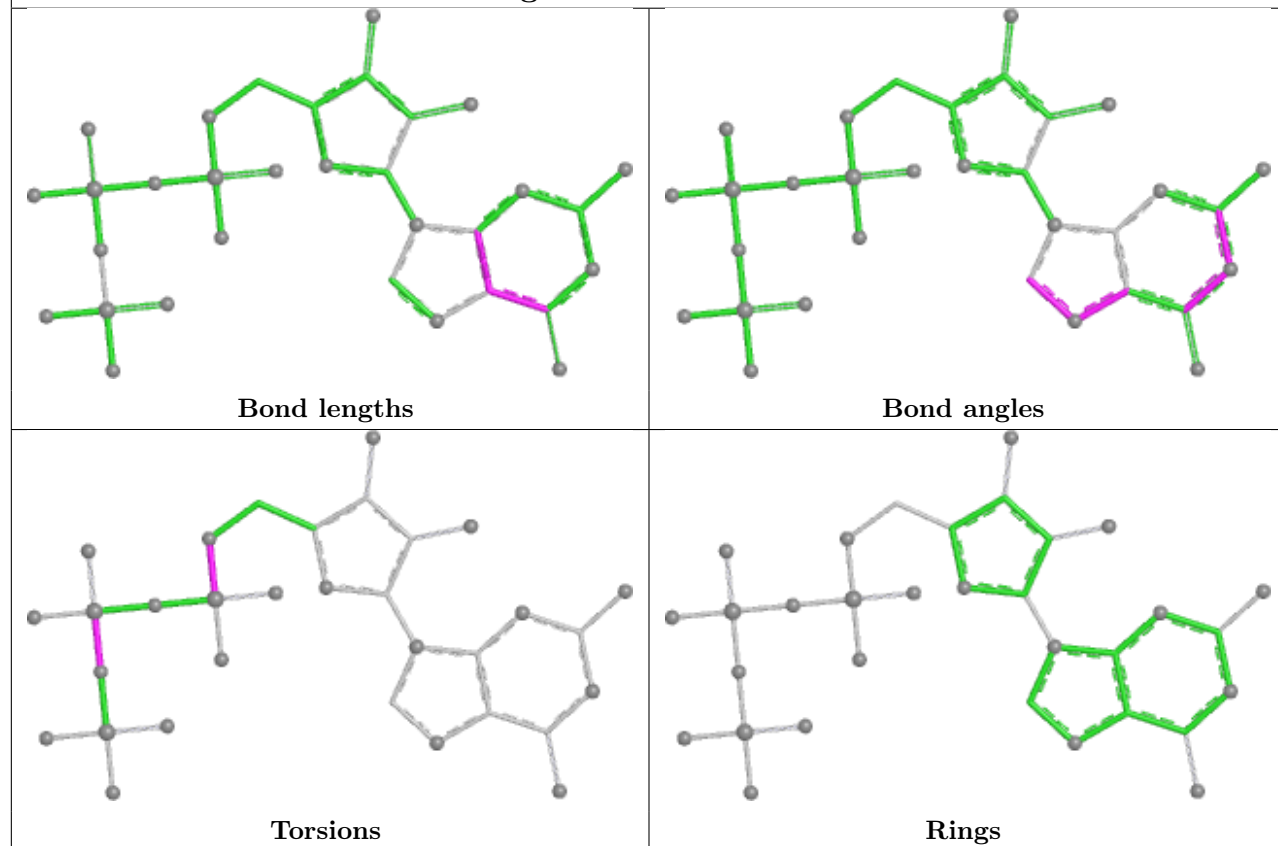
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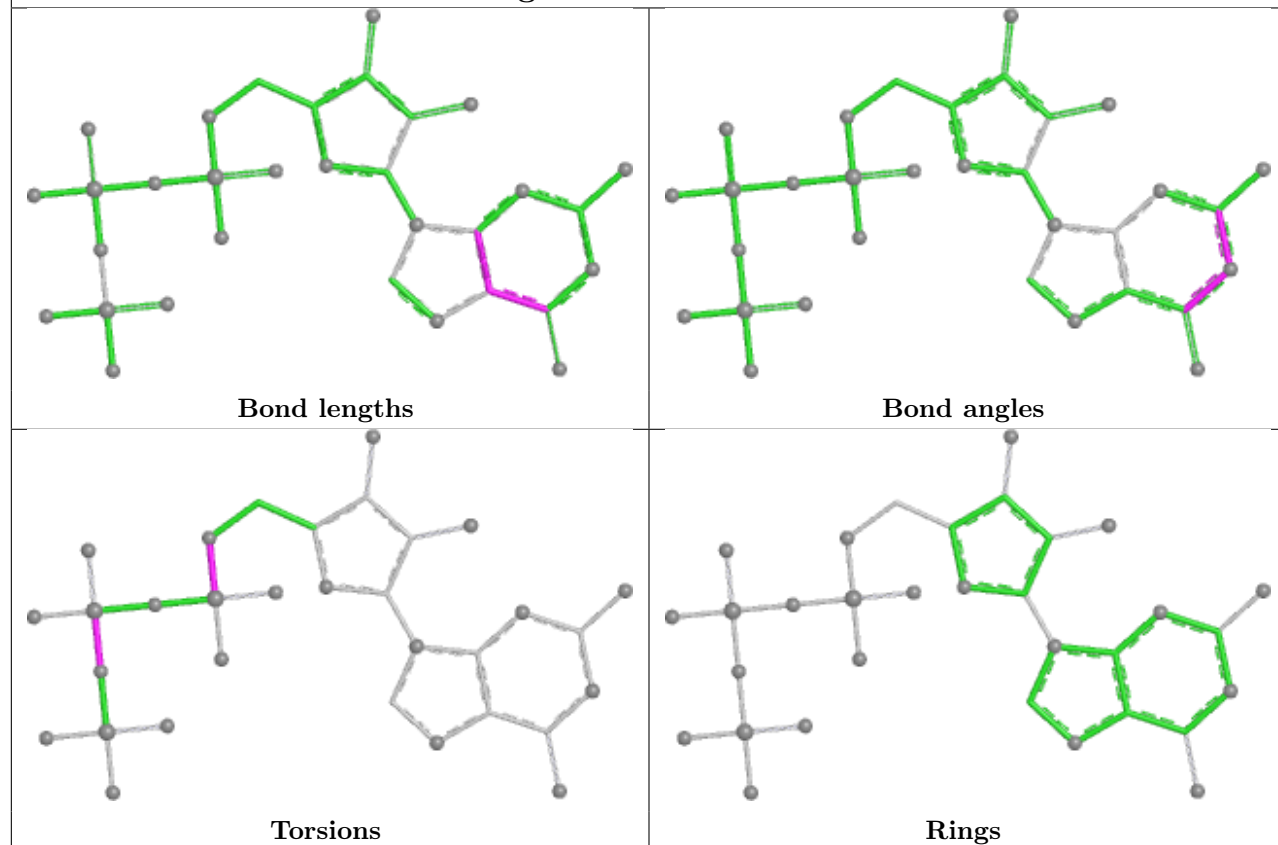
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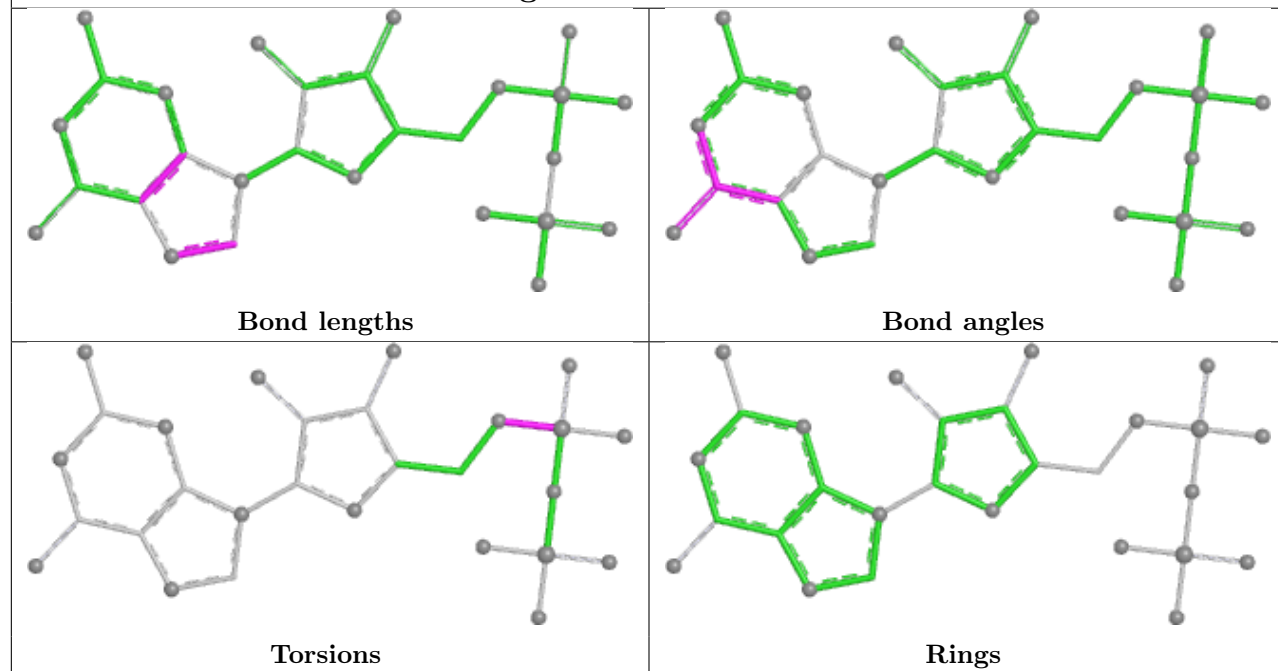
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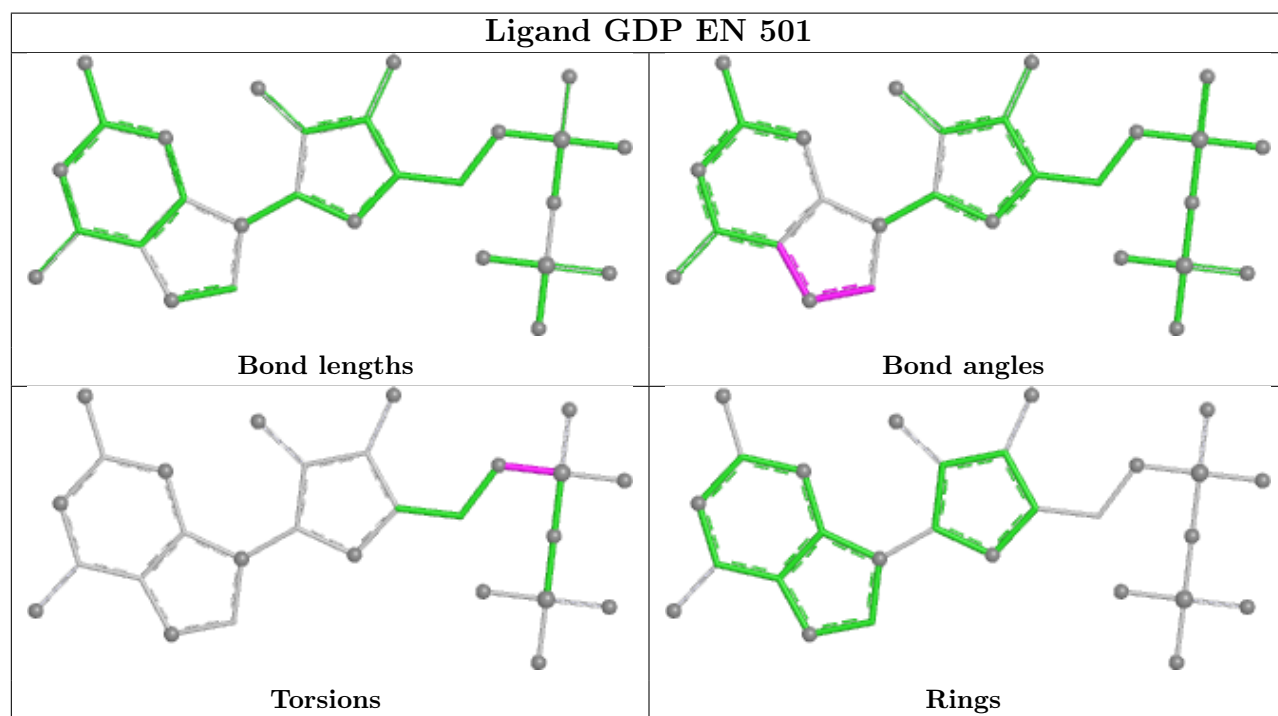
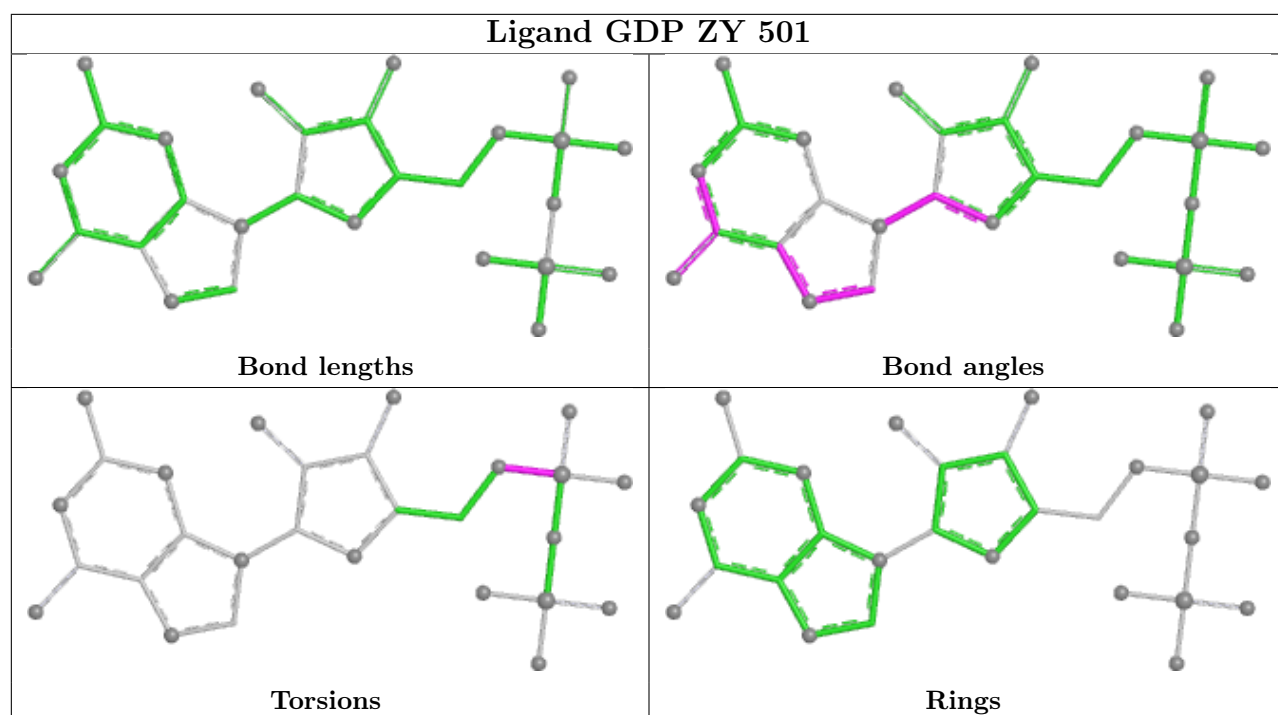


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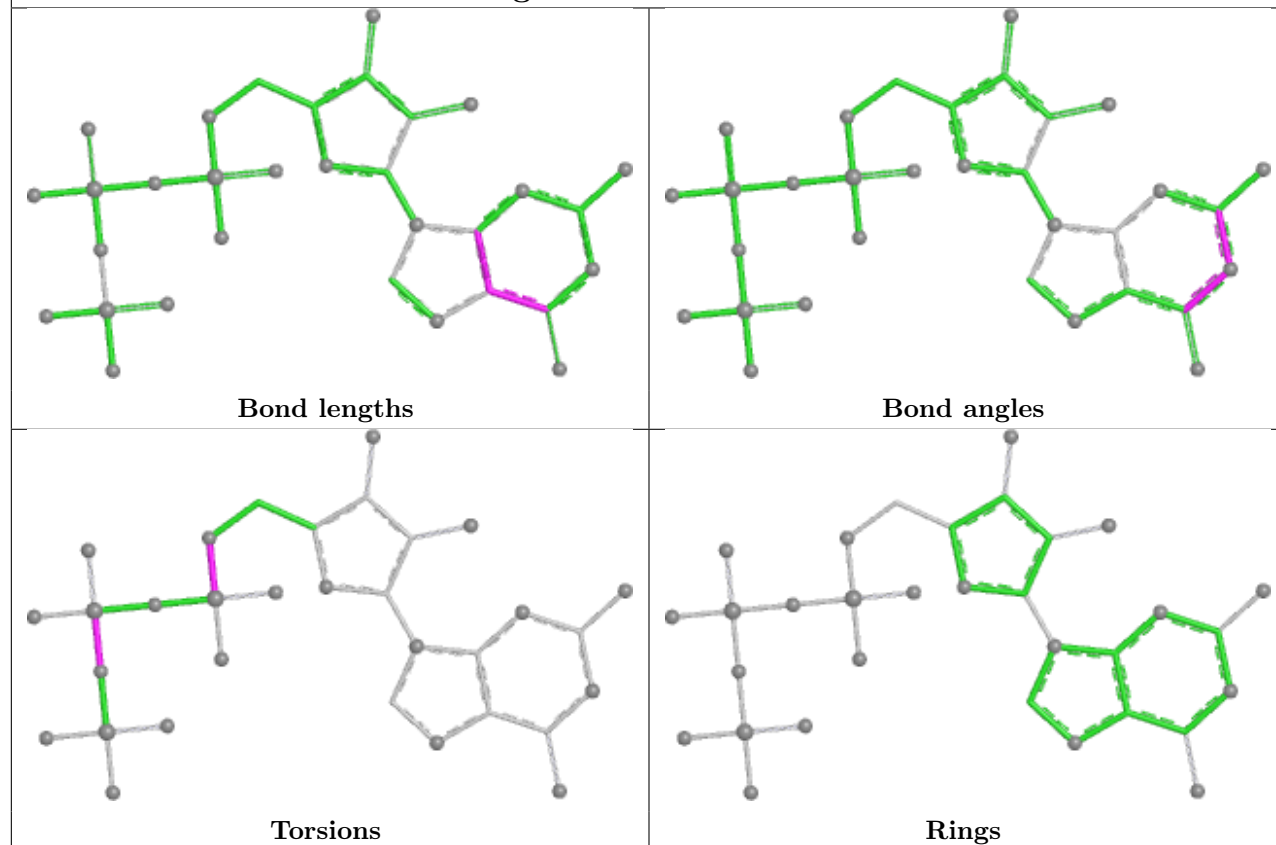


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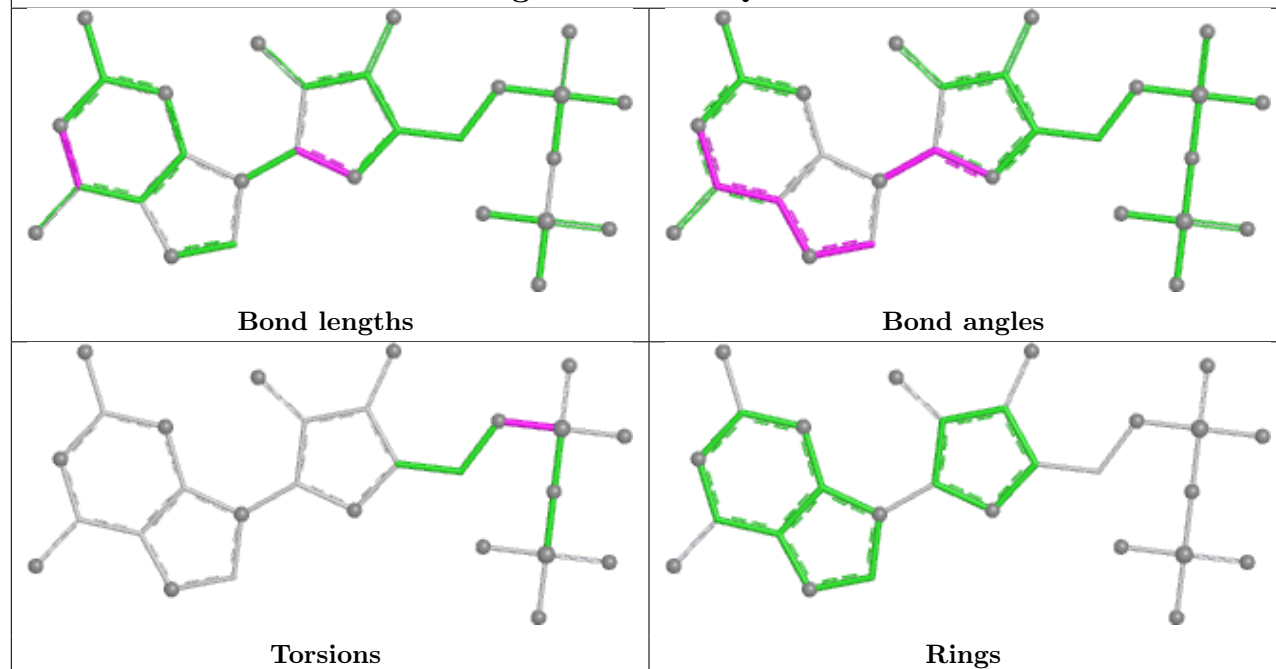




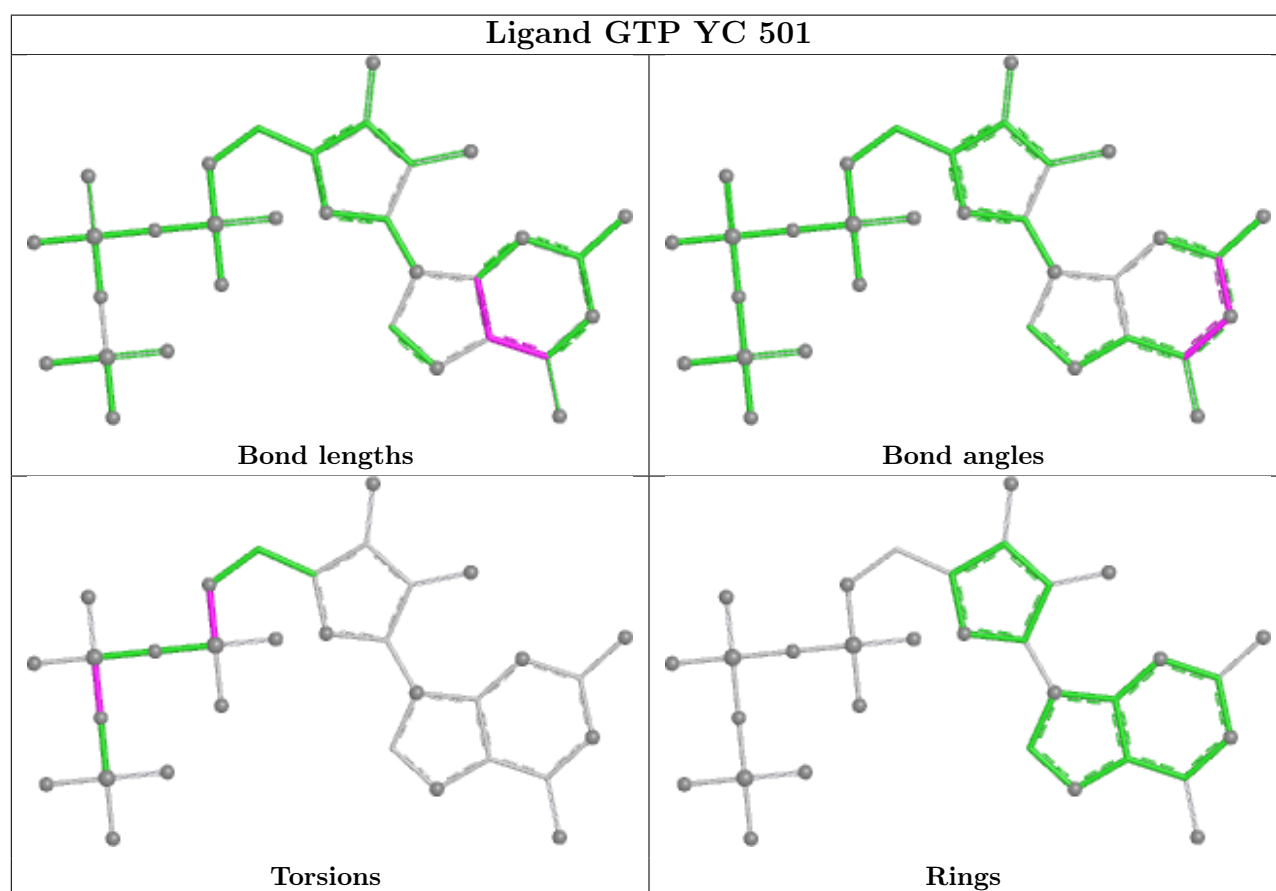
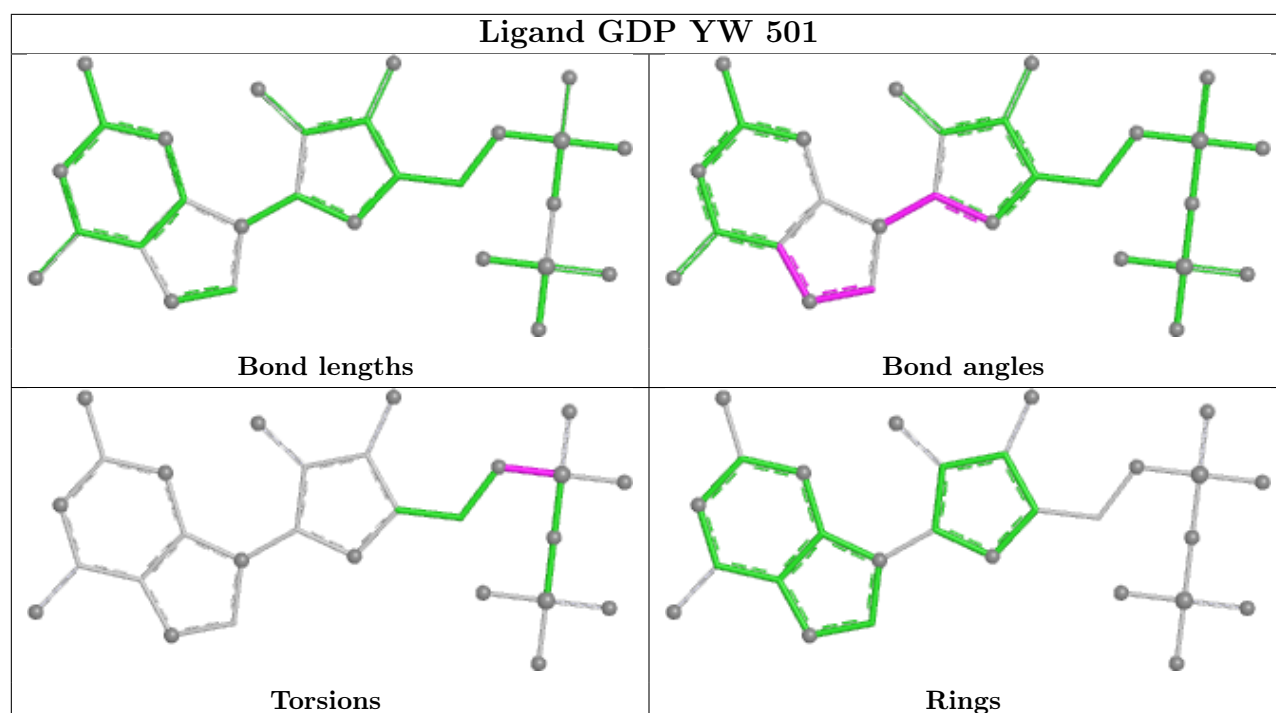
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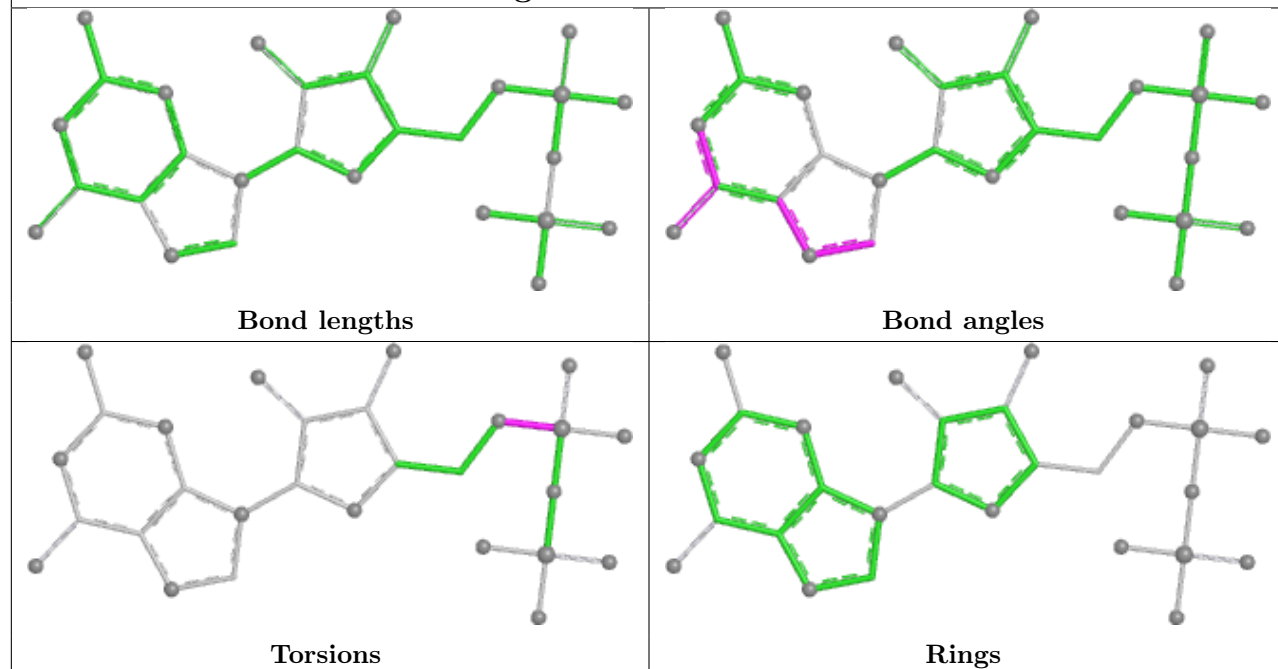
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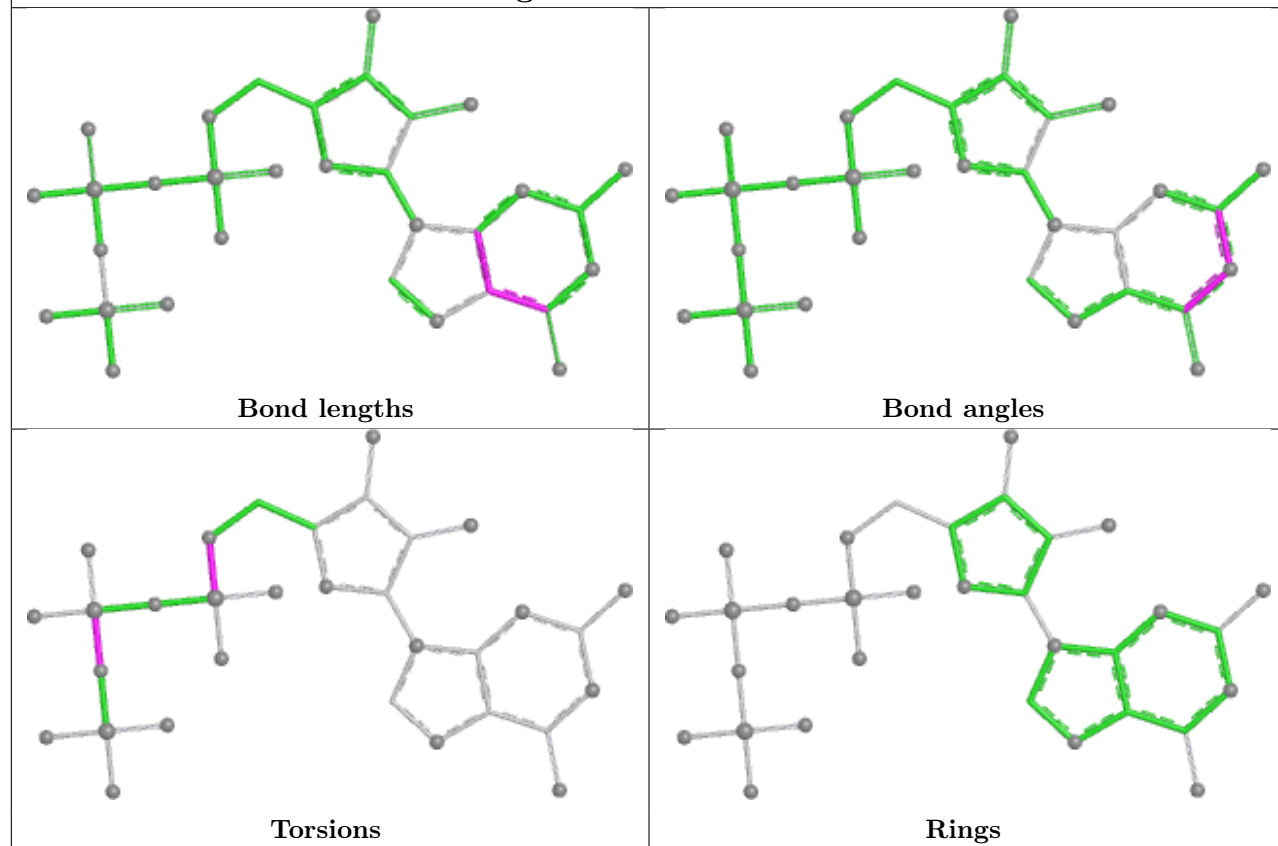


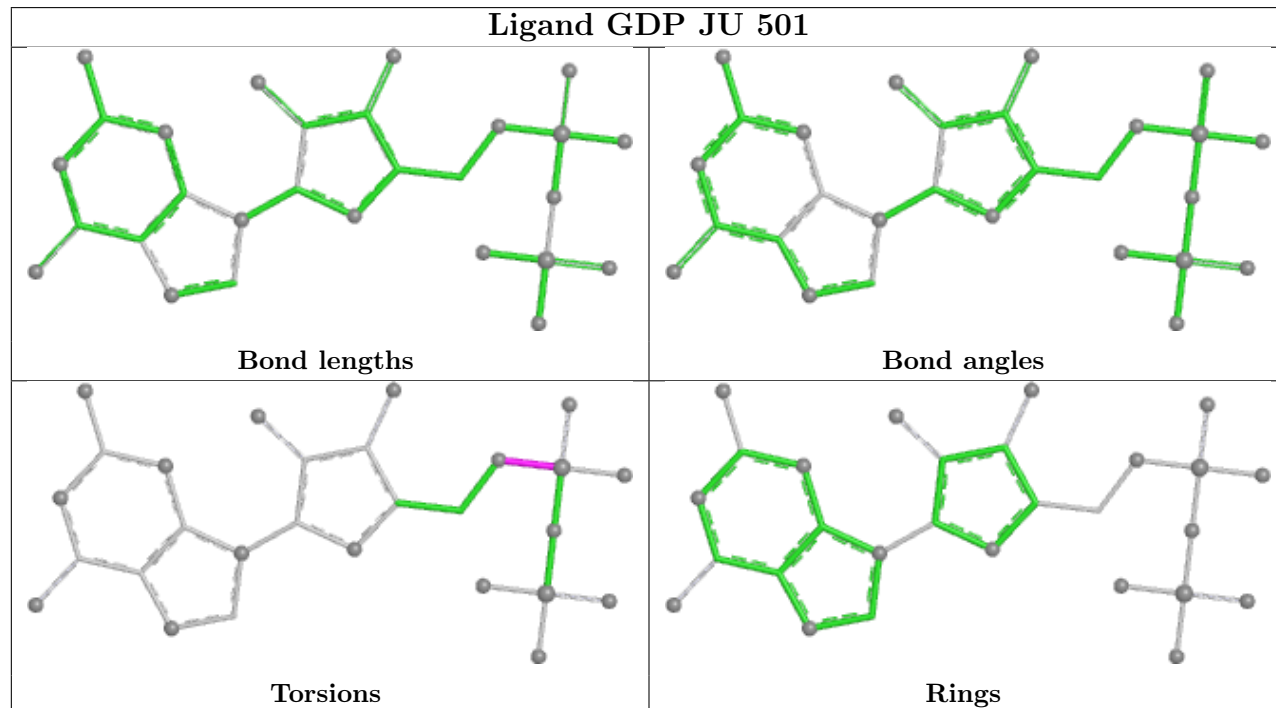
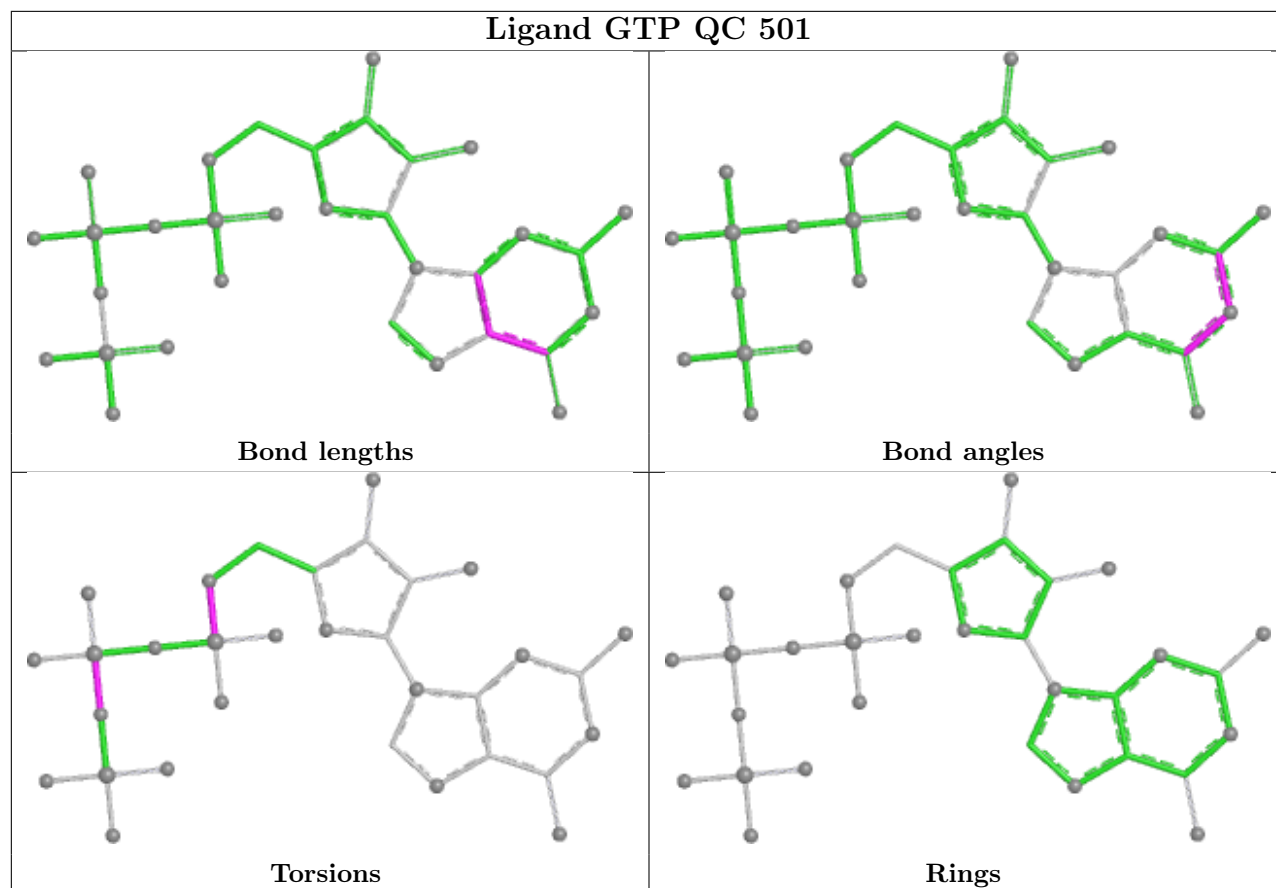


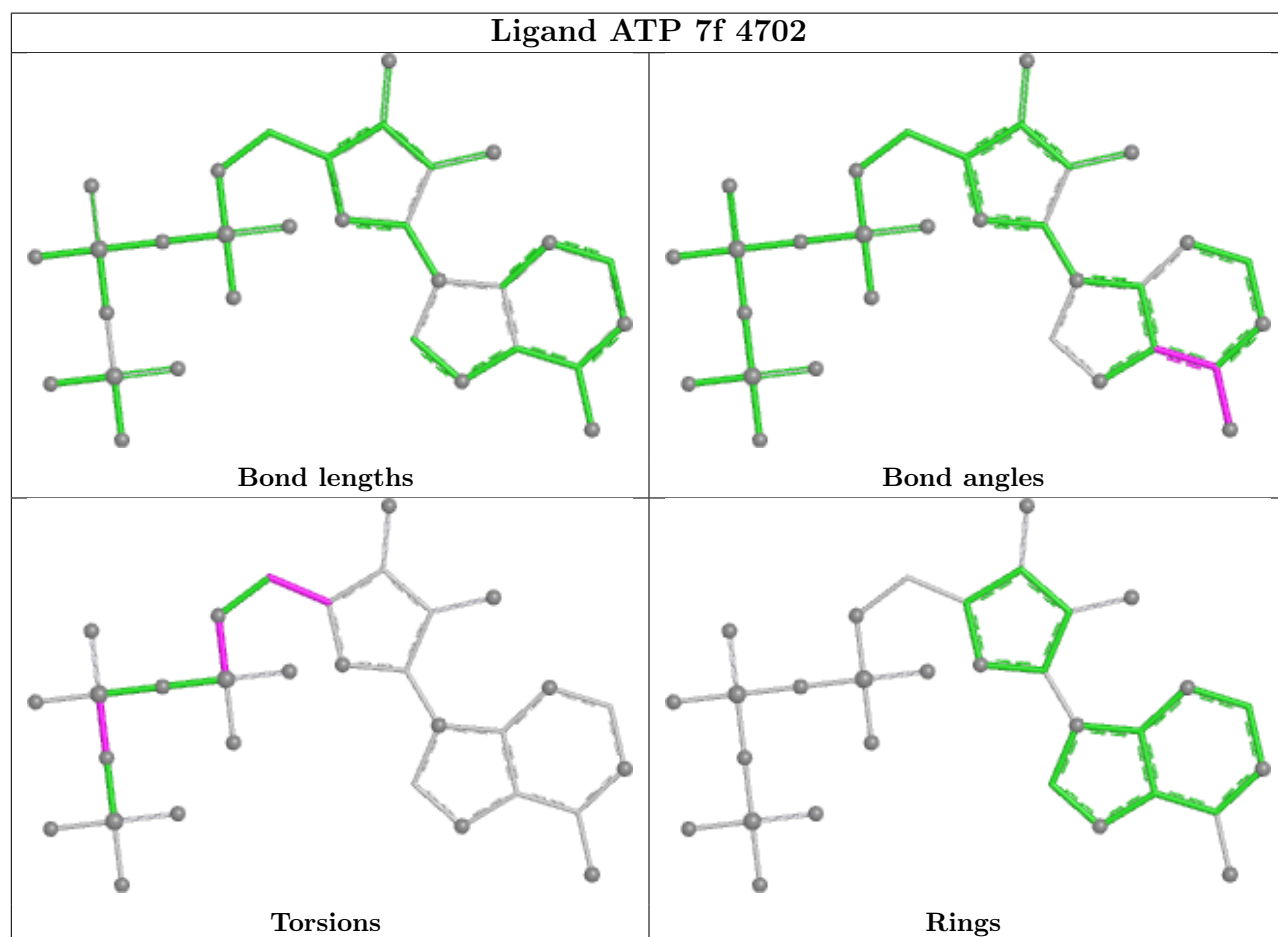
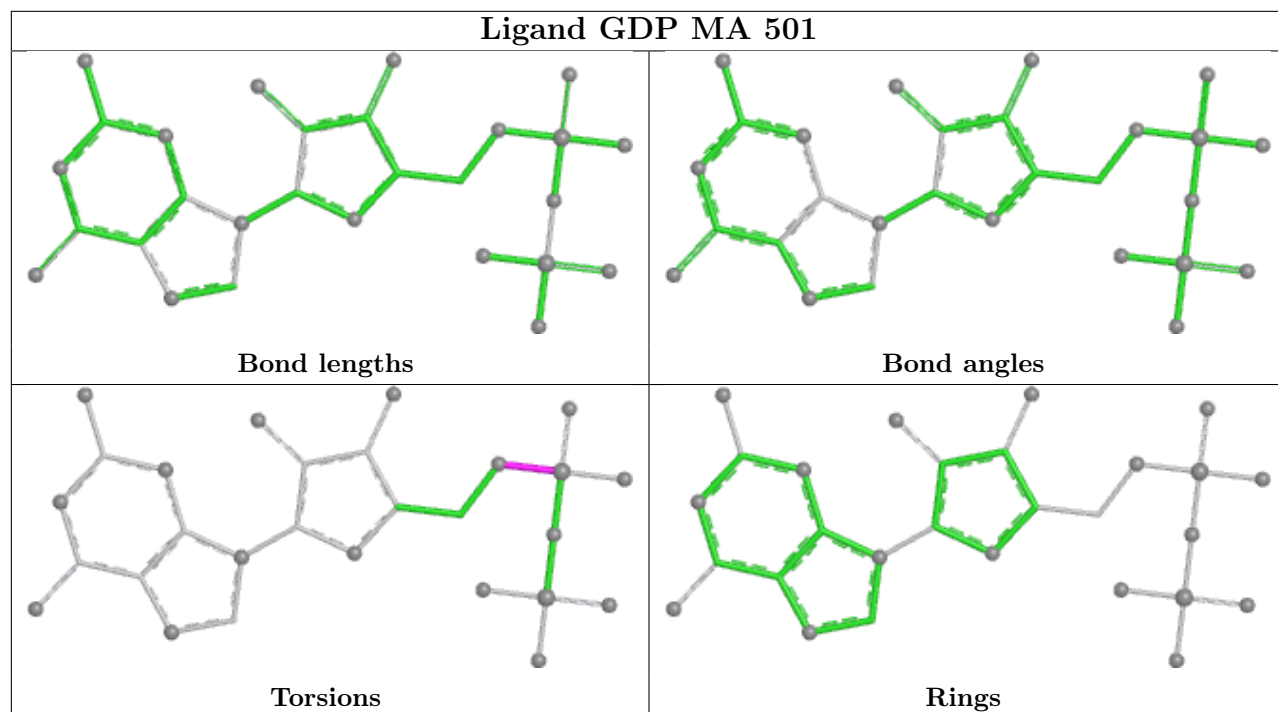
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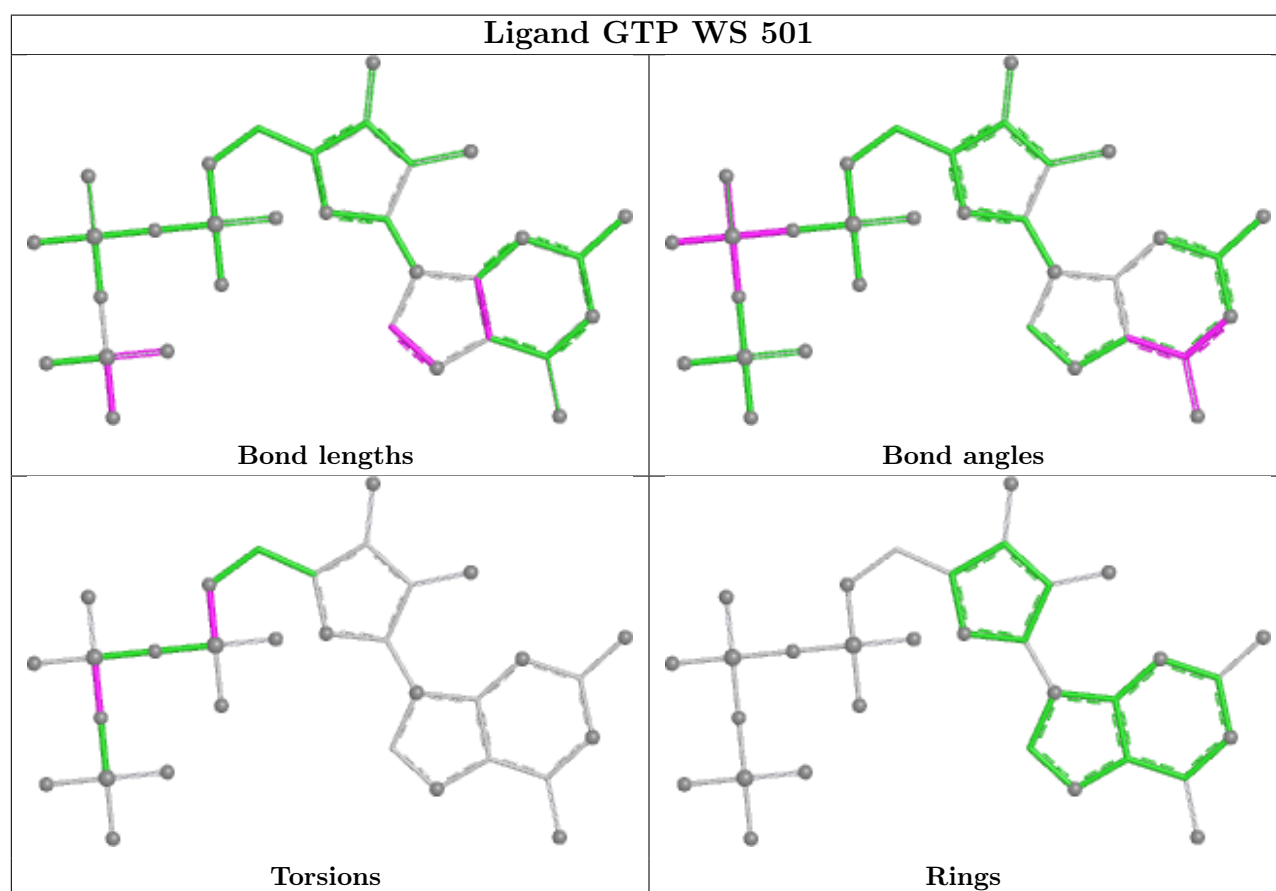
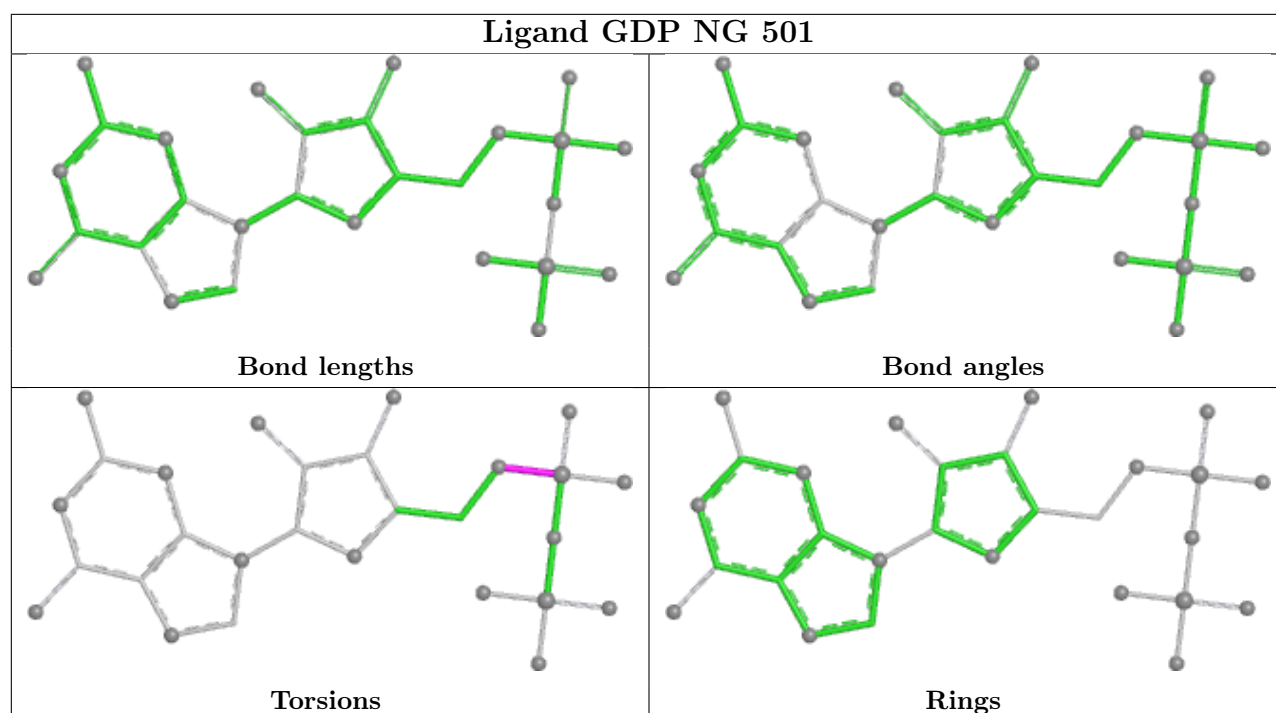


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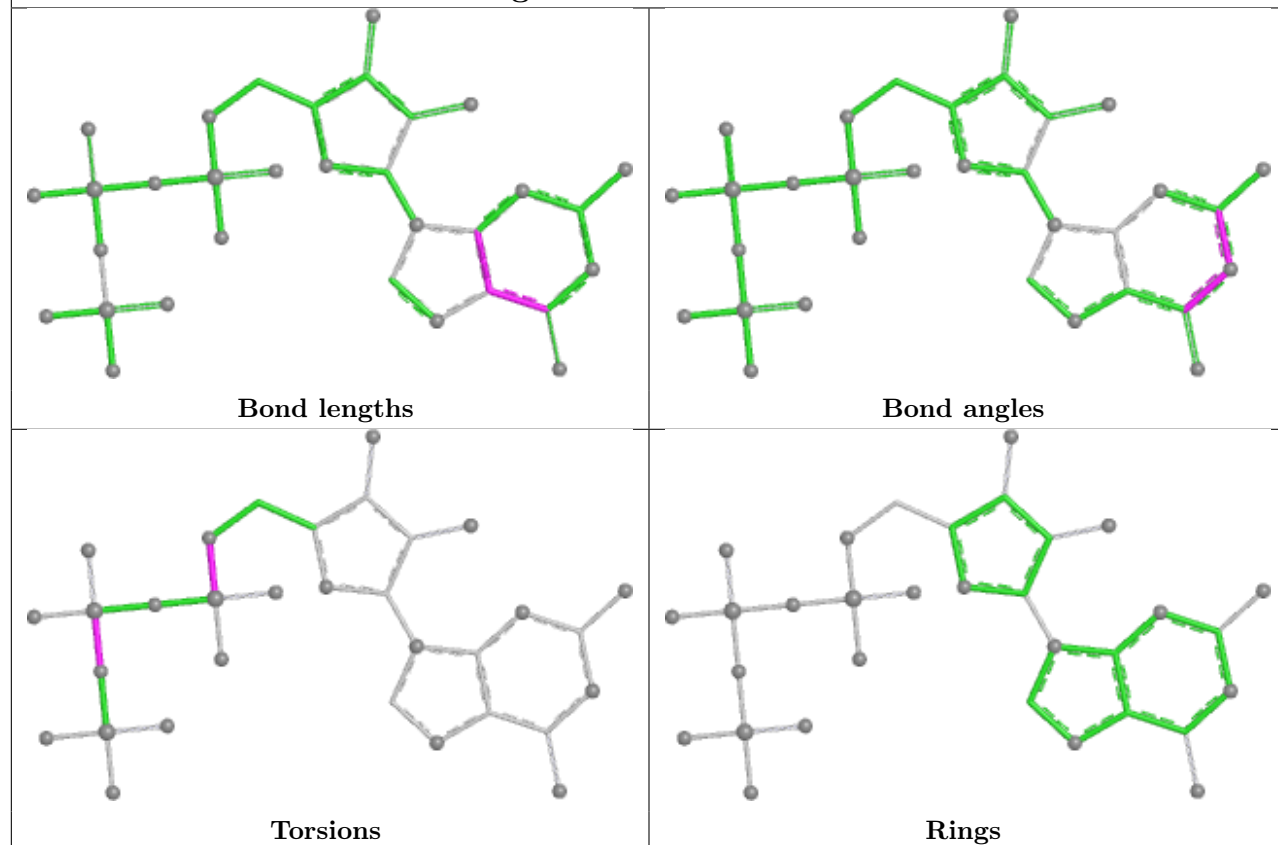




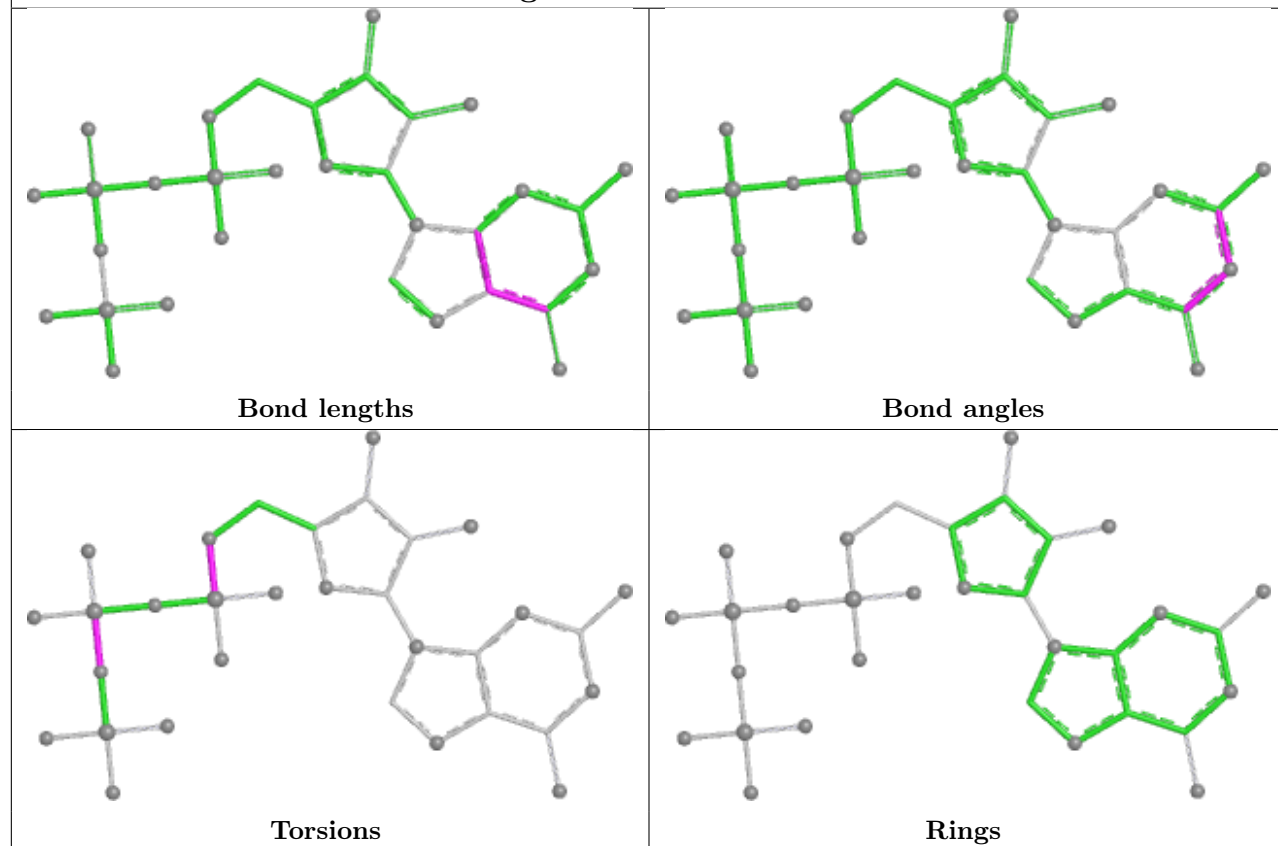


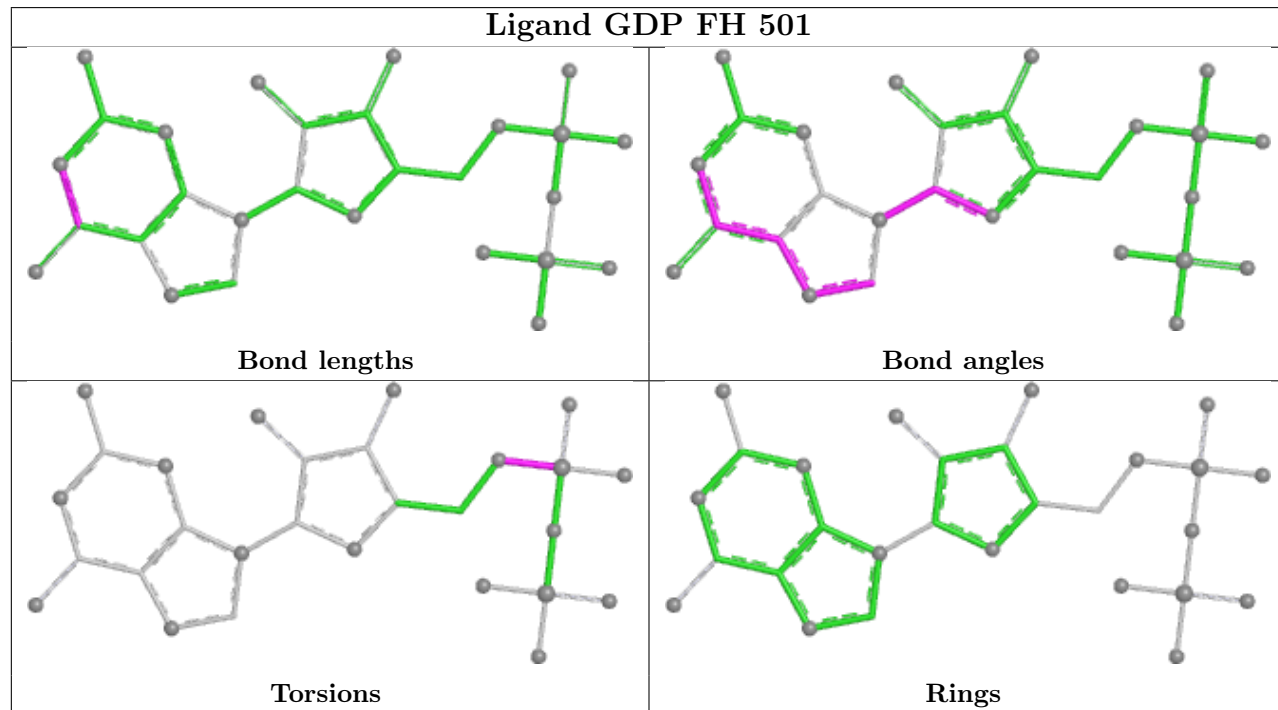
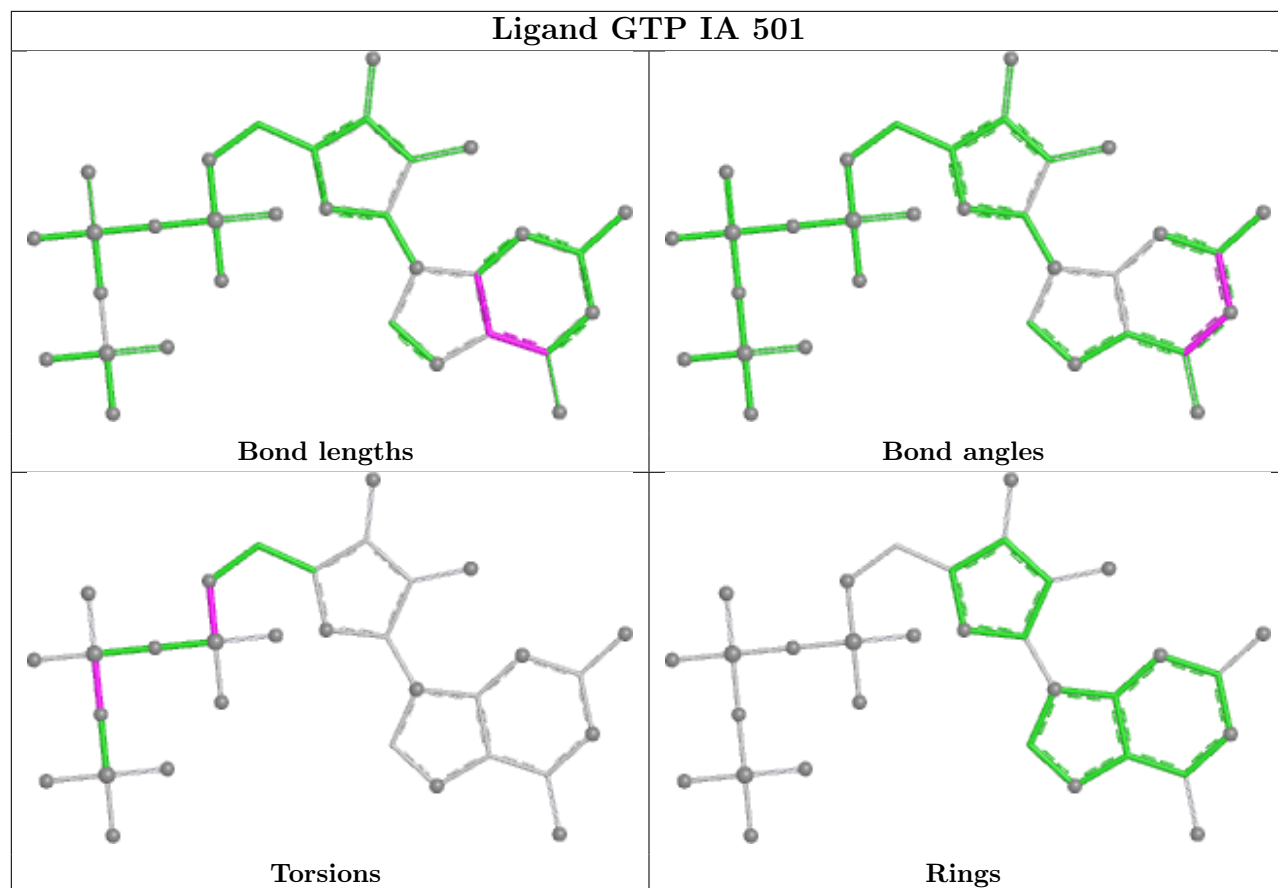


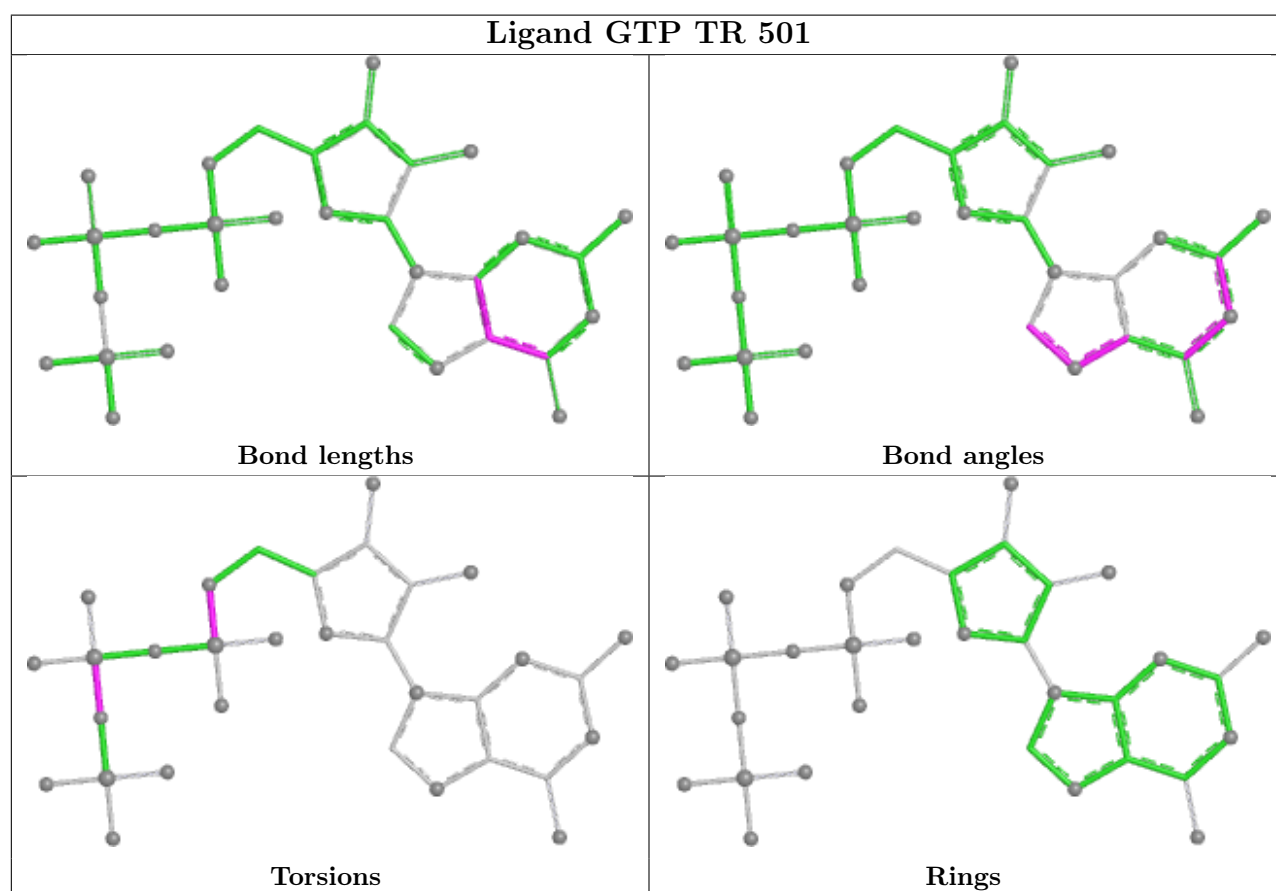
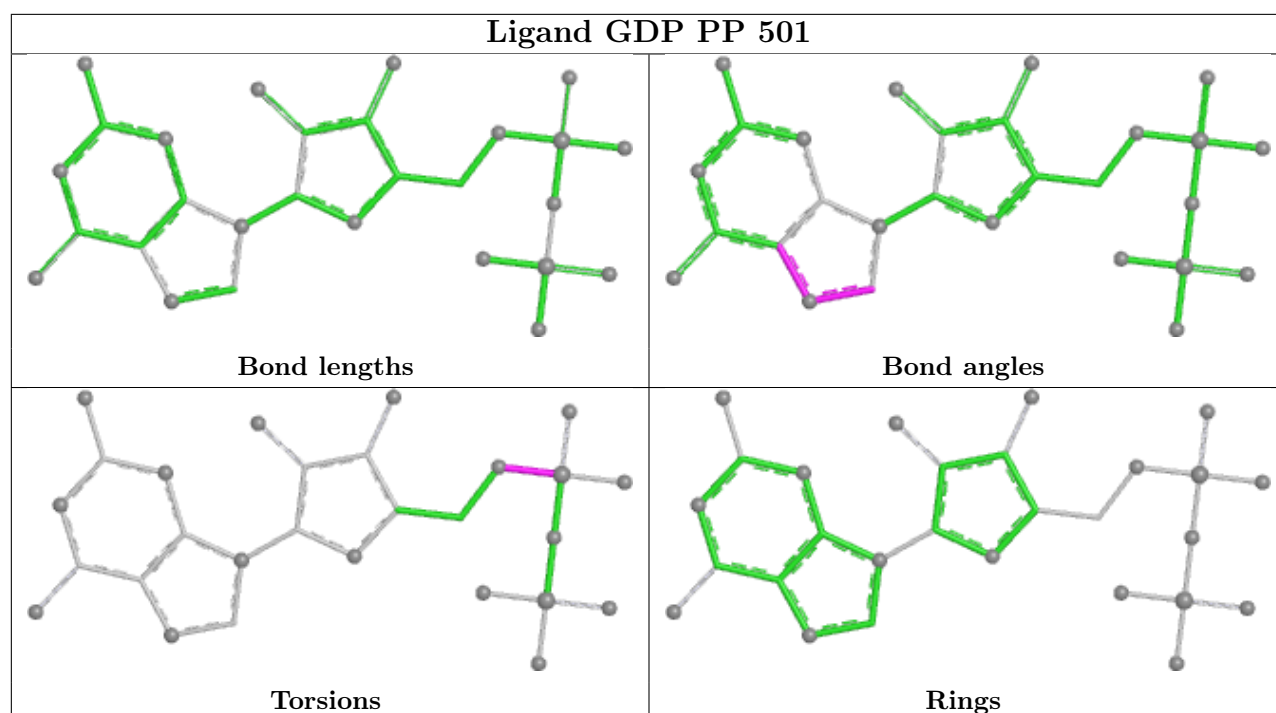
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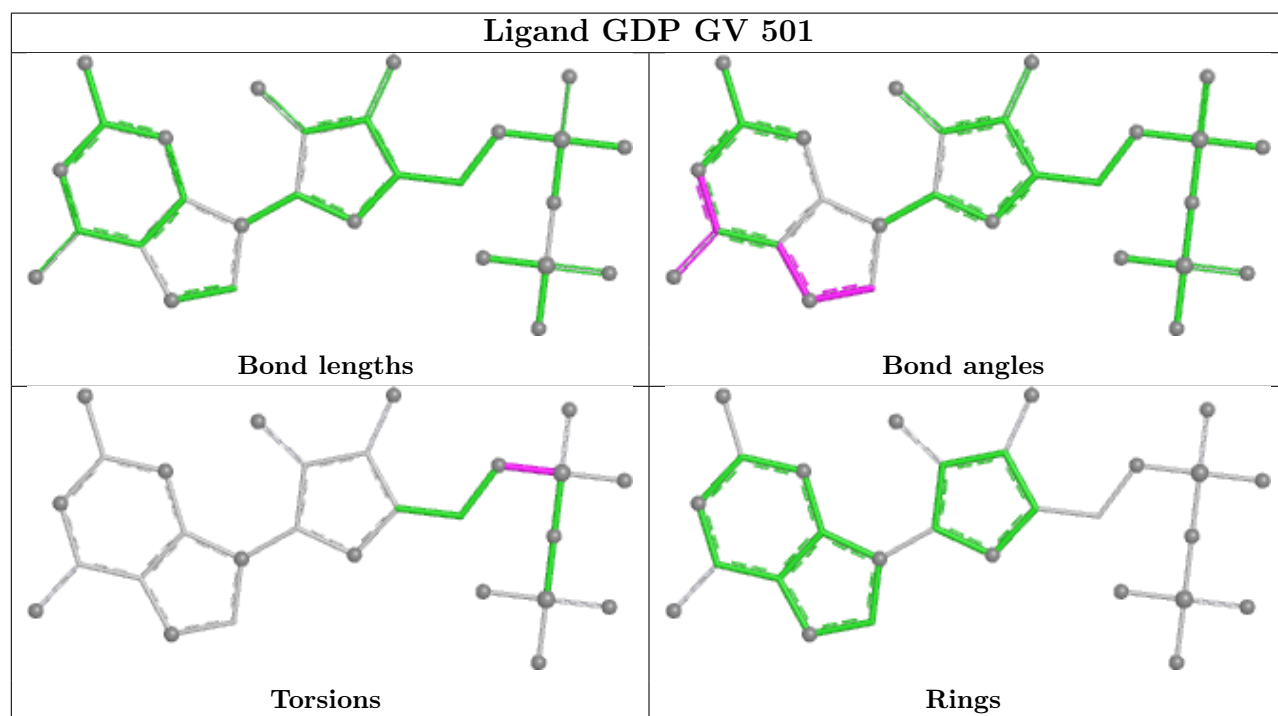
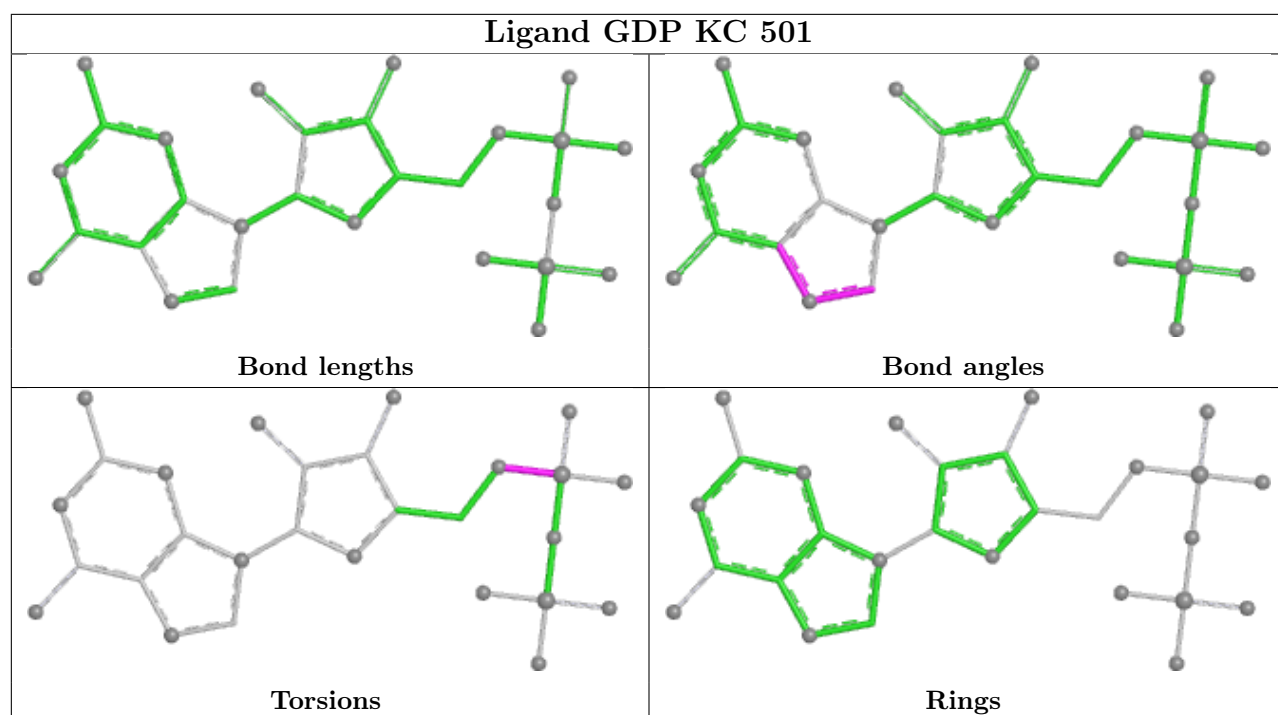
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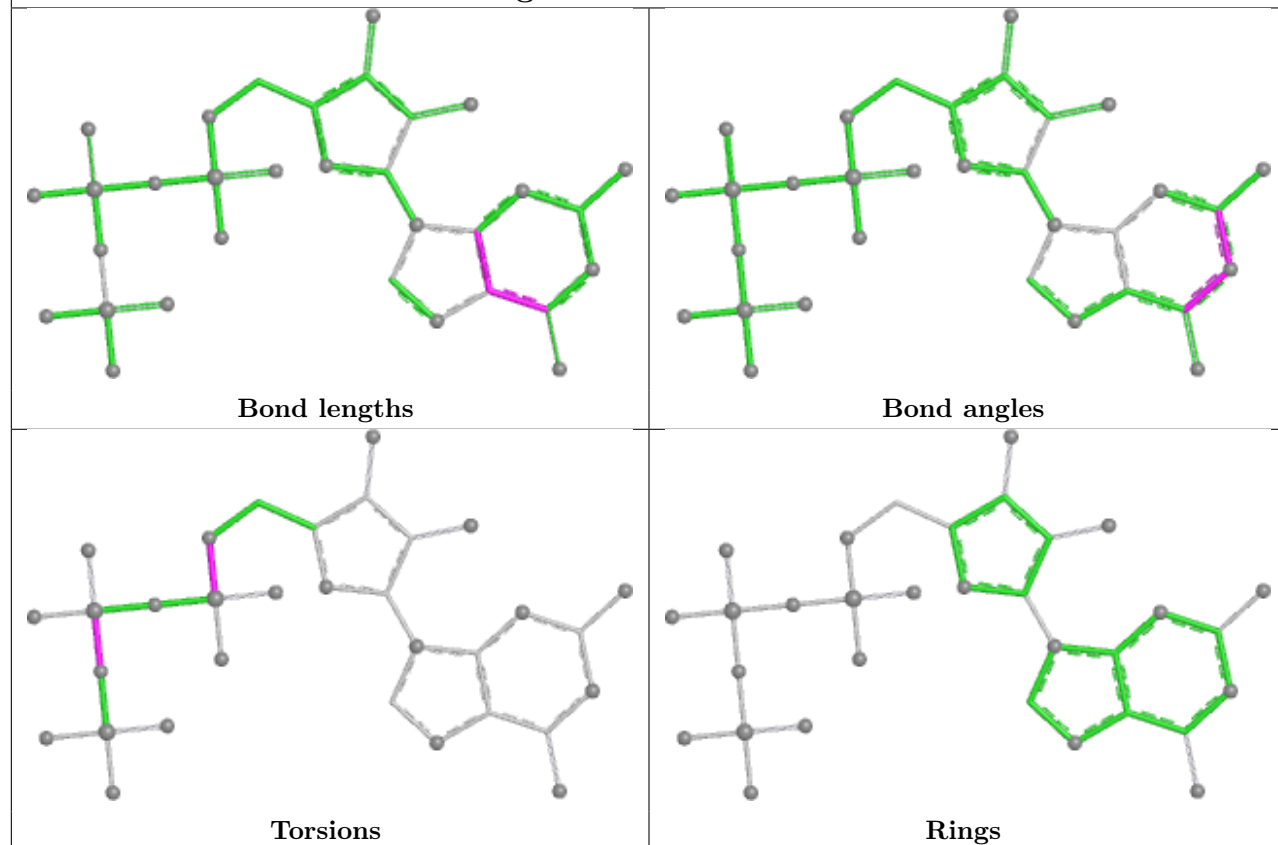




