



Full wwPDB EM Validation Report ⓘ

Jul 3, 2023 – 08:19 PM JST

PDB ID : 8IYJ
EMDB ID : EMD-35823
Title : Cryo-EM structure of the 48-nm repeat doublet microtubule from mouse sperm
Authors : Zhou, L.N.; Gui, M.; Wu, J.P.
Deposited on : 2023-04-05
Resolution : 3.50 Å (reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev50
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.34



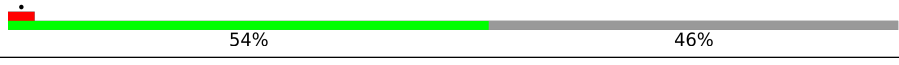

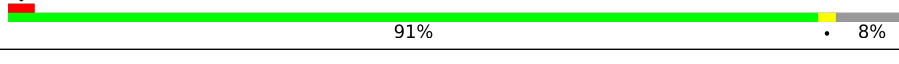
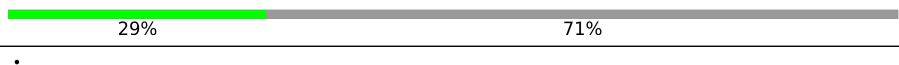
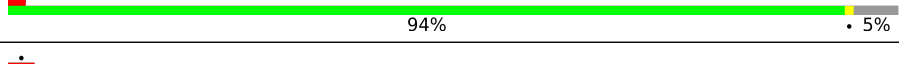
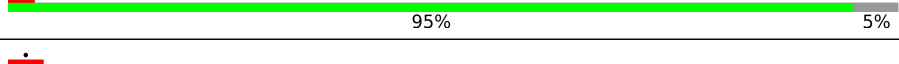
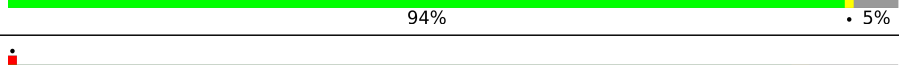
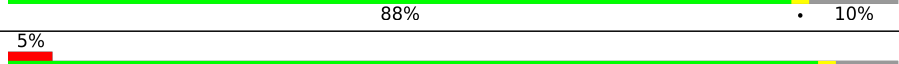
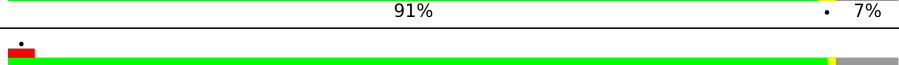
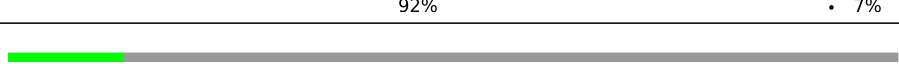
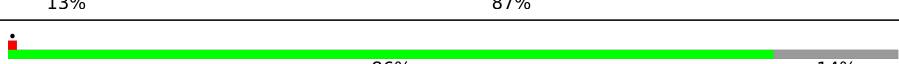
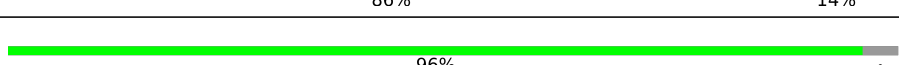
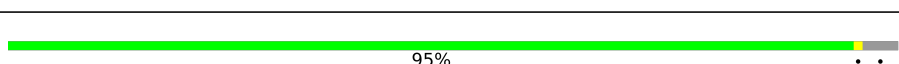
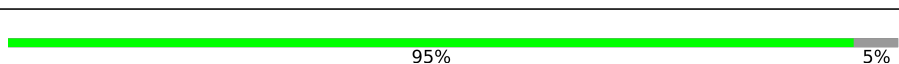

1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 Å.


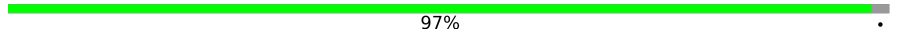
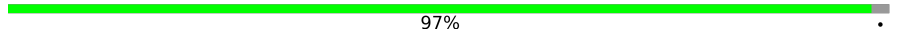
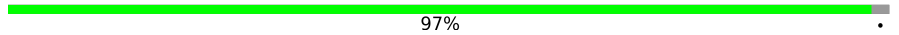
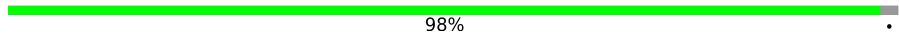
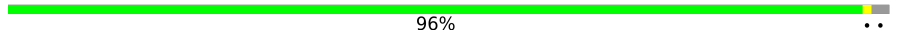
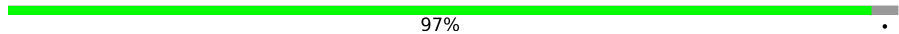
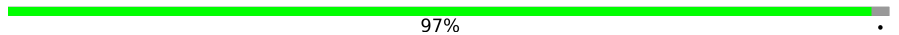
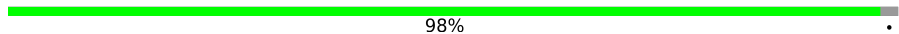
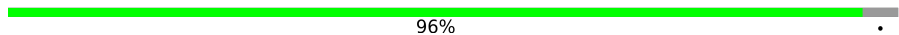
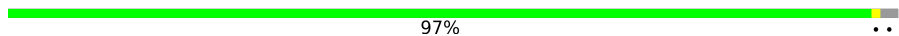
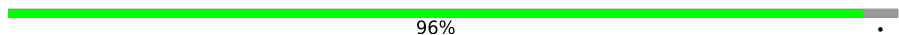
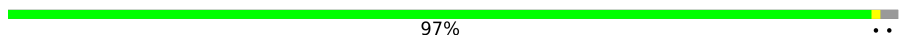
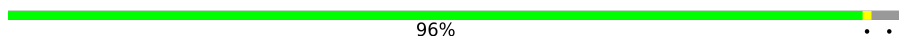
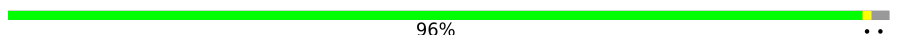
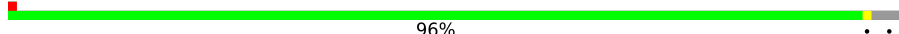
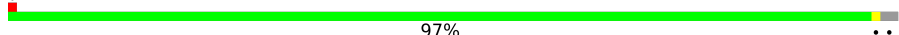
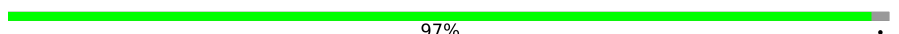
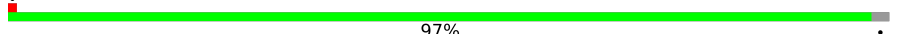
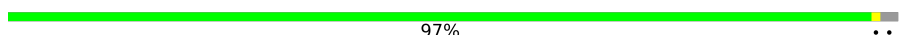
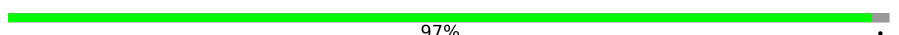
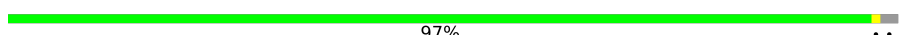
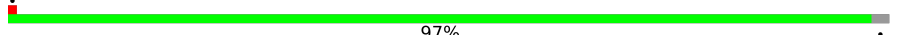

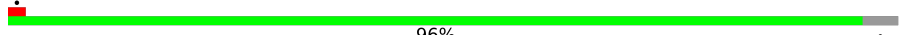
There are no overall percentile quality scores available for this entry.

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	228	 36% 64%
1	7	228	 61% 38%
2	1	853	 54% 46%
2	2	853	 31% 68%
3	3	514	 91% 8%
3	4	514	 29% 71%
4	5	395	 94% 5%
4	6	395	 95% 5%
4	j1	395	 94% 5%
5	8	196	 88% 10%
6	A	101	 5% 91% 7%
6	N1	101	 92% 7%
7	A0	418	 13% 87%
7	A1	418	 86% 14%
7	A2	418	 96%
7	A3	418	 95%
7	A4	418	 95% 5%

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Mol	Chain	Length	Quality of chain
7	A5	418	 40% 60%
8	AA	450	 97% .
8	AC	450	 97% .
8	AE	450	 97% .
8	AG	450	 98% .
8	AI	450	 96% ..
8	AK	450	 97% .
8	AM	450	 97% .
8	AO	450	 98% .
8	BC	450	 96% .
8	BE	450	 97% ..
8	BG	450	 96% .
8	BI	450	 97% ..
8	BK	450	 96% ..
8	BM	450	 96% ..
8	BO	450	 96% ..
8	CC	450	 97% ..
8	CE	450	 97% .
8	CG	450	 97% .
8	CI	450	 97% ..
8	CK	450	 97% .
8	CM	450	 97% ..
8	CO	450	 97% .
8	CQ	450	 8% 97% .
8	DC	450	 96% .

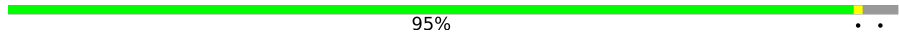
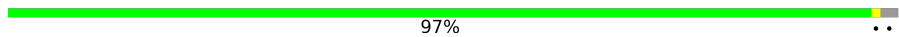
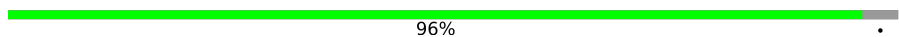
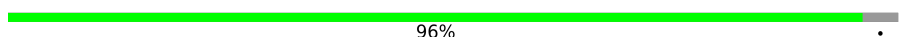
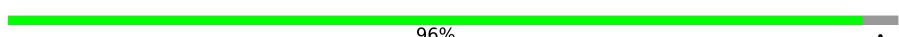
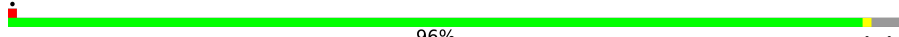




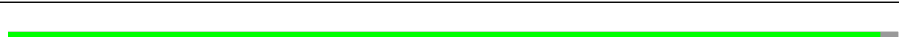


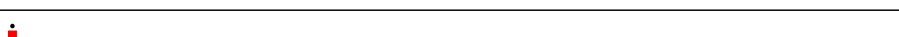
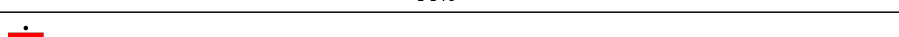
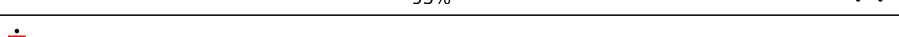
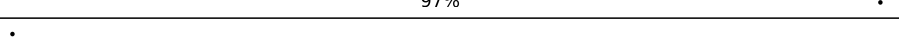
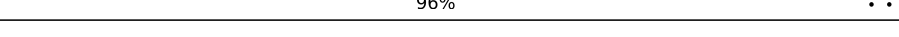
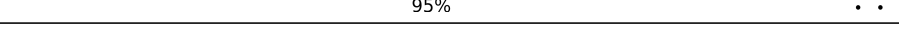
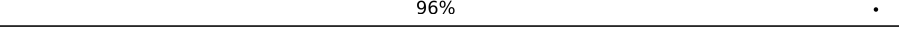
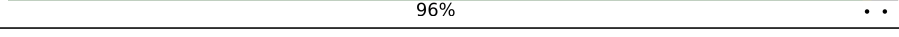
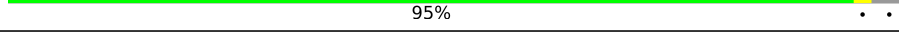
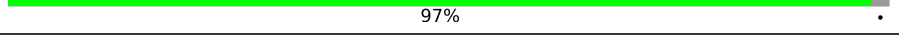
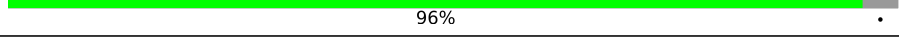
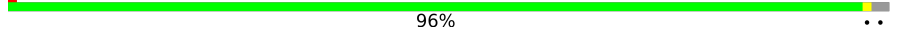
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Mol	Chain	Length	Quality of chain
8	DE	450	95%
8	DG	450	96%
8	DI	450	96%
8	DK	450	96%
8	DM	450	96%
8	DO	450	95%
8	DQ	450	95% 5%
8	EA	450	97%
8	EC	450	97%
8	EE	450	97%
8	EG	450	97%
8	EI	450	97%
8	EK	450	98%
8	EM	450	98%
8	EO	450	97% 5%
8	FA	450	94%
8	FC	450	95%
8	FE	450	96%
8	FG	450	94% 5%
8	FI	450	95%
8	FK	450	95%
8	FM	450	95%
8	FO	450	95% 5%
8	GA	450	95%
8	GC	450	95%

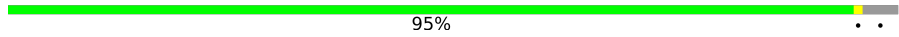
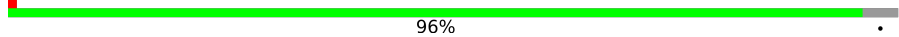
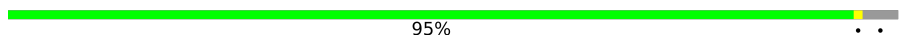
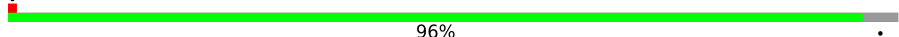
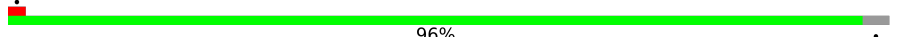
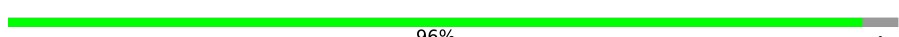
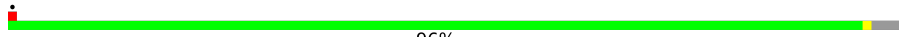



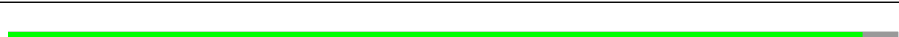


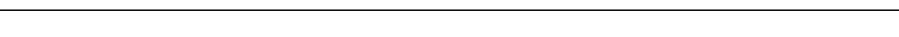
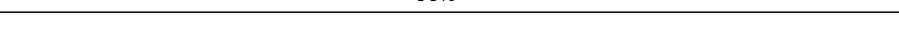
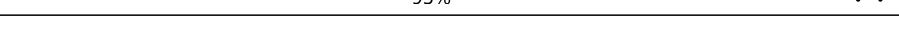
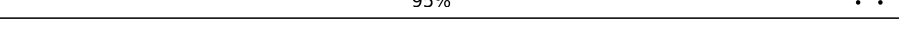
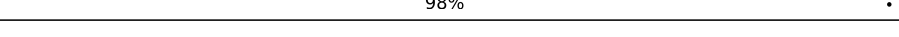
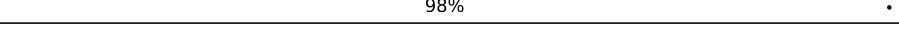
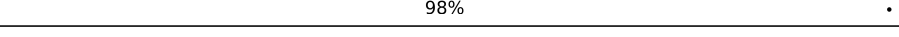
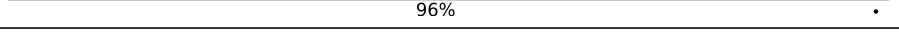
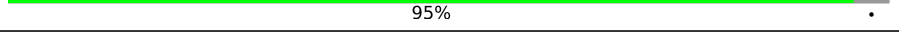
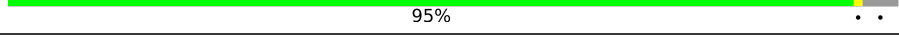
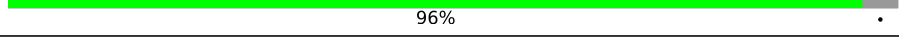
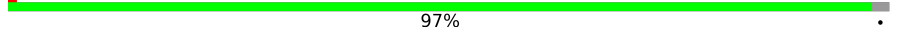
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Mol	Chain	Length	Quality of chain
8	GE	450	 95%
8	GG	450	 97%
8	GI	450	 96%
8	GK	450	 96%
8	GM	450	 96%
8	GO	450	 96%
8	HA	450	 94%
8	HC	450	 96%
8	HE	450	 97%
8	HG	450	 97%
8	HI	450	 98%
8	HK	450	 95%
8	HM	450	 96%
8	HO	450	 96%
8	IA	450	 95%
8	IC	450	 97%
8	IE	450	 96%
8	IG	450	 95%
8	II	450	 96%
8	IK	450	 96%
8	IM	450	 95%
8	IO	450	 97%
8	JC	450	 96%
8	JE	450	 96%
8	JG	450	 95%

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Mol	Chain	Length	Quality of chain
8	JI	450	 95%
8	JK	450	 96%
8	JM	450	 95%
8	JO	450	 96%
8	JQ	450	 96%
8	KA	450	 96%
8	KC	450	 96%
8	KE	450	 96%
8	KG	450	 95%
8	KI	450	 96%
8	KK	450	 96%
8	KM	450	 95%
8	KO	450	 96%
8	LA	450	 96%
8	LC	450	 95%
8	LE	450	 95%
8	LG	450	 98%
8	LI	450	 98%
8	LK	450	 98%
8	LM	450	 96%
8	LO	450	 95%
8	MA	450	 95%
8	MC	450	 96%
8	ME	450	 97%
8	MG	450	 95%

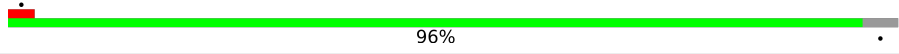
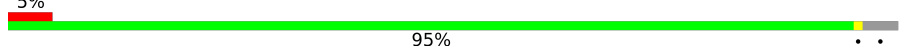
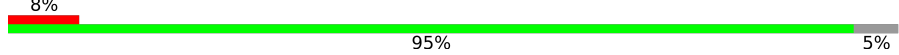
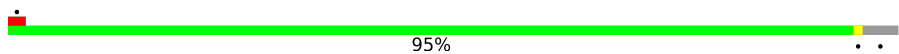
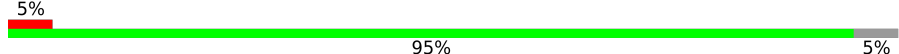
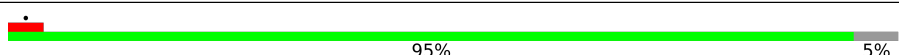
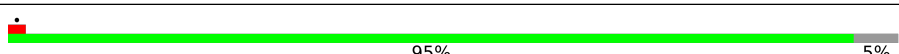
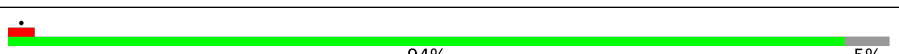
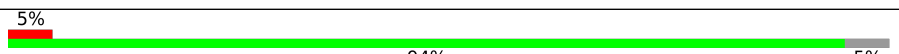
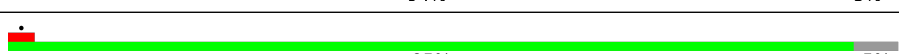
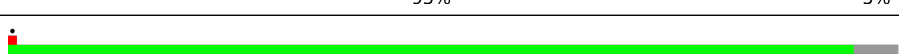
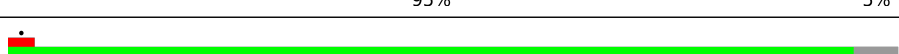
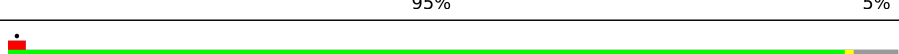
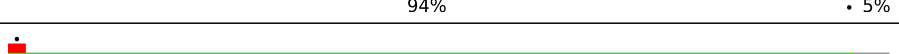
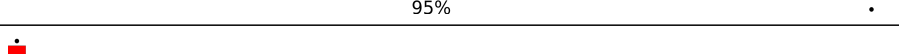
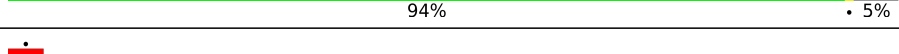
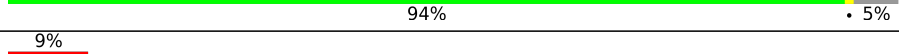
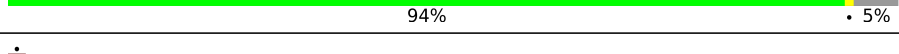
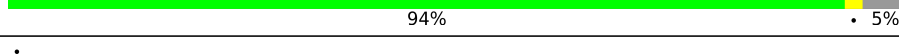
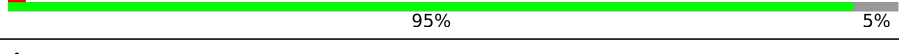
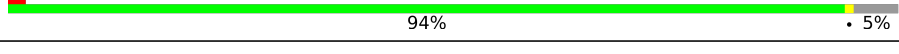
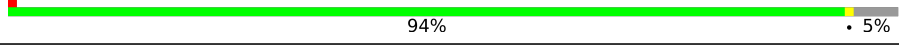
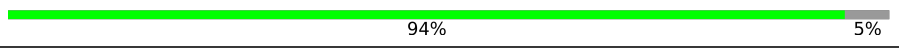
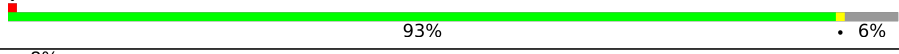
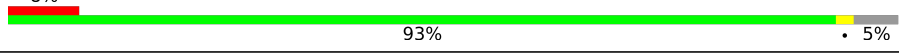
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Mol	Chain	Length	Quality of chain
8	MI	450	96% .
8	MK	450	96% ..
8	MM	450	96% .
8	MO	450	94% . 5%
8	NA	450	5% 94% . 5%
8	NC	450	6% 95% 5%
8	NE	450	. 96% .
8	NG	450	. 96% .
8	NI	450	. 95% .
8	NK	450	. 95% ..
8	NM	450	. 95% ..
8	NO	450	. 95% ..
8	OA	450	19% 95% .
8	OC	450	6% 95% ..
8	OE	450	. 95% ..
8	OG	450	. 95% ..
8	OI	450	. 95% 5%
8	OK	450	. 96% .
8	OM	450	. 95% 5%
8	OO	450	5% 94% 6%
8	PC	450	. 94% . 5%
8	PE	450	. 94% 6%
8	PG	450	. 95% .
8	PI	450	. 95% .
8	PK	450	. 94% ..

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Mol	Chain	Length	Quality of chain
8	PM	450	 96%
8	PO	450	 95%
8	QC	450	 95%
8	QE	450	 95%
8	QG	450	 95%
8	QI	450	 95%
8	QK	450	 95%
8	QM	450	 94%
8	QO	450	 94%
8	RC	450	 95%
8	RE	450	 95%
8	RG	450	 95%
8	RI	450	 94%
8	RK	450	 95%
8	RM	450	 94%
8	RO	450	 94%
8	SA	450	 94%
8	SC	450	 94%
8	SE	450	 95%
8	SG	450	 94%
8	SI	450	 94%
8	SK	450	 94%
8	SM	450	 93%
8	TA	450	 93%
8	TC	450	 94%

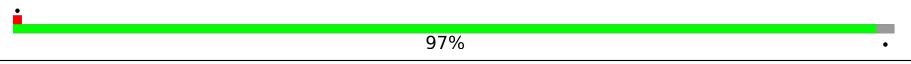
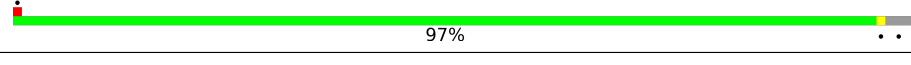
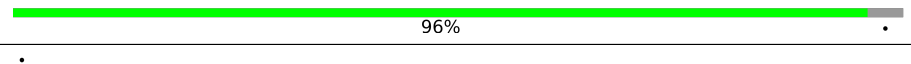
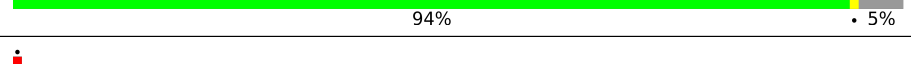
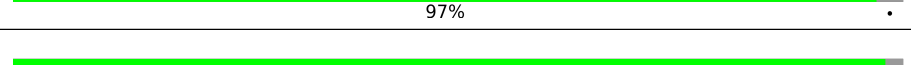
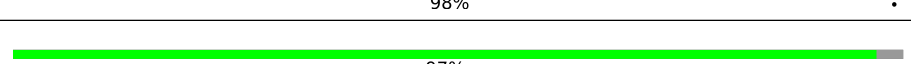
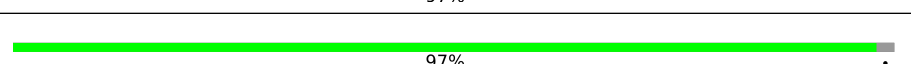
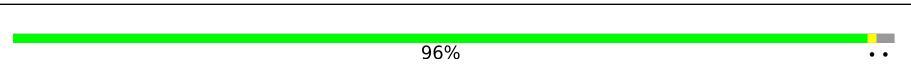
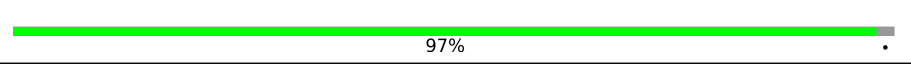
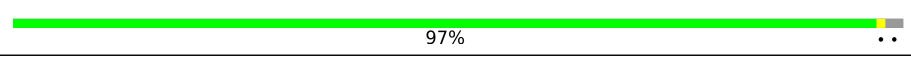
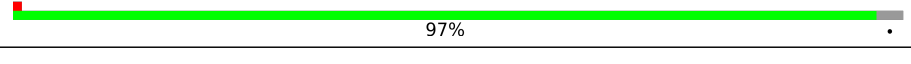
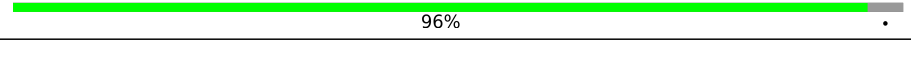
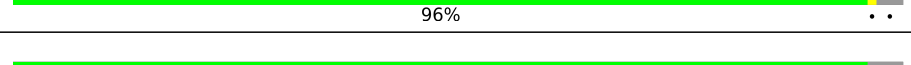
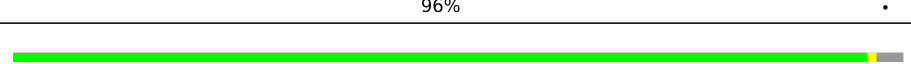
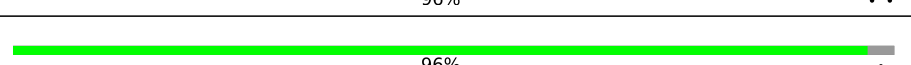
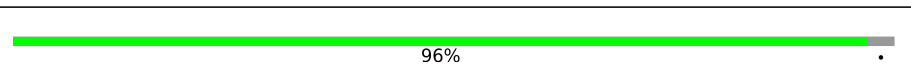
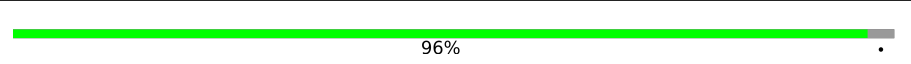
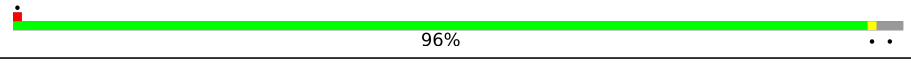
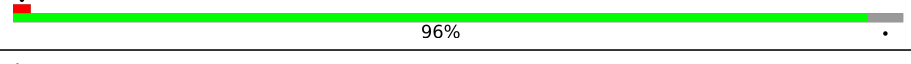
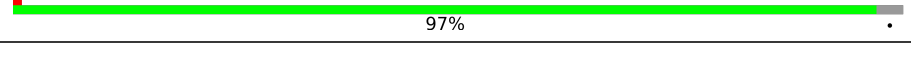
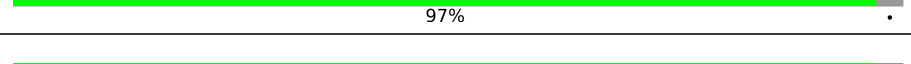
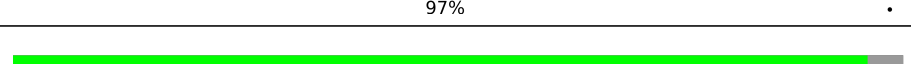
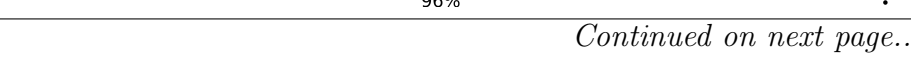


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Mol	Chain	Length	Quality of chain
8	TE	450	94% . 5%
8	TG	450	94% 5%
8	TI	450	94% 5%
8	TK	450	94% . 5%
8	TM	450	94% . 5%
8	UA	450	93% . 6%
8	UC	450	95% 5%
8	UE	450	95% 5%
8	UG	450	95% 5%
8	UI	450	95% 5%
8	UK	450	95% 5%
8	UM	450	94% . 5%
8	UO	450	94% . 5%
8	VA	450	94% . 5%
8	VC	450	97% .
8	VE	450	94% . 5%
8	VG	450	96% . .
8	VI	450	94% . 5%
8	VK	450	96% . .
8	VM	450	94% . 5%
8	VO	450	96% . .
8	WA	450	96% . .
8	WC	450	97% .
8	WE	450	96% .
8	WG	450	97% .

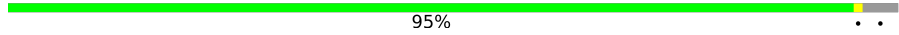
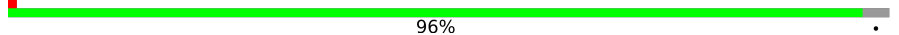
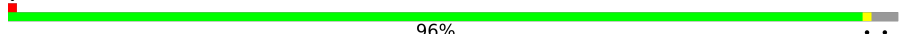
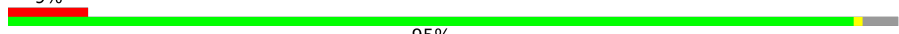


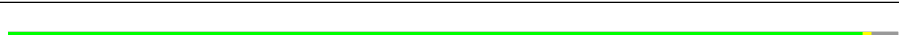
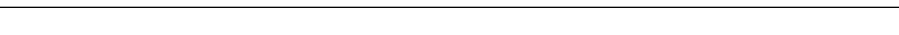
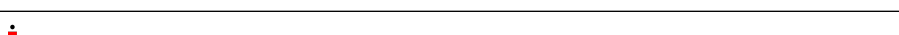
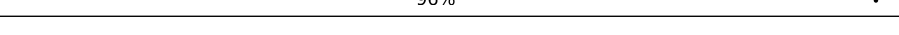
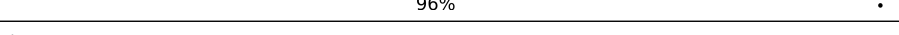
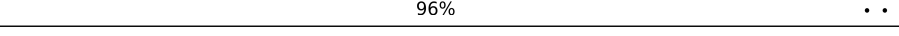
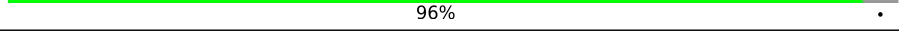
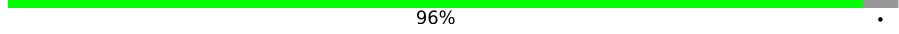
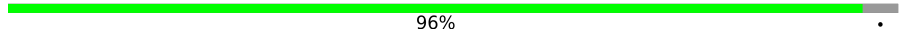
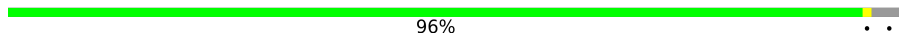
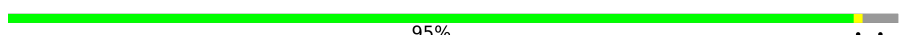
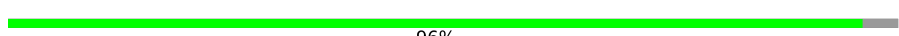





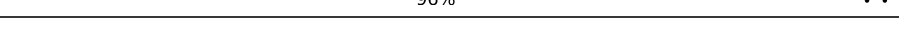
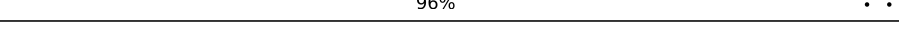
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Mol	Chain	Length	Quality of chain
8	WI	450	 97%
8	WK	450	 97%
8	WM	450	 96%
8	WO	450	 94% 5%
9	AB	445	 97%
9	AD	445	 98%
9	AF	445	 97%
9	AH	445	 97%
9	AJ	445	 96%
9	AL	445	 97%
9	AN	445	 97%
9	AP	445	 97%
9	BB	445	 96%
9	BD	445	 96%
9	BF	445	 96%
9	BH	445	 96%
9	BJ	445	 96%
9	BL	445	 96%
9	BN	445	 96%
9	BP	445	 96%
9	CB	445	 96%
9	CD	445	 97%
9	CF	445	 97%
9	CH	445	 97%
9	CJ	445	 96%

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Mol	Chain	Length	Quality of chain
9	CL	445	 95%
9	CN	445	 96%
9	CP	445	 96%
9	DB	445	 95%
9	DD	445	 96%
9	DF	445	 96%
9	DH	445	 96%
9	DJ	445	 96%
9	DL	445	 96%
9	DN	445	 96%
9	DP	445	 96%
9	EB	445	 96%
9	ED	445	 96%
9	EF	445	 96%
9	EH	445	 96%
9	EJ	445	 95%
9	EL	445	 96%
9	EN	445	 96%
9	FB	445	 96%
9	FD	445	 96%
9	FF	445	 96%
9	FH	445	 96%
9	FJ	445	 96%
9	FL	445	 96%
9	FN	445	 96%

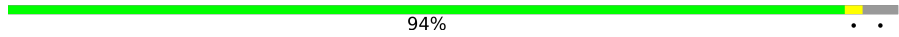
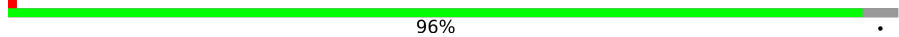
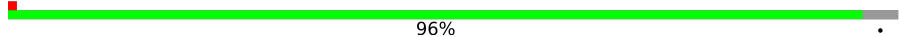
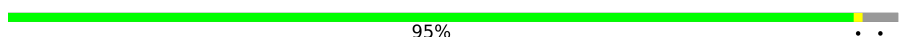
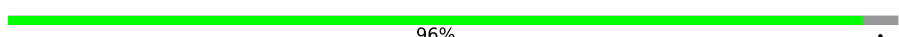
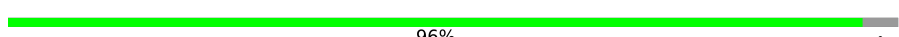
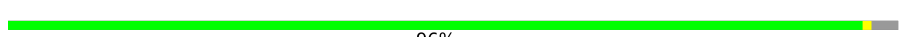



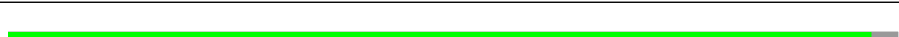


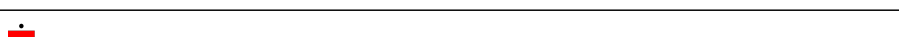
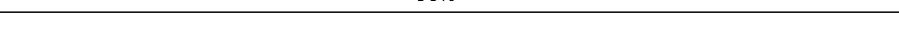
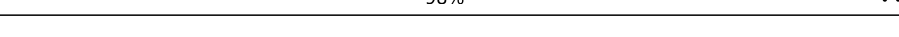
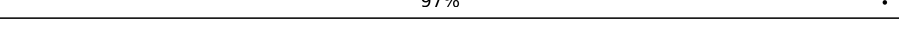
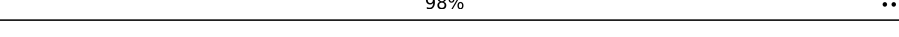
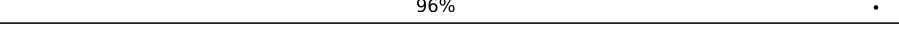
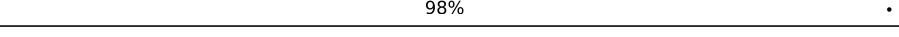
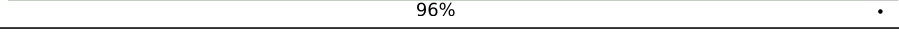
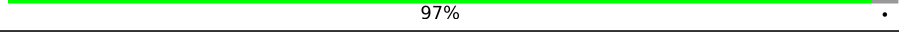
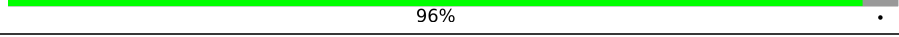
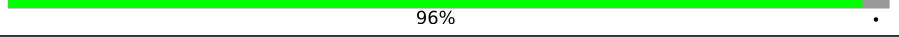
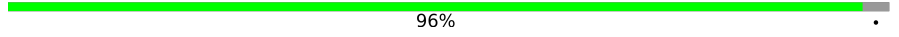
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Mol	Chain	Length	Quality of chain
9	GB	445	96%
9	GD	445	96%
9	GF	445	97%
9	GH	445	97%
9	GJ	445	97%
9	GL	445	96%
9	GN	445	96%
9	HB	445	96%
9	HD	445	95%
9	HF	445	96%
9	HH	445	96%
9	HJ	445	96%
9	HL	445	97%
9	HN	445	96%
9	HP	445	95%
9	IB	445	96%
9	ID	445	96%
9	IF	445	96%
9	IH	445	96%
9	IJ	445	96%
9	IL	445	96%
9	IN	445	96%
9	IP	445	96%
9	JB	445	96%
9	JD	445	96%

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Mol	Chain	Length	Quality of chain
9	JF	445	 94%
9	JH	445	 96%
9	JJ	445	 96%
9	JL	445	 95%
9	JN	445	 96%
9	JP	445	 96%
9	KB	445	 96%
9	KD	445	 96%
9	KF	445	 97%
9	KH	445	 96%
9	KJ	445	 97%
9	KL	445	 96%
9	KN	445	 96%
9	KP	445	 96%
9	LB	445	 98%
9	LD	445	 97%
9	LF	445	 98%
9	LH	445	 96%
9	LJ	445	 98%
9	LL	445	 96%
9	LN	445	 97%
9	LP	445	 96%
9	MB	445	 96%
9	MD	445	 96%
9	MF	445	 95%

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Mol	Chain	Length	Quality of chain
9	MH	445	96%
9	MJ	445	96%
9	ML	445	96%
9	MN	445	96%
9	MP	445	96%
9	NB	445	96%
9	ND	445	97%
9	NF	445	96%
9	NH	445	96%
9	NJ	445	96%
9	NL	445	96%
9	NN	445	96%
9	NP	445	96%
9	OB	445	95%
9	OD	445	96%
9	OF	445	96%
9	OH	445	95%
9	OJ	445	95%
9	OL	445	96%
9	ON	445	96%
9	OP	445	95%
9	PB	445	95%
9	PD	445	95%
9	PF	445	95%
9	PH	445	95%

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Mol	Chain	Length	Quality of chain
9	PJ	445	96%
9	PL	445	96%
9	PN	445	96%
9	PP	445	96%
9	QB	445	96%
9	QD	445	96%
9	QF	445	96%
9	QH	445	95%
9	QJ	445	95%
9	QL	445	96%
9	QN	445	95%
9	QP	445	95%
9	RD	445	96%
9	RF	445	96%
9	RH	445	96%
9	RJ	445	96%
9	RL	445	96%
9	RN	445	96%
9	RP	445	96%
9	SB	445	95%
9	SD	445	96%
9	SF	445	96%
9	SH	445	96%
9	SJ	445	95%
9	SL	445	95%

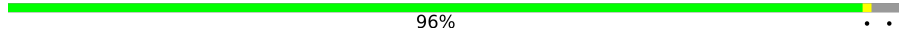
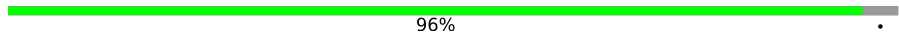
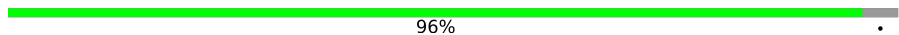
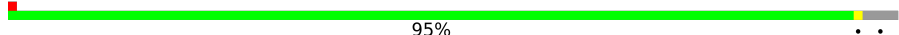
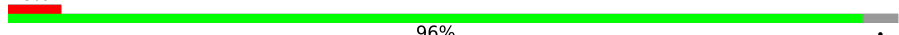






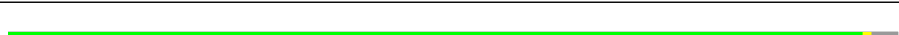

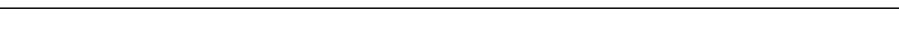
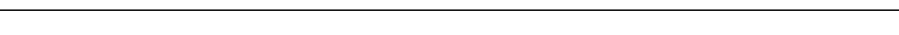
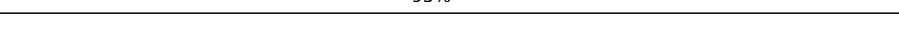
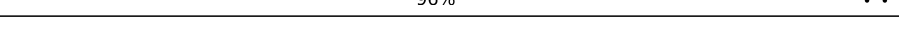
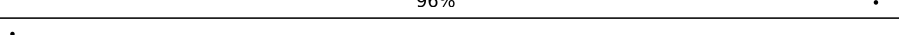







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Mol	Chain	Length	Quality of chain
9	SN	445	9% 96%
9	TB	445	95%
9	TD	445	95%
9	TF	445	95%
9	TH	445	95%
9	TJ	445	95%
9	TL	445	94%
9	TN	445	5% 95%
9	UB	445	95%
9	UD	445	96%
9	UF	445	96%
9	UH	445	96%
9	UJ	445	96%
9	UL	445	6% 96%
9	UN	445	10% 96%
9	VB	445	96%
9	VD	445	96%
9	VF	445	96%
9	VH	445	95%
9	VJ	445	95%
9	VL	445	95%
9	VN	445	95%
9	WB	445	96%
9	WD	445	96%
9	WF	445	96%



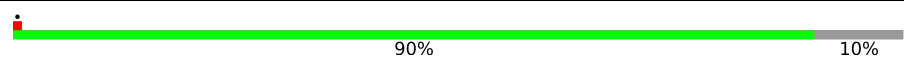
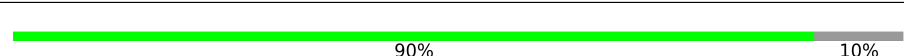
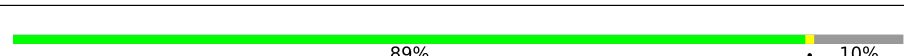
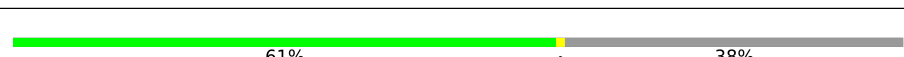
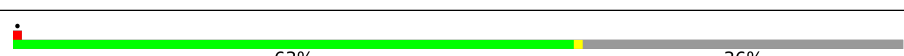
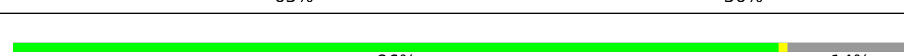
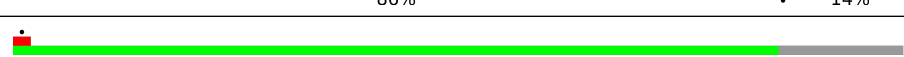

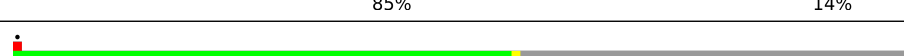
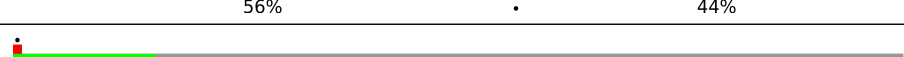

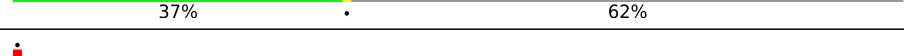
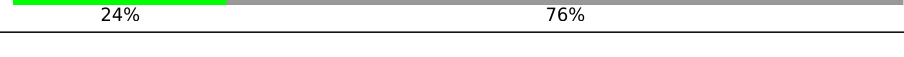
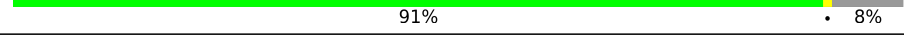
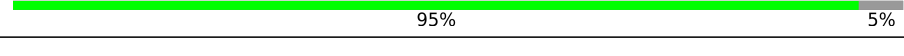
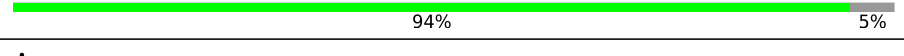
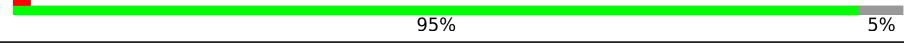


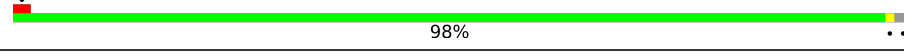
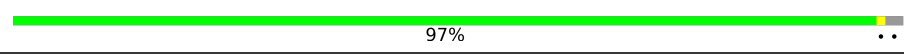
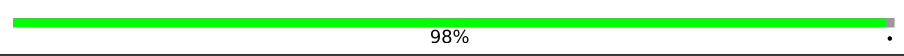

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Mol	Chain	Length	Quality of chain
9	WH	445	 96%
9	WJ	445	 96%
9	WL	445	 96%
9	WN	445	 95%
9	WP	445	 96%
10	B	491	 64% 35%
10	C	491	 56% 43%
11	B0	430	 9% 91%
11	B1	430	 83% 15%
11	B2	430	 95%
11	B3	430	 95%
11	B4	430	 96%
11	B5	430	 46% 53%
11	R0	430	 46% 54%
11	R1	430	 95%
11	R2	430	 96%
11	R3	430	 96%
11	R4	430	 85% 14%
11	R5	430	 10% 90%
12	C0	490	 36% 63%
12	C1	490	 83% 16%
12	C2	490	 83% 16%
12	C3	490	 83% 17%
12	C4	490	 74% 26%
12	C5	490	 10% 90%

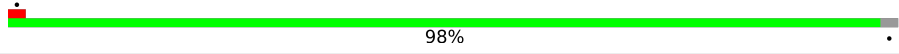
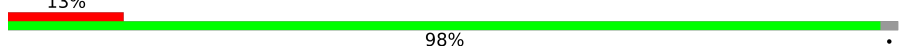
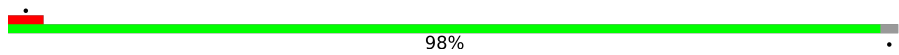


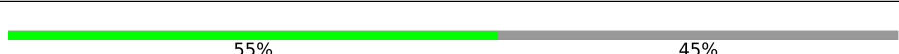
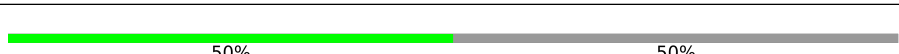
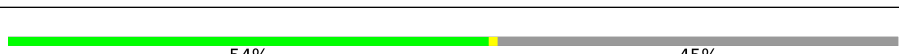
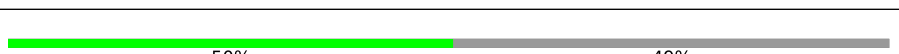
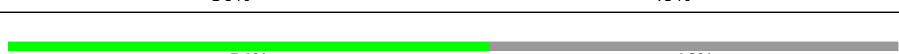

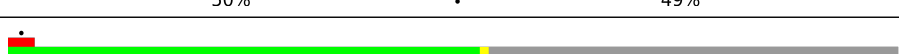

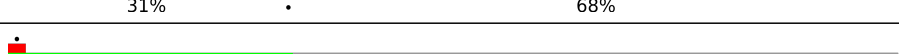
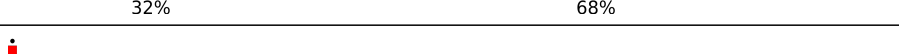








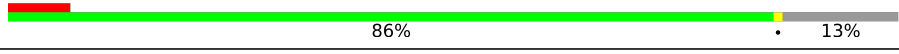

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Mol	Chain	Length	Quality of chain
12	C6	490	 9% 91%
12	S0	490	 65% 34%
12	S1	490	 90% 10%
12	S2	490	 90% 10%
12	S3	490	 89% 10%
12	S4	490	 61% 38%
12	S5	490	 63% 36%
12	S6	490	 86% 14%
12	S7	490	 86% 14%
12	S8	490	 85% 14%
12	S9	490	 56% 44%
13	D	470	 16% 84%
13	K3	470	 37% 62%
14	D0	447	 24% 76%
14	D1	447	 91% 8%
14	D2	447	 95% 5%
14	D3	447	 94% 5%
14	D4	447	 95% 5%
14	D5	447	 18% 81%
14	T0	447	 26% 73%
14	T1	447	 98% ..
14	T2	447	 97% ..
14	T3	447	 98% .
14	T4	447	 87% 12%
14	T5	447	 26% 73%


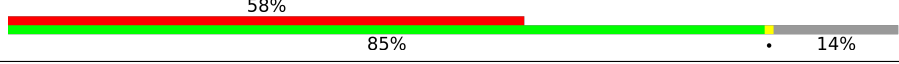
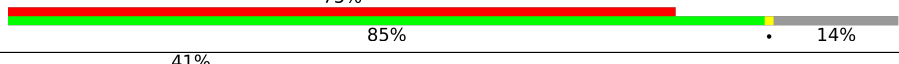


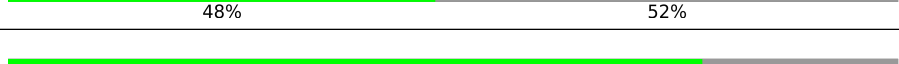
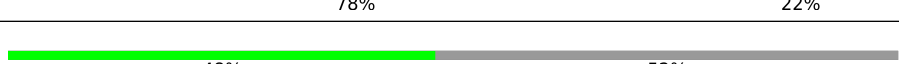
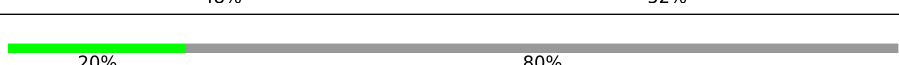
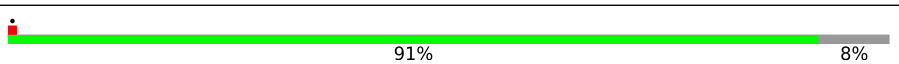

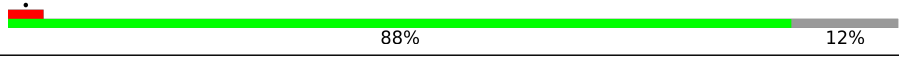
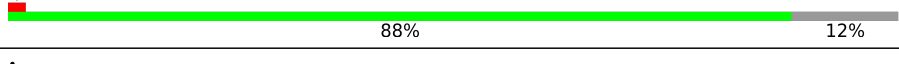
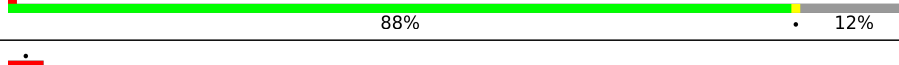
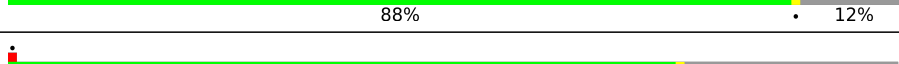

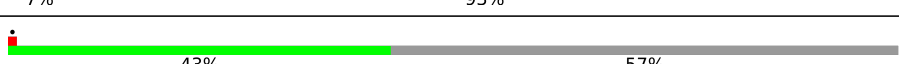









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Mol	Chain	Length	Quality of chain
15	E	303	 98%
15	F	303	 13% 98%
15	N2	303	 98%
16	G	122	 9% 74% 25%
17	H	319	 50% 49%
17	I	319	 55% 45%
17	J	319	 50% 50%
17	K	319	 54% 45%
17	L	319	 50% 49%
17	M	319	 54% 46%
17	N	319	 50% 49%
17	O7	319	 53% 46%
17	O8	319	 31% 68%
17	O9	319	 32% 68%
17	P8	319	 32% 68%
17	P9	319	 31% 68%
17	Z2	319	 16% 84%
17	Z3	319	 16% 84%
17	Z4	319	 16% 84%
17	Z5	319	 15% 84%
18	I1	166	 56% 43%
19	J1	283	 5% 39% 61%
19	J2	283	 7% 86% 13%
19	J3	283	 86% 13%
19	J4	283	 5% 86% 13%



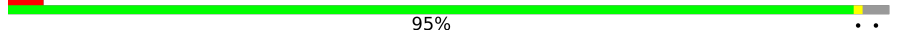
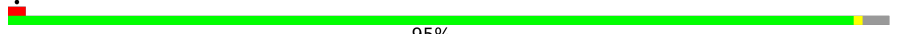


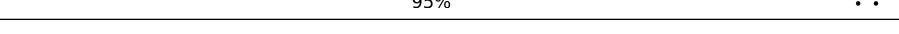

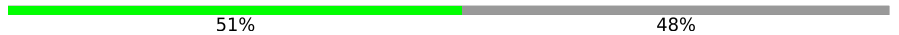


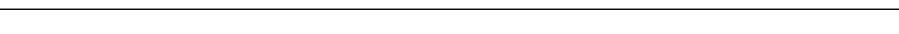
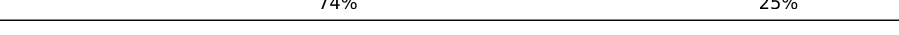




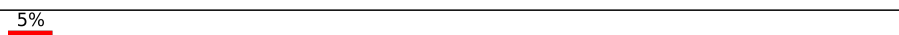







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Mol	Chain	Length	Quality of chain
19	J5	283	
20	K1	137	
20	K2	137	
21	L1	182	
22	M1	200	
22	M2	200	
22	M3	200	
22	M4	200	
23	O	379	
23	P	379	
23	Q	379	
24	O1	189	
24	O2	189	
24	O3	189	
24	O4	189	
25	O5	648	
25	O6	648	
25	T	648	
25	U	648	
25	V	648	
26	P1	131	
26	P2	131	
27	P3	180	
27	P4	180	
27	P5	180	






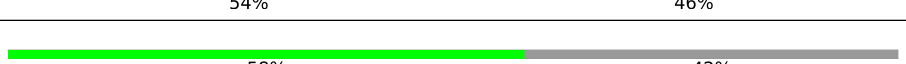
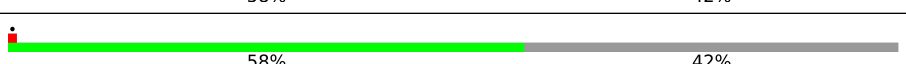
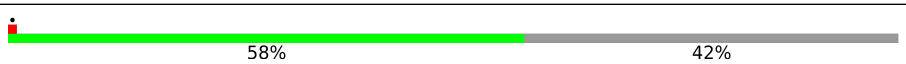

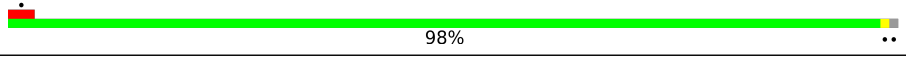
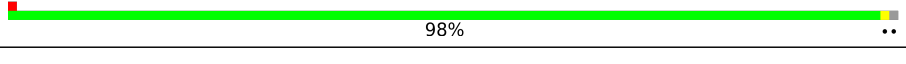
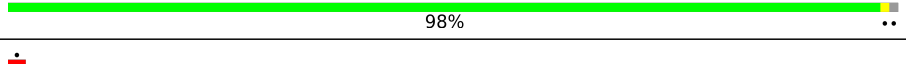
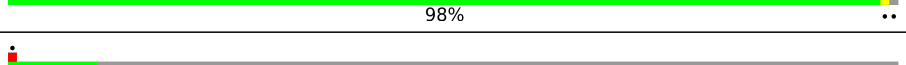
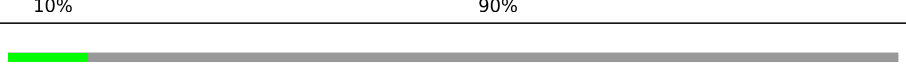
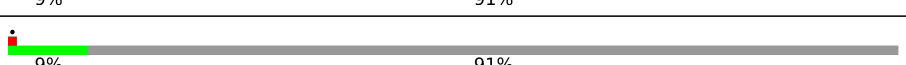
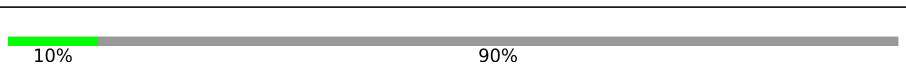


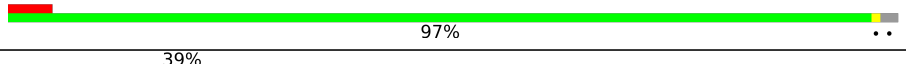
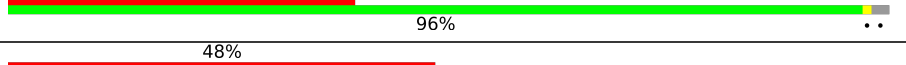
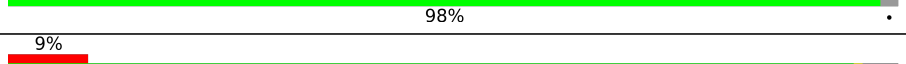
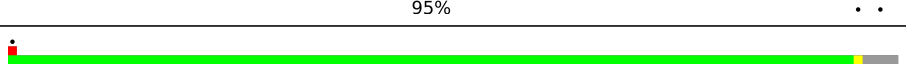
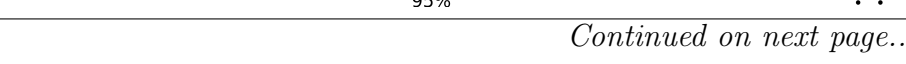


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Mol	Chain	Length	Quality of chain
27	P6	180	 85% 14%
27	P7	180	 29% 71%
28	Q1	206	 95%
28	Q2	206	 95%
28	Q3	206	 96%
28	Q4	206	 7% 95%
28	Q5	206	 8% 91%
29	R	377	 51% 48%
29	S	377	 85% 14%
30	U0	557	 63% 36%
30	U1	557	 74% 25%
30	U2	557	 73% 25%
30	U3	557	 74% 25%
30	U4	557	 36% 64%
30	U5	557	 8% 57% 43%
30	U6	557	 5% 73% 26%
30	U7	557	 73% 26%
30	U8	557	 8% 73% 26%
30	U9	557	 6% 32% 67%
30	V0	557	 26% 36% 63%
30	V1	557	 12% 69% 30%
30	V2	557	 69% 30%
30	V3	557	 11% 69% 30%
30	V4	557	 11% 51% 49%
30	V5	557	 52% 47%

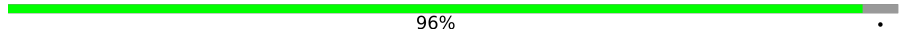
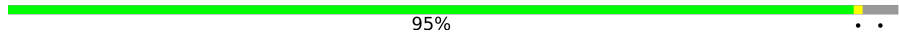
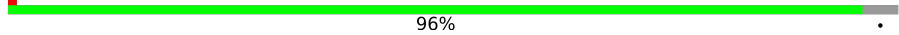
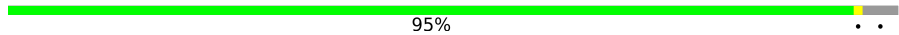
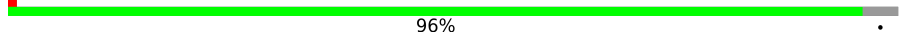
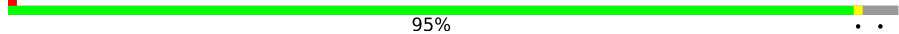

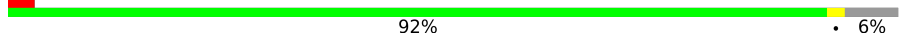

















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Mol	Chain	Length	Quality of chain
30	V6	557	
30	V7	557	
30	V8	557	
30	V9	557	
30	W0	557	
30	W2	557	
30	W4	557	
30	W5	557	
30	W6	557	
30	W7	557	
31	W	750	
31	X	750	
31	Y	750	
31	Z	750	
32	X0	260	
32	X1	260	
32	X2	260	
32	X3	260	
33	X4	427	
33	X5	427	
34	X6	273	
34	X7	273	
34	X8	273	
35	XA	193	
35	XB	193	

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Mol	Chain	Length	Quality of chain
35	XC	193	 96%
35	XD	193	 95%
35	XE	193	 96%
35	XF	193	 95%
35	XG	193	 96%
35	XH	193	 95%
36	Y0	254	 24% 75%
36	Y1	254	 92% 6%
36	Y2	254	 88% 11%
36	Y3	254	 25% 75% 6%
36	Y4	254	 71% 27% 9%
36	Y5	254	 33% 67% 6%
37	YA	241	 90% 9% 10%
37	YB	241	 91% 9%
37	YC	241	 91% 9% 11%
37	YD	241	 91% 9%
37	YE	241	 91% 9%
37	YF	241	 90% 9%
37	YG	241	 90% 9%
37	YH	241	 90% 9%
38	Z1	216	 15% 85%
39	a	551	 52% 47% 11%
39	a6	551	 13% 87%
39	b	551	 43% 56% 16%
39	c	551	 74% 25% 17%







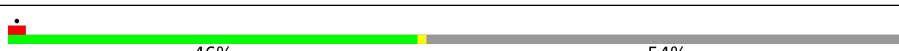

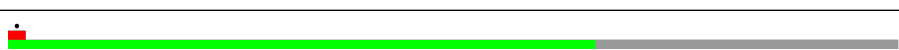
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Mol	Chain	Length	Quality of chain
39	d	551	8% 24% 75%
40	a1	229	68% 32%
40	a2	229	67% 32%
40	a3	229	67% 32%
40	a4	229	67% 32%
41	b1	499	25% 74%
41	b2	499	76% 24%
41	b3	499	76% 23%
41	b4	499	76% 23%
41	b5	499	66% 33%
42	e	620	98%
42	f	620	97%
42	g	620	98%
43	h	255	96%
43	i	255	95%
43	j	255	95%
43	k	255	96%
44	h1	141	67% 31%
44	h2	141	70% 30%
44	h3	141	70% 30%
44	h4	141	69% 30%
45	i1	189	61% 39%
45	l	189	61% 39%
45	m	189	61% 39%
45	n	189	60% 39%

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Mol	Chain	Length	Quality of chain
46	i2	1516	 12% 88%
46	i3	1516	 12% 88%
46	i4	1516	 12% 88%
47	o	547	 16% 36% 64%
47	p	547	 21% 70% 28%
48	q	168	 44% 55%
48	r	168	 46% 54%
48	s	168	 46% 54%
49	y	167	 66% 34%

2 Entry composition [i](#)

There are 52 unique types of molecules in this entry. The entry contains 1650085 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 Cilia- and flagella-associated protein 95.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	81	Total	C	N	O	S	0	0
			670	422	120	123	5		
1	7	141	Total	C	N	O	S	0	0
			1174	741	210	217	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	462	Total	C	N	O	S	0	0
			3738	2356	672	700	10		
2	2	270	Total	C	N	O	S	0	0
			2160	1381	385	386	8		

- Molecule 3 is a protein called Cilia- and flagella-associated protein 53.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	475	Total	C	N	O	S	0	0
			4023	2453	784	770	16		
3	4	148	Total	C	N	O	S	0	0
			1230	747	241	235	7		

- Molecule 4 is a protein called Nucleoside diphosphate kinase 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	5	376	Total	C	N	O	S	0	0
			2975	1885	517	553	20		
4	6	376	Total	C	N	O	S	0	0
			2975	1885	517	553	20		
4	j1	376	Total	C	N	O	S	0	0
			2975	1885	517	553	20		

- Molecule 5 is a protein called Cilia- and flagella-associated protein 107.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	8	176	Total	C	N	O	S	0	0
			1470	949	257	259	5		

- Molecule 6 is a protein called Cilia- and flagella-associated protein 141.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	94	Total	C	N	O	S	0	0
			806	507	150	145	4		
6	N1	94	Total	C	N	O	S	0	0
			806	507	150	145	4		

- Molecule 7 is a protein called Tektin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A0	54	Total	C	N	O	S	0	0
			444	271	89	83	1		
7	A1	359	Total	C	N	O	S	0	0
			2935	1818	527	580	10		
7	A2	401	Total	C	N	O	S	0	0
			3288	2038	595	645	10		
7	A3	401	Total	C	N	O	S	0	0
			3288	2038	595	645	10		
7	A4	399	Total	C	N	O	S	0	0
			3274	2029	592	643	10		
7	A5	169	Total	C	N	O	S	0	0
			1400	868	252	279	1		

- Molecule 8 is a protein called Tubulin alpha-3 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AA	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	AC	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	AE	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	AG	441	Total	C	N	O	S	0	0
			3440	2179	584	655	22		
8	AI	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	AK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	AM	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	AO	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	BC	431	Total	C	N	O	S	0	0
			3374	2140	573	639	22		
8	BE	441	Total	C	N	O	S	0	0
			3440	2179	584	655	22		
8	BG	434	Total	C	N	O	S	0	0
			3396	2153	576	645	22		
8	BI	441	Total	C	N	O	S	0	0
			3440	2179	584	655	22		
8	BK	433	Total	C	N	O	S	0	0
			3390	2150	575	643	22		
8	BM	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	BO	434	Total	C	N	O	S	0	0
			3396	2153	576	645	22		
8	CC	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	CE	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	CG	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	CI	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	CK	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	CM	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	CO	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	CQ	437	Total	C	N	O	S	0	0
			3410	2162	580	646	22		
8	DC	432	Total	C	N	O	S	0	0
			3382	2146	574	640	22		
8	DE	430	Total	C	N	O	S	0	0
			3366	2136	572	636	22		
8	DG	430	Total	C	N	O	S	0	0
			3366	2136	572	636	22		
8	DI	431	Total	C	N	O	S	0	0
			3374	2142	573	637	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	DK	431	Total	C	N	O	S	0	0
			3373	2141	573	637	22		
8	DM	432	Total	C	N	O	S	0	0
			3380	2143	574	641	22		
8	DO	431	Total	C	N	O	S	0	0
			3372	2139	573	638	22		
8	DQ	429	Total	C	N	O	S	0	0
			3360	2133	571	634	22		
8	EA	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	EC	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
8	EE	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	EG	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	EI	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	EK	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	EM	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	EO	437	Total	C	N	O	S	0	0
			3410	2162	580	646	22		
8	FA	430	Total	C	N	O	S	0	0
			3366	2136	572	636	22		
8	FC	430	Total	C	N	O	S	0	0
			3366	2136	572	636	22		
8	FE	430	Total	C	N	O	S	0	0
			3366	2136	572	636	22		
8	FG	428	Total	C	N	O	S	0	0
			3351	2127	570	632	22		
8	FI	430	Total	C	N	O	S	0	0
			3366	2136	572	636	22		
8	FK	431	Total	C	N	O	S	0	0
			3373	2141	573	637	22		
8	FM	430	Total	C	N	O	S	0	0
			3366	2136	572	636	22		
8	FO	428	Total	C	N	O	S	0	0
			3355	2129	570	634	22		
8	GA	430	Total	C	N	O	S	0	0
			3368	2137	572	637	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	GC	431	Total	C	N	O	S	0	0
			3373	2141	573	637	22		
8	GE	431	Total	C	N	O	S	0	0
			3373	2141	573	637	22		
8	GG	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	GI	433	Total	C	N	O	S	0	0
			3387	2148	575	642	22		
8	GK	433	Total	C	N	O	S	0	0
			3387	2148	575	642	22		
8	GM	434	Total	C	N	O	S	0	0
			3395	2152	576	645	22		
8	GO	434	Total	C	N	O	S	0	0
			3395	2152	576	645	22		
8	HA	431	Total	C	N	O	S	0	0
			3371	2140	573	636	22		
8	HC	434	Total	C	N	O	S	0	0
			3389	2149	576	642	22		
8	HE	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	HG	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	HI	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	HK	430	Total	C	N	O	S	0	0
			3366	2136	572	636	22		
8	HM	434	Total	C	N	O	S	0	0
			3389	2149	576	642	22		
8	HO	432	Total	C	N	O	S	0	0
			3381	2145	574	640	22		
8	IA	432	Total	C	N	O	S	0	0
			3380	2143	574	641	22		
8	IC	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	IE	441	Total	C	N	O	S	0	0
			3440	2179	584	655	22		
8	IG	433	Total	C	N	O	S	0	0
			3387	2148	575	642	22		
8	II	435	Total	C	N	O	S	0	0
			3399	2154	577	646	22		
8	IK	436	Total	C	N	O	S	0	0
			3411	2162	579	648	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	IM	434	Total	C	N	O	S	0	0
			3391	2150	576	643	22		
8	IO	440	Total	C	N	O	S	0	0
			3431	2174	583	652	22		
8	JC	434	Total	C	N	O	S	0	0
			3388	2147	576	643	22		
8	JE	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	JG	429	Total	C	N	O	S	0	0
			3360	2133	571	634	22		
8	JI	433	Total	C	N	O	S	0	0
			3390	2150	575	643	22		
8	JK	432	Total	C	N	O	S	0	0
			3381	2145	574	640	22		
8	JM	430	Total	C	N	O	S	0	0
			3366	2136	572	636	22		
8	JO	432	Total	C	N	O	S	0	0
			3379	2144	574	639	22		
8	JQ	435	Total	C	N	O	S	0	0
			3403	2158	578	645	22		
8	KA	432	Total	C	N	O	S	0	0
			3380	2143	574	641	22		
8	KC	433	Total	C	N	O	S	0	0
			3389	2149	576	642	22		
8	KE	434	Total	C	N	O	S	0	0
			3397	2153	577	645	22		
8	KG	432	Total	C	N	O	S	0	0
			3380	2143	574	641	22		
8	KI	431	Total	C	N	O	S	0	0
			3374	2140	573	639	22		
8	KK	431	Total	C	N	O	S	0	0
			3372	2139	573	638	22		
8	KM	432	Total	C	N	O	S	0	0
			3380	2143	574	641	22		
8	KO	433	Total	C	N	O	S	0	0
			3389	2149	576	642	22		
8	LA	434	Total	C	N	O	S	0	0
			3396	2153	576	645	22		
8	LC	431	Total	C	N	O	S	0	0
			3374	2140	573	639	22		
8	LE	433	Total	C	N	O	S	0	0
			3388	2149	575	642	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	LG	441	Total	C	N	O	S	0	0
			3440	2179	584	655	22		
8	LI	441	Total	C	N	O	S	0	0
			3440	2179	584	655	22		
8	LK	441	Total	C	N	O	S	0	0
			3440	2179	584	655	22		
8	LM	435	Total	C	N	O	S	0	0
			3404	2157	577	648	22		
8	LO	430	Total	C	N	O	S	0	0
			3366	2136	572	636	22		
8	MA	431	Total	C	N	O	S	0	0
			3374	2140	573	639	22		
8	MC	431	Total	C	N	O	S	0	0
			3374	2140	573	639	22		
8	ME	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	MG	432	Total	C	N	O	S	0	0
			3380	2143	574	641	22		
8	MI	432	Total	C	N	O	S	0	0
			3378	2142	574	640	22		
8	MK	433	Total	C	N	O	S	0	0
			3390	2150	575	643	22		
8	MM	432	Total	C	N	O	S	0	0
			3380	2143	574	641	22		
8	MO	428	Total	C	N	O	S	0	0
			3352	2129	570	631	22		
8	NA	428	Total	C	N	O	S	0	0
			3353	2128	570	633	22		
8	NC	428	Total	C	N	O	S	0	0
			3352	2129	570	631	22		
8	NE	434	Total	C	N	O	S	0	0
			3394	2152	576	644	22		
8	NG	432	Total	C	N	O	S	0	0
			3382	2146	574	640	22		
8	NI	431	Total	C	N	O	S	0	0
			3373	2141	573	637	22		
8	NK	431	Total	C	N	O	S	0	0
			3373	2141	573	637	22		
8	NM	432	Total	C	N	O	S	0	0
			3382	2146	574	640	22		
8	NO	432	Total	C	N	O	S	0	0
			3382	2146	574	640	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	OA	431	3374	2140	573	639	22	0	0
8	OC	430	3366	2136	572	636	22	0	0
8	OE	431	3372	2139	573	638	22	0	0
8	OG	430	3366	2136	572	636	22	0	0
8	OI	429	3360	2133	571	634	22	0	0
8	OK	431	3374	2140	573	639	22	0	0
8	OM	428	3352	2129	570	631	22	0	0
8	OO	425	3330	2114	567	628	21	0	0
8	PC	428	3352	2129	570	631	22	0	0
8	PE	425	3330	2115	566	628	21	0	0
8	PG	430	3366	2136	572	636	22	0	0
8	PI	430	3366	2136	572	636	22	0	0
8	PK	430	3367	2135	572	638	22	0	0
8	PM	432	3380	2143	574	641	22	0	0
8	PO	430	3366	2136	572	636	22	0	0
8	QC	428	3352	2129	570	631	22	0	0
8	QE	430	3366	2136	572	636	22	0	0
8	QG	428	3352	2129	570	631	22	0	0
8	QI	427	3345	2124	569	630	22	0	0
8	QK	427	3345	2124	569	630	22	0	0
8	QM	426	3338	2119	568	629	22	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	QO	427	Total	C	N	O	S	0	0
			3345	2124	569	630	22		
8	RC	428	Total	C	N	O	S	0	0
			3352	2129	570	631	22		
8	RE	428	Total	C	N	O	S	0	0
			3353	2128	570	633	22		
8	RG	428	Total	C	N	O	S	0	0
			3352	2129	570	631	22		
8	RI	429	Total	C	N	O	S	0	0
			3360	2133	571	634	22		
8	RK	430	Total	C	N	O	S	0	0
			3368	2137	572	637	22		
8	RM	429	Total	C	N	O	S	0	0
			3361	2132	571	636	22		
8	RO	428	Total	C	N	O	S	0	0
			3353	2128	570	633	22		
8	SA	429	Total	C	N	O	S	0	0
			3359	2131	571	635	22		
8	SC	428	Total	C	N	O	S	0	0
			3352	2129	570	631	22		
8	SE	428	Total	C	N	O	S	0	0
			3352	2129	570	631	22		
8	SG	427	Total	C	N	O	S	0	0
			3345	2124	569	630	22		
8	SI	429	Total	C	N	O	S	0	0
			3360	2133	571	634	22		
8	SK	427	Total	C	N	O	S	0	0
			3345	2124	569	630	22		
8	SM	425	Total	C	N	O	S	0	0
			3333	2118	567	626	22		
8	TA	426	Total	C	N	O	S	0	0
			3342	2121	568	631	22		
8	TC	426	Total	C	N	O	S	0	0
			3337	2120	568	627	22		
8	TE	429	Total	C	N	O	S	0	0
			3357	2130	571	634	22		
8	TG	426	Total	C	N	O	S	0	0
			3341	2122	568	629	22		
8	TI	427	Total	C	N	O	S	0	0
			3349	2126	569	632	22		
8	TK	428	Total	C	N	O	S	0	0
			3352	2129	570	631	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	TM	426	Total	C	N	O	S	0	0
			3341	2122	568	629	22		
8	UA	424	Total	C	N	O	S	0	0
			3327	2112	566	627	22		
8	UC	428	Total	C	N	O	S	0	0
			3351	2127	570	632	22		
8	UE	428	Total	C	N	O	S	0	0
			3351	2127	570	632	22		
8	UG	428	Total	C	N	O	S	0	0
			3353	2128	570	633	22		
8	UI	428	Total	C	N	O	S	0	0
			3352	2129	570	631	22		
8	UK	428	Total	C	N	O	S	0	0
			3353	2128	570	633	22		
8	UM	429	Total	C	N	O	S	0	0
			3359	2131	571	635	22		
8	UO	427	Total	C	N	O	S	0	0
			3347	2125	569	631	22		
8	VA	427	Total	C	N	O	S	0	0
			3345	2124	569	630	22		
8	VC	437	Total	C	N	O	S	0	0
			3410	2162	580	646	22		
8	VE	429	Total	C	N	O	S	0	0
			3358	2132	571	633	22		
8	VG	437	Total	C	N	O	S	0	0
			3410	2162	580	646	22		
8	VI	429	Total	C	N	O	S	0	0
			3360	2133	571	634	22		
8	VK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
8	VM	429	Total	C	N	O	S	0	0
			3359	2131	571	635	22		
8	VO	436	Total	C	N	O	S	0	0
			3403	2157	579	645	22		
8	WA	436	Total	C	N	O	S	0	0
			3403	2157	579	645	22		
8	WC	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	WE	433	Total	C	N	O	S	0	0
			3382	2144	575	641	22		
8	WG	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	WI	439	Total	C	N	O	S	0	0
			3424	2169	582	651	22		
8	WK	438	Total	C	N	O	S	0	0
			3418	2166	581	649	22		
8	WM	431	Total	C	N	O	S	0	0
			3374	2140	573	639	22		
8	WO	429	Total	C	N	O	S	0	0
			3358	2132	571	633	22		

- Molecule 9 is a protein called Tubulin beta-4B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AB	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
9	AD	435	Total	C	N	O	S	0	0
			3413	2141	583	663	26		
9	AF	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	AH	434	Total	C	N	O	S	0	0
			3404	2136	582	660	26		
9	AJ	434	Total	C	N	O	S	0	0
			3404	2136	582	660	26		
9	AL	434	Total	C	N	O	S	0	0
			3404	2136	582	660	26		
9	AN	434	Total	C	N	O	S	0	0
			3404	2136	582	660	26		
9	AP	432	Total	C	N	O	S	0	0
			3391	2129	580	656	26		
9	BB	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	BD	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	BF	429	Total	C	N	O	S	0	0
			3368	2116	577	649	26		
9	BH	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	BJ	431	Total	C	N	O	S	0	0
			3382	2124	579	653	26		
9	BL	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	BN	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	BP	430	3373	2119	578	650	26	0	0
9	CB	427	3356	2109	575	646	26	0	0
9	CD	431	3382	2124	579	653	26	0	0
9	CF	431	3382	2124	579	653	26	0	0
9	CH	431	3382	2124	579	653	26	0	0
9	CJ	428	3361	2112	576	647	26	0	0
9	CL	429	3368	2116	577	649	26	0	0
9	CN	431	3382	2124	579	653	26	0	0
9	CP	430	3373	2119	578	650	26	0	0
9	DB	429	3368	2116	577	649	26	0	0
9	DD	429	3368	2116	577	649	26	0	0
9	DF	430	3373	2119	578	650	26	0	0
9	DH	430	3373	2119	578	650	26	0	0
9	DJ	430	3373	2119	578	650	26	0	0
9	DL	431	3382	2124	579	653	26	0	0
9	DN	428	3361	2112	576	647	26	0	0
9	DP	430	3373	2119	578	650	26	0	0
9	EB	428	3361	2112	576	647	26	0	0
9	ED	428	3361	2112	576	647	26	0	0
9	EF	428	3361	2112	576	647	26	0	0
9	EH	428	3361	2112	576	647	26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	EJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	EL	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	EN	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	FB	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	FD	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	FF	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	FH	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	FJ	429	Total	C	N	O	S	0	0
			3368	2116	577	649	26		
9	FL	429	Total	C	N	O	S	0	0
			3368	2116	577	649	26		
9	FN	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	GB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	GD	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	GF	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	GH	431	Total	C	N	O	S	0	0
			3382	2124	579	653	26		
9	GJ	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	GL	431	Total	C	N	O	S	0	0
			3382	2124	579	653	26		
9	GN	431	Total	C	N	O	S	0	0
			3382	2124	579	653	26		
9	HB	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	HD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	HF	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	HH	431	Total	C	N	O	S	0	0
			3382	2124	579	653	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	HJ	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	HL	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	HN	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	HP	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	IB	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	ID	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	IF	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	IH	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	IJ	429	Total 3368	C 2116	N 577	O 649	S 26	0	0
9	IL	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	IN	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	IP	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	JB	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	JD	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	JF	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	JH	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	JJ	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	JL	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	JN	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	JP	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	KB	430	Total 3373	C 2119	N 578	O 650	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	KD	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	KF	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	KH	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	KJ	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	KL	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	KN	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	KP	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	LB	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
9	LD	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	LF	439	Total 3451	C 2165	N 587	O 673	S 26	0	0
9	LH	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	LJ	437	Total 3433	C 2155	N 585	O 667	S 26	0	0
9	LL	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	LN	432	Total 3391	C 2129	N 580	O 656	S 26	0	0
9	LP	429	Total 3368	C 2116	N 577	O 649	S 26	0	0
9	MB	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	MD	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	MF	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	MH	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	MJ	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	ML	430	Total 3373	C 2119	N 578	O 650	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	MN	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	MP	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	NB	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	ND	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	NF	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	NH	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	NJ	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	NL	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	NN	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	NP	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	OB	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	OD	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	OF	429	Total 3368	C 2116	N 577	O 649	S 26	0	0
9	OH	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	OJ	429	Total 3368	C 2116	N 577	O 649	S 26	0	0
9	OL	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	ON	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	OP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	PB	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	PD	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	PF	428	Total 3361	C 2112	N 576	O 647	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	PH	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	PJ	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	PL	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	PN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	PP	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	QB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	QD	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	QF	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	QH	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	QJ	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	QL	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	QN	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	QP	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	RD	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	RF	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	RH	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	RJ	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	RL	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	RN	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	RP	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	SB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	SD	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	SF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	SH	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	SJ	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	SL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	SN	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	TB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	TD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	TF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	TH	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	TJ	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	TL	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	TN	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	UB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	UD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	UF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	UH	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	UJ	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	UL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	UN	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	VB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	VD	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	VF	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	VH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	VJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	VL	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	VN	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	WB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	WD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	WF	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		
9	WH	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	WJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	WL	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	WN	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	WP	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

- Molecule 10 is a protein called Meiosis-specific nuclear structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	319	Total	C	N	O	S	0	0
			2769	1697	520	539	13		
10	C	279	Total	C	N	O	S	0	0
			2408	1493	445	459	11		

- Molecule 11 is a protein called Tektin-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	B0	39	Total	C	N	O	0	0
			334	203	66	65		

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	B1	364	Total	C	N	O	S	0	0
			2984	1840	547	586	11		
11	B2	414	Total	C	N	O	S	0	0
			3401	2093	627	667	14		
11	B3	414	Total	C	N	O	S	0	0
			3401	2093	627	667	14		
11	B4	415	Total	C	N	O	S	0	0
			3412	2099	631	668	14		
11	B5	203	Total	C	N	O	S	0	0
			1675	1036	305	325	9		
11	R0	196	Total	C	N	O	S	0	0
			1612	996	294	313	9		
11	R1	415	Total	C	N	O	S	0	0
			3412	2099	631	668	14		
11	R2	415	Total	C	N	O	S	0	0
			3412	2099	631	668	14		
11	R3	415	Total	C	N	O	S	0	0
			3412	2099	631	668	14		
11	R4	369	Total	C	N	O	S	0	0
			3025	1864	555	595	11		
11	R5	43	Total	C	N	O		0	0
			366	224	73	69			

- Molecule 12 is a protein called Tektin-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C0	179	Total	C	N	O	S	0	0
			1453	887	270	293	3		
12	C1	411	Total	C	N	O	S	0	0
			3354	2064	616	658	16		
12	C2	411	Total	C	N	O	S	0	0
			3354	2064	616	658	16		
12	C3	408	Total	C	N	O	S	0	0
			3332	2050	613	654	15		
12	C4	363	Total	C	N	O	S	0	0
			2944	1810	539	580	15		
12	C5	51	Total	C	N	O	S	0	0
			420	259	78	81	2		
12	C6	42	Total	C	N	O	S	0	0
			354	220	69	63	2		
12	S0	325	Total	C	N	O	S	0	0
			2675	1642	499	521	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	S1	441	Total	C	N	O	S	0	0
			3613	2223	669	705	16		
12	S2	441	Total	C	N	O	S	0	0
			3613	2223	669	705	16		
12	S3	441	Total	C	N	O	S	0	0
			3613	2223	669	705	16		
12	S4	303	Total	C	N	O	S	0	0
			2459	1515	446	485	13		
12	S5	313	Total	C	N	O	S	0	0
			2568	1581	472	504	11		
12	S6	422	Total	C	N	O	S	0	0
			3453	2130	633	676	14		
12	S7	422	Total	C	N	O	S	0	0
			3453	2130	633	676	14		
12	S8	420	Total	C	N	O	S	0	0
			3435	2117	631	673	14		
12	S9	276	Total	C	N	O	S	0	0
			2232	1370	409	440	13		

- Molecule 13 is a protein called Sperm-associated antigen 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	77	Total	C	N	O	S	0	0
			622	393	112	116	1		
13	K3	179	Total	C	N	O	S	0	0
			1460	911	268	274	7		

- Molecule 14 is a protein called Tektin-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D0	109	Total	C	N	O	S	0	0
			889	545	164	178	2		
14	D1	411	Total	C	N	O	S	0	0
			3370	2070	621	663	16		
14	D2	424	Total	C	N	O	S	0	0
			3480	2133	647	683	17		
14	D3	424	Total	C	N	O	S	0	0
			3480	2133	647	683	17		
14	D4	424	Total	C	N	O	S	0	0
			3480	2133	647	683	17		
14	D5	87	Total	C	N	O	S	0	0
			715	436	139	138	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	T0	119	Total	C	N	O	S	0	0
			957	588	173	193	3		
14	T1	440	Total	C	N	O	S	0	0
			3594	2206	664	706	18		
14	T2	440	Total	C	N	O	S	0	0
			3594	2206	664	706	18		
14	T3	441	Total	C	N	O	S	0	0
			3606	2215	665	708	18		
14	T4	395	Total	C	N	O	S	0	0
			3260	1997	608	639	16		
14	T5	119	Total	C	N	O	S	0	0
			975	600	180	191	4		

- Molecule 15 is a protein called Cilia- and flagella-associated protein 161.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	298	Total	C	N	O	S	0	0
			2372	1486	423	446	17		
15	F	297	Total	C	N	O	S	0	0
			2363	1481	421	444	17		
15	N2	297	Total	C	N	O	S	0	0
			2363	1481	421	444	17		

- Molecule 16 is a protein called Piercer of microtubule wall 2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	91	Total	C	N	O	S	0	0
			724	462	123	134	5		

- Molecule 17 is a protein called Protein FAM166A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H	162	Total	C	N	O	S	0	0
			1316	841	234	233	8		
17	I	175	Total	C	N	O	S	0	0
			1429	912	259	250	8		
17	J	161	Total	C	N	O	S	0	0
			1307	835	232	232	8		
17	K	174	Total	C	N	O	S	0	0
			1420	906	257	249	8		
17	L	162	Total	C	N	O	S	0	0
			1316	841	234	233	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	173	Total	C	N	O	S	0	0
			1413	902	256	247	8		
17	N	162	Total	C	N	O	S	0	0
			1316	841	234	233	8		
17	O7	173	Total	C	N	O	S	0	0
			1413	902	256	247	8		
17	O8	103	Total	C	N	O	S	0	0
			837	539	141	153	4		
17	O9	103	Total	C	N	O	S	0	0
			837	539	141	153	4		
17	P8	103	Total	C	N	O	S	0	0
			837	539	141	153	4		
17	P9	103	Total	C	N	O	S	0	0
			837	539	141	153	4		
17	Z2	51	Total	C	N	O	S	0	0
			412	265	74	69	4		
17	Z3	51	Total	C	N	O	S	0	0
			412	265	74	69	4		
17	Z4	51	Total	C	N	O	S	0	0
			412	265	74	69	4		
17	Z5	50	Total	C	N	O	S	0	0
			405	260	73	68	4		

- Molecule 18 is a protein called Cilia- and flagella-associated protein 68.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	I1	94	Total	C	N	O	S	0	0
			796	503	145	145	3		

- Molecule 19 is a protein called Cilia and flagella-associated protein 77.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	J1	111	Total	C	N	O	S	0	0
			934	596	177	158	3		
19	J2	247	Total	C	N	O	S	0	0
			2010	1269	377	353	11		
19	J3	247	Total	C	N	O	S	0	0
			2010	1269	377	353	11		
19	J4	245	Total	C	N	O	S	0	0
			1992	1259	374	348	11		
19	J5	126	Total	C	N	O	S	0	0
			1001	626	188	180	7		

- Molecule 20 is a protein called Family with sequence similarity 183, member B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	K1	118	Total	C	N	O	S	0	0
			1009	640	187	181	1		
20	K2	118	Total	C	N	O	S	0	0
			1009	640	187	181	1		

- Molecule 21 is a protein called Cilia- and flagella-associated protein 90.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L1	126	Total	C	N	O	S	0	0
			1034	652	193	187	2		

- Molecule 22 is a protein called Protein FAM166C.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	M1	96	Total	C	N	O		0	0
			826	529	148	149			
22	M2	96	Total	C	N	O		0	0
			826	529	148	149			
22	M3	156	Total	C	N	O	S	0	0
			1280	821	223	233	3		
22	M4	96	Total	C	N	O		0	0
			826	529	148	149			

- Molecule 23 is a protein called RIB43A-like with coiled-coils protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	74	Total	C	N	O	S	0	0
			627	386	124	115	2		
23	P	347	Total	C	N	O	S	0	0
			2875	1751	564	549	11		
23	Q	103	Total	C	N	O	S	0	0
			858	522	165	169	2		

- Molecule 24 is a protein called Dual specificity phosphatase 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	O1	166	Total	C	N	O	S	0	0
			1332	856	225	244	7		
24	O2	167	Total	C	N	O	S	0	0
			1344	865	226	246	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
24	O3	167	Total	C	N	O	S	0	0
			1344	865	226	246	7		
24	O4	167	Total	C	N	O	S	0	0
			1344	865	226	246	7		

- Molecule 25 is a protein called EF-hand domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	O5	491	Total	C	N	O	S	0	0
			4047	2608	682	740	17		
25	O6	48	Total	C	N	O	S	0	0
			383	240	73	69	1		
25	T	280	Total	C	N	O	S	0	0
			2365	1525	396	433	11		
25	U	503	Total	C	N	O	S	0	0
			4138	2671	694	756	17		
25	V	524	Total	C	N	O	S	0	0
			4299	2773	720	789	17		

- Molecule 26 is a protein called Testis expressed 49.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P1	76	Total	C	N	O	S	0	0
			637	409	117	109	2		
26	P2	98	Total	C	N	O	S	0	0
			825	531	152	140	2		

- Molecule 27 is a protein called Testis-expressed sequence 37 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	P3	135	Total	C	N	O	S	0	0
			1103	719	187	190	7		
27	P4	155	Total	C	N	O	S	0	0
			1272	829	211	224	8		
27	P5	155	Total	C	N	O	S	0	0
			1272	829	211	224	8		
27	P6	154	Total	C	N	O	S	0	0
			1263	824	210	221	8		
27	P7	53	Total	C	N	O	S	0	0
			447	293	70	82	2		

- Molecule 28 is a protein called Tektin bundle-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Q1	199	Total	C	N	O	S	0	0
			1634	1046	305	277	6		
28	Q2	199	Total	C	N	O	S	0	0
			1634	1046	305	277	6		
28	Q3	199	Total	C	N	O	S	0	0
			1634	1046	305	277	6		
28	Q4	199	Total	C	N	O	S	0	0
			1634	1046	305	277	6		
28	Q5	18	Total	C	N	O	S	0	0
			152	101	28	22	1		

- Molecule 29 is a protein called RIB43A-like with coiled-coils protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	R	195	Total	C	N	O	S	0	0
			1648	1010	324	304	10		
29	S	323	Total	C	N	O	S	0	0
			2728	1662	539	512	15		

- Molecule 30 is a protein called Tektin-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U0	355	Total	C	N	O	S	0	0
			2897	1793	524	557	23		
30	U1	415	Total	C	N	O	S	0	0
			3396	2101	624	646	25		
30	U2	415	Total	C	N	O	S	0	0
			3396	2101	624	646	25		
30	U3	415	Total	C	N	O	S	0	0
			3396	2101	624	646	25		
30	U4	201	Total	C	N	O	S	0	0
			1664	1019	319	319	7		
30	U5	318	Total	C	N	O	S	0	0
			2607	1604	484	501	18		
30	U6	410	Total	C	N	O	S	0	0
			3360	2079	619	638	24		
30	U7	410	Total	C	N	O	S	0	0
			3360	2079	619	638	24		
30	U8	410	Total	C	N	O	S	0	0
			3360	2079	619	638	24		
30	U9	182	Total	C	N	O	S	0	0
			1486	932	266	275	13		
30	V0	208	Total	C	N	O	S	0	0
			1695	1061	300	319	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
30	V1	389	Total	C	N	O	S	0	0
			3185	1967	583	612	23		
30	V2	389	Total	C	N	O	S	0	0
			3185	1967	583	612	23		
30	V3	389	Total	C	N	O	S	0	0
			3185	1967	583	612	23		
30	V4	284	Total	C	N	O	S	0	0
			2325	1425	429	454	17		
30	V5	294	Total	C	N	O	S	0	0
			2408	1493	432	466	17		
30	V6	364	Total	C	N	O	S	0	0
			2980	1841	542	577	20		
30	V7	334	Total	C	N	O	S	0	0
			2736	1700	493	522	21		
30	V8	303	Total	C	N	O	S	0	0
			2477	1539	442	479	17		
30	V9	99	Total	C	N	O	S	0	0
			800	507	136	153	4		
30	W0	298	Total	C	N	O	S	0	0
			2447	1513	449	465	20		
30	W2	300	Total	C	N	O	S	0	0
			2458	1522	447	469	20		
30	W4	323	Total	C	N	O	S	0	0
			2662	1655	486	502	19		
30	W5	323	Total	C	N	O	S	0	0
			2662	1655	486	502	19		
30	W6	323	Total	C	N	O	S	0	0
			2662	1655	486	502	19		
30	W7	323	Total	C	N	O	S	0	0
			2662	1655	486	502	19		

- Molecule 31 is a protein called EF-hand domain-containing family member C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	741	Total	C	N	O	S	0	0
			6116	3950	1019	1119	28		
31	X	741	Total	C	N	O	S	0	0
			6116	3950	1019	1119	28		
31	Y	742	Total	C	N	O	S	0	0
			6124	3954	1021	1121	28		
31	Z	741	Total	C	N	O	S	0	0
			6116	3950	1019	1119	28		

- Molecule 32 is a protein called Spermatid-specific manchette-related protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X0	25	Total	C	N	O	S	0	0
			200	124	34	38	4		
32	X1	24	Total	C	N	O	S	0	0
			192	118	33	37	4		
32	X2	24	Total	C	N	O	S	0	0
			192	118	33	37	4		
32	X3	25	Total	C	N	O	S	0	0
			200	124	34	38	4		

- Molecule 33 is a protein called Protein phosphatase 1 regulatory subunit 32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	X4	330	Total	C	N	O	S	0	0
			2619	1638	471	509	1		
33	X5	133	Total	C	N	O	S	0	0
			1041	658	182	196	5		

- Molecule 34 is a protein called Testis-specific serine/threonine-protein kinase 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	X6	267	Total	C	N	O	S	0	0
			2097	1335	380	374	8		
34	X7	267	Total	C	N	O	S	0	0
			2097	1335	380	374	8		
34	X8	267	Total	C	N	O	S	0	0
			2097	1335	380	374	8		

- Molecule 35 is a protein called Cilia- and flagella-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	XA	185	Total	C	N	O	S	0	0
			1540	990	269	274	7		
35	XB	185	Total	C	N	O	S	0	0
			1540	990	269	274	7		
35	XC	185	Total	C	N	O	S	0	0
			1540	990	269	274	7		
35	XD	185	Total	C	N	O	S	0	0
			1540	990	269	274	7		
35	XE	185	Total	C	N	O	S	0	0
			1540	990	269	274	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
35	XF	185	Total	C	N	O	S	0	0
			1540	990	269	274	7		
35	XG	185	Total	C	N	O	S	0	0
			1540	990	269	274	7		
35	XH	185	Total	C	N	O	S	0	0
			1540	990	269	274	7		

- Molecule 36 is a protein called Outer dense fiber protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Y0	63	Total	C	N	O	S	0	0
			483	313	87	80	3		
36	Y1	240	Total	C	N	O	S	0	0
			1828	1176	317	327	8		
36	Y2	225	Total	C	N	O	S	0	0
			1711	1101	294	309	7		
36	Y3	63	Total	C	N	O	S	0	0
			483	313	87	80	3		
36	Y4	185	Total	C	N	O	S	0	0
			1412	910	241	255	6		
36	Y5	85	Total	C	N	O	S	0	0
			644	411	110	120	3		

- Molecule 37 is a protein called Parkin coregulated gene protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	YA	220	Total	C	N	O	S	0	0
			1775	1148	300	317	10		
37	YB	220	Total	C	N	O	S	0	0
			1775	1148	300	317	10		
37	YC	220	Total	C	N	O	S	0	0
			1775	1148	300	317	10		
37	YD	220	Total	C	N	O	S	0	0
			1775	1148	300	317	10		
37	YE	220	Total	C	N	O	S	0	0
			1775	1148	300	317	10		
37	YF	220	Total	C	N	O	S	0	0
			1775	1148	300	317	10		
37	YG	220	Total	C	N	O	S	0	0
			1775	1148	300	317	10		
37	YH	220	Total	C	N	O	S	0	0
			1775	1148	300	317	10		

- Molecule 38 is a protein called Testis, prostate and placenta-expressed protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Z1	33	279	181	48	48	2	0	0

- Molecule 39 is a protein called Cilia- and flagella-associated protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	a	294	2499	1522	478	485	14	0	0
39	a6	70	572	363	99	108	2	0	0
39	b	244	2092	1266	420	399	7	0	0
39	c	413	3528	2141	692	680	15	0	0
39	d	135	1155	701	233	219	2	0	0

- Molecule 40 is a protein called Uncharacterized protein C10orf82 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	a1	156	1277	818	218	231	10	0	0
40	a2	156	1277	818	218	231	10	0	0
40	a3	156	1277	818	218	231	10	0	0
40	a4	156	1277	818	218	231	10	0	0

- Molecule 41 is a protein called Coiled-coil domain-containing protein 105.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	b1	132	1081	670	212	188	11	0	0
41	b2	381	3091	1915	598	555	23	0	0
41	b3	382	3102	1921	602	556	23	0	0
41	b4	382	3102	1921	602	556	23	0	0
41	b5	333	2705	1675	519	489	22	0	0

- Molecule 42 is a protein called Cilia- and flagella-associated protein 52.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	e	607	Total	C	N	O	S	0	0
			4689	2967	818	872	32		
42	f	607	Total	C	N	O	S	0	0
			4689	2967	818	872	32		
42	g	607	Total	C	N	O	S	0	0
			4689	2967	818	872	32		

- Molecule 43 is a protein called Enkurin.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	h	247	Total	C	N	O	S	0	0
			2014	1287	351	367	9		
43	i	245	Total	C	N	O	S	0	0
			1999	1279	349	362	9		
43	j	244	Total	C	N	O	S	0	0
			1993	1276	348	360	9		
43	k	245	Total	C	N	O	S	0	0
			1999	1279	349	362	9		

- Molecule 44 is a protein called Testis-expressed protein 43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	h1	97	Total	C	N	O	S	0	0
			787	506	139	136	6		
44	h2	99	Total	C	N	O	S	0	0
			809	518	147	138	6		
44	h3	99	Total	C	N	O	S	0	0
			809	518	147	138	6		
44	h4	98	Total	C	N	O	S	0	0
			798	512	143	137	6		

- Molecule 45 is a protein called Protein Flattop.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i1	116	Total	C	N	O	S	0	0
			909	579	162	165	3		
45	l	116	Total	C	N	O	S	0	0
			909	579	162	165	3		
45	m	116	Total	C	N	O	S	0	0
			909	579	162	165	3		
45	n	116	Total	C	N	O	S	0	0
			909	579	162	165	3		

- Molecule 46 is a protein called EF-hand calcium-binding domain-containing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	i2	180	Total	C	N	O	S	0	0
			1500	956	263	271	10		
46	i3	180	Total	C	N	O	S	0	0
			1500	956	263	271	10		
46	i4	180	Total	C	N	O	S	0	0
			1500	956	263	271	10		

- Molecule 47 is a protein called Cilia- and flagella-associated protein 210.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	o	199	Total	C	N	O	S	0	0
			1688	1040	321	322	5		
47	p	395	Total	C	N	O	S	0	0
			3300	2045	601	643	11		

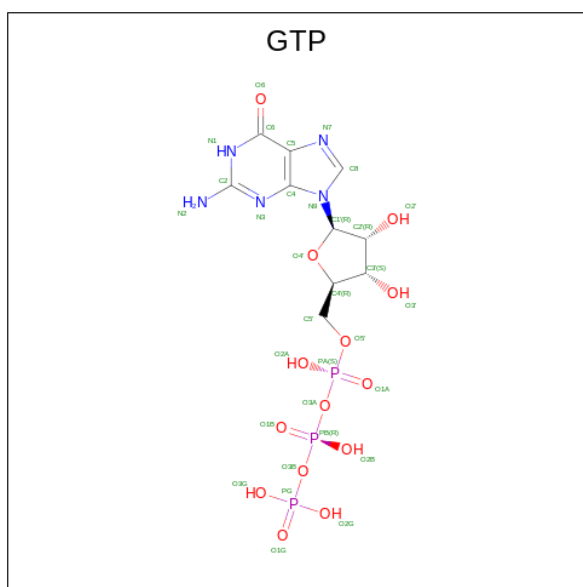
- Molecule 48 is a protein called Cilia- and flagella-associated protein 276.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
48	q	75	Total	C	N	O	0	0
			599	379	108	112		
48	r	78	Total	C	N	O	0	0
			625	395	114	116		
48	s	78	Total	C	N	O	0	0
			625	395	114	116		

- Molecule 49 is a protein called Piercer of microtubule wall 1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	y	111	Total	C	N	O	S	0	0
			911	577	165	166	3		

- Molecule 50 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
50	AA	1	Total 32	C 10	N 5	O 14	P 3	0
50	AC	1	Total 32	C 10	N 5	O 14	P 3	0
50	AE	1	Total 32	C 10	N 5	O 14	P 3	0
50	AG	1	Total 32	C 10	N 5	O 14	P 3	0
50	AI	1	Total 32	C 10	N 5	O 14	P 3	0
50	AK	1	Total 32	C 10	N 5	O 14	P 3	0
50	AM	1	Total 32	C 10	N 5	O 14	P 3	0
50	AO	1	Total 32	C 10	N 5	O 14	P 3	0
50	BC	1	Total 32	C 10	N 5	O 14	P 3	0
50	BE	1	Total 32	C 10	N 5	O 14	P 3	0
50	BG	1	Total 32	C 10	N 5	O 14	P 3	0
50	BI	1	Total 32	C 10	N 5	O 14	P 3	0
50	BK	1	Total 32	C 10	N 5	O 14	P 3	0
50	BM	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
50	BO	1	Total 32	C 10	N 5	O 14	P 3	0
50	CC	1	Total 32	C 10	N 5	O 14	P 3	0
50	CE	1	Total 32	C 10	N 5	O 14	P 3	0
50	CG	1	Total 32	C 10	N 5	O 14	P 3	0
50	CI	1	Total 32	C 10	N 5	O 14	P 3	0
50	CK	1	Total 32	C 10	N 5	O 14	P 3	0
50	CM	1	Total 32	C 10	N 5	O 14	P 3	0
50	CO	1	Total 32	C 10	N 5	O 14	P 3	0
50	CQ	1	Total 32	C 10	N 5	O 14	P 3	0
50	DC	1	Total 32	C 10	N 5	O 14	P 3	0
50	DE	1	Total 32	C 10	N 5	O 14	P 3	0
50	DG	1	Total 32	C 10	N 5	O 14	P 3	0
50	DI	1	Total 32	C 10	N 5	O 14	P 3	0
50	DK	1	Total 32	C 10	N 5	O 14	P 3	0
50	DM	1	Total 32	C 10	N 5	O 14	P 3	0
50	DO	1	Total 32	C 10	N 5	O 14	P 3	0
50	DQ	1	Total 32	C 10	N 5	O 14	P 3	0
50	EA	1	Total 32	C 10	N 5	O 14	P 3	0
50	EC	1	Total 32	C 10	N 5	O 14	P 3	0
50	EE	1	Total 32	C 10	N 5	O 14	P 3	0
50	EG	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
50	EI	1	Total 32	C 10	N 5	O 14	P 3	0
50	EK	1	Total 32	C 10	N 5	O 14	P 3	0
50	EM	1	Total 32	C 10	N 5	O 14	P 3	0
50	EO	1	Total 32	C 10	N 5	O 14	P 3	0
50	FA	1	Total 32	C 10	N 5	O 14	P 3	0
50	FC	1	Total 32	C 10	N 5	O 14	P 3	0
50	FE	1	Total 32	C 10	N 5	O 14	P 3	0
50	FG	1	Total 32	C 10	N 5	O 14	P 3	0
50	FI	1	Total 32	C 10	N 5	O 14	P 3	0
50	FK	1	Total 32	C 10	N 5	O 14	P 3	0
50	FM	1	Total 32	C 10	N 5	O 14	P 3	0
50	FO	1	Total 32	C 10	N 5	O 14	P 3	0
50	GA	1	Total 32	C 10	N 5	O 14	P 3	0
50	GC	1	Total 32	C 10	N 5	O 14	P 3	0
50	GE	1	Total 32	C 10	N 5	O 14	P 3	0
50	GG	1	Total 32	C 10	N 5	O 14	P 3	0
50	GI	1	Total 32	C 10	N 5	O 14	P 3	0
50	GK	1	Total 32	C 10	N 5	O 14	P 3	0
50	GM	1	Total 32	C 10	N 5	O 14	P 3	0
50	GO	1	Total 32	C 10	N 5	O 14	P 3	0
50	HA	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
50	HC	1	Total 32	C 10	N 5	O 14	P 3	0
50	HE	1	Total 32	C 10	N 5	O 14	P 3	0
50	HG	1	Total 32	C 10	N 5	O 14	P 3	0
50	HI	1	Total 32	C 10	N 5	O 14	P 3	0
50	HK	1	Total 32	C 10	N 5	O 14	P 3	0
50	HM	1	Total 32	C 10	N 5	O 14	P 3	0
50	HO	1	Total 32	C 10	N 5	O 14	P 3	0
50	IA	1	Total 32	C 10	N 5	O 14	P 3	0
50	IC	1	Total 32	C 10	N 5	O 14	P 3	0
50	IE	1	Total 32	C 10	N 5	O 14	P 3	0
50	IG	1	Total 32	C 10	N 5	O 14	P 3	0
50	II	1	Total 32	C 10	N 5	O 14	P 3	0
50	IK	1	Total 32	C 10	N 5	O 14	P 3	0
50	IM	1	Total 32	C 10	N 5	O 14	P 3	0
50	IO	1	Total 32	C 10	N 5	O 14	P 3	0
50	JC	1	Total 32	C 10	N 5	O 14	P 3	0
50	JE	1	Total 32	C 10	N 5	O 14	P 3	0
50	JG	1	Total 32	C 10	N 5	O 14	P 3	0
50	JI	1	Total 32	C 10	N 5	O 14	P 3	0
50	JK	1	Total 32	C 10	N 5	O 14	P 3	0
50	JM	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
50	JO	1	Total 32	C 10	N 5	O 14	P 3	0
50	JQ	1	Total 32	C 10	N 5	O 14	P 3	0
50	KA	1	Total 32	C 10	N 5	O 14	P 3	0
50	KC	1	Total 32	C 10	N 5	O 14	P 3	0
50	KE	1	Total 32	C 10	N 5	O 14	P 3	0
50	KG	1	Total 32	C 10	N 5	O 14	P 3	0
50	KI	1	Total 32	C 10	N 5	O 14	P 3	0
50	KK	1	Total 32	C 10	N 5	O 14	P 3	0
50	KM	1	Total 32	C 10	N 5	O 14	P 3	0
50	KO	1	Total 32	C 10	N 5	O 14	P 3	0
50	LA	1	Total 32	C 10	N 5	O 14	P 3	0
50	LC	1	Total 32	C 10	N 5	O 14	P 3	0
50	LE	1	Total 32	C 10	N 5	O 14	P 3	0
50	LG	1	Total 32	C 10	N 5	O 14	P 3	0
50	LI	1	Total 32	C 10	N 5	O 14	P 3	0
50	LK	1	Total 32	C 10	N 5	O 14	P 3	0
50	LM	1	Total 32	C 10	N 5	O 14	P 3	0
50	LO	1	Total 32	C 10	N 5	O 14	P 3	0
50	MA	1	Total 32	C 10	N 5	O 14	P 3	0
50	MC	1	Total 32	C 10	N 5	O 14	P 3	0
50	ME	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
50	MG	1	Total 32	C 10	N 5	O 14	P 3	0
50	MI	1	Total 32	C 10	N 5	O 14	P 3	0
50	MK	1	Total 32	C 10	N 5	O 14	P 3	0
50	MM	1	Total 32	C 10	N 5	O 14	P 3	0
50	MO	1	Total 32	C 10	N 5	O 14	P 3	0
50	NA	1	Total 32	C 10	N 5	O 14	P 3	0
50	NC	1	Total 32	C 10	N 5	O 14	P 3	0
50	NE	1	Total 32	C 10	N 5	O 14	P 3	0
50	NG	1	Total 32	C 10	N 5	O 14	P 3	0
50	NI	1	Total 32	C 10	N 5	O 14	P 3	0
50	NK	1	Total 32	C 10	N 5	O 14	P 3	0
50	NM	1	Total 32	C 10	N 5	O 14	P 3	0
50	NO	1	Total 32	C 10	N 5	O 14	P 3	0
50	OA	1	Total 32	C 10	N 5	O 14	P 3	0
50	OC	1	Total 32	C 10	N 5	O 14	P 3	0
50	OE	1	Total 32	C 10	N 5	O 14	P 3	0
50	OG	1	Total 32	C 10	N 5	O 14	P 3	0
50	OI	1	Total 32	C 10	N 5	O 14	P 3	0
50	OK	1	Total 32	C 10	N 5	O 14	P 3	0
50	OM	1	Total 32	C 10	N 5	O 14	P 3	0
50	OO	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
50	PC	1	Total 32	C 10	N 5	O 14	P 3	0
50	PE	1	Total 32	C 10	N 5	O 14	P 3	0
50	PG	1	Total 32	C 10	N 5	O 14	P 3	0
50	PI	1	Total 32	C 10	N 5	O 14	P 3	0
50	PK	1	Total 32	C 10	N 5	O 14	P 3	0
50	PM	1	Total 32	C 10	N 5	O 14	P 3	0
50	PO	1	Total 32	C 10	N 5	O 14	P 3	0
50	QC	1	Total 32	C 10	N 5	O 14	P 3	0
50	QE	1	Total 32	C 10	N 5	O 14	P 3	0
50	QG	1	Total 32	C 10	N 5	O 14	P 3	0
50	QI	1	Total 32	C 10	N 5	O 14	P 3	0
50	QK	1	Total 32	C 10	N 5	O 14	P 3	0
50	QM	1	Total 32	C 10	N 5	O 14	P 3	0
50	QO	1	Total 32	C 10	N 5	O 14	P 3	0
50	RC	1	Total 32	C 10	N 5	O 14	P 3	0
50	RE	1	Total 32	C 10	N 5	O 14	P 3	0
50	RG	1	Total 32	C 10	N 5	O 14	P 3	0
50	RI	1	Total 32	C 10	N 5	O 14	P 3	0
50	RK	1	Total 32	C 10	N 5	O 14	P 3	0
50	RM	1	Total 32	C 10	N 5	O 14	P 3	0
50	RO	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
50	SA	1	Total 32	C 10	N 5	O 14	P 3	0
50	SC	1	Total 32	C 10	N 5	O 14	P 3	0
50	SE	1	Total 32	C 10	N 5	O 14	P 3	0
50	SG	1	Total 32	C 10	N 5	O 14	P 3	0
50	SI	1	Total 32	C 10	N 5	O 14	P 3	0
50	SK	1	Total 32	C 10	N 5	O 14	P 3	0
50	SM	1	Total 32	C 10	N 5	O 14	P 3	0
50	TA	1	Total 32	C 10	N 5	O 14	P 3	0
50	TC	1	Total 32	C 10	N 5	O 14	P 3	0
50	TE	1	Total 32	C 10	N 5	O 14	P 3	0
50	TG	1	Total 32	C 10	N 5	O 14	P 3	0
50	TI	1	Total 32	C 10	N 5	O 14	P 3	0
50	TK	1	Total 32	C 10	N 5	O 14	P 3	0
50	TM	1	Total 32	C 10	N 5	O 14	P 3	0
50	UA	1	Total 32	C 10	N 5	O 14	P 3	0
50	UC	1	Total 32	C 10	N 5	O 14	P 3	0
50	UE	1	Total 32	C 10	N 5	O 14	P 3	0
50	UG	1	Total 32	C 10	N 5	O 14	P 3	0
50	UI	1	Total 32	C 10	N 5	O 14	P 3	0
50	UK	1	Total 32	C 10	N 5	O 14	P 3	0
50	UM	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
50	UO	1	32	10	5	14	3	0
50	VA	1	32	10	5	14	3	0
50	VC	1	32	10	5	14	3	0
50	VE	1	32	10	5	14	3	0
50	VG	1	32	10	5	14	3	0
50	VI	1	32	10	5	14	3	0
50	VK	1	32	10	5	14	3	0
50	VM	1	32	10	5	14	3	0
50	VO	1	32	10	5	14	3	0
50	WA	1	32	10	5	14	3	0
50	WC	1	32	10	5	14	3	0
50	WE	1	32	10	5	14	3	0
50	WG	1	32	10	5	14	3	0
50	WI	1	32	10	5	14	3	0
50	WK	1	32	10	5	14	3	0
50	WM	1	32	10	5	14	3	0
50	WO	1	32	10	5	14	3	0

- Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	AA	1	Total 1	Mg 1	0
51	AC	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
51	AE	1	Total 1	Mg 1	0
51	AG	1	Total 1	Mg 1	0
51	AI	1	Total 1	Mg 1	0
51	AK	1	Total 1	Mg 1	0
51	AM	1	Total 1	Mg 1	0
51	AO	1	Total 1	Mg 1	0
51	BC	1	Total 1	Mg 1	0
51	BE	1	Total 1	Mg 1	0
51	BG	1	Total 1	Mg 1	0
51	BI	1	Total 1	Mg 1	0
51	BK	1	Total 1	Mg 1	0
51	BM	1	Total 1	Mg 1	0
51	BO	1	Total 1	Mg 1	0
51	CC	1	Total 1	Mg 1	0
51	CE	1	Total 1	Mg 1	0
51	CG	1	Total 1	Mg 1	0
51	CI	1	Total 1	Mg 1	0
51	CK	1	Total 1	Mg 1	0
51	CM	1	Total 1	Mg 1	0
51	CO	1	Total 1	Mg 1	0
51	CQ	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
51	DC	1	1	1	0
51	DE	1	1	1	0
51	DG	1	1	1	0
51	DI	1	1	1	0
51	DK	1	1	1	0
51	DM	1	1	1	0
51	DO	1	1	1	0
51	DQ	1	1	1	0
51	EA	1	1	1	0
51	EC	1	1	1	0
51	EE	1	1	1	0
51	EG	1	1	1	0
51	EI	1	1	1	0
51	EK	1	1	1	0
51	EM	1	1	1	0
51	EO	1	1	1	0
51	FA	1	1	1	0
51	FC	1	1	1	0
51	FE	1	1	1	0
51	FG	1	1	1	0
51	FI	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
51	FK	1	1	1	0
51	FM	1	1	1	0
51	FO	1	1	1	0
51	GA	1	1	1	0
51	GC	1	1	1	0
51	GE	1	1	1	0
51	GG	1	1	1	0
51	GI	1	1	1	0
51	GK	1	1	1	0
51	GM	1	1	1	0
51	GO	1	1	1	0
51	HA	1	1	1	0
51	HC	1	1	1	0
51	HE	1	1	1	0
51	HG	1	1	1	0
51	HI	1	1	1	0
51	HK	1	1	1	0
51	HM	1	1	1	0
51	HO	1	1	1	0
51	IA	1	1	1	0
51	IC	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
51	IE	1	1	1	0
51	IG	1	1	1	0
51	II	1	1	1	0
51	IK	1	1	1	0
51	IM	1	1	1	0
51	IO	1	1	1	0
51	JC	1	1	1	0
51	JE	1	1	1	0
51	JG	1	1	1	0
51	JI	1	1	1	0
51	JK	1	1	1	0
51	JM	1	1	1	0
51	JO	1	1	1	0
51	JQ	1	1	1	0
51	KA	1	1	1	0
51	KC	1	1	1	0
51	KE	1	1	1	0
51	KG	1	1	1	0
51	KI	1	1	1	0
51	KK	1	1	1	0
51	KM	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
51	KO	1	1	1	0
51	LA	1	1	1	0
51	LC	1	1	1	0
51	LE	1	1	1	0
51	LG	1	1	1	0
51	LI	1	1	1	0
51	LK	1	1	1	0
51	LM	1	1	1	0
51	LO	1	1	1	0
51	MA	1	1	1	0
51	MC	1	1	1	0
51	ME	1	1	1	0
51	MG	1	1	1	0
51	MI	1	1	1	0
51	MK	1	1	1	0
51	MM	1	1	1	0
51	MO	1	1	1	0
51	NA	1	1	1	0
51	NC	1	1	1	0
51	NE	1	1	1	0
51	NG	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
51	NI	1	Total 1	Mg 1	0
51	NK	1	Total 1	Mg 1	0
51	NM	1	Total 1	Mg 1	0
51	NO	1	Total 1	Mg 1	0
51	OA	1	Total 1	Mg 1	0
51	OC	1	Total 1	Mg 1	0
51	OE	1	Total 1	Mg 1	0
51	OG	1	Total 1	Mg 1	0
51	OI	1	Total 1	Mg 1	0
51	OK	1	Total 1	Mg 1	0
51	OM	1	Total 1	Mg 1	0
51	OO	1	Total 1	Mg 1	0
51	PC	1	Total 1	Mg 1	0
51	PE	1	Total 1	Mg 1	0
51	PG	1	Total 1	Mg 1	0
51	PI	1	Total 1	Mg 1	0
51	PK	1	Total 1	Mg 1	0
51	PM	1	Total 1	Mg 1	0
51	PO	1	Total 1	Mg 1	0
51	QC	1	Total 1	Mg 1	0
51	QE	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
51	QG	1	Total 1	Mg 1	0
51	QI	1	Total 1	Mg 1	0
51	QK	1	Total 1	Mg 1	0
51	QM	1	Total 1	Mg 1	0
51	QO	1	Total 1	Mg 1	0
51	RC	1	Total 1	Mg 1	0
51	RE	1	Total 1	Mg 1	0
51	RG	1	Total 1	Mg 1	0
51	RI	1	Total 1	Mg 1	0
51	RK	1	Total 1	Mg 1	0
51	RM	1	Total 1	Mg 1	0
51	RO	1	Total 1	Mg 1	0
51	SA	1	Total 1	Mg 1	0
51	SC	1	Total 1	Mg 1	0
51	SE	1	Total 1	Mg 1	0
51	SG	1	Total 1	Mg 1	0
51	SI	1	Total 1	Mg 1	0
51	SK	1	Total 1	Mg 1	0
51	SM	1	Total 1	Mg 1	0
51	TA	1	Total 1	Mg 1	0
51	TC	1	Total 1	Mg 1	0

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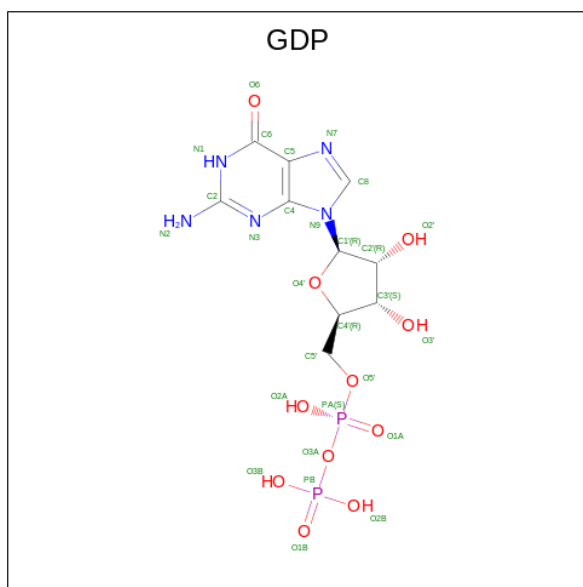
Mol	Chain	Residues	Atoms		AltConf
51	TE	1	Total 1	Mg 1	0
51	TG	1	Total 1	Mg 1	0
51	TI	1	Total 1	Mg 1	0
51	TK	1	Total 1	Mg 1	0
51	TM	1	Total 1	Mg 1	0
51	UA	1	Total 1	Mg 1	0
51	UC	1	Total 1	Mg 1	0
51	UE	1	Total 1	Mg 1	0
51	UG	1	Total 1	Mg 1	0
51	UI	1	Total 1	Mg 1	0
51	UK	1	Total 1	Mg 1	0
51	UM	1	Total 1	Mg 1	0
51	UO	1	Total 1	Mg 1	0
51	VA	1	Total 1	Mg 1	0
51	VC	1	Total 1	Mg 1	0
51	VE	1	Total 1	Mg 1	0
51	VG	1	Total 1	Mg 1	0
51	VI	1	Total 1	Mg 1	0
51	VK	1	Total 1	Mg 1	0
51	VM	1	Total 1	Mg 1	0
51	VO	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
51	WA	1	Total	Mg	0
			1	1	
51	WC	1	Total	Mg	0
			1	1	
51	WE	1	Total	Mg	0
			1	1	
51	WG	1	Total	Mg	0
			1	1	
51	WI	1	Total	Mg	0
			1	1	
51	WK	1	Total	Mg	0
			1	1	
51	WM	1	Total	Mg	0
			1	1	
51	WO	1	Total	Mg	0
			1	1	

- Molecule 52 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms				AltConf	
52	AB	1	Total	C	N	O	P	0
			28	10	5	11	2	
52	AD	1	Total	C	N	O	P	0
			28	10	5	11	2	
52	AF	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
52	AH	1	28	10	5	11	2	0
52	AJ	1	28	10	5	11	2	0
52	AL	1	28	10	5	11	2	0
52	AN	1	28	10	5	11	2	0
52	AP	1	28	10	5	11	2	0
52	BB	1	28	10	5	11	2	0
52	BD	1	28	10	5	11	2	0
52	BF	1	28	10	5	11	2	0
52	BH	1	28	10	5	11	2	0
52	BJ	1	28	10	5	11	2	0
52	BL	1	28	10	5	11	2	0
52	BN	1	28	10	5	11	2	0
52	BP	1	28	10	5	11	2	0
52	CB	1	28	10	5	11	2	0
52	CD	1	28	10	5	11	2	0
52	CF	1	28	10	5	11	2	0
52	CH	1	28	10	5	11	2	0
52	CJ	1	28	10	5	11	2	0
52	CL	1	28	10	5	11	2	0
52	CN	1	28	10	5	11	2	0
52	CP	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
52	DB	1	Total 28	C 10	N 5	O 11	P 2	0
52	DD	1	Total 28	C 10	N 5	O 11	P 2	0
52	DF	1	Total 28	C 10	N 5	O 11	P 2	0
52	DH	1	Total 28	C 10	N 5	O 11	P 2	0
52	DJ	1	Total 28	C 10	N 5	O 11	P 2	0
52	DL	1	Total 28	C 10	N 5	O 11	P 2	0
52	DN	1	Total 28	C 10	N 5	O 11	P 2	0
52	DP	1	Total 28	C 10	N 5	O 11	P 2	0
52	EB	1	Total 28	C 10	N 5	O 11	P 2	0
52	ED	1	Total 28	C 10	N 5	O 11	P 2	0
52	EF	1	Total 28	C 10	N 5	O 11	P 2	0
52	EH	1	Total 28	C 10	N 5	O 11	P 2	0
52	EJ	1	Total 28	C 10	N 5	O 11	P 2	0
52	EL	1	Total 28	C 10	N 5	O 11	P 2	0
52	EN	1	Total 28	C 10	N 5	O 11	P 2	0
52	FB	1	Total 28	C 10	N 5	O 11	P 2	0
52	FD	1	Total 28	C 10	N 5	O 11	P 2	0
52	FF	1	Total 28	C 10	N 5	O 11	P 2	0
52	FH	1	Total 28	C 10	N 5	O 11	P 2	0
52	FJ	1	Total 28	C 10	N 5	O 11	P 2	0
52	FL	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
52	FN	1	28	10	5	11	2	0
52	GB	1	28	10	5	11	2	0
52	GD	1	28	10	5	11	2	0
52	GF	1	28	10	5	11	2	0
52	GH	1	28	10	5	11	2	0
52	GJ	1	28	10	5	11	2	0
52	GL	1	28	10	5	11	2	0
52	GN	1	28	10	5	11	2	0
52	HB	1	28	10	5	11	2	0
52	HD	1	28	10	5	11	2	0
52	HF	1	28	10	5	11	2	0
52	HH	1	28	10	5	11	2	0
52	HJ	1	28	10	5	11	2	0
52	HL	1	28	10	5	11	2	0
52	HN	1	28	10	5	11	2	0
52	HP	1	28	10	5	11	2	0
52	IB	1	28	10	5	11	2	0
52	ID	1	28	10	5	11	2	0
52	IF	1	28	10	5	11	2	0
52	IH	1	28	10	5	11	2	0
52	IJ	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
52	IL	1	Total 28	C 10	N 5	O 11	P 2	0
52	IN	1	Total 28	C 10	N 5	O 11	P 2	0
52	IP	1	Total 28	C 10	N 5	O 11	P 2	0
52	JB	1	Total 28	C 10	N 5	O 11	P 2	0
52	JD	1	Total 28	C 10	N 5	O 11	P 2	0
52	JF	1	Total 28	C 10	N 5	O 11	P 2	0
52	JH	1	Total 28	C 10	N 5	O 11	P 2	0
52	JJ	1	Total 28	C 10	N 5	O 11	P 2	0
52	JL	1	Total 28	C 10	N 5	O 11	P 2	0
52	JN	1	Total 28	C 10	N 5	O 11	P 2	0
52	JP	1	Total 28	C 10	N 5	O 11	P 2	0
52	KB	1	Total 28	C 10	N 5	O 11	P 2	0
52	KD	1	Total 28	C 10	N 5	O 11	P 2	0
52	KF	1	Total 28	C 10	N 5	O 11	P 2	0
52	KH	1	Total 28	C 10	N 5	O 11	P 2	0
52	KJ	1	Total 28	C 10	N 5	O 11	P 2	0
52	KL	1	Total 28	C 10	N 5	O 11	P 2	0
52	KN	1	Total 28	C 10	N 5	O 11	P 2	0
52	KP	1	Total 28	C 10	N 5	O 11	P 2	0
52	LB	1	Total 28	C 10	N 5	O 11	P 2	0
52	LD	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
52	LF	1	28	10	5	11	2	0
52	LH	1	28	10	5	11	2	0
52	LJ	1	28	10	5	11	2	0
52	LL	1	28	10	5	11	2	0
52	LN	1	28	10	5	11	2	0
52	LP	1	28	10	5	11	2	0
52	MB	1	28	10	5	11	2	0
52	MD	1	28	10	5	11	2	0
52	MF	1	28	10	5	11	2	0
52	MH	1	28	10	5	11	2	0
52	MJ	1	28	10	5	11	2	0
52	ML	1	28	10	5	11	2	0
52	MN	1	28	10	5	11	2	0
52	MP	1	28	10	5	11	2	0
52	NB	1	28	10	5	11	2	0
52	ND	1	28	10	5	11	2	0
52	NF	1	28	10	5	11	2	0
52	NH	1	28	10	5	11	2	0
52	NJ	1	28	10	5	11	2	0
52	NL	1	28	10	5	11	2	0
52	NN	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
52	NP	1	28	10	5	11	2	0
52	OB	1	28	10	5	11	2	0
52	OD	1	28	10	5	11	2	0
52	OF	1	28	10	5	11	2	0
52	OH	1	28	10	5	11	2	0
52	OJ	1	28	10	5	11	2	0
52	OL	1	28	10	5	11	2	0
52	ON	1	28	10	5	11	2	0
52	OP	1	28	10	5	11	2	0
52	PB	1	28	10	5	11	2	0
52	PD	1	28	10	5	11	2	0
52	PF	1	28	10	5	11	2	0
52	PH	1	28	10	5	11	2	0
52	PJ	1	28	10	5	11	2	0
52	PL	1	28	10	5	11	2	0
52	PN	1	28	10	5	11	2	0
52	PP	1	28	10	5	11	2	0
52	QB	1	28	10	5	11	2	0
52	QD	1	28	10	5	11	2	0
52	QF	1	28	10	5	11	2	0
52	QH	1	28	10	5	11	2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
52	QJ	1	Total 28	C 10	N 5	O 11	P 2	0
52	QL	1	Total 28	C 10	N 5	O 11	P 2	0
52	QN	1	Total 28	C 10	N 5	O 11	P 2	0
52	QP	1	Total 28	C 10	N 5	O 11	P 2	0
52	RD	1	Total 28	C 10	N 5	O 11	P 2	0
52	RF	1	Total 28	C 10	N 5	O 11	P 2	0
52	RH	1	Total 28	C 10	N 5	O 11	P 2	0
52	RJ	1	Total 28	C 10	N 5	O 11	P 2	0
52	RL	1	Total 28	C 10	N 5	O 11	P 2	0
52	RN	1	Total 28	C 10	N 5	O 11	P 2	0
52	RP	1	Total 28	C 10	N 5	O 11	P 2	0
52	SB	1	Total 28	C 10	N 5	O 11	P 2	0
52	SD	1	Total 28	C 10	N 5	O 11	P 2	0
52	SF	1	Total 28	C 10	N 5	O 11	P 2	0
52	SH	1	Total 28	C 10	N 5	O 11	P 2	0
52	SJ	1	Total 28	C 10	N 5	O 11	P 2	0
52	SL	1	Total 28	C 10	N 5	O 11	P 2	0
52	SN	1	Total 28	C 10	N 5	O 11	P 2	0
52	TB	1	Total 28	C 10	N 5	O 11	P 2	0
52	TD	1	Total 28	C 10	N 5	O 11	P 2	0
52	TF	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
52	TH	1	28	10	5	11	2	0
52	TJ	1	28	10	5	11	2	0
52	TL	1	28	10	5	11	2	0
52	TN	1	28	10	5	11	2	0
52	UB	1	28	10	5	11	2	0
52	UD	1	28	10	5	11	2	0
52	UF	1	28	10	5	11	2	0
52	UH	1	28	10	5	11	2	0
52	UJ	1	28	10	5	11	2	0
52	UL	1	28	10	5	11	2	0
52	UN	1	28	10	5	11	2	0
52	VB	1	28	10	5	11	2	0
52	VD	1	28	10	5	11	2	0
52	VF	1	28	10	5	11	2	0
52	VH	1	28	10	5	11	2	0
52	VJ	1	28	10	5	11	2	0
52	VL	1	28	10	5	11	2	0
52	VN	1	28	10	5	11	2	0
52	WB	1	28	10	5	11	2	0
52	WD	1	28	10	5	11	2	0
52	WF	1	28	10	5	11	2	0

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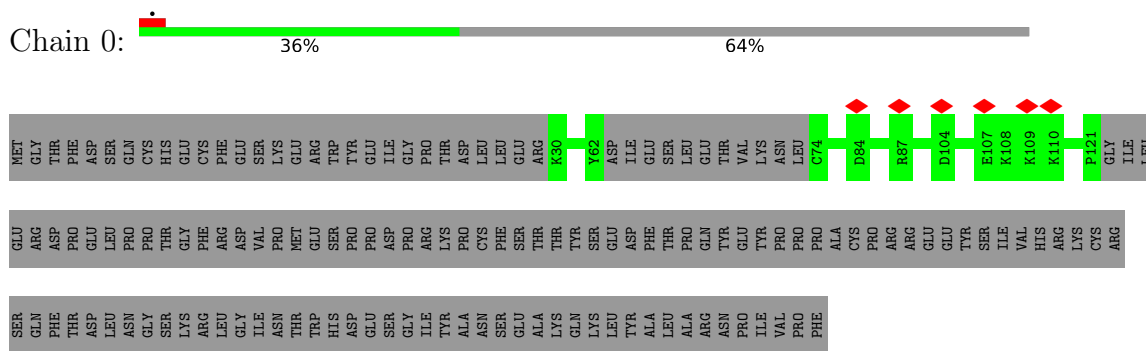
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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
52	WH	1	Total 28	C 10	N 5	O 11	P 2	0
52	WJ	1	Total 28	C 10	N 5	O 11	P 2	0
52	WL	1	Total 28	C 10	N 5	O 11	P 2	0
52	WN	1	Total 28	C 10	N 5	O 11	P 2	0
52	WP	1	Total 28	C 10	N 5	O 11	P 2	0

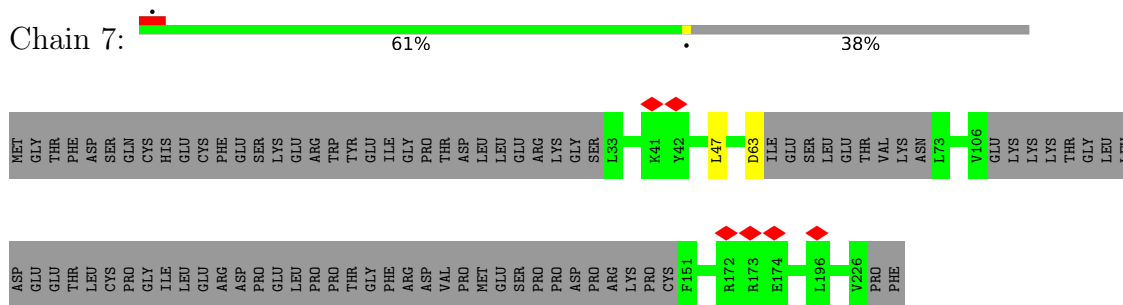
3 Residue-property plots i

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 and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Cilia- and flagella-associated protein 95

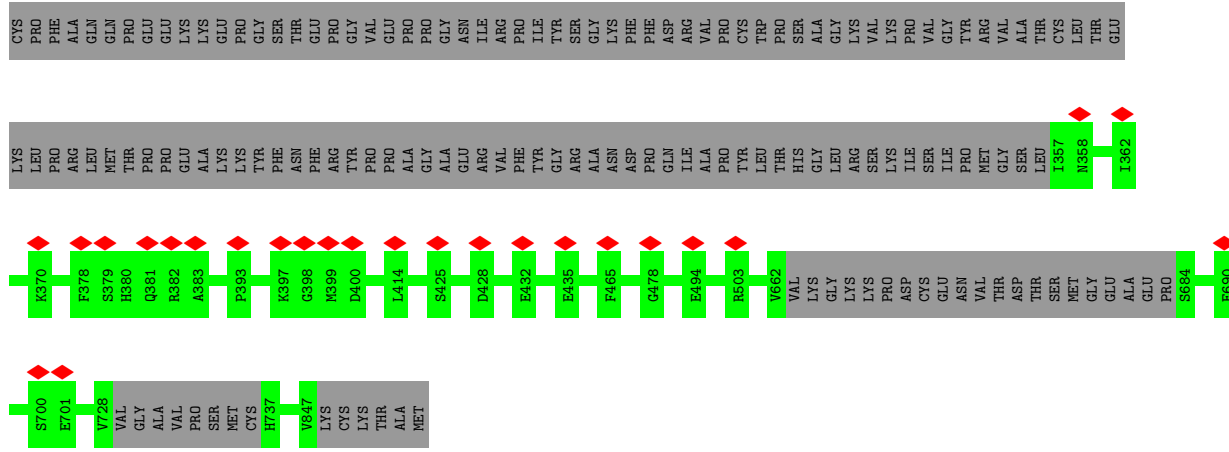


- Molecule 1: Cilia- and flagella-associated protein 95

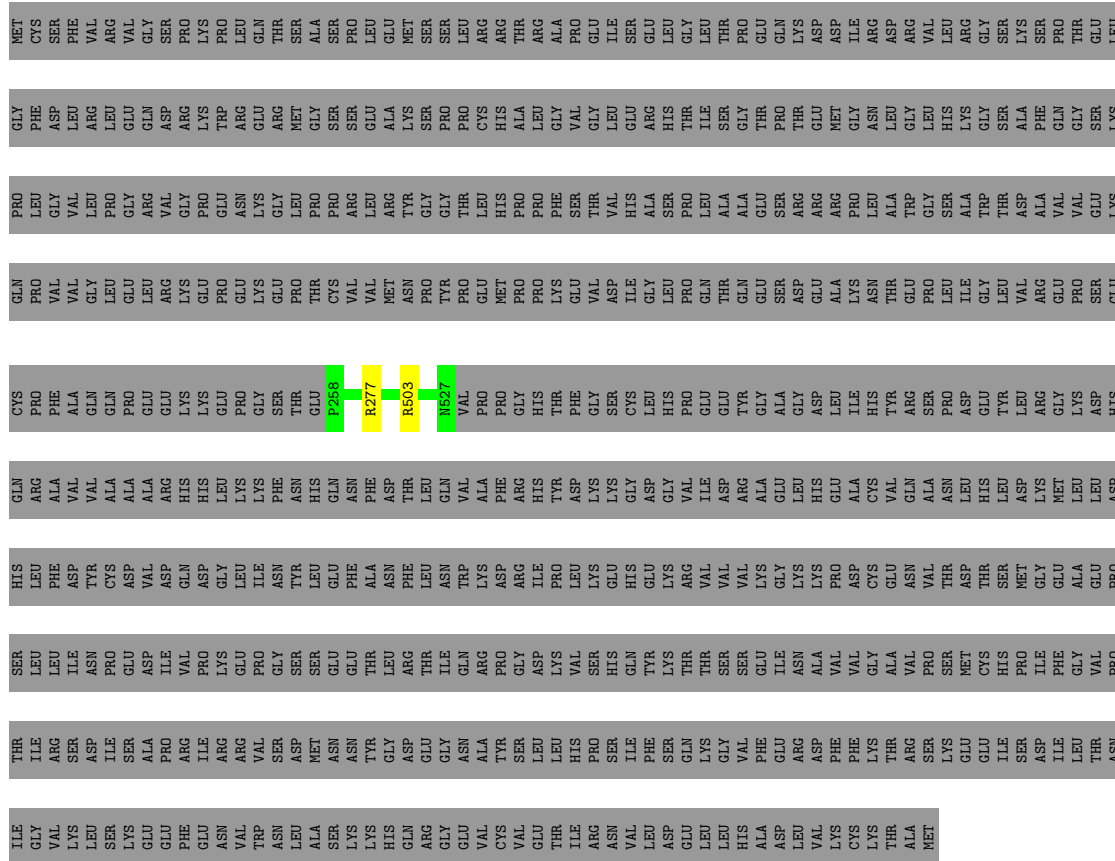


- Molecule 2: EF-hand domain-containing family member B

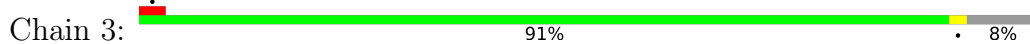




● Molecule 2: EF-hand domain-containing family member B



● Molecule 3: Cilia- and flagella-associated protein 53



ILE
ARG
ALA
GLU
ALA
ILE
CYS

• Molecule 7: Tektin-1



MET
A2
D89
G402
ASP
ASP
HIS
GLY
ALA
TRP
GLU
GLY
GLY
ILE
ARG
ALA
GLU
ALA
ILE
CYS

• Molecule 7: Tektin-1



MET
A2
D78
E202
K203
V204
L232
L389
G402
ASP
ASP
HIS
GLY
ALA
TRP
GLU
GLY
ILE
ARG
ALA
GLU
ALA
ILE
CYS

• Molecule 7: Tektin-1



MET
ALA
LYS
L4
E202
K203
D264
G402
ASP
ASP
HIS
GLY
ALA
TRP
GLY
GLY
ILE
ARG
ALA
ILE
CYS

• Molecule 7: Tektin-1



MET
A2
D90
LEU
THR
LYR
THR
LYR
THR
ARG
LEU
SER
GLU
ARG
SER
LEU
LEU
LEU
SER
TYR
LYS
LEU
PRO
LEU
HIS
ILE
THR
GLU
GLY
CYS
LEU
GLY
TYR
ARG
GLY
VAL
ASP
LEU
VAL
HIS
ASP
ASP
VAL
PHE
VAL
ILE
ASN
GLN
GLY
LEU
LEU
GLN
LYS
GLU
THR
LYS
ALA
ASP
ALA
ILE
ILE
HIS
GLY
VAL

MET
ASN
LEU
LEU
ILE
ARG
THR
LEU
THR
GLU
SER
THR
G186
V204
L232
K239
LEU
LEU
ASN
ALA
VAL
ASP
GLN
ILE
LEU
SER
GLN
THR
ALA
ASN
ASP
LEU
ARG
ARG
GLN
GLY
VAL
VAL
ASP
GLU
VAL
ASP
GLU
PHE
ASN
ILE
ASN
GLY
LEU
LEU
CYS
ARG
THR
LYS
ALA
ASP
ALA
TYR
ARG
ASN
LEU
ILE
LYS

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

GLU
ILE
GLN
GLU
ASP
ASN
HIS
ASN
VAL
TRP
VAL
GLU
ALA
ARG
LEU
SER
GLY
LYS
GLU
THR
LEU
ALA
GLN
ALA
G186
THR
GLN
LEU
ASN
ALA
VAL
ILE
THR
GLN
GLN
TYR
ARG
GLY
PRO
GLN
ALA
LEU
VAL
LEU
THR
THR
ASN
THR
HIS
ILE
TYR
ILE
ASP
VAL
GLN
VAL
LEU
CYS
ARG
MET
MET
MET
ARG
GLN
TYR
ARG
SER
ILE
PRO
PRO

ARG
ASP
GLY
ASP
ASP
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GLY
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ARG
ALA
ALA
ALA
ILE
ILE
CYS

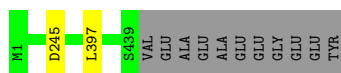
• Molecule 8: Tubulin alpha-3 chain



K1
M36
I83
D367
S439
VAL
GLU
ALA
GLU
ALA
GLU
GLY
GLU
GLU
TYR

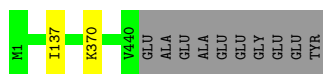
• Molecule 8: Tubulin alpha-3 chain

Chain AC:  97%



- Molecule 8: Tubulin alpha-3 chain

Chain AE:  97%



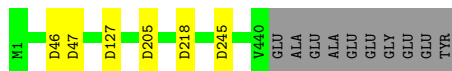
- Molecule 8: Tubulin alpha-3 chain

Chain AG:  98%



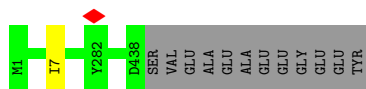
- Molecule 8: Tubulin alpha-3 chain

Chain AI:  96%



- Molecule 8: Tubulin alpha-3 chain

Chain AK:  97%



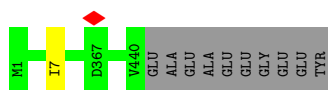
- Molecule 8: Tubulin alpha-3 chain

Chain AM:  97%



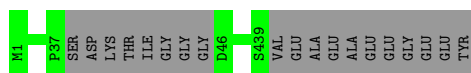
- Molecule 8: Tubulin alpha-3 chain

Chain AO:  98%



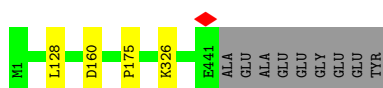
- Molecule 8: Tubulin alpha-3 chain

Chain BC:  96%



• Molecule 8: Tubulin alpha-3 chain

Chain BE:  97%



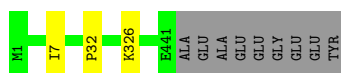
• Molecule 8: Tubulin alpha-3 chain

Chain BG:  96%



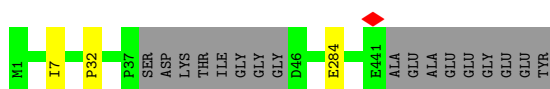
• Molecule 8: Tubulin alpha-3 chain

Chain BI:  97%



• Molecule 8: Tubulin alpha-3 chain

Chain BK:  96%



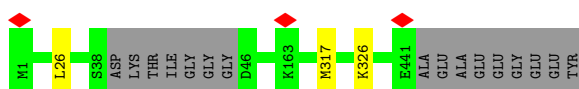
• Molecule 8: Tubulin alpha-3 chain

Chain BM:  96%



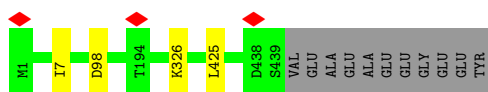
• Molecule 8: Tubulin alpha-3 chain

Chain BO:  96%



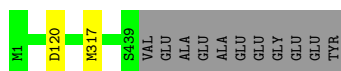
• Molecule 8: Tubulin alpha-3 chain

Chain CC:  97%



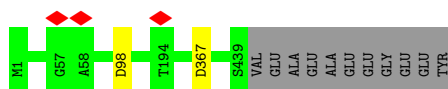
- Molecule 8: Tubulin alpha-3 chain

Chain CE:  97%



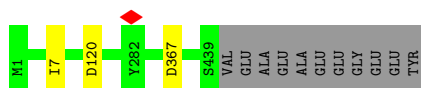
- Molecule 8: Tubulin alpha-3 chain

Chain CG:  97%



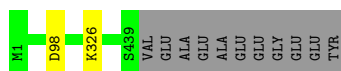
- Molecule 8: Tubulin alpha-3 chain

Chain CI:  97%



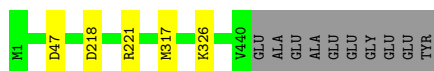
- Molecule 8: Tubulin alpha-3 chain

Chain CK:  97%



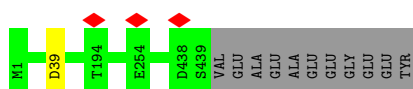
- Molecule 8: Tubulin alpha-3 chain

Chain CM:  97%

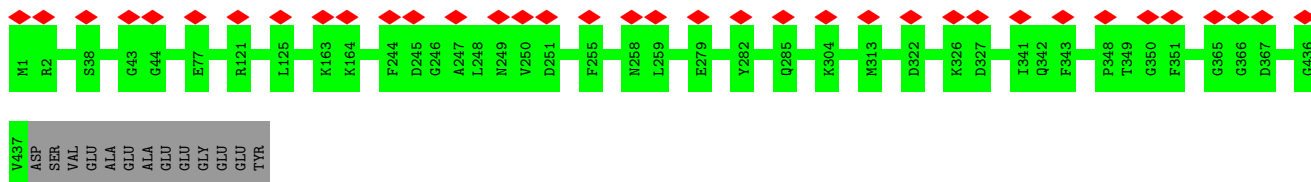


- Molecule 8: Tubulin alpha-3 chain

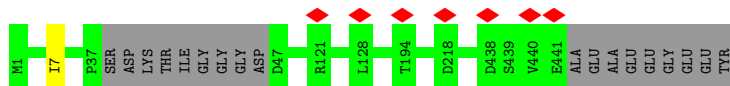
Chain CO:  97%



- Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



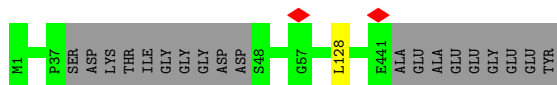
• Molecule 8: Tubulin alpha-3 chain



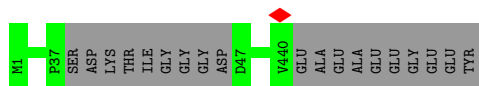
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain

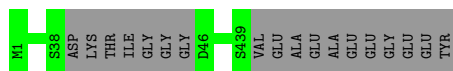


• Molecule 8: Tubulin alpha-3 chain

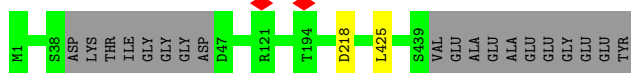


• Molecule 8: Tubulin alpha-3 chain

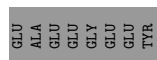
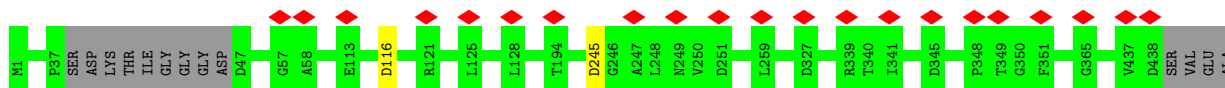




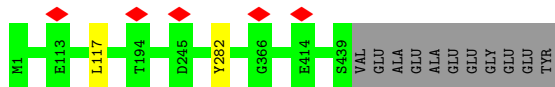
• Molecule 8: Tubulin alpha-3 chain



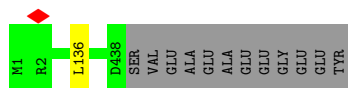
• Molecule 8: Tubulin alpha-3 chain



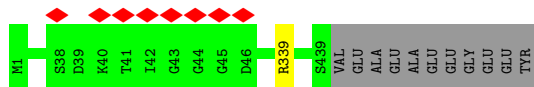
• Molecule 8: Tubulin alpha-3 chain



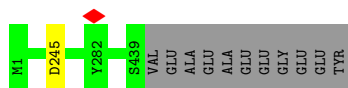
• Molecule 8: Tubulin alpha-3 chain



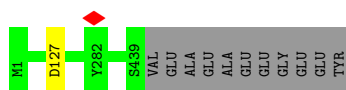
• Molecule 8: Tubulin alpha-3 chain



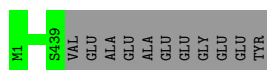
• Molecule 8: Tubulin alpha-3 chain



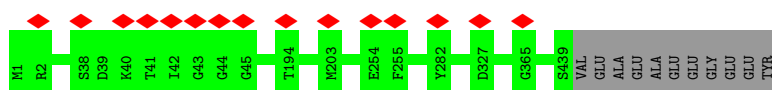
• Molecule 8: Tubulin alpha-3 chain



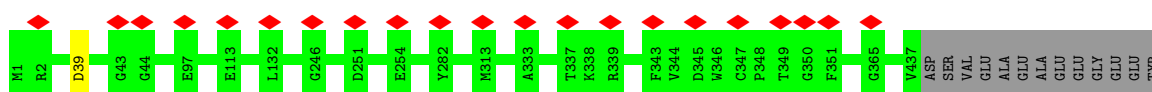
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



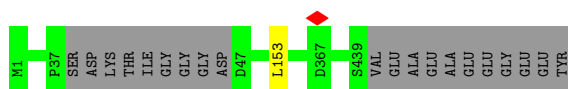
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain

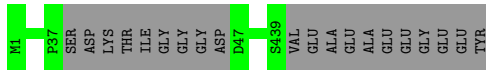


• Molecule 8: Tubulin alpha-3 chain



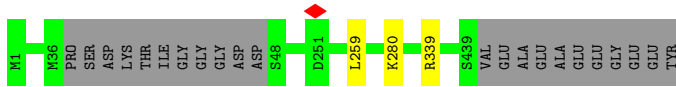
• Molecule 8: Tubulin alpha-3 chain





- Molecule 8: Tubulin alpha-3 chain

Chain FG: 94% 5%



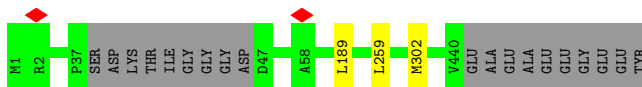
- Molecule 8: Tubulin alpha-3 chain

Chain FI: 95% 5%



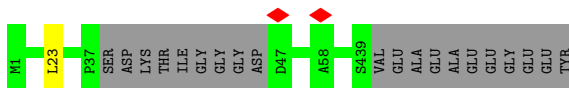
- Molecule 8: Tubulin alpha-3 chain

Chain FK: 95% 5%



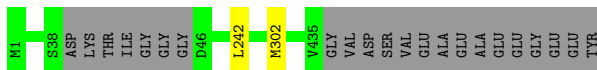
- Molecule 8: Tubulin alpha-3 chain

Chain FM: 95% 5%



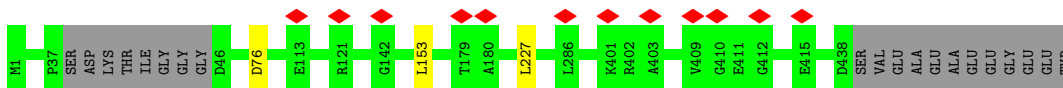
- Molecule 8: Tubulin alpha-3 chain

Chain FO: 95% 5%

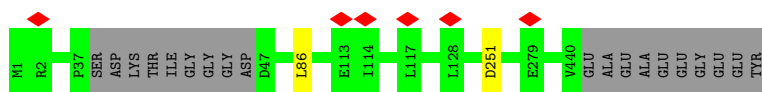


- Molecule 8: Tubulin alpha-3 chain

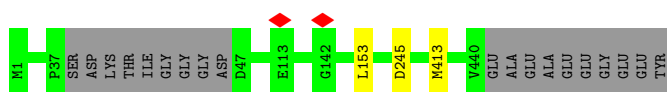
Chain GA: 95% 5%



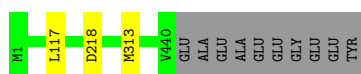
- Molecule 8: Tubulin alpha-3 chain



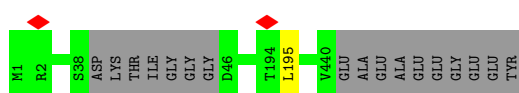
• Molecule 8: Tubulin alpha-3 chain



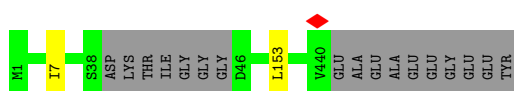
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



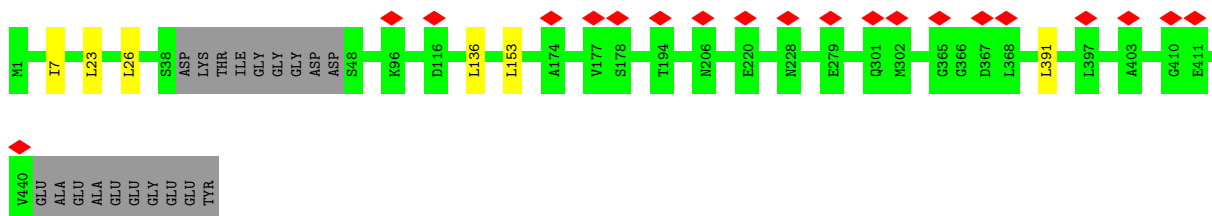
• Molecule 8: Tubulin alpha-3 chain



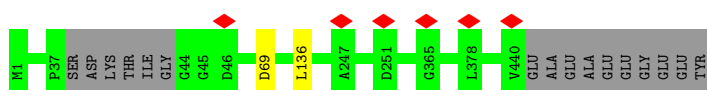
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



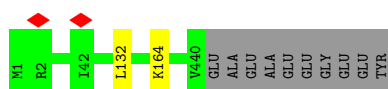
• Molecule 8: Tubulin alpha-3 chain



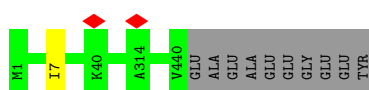
• Molecule 8: Tubulin alpha-3 chain



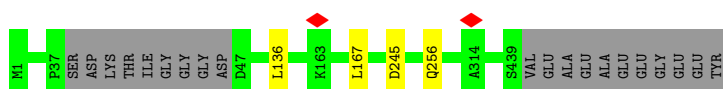
• Molecule 8: Tubulin alpha-3 chain



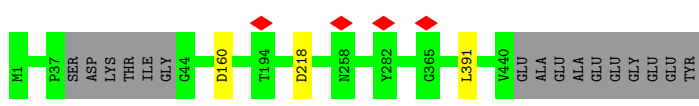
• Molecule 8: Tubulin alpha-3 chain



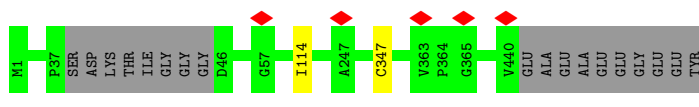
• Molecule 8: Tubulin alpha-3 chain



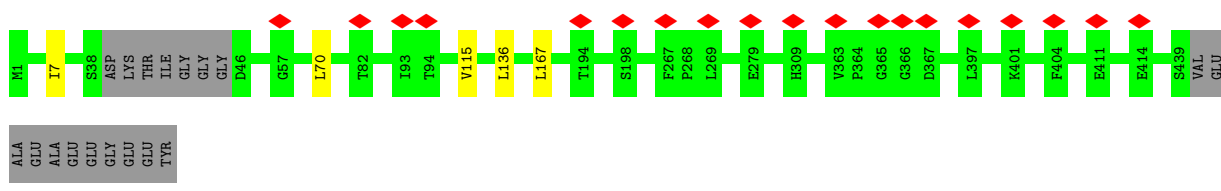
• Molecule 8: Tubulin alpha-3 chain



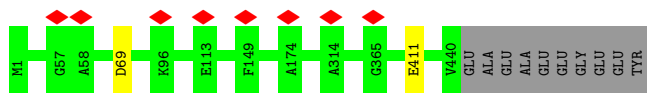
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



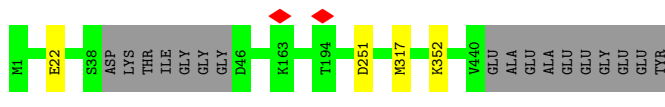
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain

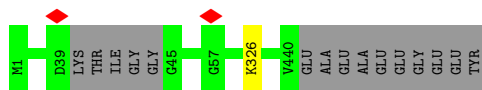


• Molecule 8: Tubulin alpha-3 chain

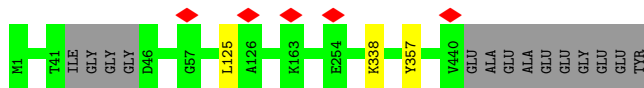


• Molecule 8: Tubulin alpha-3 chain

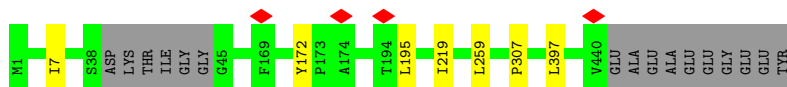




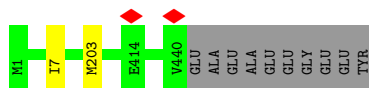
- Molecule 8: Tubulin alpha-3 chain



- Molecule 8: Tubulin alpha-3 chain



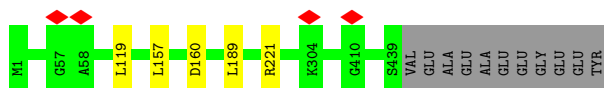
- Molecule 8: Tubulin alpha-3 chain



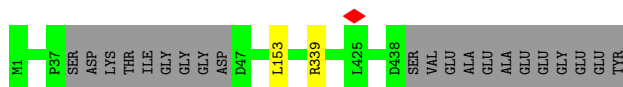
- Molecule 8: Tubulin alpha-3 chain



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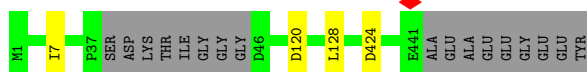


- Molecule 8: Tubulin alpha-3 chain



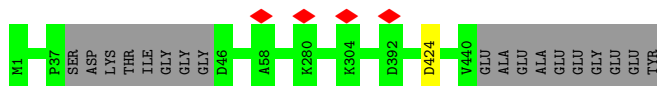
- Molecule 8: Tubulin alpha-3 chain

Chain JI:  95%



- Molecule 8: Tubulin alpha-3 chain

Chain JK:  96%



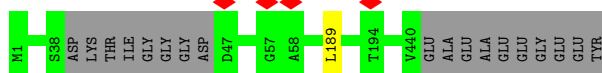
- Molecule 8: Tubulin alpha-3 chain

Chain JM:  95%



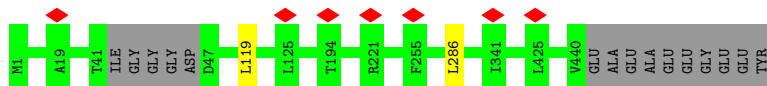
- Molecule 8: Tubulin alpha-3 chain

Chain JO:  96%



- Molecule 8: Tubulin alpha-3 chain

Chain JQ:  96%



- Molecule 8: Tubulin alpha-3 chain

Chain KA:  96%

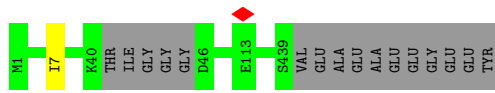


- Molecule 8: Tubulin alpha-3 chain

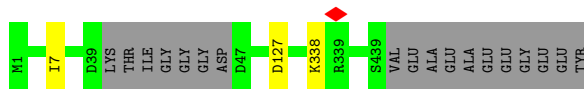
Chain KC:  96%



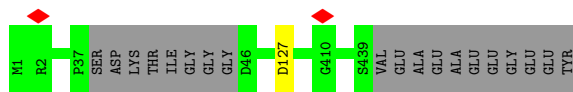
• Molecule 8: Tubulin alpha-3 chain



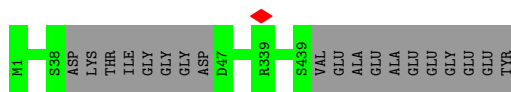
• Molecule 8: Tubulin alpha-3 chain



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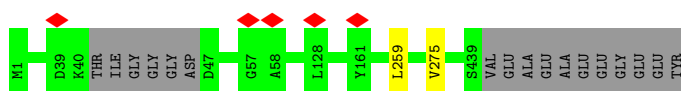
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain

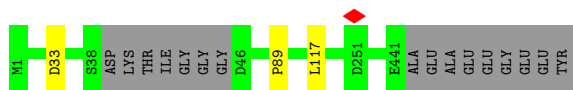


• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain





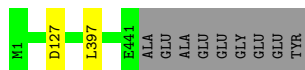
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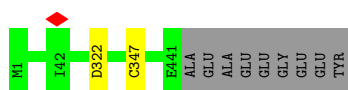
• Molecule 8: Tubulin alpha-3 chain



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• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain

Chain LO:  95%



- Molecule 8: Tubulin alpha-3 chain

Chain MA:  95%



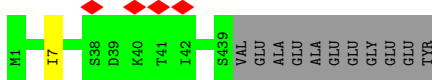
- Molecule 8: Tubulin alpha-3 chain

Chain MC:  96%



- Molecule 8: Tubulin alpha-3 chain

Chain ME:  97%



- Molecule 8: Tubulin alpha-3 chain

Chain MG:  95%



- Molecule 8: Tubulin alpha-3 chain

Chain MI:  96%



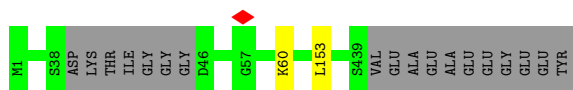
- Molecule 8: Tubulin alpha-3 chain

Chain MK:  96%



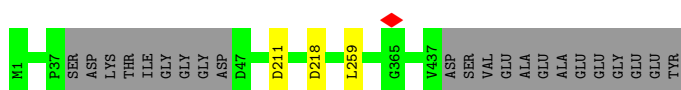
- Molecule 8: Tubulin alpha-3 chain

Chain MM:  96%



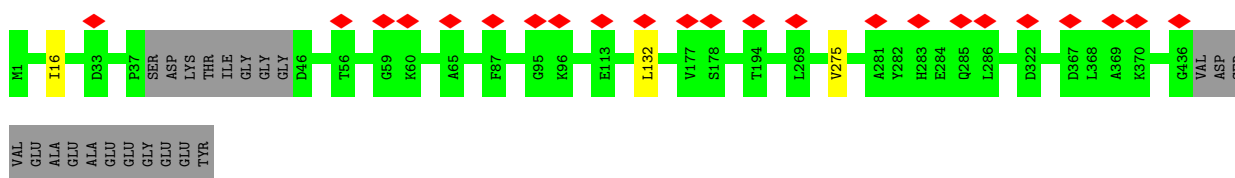
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Chain MO:  94%



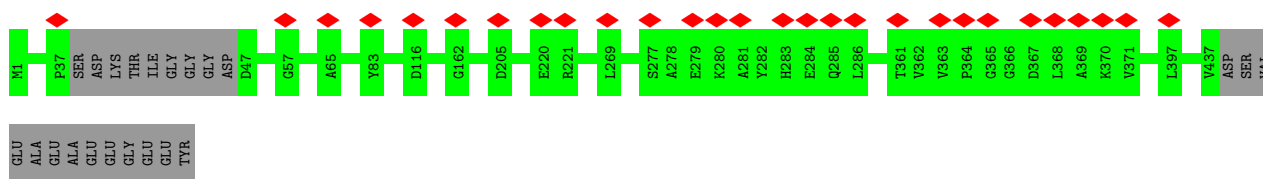
• Molecule 8: Tubulin alpha-3 chain

Chain NA:  94%



• Molecule 8: Tubulin alpha-3 chain

Chain NC:  95%



• Molecule 8: Tubulin alpha-3 chain

Chain NE:  96%

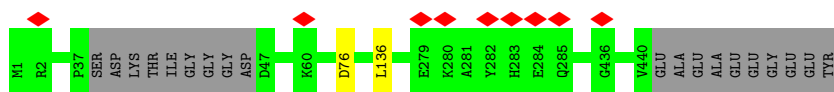


• Molecule 8: Tubulin alpha-3 chain

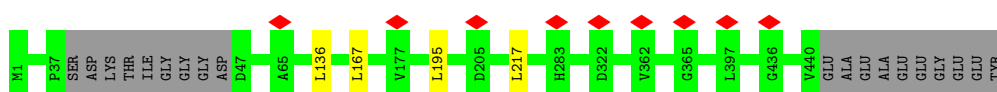
Chain NG:  96%



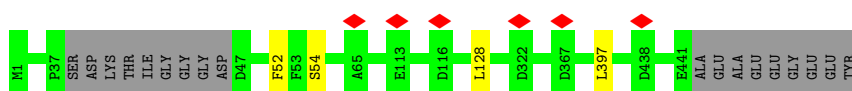
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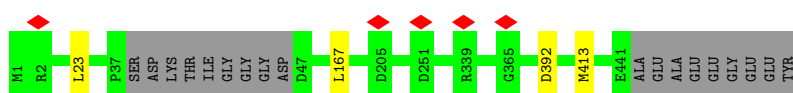
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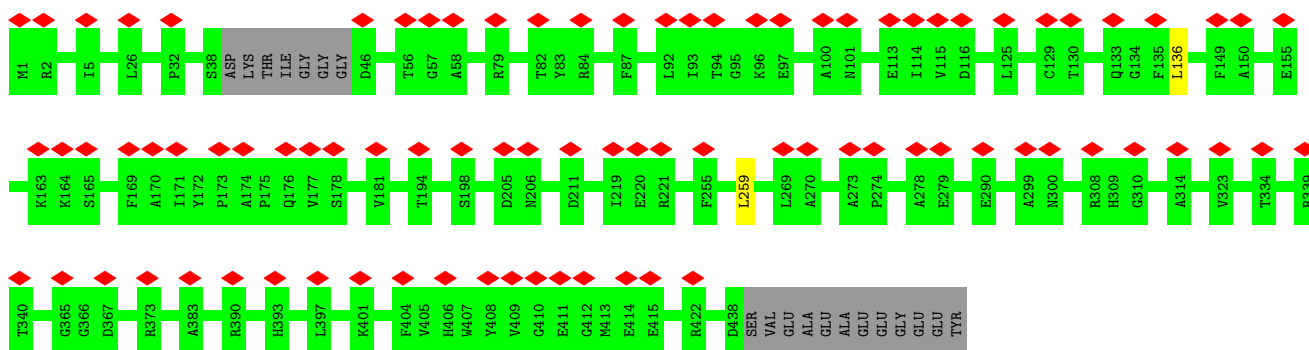
• Molecule 8: Tubulin alpha-3 chain



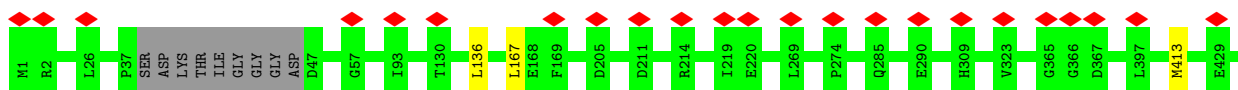
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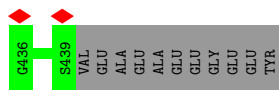


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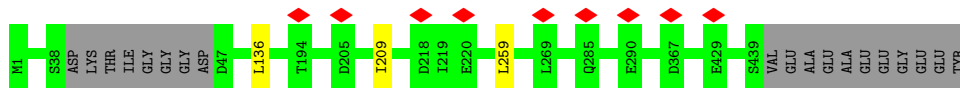


• Molecule 8: Tubulin alpha-3 chain

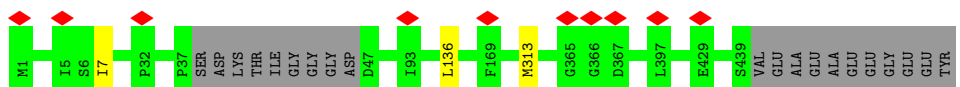




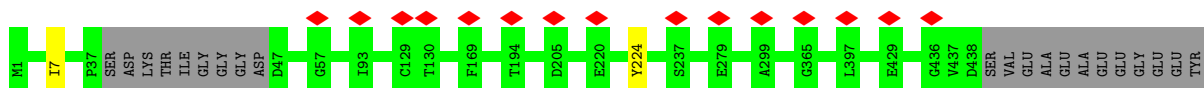
• Molecule 8: Tubulin alpha-3 chain



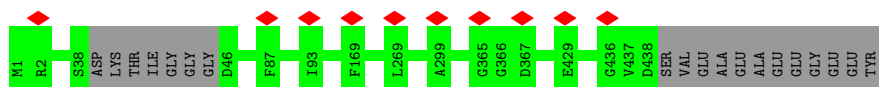
• Molecule 8: Tubulin alpha-3 chain



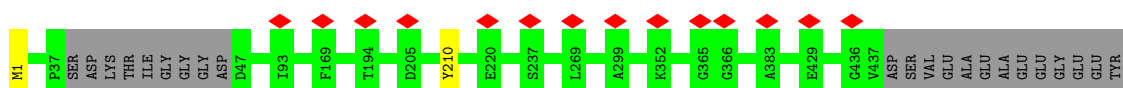
• Molecule 8: Tubulin alpha-3 chain



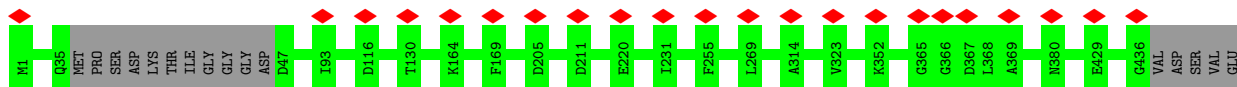
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



ALA
GLU
ALA
GLU
GLU
GLU
TYR

• Molecule 8: Tubulin alpha-3 chain

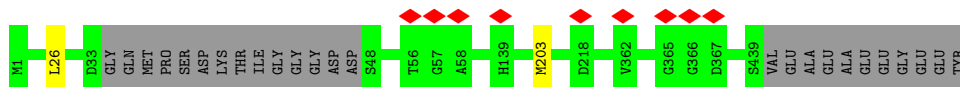
Chain PC:  94% 5%



ALA
GLU
ALA
GLU
GLU
GLU
TYR

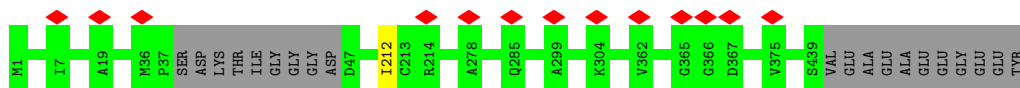
• Molecule 8: Tubulin alpha-3 chain

Chain PE:  94% 6%



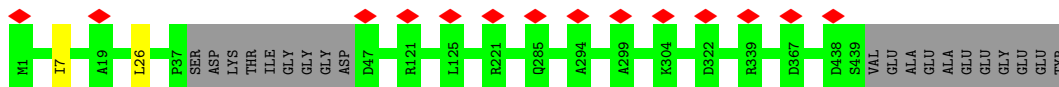
• Molecule 8: Tubulin alpha-3 chain

Chain PG:  95%



• Molecule 8: Tubulin alpha-3 chain

Chain PI:  95%



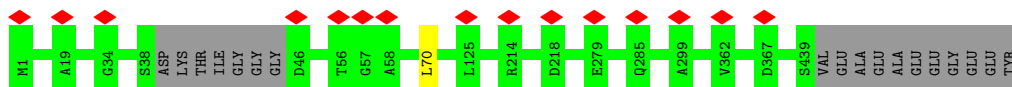
• Molecule 8: Tubulin alpha-3 chain

Chain PK:  94%

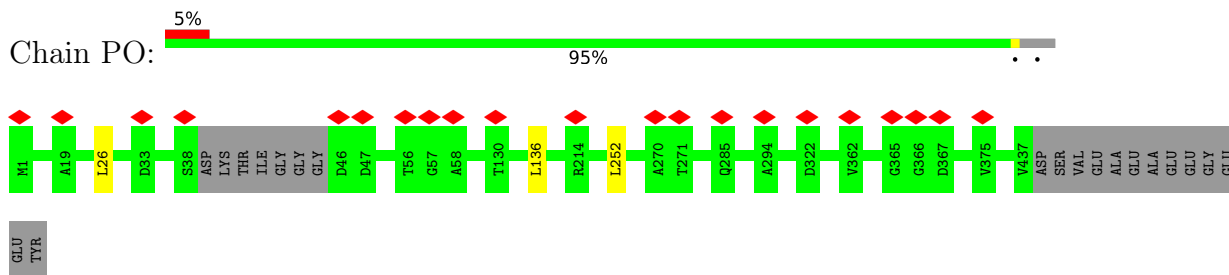


• Molecule 8: Tubulin alpha-3 chain

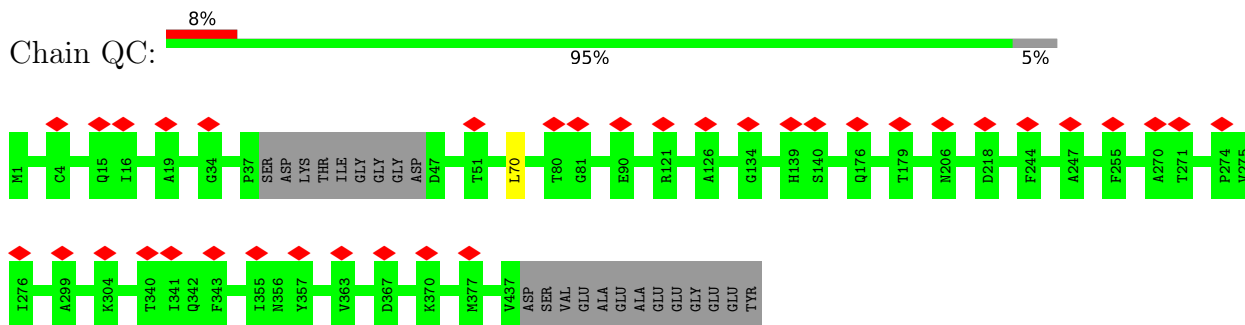
Chain PM:  96%



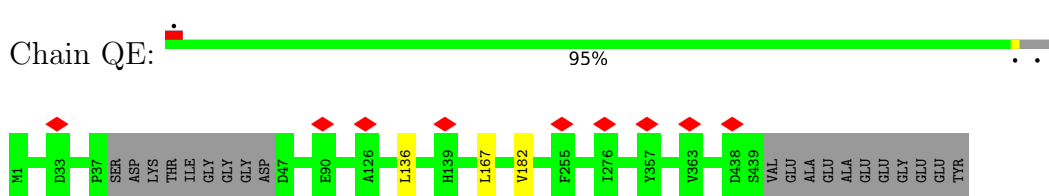
• Molecule 8: Tubulin alpha-3 chain



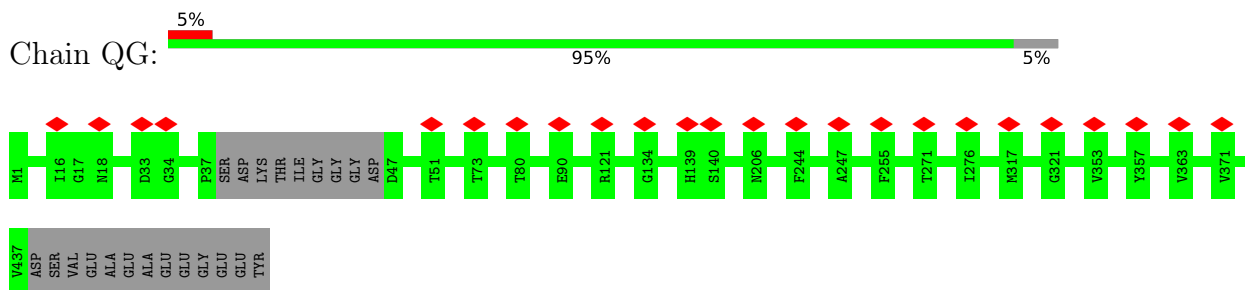
• Molecule 8: Tubulin alpha-3 chain



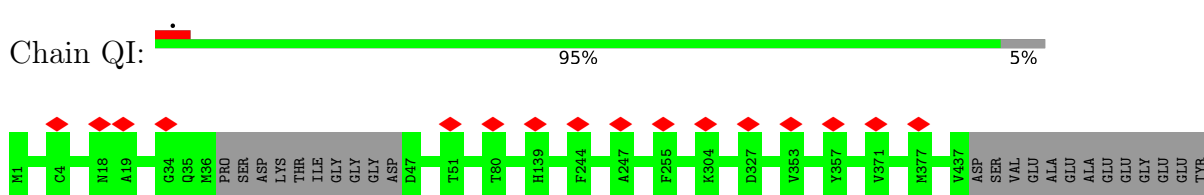
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain

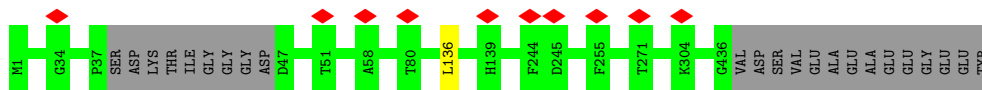


• Molecule 8: Tubulin alpha-3 chain



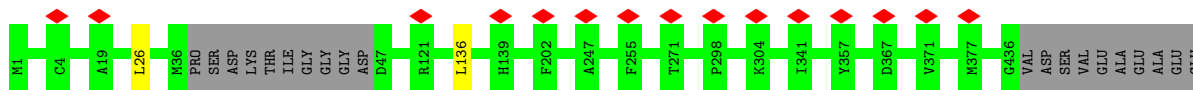
• Molecule 8: Tubulin alpha-3 chain





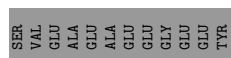
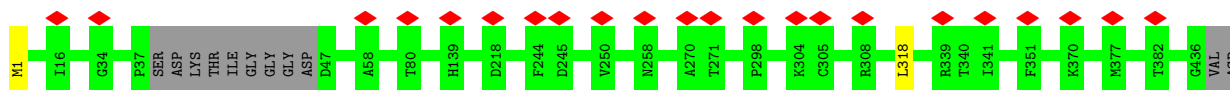
- Molecule 8: Tubulin alpha-3 chain

Chain QM: 94% 5%



- Molecule 8: Tubulin alpha-3 chain

Chain QO: 5% 94% 5%



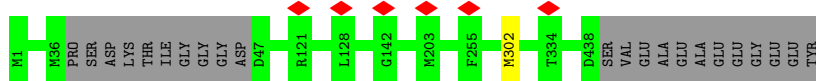
- Molecule 8: Tubulin alpha-3 chain

Chain RC: 5% 95% 5%



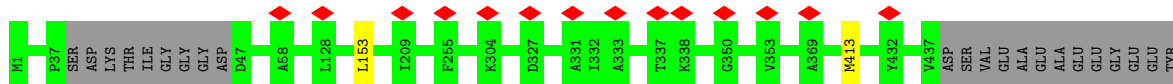
- Molecule 8: Tubulin alpha-3 chain

Chain RE: 5% 95% 5%



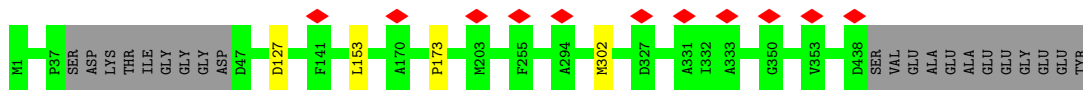
- Molecule 8: Tubulin alpha-3 chain

Chain RG: 5% 95% 5%

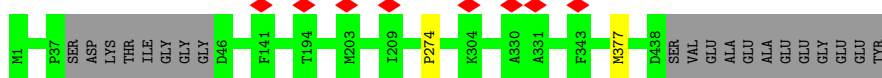


- Molecule 8: Tubulin alpha-3 chain

Chain RI: 5% 94% 5%



• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain

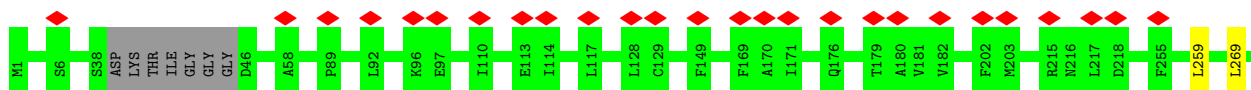


• Molecule 8: Tubulin alpha-3 chain

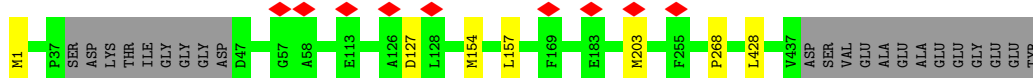


GLU
TYR

• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain

Chain SE:  95% 5%



• Molecule 8: Tubulin alpha-3 chain

Chain SG:  94% 5%



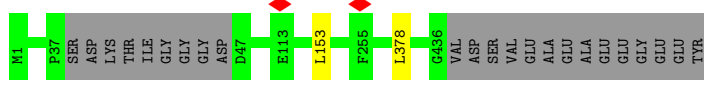
• Molecule 8: Tubulin alpha-3 chain

Chain SI:  94% 5%



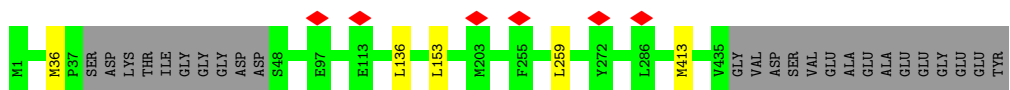
• Molecule 8: Tubulin alpha-3 chain

Chain SK:  94% 5%

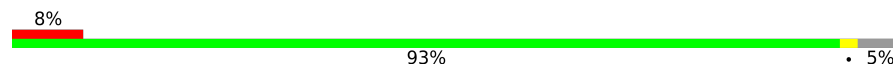


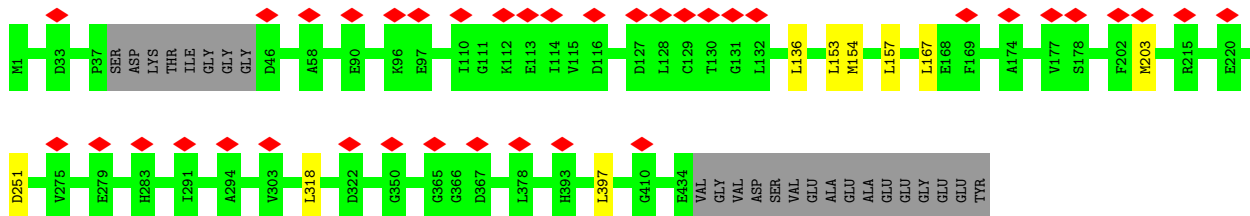
• Molecule 8: Tubulin alpha-3 chain

Chain SM:  93% 6%



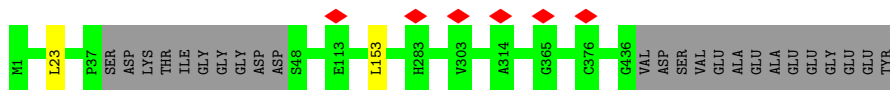
• Molecule 8: Tubulin alpha-3 chain

Chain TA:  8% 93% 5%

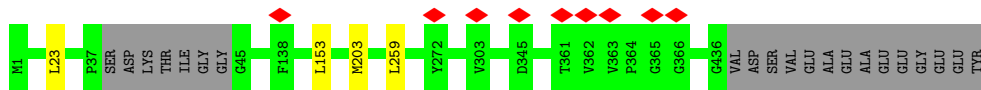


• Molecule 8: Tubulin alpha-3 chain

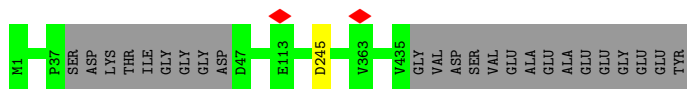
Chain TC:  94% 5%



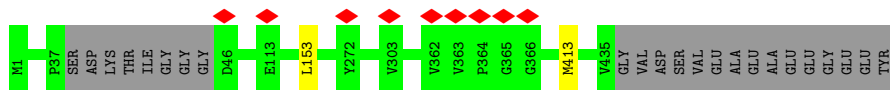
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



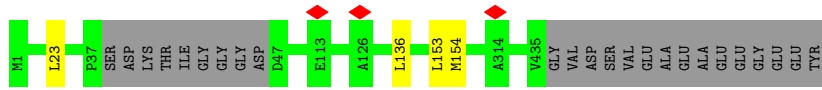
• Molecule 8: Tubulin alpha-3 chain



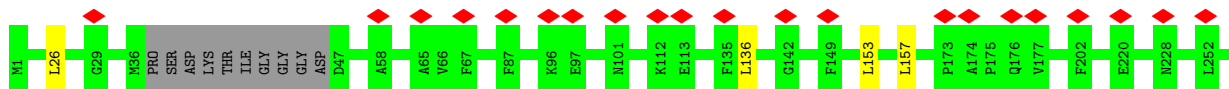
• Molecule 8: Tubulin alpha-3 chain

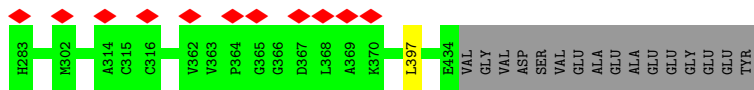


• Molecule 8: Tubulin alpha-3 chain

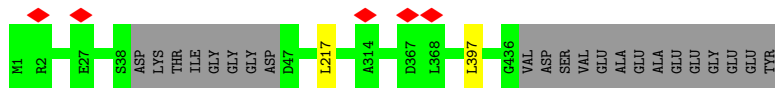


• Molecule 8: Tubulin alpha-3 chain

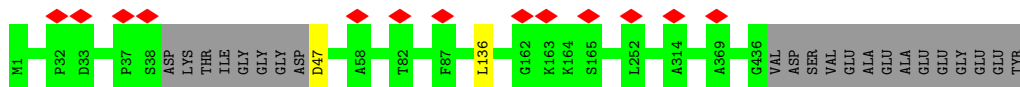




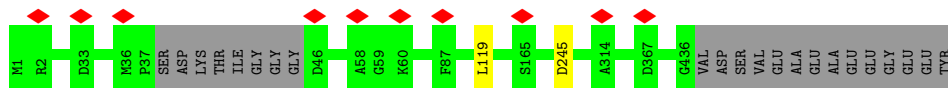
• Molecule 8: Tubulin alpha-3 chain



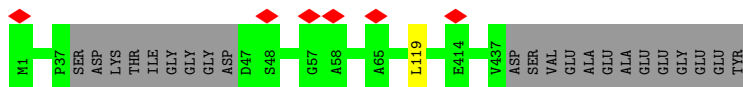
• Molecule 8: Tubulin alpha-3 chain



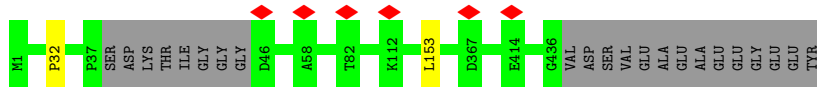
• Molecule 8: Tubulin alpha-3 chain



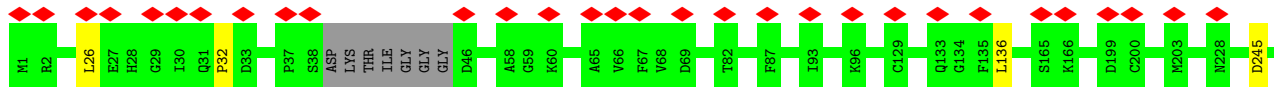
• Molecule 8: Tubulin alpha-3 chain

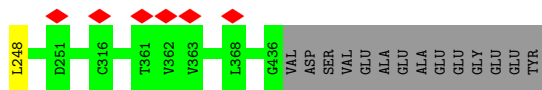


• Molecule 8: Tubulin alpha-3 chain

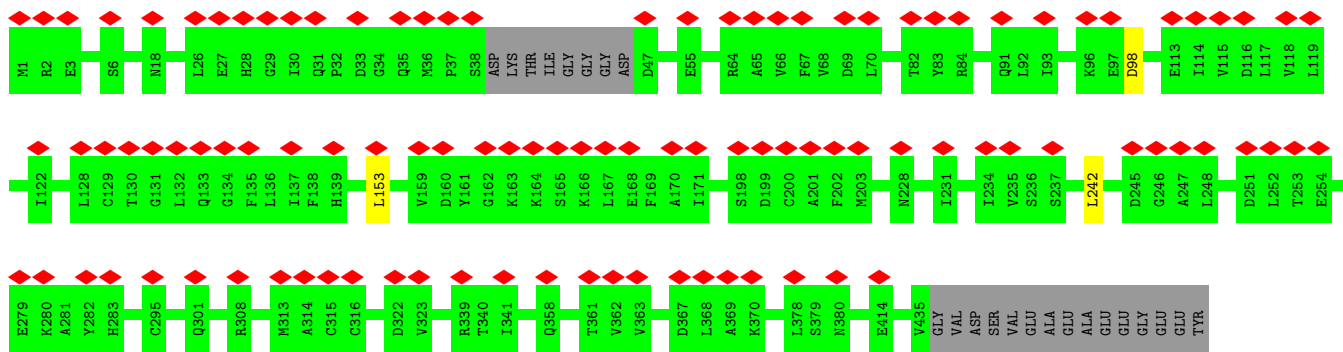


• Molecule 8: Tubulin alpha-3 chain

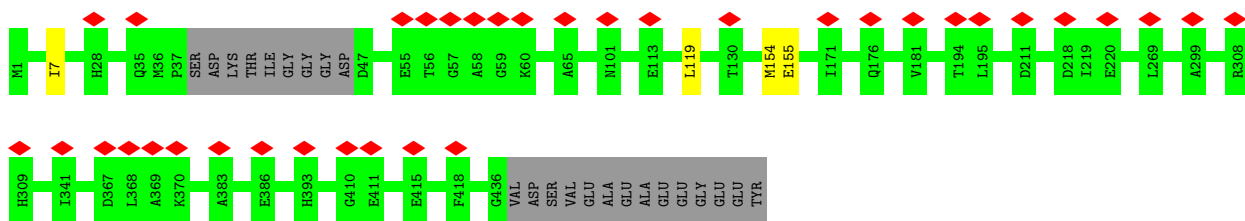




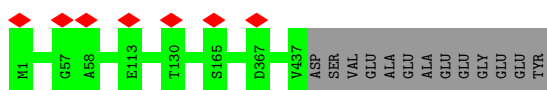
• Molecule 8: Tubulin alpha-3 chain



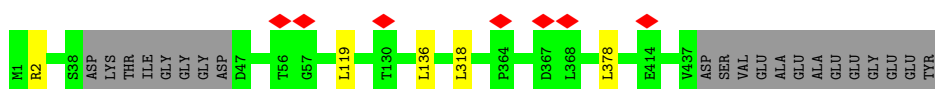
• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain



• Molecule 8: Tubulin alpha-3 chain





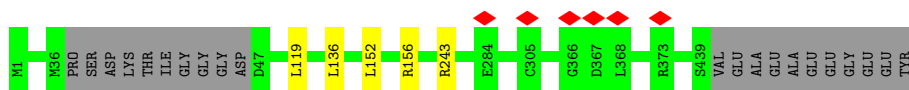
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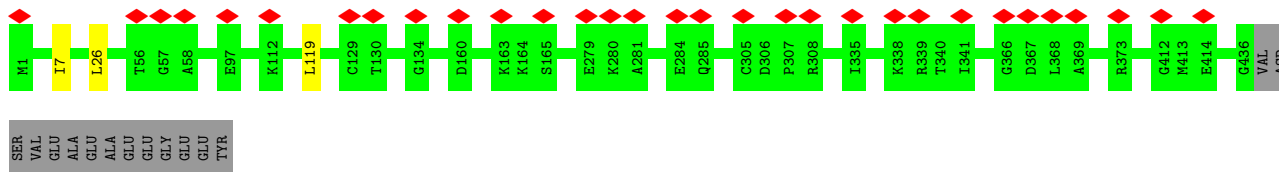
• Molecule 8: Tubulin alpha-3 chain



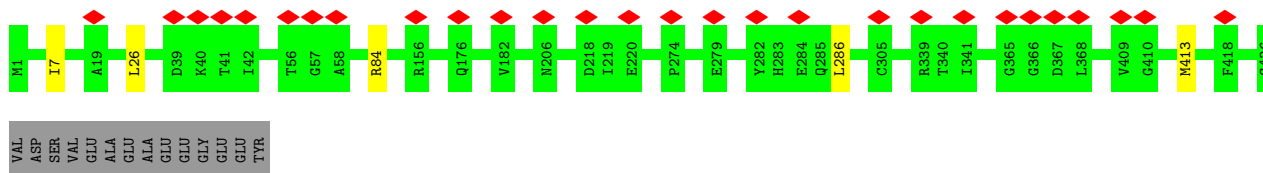
• Molecule 8: Tubulin alpha-3 chain



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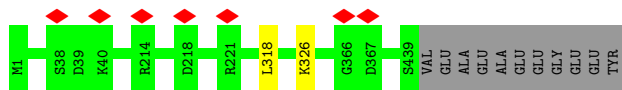


• Molecule 8: Tubulin alpha-3 chain

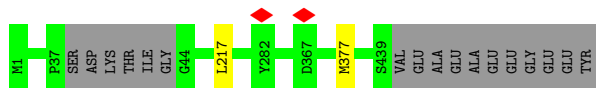


• Molecule 8: Tubulin alpha-3 chain

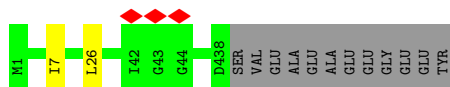




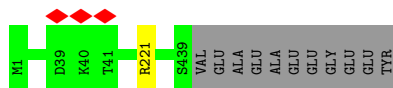
• Molecule 8: Tubulin alpha-3 chain



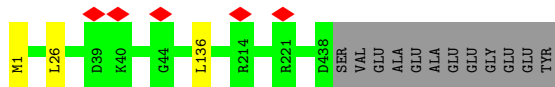
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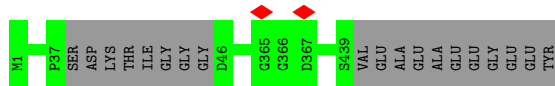
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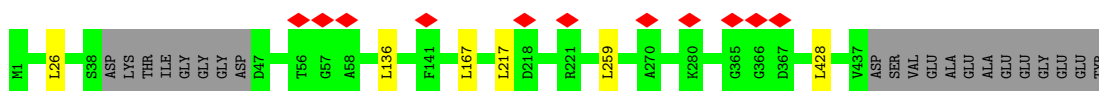
• Molecule 8: Tubulin alpha-3 chain



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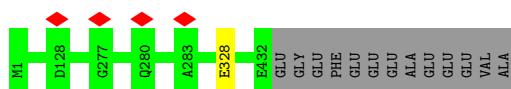


• Molecule 8: Tubulin alpha-3 chain



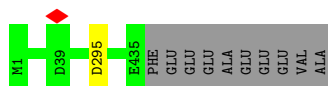
• Molecule 9: Tubulin beta-4B chain

Chain AB:  97%



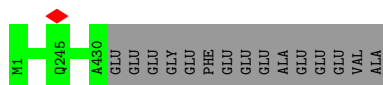
- Molecule 9: Tubulin beta-4B chain

Chain AD:  98%



- Molecule 9: Tubulin beta-4B chain

Chain AF:  97%



- Molecule 9: Tubulin beta-4B chain

Chain AH:  97%



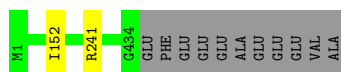
- Molecule 9: Tubulin beta-4B chain

Chain AJ:  96%



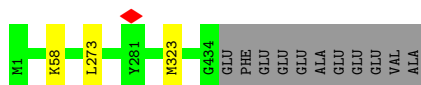
- Molecule 9: Tubulin beta-4B chain

Chain AL:  97%



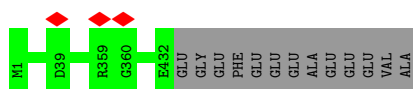
- Molecule 9: Tubulin beta-4B chain

Chain AN:  97%



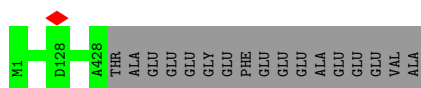
- Molecule 9: Tubulin beta-4B chain

Chain AP:  97%



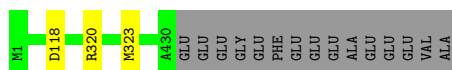
- Molecule 9: Tubulin beta-4B chain

Chain BB:  96%



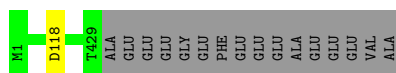
- Molecule 9: Tubulin beta-4B chain

Chain BD:  96%



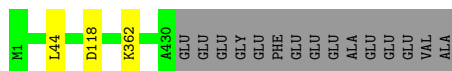
- Molecule 9: Tubulin beta-4B chain

Chain BF:  96%



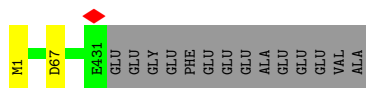
- Molecule 9: Tubulin beta-4B chain

Chain BH:  96%



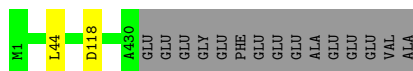
- Molecule 9: Tubulin beta-4B chain

Chain BJ:  96%



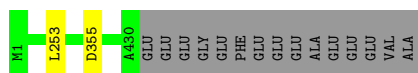
- Molecule 9: Tubulin beta-4B chain

Chain BL:  96%



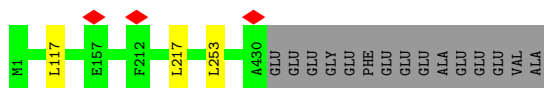
- Molecule 9: Tubulin beta-4B chain

Chain BN:  96%



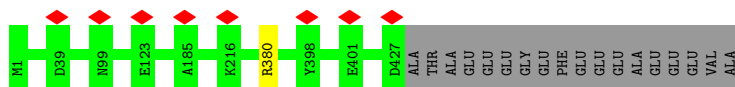
● Molecule 9: Tubulin beta-4B chain

Chain BP:  96%



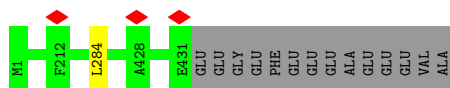
● Molecule 9: Tubulin beta-4B chain

Chain CB:  96%



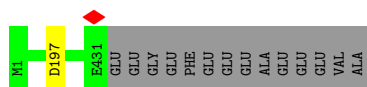
● Molecule 9: Tubulin beta-4B chain

Chain CD:  97%



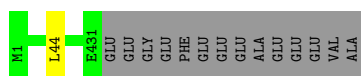
● Molecule 9: Tubulin beta-4B chain

Chain CF:  97%



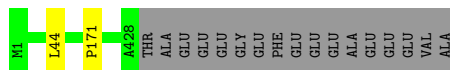
● Molecule 9: Tubulin beta-4B chain

Chain CH:  97%



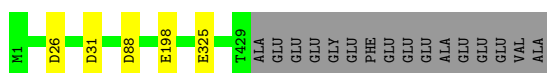
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Chain CJ:  96%



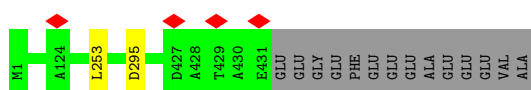
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Chain CL:  95%



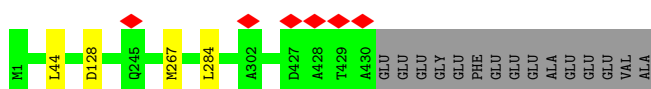
• Molecule 9: Tubulin beta-4B chain

Chain CN:  96%



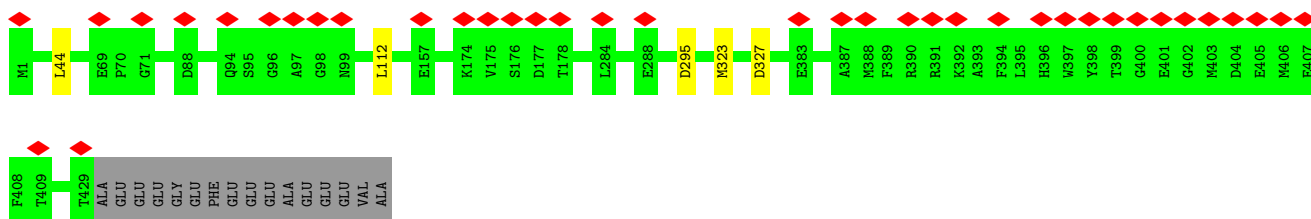
• Molecule 9: Tubulin beta-4B chain

Chain CP:  96%



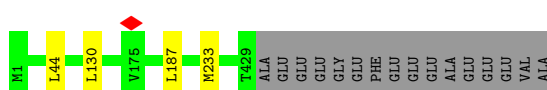
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Chain DB:  95%



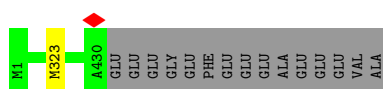
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Chain DD:  96%



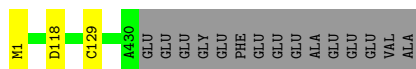
• Molecule 9: Tubulin beta-4B chain

Chain DF:  96%

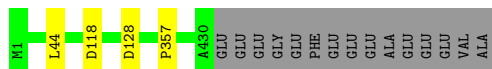


• Molecule 9: Tubulin beta-4B chain

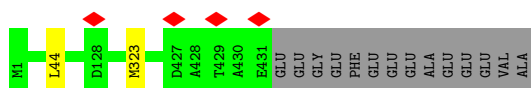
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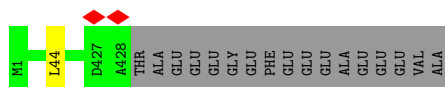
• Molecule 9: Tubulin beta-4B chain



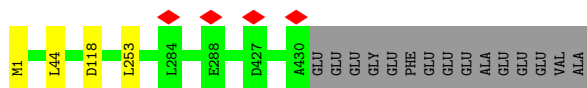
• Molecule 9: Tubulin beta-4B chain



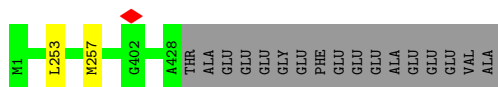
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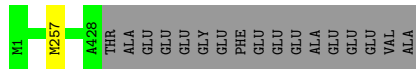
• Molecule 9: Tubulin beta-4B chain



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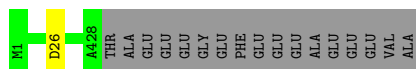


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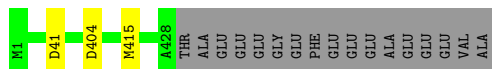
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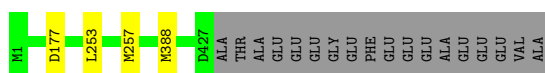
- Molecule 9: Tubulin beta-4B chain

Chain EH: 96%



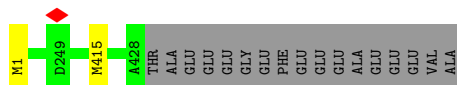
- Molecule 9: Tubulin beta-4B chain

Chain EJ: 95%



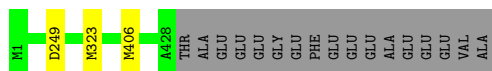
- Molecule 9: Tubulin beta-4B chain

Chain EL: 96%



- Molecule 9: Tubulin beta-4B chain

Chain EN: 96%



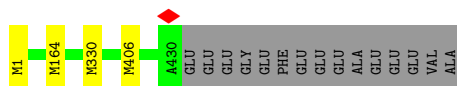
- Molecule 9: Tubulin beta-4B chain

Chain FB: 96%



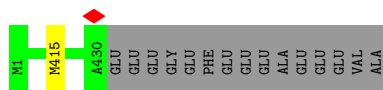
- Molecule 9: Tubulin beta-4B chain

Chain FD: 96%



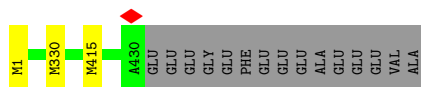
- Molecule 9: Tubulin beta-4B chain

Chain FF: 96%



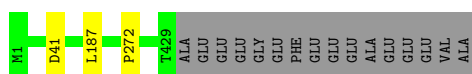
- Molecule 9: Tubulin beta-4B chain

Chain FH: 96%



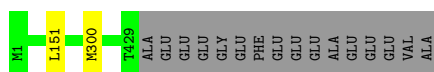
- Molecule 9: Tubulin beta-4B chain

Chain FJ: 96%



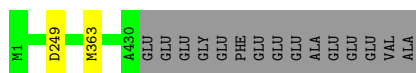
- Molecule 9: Tubulin beta-4B chain

Chain FL: 96%



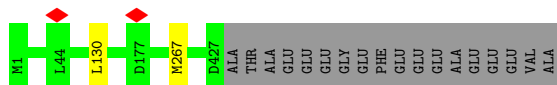
- Molecule 9: Tubulin beta-4B chain

Chain FN: 96%



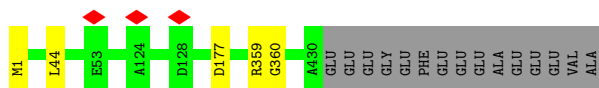
- Molecule 9: Tubulin beta-4B chain

Chain GB: 96%



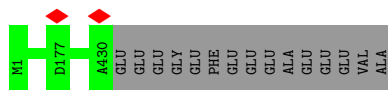
- Molecule 9: Tubulin beta-4B chain

Chain GD: 96%

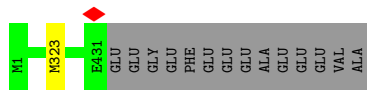


- Molecule 9: Tubulin beta-4B chain

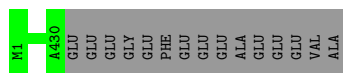
Chain GF: 97%



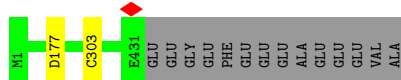
• Molecule 9: Tubulin beta-4B chain



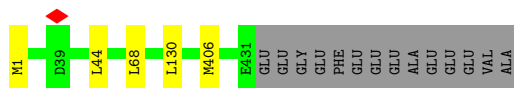
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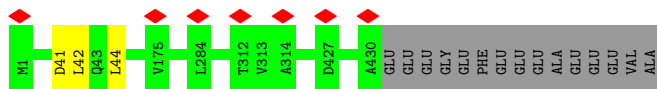
• Molecule 9: Tubulin beta-4B chain



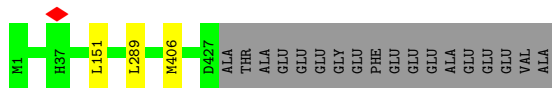
• Molecule 9: Tubulin beta-4B chain



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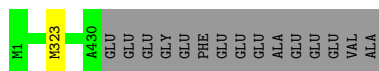


• Molecule 9: Tubulin beta-4B chain

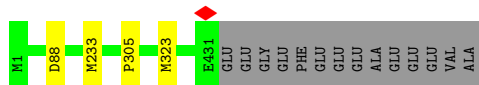


• Molecule 9: Tubulin beta-4B chain

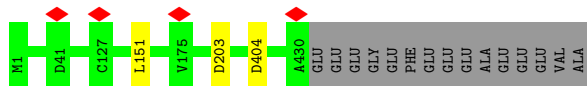




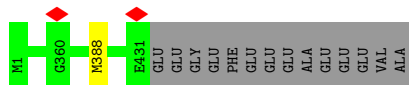
• Molecule 9: Tubulin beta-4B chain



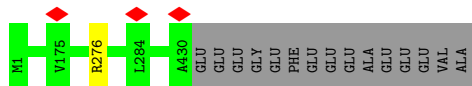
• Molecule 9: Tubulin beta-4B chain



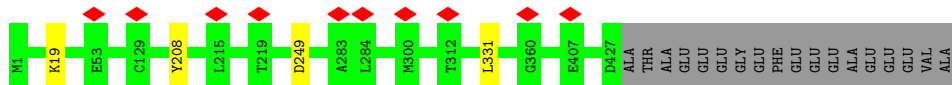
• Molecule 9: Tubulin beta-4B chain



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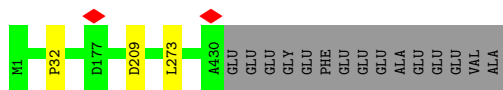


• Molecule 9: Tubulin beta-4B chain

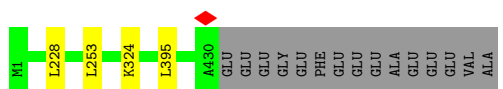


• Molecule 9: Tubulin beta-4B chain

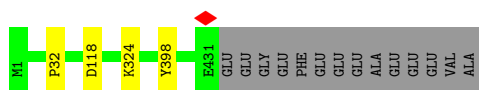




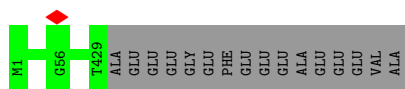
• Molecule 9: Tubulin beta-4B chain



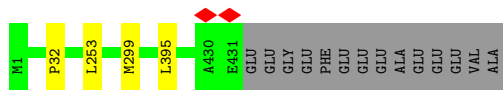
• Molecule 9: Tubulin beta-4B chain



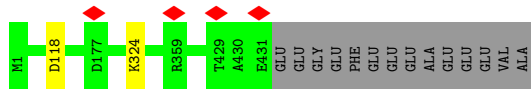
• Molecule 9: Tubulin beta-4B chain



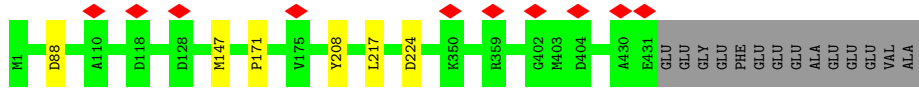
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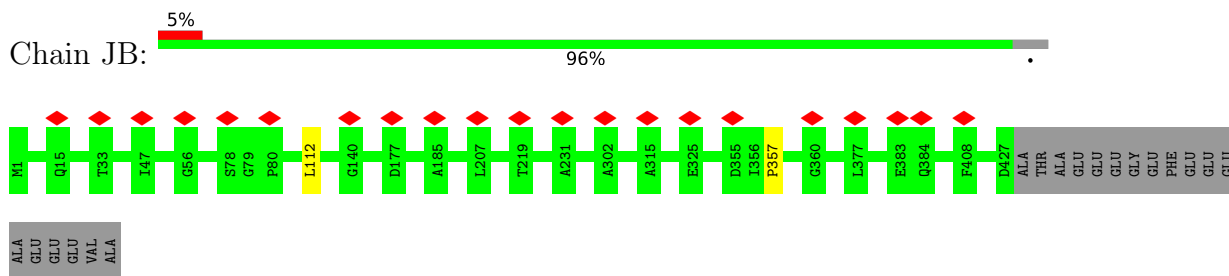
• Molecule 9: Tubulin beta-4B chain



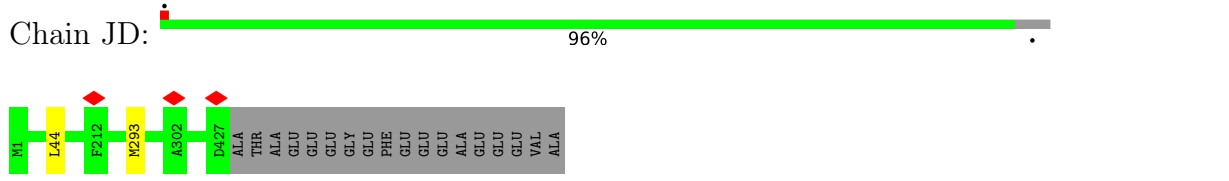
• Molecule 9: Tubulin beta-4B chain



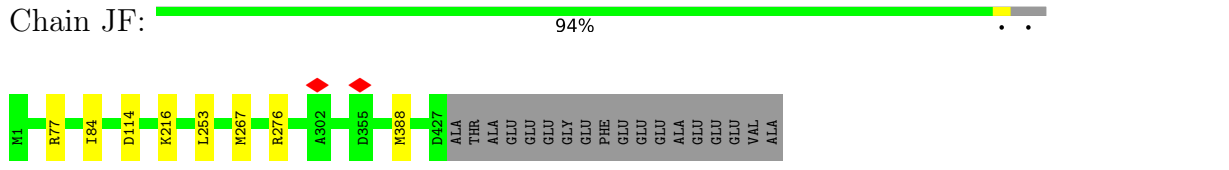
• Molecule 9: Tubulin beta-4B chain



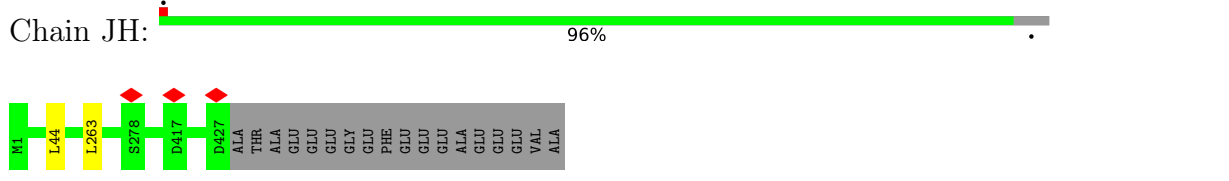
• Molecule 9: Tubulin beta-4B chain



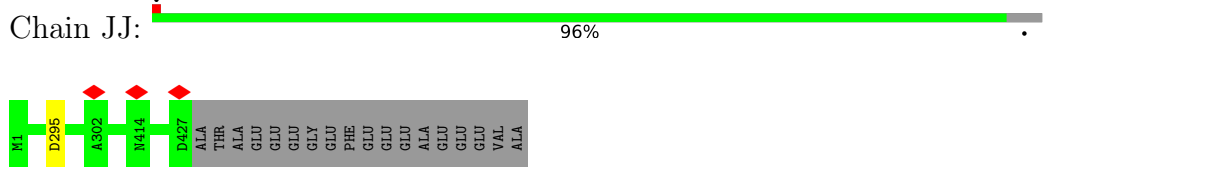
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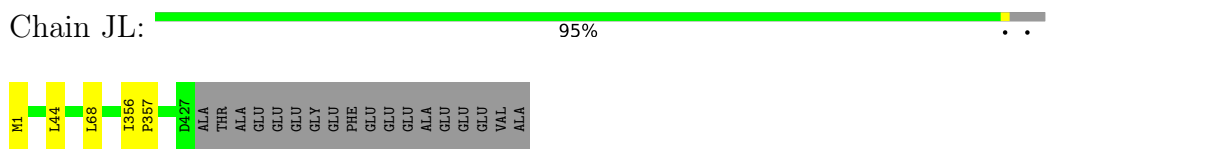
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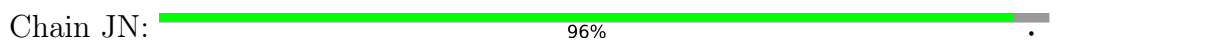
• Molecule 9: Tubulin beta-4B chain

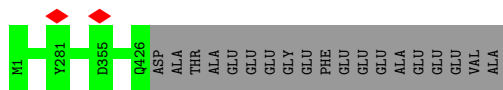


• Molecule 9: Tubulin beta-4B chain

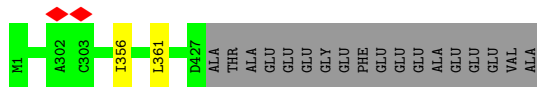


• Molecule 9: Tubulin beta-4B chain

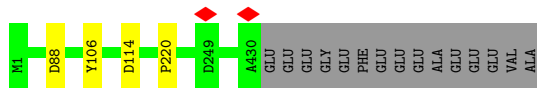




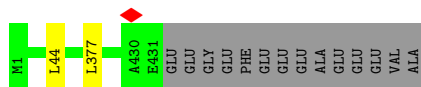
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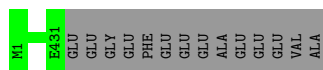
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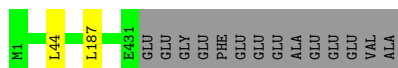
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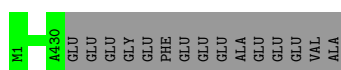
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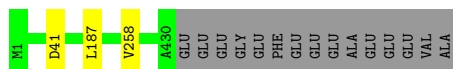


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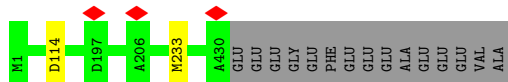


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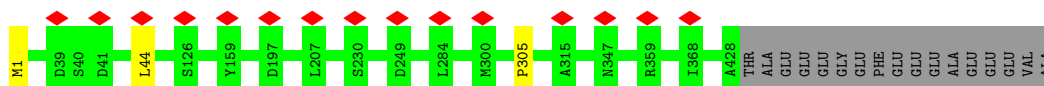




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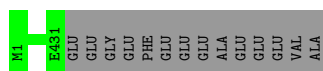
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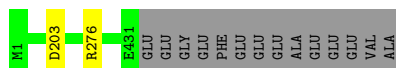
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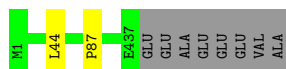


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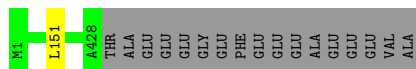
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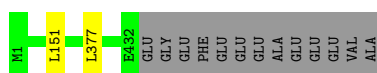
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Chain LL: 96%



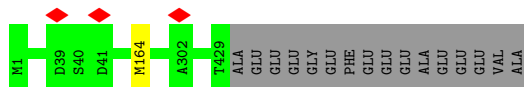
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Chain LN: 97%



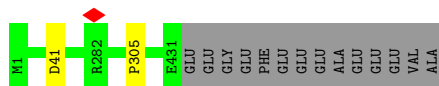
- Molecule 9: Tubulin beta-4B chain

Chain LP: 96%



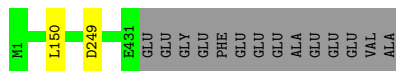
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Chain MB: 96%



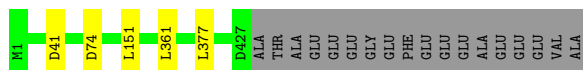
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Chain MD: 96%



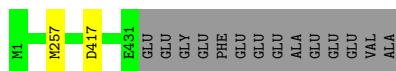
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Chain MF: 95%

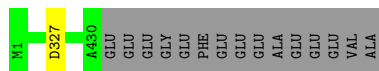


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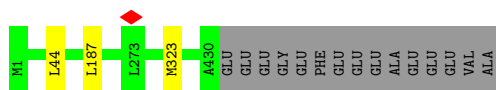
Chain MH: 96%



• Molecule 9: Tubulin beta-4B chain



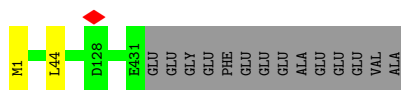
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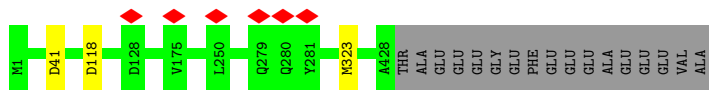


• Molecule 9: Tubulin beta-4B chain



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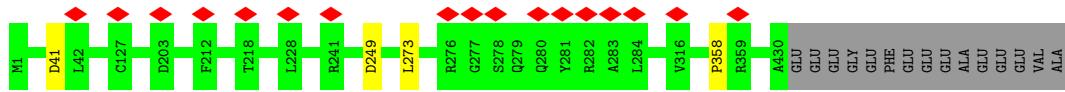




