wwPDB EM Validation Summary 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)

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

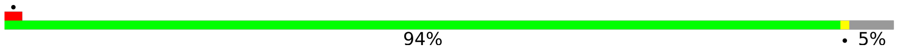
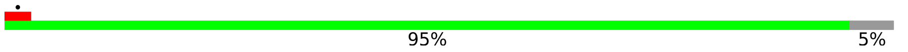
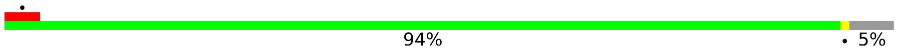
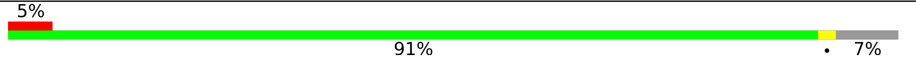
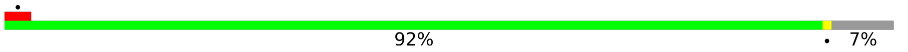
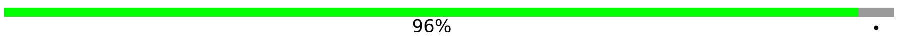
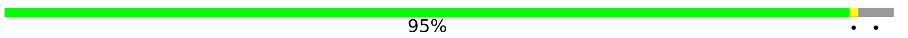
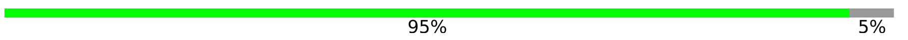
1 Overall quality at a glance ⓘ

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 <=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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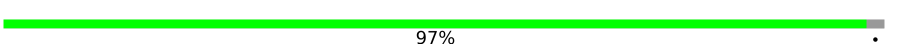
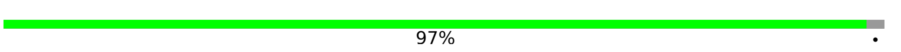
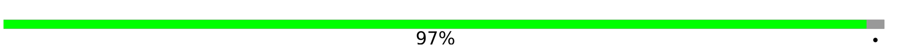
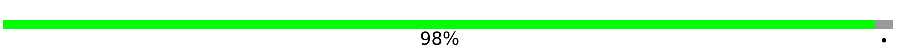
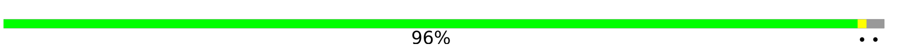
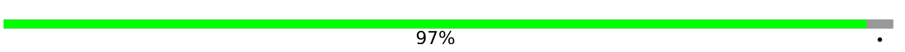
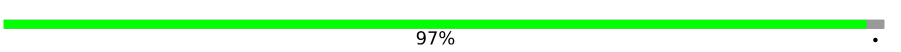
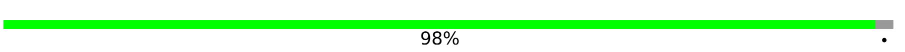
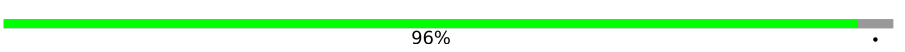
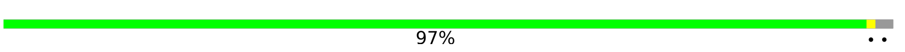
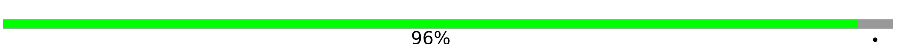
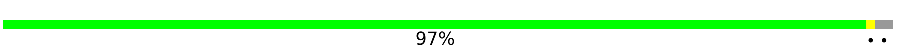
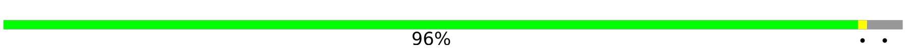
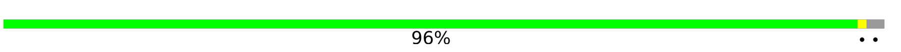
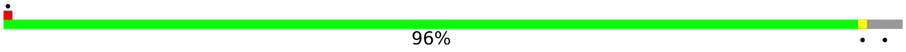
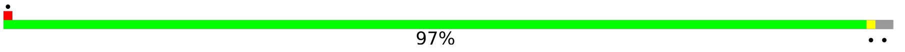
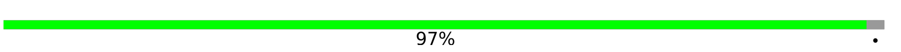
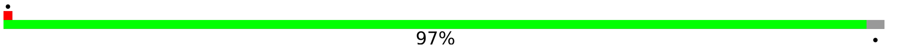
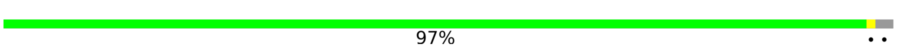
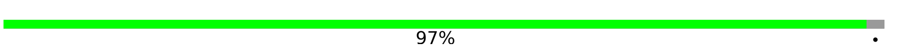
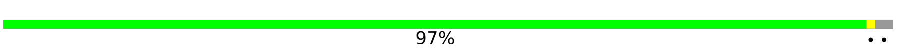
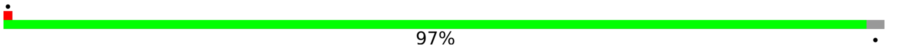
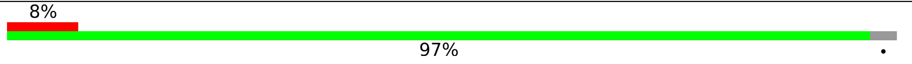
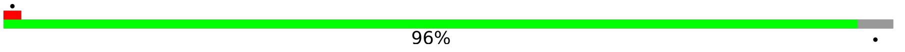
Mol	Chain	Length	Quality of chain
7	A5	418	
8	AA	450	
8	AC	450	
8	AE	450	
8	AG	450	
8	AI	450	
8	AK	450	
8	AM	450	
8	AO	450	
8	BC	450	
8	BE	450	
8	BG	450	
8	BI	450	
8	BK	450	
8	BM	450	
8	BO	450	
8	CC	450	
8	CE	450	
8	CG	450	
8	CI	450	
8	CK	450	
8	CM	450	
8	CO	450	
8	CQ	450	
8	DC	450	

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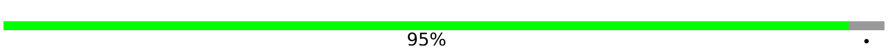
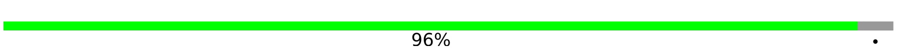
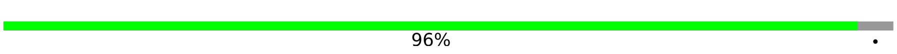
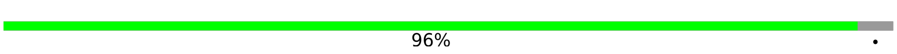
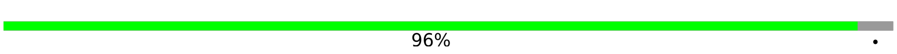
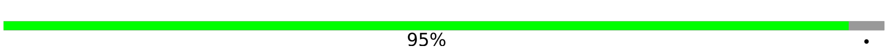
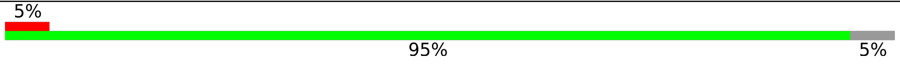
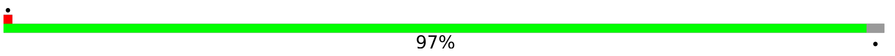
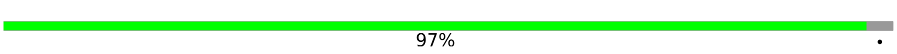
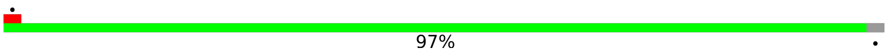
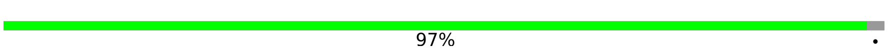
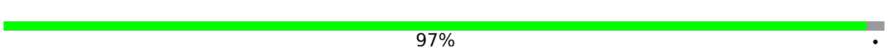
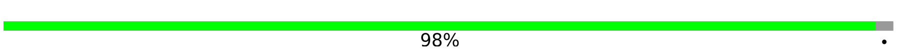
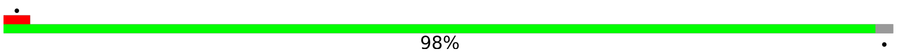
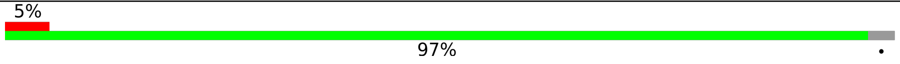
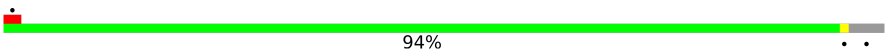
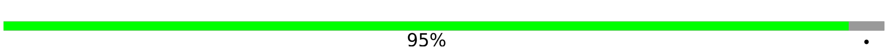
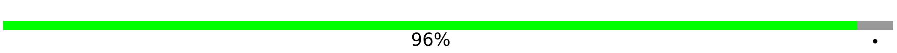
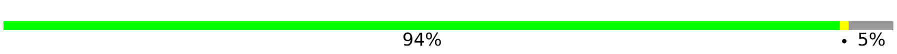
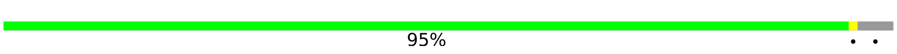
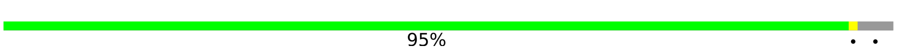
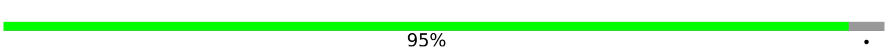
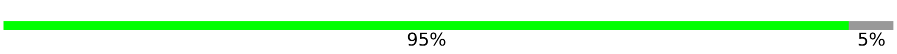
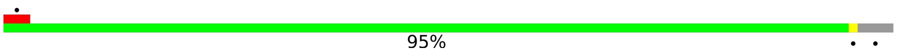
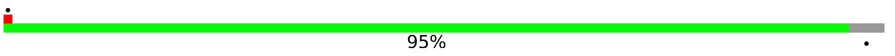
Mol	Chain	Length	Quality of chain
8	DE	450	
8	DG	450	
8	DI	450	
8	DK	450	
8	DM	450	
8	DO	450	
8	DQ	450	
8	EA	450	
8	EC	450	
8	EE	450	
8	EG	450	
8	EI	450	
8	EK	450	
8	EM	450	
8	EO	450	
8	FA	450	
8	FC	450	
8	FE	450	
8	FG	450	
8	FI	450	
8	FK	450	
8	FM	450	
8	FO	450	
8	GA	450	
8	GC	450	

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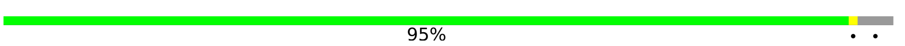
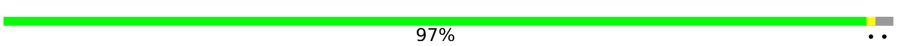
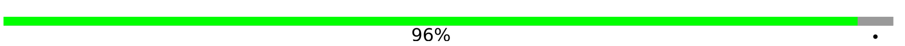
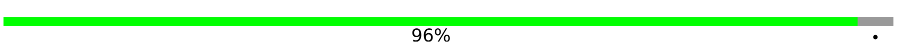
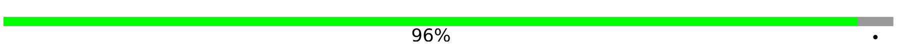
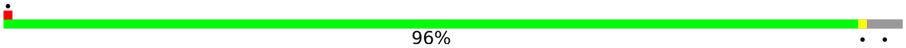
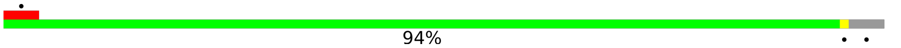
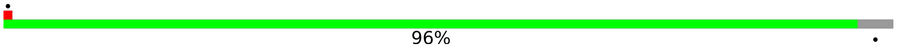
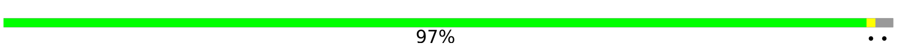
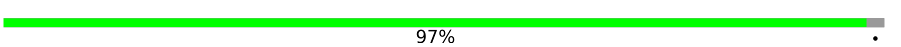
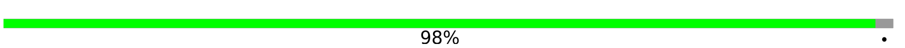
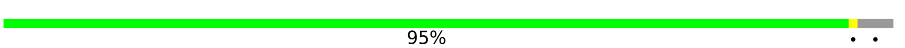
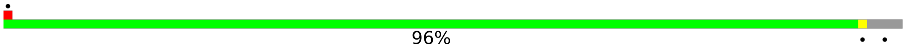
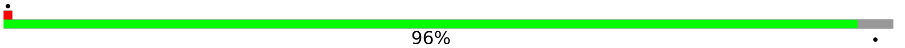
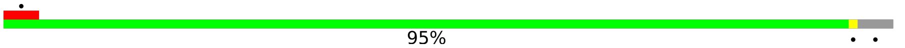
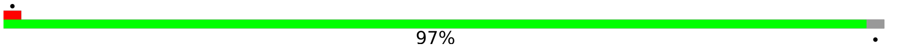
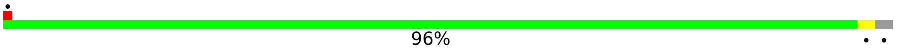
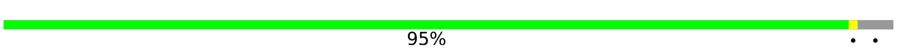
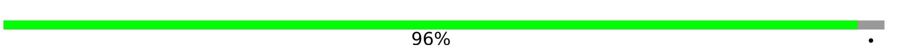
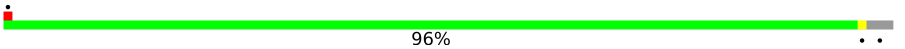
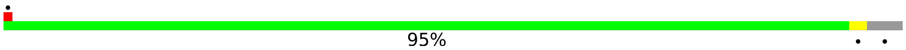
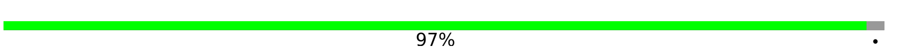
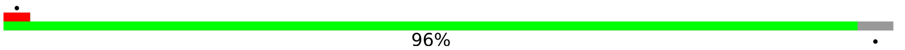
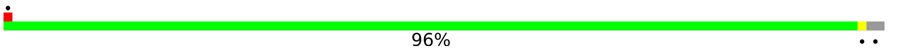
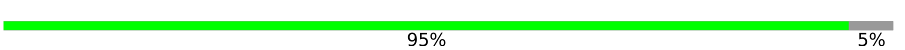
Mol	Chain	Length	Quality of chain
8	GE	450	
8	GG	450	
8	GI	450	
8	GK	450	
8	GM	450	
8	GO	450	
8	HA	450	
8	HC	450	
8	HE	450	
8	HG	450	
8	HI	450	
8	HK	450	
8	HM	450	
8	HO	450	
8	IA	450	
8	IC	450	
8	IE	450	
8	IG	450	
8	II	450	
8	IK	450	
8	IM	450	
8	IO	450	
8	JC	450	
8	JE	450	
8	JG	450	

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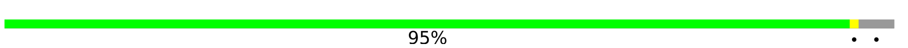
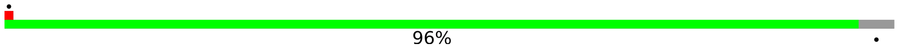
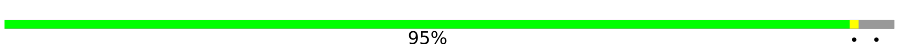
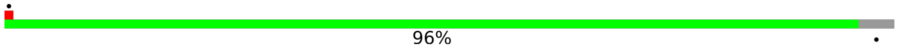
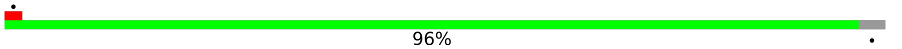
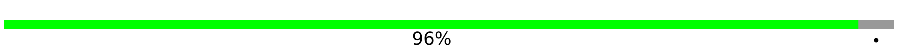
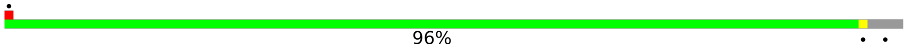
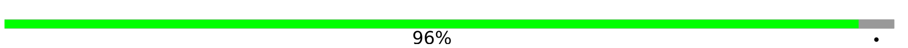
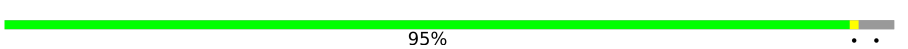
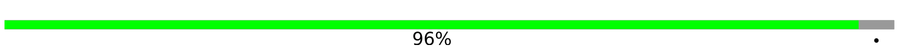
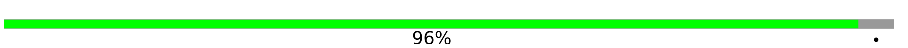
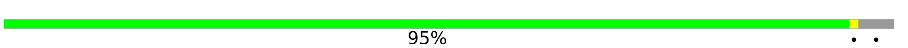
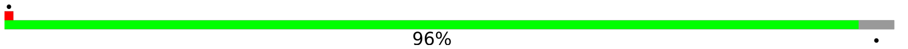
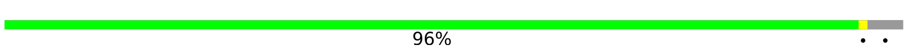
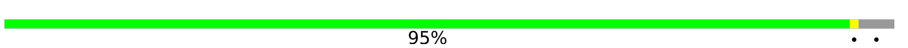
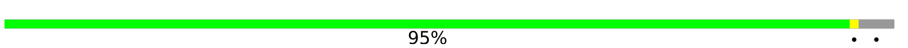
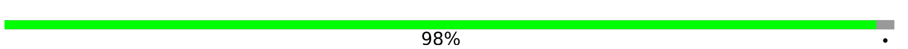
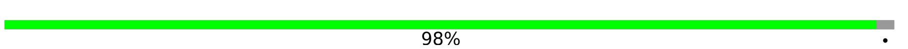
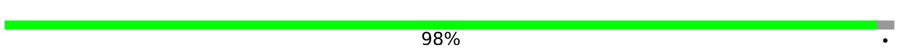
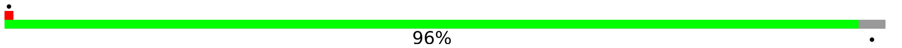
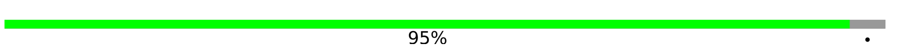
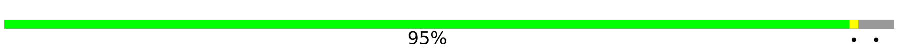
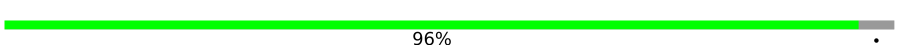
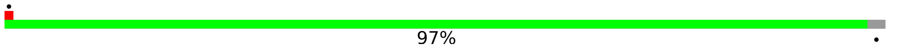
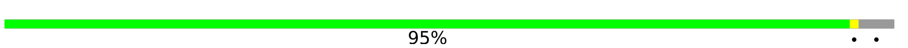
Mol	Chain	Length	Quality of chain
8	JI	450	
8	JK	450	
8	JM	450	
8	JO	450	
8	JQ	450	
8	KA	450	
8	KC	450	
8	KE	450	
8	KG	450	
8	KI	450	
8	KK	450	
8	KM	450	
8	KO	450	
8	LA	450	
8	LC	450	
8	LE	450	
8	LG	450	
8	LI	450	
8	LK	450	
8	LM	450	
8	LO	450	
8	MA	450	
8	MC	450	
8	ME	450	
8	MG	450	

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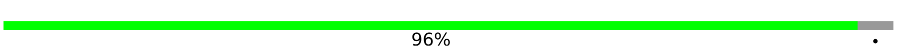
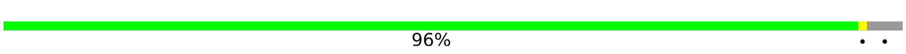
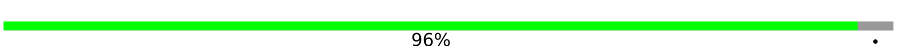
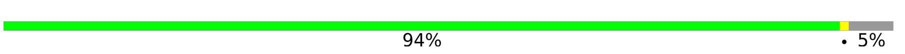
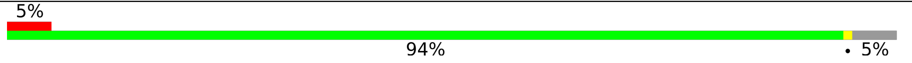
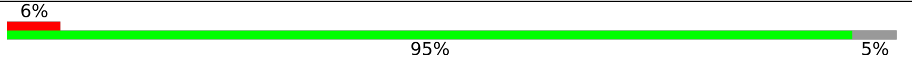
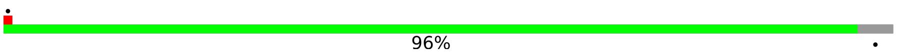
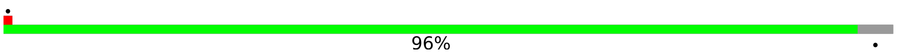
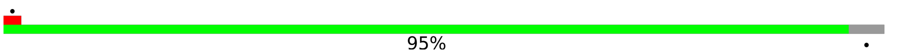
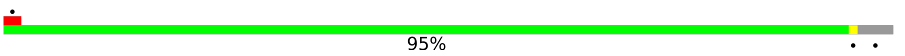
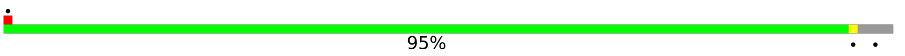
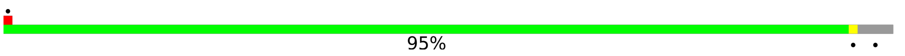
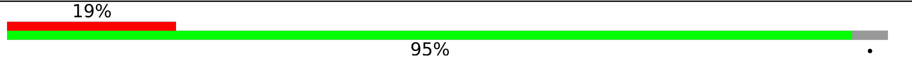
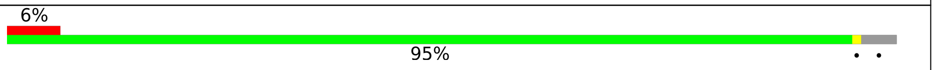
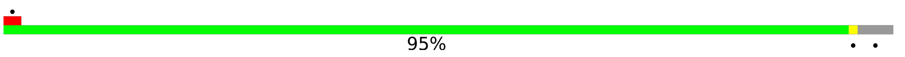
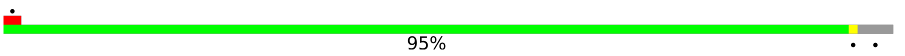
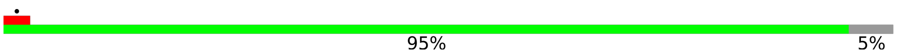
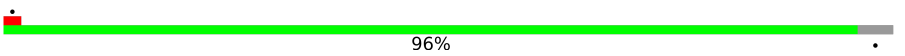
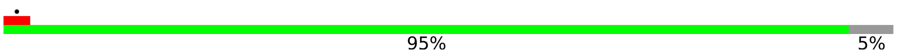
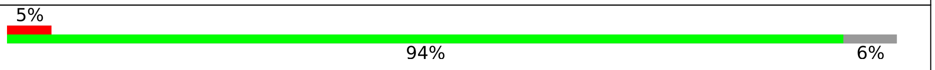
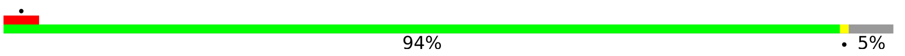
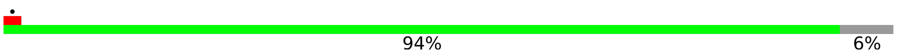
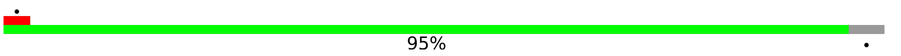
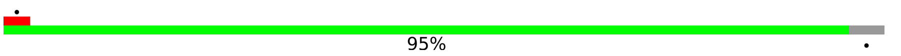
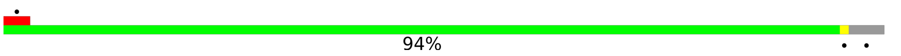
Mol	Chain	Length	Quality of chain
8	MI	450	
8	MK	450	
8	MM	450	
8	MO	450	
8	NA	450	
8	NC	450	
8	NE	450	
8	NG	450	
8	NI	450	
8	NK	450	
8	NM	450	
8	NO	450	
8	OA	450	
8	OC	450	
8	OE	450	
8	OG	450	
8	OI	450	
8	OK	450	
8	OM	450	
8	OO	450	
8	PC	450	
8	PE	450	
8	PG	450	
8	PI	450	
8	PK	450	

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Mol	Chain	Length	Quality of chain
8	PM	450	• 96% •
8	PO	450	5% 95% • •
8	QC	450	8% 95% 5%
8	QE	450	• 95% • •
8	QG	450	5% 95% 5%
8	QI	450	• 95% 5%
8	QK	450	• 95% 5%
8	QM	450	• 94% 5%
8	QO	450	5% 94% 5%
8	RC	450	• 95% 5%
8	RE	450	• 95% 5%
8	RG	450	• 95% 5%
8	RI	450	• 94% • 5%
8	RK	450	• 95% •
8	RM	450	• 94% • 5%
8	RO	450	• 94% • 5%
8	SA	450	9% 94% • 5%
8	SC	450	• 94% • 5%
8	SE	450	• 95% 5%
8	SG	450	• 94% • 5%
8	SI	450	• 94% • 5%
8	SK	450	94% 5%
8	SM	450	• 93% • 6%
8	TA	450	8% 93% • 5%
8	TC	450	• 94% 5%