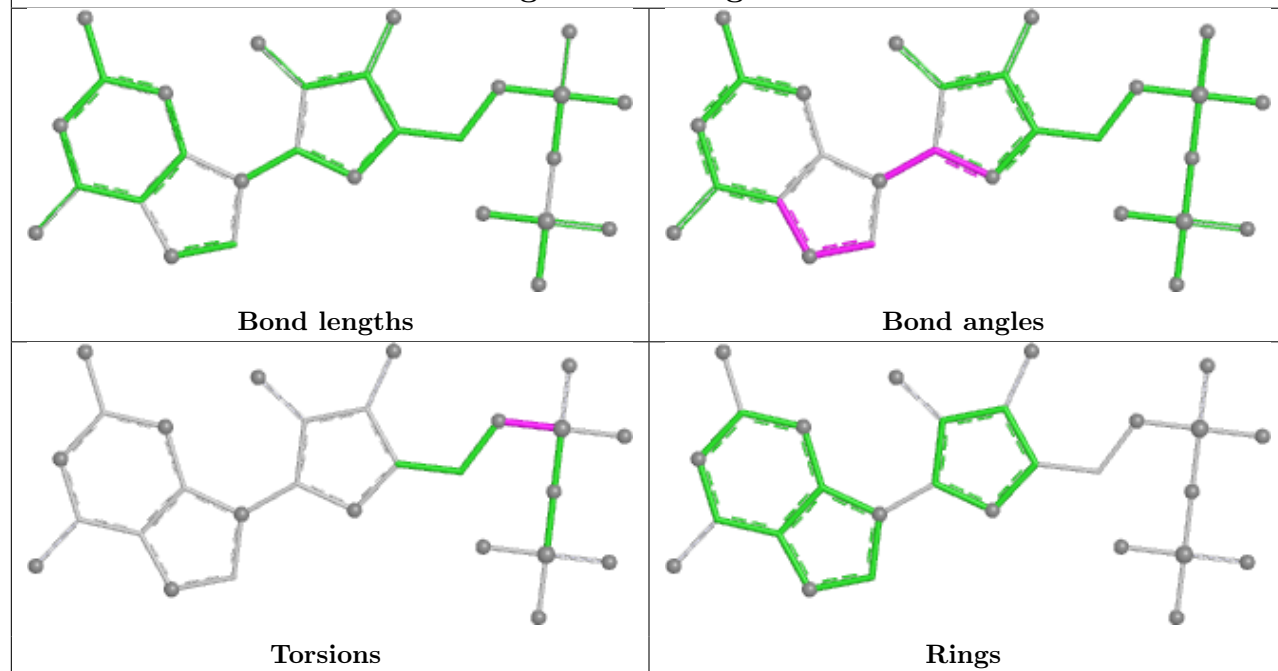




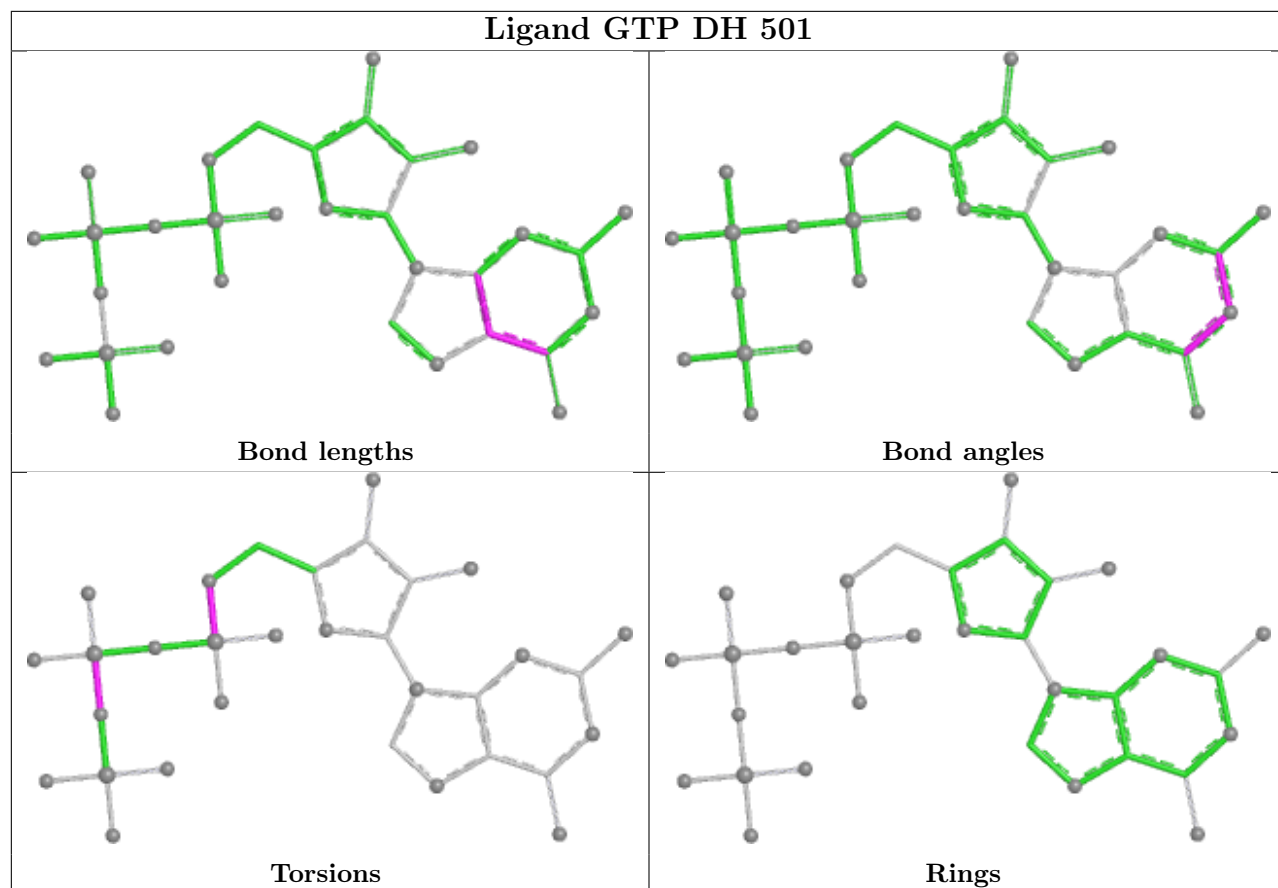
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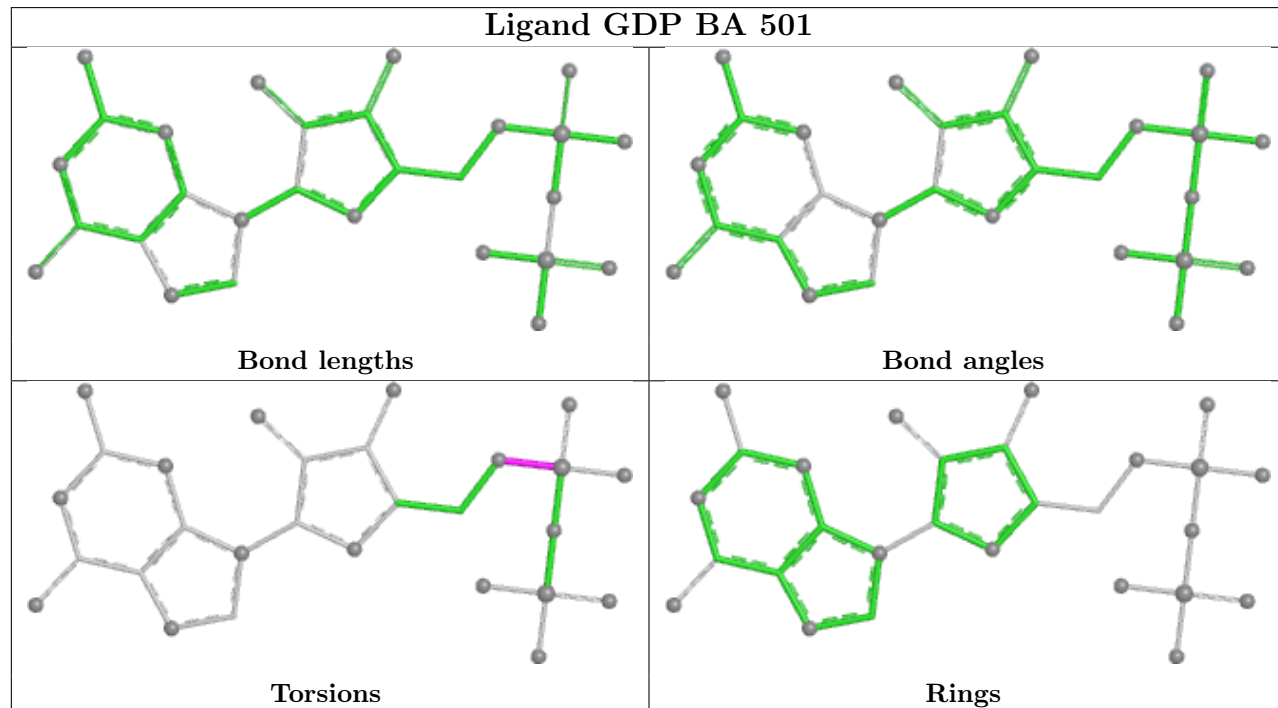
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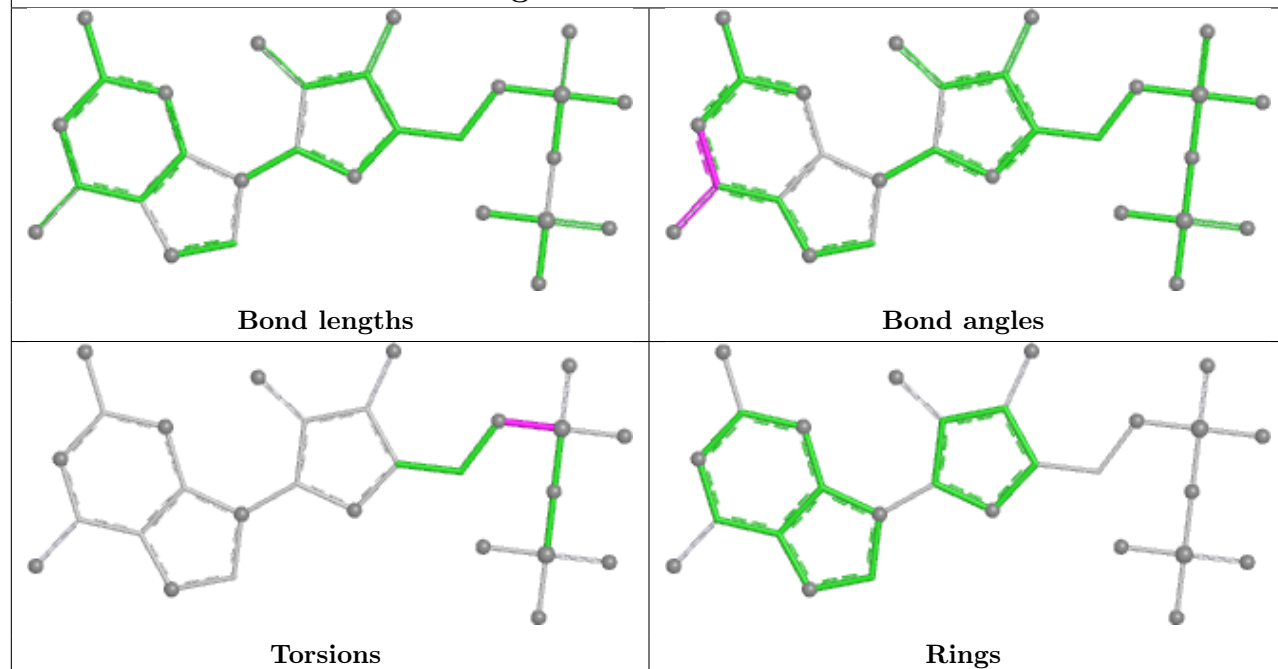
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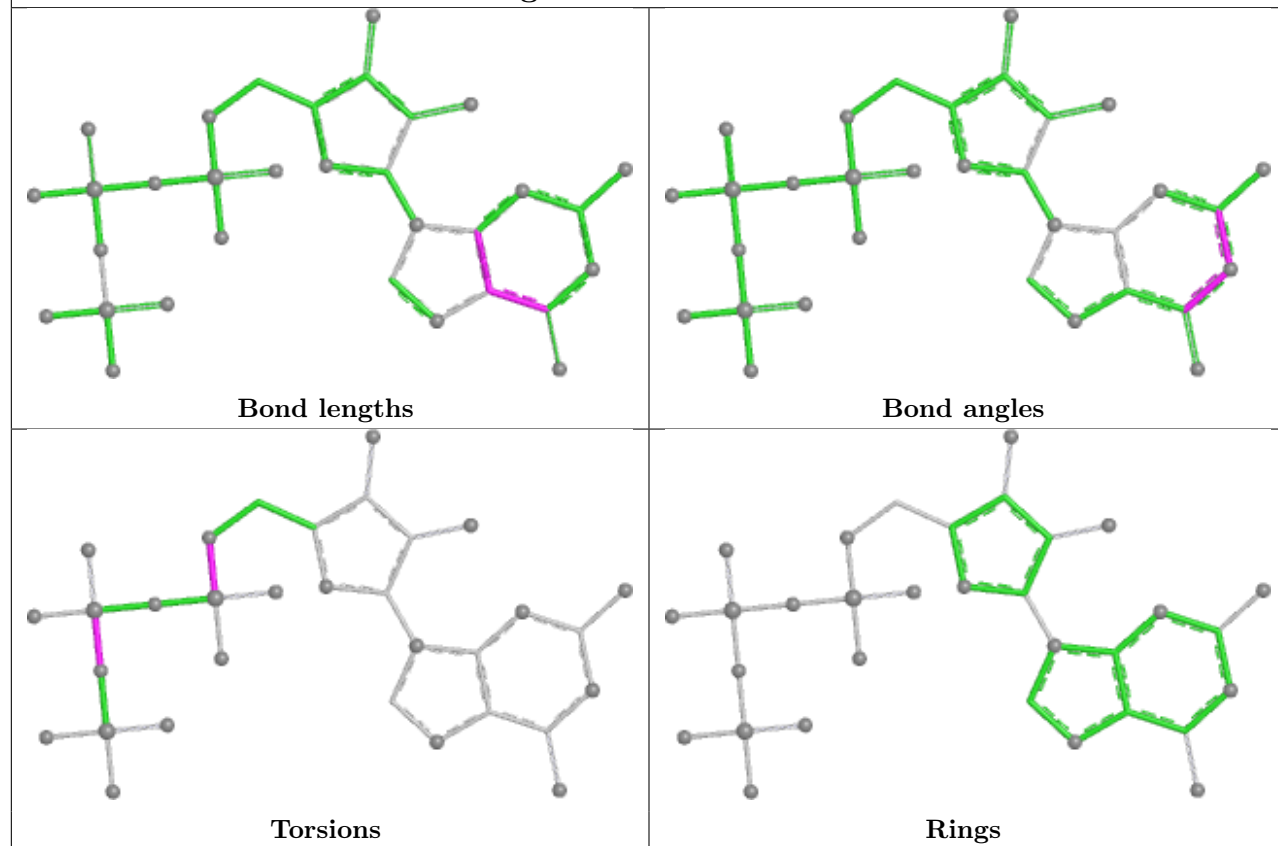
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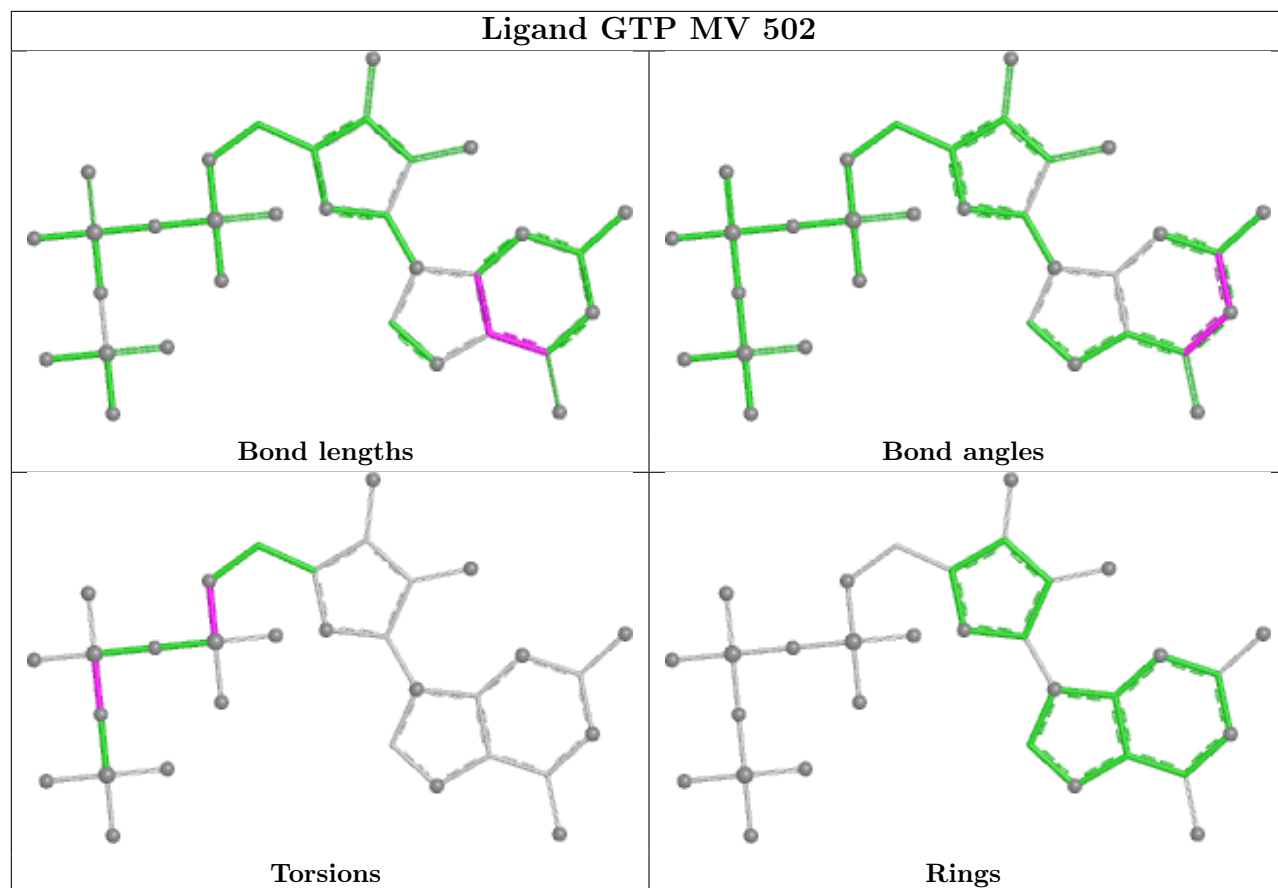
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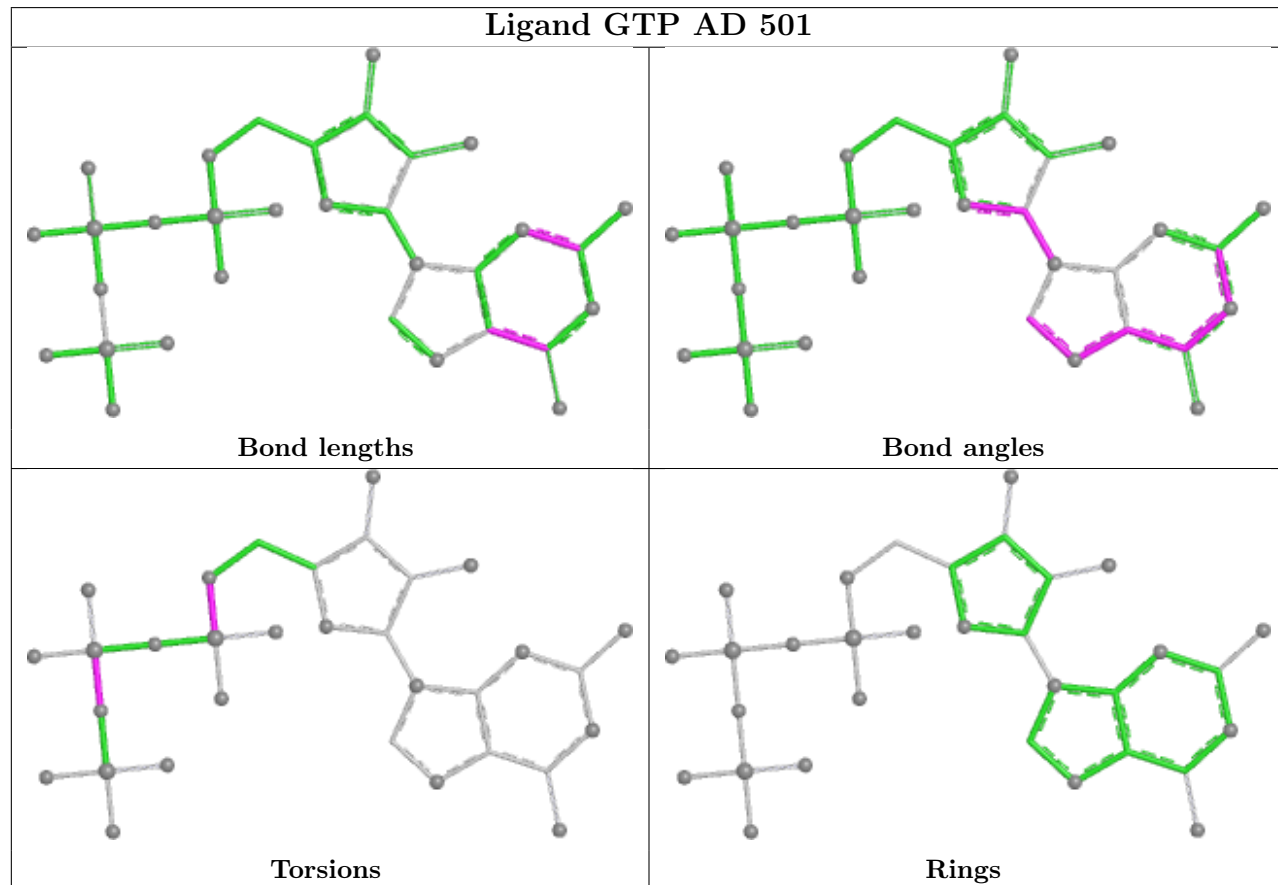
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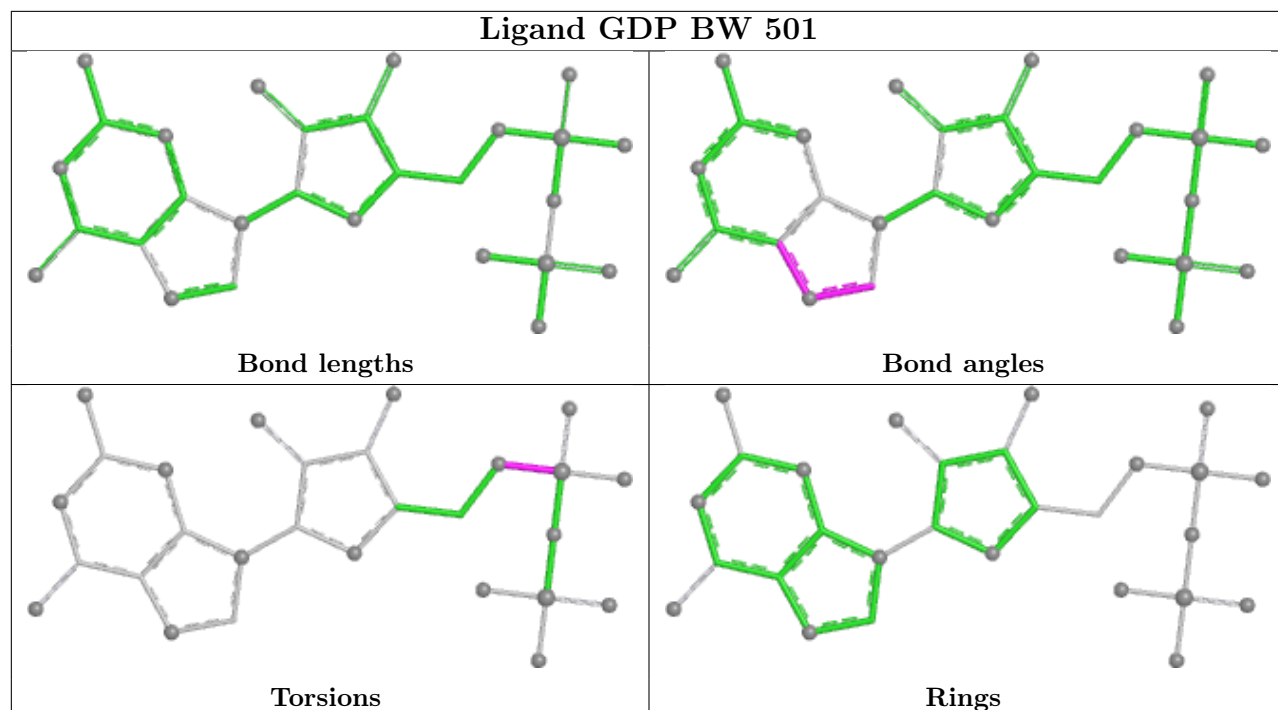
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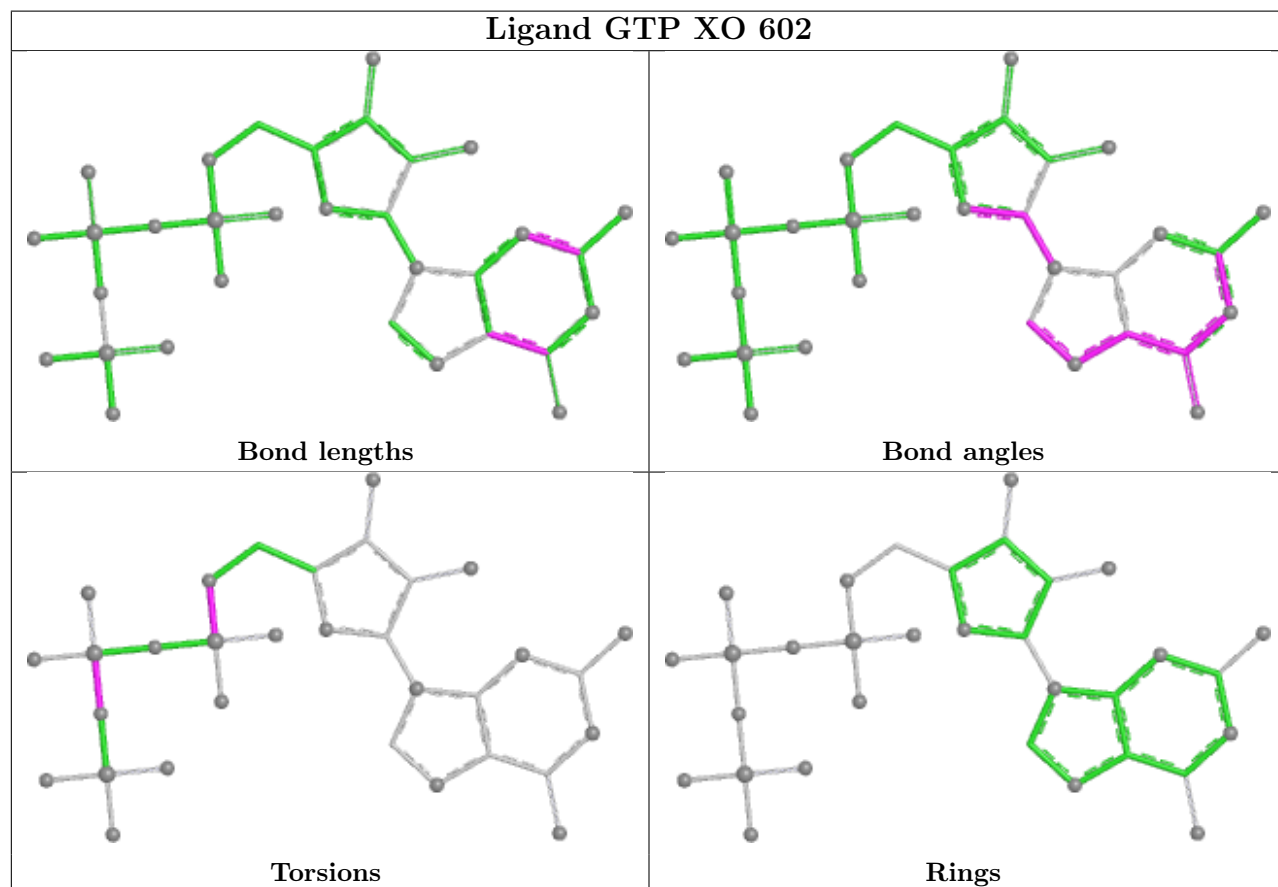
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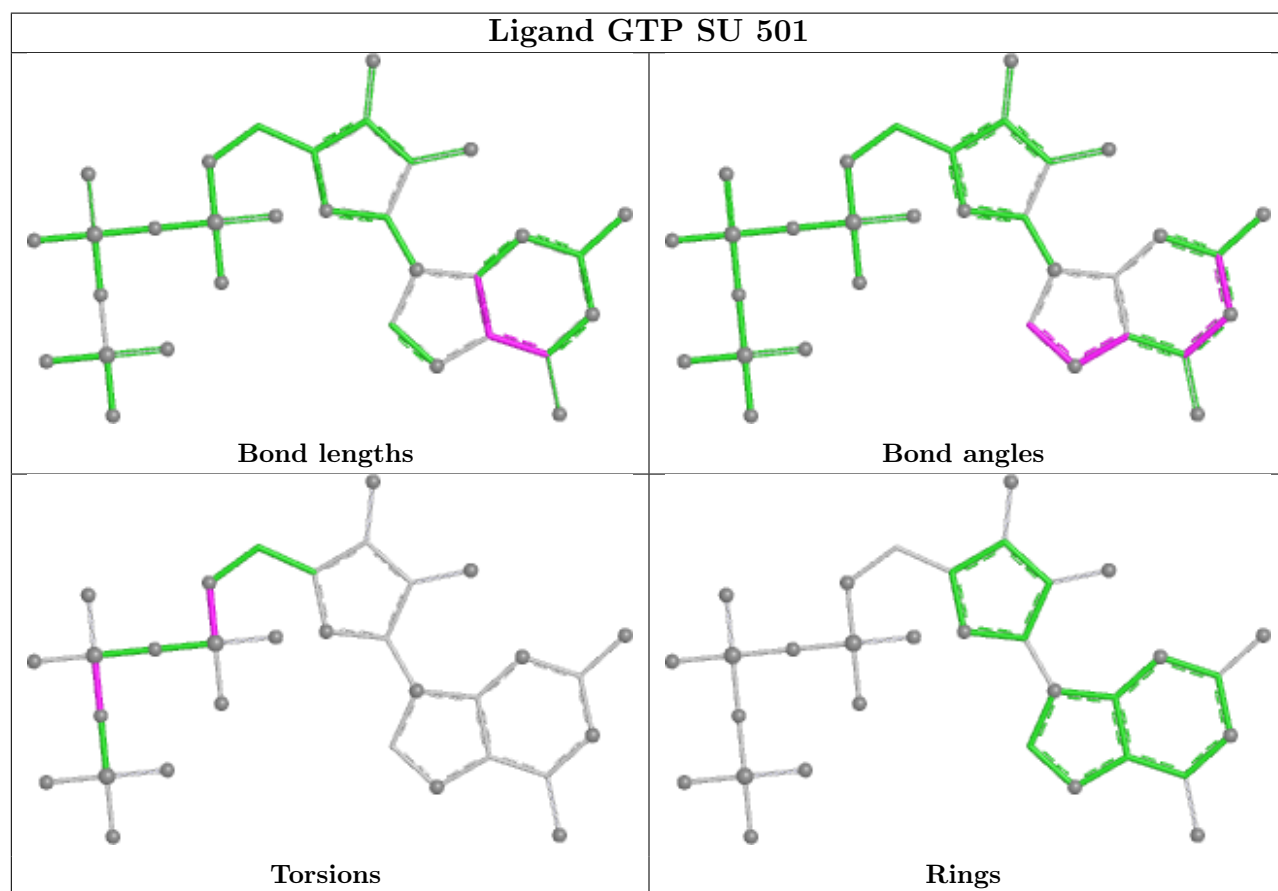
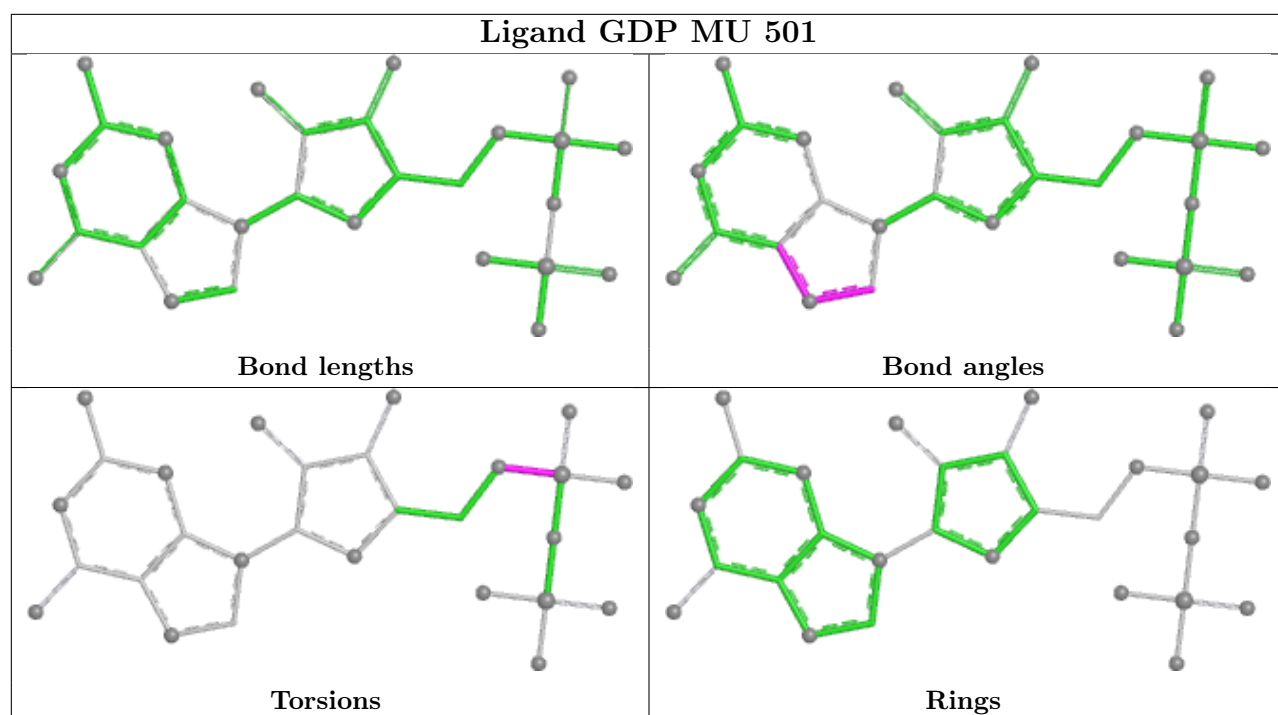


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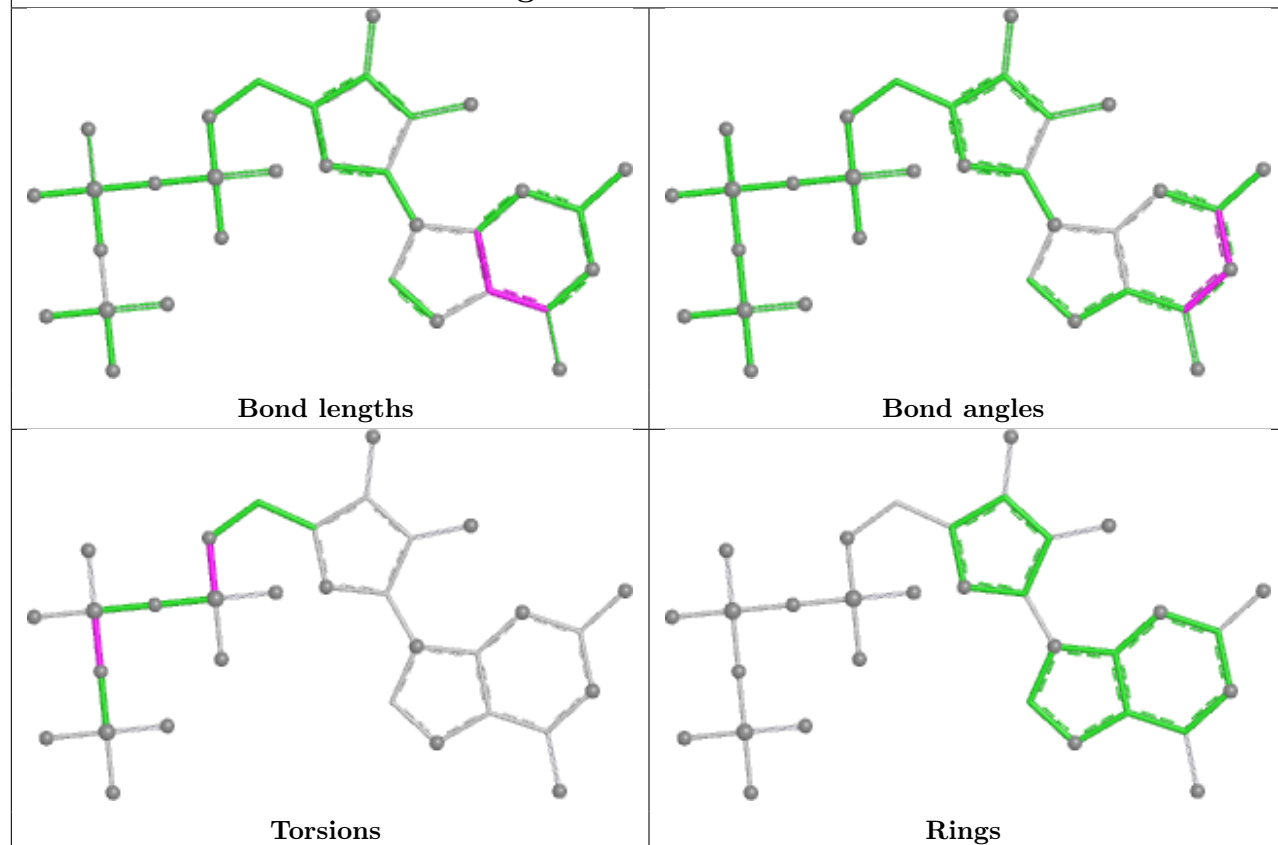


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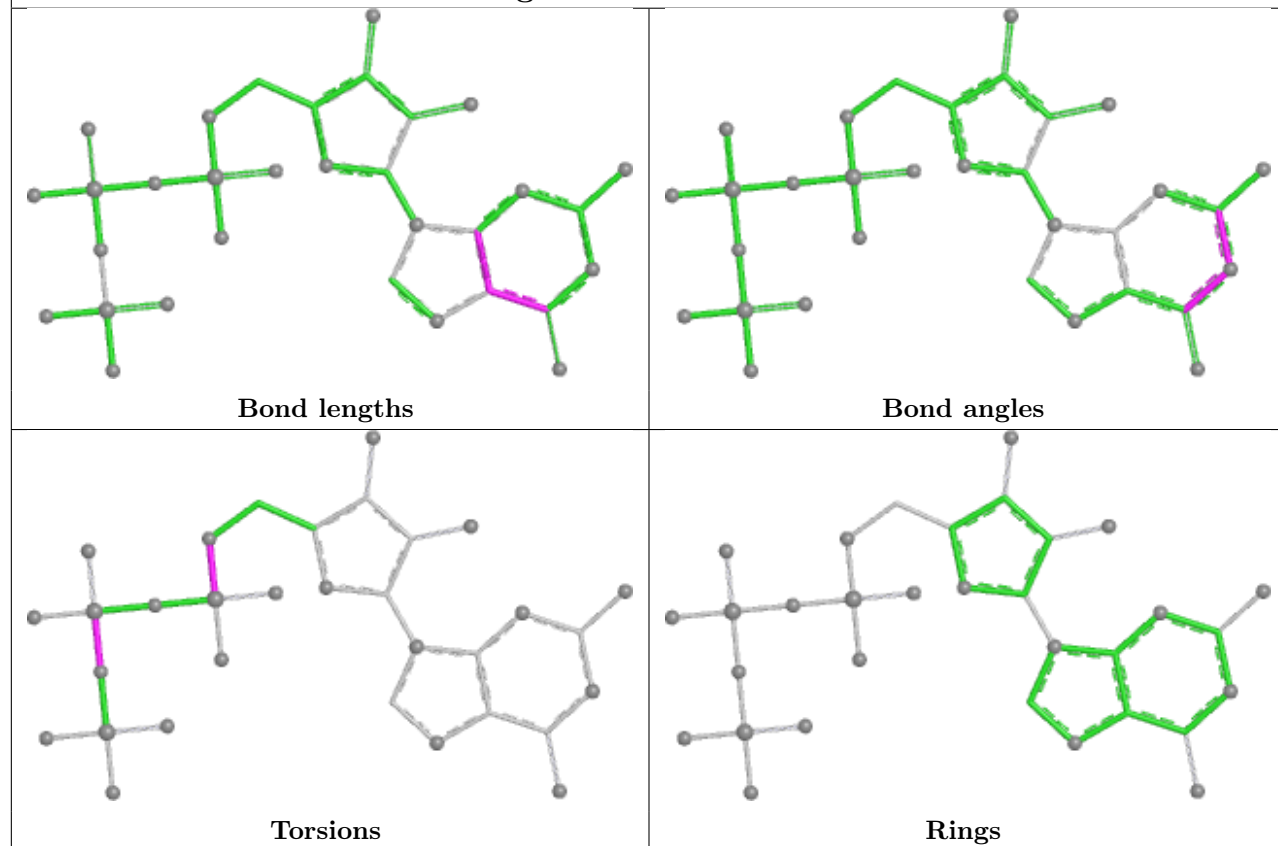




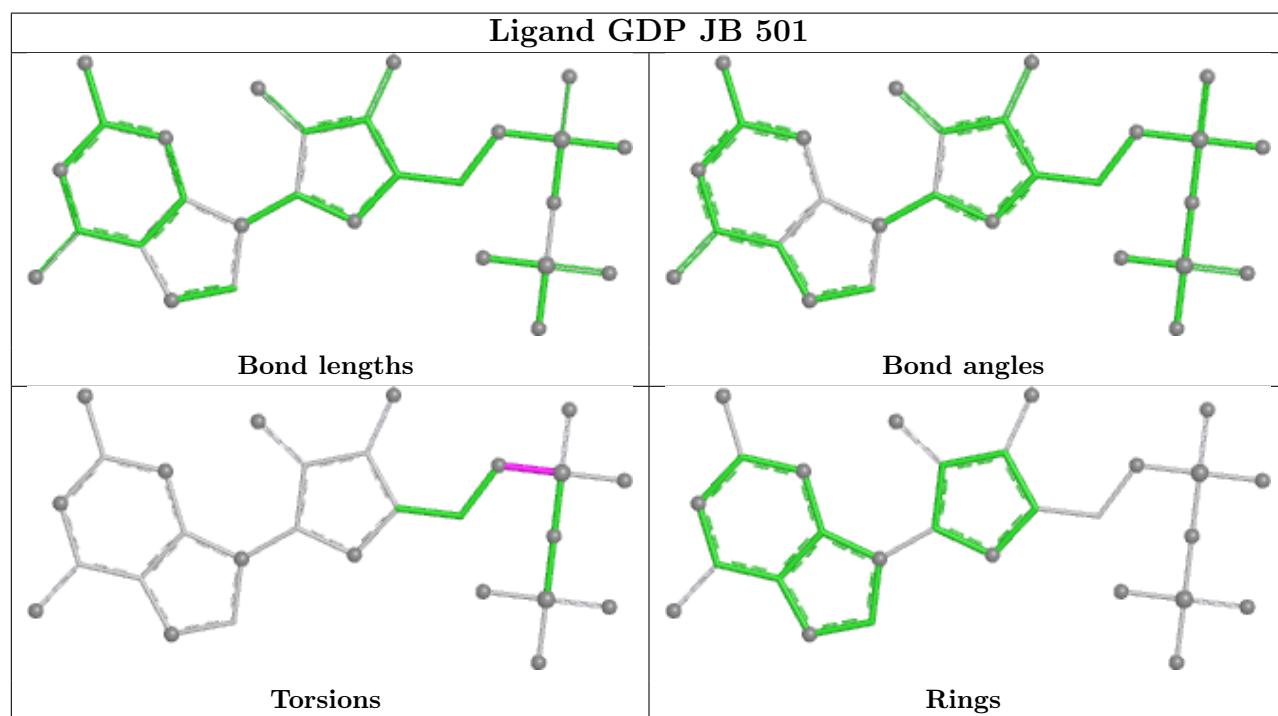
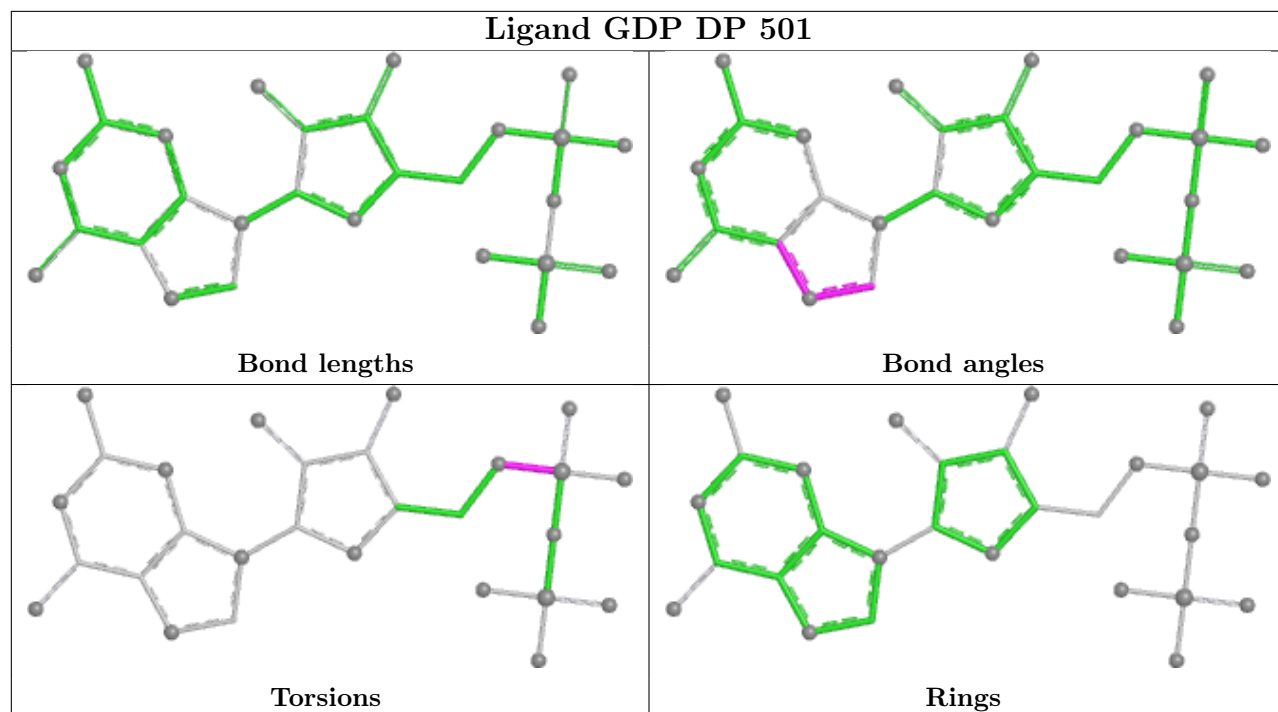
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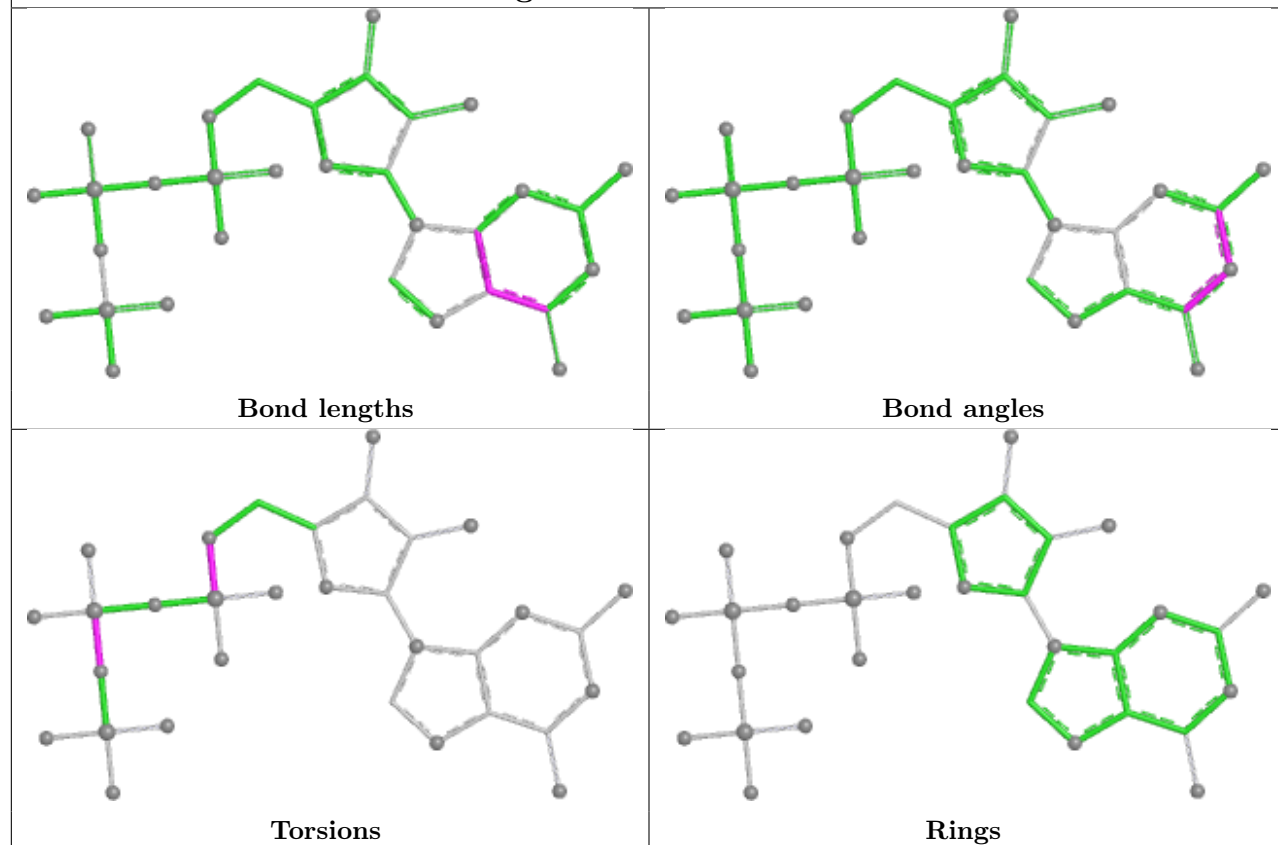
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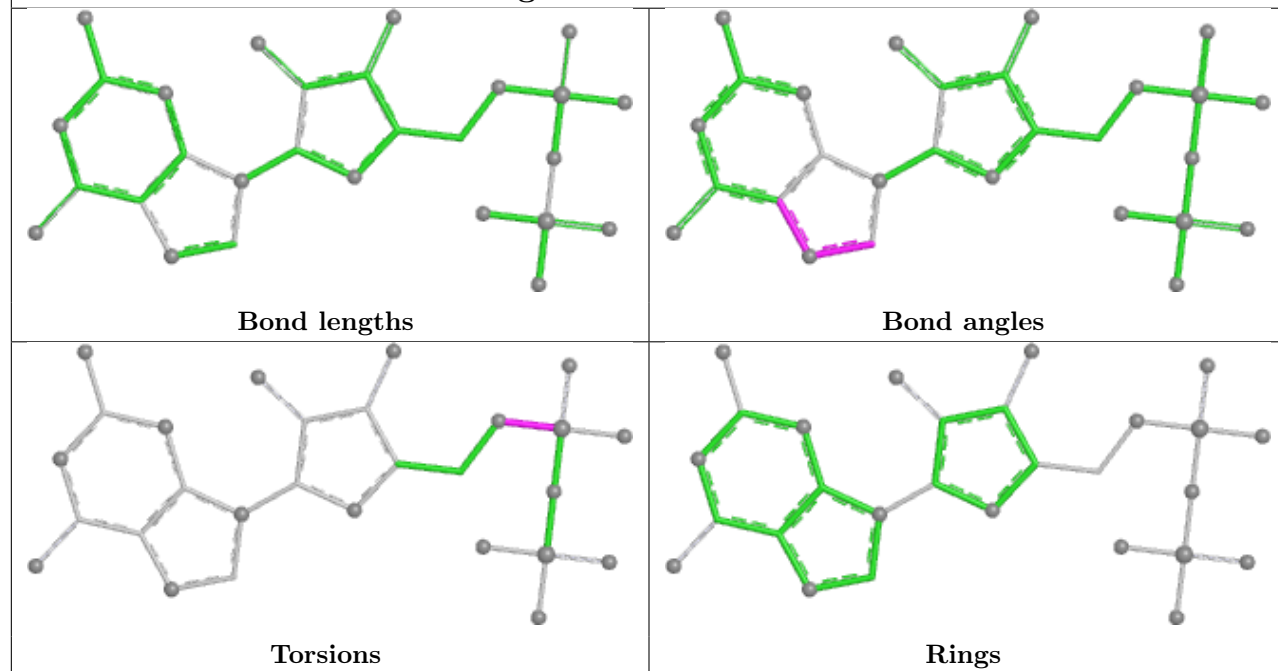


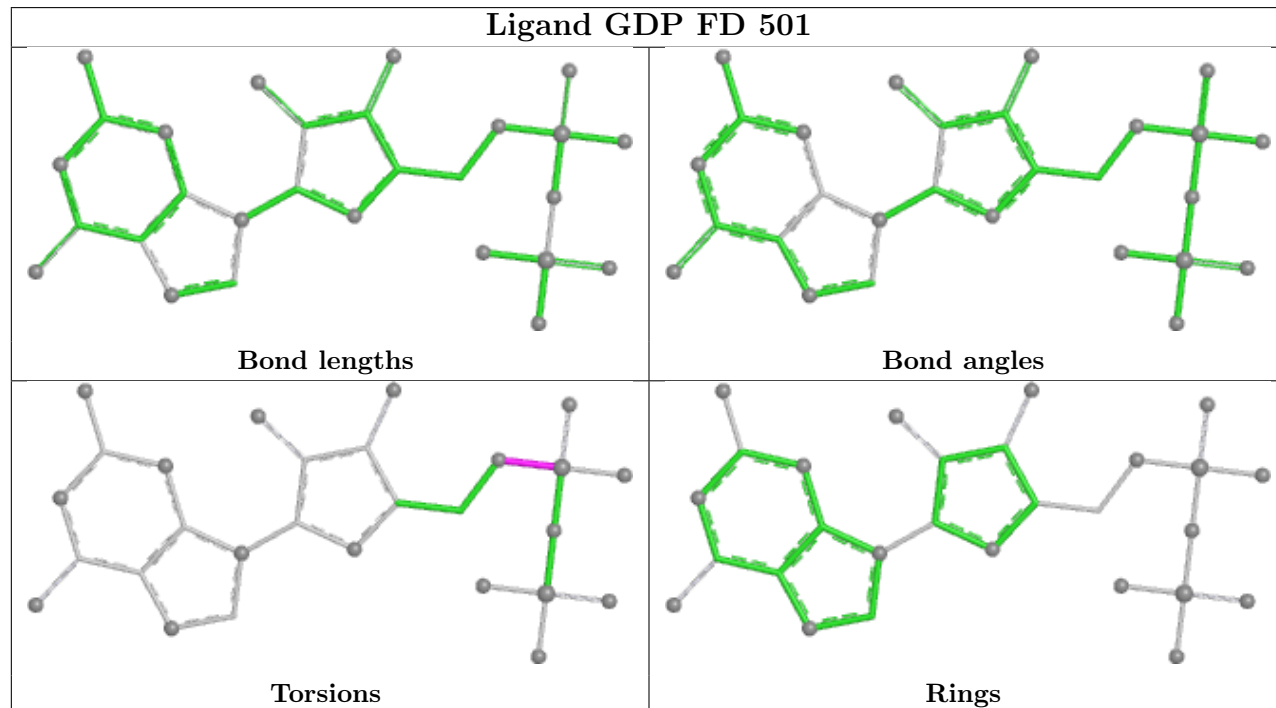
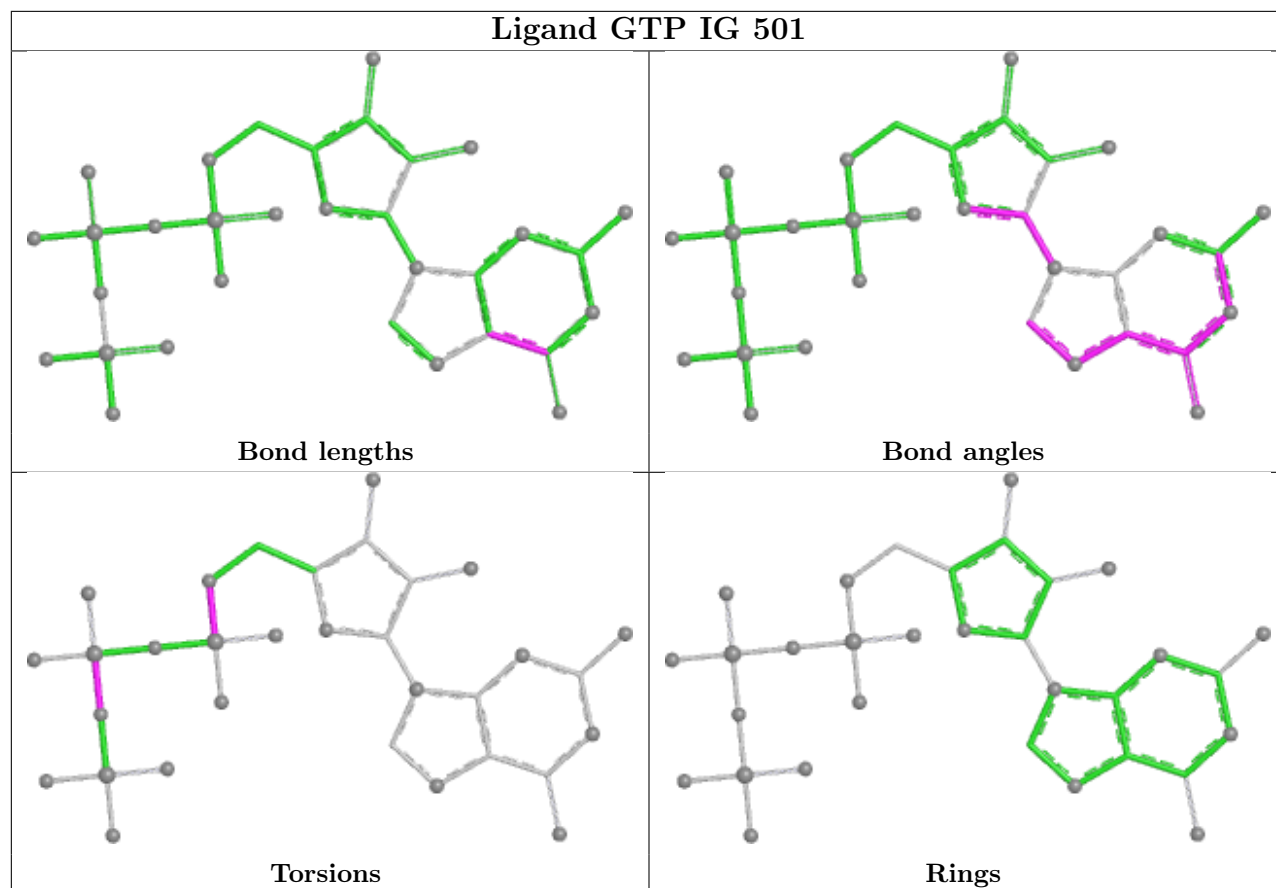


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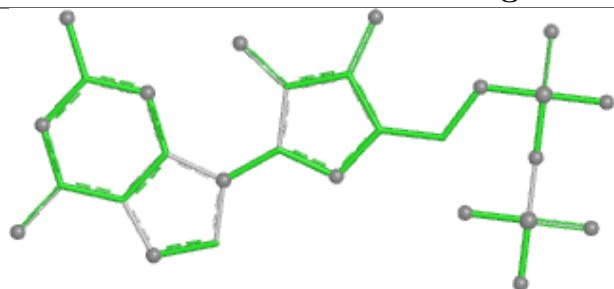


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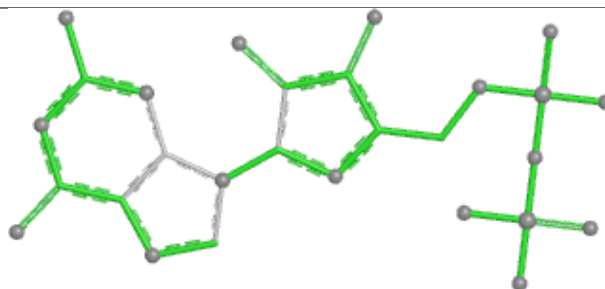




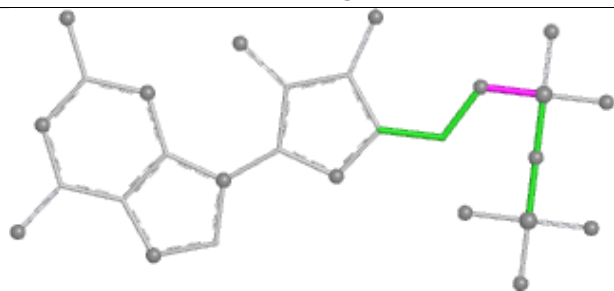
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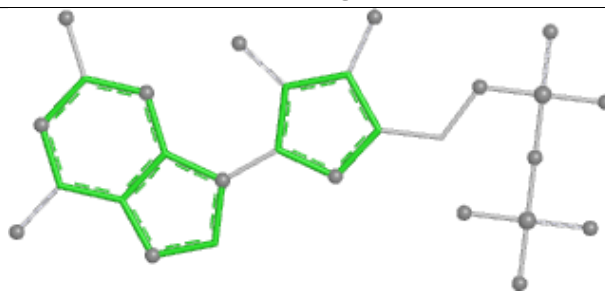
Bond lengths



Bond angles

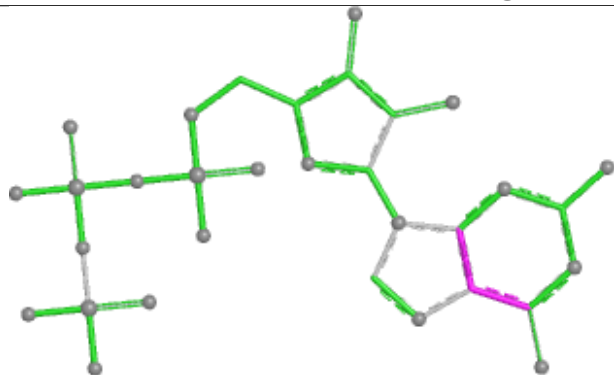


Torsions

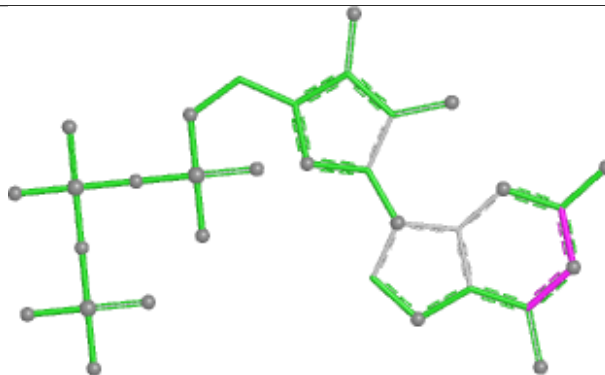


Rings

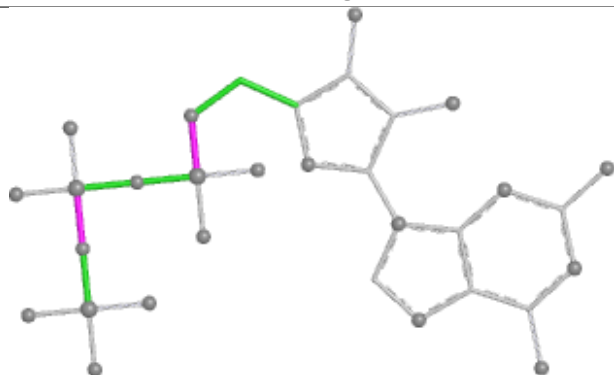
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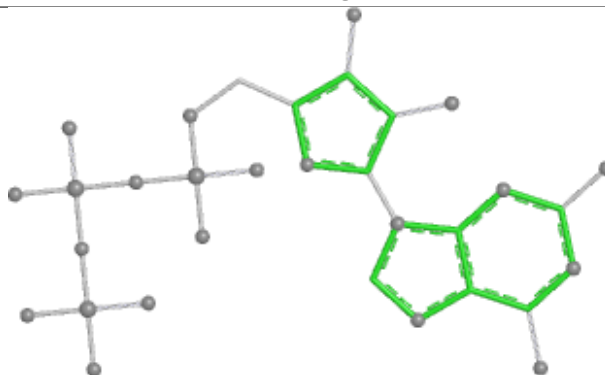
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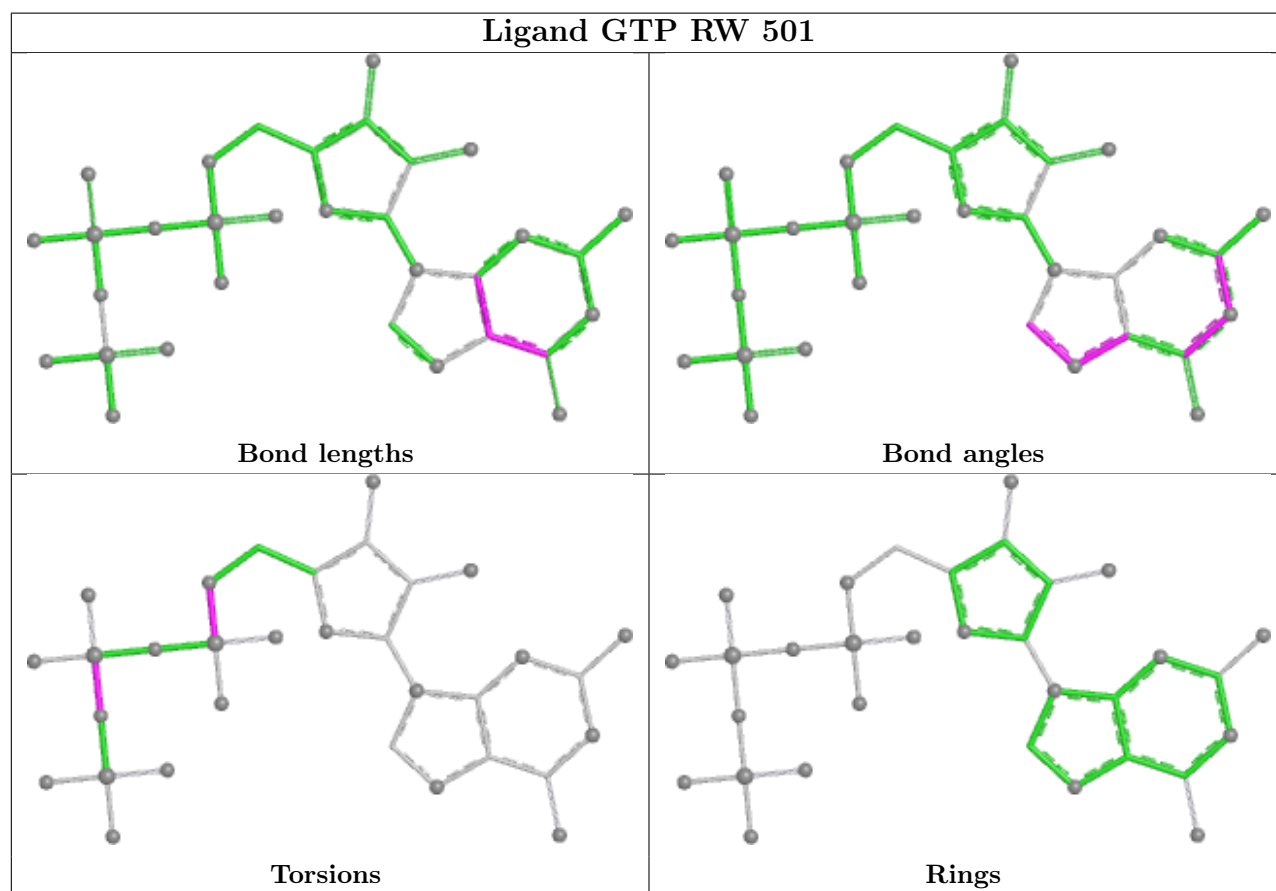
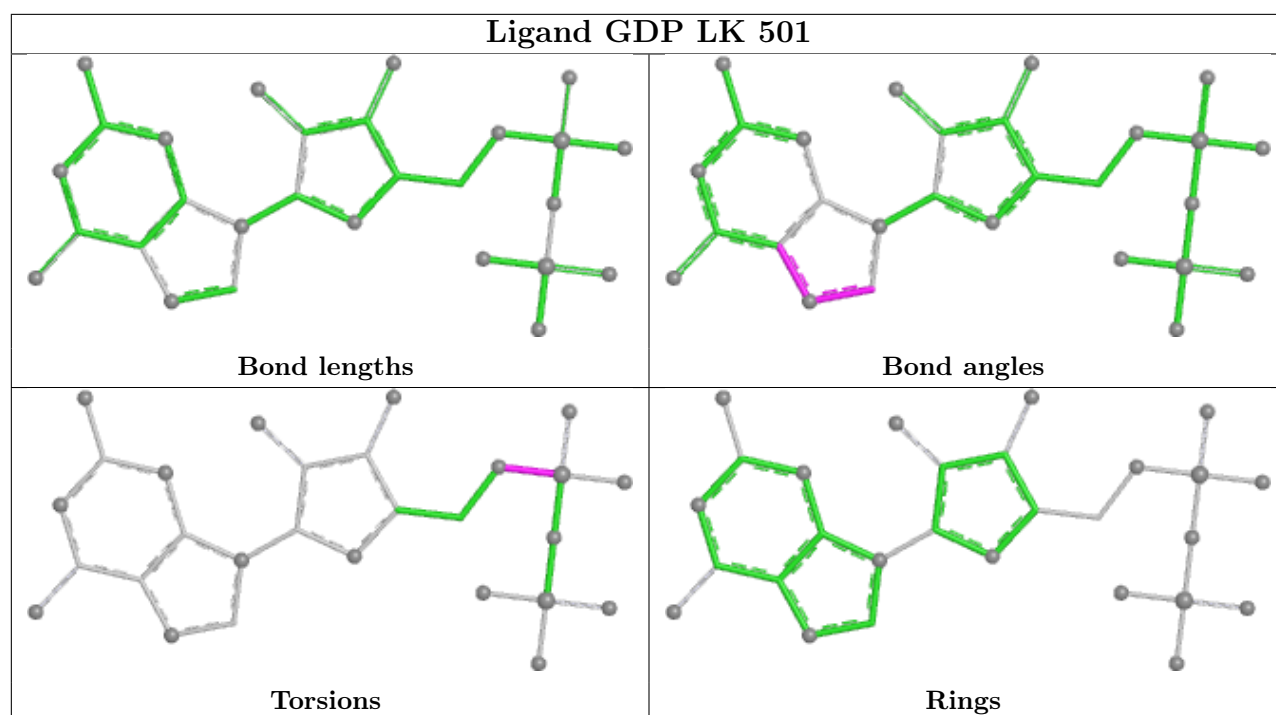
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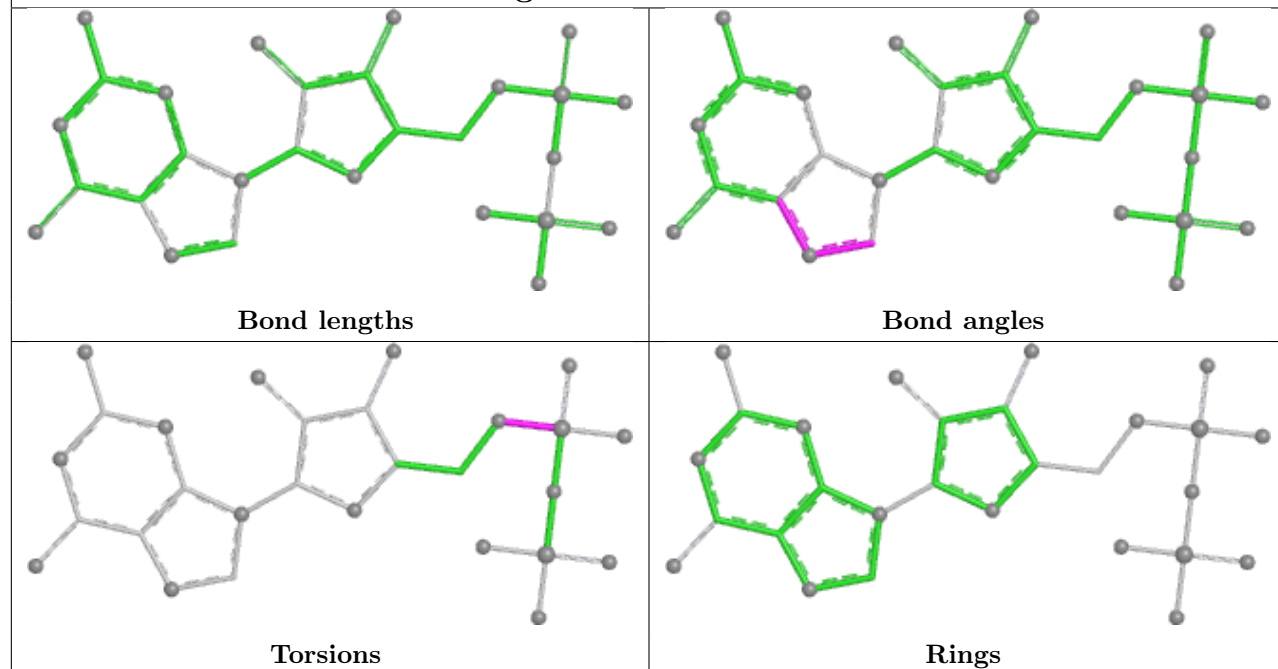
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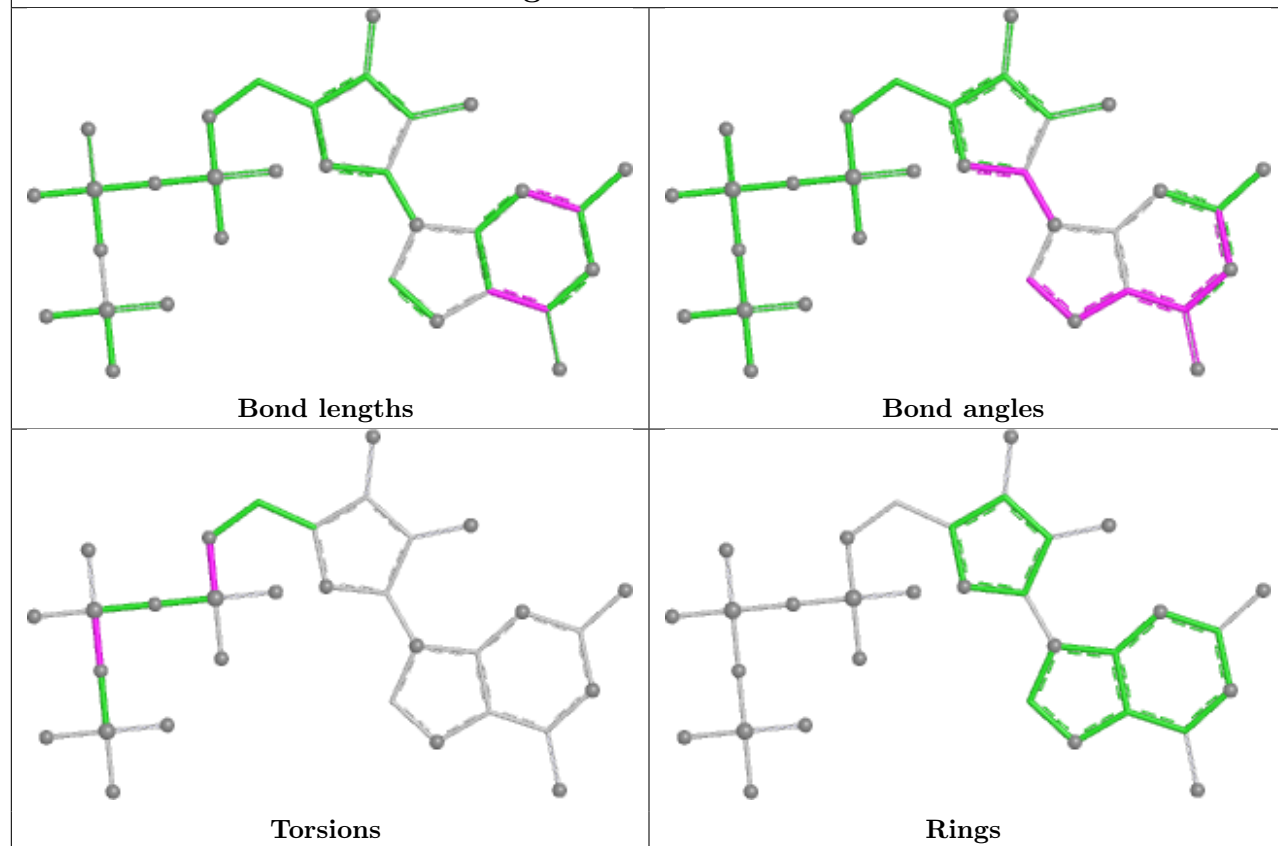
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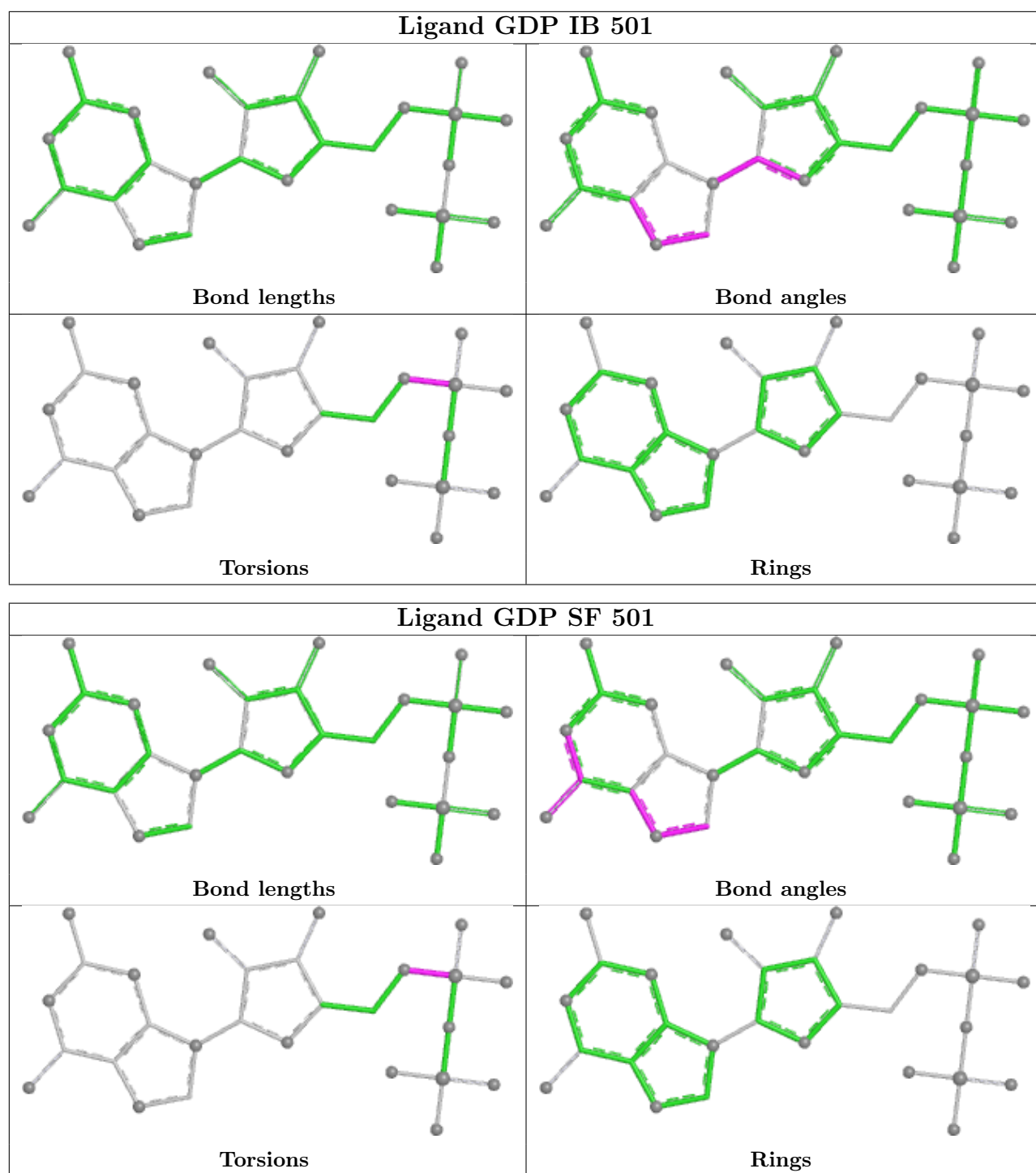