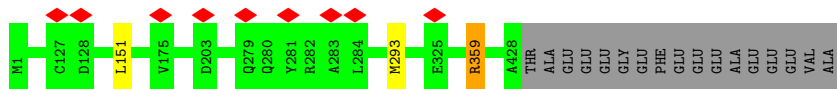
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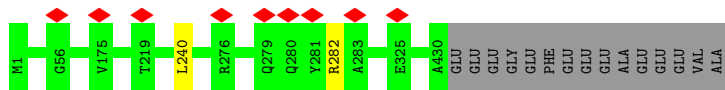
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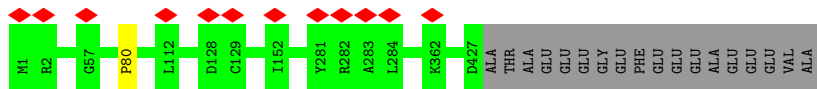
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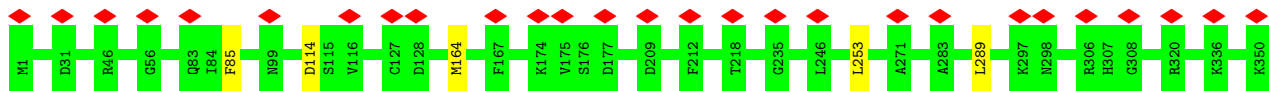
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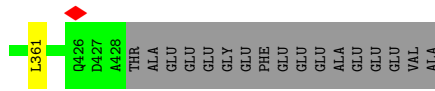


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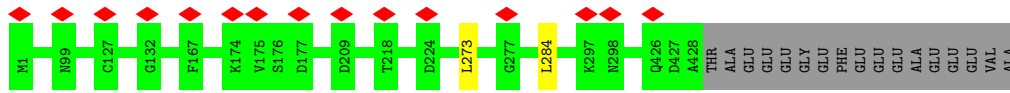


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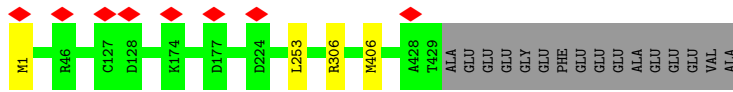




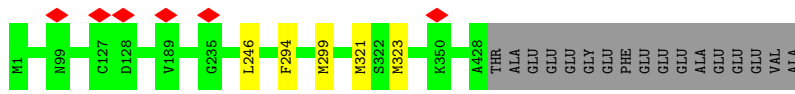
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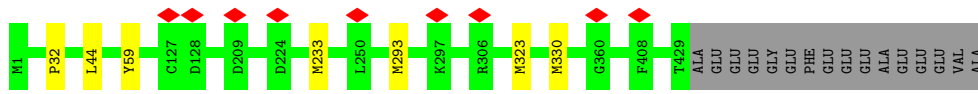
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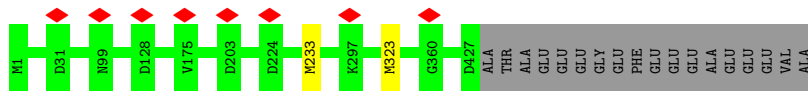
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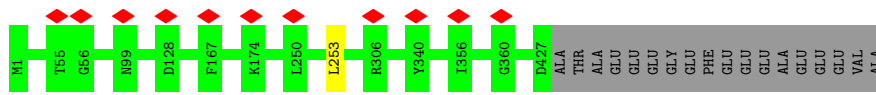
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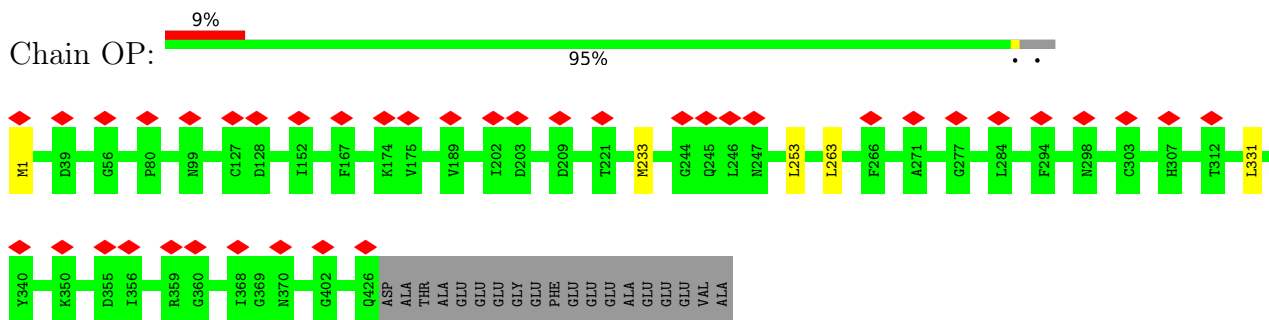
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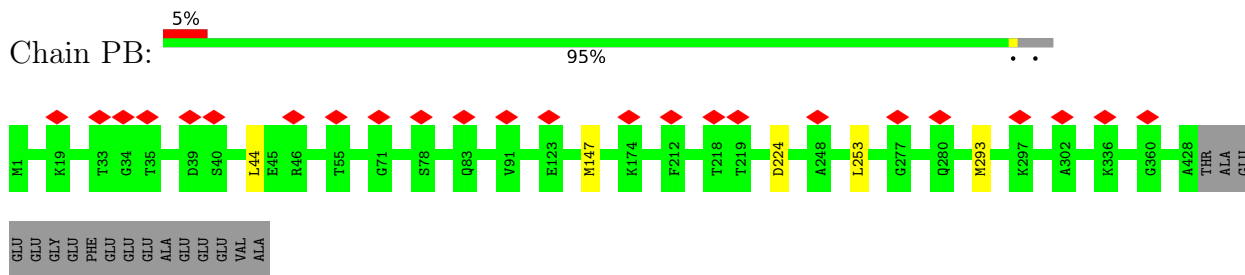
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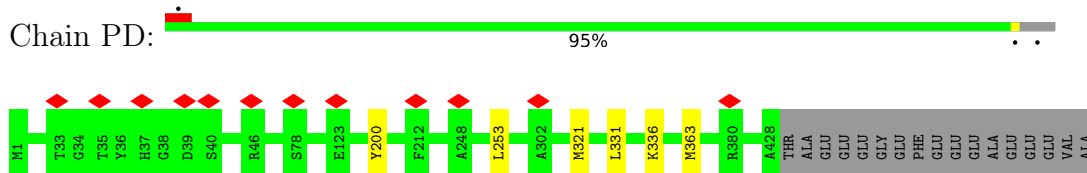
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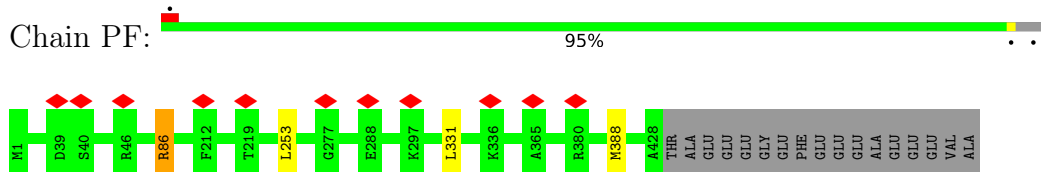
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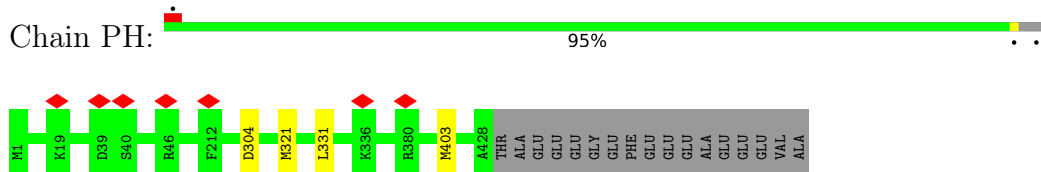
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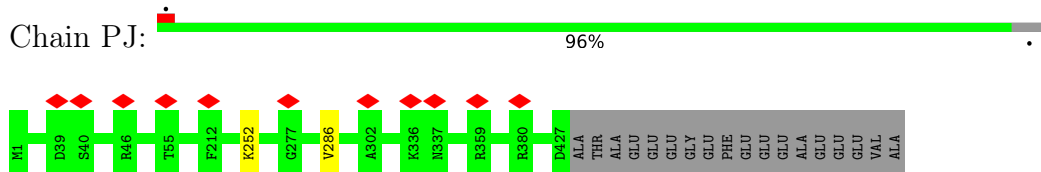
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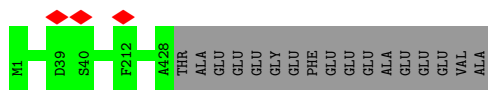
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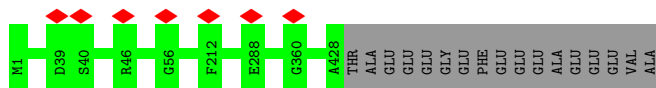
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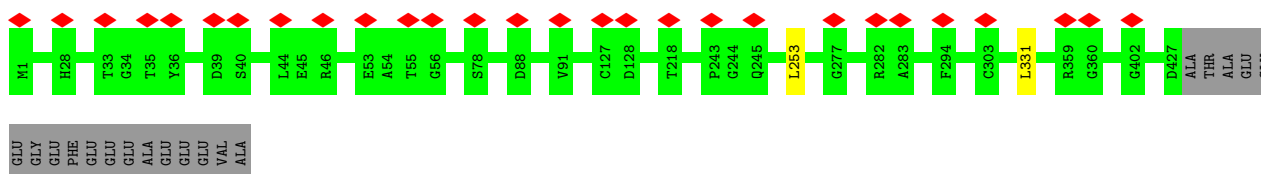
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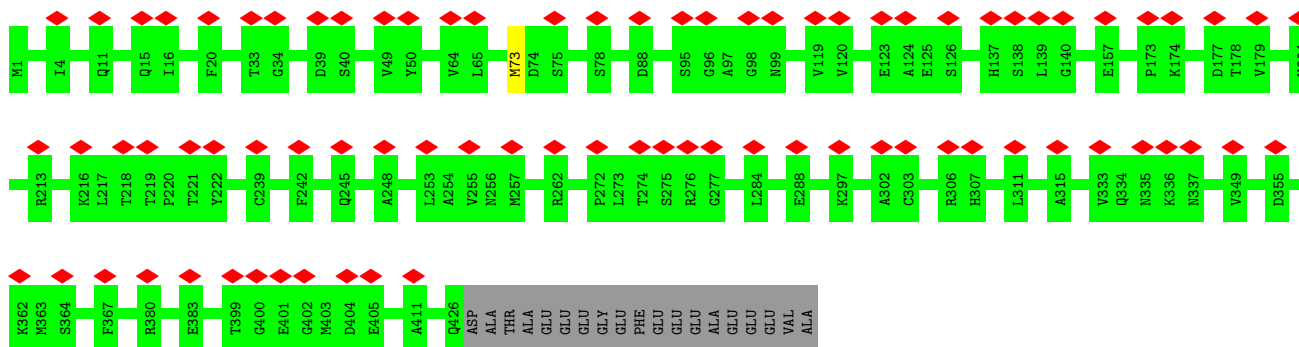
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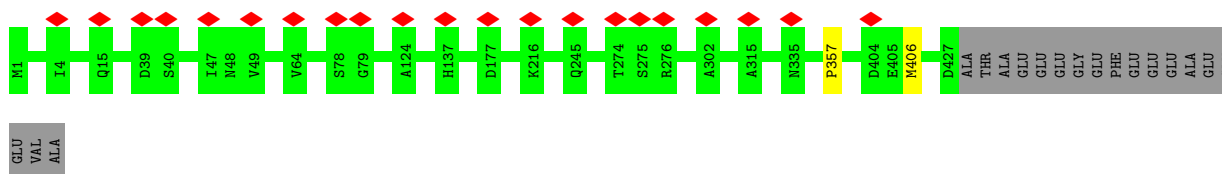
• Molecule 9: Tubulin beta-4B chain



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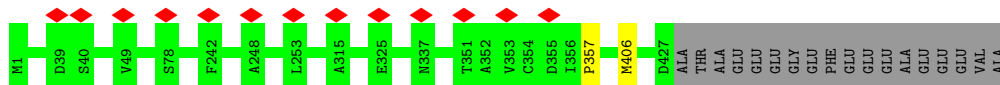


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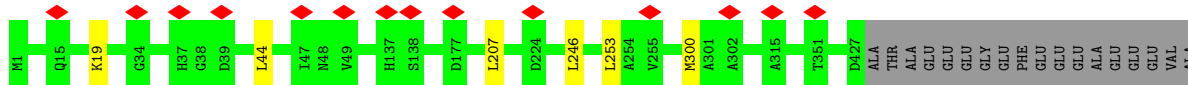
• Molecule 9: Tubulin beta-4B chain

Chain QF:  96%



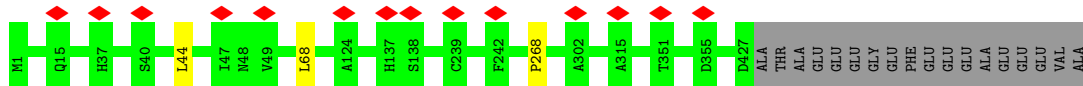
• Molecule 9: Tubulin beta-4B chain

Chain QH:  95%



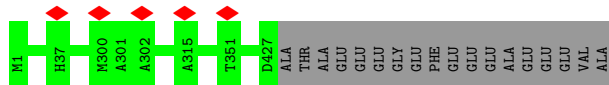
• Molecule 9: Tubulin beta-4B chain

Chain QJ:  95%



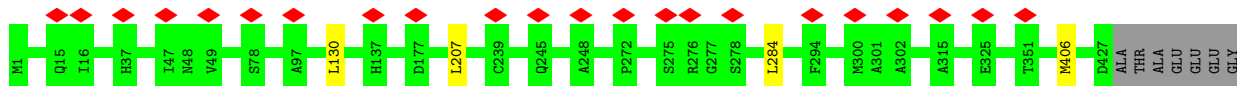
• Molecule 9: Tubulin beta-4B chain

Chain QL:  96%



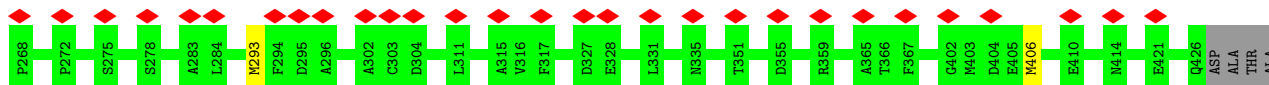
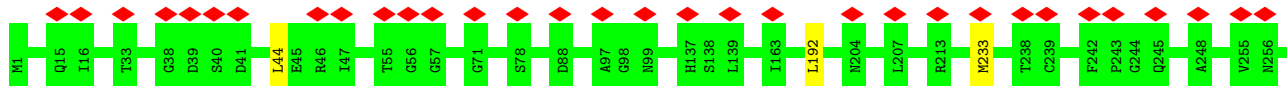
• Molecule 9: Tubulin beta-4B chain

Chain QN:  5%  95%



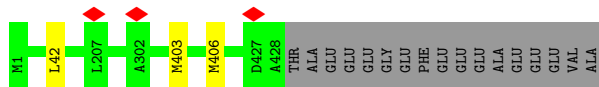
• Molecule 9: Tubulin beta-4B chain

Chain QP:  14%  95%

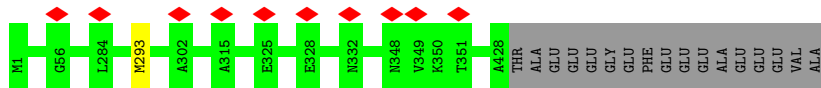


GLU
GLU
GLY
GLU
PHE
GLU
GLU
GLU
ALA
GLU
GLU
VAL
ALA

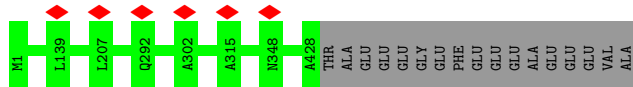
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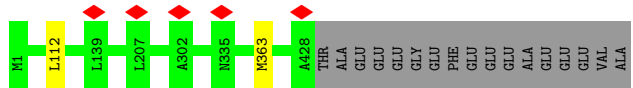
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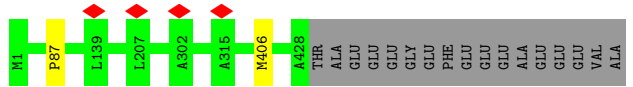
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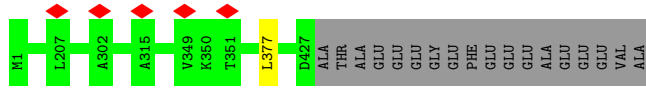
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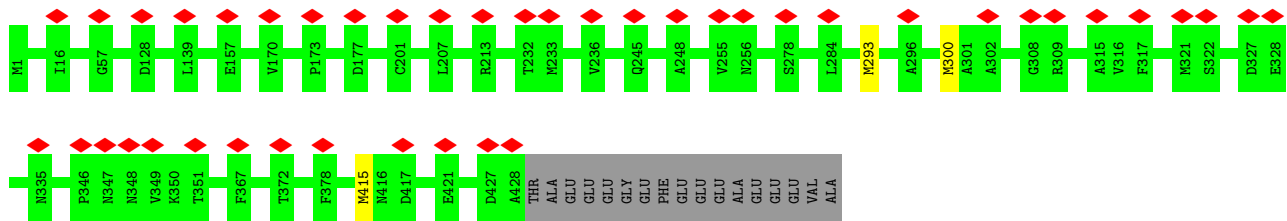


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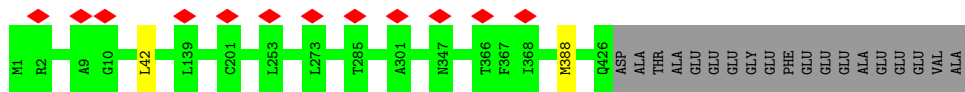


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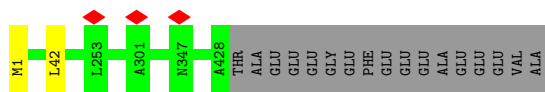




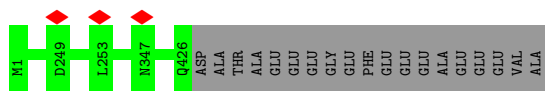
• Molecule 9: Tubulin beta-4B chain



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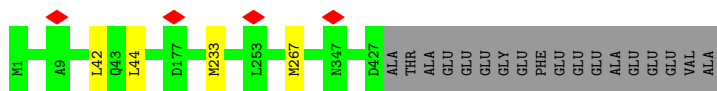
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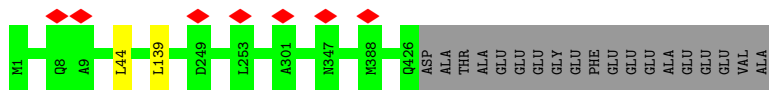


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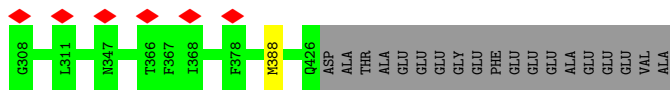


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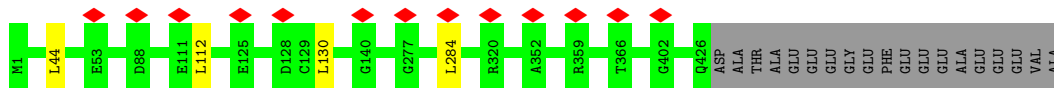




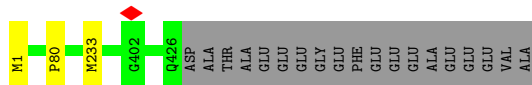
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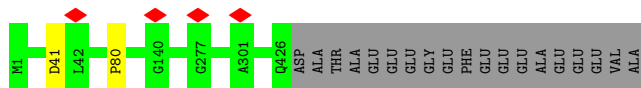
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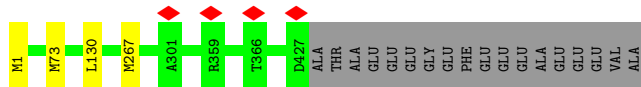
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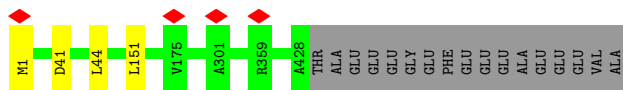


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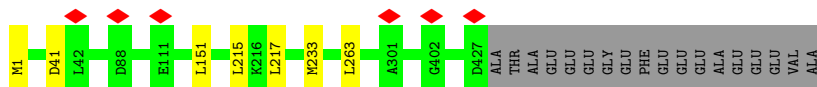


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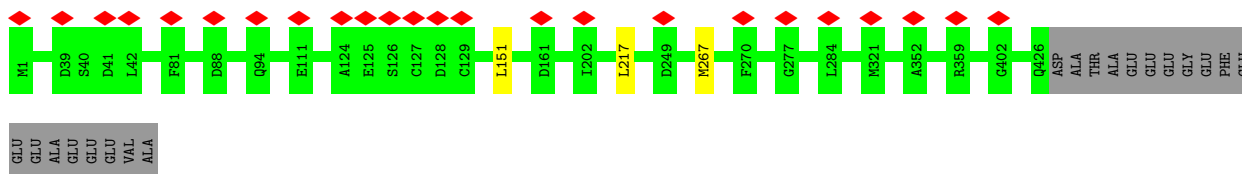




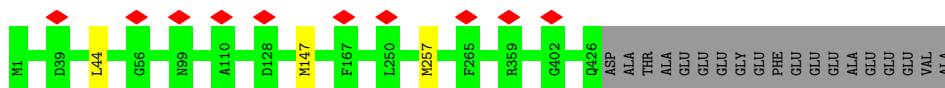
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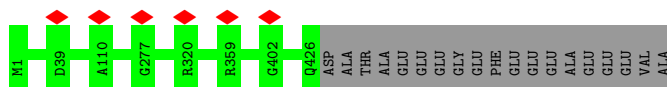
• Molecule 9: Tubulin beta-4B chain



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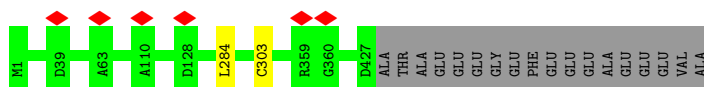
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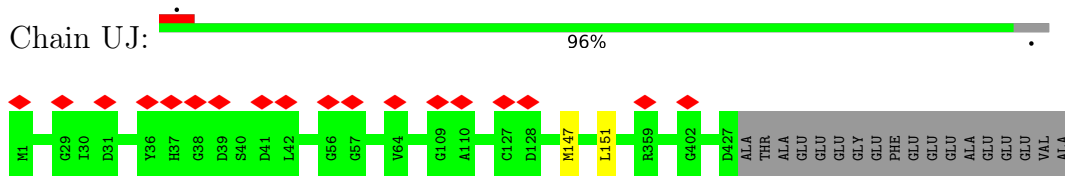
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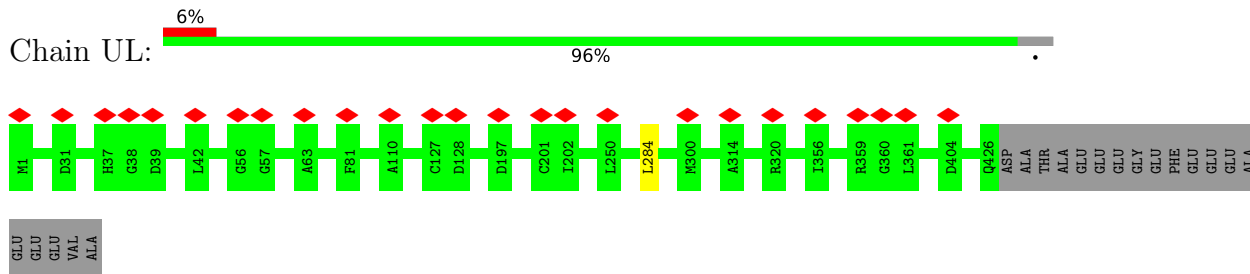
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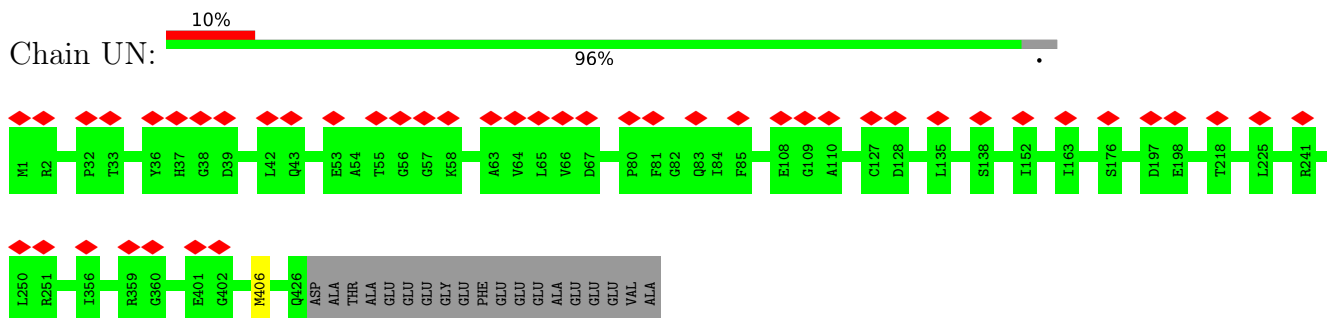
• Molecule 9: Tubulin beta-4B chain



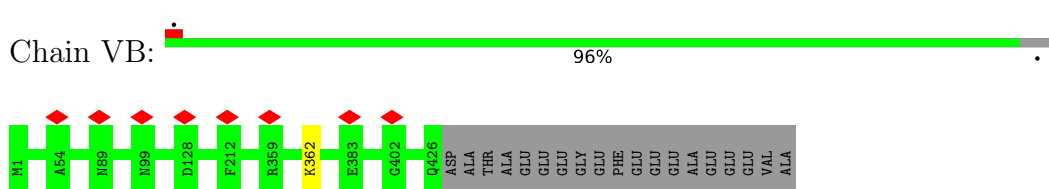
• Molecule 9: Tubulin beta-4B chain



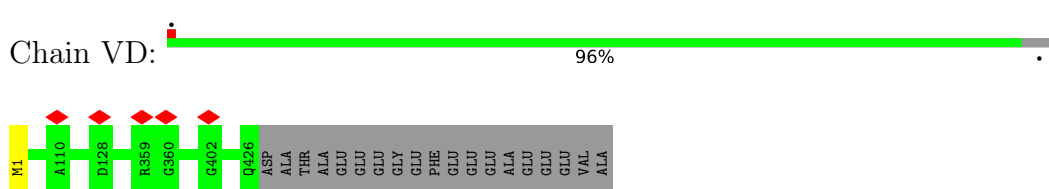
• Molecule 9: Tubulin beta-4B chain



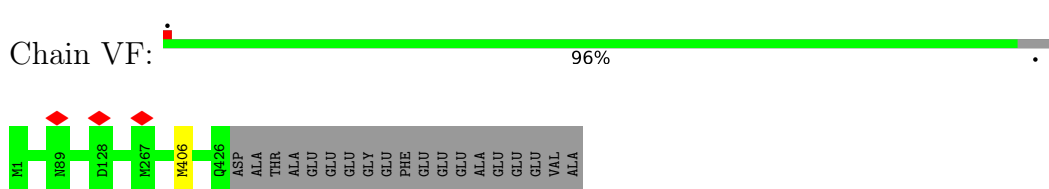
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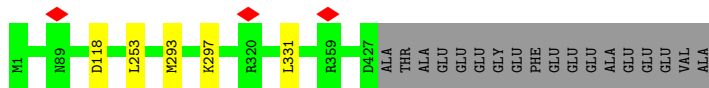
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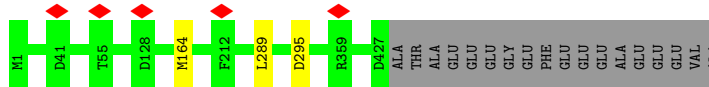
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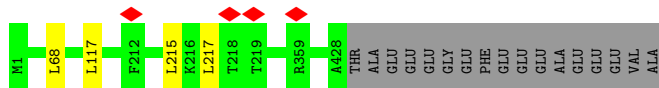
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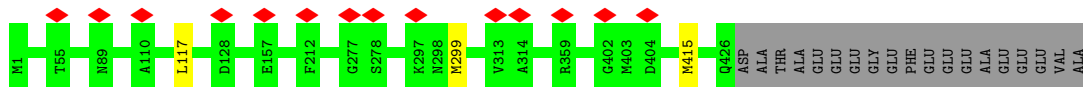
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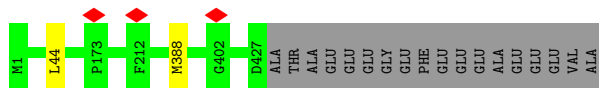
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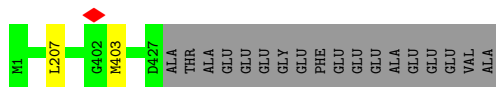
• Molecule 9: Tubulin beta-4B chain



• Molecule 9: Tubulin beta-4B chain

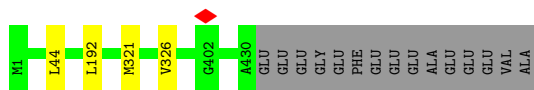


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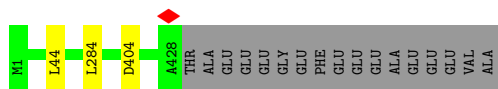


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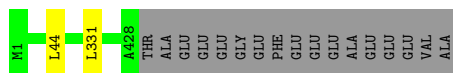




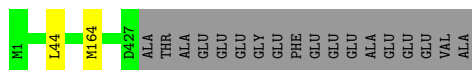
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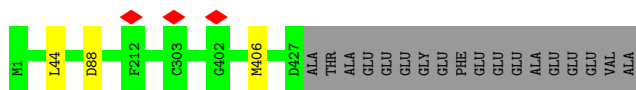
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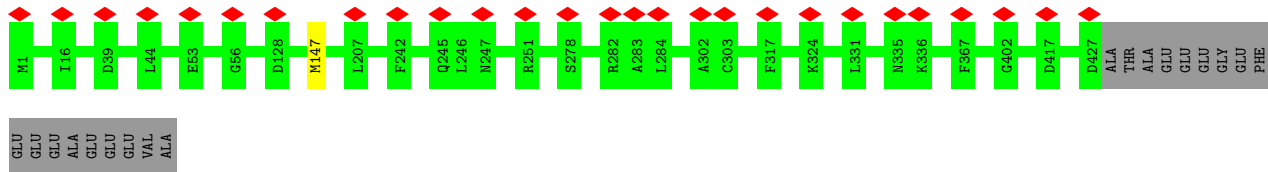
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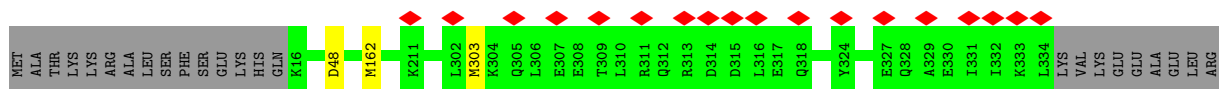
• Molecule 9: Tubulin beta-4B chain



• Molecule 9: Tubulin beta-4B chain

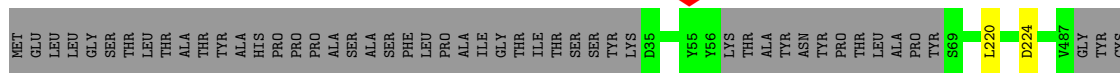


• Molecule 10: Meiosis-specific nuclear structural protein 1



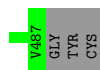
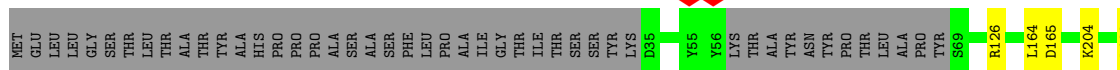
• Molecule 12: Tektin-3

Chain S2:  90% 10%



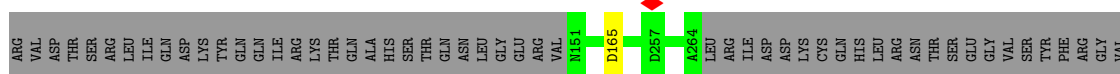
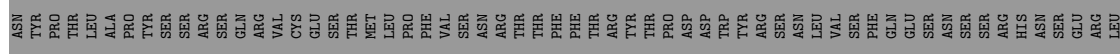
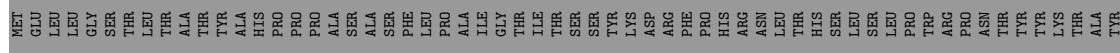
• Molecule 12: Tektin-3

Chain S3:  89% 10%



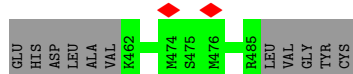
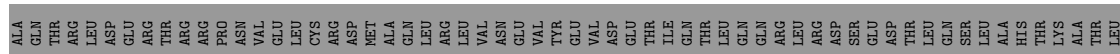
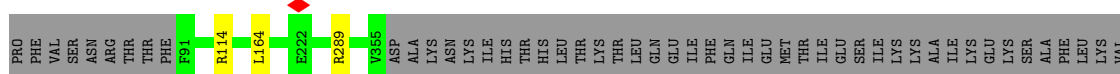
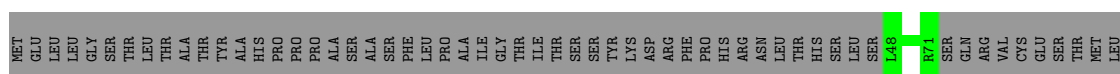
• Molecule 12: Tektin-3

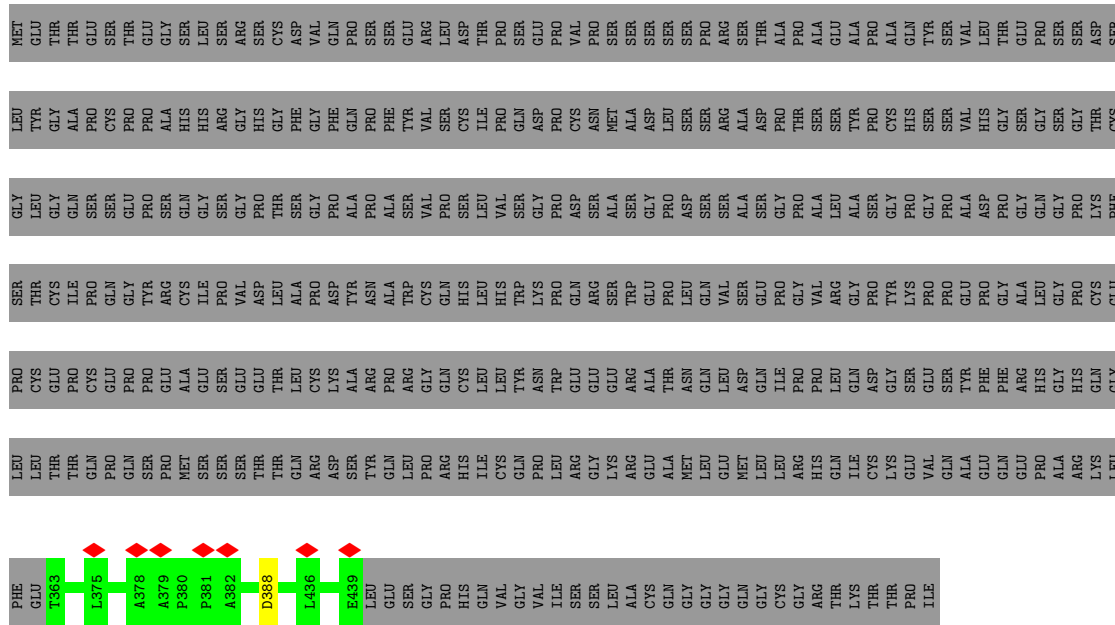
Chain S4:  61% 38%



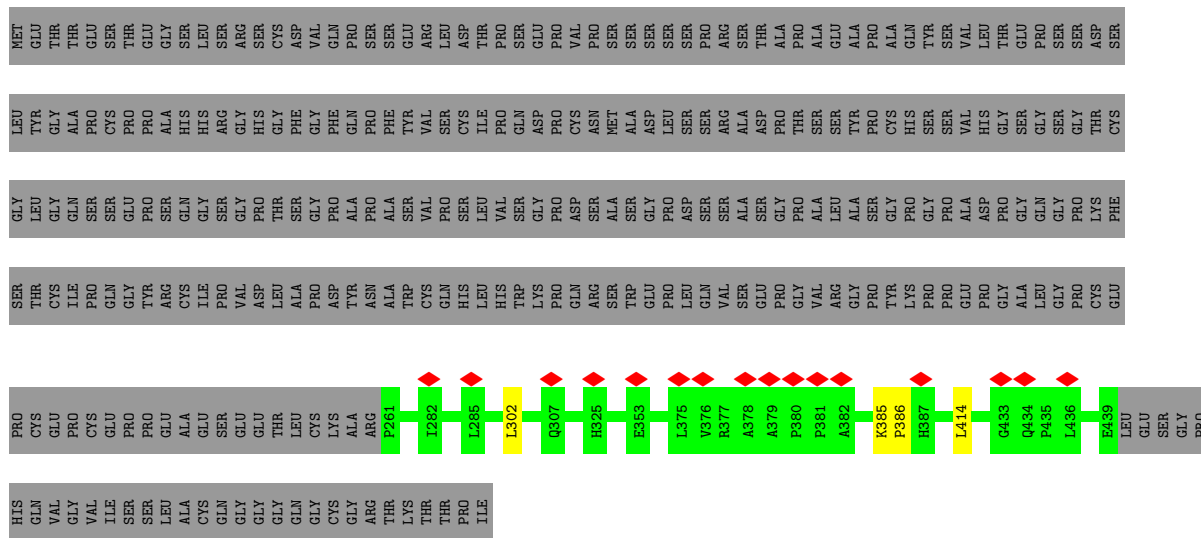
• Molecule 12: Tektin-3

Chain S5:  63% 36%

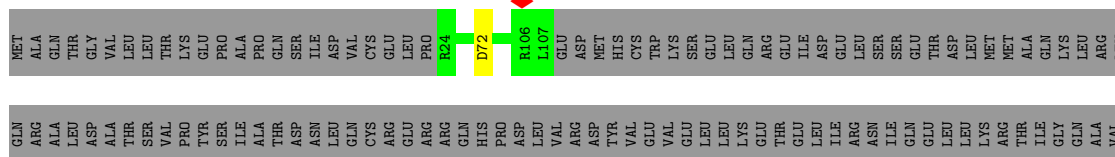


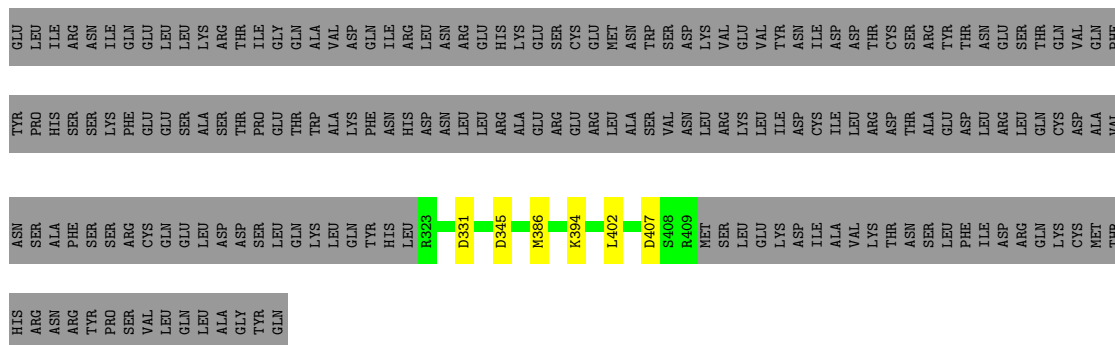


• Molecule 13: Sperm-associated antigen 8

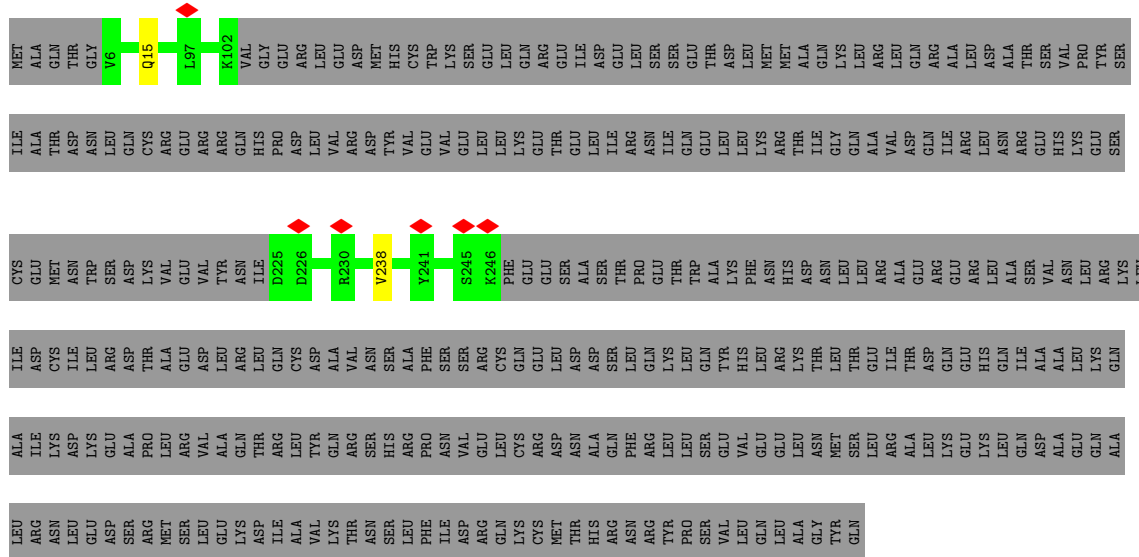


• Molecule 14: Tektin-4

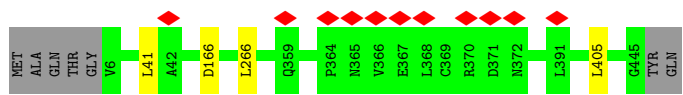




• Molecule 14: Tektin-4



• Molecule 14: Tektin-4



• Molecule 14: Tektin-4

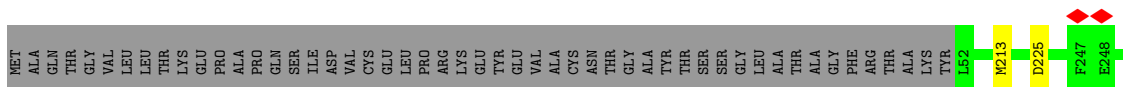
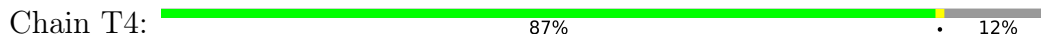


• Molecule 14: Tektin-4

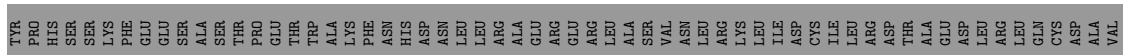
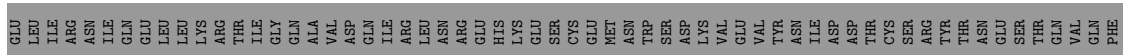
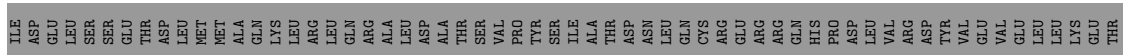
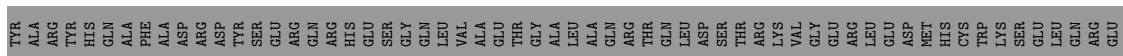
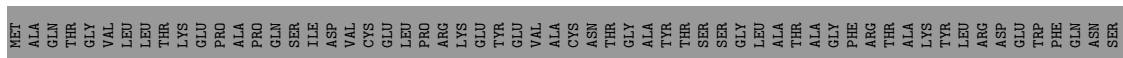




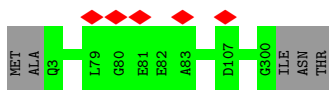
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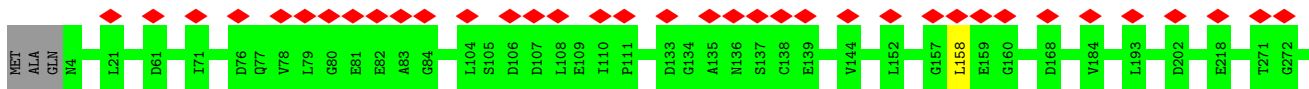
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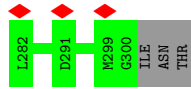


• Molecule 15: Cilia- and flagella-associated protein 161

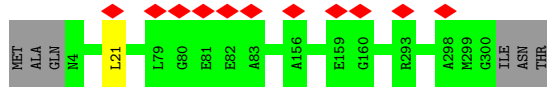


• Molecule 15: Cilia- and flagella-associated protein 161

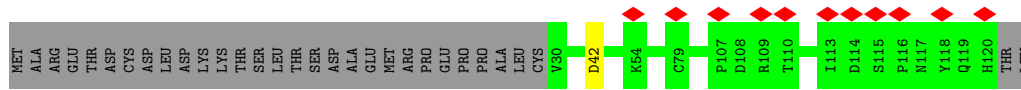
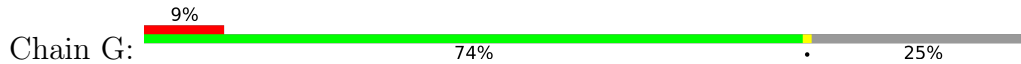




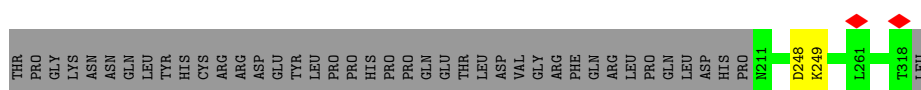
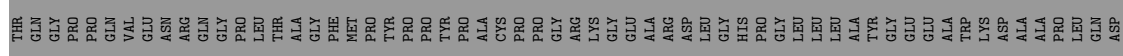
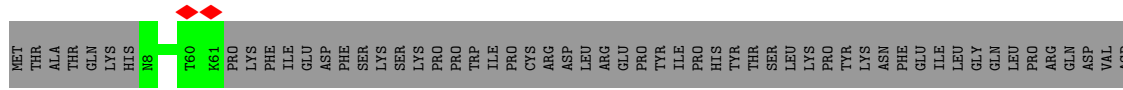
- Molecule 15: Cilia- and flagella-associated protein 161



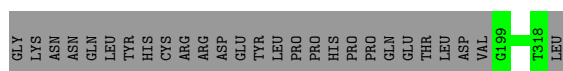
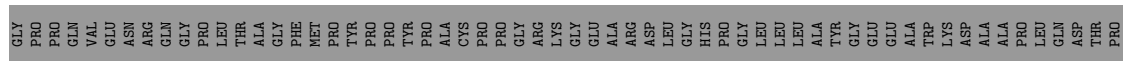
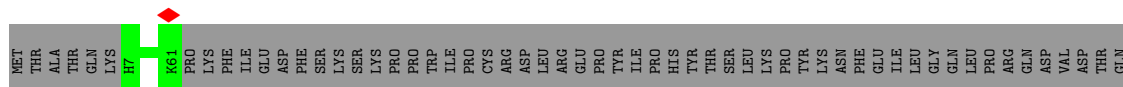
- Molecule 16: Piercer of microtubule wall 2 protein



- Molecule 17: Protein FAM166A



- Molecule 17: Protein FAM166A



- Molecule 17: Protein FAM166A



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

• Molecule 18: Cilia- and flagella-associated protein 68



MET ALA VAL SER PRO CYS SER ASN HIS THR TYR ALA GLN THR ARG GLN ASN SER VAL CYS TYR THR TYR GLY ASP ARG ARG ARG ARG HIS THR LEU W54 R94 P87 S147

GLU PRO GLN THR HIS TYR SER CYS CYS VAL ASP PRO SER VAL GLN SER

• Molecule 19: Cilia and flagella-associated protein 77



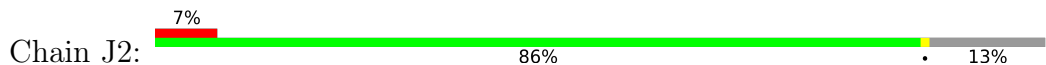
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PRO LEU ILE VAL LYS ALA GLU LEU ARG ARG SER CYS SER LEU PRO GLN PRO ILE VAL ASN PHE ARG THR ASN TYR GLY THR TYR ILE CYS ARG PRO GLY LEU LEU VAL THR VAL ALA ILE ASP ILE ARG HIS TRP ASN VAL PHE LYS GLN ARG PRO THR CYS VAL VAL ARG ASP MET THR ARG ASN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

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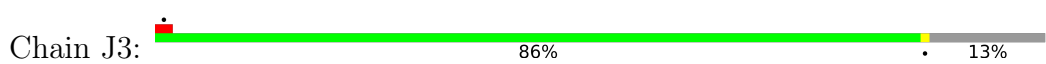
• Molecule 19: Cilia and flagella-associated protein 77



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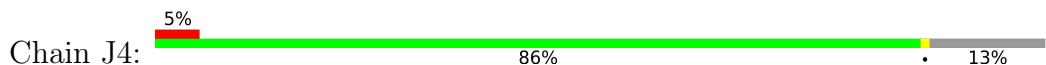
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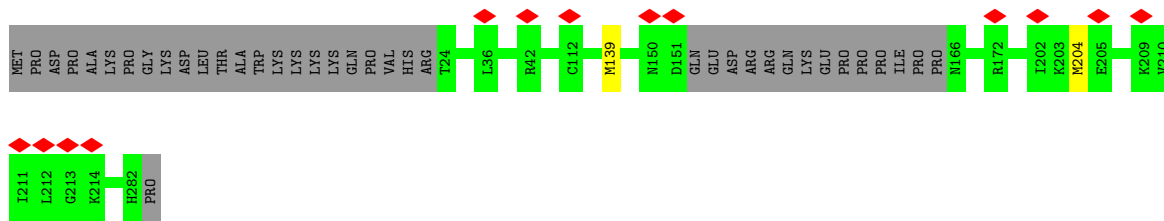
• Molecule 19: Cilia and flagella-associated protein 77



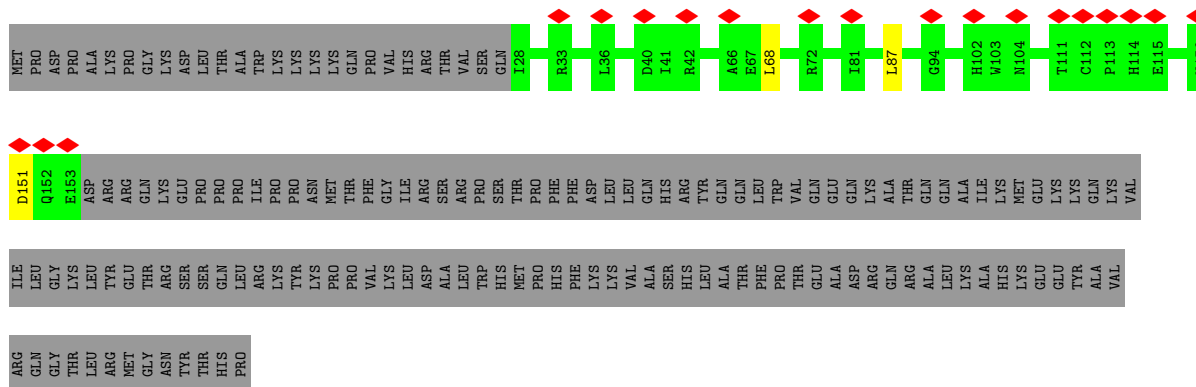
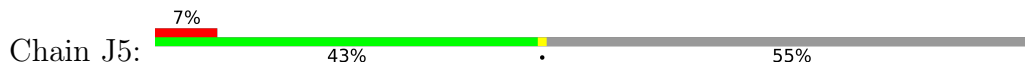
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• Molecule 19: Cilia and flagella-associated protein 77

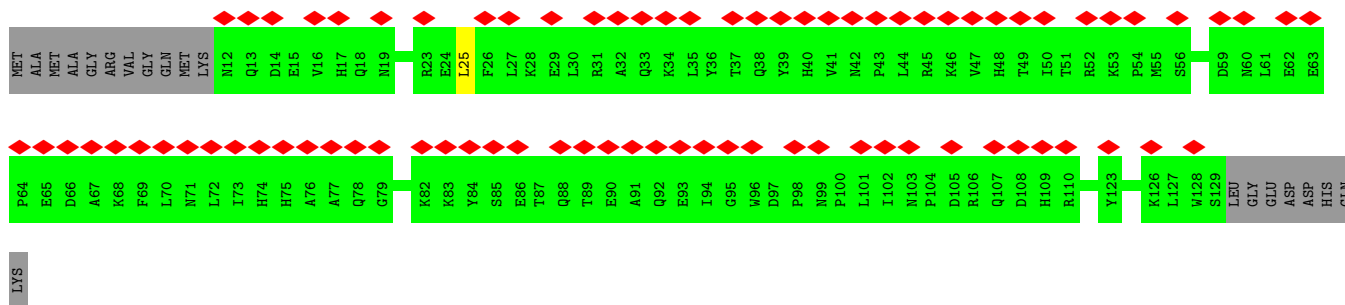
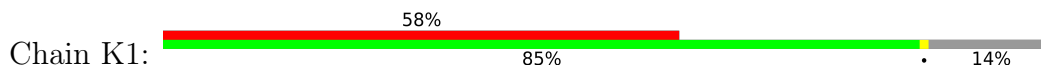




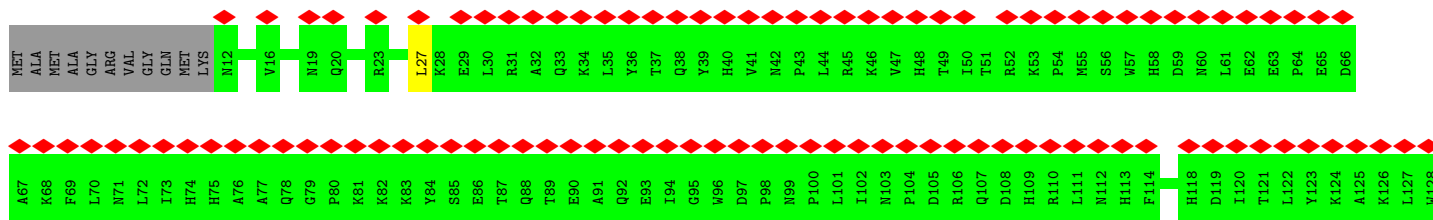
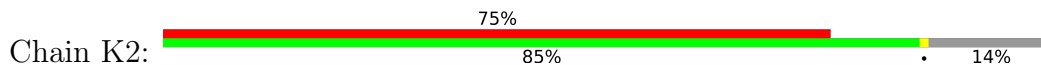
• Molecule 19: Cilia and flagella-associated protein 77

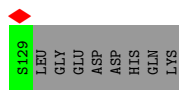


• Molecule 20: Family with sequence similarity 183, member B

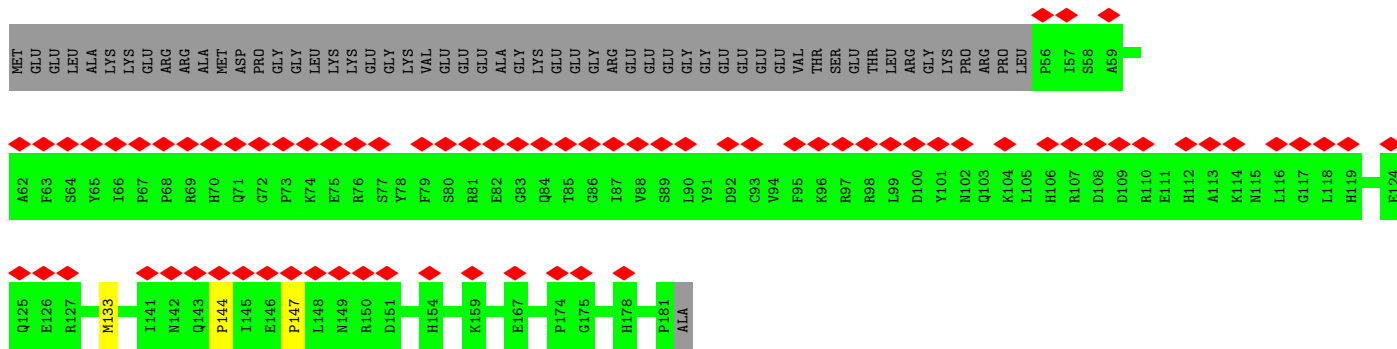
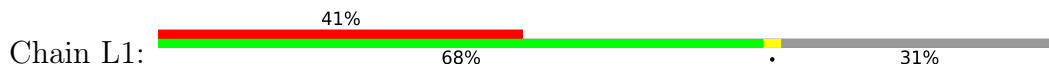


• Molecule 20: Family with sequence similarity 183, member B

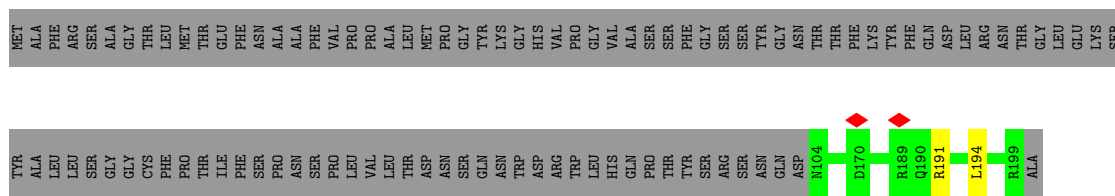




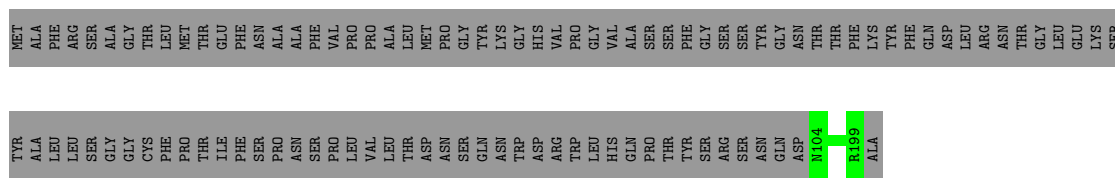
• Molecule 21: Cilia- and flagella-associated protein 90



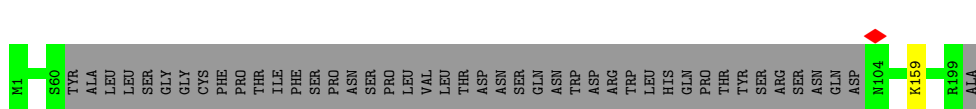
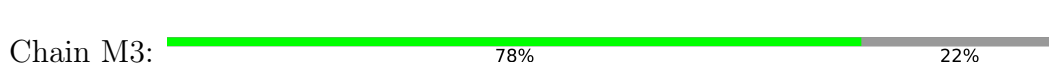
• Molecule 22: Protein FAM166C



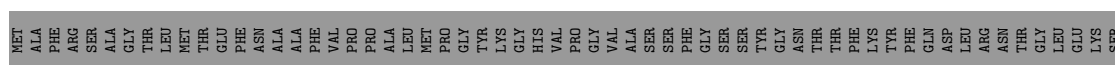
• Molecule 22: Protein FAM166C

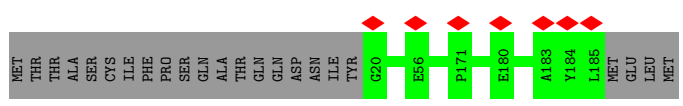
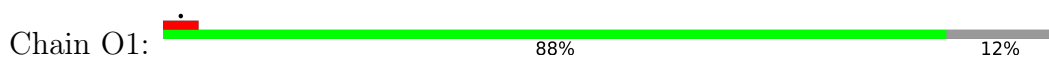


• Molecule 22: Protein FAM166C

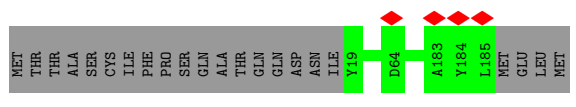


• Molecule 22: Protein FAM166C

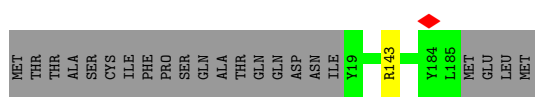
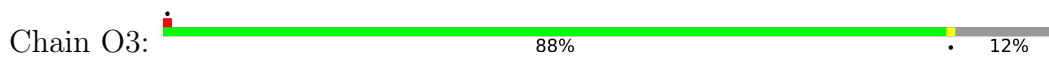




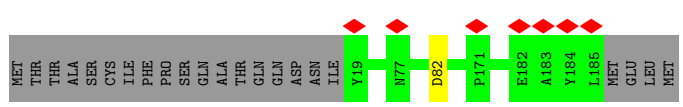
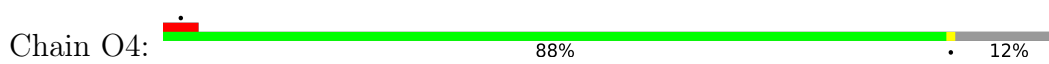
• Molecule 24: Dual specificity phosphatase 21



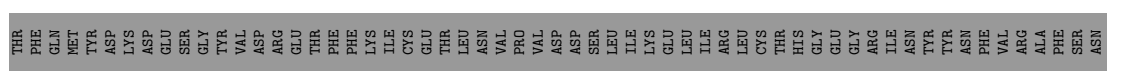
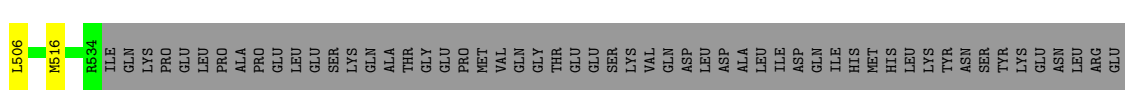
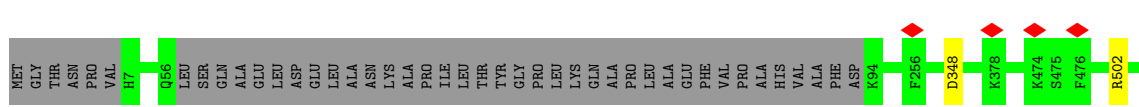
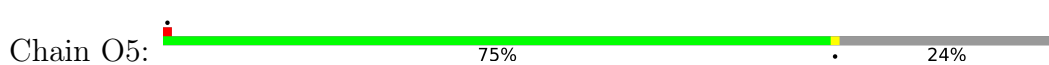
• Molecule 24: Dual specificity phosphatase 21



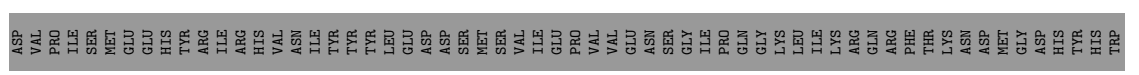
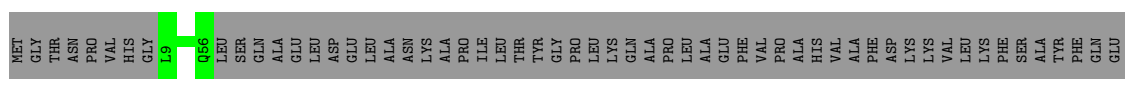
• Molecule 24: Dual specificity phosphatase 21

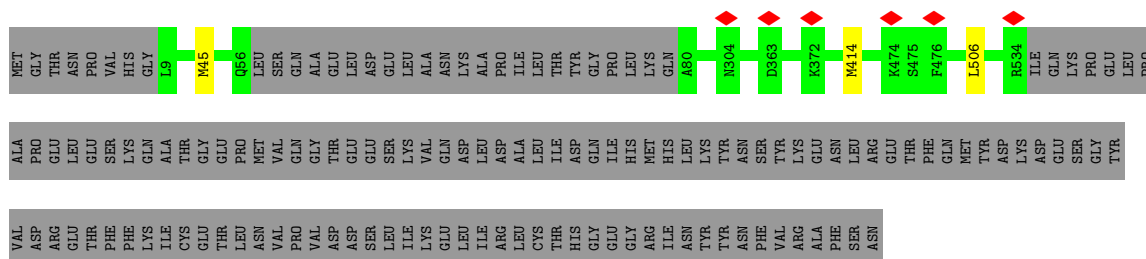


• Molecule 25: EF-hand domain-containing protein 1

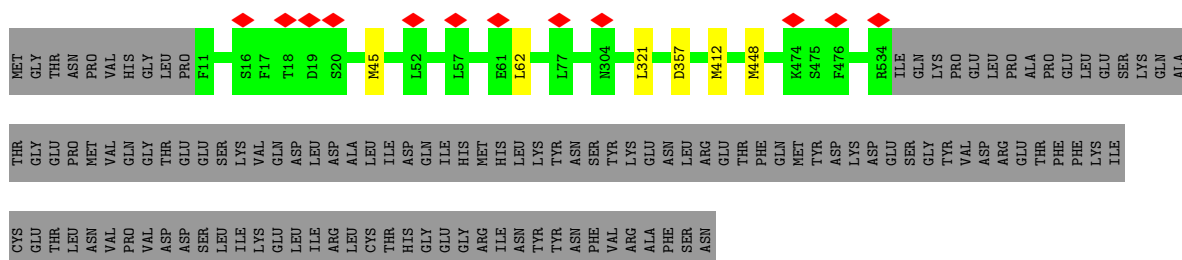
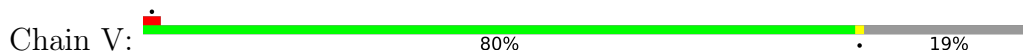


• Molecule 25: EF-hand domain-containing protein 1

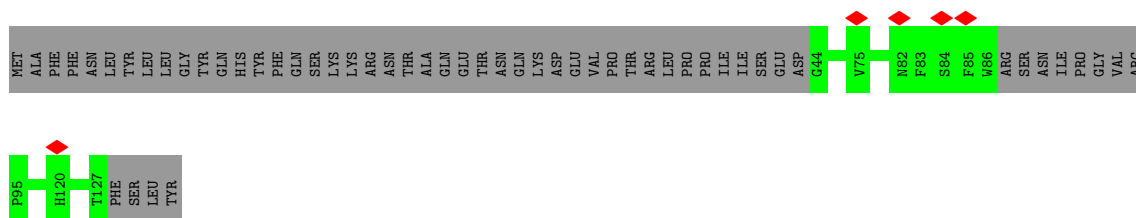




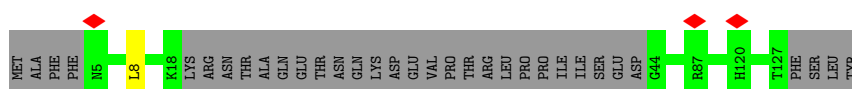
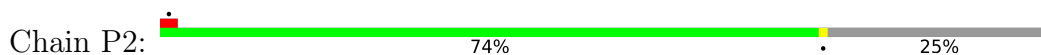
- Molecule 25: EF-hand domain-containing protein 1



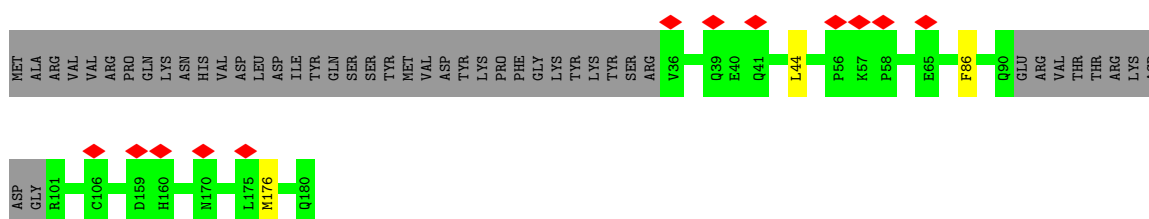
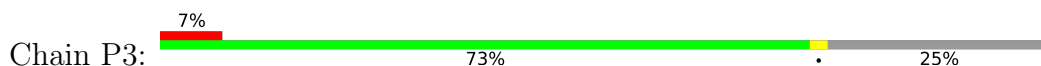
- Molecule 26: Testis expressed 49

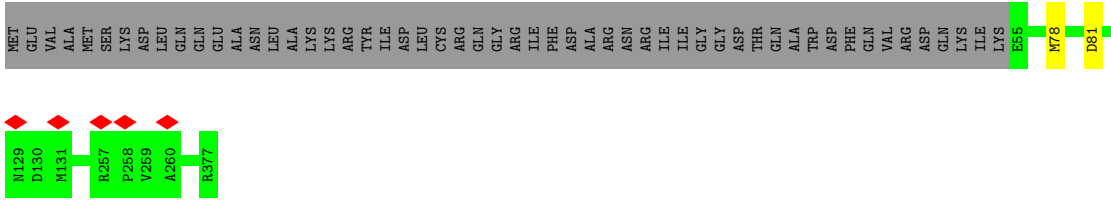


- Molecule 26: Testis expressed 49

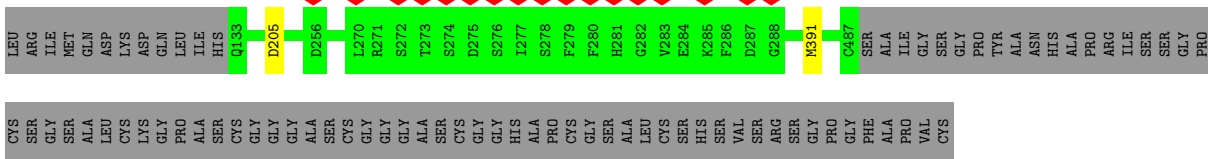
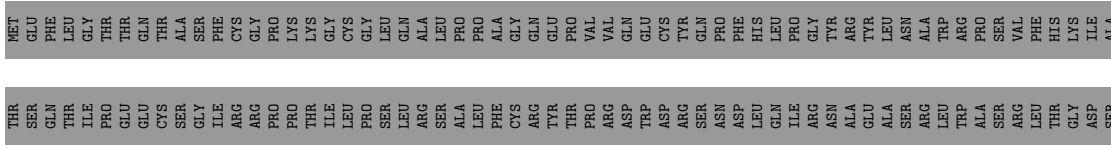


- Molecule 27: Testis-expressed sequence 37 protein

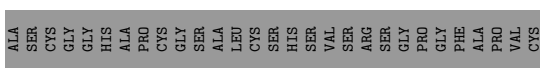
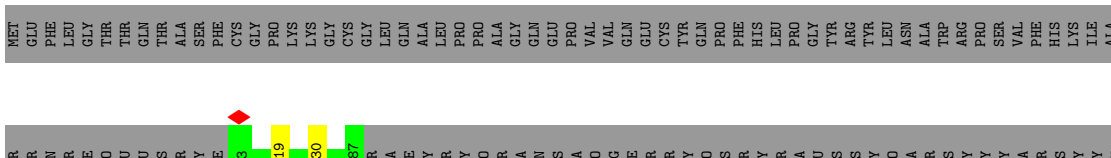
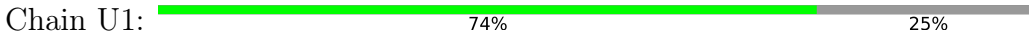




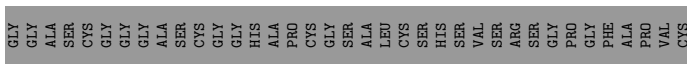
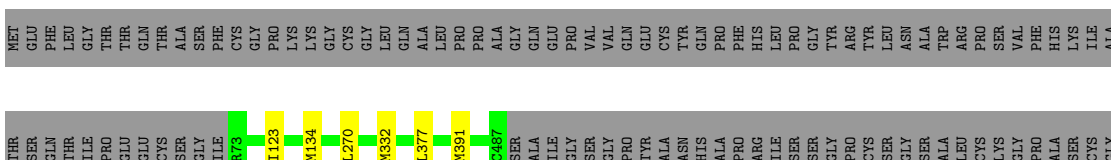
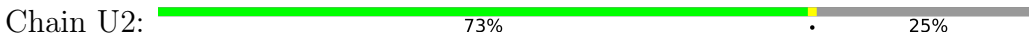
• Molecule 30: Tektin-5



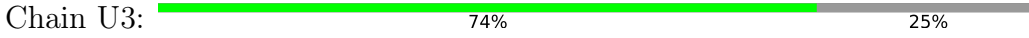
• Molecule 30: Tektin-5

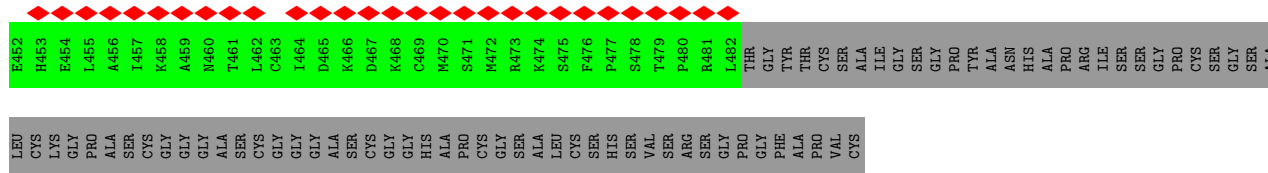


• Molecule 30: Tektin-5

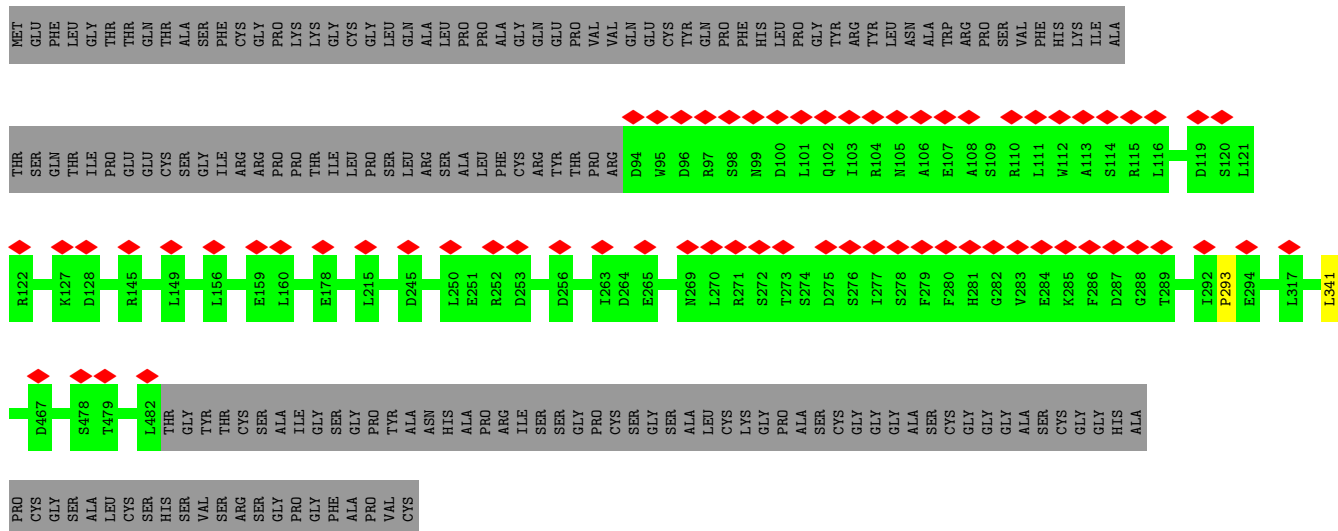


• Molecule 30: Tektin-5

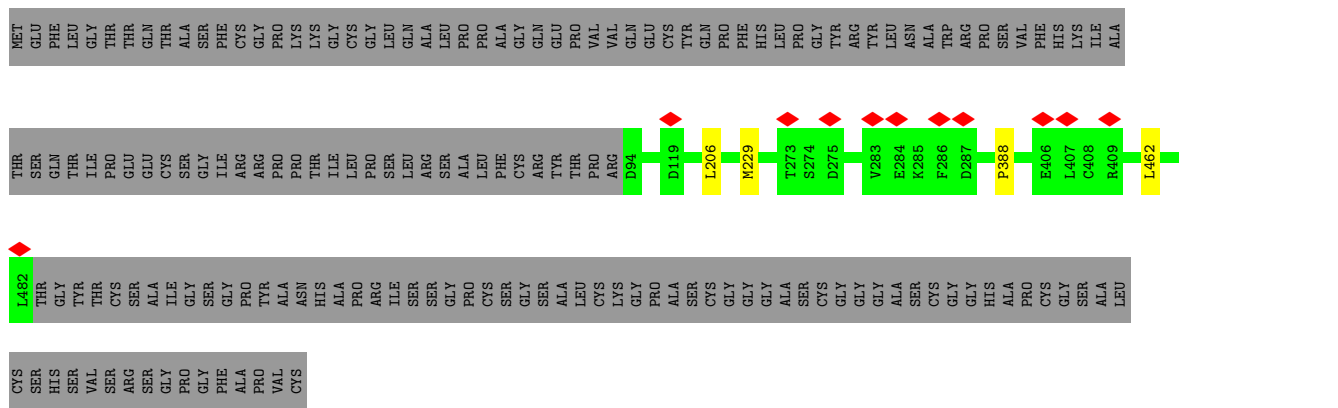




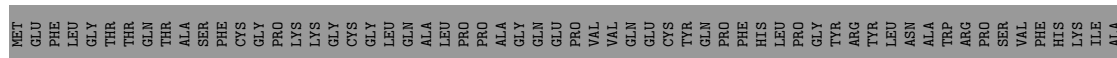
● Molecule 30: Tektin-5

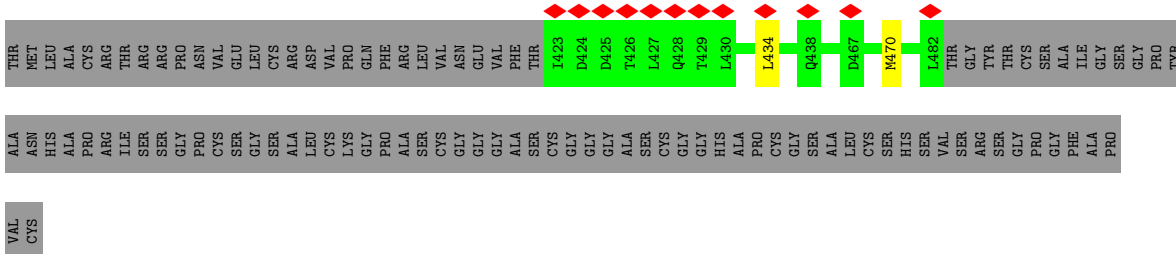


● Molecule 30: Tektin-5

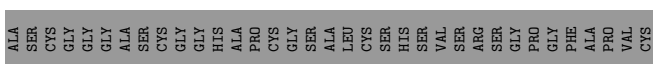
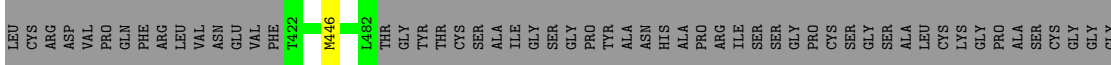
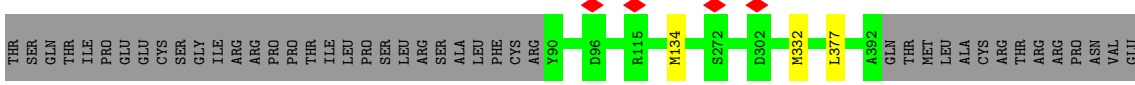
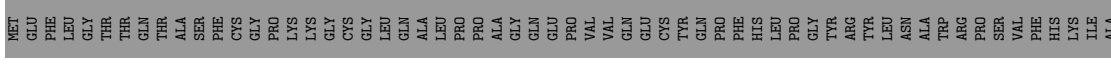


● Molecule 30: Tektin-5

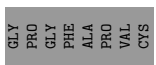
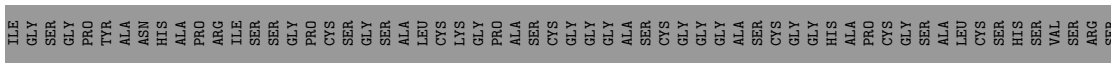
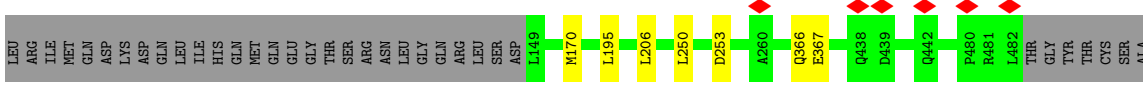
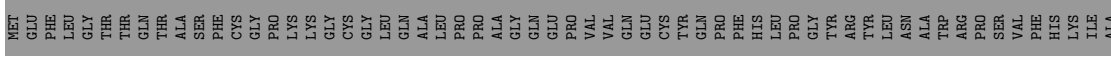




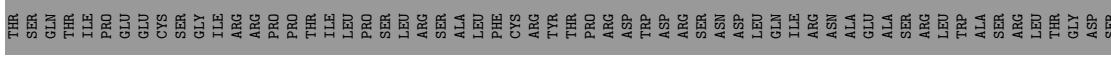
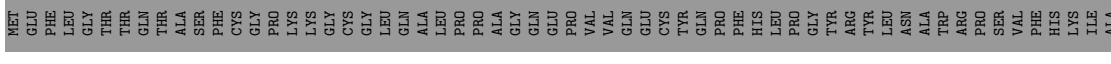
• Molecule 30: Tektin-5

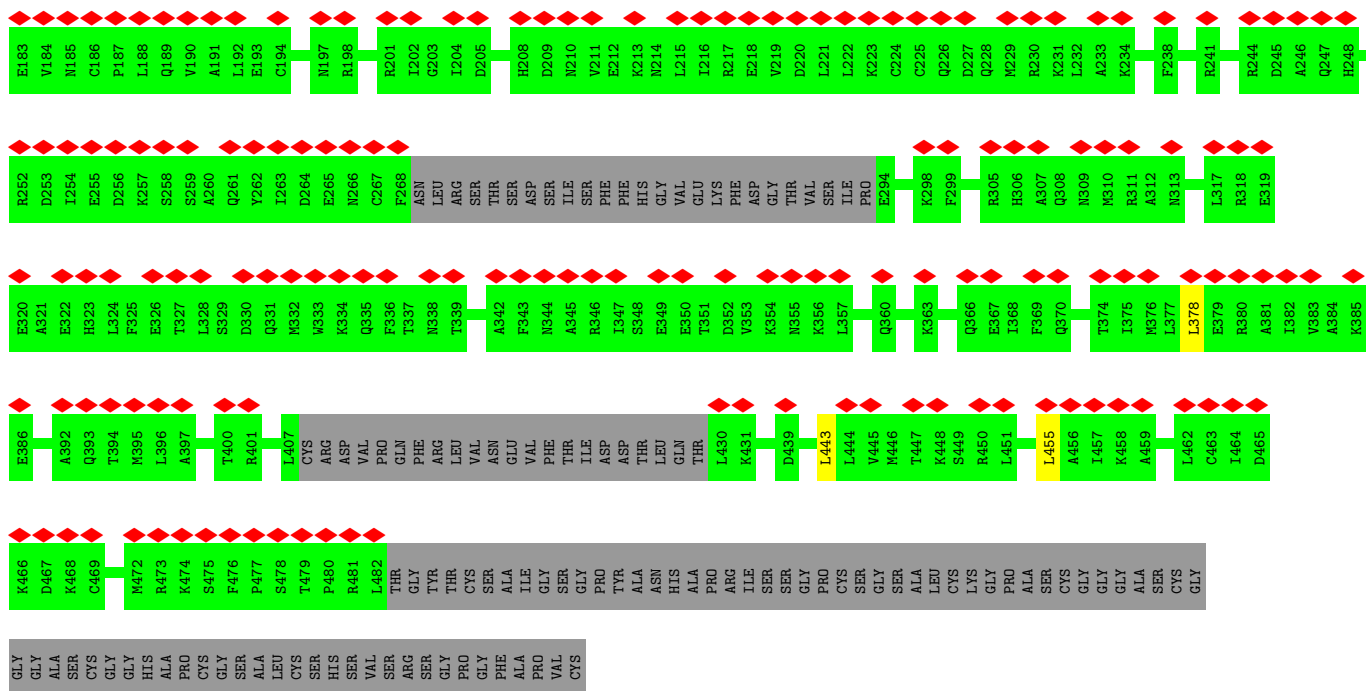


• Molecule 30: Tektin-5

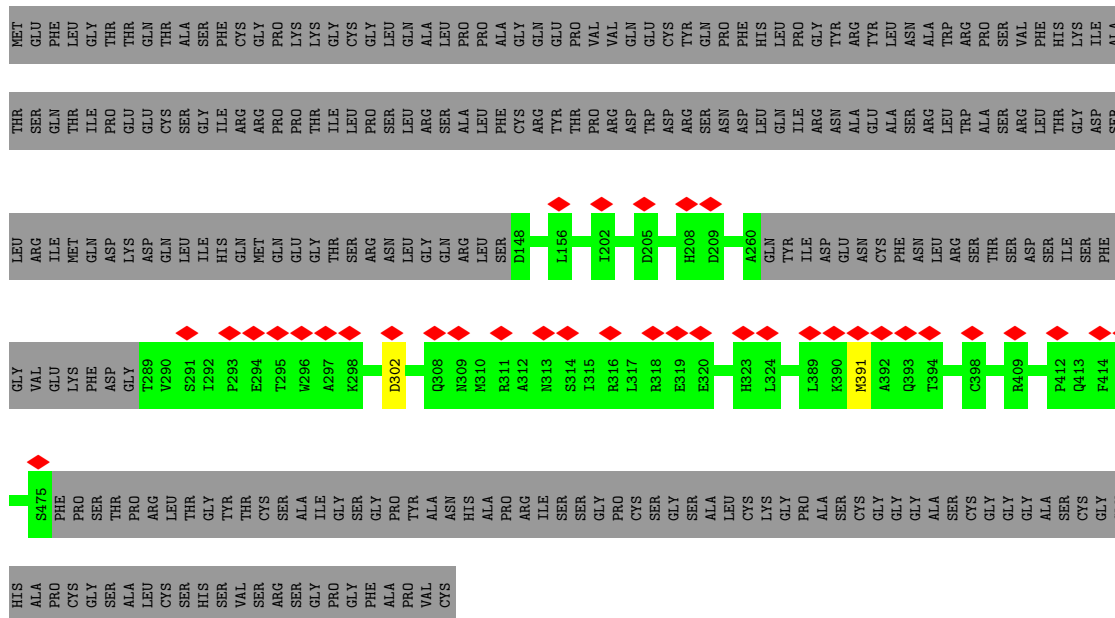


• Molecule 30: Tektin-5

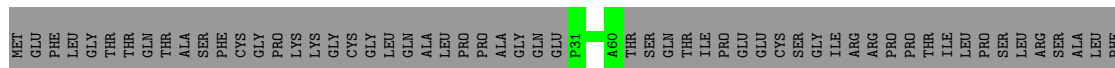




• Molecule 30: Tektin-5

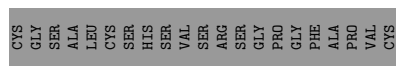
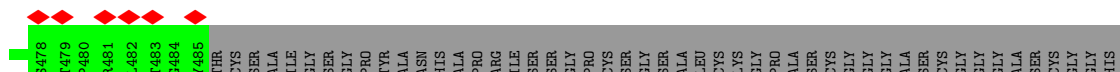
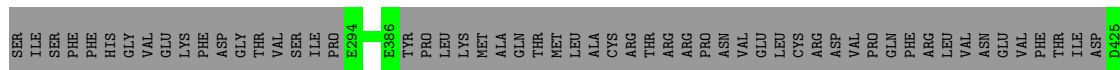
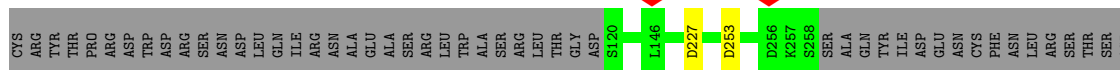
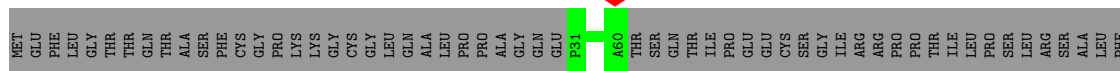


• Molecule 30: Tektin-5



• Molecule 30: Tektin-5

Chain W7:  58% 42%



• Molecule 31: EF-hand domain-containing family member C2

Chain W:  98%



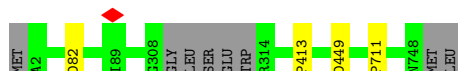
• Molecule 31: EF-hand domain-containing family member C2

Chain X:  98%



• Molecule 31: EF-hand domain-containing family member C2

Chain Y:  98%



• Molecule 31: EF-hand domain-containing family member C2

Chain Z:  98%



• Molecule 32: Spermatid-specific manchette-related protein 1

Chain X0:  10% 90%



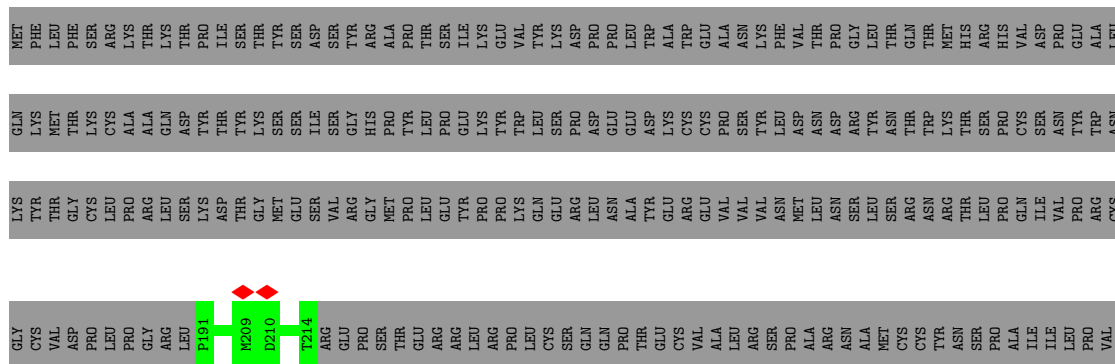
• Molecule 32: Spermatid-specific manchette-related protein 1

Chain X1:  9% 91%



• Molecule 32: Spermatid-specific manchette-related protein 1

Chain X2:  9% 91%



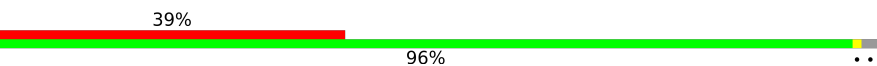
SER
VAL
ASP
PRO
PHE
TYR
ARG
ASP
MET
PRO
HIS
SER
SER
ARG
TYR
PRO
ALA
SER
SER

- Molecule 34: Testis-specific serine/threonine-protein kinase 6

Chain X6:  5% 97%

MET SER G3 D4 E9 G19 K65 P68 R59 S62 P70 H74 E77 N83 G84 L198 L248 S253 A258 L267 R268 A269 GLY ASP SER SER GLY

- Molecule 34: Testis-specific serine/threonine-protein kinase 6

Chain X7:  39% 96%

MET SER G3 D4 K5 L6 L7 S8 E9 L10 K13 R16 E20 G21 S22 A29 T30 S31 K32 G33 Y34 K35 G36 T37 V38 A39 D44 R47 A48 K55 F56 L57 P58 R59 E60 L61 S62 I63 G66 H74 E80 V81 C82 N83 G84 V89 A100

R103 N104 I107 F108 G109 S110 Q111 A112 R113 E114 L115 F116 H129 H130 L131 L142 L143 S144 P145 D146 E147 R148 R149 D154 F155 G156 F157 Q160 A161 H162 Q163 Y164 P165 D166 L167 C172 A178 L183 P187 Y188 D189 D194 V195 M205 V206 T207 G208 D214

S215 D216 I217 A218 R222 K225 R226 G227 V228 E129 L234 E235 L236 S237 R239 C240 S242 E246 L247 Q249 S253 A254 R255 S257 A258 Q259 Q260 V261 W266 L267 R268 A269 GLY ASP SER SER GLY

- Molecule 34: Testis-specific serine/threonine-protein kinase 6

Chain X8:  48% 98%

MET SER G3 D4 K5 L6 L7 S8 E9 L10 G11 Y12 K13 R16 T17 E20 G21 S22 V28 A29 K33 Y34 K35 G36 T37 V38 A39 D44 R45 R46 R47 A48 F52 V53 N54 K55 F56 L57 P58 L61 S62 I63 L64 H74 V75 F76 V81 C82 N83 G84 K85

L86 V89 A92 Q102 R103 N104 G105 R106 I107 P108 G109 S110 Q111 A112 F116 L126 H129 H130 L131 V132 L142 L143 D145 E147 R148 R149 V150 D154 F155 G156 F157 F158 G158 R159 Q160 A161 H162 G163 Y164 P165 D166 L167 C172 G173 S174 A175 A176 Y177 V182

V206 T207 G208 C209 M210 P211 F212 D213 D214 S215 D216 I217 A218 P221 R222 R223 Q224 K225 R226 G227 V228 L229 Y230 P231 D232 G233 L234 E235 L236 R239 L247 L248 Q249 F250 S253 A254 R255 P256 S257 A258 G259 Q260 V261 W266 L267 R268 A269 GLY ASP SER SER GLY

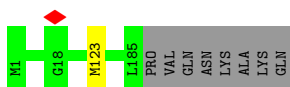
- Molecule 35: Cilia- and flagella-associated protein 20

Chain XA:  9% 95%

M1 S16 I17 G18 S19 K27 M40 Q43 S44 L47 D126 L171 E174 D175 E176 P177 P178 A179 E180 L183 Y184 L185 PRO VAL GLN ASN LYS ALA LYS GLN

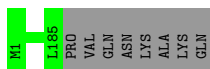
- Molecule 35: Cilia- and flagella-associated protein 20

Chain XB:  95%



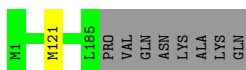
- Molecule 35: Cilia- and flagella-associated protein 20

Chain XC:  96%



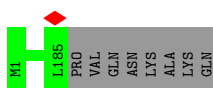
- Molecule 35: Cilia- and flagella-associated protein 20

Chain XD:  95%



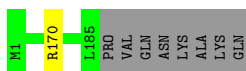
- Molecule 35: Cilia- and flagella-associated protein 20

Chain XE:  96%



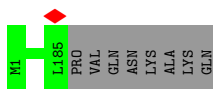
- Molecule 35: Cilia- and flagella-associated protein 20

Chain XF:  95%



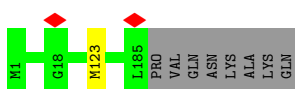
- Molecule 35: Cilia- and flagella-associated protein 20

Chain XG:  96%



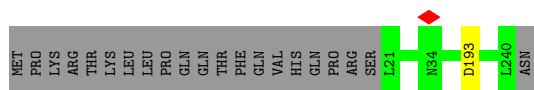
- Molecule 35: Cilia- and flagella-associated protein 20

Chain XH:  95%



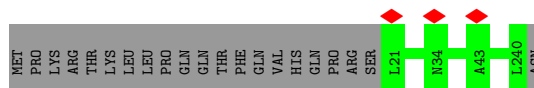
- Molecule 36: Outer dense fiber protein 3

Chain YD:  91% 9%



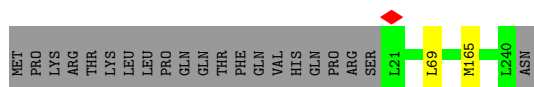
- Molecule 37: Parkin coregulated gene protein homolog

Chain YE:  91% 9%



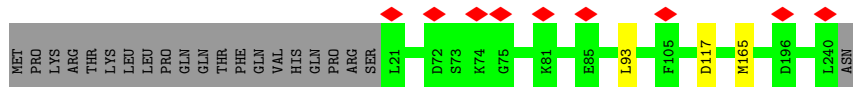
- Molecule 37: Parkin coregulated gene protein homolog

Chain YF:  90% 9%



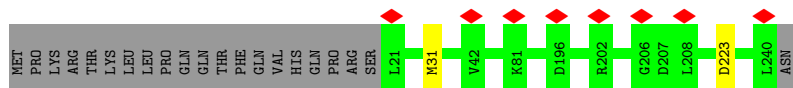
- Molecule 37: Parkin coregulated gene protein homolog

Chain YG:  90% 9%



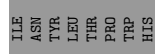
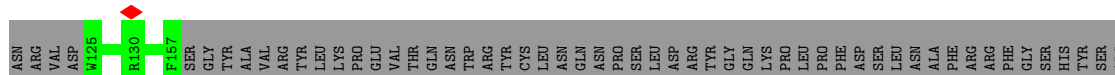
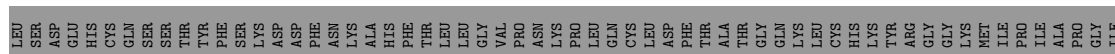
- Molecule 37: Parkin coregulated gene protein homolog

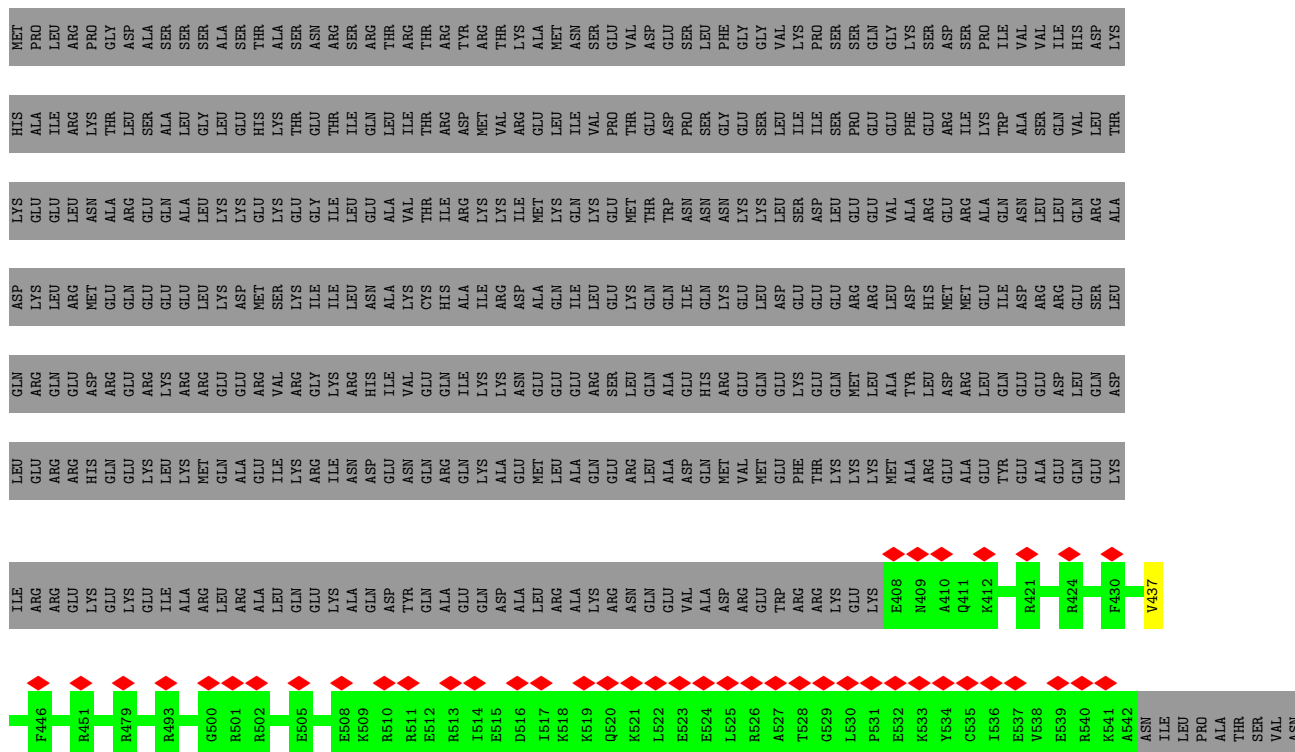
Chain YH:  90% 9%



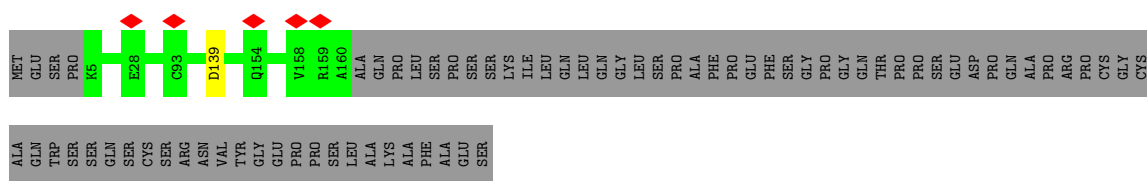
- Molecule 38: Testis, prostate and placenta-expressed protein

Chain Z1:  15% 85%

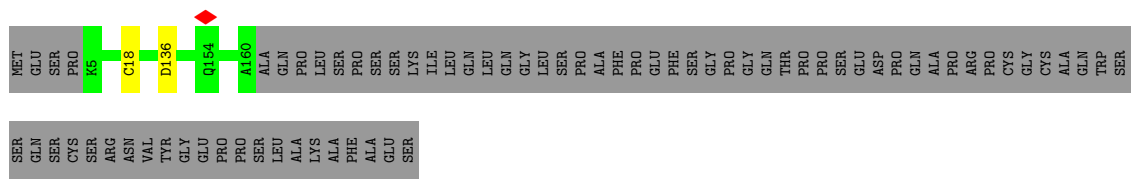




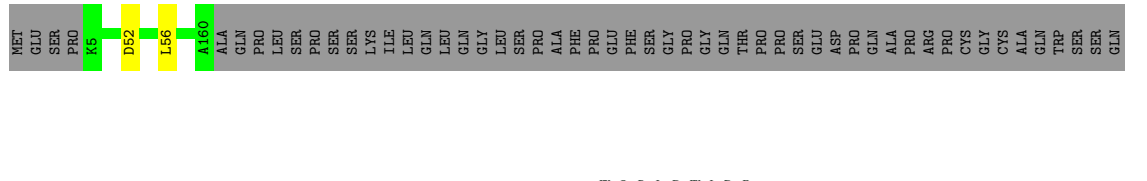
• Molecule 40: Uncharacterized protein C10orf82 homolog

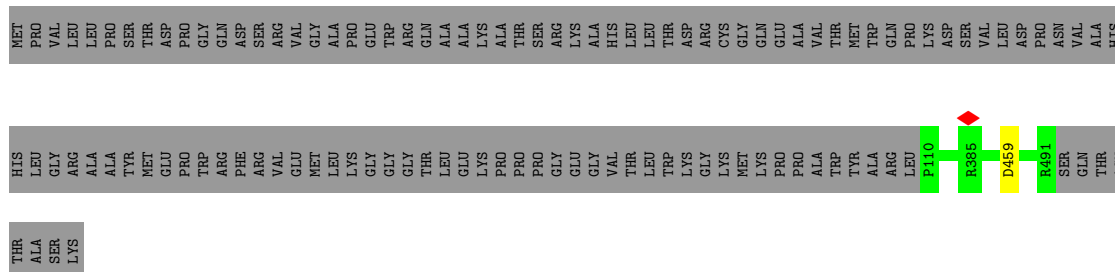


• Molecule 40: Uncharacterized protein C10orf82 homolog

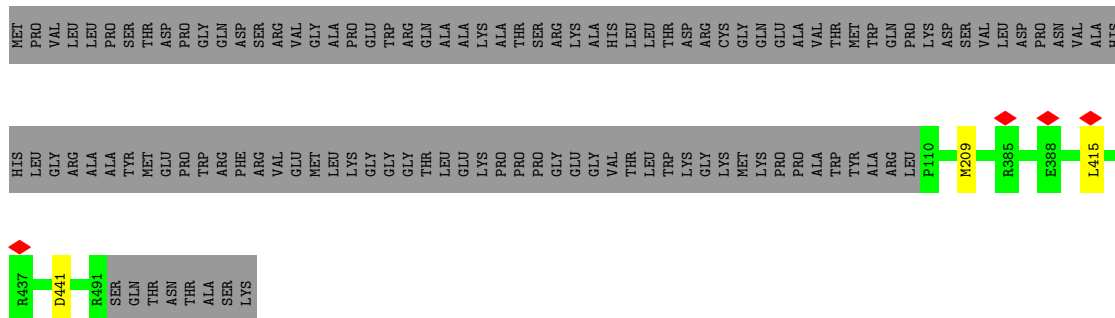
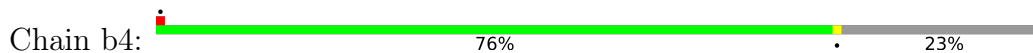


• Molecule 40: Uncharacterized protein C10orf82 homolog

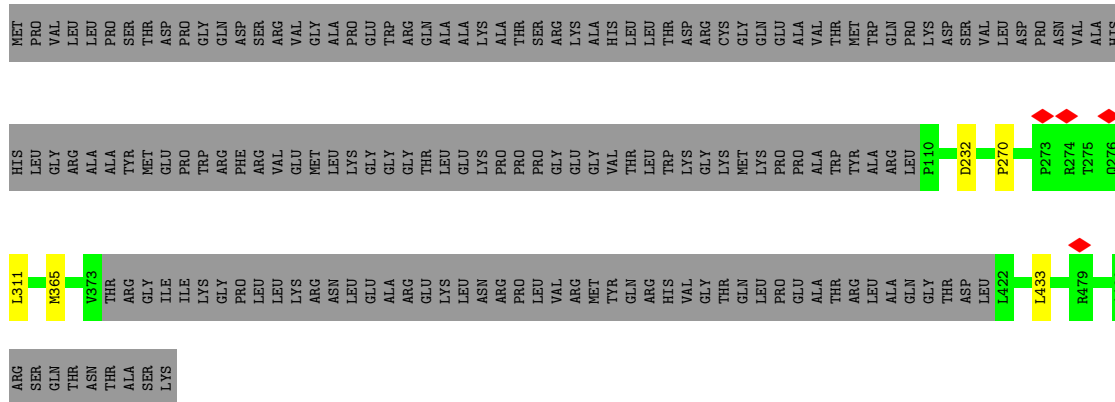




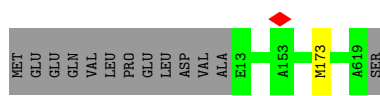
• Molecule 41: Coiled-coil domain-containing protein 105



• Molecule 41: Coiled-coil domain-containing protein 105

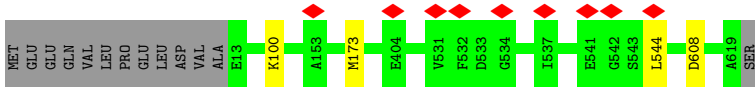


• Molecule 42: Cilia- and flagella-associated protein 52

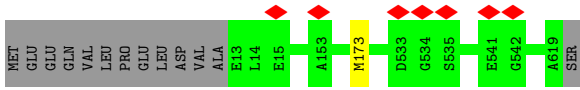


• Molecule 42: Cilia- and flagella-associated protein 52

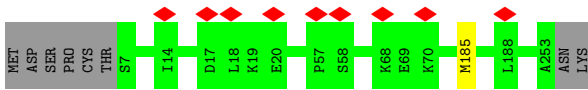




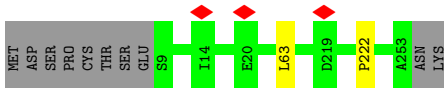
• Molecule 42: Cilia- and flagella-associated protein 52



• Molecule 43: Enkurin



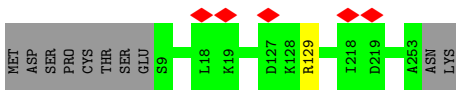
• Molecule 43: Enkurin



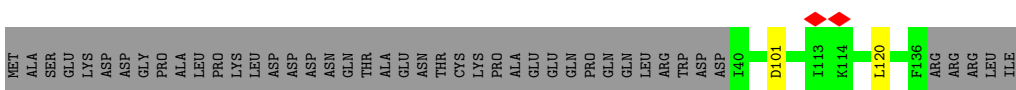
• Molecule 43: Enkurin



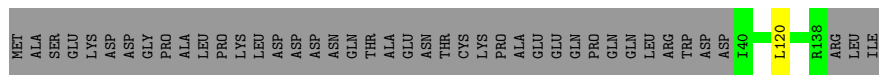
• Molecule 43: Enkurin



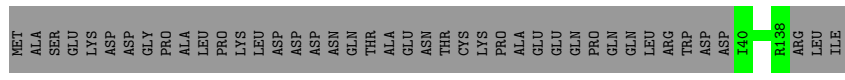
• Molecule 44: Testis-expressed protein 43



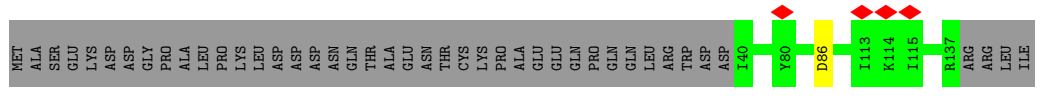
• Molecule 44: Testis-expressed protein 43



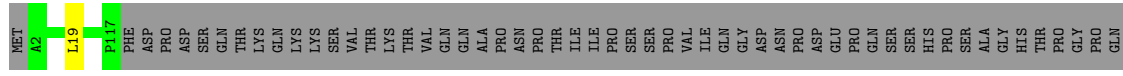
• Molecule 44: Testis-expressed protein 43



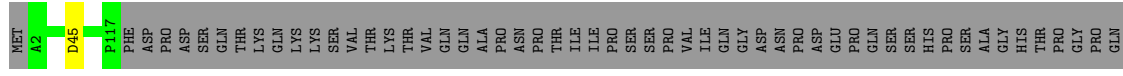
• Molecule 44: Testis-expressed protein 43



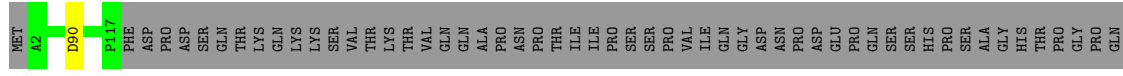
• Molecule 45: Protein Flattop



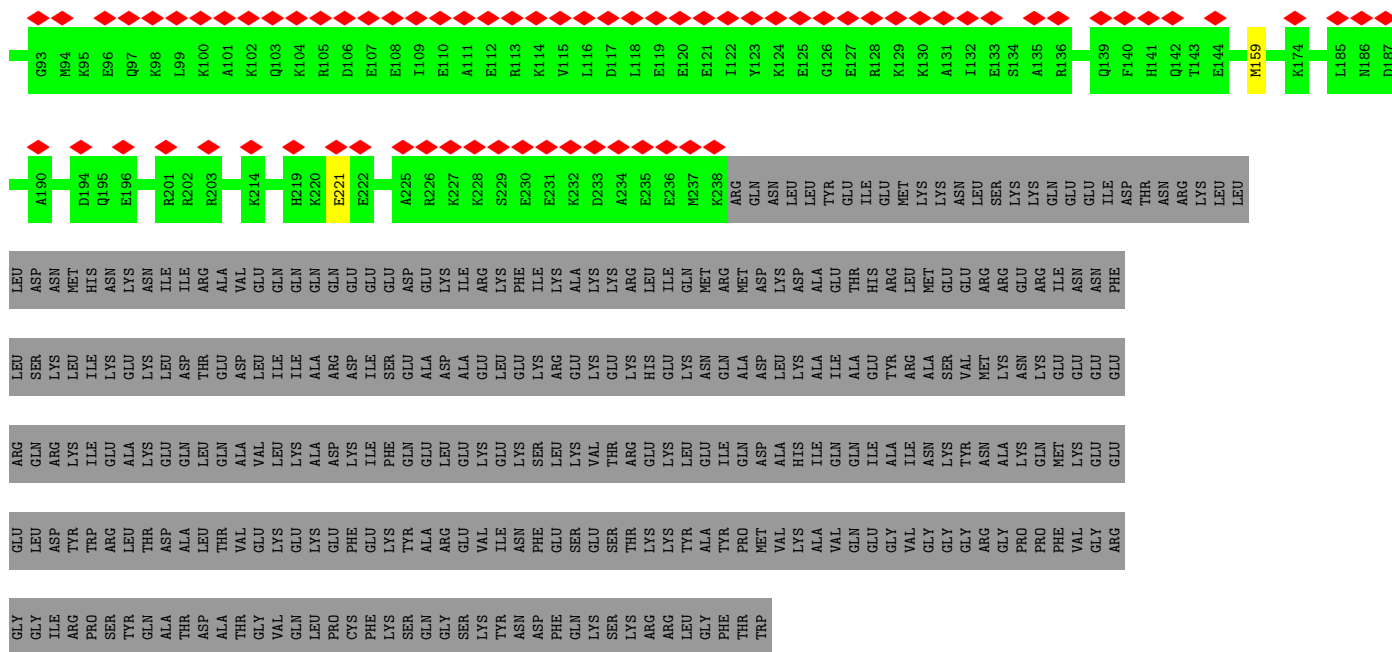
• Molecule 45: Protein Flattop



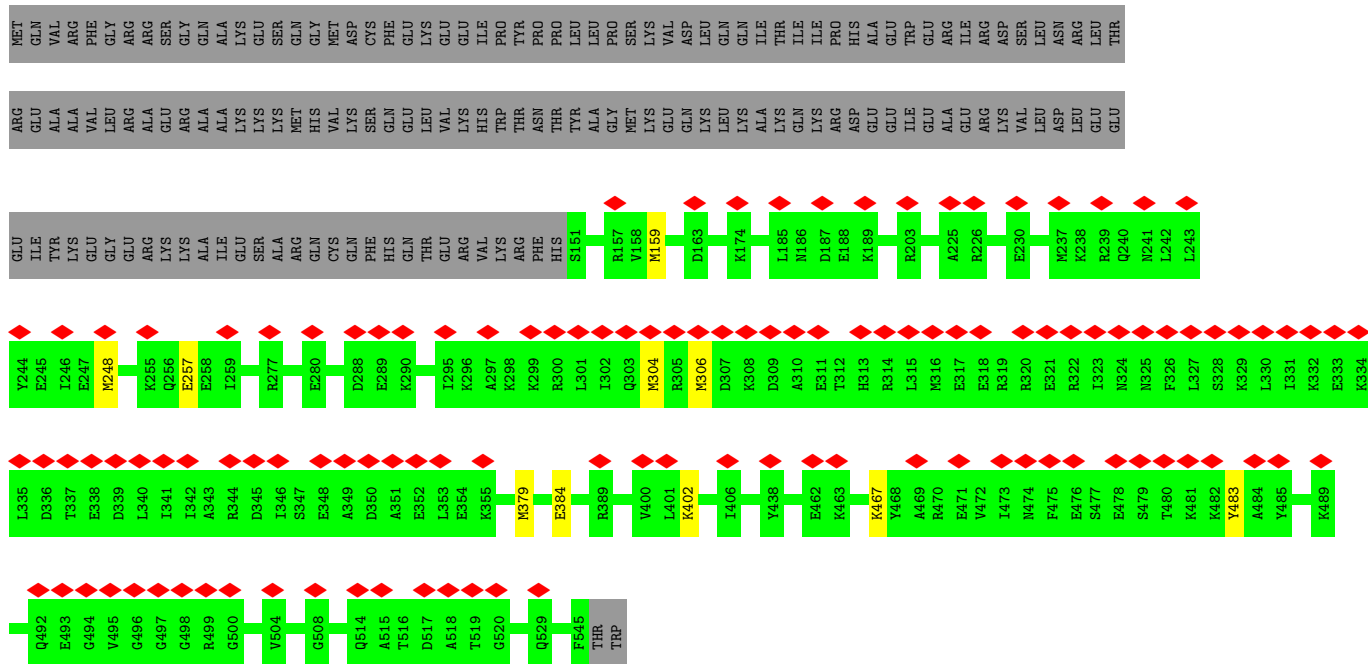
• Molecule 45: Protein Flattop



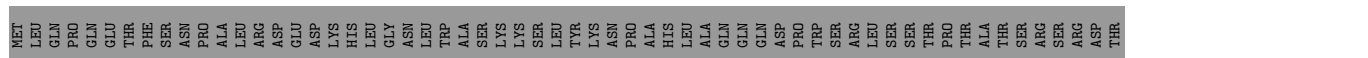
• Molecule 45: Protein Flattop



• Molecule 47: Cilia- and flagella-associated protein 210



• Molecule 48: Cilia- and flagella-associated protein 276



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	95290	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.821	Depositor
Minimum map value	0.000	Depositor
Average map value	0.073	Depositor
Map value standard deviation	0.176	Depositor
Recommended contour level	0.3	Depositor
Map size (\AA)	576.11, 463.062, 869.60004	wwPDB
Map dimensions	530, 426, 800	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.087, 1.087, 1.087	Depositor

5 Model quality i

5.1 Standard geometry i

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.39	0/685	0.78	0/918
1	7	0.35	0/1206	0.72	2/1629 (0.1%)
2	1	0.33	0/3827	0.59	0/5169
2	2	0.37	0/2224	0.65	0/3010
3	3	0.35	0/4056	0.64	7/5386 (0.1%)
3	4	0.33	0/1237	0.67	1/1646 (0.1%)
4	5	0.31	0/3038	0.58	2/4102 (0.0%)
4	6	0.29	0/3038	0.57	0/4102
4	j1	0.34	0/3038	0.67	2/4102 (0.0%)
5	8	0.33	0/1523	0.75	4/2073 (0.2%)
6	A	0.35	0/819	0.74	2/1097 (0.2%)
6	N1	0.44	0/819	0.71	1/1097 (0.1%)
7	A0	0.34	0/449	0.61	0/605
7	A1	0.32	0/2965	0.55	0/3994
7	A2	0.34	0/3327	0.54	1/4483 (0.0%)
7	A3	0.36	0/3327	0.58	3/4483 (0.1%)
7	A4	0.34	0/3313	0.56	1/4465 (0.0%)
7	A5	0.36	0/1419	0.59	1/1910 (0.1%)
8	AA	0.27	0/3502	0.56	1/4755 (0.0%)
8	AC	0.30	0/3502	0.55	2/4755 (0.0%)
8	AE	0.35	0/3509	0.64	2/4765 (0.0%)
8	AG	0.37	1/3518 (0.0%)	0.59	1/4777 (0.0%)
8	AI	0.35	0/3509	0.64	6/4765 (0.1%)
8	AK	0.33	0/3496	0.56	1/4747 (0.0%)
8	AM	0.34	0/3509	0.60	1/4765 (0.0%)
8	AO	0.32	0/3509	0.60	1/4765 (0.0%)
8	BC	0.29	0/3451	0.54	0/4686
8	BE	0.34	0/3518	0.64	5/4777 (0.1%)
8	BG	0.32	0/3473	0.57	0/4716
8	BI	0.35	0/3518	0.61	3/4777 (0.1%)
8	BK	0.33	0/3467	0.60	3/4708 (0.1%)
8	BM	0.33	0/3502	0.63	6/4755 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	BO	0.33	0/3473	0.62	3/4716 (0.1%)
8	CC	0.31	0/3502	0.57	5/4755 (0.1%)
8	CE	0.30	0/3502	0.58	2/4755 (0.0%)
8	CG	0.30	0/3502	0.57	2/4755 (0.0%)
8	CI	0.32	0/3502	0.58	3/4755 (0.1%)
8	CK	0.32	0/3502	0.56	2/4755 (0.0%)
8	CM	0.34	0/3509	0.63	4/4765 (0.1%)
8	CO	0.29	0/3502	0.55	1/4755 (0.0%)
8	CQ	0.31	0/3488	0.59	0/4736
8	DC	0.32	0/3459	0.57	1/4697 (0.0%)
8	DE	0.29	0/3443	0.56	3/4675 (0.1%)
8	DG	0.31	0/3443	0.54	0/4675
8	DI	0.31	0/3451	0.57	1/4686 (0.0%)
8	DK	0.29	0/3450	0.52	0/4685
8	DM	0.29	0/3457	0.54	0/4694
8	DO	0.28	0/3449	0.55	2/4683 (0.0%)
8	DQ	0.27	0/3437	0.56	2/4667 (0.0%)
8	EA	0.32	1/3502 (0.0%)	0.58	1/4755 (0.0%)
8	EC	0.28	0/3496	0.55	1/4747 (0.0%)
8	EE	0.27	0/3502	0.52	0/4755
8	EG	0.28	0/3502	0.55	1/4755 (0.0%)
8	EI	0.30	0/3502	0.56	1/4755 (0.0%)
8	EK	0.30	0/3502	0.54	0/4755
8	EM	0.27	0/3502	0.52	0/4755
8	EO	0.28	0/3488	0.57	1/4736 (0.0%)
8	FA	0.32	0/3443	0.62	4/4675 (0.1%)
8	FC	0.30	0/3443	0.58	1/4675 (0.0%)
8	FE	0.27	0/3443	0.53	0/4675
8	FG	0.30	0/3427	0.60	3/4652 (0.1%)
8	FI	0.33	0/3443	0.57	3/4675 (0.1%)
8	FK	0.27	0/3450	0.55	3/4685 (0.1%)
8	FM	0.28	0/3443	0.56	1/4675 (0.0%)
8	FO	0.28	0/3432	0.59	2/4660 (0.0%)
8	GA	0.27	0/3445	0.55	3/4678 (0.1%)
8	GC	0.30	0/3450	0.60	2/4685 (0.0%)
8	GE	0.33	0/3450	0.62	3/4685 (0.1%)
8	GG	0.34	0/3509	0.62	3/4765 (0.1%)
8	GI	0.30	0/3464	0.58	1/4704 (0.0%)
8	GK	0.31	0/3464	0.61	2/4704 (0.0%)
8	GM	0.31	0/3472	0.61	2/4715 (0.0%)
8	GO	0.30	0/3472	0.63	4/4715 (0.1%)
8	HA	0.30	0/3448	0.63	6/4682 (0.1%)
8	HC	0.33	0/3466	0.65	2/4706 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	HE	0.32	0/3509	0.64	3/4765 (0.1%)
8	HG	0.36	1/3509 (0.0%)	0.60	1/4765 (0.0%)
8	HI	0.33	0/3509	0.59	1/4765 (0.0%)
8	HK	0.32	0/3443	0.64	4/4675 (0.1%)
8	HM	0.36	0/3466	0.66	3/4706 (0.1%)
8	HO	0.34	0/3458	0.66	2/4696 (0.0%)
8	IA	0.30	0/3457	0.64	5/4694 (0.1%)
8	IC	0.36	2/3509 (0.1%)	0.65	1/4765 (0.0%)
8	IE	0.33	0/3518	0.67	7/4777 (0.1%)
8	IG	0.43	2/3464 (0.1%)	0.68	4/4704 (0.1%)
8	II	0.38	0/3476	0.62	1/4720 (0.0%)
8	IK	0.38	1/3488 (0.0%)	0.64	2/4736 (0.0%)
8	IM	0.39	1/3468 (0.0%)	0.69	8/4709 (0.2%)
8	IO	0.35	0/3509	0.67	2/4765 (0.0%)
8	JC	0.30	0/3465	0.59	2/4704 (0.0%)
8	JE	0.35	0/3502	0.67	5/4755 (0.1%)
8	JG	0.33	0/3437	0.60	2/4667 (0.0%)
8	JI	0.37	0/3467	0.67	4/4708 (0.1%)
8	JK	0.33	0/3458	0.60	1/4696 (0.0%)
8	JM	0.32	0/3443	0.59	3/4675 (0.1%)
8	JO	0.35	0/3456	0.65	1/4693 (0.0%)
8	JQ	0.31	0/3480	0.64	2/4725 (0.0%)
8	KA	0.31	0/3457	0.58	2/4694 (0.0%)
8	KC	0.32	0/3466	0.59	3/4705 (0.1%)
8	KE	0.34	0/3474	0.60	1/4716 (0.0%)
8	KG	0.33	0/3457	0.58	3/4694 (0.1%)
8	KI	0.35	0/3451	0.59	1/4686 (0.0%)
8	KK	0.30	0/3449	0.57	0/4683
8	KM	0.33	0/3457	0.64	5/4694 (0.1%)
8	KO	0.34	0/3466	0.62	2/4705 (0.0%)
8	LA	0.31	0/3473	0.61	3/4716 (0.1%)
8	LC	0.34	0/3451	0.60	3/4686 (0.1%)
8	LE	0.37	1/3465 (0.0%)	0.61	5/4705 (0.1%)
8	LG	0.33	0/3518	0.57	2/4777 (0.0%)
8	LI	0.34	0/3518	0.58	2/4777 (0.0%)
8	LK	0.33	0/3518	0.58	2/4777 (0.0%)
8	LM	0.30	0/3481	0.57	2/4727 (0.0%)
8	LO	0.32	0/3443	0.59	2/4675 (0.0%)
8	MA	0.27	0/3451	0.57	3/4686 (0.1%)
8	MC	0.32	0/3451	0.56	1/4686 (0.0%)
8	ME	0.32	0/3502	0.56	1/4755 (0.0%)
8	MG	0.32	0/3457	0.57	3/4694 (0.1%)
8	MI	0.34	0/3455	0.57	1/4691 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	MK	0.37	0/3467	0.59	3/4708 (0.1%)
8	MM	0.31	0/3457	0.57	2/4694 (0.0%)
8	MO	0.29	0/3429	0.58	3/4656 (0.1%)
8	NA	0.28	0/3430	0.58	3/4657 (0.1%)
8	NC	0.27	0/3429	0.54	0/4656
8	NE	0.30	0/3471	0.58	2/4713 (0.0%)
8	NG	0.32	0/3459	0.61	1/4697 (0.0%)
8	NI	0.33	0/3450	0.60	2/4685 (0.0%)
8	NK	0.34	0/3450	0.69	4/4685 (0.1%)
8	NM	0.34	1/3459 (0.0%)	0.63	3/4697 (0.1%)
8	NO	0.31	0/3459	0.63	4/4697 (0.1%)
8	OA	0.28	0/3451	0.58	2/4686 (0.0%)
8	OC	0.28	0/3443	0.59	3/4675 (0.1%)
8	OE	0.31	0/3449	0.60	3/4683 (0.1%)
8	OG	0.30	0/3443	0.58	3/4675 (0.1%)
8	OI	0.33	1/3437 (0.0%)	0.58	1/4667 (0.0%)
8	OK	0.32	0/3451	0.59	0/4686
8	OM	0.31	1/3429 (0.0%)	0.58	1/4656 (0.0%)
8	OO	0.31	0/3406	0.62	0/4624
8	PC	0.33	1/3429 (0.0%)	0.61	4/4656 (0.1%)
8	PE	0.29	0/3406	0.57	2/4625 (0.0%)
8	PG	0.28	0/3443	0.57	1/4675 (0.0%)
8	PI	0.33	0/3443	0.60	2/4675 (0.0%)
8	PK	0.32	1/3443 (0.0%)	0.62	4/4674 (0.1%)
8	PM	0.31	0/3457	0.60	2/4694 (0.0%)
8	PO	0.29	0/3443	0.60	3/4675 (0.1%)
8	QC	0.28	0/3429	0.59	1/4656 (0.0%)
8	QE	0.33	1/3443 (0.0%)	0.60	2/4675 (0.0%)
8	QG	0.29	0/3429	0.55	0/4656
8	QI	0.29	0/3421	0.58	0/4644
8	QK	0.28	0/3422	0.56	1/4646 (0.0%)
8	QM	0.30	0/3414	0.61	2/4634 (0.0%)
8	QO	0.29	0/3422	0.59	2/4646 (0.0%)
8	RC	0.27	0/3429	0.56	1/4656 (0.0%)
8	RE	0.28	0/3429	0.57	1/4655 (0.0%)
8	RG	0.27	0/3429	0.57	3/4656 (0.1%)
8	RI	0.29	0/3437	0.58	4/4667 (0.1%)
8	RK	0.30	0/3445	0.58	2/4678 (0.0%)
8	RM	0.33	1/3437 (0.0%)	0.59	3/4666 (0.1%)
8	RO	0.30	0/3429	0.61	4/4655 (0.1%)
8	SA	0.27	0/3436	0.58	4/4665 (0.1%)
8	SC	0.34	1/3429 (0.0%)	0.64	8/4656 (0.2%)
8	SE	0.29	0/3429	0.59	1/4656 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	SG	0.29	0/3422	0.60	5/4646 (0.1%)
8	SI	0.37	2/3437 (0.1%)	0.69	7/4667 (0.1%)
8	SK	0.29	0/3422	0.58	2/4646 (0.0%)
8	SM	0.30	0/3410	0.64	6/4630 (0.1%)
8	TA	0.31	0/3419	0.66	9/4642 (0.2%)
8	TC	0.31	0/3414	0.63	2/4635 (0.0%)
8	TE	0.31	0/3434	0.62	4/4662 (0.1%)
8	TG	0.27	0/3418	0.56	1/4641 (0.0%)
8	TI	0.32	0/3426	0.58	2/4652 (0.0%)
8	TK	0.27	0/3429	0.57	3/4656 (0.1%)
8	TM	0.29	0/3418	0.63	5/4641 (0.1%)
8	UA	0.30	0/3403	0.65	6/4619 (0.1%)
8	UC	0.28	0/3428	0.59	2/4654 (0.0%)
8	UE	0.28	0/3428	0.59	2/4654 (0.0%)
8	UG	0.27	0/3430	0.58	2/4657 (0.0%)
8	UI	0.30	0/3429	0.57	1/4656 (0.0%)
8	UK	0.28	0/3430	0.61	2/4657 (0.0%)
8	UM	0.30	0/3436	0.62	5/4665 (0.1%)
8	UO	0.28	0/3424	0.60	3/4649 (0.1%)
8	VA	0.28	0/3422	0.57	4/4646 (0.1%)
8	VC	0.28	0/3488	0.56	0/4736
8	VE	0.30	0/3435	0.59	4/4664 (0.1%)
8	VG	0.31	0/3488	0.64	6/4736 (0.1%)
8	VI	0.32	0/3437	0.66	4/4667 (0.1%)
8	VK	0.31	0/3496	0.60	4/4747 (0.1%)
8	VM	0.32	0/3435	0.61	4/4663 (0.1%)
8	VO	0.28	0/3481	0.58	3/4726 (0.1%)
8	WA	0.32	0/3481	0.61	5/4726 (0.1%)
8	WC	0.28	0/3502	0.59	2/4755 (0.0%)
8	WE	0.28	0/3459	0.60	3/4696 (0.1%)
8	WG	0.28	0/3496	0.57	2/4747 (0.0%)
8	WI	0.28	0/3502	0.55	0/4755
8	WK	0.29	0/3496	0.57	3/4747 (0.1%)
8	WM	0.28	0/3451	0.57	0/4686
8	WO	0.29	0/3435	0.61	6/4664 (0.1%)
9	AB	0.30	0/3466	0.58	1/4697 (0.0%)
9	AD	0.31	0/3488	0.59	1/4726 (0.0%)
9	AF	0.32	0/3448	0.56	0/4673
9	AH	0.34	0/3479	0.59	2/4714 (0.0%)
9	AJ	0.38	0/3479	0.64	5/4714 (0.1%)
9	AL	0.34	0/3479	0.60	1/4714 (0.0%)
9	AN	0.32	0/3479	0.62	3/4714 (0.1%)
9	AP	0.30	0/3466	0.57	0/4697

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	BB	0.28	0/3436	0.55	0/4656
9	BD	0.29	0/3448	0.57	2/4673 (0.0%)
9	BF	0.32	0/3443	0.57	1/4666 (0.0%)
9	BH	0.34	0/3448	0.59	3/4673 (0.1%)
9	BJ	0.33	0/3457	0.58	2/4685 (0.0%)
9	BL	0.32	0/3448	0.59	2/4673 (0.0%)
9	BN	0.31	0/3448	0.59	2/4673 (0.0%)
9	BP	0.28	0/3448	0.58	3/4673 (0.1%)
9	CB	0.31	0/3431	0.61	1/4649 (0.0%)
9	CD	0.29	0/3457	0.60	2/4685 (0.0%)
9	CF	0.30	0/3457	0.56	1/4685 (0.0%)
9	CH	0.30	0/3457	0.57	1/4685 (0.0%)
9	CJ	0.29	0/3436	0.55	2/4656 (0.0%)
9	CL	0.35	2/3443 (0.1%)	0.62	4/4666 (0.1%)
9	CN	0.29	0/3457	0.56	2/4685 (0.0%)
9	CP	0.29	0/3448	0.58	4/4673 (0.1%)
9	DB	0.28	0/3443	0.59	5/4666 (0.1%)
9	DD	0.29	0/3443	0.59	4/4666 (0.1%)
9	DF	0.28	0/3448	0.55	1/4673 (0.0%)
9	DH	0.30	1/3448 (0.0%)	0.56	2/4673 (0.0%)
9	DJ	0.29	0/3448	0.56	4/4673 (0.1%)
9	DL	0.28	0/3457	0.56	3/4685 (0.1%)
9	DN	0.28	0/3436	0.56	1/4656 (0.0%)
9	DP	0.27	0/3448	0.59	4/4673 (0.1%)
9	EB	0.31	0/3436	0.58	3/4656 (0.1%)
9	ED	0.28	0/3436	0.56	1/4656 (0.0%)
9	EF	0.29	0/3436	0.58	1/4656 (0.0%)
9	EH	0.28	0/3436	0.57	3/4656 (0.1%)
9	EJ	0.29	0/3431	0.58	4/4649 (0.1%)
9	EL	0.28	0/3436	0.57	2/4656 (0.0%)
9	EN	0.28	0/3436	0.59	3/4656 (0.1%)
9	FB	0.31	0/3448	0.64	5/4673 (0.1%)
9	FD	0.29	0/3448	0.58	4/4673 (0.1%)
9	FF	0.28	0/3448	0.57	1/4673 (0.0%)
9	FH	0.28	0/3448	0.58	3/4673 (0.1%)
9	FJ	0.30	0/3443	0.57	3/4666 (0.1%)
9	FL	0.29	0/3443	0.58	2/4666 (0.0%)
9	FN	0.29	0/3448	0.58	2/4673 (0.0%)
9	GB	0.29	0/3431	0.59	2/4649 (0.0%)
9	GD	0.31	1/3448 (0.0%)	0.61	4/4673 (0.1%)
9	GF	0.29	0/3448	0.56	0/4673
9	GH	0.28	0/3457	0.57	1/4685 (0.0%)
9	GJ	0.30	0/3448	0.57	0/4673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	GL	0.35	1/3457 (0.0%)	0.59	1/4685 (0.0%)
9	GN	0.31	0/3457	0.61	5/4685 (0.1%)
9	HB	0.31	0/3448	0.65	3/4673 (0.1%)
9	HD	0.33	0/3431	0.62	3/4649 (0.1%)
9	HF	0.32	0/3448	0.61	2/4673 (0.0%)
9	HH	0.31	0/3457	0.61	5/4685 (0.1%)
9	HJ	0.33	0/3448	0.66	3/4673 (0.1%)
9	HL	0.33	0/3457	0.62	1/4685 (0.0%)
9	HN	0.33	0/3448	0.60	0/4673
9	HP	0.33	0/3431	0.64	5/4649 (0.1%)
9	IB	0.34	0/3448	0.67	4/4673 (0.1%)
9	ID	0.32	0/3448	0.64	3/4673 (0.1%)
9	IF	0.36	1/3448 (0.0%)	0.63	3/4673 (0.1%)
9	IH	0.37	0/3457	0.69	5/4685 (0.1%)
9	IJ	0.31	0/3443	0.56	0/4666
9	IL	0.39	1/3457 (0.0%)	0.69	5/4685 (0.1%)
9	IN	0.35	0/3457	0.63	2/4685 (0.0%)
9	IP	0.37	1/3457 (0.0%)	0.74	7/4685 (0.1%)
9	JB	0.31	0/3431	0.61	3/4649 (0.1%)
9	JD	0.34	0/3431	0.66	2/4649 (0.0%)
9	JF	0.37	0/3431	0.69	7/4649 (0.2%)
9	JH	0.34	0/3431	0.63	2/4649 (0.0%)
9	JJ	0.34	0/3431	0.62	1/4649 (0.0%)
9	JL	0.34	0/3431	0.69	5/4649 (0.1%)
9	JN	0.34	0/3423	0.60	0/4638
9	JP	0.33	0/3431	0.62	2/4649 (0.0%)
9	KB	0.36	1/3448 (0.0%)	0.63	3/4673 (0.1%)
9	KD	0.34	0/3457	0.62	2/4685 (0.0%)
9	KF	0.31	0/3457	0.55	0/4685
9	KH	0.31	0/3457	0.60	2/4685 (0.0%)
9	KJ	0.31	0/3448	0.58	0/4673
9	KL	0.32	0/3448	0.63	3/4673 (0.1%)
9	KN	0.33	0/3448	0.60	2/4673 (0.0%)
9	KP	0.33	0/3436	0.64	4/4656 (0.1%)
9	LB	0.33	0/3509	0.63	3/4754 (0.1%)
9	LD	0.31	0/3457	0.55	0/4685
9	LF	0.34	0/3527	0.63	4/4778 (0.1%)
9	LH	0.33	0/3457	0.57	1/4685 (0.0%)
9	LJ	0.33	0/3509	0.60	2/4754 (0.0%)
9	LL	0.31	0/3436	0.57	1/4656 (0.0%)
9	LN	0.30	0/3466	0.58	2/4697 (0.0%)
9	LP	0.27	0/3443	0.54	1/4666 (0.0%)
9	MB	0.30	0/3457	0.59	2/4685 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	MD	0.34	0/3457	0.58	2/4685 (0.0%)
9	MF	0.31	0/3431	0.59	5/4649 (0.1%)
9	MH	0.32	0/3457	0.58	2/4685 (0.0%)
9	MJ	0.33	0/3448	0.57	1/4673 (0.0%)
9	ML	0.32	0/3448	0.59	3/4673 (0.1%)
9	MN	0.30	0/3457	0.59	4/4685 (0.1%)
9	MP	0.31	0/3457	0.57	2/4685 (0.0%)
9	NB	0.28	0/3436	0.60	3/4656 (0.1%)
9	ND	0.29	0/3457	0.57	0/4685
9	NF	0.35	0/3436	0.65	4/4656 (0.1%)
9	NH	0.32	0/3431	0.60	1/4649 (0.0%)
9	NJ	0.33	0/3448	0.66	4/4673 (0.1%)
9	NL	0.34	0/3436	0.64	3/4656 (0.1%)
9	NN	0.31	0/3448	0.62	1/4673 (0.0%)
9	NP	0.28	0/3431	0.56	1/4649 (0.0%)
9	OB	0.33	0/3436	0.64	6/4656 (0.1%)
9	OD	0.29	0/3436	0.60	2/4656 (0.0%)
9	OF	0.34	0/3443	0.61	3/4666 (0.1%)
9	OH	0.37	2/3436 (0.1%)	0.64	5/4656 (0.1%)
9	OJ	0.36	0/3443	0.72	8/4666 (0.2%)
9	OL	0.31	0/3431	0.61	2/4649 (0.0%)
9	ON	0.31	0/3431	0.59	1/4649 (0.0%)
9	OP	0.31	0/3423	0.66	6/4638 (0.1%)
9	PB	0.30	1/3436 (0.0%)	0.60	4/4656 (0.1%)
9	PD	0.33	0/3436	0.67	7/4656 (0.2%)
9	PF	0.28	0/3436	0.60	4/4656 (0.1%)
9	PH	0.32	0/3436	0.62	4/4656 (0.1%)
9	PJ	0.30	0/3431	0.62	2/4649 (0.0%)
9	PL	0.29	0/3436	0.57	0/4656
9	PN	0.29	0/3436	0.58	0/4656
9	PP	0.27	0/3431	0.56	2/4649 (0.0%)
9	QB	0.31	0/3423	0.63	1/4638 (0.0%)
9	QD	0.29	0/3431	0.60	2/4649 (0.0%)
9	QF	0.28	0/3431	0.59	2/4649 (0.0%)
9	QH	0.32	0/3431	0.64	6/4649 (0.1%)
9	QJ	0.30	0/3431	0.61	3/4649 (0.1%)
9	QL	0.28	0/3431	0.56	0/4649
9	QN	0.29	0/3431	0.62	4/4649 (0.1%)
9	QP	0.30	0/3423	0.60	5/4638 (0.1%)
9	RD	0.28	0/3436	0.58	3/4656 (0.1%)
9	RF	0.28	0/3436	0.57	1/4656 (0.0%)
9	RH	0.28	0/3436	0.54	0/4656
9	RJ	0.29	0/3436	0.57	2/4656 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	RL	0.31	0/3436	0.60	2/4656 (0.0%)
9	RN	0.28	0/3431	0.56	1/4649 (0.0%)
9	RP	0.27	0/3436	0.56	3/4656 (0.1%)
9	SB	0.28	0/3423	0.58	2/4638 (0.0%)
9	SD	0.29	0/3436	0.58	2/4656 (0.0%)
9	SF	0.33	0/3423	0.59	0/4638
9	SH	0.29	0/3431	0.61	2/4649 (0.0%)
9	SJ	0.30	0/3431	0.63	4/4649 (0.1%)
9	SL	0.29	0/3423	0.60	2/4638 (0.0%)
9	SN	0.28	0/3423	0.59	2/4638 (0.0%)
9	TB	0.30	0/3423	0.62	4/4638 (0.1%)
9	TD	0.31	1/3423 (0.0%)	0.63	4/4638 (0.1%)
9	TF	0.28	0/3423	0.58	2/4638 (0.0%)
9	TH	0.29	0/3431	0.61	5/4649 (0.1%)
9	TJ	0.28	0/3436	0.60	4/4656 (0.1%)
9	TL	0.32	0/3431	0.63	7/4649 (0.2%)
9	TN	0.29	0/3423	0.59	3/4638 (0.1%)
9	UB	0.28	0/3423	0.64	4/4638 (0.1%)
9	UD	0.27	0/3423	0.55	0/4638
9	UF	0.29	0/3423	0.60	1/4638 (0.0%)
9	UH	0.30	1/3431 (0.0%)	0.59	1/4649 (0.0%)
9	UJ	0.30	0/3431	0.60	2/4649 (0.0%)
9	UL	0.28	0/3423	0.57	1/4638 (0.0%)
9	UN	0.27	0/3423	0.58	1/4638 (0.0%)
9	VB	0.27	0/3423	0.53	1/4638 (0.0%)
9	VD	0.26	0/3423	0.58	1/4638 (0.0%)
9	VF	0.29	0/3423	0.60	1/4638 (0.0%)
9	VH	0.28	0/3431	0.62	5/4649 (0.1%)
9	VJ	0.30	0/3431	0.62	3/4649 (0.1%)
9	VL	0.28	0/3436	0.57	4/4656 (0.1%)
9	VN	0.29	0/3423	0.64	3/4638 (0.1%)
9	WB	0.30	0/3431	0.58	2/4649 (0.0%)
9	WD	0.28	0/3431	0.56	2/4649 (0.0%)
9	WF	0.32	1/3448 (0.0%)	0.62	3/4673 (0.1%)
9	WH	0.29	0/3436	0.60	3/4656 (0.1%)
9	WJ	0.29	0/3436	0.60	2/4656 (0.0%)
9	WL	0.30	0/3431	0.58	3/4649 (0.1%)
9	WN	0.29	0/3431	0.61	3/4649 (0.1%)
9	WP	0.30	0/3431	0.59	1/4649 (0.0%)
10	B	0.33	0/2787	0.64	3/3696 (0.1%)
10	C	0.37	0/2427	0.70	6/3218 (0.2%)
11	B0	0.43	0/340	0.81	0/457
11	B1	0.35	0/3018	0.65	6/4069 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	B2	0.37	0/3440	0.66	6/4638 (0.1%)
11	B3	0.39	1/3440 (0.0%)	0.64	4/4638 (0.1%)
11	B4	0.35	2/3451 (0.1%)	0.61	3/4652 (0.1%)
11	B5	0.38	0/1691	0.76	4/2274 (0.2%)
11	R0	0.34	0/1625	0.62	0/2184
11	R1	0.32	0/3451	0.63	5/4652 (0.1%)
11	R2	0.33	0/3451	0.62	3/4652 (0.1%)
11	R3	0.36	0/3451	0.62	1/4652 (0.0%)
11	R4	0.37	0/3059	0.68	4/4124 (0.1%)
11	R5	0.41	0/372	0.79	0/500
12	C0	0.35	0/1476	0.59	1/1991 (0.1%)
12	C1	0.39	2/3399 (0.1%)	0.58	1/4581 (0.0%)
12	C2	0.35	0/3399	0.57	2/4581 (0.0%)
12	C3	0.35	0/3376	0.57	2/4550 (0.0%)
12	C4	0.33	0/2978	0.56	2/4010 (0.0%)
12	C5	0.38	0/422	0.81	1/567 (0.2%)
12	C6	0.31	0/364	0.71	0/493
12	S0	0.36	0/2719	0.69	5/3665 (0.1%)
12	S1	0.30	0/3666	0.55	1/4944 (0.0%)
12	S2	0.32	0/3666	0.59	2/4944 (0.0%)
12	S3	0.38	0/3666	0.65	5/4944 (0.1%)
12	S4	0.34	0/2485	0.61	3/3344 (0.1%)
12	S5	0.33	0/2610	0.59	2/3522 (0.1%)
12	S6	0.32	0/3504	0.58	2/4728 (0.0%)
12	S7	0.38	0/3504	0.62	2/4728 (0.0%)
12	S8	0.40	0/3485	0.65	2/4702 (0.0%)
12	S9	0.38	0/2252	0.70	3/3028 (0.1%)
13	D	0.31	0/642	0.70	1/879 (0.1%)
13	K3	0.31	0/1500	0.71	4/2037 (0.2%)
14	D0	0.34	0/906	0.63	1/1219 (0.1%)
14	D1	0.37	0/3416	0.61	3/4598 (0.1%)
14	D2	0.36	0/3529	0.60	1/4752 (0.0%)
14	D3	0.36	0/3529	0.60	1/4752 (0.0%)
14	D4	0.36	0/3529	0.61	1/4752 (0.0%)
14	D5	0.54	1/720 (0.1%)	0.98	7/965 (0.7%)
14	T0	0.44	1/976 (0.1%)	0.76	1/1319 (0.1%)
14	T1	0.29	0/3645	0.62	4/4913 (0.1%)
14	T2	0.38	1/3645 (0.0%)	0.68	6/4913 (0.1%)
14	T3	0.36	0/3658	0.62	2/4931 (0.0%)
14	T4	0.37	0/3305	0.65	5/4450 (0.1%)
14	T5	0.42	0/983	0.87	6/1319 (0.5%)
15	E	0.33	0/2415	0.63	0/3259
15	F	0.29	0/2406	0.62	1/3247 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
15	N2	0.30	0/2406	0.60	1/3247 (0.0%)
16	G	0.32	0/747	0.66	1/1015 (0.1%)
17	H	0.36	0/1356	0.68	2/1840 (0.1%)
17	I	0.31	0/1474	0.65	0/2000
17	J	0.36	0/1347	0.57	0/1829
17	K	0.33	0/1465	0.66	2/1989 (0.1%)
17	L	0.34	0/1356	0.63	1/1840 (0.1%)
17	M	0.35	0/1458	0.65	0/1979
17	N	0.34	0/1356	0.74	5/1840 (0.3%)
17	O7	0.37	0/1458	0.71	3/1979 (0.2%)
17	O8	0.33	0/862	0.68	2/1170 (0.2%)
17	O9	0.36	0/862	0.66	1/1170 (0.1%)
17	P8	0.35	0/862	0.65	1/1170 (0.1%)
17	P9	0.35	0/862	0.72	3/1170 (0.3%)
17	Z2	0.31	0/424	0.65	1/571 (0.2%)
17	Z3	0.33	0/424	0.66	0/571
17	Z4	0.32	0/424	0.59	0/571
17	Z5	0.36	0/416	0.78	1/560 (0.2%)
18	I1	0.49	1/826 (0.1%)	0.82	2/1123 (0.2%)
19	J1	0.32	0/958	0.77	2/1287 (0.2%)
19	J2	0.40	1/2055 (0.0%)	0.73	3/2772 (0.1%)
19	J3	0.34	0/2055	0.69	3/2772 (0.1%)
19	J4	0.38	0/2037	0.71	3/2748 (0.1%)
19	J5	0.35	0/1021	0.77	3/1382 (0.2%)
20	K1	0.31	0/1038	0.68	1/1407 (0.1%)
20	K2	0.28	0/1038	0.58	1/1407 (0.1%)
21	L1	0.37	1/1063 (0.1%)	0.78	3/1435 (0.2%)
22	M1	0.33	0/849	0.69	2/1148 (0.2%)
22	M2	0.38	0/849	0.67	0/1148
22	M3	0.37	0/1316	0.68	1/1778 (0.1%)
22	M4	0.43	1/849 (0.1%)	0.70	0/1148
23	O	0.33	0/635	0.66	0/846
23	P	0.36	0/2911	0.61	1/3896 (0.0%)
23	Q	0.36	0/868	0.78	5/1161 (0.4%)
24	O1	0.29	0/1366	0.54	0/1862
24	O2	0.31	0/1379	0.55	0/1880
24	O3	0.31	0/1379	0.55	0/1880
24	O4	0.33	0/1379	0.61	1/1880 (0.1%)
25	O5	0.32	0/4158	0.61	4/5631 (0.1%)
25	O6	0.31	0/393	0.77	0/531
25	T	0.30	0/2429	0.60	3/3285 (0.1%)
25	U	0.35	0/4253	0.61	3/5764 (0.1%)
25	V	0.33	0/4417	0.66	9/5988 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	P1	0.31	0/658	0.58	0/892
26	P2	0.37	0/852	0.70	1/1155 (0.1%)
27	P3	0.43	0/1145	0.71	3/1564 (0.2%)
27	P4	0.33	0/1319	0.65	2/1799 (0.1%)
27	P5	0.39	0/1319	0.61	0/1799
27	P6	0.43	0/1310	0.65	1/1787 (0.1%)
27	P7	0.37	0/460	0.68	1/621 (0.2%)
28	Q1	0.36	0/1696	0.77	5/2315 (0.2%)
28	Q2	0.44	1/1696 (0.1%)	0.72	3/2315 (0.1%)
28	Q3	0.36	0/1696	0.69	1/2315 (0.0%)
28	Q4	0.38	0/1696	0.75	2/2315 (0.1%)
28	Q5	0.49	0/158	0.81	1/213 (0.5%)
29	R	0.31	0/1674	0.63	1/2232 (0.0%)
29	S	0.34	0/2770	0.66	2/3701 (0.1%)
30	U0	0.32	0/2934	0.57	2/3946 (0.1%)
30	U1	0.29	0/3444	0.60	2/4637 (0.0%)
30	U2	0.29	0/3444	0.63	6/4637 (0.1%)
30	U3	0.33	0/3444	0.59	2/4637 (0.0%)
30	U4	0.31	0/1691	0.61	1/2271 (0.0%)
30	U5	0.33	0/2646	0.65	4/3557 (0.1%)
30	U6	0.29	0/3407	0.59	4/4586 (0.1%)
30	U7	0.32	0/3407	0.61	4/4586 (0.1%)
30	U8	0.35	0/3407	0.70	5/4586 (0.1%)
30	U9	0.32	0/1499	0.64	2/2018 (0.1%)
30	V0	0.39	1/1713 (0.1%)	0.82	7/2307 (0.3%)
30	V1	0.28	0/3226	0.61	2/4339 (0.0%)
30	V2	0.30	0/3226	0.64	4/4339 (0.1%)
30	V3	0.37	0/3226	0.73	7/4339 (0.2%)
30	V4	0.40	0/2357	0.65	1/3165 (0.0%)
30	V5	0.34	0/2437	0.67	7/3274 (0.2%)
30	V6	0.32	0/3018	0.62	4/4057 (0.1%)
30	V7	0.39	1/2772 (0.0%)	0.69	7/3729 (0.2%)
30	V8	0.35	0/2507	0.67	3/3371 (0.1%)
30	V9	0.41	0/804	0.80	0/1080
30	W0	0.36	0/2473	0.72	5/3317 (0.2%)
30	W2	0.36	0/2484	0.65	2/3338 (0.1%)
30	W4	0.26	0/2697	0.57	2/3621 (0.1%)
30	W5	0.29	0/2697	0.61	2/3621 (0.1%)
30	W6	0.27	0/2697	0.54	0/3621
30	W7	0.31	0/2697	0.63	2/3621 (0.1%)
31	W	0.32	0/6283	0.61	4/8495 (0.0%)
31	X	0.32	0/6283	0.60	5/8495 (0.1%)
31	Y	0.33	0/6291	0.60	4/8506 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Z	0.33	1/6283 (0.0%)	0.61	4/8495 (0.0%)
32	X0	0.33	0/206	0.63	0/278
32	X1	0.35	0/198	0.73	1/266 (0.4%)
32	X2	0.33	0/198	0.64	0/266
32	X3	0.29	0/206	0.70	0/278
33	X4	0.32	0/2694	0.66	3/3661 (0.1%)
33	X5	0.35	0/1072	0.68	1/1454 (0.1%)
34	X6	0.35	0/2144	0.66	3/2899 (0.1%)
34	X7	0.34	0/2144	0.70	4/2899 (0.1%)
34	X8	0.29	0/2144	0.64	0/2899
35	XA	0.29	0/1573	0.63	2/2122 (0.1%)
35	XB	0.29	0/1573	0.62	1/2122 (0.0%)
35	XC	0.26	0/1573	0.57	0/2122
35	XD	0.28	0/1573	0.62	1/2122 (0.0%)
35	XE	0.34	0/1573	0.59	0/2122
35	XF	0.30	0/1573	0.61	0/2122
35	XG	0.31	0/1573	0.61	0/2122
35	XH	0.31	0/1573	0.63	1/2122 (0.0%)
36	Y0	0.36	0/503	0.75	1/688 (0.1%)
36	Y1	0.39	0/1890	0.83	6/2576 (0.2%)
36	Y2	0.30	0/1767	0.62	2/2408 (0.1%)
36	Y3	0.31	0/503	0.66	0/688
36	Y4	0.37	0/1458	0.86	6/1984 (0.3%)
36	Y5	0.38	0/663	0.73	0/903
37	YA	0.31	0/1817	0.63	3/2455 (0.1%)
37	YB	0.31	0/1817	0.59	1/2455 (0.0%)
37	YC	0.27	0/1817	0.50	0/2455
37	YD	0.34	1/1817 (0.1%)	0.57	1/2455 (0.0%)
37	YE	0.31	0/1817	0.61	0/2455
37	YF	0.28	0/1817	0.62	3/2455 (0.1%)
37	YG	0.30	0/1817	0.63	5/2455 (0.2%)
37	YH	0.29	0/1817	0.61	2/2455 (0.1%)
38	Z1	0.36	0/288	0.75	0/387
39	a	0.34	0/2512	0.74	5/3331 (0.2%)
39	a6	0.29	0/575	0.62	1/767 (0.1%)
39	b	0.40	0/2105	0.81	5/2785 (0.2%)
39	c	0.33	0/3549	0.72	4/4707 (0.1%)
39	d	0.37	1/1162 (0.1%)	0.69	0/1538
40	a1	0.29	0/1313	0.60	1/1779 (0.1%)
40	a2	0.39	1/1313 (0.1%)	0.62	1/1779 (0.1%)
40	a3	0.33	0/1313	0.63	2/1779 (0.1%)
40	a4	0.37	0/1313	0.71	2/1779 (0.1%)
41	b1	0.40	0/1095	0.83	6/1465 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
41	b2	0.38	1/3141 (0.0%)	0.66	4/4226 (0.1%)
41	b3	0.29	0/3152	0.62	1/4240 (0.0%)
41	b4	0.35	0/3152	0.67	4/4240 (0.1%)
41	b5	0.34	0/2749	0.69	5/3697 (0.1%)
42	e	0.28	0/4786	0.58	1/6472 (0.0%)
42	f	0.30	0/4786	0.64	5/6472 (0.1%)
42	g	0.29	0/4786	0.60	1/6472 (0.0%)
43	h	0.31	0/2057	0.58	1/2757 (0.0%)
43	i	0.29	0/2042	0.59	2/2737 (0.1%)
43	j	0.32	0/2036	0.59	1/2729 (0.0%)
43	k	0.35	2/2042 (0.1%)	0.61	1/2737 (0.0%)
44	h1	0.39	0/809	0.76	3/1091 (0.3%)
44	h2	0.45	0/831	0.71	1/1119 (0.1%)
44	h3	0.39	0/831	0.69	0/1119
44	h4	0.32	0/820	0.70	1/1105 (0.1%)
45	i1	0.30	0/937	0.60	1/1281 (0.1%)
45	l	0.36	0/937	0.59	1/1281 (0.1%)
45	m	0.31	0/937	0.56	1/1281 (0.1%)
45	n	0.32	0/937	0.65	3/1281 (0.2%)
46	i2	0.28	0/1526	0.58	1/2039 (0.0%)
46	i3	0.33	0/1526	0.64	2/2039 (0.1%)
46	i4	0.29	0/1526	0.61	0/2039
47	o	0.38	0/1707	0.77	3/2264 (0.1%)
47	p	0.40	2/3334 (0.1%)	0.70	10/4428 (0.2%)
48	q	0.31	0/614	0.63	1/827 (0.1%)
48	r	0.40	0/640	0.69	1/862 (0.1%)
48	s	0.32	0/640	0.55	0/862
49	y	0.36	0/942	0.67	0/1279
All	All	0.32	59/1674605 (0.0%)	0.61	1363/2267788 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	2	0	2
3	3	0	1
4	5	0	1
4	j1	0	1
8	AM	0	1
8	CM	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	EE	0	1
8	FA	0	1
8	IE	0	1
8	JE	0	1
8	JM	0	1
8	NG	0	1
8	VE	0	1
8	VM	0	1
8	WI	0	1
9	AJ	0	1
9	AL	0	1
9	BD	0	1
9	HN	0	1
9	IB	0	1
9	JF	0	1
9	LF	0	1
9	LH	0	1
9	NL	0	1
9	NN	0	1
9	OF	0	1
9	PF	0	1
11	B5	0	1
12	S0	0	1
12	S3	0	1
12	S5	0	1
12	S6	0	1
12	S9	0	1
14	D3	0	1
14	T2	0	1
17	O8	0	1
22	M1	0	1
24	O3	0	1
25	O5	0	1
28	Q1	0	1
28	Q2	0	1
28	Q3	0	1
28	Q4	0	1
28	Q5	0	1
30	U3	0	1
30	U8	0	1
31	Z	0	1
35	XF	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
36	Y5	0	1
40	a4	0	1
46	i3	0	1
All	All	0	52

All (59) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	p	483	TYR	CD2-CE2	-9.30	1.25	1.39
9	OH	294	PHE	CD1-CE1	-8.75	1.21	1.39
8	LE	175	PRO	CG-CD	-8.32	1.23	1.50
18	I1	87	PRO	CG-CD	-8.13	1.23	1.50
19	J2	187	TYR	CD1-CE1	-7.27	1.28	1.39
30	V0	403	PRO	CG-CD	-7.18	1.26	1.50
9	IL	32	PRO	CG-CD	-7.02	1.27	1.50
9	WF	326	VAL	CB-CG2	-7.02	1.38	1.52
8	IG	22	GLU	CG-CD	-7.01	1.41	1.51
8	HG	164	LYS	CE-NZ	-6.87	1.31	1.49
47	p	483	TYR	CB-CG	-6.86	1.41	1.51
37	YD	193	ASP	CA-CB	6.82	1.69	1.53
40	a2	18	CYS	CB-SG	-6.81	1.70	1.82
8	OI	224	TYR	CD1-CE1	-6.65	1.29	1.39
9	IF	324	LYS	CD-CE	-6.54	1.34	1.51
43	k	129	ARG	CG-CD	-6.42	1.35	1.51
41	b2	152	ARG	CB-CG	-6.35	1.35	1.52
8	SI	268	PRO	CG-CD	-6.23	1.30	1.50
11	B4	328	GLU	CB-CG	-6.21	1.40	1.52
9	IP	171	PRO	CG-CD	-6.19	1.30	1.50
8	NM	54	SER	CA-CB	-6.11	1.43	1.52
8	SI	171	ILE	C-N	6.11	1.48	1.34
8	QE	182	VAL	CB-CG2	-6.08	1.40	1.52
9	TD	80	PRO	CG-CD	-6.03	1.30	1.50
8	EA	282	TYR	CE1-CZ	-5.97	1.30	1.38
11	B3	328	GLU	CD-OE2	-5.96	1.19	1.25
8	RM	207	GLU	CD-OE1	-5.86	1.19	1.25
9	DH	129	CYS	CB-SG	-5.85	1.72	1.81
8	IK	357	TYR	CE1-CZ	-5.82	1.30	1.38
11	B4	328	GLU	CD-OE2	-5.79	1.19	1.25
12	C1	203	GLU	CG-CD	-5.74	1.43	1.51
39	d	437	VAL	CB-CG1	-5.72	1.40	1.52
9	GL	303	CYS	CB-SG	-5.63	1.72	1.81
8	AG	388	TRP	CB-CG	-5.62	1.40	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	IG	352	LYS	CD-CE	-5.54	1.37	1.51
9	CL	198	GLU	CD-OE2	-5.53	1.19	1.25
8	OM	210	TYR	CE2-CZ	-5.51	1.31	1.38
31	Z	715	GLU	CD-OE1	-5.51	1.19	1.25
9	GD	360	GLY	N-CA	-5.38	1.38	1.46
8	IM	172	TYR	CG-CD1	-5.36	1.32	1.39
8	SC	268	PRO	CG-CD	-5.33	1.33	1.50
8	IC	411	GLU	CG-CD	-5.33	1.44	1.51
21	L1	133	MET	CG-SD	-5.33	1.67	1.81
8	PK	168	GLU	CD-OE1	-5.27	1.19	1.25
14	T0	238	VAL	CB-CG1	-5.26	1.41	1.52
9	PB	44	LEU	CA-CB	5.26	1.65	1.53
30	V7	367	GLU	CD-OE2	-5.26	1.19	1.25
43	k	129	ARG	CB-CG	-5.26	1.38	1.52
14	D5	394	LYS	CB-CG	-5.26	1.38	1.52
14	T2	23	PRO	CG-CD	-5.25	1.33	1.50
28	Q2	192	CYS	CB-SG	-5.24	1.73	1.81
9	OH	294	PHE	CB-CG	-5.23	1.42	1.51
9	KB	106	TYR	CD1-CE1	-5.19	1.31	1.39
12	C1	203	GLU	CB-CG	-5.17	1.42	1.52
22	M4	184	VAL	CB-CG1	-5.16	1.42	1.52
8	PC	315	CYS	CB-SG	-5.15	1.73	1.81
9	UH	303	CYS	CB-SG	-5.09	1.73	1.81
9	CL	198	GLU	CD-OE1	-5.07	1.20	1.25
8	IC	411	GLU	CB-CG	-5.01	1.42	1.52

All (1363) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	IP	217	LEU	CB-CG-CD1	-15.19	85.19	111.00
42	f	544	LEU	CB-CG-CD2	-14.72	85.97	111.00
36	Y4	89	ILE	CG1-CB-CG2	-13.71	81.25	111.40
8	IG	352	LYS	CD-CE-NZ	-13.40	80.88	111.70
30	V0	403	PRO	CA-N-CD	-13.16	93.07	111.50
9	PD	321	MET	CG-SD-CE	13.15	121.25	100.20
18	I1	87	PRO	CA-N-CD	-12.66	93.77	111.50
9	IP	171	PRO	CA-N-CD	-12.56	93.91	111.50
9	WN	88	ASP	CB-CG-OD1	12.54	129.59	118.30
9	TD	80	PRO	CA-N-CD	-12.52	93.97	111.50
37	YF	69	LEU	CB-CG-CD2	-12.39	89.93	111.00
9	RL	87	PRO	CA-N-CD	-12.28	94.31	111.50
9	OJ	32	PRO	CA-N-CD	-12.16	94.47	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	SI	268	PRO	CA-N-CD	-12.08	94.59	111.50
9	JL	357	PRO	CA-N-CD	-11.91	94.82	111.50
14	T2	23	PRO	CA-N-CD	-11.86	94.89	111.50
47	o	159	MET	CA-CB-CG	11.79	133.34	113.30
9	IL	32	PRO	CA-N-CD	-11.74	95.06	111.50
9	IH	32	PRO	CA-N-CD	-11.71	95.10	111.50
9	JL	356	ILE	C-N-CD	-11.59	95.11	120.60
9	JB	357	PRO	CA-N-CD	-11.56	95.32	111.50
9	OP	253	LEU	CA-CB-CG	11.42	141.56	115.30
8	BE	175	PRO	CA-N-CD	-11.41	95.53	111.50
9	WL	164	MET	CG-SD-CE	-11.38	81.99	100.20
8	AE	370	LYS	CD-CE-NZ	-11.26	85.81	111.70
9	HF	323	MET	CG-SD-CE	-11.06	82.51	100.20
8	GG	218	ASP	CB-CG-OD1	10.96	128.17	118.30
9	QD	357	PRO	CA-N-CD	-10.91	96.22	111.50
8	TM	153	LEU	CA-CB-CG	10.75	140.02	115.30
31	Y	413	PRO	CA-N-CD	-10.61	96.64	111.50
23	Q	324	LEU	CB-CG-CD1	-10.52	93.11	111.00
30	U7	127	LYS	CD-CE-NZ	10.38	135.57	111.70
36	Y4	117	ASP	CB-CG-OD2	10.28	127.55	118.30
8	UK	32	PRO	CA-N-CD	-10.14	97.31	111.50
8	RC	218	ASP	CB-CG-OD1	10.12	127.41	118.30
36	Y1	34	PRO	CA-N-CD	-10.08	97.39	111.50
30	U8	425	ASP	CB-CG-OD2	10.06	127.36	118.30
9	WF	321	MET	CG-SD-CE	-9.84	84.46	100.20
21	L1	144	PRO	CA-N-CD	-9.81	97.76	111.50
25	V	62	LEU	CB-CG-CD2	-9.78	94.37	111.00
8	CM	47	ASP	CB-CG-OD1	9.78	127.10	118.30
41	b5	270	PRO	CA-N-CD	-9.71	97.90	111.50
8	MG	428	LEU	CB-CG-CD2	-9.67	94.56	111.00
9	AN	323	MET	CG-SD-CE	-9.65	84.77	100.20
9	IP	224	ASP	CB-CG-OD1	9.65	126.98	118.30
9	OL	233	MET	CG-SD-CE	9.64	115.63	100.20
5	8	61	ASP	CB-CG-OD2	9.61	126.95	118.30
8	BI	32	PRO	CA-N-CD	-9.60	98.06	111.50
42	f	544	LEU	CB-CG-CD1	9.57	127.27	111.00
18	I1	87	PRO	N-CD-CG	-9.53	88.90	103.20
47	o	159	MET	CB-CG-SD	9.45	140.74	112.40
11	R2	205	PRO	CA-N-CD	-9.39	98.35	111.50
11	B1	387	ASP	CB-CG-OD1	9.35	126.72	118.30
30	V2	388	PRO	CA-N-CD	-9.30	98.49	111.50
9	NJ	273	LEU	CB-CG-CD2	-9.21	95.34	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	Q1	158	ALA	O-C-N	-9.20	107.98	122.70
30	U2	270	LEU	CB-CG-CD2	-9.18	95.40	111.00
8	LK	7	ILE	CG1-CB-CG2	-9.16	91.25	111.40
36	Y1	240	ILE	CG1-CB-CG2	-9.09	91.41	111.40
36	Y1	139	PRO	CA-N-CD	-9.08	98.79	111.50
11	B5	109	PRO	CA-N-CD	-9.03	98.86	111.50
9	QJ	268	PRO	CA-N-CD	-8.98	98.92	111.50
30	V0	403	PRO	N-CD-CG	-8.95	89.77	103.20
48	r	148	PRO	CA-N-CD	-8.95	98.97	111.50
9	NF	323	MET	CG-SD-CE	-8.92	85.93	100.20
8	HM	218	ASP	CB-CG-OD2	8.85	126.27	118.30
9	RF	293	MET	CG-SD-CE	-8.84	86.06	100.20
8	LA	89	PRO	CA-N-CD	-8.81	99.17	111.50
8	LE	175	PRO	CA-N-CD	-8.77	99.22	111.50
31	X	460	ASP	CB-CG-OD1	8.76	126.18	118.30
9	IL	32	PRO	N-CD-CG	-8.75	90.08	103.20
30	V0	396	LEU	CB-CG-CD2	-8.73	96.15	111.00
11	B4	205	PRO	CA-N-CD	-8.69	99.33	111.50
30	V1	293	PRO	CA-N-CD	-8.68	99.35	111.50
5	8	59	MET	CA-CB-CG	8.65	128.00	113.30
19	J2	232	LEU	CA-CB-CG	8.64	135.18	115.30
37	YB	106	PRO	CA-N-CD	-8.63	99.42	111.50
30	W0	378	LEU	CB-CG-CD1	-8.62	96.34	111.00
8	VO	7	ILE	CG1-CB-CG2	-8.62	92.44	111.40
8	LE	175	PRO	N-CD-CG	-8.61	90.28	103.20
9	QH	207	LEU	CB-CG-CD2	-8.54	96.48	111.00
13	K3	386	PRO	CA-N-CD	-8.53	99.56	111.50
9	HB	42	LEU	CB-CG-CD2	-8.49	96.57	111.00
8	UM	32	PRO	CA-N-CD	-8.49	99.61	111.50
8	UA	153	LEU	CA-CB-CG	8.47	134.79	115.30
9	OP	233	MET	CG-SD-CE	8.47	113.75	100.20
8	DO	218	ASP	CB-CG-OD2	8.46	125.91	118.30
20	K1	25	LEU	CA-CB-CG	8.43	134.69	115.30
9	ID	273	LEU	CB-CG-CD2	-8.39	96.73	111.00
9	KN	233	MET	CG-SD-CE	8.37	113.59	100.20
28	Q2	14	PRO	CA-N-CD	-8.37	99.78	111.50
9	IB	330	MET	CA-CB-CG	8.32	127.45	113.30
8	PG	212	ILE	CG1-CB-CG2	-8.32	93.09	111.40
8	GK	153	LEU	CA-CB-CG	8.25	134.27	115.30
43	k	129	ARG	CG-CD-NE	-8.24	94.50	111.80
8	NK	167	LEU	CA-CB-CG	8.19	134.13	115.30
14	T2	22	LEU	CA-CB-CG	8.18	134.11	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	UK	153	LEU	CA-CB-CG	8.18	134.11	115.30
9	VN	299	MET	CB-CG-SD	-8.15	87.95	112.40
17	N	43	LEU	CA-CB-CG	8.13	134.01	115.30
39	b	450	LEU	CA-CB-CG	8.12	133.98	115.30
21	L1	133	MET	CA-CB-CG	-8.12	99.50	113.30
33	X4	313	VAL	CG1-CB-CG2	-8.10	97.94	110.90
30	U2	123	ILE	CG1-CB-CG2	-8.10	93.58	111.40
30	V3	192	LEU	CA-CB-CG	8.07	133.86	115.30
41	b4	436	LEU	CA-CB-CG	8.05	133.81	115.30
11	R1	329	LEU	CA-CB-CG	8.03	133.76	115.30
8	KC	205	ASP	CB-CG-OD2	8.03	125.52	118.30
12	S4	438	LEU	CB-CG-CD2	8.03	124.64	111.00
9	AJ	323	MET	CG-SD-CE	-8.02	87.37	100.20
9	QF	357	PRO	CA-N-CD	-7.98	100.32	111.50
8	RO	274	PRO	CA-N-CD	-7.98	100.32	111.50
9	CL	26	ASP	CB-CG-OD1	7.94	125.45	118.30
8	OG	7	ILE	CG1-CB-CG2	-7.92	93.97	111.40
30	U2	134	MET	CB-CG-SD	-7.92	88.65	112.40
8	BK	32	PRO	CA-N-CD	-7.90	100.44	111.50
8	VG	7	ILE	CG1-CB-CG2	-7.89	94.05	111.40
39	b	341	MET	CA-CB-CG	7.88	126.70	113.30
31	X	91	ASP	CB-CG-OD1	7.88	125.39	118.30
9	FB	415	MET	CG-SD-CE	-7.86	87.62	100.20
9	CH	44	LEU	CA-CB-CG	7.86	133.38	115.30
14	T5	386	MET	CA-CB-CG	7.86	126.66	113.30
8	SM	153	LEU	CA-CB-CG	7.86	133.37	115.30
9	LF	427	ASP	CB-CG-OD1	7.85	125.37	118.30
8	UG	245	ASP	CB-CG-OD1	7.83	125.35	118.30
9	NJ	358	PRO	CA-N-CD	-7.83	100.54	111.50
9	MB	305	PRO	CA-N-CD	-7.83	100.54	111.50
14	T2	443	LEU	CA-CB-CG	7.82	133.28	115.30
9	VN	117	LEU	CA-CB-CG	7.78	133.20	115.30
14	T1	166	ASP	CB-CG-OD2	7.78	125.30	118.30
34	X7	194	ASP	CB-CG-OD2	7.77	125.29	118.30
8	WO	428	LEU	CB-CG-CD2	-7.75	97.82	111.00
41	b2	152	ARG	CG-CD-NE	-7.73	95.57	111.80
8	HA	23	LEU	CA-CB-CG	7.72	133.06	115.30
30	V6	377	LEU	CA-CB-CG	7.72	133.06	115.30
39	a	232	MET	CA-CB-CG	7.70	126.40	113.30
14	T4	283	ASP	CB-CG-OD2	7.70	125.23	118.30
9	LB	324	LYS	CD-CE-NZ	-7.69	94.00	111.70
30	U4	134	MET	CB-CG-SD	-7.69	89.32	112.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	b4	415	LEU	CA-CB-CG	7.69	132.98	115.30
8	TA	203	MET	CG-SD-CE	7.68	112.50	100.20
8	RO	154	MET	CA-CB-CG	7.68	126.36	113.30
8	OE	136	LEU	CA-CB-CG	7.66	132.92	115.30
34	X7	115	LEU	CA-CB-CG	7.66	132.92	115.30
12	S0	484	LEU	CA-CB-CG	7.65	132.89	115.30
9	OD	284	LEU	CA-CB-CG	7.65	132.89	115.30
21	L1	147	PRO	CA-N-CD	-7.63	100.81	111.50
9	CF	197	ASP	CB-CG-OD1	7.61	125.15	118.30
17	P9	188	PRO	CA-N-CD	-7.60	100.86	111.50
8	RG	413	MET	CG-SD-CE	7.59	112.34	100.20
8	NO	23	LEU	CA-CB-CG	7.56	132.70	115.30
8	VG	119	LEU	CA-CB-CG	7.56	132.69	115.30
8	GO	153	LEU	CA-CB-CG	7.55	132.67	115.30
44	h2	120	LEU	CA-CB-CG	7.55	132.67	115.30
8	VM	152	LEU	CA-CB-CG	7.55	132.66	115.30
25	V	321	LEU	CA-CB-CG	7.54	132.63	115.30
8	KE	7	ILE	CG1-CB-CG2	-7.52	94.85	111.40
10	B	303	MET	CA-CB-CG	7.52	126.09	113.30
8	MO	211	ASP	CB-CG-OD1	7.52	125.07	118.30
8	HA	26	LEU	CB-CG-CD2	-7.52	98.22	111.00
8	IM	219	ILE	CG1-CB-CG2	-7.51	94.89	111.40
8	DQ	245	ASP	CB-CG-OD2	7.50	125.05	118.30
9	GD	177	ASP	CB-CG-OD2	7.50	125.05	118.30
8	BE	326	LYS	CD-CE-NZ	-7.50	94.46	111.70
43	j	15	PRO	CA-N-CD	-7.49	101.01	111.50
39	b	442	ASP	CB-CG-OD1	7.49	125.04	118.30
13	D	388	ASP	CB-CG-OD1	7.48	125.03	118.30
14	D1	331	ASP	CB-CG-OD2	7.48	125.03	118.30
9	TL	41	ASP	CB-CG-OD2	7.48	125.03	118.30
8	LC	218	ASP	CB-CG-OD2	7.47	125.03	118.30
12	C4	269	ASP	CB-CG-OD1	7.47	125.02	118.30
30	W4	220	ASP	CB-CG-OD2	7.47	125.02	118.30
9	HH	305	PRO	CA-N-CD	-7.46	101.06	111.50
9	HH	323	MET	CG-SD-CE	-7.46	88.26	100.20
9	KD	44	LEU	CA-CB-CG	7.45	132.44	115.30
8	SC	203	MET	CG-SD-CE	7.45	112.12	100.20
25	V	412	MET	CA-CB-CG	7.45	125.96	113.30
8	TC	153	LEU	CA-CB-CG	7.45	132.42	115.30
9	IP	88	ASP	CB-CG-OD1	7.44	125.00	118.30
17	O9	52	PRO	CA-N-CD	-7.43	101.10	111.50
44	h4	86	ASP	CB-CG-OD2	7.42	124.98	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	J1	190	LEU	CB-CG-CD2	-7.42	98.39	111.00
9	NF	41	ASP	CB-CG-OD2	7.41	124.97	118.30
8	VI	119	LEU	CA-CB-CG	7.41	132.34	115.30
9	PF	331	LEU	CA-CB-CG	7.40	132.31	115.30
17	Z5	238	ASP	CB-CG-OD2	7.39	124.95	118.30
9	BF	118	ASP	CB-CG-OD1	7.38	124.94	118.30
9	GH	323	MET	CG-SD-CE	-7.38	88.40	100.20
6	A	39	LEU	CA-CB-CG	7.38	132.26	115.30
9	KP	44	LEU	CB-CG-CD1	7.38	123.54	111.00
9	UF	41	ASP	CB-CG-OD2	7.37	124.94	118.30
30	V3	439	ASP	CB-CG-OD1	7.37	124.93	118.30
9	TD	80	PRO	N-CD-CG	-7.37	92.15	103.20
8	MI	218	ASP	CB-CG-OD2	7.35	124.91	118.30
8	WC	326	LYS	CD-CE-NZ	-7.34	94.81	111.70
9	DP	118	ASP	CB-CG-OD2	7.34	124.91	118.30
28	Q4	62	VAL	CG1-CB-CG2	-7.34	99.16	110.90
8	JE	189	LEU	CB-CG-CD1	7.33	123.47	111.00
12	C1	123	ASP	CB-CG-OD1	7.31	124.88	118.30
8	UI	119	LEU	CA-CB-CG	7.31	132.10	115.30
8	CM	218	ASP	CB-CG-OD1	7.30	124.87	118.30
8	MA	218	ASP	CB-CG-OD1	7.30	124.87	118.30
9	JF	267	MET	CG-SD-CE	7.29	111.87	100.20
7	A3	78	ASP	CB-CG-OD1	7.29	124.86	118.30
8	SM	136	LEU	CA-CB-CG	7.28	132.05	115.30
11	B3	219	ASP	CB-CG-OD1	7.28	124.85	118.30
12	C2	401	ASP	CB-CG-OD2	7.28	124.85	118.30
9	IL	395	LEU	CB-CG-CD1	-7.27	98.64	111.00
8	IM	259	LEU	CB-CG-CD2	-7.27	98.64	111.00
9	KP	305	PRO	CA-N-CD	-7.27	101.32	111.50
17	H	248	ASP	CB-CG-OD2	7.26	124.84	118.30
9	BP	253	LEU	CA-CB-CG	7.26	132.00	115.30
8	SI	203	MET	CA-CB-CG	-7.24	101.00	113.30
8	RM	173	PRO	CA-N-CD	-7.23	101.38	111.50
17	P8	147	ASP	CB-CG-OD1	7.23	124.81	118.30
3	3	367	ILE	CG1-CB-CG2	-7.22	95.50	111.40
9	KB	88	ASP	CB-CG-OD1	7.22	124.80	118.30
8	SC	268	PRO	CA-N-CD	-7.22	101.39	111.50
8	IM	7	ILE	CG1-CB-CG2	-7.22	95.52	111.40
14	T4	225	ASP	CB-CG-OD1	7.21	124.78	118.30
8	EO	39	ASP	CB-CG-OD1	7.20	124.78	118.30
20	K2	27	LEU	CA-CB-CG	7.20	131.86	115.30
11	B3	111	ASP	CB-CG-OD2	7.19	124.77	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	NK	136	LEU	CA-CB-CG	7.19	131.84	115.30
5	8	59	MET	CB-CG-SD	7.19	133.97	112.40
8	TM	23	LEU	CA-CB-CG	7.18	131.81	115.30
8	GO	157	LEU	CB-CG-CD2	7.17	123.19	111.00
8	GE	153	LEU	CA-CB-CG	7.16	131.78	115.30
8	AI	218	ASP	CB-CG-OD2	7.16	124.75	118.30
11	R3	111	ASP	CB-CG-OD1	7.16	124.75	118.30
8	HM	391	LEU	CA-CB-CG	7.14	131.71	115.30
9	KH	44	LEU	CA-CB-CG	7.13	131.71	115.30
8	NK	217	LEU	CA-CB-CG	7.13	131.71	115.30
9	OB	253	LEU	CA-CB-CG	7.13	131.70	115.30
8	UO	153	LEU	CA-CB-CG	7.13	131.69	115.30
14	D0	72	ASP	CB-CG-OD1	7.12	124.70	118.30
9	JF	114	ASP	CB-CG-OD1	7.11	124.70	118.30
8	RI	173	PRO	CA-N-CD	-7.11	101.54	111.50
9	NL	293	MET	CG-SD-CE	-7.11	88.83	100.20
19	J5	151	ASP	CB-CG-OD2	7.11	124.70	118.30
8	RE	302	MET	CB-CG-SD	7.10	133.70	112.40
17	N	248	ASP	CB-CG-OD2	7.09	124.69	118.30
9	BD	323	MET	CA-CB-CG	-7.08	101.27	113.30
8	JI	128	LEU	CA-CB-CG	7.08	131.58	115.30
8	TG	245	ASP	CB-CG-OD2	7.07	124.67	118.30
12	S8	369	LEU	CA-CB-CG	7.07	131.57	115.30
30	V2	229	MET	CA-CB-CG	7.07	125.32	113.30
9	UL	284	LEU	CA-CB-CG	7.05	131.53	115.30
8	HE	7	ILE	CG1-CB-CG2	-7.05	95.88	111.40
9	BL	118	ASP	CB-CG-OD1	7.05	124.64	118.30
11	B3	69	ASP	CB-CG-OD1	7.05	124.64	118.30
40	a4	140	LEU	CA-CB-CG	7.05	131.51	115.30
14	D2	283	ASP	CB-CG-OD1	7.04	124.64	118.30
8	TK	153	LEU	CA-CB-CG	7.04	131.50	115.30
33	X5	81	ASP	CB-CG-OD2	7.04	124.64	118.30
8	HC	69	ASP	CB-CG-OD1	7.04	124.64	118.30
8	KG	7	ILE	CG1-CB-CG2	-7.03	95.93	111.40
9	TL	233	MET	CB-CG-SD	-7.03	91.31	112.40
9	PH	403	MET	CA-CB-CG	7.02	125.24	113.30
30	V0	441	LEU	CA-CB-CG	7.00	131.41	115.30
27	P4	24	ASP	CB-CG-OD2	6.99	124.59	118.30
17	N	294	ASP	CB-CG-OD2	6.99	124.59	118.30
8	BE	128	LEU	CA-CB-CG	6.97	131.34	115.30
10	C	217	ASP	CB-CG-OD1	6.97	124.57	118.30
8	MO	259	LEU	CA-CB-CG	6.97	131.32	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	W0	455	LEU	CA-CB-CG	6.97	131.32	115.30
17	O8	45	ASP	CB-CG-OD2	6.96	124.57	118.30
8	DQ	116	ASP	CB-CG-OD2	6.96	124.57	118.30
41	b5	365	MET	CA-CB-CG	6.96	125.14	113.30
8	TE	23	LEU	CA-CB-CG	6.96	131.31	115.30
9	NL	359	ARG	CG-CD-NE	-6.96	97.19	111.80
9	DL	323	MET	CB-CG-SD	-6.96	91.53	112.40
43	i	222	PRO	CA-N-CD	-6.96	101.76	111.50
12	C2	176	ASP	CB-CG-OD1	6.94	124.55	118.30
8	VM	119	LEU	CA-CB-CG	6.94	131.25	115.30
8	FG	280	LYS	CA-CB-CG	6.93	128.65	113.40
8	AI	127	ASP	CB-CG-OD1	6.93	124.54	118.30
8	FK	302	MET	CA-CB-CG	6.93	125.08	113.30
14	D5	386	MET	CA-CB-CG	6.93	125.08	113.30
8	OE	209	ILE	CG1-CB-CG2	-6.92	96.18	111.40
37	YD	193	ASP	CB-CG-OD1	6.92	124.53	118.30
11	B2	180	MET	CG-SD-CE	-6.91	89.14	100.20
9	JJ	295	ASP	CB-CG-OD2	6.91	124.52	118.30
12	S0	199	LEU	CA-CB-CG	6.90	131.18	115.30
30	U5	341	LEU	CA-CB-CG	6.90	131.16	115.30
8	MA	259	LEU	CA-CB-CG	6.88	131.13	115.30
8	AI	245	ASP	CB-CG-OD2	6.88	124.49	118.30
28	Q2	116	MET	CG-SD-CE	-6.88	89.19	100.20
8	VG	136	LEU	CA-CB-CG	6.88	131.13	115.30
30	U6	378	LEU	CA-CB-CG	6.87	131.11	115.30
9	TH	267	MET	CA-CB-CG	6.86	124.97	113.30
14	T3	199	ASP	CB-CG-OD2	6.86	124.48	118.30
8	II	326	LYS	CD-CE-NZ	6.86	127.48	111.70
8	BI	326	LYS	CD-CE-NZ	-6.86	95.93	111.70
11	R1	387	ASP	CB-CG-OD1	6.86	124.47	118.30
31	X	171	ASP	CB-CG-OD1	6.84	124.46	118.30
8	LE	218	ASP	CB-CG-OD1	6.84	124.46	118.30
8	TA	318	LEU	CA-CB-CG	6.84	131.03	115.30
12	S6	443	ASP	CB-CG-OD1	6.83	124.45	118.30
30	V3	357	LEU	CA-CB-CG	6.83	131.02	115.30
9	PD	200	TYR	CB-CG-CD2	-6.83	116.90	121.00
9	MF	151	LEU	CA-CB-CG	6.83	131.00	115.30
8	IA	115	VAL	CG1-CB-CG2	-6.83	99.98	110.90
7	A5	232	LEU	CA-CB-CG	6.81	130.97	115.30
9	HP	331	LEU	CA-CB-CG	6.81	130.96	115.30
14	T5	339	LEU	CA-CB-CG	6.81	130.96	115.30
12	S8	443	ASP	CB-CG-OD1	6.80	124.42	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	VG	217	LEU	CA-CB-CG	6.80	130.94	115.30
31	W	458	LEU	CB-CG-CD2	-6.80	99.44	111.00
25	U	414	MET	CG-SD-CE	-6.80	89.32	100.20
9	IH	324	LYS	CD-CE-NZ	-6.80	96.07	111.70
28	Q1	105	LEU	CB-CG-CD1	-6.80	99.45	111.00
8	CI	367	ASP	CB-CG-OD1	6.79	124.42	118.30
9	BH	118	ASP	CB-CG-OD1	6.79	124.41	118.30
14	D5	407	ASP	CB-CG-OD1	6.79	124.41	118.30
37	YF	165	MET	CA-CB-CG	6.79	124.83	113.30
28	Q2	158	ALA	O-C-N	-6.78	111.85	122.70
8	IA	136	LEU	CA-CB-CG	6.78	130.89	115.30
30	V5	377	LEU	CA-CB-CG	6.78	130.88	115.30
8	BM	7	ILE	CG1-CB-CG2	-6.77	96.50	111.40
8	SG	36	MET	CG-SD-CE	6.77	111.03	100.20
36	Y4	105	ASP	CB-CG-OD1	6.77	124.39	118.30
9	CN	295	ASP	CB-CG-OD1	6.76	124.39	118.30
9	MF	74	ASP	CB-CG-OD1	6.76	124.38	118.30
8	FO	302	MET	CA-CB-CG	6.76	124.79	113.30
30	V7	250	LEU	CB-CG-CD2	-6.75	99.52	111.00
9	JF	84	ILE	CG1-CB-CG2	-6.75	96.54	111.40
9	WN	406	MET	CA-CB-CG	6.75	124.77	113.30
22	M1	194	LEU	CA-CB-CG	6.74	130.80	115.30
8	WE	217	LEU	CA-CB-CG	6.73	130.78	115.30
31	W	713	LEU	CA-CB-CG	6.73	130.78	115.30
9	JH	263	LEU	CA-CB-CG	6.73	130.77	115.30
8	AO	7	ILE	CG1-CB-CG2	-6.73	96.60	111.40
9	EN	323	MET	CG-SD-CE	-6.72	89.44	100.20
25	O5	348	ASP	CB-CG-OD1	6.72	124.35	118.30
8	AI	46	ASP	CB-CG-OD1	6.72	124.35	118.30
8	CC	7	ILE	CG1-CB-CG2	-6.72	96.62	111.40
9	TF	41	ASP	CB-CG-OD1	6.71	124.34	118.30
30	U1	130	LEU	CA-CB-CG	6.71	130.73	115.30
9	EN	249	ASP	CB-CG-OD1	6.70	124.33	118.30
8	QO	318	LEU	CB-CG-CD1	-6.70	99.61	111.00
9	HP	208	TYR	CB-CG-CD1	-6.69	116.98	121.00
17	P9	164	ASP	CB-CG-OD1	6.68	124.32	118.30
9	QH	253	LEU	CA-CB-CG	6.68	130.66	115.30
41	b1	443	LEU	CB-CG-CD2	6.68	122.35	111.00
8	IA	167	LEU	CB-CG-CD1	-6.66	99.67	111.00
9	UB	257	MET	CB-CG-SD	6.66	132.39	112.40
8	LM	157	LEU	CA-CB-CG	6.66	130.62	115.30
9	QH	44	LEU	CA-CB-CG	6.66	130.62	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	W7	253	ASP	CB-CG-OD1	6.66	124.29	118.30
8	UA	157	LEU	CB-CG-CD1	-6.65	99.69	111.00
11	B5	125	ASP	CB-CG-OD1	6.65	124.28	118.30
9	MD	249	ASP	CB-CG-OD1	6.64	124.28	118.30
9	OJ	44	LEU	CA-CB-CG	6.64	130.58	115.30
8	JE	189	LEU	CB-CG-CD2	-6.64	99.71	111.00
12	S7	443	ASP	CB-CG-OD1	6.64	124.27	118.30
9	FB	41	ASP	CB-CG-OD2	6.63	124.27	118.30
8	KM	317	MET	CB-CG-SD	6.63	132.29	112.40
30	V3	328	LEU	CA-CB-CG	6.63	130.55	115.30
8	IO	7	ILE	CG1-CB-CG2	-6.63	96.82	111.40
8	JM	116	ASP	CB-CG-OD1	6.63	124.27	118.30
30	W4	206	LEU	CA-CB-CG	6.63	130.54	115.30
34	X6	198	LEU	CA-CB-CG	6.63	130.54	115.30
8	FA	153	LEU	CA-CB-CG	6.62	130.54	115.30
9	GN	1	MET	CA-CB-CG	6.62	124.56	113.30
30	V6	446	MET	CA-CB-CG	6.62	124.55	113.30
3	3	311	MET	CA-CB-CG	6.62	124.55	113.30
10	B	162	MET	CA-CB-CG	6.62	124.55	113.30
8	EG	245	ASP	CB-CG-OD2	6.62	124.25	118.30
31	Z	82	ASP	CB-CG-OD1	6.61	124.25	118.30
17	N	246	ASP	CB-CG-OD2	6.60	124.24	118.30
9	TH	73	MET	CB-CG-SD	-6.60	92.60	112.40
9	OJ	32	PRO	N-CD-CG	-6.59	93.31	103.20
40	a3	56	LEU	CB-CG-CD2	-6.59	99.80	111.00
9	HJ	151	LEU	CB-CG-CD2	-6.59	99.80	111.00
8	FC	153	LEU	CA-CB-CG	6.58	130.44	115.30
9	DJ	357	PRO	CA-N-CD	-6.58	102.28	111.50
8	LC	322	ASP	CB-CG-OD1	6.58	124.22	118.30
8	WE	377	MET	CG-SD-CE	6.57	110.71	100.20
9	HP	249	ASP	CB-CG-OD1	6.57	124.21	118.30
8	OC	136	LEU	CA-CB-CG	6.56	130.40	115.30
47	p	379	MET	CA-CB-CG	6.56	124.46	113.30
8	PO	252	LEU	CA-CB-CG	6.56	130.40	115.30
25	V	62	LEU	CB-CG-CD1	-6.56	99.85	111.00
8	GE	245	ASP	CB-CG-OD2	6.56	124.20	118.30
11	R2	114	ILE	CG1-CB-CG2	-6.55	96.98	111.40
30	W0	455	LEU	CB-CG-CD2	-6.55	99.86	111.00
30	V7	170	MET	CG-SD-CE	-6.55	89.72	100.20
17	Z2	246	ASP	CB-CG-OD2	6.55	124.19	118.30
8	NI	76	ASP	CB-CG-OD2	6.54	124.18	118.30
8	TC	23	LEU	CA-CB-CG	6.54	130.33	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	BO	326	LYS	CA-CB-CG	-6.53	99.03	113.40
9	PD	331	LEU	CA-CB-CG	6.50	130.26	115.30
12	S4	165	ASP	CB-CG-OD2	6.50	124.15	118.30
3	4	443	LEU	CA-CB-CG	6.50	130.24	115.30
9	FJ	187	LEU	CA-CB-CG	6.50	130.24	115.30
8	HG	132	LEU	CB-CG-CD2	6.50	122.04	111.00
19	J1	204	MET	CA-CB-CG	6.49	124.34	113.30
11	B1	387	ASP	CB-CG-OD2	-6.49	112.46	118.30
8	TA	136	LEU	CA-CB-CG	6.49	130.22	115.30
48	q	72	ASP	CB-CG-OD2	6.49	124.14	118.30
9	BH	362	LYS	CD-CE-NZ	6.47	126.59	111.70
12	S2	224	ASP	CB-CG-OD2	6.47	124.12	118.30
9	DH	1	MET	CA-CB-CG	6.47	124.29	113.30
9	PH	304	ASP	CB-CG-OD2	6.46	124.12	118.30
10	B	48	ASP	CB-CG-OD2	6.46	124.11	118.30
8	UE	136	LEU	CA-CB-CG	6.45	130.13	115.30
9	OP	263	LEU	CA-CB-CG	6.44	130.12	115.30
30	V5	206	LEU	CA-CB-CG	6.44	130.12	115.30
12	S7	104	LEU	CA-CB-CG	6.44	130.10	115.30
9	FJ	41	ASP	CB-CG-OD2	6.43	124.09	118.30
8	CE	120	ASP	CB-CG-OD1	6.43	124.08	118.30
8	PE	26	LEU	CA-CB-CG	6.43	130.08	115.30
8	HE	69	ASP	CB-CG-OD2	6.42	124.08	118.30
9	ID	32	PRO	CA-N-CD	-6.42	102.52	111.50
8	SI	203	MET	CG-SD-CE	-6.42	89.94	100.20
12	S1	411	LEU	CA-CB-CG	6.41	130.05	115.30
30	V2	462	LEU	CA-CB-CG	6.41	130.05	115.30
8	KG	127	ASP	CB-CG-OD1	6.41	124.07	118.30
9	TB	44	LEU	CB-CG-CD2	-6.40	100.12	111.00
11	B1	211	ASP	CB-CG-OD1	6.40	124.06	118.30
8	EI	127	ASP	CB-CG-OD2	6.40	124.06	118.30
30	W2	302	ASP	CB-CG-OD2	6.39	124.05	118.30
9	TF	80	PRO	CA-N-CD	-6.39	102.56	111.50
9	IN	324	LYS	CD-CE-NZ	-6.38	97.01	111.70
41	b5	232	ASP	CB-CG-OD1	6.38	124.04	118.30
8	LA	33	ASP	CB-CG-OD1	6.38	124.04	118.30
41	b3	459	ASP	CB-CG-OD2	6.38	124.04	118.30
8	HK	167	LEU	CA-CB-CG	6.37	129.95	115.30
25	O5	348	ASP	CB-CG-OD2	-6.37	112.57	118.30
23	Q	324	LEU	CB-CG-CD2	6.37	121.83	111.00
9	JD	44	LEU	CA-CB-CG	6.37	129.94	115.30
8	SC	268	PRO	N-CD-CG	-6.36	93.66	103.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	RD	406	MET	CA-CB-CG	6.36	124.11	113.30
8	VE	318	LEU	CB-CG-CD1	-6.36	100.19	111.00
12	S3	438	LEU	CB-CG-CD1	-6.35	100.20	111.00
9	PD	363	MET	CB-CG-SD	-6.35	93.34	112.40
30	U8	444	LEU	CA-CB-CG	6.35	129.91	115.30
8	JI	120	ASP	CB-CG-OD2	6.35	124.02	118.30
8	UA	26	LEU	CA-CB-CG	6.35	129.90	115.30
39	a	286	MET	CG-SD-CE	-6.35	90.04	100.20
9	MH	417	ASP	CB-CG-OD2	6.35	124.01	118.30
8	SA	259	LEU	CA-CB-CG	6.35	129.90	115.30
37	YG	165	MET	CA-CB-CG	6.35	124.09	113.30
31	Z	169	ASP	CB-CG-OD2	6.35	124.01	118.30
37	YG	93	LEU	CB-CG-CD2	-6.35	100.21	111.00
9	CL	31	ASP	CB-CG-OD2	6.34	124.01	118.30
11	R4	376	ASP	CB-CG-OD2	6.34	124.01	118.30
30	V3	220	ASP	CB-CG-OD2	6.34	124.01	118.30
33	X4	153	LEU	CA-CB-CG	6.34	129.88	115.30
30	W7	227	ASP	CB-CG-OD2	6.34	124.00	118.30
8	GA	76	ASP	CB-CG-OD1	6.33	124.00	118.30
8	IC	69	ASP	CB-CG-OD1	6.33	124.00	118.30
8	VK	119	LEU	CA-CB-CG	6.33	129.86	115.30
9	MB	41	ASP	CB-CG-OD2	6.33	124.00	118.30
8	SM	136	LEU	CB-CG-CD2	6.32	121.75	111.00
8	BM	322	ASP	CB-CG-OD1	6.32	123.99	118.30
9	HP	19	LYS	CD-CE-NZ	6.32	126.24	111.70
9	BL	44	LEU	CA-CB-CG	6.32	129.83	115.30
8	QE	136	LEU	CA-CB-CG	6.31	129.82	115.30
8	CI	120	ASP	CB-CG-OD2	6.31	123.98	118.30
9	OB	289	LEU	CA-CB-CG	6.31	129.81	115.30
30	U2	332	MET	CA-CB-CG	6.31	124.02	113.30
8	WO	26	LEU	CA-CB-CG	6.31	129.81	115.30
9	JF	216	LYS	CA-CB-CG	6.30	127.26	113.40
9	SJ	233	MET	CA-CB-CG	6.30	124.01	113.30
30	U6	462	LEU	CA-CB-CG	6.30	129.78	115.30
8	TA	153	LEU	CA-CB-CG	6.29	129.78	115.30
11	B5	384	LEU	CA-CB-CG	6.29	129.76	115.30
14	T5	345	ASP	CB-CG-OD2	6.29	123.96	118.30
37	YH	31	MET	CA-CB-CG	6.28	123.98	113.30
28	Q1	105	LEU	CA-CB-CG	6.27	129.71	115.30
25	V	357	ASP	CB-CG-OD2	6.26	123.94	118.30
9	OP	253	LEU	CB-CG-CD1	6.26	121.65	111.00
9	IF	395	LEU	CA-CB-CG	6.26	129.69	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	J2	204	MET	CA-CB-CG	6.26	123.94	113.30
37	YG	117	ASP	CB-CG-OD2	6.25	123.93	118.30
8	PK	26	LEU	CA-CB-CG	6.25	129.68	115.30
30	U5	461	THR	OG1-CB-CG2	-6.25	95.62	110.00
8	IA	7	ILE	CG1-CB-CG2	-6.25	97.65	111.40
9	GB	267	MET	CA-CB-CG	6.25	123.92	113.30
9	TJ	41	ASP	CB-CG-OD2	6.25	123.92	118.30
8	RM	153	LEU	CA-CB-CG	6.25	129.67	115.30
8	VG	127	ASP	CB-CG-OD2	6.25	123.92	118.30
8	PM	70	LEU	CA-CB-CG	6.24	129.66	115.30
25	O5	516	MET	CG-SD-CE	6.24	110.19	100.20
8	PI	7	ILE	CG1-CB-CG2	-6.24	97.67	111.40
47	p	248	MET	CA-CB-CG	6.24	123.90	113.30
8	IK	125	LEU	CB-CG-CD2	-6.23	100.40	111.00
9	WF	44	LEU	CA-CB-CG	6.23	129.64	115.30
3	3	101	LEU	CB-CG-CD1	-6.23	100.41	111.00
17	O7	56	LEU	CA-CB-CG	6.23	129.63	115.30
11	B4	111	ASP	CB-CG-OD2	6.23	123.91	118.30
28	Q4	57	ASP	CB-CG-OD1	6.23	123.90	118.30
8	BE	326	LYS	CA-CB-CG	-6.22	99.71	113.40
9	FB	330	MET	CB-CG-SD	-6.22	93.73	112.40
9	FJ	272	PRO	CA-N-CD	-6.22	102.78	111.50
9	JF	388	MET	CA-CB-CG	6.22	123.88	113.30
9	EH	41	ASP	CB-CG-OD2	6.22	123.90	118.30
9	PB	147	MET	CA-CB-CG	6.22	123.88	113.30
9	VH	297	LYS	CD-CE-NZ	-6.22	97.39	111.70
45	m	90	ASP	CB-CG-OD2	6.22	123.90	118.30
8	EC	136	LEU	CA-CB-CG	6.22	129.60	115.30
8	SC	127	ASP	CB-CG-OD2	6.21	123.89	118.30
30	U8	378	LEU	CA-CB-CG	6.21	129.59	115.30
9	IN	118	ASP	CB-CG-OD2	6.21	123.89	118.30
47	o	221	GLU	CA-CB-CG	6.21	127.06	113.40
8	NA	16	ILE	CG1-CB-CG2	-6.21	97.74	111.40
8	HK	136	LEU	CA-CB-CG	6.21	129.58	115.30
8	TA	167	LEU	CA-CB-CG	6.21	129.58	115.30
8	BO	26	LEU	CA-CB-CG	6.20	129.57	115.30
8	KO	275	VAL	CG1-CB-CG2	-6.20	100.98	110.90
8	TM	136	LEU	CA-CB-CG	6.20	129.56	115.30
8	SC	154	MET	CG-SD-CE	-6.20	90.29	100.20
8	SG	397	LEU	CA-CB-CG	6.20	129.55	115.30
9	WL	164	MET	CB-CG-SD	-6.20	93.82	112.40
17	L	313	ASP	CB-CG-OD2	6.19	123.87	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	TB	112	LEU	CA-CB-CG	6.19	129.54	115.30
9	QP	233	MET	CG-SD-CE	-6.19	90.30	100.20
9	HL	388	MET	CA-CB-CG	6.19	123.82	113.30
9	KL	41	ASP	CB-CG-OD2	6.19	123.87	118.30
8	SC	157	LEU	CA-CB-CG	6.19	129.53	115.30
7	A2	89	ASP	CB-CG-OD1	6.18	123.87	118.30
17	N	43	LEU	CB-CG-CD2	6.18	121.51	111.00
8	DE	189	LEU	CB-CG-CD2	-6.18	100.50	111.00
9	CD	284	LEU	CA-CB-CG	6.17	129.50	115.30
8	JQ	286	LEU	CA-CB-CG	6.17	129.50	115.30
8	WK	1	MET	CA-CB-CG	6.17	123.79	113.30
12	S0	176	ASP	CB-CG-OD2	6.17	123.85	118.30
40	a3	52	ASP	CB-CG-OD2	6.17	123.85	118.30
9	QP	293	MET	CA-CB-CG	6.16	123.78	113.30
12	S3	164	LEU	CA-CB-CG	6.16	129.47	115.30
8	VI	125	LEU	CA-CB-CG	6.16	129.47	115.30
9	OH	299	MET	CB-CG-SD	-6.16	93.92	112.40
8	SI	153	LEU	CA-CB-CG	6.16	129.47	115.30
9	NF	118	ASP	CB-CG-OD2	6.16	123.84	118.30
30	U5	477	PRO	CA-N-CD	-6.16	102.88	111.50
9	WH	404	ASP	CB-CG-OD2	6.16	123.84	118.30
9	GN	406	MET	CB-CG-SD	6.15	130.86	112.40
9	PD	336	LYS	CD-CE-NZ	-6.15	97.55	111.70
8	MA	76	ASP	CB-CG-OD1	6.15	123.83	118.30
9	WD	403	MET	CA-CB-CG	6.15	123.75	113.30
35	XA	47	LEU	CA-CB-CG	6.14	129.43	115.30
8	CM	317	MET	CA-CB-CG	6.14	123.73	113.30
8	RO	154	MET	CG-SD-CE	6.14	110.02	100.20
37	YA	223	ASP	CB-CG-OD2	6.13	123.82	118.30
8	PK	1	MET	CA-CB-CG	6.13	123.71	113.30
9	DJ	44	LEU	CA-CB-CG	6.12	129.38	115.30
14	T4	213	MET	CA-CB-CG	6.12	123.71	113.30
42	g	173	MET	CB-CG-SD	6.12	130.77	112.40
12	S0	484	LEU	CB-CG-CD2	-6.12	100.60	111.00
25	V	62	LEU	CA-CB-CG	6.12	129.37	115.30
8	KI	127	ASP	CB-CG-OD2	6.11	123.80	118.30
9	LB	44	LEU	CA-CB-CG	6.11	129.35	115.30
37	YA	32	MET	CG-SD-CE	-6.11	90.43	100.20
3	3	116	MET	CB-CG-SD	-6.10	94.09	112.40
9	CP	128	ASP	CB-CG-OD2	6.09	123.78	118.30
11	R4	111	ASP	CB-CG-OD1	6.09	123.78	118.30
45	i1	19	LEU	CB-CG-CD2	-6.09	100.64	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	Y4	134	ASP	CB-CG-OD1	6.08	123.78	118.30
30	V8	270	LEU	CA-CB-CG	6.08	129.28	115.30
14	D3	312	ASP	CB-CG-OD1	6.08	123.77	118.30
8	LO	153	LEU	CA-CB-CG	6.08	129.28	115.30
9	BP	117	LEU	CA-CB-CG	6.07	129.27	115.30
8	LC	173	PRO	CA-N-CD	-6.07	103.00	111.50
9	OF	406	MET	CA-CB-CG	6.07	123.62	113.30
9	VH	118	ASP	CB-CG-OD2	6.07	123.76	118.30
8	JI	7	ILE	CG1-CB-CG2	-6.07	98.06	111.40
9	LJ	44	LEU	CA-CB-CG	6.07	129.25	115.30
9	OH	299	MET	CG-SD-CE	6.07	109.91	100.20
25	V	448	MET	CB-CG-SD	6.07	130.60	112.40
9	BN	355	ASP	CB-CG-OD2	6.06	123.76	118.30
19	J4	139	MET	CA-CB-CG	-6.06	103.00	113.30
9	KB	114	ASP	CB-CG-OD2	6.06	123.75	118.30
17	K	27	LEU	CB-CG-CD2	-6.05	100.71	111.00
8	UM	26	LEU	CA-CB-CG	6.05	129.23	115.30
30	V7	195	LEU	CB-CG-CD2	-6.05	100.71	111.00
9	TL	215	LEU	CA-CB-CG	6.05	129.22	115.30
9	ML	187	LEU	CA-CB-CG	6.04	129.20	115.30
41	b4	441	ASP	CB-CG-OD2	6.04	123.74	118.30
9	DB	112	LEU	CA-CB-CG	6.04	129.20	115.30
6	N1	51	MET	CG-SD-CE	-6.04	90.53	100.20
8	RI	302	MET	CB-CG-SD	6.04	130.51	112.40
19	J4	139	MET	CB-CG-SD	-6.04	94.29	112.40
8	QO	1	MET	CA-CB-CG	6.04	123.56	113.30
9	GL	177	ASP	CB-CG-OD1	6.03	123.73	118.30
13	K3	302	LEU	CA-CB-CG	6.03	129.17	115.30
8	SI	268	PRO	N-CD-CG	-6.03	94.16	103.20
8	LG	127	ASP	CB-CG-OD2	6.03	123.72	118.30
26	P2	8	LEU	CA-CB-CG	6.02	129.16	115.30
32	X1	209	MET	CA-CB-CG	6.02	123.53	113.30
8	IM	307	PRO	N-CD-CG	-6.02	94.17	103.20
41	b5	311	LEU	CA-CB-CG	6.01	129.13	115.30
9	MF	41	ASP	CB-CG-OD1	6.01	123.71	118.30
8	CG	98	ASP	CB-CG-OD1	6.01	123.71	118.30
9	UB	147	MET	CA-CB-CG	6.01	123.52	113.30
8	QM	26	LEU	CA-CB-CG	6.00	129.10	115.30
9	HB	41	ASP	CB-CG-OD1	6.00	123.70	118.30
8	JG	339	ARG	CA-CB-CG	6.00	126.60	113.40
42	e	173	MET	CB-CG-SD	6.00	130.39	112.40
12	C3	270	LYS	CD-CE-NZ	-6.00	97.91	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	V4	240	ILE	CG1-CB-CG2	-6.00	98.21	111.40
8	VK	7	ILE	CG1-CB-CG2	-5.99	98.22	111.40
9	CJ	171	PRO	C-N-CA	5.99	136.67	121.70
9	OH	323	MET	CG-SD-CE	-5.99	90.62	100.20
8	TE	153	LEU	CA-CB-CG	5.98	129.06	115.30
9	MJ	327	ASP	CB-CG-OD2	5.98	123.68	118.30
28	Q3	14	PRO	CA-N-CD	-5.98	103.13	111.50
9	DB	327	ASP	CB-CG-OD1	5.97	123.67	118.30
30	U6	377	LEU	CA-CB-CG	5.97	129.04	115.30
11	B2	111	ASP	CB-CG-OD1	5.97	123.67	118.30
9	QB	73	MET	CG-SD-CE	-5.97	90.65	100.20
8	GO	154	MET	CA-CB-CG	5.96	123.44	113.30
8	IE	424	ASP	CB-CG-OD2	5.96	123.67	118.30
8	PO	136	LEU	CB-CG-CD1	5.96	121.14	111.00
9	NB	361	LEU	CA-CB-CG	5.96	129.01	115.30
8	PE	203	MET	CB-CG-SD	5.96	130.27	112.40
8	GO	397	LEU	CA-CB-CG	5.95	128.99	115.30
9	QH	246	LEU	CA-CB-CG	5.95	128.99	115.30
13	K3	385	LYS	CA-CB-CG	5.95	126.50	113.40
8	LE	211	ASP	CB-CG-OD1	5.95	123.66	118.30
8	IM	195	LEU	CA-CB-CG	5.95	128.98	115.30
9	TH	130	LEU	CA-CB-CG	5.95	128.98	115.30
8	IM	259	LEU	CB-CG-CD1	5.95	121.11	111.00
9	QN	284	LEU	CA-CB-CG	5.94	128.97	115.30
8	JQ	119	LEU	CA-CB-CG	5.94	128.97	115.30
15	N2	21	LEU	CA-CB-CG	5.94	128.97	115.30
9	VF	406	MET	CA-CB-CG	5.94	123.39	113.30
31	Z	591	MET	CA-CB-CG	5.93	123.39	113.30
8	AK	7	ILE	CG1-CB-CG2	-5.93	98.35	111.40
8	SK	153	LEU	CA-CB-CG	5.93	128.94	115.30
8	HA	136	LEU	CA-CB-CG	5.93	128.94	115.30
9	CP	284	LEU	CA-CB-CG	5.92	128.92	115.30
19	J4	204	MET	CA-CB-CG	5.92	123.37	113.30
8	UC	217	LEU	CA-CB-CG	5.92	128.91	115.30
9	DJ	128	ASP	CB-CG-OD1	5.92	123.62	118.30
9	IH	118	ASP	CB-CG-OD2	5.91	123.62	118.30
8	JM	251	ASP	CB-CG-OD1	5.91	123.62	118.30
8	OC	167	LEU	CA-CB-CG	5.91	128.90	115.30
8	FI	326	LYS	CB-CG-CD	-5.91	96.24	111.60
8	WK	26	LEU	CA-CB-CG	5.91	128.88	115.30
45	n	90	ASP	CB-CG-OD2	5.91	123.61	118.30
9	HF	323	MET	CA-CB-CG	-5.90	103.27	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	IL	253	LEU	CA-CB-CG	5.90	128.87	115.30
9	MN	263	LEU	CA-CB-CG	5.90	128.87	115.30
9	PP	331	LEU	CA-CB-CG	5.90	128.87	115.30
9	FD	406	MET	CB-CG-SD	5.90	130.09	112.40
9	MF	361	LEU	CA-CB-CG	5.90	128.86	115.30
41	b1	397	LEU	CA-CB-CG	5.90	128.86	115.30
22	M1	194	LEU	CB-CG-CD2	5.90	121.02	111.00
19	J5	87	LEU	CA-CB-CG	5.89	128.85	115.30
8	IE	7	ILE	CG1-CB-CG2	-5.89	98.44	111.40
8	JC	302	MET	CA-CB-CG	5.89	123.31	113.30
9	IP	171	PRO	N-CD-CG	-5.89	94.37	103.20
8	KO	259	LEU	CA-CB-CG	5.88	128.84	115.30
9	LJ	87	PRO	CA-N-CD	-5.88	103.26	111.50
30	V5	470	MET	CB-CG-SD	5.88	130.05	112.40
8	FK	259	LEU	CA-CB-CG	5.88	128.83	115.30
9	EH	404	ASP	CB-CG-OD1	5.88	123.59	118.30
9	SD	1	MET	CA-CB-CG	5.88	123.29	113.30
30	V5	434	LEU	CB-CG-CD1	-5.87	101.02	111.00
27	P3	44	LEU	CA-CB-CG	5.87	128.79	115.30
8	UG	119	LEU	CA-CB-CG	5.87	128.79	115.30
8	PC	33	ASP	CB-CG-OD2	5.87	123.58	118.30
30	V6	332	MET	CA-CB-CG	5.87	123.27	113.30
9	FL	151	LEU	CA-CB-CG	5.86	128.78	115.30
17	K	45	ASP	CB-CG-OD2	5.86	123.57	118.30
8	VA	155	GLU	CA-CB-CG	5.86	126.29	113.40
9	CP	44	LEU	CA-CB-CG	5.86	128.77	115.30
9	IB	284	LEU	CB-CG-CD2	5.86	120.96	111.00
8	VE	136	LEU	CA-CB-CG	5.86	128.77	115.30
9	FN	249	ASP	CB-CG-OD2	5.86	123.57	118.30
9	QP	406	MET	CA-CB-CG	5.86	123.25	113.30
9	OJ	233	MET	CG-SD-CE	5.85	109.57	100.20
14	D5	402	LEU	CA-CB-CG	5.85	128.76	115.30
4	5	70	LYS	CD-CE-NZ	5.85	125.15	111.70
9	PB	293	MET	CA-CB-CG	5.85	123.24	113.30
9	LB	305	PRO	CA-N-CD	-5.85	103.32	111.50
9	HH	323	MET	CA-CB-CG	-5.84	103.36	113.30
30	W0	170	MET	CB-CG-SD	-5.84	94.87	112.40
44	h1	120	LEU	CB-CG-CD2	5.84	120.93	111.00
8	KM	128	LEU	CA-CB-CG	5.84	128.73	115.30
10	C	303	MET	CA-CB-CG	5.84	123.22	113.30
8	UO	242	LEU	CB-CG-CD2	-5.84	101.08	111.00
8	VE	119	LEU	CA-CB-CG	5.84	128.72	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	LM	153	LEU	CA-CB-CG	5.83	128.72	115.30
9	FD	1	MET	CA-CB-CG	5.83	123.22	113.30
11	R1	23	LEU	CA-CB-CG	5.83	128.72	115.30
9	PD	321	MET	CB-CG-SD	-5.83	94.91	112.40
12	S9	434	LEU	CB-CG-CD2	5.83	120.91	111.00
8	NM	128	LEU	CA-CB-CG	5.83	128.71	115.30
8	NE	136	LEU	CA-CB-CG	5.83	128.70	115.30
9	BD	118	ASP	CB-CG-OD1	5.82	123.54	118.30
8	UA	397	LEU	CA-CB-CG	5.82	128.69	115.30
9	TL	1	MET	CA-CB-CG	5.82	123.19	113.30
39	a	191	LEU	CB-CG-CD1	-5.81	101.12	111.00
8	BM	120	ASP	CB-CG-OD2	5.81	123.53	118.30
9	SB	42	LEU	CA-CB-CG	5.81	128.66	115.30
9	SH	41	ASP	CB-CG-OD2	5.81	123.53	118.30
14	T2	23	PRO	N-CD-CG	-5.81	94.49	103.20
9	WH	284	LEU	CB-CG-CD2	5.80	120.86	111.00
8	MO	218	ASP	CB-CG-OD2	5.80	123.52	118.30
17	O8	147	ASP	CB-CG-OD1	5.80	123.52	118.30
30	U7	302	ASP	CB-CG-OD2	5.80	123.52	118.30
8	TE	259	LEU	CA-CB-CG	5.79	128.63	115.30
11	B2	329	LEU	CA-CB-CG	5.79	128.63	115.30
28	Q1	191	PRO	CA-N-CD	-5.79	103.39	111.50
8	WE	377	MET	CB-CG-SD	5.79	129.78	112.40
8	FA	1	MET	CA-CB-CG	5.79	123.14	113.30
8	NO	392	ASP	CB-CG-OD1	5.79	123.51	118.30
8	SA	377	MET	CB-CG-SD	5.79	129.76	112.40
9	DD	233	MET	CA-CB-CG	5.79	123.13	113.30
9	PB	224	ASP	CB-CG-OD2	5.79	123.51	118.30
8	JO	189	LEU	CA-CB-CG	5.78	128.60	115.30
8	NG	114	ILE	CG1-CB-CG2	-5.78	98.68	111.40
9	RP	293	MET	CA-CB-CG	5.78	123.13	113.30
8	FA	157	LEU	CA-CB-CG	5.78	128.60	115.30
9	QN	130	LEU	CA-CB-CG	5.78	128.59	115.30
9	JB	112	LEU	CA-CB-CG	5.78	128.59	115.30
14	T4	278	LEU	CB-CG-CD2	5.78	120.82	111.00
9	BJ	1	MET	CA-CB-CG	-5.78	103.48	113.30
9	WJ	331	LEU	CB-CG-CD2	5.78	120.82	111.00
40	a1	139	ASP	CB-CG-OD2	5.78	123.50	118.30
8	GA	153	LEU	CA-CB-CG	5.78	128.59	115.30
17	O7	289	ILE	CG1-CB-CG2	-5.78	98.70	111.40
8	SI	157	LEU	CA-CB-CG	5.78	128.59	115.30
8	BM	152	LEU	CB-CG-CD2	-5.77	101.19	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	IK	338	LYS	CD-CE-NZ	-5.77	98.42	111.70
8	SI	398	MET	CG-SD-CE	-5.77	90.96	100.20
34	X6	70	PRO	CA-N-CD	-5.77	103.42	111.50
27	P3	176	MET	CA-CB-CG	5.77	123.11	113.30
9	FB	280	GLN	CA-CB-CG	5.77	126.09	113.40
8	OC	413	MET	CA-CB-CG	5.77	123.10	113.30
8	RI	153	LEU	CA-CB-CG	5.76	128.55	115.30
9	WL	44	LEU	CA-CB-CG	5.76	128.55	115.30
30	U5	461	THR	CA-CB-CG2	-5.76	104.34	112.40
19	J2	36	LEU	CB-CG-CD2	5.75	120.78	111.00
9	EL	1	MET	CA-CB-CG	5.74	123.06	113.30
9	WH	44	LEU	CA-CB-CG	5.74	128.50	115.30
8	CG	367	ASP	CB-CG-OD1	5.74	123.46	118.30
28	Q1	20	LEU	CA-CB-CG	5.73	128.49	115.30
30	U2	377	LEU	CA-CB-CG	5.73	128.48	115.30
9	IB	323	MET	CG-SD-CE	-5.73	91.03	100.20
8	RO	317	MET	CA-CB-CG	5.73	123.04	113.30
9	WJ	44	LEU	CA-CB-CG	5.73	128.48	115.30
34	X7	216	ASP	CB-CG-OD1	5.73	123.46	118.30
8	OG	136	LEU	CA-CB-CG	5.73	128.48	115.30
14	D5	386	MET	CB-CG-SD	5.73	129.58	112.40
9	PF	388	MET	CA-CB-CG	5.73	123.04	113.30
39	c	478	LEU	CA-CB-CG	5.73	128.47	115.30
41	b2	357	MET	CG-SD-CE	-5.73	91.04	100.20
42	f	608	ASP	CB-CG-OD2	5.73	123.45	118.30
9	EF	26	ASP	CB-CG-OD2	5.72	123.45	118.30
9	OJ	323	MET	CA-CB-CG	5.72	123.03	113.30
9	DB	295	ASP	CB-CG-OD2	5.72	123.45	118.30
8	IM	397	LEU	CA-CB-CG	5.72	128.45	115.30
22	M3	159	LYS	CD-CE-NZ	5.72	124.86	111.70
8	HA	391	LEU	CA-CB-CG	5.71	128.44	115.30
8	WO	259	LEU	CA-CB-CG	5.71	128.44	115.30
9	FH	415	MET	CA-CB-CG	5.71	123.01	113.30
30	V0	446	MET	CA-CB-CG	5.71	123.01	113.30
30	U2	391	MET	CB-CG-SD	5.71	129.51	112.40
9	SJ	42	LEU	CA-CB-CG	5.70	128.42	115.30
8	NI	136	LEU	CA-CB-CG	5.70	128.41	115.30
9	RJ	363	MET	CG-SD-CE	5.70	109.31	100.20
9	SL	44	LEU	CA-CB-CG	5.70	128.40	115.30
9	HJ	203	ASP	CB-CG-OD1	5.69	123.42	118.30
19	J3	87	LEU	CA-CB-CG	5.69	128.39	115.30
23	P	251	ASP	CB-CG-OD2	5.69	123.42	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	DP	1	MET	CA-CB-CG	5.69	122.97	113.30
8	MK	160	ASP	CB-CG-OD1	5.69	123.42	118.30
8	QM	136	LEU	CA-CB-CG	5.69	128.39	115.30
8	VI	136	LEU	CA-CB-CG	5.69	128.39	115.30
12	S3	204	LYS	CD-CE-NZ	-5.69	98.62	111.70
9	SN	388	MET	CA-CB-CG	5.69	122.97	113.30
9	OP	1	MET	CA-CB-CG	5.68	122.97	113.30
27	P7	169	LEU	CA-CB-CG	5.68	128.38	115.30
31	Y	449	ASP	CB-CG-OD1	5.68	123.41	118.30
8	QC	70	LEU	CA-CB-CG	5.68	128.36	115.30
8	GM	86	LEU	CA-CB-CG	5.68	128.36	115.30
9	PF	253	LEU	CA-CB-CG	5.67	128.35	115.30
8	OE	259	LEU	CA-CB-CG	5.67	128.35	115.30
47	p	306	MET	CA-CB-CG	5.67	122.94	113.30
8	GA	227	LEU	CA-CB-CG	5.67	128.34	115.30
9	PF	86	ARG	CA-CB-CG	5.67	125.87	113.40
9	TL	151	LEU	CA-CB-CG	5.67	128.33	115.30
44	h1	120	LEU	CA-CB-CG	5.66	128.32	115.30
9	DL	44	LEU	CA-CB-CG	5.66	128.32	115.30
8	SM	413	MET	CA-CB-CG	5.66	122.92	113.30
9	VH	253	LEU	CA-CB-CG	5.66	128.32	115.30
11	B2	178	ASP	CB-CG-OD1	5.66	123.39	118.30
9	JL	1	MET	CA-CB-CG	5.66	122.92	113.30
14	T3	22	LEU	CA-CB-CG	5.66	128.31	115.30
8	TA	251	ASP	CB-CG-OD1	5.66	123.39	118.30
25	O5	506	LEU	CA-CB-CG	5.66	128.31	115.30
19	J3	68	LEU	CA-CB-CG	5.65	128.29	115.30
9	EL	415	MET	CA-CB-CG	5.65	122.90	113.30
8	FG	259	LEU	CA-CB-CG	5.65	128.29	115.30
8	WO	136	LEU	CA-CB-CG	5.65	128.29	115.30
8	GC	86	LEU	CA-CB-CG	5.64	128.28	115.30
9	LL	151	LEU	CA-CB-CG	5.64	128.28	115.30
8	JE	157	LEU	CA-CB-CG	5.64	128.28	115.30
9	JP	361	LEU	CB-CG-CD2	5.64	120.59	111.00
8	FI	153	LEU	CA-CB-CG	5.64	128.27	115.30
9	WN	44	LEU	CA-CB-CG	5.64	128.27	115.30
10	C	459	LEU	CA-CB-CG	5.64	128.27	115.30
8	IE	160	ASP	CB-CG-OD2	5.64	123.37	118.30
8	RK	274	PRO	CA-N-CD	-5.64	103.61	111.50
8	AA	36	MET	CB-CG-SD	5.63	129.31	112.40
12	C3	458	ASP	CB-CG-OD2	5.63	123.37	118.30
8	GK	7	ILE	CG1-CB-CG2	-5.63	99.01	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	QH	300	MET	CA-CB-CG	5.63	122.88	113.30
9	UJ	151	LEU	CA-CB-CG	5.63	128.26	115.30
44	h1	101	ASP	CB-CG-OD2	5.63	123.37	118.30
9	GD	1	MET	CA-CB-CG	5.63	122.87	113.30
9	KP	44	LEU	CB-CG-CD2	-5.63	101.43	111.00
8	FK	189	LEU	CA-CB-CG	5.63	128.25	115.30
8	UM	248	LEU	CA-CB-CG	5.63	128.25	115.30
9	JP	356	ILE	CG1-CB-CG2	-5.63	99.02	111.40
8	NA	132	LEU	CA-CB-CG	5.63	128.25	115.30
9	GB	130	LEU	CA-CB-CG	5.63	128.24	115.30
8	MM	153	LEU	CA-CB-CG	5.63	128.24	115.30
8	TK	157	LEU	CA-CB-CG	5.63	128.24	115.30
31	Z	697	LEU	CB-CG-CD1	5.63	120.57	111.00
9	HB	44	LEU	CA-CB-CG	5.62	128.22	115.30
9	JL	44	LEU	CA-CB-CG	5.62	128.22	115.30
37	YH	223	ASP	CB-CG-OD1	5.62	123.35	118.30
9	LF	305	PRO	CA-N-CD	-5.61	103.64	111.50
31	Y	711	PRO	CA-N-CD	-5.61	103.64	111.50
9	FH	330	MET	CA-CB-CG	5.61	122.84	113.30
9	HH	233	MET	CA-CB-CG	5.61	122.84	113.30
31	W	684	LYS	CA-CB-CG	5.61	125.74	113.40
9	TN	151	LEU	CA-CB-CG	5.61	128.20	115.30
16	G	42	ASP	CB-CG-OD1	5.61	123.34	118.30
8	CK	98	ASP	CB-CG-OD1	5.60	123.34	118.30
14	T5	331	ASP	CB-CG-OD2	5.60	123.34	118.30
43	h	185	MET	CB-CG-SD	-5.60	95.59	112.40
8	GI	195	LEU	CB-CG-CD1	5.60	120.52	111.00
8	PC	221	ARG	CA-CB-CG	5.60	125.72	113.40
39	c	232	MET	CA-CB-CG	5.60	122.82	113.30
9	AD	295	ASP	CB-CG-OD2	5.60	123.34	118.30
8	HE	136	LEU	CA-CB-CG	5.60	128.17	115.30
25	V	45	MET	CA-CB-CG	5.60	122.82	113.30
8	WA	26	LEU	CA-CB-CG	5.60	128.17	115.30
9	QH	19	LYS	CD-CE-NZ	-5.59	98.83	111.70
30	U8	130	LEU	CA-CB-CG	5.59	128.17	115.30
33	X4	175	MET	CA-CB-CG	5.59	122.81	113.30
9	AJ	377	LEU	CA-CB-CG	5.59	128.15	115.30
14	D1	167	LEU	CA-CB-CG	5.58	128.14	115.30
9	IF	253	LEU	CA-CB-CG	5.58	128.14	115.30
30	W5	206	LEU	CA-CB-CG	5.58	128.14	115.30
47	p	159	MET	CA-CB-CG	5.58	122.79	113.30
1	7	47	LEU	CA-CB-CG	5.58	128.13	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	UE	47	ASP	CB-CG-OD2	5.58	123.32	118.30
30	V5	195	LEU	CB-CG-CD2	-5.58	101.51	111.00
9	LF	330	MET	CA-CB-CG	-5.58	103.82	113.30
9	MN	273	LEU	CA-CB-CG	5.58	128.13	115.30
9	IF	228	LEU	CB-CG-CD2	-5.58	101.52	111.00
8	OI	7	ILE	CG1-CB-CG2	-5.58	99.13	111.40
9	FD	330	MET	CA-CB-CG	5.57	122.77	113.30
41	b1	382	LEU	CA-CB-CG	5.57	128.12	115.30
9	MN	1	MET	CA-CB-CG	5.57	122.77	113.30
8	FG	339	ARG	CA-CB-CG	5.56	125.64	113.40
9	EN	406	MET	CA-CB-CG	5.56	122.75	113.30
8	LG	397	LEU	CA-CB-CG	5.56	128.10	115.30
9	OH	321	MET	CA-CB-CG	5.56	122.75	113.30
30	U7	232	LEU	CB-CG-CD1	-5.56	101.55	111.00
11	B1	269	LEU	CB-CG-CD2	-5.56	101.55	111.00
8	AC	245	ASP	CB-CG-OD2	5.56	123.30	118.30
8	UA	136	LEU	CA-CB-CG	5.56	128.09	115.30
9	JD	293	MET	CA-CB-CG	5.56	122.75	113.30
9	TH	267	MET	CB-CG-SD	5.56	129.07	112.40
8	NO	167	LEU	CA-CB-CG	5.55	128.08	115.30
35	XB	123	MET	CA-CB-CG	5.55	122.74	113.30
37	YG	93	LEU	CA-CB-CG	5.55	128.07	115.30
9	GD	44	LEU	CA-CB-CG	5.55	128.06	115.30
9	OL	323	MET	CB-CG-SD	5.55	129.04	112.40
8	HI	7	ILE	CG1-CB-CG2	-5.54	99.21	111.40
23	Q	324	LEU	CA-CB-CG	5.54	128.05	115.30
8	TK	251	ASP	CB-CG-OD2	5.54	123.29	118.30
8	OA	136	LEU	CA-CB-CG	5.54	128.05	115.30
9	JH	44	LEU	CA-CB-CG	5.54	128.04	115.30
8	VM	156	ARG	CA-CB-CG	5.54	125.58	113.40
9	MP	1	MET	CA-CB-CG	5.54	122.71	113.30
9	DP	44	LEU	CA-CB-CG	5.53	128.03	115.30
30	V3	391	MET	CA-CB-CG	-5.53	103.90	113.30
35	XA	171	LEU	CB-CG-CD2	-5.53	101.60	111.00
41	b2	113	MET	CA-CB-CG	5.53	122.70	113.30
9	CJ	44	LEU	CA-CB-CG	5.53	128.01	115.30
9	CL	325	GLU	CA-CB-CG	5.53	125.55	113.40
9	OB	114	ASP	CB-CG-OD1	5.53	123.27	118.30
8	IG	317	MET	CA-CB-CG	5.52	122.69	113.30
11	B4	108	LEU	CB-CG-CD1	-5.52	101.62	111.00
30	W5	237	ASP	CB-CG-OD1	5.51	123.26	118.30
4	j1	317	MET	CA-CB-CG	5.51	122.67	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	TI	413	MET	CA-CB-CG	5.51	122.67	113.30
30	V3	455	LEU	CA-CB-CG	5.51	127.97	115.30
9	FL	300	MET	CB-CG-SD	5.50	128.92	112.40
39	a	240	LEU	CA-CB-CG	5.50	127.96	115.30
8	RG	413	MET	CB-CG-SD	-5.50	95.89	112.40
8	VI	203	MET	CB-CG-SD	5.50	128.91	112.40
9	SD	42	LEU	CA-CB-CG	5.50	127.95	115.30
30	U9	446	MET	CA-CB-CG	5.50	122.65	113.30
45	n	109	LEU	CA-CB-CG	5.50	127.95	115.30
9	IH	32	PRO	N-CD-CG	-5.50	94.96	103.20
8	IE	397	LEU	CA-CB-CG	5.50	127.94	115.30
9	DN	44	LEU	CA-CB-CG	5.49	127.94	115.30
9	TL	217	LEU	CA-CB-CG	5.49	127.93	115.30
41	b1	344	LEU	CA-CB-CG	5.49	127.93	115.30
11	R1	287	LEU	CA-CB-CG	5.49	127.93	115.30
9	EH	415	MET	CB-CG-SD	5.49	128.87	112.40
9	EJ	388	MET	CA-CB-CG	5.49	122.63	113.30
9	GN	130	LEU	CA-CB-CG	5.49	127.92	115.30
8	WG	26	LEU	CA-CB-CG	5.49	127.92	115.30
8	BE	160	ASP	CB-CG-OD2	5.49	123.24	118.30
8	HO	347	CYS	CA-CB-SG	5.49	123.88	114.00
29	S	81	ASP	CB-CG-OD2	5.49	123.24	118.30
41	b5	433	LEU	CB-CG-CD1	5.49	120.33	111.00
8	VE	378	LEU	CA-CB-CG	5.48	127.91	115.30
9	GN	68	LEU	CB-CG-CD2	-5.48	101.68	111.00
8	MK	195	LEU	CA-CB-CG	5.48	127.90	115.30
12	S5	164	LEU	CB-CG-CD1	-5.48	101.69	111.00
46	i3	1515	LEU	CA-CB-CG	5.48	127.89	115.30
8	GM	98	ASP	CB-CG-OD1	5.47	123.23	118.30
8	MG	153	LEU	CA-CB-CG	5.47	127.89	115.30
3	3	51	LEU	CA-CB-CG	5.47	127.89	115.30
8	AI	205	ASP	CB-CG-OD1	5.47	123.22	118.30
31	X	458	LEU	CB-CG-CD2	-5.47	101.70	111.00
8	JC	398	MET	CG-SD-CE	-5.47	91.45	100.20
47	p	467	LYS	CA-CB-CG	5.47	125.42	113.40
8	LA	117	LEU	CA-CB-CG	5.46	127.87	115.30
8	WA	286	LEU	CB-CG-CD2	5.46	120.29	111.00
12	C4	167	MET	CB-CG-SD	5.46	128.79	112.40
9	LP	164	MET	CG-SD-CE	5.46	108.94	100.20
9	KD	377	LEU	CA-CB-CG	5.46	127.85	115.30
9	OB	85	PHE	C-N-CA	5.46	135.34	121.70
9	HH	88	ASP	CB-CG-OD2	5.45	123.21	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	VL	215	LEU	CA-CB-CG	5.45	127.84	115.30
9	DD	130	LEU	CA-CB-CG	5.45	127.84	115.30
8	IE	117	LEU	CA-CB-CG	5.45	127.84	115.30
9	DF	323	MET	CB-CG-SD	-5.45	96.05	112.40
8	MG	425	LEU	CB-CG-CD1	-5.45	101.74	111.00
9	DB	44	LEU	CA-CB-CG	5.45	127.83	115.30
9	AJ	323	MET	CA-CB-CG	-5.44	104.05	113.30
36	Y4	89	ILE	CA-CB-CG1	5.44	121.34	111.00
14	D5	394	LYS	CB-CG-CD	-5.44	97.46	111.60
9	DL	323	MET	CG-SD-CE	-5.44	91.50	100.20
8	TA	154	MET	CA-CB-CG	5.44	122.54	113.30
9	AH	39	ASP	CB-CG-OD1	5.43	123.19	118.30
8	TM	154	MET	CA-CB-CG	5.43	122.53	113.30
9	WB	44	LEU	CA-CB-CG	5.43	127.80	115.30
9	DP	253	LEU	CA-CB-CG	5.43	127.79	115.30
11	R1	114	ILE	CG1-CB-CG2	-5.43	99.45	111.40
8	VM	136	LEU	CA-CB-CG	5.43	127.79	115.30
8	WK	136	LEU	CA-CB-CG	5.43	127.79	115.30
12	C0	269	ASP	CB-CG-OD2	5.43	123.19	118.30
8	SG	413	MET	CA-CB-CG	5.43	122.53	113.30
9	OB	164	MET	CA-CB-CG	5.42	122.52	113.30
8	IA	70	LEU	CA-CB-CG	5.42	127.77	115.30
9	KN	114	ASP	CB-CG-OD1	5.42	123.18	118.30
8	VA	7	ILE	CG1-CB-CG2	-5.42	99.47	111.40
9	HP	208	TYR	CB-CG-CD2	5.42	124.25	121.00
9	NN	240	LEU	CA-CB-CG	5.42	127.76	115.30
36	Y1	20	MET	CB-CG-SD	5.42	128.65	112.40
25	T	232	LEU	CA-CB-CG	5.42	127.75	115.30
8	WO	217	LEU	CA-CB-CG	5.42	127.75	115.30
8	GG	117	LEU	CA-CB-CG	5.41	127.75	115.30
8	NO	413	MET	CA-CB-CG	5.41	122.50	113.30
9	EB	253	LEU	CA-CB-CG	5.41	127.75	115.30
8	PC	26	LEU	CA-CB-CG	5.41	127.74	115.30
8	LI	347	CYS	CA-CB-SG	5.41	123.74	114.00
8	OM	1	MET	CA-CB-CG	5.41	122.49	113.30
8	JG	153	LEU	CA-CB-CG	5.41	127.73	115.30
17	O7	292	MET	CG-SD-CE	5.40	108.85	100.20
8	VA	119	LEU	CA-CB-CG	5.40	127.72	115.30
9	OF	1	MET	CA-CB-CG	5.40	122.48	113.30
14	T1	41	LEU	CB-CG-CD2	-5.40	101.83	111.00
8	UO	98	ASP	CB-CG-OD1	5.39	123.15	118.30
41	b2	152	ARG	NE-CZ-NH2	-5.39	117.61	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	TH	1	MET	CA-CB-CG	5.39	122.46	113.30
23	Q	357	LEU	CA-CB-CG	5.38	127.68	115.30
9	OJ	330	MET	CA-CB-CG	5.38	122.45	113.30
14	T4	368	LEU	CA-CB-CG	5.38	127.68	115.30
40	a2	136	ASP	CB-CG-OD2	5.38	123.14	118.30
9	BN	253	LEU	CA-CB-CG	5.38	127.67	115.30
8	CK	326	LYS	CD-CE-NZ	-5.38	99.33	111.70
9	TN	267	MET	CA-CB-CG	5.38	122.44	113.30
30	V6	134	MET	CB-CG-SD	-5.38	96.27	112.40
11	B1	33	ASP	CB-CG-OD1	5.37	123.13	118.30
8	BK	284	GLU	CA-CB-CG	5.37	125.22	113.40
41	b4	209	MET	CA-CB-CG	5.37	122.43	113.30
30	U7	127	LYS	CG-CD-CE	-5.37	95.79	111.90
9	CL	88	ASP	CB-CG-OD2	5.37	123.13	118.30
45	n	45	ASP	CB-CG-OD2	5.37	123.13	118.30
8	RG	153	LEU	CA-CB-CG	5.37	127.64	115.30
9	QJ	68	LEU	CA-CB-CG	5.36	127.64	115.30
11	R4	387	ASP	CB-CG-OD1	5.36	123.13	118.30
8	VA	154	MET	CG-SD-CE	-5.36	91.62	100.20
39	a	185	MET	CA-CB-CG	5.36	122.42	113.30
9	JF	276	ARG	CG-CD-NE	5.36	123.06	111.80
8	JM	7	ILE	CG1-CB-CG2	-5.36	99.61	111.40
9	AN	273	LEU	CA-CB-CG	5.36	127.62	115.30
8	CC	98	ASP	CB-CG-OD2	5.36	123.12	118.30
15	F	158	LEU	CA-CB-CG	5.36	127.62	115.30
9	RL	406	MET	CB-CG-SD	5.36	128.47	112.40
8	RM	302	MET	CA-CB-CG	5.35	122.40	113.30
29	S	78	MET	CG-SD-CE	-5.35	91.63	100.20
42	f	173	MET	CA-CB-CG	5.35	122.40	113.30
9	UB	257	MET	CG-SD-CE	5.35	108.76	100.20
9	VL	68	LEU	CA-CB-CG	5.35	127.61	115.30
8	JI	424	ASP	CB-CG-OD1	5.35	123.12	118.30
8	PM	70	LEU	CB-CG-CD1	-5.35	101.90	111.00
8	RK	377	MET	CB-CG-SD	-5.35	96.35	112.40
36	Y1	114	TYR	CA-CB-CG	-5.35	103.23	113.40
8	AG	171	ILE	C-N-CA	5.35	135.07	121.70
17	H	249	LYS	CA-CB-CG	5.35	125.17	113.40
8	ME	7	ILE	CG1-CB-CG2	-5.35	99.64	111.40
12	S5	114	ARG	CG-CD-NE	-5.35	100.57	111.80
9	TL	263	LEU	CA-CB-CG	5.35	127.60	115.30
8	HM	160	ASP	CB-CG-OD1	5.34	123.11	118.30
8	PO	26	LEU	CA-CB-CG	5.34	127.58	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	TE	203	MET	CG-SD-CE	5.34	108.75	100.20
8	BM	347	CYS	CA-CB-SG	5.34	123.61	114.00
31	W	745	LEU	CA-CB-CG	5.34	127.58	115.30
12	C5	426	GLU	CA-CB-CG	5.34	125.14	113.40
8	SM	36	MET	CG-SD-CE	5.34	108.74	100.20
9	BJ	67	ASP	CB-CG-OD1	5.33	123.10	118.30
30	V0	332	MET	CA-CB-CG	5.33	122.37	113.30
9	IP	208	TYR	CB-CG-CD2	-5.33	117.80	121.00
8	HA	153	LEU	CA-CB-CG	5.33	127.56	115.30
9	FD	164	MET	CB-CG-SD	-5.33	96.41	112.40
30	V8	192	LEU	CA-CB-CG	5.33	127.56	115.30
30	V7	206	LEU	CA-CB-CG	5.33	127.55	115.30
8	KA	215	ARG	CA-CB-CG	5.33	125.12	113.40
3	3	105	LEU	CA-CB-CG	5.32	127.54	115.30
9	OF	253	LEU	CA-CB-CG	5.32	127.55	115.30
8	PK	7	ILE	CG1-CB-CG2	-5.32	99.69	111.40
8	HK	256	GLN	CA-CB-CG	5.32	125.11	113.40
9	VH	331	LEU	CA-CB-CG	5.32	127.53	115.30
31	X	533	MET	CG-SD-CE	5.32	108.71	100.20
8	VG	26	LEU	CA-CB-CG	5.32	127.52	115.30
9	LN	151	LEU	CA-CB-CG	5.31	127.52	115.30
36	Y4	89	ILE	CB-CG1-CD1	5.31	128.78	113.90
9	KL	258	VAL	CA-CB-CG2	5.31	118.86	110.90
12	S6	176	ASP	CB-CG-OD2	5.31	123.08	118.30
8	AC	397	LEU	CA-CB-CG	5.31	127.50	115.30
9	NH	44	LEU	CA-CB-CG	5.31	127.51	115.30
9	PD	253	LEU	CA-CB-CG	5.31	127.50	115.30
9	TN	217	LEU	CB-CG-CD2	5.31	120.02	111.00
8	CC	326	LYS	CD-CE-NZ	-5.30	99.50	111.70
19	J3	55	ASP	CB-CG-OD1	5.30	123.07	118.30
9	AH	249	ASP	CB-CG-OD2	5.30	123.07	118.30
7	A4	261	ASP	CB-CG-OD2	5.30	123.07	118.30
9	ED	257	MET	CG-SD-CE	5.30	108.68	100.20
45	I	45	ASP	CB-CG-OD1	5.30	123.07	118.30
9	SH	363	MET	CB-CG-SD	5.30	128.29	112.40
11	B5	384	LEU	CB-CG-CD2	5.29	120.00	111.00
9	QP	192	LEU	CA-CB-CG	5.29	127.47	115.30
14	T2	395	LEU	CA-CB-CG	5.29	127.47	115.30
8	AM	425	LEU	CB-CG-CD2	5.29	119.99	111.00
8	LO	157	LEU	CA-CB-CG	5.29	127.47	115.30
9	CD	284	LEU	CB-CG-CD2	-5.28	102.02	111.00
9	QN	207	LEU	CA-CB-CG	5.28	127.45	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	UM	136	LEU	CA-CB-CG	5.28	127.45	115.30
11	B2	180	MET	CA-CB-CG	5.28	122.28	113.30
30	U1	119	ASP	CB-CG-OD2	5.28	123.05	118.30
9	WD	207	LEU	CA-CB-CG	5.28	127.44	115.30
8	JE	160	ASP	CB-CG-OD2	5.28	123.05	118.30
8	UM	245	ASP	CB-CG-OD2	5.28	123.05	118.30
8	NE	413	MET	CG-SD-CE	-5.28	91.76	100.20
9	NP	80	PRO	CA-N-CD	-5.28	104.11	111.50
39	c	339	MET	CA-CB-CG	5.28	122.27	113.30
9	FH	1	MET	CA-CB-CG	5.27	122.27	113.30
9	HD	151	LEU	CA-CB-CG	5.27	127.43	115.30
8	JE	119	LEU	CA-CB-CG	5.27	127.43	115.30
35	XD	121	MET	CA-CB-CG	5.27	122.27	113.30
36	Y1	106	TYR	CB-CA-C	-5.27	99.85	110.40
37	YG	93	LEU	CB-CG-CD1	5.27	119.97	111.00
9	LF	284	LEU	CA-CB-CG	5.27	127.42	115.30
37	YF	69	LEU	CA-CB-CG	5.27	127.42	115.30
9	AN	58	LYS	CA-CB-CG	-5.27	101.81	113.40
8	BM	219	ILE	CG1-CB-CG2	-5.27	99.82	111.40
27	P4	169	LEU	CA-CB-CG	5.26	127.41	115.30
28	Q5	56	ARG	CG-CD-NE	-5.26	100.75	111.80
10	C	334	LEU	CA-CB-CG	5.26	127.40	115.30
11	R2	69	ASP	CB-CG-OD2	5.26	123.03	118.30
8	KM	160	ASP	CB-CG-OD1	5.26	123.03	118.30
9	VB	362	LYS	CD-CE-NZ	-5.26	99.61	111.70
31	Y	82	ASP	CB-CG-OD2	5.26	123.03	118.30
8	AE	137	ILE	CG1-CB-CG2	-5.25	99.84	111.40
14	D1	394	LYS	CB-CG-CD	-5.25	97.94	111.60
24	O4	82	ASP	CB-CG-OD2	5.25	123.03	118.30
9	EB	257	MET	CG-SD-CE	5.25	108.60	100.20
9	JB	357	PRO	N-CD-CG	-5.25	95.32	103.20
9	NB	228	LEU	CA-CB-CG	5.25	127.38	115.30
9	OB	361	LEU	CA-CB-CG	5.25	127.38	115.30
9	TD	233	MET	CA-CB-CG	5.25	122.23	113.30
30	V8	451	LEU	CB-CG-CD2	-5.25	102.07	111.00
9	WB	388	MET	CA-CB-CG	5.25	122.23	113.30
8	GC	251	ASP	CB-CG-OD2	5.25	123.02	118.30
30	V2	206	LEU	CA-CB-CG	5.25	127.37	115.30
9	VL	217	LEU	CA-CB-CG	5.25	127.37	115.30
9	IH	398	TYR	CB-CG-CD2	-5.25	117.85	121.00
8	TA	157	LEU	CA-CB-CG	5.24	127.36	115.30
47	p	304	MET	CA-CB-CG	5.24	122.21	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	OG	313	MET	CG-SD-CE	-5.24	91.81	100.20
34	X7	142	LEU	CA-CB-CG	5.24	127.35	115.30
47	p	384	GLU	CA-CB-CG	5.24	124.92	113.40
9	OP	331	LEU	CA-CB-CG	5.24	127.34	115.30
25	V	448	MET	CG-SD-CE	5.23	108.58	100.20
9	AJ	225	LEU	CA-CB-CG	5.23	127.33	115.30
9	CN	253	LEU	CA-CB-CG	5.23	127.33	115.30
14	D4	331	ASP	CB-CG-OD1	5.23	123.01	118.30
8	HK	245	ASP	CB-CG-OD2	5.23	123.01	118.30
9	KP	1	MET	CA-CB-CG	5.23	122.19	113.30
9	VH	293	MET	CA-CB-CG	5.23	122.19	113.30
30	U8	173	LEU	CA-CB-CG	5.23	127.32	115.30
8	EA	117	LEU	CA-CB-CG	5.23	127.32	115.30
8	CM	326	LYS	CA-CB-CG	-5.22	101.91	113.40
9	ML	323	MET	CG-SD-CE	-5.22	91.84	100.20
35	XH	123	MET	CA-CB-CG	5.22	122.18	113.30
17	P9	187	LEU	CA-CB-CG	5.22	127.31	115.30
9	RD	403	MET	CA-CB-CG	5.22	122.18	113.30
8	AI	47	ASP	CB-CG-OD2	5.22	123.00	118.30
19	J5	68	LEU	CA-CB-CG	5.22	127.31	115.30
8	LK	153	LEU	CB-CG-CD2	-5.22	102.13	111.00
9	NJ	41	ASP	CB-CG-OD1	5.22	123.00	118.30
8	RI	127	ASP	CB-CG-OD2	5.22	123.00	118.30
9	AL	152	ILE	CG1-CB-CG2	-5.22	99.92	111.40
8	LE	335	ILE	CG1-CB-CG2	-5.22	99.92	111.40
8	BI	7	ILE	CG1-CB-CG2	-5.22	99.92	111.40
8	HC	136	LEU	CA-CB-CG	5.22	127.30	115.30
12	S9	197	GLU	CA-CB-CG	5.22	124.88	113.40
9	PP	253	LEU	CA-CB-CG	5.21	127.29	115.30
11	B2	69	ASP	CB-CG-OD2	5.21	122.99	118.30
8	CE	317	MET	CB-CG-SD	5.21	128.04	112.40
8	NK	195	LEU	CB-CG-CD1	-5.21	102.14	111.00
8	GE	413	MET	CA-CB-CG	5.21	122.16	113.30
8	PK	398	MET	CA-CB-CG	5.21	122.16	113.30
8	WA	413	MET	CG-SD-CE	-5.21	91.86	100.20
8	KC	7	ILE	CG1-CB-CG2	-5.21	99.94	111.40
12	S0	309	LEU	CA-CB-CG	5.21	127.28	115.30
9	SB	388	MET	CG-SD-CE	5.21	108.53	100.20
39	b	443	ARG	CB-CG-CD	5.21	125.14	111.60
9	RP	415	MET	CA-CB-CG	5.20	122.15	113.30
39	b	461	LYS	CA-CB-CG	5.20	124.85	113.40
46	i3	1344	LEU	CB-CG-CD2	5.20	119.84	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	FF	415	MET	CA-CB-CG	5.20	122.14	113.30
9	FN	363	MET	CG-SD-CE	5.20	108.52	100.20
27	P3	86	PHE	C-N-CA	5.20	134.70	121.70
41	b1	357	MET	CG-SD-CE	-5.20	91.88	100.20
8	IG	251	ASP	CB-CG-OD1	5.20	122.98	118.30
9	TB	284	LEU	CB-CG-CD2	-5.20	102.16	111.00
9	UB	44	LEU	CA-CB-CG	5.20	127.26	115.30
9	DJ	118	ASP	CB-CG-OD2	5.20	122.98	118.30
9	RD	42	LEU	CB-CG-CD1	5.20	119.84	111.00
8	TI	153	LEU	CA-CB-CG	5.20	127.26	115.30
25	U	45	MET	CA-CB-CG	5.20	122.14	113.30
9	BP	217	LEU	CA-CB-CG	5.20	127.25	115.30
9	ON	253	LEU	CA-CB-CG	5.20	127.25	115.30
9	UJ	147	MET	CA-CB-CG	5.20	122.13	113.30
9	PH	321	MET	CA-CB-CG	5.19	122.13	113.30
9	RJ	112	LEU	CB-CG-CD1	-5.19	102.17	111.00
9	TD	1	MET	CA-CB-CG	5.19	122.13	113.30
27	P6	111	PRO	CA-N-CD	-5.19	104.23	111.50
9	TJ	44	LEU	CA-CB-CG	5.19	127.23	115.30
8	DC	7	ILE	CG1-CB-CG2	-5.19	99.99	111.40
8	SC	1	MET	CA-CB-CG	5.19	122.12	113.30
9	EJ	253	LEU	CA-CB-CG	5.19	127.23	115.30
8	KA	339	ARG	CA-CB-CG	5.19	124.81	113.40
8	LI	322	ASP	CB-CG-OD2	5.19	122.97	118.30
8	BK	7	ILE	CG1-CB-CG2	-5.18	100.00	111.40
8	CC	326	LYS	CB-CG-CD	-5.18	98.12	111.60
14	D5	345	ASP	CB-CG-OD1	5.18	122.97	118.30
8	VO	119	LEU	CA-CB-CG	5.18	127.22	115.30
8	DE	189	LEU	CB-CG-CD1	5.18	119.81	111.00
9	EJ	177	ASP	CB-CG-OD2	5.18	122.96	118.30
8	HA	7	ILE	CG1-CB-CG2	-5.18	100.00	111.40
8	IE	92	LEU	CB-CG-CD2	5.18	119.81	111.00
9	OD	273	LEU	CA-CB-CG	5.18	127.22	115.30
8	SC	428	LEU	CA-CB-CG	5.18	127.21	115.30
9	WF	192	LEU	CA-CB-CG	5.18	127.21	115.30
8	QE	167	LEU	CA-CB-CG	5.18	127.21	115.30
8	DE	116	ASP	CB-CG-OD2	5.18	122.96	118.30
8	GG	313	MET	CA-CB-CG	5.18	122.10	113.30
9	QP	44	LEU	CA-CB-CG	5.18	127.20	115.30
9	VJ	164	MET	CB-CG-SD	5.18	127.93	112.40
8	WA	84	ARG	CG-CD-NE	5.17	122.66	111.80
10	C	306	LEU	CA-CB-CG	5.17	127.19	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	IB	330	MET	CB-CG-SD	5.17	127.91	112.40
8	NM	52	PHE	C-N-CA	5.17	134.63	121.70
30	U9	470	MET	CG-SD-CE	5.17	108.47	100.20
30	V0	192	LEU	CA-CB-CG	5.17	127.19	115.30
41	b1	400	MET	CG-SD-CE	-5.17	91.93	100.20
39	a6	121	LYS	CA-CB-CG	5.17	124.77	113.40
8	BO	317	MET	CA-CB-CG	5.16	122.08	113.30
9	OJ	293	MET	CA-CB-CG	5.16	122.08	113.30
9	PB	253	LEU	CA-CB-CG	5.16	127.17	115.30
14	T5	339	LEU	CB-CG-CD2	-5.16	102.22	111.00
9	VD	1	MET	CB-CG-SD	-5.16	96.91	112.40
8	CO	39	ASP	CB-CG-OD2	5.16	122.94	118.30
9	NL	151	LEU	CA-CB-CG	5.16	127.17	115.30
9	PJ	252	LYS	CB-CG-CD	5.16	125.01	111.60
8	SM	259	LEU	CA-CB-CG	5.16	127.16	115.30
14	T1	266	LEU	CA-CB-CG	5.16	127.16	115.30
8	PC	70	LEU	CA-CB-CG	5.15	127.15	115.30
9	QJ	44	LEU	CA-CB-CG	5.15	127.15	115.30
8	WO	167	LEU	CA-CB-CG	5.15	127.15	115.30
14	D5	331	ASP	CB-CG-OD1	5.15	122.94	118.30
8	SA	269	LEU	CA-CB-CG	5.15	127.15	115.30
8	KC	327	ASP	CB-CG-OD2	5.15	122.93	118.30
8	NA	275	VAL	CG1-CB-CG2	-5.15	102.67	110.90
9	AJ	130	LEU	CA-CB-CG	5.14	127.13	115.30
9	GN	44	LEU	CA-CB-CG	5.14	127.13	115.30
1	7	63	ASP	CB-CG-OD1	5.14	122.93	118.30
11	B1	125	ASP	CB-CG-OD1	5.14	122.93	118.30
8	VO	26	LEU	CA-CB-CG	5.14	127.13	115.30
11	B3	175	ASP	CB-CG-OD2	5.14	122.93	118.30
8	NM	397	LEU	CA-CB-CG	5.14	127.12	115.30
47	p	483	TYR	OH-CZ-CE2	-5.14	106.22	120.10
14	T2	380	GLU	CA-CB-CG	-5.14	102.10	113.40
7	A3	232	LEU	CA-CB-CG	5.14	127.11	115.30
10	C	375	PHE	CB-CG-CD2	-5.14	117.20	120.80
9	MP	44	LEU	CA-CB-CG	5.14	127.11	115.30
9	DD	44	LEU	CA-CB-CG	5.13	127.11	115.30
9	EB	257	MET	CB-CG-SD	5.13	127.80	112.40
9	SN	388	MET	CG-SD-CE	5.13	108.41	100.20
8	IE	252	LEU	CA-CB-CG	5.13	127.10	115.30
14	T5	339	LEU	CB-CG-CD1	5.13	119.72	111.00
30	V1	341	LEU	CA-CB-CG	5.13	127.10	115.30
34	X6	248	LEU	CA-CB-CG	5.13	127.10	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	34	MET	CG-SD-CE	5.13	108.41	100.20
9	TJ	151	LEU	CA-CB-CG	5.13	127.10	115.30
8	VK	413	MET	CA-CB-CG	5.13	122.02	113.30
9	CB	380	ARG	CG-CD-NE	-5.13	101.03	111.80
8	FM	23	LEU	CA-CB-CG	5.13	127.09	115.30
30	V7	367	GLU	OE1-CD-OE2	-5.13	117.15	123.30
25	T	321	LEU	CA-CB-CG	5.12	127.09	115.30
9	HD	289	LEU	CA-CB-CG	5.12	127.08	115.30
30	U0	391	MET	CG-SD-CE	-5.12	92.00	100.20
36	Y2	214	LEU	CA-CB-CG	5.12	127.08	115.30
8	JK	424	ASP	CB-CG-OD2	5.12	122.91	118.30
30	V7	253	ASP	CB-CG-OD2	5.12	122.91	118.30
9	OH	246	LEU	CB-CG-CD1	-5.12	102.30	111.00
12	S3	438	LEU	CA-CB-CG	5.12	127.07	115.30
9	NF	323	MET	CA-CB-CG	-5.12	104.61	113.30
8	DO	425	LEU	CA-CB-CG	5.11	127.06	115.30
30	U3	310	MET	CB-CG-SD	5.11	127.74	112.40
40	a4	101	GLN	CA-CB-CG	5.11	124.65	113.40
30	U6	101	LEU	CA-CB-CG	5.11	127.05	115.30
9	BH	44	LEU	CA-CB-CG	5.11	127.05	115.30
9	MN	323	MET	CG-SD-CE	-5.11	92.03	100.20
9	DD	187	LEU	CA-CB-CG	5.11	127.04	115.30
9	GD	359	ARG	C-N-CA	-5.10	111.58	122.30
8	SE	398	MET	CG-SD-CE	-5.10	92.03	100.20
9	UH	284	LEU	CA-CB-CG	5.10	127.04	115.30
4	5	316	ASP	CB-CG-OD2	5.10	122.89	118.30
9	JF	253	LEU	CA-CB-CG	5.10	127.04	115.30
8	QK	136	LEU	CA-CB-CG	5.10	127.03	115.30
9	MH	257	MET	CA-CB-CG	-5.10	104.63	113.30
8	VK	375	VAL	CG1-CB-CG2	-5.10	102.74	110.90
8	PI	26	LEU	CA-CB-CG	5.10	127.03	115.30
8	SG	269	LEU	CA-CB-CG	5.10	127.03	115.30
8	MM	60	LYS	CD-CE-NZ	-5.10	99.98	111.70
9	OJ	59	TYR	CB-CG-CD2	-5.09	117.94	121.00
36	Y2	246	MET	CG-SD-CE	-5.09	92.05	100.20
8	TM	154	MET	CG-SD-CE	5.09	108.35	100.20
30	U0	205	ASP	CB-CG-OD1	5.09	122.88	118.30
8	IG	317	MET	CB-CG-SD	5.09	127.67	112.40
8	SA	302	MET	CA-CB-CG	5.09	121.95	113.30
9	VJ	295	ASP	CB-CG-OD1	5.09	122.88	118.30
9	WP	147	MET	CA-CB-CG	5.09	121.95	113.30
3	3	390	MET	CA-CB-CG	5.09	121.95	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	8	134	PRO	CA-N-CD	-5.09	104.38	111.50
9	DB	323	MET	CA-CB-CG	-5.09	104.65	113.30
9	QN	406	MET	CA-CB-CG	5.09	121.95	113.30
9	UN	406	MET	CA-CB-CG	5.09	121.95	113.30
9	DH	118	ASP	CB-CG-OD2	5.08	122.87	118.30
8	IM	307	PRO	CA-CB-CG	-5.08	94.35	104.00
8	UC	397	LEU	CA-CB-CG	5.08	126.99	115.30
37	YA	87	LEU	CB-CG-CD2	5.08	119.64	111.00
9	QF	406	MET	CA-CB-CG	5.08	121.93	113.30
42	f	100	LYS	CA-CB-CG	5.08	124.57	113.40
9	AB	328	GLU	CA-CB-CG	5.08	124.57	113.40
47	p	257	GLU	CA-CB-CG	5.08	124.56	113.40
9	IL	299	MET	CB-CG-SD	-5.07	97.18	112.40
9	QD	406	MET	CA-CB-CG	5.07	121.92	113.30
9	SJ	44	LEU	CA-CB-CG	5.07	126.97	115.30
39	c	274	LEU	CA-CB-CG	5.07	126.97	115.30
9	KB	220	PRO	N-CD-CG	-5.07	95.59	103.20
30	W0	443	LEU	CA-CB-CG	5.07	126.97	115.30
9	IP	147	MET	CA-CB-CG	5.07	121.92	113.30
23	Q	300	ARG	CG-CD-NE	5.07	122.45	111.80
8	FO	242	LEU	CA-CB-CG	5.07	126.96	115.30
8	CI	7	ILE	CG1-CB-CG2	-5.07	100.25	111.40
8	MK	322	ASP	CB-CG-OD1	5.07	122.86	118.30
9	RN	377	LEU	CA-CB-CG	5.07	126.95	115.30
9	LH	203	ASP	CB-CG-OD1	5.07	122.86	118.30
9	NJ	249	ASP	CB-CG-OD2	5.07	122.86	118.30
9	PH	331	LEU	CA-CB-CG	5.07	126.95	115.30
14	T1	405	LEU	CA-CB-CG	5.07	126.95	115.30
8	KM	117	LEU	CA-CB-CG	5.06	126.94	115.30
9	SL	139	LEU	CB-CG-CD2	-5.06	102.39	111.00
30	V5	470	MET	CG-SD-CE	5.06	108.30	100.20
8	UA	157	LEU	CB-CG-CD2	5.06	119.60	111.00
8	WC	318	LEU	CA-CB-CG	5.06	126.94	115.30
8	KM	189	LEU	CA-CB-CG	5.06	126.93	115.30
25	U	506	LEU	CA-CB-CG	5.06	126.93	115.30
9	HJ	404	ASP	CB-CG-OD1	5.06	122.85	118.30
9	MD	150	LEU	CB-CG-CD2	5.05	119.59	111.00
8	IO	203	MET	CB-CG-SD	5.05	127.56	112.40
12	S2	220	LEU	CA-CB-CG	5.05	126.92	115.30
9	CP	267	MET	CA-CB-CG	5.05	121.89	113.30
9	MF	377	LEU	CA-CB-CG	5.05	126.91	115.30
8	OA	259	LEU	CA-CB-CG	5.05	126.91	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	S4	306	ASP	CB-CG-OD1	5.05	122.84	118.30
9	VL	117	LEU	CB-CG-CD2	5.05	119.59	111.00
9	TJ	1	MET	CA-CB-CG	5.05	121.88	113.30
8	FI	345	ASP	CB-CG-OD2	5.05	122.84	118.30
9	RP	300	MET	CA-CB-CG	5.05	121.88	113.30
9	VN	415	MET	CA-CB-CG	5.05	121.88	113.30
25	T	321	LEU	CB-CG-CD2	5.04	119.58	111.00
8	CC	425	LEU	CB-CG-CD2	-5.04	102.43	111.00
8	SK	378	LEU	CA-CB-CG	5.04	126.90	115.30
30	W2	391	MET	CG-SD-CE	5.04	108.26	100.20
9	PJ	286	VAL	CA-CB-CG2	-5.04	103.34	110.90
8	WA	7	ILE	CG1-CB-CG2	-5.04	100.32	111.40
8	WG	7	ILE	CG1-CB-CG2	-5.03	100.34	111.40
14	T0	15	GLN	CA-CB-CG	5.03	124.46	113.40
9	HD	406	MET	CA-CB-CG	5.03	121.84	113.30
9	VJ	289	LEU	CA-CB-CG	5.03	126.86	115.30
46	i2	1494	LEU	CA-CB-CG	5.03	126.86	115.30
9	TB	130	LEU	CA-CB-CG	5.02	126.85	115.30
30	U3	310	MET	CG-SD-CE	5.02	108.23	100.20
30	V5	310	MET	CB-CG-SD	-5.02	97.33	112.40
9	EJ	257	MET	CB-CG-SD	5.02	127.46	112.40
8	HO	114	ILE	CG1-CB-CG2	-5.02	100.35	111.40
9	LN	377	LEU	CA-CB-CG	5.02	126.85	115.30
8	TA	397	LEU	CA-CB-CG	5.02	126.84	115.30
43	i	63	LEU	CB-CG-CD2	-5.02	102.47	111.00
4	j1	273	LEU	CA-CB-CG	5.02	126.84	115.30
47	p	402	LYS	CA-CB-CG	5.02	124.44	113.40
9	ID	209	ASP	CB-CG-OD2	5.02	122.82	118.30
9	ML	44	LEU	CA-CB-CG	5.02	126.84	115.30
29	R	69	MET	CB-CG-SD	-5.02	97.35	112.40
8	DI	128	LEU	CA-CB-CG	5.02	126.84	115.30
13	K3	414	LEU	CA-CB-CG	5.02	126.84	115.30
8	KG	338	LYS	CA-CB-CG	5.02	124.43	113.40
11	R4	108	LEU	CA-CB-CG	5.02	126.84	115.30
30	V7	366	GLN	CA-CB-CG	5.02	124.44	113.40
8	FA	280	LYS	CA-CB-CG	5.01	124.43	113.40
9	FB	311	LEU	CA-CB-CG	5.01	126.83	115.30
9	KH	187	LEU	CB-CG-CD1	5.01	119.53	111.00
9	KL	187	LEU	CB-CG-CD1	5.01	119.52	111.00
7	A3	389	LEU	CA-CB-CG	5.01	126.83	115.30
8	SG	128	LEU	CA-CB-CG	5.01	126.83	115.30
36	Y0	19	ILE	CG1-CB-CG2	-5.01	100.38	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	S3	165	ASP	CB-CG-OD1	5.01	122.81	118.30
9	JL	68	LEU	CB-CG-CD1	-5.00	102.49	111.00
8	MC	242	LEU	CA-CB-CG	5.00	126.81	115.30
9	NB	44	LEU	CA-CB-CG	5.00	126.81	115.30
12	S9	484	LEU	CA-CB-CG	5.00	126.81	115.30
9	SJ	267	MET	CA-CB-CG	5.00	121.80	113.30