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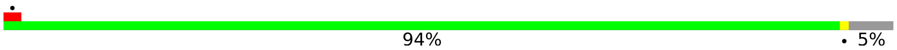
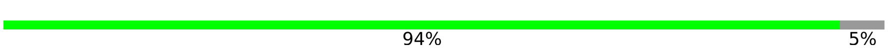
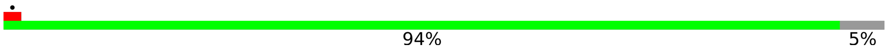
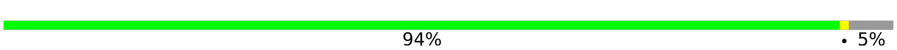
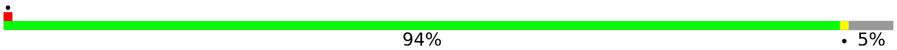
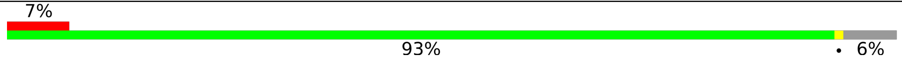
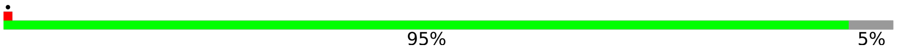
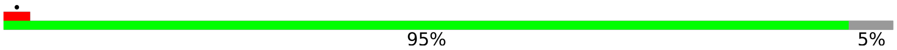
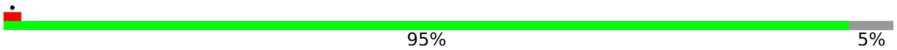
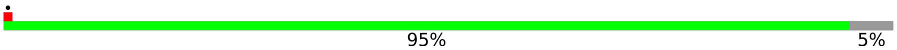
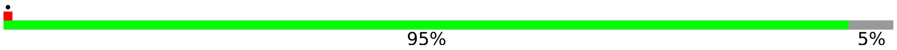
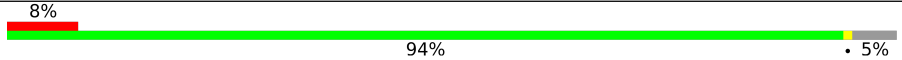
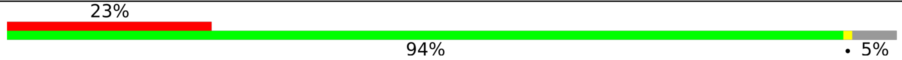
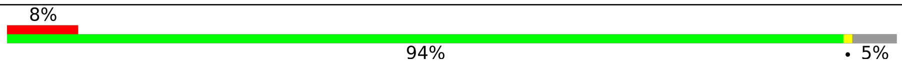
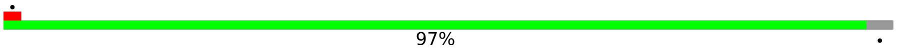
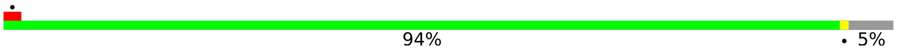
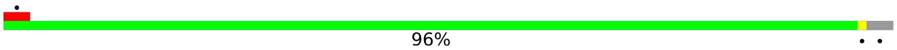
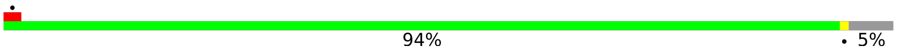
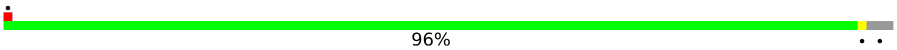
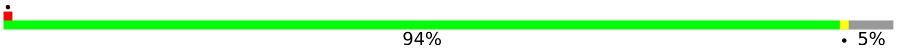
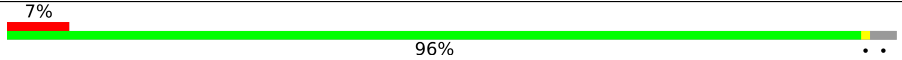
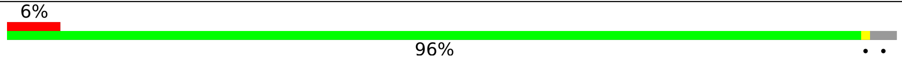
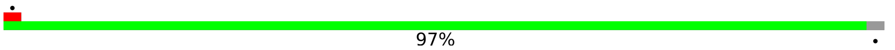
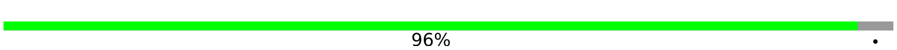
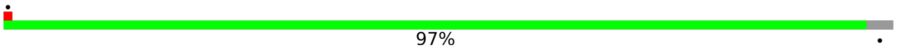
Mol	Chain	Length	Quality of chain
8	TE	450	
8	TG	450	
8	TI	450	
8	TK	450	
8	TM	450	
8	UA	450	
8	UC	450	
8	UE	450	
8	UG	450	
8	UI	450	
8	UK	450	
8	UM	450	
8	UO	450	
8	VA	450	
8	VC	450	
8	VE	450	
8	VG	450	
8	VI	450	
8	VK	450	
8	VM	450	
8	VO	450	
8	WA	450	
8	WC	450	
8	WE	450	
8	WG	450	

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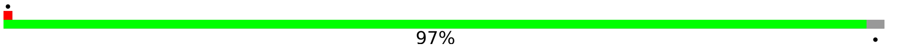
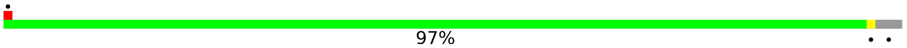
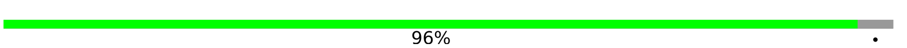
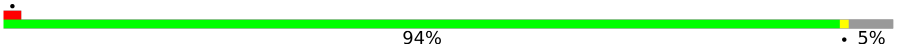
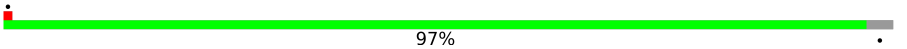
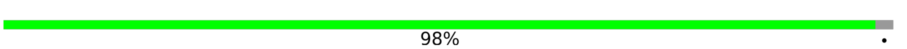
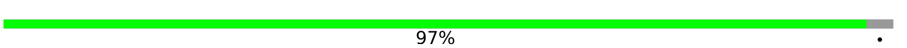
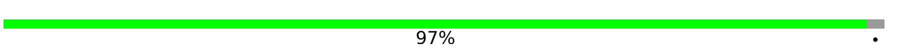
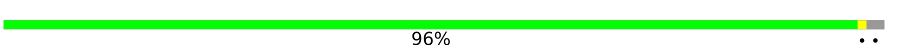
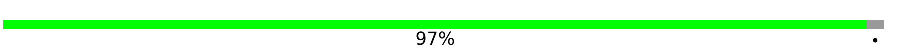
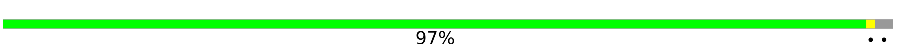
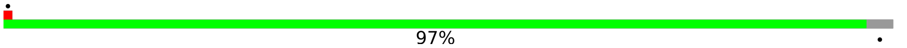
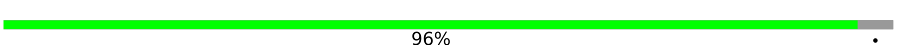
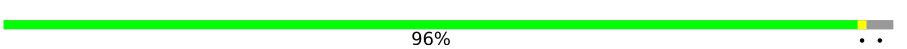
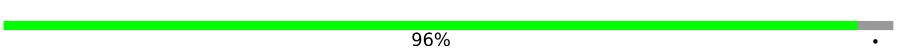
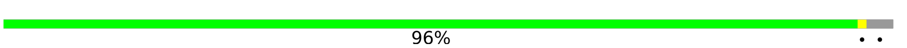
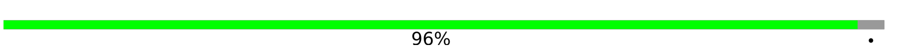
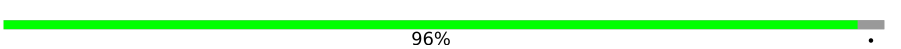
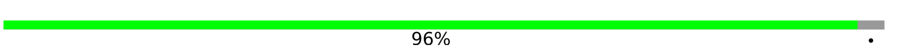
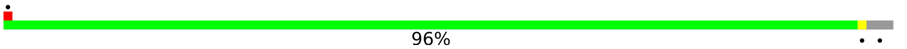
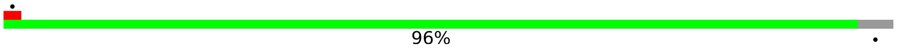
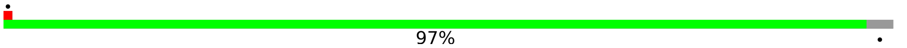
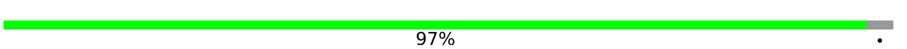
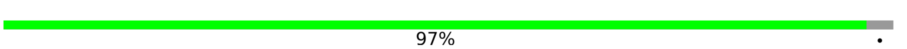
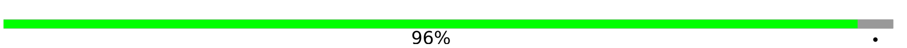
Mol	Chain	Length	Quality of chain
8	WI	450	
8	WK	450	
8	WM	450	
8	WO	450	
9	AB	445	
9	AD	445	
9	AF	445	
9	AH	445	
9	AJ	445	
9	AL	445	
9	AN	445	
9	AP	445	
9	BB	445	
9	BD	445	
9	BF	445	
9	BH	445	
9	BJ	445	
9	BL	445	
9	BN	445	
9	BP	445	
9	CB	445	
9	CD	445	
9	CF	445	
9	CH	445	
9	CJ	445	

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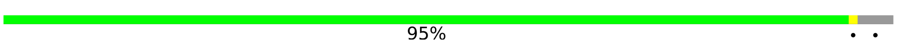
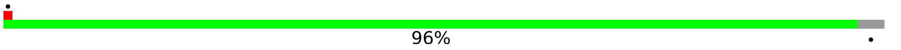
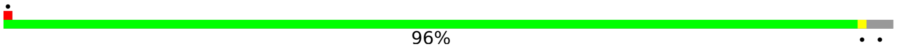
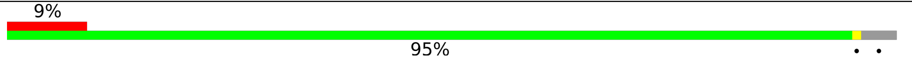
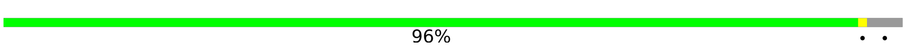
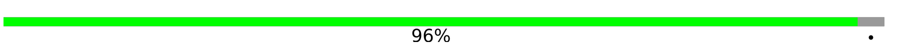
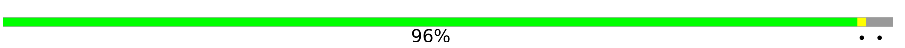
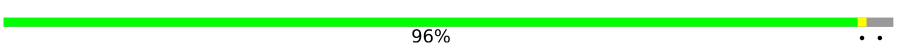
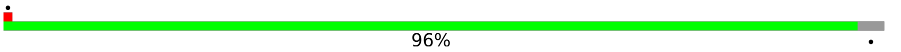
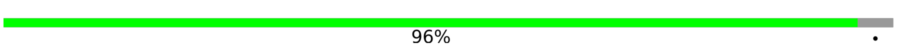
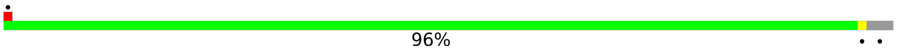
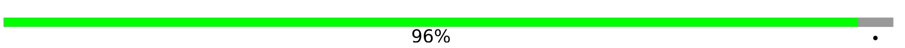
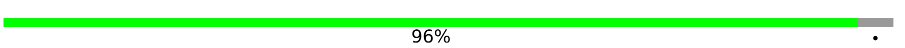
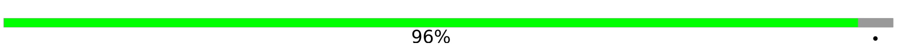
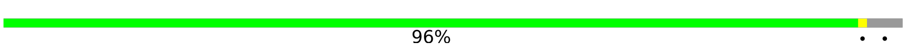
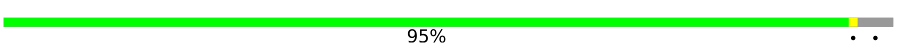
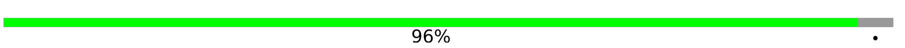
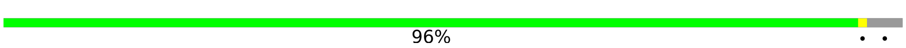
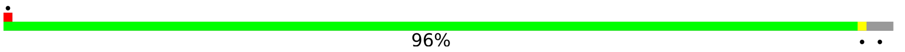
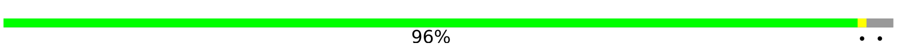
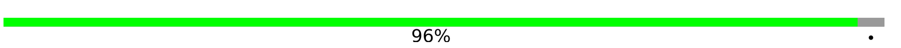
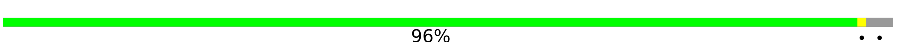
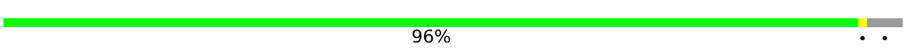
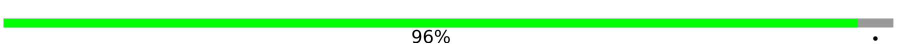
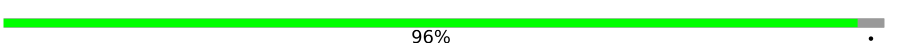
Mol	Chain	Length	Quality of chain
9	CL	445	
9	CN	445	
9	CP	445	
9	DB	445	
9	DD	445	
9	DF	445	
9	DH	445	
9	DJ	445	
9	DL	445	
9	DN	445	
9	DP	445	
9	EB	445	
9	ED	445	
9	EF	445	
9	EH	445	
9	EJ	445	
9	EL	445	
9	EN	445	
9	FB	445	
9	FD	445	
9	FF	445	
9	FH	445	
9	FJ	445	
9	FL	445	
9	FN	445	

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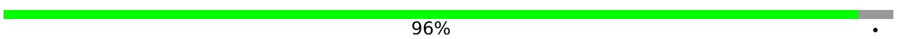
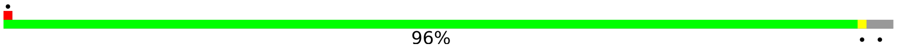
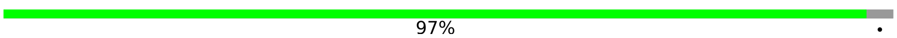
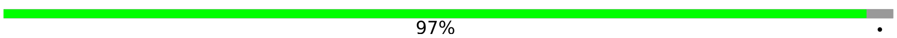
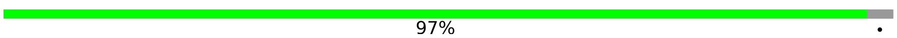
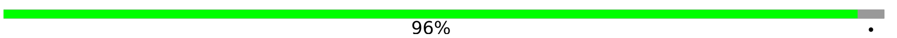
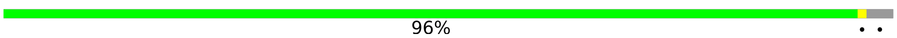
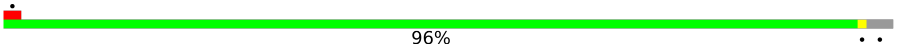
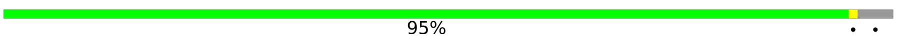
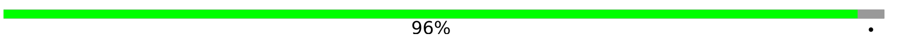
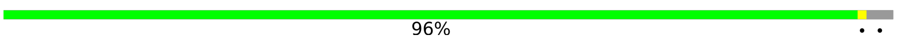
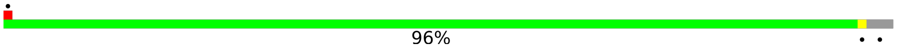
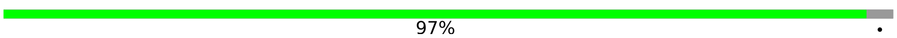
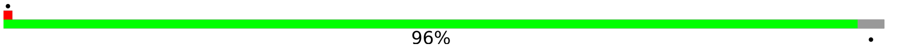
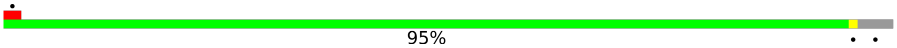
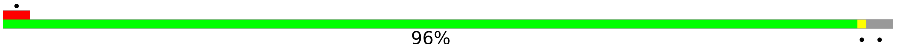
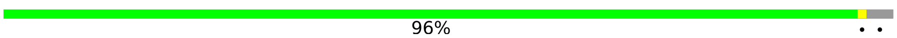
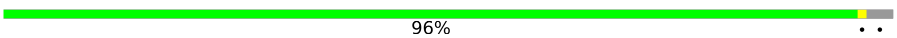
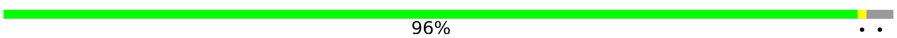
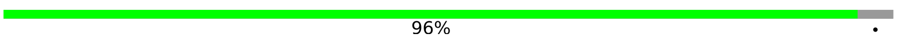
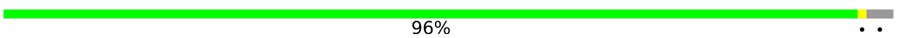
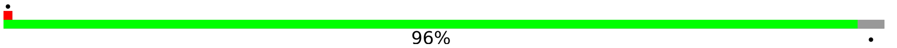
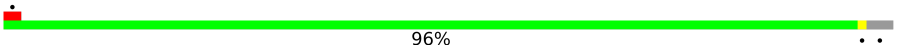
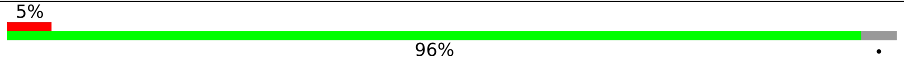
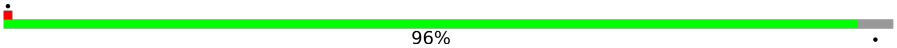
Mol	Chain	Length	Quality of chain
9	GB	445	
9	GD	445	
9	GF	445	
9	GH	445	
9	GJ	445	
9	GL	445	
9	GN	445	
9	HB	445	
9	HD	445	
9	HF	445	
9	HH	445	
9	HJ	445	
9	HL	445	
9	HN	445	
9	HP	445	
9	IB	445	
9	ID	445	
9	IF	445	
9	IH	445	
9	IJ	445	
9	IL	445	
9	IN	445	
9	IP	445	
9	JB	445	
9	JD	445	

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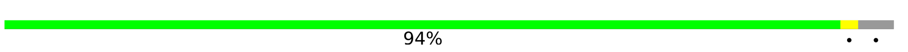
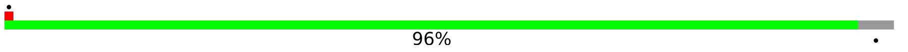
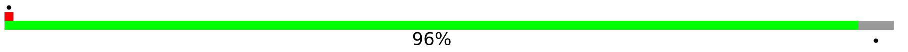
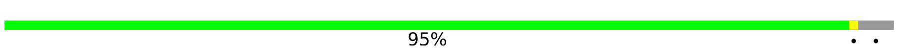
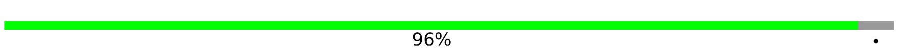
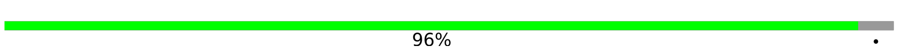
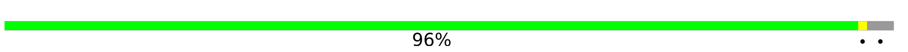
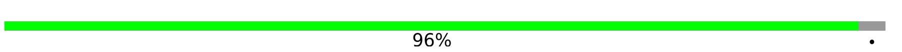
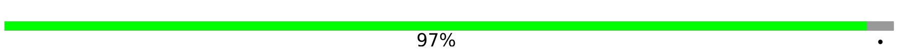
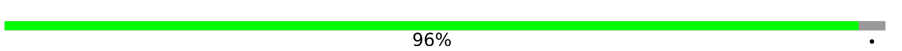
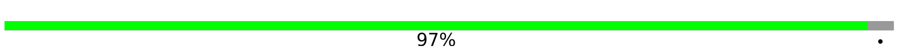
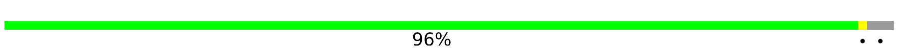
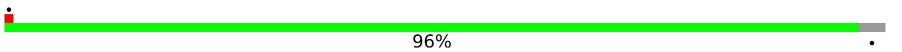
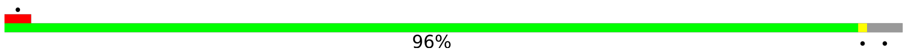
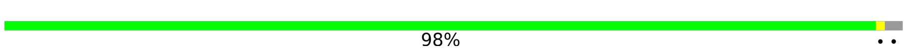
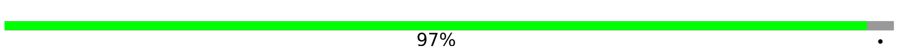
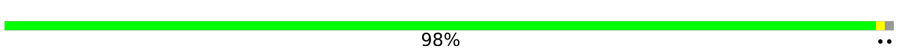
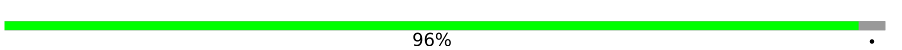
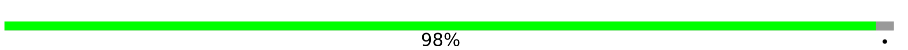
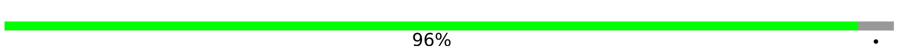
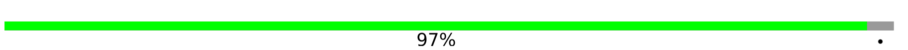
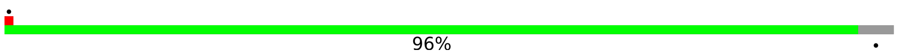
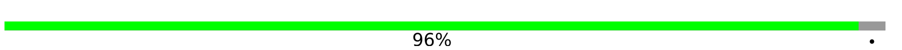
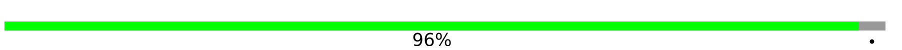
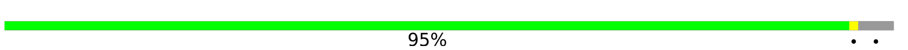
Mol	Chain	Length	Quality of chain
9	JF	445	
9	JH	445	
9	JJ	445	
9	JL	445	
9	JN	445	
9	JP	445	
9	KB	445	
9	KD	445	
9	KF	445	
9	KH	445	
9	KJ	445	
9	KL	445	
9	KN	445	
9	KP	445	
9	LB	445	
9	LD	445	
9	LF	445	
9	LH	445	
9	LJ	445	
9	LL	445	
9	LN	445	
9	LP	445	
9	MB	445	
9	MD	445	
9	MF	445	

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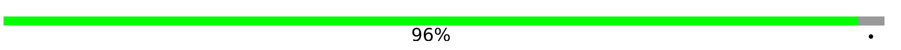
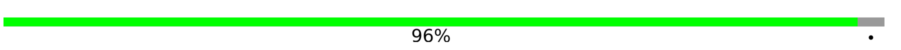
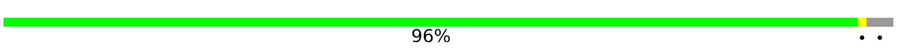
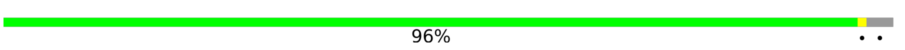
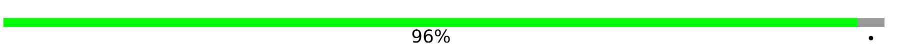
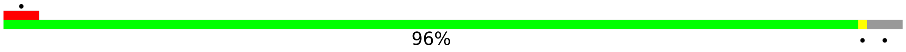
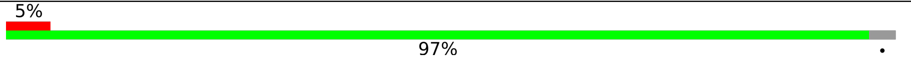
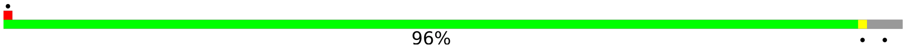
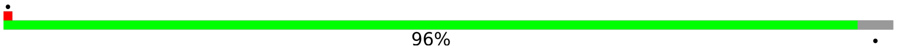
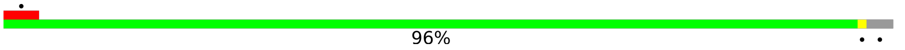
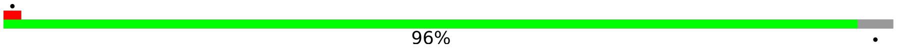
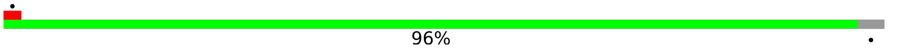
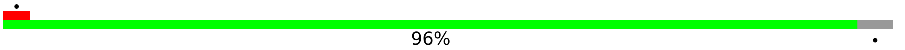
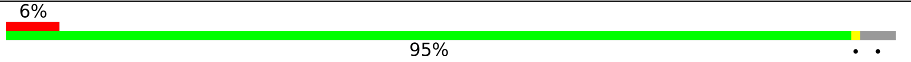
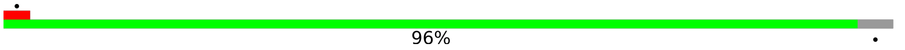
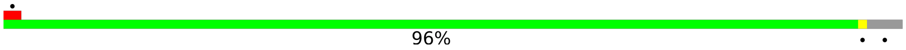
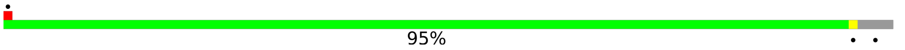
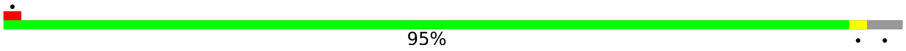
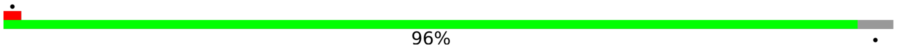
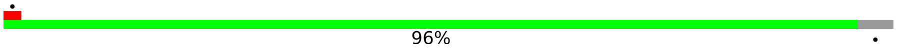
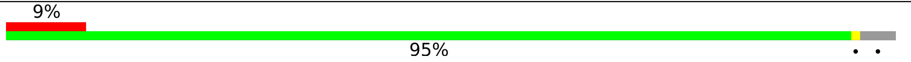
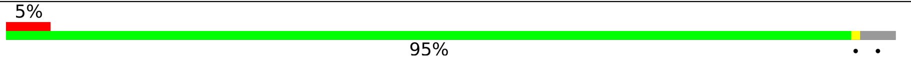
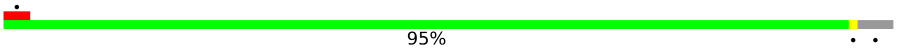
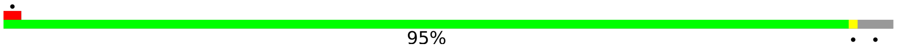
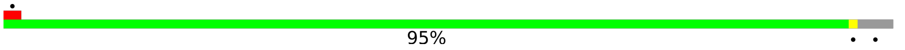
Mol	Chain	Length	Quality of chain
9	MH	445	
9	MJ	445	
9	ML	445	
9	MN	445	
9	MP	445	
9	NB	445	
9	ND	445	
9	NF	445	
9	NH	445	
9	NJ	445	
9	NL	445	
9	NN	445	
9	NP	445	
9	OB	445	
9	OD	445	
9	OF	445	
9	OH	445	
9	OJ	445	
9	OL	445	
9	ON	445	
9	OP	445	
9	PB	445	
9	PD	445	
9	PF	445	
9	PH	445	