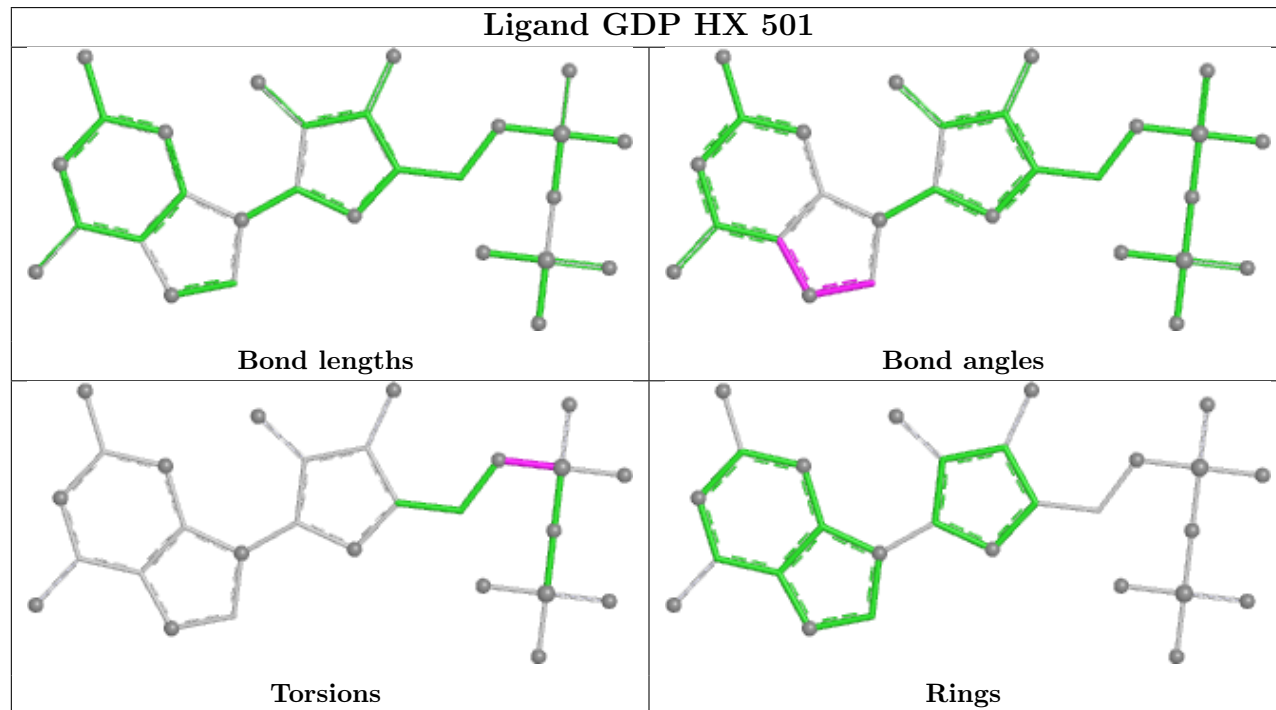
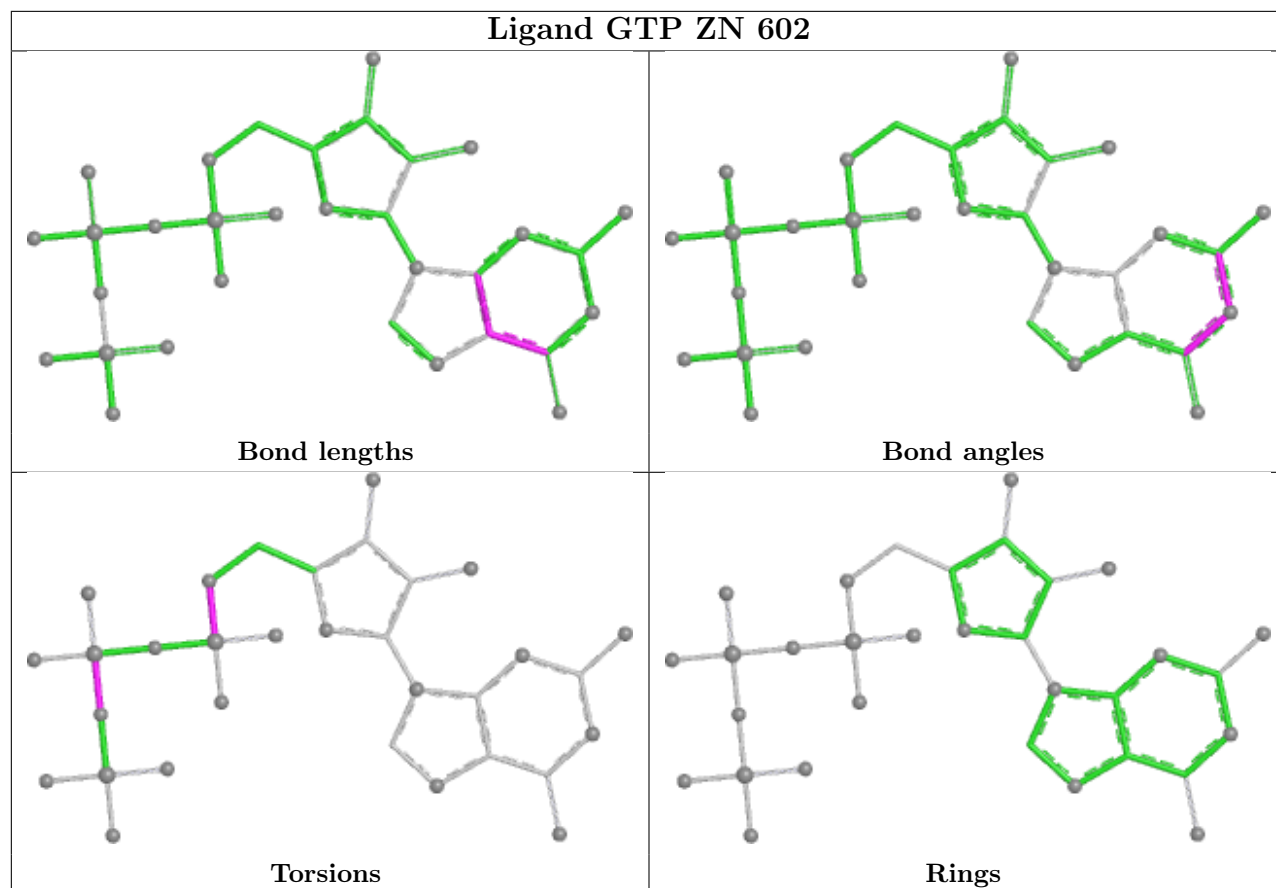
## Ligand GDP DX 501



## Ligand GTP IU 501

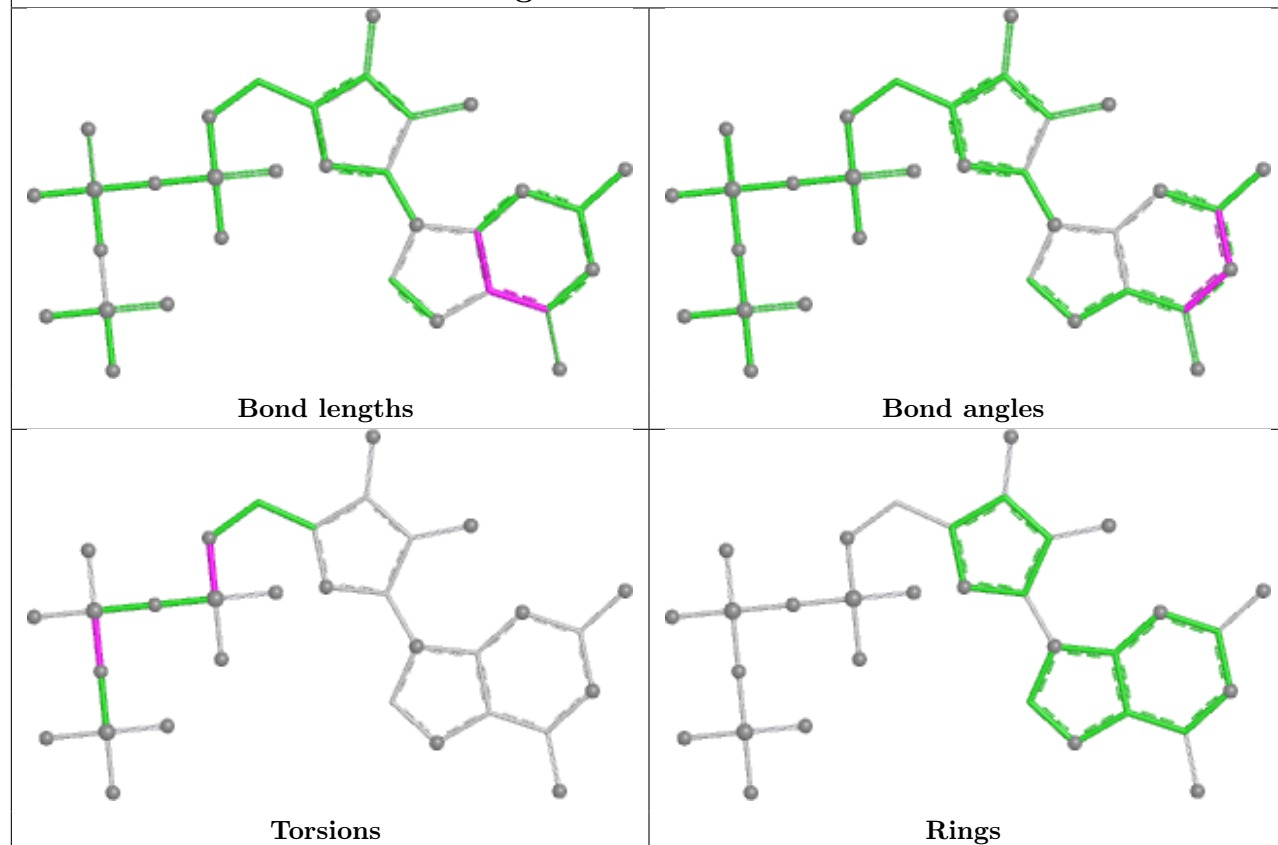




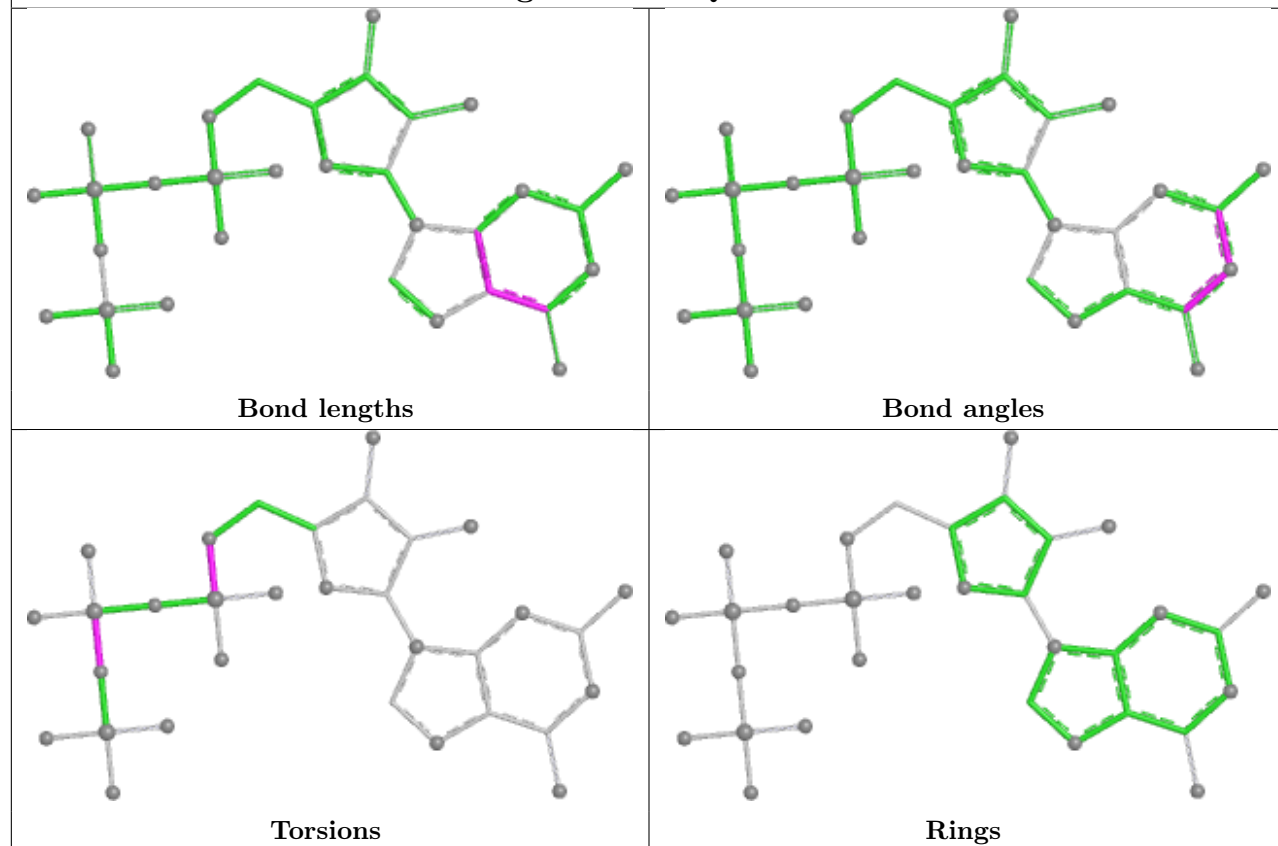


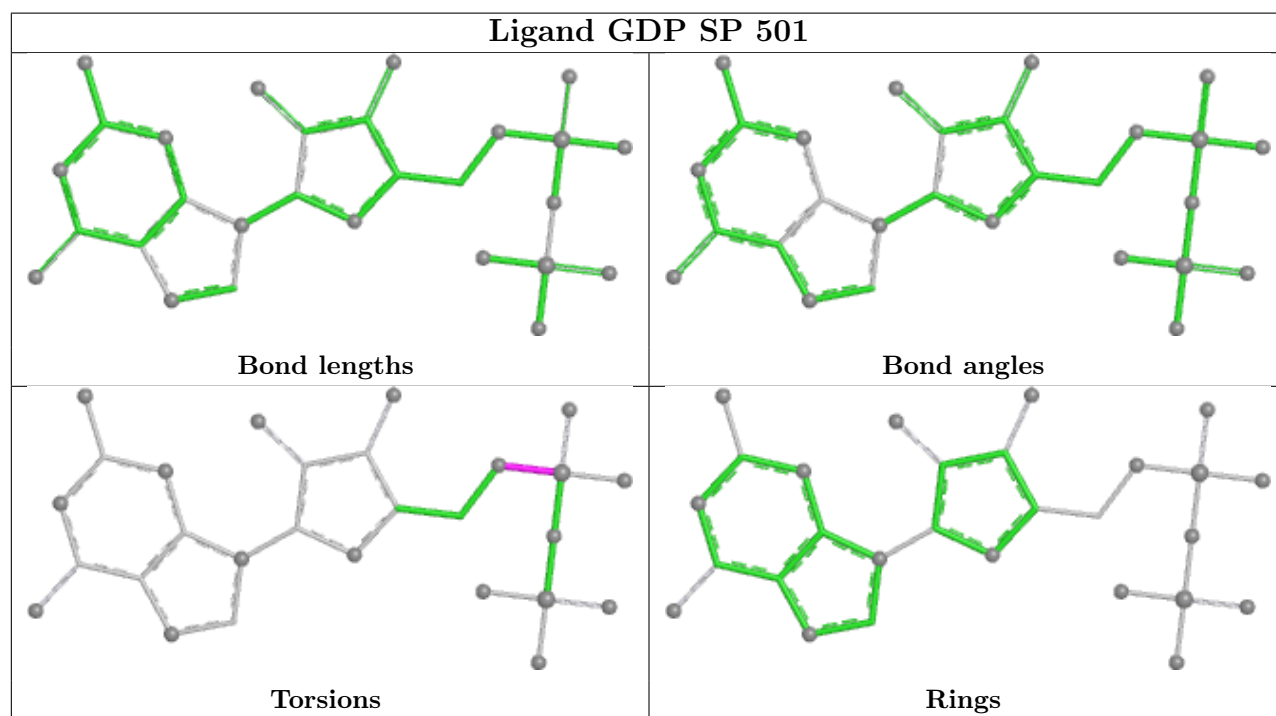
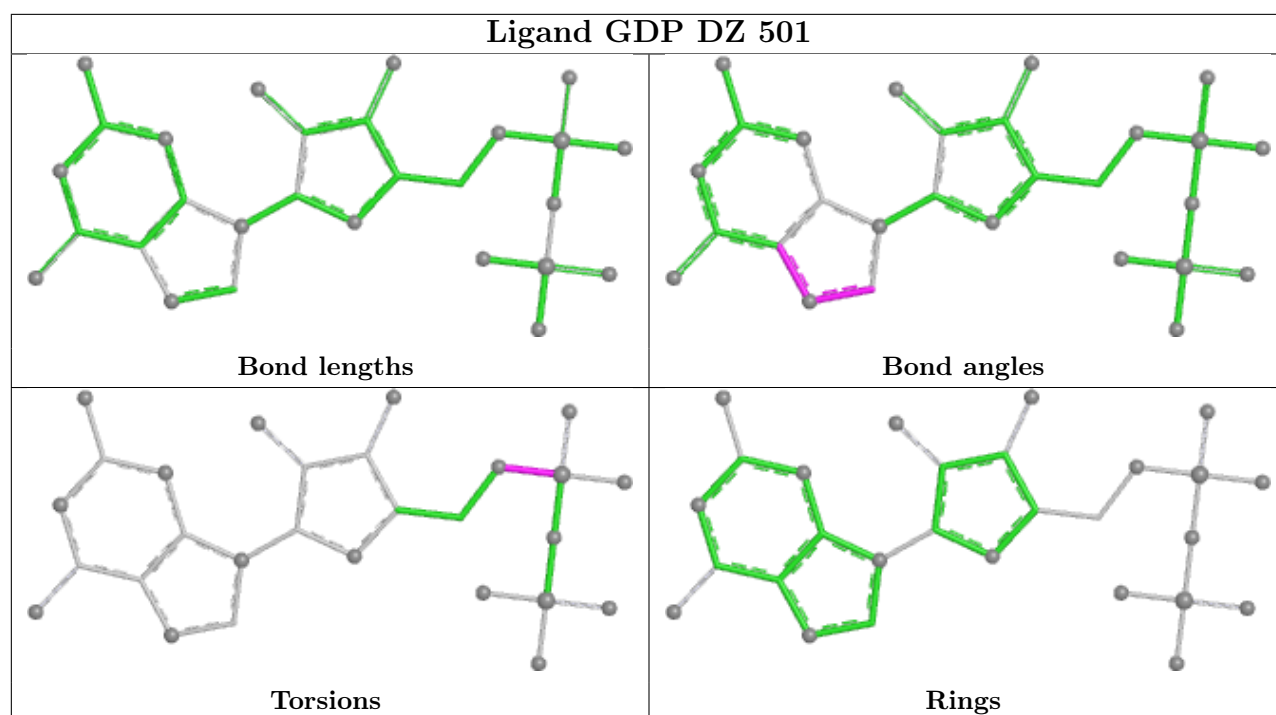


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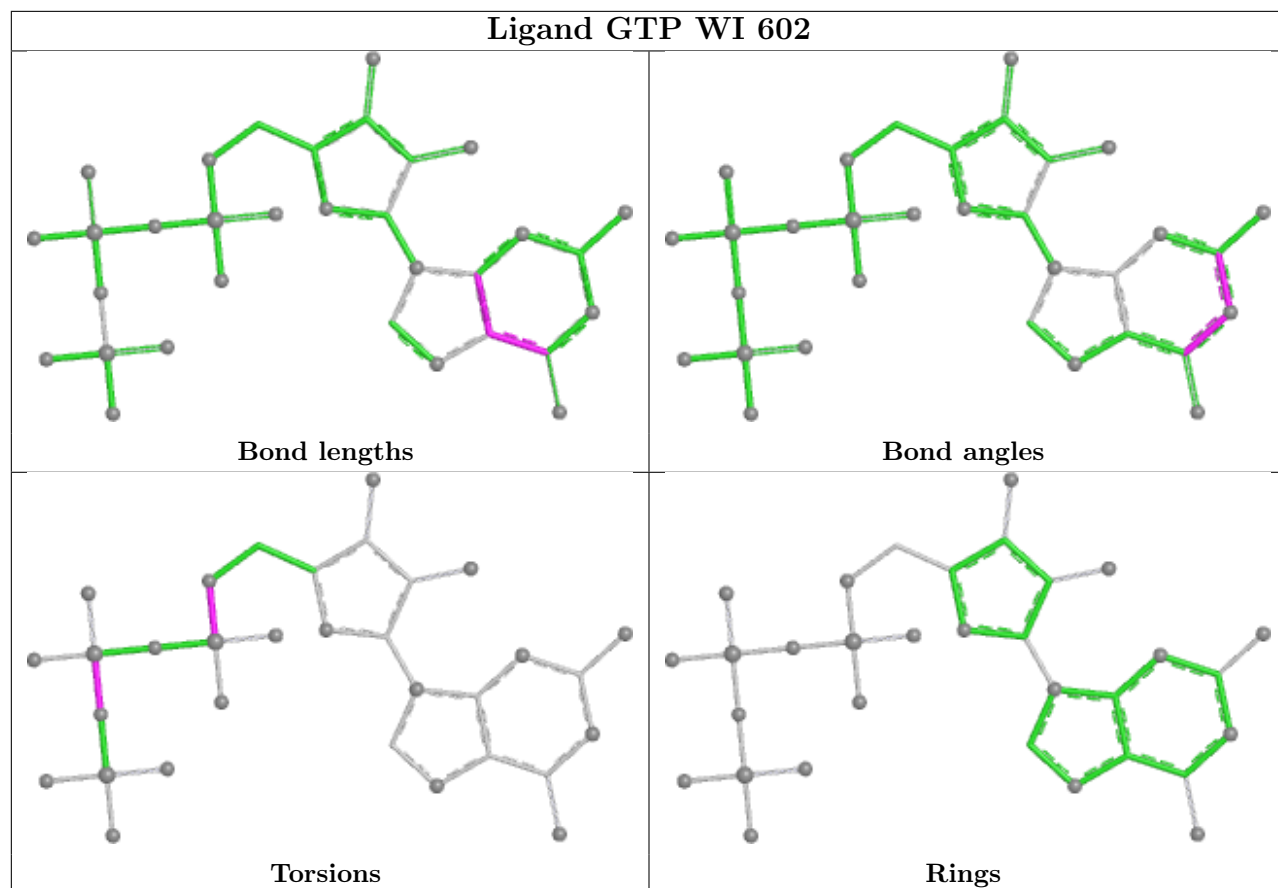


## Ligand GTP QU 602

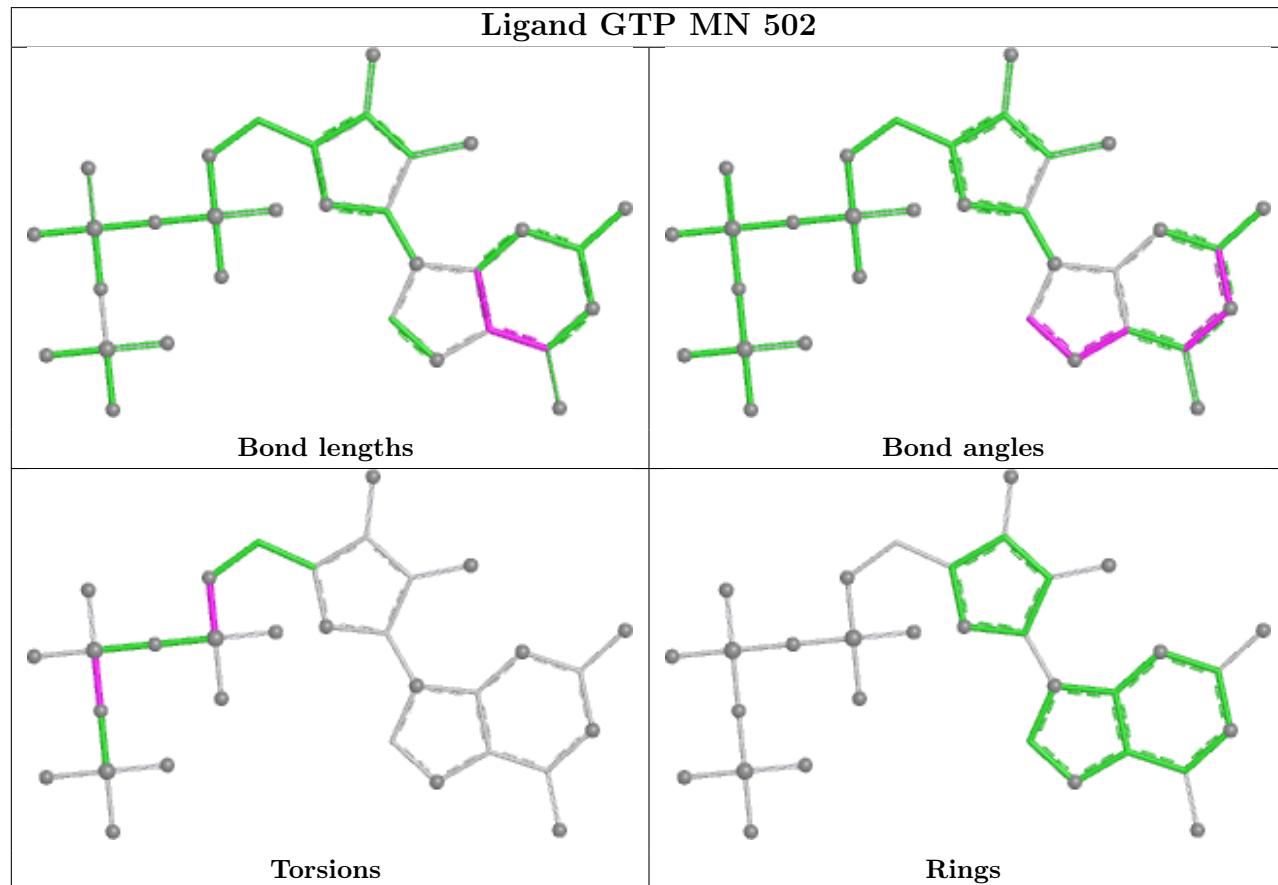


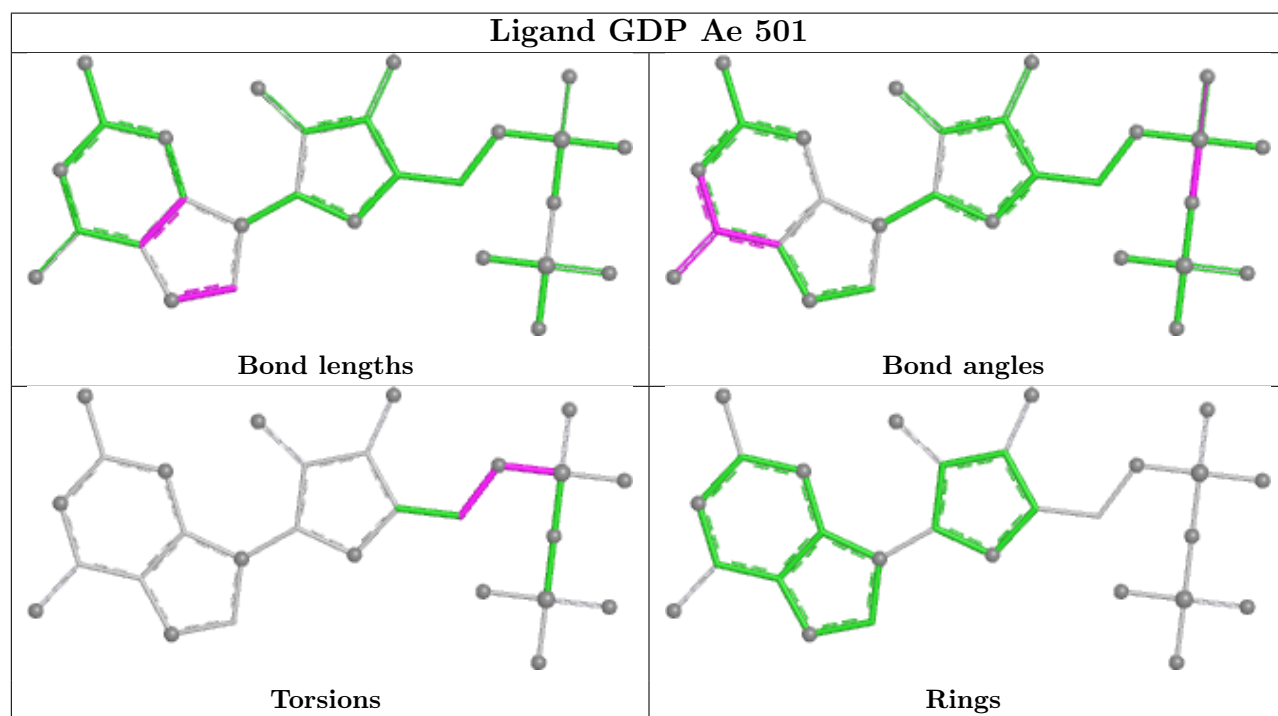
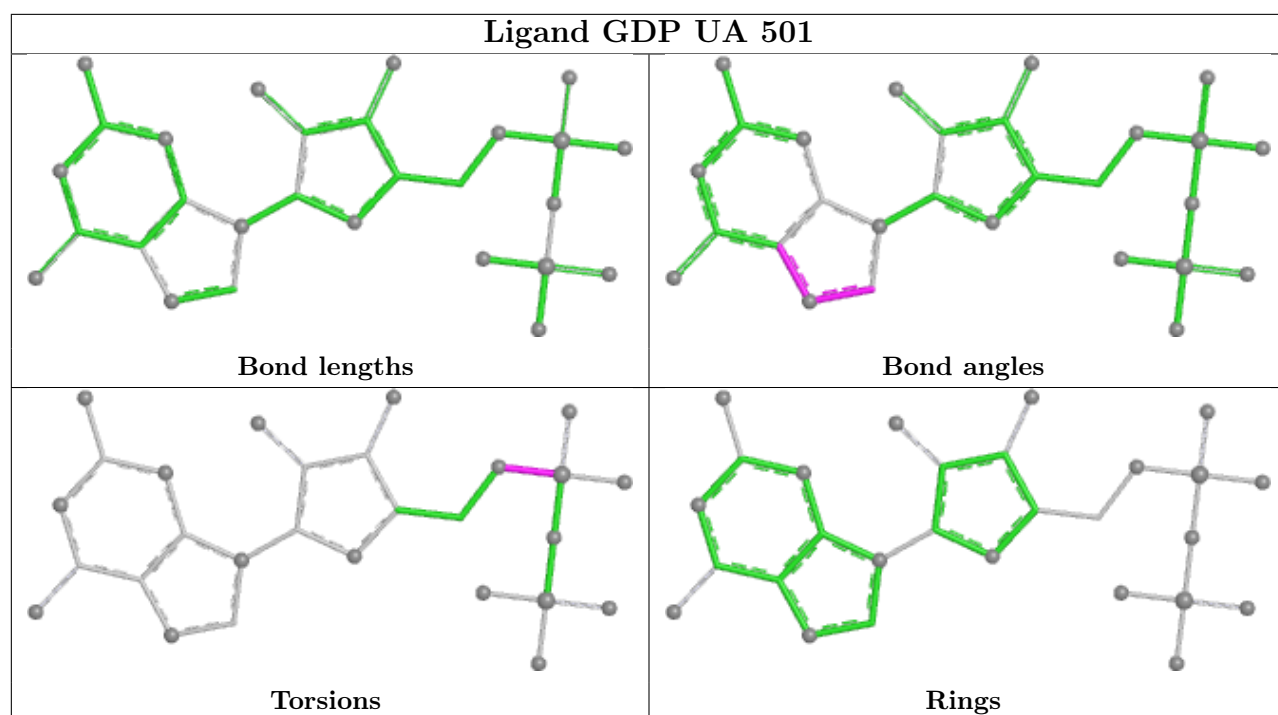


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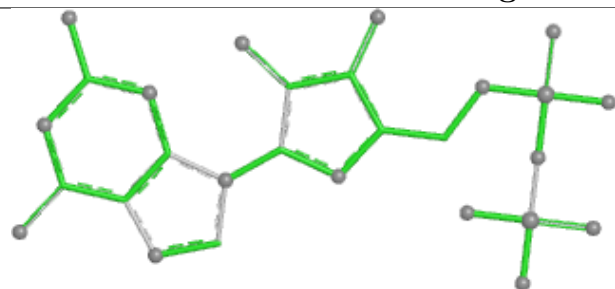


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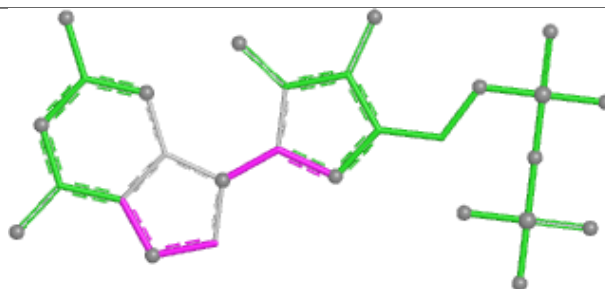




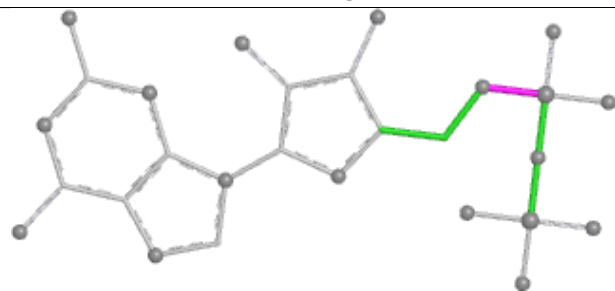
## Ligand GDP OK 501



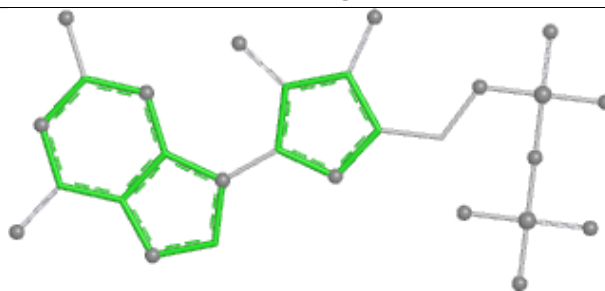
Bond lengths



Bond angles

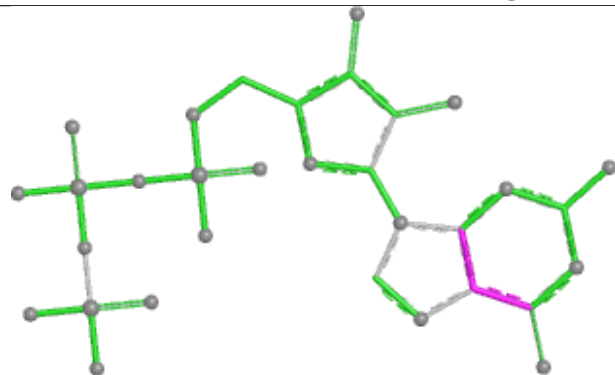


Torsions

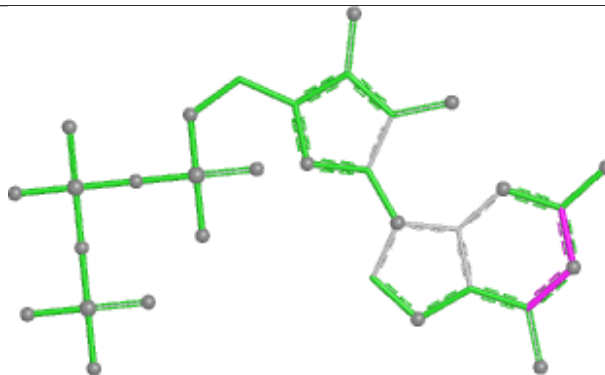


Rings

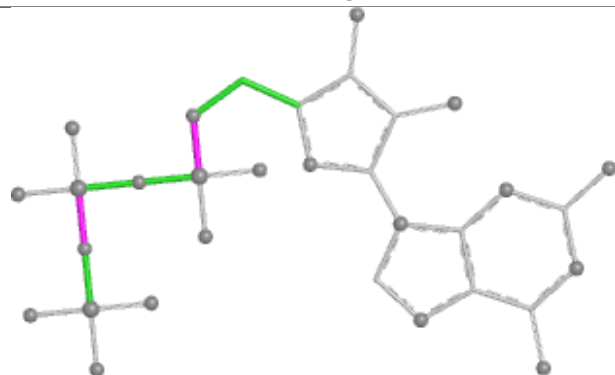
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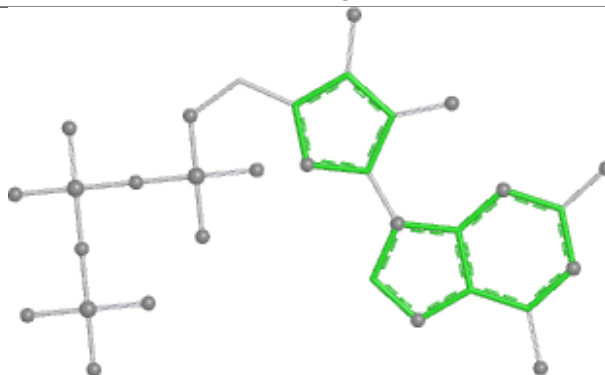
Bond lengths



Bond angles

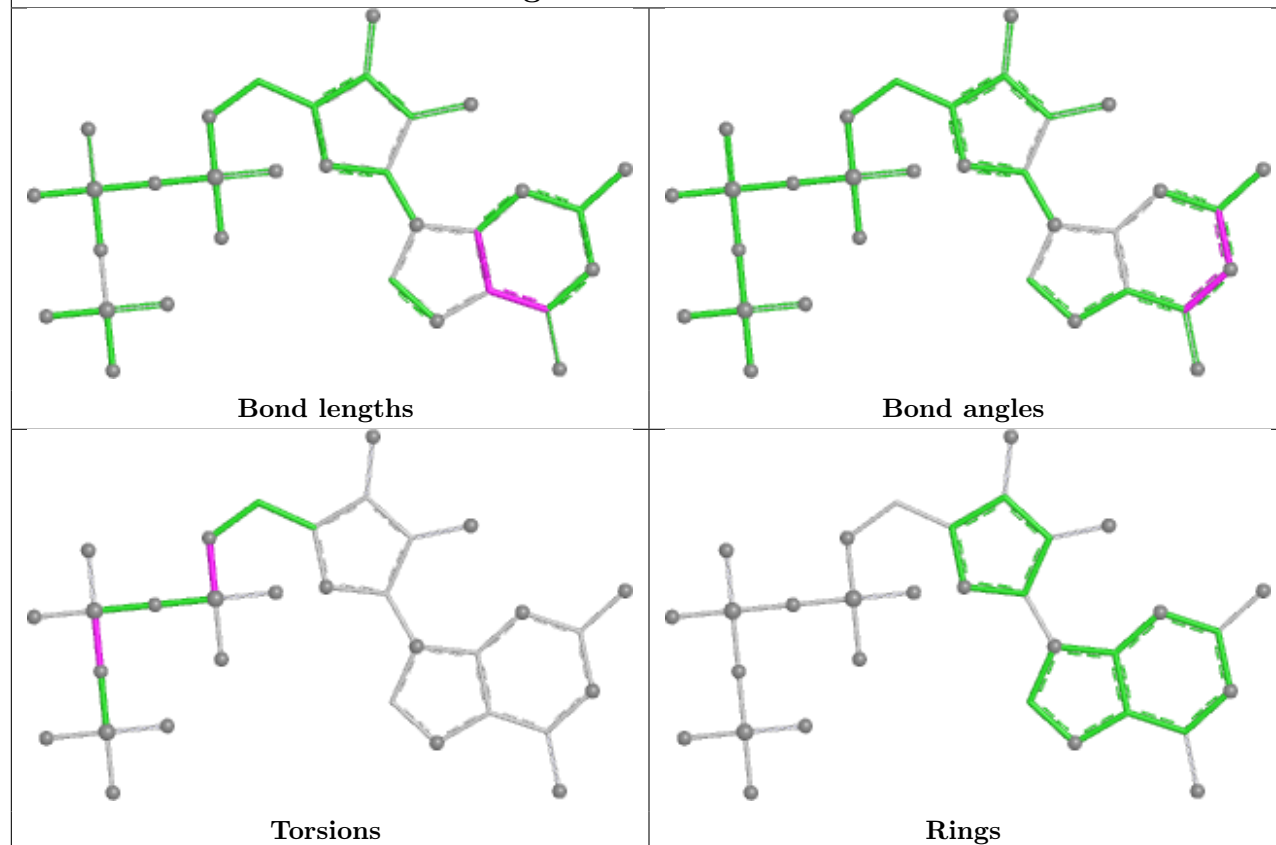


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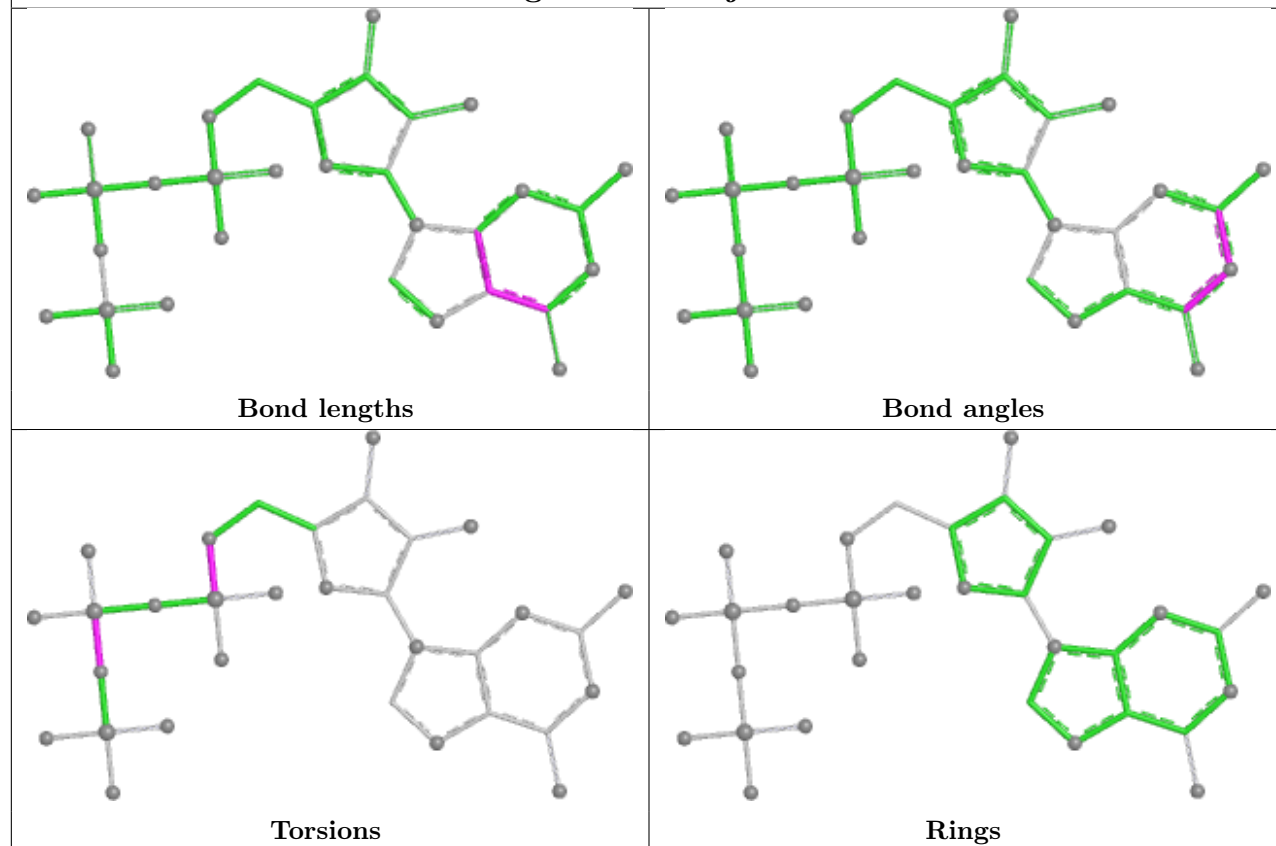


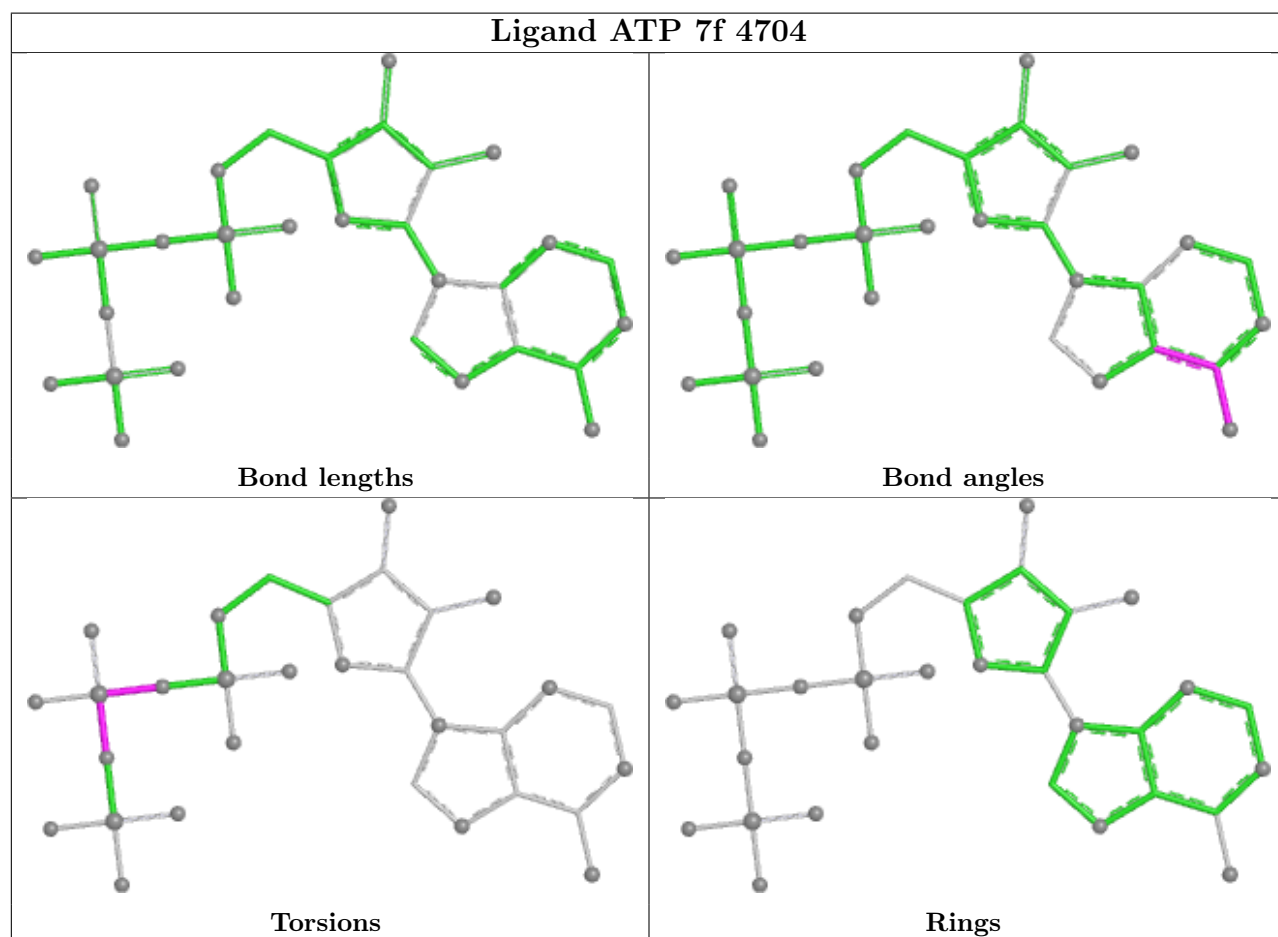
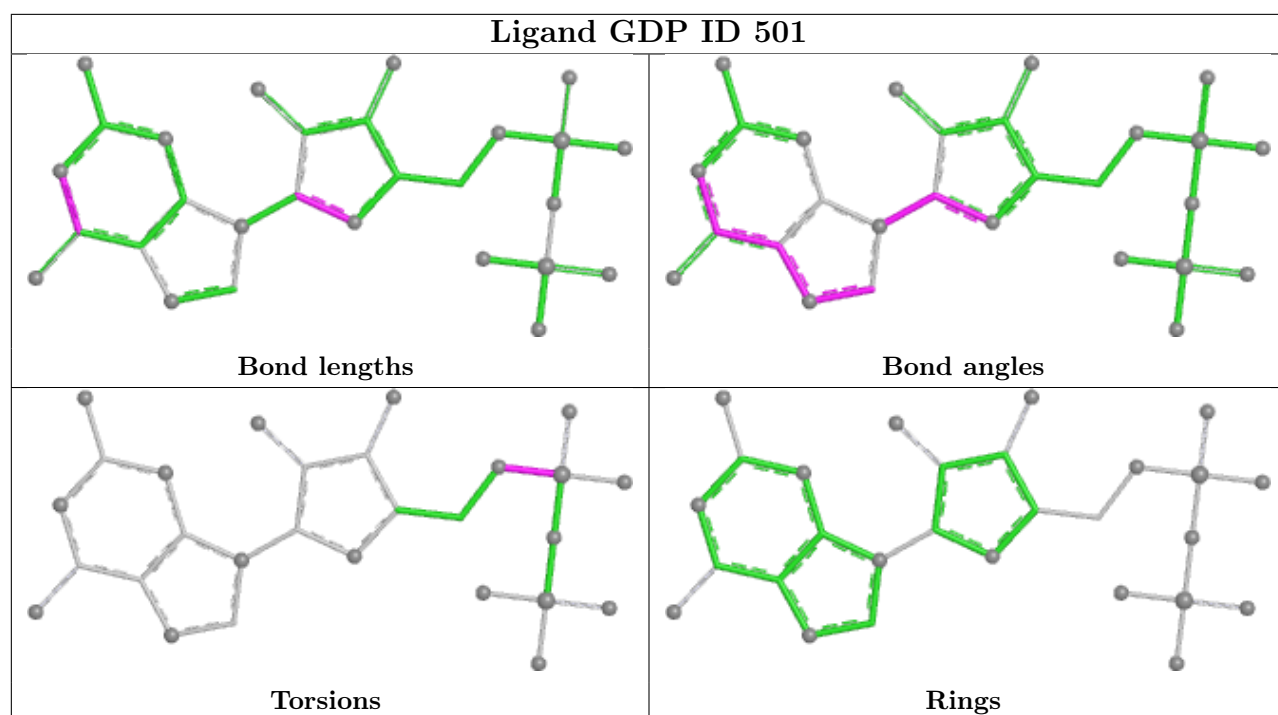
Rings

## Ligand GTP VI 501

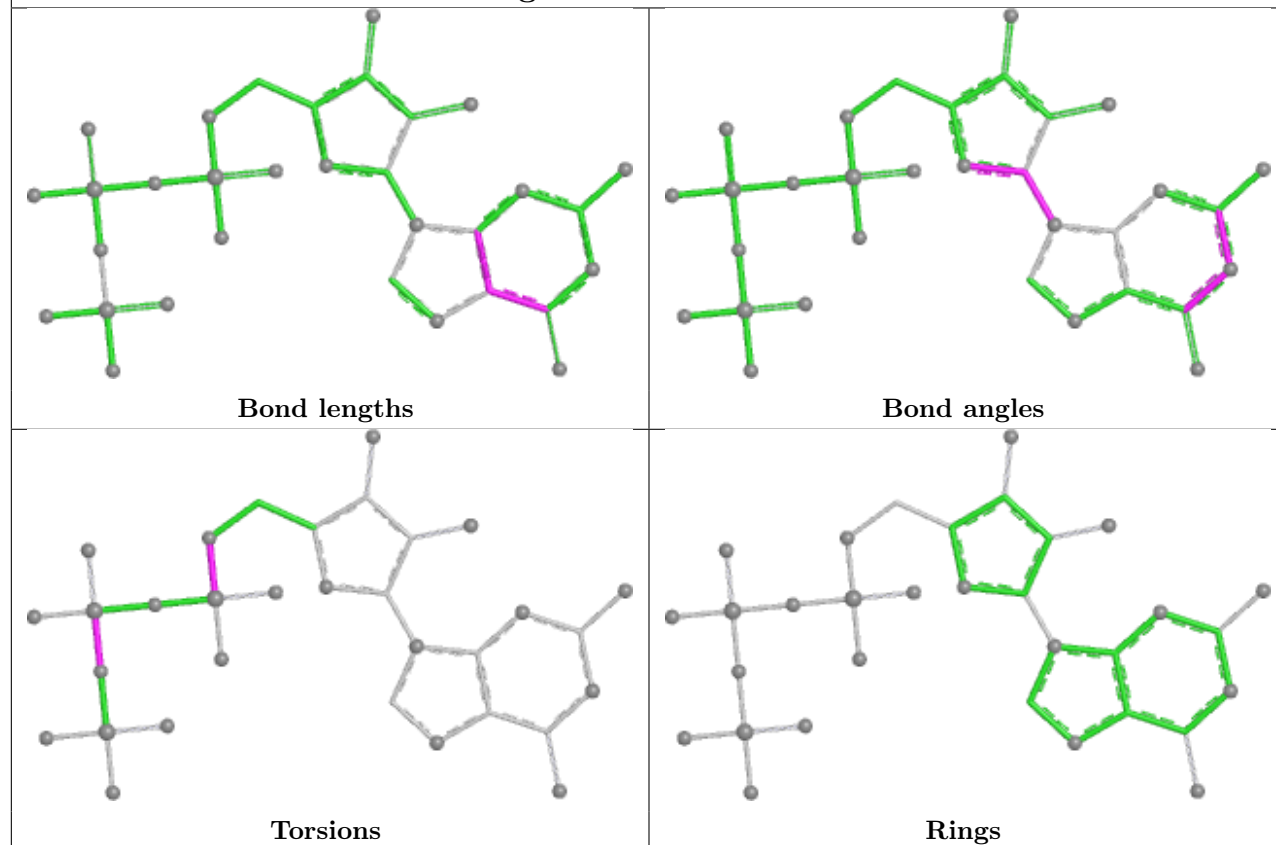


## Ligand GTP Aj 501

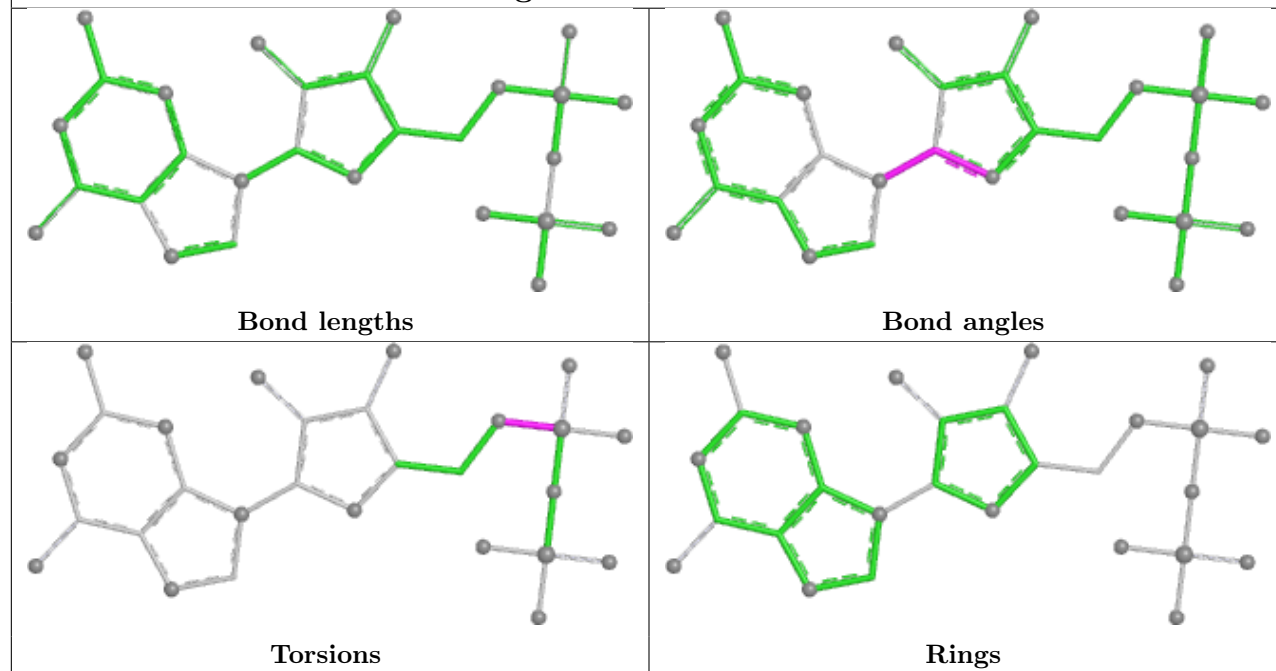




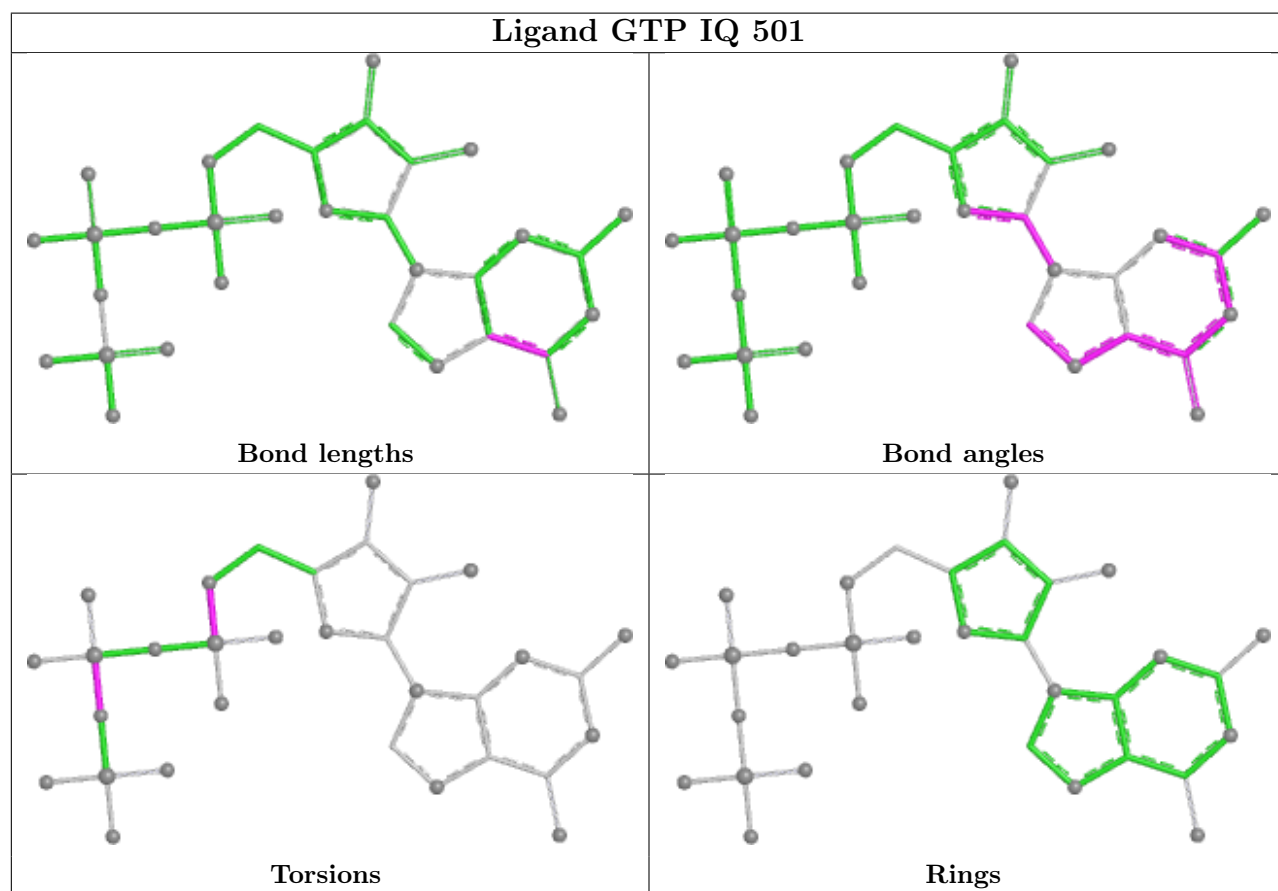
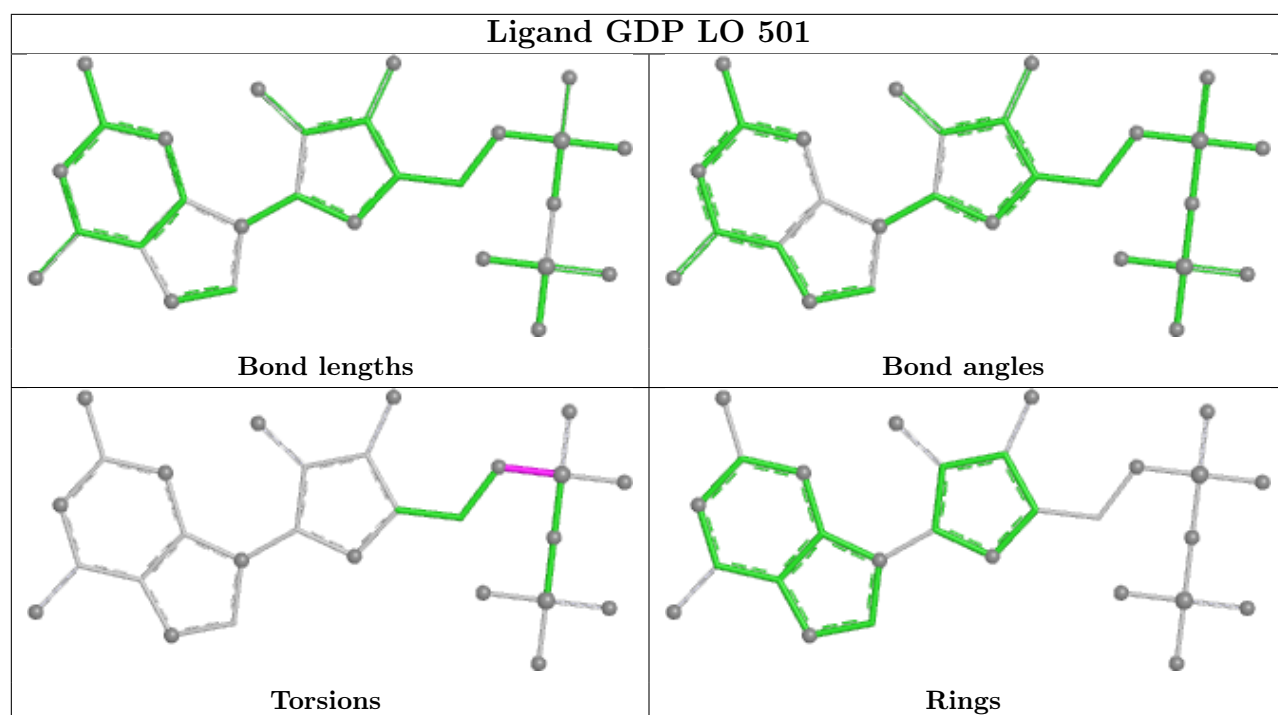
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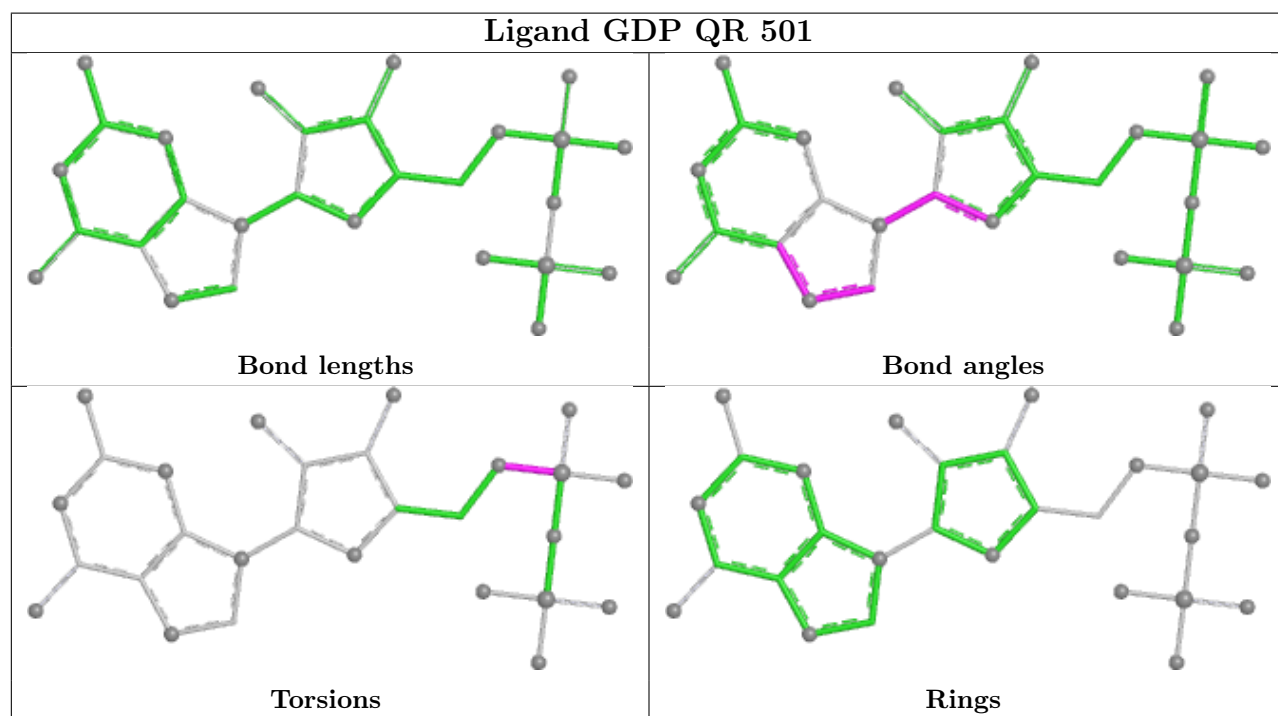
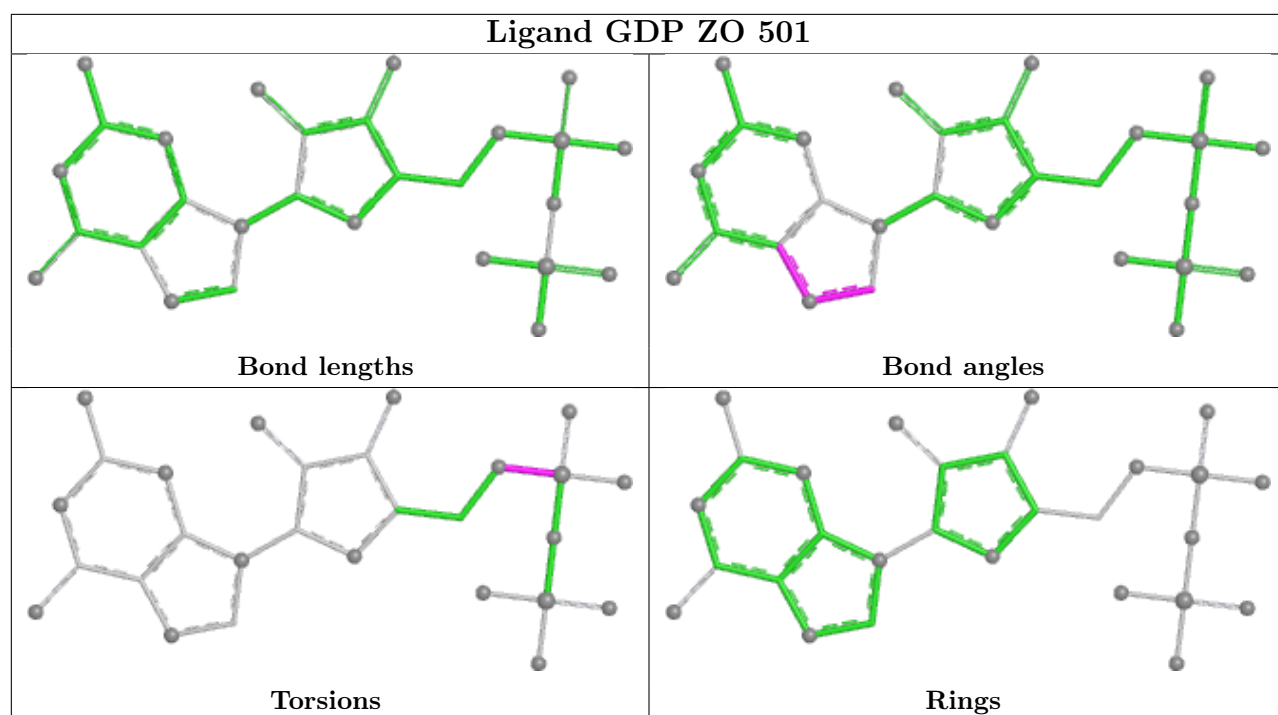


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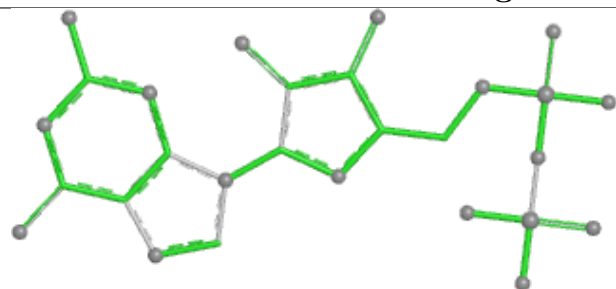




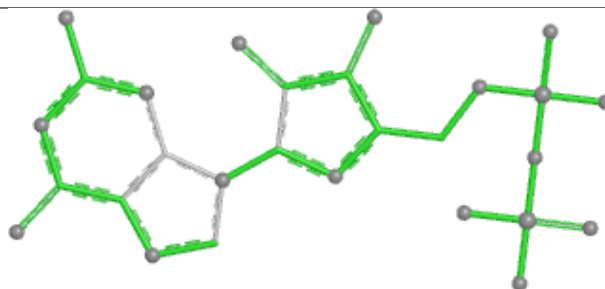




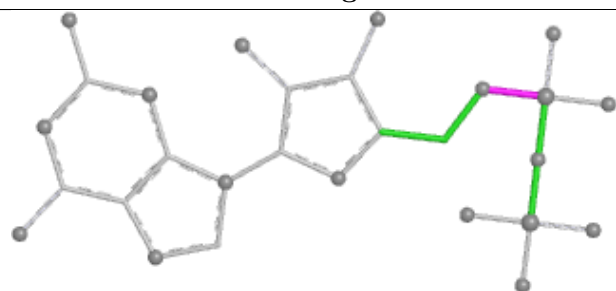
## Ligand GDP WB 501



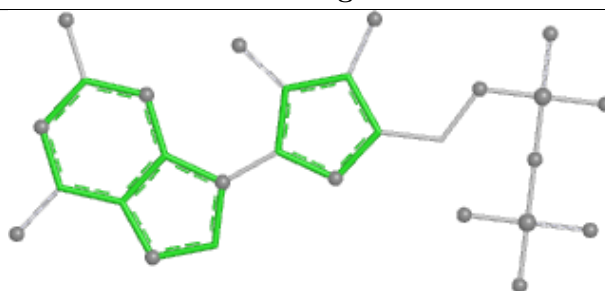
Bond lengths



Bond angles

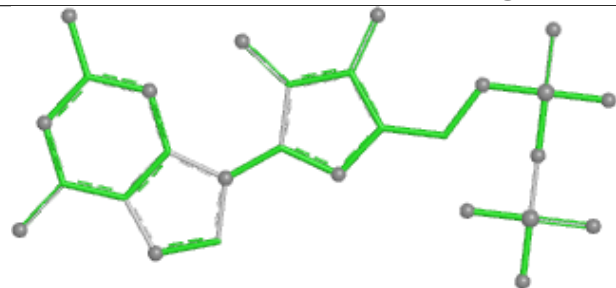


Torsions

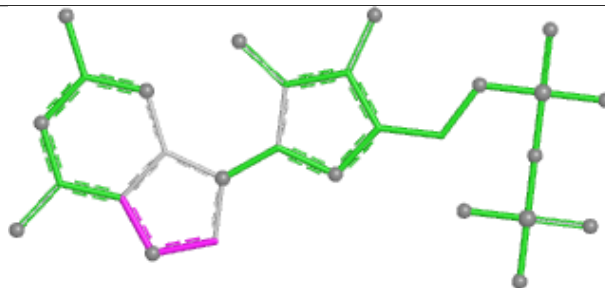


Rings

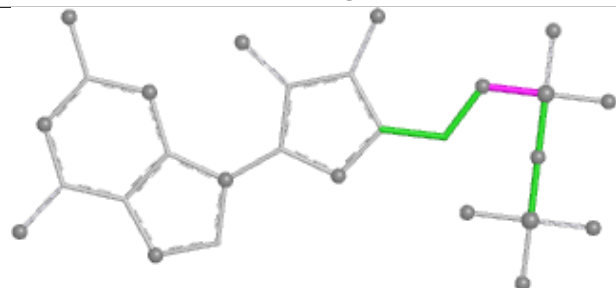
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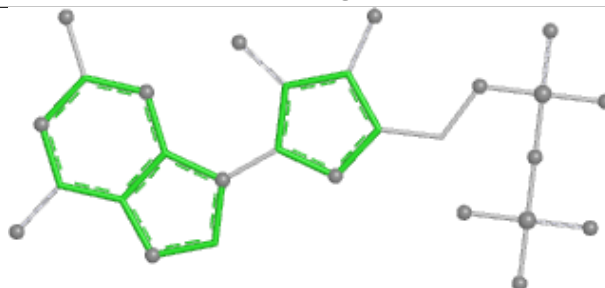
Bond lengths