There are no chirality outliers.

All (52) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	2	277	ARG	Sidechain
2	2	503	ARG	Sidechain
3	3	339	GLN	Mainchain
4	5	62	ARG	Sidechain
9	AJ	262	ARG	Sidechain
9	AL	241	ARG	Sidechain
8	AM	221	ARG	Sidechain
11	B5	266	ARG	Sidechain
9	BD	320	ARG	Sidechain
8	CM	221	ARG	Sidechain
14	D3	230	ARG	Sidechain
8	EE	339	ARG	Sidechain
8	FA	123	ARG	Sidechain
9	HN	276	ARG	Sidechain
9	IB	306	ARG	Sidechain
8	IE	84	ARG	Sidechain
8	JE	221	ARG	Sidechain
9	JF	77	ARG	Sidechain
8	JM	221	ARG	Sidechain
9	LF	390	ARG	Sidechain
9	LH	276	ARG	Sidechain
22	M1	191	ARG	Sidechain
8	NG	221	ARG	Sidechain
9	NL	359	ARG	Sidechain
9	NN	282	ARG	Sidechain
24	O3	143	ARG	Sidechain
25	O5	502	ARG	Sidechain
17	O8	183	ARG	Sidechain
9	OF	306	ARG	Sidechain
9	PF	86	ARG	Sidechain
28	Q1	158	ALA	Mainchain

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Mol	Chain	Res	Type	Group
28	Q2	158	ALA	Mainchain
28	Q3	158	ALA	Mainchain
28	Q4	158	ALA	Mainchain
28	Q5	56	ARG	Sidechain
12	S0	485	ARG	Sidechain
12	S3	126	ARG	Sidechain
12	S5	289	ARG	Sidechain
12	S6	183	ARG	Sidechain
12	S9	439	ARG	Sidechain
14	T2	403	ARG	Sidechain
30	U3	73	ARG	Sidechain
30	U8	415	ARG	Sidechain
8	VE	2	ARG	Sidechain
8	VM	243	ARG	Sidechain
8	WI	221	ARG	Sidechain
35	XF	170	ARG	Sidechain
36	Y5	205	ARG	Sidechain
31	Z	280	ARG	Sidechain
40	a4	159	ARG	Sidechain
46	i3	1475	ARG	Sidechain
4	j1	63	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 532 ligands modelled in this entry, 178 are monoatomic - leaving 354 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
52	GDP	FL	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.36	4 (13%)
50	GTP	OG	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.61	7 (21%)
52	GDP	OL	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.32	4 (13%)
52	GDP	HD	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.26	4 (13%)
50	GTP	NG	501	-	26,34,34	1.20	2 (7%)	32,54,54	1.65	7 (21%)
50	GTP	SK	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.54	7 (21%)
52	GDP	JD	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.27	4 (13%)
50	GTP	JM	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.62	6 (18%)
52	GDP	QD	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.28	4 (13%)
50	GTP	JG	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.59	6 (18%)
50	GTP	UI	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	AE	501	-	26,34,34	1.19	2 (7%)	32,54,54	1.60	7 (21%)
50	GTP	WM	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.58	7 (21%)
50	GTP	EG	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.61	7 (21%)
52	GDP	IH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.30	4 (13%)
50	GTP	WI	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	VA	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	SA	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.54	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	GTP	BO	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.60	7 (21%)
52	GDP	DL	502	-	24,30,30	0.98	1 (4%)	30,47,47	1.28	5 (16%)
52	GDP	NL	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.30	4 (13%)
50	GTP	OC	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.61	7 (21%)
50	GTP	OM	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	CG	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.60	7 (21%)
52	GDP	HH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	4 (13%)
50	GTP	DG	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	VB	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	FJ	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.30	3 (10%)
50	GTP	AG	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.62	7 (21%)
52	GDP	VJ	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.27	4 (13%)
50	GTP	OK	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	IC	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	LK	501	-	26,34,34	1.20	2 (7%)	32,54,54	1.60	7 (21%)
52	GDP	RN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.30	4 (13%)
50	GTP	SE	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.52	7 (21%)
52	GDP	BL	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.32	4 (13%)
50	GTP	SI	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.52	7 (21%)
52	GDP	WF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.27	4 (13%)
52	GDP	MF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.38	4 (13%)
52	GDP	ID	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	UN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.28	4 (13%)
50	GTP	OO	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.60	7 (21%)
52	GDP	KJ	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.40	5 (16%)
52	GDP	OJ	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.37	6 (20%)
52	GDP	FH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.32	4 (13%)
50	GTP	PC	501	-	26,34,34	1.11	2 (7%)	32,54,54	1.55	6 (18%)
50	GTP	LM	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	RO	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	AB	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	BM	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.61	7 (21%)
50	GTP	CK	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.67	7 (21%)
52	GDP	DJ	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	RC	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.54	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
52	GDP	CB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	HF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	DK	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.59	7 (21%)
52	GDP	PF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.30	4 (13%)
50	GTP	AO	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.59	7 (21%)
52	GDP	LH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.28	5 (16%)
50	GTP	OE	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.57	6 (18%)
52	GDP	KL	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	UM	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	CN	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	GB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.24	4 (13%)
50	GTP	JI	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.61	7 (21%)
52	GDP	EH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	LC	501	-	26,34,34	1.22	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	LN	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.34	4 (13%)
52	GDP	VH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	SB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	JJ	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.34	4 (13%)
50	GTP	TE	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.54	7 (21%)
52	GDP	HN	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	GM	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	AL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.38	4 (13%)
50	GTP	QO	501	-	26,34,34	1.10	1 (3%)	32,54,54	1.56	6 (18%)
52	GDP	OD	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	MD	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.28	4 (13%)
50	GTP	CM	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.60	7 (21%)
52	GDP	TJ	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.30	4 (13%)
50	GTP	KO	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	CF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	TN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	FI	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.58	7 (21%)
50	GTP	ME	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.64	6 (18%)
52	GDP	NB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	DP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.28	4 (13%)
52	GDP	FB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.30	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	GTP	VE	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.58	7 (21%)
50	GTP	VM	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	PO	501	-	26,34,34	1.11	2 (7%)	32,54,54	1.58	6 (18%)
52	GDP	MJ	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.43	4 (13%)
52	GDP	QH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.23	4 (13%)
52	GDP	HL	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.32	4 (13%)
52	GDP	KB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
52	GDP	TL	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	BK	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.60	7 (21%)
50	GTP	NK	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	QM	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	MG	501	-	26,34,34	1.20	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	UD	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	GF	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.28	5 (16%)
50	GTP	FK	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.55	7 (21%)
52	GDP	GN	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	RL	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.30	4 (13%)
50	GTP	HM	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	MM	501	-	26,34,34	1.17	1 (3%)	32,54,54	1.65	7 (21%)
50	GTP	RK	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.56	7 (21%)
50	GTP	EC	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.61	7 (21%)
50	GTP	DI	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.61	7 (21%)
52	GDP	NF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
52	GDP	NH	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.43	4 (13%)
50	GTP	UE	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.54	6 (18%)
50	GTP	FC	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.60	7 (21%)
50	GTP	OI	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.57	6 (18%)
52	GDP	UB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.33	4 (13%)
50	GTP	EO	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	AA	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.57	7 (21%)
50	GTP	HE	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	KC	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.57	7 (21%)
52	GDP	RF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	CP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.27	4 (13%)
52	GDP	EB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.27	5 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	GTP	FE	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.54	7 (21%)
50	GTP	CC	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.55	7 (21%)
52	GDP	DH	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.28	4 (13%)
50	GTP	SM	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.53	7 (21%)
50	GTP	UK	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.57	7 (21%)
50	GTP	LO	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	VD	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.34	4 (13%)
50	GTP	LG	501	-	26,34,34	1.19	2 (7%)	32,54,54	1.62	7 (21%)
52	GDP	IB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	IM	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.62	7 (21%)
52	GDP	LF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.40	4 (13%)
50	GTP	NA	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	EF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.28	5 (16%)
50	GTP	EM	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.54	7 (21%)
50	GTP	MC	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.51	6 (18%)
52	GDP	BB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	FF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	NJ	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.41	4 (13%)
52	GDP	MP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	4 (13%)
50	GTP	HO	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.58	8 (25%)
52	GDP	CJ	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.36	4 (13%)
52	GDP	BF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.34	4 (13%)
52	GDP	BJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	SJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	EE	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.59	7 (21%)
52	GDP	WP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	NP	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.32	4 (13%)
50	GTP	BI	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.65	7 (21%)
50	GTP	RI	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	HB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.27	4 (13%)
52	GDP	DB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.30	4 (13%)
50	GTP	IE	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.57	7 (21%)
52	GDP	MB	502	-	24,30,30	0.90	1 (4%)	30,47,47	1.25	4 (13%)
50	GTP	TC	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	LB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.29	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
52	GDP	GH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.34	4 (13%)
50	GTP	UG	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.58	7 (21%)
50	GTP	TG	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.57	7 (21%)
52	GDP	MN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	4 (13%)
50	GTP	FA	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.54	7 (21%)
50	GTP	CQ	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.55	7 (21%)
52	GDP	QB	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	DM	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.55	7 (21%)
52	GDP	ND	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	GO	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.56	6 (18%)
50	GTP	SG	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.51	6 (18%)
50	GTP	AK	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.62	7 (21%)
50	GTP	VI	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.57	6 (18%)
50	GTP	MO	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.59	7 (21%)
52	GDP	JL	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.27	4 (13%)
50	GTP	NC	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.58	7 (21%)
50	GTP	CO	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	WB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.28	4 (13%)
50	GTP	VG	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.58	7 (21%)
52	GDP	CH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.33	4 (13%)
52	GDP	GL	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.34	4 (13%)
50	GTP	WC	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.58	7 (21%)
50	GTP	TI	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.54	7 (21%)
52	GDP	VL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	GA	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	BE	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.61	7 (21%)
50	GTP	QC	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.56	7 (21%)
50	GTP	NM	501	-	26,34,34	1.13	1 (3%)	32,54,54	1.60	7 (21%)
52	GDP	SN	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	JB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.27	4 (13%)
52	GDP	AP	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.33	4 (13%)
52	GDP	TD	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	DF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	RJ	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.28	4 (13%)
50	GTP	RG	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.56	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
52	GDP	SH	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.27	4 (13%)
50	GTP	LE	501	-	26,34,34	1.20	2 (7%)	32,54,54	1.56	7 (21%)
50	GTP	IA	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.55	7 (21%)
52	GDP	OP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	4 (13%)
52	GDP	IJ	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	JH	502	-	24,30,30	1.01	1 (4%)	30,47,47	1.36	4 (13%)
50	GTP	TM	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	WE	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	TH	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	RM	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.54	7 (21%)
52	GDP	SF	502	-	24,30,30	0.91	1 (4%)	30,47,47	1.34	5 (16%)
52	GDP	QP	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.32	5 (16%)
50	GTP	PI	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.61	7 (21%)
50	GTP	JK	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.67	7 (21%)
52	GDP	KN	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	CD	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	IO	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.65	6 (18%)
52	GDP	LJ	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.38	4 (13%)
50	GTP	BG	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.63	7 (21%)
50	GTP	WK	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.57	6 (18%)
52	GDP	LL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	5 (16%)
52	GDP	DD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	MH	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.27	4 (13%)
52	GDP	PL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.28	4 (13%)
52	GDP	IF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	KD	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.33	4 (13%)
52	GDP	JN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.28	4 (13%)
52	GDP	LP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.25	4 (13%)
50	GTP	KE	501	-	26,34,34	1.19	1 (3%)	32,54,54	1.53	7 (21%)
50	GTP	GC	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.54	6 (18%)
52	GDP	ML	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	5 (16%)
52	GDP	DN	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	SD	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	PD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	LI	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.60	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	GTP	JO	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.69	7 (21%)
50	GTP	JE	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.59	7 (21%)
52	GDP	LD	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.31	5 (16%)
52	GDP	WH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	AD	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.37	4 (13%)
52	GDP	IL	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.31	4 (13%)
52	GDP	ED	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	DE	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.59	7 (21%)
52	GDP	AJ	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.34	4 (13%)
52	GDP	ON	502	-	24,30,30	0.99	1 (4%)	30,47,47	1.28	5 (16%)
50	GTP	GI	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.59	7 (21%)
52	GDP	UF	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	FN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	4 (13%)
50	GTP	TA	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.53	7 (21%)
52	GDP	WJ	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.27	4 (13%)
50	GTP	EI	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.57	7 (21%)
50	GTP	WG	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	PM	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.57	6 (18%)
52	GDP	SL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	AH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.36	4 (13%)
52	GDP	WD	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	FD	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.32	4 (13%)
50	GTP	BC	501	-	26,34,34	1.11	2 (7%)	32,54,54	1.61	6 (18%)
52	GDP	RP	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	AI	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.64	7 (21%)
50	GTP	PK	501	-	26,34,34	1.11	2 (7%)	32,54,54	1.55	6 (18%)
50	GTP	DC	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.58	7 (21%)
52	GDP	EN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	TB	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.34	5 (16%)
52	GDP	QN	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.28	4 (13%)
50	GTP	GK	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.53	7 (21%)
50	GTP	PG	501	-	26,34,34	1.09	1 (3%)	32,54,54	1.62	7 (21%)
50	GTP	FM	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	MA	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.53	7 (21%)
50	GTP	KI	501	-	26,34,34	1.20	2 (7%)	32,54,54	1.55	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
52	GDP	OH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	BH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.34	4 (13%)
52	GDP	WN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.26	4 (13%)
50	GTP	NO	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.56	7 (21%)
50	GTP	IG	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.63	6 (18%)
52	GDP	JF	502	-	24,30,30	0.92	1 (4%)	30,47,47	1.29	3 (10%)
52	GDP	PN	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.28	4 (13%)
50	GTP	TK	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.56	7 (21%)
50	GTP	QE	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.57	7 (21%)
52	GDP	BN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.28	4 (13%)
50	GTP	HG	501	-	26,34,34	1.19	2 (7%)	32,54,54	1.62	7 (21%)
50	GTP	HA	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.53	7 (21%)
50	GTP	MK	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.61	7 (21%)
50	GTP	HK	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.57	7 (21%)
50	GTP	NE	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.52	7 (21%)
52	GDP	VN	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.27	4 (13%)
50	GTP	HI	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.61	7 (21%)
52	GDP	UJ	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.26	4 (13%)
50	GTP	AM	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	WA	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.54	7 (21%)
50	GTP	MI	501	-	26,34,34	1.20	1 (3%)	32,54,54	1.59	7 (21%)
50	GTP	OA	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.55	7 (21%)
52	GDP	QL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.28	4 (13%)
52	GDP	UH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.34	4 (13%)
52	GDP	GD	502	-	24,30,30	1.03	1 (4%)	30,47,47	1.24	4 (13%)
50	GTP	KM	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.54	7 (21%)
52	GDP	IP	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.43	5 (16%)
52	GDP	GJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.25	5 (16%)
52	GDP	KP	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.27	4 (13%)
52	GDP	PP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	JC	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.56	7 (21%)
50	GTP	VO	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.58	7 (21%)
52	GDP	EJ	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	II	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.62	7 (21%)
50	GTP	KA	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.55	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
52	GDP	WL	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.30	4 (13%)
50	GTP	AC	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.61	7 (21%)
50	GTP	DQ	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.57	7 (21%)
50	GTP	PE	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.57	6 (18%)
50	GTP	VC	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.56	7 (21%)
50	GTP	FO	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	GE	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	JQ	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.59	7 (21%)
52	GDP	AF	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	KH	502	-	24,30,30	0.97	1 (4%)	30,47,47	1.27	4 (13%)
52	GDP	PB	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.30	4 (13%)
52	GDP	RH	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	VK	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.59	7 (21%)
52	GDP	BP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	PH	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	NN	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.34	4 (13%)
50	GTP	DO	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.57	7 (21%)
50	GTP	QI	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.60	6 (18%)
50	GTP	EK	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	LA	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	CE	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.59	7 (21%)
52	GDP	AN	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.35	4 (13%)
50	GTP	HC	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.55	7 (21%)
50	GTP	QG	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.58	7 (21%)
52	GDP	BD	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.31	4 (13%)
50	GTP	UC	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.60	7 (21%)
52	GDP	RD	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.32	4 (13%)
52	GDP	VF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.27	4 (13%)
52	GDP	UL	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.29	4 (13%)
52	GDP	OF	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.33	4 (13%)
50	GTP	NI	501	-	26,34,34	1.15	2 (7%)	32,54,54	1.63	7 (21%)
52	GDP	HP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.26	4 (13%)
50	GTP	RE	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.56	7 (21%)
50	GTP	QK	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.58	7 (21%)
50	GTP	EA	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.56	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	GTP	UA	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.55	7 (21%)
52	GDP	HJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.23	4 (13%)
52	GDP	QF	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.26	4 (13%)
50	GTP	GG	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.54	6 (18%)
52	GDP	PJ	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.32	4 (13%)
52	GDP	QJ	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.24	4 (13%)
50	GTP	UO	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.57	7 (21%)
52	GDP	OB	502	-	24,30,30	1.01	1 (4%)	30,47,47	1.36	4 (13%)
50	GTP	IK	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.64	7 (21%)
52	GDP	EL	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.28	4 (13%)
52	GDP	KF	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.33	5 (16%)
50	GTP	FG	501	-	26,34,34	1.16	2 (7%)	32,54,54	1.56	7 (21%)
50	GTP	KG	501	-	26,34,34	1.19	2 (7%)	32,54,54	1.57	7 (21%)
52	GDP	TF	502	-	24,30,30	0.93	1 (4%)	30,47,47	1.29	4 (13%)
50	GTP	SC	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.52	7 (21%)
52	GDP	CL	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.30	4 (13%)
50	GTP	CI	501	-	26,34,34	1.17	2 (7%)	32,54,54	1.59	7 (21%)
50	GTP	KK	501	-	26,34,34	1.18	2 (7%)	32,54,54	1.57	7 (21%)
50	GTP	WO	501	-	26,34,34	1.14	2 (7%)	32,54,54	1.56	7 (21%)
52	GDP	JP	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.26	4 (13%)
52	GDP	IN	502	-	24,30,30	0.95	1 (4%)	30,47,47	1.33	4 (13%)

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
52	GDP	FL	502	-	-	0/12/32/32	0/3/3/3
50	GTP	OG	501	-	-	8/18/38/38	0/3/3/3
52	GDP	OL	502	-	-	1/12/32/32	0/3/3/3
52	GDP	HD	502	-	-	1/12/32/32	0/3/3/3
50	GTP	NG	501	-	-	9/18/38/38	0/3/3/3
50	GTP	SK	501	-	-	8/18/38/38	0/3/3/3
52	GDP	JD	502	-	-	1/12/32/32	0/3/3/3
50	GTP	JM	501	-	-	6/18/38/38	0/3/3/3
52	GDP	QD	502	-	-	0/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	JG	501	-	-	6/18/38/38	0/3/3/3
50	GTP	UI	501	-	-	8/18/38/38	0/3/3/3
50	GTP	AE	501	-	-	9/18/38/38	0/3/3/3
50	GTP	WM	501	-	-	6/18/38/38	0/3/3/3
50	GTP	EG	501	-	-	7/18/38/38	0/3/3/3
52	GDP	IH	502	-	-	0/12/32/32	0/3/3/3
50	GTP	WI	501	-	-	6/18/38/38	0/3/3/3
50	GTP	VA	501	-	-	8/18/38/38	0/3/3/3
50	GTP	SA	501	-	-	8/18/38/38	0/3/3/3
50	GTP	BO	501	-	-	8/18/38/38	0/3/3/3
52	GDP	DL	502	-	-	2/12/32/32	0/3/3/3
52	GDP	NL	502	-	-	1/12/32/32	0/3/3/3
50	GTP	OC	501	-	-	8/18/38/38	0/3/3/3
50	GTP	OM	501	-	-	8/18/38/38	0/3/3/3
50	GTP	CG	501	-	-	6/18/38/38	0/3/3/3
52	GDP	HH	502	-	-	0/12/32/32	0/3/3/3
50	GTP	DG	501	-	-	8/18/38/38	0/3/3/3
52	GDP	VB	502	-	-	4/12/32/32	0/3/3/3
52	GDP	FJ	502	-	-	1/12/32/32	0/3/3/3
50	GTP	AG	501	-	-	6/18/38/38	0/3/3/3
52	GDP	VJ	502	-	-	1/12/32/32	0/3/3/3
50	GTP	OK	501	-	-	8/18/38/38	0/3/3/3
50	GTP	IC	501	-	-	7/18/38/38	0/3/3/3
50	GTP	LK	501	-	-	7/18/38/38	0/3/3/3
52	GDP	RN	502	-	-	0/12/32/32	0/3/3/3
50	GTP	SE	501	-	-	6/18/38/38	0/3/3/3
52	GDP	BL	502	-	-	2/12/32/32	0/3/3/3
50	GTP	SI	501	-	-	8/18/38/38	0/3/3/3
52	GDP	WF	502	-	-	1/12/32/32	0/3/3/3
52	GDP	MF	502	-	-	1/12/32/32	0/3/3/3
52	GDP	ID	502	-	-	0/12/32/32	0/3/3/3
52	GDP	UN	502	-	-	1/12/32/32	0/3/3/3
50	GTP	OO	501	-	-	9/18/38/38	0/3/3/3
52	GDP	KJ	502	-	-	1/12/32/32	0/3/3/3
52	GDP	OJ	502	-	-	4/12/32/32	0/3/3/3
52	GDP	FH	502	-	-	1/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	PC	501	-	-	8/18/38/38	0/3/3/3
50	GTP	LM	501	-	-	6/18/38/38	0/3/3/3
50	GTP	RO	501	-	-	8/18/38/38	0/3/3/3
52	GDP	AB	502	-	-	0/12/32/32	0/3/3/3
50	GTP	BM	501	-	-	7/18/38/38	0/3/3/3
50	GTP	CK	501	-	-	5/18/38/38	0/3/3/3
52	GDP	DJ	502	-	-	1/12/32/32	0/3/3/3
50	GTP	RC	501	-	-	8/18/38/38	0/3/3/3
52	GDP	CB	502	-	-	1/12/32/32	0/3/3/3
52	GDP	HF	502	-	-	0/12/32/32	0/3/3/3
50	GTP	DK	501	-	-	6/18/38/38	0/3/3/3
52	GDP	PF	502	-	-	1/12/32/32	0/3/3/3
50	GTP	AO	501	-	-	8/18/38/38	0/3/3/3
52	GDP	LH	502	-	-	3/12/32/32	0/3/3/3
50	GTP	OE	501	-	-	8/18/38/38	0/3/3/3
52	GDP	KL	502	-	-	1/12/32/32	0/3/3/3
50	GTP	UM	501	-	-	8/18/38/38	0/3/3/3
52	GDP	CN	502	-	-	1/12/32/32	0/3/3/3
52	GDP	GB	502	-	-	1/12/32/32	0/3/3/3
50	GTP	JI	501	-	-	8/18/38/38	0/3/3/3
52	GDP	EH	502	-	-	1/12/32/32	0/3/3/3
50	GTP	LC	501	-	-	6/18/38/38	0/3/3/3
52	GDP	LN	502	-	-	1/12/32/32	0/3/3/3
52	GDP	VH	502	-	-	1/12/32/32	0/3/3/3
52	GDP	SB	502	-	-	1/12/32/32	0/3/3/3
52	GDP	JJ	502	-	-	2/12/32/32	0/3/3/3
50	GTP	TE	501	-	-	8/18/38/38	0/3/3/3
52	GDP	HN	502	-	-	0/12/32/32	0/3/3/3
50	GTP	GM	501	-	-	6/18/38/38	0/3/3/3
52	GDP	AL	502	-	-	1/12/32/32	0/3/3/3
50	GTP	QO	501	-	-	7/18/38/38	0/3/3/3
52	GDP	OD	502	-	-	3/12/32/32	0/3/3/3
52	GDP	MD	502	-	-	4/12/32/32	0/3/3/3
50	GTP	CM	501	-	-	5/18/38/38	0/3/3/3
52	GDP	TJ	502	-	-	1/12/32/32	0/3/3/3
50	GTP	KO	501	-	-	5/18/38/38	0/3/3/3
52	GDP	CF	502	-	-	1/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
52	GDP	TN	502	-	-	1/12/32/32	0/3/3/3
50	GTP	FI	501	-	-	6/18/38/38	0/3/3/3
50	GTP	ME	501	-	-	4/18/38/38	0/3/3/3
52	GDP	NB	502	-	-	1/12/32/32	0/3/3/3
52	GDP	DP	502	-	-	4/12/32/32	0/3/3/3
52	GDP	FB	502	-	-	1/12/32/32	0/3/3/3
50	GTP	VE	501	-	-	7/18/38/38	0/3/3/3
50	GTP	VM	501	-	-	7/18/38/38	0/3/3/3
50	GTP	PO	501	-	-	8/18/38/38	0/3/3/3
52	GDP	MJ	502	-	-	1/12/32/32	0/3/3/3
52	GDP	QH	502	-	-	1/12/32/32	0/3/3/3
52	GDP	HL	502	-	-	1/12/32/32	0/3/3/3
52	GDP	KB	502	-	-	2/12/32/32	0/3/3/3
52	GDP	TL	502	-	-	1/12/32/32	0/3/3/3
50	GTP	BK	501	-	-	7/18/38/38	0/3/3/3
50	GTP	NK	501	-	-	9/18/38/38	0/3/3/3
50	GTP	QM	501	-	-	8/18/38/38	0/3/3/3
50	GTP	MG	501	-	-	6/18/38/38	0/3/3/3
52	GDP	UD	502	-	-	4/12/32/32	0/3/3/3
52	GDP	GF	502	-	-	0/12/32/32	0/3/3/3
50	GTP	FK	501	-	-	8/18/38/38	0/3/3/3
52	GDP	GN	502	-	-	1/12/32/32	0/3/3/3
52	GDP	RL	502	-	-	0/12/32/32	0/3/3/3
50	GTP	HM	501	-	-	7/18/38/38	0/3/3/3
50	GTP	MM	501	-	-	9/18/38/38	0/3/3/3
50	GTP	RK	501	-	-	9/18/38/38	0/3/3/3
50	GTP	EC	501	-	-	7/18/38/38	0/3/3/3
50	GTP	DI	501	-	-	7/18/38/38	0/3/3/3
52	GDP	NF	502	-	-	1/12/32/32	0/3/3/3
52	GDP	NH	502	-	-	2/12/32/32	0/3/3/3
50	GTP	UE	501	-	-	8/18/38/38	0/3/3/3
50	GTP	FC	501	-	-	7/18/38/38	0/3/3/3
50	GTP	OI	501	-	-	8/18/38/38	0/3/3/3
52	GDP	UB	502	-	-	1/12/32/32	0/3/3/3
50	GTP	EO	501	-	-	8/18/38/38	0/3/3/3
50	GTP	AA	501	-	-	8/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	HE	501	-	-	7/18/38/38	0/3/3/3
50	GTP	KC	501	-	-	5/18/38/38	0/3/3/3
52	GDP	RF	502	-	-	0/12/32/32	0/3/3/3
52	GDP	CP	502	-	-	1/12/32/32	0/3/3/3
52	GDP	EB	502	-	-	1/12/32/32	0/3/3/3
50	GTP	FE	501	-	-	5/18/38/38	0/3/3/3
50	GTP	CC	501	-	-	8/18/38/38	0/3/3/3
52	GDP	DH	502	-	-	0/12/32/32	0/3/3/3
50	GTP	SM	501	-	-	7/18/38/38	0/3/3/3
50	GTP	UK	501	-	-	9/18/38/38	0/3/3/3
50	GTP	LO	501	-	-	6/18/38/38	0/3/3/3
52	GDP	VD	502	-	-	1/12/32/32	0/3/3/3
50	GTP	LG	501	-	-	7/18/38/38	0/3/3/3
52	GDP	IB	502	-	-	2/12/32/32	0/3/3/3
50	GTP	IM	501	-	-	7/18/38/38	0/3/3/3
52	GDP	LF	502	-	-	2/12/32/32	0/3/3/3
50	GTP	NA	501	-	-	8/18/38/38	0/3/3/3
52	GDP	EF	502	-	-	1/12/32/32	0/3/3/3
50	GTP	EM	501	-	-	7/18/38/38	0/3/3/3
50	GTP	MC	501	-	-	6/18/38/38	0/3/3/3
52	GDP	BB	502	-	-	0/12/32/32	0/3/3/3
52	GDP	FF	502	-	-	1/12/32/32	0/3/3/3
52	GDP	NJ	502	-	-	1/12/32/32	0/3/3/3
52	GDP	MP	502	-	-	2/12/32/32	0/3/3/3
50	GTP	HO	501	-	-	7/18/38/38	0/3/3/3
52	GDP	CJ	502	-	-	1/12/32/32	0/3/3/3
52	GDP	BF	502	-	-	1/12/32/32	0/3/3/3
52	GDP	BJ	502	-	-	0/12/32/32	0/3/3/3
52	GDP	SJ	502	-	-	2/12/32/32	0/3/3/3
50	GTP	EE	501	-	-	7/18/38/38	0/3/3/3
52	GDP	WP	502	-	-	1/12/32/32	0/3/3/3
52	GDP	NP	502	-	-	1/12/32/32	0/3/3/3
50	GTP	BI	501	-	-	7/18/38/38	0/3/3/3
50	GTP	RI	501	-	-	7/18/38/38	0/3/3/3
52	GDP	HB	502	-	-	2/12/32/32	0/3/3/3
52	GDP	DB	502	-	-	1/12/32/32	0/3/3/3
50	GTP	IE	501	-	-	8/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
52	GDP	MB	502	-	-	1/12/32/32	0/3/3/3
50	GTP	TC	501	-	-	8/18/38/38	0/3/3/3
52	GDP	LB	502	-	-	1/12/32/32	0/3/3/3
52	GDP	GH	502	-	-	1/12/32/32	0/3/3/3
50	GTP	UG	501	-	-	9/18/38/38	0/3/3/3
50	GTP	TG	501	-	-	8/18/38/38	0/3/3/3
52	GDP	MN	502	-	-	2/12/32/32	0/3/3/3
50	GTP	FA	501	-	-	7/18/38/38	0/3/3/3
50	GTP	CQ	501	-	-	8/18/38/38	0/3/3/3
52	GDP	QB	502	-	-	1/12/32/32	0/3/3/3
50	GTP	DM	501	-	-	8/18/38/38	0/3/3/3
52	GDP	ND	502	-	-	2/12/32/32	0/3/3/3
50	GTP	GO	501	-	-	6/18/38/38	0/3/3/3
50	GTP	SG	501	-	-	8/18/38/38	0/3/3/3
50	GTP	AK	501	-	-	6/18/38/38	0/3/3/3
50	GTP	VI	501	-	-	8/18/38/38	0/3/3/3
50	GTP	MO	501	-	-	6/18/38/38	0/3/3/3
52	GDP	JL	502	-	-	1/12/32/32	0/3/3/3
50	GTP	NC	501	-	-	6/18/38/38	0/3/3/3
50	GTP	CO	501	-	-	8/18/38/38	0/3/3/3
52	GDP	WB	502	-	-	0/12/32/32	0/3/3/3
50	GTP	VG	501	-	-	8/18/38/38	0/3/3/3
52	GDP	CH	502	-	-	0/12/32/32	0/3/3/3
52	GDP	GL	502	-	-	1/12/32/32	0/3/3/3
50	GTP	WC	501	-	-	7/18/38/38	0/3/3/3
50	GTP	TI	501	-	-	8/18/38/38	0/3/3/3
52	GDP	VL	502	-	-	1/12/32/32	0/3/3/3
50	GTP	GA	501	-	-	8/18/38/38	0/3/3/3
50	GTP	BE	501	-	-	8/18/38/38	0/3/3/3
50	GTP	QC	501	-	-	8/18/38/38	0/3/3/3
50	GTP	NM	501	-	-	8/18/38/38	0/3/3/3
52	GDP	SN	502	-	-	1/12/32/32	0/3/3/3
52	GDP	JB	502	-	-	1/12/32/32	0/3/3/3
52	GDP	AP	502	-	-	1/12/32/32	0/3/3/3
52	GDP	TD	502	-	-	1/12/32/32	0/3/3/3
52	GDP	DF	502	-	-	0/12/32/32	0/3/3/3
52	GDP	RJ	502	-	-	0/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	RG	501	-	-	7/18/38/38	0/3/3/3
52	GDP	SH	502	-	-	1/12/32/32	0/3/3/3
50	GTP	LE	501	-	-	5/18/38/38	0/3/3/3
50	GTP	IA	501	-	-	8/18/38/38	0/3/3/3
52	GDP	OP	502	-	-	1/12/32/32	0/3/3/3
52	GDP	IJ	502	-	-	1/12/32/32	0/3/3/3
52	GDP	JH	502	-	-	0/12/32/32	0/3/3/3
50	GTP	TM	501	-	-	9/18/38/38	0/3/3/3
50	GTP	WE	501	-	-	7/18/38/38	0/3/3/3
52	GDP	TH	502	-	-	1/12/32/32	0/3/3/3
50	GTP	RM	501	-	-	7/18/38/38	0/3/3/3
52	GDP	SF	502	-	-	2/12/32/32	0/3/3/3
52	GDP	QP	502	-	-	0/12/32/32	0/3/3/3
50	GTP	PI	501	-	-	8/18/38/38	0/3/3/3
50	GTP	JK	501	-	-	4/18/38/38	0/3/3/3
52	GDP	KN	502	-	-	1/12/32/32	0/3/3/3
52	GDP	CD	502	-	-	1/12/32/32	0/3/3/3
50	GTP	IO	501	-	-	8/18/38/38	0/3/3/3
52	GDP	LJ	502	-	-	1/12/32/32	0/3/3/3
50	GTP	BG	501	-	-	6/18/38/38	0/3/3/3
50	GTP	WK	501	-	-	6/18/38/38	0/3/3/3
52	GDP	LL	502	-	-	3/12/32/32	0/3/3/3
52	GDP	DD	502	-	-	1/12/32/32	0/3/3/3
52	GDP	MH	502	-	-	4/12/32/32	0/3/3/3
52	GDP	PL	502	-	-	0/12/32/32	0/3/3/3
52	GDP	IF	502	-	-	1/12/32/32	0/3/3/3
52	GDP	KD	502	-	-	2/12/32/32	0/3/3/3
52	GDP	JN	502	-	-	1/12/32/32	0/3/3/3
52	GDP	LP	502	-	-	1/12/32/32	0/3/3/3
50	GTP	KE	501	-	-	7/18/38/38	0/3/3/3
50	GTP	GC	501	-	-	6/18/38/38	0/3/3/3
52	GDP	ML	502	-	-	3/12/32/32	0/3/3/3
52	GDP	DN	502	-	-	1/12/32/32	0/3/3/3
52	GDP	SD	502	-	-	2/12/32/32	0/3/3/3
52	GDP	PD	502	-	-	1/12/32/32	0/3/3/3
50	GTP	LI	501	-	-	7/18/38/38	0/3/3/3
50	GTP	JO	501	-	-	6/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	JE	501	-	-	6/18/38/38	0/3/3/3
52	GDP	LD	502	-	-	3/12/32/32	0/3/3/3
52	GDP	WH	502	-	-	0/12/32/32	0/3/3/3
52	GDP	AD	502	-	-	1/12/32/32	0/3/3/3
52	GDP	IL	502	-	-	0/12/32/32	0/3/3/3
52	GDP	ED	502	-	-	1/12/32/32	0/3/3/3
50	GTP	DE	501	-	-	7/18/38/38	0/3/3/3
52	GDP	AJ	502	-	-	1/12/32/32	0/3/3/3
52	GDP	ON	502	-	-	2/12/32/32	0/3/3/3
50	GTP	GI	501	-	-	4/18/38/38	0/3/3/3
52	GDP	UF	502	-	-	0/12/32/32	0/3/3/3
52	GDP	FN	502	-	-	1/12/32/32	0/3/3/3
50	GTP	TA	501	-	-	8/18/38/38	0/3/3/3
52	GDP	WJ	502	-	-	1/12/32/32	0/3/3/3
50	GTP	EI	501	-	-	7/18/38/38	0/3/3/3
50	GTP	WG	501	-	-	8/18/38/38	0/3/3/3
50	GTP	PM	501	-	-	8/18/38/38	0/3/3/3
52	GDP	SL	502	-	-	2/12/32/32	0/3/3/3
52	GDP	AH	502	-	-	1/12/32/32	0/3/3/3
52	GDP	WD	502	-	-	1/12/32/32	0/3/3/3
52	GDP	FD	502	-	-	0/12/32/32	0/3/3/3
50	GTP	BC	501	-	-	8/18/38/38	0/3/3/3
52	GDP	RP	502	-	-	0/12/32/32	0/3/3/3
50	GTP	AI	501	-	-	9/18/38/38	0/3/3/3
50	GTP	PK	501	-	-	7/18/38/38	0/3/3/3
50	GTP	DC	501	-	-	7/18/38/38	0/3/3/3
52	GDP	EN	502	-	-	1/12/32/32	0/3/3/3
52	GDP	TB	502	-	-	1/12/32/32	0/3/3/3
52	GDP	QN	502	-	-	1/12/32/32	0/3/3/3
50	GTP	GK	501	-	-	7/18/38/38	0/3/3/3
50	GTP	PG	501	-	-	8/18/38/38	0/3/3/3
50	GTP	FM	501	-	-	8/18/38/38	0/3/3/3
50	GTP	MA	501	-	-	6/18/38/38	0/3/3/3
50	GTP	KI	501	-	-	7/18/38/38	0/3/3/3
52	GDP	OH	502	-	-	2/12/32/32	0/3/3/3
52	GDP	BH	502	-	-	1/12/32/32	0/3/3/3
52	GDP	WN	502	-	-	0/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	NO	501	-	-	9/18/38/38	0/3/3/3
50	GTP	IG	501	-	-	8/18/38/38	0/3/3/3
52	GDP	JF	502	-	-	0/12/32/32	0/3/3/3
52	GDP	PN	502	-	-	3/12/32/32	0/3/3/3
50	GTP	TK	501	-	-	8/18/38/38	0/3/3/3
50	GTP	QE	501	-	-	7/18/38/38	0/3/3/3
52	GDP	BN	502	-	-	0/12/32/32	0/3/3/3
50	GTP	HG	501	-	-	9/18/38/38	0/3/3/3
50	GTP	HA	501	-	-	9/18/38/38	0/3/3/3
50	GTP	MK	501	-	-	6/18/38/38	0/3/3/3
50	GTP	HK	501	-	-	7/18/38/38	0/3/3/3
50	GTP	NE	501	-	-	7/18/38/38	0/3/3/3
52	GDP	VN	502	-	-	1/12/32/32	0/3/3/3
50	GTP	HI	501	-	-	9/18/38/38	0/3/3/3
52	GDP	UJ	502	-	-	1/12/32/32	0/3/3/3
50	GTP	AM	501	-	-	9/18/38/38	0/3/3/3
50	GTP	WA	501	-	-	8/18/38/38	0/3/3/3
50	GTP	MI	501	-	-	5/18/38/38	0/3/3/3
50	GTP	OA	501	-	-	7/18/38/38	0/3/3/3
52	GDP	QL	502	-	-	0/12/32/32	0/3/3/3
52	GDP	UH	502	-	-	1/12/32/32	0/3/3/3
52	GDP	GD	502	-	-	2/12/32/32	0/3/3/3
50	GTP	KM	501	-	-	5/18/38/38	0/3/3/3
52	GDP	IP	502	-	-	1/12/32/32	0/3/3/3
52	GDP	GJ	502	-	-	3/12/32/32	0/3/3/3
52	GDP	KP	502	-	-	2/12/32/32	0/3/3/3
52	GDP	PP	502	-	-	1/12/32/32	0/3/3/3
50	GTP	JC	501	-	-	7/18/38/38	0/3/3/3
50	GTP	VO	501	-	-	8/18/38/38	0/3/3/3
52	GDP	EJ	502	-	-	0/12/32/32	0/3/3/3
50	GTP	II	501	-	-	7/18/38/38	0/3/3/3
50	GTP	KA	501	-	-	5/18/38/38	0/3/3/3
52	GDP	WL	502	-	-	1/12/32/32	0/3/3/3
50	GTP	AC	501	-	-	6/18/38/38	0/3/3/3
50	GTP	DQ	501	-	-	8/18/38/38	0/3/3/3
50	GTP	PE	501	-	-	7/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	VC	501	-	-	8/18/38/38	0/3/3/3
50	GTP	FO	501	-	-	9/18/38/38	0/3/3/3
50	GTP	GE	501	-	-	7/18/38/38	0/3/3/3
50	GTP	JQ	501	-	-	6/18/38/38	0/3/3/3
52	GDP	AF	502	-	-	0/12/32/32	0/3/3/3
52	GDP	KH	502	-	-	1/12/32/32	0/3/3/3
52	GDP	PB	502	-	-	1/12/32/32	0/3/3/3
52	GDP	RH	502	-	-	1/12/32/32	0/3/3/3
50	GTP	VK	501	-	-	7/18/38/38	0/3/3/3
52	GDP	BP	502	-	-	1/12/32/32	0/3/3/3
52	GDP	PH	502	-	-	1/12/32/32	0/3/3/3
52	GDP	NN	502	-	-	4/12/32/32	0/3/3/3
50	GTP	DO	501	-	-	8/18/38/38	0/3/3/3
50	GTP	QI	501	-	-	8/18/38/38	0/3/3/3
50	GTP	EK	501	-	-	6/18/38/38	0/3/3/3
50	GTP	LA	501	-	-	6/18/38/38	0/3/3/3
50	GTP	CE	501	-	-	6/18/38/38	0/3/3/3
52	GDP	AN	502	-	-	0/12/32/32	0/3/3/3
50	GTP	HC	501	-	-	9/18/38/38	0/3/3/3
50	GTP	QG	501	-	-	8/18/38/38	0/3/3/3
52	GDP	BD	502	-	-	1/12/32/32	0/3/3/3
50	GTP	UC	501	-	-	8/18/38/38	0/3/3/3
52	GDP	RD	502	-	-	0/12/32/32	0/3/3/3
52	GDP	VF	502	-	-	1/12/32/32	0/3/3/3
52	GDP	UL	502	-	-	1/12/32/32	0/3/3/3
52	GDP	OF	502	-	-	3/12/32/32	0/3/3/3
50	GTP	NI	501	-	-	8/18/38/38	0/3/3/3
52	GDP	HP	502	-	-	1/12/32/32	0/3/3/3
50	GTP	RE	501	-	-	8/18/38/38	0/3/3/3
50	GTP	QK	501	-	-	8/18/38/38	0/3/3/3
50	GTP	EA	501	-	-	7/18/38/38	0/3/3/3
50	GTP	UA	501	-	-	8/18/38/38	0/3/3/3
52	GDP	HJ	502	-	-	0/12/32/32	0/3/3/3
52	GDP	QF	502	-	-	1/12/32/32	0/3/3/3
50	GTP	GG	501	-	-	6/18/38/38	0/3/3/3
52	GDP	PJ	502	-	-	1/12/32/32	0/3/3/3
52	GDP	QJ	502	-	-	0/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	UO	501	-	-	7/18/38/38	0/3/3/3
52	GDP	OB	502	-	-	4/12/32/32	0/3/3/3
50	GTP	IK	501	-	-	7/18/38/38	0/3/3/3
52	GDP	EL	502	-	-	1/12/32/32	0/3/3/3
52	GDP	KF	502	-	-	1/12/32/32	0/3/3/3
50	GTP	FG	501	-	-	6/18/38/38	0/3/3/3
50	GTP	KG	501	-	-	5/18/38/38	0/3/3/3
52	GDP	TF	502	-	-	1/12/32/32	0/3/3/3
50	GTP	SC	501	-	-	7/18/38/38	0/3/3/3
52	GDP	CL	502	-	-	1/12/32/32	0/3/3/3
50	GTP	CI	501	-	-	5/18/38/38	0/3/3/3
50	GTP	KK	501	-	-	6/18/38/38	0/3/3/3
50	GTP	WO	501	-	-	6/18/38/38	0/3/3/3
52	GDP	JP	502	-	-	0/12/32/32	0/3/3/3
52	GDP	IN	502	-	-	1/12/32/32	0/3/3/3

All (526) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	LC	501	GTP	C5-C6	-4.36	1.38	1.47
50	NG	501	GTP	C5-C6	-4.35	1.38	1.47
50	HG	501	GTP	C5-C6	-4.29	1.38	1.47
50	KI	501	GTP	C5-C6	-4.28	1.38	1.47
50	LG	501	GTP	C5-C6	-4.28	1.38	1.47
50	KE	501	GTP	C5-C6	-4.27	1.38	1.47
50	MI	501	GTP	C5-C6	-4.27	1.38	1.47
50	LK	501	GTP	C5-C6	-4.26	1.38	1.47
50	LE	501	GTP	C5-C6	-4.26	1.38	1.47
50	MG	501	GTP	C5-C6	-4.26	1.38	1.47
50	MO	501	GTP	C5-C6	-4.24	1.38	1.47
50	KG	501	GTP	C5-C6	-4.23	1.38	1.47
50	KC	501	GTP	C5-C6	-4.22	1.38	1.47
50	BE	501	GTP	C5-C6	-4.21	1.38	1.47
50	BM	501	GTP	C5-C6	-4.20	1.38	1.47
50	FK	501	GTP	C5-C6	-4.20	1.38	1.47
50	HO	501	GTP	C5-C6	-4.20	1.38	1.47
50	BI	501	GTP	C5-C6	-4.20	1.38	1.47
50	LI	501	GTP	C5-C6	-4.20	1.38	1.47
50	MM	501	GTP	C5-C6	-4.20	1.38	1.47
50	GM	501	GTP	C5-C6	-4.19	1.38	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	KK	501	GTP	C5-C6	-4.19	1.38	1.47
50	EE	501	GTP	C5-C6	-4.18	1.38	1.47
50	AE	501	GTP	C5-C6	-4.17	1.38	1.47
50	AC	501	GTP	C5-C6	-4.17	1.38	1.47
50	EO	501	GTP	C5-C6	-4.17	1.39	1.47
50	EI	501	GTP	C5-C6	-4.16	1.39	1.47
50	FO	501	GTP	C5-C6	-4.16	1.39	1.47
50	LO	501	GTP	C5-C6	-4.16	1.39	1.47
50	GI	501	GTP	C5-C6	-4.16	1.39	1.47
50	FC	501	GTP	C5-C6	-4.16	1.39	1.47
50	MA	501	GTP	C5-C6	-4.15	1.39	1.47
50	EM	501	GTP	C5-C6	-4.15	1.39	1.47
50	GK	501	GTP	C5-C6	-4.15	1.39	1.47
50	EG	501	GTP	C5-C6	-4.15	1.39	1.47
50	BK	501	GTP	C5-C6	-4.15	1.39	1.47
50	II	501	GTP	C5-C6	-4.14	1.39	1.47
50	HK	501	GTP	C5-C6	-4.14	1.39	1.47
50	HM	501	GTP	C5-C6	-4.14	1.39	1.47
50	FI	501	GTP	C5-C6	-4.14	1.39	1.47
50	NO	501	GTP	C5-C6	-4.14	1.39	1.47
50	AG	501	GTP	C5-C6	-4.14	1.39	1.47
50	FM	501	GTP	C5-C6	-4.13	1.39	1.47
50	MK	501	GTP	C5-C6	-4.13	1.39	1.47
50	DK	501	GTP	C5-C6	-4.13	1.39	1.47
50	HI	501	GTP	C5-C6	-4.13	1.39	1.47
50	KM	501	GTP	C5-C6	-4.13	1.39	1.47
50	WM	501	GTP	C5-C6	-4.13	1.39	1.47
50	GE	501	GTP	C5-C6	-4.13	1.39	1.47
50	CI	501	GTP	C5-C6	-4.13	1.39	1.47
50	CM	501	GTP	C5-C6	-4.13	1.39	1.47
50	QG	501	GTP	C5-C6	-4.12	1.39	1.47
50	JI	501	GTP	C5-C6	-4.12	1.39	1.47
50	IE	501	GTP	C5-C6	-4.12	1.39	1.47
50	MC	501	GTP	C5-C6	-4.11	1.39	1.47
50	AK	501	GTP	C5-C6	-4.11	1.39	1.47
50	AI	501	GTP	C5-C6	-4.11	1.39	1.47
50	KO	501	GTP	C5-C6	-4.11	1.39	1.47
50	HC	501	GTP	C5-C6	-4.10	1.39	1.47
50	LM	501	GTP	C5-C6	-4.10	1.39	1.47
50	NE	501	GTP	C5-C6	-4.10	1.39	1.47
50	DM	501	GTP	C5-C6	-4.10	1.39	1.47
50	EK	501	GTP	C5-C6	-4.10	1.39	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	FG	501	GTP	C5-C6	-4.10	1.39	1.47
50	SK	501	GTP	C5-C6	-4.09	1.39	1.47
50	BG	501	GTP	C5-C6	-4.09	1.39	1.47
50	KA	501	GTP	C5-C6	-4.09	1.39	1.47
50	AO	501	GTP	C5-C6	-4.09	1.39	1.47
50	FE	501	GTP	C5-C6	-4.09	1.39	1.47
50	UI	501	GTP	C5-C6	-4.08	1.39	1.47
50	SI	501	GTP	C5-C6	-4.08	1.39	1.47
50	TC	501	GTP	C5-C6	-4.08	1.39	1.47
50	DE	501	GTP	C5-C6	-4.08	1.39	1.47
50	JK	501	GTP	C5-C6	-4.08	1.39	1.47
50	SC	501	GTP	C5-C6	-4.08	1.39	1.47
50	BO	501	GTP	C5-C6	-4.08	1.39	1.47
50	NI	501	GTP	C5-C6	-4.08	1.39	1.47
50	AM	501	GTP	C5-C6	-4.07	1.39	1.47
50	OK	501	GTP	C5-C6	-4.07	1.39	1.47
50	VI	501	GTP	C5-C6	-4.07	1.39	1.47
50	OG	501	GTP	C5-C6	-4.07	1.39	1.47
50	UE	501	GTP	C5-C6	-4.07	1.39	1.47
50	NK	501	GTP	C5-C6	-4.07	1.39	1.47
50	CK	501	GTP	C5-C6	-4.07	1.39	1.47
50	LA	501	GTP	C5-C6	-4.06	1.39	1.47
50	GO	501	GTP	C5-C6	-4.06	1.39	1.47
50	ME	501	GTP	C5-C6	-4.06	1.39	1.47
50	CO	501	GTP	C5-C6	-4.06	1.39	1.47
50	DI	501	GTP	C5-C6	-4.06	1.39	1.47
50	CC	501	GTP	C5-C6	-4.06	1.39	1.47
50	IM	501	GTP	C5-C6	-4.06	1.39	1.47
50	RG	501	GTP	C5-C6	-4.06	1.39	1.47
50	UG	501	GTP	C5-C6	-4.05	1.39	1.47
50	RM	501	GTP	C5-C6	-4.05	1.39	1.47
50	OM	501	GTP	C5-C6	-4.05	1.39	1.47
50	UO	501	GTP	C5-C6	-4.05	1.39	1.47
50	DQ	501	GTP	C5-C6	-4.05	1.39	1.47
50	TK	501	GTP	C5-C6	-4.05	1.39	1.47
50	RI	501	GTP	C5-C6	-4.05	1.39	1.47
50	OI	501	GTP	C5-C6	-4.04	1.39	1.47
50	DO	501	GTP	C5-C6	-4.04	1.39	1.47
50	WG	501	GTP	C5-C6	-4.04	1.39	1.47
50	HA	501	GTP	C5-C6	-4.04	1.39	1.47
50	RK	501	GTP	C5-C6	-4.04	1.39	1.47
50	CE	501	GTP	C5-C6	-4.04	1.39	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	EA	501	GTP	C5-C6	-4.04	1.39	1.47
50	PI	501	GTP	C5-C6	-4.04	1.39	1.47
50	TM	501	GTP	C5-C6	-4.04	1.39	1.47
50	RO	501	GTP	C5-C6	-4.04	1.39	1.47
50	SG	501	GTP	C5-C6	-4.04	1.39	1.47
50	EC	501	GTP	C5-C6	-4.03	1.39	1.47
50	CQ	501	GTP	C5-C6	-4.03	1.39	1.47
50	WI	501	GTP	C5-C6	-4.03	1.39	1.47
50	UM	501	GTP	C5-C6	-4.03	1.39	1.47
50	DG	501	GTP	C5-C6	-4.03	1.39	1.47
50	VC	501	GTP	C5-C6	-4.03	1.39	1.47
50	CG	501	GTP	C5-C6	-4.03	1.39	1.47
50	UK	501	GTP	C5-C6	-4.03	1.39	1.47
50	VM	501	GTP	C5-C6	-4.03	1.39	1.47
50	WK	501	GTP	C5-C6	-4.02	1.39	1.47
50	GC	501	GTP	C5-C6	-4.02	1.39	1.47
50	NC	501	GTP	C5-C6	-4.02	1.39	1.47
50	PE	501	GTP	C5-C6	-4.02	1.39	1.47
50	WO	501	GTP	C5-C6	-4.02	1.39	1.47
50	UC	501	GTP	C5-C6	-4.02	1.39	1.47
50	DC	501	GTP	C5-C6	-4.02	1.39	1.47
50	FA	501	GTP	C5-C6	-4.02	1.39	1.47
50	SE	501	GTP	C5-C6	-4.02	1.39	1.47
50	VK	501	GTP	C5-C6	-4.01	1.39	1.47
50	TE	501	GTP	C5-C6	-4.01	1.39	1.47
50	WE	501	GTP	C5-C6	-4.01	1.39	1.47
50	TI	501	GTP	C5-C6	-4.01	1.39	1.47
50	IA	501	GTP	C5-C6	-4.01	1.39	1.47
50	UA	501	GTP	C5-C6	-4.01	1.39	1.47
50	OO	501	GTP	C5-C6	-4.01	1.39	1.47
50	VG	501	GTP	C5-C6	-4.01	1.39	1.47
50	VO	501	GTP	C5-C6	-4.00	1.39	1.47
50	QE	501	GTP	C5-C6	-4.00	1.39	1.47
50	AA	501	GTP	C5-C6	-3.99	1.39	1.47
50	HE	501	GTP	C5-C6	-3.99	1.39	1.47
50	QI	501	GTP	C5-C6	-3.99	1.39	1.47
50	RC	501	GTP	C5-C6	-3.99	1.39	1.47
50	TG	501	GTP	C5-C6	-3.99	1.39	1.47
50	IC	501	GTP	C5-C6	-3.99	1.39	1.47
50	NA	501	GTP	C5-C6	-3.99	1.39	1.47
50	SM	501	GTP	C5-C6	-3.99	1.39	1.47
50	WC	501	GTP	C5-C6	-3.99	1.39	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	IG	501	GTP	C5-C6	-3.98	1.39	1.47
50	GG	501	GTP	C5-C6	-3.98	1.39	1.47
50	SA	501	GTP	C5-C6	-3.97	1.39	1.47
50	JM	501	GTP	C5-C6	-3.97	1.39	1.47
50	GA	501	GTP	C5-C6	-3.97	1.39	1.47
50	VE	501	GTP	C5-C6	-3.97	1.39	1.47
50	IK	501	GTP	C5-C6	-3.97	1.39	1.47
50	JE	501	GTP	C5-C6	-3.97	1.39	1.47
50	WA	501	GTP	C5-C6	-3.97	1.39	1.47
50	PM	501	GTP	C5-C6	-3.96	1.39	1.47
50	QM	501	GTP	C5-C6	-3.96	1.39	1.47
50	RE	501	GTP	C5-C6	-3.96	1.39	1.47
50	NM	501	GTP	C5-C6	-3.96	1.39	1.47
50	OE	501	GTP	C5-C6	-3.96	1.39	1.47
50	PK	501	GTP	C5-C6	-3.95	1.39	1.47
50	OA	501	GTP	C5-C6	-3.95	1.39	1.47
50	VA	501	GTP	C5-C6	-3.95	1.39	1.47
50	QK	501	GTP	C5-C6	-3.95	1.39	1.47
50	TA	501	GTP	C5-C6	-3.95	1.39	1.47
50	OC	501	GTP	C5-C6	-3.94	1.39	1.47
50	QC	501	GTP	C5-C6	-3.94	1.39	1.47
50	IO	501	GTP	C5-C6	-3.94	1.39	1.47
50	JQ	501	GTP	C5-C6	-3.94	1.39	1.47
50	PC	501	GTP	C5-C6	-3.93	1.39	1.47
50	JC	501	GTP	C5-C6	-3.93	1.39	1.47
50	JG	501	GTP	C5-C6	-3.92	1.39	1.47
50	PO	501	GTP	C5-C6	-3.92	1.39	1.47
50	BC	501	GTP	C5-C6	-3.82	1.39	1.47
50	JO	501	GTP	C5-C6	-3.80	1.39	1.47
50	QO	501	GTP	C5-C6	-3.76	1.39	1.47
50	PG	501	GTP	C5-C6	-3.73	1.39	1.47
52	GD	502	GDP	C6-N1	-3.00	1.33	1.37
52	JH	502	GDP	C6-N1	-2.87	1.33	1.37
52	KH	502	GDP	C6-N1	-2.72	1.33	1.37
52	AD	502	GDP	C6-N1	-2.68	1.33	1.37
52	KJ	502	GDP	C6-N1	-2.68	1.33	1.37
52	OB	502	GDP	C6-N1	-2.66	1.33	1.37
52	PN	502	GDP	C6-N1	-2.65	1.33	1.37
52	LB	502	GDP	C6-N1	-2.64	1.33	1.37
52	KL	502	GDP	C6-N1	-2.63	1.34	1.37
52	DL	502	GDP	C6-N1	-2.62	1.34	1.37
52	IL	502	GDP	C6-N1	-2.58	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	IJ	502	GDP	C6-N1	-2.58	1.34	1.37
52	IN	502	GDP	C6-N1	-2.58	1.34	1.37
52	DJ	502	GDP	C6-N1	-2.58	1.34	1.37
52	NL	502	GDP	C6-N1	-2.57	1.34	1.37
52	CN	502	GDP	C6-N1	-2.56	1.34	1.37
52	GL	502	GDP	C6-N1	-2.55	1.34	1.37
52	BF	502	GDP	C6-N1	-2.55	1.34	1.37
52	CL	502	GDP	C6-N1	-2.55	1.34	1.37
52	AJ	502	GDP	C6-N1	-2.55	1.34	1.37
52	KB	502	GDP	C6-N1	-2.55	1.34	1.37
52	LJ	502	GDP	C6-N1	-2.54	1.34	1.37
52	FL	502	GDP	C6-N1	-2.54	1.34	1.37
52	CH	502	GDP	C6-N1	-2.53	1.34	1.37
52	EJ	502	GDP	C6-N1	-2.53	1.34	1.37
52	MD	502	GDP	C6-N1	-2.53	1.34	1.37
50	VI	501	GTP	C2-N3	2.53	1.39	1.33
52	HN	502	GDP	C6-N1	-2.53	1.34	1.37
52	LD	502	GDP	C6-N1	-2.53	1.34	1.37
52	DN	502	GDP	C6-N1	-2.53	1.34	1.37
52	NF	502	GDP	C6-N1	-2.53	1.34	1.37
52	LF	502	GDP	C6-N1	-2.52	1.34	1.37
52	CF	502	GDP	C6-N1	-2.52	1.34	1.37
52	JL	502	GDP	C6-N1	-2.52	1.34	1.37
52	ID	502	GDP	C6-N1	-2.52	1.34	1.37
52	KD	502	GDP	C6-N1	-2.52	1.34	1.37
52	JN	502	GDP	C6-N1	-2.51	1.34	1.37
52	AH	502	GDP	C6-N1	-2.51	1.34	1.37
52	WJ	502	GDP	C6-N1	-2.51	1.34	1.37
52	CJ	502	GDP	C6-N1	-2.50	1.34	1.37
52	EL	502	GDP	C6-N1	-2.49	1.34	1.37
52	UB	502	GDP	C6-N1	-2.49	1.34	1.37
52	RH	502	GDP	C6-N1	-2.49	1.34	1.37
52	EH	502	GDP	C6-N1	-2.49	1.34	1.37
52	DH	502	GDP	C6-N1	-2.49	1.34	1.37
52	FD	502	GDP	C6-N1	-2.49	1.34	1.37
52	FF	502	GDP	C6-N1	-2.49	1.34	1.37
52	PP	502	GDP	C6-N1	-2.48	1.34	1.37
52	IH	502	GDP	C6-N1	-2.48	1.34	1.37
52	CD	502	GDP	C6-N1	-2.48	1.34	1.37
52	GJ	502	GDP	C6-N1	-2.48	1.34	1.37
52	DF	502	GDP	C6-N1	-2.48	1.34	1.37
52	FH	502	GDP	C6-N1	-2.48	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	OH	502	GDP	C6-N1	-2.48	1.34	1.37
52	HH	502	GDP	C6-N1	-2.48	1.34	1.37
52	SL	502	GDP	C6-N1	-2.48	1.34	1.37
52	WD	502	GDP	C6-N1	-2.48	1.34	1.37
52	GH	502	GDP	C6-N1	-2.47	1.34	1.37
52	BD	502	GDP	C6-N1	-2.47	1.34	1.37
52	RL	502	GDP	C6-N1	-2.47	1.34	1.37
52	UF	502	GDP	C6-N1	-2.47	1.34	1.37
52	RF	502	GDP	C6-N1	-2.47	1.34	1.37
52	KF	502	GDP	C6-N1	-2.46	1.34	1.37
52	WF	502	GDP	C6-N1	-2.46	1.34	1.37
52	QD	502	GDP	C6-N1	-2.46	1.34	1.37
52	GF	502	GDP	C6-N1	-2.46	1.34	1.37
52	BN	502	GDP	C6-N1	-2.46	1.34	1.37
52	WN	502	GDP	C6-N1	-2.46	1.34	1.37
52	MH	502	GDP	C6-N1	-2.46	1.34	1.37
52	AF	502	GDP	C6-N1	-2.46	1.34	1.37
52	HF	502	GDP	C6-N1	-2.45	1.34	1.37
52	LL	502	GDP	C6-N1	-2.45	1.34	1.37
52	HL	502	GDP	C6-N1	-2.45	1.34	1.37
52	NJ	502	GDP	C6-N1	-2.45	1.34	1.37
52	VJ	502	GDP	C6-N1	-2.45	1.34	1.37
52	FN	502	GDP	C6-N1	-2.45	1.34	1.37
52	MJ	502	GDP	C6-N1	-2.45	1.34	1.37
52	IF	502	GDP	C6-N1	-2.45	1.34	1.37
52	ML	502	GDP	C6-N1	-2.45	1.34	1.37
52	VD	502	GDP	C6-N1	-2.45	1.34	1.37
52	MP	502	GDP	C6-N1	-2.45	1.34	1.37
52	RP	502	GDP	C6-N1	-2.44	1.34	1.37
52	ED	502	GDP	C6-N1	-2.44	1.34	1.37
52	MF	502	GDP	C6-N1	-2.44	1.34	1.37
52	PJ	502	GDP	C6-N1	-2.44	1.34	1.37
52	OJ	502	GDP	C6-N1	-2.44	1.34	1.37
52	SB	502	GDP	C6-N1	-2.44	1.34	1.37
52	TH	502	GDP	C6-N1	-2.44	1.34	1.37
52	VH	502	GDP	C6-N1	-2.44	1.34	1.37
52	AP	502	GDP	C6-N1	-2.44	1.34	1.37
52	KP	502	GDP	C6-N1	-2.44	1.34	1.37
52	QF	502	GDP	C6-N1	-2.44	1.34	1.37
52	AL	502	GDP	C6-N1	-2.43	1.34	1.37
52	DP	502	GDP	C6-N1	-2.43	1.34	1.37
52	MN	502	GDP	C6-N1	-2.43	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	PB	502	GDP	C6-N1	-2.43	1.34	1.37
52	GB	502	GDP	C6-N1	-2.43	1.34	1.37
52	UJ	502	GDP	C6-N1	-2.43	1.34	1.37
52	OL	502	GDP	C6-N1	-2.43	1.34	1.37
52	BL	502	GDP	C6-N1	-2.43	1.34	1.37
52	NB	502	GDP	C6-N1	-2.43	1.34	1.37
52	BP	502	GDP	C6-N1	-2.43	1.34	1.37
52	IB	502	GDP	C6-N1	-2.43	1.34	1.37
50	QG	501	GTP	C2-N3	2.43	1.39	1.33
52	PH	502	GDP	C6-N1	-2.43	1.34	1.37
52	BB	502	GDP	C6-N1	-2.43	1.34	1.37
52	BJ	502	GDP	C6-N1	-2.43	1.34	1.37
52	LH	502	GDP	C6-N1	-2.42	1.34	1.37
52	NN	502	GDP	C6-N1	-2.42	1.34	1.37
52	EN	502	GDP	C6-N1	-2.42	1.34	1.37
52	BH	502	GDP	C6-N1	-2.42	1.34	1.37
52	TL	502	GDP	C6-N1	-2.42	1.34	1.37
52	AB	502	GDP	C6-N1	-2.42	1.34	1.37
52	PL	502	GDP	C6-N1	-2.42	1.34	1.37
52	TJ	502	GDP	C6-N1	-2.42	1.34	1.37
52	RJ	502	GDP	C6-N1	-2.42	1.34	1.37
52	UH	502	GDP	C6-N1	-2.42	1.34	1.37
52	DD	502	GDP	C6-N1	-2.42	1.34	1.37
52	ON	502	GDP	C6-N1	-2.42	1.34	1.37
52	PD	502	GDP	C6-N1	-2.42	1.34	1.37
52	GN	502	GDP	C6-N1	-2.41	1.34	1.37
52	PF	502	GDP	C6-N1	-2.41	1.34	1.37
52	LN	502	GDP	C6-N1	-2.41	1.34	1.37
52	TN	502	GDP	C6-N1	-2.41	1.34	1.37
52	EF	502	GDP	C6-N1	-2.41	1.34	1.37
52	JP	502	GDP	C6-N1	-2.41	1.34	1.37
52	JB	502	GDP	C6-N1	-2.41	1.34	1.37
52	WL	502	GDP	C6-N1	-2.41	1.34	1.37
52	JD	502	GDP	C6-N1	-2.41	1.34	1.37
52	WB	502	GDP	C6-N1	-2.40	1.34	1.37
52	CP	502	GDP	C6-N1	-2.40	1.34	1.37
52	TF	502	GDP	C6-N1	-2.40	1.34	1.37
52	HP	502	GDP	C6-N1	-2.40	1.34	1.37
52	NH	502	GDP	C6-N1	-2.40	1.34	1.37
52	CB	502	GDP	C6-N1	-2.40	1.34	1.37
52	OP	502	GDP	C6-N1	-2.40	1.34	1.37
52	OF	502	GDP	C6-N1	-2.40	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	QH	502	GDP	C6-N1	-2.40	1.34	1.37
52	QL	502	GDP	C6-N1	-2.40	1.34	1.37
52	RN	502	GDP	C6-N1	-2.39	1.34	1.37
52	VL	502	GDP	C6-N1	-2.39	1.34	1.37
52	IP	502	GDP	C6-N1	-2.39	1.34	1.37
52	SJ	502	GDP	C6-N1	-2.39	1.34	1.37
52	UN	502	GDP	C6-N1	-2.39	1.34	1.37
52	ND	502	GDP	C6-N1	-2.38	1.34	1.37
52	UL	502	GDP	C6-N1	-2.38	1.34	1.37
52	JJ	502	GDP	C6-N1	-2.38	1.34	1.37
52	SH	502	GDP	C6-N1	-2.38	1.34	1.37
52	WH	502	GDP	C6-N1	-2.38	1.34	1.37
52	QN	502	GDP	C6-N1	-2.38	1.34	1.37
52	OD	502	GDP	C6-N1	-2.38	1.34	1.37
52	AN	502	GDP	C6-N1	-2.38	1.34	1.37
52	EB	502	GDP	C6-N1	-2.38	1.34	1.37
52	HD	502	GDP	C6-N1	-2.38	1.34	1.37
52	NP	502	GDP	C6-N1	-2.38	1.34	1.37
52	LP	502	GDP	C6-N1	-2.38	1.34	1.37
52	QJ	502	GDP	C6-N1	-2.37	1.34	1.37
52	DB	502	GDP	C6-N1	-2.37	1.34	1.37
52	UD	502	GDP	C6-N1	-2.37	1.34	1.37
52	TD	502	GDP	C6-N1	-2.36	1.34	1.37
52	VF	502	GDP	C6-N1	-2.36	1.34	1.37
52	KN	502	GDP	C6-N1	-2.35	1.34	1.37
52	SN	502	GDP	C6-N1	-2.35	1.34	1.37
52	SF	502	GDP	C6-N1	-2.35	1.34	1.37
52	FB	502	GDP	C6-N1	-2.35	1.34	1.37
52	RD	502	GDP	C6-N1	-2.35	1.34	1.37
52	WP	502	GDP	C6-N1	-2.34	1.34	1.37
52	VB	502	GDP	C6-N1	-2.34	1.34	1.37
52	HB	502	GDP	C6-N1	-2.34	1.34	1.37
52	HJ	502	GDP	C6-N1	-2.33	1.34	1.37
52	SD	502	GDP	C6-N1	-2.32	1.34	1.37
52	VN	502	GDP	C6-N1	-2.32	1.34	1.37
52	QB	502	GDP	C6-N1	-2.32	1.34	1.37
50	JO	501	GTP	C2-N3	2.32	1.38	1.33
50	IE	501	GTP	C2-N3	2.32	1.38	1.33
50	VK	501	GTP	C2-N3	2.31	1.38	1.33
50	UO	501	GTP	C2-N3	2.30	1.38	1.33
52	QP	502	GDP	C6-N1	-2.30	1.34	1.37
50	CK	501	GTP	C2-N3	2.28	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	WE	501	GTP	C2-N3	2.28	1.38	1.33
50	RM	501	GTP	C2-N3	2.27	1.38	1.33
50	UM	501	GTP	C2-N3	2.27	1.38	1.33
50	HA	501	GTP	C2-N3	2.26	1.38	1.33
50	IK	501	GTP	C2-N3	2.26	1.38	1.33
50	UK	501	GTP	C2-N3	2.26	1.38	1.33
50	FO	501	GTP	C2-N3	2.26	1.38	1.33
50	VM	501	GTP	C2-N3	2.26	1.38	1.33
50	WO	501	GTP	C2-N3	2.26	1.38	1.33
50	RK	501	GTP	C2-N3	2.25	1.38	1.33
50	GC	501	GTP	C2-N3	2.25	1.38	1.33
50	QC	501	GTP	C2-N3	2.25	1.38	1.33
50	CQ	501	GTP	C2-N3	2.25	1.38	1.33
50	VG	501	GTP	C2-N3	2.25	1.38	1.33
50	VA	501	GTP	C2-N3	2.25	1.38	1.33
50	IO	501	GTP	C2-N3	2.25	1.38	1.33
50	RI	501	GTP	C2-N3	2.24	1.38	1.33
50	RC	501	GTP	C2-N3	2.24	1.38	1.33
50	SC	501	GTP	C2-N3	2.24	1.38	1.33
52	TB	502	GDP	C6-N1	-2.24	1.34	1.37
50	IG	501	GTP	C2-N3	2.24	1.38	1.33
50	HK	501	GTP	C2-N3	2.24	1.38	1.33
50	TC	501	GTP	C2-N3	2.24	1.38	1.33
50	QE	501	GTP	C2-N3	2.24	1.38	1.33
50	VE	501	GTP	C2-N3	2.24	1.38	1.33
50	GM	501	GTP	C2-N3	2.23	1.38	1.33
50	PE	501	GTP	C2-N3	2.23	1.38	1.33
50	LA	501	GTP	C2-N3	2.23	1.38	1.33
50	CM	501	GTP	C2-N3	2.23	1.38	1.33
50	QI	501	GTP	C2-N3	2.23	1.38	1.33
50	AO	501	GTP	C2-N3	2.23	1.38	1.33
50	RO	501	GTP	C2-N3	2.22	1.38	1.33
50	JK	501	GTP	C2-N3	2.22	1.38	1.33
50	SG	501	GTP	C2-N3	2.22	1.38	1.33
50	OA	501	GTP	C2-N3	2.22	1.38	1.33
50	SE	501	GTP	C2-N3	2.22	1.38	1.33
50	VO	501	GTP	C2-N3	2.22	1.38	1.33
50	UA	501	GTP	C2-N3	2.21	1.38	1.33
50	WI	501	GTP	C2-N3	2.21	1.38	1.33
50	IA	501	GTP	C2-N3	2.21	1.38	1.33
50	TA	501	GTP	C2-N3	2.21	1.38	1.33
50	RG	501	GTP	C2-N3	2.21	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	DK	501	GTP	C2-N3	2.21	1.38	1.33
50	BC	501	GTP	C2-N3	2.21	1.38	1.33
50	SK	501	GTP	C2-N3	2.20	1.38	1.33
50	DM	501	GTP	C2-N3	2.20	1.38	1.33
50	VC	501	GTP	C2-N3	2.20	1.38	1.33
50	IC	501	GTP	C2-N3	2.20	1.38	1.33
50	NE	501	GTP	C2-N3	2.20	1.38	1.33
50	UE	501	GTP	C2-N3	2.20	1.38	1.33
50	II	501	GTP	C2-N3	2.20	1.38	1.33
50	EE	501	GTP	C2-N3	2.20	1.38	1.33
50	WA	501	GTP	C2-N3	2.20	1.38	1.33
50	PI	501	GTP	C2-N3	2.20	1.38	1.33
50	OK	501	GTP	C2-N3	2.20	1.38	1.33
50	GA	501	GTP	C2-N3	2.20	1.38	1.33
50	OE	501	GTP	C2-N3	2.20	1.38	1.33
50	EA	501	GTP	C2-N3	2.19	1.38	1.33
50	PO	501	GTP	C2-N3	2.19	1.38	1.33
50	CG	501	GTP	C2-N3	2.19	1.38	1.33
50	QM	501	GTP	C2-N3	2.19	1.38	1.33
50	DQ	501	GTP	C2-N3	2.19	1.38	1.33
50	CO	501	GTP	C2-N3	2.19	1.38	1.33
50	OG	501	GTP	C2-N3	2.19	1.38	1.33
50	WC	501	GTP	C2-N3	2.19	1.38	1.33
50	CE	501	GTP	C2-N3	2.19	1.38	1.33
50	DC	501	GTP	C2-N3	2.19	1.38	1.33
50	NO	501	GTP	C2-N3	2.19	1.38	1.33
50	CC	501	GTP	C2-N3	2.18	1.38	1.33
50	EK	501	GTP	C2-N3	2.18	1.38	1.33
50	UI	501	GTP	C2-N3	2.18	1.38	1.33
50	LM	501	GTP	C2-N3	2.18	1.38	1.33
50	FG	501	GTP	C2-N3	2.18	1.38	1.33
50	NC	501	GTP	C2-N3	2.18	1.38	1.33
50	NI	501	GTP	C2-N3	2.18	1.38	1.33
50	HC	501	GTP	C2-N3	2.18	1.38	1.33
50	OM	501	GTP	C2-N3	2.18	1.38	1.33
50	DI	501	GTP	C2-N3	2.18	1.38	1.33
50	AA	501	GTP	C2-N3	2.18	1.38	1.33
50	CI	501	GTP	C2-N3	2.18	1.38	1.33
50	JC	501	GTP	C2-N3	2.18	1.38	1.33
50	FA	501	GTP	C2-N3	2.18	1.38	1.33
50	JE	501	GTP	C2-N3	2.18	1.38	1.33
50	GO	501	GTP	C2-N3	2.18	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	BO	501	GTP	C2-N3	2.18	1.38	1.33
50	UC	501	GTP	C2-N3	2.18	1.38	1.33
50	PK	501	GTP	C2-N3	2.18	1.38	1.33
50	QK	501	GTP	C2-N3	2.17	1.38	1.33
50	LG	501	GTP	C2-N3	2.17	1.38	1.33
50	RE	501	GTP	C2-N3	2.17	1.38	1.33
50	SA	501	GTP	C2-N3	2.17	1.38	1.33
50	IM	501	GTP	C2-N3	2.17	1.38	1.33
50	TK	501	GTP	C2-N3	2.17	1.38	1.33
50	FC	501	GTP	C2-N3	2.17	1.38	1.33
50	WM	501	GTP	C2-N3	2.17	1.38	1.33
50	LE	501	GTP	C2-N3	2.17	1.38	1.33
50	HE	501	GTP	C2-N3	2.17	1.38	1.33
50	HO	501	GTP	C2-N3	2.17	1.38	1.33
50	GI	501	GTP	C2-N3	2.17	1.38	1.33
50	MA	501	GTP	C2-N3	2.17	1.38	1.33
50	UG	501	GTP	C2-N3	2.17	1.38	1.33
50	NA	501	GTP	C2-N3	2.16	1.38	1.33
50	BE	501	GTP	C2-N3	2.16	1.38	1.33
50	EI	501	GTP	C2-N3	2.16	1.38	1.33
50	EO	501	GTP	C2-N3	2.16	1.38	1.33
50	TE	501	GTP	C2-N3	2.16	1.38	1.33
50	KK	501	GTP	C2-N3	2.16	1.38	1.33
50	OC	501	GTP	C2-N3	2.16	1.38	1.33
50	AC	501	GTP	C2-N3	2.16	1.38	1.33
50	EC	501	GTP	C2-N3	2.16	1.38	1.33
50	EG	501	GTP	C2-N3	2.16	1.38	1.33
50	NG	501	GTP	C2-N3	2.16	1.38	1.33
50	TI	501	GTP	C2-N3	2.16	1.38	1.33
50	ME	501	GTP	C2-N3	2.16	1.38	1.33
50	HM	501	GTP	C2-N3	2.15	1.38	1.33
50	BM	501	GTP	C2-N3	2.15	1.38	1.33
50	BK	501	GTP	C2-N3	2.15	1.38	1.33
50	DG	501	GTP	C2-N3	2.15	1.38	1.33
50	EM	501	GTP	C2-N3	2.15	1.38	1.33
50	DE	501	GTP	C2-N3	2.15	1.38	1.33
50	DO	501	GTP	C2-N3	2.15	1.38	1.33
50	MO	501	GTP	C2-N3	2.14	1.38	1.33
50	LC	501	GTP	C2-N3	2.14	1.38	1.33
50	AE	501	GTP	C2-N3	2.14	1.38	1.33
52	JF	502	GDP	C6-N1	-2.14	1.34	1.37
50	JM	501	GTP	C2-N3	2.14	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	FM	501	GTP	C2-N3	2.14	1.38	1.33
50	TG	501	GTP	C2-N3	2.14	1.38	1.33
50	OO	501	GTP	C2-N3	2.14	1.38	1.33
52	FJ	502	GDP	C6-N1	-2.14	1.34	1.37
50	SI	501	GTP	C2-N3	2.14	1.38	1.33
50	GG	501	GTP	C2-N3	2.14	1.38	1.33
50	SM	501	GTP	C2-N3	2.14	1.38	1.33
50	WG	501	GTP	C2-N3	2.13	1.38	1.33
52	MB	502	GDP	C6-N1	-2.13	1.34	1.37
50	HI	501	GTP	C2-N3	2.13	1.38	1.33
50	BI	501	GTP	C2-N3	2.13	1.38	1.33
50	WK	501	GTP	C2-N3	2.12	1.38	1.33
50	OI	501	GTP	C2-N3	2.12	1.38	1.33
50	JG	501	GTP	C2-N3	2.12	1.38	1.33
50	TM	501	GTP	C2-N3	2.12	1.38	1.33
50	KM	501	GTP	C2-N3	2.11	1.38	1.33
50	JQ	501	GTP	C2-N3	2.11	1.38	1.33
50	MK	501	GTP	C2-N3	2.11	1.38	1.33
50	KO	501	GTP	C2-N3	2.11	1.38	1.33
50	PC	501	GTP	C2-N3	2.11	1.38	1.33
50	FE	501	GTP	C2-N3	2.10	1.38	1.33
50	AK	501	GTP	C2-N3	2.10	1.38	1.33
50	FK	501	GTP	C2-N3	2.10	1.38	1.33
50	GE	501	GTP	C2-N3	2.10	1.38	1.33
50	LO	501	GTP	C2-N3	2.10	1.38	1.33
50	NK	501	GTP	C2-N3	2.09	1.38	1.33
50	FI	501	GTP	C2-N3	2.09	1.38	1.33
50	LI	501	GTP	C2-N3	2.09	1.38	1.33
50	GK	501	GTP	C2-N3	2.09	1.38	1.33
50	AG	501	GTP	C2-N3	2.08	1.38	1.33
50	KI	501	GTP	C2-N3	2.08	1.38	1.33
50	KA	501	GTP	C2-N3	2.08	1.38	1.33
50	PM	501	GTP	C2-N3	2.08	1.38	1.33
50	AM	501	GTP	C2-N3	2.08	1.38	1.33
50	BG	501	GTP	C2-N3	2.08	1.38	1.33
50	LK	501	GTP	C2-N3	2.08	1.38	1.33
50	AI	501	GTP	C2-N3	2.07	1.38	1.33
50	MC	501	GTP	C2-N3	2.06	1.38	1.33
50	MG	501	GTP	C2-N3	2.06	1.38	1.33
50	KG	501	GTP	C2-N3	2.04	1.38	1.33
50	HG	501	GTP	C2-N3	2.03	1.38	1.33
50	KC	501	GTP	C2-N3	2.03	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	JI	501	GTP	C2-N3	2.02	1.38	1.33

All (1944) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	MJ	502	GDP	PA-O3A-PB	-4.58	117.09	132.83
52	LF	502	GDP	PA-O3A-PB	-4.52	117.31	132.83
50	II	501	GTP	PB-O3B-PG	-4.51	117.34	132.83
52	KB	502	GDP	PA-O3A-PB	-4.39	117.75	132.83
50	MM	501	GTP	PA-O3A-PB	-4.34	117.94	132.83
52	LJ	502	GDP	PA-O3A-PB	-4.29	118.09	132.83
52	AD	502	GDP	PA-O3A-PB	-4.25	118.24	132.83
52	CH	502	GDP	PA-O3A-PB	-4.25	118.24	132.83
52	AL	502	GDP	PA-O3A-PB	-4.23	118.31	132.83
52	CJ	502	GDP	PA-O3A-PB	-4.19	118.46	132.83
52	HH	502	GDP	PA-O3A-PB	-4.17	118.53	132.83
50	BC	501	GTP	PB-O3B-PG	-4.16	118.56	132.83
52	NH	502	GDP	PA-O3A-PB	-4.15	118.57	132.83
52	MF	502	GDP	PA-O3A-PB	-4.15	118.60	132.83
50	NI	501	GTP	PB-O3B-PG	-4.14	118.62	132.83
52	AJ	502	GDP	PA-O3A-PB	-4.14	118.62	132.83
50	JO	501	GTP	PA-O3A-PB	-4.12	118.70	132.83
50	OO	501	GTP	PB-O3B-PG	-4.11	118.72	132.83
50	QI	501	GTP	PB-O3B-PG	-4.10	118.75	132.83
50	IO	501	GTP	PA-O3A-PB	-4.10	118.76	132.83
52	NJ	502	GDP	PA-O3A-PB	-4.09	118.79	132.83
52	AN	502	GDP	PA-O3A-PB	-4.07	118.87	132.83
52	BH	502	GDP	PA-O3A-PB	-4.07	118.87	132.83
50	FC	501	GTP	PB-O3B-PG	-4.06	118.90	132.83
50	UC	501	GTP	PB-O3B-PG	-4.06	118.90	132.83
50	BM	501	GTP	PB-O3B-PG	-4.06	118.91	132.83
52	AH	502	GDP	PA-O3A-PB	-4.02	119.03	132.83
52	LL	502	GDP	PA-O3A-PB	-4.02	119.04	132.83
52	IN	502	GDP	PA-O3A-PB	-4.02	119.05	132.83
50	CK	501	GTP	PB-O3B-PG	-4.02	119.05	132.83
50	AK	501	GTP	PA-O3A-PB	-4.01	119.06	132.83
52	FL	502	GDP	PA-O3A-PB	-4.01	119.06	132.83
50	GI	501	GTP	PB-O3B-PG	-4.01	119.07	132.83
52	IP	502	GDP	PA-O3A-PB	-3.98	119.16	132.83
50	NG	501	GTP	PB-O3B-PG	-3.98	119.18	132.83
52	KJ	502	GDP	PA-O3A-PB	-3.97	119.20	132.83
50	OC	501	GTP	PB-O3B-PG	-3.95	119.26	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	MO	501	GTP	PA-O3A-PB	-3.95	119.26	132.83
52	IJ	502	GDP	PA-O3A-PB	-3.95	119.26	132.83
50	VI	501	GTP	PB-O3B-PG	-3.95	119.27	132.83
50	AO	501	GTP	PB-O3B-PG	-3.94	119.29	132.83
50	EK	501	GTP	PB-O3B-PG	-3.94	119.31	132.83
50	IE	501	GTP	PB-O3B-PG	-3.94	119.32	132.83
52	KF	502	GDP	PA-O3A-PB	-3.94	119.32	132.83
50	PI	501	GTP	PB-O3B-PG	-3.93	119.33	132.83
52	FH	502	GDP	PA-O3A-PB	-3.93	119.34	132.83
52	LN	502	GDP	PA-O3A-PB	-3.93	119.34	132.83
52	FD	502	GDP	PA-O3A-PB	-3.92	119.36	132.83
50	BG	501	GTP	PB-O3B-PG	-3.92	119.37	132.83
50	AI	501	GTP	PB-O3B-PG	-3.92	119.37	132.83
52	JH	502	GDP	PA-O3A-PB	-3.91	119.41	132.83
50	HK	501	GTP	PB-O3B-PG	-3.90	119.44	132.83
50	JO	501	GTP	PB-O3B-PG	-3.90	119.45	132.83
50	HI	501	GTP	PB-O3B-PG	-3.89	119.47	132.83
50	IK	501	GTP	PB-O3B-PG	-3.89	119.47	132.83
52	NF	502	GDP	PA-O3A-PB	-3.89	119.48	132.83
50	BK	501	GTP	PB-O3B-PG	-3.89	119.49	132.83
50	BI	501	GTP	PB-O3B-PG	-3.89	119.49	132.83
50	CI	501	GTP	PB-O3B-PG	-3.89	119.49	132.83
52	KN	502	GDP	PA-O3A-PB	-3.88	119.51	132.83
50	WG	501	GTP	PB-O3B-PG	-3.88	119.51	132.83
50	HM	501	GTP	PB-O3B-PG	-3.87	119.53	132.83
50	EE	501	GTP	PB-O3B-PG	-3.87	119.55	132.83
52	AF	502	GDP	PA-O3A-PB	-3.87	119.56	132.83
50	GE	501	GTP	PA-O3A-PB	-3.87	119.56	132.83
50	NG	501	GTP	PA-O3A-PB	-3.86	119.56	132.83
50	QK	501	GTP	PB-O3B-PG	-3.86	119.59	132.83
50	RK	501	GTP	PB-O3B-PG	-3.85	119.60	132.83
50	QE	501	GTP	PB-O3B-PG	-3.85	119.62	132.83
50	IC	501	GTP	PB-O3B-PG	-3.84	119.64	132.83
50	IG	501	GTP	PB-O3B-PG	-3.84	119.64	132.83
52	LB	502	GDP	PA-O3A-PB	-3.84	119.65	132.83
50	PE	501	GTP	PB-O3B-PG	-3.84	119.65	132.83
50	IO	501	GTP	PB-O3B-PG	-3.83	119.68	132.83
50	HG	501	GTP	PA-O3A-PB	-3.83	119.69	132.83
50	AC	501	GTP	PB-O3B-PG	-3.83	119.69	132.83
52	GH	502	GDP	PA-O3A-PB	-3.82	119.70	132.83
50	JI	501	GTP	PB-O3B-PG	-3.82	119.71	132.83
50	CE	501	GTP	PB-O3B-PG	-3.81	119.74	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	CM	501	GTP	PB-O3B-PG	-3.81	119.74	132.83
50	JK	501	GTP	PA-O3A-PB	-3.81	119.74	132.83
52	BF	502	GDP	PA-O3A-PB	-3.81	119.76	132.83
52	JJ	502	GDP	PA-O3A-PB	-3.81	119.76	132.83
50	JK	501	GTP	PB-O3B-PG	-3.81	119.77	132.83
50	JM	501	GTP	PB-O3B-PG	-3.80	119.78	132.83
50	MK	501	GTP	PA-O3A-PB	-3.80	119.78	132.83
52	CF	502	GDP	PA-O3A-PB	-3.80	119.79	132.83
50	FM	501	GTP	PB-O3B-PG	-3.80	119.80	132.83
52	BL	502	GDP	PA-O3A-PB	-3.79	119.81	132.83
50	PG	501	GTP	PB-O3B-PG	-3.79	119.83	132.83
52	CB	502	GDP	PA-O3A-PB	-3.79	119.83	132.83
50	JG	501	GTP	PB-O3B-PG	-3.78	119.84	132.83
50	UO	501	GTP	PB-O3B-PG	-3.78	119.87	132.83
50	WM	501	GTP	PB-O3B-PG	-3.77	119.89	132.83
52	KD	502	GDP	PA-O3A-PB	-3.77	119.90	132.83
50	NM	501	GTP	PB-O3B-PG	-3.77	119.90	132.83
52	MD	502	GDP	PA-O3A-PB	-3.77	119.91	132.83
50	WI	501	GTP	PB-O3B-PG	-3.76	119.91	132.83
50	IM	501	GTP	PB-O3B-PG	-3.76	119.92	132.83
52	EH	502	GDP	PA-O3A-PB	-3.76	119.93	132.83
50	BO	501	GTP	PB-O3B-PG	-3.76	119.94	132.83
52	SJ	502	GDP	PA-O3A-PB	-3.75	119.94	132.83
52	LD	502	GDP	PA-O3A-PB	-3.75	119.95	132.83
50	OG	501	GTP	PB-O3B-PG	-3.75	119.96	132.83
52	KL	502	GDP	PA-O3A-PB	-3.75	119.96	132.83
50	JM	501	GTP	PA-O3A-PB	-3.75	119.97	132.83
52	FF	502	GDP	PA-O3A-PB	-3.74	119.98	132.83
50	CK	501	GTP	PA-O3A-PB	-3.74	119.99	132.83
50	UI	501	GTP	PB-O3B-PG	-3.74	119.99	132.83
50	JQ	501	GTP	PB-O3B-PG	-3.74	120.00	132.83
50	UG	501	GTP	PB-O3B-PG	-3.74	120.01	132.83
52	CD	502	GDP	PA-O3A-PB	-3.74	120.01	132.83
50	MI	501	GTP	PA-O3A-PB	-3.73	120.01	132.83
50	AG	501	GTP	PB-O3B-PG	-3.73	120.02	132.83
50	VO	501	GTP	PA-O3A-PB	-3.72	120.05	132.83
50	EI	501	GTP	PB-O3B-PG	-3.72	120.05	132.83
50	DE	501	GTP	PB-O3B-PG	-3.72	120.05	132.83
50	VK	501	GTP	PB-O3B-PG	-3.72	120.06	132.83
50	OK	501	GTP	PB-O3B-PG	-3.72	120.07	132.83
50	NK	501	GTP	PB-O3B-PG	-3.72	120.08	132.83
52	DF	502	GDP	PA-O3A-PB	-3.72	120.08	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	BE	501	GTP	PB-O3B-PG	-3.71	120.08	132.83
52	EN	502	GDP	PA-O3A-PB	-3.71	120.09	132.83
50	QO	501	GTP	PB-O3B-PG	-3.71	120.10	132.83
52	FN	502	GDP	PA-O3A-PB	-3.71	120.10	132.83
52	WH	502	GDP	PA-O3A-PB	-3.71	120.10	132.83
52	FB	502	GDP	PA-O3A-PB	-3.71	120.10	132.83
50	DI	501	GTP	PA-O3A-PB	-3.71	120.11	132.83
50	EG	501	GTP	PB-O3B-PG	-3.70	120.12	132.83
50	HG	501	GTP	PB-O3B-PG	-3.70	120.13	132.83
52	HL	502	GDP	PA-O3A-PB	-3.70	120.13	132.83
50	VG	501	GTP	PB-O3B-PG	-3.70	120.14	132.83
50	CO	501	GTP	PB-O3B-PG	-3.70	120.14	132.83
52	UH	502	GDP	PA-O3A-PB	-3.70	120.14	132.83
52	BJ	502	GDP	PA-O3A-PB	-3.70	120.14	132.83
52	GL	502	GDP	PA-O3A-PB	-3.69	120.17	132.83
50	IM	501	GTP	PA-O3A-PB	-3.68	120.19	132.83
52	IF	502	GDP	PA-O3A-PB	-3.68	120.19	132.83
50	LK	501	GTP	PB-O3B-PG	-3.68	120.21	132.83
50	WE	501	GTP	PB-O3B-PG	-3.68	120.21	132.83
50	DG	501	GTP	PB-O3B-PG	-3.67	120.23	132.83
50	DI	501	GTP	PB-O3B-PG	-3.67	120.23	132.83
50	CG	501	GTP	PB-O3B-PG	-3.67	120.23	132.83
50	DO	501	GTP	PB-O3B-PG	-3.67	120.24	132.83
50	CC	501	GTP	PB-O3B-PG	-3.67	120.25	132.83
50	NI	501	GTP	PA-O3A-PB	-3.66	120.27	132.83
50	VM	501	GTP	PB-O3B-PG	-3.66	120.28	132.83
52	JP	502	GDP	PA-O3A-PB	-3.66	120.28	132.83
52	SF	502	GDP	PA-O3A-PB	-3.66	120.28	132.83
50	WC	501	GTP	PB-O3B-PG	-3.66	120.28	132.83
50	KE	501	GTP	PB-O3B-PG	-3.65	120.29	132.83
50	QC	501	GTP	PB-O3B-PG	-3.65	120.29	132.83
50	BI	501	GTP	PA-O3A-PB	-3.65	120.30	132.83
52	DN	502	GDP	PA-O3A-PB	-3.65	120.30	132.83
50	HO	501	GTP	PA-O3A-PB	-3.65	120.30	132.83
52	EJ	502	GDP	PA-O3A-PB	-3.65	120.30	132.83
50	WK	501	GTP	PB-O3B-PG	-3.65	120.30	132.83
50	WO	501	GTP	PB-O3B-PG	-3.65	120.30	132.83
50	RE	501	GTP	PB-O3B-PG	-3.65	120.31	132.83
50	LC	501	GTP	PB-O3B-PG	-3.65	120.31	132.83
50	ME	501	GTP	PA-O3A-PB	-3.64	120.32	132.83
52	HF	502	GDP	PA-O3A-PB	-3.64	120.34	132.83
50	AI	501	GTP	PA-O3A-PB	-3.64	120.35	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	FJ	502	GDP	PA-O3A-PB	-3.63	120.36	132.83
50	DC	501	GTP	PA-O3A-PB	-3.63	120.36	132.83
52	JF	502	GDP	PA-O3A-PB	-3.63	120.37	132.83
50	LG	501	GTP	PA-O3A-PB	-3.63	120.37	132.83
52	IH	502	GDP	PA-O3A-PB	-3.63	120.38	132.83
50	JE	501	GTP	PA-O3A-PB	-3.63	120.38	132.83
50	DQ	501	GTP	PB-O3B-PG	-3.63	120.38	132.83
50	OM	501	GTP	PB-O3B-PG	-3.62	120.39	132.83
50	EC	501	GTP	PB-O3B-PG	-3.62	120.42	132.83
50	MM	501	GTP	PB-O3B-PG	-3.61	120.43	132.83
50	AM	501	GTP	PA-O3A-PB	-3.61	120.44	132.83
50	LE	501	GTP	PB-O3B-PG	-3.61	120.44	132.83
50	GO	501	GTP	PB-O3B-PG	-3.61	120.45	132.83
52	CL	502	GDP	PA-O3A-PB	-3.60	120.47	132.83
50	MC	501	GTP	PB-O3B-PG	-3.60	120.48	132.83
52	IL	502	GDP	PA-O3A-PB	-3.60	120.48	132.83
50	AM	501	GTP	PB-O3B-PG	-3.60	120.48	132.83
52	MP	502	GDP	PA-O3A-PB	-3.60	120.48	132.83
50	EG	501	GTP	PA-O3A-PB	-3.60	120.49	132.83
52	TB	502	GDP	PA-O3A-PB	-3.59	120.49	132.83
52	MH	502	GDP	PA-O3A-PB	-3.59	120.49	132.83
52	AP	502	GDP	PA-O3A-PB	-3.59	120.51	132.83
52	KH	502	GDP	PA-O3A-PB	-3.59	120.51	132.83
52	MN	502	GDP	PA-O3A-PB	-3.59	120.51	132.83
50	DK	501	GTP	PB-O3B-PG	-3.58	120.54	132.83
50	RG	501	GTP	PB-O3B-PG	-3.58	120.54	132.83
52	NN	502	GDP	PA-O3A-PB	-3.58	120.54	132.83
50	EO	501	GTP	PB-O3B-PG	-3.58	120.54	132.83
52	HN	502	GDP	PA-O3A-PB	-3.58	120.54	132.83
50	FE	501	GTP	PB-O3B-PG	-3.58	120.55	132.83
50	PM	501	GTP	PB-O3B-PG	-3.58	120.55	132.83
52	TJ	502	GDP	PA-O3A-PB	-3.58	120.56	132.83
50	TG	501	GTP	PB-O3B-PG	-3.57	120.57	132.83
50	KC	501	GTP	PB-O3B-PG	-3.57	120.57	132.83
50	NC	501	GTP	PB-O3B-PG	-3.57	120.57	132.83
52	BN	502	GDP	PA-O3A-PB	-3.57	120.58	132.83
50	KO	501	GTP	PB-O3B-PG	-3.57	120.58	132.83
52	SB	502	GDP	PA-O3A-PB	-3.57	120.58	132.83
52	PH	502	GDP	PA-O3A-PB	-3.57	120.59	132.83
50	LI	501	GTP	PB-O3B-PG	-3.56	120.59	132.83
50	VE	501	GTP	PB-O3B-PG	-3.56	120.59	132.83
50	JC	501	GTP	PB-O3B-PG	-3.56	120.60	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	MB	502	GDP	PA-O3A-PB	-3.56	120.61	132.83
50	KM	501	GTP	PB-O3B-PG	-3.56	120.61	132.83
50	MG	501	GTP	PB-O3B-PG	-3.56	120.62	132.83
50	LG	501	GTP	PB-O3B-PG	-3.56	120.62	132.83
52	CN	502	GDP	PA-O3A-PB	-3.56	120.62	132.83
50	PO	501	GTP	PB-O3B-PG	-3.55	120.63	132.83
50	PG	501	GTP	PA-O3A-PB	-3.55	120.63	132.83
50	UK	501	GTP	PB-O3B-PG	-3.55	120.65	132.83
52	EB	502	GDP	PA-O3A-PB	-3.54	120.67	132.83
50	QG	501	GTP	PB-O3B-PG	-3.54	120.67	132.83
50	FO	501	GTP	PB-O3B-PG	-3.54	120.68	132.83
50	GM	501	GTP	PB-O3B-PG	-3.54	120.68	132.83
50	UE	501	GTP	PB-O3B-PG	-3.54	120.68	132.83
52	DH	502	GDP	PA-O3A-PB	-3.54	120.69	132.83
50	AK	501	GTP	PB-O3B-PG	-3.53	120.70	132.83
50	AE	501	GTP	PB-O3B-PG	-3.53	120.70	132.83
50	JO	501	GTP	C5-C6-N1	3.53	120.19	113.95
52	RF	502	GDP	PA-O3A-PB	-3.53	120.70	132.83
52	RP	502	GDP	PA-O3A-PB	-3.53	120.71	132.83
50	OE	501	GTP	PB-O3B-PG	-3.53	120.72	132.83
52	EF	502	GDP	PA-O3A-PB	-3.53	120.72	132.83
50	UM	501	GTP	PB-O3B-PG	-3.52	120.73	132.83
50	JE	501	GTP	PB-O3B-PG	-3.52	120.73	132.83
50	ME	501	GTP	PB-O3B-PG	-3.52	120.74	132.83
50	FO	501	GTP	PA-O3A-PB	-3.52	120.75	132.83
52	GF	502	GDP	PA-O3A-PB	-3.52	120.75	132.83
50	QM	501	GTP	PB-O3B-PG	-3.52	120.76	132.83
50	LK	501	GTP	PA-O3A-PB	-3.52	120.76	132.83
50	EA	501	GTP	PB-O3B-PG	-3.51	120.77	132.83
52	LP	502	GDP	PA-O3A-PB	-3.51	120.77	132.83
50	VC	501	GTP	PB-O3B-PG	-3.51	120.78	132.83
50	VO	501	GTP	PB-O3B-PG	-3.51	120.78	132.83
50	QG	501	GTP	C5-C6-N1	3.51	120.14	113.95
52	DJ	502	GDP	PA-O3A-PB	-3.50	120.82	132.83
50	GC	501	GTP	PB-O3B-PG	-3.50	120.82	132.83
52	GB	502	GDP	PA-O3A-PB	-3.50	120.82	132.83
52	WF	502	GDP	PA-O3A-PB	-3.50	120.82	132.83
50	TK	501	GTP	PB-O3B-PG	-3.50	120.83	132.83
50	FI	501	GTP	PA-O3A-PB	-3.50	120.83	132.83
50	RI	501	GTP	PB-O3B-PG	-3.50	120.83	132.83
50	GG	501	GTP	PB-O3B-PG	-3.50	120.83	132.83
50	NK	501	GTP	PA-O3A-PB	-3.49	120.83	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	BG	501	GTP	PA-O3A-PB	-3.49	120.84	132.83
50	MI	501	GTP	PB-O3B-PG	-3.49	120.84	132.83
52	RD	502	GDP	PA-O3A-PB	-3.49	120.85	132.83
52	TN	502	GDP	PA-O3A-PB	-3.49	120.86	132.83
52	OB	502	GDP	C3'-C2'-C1'	3.49	106.23	100.98
50	MK	501	GTP	PB-O3B-PG	-3.49	120.86	132.83
50	TM	501	GTP	PB-O3B-PG	-3.48	120.88	132.83
50	PC	501	GTP	PB-O3B-PG	-3.48	120.88	132.83
50	AA	501	GTP	PB-O3B-PG	-3.48	120.88	132.83
50	LO	501	GTP	PB-O3B-PG	-3.48	120.89	132.83
52	RN	502	GDP	PA-O3A-PB	-3.48	120.89	132.83
50	CQ	501	GTP	PB-O3B-PG	-3.48	120.90	132.83
52	JN	502	GDP	PA-O3A-PB	-3.47	120.91	132.83
50	DM	501	GTP	PB-O3B-PG	-3.47	120.92	132.83
50	GM	501	GTP	PA-O3A-PB	-3.47	120.92	132.83
52	TD	502	GDP	PA-O3A-PB	-3.47	120.92	132.83
52	SH	502	GDP	PA-O3A-PB	-3.47	120.93	132.83
52	SL	502	GDP	PA-O3A-PB	-3.47	120.93	132.83
52	PJ	502	GDP	PA-O3A-PB	-3.46	120.94	132.83
50	OI	501	GTP	PB-O3B-PG	-3.46	120.94	132.83
50	PO	501	GTP	PA-O3A-PB	-3.46	120.94	132.83
52	CP	502	GDP	PA-O3A-PB	-3.46	120.95	132.83
52	LH	502	GDP	PA-O3A-PB	-3.46	120.96	132.83
50	NA	501	GTP	PB-O3B-PG	-3.46	120.96	132.83
50	AE	501	GTP	C5-C6-N1	3.46	120.05	113.95
50	TC	501	GTP	PB-O3B-PG	-3.45	120.97	132.83
52	BD	502	GDP	PA-O3A-PB	-3.45	120.98	132.83
50	LA	501	GTP	PB-O3B-PG	-3.45	120.98	132.83
52	QP	502	GDP	PA-O3A-PB	-3.45	121.00	132.83
52	HJ	502	GDP	PA-O3A-PB	-3.45	121.00	132.83
52	WB	502	GDP	PA-O3A-PB	-3.44	121.01	132.83
52	WJ	502	GDP	PA-O3A-PB	-3.44	121.01	132.83
50	GK	501	GTP	PB-O3B-PG	-3.44	121.01	132.83
50	PK	501	GTP	PB-O3B-PG	-3.44	121.01	132.83
50	HE	501	GTP	PB-O3B-PG	-3.44	121.01	132.83
52	AB	502	GDP	PA-O3A-PB	-3.44	121.02	132.83
50	KI	501	GTP	PB-O3B-PG	-3.44	121.02	132.83
50	NM	501	GTP	PA-O3A-PB	-3.44	121.03	132.83
50	FM	501	GTP	PA-O3A-PB	-3.44	121.03	132.83
50	JQ	501	GTP	PA-O3A-PB	-3.44	121.03	132.83
50	TG	501	GTP	PA-O3A-PB	-3.44	121.04	132.83
50	IA	501	GTP	PB-O3B-PG	-3.43	121.05	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	IG	501	GTP	PA-O3A-PB	-3.43	121.05	132.83
50	KK	501	GTP	C5-C6-N1	3.43	120.00	113.95
52	JD	502	GDP	PA-O3A-PB	-3.43	121.06	132.83
50	DK	501	GTP	PA-O3A-PB	-3.43	121.07	132.83
52	PN	502	GDP	PA-O3A-PB	-3.43	121.07	132.83
52	ED	502	GDP	PA-O3A-PB	-3.43	121.07	132.83
52	NP	502	GDP	PA-O3A-PB	-3.43	121.07	132.83
50	FC	501	GTP	C5-C6-N1	3.43	120.00	113.95
50	LM	501	GTP	PB-O3B-PG	-3.42	121.09	132.83
50	UA	501	GTP	PB-O3B-PG	-3.42	121.09	132.83
50	KI	501	GTP	C5-C6-N1	3.42	119.99	113.95
50	LO	501	GTP	PA-O3A-PB	-3.42	121.10	132.83
50	OE	501	GTP	PA-O3A-PB	-3.41	121.11	132.83
52	ID	502	GDP	PA-O3A-PB	-3.41	121.11	132.83
50	BO	501	GTP	PA-O3A-PB	-3.41	121.11	132.83
50	AC	501	GTP	PA-O3A-PB	-3.41	121.11	132.83
50	RO	501	GTP	PB-O3B-PG	-3.41	121.13	132.83
50	RG	501	GTP	C5-C6-N1	3.41	119.97	113.95
52	DD	502	GDP	PA-O3A-PB	-3.40	121.14	132.83
50	AG	501	GTP	PA-O3A-PB	-3.40	121.15	132.83
52	VD	502	GDP	PA-O3A-PB	-3.40	121.15	132.83
50	HC	501	GTP	PB-O3B-PG	-3.40	121.16	132.83
52	NL	502	GDP	PA-O3A-PB	-3.40	121.16	132.83
52	PF	502	GDP	PA-O3A-PB	-3.40	121.17	132.83
52	WD	502	GDP	PA-O3A-PB	-3.40	121.17	132.83
52	UF	502	GDP	PA-O3A-PB	-3.40	121.17	132.83
50	IK	501	GTP	C5-C6-N1	3.40	119.95	113.95
50	RO	501	GTP	C5-C6-N1	3.40	119.95	113.95
50	HI	501	GTP	PA-O3A-PB	-3.40	121.18	132.83
50	OA	501	GTP	PB-O3B-PG	-3.39	121.18	132.83
52	RL	502	GDP	PA-O3A-PB	-3.39	121.18	132.83
50	RM	501	GTP	C5-C6-N1	3.39	119.94	113.95
52	VH	502	GDP	PA-O3A-PB	-3.39	121.18	132.83
50	JK	501	GTP	C5-C6-N1	3.39	119.94	113.95
50	FK	501	GTP	PB-O3B-PG	-3.39	121.19	132.83
50	FG	501	GTP	PB-O3B-PG	-3.39	121.19	132.83
50	NO	501	GTP	PA-O3A-PB	-3.39	121.19	132.83
50	WA	501	GTP	PB-O3B-PG	-3.39	121.19	132.83
50	VA	501	GTP	PB-O3B-PG	-3.39	121.20	132.83
50	EC	501	GTP	C5-C6-N1	3.39	119.93	113.95
52	RH	502	GDP	PA-O3A-PB	-3.39	121.21	132.83
50	NO	501	GTP	PB-O3B-PG	-3.38	121.21	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	SM	501	GTP	PB-O3B-PG	-3.38	121.22	132.83
50	KG	501	GTP	C3'-C2'-C1'	3.38	106.07	100.98
50	AG	501	GTP	C5-C6-N1	3.38	119.92	113.95
50	LI	501	GTP	PA-O3A-PB	-3.38	121.22	132.83
50	VM	501	GTP	PA-O3A-PB	-3.38	121.23	132.83
52	WL	502	GDP	PA-O3A-PB	-3.38	121.23	132.83
50	AK	501	GTP	C5-C6-N1	3.37	119.91	113.95
50	VK	501	GTP	C5-C6-N1	3.37	119.91	113.95
50	JG	501	GTP	PA-O3A-PB	-3.37	121.25	132.83
50	MK	501	GTP	C5-C6-N1	3.37	119.91	113.95
50	AE	501	GTP	PA-O3A-PB	-3.37	121.26	132.83
50	HC	501	GTP	C5-C6-N1	3.37	119.90	113.95
50	PI	501	GTP	C5-C6-N1	3.37	119.90	113.95
50	RE	501	GTP	C5-C6-N1	3.37	119.89	113.95
50	PM	501	GTP	PA-O3A-PB	-3.37	121.28	132.83
50	FK	501	GTP	PA-O3A-PB	-3.36	121.28	132.83
50	EA	501	GTP	C5-C6-N1	3.36	119.89	113.95
50	KA	501	GTP	C5-C6-N1	3.36	119.89	113.95
52	UB	502	GDP	PA-O3A-PB	-3.36	121.29	132.83
50	AI	501	GTP	C5-C6-N1	3.36	119.88	113.95
50	WC	501	GTP	C5-C6-N1	3.36	119.88	113.95
50	JI	501	GTP	C5-C6-N1	3.36	119.88	113.95
50	BI	501	GTP	C5-C6-N1	3.35	119.88	113.95
50	SI	501	GTP	PA-O3A-PB	-3.35	121.32	132.83
52	TH	502	GDP	PA-O3A-PB	-3.35	121.32	132.83
52	HD	502	GDP	PA-O3A-PB	-3.35	121.32	132.83
50	KC	501	GTP	C5-C6-N1	3.35	119.87	113.95
50	RK	501	GTP	C5-C6-N1	3.35	119.86	113.95
50	EC	501	GTP	PA-O3A-PB	-3.35	121.34	132.83
50	FG	501	GTP	PA-O3A-PB	-3.35	121.34	132.83
50	QI	501	GTP	C5-C6-N1	3.35	119.86	113.95
52	OL	502	GDP	PA-O3A-PB	-3.35	121.34	132.83
50	AC	501	GTP	C5-C6-N1	3.35	119.86	113.95
50	NC	501	GTP	PA-O3A-PB	-3.34	121.35	132.83
50	EM	501	GTP	C5-C6-N1	3.34	119.86	113.95
50	OI	501	GTP	PA-O3A-PB	-3.34	121.35	132.83
50	RC	501	GTP	C5-C6-N1	3.34	119.85	113.95
50	TE	501	GTP	PB-O3B-PG	-3.34	121.36	132.83
50	CK	501	GTP	C5-C6-N1	3.34	119.84	113.95
50	CM	501	GTP	C5-C6-N1	3.34	119.84	113.95
52	NJ	502	GDP	C3'-C2'-C1'	3.33	106.00	100.98
52	ND	502	GDP	PA-O3A-PB	-3.33	121.39	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	FO	501	GTP	C5-C6-N1	3.33	119.84	113.95
50	CG	501	GTP	C5-C6-N1	3.33	119.83	113.95
50	ME	501	GTP	C5-C6-N1	3.33	119.83	113.95
50	OC	501	GTP	PA-O3A-PB	-3.33	121.41	132.83
50	KG	501	GTP	C5-C6-N1	3.33	119.83	113.95
50	TC	501	GTP	C5-C6-N1	3.33	119.82	113.95
52	ML	502	GDP	PA-O3A-PB	-3.33	121.42	132.83
50	EK	501	GTP	C5-C6-N1	3.32	119.82	113.95
50	FI	501	GTP	PB-O3B-PG	-3.32	121.42	132.83
52	TF	502	GDP	PA-O3A-PB	-3.32	121.42	132.83
50	PO	501	GTP	C5-C6-N1	3.32	119.82	113.95
52	VL	502	GDP	PA-O3A-PB	-3.32	121.43	132.83
50	PE	501	GTP	C5-C6-N1	3.32	119.82	113.95
50	LG	501	GTP	C5-C6-N1	3.32	119.82	113.95
50	HA	501	GTP	PB-O3B-PG	-3.32	121.43	132.83
50	TI	501	GTP	PB-O3B-PG	-3.32	121.44	132.83
50	EI	501	GTP	C5-C6-N1	3.32	119.81	113.95
50	LE	501	GTP	C5-C6-N1	3.32	119.81	113.95
50	QC	501	GTP	C5-C6-N1	3.32	119.81	113.95
50	LI	501	GTP	C5-C6-N1	3.32	119.81	113.95
50	IK	501	GTP	PA-O3A-PB	-3.32	121.44	132.83
52	GN	502	GDP	PA-O3A-PB	-3.32	121.45	132.83
50	EE	501	GTP	C5-C6-N1	3.31	119.80	113.95
52	PL	502	GDP	PA-O3A-PB	-3.31	121.46	132.83
50	OG	501	GTP	C5-C6-N1	3.31	119.80	113.95
50	WI	501	GTP	C5-C6-N1	3.31	119.80	113.95
50	VE	501	GTP	PA-O3A-PB	-3.31	121.46	132.83
50	EG	501	GTP	C5-C6-N1	3.31	119.80	113.95
50	BG	501	GTP	C5-C6-N1	3.31	119.80	113.95
50	FI	501	GTP	C5-C6-N1	3.31	119.80	113.95
50	WG	501	GTP	C5-C6-N1	3.31	119.80	113.95
50	FA	501	GTP	C5-C6-N1	3.31	119.79	113.95
50	GE	501	GTP	PB-O3B-PG	-3.31	121.48	132.83
50	DK	501	GTP	C5-C6-N1	3.31	119.79	113.95
50	KE	501	GTP	C5-C6-N1	3.31	119.79	113.95
50	WK	501	GTP	PA-O3A-PB	-3.31	121.48	132.83
50	DM	501	GTP	C5-C6-N1	3.30	119.79	113.95
50	NE	501	GTP	PB-O3B-PG	-3.30	121.49	132.83
52	SD	502	GDP	PA-O3A-PB	-3.30	121.49	132.83
52	PD	502	GDP	PA-O3A-PB	-3.30	121.50	132.83
50	AA	501	GTP	C5-C6-N1	3.30	119.78	113.95
50	SK	501	GTP	PB-O3B-PG	-3.30	121.51	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	DE	501	GTP	C5-C6-N1	3.30	119.77	113.95
50	LC	501	GTP	C5-C6-N1	3.30	119.77	113.95
50	QK	501	GTP	C5-C6-N1	3.30	119.77	113.95
50	WE	501	GTP	C5-C6-N1	3.30	119.77	113.95
50	OI	501	GTP	C5-C6-N1	3.30	119.77	113.95
52	SN	502	GDP	PA-O3A-PB	-3.30	121.52	132.83
50	NO	501	GTP	C5-C6-N1	3.29	119.77	113.95
50	GA	501	GTP	PB-O3B-PG	-3.29	121.52	132.83
50	JE	501	GTP	C5-C6-N1	3.29	119.77	113.95
50	MA	501	GTP	PA-O3A-PB	-3.29	121.52	132.83
52	UL	502	GDP	PA-O3A-PB	-3.29	121.54	132.83
50	GK	501	GTP	PA-O3A-PB	-3.29	121.54	132.83
50	VG	501	GTP	PA-O3A-PB	-3.29	121.55	132.83
50	ME	501	GTP	C3'-C2'-C1'	3.29	105.93	100.98
50	BE	501	GTP	C5-C6-N1	3.29	119.75	113.95
50	NG	501	GTP	C5-C6-N1	3.29	119.75	113.95
50	DC	501	GTP	C5-C6-N1	3.29	119.75	113.95
50	SA	501	GTP	PA-O3A-PB	-3.29	121.55	132.83
52	RJ	502	GDP	PA-O3A-PB	-3.29	121.55	132.83
52	OH	502	GDP	PA-O3A-PB	-3.28	121.56	132.83
50	BK	501	GTP	C5-C6-N1	3.28	119.75	113.95
50	WM	501	GTP	C5-C6-N1	3.28	119.75	113.95
50	OC	501	GTP	C5-C6-N1	3.28	119.75	113.95
50	RI	501	GTP	C5-C6-N1	3.28	119.75	113.95
52	NP	502	GDP	C3'-C2'-C1'	3.28	105.92	100.98
50	GO	501	GTP	C5-C6-N1	3.28	119.75	113.95
50	IG	501	GTP	C5-C6-N1	3.28	119.74	113.95
50	NI	501	GTP	C5-C6-N1	3.28	119.74	113.95
50	NK	501	GTP	C5-C6-N1	3.28	119.74	113.95
50	HM	501	GTP	PA-O3A-PB	-3.28	121.58	132.83
50	SG	501	GTP	PB-O3B-PG	-3.28	121.58	132.83
50	LM	501	GTP	C5-C6-N1	3.28	119.74	113.95
52	QB	502	GDP	PA-O3A-PB	-3.28	121.59	132.83
52	VB	502	GDP	PA-O3A-PB	-3.27	121.59	132.83
52	UF	502	GDP	C3'-C2'-C1'	3.27	105.91	100.98
50	TE	501	GTP	C5-C6-N1	3.27	119.73	113.95
50	TK	501	GTP	PA-O3A-PB	-3.27	121.61	132.83
50	JM	501	GTP	C5-C6-N1	3.27	119.72	113.95
50	CO	501	GTP	C5-C6-N1	3.27	119.72	113.95
50	RC	501	GTP	PB-O3B-PG	-3.27	121.61	132.83
50	DQ	501	GTP	C5-C6-N1	3.27	119.72	113.95
50	VI	501	GTP	C5-C6-N1	3.27	119.72	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	OO	501	GTP	PA-O3A-PB	-3.27	121.61	132.83
50	UK	501	GTP	PA-O3A-PB	-3.27	121.61	132.83
50	MO	501	GTP	C5-C6-N1	3.27	119.72	113.95
50	VC	501	GTP	C5-C6-N1	3.27	119.72	113.95
50	UE	501	GTP	C5-C6-N1	3.26	119.72	113.95
52	ID	502	GDP	C3'-C2'-C1'	3.26	105.89	100.98
50	HI	501	GTP	C5-C6-N1	3.26	119.71	113.95
50	OK	501	GTP	C5-C6-N1	3.26	119.71	113.95
50	PK	501	GTP	C5-C6-N1	3.26	119.71	113.95
50	AO	501	GTP	C5-C6-N1	3.26	119.71	113.95
50	CQ	501	GTP	C5-C6-N1	3.26	119.71	113.95
52	PB	502	GDP	PA-O3A-PB	-3.26	121.63	132.83
50	BO	501	GTP	C5-C6-N1	3.26	119.71	113.95
50	HM	501	GTP	C5-C6-N1	3.26	119.71	113.95
50	PC	501	GTP	PA-O3A-PB	-3.26	121.64	132.83
52	DB	502	GDP	PA-O3A-PB	-3.26	121.64	132.83
50	IE	501	GTP	C5-C6-N1	3.26	119.71	113.95
50	KM	501	GTP	C5-C6-N1	3.26	119.71	113.95
50	AA	501	GTP	PA-O3A-PB	-3.26	121.65	132.83
52	BB	502	GDP	PA-O3A-PB	-3.26	121.65	132.83
50	WK	501	GTP	C5-C6-N1	3.26	119.70	113.95
52	OB	502	GDP	PA-O3A-PB	-3.26	121.65	132.83
52	UB	502	GDP	C3'-C2'-C1'	3.26	105.88	100.98
50	SK	501	GTP	C5-C6-N1	3.26	119.70	113.95
50	AM	501	GTP	C5-C6-N1	3.26	119.70	113.95
50	FK	501	GTP	C5-C6-N1	3.26	119.70	113.95
50	KK	501	GTP	PB-O3B-PG	-3.25	121.66	132.83
52	BP	502	GDP	PA-O3A-PB	-3.25	121.66	132.83
50	MO	501	GTP	PB-O3B-PG	-3.25	121.66	132.83
50	QM	501	GTP	C5-C6-N1	3.25	119.69	113.95
50	OG	501	GTP	PA-O3A-PB	-3.25	121.67	132.83
52	QB	502	GDP	C3'-C2'-C1'	3.25	105.87	100.98
50	GA	501	GTP	C5-C6-N1	3.25	119.69	113.95
50	HK	501	GTP	C5-C6-N1	3.25	119.69	113.95
52	DL	502	GDP	PA-O3A-PB	-3.25	121.67	132.83
50	JC	501	GTP	C5-C6-N1	3.25	119.69	113.95
50	EO	501	GTP	C5-C6-N1	3.25	119.69	113.95
50	HO	501	GTP	C5-C6-N1	3.25	119.69	113.95
50	KO	501	GTP	C5-C6-N1	3.25	119.69	113.95
52	KP	502	GDP	PA-O3A-PB	-3.25	121.69	132.83
50	DE	501	GTP	PA-O3A-PB	-3.25	121.69	132.83
50	PG	501	GTP	C5-C6-N1	3.24	119.68	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	VA	501	GTP	C5-C6-N1	3.24	119.68	113.95
50	NA	501	GTP	PA-O3A-PB	-3.24	121.70	132.83
50	LA	501	GTP	C5-C6-N1	3.24	119.68	113.95
50	QE	501	GTP	C5-C6-N1	3.24	119.68	113.95
50	CC	501	GTP	C5-C6-N1	3.24	119.68	113.95
50	DI	501	GTP	C5-C6-N1	3.24	119.68	113.95
50	UM	501	GTP	C5-C6-N1	3.24	119.68	113.95
50	FG	501	GTP	C5-C6-N1	3.24	119.67	113.95
50	DG	501	GTP	C5-C6-N1	3.24	119.67	113.95
50	IC	501	GTP	PA-O3A-PB	-3.24	121.71	132.83
50	GC	501	GTP	C5-C6-N1	3.24	119.67	113.95
50	LK	501	GTP	C5-C6-N1	3.24	119.67	113.95
50	TI	501	GTP	PA-O3A-PB	-3.24	121.72	132.83
50	BM	501	GTP	C5-C6-N1	3.24	119.67	113.95
50	OK	501	GTP	PA-O3A-PB	-3.24	121.72	132.83
50	IM	501	GTP	C5-C6-N1	3.24	119.67	113.95
50	WO	501	GTP	C5-C6-N1	3.24	119.67	113.95
50	BC	501	GTP	C5-C6-N1	3.23	119.66	113.95
50	HG	501	GTP	C5-C6-N1	3.23	119.66	113.95
52	FL	502	GDP	C3'-C2'-C1'	3.23	105.84	100.98
50	CM	501	GTP	PA-O3A-PB	-3.23	121.74	132.83
50	DO	501	GTP	C5-C6-N1	3.23	119.66	113.95
50	TI	501	GTP	C5-C6-N1	3.23	119.65	113.95
50	MM	501	GTP	C5-C6-N1	3.23	119.65	113.95
50	TA	501	GTP	C5-C6-N1	3.23	119.65	113.95
50	GG	501	GTP	C5-C6-N1	3.23	119.65	113.95
52	WP	502	GDP	PA-O3A-PB	-3.23	121.76	132.83
50	AE	501	GTP	C2-N1-C6	-3.23	119.16	125.10
50	PM	501	GTP	C5-C6-N1	3.23	119.65	113.95
50	MA	501	GTP	C5-C6-N1	3.22	119.65	113.95
50	IA	501	GTP	C5-C6-N1	3.22	119.64	113.95
52	JB	502	GDP	PA-O3A-PB	-3.22	121.77	132.83
50	NE	501	GTP	C5-C6-N1	3.22	119.64	113.95
50	HA	501	GTP	C5-C6-N1	3.22	119.64	113.95
50	MA	501	GTP	PB-O3B-PG	-3.22	121.78	132.83
50	LO	501	GTP	C5-C6-N1	3.22	119.64	113.95
50	SE	501	GTP	C5-C6-N1	3.22	119.64	113.95
50	TG	501	GTP	C5-C6-N1	3.22	119.64	113.95
52	PB	502	GDP	C3'-C2'-C1'	3.22	105.82	100.98
50	CE	501	GTP	C5-C6-N1	3.22	119.63	113.95
50	SA	501	GTP	C5-C6-N1	3.22	119.63	113.95
50	BE	501	GTP	PA-O3A-PB	-3.22	121.78	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	TL	502	GDP	PA-O3A-PB	-3.22	121.79	132.83
50	SA	501	GTP	PB-O3B-PG	-3.22	121.79	132.83
50	SK	501	GTP	PA-O3A-PB	-3.22	121.79	132.83
52	NB	502	GDP	C3'-C2'-C1'	3.21	105.82	100.98
52	UD	502	GDP	PA-O3A-PB	-3.21	121.80	132.83
50	MI	501	GTP	C5-C6-N1	3.21	119.63	113.95
52	WL	502	GDP	C3'-C2'-C1'	3.21	105.82	100.98
50	MG	501	GTP	PA-O3A-PB	-3.21	121.80	132.83
50	UA	501	GTP	C5-C6-N1	3.21	119.62	113.95
50	VE	501	GTP	C5-C6-N1	3.21	119.62	113.95
50	TA	501	GTP	PB-O3B-PG	-3.21	121.81	132.83
50	FM	501	GTP	C5-C6-N1	3.21	119.62	113.95
50	VK	501	GTP	PA-O3A-PB	-3.21	121.81	132.83
50	JQ	501	GTP	C5-C6-N1	3.21	119.62	113.95
50	SM	501	GTP	C5-C6-N1	3.21	119.62	113.95
50	OA	501	GTP	PA-O3A-PB	-3.21	121.82	132.83
50	CI	501	GTP	PA-O3A-PB	-3.21	121.82	132.83
52	NH	502	GDP	C3'-C2'-C1'	3.21	105.81	100.98
52	WP	502	GDP	C3'-C2'-C1'	3.21	105.81	100.98
52	MF	502	GDP	C3'-C2'-C1'	3.21	105.80	100.98
50	NA	501	GTP	C5-C6-N1	3.20	119.61	113.95
50	VM	501	GTP	C5-C6-N1	3.20	119.61	113.95
50	FE	501	GTP	C5-C6-N1	3.20	119.61	113.95
52	PP	502	GDP	PA-O3A-PB	-3.20	121.84	132.83
50	GM	501	GTP	C5-C6-N1	3.20	119.60	113.95
52	NF	502	GDP	C3'-C2'-C1'	3.20	105.80	100.98
52	MN	502	GDP	C3'-C2'-C1'	3.20	105.80	100.98
50	UK	501	GTP	C5-C6-N1	3.20	119.60	113.95
52	EL	502	GDP	PA-O3A-PB	-3.20	121.85	132.83
50	HE	501	GTP	C5-C6-N1	3.20	119.60	113.95
52	NB	502	GDP	PA-O3A-PB	-3.20	121.85	132.83
50	CI	501	GTP	C5-C6-N1	3.20	119.60	113.95
50	MG	501	GTP	C5-C6-N1	3.20	119.60	113.95
50	DO	501	GTP	PA-O3A-PB	-3.20	121.86	132.83
50	UO	501	GTP	C5-C6-N1	3.20	119.60	113.95
50	WI	501	GTP	PA-O3A-PB	-3.19	121.86	132.83
50	UG	501	GTP	C5-C6-N1	3.19	119.59	113.95
50	SC	501	GTP	PB-O3B-PG	-3.19	121.86	132.83
50	TK	501	GTP	C5-C6-N1	3.19	119.59	113.95
50	FA	501	GTP	PA-O3A-PB	-3.19	121.87	132.83
50	KC	501	GTP	PA-O3A-PB	-3.19	121.87	132.83
50	QG	501	GTP	PA-O3A-PB	-3.19	121.87	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	WC	501	GTP	PA-O3A-PB	-3.19	121.87	132.83
52	OP	502	GDP	PA-O3A-PB	-3.19	121.87	132.83
50	VG	501	GTP	C5-C6-N1	3.19	119.59	113.95
52	SF	502	GDP	C3'-C2'-C1'	3.19	105.78	100.98
50	NM	501	GTP	C5-C6-N1	3.19	119.58	113.95
50	GI	501	GTP	C5-C6-N1	3.19	119.58	113.95
50	JG	501	GTP	C5-C6-N1	3.19	119.58	113.95
50	OA	501	GTP	C5-C6-N1	3.19	119.58	113.95
50	VO	501	GTP	C5-C6-N1	3.19	119.58	113.95
50	IA	501	GTP	PA-O3A-PB	-3.19	121.89	132.83
50	UI	501	GTP	C5-C6-N1	3.19	119.58	113.95
52	SN	502	GDP	C3'-C2'-C1'	3.19	105.77	100.98
52	WD	502	GDP	C3'-C2'-C1'	3.19	105.77	100.98
50	TM	501	GTP	C5-C6-N1	3.19	119.58	113.95
52	RP	502	GDP	C3'-C2'-C1'	3.18	105.77	100.98
50	NC	501	GTP	C5-C6-N1	3.18	119.58	113.95
50	SG	501	GTP	C5-C6-N1	3.18	119.57	113.95
50	WA	501	GTP	C5-C6-N1	3.18	119.57	113.95
50	PC	501	GTP	C5-C6-N1	3.18	119.56	113.95
50	GI	501	GTP	PA-O3A-PB	-3.18	121.93	132.83
50	GO	501	GTP	PA-O3A-PB	-3.18	121.93	132.83
50	UA	501	GTP	PA-O3A-PB	-3.18	121.93	132.83
50	OE	501	GTP	C5-C6-N1	3.17	119.56	113.95
52	AP	502	GDP	C3'-C2'-C1'	3.17	105.75	100.98
50	VC	501	GTP	PA-O3A-PB	-3.17	121.94	132.83
50	TA	501	GTP	PA-O3A-PB	-3.17	121.94	132.83
52	DP	502	GDP	PA-O3A-PB	-3.17	121.95	132.83
52	AL	502	GDP	C3'-C2'-C1'	3.17	105.75	100.98
50	UC	501	GTP	C5-C6-N1	3.17	119.55	113.95
50	GK	501	GTP	C5-C6-N1	3.17	119.55	113.95
50	SG	501	GTP	PA-O3A-PB	-3.17	121.96	132.83
50	SM	501	GTP	PA-O3A-PB	-3.17	121.96	132.83
50	UC	501	GTP	PA-O3A-PB	-3.17	121.96	132.83
50	EM	501	GTP	PA-O3A-PB	-3.17	121.97	132.83
50	IO	501	GTP	C5-C6-N1	3.16	119.54	113.95
52	IB	502	GDP	PA-O3A-PB	-3.16	121.97	132.83
50	EM	501	GTP	PB-O3B-PG	-3.16	121.97	132.83
52	QN	502	GDP	PA-O3A-PB	-3.16	121.98	132.83
50	MC	501	GTP	C5-C6-N1	3.16	119.53	113.95
50	SI	501	GTP	PB-O3B-PG	-3.16	121.98	132.83
50	TC	501	GTP	PA-O3A-PB	-3.16	121.98	132.83
50	JI	501	GTP	PA-O3A-PB	-3.16	121.99	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	VB	502	GDP	C3'-C2'-C1'	3.16	105.73	100.98
50	IK	501	GTP	C8-N7-C5	3.16	109.00	102.99
50	KA	501	GTP	PB-O3B-PG	-3.16	122.00	132.83
50	WA	501	GTP	PA-O3A-PB	-3.16	122.00	132.83
50	SE	501	GTP	PA-O3A-PB	-3.15	122.00	132.83
50	HE	501	GTP	PA-O3A-PB	-3.15	122.01	132.83
50	IC	501	GTP	C5-C6-N1	3.15	119.52	113.95
52	OF	502	GDP	PA-O3A-PB	-3.15	122.01	132.83
52	UN	502	GDP	C3'-C2'-C1'	3.15	105.72	100.98
50	SC	501	GTP	C5-C6-N1	3.15	119.51	113.95
50	IM	501	GTP	C8-N7-C5	3.15	108.99	102.99
50	SI	501	GTP	C5-C6-N1	3.15	119.51	113.95
50	FA	501	GTP	PB-O3B-PG	-3.15	122.02	132.83
50	SC	501	GTP	PA-O3A-PB	-3.15	122.02	132.83
50	BK	501	GTP	PA-O3A-PB	-3.15	122.03	132.83
50	KG	501	GTP	PB-O3B-PG	-3.14	122.03	132.83
50	QK	501	GTP	PA-O3A-PB	-3.14	122.04	132.83
50	GA	501	GTP	PA-O3A-PB	-3.14	122.04	132.83
50	IG	501	GTP	C8-N7-C5	3.14	108.98	102.99
50	IO	501	GTP	C8-N7-C5	3.14	108.98	102.99
50	WO	501	GTP	PA-O3A-PB	-3.14	122.05	132.83
50	BM	501	GTP	PA-O3A-PB	-3.14	122.05	132.83
50	TE	501	GTP	PA-O3A-PB	-3.14	122.05	132.83
52	VF	502	GDP	PA-O3A-PB	-3.14	122.05	132.83
52	OJ	502	GDP	PA-O3A-PB	-3.14	122.05	132.83
50	OM	501	GTP	C5-C6-N1	3.14	119.49	113.95
52	MJ	502	GDP	C3'-C2'-C1'	3.14	105.70	100.98
50	TM	501	GTP	PA-O3A-PB	-3.14	122.06	132.83
52	JL	502	GDP	PA-O3A-PB	-3.14	122.06	132.83
50	BC	501	GTP	C8-N7-C5	3.14	108.97	102.99
50	GC	501	GTP	PA-O3A-PB	-3.13	122.07	132.83
50	SE	501	GTP	PB-O3B-PG	-3.13	122.08	132.83
50	QO	501	GTP	C8-N7-C5	3.13	108.96	102.99
50	RI	501	GTP	C8-N7-C5	3.13	108.95	102.99
52	AD	502	GDP	C3'-C2'-C1'	3.13	105.69	100.98
50	JO	501	GTP	C8-N7-C5	3.13	108.95	102.99
50	PG	501	GTP	C8-N7-C5	3.13	108.95	102.99
52	NN	502	GDP	C3'-C2'-C1'	3.13	105.69	100.98
50	CG	501	GTP	C8-N7-C5	3.13	108.95	102.99
50	PK	501	GTP	PA-O3A-PB	-3.13	122.09	132.83
52	WH	502	GDP	C3'-C2'-C1'	3.13	105.69	100.98
50	GE	501	GTP	C5-C6-N1	3.13	119.47	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	PP	502	GDP	C3'-C2'-C1'	3.13	105.69	100.98
50	UG	501	GTP	PA-O3A-PB	-3.13	122.10	132.83
50	OO	501	GTP	C5-C6-N1	3.13	119.47	113.95
50	CG	501	GTP	C2-N1-C6	-3.12	119.34	125.10
52	OF	502	GDP	C3'-C2'-C1'	3.12	105.68	100.98
50	CE	501	GTP	C8-N7-C5	3.12	108.94	102.99
50	AO	501	GTP	PA-O3A-PB	-3.12	122.12	132.83
52	FN	502	GDP	C3'-C2'-C1'	3.12	105.68	100.98
50	JI	501	GTP	C2-N1-C6	-3.12	119.36	125.10
50	CG	501	GTP	PA-O3A-PB	-3.12	122.13	132.83
50	KA	501	GTP	PA-O3A-PB	-3.11	122.14	132.83
52	PF	502	GDP	C3'-C2'-C1'	3.11	105.67	100.98
52	VL	502	GDP	C3'-C2'-C1'	3.11	105.66	100.98
52	OD	502	GDP	PA-O3A-PB	-3.11	122.15	132.83
50	PK	501	GTP	C8-N7-C5	3.11	108.91	102.99
50	DM	501	GTP	PA-O3A-PB	-3.11	122.16	132.83
50	HO	501	GTP	PB-O3B-PG	-3.10	122.18	132.83
50	EO	501	GTP	PA-O3A-PB	-3.10	122.18	132.83
52	SB	502	GDP	C3'-C2'-C1'	3.10	105.65	100.98
50	JK	501	GTP	C2-N1-C6	-3.10	119.39	125.10
50	JQ	501	GTP	C8-N7-C5	3.10	108.90	102.99
52	HB	502	GDP	PA-O3A-PB	-3.10	122.19	132.83
52	UD	502	GDP	C3'-C2'-C1'	3.10	105.64	100.98
50	JG	501	GTP	C8-N7-C5	3.10	108.89	102.99
50	EC	501	GTP	C8-N7-C5	3.09	108.88	102.99
50	QC	501	GTP	C8-N7-C5	3.09	108.88	102.99
50	PI	501	GTP	PA-O3A-PB	-3.09	122.22	132.83
50	DC	501	GTP	PB-O3B-PG	-3.09	122.22	132.83
50	ME	501	GTP	C2-N1-C6	-3.09	119.41	125.10
52	CN	502	GDP	C3'-C2'-C1'	3.09	105.63	100.98
52	DN	502	GDP	C3'-C2'-C1'	3.09	105.62	100.98
50	DC	501	GTP	C8-N7-C5	3.09	108.87	102.99
50	QE	501	GTP	C8-N7-C5	3.08	108.87	102.99
50	QK	501	GTP	C8-N7-C5	3.08	108.87	102.99
52	QD	502	GDP	PA-O3A-PB	-3.08	122.25	132.83
50	IC	501	GTP	C3'-C2'-C1'	3.08	105.62	100.98
50	OM	501	GTP	PA-O3A-PB	-3.08	122.26	132.83
52	TL	502	GDP	C3'-C2'-C1'	3.08	105.61	100.98
50	II	501	GTP	C5-C6-N1	3.08	119.39	113.95
50	JC	501	GTP	PA-O3A-PB	-3.08	122.27	132.83
50	QM	501	GTP	C8-N7-C5	3.08	108.85	102.99
50	CK	501	GTP	C2-N1-C6	-3.07	119.44	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	IK	501	GTP	C2-N1-C6	-3.07	119.44	125.10
50	VK	501	GTP	C8-N7-C5	3.07	108.84	102.99
50	BK	501	GTP	C8-N7-C5	3.07	108.84	102.99
50	PM	501	GTP	C8-N7-C5	3.07	108.84	102.99
50	OE	501	GTP	C8-N7-C5	3.07	108.84	102.99
50	PC	501	GTP	C8-N7-C5	3.07	108.84	102.99
52	CB	502	GDP	C3'-C2'-C1'	3.07	105.60	100.98
50	HI	501	GTP	C8-N7-C5	3.07	108.83	102.99
50	EK	501	GTP	C3'-C2'-C1'	3.07	105.60	100.98
50	VI	501	GTP	C3'-C2'-C1'	3.07	105.60	100.98
50	IC	501	GTP	C8-N7-C5	3.07	108.83	102.99
50	JE	501	GTP	C8-N7-C5	3.07	108.83	102.99
52	BF	502	GDP	C3'-C2'-C1'	3.07	105.60	100.98
50	PO	501	GTP	C8-N7-C5	3.07	108.83	102.99
50	JC	501	GTP	C8-N7-C5	3.07	108.83	102.99
50	QI	501	GTP	C8-N7-C5	3.07	108.83	102.99
50	AG	501	GTP	C8-N7-C5	3.06	108.83	102.99
50	JM	501	GTP	C8-N7-C5	3.06	108.83	102.99
50	HA	501	GTP	PA-O3A-PB	-3.06	122.31	132.83
50	BC	501	GTP	PA-O3A-PB	-3.06	122.32	132.83
50	BO	501	GTP	C8-N7-C5	3.06	108.82	102.99
50	CE	501	GTP	PA-O3A-PB	-3.06	122.32	132.83
50	ME	501	GTP	C8-N7-C5	3.06	108.82	102.99
50	VE	501	GTP	C8-N7-C5	3.06	108.82	102.99
50	WM	501	GTP	PA-O3A-PB	-3.06	122.33	132.83
50	AI	501	GTP	C8-N7-C5	3.06	108.82	102.99
50	CI	501	GTP	C2-N1-C6	-3.06	119.47	125.10
50	VM	501	GTP	C8-N7-C5	3.06	108.82	102.99
50	AI	501	GTP	C2-N1-C6	-3.06	119.47	125.10
50	OO	501	GTP	C8-N7-C5	3.06	108.81	102.99
50	UE	501	GTP	PA-O3A-PB	-3.06	122.34	132.83
50	LM	501	GTP	PA-O3A-PB	-3.06	122.34	132.83
50	AG	501	GTP	C2-N1-C6	-3.06	119.47	125.10
50	VA	501	GTP	C8-N7-C5	3.06	108.81	102.99
50	CK	501	GTP	C8-N7-C5	3.05	108.81	102.99
52	TN	502	GDP	C3'-C2'-C1'	3.05	105.58	100.98
50	LI	501	GTP	C8-N7-C5	3.05	108.81	102.99
50	SA	501	GTP	C8-N7-C5	3.05	108.81	102.99
50	OG	501	GTP	C8-N7-C5	3.05	108.81	102.99
50	QO	501	GTP	C5-C6-N1	3.05	119.34	113.95
50	AA	501	GTP	C8-N7-C5	3.05	108.80	102.99
50	VA	501	GTP	PA-O3A-PB	-3.05	122.36	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	GG	501	GTP	C3'-C2'-C1'	3.05	105.57	100.98
50	DE	501	GTP	C8-N7-C5	3.05	108.80	102.99
50	HC	501	GTP	C8-N7-C5	3.05	108.80	102.99
50	HM	501	GTP	C8-N7-C5	3.05	108.80	102.99
50	DQ	501	GTP	C8-N7-C5	3.05	108.80	102.99
50	BG	501	GTP	C8-N7-C5	3.05	108.79	102.99
50	CQ	501	GTP	C8-N7-C5	3.05	108.79	102.99
50	GA	501	GTP	C8-N7-C5	3.05	108.79	102.99
50	NK	501	GTP	C8-N7-C5	3.05	108.79	102.99
50	VO	501	GTP	C8-N7-C5	3.05	108.79	102.99
50	IE	501	GTP	C3'-C2'-C1'	3.05	105.56	100.98
50	OC	501	GTP	C8-N7-C5	3.05	108.79	102.99
50	IA	501	GTP	C8-N7-C5	3.04	108.79	102.99
50	UC	501	GTP	C8-N7-C5	3.04	108.79	102.99
50	UA	501	GTP	C8-N7-C5	3.04	108.79	102.99
50	IG	501	GTP	C3'-C2'-C1'	3.04	105.56	100.98
52	PD	502	GDP	C3'-C2'-C1'	3.04	105.56	100.98
50	VG	501	GTP	C8-N7-C5	3.04	108.78	102.99
52	BN	502	GDP	C3'-C2'-C1'	3.04	105.56	100.98
50	LG	501	GTP	C2-N1-C6	-3.04	119.50	125.10
50	RC	501	GTP	C8-N7-C5	3.04	108.78	102.99
50	HE	501	GTP	C8-N7-C5	3.04	108.78	102.99
50	DI	501	GTP	C8-N7-C5	3.04	108.77	102.99
50	EI	501	GTP	C3'-C2'-C1'	3.04	105.55	100.98
50	NM	501	GTP	C2-N1-C6	-3.04	119.51	125.10
50	JO	501	GTP	C2-N1-C6	-3.03	119.51	125.10
52	QL	502	GDP	PA-O3A-PB	-3.03	122.42	132.83
50	SG	501	GTP	C8-N7-C5	3.03	108.77	102.99
52	QJ	502	GDP	PA-O3A-PB	-3.03	122.42	132.83
50	RK	501	GTP	C8-N7-C5	3.03	108.76	102.99
50	WC	501	GTP	C8-N7-C5	3.03	108.76	102.99
52	UH	502	GDP	C3'-C2'-C1'	3.03	105.54	100.98
50	CI	501	GTP	C8-N7-C5	3.03	108.76	102.99
50	DG	501	GTP	C8-N7-C5	3.03	108.76	102.99
50	RE	501	GTP	C8-N7-C5	3.03	108.76	102.99
50	RM	501	GTP	C8-N7-C5	3.03	108.76	102.99
50	OM	501	GTP	C3'-C2'-C1'	3.03	105.54	100.98
50	BI	501	GTP	C2-N1-C6	-3.03	119.53	125.10
50	EM	501	GTP	C8-N7-C5	3.03	108.75	102.99
50	AO	501	GTP	C8-N7-C5	3.03	108.75	102.99
50	OA	501	GTP	C8-N7-C5	3.03	108.75	102.99
50	WO	501	GTP	C8-N7-C5	3.03	108.75	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	OH	502	GDP	C3'-C2'-C1'	3.03	105.53	100.98
50	SM	501	GTP	C8-N7-C5	3.03	108.75	102.99
50	TE	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	TI	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	EK	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	KI	501	GTP	PA-O3A-PB	-3.02	122.45	132.83
50	VC	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	QO	501	GTP	PA-O3A-PB	-3.02	122.45	132.83
50	GI	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	IE	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	UG	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	PM	501	GTP	C2-N1-C6	-3.02	119.53	125.10
50	AM	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	NM	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	DK	501	GTP	C2-N1-C6	-3.02	119.53	125.10
50	PI	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	UO	501	GTP	C8-N7-C5	3.02	108.75	102.99
50	BE	501	GTP	C8-N7-C5	3.02	108.74	102.99
50	CC	501	GTP	C8-N7-C5	3.02	108.74	102.99
50	EO	501	GTP	C8-N7-C5	3.02	108.74	102.99
50	GO	501	GTP	C8-N7-C5	3.02	108.74	102.99
50	WI	501	GTP	C8-N7-C5	3.02	108.74	102.99
52	SL	502	GDP	C3'-C2'-C1'	3.02	105.53	100.98
50	GG	501	GTP	C8-N7-C5	3.02	108.74	102.99
50	KO	501	GTP	PA-O3A-PB	-3.02	122.46	132.83
50	EI	501	GTP	C8-N7-C5	3.02	108.74	102.99
50	UM	501	GTP	C8-N7-C5	3.02	108.74	102.99
50	TA	501	GTP	C8-N7-C5	3.02	108.74	102.99
50	GC	501	GTP	C8-N7-C5	3.02	108.74	102.99
52	HP	502	GDP	PA-O3A-PB	-3.02	122.48	132.83
50	WA	501	GTP	C8-N7-C5	3.02	108.73	102.99
50	LE	501	GTP	C2-N1-C6	-3.02	119.55	125.10
50	CM	501	GTP	C8-N7-C5	3.02	108.73	102.99
50	II	501	GTP	PA-O3A-PB	-3.02	122.48	132.83
52	IB	502	GDP	C3'-C2'-C1'	3.01	105.52	100.98
52	ND	502	GDP	C3'-C2'-C1'	3.01	105.52	100.98
52	OP	502	GDP	C3'-C2'-C1'	3.01	105.52	100.98
50	CO	501	GTP	C8-N7-C5	3.01	108.73	102.99
50	DO	501	GTP	C8-N7-C5	3.01	108.73	102.99
50	EG	501	GTP	C8-N7-C5	3.01	108.73	102.99
50	BE	501	GTP	C2-N1-C6	-3.01	119.55	125.10
52	GD	502	GDP	PA-O3A-PB	-3.01	122.49	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	NA	501	GTP	C8-N7-C5	3.01	108.73	102.99
50	UI	501	GTP	C8-N7-C5	3.01	108.72	102.99
50	WE	501	GTP	C8-N7-C5	3.01	108.72	102.99
50	JI	501	GTP	C8-N7-C5	3.01	108.72	102.99
50	TM	501	GTP	C8-N7-C5	3.01	108.72	102.99
50	BM	501	GTP	C8-N7-C5	3.01	108.72	102.99
52	TF	502	GDP	C3'-C2'-C1'	3.01	105.51	100.98
50	AE	501	GTP	C8-N7-C5	3.01	108.72	102.99
50	DM	501	GTP	C2-N1-C6	-3.01	119.56	125.10
50	LA	501	GTP	C8-N7-C5	3.01	108.72	102.99
50	RO	501	GTP	C8-N7-C5	3.01	108.72	102.99
52	QD	502	GDP	C3'-C2'-C1'	3.01	105.50	100.98
52	GN	502	GDP	C3'-C2'-C1'	3.01	105.50	100.98
50	MK	501	GTP	C2-N1-C6	-3.01	119.56	125.10
50	WG	501	GTP	C8-N7-C5	3.01	108.72	102.99
50	NC	501	GTP	C3'-C2'-C1'	3.00	105.50	100.98
50	KO	501	GTP	C8-N7-C5	3.00	108.71	102.99
50	OK	501	GTP	C8-N7-C5	3.00	108.71	102.99
50	RC	501	GTP	PA-O3A-PB	-3.00	122.52	132.83
52	DJ	502	GDP	C3'-C2'-C1'	3.00	105.50	100.98
52	PJ	502	GDP	C3'-C2'-C1'	3.00	105.50	100.98
50	HK	501	GTP	PA-O3A-PB	-3.00	122.52	132.83
50	SE	501	GTP	C8-N7-C5	3.00	108.71	102.99
50	AC	501	GTP	C8-N7-C5	3.00	108.71	102.99
50	WK	501	GTP	C8-N7-C5	3.00	108.71	102.99
50	RG	501	GTP	C8-N7-C5	3.00	108.71	102.99
52	KJ	502	GDP	C3'-C2'-C1'	3.00	105.50	100.98
50	KK	501	GTP	PA-O3A-PB	-3.00	122.53	132.83
50	JE	501	GTP	C2-N1-C6	-3.00	119.57	125.10
50	EE	501	GTP	C8-N7-C5	3.00	108.70	102.99
50	KK	501	GTP	C8-N7-C5	3.00	108.70	102.99
50	EA	501	GTP	C8-N7-C5	3.00	108.70	102.99
50	CM	501	GTP	C2-N1-C6	-3.00	119.58	125.10
50	FC	501	GTP	C3'-C2'-C1'	3.00	105.49	100.98
52	AB	502	GDP	C3'-C2'-C1'	3.00	105.49	100.98
50	TK	501	GTP	C8-N7-C5	3.00	108.70	102.99
50	PG	501	GTP	C2-N1-C6	-3.00	119.58	125.10
50	FO	501	GTP	C8-N7-C5	3.00	108.70	102.99
50	OA	501	GTP	C3'-C2'-C1'	3.00	105.49	100.98
50	PE	501	GTP	C8-N7-C5	3.00	108.70	102.99
50	MK	501	GTP	C8-N7-C5	3.00	108.70	102.99
50	UE	501	GTP	C8-N7-C5	3.00	108.70	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	CQ	501	GTP	PA-O3A-PB	-2.99	122.55	132.83
50	LM	501	GTP	C8-N7-C5	2.99	108.69	102.99
50	QG	501	GTP	C2-N1-C6	-2.99	119.59	125.10
50	UM	501	GTP	PA-O3A-PB	-2.99	122.56	132.83
50	KK	501	GTP	C2-N1-C6	-2.99	119.59	125.10
50	QE	501	GTP	C3'-C2'-C1'	2.99	105.48	100.98
52	GL	502	GDP	C3'-C2'-C1'	2.99	105.48	100.98
50	QG	501	GTP	C8-N7-C5	2.99	108.69	102.99
52	RH	502	GDP	C3'-C2'-C1'	2.99	105.48	100.98
50	EE	501	GTP	C3'-C2'-C1'	2.99	105.48	100.98
52	BB	502	GDP	C3'-C2'-C1'	2.99	105.48	100.98
50	BI	501	GTP	C8-N7-C5	2.99	108.69	102.99
50	DK	501	GTP	C8-N7-C5	2.99	108.69	102.99
52	AN	502	GDP	C3'-C2'-C1'	2.99	105.48	100.98
50	LI	501	GTP	C2-N1-C6	-2.99	119.59	125.10
50	AK	501	GTP	C2-N1-C6	-2.99	119.59	125.10
50	RK	501	GTP	C2-N1-C6	-2.99	119.60	125.10
52	VJ	502	GDP	C3'-C2'-C1'	2.99	105.47	100.98
50	BG	501	GTP	C2-N1-C6	-2.99	119.60	125.10
50	CK	501	GTP	C3'-C2'-C1'	2.99	105.47	100.98
52	BJ	502	GDP	C3'-C2'-C1'	2.99	105.47	100.98
50	WM	501	GTP	C8-N7-C5	2.99	108.68	102.99
52	QN	502	GDP	C3'-C2'-C1'	2.99	105.47	100.98
52	UJ	502	GDP	C3'-C2'-C1'	2.99	105.47	100.98
50	WE	501	GTP	PA-O3A-PB	-2.99	122.58	132.83
50	WI	501	GTP	C2-N1-C6	-2.98	119.60	125.10
50	HA	501	GTP	C8-N7-C5	2.98	108.67	102.99
52	UL	502	GDP	C3'-C2'-C1'	2.98	105.47	100.98
50	FC	501	GTP	C2-N1-C6	-2.98	119.61	125.10
50	EA	501	GTP	C2-N1-C6	-2.98	119.61	125.10
50	UK	501	GTP	C3'-C2'-C1'	2.98	105.47	100.98
52	BD	502	GDP	C3'-C2'-C1'	2.98	105.47	100.98
50	PI	501	GTP	C3'-C2'-C1'	2.98	105.47	100.98
50	MI	501	GTP	C8-N7-C5	2.98	108.67	102.99
50	DQ	501	GTP	PA-O3A-PB	-2.98	122.60	132.83
50	DM	501	GTP	C8-N7-C5	2.98	108.67	102.99
50	NO	501	GTP	C8-N7-C5	2.98	108.67	102.99
50	GE	501	GTP	C3'-C2'-C1'	2.98	105.46	100.98
50	IA	501	GTP	C3'-C2'-C1'	2.98	105.46	100.98
52	WN	502	GDP	PA-O3A-PB	-2.98	122.60	132.83
50	KM	501	GTP	C8-N7-C5	2.98	108.67	102.99
52	VJ	502	GDP	PA-O3A-PB	-2.98	122.61	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	IG	501	GTP	C2-N1-C6	-2.98	119.61	125.10
50	GE	501	GTP	C8-N7-C5	2.98	108.66	102.99
50	OI	501	GTP	C3'-C2'-C1'	2.98	105.46	100.98
50	RM	501	GTP	C2-N1-C6	-2.98	119.62	125.10
50	NG	501	GTP	C8-N7-C5	2.98	108.66	102.99
50	WE	501	GTP	C3'-C2'-C1'	2.98	105.46	100.98
50	LC	501	GTP	C2-N1-C6	-2.98	119.62	125.10
50	WE	501	GTP	C2-N1-C6	-2.98	119.62	125.10
50	FK	501	GTP	C8-N7-C5	2.98	108.66	102.99
50	LE	501	GTP	C8-N7-C5	2.98	108.66	102.99
50	OO	501	GTP	C3'-C2'-C1'	2.97	105.46	100.98
50	FE	501	GTP	C8-N7-C5	2.97	108.66	102.99
50	FO	501	GTP	C2-N1-C6	-2.97	119.62	125.10
50	FA	501	GTP	C8-N7-C5	2.97	108.66	102.99
50	LO	501	GTP	C8-N7-C5	2.97	108.66	102.99
52	TH	502	GDP	C3'-C2'-C1'	2.97	105.45	100.98
52	WB	502	GDP	C3'-C2'-C1'	2.97	105.45	100.98
50	VC	501	GTP	C3'-C2'-C1'	2.97	105.45	100.98
50	EC	501	GTP	C2-N1-C6	-2.97	119.62	125.10
50	HK	501	GTP	C2-N1-C6	-2.97	119.63	125.10
52	JH	502	GDP	C3'-C2'-C1'	2.97	105.45	100.98
50	TG	501	GTP	C8-N7-C5	2.97	108.65	102.99
50	VI	501	GTP	C8-N7-C5	2.97	108.65	102.99
50	IE	501	GTP	C2-N1-C6	-2.97	119.63	125.10
50	EA	501	GTP	PA-O3A-PB	-2.97	122.63	132.83
50	UO	501	GTP	PA-O3A-PB	-2.97	122.64	132.83
50	MO	501	GTP	C8-N7-C5	2.97	108.65	102.99
50	NC	501	GTP	C8-N7-C5	2.97	108.65	102.99
50	FC	501	GTP	C8-N7-C5	2.97	108.64	102.99
50	HG	501	GTP	C8-N7-C5	2.97	108.64	102.99
50	OC	501	GTP	C3'-C2'-C1'	2.97	105.45	100.98
50	WG	501	GTP	PA-O3A-PB	-2.97	122.64	132.83
50	WK	501	GTP	C3'-C2'-C1'	2.97	105.44	100.98
50	VA	501	GTP	C3'-C2'-C1'	2.97	105.44	100.98
52	ON	502	GDP	PA-O3A-PB	-2.97	122.65	132.83
50	EM	501	GTP	C2-N1-C6	-2.96	119.64	125.10
50	HK	501	GTP	C8-N7-C5	2.96	108.64	102.99
50	FI	501	GTP	C2-N1-C6	-2.96	119.64	125.10
50	HC	501	GTP	C2-N1-C6	-2.96	119.64	125.10
50	OG	501	GTP	C3'-C2'-C1'	2.96	105.44	100.98
52	ED	502	GDP	C3'-C2'-C1'	2.96	105.44	100.98
50	MA	501	GTP	C8-N7-C5	2.96	108.64	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	LK	501	GTP	C8-N7-C5	2.96	108.63	102.99
50	OI	501	GTP	C8-N7-C5	2.96	108.63	102.99
50	FC	501	GTP	PA-O3A-PB	-2.96	122.66	132.83
50	UG	501	GTP	C3'-C2'-C1'	2.96	105.44	100.98
50	EI	501	GTP	PA-O3A-PB	-2.96	122.67	132.83
50	PE	501	GTP	PA-O3A-PB	-2.96	122.67	132.83
50	UC	501	GTP	C3'-C2'-C1'	2.96	105.44	100.98
50	RM	501	GTP	PB-O3B-PG	-2.96	122.67	132.83
52	UN	502	GDP	PA-O3A-PB	-2.96	122.67	132.83
50	BM	501	GTP	C2-N1-C6	-2.96	119.65	125.10
50	AC	501	GTP	C2-N1-C6	-2.96	119.65	125.10
50	IO	501	GTP	C2-N1-C6	-2.96	119.65	125.10
50	LM	501	GTP	C2-N1-C6	-2.96	119.65	125.10
50	EA	501	GTP	C3'-C2'-C1'	2.96	105.43	100.98
50	KC	501	GTP	C2-N1-C6	-2.96	119.65	125.10
50	CO	501	GTP	PA-O3A-PB	-2.96	122.67	132.83
50	VE	501	GTP	C3'-C2'-C1'	2.96	105.43	100.98
52	VH	502	GDP	C3'-C2'-C1'	2.96	105.43	100.98
50	WC	501	GTP	C2-N1-C6	-2.96	119.65	125.10
52	TJ	502	GDP	C3'-C2'-C1'	2.96	105.43	100.98
50	BO	501	GTP	C2-N1-C6	-2.96	119.65	125.10
50	LC	501	GTP	C8-N7-C5	2.96	108.62	102.99
50	HO	501	GTP	C2-N1-C6	-2.96	119.66	125.10
50	FM	501	GTP	C8-N7-C5	2.95	108.62	102.99
50	TC	501	GTP	C8-N7-C5	2.95	108.62	102.99
50	RG	501	GTP	C2-N1-C6	-2.95	119.66	125.10
50	PI	501	GTP	C2-N1-C6	-2.95	119.66	125.10
52	MP	502	GDP	C3'-C2'-C1'	2.95	105.42	100.98
50	IM	501	GTP	C2-N1-C6	-2.95	119.66	125.10
50	GM	501	GTP	C8-N7-C5	2.95	108.61	102.99
50	EI	501	GTP	C2-N1-C6	-2.95	119.67	125.10
50	SI	501	GTP	C8-N7-C5	2.95	108.61	102.99
50	KG	501	GTP	C8-N7-C5	2.95	108.61	102.99
50	EE	501	GTP	C2-N1-C6	-2.95	119.67	125.10
50	RO	501	GTP	C2-N1-C6	-2.95	119.67	125.10
50	KA	501	GTP	C8-N7-C5	2.95	108.61	102.99
50	MC	501	GTP	C8-N7-C5	2.95	108.61	102.99
50	UO	501	GTP	C3'-C2'-C1'	2.95	105.42	100.98
50	NE	501	GTP	C8-N7-C5	2.95	108.60	102.99
50	DI	501	GTP	C2-N1-C6	-2.95	119.67	125.10
50	KI	501	GTP	C2-N1-C6	-2.95	119.67	125.10
50	CQ	501	GTP	C2-N1-C6	-2.94	119.67	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	JC	501	GTP	C2-N1-C6	-2.94	119.67	125.10
52	OJ	502	GDP	C5-C6-N1	2.94	119.15	113.95
50	OM	501	GTP	C8-N7-C5	2.94	108.60	102.99
50	RO	501	GTP	PA-O3A-PB	-2.94	122.72	132.83
52	SJ	502	GDP	C3'-C2'-C1'	2.94	105.41	100.98
52	SD	502	GDP	C3'-C2'-C1'	2.94	105.41	100.98
50	UK	501	GTP	C8-N7-C5	2.94	108.59	102.99
50	SC	501	GTP	C8-N7-C5	2.94	108.59	102.99
50	WO	501	GTP	C3'-C2'-C1'	2.94	105.41	100.98
50	RC	501	GTP	C2-N1-C6	-2.94	119.69	125.10
50	DC	501	GTP	C3'-C2'-C1'	2.94	105.40	100.98
50	EK	501	GTP	C2-N1-C6	-2.94	119.69	125.10
50	OE	501	GTP	C3'-C2'-C1'	2.94	105.40	100.98
50	RI	501	GTP	C2-N1-C6	-2.94	119.69	125.10
50	PO	501	GTP	C2-N1-C6	-2.94	119.69	125.10
50	HC	501	GTP	PA-O3A-PB	-2.94	122.75	132.83
50	MO	501	GTP	C2-N1-C6	-2.94	119.69	125.10
50	PE	501	GTP	C2-N1-C6	-2.94	119.69	125.10
50	FI	501	GTP	C8-N7-C5	2.94	108.58	102.99
50	VK	501	GTP	C2-N1-C6	-2.94	119.69	125.10
52	TD	502	GDP	C3'-C2'-C1'	2.94	105.40	100.98
50	AA	501	GTP	C2-N1-C6	-2.93	119.69	125.10
50	JK	501	GTP	C8-N7-C5	2.93	108.58	102.99
50	LG	501	GTP	C8-N7-C5	2.93	108.58	102.99
50	KA	501	GTP	C2-N1-C6	-2.93	119.70	125.10
50	KC	501	GTP	C8-N7-C5	2.93	108.58	102.99
50	RM	501	GTP	PA-O3A-PB	-2.93	122.77	132.83
50	GC	501	GTP	C3'-C2'-C1'	2.93	105.39	100.98
52	UJ	502	GDP	PA-O3A-PB	-2.93	122.77	132.83
52	JB	502	GDP	C3'-C2'-C1'	2.93	105.39	100.98
50	LA	501	GTP	C2-N1-C6	-2.93	119.70	125.10
50	DE	501	GTP	C2-N1-C6	-2.93	119.70	125.10
50	PE	501	GTP	C3'-C2'-C1'	2.93	105.39	100.98
50	MG	501	GTP	C8-N7-C5	2.93	108.56	102.99
50	VG	501	GTP	C2-N1-C6	-2.93	119.71	125.10
52	QF	502	GDP	PA-O3A-PB	-2.93	122.78	132.83
50	WA	501	GTP	C3'-C2'-C1'	2.93	105.38	100.98
50	BK	501	GTP	C2-N1-C6	-2.93	119.71	125.10
50	AO	501	GTP	C2-N1-C6	-2.92	119.71	125.10
50	DQ	501	GTP	C2-N1-C6	-2.92	119.71	125.10
50	JM	501	GTP	C2-N1-C6	-2.92	119.72	125.10
50	RE	501	GTP	C2-N1-C6	-2.92	119.72	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	VG	501	GTP	C3'-C2'-C1'	2.92	105.38	100.98
50	EE	501	GTP	PA-O3A-PB	-2.92	122.80	132.83
50	DG	501	GTP	C2-N1-C6	-2.92	119.72	125.10
50	KG	501	GTP	C2-N1-C6	-2.92	119.72	125.10
52	RF	502	GDP	C3'-C2'-C1'	2.92	105.37	100.98
50	WM	501	GTP	C2-N1-C6	-2.92	119.72	125.10
50	VA	501	GTP	C2-N1-C6	-2.92	119.72	125.10
50	QI	501	GTP	PA-O3A-PB	-2.92	122.81	132.83
50	VC	501	GTP	C2-N1-C6	-2.92	119.72	125.10
50	UM	501	GTP	C2-N1-C6	-2.92	119.73	125.10
50	WO	501	GTP	C2-N1-C6	-2.92	119.73	125.10
50	BM	501	GTP	C3'-C2'-C1'	2.92	105.37	100.98
50	CO	501	GTP	C3'-C2'-C1'	2.92	105.37	100.98
50	NA	501	GTP	C3'-C2'-C1'	2.92	105.37	100.98
50	WM	501	GTP	C3'-C2'-C1'	2.92	105.37	100.98
50	CO	501	GTP	C2-N1-C6	-2.92	119.73	125.10
50	QI	501	GTP	C2-N1-C6	-2.92	119.73	125.10
50	JO	501	GTP	C3'-C2'-C1'	2.91	105.37	100.98
52	RD	502	GDP	C3'-C2'-C1'	2.91	105.37	100.98
50	MI	501	GTP	C2-N1-C6	-2.91	119.73	125.10
50	BC	501	GTP	C2-N1-C6	-2.91	119.73	125.10
50	MM	501	GTP	C8-N7-C5	2.91	108.54	102.99
50	UA	501	GTP	C3'-C2'-C1'	2.91	105.36	100.98
52	CJ	502	GDP	C3'-C2'-C1'	2.91	105.36	100.98
52	IP	502	GDP	C3'-C2'-C1'	2.91	105.36	100.98
50	DG	501	GTP	PA-O3A-PB	-2.91	122.83	132.83
50	GA	501	GTP	C3'-C2'-C1'	2.91	105.36	100.98
50	UM	501	GTP	C3'-C2'-C1'	2.91	105.36	100.98
50	WG	501	GTP	C2-N1-C6	-2.91	119.74	125.10
50	SK	501	GTP	C8-N7-C5	2.91	108.54	102.99
50	PC	501	GTP	C3'-C2'-C1'	2.91	105.36	100.98
50	FE	501	GTP	PA-O3A-PB	-2.91	122.84	132.83
50	GK	501	GTP	C8-N7-C5	2.91	108.53	102.99
50	EG	501	GTP	C2-N1-C6	-2.91	119.74	125.10
50	FG	501	GTP	C8-N7-C5	2.91	108.53	102.99
50	RO	501	GTP	C3'-C2'-C1'	2.91	105.35	100.98
50	JC	501	GTP	C3'-C2'-C1'	2.90	105.35	100.98
50	FA	501	GTP	C2-N1-C6	-2.90	119.75	125.10
50	OG	501	GTP	C2-N1-C6	-2.90	119.75	125.10
50	CQ	501	GTP	C3'-C2'-C1'	2.90	105.35	100.98
52	TB	502	GDP	C3'-C2'-C1'	2.90	105.35	100.98
50	QM	501	GTP	C2-N1-C6	-2.90	119.76	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	QM	501	GTP	C3'-C2'-C1'	2.90	105.34	100.98
52	GH	502	GDP	C3'-C2'-C1'	2.90	105.34	100.98
50	LK	501	GTP	C2-N1-C6	-2.90	119.76	125.10
52	VD	502	GDP	C3'-C2'-C1'	2.90	105.34	100.98
52	HP	502	GDP	C3'-C2'-C1'	2.90	105.34	100.98
50	AA	501	GTP	C3'-C2'-C1'	2.90	105.34	100.98
50	NI	501	GTP	C8-N7-C5	2.90	108.51	102.99
50	CE	501	GTP	C2-N1-C6	-2.90	119.76	125.10
50	CC	501	GTP	C2-N1-C6	-2.90	119.77	125.10
50	II	501	GTP	C2-N1-C6	-2.89	119.77	125.10
50	MG	501	GTP	C2-N1-C6	-2.89	119.77	125.10
50	QE	501	GTP	C2-N1-C6	-2.89	119.77	125.10
50	GA	501	GTP	C2-N1-C6	-2.89	119.77	125.10
50	HO	501	GTP	C8-N7-C5	2.89	108.50	102.99
52	RL	502	GDP	C3'-C2'-C1'	2.89	105.33	100.98
50	KO	501	GTP	C2-N1-C6	-2.89	119.78	125.10
50	KM	501	GTP	C2-N1-C6	-2.89	119.78	125.10
50	GG	501	GTP	PA-O3A-PB	-2.89	122.92	132.83
50	UI	501	GTP	C3'-C2'-C1'	2.89	105.33	100.98
50	JG	501	GTP	C2-N1-C6	-2.89	119.78	125.10
50	KG	501	GTP	PA-O3A-PB	-2.89	122.92	132.83
50	CM	501	GTP	C3'-C2'-C1'	2.89	105.33	100.98
50	UE	501	GTP	C3'-C2'-C1'	2.89	105.32	100.98
50	CC	501	GTP	PA-O3A-PB	-2.89	122.92	132.83
50	CG	501	GTP	C3'-C2'-C1'	2.89	105.32	100.98
50	AM	501	GTP	C2-N1-C6	-2.89	119.78	125.10
50	HM	501	GTP	C2-N1-C6	-2.88	119.79	125.10
50	IK	501	GTP	C3'-C2'-C1'	2.88	105.32	100.98
50	IA	501	GTP	C2-N1-C6	-2.88	119.79	125.10
50	DG	501	GTP	C3'-C2'-C1'	2.88	105.32	100.98
50	SC	501	GTP	C2-N1-C6	-2.88	119.79	125.10
52	QP	502	GDP	C3'-C2'-C1'	2.88	105.32	100.98
50	DI	501	GTP	C3'-C2'-C1'	2.88	105.32	100.98
52	PH	502	GDP	C3'-C2'-C1'	2.88	105.32	100.98
50	AK	501	GTP	C8-N7-C5	2.88	108.48	102.99
50	NK	501	GTP	C2-N1-C6	-2.88	119.79	125.10
50	PK	501	GTP	C2-N1-C6	-2.88	119.79	125.10
50	KI	501	GTP	C8-N7-C5	2.88	108.48	102.99
50	VI	501	GTP	PA-O3A-PB	-2.88	122.94	132.83
50	EO	501	GTP	C2-N1-C6	-2.88	119.79	125.10
50	DC	501	GTP	C2-N1-C6	-2.88	119.80	125.10
52	IL	502	GDP	C3'-C2'-C1'	2.88	105.31	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	PN	502	GDP	C3'-C2'-C1'	2.88	105.31	100.98
50	UO	501	GTP	C2-N1-C6	-2.88	119.80	125.10
52	QL	502	GDP	C3'-C2'-C1'	2.88	105.31	100.98
50	HK	501	GTP	C3'-C2'-C1'	2.88	105.31	100.98
50	TG	501	GTP	C3'-C2'-C1'	2.87	105.31	100.98
52	HN	502	GDP	C3'-C2'-C1'	2.87	105.31	100.98
50	OO	501	GTP	C2-N1-C6	-2.87	119.81	125.10
50	UA	501	GTP	C2-N1-C6	-2.87	119.81	125.10
50	TK	501	GTP	C3'-C2'-C1'	2.87	105.30	100.98
50	NO	501	GTP	C2-N1-C6	-2.87	119.81	125.10
50	OK	501	GTP	C3'-C2'-C1'	2.87	105.30	100.98
50	OK	501	GTP	C2-N1-C6	-2.87	119.81	125.10
52	HB	502	GDP	C3'-C2'-C1'	2.87	105.30	100.98
50	CE	501	GTP	C3'-C2'-C1'	2.87	105.30	100.98
52	LN	502	GDP	C3'-C2'-C1'	2.87	105.30	100.98
50	SA	501	GTP	C3'-C2'-C1'	2.87	105.30	100.98
50	VM	501	GTP	C3'-C2'-C1'	2.87	105.30	100.98
50	FG	501	GTP	C2-N1-C6	-2.87	119.81	125.10
50	UC	501	GTP	C2-N1-C6	-2.87	119.81	125.10
50	WI	501	GTP	C3'-C2'-C1'	2.87	105.30	100.98
52	HF	502	GDP	C3'-C2'-C1'	2.87	105.30	100.98
50	PC	501	GTP	C2-N1-C6	-2.87	119.81	125.10
50	QK	501	GTP	C2-N1-C6	-2.87	119.81	125.10
50	LA	501	GTP	PA-O3A-PB	-2.87	122.98	132.83
50	GI	501	GTP	C2-N1-C6	-2.87	119.82	125.10
50	VM	501	GTP	C2-N1-C6	-2.87	119.82	125.10
50	HE	501	GTP	C3'-C2'-C1'	2.87	105.30	100.98
50	MM	501	GTP	C2-N1-C6	-2.87	119.82	125.10
50	WA	501	GTP	C2-N1-C6	-2.87	119.82	125.10
52	VN	502	GDP	PA-O3A-PB	-2.87	122.99	132.83
50	TC	501	GTP	C3'-C2'-C1'	2.87	105.29	100.98
52	FH	502	GDP	C3'-C2'-C1'	2.87	105.29	100.98
50	NE	501	GTP	C2-N1-C6	-2.87	119.82	125.10
52	QF	502	GDP	C3'-C2'-C1'	2.87	105.29	100.98
50	MA	501	GTP	C2-N1-C6	-2.87	119.82	125.10
50	FO	501	GTP	C3'-C2'-C1'	2.86	105.29	100.98
50	PK	501	GTP	C3'-C2'-C1'	2.86	105.29	100.98
50	RC	501	GTP	C3'-C2'-C1'	2.86	105.29	100.98
50	HI	501	GTP	C2-N1-C6	-2.86	119.83	125.10
50	TE	501	GTP	C3'-C2'-C1'	2.86	105.29	100.98
50	GO	501	GTP	C2-N1-C6	-2.86	119.83	125.10
50	WK	501	GTP	C2-N1-C6	-2.86	119.83	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	SA	501	GTP	C2-N1-C6	-2.86	119.83	125.10
50	IC	501	GTP	C2-N1-C6	-2.86	119.83	125.10
52	GJ	502	GDP	C3'-C2'-C1'	2.86	105.28	100.98
50	OI	501	GTP	C2-N1-C6	-2.86	119.83	125.10
50	TC	501	GTP	C2-N1-C6	-2.86	119.83	125.10
50	PO	501	GTP	C3'-C2'-C1'	2.86	105.28	100.98
50	UE	501	GTP	C2-N1-C6	-2.86	119.84	125.10
50	KE	501	GTP	C8-N7-C5	2.86	108.43	102.99
50	DO	501	GTP	C2-N1-C6	-2.85	119.84	125.10
50	VE	501	GTP	C2-N1-C6	-2.85	119.84	125.10
50	BC	501	GTP	C3'-C2'-C1'	2.85	105.28	100.98
50	HE	501	GTP	C2-N1-C6	-2.85	119.85	125.10
50	RG	501	GTP	C3'-C2'-C1'	2.85	105.27	100.98
50	LO	501	GTP	C2-N1-C6	-2.85	119.85	125.10
52	DB	502	GDP	C3'-C2'-C1'	2.85	105.27	100.98
50	HG	501	GTP	C2-N1-C6	-2.85	119.85	125.10
50	JQ	501	GTP	C2-N1-C6	-2.85	119.85	125.10
50	SM	501	GTP	C3'-C2'-C1'	2.85	105.27	100.98
50	UI	501	GTP	C2-N1-C6	-2.85	119.86	125.10
50	GC	501	GTP	C2-N1-C6	-2.85	119.86	125.10
50	KE	501	GTP	C2-N1-C6	-2.85	119.86	125.10
50	PM	501	GTP	C3'-C2'-C1'	2.85	105.26	100.98
52	WN	502	GDP	C3'-C2'-C1'	2.85	105.26	100.98
50	IE	501	GTP	PA-O3A-PB	-2.85	123.06	132.83
50	FK	501	GTP	C2-N1-C6	-2.85	119.86	125.10
50	FA	501	GTP	C3'-C2'-C1'	2.84	105.26	100.98
50	OA	501	GTP	C2-N1-C6	-2.84	119.86	125.10
50	SE	501	GTP	C3'-C2'-C1'	2.84	105.26	100.98
50	NC	501	GTP	C2-N1-C6	-2.84	119.86	125.10
50	RM	501	GTP	C3'-C2'-C1'	2.84	105.26	100.98
50	TA	501	GTP	C3'-C2'-C1'	2.84	105.26	100.98
50	TA	501	GTP	C2-N1-C6	-2.84	119.86	125.10
50	OM	501	GTP	C2-N1-C6	-2.84	119.87	125.10
50	BE	501	GTP	C3'-C2'-C1'	2.84	105.25	100.98
50	NI	501	GTP	C2-N1-C6	-2.84	119.87	125.10
52	DP	502	GDP	C3'-C2'-C1'	2.84	105.25	100.98
50	OC	501	GTP	C2-N1-C6	-2.84	119.87	125.10
50	UG	501	GTP	C2-N1-C6	-2.84	119.87	125.10
52	PL	502	GDP	C3'-C2'-C1'	2.84	105.25	100.98
50	UK	501	GTP	C2-N1-C6	-2.84	119.87	125.10
50	TM	501	GTP	C3'-C2'-C1'	2.84	105.25	100.98
50	SK	501	GTP	C2-N1-C6	-2.84	119.88	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	RI	501	GTP	C3'-C2'-C1'	2.84	105.25	100.98
50	MA	501	GTP	C3'-C2'-C1'	2.84	105.25	100.98
50	TI	501	GTP	C2-N1-C6	-2.83	119.88	125.10
50	QM	501	GTP	PA-O3A-PB	-2.83	123.10	132.83
50	NA	501	GTP	C2-N1-C6	-2.83	119.88	125.10
52	EH	502	GDP	C3'-C2'-C1'	2.83	105.24	100.98
50	MC	501	GTP	C2-N1-C6	-2.83	119.89	125.10
50	VK	501	GTP	C3'-C2'-C1'	2.83	105.24	100.98
50	BO	501	GTP	C3'-C2'-C1'	2.83	105.24	100.98
50	II	501	GTP	C8-N7-C5	2.83	108.38	102.99
50	FM	501	GTP	C2-N1-C6	-2.83	119.89	125.10
50	KA	501	GTP	C3'-C2'-C1'	2.83	105.23	100.98
50	VO	501	GTP	C3'-C2'-C1'	2.83	105.23	100.98
52	DF	502	GDP	C3'-C2'-C1'	2.83	105.23	100.98
50	QC	501	GTP	PA-O3A-PB	-2.83	123.13	132.83
50	HA	501	GTP	C2-N1-C6	-2.82	119.90	125.10
50	SM	501	GTP	C2-N1-C6	-2.82	119.90	125.10
50	VO	501	GTP	C2-N1-C6	-2.82	119.90	125.10
50	SG	501	GTP	C2-N1-C6	-2.82	119.90	125.10
50	DQ	501	GTP	C3'-C2'-C1'	2.82	105.22	100.98
50	GE	501	GTP	C2-N1-C6	-2.82	119.91	125.10
50	SE	501	GTP	C2-N1-C6	-2.82	119.91	125.10
50	GM	501	GTP	C2-N1-C6	-2.82	119.91	125.10
52	VN	502	GDP	C3'-C2'-C1'	2.81	105.22	100.98
50	QC	501	GTP	C2-N1-C6	-2.81	119.92	125.10
50	VI	501	GTP	C2-N1-C6	-2.81	119.92	125.10
50	QK	501	GTP	C3'-C2'-C1'	2.81	105.21	100.98
50	NE	501	GTP	PA-O3A-PB	-2.81	123.19	132.83
50	II	501	GTP	C3'-C2'-C1'	2.81	105.21	100.98
50	JE	501	GTP	C3'-C2'-C1'	2.81	105.20	100.98
50	FG	501	GTP	C3'-C2'-C1'	2.80	105.20	100.98
50	SI	501	GTP	C3'-C2'-C1'	2.80	105.20	100.98
50	FE	501	GTP	C2-N1-C6	-2.80	119.93	125.10
50	LO	501	GTP	C3'-C2'-C1'	2.80	105.20	100.98
50	EM	501	GTP	C3'-C2'-C1'	2.80	105.20	100.98
50	NG	501	GTP	C2-N1-C6	-2.80	119.94	125.10
50	GG	501	GTP	C2-N1-C6	-2.80	119.95	125.10
50	CC	501	GTP	C3'-C2'-C1'	2.80	105.19	100.98
50	NE	501	GTP	C3'-C2'-C1'	2.79	105.19	100.98
50	RE	501	GTP	PA-O3A-PB	-2.79	123.24	132.83
50	OE	501	GTP	C2-N1-C6	-2.79	119.96	125.10
50	SC	501	GTP	C3'-C2'-C1'	2.79	105.18	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	AH	502	GDP	C3'-C2'-C1'	2.79	105.18	100.98
52	GD	502	GDP	C3'-C2'-C1'	2.79	105.18	100.98
52	KD	502	GDP	C3'-C2'-C1'	2.79	105.18	100.98
50	EG	501	GTP	C3'-C2'-C1'	2.79	105.18	100.98
50	WG	501	GTP	C3'-C2'-C1'	2.79	105.17	100.98
50	FM	501	GTP	C3'-C2'-C1'	2.79	105.17	100.98
52	JN	502	GDP	C3'-C2'-C1'	2.79	105.17	100.98
52	BH	502	GDP	C3'-C2'-C1'	2.78	105.17	100.98
50	RI	501	GTP	PA-O3A-PB	-2.78	123.27	132.83
50	TE	501	GTP	C2-N1-C6	-2.78	119.97	125.10
50	TK	501	GTP	C2-N1-C6	-2.78	119.97	125.10
50	SK	501	GTP	C3'-C2'-C1'	2.78	105.17	100.98
50	QE	501	GTP	PA-O3A-PB	-2.78	123.28	132.83
50	MK	501	GTP	C3'-C2'-C1'	2.78	105.16	100.98
52	WJ	502	GDP	C3'-C2'-C1'	2.78	105.16	100.98
50	DO	501	GTP	C3'-C2'-C1'	2.78	105.16	100.98
50	KM	501	GTP	PA-O3A-PB	-2.78	123.29	132.83
52	WF	502	GDP	C3'-C2'-C1'	2.78	105.16	100.98
50	LA	501	GTP	C3'-C2'-C1'	2.77	105.16	100.98
50	TM	501	GTP	C2-N1-C6	-2.77	119.99	125.10
50	TG	501	GTP	C2-N1-C6	-2.77	119.99	125.10
50	UI	501	GTP	PA-O3A-PB	-2.77	123.32	132.83
50	NG	501	GTP	C3'-C2'-C1'	2.77	105.15	100.98
50	NO	501	GTP	C3'-C2'-C1'	2.77	105.15	100.98
50	RE	501	GTP	C3'-C2'-C1'	2.77	105.15	100.98
52	VF	502	GDP	C3'-C2'-C1'	2.77	105.15	100.98
52	BP	502	GDP	C3'-C2'-C1'	2.77	105.15	100.98
52	ON	502	GDP	C3'-C2'-C1'	2.77	105.15	100.98
50	BK	501	GTP	C3'-C2'-C1'	2.77	105.14	100.98
50	IM	501	GTP	C3'-C2'-C1'	2.77	105.14	100.98
50	QO	501	GTP	C3'-C2'-C1'	2.76	105.14	100.98
52	EL	502	GDP	C3'-C2'-C1'	2.76	105.14	100.98
52	IJ	502	GDP	C3'-C2'-C1'	2.76	105.13	100.98
50	GK	501	GTP	C2-N1-C6	-2.75	120.03	125.10
50	SI	501	GTP	C2-N1-C6	-2.75	120.03	125.10
50	HM	501	GTP	C3'-C2'-C1'	2.75	105.12	100.98
50	HO	501	GTP	C3'-C2'-C1'	2.75	105.12	100.98
50	HA	501	GTP	C3'-C2'-C1'	2.75	105.11	100.98
50	WC	501	GTP	C3'-C2'-C1'	2.75	105.11	100.98
52	JL	502	GDP	C3'-C2'-C1'	2.75	105.11	100.98
50	KM	501	GTP	C3'-C2'-C1'	2.75	105.11	100.98
50	AO	501	GTP	C3'-C2'-C1'	2.74	105.11	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	LE	501	GTP	PA-O3A-PB	-2.74	123.42	132.83
50	DE	501	GTP	C3'-C2'-C1'	2.74	105.10	100.98
52	QH	502	GDP	C3'-C2'-C1'	2.74	105.10	100.98
50	BI	501	GTP	C3'-C2'-C1'	2.74	105.10	100.98
52	RN	502	GDP	C3'-C2'-C1'	2.74	105.10	100.98
50	MC	501	GTP	C3'-C2'-C1'	2.73	105.09	100.98
50	RG	501	GTP	PA-O3A-PB	-2.73	123.46	132.83
50	DK	501	GTP	C3'-C2'-C1'	2.73	105.09	100.98
50	HG	501	GTP	C3'-C2'-C1'	2.73	105.09	100.98
50	LG	501	GTP	C3'-C2'-C1'	2.73	105.09	100.98
52	IN	502	GDP	C3'-C2'-C1'	2.73	105.08	100.98
50	DM	501	GTP	C3'-C2'-C1'	2.73	105.08	100.98
50	JM	501	GTP	C3'-C2'-C1'	2.72	105.08	100.98
52	FD	502	GDP	C3'-C2'-C1'	2.72	105.07	100.98
52	SH	502	GDP	C3'-C2'-C1'	2.72	105.07	100.98
50	LC	501	GTP	PA-O3A-PB	-2.72	123.50	132.83
50	NI	501	GTP	C3'-C2'-C1'	2.72	105.07	100.98
52	HL	502	GDP	C3'-C2'-C1'	2.71	105.06	100.98
50	JQ	501	GTP	C3'-C2'-C1'	2.71	105.06	100.98
50	FI	501	GTP	C3'-C2'-C1'	2.71	105.06	100.98
50	GI	501	GTP	C3'-C2'-C1'	2.71	105.05	100.98
52	FJ	502	GDP	C3'-C2'-C1'	2.70	105.05	100.98
52	BL	502	GDP	C3'-C2'-C1'	2.70	105.04	100.98
52	CP	502	GDP	C3'-C2'-C1'	2.70	105.04	100.98
50	FE	501	GTP	C3'-C2'-C1'	2.70	105.04	100.98
52	RJ	502	GDP	C3'-C2'-C1'	2.69	105.02	100.98
50	GO	501	GTP	C3'-C2'-C1'	2.69	105.02	100.98
50	QI	501	GTP	C3'-C2'-C1'	2.69	105.02	100.98
50	AM	501	GTP	C3'-C2'-C1'	2.68	105.02	100.98
50	PG	501	GTP	C3'-C2'-C1'	2.68	105.02	100.98
52	JJ	502	GDP	C3'-C2'-C1'	2.68	105.02	100.98
50	KK	501	GTP	C3'-C2'-C1'	2.67	105.00	100.98
52	DL	502	GDP	C3'-C2'-C1'	2.67	104.99	100.98
52	LJ	502	GDP	C3'-C2'-C1'	2.67	104.99	100.98
50	MO	501	GTP	C3'-C2'-C1'	2.67	104.99	100.98
52	KP	502	GDP	C3'-C2'-C1'	2.67	104.99	100.98
50	EK	501	GTP	PA-O3A-PB	-2.67	123.68	132.83
50	JI	501	GTP	C3'-C2'-C1'	2.66	104.99	100.98
50	HC	501	GTP	C3'-C2'-C1'	2.66	104.99	100.98
52	FF	502	GDP	C3'-C2'-C1'	2.66	104.98	100.98
50	RK	501	GTP	C3'-C2'-C1'	2.66	104.98	100.98
52	NL	502	GDP	C3'-C2'-C1'	2.65	104.97	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	JK	501	GTP	C3'-C2'-C1'	2.65	104.97	100.98
52	EJ	502	GDP	C3'-C2'-C1'	2.65	104.97	100.98
52	HH	502	GDP	C3'-C2'-C1'	2.65	104.97	100.98
52	EN	502	GDP	C3'-C2'-C1'	2.65	104.97	100.98
50	QG	501	GTP	C3'-C2'-C1'	2.64	104.95	100.98
50	EC	501	GTP	C3'-C2'-C1'	2.64	104.95	100.98
50	IO	501	GTP	C3'-C2'-C1'	2.64	104.95	100.98
50	AG	501	GTP	C3'-C2'-C1'	2.63	104.94	100.98
50	MC	501	GTP	PA-O3A-PB	-2.63	123.80	132.83
50	BG	501	GTP	C3'-C2'-C1'	2.61	104.92	100.98
50	TI	501	GTP	C3'-C2'-C1'	2.61	104.91	100.98
50	CI	501	GTP	C3'-C2'-C1'	2.61	104.91	100.98
50	GM	501	GTP	C3'-C2'-C1'	2.61	104.91	100.98
50	LC	501	GTP	C3'-C2'-C1'	2.59	104.88	100.98
50	JG	501	GTP	C3'-C2'-C1'	2.59	104.87	100.98
52	OJ	502	GDP	O6-C6-C5	-2.58	119.33	124.37
52	ML	502	GDP	C3'-C2'-C1'	2.58	104.86	100.98
52	QP	502	GDP	C5-C6-N1	2.57	118.50	113.95
52	QH	502	GDP	PA-O3A-PB	-2.57	123.99	132.83
52	OL	502	GDP	C5-C6-N1	2.57	118.50	113.95
50	LM	501	GTP	C3'-C2'-C1'	2.57	104.85	100.98
50	MM	501	GTP	C3'-C2'-C1'	2.57	104.85	100.98
50	AE	501	GTP	C3'-C2'-C1'	2.57	104.84	100.98
50	NM	501	GTP	C3'-C2'-C1'	2.57	104.84	100.98
52	AF	502	GDP	C3'-C2'-C1'	2.56	104.83	100.98
52	JF	502	GDP	C8-N7-C5	2.56	107.86	102.99
50	MG	501	GTP	C3'-C2'-C1'	2.55	104.82	100.98
52	QJ	502	GDP	C3'-C2'-C1'	2.55	104.82	100.98
50	KI	501	GTP	C3'-C2'-C1'	2.55	104.82	100.98
50	QC	501	GTP	C3'-C2'-C1'	2.55	104.81	100.98
52	JD	502	GDP	C3'-C2'-C1'	2.54	104.80	100.98
50	KE	501	GTP	PA-O3A-PB	-2.53	124.14	132.83
50	KC	501	GTP	C3'-C2'-C1'	2.53	104.78	100.98
52	OL	502	GDP	C3'-C2'-C1'	2.53	104.78	100.98
52	OD	502	GDP	C3'-C2'-C1'	2.52	104.77	100.98
50	AC	501	GTP	C3'-C2'-C1'	2.52	104.77	100.98
52	FB	502	GDP	C3'-C2'-C1'	2.52	104.77	100.98
50	SG	501	GTP	C3'-C2'-C1'	2.51	104.76	100.98
52	IP	502	GDP	O3B-PB-O3A	2.51	113.05	104.64
52	KH	502	GDP	C3'-C2'-C1'	2.51	104.75	100.98
50	KO	501	GTP	C3'-C2'-C1'	2.50	104.74	100.98
52	OD	502	GDP	C5-C6-N1	2.49	118.35	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	CD	502	GDP	C3'-C2'-C1'	2.48	104.71	100.98
52	HD	502	GDP	C3'-C2'-C1'	2.48	104.71	100.98
52	IF	502	GDP	C3'-C2'-C1'	2.48	104.71	100.98
50	LE	501	GTP	C3'-C2'-C1'	2.47	104.70	100.98
52	GF	502	GDP	C8-N7-C5	2.47	107.69	102.99
52	JF	502	GDP	C5-C6-N1	2.47	118.31	113.95
52	OB	502	GDP	C8-N7-C5	2.47	107.69	102.99
52	RD	502	GDP	C5-C6-N1	2.46	118.30	113.95
50	HI	501	GTP	C3'-C2'-C1'	2.46	104.68	100.98
52	DJ	502	GDP	C8-N7-C5	2.46	107.68	102.99
52	DD	502	GDP	C3'-C2'-C1'	2.46	104.68	100.98
52	CL	502	GDP	C5-C6-N1	2.46	118.29	113.95
52	IF	502	GDP	C8-N7-C5	2.45	107.66	102.99
52	NL	502	GDP	C8-N7-C5	2.45	107.66	102.99
52	DH	502	GDP	C8-N7-C5	2.45	107.66	102.99
50	EO	501	GTP	C3'-C2'-C1'	2.45	104.66	100.98
52	JH	502	GDP	C5-C6-N1	2.45	118.27	113.95
50	KE	501	GTP	C3'-C2'-C1'	2.45	104.66	100.98
52	UJ	502	GDP	C8-N7-C5	2.44	107.65	102.99
52	AJ	502	GDP	C3'-C2'-C1'	2.44	104.66	100.98
50	AE	501	GTP	O6-C6-C5	-2.44	119.61	124.37
52	IH	502	GDP	C3'-C2'-C1'	2.43	104.64	100.98
52	SD	502	GDP	C5-C6-N1	2.43	118.25	113.95
52	CF	502	GDP	C3'-C2'-C1'	2.43	104.64	100.98
52	KL	502	GDP	C3'-C2'-C1'	2.43	104.63	100.98
52	LB	502	GDP	C5-C6-N1	2.43	118.23	113.95
52	IL	502	GDP	C5-C6-N1	2.42	118.23	113.95
50	QG	501	GTP	O6-C6-C5	-2.42	119.64	124.37
52	LH	502	GDP	C5-C6-N1	2.42	118.23	113.95
52	FL	502	GDP	C5-C6-N1	2.42	118.22	113.95
52	CF	502	GDP	C5-C6-N1	2.42	118.22	113.95
52	DF	502	GDP	C8-N7-C5	2.42	107.59	102.99
52	KF	502	GDP	C3'-C2'-C1'	2.42	104.61	100.98
52	EF	502	GDP	C8-N7-C5	2.41	107.59	102.99
52	GD	502	GDP	C5-C6-N1	2.41	118.22	113.95
52	VD	502	GDP	C8-N7-C5	2.41	107.59	102.99
50	NG	501	GTP	O6-C6-C5	-2.41	119.66	124.37
52	QJ	502	GDP	C8-N7-C5	2.41	107.58	102.99
52	BF	502	GDP	C5-C6-N1	2.41	118.21	113.95
52	BB	502	GDP	C8-N7-C5	2.41	107.58	102.99
52	DH	502	GDP	C3'-C2'-C1'	2.41	104.60	100.98
52	IL	502	GDP	C8-N7-C5	2.41	107.58	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	HN	502	GDP	C8-N7-C5	2.41	107.57	102.99
52	AJ	502	GDP	C5-C6-N1	2.40	118.20	113.95
52	JL	502	GDP	C8-N7-C5	2.40	107.57	102.99
50	QO	501	GTP	C2-N1-C6	-2.40	120.67	125.10
52	VH	502	GDP	C8-N7-C5	2.40	107.57	102.99
52	KL	502	GDP	C5-C6-N1	2.40	118.19	113.95
52	UH	502	GDP	C8-N7-C5	2.40	107.56	102.99
52	KJ	502	GDP	C5-C6-N1	2.40	118.19	113.95
50	AI	501	GTP	C3'-C2'-C1'	2.40	104.58	100.98
52	HN	502	GDP	C5-C6-N1	2.39	118.18	113.95
52	NF	502	GDP	C5-C6-N1	2.39	118.18	113.95
52	HP	502	GDP	C8-N7-C5	2.39	107.55	102.99
52	QH	502	GDP	C8-N7-C5	2.39	107.55	102.99
52	IH	502	GDP	C8-N7-C5	2.39	107.55	102.99
52	PJ	502	GDP	C8-N7-C5	2.39	107.55	102.99
52	VL	502	GDP	C8-N7-C5	2.39	107.55	102.99
52	IJ	502	GDP	C5-C6-N1	2.39	118.17	113.95
50	BE	501	GTP	O6-C6-C5	-2.39	119.70	124.37
52	JP	502	GDP	C8-N7-C5	2.39	107.54	102.99
52	PF	502	GDP	C8-N7-C5	2.39	107.54	102.99
52	LF	502	GDP	C3'-C2'-C1'	2.39	104.57	100.98
52	GB	502	GDP	C5-C6-N1	2.39	118.17	113.95
52	JL	502	GDP	C5-C6-N1	2.39	118.17	113.95
50	NK	501	GTP	C3'-C2'-C1'	2.39	104.57	100.98
52	GJ	502	GDP	PA-O3A-PB	-2.38	124.64	132.83
52	PH	502	GDP	C8-N7-C5	2.38	107.53	102.99
52	JN	502	GDP	C8-N7-C5	2.38	107.53	102.99
52	EF	502	GDP	C3'-C2'-C1'	2.38	104.56	100.98
52	HL	502	GDP	C8-N7-C5	2.38	107.53	102.99
52	NP	502	GDP	C8-N7-C5	2.38	107.53	102.99
52	EB	502	GDP	C8-N7-C5	2.38	107.52	102.99
52	NL	502	GDP	C5-C6-N1	2.38	118.15	113.95
52	TB	502	GDP	C5-C6-N1	2.38	118.15	113.95
52	PL	502	GDP	C8-N7-C5	2.38	107.52	102.99
52	VJ	502	GDP	C8-N7-C5	2.38	107.52	102.99
52	ON	502	GDP	C8-N7-C5	2.38	107.52	102.99
52	JN	502	GDP	C5-C6-N1	2.38	118.15	113.95
52	DD	502	GDP	C5-C6-N1	2.38	118.15	113.95
52	KF	502	GDP	C5-C6-N1	2.38	118.15	113.95
52	WN	502	GDP	C8-N7-C5	2.38	107.52	102.99
52	AP	502	GDP	C5-C6-N1	2.38	118.15	113.95
52	CN	502	GDP	C5-C6-N1	2.37	118.14	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	UN	502	GDP	C8-N7-C5	2.37	107.51	102.99
52	CD	502	GDP	C5-C6-N1	2.37	118.14	113.95
52	PP	502	GDP	C8-N7-C5	2.37	107.51	102.99
52	IJ	502	GDP	C8-N7-C5	2.37	107.51	102.99
52	VB	502	GDP	C8-N7-C5	2.37	107.51	102.99
52	GJ	502	GDP	C8-N7-C5	2.37	107.51	102.99
52	BP	502	GDP	C5-C6-N1	2.37	118.14	113.95
52	GL	502	GDP	C5-C6-N1	2.37	118.14	113.95
52	UB	502	GDP	C8-N7-C5	2.37	107.50	102.99
52	KN	502	GDP	C8-N7-C5	2.37	107.50	102.99
52	RF	502	GDP	C5-C6-N1	2.37	118.13	113.95
52	OF	502	GDP	C8-N7-C5	2.37	107.50	102.99
52	DL	502	GDP	C5-C6-N1	2.37	118.13	113.95
52	HF	502	GDP	C5-C6-N1	2.37	118.13	113.95
52	ID	502	GDP	C5-C6-N1	2.37	118.13	113.95
50	AC	501	GTP	O6-C6-C5	-2.36	119.75	124.37
52	CH	502	GDP	C5-C6-N1	2.36	118.13	113.95
52	BD	502	GDP	C5-C6-N1	2.36	118.13	113.95
52	BL	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	PP	502	GDP	C5-C6-N1	2.36	118.13	113.95
52	RH	502	GDP	C5-C6-N1	2.36	118.13	113.95
52	CP	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	UD	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	WF	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	PJ	502	GDP	C5-C6-N1	2.36	118.12	113.95
52	PD	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	PH	502	GDP	C5-C6-N1	2.36	118.12	113.95
52	EJ	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	TJ	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	EH	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	KH	502	GDP	C5-C6-N1	2.36	118.12	113.95
52	AN	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	RD	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	WJ	502	GDP	C8-N7-C5	2.36	107.49	102.99
52	QL	502	GDP	C5-C6-N1	2.36	118.12	113.95
52	QB	502	GDP	C5-C6-N1	2.36	118.12	113.95
52	VN	502	GDP	C8-N7-C5	2.36	107.48	102.99
52	AB	502	GDP	C8-N7-C5	2.36	107.48	102.99
52	WB	502	GDP	C8-N7-C5	2.36	107.48	102.99
52	JJ	502	GDP	C8-N7-C5	2.36	107.48	102.99
50	RK	501	GTP	PA-O3A-PB	-2.36	124.74	132.83
52	AP	502	GDP	C8-N7-C5	2.36	107.48	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	TB	502	GDP	C8-N7-C5	2.36	107.48	102.99
52	UF	502	GDP	C8-N7-C5	2.36	107.48	102.99
52	BJ	502	GDP	C8-N7-C5	2.36	107.48	102.99
52	EL	502	GDP	C5-C6-N1	2.36	118.11	113.95
52	WH	502	GDP	C8-N7-C5	2.35	107.47	102.99
52	JD	502	GDP	C8-N7-C5	2.35	107.47	102.99
52	AF	502	GDP	C8-N7-C5	2.35	107.47	102.99
52	CD	502	GDP	C8-N7-C5	2.35	107.47	102.99
52	ED	502	GDP	C8-N7-C5	2.35	107.47	102.99
52	VF	502	GDP	C8-N7-C5	2.35	107.47	102.99
52	AH	502	GDP	C5-C6-N1	2.35	118.11	113.95
52	OF	502	GDP	C5-C6-N1	2.35	118.11	113.95
52	QD	502	GDP	C5-C6-N1	2.35	118.11	113.95
52	NJ	502	GDP	C5-C6-N1	2.35	118.10	113.95
52	VB	502	GDP	C5-C6-N1	2.35	118.10	113.95
52	QN	502	GDP	C8-N7-C5	2.35	107.47	102.99
52	OP	502	GDP	C5-C6-N1	2.35	118.10	113.95
52	TF	502	GDP	C8-N7-C5	2.35	107.47	102.99
52	OH	502	GDP	C5-C6-N1	2.35	118.10	113.95
50	AK	501	GTP	C3'-C2'-C1'	2.35	104.51	100.98
52	JB	502	GDP	C5-C6-N1	2.35	118.10	113.95
52	BP	502	GDP	C8-N7-C5	2.35	107.46	102.99
52	TL	502	GDP	C8-N7-C5	2.35	107.46	102.99
52	PD	502	GDP	C5-C6-N1	2.35	118.10	113.95
52	AB	502	GDP	C5-C6-N1	2.35	118.09	113.95
52	WN	502	GDP	C5-C6-N1	2.35	118.09	113.95
52	DH	502	GDP	C5-C6-N1	2.35	118.09	113.95
52	FF	502	GDP	C5-C6-N1	2.35	118.09	113.95
52	PN	502	GDP	C5-C6-N1	2.35	118.09	113.95
52	QF	502	GDP	C5-C6-N1	2.35	118.09	113.95
52	WJ	502	GDP	C5-C6-N1	2.34	118.09	113.95
52	LB	502	GDP	C8-N7-C5	2.34	107.46	102.99
52	TD	502	GDP	C8-N7-C5	2.34	107.46	102.99
52	NH	502	GDP	C5-C6-N1	2.34	118.09	113.95
52	CB	502	GDP	C5-C6-N1	2.34	118.09	113.95
52	TH	502	GDP	C5-C6-N1	2.34	118.09	113.95
52	FN	502	GDP	C5-C6-N1	2.34	118.09	113.95
52	CF	502	GDP	C8-N7-C5	2.34	107.45	102.99
52	FD	502	GDP	C5-C6-N1	2.34	118.09	113.95
52	WD	502	GDP	C8-N7-C5	2.34	107.45	102.99
52	UL	502	GDP	C8-N7-C5	2.34	107.45	102.99
52	KB	502	GDP	C5-C6-N1	2.34	118.08	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	DB	502	GDP	C8-N7-C5	2.34	107.45	102.99
52	TN	502	GDP	C8-N7-C5	2.34	107.45	102.99
52	UH	502	GDP	C5-C6-N1	2.34	118.08	113.95
52	VD	502	GDP	C5-C6-N1	2.34	118.08	113.95
50	KI	501	GTP	O6-C6-C5	-2.34	119.81	124.37
52	AH	502	GDP	C8-N7-C5	2.34	107.44	102.99
52	LP	502	GDP	C8-N7-C5	2.34	107.44	102.99
52	CL	502	GDP	C3'-C2'-C1'	2.34	104.50	100.98
52	DB	502	GDP	C5-C6-N1	2.34	118.08	113.95
52	BD	502	GDP	C8-N7-C5	2.34	107.44	102.99
52	DD	502	GDP	C8-N7-C5	2.34	107.44	102.99
52	WL	502	GDP	C8-N7-C5	2.34	107.44	102.99
52	AL	502	GDP	C5-C6-N1	2.34	118.08	113.95
52	MB	502	GDP	C3'-C2'-C1'	2.34	104.50	100.98
52	TH	502	GDP	C8-N7-C5	2.34	107.44	102.99
52	GH	502	GDP	C5-C6-N1	2.34	118.08	113.95
52	GL	502	GDP	C8-N7-C5	2.34	107.44	102.99
52	HB	502	GDP	C8-N7-C5	2.34	107.44	102.99
52	HJ	502	GDP	C8-N7-C5	2.34	107.44	102.99
52	PL	502	GDP	C5-C6-N1	2.33	118.08	113.95
52	DJ	502	GDP	C5-C6-N1	2.33	118.07	113.95
52	RF	502	GDP	C8-N7-C5	2.33	107.44	102.99
52	NB	502	GDP	C5-C6-N1	2.33	118.07	113.95
52	QF	502	GDP	C8-N7-C5	2.33	107.44	102.99
52	PB	502	GDP	C8-N7-C5	2.33	107.43	102.99
52	OD	502	GDP	C8-N7-C5	2.33	107.43	102.99
52	CJ	502	GDP	C5-C6-N1	2.33	118.07	113.95
52	AD	502	GDP	C5-C6-N1	2.33	118.07	113.95
52	SF	502	GDP	C5-C6-N1	2.33	118.07	113.95
52	IB	502	GDP	C8-N7-C5	2.33	107.43	102.99
52	JD	502	GDP	C5-C6-N1	2.33	118.07	113.95
52	CN	502	GDP	C8-N7-C5	2.33	107.43	102.99
52	PN	502	GDP	C8-N7-C5	2.33	107.43	102.99
52	CJ	502	GDP	C8-N7-C5	2.33	107.43	102.99
52	HL	502	GDP	C5-C6-N1	2.33	118.06	113.95
52	CH	502	GDP	C8-N7-C5	2.33	107.42	102.99
52	EN	502	GDP	C8-N7-C5	2.33	107.42	102.99
52	SN	502	GDP	C8-N7-C5	2.33	107.42	102.99
52	IF	502	GDP	C5-C6-N1	2.33	118.06	113.95
52	KP	502	GDP	C5-C6-N1	2.33	118.06	113.95
52	WP	502	GDP	C8-N7-C5	2.33	107.42	102.99
52	DN	502	GDP	C5-C6-N1	2.33	118.06	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	QL	502	GDP	C8-N7-C5	2.33	107.42	102.99
52	SB	502	GDP	C5-C6-N1	2.33	118.06	113.95
52	ND	502	GDP	C5-C6-N1	2.33	118.06	113.95
52	QJ	502	GDP	C5-C6-N1	2.33	118.06	113.95
52	DL	502	GDP	C8-N7-C5	2.32	107.42	102.99
52	MH	502	GDP	C3'-C2'-C1'	2.32	104.48	100.98
52	MP	502	GDP	C8-N7-C5	2.32	107.42	102.99
52	SD	502	GDP	C8-N7-C5	2.32	107.42	102.99
52	LD	502	GDP	C5-C6-N1	2.32	118.05	113.95
52	GH	502	GDP	C8-N7-C5	2.32	107.41	102.99
52	RP	502	GDP	C8-N7-C5	2.32	107.41	102.99
52	MP	502	GDP	C5-C6-N1	2.32	118.05	113.95
52	GF	502	GDP	C5-C6-N1	2.32	118.05	113.95
52	LL	502	GDP	C5-C6-N1	2.32	118.05	113.95
52	BH	502	GDP	C8-N7-C5	2.32	107.41	102.99
52	TL	502	GDP	C5-C6-N1	2.32	118.05	113.95
52	CB	502	GDP	C8-N7-C5	2.32	107.41	102.99
52	HD	502	GDP	C8-N7-C5	2.32	107.41	102.99
50	KE	501	GTP	O6-C6-C5	-2.32	119.84	124.37
52	RL	502	GDP	C8-N7-C5	2.32	107.41	102.99
52	UB	502	GDP	C5-C6-N1	2.32	118.05	113.95
52	BF	502	GDP	C8-N7-C5	2.32	107.41	102.99
52	DN	502	GDP	C8-N7-C5	2.32	107.41	102.99
52	KL	502	GDP	C8-N7-C5	2.32	107.41	102.99
52	IB	502	GDP	C5-C6-N1	2.32	118.05	113.95
52	UD	502	GDP	C5-C6-N1	2.32	118.05	113.95
52	MD	502	GDP	C5-C6-N1	2.32	118.04	113.95
52	RN	502	GDP	C5-C6-N1	2.32	118.04	113.95
52	TJ	502	GDP	C5-C6-N1	2.32	118.04	113.95
52	LN	502	GDP	C5-C6-N1	2.32	118.04	113.95
52	AN	502	GDP	C5-C6-N1	2.31	118.04	113.95
52	CL	502	GDP	C8-N7-C5	2.31	107.40	102.99
52	GN	502	GDP	C8-N7-C5	2.31	107.40	102.99
52	JB	502	GDP	C8-N7-C5	2.31	107.40	102.99
52	SJ	502	GDP	C5-C6-N1	2.31	118.04	113.95
52	NB	502	GDP	C8-N7-C5	2.31	107.39	102.99
52	SB	502	GDP	C8-N7-C5	2.31	107.39	102.99
52	DP	502	GDP	C8-N7-C5	2.31	107.39	102.99
52	FB	502	GDP	C5-C6-N1	2.31	118.03	113.95
52	RN	502	GDP	C8-N7-C5	2.31	107.39	102.99
52	EN	502	GDP	C5-C6-N1	2.31	118.03	113.95
52	WD	502	GDP	C5-C6-N1	2.31	118.03	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	AJ	502	GDP	C8-N7-C5	2.31	107.39	102.99
52	GJ	502	GDP	O3B-PB-O3A	2.31	112.37	104.64
52	WP	502	GDP	C5-C6-N1	2.31	118.03	113.95
52	QN	502	GDP	C5-C6-N1	2.31	118.02	113.95
52	RJ	502	GDP	C8-N7-C5	2.31	107.38	102.99
52	VH	502	GDP	C5-C6-N1	2.31	118.02	113.95
52	FH	502	GDP	C5-C6-N1	2.30	118.02	113.95
52	MN	502	GDP	C5-C6-N1	2.30	118.02	113.95
50	BI	501	GTP	O6-C6-C5	-2.30	119.87	124.37
52	RL	502	GDP	C5-C6-N1	2.30	118.02	113.95
52	RP	502	GDP	C5-C6-N1	2.30	118.02	113.95
52	MB	502	GDP	C8-N7-C5	2.30	107.38	102.99
52	PF	502	GDP	C5-C6-N1	2.30	118.02	113.95
52	JJ	502	GDP	C5-C6-N1	2.30	118.02	113.95
52	TD	502	GDP	C5-C6-N1	2.30	118.02	113.95
52	MH	502	GDP	C5-C6-N1	2.30	118.02	113.95
52	VJ	502	GDP	C5-C6-N1	2.30	118.02	113.95
50	BO	501	GTP	O6-C6-C5	-2.30	119.88	124.37
52	QB	502	GDP	C8-N7-C5	2.30	107.38	102.99
52	IN	502	GDP	C8-N7-C5	2.30	107.37	102.99
52	SL	502	GDP	C5-C6-N1	2.30	118.02	113.95
52	QH	502	GDP	C5-C6-N1	2.30	118.01	113.95
52	VN	502	GDP	C5-C6-N1	2.30	118.01	113.95
52	OH	502	GDP	C8-N7-C5	2.30	107.37	102.99
52	OP	502	GDP	C8-N7-C5	2.30	107.37	102.99
52	DP	502	GDP	C5-C6-N1	2.30	118.01	113.95
52	LP	502	GDP	C5-C6-N1	2.30	118.01	113.95
52	UL	502	GDP	C5-C6-N1	2.30	118.01	113.95
52	QD	502	GDP	C8-N7-C5	2.30	107.37	102.99
52	LJ	502	GDP	C5-C6-N1	2.30	118.01	113.95
52	LN	502	GDP	C8-N7-C5	2.30	107.36	102.99
52	PB	502	GDP	C5-C6-N1	2.30	118.01	113.95
52	NN	502	GDP	C5-C6-N1	2.30	118.00	113.95
52	EL	502	GDP	C8-N7-C5	2.29	107.36	102.99
52	NF	502	GDP	C8-N7-C5	2.29	107.36	102.99
52	CP	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	KD	502	GDP	C5-C6-N1	2.29	118.00	113.95
50	FK	501	GTP	C3'-C2'-C1'	2.29	104.43	100.98
52	HD	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	IN	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	VL	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	ML	502	GDP	C8-N7-C5	2.29	107.36	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	EF	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	MN	502	GDP	C8-N7-C5	2.29	107.36	102.99
52	KN	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	RJ	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	AL	502	GDP	C8-N7-C5	2.29	107.36	102.99
52	FD	502	GDP	C8-N7-C5	2.29	107.36	102.99
52	LL	502	GDP	C8-N7-C5	2.29	107.35	102.99
52	IP	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	MF	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	UF	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	SN	502	GDP	C5-C6-N1	2.29	118.00	113.95
52	MH	502	GDP	C8-N7-C5	2.29	107.35	102.99
52	BN	502	GDP	C8-N7-C5	2.29	107.35	102.99
52	UN	502	GDP	C5-C6-N1	2.29	117.99	113.95
52	GN	502	GDP	C5-C6-N1	2.29	117.99	113.95
52	LF	502	GDP	C5-C6-N1	2.29	117.99	113.95
52	BH	502	GDP	C5-C6-N1	2.29	117.99	113.95
52	SL	502	GDP	C8-N7-C5	2.28	107.34	102.99
52	HJ	502	GDP	C5-C6-N1	2.28	117.98	113.95
52	FL	502	GDP	C8-N7-C5	2.28	107.34	102.99
52	FB	502	GDP	C8-N7-C5	2.28	107.34	102.99
52	BB	502	GDP	C5-C6-N1	2.28	117.98	113.95
52	JP	502	GDP	C5-C6-N1	2.28	117.98	113.95
52	LF	502	GDP	C8-N7-C5	2.28	107.33	102.99
52	GJ	502	GDP	C5-C6-N1	2.28	117.98	113.95
52	HB	502	GDP	C5-C6-N1	2.28	117.98	113.95
52	WB	502	GDP	C5-C6-N1	2.28	117.98	113.95
52	FH	502	GDP	C8-N7-C5	2.28	107.33	102.99
52	WF	502	GDP	C5-C6-N1	2.28	117.98	113.95
52	TN	502	GDP	C5-C6-N1	2.28	117.98	113.95
52	MD	502	GDP	C8-N7-C5	2.28	107.33	102.99
52	LJ	502	GDP	C8-N7-C5	2.28	107.33	102.99
52	JP	502	GDP	C3'-C2'-C1'	2.28	104.41	100.98
50	MO	501	GTP	O6-C6-C5	-2.28	119.92	124.37
52	HP	502	GDP	C5-C6-N1	2.28	117.97	113.95
52	IH	502	GDP	C5-C6-N1	2.28	117.97	113.95
52	AF	502	GDP	C5-C6-N1	2.27	117.97	113.95
50	LK	501	GTP	C3'-C2'-C1'	2.27	104.40	100.98
52	GB	502	GDP	C8-N7-C5	2.27	107.32	102.99
52	BL	502	GDP	C5-C6-N1	2.27	117.96	113.95
52	EB	502	GDP	C5-C6-N1	2.27	117.96	113.95
52	ND	502	GDP	C8-N7-C5	2.27	107.31	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	GF	502	GDP	C3'-C2'-C1'	2.27	104.40	100.98
52	FF	502	GDP	C8-N7-C5	2.27	107.31	102.99
52	UJ	502	GDP	C5-C6-N1	2.27	117.96	113.95
52	MJ	502	GDP	C5-C6-N1	2.27	117.96	113.95
52	EJ	502	GDP	C5-C6-N1	2.27	117.95	113.95
52	NP	502	GDP	C5-C6-N1	2.27	117.95	113.95
52	ML	502	GDP	C5-C6-N1	2.26	117.95	113.95
52	NH	502	GDP	C8-N7-C5	2.26	107.30	102.99
52	KP	502	GDP	C8-N7-C5	2.26	107.30	102.99
52	MF	502	GDP	C8-N7-C5	2.26	107.30	102.99
52	ED	502	GDP	C5-C6-N1	2.26	117.95	113.95
52	IP	502	GDP	C8-N7-C5	2.26	107.30	102.99
52	TF	502	GDP	C5-C6-N1	2.26	117.94	113.95
50	II	501	GTP	O6-C6-C5	-2.26	119.96	124.37
52	HF	502	GDP	C8-N7-C5	2.26	107.29	102.99
50	LC	501	GTP	O6-C6-C5	-2.26	119.96	124.37
50	LG	501	GTP	O6-C6-C5	-2.26	119.96	124.37
52	OL	502	GDP	C8-N7-C5	2.26	107.29	102.99
52	EH	502	GDP	C5-C6-N1	2.25	117.93	113.95
52	LP	502	GDP	C3'-C2'-C1'	2.25	104.37	100.98
52	FN	502	GDP	C8-N7-C5	2.25	107.28	102.99
52	HH	502	GDP	C8-N7-C5	2.25	107.28	102.99
50	NK	501	GTP	O6-C6-C5	-2.25	119.97	124.37
52	WL	502	GDP	C5-C6-N1	2.25	117.92	113.95
50	AG	501	GTP	O6-C6-C5	-2.25	119.98	124.37
50	FI	501	GTP	O6-C6-C5	-2.25	119.98	124.37
52	GD	502	GDP	C8-N7-C5	2.25	107.27	102.99
52	LD	502	GDP	C8-N7-C5	2.25	107.27	102.99
52	RH	502	GDP	C8-N7-C5	2.25	107.27	102.99
52	SJ	502	GDP	C8-N7-C5	2.25	107.27	102.99
50	GK	501	GTP	O6-C6-C5	-2.25	119.98	124.37
50	NA	501	GTP	O6-C6-C5	-2.25	119.98	124.37
52	AD	502	GDP	C8-N7-C5	2.25	107.27	102.99
52	MJ	502	GDP	C8-N7-C5	2.25	107.27	102.99
52	DF	502	GDP	C5-C6-N1	2.25	117.92	113.95
50	MG	501	GTP	O6-C6-C5	-2.24	119.99	124.37
52	KB	502	GDP	C3'-C2'-C1'	2.24	104.36	100.98
52	TB	502	GDP	O2B-PB-O3A	2.24	112.16	104.64
52	BJ	502	GDP	C5-C6-N1	2.24	117.91	113.95
52	KB	502	GDP	C8-N7-C5	2.24	107.26	102.99
52	MB	502	GDP	C5-C6-N1	2.24	117.91	113.95
52	OB	502	GDP	C5-C6-N1	2.24	117.91	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	BN	502	GDP	C5-C6-N1	2.24	117.90	113.95
50	LI	501	GTP	C3'-C2'-C1'	2.24	104.35	100.98
50	NO	501	GTP	O6-C6-C5	-2.24	120.00	124.37
52	SH	502	GDP	C5-C6-N1	2.24	117.90	113.95
52	WH	502	GDP	C5-C6-N1	2.24	117.90	113.95
52	GB	502	GDP	C2'-C3'-C4'	2.24	106.98	102.64
52	OJ	502	GDP	C3'-C2'-C1'	2.23	104.34	100.98
50	IE	501	GTP	O6-C6-C5	-2.23	120.01	124.37
52	NJ	502	GDP	C8-N7-C5	2.23	107.24	102.99
52	SH	502	GDP	C8-N7-C5	2.23	107.23	102.99
50	CK	501	GTP	O6-C6-C5	-2.23	120.02	124.37
52	QP	502	GDP	C8-N7-C5	2.23	107.23	102.99
52	VF	502	GDP	C5-C6-N1	2.22	117.88	113.95
50	NE	501	GTP	O6-C6-C5	-2.22	120.03	124.37
52	HH	502	GDP	C5-C6-N1	2.22	117.87	113.95
50	OG	501	GTP	O6-C6-C5	-2.22	120.04	124.37
52	NN	502	GDP	C8-N7-C5	2.22	107.21	102.99
52	LH	502	GDP	C8-N7-C5	2.21	107.20	102.99
50	AO	501	GTP	O6-C6-C5	-2.21	120.06	124.37
52	SF	502	GDP	C8-N7-C5	2.21	107.20	102.99
50	NC	501	GTP	O6-C6-C5	-2.21	120.06	124.37
52	ID	502	GDP	C8-N7-C5	2.21	107.20	102.99
50	HC	501	GTP	O6-C6-C5	-2.21	120.06	124.37
50	LA	501	GTP	O6-C6-C5	-2.21	120.06	124.37
50	NI	501	GTP	O6-C6-C5	-2.21	120.06	124.37
50	KC	501	GTP	O6-C6-C5	-2.20	120.07	124.37
52	KH	502	GDP	C8-N7-C5	2.20	107.19	102.99
52	JH	502	GDP	C8-N7-C5	2.20	107.19	102.99
50	MI	501	GTP	O6-C6-C5	-2.20	120.08	124.37
52	LB	502	GDP	C3'-C2'-C1'	2.20	104.29	100.98
50	KG	501	GTP	O6-C6-C5	-2.20	120.08	124.37
50	AK	501	GTP	O6-C6-C5	-2.19	120.09	124.37
50	SC	501	GTP	O6-C6-C5	-2.19	120.09	124.37
52	LH	502	GDP	C2'-C3'-C4'	2.19	106.90	102.64
52	LH	502	GDP	O6-C6-C5	-2.19	120.10	124.37
50	FM	501	GTP	O6-C6-C5	-2.19	120.10	124.37
50	LK	501	GTP	O6-C6-C5	-2.19	120.10	124.37
50	LE	501	GTP	O6-C6-C5	-2.18	120.11	124.37
52	KJ	502	GDP	C8-N7-C5	2.18	107.15	102.99
52	KN	502	GDP	C3'-C2'-C1'	2.18	104.27	100.98
52	KD	502	GDP	C8-N7-C5	2.18	107.15	102.99
50	RI	501	GTP	O6-C6-C5	-2.18	120.11	124.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	LM	501	GTP	O6-C6-C5	-2.18	120.11	124.37
50	BM	501	GTP	O6-C6-C5	-2.18	120.11	124.37
50	HK	501	GTP	O6-C6-C5	-2.18	120.11	124.37
50	MK	501	GTP	O6-C6-C5	-2.18	120.12	124.37
50	HO	501	GTP	O3G-PG-O3B	2.18	111.94	104.64
50	BG	501	GTP	O6-C6-C5	-2.18	120.12	124.37
52	EB	502	GDP	C2'-C3'-C4'	2.18	106.87	102.64
50	SK	501	GTP	O6-C6-C5	-2.18	120.12	124.37
50	HM	501	GTP	O6-C6-C5	-2.18	120.12	124.37
52	KF	502	GDP	C8-N7-C5	2.17	107.13	102.99
50	DI	501	GTP	O6-C6-C5	-2.17	120.13	124.37
50	LI	501	GTP	O6-C6-C5	-2.17	120.13	124.37
50	LO	501	GTP	O6-C6-C5	-2.17	120.14	124.37
52	KJ	502	GDP	O6-C6-C5	-2.17	120.14	124.37
50	NM	501	GTP	O6-C6-C5	-2.16	120.15	124.37
52	ON	502	GDP	C2'-C3'-C4'	2.16	106.84	102.64
50	EM	501	GTP	O6-C6-C5	-2.16	120.15	124.37
50	GA	501	GTP	O6-C6-C5	-2.16	120.15	124.37
50	HI	501	GTP	O6-C6-C5	-2.16	120.15	124.37
52	OJ	502	GDP	C8-N7-C5	2.16	107.11	102.99
50	IM	501	GTP	O6-C6-C5	-2.16	120.15	124.37
50	HG	501	GTP	O6-C6-C5	-2.16	120.15	124.37
50	IA	501	GTP	O6-C6-C5	-2.16	120.15	124.37
50	KA	501	GTP	O6-C6-C5	-2.16	120.16	124.37
50	JI	501	GTP	O6-C6-C5	-2.16	120.16	124.37
50	FG	501	GTP	O6-C6-C5	-2.16	120.16	124.37
50	CC	501	GTP	O6-C6-C5	-2.16	120.16	124.37
50	MM	501	GTP	O6-C6-C5	-2.16	120.16	124.37
52	CH	502	GDP	C3'-C2'-C1'	2.16	104.22	100.98
50	RG	501	GTP	O6-C6-C5	-2.16	120.16	124.37
50	TK	501	GTP	O6-C6-C5	-2.15	120.17	124.37
50	DE	501	GTP	O6-C6-C5	-2.15	120.17	124.37
50	FC	501	GTP	O6-C6-C5	-2.15	120.17	124.37
50	GI	501	GTP	O6-C6-C5	-2.15	120.17	124.37
50	OO	501	GTP	O6-C6-C5	-2.15	120.18	124.37
50	CM	501	GTP	O6-C6-C5	-2.15	120.18	124.37
50	KM	501	GTP	O6-C6-C5	-2.15	120.18	124.37
50	AI	501	GTP	O6-C6-C5	-2.14	120.18	124.37
50	KO	501	GTP	O6-C6-C5	-2.14	120.18	124.37
50	TA	501	GTP	O6-C6-C5	-2.14	120.18	124.37
50	DQ	501	GTP	O6-C6-C5	-2.14	120.19	124.37
50	VA	501	GTP	O6-C6-C5	-2.14	120.19	124.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	EG	501	GTP	O6-C6-C5	-2.14	120.19	124.37
50	AA	501	GTP	O6-C6-C5	-2.14	120.19	124.37
50	UA	501	GTP	O6-C6-C5	-2.14	120.19	124.37
50	FE	501	GTP	O6-C6-C5	-2.14	120.19	124.37
50	FK	501	GTP	O6-C6-C5	-2.14	120.19	124.37
50	CI	501	GTP	O6-C6-C5	-2.14	120.19	124.37
50	WI	501	GTP	O6-C6-C5	-2.14	120.19	124.37
50	TM	501	GTP	O6-C6-C5	-2.14	120.20	124.37
50	EI	501	GTP	O6-C6-C5	-2.14	120.20	124.37
50	SI	501	GTP	O6-C6-C5	-2.14	120.20	124.37
50	EA	501	GTP	O6-C6-C5	-2.14	120.20	124.37
50	RM	501	GTP	O6-C6-C5	-2.14	120.20	124.37
50	DM	501	GTP	O6-C6-C5	-2.13	120.20	124.37
50	DO	501	GTP	O6-C6-C5	-2.13	120.20	124.37
50	HO	501	GTP	O6-C6-C5	-2.13	120.21	124.37
50	PG	501	GTP	N2-C2-N1	2.13	121.25	116.71
50	OK	501	GTP	O6-C6-C5	-2.13	120.22	124.37
50	DK	501	GTP	O6-C6-C5	-2.13	120.22	124.37
50	GE	501	GTP	O6-C6-C5	-2.13	120.22	124.37
52	KF	502	GDP	O6-C6-C5	-2.13	120.22	124.37
50	TC	501	GTP	O6-C6-C5	-2.12	120.23	124.37
50	WA	501	GTP	O6-C6-C5	-2.12	120.23	124.37
50	TI	501	GTP	O6-C6-C5	-2.12	120.23	124.37
50	UM	501	GTP	O6-C6-C5	-2.12	120.24	124.37
52	LL	502	GDP	C3'-C2'-C1'	2.11	104.16	100.98
52	FJ	502	GDP	C8-N7-C5	2.11	107.01	102.99
50	CO	501	GTP	O6-C6-C5	-2.11	120.25	124.37
50	EE	501	GTP	O6-C6-C5	-2.11	120.26	124.37
52	OJ	502	GDP	C2'-C3'-C4'	2.11	106.73	102.64
50	JE	501	GTP	O6-C6-C5	-2.11	120.26	124.37
50	UG	501	GTP	O6-C6-C5	-2.11	120.26	124.37
50	OA	501	GTP	O6-C6-C5	-2.10	120.26	124.37
50	EK	501	GTP	O6-C6-C5	-2.10	120.27	124.37
50	RC	501	GTP	O6-C6-C5	-2.10	120.27	124.37
50	UO	501	GTP	O6-C6-C5	-2.10	120.27	124.37
50	UK	501	GTP	O6-C6-C5	-2.10	120.27	124.37
50	VM	501	GTP	O6-C6-C5	-2.10	120.27	124.37
50	VO	501	GTP	O6-C6-C5	-2.10	120.27	124.37
52	HJ	502	GDP	C3'-C2'-C1'	2.10	104.14	100.98
50	WM	501	GTP	O6-C6-C5	-2.10	120.27	124.37
50	GM	501	GTP	O6-C6-C5	-2.10	120.28	124.37
50	RK	501	GTP	O6-C6-C5	-2.10	120.28	124.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	SE	501	GTP	O6-C6-C5	-2.10	120.28	124.37
50	VC	501	GTP	O6-C6-C5	-2.10	120.28	124.37
50	FA	501	GTP	O6-C6-C5	-2.10	120.28	124.37
50	HE	501	GTP	O6-C6-C5	-2.09	120.28	124.37
52	QP	502	GDP	O6-C6-C5	-2.09	120.28	124.37
50	UC	501	GTP	O6-C6-C5	-2.09	120.28	124.37
52	EB	502	GDP	C3'-C2'-C1'	2.09	104.13	100.98
50	GK	501	GTP	C3'-C2'-C1'	2.09	104.13	100.98
50	CG	501	GTP	O6-C6-C5	-2.09	120.29	124.37
50	BK	501	GTP	O6-C6-C5	-2.09	120.29	124.37
50	CE	501	GTP	O6-C6-C5	-2.09	120.29	124.37
50	TE	501	GTP	O6-C6-C5	-2.09	120.30	124.37
50	HA	501	GTP	O6-C6-C5	-2.08	120.30	124.37
50	QM	501	GTP	O6-C6-C5	-2.08	120.30	124.37
50	SA	501	GTP	O6-C6-C5	-2.08	120.30	124.37
50	KK	501	GTP	O6-C6-C5	-2.08	120.30	124.37
50	UI	501	GTP	O6-C6-C5	-2.08	120.31	124.37
50	WE	501	GTP	O6-C6-C5	-2.08	120.31	124.37
50	MA	501	GTP	O6-C6-C5	-2.08	120.31	124.37
52	ON	502	GDP	C5-C6-N1	2.08	117.62	113.95
52	MD	502	GDP	C3'-C2'-C1'	2.08	104.10	100.98
50	EO	501	GTP	O6-C6-C5	-2.08	120.32	124.37
50	MI	501	GTP	C3'-C2'-C1'	2.07	104.10	100.98
50	AM	501	GTP	O6-C6-C5	-2.07	120.32	124.37
50	DC	501	GTP	O6-C6-C5	-2.07	120.32	124.37
50	IK	501	GTP	O6-C6-C5	-2.07	120.32	124.37
50	DG	501	GTP	O6-C6-C5	-2.07	120.33	124.37
50	EC	501	GTP	O6-C6-C5	-2.07	120.33	124.37
52	DL	502	GDP	C2'-C3'-C4'	2.07	106.66	102.64
52	GF	502	GDP	C2'-C3'-C4'	2.07	106.66	102.64
50	OM	501	GTP	O6-C6-C5	-2.07	120.34	124.37
50	RO	501	GTP	O6-C6-C5	-2.06	120.34	124.37
50	QE	501	GTP	O6-C6-C5	-2.06	120.35	124.37
50	TG	501	GTP	O6-C6-C5	-2.06	120.36	124.37
50	SM	501	GTP	O6-C6-C5	-2.05	120.36	124.37
50	VK	501	GTP	O6-C6-C5	-2.05	120.36	124.37
52	SF	502	GDP	O6-C6-C5	-2.05	120.36	124.37
50	CQ	501	GTP	O6-C6-C5	-2.05	120.37	124.37
50	WO	501	GTP	O6-C6-C5	-2.05	120.37	124.37
52	LD	502	GDP	O6-C6-C5	-2.04	120.38	124.37
50	FO	501	GTP	O6-C6-C5	-2.04	120.38	124.37
50	JQ	501	GTP	O6-C6-C5	-2.04	120.39	124.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	RE	501	GTP	O6-C6-C5	-2.03	120.40	124.37
50	IC	501	GTP	O6-C6-C5	-2.03	120.40	124.37
50	JK	501	GTP	O6-C6-C5	-2.03	120.40	124.37
50	VG	501	GTP	O6-C6-C5	-2.03	120.41	124.37
50	PI	501	GTP	O6-C6-C5	-2.03	120.41	124.37
52	EF	502	GDP	C2'-C3'-C4'	2.03	106.58	102.64
52	LD	502	GDP	C3'-C2'-C1'	2.03	104.03	100.98
50	WG	501	GTP	O6-C6-C5	-2.03	120.41	124.37
50	JC	501	GTP	O6-C6-C5	-2.03	120.41	124.37
50	QK	501	GTP	O6-C6-C5	-2.02	120.43	124.37
52	LL	502	GDP	O6-C6-C5	-2.02	120.43	124.37
50	QC	501	GTP	O6-C6-C5	-2.02	120.43	124.37
50	VE	501	GTP	O6-C6-C5	-2.02	120.43	124.37
50	JO	501	GTP	O6-C6-N1	-2.01	118.27	120.65
52	ML	502	GDP	C2'-C3'-C4'	2.01	106.55	102.64
50	WC	501	GTP	O6-C6-C5	-2.00	120.46	124.37
50	OC	501	GTP	O6-C6-C5	-2.00	120.46	124.37