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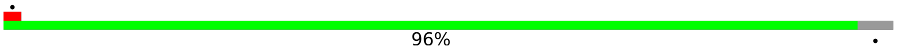
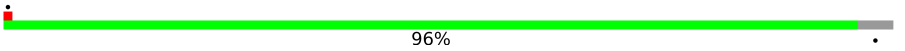
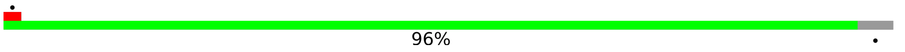
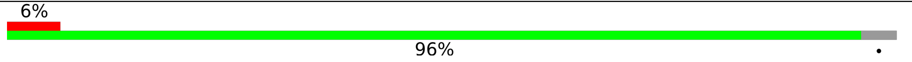
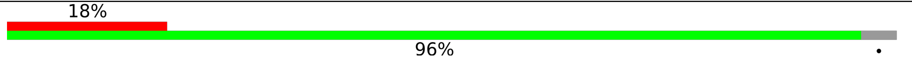
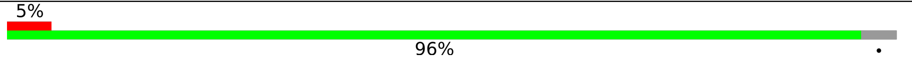
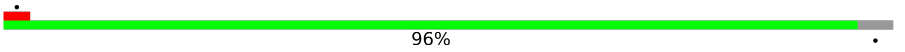
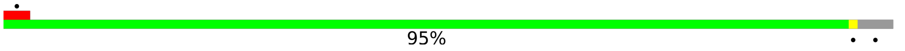
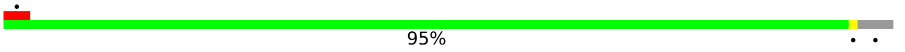
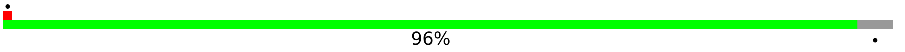
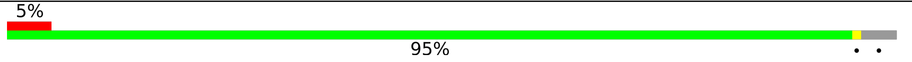
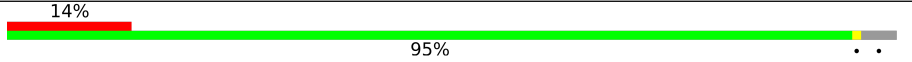
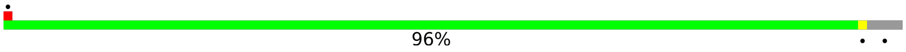
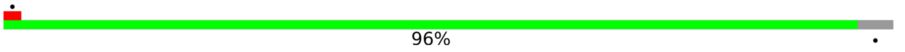
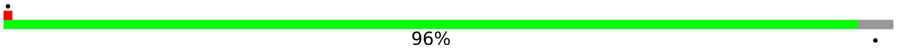
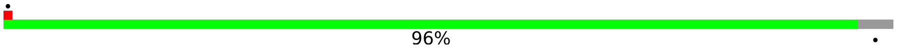
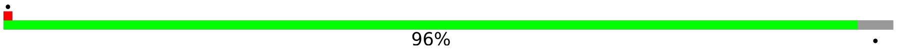
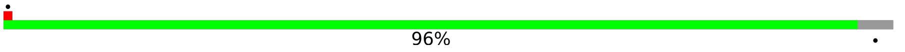
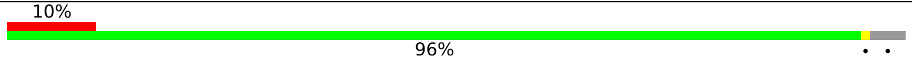
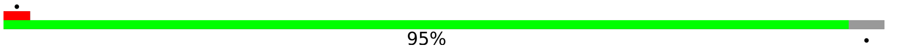
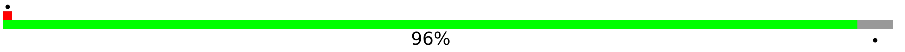
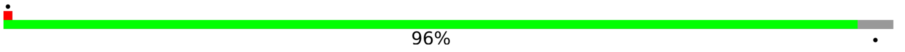
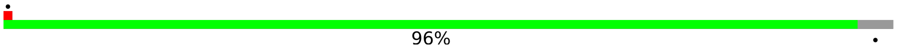
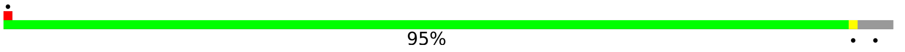
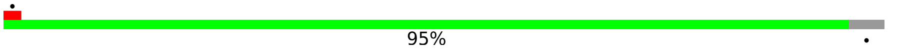
Mol	Chain	Length	Quality of chain
9	PJ	445	
9	PL	445	
9	PN	445	
9	PP	445	
9	QB	445	
9	QD	445	
9	QF	445	
9	QH	445	
9	QJ	445	
9	QL	445	
9	QN	445	
9	QP	445	
9	RD	445	
9	RF	445	
9	RH	445	
9	RJ	445	
9	RL	445	
9	RN	445	
9	RP	445	
9	SB	445	
9	SD	445	
9	SF	445	
9	SH	445	
9	SJ	445	
9	SL	445	

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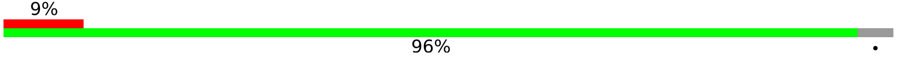
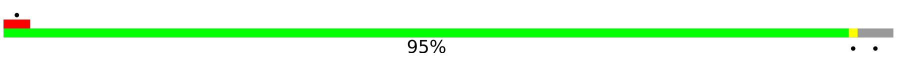
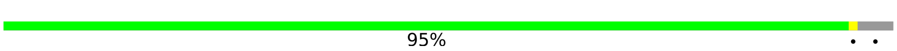
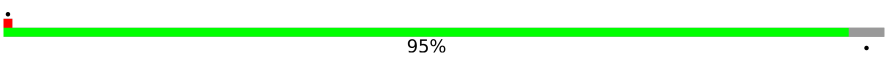
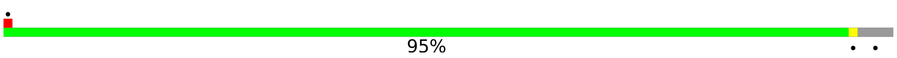
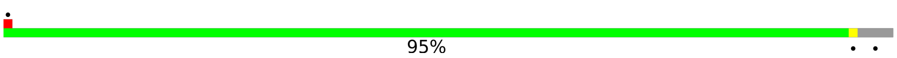
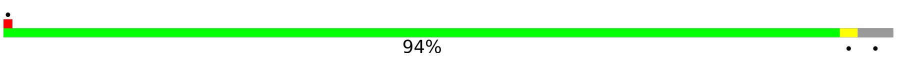
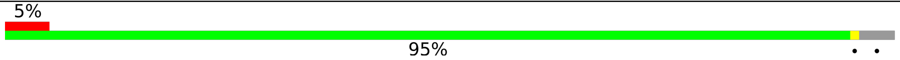
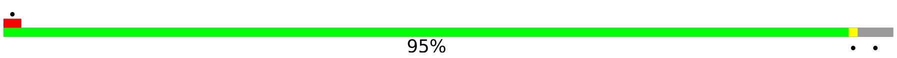
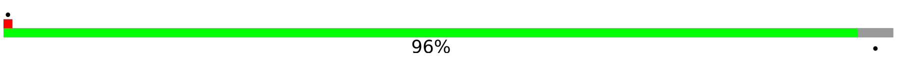
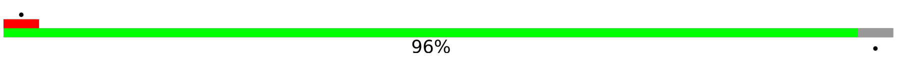
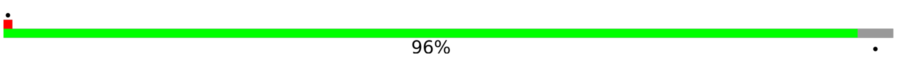
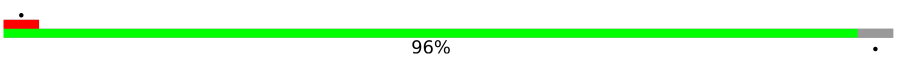
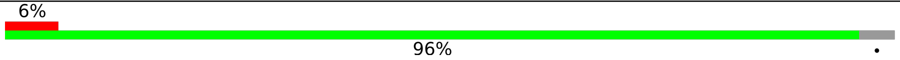
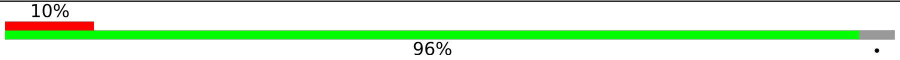
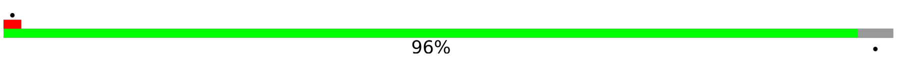
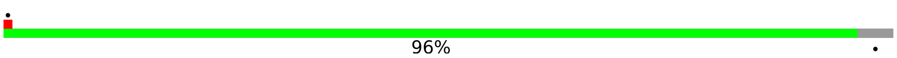
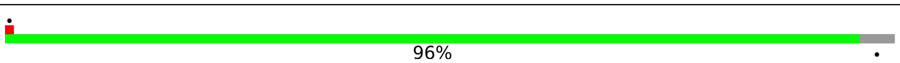
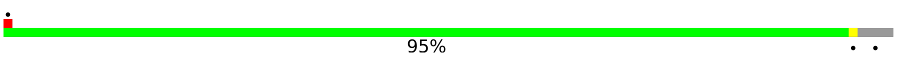
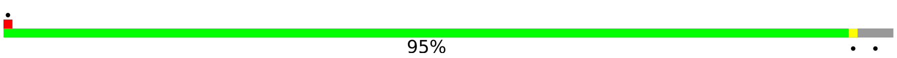
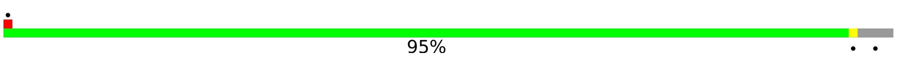
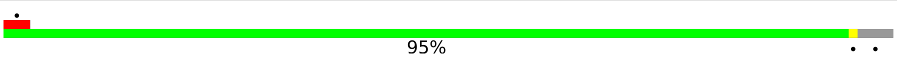
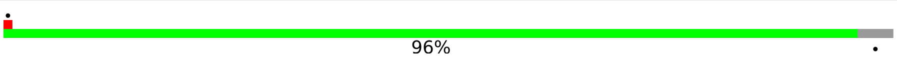
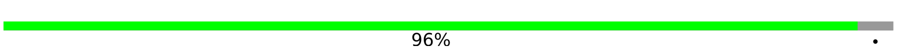
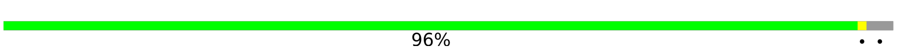
Mol	Chain	Length	Quality of chain
9	SN	445	
9	TB	445	
9	TD	445	
9	TF	445	
9	TH	445	
9	TJ	445	
9	TL	445	
9	TN	445	
9	UB	445	
9	UD	445	
9	UF	445	
9	UH	445	
9	UJ	445	
9	UL	445	
9	UN	445	
9	VB	445	
9	VD	445	
9	VF	445	
9	VH	445	
9	VJ	445	
9	VL	445	
9	VN	445	
9	WB	445	
9	WD	445	
9	WF	445	

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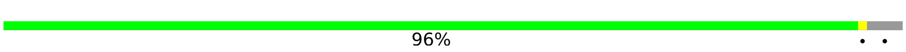
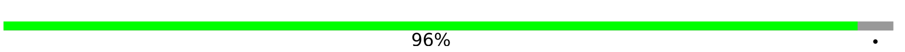
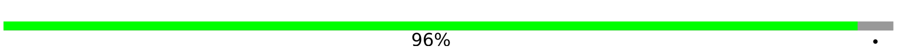
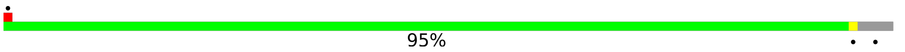
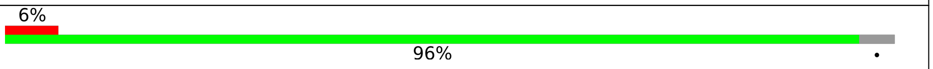
Mol	Chain	Length	Quality of chain
9	WH	445	
9	WJ	445	
9	WL	445	
9	WN	445	
9	WP	445	
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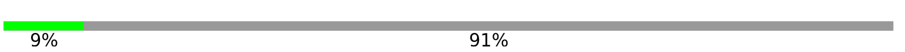
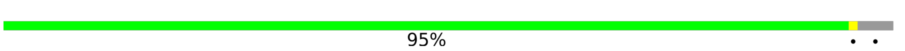
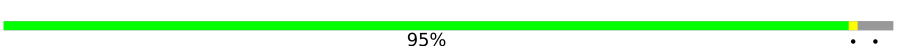
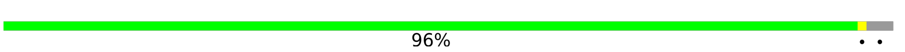
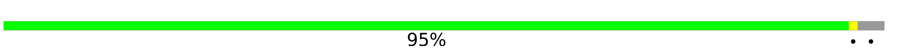
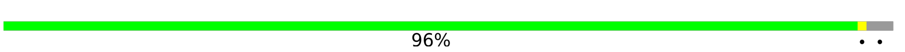
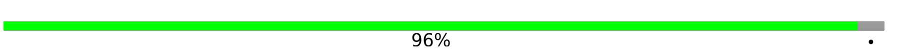
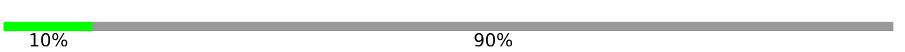
10	C	491	
11	B0	430	
11	B1	430	
11	B2	430	
11	B3	430	
11	B4	430	
11	B5	430	
11	R0	430	
11	R1	430	
11	R2	430	
11	R3	430	
11	R4	430	
11	R5	430	
12	C0	490	
12	C1	490	
12	C2	490	
12	C3	490	
12	C4	490	
12	C5	490	

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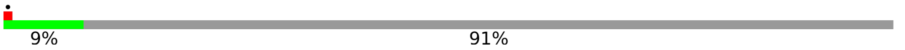
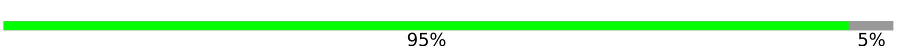
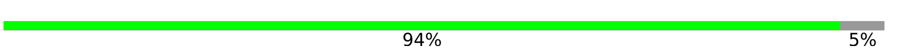
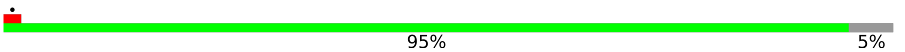
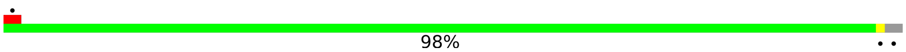
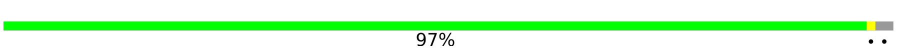
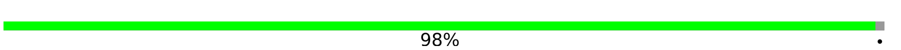
Mol	Chain	Length	Quality of chain
12	C6	490	 9% 91%
12	S0	490	 65% 34%
12	S1	490	 90% 10%
12	S2	490	 90% 10%
12	S3	490	 89% 10%
12	S4	490	 61% 38%
12	S5	490	 63% 36%
12	S6	490	 86% 14%
12	S7	490	 86% 14%
12	S8	490	 85% 14%
12	S9	490	 56% 44%
13	D	470	 16% 84%
13	K3	470	 37% 62%
14	D0	447	 24% 76%
14	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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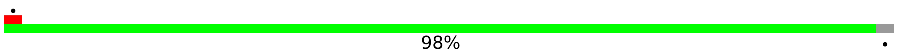
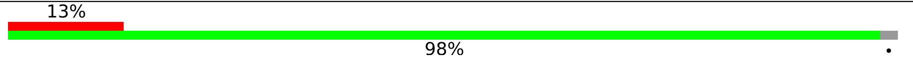
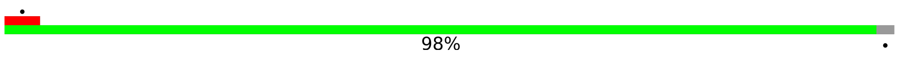
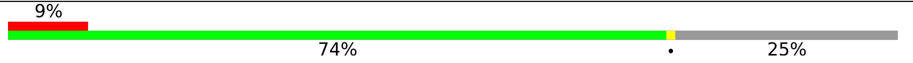
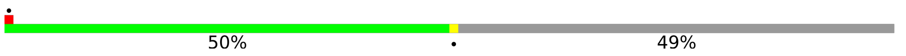
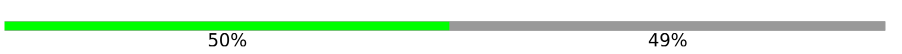
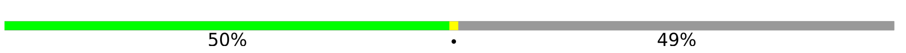
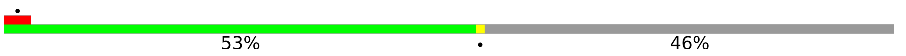
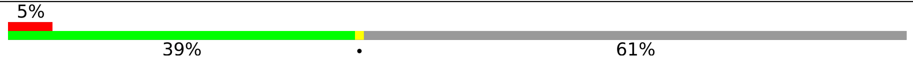
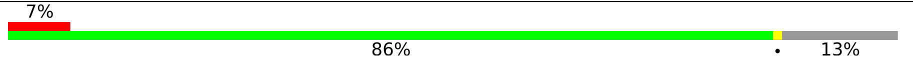
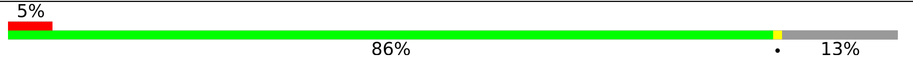
Mol	Chain	Length	Quality of chain
15	E	303	 98%
15	F	303	 13% 98%
15	N2	303	 98%
16	G	122	 9% 74% 25%
17	H	319	 50% 49%
17	I	319	 55% 45%
17	J	319	 50% 50%
17	K	319	 54% 45%
17	L	319	 50% 49%
17	M	319	 54% 46%
17	N	319	 50% 49%
17	O7	319	 53% 46%
17	O8	319	 31% 68%
17	O9	319	 32% 68%
17	P8	319	 32% 68%
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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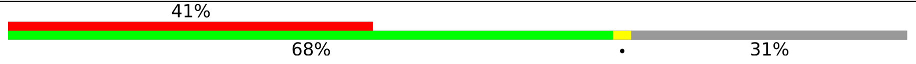
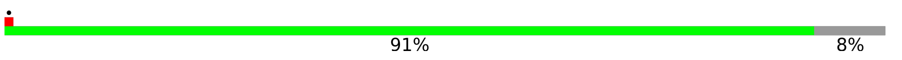
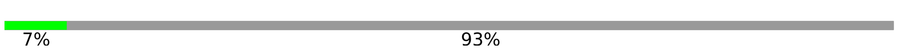
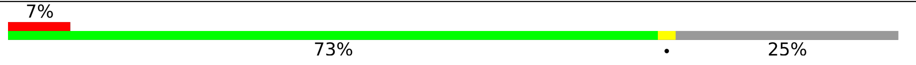
Mol	Chain	Length	Quality of chain
19	J5	283	
20	K1	137	
20	K2	137	
21	L1	182	
22	M1	200	
22	M2	200	
22	M3	200	
22	M4	200	
23	O	379	
23	P	379	
23	Q	379	
24	O1	189	
24	O2	189	
24	O3	189	
24	O4	189	
25	O5	648	
25	O6	648	
25	T	648	
25	U	648	
25	V	648	
26	P1	131	
26	P2	131	
27	P3	180	
27	P4	180	
27	P5	180	

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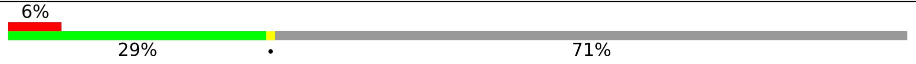
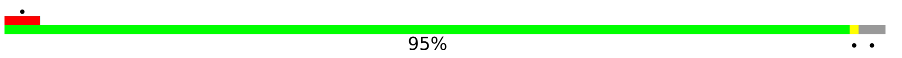
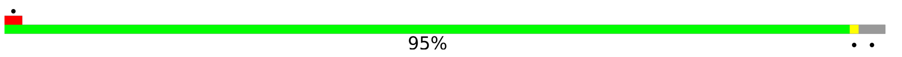
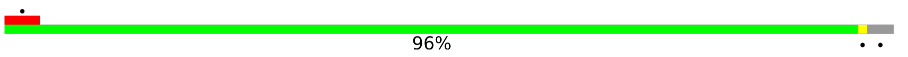
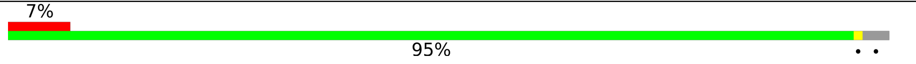
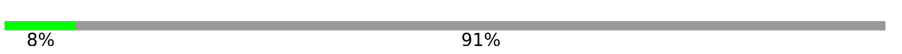
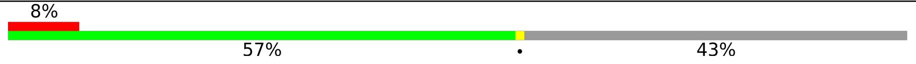
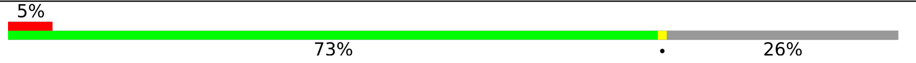
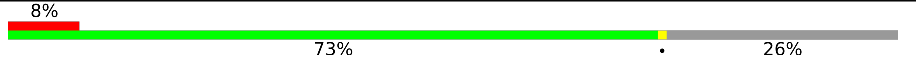
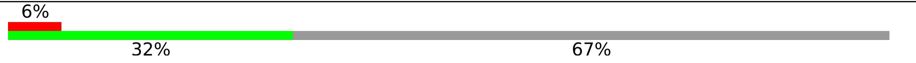
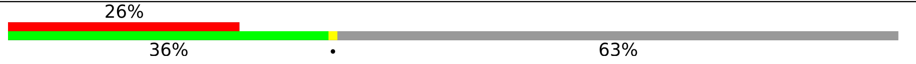
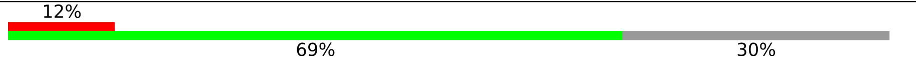
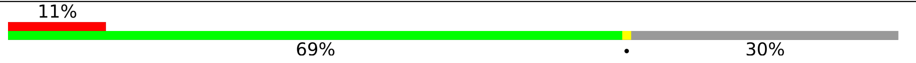
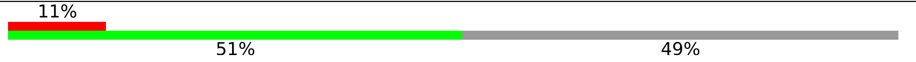
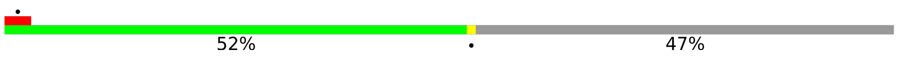
Mol	Chain	Length	Quality of chain
27	P6	180	
27	P7	180	
28	Q1	206	
28	Q2	206	
28	Q3	206	
28	Q4	206	
28	Q5	206	
29	R	377	
29	S	377	
30	U0	557	
30	U1	557	
30	U2	557	
30	U3	557	
30	U4	557	
30	U5	557	
30	U6	557	
30	U7	557	
30	U8	557	
30	U9	557	
30	V0	557	
30	V1	557	
30	V2	557	
30	V3	557	
30	V4	557	
30	V5	557	

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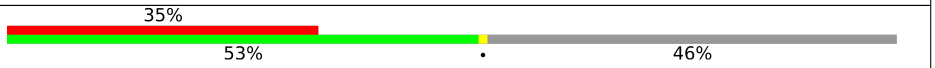
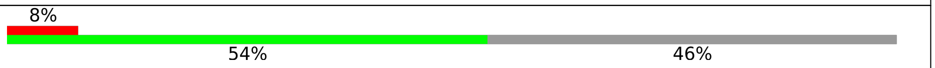
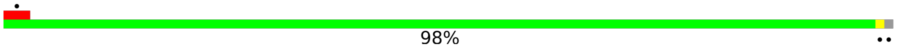
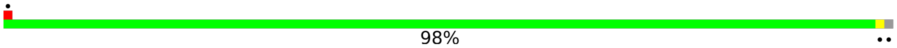
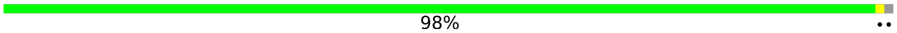
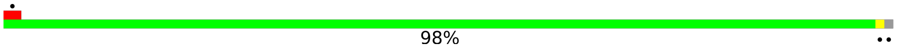
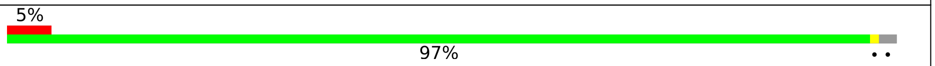
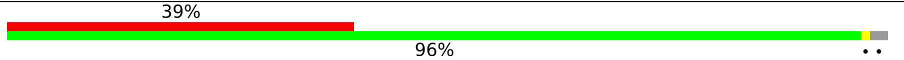
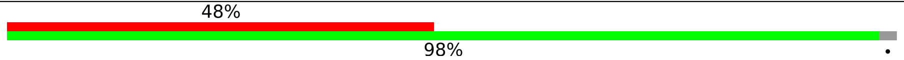
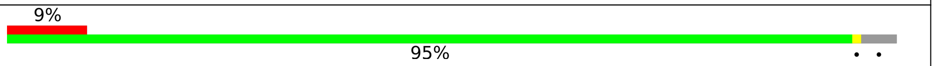
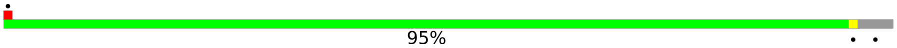
Mol	Chain	Length	Quality of chain
30	V6	557	
30	V7	557	
30	V8	557	
30	V9	557	
30	W0	557	
30	W2	557	
30	W4	557	
30	W5	557	
30	W6	557	
30	W7	557	
31	W	750	
31	X	750	
31	Y	750	
31	Z	750	
32	X0	260	
32	X1	260	
32	X2	260	
32	X3	260	
33	X4	427	
33	X5	427	
34	X6	273	
34	X7	273	
34	X8	273	
35	XA	193	
35	XB	193	

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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	6% 25% 75%
36	Y4	254	9% 71% • 27%
36	Y5	254	6% 33% 67%
37	YA	241	10% 90% • 9%
37	YB	241	91% 9%
37	YC	241	11% 91% 9%
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	11% 52% • 47%
39	a6	551	• 13% 87%
39	b	551	16% 43% • 56%
39	c	551	17% 74% • 25%

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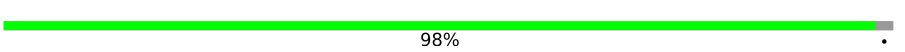
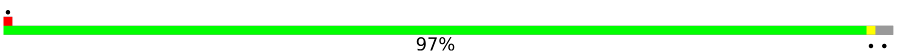
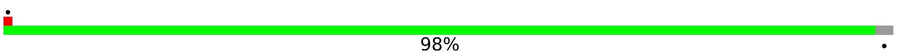
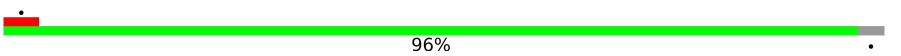
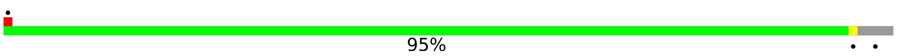
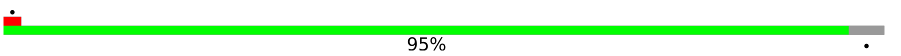
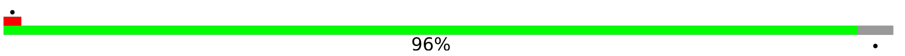
Mol	Chain	Length	Quality of chain
39	d	551	
40	a1	229	
40	a2	229	
40	a3	229	
40	a4	229	
41	b1	499	
41	b2	499	
41	b3	499	
41	b4	499	
41	b5	499	
42	e	620	
42	f	620	
42	g	620	
43	h	255	
43	i	255	
43	j	255	
43	k	255	
44	h1	141	
44	h2	141	
44	h3	141	
44	h4	141	
45	i1	189	
45	l	189	
45	m	189	
45	n	189	

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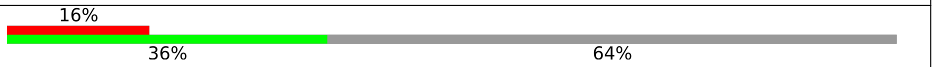
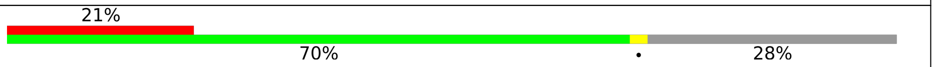
Mol	Chain	Length	Quality of chain
46	i2	1516	
46	i3	1516	
46	i4	1516	
47	o	547	
47	p	547	
48	q	168	
48	r	168	
48	s	168	
49	y	167	

2 Entry composition

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
1	0	81	Total C N O S 670 422 120 123 5	0	0
1	7	141	Total C N O S 1174 741 210 217 6	0	0

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

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

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

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

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

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

- 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 1470 949 257 259 5	0	0

- 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 806 507 150 145 4	0	0
6	N1	94	Total C N O S 806 507 150 145 4	0	0

- Molecule 7 is a protein called Tektin-1.