Bond angles

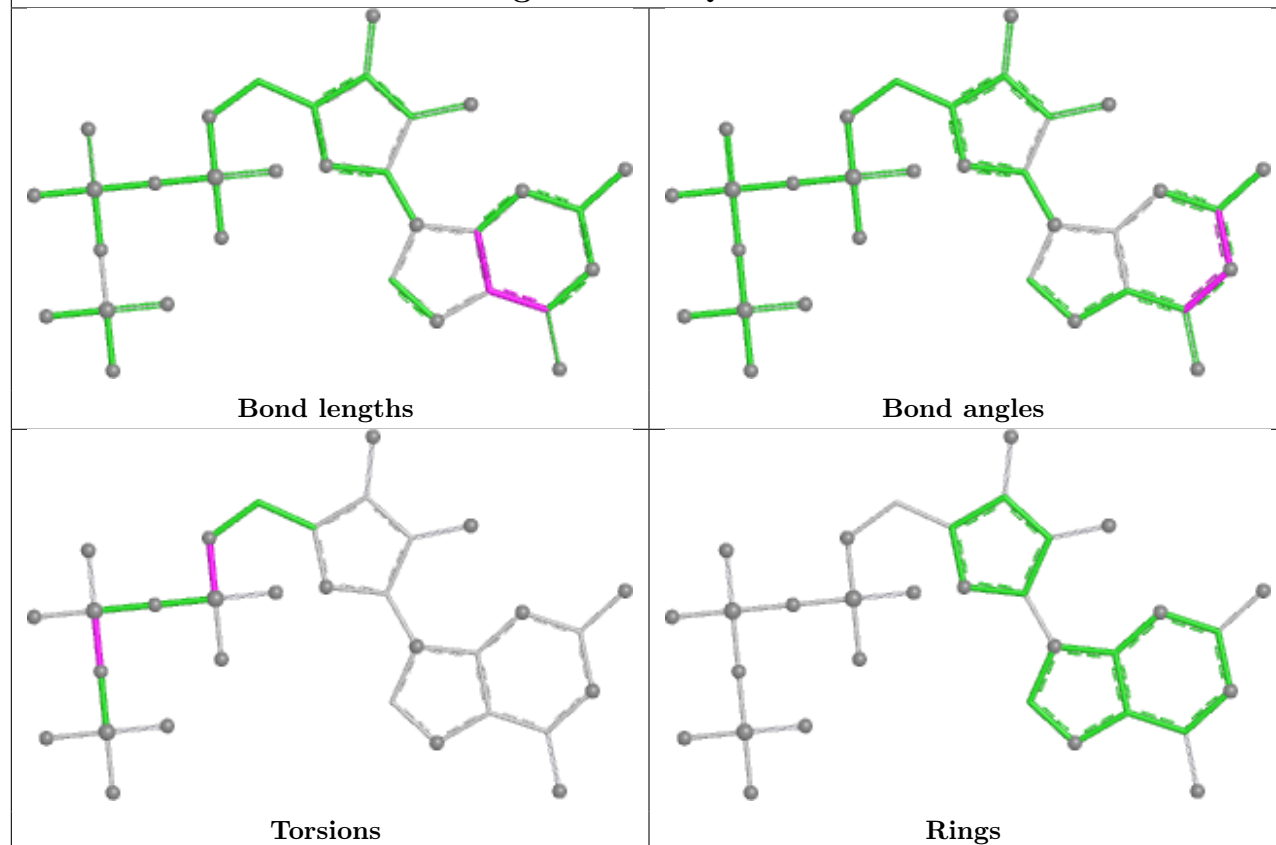


Torsions

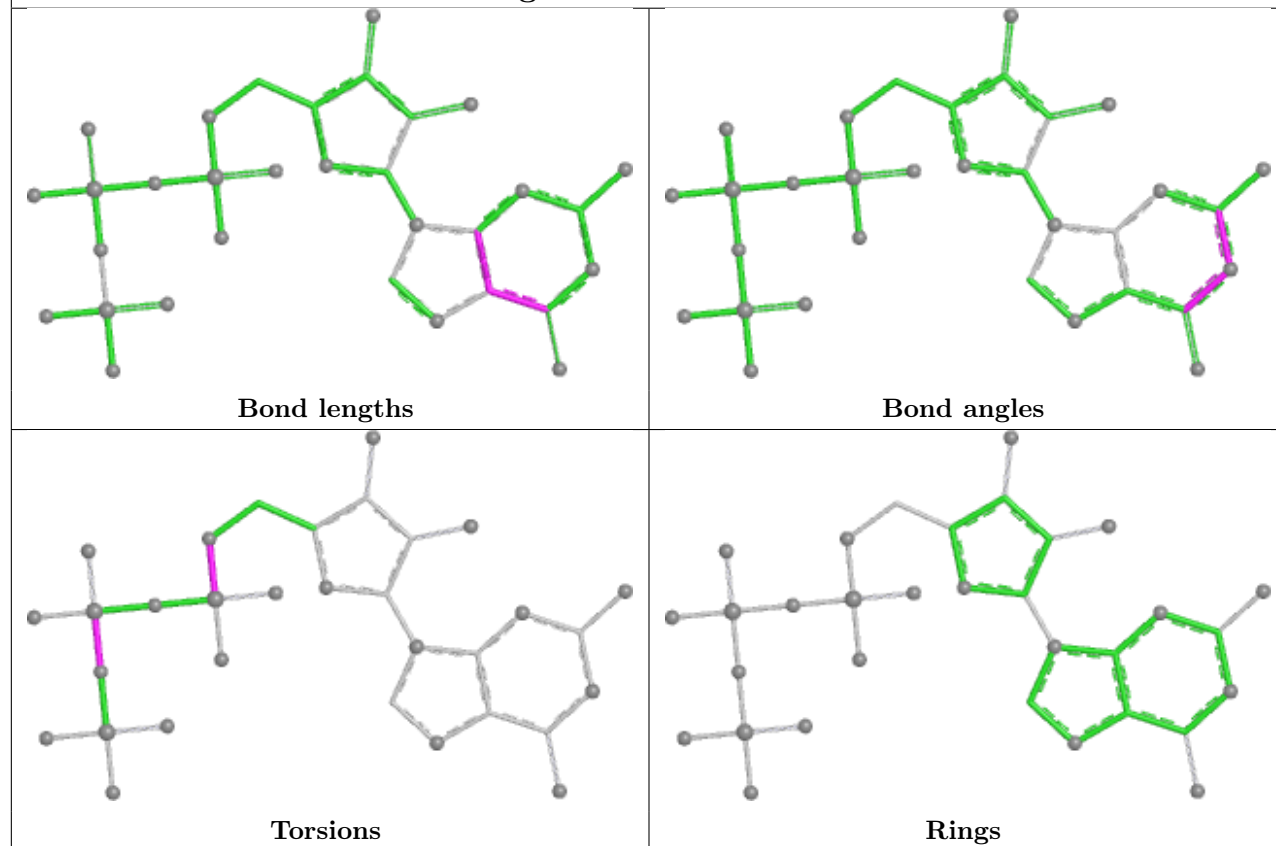


Rings

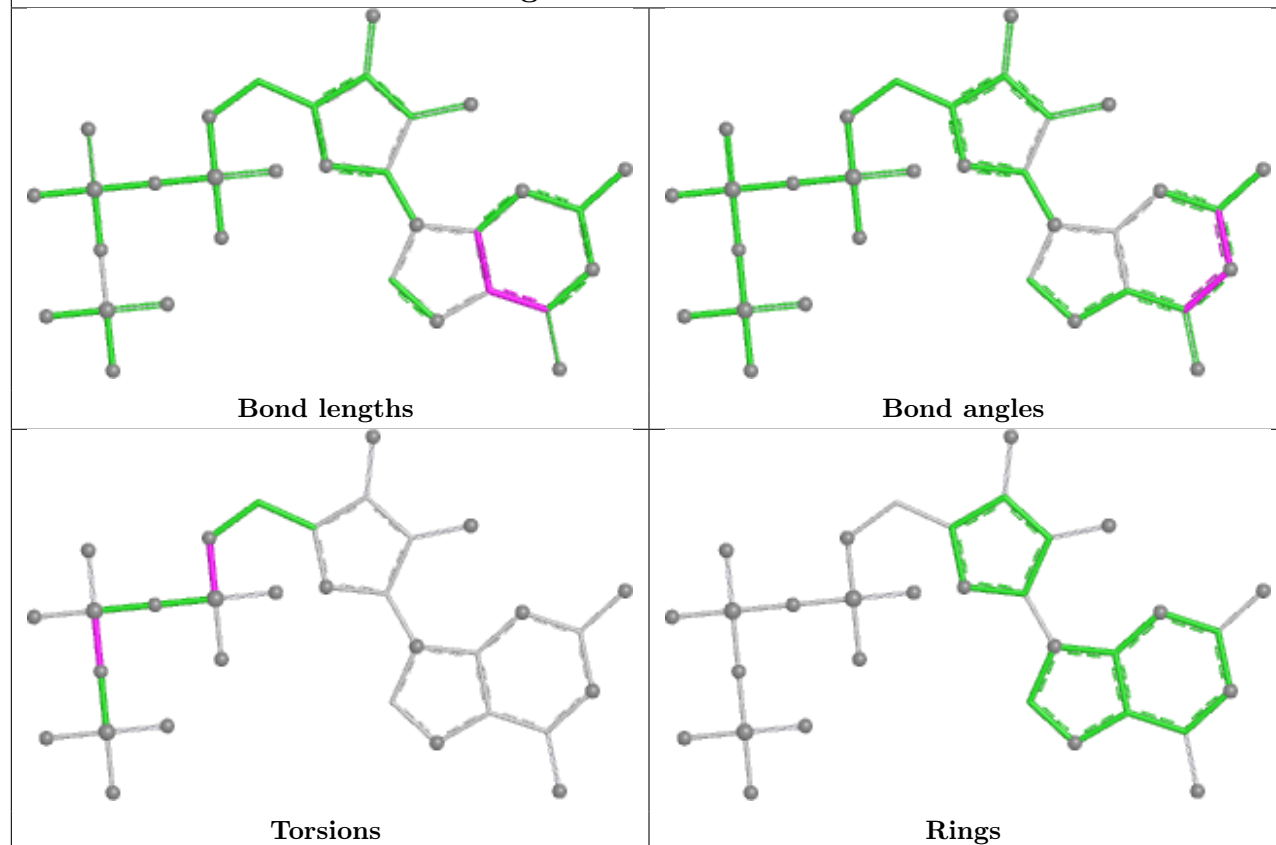
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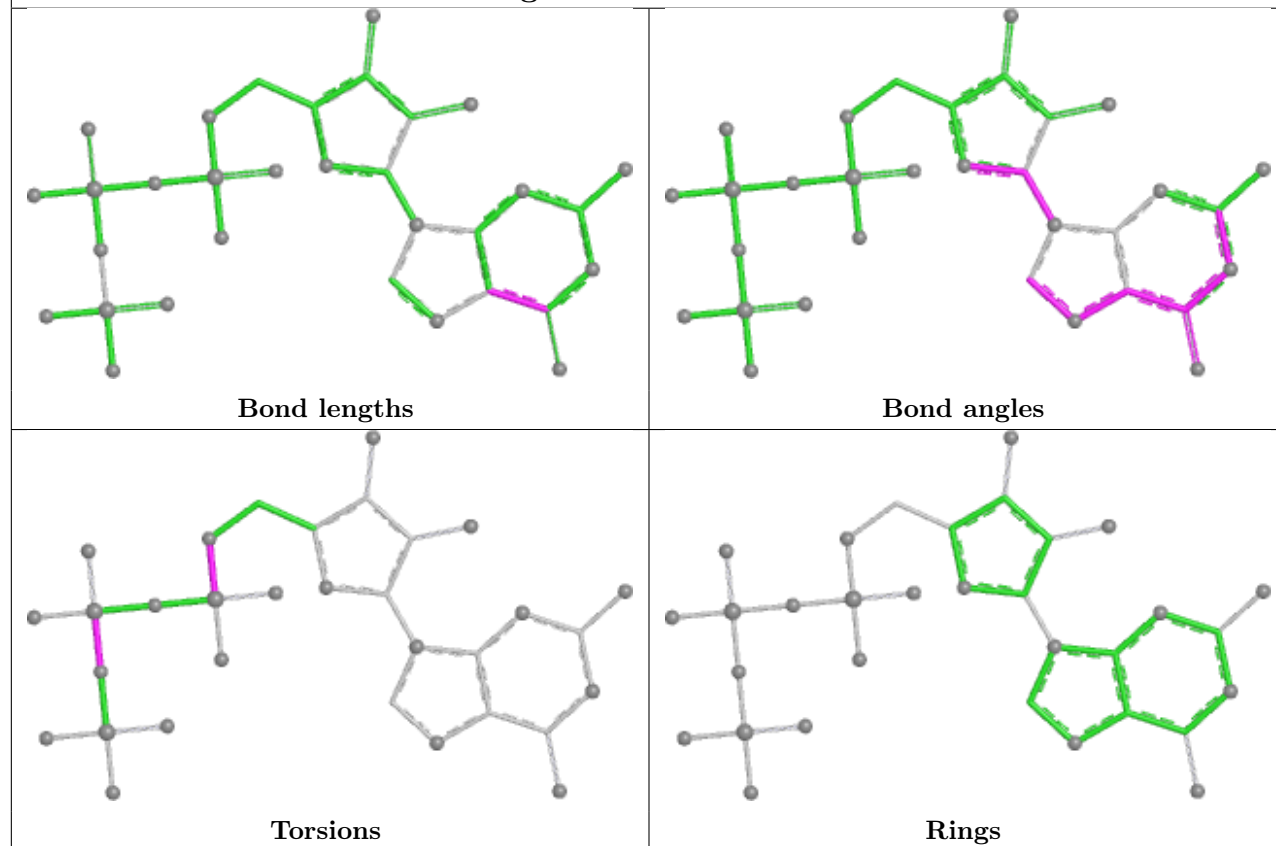
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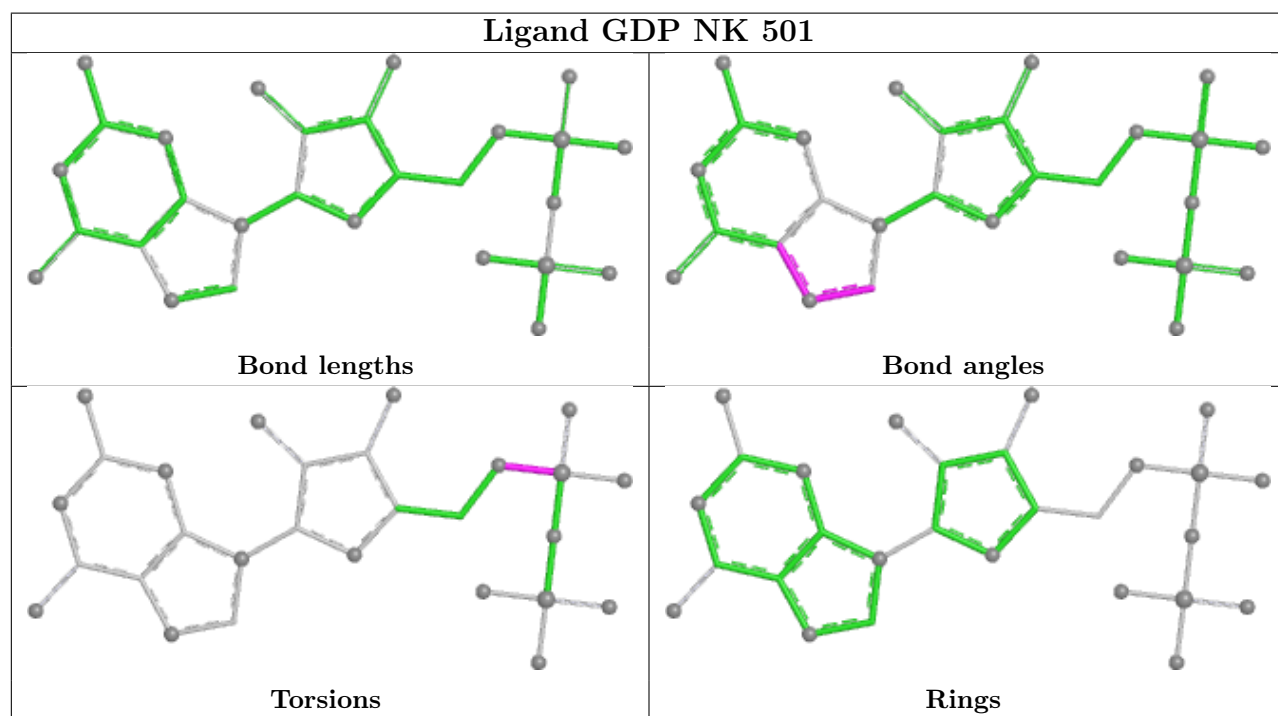
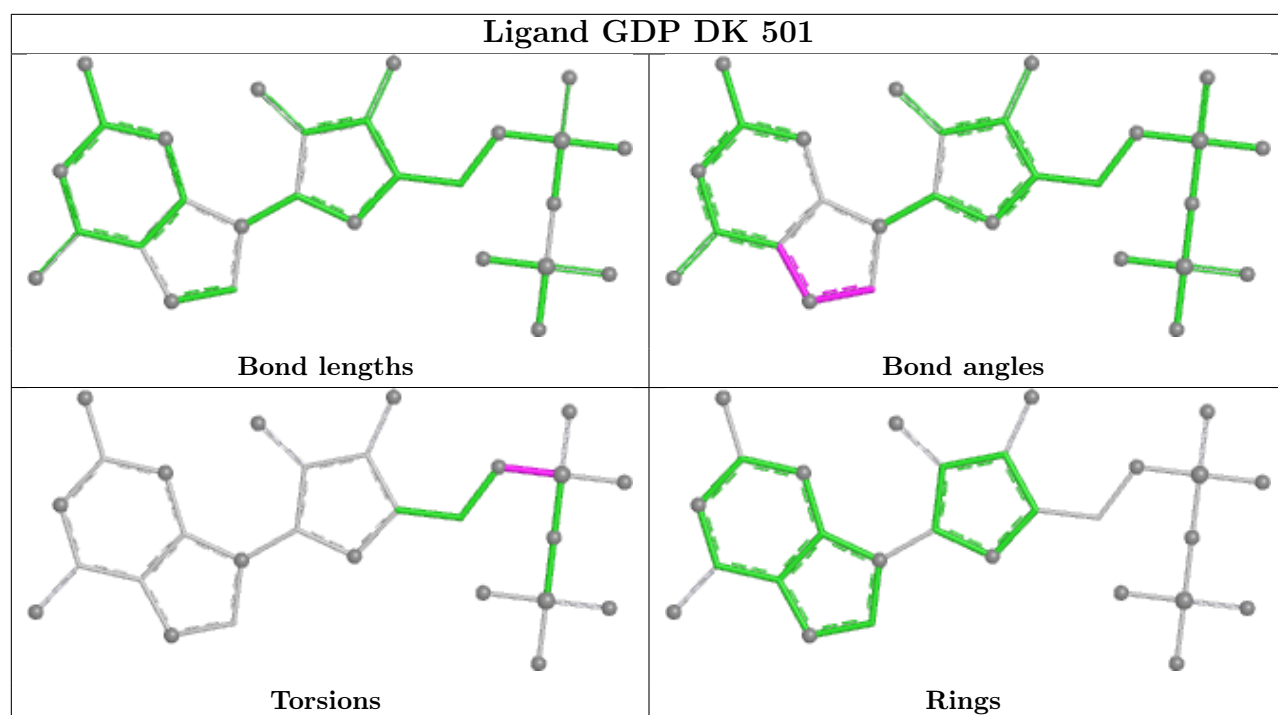


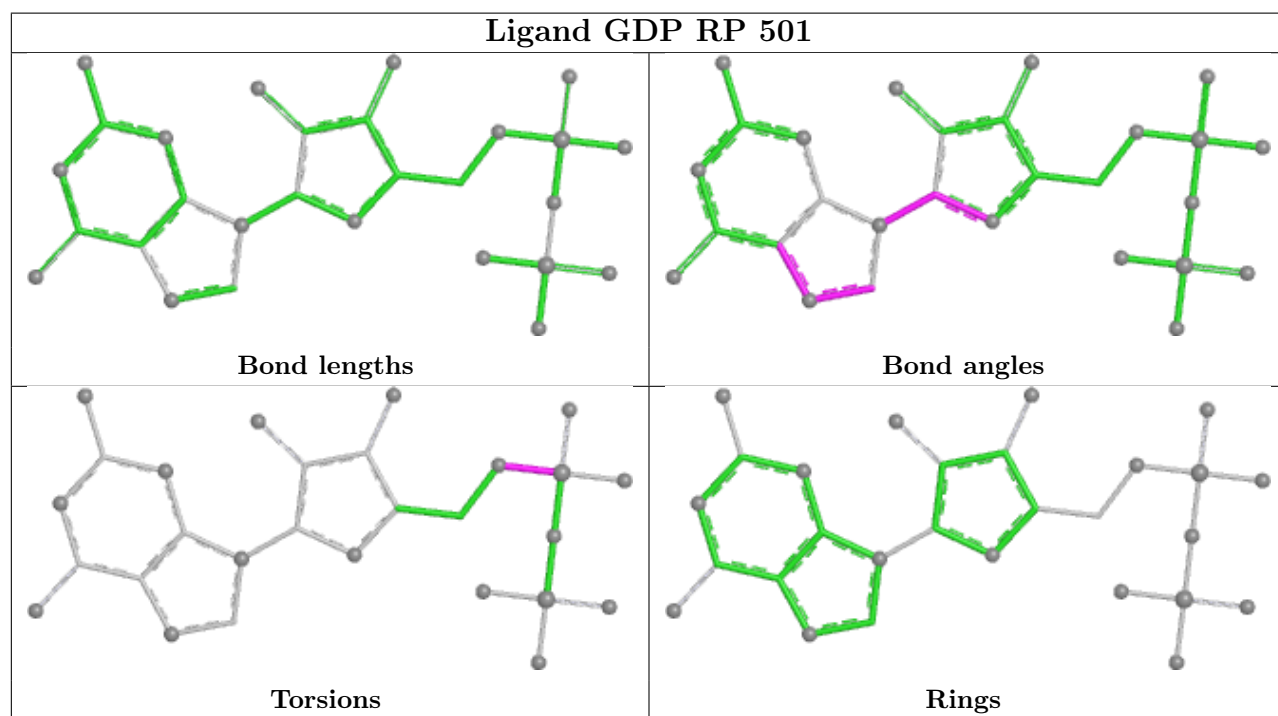
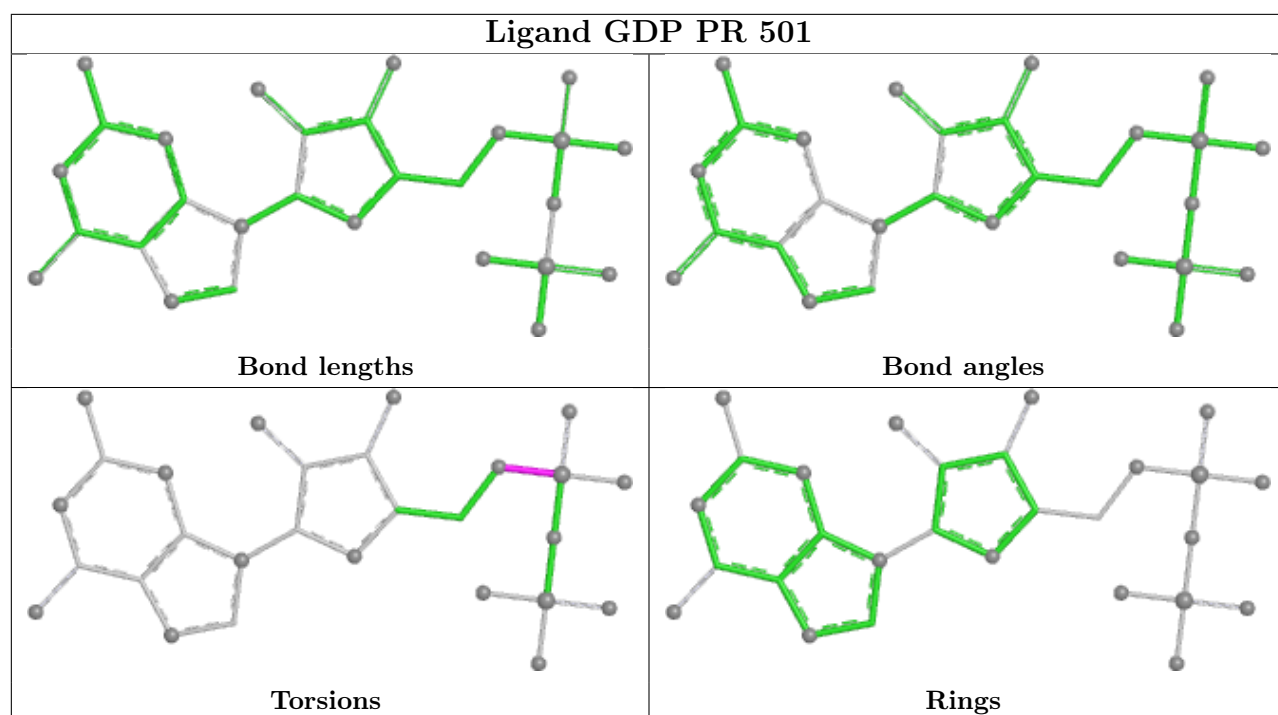
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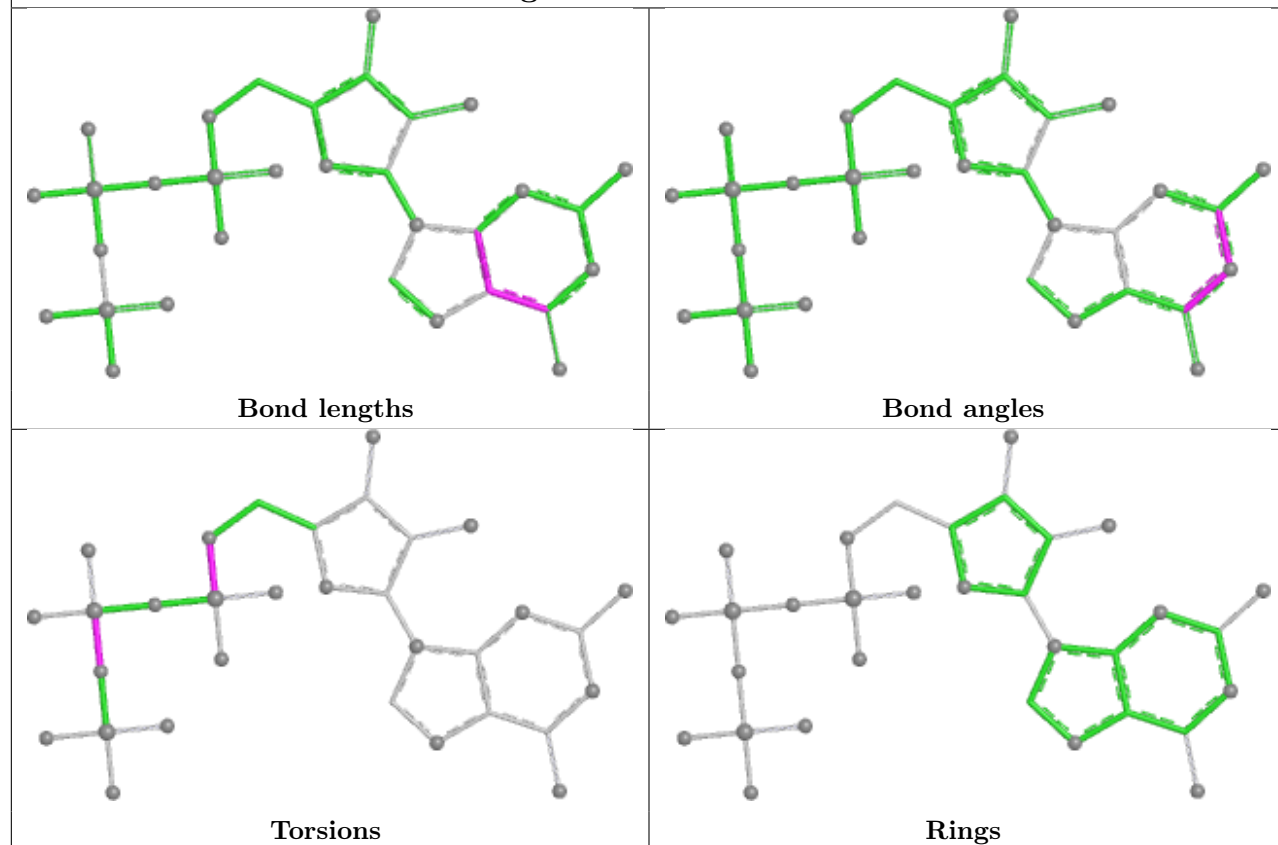
## Ligand GTP JH 602



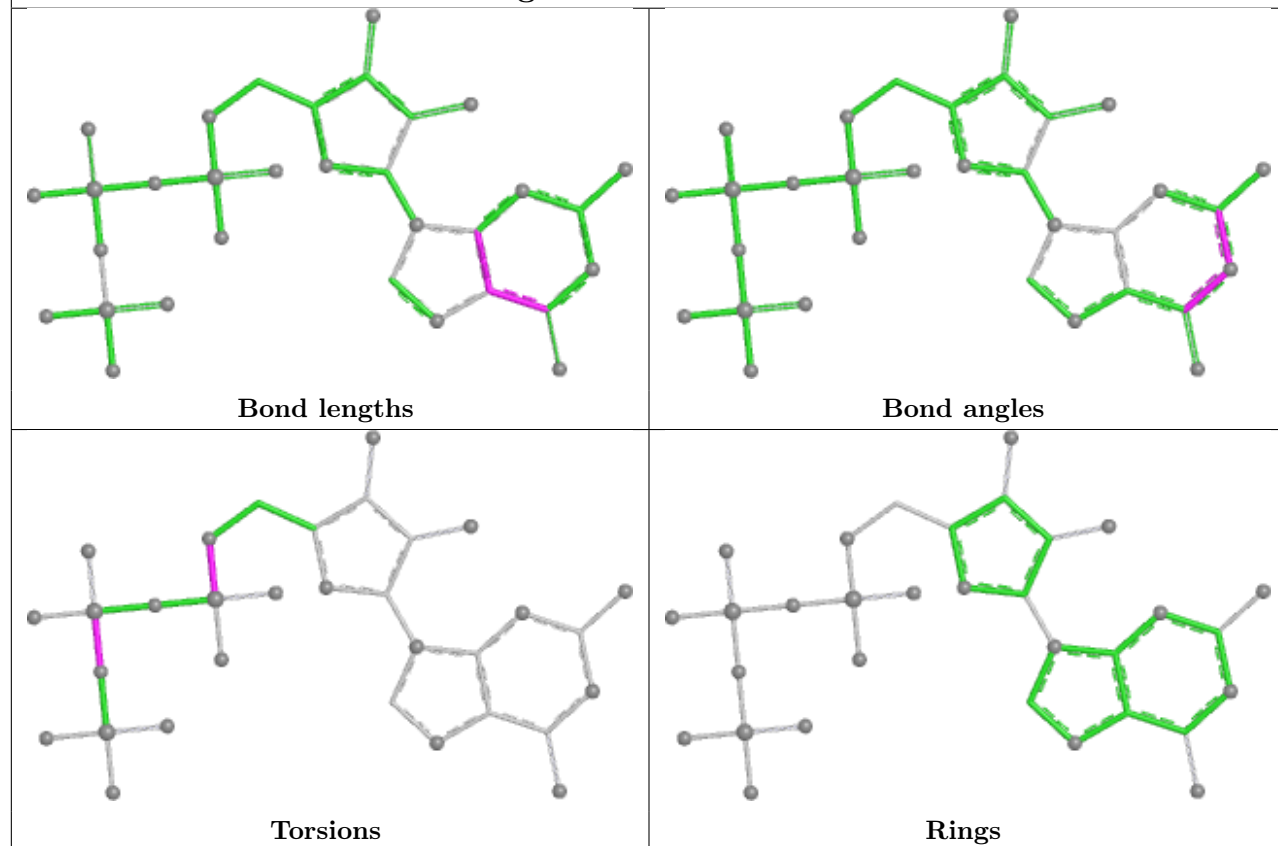




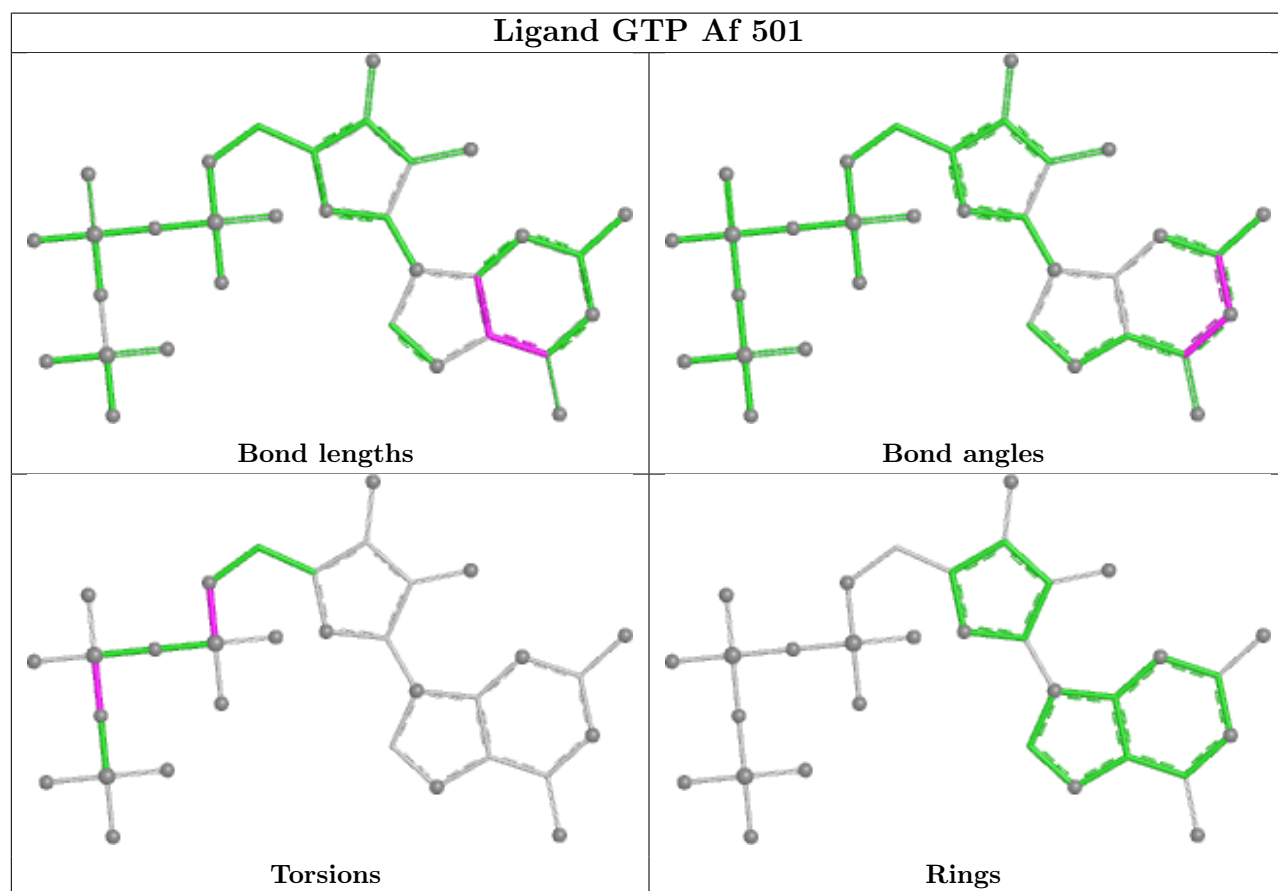
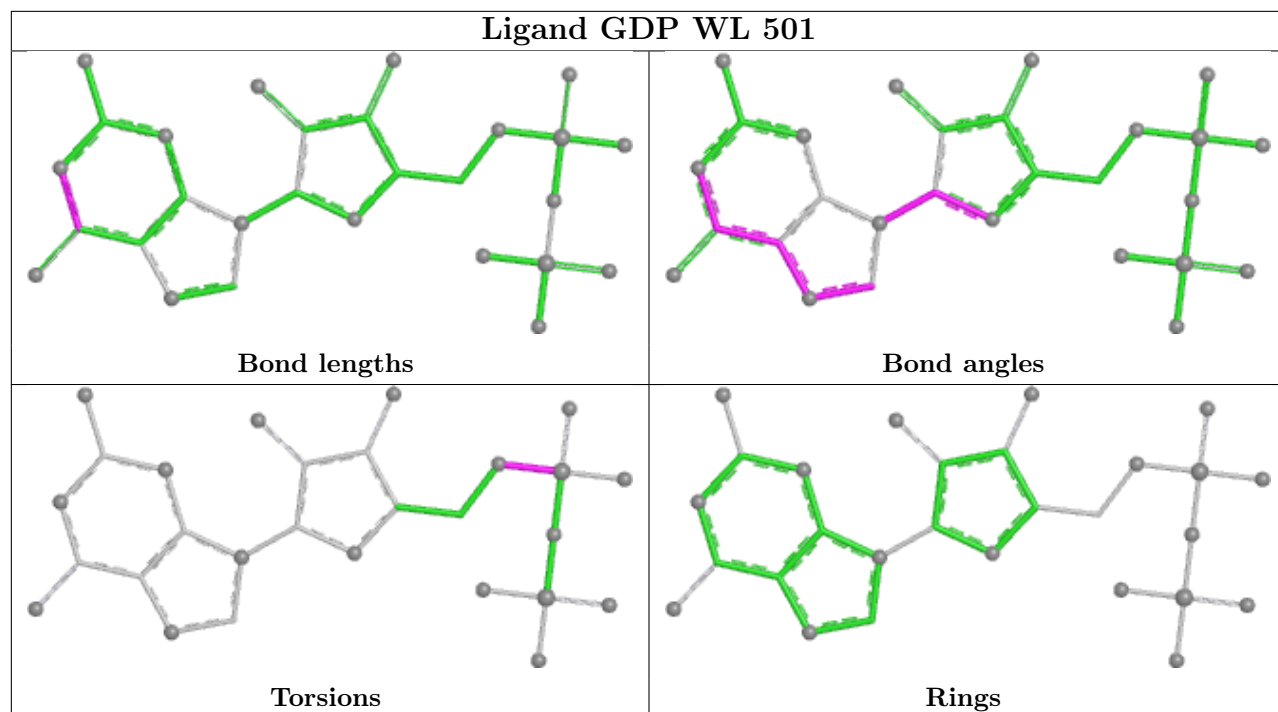
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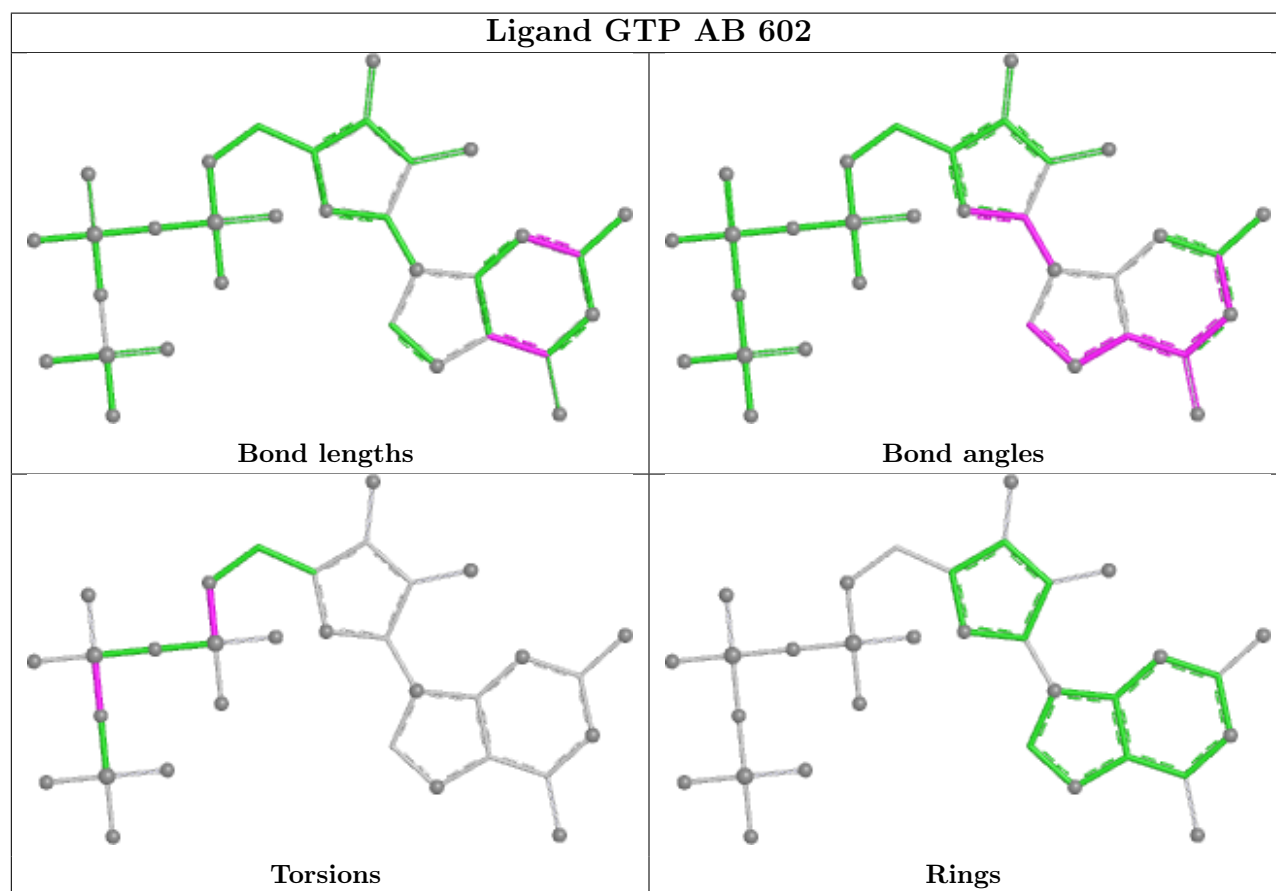
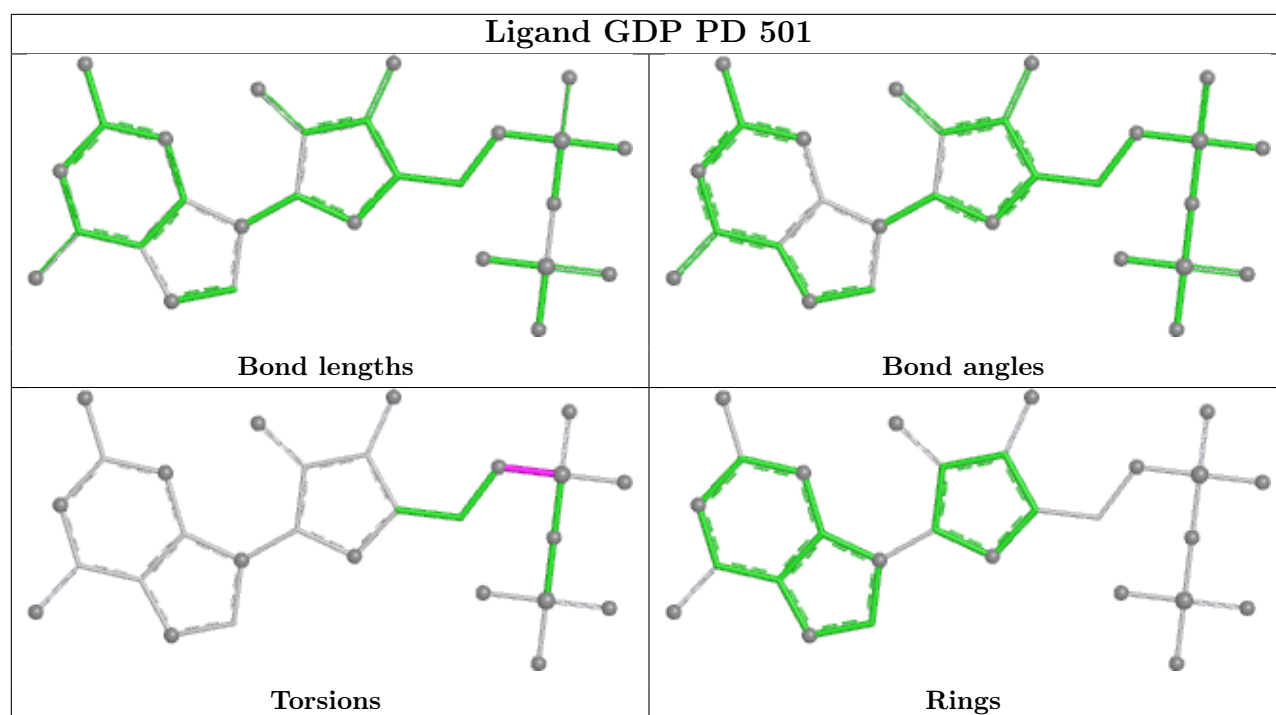


## Ligand GTP XC 602

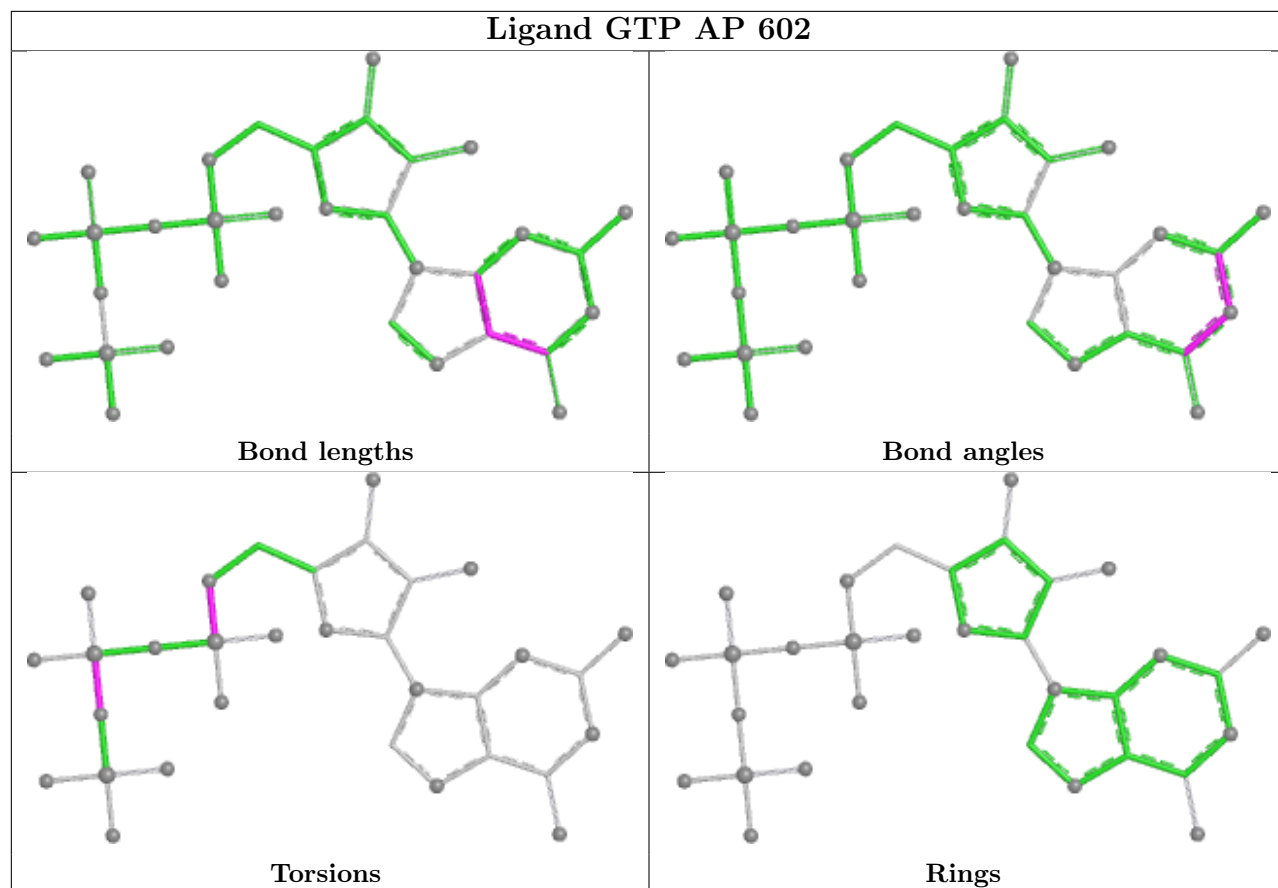




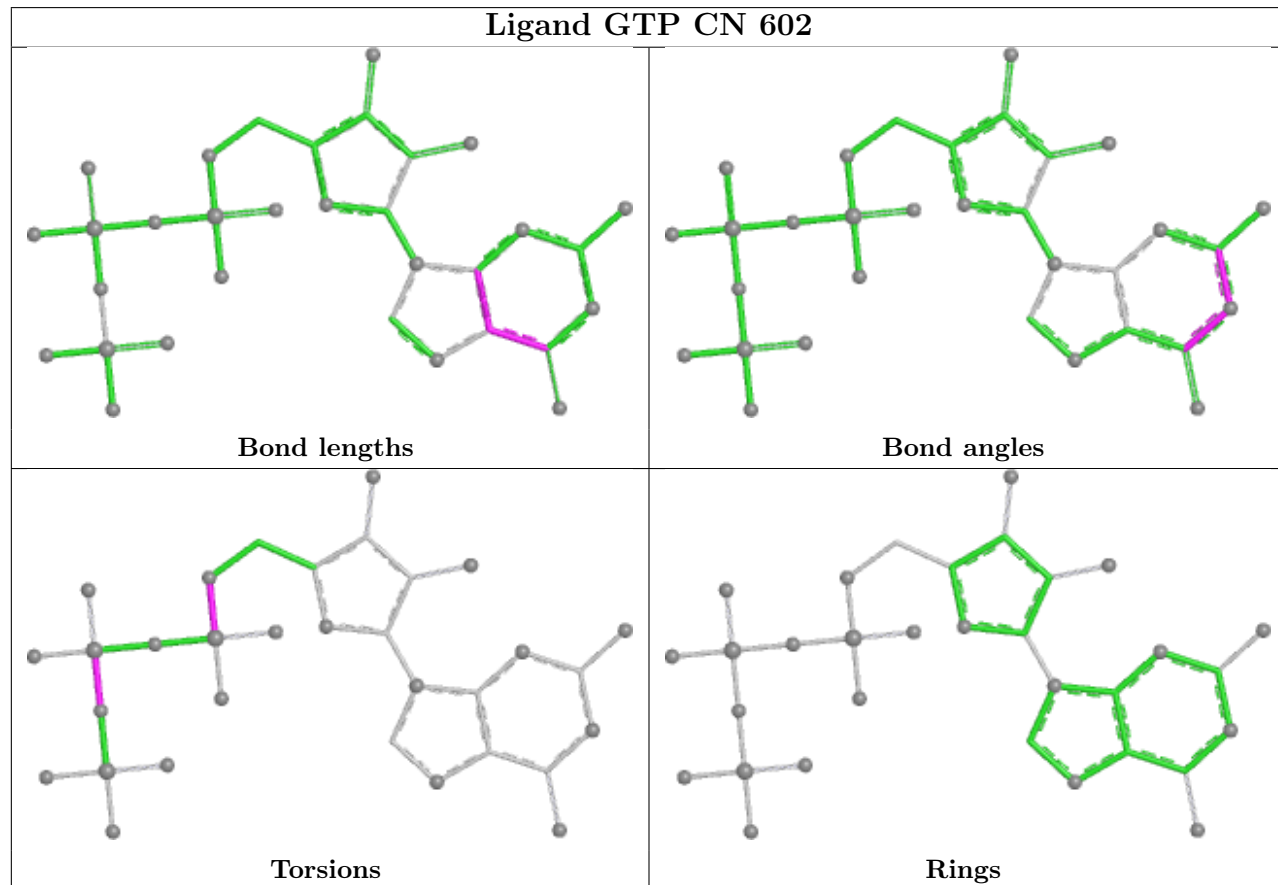


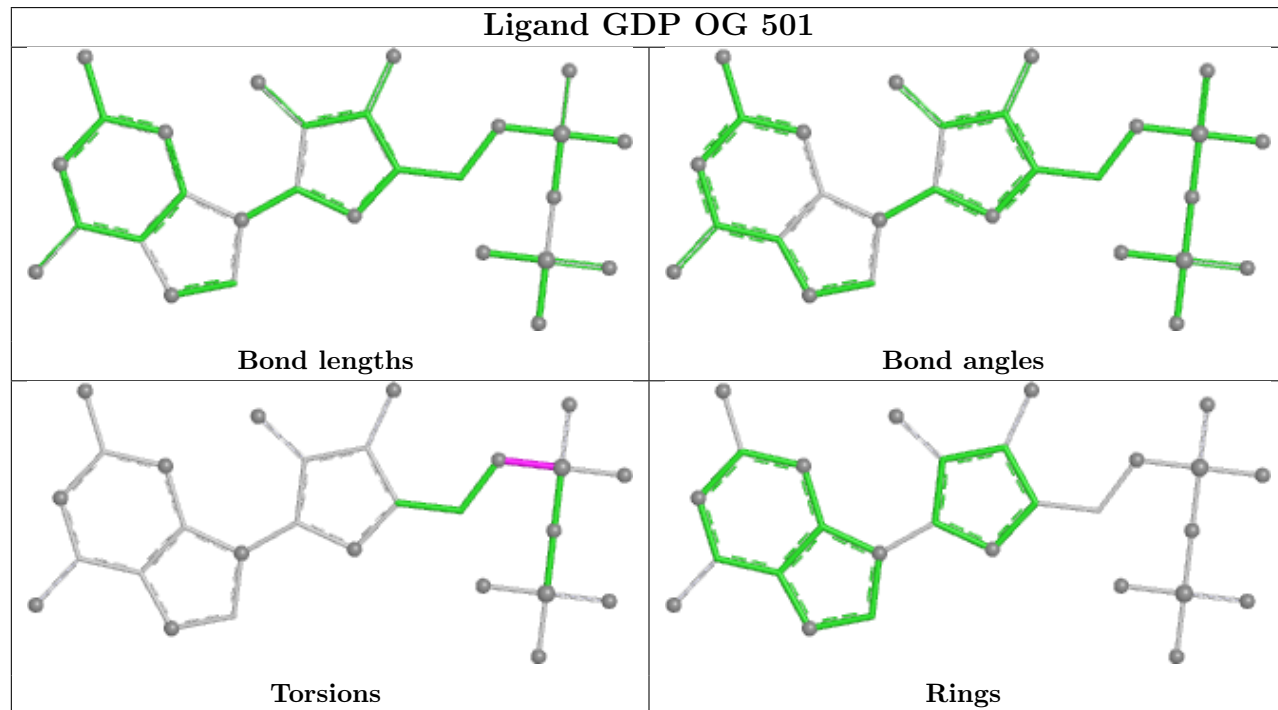
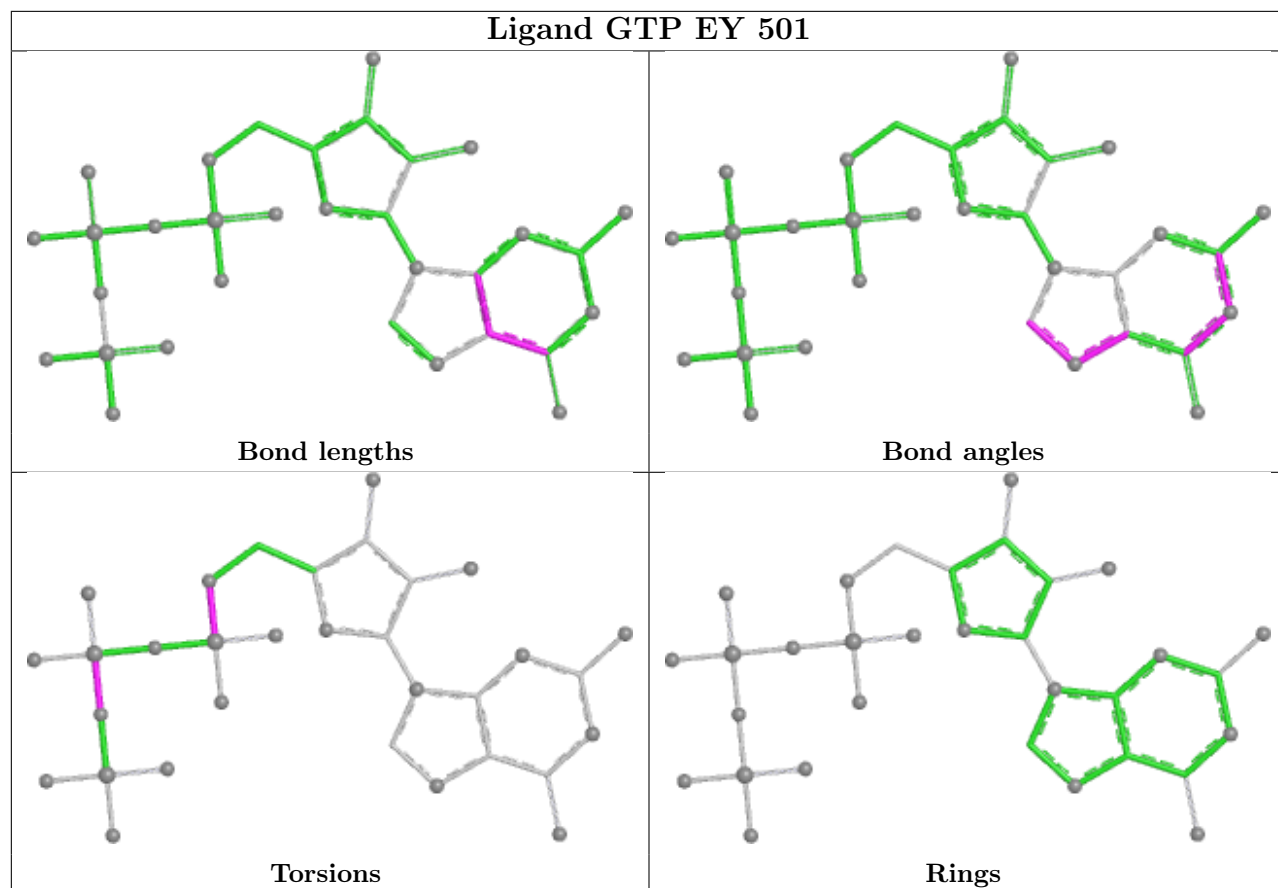