There are no chirality outliers.

All (1477) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
50	AA	501	GTP	C5'-O5'-PA-O1A
50	AA	501	GTP	C5'-O5'-PA-O2A
50	AC	501	GTP	C5'-O5'-PA-O1A
50	AC	501	GTP	C5'-O5'-PA-O2A
50	AE	501	GTP	PB-O3A-PA-O5'
50	AE	501	GTP	C5'-O5'-PA-O1A
50	AE	501	GTP	C5'-O5'-PA-O2A
50	AG	501	GTP	PB-O3A-PA-O5'
50	AG	501	GTP	C5'-O5'-PA-O3A
50	AG	501	GTP	C5'-O5'-PA-O2A
50	AI	501	GTP	PB-O3A-PA-O5'
50	AI	501	GTP	C5'-O5'-PA-O1A
50	AI	501	GTP	C5'-O5'-PA-O2A
50	AK	501	GTP	C5'-O5'-PA-O1A
50	AK	501	GTP	C5'-O5'-PA-O2A
50	AM	501	GTP	C5'-O5'-PA-O1A
50	AM	501	GTP	C5'-O5'-PA-O2A
50	AO	501	GTP	C5'-O5'-PA-O1A
50	AO	501	GTP	C5'-O5'-PA-O2A
50	BC	501	GTP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
50	BC	501	GTP	C5'-O5'-PA-O2A
50	BE	501	GTP	C5'-O5'-PA-O1A
50	BE	501	GTP	C5'-O5'-PA-O2A
50	BG	501	GTP	C5'-O5'-PA-O1A
50	BG	501	GTP	C5'-O5'-PA-O2A
50	BI	501	GTP	C5'-O5'-PA-O1A
50	BK	501	GTP	C5'-O5'-PA-O1A
50	BK	501	GTP	C5'-O5'-PA-O2A
50	BM	501	GTP	C5'-O5'-PA-O1A
50	BO	501	GTP	C5'-O5'-PA-O1A
50	BO	501	GTP	C5'-O5'-PA-O2A
50	CC	501	GTP	C5'-O5'-PA-O1A
50	CC	501	GTP	C5'-O5'-PA-O2A
50	CE	501	GTP	C5'-O5'-PA-O1A
50	CE	501	GTP	C5'-O5'-PA-O2A
50	CG	501	GTP	C5'-O5'-PA-O1A
50	CG	501	GTP	C5'-O5'-PA-O2A
50	CI	501	GTP	C5'-O5'-PA-O1A
50	CI	501	GTP	C5'-O5'-PA-O2A
50	CK	501	GTP	C5'-O5'-PA-O1A
50	CM	501	GTP	C5'-O5'-PA-O1A
50	CM	501	GTP	C5'-O5'-PA-O2A
50	CO	501	GTP	C5'-O5'-PA-O1A
50	CO	501	GTP	C5'-O5'-PA-O2A
50	CQ	501	GTP	C5'-O5'-PA-O1A
50	CQ	501	GTP	C5'-O5'-PA-O2A
50	DC	501	GTP	C5'-O5'-PA-O1A
50	DE	501	GTP	C5'-O5'-PA-O1A
50	DE	501	GTP	C5'-O5'-PA-O2A
50	DG	501	GTP	C5'-O5'-PA-O1A
50	DG	501	GTP	C5'-O5'-PA-O2A
50	DI	501	GTP	C5'-O5'-PA-O1A
50	DK	501	GTP	C5'-O5'-PA-O3A
50	DK	501	GTP	C5'-O5'-PA-O1A
50	DK	501	GTP	C5'-O5'-PA-O2A
50	DM	501	GTP	C5'-O5'-PA-O1A
50	DM	501	GTP	C5'-O5'-PA-O2A
50	DO	501	GTP	C5'-O5'-PA-O1A
50	DO	501	GTP	C5'-O5'-PA-O2A
50	DQ	501	GTP	C5'-O5'-PA-O1A
50	DQ	501	GTP	C5'-O5'-PA-O2A
50	EA	501	GTP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
50	EA	501	GTP	C5'-O5'-PA-O2A
50	EC	501	GTP	C5'-O5'-PA-O1A
50	EC	501	GTP	C5'-O5'-PA-O2A
50	EE	501	GTP	C5'-O5'-PA-O1A
50	EE	501	GTP	C5'-O5'-PA-O2A
50	EG	501	GTP	C5'-O5'-PA-O1A
50	EG	501	GTP	C5'-O5'-PA-O2A
50	EI	501	GTP	C5'-O5'-PA-O1A
50	EI	501	GTP	C5'-O5'-PA-O2A
50	EK	501	GTP	C5'-O5'-PA-O1A
50	EK	501	GTP	C5'-O5'-PA-O2A
50	EM	501	GTP	C5'-O5'-PA-O1A
50	EM	501	GTP	C5'-O5'-PA-O2A
50	EO	501	GTP	C5'-O5'-PA-O1A
50	EO	501	GTP	C5'-O5'-PA-O2A
50	FA	501	GTP	C5'-O5'-PA-O1A
50	FA	501	GTP	C5'-O5'-PA-O2A
50	FC	501	GTP	C5'-O5'-PA-O1A
50	FC	501	GTP	C5'-O5'-PA-O2A
50	FE	501	GTP	C5'-O5'-PA-O3A
50	FE	501	GTP	C5'-O5'-PA-O1A
50	FE	501	GTP	C5'-O5'-PA-O2A
50	FG	501	GTP	C5'-O5'-PA-O1A
50	FG	501	GTP	C5'-O5'-PA-O2A
50	FI	501	GTP	C5'-O5'-PA-O3A
50	FI	501	GTP	C5'-O5'-PA-O2A
50	FK	501	GTP	C5'-O5'-PA-O1A
50	FK	501	GTP	C5'-O5'-PA-O2A
50	FM	501	GTP	C5'-O5'-PA-O1A
50	FM	501	GTP	C5'-O5'-PA-O2A
50	FO	501	GTP	C5'-O5'-PA-O1A
50	FO	501	GTP	C5'-O5'-PA-O2A
50	GA	501	GTP	C5'-O5'-PA-O3A
50	GA	501	GTP	C5'-O5'-PA-O2A
50	GC	501	GTP	C5'-O5'-PA-O3A
50	GC	501	GTP	C5'-O5'-PA-O2A
50	GE	501	GTP	C5'-O5'-PA-O1A
50	GE	501	GTP	C5'-O5'-PA-O2A
50	GG	501	GTP	C5'-O5'-PA-O3A
50	GG	501	GTP	C5'-O5'-PA-O1A
50	GG	501	GTP	C5'-O5'-PA-O2A
50	GI	501	GTP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
50	GI	501	GTP	C5'-O5'-PA-O2A
50	GK	501	GTP	C5'-O5'-PA-O3A
50	GK	501	GTP	C5'-O5'-PA-O1A
50	GK	501	GTP	C5'-O5'-PA-O2A
50	GM	501	GTP	C5'-O5'-PA-O3A
50	GM	501	GTP	C5'-O5'-PA-O1A
50	GM	501	GTP	C5'-O5'-PA-O2A
50	GO	501	GTP	C5'-O5'-PA-O1A
50	GO	501	GTP	C5'-O5'-PA-O2A
50	HA	501	GTP	PB-O3A-PA-O5'
50	HA	501	GTP	C5'-O5'-PA-O3A
50	HA	501	GTP	C5'-O5'-PA-O1A
50	HA	501	GTP	C5'-O5'-PA-O2A
50	HC	501	GTP	C5'-O5'-PA-O1A
50	HC	501	GTP	C5'-O5'-PA-O2A
50	HE	501	GTP	PB-O3A-PA-O5'
50	HE	501	GTP	C5'-O5'-PA-O3A
50	HE	501	GTP	C5'-O5'-PA-O1A
50	HE	501	GTP	C5'-O5'-PA-O2A
50	HG	501	GTP	C5'-O5'-PA-O1A
50	HG	501	GTP	C5'-O5'-PA-O2A
50	HI	501	GTP	PB-O3A-PA-O5'
50	HI	501	GTP	C5'-O5'-PA-O1A
50	HI	501	GTP	C5'-O5'-PA-O2A
50	HK	501	GTP	PB-O3A-PA-O5'
50	HK	501	GTP	C5'-O5'-PA-O3A
50	HK	501	GTP	C5'-O5'-PA-O2A
50	HM	501	GTP	C5'-O5'-PA-O1A
50	HM	501	GTP	C5'-O5'-PA-O2A
50	HO	501	GTP	PB-O3A-PA-O5'
50	HO	501	GTP	C5'-O5'-PA-O3A
50	HO	501	GTP	C5'-O5'-PA-O2A
50	IA	501	GTP	C5'-O5'-PA-O1A
50	IA	501	GTP	C5'-O5'-PA-O2A
50	IC	501	GTP	C5'-O5'-PA-O1A
50	IC	501	GTP	C5'-O5'-PA-O2A
50	IE	501	GTP	C5'-O5'-PA-O1A
50	IE	501	GTP	C5'-O5'-PA-O2A
50	IG	501	GTP	C5'-O5'-PA-O1A
50	IG	501	GTP	C5'-O5'-PA-O2A
50	II	501	GTP	C5'-O5'-PA-O1A
50	IK	501	GTP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
50	IK	501	GTP	C5'-O5'-PA-O2A
50	IM	501	GTP	C5'-O5'-PA-O1A
50	IO	501	GTP	C5'-O5'-PA-O1A
50	IO	501	GTP	C3'-C4'-C5'-O5'
50	JC	501	GTP	C5'-O5'-PA-O1A
50	JC	501	GTP	C5'-O5'-PA-O2A
50	JE	501	GTP	C5'-O5'-PA-O1A
50	JE	501	GTP	C5'-O5'-PA-O2A
50	JG	501	GTP	C5'-O5'-PA-O1A
50	JG	501	GTP	C5'-O5'-PA-O2A
50	JI	501	GTP	C5'-O5'-PA-O1A
50	JI	501	GTP	C5'-O5'-PA-O2A
50	JK	501	GTP	C5'-O5'-PA-O1A
50	JK	501	GTP	C5'-O5'-PA-O2A
50	JM	501	GTP	C5'-O5'-PA-O1A
50	JM	501	GTP	C5'-O5'-PA-O2A
50	JO	501	GTP	C5'-O5'-PA-O1A
50	JO	501	GTP	C5'-O5'-PA-O2A
50	JQ	501	GTP	C5'-O5'-PA-O1A
50	JQ	501	GTP	C5'-O5'-PA-O2A
50	KA	501	GTP	C5'-O5'-PA-O3A
50	KA	501	GTP	C5'-O5'-PA-O1A
50	KA	501	GTP	C5'-O5'-PA-O2A
50	KC	501	GTP	C5'-O5'-PA-O1A
50	KC	501	GTP	C5'-O5'-PA-O2A
50	KE	501	GTP	C5'-O5'-PA-O1A
50	KE	501	GTP	C5'-O5'-PA-O2A
50	KG	501	GTP	C5'-O5'-PA-O3A
50	KG	501	GTP	C5'-O5'-PA-O1A
50	KG	501	GTP	C5'-O5'-PA-O2A
50	KI	501	GTP	C5'-O5'-PA-O1A
50	KI	501	GTP	C5'-O5'-PA-O2A
50	KK	501	GTP	C5'-O5'-PA-O3A
50	KK	501	GTP	C5'-O5'-PA-O1A
50	KK	501	GTP	C5'-O5'-PA-O2A
50	KM	501	GTP	C5'-O5'-PA-O1A
50	KM	501	GTP	C5'-O5'-PA-O2A
50	KO	501	GTP	C5'-O5'-PA-O1A
50	KO	501	GTP	C5'-O5'-PA-O2A
50	LA	501	GTP	C5'-O5'-PA-O1A
50	LA	501	GTP	C5'-O5'-PA-O2A
50	LC	501	GTP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
50	LC	501	GTP	C5'-O5'-PA-O2A
50	LE	501	GTP	C5'-O5'-PA-O3A
50	LG	501	GTP	C5'-O5'-PA-O1A
50	LG	501	GTP	C5'-O5'-PA-O2A
50	LG	501	GTP	O4'-C4'-C5'-O5'
50	LG	501	GTP	C3'-C4'-C5'-O5'
50	LI	501	GTP	C5'-O5'-PA-O1A
50	LI	501	GTP	C5'-O5'-PA-O2A
50	LK	501	GTP	C5'-O5'-PA-O1A
50	LK	501	GTP	C5'-O5'-PA-O2A
50	LM	501	GTP	C5'-O5'-PA-O1A
50	LM	501	GTP	C5'-O5'-PA-O2A
50	LO	501	GTP	C5'-O5'-PA-O1A
50	LO	501	GTP	C5'-O5'-PA-O2A
50	MA	501	GTP	C5'-O5'-PA-O1A
50	MA	501	GTP	C5'-O5'-PA-O2A
50	MC	501	GTP	C5'-O5'-PA-O1A
50	MC	501	GTP	C5'-O5'-PA-O2A
50	ME	501	GTP	C5'-O5'-PA-O1A
50	MG	501	GTP	C5'-O5'-PA-O1A
50	MG	501	GTP	C5'-O5'-PA-O2A
50	MI	501	GTP	C5'-O5'-PA-O1A
50	MI	501	GTP	C5'-O5'-PA-O2A
50	MK	501	GTP	C5'-O5'-PA-O1A
50	MK	501	GTP	C5'-O5'-PA-O2A
50	MM	501	GTP	PB-O3A-PA-O5'
50	MM	501	GTP	C5'-O5'-PA-O1A
50	MM	501	GTP	C5'-O5'-PA-O2A
50	MO	501	GTP	C5'-O5'-PA-O1A
50	MO	501	GTP	C5'-O5'-PA-O2A
50	NA	501	GTP	C5'-O5'-PA-O1A
50	NA	501	GTP	C5'-O5'-PA-O2A
50	NC	501	GTP	PB-O3A-PA-O5'
50	NC	501	GTP	C5'-O5'-PA-O3A
50	NC	501	GTP	C5'-O5'-PA-O2A
50	NE	501	GTP	PB-O3A-PA-O5'
50	NE	501	GTP	C5'-O5'-PA-O3A
50	NE	501	GTP	C5'-O5'-PA-O2A
50	NG	501	GTP	C5'-O5'-PA-O1A
50	NG	501	GTP	C5'-O5'-PA-O2A
50	NI	501	GTP	C5'-O5'-PA-O1A
50	NI	501	GTP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
50	NI	501	GTP	C3'-C4'-C5'-O5'
50	NK	501	GTP	C5'-O5'-PA-O1A
50	NK	501	GTP	C5'-O5'-PA-O2A
50	NM	501	GTP	C5'-O5'-PA-O1A
50	NM	501	GTP	C5'-O5'-PA-O2A
50	NO	501	GTP	C5'-O5'-PA-O1A
50	NO	501	GTP	C5'-O5'-PA-O2A
50	OA	501	GTP	C5'-O5'-PA-O1A
50	OA	501	GTP	C5'-O5'-PA-O2A
50	OC	501	GTP	C5'-O5'-PA-O1A
50	OC	501	GTP	C5'-O5'-PA-O2A
50	OE	501	GTP	C5'-O5'-PA-O1A
50	OE	501	GTP	C5'-O5'-PA-O2A
50	OG	501	GTP	C5'-O5'-PA-O1A
50	OG	501	GTP	C5'-O5'-PA-O2A
50	OI	501	GTP	C5'-O5'-PA-O1A
50	OI	501	GTP	C5'-O5'-PA-O2A
50	OK	501	GTP	C5'-O5'-PA-O1A
50	OK	501	GTP	C5'-O5'-PA-O2A
50	OK	501	GTP	C3'-C4'-C5'-O5'
50	OM	501	GTP	C5'-O5'-PA-O1A
50	OM	501	GTP	C5'-O5'-PA-O2A
50	OO	501	GTP	C5'-O5'-PA-O1A
50	OO	501	GTP	C5'-O5'-PA-O2A
50	PC	501	GTP	C5'-O5'-PA-O1A
50	PC	501	GTP	C5'-O5'-PA-O2A
50	PE	501	GTP	C5'-O5'-PA-O1A
50	PE	501	GTP	C5'-O5'-PA-O2A
50	PG	501	GTP	C5'-O5'-PA-O1A
50	PG	501	GTP	C5'-O5'-PA-O2A
50	PI	501	GTP	C5'-O5'-PA-O1A
50	PI	501	GTP	C5'-O5'-PA-O2A
50	PK	501	GTP	C5'-O5'-PA-O1A
50	PK	501	GTP	C5'-O5'-PA-O2A
50	PM	501	GTP	C5'-O5'-PA-O1A
50	PM	501	GTP	C5'-O5'-PA-O2A
50	PO	501	GTP	C5'-O5'-PA-O1A
50	PO	501	GTP	C5'-O5'-PA-O2A
50	QC	501	GTP	C5'-O5'-PA-O1A
50	QC	501	GTP	C5'-O5'-PA-O2A
50	QE	501	GTP	C5'-O5'-PA-O1A
50	QE	501	GTP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
50	QG	501	GTP	C5'-O5'-PA-O1A
50	QG	501	GTP	C5'-O5'-PA-O2A
50	QI	501	GTP	C5'-O5'-PA-O3A
50	QI	501	GTP	C5'-O5'-PA-O2A
50	QK	501	GTP	C5'-O5'-PA-O3A
50	QK	501	GTP	C5'-O5'-PA-O1A
50	QK	501	GTP	C5'-O5'-PA-O2A
50	QM	501	GTP	C5'-O5'-PA-O1A
50	QM	501	GTP	C5'-O5'-PA-O2A
50	QO	501	GTP	C5'-O5'-PA-O1A
50	RC	501	GTP	C5'-O5'-PA-O1A
50	RC	501	GTP	C5'-O5'-PA-O2A
50	RE	501	GTP	C5'-O5'-PA-O1A
50	RE	501	GTP	C5'-O5'-PA-O2A
50	RG	501	GTP	C5'-O5'-PA-O1A
50	RG	501	GTP	C5'-O5'-PA-O2A
50	RI	501	GTP	C5'-O5'-PA-O1A
50	RI	501	GTP	C5'-O5'-PA-O2A
50	RK	501	GTP	C5'-O5'-PA-O1A
50	RK	501	GTP	C5'-O5'-PA-O2A
50	RK	501	GTP	C3'-C4'-C5'-O5'
50	RM	501	GTP	C5'-O5'-PA-O1A
50	RM	501	GTP	C5'-O5'-PA-O2A
50	RO	501	GTP	C5'-O5'-PA-O1A
50	RO	501	GTP	C5'-O5'-PA-O2A
50	SA	501	GTP	C5'-O5'-PA-O1A
50	SA	501	GTP	C5'-O5'-PA-O2A
50	SC	501	GTP	C5'-O5'-PA-O1A
50	SC	501	GTP	C5'-O5'-PA-O2A
50	SE	501	GTP	C5'-O5'-PA-O3A
50	SE	501	GTP	C5'-O5'-PA-O1A
50	SE	501	GTP	C5'-O5'-PA-O2A
50	SG	501	GTP	C5'-O5'-PA-O1A
50	SG	501	GTP	C5'-O5'-PA-O2A
50	SI	501	GTP	PB-O3A-PA-O5'
50	SI	501	GTP	C5'-O5'-PA-O3A
50	SI	501	GTP	C5'-O5'-PA-O2A
50	SK	501	GTP	C5'-O5'-PA-O3A
50	SK	501	GTP	C5'-O5'-PA-O1A
50	SK	501	GTP	C5'-O5'-PA-O2A
50	SM	501	GTP	C5'-O5'-PA-O3A
50	SM	501	GTP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
50	SM	501	GTP	C5'-O5'-PA-O2A
50	TA	501	GTP	C5'-O5'-PA-O1A
50	TA	501	GTP	C5'-O5'-PA-O2A
50	TC	501	GTP	C5'-O5'-PA-O1A
50	TC	501	GTP	C5'-O5'-PA-O2A
50	TE	501	GTP	C5'-O5'-PA-O3A
50	TE	501	GTP	C5'-O5'-PA-O1A
50	TE	501	GTP	C5'-O5'-PA-O2A
50	TG	501	GTP	C5'-O5'-PA-O3A
50	TG	501	GTP	C5'-O5'-PA-O1A
50	TG	501	GTP	C5'-O5'-PA-O2A
50	TI	501	GTP	C5'-O5'-PA-O1A
50	TI	501	GTP	C5'-O5'-PA-O2A
50	TK	501	GTP	C5'-O5'-PA-O1A
50	TK	501	GTP	C5'-O5'-PA-O2A
50	TM	501	GTP	C5'-O5'-PA-O3A
50	TM	501	GTP	C5'-O5'-PA-O1A
50	TM	501	GTP	C5'-O5'-PA-O2A
50	UA	501	GTP	C5'-O5'-PA-O1A
50	UA	501	GTP	C5'-O5'-PA-O2A
50	UC	501	GTP	PB-O3A-PA-O5'
50	UC	501	GTP	C5'-O5'-PA-O3A
50	UC	501	GTP	C5'-O5'-PA-O1A
50	UC	501	GTP	C5'-O5'-PA-O2A
50	UE	501	GTP	PB-O3A-PA-O5'
50	UE	501	GTP	C5'-O5'-PA-O1A
50	UE	501	GTP	C5'-O5'-PA-O2A
50	UG	501	GTP	C5'-O5'-PA-O1A
50	UG	501	GTP	C5'-O5'-PA-O2A
50	UI	501	GTP	PB-O3A-PA-O5'
50	UI	501	GTP	C5'-O5'-PA-O1A
50	UI	501	GTP	C5'-O5'-PA-O2A
50	UK	501	GTP	C5'-O5'-PA-O1A
50	UK	501	GTP	C5'-O5'-PA-O2A
50	UM	501	GTP	C5'-O5'-PA-O1A
50	UM	501	GTP	C5'-O5'-PA-O2A
50	UO	501	GTP	C5'-O5'-PA-O3A
50	UO	501	GTP	C5'-O5'-PA-O1A
50	UO	501	GTP	C5'-O5'-PA-O2A
50	VA	501	GTP	C5'-O5'-PA-O1A
50	VA	501	GTP	C5'-O5'-PA-O2A
50	VC	501	GTP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
50	VC	501	GTP	C5'-O5'-PA-O2A
50	VE	501	GTP	C5'-O5'-PA-O1A
50	VE	501	GTP	C5'-O5'-PA-O2A
50	VG	501	GTP	C5'-O5'-PA-O1A
50	VI	501	GTP	C5'-O5'-PA-O1A
50	VI	501	GTP	C5'-O5'-PA-O2A
50	VK	501	GTP	C5'-O5'-PA-O1A
50	VK	501	GTP	C5'-O5'-PA-O2A
50	VK	501	GTP	C3'-C4'-C5'-O5'
50	VM	501	GTP	C5'-O5'-PA-O1A
50	VM	501	GTP	C5'-O5'-PA-O2A
50	VO	501	GTP	C5'-O5'-PA-O1A
50	VO	501	GTP	C5'-O5'-PA-O2A
50	VO	501	GTP	O4'-C4'-C5'-O5'
50	VO	501	GTP	C3'-C4'-C5'-O5'
50	WA	501	GTP	C5'-O5'-PA-O1A
50	WA	501	GTP	C5'-O5'-PA-O2A
50	WC	501	GTP	C5'-O5'-PA-O1A
50	WC	501	GTP	C5'-O5'-PA-O2A
50	WE	501	GTP	C5'-O5'-PA-O1A
50	WE	501	GTP	C5'-O5'-PA-O2A
50	WG	501	GTP	C5'-O5'-PA-O1A
50	WG	501	GTP	C5'-O5'-PA-O2A
50	WI	501	GTP	C5'-O5'-PA-O1A
50	WI	501	GTP	C5'-O5'-PA-O2A
50	WK	501	GTP	C5'-O5'-PA-O1A
50	WK	501	GTP	C5'-O5'-PA-O2A
50	WM	501	GTP	C5'-O5'-PA-O1A
50	WM	501	GTP	C5'-O5'-PA-O2A
50	WO	501	GTP	C5'-O5'-PA-O1A
50	WO	501	GTP	C5'-O5'-PA-O2A
52	AD	502	GDP	C5'-O5'-PA-O1A
52	BH	502	GDP	C5'-O5'-PA-O1A
52	BL	502	GDP	C5'-O5'-PA-O1A
52	CL	502	GDP	C5'-O5'-PA-O1A
52	CN	502	GDP	C5'-O5'-PA-O1A
52	DJ	502	GDP	C5'-O5'-PA-O1A
52	DL	502	GDP	C5'-O5'-PA-O3A
52	DL	502	GDP	C5'-O5'-PA-O1A
52	DN	502	GDP	C5'-O5'-PA-O1A
52	DP	502	GDP	C5'-O5'-PA-O3A
52	DP	502	GDP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
52	EL	502	GDP	C5'-O5'-PA-O1A
52	GD	502	GDP	C5'-O5'-PA-O3A
52	GD	502	GDP	C5'-O5'-PA-O1A
52	GJ	502	GDP	PA-O3A-PB-O3B
52	GL	502	GDP	C5'-O5'-PA-O1A
52	HB	502	GDP	C5'-O5'-PA-O1A
52	HP	502	GDP	C5'-O5'-PA-O1A
52	JJ	502	GDP	C5'-O5'-PA-O1A
52	JL	502	GDP	C5'-O5'-PA-O1A
52	KB	502	GDP	C5'-O5'-PA-O3A
52	KB	502	GDP	C5'-O5'-PA-O1A
52	KD	502	GDP	C5'-O5'-PA-O1A
52	KJ	502	GDP	C5'-O5'-PA-O1A
52	KP	502	GDP	C5'-O5'-PA-O1A
52	LB	502	GDP	C5'-O5'-PA-O1A
52	LD	502	GDP	C5'-O5'-PA-O1A
52	LH	502	GDP	C5'-O5'-PA-O1A
52	LL	502	GDP	C5'-O5'-PA-O1A
52	LN	502	GDP	C5'-O5'-PA-O1A
52	MB	502	GDP	C5'-O5'-PA-O1A
52	MD	502	GDP	C5'-O5'-PA-O3A
52	MF	502	GDP	C5'-O5'-PA-O1A
52	MH	502	GDP	C5'-O5'-PA-O3A
52	MH	502	GDP	C5'-O5'-PA-O1A
52	MJ	502	GDP	C5'-O5'-PA-O1A
52	ML	502	GDP	C5'-O5'-PA-O1A
52	MN	502	GDP	C5'-O5'-PA-O1A
52	MP	502	GDP	C5'-O5'-PA-O1A
52	ND	502	GDP	C5'-O5'-PA-O1A
52	NF	502	GDP	C5'-O5'-PA-O1A
52	NH	502	GDP	C5'-O5'-PA-O1A
52	NJ	502	GDP	C5'-O5'-PA-O1A
52	NN	502	GDP	C5'-O5'-PA-O1A
52	OB	502	GDP	C5'-O5'-PA-O3A
52	OB	502	GDP	C5'-O5'-PA-O1A
52	OF	502	GDP	C5'-O5'-PA-O1A
52	OH	502	GDP	C5'-O5'-PA-O1A
52	OJ	502	GDP	C5'-O5'-PA-O3A
52	OJ	502	GDP	C5'-O5'-PA-O1A
52	OP	502	GDP	C5'-O5'-PA-O1A
52	PP	502	GDP	C5'-O5'-PA-O1A
52	SD	502	GDP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
52	SF	502	GDP	C5'-O5'-PA-O1A
52	SH	502	GDP	C5'-O5'-PA-O1A
52	SJ	502	GDP	C5'-O5'-PA-O1A
52	SL	502	GDP	C5'-O5'-PA-O1A
52	SN	502	GDP	C5'-O5'-PA-O1A
52	TH	502	GDP	C5'-O5'-PA-O1A
52	UD	502	GDP	C5'-O5'-PA-O1A
52	VB	502	GDP	C5'-O5'-PA-O1A
50	BC	501	GTP	C3'-C4'-C5'-O5'
50	BI	501	GTP	C3'-C4'-C5'-O5'
50	DC	501	GTP	O4'-C4'-C5'-O5'
50	DC	501	GTP	C3'-C4'-C5'-O5'
50	EM	501	GTP	C3'-C4'-C5'-O5'
50	FO	501	GTP	C3'-C4'-C5'-O5'
50	HG	501	GTP	C3'-C4'-C5'-O5'
50	HI	501	GTP	C3'-C4'-C5'-O5'
50	HM	501	GTP	O4'-C4'-C5'-O5'
50	HM	501	GTP	C3'-C4'-C5'-O5'
50	HO	501	GTP	C3'-C4'-C5'-O5'
50	IE	501	GTP	O4'-C4'-C5'-O5'
50	IE	501	GTP	C3'-C4'-C5'-O5'
50	IG	501	GTP	O4'-C4'-C5'-O5'
50	IG	501	GTP	C3'-C4'-C5'-O5'
50	IK	501	GTP	O4'-C4'-C5'-O5'
50	IK	501	GTP	C3'-C4'-C5'-O5'
50	IO	501	GTP	O4'-C4'-C5'-O5'
50	LK	501	GTP	O4'-C4'-C5'-O5'
50	LK	501	GTP	C3'-C4'-C5'-O5'
50	NI	501	GTP	O4'-C4'-C5'-O5'
50	OK	501	GTP	O4'-C4'-C5'-O5'
50	PG	501	GTP	O4'-C4'-C5'-O5'
50	PG	501	GTP	C3'-C4'-C5'-O5'
50	QG	501	GTP	C3'-C4'-C5'-O5'
50	QK	501	GTP	C3'-C4'-C5'-O5'
50	QO	501	GTP	C3'-C4'-C5'-O5'
50	RK	501	GTP	O4'-C4'-C5'-O5'
50	UK	501	GTP	C3'-C4'-C5'-O5'
50	VG	501	GTP	O4'-C4'-C5'-O5'
50	VG	501	GTP	C3'-C4'-C5'-O5'
50	VK	501	GTP	O4'-C4'-C5'-O5'
50	WG	501	GTP	C3'-C4'-C5'-O5'
52	OB	502	GDP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
52	OJ	502	GDP	O4'-C4'-C5'-O5'
52	OJ	502	GDP	C3'-C4'-C5'-O5'
50	BC	501	GTP	O4'-C4'-C5'-O5'
50	BI	501	GTP	O4'-C4'-C5'-O5'
50	DE	501	GTP	C3'-C4'-C5'-O5'
50	EM	501	GTP	O4'-C4'-C5'-O5'
50	FO	501	GTP	O4'-C4'-C5'-O5'
50	HG	501	GTP	O4'-C4'-C5'-O5'
50	HI	501	GTP	O4'-C4'-C5'-O5'
50	HK	501	GTP	O4'-C4'-C5'-O5'
50	HK	501	GTP	C3'-C4'-C5'-O5'
50	HO	501	GTP	O4'-C4'-C5'-O5'
50	II	501	GTP	O4'-C4'-C5'-O5'
50	II	501	GTP	C3'-C4'-C5'-O5'
50	OC	501	GTP	O4'-C4'-C5'-O5'
50	OC	501	GTP	C3'-C4'-C5'-O5'
50	QG	501	GTP	O4'-C4'-C5'-O5'
50	QK	501	GTP	O4'-C4'-C5'-O5'
50	QO	501	GTP	O4'-C4'-C5'-O5'
50	TC	501	GTP	O4'-C4'-C5'-O5'
50	TC	501	GTP	C3'-C4'-C5'-O5'
50	UK	501	GTP	O4'-C4'-C5'-O5'
50	VE	501	GTP	O4'-C4'-C5'-O5'
50	VE	501	GTP	C3'-C4'-C5'-O5'
50	VM	501	GTP	O4'-C4'-C5'-O5'
50	VM	501	GTP	C3'-C4'-C5'-O5'
50	WG	501	GTP	O4'-C4'-C5'-O5'
52	OB	502	GDP	O4'-C4'-C5'-O5'
50	BM	501	GTP	O4'-C4'-C5'-O5'
50	DE	501	GTP	O4'-C4'-C5'-O5'
50	JC	501	GTP	O4'-C4'-C5'-O5'
50	JC	501	GTP	C3'-C4'-C5'-O5'
50	PI	501	GTP	O4'-C4'-C5'-O5'
50	PI	501	GTP	C3'-C4'-C5'-O5'
50	QI	501	GTP	C3'-C4'-C5'-O5'
50	UE	501	GTP	O4'-C4'-C5'-O5'
50	UE	501	GTP	C3'-C4'-C5'-O5'
50	AA	501	GTP	C3'-C4'-C5'-O5'
50	AO	501	GTP	C3'-C4'-C5'-O5'
50	BM	501	GTP	C3'-C4'-C5'-O5'
50	EC	501	GTP	C3'-C4'-C5'-O5'
50	FK	501	GTP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
50	FM	501	GTP	C3'-C4'-C5'-O5'
50	GE	501	GTP	C3'-C4'-C5'-O5'
50	HA	501	GTP	C3'-C4'-C5'-O5'
50	HC	501	GTP	C3'-C4'-C5'-O5'
50	HE	501	GTP	C3'-C4'-C5'-O5'
50	JG	501	GTP	C3'-C4'-C5'-O5'
50	LI	501	GTP	C3'-C4'-C5'-O5'
50	NA	501	GTP	C3'-C4'-C5'-O5'
50	NK	501	GTP	C3'-C4'-C5'-O5'
50	NM	501	GTP	C3'-C4'-C5'-O5'
50	OI	501	GTP	C3'-C4'-C5'-O5'
50	PO	501	GTP	C3'-C4'-C5'-O5'
50	QE	501	GTP	C3'-C4'-C5'-O5'
50	UC	501	GTP	C3'-C4'-C5'-O5'
50	UG	501	GTP	C3'-C4'-C5'-O5'
50	VC	501	GTP	C3'-C4'-C5'-O5'
50	VI	501	GTP	C3'-C4'-C5'-O5'
50	WA	501	GTP	C3'-C4'-C5'-O5'
52	MD	502	GDP	C3'-C4'-C5'-O5'
52	PN	502	GDP	C3'-C4'-C5'-O5'
50	AO	501	GTP	O4'-C4'-C5'-O5'
50	BO	501	GTP	C3'-C4'-C5'-O5'
50	CO	501	GTP	C3'-C4'-C5'-O5'
50	DO	501	GTP	C3'-C4'-C5'-O5'
50	EE	501	GTP	C3'-C4'-C5'-O5'
50	FM	501	GTP	O4'-C4'-C5'-O5'
50	GE	501	GTP	O4'-C4'-C5'-O5'
50	HE	501	GTP	O4'-C4'-C5'-O5'
50	IM	501	GTP	C3'-C4'-C5'-O5'
50	JG	501	GTP	O4'-C4'-C5'-O5'
50	LI	501	GTP	O4'-C4'-C5'-O5'
50	NA	501	GTP	O4'-C4'-C5'-O5'
50	NE	501	GTP	C3'-C4'-C5'-O5'
50	NK	501	GTP	O4'-C4'-C5'-O5'
50	PE	501	GTP	C3'-C4'-C5'-O5'
50	QC	501	GTP	C3'-C4'-C5'-O5'
50	QE	501	GTP	O4'-C4'-C5'-O5'
50	QI	501	GTP	O4'-C4'-C5'-O5'
50	SA	501	GTP	C3'-C4'-C5'-O5'
50	SK	501	GTP	C3'-C4'-C5'-O5'
50	UG	501	GTP	O4'-C4'-C5'-O5'
50	VC	501	GTP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
50	VI	501	GTP	O4'-C4'-C5'-O5'
50	WA	501	GTP	O4'-C4'-C5'-O5'
52	PN	502	GDP	O4'-C4'-C5'-O5'
52	UD	502	GDP	C3'-C4'-C5'-O5'
50	AM	501	GTP	C3'-C4'-C5'-O5'
50	DG	501	GTP	C3'-C4'-C5'-O5'
50	EC	501	GTP	O4'-C4'-C5'-O5'
50	FK	501	GTP	O4'-C4'-C5'-O5'
50	IA	501	GTP	C3'-C4'-C5'-O5'
50	JM	501	GTP	C3'-C4'-C5'-O5'
50	OI	501	GTP	O4'-C4'-C5'-O5'
50	PK	501	GTP	C3'-C4'-C5'-O5'
50	SG	501	GTP	C3'-C4'-C5'-O5'
50	TE	501	GTP	C3'-C4'-C5'-O5'
50	UC	501	GTP	O4'-C4'-C5'-O5'
50	WC	501	GTP	C3'-C4'-C5'-O5'
52	QH	502	GDP	PA-O3A-PB-O1B
50	HA	501	GTP	PA-O3A-PB-O1B
50	HC	501	GTP	PA-O3A-PB-O1B
50	HK	501	GTP	PA-O3A-PB-O1B
50	JI	501	GTP	PB-O3A-PA-O1A
50	KE	501	GTP	PB-O3A-PA-O1A
50	OK	501	GTP	PA-O3A-PB-O1B
50	OO	501	GTP	PA-O3A-PB-O1B
50	SE	501	GTP	PA-O3A-PB-O1B
50	SI	501	GTP	PA-O3A-PB-O1B
50	SK	501	GTP	PA-O3A-PB-O1B
50	TE	501	GTP	PA-O3A-PB-O1B
50	TM	501	GTP	PA-O3A-PB-O1B
50	UE	501	GTP	PA-O3A-PB-O1B
50	UK	501	GTP	PA-O3A-PB-O1B
50	UO	501	GTP	PA-O3A-PB-O1B
50	CC	501	GTP	C3'-C4'-C5'-O5'
50	CQ	501	GTP	C3'-C4'-C5'-O5'
50	DI	501	GTP	C3'-C4'-C5'-O5'
50	DM	501	GTP	C3'-C4'-C5'-O5'
50	HA	501	GTP	O4'-C4'-C5'-O5'
50	IC	501	GTP	C3'-C4'-C5'-O5'
50	JE	501	GTP	C3'-C4'-C5'-O5'
50	OE	501	GTP	C3'-C4'-C5'-O5'
50	OM	501	GTP	C3'-C4'-C5'-O5'
50	PM	501	GTP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
50	RC	501	GTP	C3'-C4'-C5'-O5'
50	RE	501	GTP	C3'-C4'-C5'-O5'
50	RO	501	GTP	C3'-C4'-C5'-O5'
50	SC	501	GTP	C3'-C4'-C5'-O5'
50	TA	501	GTP	C3'-C4'-C5'-O5'
50	TK	501	GTP	C3'-C4'-C5'-O5'
50	TM	501	GTP	C3'-C4'-C5'-O5'
50	UM	501	GTP	C3'-C4'-C5'-O5'
50	UO	501	GTP	C3'-C4'-C5'-O5'
50	VA	501	GTP	C3'-C4'-C5'-O5'
52	NN	502	GDP	C3'-C4'-C5'-O5'
50	LE	501	GTP	C4'-C5'-O5'-PA
50	AA	501	GTP	O4'-C4'-C5'-O5'
50	BO	501	GTP	O4'-C4'-C5'-O5'
50	CO	501	GTP	O4'-C4'-C5'-O5'
50	EE	501	GTP	O4'-C4'-C5'-O5'
50	HC	501	GTP	O4'-C4'-C5'-O5'
50	IM	501	GTP	O4'-C4'-C5'-O5'
50	NM	501	GTP	O4'-C4'-C5'-O5'
50	NO	501	GTP	C3'-C4'-C5'-O5'
50	PE	501	GTP	O4'-C4'-C5'-O5'
50	PO	501	GTP	O4'-C4'-C5'-O5'
50	QC	501	GTP	O4'-C4'-C5'-O5'
50	SK	501	GTP	O4'-C4'-C5'-O5'
50	UI	501	GTP	C3'-C4'-C5'-O5'
52	MD	502	GDP	O4'-C4'-C5'-O5'
50	CE	501	GTP	C4'-C5'-O5'-PA
50	DI	501	GTP	C4'-C5'-O5'-PA
50	DQ	501	GTP	C4'-C5'-O5'-PA
50	EC	501	GTP	C4'-C5'-O5'-PA
50	EM	501	GTP	C4'-C5'-O5'-PA
50	FA	501	GTP	C4'-C5'-O5'-PA
50	GG	501	GTP	C4'-C5'-O5'-PA
50	GI	501	GTP	C4'-C5'-O5'-PA
50	IK	501	GTP	C4'-C5'-O5'-PA
50	IO	501	GTP	C4'-C5'-O5'-PA
50	JC	501	GTP	C4'-C5'-O5'-PA
50	JE	501	GTP	C4'-C5'-O5'-PA
50	KC	501	GTP	C4'-C5'-O5'-PA
50	LC	501	GTP	C4'-C5'-O5'-PA
50	LM	501	GTP	C4'-C5'-O5'-PA
50	MG	501	GTP	C4'-C5'-O5'-PA

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Mol	Chain	Res	Type	Atoms
50	MK	501	GTP	C4'-C5'-O5'-PA
50	MM	501	GTP	C4'-C5'-O5'-PA
50	MO	501	GTP	C4'-C5'-O5'-PA
50	PI	501	GTP	C4'-C5'-O5'-PA
50	QC	501	GTP	C4'-C5'-O5'-PA
50	VO	501	GTP	C4'-C5'-O5'-PA
50	WA	501	GTP	C4'-C5'-O5'-PA
50	WE	501	GTP	C4'-C5'-O5'-PA
50	WI	501	GTP	C4'-C5'-O5'-PA
50	AM	501	GTP	PB-O3A-PA-O5'
50	FO	501	GTP	PB-O3A-PA-O5'
50	GO	501	GTP	PB-O3A-PA-O5'
50	HC	501	GTP	PB-O3A-PA-O5'
50	HG	501	GTP	PB-O3A-PA-O5'
50	IG	501	GTP	PB-O3A-PA-O5'
50	NG	501	GTP	PB-O3A-PA-O5'
50	NK	501	GTP	PB-O3A-PA-O5'
50	NO	501	GTP	PB-O3A-PA-O5'
50	OE	501	GTP	PB-O3A-PA-O5'
50	OO	501	GTP	PB-O3A-PA-O5'
50	RK	501	GTP	PB-O3A-PA-O5'
50	TM	501	GTP	PB-O3A-PA-O5'
50	UK	501	GTP	PB-O3A-PA-O5'
50	DO	501	GTP	O4'-C4'-C5'-O5'
50	NE	501	GTP	O4'-C4'-C5'-O5'
50	SA	501	GTP	O4'-C4'-C5'-O5'
52	UD	502	GDP	O4'-C4'-C5'-O5'
50	BO	501	GTP	C4'-C5'-O5'-PA
50	CI	501	GTP	C4'-C5'-O5'-PA
50	CO	501	GTP	C4'-C5'-O5'-PA
50	DM	501	GTP	C4'-C5'-O5'-PA
50	EA	501	GTP	C4'-C5'-O5'-PA
50	EG	501	GTP	C4'-C5'-O5'-PA
50	EI	501	GTP	C4'-C5'-O5'-PA
50	FC	501	GTP	C4'-C5'-O5'-PA
50	FG	501	GTP	C4'-C5'-O5'-PA
50	FK	501	GTP	C4'-C5'-O5'-PA
50	FO	501	GTP	C4'-C5'-O5'-PA
50	GM	501	GTP	C4'-C5'-O5'-PA
50	GO	501	GTP	C4'-C5'-O5'-PA
50	HC	501	GTP	C4'-C5'-O5'-PA
50	HM	501	GTP	C4'-C5'-O5'-PA

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Mol	Chain	Res	Type	Atoms
50	IA	501	GTP	C4'-C5'-O5'-PA
50	IC	501	GTP	C4'-C5'-O5'-PA
50	II	501	GTP	C4'-C5'-O5'-PA
50	JG	501	GTP	C4'-C5'-O5'-PA
50	JM	501	GTP	C4'-C5'-O5'-PA
50	KO	501	GTP	C4'-C5'-O5'-PA
50	LA	501	GTP	C4'-C5'-O5'-PA
50	LI	501	GTP	C4'-C5'-O5'-PA
50	LO	501	GTP	C4'-C5'-O5'-PA
50	MA	501	GTP	C4'-C5'-O5'-PA
50	MI	501	GTP	C4'-C5'-O5'-PA
50	NA	501	GTP	C4'-C5'-O5'-PA
50	NG	501	GTP	C4'-C5'-O5'-PA
50	NI	501	GTP	C4'-C5'-O5'-PA
50	NM	501	GTP	C4'-C5'-O5'-PA
50	NO	501	GTP	C4'-C5'-O5'-PA
50	OC	501	GTP	C4'-C5'-O5'-PA
50	OM	501	GTP	C4'-C5'-O5'-PA
50	PE	501	GTP	C4'-C5'-O5'-PA
50	PK	501	GTP	C4'-C5'-O5'-PA
50	QG	501	GTP	C4'-C5'-O5'-PA
50	QK	501	GTP	C4'-C5'-O5'-PA
50	QO	501	GTP	C4'-C5'-O5'-PA
50	RI	501	GTP	C4'-C5'-O5'-PA
50	RM	501	GTP	C4'-C5'-O5'-PA
50	UA	501	GTP	C4'-C5'-O5'-PA
50	UE	501	GTP	C4'-C5'-O5'-PA
50	UK	501	GTP	C4'-C5'-O5'-PA
50	UM	501	GTP	C4'-C5'-O5'-PA
50	UO	501	GTP	C4'-C5'-O5'-PA
50	VG	501	GTP	C4'-C5'-O5'-PA
50	VI	501	GTP	C4'-C5'-O5'-PA
50	VK	501	GTP	C4'-C5'-O5'-PA
50	VM	501	GTP	C4'-C5'-O5'-PA
50	WM	501	GTP	C4'-C5'-O5'-PA
50	WO	501	GTP	C4'-C5'-O5'-PA
50	AE	501	GTP	C5'-O5'-PA-O3A
50	BM	501	GTP	C5'-O5'-PA-O3A
50	CE	501	GTP	C5'-O5'-PA-O3A
50	CK	501	GTP	C5'-O5'-PA-O3A
50	CQ	501	GTP	C5'-O5'-PA-O3A
50	DI	501	GTP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
50	DQ	501	GTP	C5'-O5'-PA-O3A
50	EE	501	GTP	C5'-O5'-PA-O3A
50	EK	501	GTP	C5'-O5'-PA-O3A
50	FG	501	GTP	C5'-O5'-PA-O3A
50	FM	501	GTP	C5'-O5'-PA-O3A
50	GO	501	GTP	C5'-O5'-PA-O3A
50	HC	501	GTP	C5'-O5'-PA-O3A
50	HG	501	GTP	C5'-O5'-PA-O3A
50	II	501	GTP	C5'-O5'-PA-O3A
50	IM	501	GTP	C5'-O5'-PA-O3A
50	IO	501	GTP	C5'-O5'-PA-O3A
50	KO	501	GTP	C5'-O5'-PA-O3A
50	MA	501	GTP	C5'-O5'-PA-O3A
50	ME	501	GTP	C5'-O5'-PA-O3A
50	MM	501	GTP	C5'-O5'-PA-O3A
50	OC	501	GTP	C5'-O5'-PA-O3A
50	QO	501	GTP	C5'-O5'-PA-O3A
50	RE	501	GTP	C5'-O5'-PA-O3A
50	RG	501	GTP	C5'-O5'-PA-O3A
50	RM	501	GTP	C5'-O5'-PA-O3A
50	RO	501	GTP	C5'-O5'-PA-O3A
50	SG	501	GTP	C5'-O5'-PA-O3A
50	TA	501	GTP	C5'-O5'-PA-O3A
50	TC	501	GTP	C5'-O5'-PA-O3A
50	TI	501	GTP	C5'-O5'-PA-O3A
50	TK	501	GTP	C5'-O5'-PA-O3A
50	UE	501	GTP	C5'-O5'-PA-O3A
50	UG	501	GTP	C5'-O5'-PA-O3A
50	UI	501	GTP	C5'-O5'-PA-O3A
50	UK	501	GTP	C5'-O5'-PA-O3A
50	UM	501	GTP	C5'-O5'-PA-O3A
50	VG	501	GTP	C5'-O5'-PA-O3A
50	VK	501	GTP	C5'-O5'-PA-O3A
50	WM	501	GTP	C5'-O5'-PA-O3A
52	JJ	502	GDP	C5'-O5'-PA-O3A
52	KP	502	GDP	C5'-O5'-PA-O3A
52	ML	502	GDP	C5'-O5'-PA-O3A
52	MP	502	GDP	C5'-O5'-PA-O3A
50	AM	501	GTP	O4'-C4'-C5'-O5'
50	EA	501	GTP	C3'-C4'-C5'-O5'
50	FC	501	GTP	C3'-C4'-C5'-O5'
50	JO	501	GTP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
50	JQ	501	GTP	C3'-C4'-C5'-O5'
50	NC	501	GTP	C3'-C4'-C5'-O5'
50	OG	501	GTP	C3'-C4'-C5'-O5'
50	OO	501	GTP	C3'-C4'-C5'-O5'
50	RG	501	GTP	C3'-C4'-C5'-O5'
50	TE	501	GTP	O4'-C4'-C5'-O5'
50	AC	501	GTP	PA-O3A-PB-O2B
50	AI	501	GTP	PA-O3A-PB-O2B
50	BC	501	GTP	PA-O3A-PB-O2B
50	BE	501	GTP	PA-O3A-PB-O2B
50	BM	501	GTP	PA-O3A-PB-O2B
50	BO	501	GTP	PA-O3A-PB-O2B
50	CO	501	GTP	PA-O3A-PB-O2B
50	DC	501	GTP	PA-O3A-PB-O2B
50	DE	501	GTP	PA-O3A-PB-O2B
50	DM	501	GTP	PA-O3A-PB-O2B
50	DO	501	GTP	PA-O3A-PB-O2B
50	EA	501	GTP	PA-O3A-PB-O2B
50	EC	501	GTP	PA-O3A-PB-O2B
50	EK	501	GTP	PA-O3A-PB-O2B
50	EM	501	GTP	PA-O3A-PB-O2B
50	FA	501	GTP	PA-O3A-PB-O2B
50	FE	501	GTP	PA-O3A-PB-O2B
50	FG	501	GTP	PA-O3A-PB-O2B
50	FI	501	GTP	PA-O3A-PB-O2B
50	FK	501	GTP	PA-O3A-PB-O2B
50	GA	501	GTP	PA-O3A-PB-O2B
50	GE	501	GTP	PA-O3A-PB-O2B
50	GG	501	GTP	PA-O3A-PB-O2B
50	GI	501	GTP	PA-O3A-PB-O2B
50	GO	501	GTP	PA-O3A-PB-O2B
50	HM	501	GTP	PA-O3A-PB-O2B
50	II	501	GTP	PA-O3A-PB-O2B
50	IK	501	GTP	PA-O3A-PB-O2B
50	IM	501	GTP	PA-O3A-PB-O2B
50	JC	501	GTP	PA-O3A-PB-O2B
50	KE	501	GTP	PA-O3A-PB-O2B
50	KI	501	GTP	PA-O3A-PB-O2B
50	KM	501	GTP	PA-O3A-PB-O2B
50	KO	501	GTP	PA-O3A-PB-O2B
50	LA	501	GTP	PA-O3A-PB-O2B
50	LC	501	GTP	PA-O3A-PB-O2B

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Mol	Chain	Res	Type	Atoms
50	LG	501	GTP	PA-O3A-PB-O2B
50	LK	501	GTP	PA-O3A-PB-O2B
50	LM	501	GTP	PA-O3A-PB-O2B
50	LO	501	GTP	PA-O3A-PB-O2B
50	MC	501	GTP	PA-O3A-PB-O2B
50	MK	501	GTP	PA-O3A-PB-O2B
50	MM	501	GTP	PA-O3A-PB-O1B
50	MO	501	GTP	PA-O3A-PB-O2B
50	NG	501	GTP	PA-O3A-PB-O1B
50	NK	501	GTP	PA-O3A-PB-O1B
50	NM	501	GTP	PA-O3A-PB-O1B
50	PM	501	GTP	PA-O3A-PB-O2B
50	QE	501	GTP	PA-O3A-PB-O2B
50	QM	501	GTP	PA-O3A-PB-O2B
50	RI	501	GTP	PA-O3A-PB-O2B
50	RK	501	GTP	PA-O3A-PB-O2B
50	SC	501	GTP	PA-O3A-PB-O2B
50	SG	501	GTP	PA-O3A-PB-O1B
50	TC	501	GTP	PA-O3A-PB-O1B
50	VE	501	GTP	PA-O3A-PB-O2B
50	VG	501	GTP	PA-O3A-PB-O2B
50	VI	501	GTP	PA-O3A-PB-O2B
50	VK	501	GTP	PA-O3A-PB-O2B
50	VM	501	GTP	PA-O3A-PB-O2B
50	WA	501	GTP	PA-O3A-PB-O2B
50	WC	501	GTP	PA-O3A-PB-O2B
50	WG	501	GTP	PA-O3A-PB-O2B
50	WM	501	GTP	PA-O3A-PB-O2B
50	WO	501	GTP	PA-O3A-PB-O2B
50	AA	501	GTP	C4'-C5'-O5'-PA
50	AC	501	GTP	C4'-C5'-O5'-PA
50	AG	501	GTP	C4'-C5'-O5'-PA
50	AI	501	GTP	C4'-C5'-O5'-PA
50	AK	501	GTP	C4'-C5'-O5'-PA
50	AM	501	GTP	C4'-C5'-O5'-PA
50	AO	501	GTP	C4'-C5'-O5'-PA
50	BC	501	GTP	C4'-C5'-O5'-PA
50	BE	501	GTP	C4'-C5'-O5'-PA
50	BG	501	GTP	C4'-C5'-O5'-PA
50	BI	501	GTP	C4'-C5'-O5'-PA
50	BK	501	GTP	C4'-C5'-O5'-PA
50	BM	501	GTP	C4'-C5'-O5'-PA

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Mol	Chain	Res	Type	Atoms
50	CC	501	GTP	C4'-C5'-O5'-PA
50	CG	501	GTP	C4'-C5'-O5'-PA
50	CK	501	GTP	C4'-C5'-O5'-PA
50	CM	501	GTP	C4'-C5'-O5'-PA
50	CQ	501	GTP	C4'-C5'-O5'-PA
50	DC	501	GTP	C4'-C5'-O5'-PA
50	DE	501	GTP	C4'-C5'-O5'-PA
50	DG	501	GTP	C4'-C5'-O5'-PA
50	DK	501	GTP	C4'-C5'-O5'-PA
50	DO	501	GTP	C4'-C5'-O5'-PA
50	EO	501	GTP	C4'-C5'-O5'-PA
50	FE	501	GTP	C4'-C5'-O5'-PA
50	FI	501	GTP	C4'-C5'-O5'-PA
50	FM	501	GTP	C4'-C5'-O5'-PA
50	GA	501	GTP	C4'-C5'-O5'-PA
50	GC	501	GTP	C4'-C5'-O5'-PA
50	GE	501	GTP	C4'-C5'-O5'-PA
50	GK	501	GTP	C4'-C5'-O5'-PA
50	HA	501	GTP	C4'-C5'-O5'-PA
50	HE	501	GTP	C4'-C5'-O5'-PA
50	HG	501	GTP	C4'-C5'-O5'-PA
50	HI	501	GTP	C4'-C5'-O5'-PA
50	HK	501	GTP	C4'-C5'-O5'-PA
50	HO	501	GTP	C4'-C5'-O5'-PA
50	IE	501	GTP	C4'-C5'-O5'-PA
50	IM	501	GTP	C4'-C5'-O5'-PA
50	JQ	501	GTP	C4'-C5'-O5'-PA
50	KA	501	GTP	C4'-C5'-O5'-PA
50	KI	501	GTP	C4'-C5'-O5'-PA
50	KK	501	GTP	C4'-C5'-O5'-PA
50	KM	501	GTP	C4'-C5'-O5'-PA
50	LG	501	GTP	C4'-C5'-O5'-PA
50	LK	501	GTP	C4'-C5'-O5'-PA
50	MC	501	GTP	C4'-C5'-O5'-PA
50	ME	501	GTP	C4'-C5'-O5'-PA
50	NC	501	GTP	C4'-C5'-O5'-PA
50	NE	501	GTP	C4'-C5'-O5'-PA
50	NK	501	GTP	C4'-C5'-O5'-PA
50	OA	501	GTP	C4'-C5'-O5'-PA
50	OE	501	GTP	C4'-C5'-O5'-PA
50	OG	501	GTP	C4'-C5'-O5'-PA
50	OI	501	GTP	C4'-C5'-O5'-PA

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Mol	Chain	Res	Type	Atoms
50	OK	501	GTP	C4'-C5'-O5'-PA
50	OO	501	GTP	C4'-C5'-O5'-PA
50	PC	501	GTP	C4'-C5'-O5'-PA
50	PG	501	GTP	C4'-C5'-O5'-PA
50	PM	501	GTP	C4'-C5'-O5'-PA
50	PO	501	GTP	C4'-C5'-O5'-PA
50	QE	501	GTP	C4'-C5'-O5'-PA
50	QI	501	GTP	C4'-C5'-O5'-PA
50	QM	501	GTP	C4'-C5'-O5'-PA
50	RC	501	GTP	C4'-C5'-O5'-PA
50	RE	501	GTP	C4'-C5'-O5'-PA
50	RG	501	GTP	C4'-C5'-O5'-PA
50	RK	501	GTP	C4'-C5'-O5'-PA
50	RO	501	GTP	C4'-C5'-O5'-PA
50	SA	501	GTP	C4'-C5'-O5'-PA
50	SE	501	GTP	C4'-C5'-O5'-PA
50	SG	501	GTP	C4'-C5'-O5'-PA
50	SI	501	GTP	C4'-C5'-O5'-PA
50	SK	501	GTP	C4'-C5'-O5'-PA
50	SM	501	GTP	C4'-C5'-O5'-PA
50	TA	501	GTP	C4'-C5'-O5'-PA
50	TE	501	GTP	C4'-C5'-O5'-PA
50	TG	501	GTP	C4'-C5'-O5'-PA
50	TI	501	GTP	C4'-C5'-O5'-PA
50	TK	501	GTP	C4'-C5'-O5'-PA
50	UG	501	GTP	C4'-C5'-O5'-PA
50	UI	501	GTP	C4'-C5'-O5'-PA
50	VA	501	GTP	C4'-C5'-O5'-PA
50	VC	501	GTP	C4'-C5'-O5'-PA
50	VE	501	GTP	C4'-C5'-O5'-PA
50	WC	501	GTP	C4'-C5'-O5'-PA
50	WG	501	GTP	C4'-C5'-O5'-PA
50	WK	501	GTP	C4'-C5'-O5'-PA
50	BI	501	GTP	C5'-O5'-PA-O2A
50	BM	501	GTP	C5'-O5'-PA-O2A
50	CK	501	GTP	C5'-O5'-PA-O2A
50	DC	501	GTP	C5'-O5'-PA-O2A
50	DI	501	GTP	C5'-O5'-PA-O2A
50	GA	501	GTP	C5'-O5'-PA-O1A
50	GC	501	GTP	C5'-O5'-PA-O1A
50	II	501	GTP	C5'-O5'-PA-O2A
50	IM	501	GTP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
50	IO	501	GTP	C5'-O5'-PA-O2A
50	LE	501	GTP	C5'-O5'-PA-O2A
50	ME	501	GTP	C5'-O5'-PA-O2A
50	QI	501	GTP	C5'-O5'-PA-O1A
50	QO	501	GTP	C5'-O5'-PA-O2A
50	SI	501	GTP	C5'-O5'-PA-O1A
50	VG	501	GTP	C5'-O5'-PA-O2A
52	MD	502	GDP	C5'-O5'-PA-O1A
52	OD	502	GDP	C5'-O5'-PA-O1A
50	BE	501	GTP	C3'-C4'-C5'-O5'
50	DQ	501	GTP	C3'-C4'-C5'-O5'
50	EG	501	GTP	C3'-C4'-C5'-O5'
50	EO	501	GTP	C3'-C4'-C5'-O5'
50	FA	501	GTP	C3'-C4'-C5'-O5'
50	JI	501	GTP	C3'-C4'-C5'-O5'
50	KI	501	GTP	C3'-C4'-C5'-O5'
50	MM	501	GTP	C3'-C4'-C5'-O5'
50	OA	501	GTP	C3'-C4'-C5'-O5'
50	PK	501	GTP	O4'-C4'-C5'-O5'
50	QM	501	GTP	C3'-C4'-C5'-O5'
50	TG	501	GTP	C3'-C4'-C5'-O5'
50	TI	501	GTP	C3'-C4'-C5'-O5'
50	UA	501	GTP	C3'-C4'-C5'-O5'
50	WC	501	GTP	O4'-C4'-C5'-O5'
52	MH	502	GDP	C3'-C4'-C5'-O5'
50	AE	501	GTP	C4'-C5'-O5'-PA
50	EE	501	GTP	C4'-C5'-O5'-PA
50	EK	501	GTP	C4'-C5'-O5'-PA
50	IG	501	GTP	C4'-C5'-O5'-PA
50	KE	501	GTP	C4'-C5'-O5'-PA
50	KG	501	GTP	C4'-C5'-O5'-PA
50	TC	501	GTP	C4'-C5'-O5'-PA
50	TM	501	GTP	C4'-C5'-O5'-PA
50	UC	501	GTP	C4'-C5'-O5'-PA
50	AE	501	GTP	C3'-C4'-C5'-O5'
50	CC	501	GTP	O4'-C4'-C5'-O5'
50	CQ	501	GTP	O4'-C4'-C5'-O5'
50	DG	501	GTP	O4'-C4'-C5'-O5'
50	DI	501	GTP	O4'-C4'-C5'-O5'
50	FI	501	GTP	C3'-C4'-C5'-O5'
50	GA	501	GTP	C3'-C4'-C5'-O5'
50	IA	501	GTP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
50	IC	501	GTP	O4'-C4'-C5'-O5'
50	JE	501	GTP	O4'-C4'-C5'-O5'
50	JM	501	GTP	O4'-C4'-C5'-O5'
50	NG	501	GTP	C3'-C4'-C5'-O5'
50	OE	501	GTP	O4'-C4'-C5'-O5'
50	PC	501	GTP	C3'-C4'-C5'-O5'
50	PM	501	GTP	O4'-C4'-C5'-O5'
50	RC	501	GTP	O4'-C4'-C5'-O5'
50	RE	501	GTP	O4'-C4'-C5'-O5'
50	RO	501	GTP	O4'-C4'-C5'-O5'
50	SC	501	GTP	O4'-C4'-C5'-O5'
50	SG	501	GTP	O4'-C4'-C5'-O5'
50	SI	501	GTP	C3'-C4'-C5'-O5'
50	TA	501	GTP	O4'-C4'-C5'-O5'
50	TK	501	GTP	O4'-C4'-C5'-O5'
50	TM	501	GTP	O4'-C4'-C5'-O5'
50	UM	501	GTP	O4'-C4'-C5'-O5'
50	VA	501	GTP	O4'-C4'-C5'-O5'
50	WK	501	GTP	C3'-C4'-C5'-O5'
52	DP	502	GDP	C3'-C4'-C5'-O5'
52	NN	502	GDP	O4'-C4'-C5'-O5'
52	OD	502	GDP	C3'-C4'-C5'-O5'
50	CK	501	GTP	C3'-C4'-C5'-O5'
50	DM	501	GTP	O4'-C4'-C5'-O5'
50	NO	501	GTP	O4'-C4'-C5'-O5'
50	OM	501	GTP	O4'-C4'-C5'-O5'
50	RG	501	GTP	O4'-C4'-C5'-O5'
50	SE	501	GTP	C3'-C4'-C5'-O5'
50	UI	501	GTP	O4'-C4'-C5'-O5'
50	UO	501	GTP	O4'-C4'-C5'-O5'
52	VB	502	GDP	C3'-C4'-C5'-O5'
50	AE	501	GTP	PA-O3A-PB-O2B
50	AG	501	GTP	PA-O3A-PB-O2B
50	AK	501	GTP	PA-O3A-PB-O2B
50	AM	501	GTP	PA-O3A-PB-O2B
50	AO	501	GTP	PA-O3A-PB-O2B
50	BG	501	GTP	PA-O3A-PB-O2B
50	BI	501	GTP	PA-O3A-PB-O2B
50	BK	501	GTP	PA-O3A-PB-O2B
50	CC	501	GTP	PA-O3A-PB-O2B
50	CE	501	GTP	PA-O3A-PB-O2B
50	CG	501	GTP	PB-O3A-PA-O1A

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Mol	Chain	Res	Type	Atoms
50	CI	501	GTP	PA-O3A-PB-O2B
50	CM	501	GTP	PA-O3A-PB-O2B
50	CQ	501	GTP	PA-O3A-PB-O2B
50	DG	501	GTP	PA-O3A-PB-O2B
50	DI	501	GTP	PA-O3A-PB-O2B
50	DQ	501	GTP	PA-O3A-PB-O2B
50	EE	501	GTP	PA-O3A-PB-O2B
50	EO	501	GTP	PA-O3A-PB-O2B
50	FC	501	GTP	PA-O3A-PB-O2B
50	FM	501	GTP	PA-O3A-PB-O2B
50	FO	501	GTP	PA-O3A-PB-O2B
50	GC	501	GTP	PA-O3A-PB-O2B
50	GK	501	GTP	PA-O3A-PB-O2B
50	GM	501	GTP	PA-O3A-PB-O2B
50	HG	501	GTP	PA-O3A-PB-O2B
50	HI	501	GTP	PA-O3A-PB-O2B
50	IA	501	GTP	PA-O3A-PB-O2B
50	IC	501	GTP	PA-O3A-PB-O2B
50	IE	501	GTP	PA-O3A-PB-O2B
50	IG	501	GTP	PA-O3A-PB-O2B
50	KA	501	GTP	PA-O3A-PB-O2B
50	KC	501	GTP	PA-O3A-PB-O2B
50	KG	501	GTP	PA-O3A-PB-O2B
50	KK	501	GTP	PA-O3A-PB-O2B
50	LE	501	GTP	PA-O3A-PB-O2B
50	LI	501	GTP	PA-O3A-PB-O2B
50	MA	501	GTP	PA-O3A-PB-O2B
50	MG	501	GTP	PA-O3A-PB-O2B
50	MI	501	GTP	PA-O3A-PB-O2B
50	NA	501	GTP	PA-O3A-PB-O1B
50	NI	501	GTP	PA-O3A-PB-O1B
50	NO	501	GTP	PA-O3A-PB-O1B
50	OA	501	GTP	PA-O3A-PB-O2B
50	OC	501	GTP	PA-O3A-PB-O2B
50	OE	501	GTP	PA-O3A-PB-O2B
50	OG	501	GTP	PA-O3A-PB-O1B
50	OI	501	GTP	PA-O3A-PB-O2B
50	OM	501	GTP	PA-O3A-PB-O2B
50	PC	501	GTP	PA-O3A-PB-O2B
50	PE	501	GTP	PA-O3A-PB-O2B
50	PG	501	GTP	PA-O3A-PB-O2B
50	PI	501	GTP	PA-O3A-PB-O2B

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Mol	Chain	Res	Type	Atoms
50	PK	501	GTP	PA-O3A-PB-O2B
50	PO	501	GTP	PA-O3A-PB-O2B
50	QC	501	GTP	PA-O3A-PB-O2B
50	QG	501	GTP	PA-O3A-PB-O2B
50	QK	501	GTP	PA-O3A-PB-O2B
50	QO	501	GTP	PA-O3A-PB-O2B
50	RC	501	GTP	PA-O3A-PB-O2B
50	RE	501	GTP	PA-O3A-PB-O2B
50	RG	501	GTP	PA-O3A-PB-O2B
50	RM	501	GTP	PA-O3A-PB-O2B
50	RO	501	GTP	PA-O3A-PB-O1B
50	SA	501	GTP	PA-O3A-PB-O2B
50	SM	501	GTP	PA-O3A-PB-O1B
50	TG	501	GTP	PA-O3A-PB-O2B
50	TI	501	GTP	PA-O3A-PB-O2B
50	TK	501	GTP	PA-O3A-PB-O2B
50	UA	501	GTP	PA-O3A-PB-O1B
50	UC	501	GTP	PA-O3A-PB-O1B
50	UG	501	GTP	PA-O3A-PB-O1B
50	VC	501	GTP	PA-O3A-PB-O2B
50	VO	501	GTP	PA-O3A-PB-O2B
50	WE	501	GTP	PA-O3A-PB-O2B
50	WI	501	GTP	PA-O3A-PB-O2B
50	JO	501	GTP	C4'-C5'-O5'-PA
50	SC	501	GTP	C4'-C5'-O5'-PA
50	AI	501	GTP	C3'-C4'-C5'-O5'
50	MO	501	GTP	C3'-C4'-C5'-O5'
50	SM	501	GTP	C3'-C4'-C5'-O5'
52	ON	502	GDP	C3'-C4'-C5'-O5'
50	BG	501	GTP	C3'-C4'-C5'-O5'
50	NC	501	GTP	O4'-C4'-C5'-O5'
52	ML	502	GDP	C3'-C4'-C5'-O5'
50	JI	501	GTP	C4'-C5'-O5'-PA
50	FC	501	GTP	O4'-C4'-C5'-O5'
50	AA	501	GTP	PA-O3A-PB-O1B
50	AE	501	GTP	PA-O3A-PB-O1B
50	HI	501	GTP	PA-O3A-PB-O1B
50	MG	501	GTP	PA-O3A-PB-O1B
50	NG	501	GTP	PA-O3A-PB-O2B
50	NI	501	GTP	PA-O3A-PB-O2B
50	NO	501	GTP	PA-O3A-PB-O2B
50	OC	501	GTP	PA-O3A-PB-O1B

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Mol	Chain	Res	Type	Atoms
50	OK	501	GTP	PA-O3A-PB-O2B
50	RE	501	GTP	PA-O3A-PB-O1B
50	SG	501	GTP	PA-O3A-PB-O2B
50	SM	501	GTP	PA-O3A-PB-O2B
50	TA	501	GTP	PA-O3A-PB-O1B
50	TA	501	GTP	PA-O3A-PB-O2B
50	UI	501	GTP	PA-O3A-PB-O1B
50	UM	501	GTP	PA-O3A-PB-O1B
50	UM	501	GTP	PA-O3A-PB-O2B
50	VA	501	GTP	PA-O3A-PB-O1B
50	BE	501	GTP	O4'-C4'-C5'-O5'
50	BK	501	GTP	C3'-C4'-C5'-O5'
50	DQ	501	GTP	O4'-C4'-C5'-O5'
50	EA	501	GTP	O4'-C4'-C5'-O5'
50	EO	501	GTP	O4'-C4'-C5'-O5'
50	JO	501	GTP	O4'-C4'-C5'-O5'
50	JQ	501	GTP	O4'-C4'-C5'-O5'
50	MM	501	GTP	O4'-C4'-C5'-O5'
50	OA	501	GTP	O4'-C4'-C5'-O5'
50	OG	501	GTP	O4'-C4'-C5'-O5'
50	OO	501	GTP	O4'-C4'-C5'-O5'
50	QM	501	GTP	O4'-C4'-C5'-O5'
50	TG	501	GTP	O4'-C4'-C5'-O5'
50	TI	501	GTP	O4'-C4'-C5'-O5'
50	UA	501	GTP	O4'-C4'-C5'-O5'
52	LL	502	GDP	C3'-C4'-C5'-O5'
50	UG	501	GTP	PB-O3A-PA-O5'
50	CE	501	GTP	C3'-C4'-C5'-O5'
50	CG	501	GTP	C3'-C4'-C5'-O5'
50	EG	501	GTP	O4'-C4'-C5'-O5'
50	FA	501	GTP	O4'-C4'-C5'-O5'
50	JI	501	GTP	O4'-C4'-C5'-O5'
50	KI	501	GTP	O4'-C4'-C5'-O5'
50	RI	501	GTP	C3'-C4'-C5'-O5'
52	MH	502	GDP	O4'-C4'-C5'-O5'
50	AE	501	GTP	O4'-C4'-C5'-O5'
50	LO	501	GTP	C3'-C4'-C5'-O5'
50	NG	501	GTP	O4'-C4'-C5'-O5'
50	SI	501	GTP	O4'-C4'-C5'-O5'
52	IB	502	GDP	C3'-C4'-C5'-O5'
52	OD	502	GDP	O4'-C4'-C5'-O5'
50	AA	501	GTP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
50	AC	501	GTP	C5'-O5'-PA-O3A
50	AI	501	GTP	C5'-O5'-PA-O3A
50	AK	501	GTP	C5'-O5'-PA-O3A
50	AM	501	GTP	C5'-O5'-PA-O3A
50	AO	501	GTP	C5'-O5'-PA-O3A
50	BC	501	GTP	C5'-O5'-PA-O3A
50	BE	501	GTP	C5'-O5'-PA-O3A
50	BG	501	GTP	C5'-O5'-PA-O3A
50	BI	501	GTP	C5'-O5'-PA-O3A
50	BK	501	GTP	C5'-O5'-PA-O3A
50	BO	501	GTP	C5'-O5'-PA-O3A
50	CC	501	GTP	C5'-O5'-PA-O3A
50	CG	501	GTP	C5'-O5'-PA-O3A
50	CI	501	GTP	C5'-O5'-PA-O3A
50	CM	501	GTP	C5'-O5'-PA-O3A
50	CO	501	GTP	C5'-O5'-PA-O3A
50	DC	501	GTP	C5'-O5'-PA-O3A
50	DE	501	GTP	C5'-O5'-PA-O3A
50	DG	501	GTP	C5'-O5'-PA-O3A
50	DM	501	GTP	C5'-O5'-PA-O3A
50	DO	501	GTP	C5'-O5'-PA-O3A
50	EA	501	GTP	C5'-O5'-PA-O3A
50	EC	501	GTP	C5'-O5'-PA-O3A
50	EG	501	GTP	C5'-O5'-PA-O3A
50	EI	501	GTP	C5'-O5'-PA-O3A
50	EM	501	GTP	C5'-O5'-PA-O3A
50	EO	501	GTP	C5'-O5'-PA-O3A
50	FA	501	GTP	C5'-O5'-PA-O3A
50	FC	501	GTP	C5'-O5'-PA-O3A
50	FK	501	GTP	C5'-O5'-PA-O3A
50	FO	501	GTP	C5'-O5'-PA-O3A
50	GE	501	GTP	C5'-O5'-PA-O3A
50	HI	501	GTP	C5'-O5'-PA-O3A
50	HM	501	GTP	C5'-O5'-PA-O3A
50	IA	501	GTP	C5'-O5'-PA-O3A
50	IC	501	GTP	C5'-O5'-PA-O3A
50	IE	501	GTP	C5'-O5'-PA-O3A
50	IG	501	GTP	C5'-O5'-PA-O3A
50	IK	501	GTP	C5'-O5'-PA-O3A
50	JC	501	GTP	C5'-O5'-PA-O3A
50	JE	501	GTP	C5'-O5'-PA-O3A
50	JG	501	GTP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
50	JI	501	GTP	C5'-O5'-PA-O3A
50	JK	501	GTP	C5'-O5'-PA-O3A
50	JM	501	GTP	C5'-O5'-PA-O3A
50	JO	501	GTP	C5'-O5'-PA-O3A
50	JQ	501	GTP	C5'-O5'-PA-O3A
50	KC	501	GTP	C5'-O5'-PA-O3A
50	KE	501	GTP	C5'-O5'-PA-O3A
50	KI	501	GTP	C5'-O5'-PA-O3A
50	KM	501	GTP	C5'-O5'-PA-O3A
50	LA	501	GTP	C5'-O5'-PA-O3A
50	LC	501	GTP	C5'-O5'-PA-O3A
50	LG	501	GTP	C5'-O5'-PA-O3A
50	LI	501	GTP	C5'-O5'-PA-O3A
50	LK	501	GTP	C5'-O5'-PA-O3A
50	LM	501	GTP	C5'-O5'-PA-O3A
50	LO	501	GTP	C5'-O5'-PA-O3A
50	MC	501	GTP	C5'-O5'-PA-O3A
50	MG	501	GTP	C5'-O5'-PA-O3A
50	MI	501	GTP	C5'-O5'-PA-O3A
50	MK	501	GTP	C5'-O5'-PA-O3A
50	MO	501	GTP	C5'-O5'-PA-O3A
50	NA	501	GTP	C5'-O5'-PA-O3A
50	NG	501	GTP	C5'-O5'-PA-O3A
50	NI	501	GTP	C5'-O5'-PA-O3A
50	NK	501	GTP	C5'-O5'-PA-O3A
50	NM	501	GTP	C5'-O5'-PA-O3A
50	NO	501	GTP	C5'-O5'-PA-O3A
50	OA	501	GTP	C5'-O5'-PA-O3A
50	OE	501	GTP	C5'-O5'-PA-O3A
50	OG	501	GTP	C5'-O5'-PA-O3A
50	OI	501	GTP	C5'-O5'-PA-O3A
50	OK	501	GTP	C5'-O5'-PA-O3A
50	OM	501	GTP	C5'-O5'-PA-O3A
50	OO	501	GTP	C5'-O5'-PA-O3A
50	PC	501	GTP	C5'-O5'-PA-O3A
50	PE	501	GTP	C5'-O5'-PA-O3A
50	PG	501	GTP	C5'-O5'-PA-O3A
50	PI	501	GTP	C5'-O5'-PA-O3A
50	PK	501	GTP	C5'-O5'-PA-O3A
50	PM	501	GTP	C5'-O5'-PA-O3A
50	PO	501	GTP	C5'-O5'-PA-O3A
50	QC	501	GTP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
50	QE	501	GTP	C5'-O5'-PA-O3A
50	QG	501	GTP	C5'-O5'-PA-O3A
50	QM	501	GTP	C5'-O5'-PA-O3A
50	RC	501	GTP	C5'-O5'-PA-O3A
50	RI	501	GTP	C5'-O5'-PA-O3A
50	RK	501	GTP	C5'-O5'-PA-O3A
50	SA	501	GTP	C5'-O5'-PA-O3A
50	SC	501	GTP	C5'-O5'-PA-O3A
50	UA	501	GTP	C5'-O5'-PA-O3A
50	VA	501	GTP	C5'-O5'-PA-O3A
50	VC	501	GTP	C5'-O5'-PA-O3A
50	VE	501	GTP	C5'-O5'-PA-O3A
50	VI	501	GTP	C5'-O5'-PA-O3A
50	VM	501	GTP	C5'-O5'-PA-O3A
50	VO	501	GTP	C5'-O5'-PA-O3A
50	WA	501	GTP	C5'-O5'-PA-O3A
50	WC	501	GTP	C5'-O5'-PA-O3A
50	WE	501	GTP	C5'-O5'-PA-O3A
50	WG	501	GTP	C5'-O5'-PA-O3A
50	WI	501	GTP	C5'-O5'-PA-O3A
50	WK	501	GTP	C5'-O5'-PA-O3A
50	WO	501	GTP	C5'-O5'-PA-O3A
52	BL	502	GDP	C5'-O5'-PA-O3A
52	HB	502	GDP	C5'-O5'-PA-O3A
52	IJ	502	GDP	C5'-O5'-PA-O3A
52	KD	502	GDP	C5'-O5'-PA-O3A
52	LD	502	GDP	C5'-O5'-PA-O3A
52	LH	502	GDP	C5'-O5'-PA-O3A
52	LL	502	GDP	C5'-O5'-PA-O3A
52	MN	502	GDP	C5'-O5'-PA-O3A
52	ND	502	GDP	C5'-O5'-PA-O3A
52	NH	502	GDP	C5'-O5'-PA-O3A
52	NN	502	GDP	C5'-O5'-PA-O3A
52	OF	502	GDP	C5'-O5'-PA-O3A
52	SD	502	GDP	C5'-O5'-PA-O3A
52	SF	502	GDP	C5'-O5'-PA-O3A
52	SJ	502	GDP	C5'-O5'-PA-O3A
52	SL	502	GDP	C5'-O5'-PA-O3A
52	UD	502	GDP	C5'-O5'-PA-O3A
52	VB	502	GDP	C5'-O5'-PA-O3A
50	JK	501	GTP	C4'-C5'-O5'-PA
50	AI	501	GTP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
50	FI	501	GTP	O4'-C4'-C5'-O5'
50	GA	501	GTP	O4'-C4'-C5'-O5'
50	GK	501	GTP	C3'-C4'-C5'-O5'
50	LM	501	GTP	C3'-C4'-C5'-O5'
50	PC	501	GTP	O4'-C4'-C5'-O5'
50	RM	501	GTP	C3'-C4'-C5'-O5'
50	WM	501	GTP	C3'-C4'-C5'-O5'
50	WO	501	GTP	C3'-C4'-C5'-O5'
52	DP	502	GDP	O4'-C4'-C5'-O5'
52	LD	502	GDP	C3'-C4'-C5'-O5'
52	LH	502	GDP	C3'-C4'-C5'-O5'
52	OF	502	GDP	C3'-C4'-C5'-O5'
52	VB	502	GDP	O4'-C4'-C5'-O5'
50	AA	501	GTP	PA-O3A-PB-O2B
50	AC	501	GTP	PA-O3A-PB-O1B
50	AG	501	GTP	PA-O3A-PB-O1B
50	AI	501	GTP	PA-O3A-PB-O1B
50	AK	501	GTP	PA-O3A-PB-O1B
50	AM	501	GTP	PA-O3A-PB-O1B
50	AO	501	GTP	PA-O3A-PB-O1B
50	BC	501	GTP	PA-O3A-PB-O1B
50	BE	501	GTP	PA-O3A-PB-O1B
50	BK	501	GTP	PA-O3A-PB-O1B
50	BO	501	GTP	PA-O3A-PB-O1B
50	CC	501	GTP	PA-O3A-PB-O1B
50	CO	501	GTP	PA-O3A-PB-O1B
50	CQ	501	GTP	PA-O3A-PB-O1B
50	DG	501	GTP	PA-O3A-PB-O1B
50	DK	501	GTP	PA-O3A-PB-O1B
50	DK	501	GTP	PA-O3A-PB-O2B
50	DM	501	GTP	PA-O3A-PB-O1B
50	DO	501	GTP	PA-O3A-PB-O1B
50	DQ	501	GTP	PA-O3A-PB-O1B
50	EG	501	GTP	PA-O3A-PB-O2B
50	EI	501	GTP	PA-O3A-PB-O1B
50	EI	501	GTP	PA-O3A-PB-O2B
50	EO	501	GTP	PA-O3A-PB-O1B
50	FG	501	GTP	PA-O3A-PB-O1B
50	FK	501	GTP	PA-O3A-PB-O1B
50	FM	501	GTP	PA-O3A-PB-O1B
50	FO	501	GTP	PA-O3A-PB-O1B
50	GA	501	GTP	PA-O3A-PB-O1B

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Mol	Chain	Res	Type	Atoms
50	GC	501	GTP	PA-O3A-PB-O1B
50	GG	501	GTP	PA-O3A-PB-O1B
50	GK	501	GTP	PA-O3A-PB-O1B
50	GM	501	GTP	PA-O3A-PB-O1B
50	HA	501	GTP	PA-O3A-PB-O2B
50	HC	501	GTP	PA-O3A-PB-O2B
50	HG	501	GTP	PA-O3A-PB-O1B
50	HO	501	GTP	PB-O3A-PA-O1A
50	IA	501	GTP	PA-O3A-PB-O1B
50	IE	501	GTP	PA-O3A-PB-O1B
50	IO	501	GTP	PA-O3A-PB-O1B
50	IO	501	GTP	PA-O3A-PB-O2B
50	JI	501	GTP	PB-O3A-PA-O2A
50	KE	501	GTP	PB-O3A-PA-O2A
50	KK	501	GTP	PA-O3A-PB-O1B
50	LA	501	GTP	PA-O3A-PB-O1B
50	LC	501	GTP	PA-O3A-PB-O1B
50	LE	501	GTP	PA-O3A-PB-O1B
50	MA	501	GTP	PA-O3A-PB-O1B
50	MC	501	GTP	PB-O3A-PA-O1A
50	MM	501	GTP	PA-O3A-PB-O2B
50	NA	501	GTP	PA-O3A-PB-O2B
50	NK	501	GTP	PA-O3A-PB-O2B
50	NM	501	GTP	PA-O3A-PB-O2B
50	OG	501	GTP	PA-O3A-PB-O2B
50	OI	501	GTP	PA-O3A-PB-O1B
50	OM	501	GTP	PA-O3A-PB-O1B
50	OO	501	GTP	PA-O3A-PB-O2B
50	PC	501	GTP	PA-O3A-PB-O1B
50	PG	501	GTP	PA-O3A-PB-O1B
50	PI	501	GTP	PA-O3A-PB-O1B
50	PM	501	GTP	PA-O3A-PB-O1B
50	PO	501	GTP	PA-O3A-PB-O1B
50	QC	501	GTP	PA-O3A-PB-O1B
50	QG	501	GTP	PA-O3A-PB-O1B
50	QI	501	GTP	PA-O3A-PB-O1B
50	QI	501	GTP	PA-O3A-PB-O2B
50	QK	501	GTP	PA-O3A-PB-O1B
50	QM	501	GTP	PA-O3A-PB-O1B
50	RC	501	GTP	PA-O3A-PB-O1B
50	RI	501	GTP	PA-O3A-PB-O1B
50	RK	501	GTP	PA-O3A-PB-O1B

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Mol	Chain	Res	Type	Atoms
50	RM	501	GTP	PA-O3A-PB-O1B
50	RO	501	GTP	PA-O3A-PB-O2B
50	SA	501	GTP	PA-O3A-PB-O1B
50	SK	501	GTP	PA-O3A-PB-O2B
50	TC	501	GTP	PA-O3A-PB-O2B
50	TE	501	GTP	PA-O3A-PB-O2B
50	TG	501	GTP	PA-O3A-PB-O1B
50	TI	501	GTP	PA-O3A-PB-O1B
50	TK	501	GTP	PA-O3A-PB-O1B
50	TM	501	GTP	PA-O3A-PB-O2B
50	UA	501	GTP	PA-O3A-PB-O2B
50	UG	501	GTP	PA-O3A-PB-O2B
50	UK	501	GTP	PA-O3A-PB-O2B
50	VA	501	GTP	PA-O3A-PB-O2B
50	VC	501	GTP	PA-O3A-PB-O1B
50	VG	501	GTP	PA-O3A-PB-O1B
50	VI	501	GTP	PA-O3A-PB-O1B
50	VO	501	GTP	PA-O3A-PB-O1B
50	WA	501	GTP	PA-O3A-PB-O1B
50	WE	501	GTP	PA-O3A-PB-O1B
50	WG	501	GTP	PA-O3A-PB-O1B
50	WI	501	GTP	PA-O3A-PB-O1B
50	NE	501	GTP	C5'-O5'-PA-O1A
52	AH	502	GDP	C5'-O5'-PA-O1A
52	AJ	502	GDP	C5'-O5'-PA-O1A
52	AL	502	GDP	C5'-O5'-PA-O1A
52	AP	502	GDP	C5'-O5'-PA-O1A
52	BD	502	GDP	C5'-O5'-PA-O1A
52	BF	502	GDP	C5'-O5'-PA-O1A
52	BP	502	GDP	C5'-O5'-PA-O1A
52	CB	502	GDP	C5'-O5'-PA-O1A
52	CD	502	GDP	C5'-O5'-PA-O1A
52	CF	502	GDP	C5'-O5'-PA-O1A
52	CJ	502	GDP	C5'-O5'-PA-O1A
52	CP	502	GDP	C5'-O5'-PA-O1A
52	DB	502	GDP	C5'-O5'-PA-O1A
52	DD	502	GDP	C5'-O5'-PA-O1A
52	EB	502	GDP	C5'-O5'-PA-O1A
52	ED	502	GDP	C5'-O5'-PA-O1A
52	EF	502	GDP	C5'-O5'-PA-O1A
52	EH	502	GDP	C5'-O5'-PA-O1A
52	EN	502	GDP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
52	FB	502	GDP	C5'-O5'-PA-O1A
52	FF	502	GDP	C5'-O5'-PA-O1A
52	FH	502	GDP	C5'-O5'-PA-O1A
52	FJ	502	GDP	C5'-O5'-PA-O1A
52	FN	502	GDP	C5'-O5'-PA-O1A
52	GB	502	GDP	C5'-O5'-PA-O1A
52	GH	502	GDP	C5'-O5'-PA-O1A
52	GJ	502	GDP	C5'-O5'-PA-O1A
52	GN	502	GDP	C5'-O5'-PA-O1A
52	HD	502	GDP	C5'-O5'-PA-O1A
52	HL	502	GDP	C5'-O5'-PA-O1A
52	IB	502	GDP	C5'-O5'-PA-O1A
52	IF	502	GDP	C5'-O5'-PA-O1A
52	IN	502	GDP	C5'-O5'-PA-O1A
52	IP	502	GDP	C5'-O5'-PA-O1A
52	JB	502	GDP	C5'-O5'-PA-O1A
52	JD	502	GDP	C5'-O5'-PA-O1A
52	JN	502	GDP	C5'-O5'-PA-O1A
52	KF	502	GDP	C5'-O5'-PA-O1A
52	KH	502	GDP	C5'-O5'-PA-O1A
52	KL	502	GDP	C5'-O5'-PA-O1A
52	KN	502	GDP	C5'-O5'-PA-O1A
52	LF	502	GDP	C5'-O5'-PA-O1A
52	LJ	502	GDP	C5'-O5'-PA-O1A
52	LP	502	GDP	C5'-O5'-PA-O1A
52	NB	502	GDP	C5'-O5'-PA-O1A
52	NL	502	GDP	C5'-O5'-PA-O1A
52	NP	502	GDP	C5'-O5'-PA-O1A
52	OL	502	GDP	C5'-O5'-PA-O1A
52	ON	502	GDP	C5'-O5'-PA-O1A
52	PB	502	GDP	C5'-O5'-PA-O1A
52	PD	502	GDP	C5'-O5'-PA-O1A
52	PF	502	GDP	C5'-O5'-PA-O1A
52	PH	502	GDP	C5'-O5'-PA-O1A
52	PJ	502	GDP	C5'-O5'-PA-O1A
52	PN	502	GDP	C5'-O5'-PA-O1A
52	QB	502	GDP	C5'-O5'-PA-O1A
52	QF	502	GDP	C5'-O5'-PA-O1A
52	QN	502	GDP	C5'-O5'-PA-O1A
52	RH	502	GDP	C5'-O5'-PA-O1A
52	SB	502	GDP	C5'-O5'-PA-O1A
52	TB	502	GDP	C5'-O5'-PA-O1A

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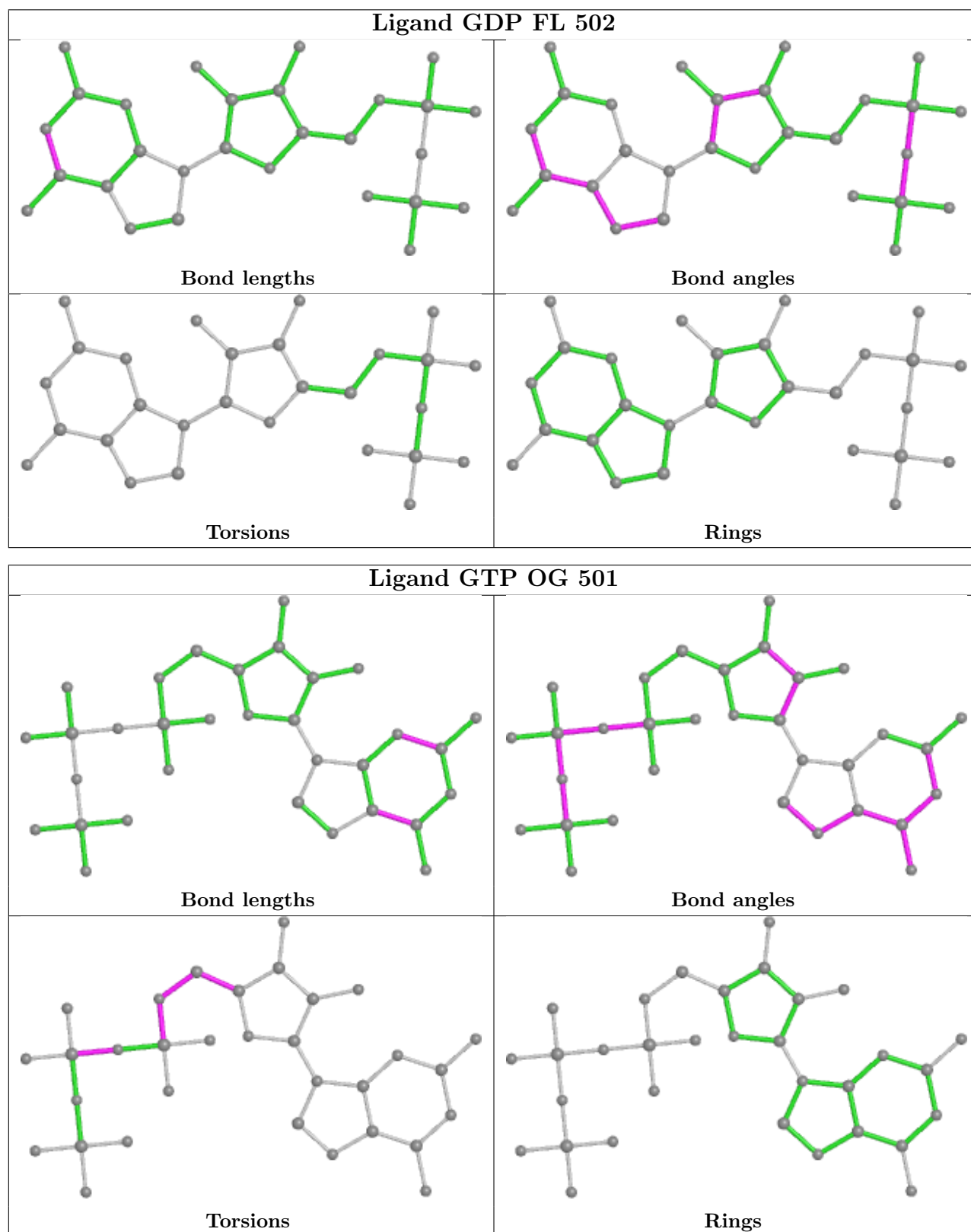
Mol	Chain	Res	Type	Atoms
52	TD	502	GDP	C5'-O5'-PA-O1A
52	TF	502	GDP	C5'-O5'-PA-O1A
52	TJ	502	GDP	C5'-O5'-PA-O1A
52	TL	502	GDP	C5'-O5'-PA-O1A
52	TN	502	GDP	C5'-O5'-PA-O1A
52	UB	502	GDP	C5'-O5'-PA-O1A
52	UH	502	GDP	C5'-O5'-PA-O1A
52	UJ	502	GDP	C5'-O5'-PA-O1A
52	UL	502	GDP	C5'-O5'-PA-O1A
52	UN	502	GDP	C5'-O5'-PA-O1A
52	VD	502	GDP	C5'-O5'-PA-O1A
52	VF	502	GDP	C5'-O5'-PA-O1A
52	VH	502	GDP	C5'-O5'-PA-O1A
52	VJ	502	GDP	C5'-O5'-PA-O1A
52	VL	502	GDP	C5'-O5'-PA-O1A
52	VN	502	GDP	C5'-O5'-PA-O1A
52	WD	502	GDP	C5'-O5'-PA-O1A
52	WF	502	GDP	C5'-O5'-PA-O1A
52	WJ	502	GDP	C5'-O5'-PA-O1A
52	WL	502	GDP	C5'-O5'-PA-O1A
52	WP	502	GDP	C5'-O5'-PA-O1A
50	EI	501	GTP	C3'-C4'-C5'-O5'
50	WK	501	GTP	O4'-C4'-C5'-O5'
52	GJ	502	GDP	PA-O3A-PB-O1B
50	EK	501	GTP	C3'-C4'-C5'-O5'
50	MK	501	GTP	C3'-C4'-C5'-O5'
50	WE	501	GTP	C3'-C4'-C5'-O5'
52	LF	502	GDP	C3'-C4'-C5'-O5'
52	OH	502	GDP	C3'-C4'-C5'-O5'

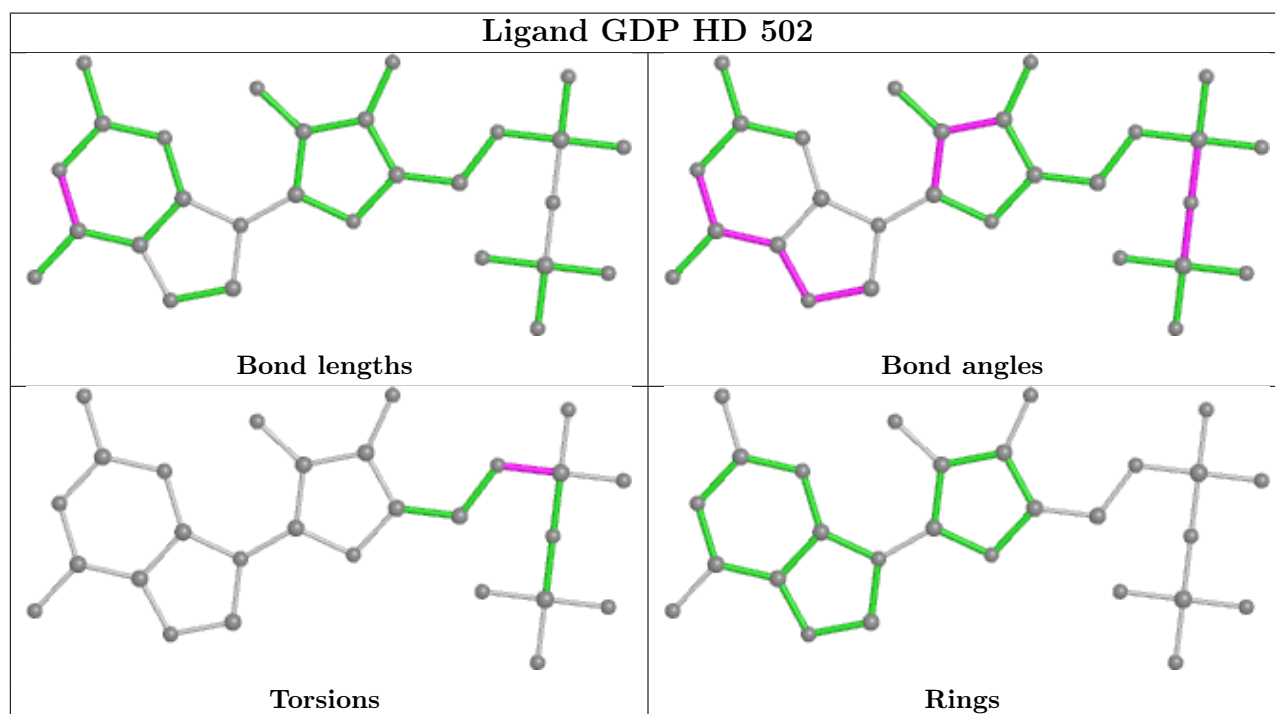
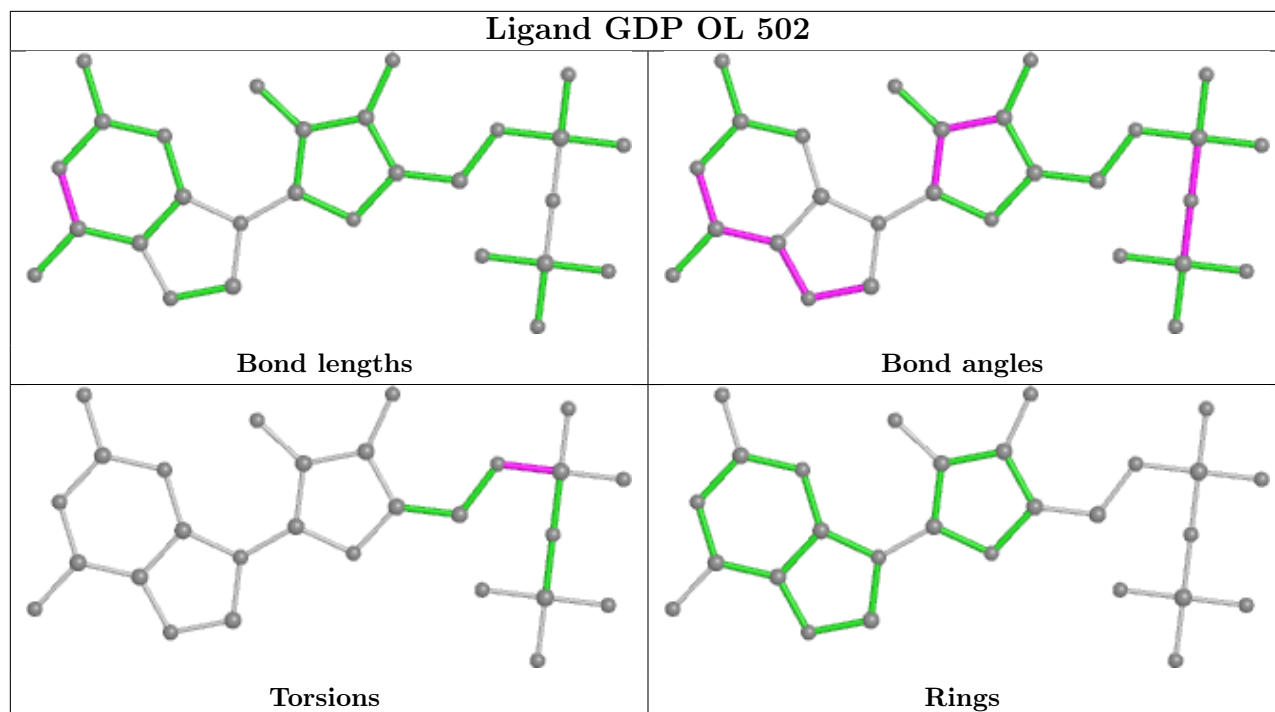
There are no ring outliers.

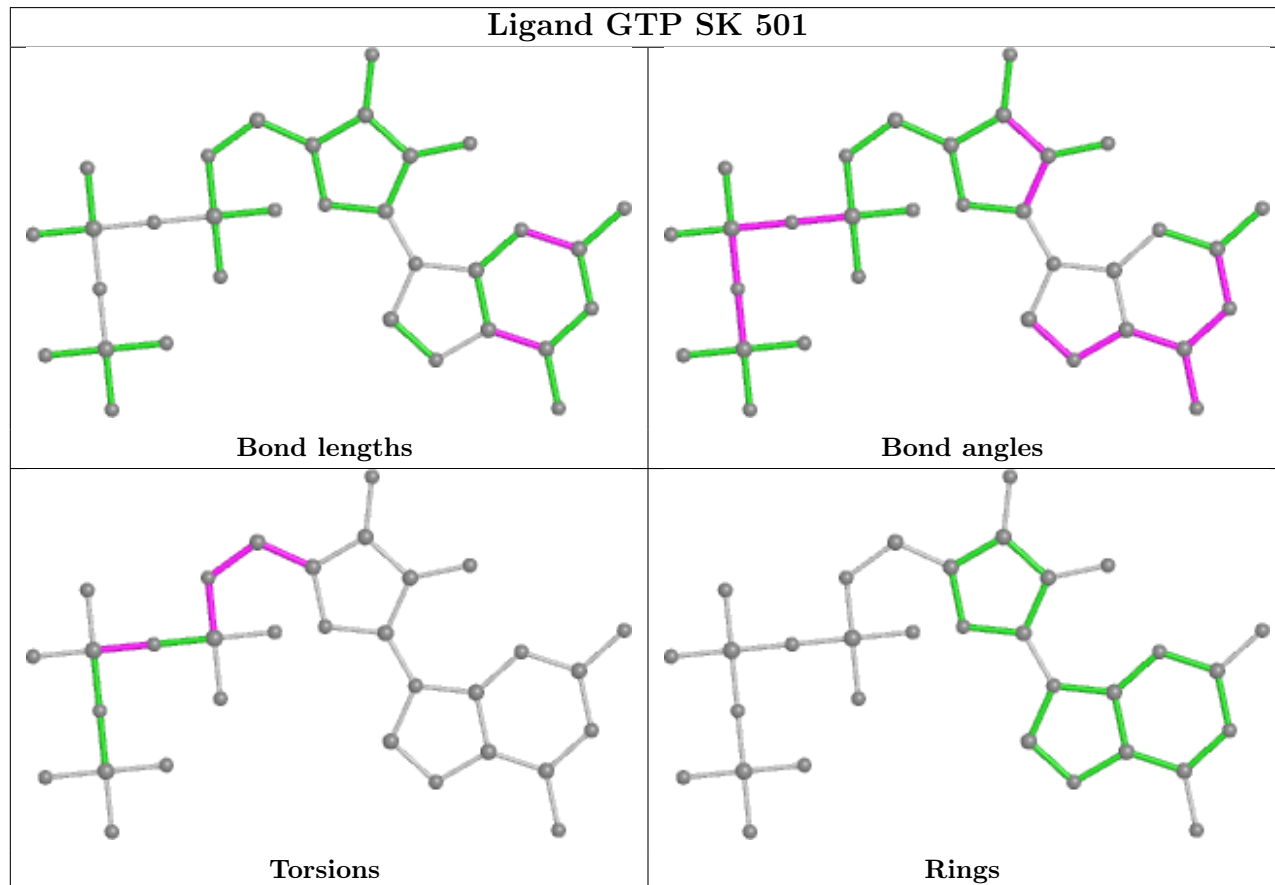
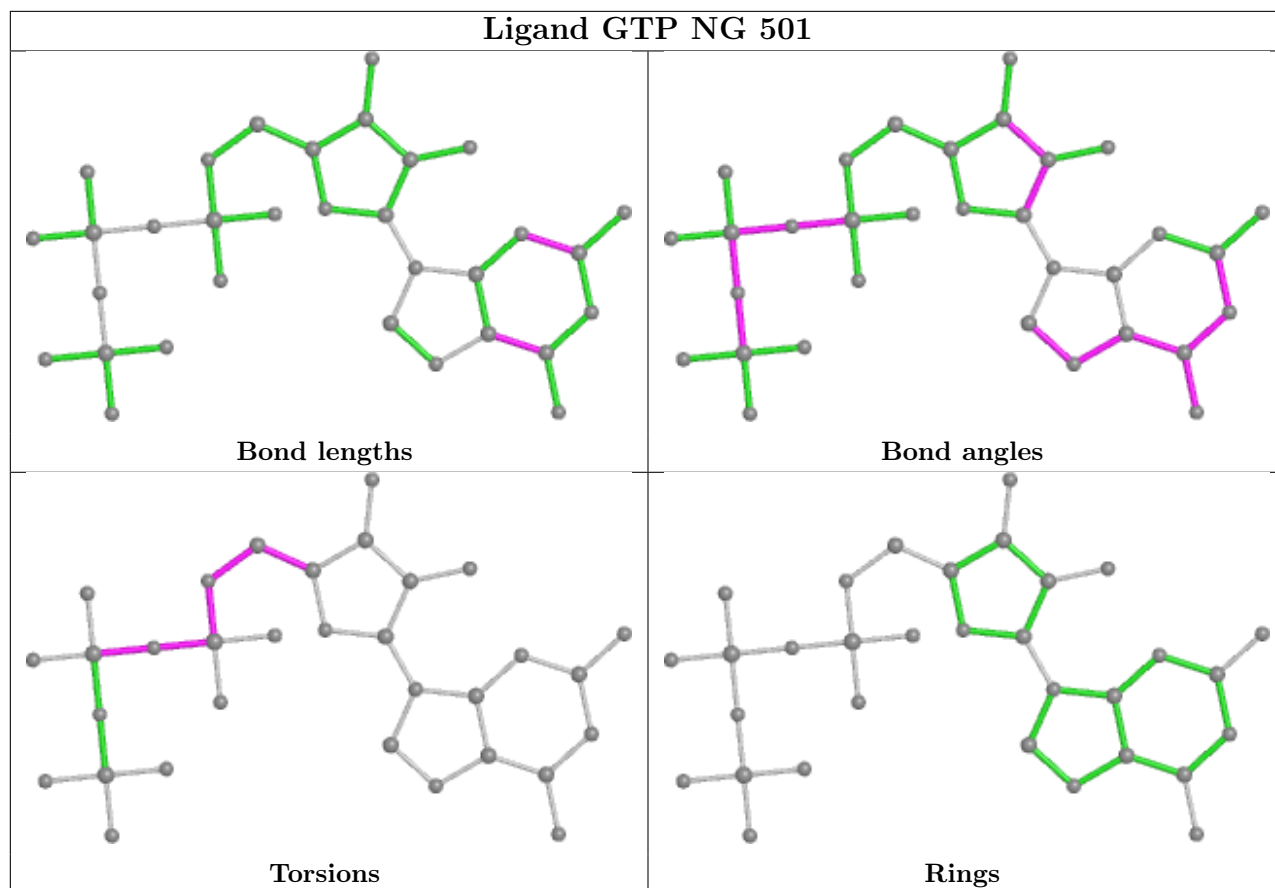
No monomer is involved in short contacts.

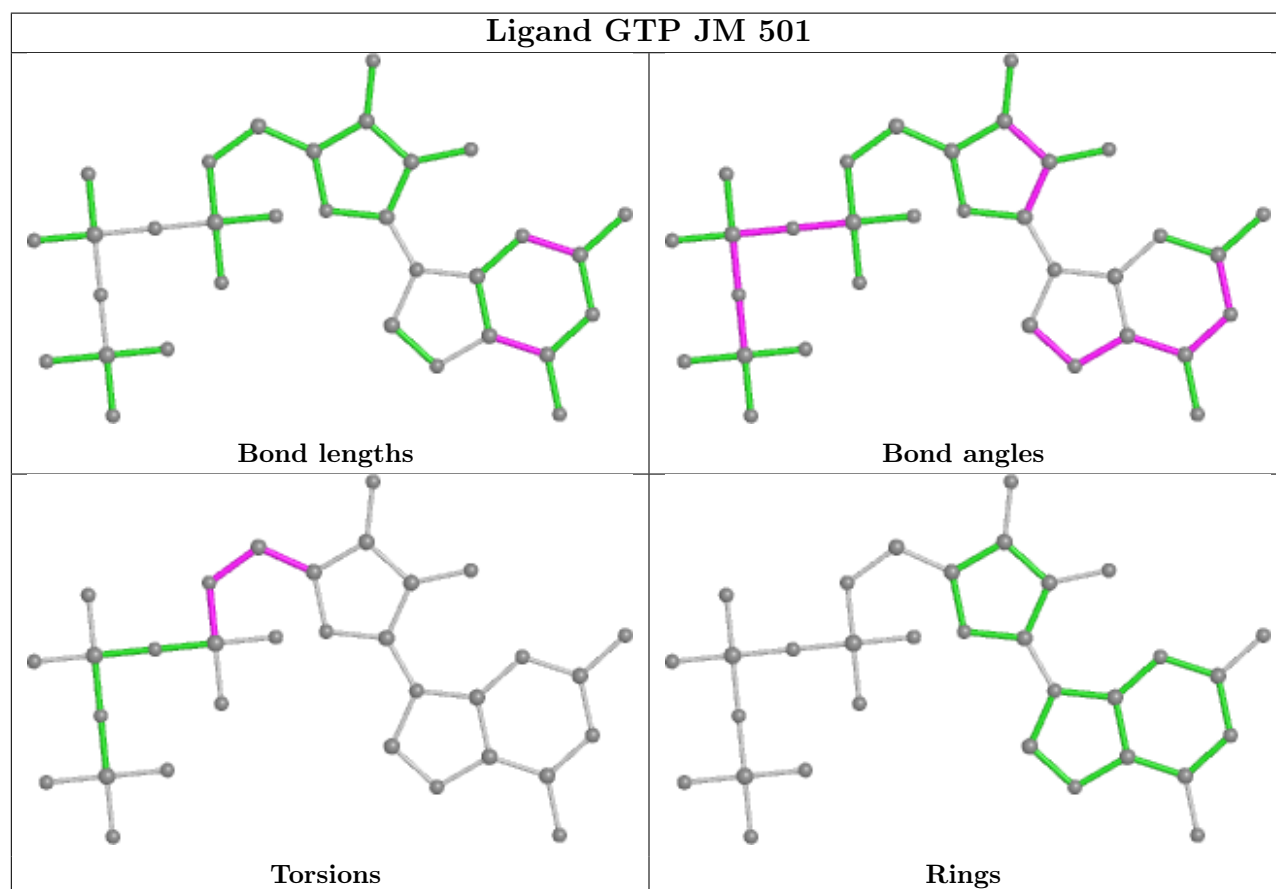
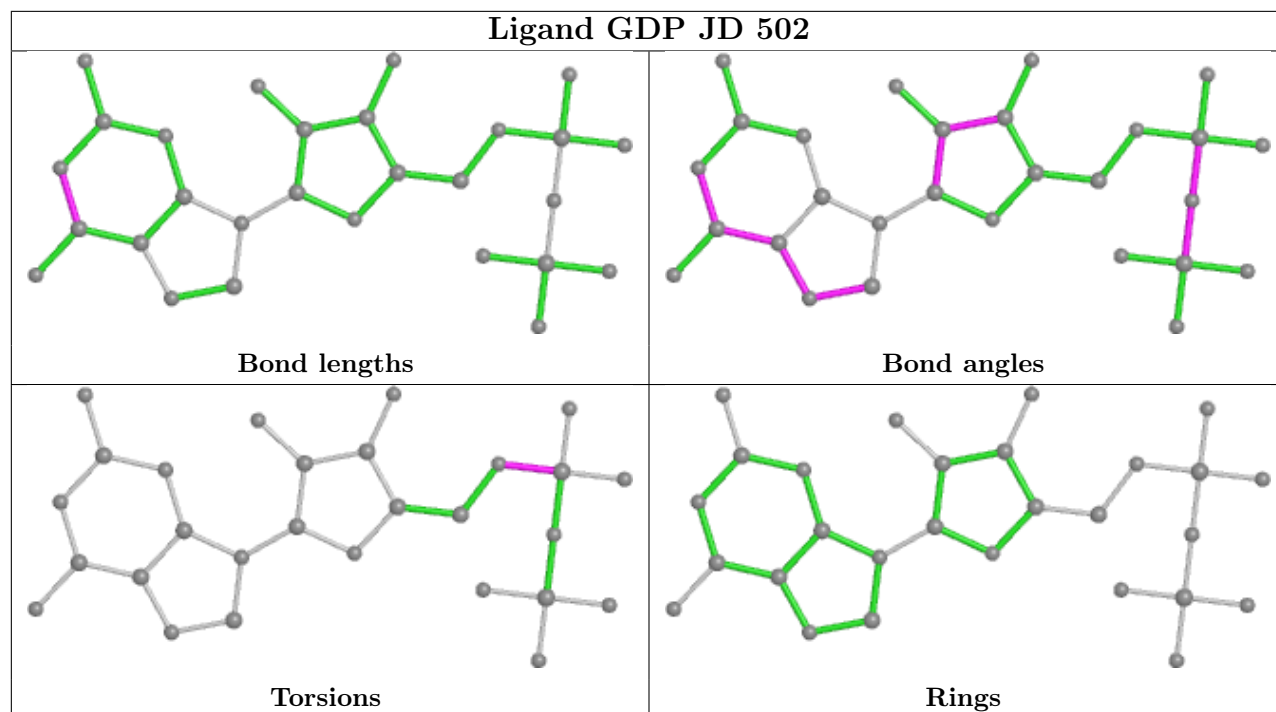
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

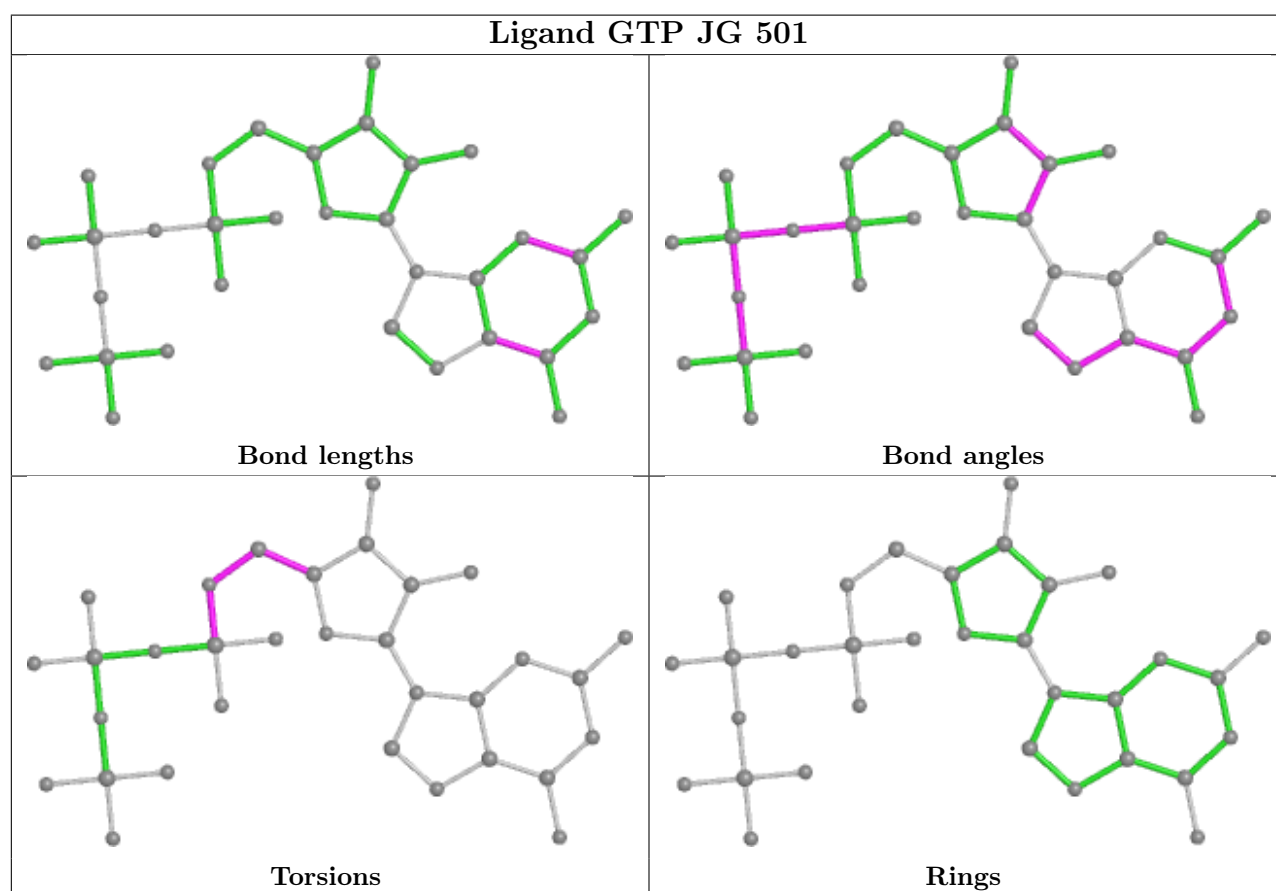
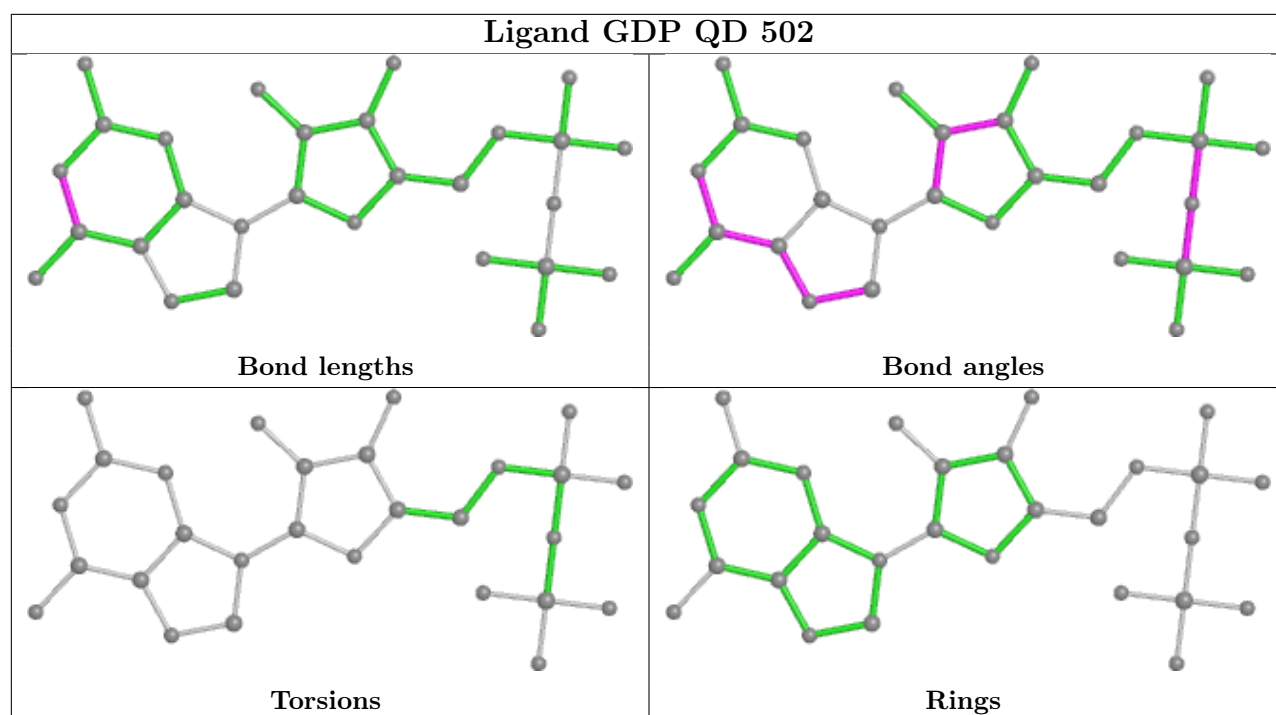
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

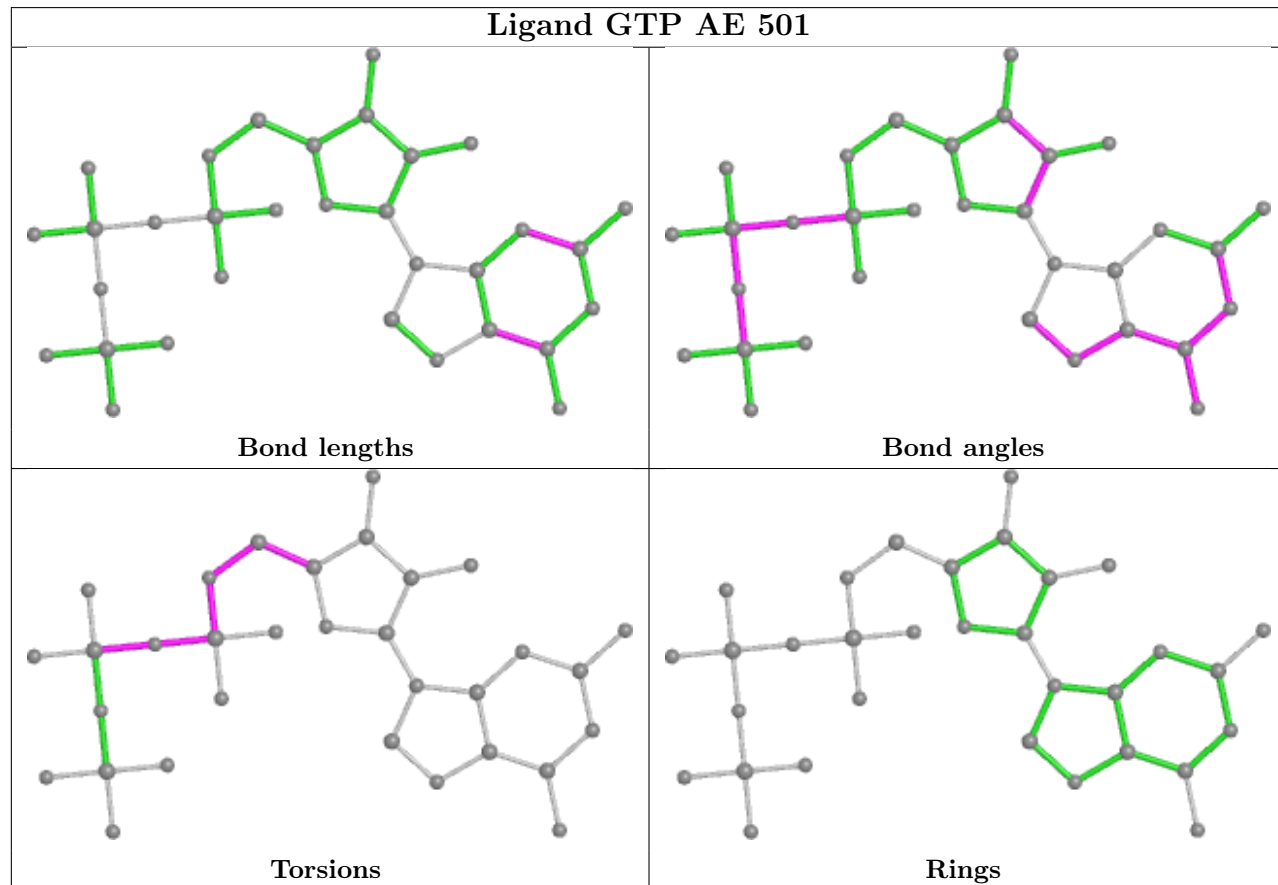
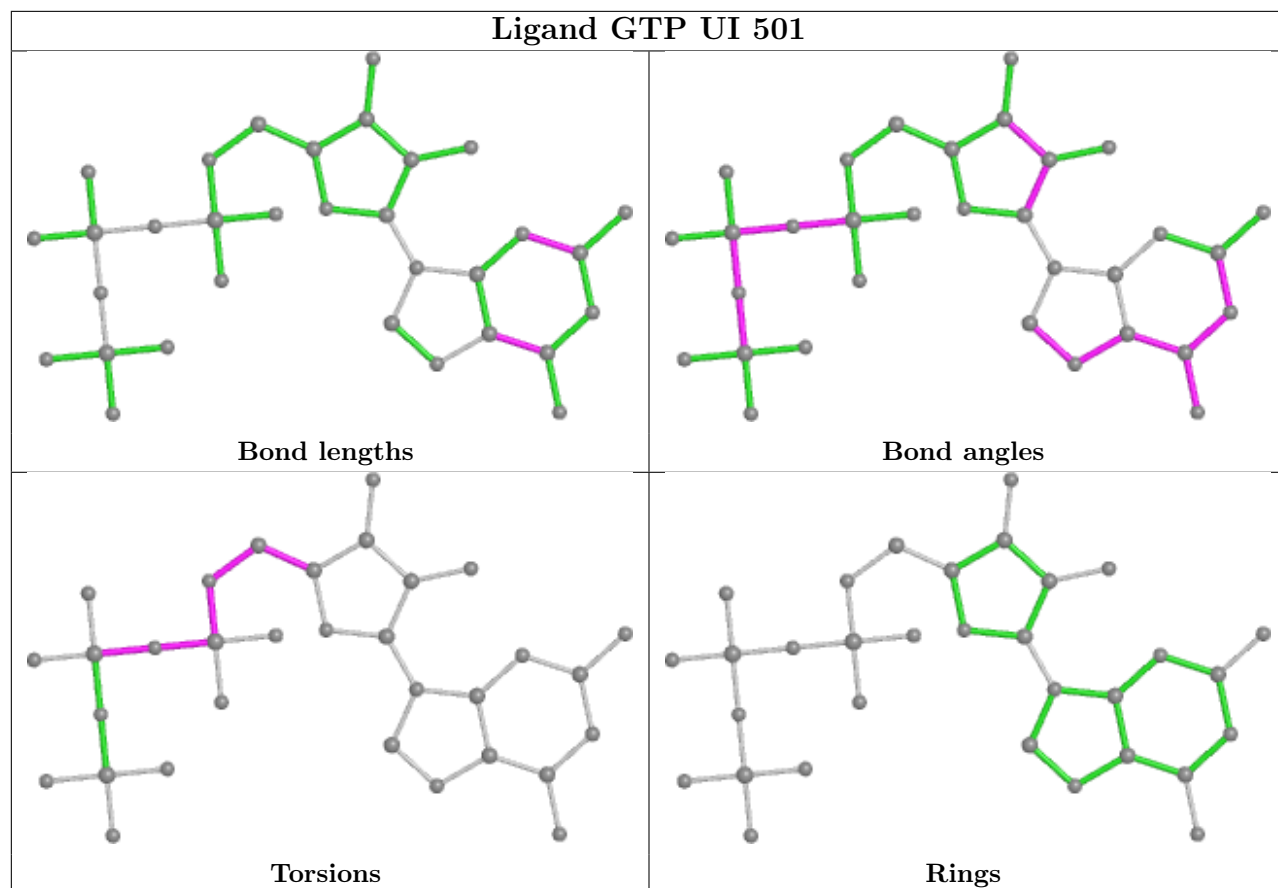


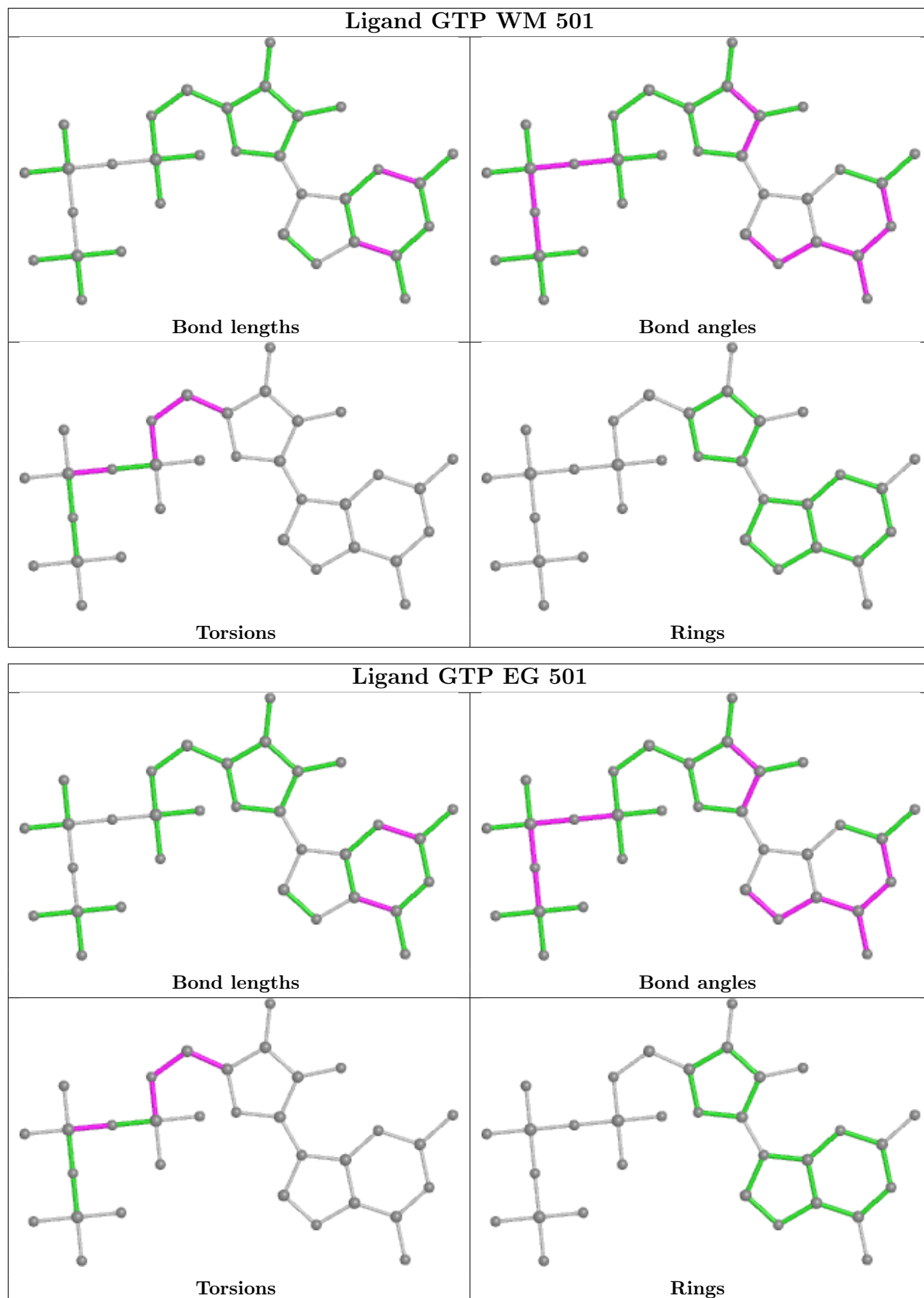


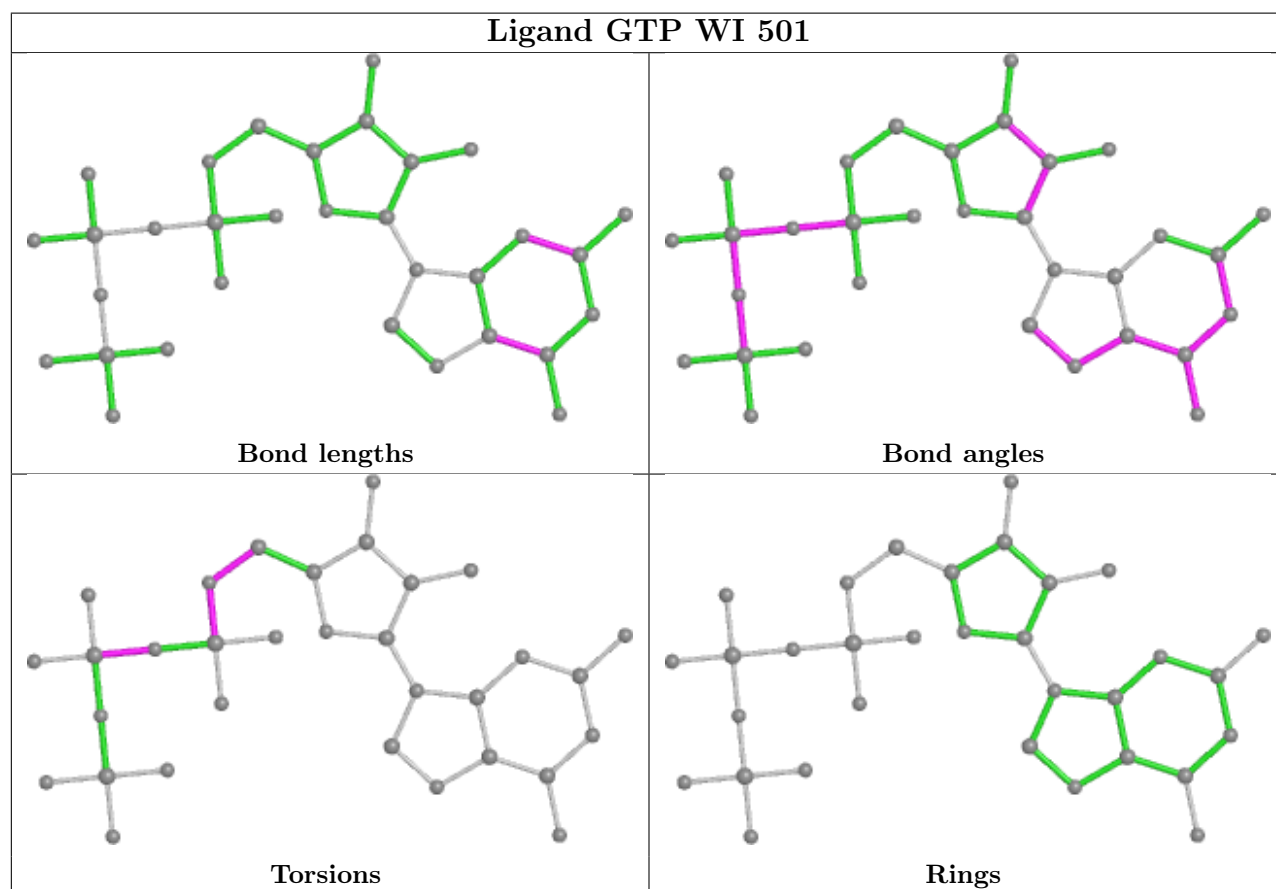
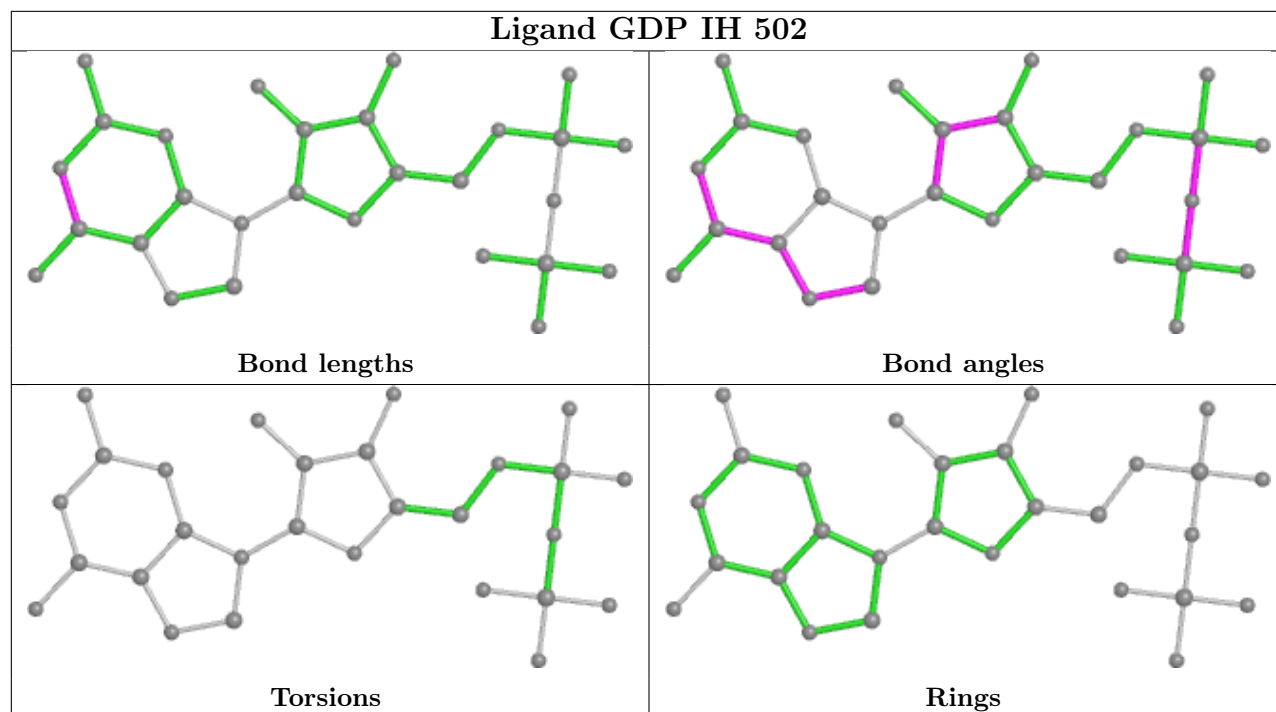


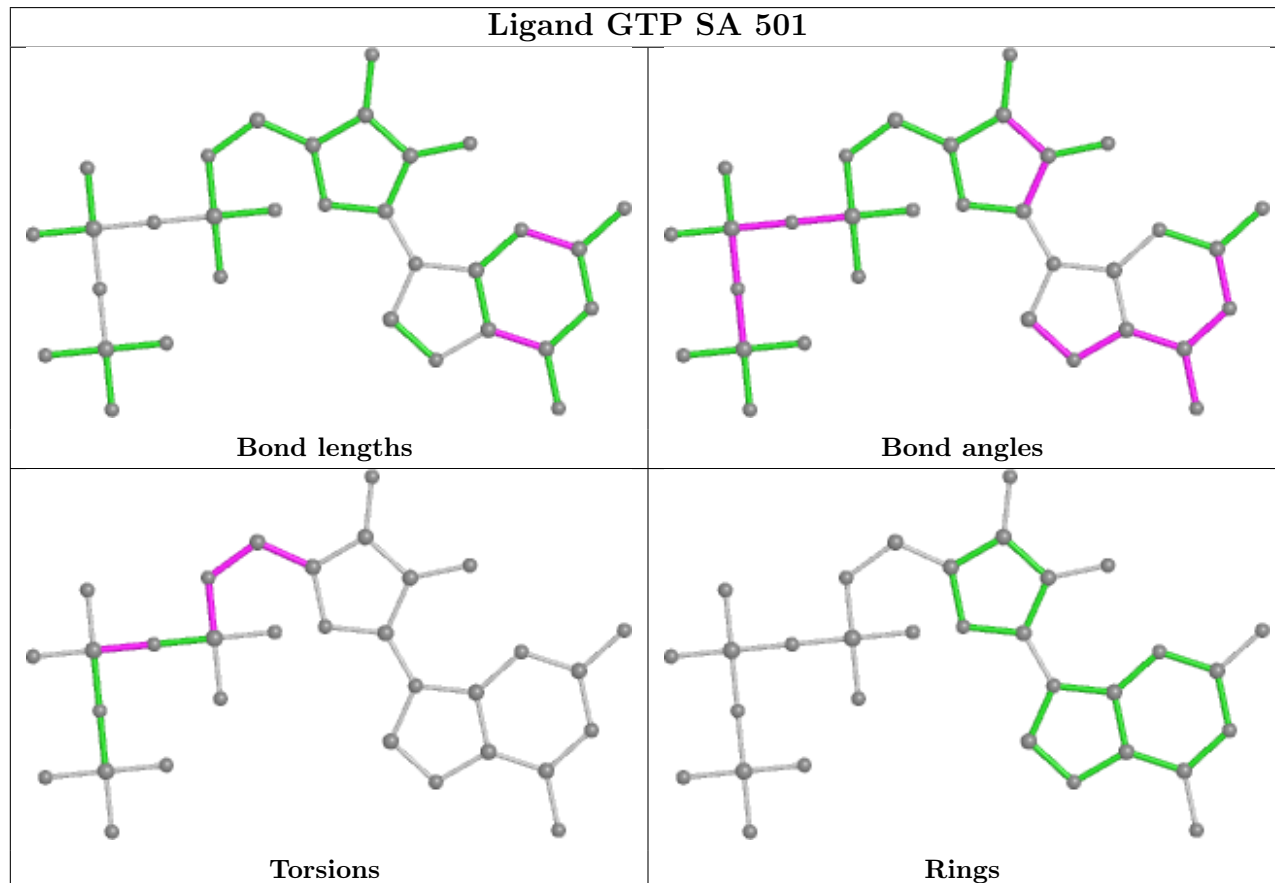
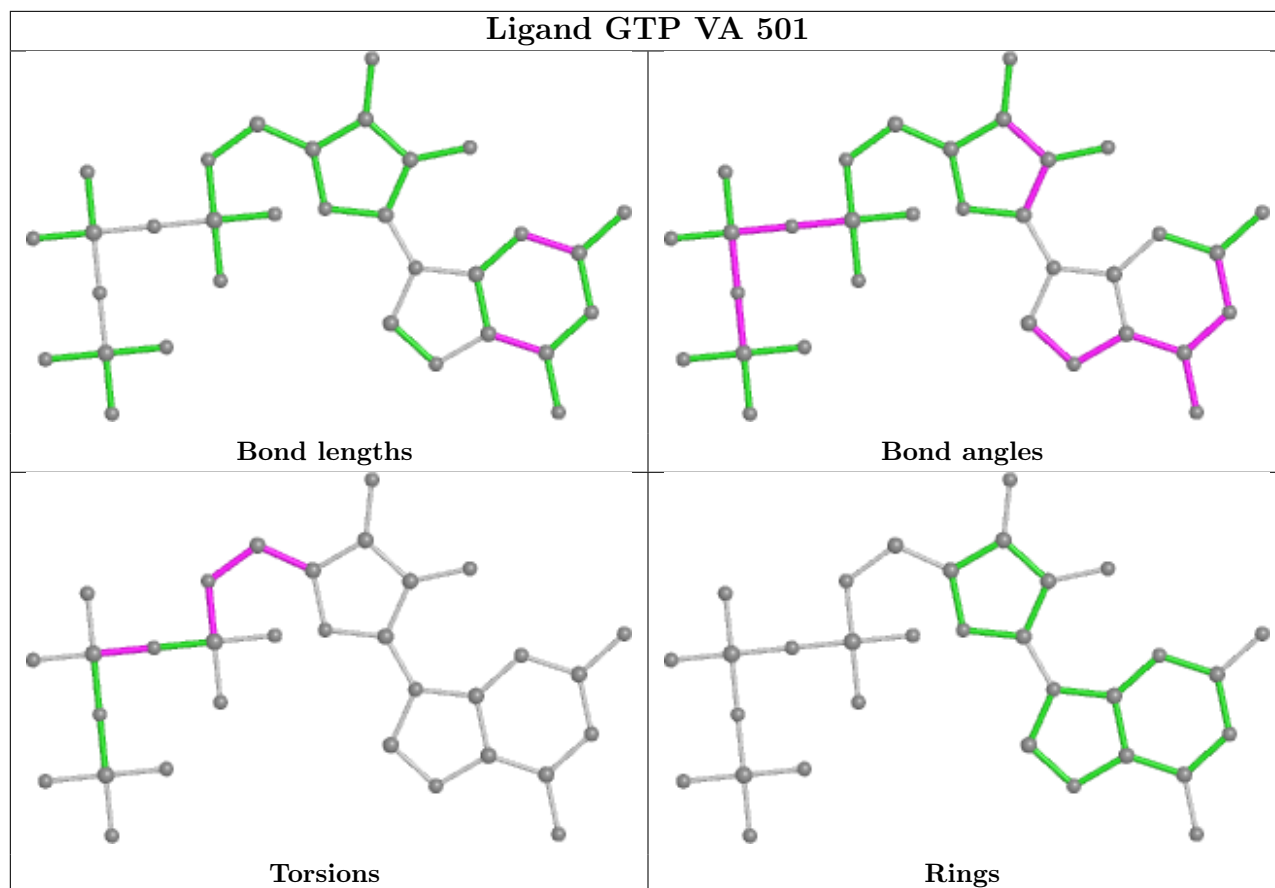


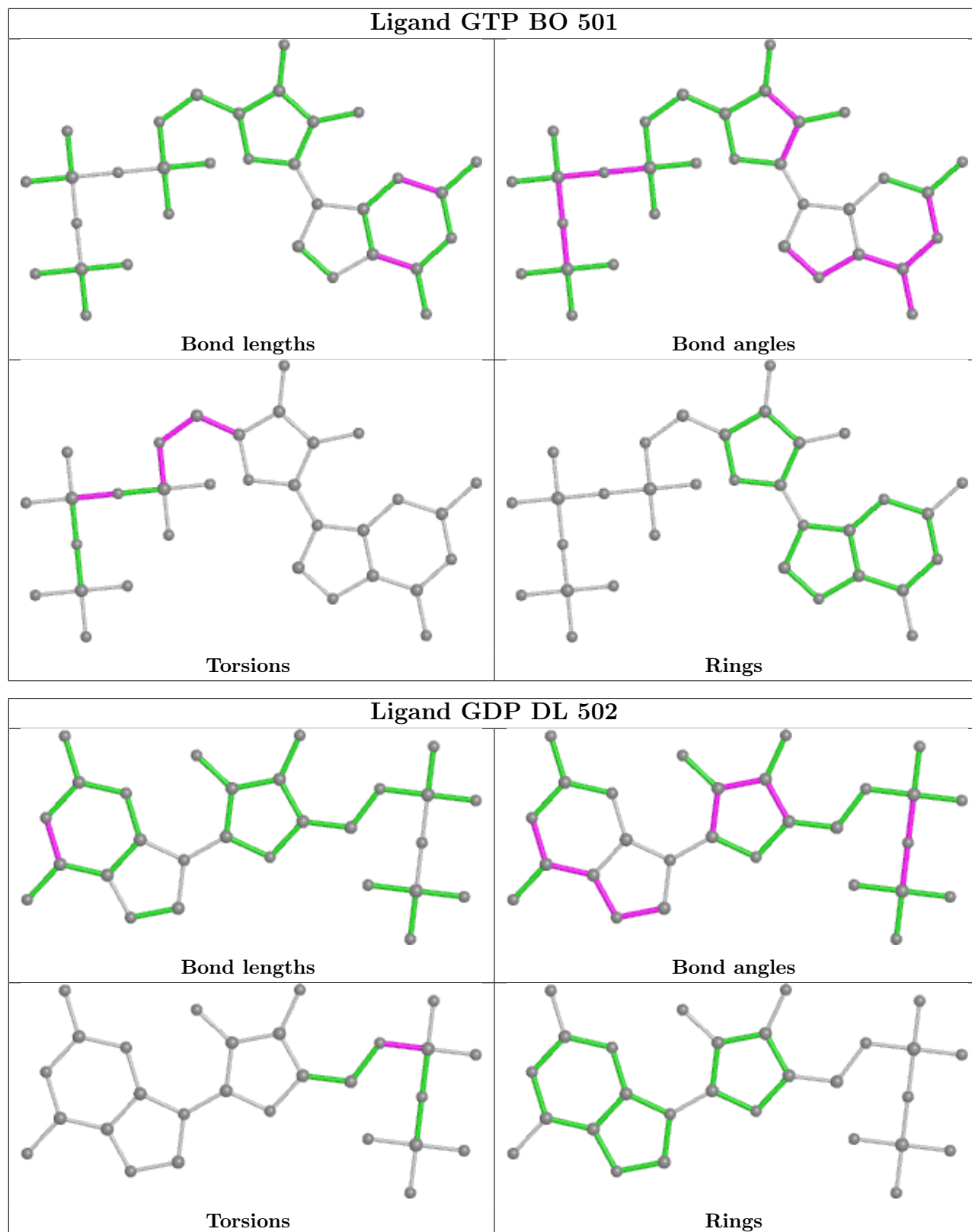


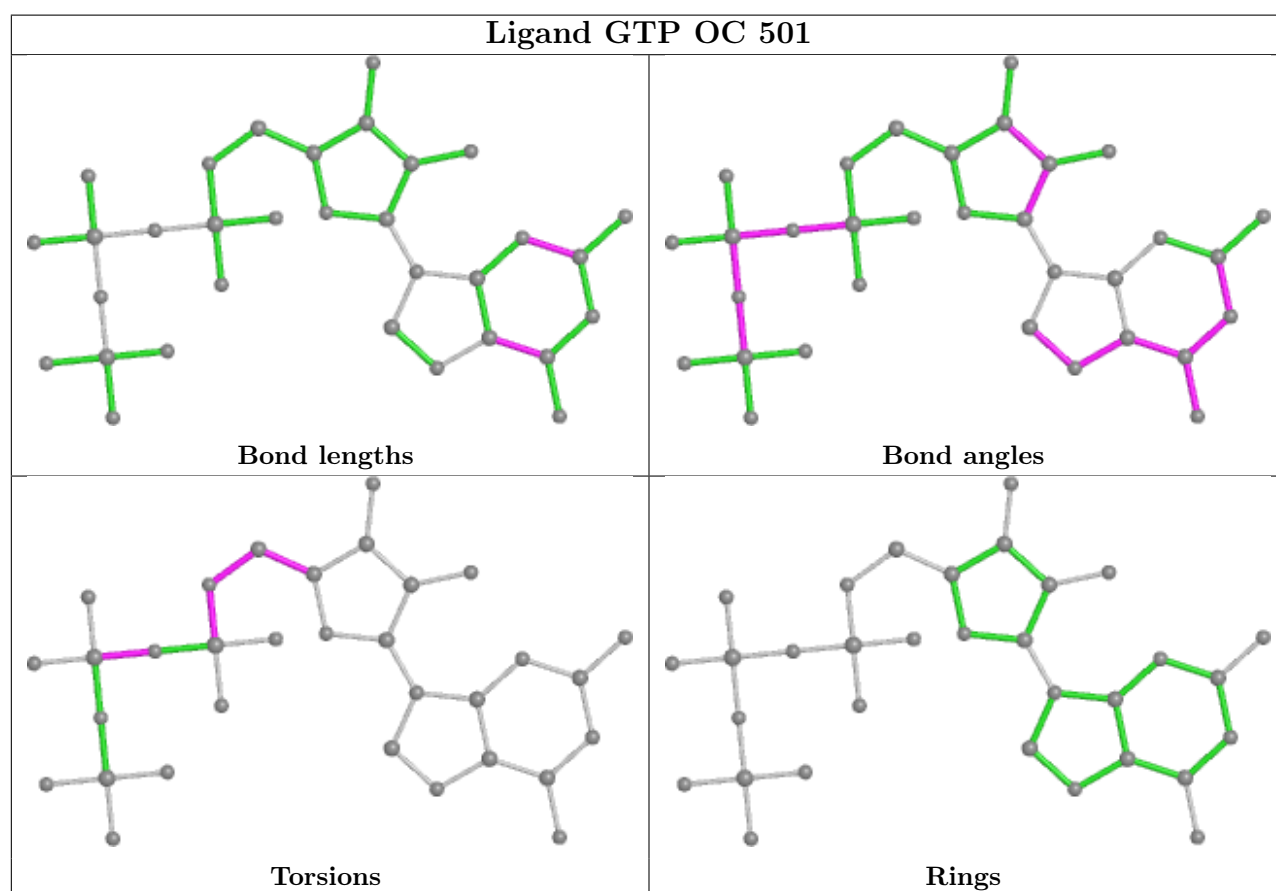
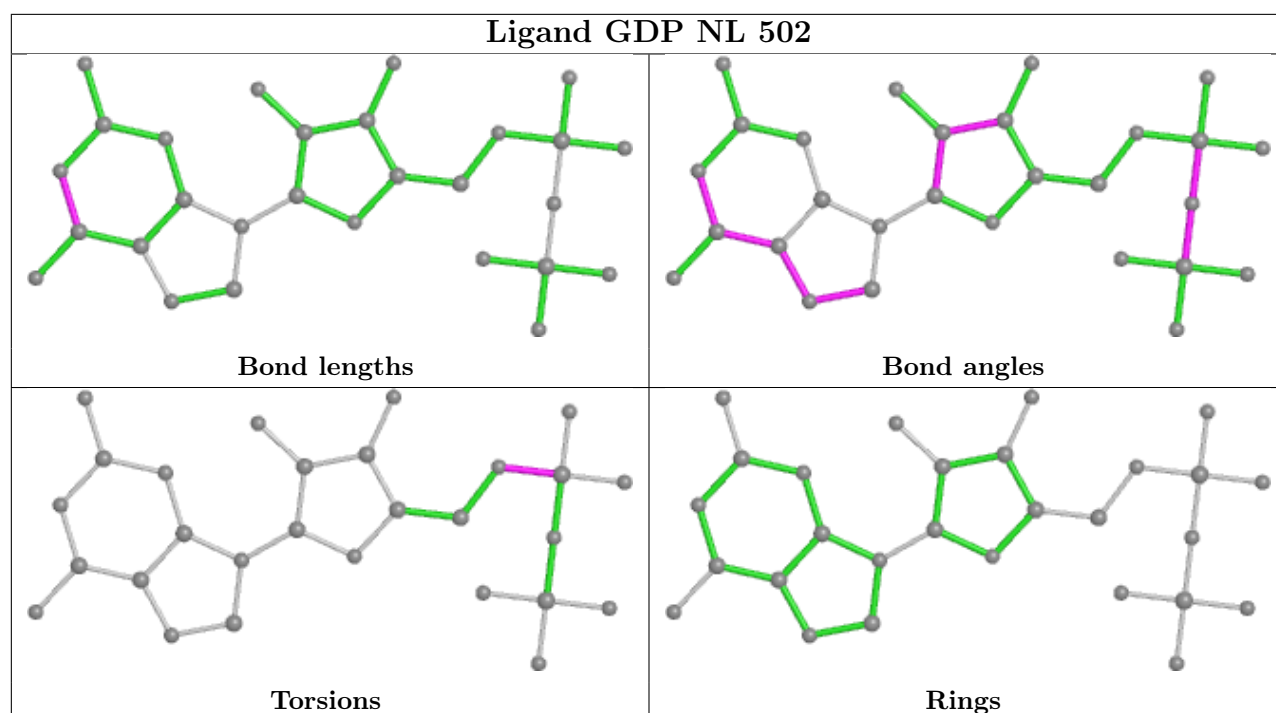


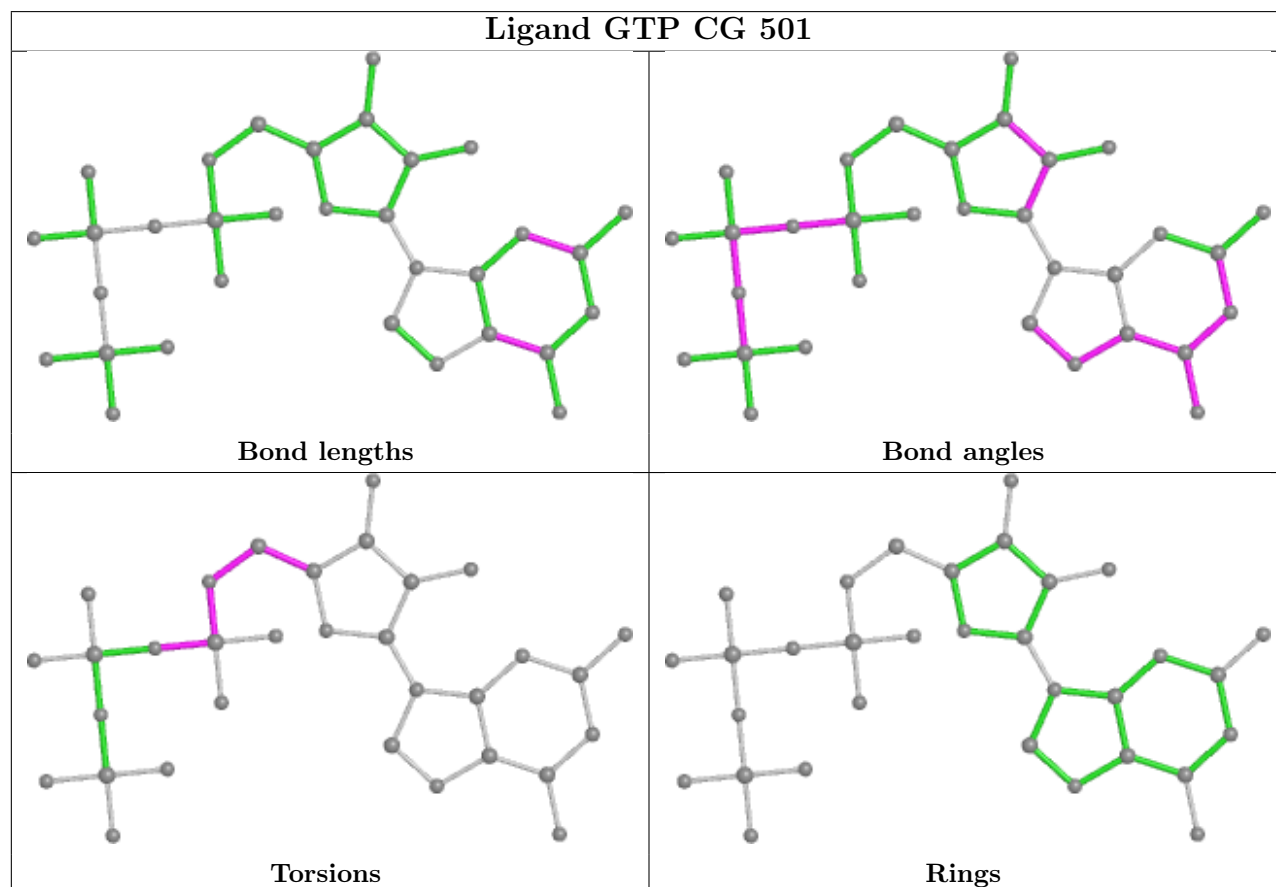
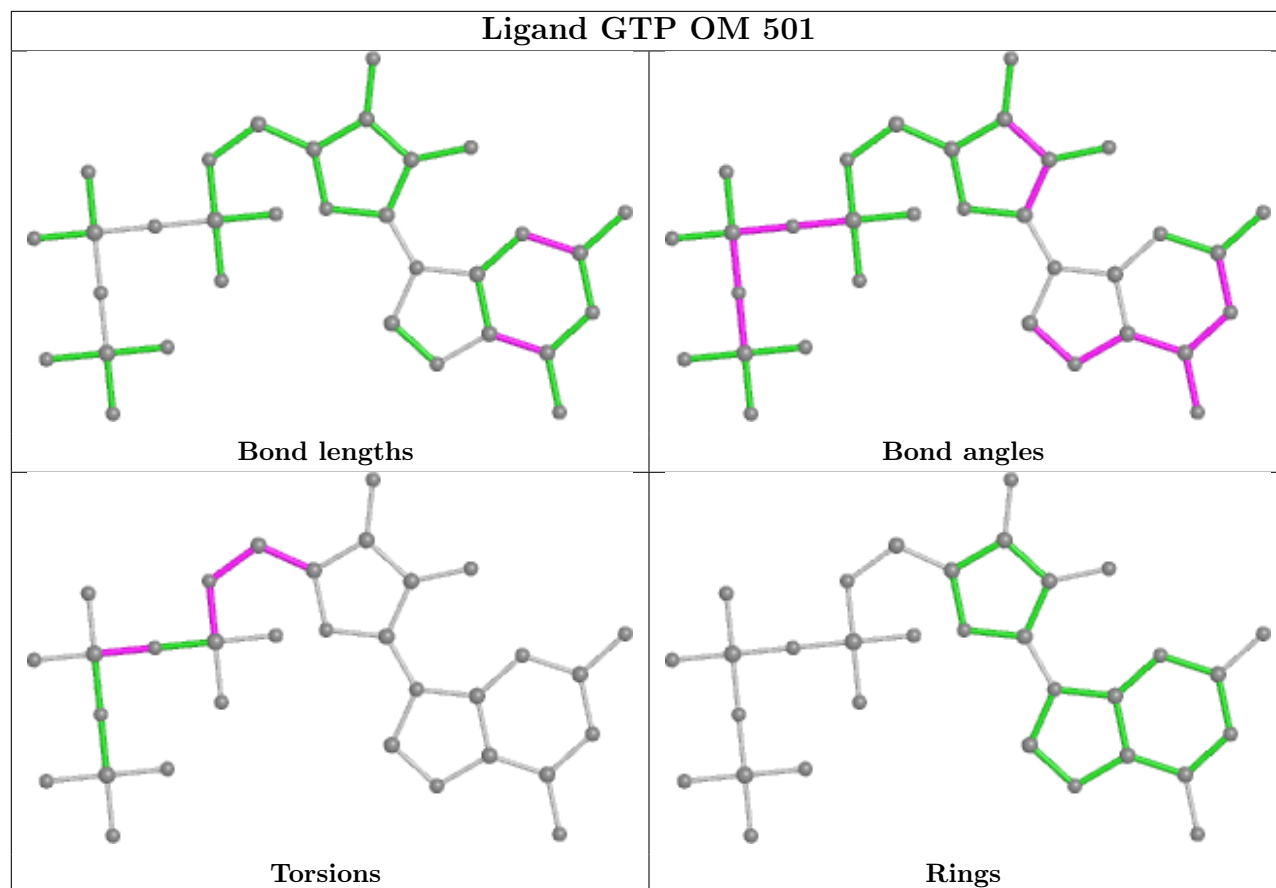