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

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

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

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

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

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

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

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

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

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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 3424	C 2169	N 582	O 651	S 22	0	0
8	WK	438	Total 3418	C 2166	N 581	O 649	S 22	0	0
8	WM	431	Total 3374	C 2140	N 573	O 639	S 22	0	0
8	WO	429	Total 3358	C 2132	N 571	O 633	S 22	0	0

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

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	BP	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	CB	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	CD	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	CF	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	CH	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	CJ	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	CL	429	Total 3368	C 2116	N 577	O 649	S 26	0	0
9	CN	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	CP	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	DB	429	Total 3368	C 2116	N 577	O 649	S 26	0	0
9	DD	429	Total 3368	C 2116	N 577	O 649	S 26	0	0
9	DF	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	DH	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	DJ	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	DL	431	Total 3382	C 2124	N 579	O 653	S 26	0	0
9	DN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	DP	430	Total 3373	C 2119	N 578	O 650	S 26	0	0
9	EB	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	ED	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	EF	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	EH	428	Total 3361	C 2112	N 576	O 647	S 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
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	3382	2124	579	653	26	0	0
9	KF	431	3382	2124	579	653	26	0	0
9	KH	431	3382	2124	579	653	26	0	0
9	KJ	430	3373	2119	578	650	26	0	0
9	KL	430	3373	2119	578	650	26	0	0
9	KN	430	3373	2119	578	650	26	0	0
9	KP	428	3361	2112	576	647	26	0	0
9	LB	437	3433	2155	585	667	26	0	0
9	LD	431	3382	2124	579	653	26	0	0
9	LF	439	3451	2165	587	673	26	0	0
9	LH	431	3382	2124	579	653	26	0	0
9	LJ	437	3433	2155	585	667	26	0	0
9	LL	428	3361	2112	576	647	26	0	0
9	LN	432	3391	2129	580	656	26	0	0
9	LP	429	3368	2116	577	649	26	0	0
9	MB	431	3382	2124	579	653	26	0	0
9	MD	431	3382	2124	579	653	26	0	0
9	MF	427	3356	2109	575	646	26	0	0
9	MH	431	3382	2124	579	653	26	0	0
9	MJ	430	3373	2119	578	650	26	0	0
9	ML	430	3373	2119	578	650	26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
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 C N O S 3361 2112 576 647 26	0	0
9	PJ	427	Total C N O S 3356 2109 575 646 26	0	0
9	PL	428	Total C N O S 3361 2112 576 647 26	0	0
9	PN	428	Total C N O S 3361 2112 576 647 26	0	0
9	PP	427	Total C N O S 3356 2109 575 646 26	0	0
9	QB	426	Total C N O S 3348 2105 574 643 26	0	0
9	QD	427	Total C N O S 3356 2109 575 646 26	0	0
9	QF	427	Total C N O S 3356 2109 575 646 26	0	0
9	QH	427	Total C N O S 3356 2109 575 646 26	0	0
9	QJ	427	Total C N O S 3356 2109 575 646 26	0	0
9	QL	427	Total C N O S 3356 2109 575 646 26	0	0
9	QN	427	Total C N O S 3356 2109 575 646 26	0	0
9	QP	426	Total C N O S 3348 2105 574 643 26	0	0
9	RD	428	Total C N O S 3361 2112 576 647 26	0	0
9	RF	428	Total C N O S 3361 2112 576 647 26	0	0
9	RH	428	Total C N O S 3361 2112 576 647 26	0	0
9	RJ	428	Total C N O S 3361 2112 576 647 26	0	0
9	RL	428	Total C N O S 3361 2112 576 647 26	0	0
9	RN	427	Total C N O S 3356 2109 575 646 26	0	0
9	RP	428	Total C N O S 3361 2112 576 647 26	0	0
9	SB	426	Total C N O S 3348 2105 574 643 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 3348 2105 574 643 26	0	0
9	VF	426	Total C N O S 3348 2105 574 643 26	0	0
9	VH	427	Total C N O S 3356 2109 575 646 26	0	0
9	VJ	427	Total C N O S 3356 2109 575 646 26	0	0
9	VL	428	Total C N O S 3361 2112 576 647 26	0	0
9	VN	426	Total C N O S 3348 2105 574 643 26	0	0
9	WB	427	Total C N O S 3356 2109 575 646 26	0	0
9	WD	427	Total C N O S 3356 2109 575 646 26	0	0
9	WF	430	Total C N O S 3373 2119 578 650 26	0	0
9	WH	428	Total C N O S 3361 2112 576 647 26	0	0
9	WJ	428	Total C N O S 3361 2112 576 647 26	0	0
9	WL	427	Total C N O S 3356 2109 575 646 26	0	0
9	WN	427	Total C N O S 3356 2109 575 646 26	0	0
9	WP	427	Total C N O S 3356 2109 575 646 26	0	0

- 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 2769 1697 520 539 13	0	0
10	C	279	Total C N O S 2408 1493 445 459 11	0	0

- Molecule 11 is a protein called Tektin-2.

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

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

- Molecule 12 is a protein called Tektin-3.

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

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

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

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

- Molecule 14 is a protein called Tektin-4.

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

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

- 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 2372 1486 423 446 17	0	0
15	F	297	Total C N O S 2363 1481 421 444 17	0	0
15	N2	297	Total C N O S 2363 1481 421 444 17	0	0

- 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 724 462 123 134 5	0	0

- Molecule 17 is a protein called Protein FAM166A.

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

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

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

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

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

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

- 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 1009 640 187 181 1	0	0
20	K2	118	Total C N O S 1009 640 187 181 1	0	0

- 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 1034 652 193 187 2	0	0

- Molecule 22 is a protein called Protein FAM166C.

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

- 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 627 386 124 115 2	0	0
23	P	347	Total C N O S 2875 1751 564 549 11	0	0
23	Q	103	Total C N O S 858 522 165 169 2	0	0

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

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

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

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

- Molecule 26 is a protein called Testis expressed 49.

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

- 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 1103 719 187 190 7	0	0
27	P4	155	Total C N O S 1272 829 211 224 8	0	0
27	P5	155	Total C N O S 1272 829 211 224 8	0	0
27	P6	154	Total C N O S 1263 824 210 221 8	0	0
27	P7	53	Total C N O S 447 293 70 82 2	0	0

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

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

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

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

- Molecule 30 is a protein called Tektin-5.

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

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

- 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 6116 3950 1019 1119 28	0	0
31	X	741	Total C N O S 6116 3950 1019 1119 28	0	0
31	Y	742	Total C N O S 6124 3954 1021 1121 28	0	0
31	Z	741	Total C N O S 6116 3950 1019 1119 28	0	0

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

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

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

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

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

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

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

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

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

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

- 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 1775 1148 300 317 10	0	0
37	YB	220	Total C N O S 1775 1148 300 317 10	0	0
37	YC	220	Total C N O S 1775 1148 300 317 10	0	0
37	YD	220	Total C N O S 1775 1148 300 317 10	0	0
37	YE	220	Total C N O S 1775 1148 300 317 10	0	0
37	YF	220	Total C N O S 1775 1148 300 317 10	0	0
37	YG	220	Total C N O S 1775 1148 300 317 10	0	0
37	YH	220	Total C N O S 1775 1148 300 317 10	0	0

- 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
			Total	C	N	O	S		
42	e	607	4689	2967	818	872	32	0	0
42	f	607	4689	2967	818	872	32	0	0
42	g	607	4689	2967	818	872	32	0	0

- Molecule 43 is a protein called Enkurin.

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

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

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

- Molecule 45 is a protein called Protein Flattop.

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

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

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

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

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

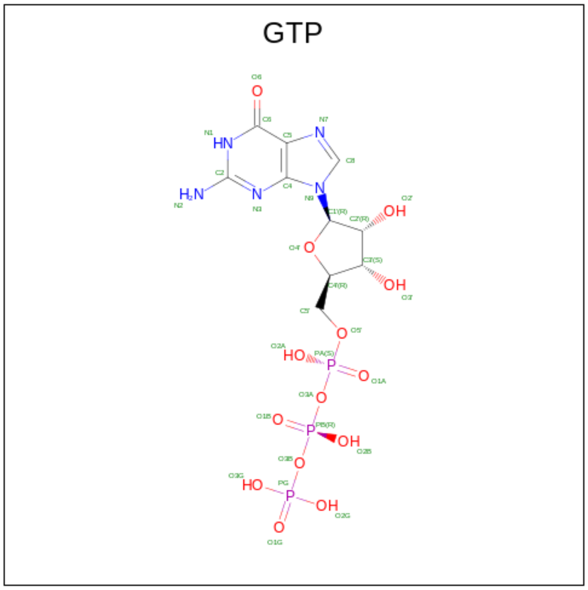
- Molecule 48 is a protein called Cilia- and flagella-associated protein 276.

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

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

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

- Molecule 50 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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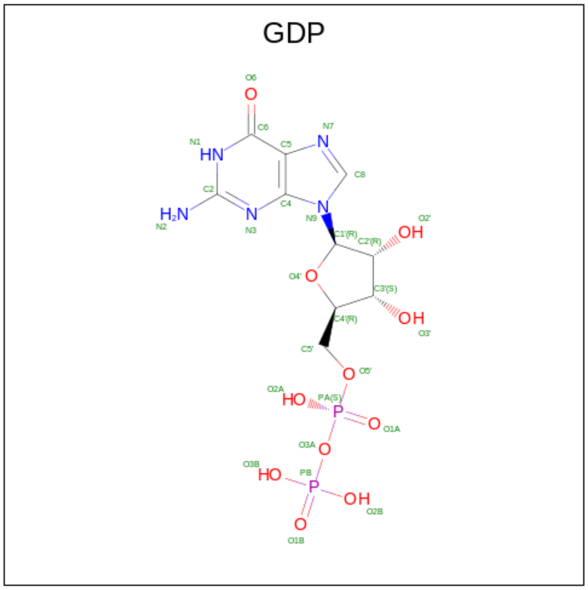
Mol	Chain	Residues	Atoms	AltConf
51	WA	1	Total Mg 1 1	0
51	WC	1	Total Mg 1 1	0
51	WE	1	Total Mg 1 1	0
51	WG	1	Total Mg 1 1	0
51	WI	1	Total Mg 1 1	0
51	WK	1	Total Mg 1 1	0
51	WM	1	Total Mg 1 1	0
51	WO	1	Total Mg 1 1	0

- 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 28 10 5 11 2	0
52	AD	1	Total C N O P 28 10 5 11 2	0
52	AF	1	Total C N O P 28 10 5 11 2	0

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

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

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

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

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

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

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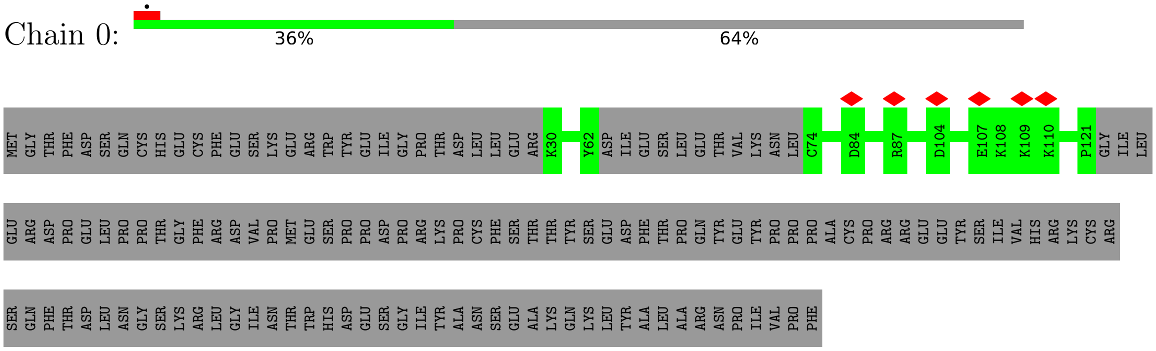
Mol	Chain	Residues	Atoms					AltConf
52	WH	1	Total 28	C 10	N 5	O 11	P 2	0
52	WJ	1	Total 28	C 10	N 5	O 11	P 2	0
52	WL	1	Total 28	C 10	N 5	O 11	P 2	0
52	WN	1	Total 28	C 10	N 5	O 11	P 2	0
52	WP	1	Total 28	C 10	N 5	O 11	P 2	0

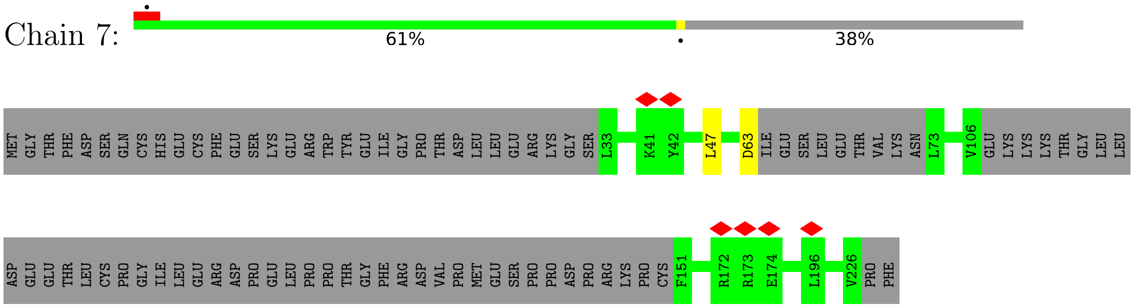
3 Residue-property plots ⓘ

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.

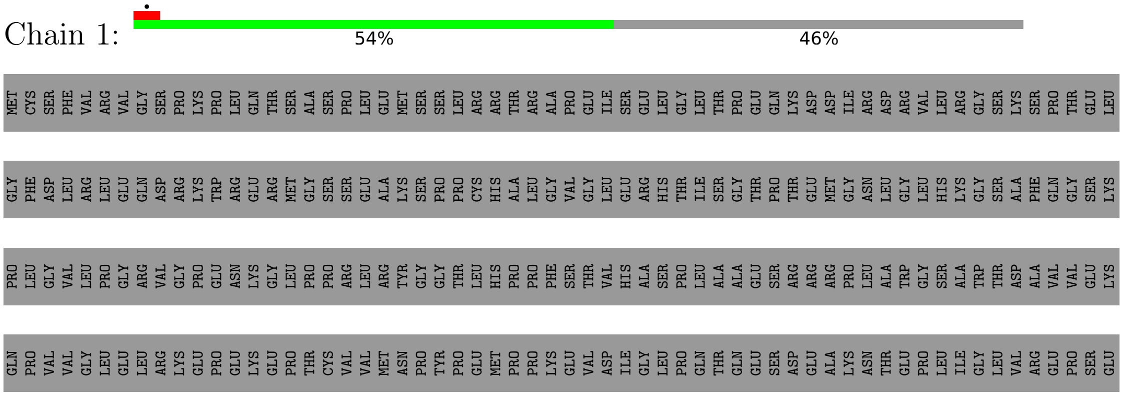
- Molecule 1: Cilia- and flagella-associated protein 95

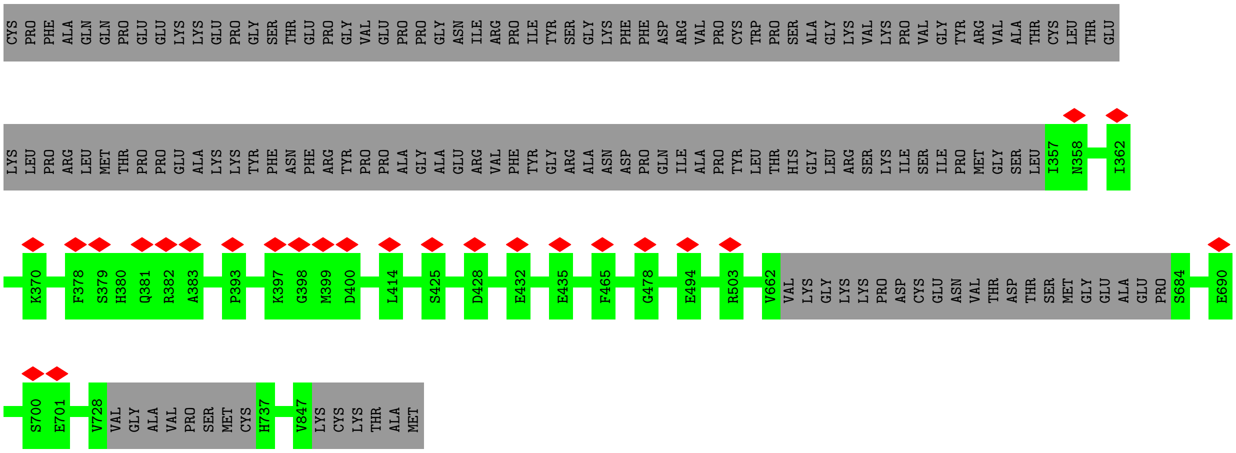


- Molecule 1: Cilia- and flagella-associated protein 95

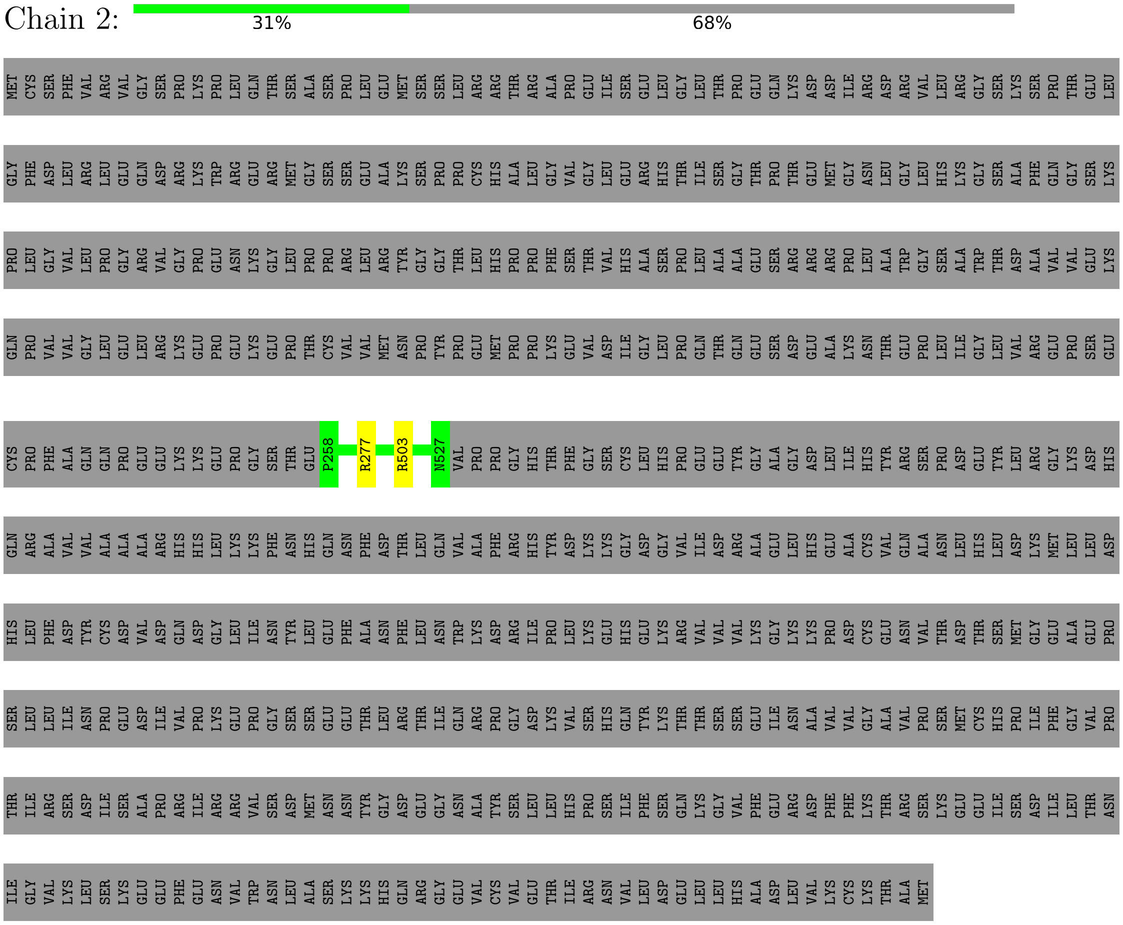


- Molecule 2: EF-hand domain-containing family member B

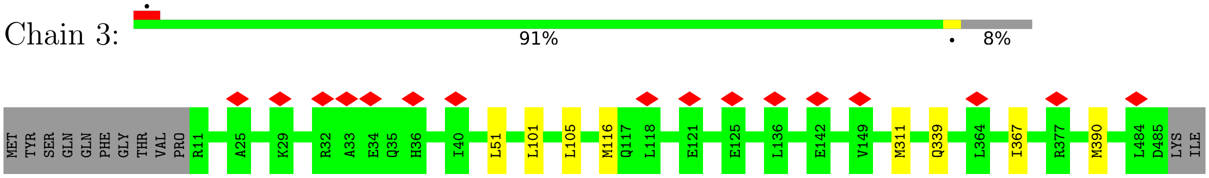




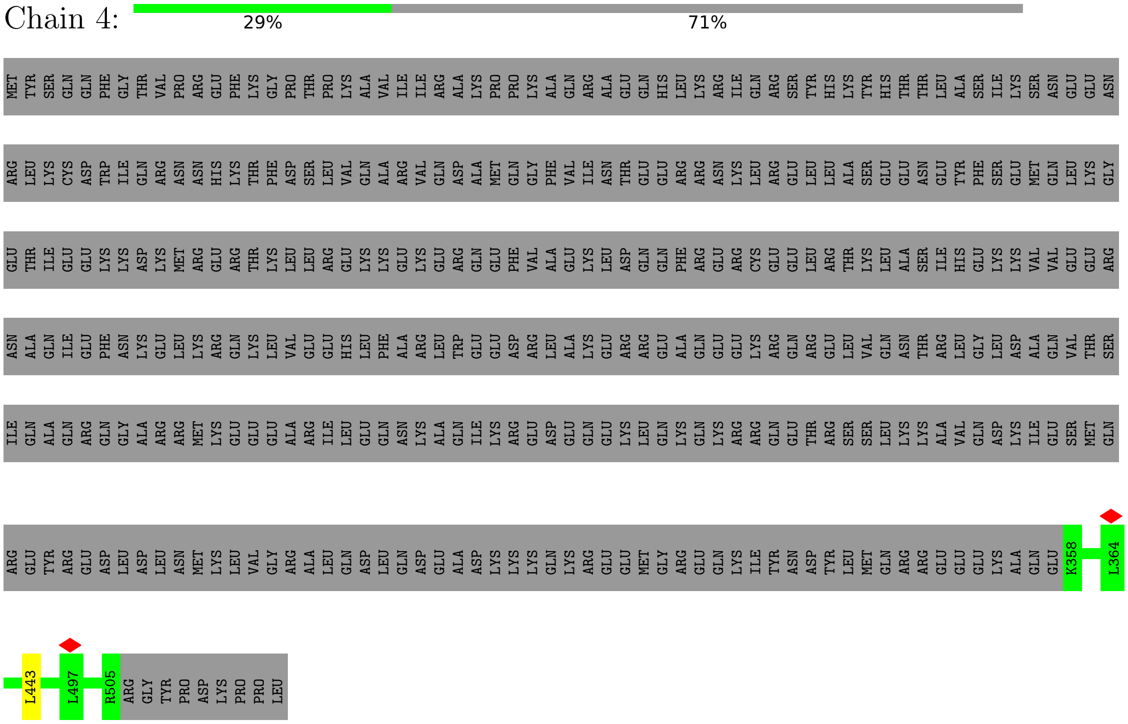
- Molecule 2: EF-hand domain-containing family member B



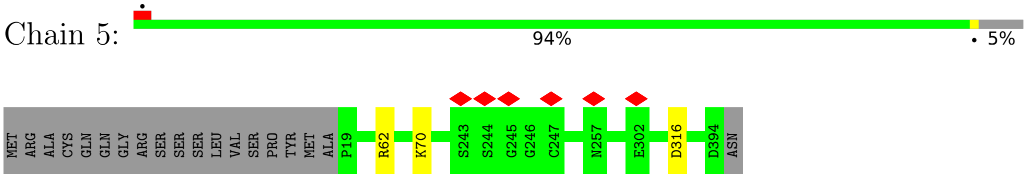
- Molecule 3: Cilia- and flagella-associated protein 53



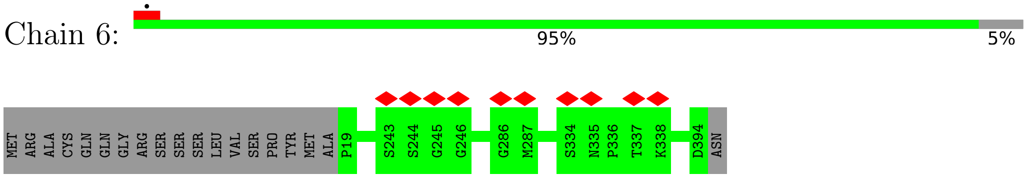
- Molecule 3: Cilia- and flagella-associated protein 53



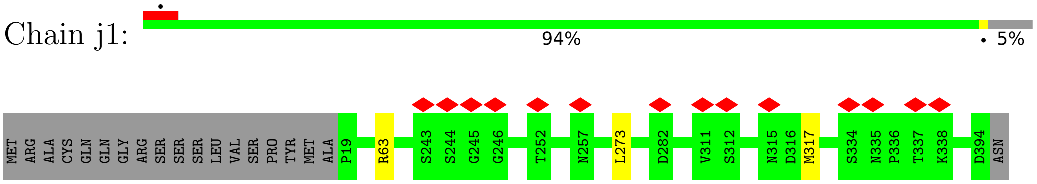
- Molecule 4: Nucleoside diphosphate kinase 7