## Ligand GTP AP 602

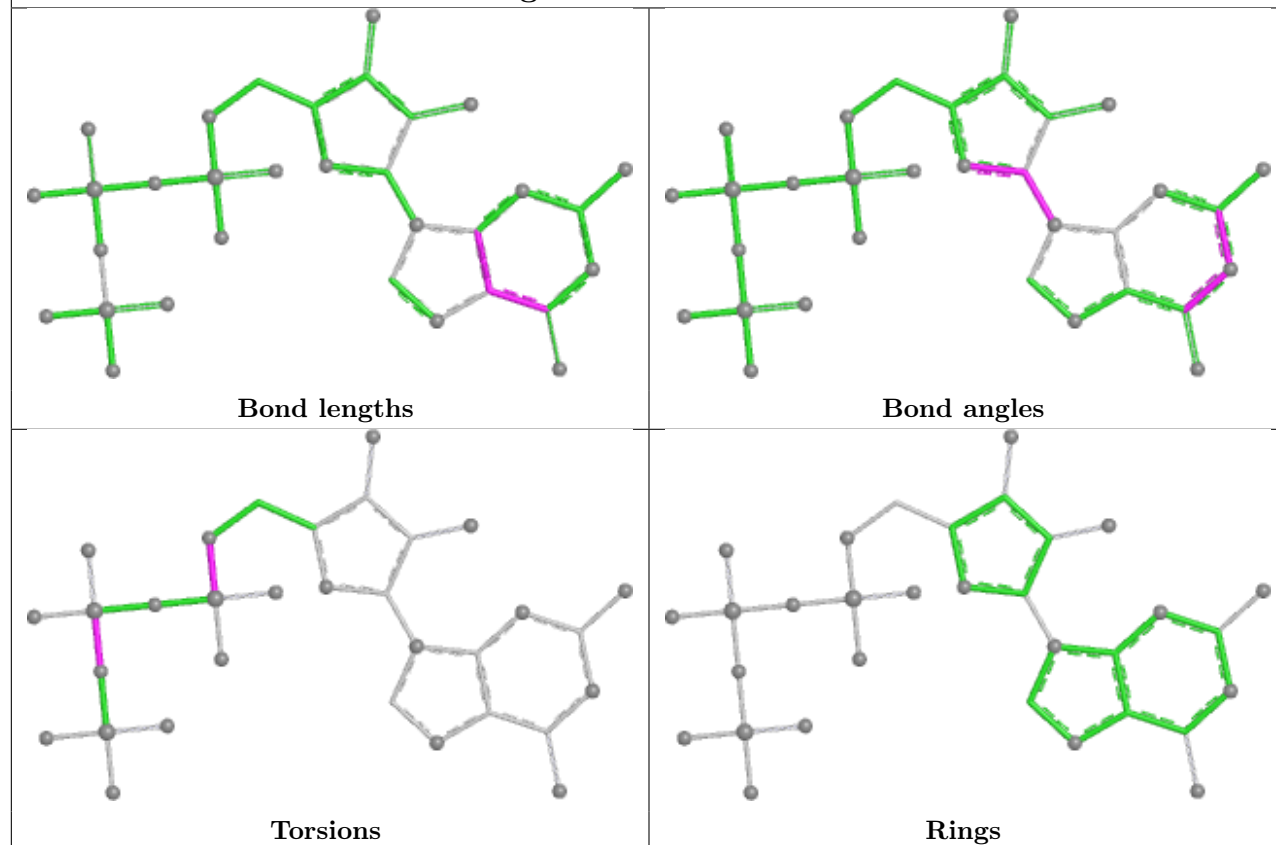


## Ligand GTP CN 602

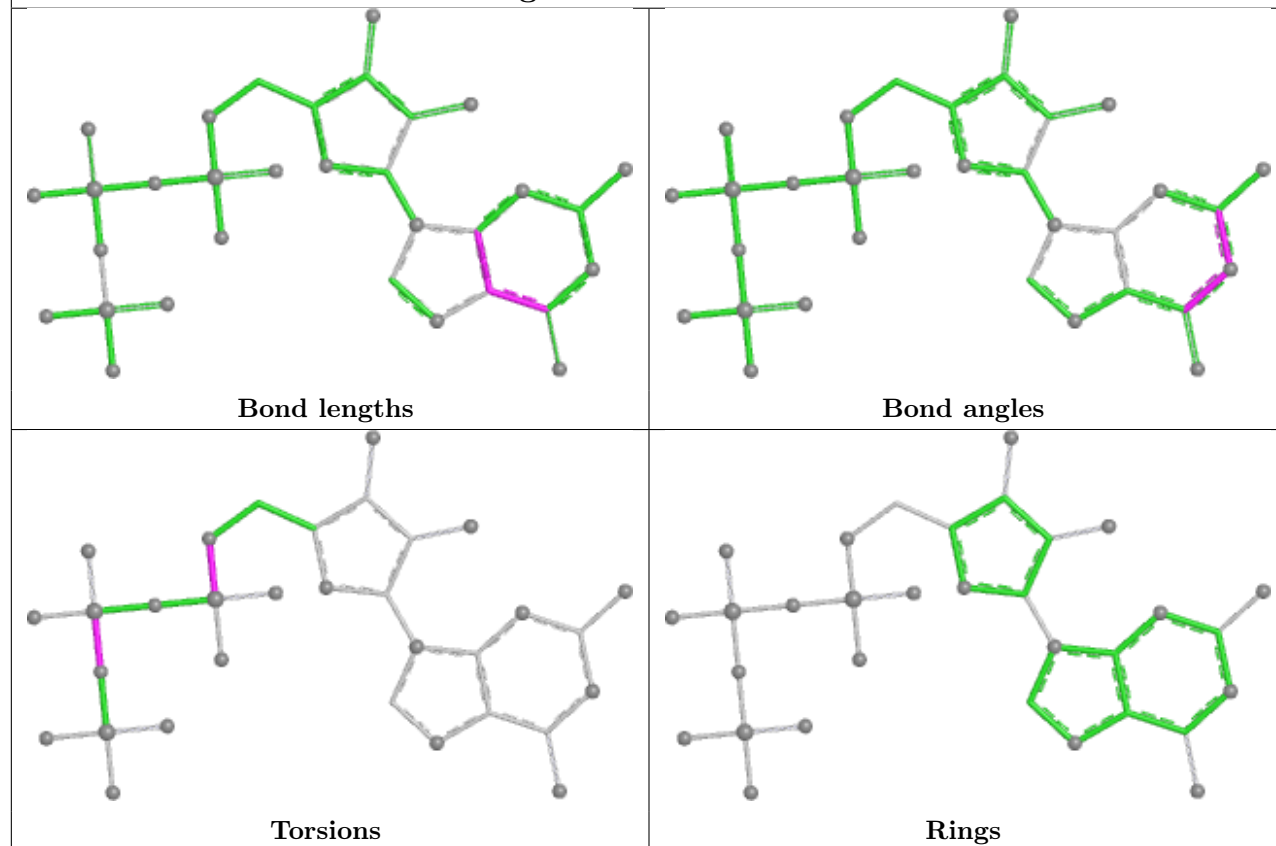




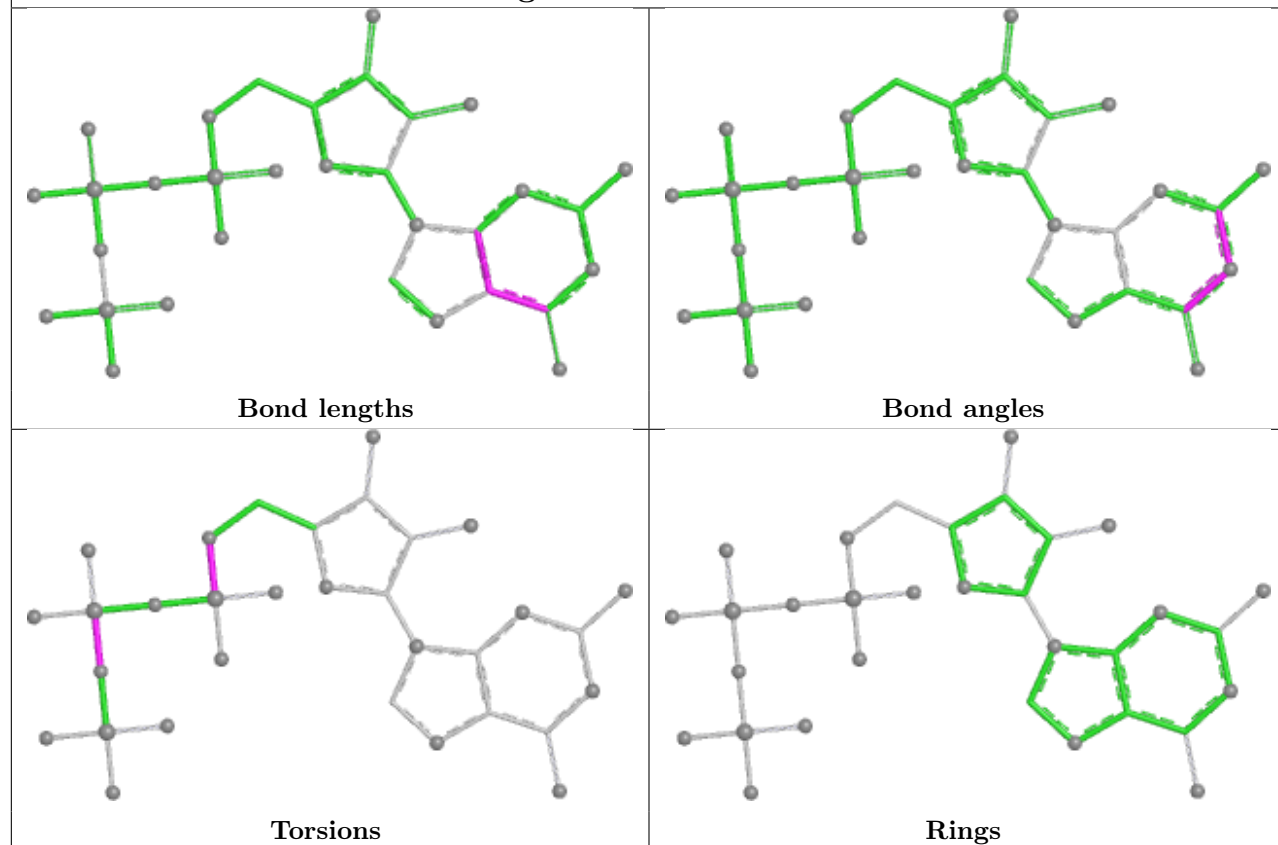
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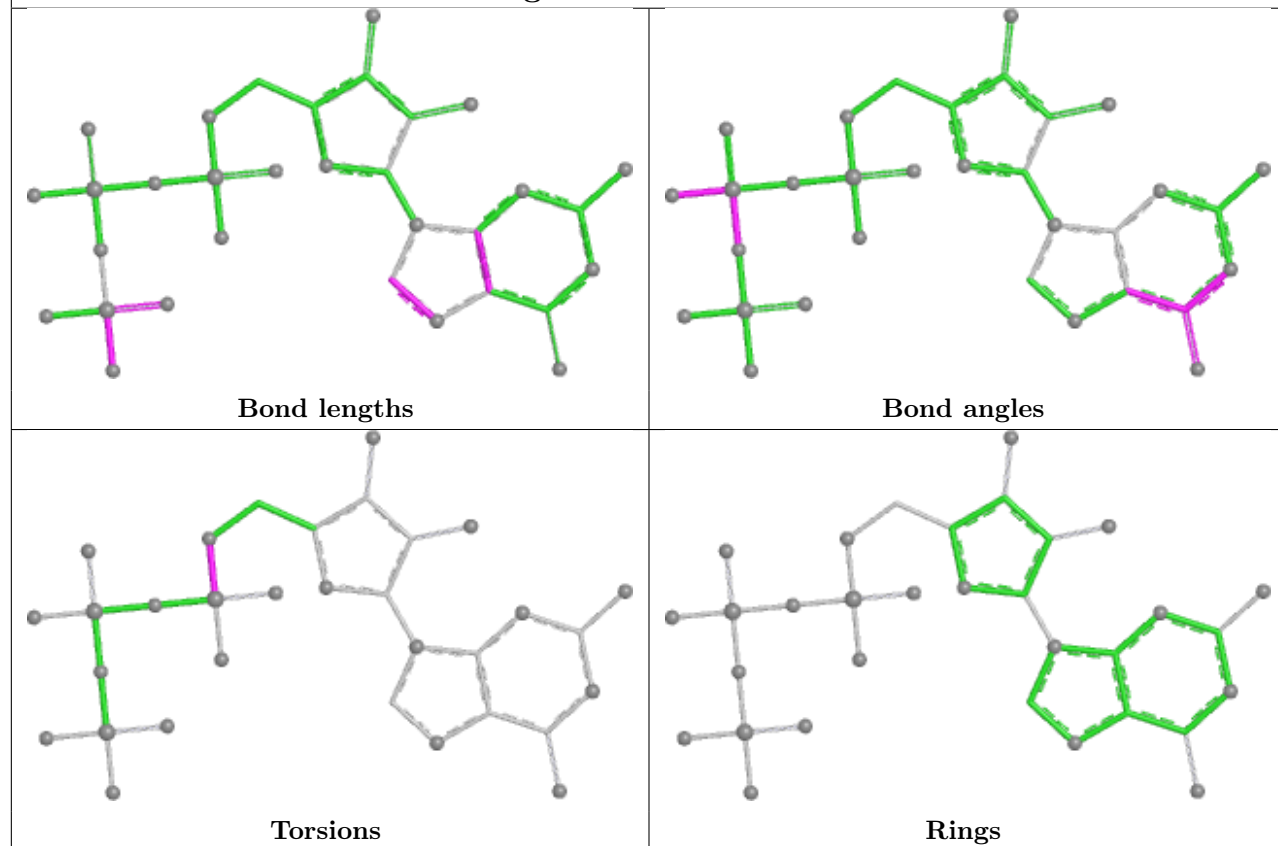
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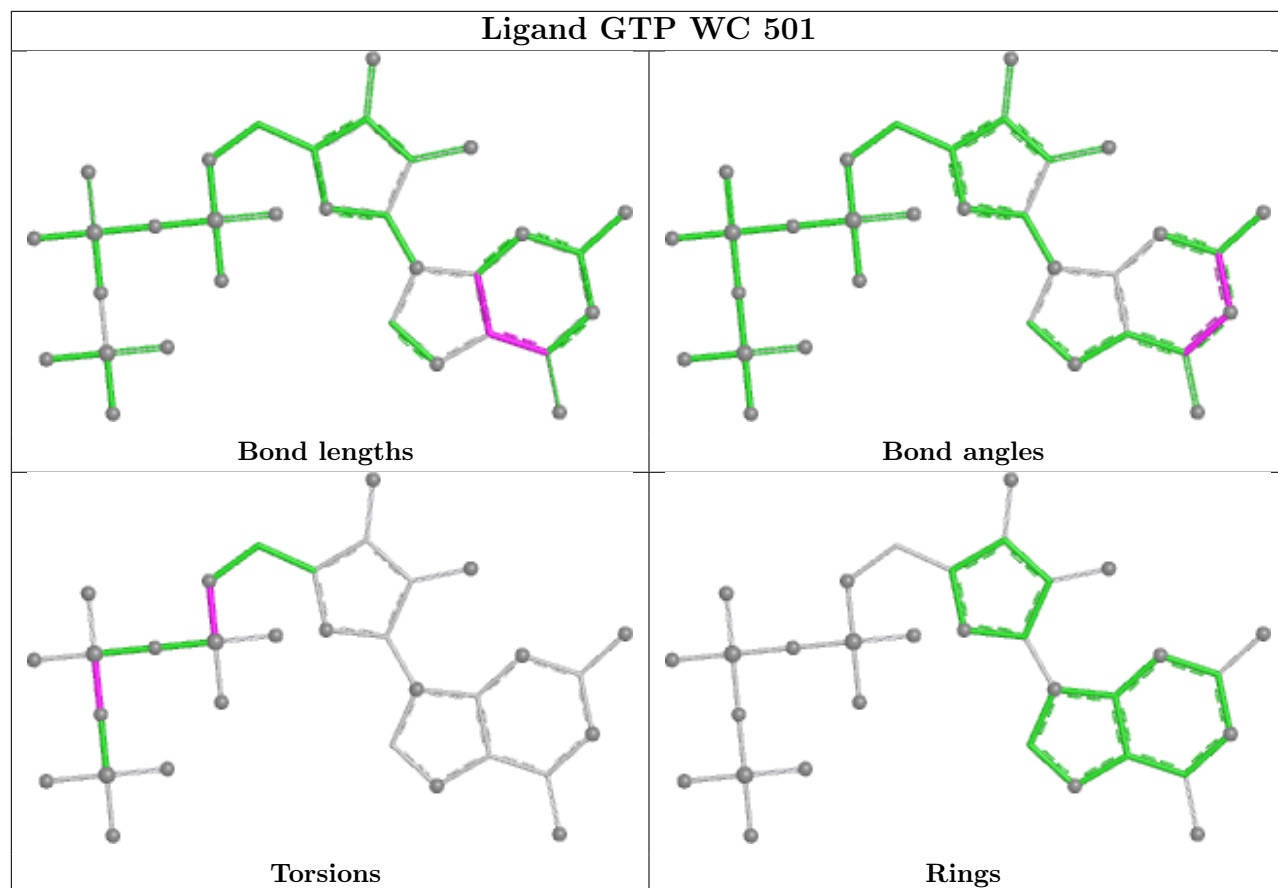
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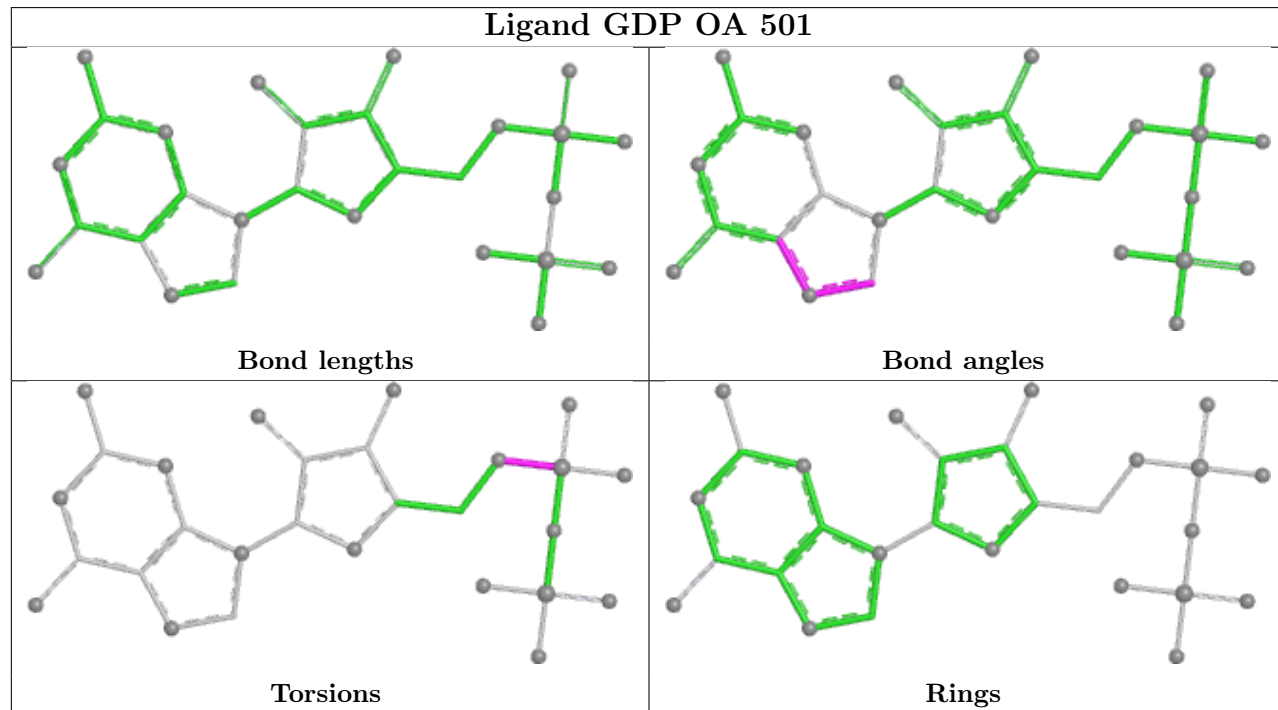
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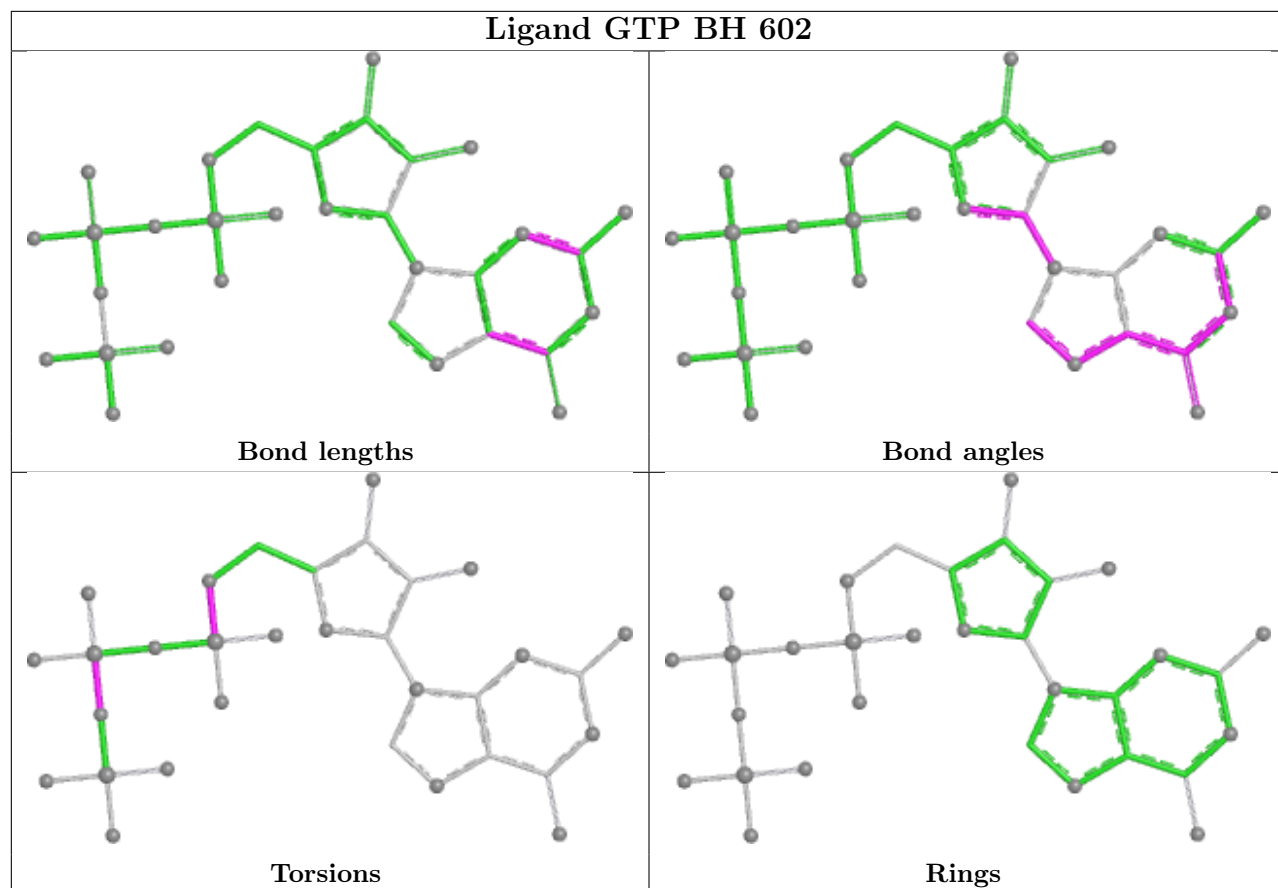
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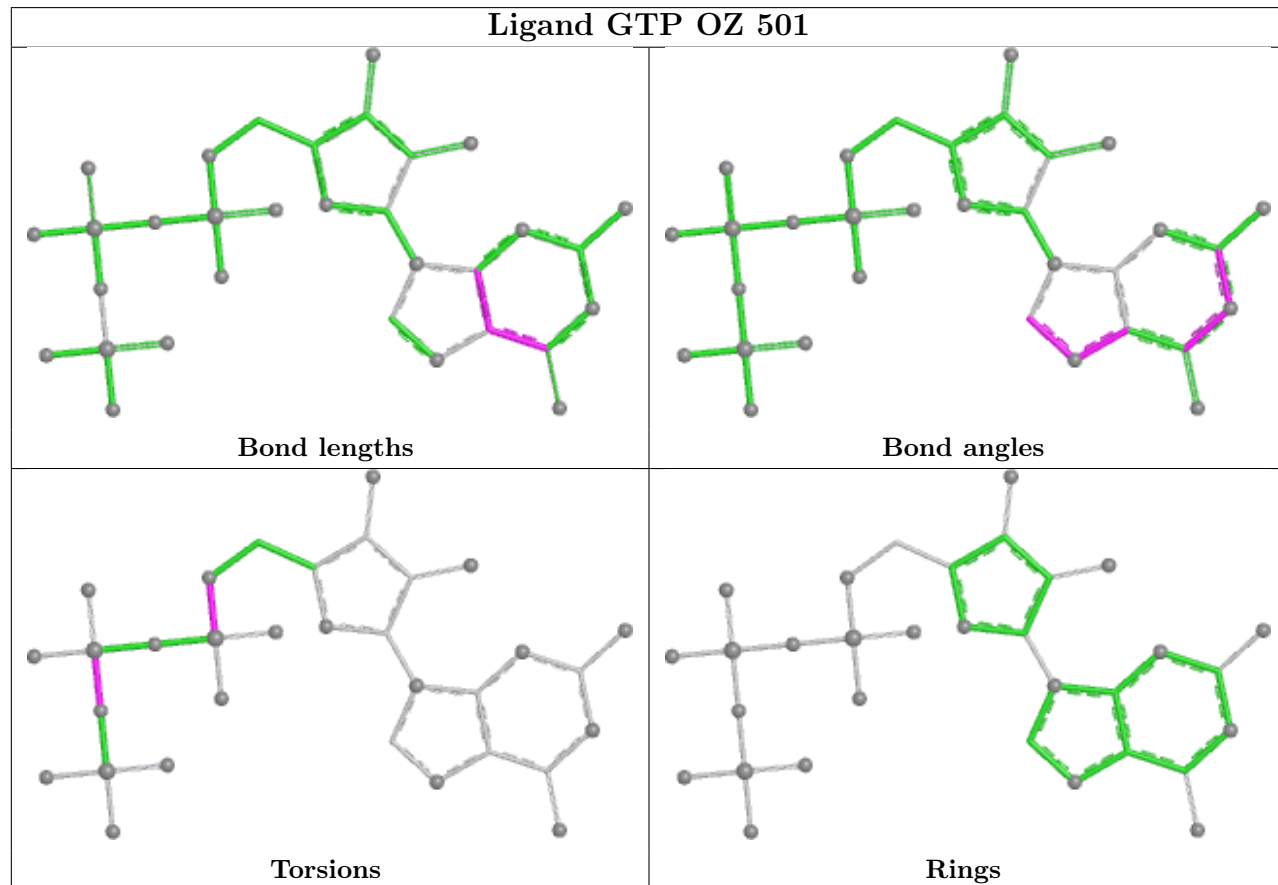
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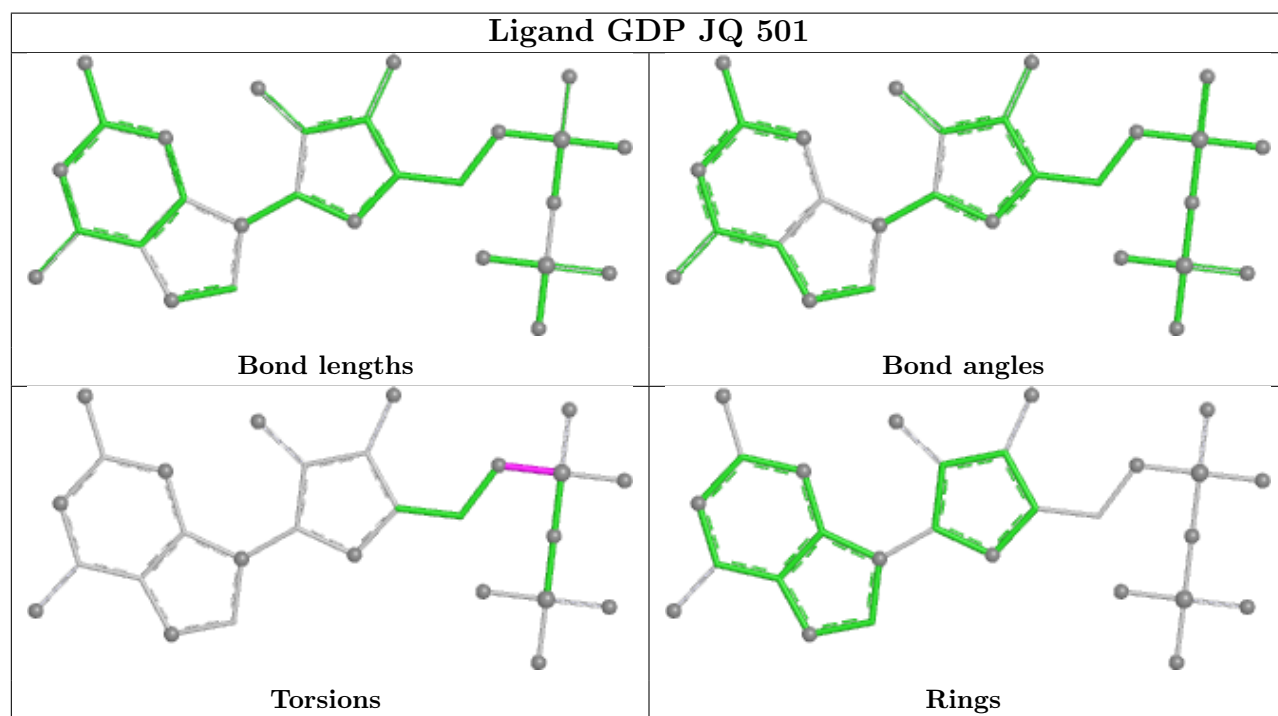
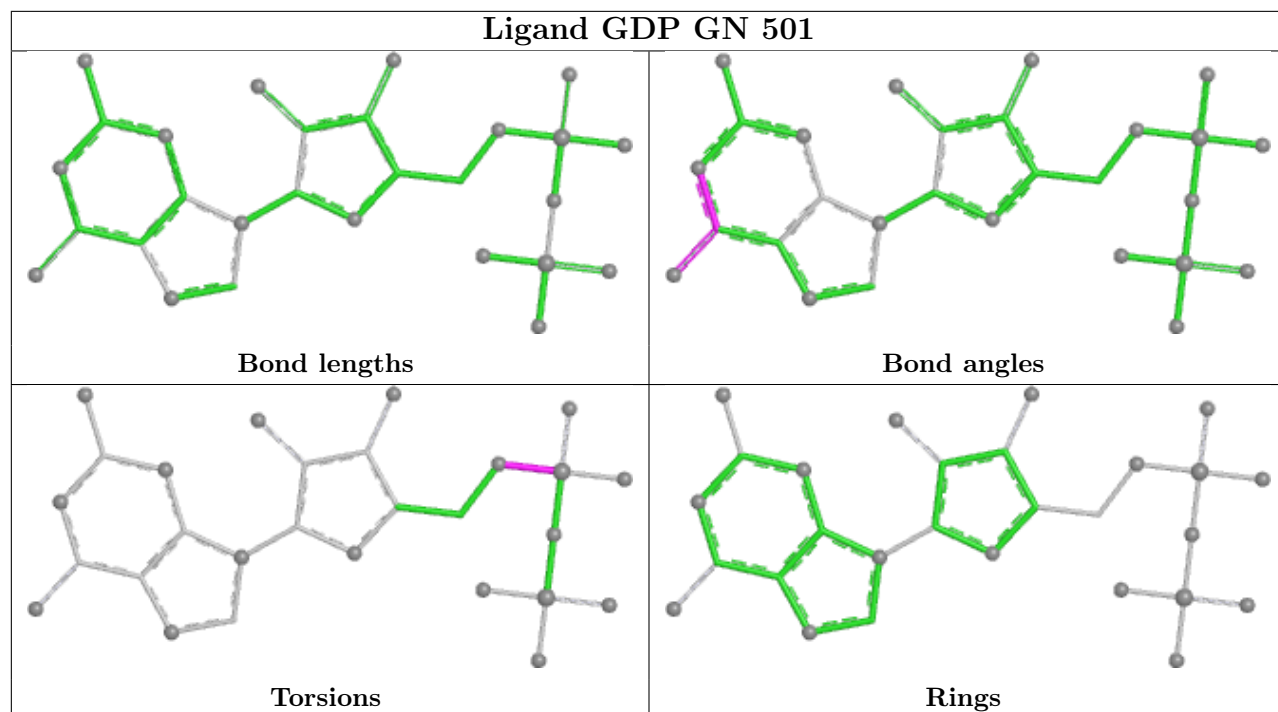
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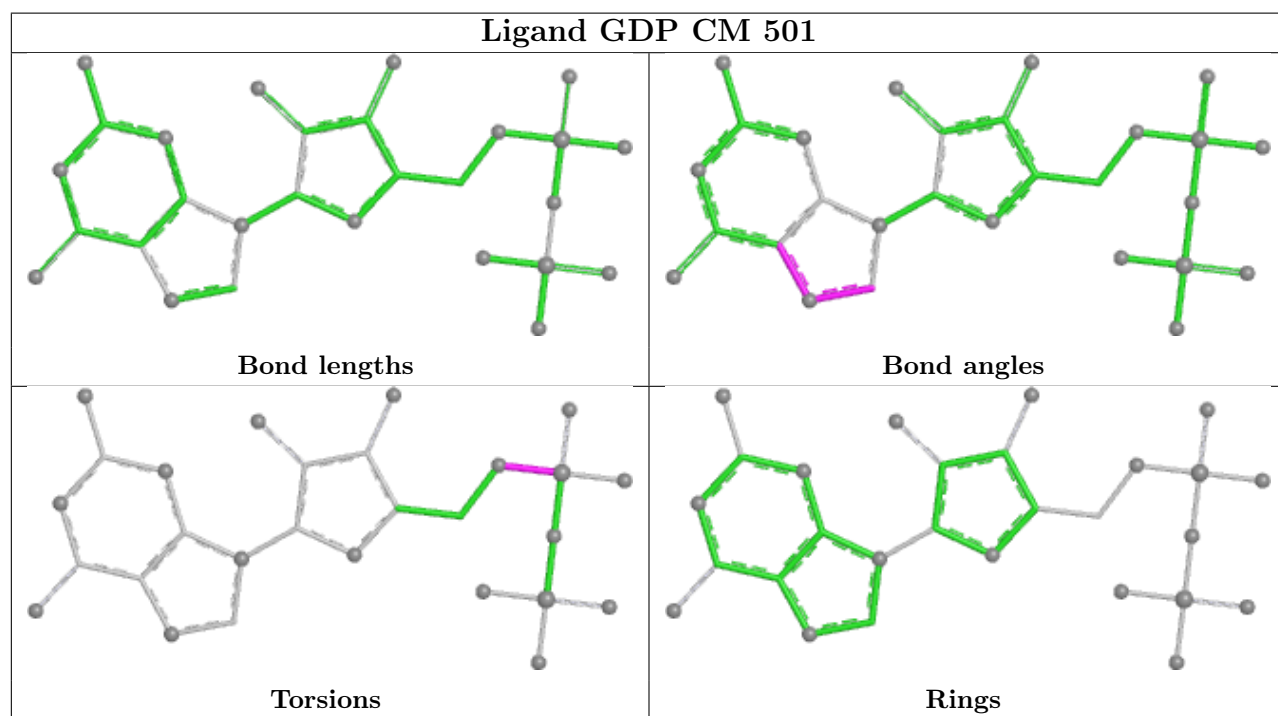
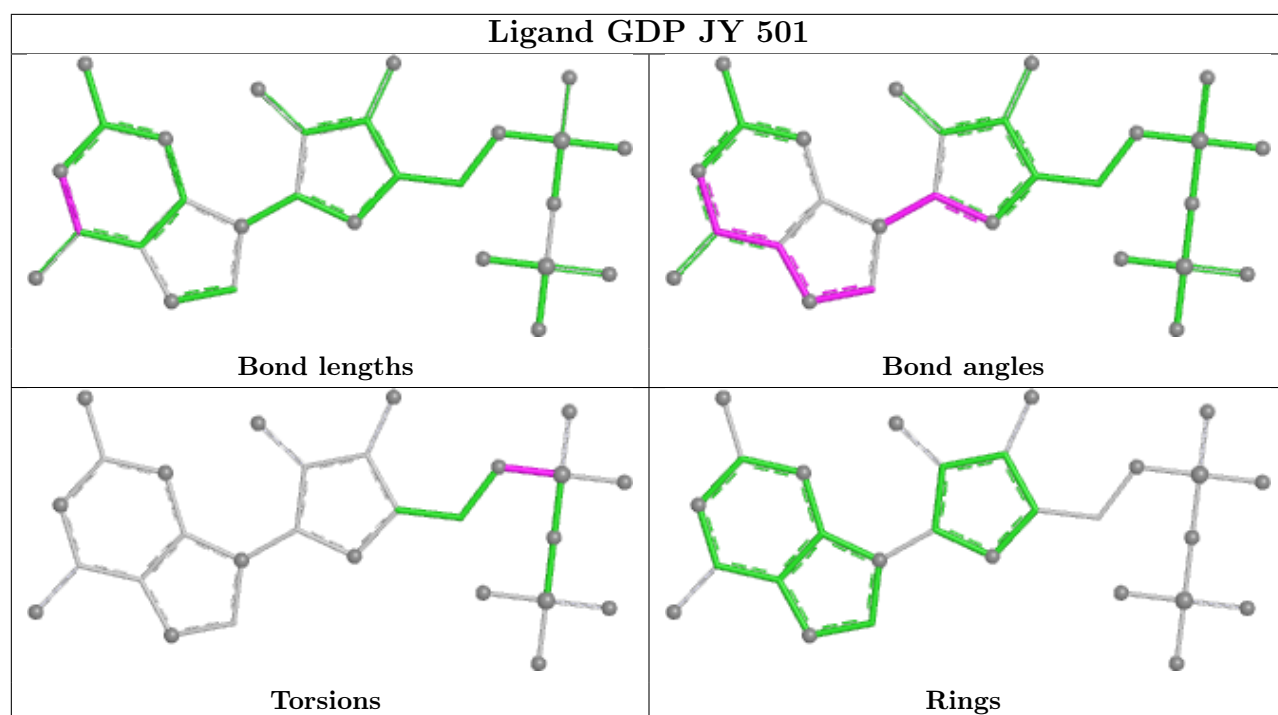


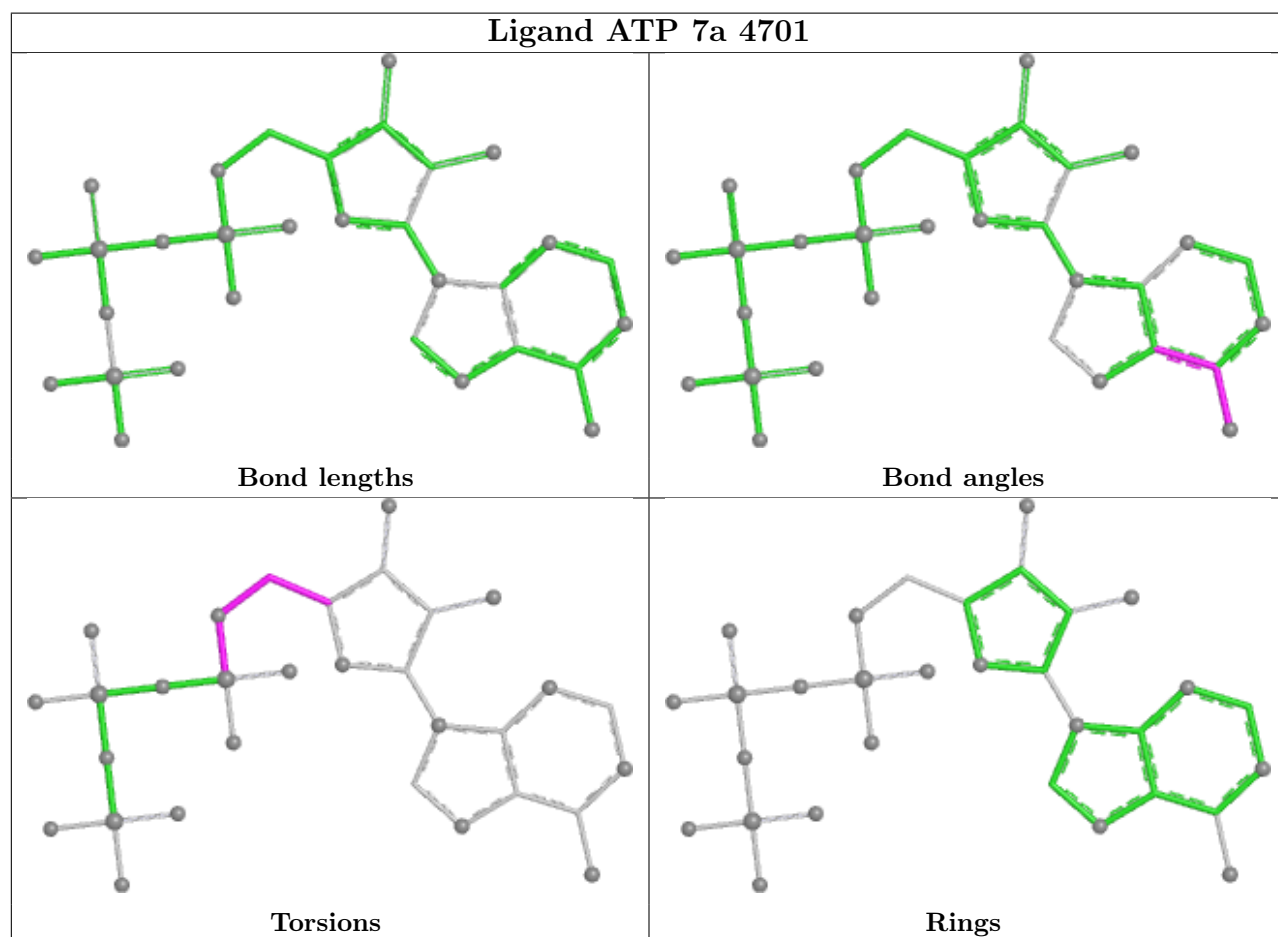
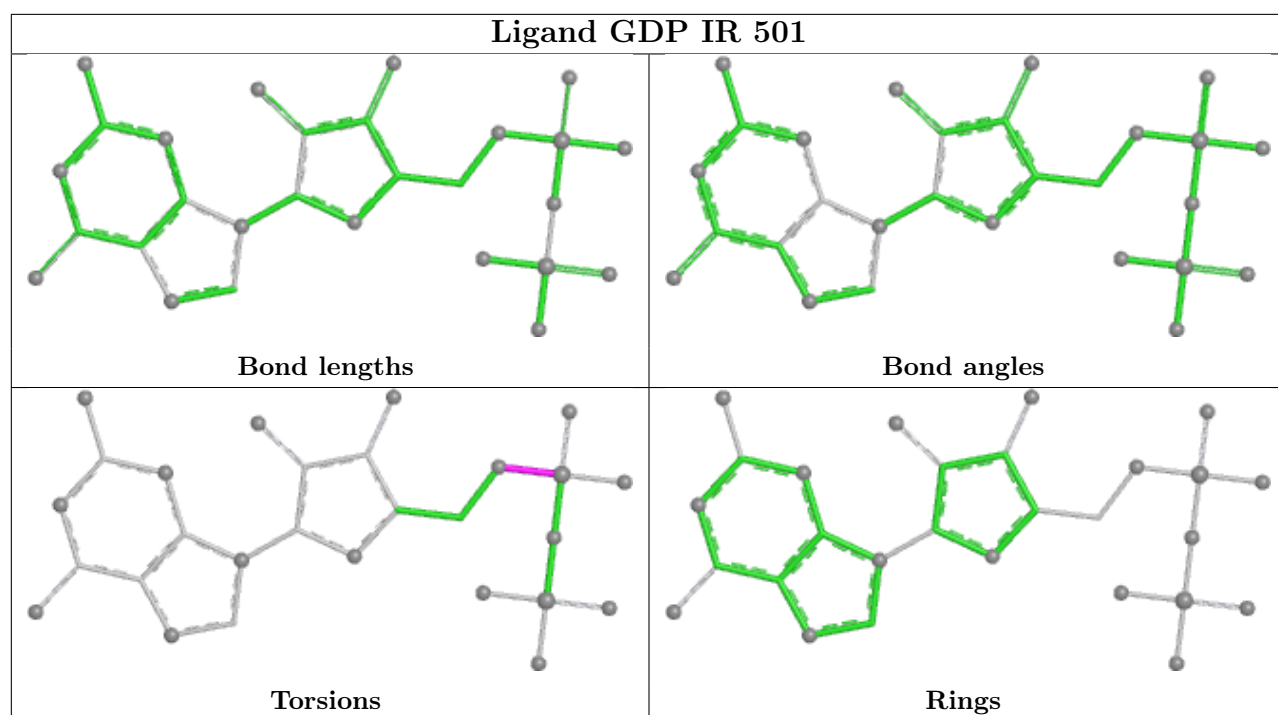
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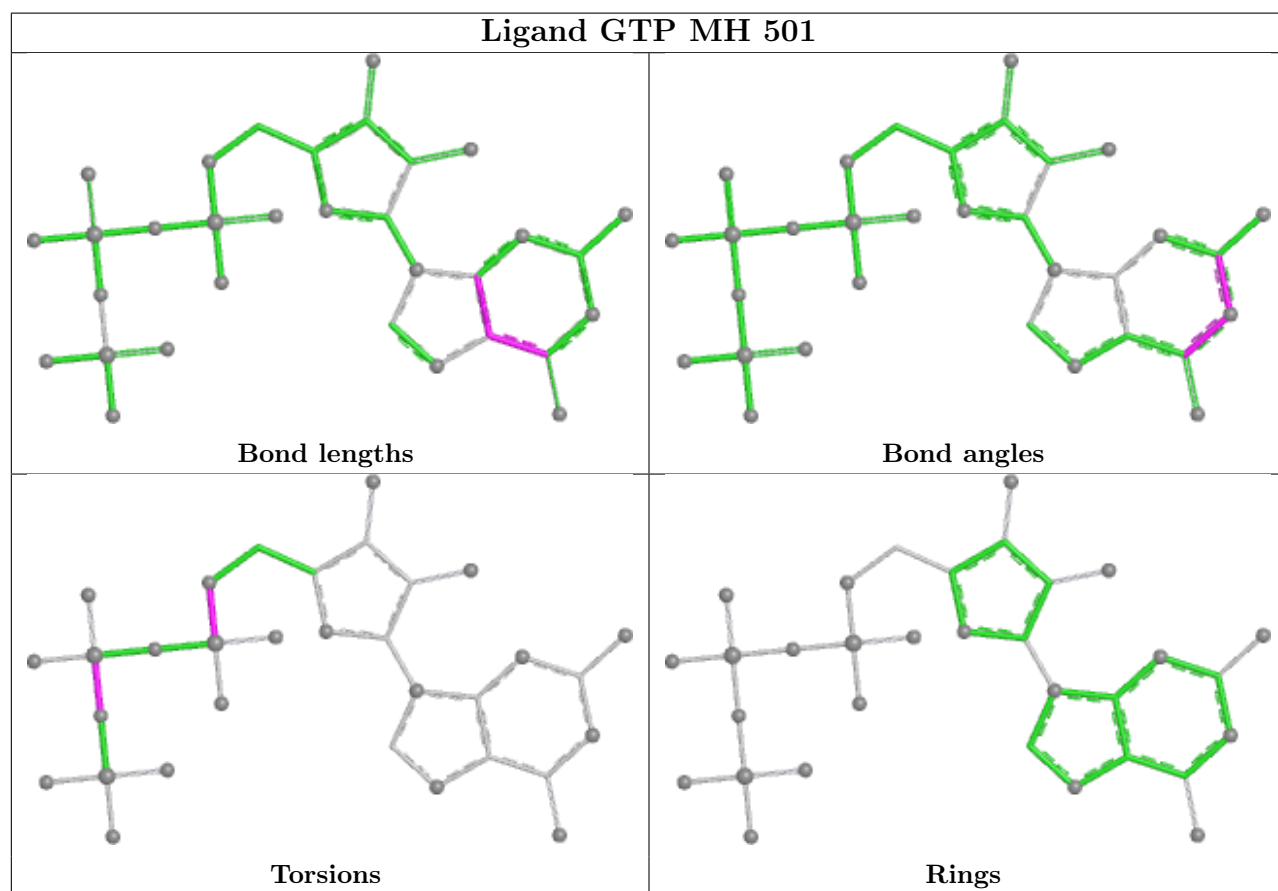
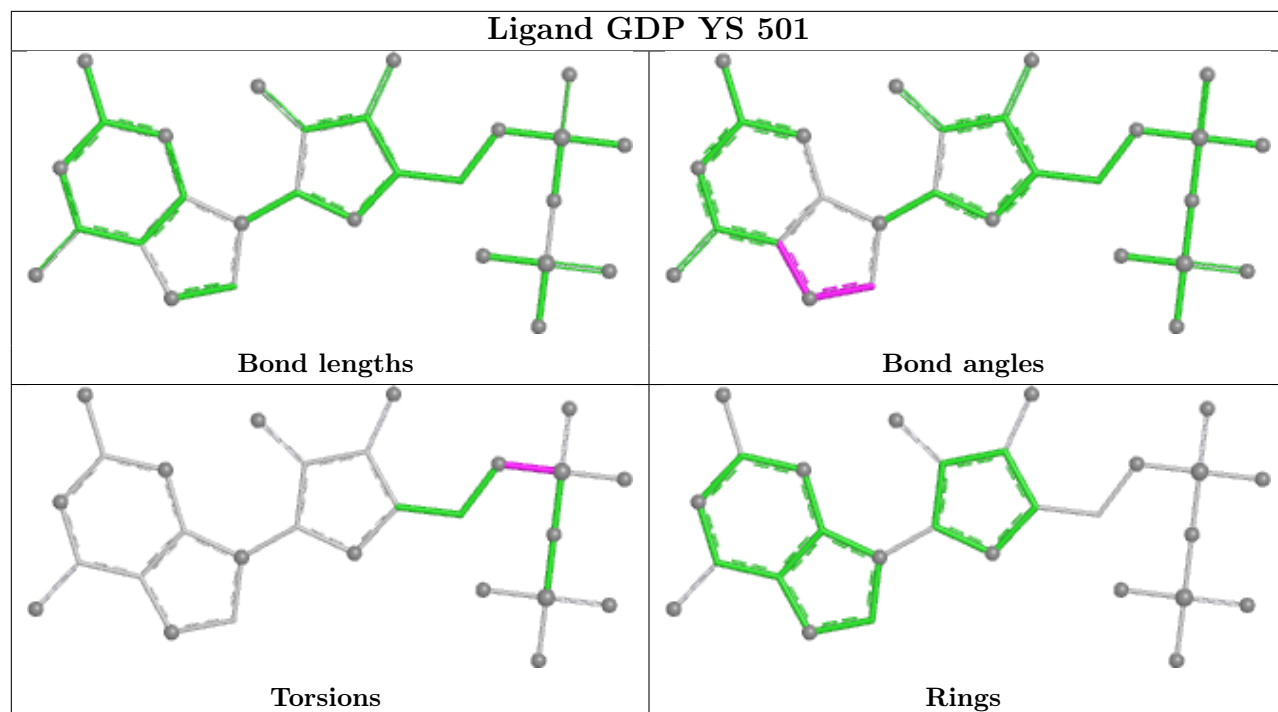




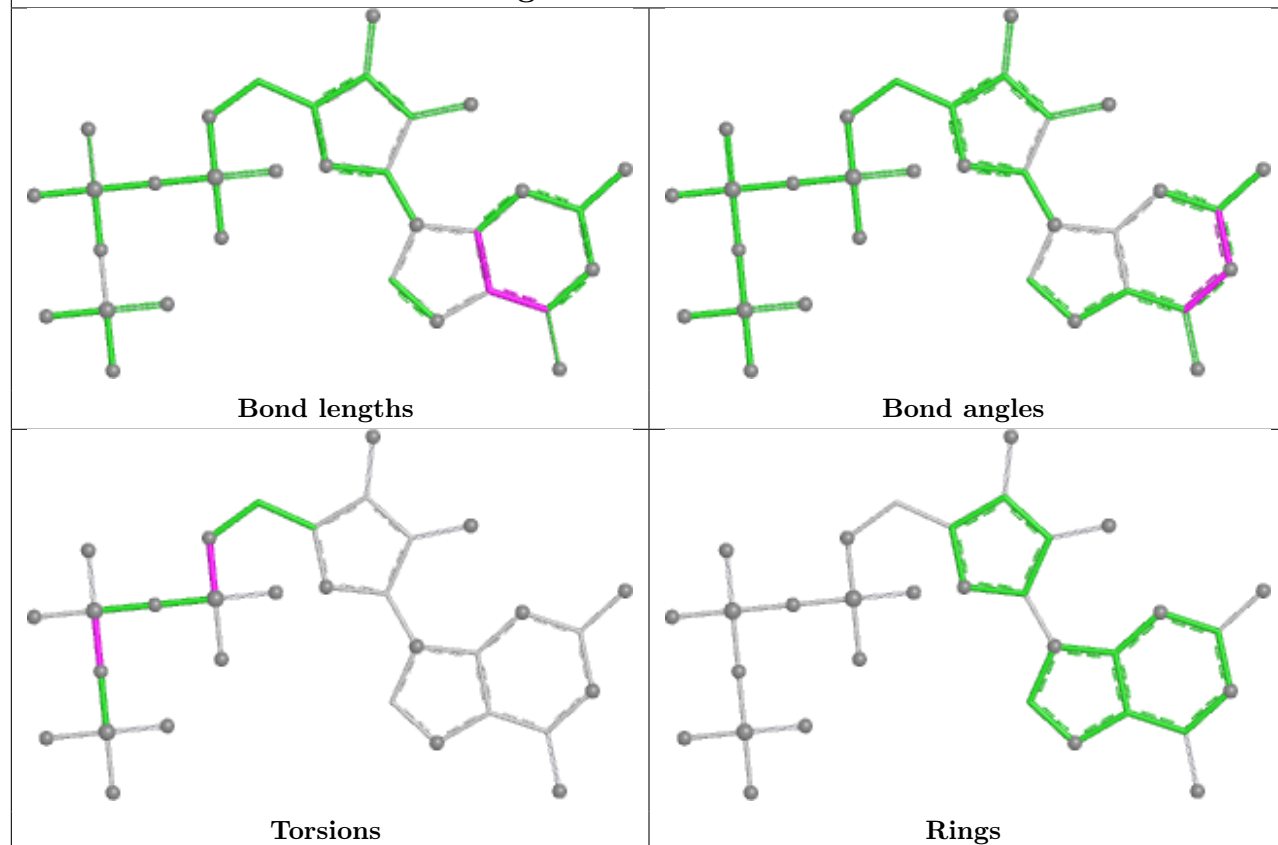




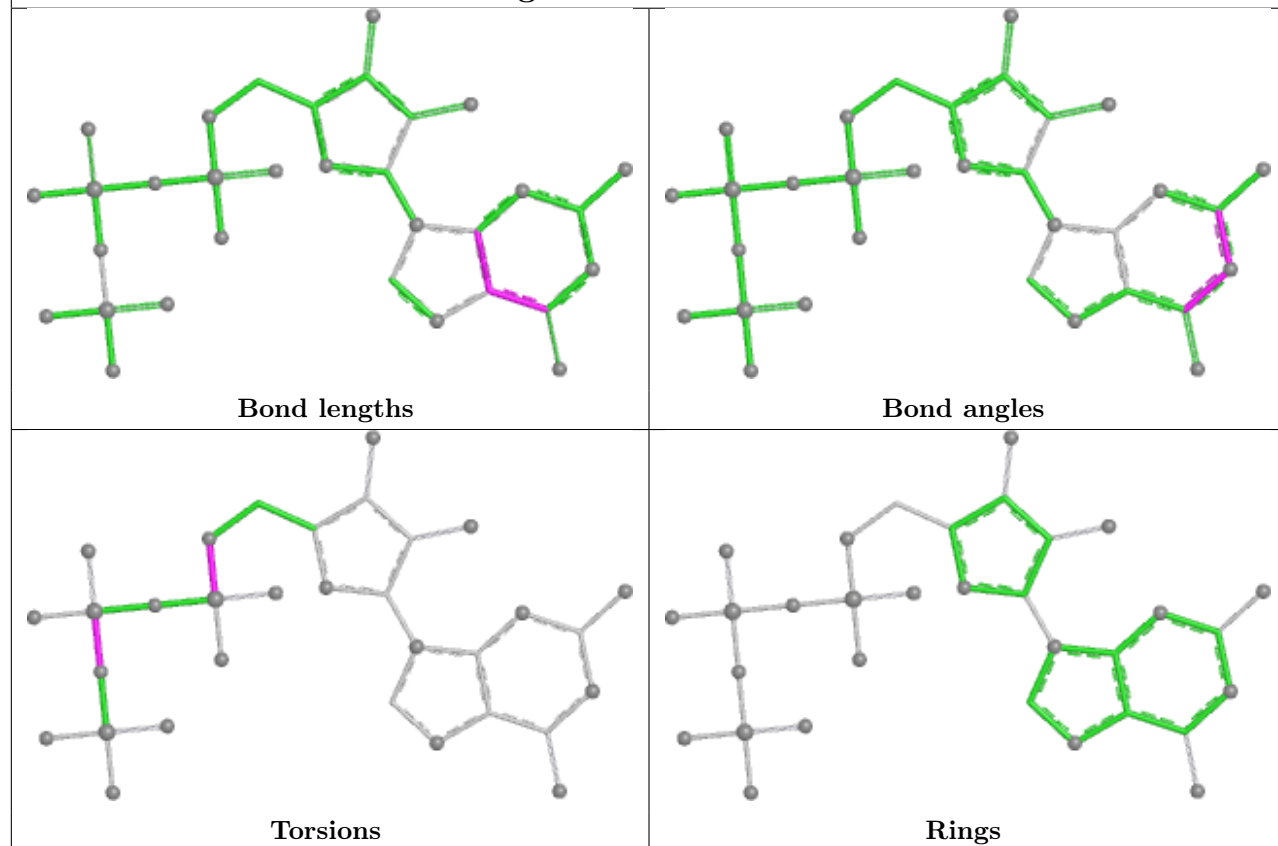




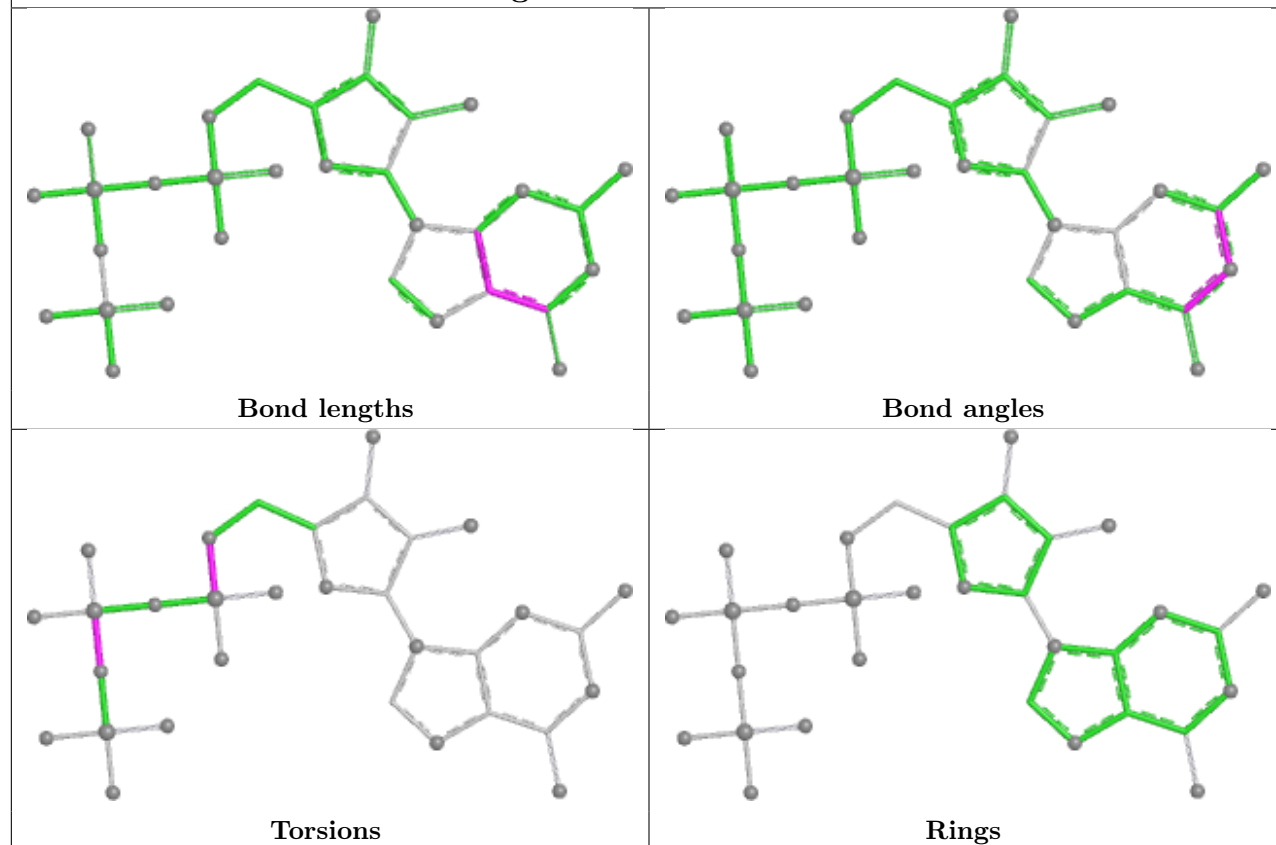
## Ligand GTP EG 501



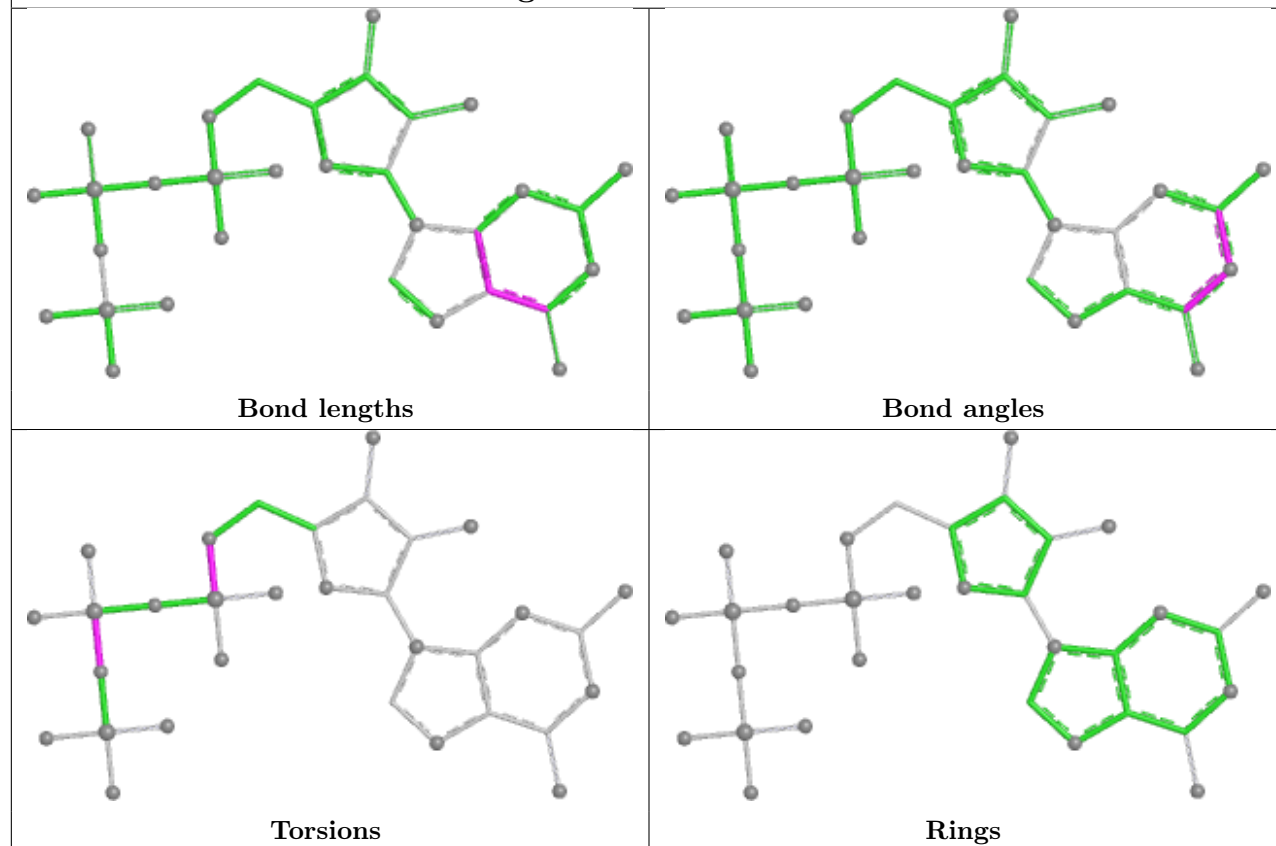
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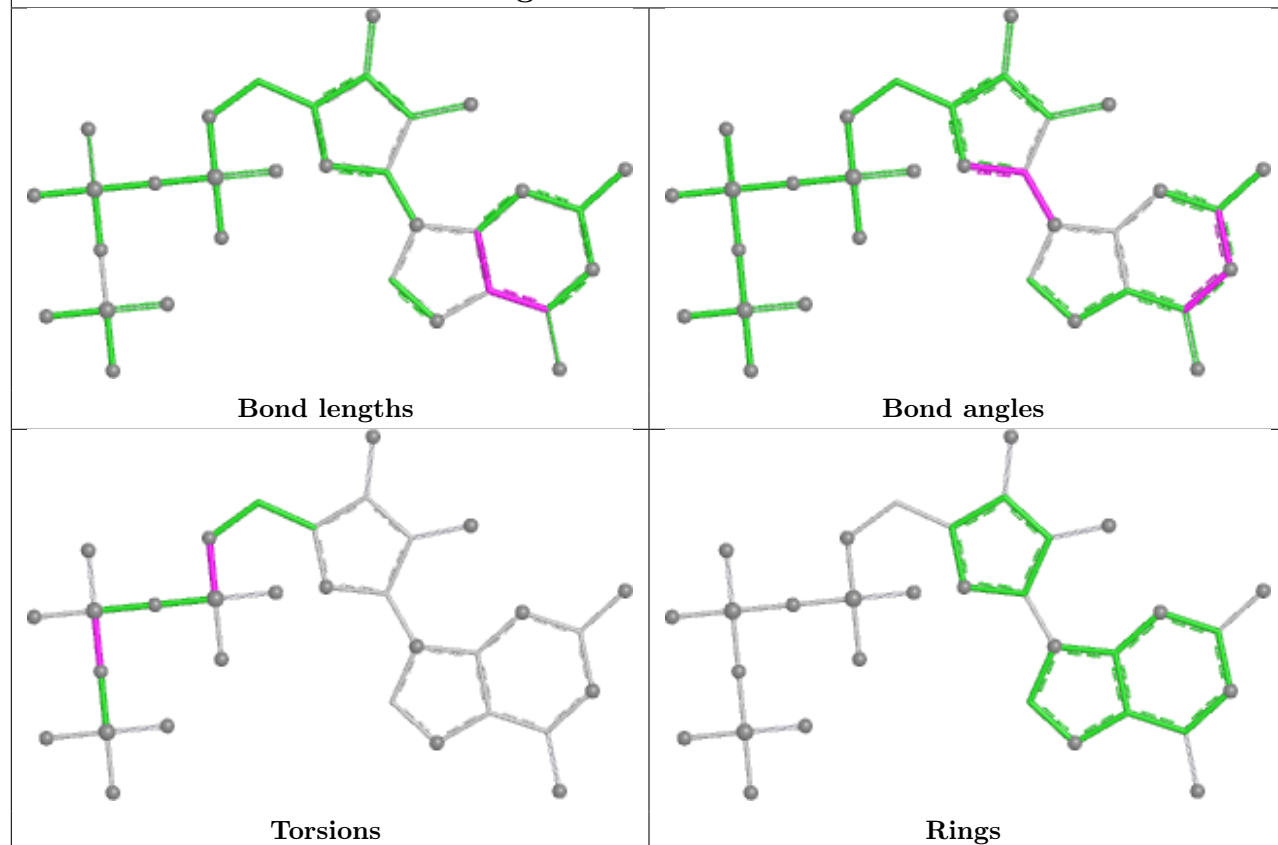
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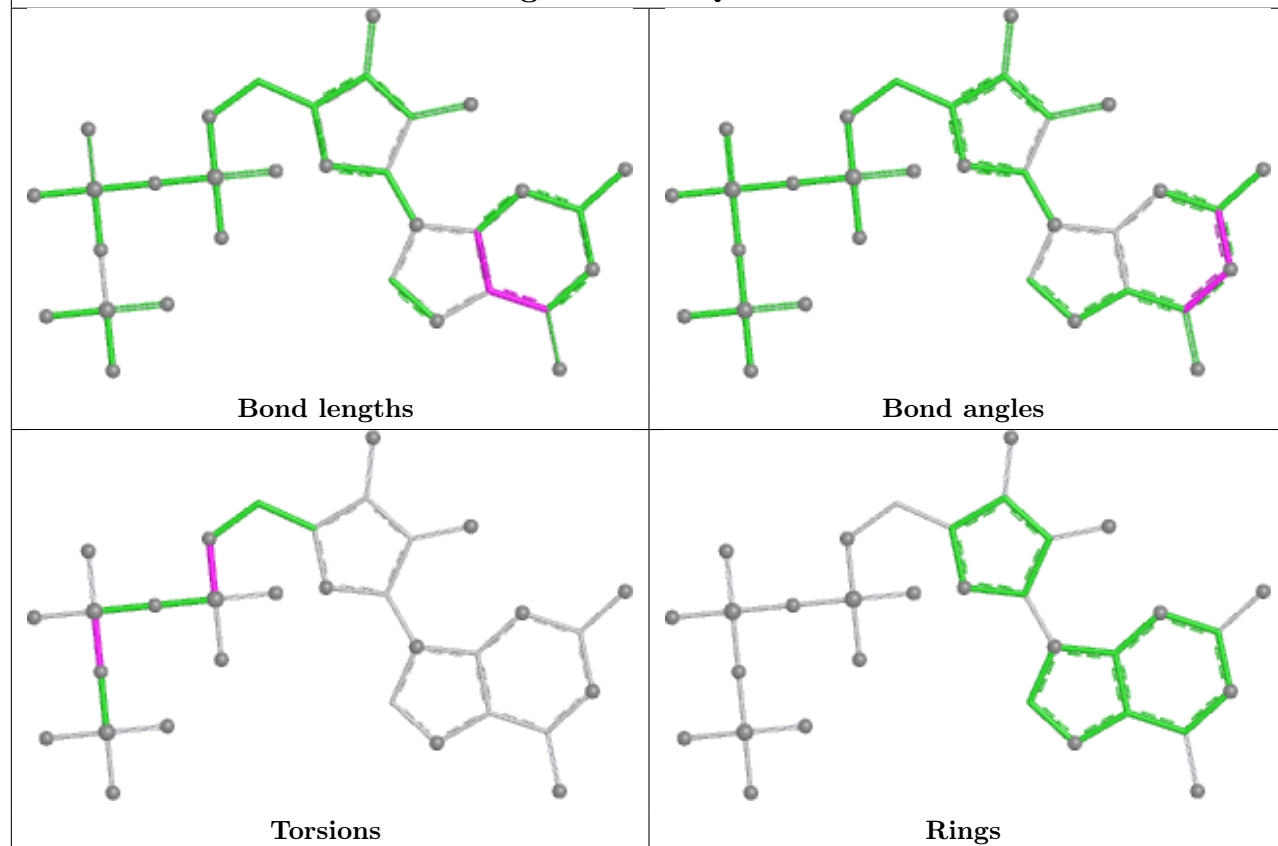
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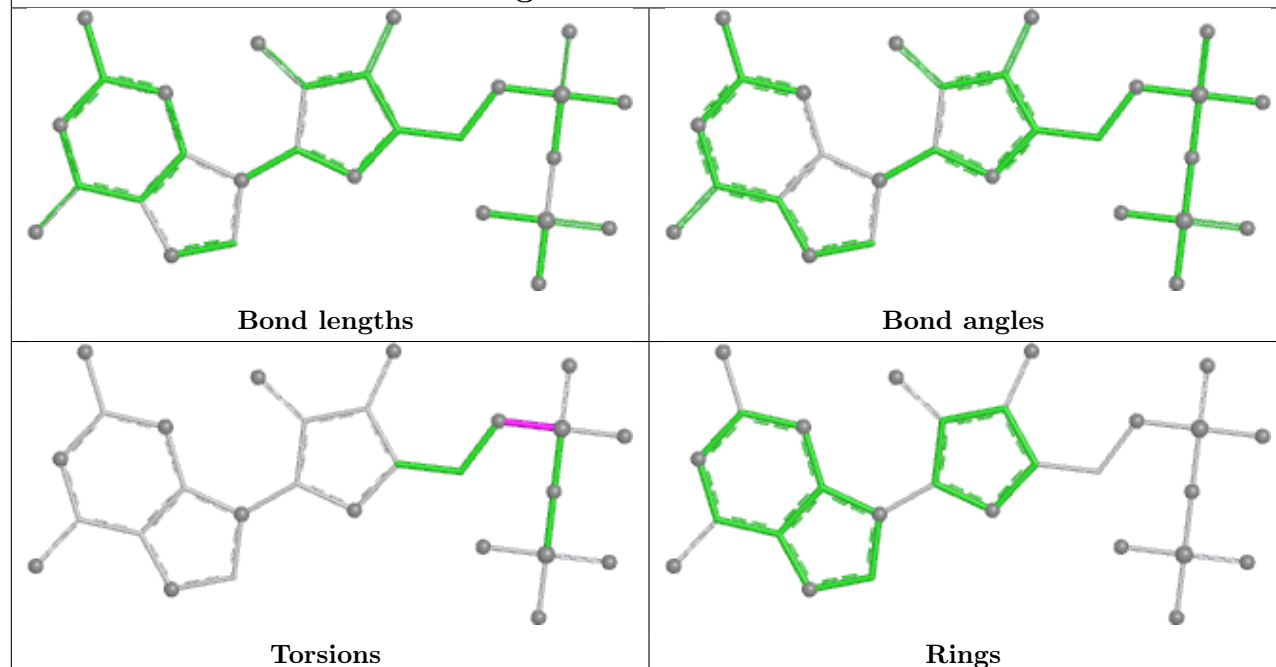
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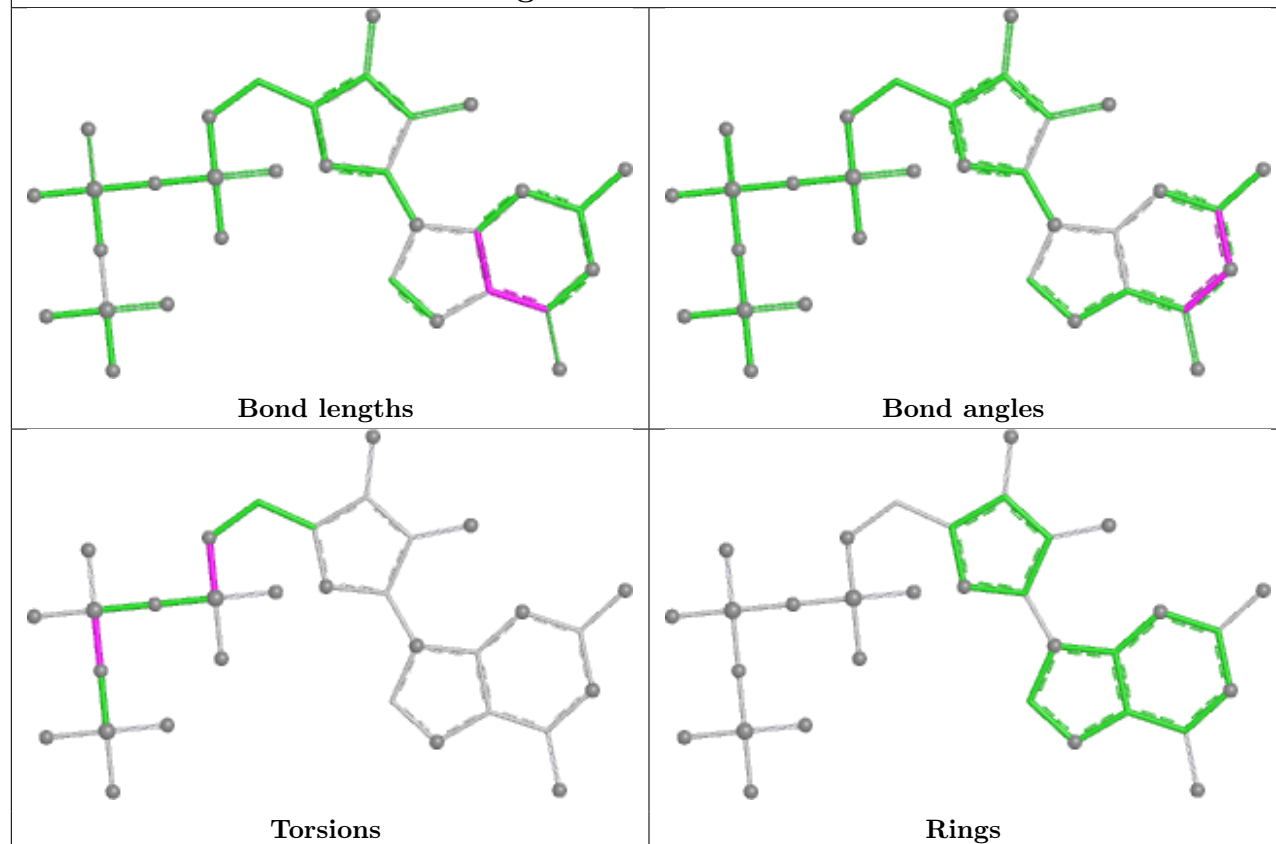
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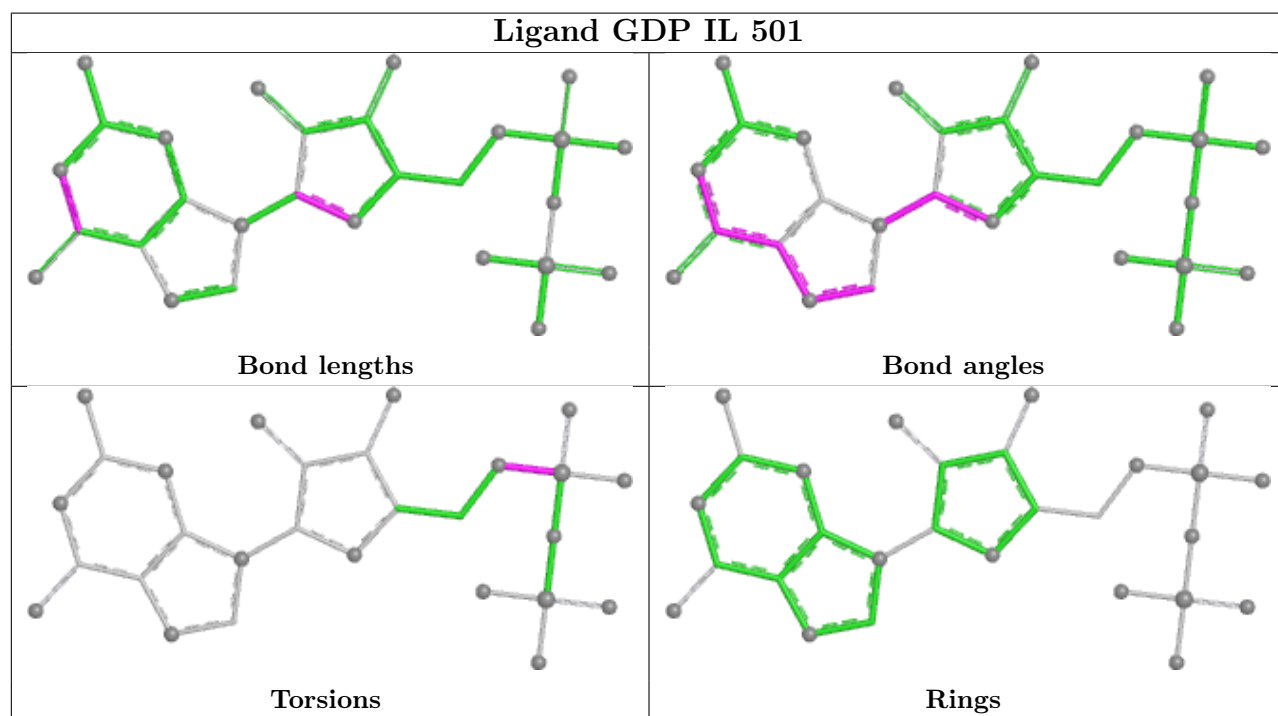
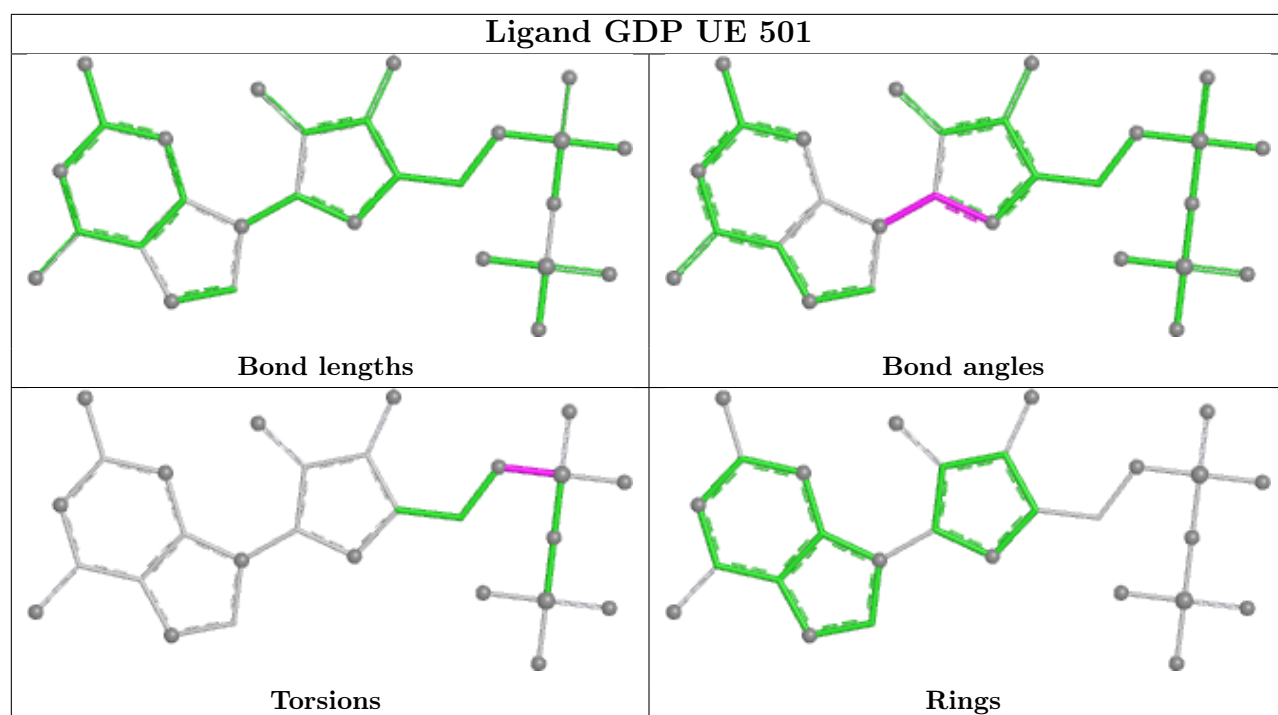
## Ligand GDP JM 501

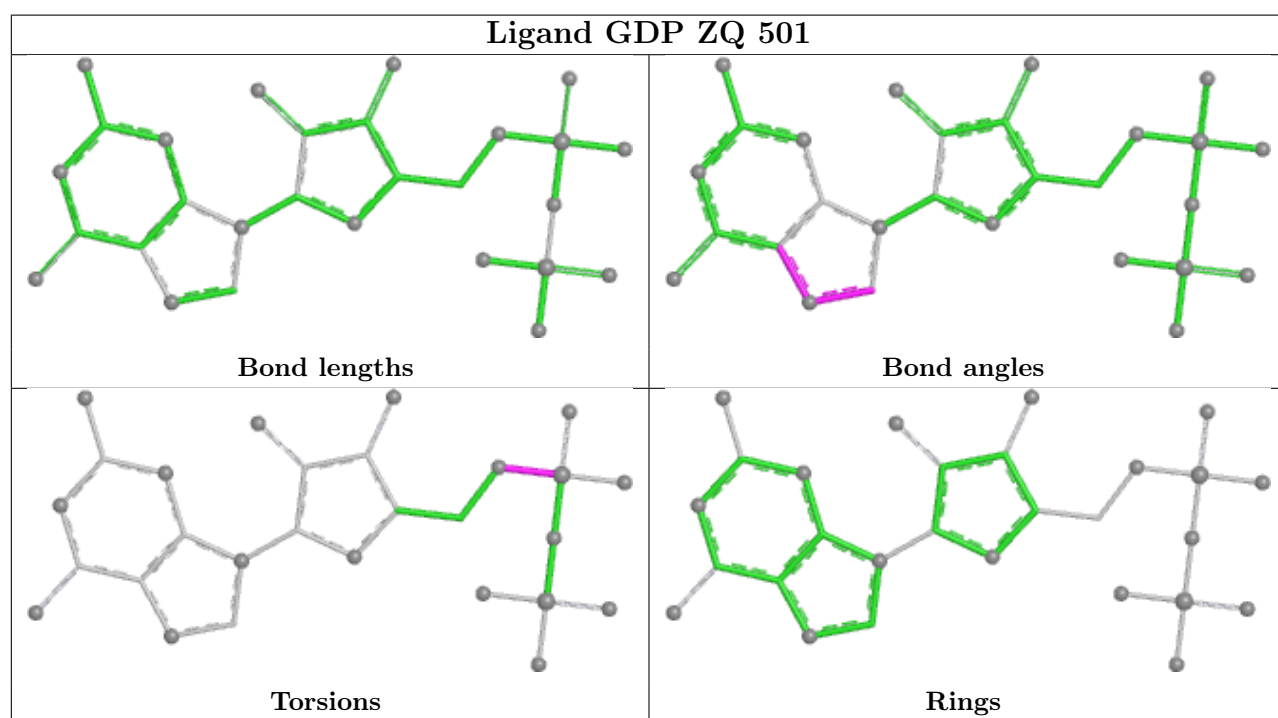
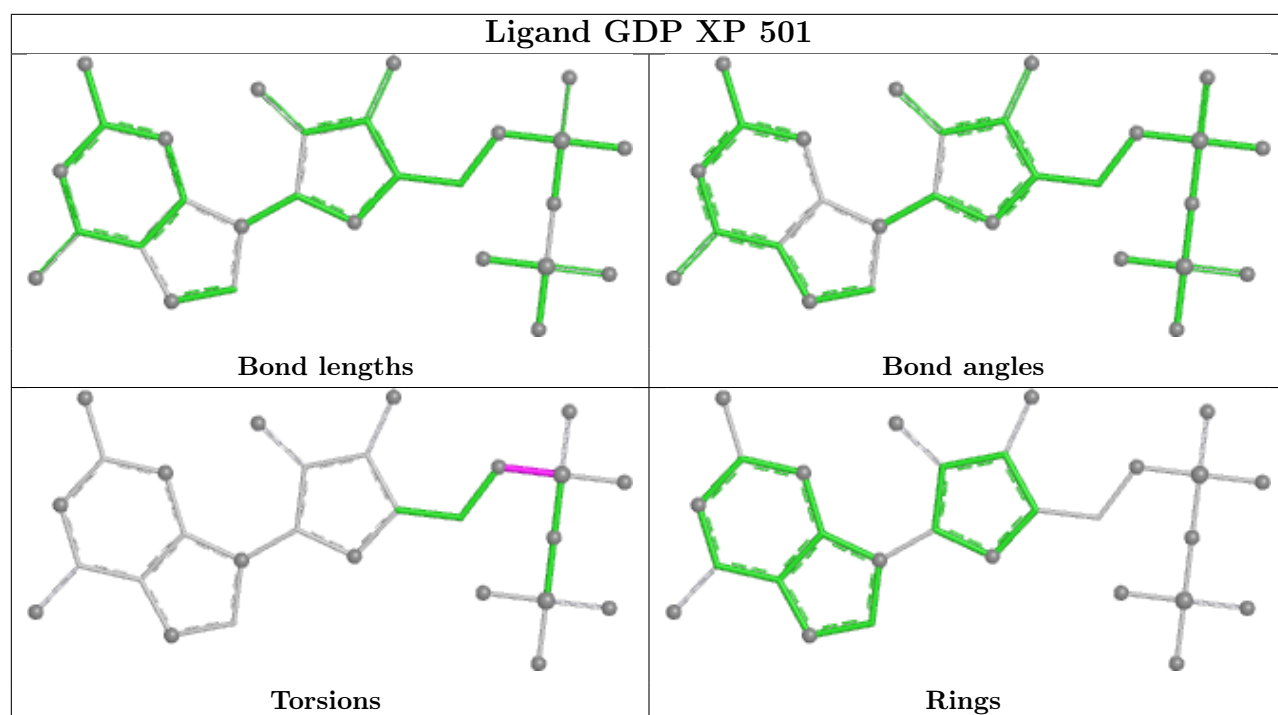


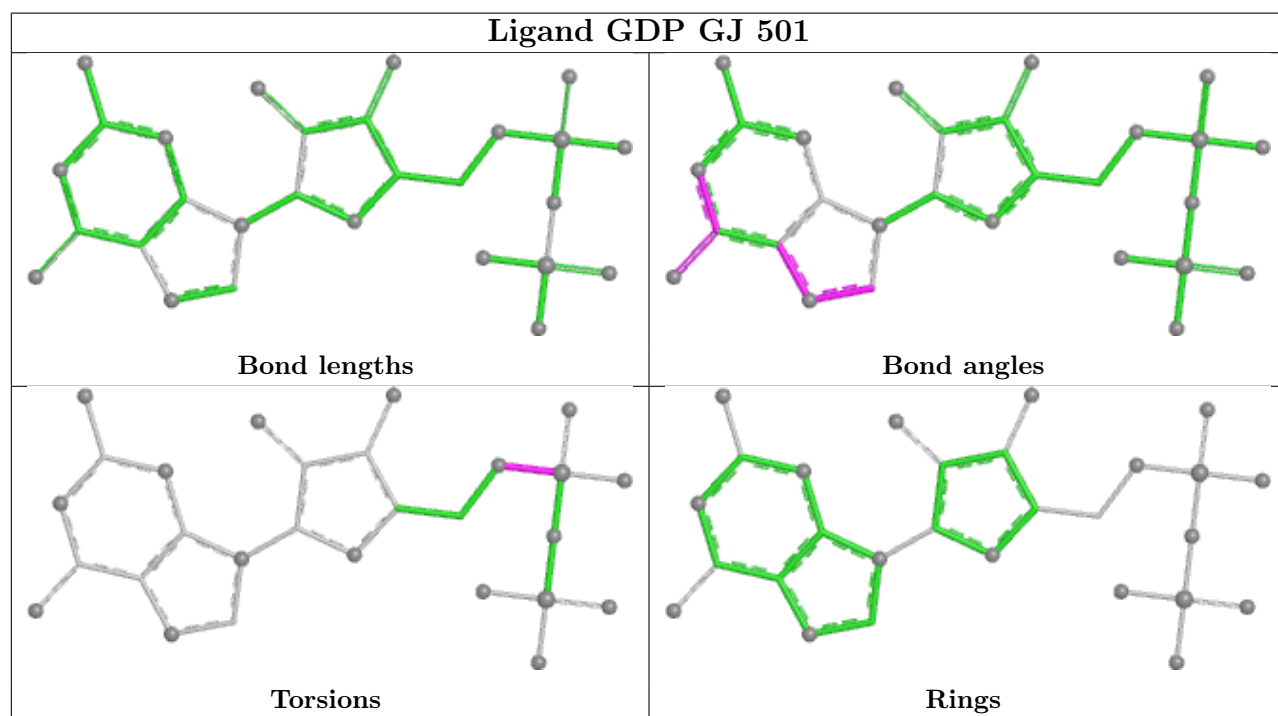
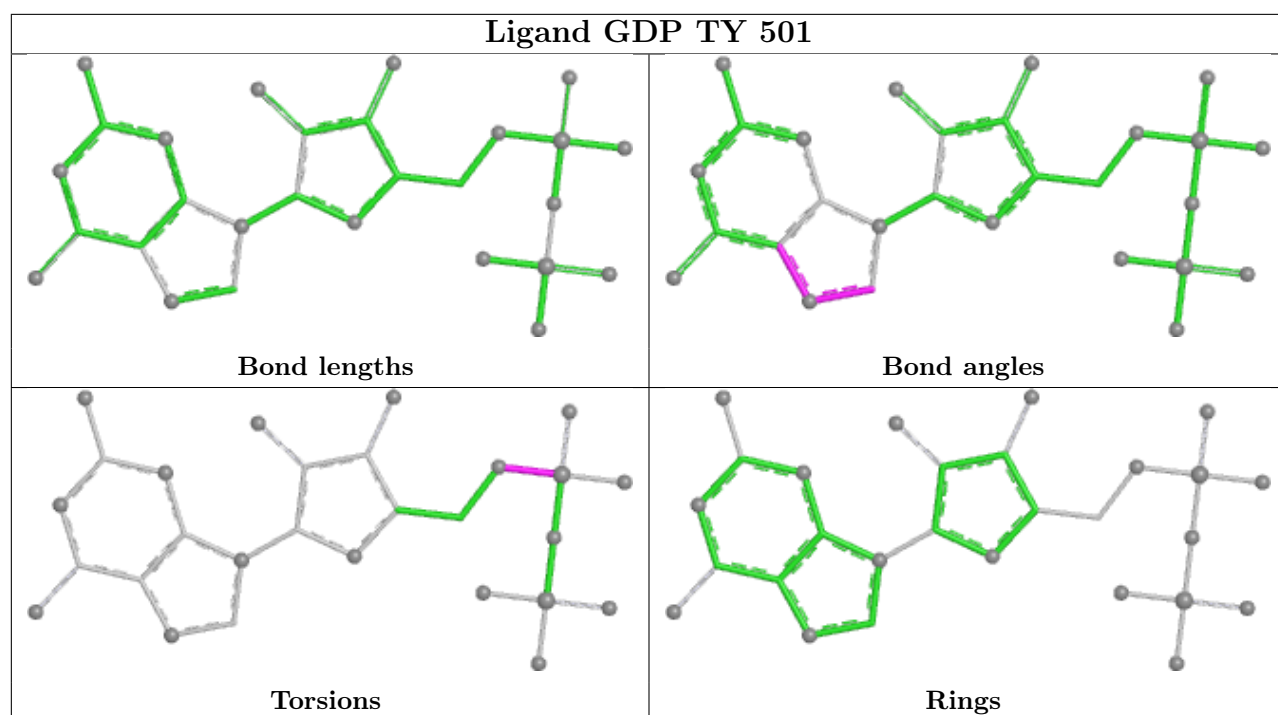
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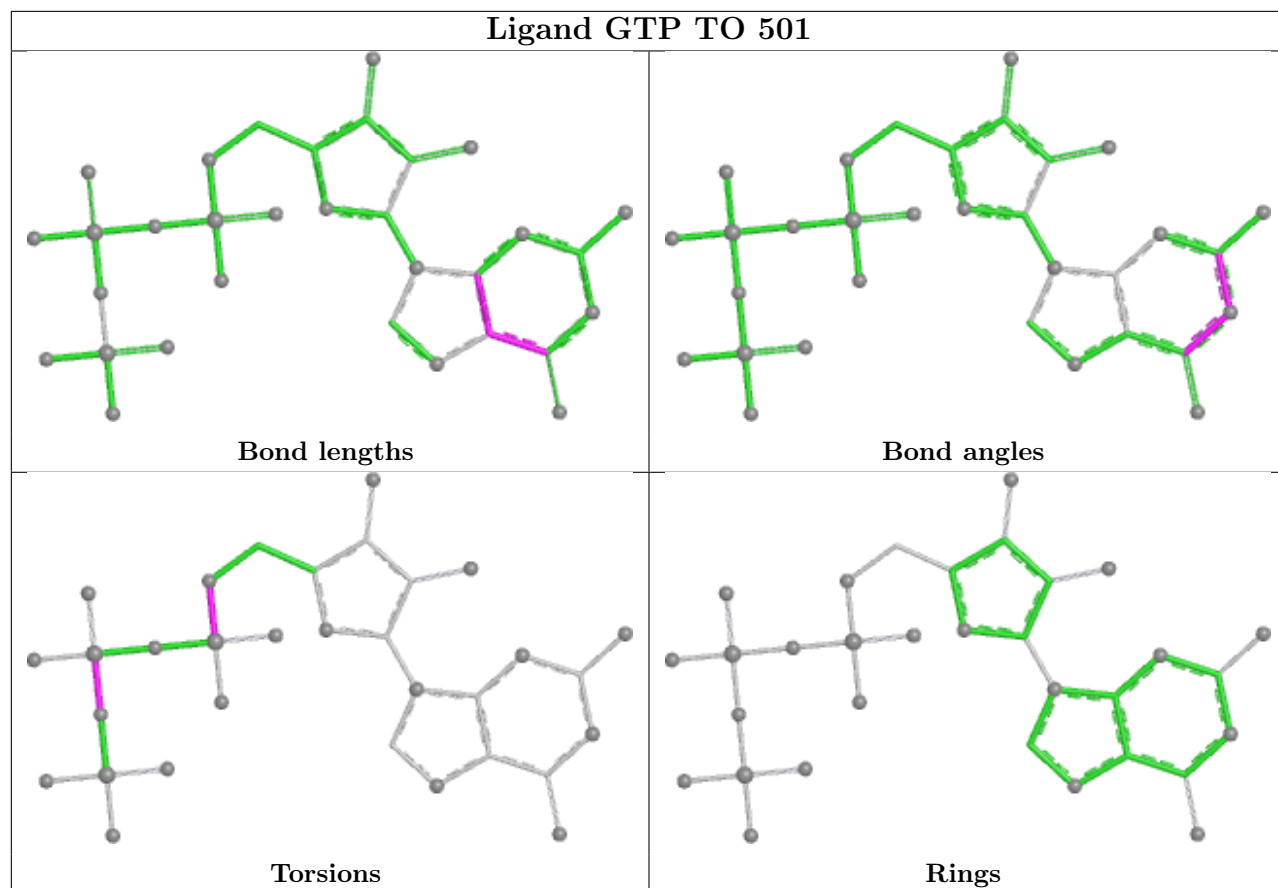