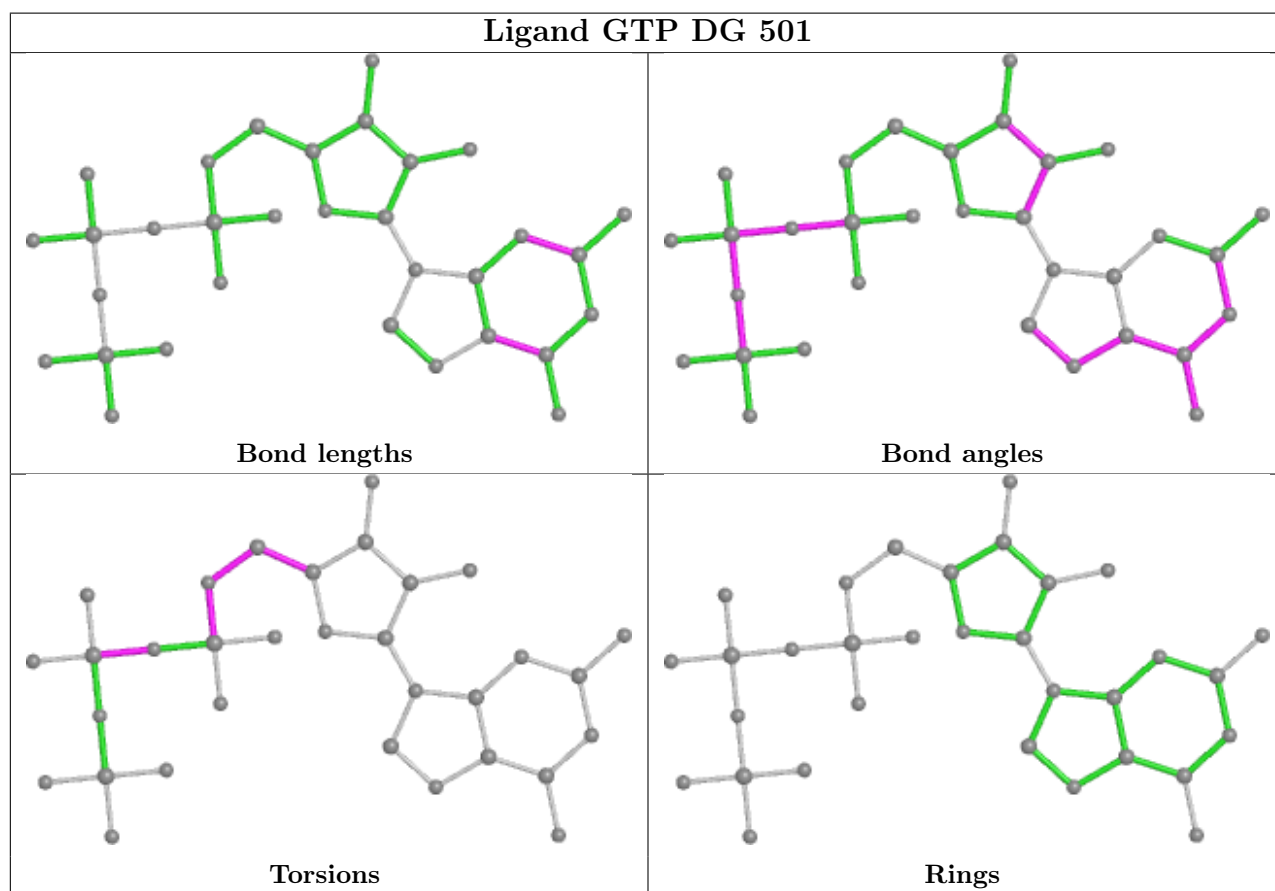
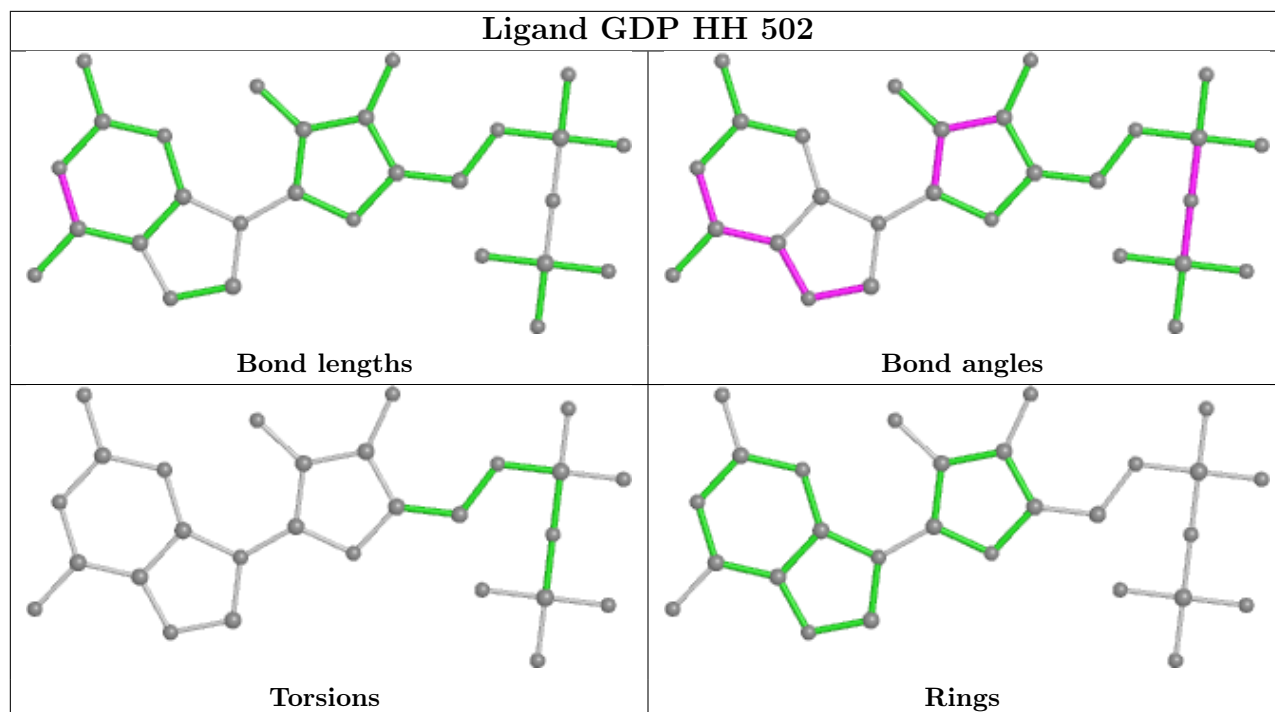


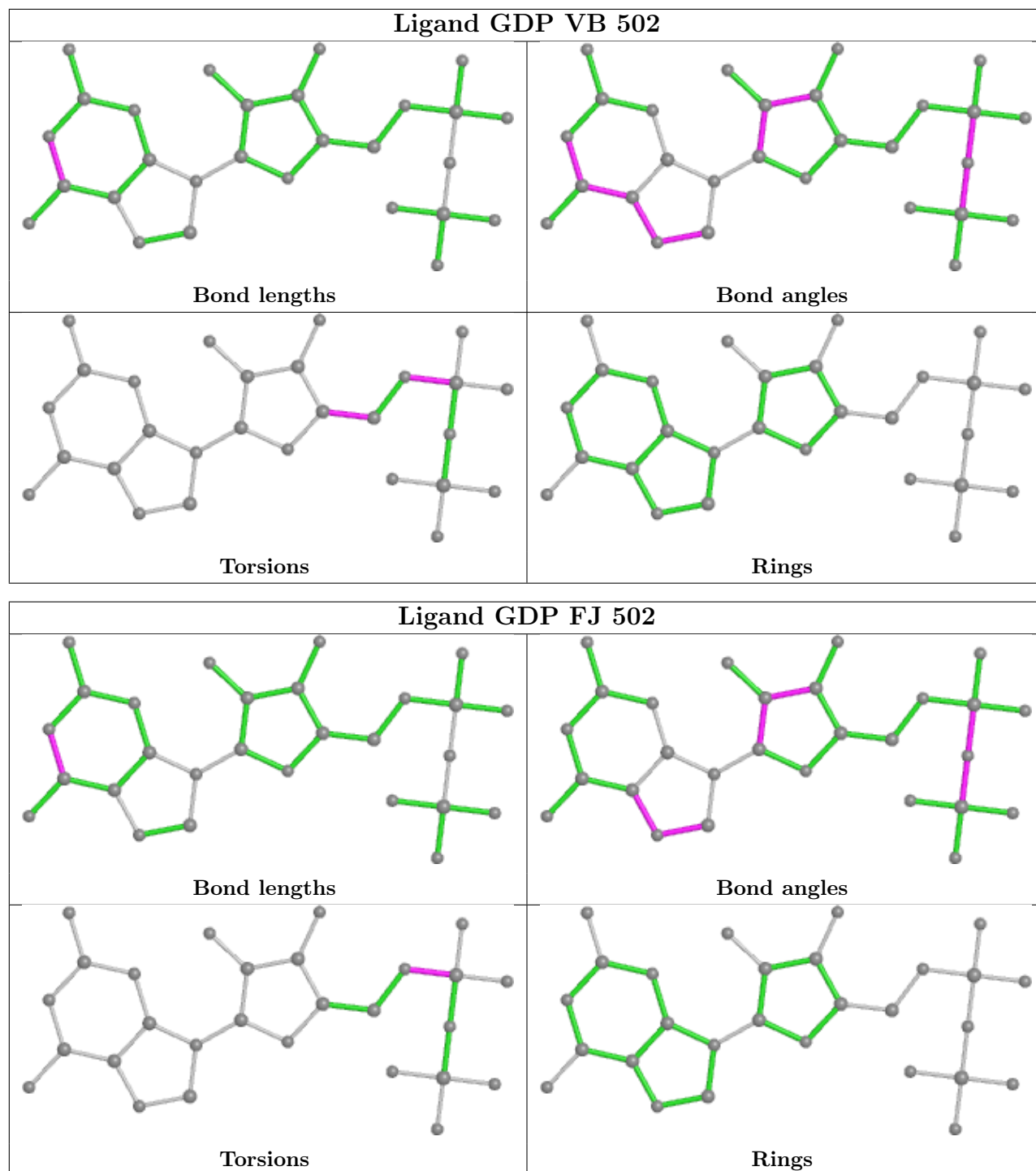


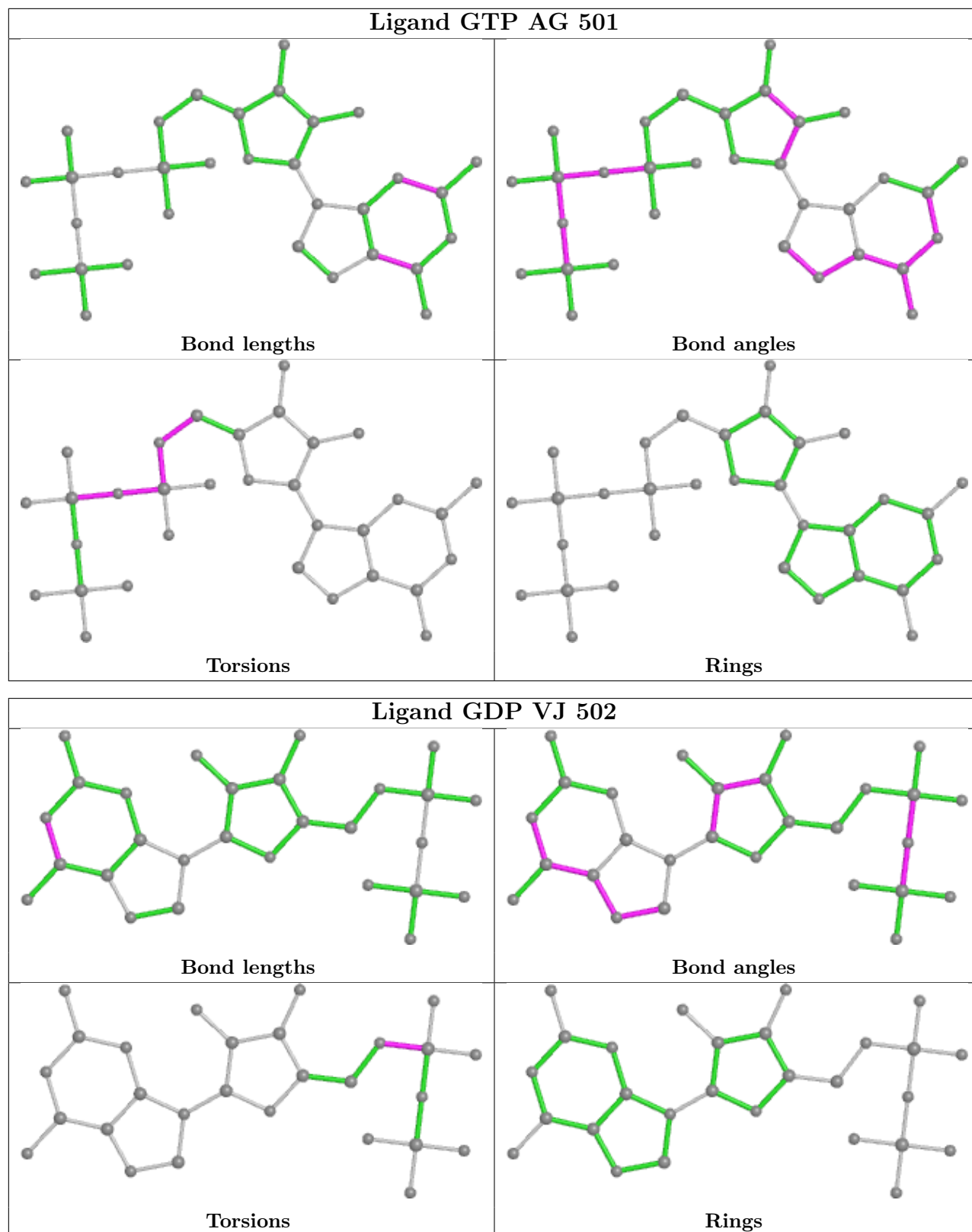


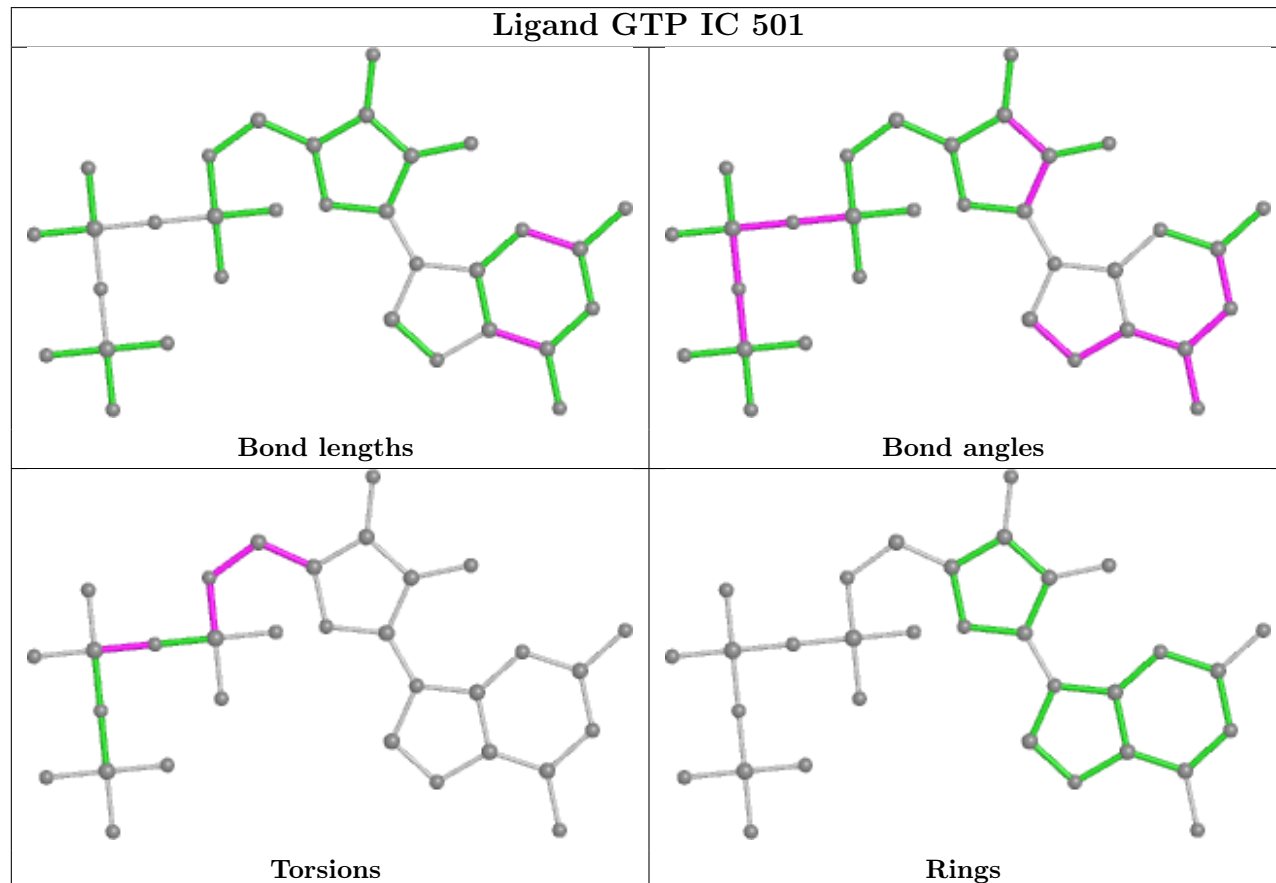
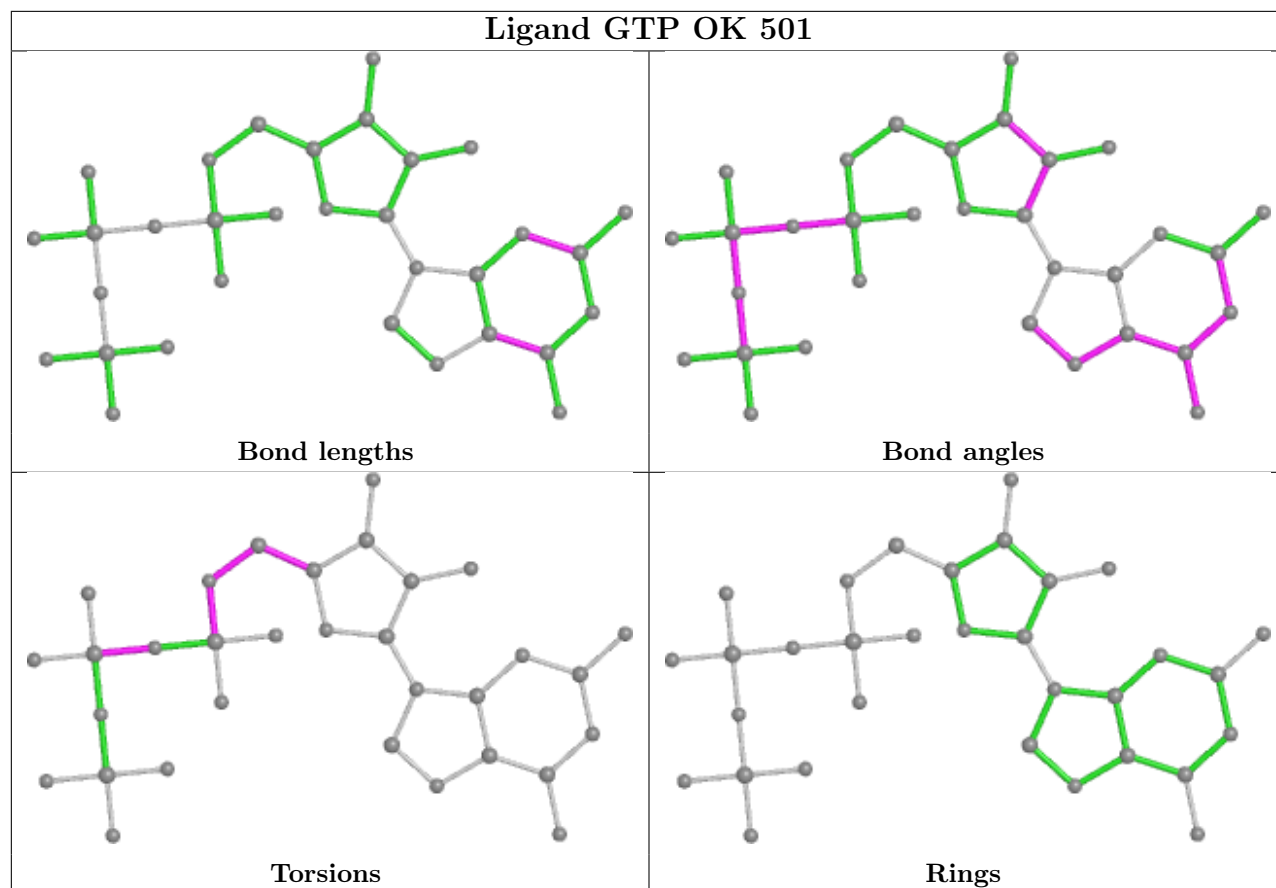


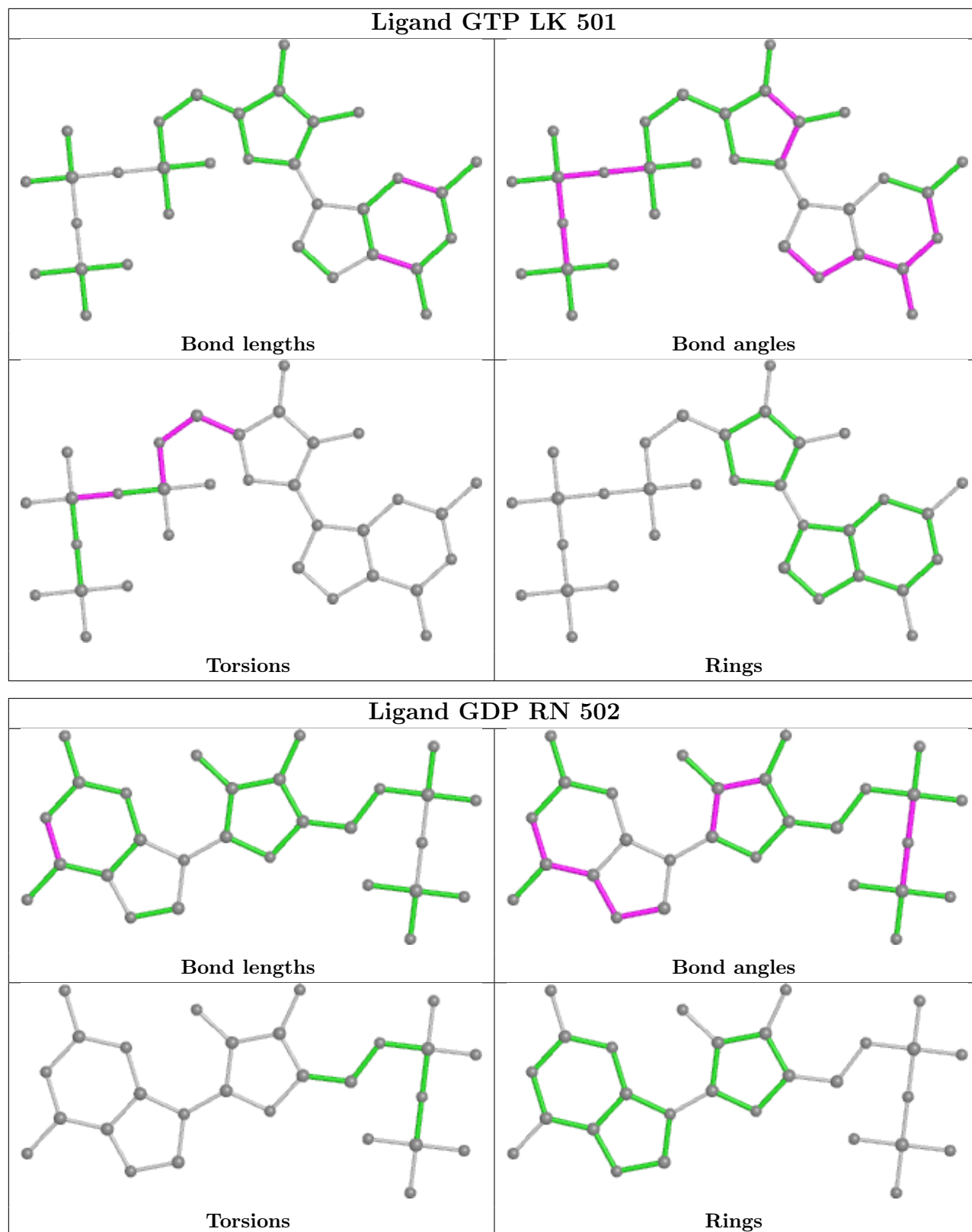


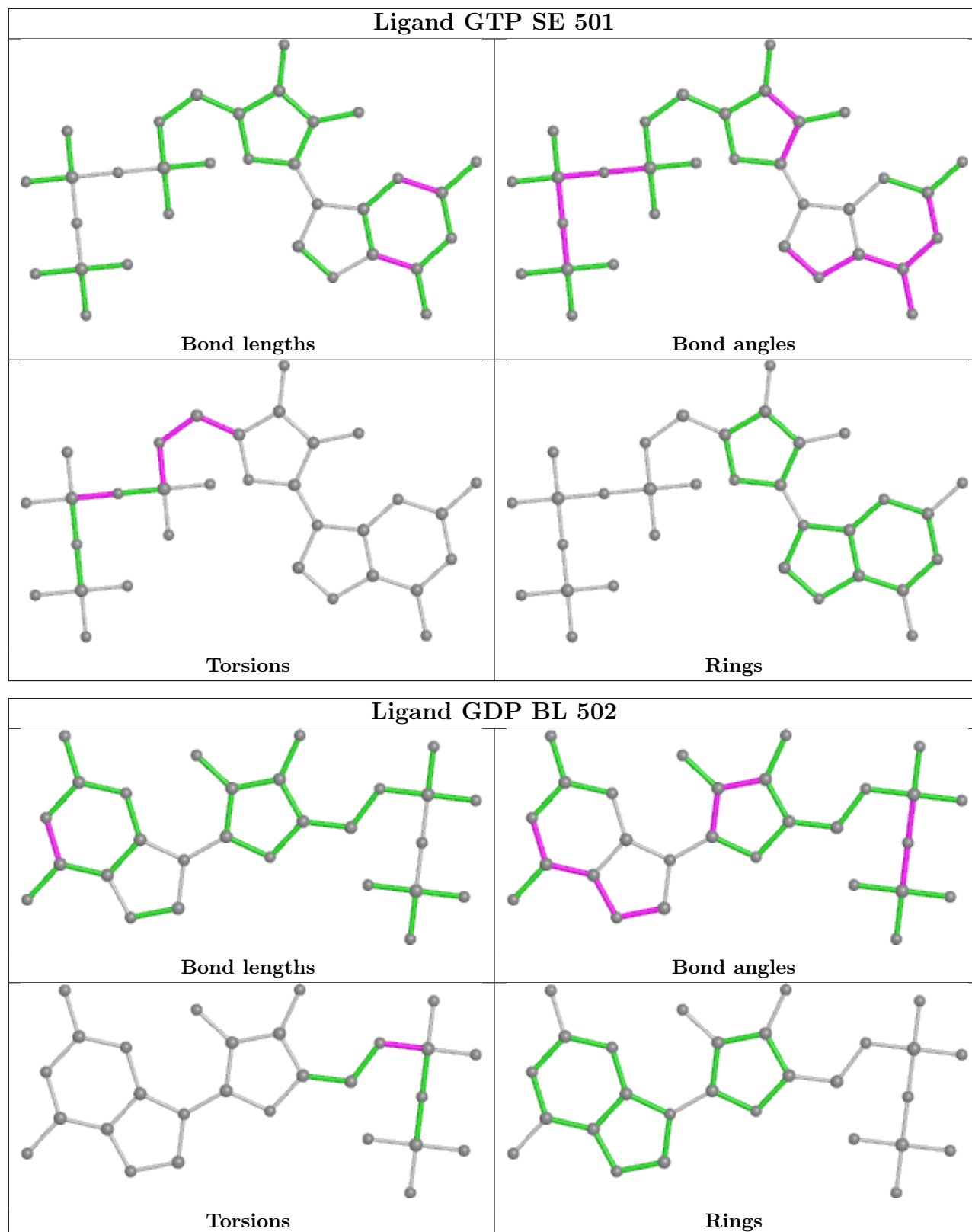


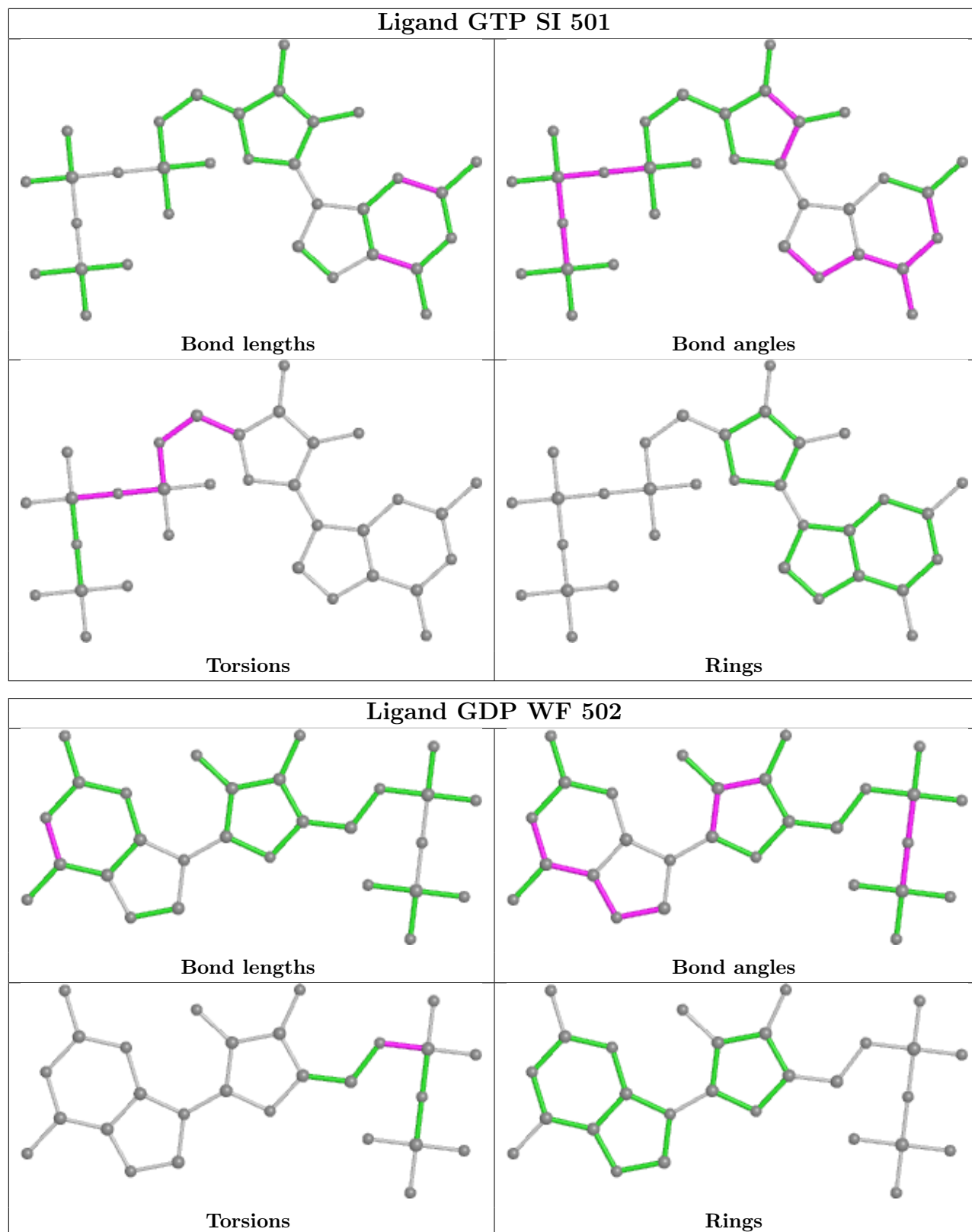


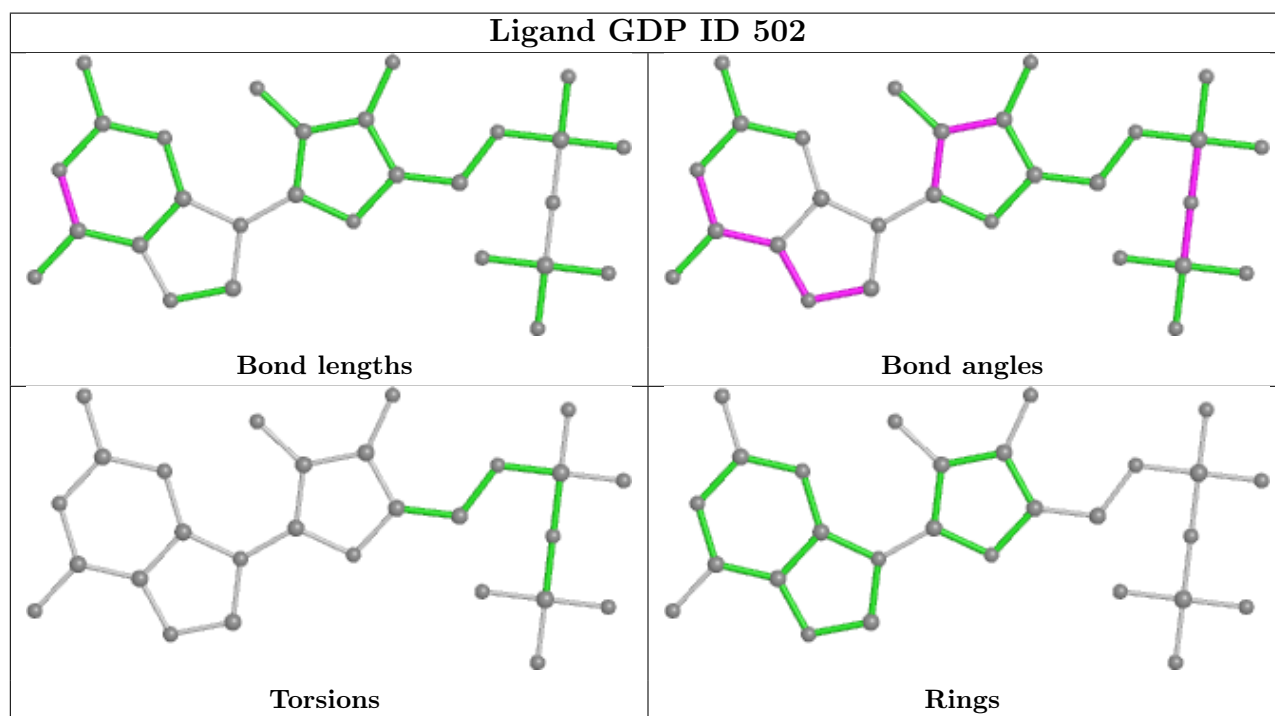
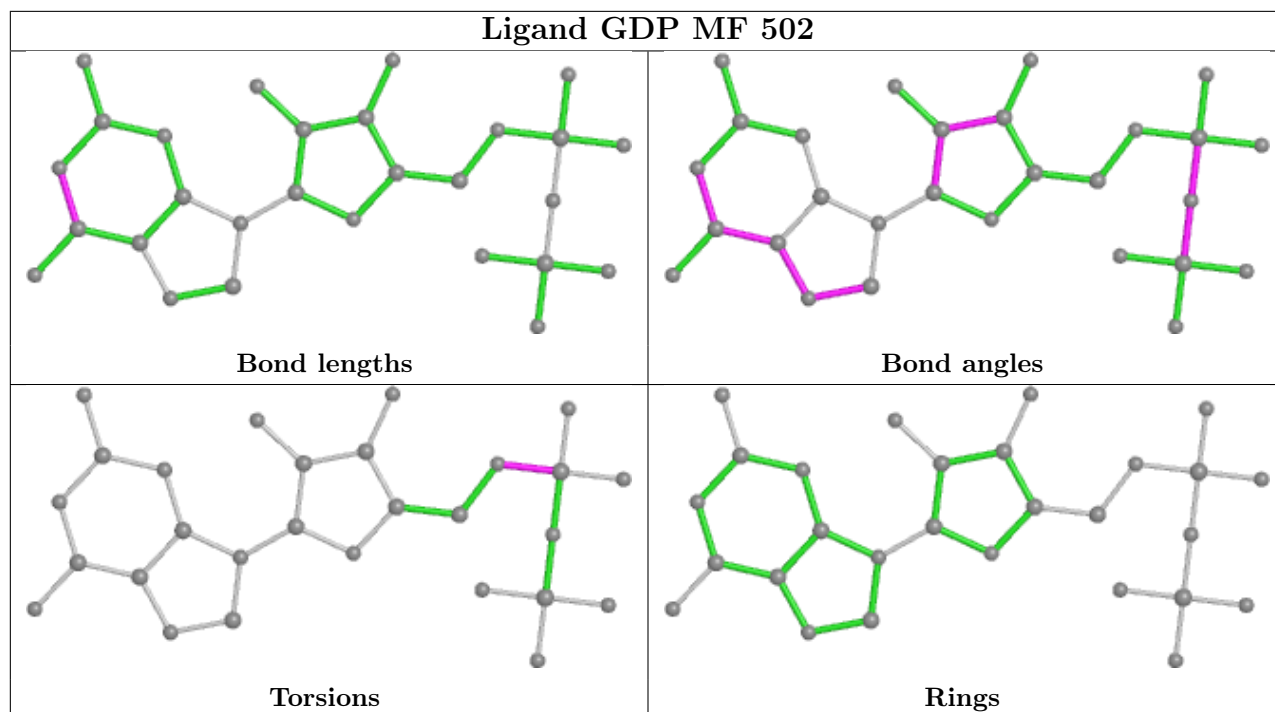


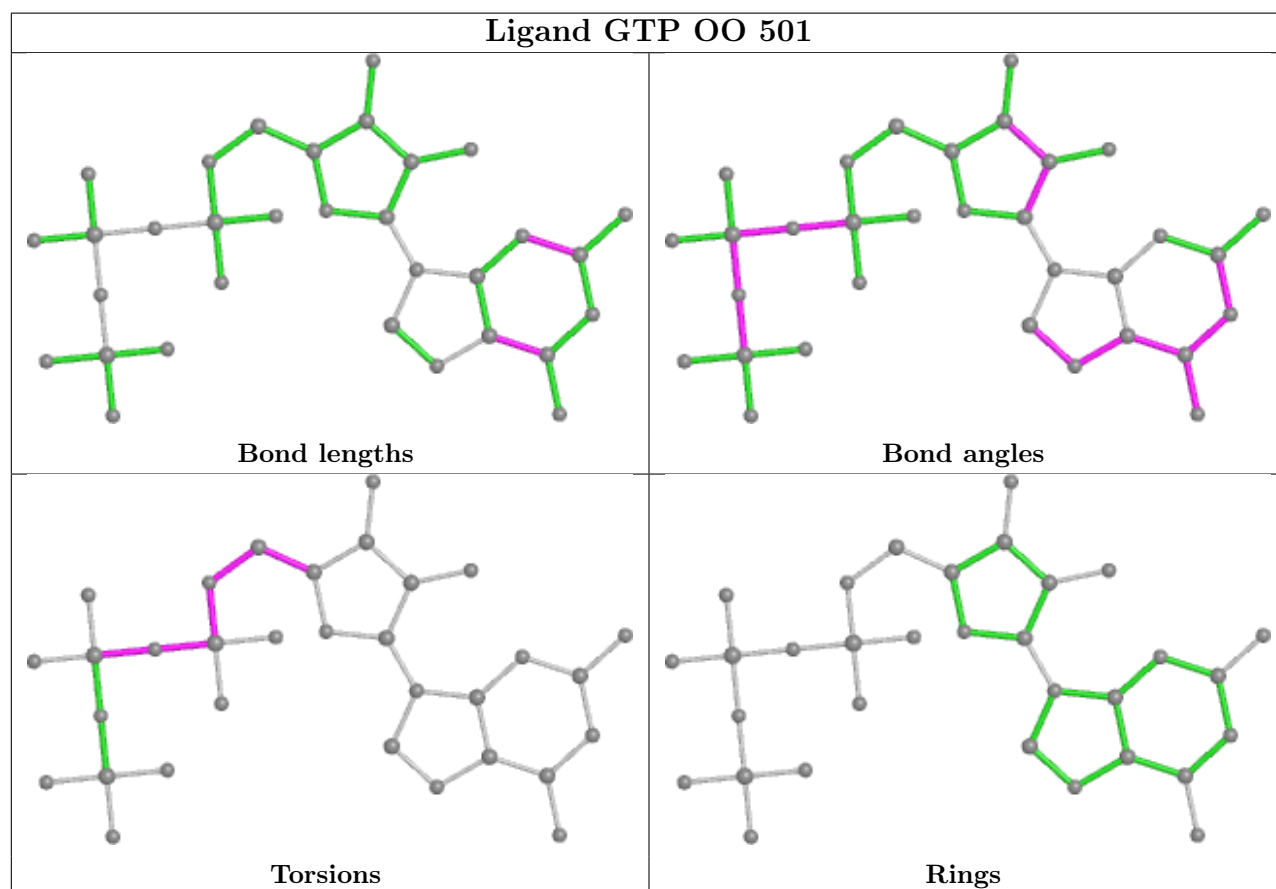
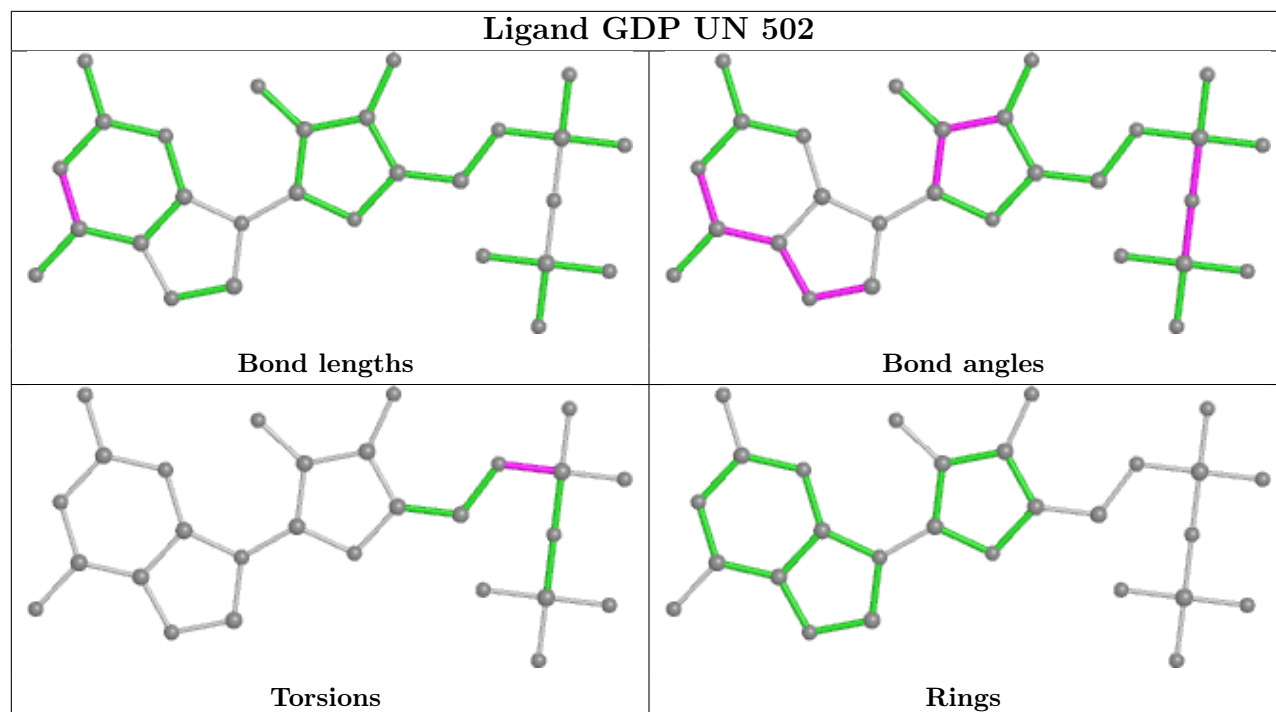


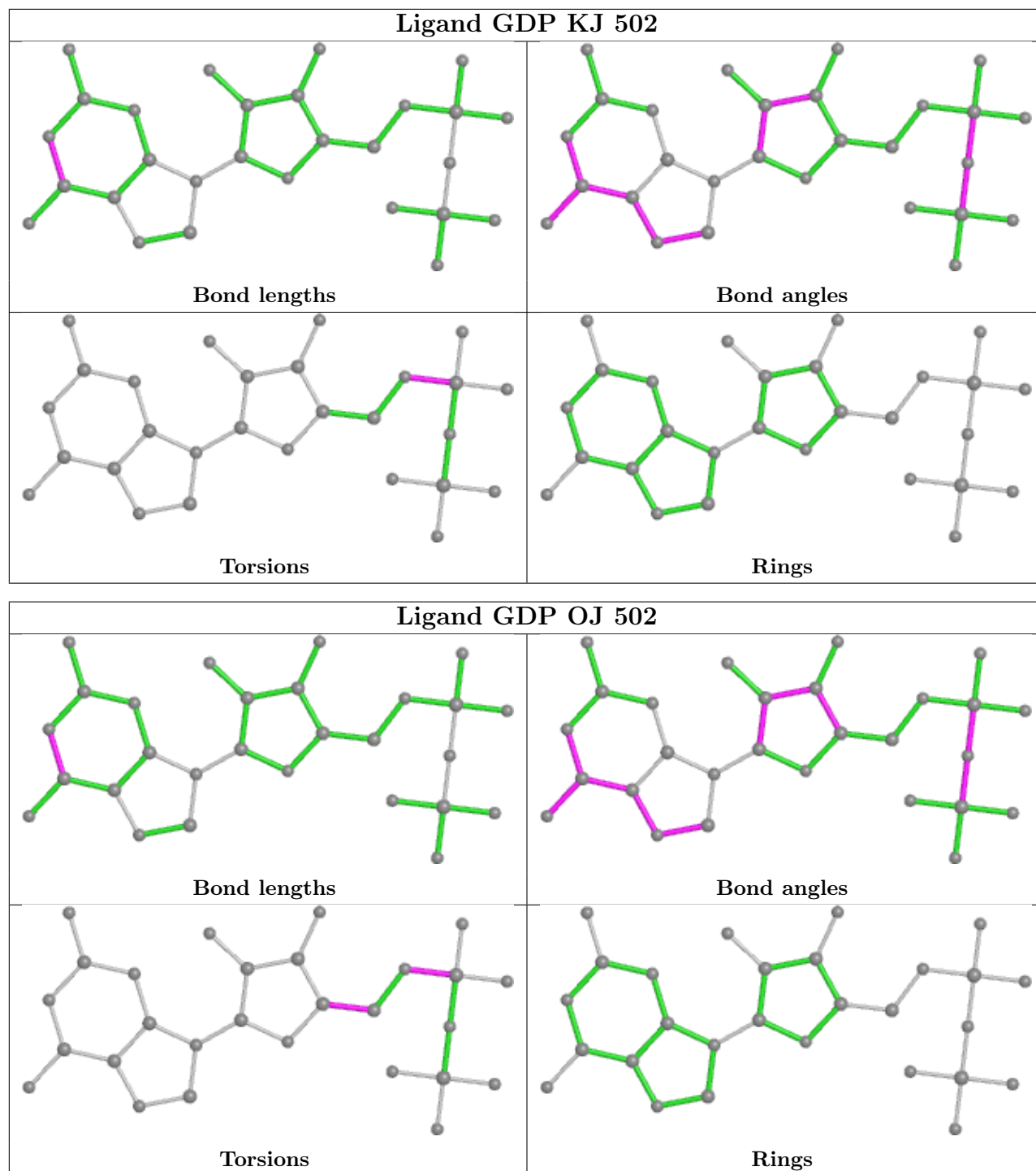


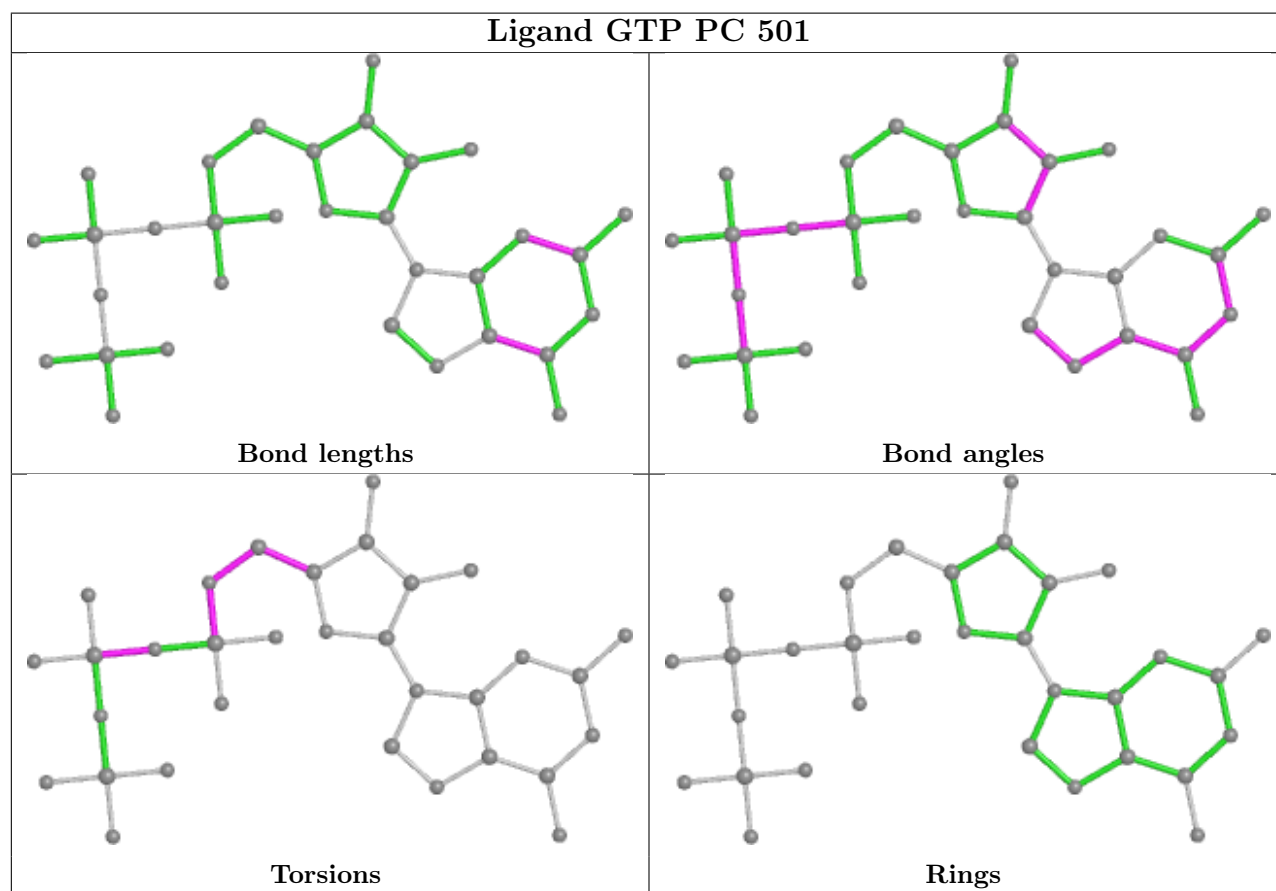
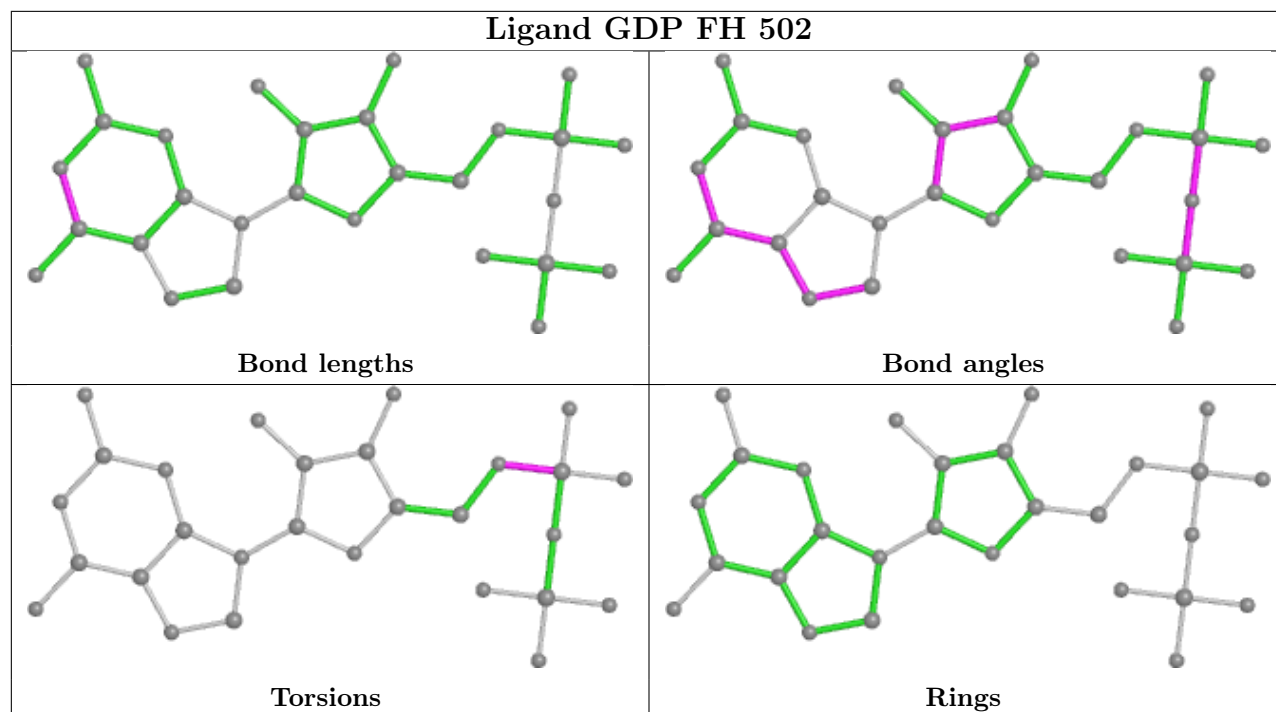


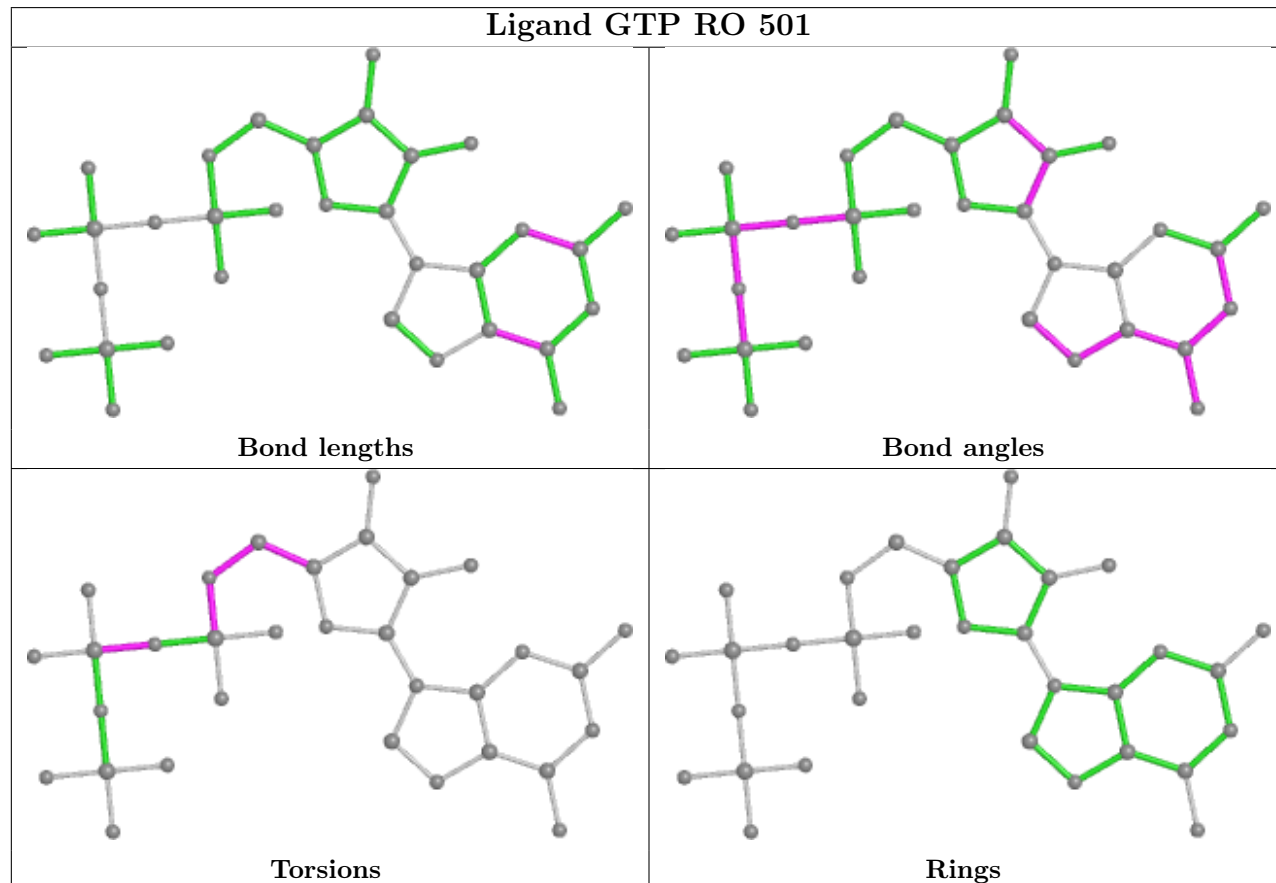
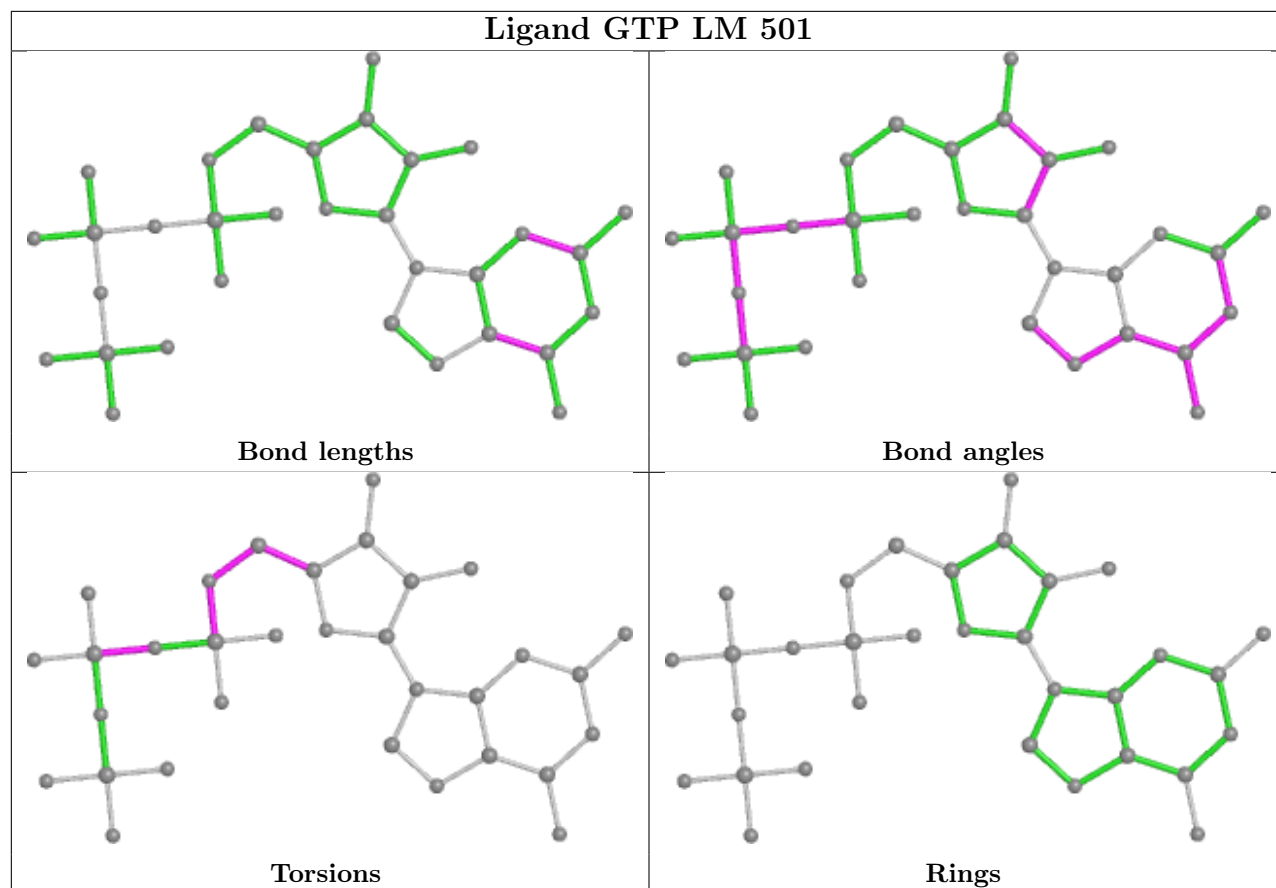


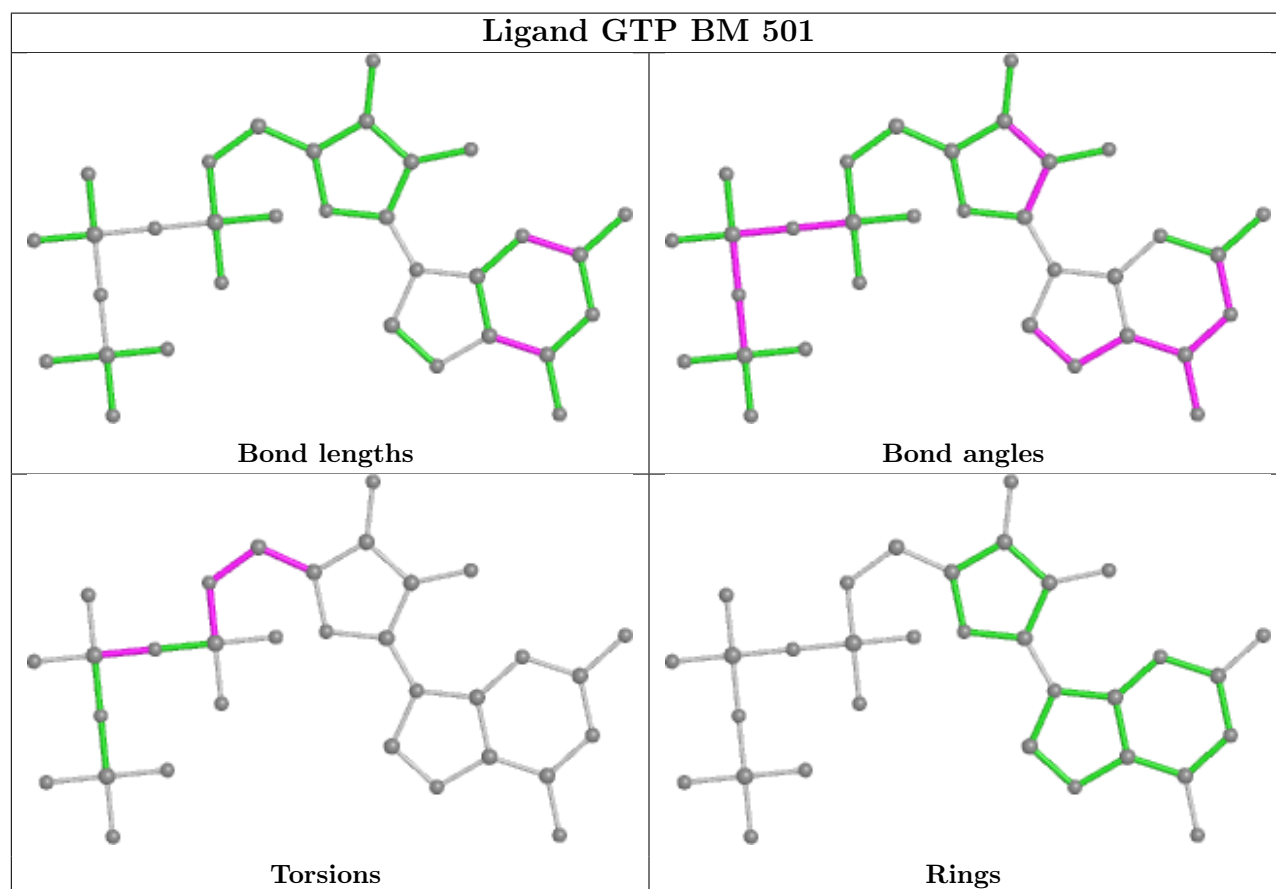
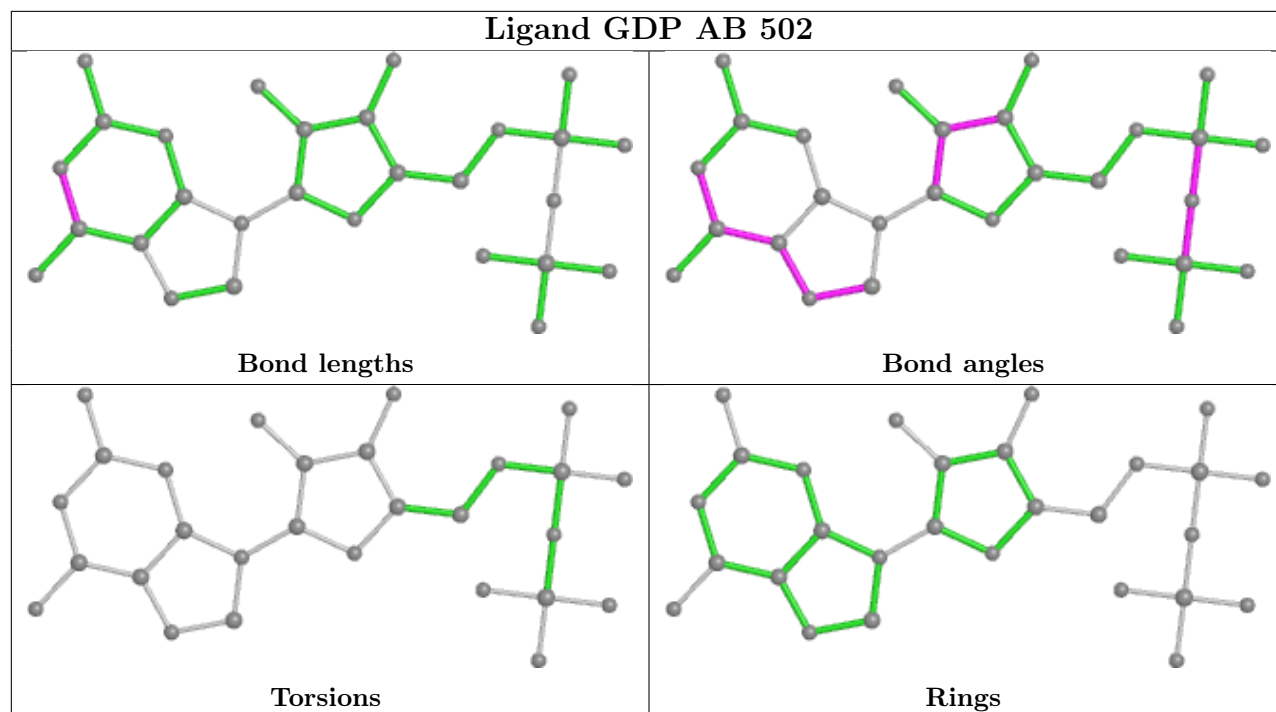


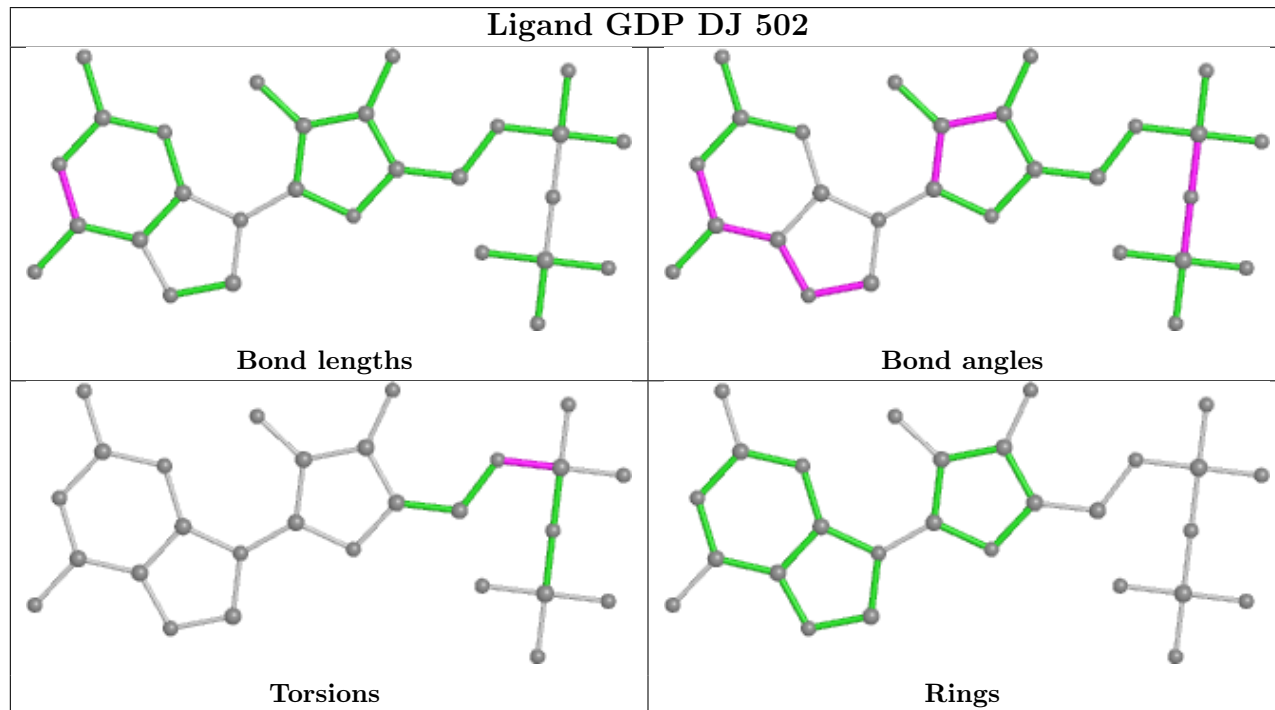
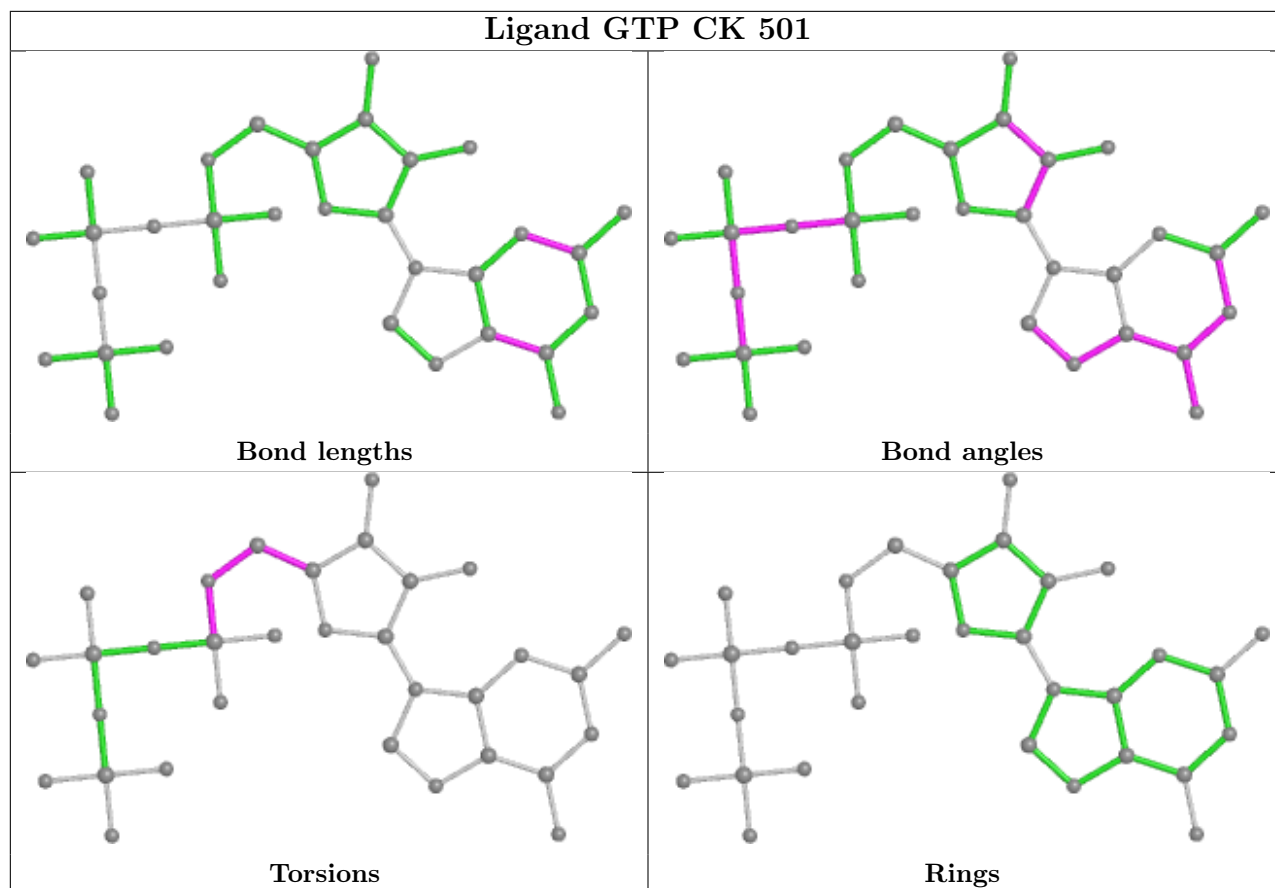


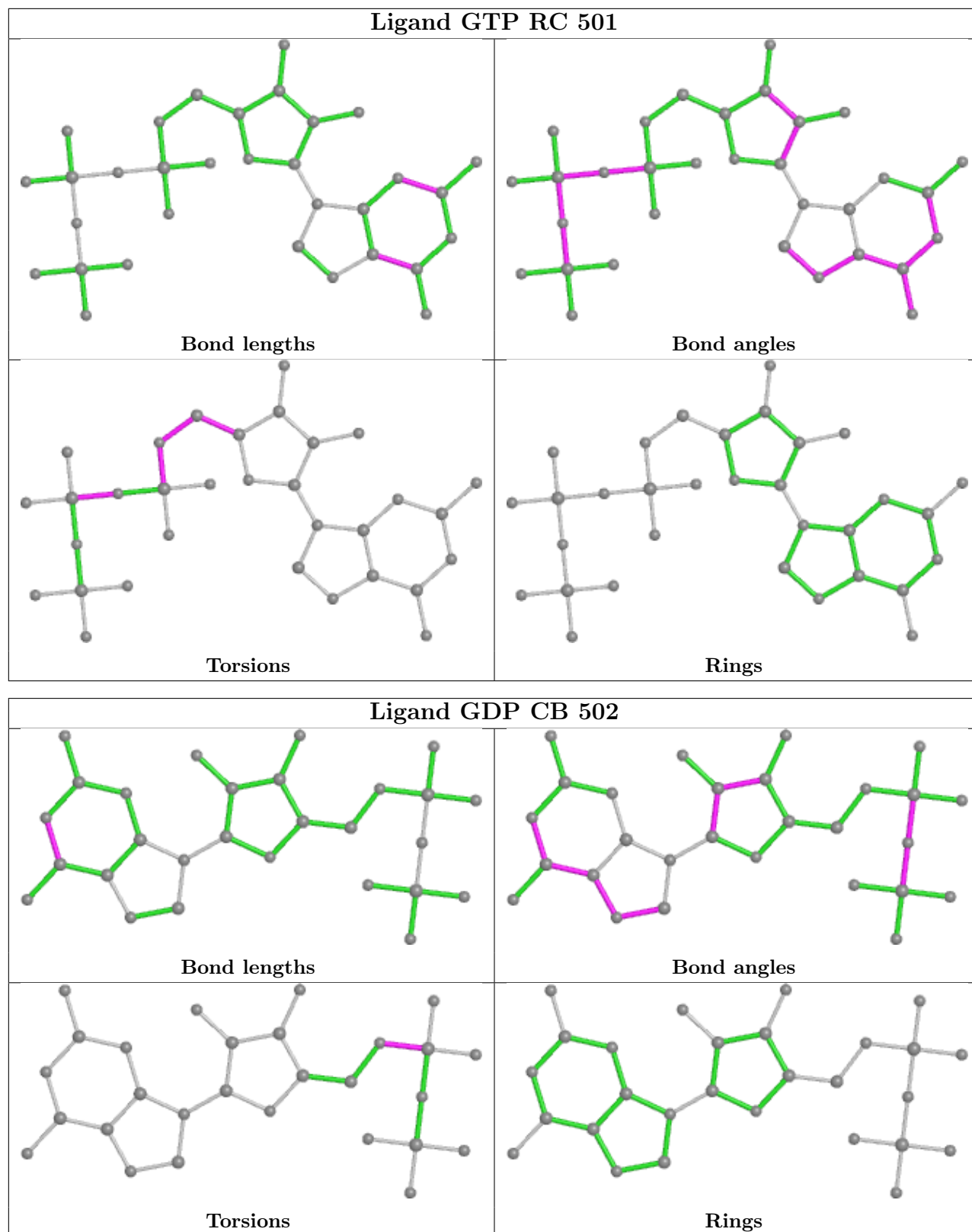


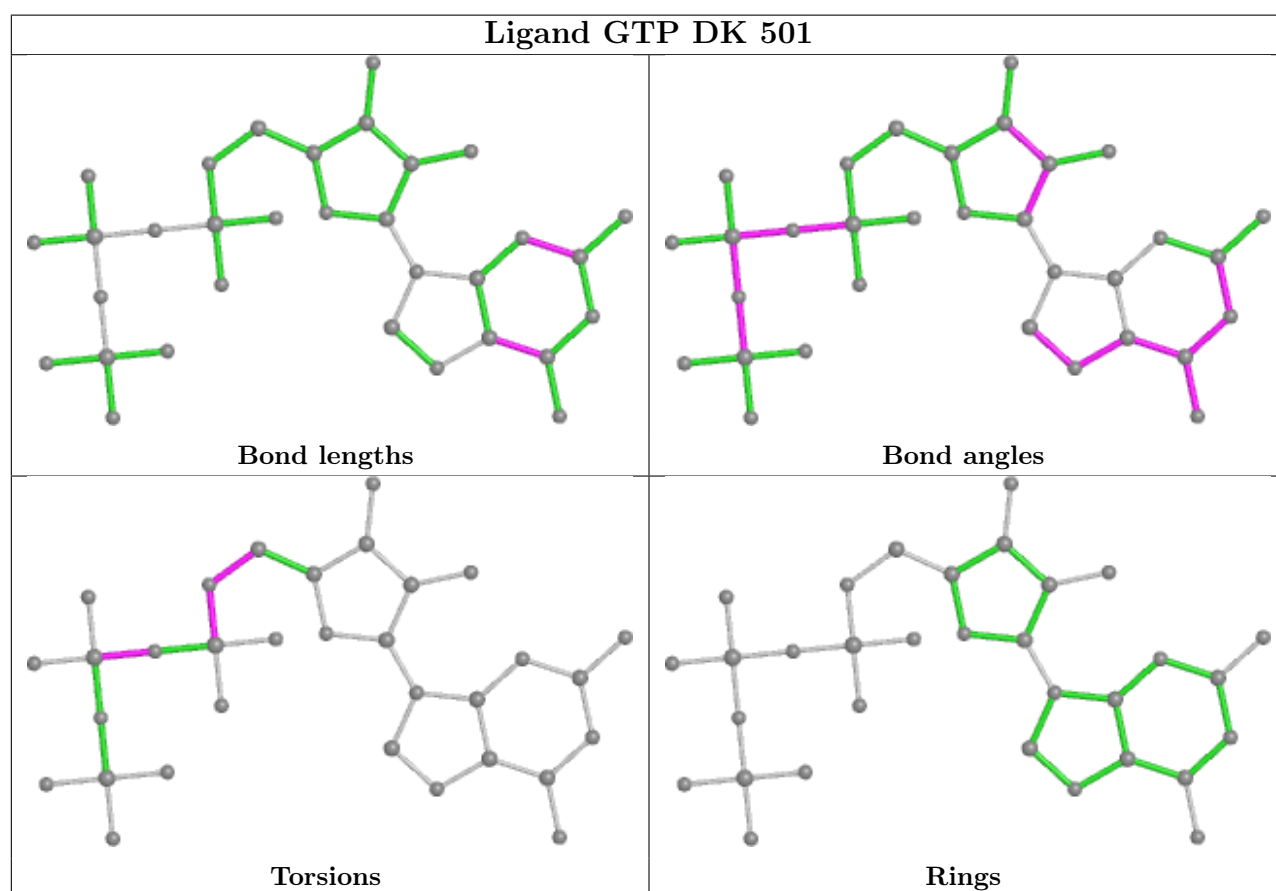
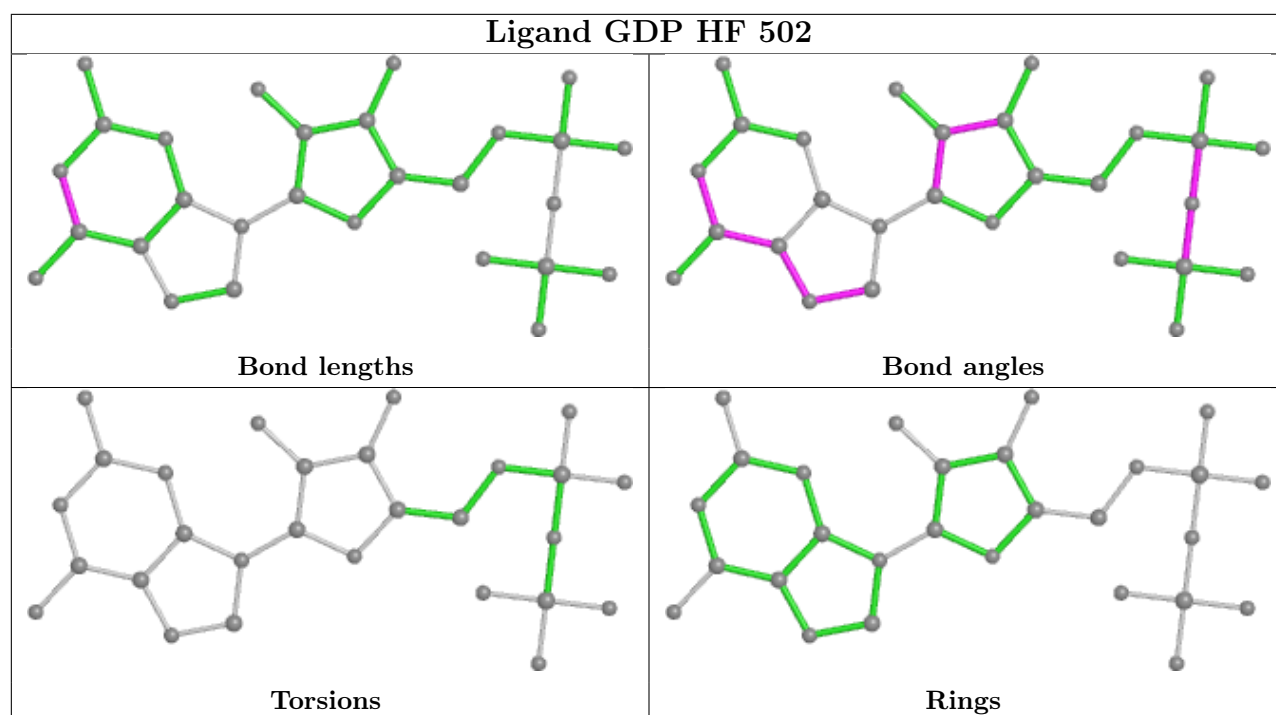


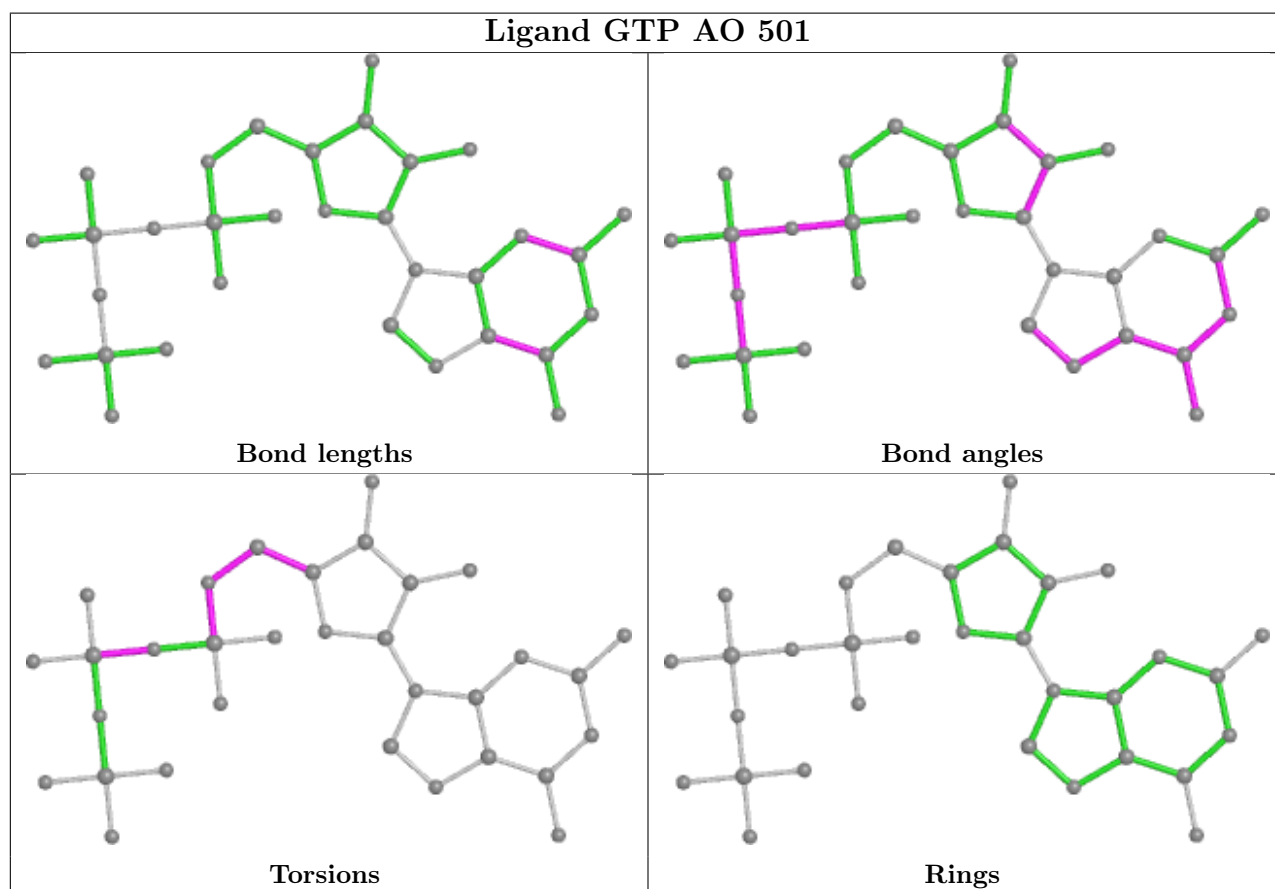
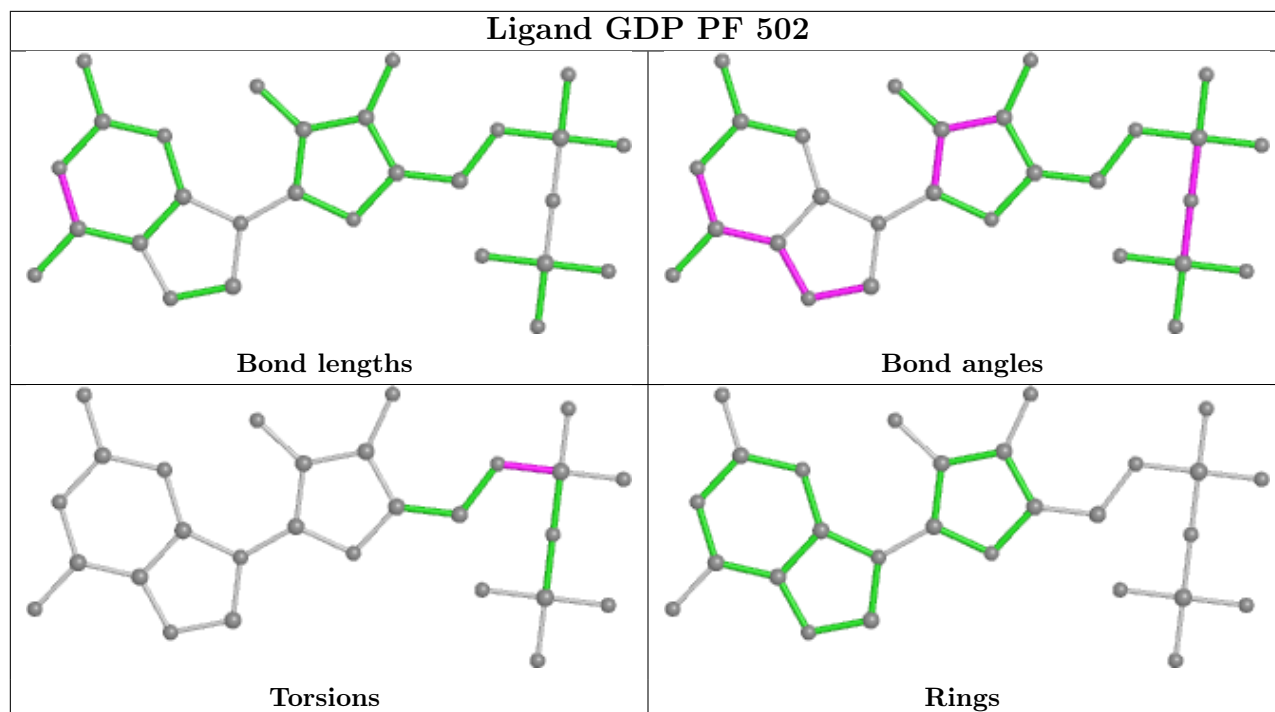


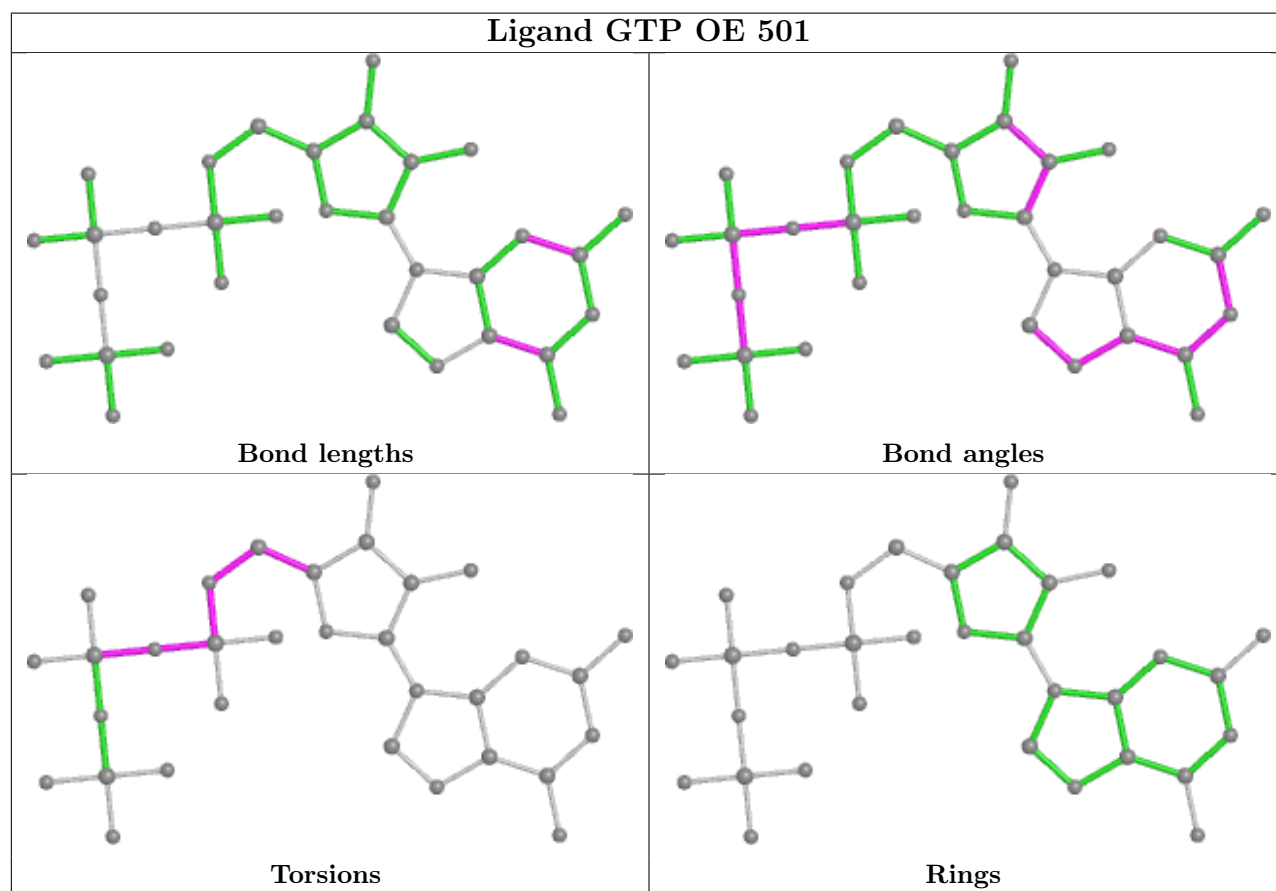
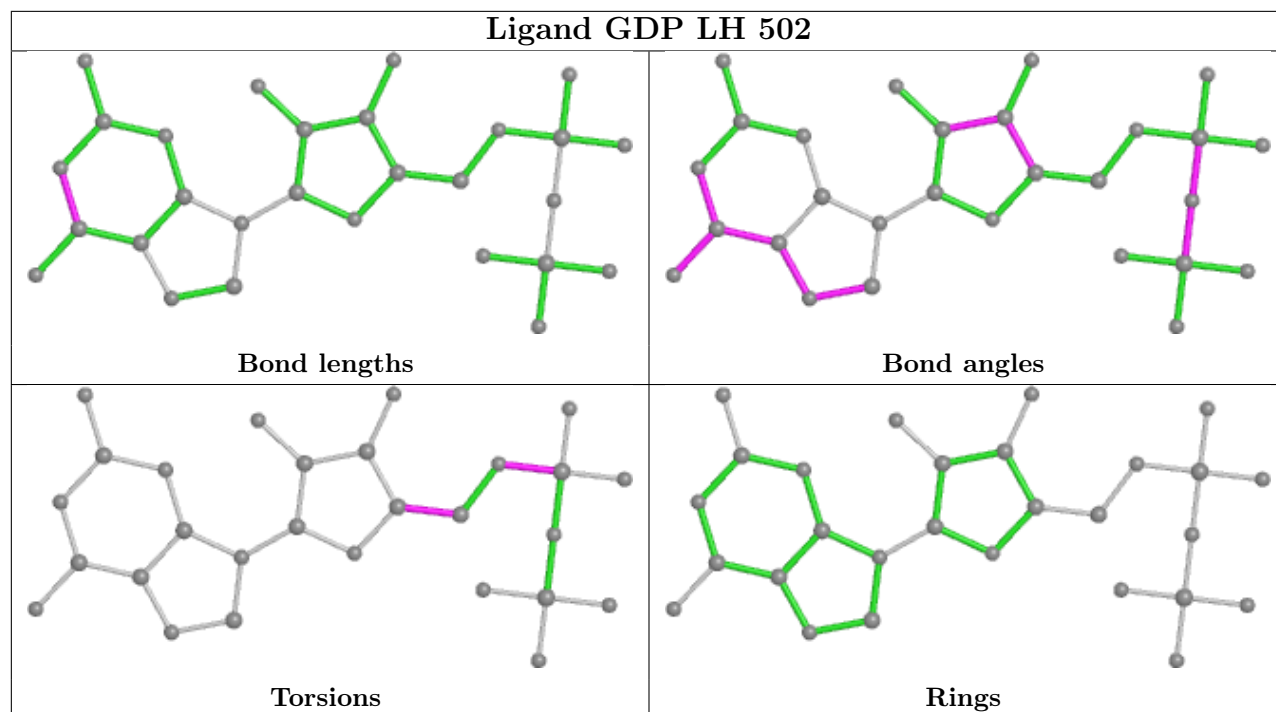


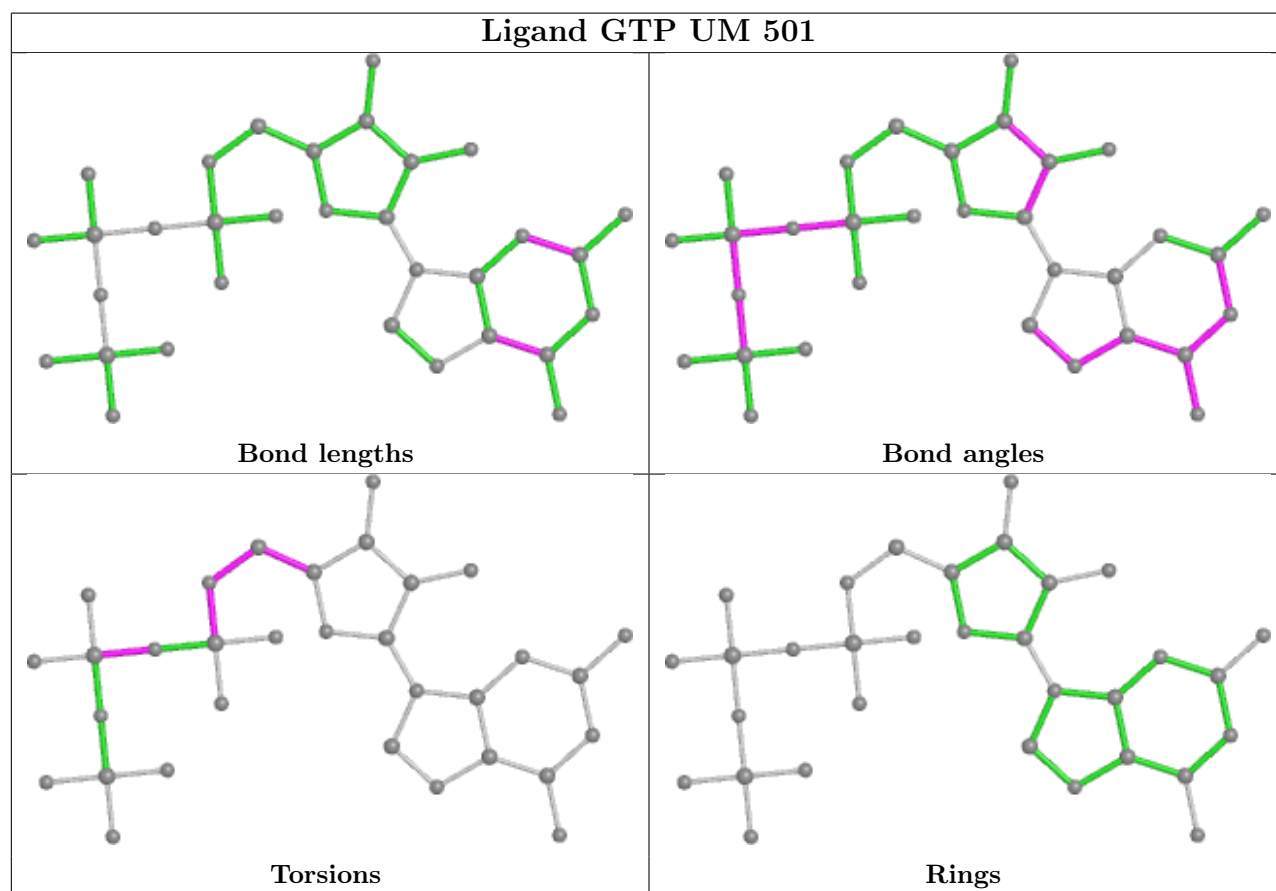
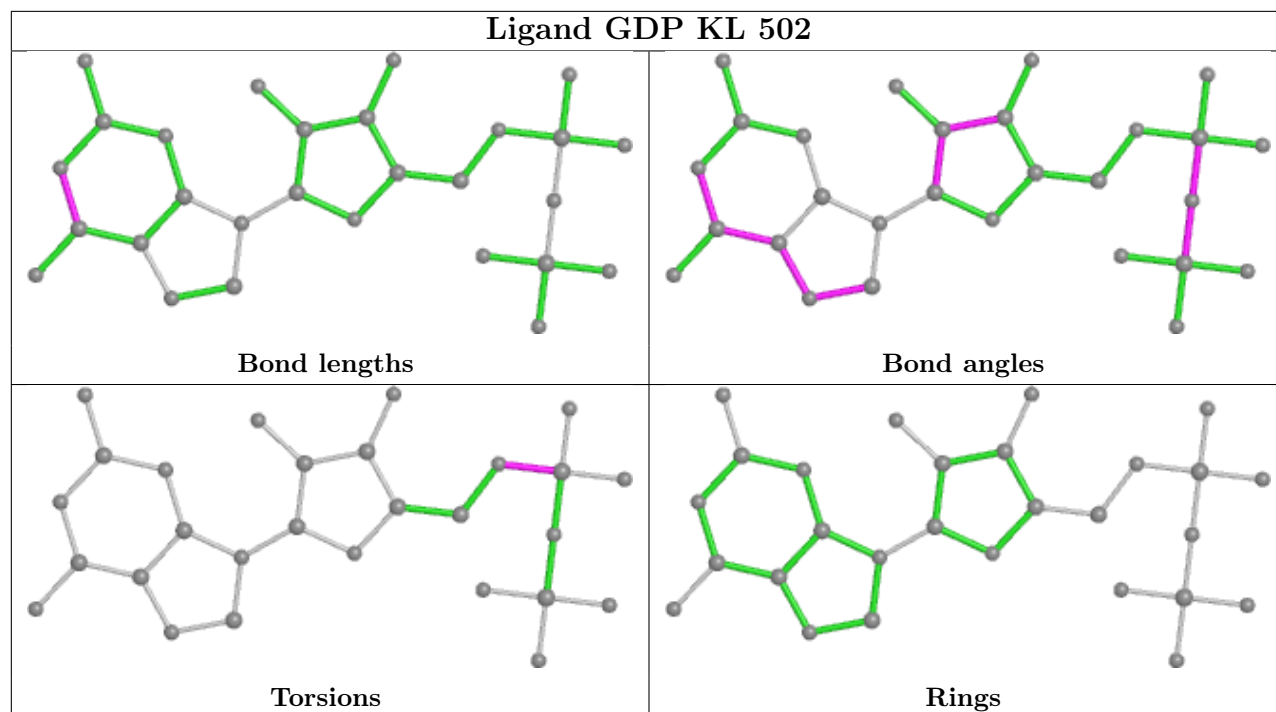


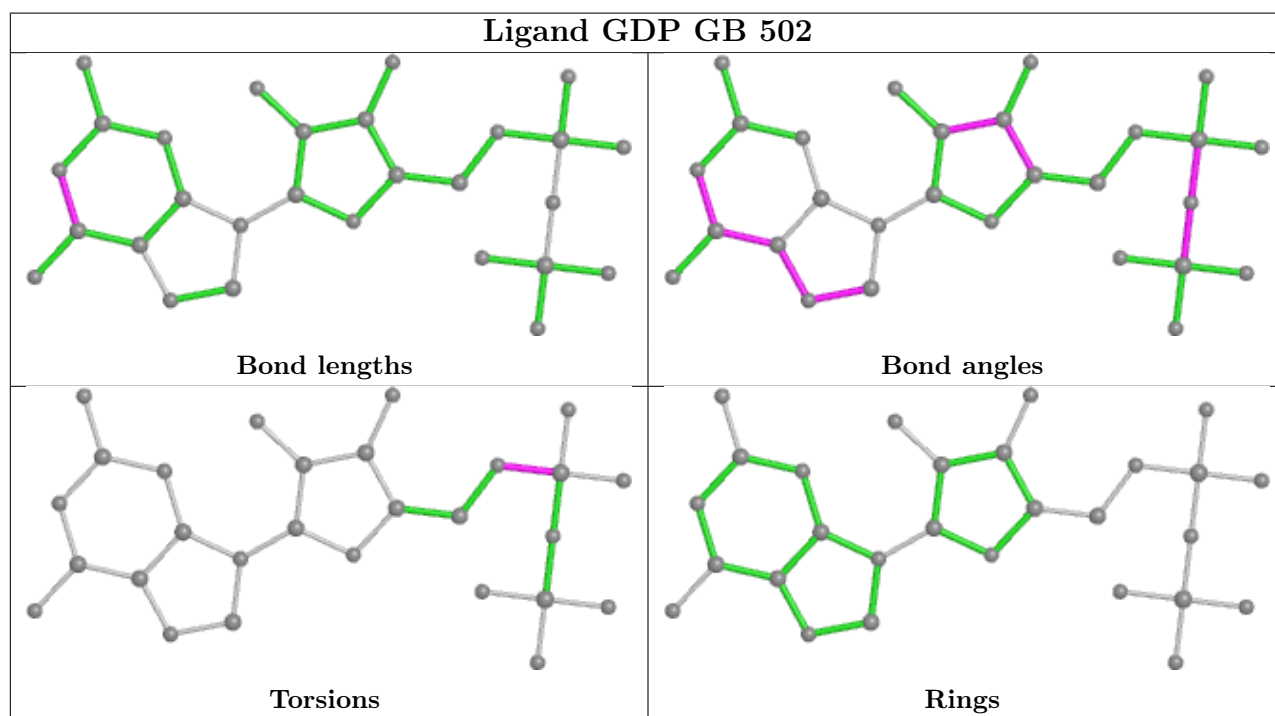
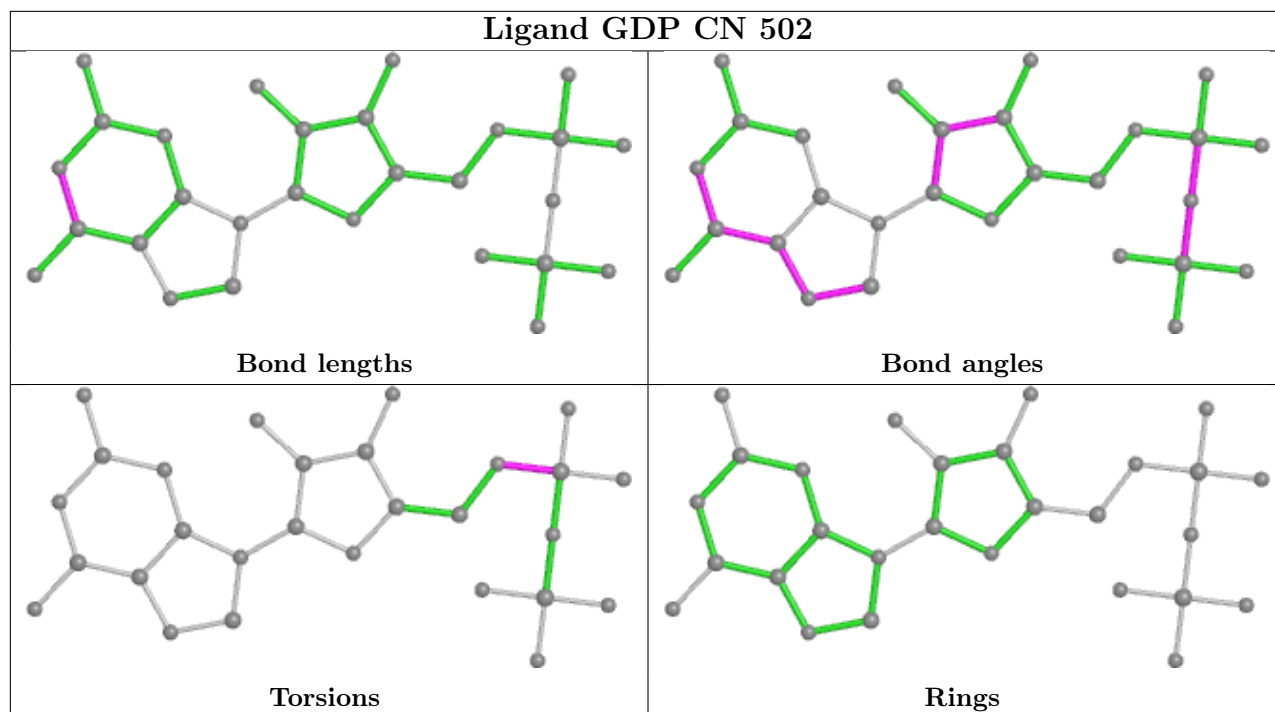


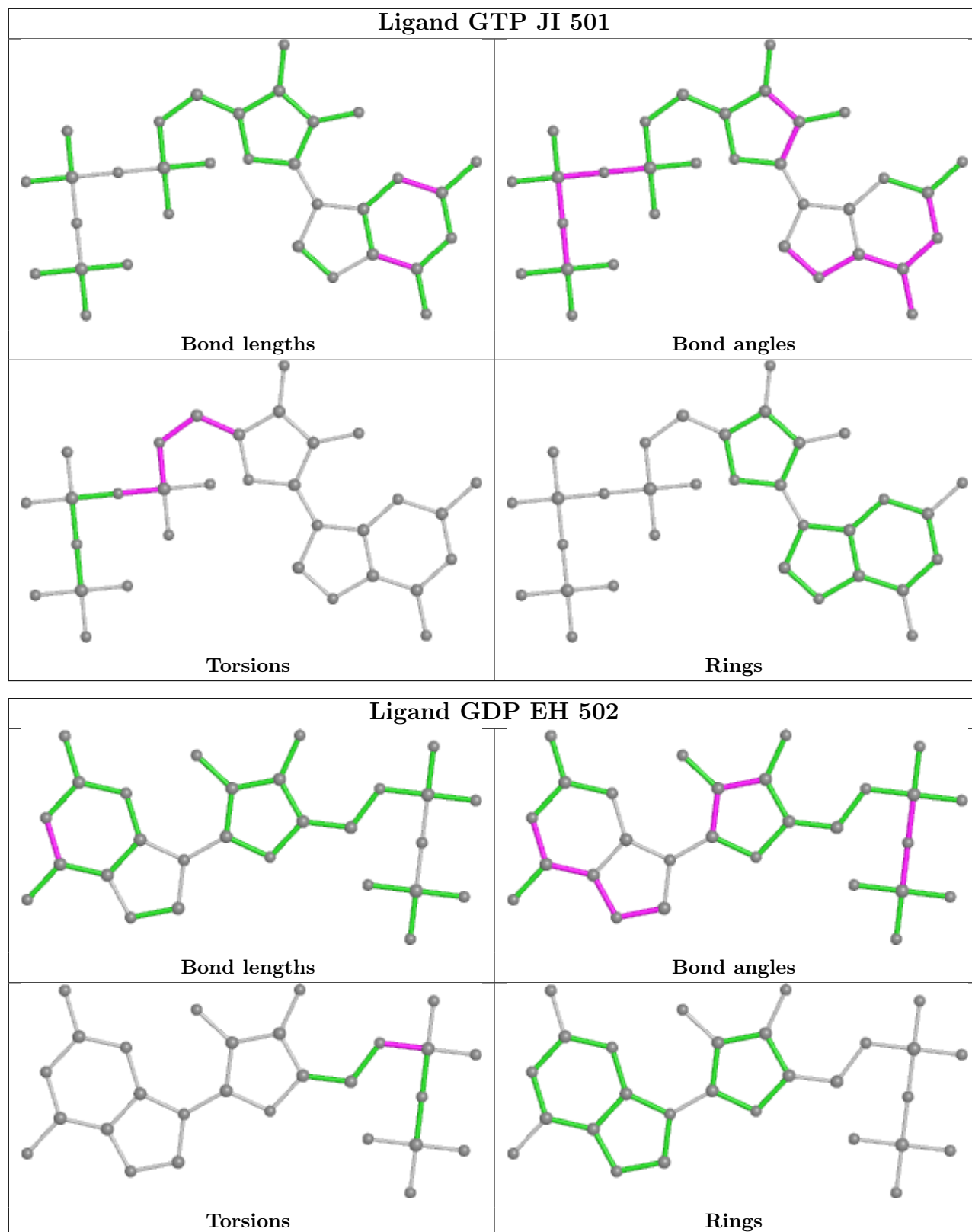


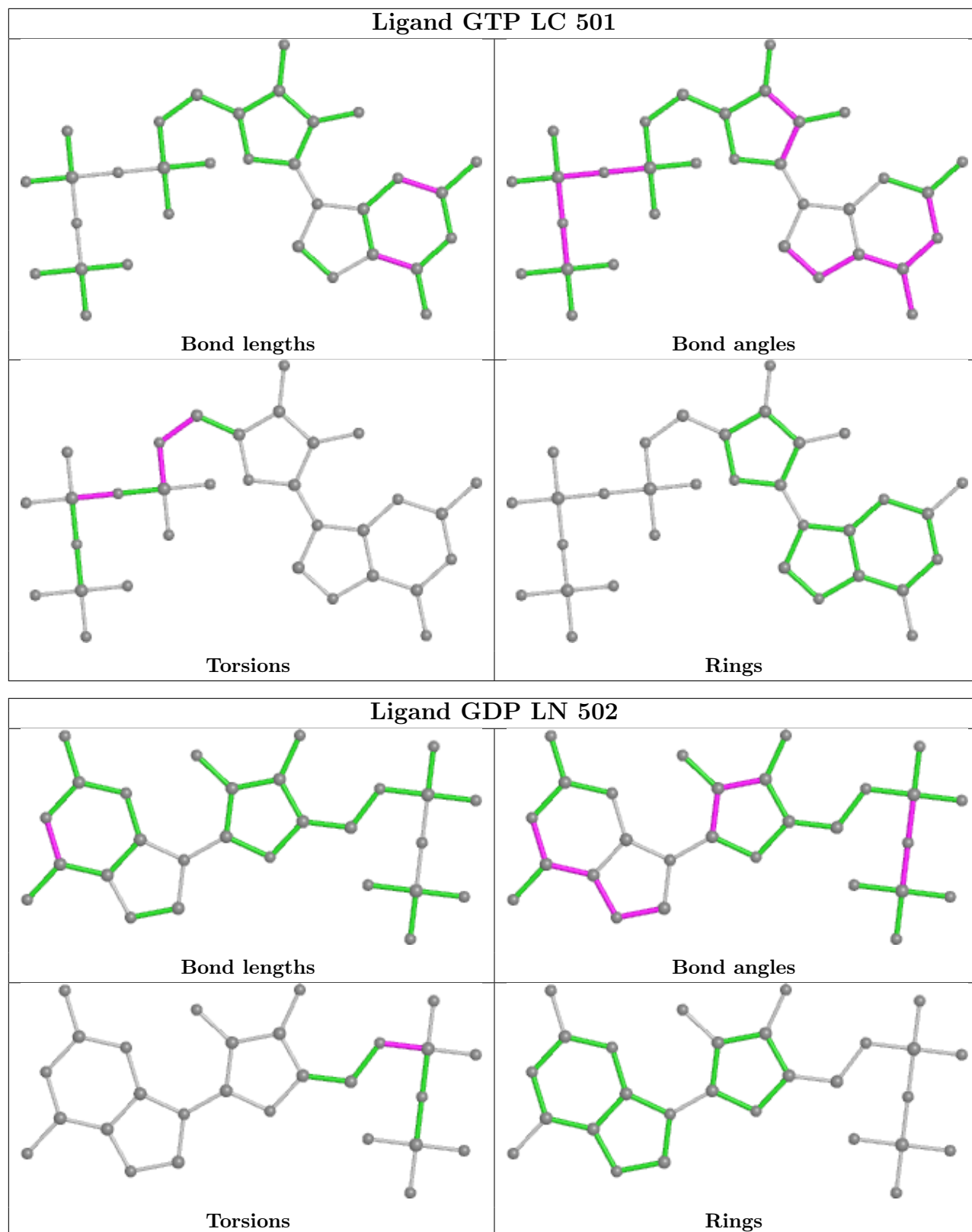


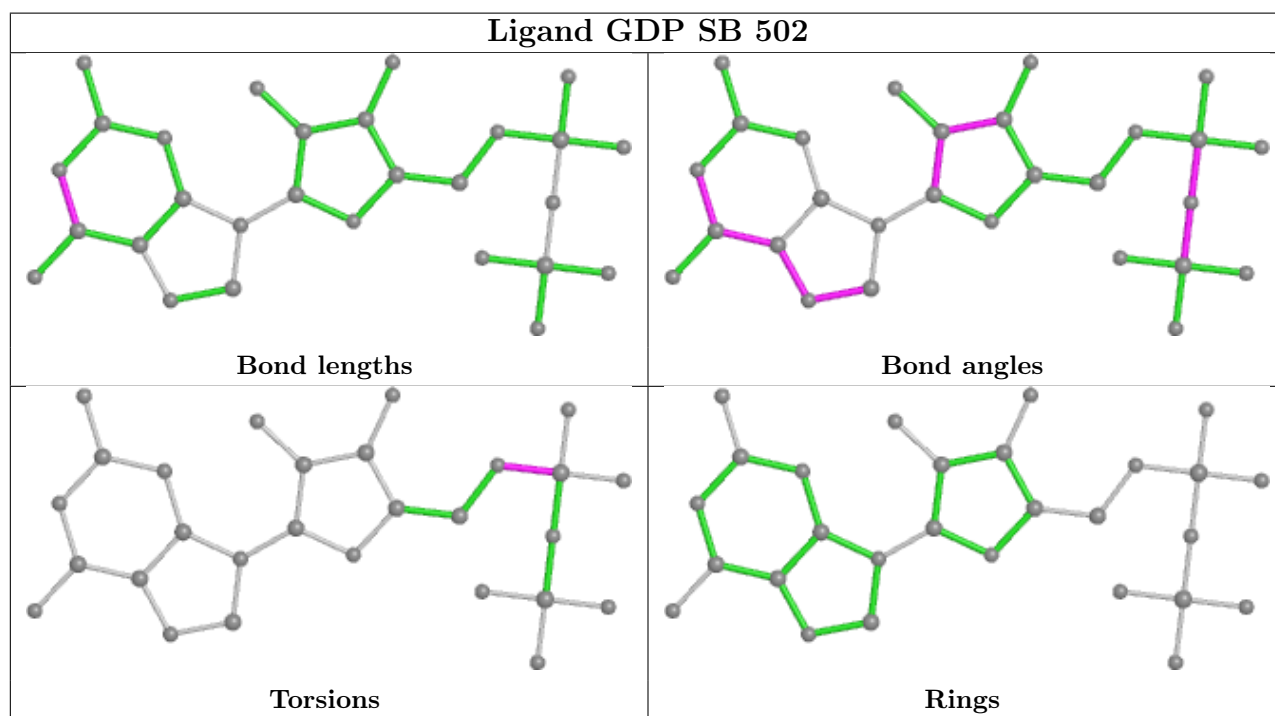
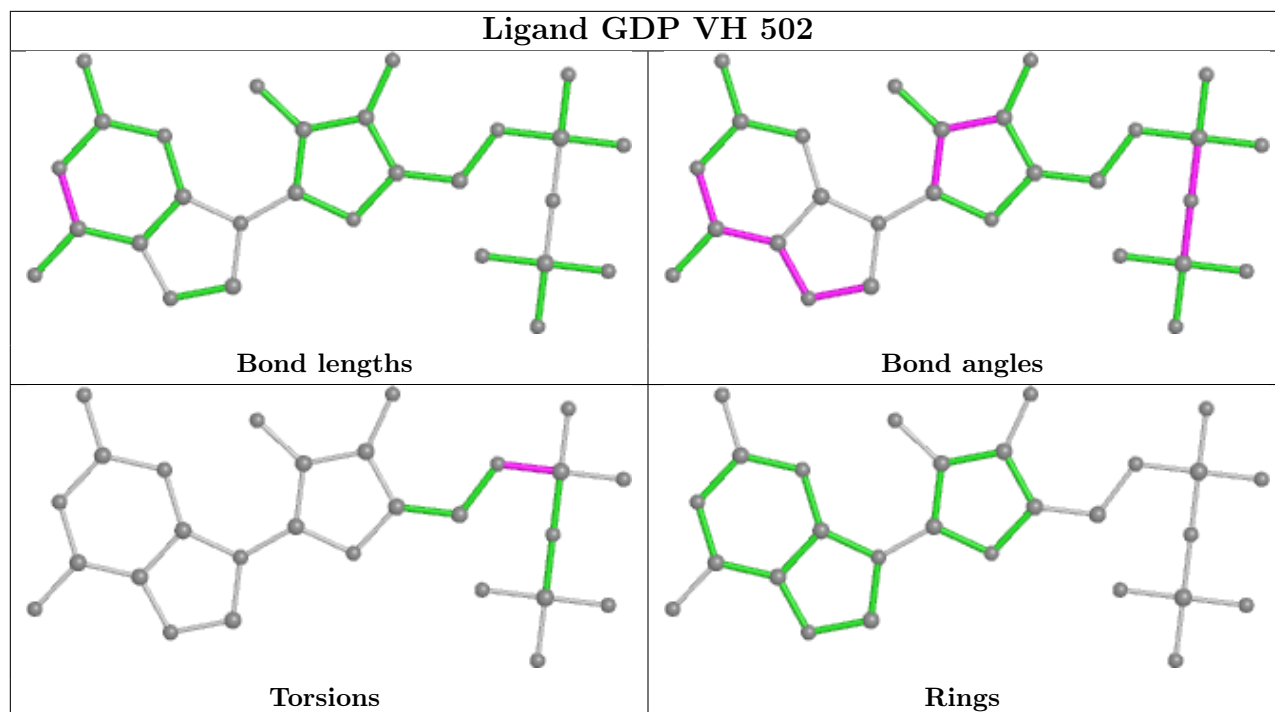


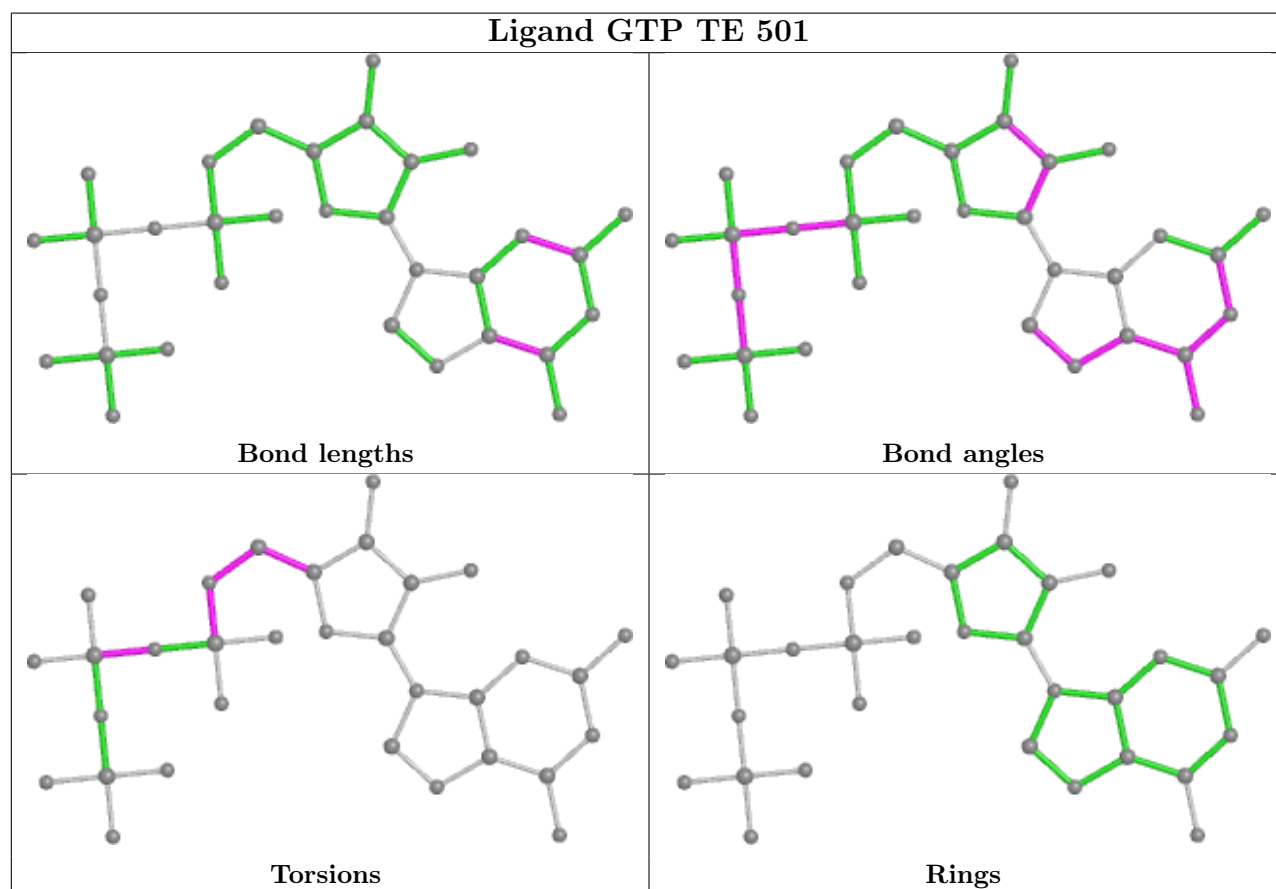
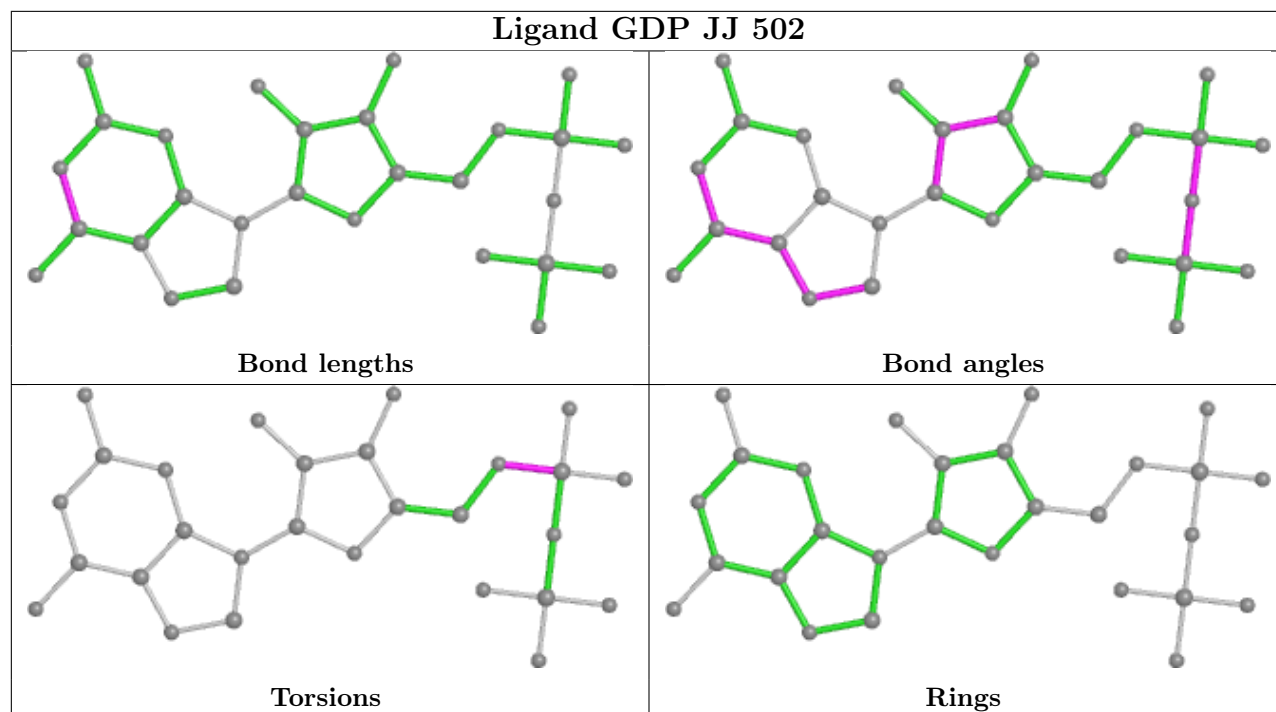


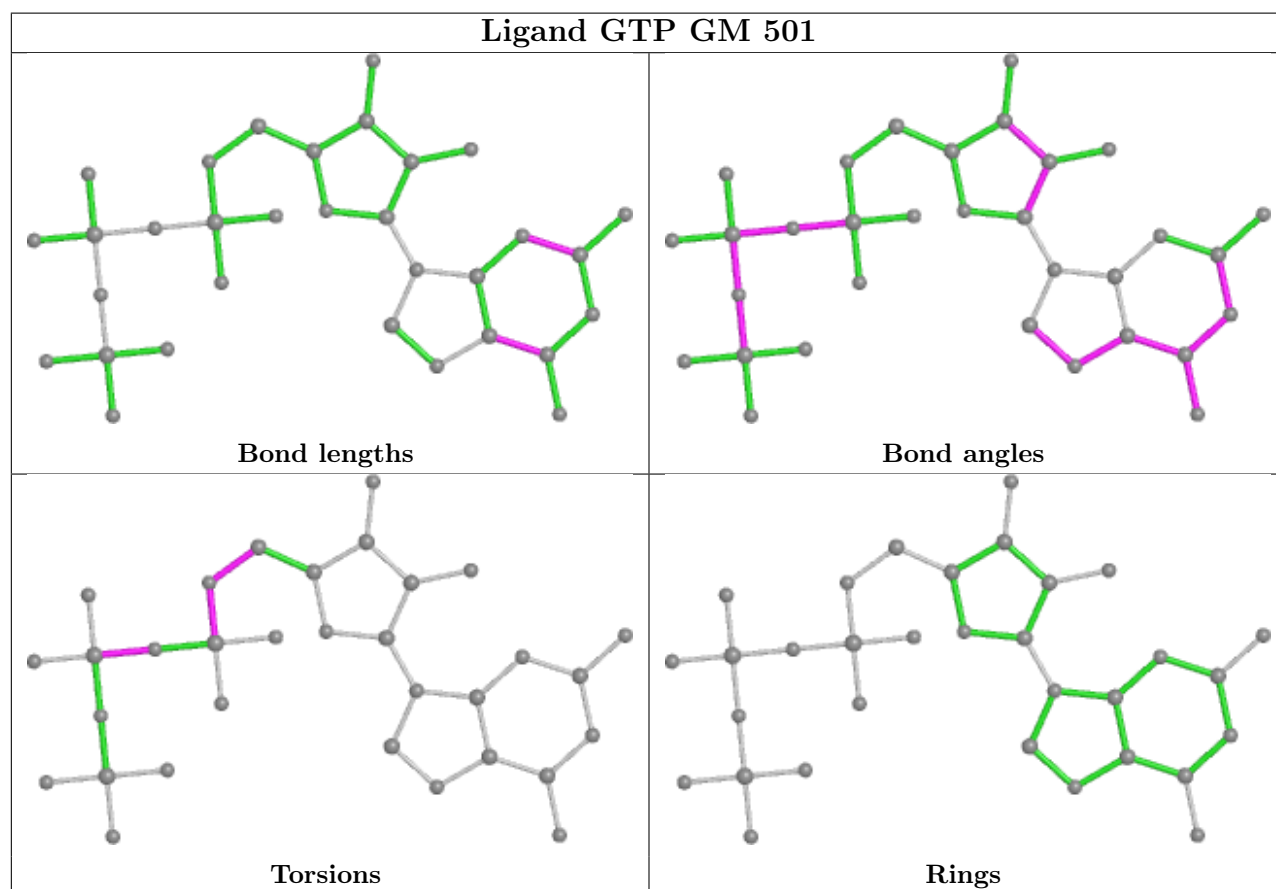
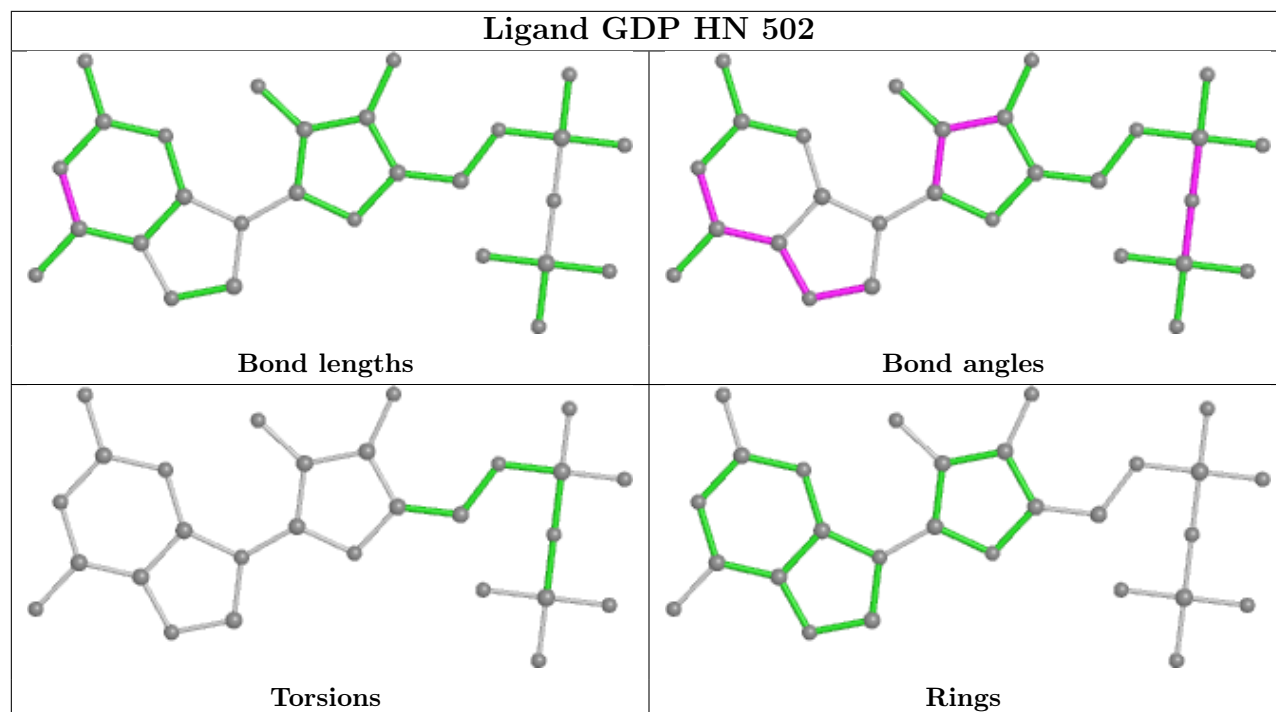


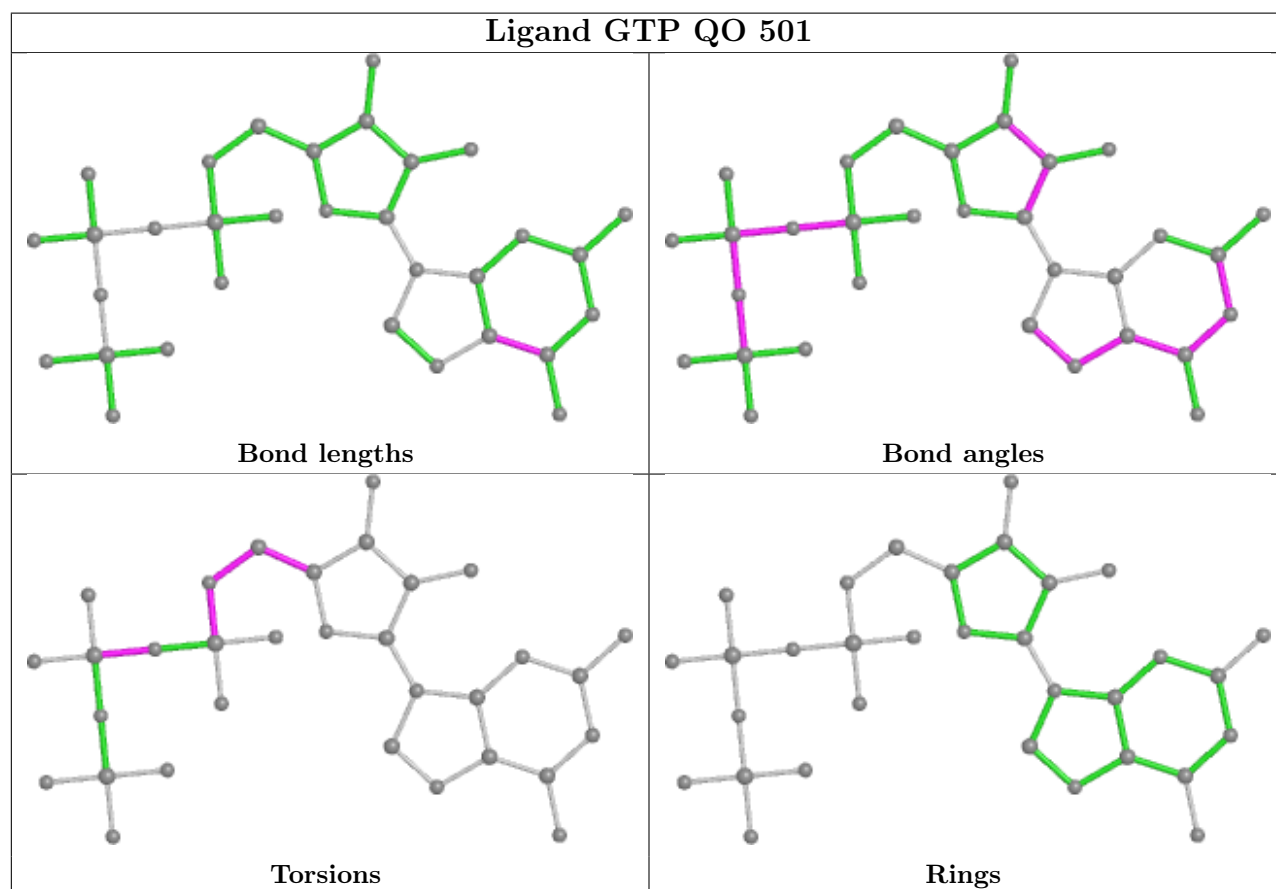
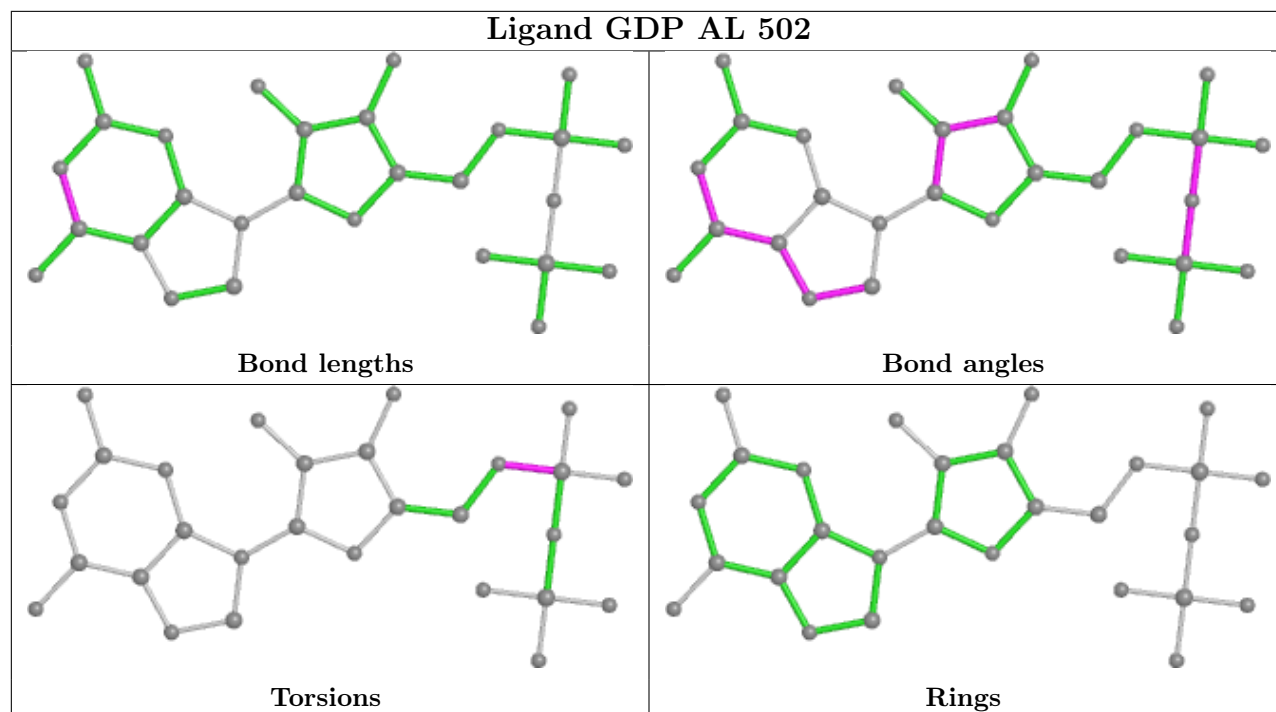


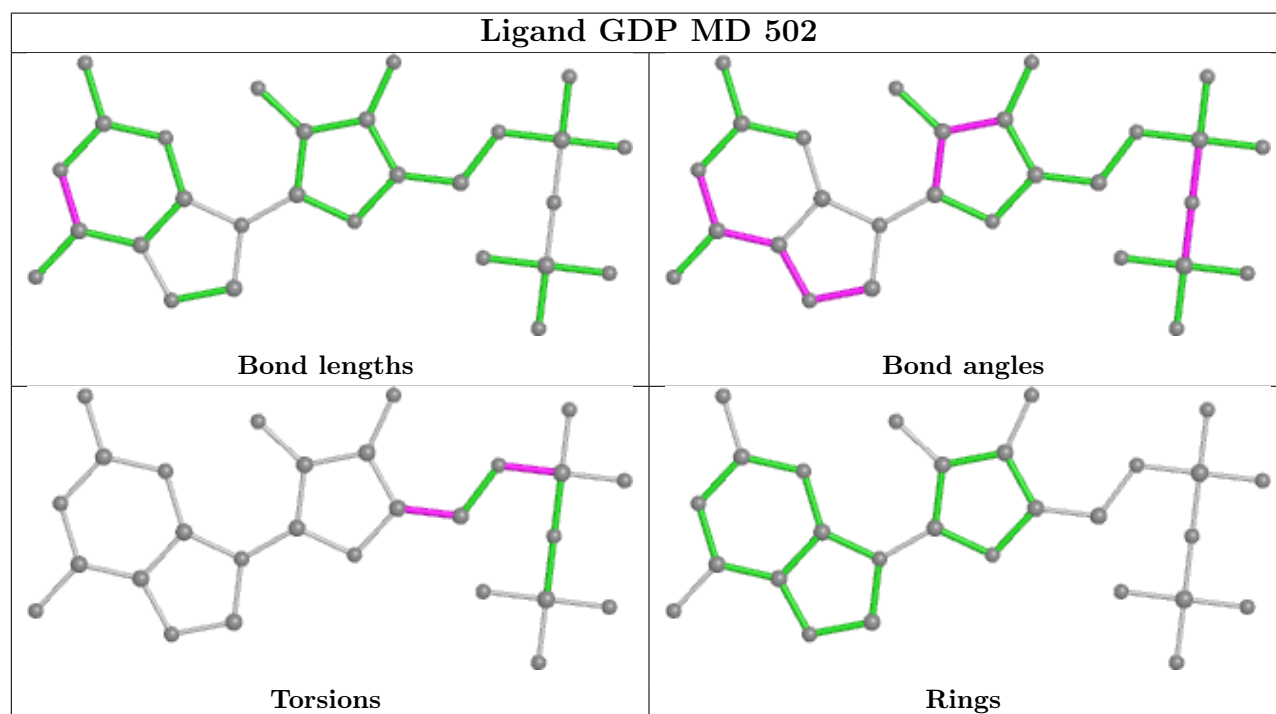
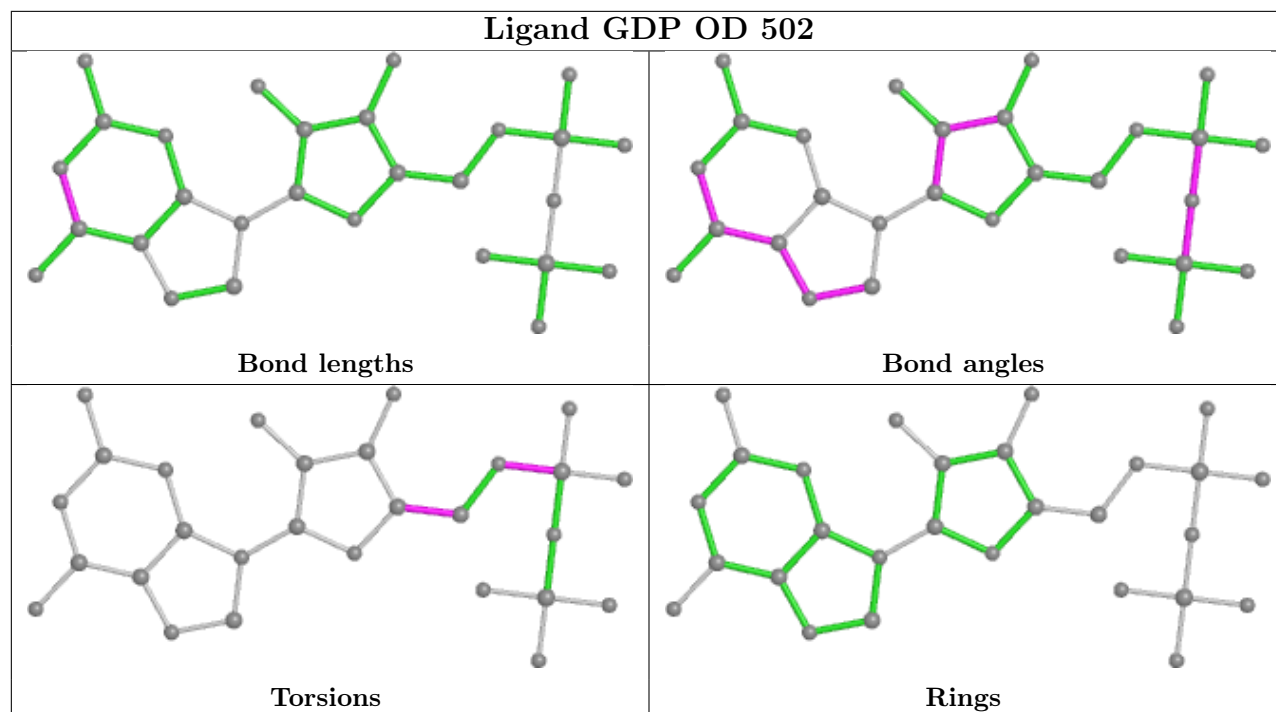


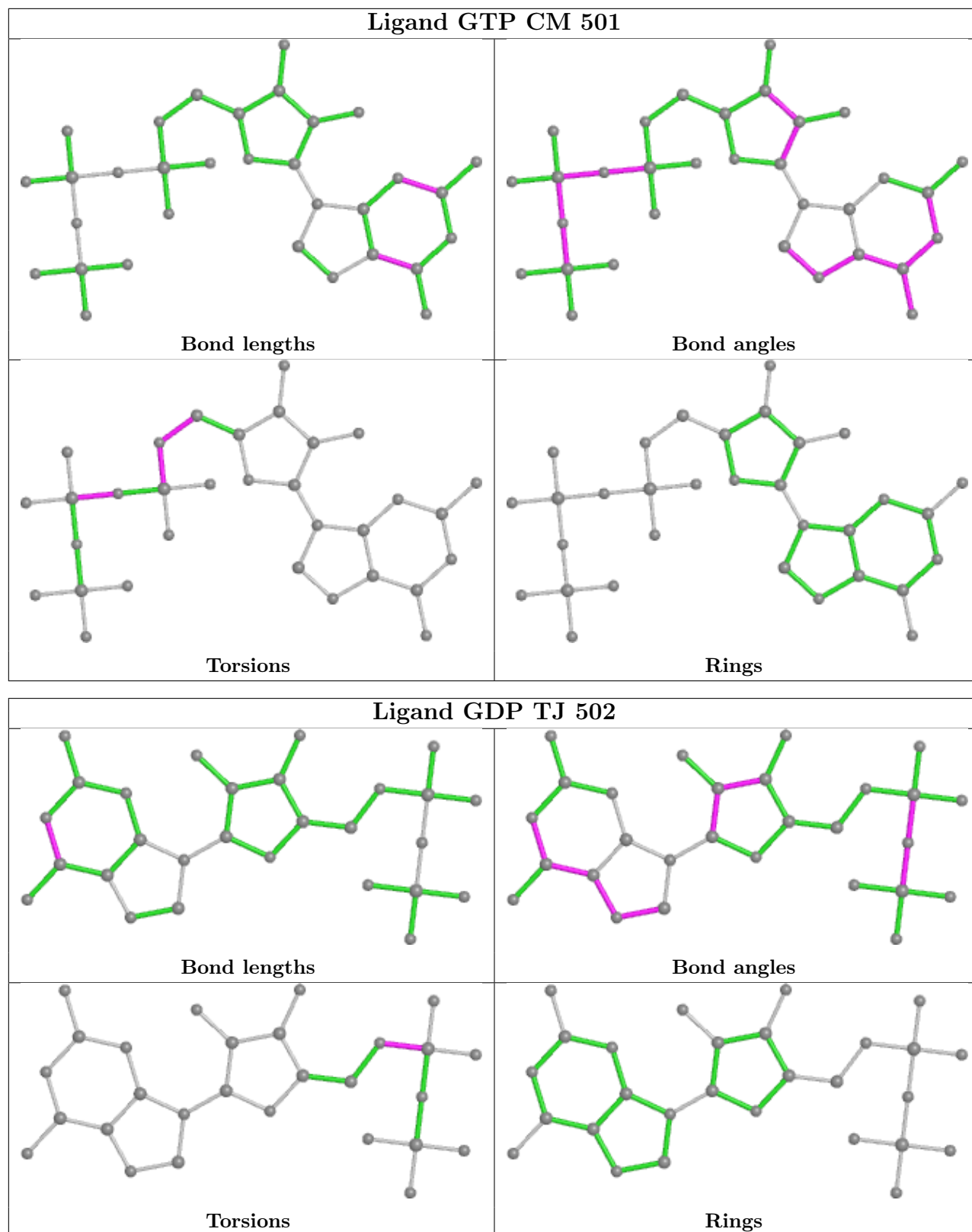


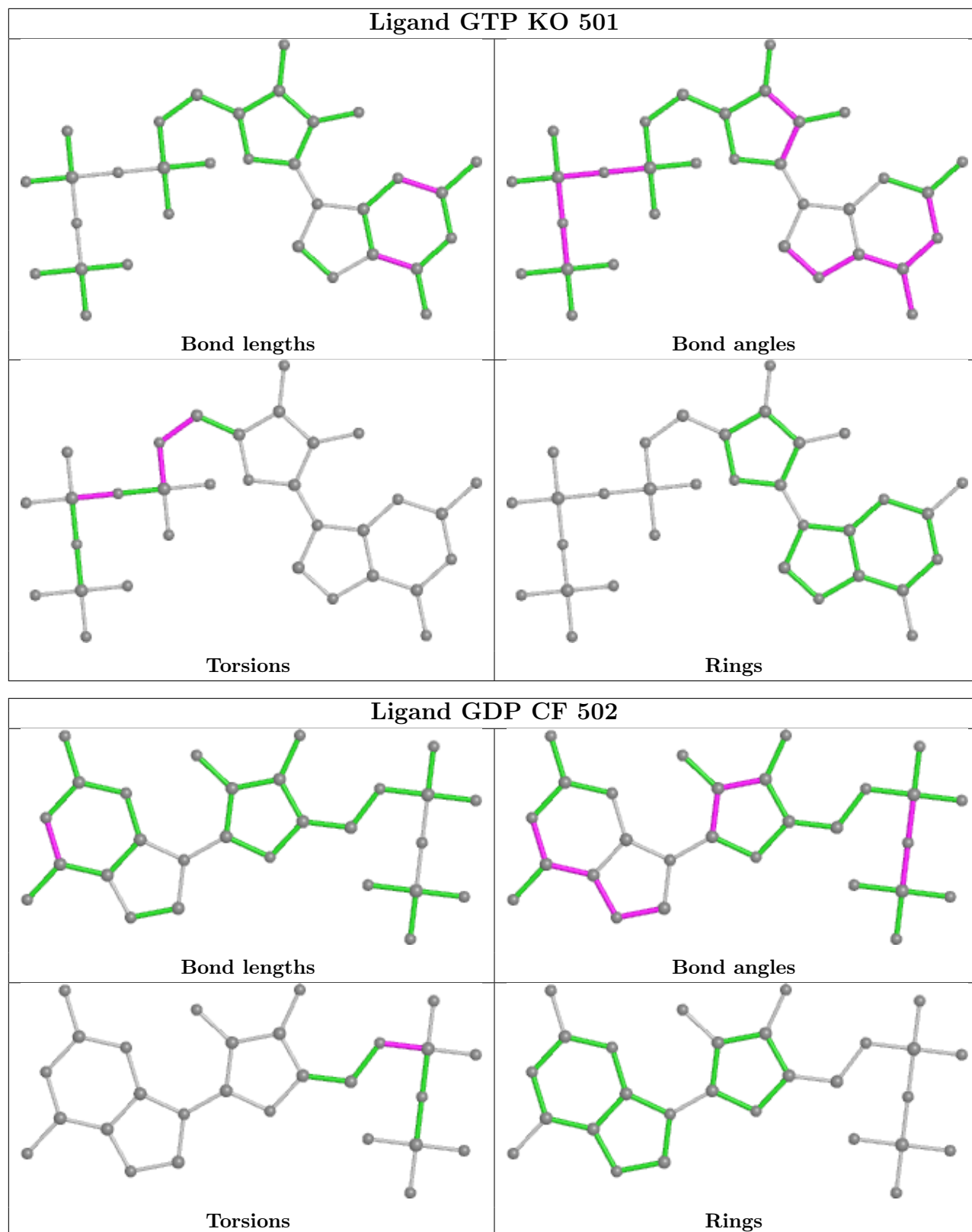


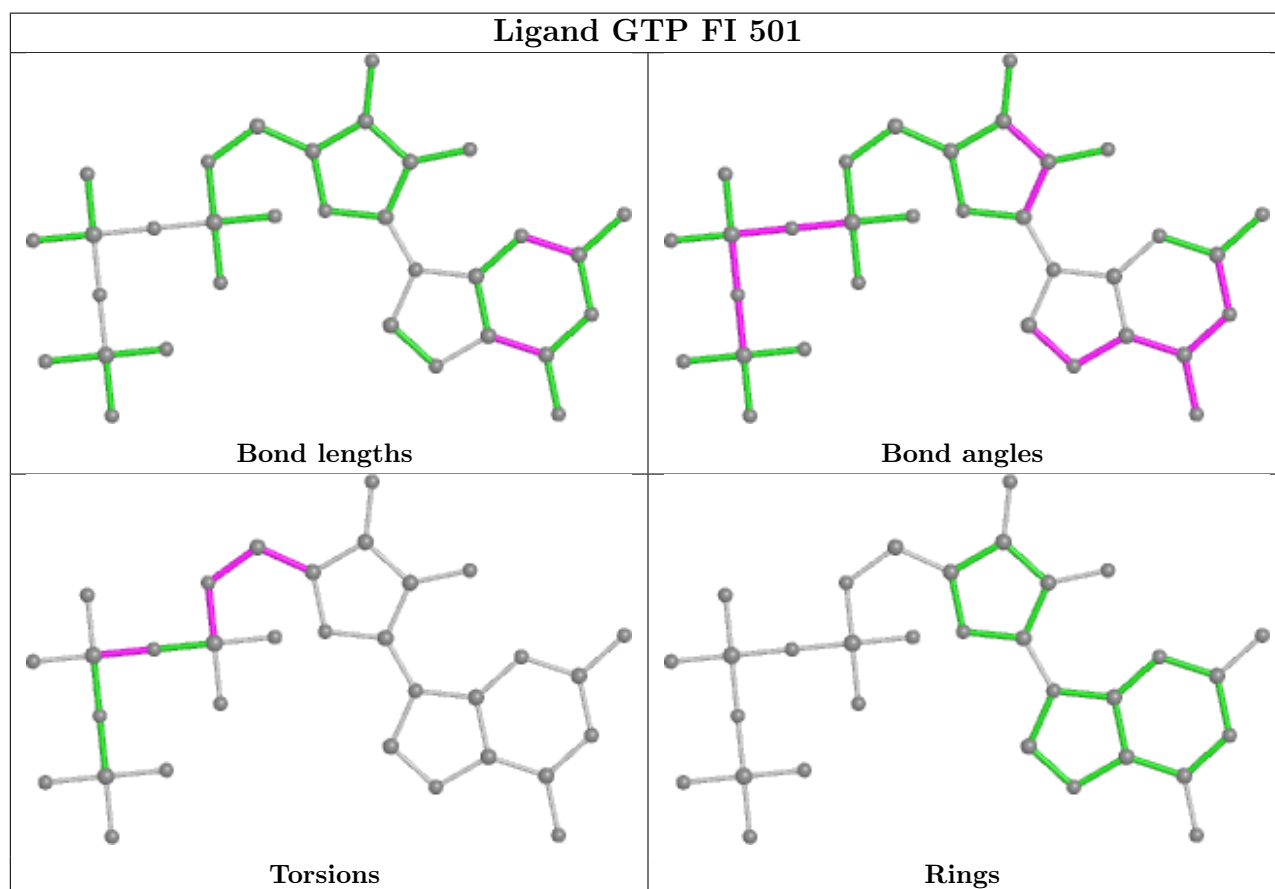
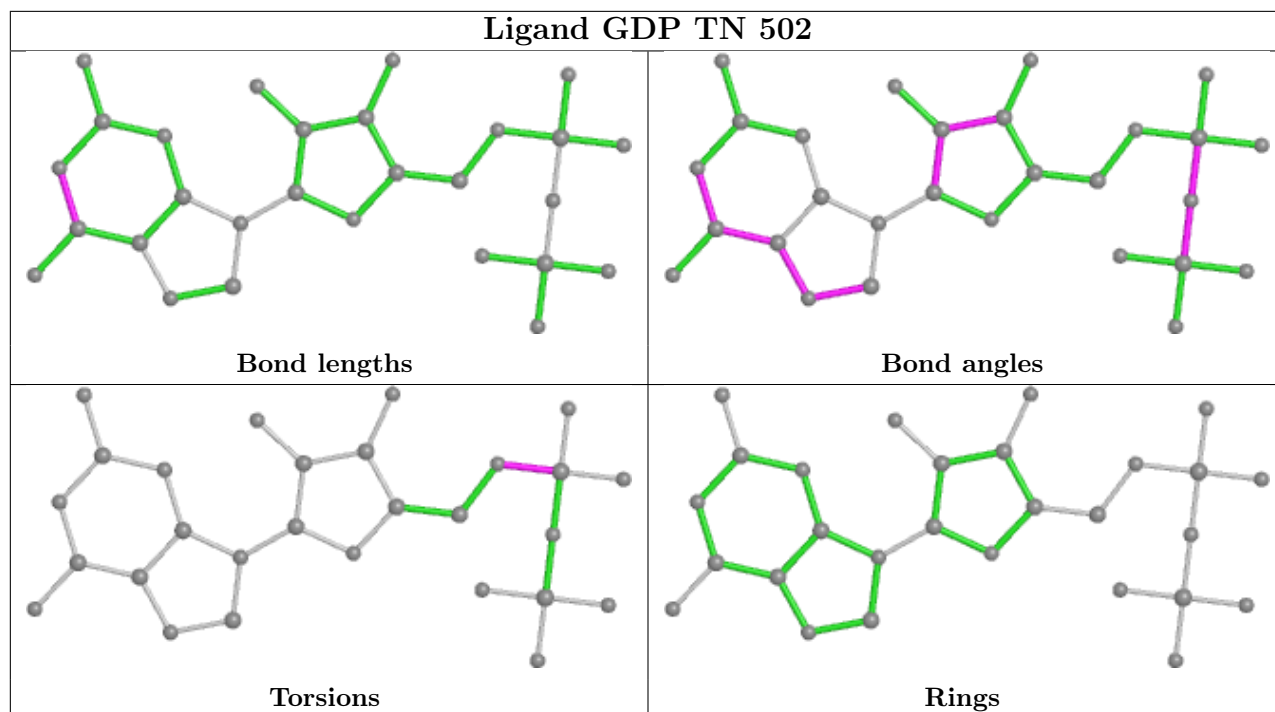


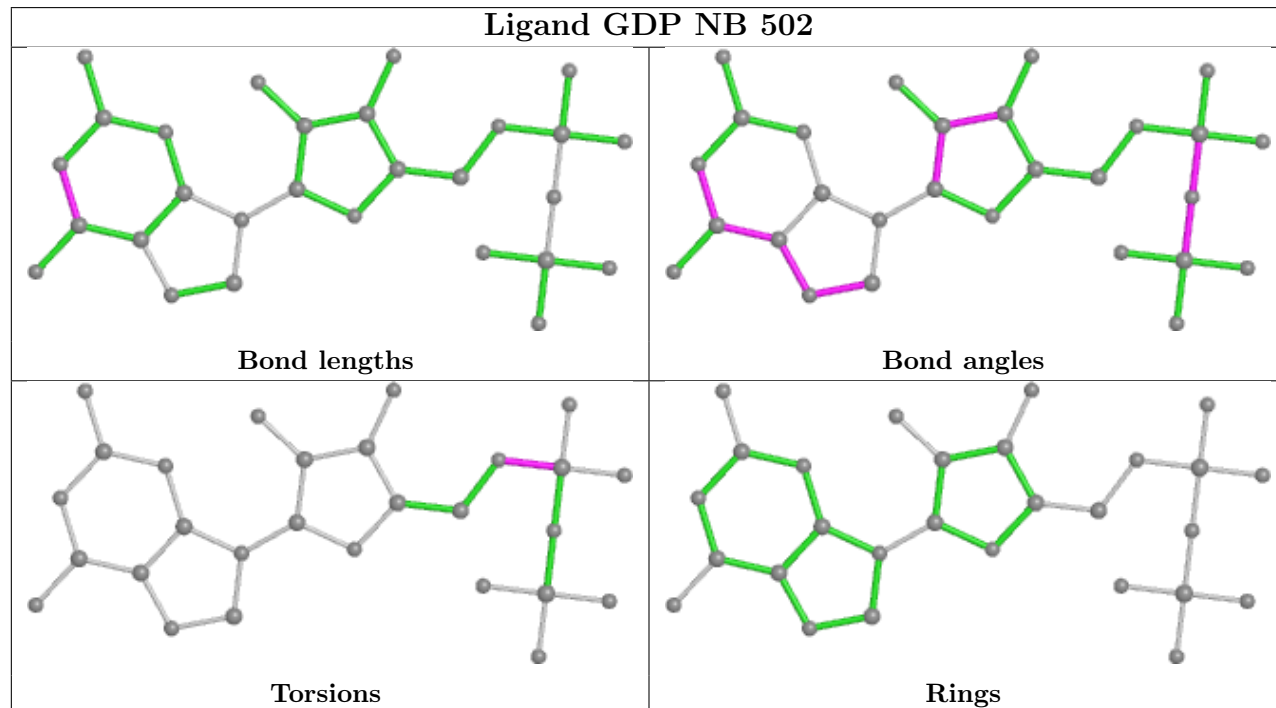
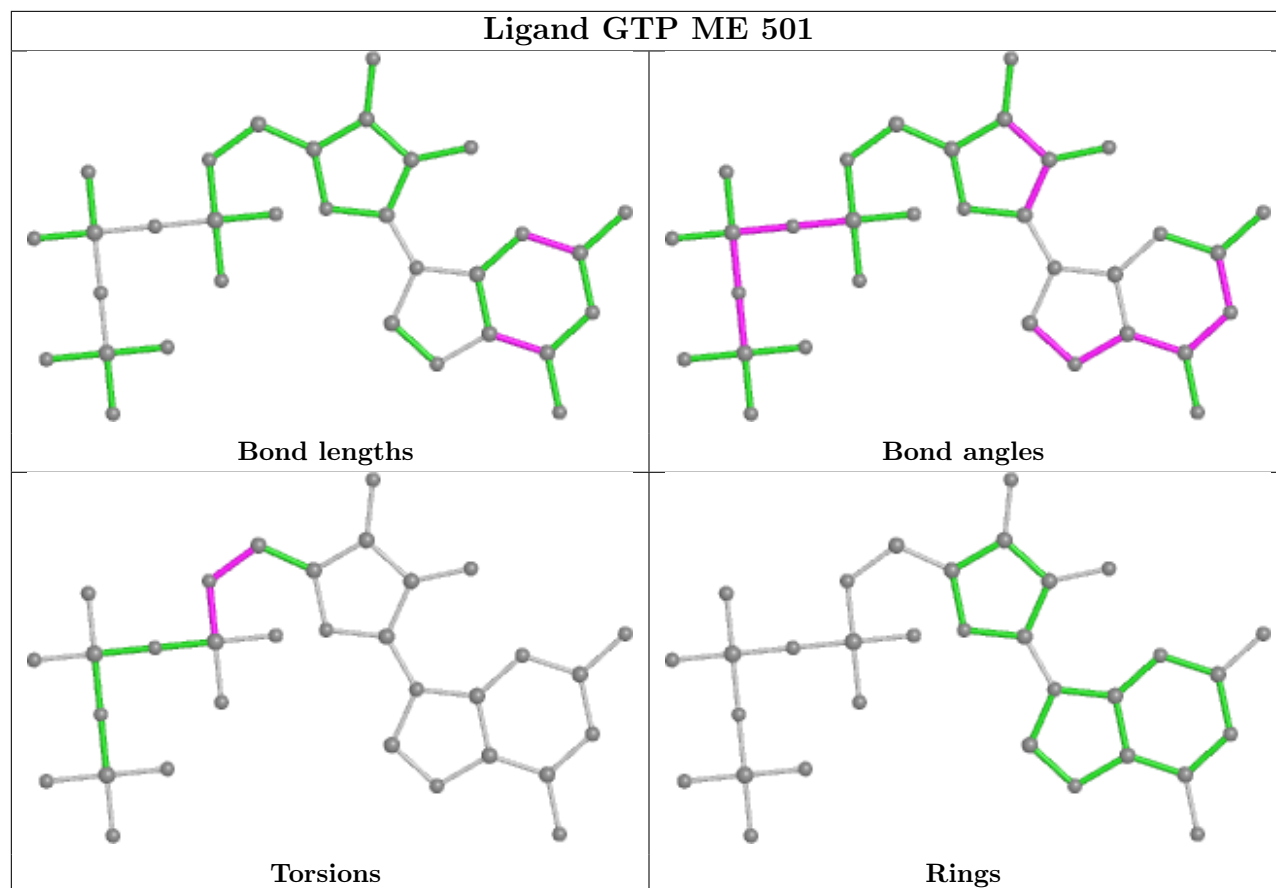


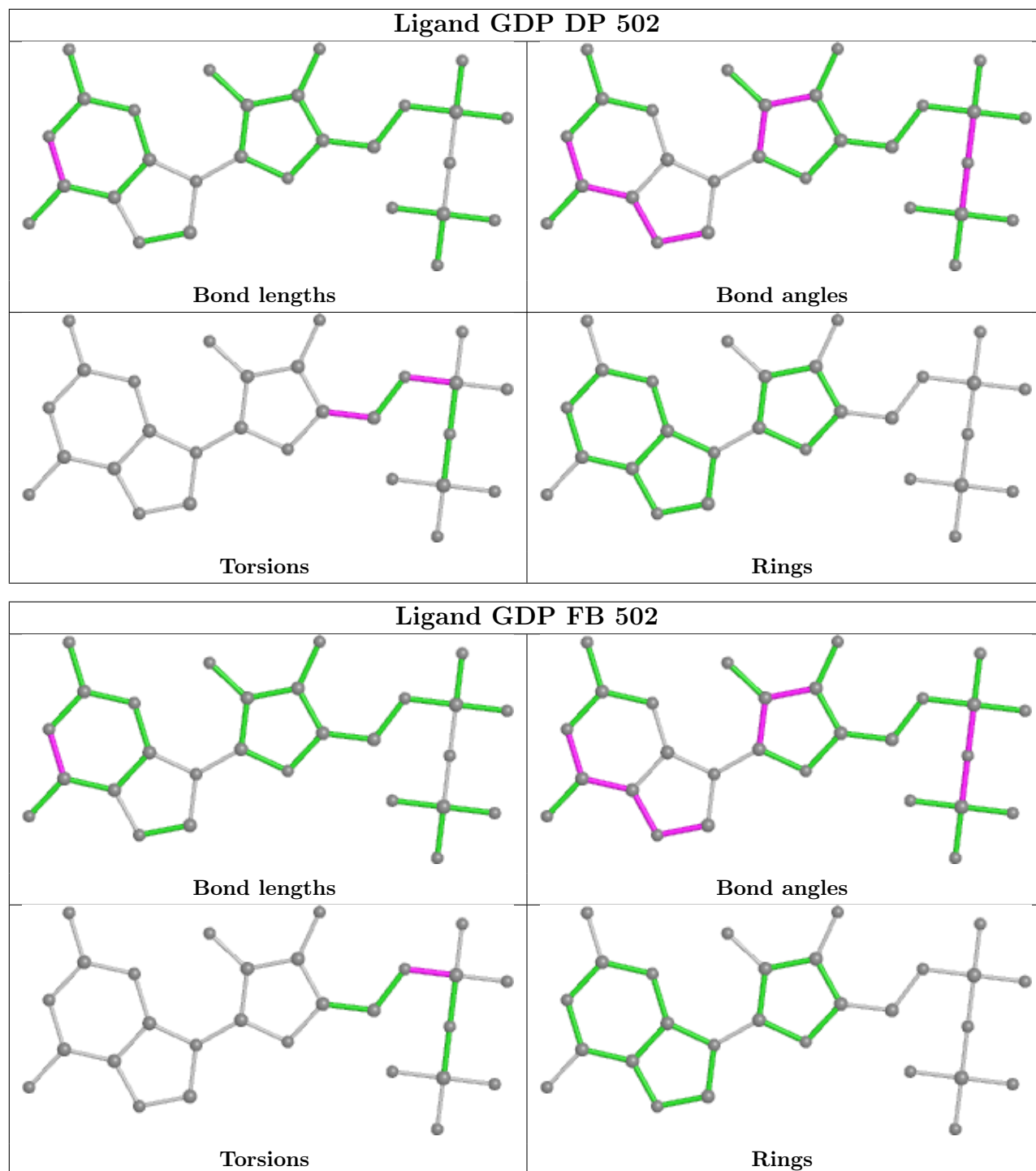


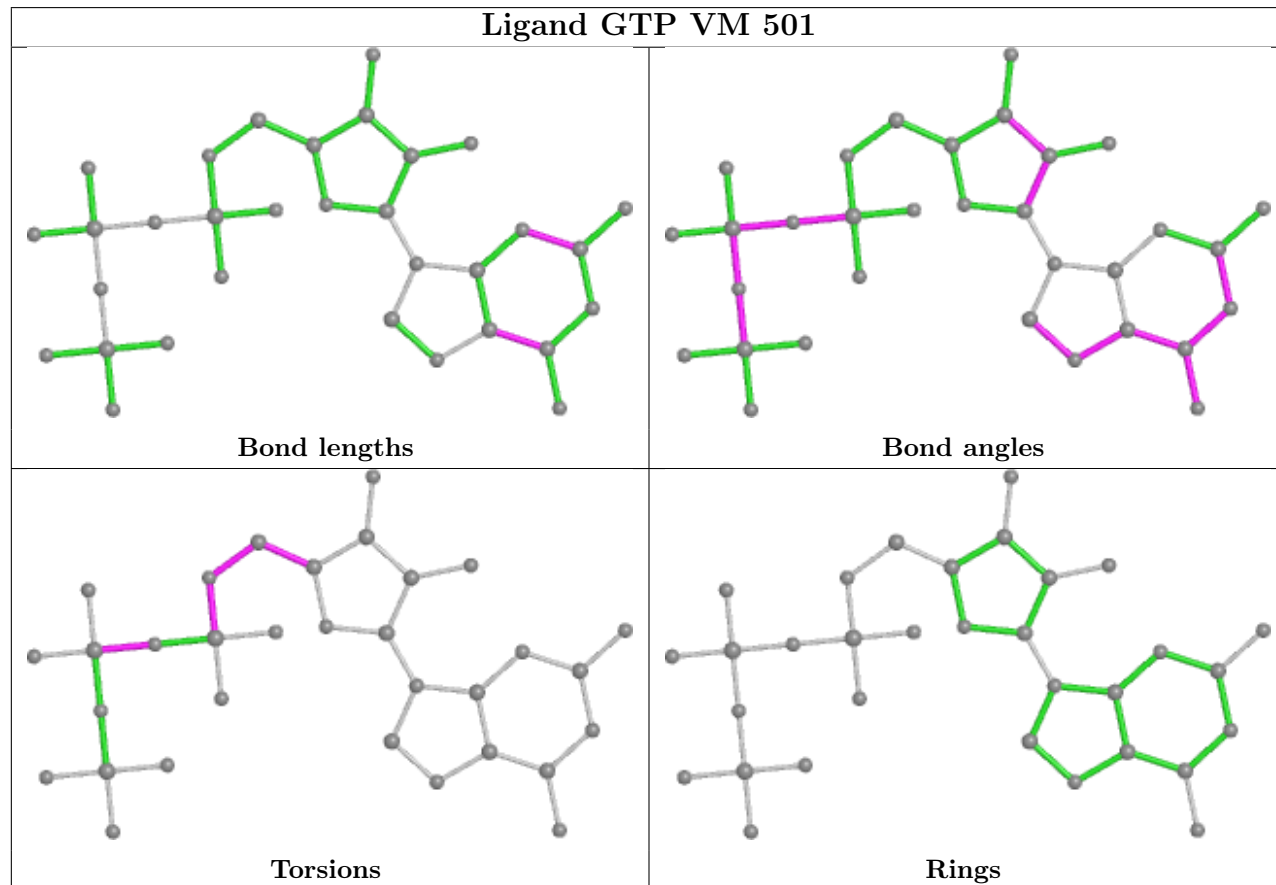
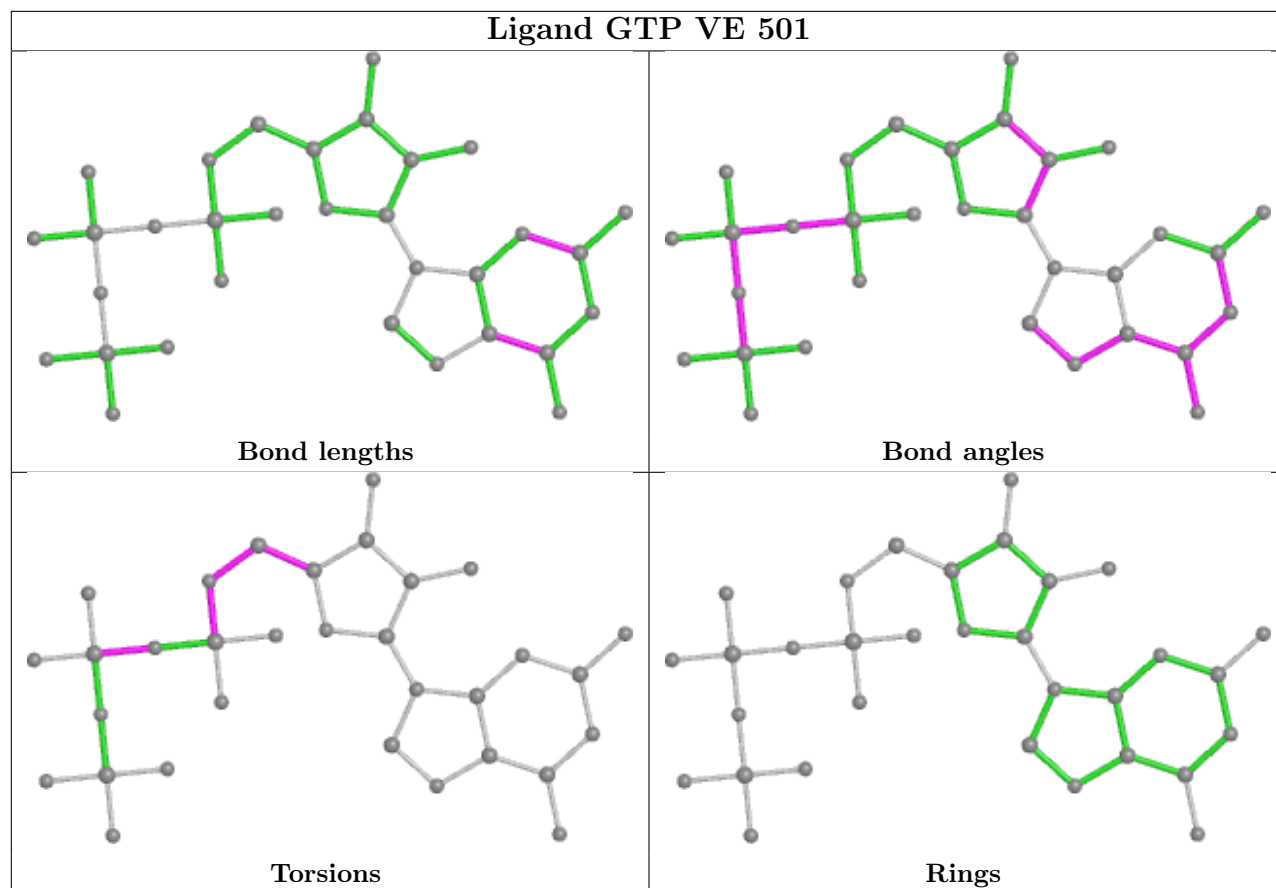


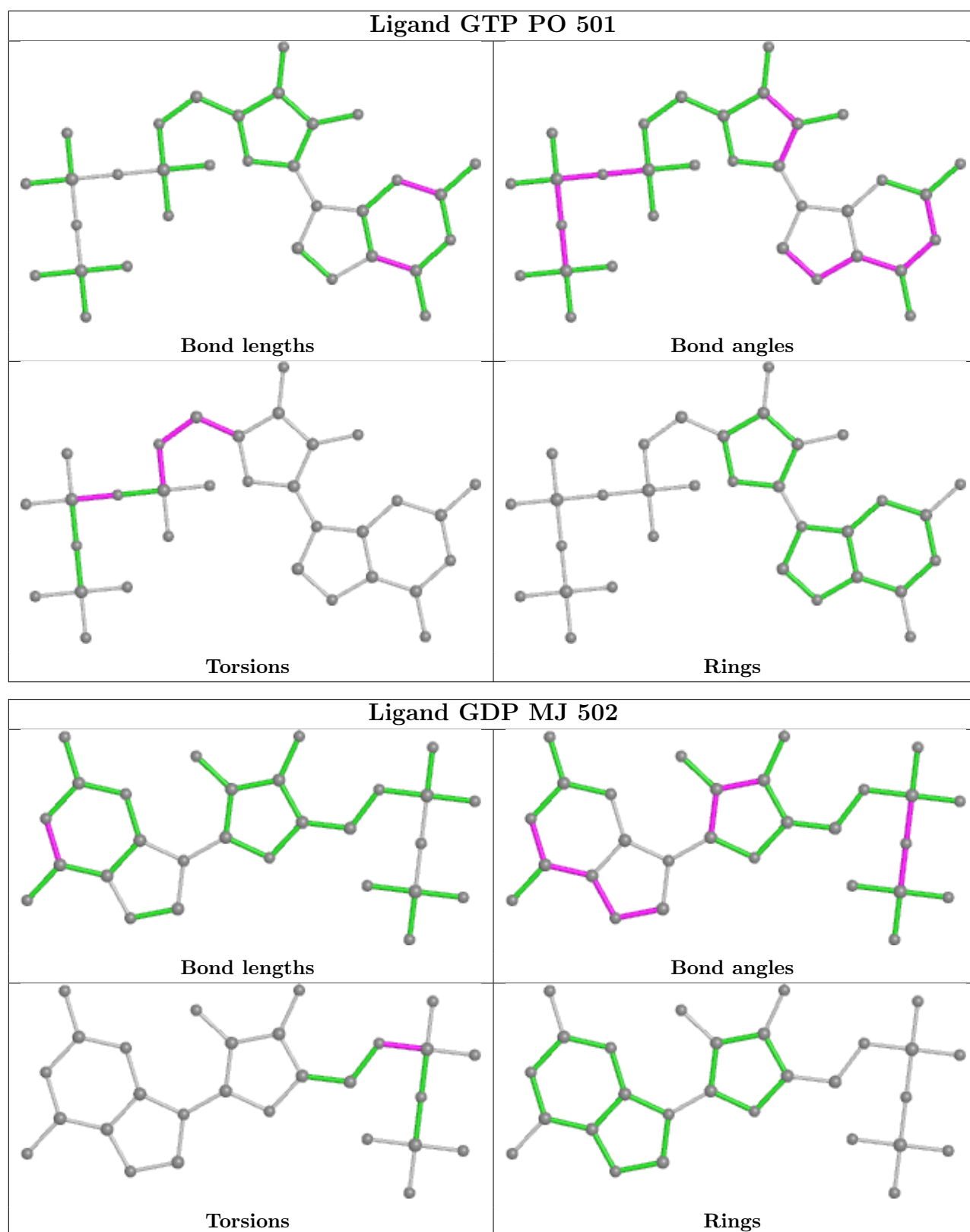


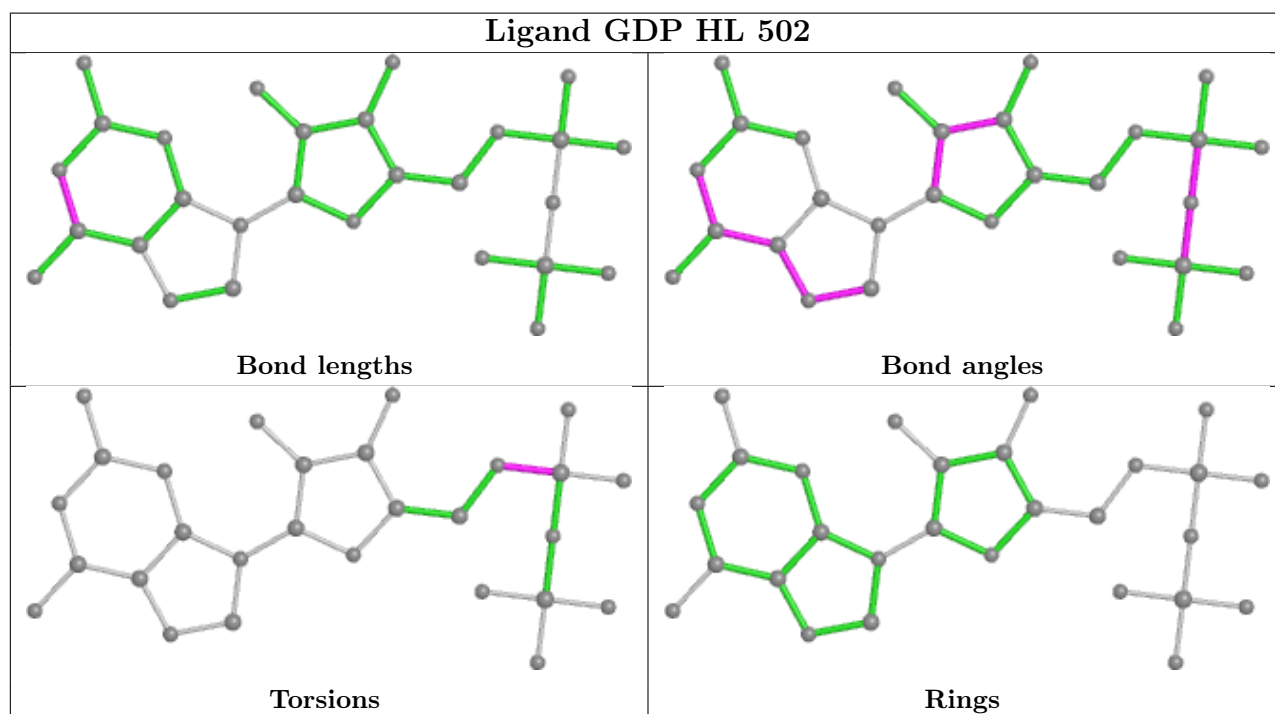
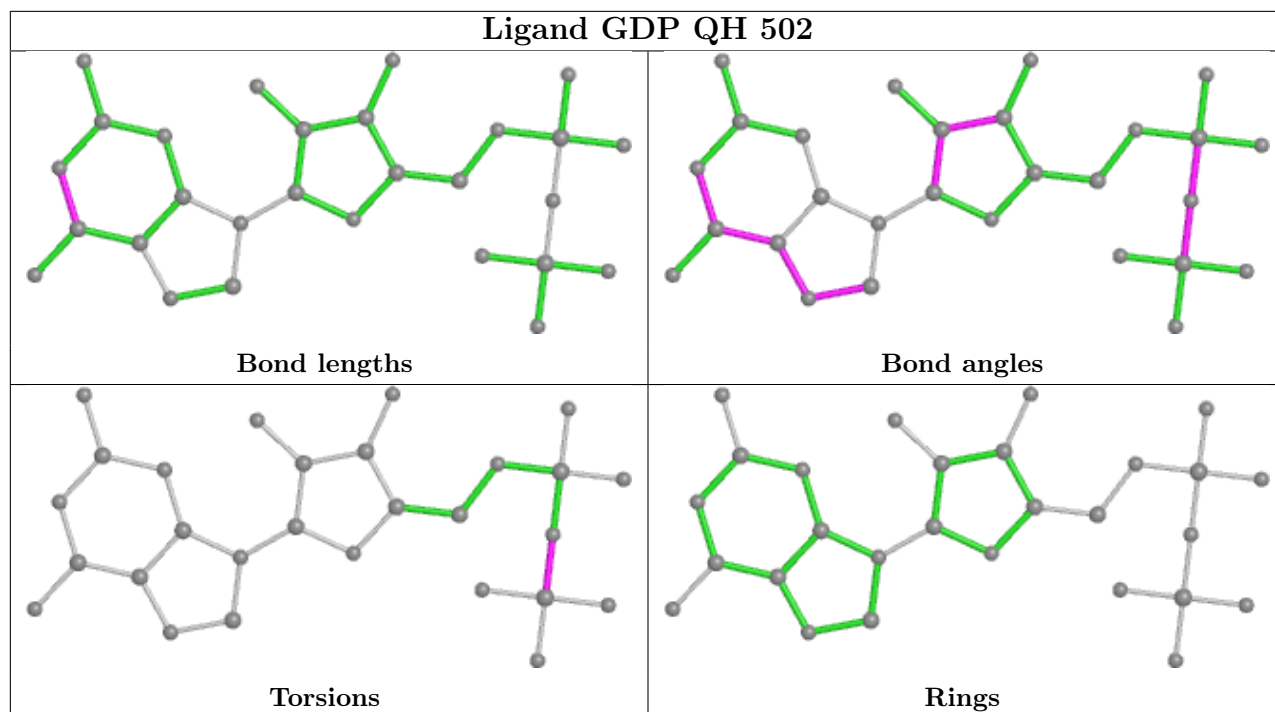


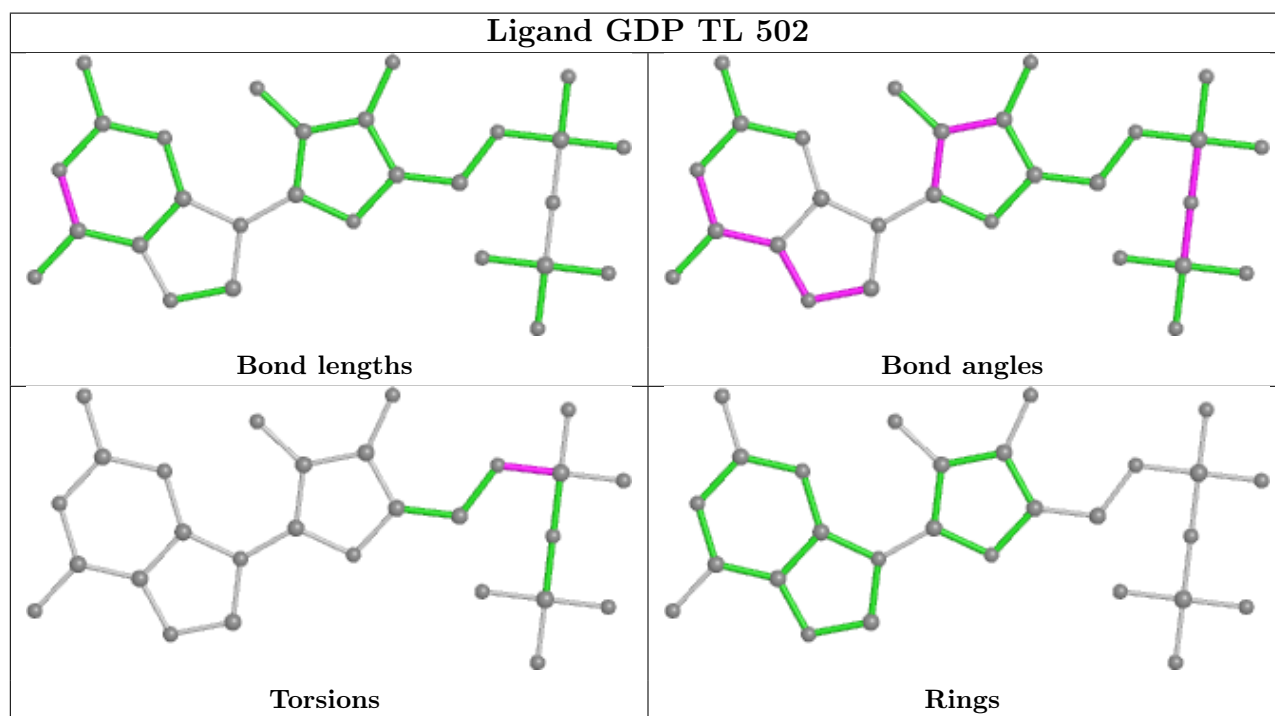
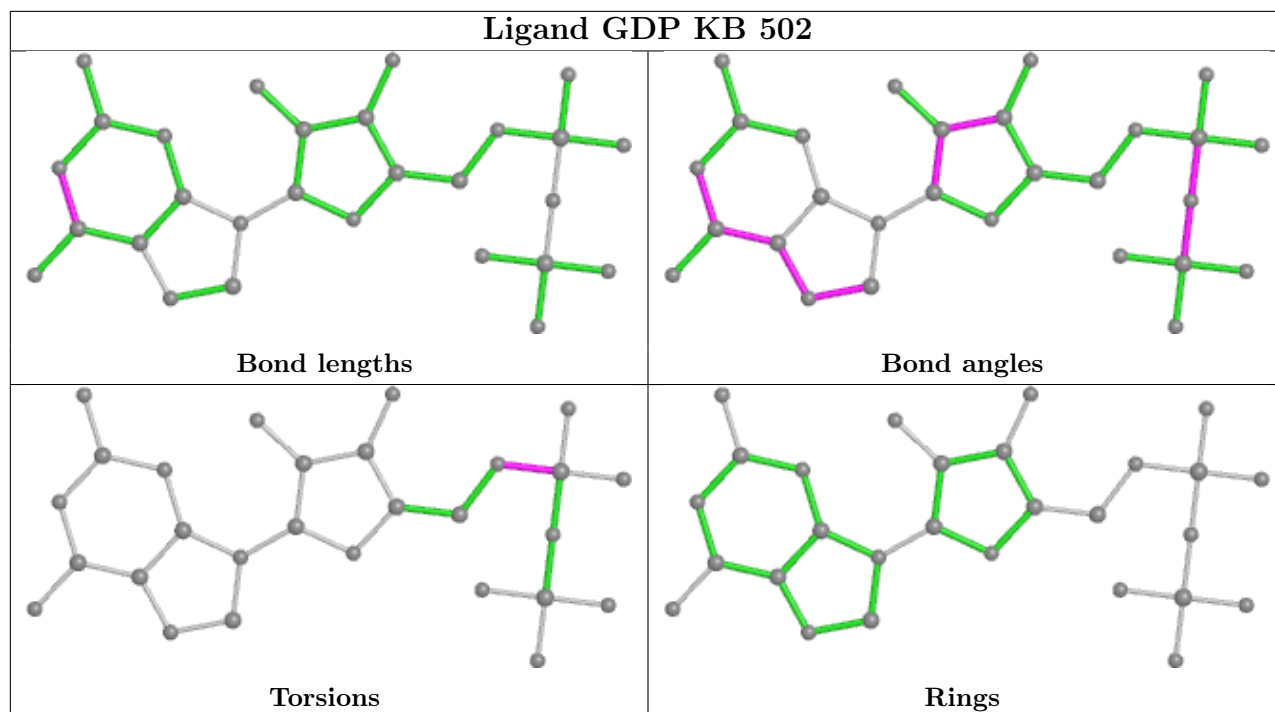


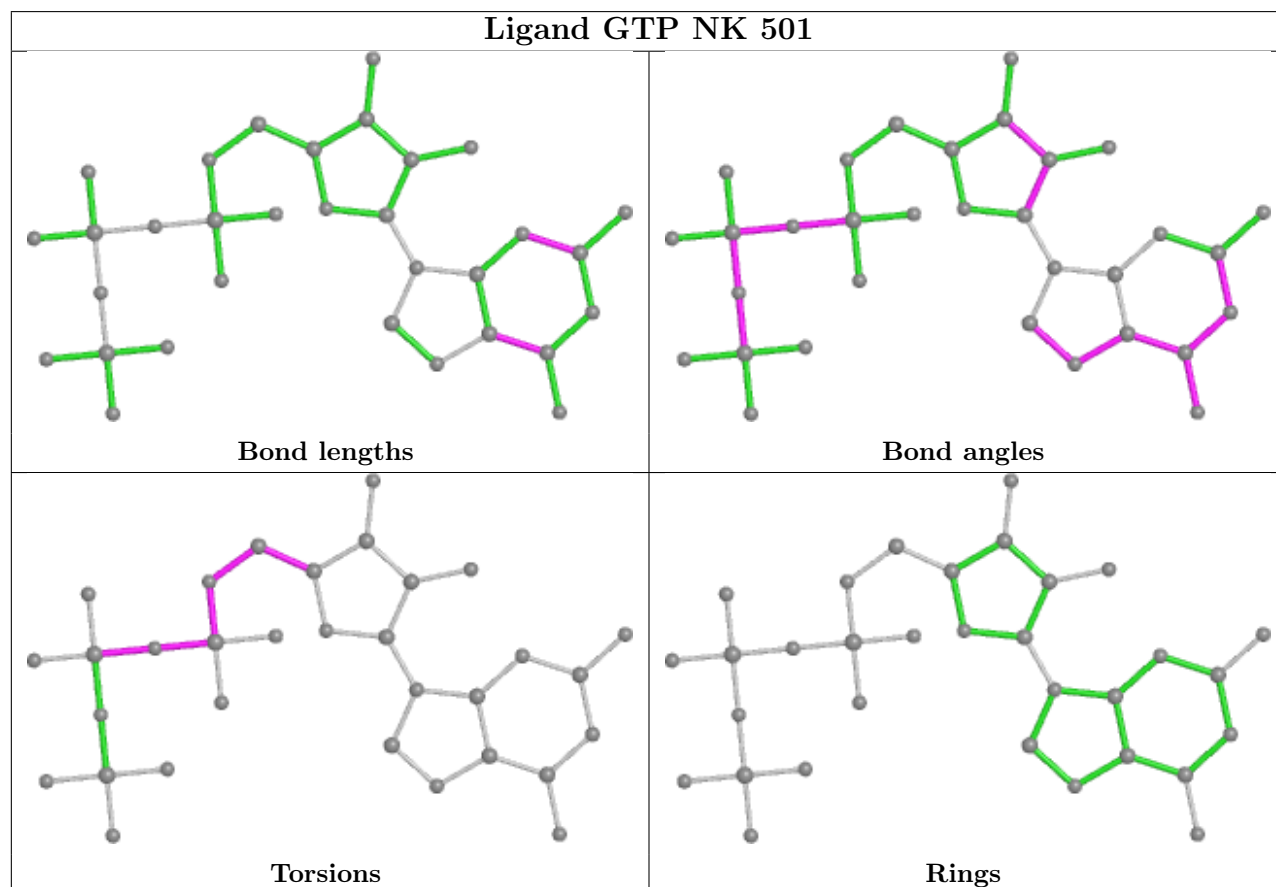
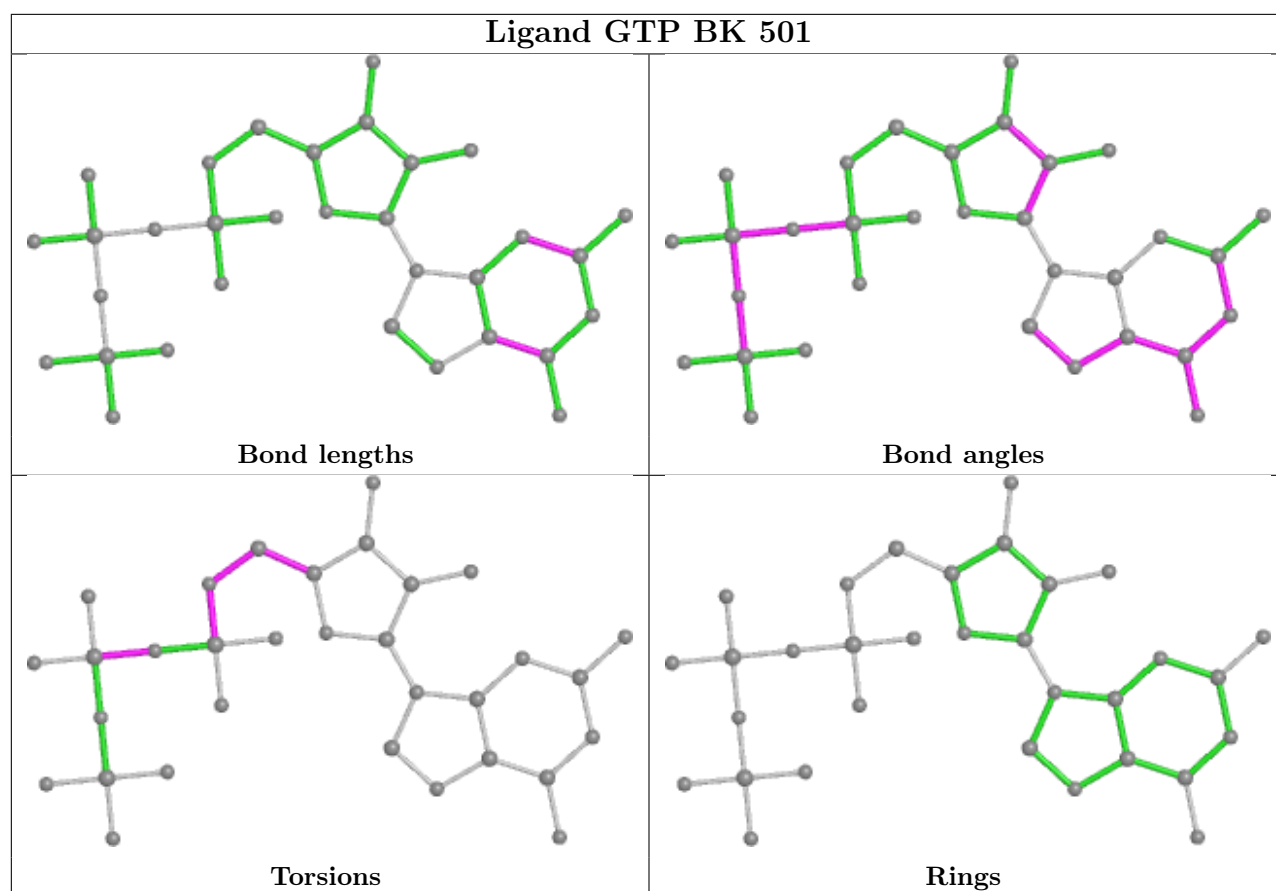


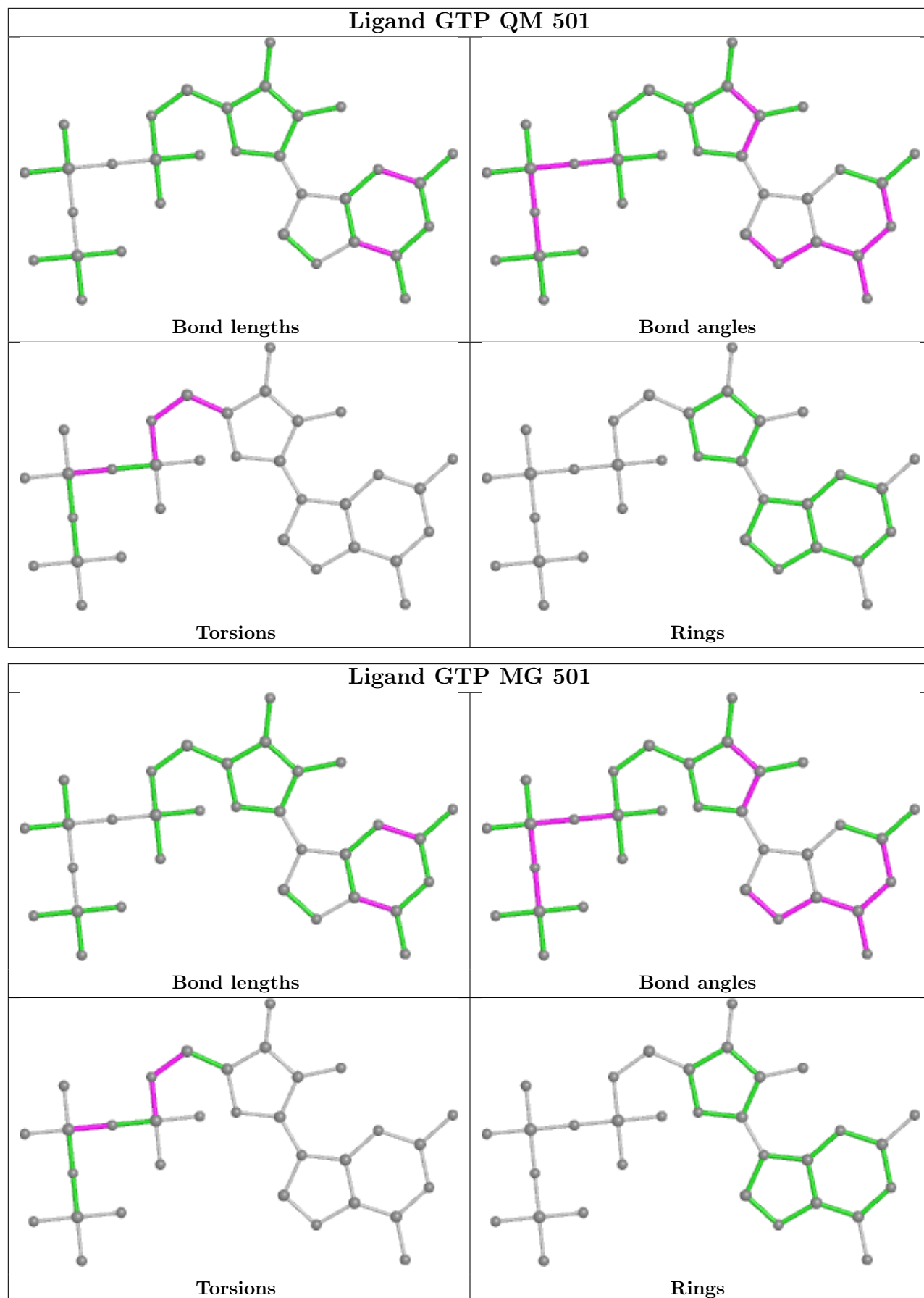


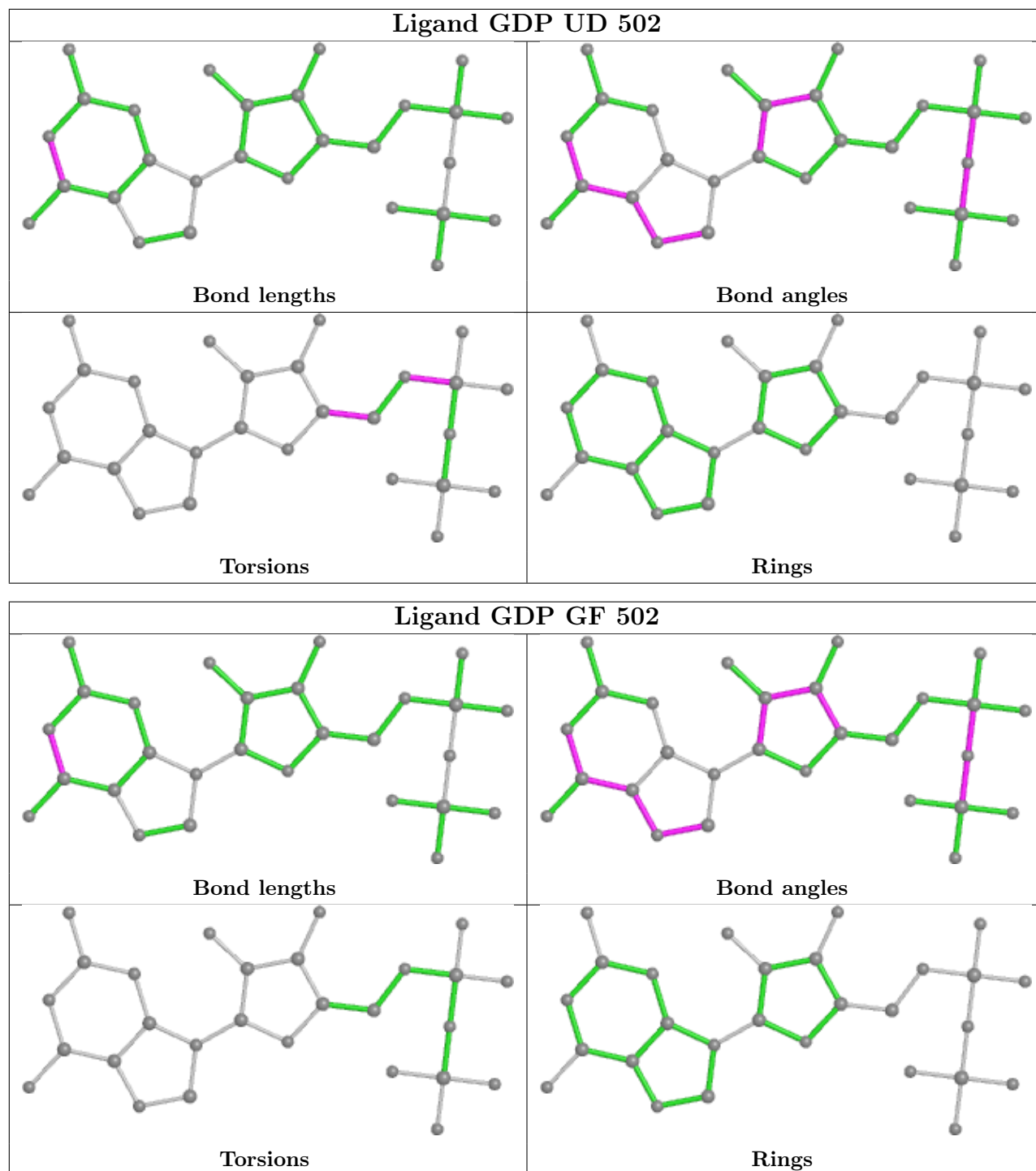


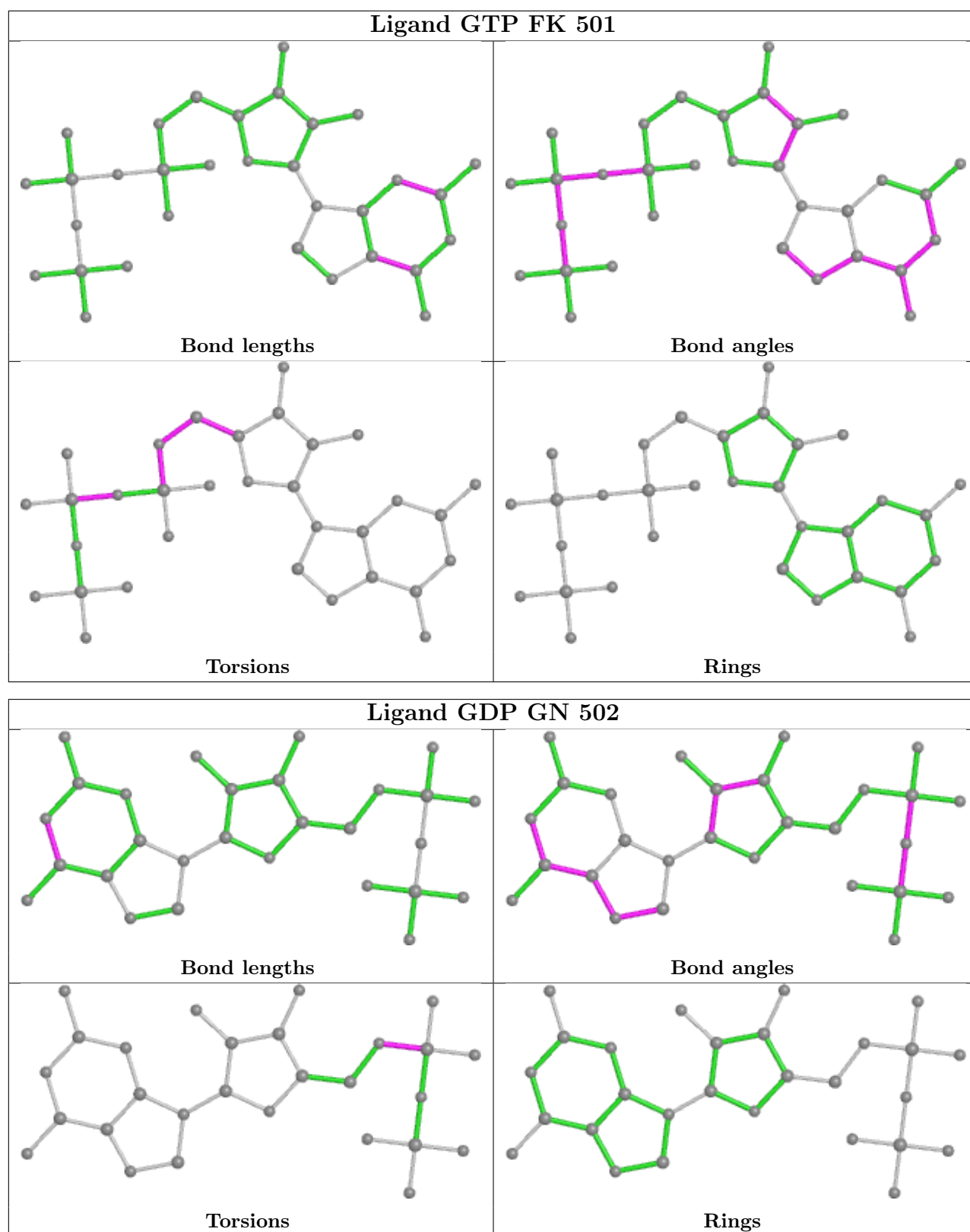


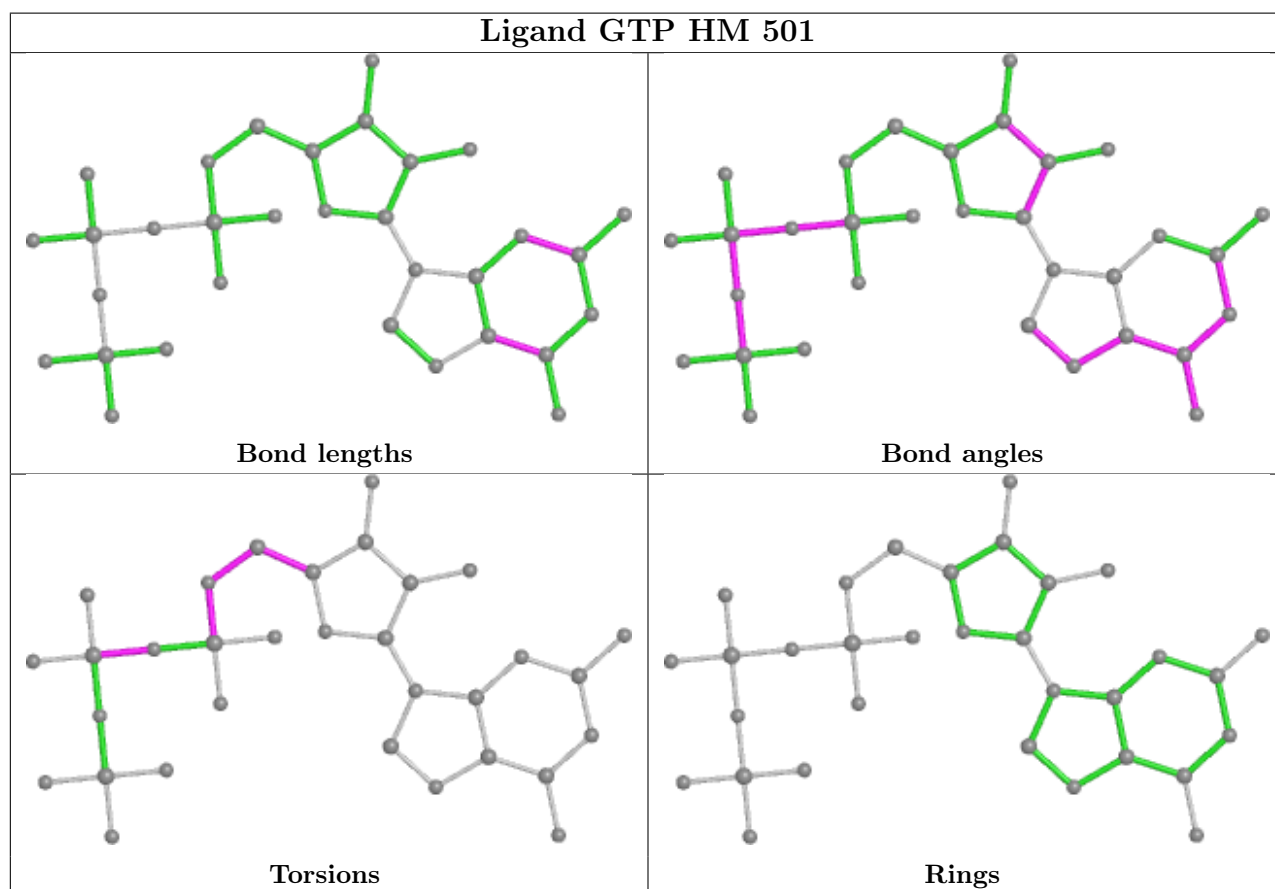
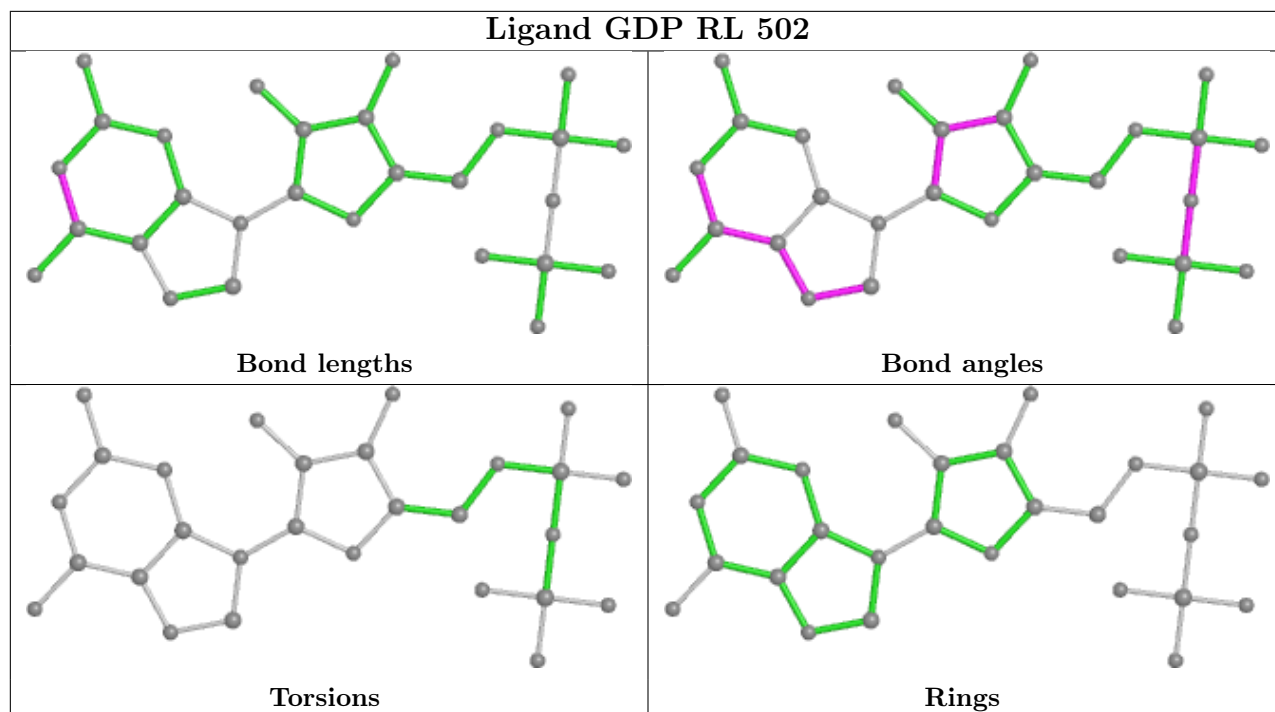