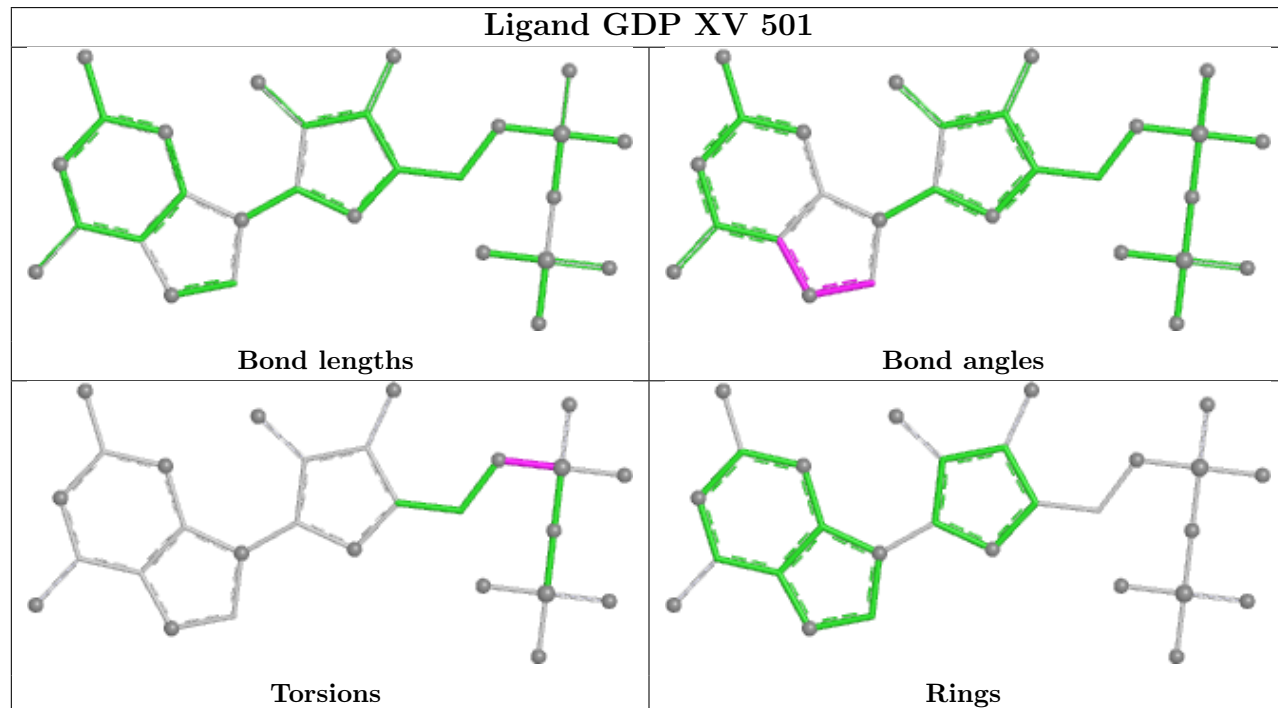




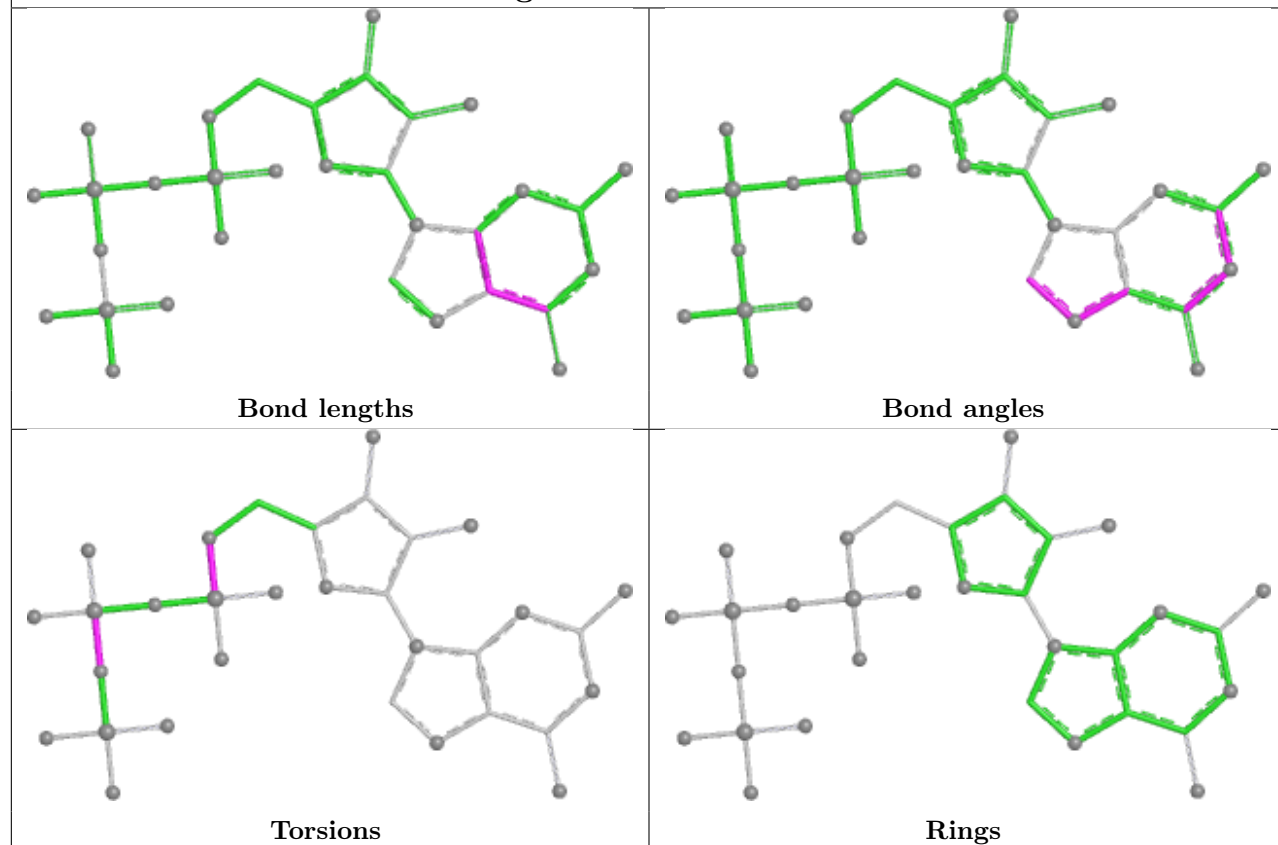
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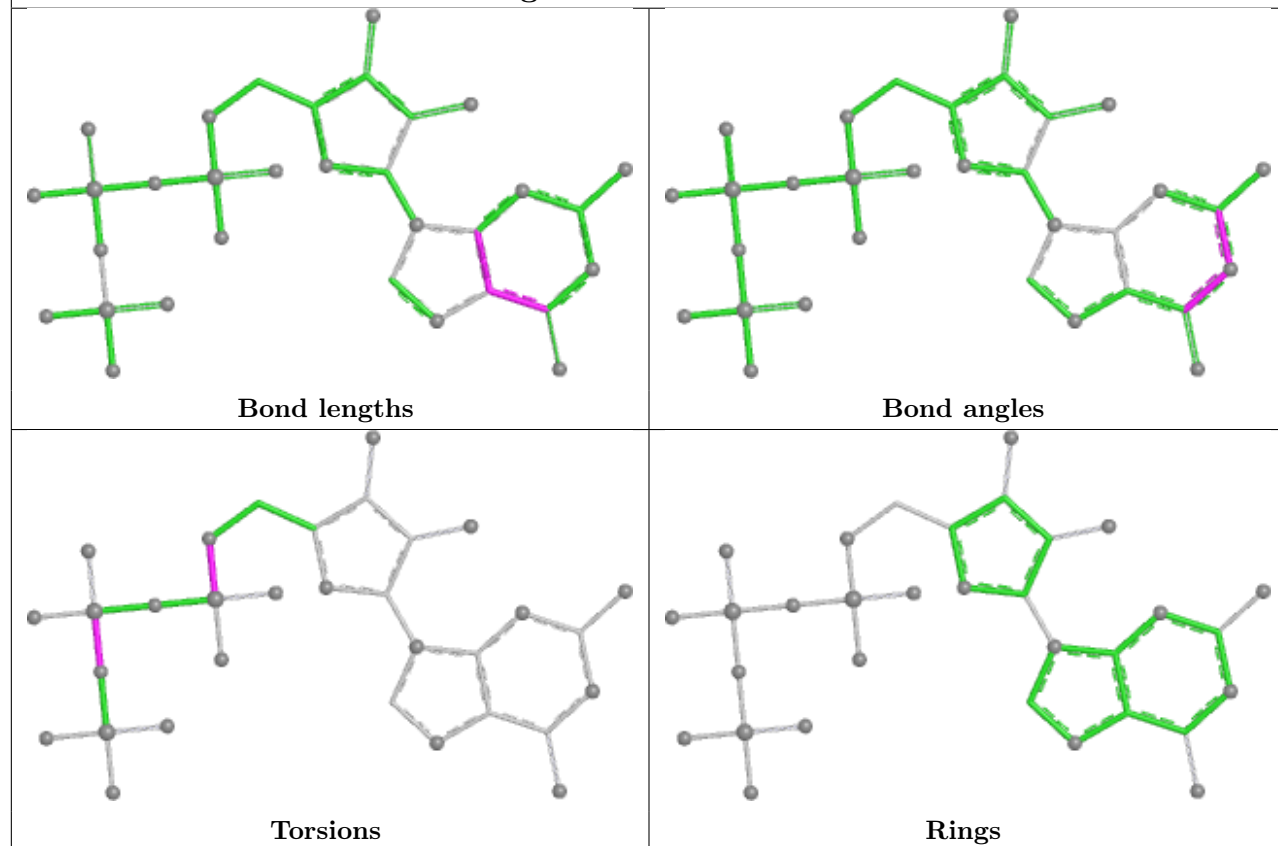
## Ligand GDP XV 501



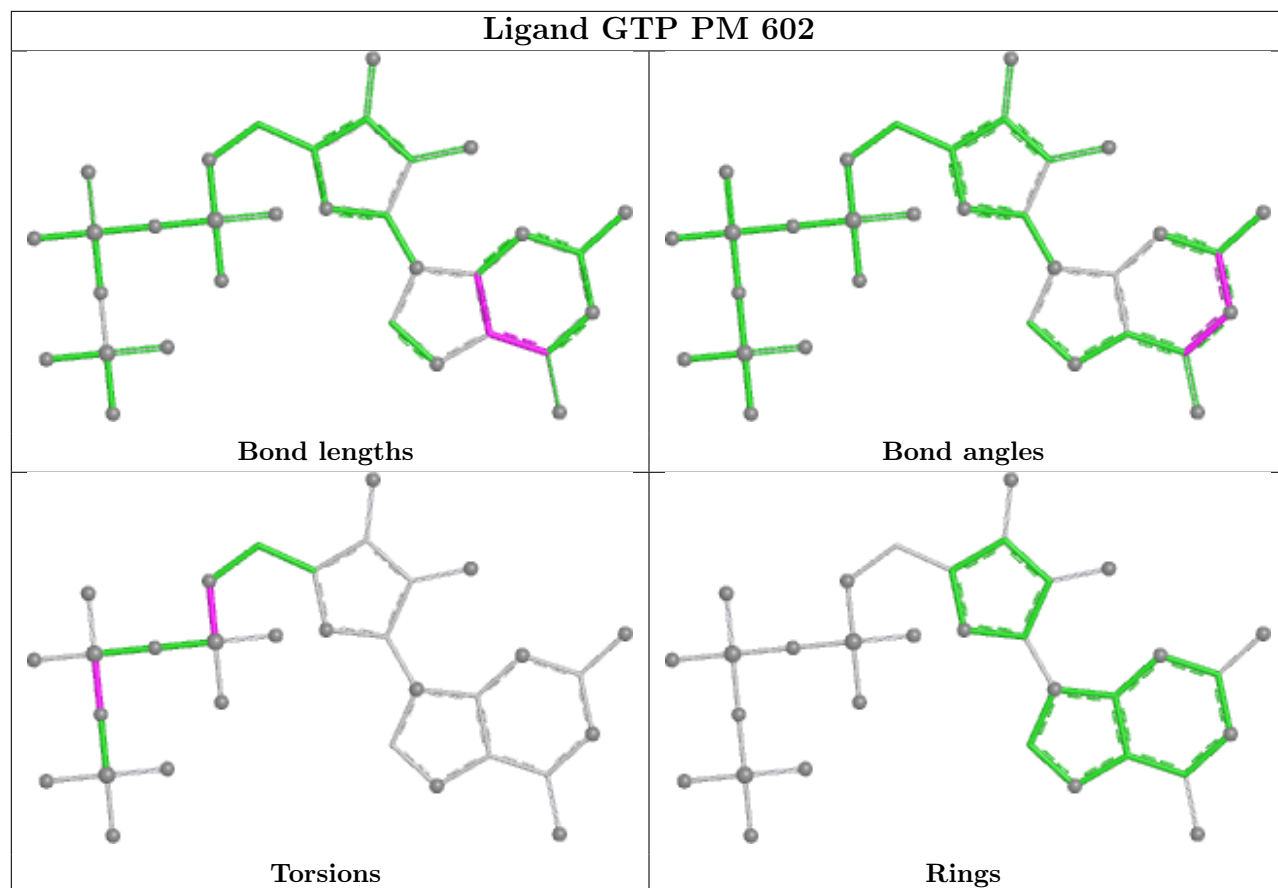
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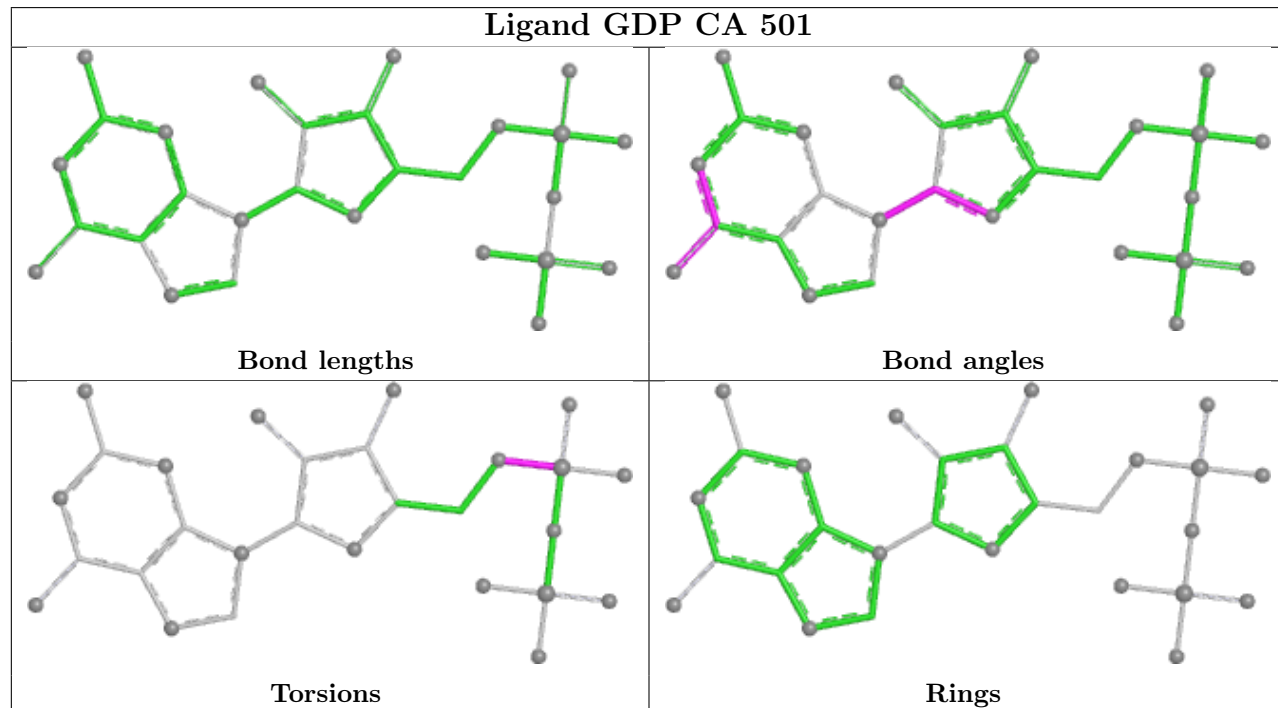
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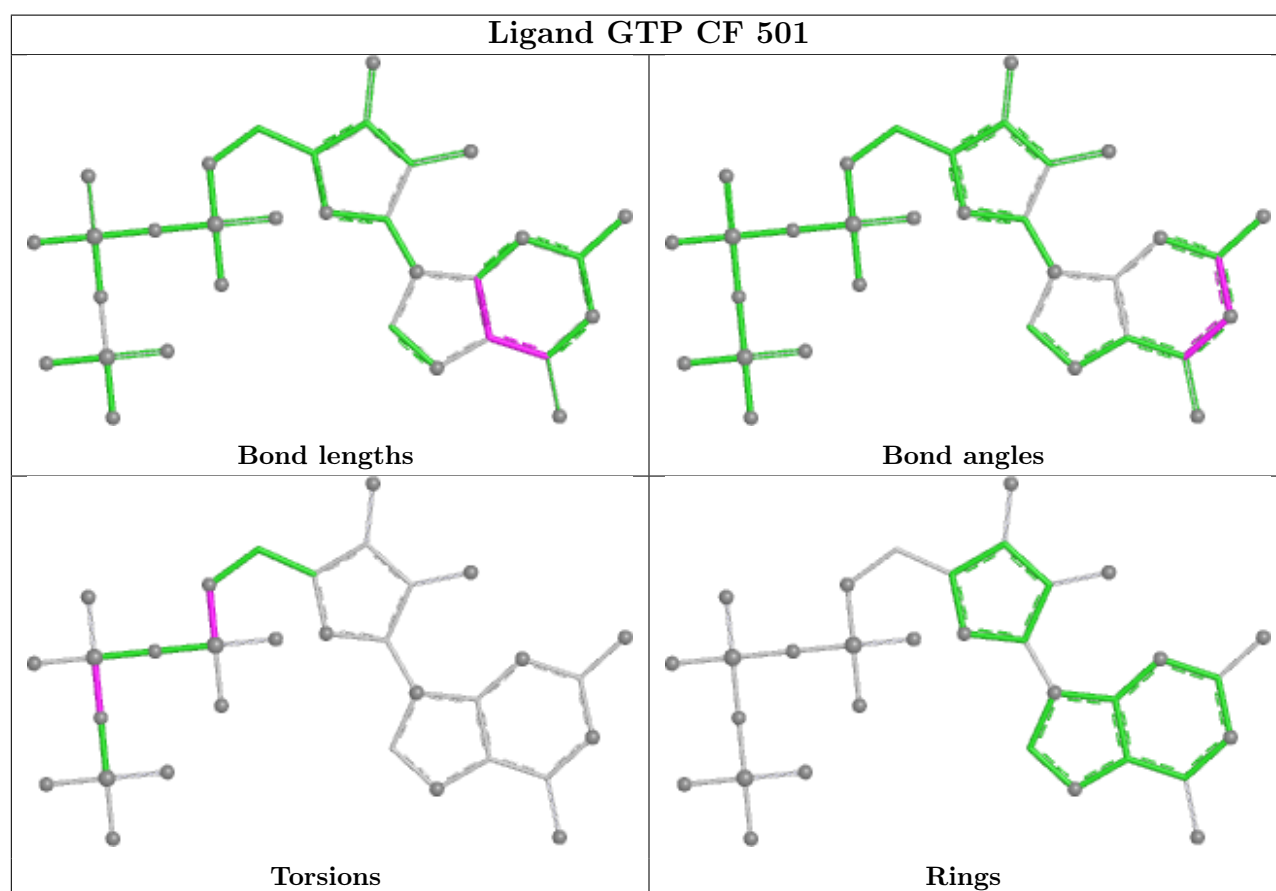
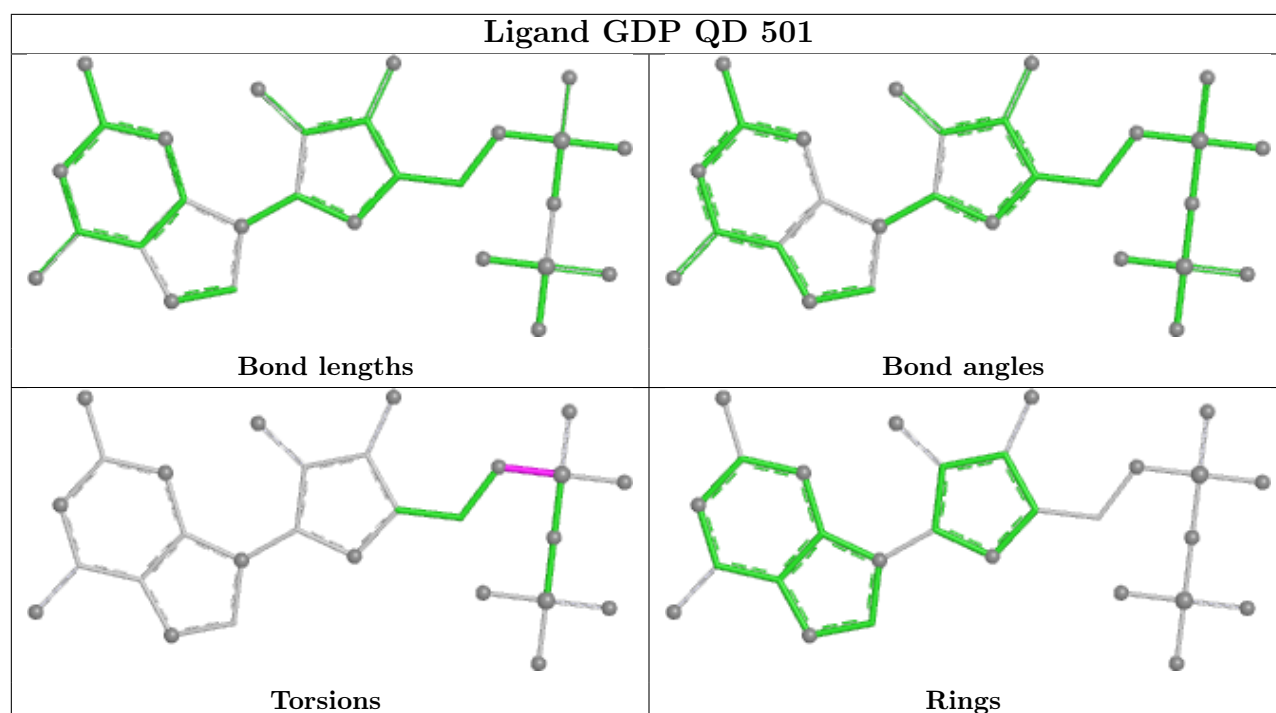


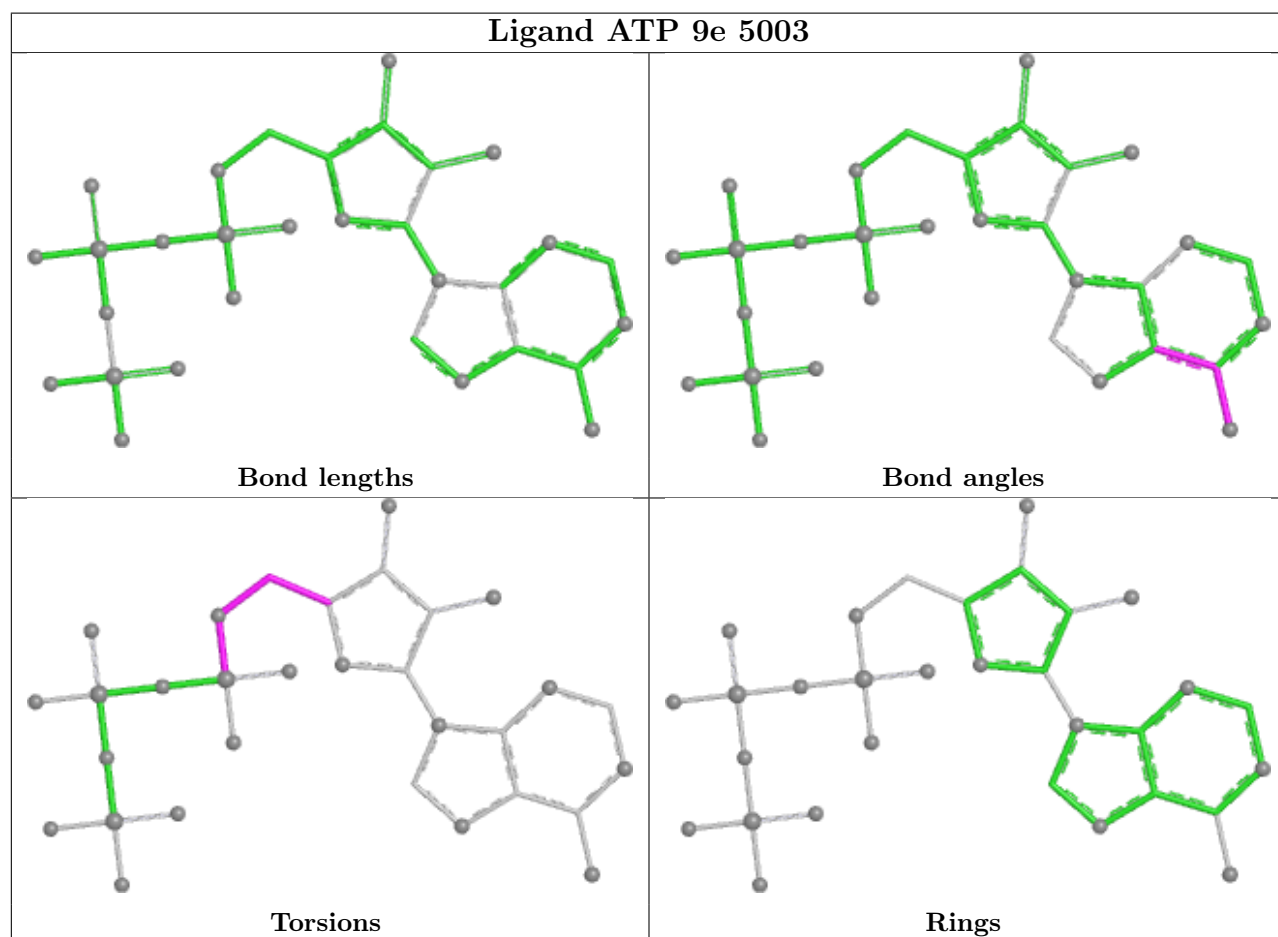
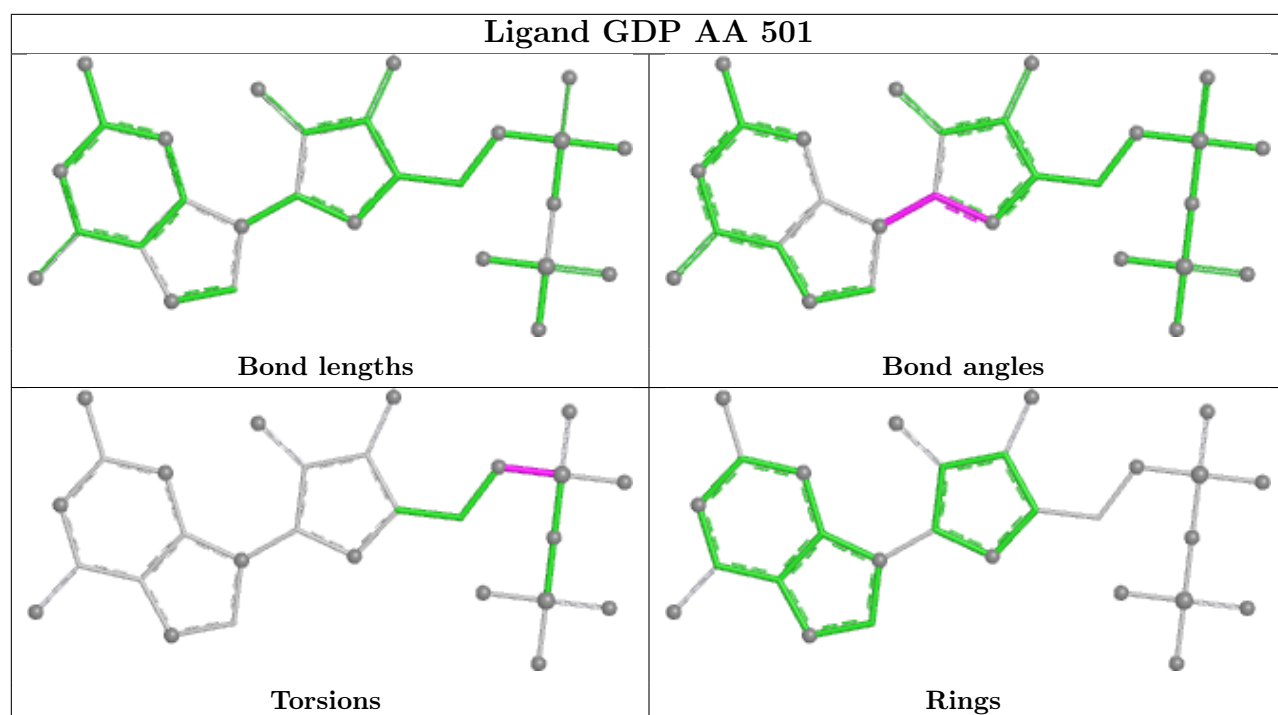
## Ligand GTP PM 602



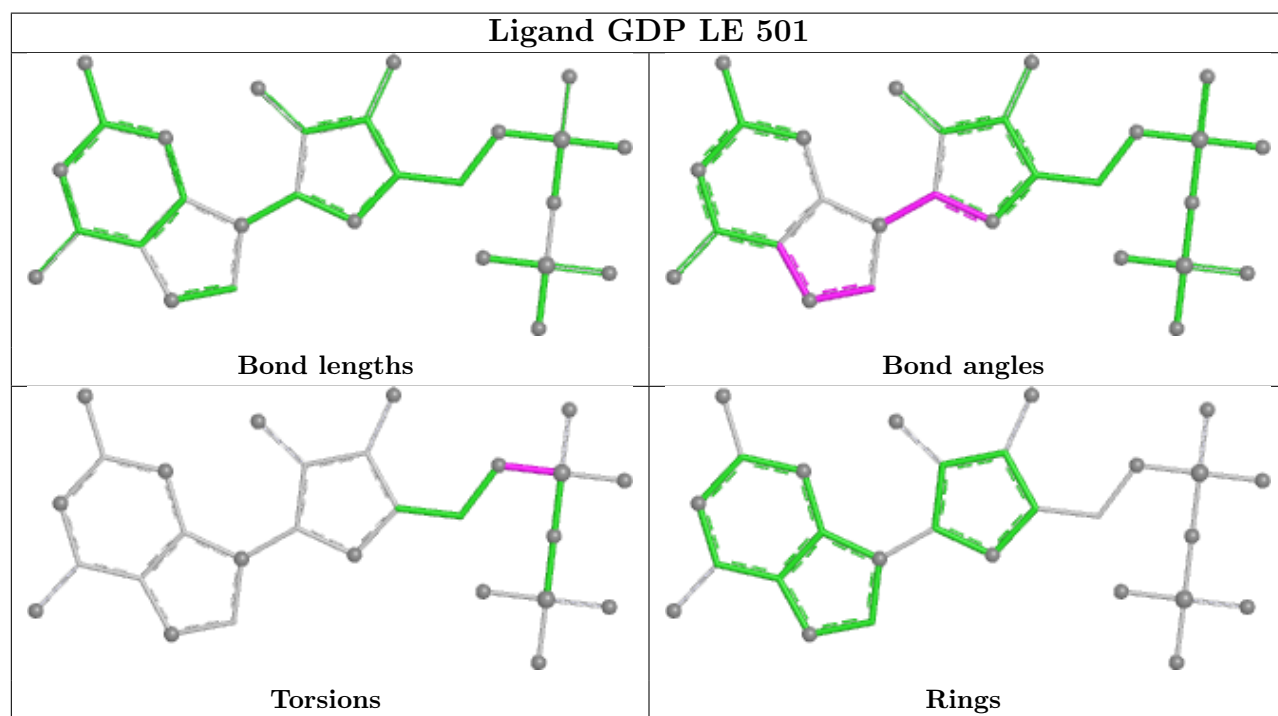
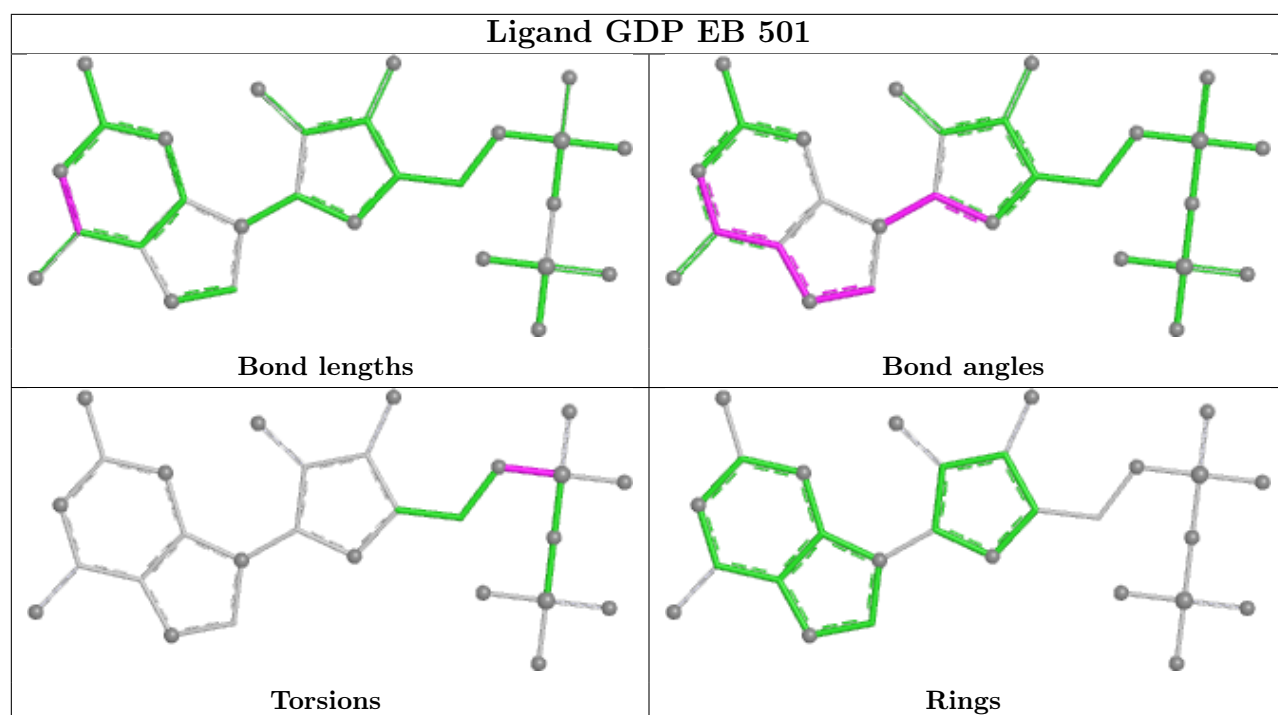
## Ligand GDP CA 501

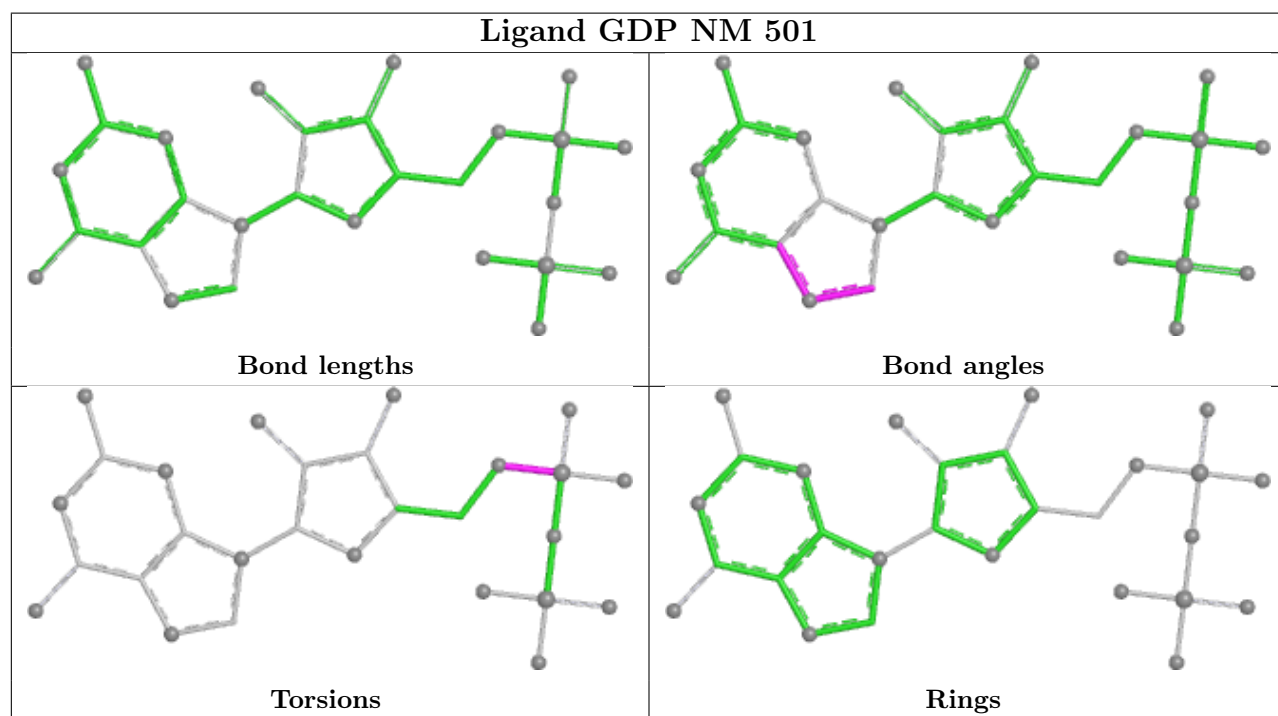
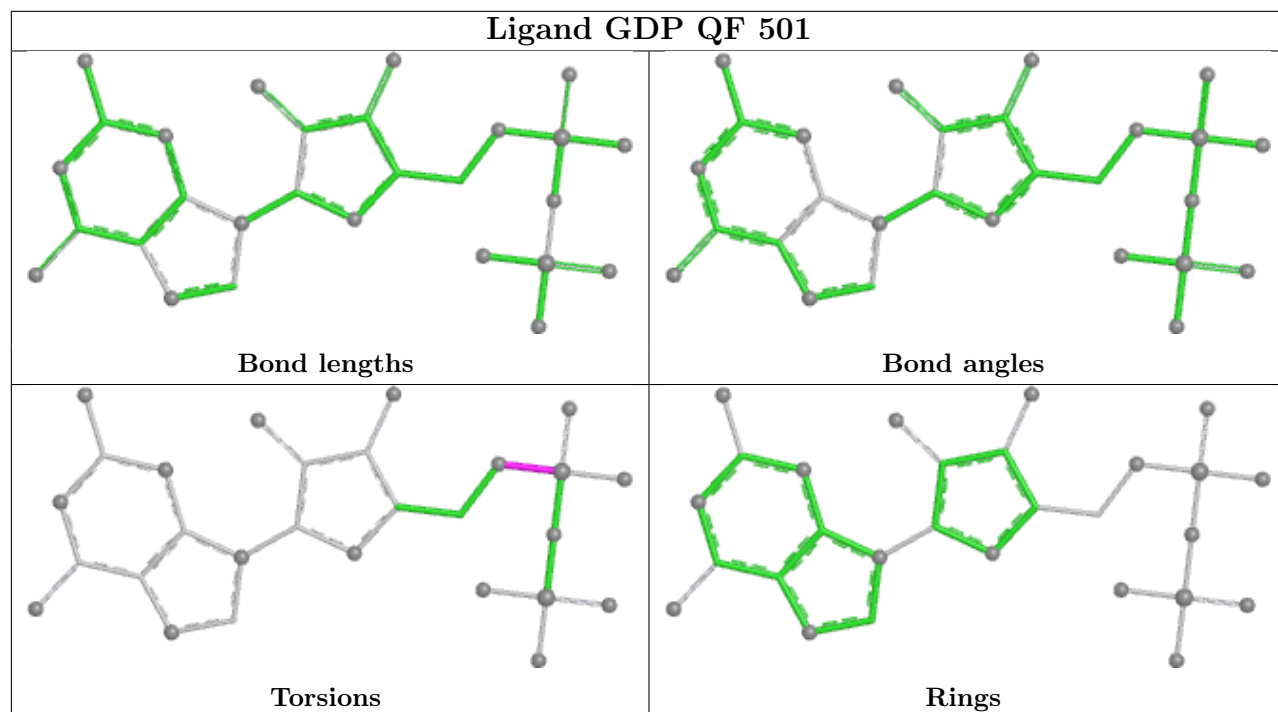


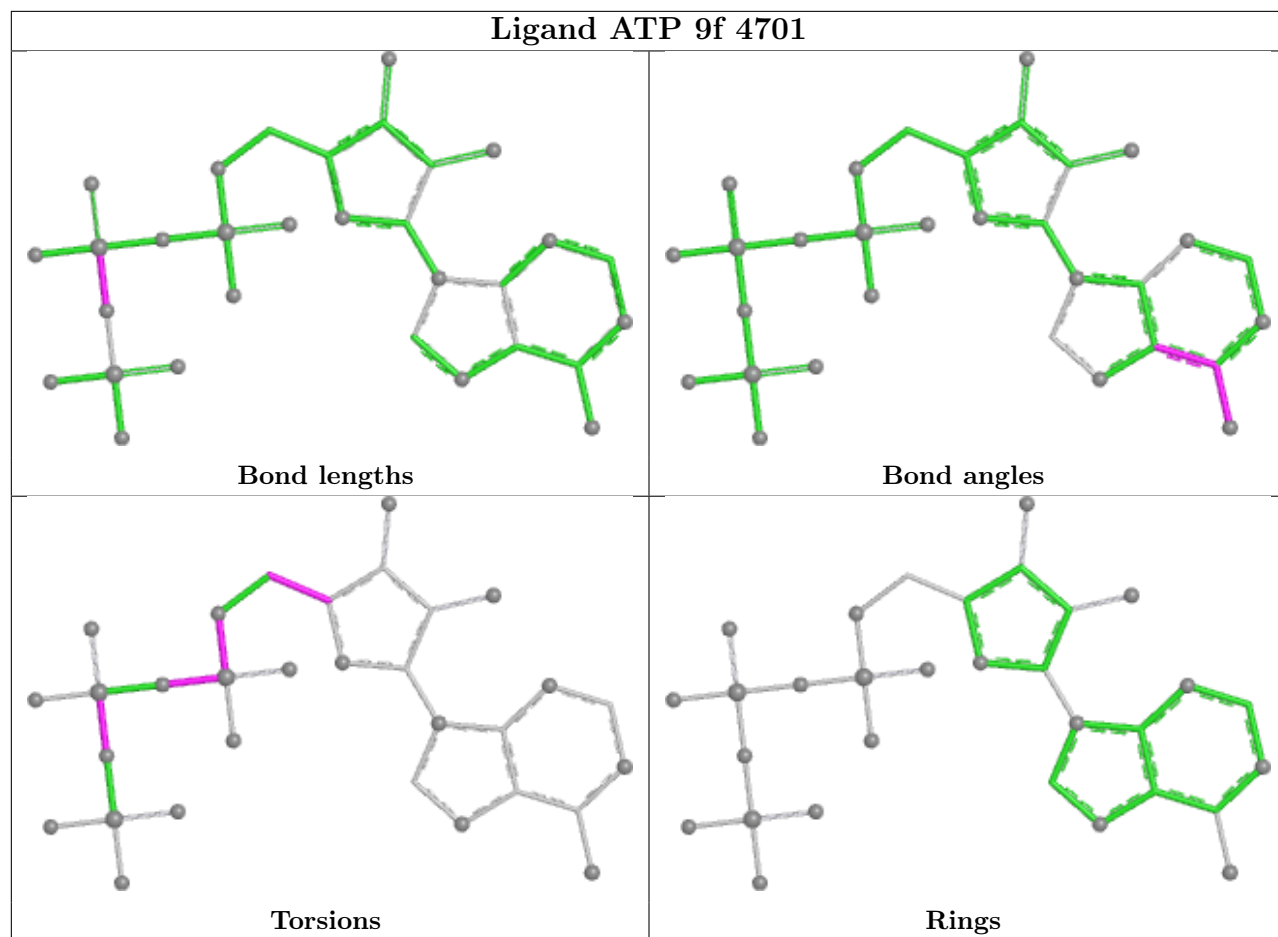


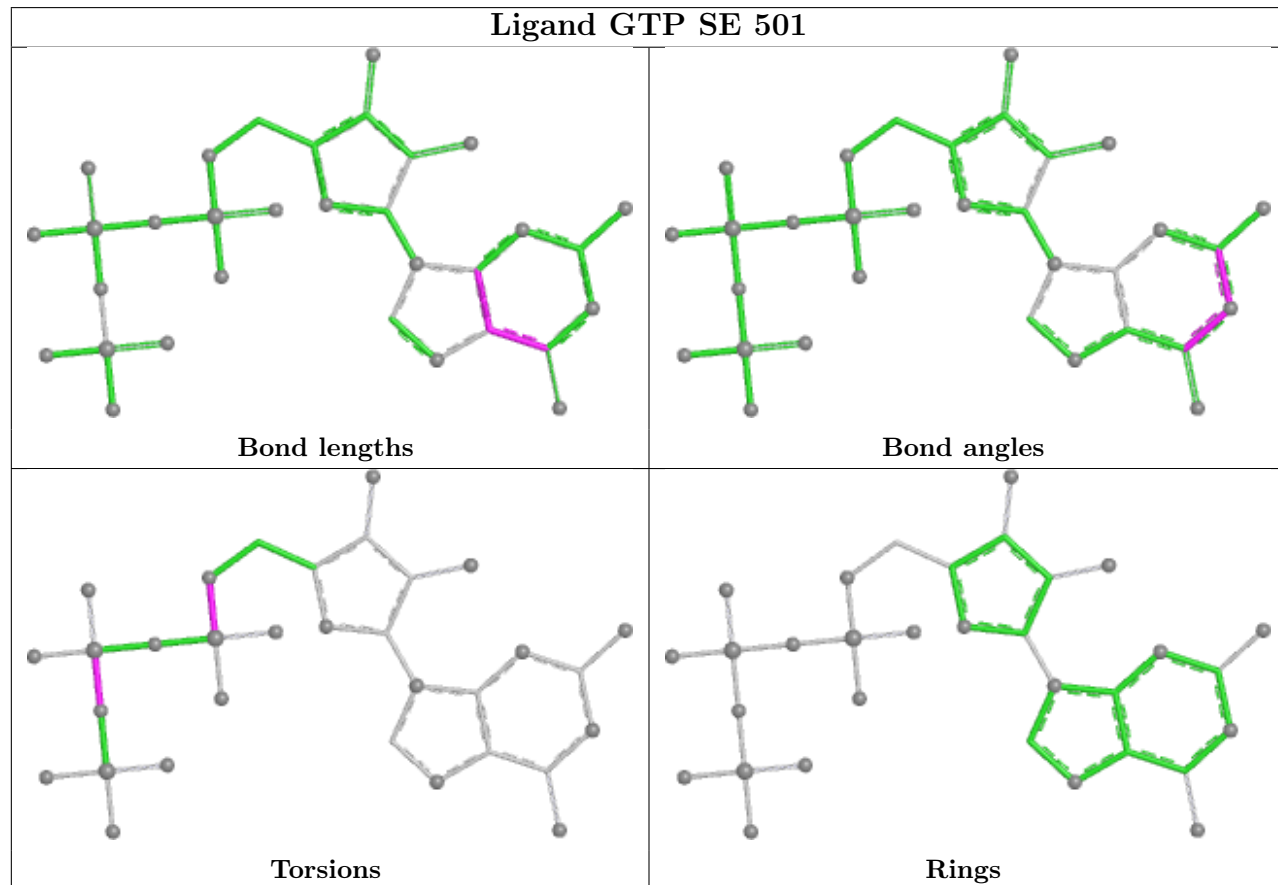
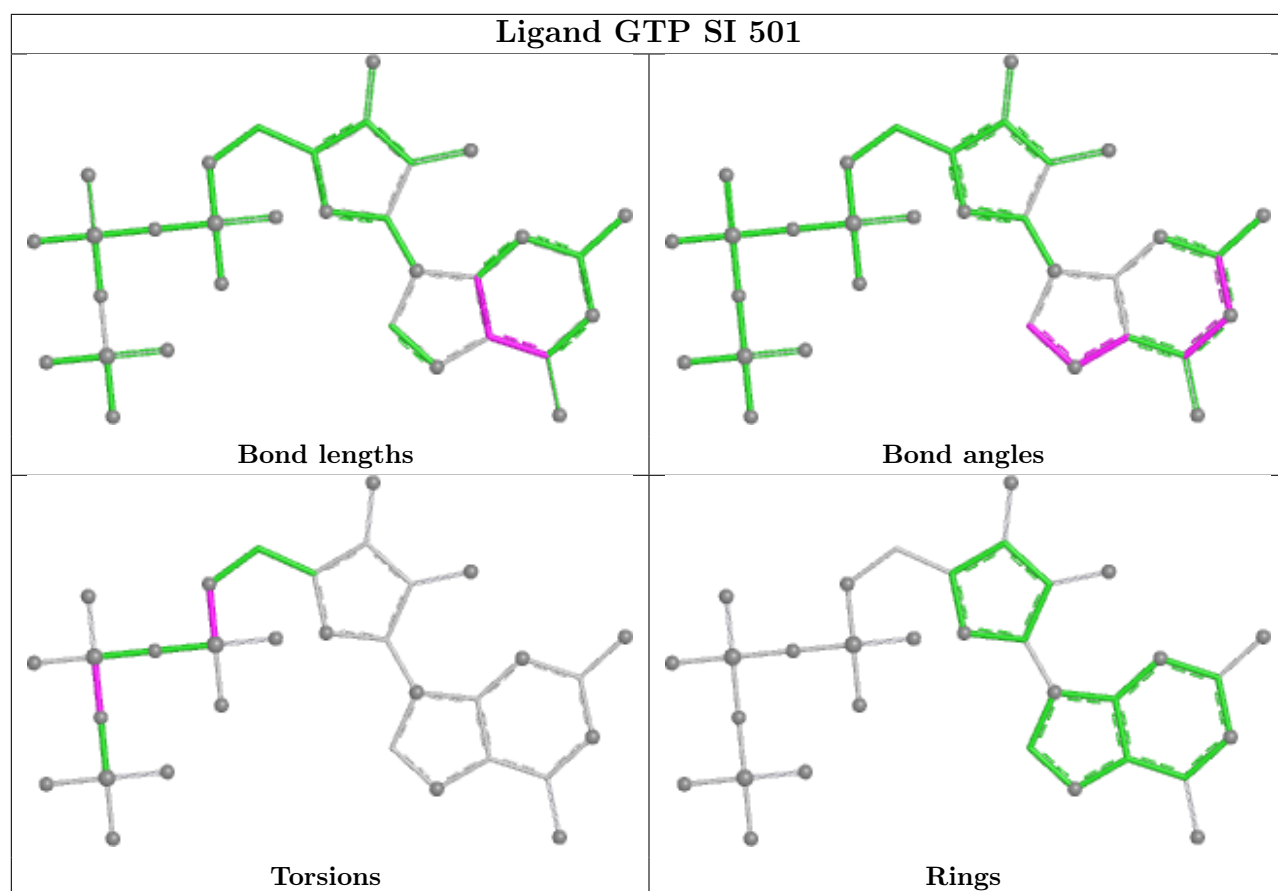


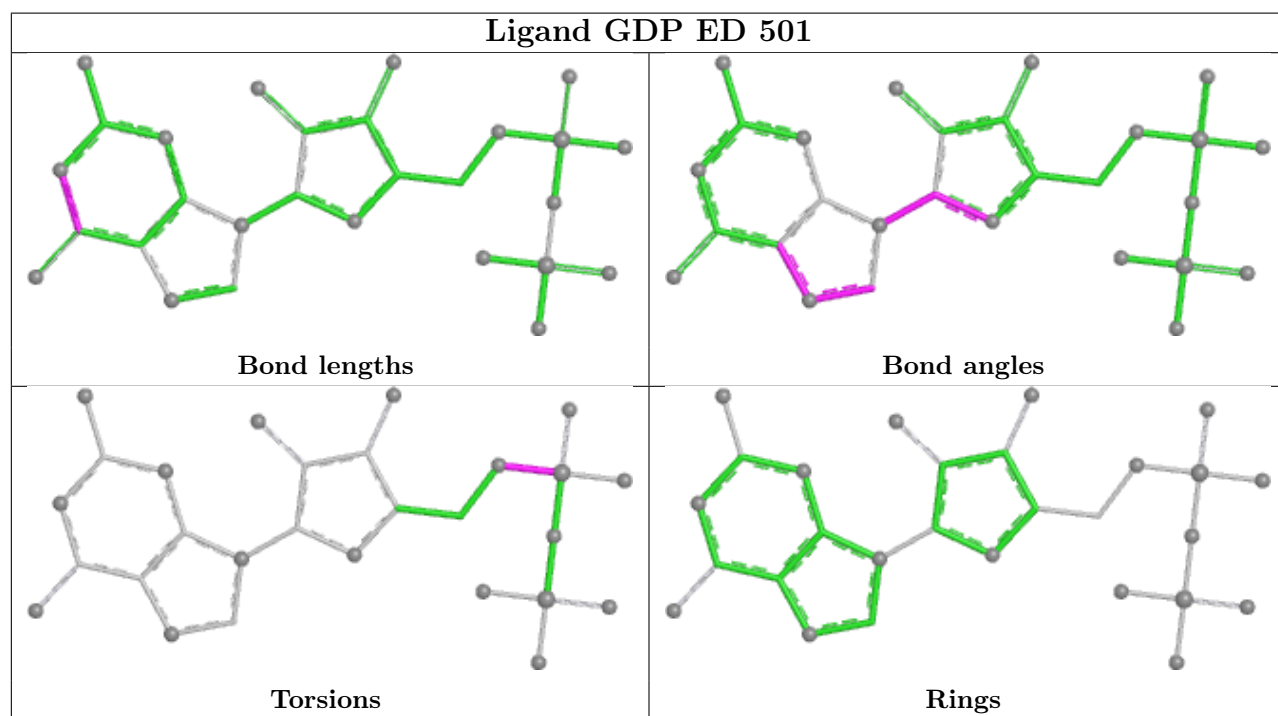
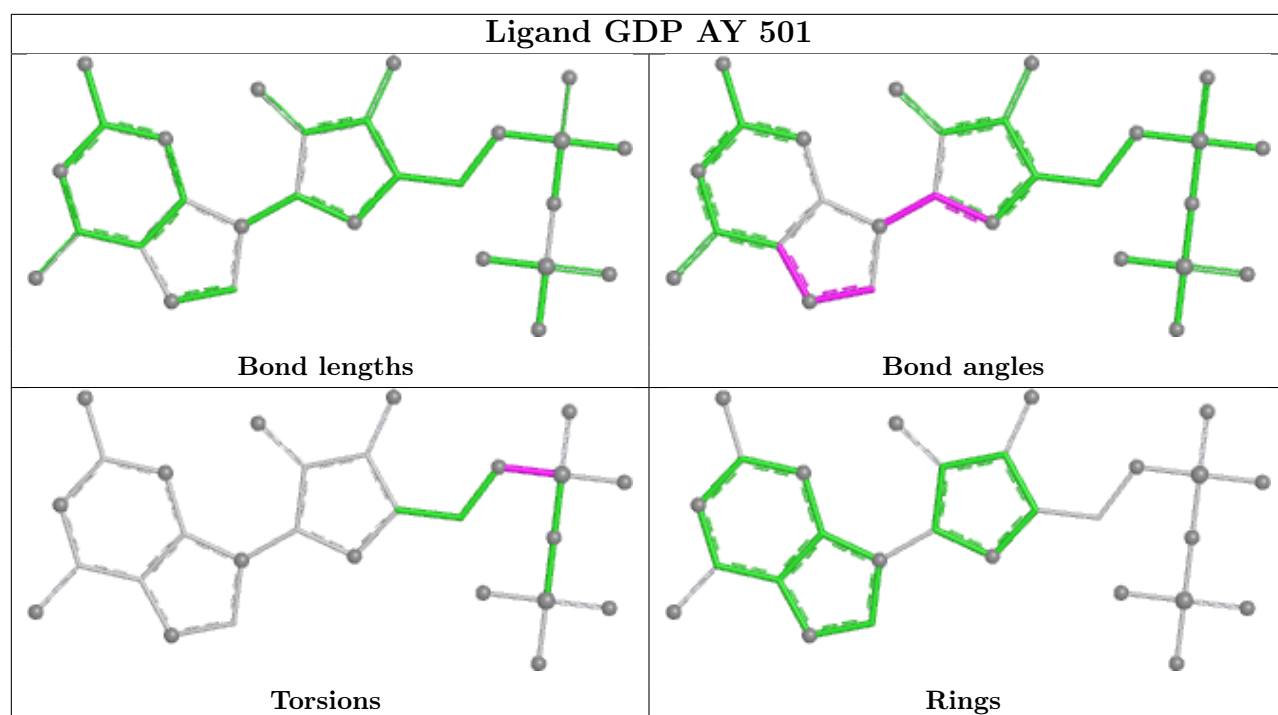




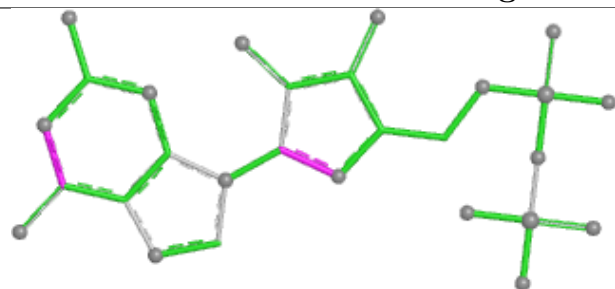




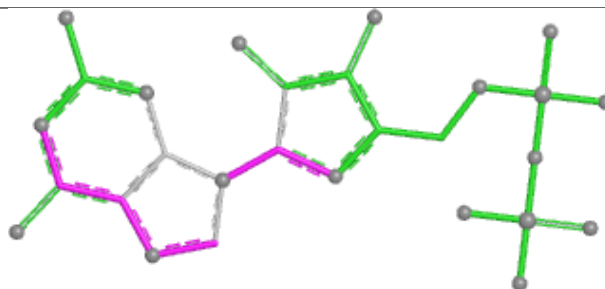




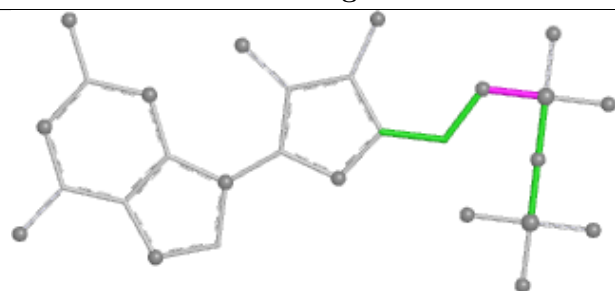
## Ligand GDP JW 501



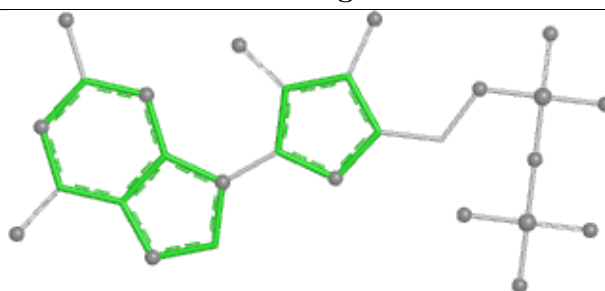
Bond lengths



Bond angles

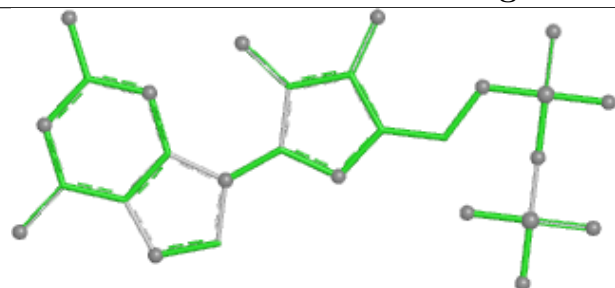


Torsions

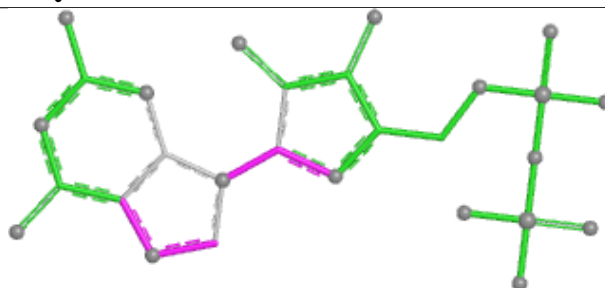


Rings

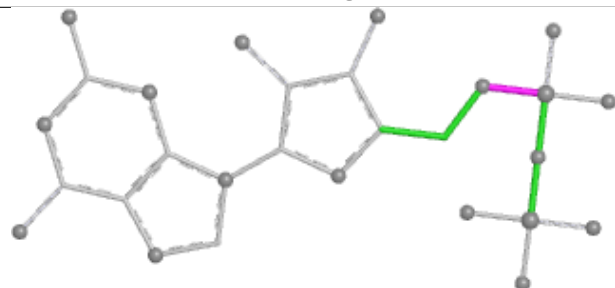
## Ligand GDP QX 501



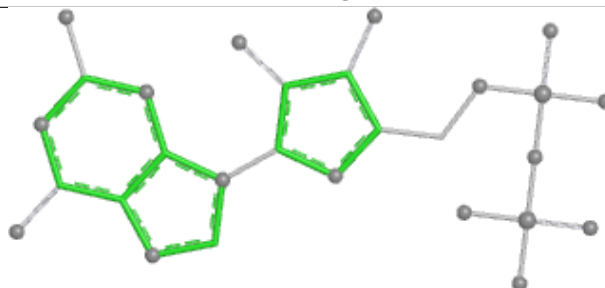
Bond lengths



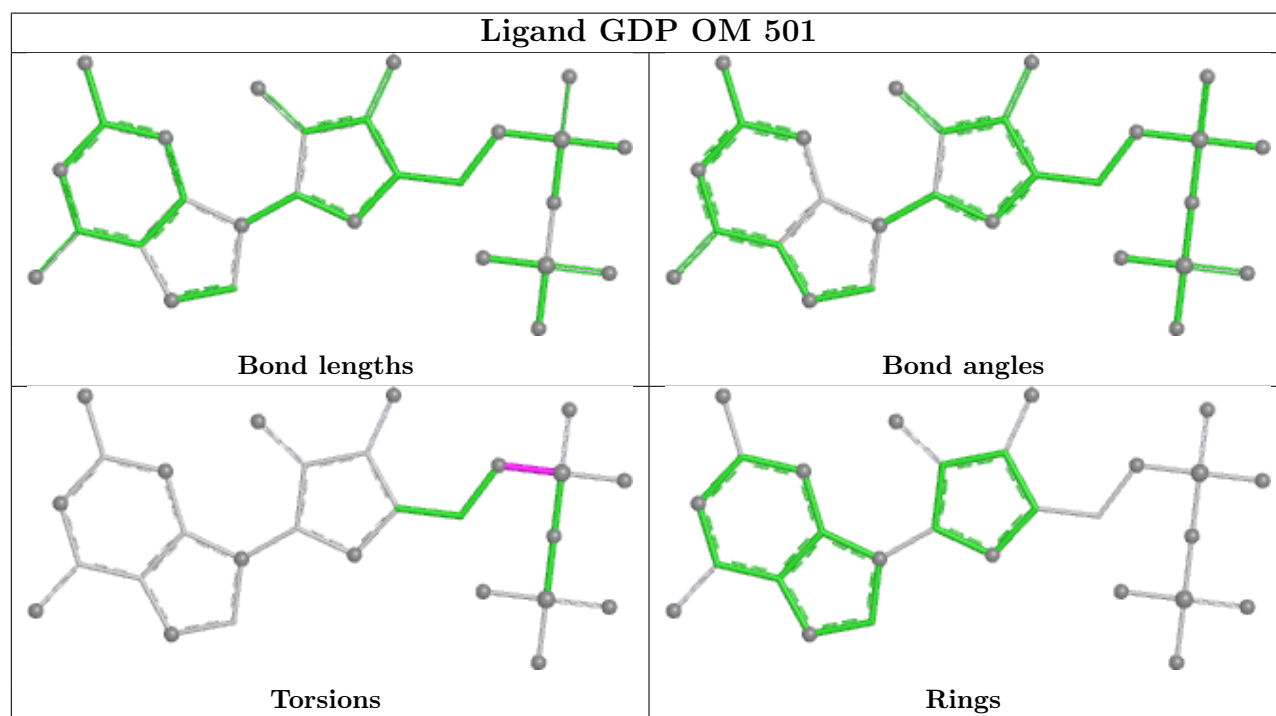
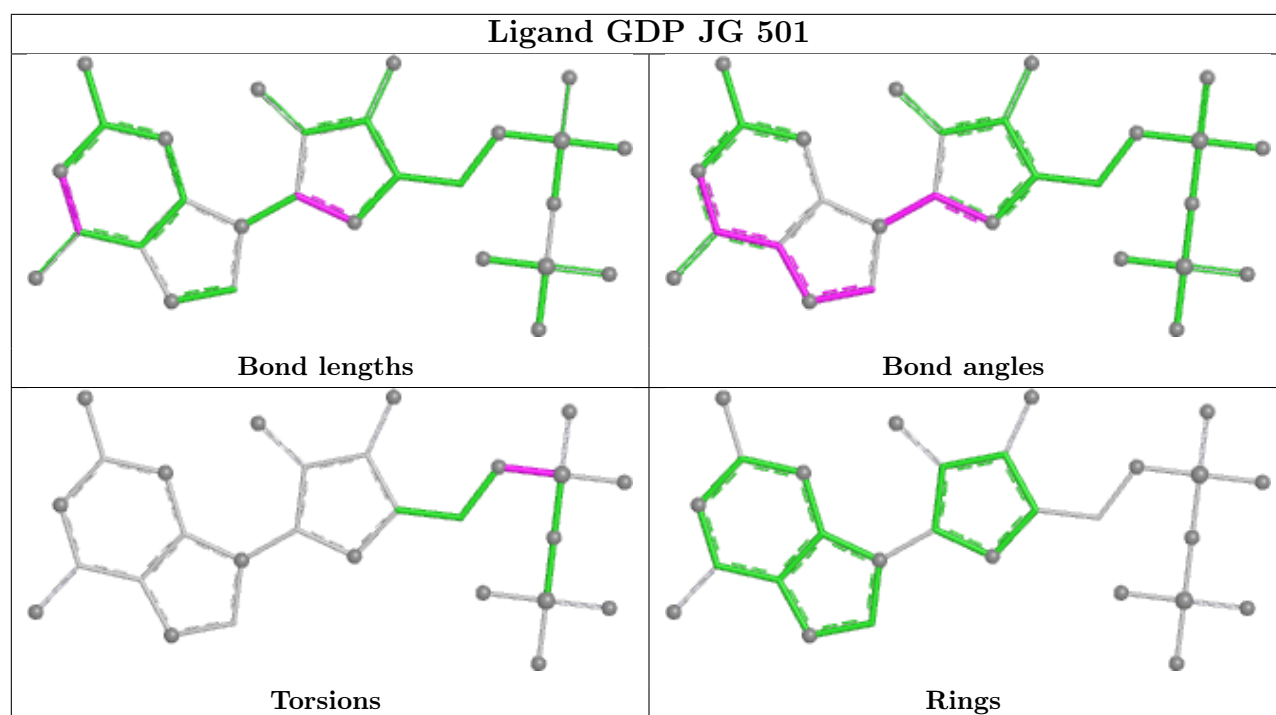
Bond angles



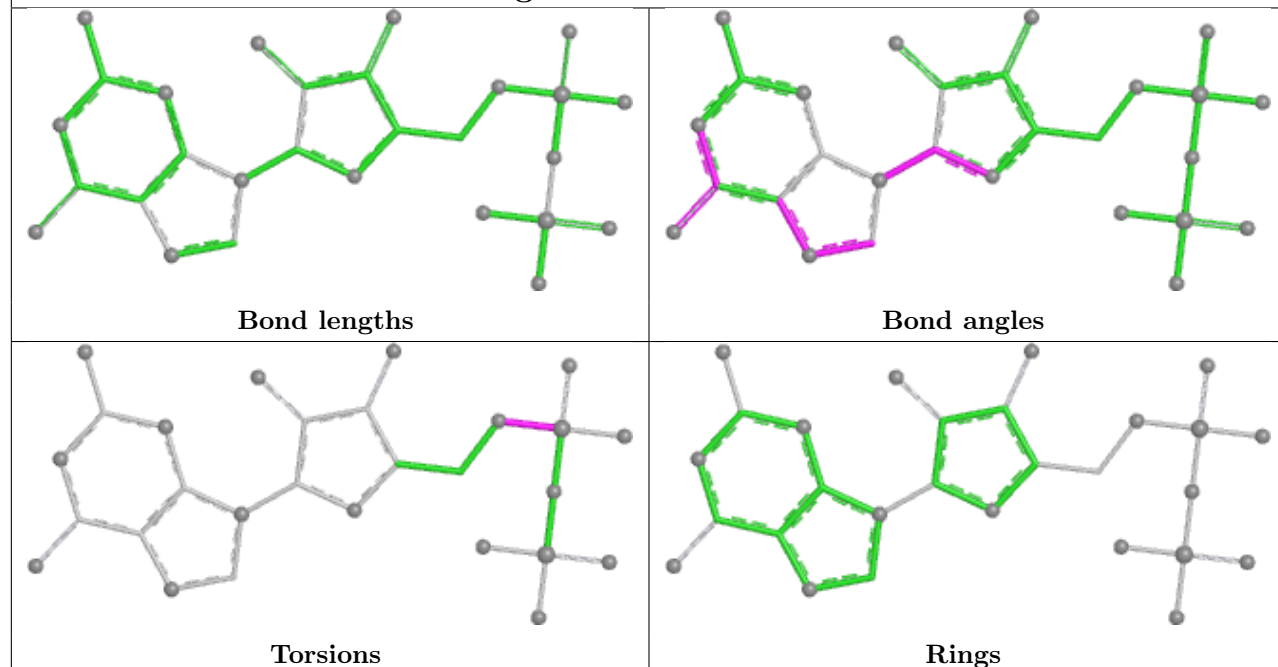
Torsions



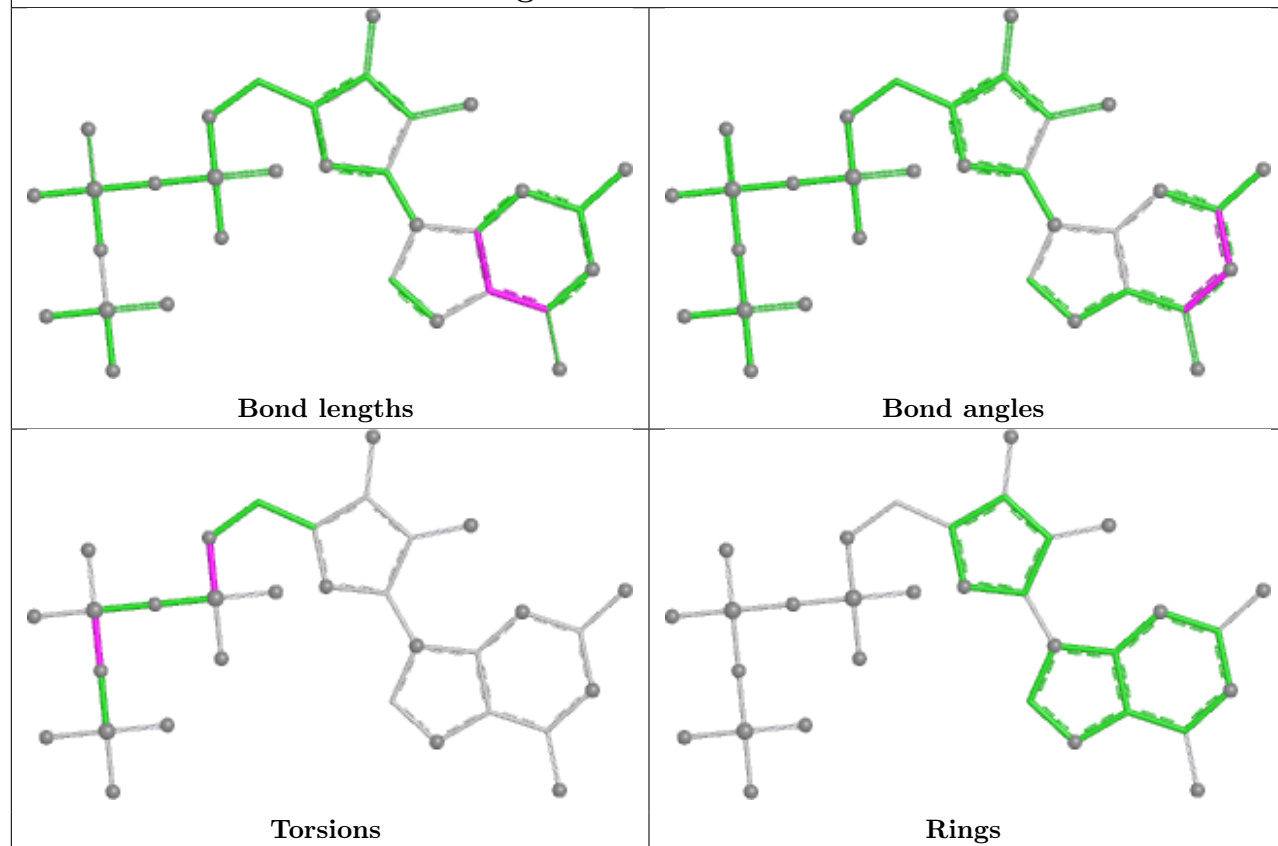
Rings



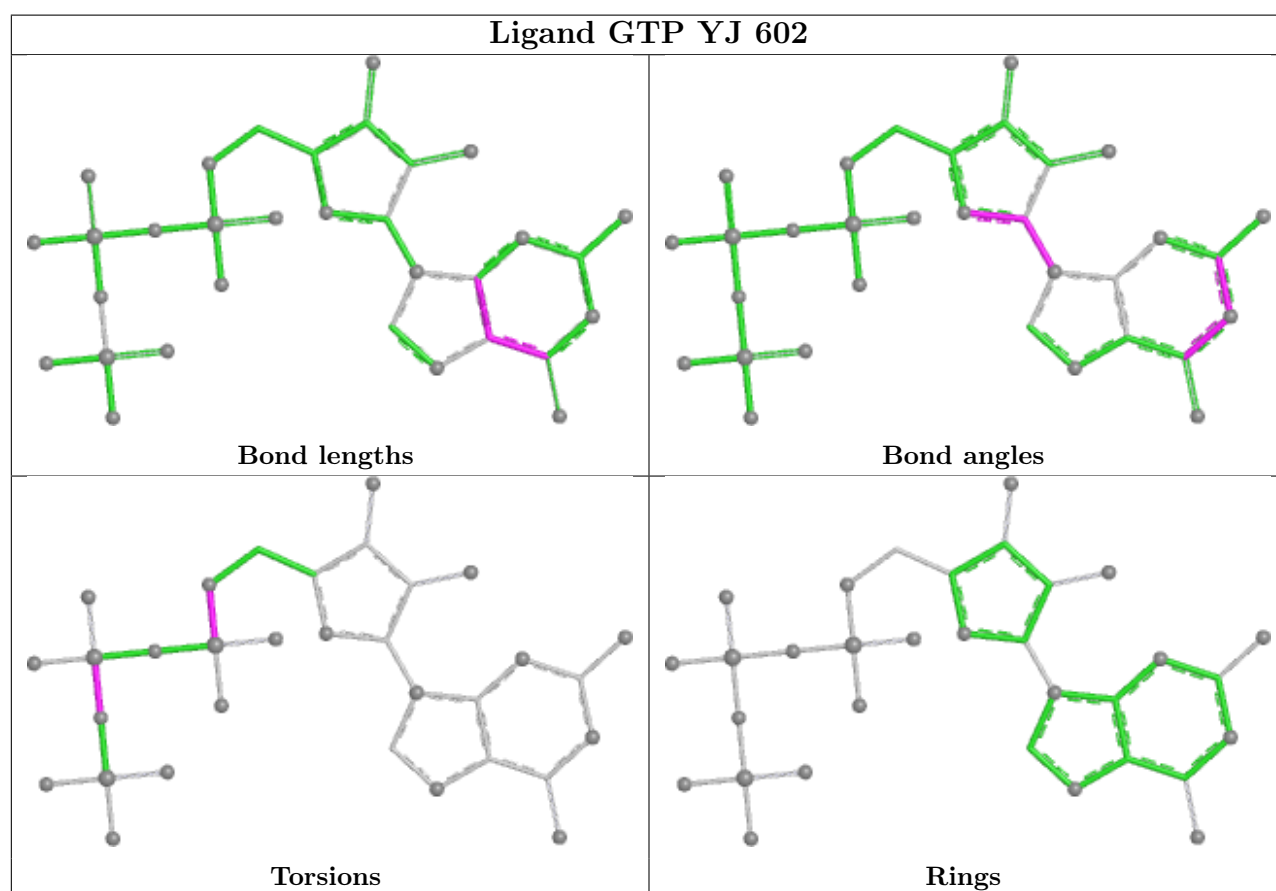
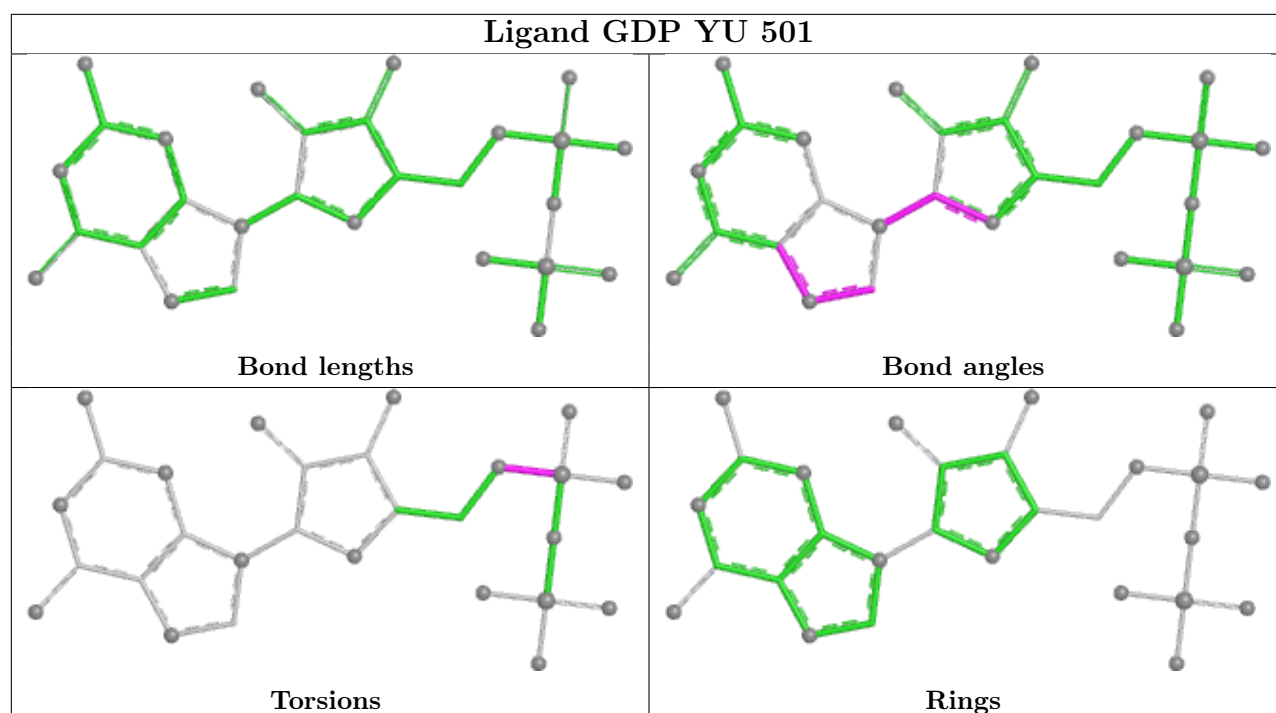
## Ligand GDP RX 501