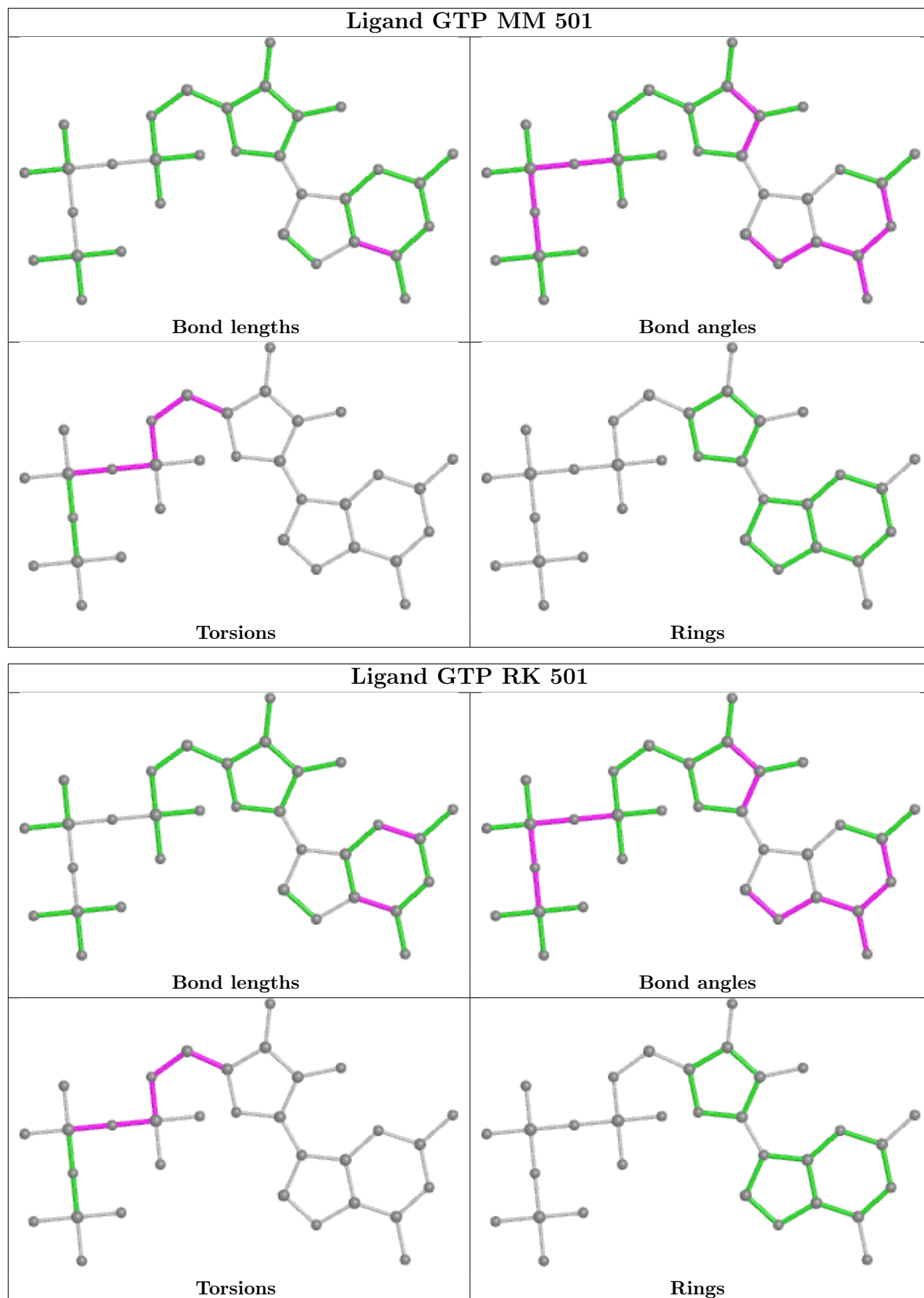


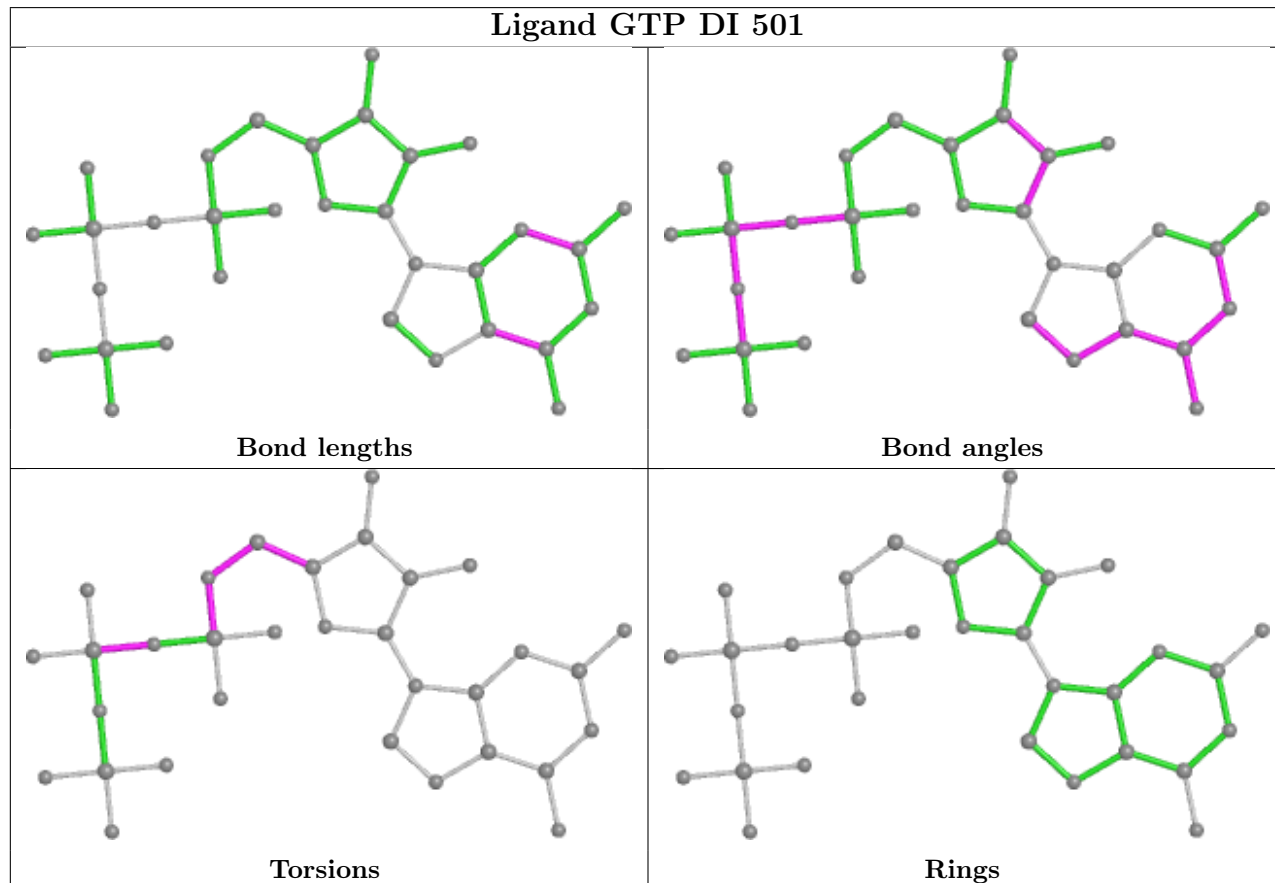
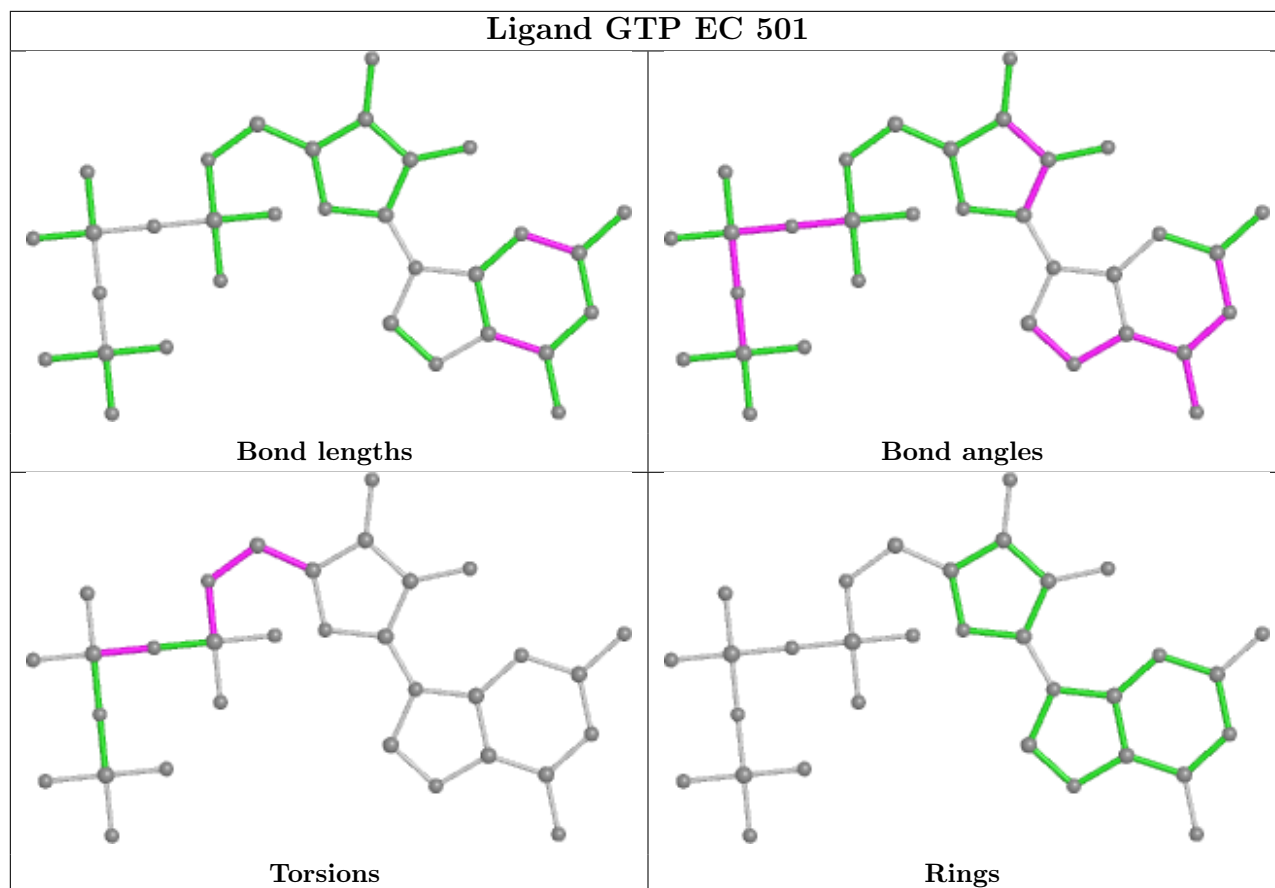


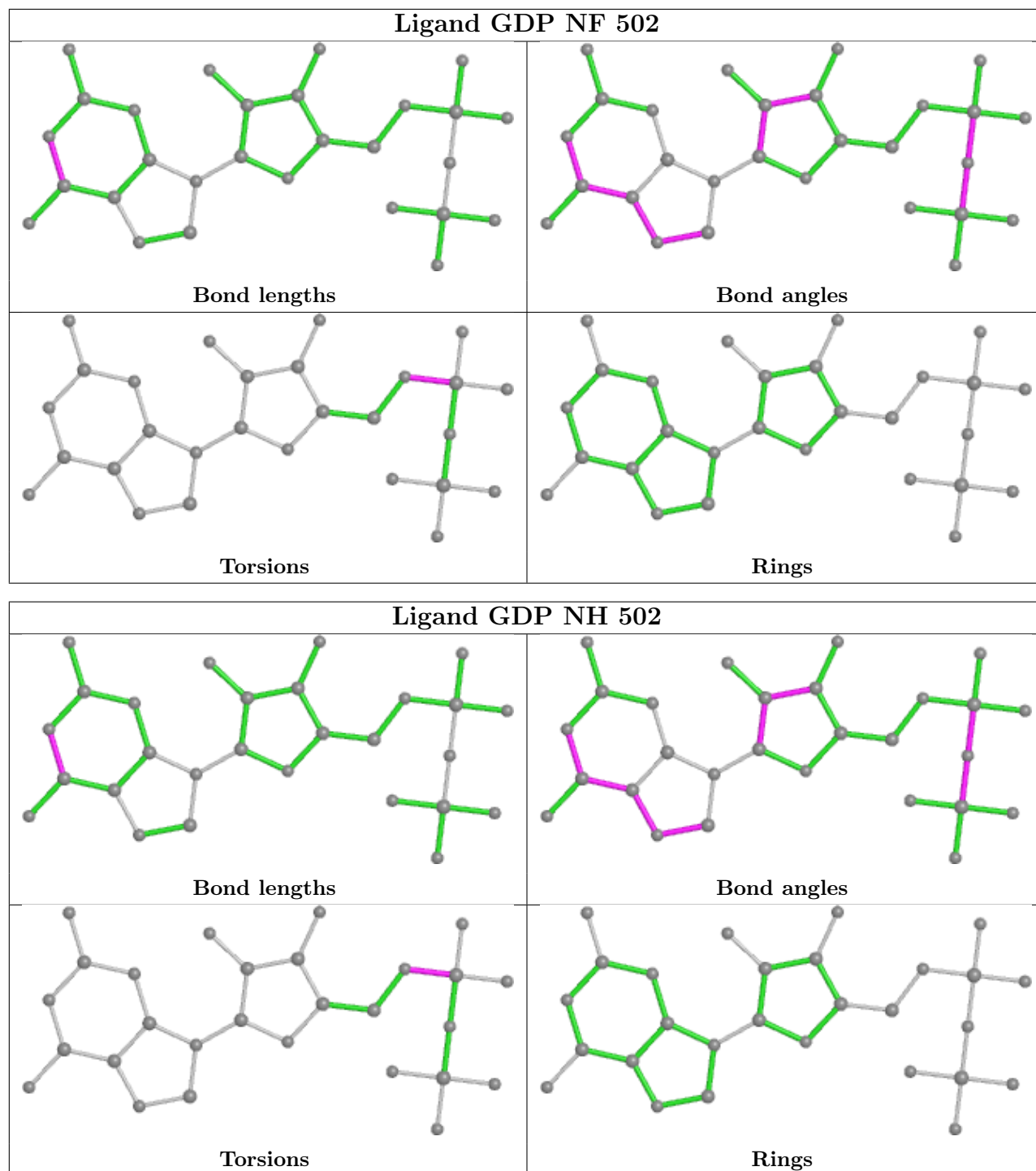


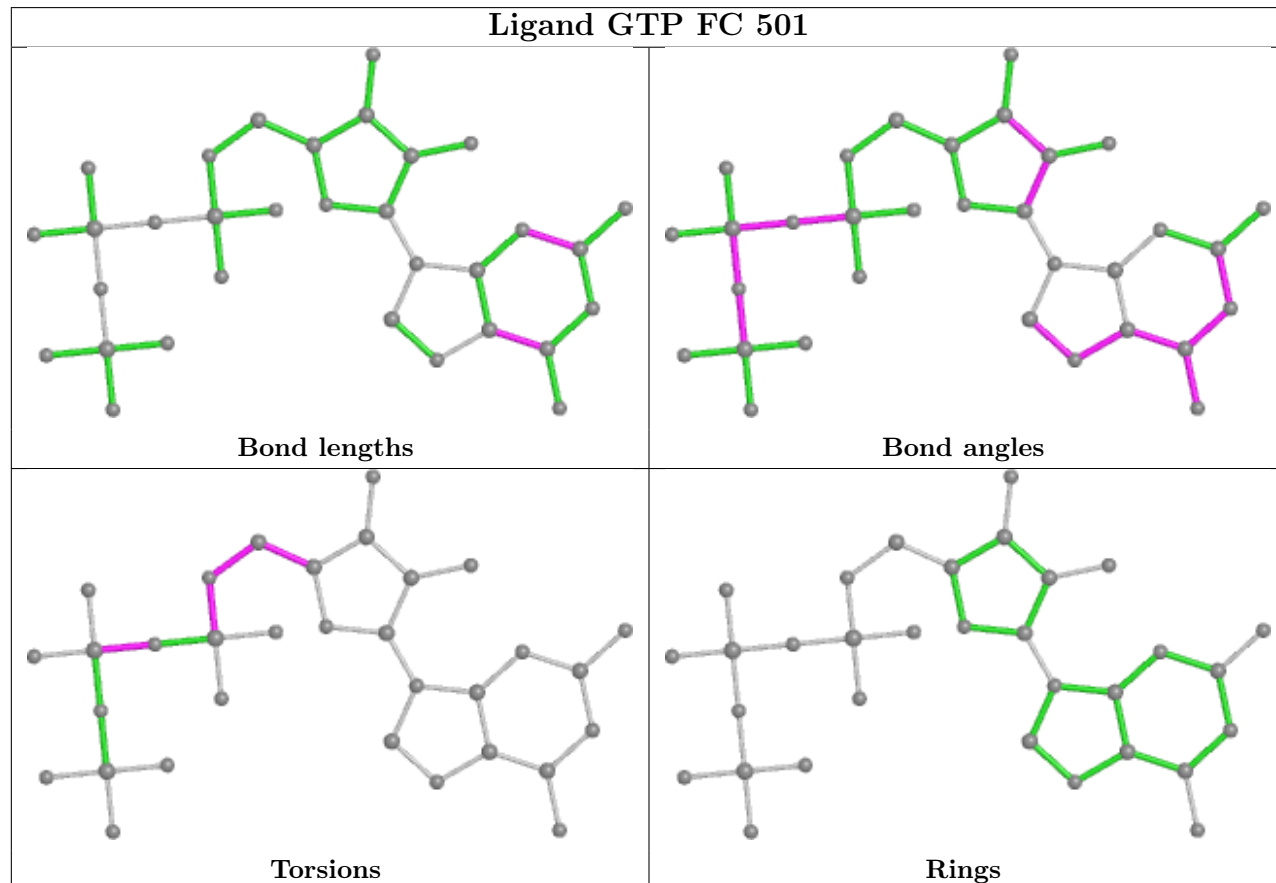
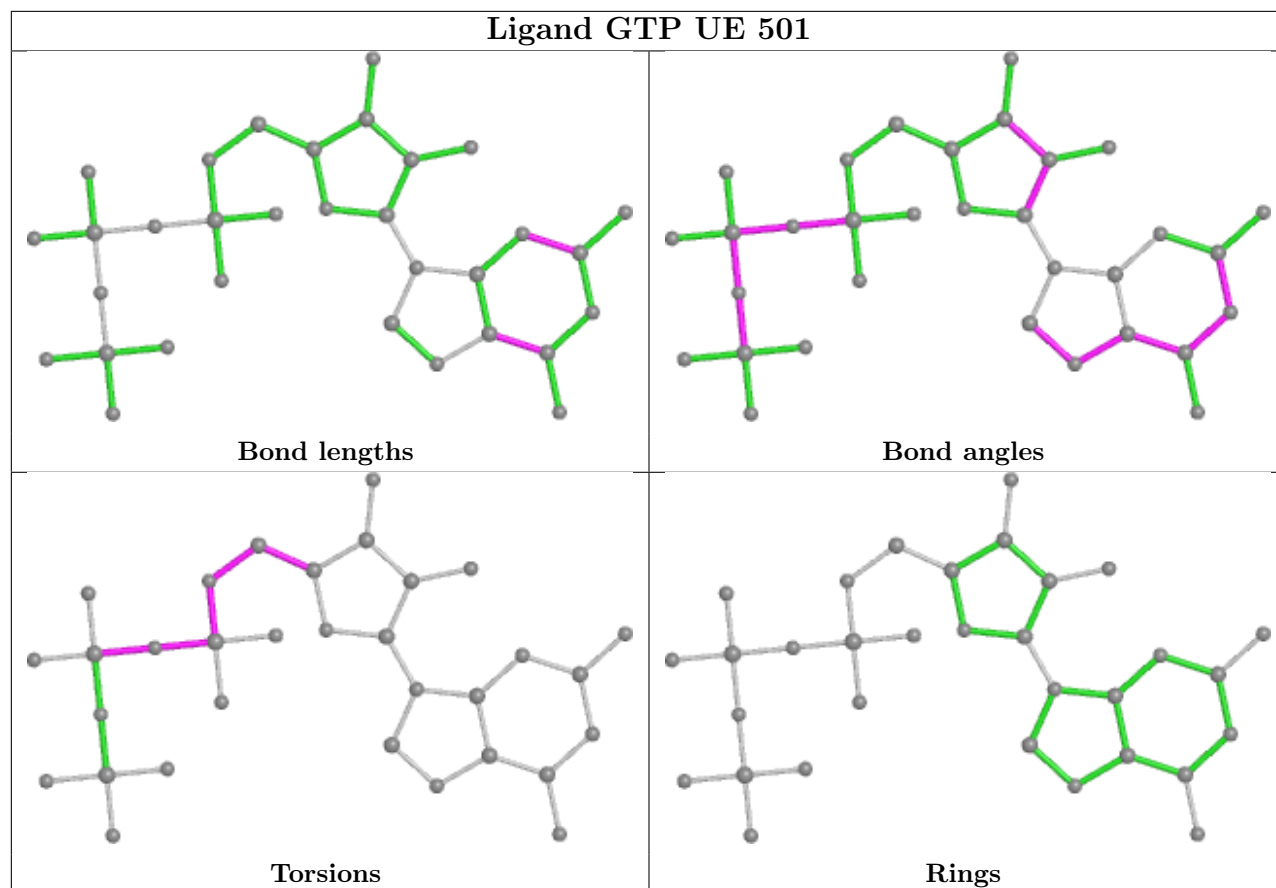


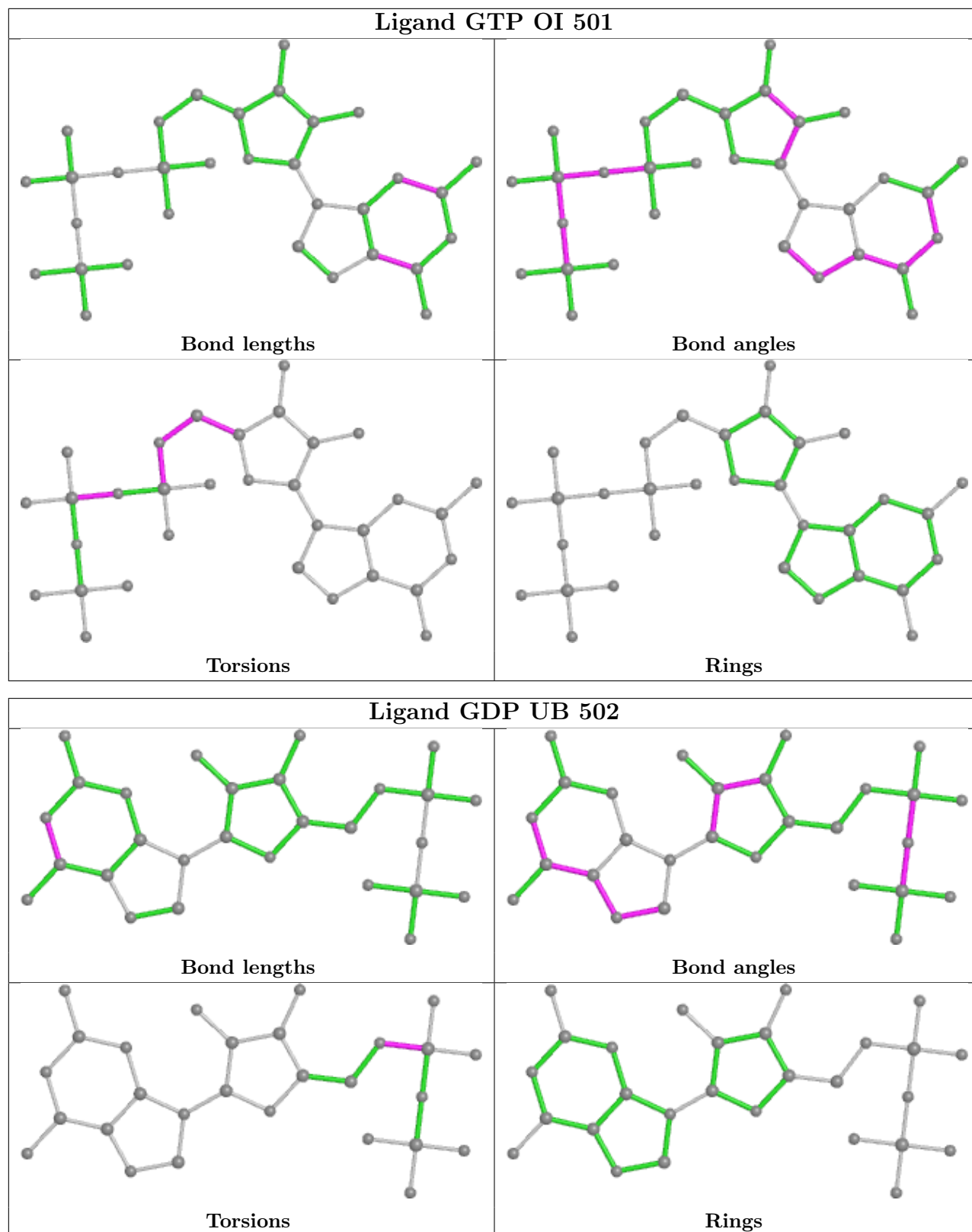


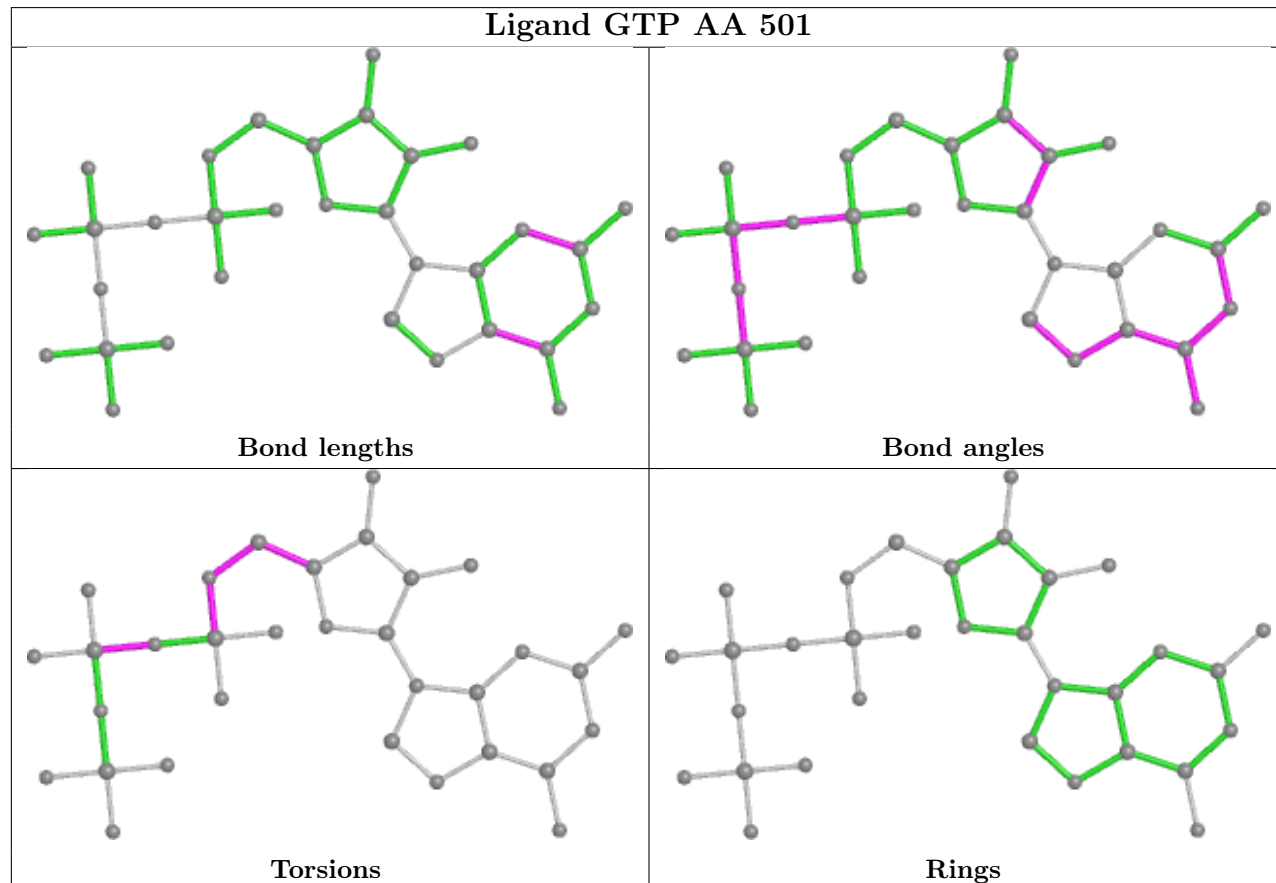
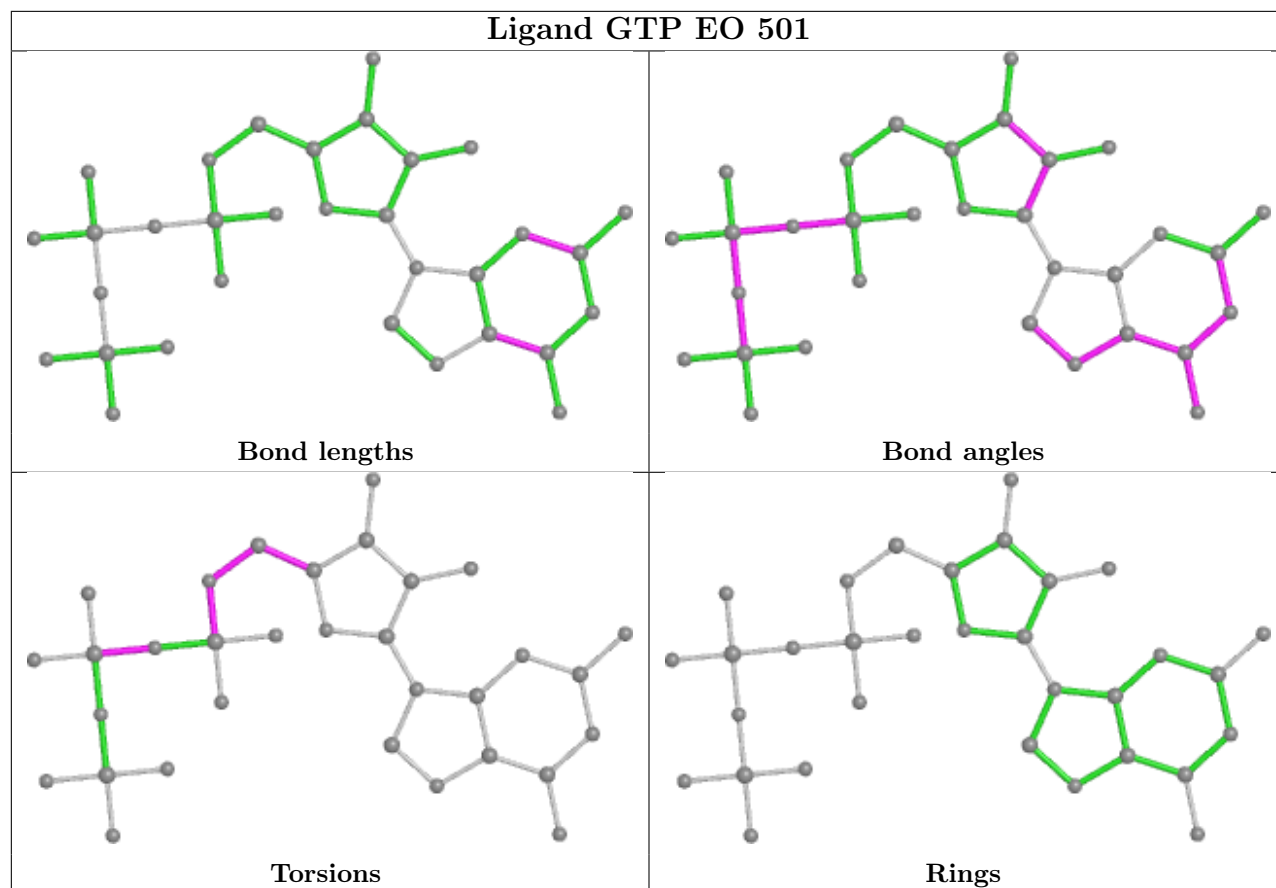


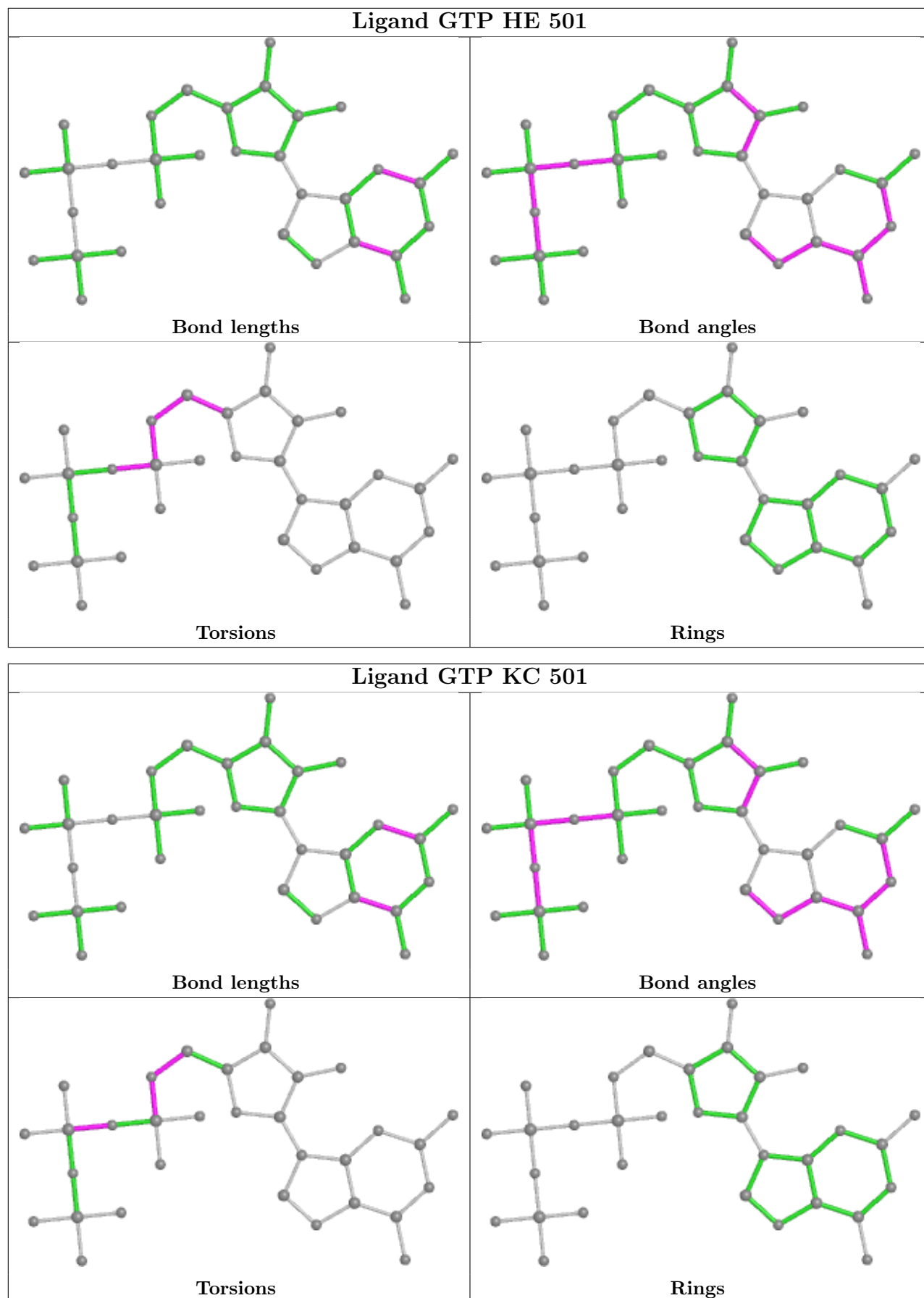


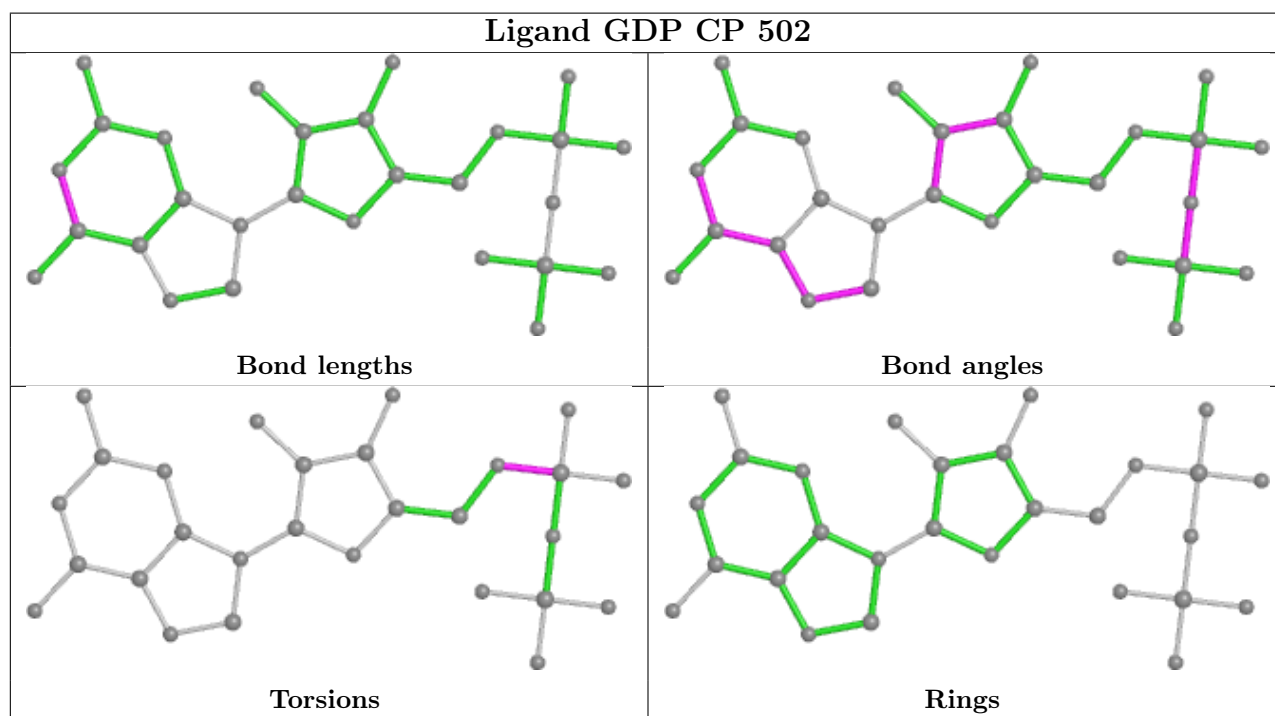
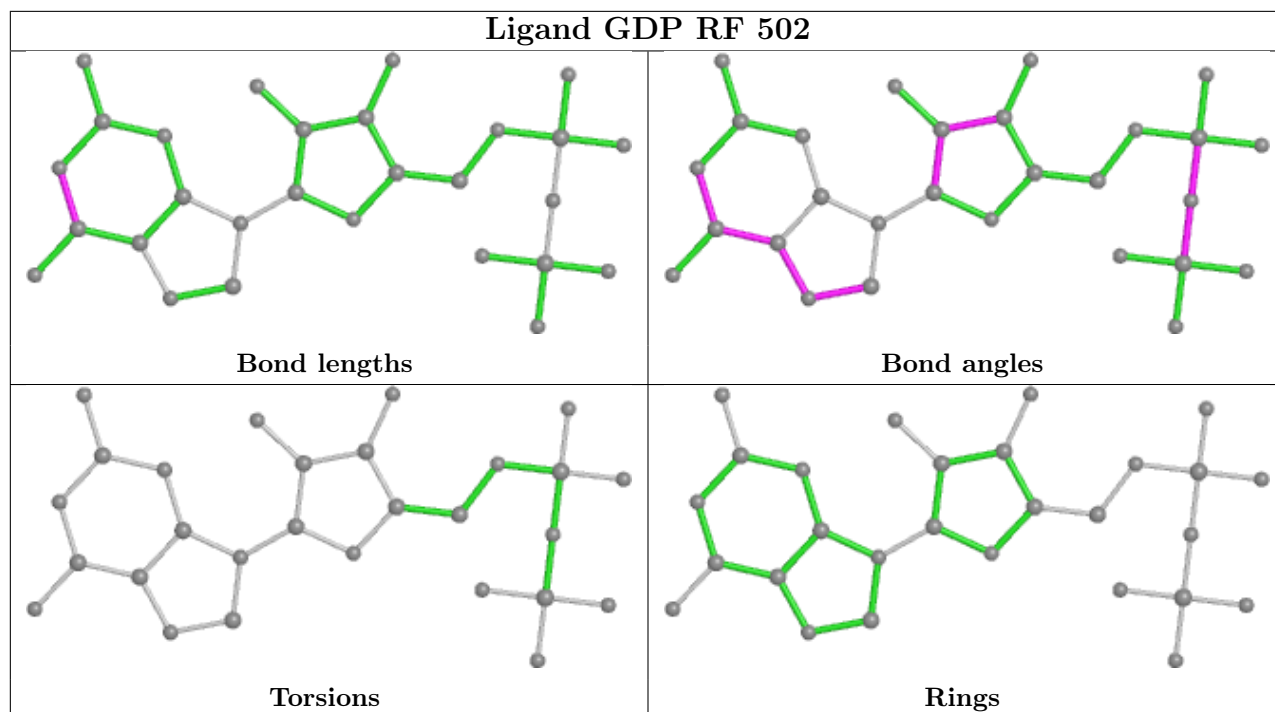


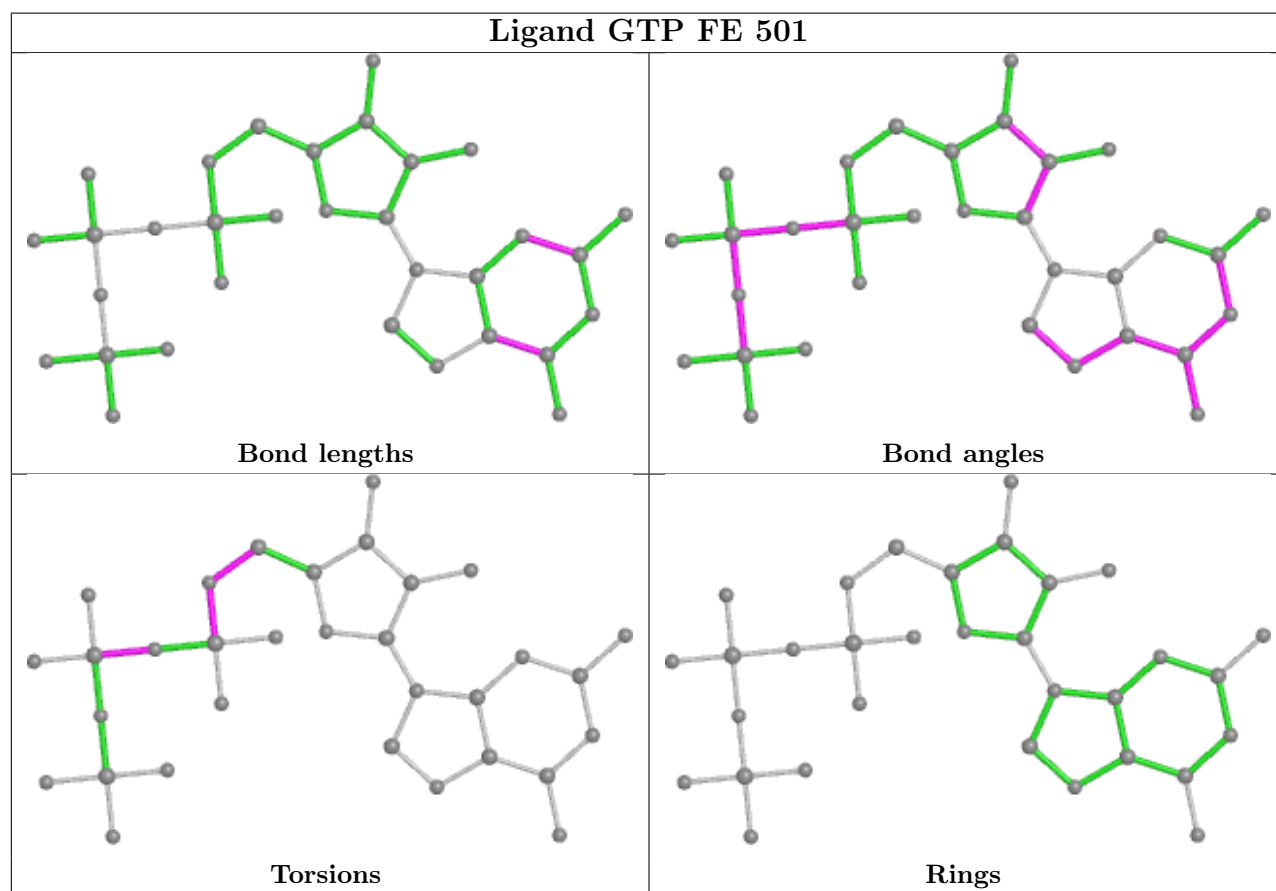
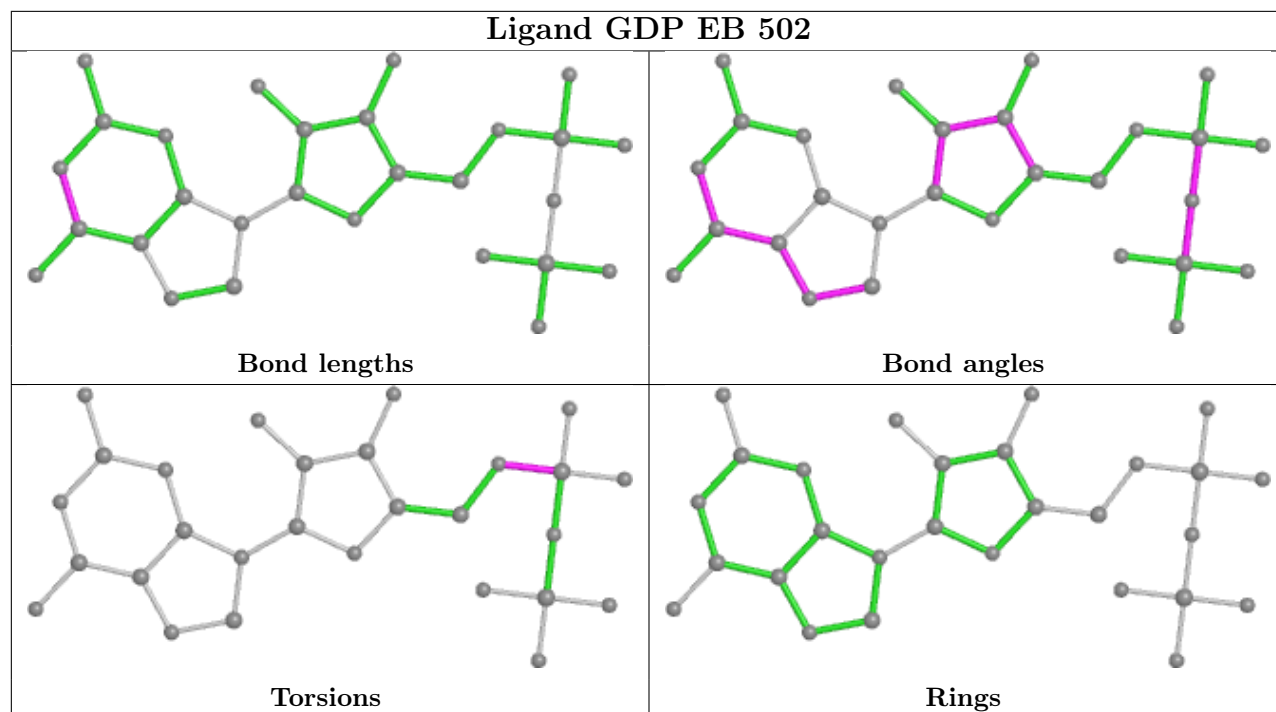


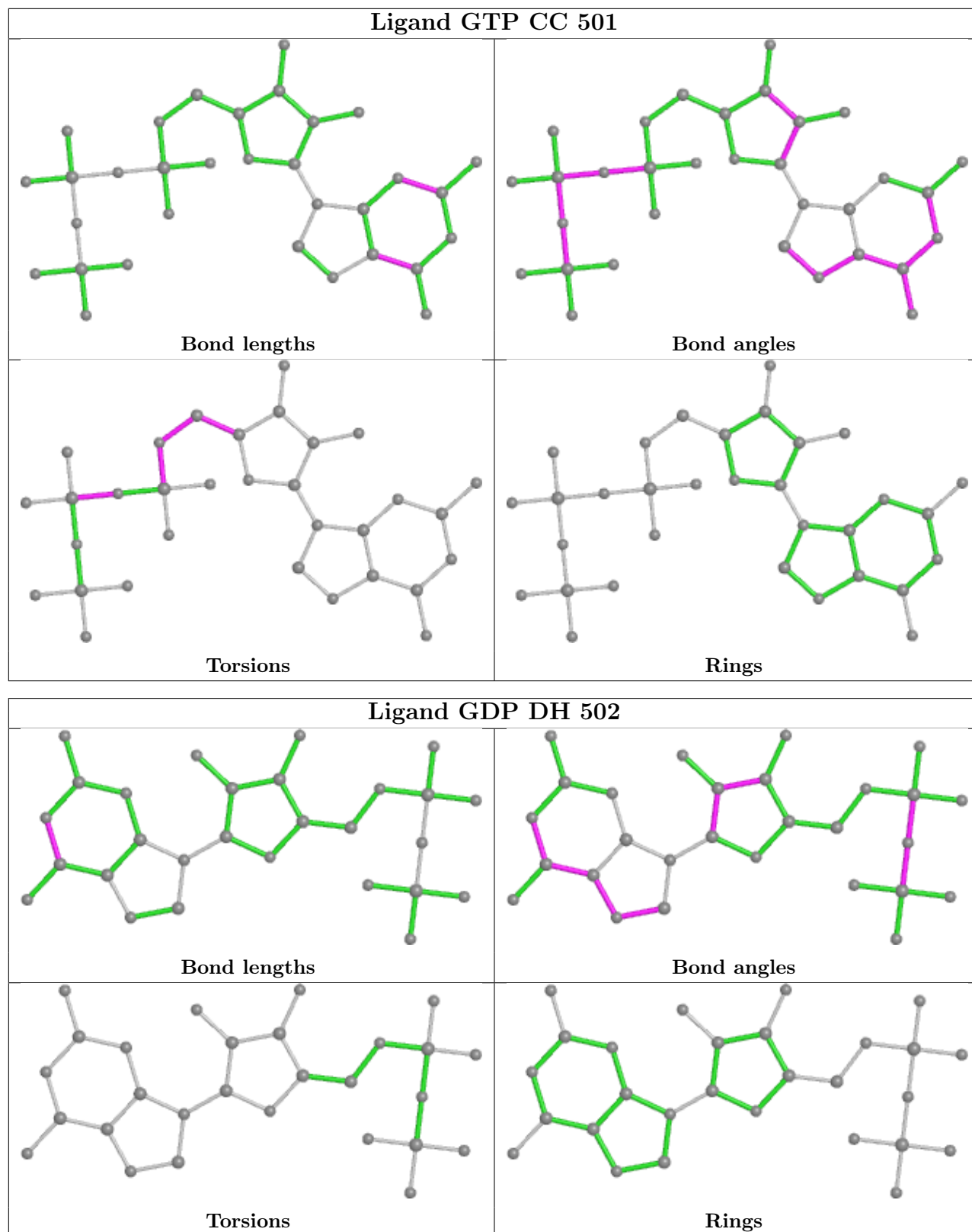


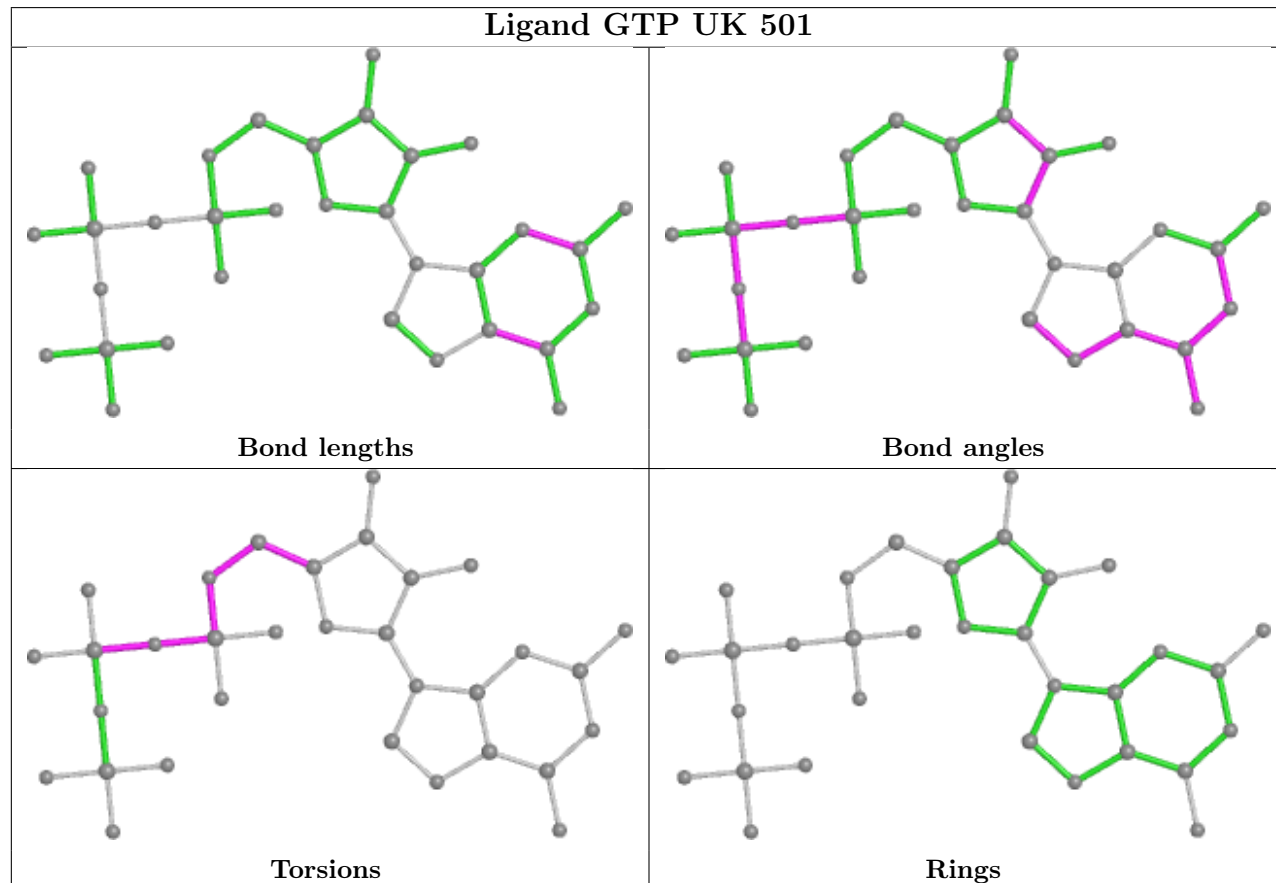
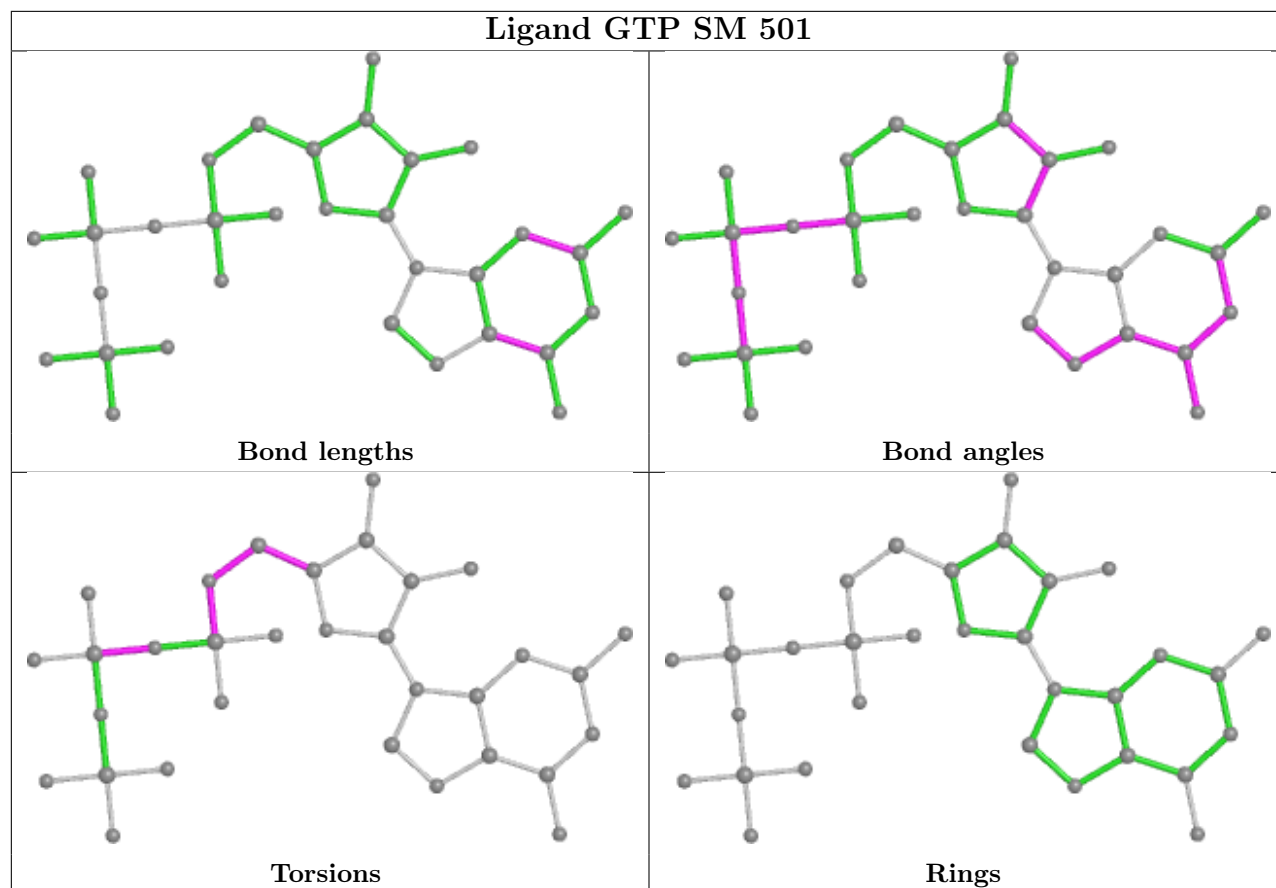


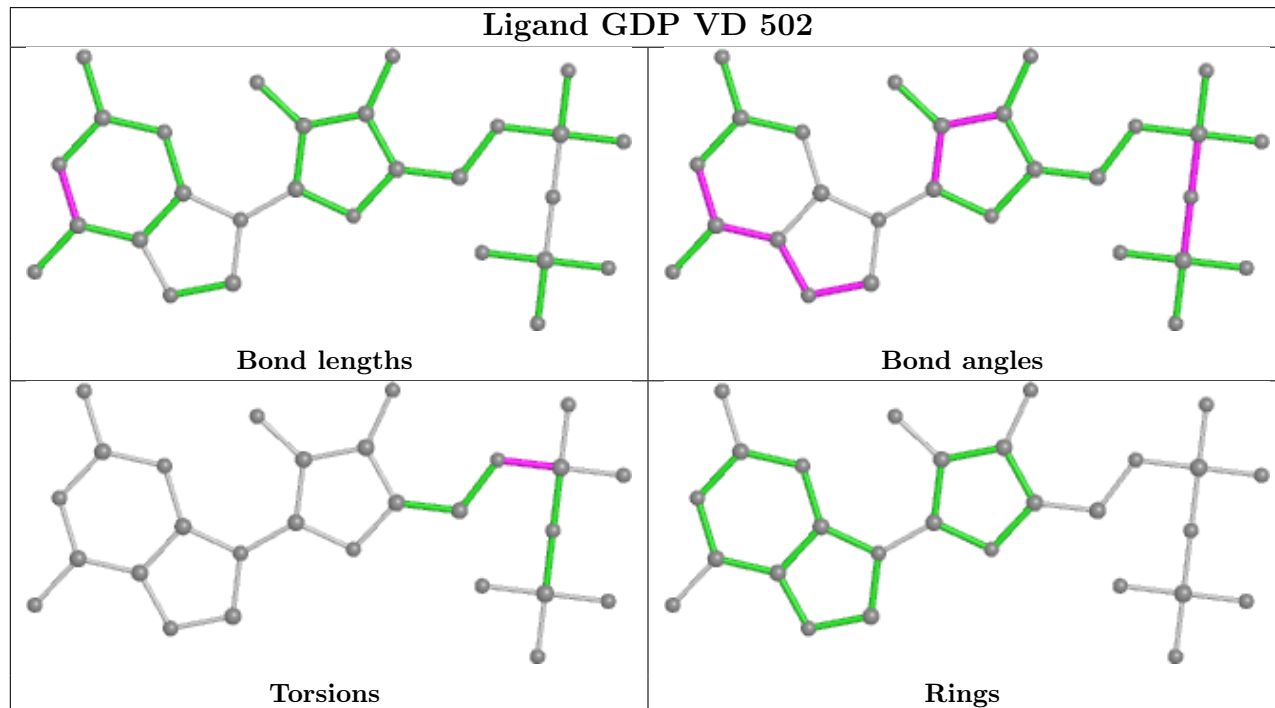
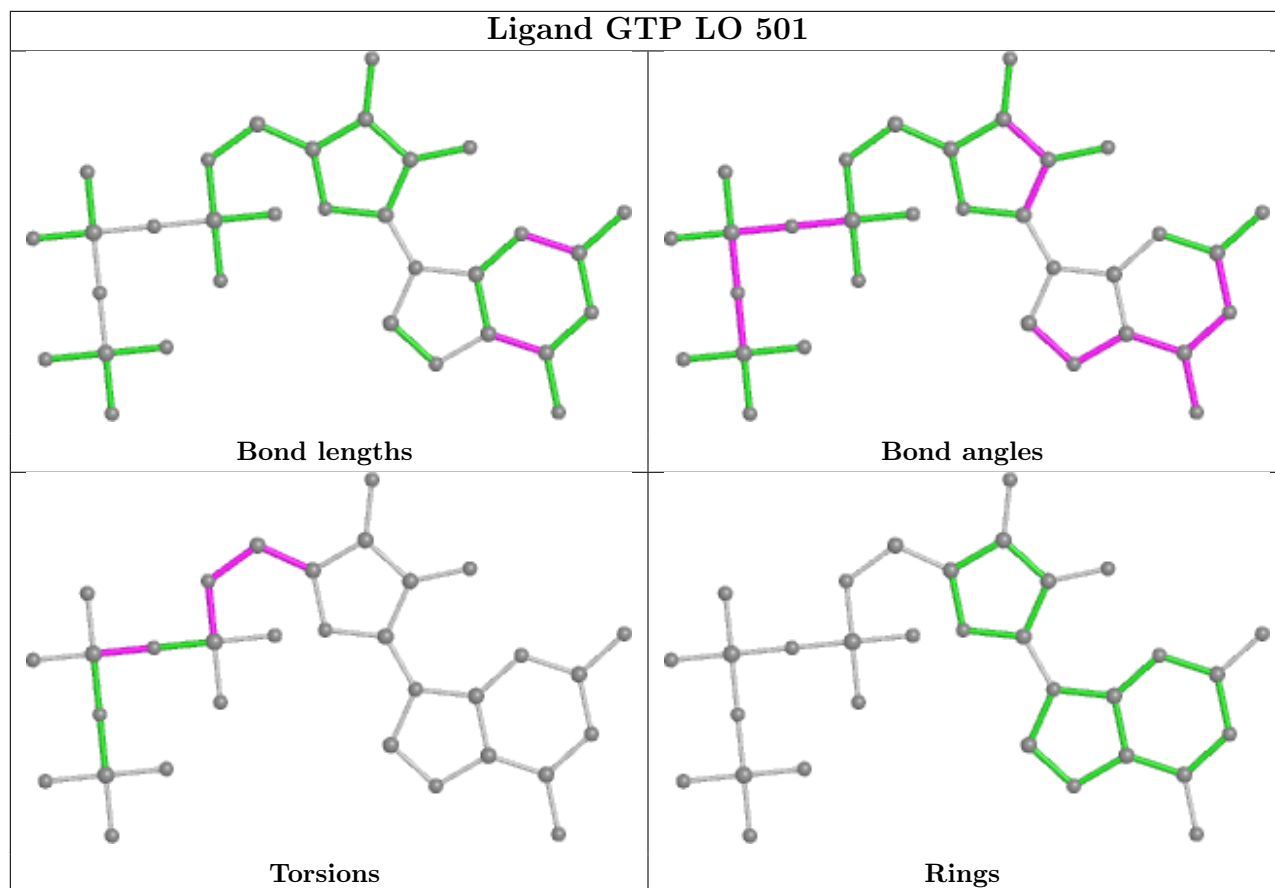


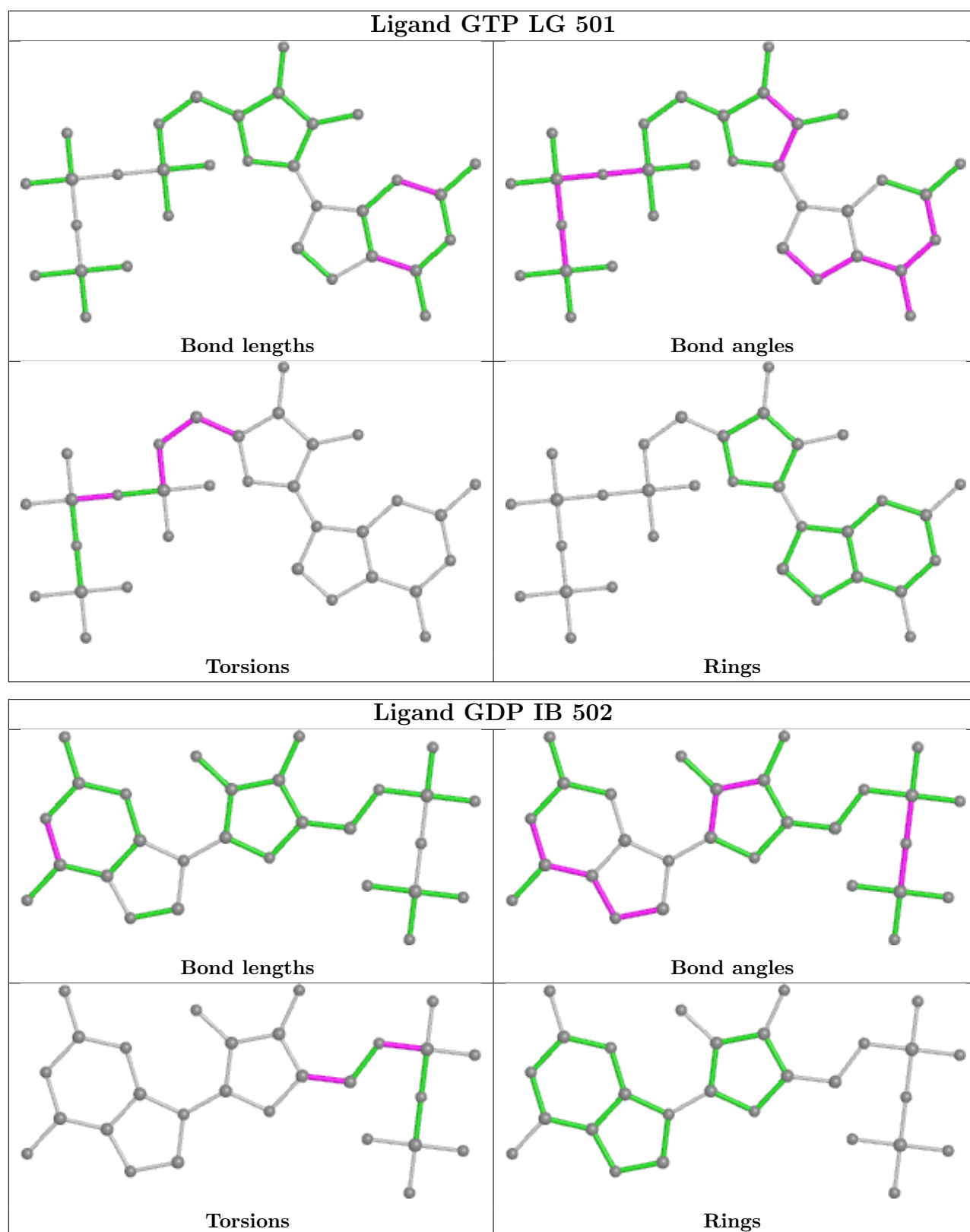


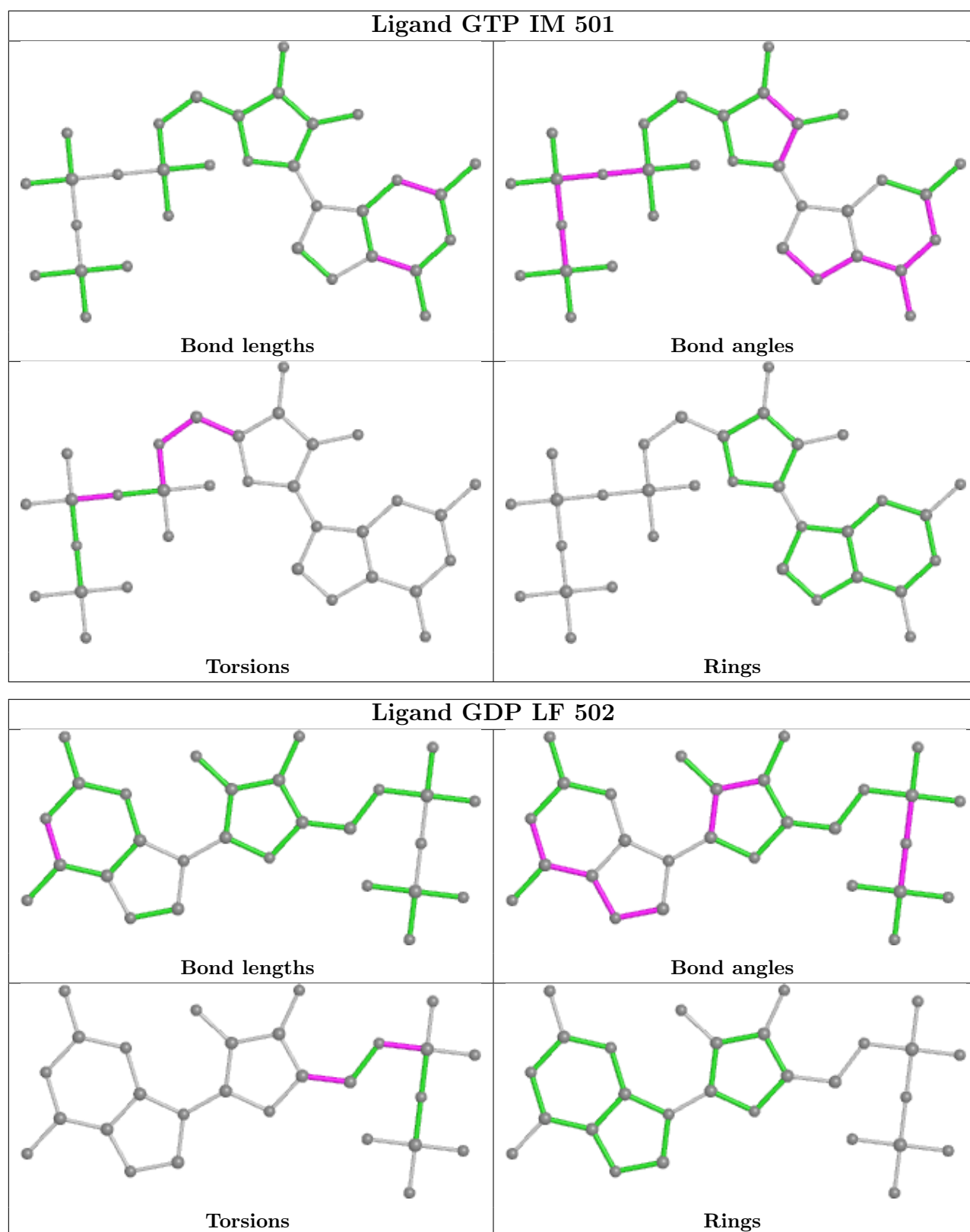


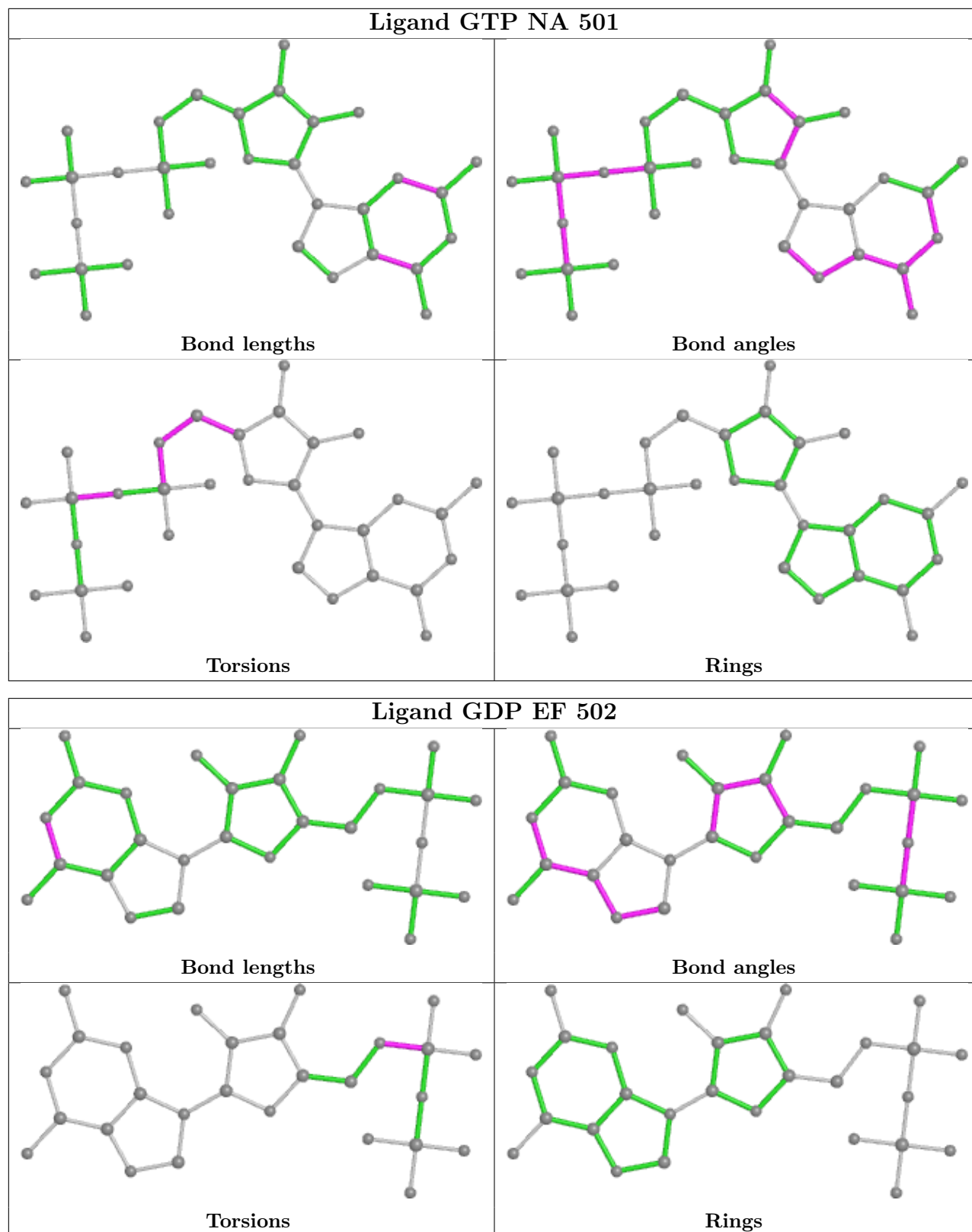


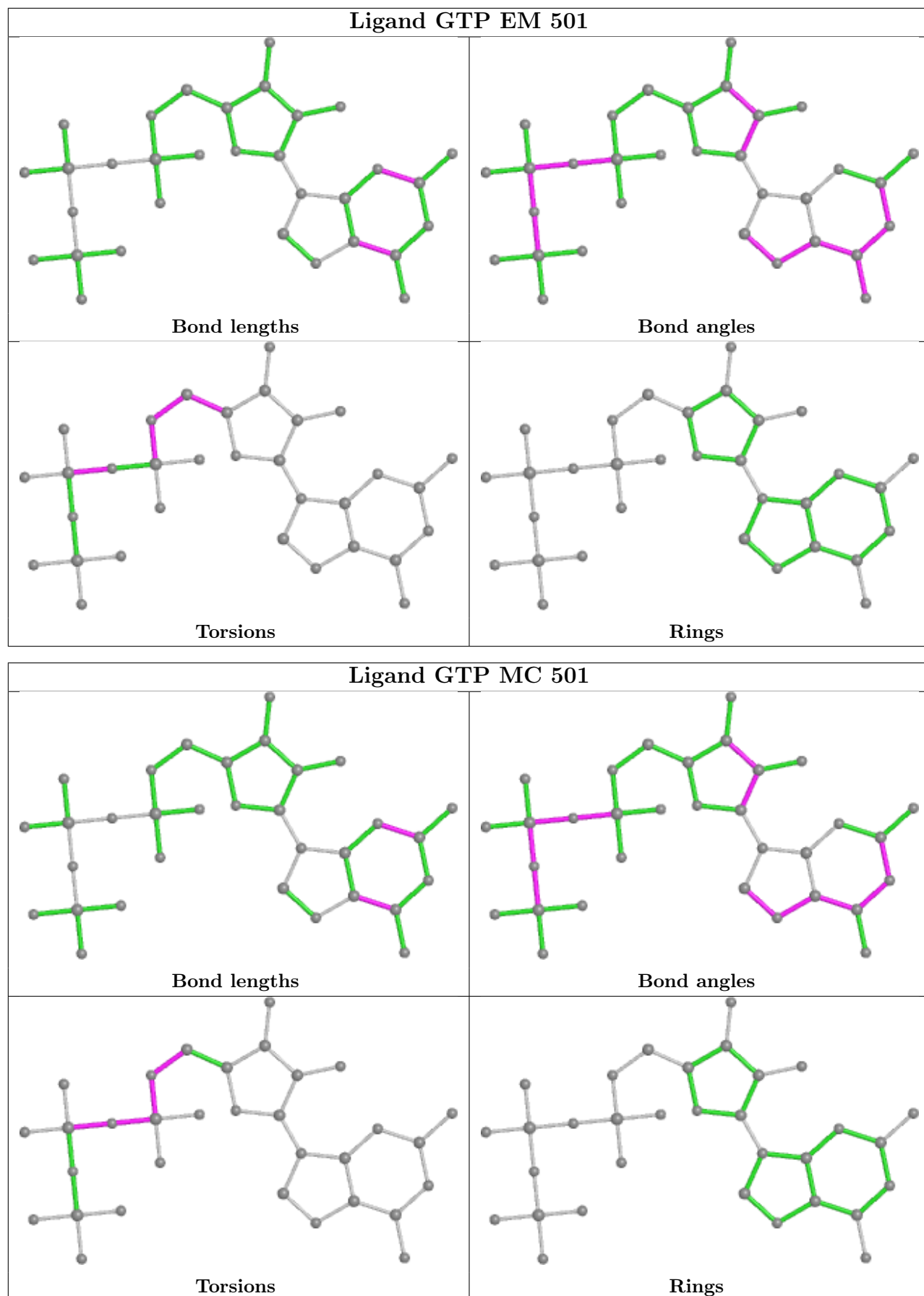


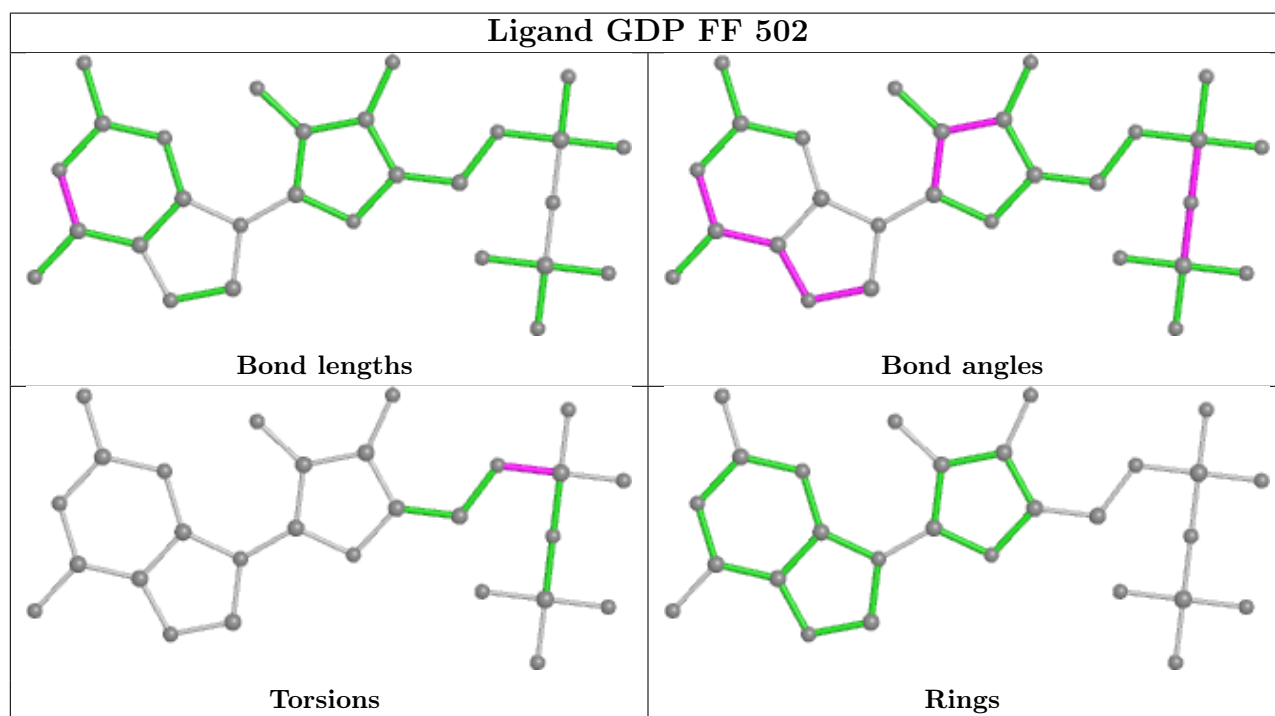
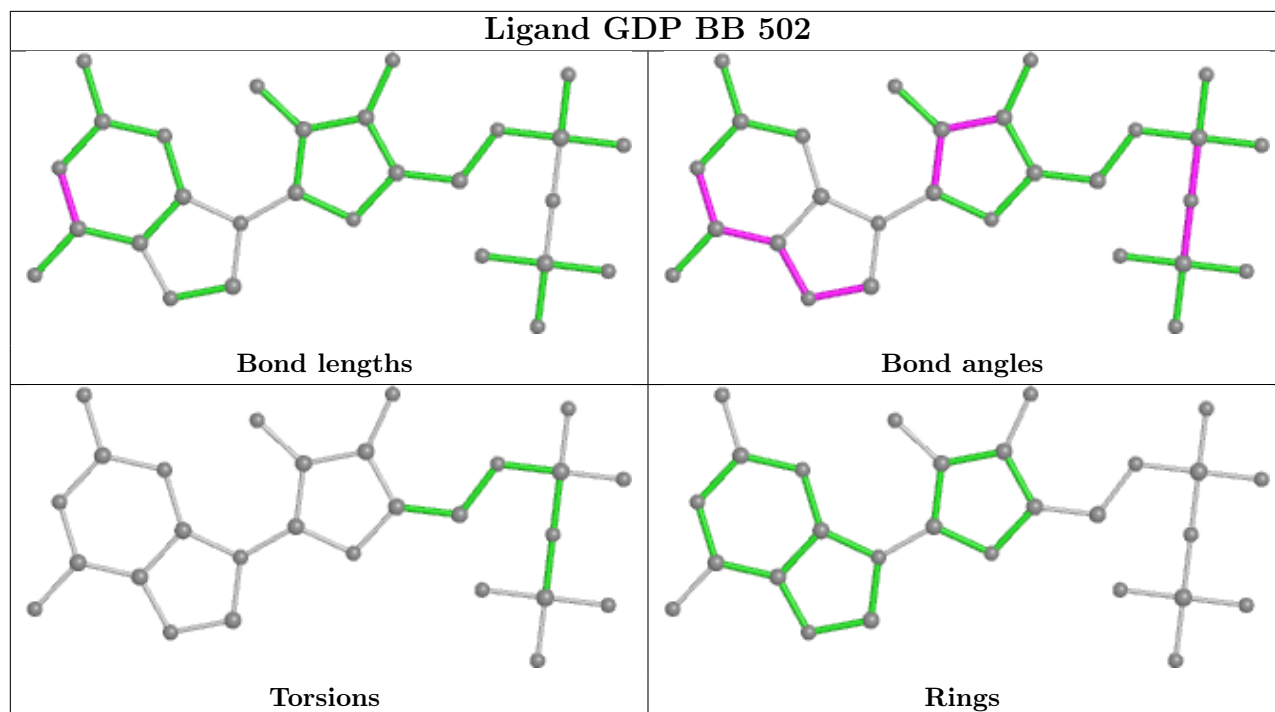


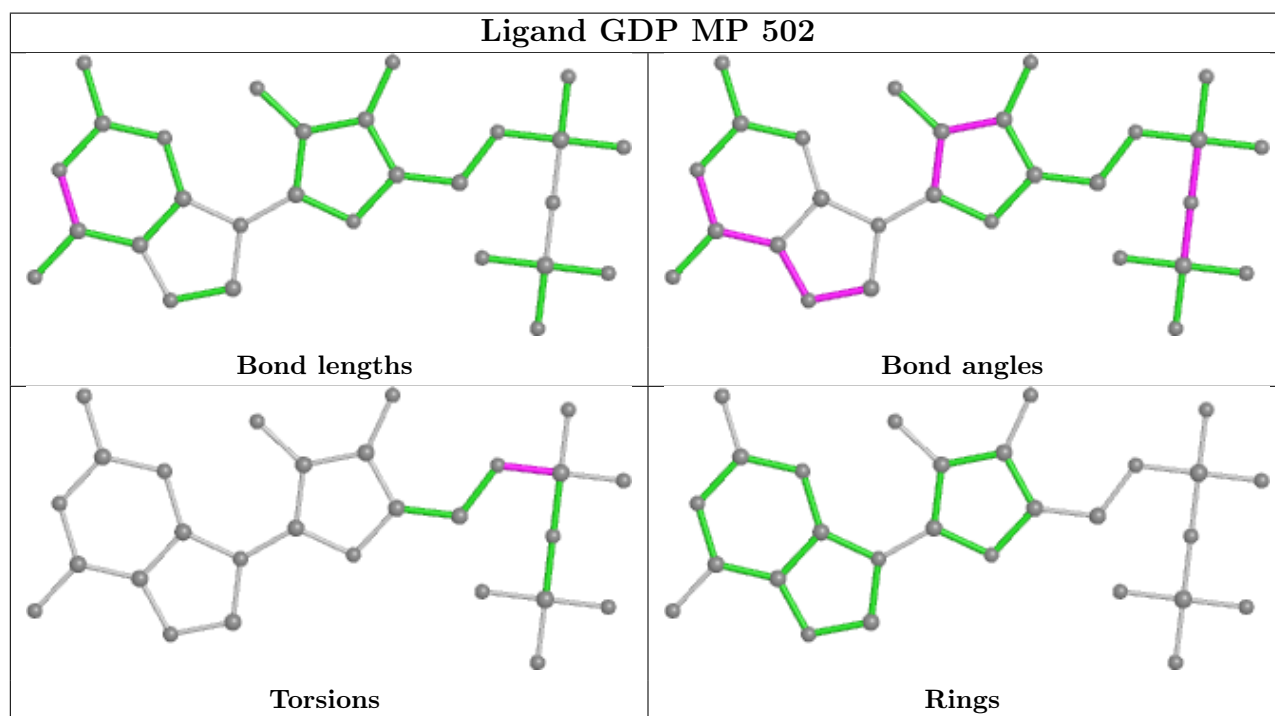
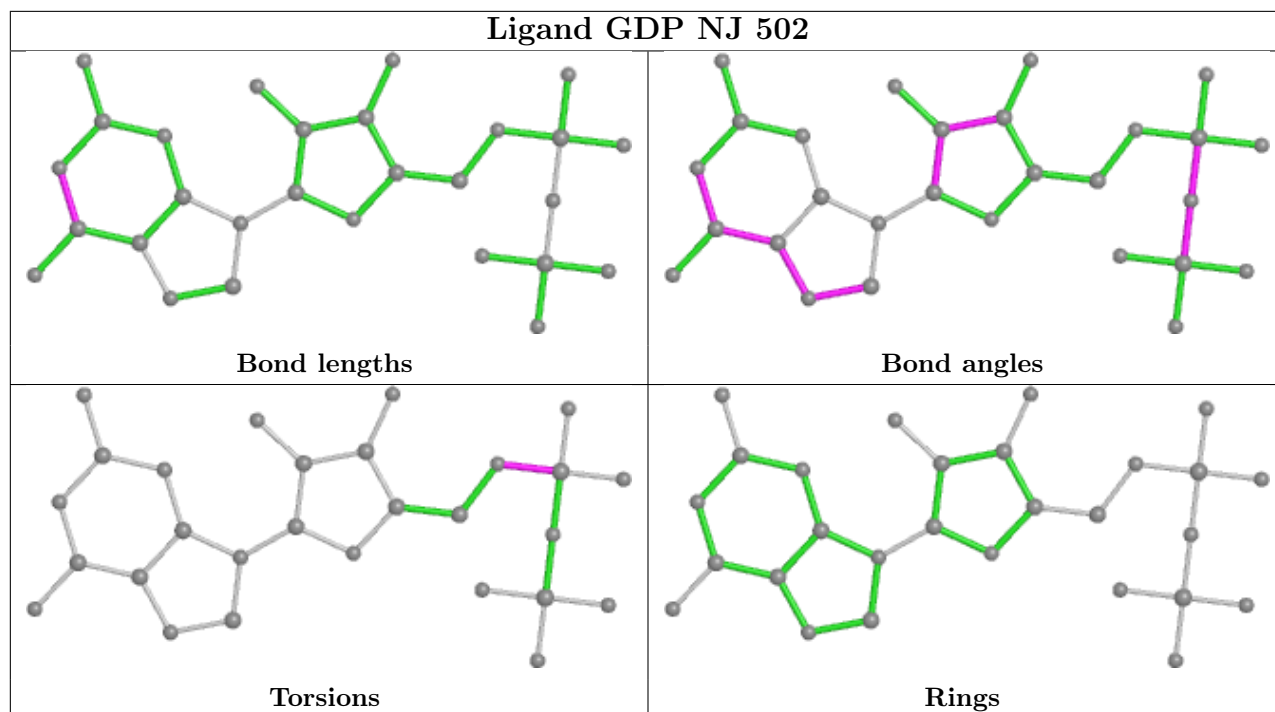


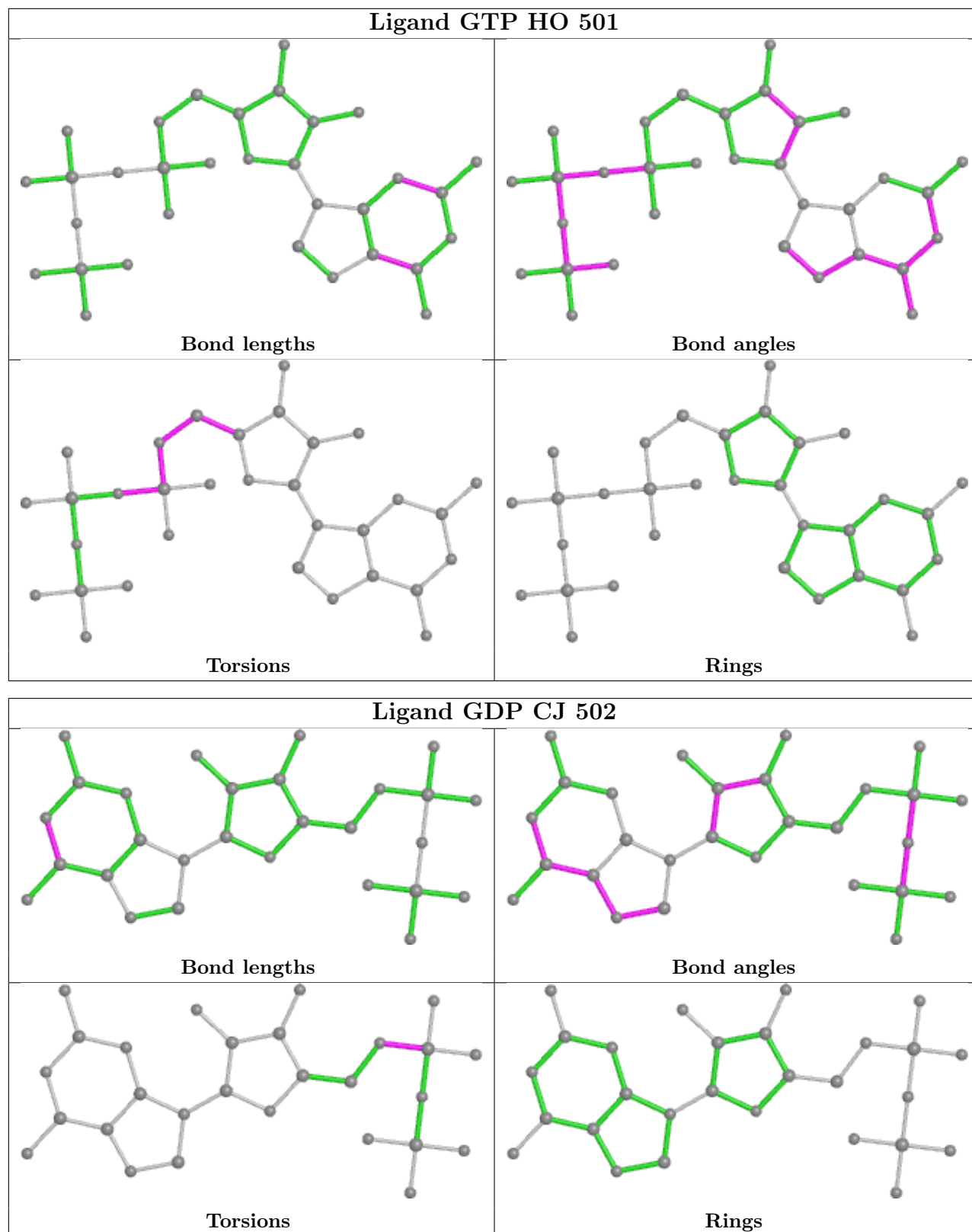


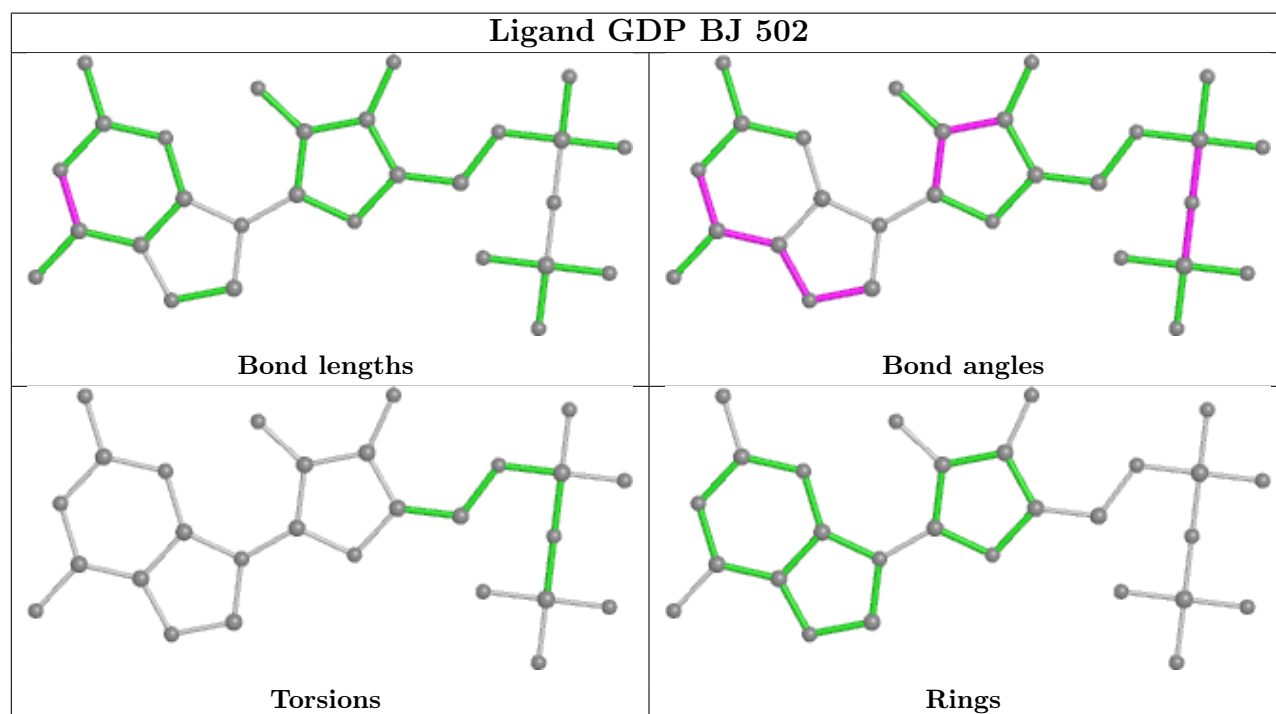
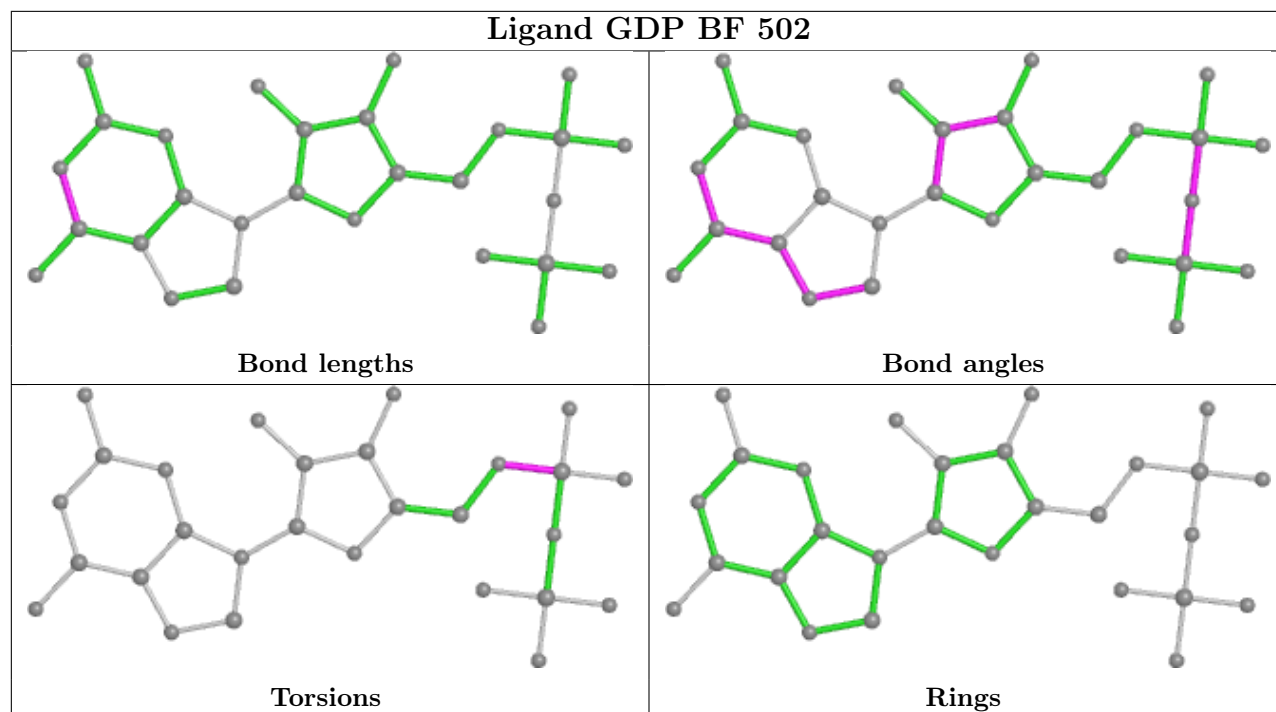


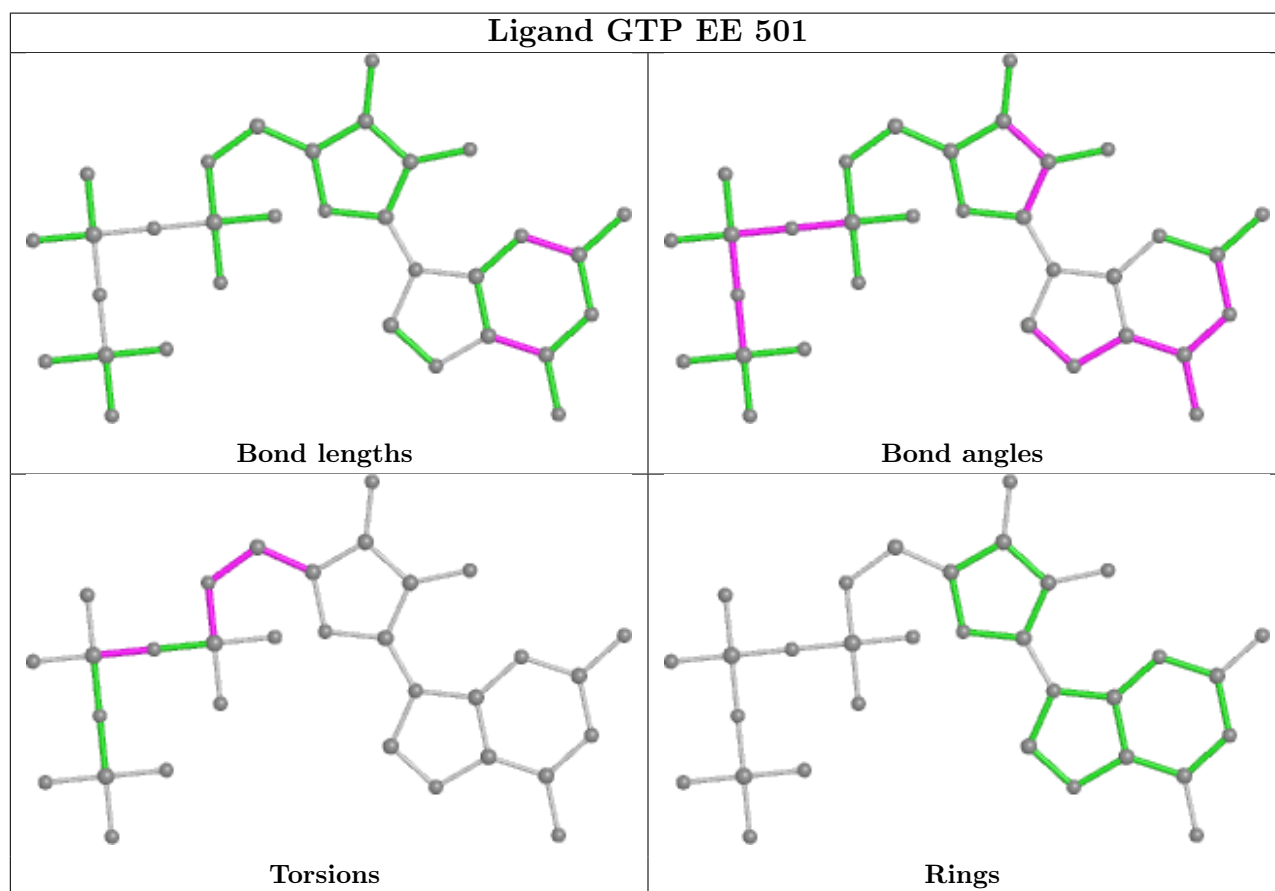
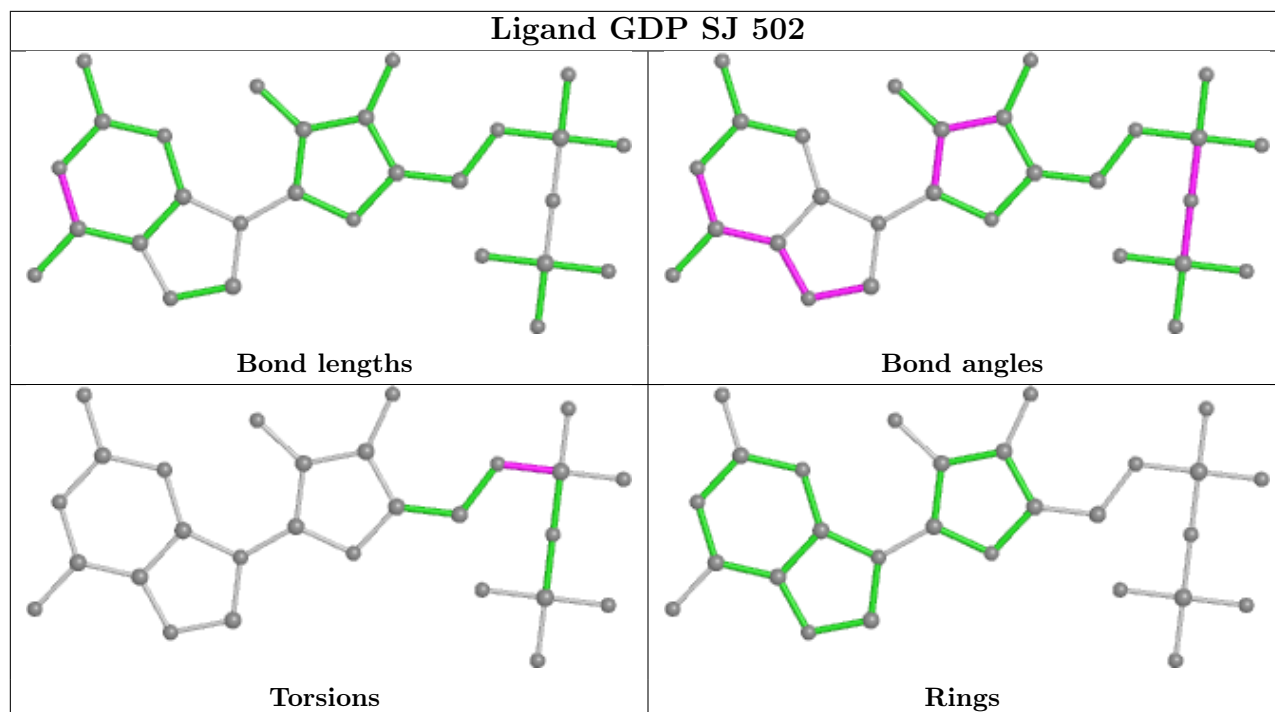


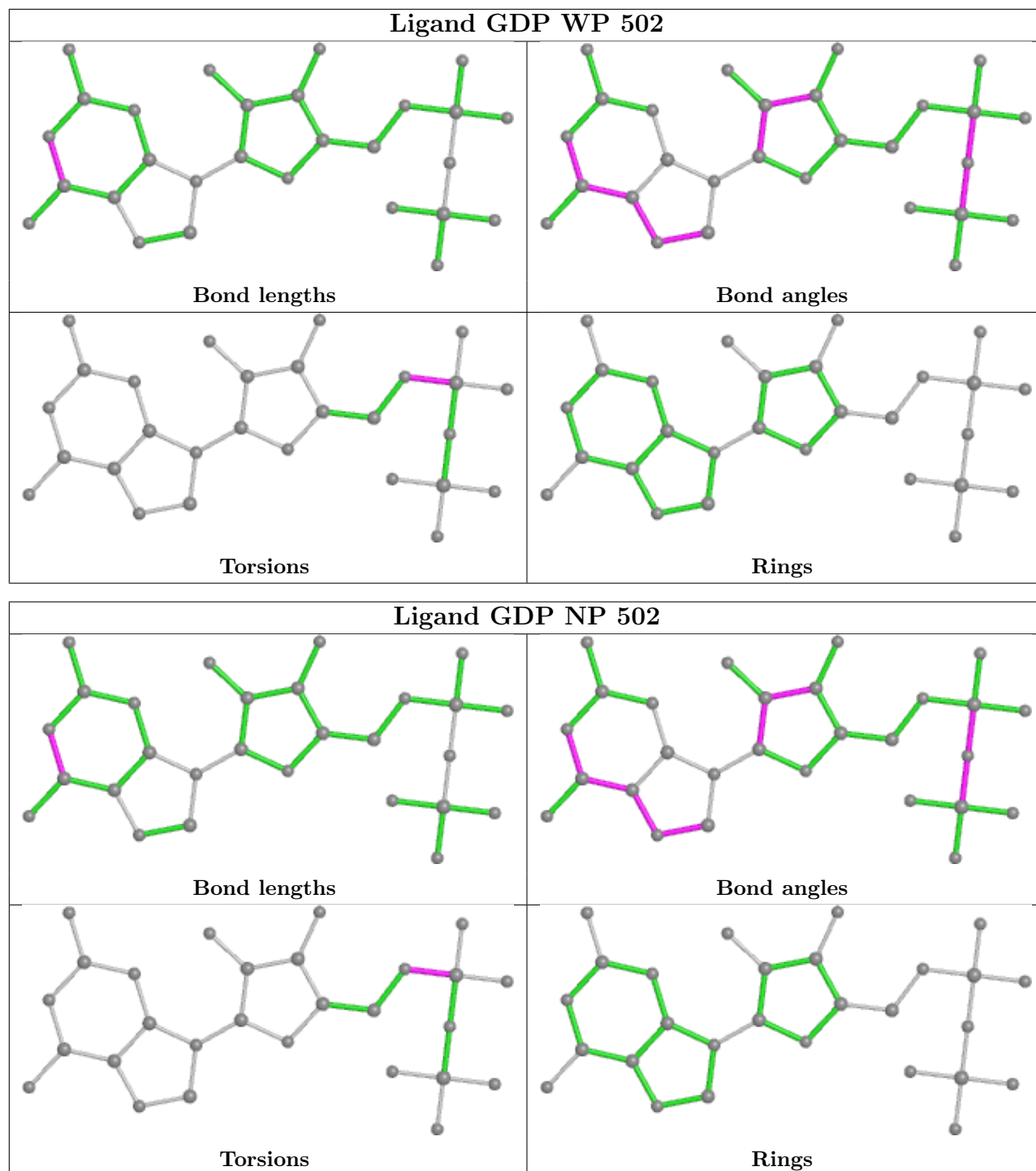


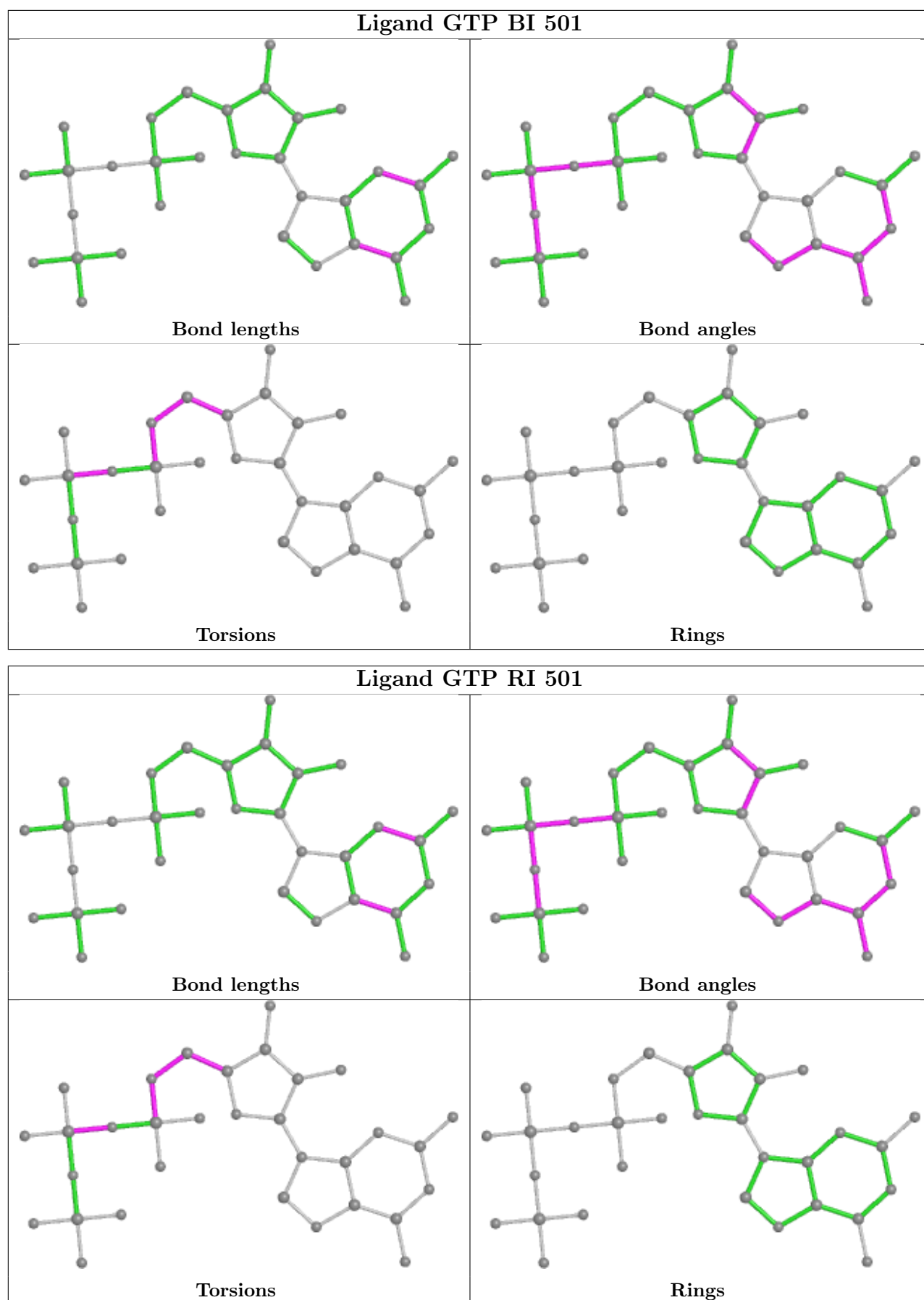


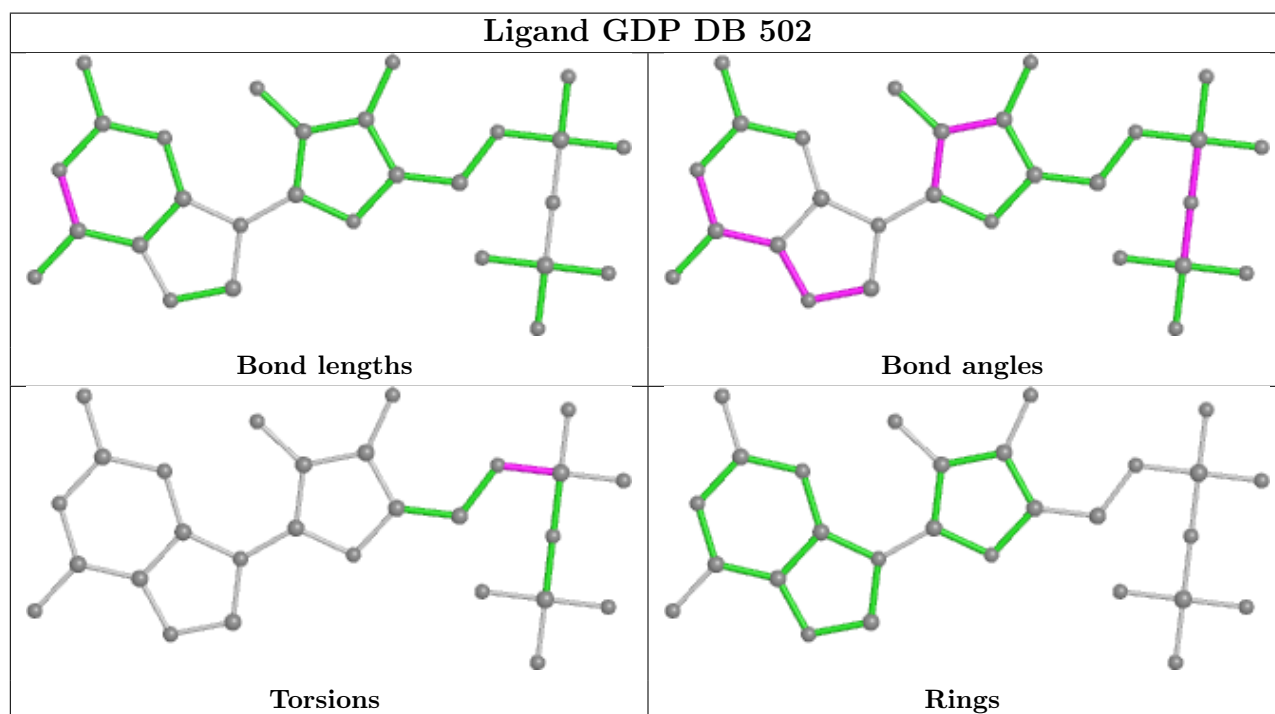
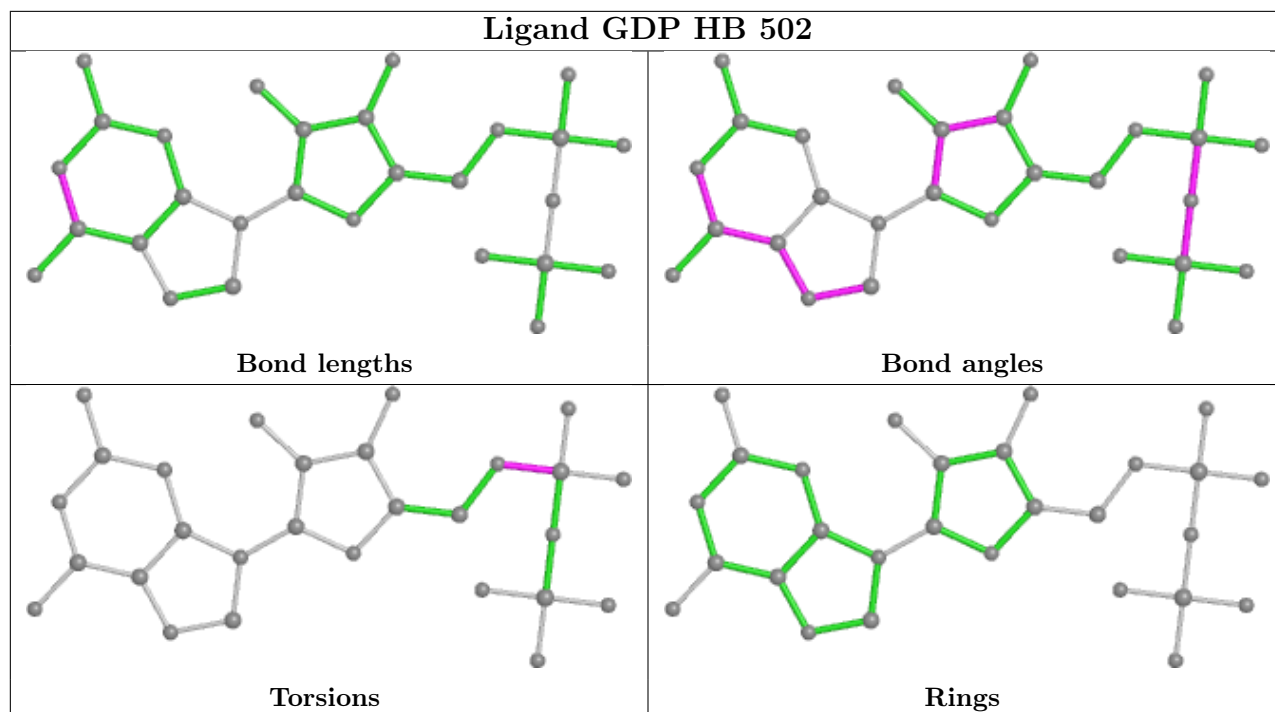


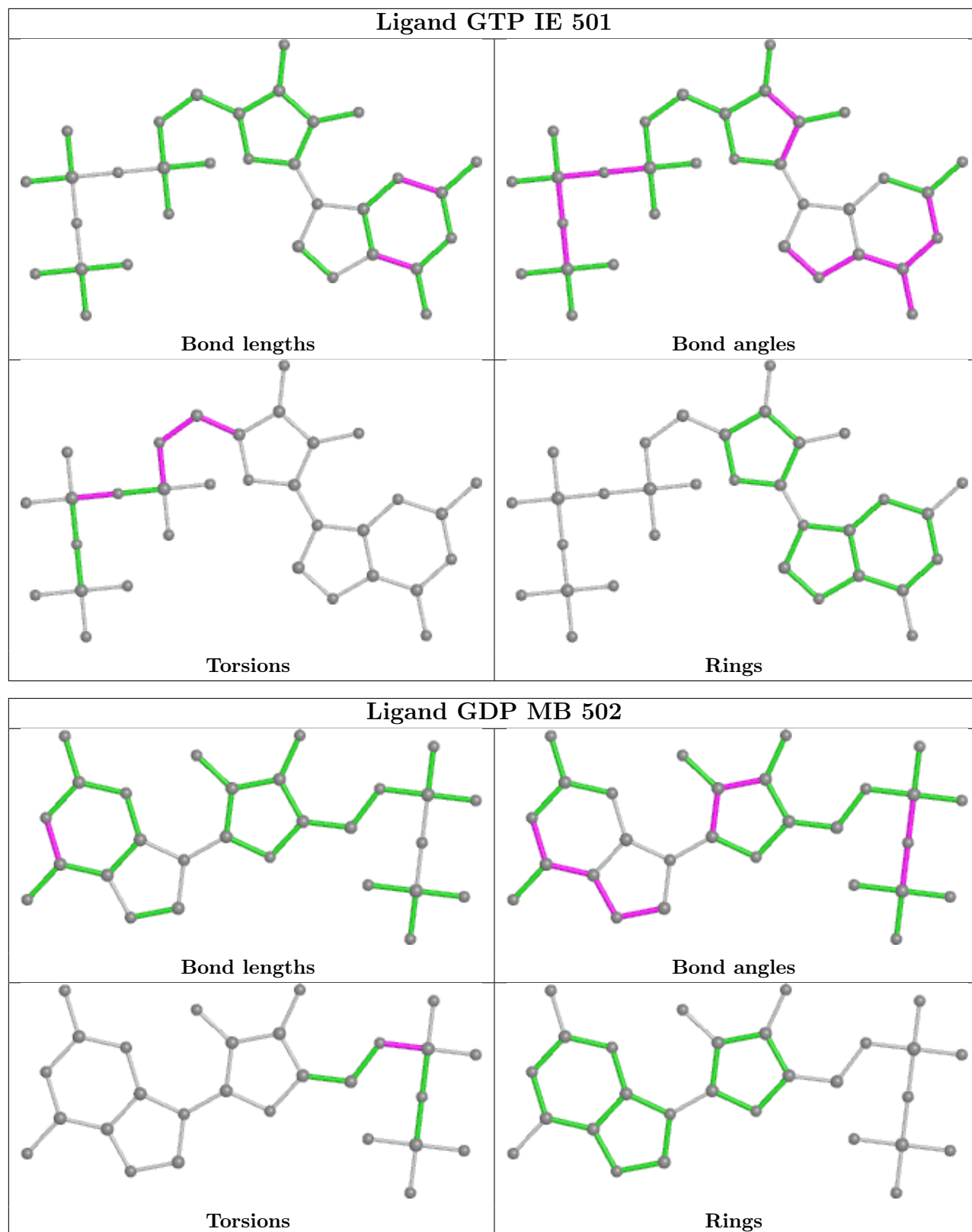


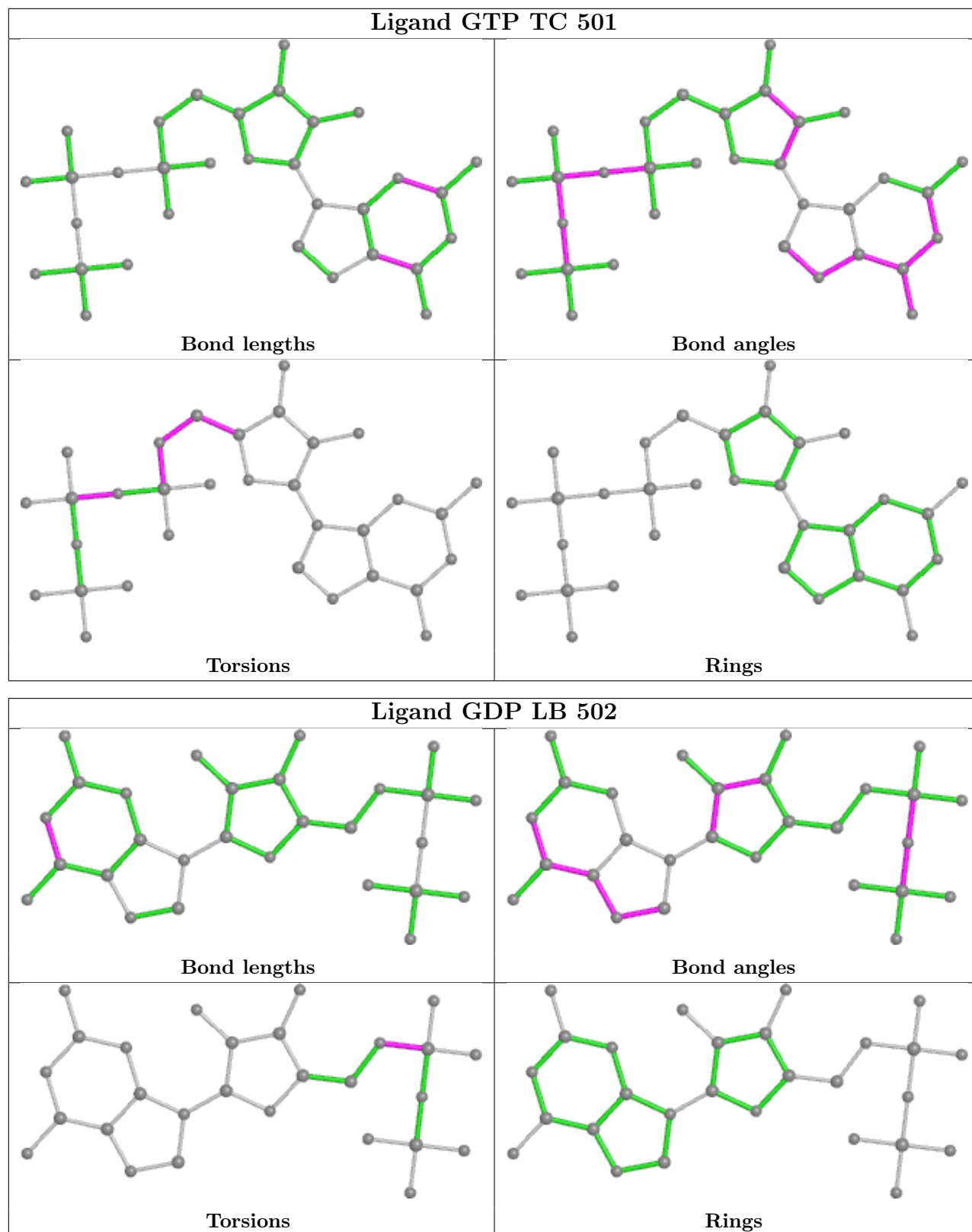


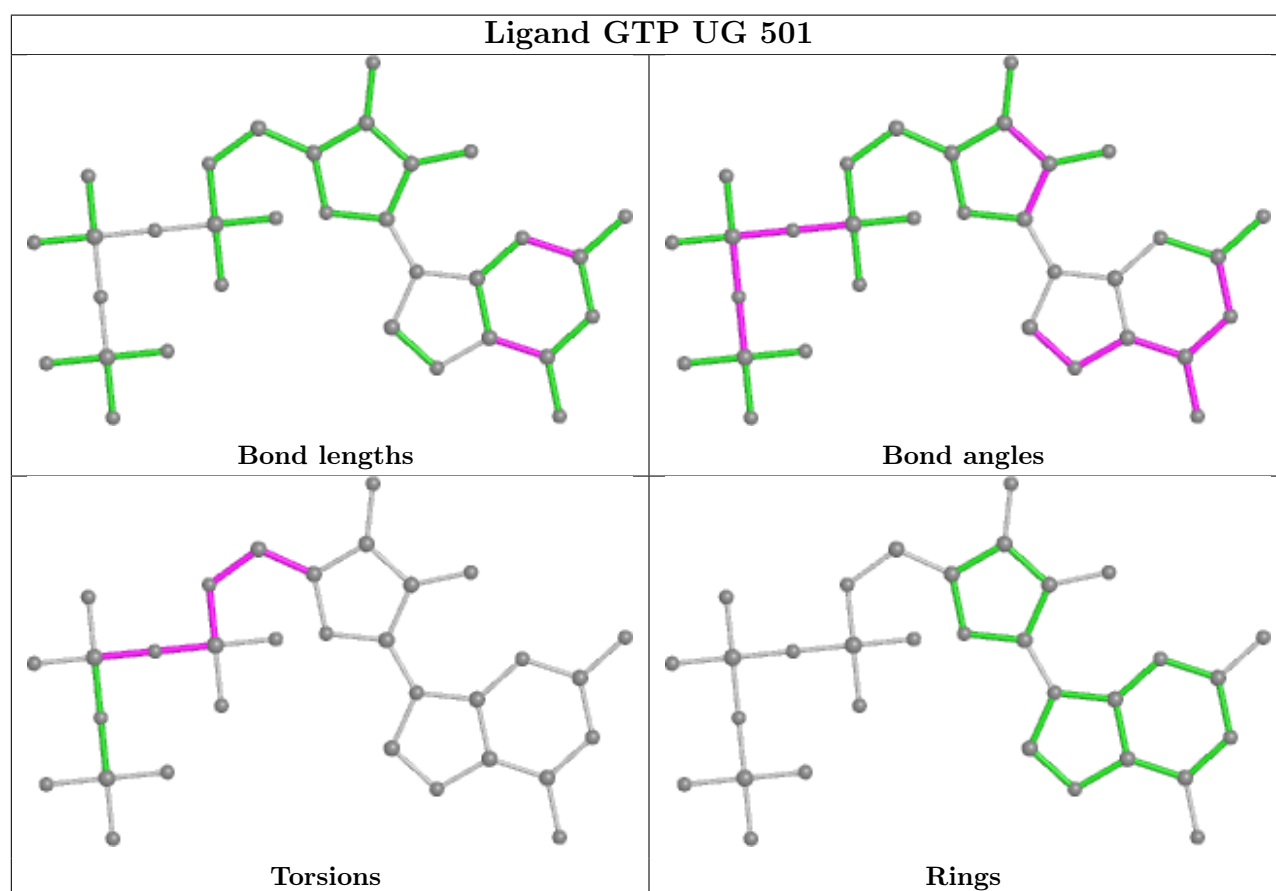
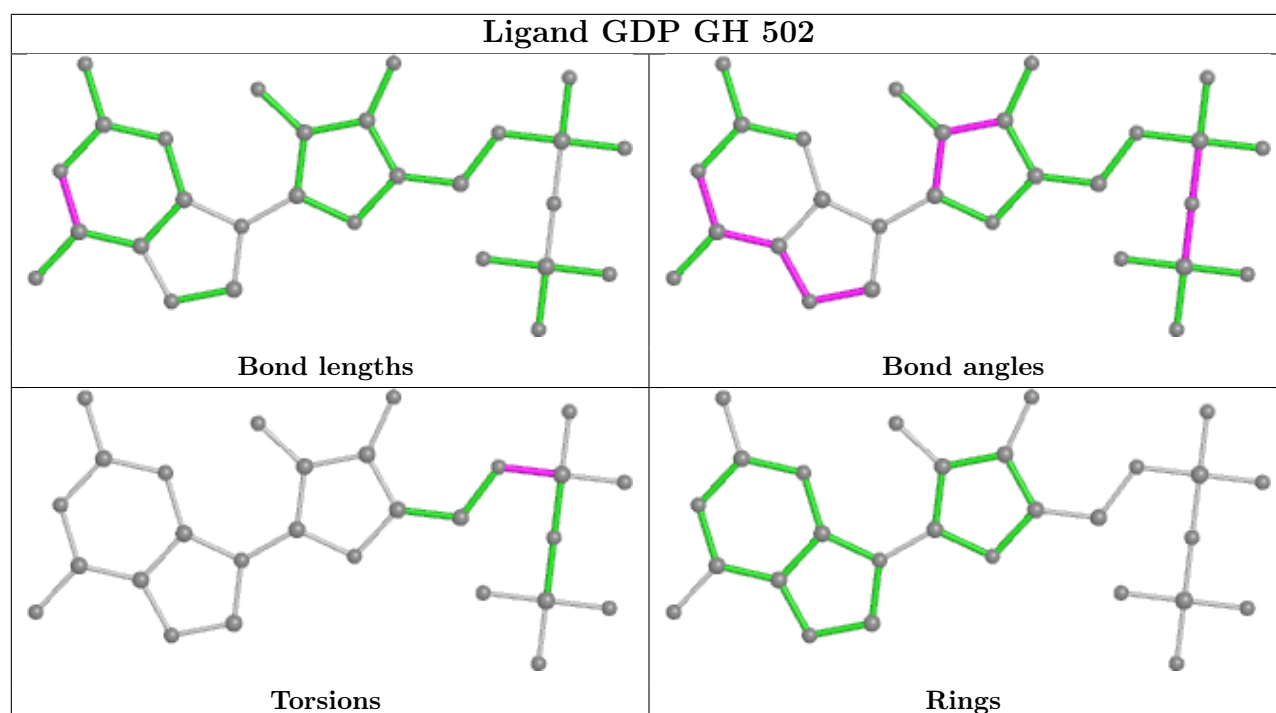


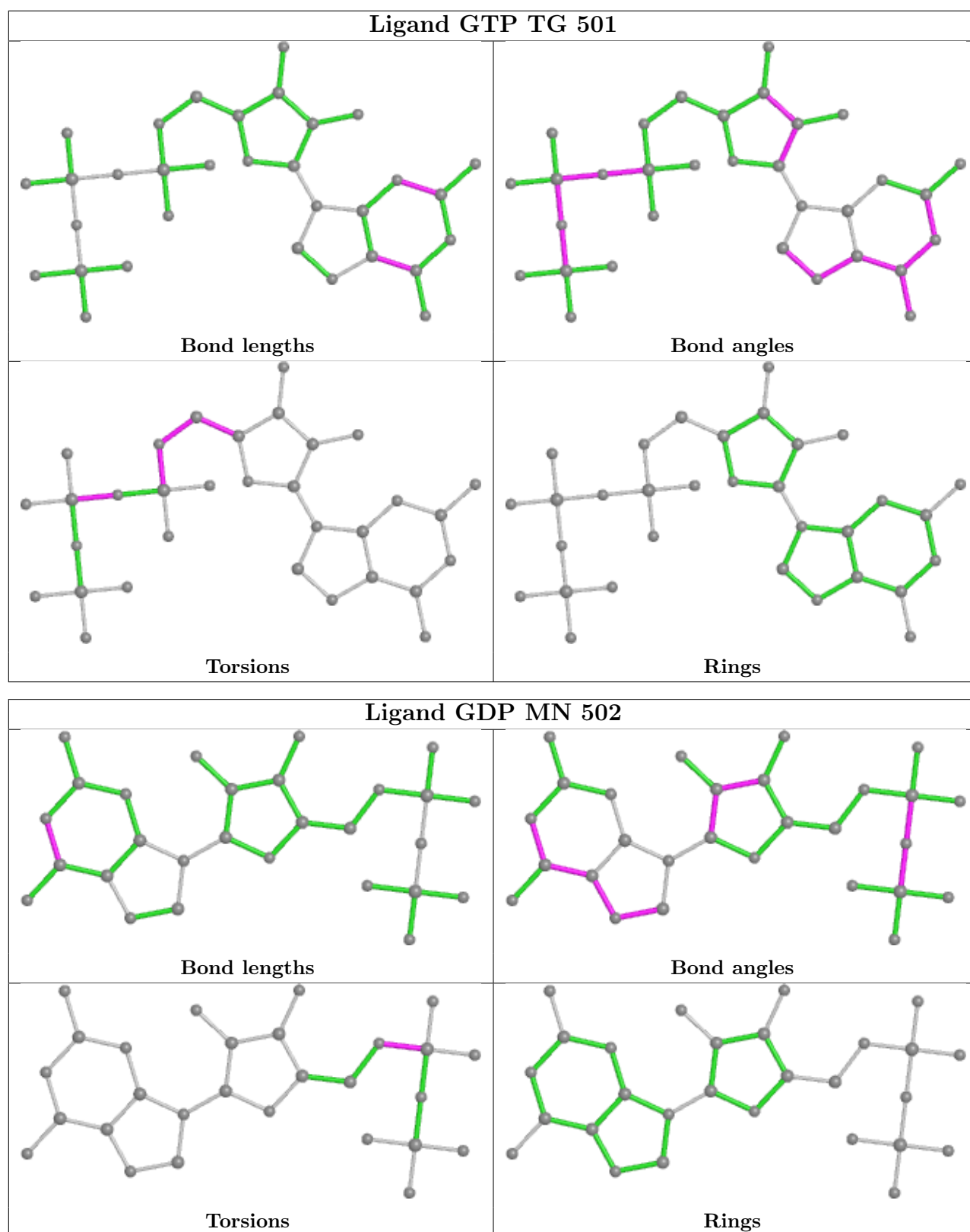


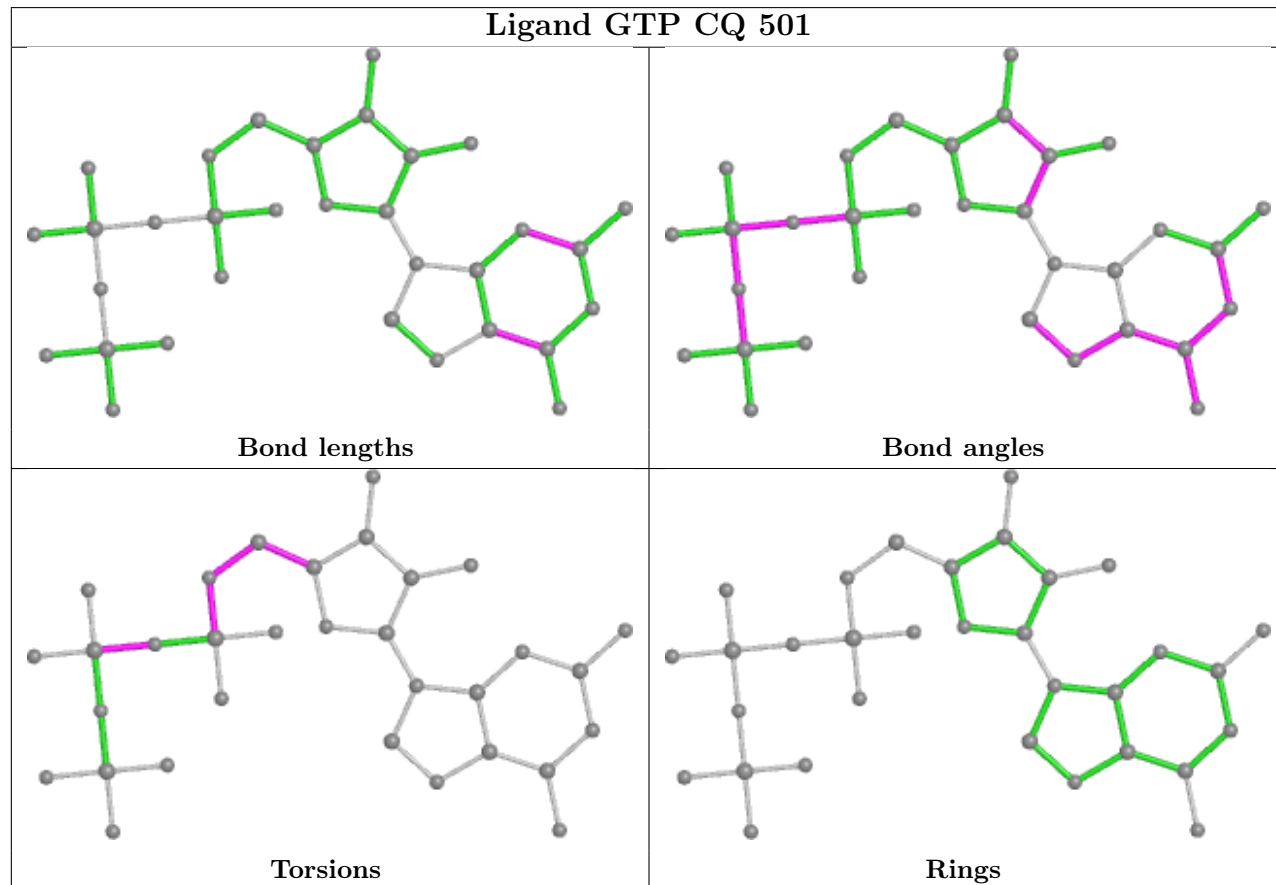
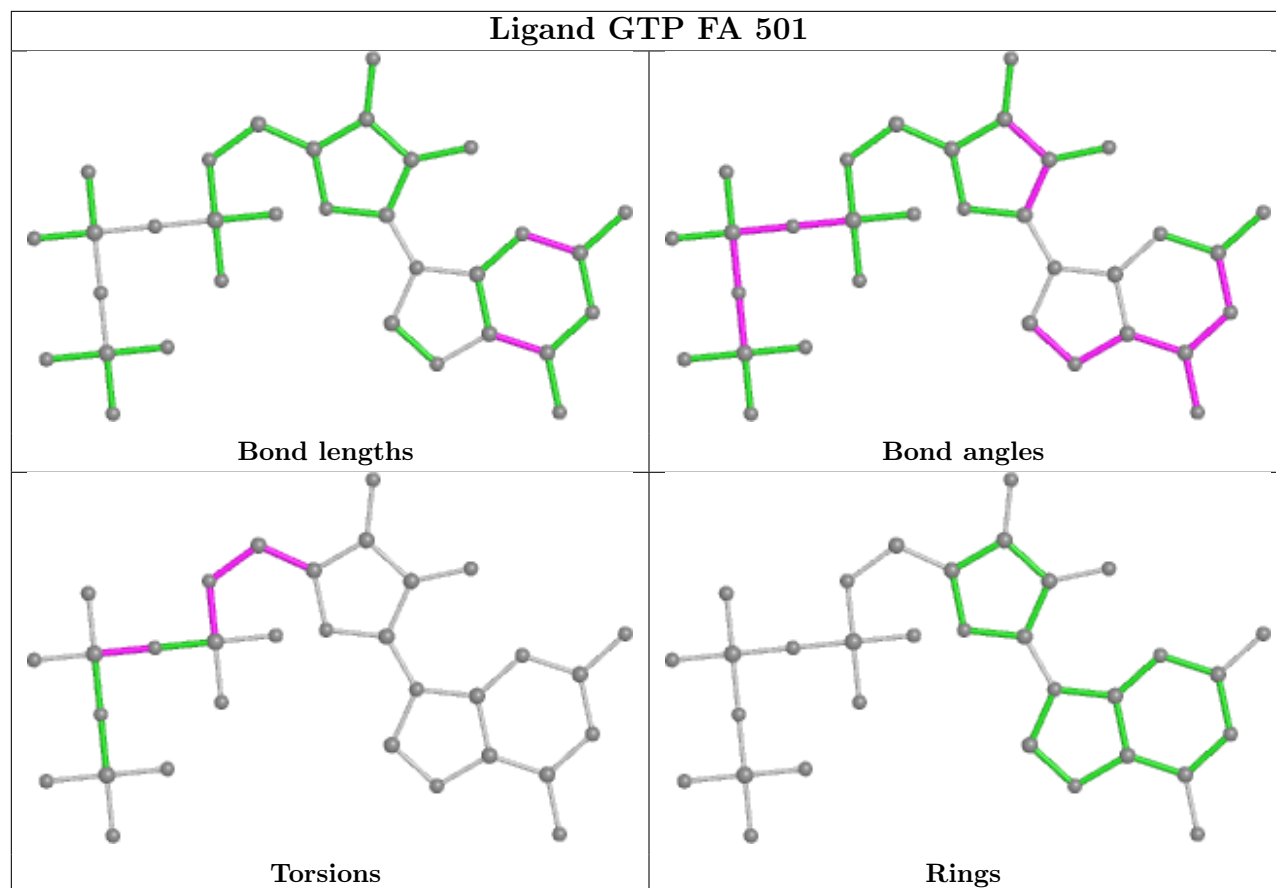


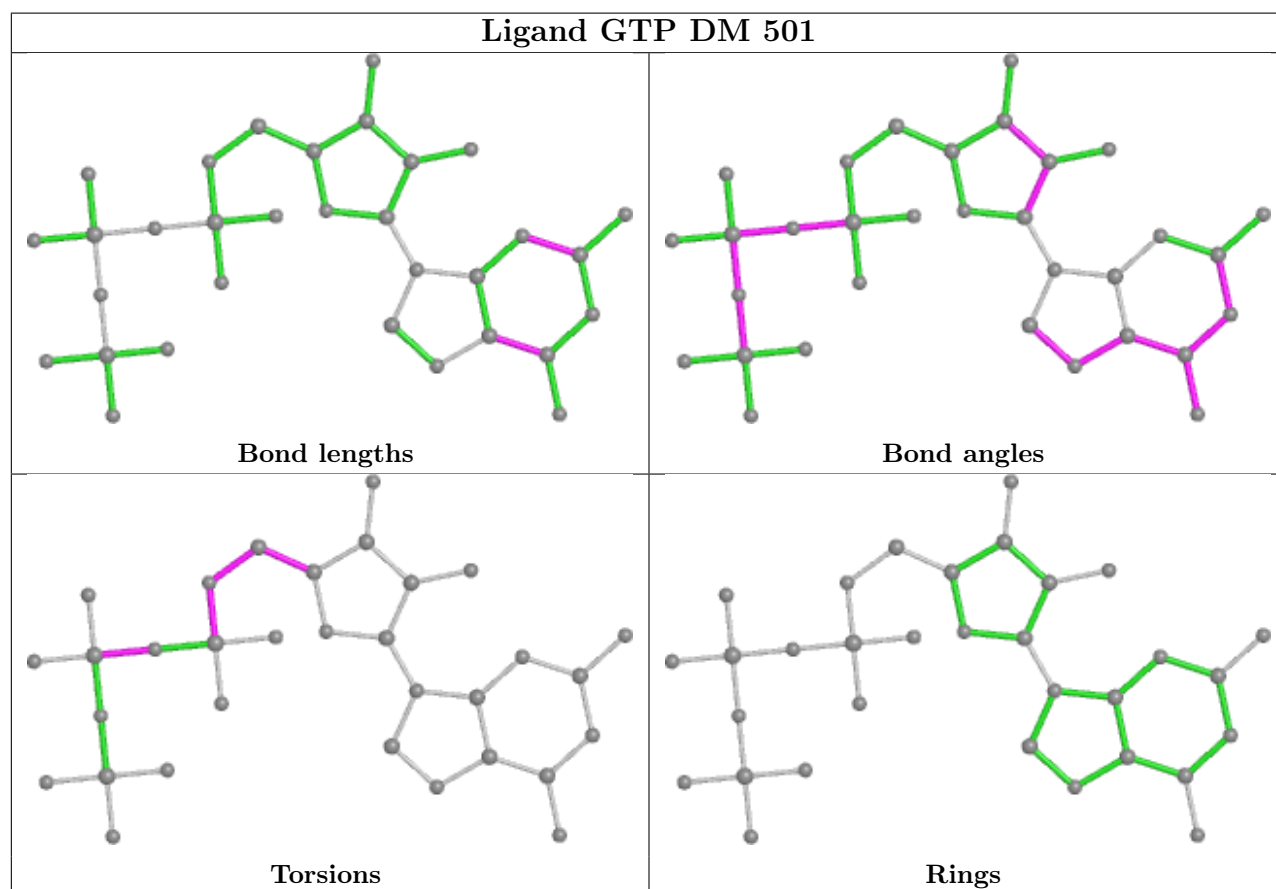
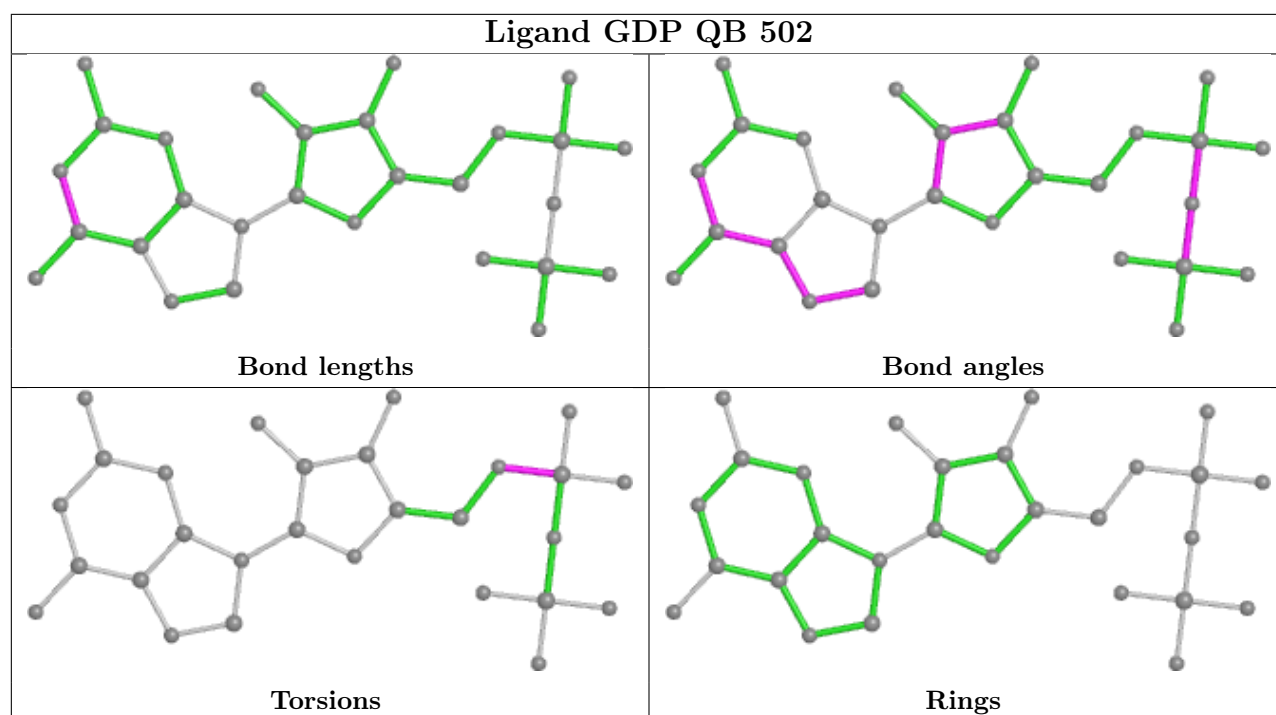


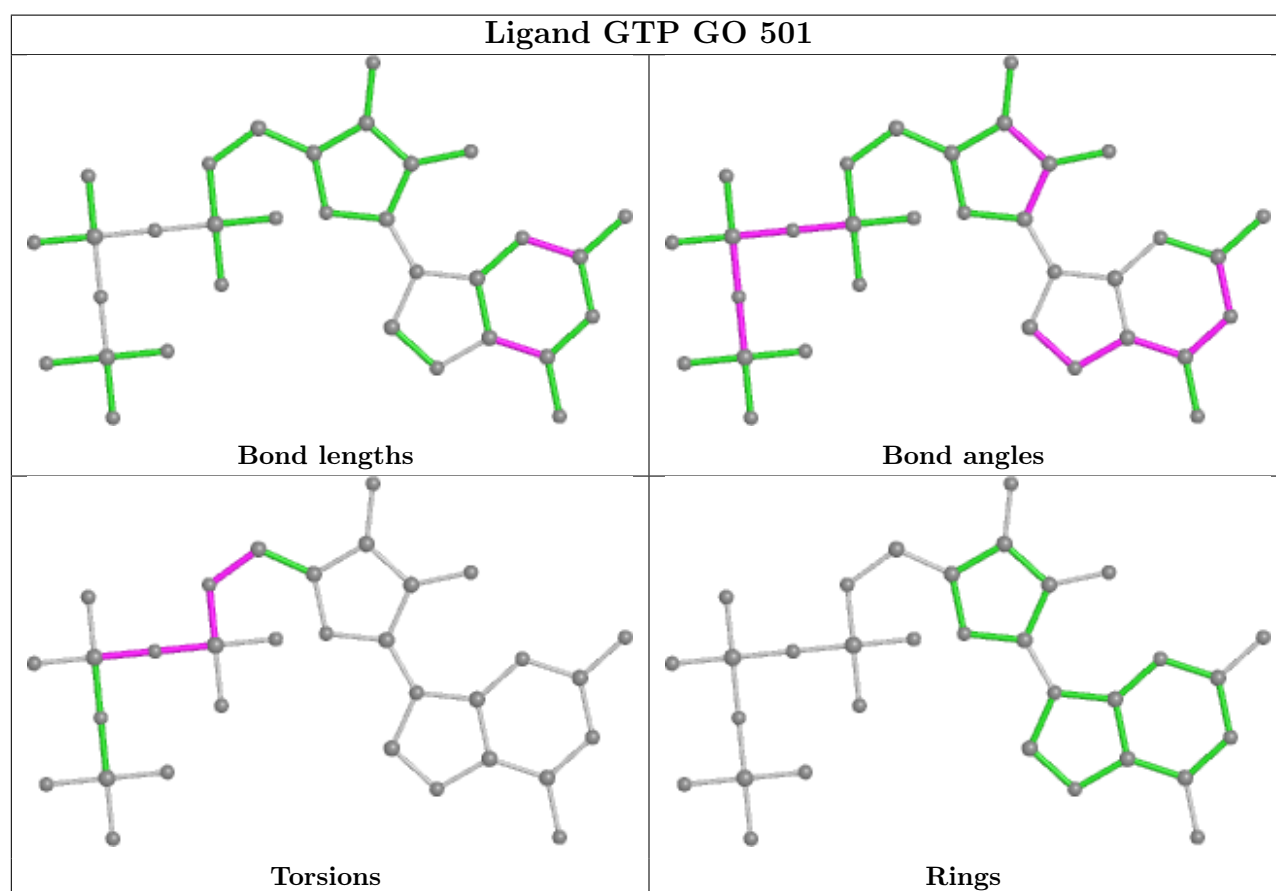
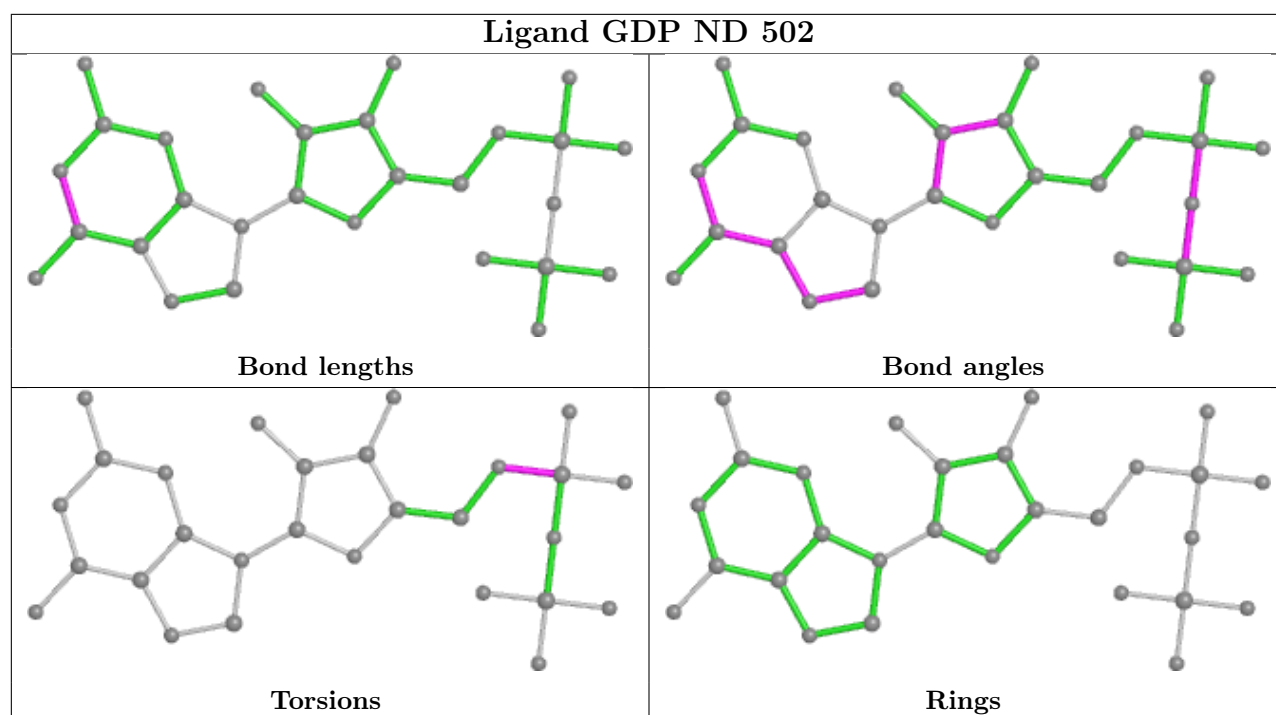


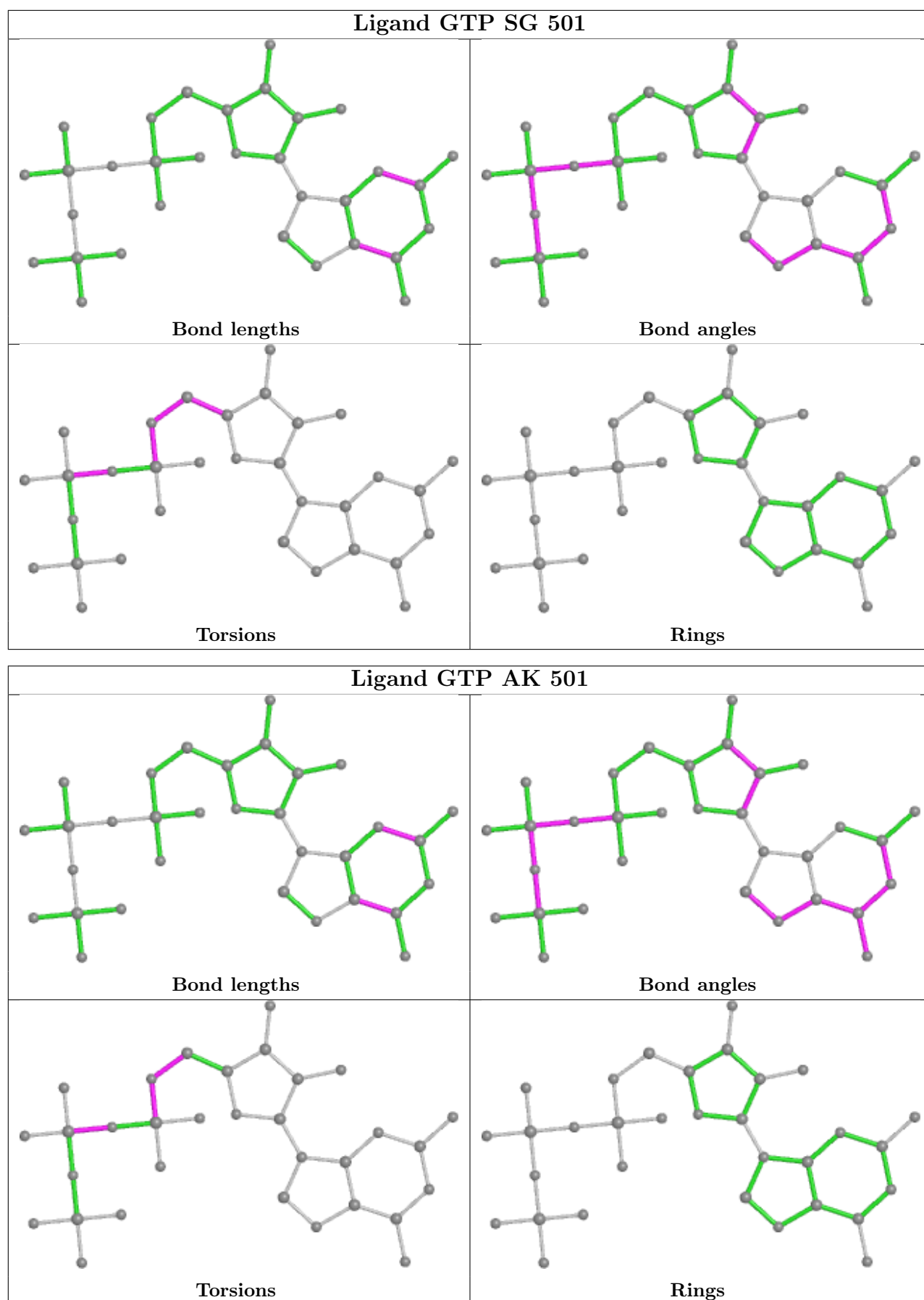


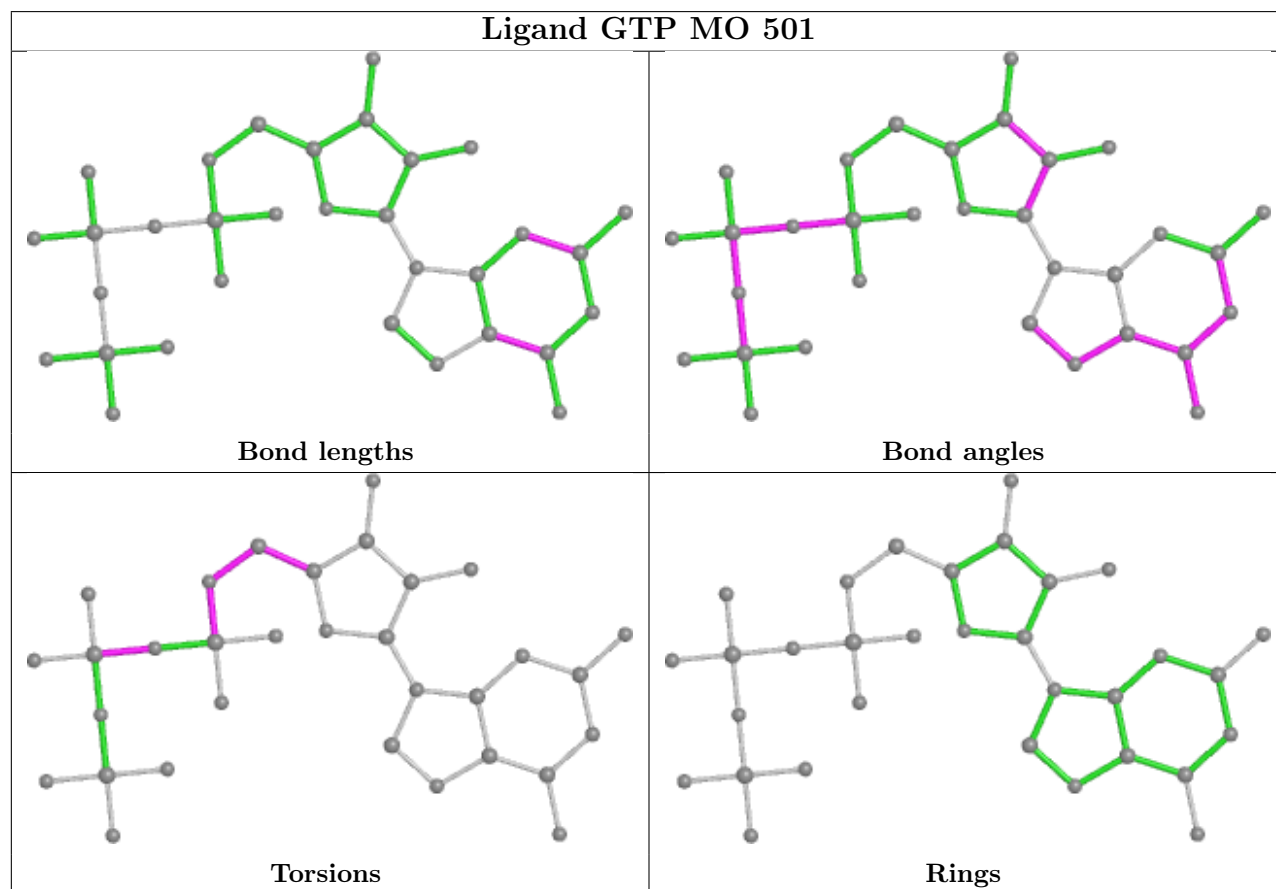
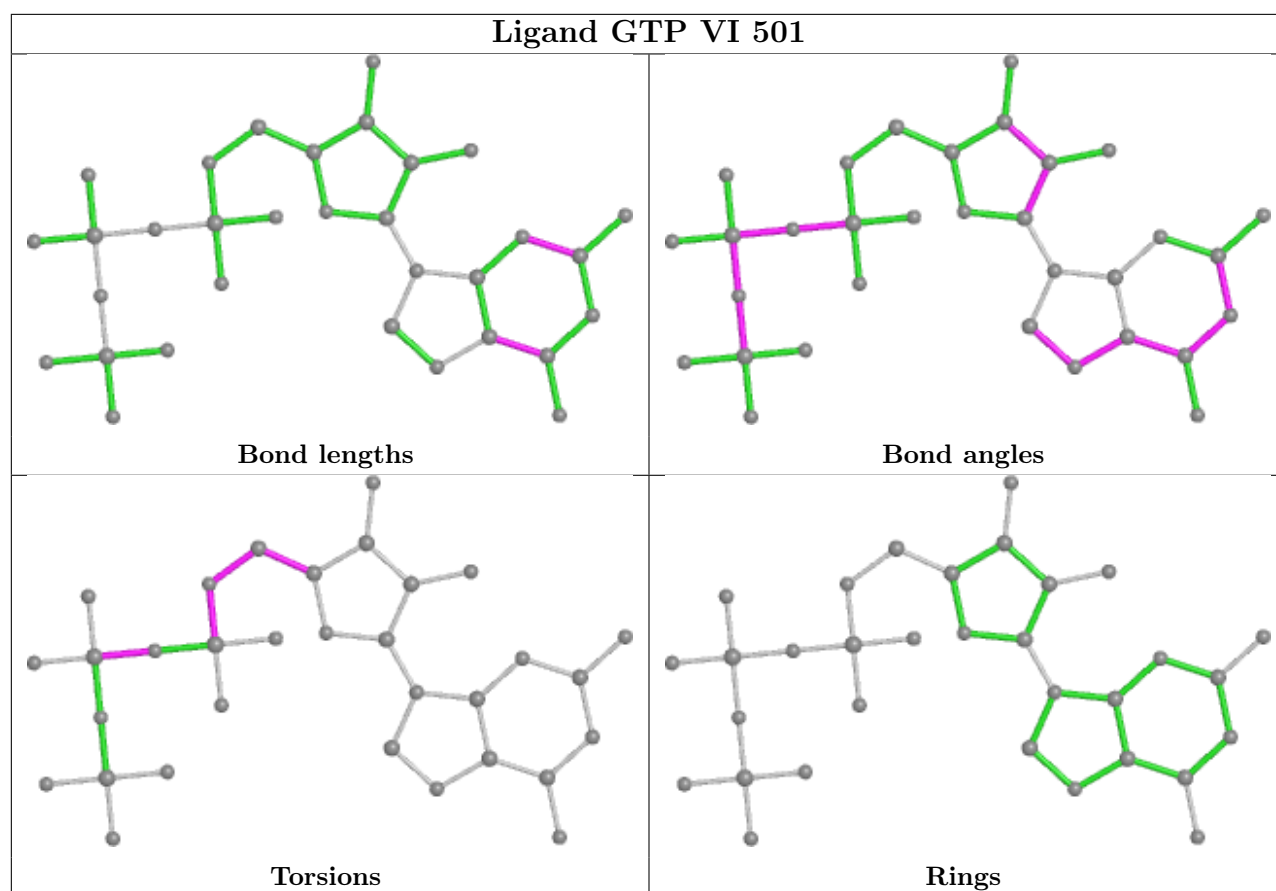


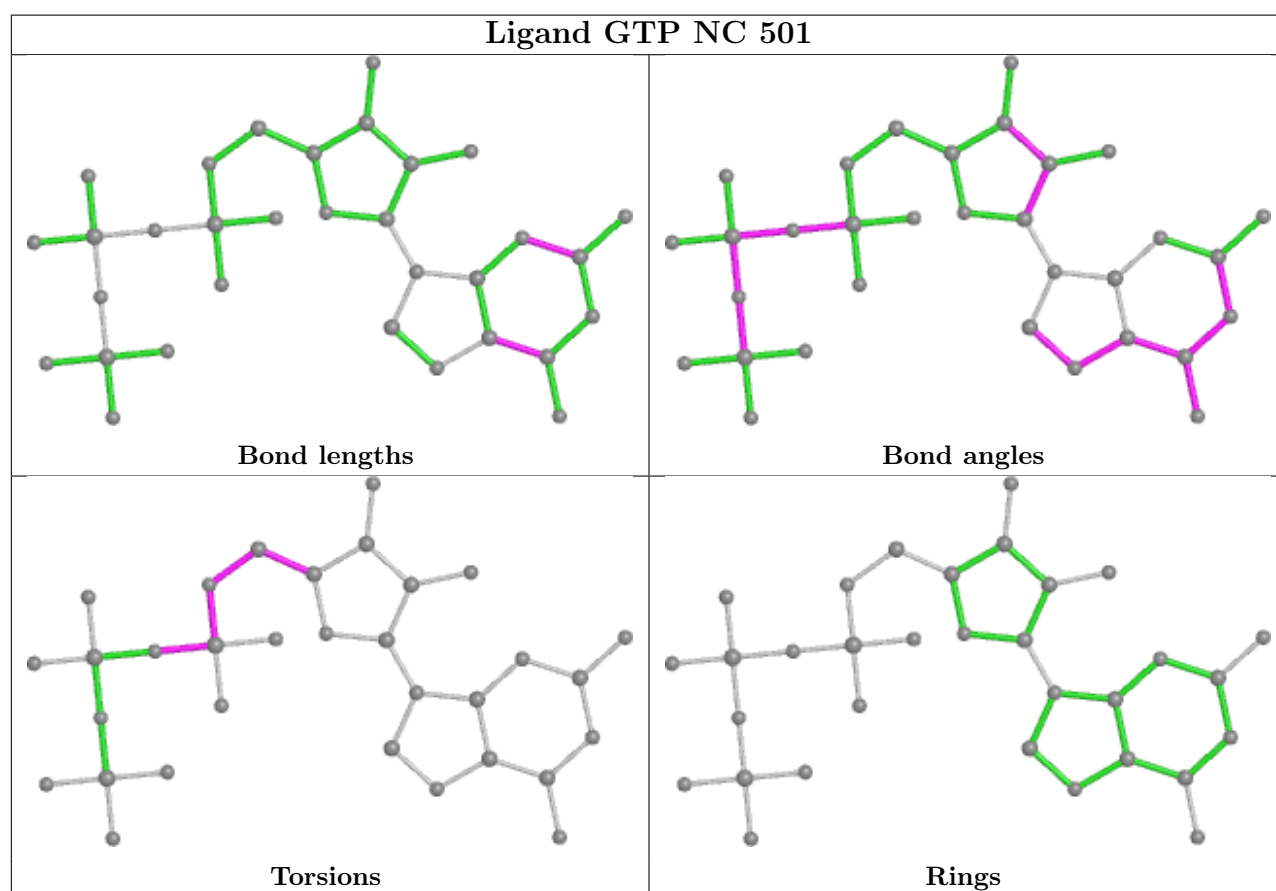
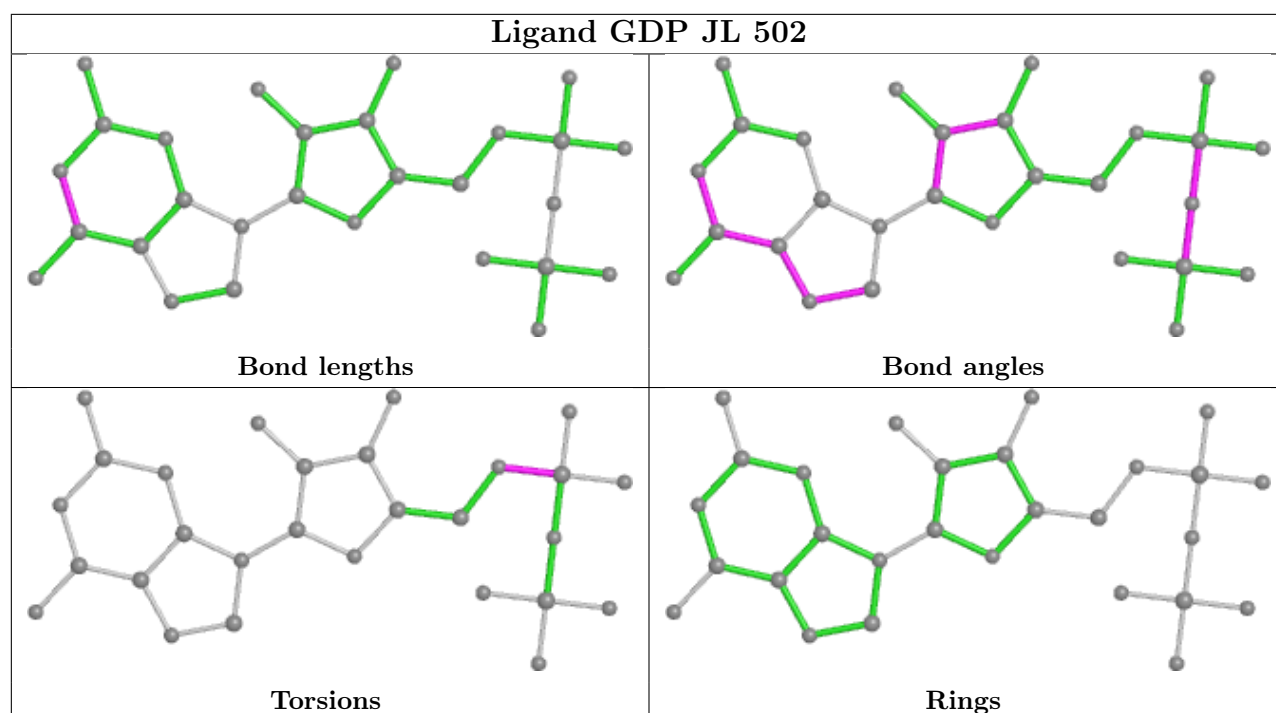


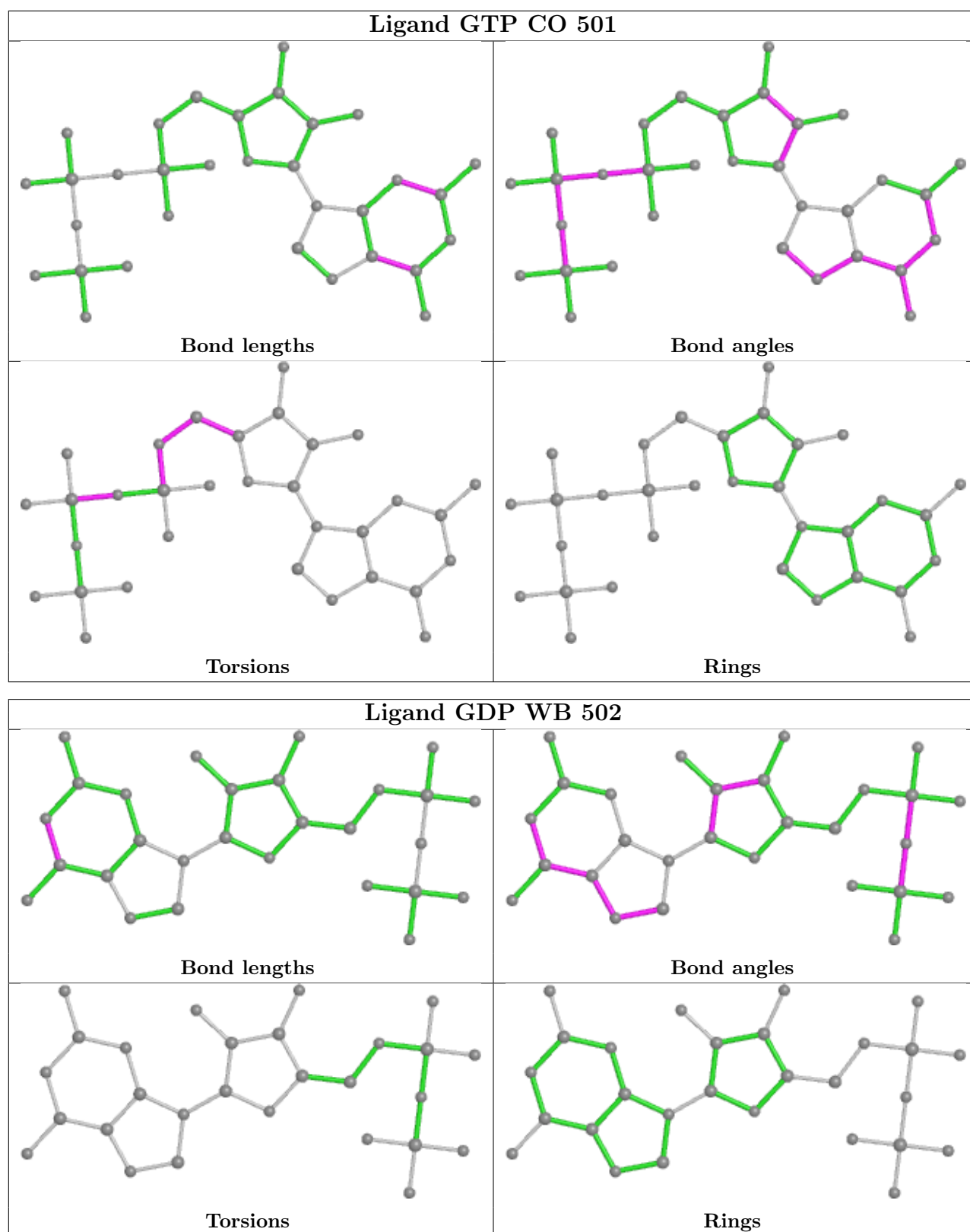


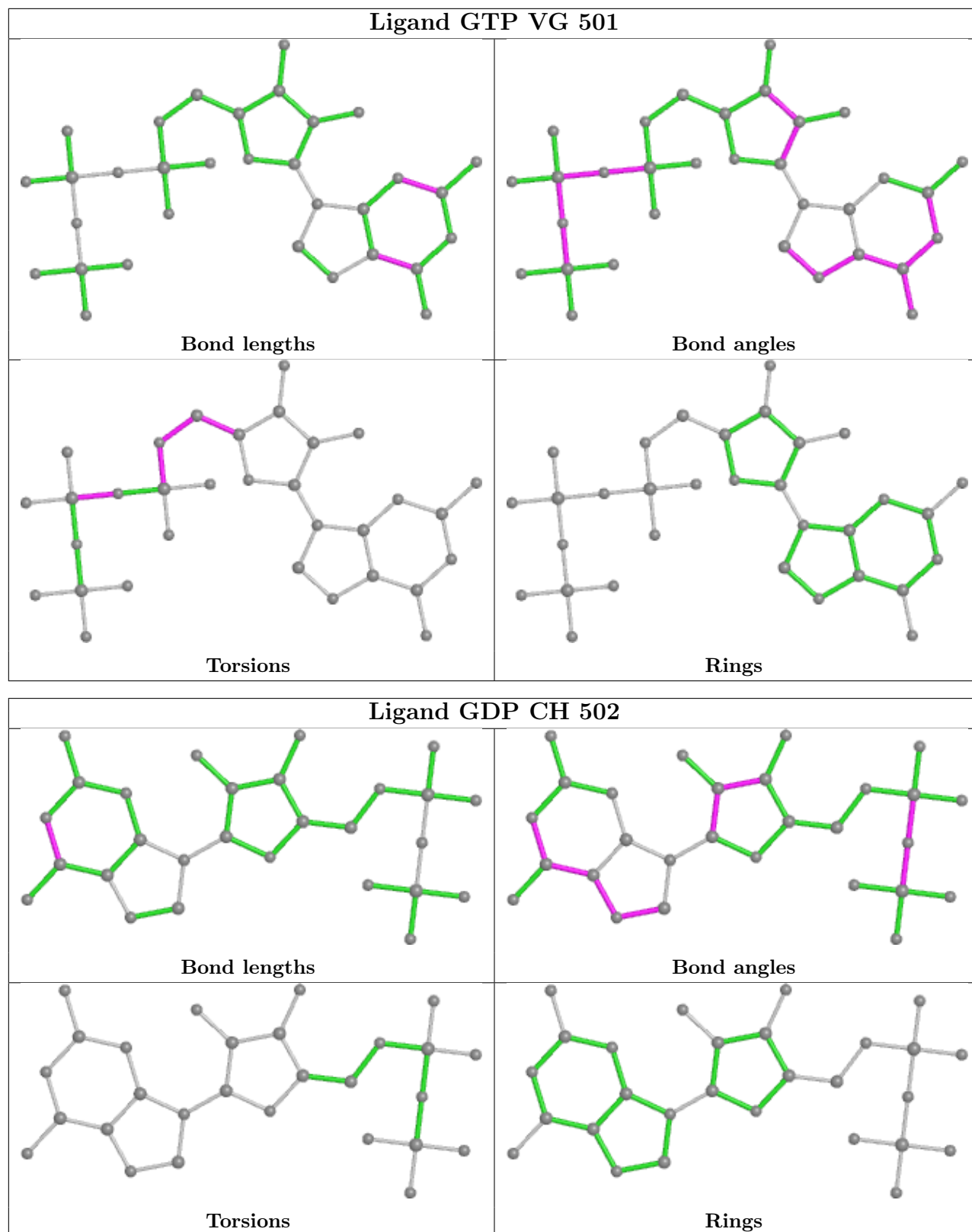


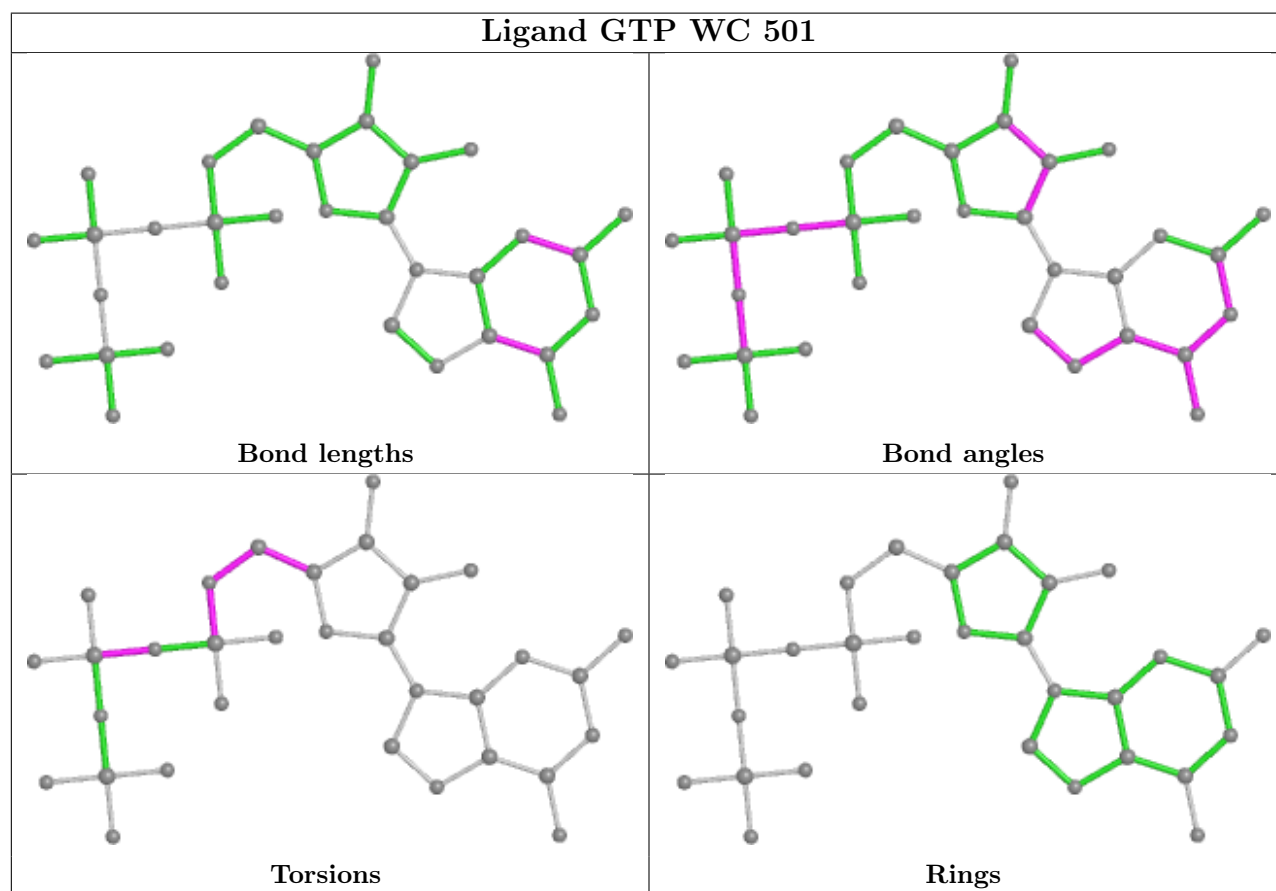
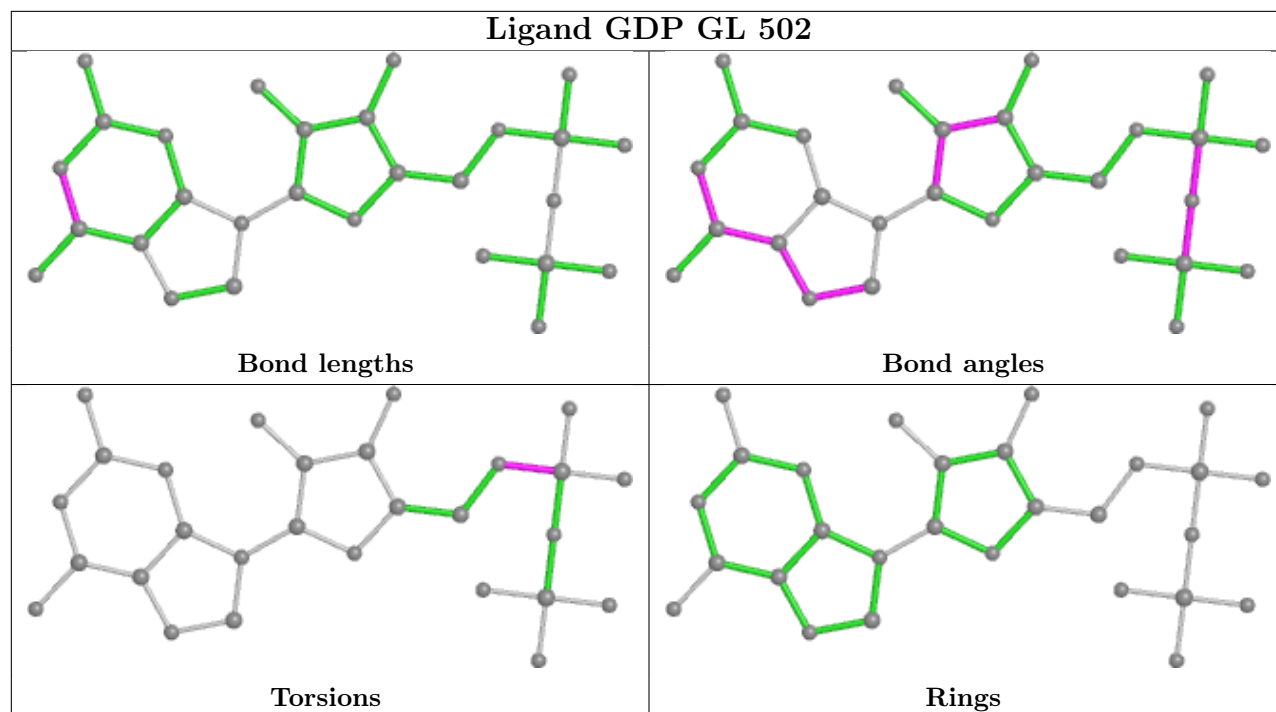


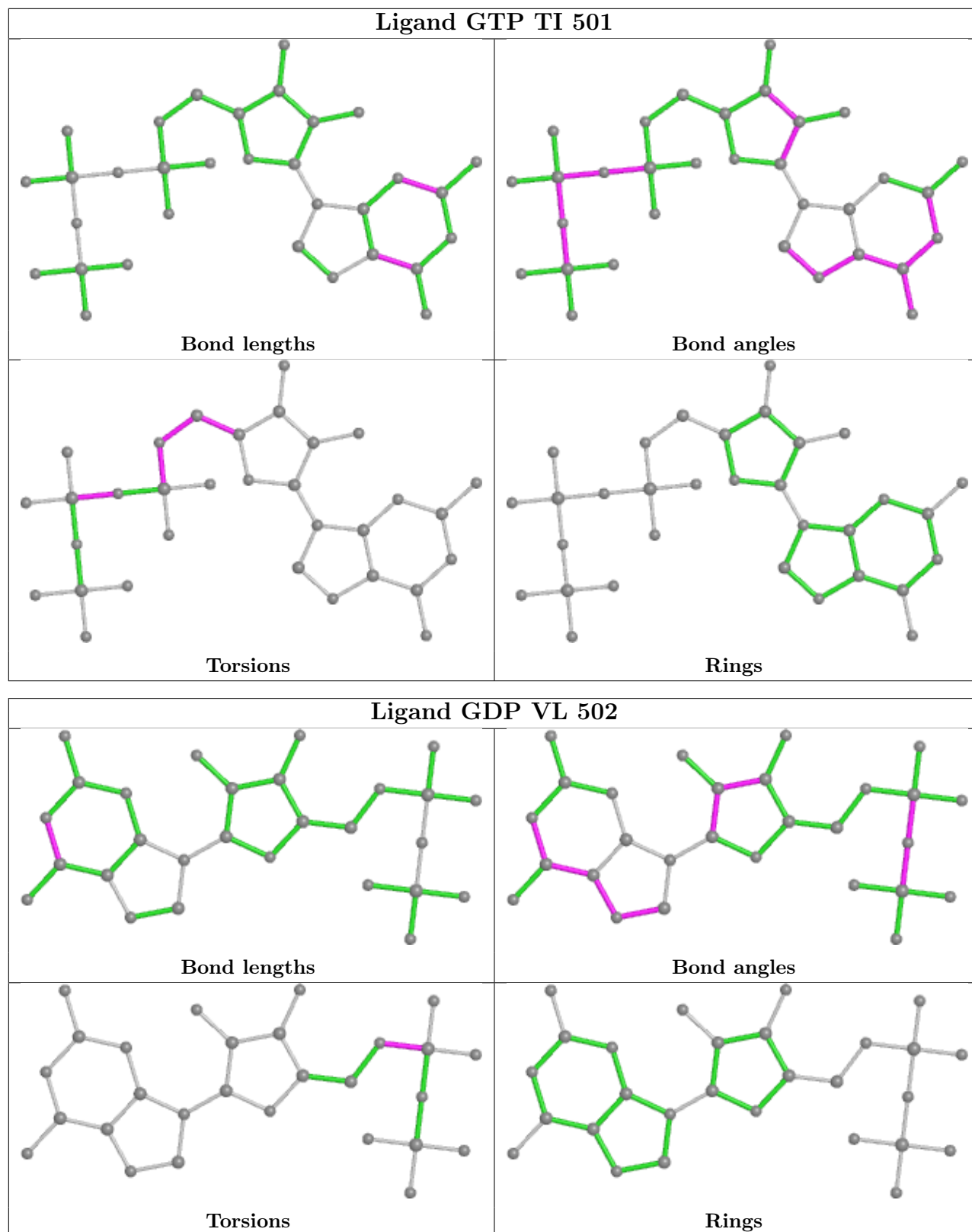


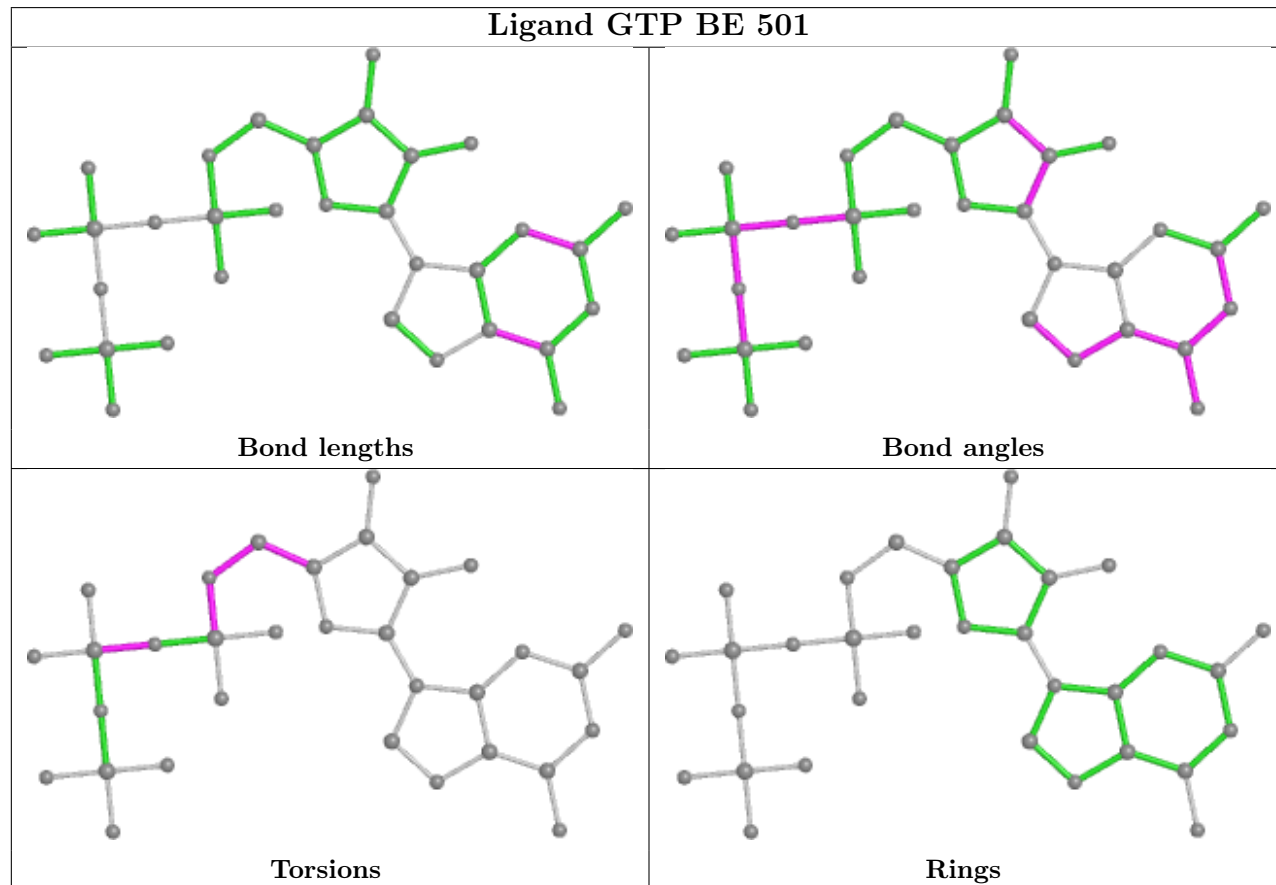
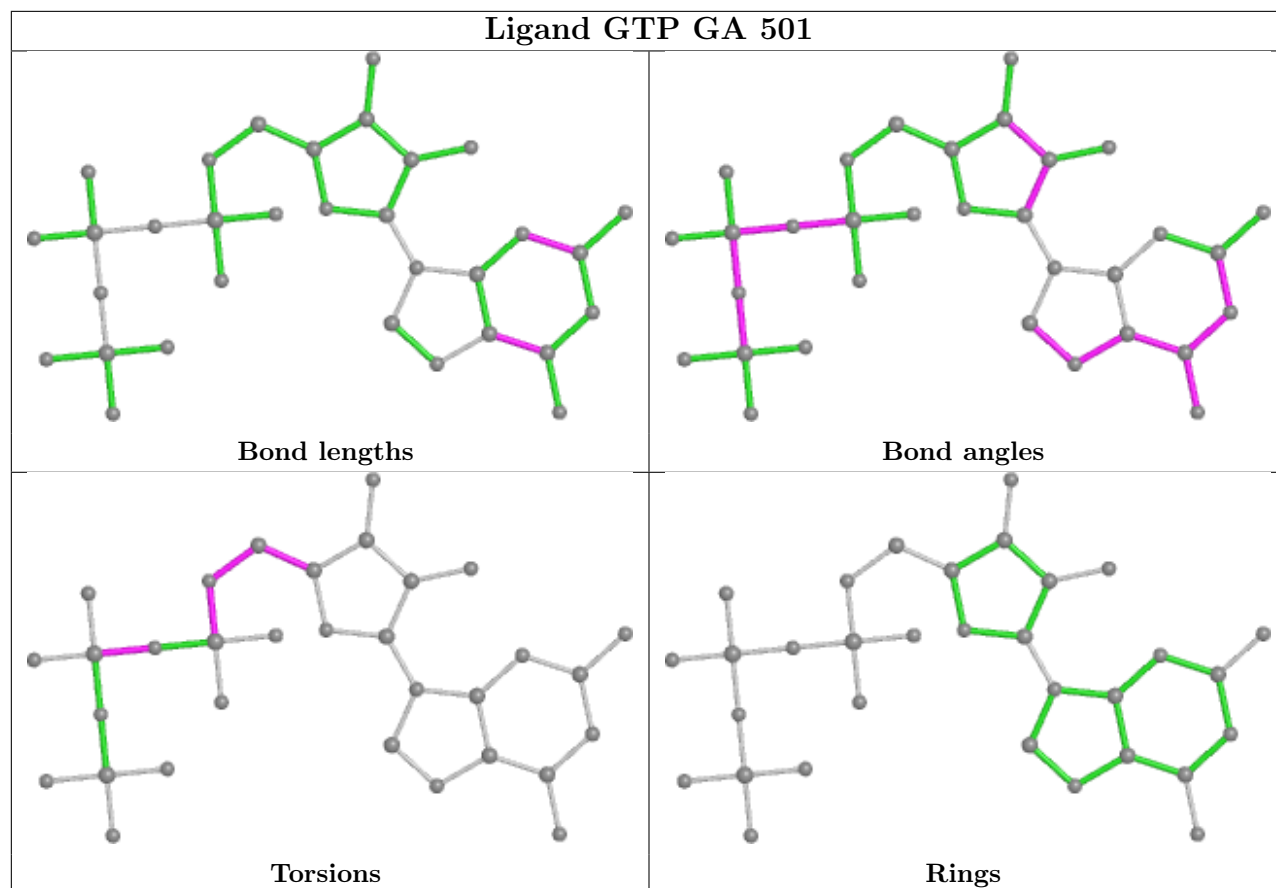


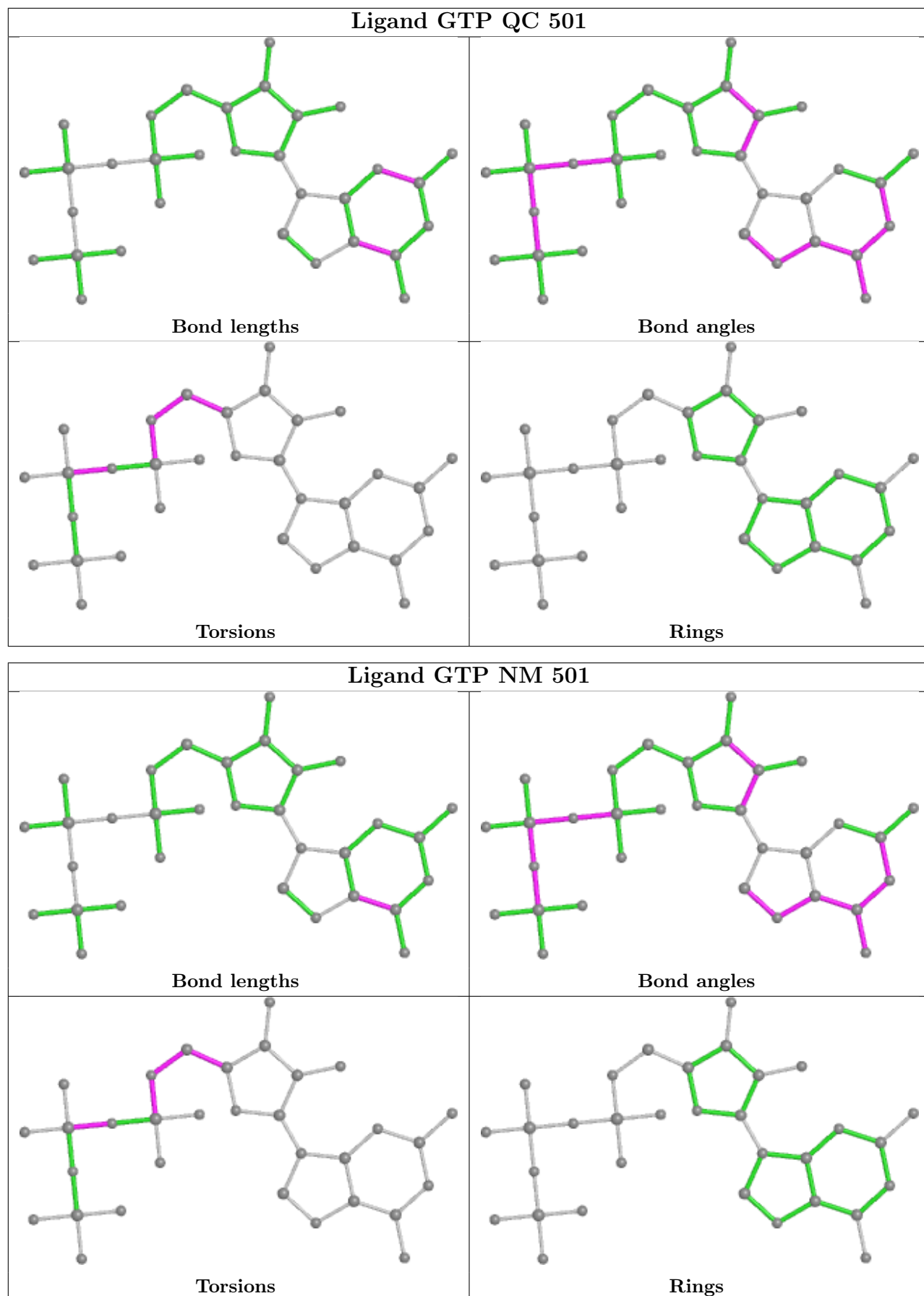


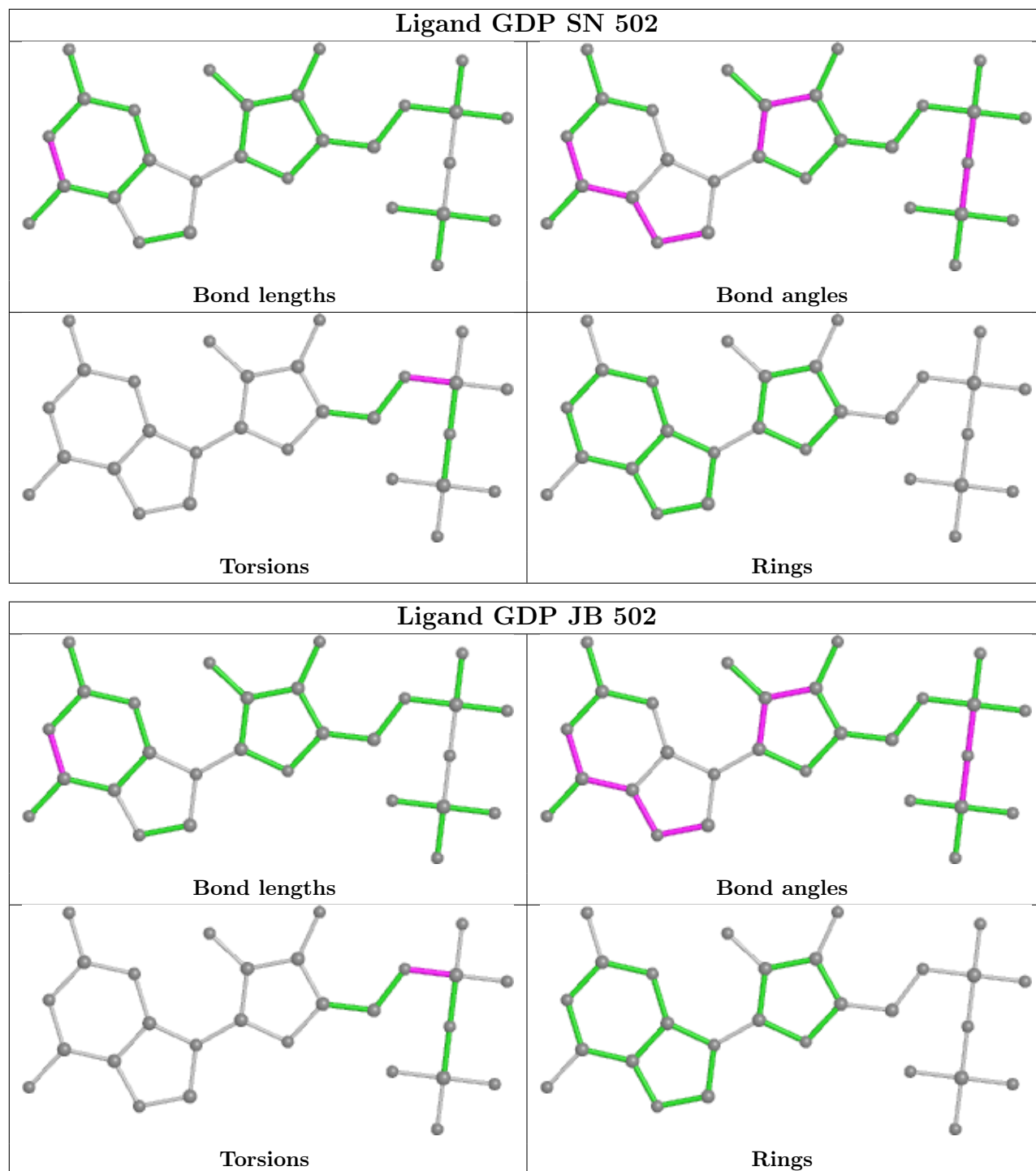


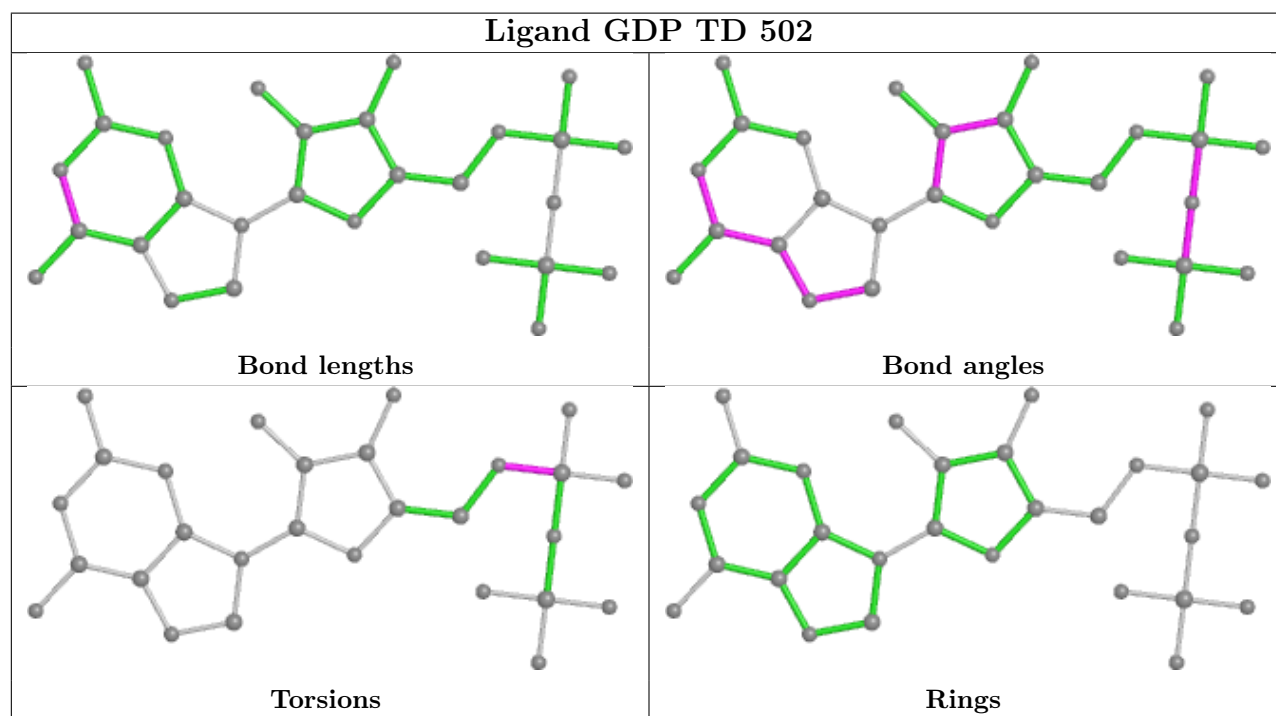
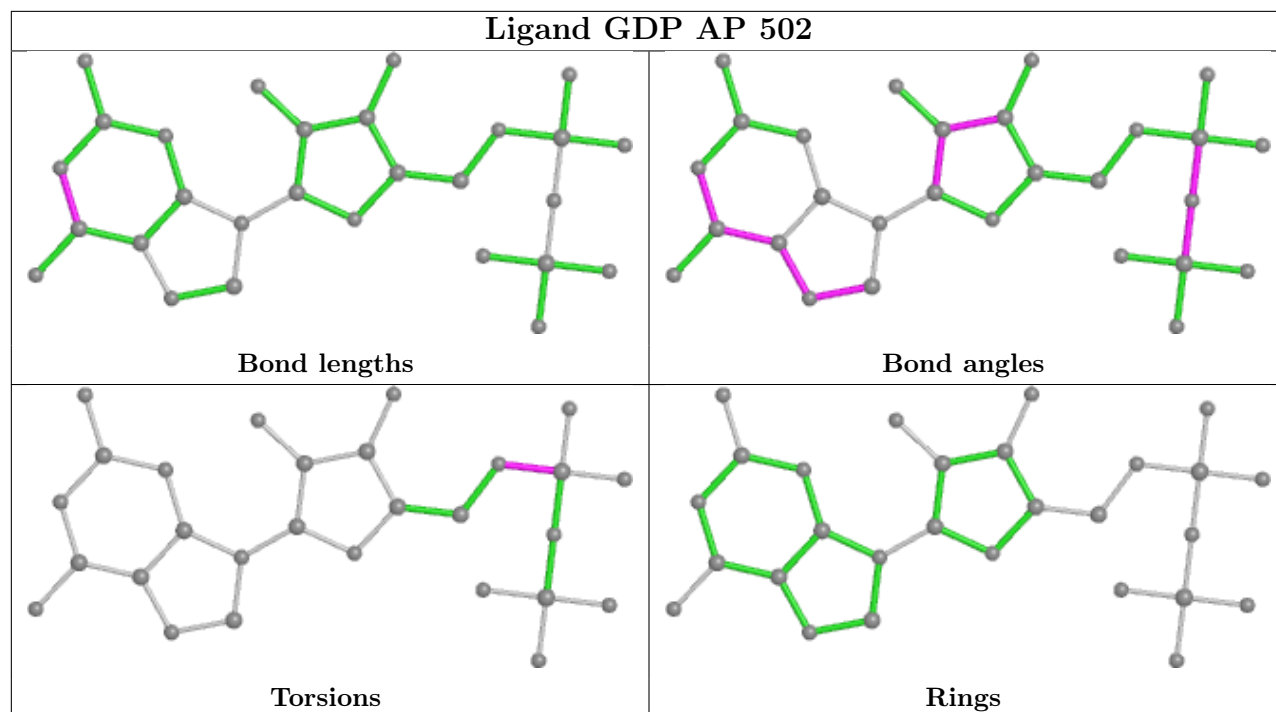


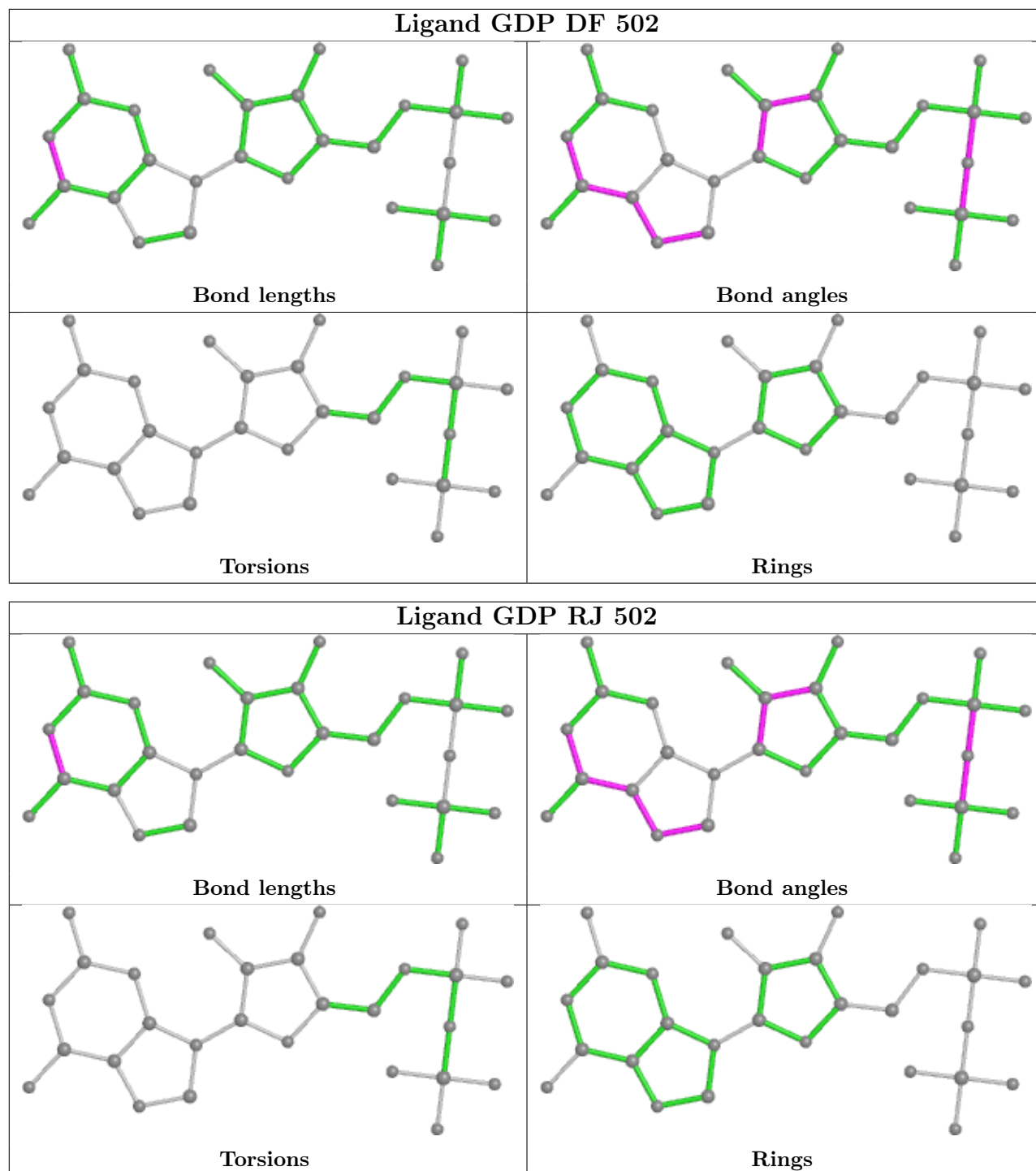


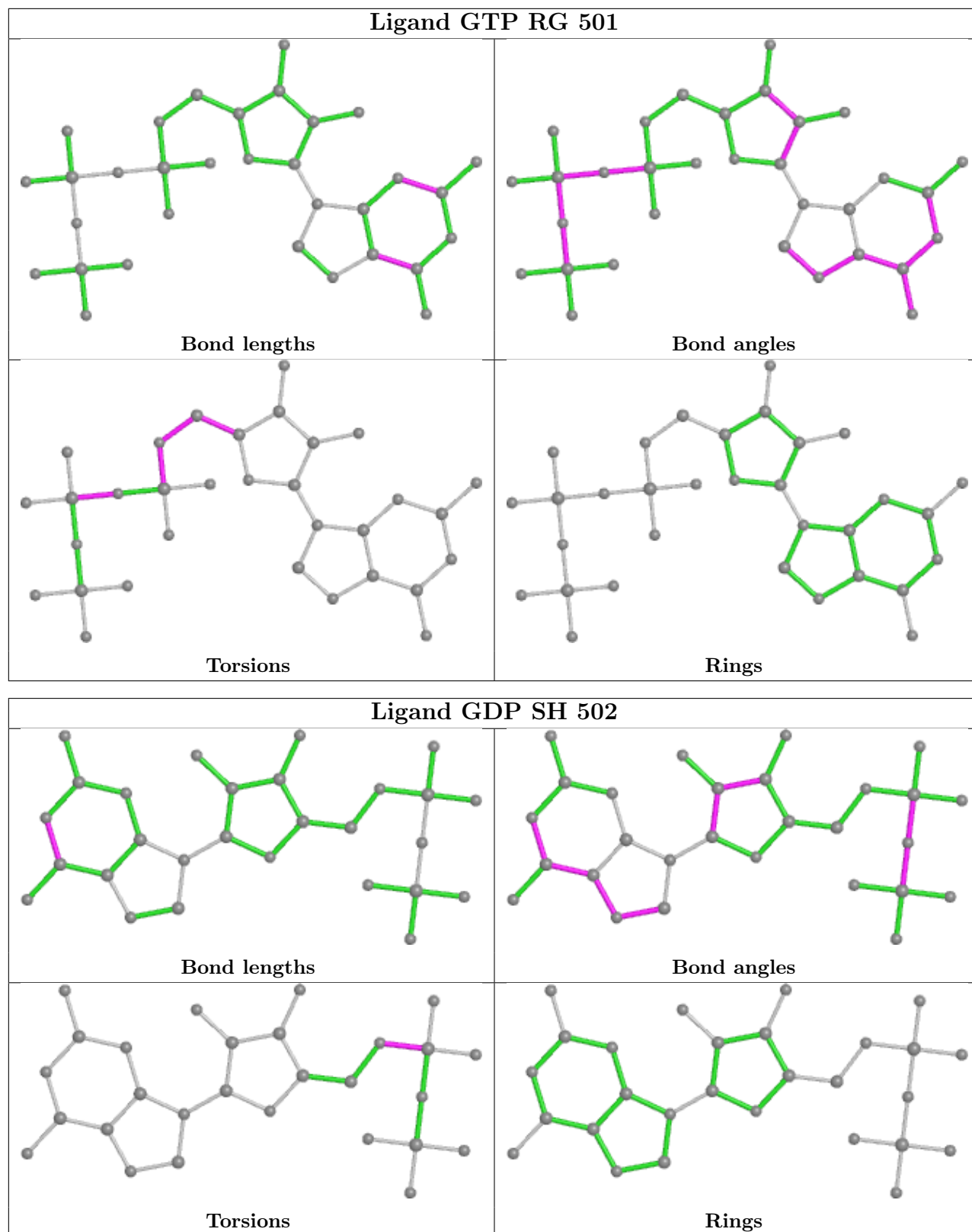


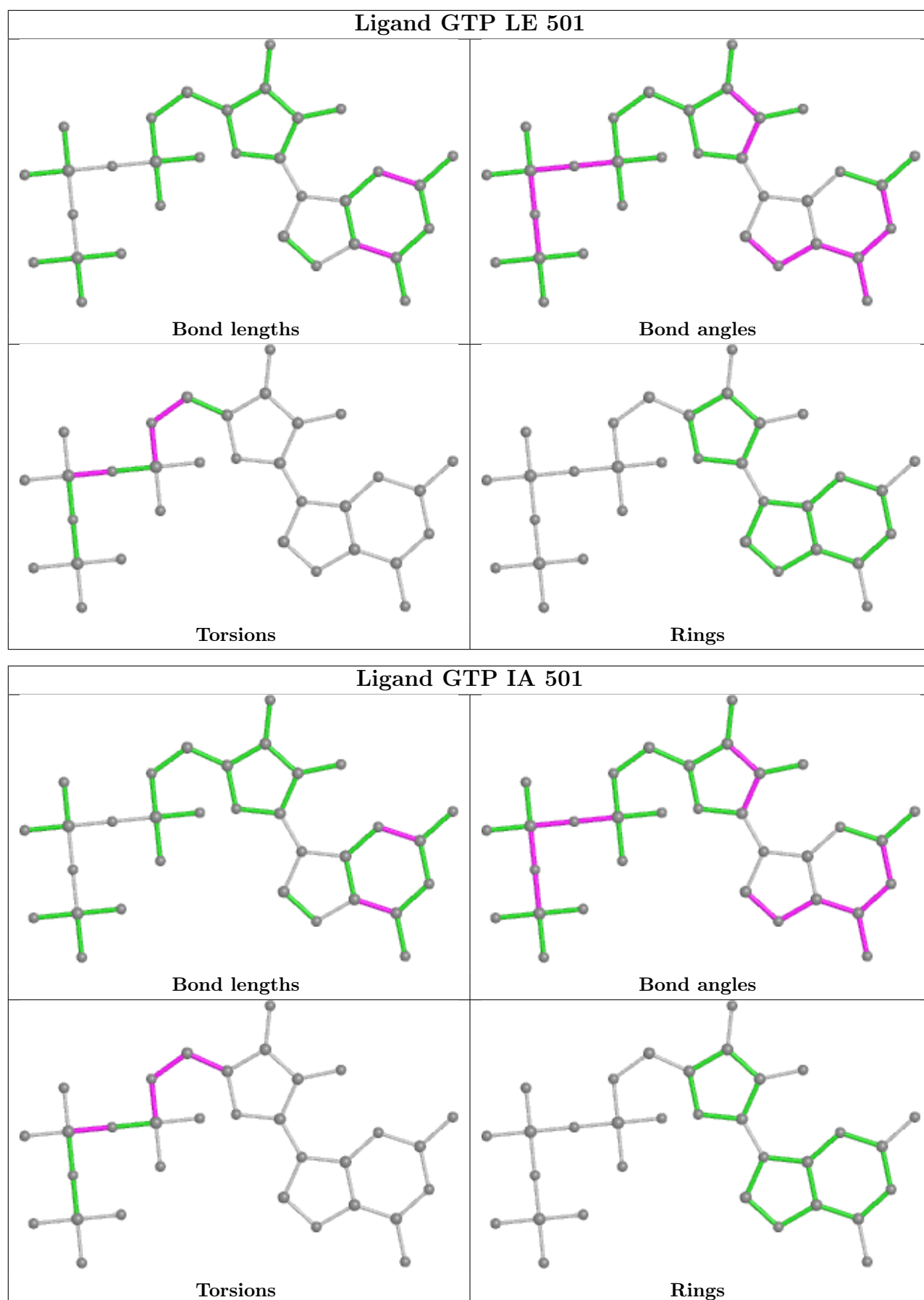


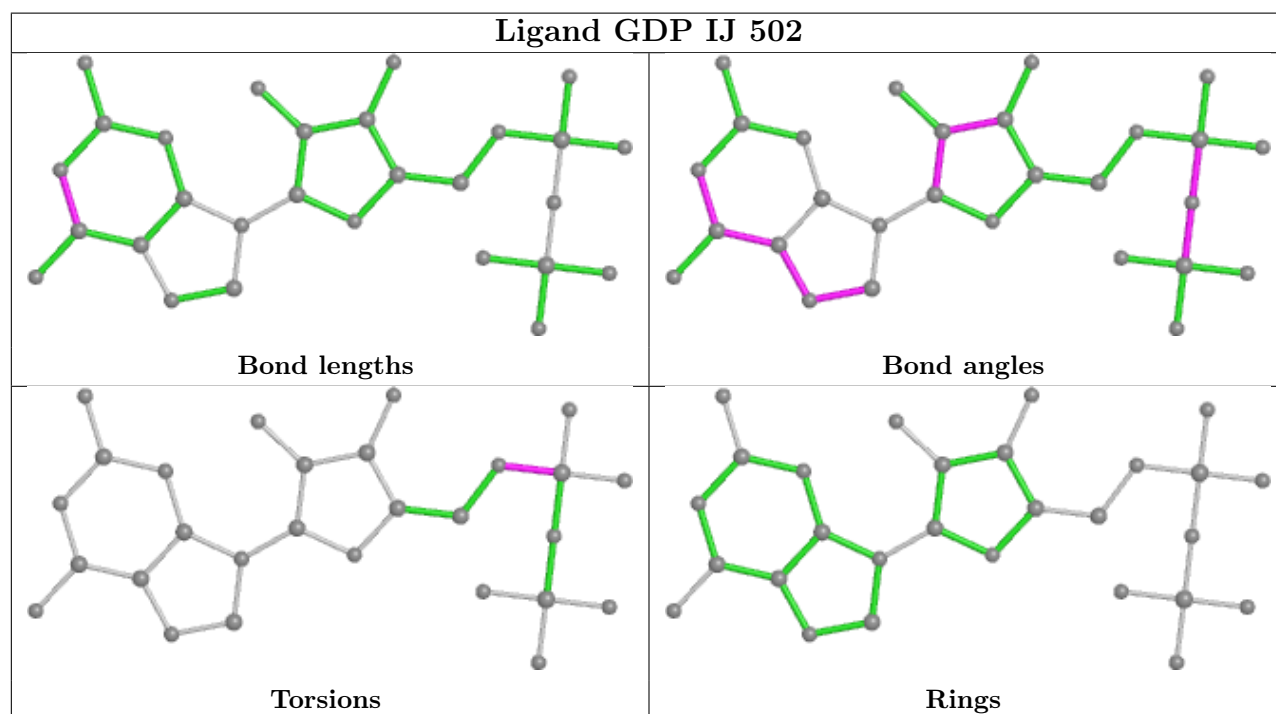
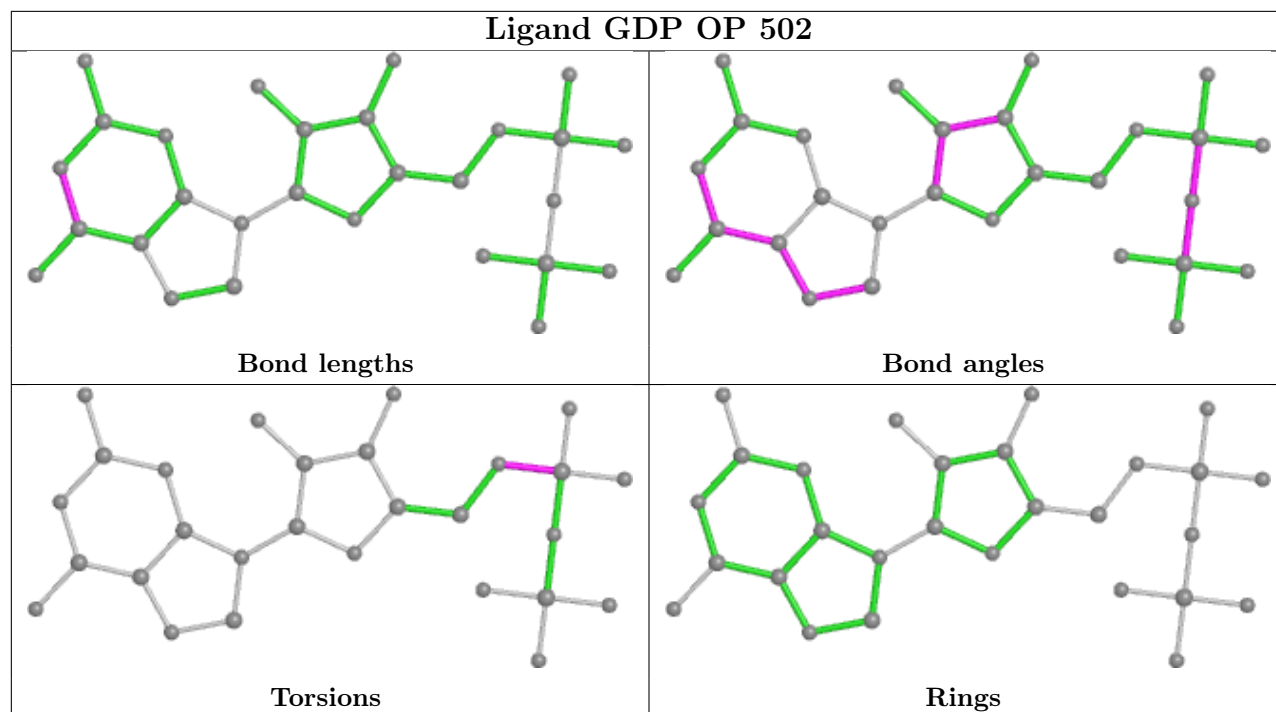