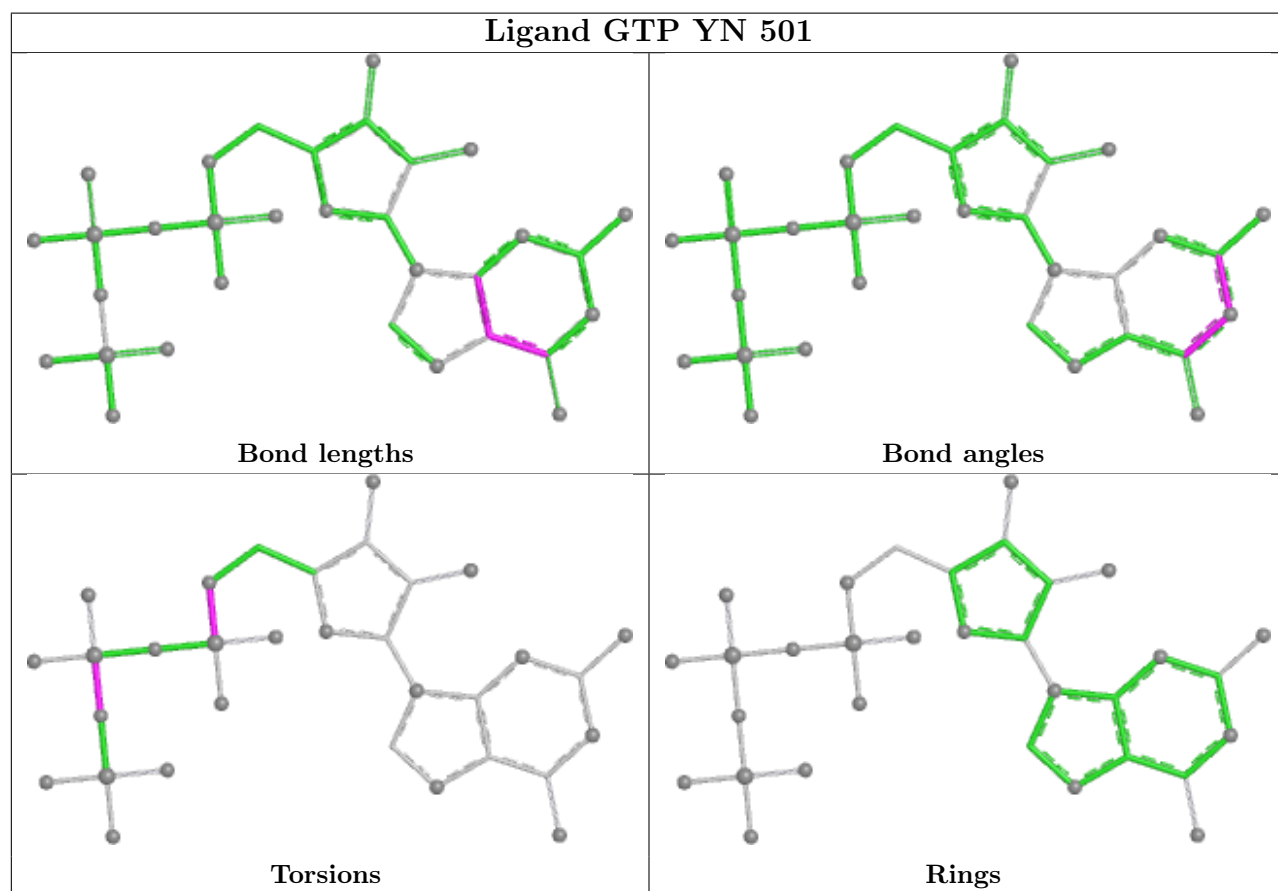
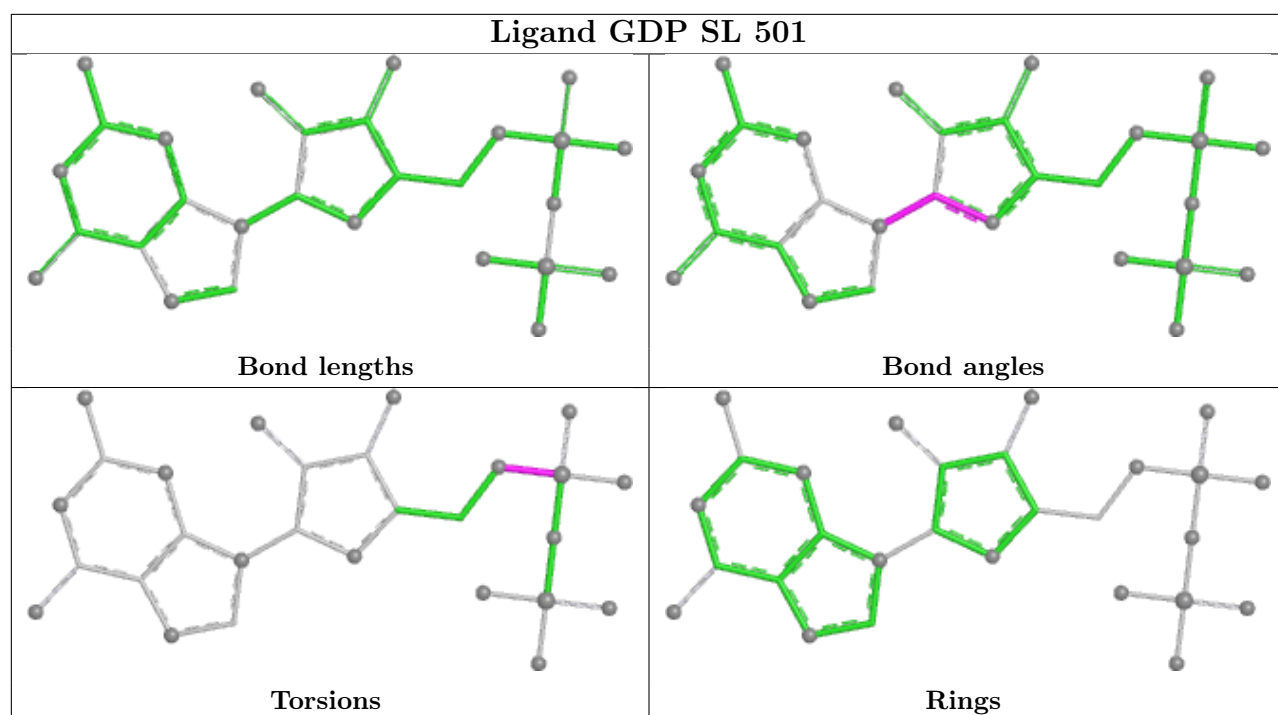


## Ligand GTP RA 602

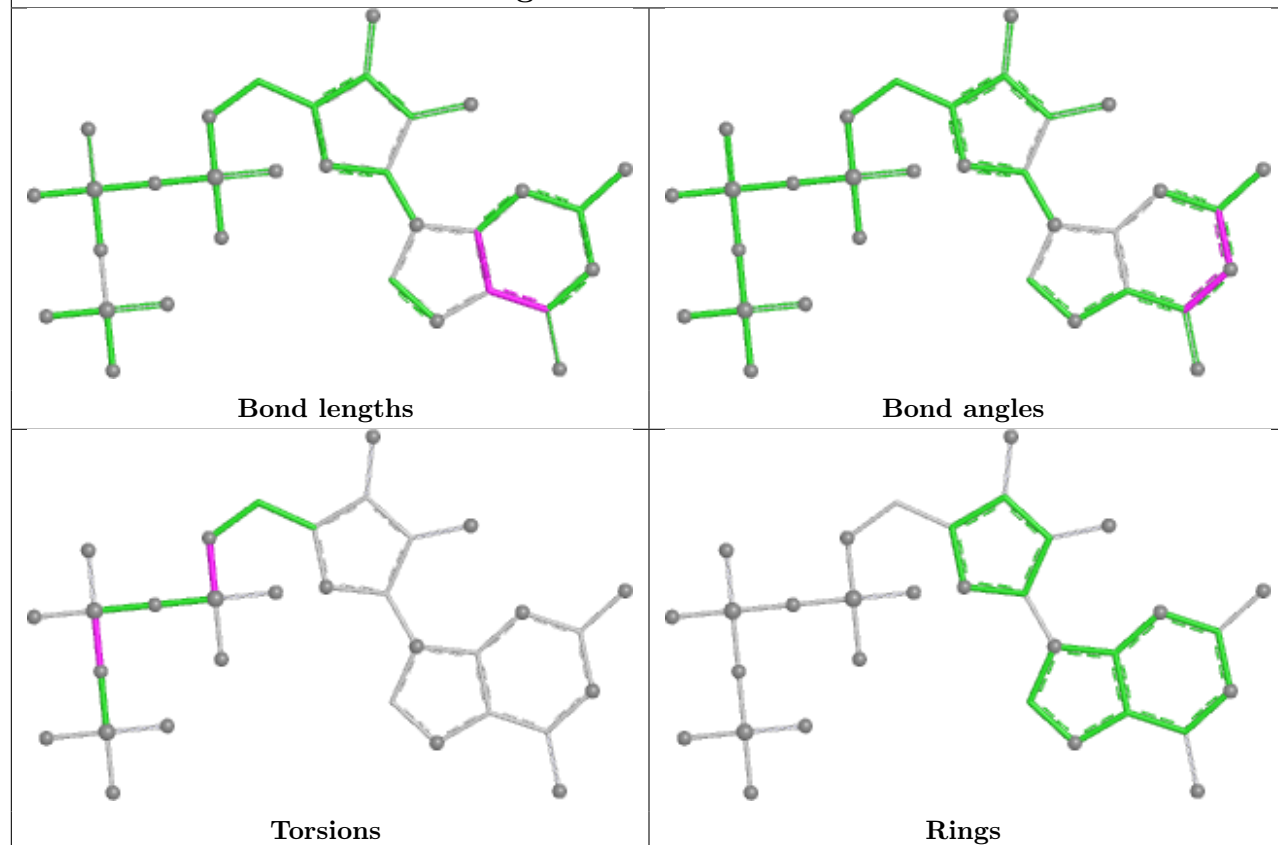




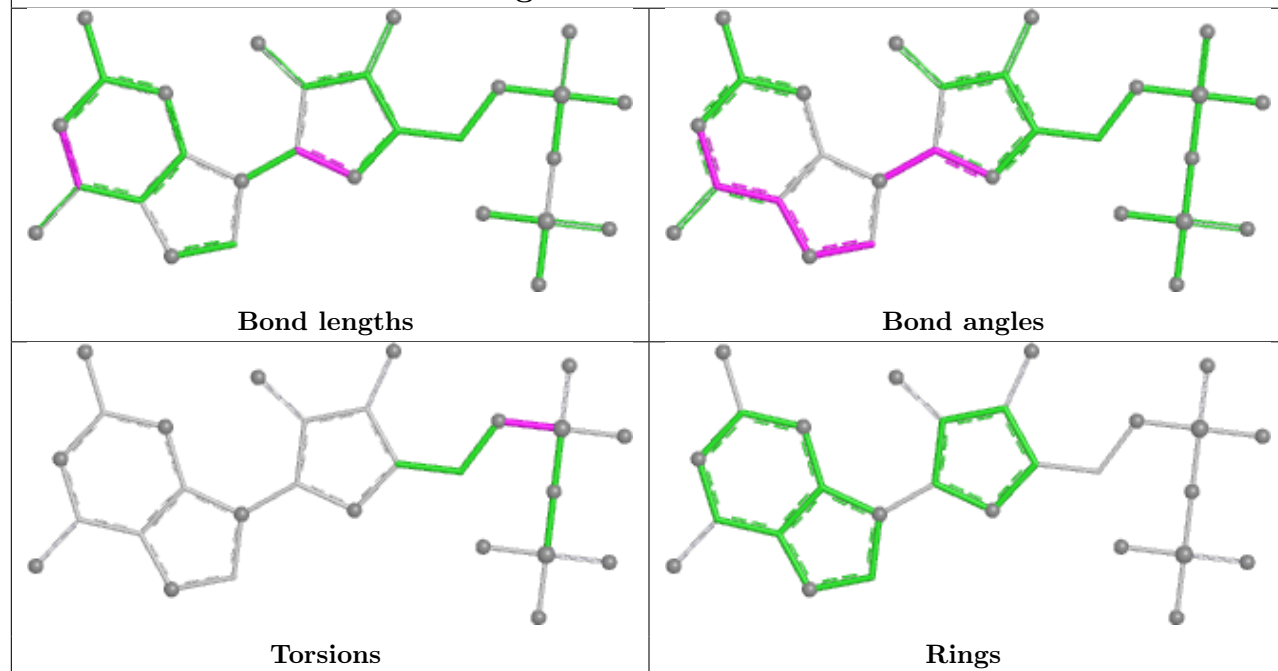




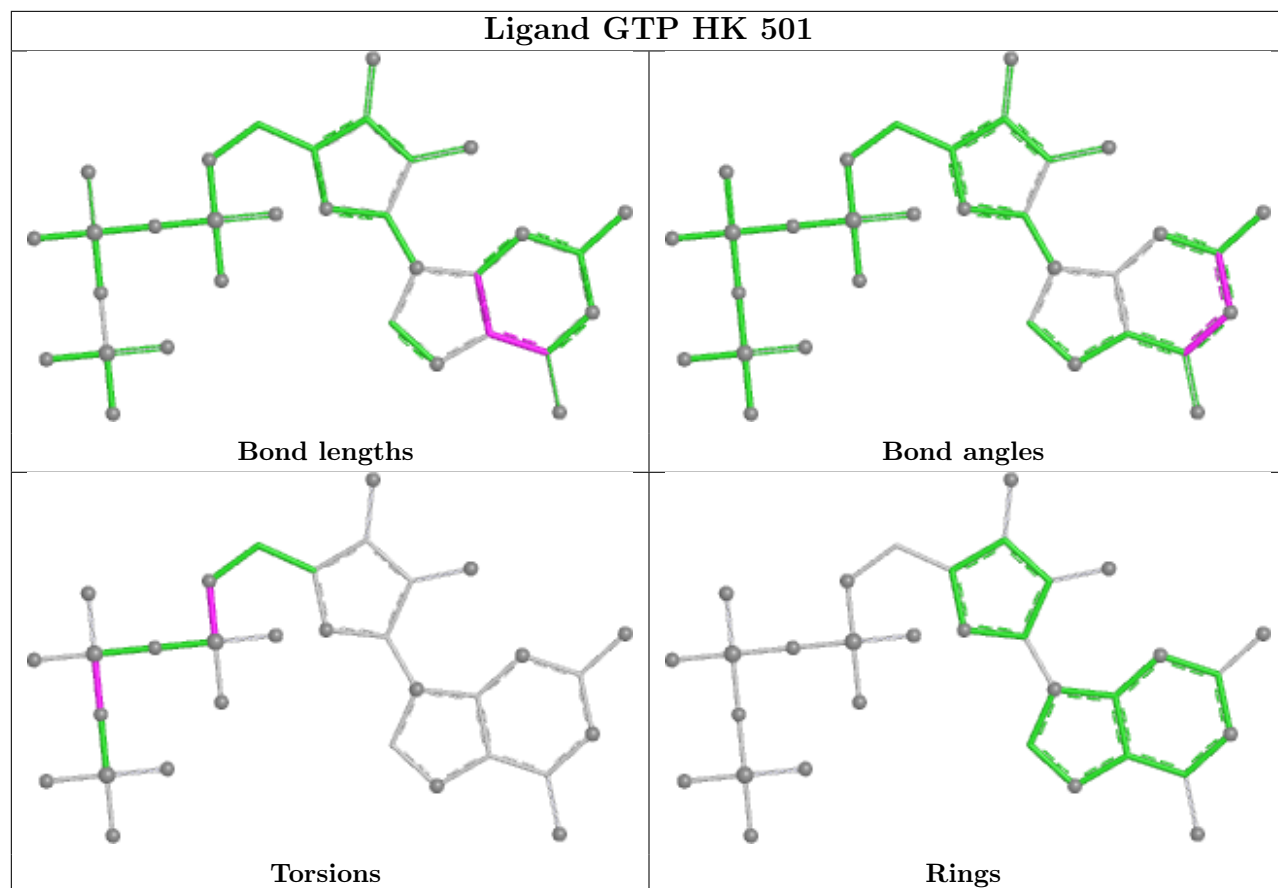
## Ligand GTP KR 602



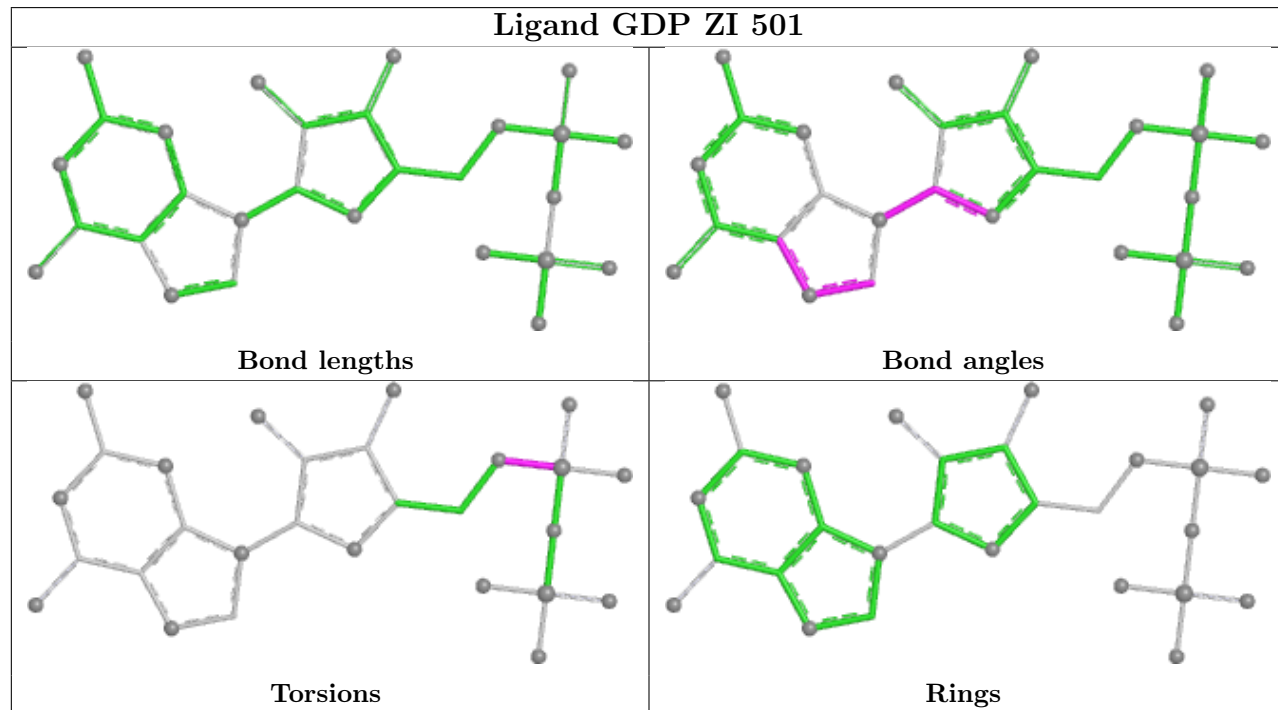
## Ligand GDP CU 501



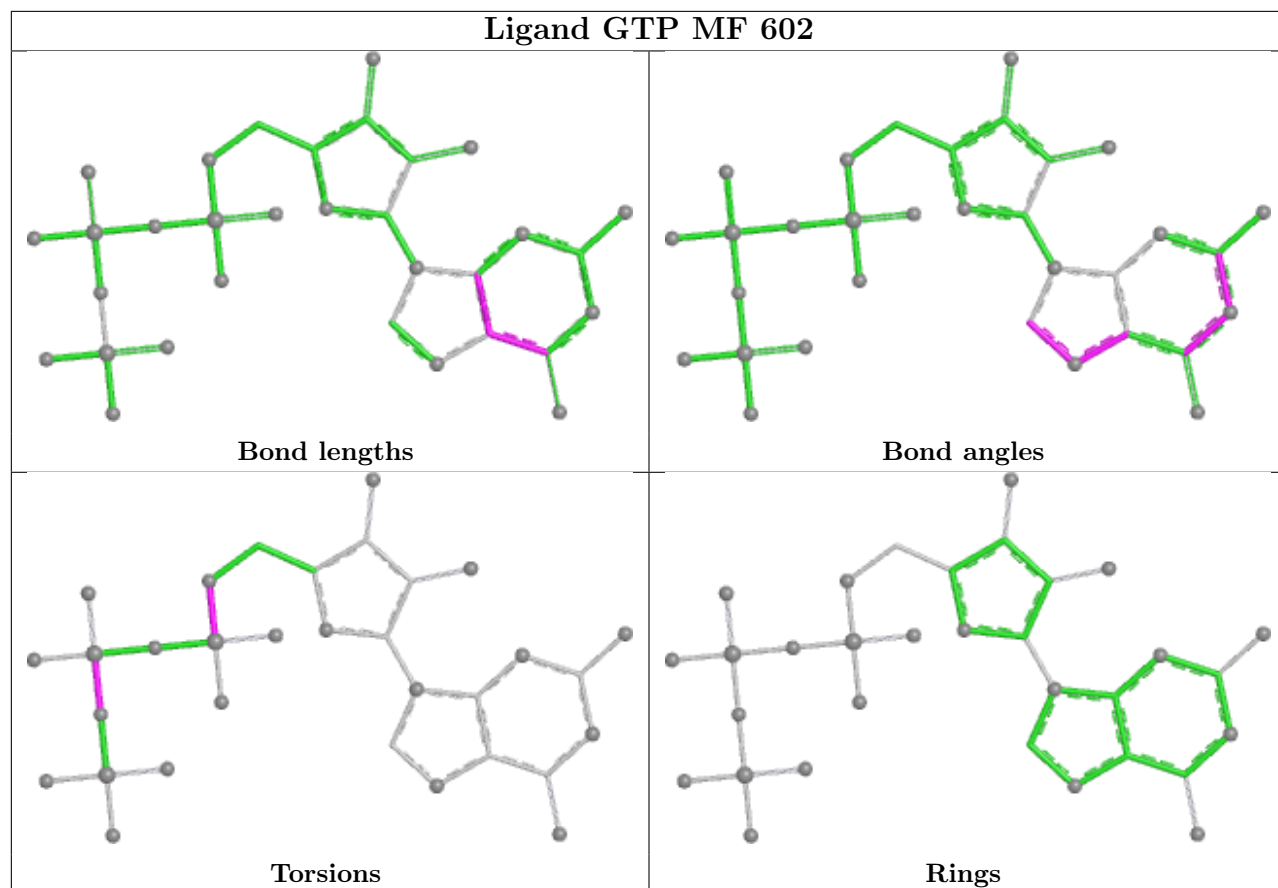
## Ligand GTP HK 501



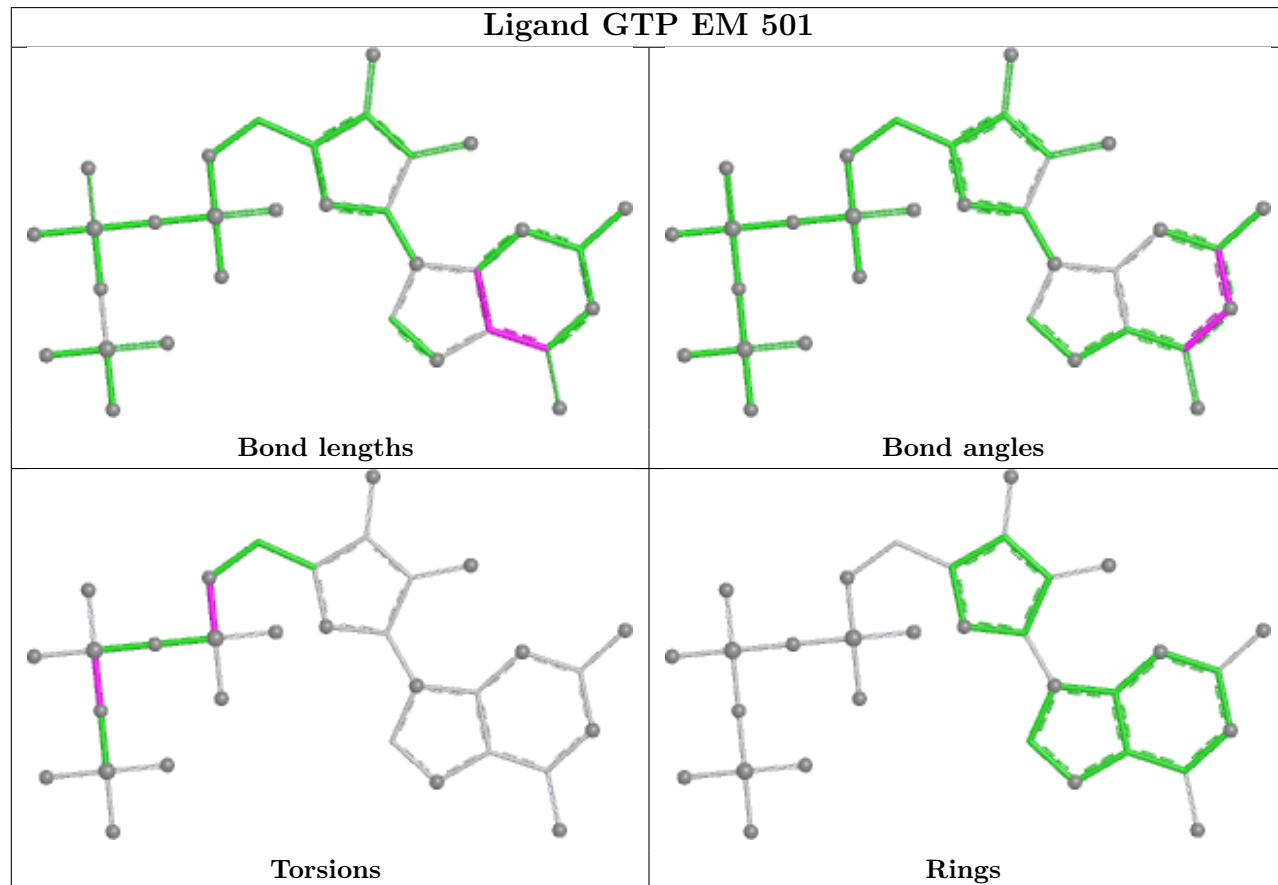
## Ligand GDP ZI 501



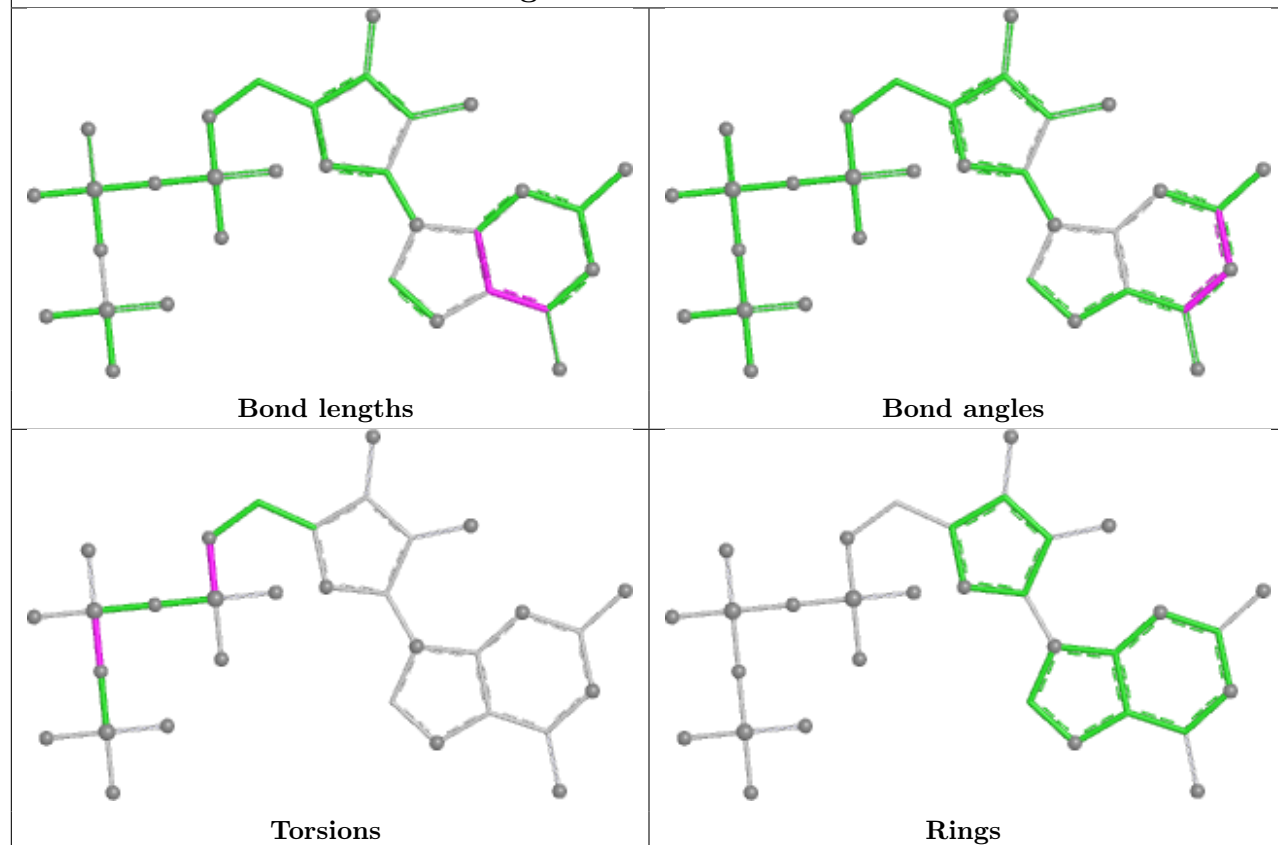
## Ligand GTP MF 602



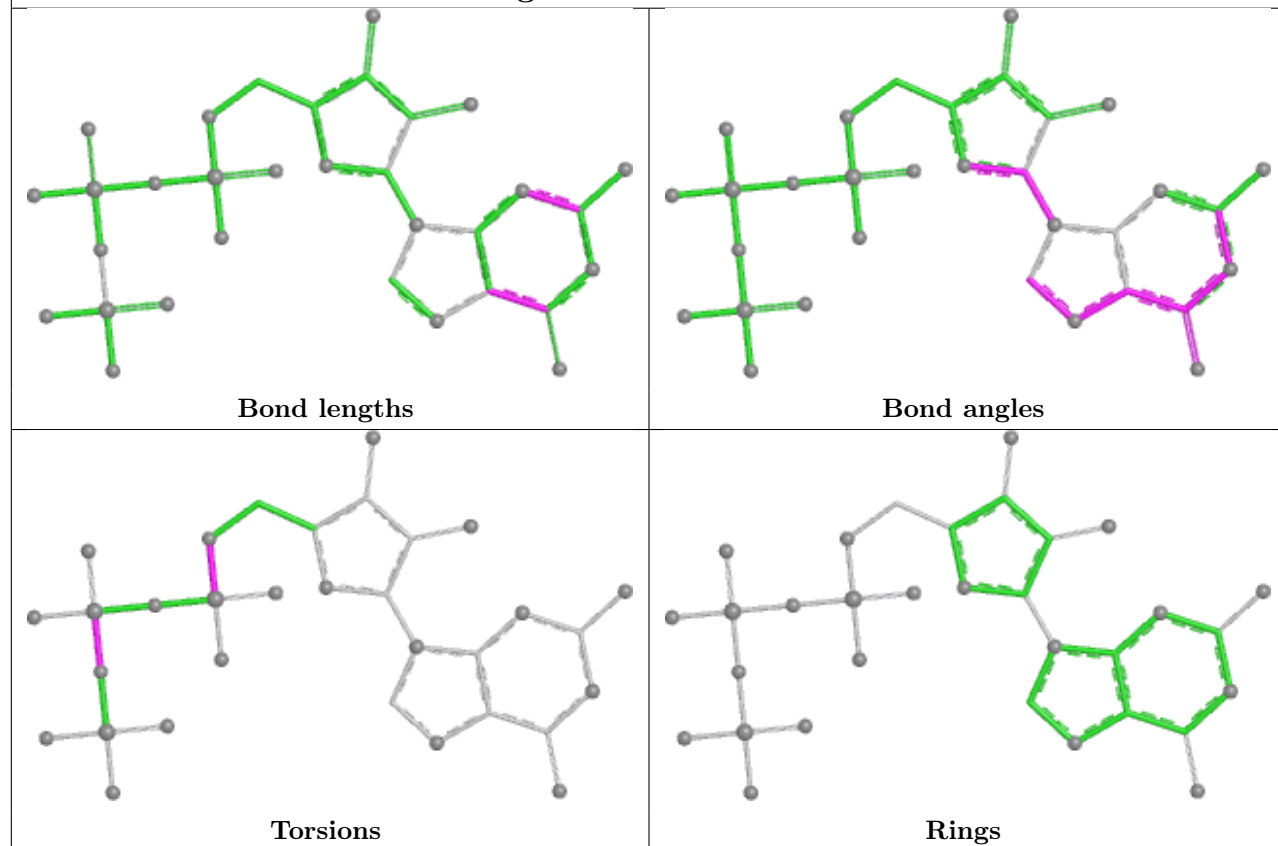
## Ligand GTP EM 501

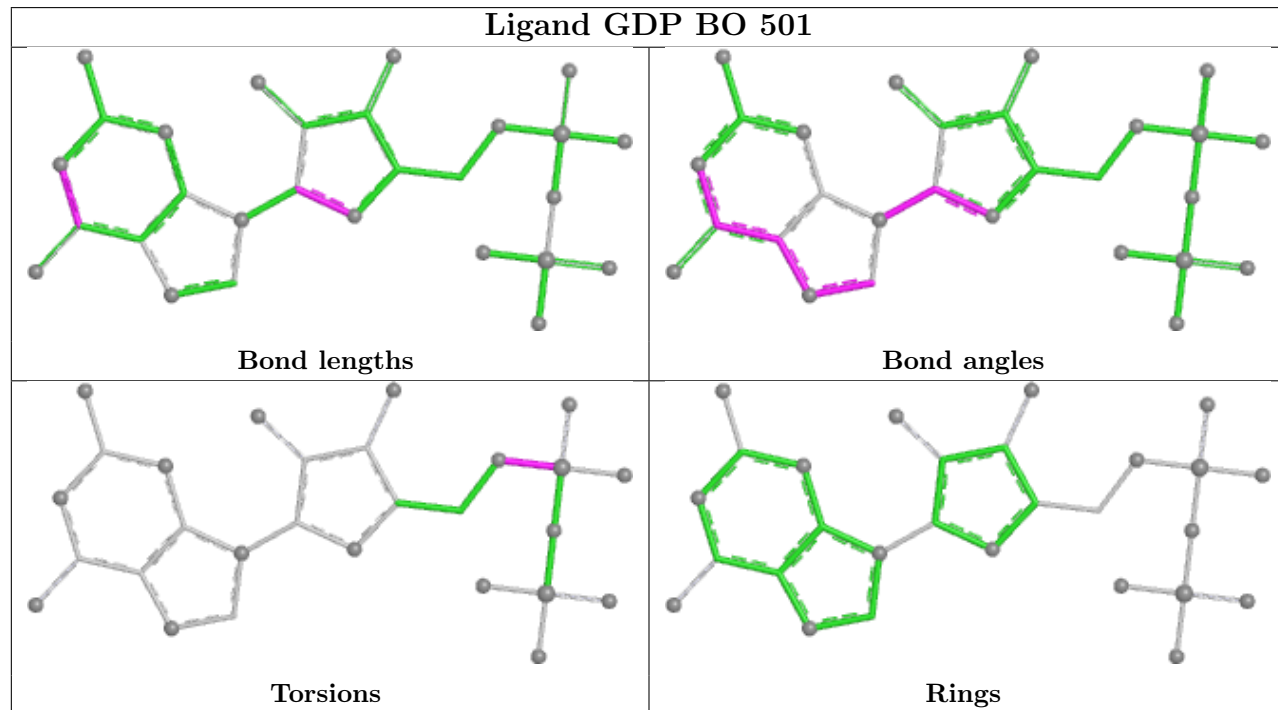
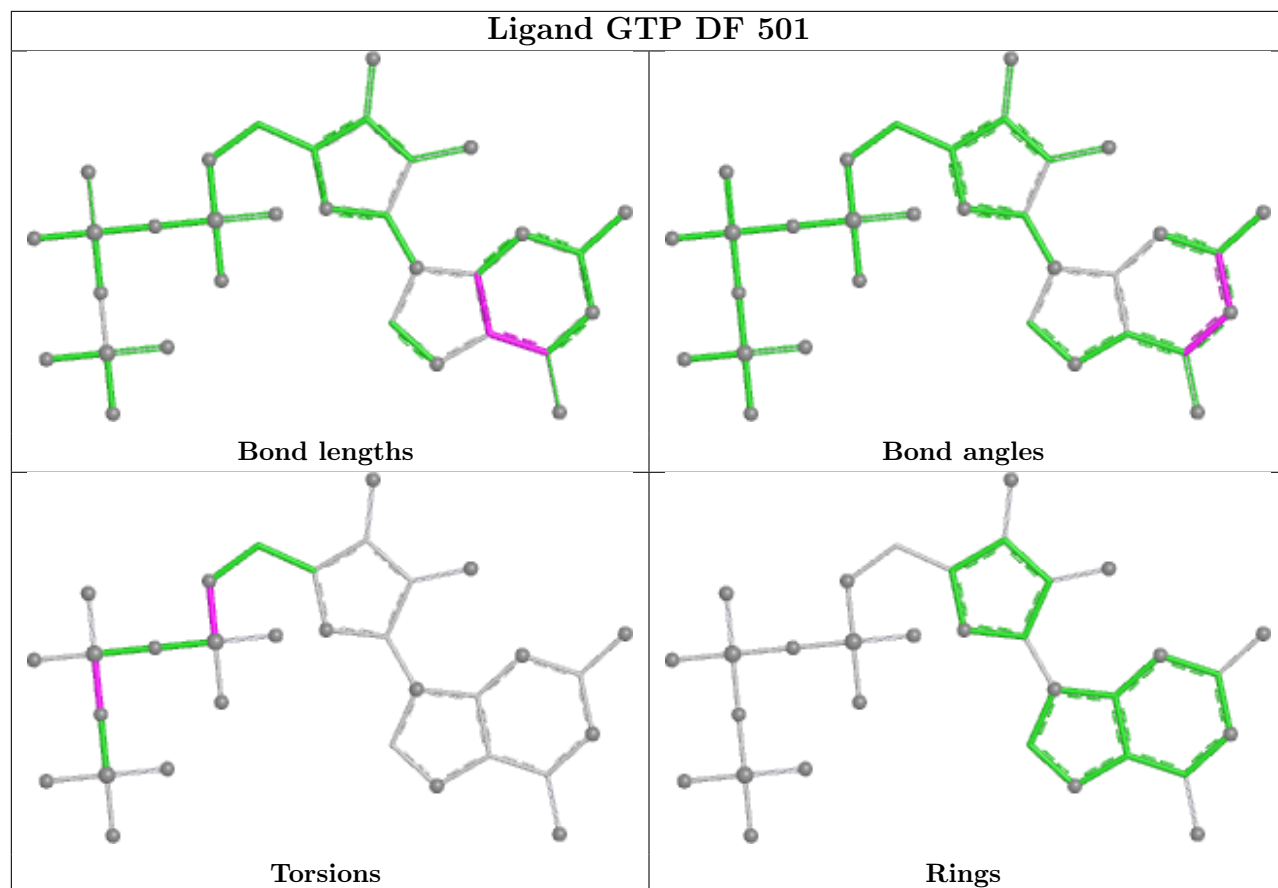


## Ligand GTP ZB 501

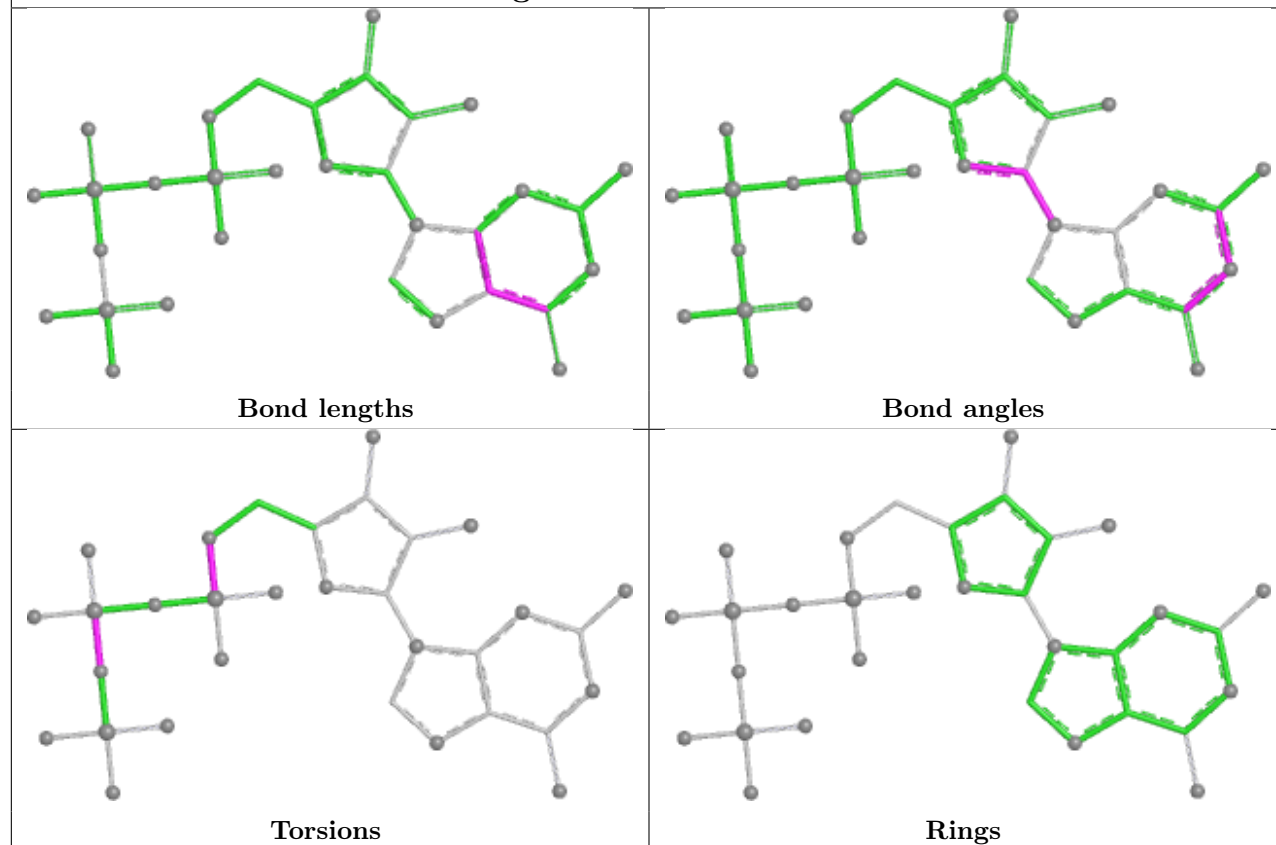


## Ligand GTP BN 602

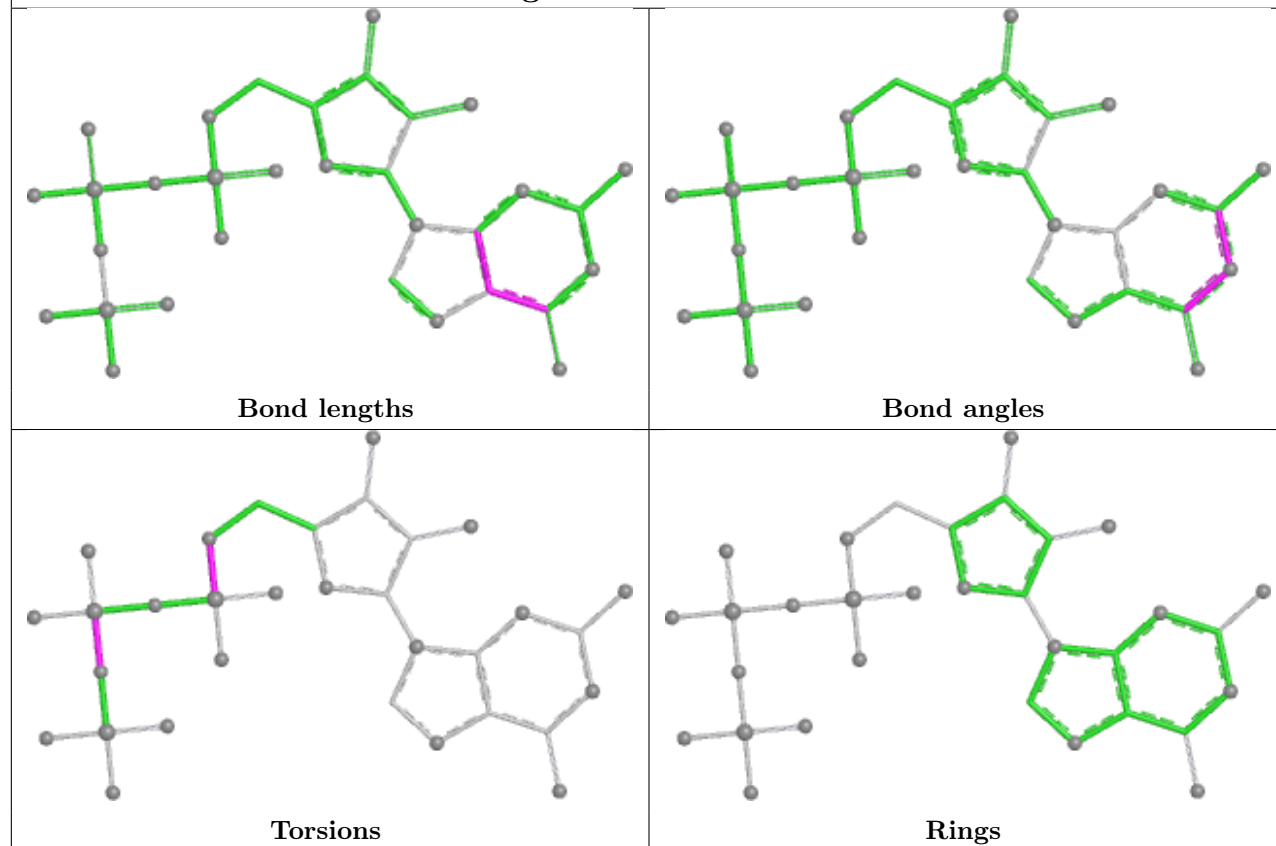




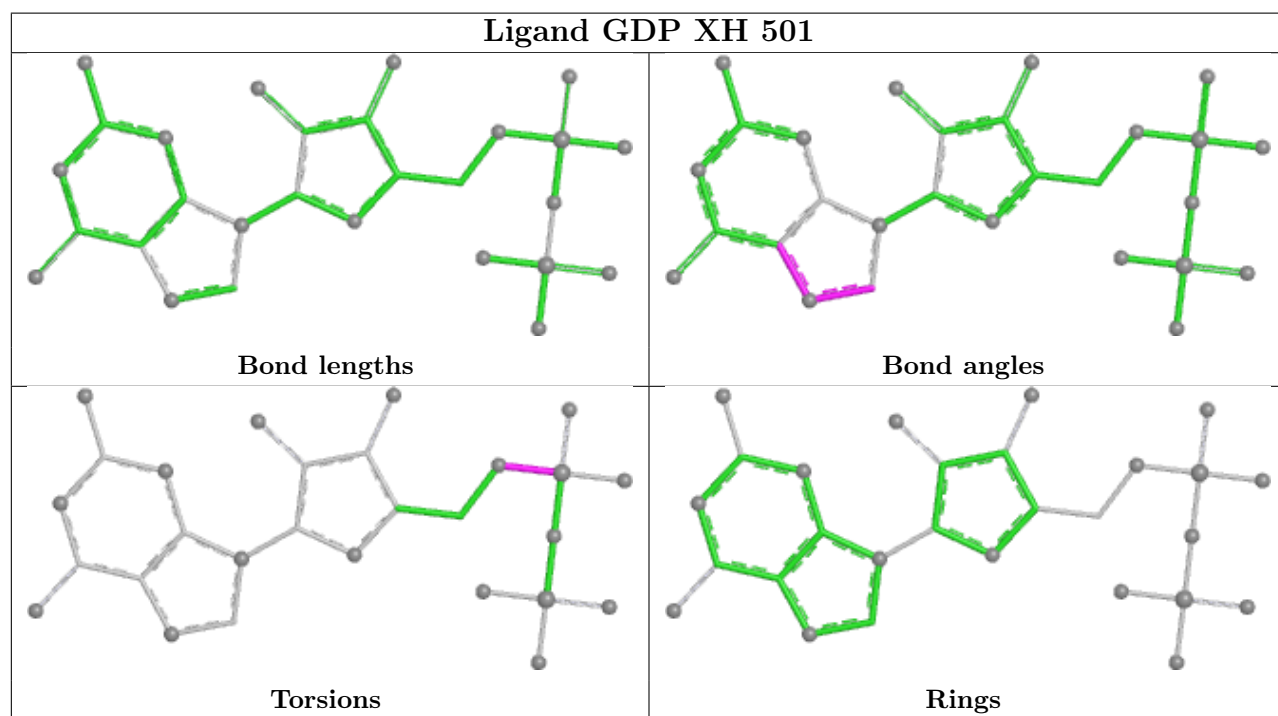
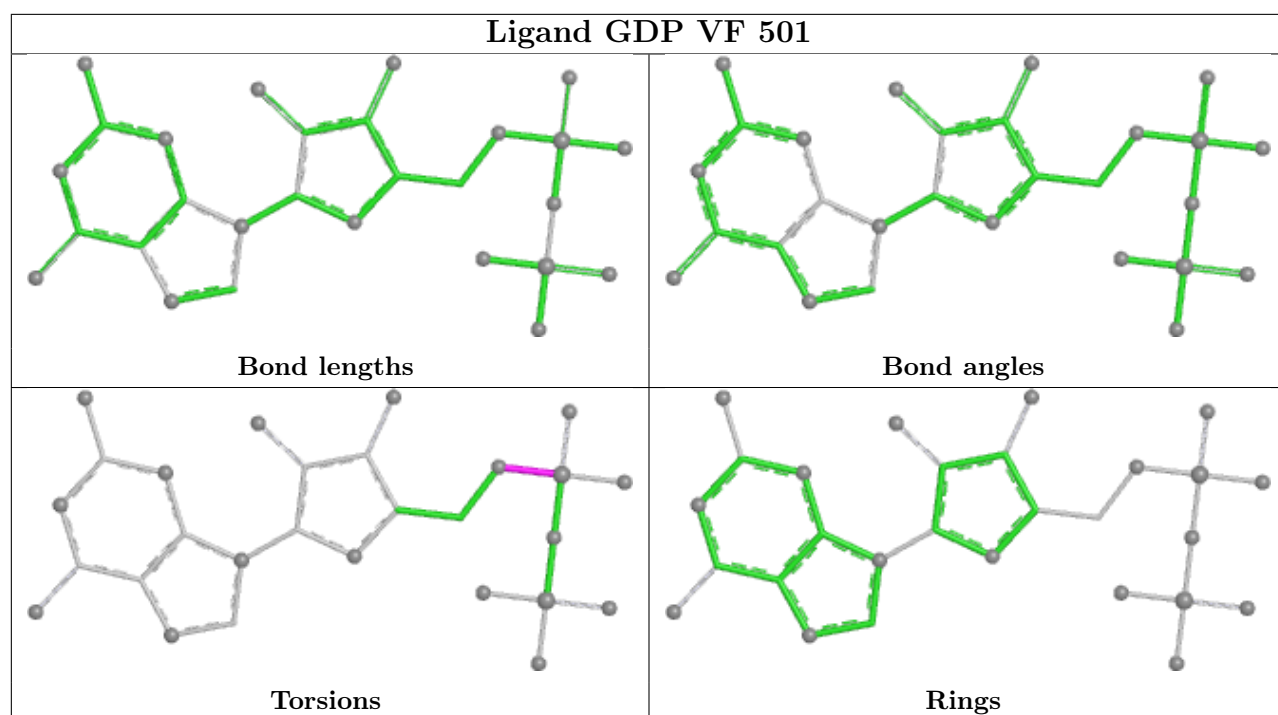
## Ligand GTP HM 602

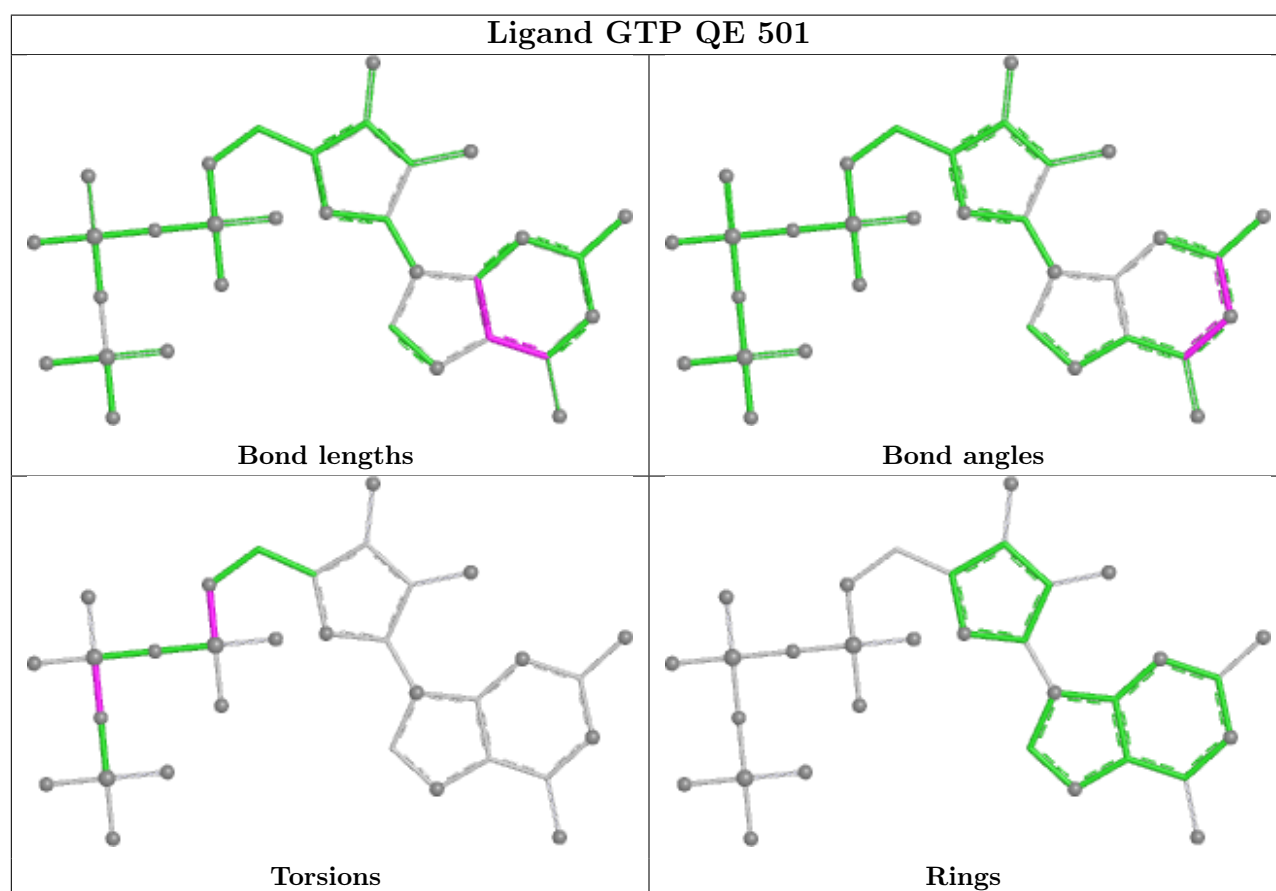
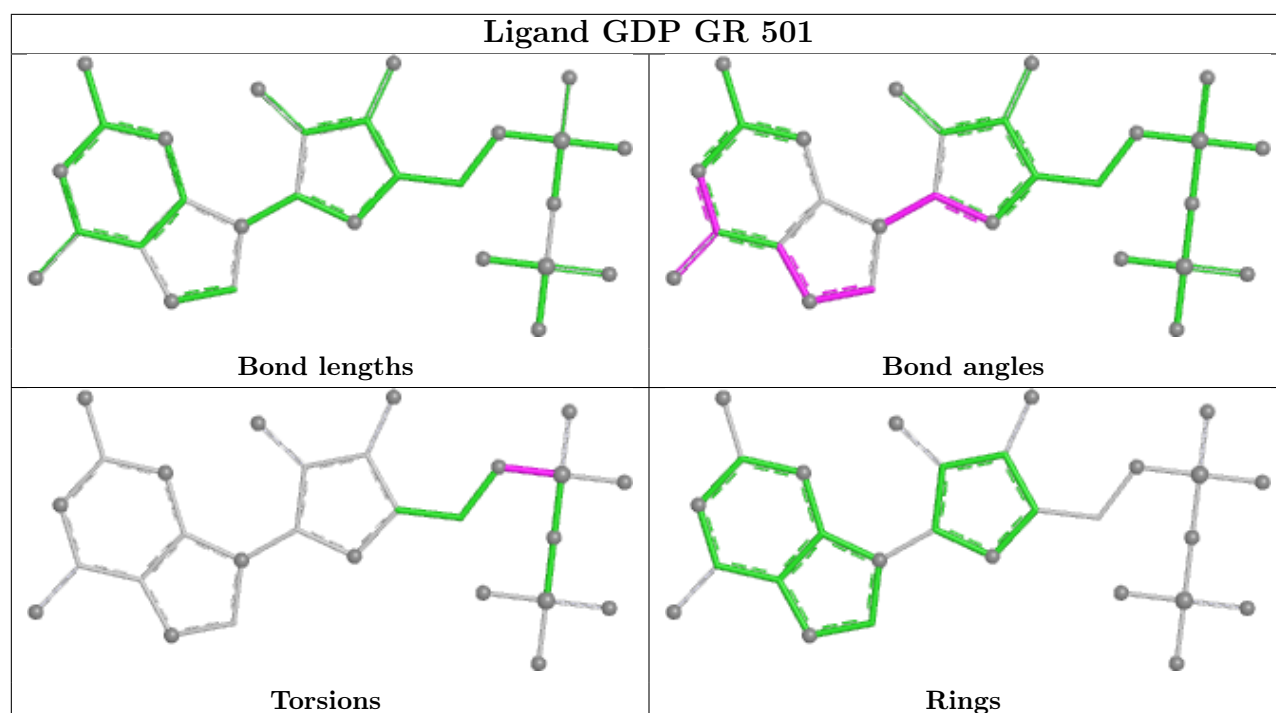


## Ligand GTP LL 501

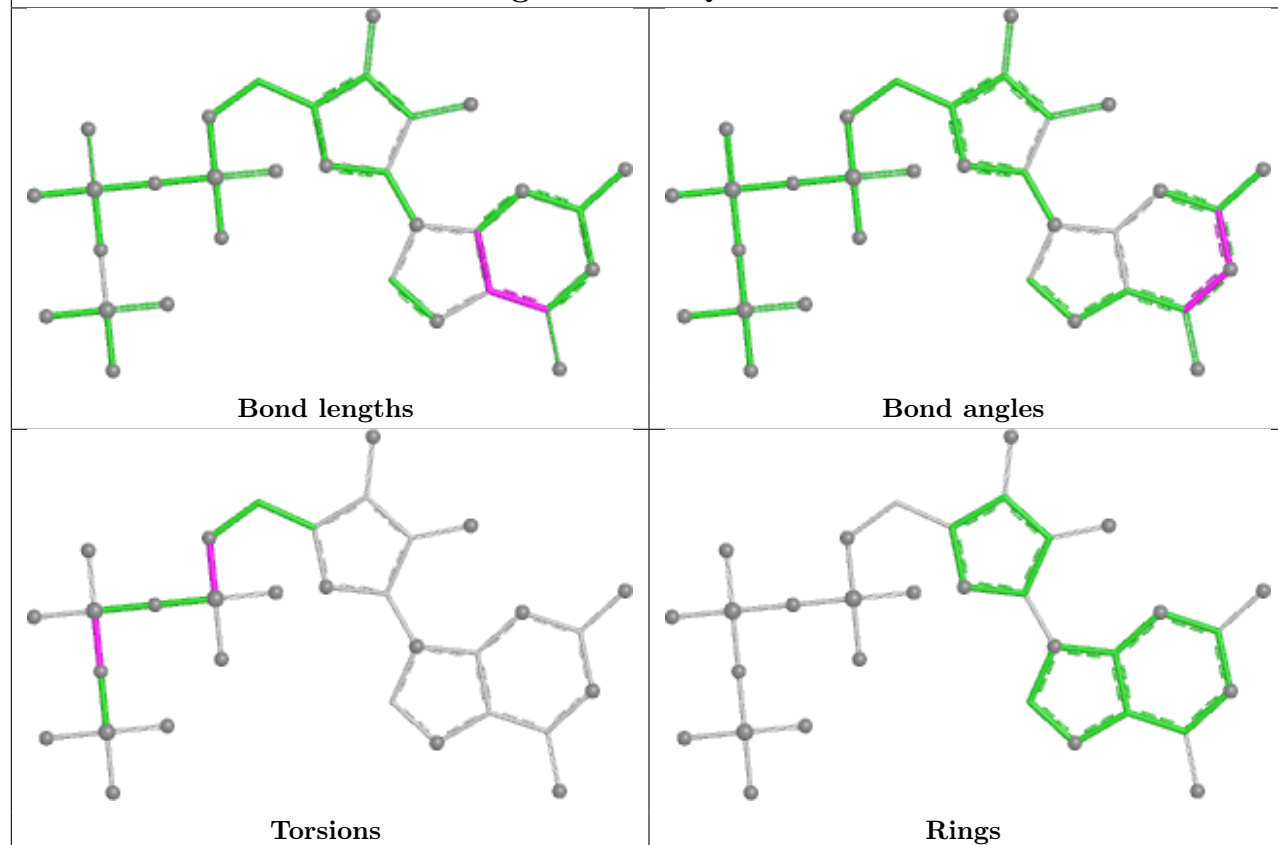




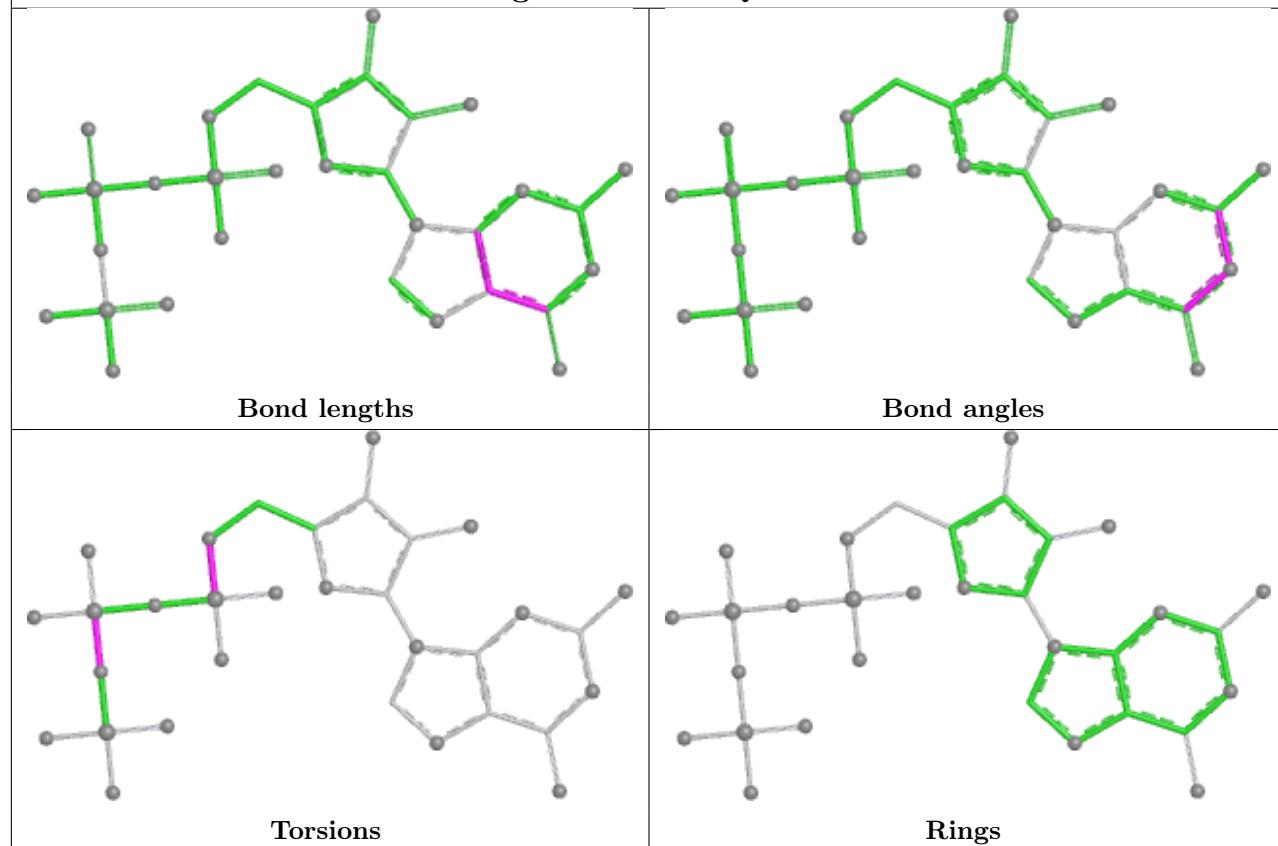




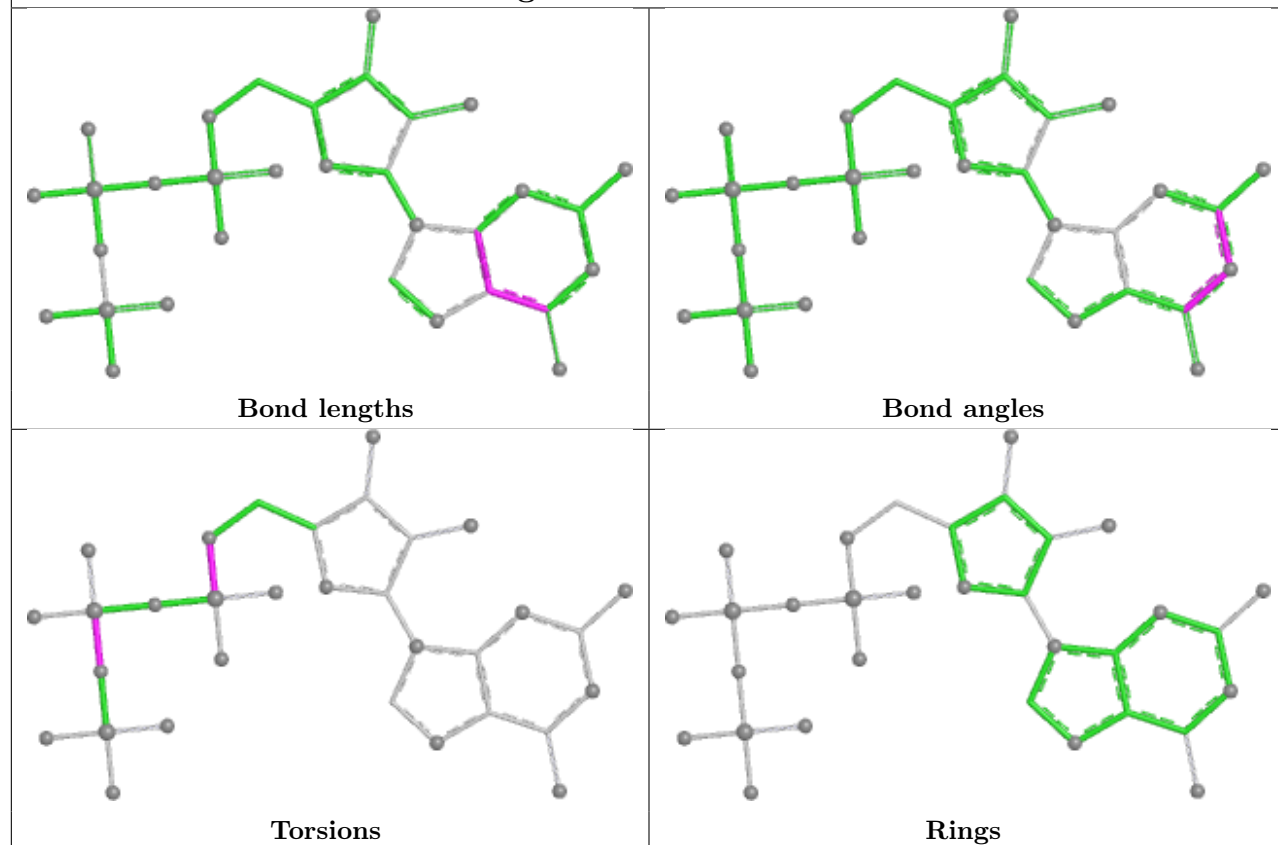
## Ligand GTP QW 501



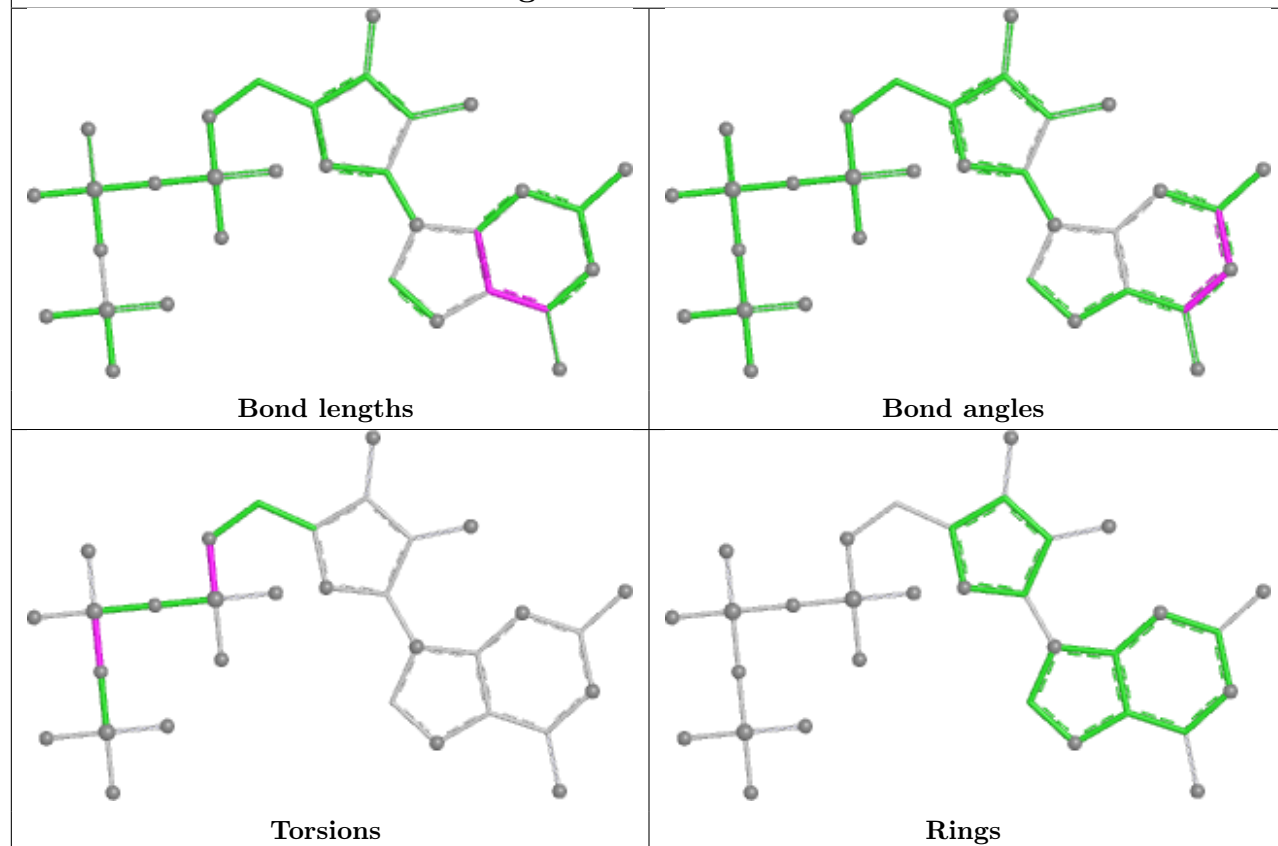
## Ligand GTP WQ 602

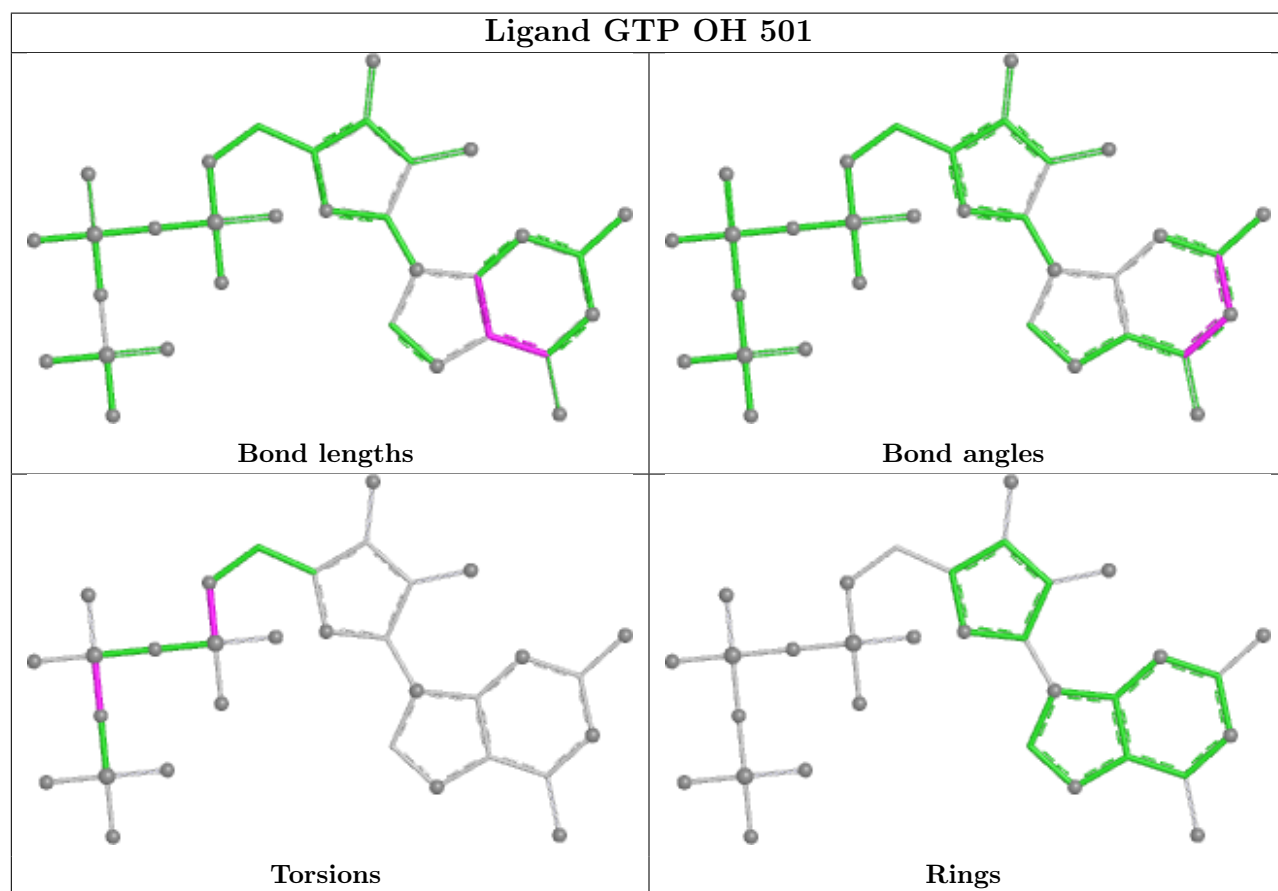
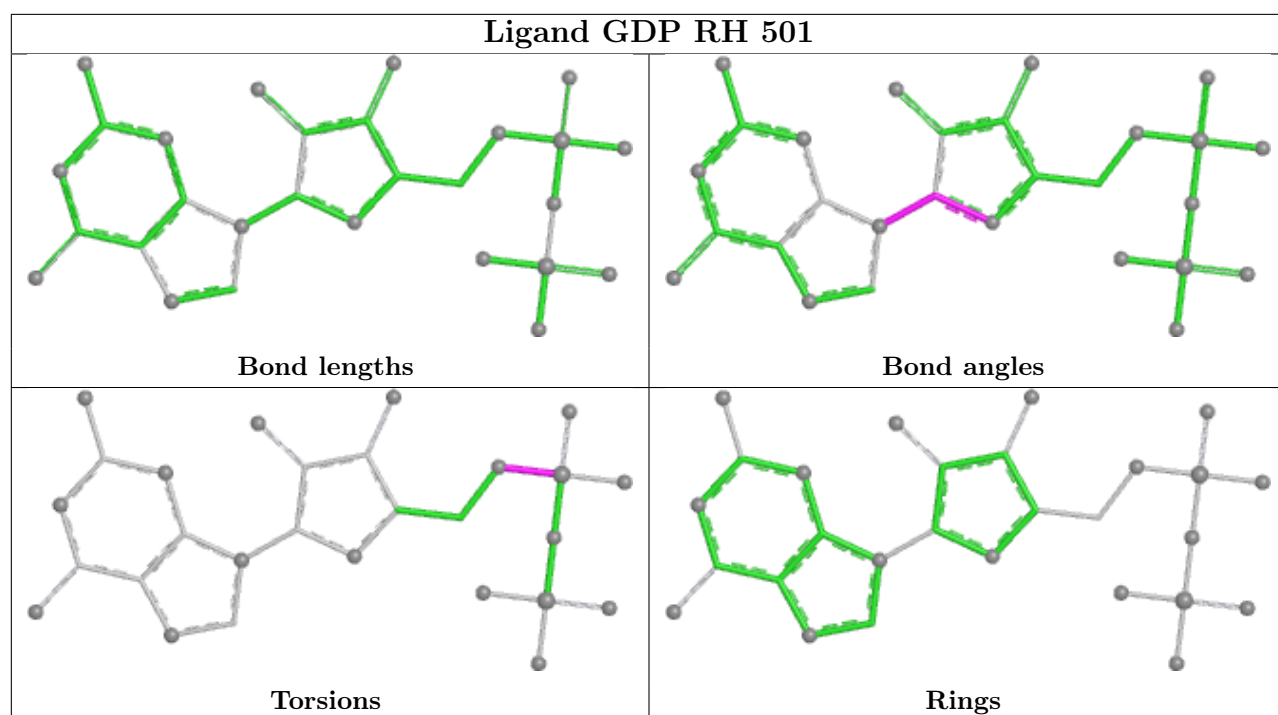