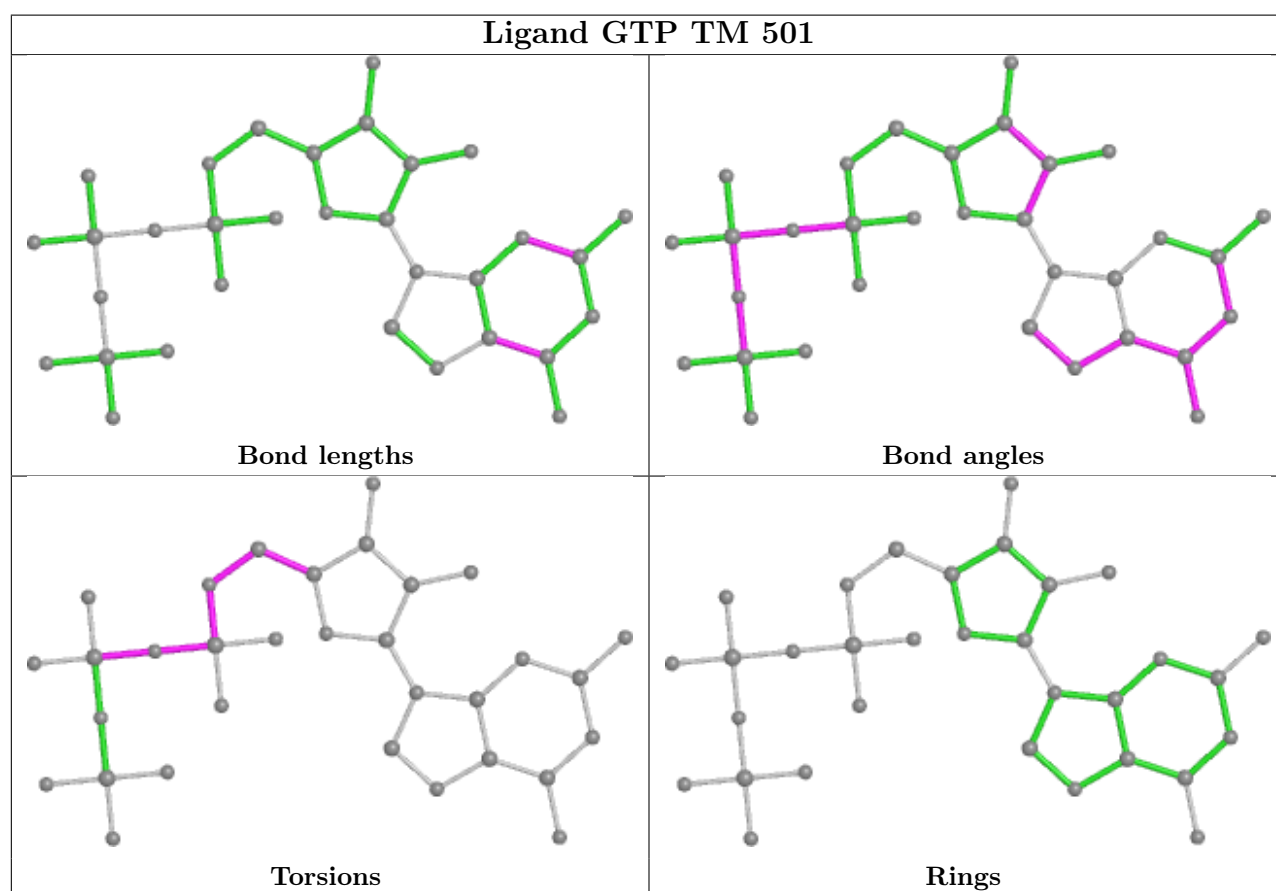
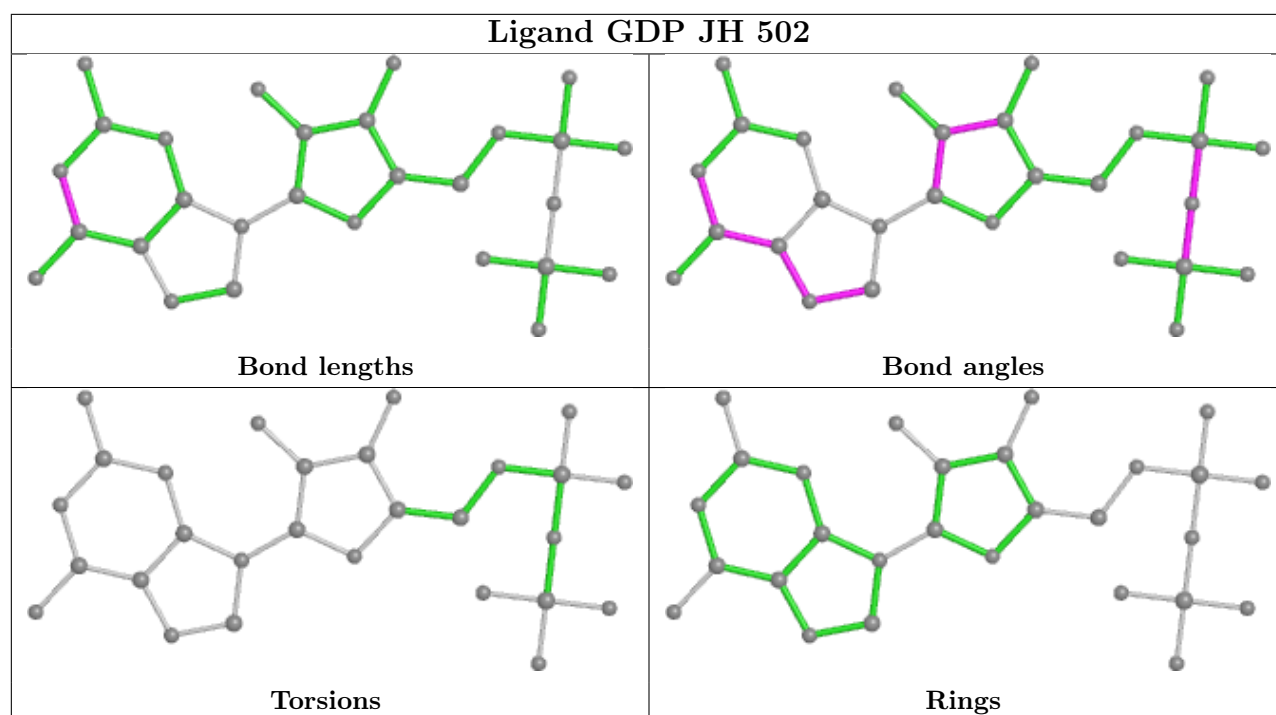


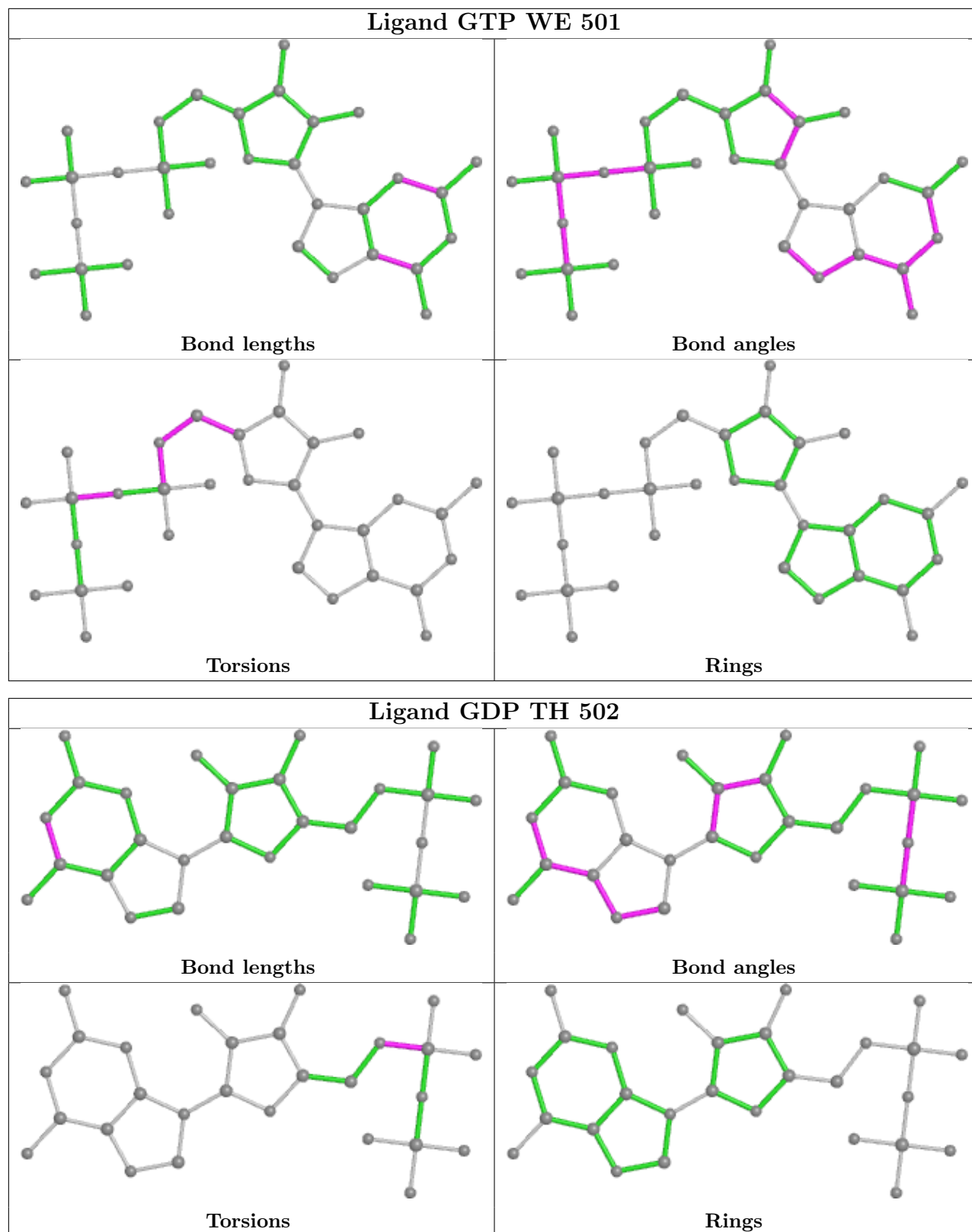


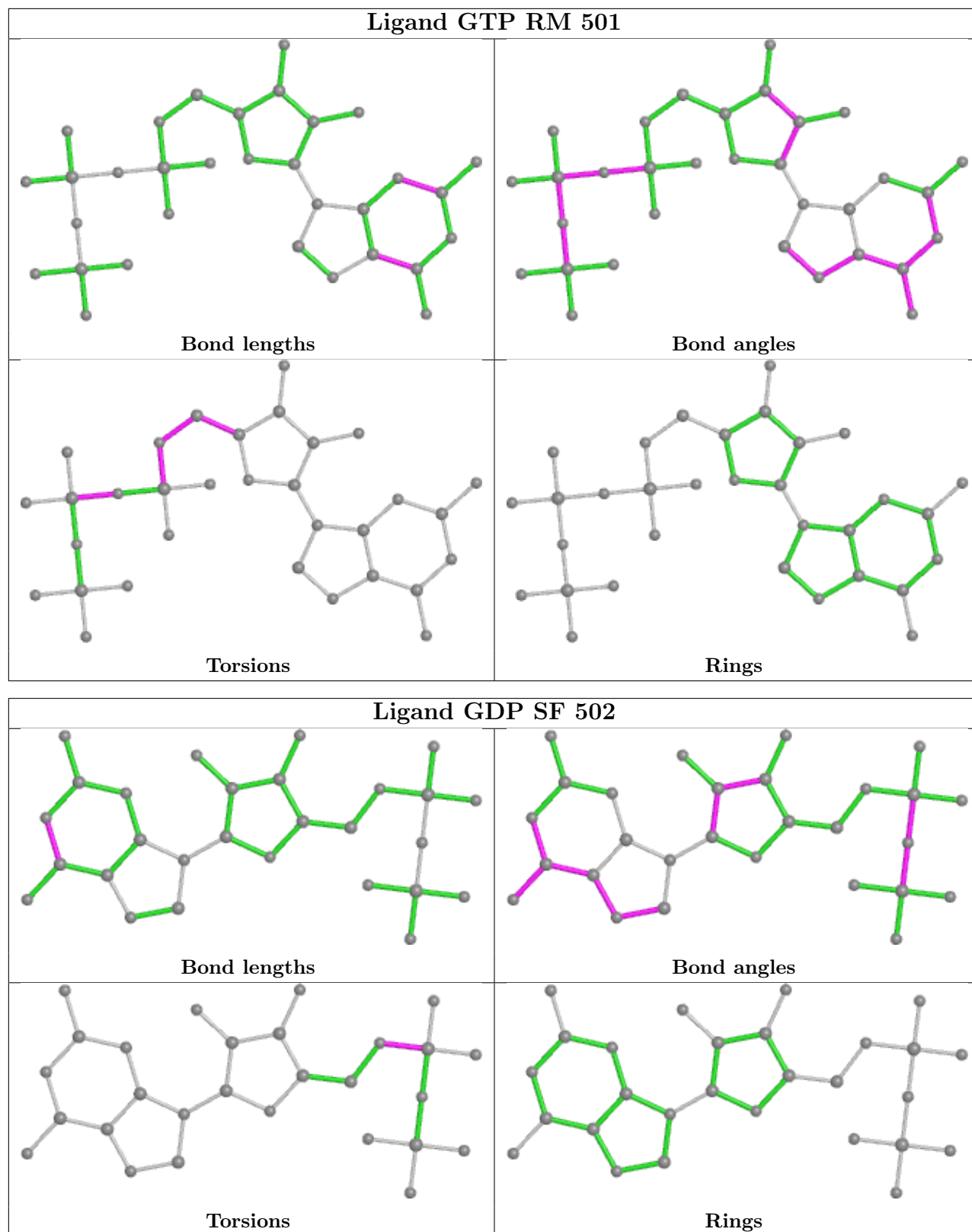


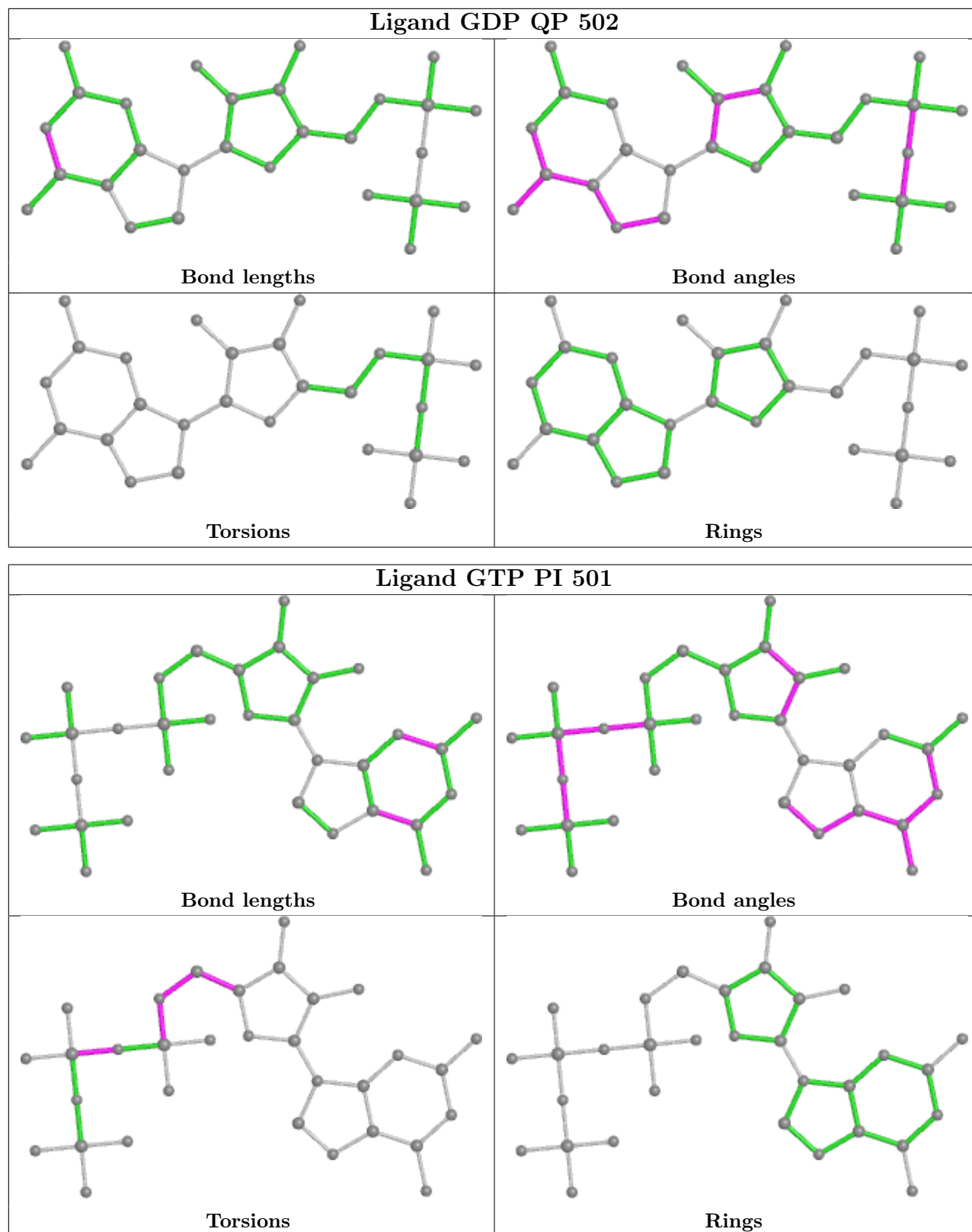


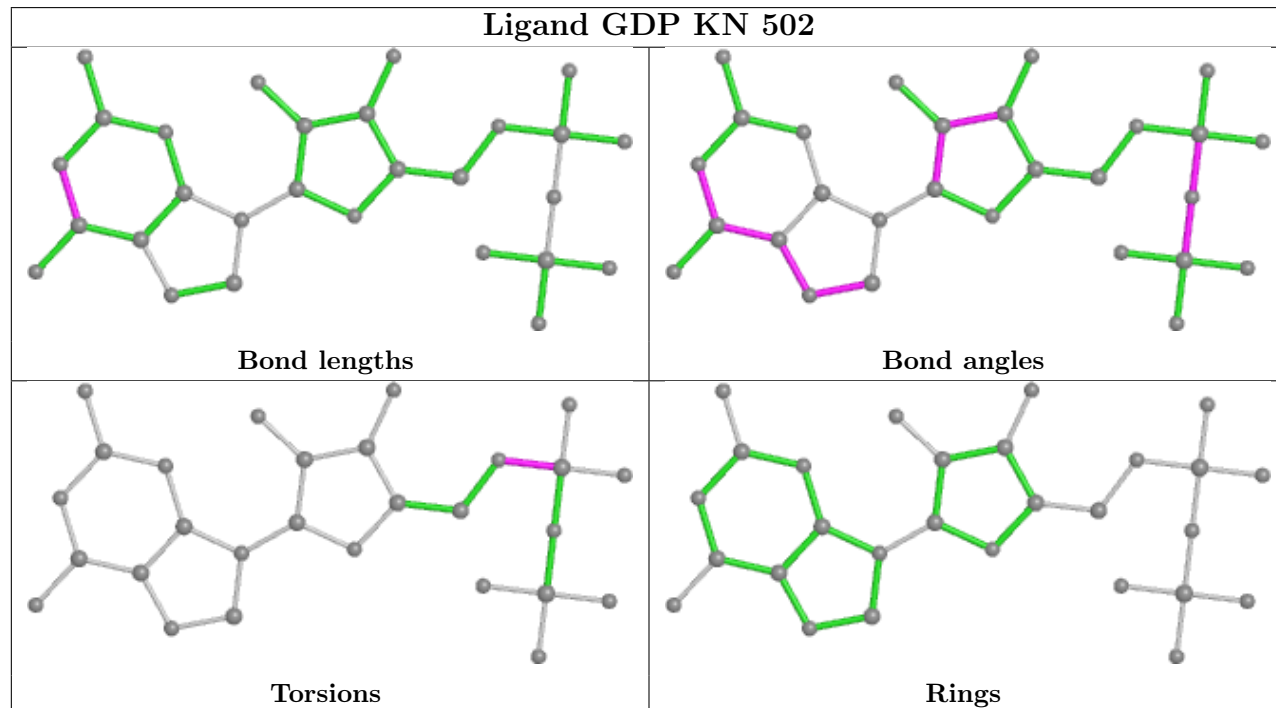
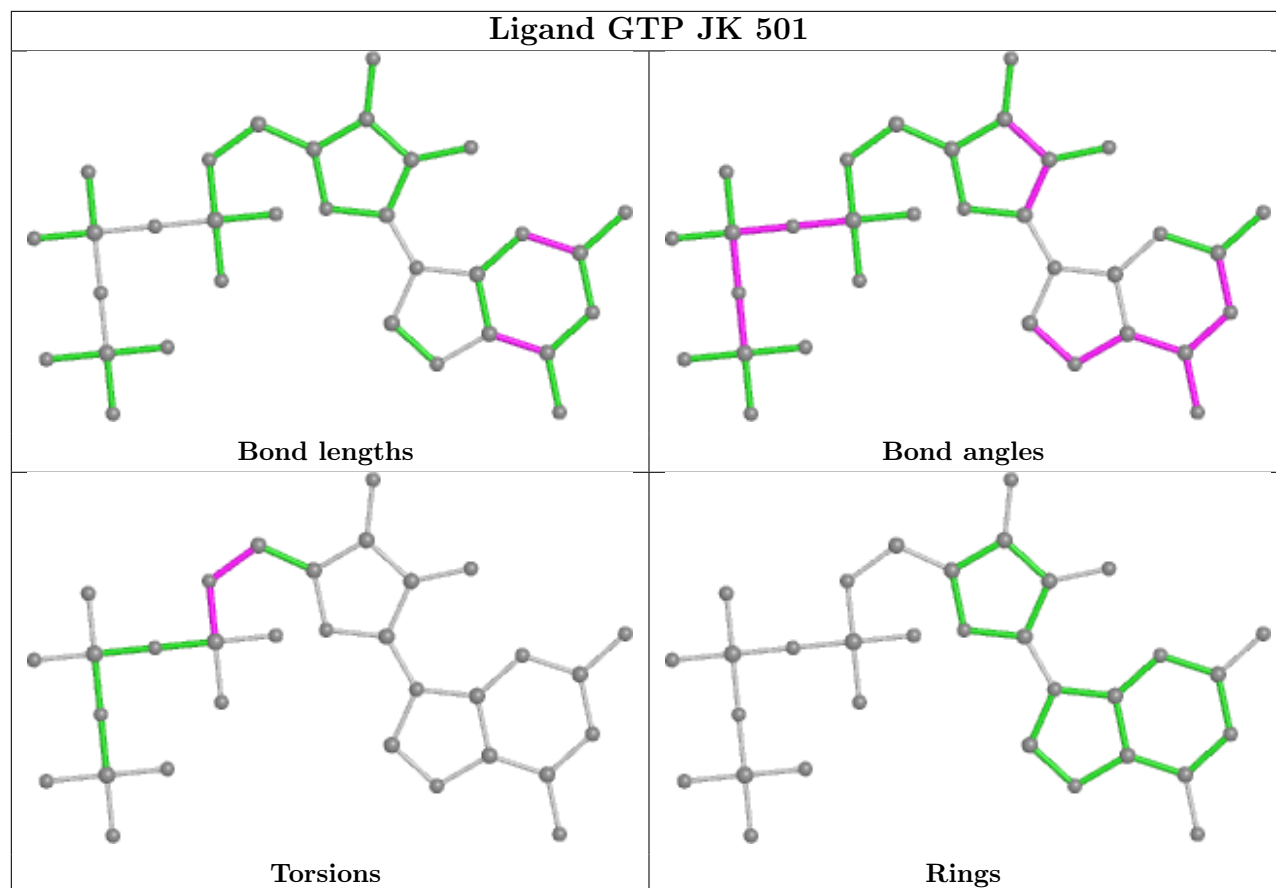


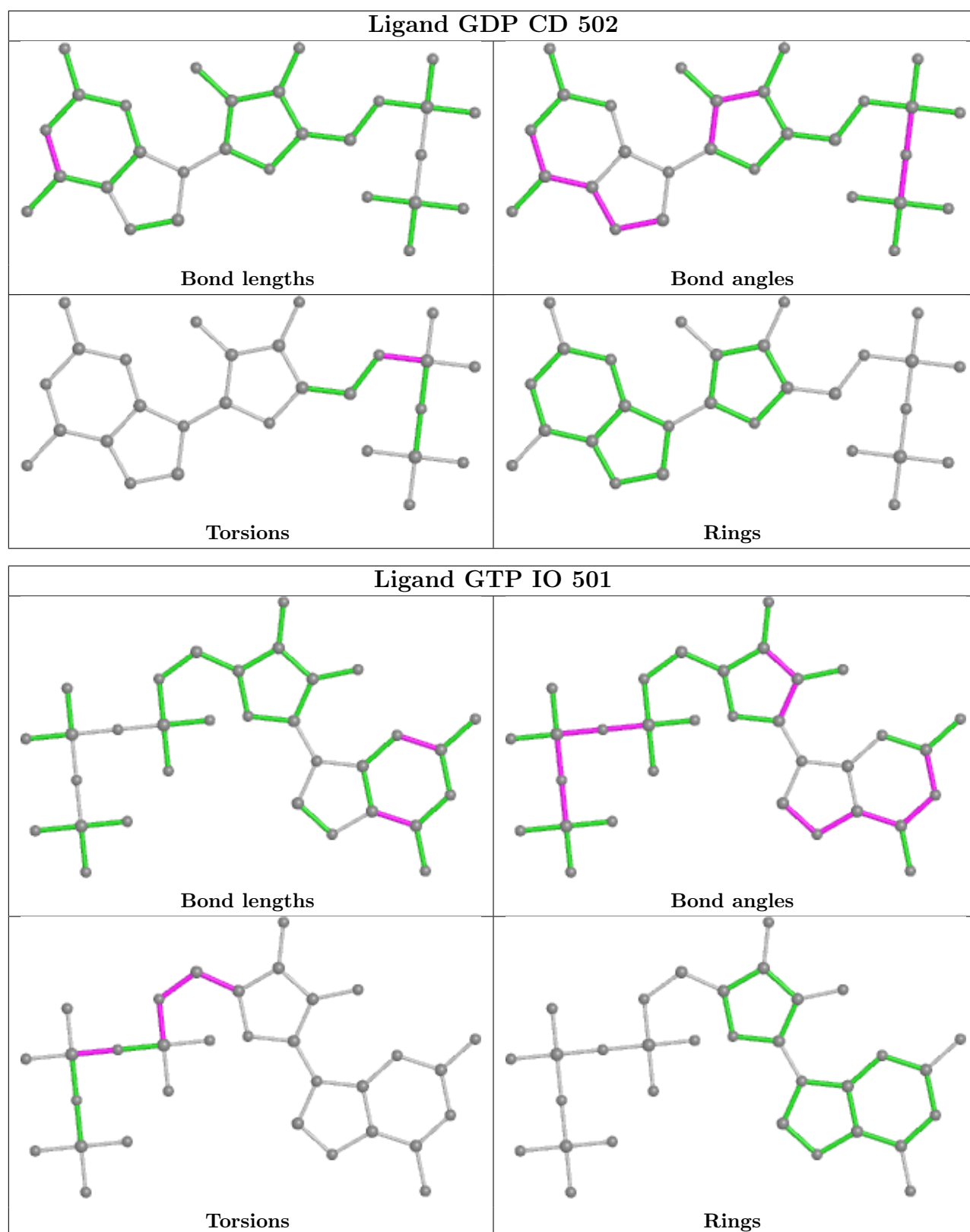


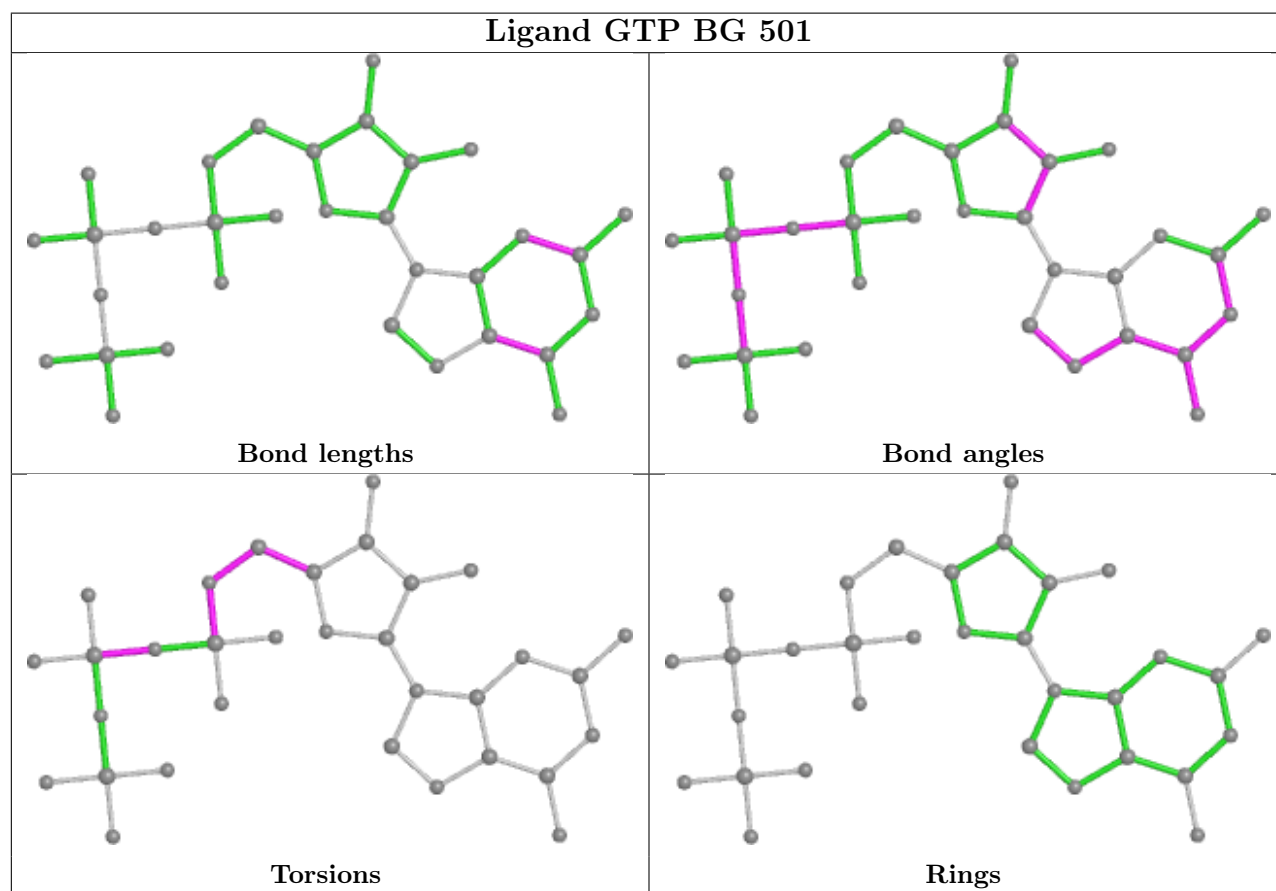
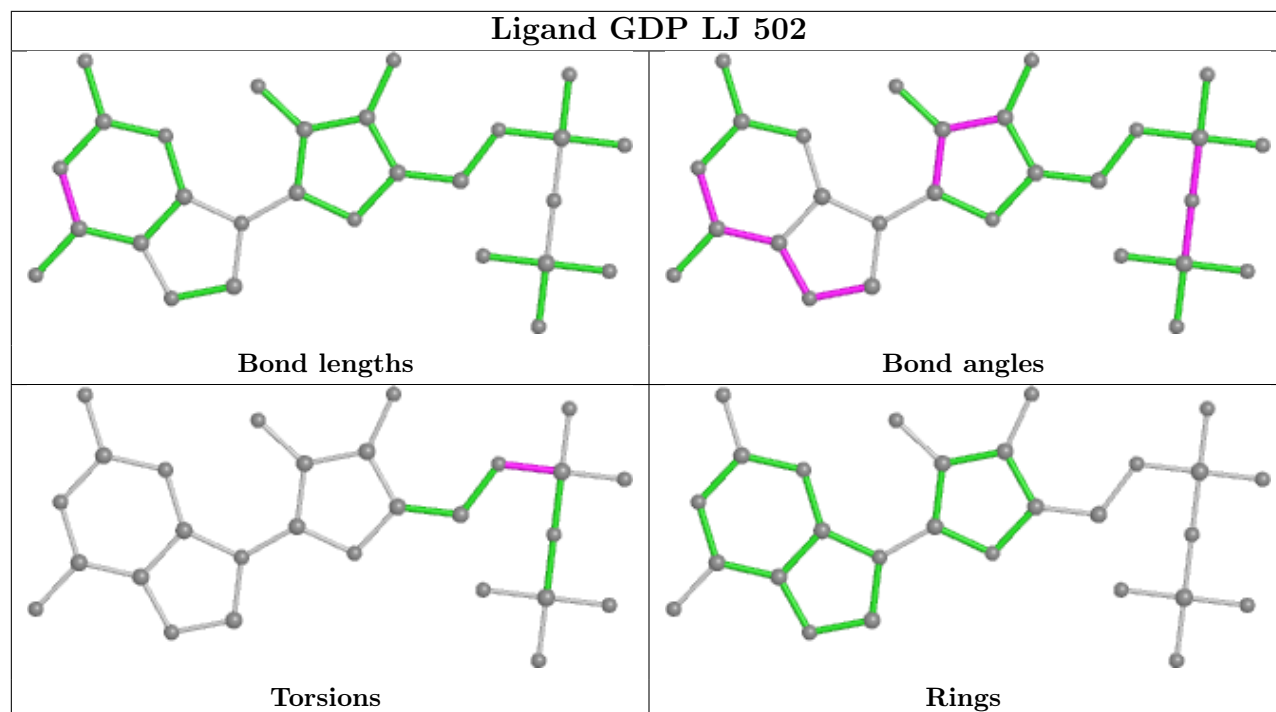


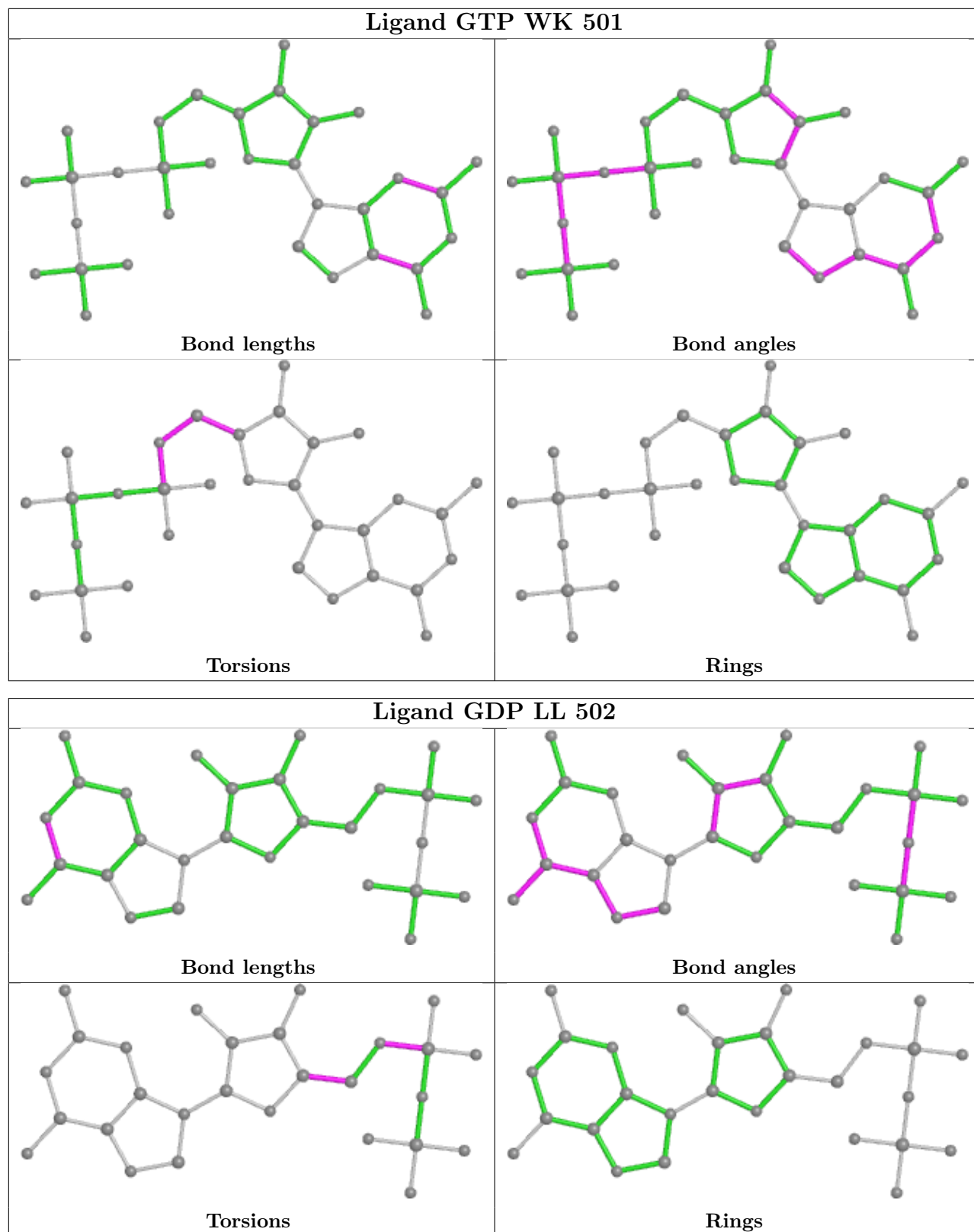


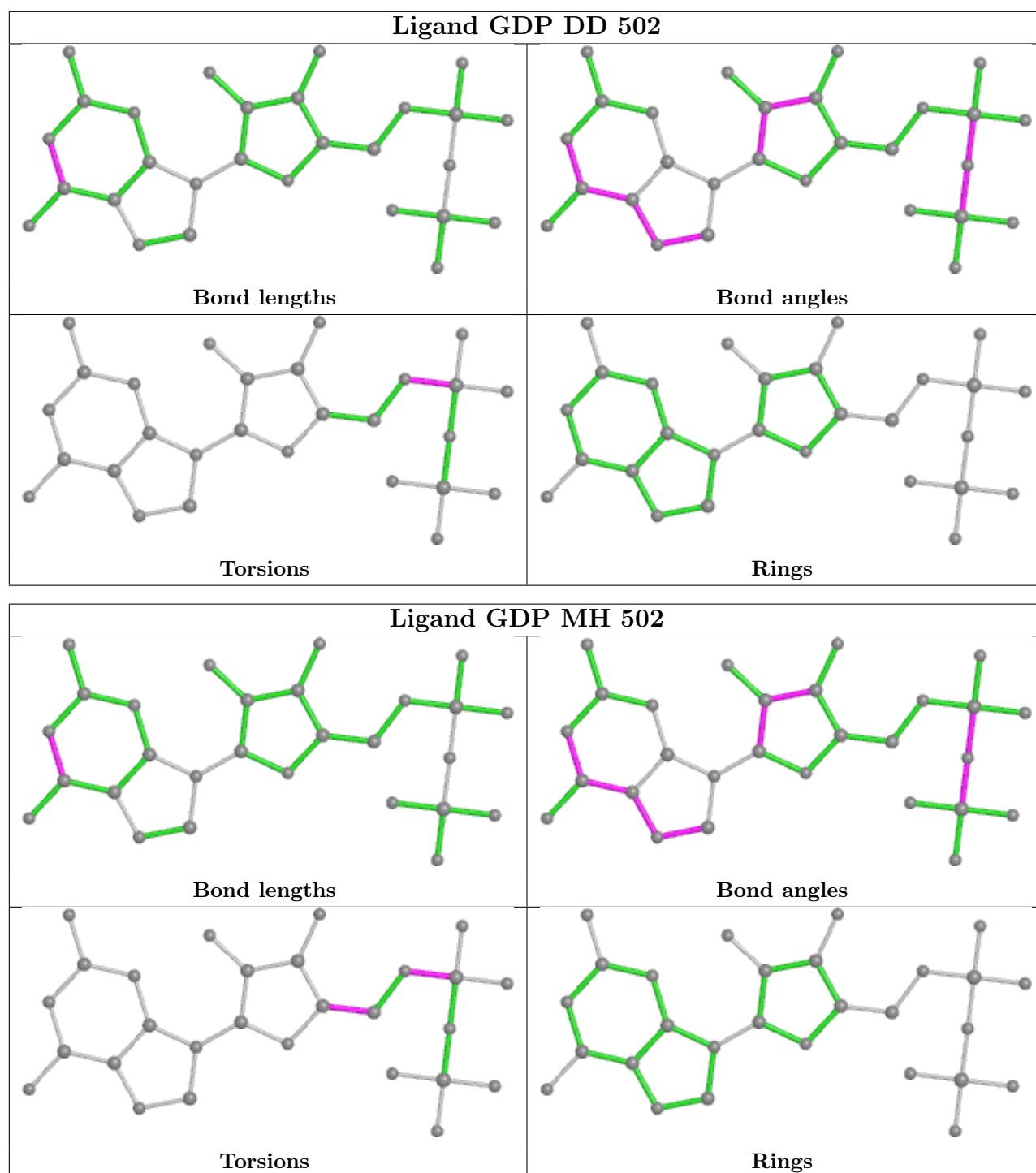


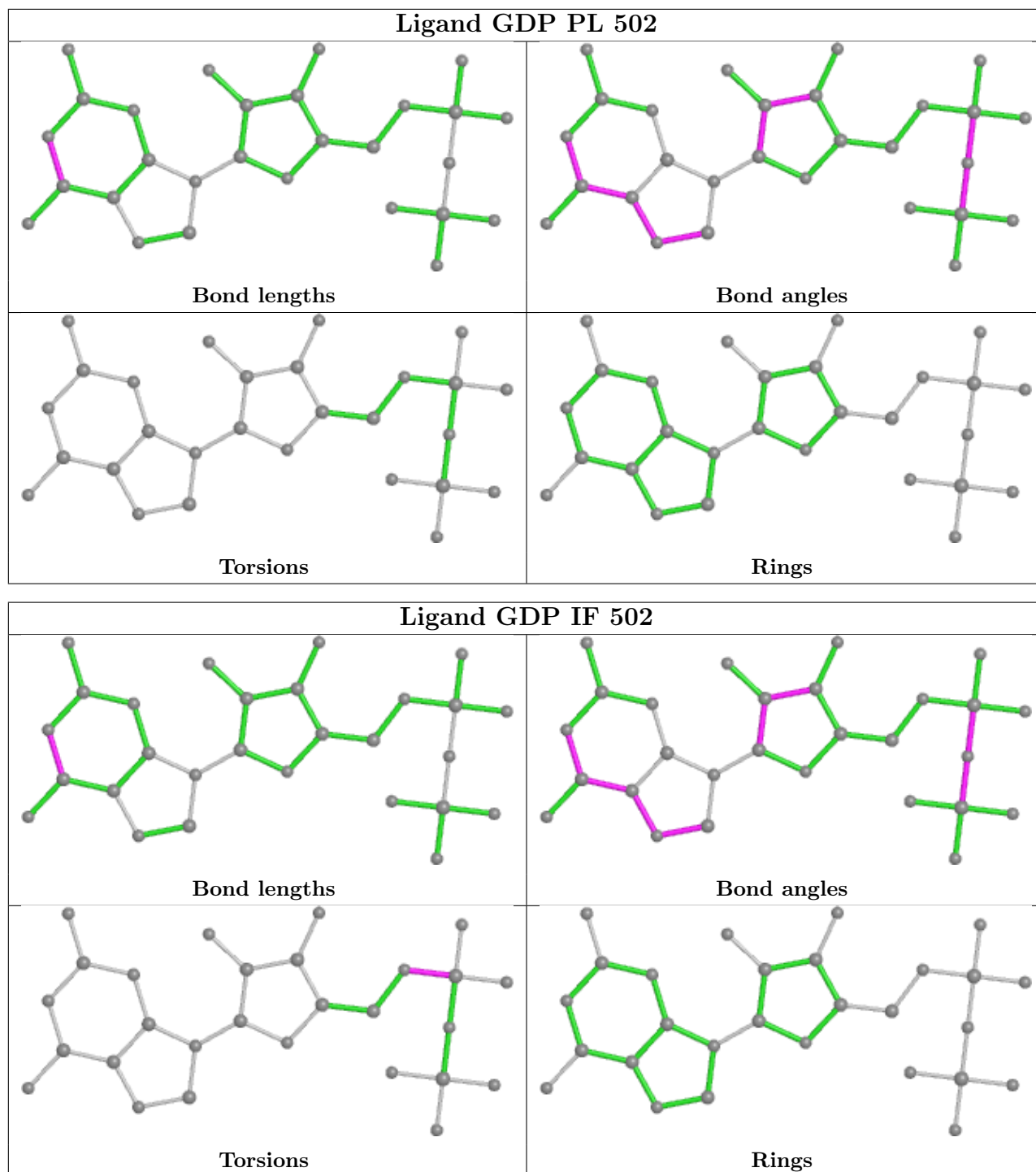


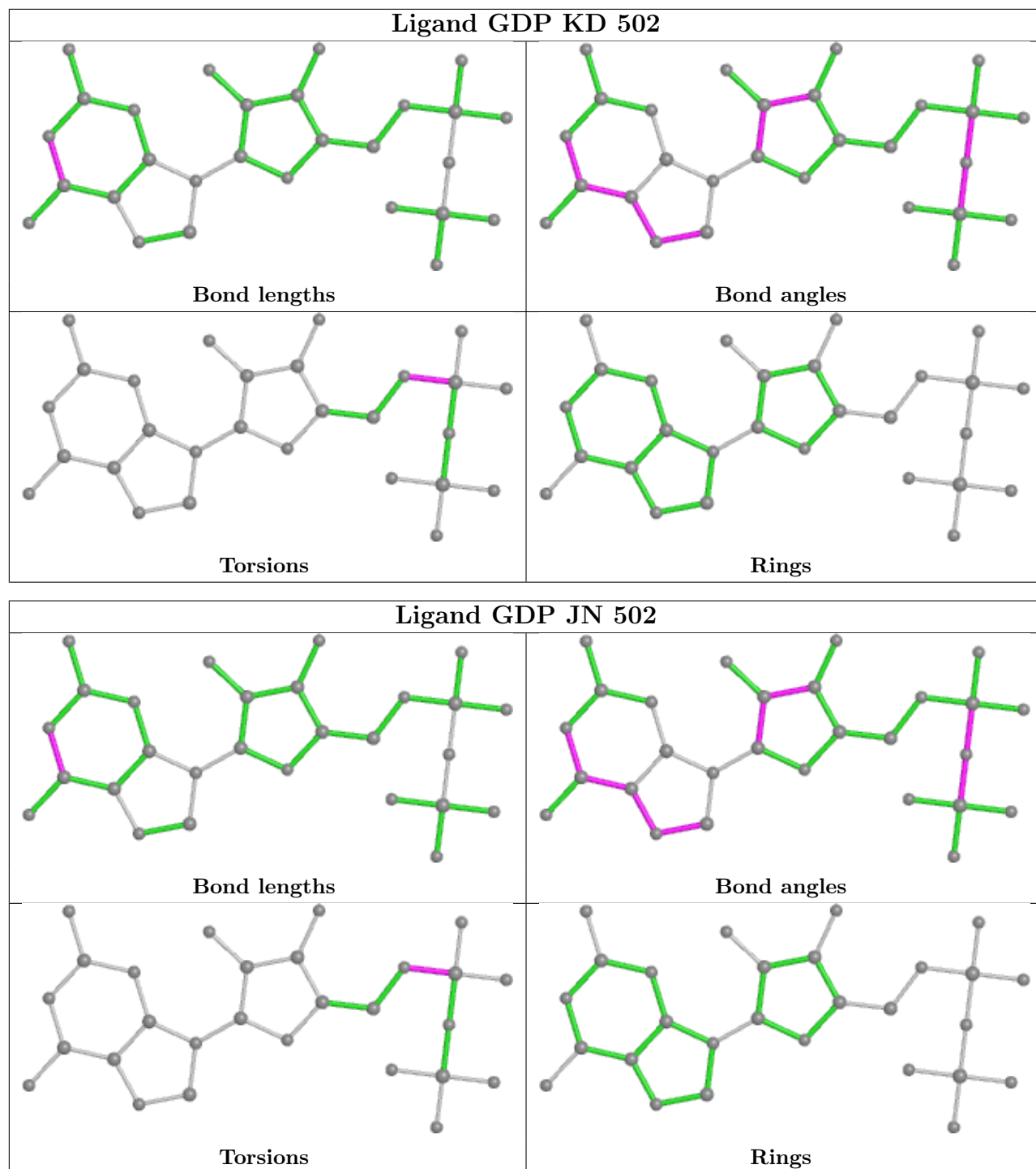


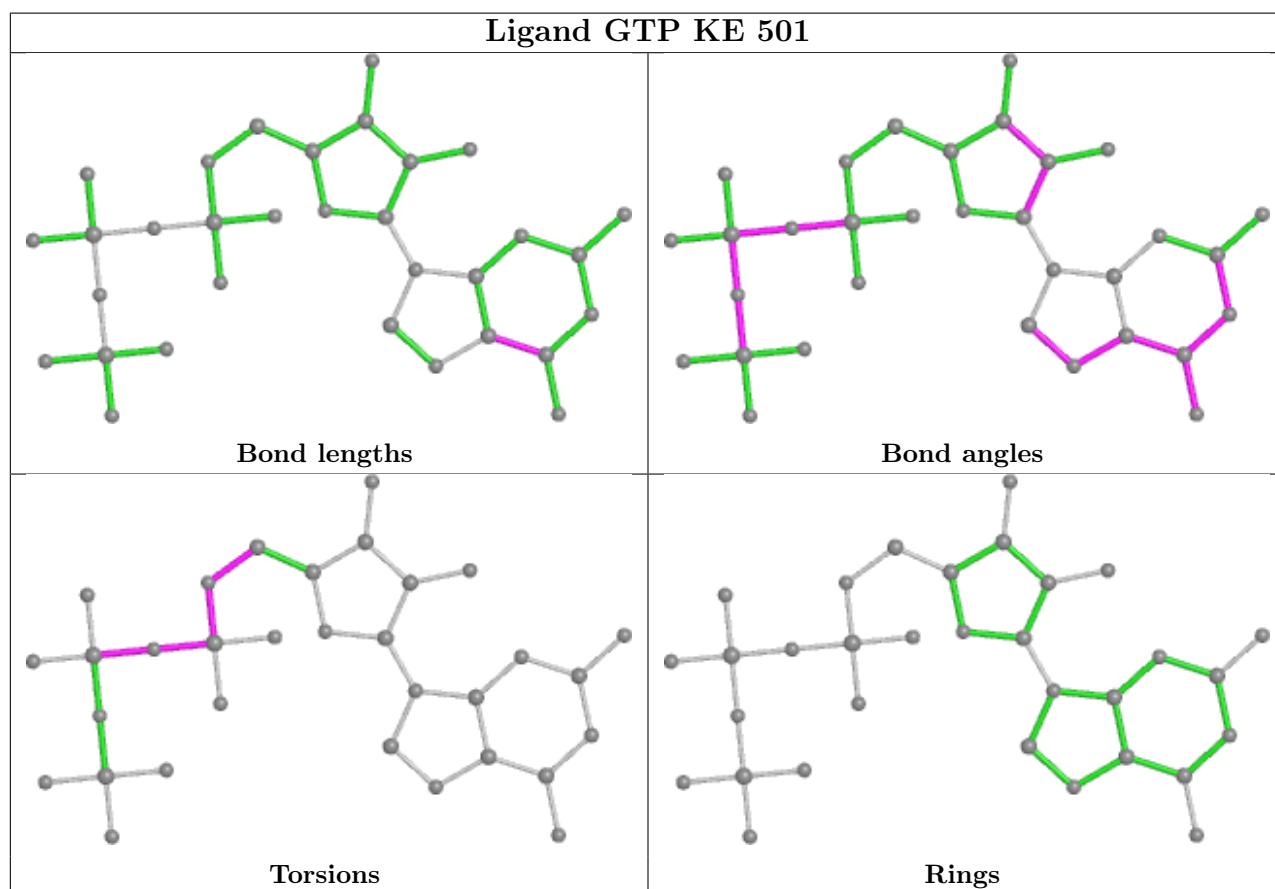
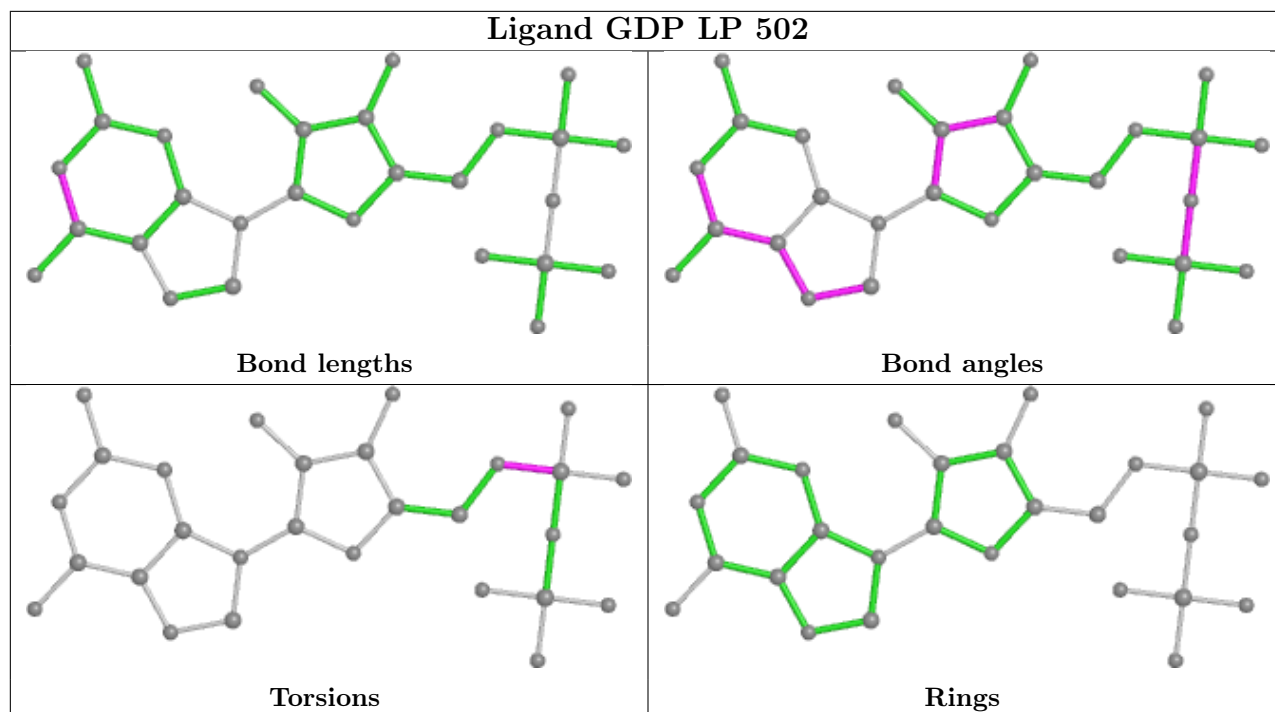


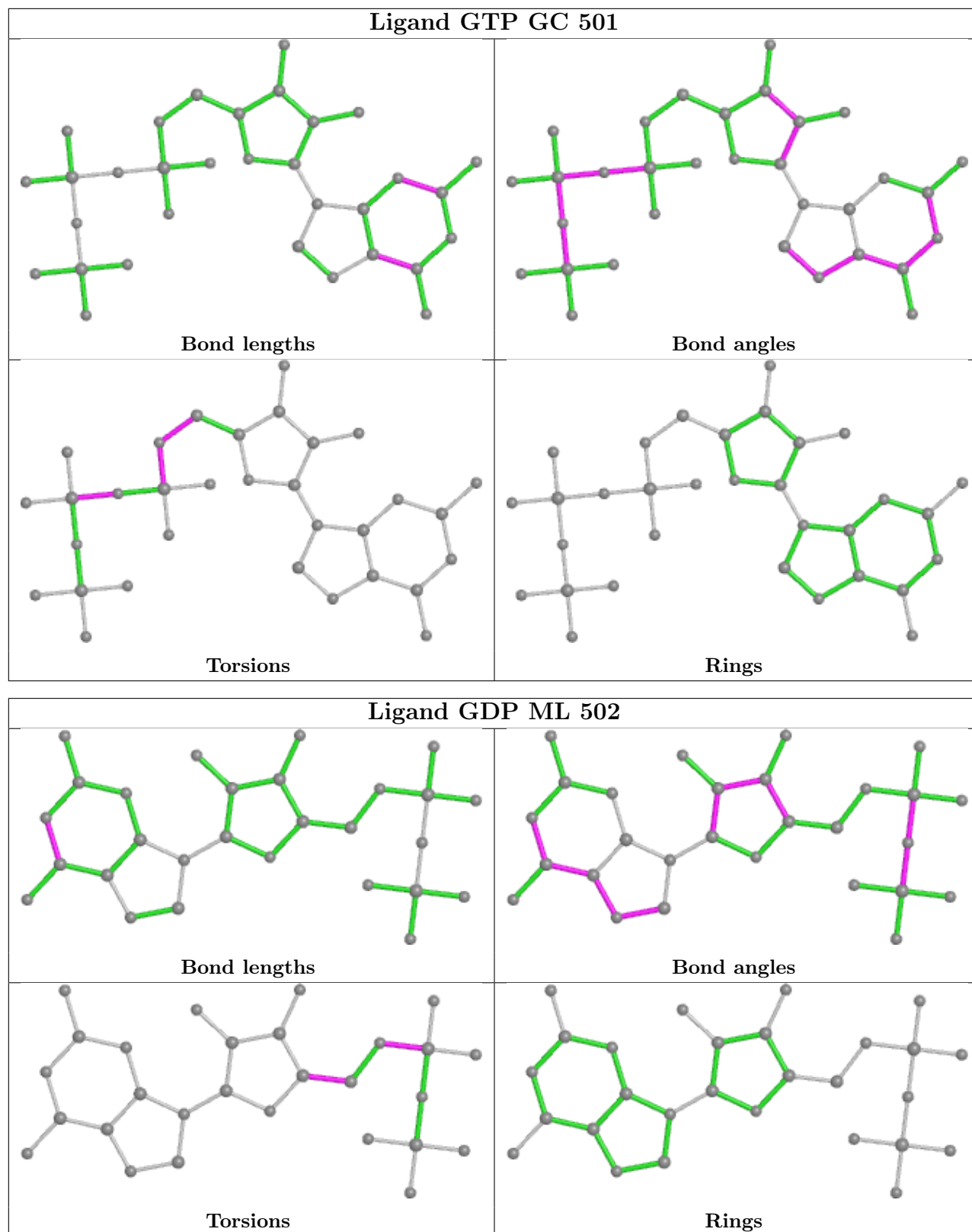


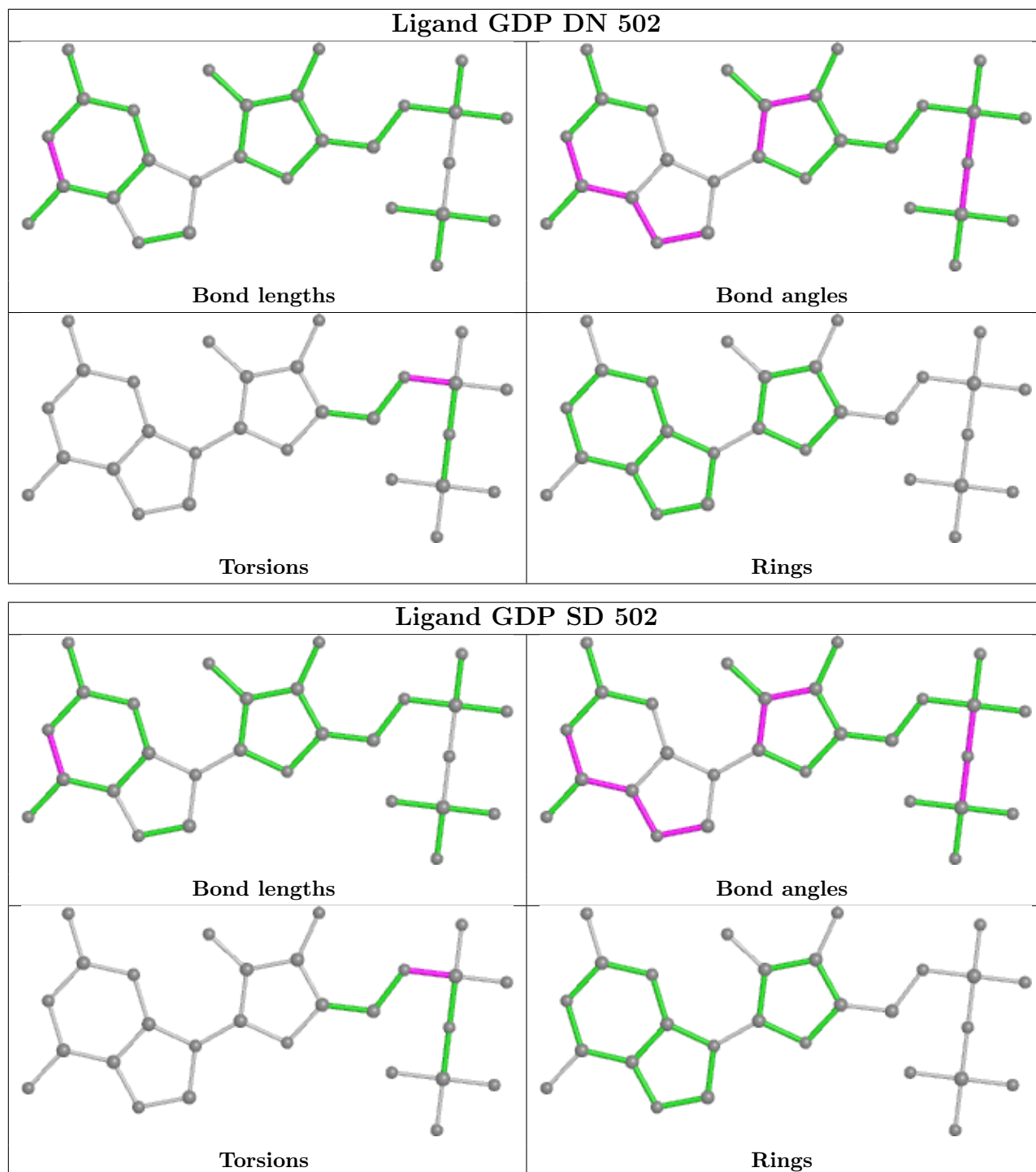


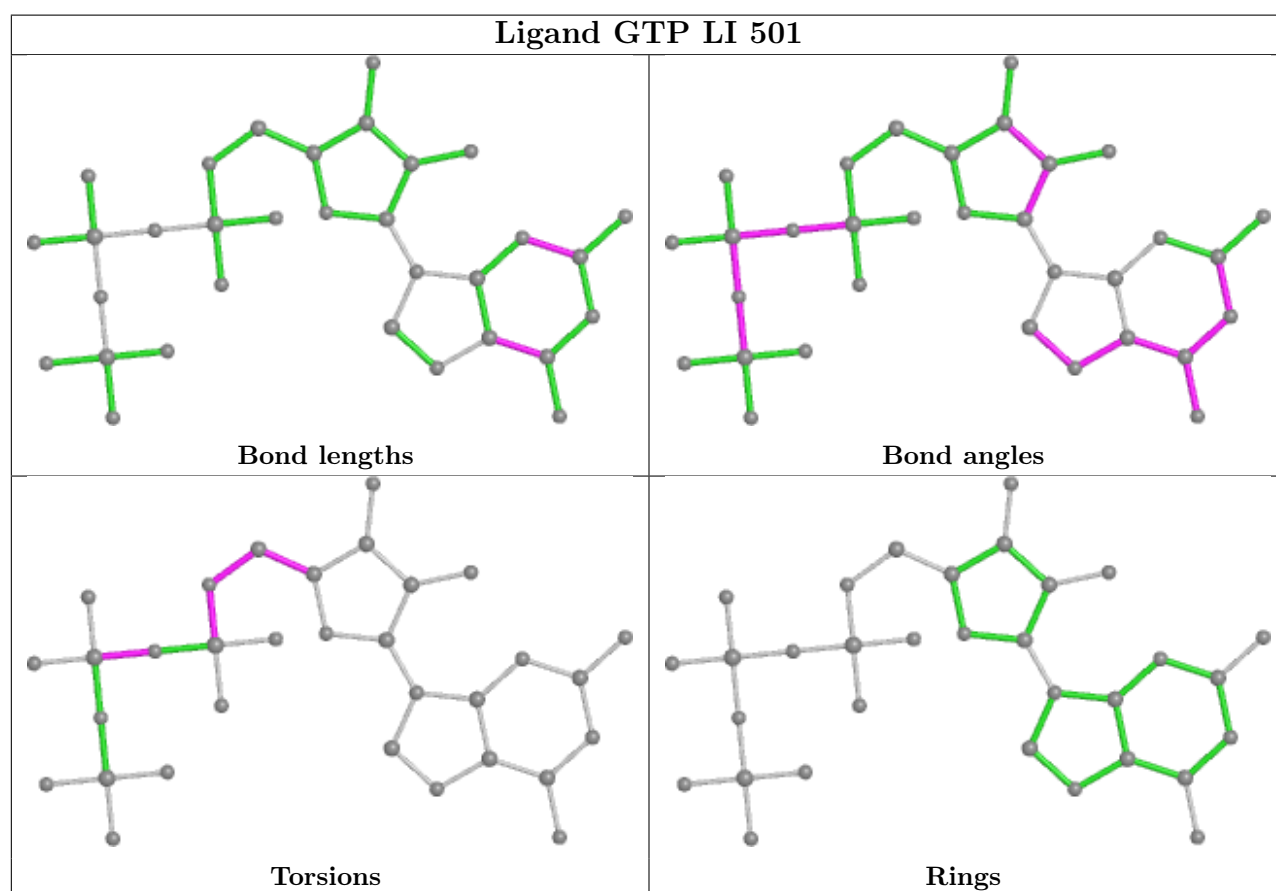
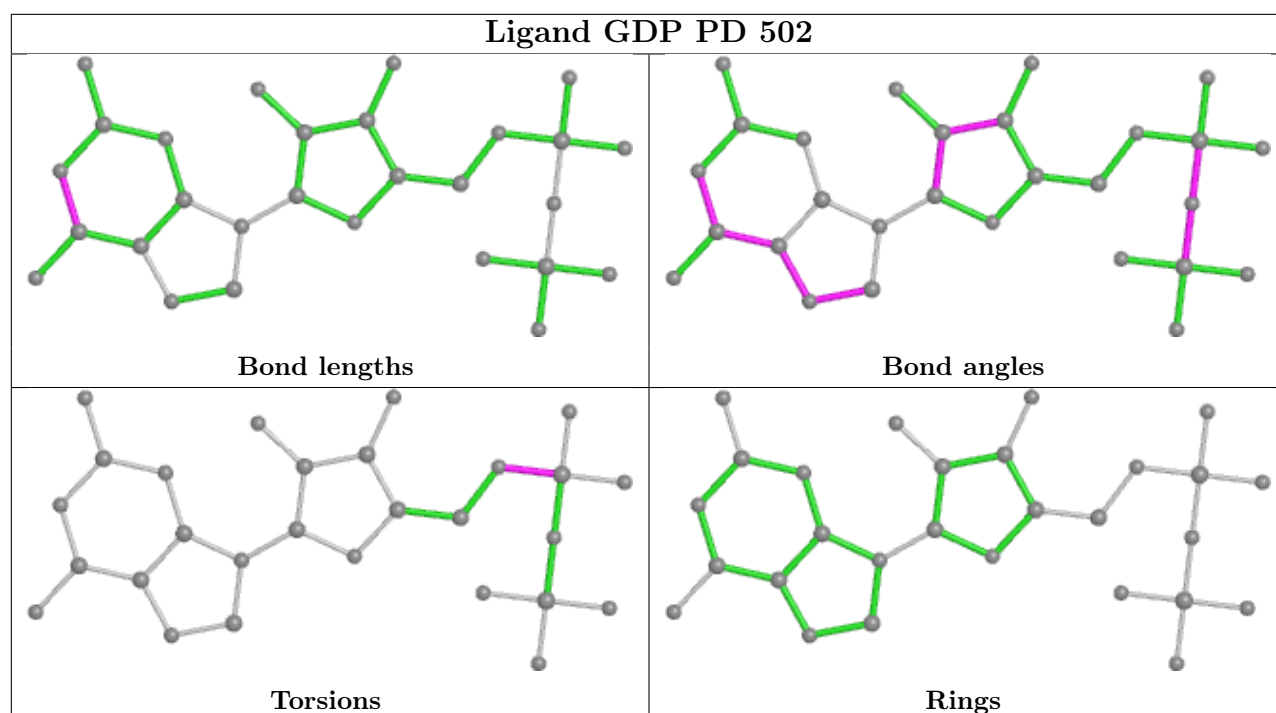


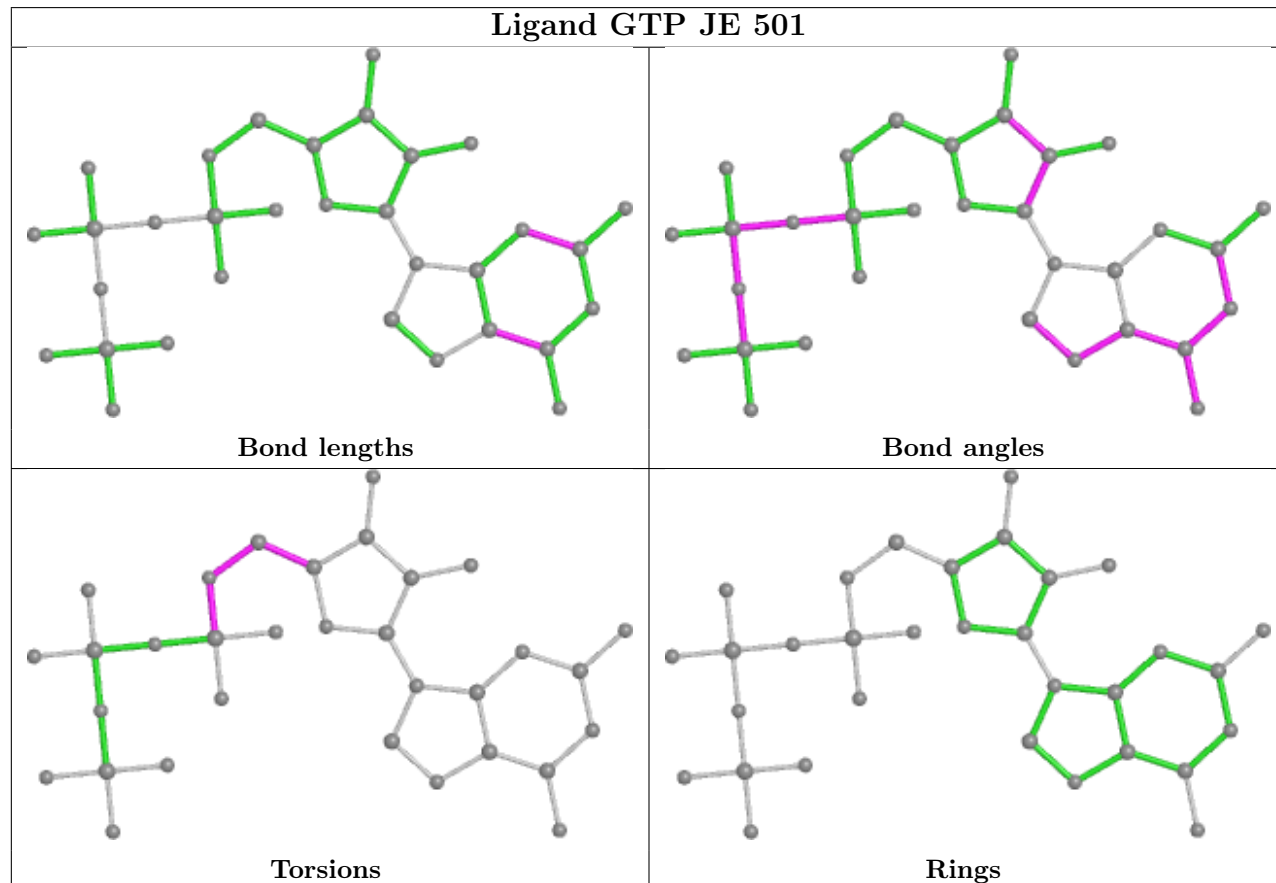
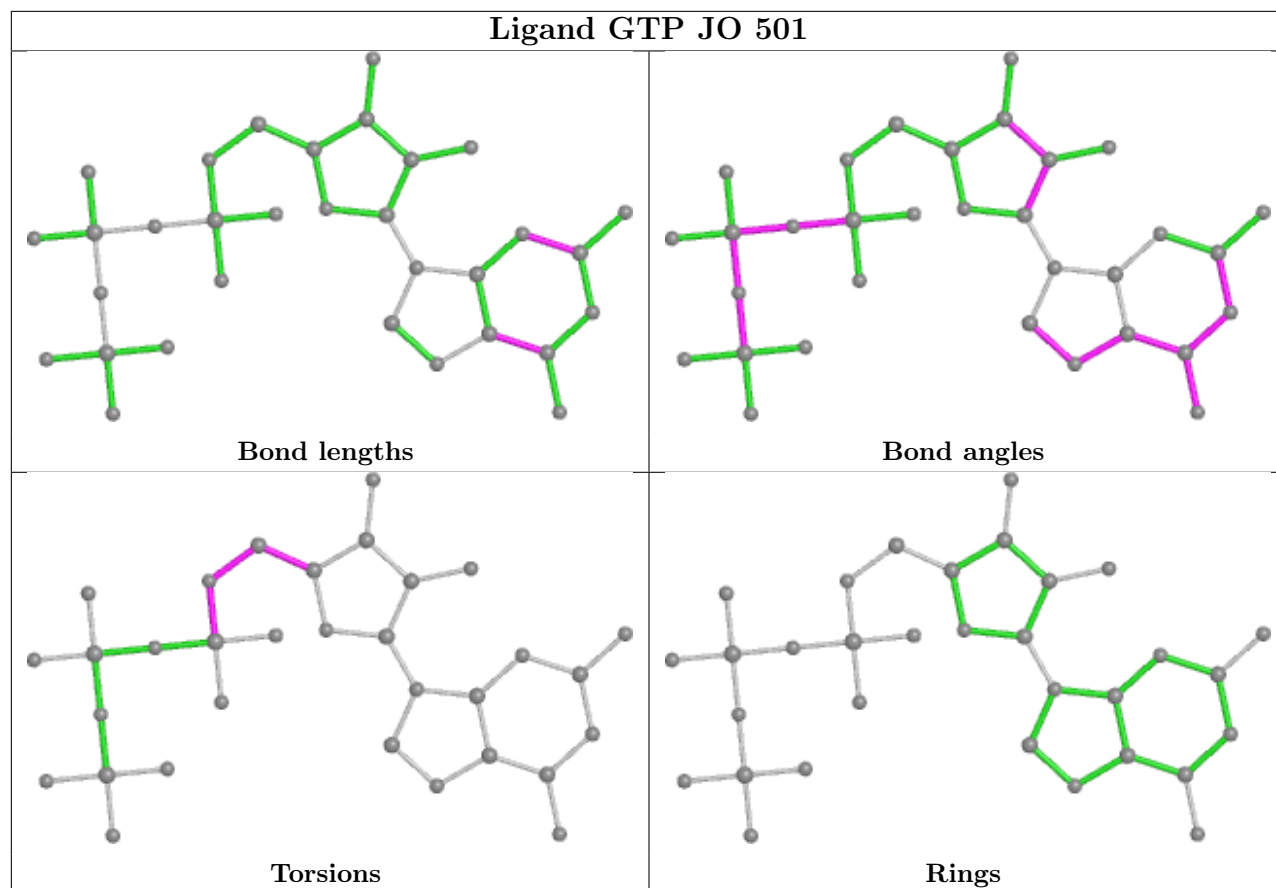


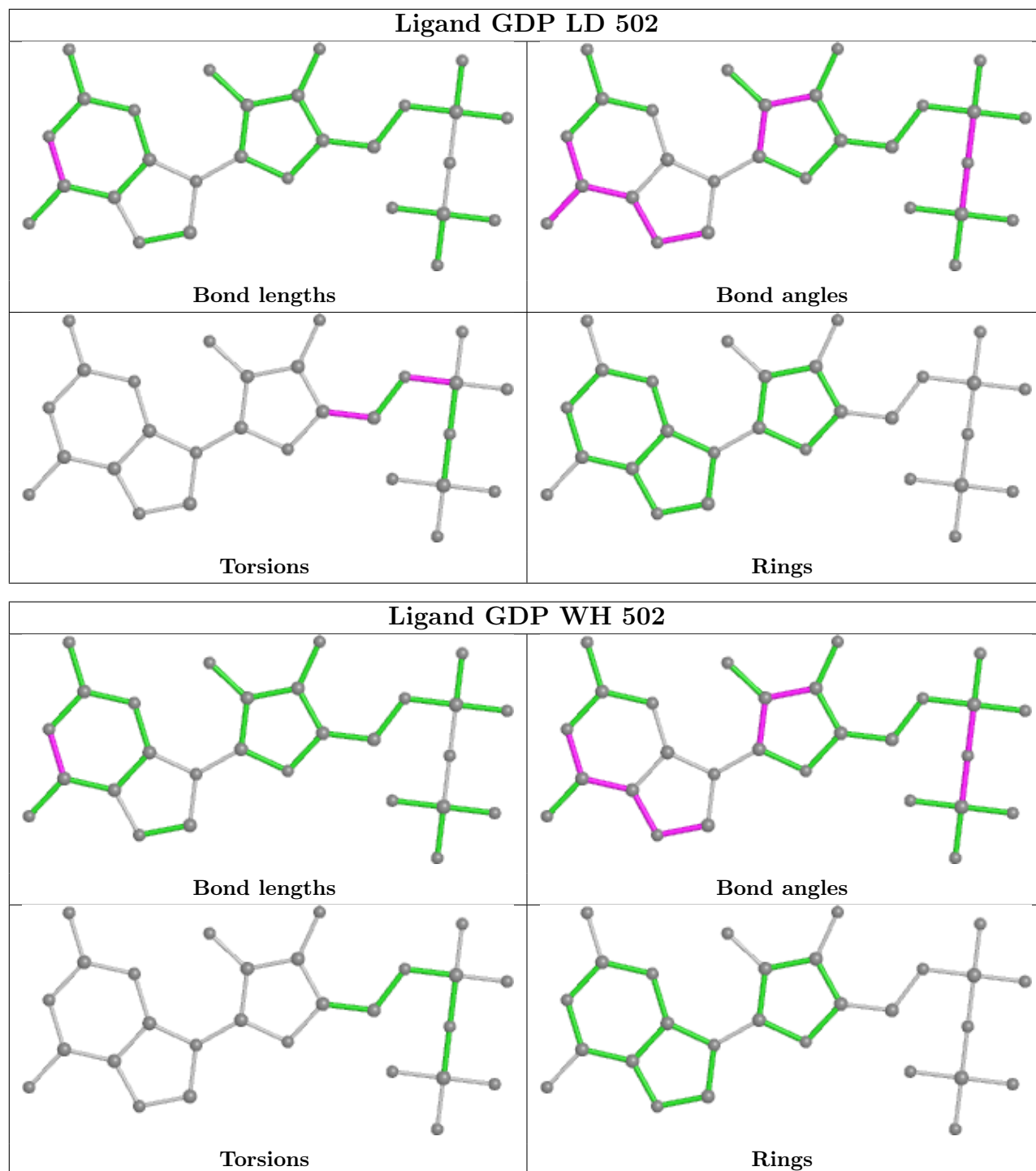


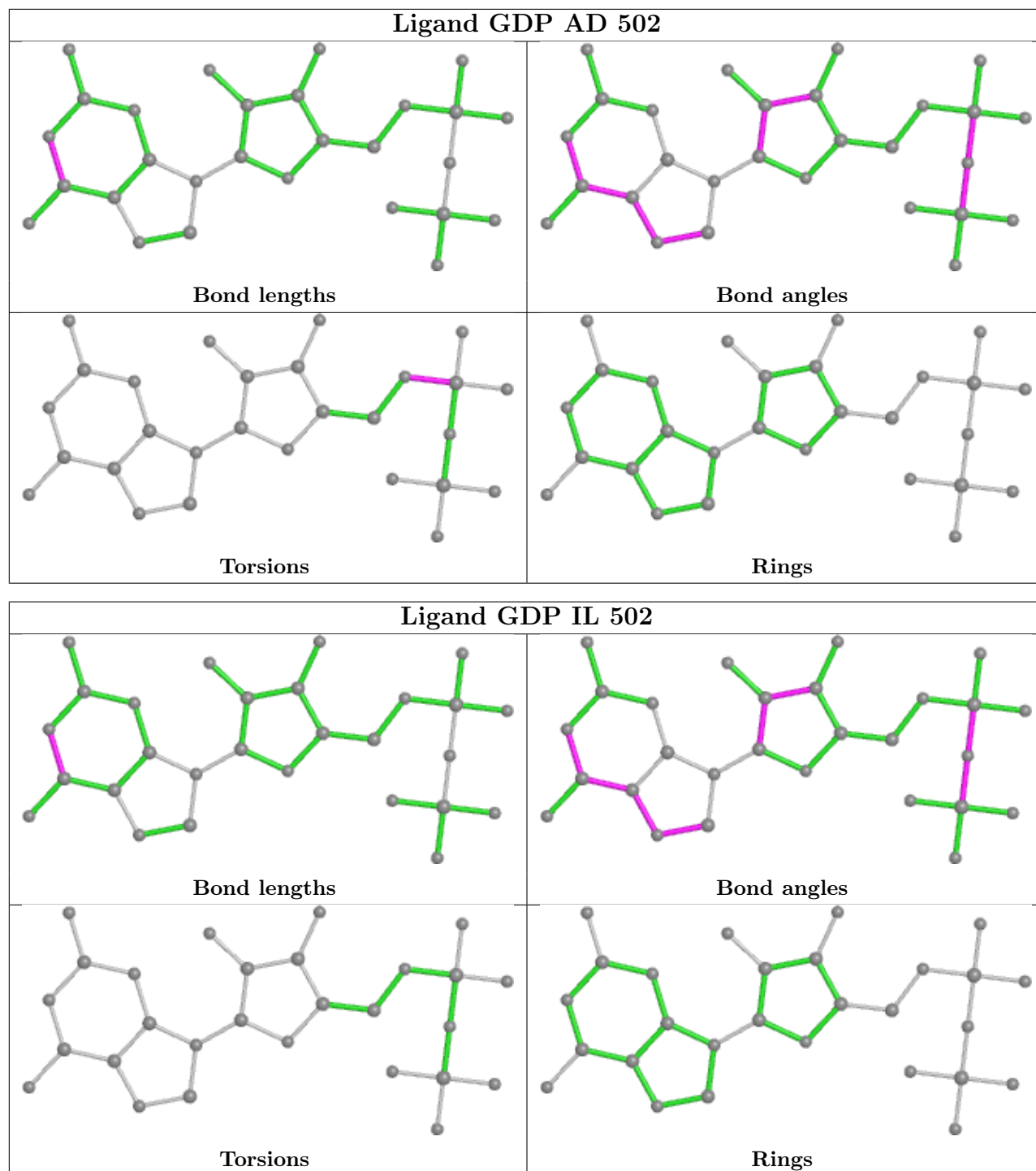


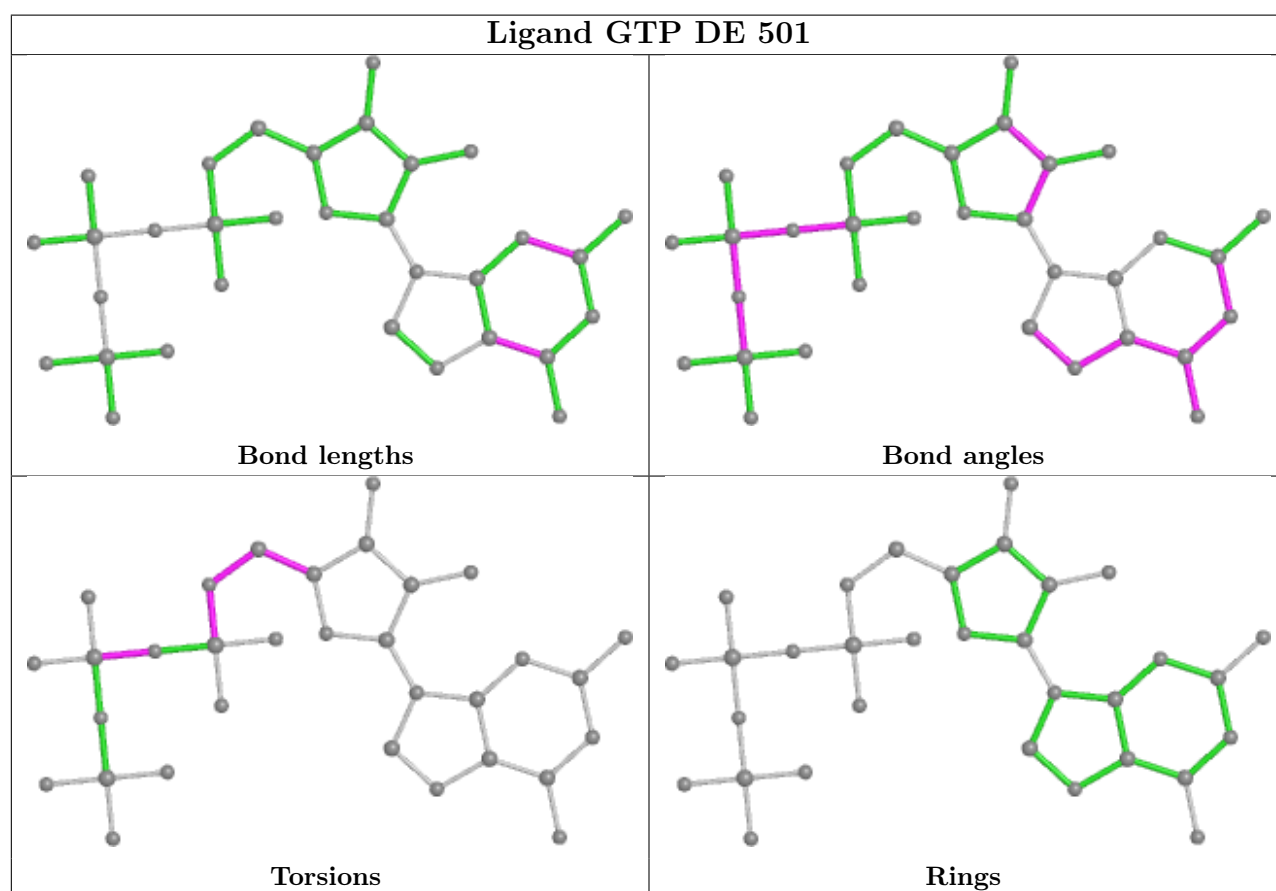
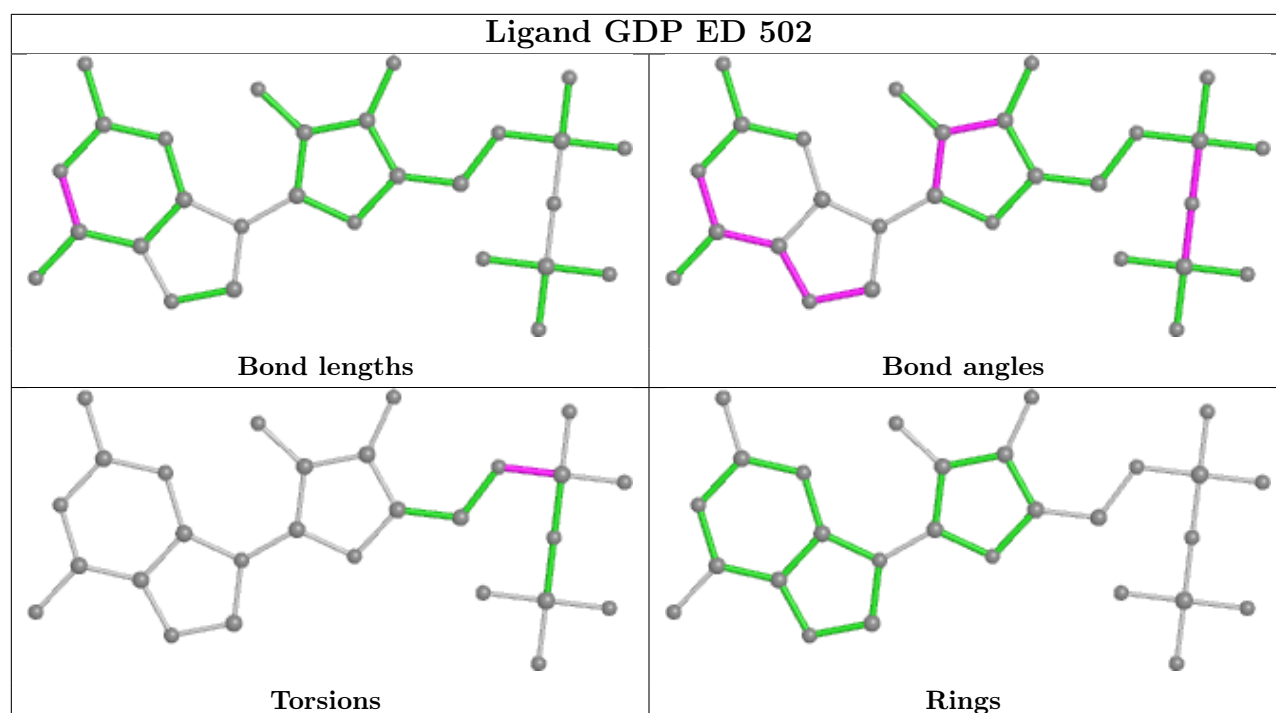


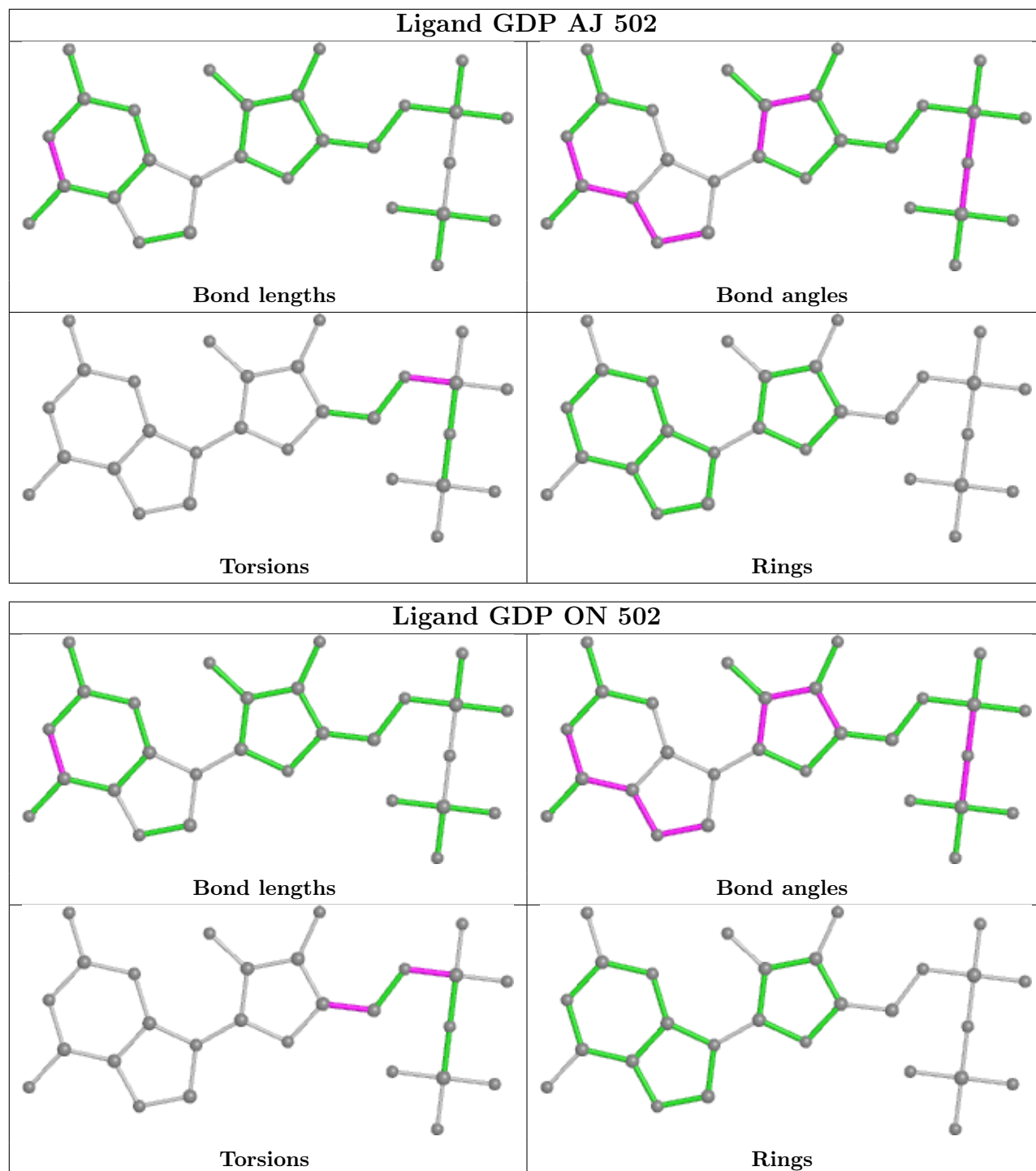


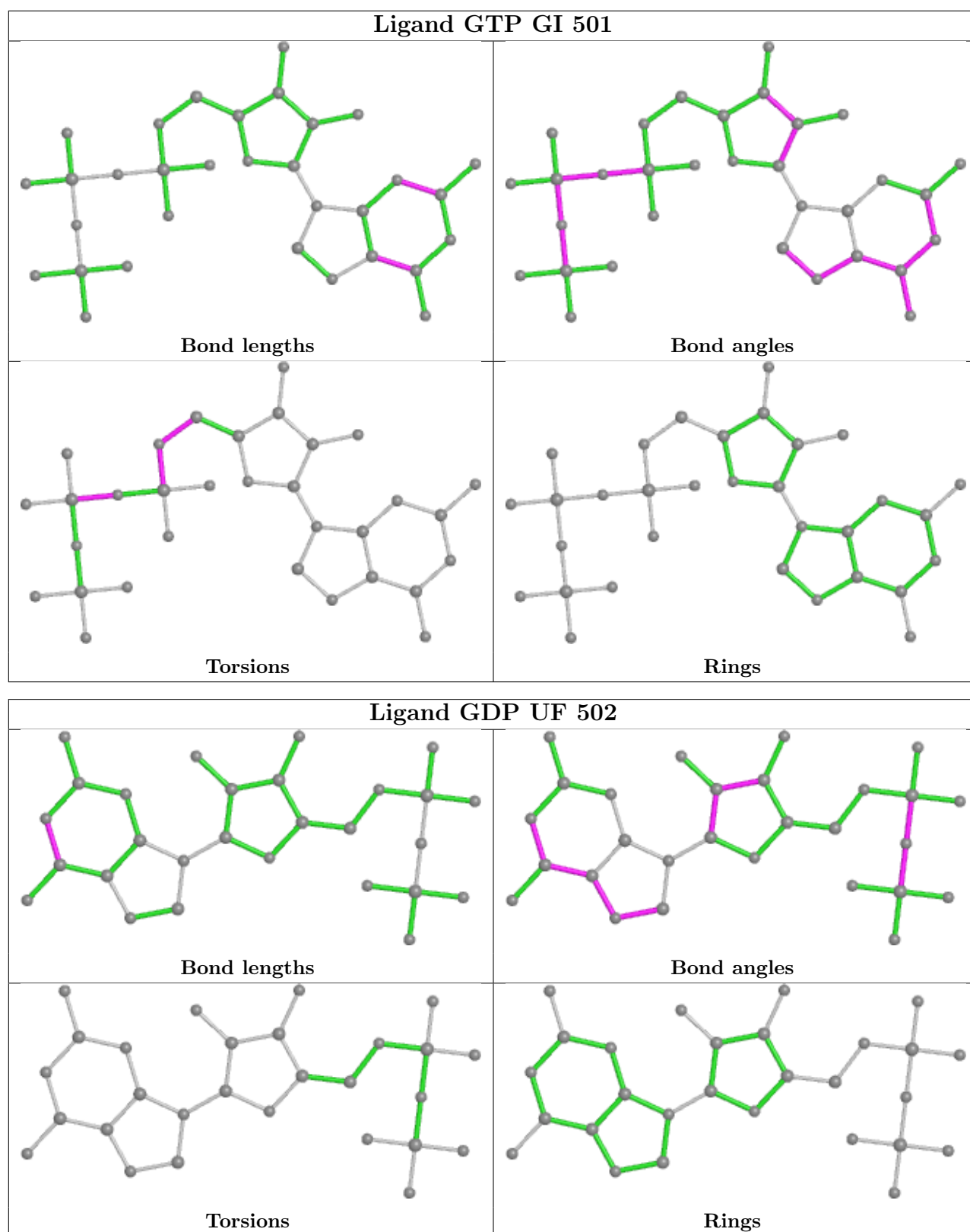


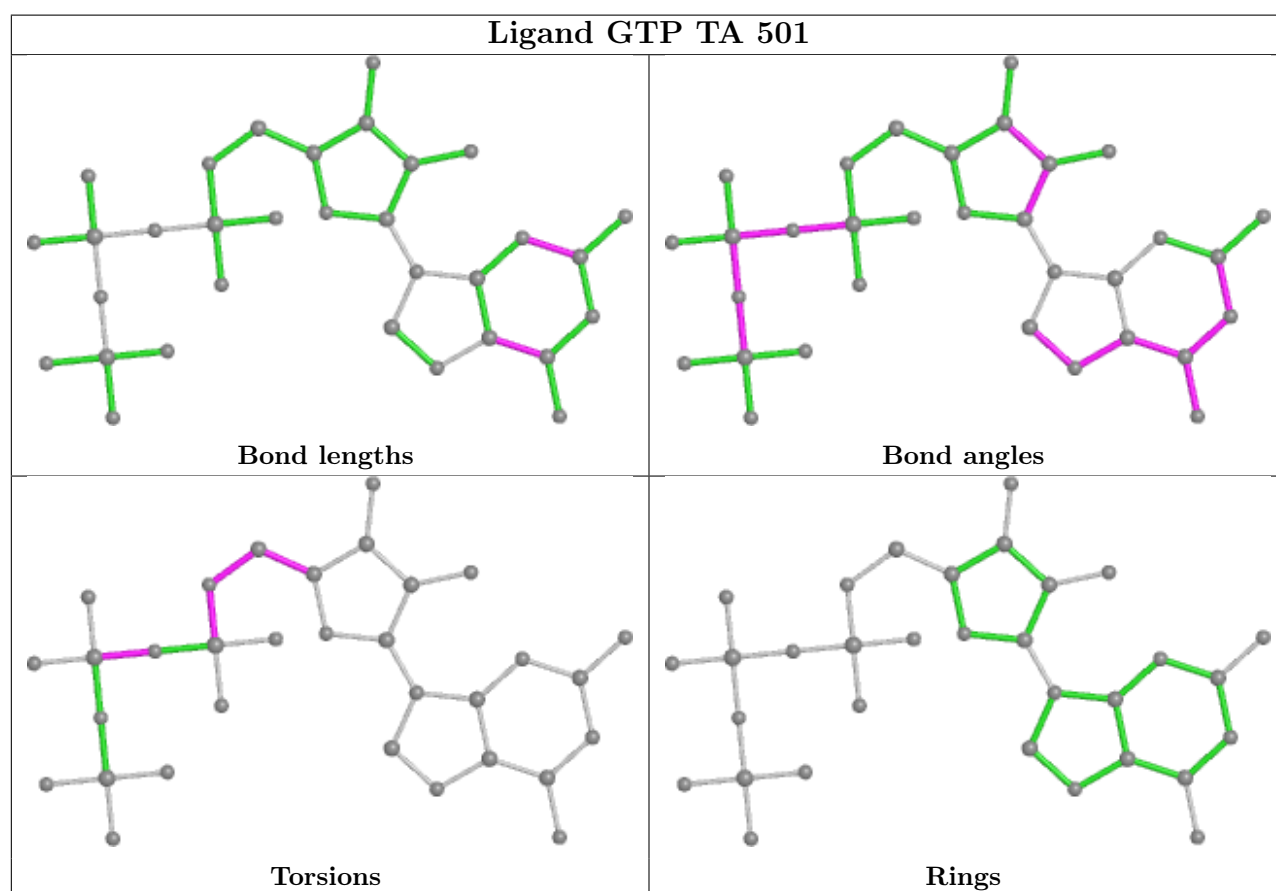
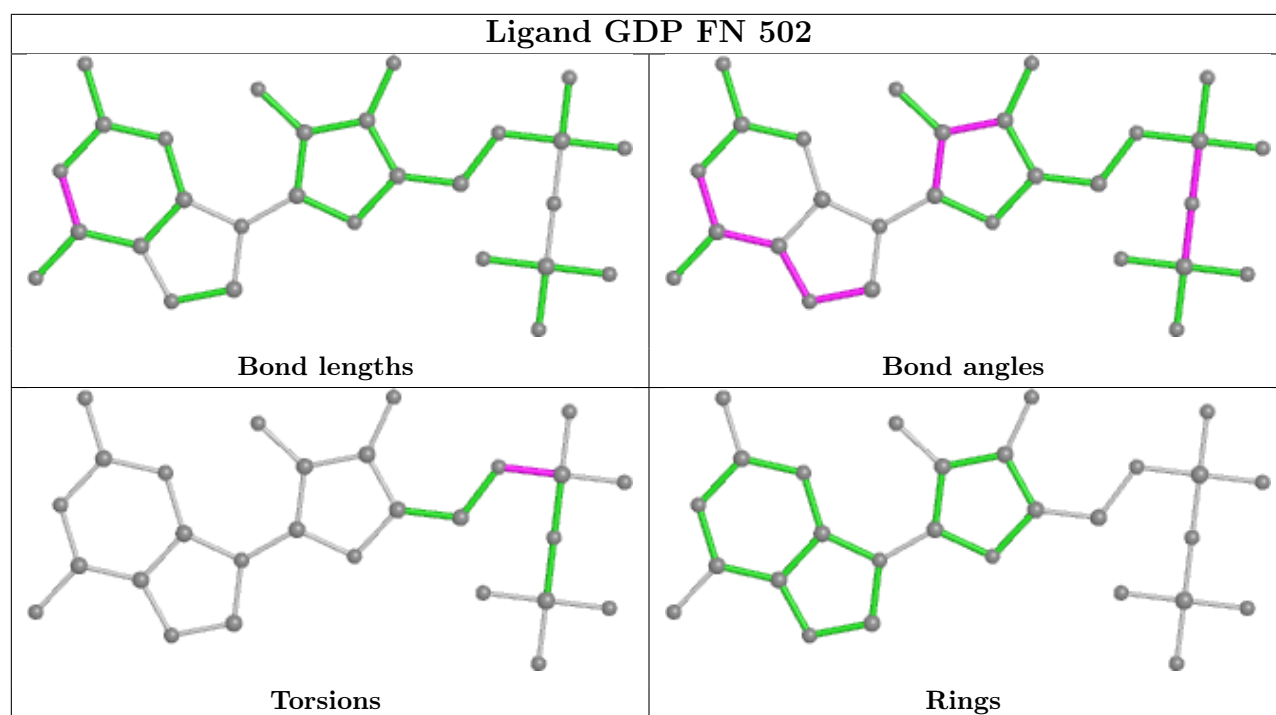


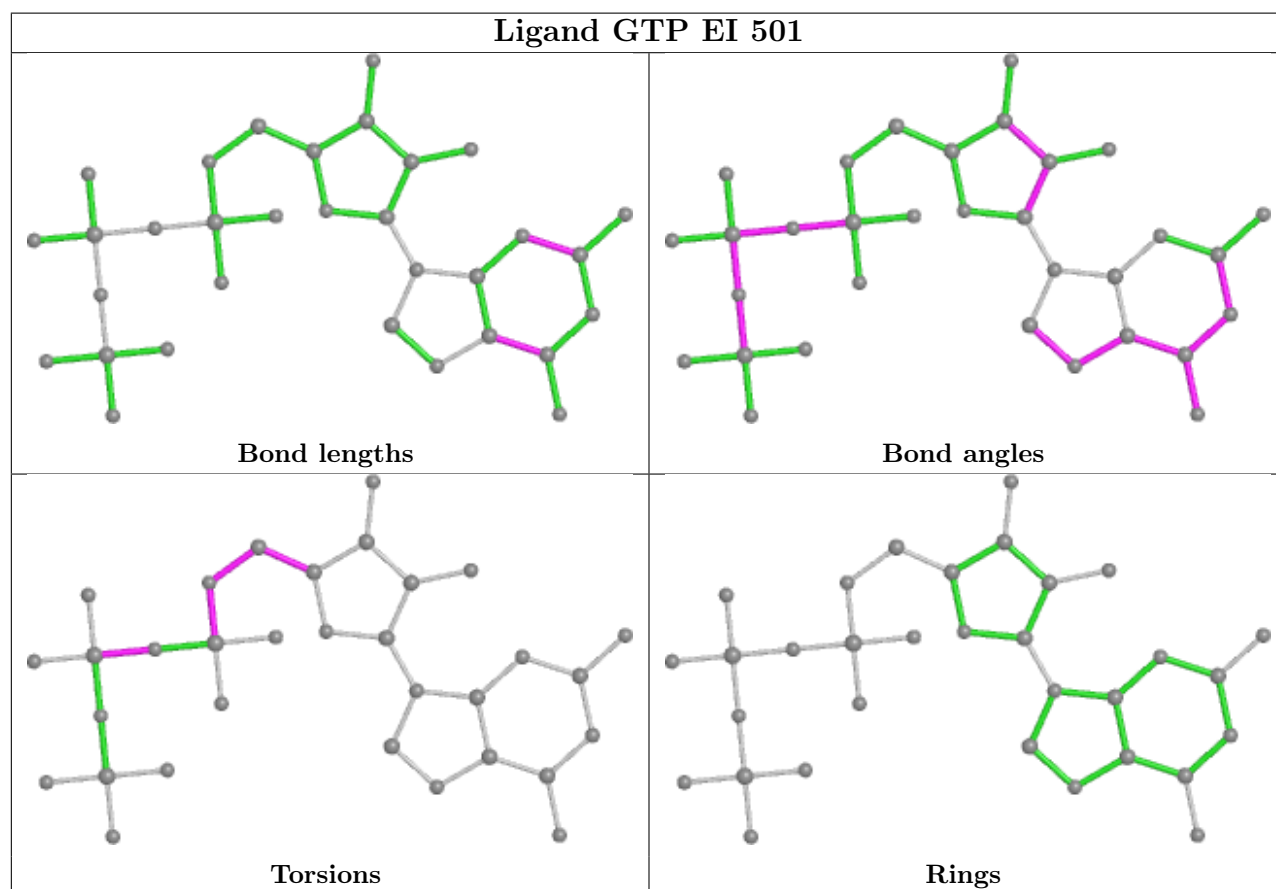
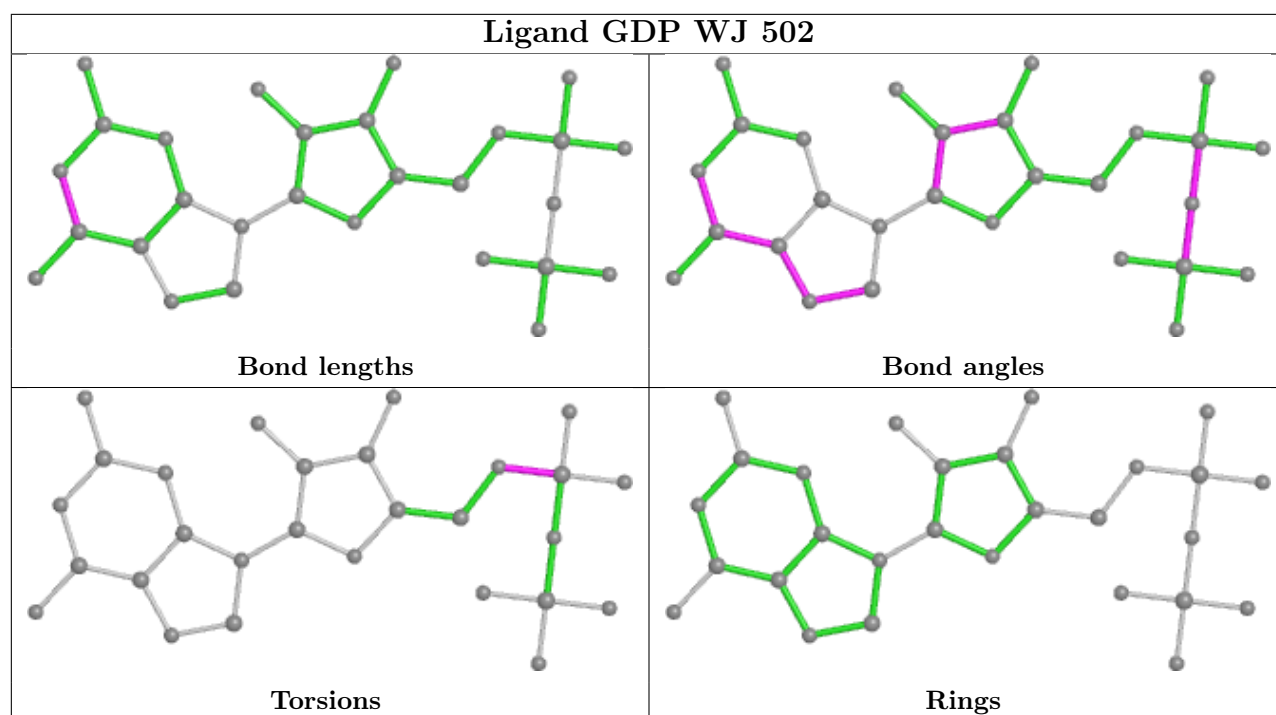


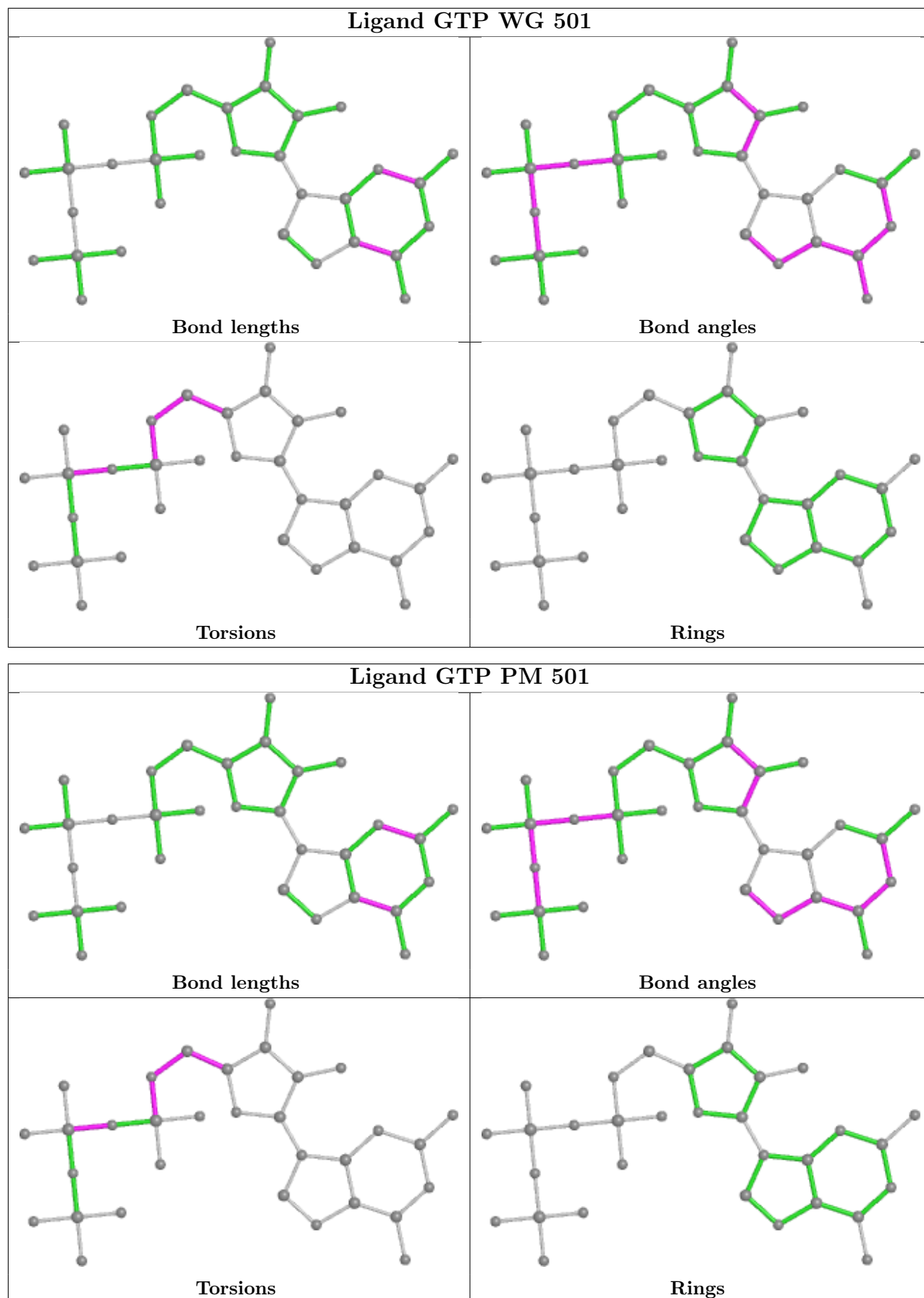


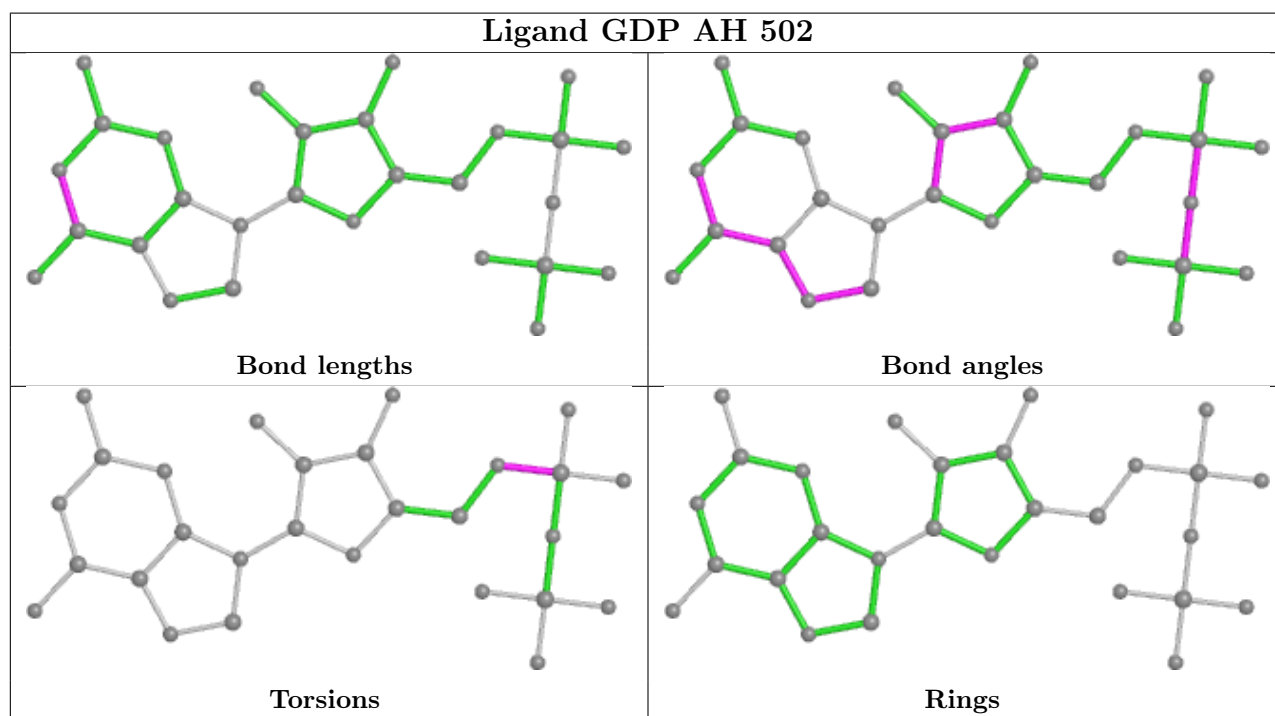
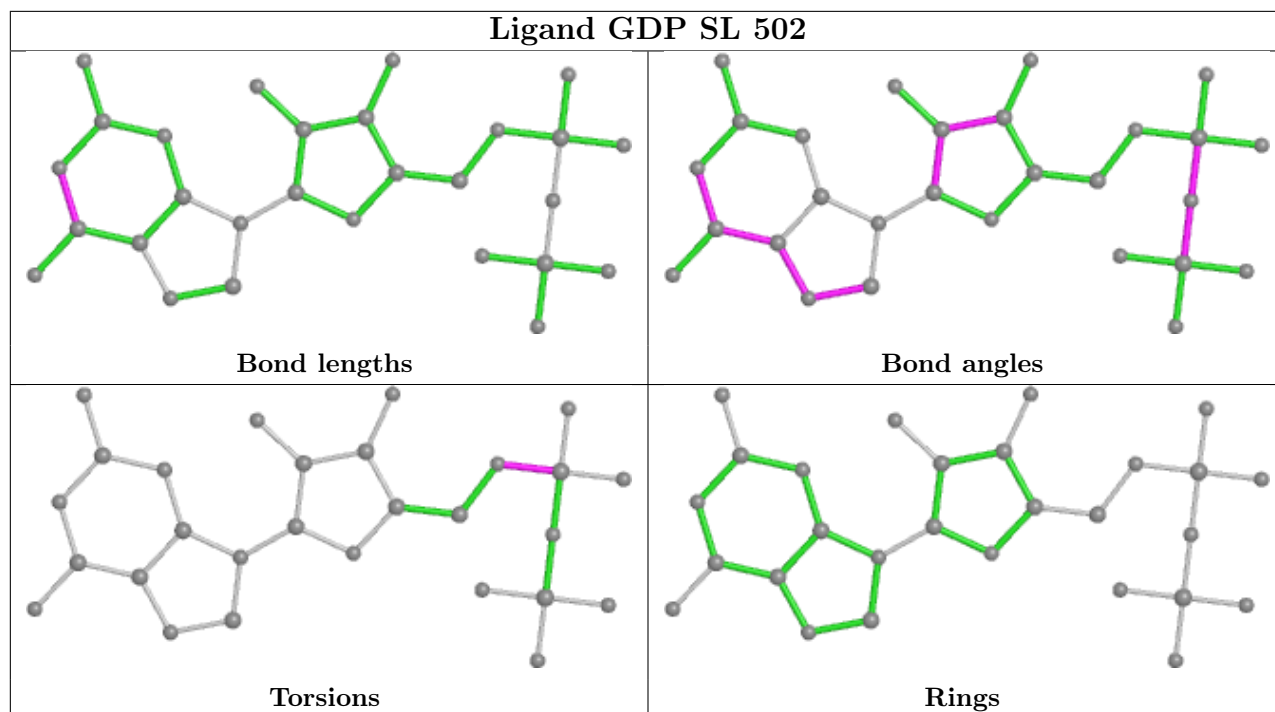


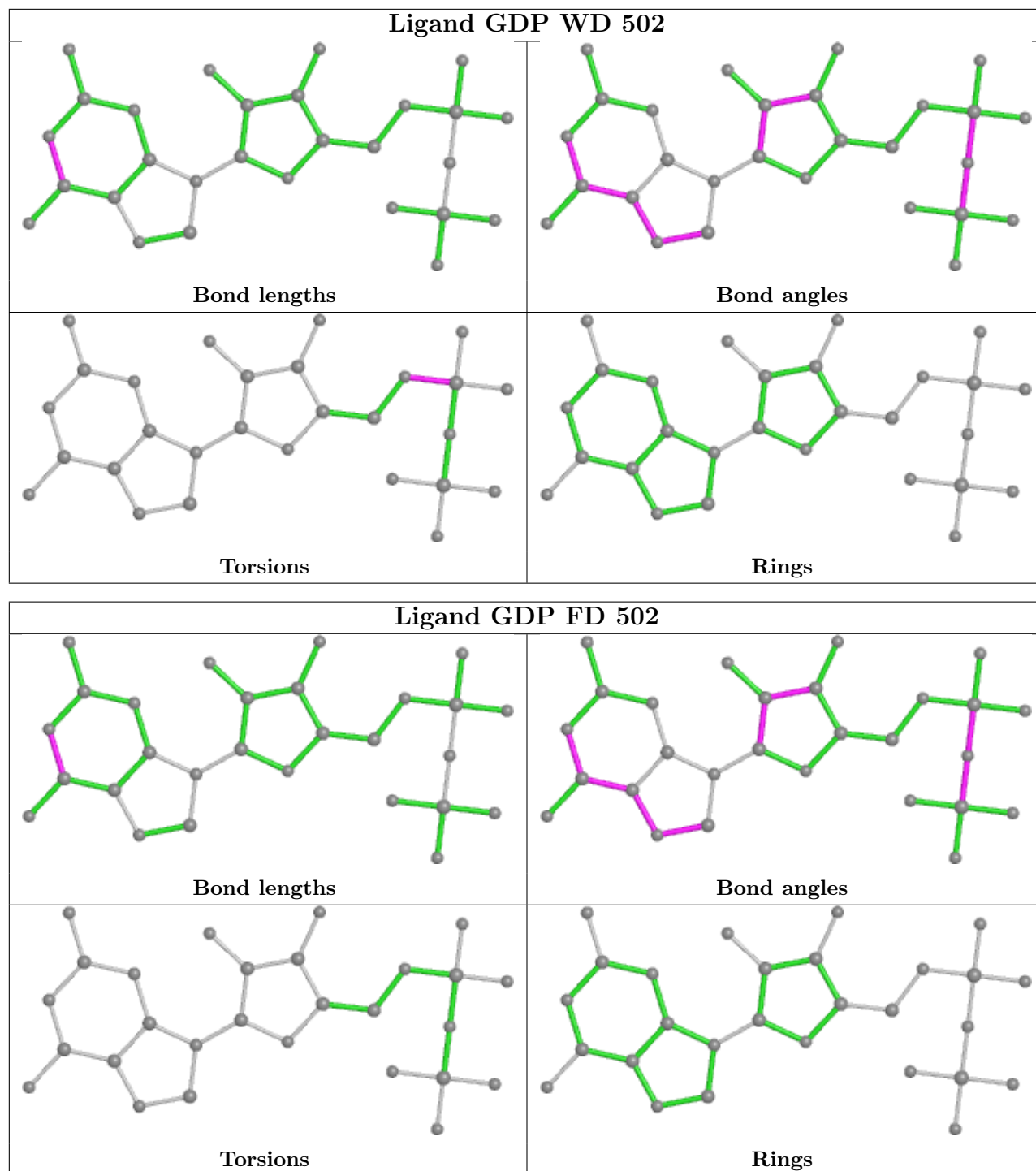


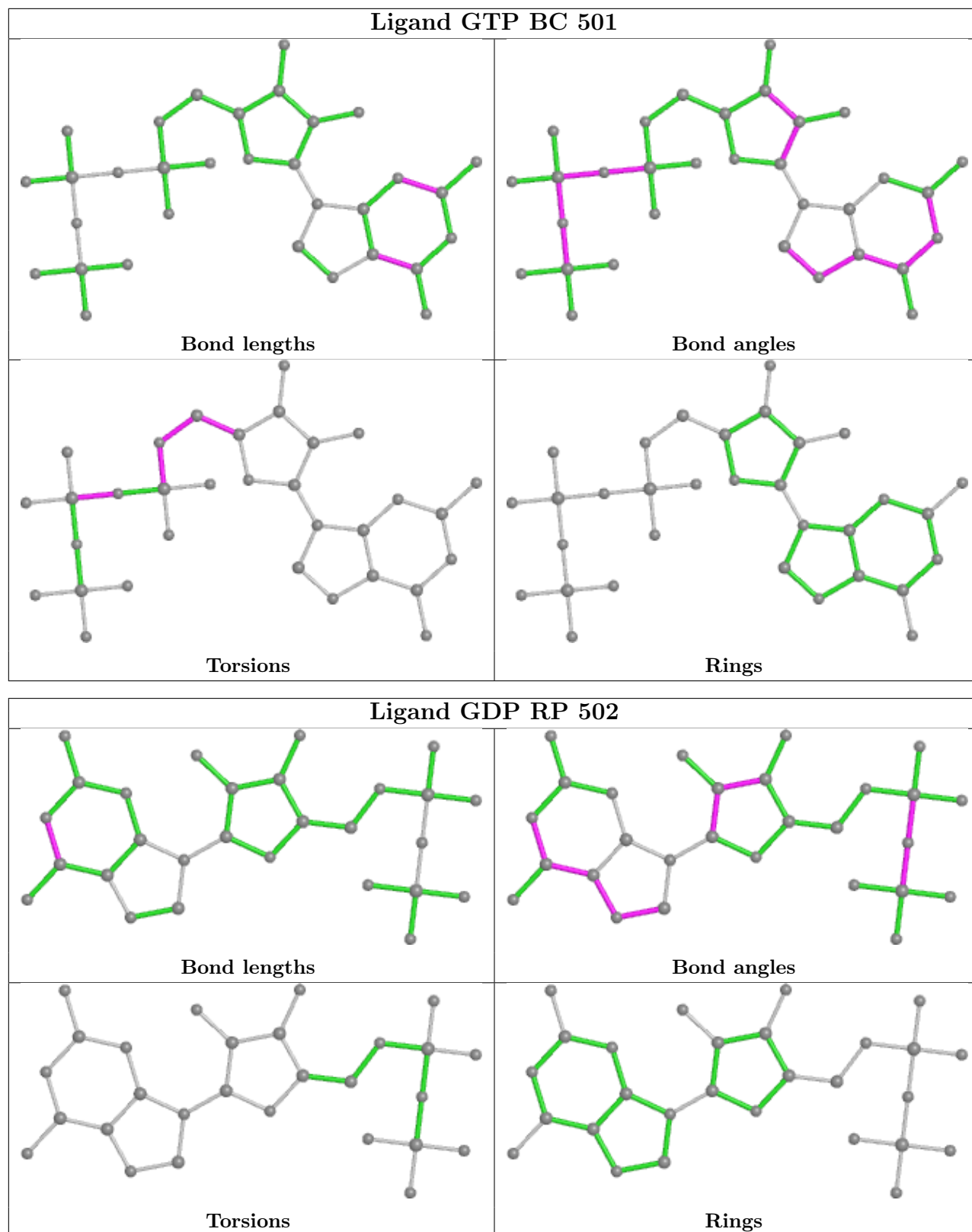


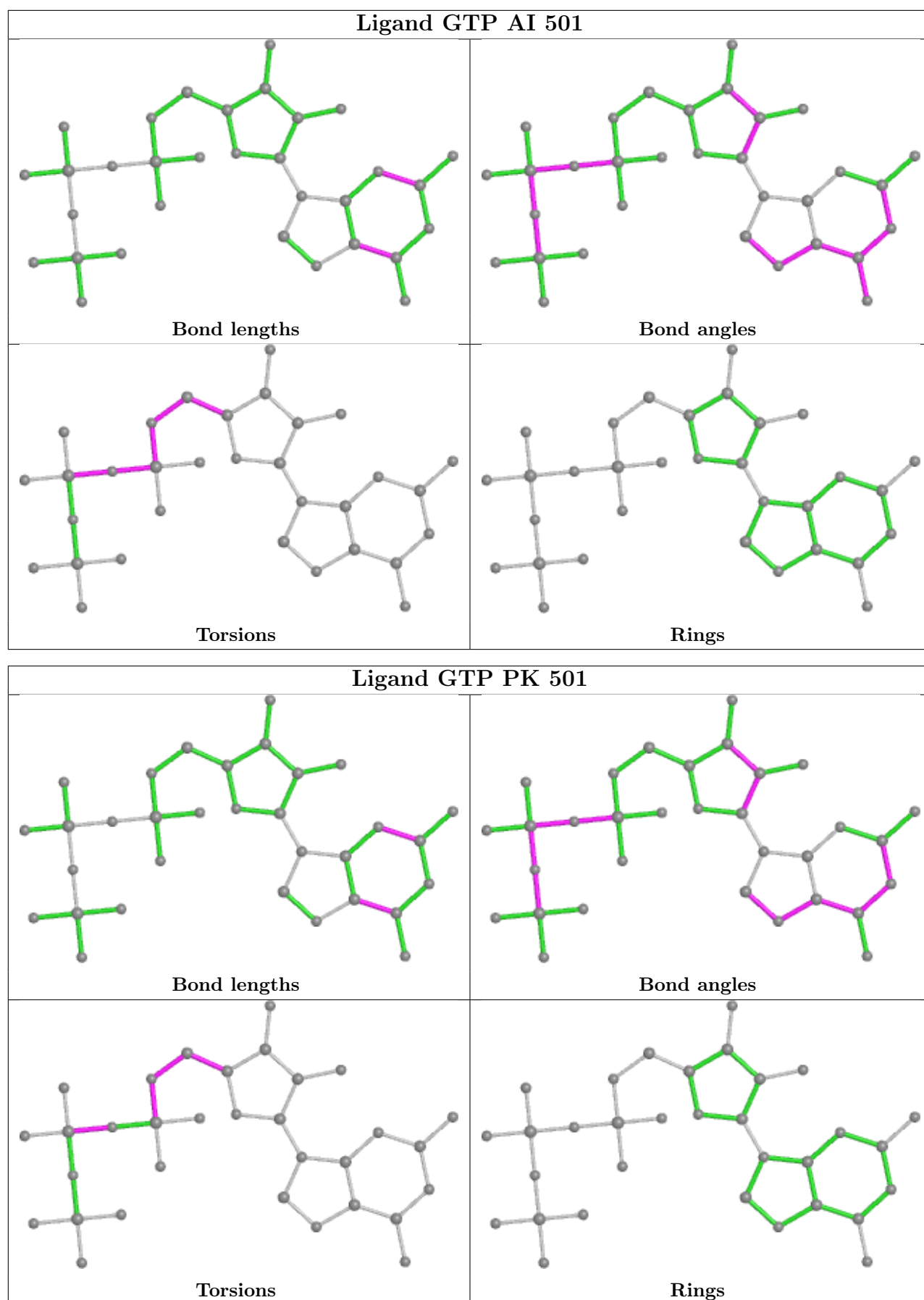


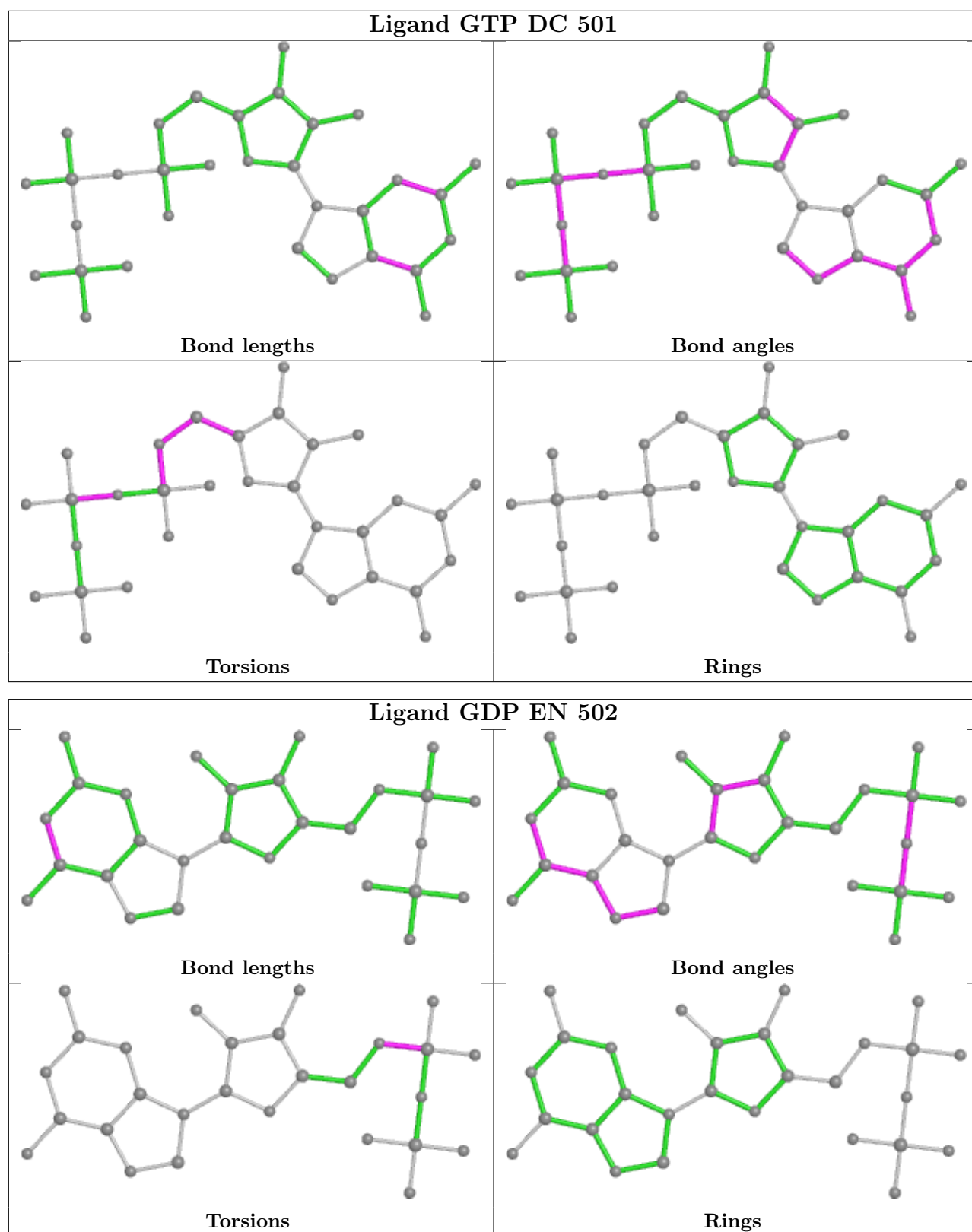


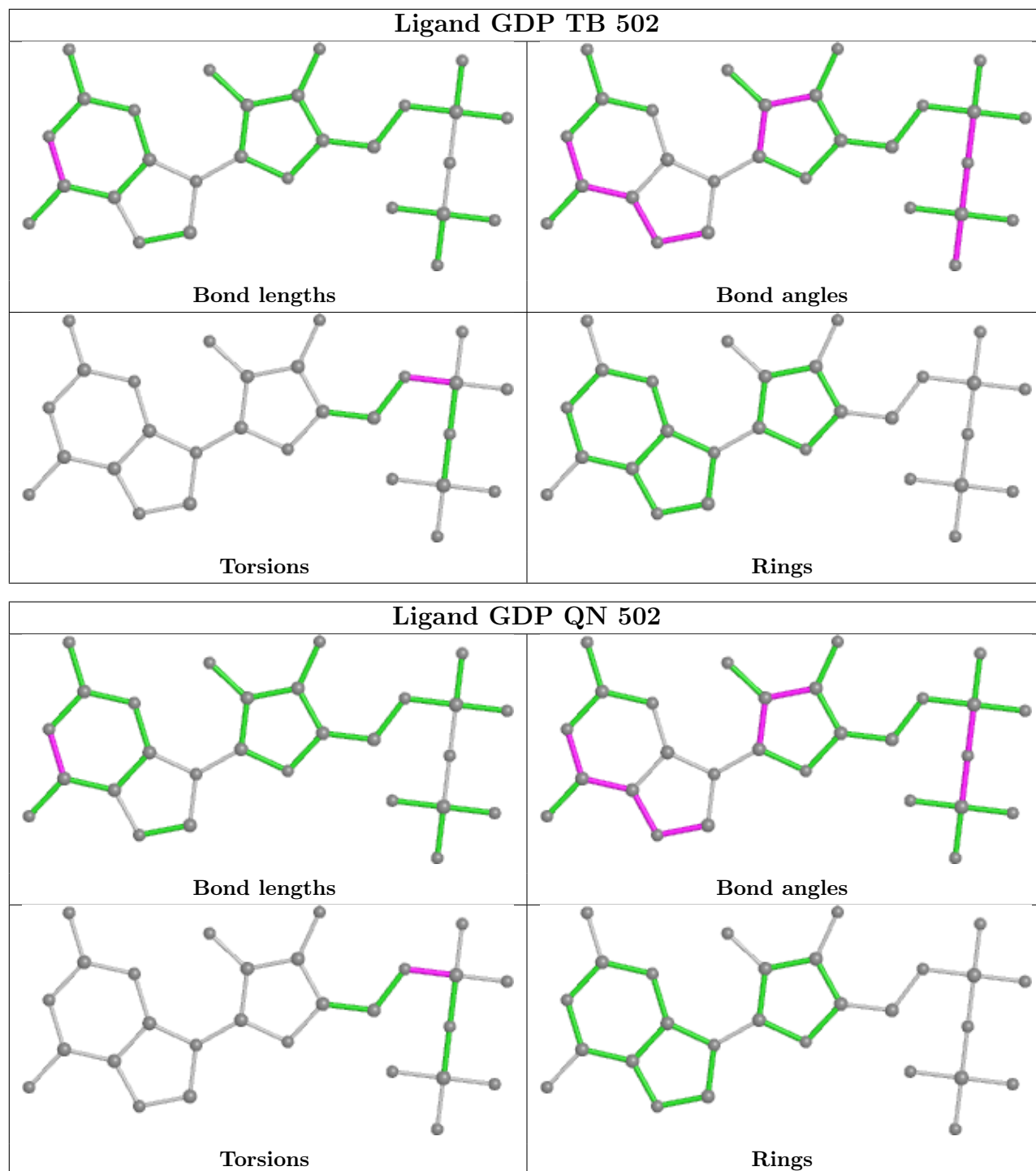


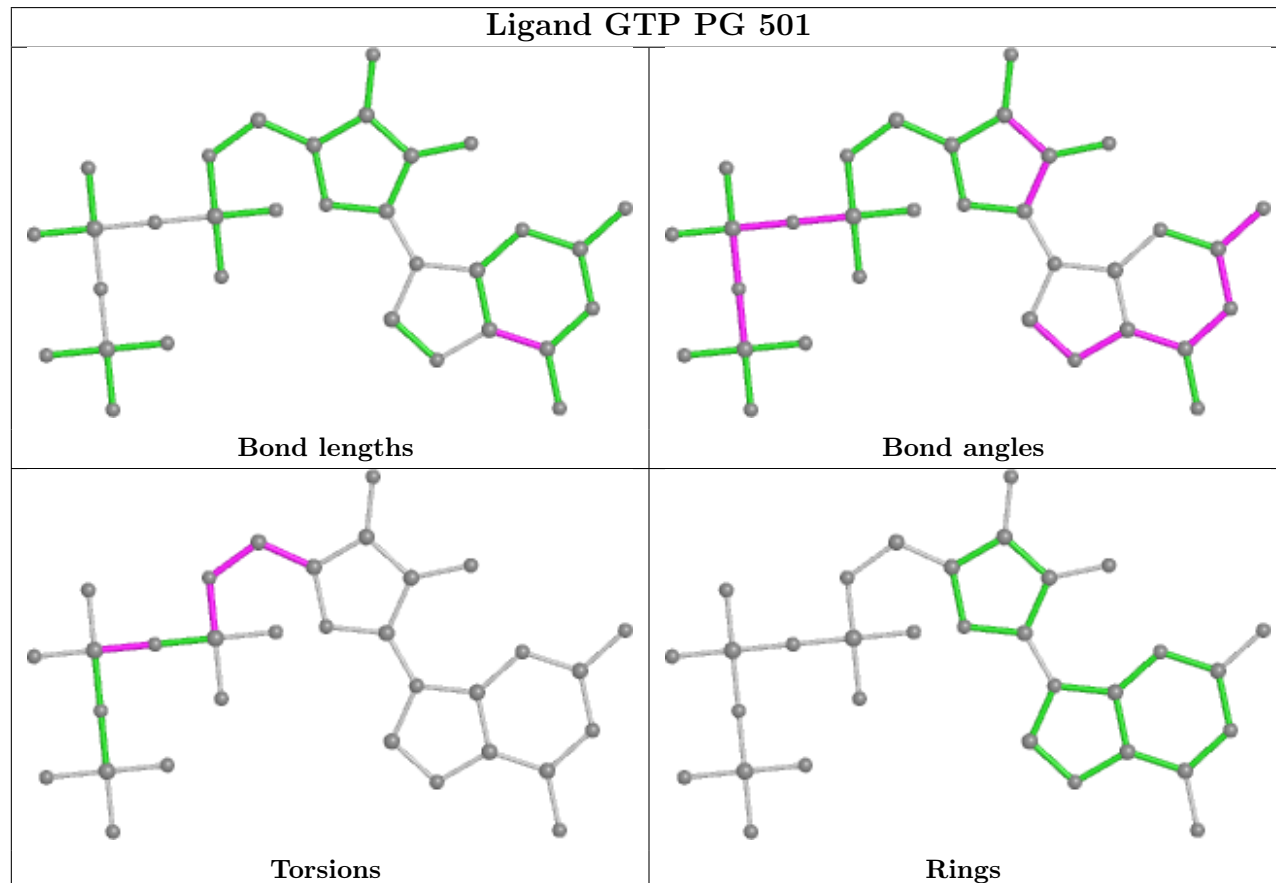
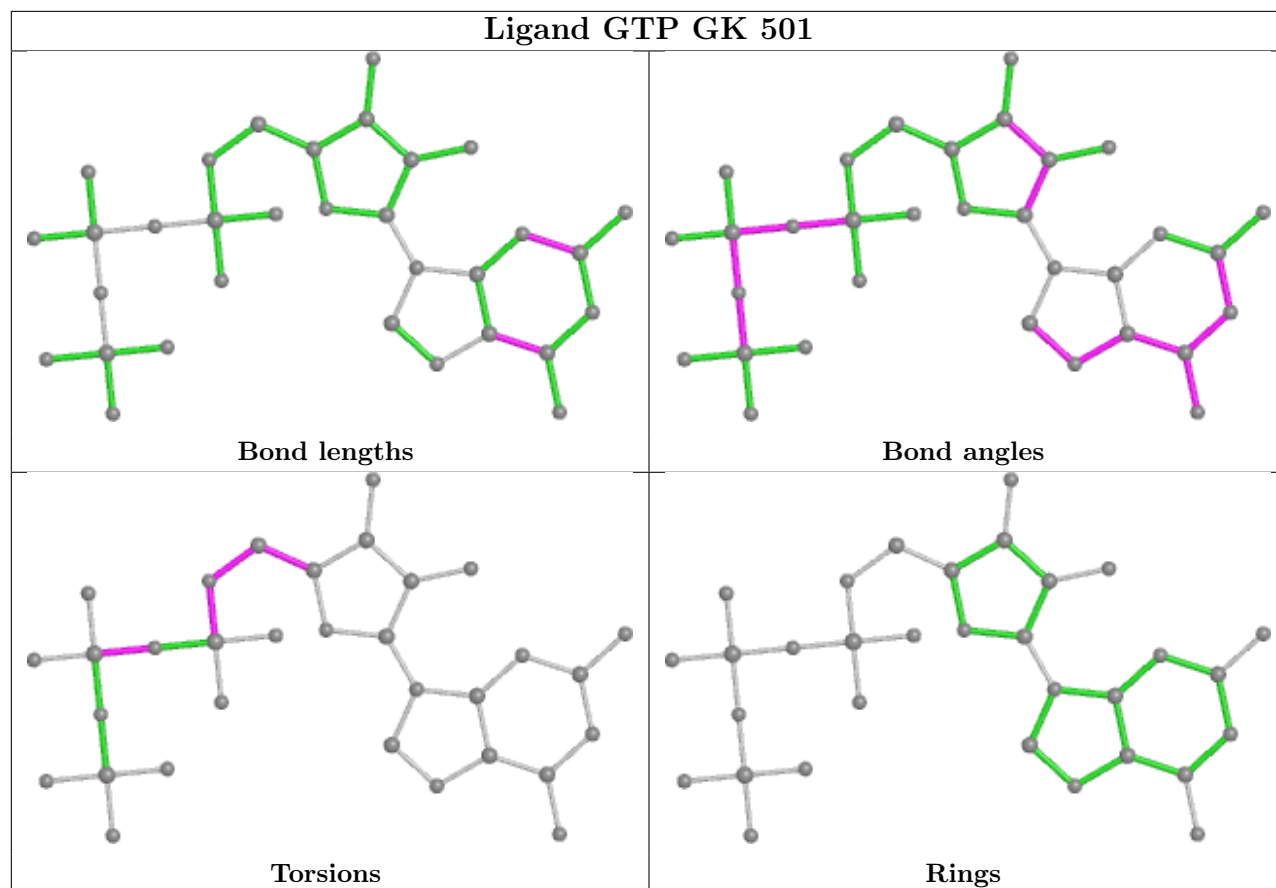


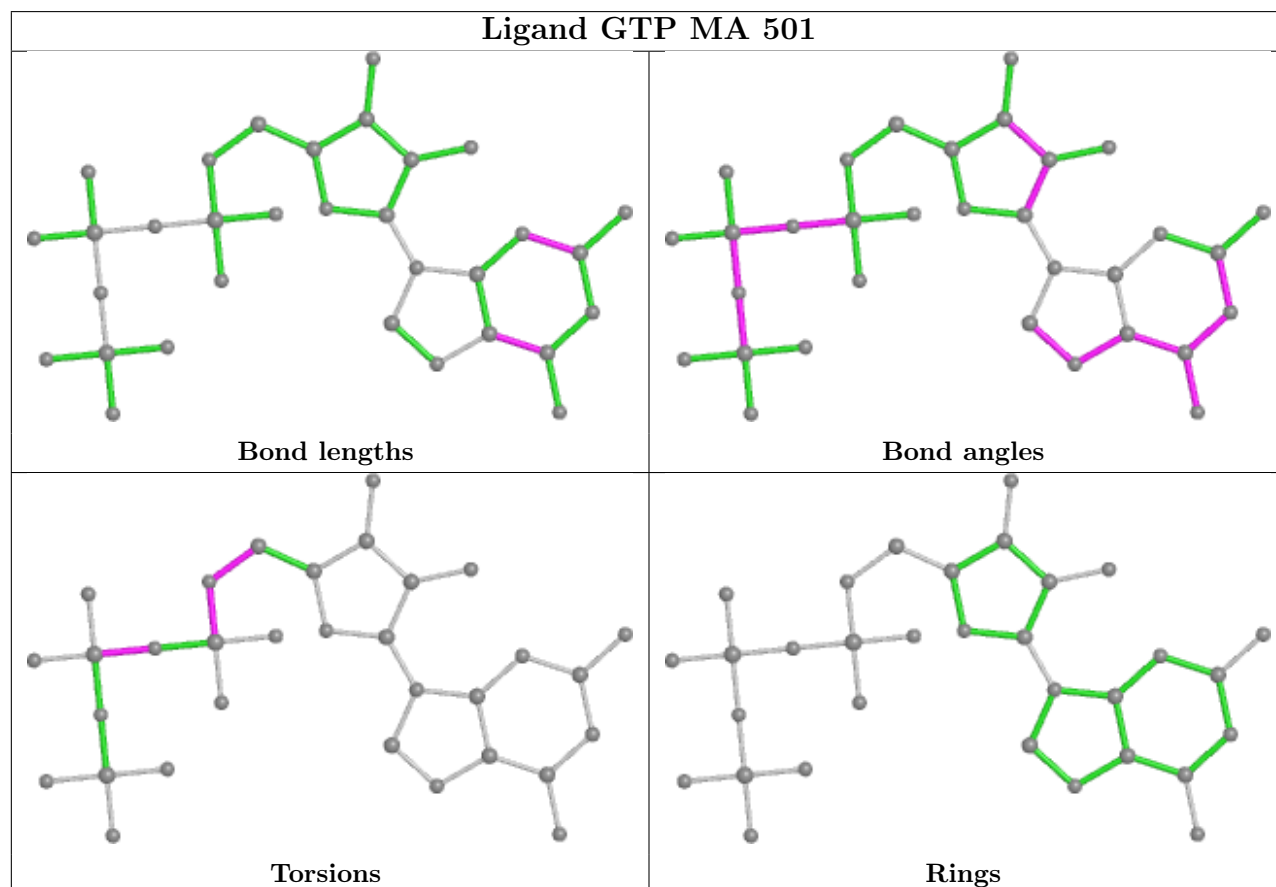
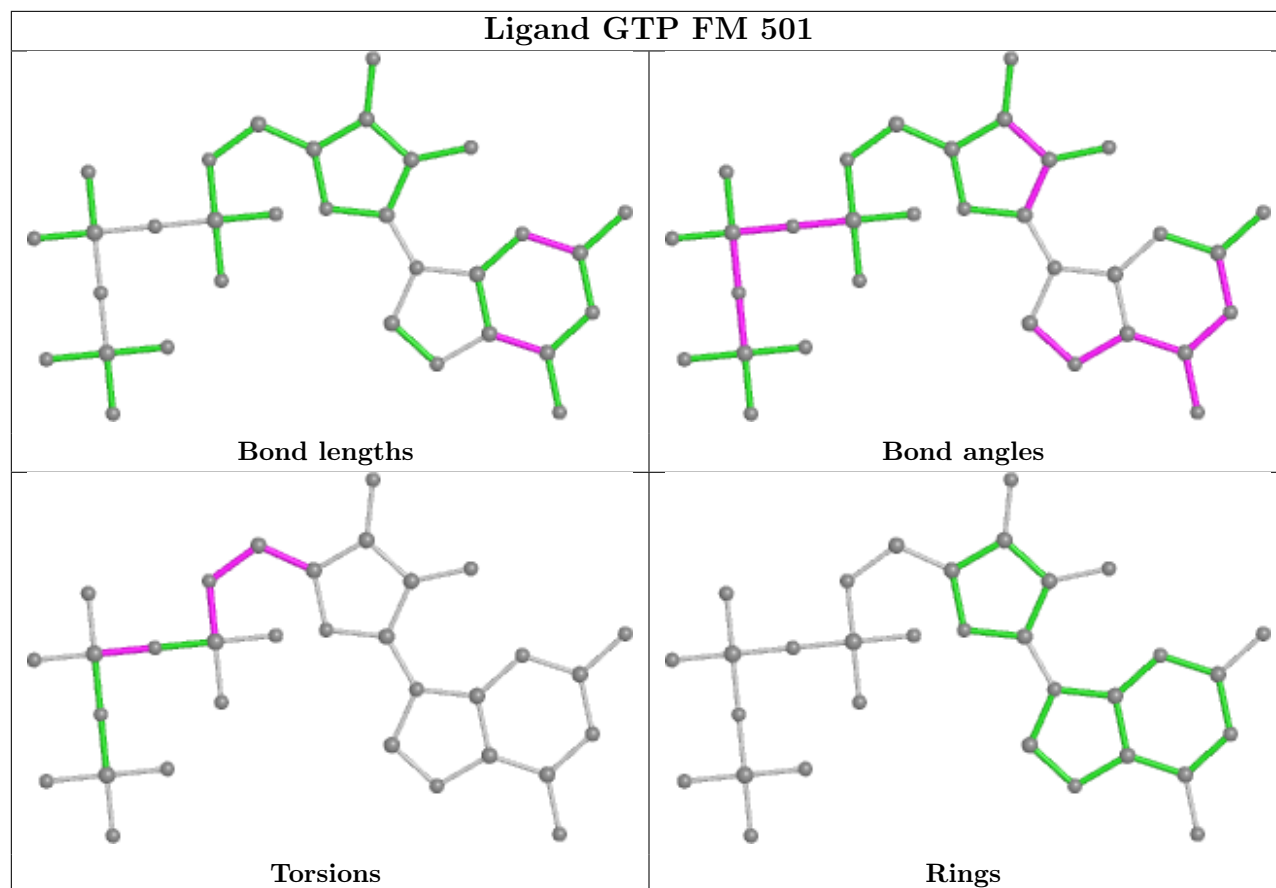


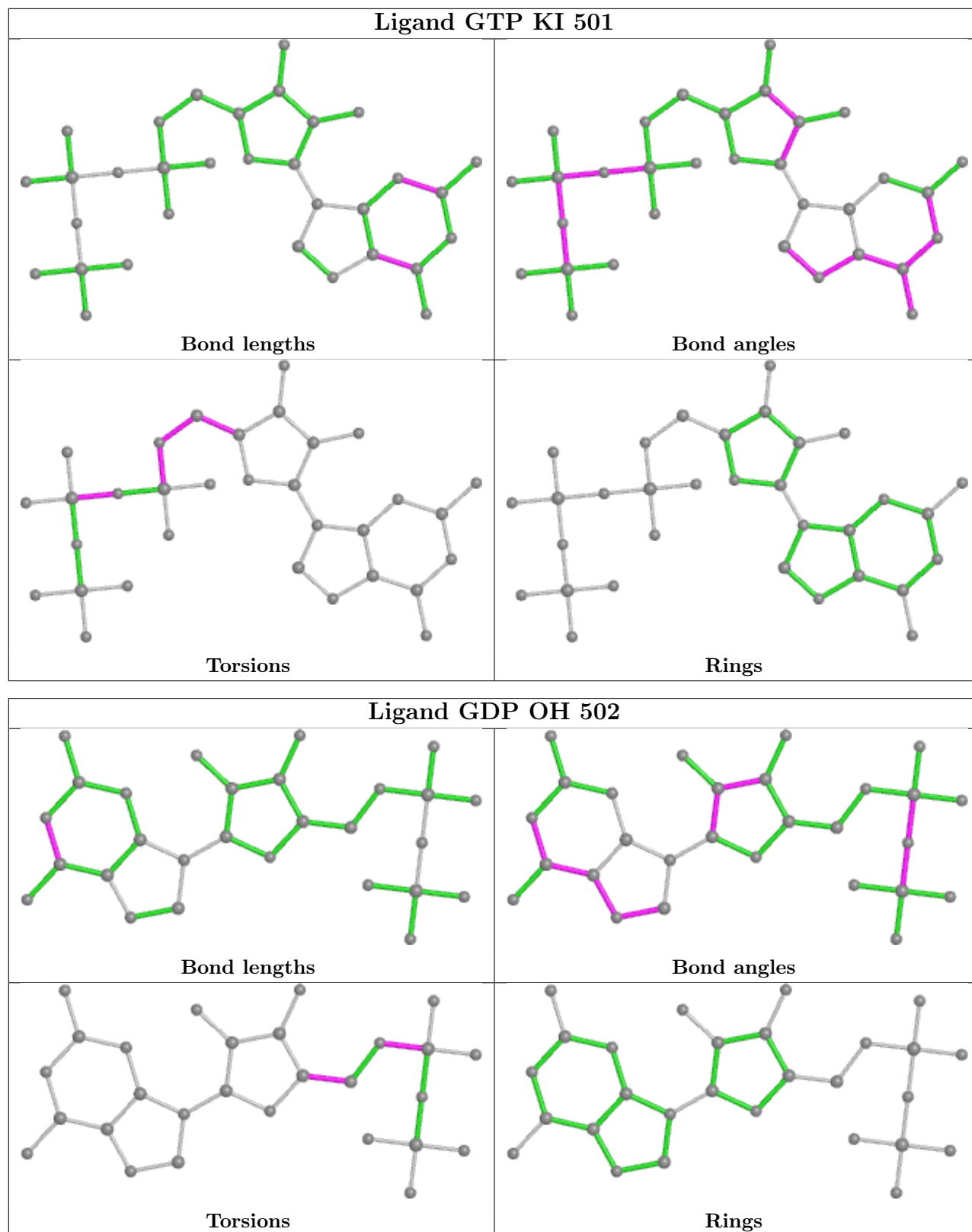


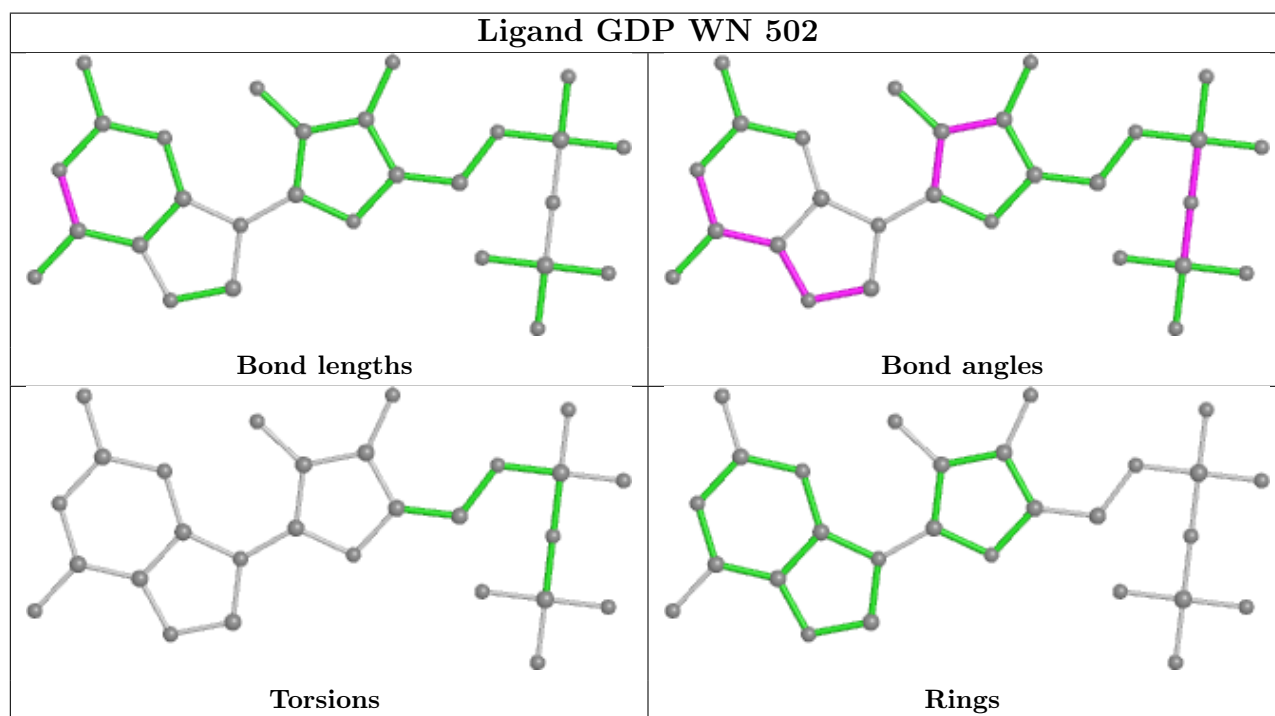
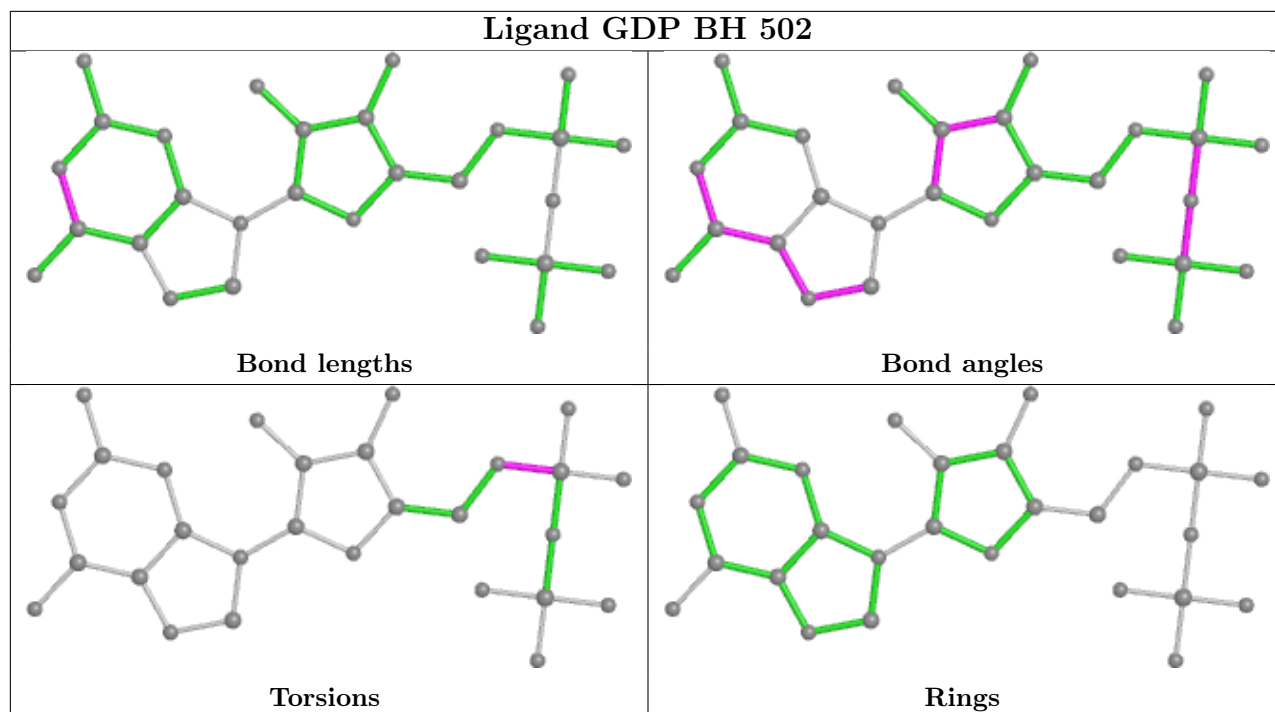


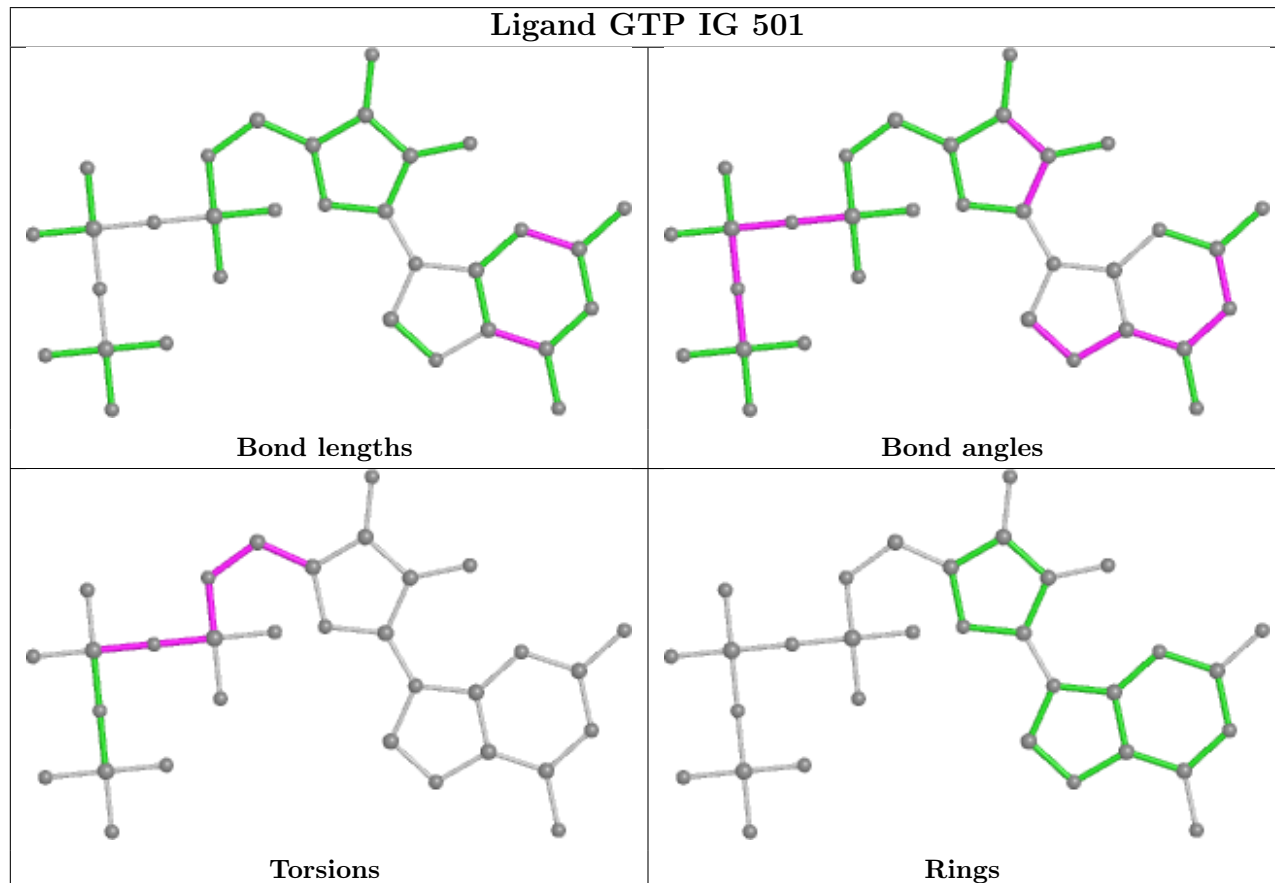
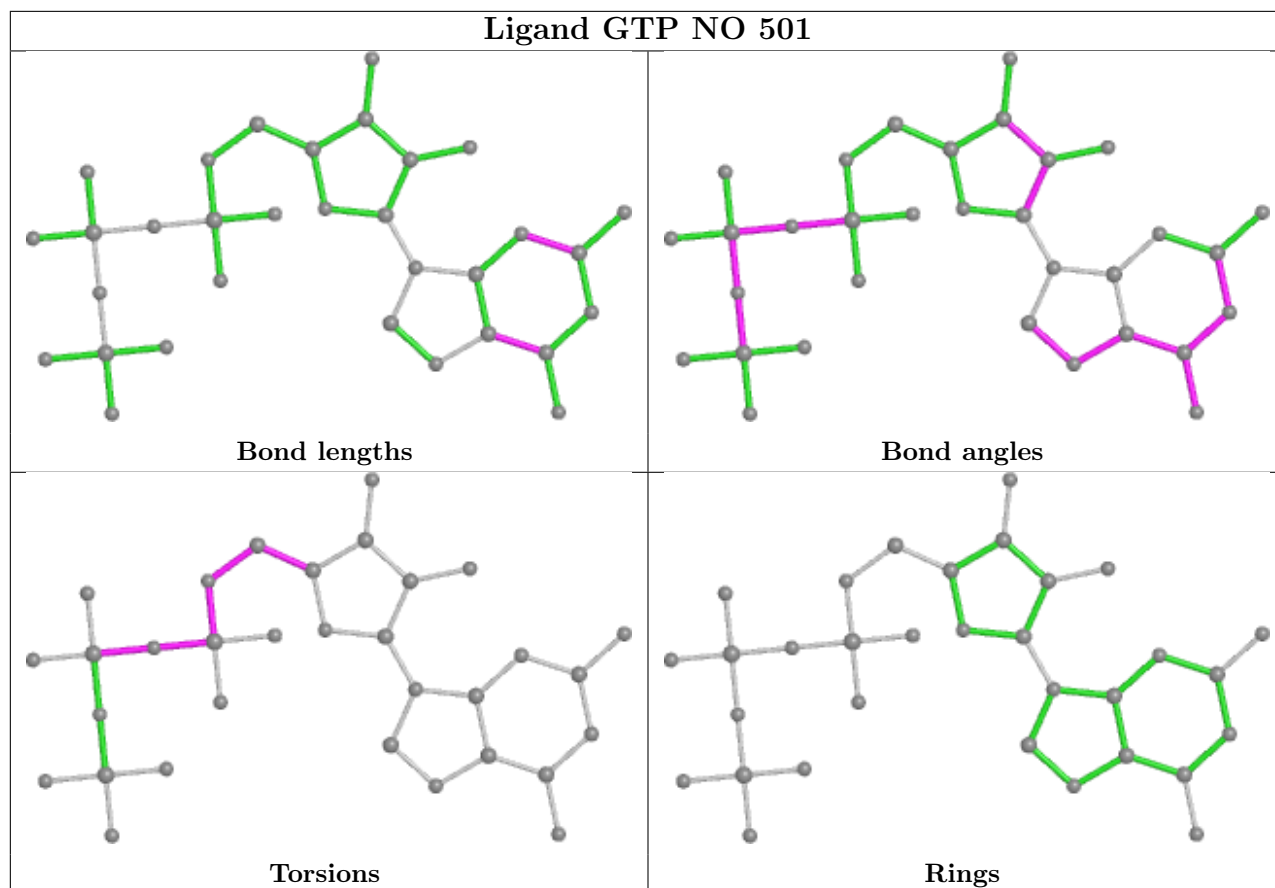


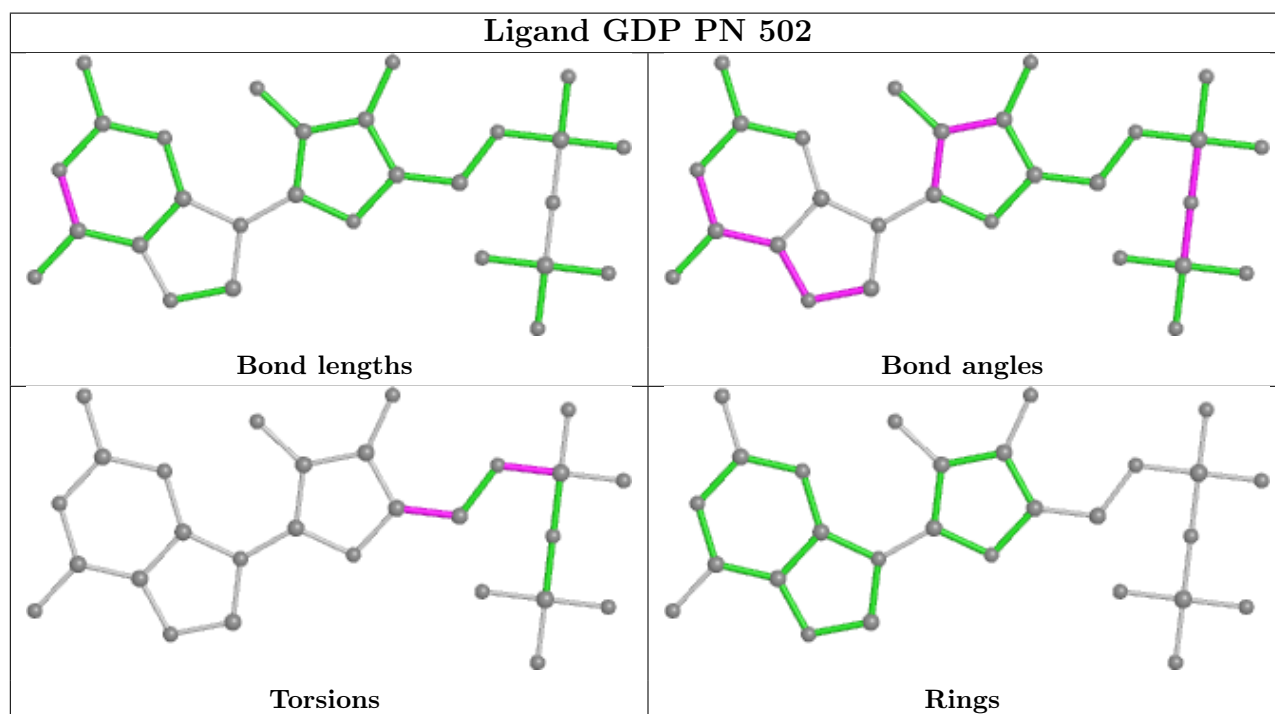
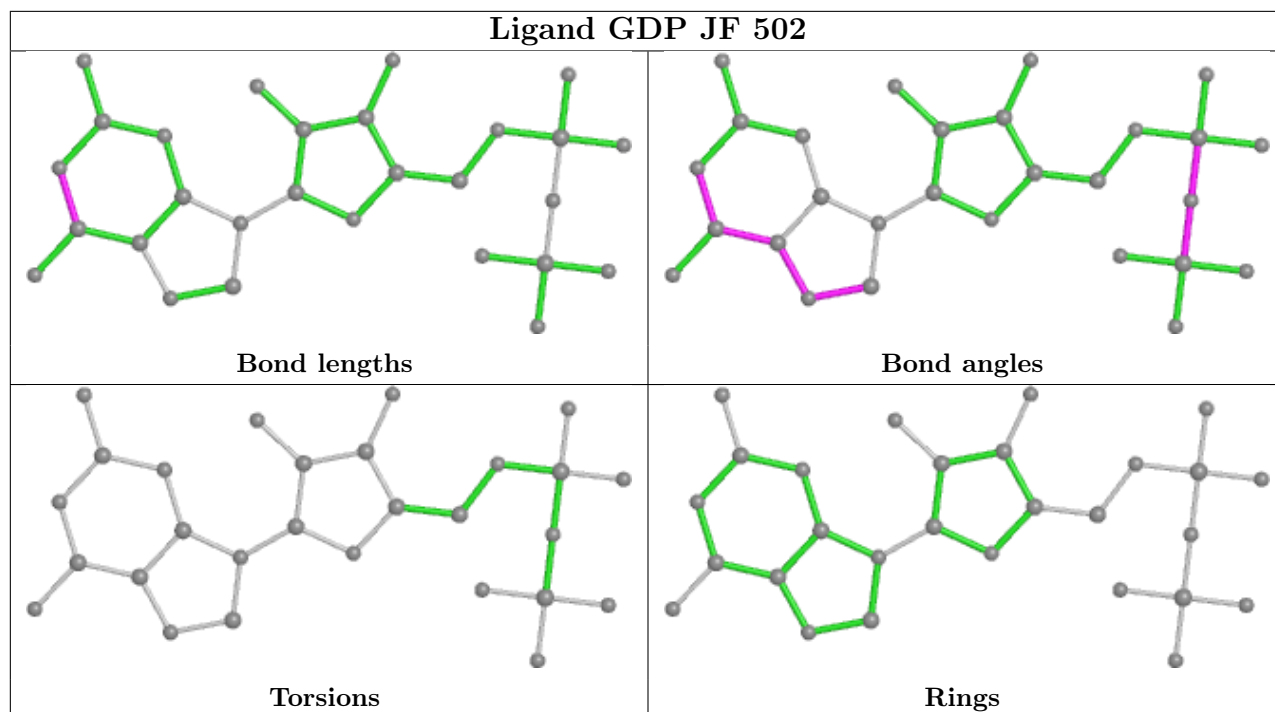


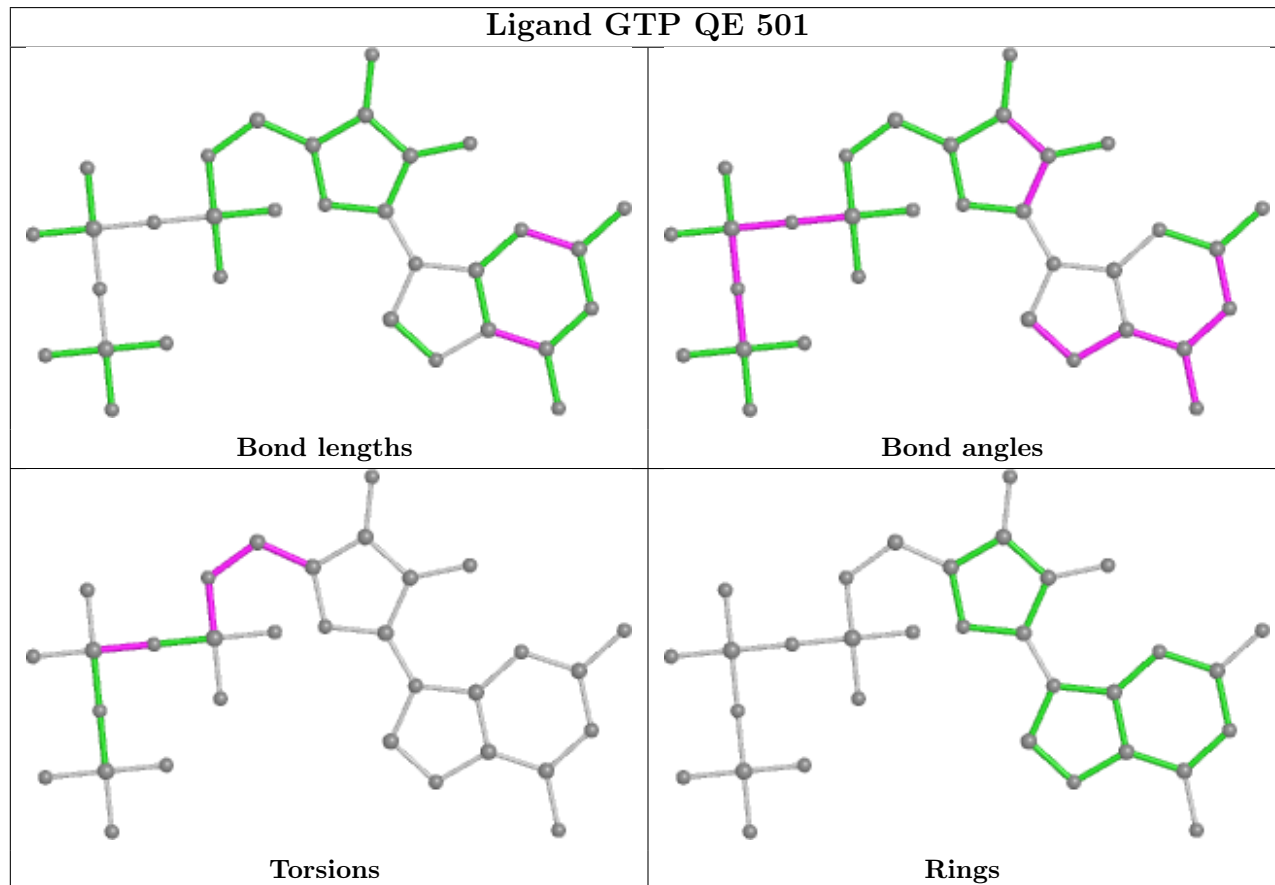
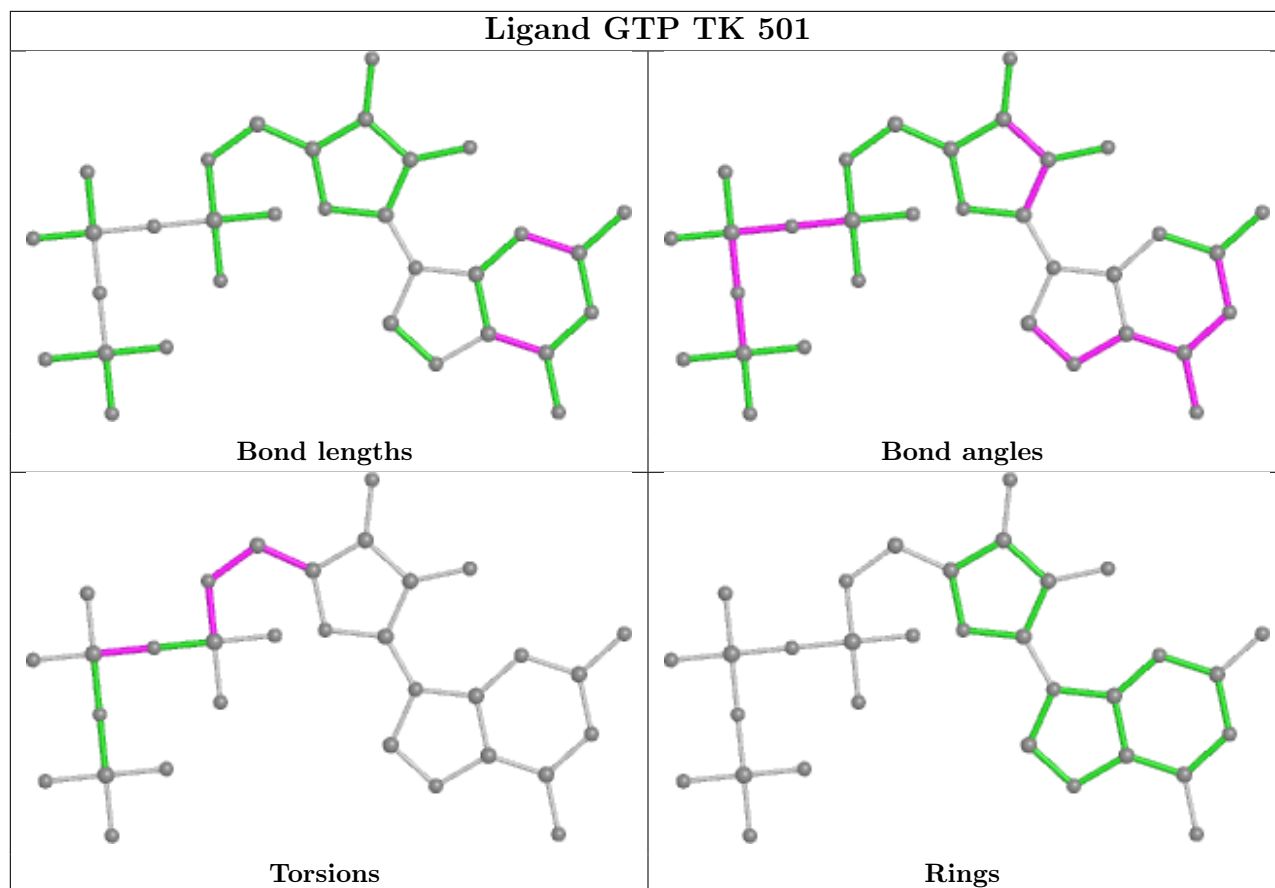


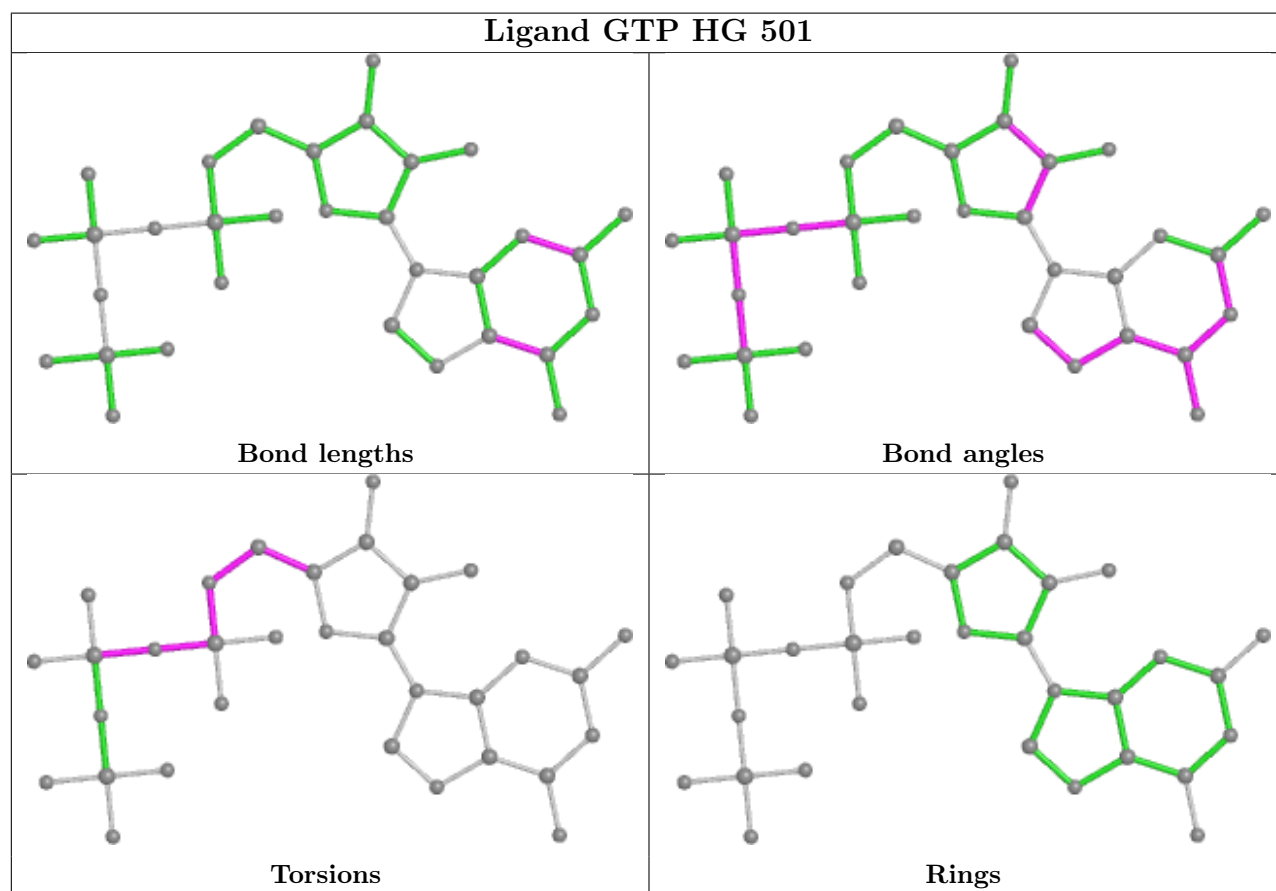
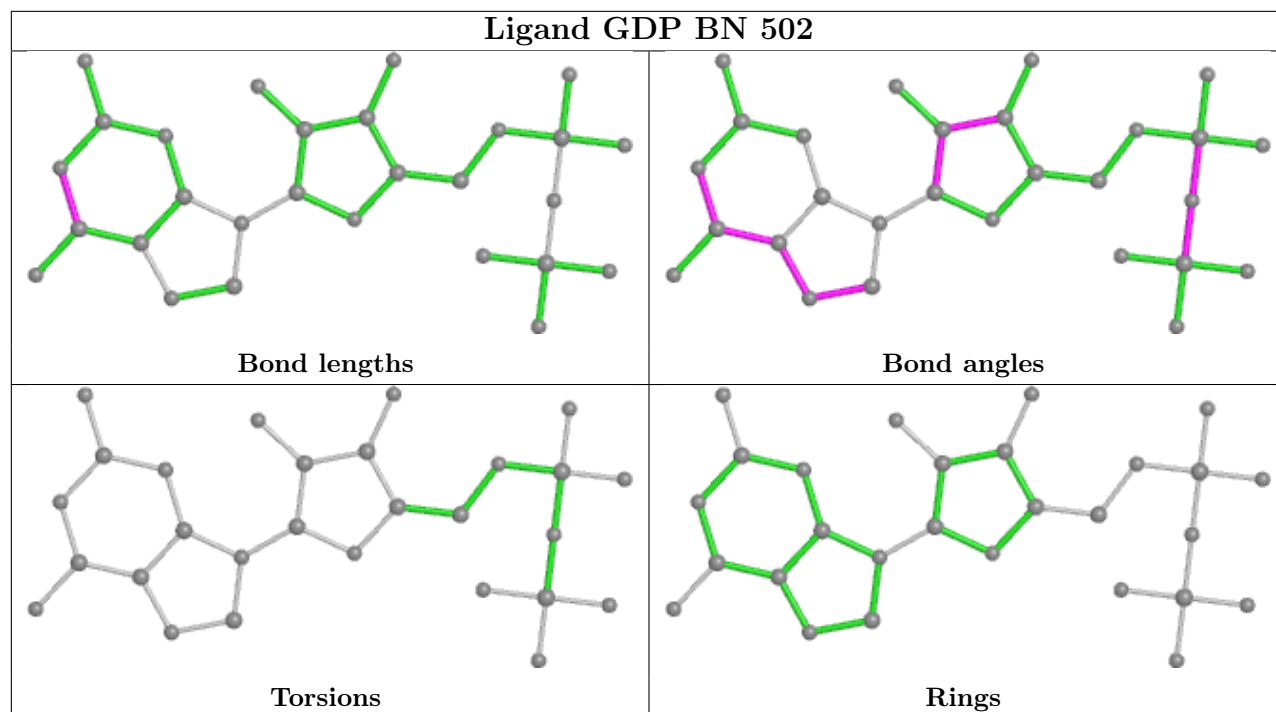


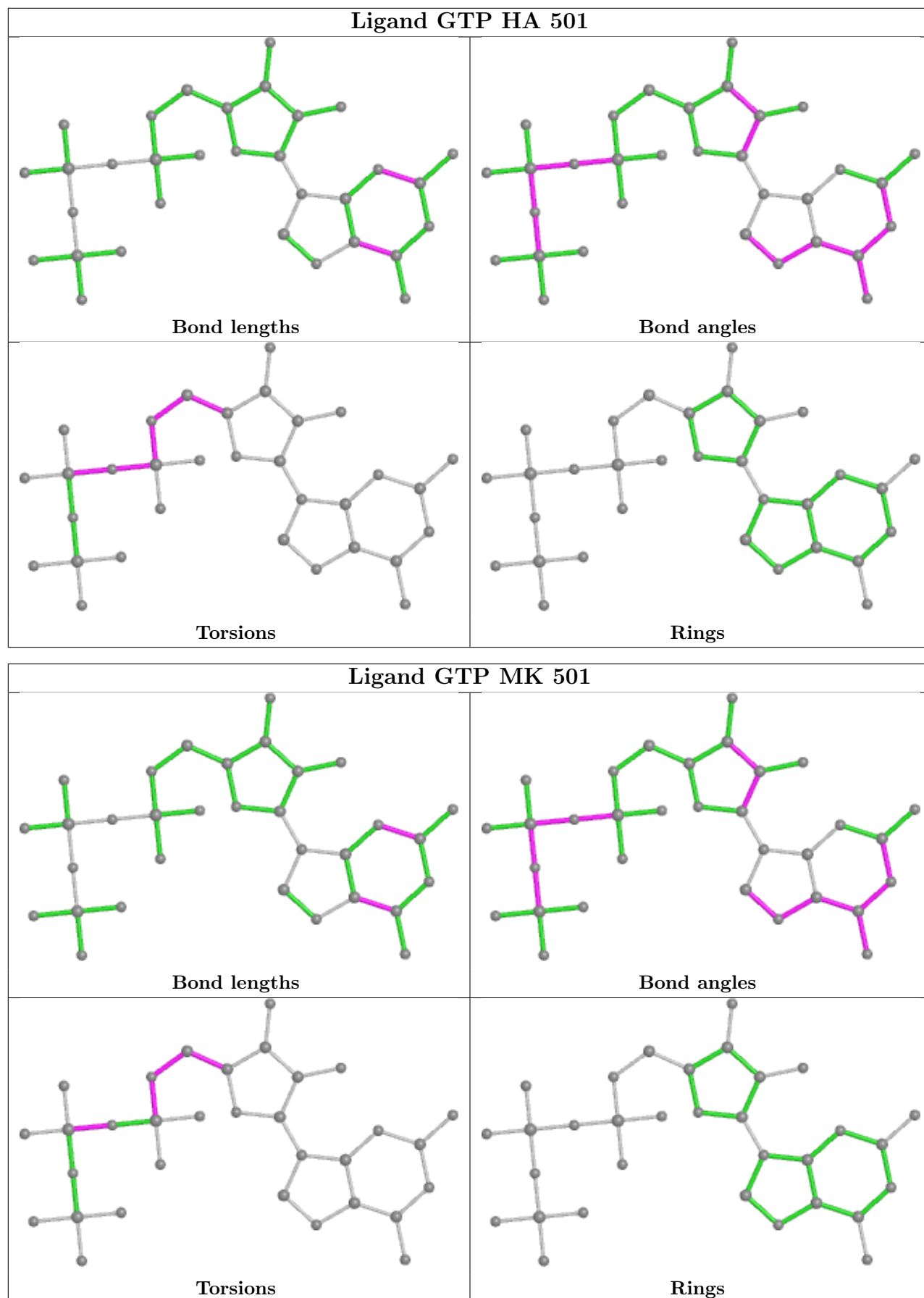


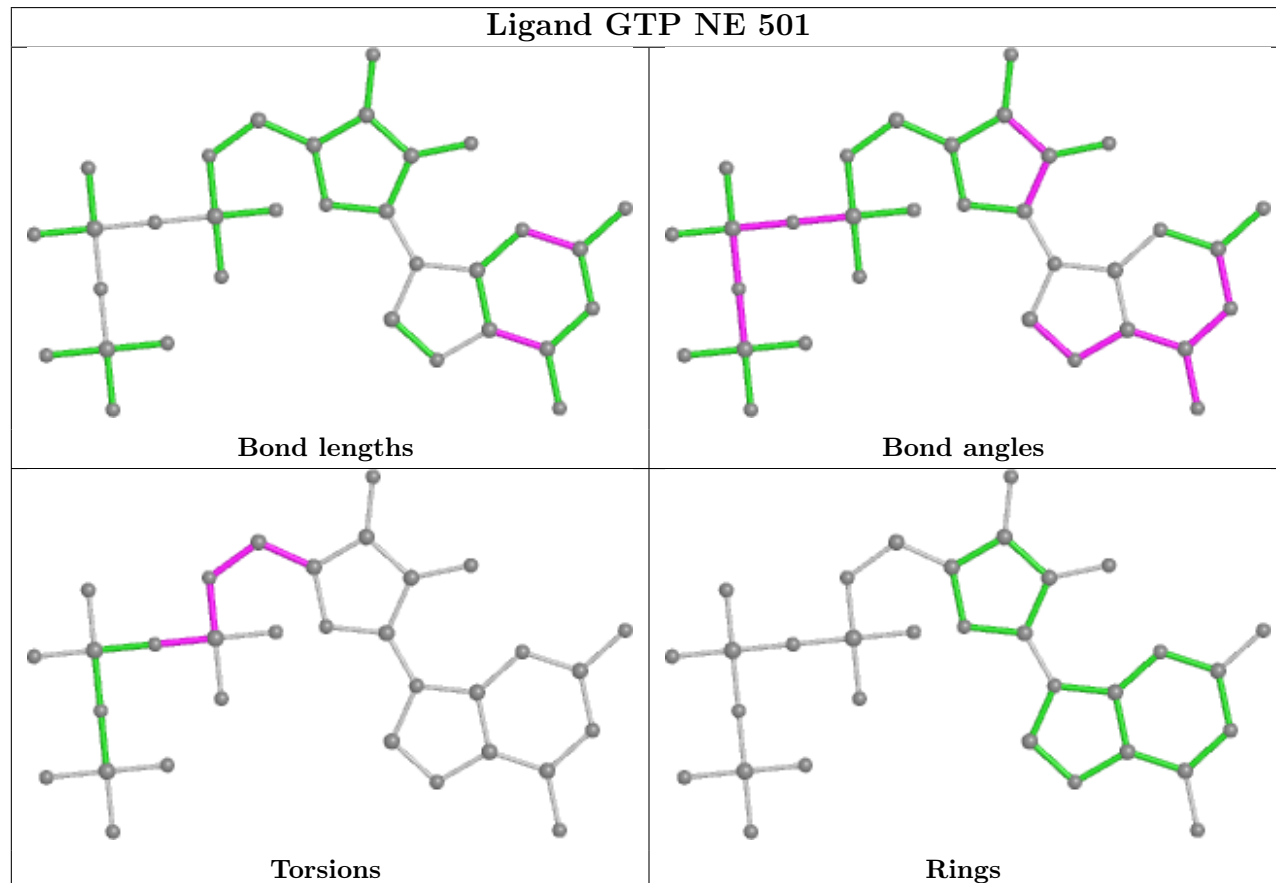
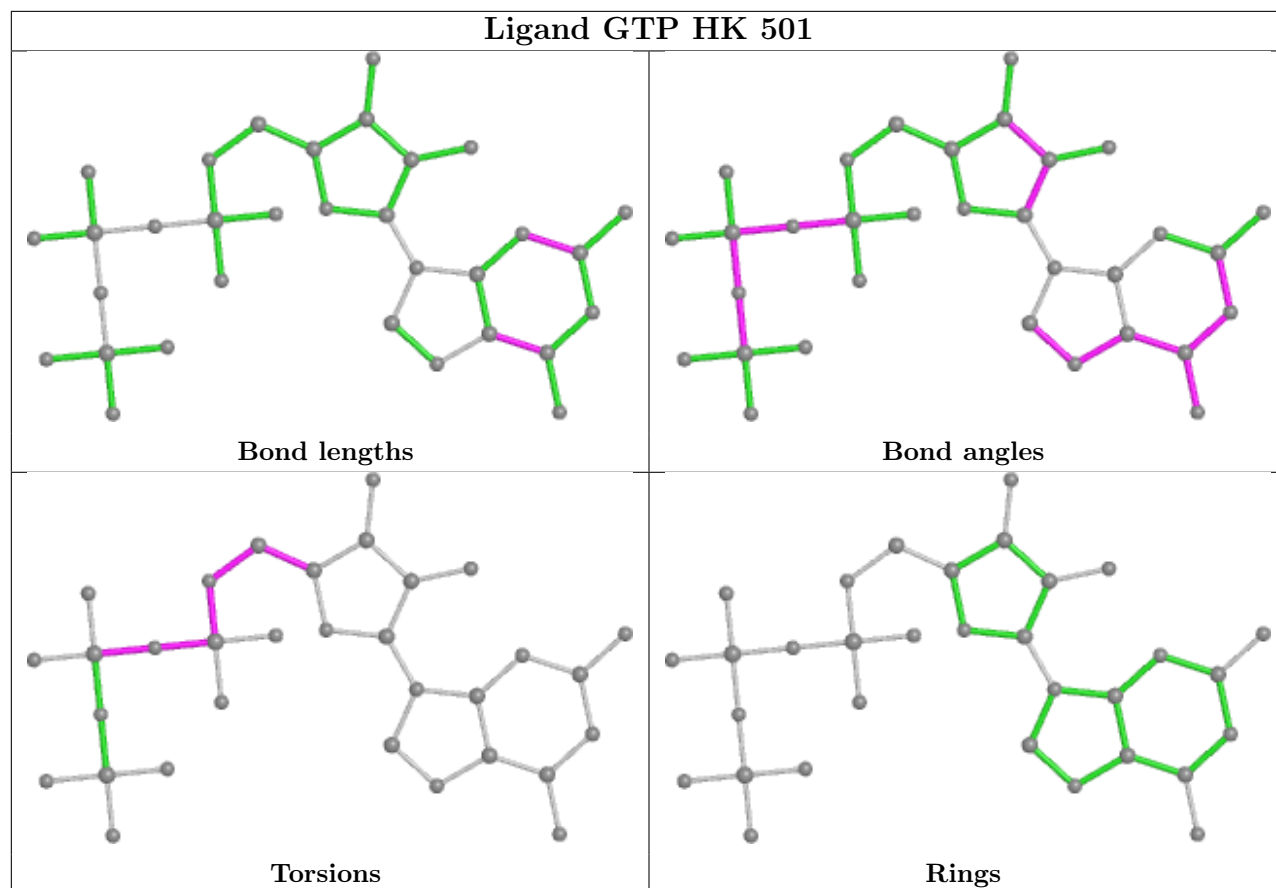


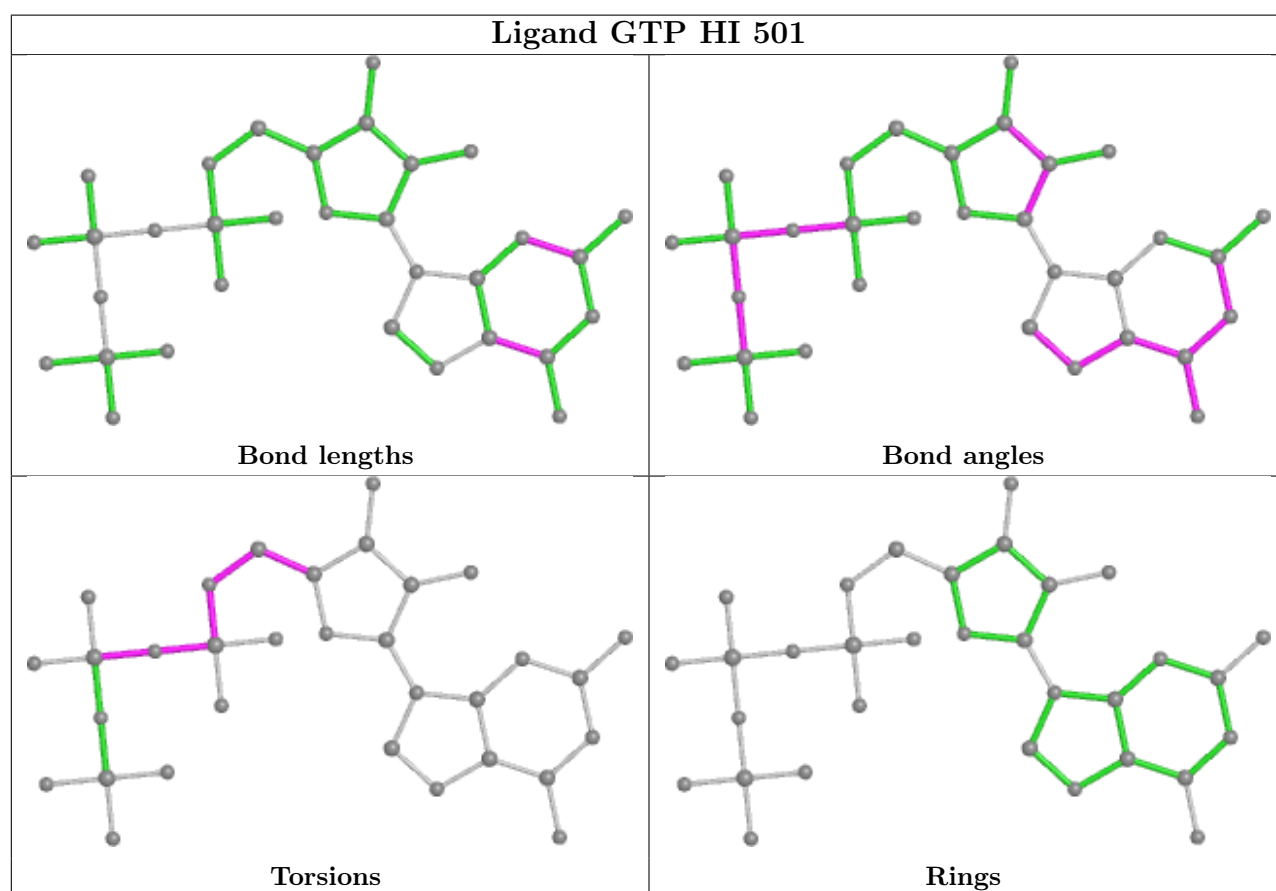
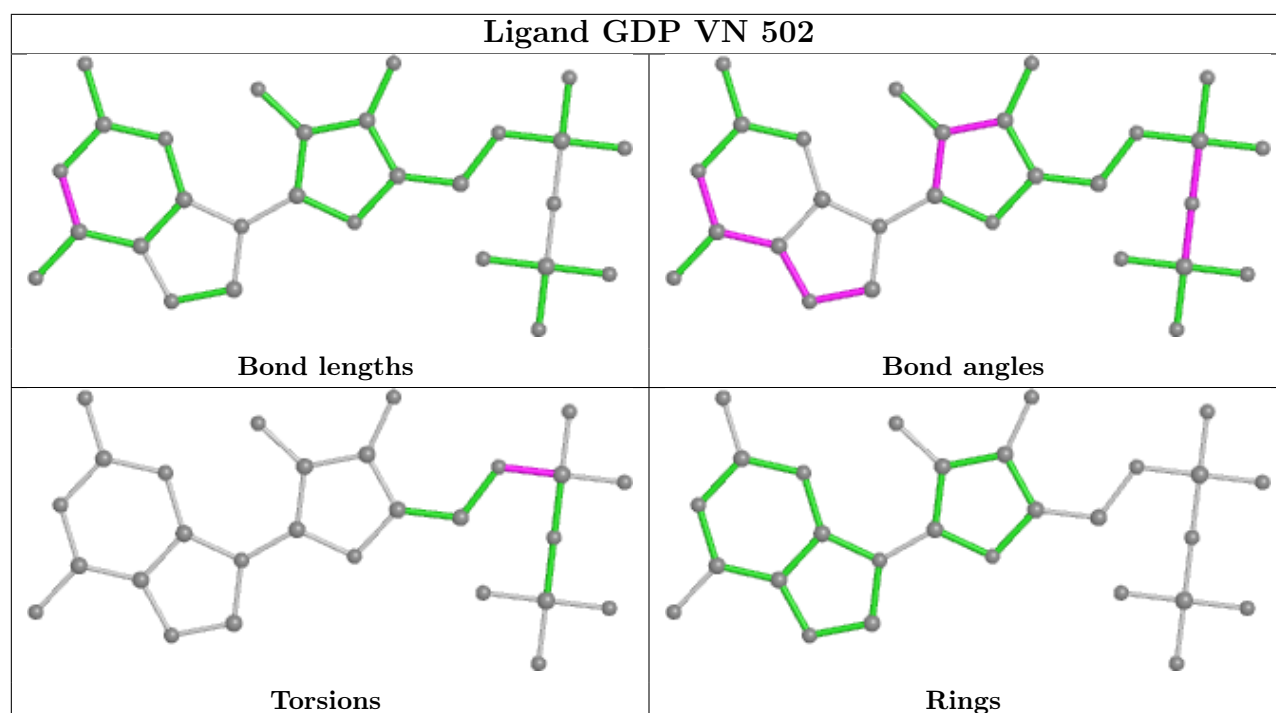


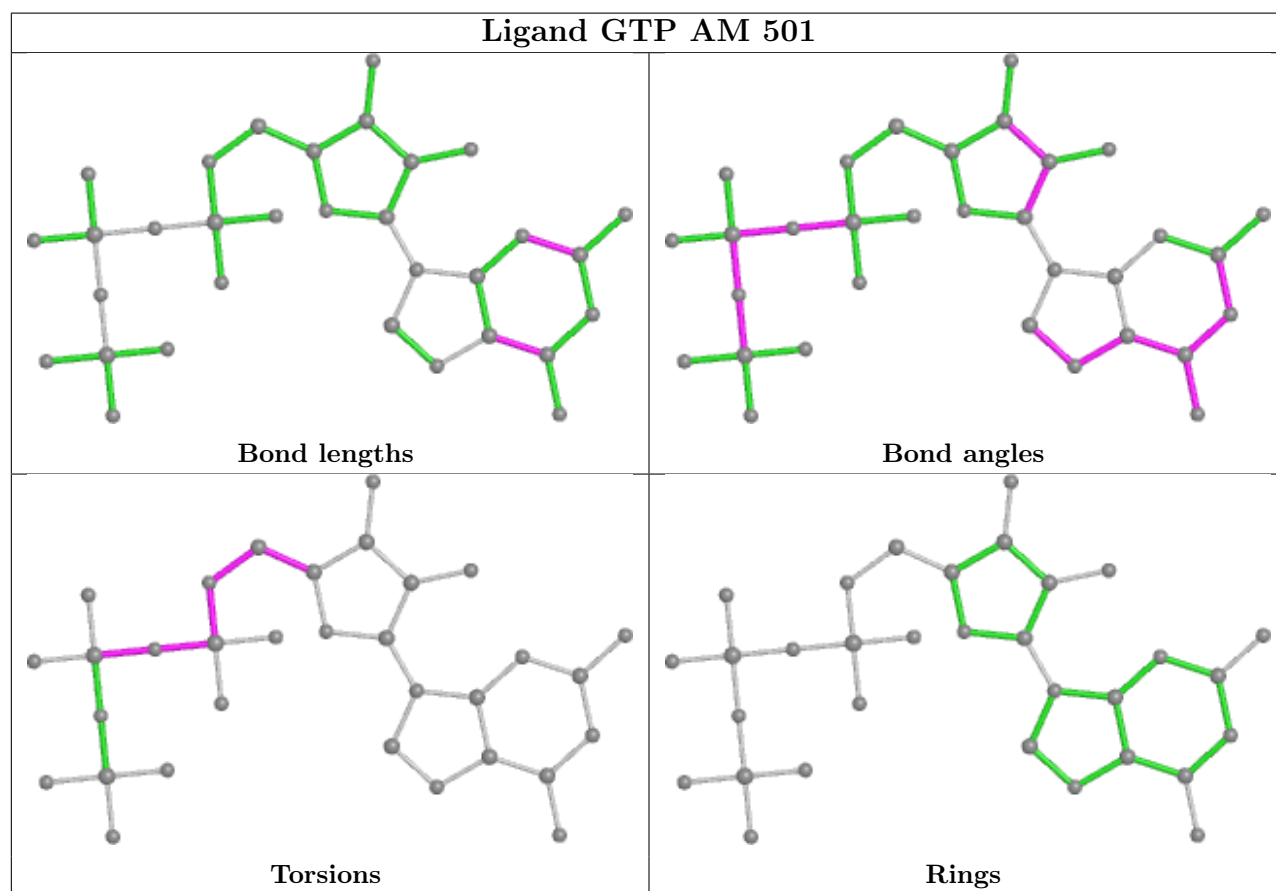
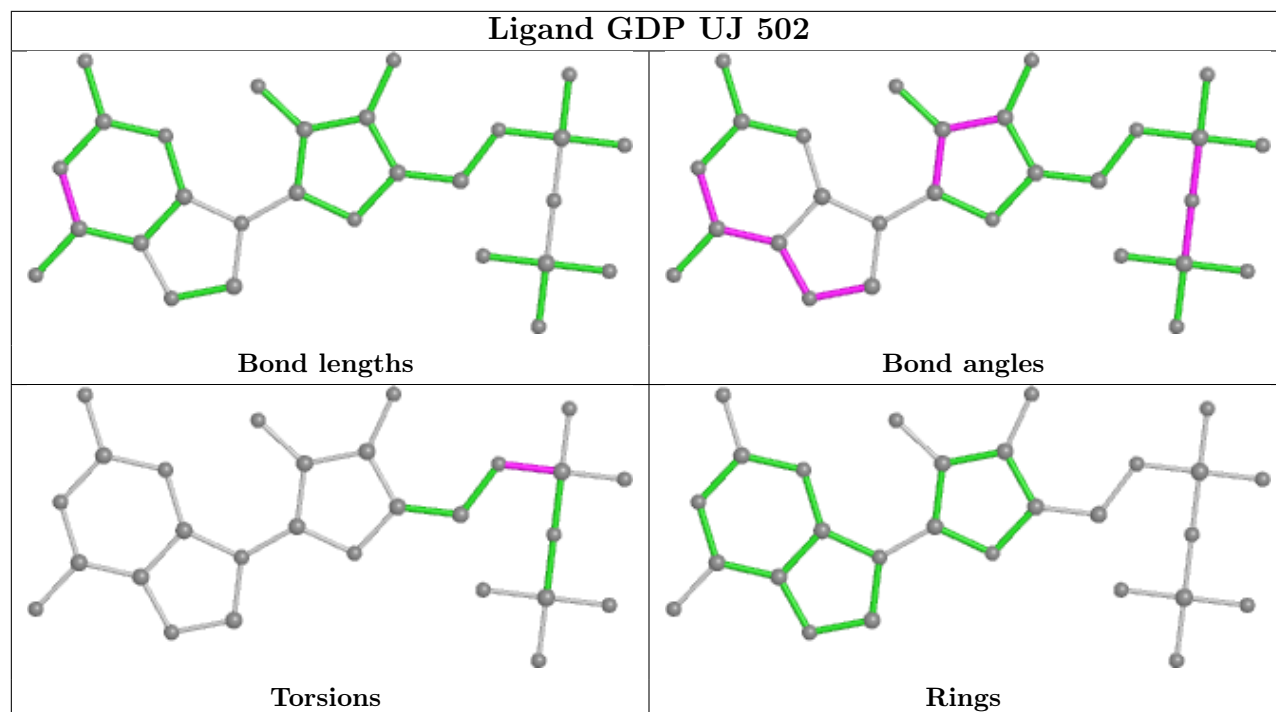


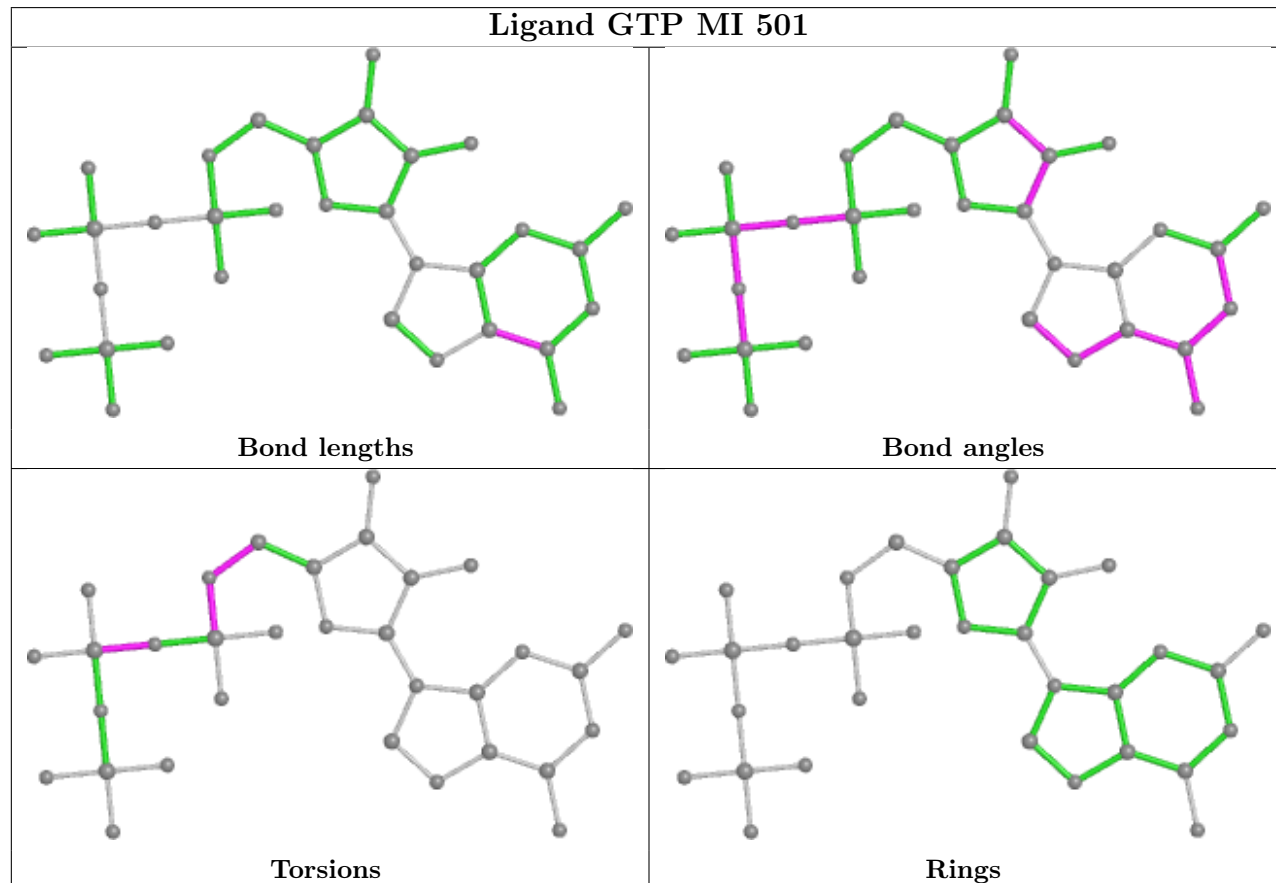
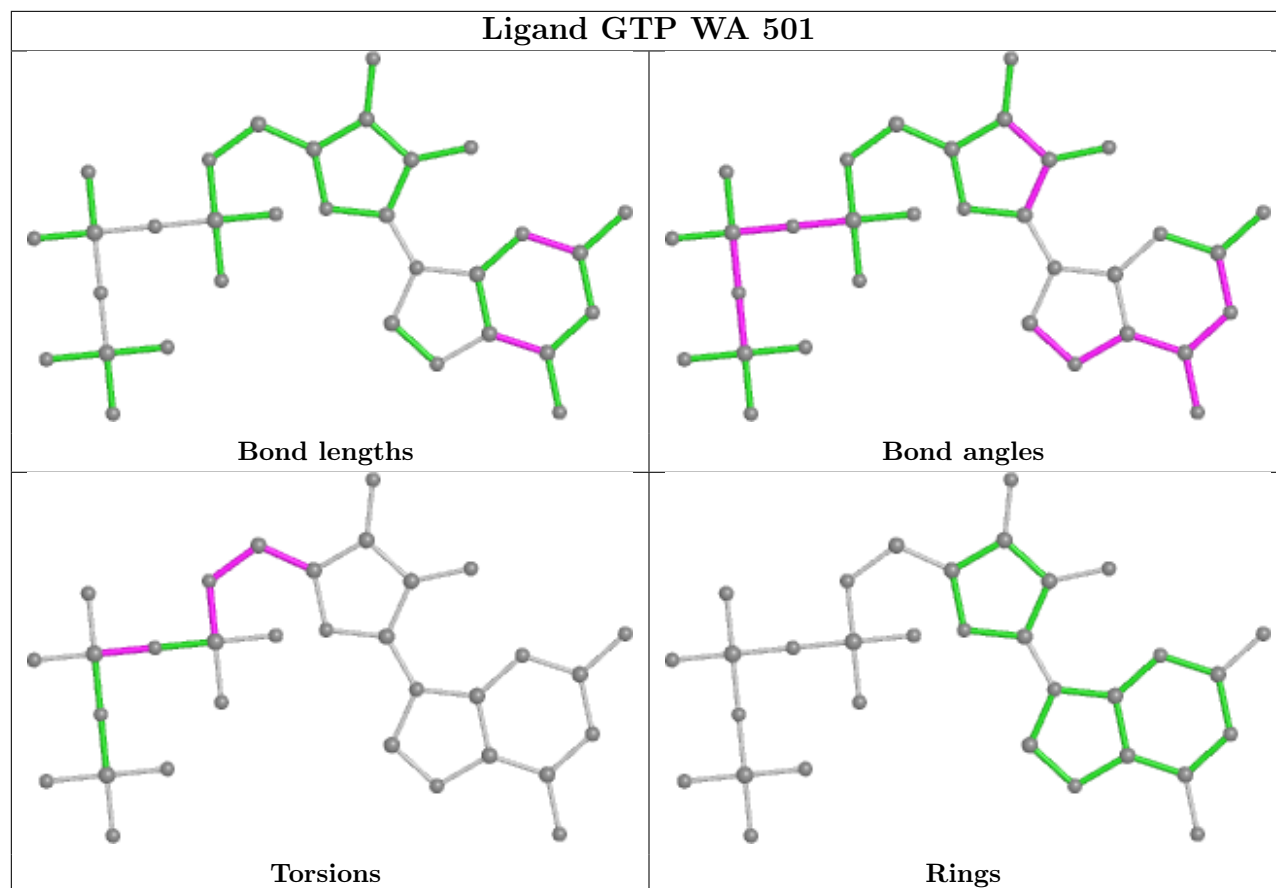


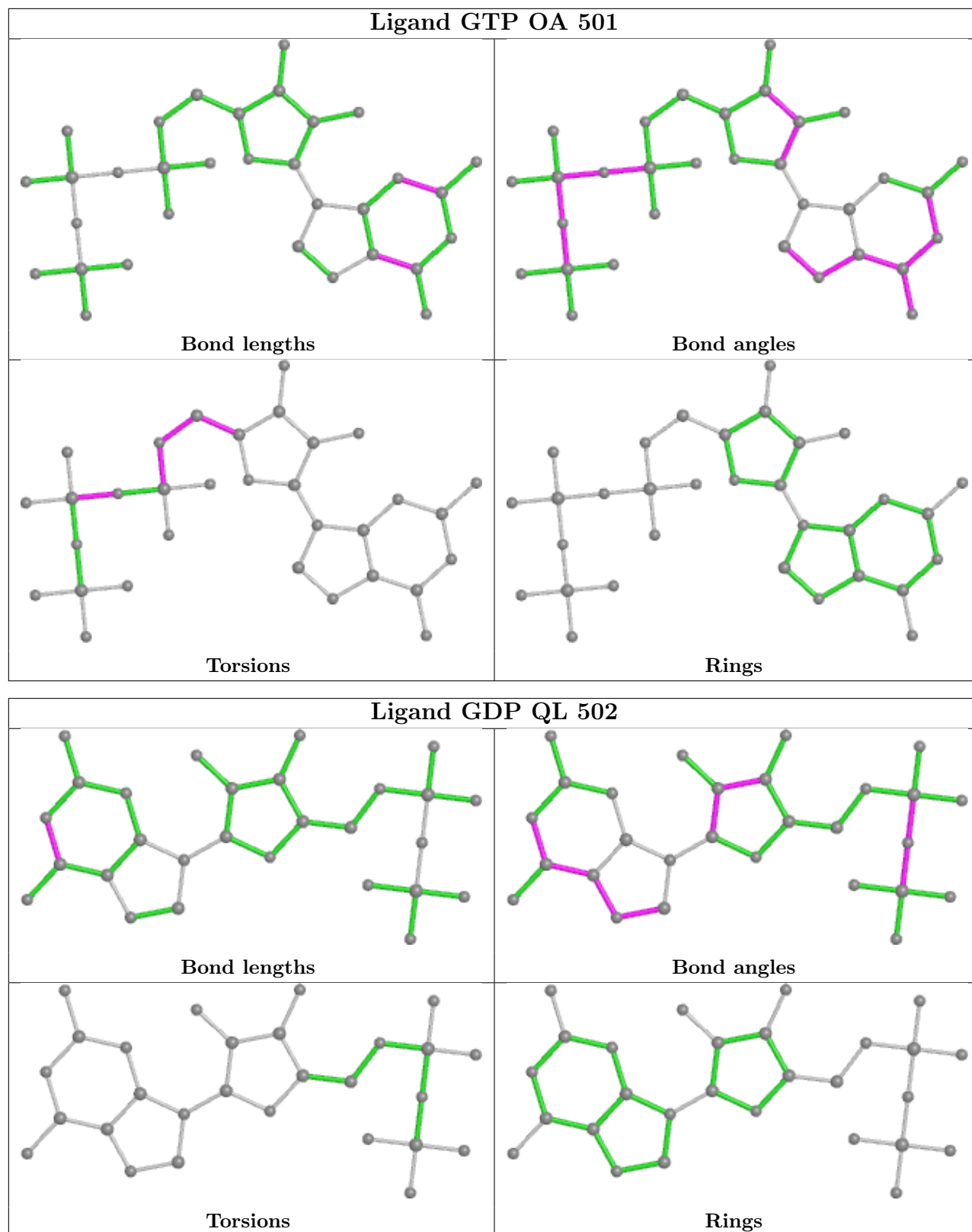


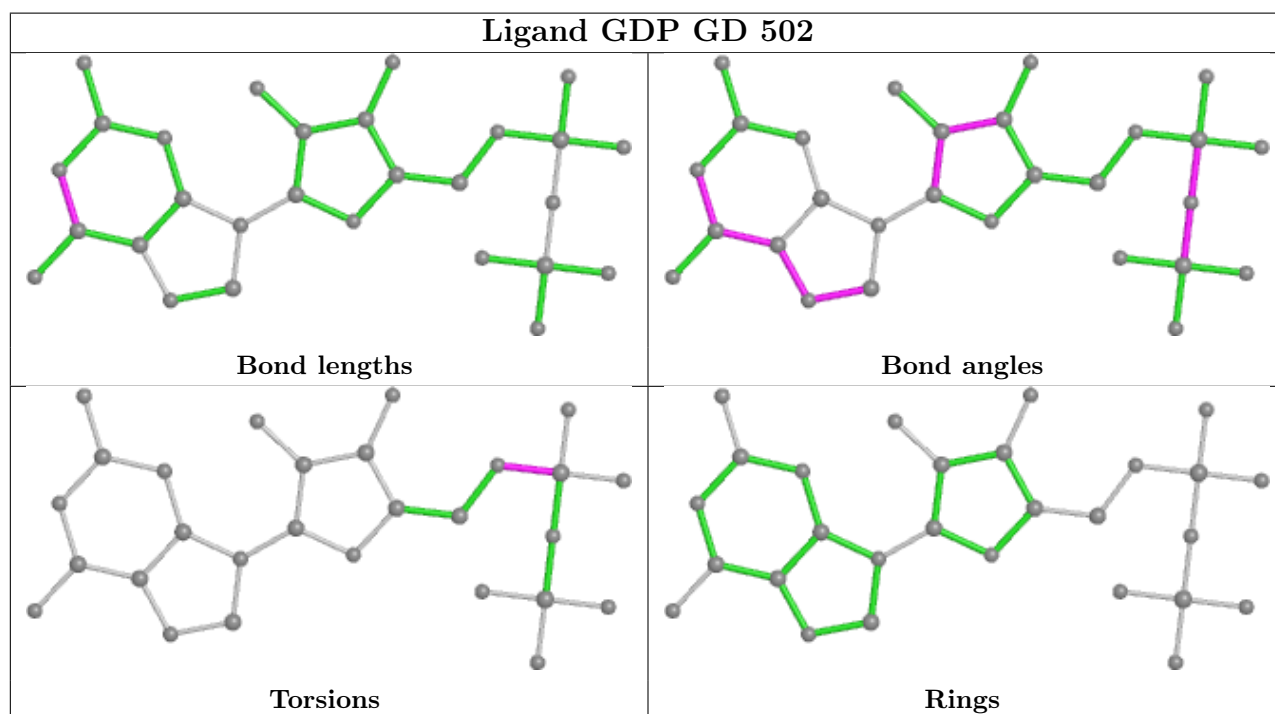
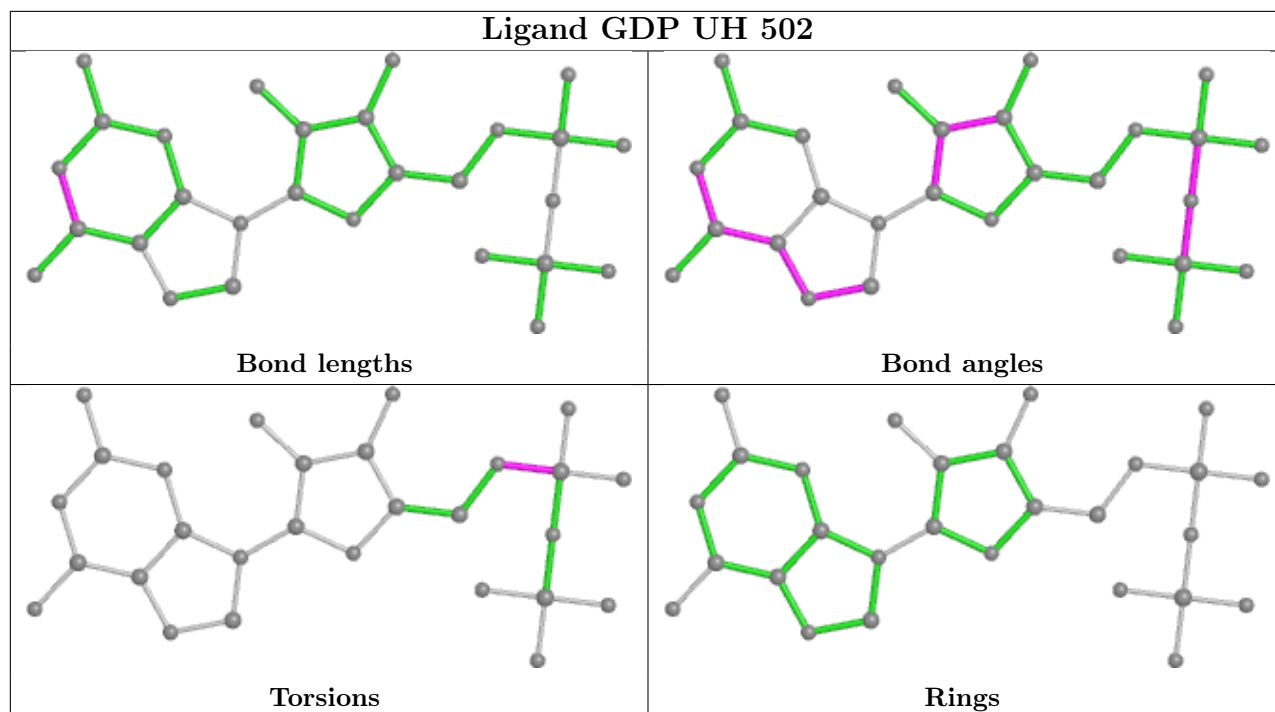


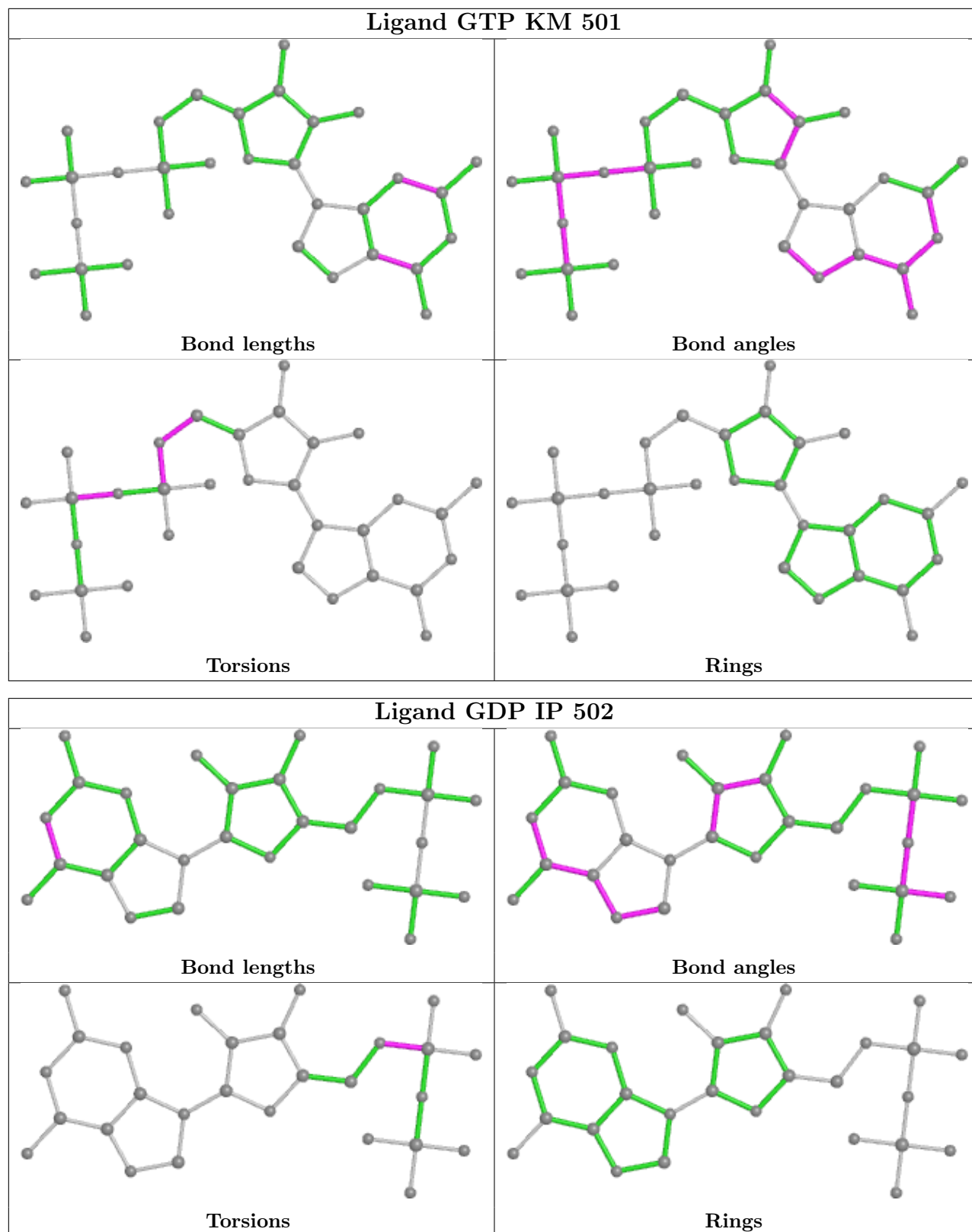


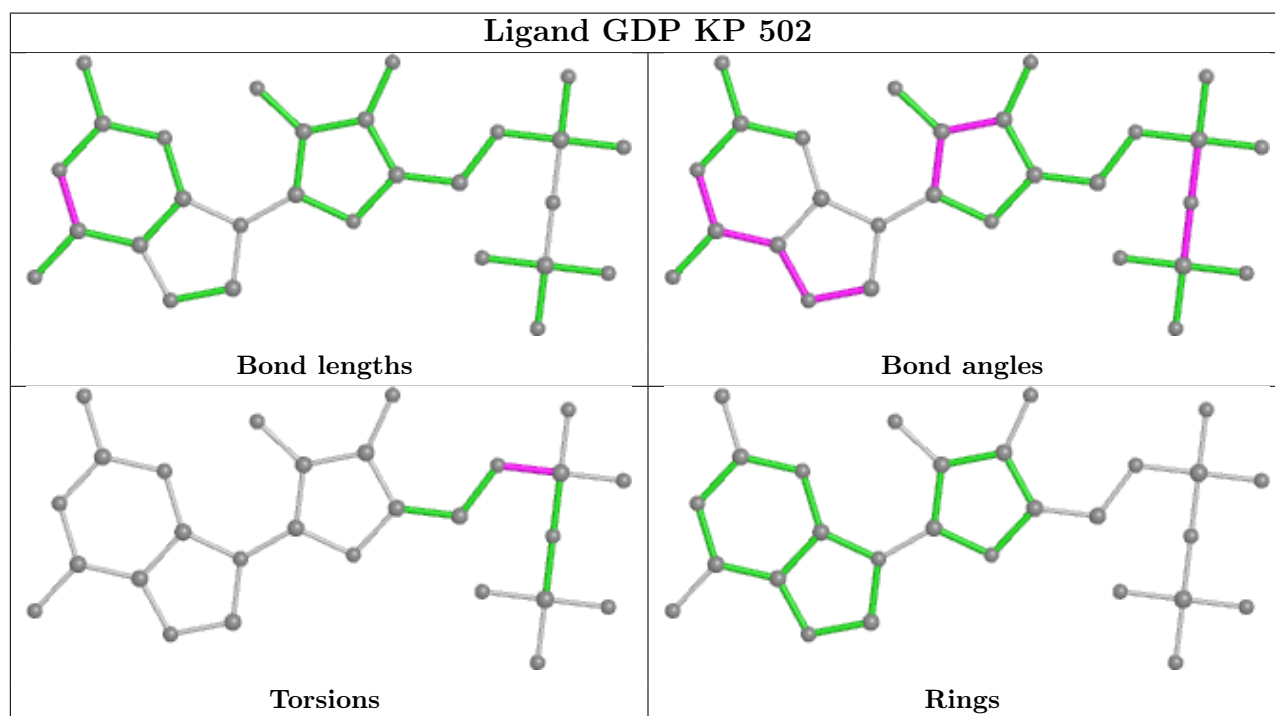
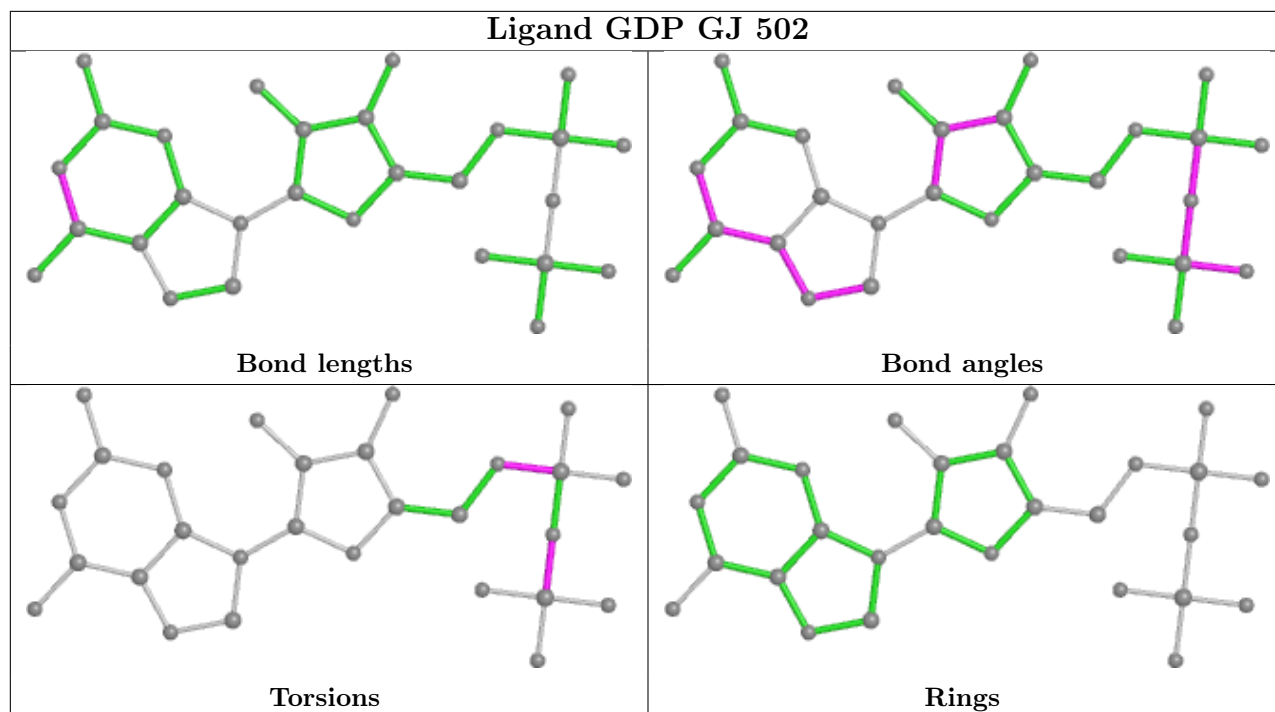


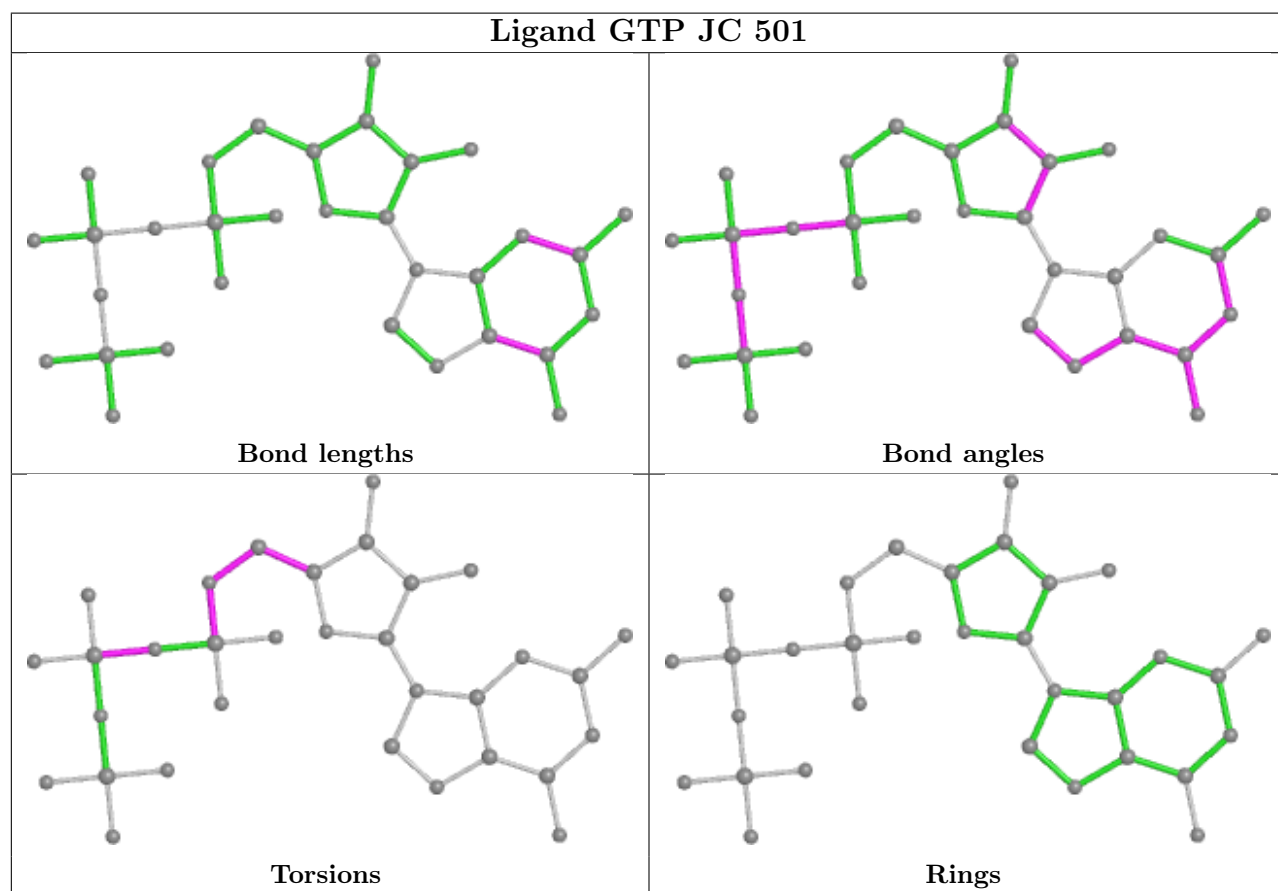
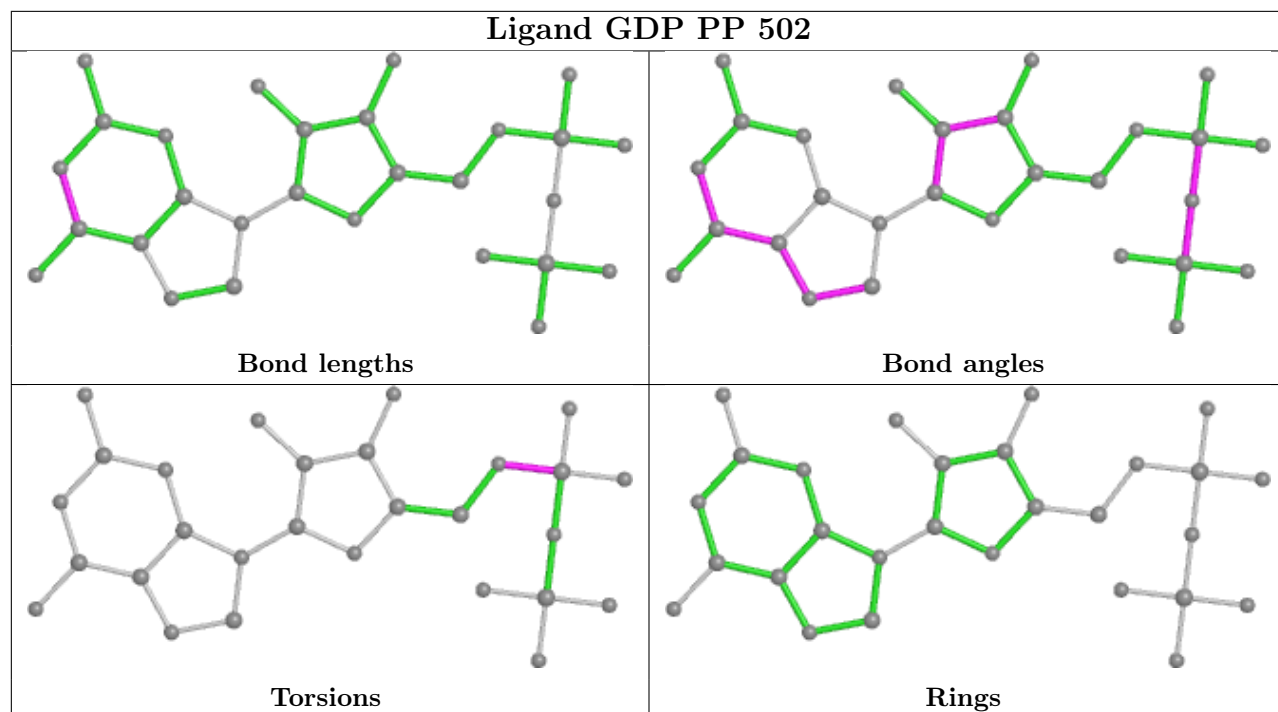


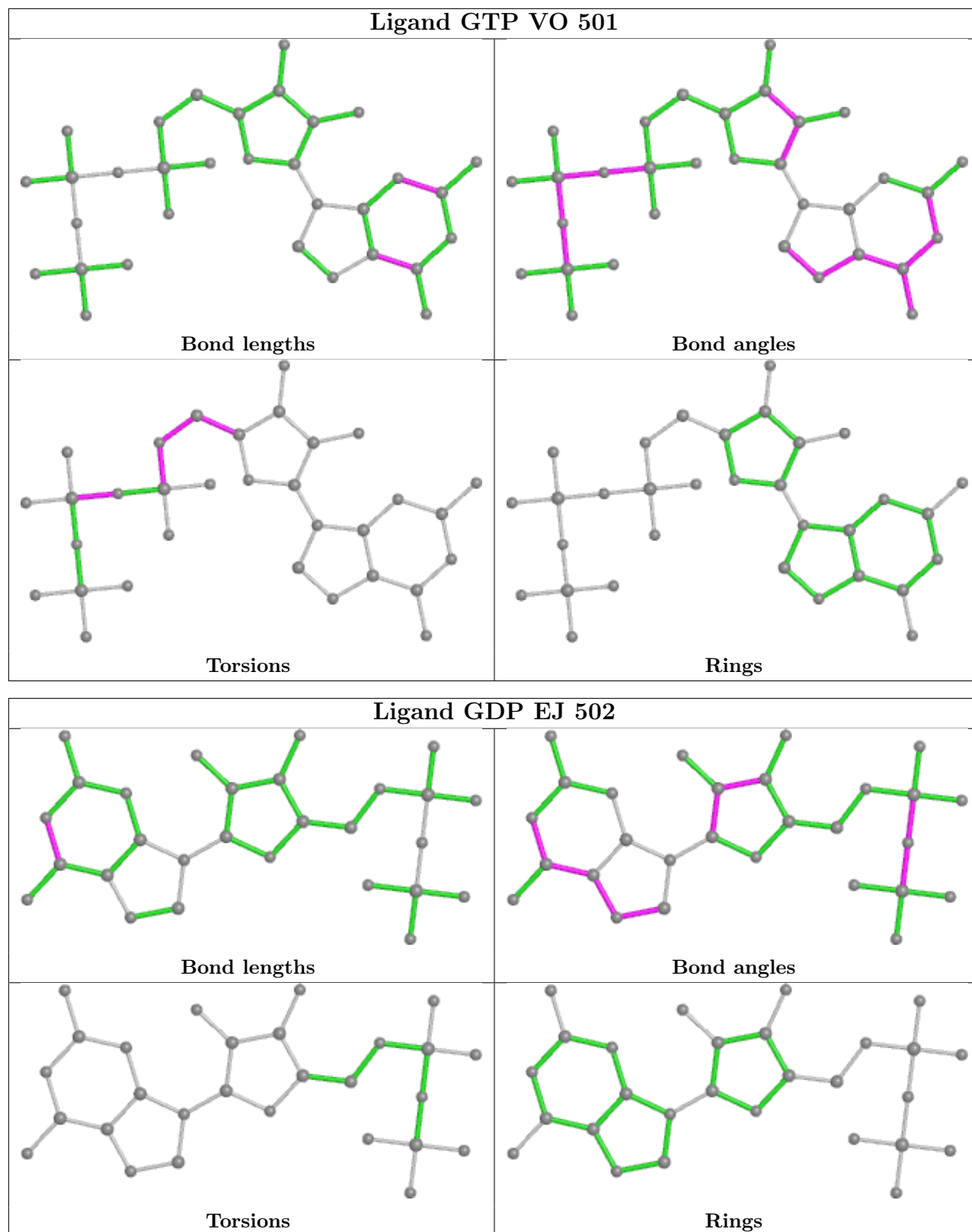


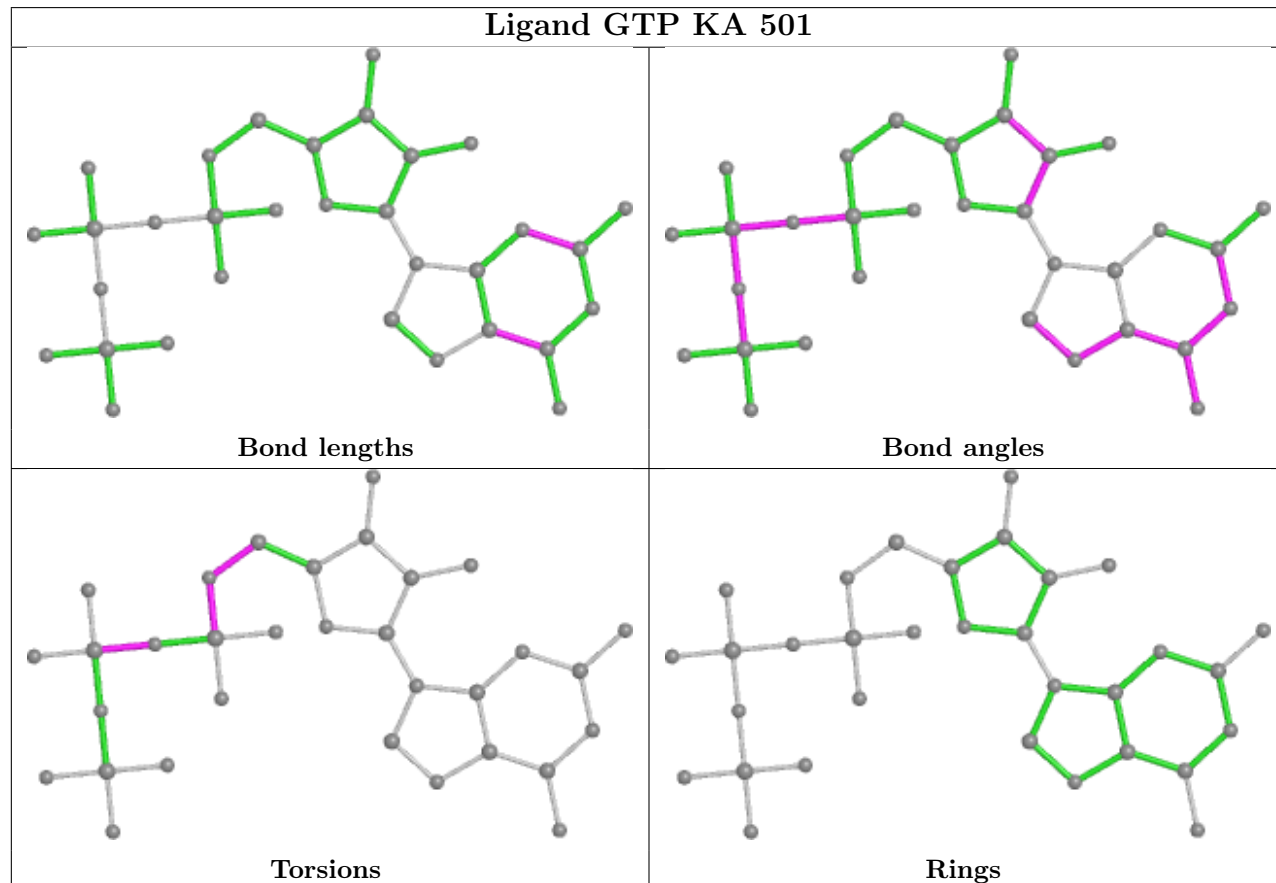
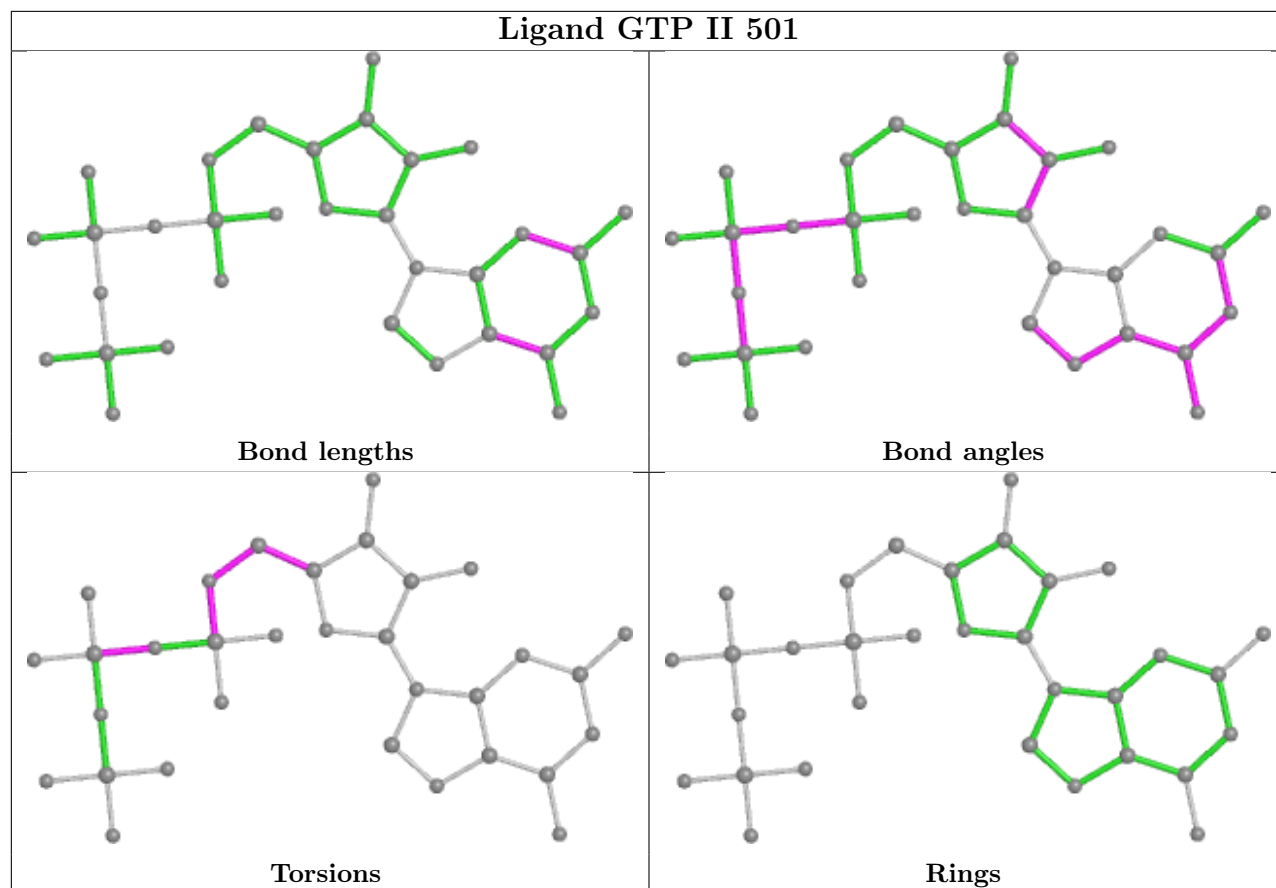


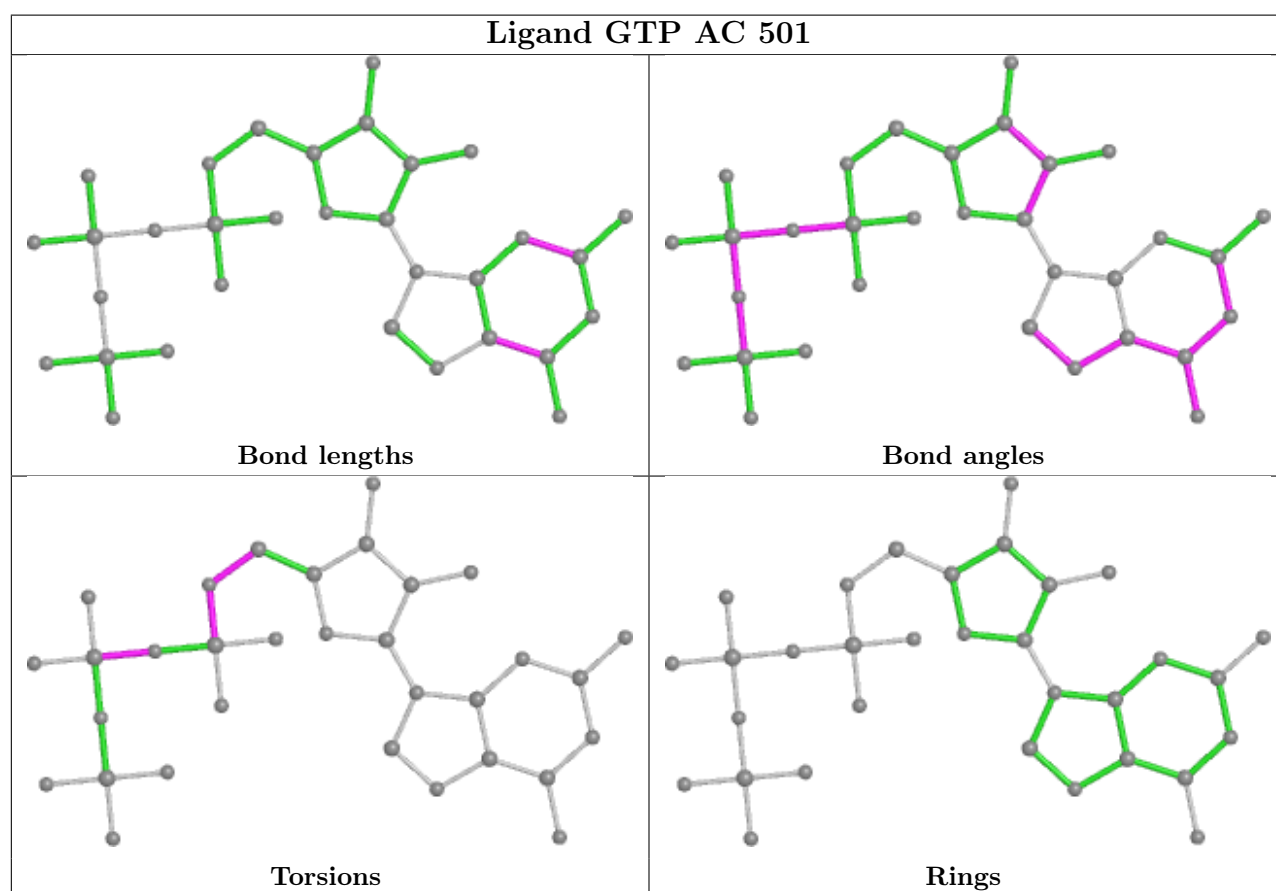
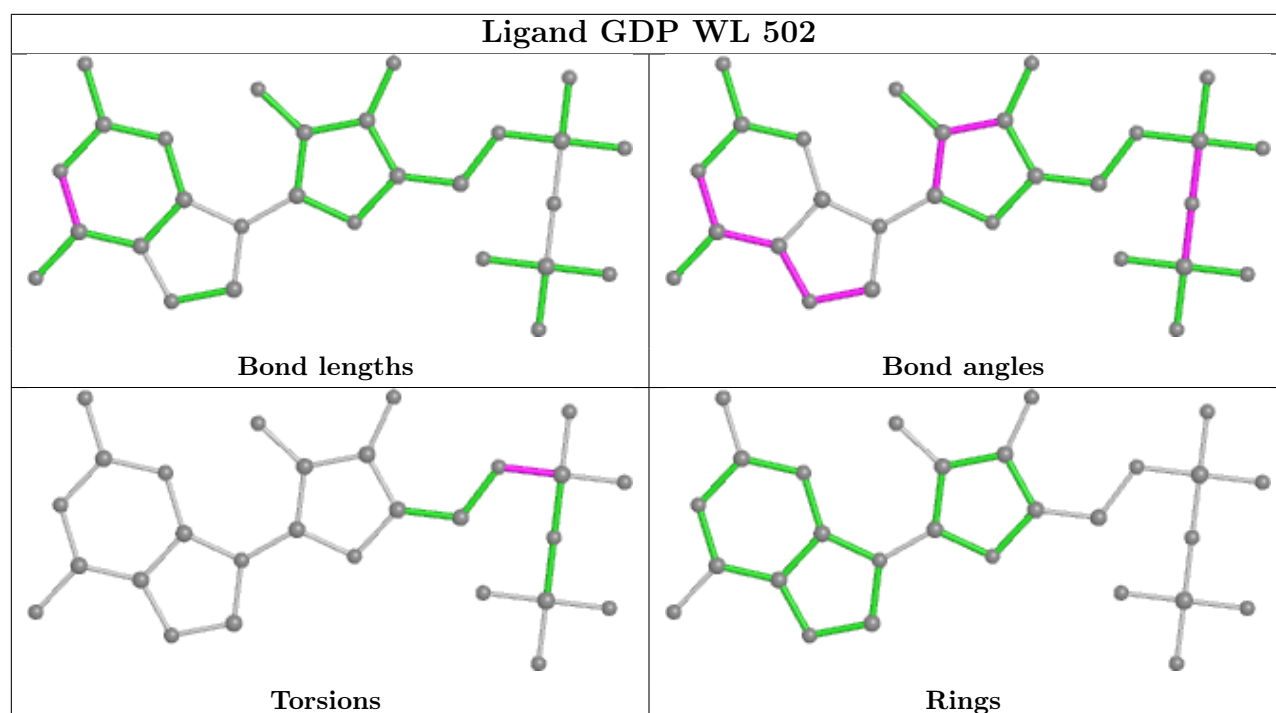


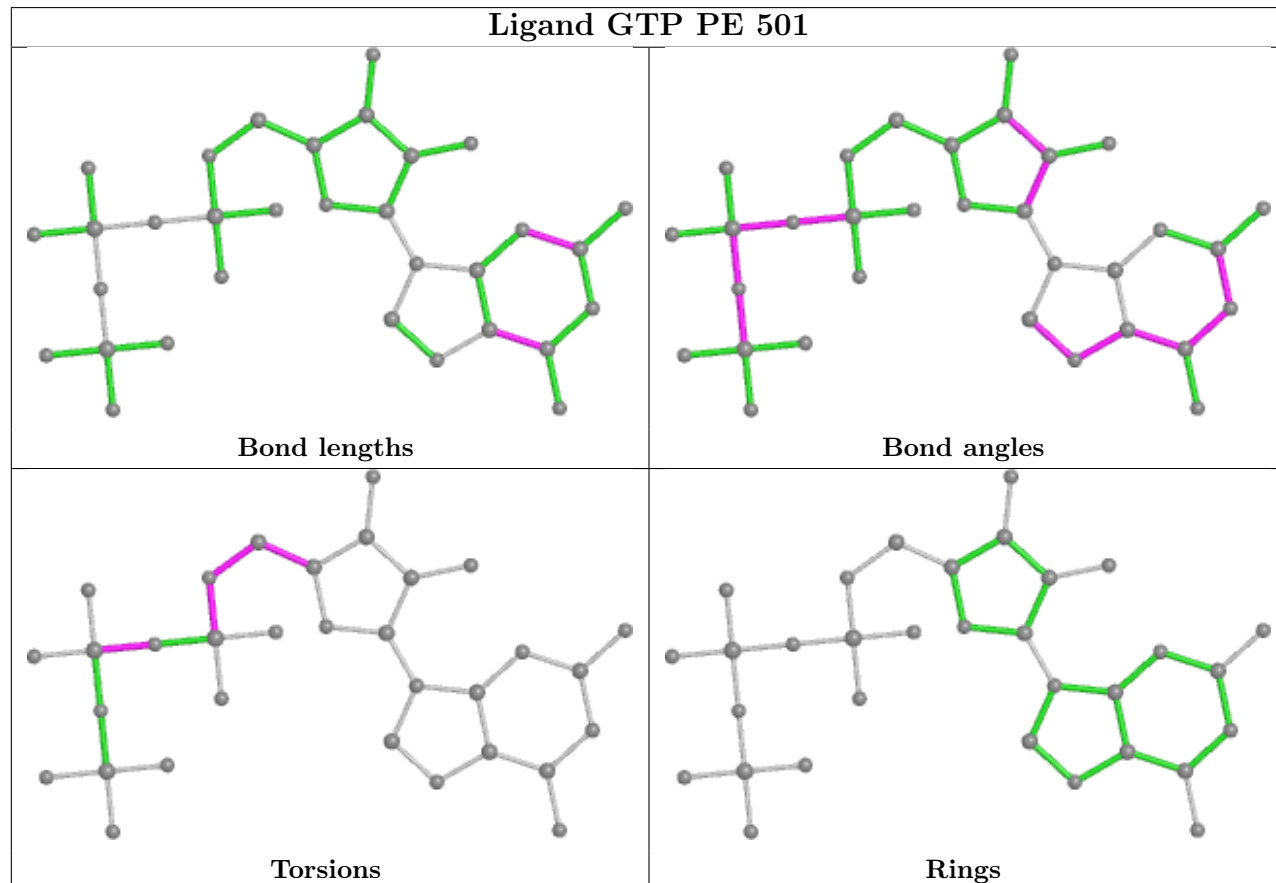
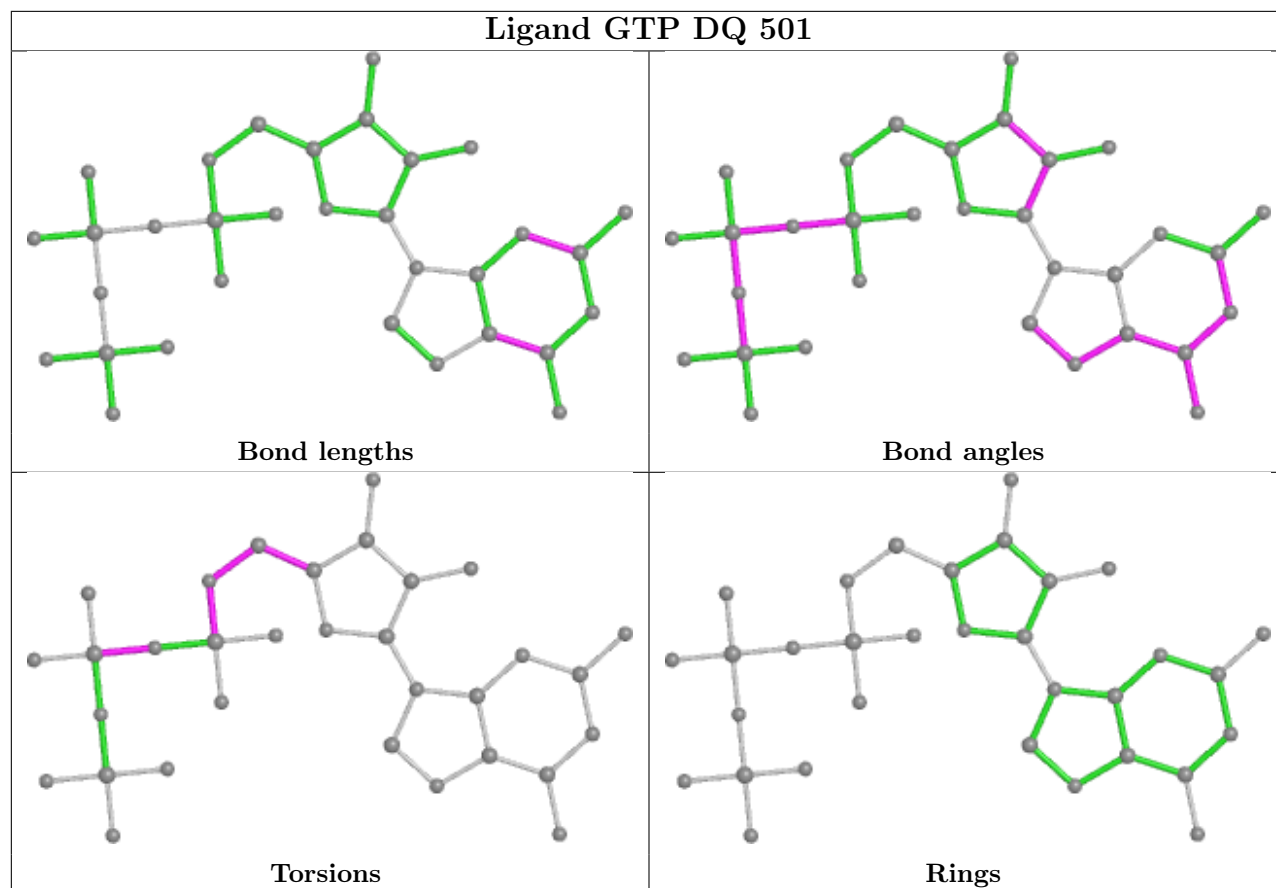


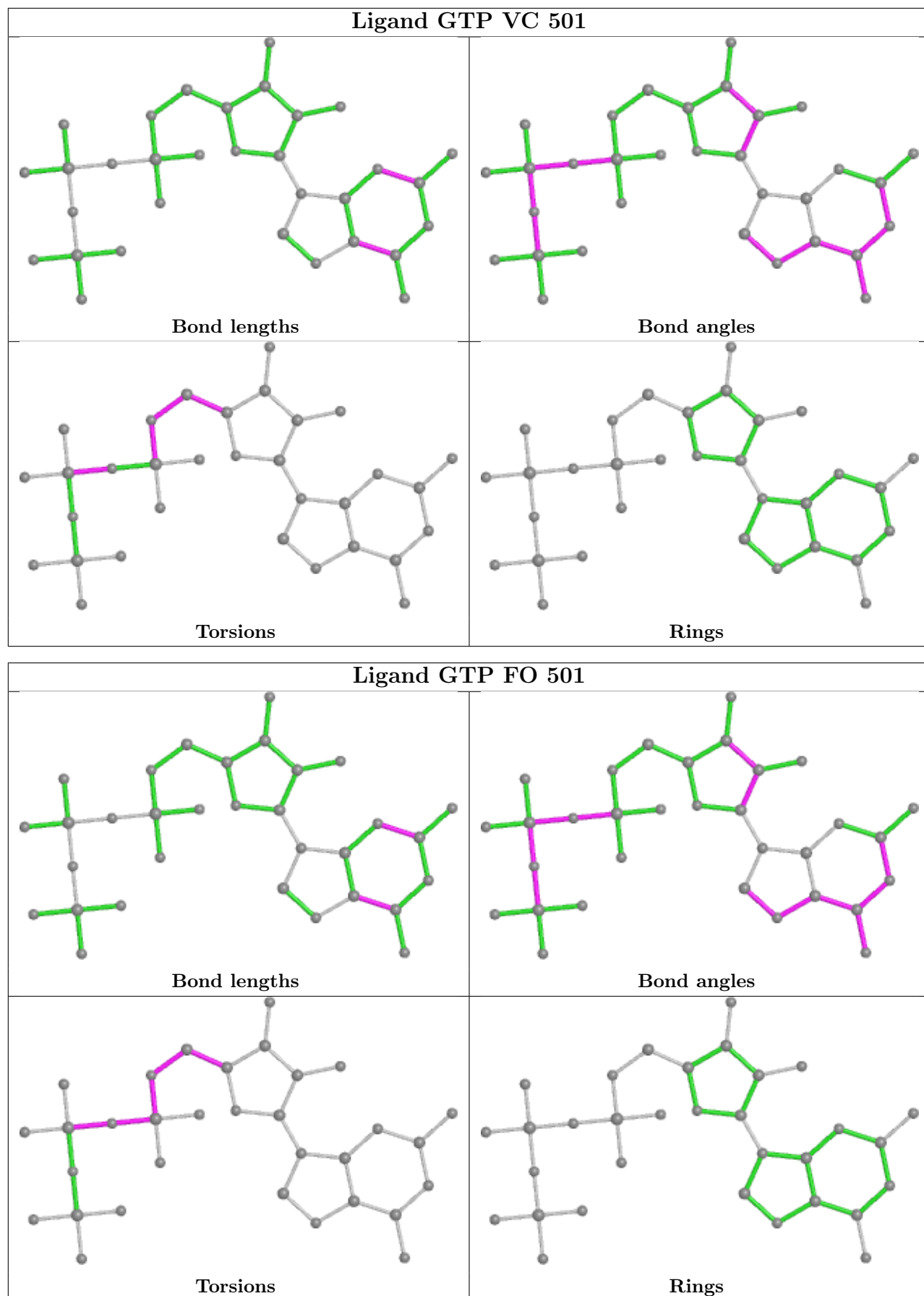


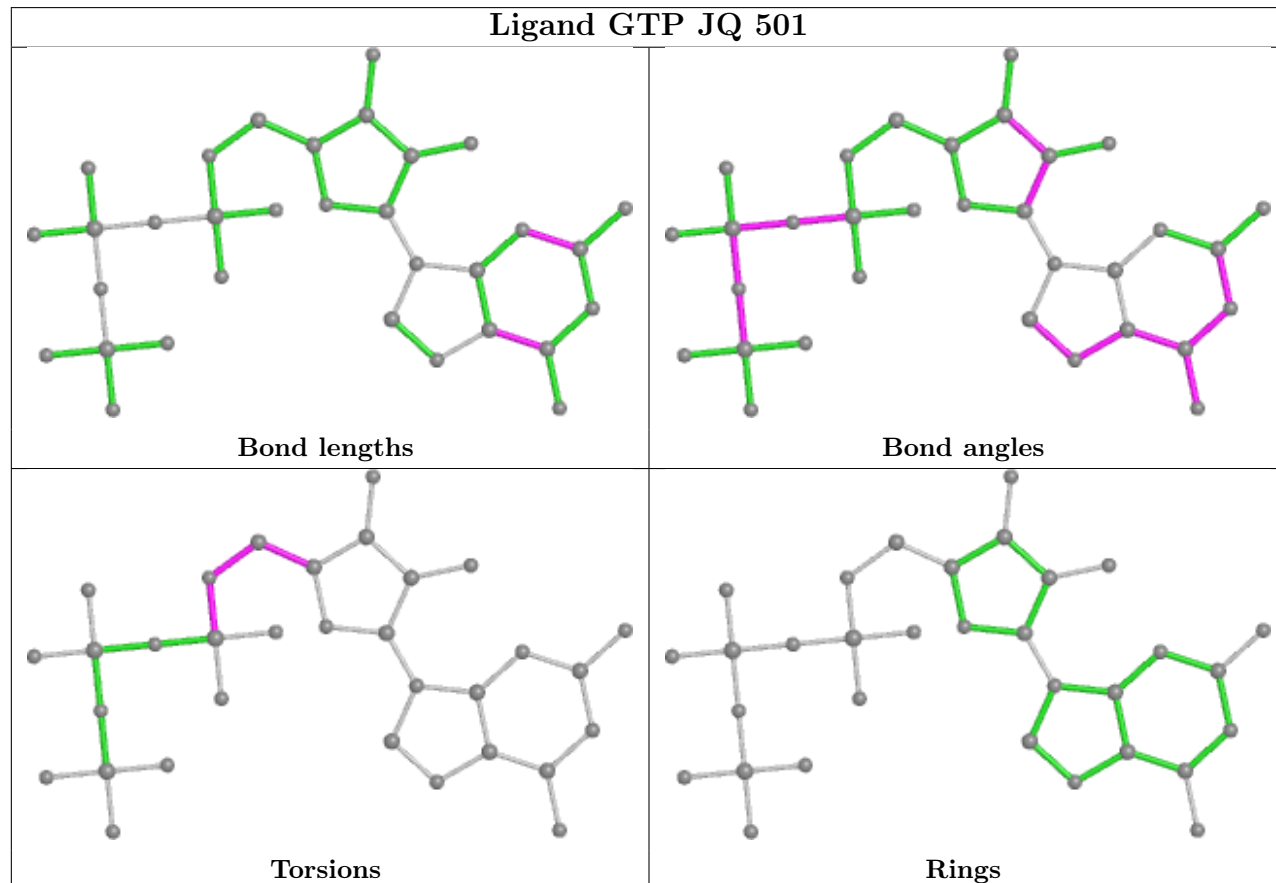
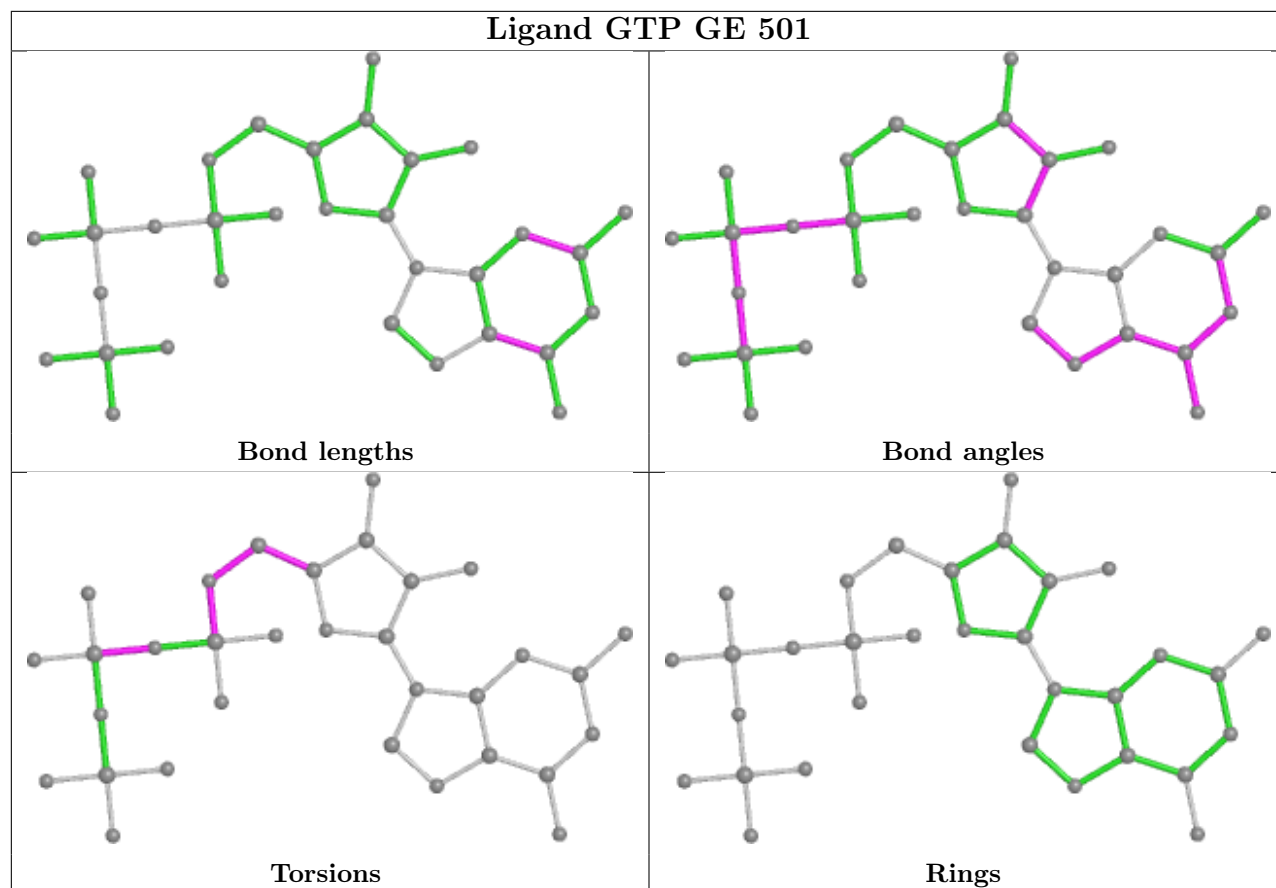


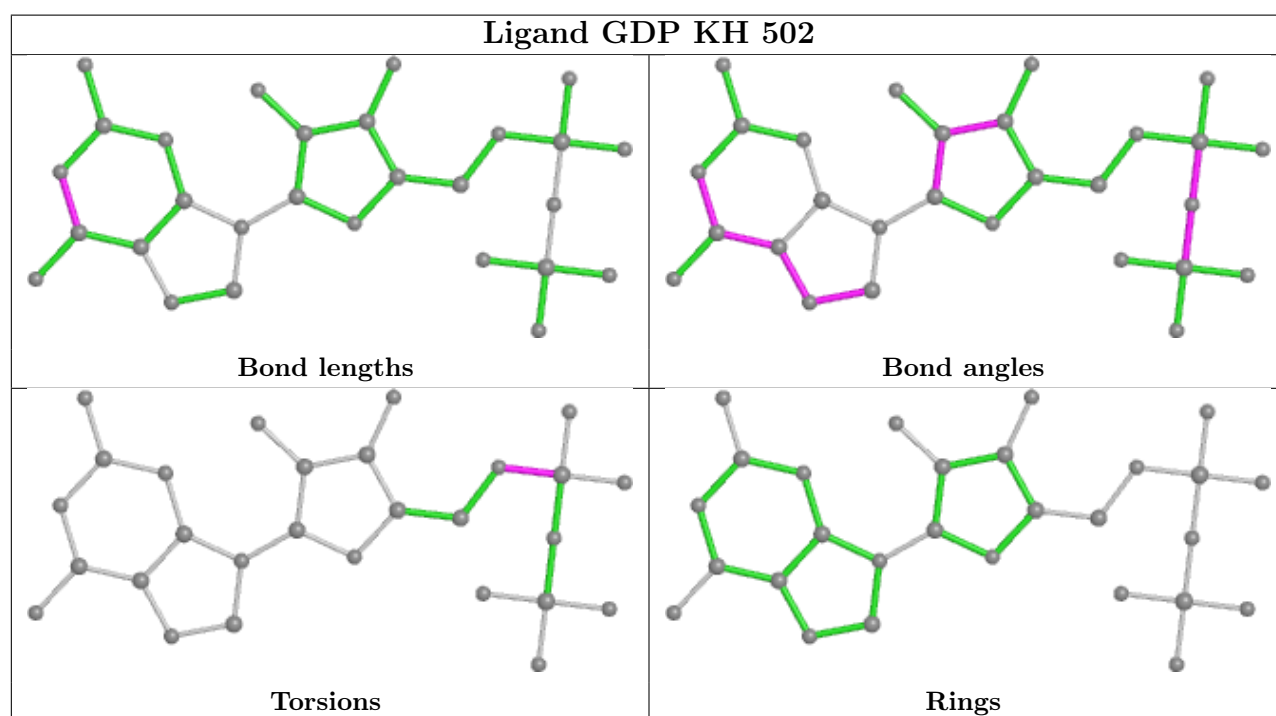
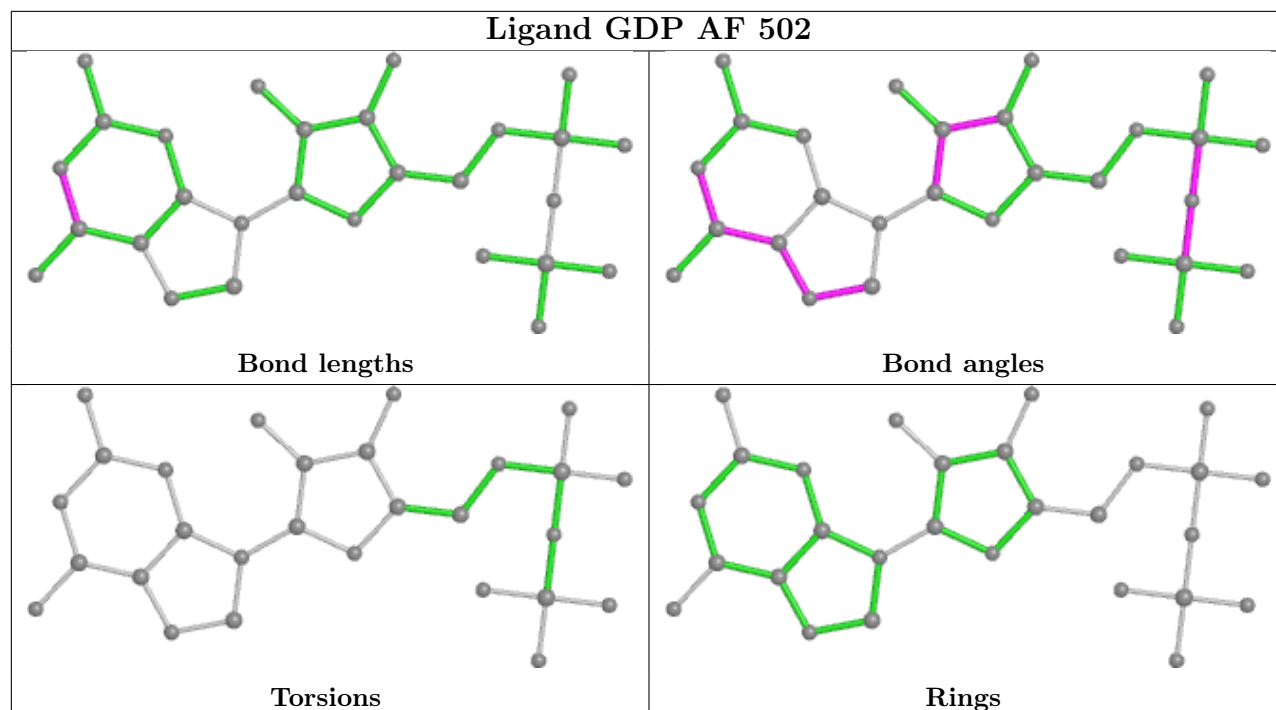


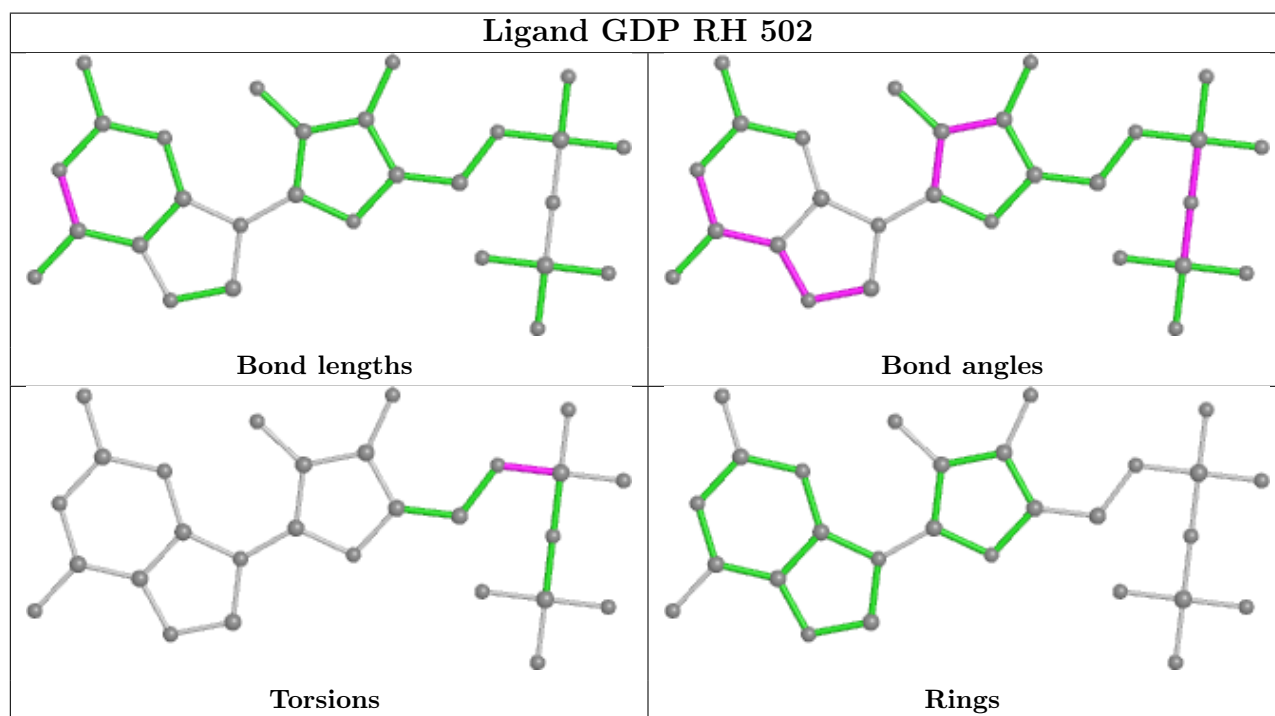
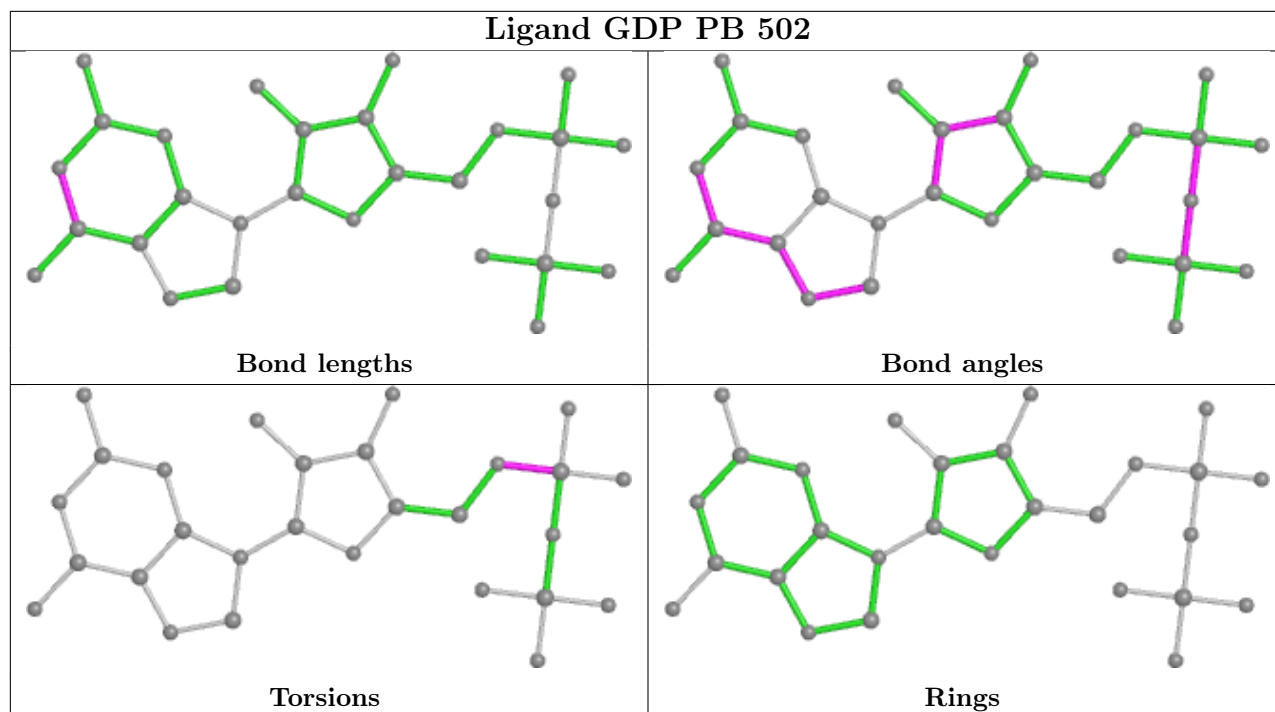


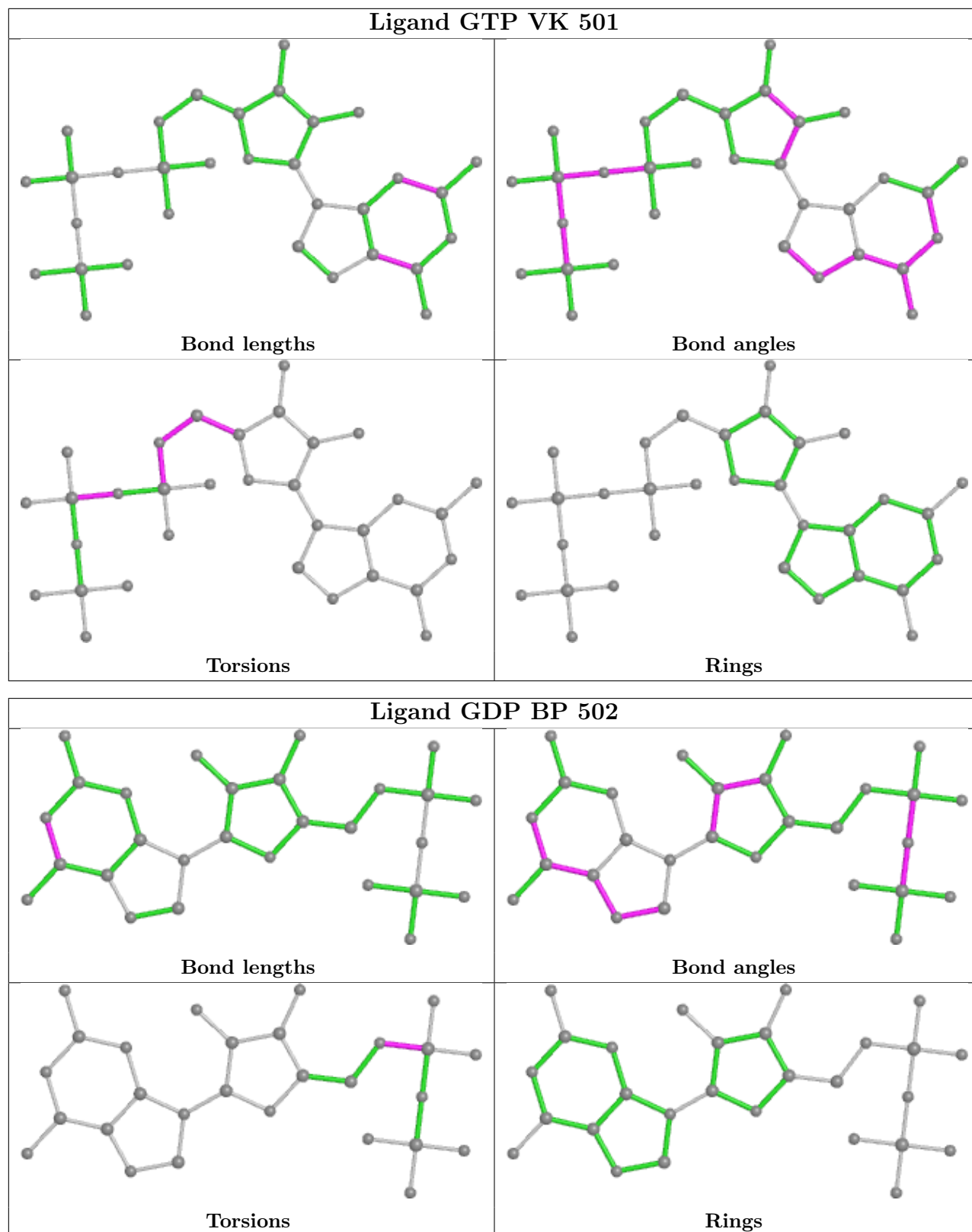


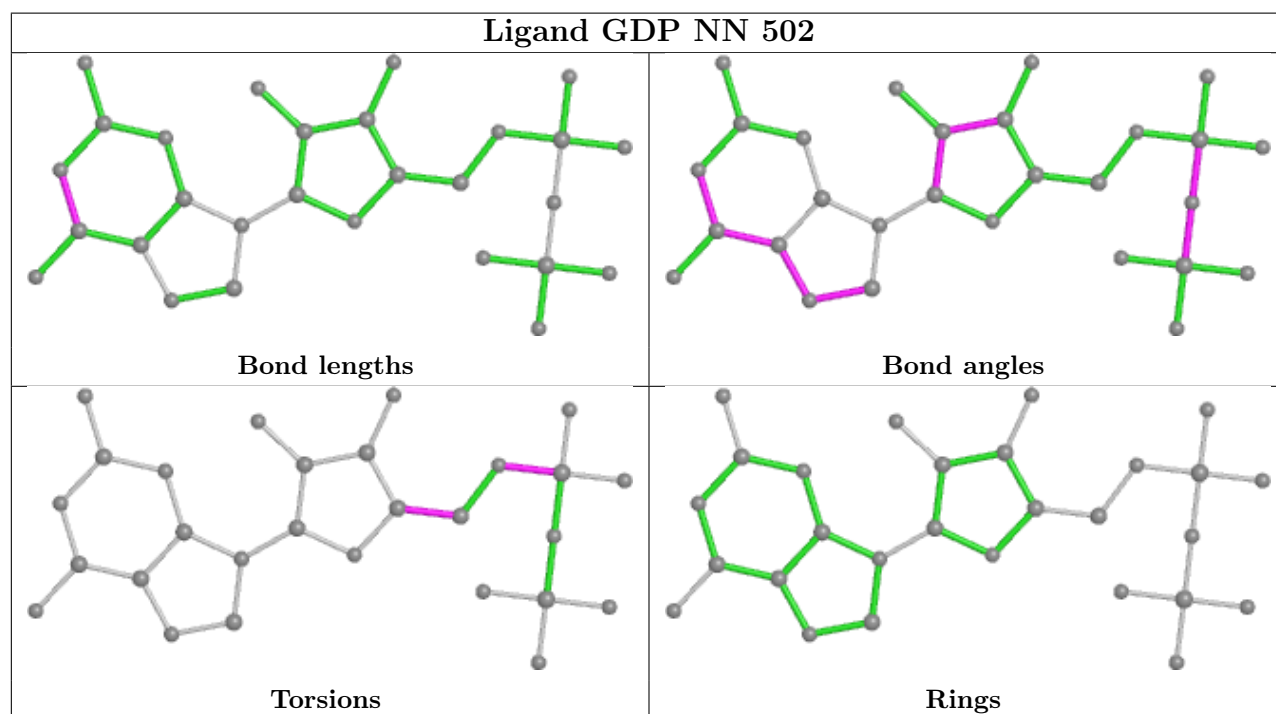
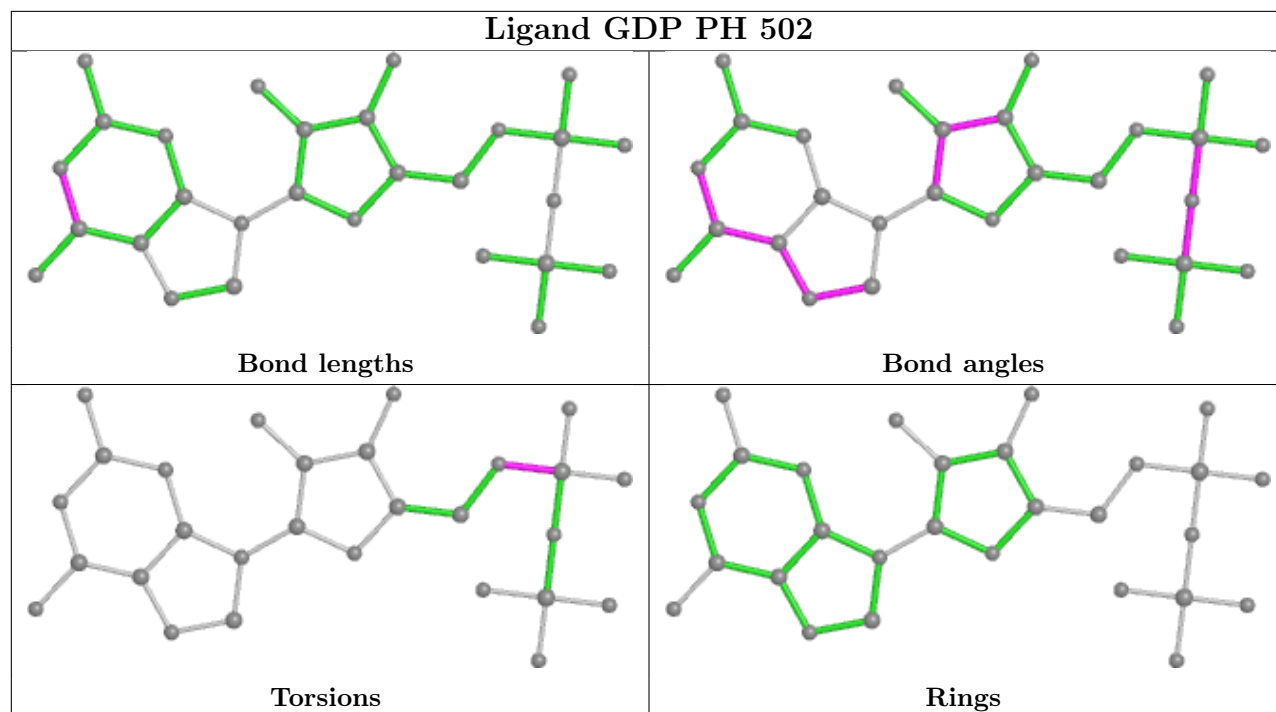


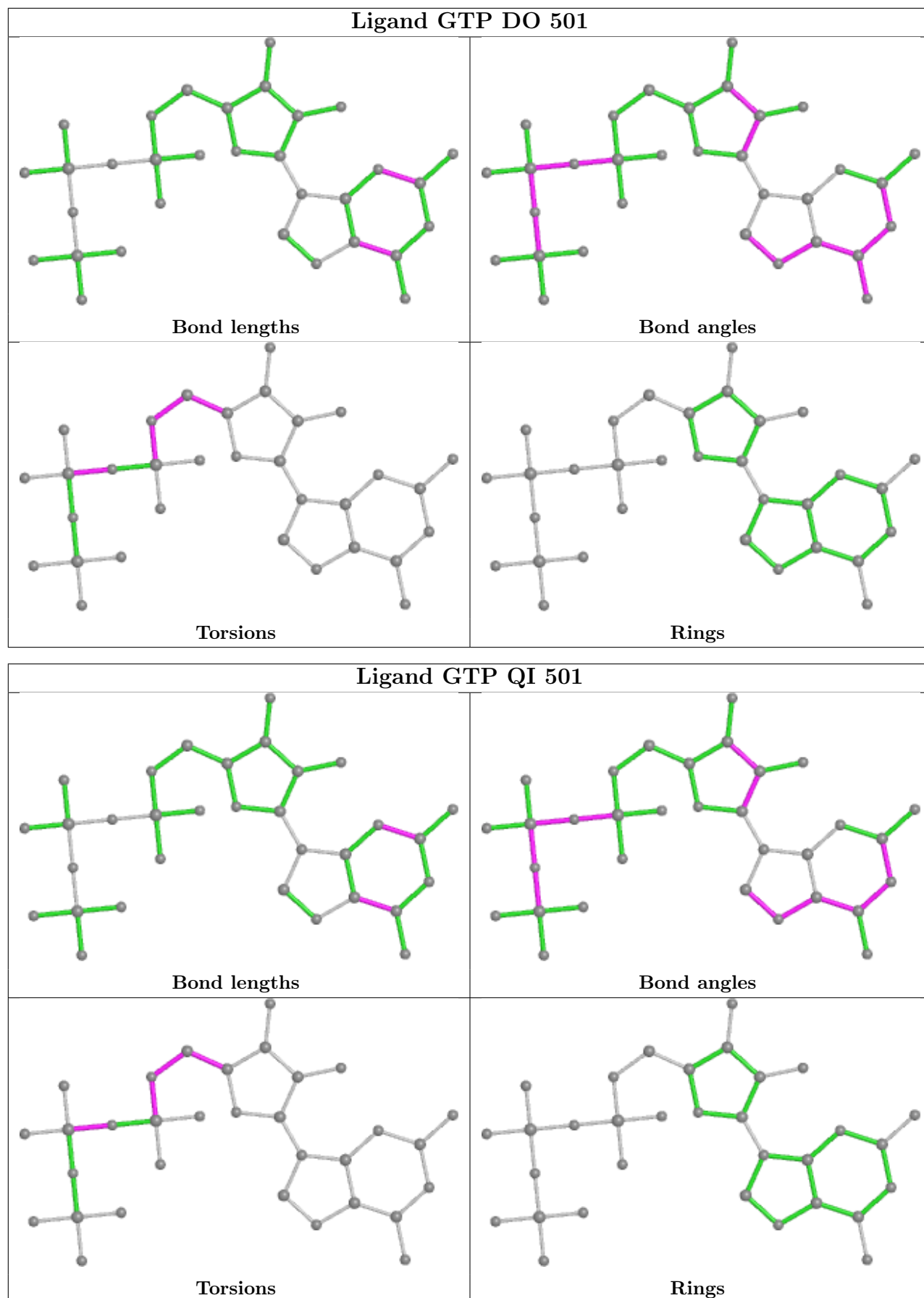


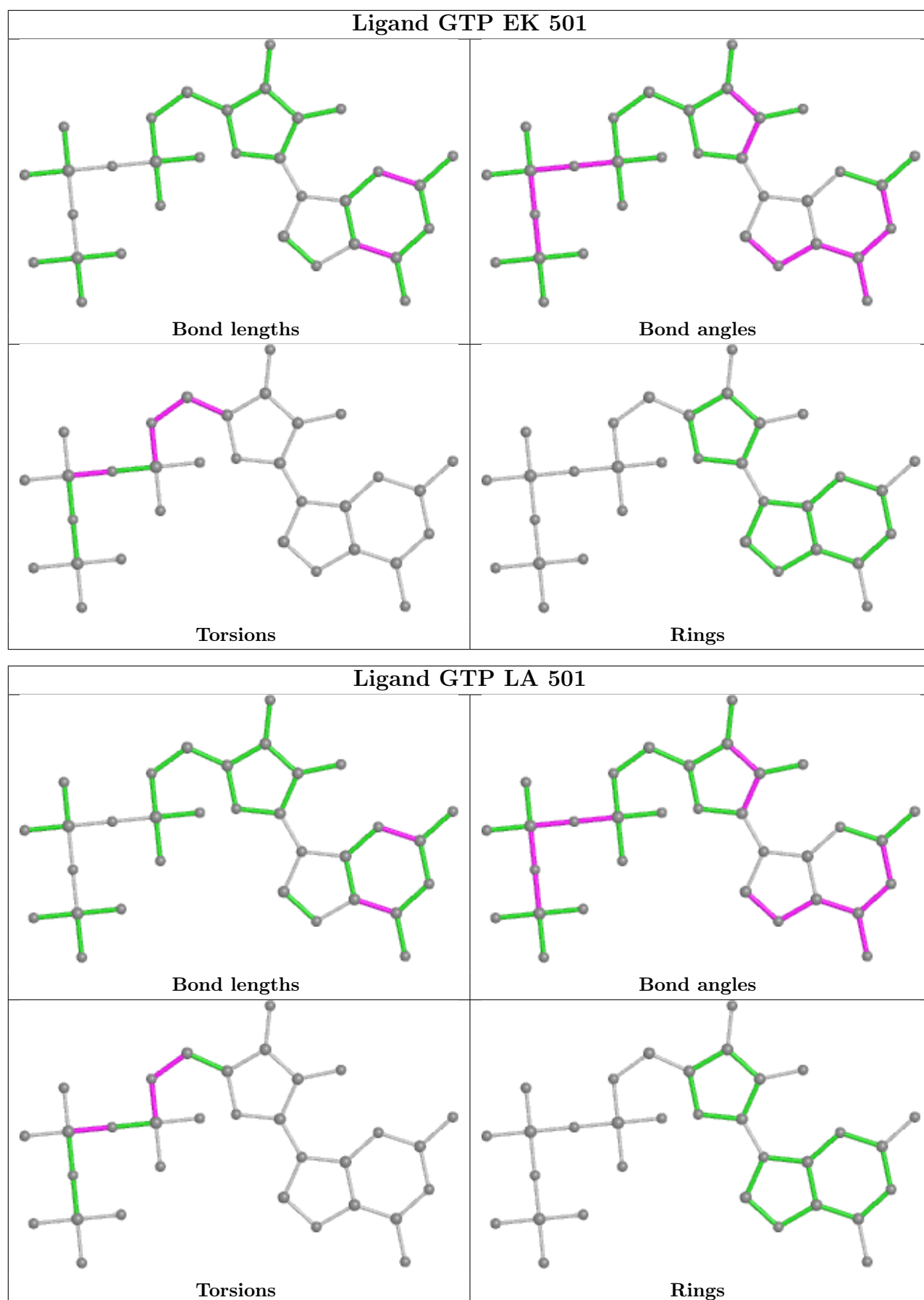


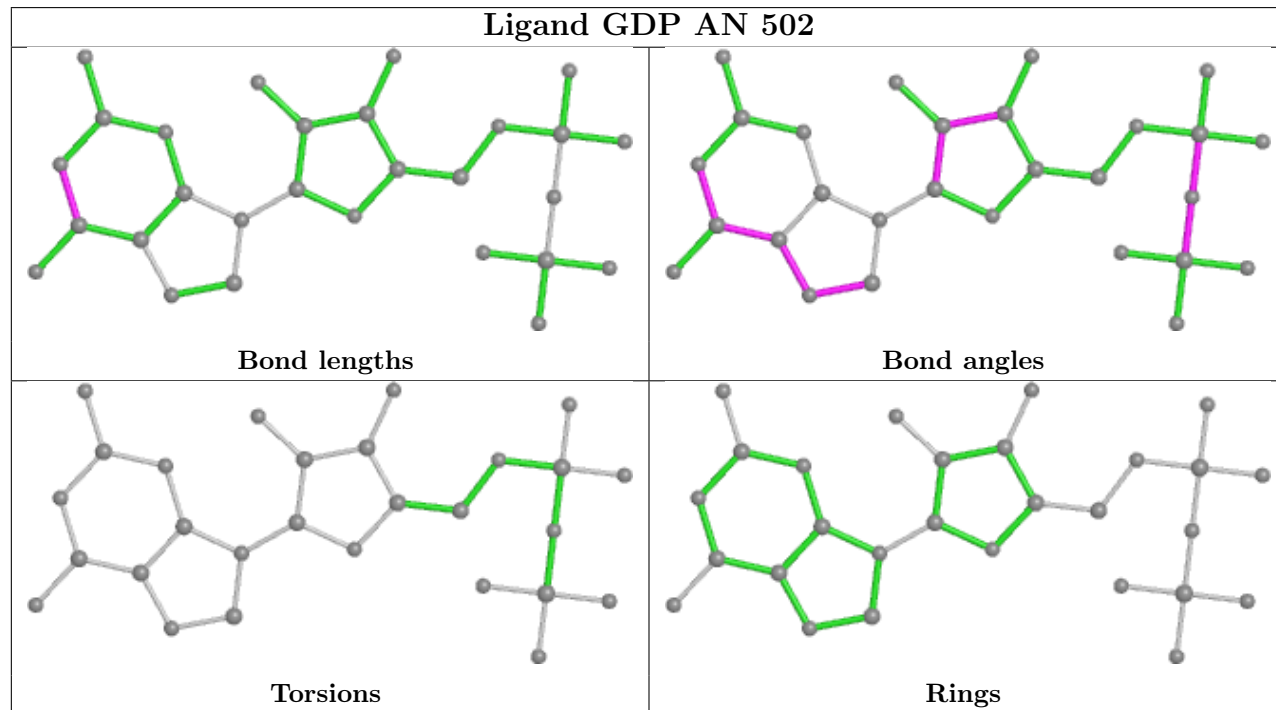
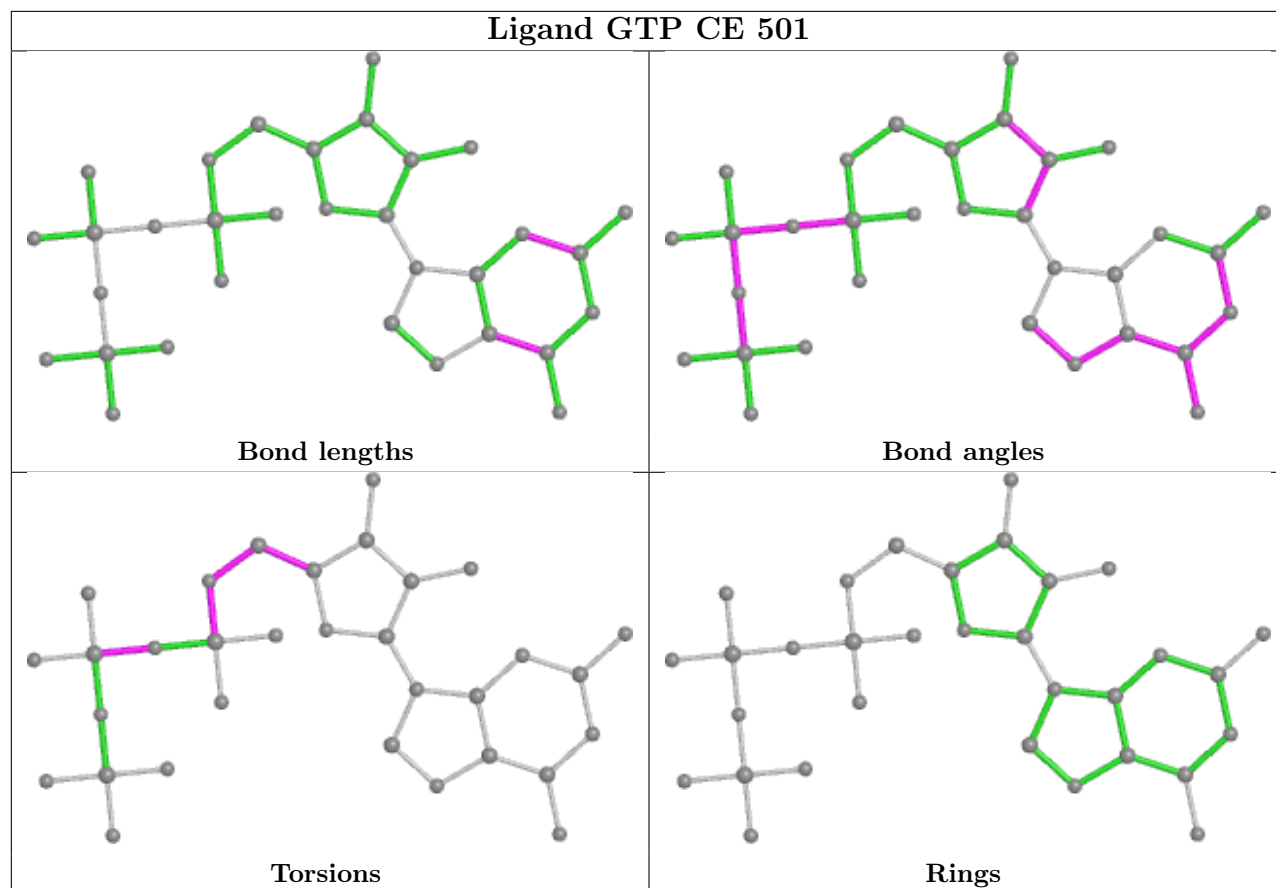


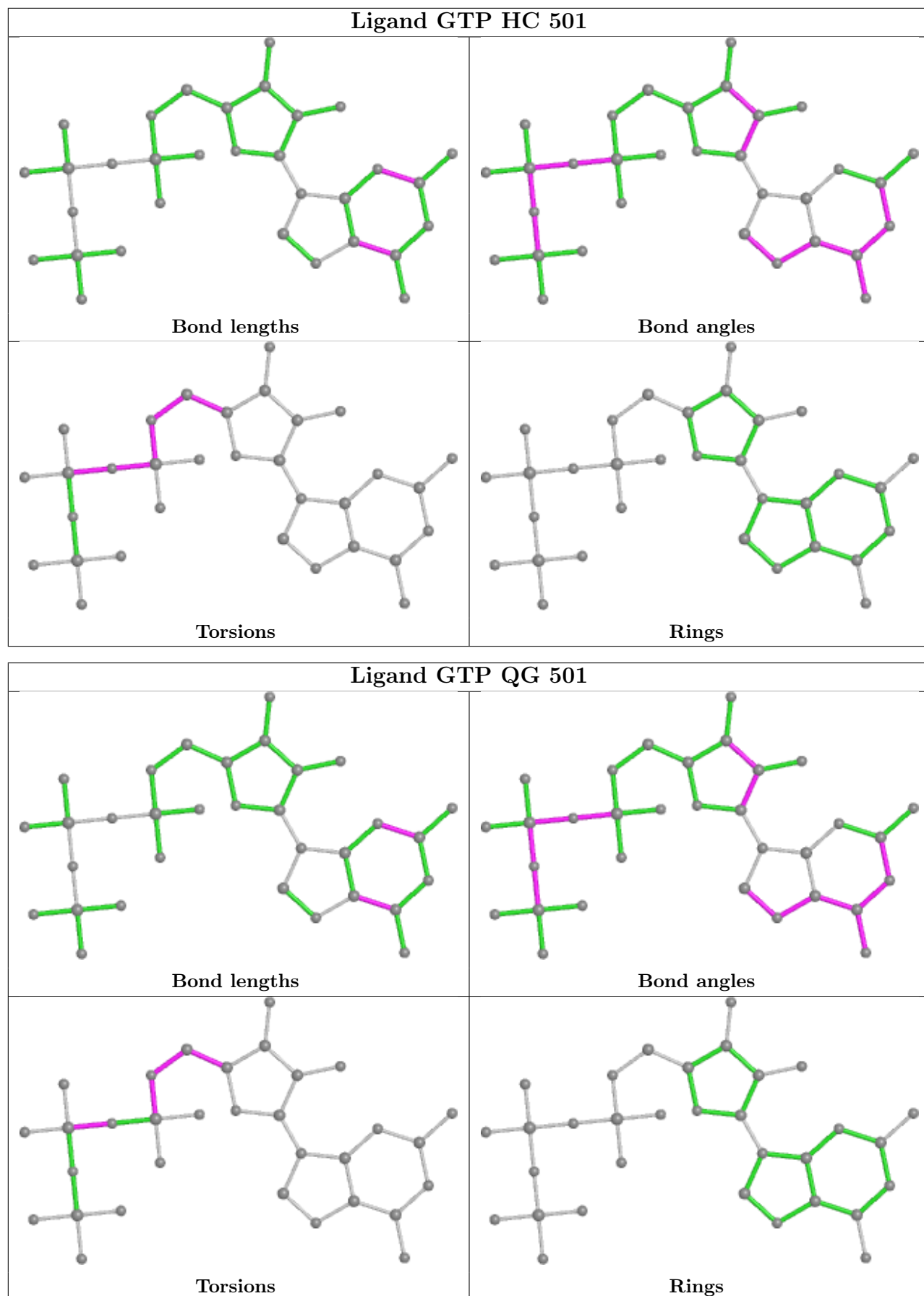


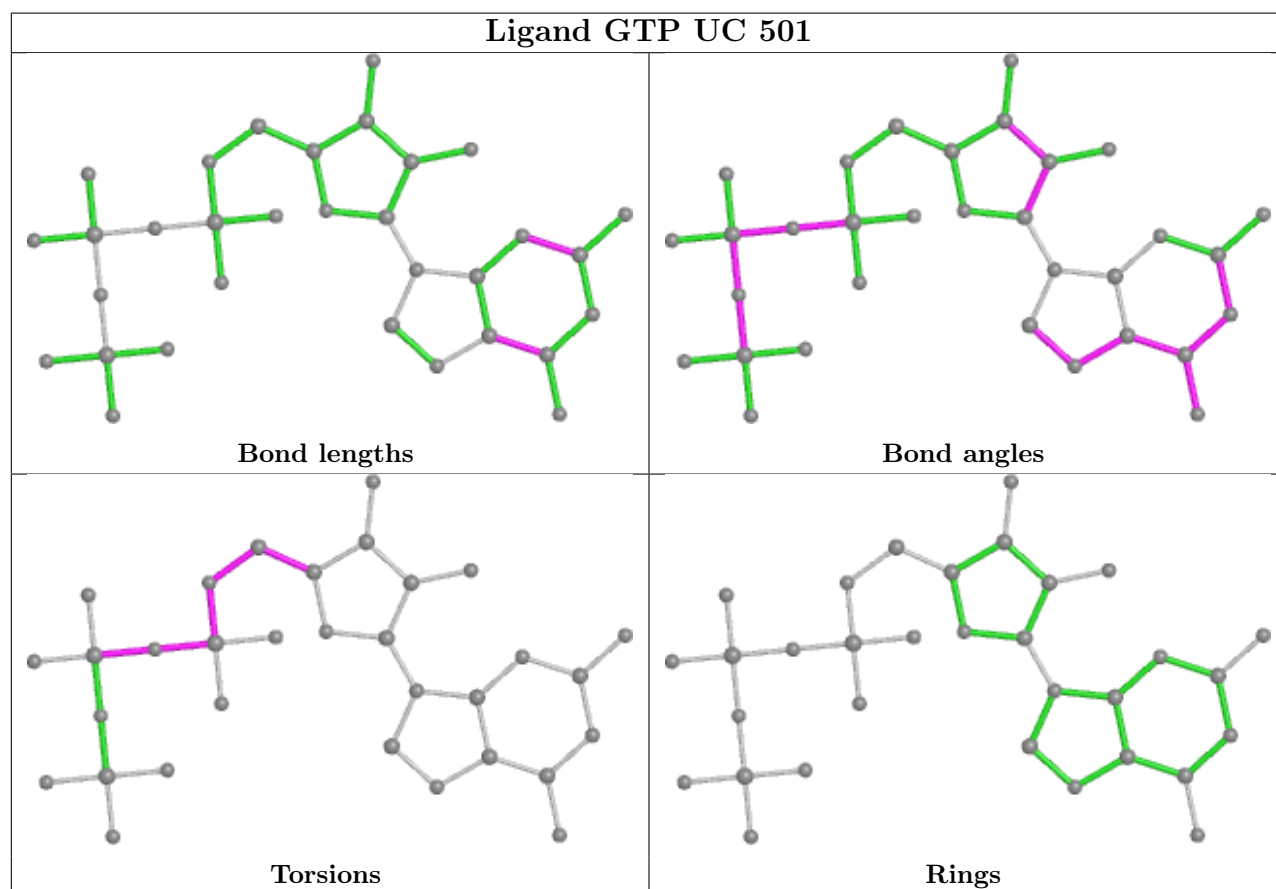
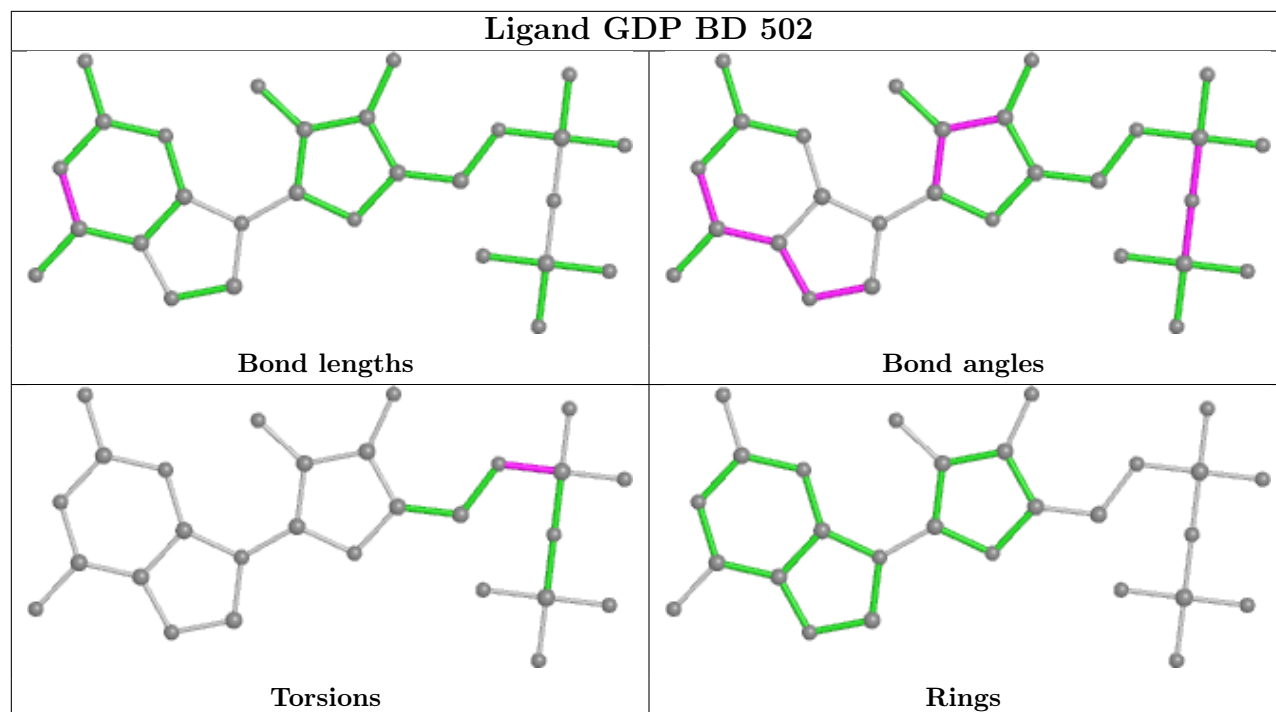


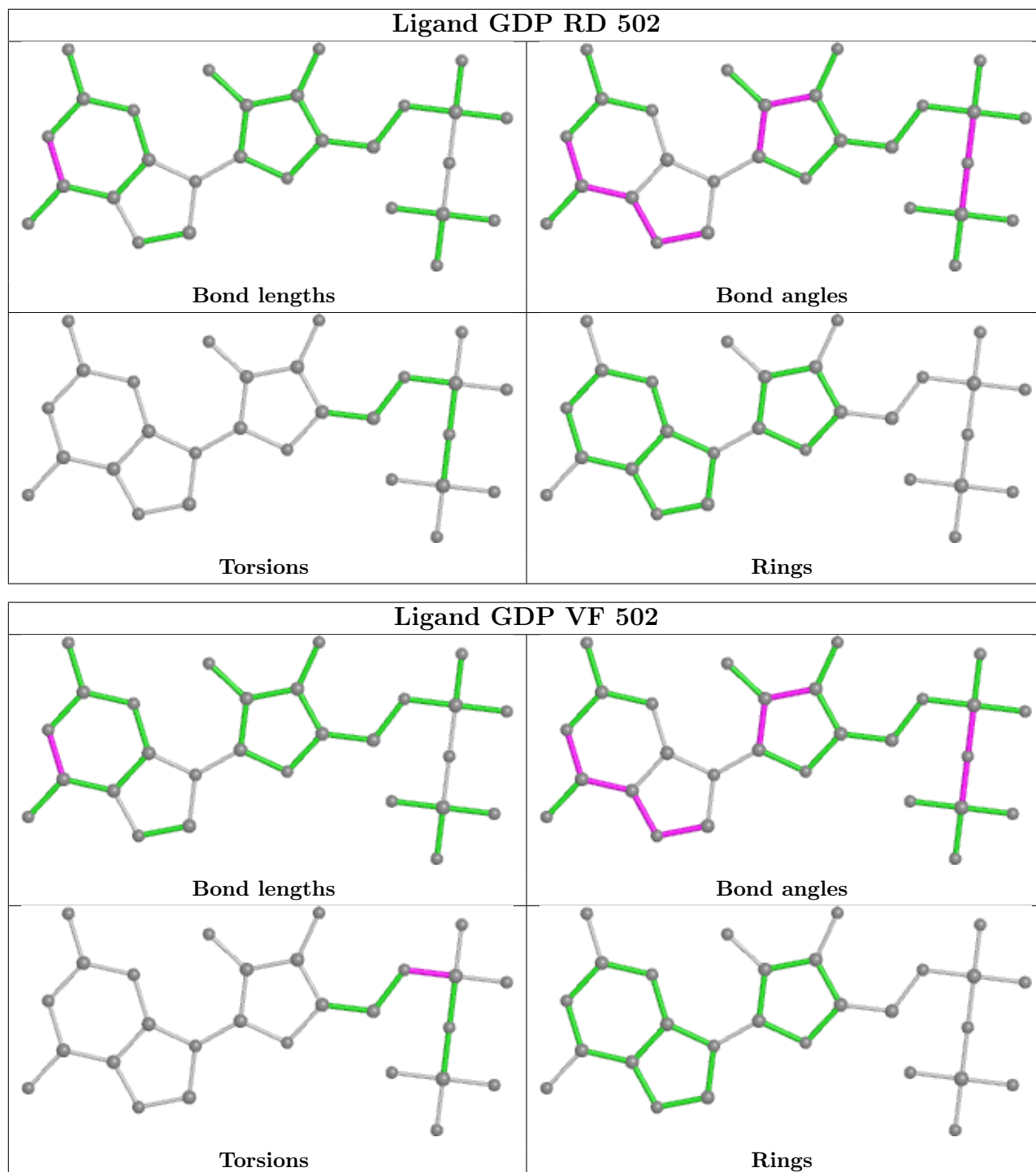


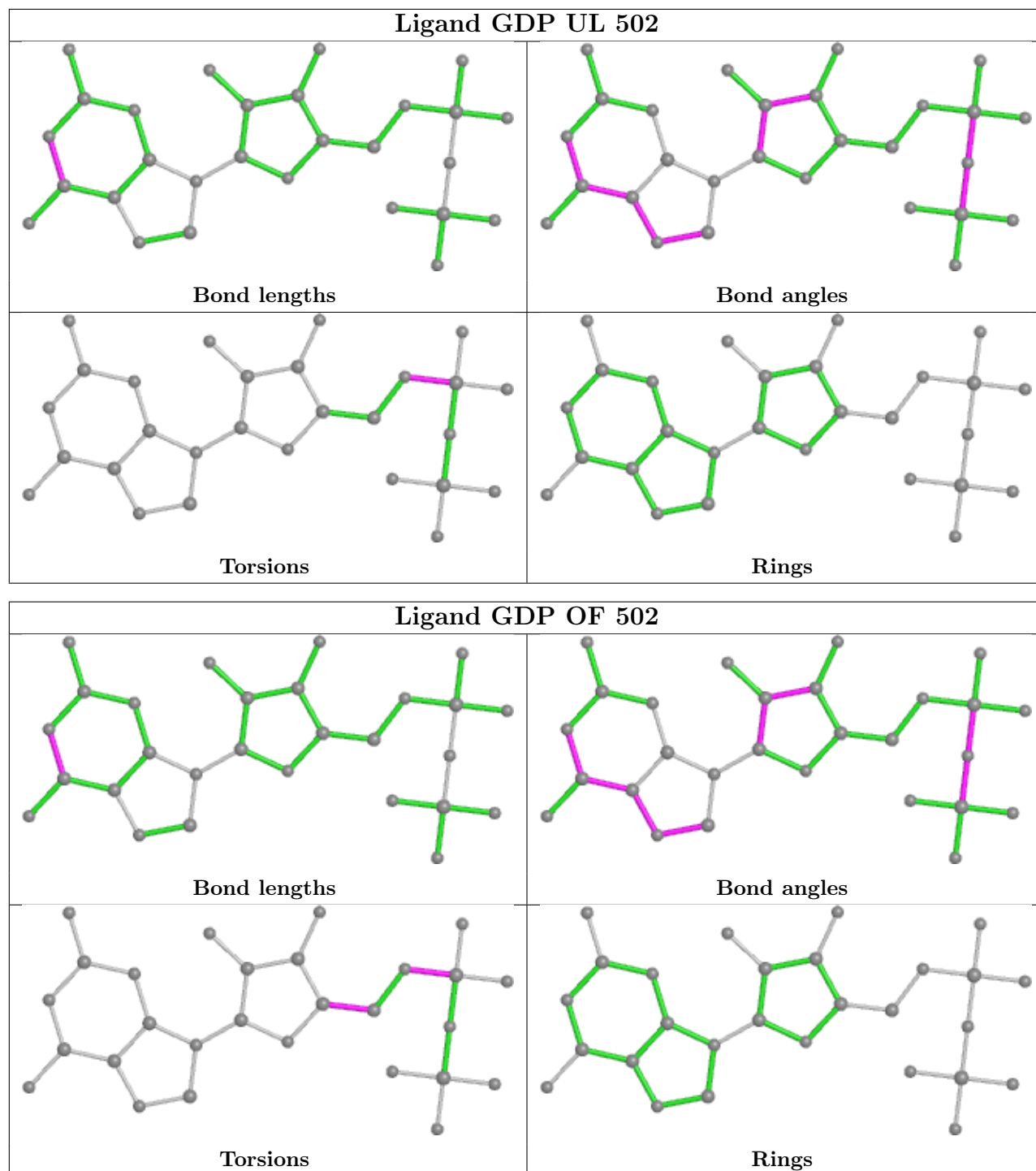


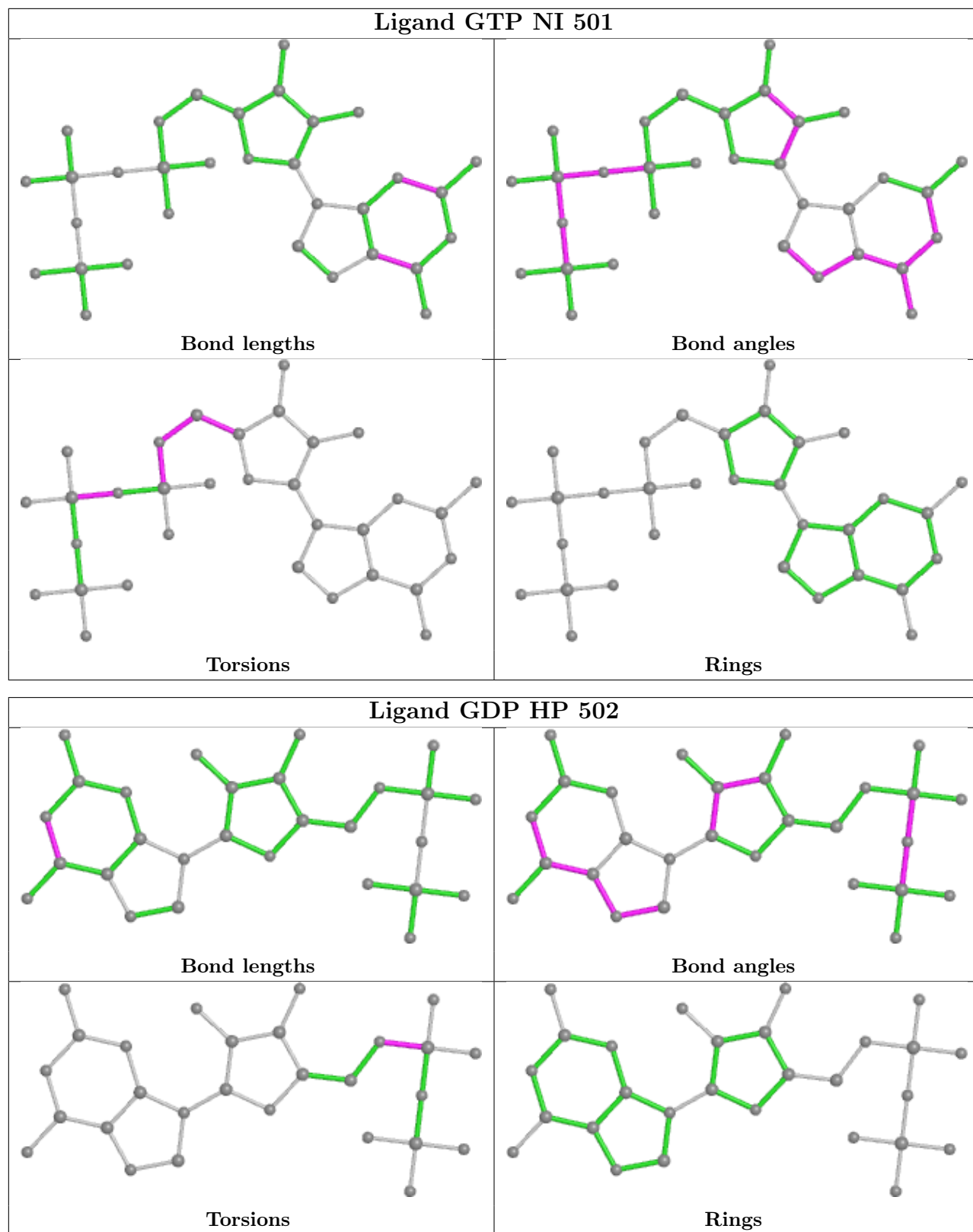


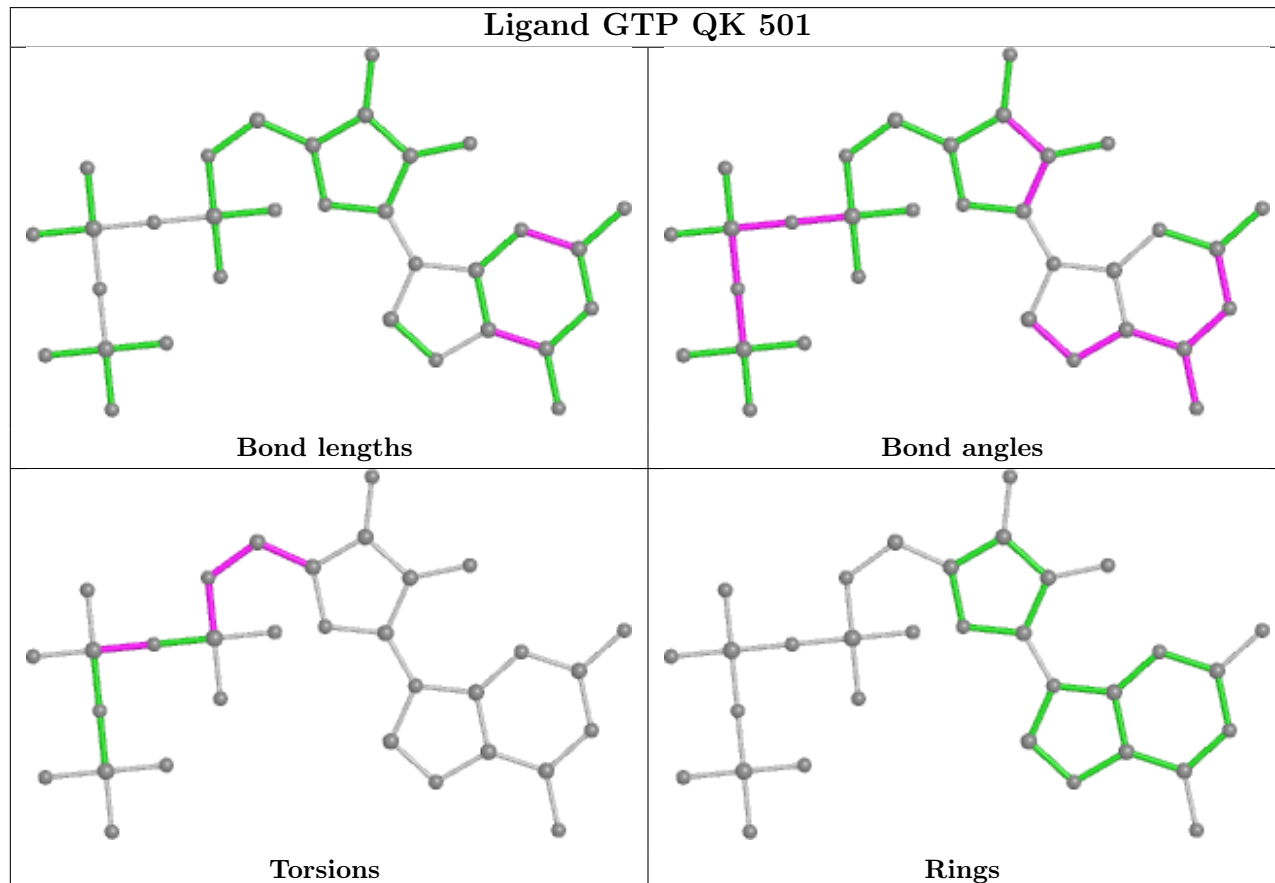
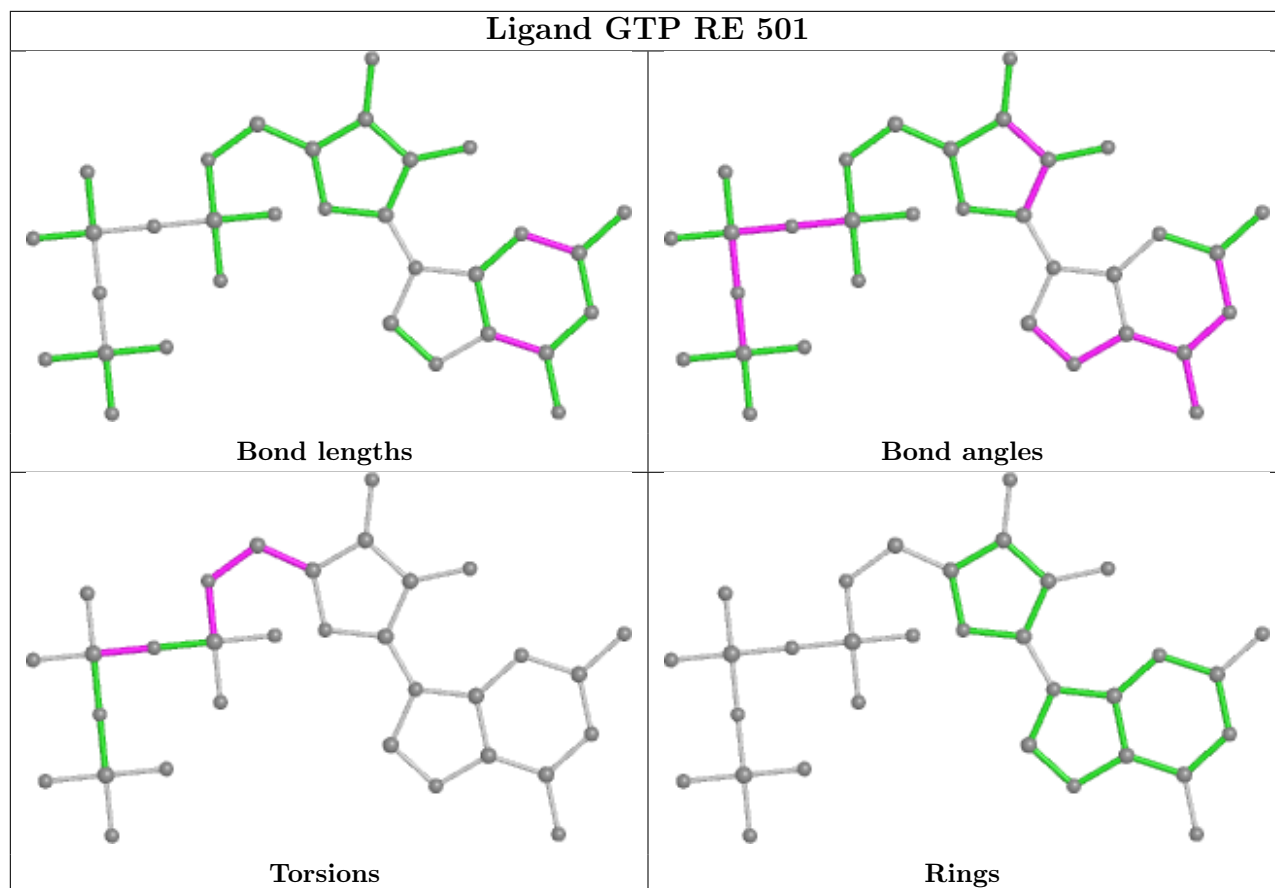


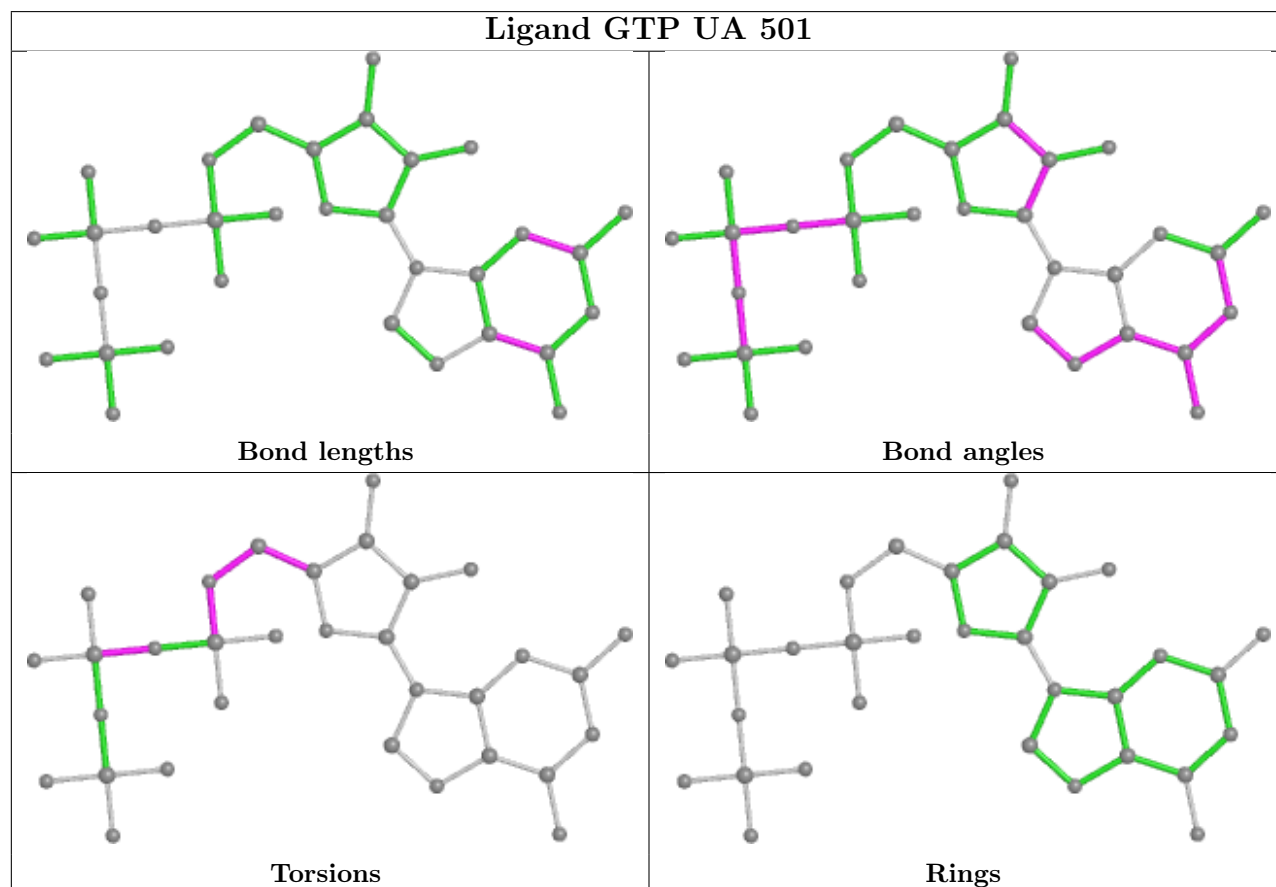
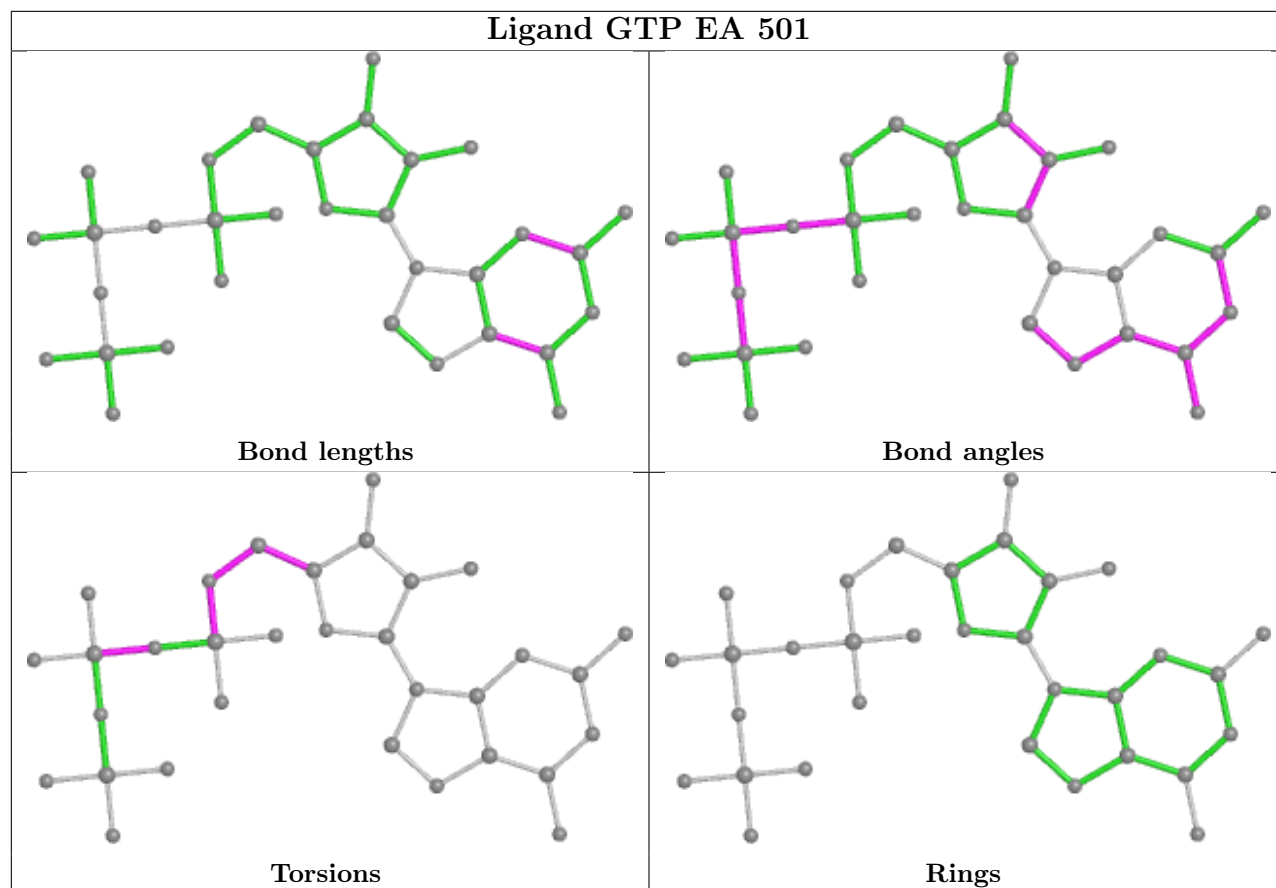


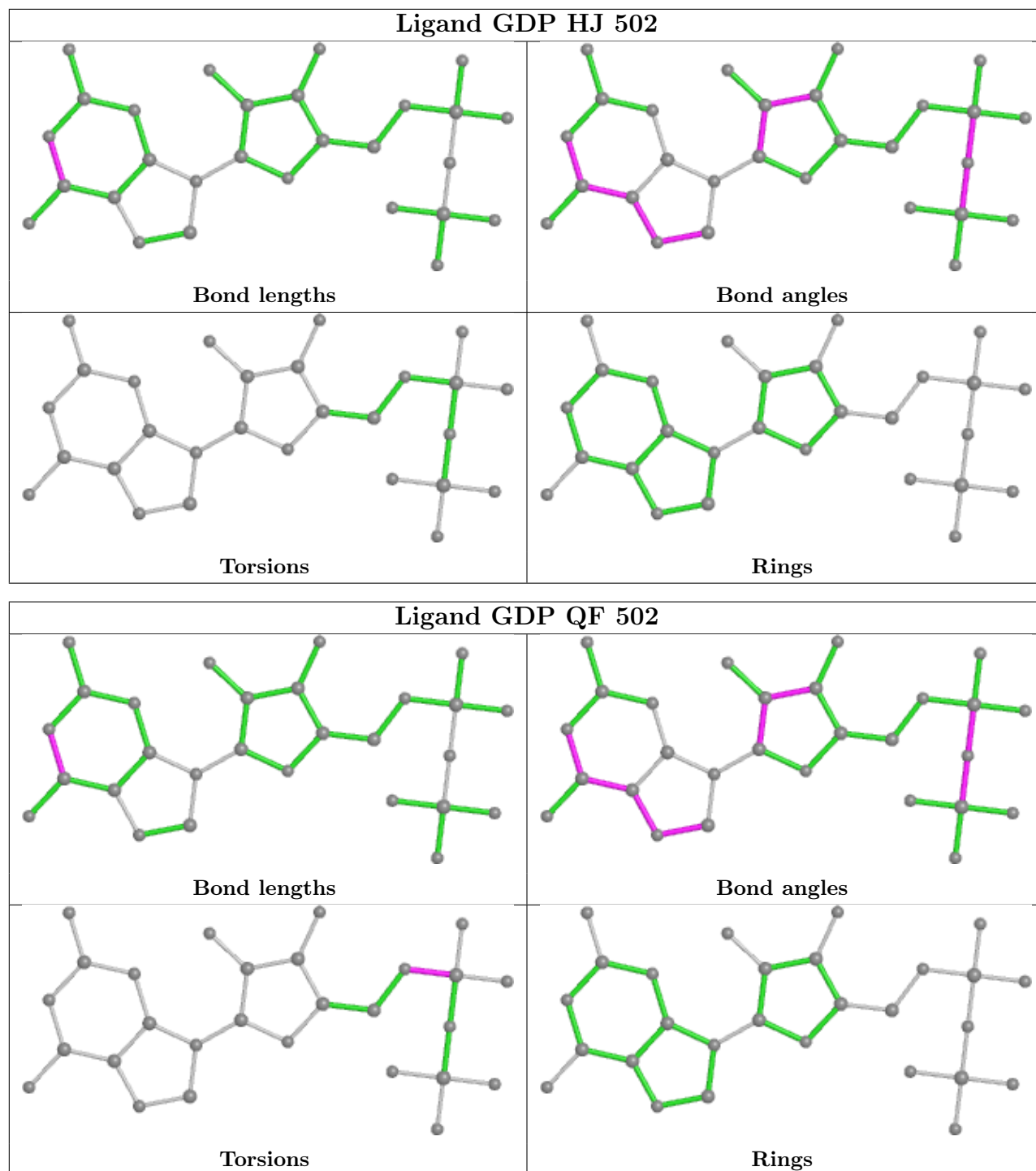


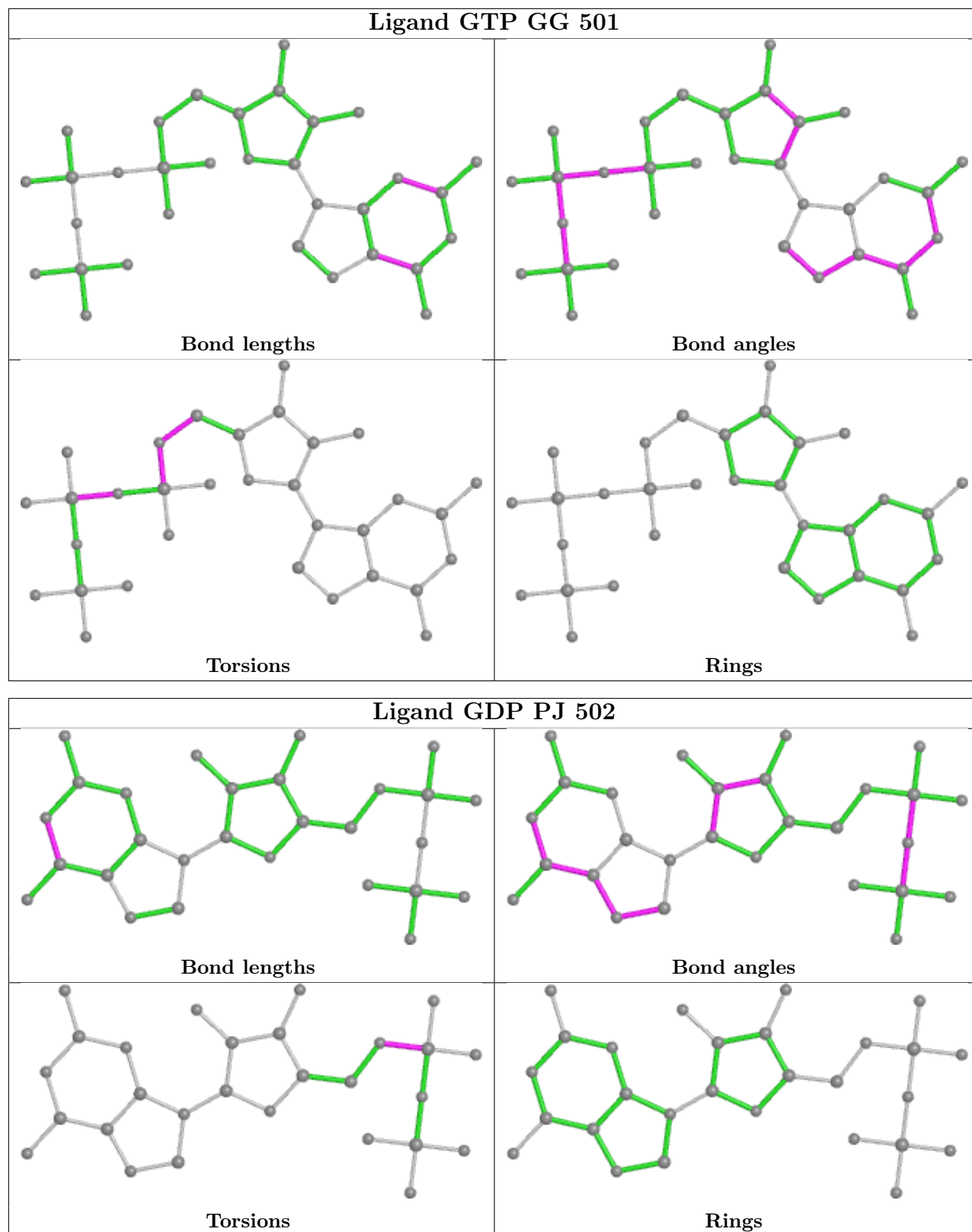


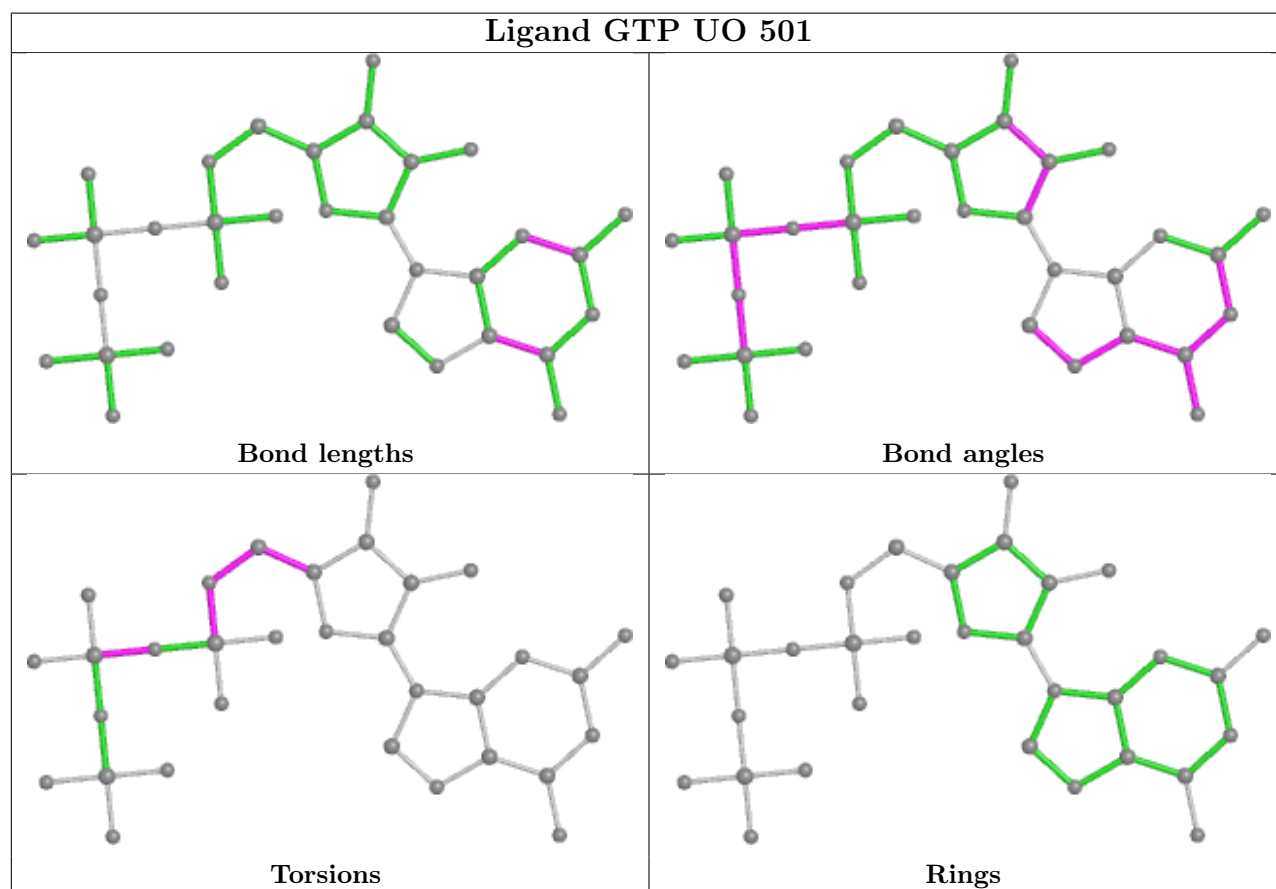
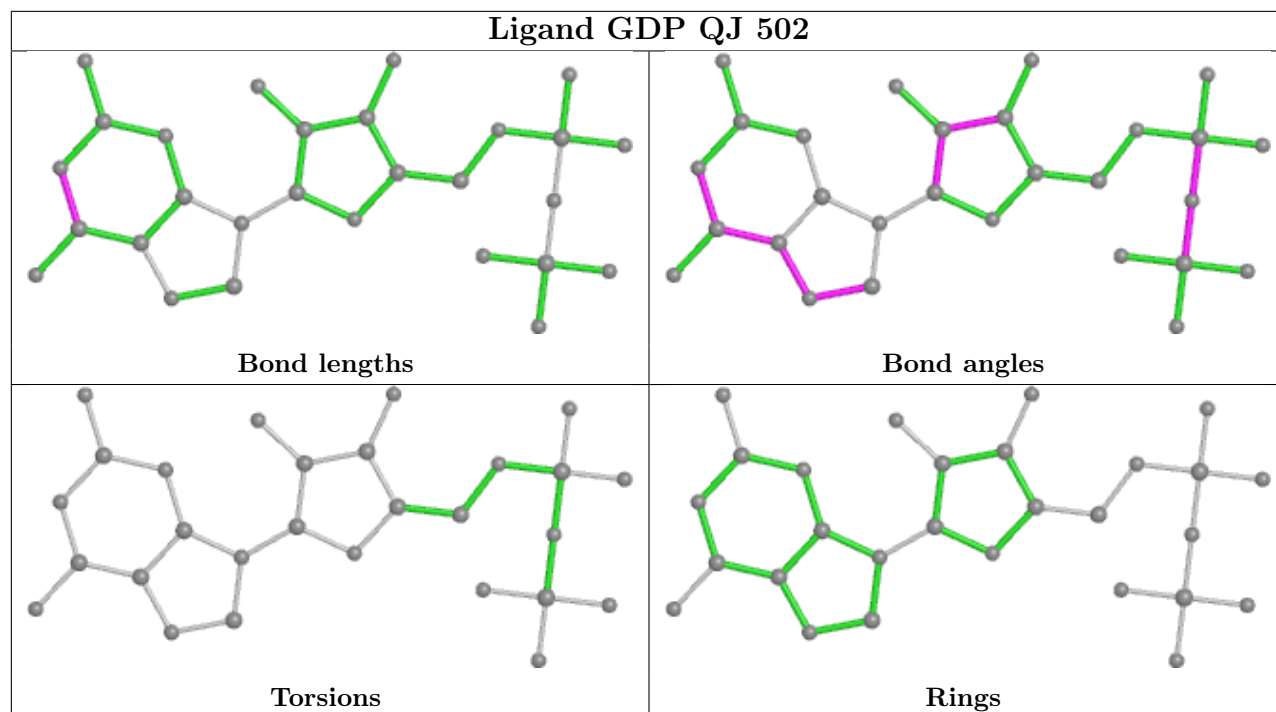


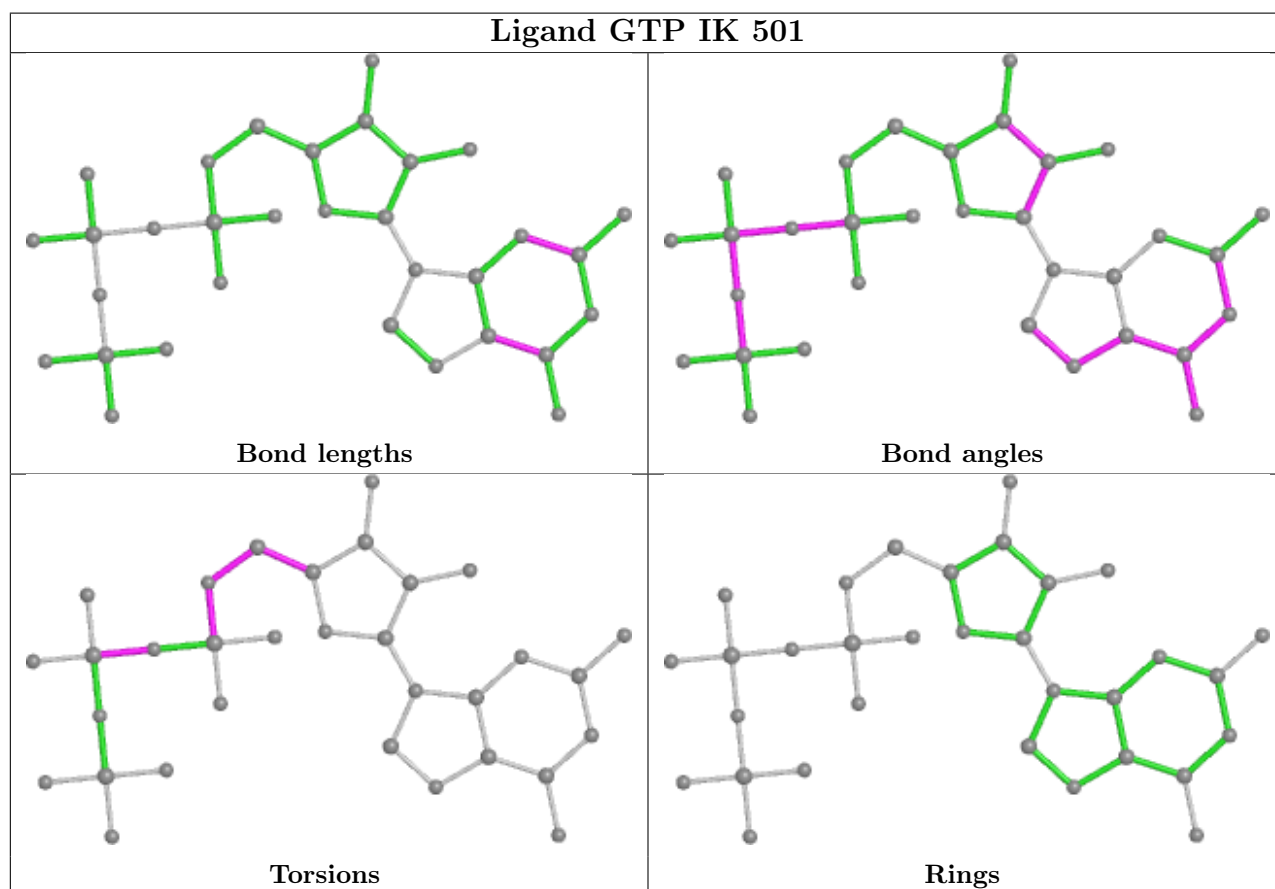
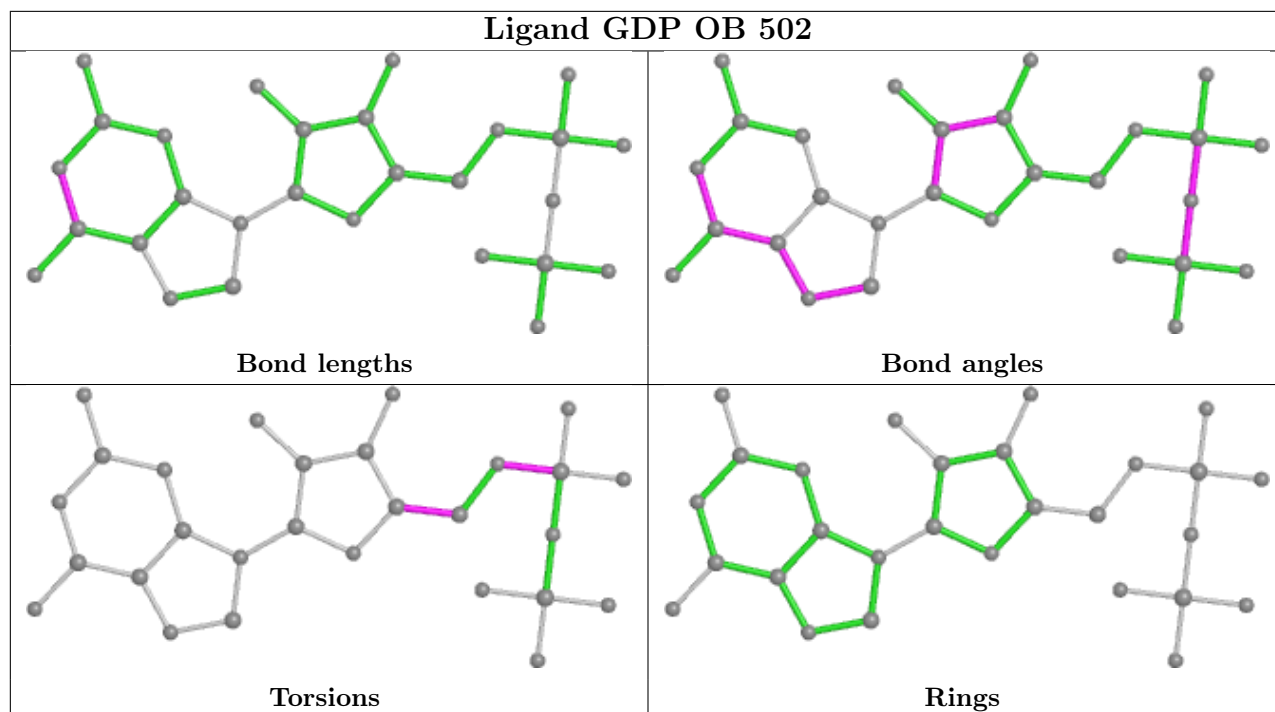


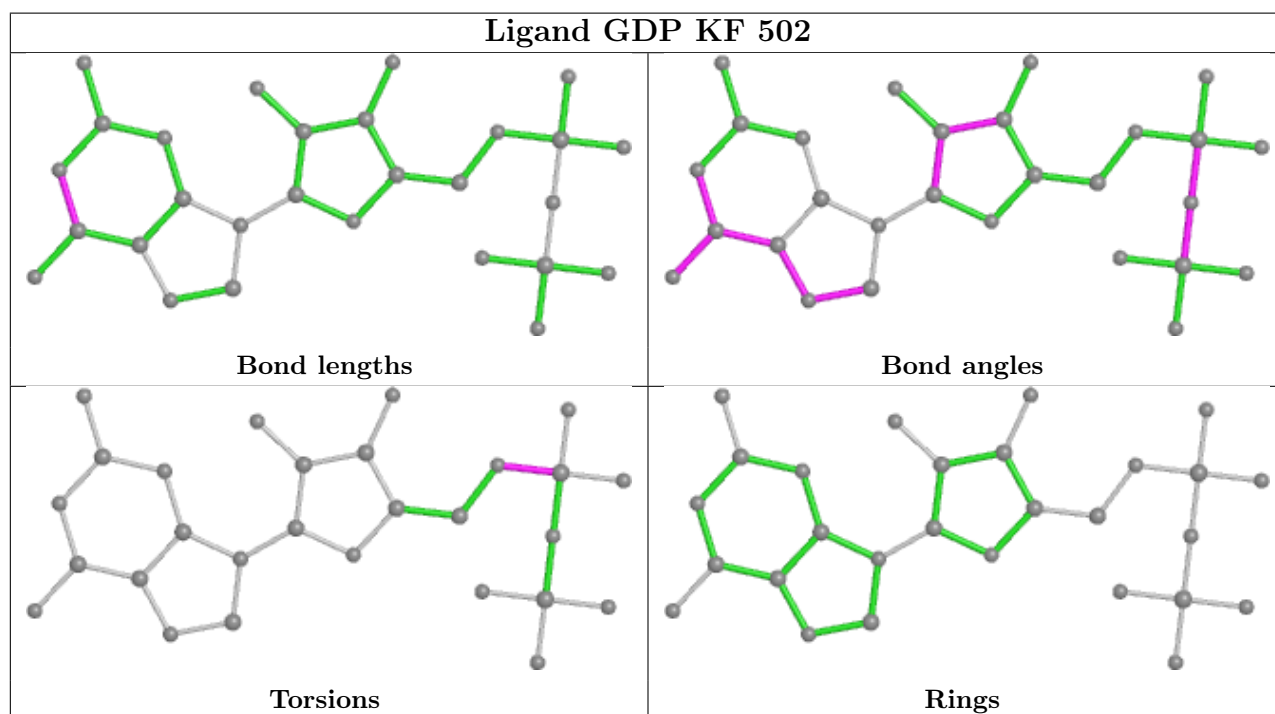
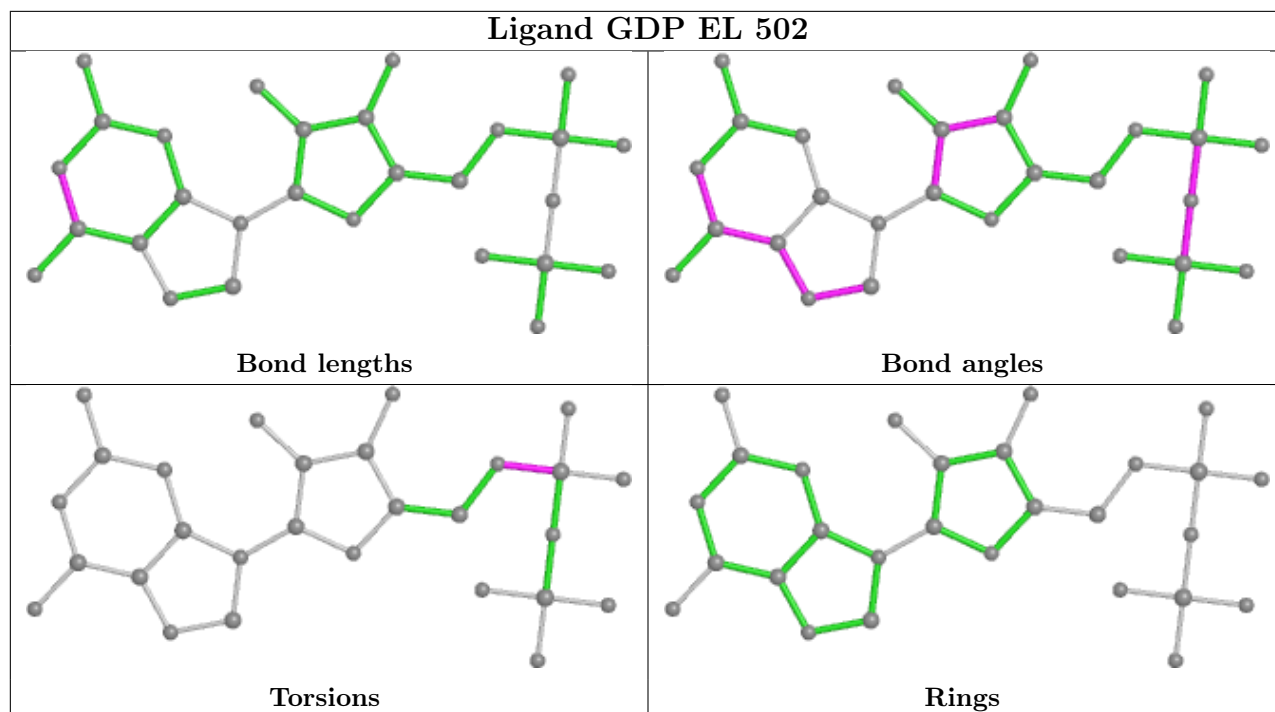


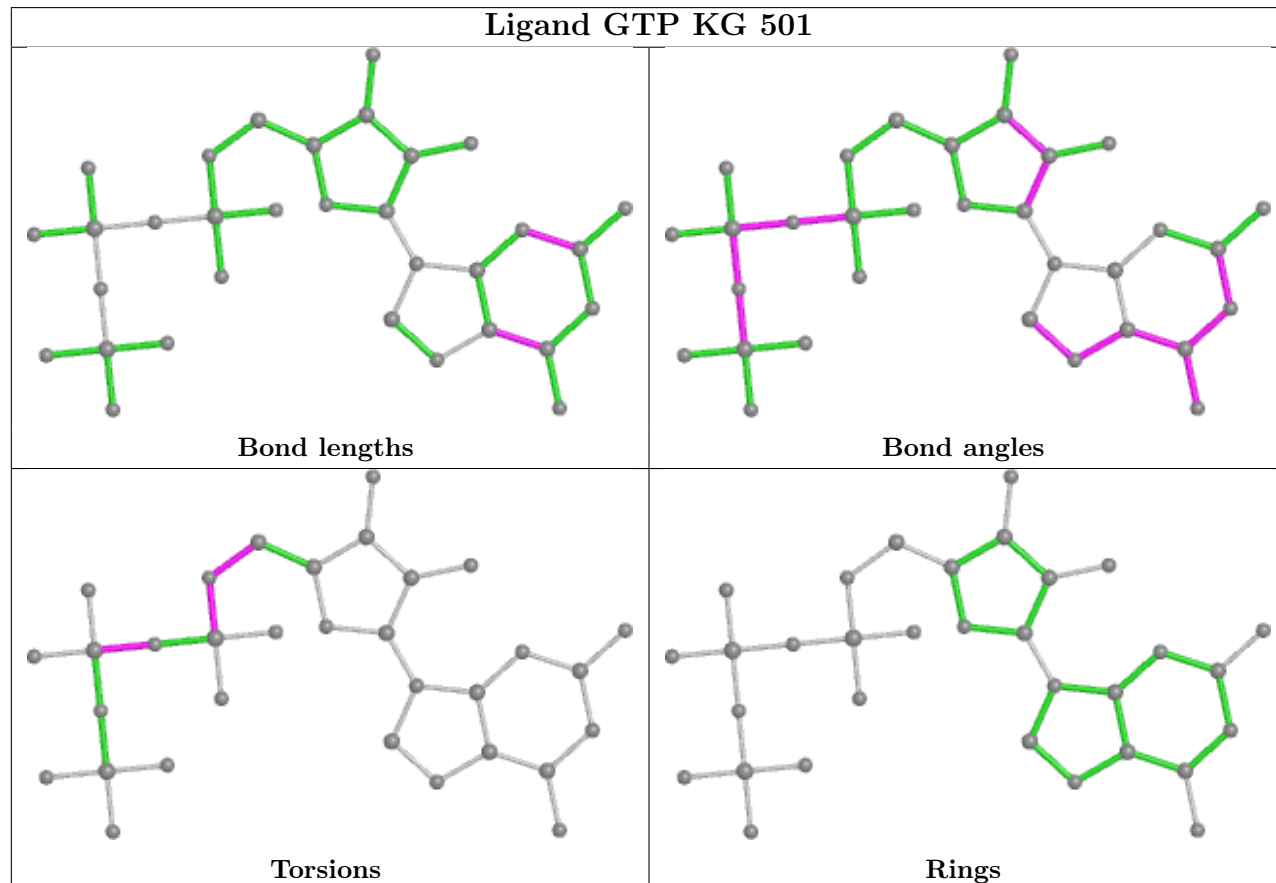
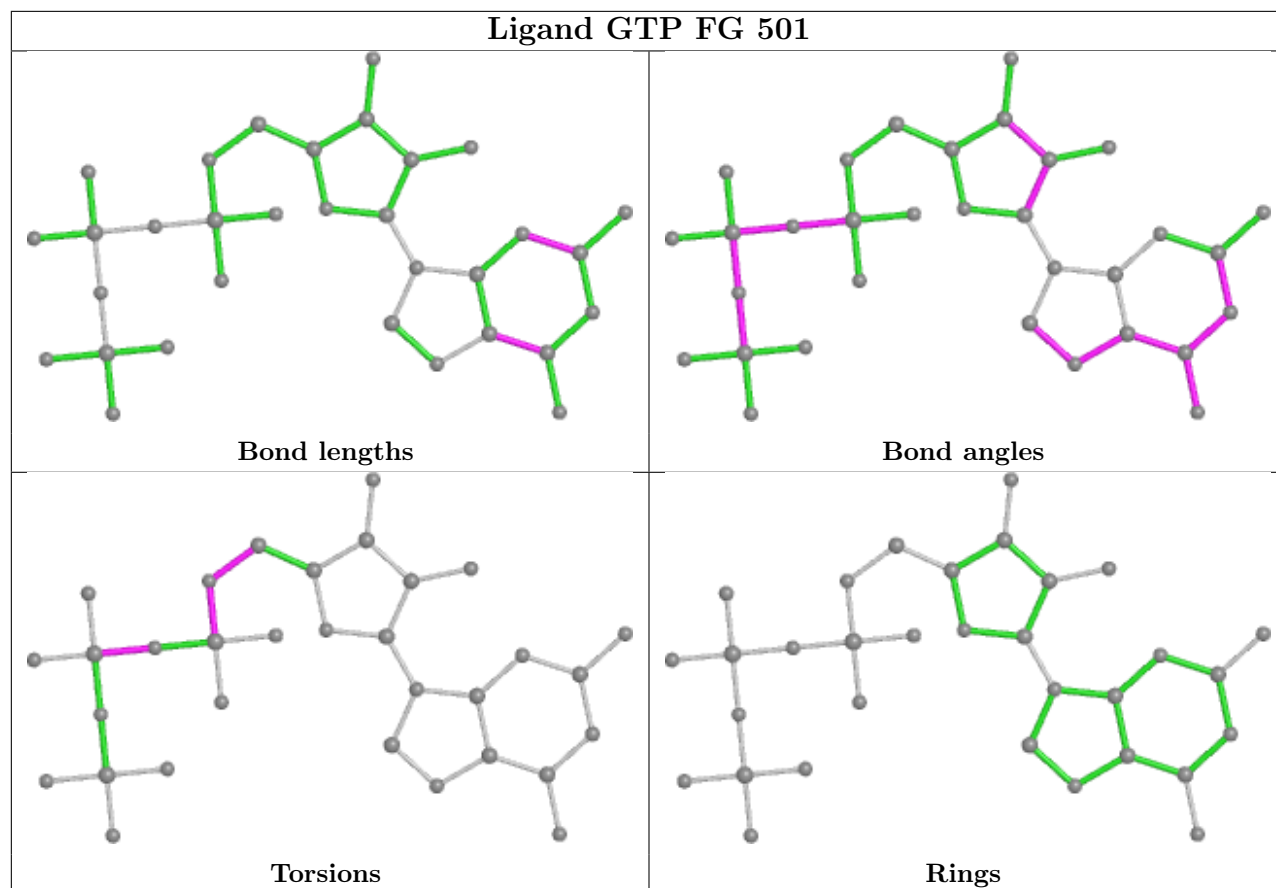


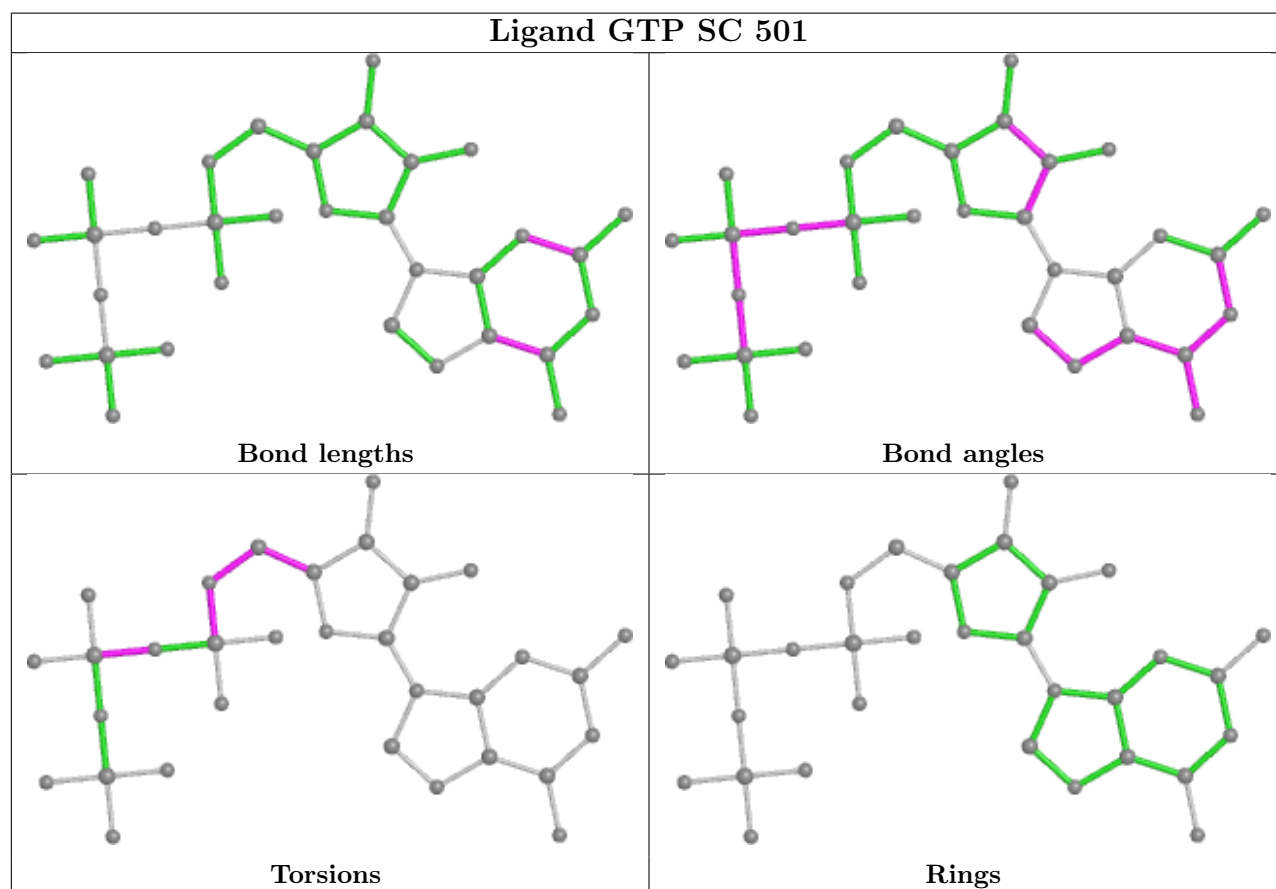
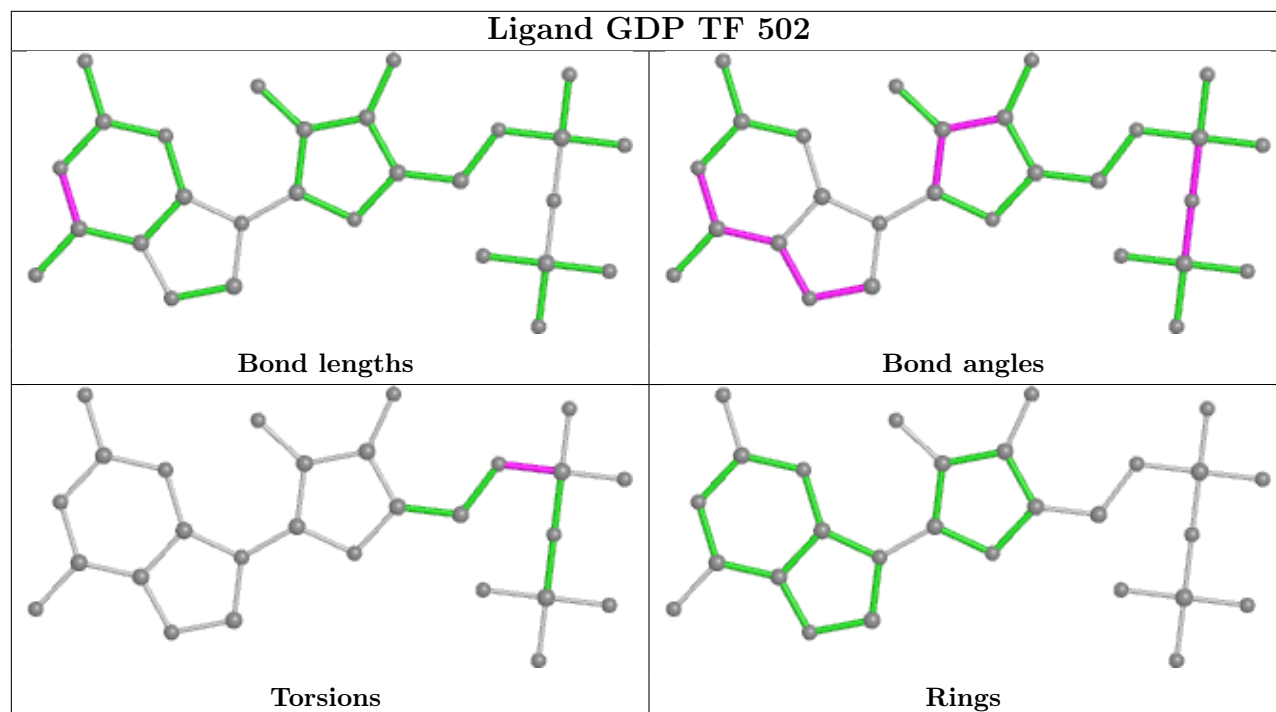


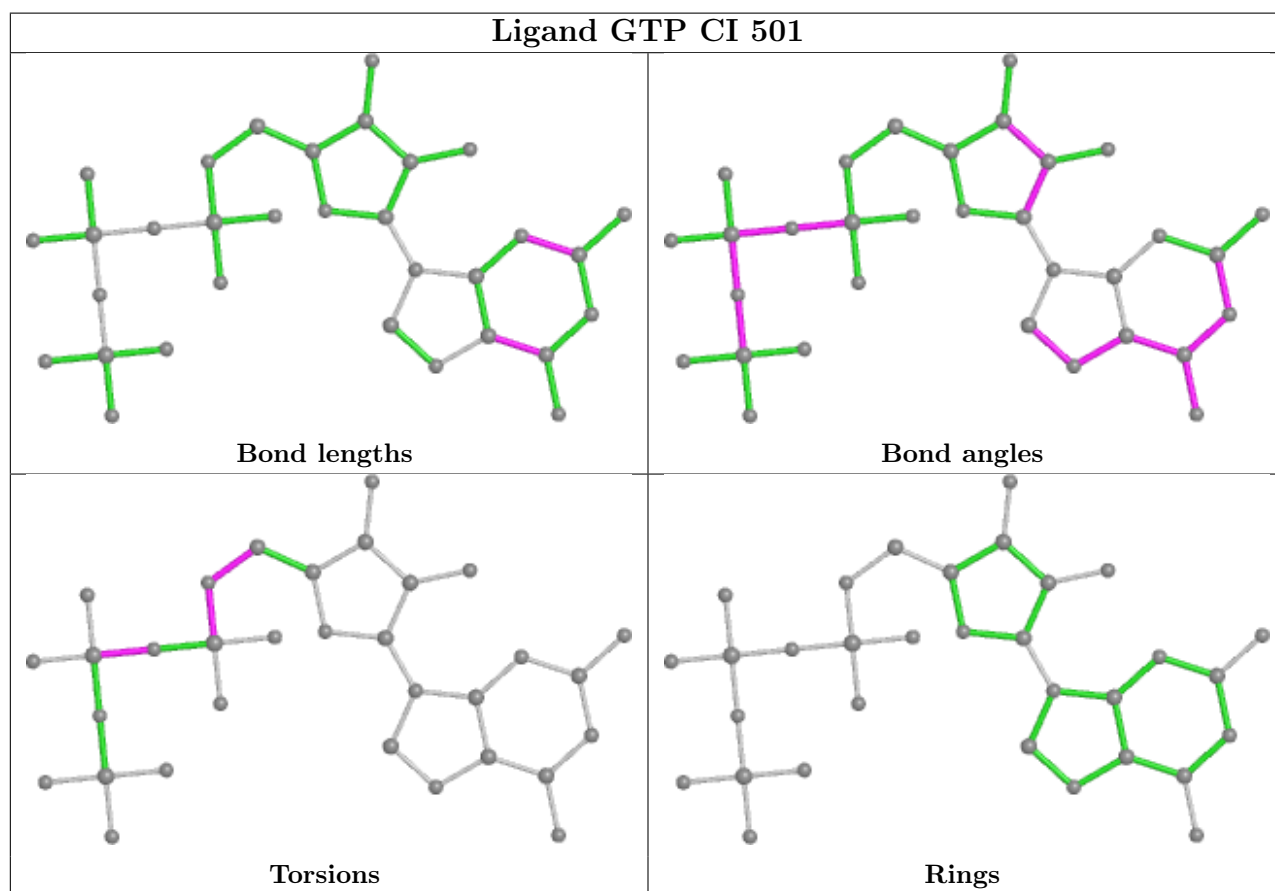
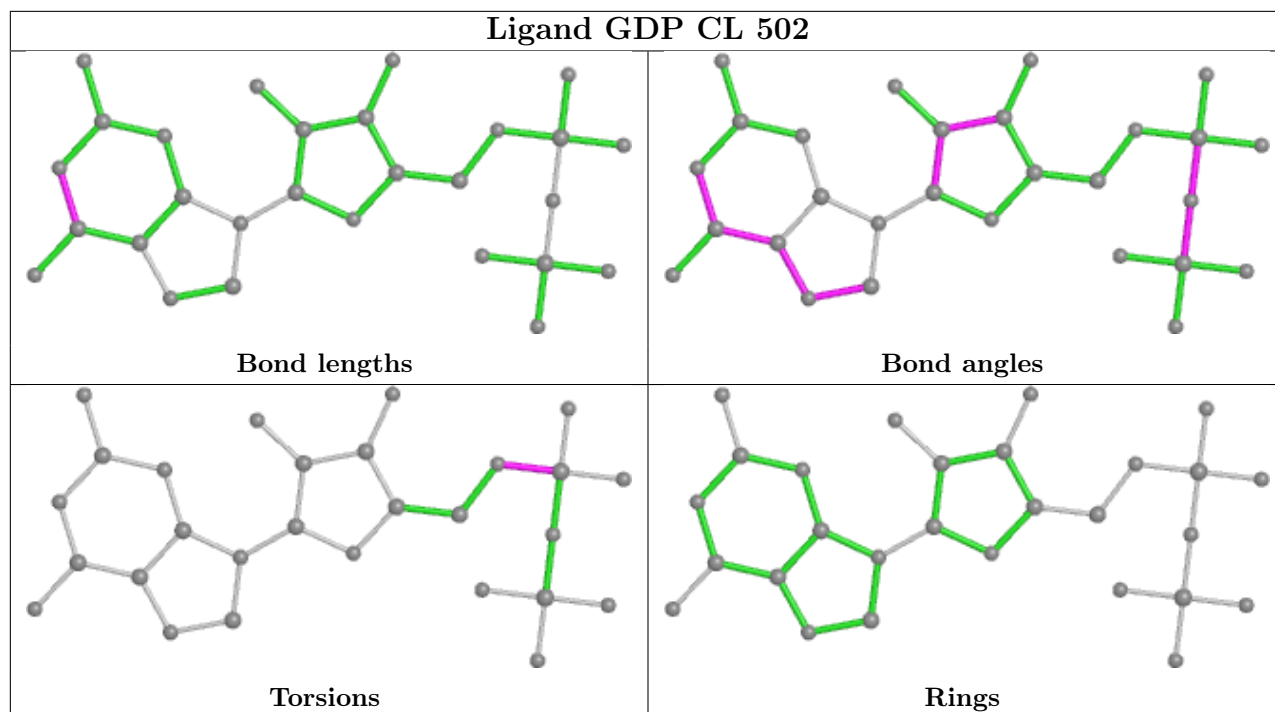


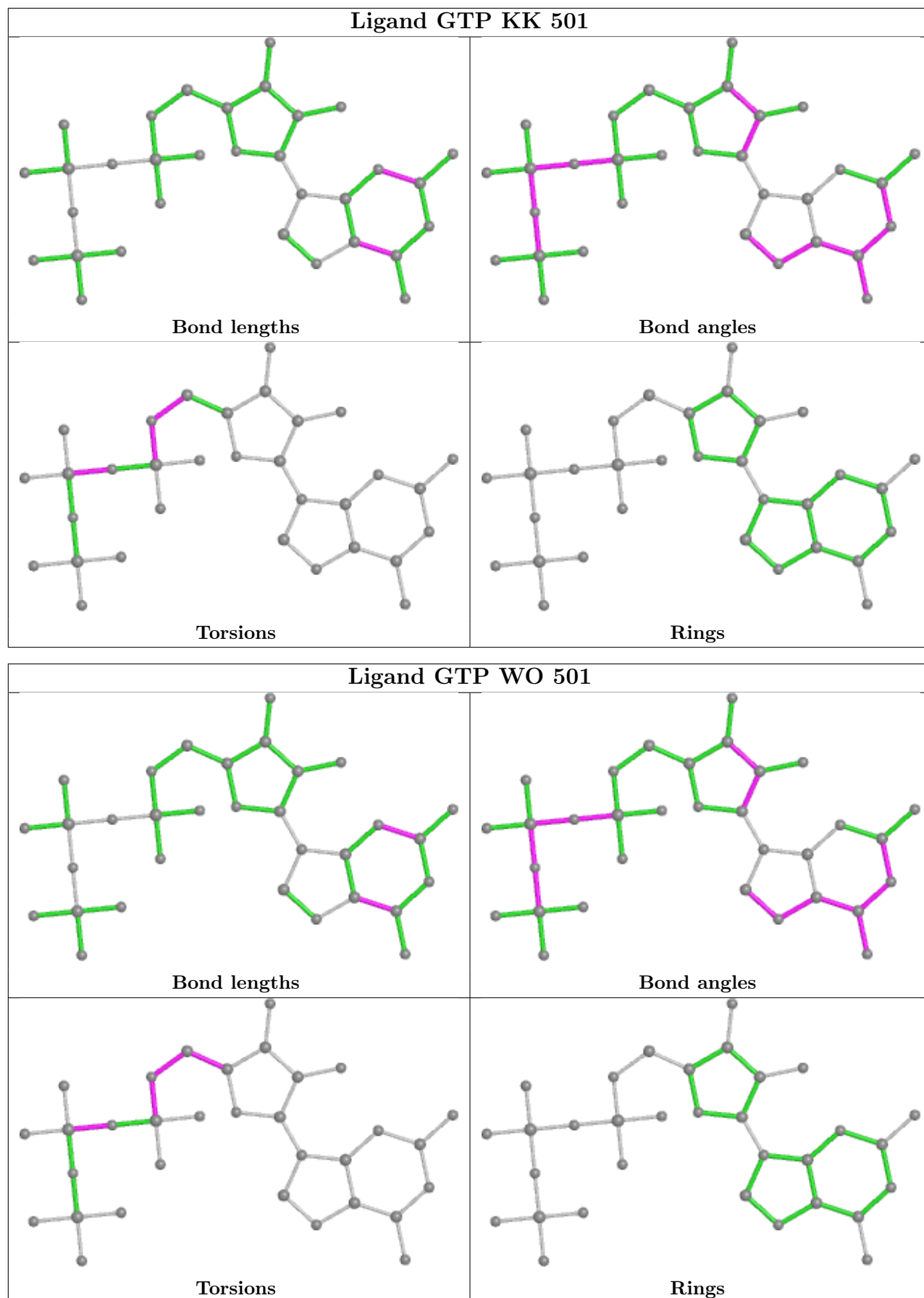


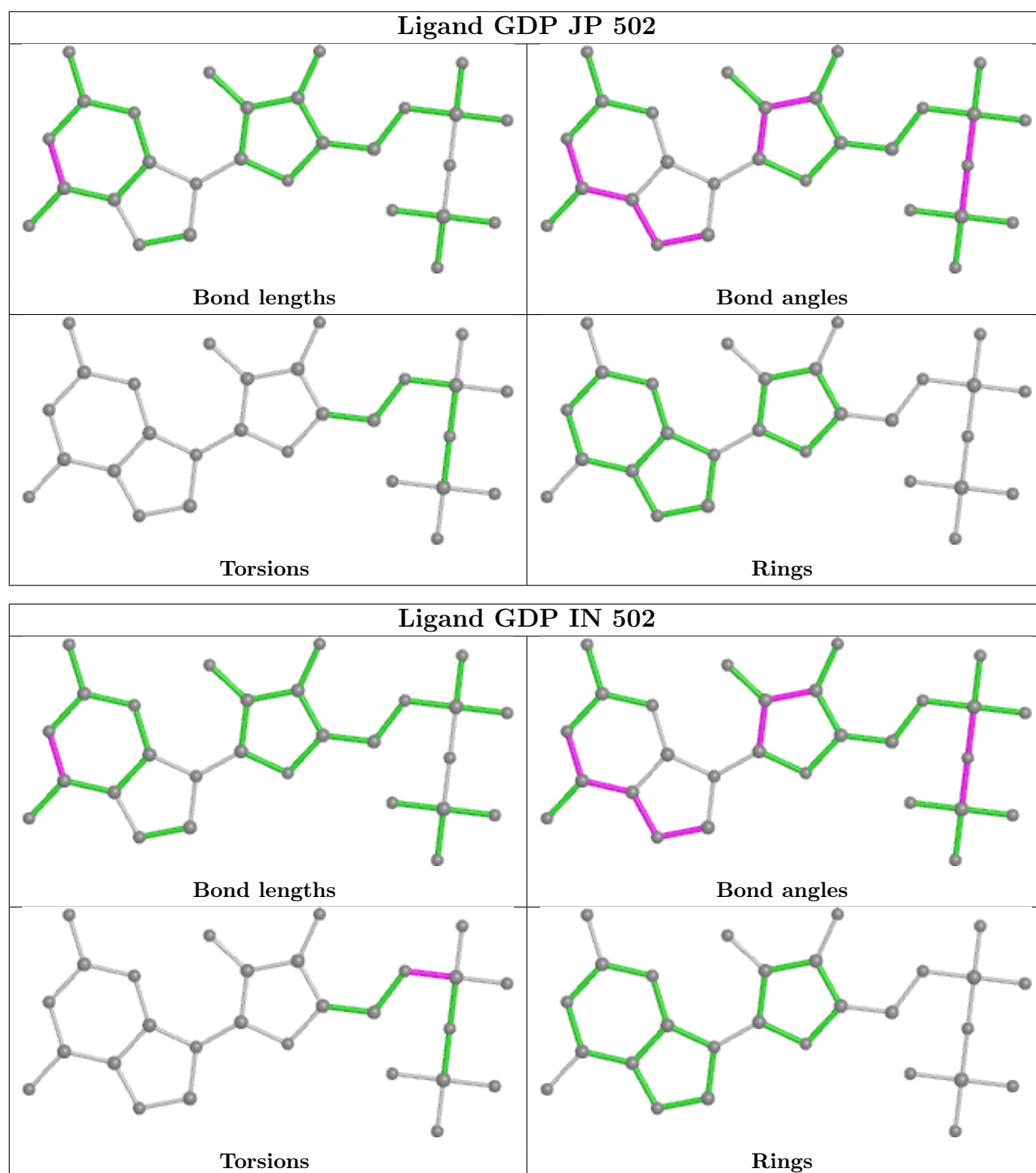












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

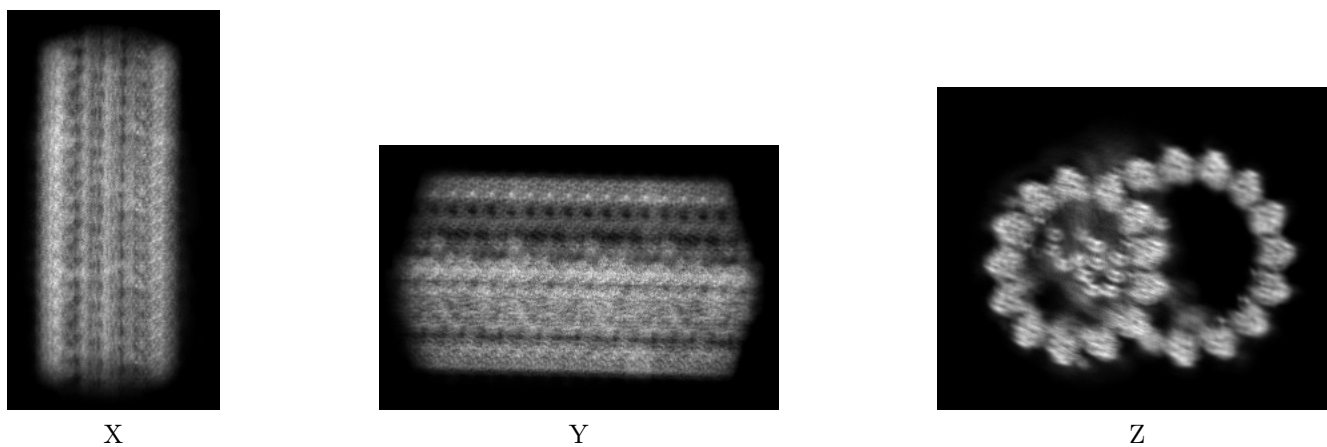
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35823. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

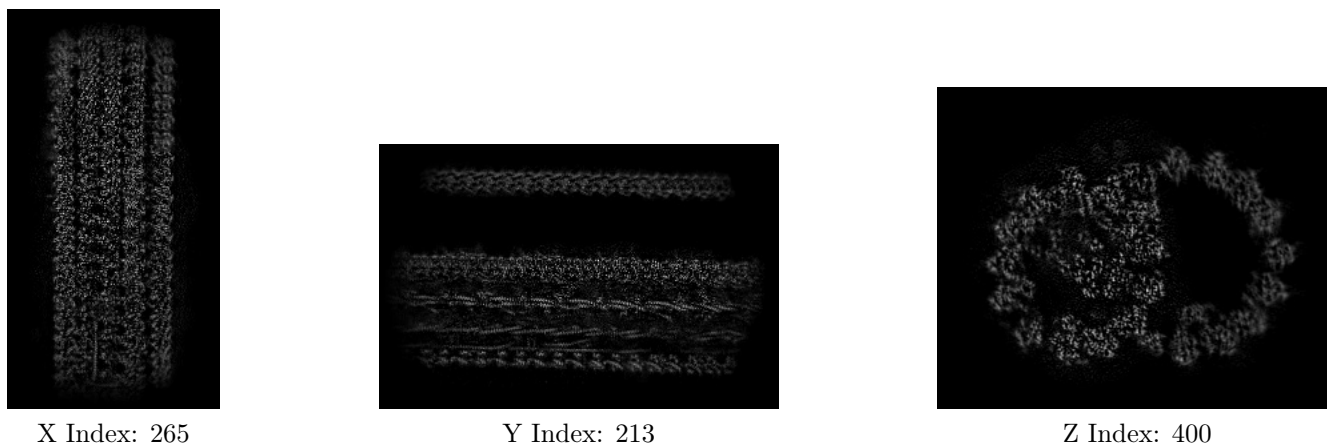
6.1.1 Primary map



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

6.2 Central slices [i](#)

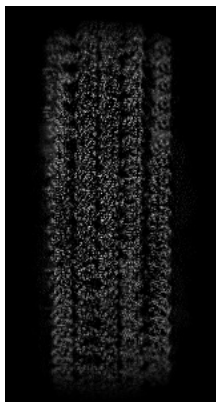
6.2.1 Primary map



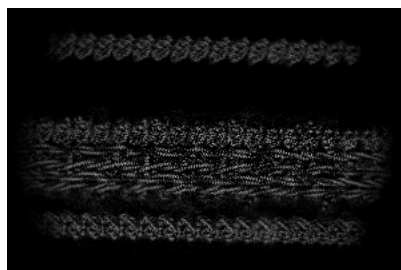
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

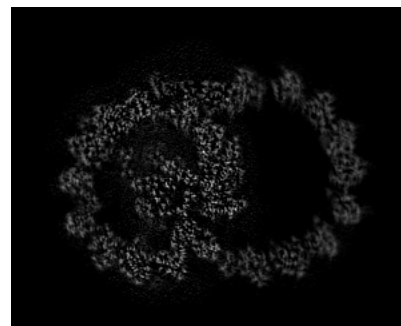
6.3.1 Primary map



X Index: 270



Y Index: 196

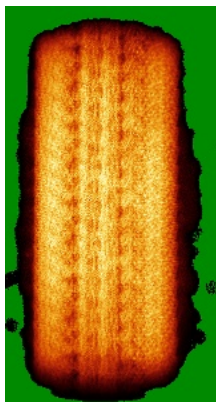


Z Index: 448

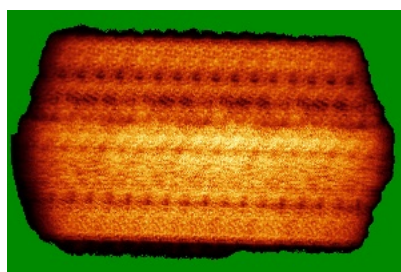
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

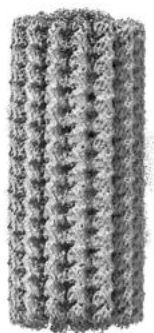


Z

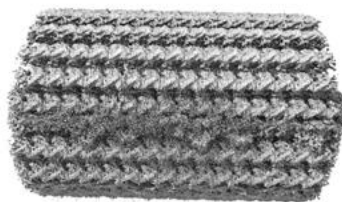
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

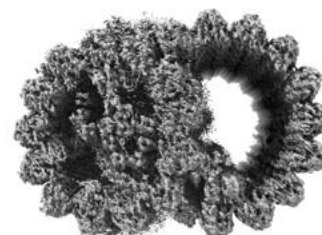
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

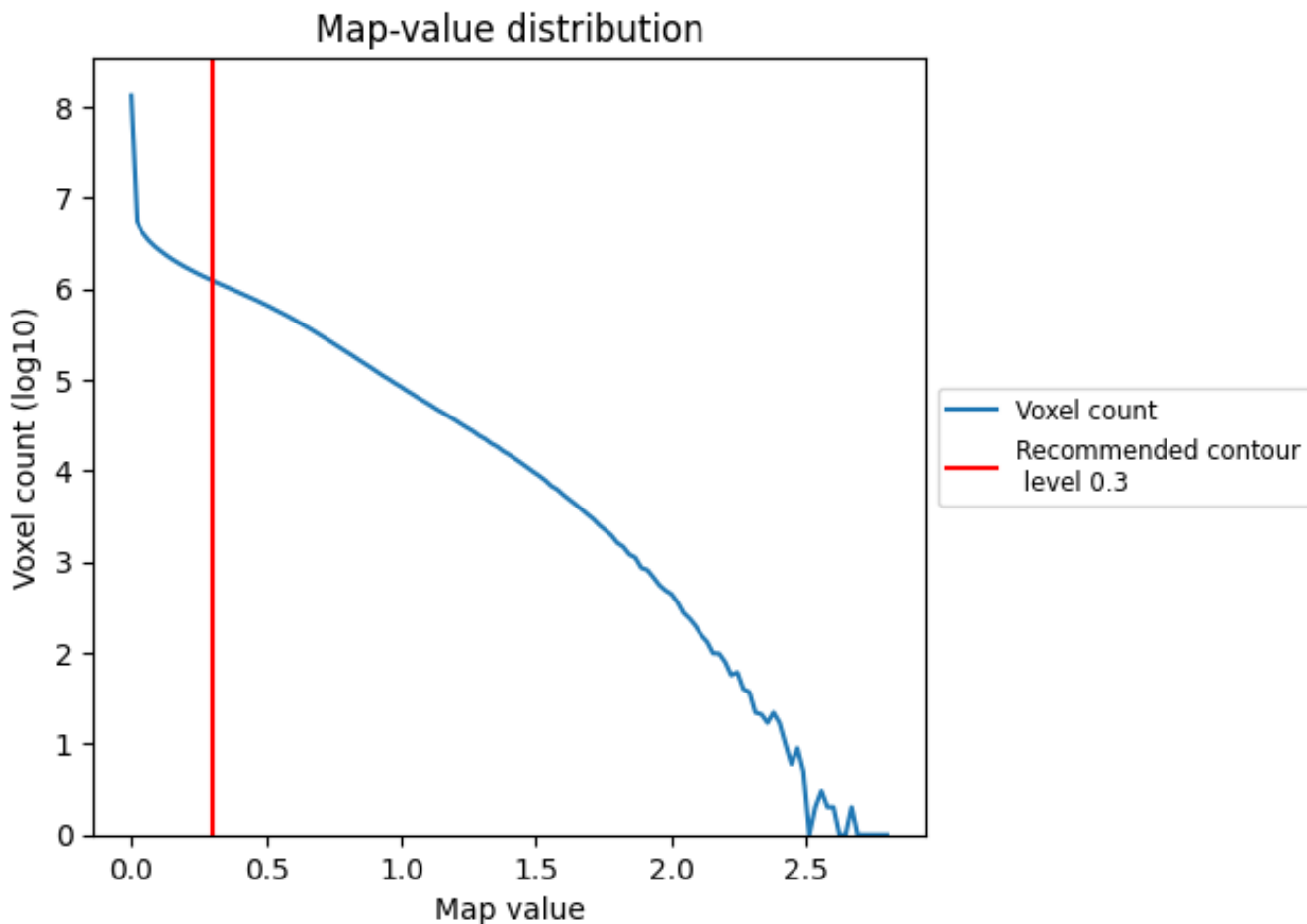
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

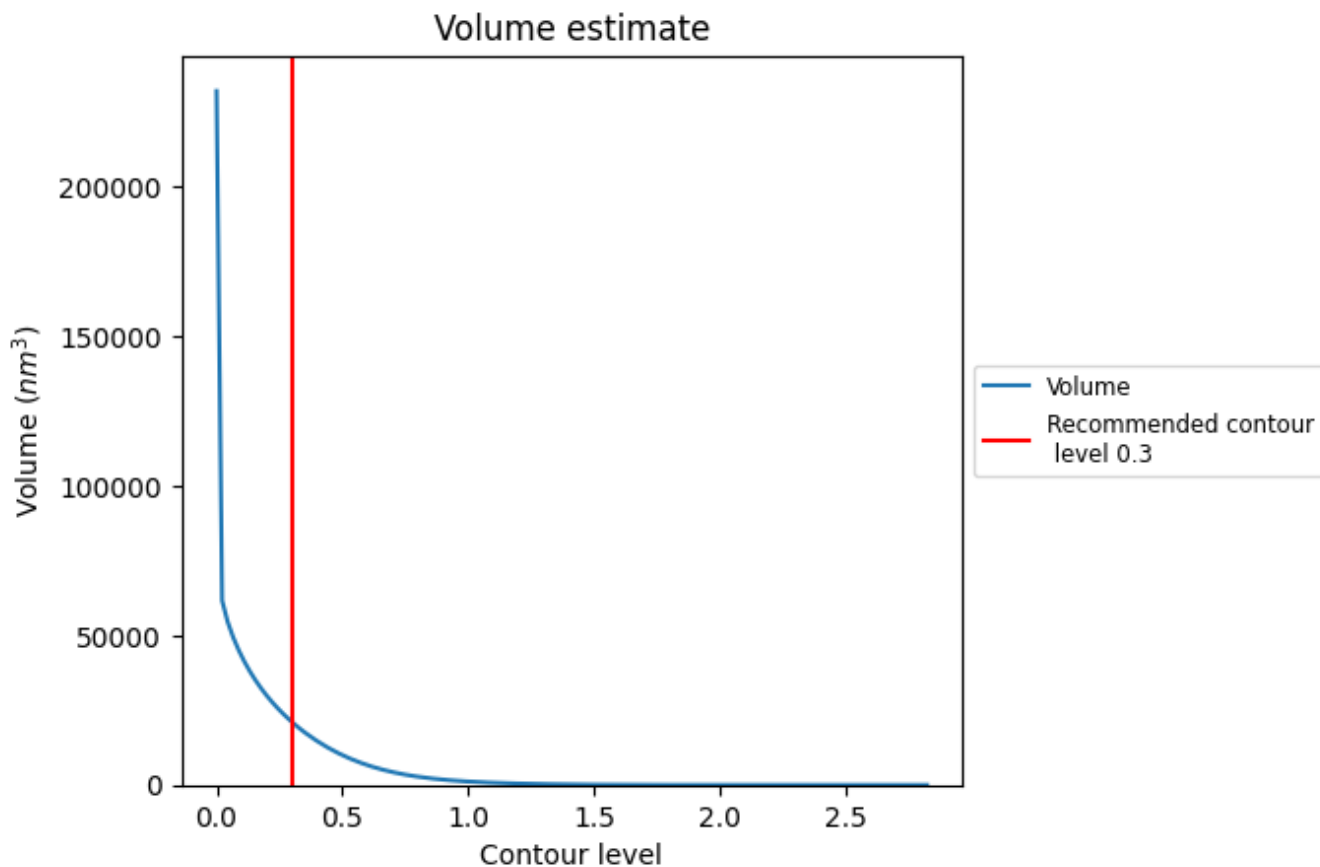
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 21016 nm³; this corresponds to an approximate mass of 18985 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

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

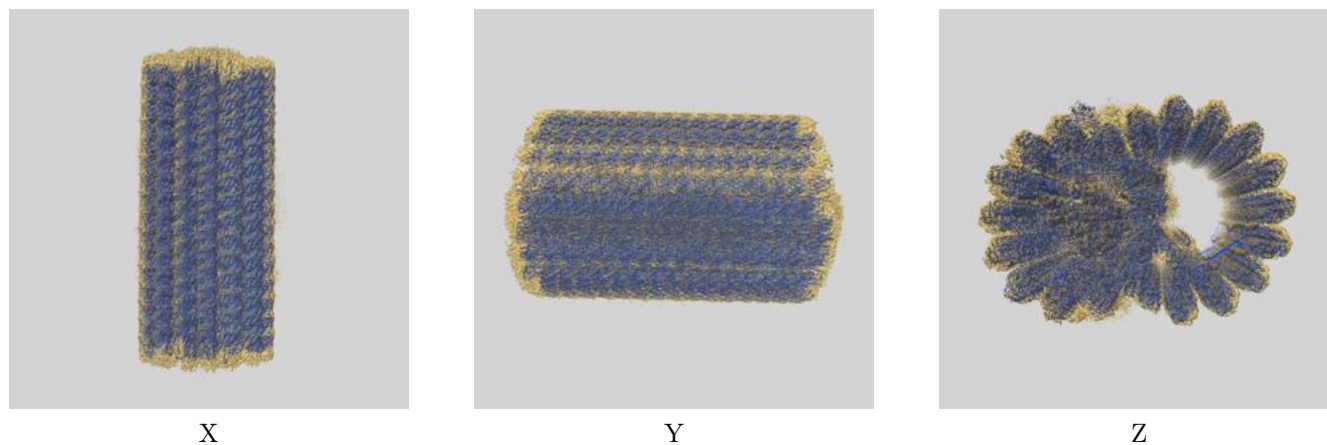
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35823 and PDB model 8IYJ. Per-residue inclusion information can be found in section 3 on page 85.

9.1 Map-model overlay [i](#)

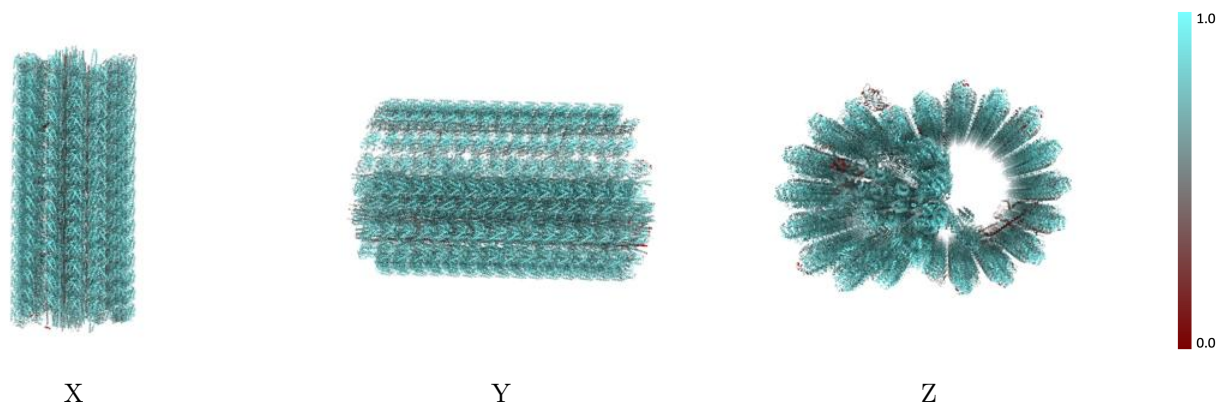


The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

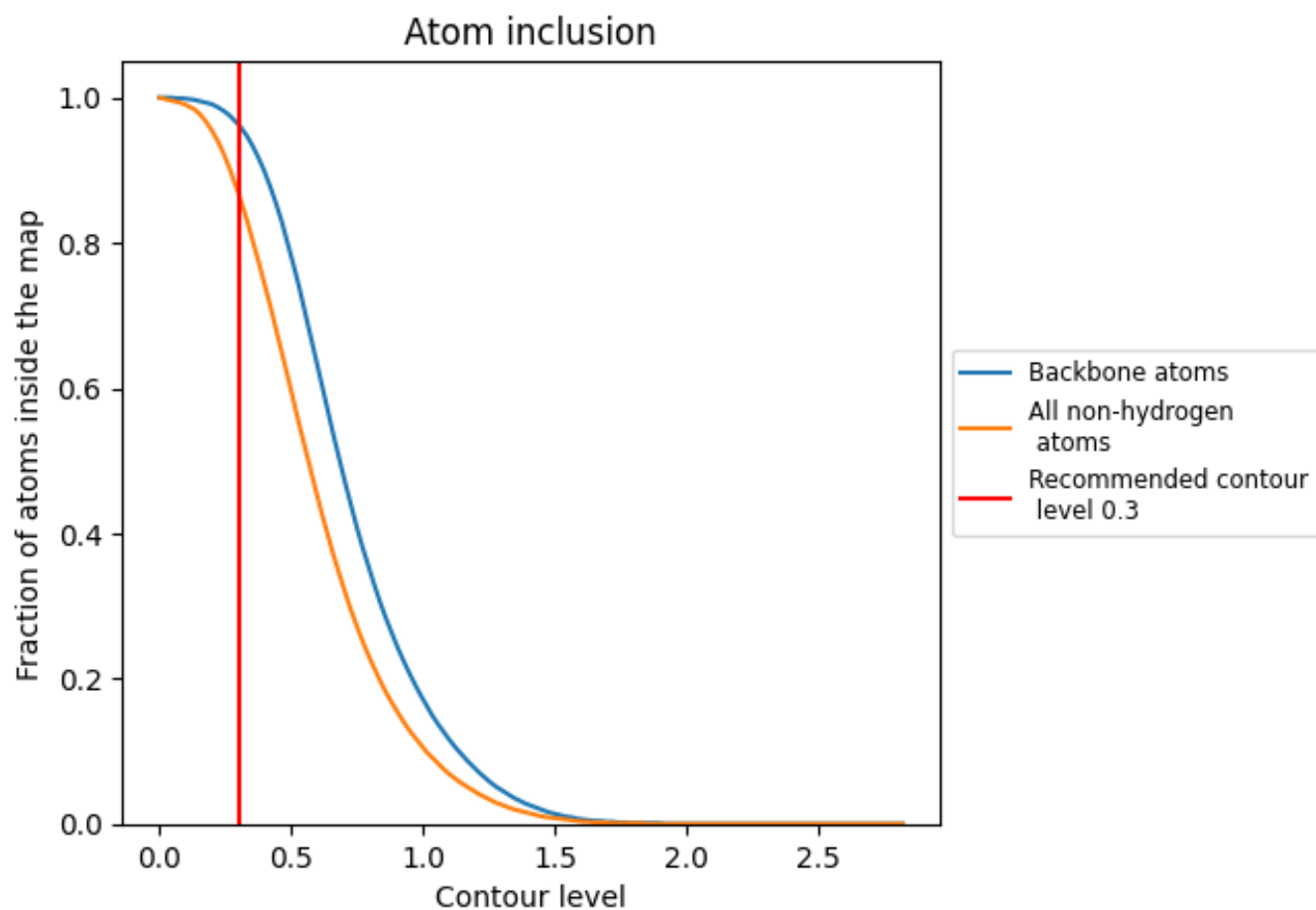
This section was not generated.

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)











































The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	0.8680
0	0.7450
1	0.8190
2	0.8610
3	0.7760
4	0.7930
5	0.8770
6	0.8500
7	0.8190
8	0.9100
A	0.7950
A0	0.8820
A1	0.8990
A2	0.9230
A3	0.9280
A4	0.9010
A5	0.8410
AA	0.8650
AB	0.9190
AC	0.9390
AD	0.9280
AE	0.9290
AF	0.9250
AG	0.9500
AH	0.9330
AI	0.9300
AJ	0.9220
AK	0.9270
AL	0.9370
AM	0.9220
AN	0.9420
AO	0.9110
AP	0.8850
B	0.7980
B0	0.8720













































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Chain	Atom inclusion
B1	 0.8860
B2	 0.9190
B3	 0.9200
B4	 0.8860
B5	 0.7900
BB	 0.9060
BC	 0.9180
BD	 0.9420
BE	 0.9140
BF	 0.9410
BG	 0.9530
BH	 0.9520
BI	 0.9580
BJ	 0.9440
BK	 0.9540
BL	 0.9250
BM	 0.9190
BN	 0.9380
BO	 0.8930
BP	 0.8510
C	 0.8290
C0	 0.8950
C1	 0.9270
C2	 0.9450
C3	 0.9300
C4	 0.8790
C5	 0.8230
C6	 0.6400
CB	 0.8430
CC	 0.8710
CD	 0.9060
CE	 0.9270
CF	 0.9470
CG	 0.9510
CH	 0.9550
CI	 0.9490
CJ	 0.9520
CK	 0.9480
CL	 0.9360
CM	 0.9200
CN	 0.9170
CO	 0.8580

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Chain	Atom inclusion
CP	 0.8390
CQ	 0.7210
D	 0.7960
D0	 0.8360
D1	 0.8890
D2	 0.9110
D3	 0.9250
D4	 0.8580
D5	 0.8620
DB	 0.7410
DC	 0.8540
DD	 0.8990
DE	 0.9230
DF	 0.9730
DG	 0.9570
DH	 0.9490
DI	 0.9320
DJ	 0.9520
DK	 0.9470
DL	 0.9430
DM	 0.9360
DN	 0.9080
DO	 0.8770
DP	 0.8510
DQ	 0.7420
E	 0.9300
EA	 0.8070
EB	 0.8810
EC	 0.8840
ED	 0.9430
EE	 0.9300
EF	 0.9240
EG	 0.9340
EH	 0.9360
EI	 0.9290
EJ	 0.9370
EK	 0.9320
EL	 0.8850
EM	 0.8300
EN	 0.8540
EO	 0.7560
F	 0.6990











































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Chain	Atom inclusion
FA	0.8130
FB	0.8760
FC	0.9030
FD	0.9410
FE	0.9640
FF	0.9340
FG	0.9060
FH	0.9120
FI	0.9100
FJ	0.9110
FK	0.9180
FL	0.9250
FM	0.8840
FN	0.8930
FO	0.8540
G	0.7720
GA	0.7870
GB	0.8800
GC	0.8600
GD	0.8880
GE	0.9080
GF	0.9190
GG	0.9200
GH	0.9210
GI	0.9000
GJ	0.9360
GK	0.9310
GL	0.9270
GM	0.9090
GN	0.9080
GO	0.8720
H	0.8750
HA	0.7880
HB	0.8590
HC	0.8520
HD	0.8810
HE	0.8950
HF	0.9350
HG	0.9200
HH	0.9480
HI	0.9340
HJ	0.9090











































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Chain	Atom inclusion
HK	 0.9160
HL	 0.9090
HM	 0.8930
HN	 0.9100
HO	 0.8800
HP	 0.8350
I	 0.9050
I1	 0.8500
IA	 0.8200
IB	 0.8380
IC	 0.8470
ID	 0.8650
IE	 0.9100
IF	 0.9220
IG	 0.9010
IH	 0.9140
II	 0.9190
IJ	 0.9420
IK	 0.9110
IL	 0.9140
IM	 0.8890
IN	 0.8950
IO	 0.8930
IP	 0.8520
J	 0.9580
J1	 0.8120
J2	 0.7990
J3	 0.8590
J4	 0.8080
J5	 0.6680
JB	 0.8110
JC	 0.8560
JD	 0.8700
JE	 0.8660
JF	 0.9030
JG	 0.9050
JH	 0.9150
JI	 0.9140
JJ	 0.9220
JK	 0.9310
JL	 0.9040
JM	 0.8920

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Chain	Atom inclusion
JN	 0.8860
JO	 0.8880
JP	 0.8710
JQ	 0.8460
K	 0.9290
K1	 0.3040
K2	 0.1240
K3	 0.7560
KA	 0.8940
KB	 0.8960
KC	 0.9030
KD	 0.9150
KE	 0.9210
KF	 0.9410
KG	 0.9510
KH	 0.9490
KI	 0.9080
KJ	 0.9020
KK	 0.9360
KL	 0.9320
KM	 0.8980
KN	 0.8820
KO	 0.8700
KP	 0.7800
L	 0.9540
L1	 0.3750
LA	 0.9200
LB	 0.9230
LC	 0.9320
LD	 0.9330
LE	 0.9270
LF	 0.9340
LG	 0.9460
LH	 0.9350
LI	 0.9270
LJ	 0.9330
LK	 0.9250
LL	 0.9440
LM	 0.9150
LN	 0.8880
LO	 0.8720
LP	 0.8770











































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Chain	Atom inclusion
M	0.9390
M1	0.8740
M2	0.9280
M3	0.8930
M4	0.9420
MA	0.9250
MB	0.9250
MC	0.9190
MD	0.9270
ME	0.9160
MF	0.9310
MG	0.9410
MH	0.9430
MI	0.9290
MJ	0.9340
MK	0.9110
ML	0.9270
MM	0.9220
MN	0.9100
MO	0.8830
MP	0.8770
N	0.8580
N1	0.7580
N2	0.8480
NA	0.8040
NB	0.8590
NC	0.8320
ND	0.8590
NE	0.8990
NF	0.8930
NG	0.8770
NH	0.8800
NI	0.8820
NJ	0.8630
NK	0.8590
NL	0.8630
NM	0.8370
NN	0.8550
NO	0.8520
NP	0.8130
O	0.8340
O1	0.8260

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Chain	Atom inclusion
O2	 0.8570
O3	 0.8790
O4	 0.8290
O5	 0.8840
O6	 0.8270
O7	 0.7630
O8	 0.8410
O9	 0.8720
OA	 0.6500
OB	 0.7760
OC	 0.7920
OD	 0.8330
OE	 0.8370
OF	 0.8870
OG	 0.8930
OH	 0.9030
OI	 0.8780
OJ	 0.8710
OK	 0.8730
OL	 0.8920
OM	 0.8590
ON	 0.8320
OO	 0.8050
OP	 0.7350
P	 0.8590
P1	 0.7340
P2	 0.8260
P3	 0.7070
P4	 0.8340
P5	 0.8210
P6	 0.8680
P7	 0.6220
P8	 0.8710
P9	 0.8010
PB	 0.8240
PC	 0.8430
PD	 0.8690
PE	 0.8960
PF	 0.8830
PG	 0.8680
PH	 0.8840
PI	 0.8800











































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Chain	Atom inclusion
PJ	0.8850
PK	0.8730
PL	0.9120
PM	0.8850
PN	0.8880
PO	0.8520
PP	0.7940
Q	0.7590
Q1	0.8530
Q2	0.8780
Q3	0.8610
Q4	0.8150
Q5	0.7470
QB	0.6730
QC	0.7690
QD	0.8170
QE	0.8750
QF	0.8640
QG	0.8360
QH	0.8650
QI	0.8470
QJ	0.8660
QK	0.8590
QL	0.8810
QM	0.8380
QN	0.8140
QO	0.7980
QP	0.6950
R	0.8810
R0	0.8700
R1	0.9040
R2	0.9220
R3	0.9260
R4	0.8520
R5	0.8110
RC	0.8530
RD	0.8990
RE	0.9030
RF	0.9070
RG	0.8840
RH	0.9070
RI	0.8940

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Chain	Atom inclusion
RJ	 0.9150
RK	 0.9030
RL	 0.9190
RM	 0.8990
RN	 0.9000
RO	 0.8680
RP	 0.7710
S	 0.8470
S0	 0.8060
S1	 0.9270
S2	 0.9350
S3	 0.9250
S4	 0.8740
S5	 0.8590
S6	 0.9190
S7	 0.9020
S8	 0.9220
S9	 0.8440
SA	 0.7240
SB	 0.8390
SC	 0.8500
SD	 0.9010
SE	 0.8460
SF	 0.8770
SG	 0.8640
SH	 0.8890
SI	 0.8700
SJ	 0.8850
SK	 0.8830
SL	 0.8670
SM	 0.8260
SN	 0.7240
T	 0.8320
T0	 0.8040
T1	 0.8710
T2	 0.9220
T3	 0.9180
T4	 0.9040
T5	 0.7980
TA	 0.7380
TB	 0.8190
TC	 0.8450

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Chain	Atom inclusion
TD	0.9110
TE	0.8590
TF	0.8680
TG	0.8700
TH	0.8760
TI	0.8540
TJ	0.8660
TK	0.8960
TL	0.8610
TM	0.8500
TN	0.7700
U	0.8880
U0	0.8070
U1	0.9130
U2	0.9180
U3	0.8930
U4	0.7930
U5	0.6360
U6	0.7690
U7	0.8590
U8	0.7320
U9	0.6040
UA	0.7360
UB	0.8440
UC	0.8430
UD	0.8920
UE	0.8580
UF	0.8660
UG	0.8640
UH	0.8800
UI	0.8780
UJ	0.8590
UK	0.8780
UL	0.8060
UM	0.7860
UN	0.7390
UO	0.6310
V	0.8930
V0	0.2680
V1	0.6600
V2	0.8200
V3	0.6700











































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Chain	Atom inclusion
V4	0.5980
V5	0.7330
V6	0.8660
V7	0.8460
V8	0.7510
V9	0.7430
VA	0.7630
VB	0.8560
VC	0.8590
VD	0.9000
VE	0.8690
VF	0.8590
VG	0.8500
VH	0.8860
VI	0.8650
VJ	0.8680
VK	0.8870
VL	0.8870
VM	0.8490
VN	0.8290
VO	0.7700
W	0.8300
W0	0.3180
W2	0.6400
W4	0.8310
W5	0.8800
W6	0.8760
W7	0.7690
WA	0.7630
WB	0.8580
WC	0.8550
WD	0.9140
WE	0.9030
WF	0.9100
WG	0.8940
WH	0.9190
WI	0.8880
WJ	0.9150
WK	0.9000
WL	0.9310
WM	0.8720
WN	0.8850







































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Chain	Atom inclusion
WO	 0.8350
WP	 0.7660
X	 0.9030
X0	 0.7600
X1	 0.7070
X2	 0.7720
X3	 0.7500
X4	 0.8110
X5	 0.7700
X6	 0.7830
X7	 0.4670
X8	 0.4050
XA	 0.7370
XB	 0.9040
XC	 0.9740
XD	 0.9560
XE	 0.9500
XF	 0.9450
XG	 0.9430
XH	 0.9190
Y	 0.8980
Y0	 0.8170
Y1	 0.8540
Y2	 0.8790
Y3	 0.7040
Y4	 0.7680
Y5	 0.6860
YA	 0.7140
YB	 0.8500
YC	 0.7350
YD	 0.9020
YE	 0.8340
YF	 0.9020
YG	 0.8000
YH	 0.7570
Z	 0.8110
Z1	 0.8040
Z2	 0.7830
Z3	 0.9100
Z4	 0.8900
Z5	 0.8200
a	 0.5800

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Chain	Atom inclusion
a1	 0.8360
a2	 0.9120
a3	 0.9160
a4	 0.8200
a6	 0.5760
b	 0.4820
b1	 0.8640
b2	 0.8880
b3	 0.9300
b4	 0.8990
b5	 0.8220
c	 0.5560
d	 0.4670
e	 0.8750
f	 0.8700
g	 0.8630
h	 0.8200
h1	 0.9130
h2	 0.9060
h3	 0.8960
h4	 0.8470
i	 0.8750
i1	 0.9330
i2	 0.8110
i3	 0.7840
i4	 0.8250
j	 0.8740
j1	 0.8270
k	 0.8450
l	 0.9480
m	 0.9580
n	 0.9480
o	 0.4630
p	 0.5340
q	 0.8580
r	 0.8490
s	 0.8670
y	 0.8330