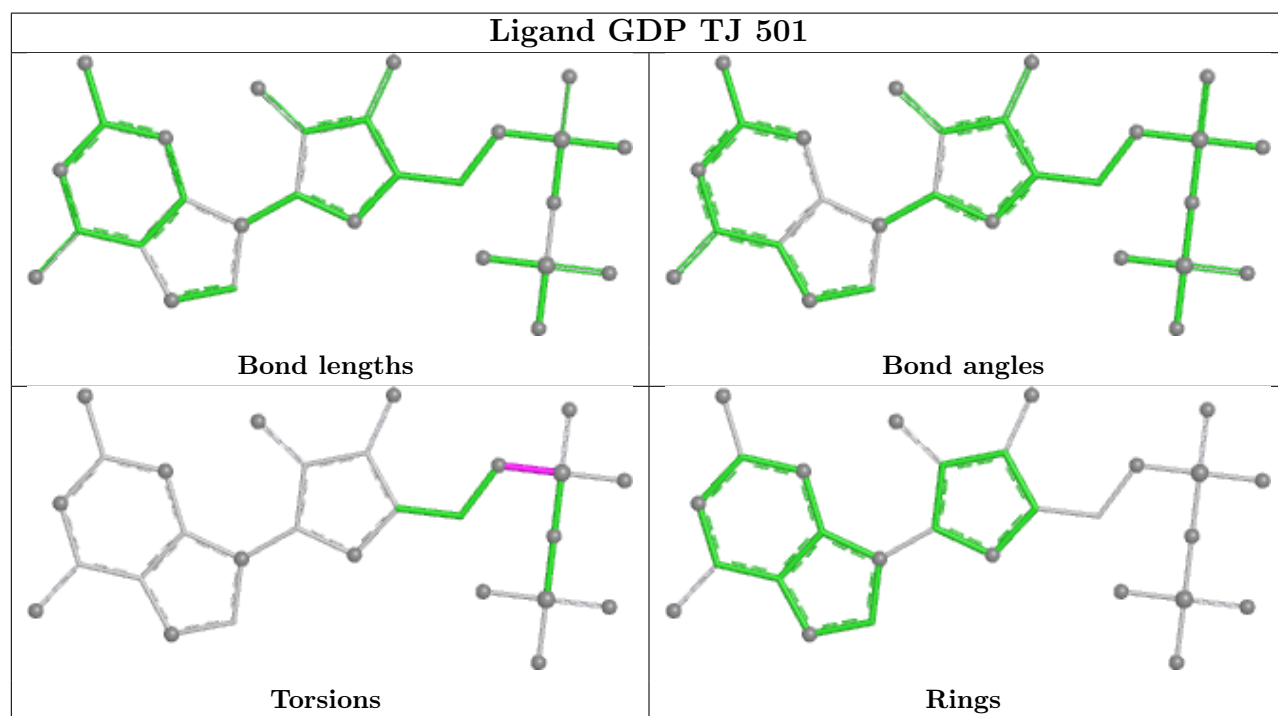
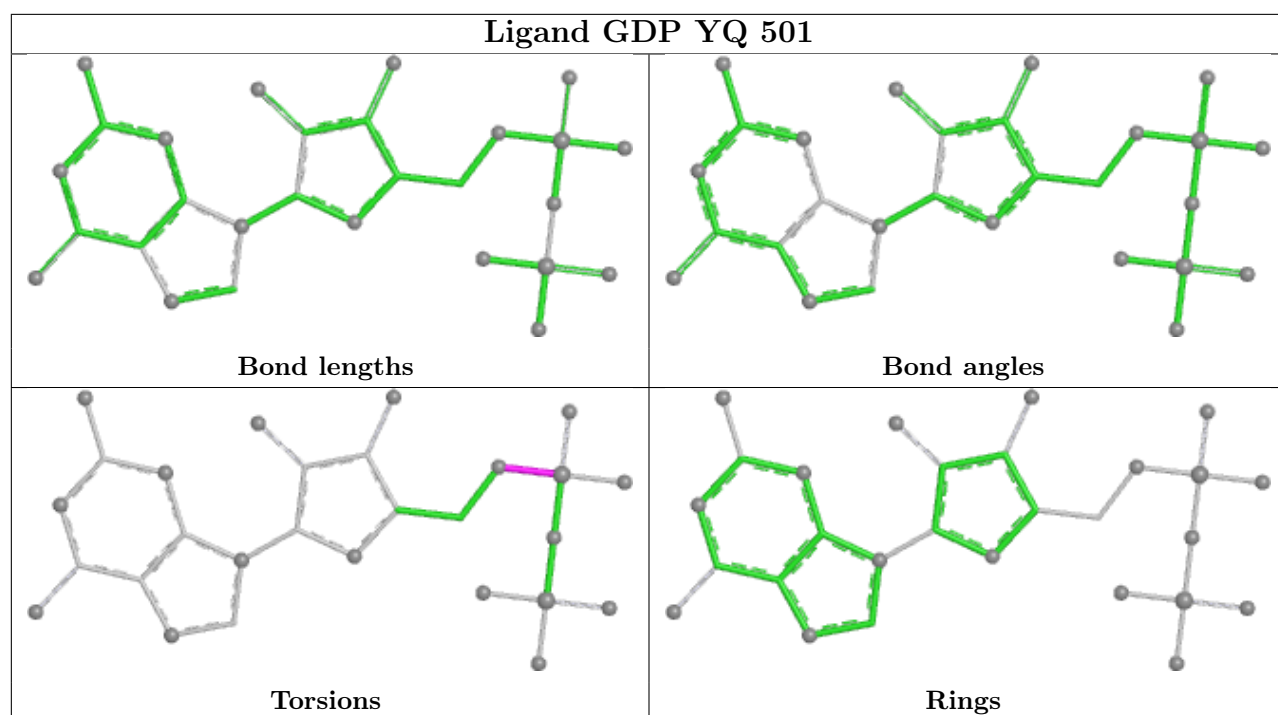
## Ligand GTP TV 501

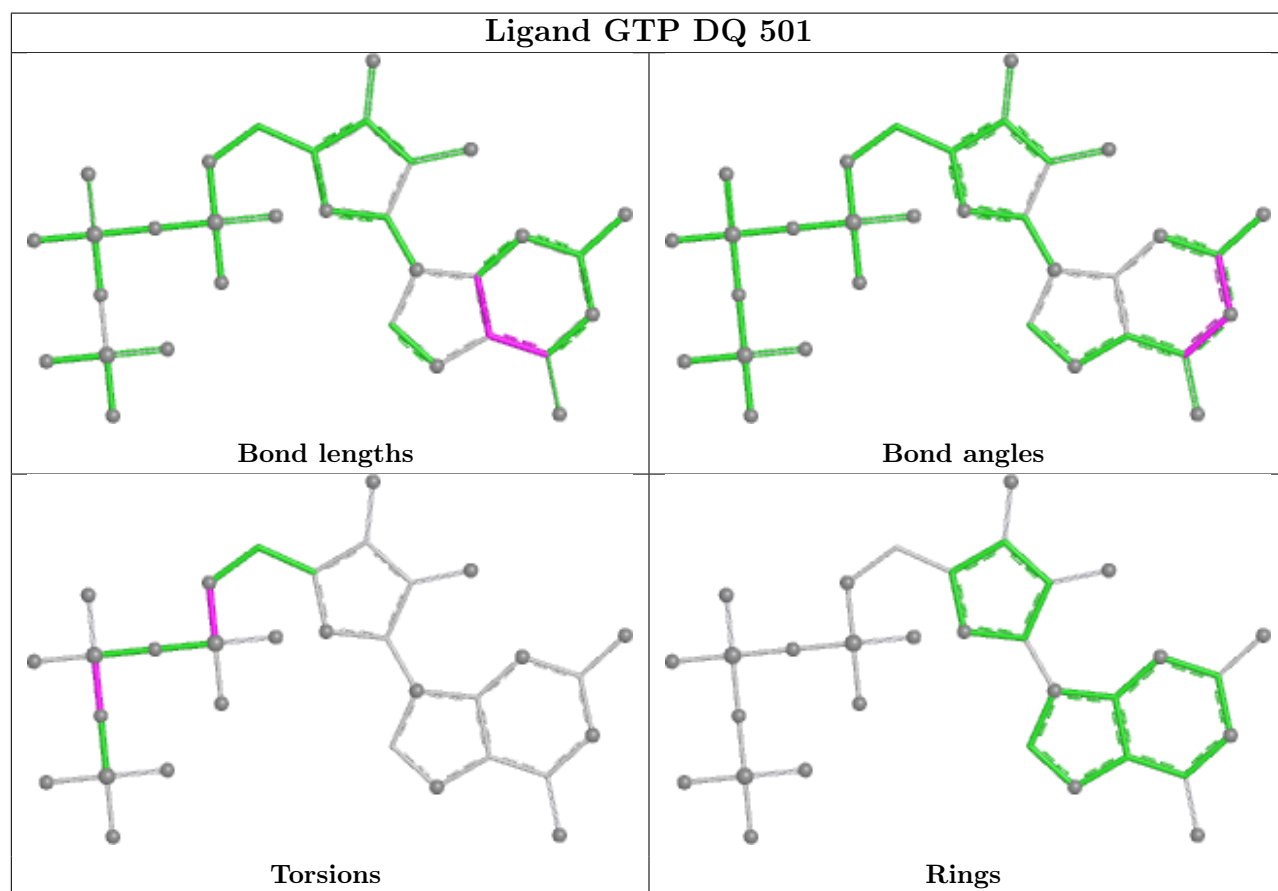
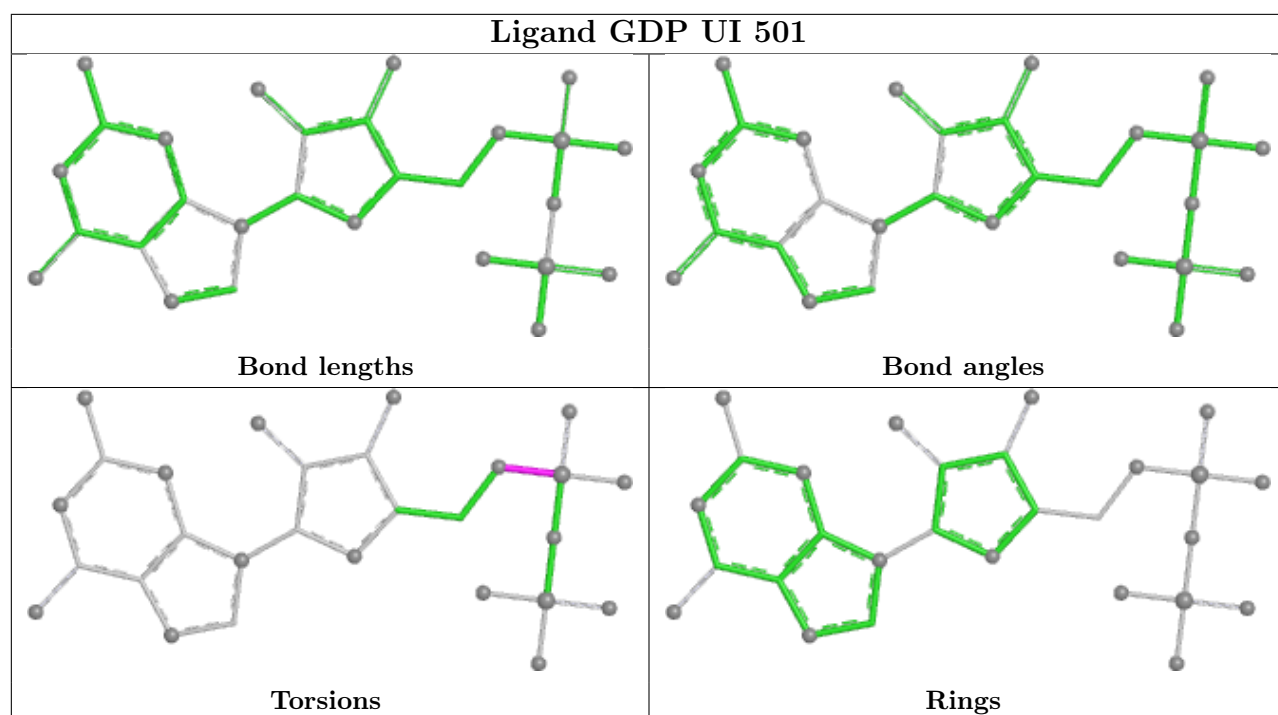


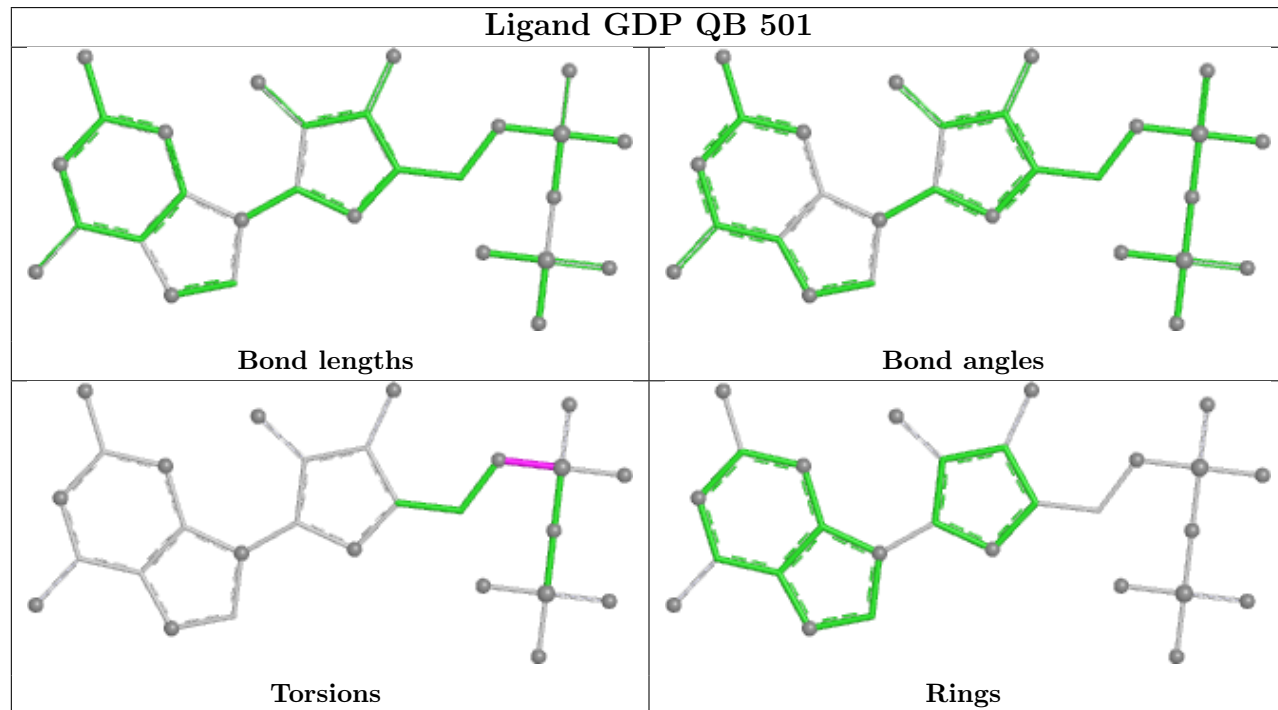
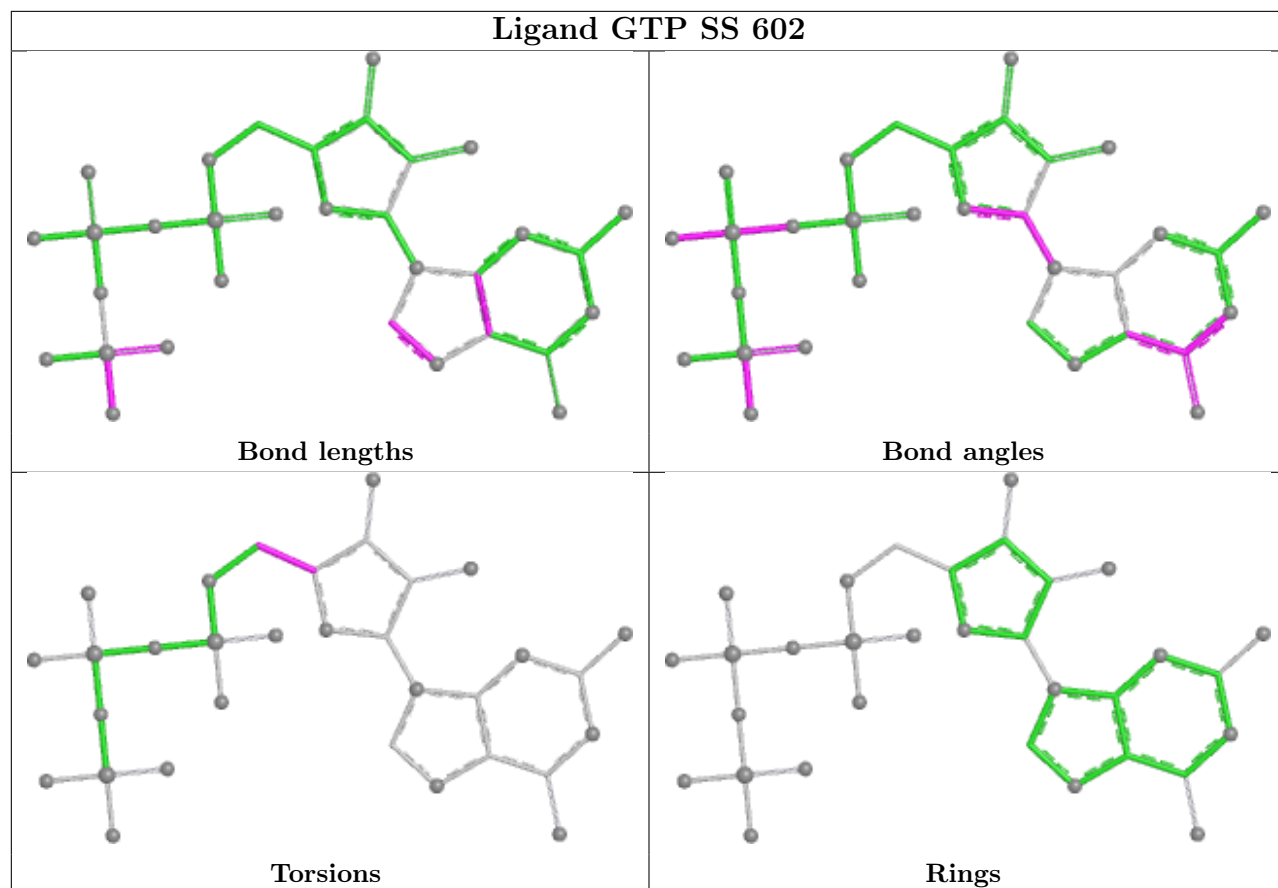
## Ligand GTP EO 501



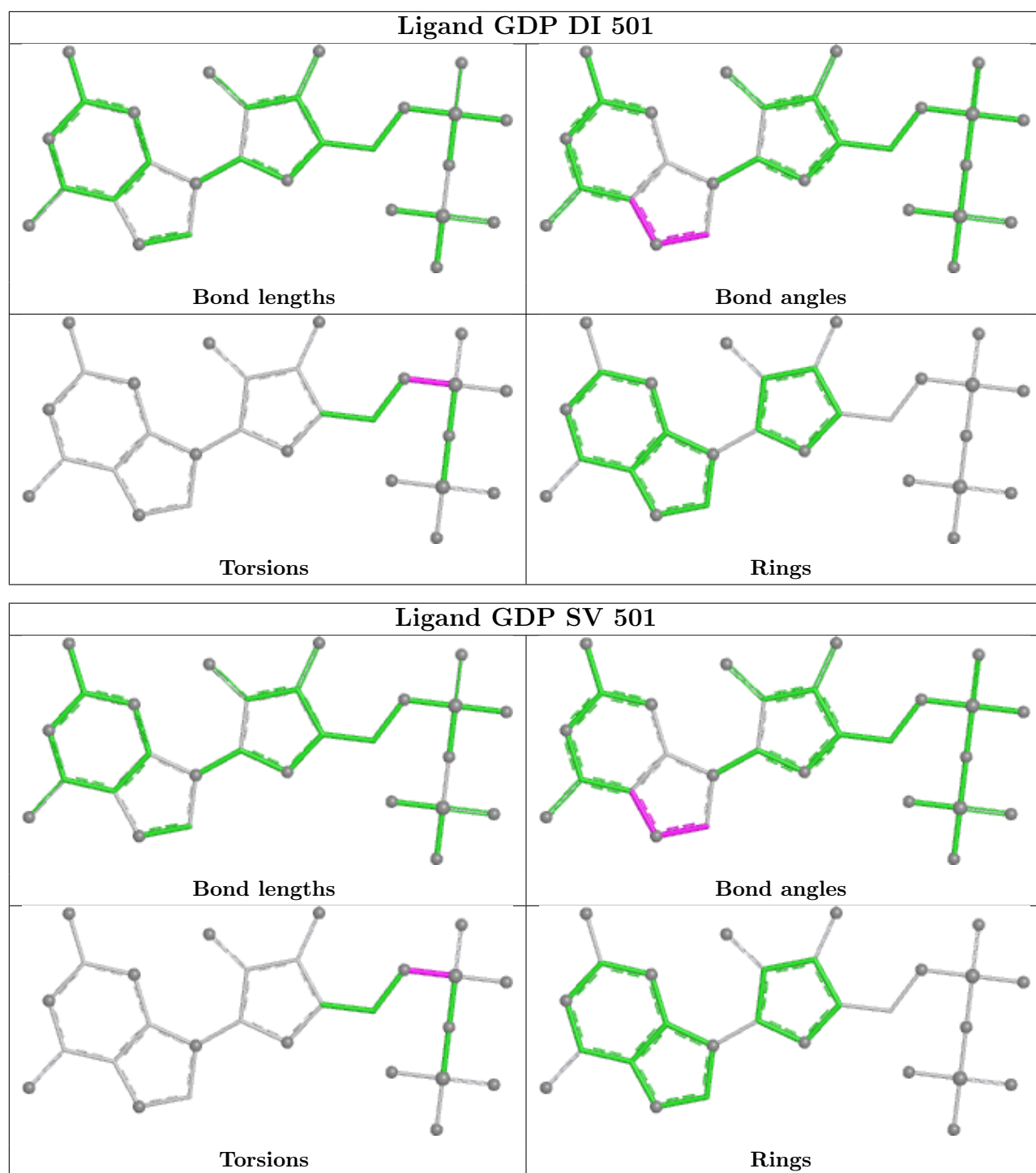




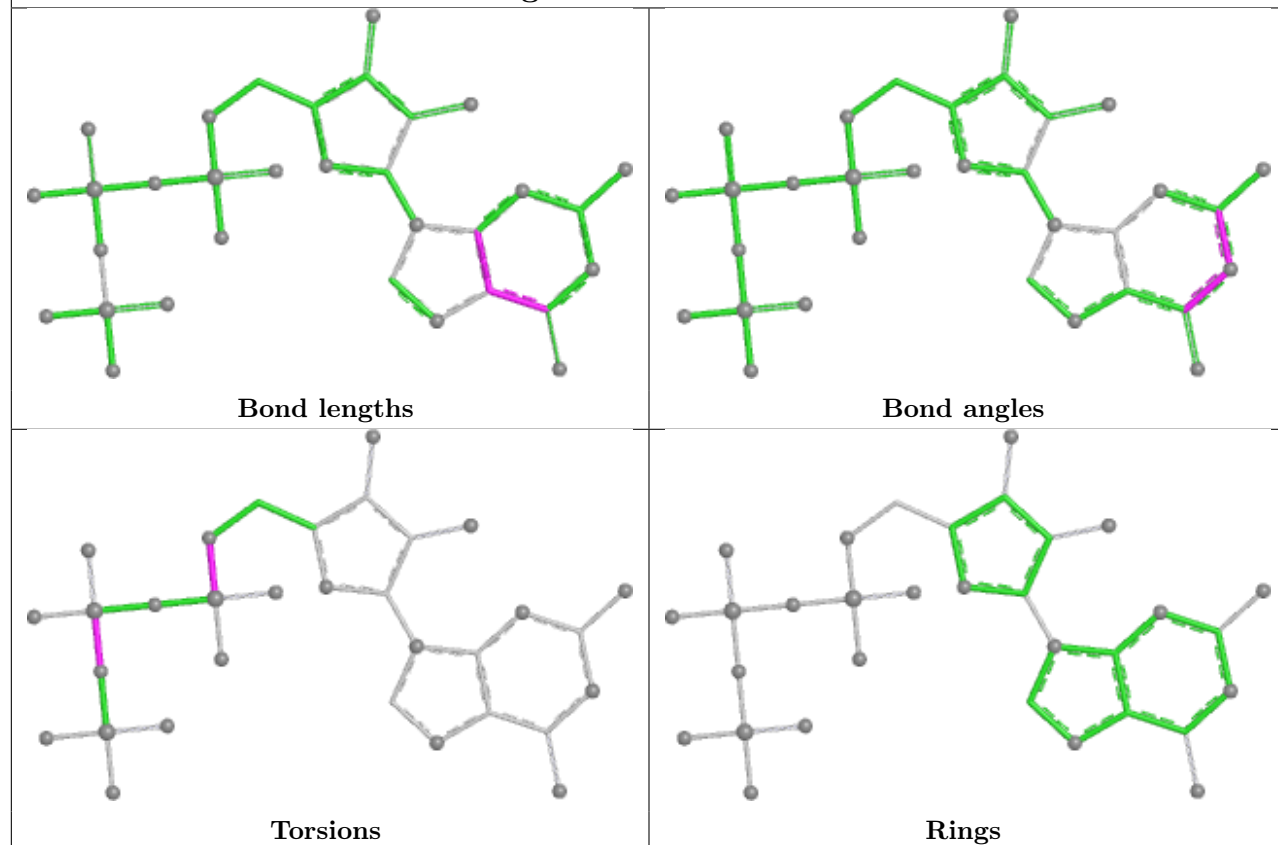




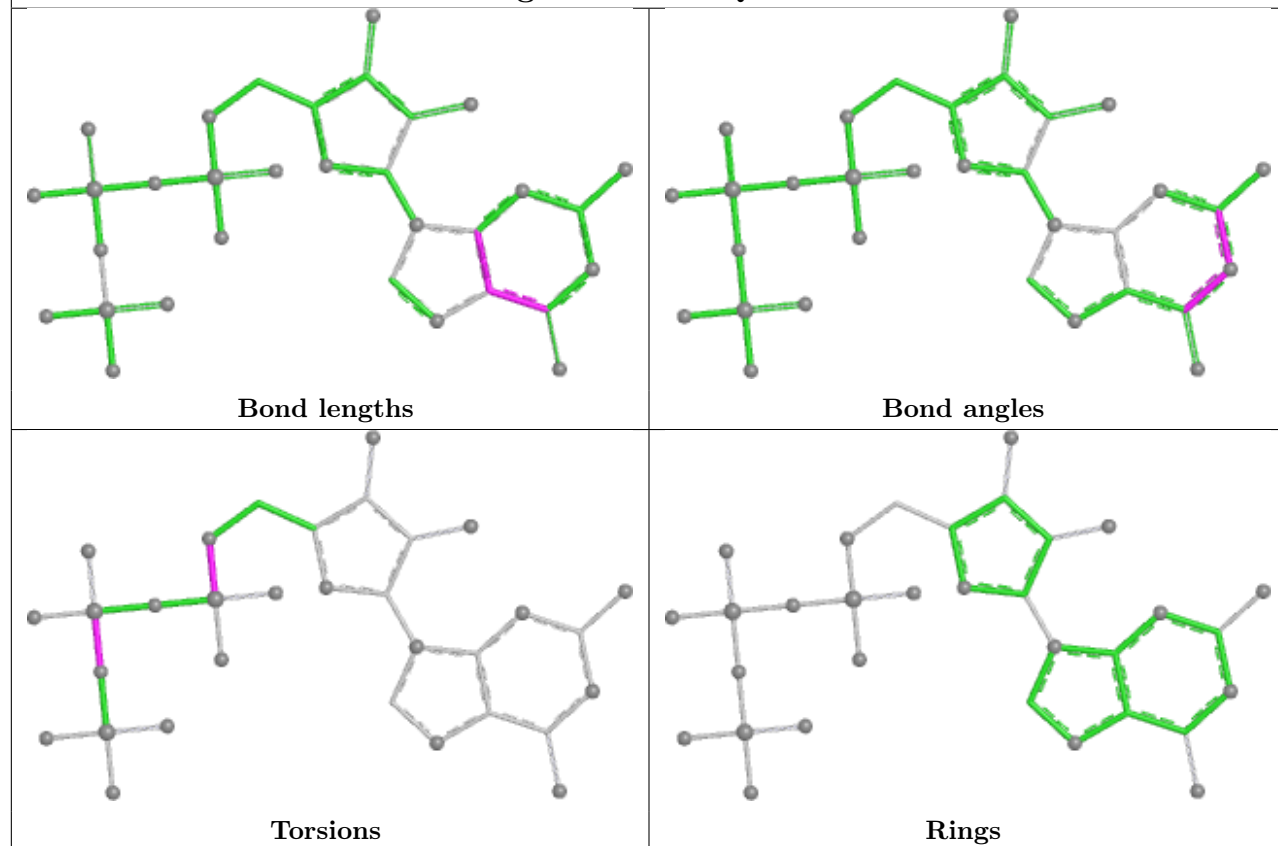




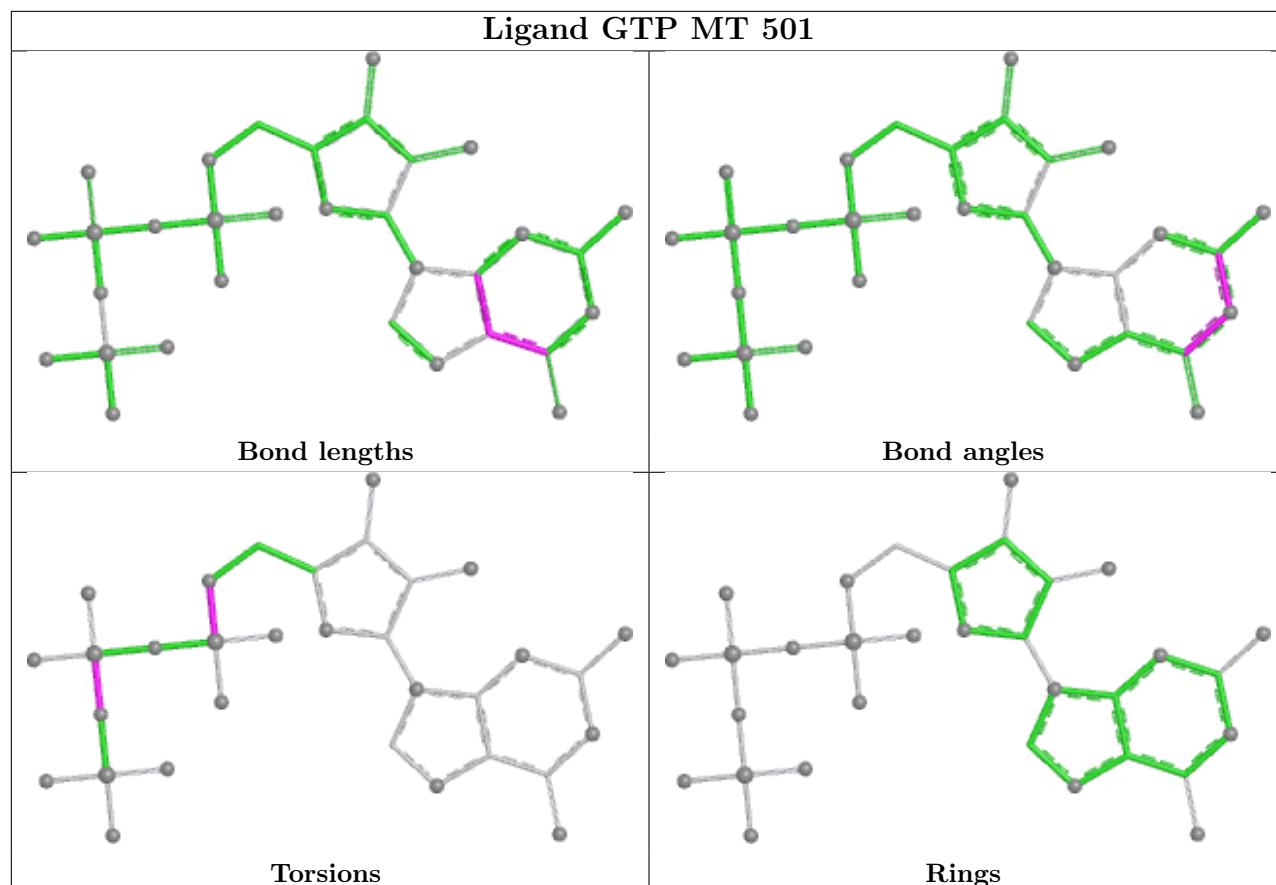
## Ligand GTP ZF 602



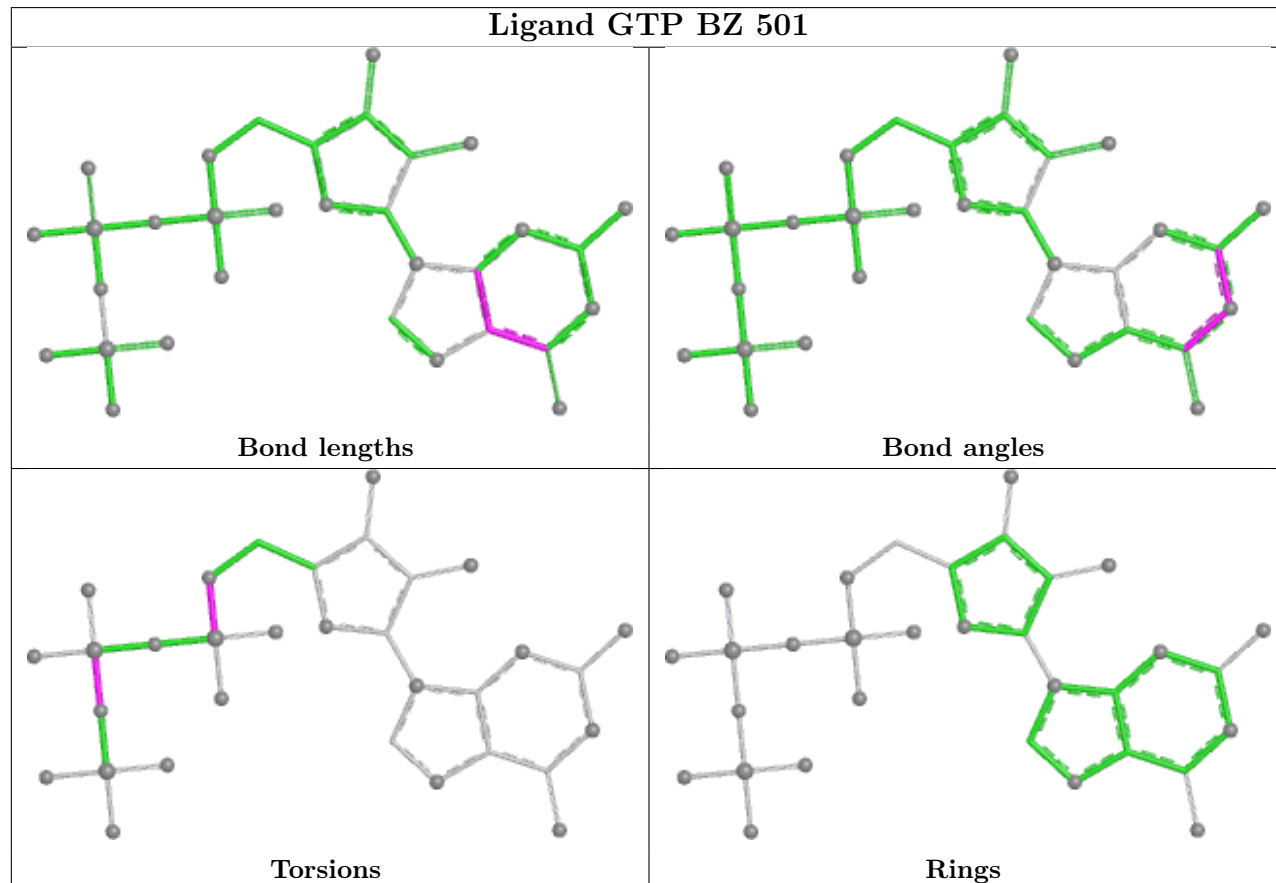
## Ligand GTP VQ 501

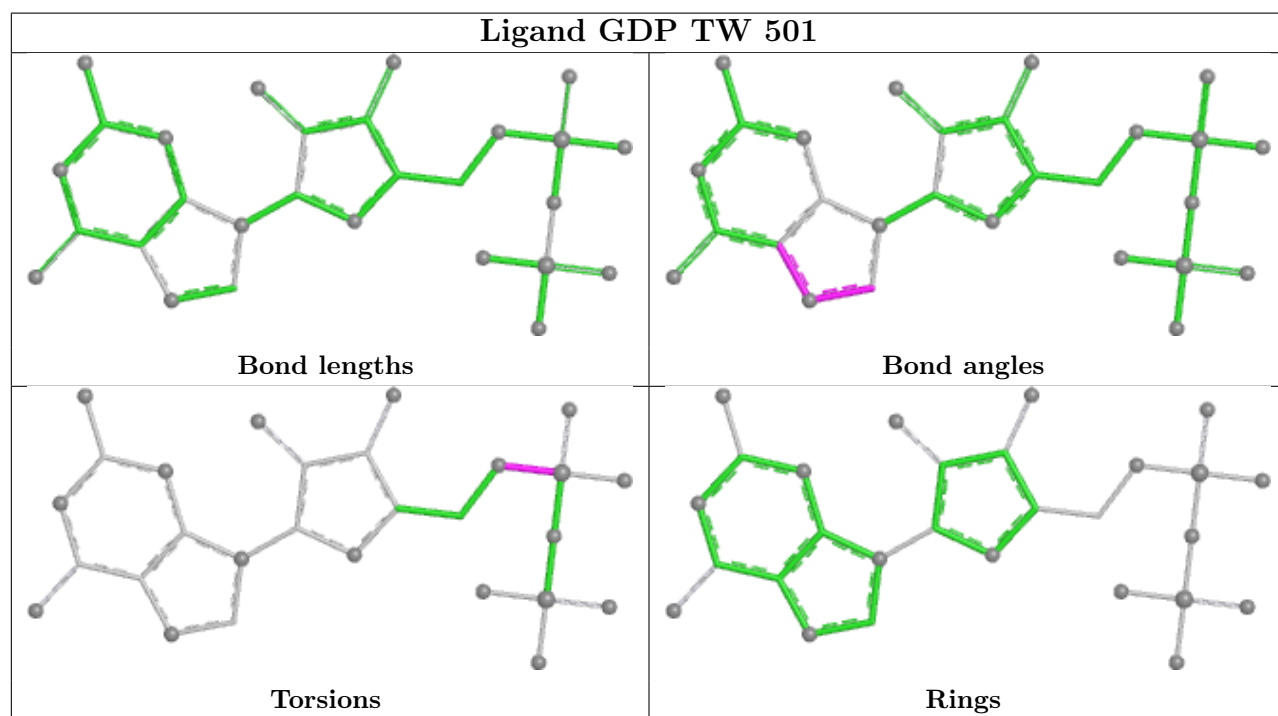
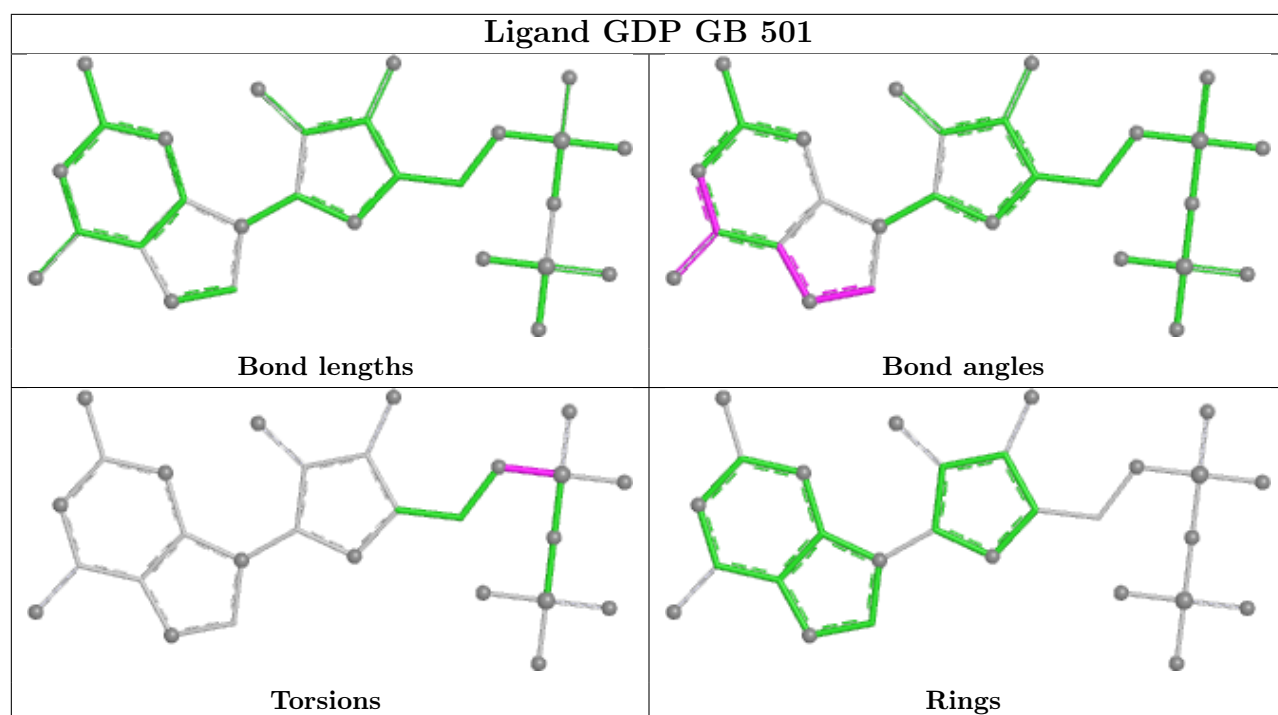


## Ligand GTP MT 501

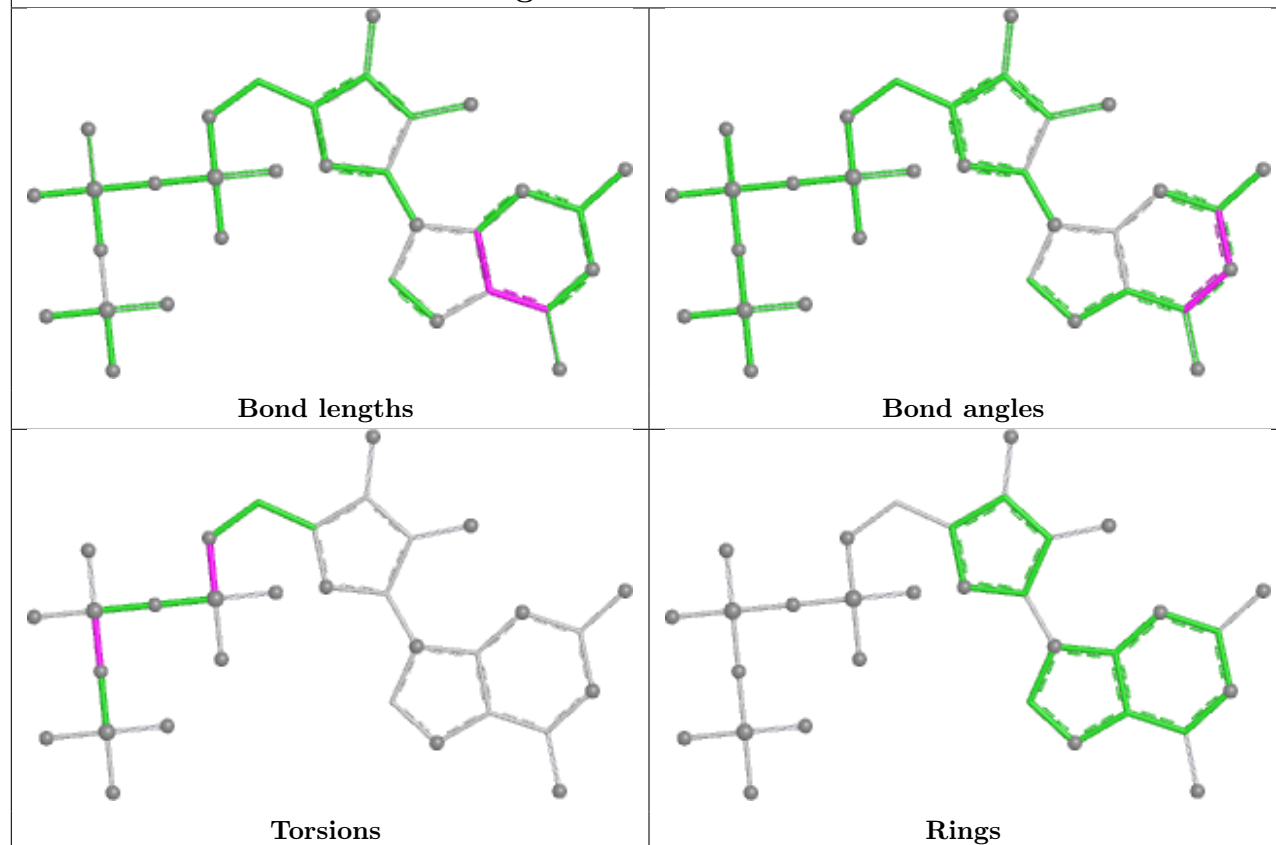


## Ligand GTP BZ 501

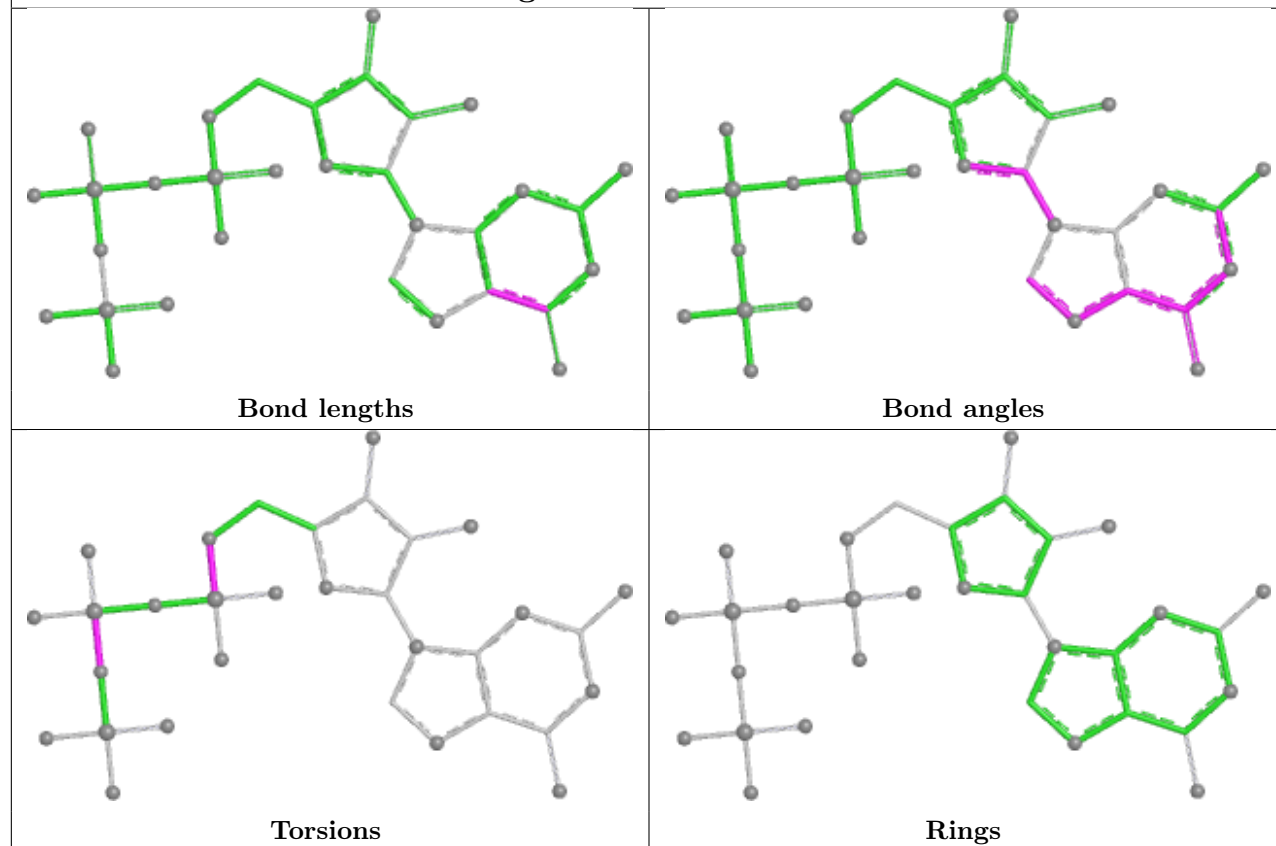




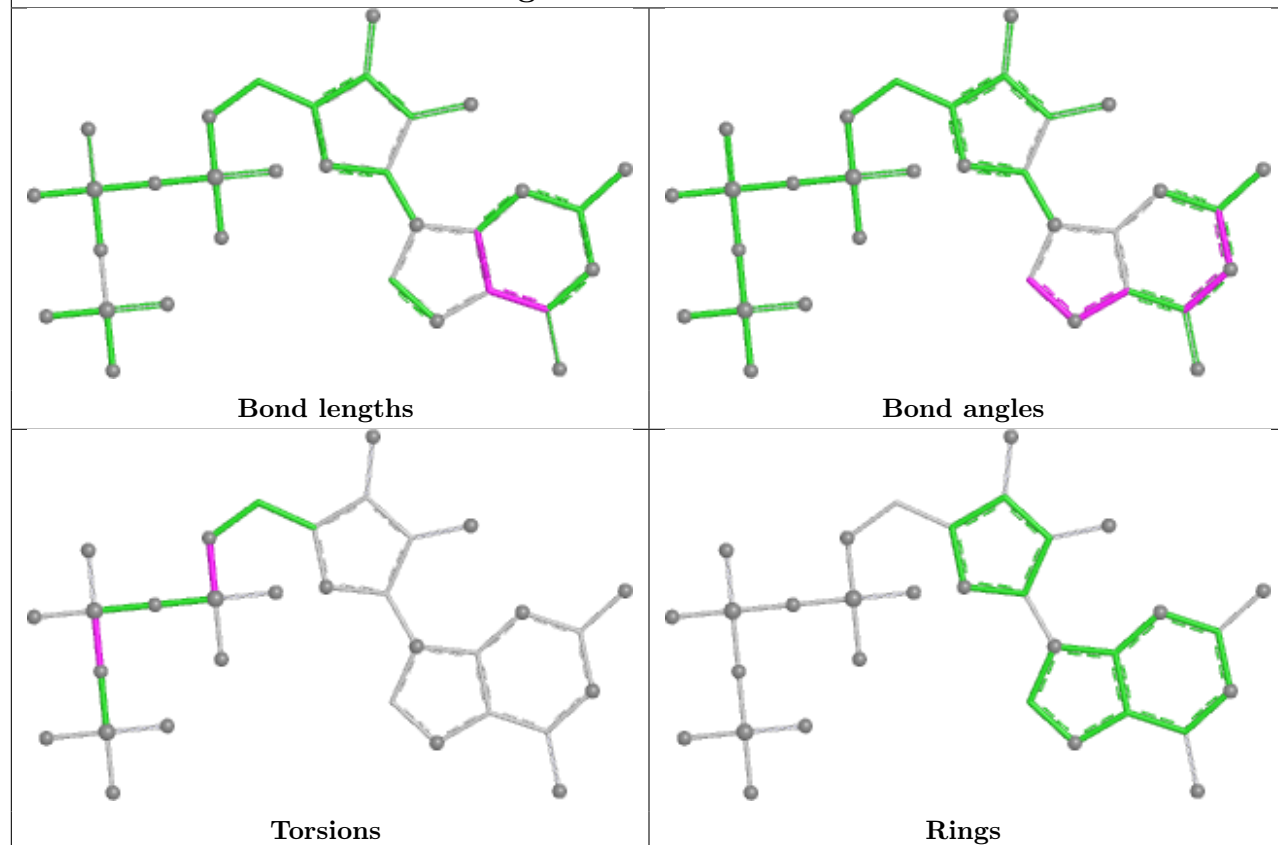
## Ligand GTP UH 501



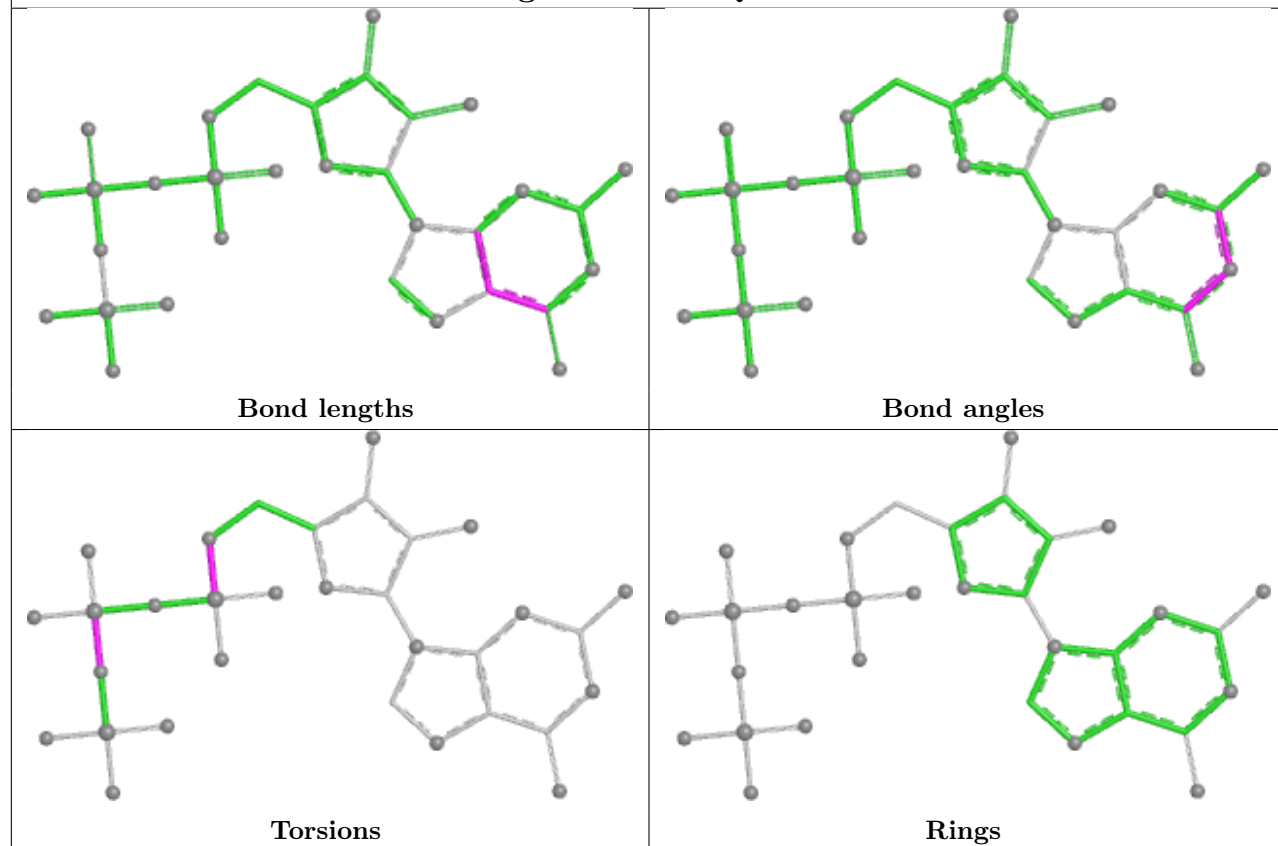
## Ligand GTP PC 602



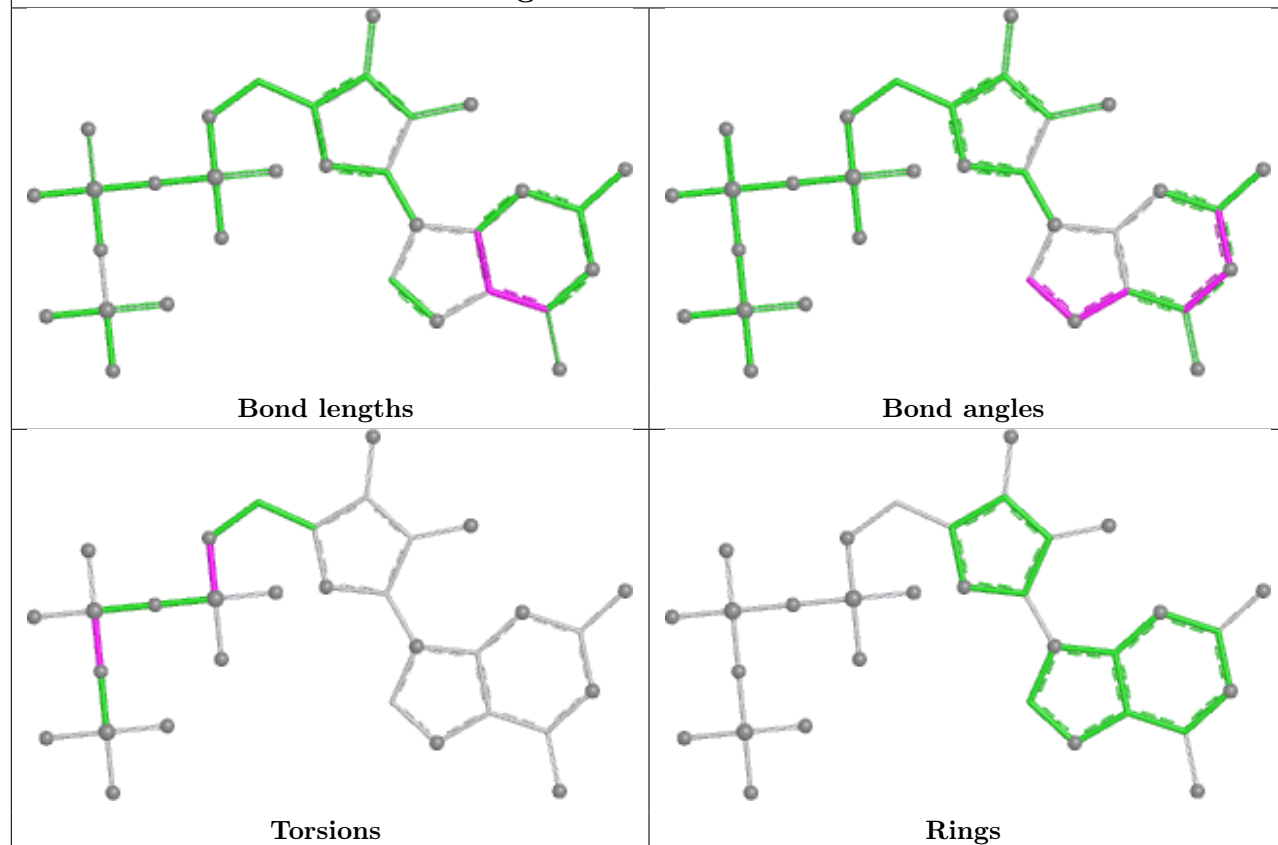
## Ligand GTP EU 501



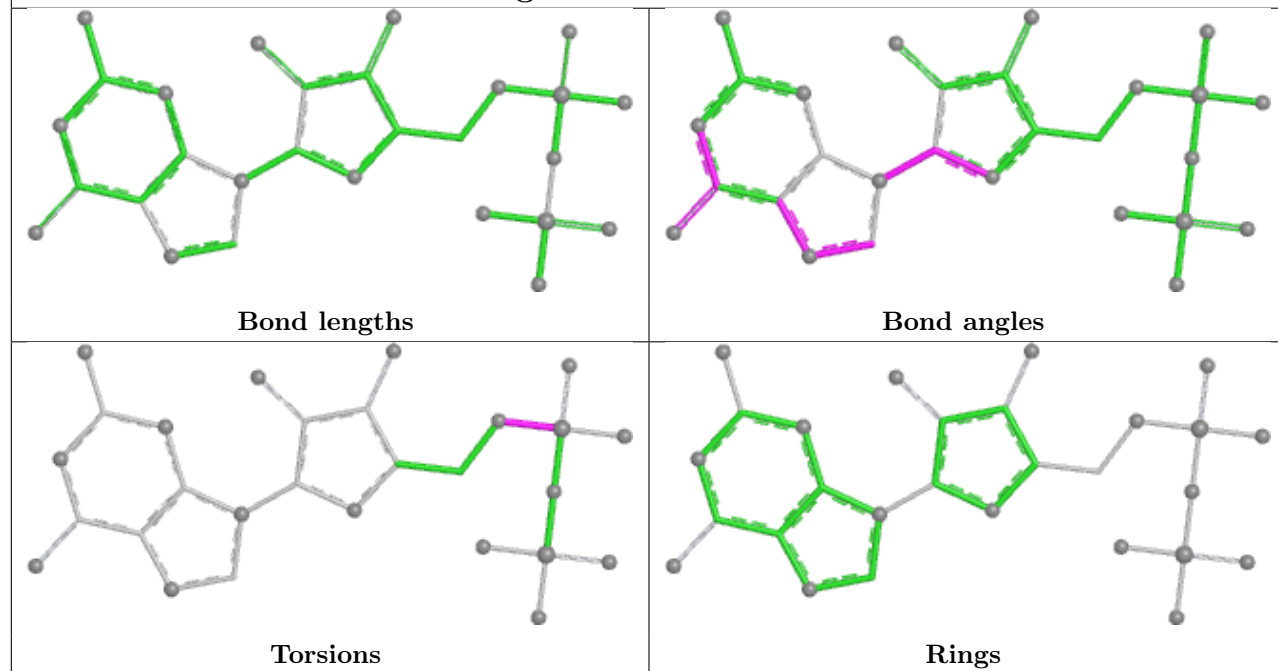
## Ligand GTP PQ 501



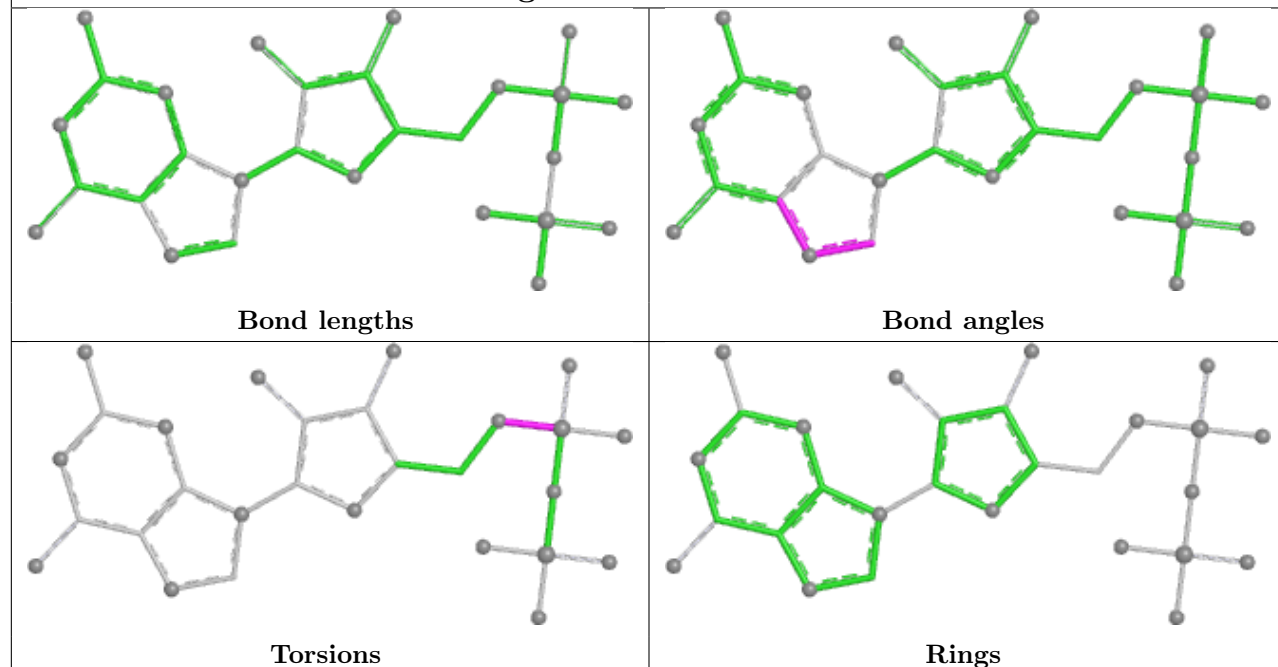
## Ligand GTP UB 501



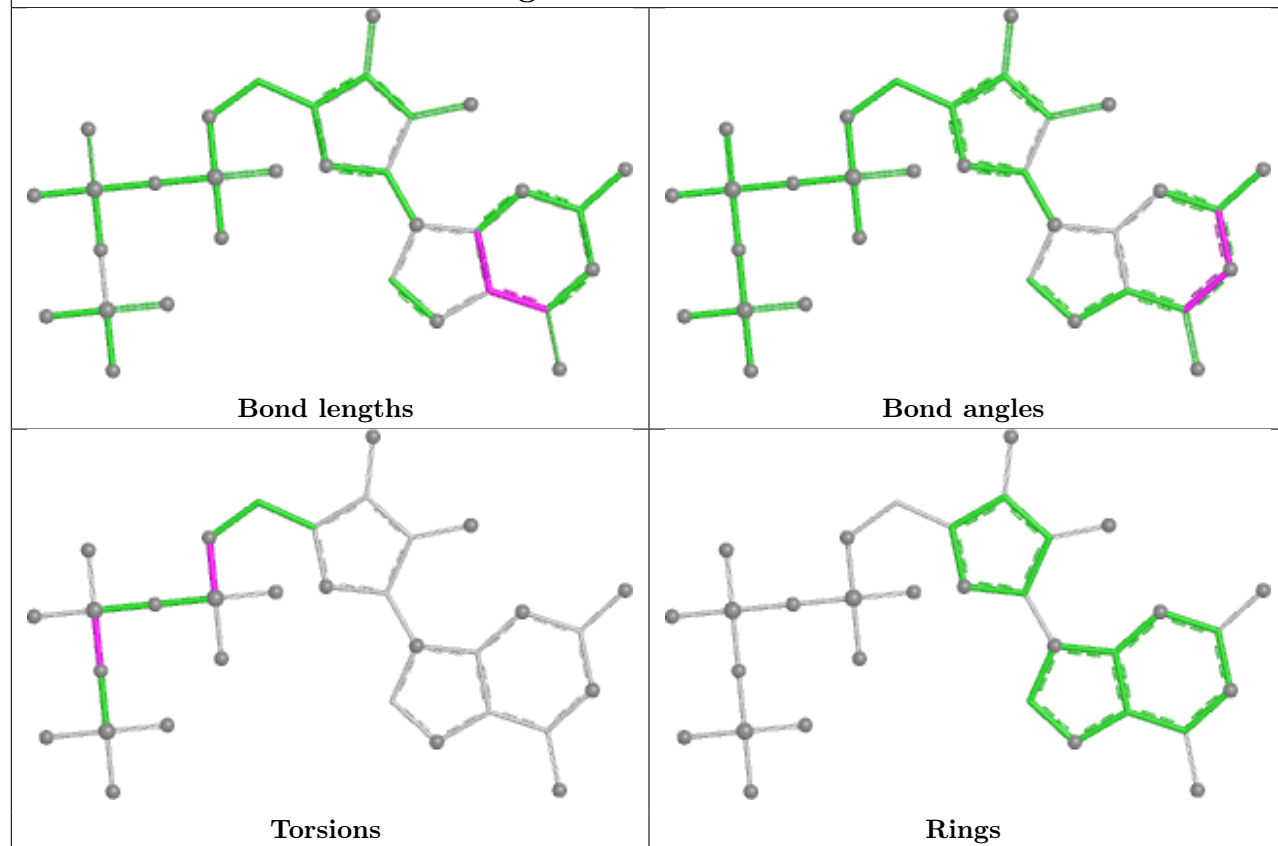
## Ligand GDP TD 501



## Ligand GDP ZA 501

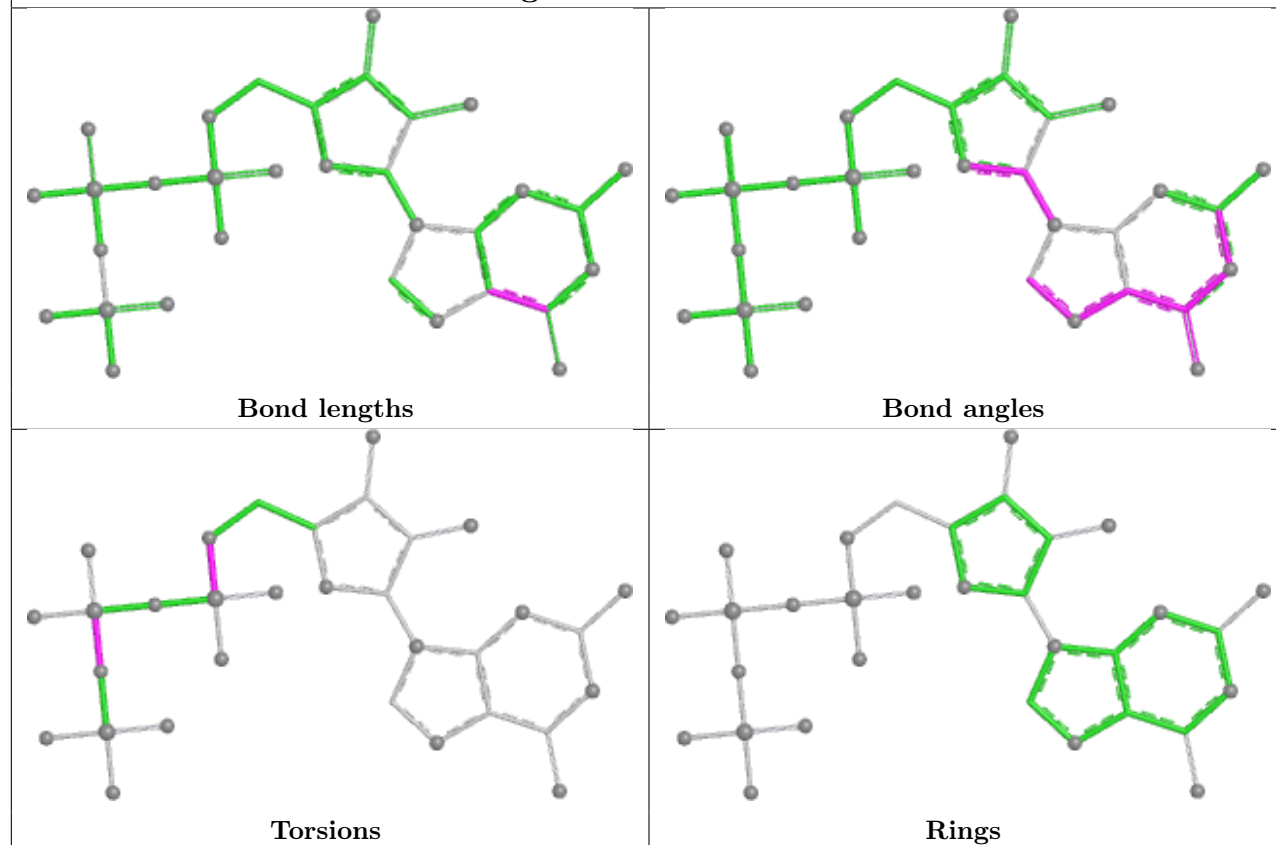


## Ligand GTP CP 602

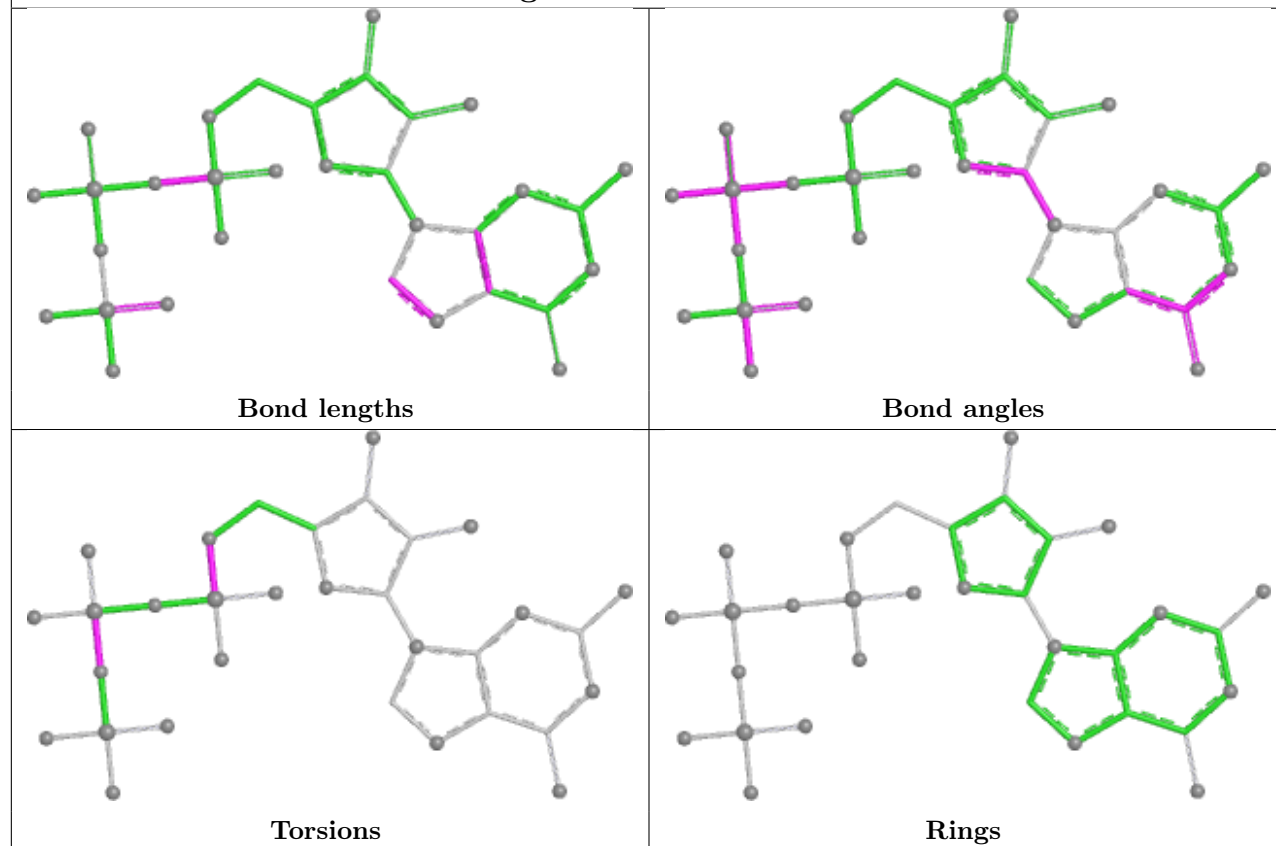




## Ligand GTP JR 602



## Ligand GTP SA 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

This section contains visualisations of the EMDB entry EMD-47524. 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

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

### 6.5 Orthogonal surface views

This section was not generated.

### 6.6 Mask visualisation

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

## 7 Map analysis ⓘ

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

### 7.1 Map-value distribution ⓘ

This section was not generated.

### 7.2 Volume estimate versus contour level ⓘ

This section was not generated.

### 7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 8 Fourier-Shell correlation

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

## 9 Map-model fit

This section was not generated.