- Molecule 4: Nucleoside diphosphate kinase 7

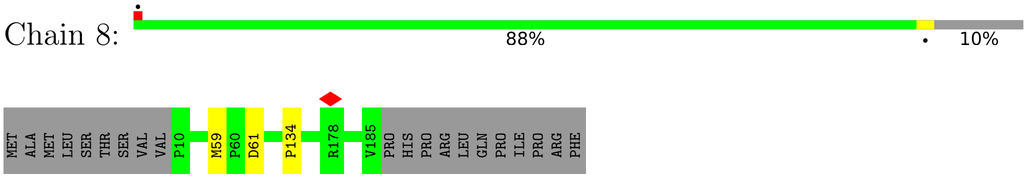


- Molecule 4: Nucleoside diphosphate kinase 7



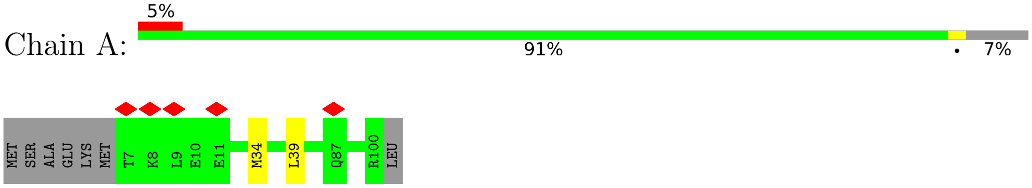
- Molecule 5: Cilia- and flagella-associated protein 107

Chain 8:



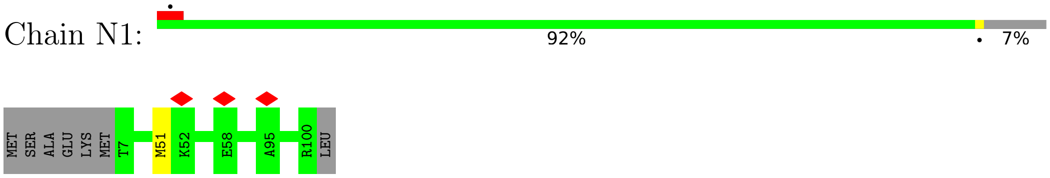
- Molecule 6: Cilia- and flagella-associated protein 141

Chain A:



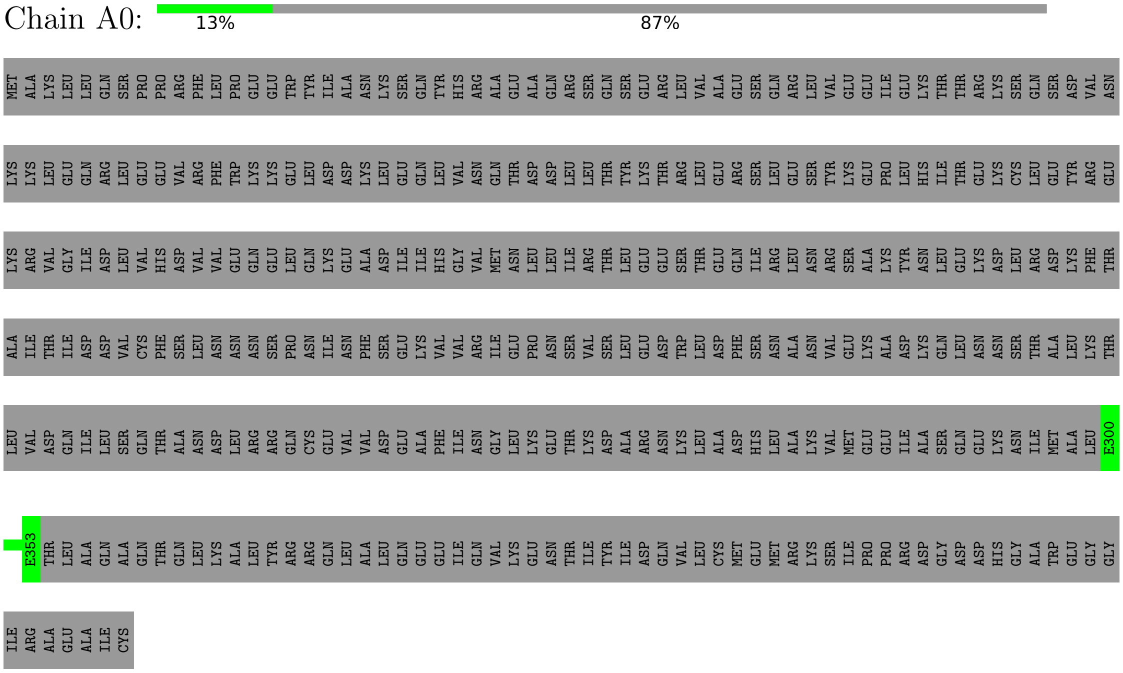
- Molecule 6: Cilia- and flagella-associated protein 141

Chain N1:



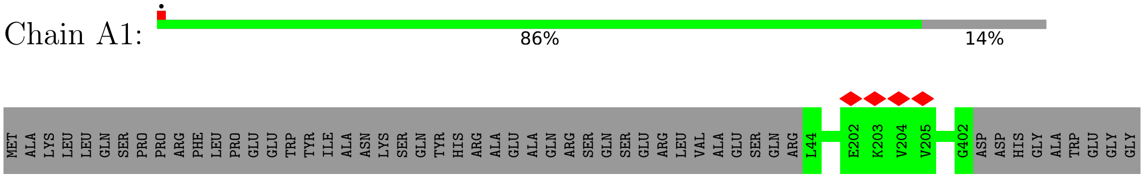
- Molecule 7: Tektin-1

Chain A0:

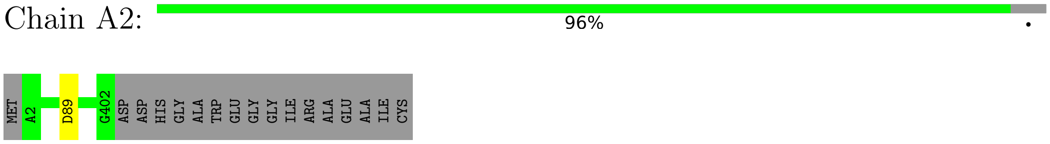


- Molecule 7: Tektin-1

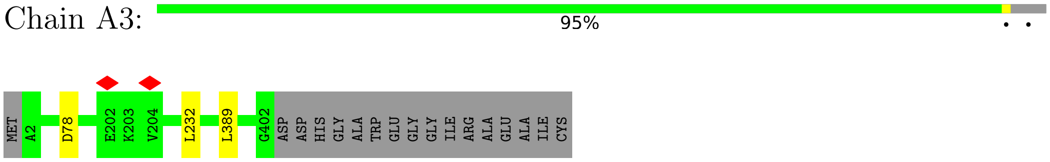
Chain A1:



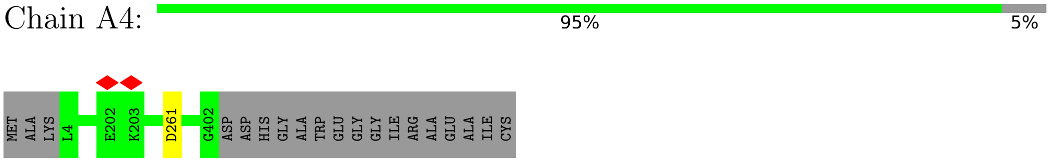
- Molecule 7: Tektin-1



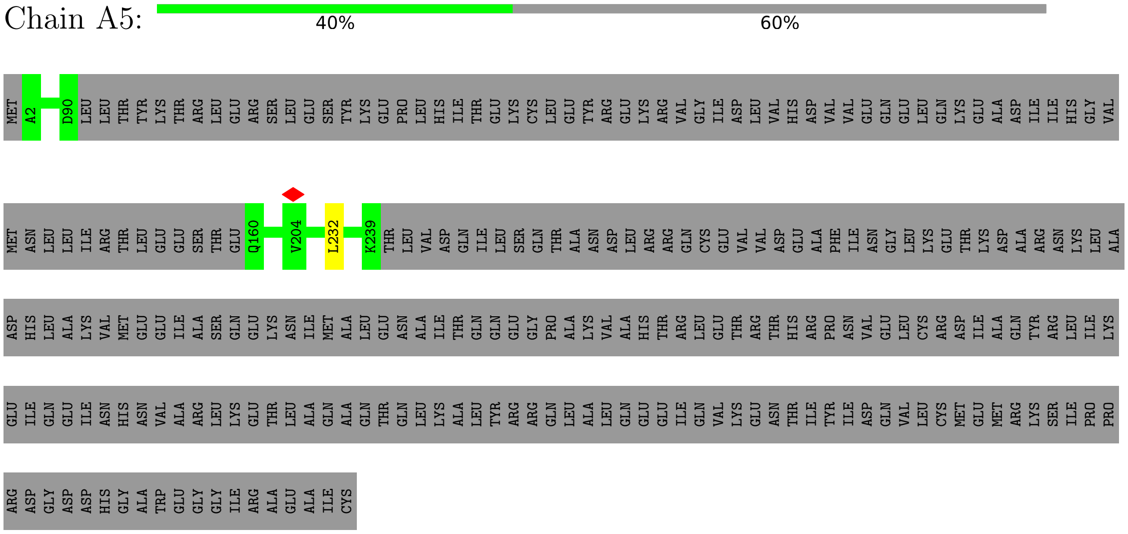
- Molecule 7: Tektin-1



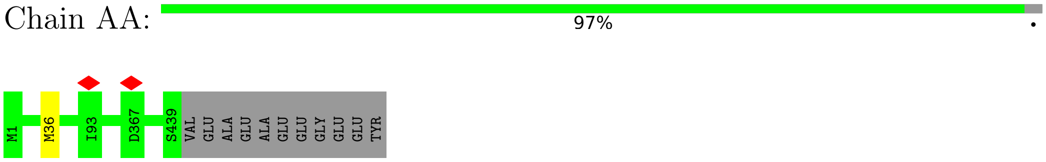
- Molecule 7: Tektin-1



- Molecule 7: Tektin-1

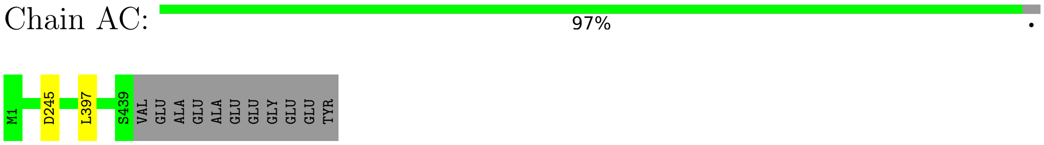


- Molecule 8: Tubulin alpha-3 chain



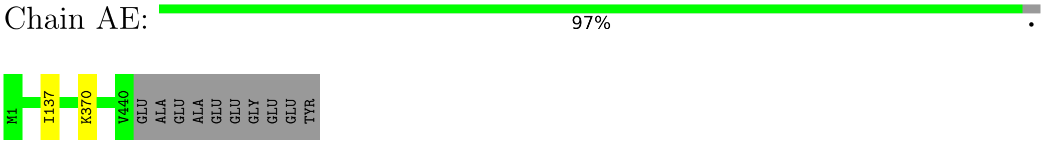
- Molecule 8: Tubulin alpha-3 chain

Chain AC:



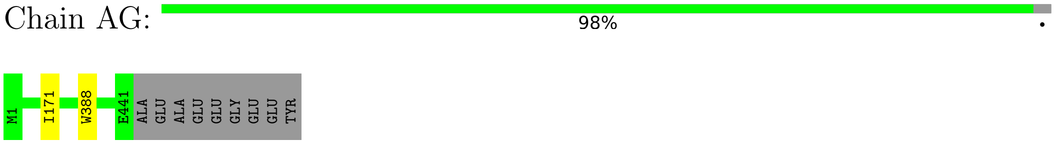
- Molecule 8: Tubulin alpha-3 chain

Chain AE:



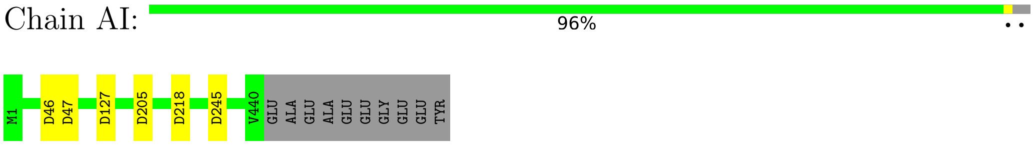
- Molecule 8: Tubulin alpha-3 chain

Chain AG:



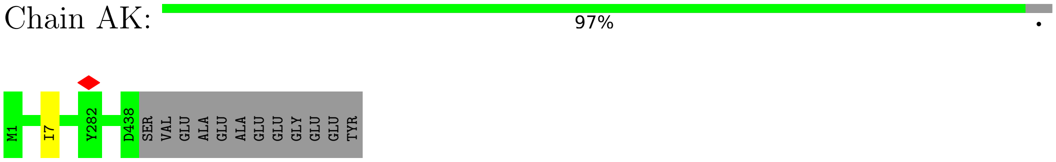
- Molecule 8: Tubulin alpha-3 chain

Chain AI:



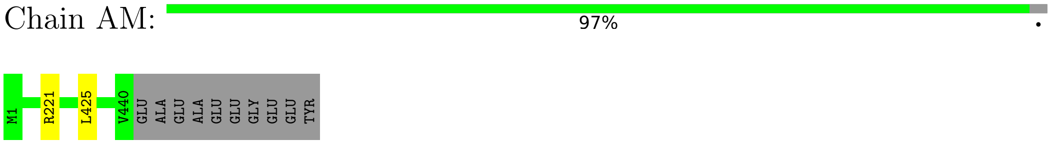
- Molecule 8: Tubulin alpha-3 chain

Chain AK:



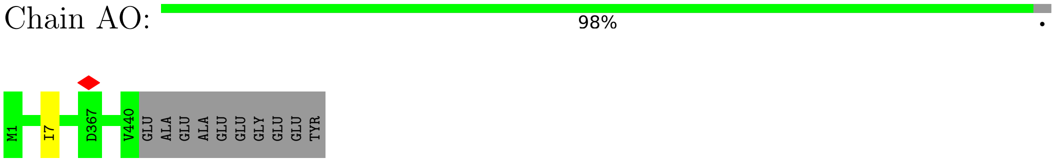
- Molecule 8: Tubulin alpha-3 chain

Chain AM:



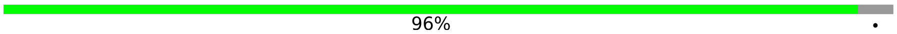
- Molecule 8: Tubulin alpha-3 chain

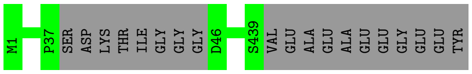
Chain AO:



- Molecule 8: Tubulin alpha-3 chain

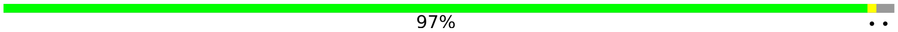
Chain BC:

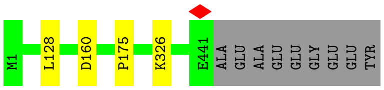




- Molecule 8: Tubulin alpha-3 chain

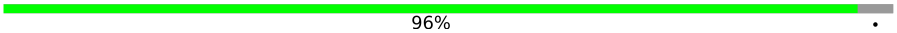
Chain BE:

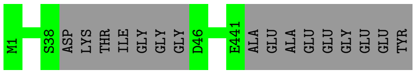




- Molecule 8: Tubulin alpha-3 chain

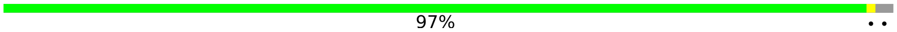
Chain BG:

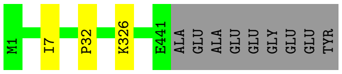




- Molecule 8: Tubulin alpha-3 chain

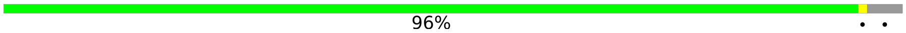
Chain BI:

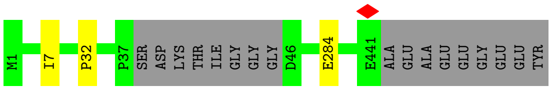




- Molecule 8: Tubulin alpha-3 chain

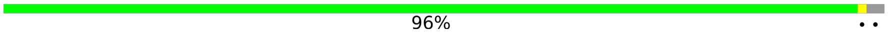
Chain BK:

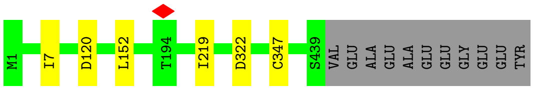




- Molecule 8: Tubulin alpha-3 chain

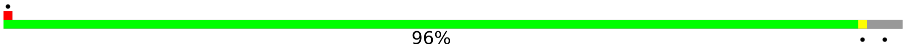
Chain BM:

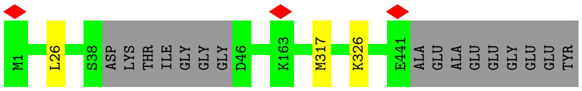




- Molecule 8: Tubulin alpha-3 chain

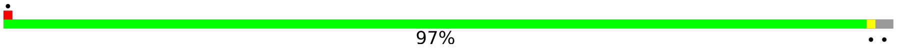
Chain BO:

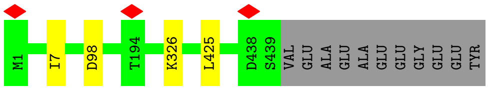




- Molecule 8: Tubulin alpha-3 chain

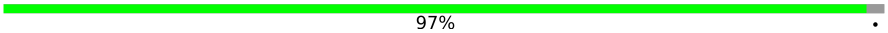
Chain CC:





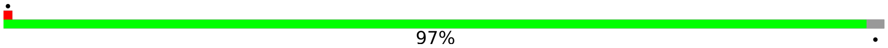
- Molecule 8: Tubulin alpha-3 chain

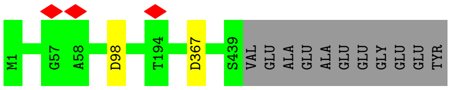
Chain CE:



- Molecule 8: Tubulin alpha-3 chain

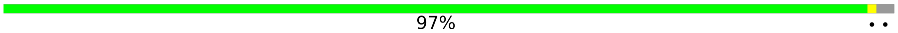
Chain CG:

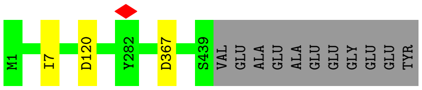




- Molecule 8: Tubulin alpha-3 chain

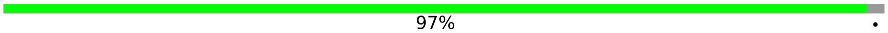
Chain CI:





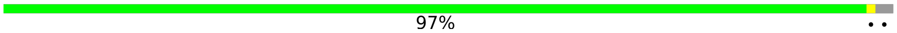
- Molecule 8: Tubulin alpha-3 chain

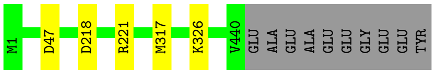
Chain CK:



- Molecule 8: Tubulin alpha-3 chain

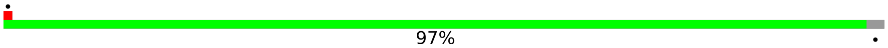
Chain CM:

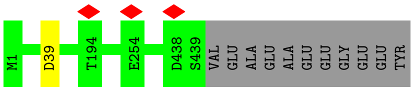




- Molecule 8: Tubulin alpha-3 chain

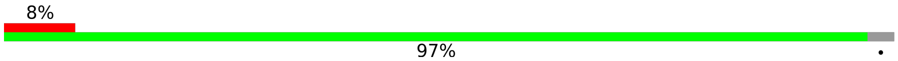
Chain CO:

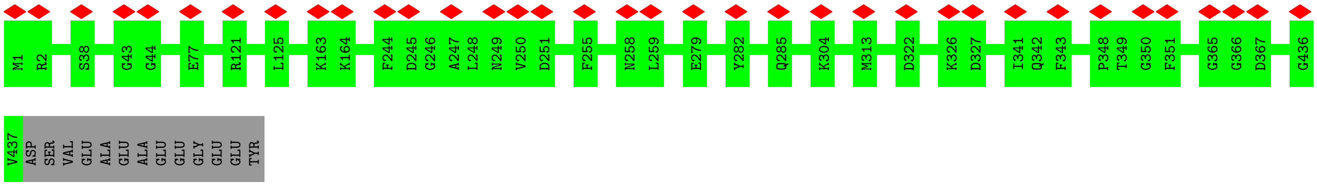




- Molecule 8: Tubulin alpha-3 chain

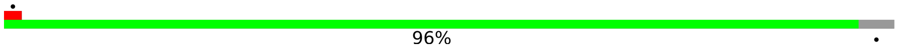
Chain CQ:

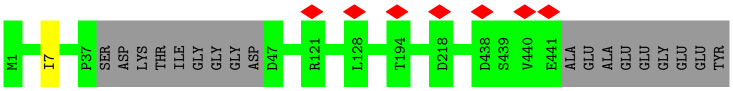




- Molecule 8: Tubulin alpha-3 chain

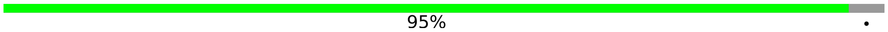
Chain DC:

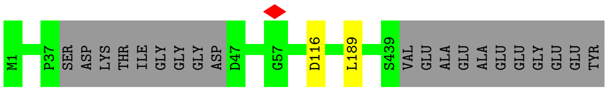




- Molecule 8: Tubulin alpha-3 chain

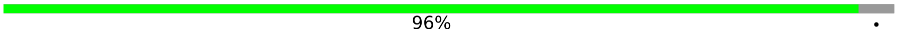
Chain DE:

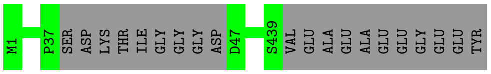




- Molecule 8: Tubulin alpha-3 chain

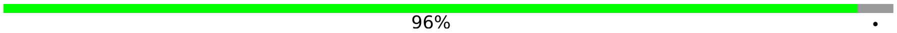
Chain DG:

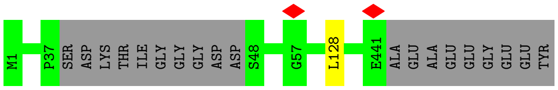




- Molecule 8: Tubulin alpha-3 chain

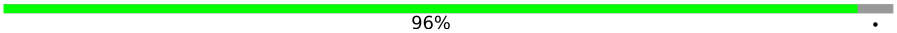
Chain DI:

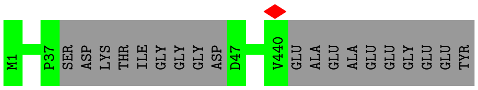




- Molecule 8: Tubulin alpha-3 chain

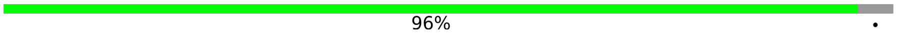
Chain DK:

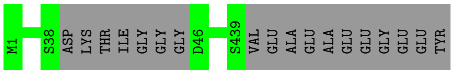




- Molecule 8: Tubulin alpha-3 chain

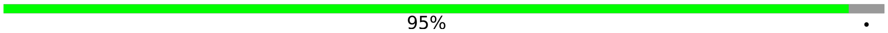
Chain DM:

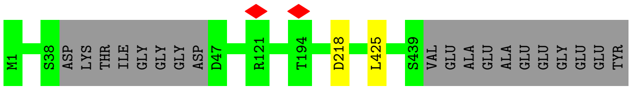




- Molecule 8: Tubulin alpha-3 chain

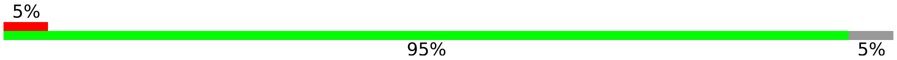
Chain DO:

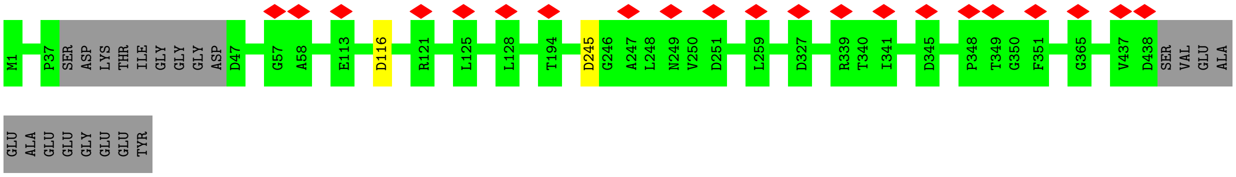




- Molecule 8: Tubulin alpha-3 chain

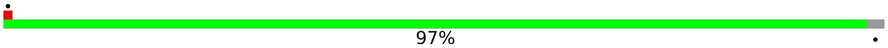
Chain DQ:

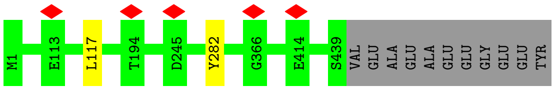




- Molecule 8: Tubulin alpha-3 chain

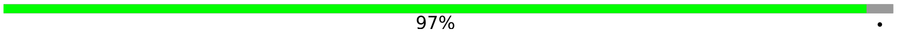
Chain EA:

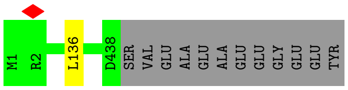




- Molecule 8: Tubulin alpha-3 chain

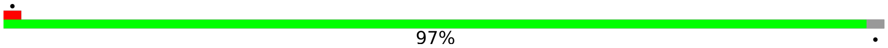
Chain EC:

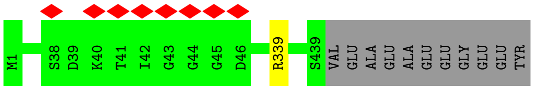




- Molecule 8: Tubulin alpha-3 chain

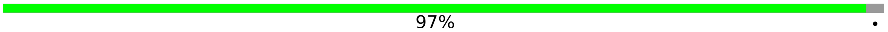
Chain EE:

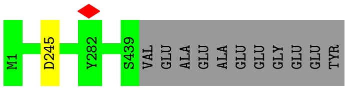




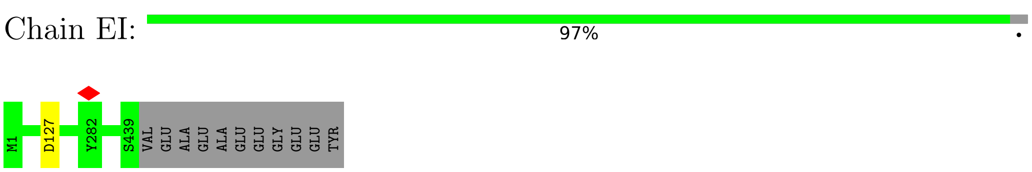
- Molecule 8: Tubulin alpha-3 chain

Chain EG:

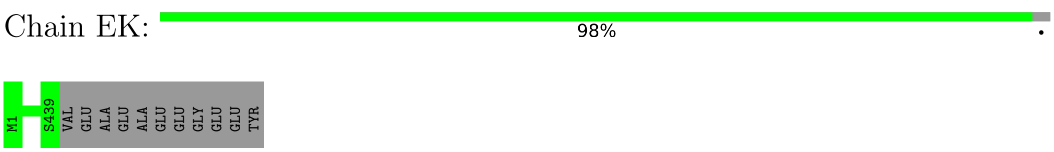




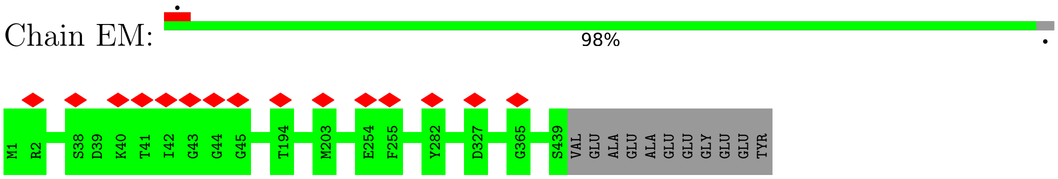
- Molecule 8: Tubulin alpha-3 chain



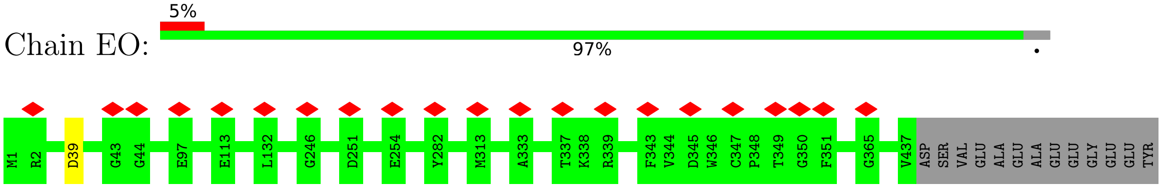
- Molecule 8: Tubulin alpha-3 chain



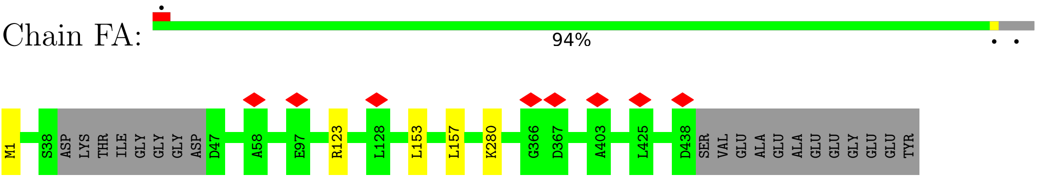
- Molecule 8: Tubulin alpha-3 chain



- Molecule 8: Tubulin alpha-3 chain



- Molecule 8: Tubulin alpha-3 chain



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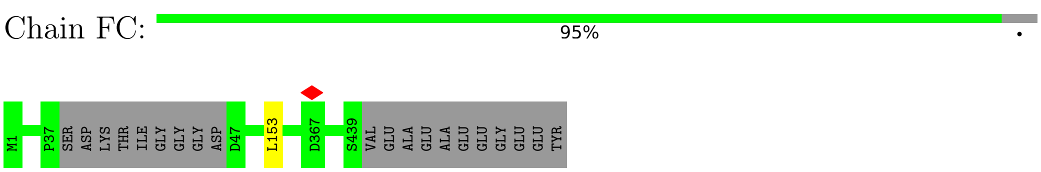

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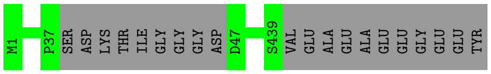
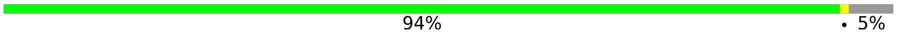
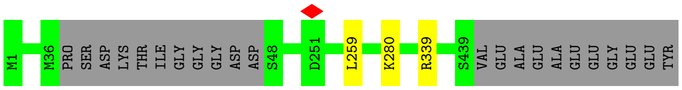


- Molecule 8: Tubulin alpha-3 chain

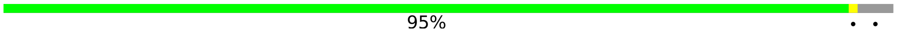
Chain FG:

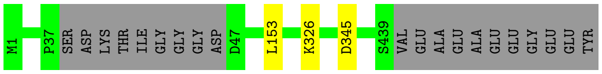




- Molecule 8: Tubulin alpha-3 chain

Chain FI:





- Molecule 8: Tubulin alpha-3 chain

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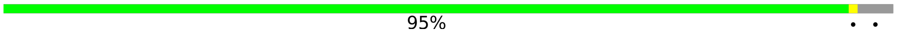
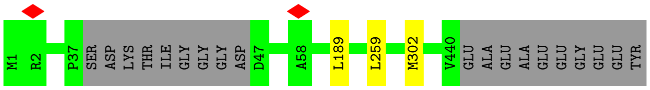
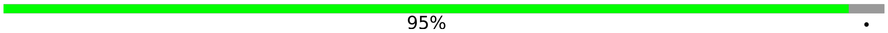
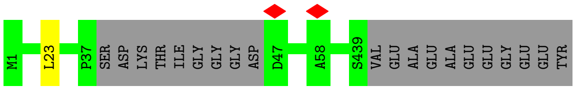




- Molecule 8: Tubulin alpha-3 chain

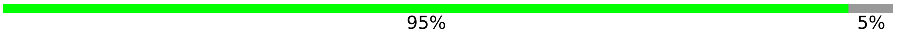
Chain FM:

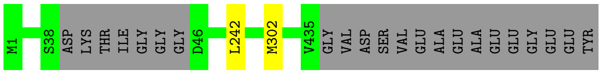




- Molecule 8: Tubulin alpha-3 chain

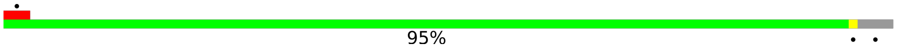
Chain FO:

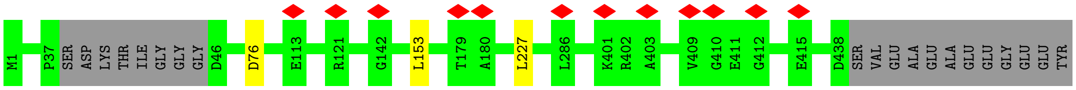




- Molecule 8: Tubulin alpha-3 chain

Chain GA:





- Molecule 8: Tubulin alpha-3 chain

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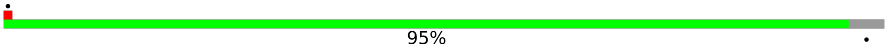
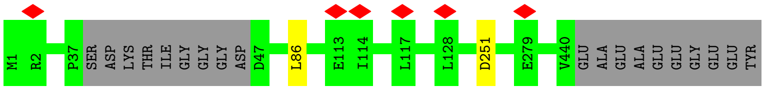
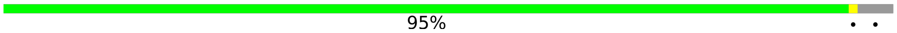
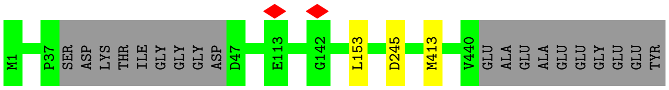




- Molecule 8: Tubulin alpha-3 chain

Chain GE:





- Molecule 8: Tubulin alpha-3 chain

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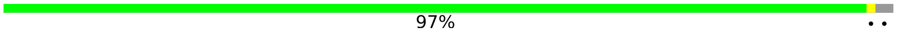
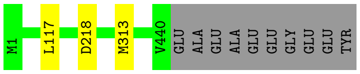
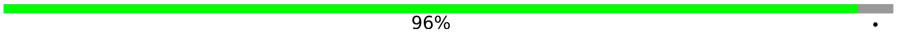
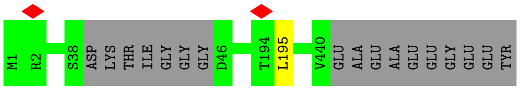




- Molecule 8: Tubulin alpha-3 chain

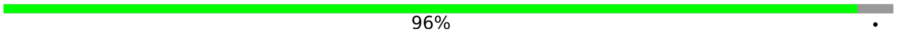
Chain GI:

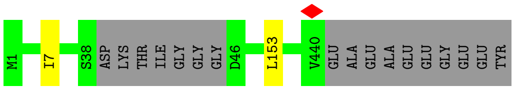




- Molecule 8: Tubulin alpha-3 chain

Chain GK:





- Molecule 8: Tubulin alpha-3 chain

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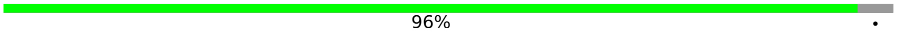
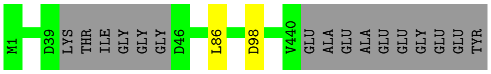
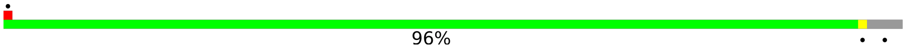
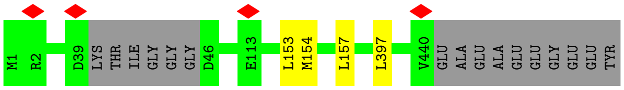




- Molecule 8: Tubulin alpha-3 chain

Chain GO:





- Molecule 8: Tubulin alpha-3 chain

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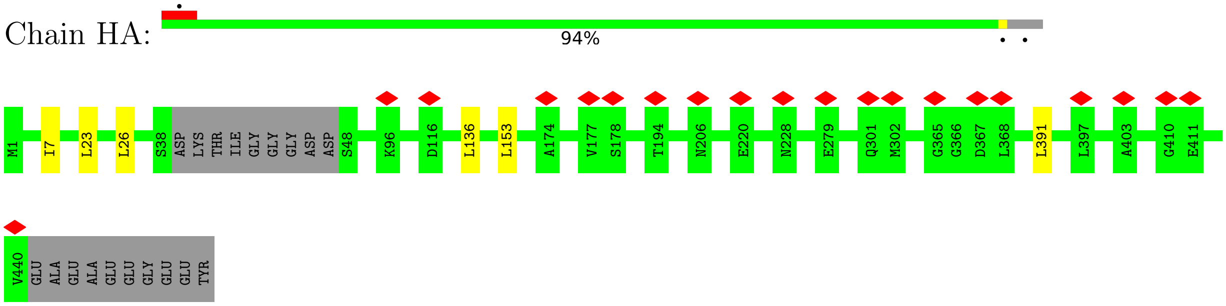
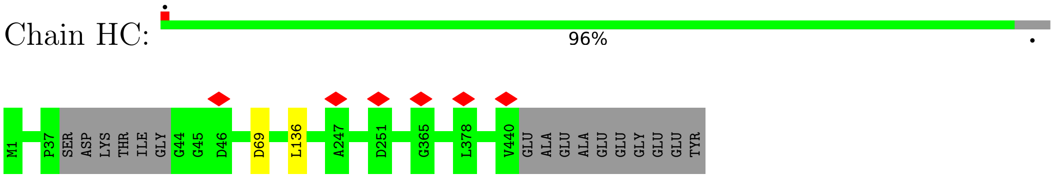


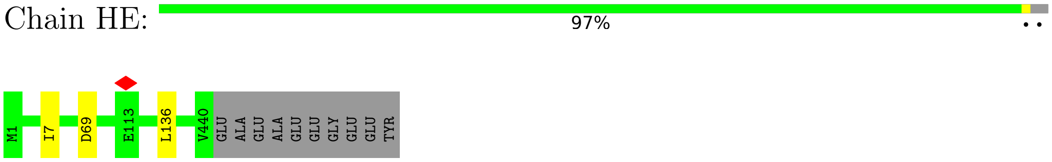
- Molecule 8: Tubulin alpha-3 chain

Chain HC:



- Molecule 8: Tubulin alpha-3 chain

Chain HE:



- Molecule 8: Tubulin alpha-3 chain

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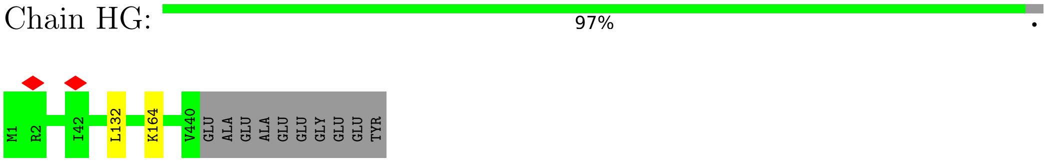

- Molecule 8: Tubulin alpha-3 chain

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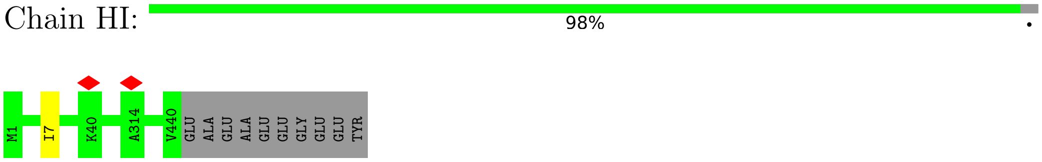

- Molecule 8: Tubulin alpha-3 chain

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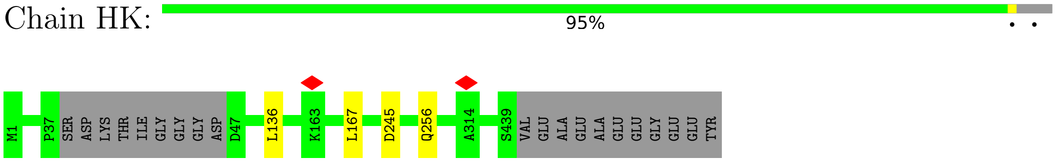

- Molecule 8: Tubulin alpha-3 chain

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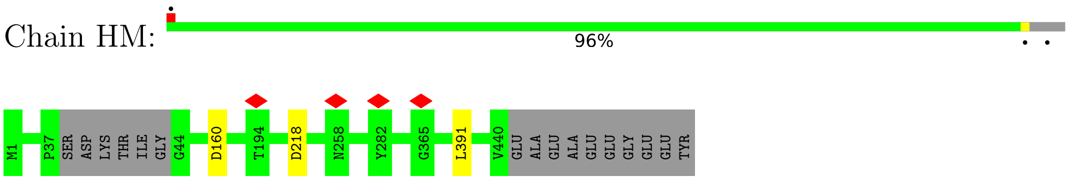
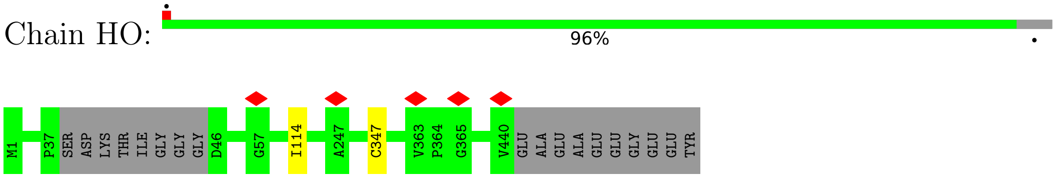


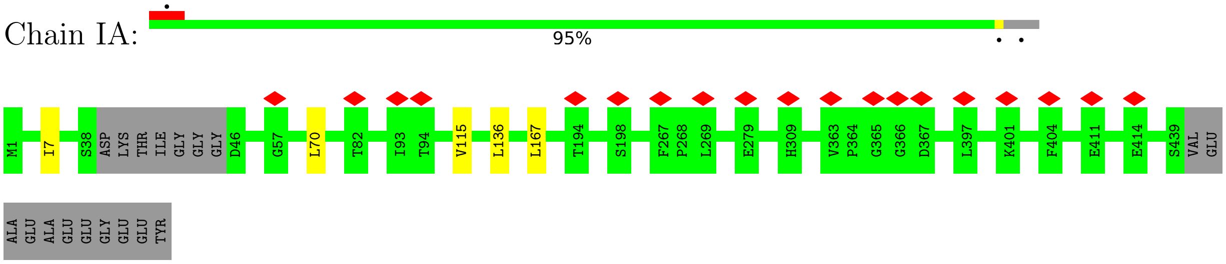
- Molecule 8: Tubulin alpha-3 chain

Chain HO:



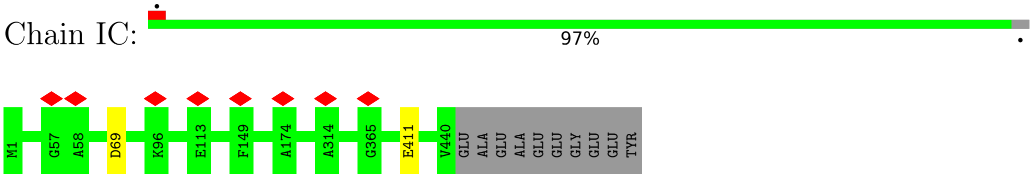
- Molecule 8: Tubulin alpha-3 chain

Chain IA:



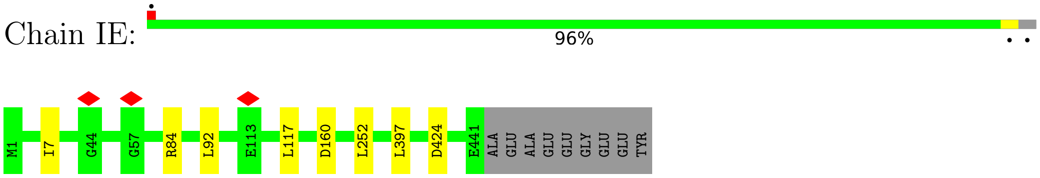
- Molecule 8: Tubulin alpha-3 chain

Chain IC:



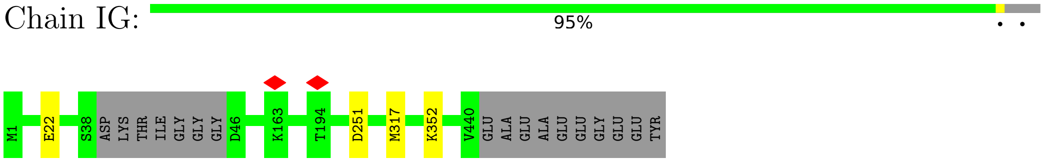
- Molecule 8: Tubulin alpha-3 chain

Chain IE:



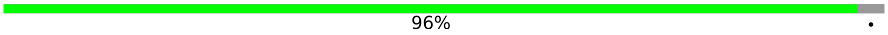
- Molecule 8: Tubulin alpha-3 chain

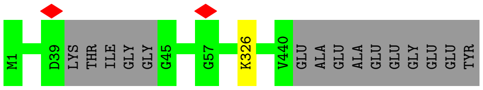
Chain IG:



- Molecule 8: Tubulin alpha-3 chain

Chain II:





- Molecule 8: Tubulin alpha-3 chain

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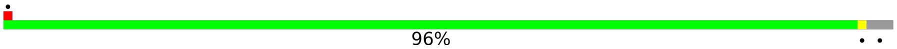
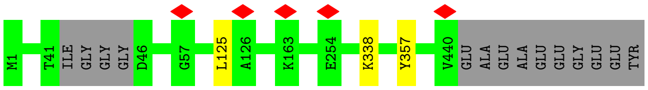
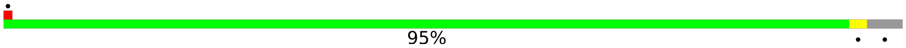
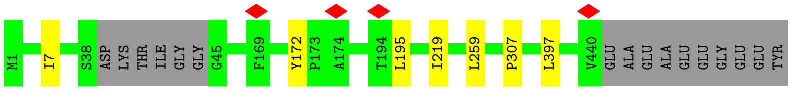




- Molecule 8: Tubulin alpha-3 chain

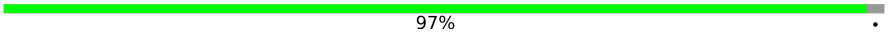
Chain IM:

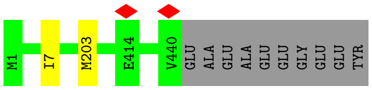




- Molecule 8: Tubulin alpha-3 chain

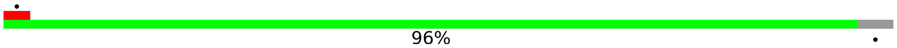
Chain IO:

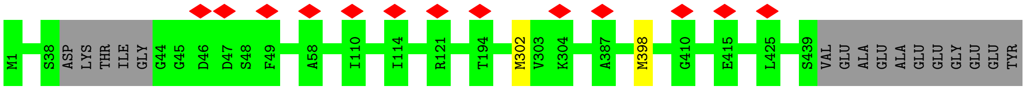




- Molecule 8: Tubulin alpha-3 chain

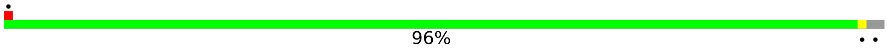
Chain JC:

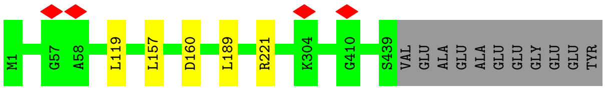




- Molecule 8: Tubulin alpha-3 chain

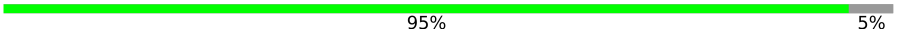
Chain JE:

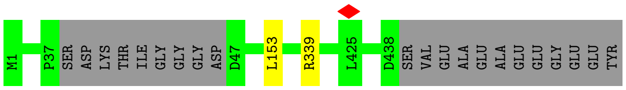




- Molecule 8: Tubulin alpha-3 chain

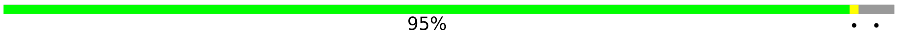
Chain JG:

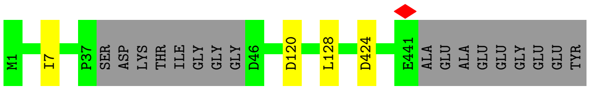




- Molecule 8: Tubulin alpha-3 chain

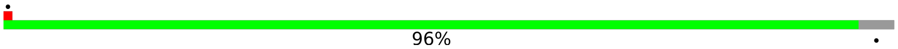
Chain JI:

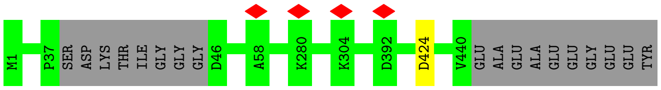




- Molecule 8: Tubulin alpha-3 chain

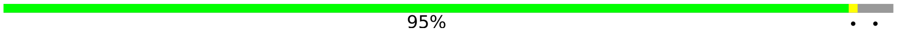
Chain JK:

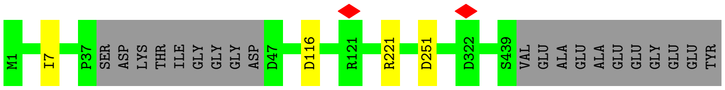




- Molecule 8: Tubulin alpha-3 chain

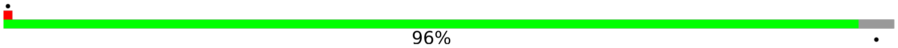
Chain JM:

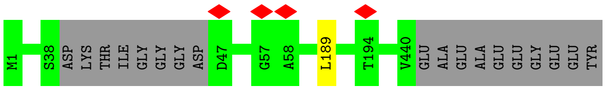




- Molecule 8: Tubulin alpha-3 chain

Chain JO:





- Molecule 8: Tubulin alpha-3 chain

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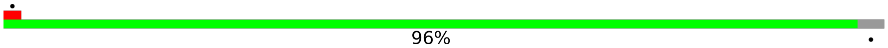
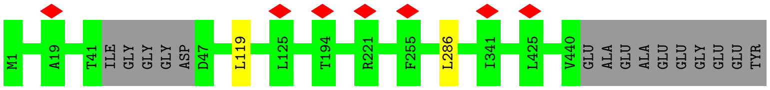
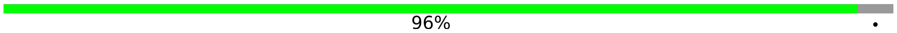
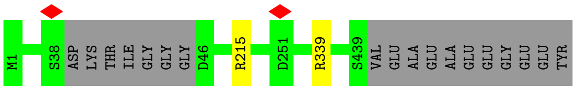




- Molecule 8: Tubulin alpha-3 chain

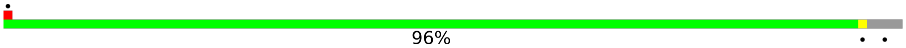
Chain KA:

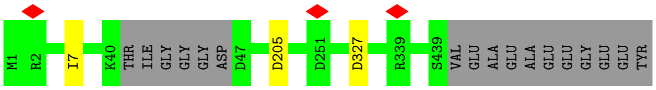




- Molecule 8: Tubulin alpha-3 chain

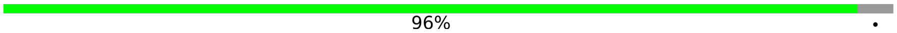
Chain KC:

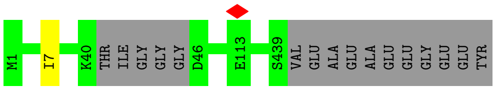




- Molecule 8: Tubulin alpha-3 chain

Chain KE:





- Molecule 8: Tubulin alpha-3 chain

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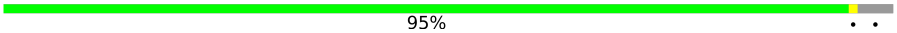
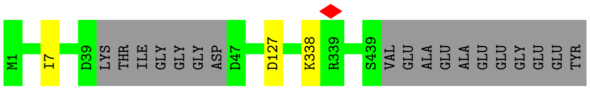
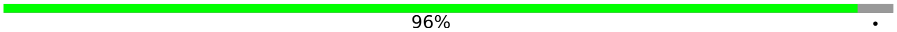
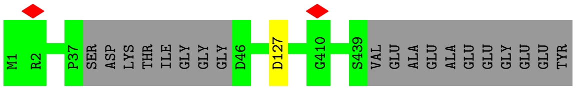




- Molecule 8: Tubulin alpha-3 chain

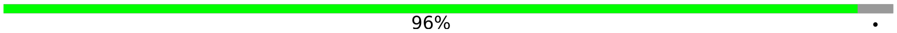
Chain KI:

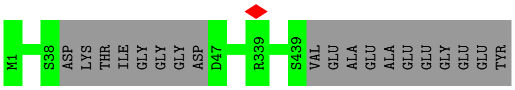




- Molecule 8: Tubulin alpha-3 chain

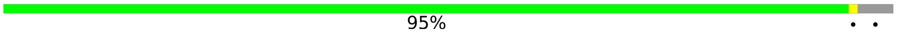
Chain KK:

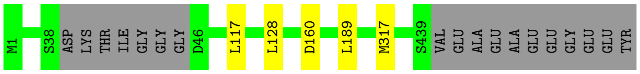




- Molecule 8: Tubulin alpha-3 chain

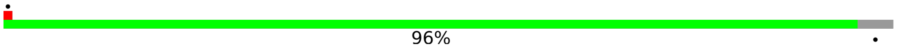
Chain KM:

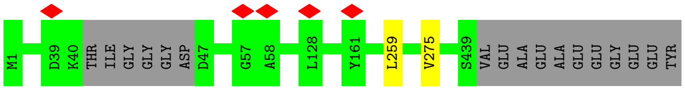




- Molecule 8: Tubulin alpha-3 chain

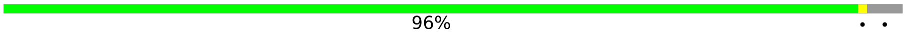
Chain KO:

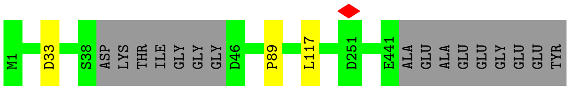




- Molecule 8: Tubulin alpha-3 chain

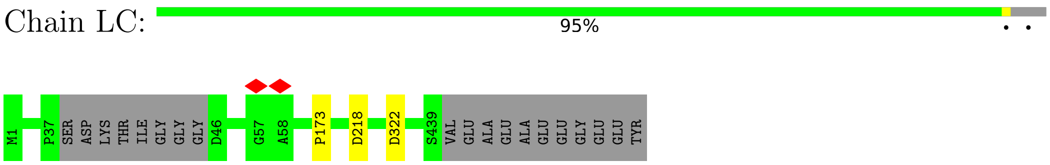
Chain LA:





- Molecule 8: Tubulin alpha-3 chain

Chain LC:



- Molecule 8: Tubulin alpha-3 chain

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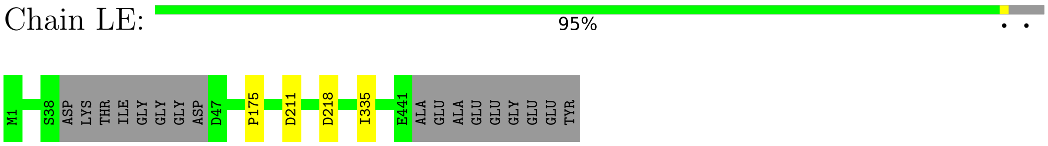
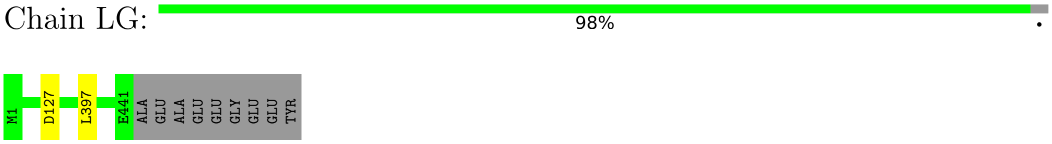


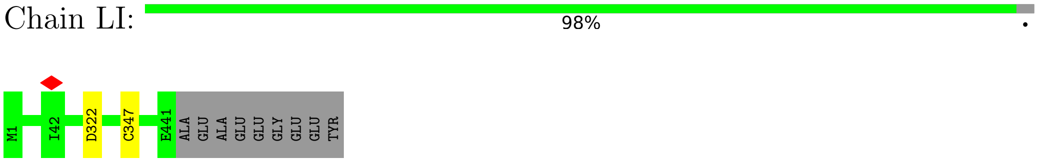
- Molecule 8: Tubulin alpha-3 chain

Chain LG:



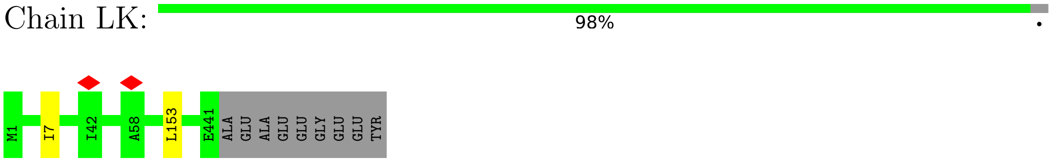
- Molecule 8: Tubulin alpha-3 chain

Chain LI:



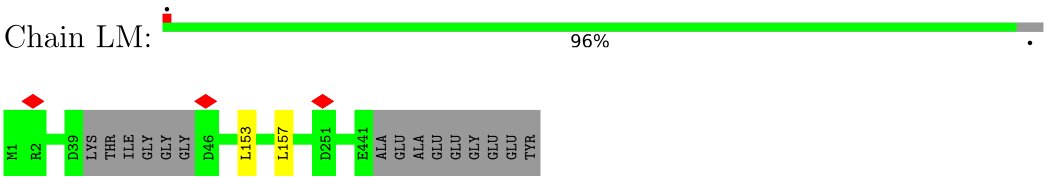
- Molecule 8: Tubulin alpha-3 chain

Chain LK:



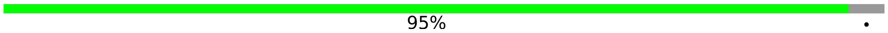
- Molecule 8: Tubulin alpha-3 chain

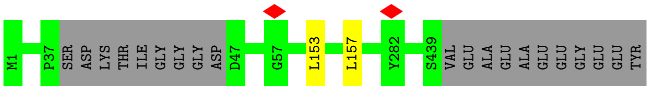
Chain LM:



- Molecule 8: Tubulin alpha-3 chain

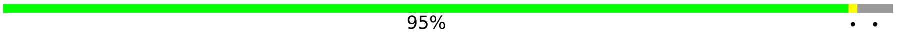
Chain LO:

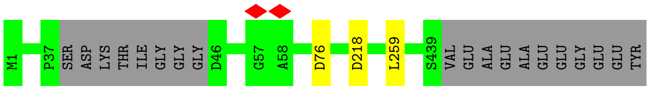




- Molecule 8: Tubulin alpha-3 chain

Chain MA:





- Molecule 8: Tubulin alpha-3 chain

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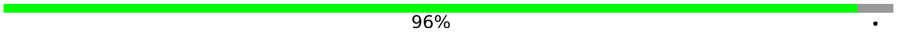
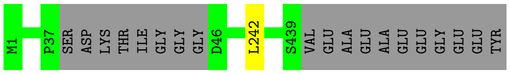
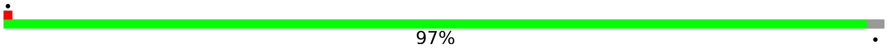
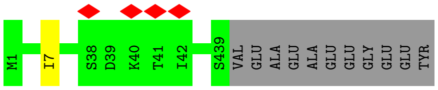




- Molecule 8: Tubulin alpha-3 chain

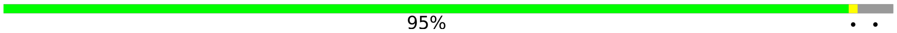
Chain ME:

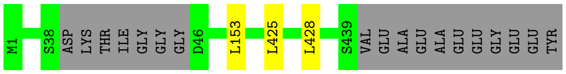




- Molecule 8: Tubulin alpha-3 chain

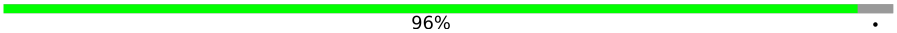
Chain MG:

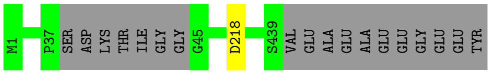




- Molecule 8: Tubulin alpha-3 chain

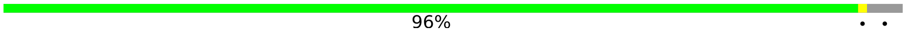
Chain MI:

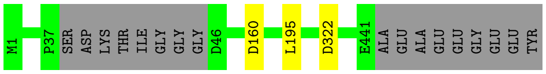




- Molecule 8: Tubulin alpha-3 chain

Chain MK:





- Molecule 8: Tubulin alpha-3 chain

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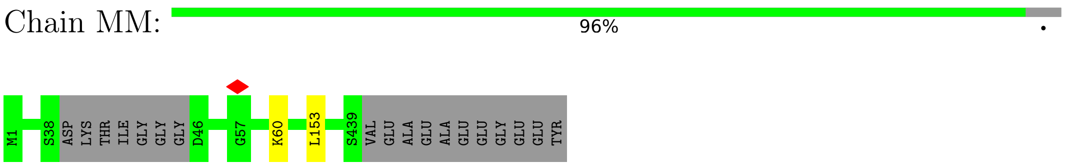

- Molecule 8: Tubulin alpha-3 chain

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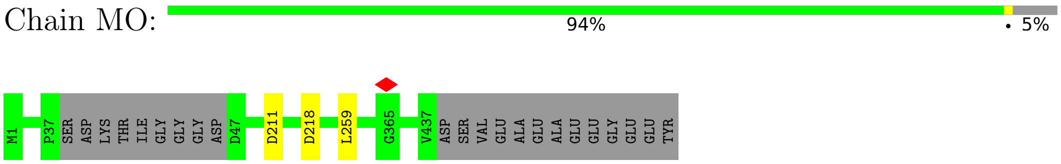

- Molecule 8: Tubulin alpha-3 chain

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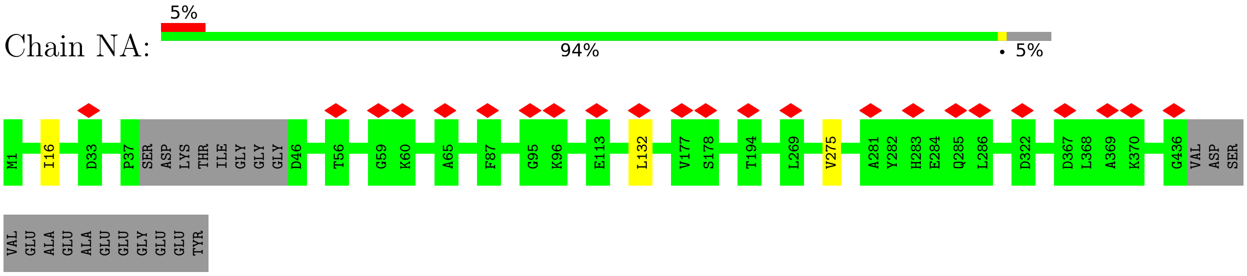
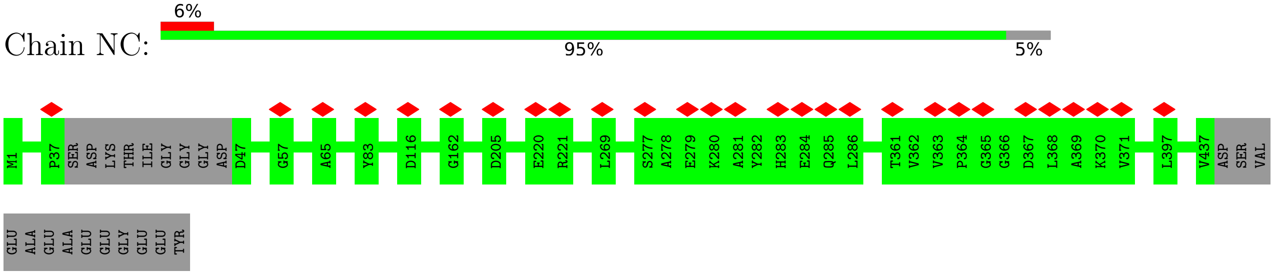


- Molecule 8: Tubulin alpha-3 chain

Chain NC:



- Molecule 8: Tubulin alpha-3 chain

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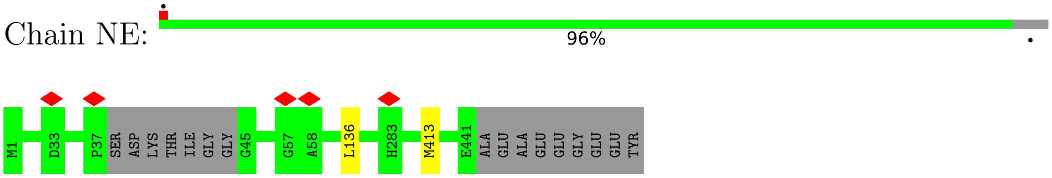

- Molecule 8: Tubulin alpha-3 chain

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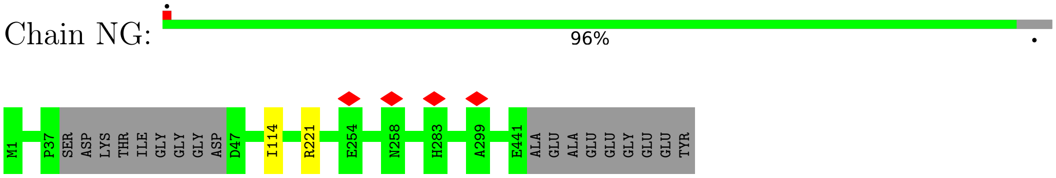
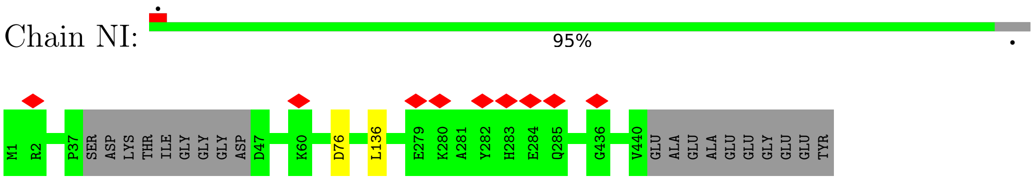


- Molecule 8: Tubulin alpha-3 chain



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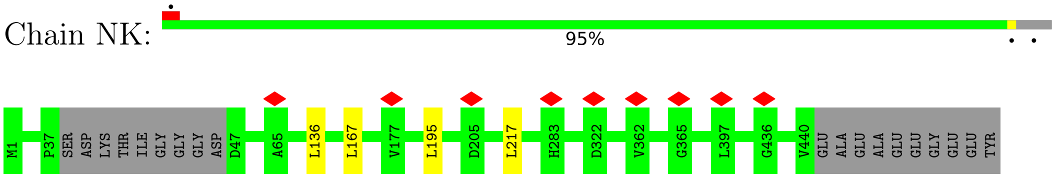
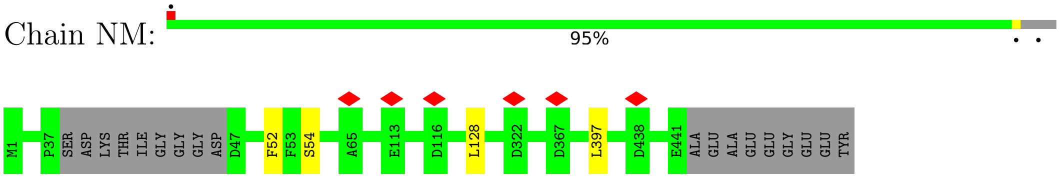


- Molecule 8: Tubulin alpha-3 chain



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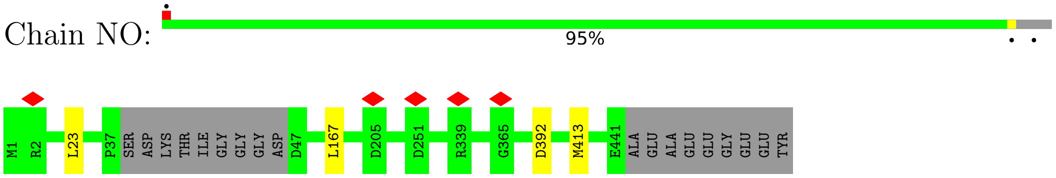
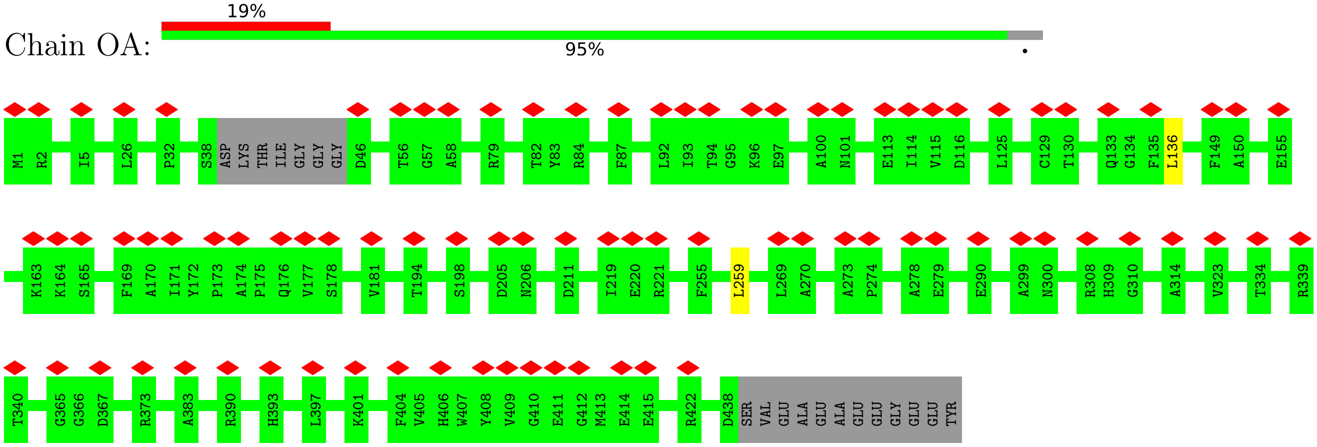


- Molecule 8: Tubulin alpha-3 chain



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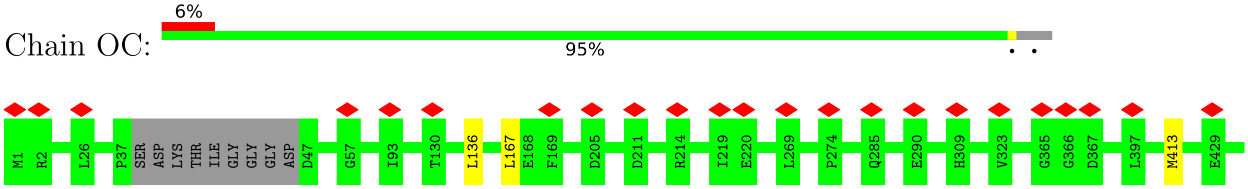

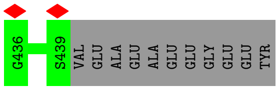

- Molecule 8: Tubulin alpha-3 chain

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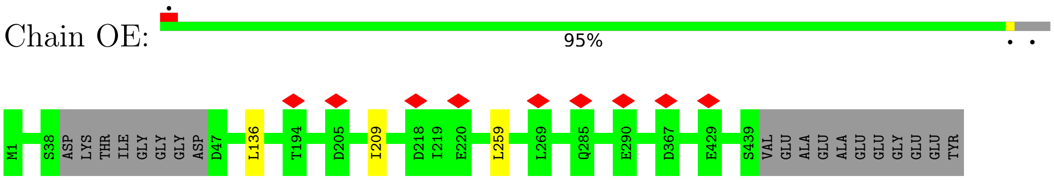

- Molecule 8: Tubulin alpha-3 chain

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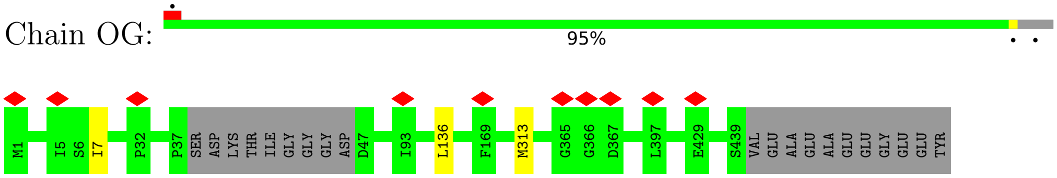

- Molecule 8: Tubulin alpha-3 chain

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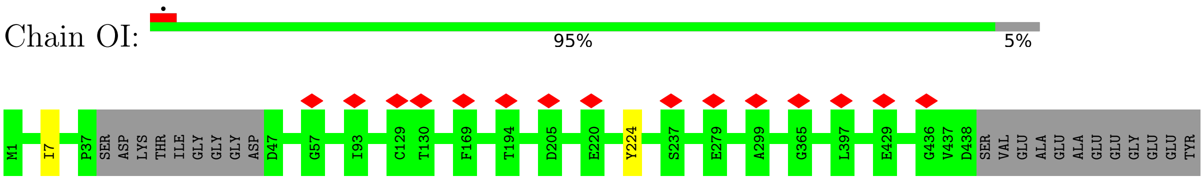

- Molecule 8: Tubulin alpha-3 chain

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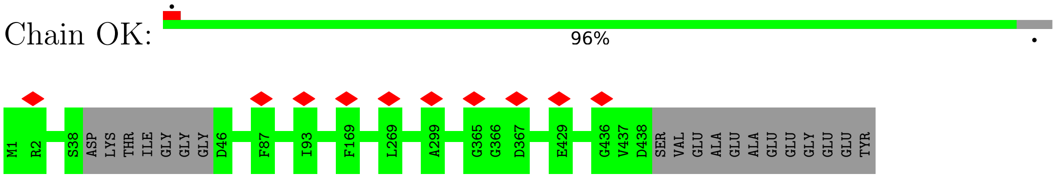

- Molecule 8: Tubulin alpha-3 chain

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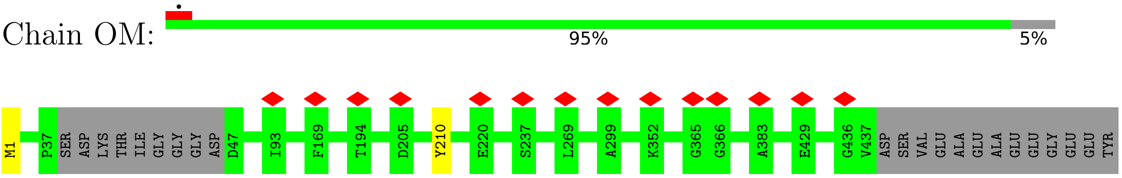

- Molecule 8: Tubulin alpha-3 chain

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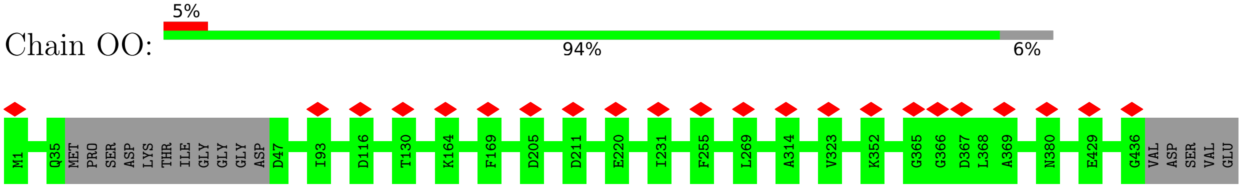

- Molecule 8: Tubulin alpha-3 chain

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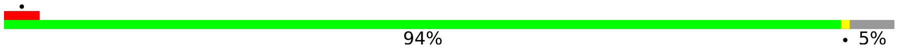

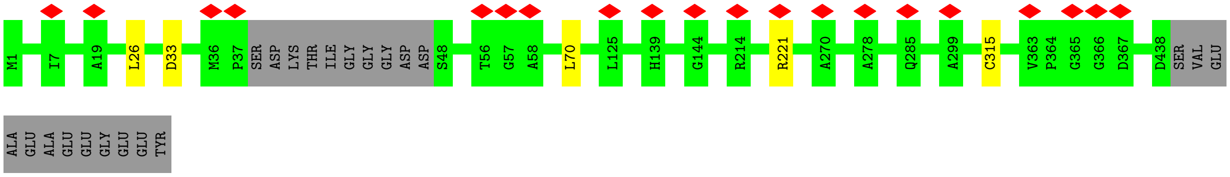

- Molecule 8: Tubulin alpha-3 chain

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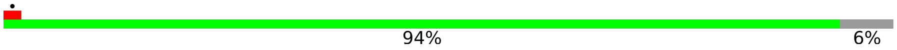

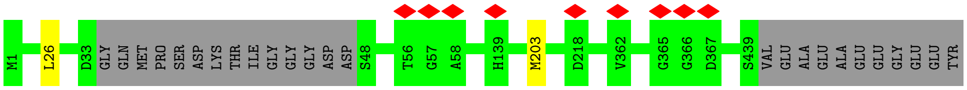

- Molecule 8: Tubulin alpha-3 chain

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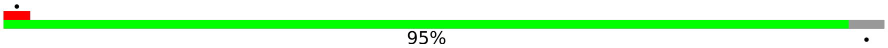
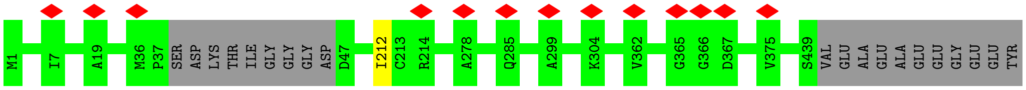
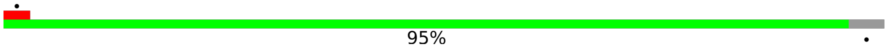
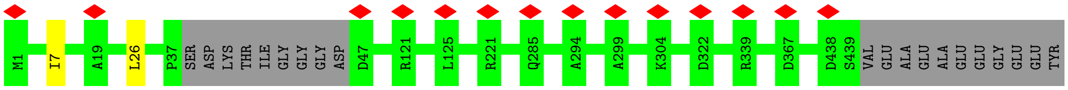




- Molecule 8: Tubulin alpha-3 chain

Chain PI:





- Molecule 8: Tubulin alpha-3 chain

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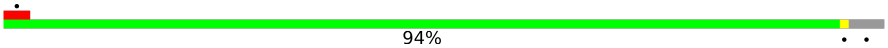

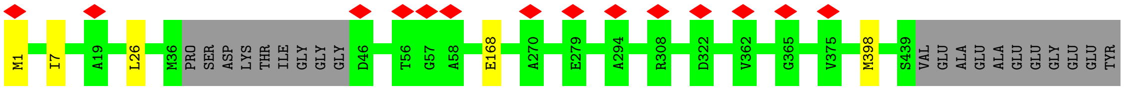

- Molecule 8: Tubulin alpha-3 chain

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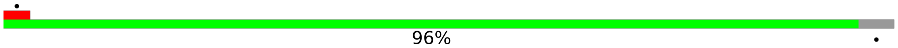

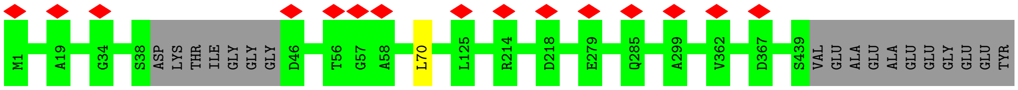

- Molecule 8: Tubulin alpha-3 chain

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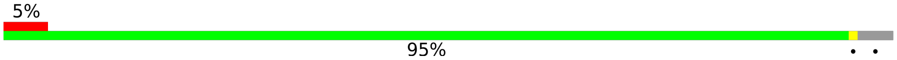
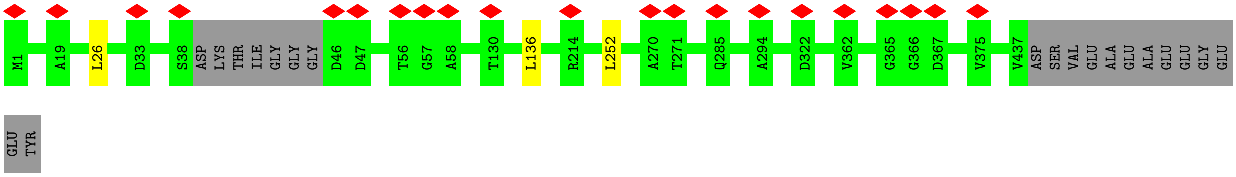
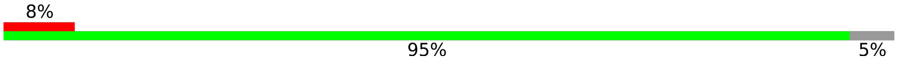
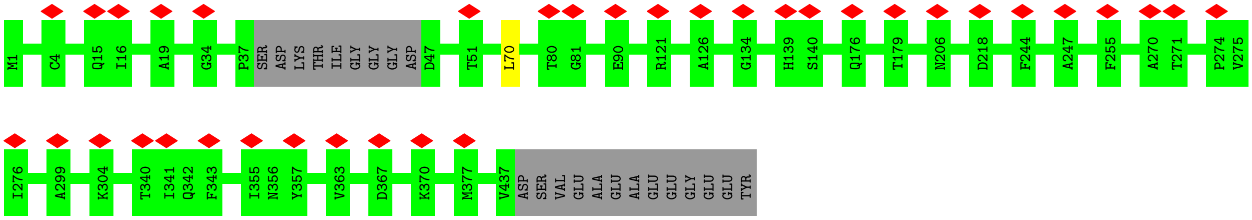




- Molecule 8: Tubulin alpha-3 chain

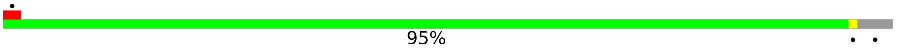
Chain QC:

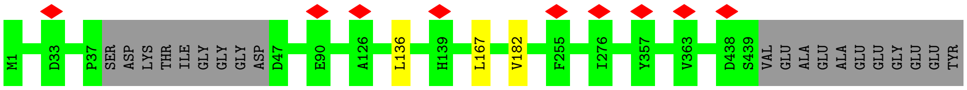




- Molecule 8: Tubulin alpha-3 chain

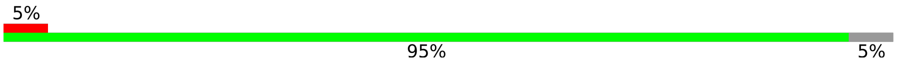
Chain QE:

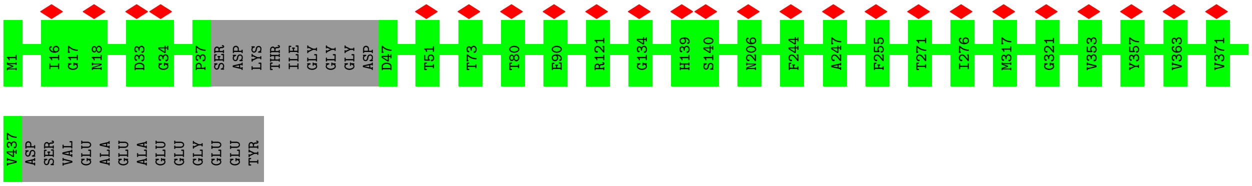




- Molecule 8: Tubulin alpha-3 chain

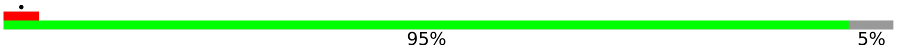
Chain QG:

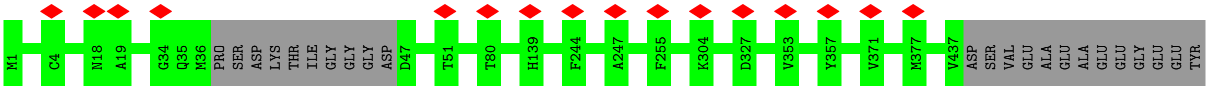




- Molecule 8: Tubulin alpha-3 chain

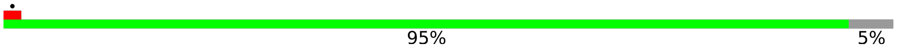
Chain QI:

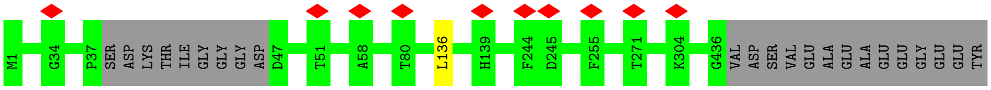




- Molecule 8: Tubulin alpha-3 chain

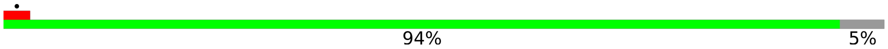
Chain QK:

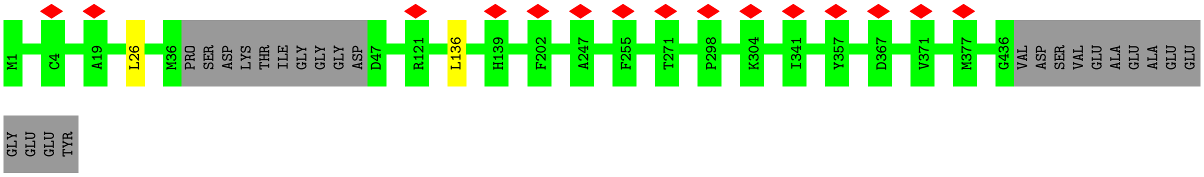




- Molecule 8: Tubulin alpha-3 chain

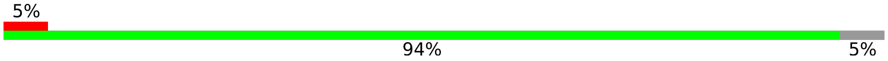
Chain QM:

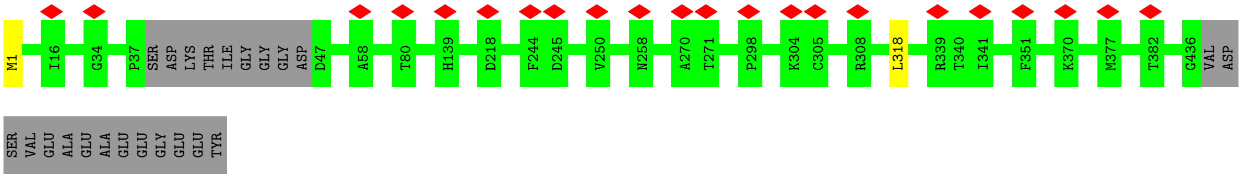




- Molecule 8: Tubulin alpha-3 chain

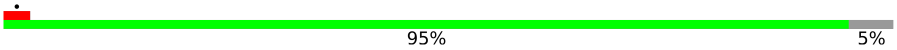
Chain QO:

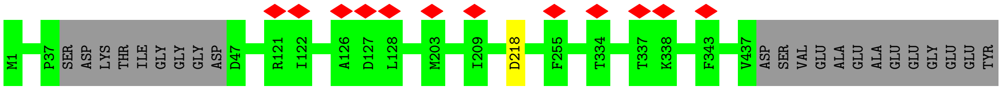




- Molecule 8: Tubulin alpha-3 chain

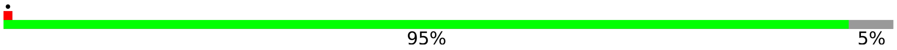
Chain RC:

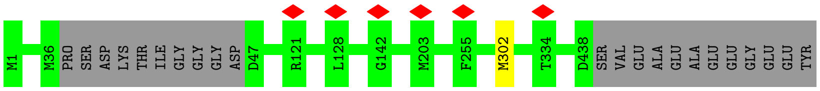




- Molecule 8: Tubulin alpha-3 chain

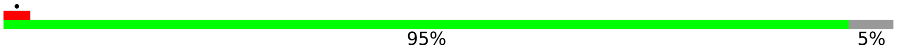
Chain RE:

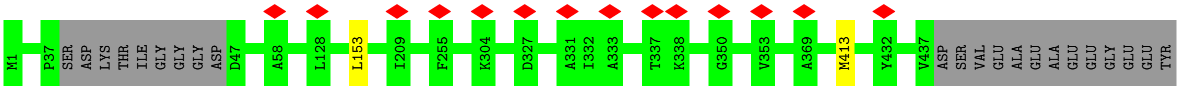




- Molecule 8: Tubulin alpha-3 chain

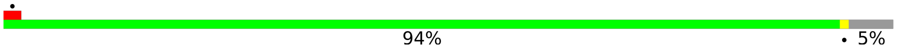
Chain RG:

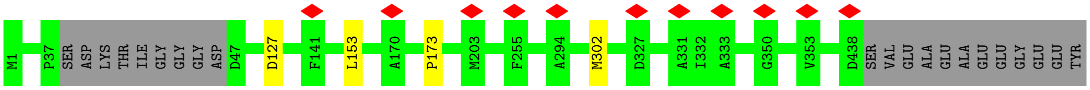




- Molecule 8: Tubulin alpha-3 chain

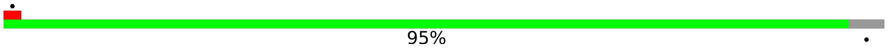
Chain RI:

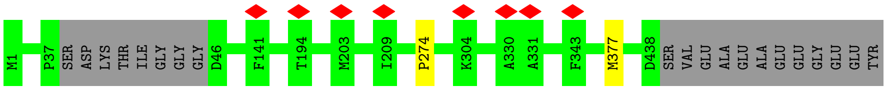




- Molecule 8: Tubulin alpha-3 chain

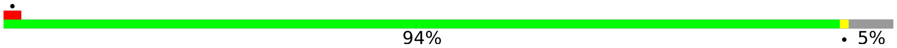
Chain RK:

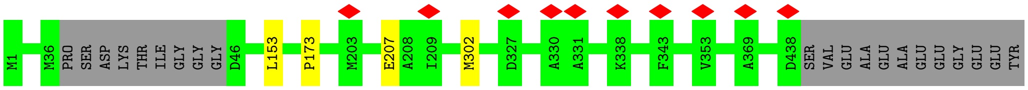




- Molecule 8: Tubulin alpha-3 chain

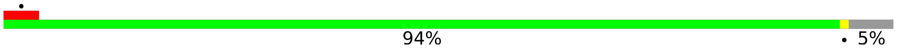
Chain RM:

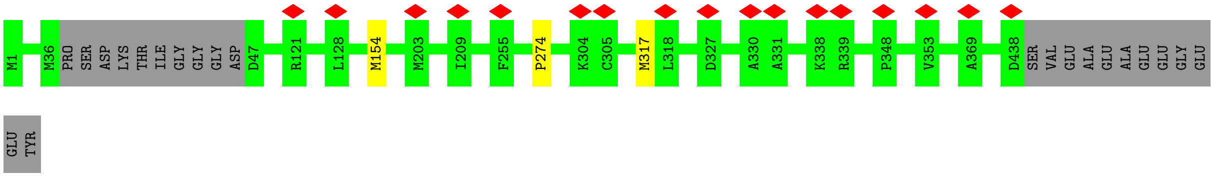




- Molecule 8: Tubulin alpha-3 chain

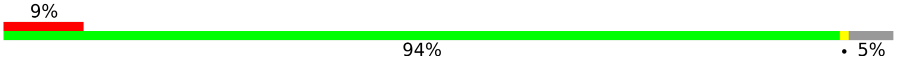
Chain RO:

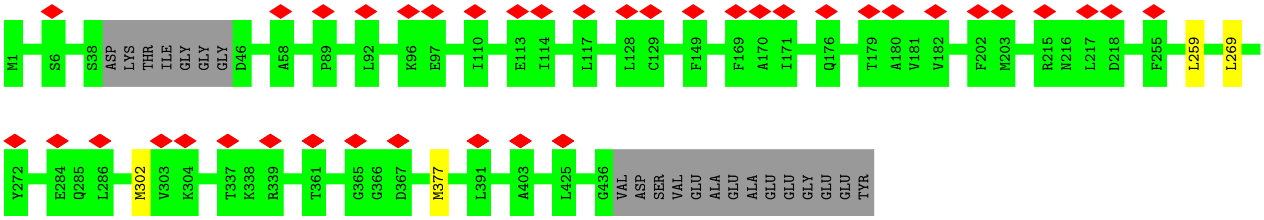




- Molecule 8: Tubulin alpha-3 chain

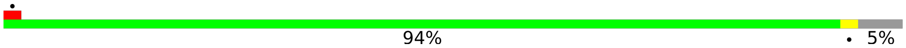
Chain SA:

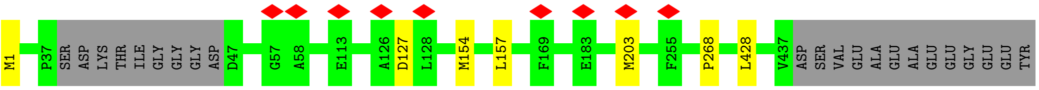




- Molecule 8: Tubulin alpha-3 chain

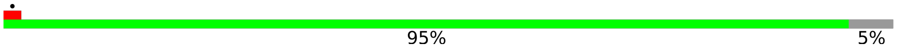
Chain SC:

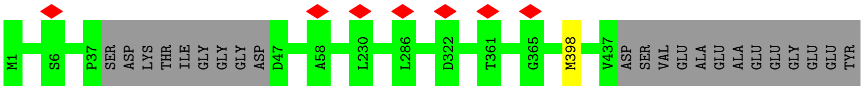




- Molecule 8: Tubulin alpha-3 chain

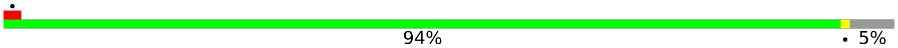
Chain SE:

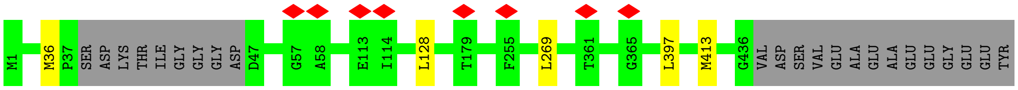




- Molecule 8: Tubulin alpha-3 chain

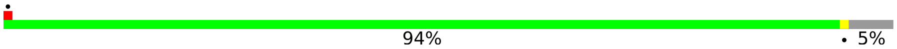
Chain SG:





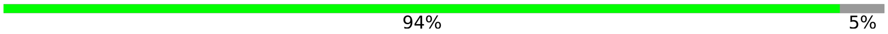
- Molecule 8: Tubulin alpha-3 chain

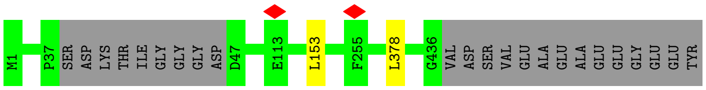
Chain SI:



- Molecule 8: Tubulin alpha-3 chain

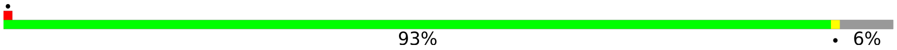
Chain SK:

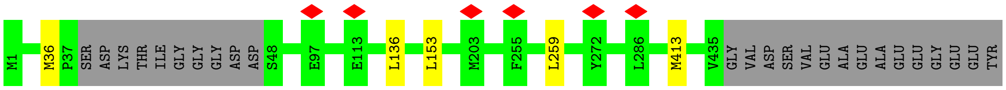




- Molecule 8: Tubulin alpha-3 chain

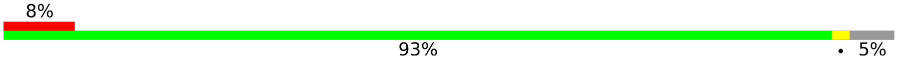
Chain SM:

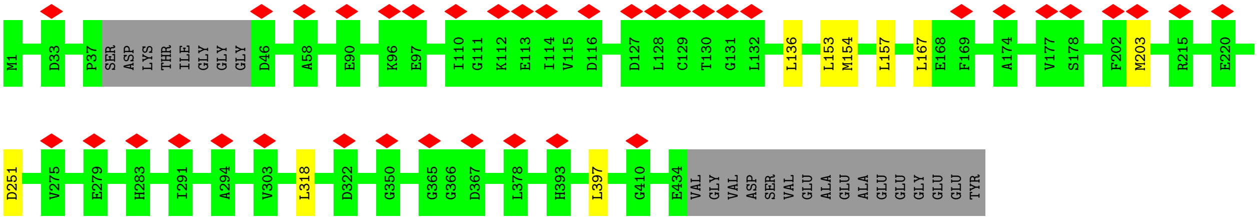




- Molecule 8: Tubulin alpha-3 chain

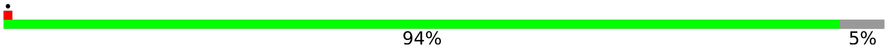
Chain TA:

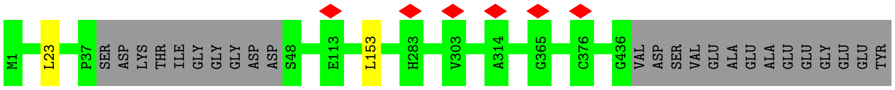




- Molecule 8: Tubulin alpha-3 chain

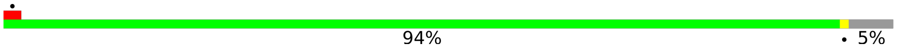
Chain TC:

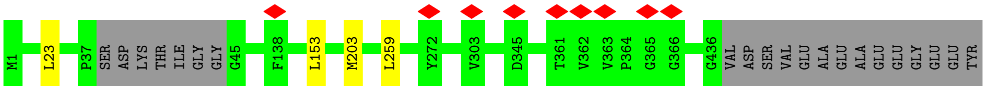




- Molecule 8: Tubulin alpha-3 chain

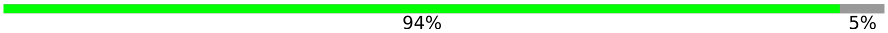
Chain TE:

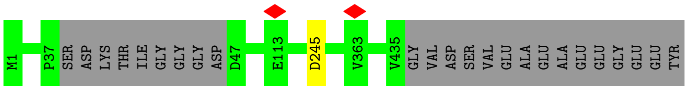




- Molecule 8: Tubulin alpha-3 chain

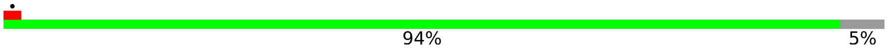
Chain TG:

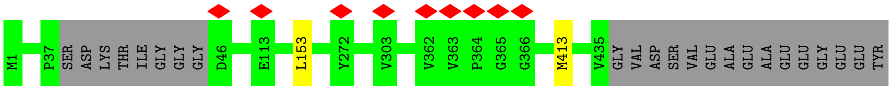




- Molecule 8: Tubulin alpha-3 chain

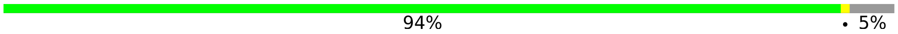
Chain TI:

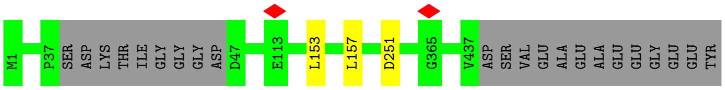




- Molecule 8: Tubulin alpha-3 chain

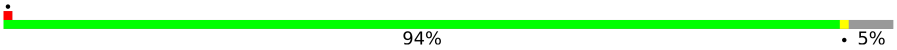
Chain TK:

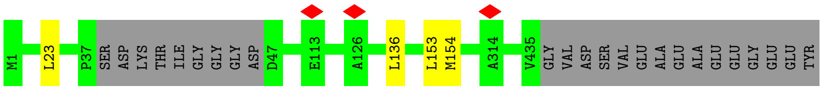




- Molecule 8: Tubulin alpha-3 chain

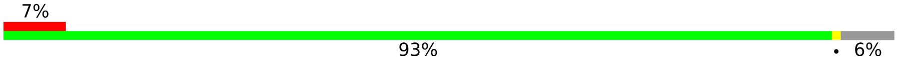
Chain TM:

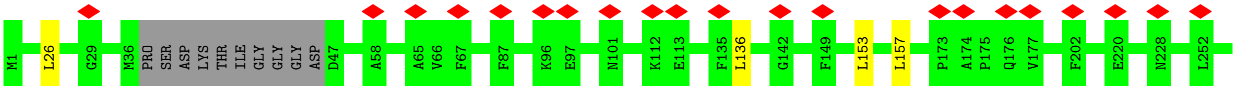


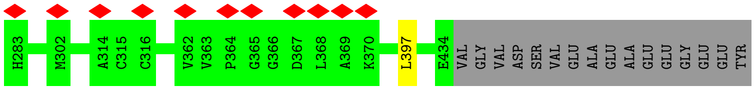


- Molecule 8: Tubulin alpha-3 chain

Chain UA:

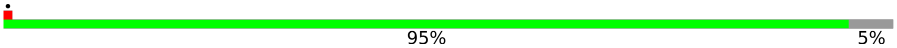


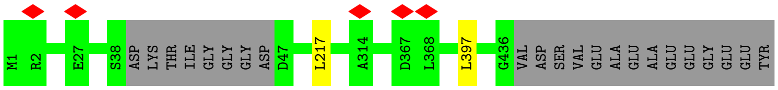




- Molecule 8: Tubulin alpha-3 chain

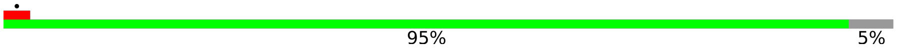
Chain UC:

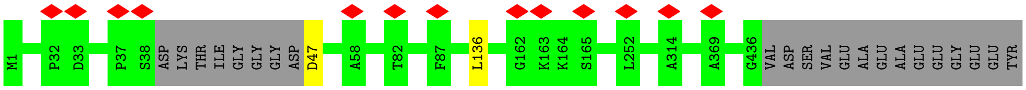




- Molecule 8: Tubulin alpha-3 chain

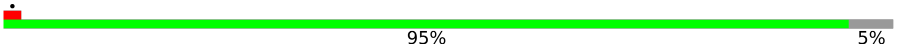
Chain UE:

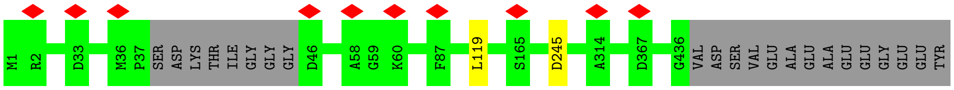




- Molecule 8: Tubulin alpha-3 chain

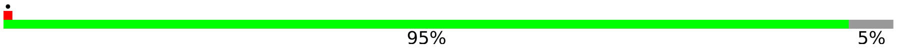
Chain UG:

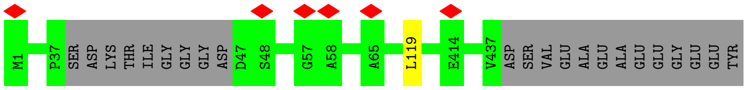




- Molecule 8: Tubulin alpha-3 chain

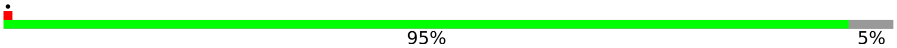
Chain UI:

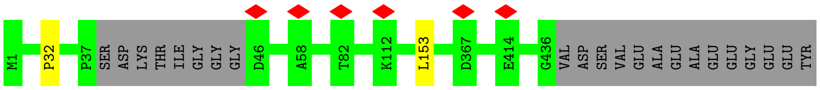




- Molecule 8: Tubulin alpha-3 chain

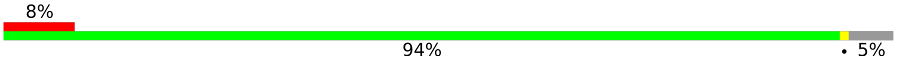
Chain UK:

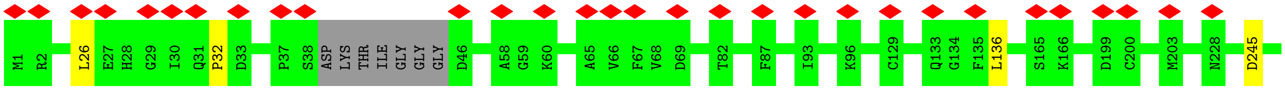


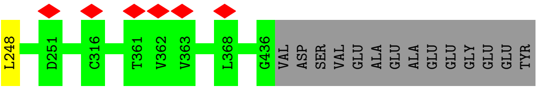


- Molecule 8: Tubulin alpha-3 chain

Chain UM:

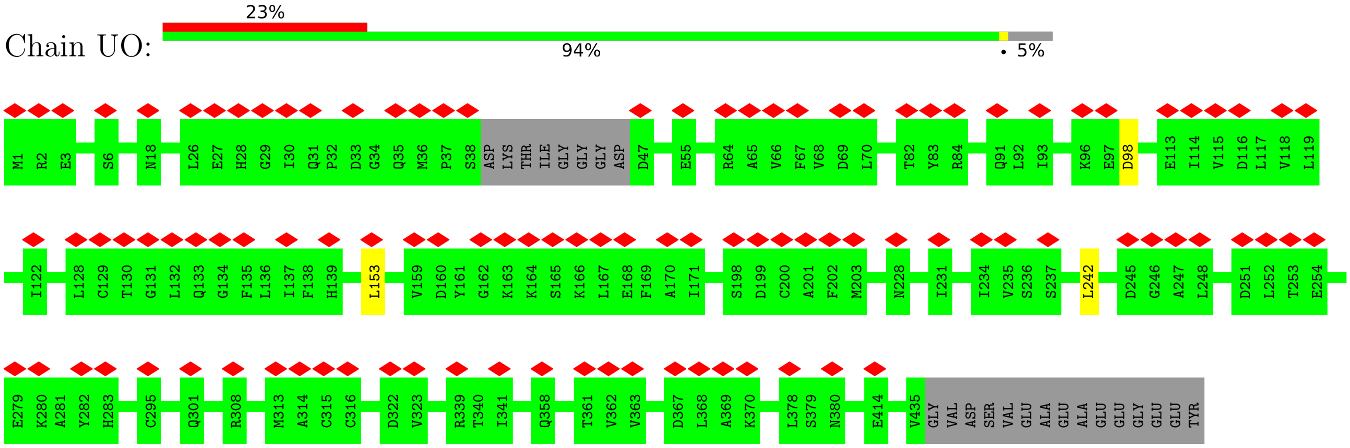






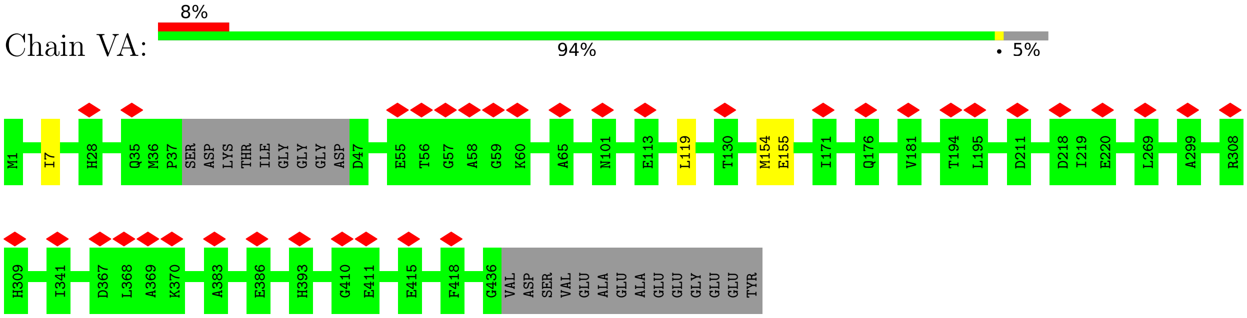
- Molecule 8: Tubulin alpha-3 chain

Chain UO:



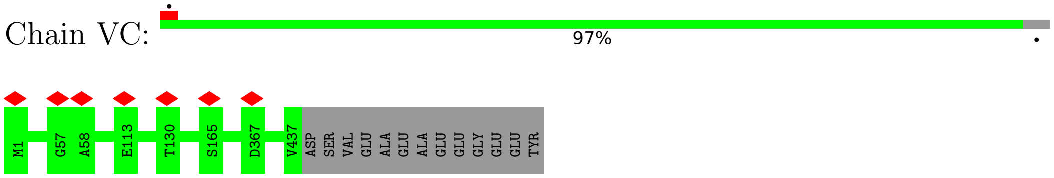
- Molecule 8: Tubulin alpha-3 chain

Chain VA:



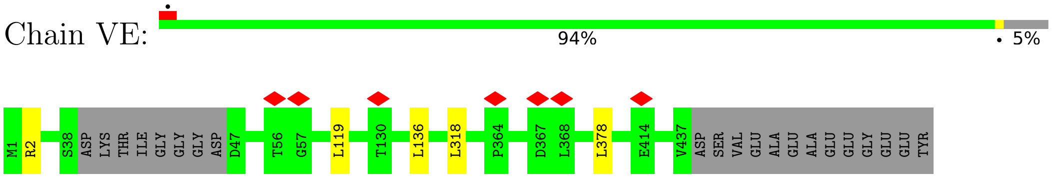
- Molecule 8: Tubulin alpha-3 chain

Chain VC:



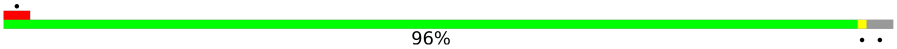
- Molecule 8: Tubulin alpha-3 chain

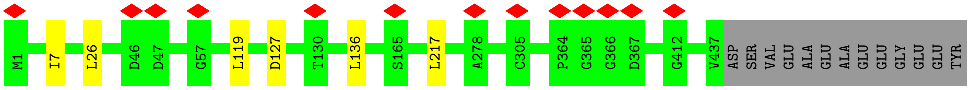
Chain VE:



- Molecule 8: Tubulin alpha-3 chain

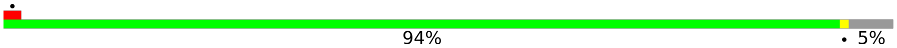
Chain VG:

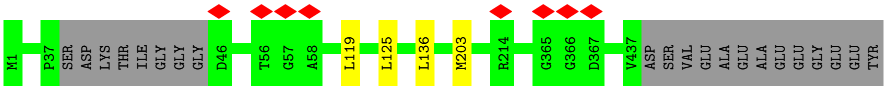




- Molecule 8: Tubulin alpha-3 chain

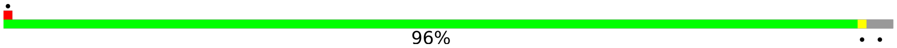
Chain VI:

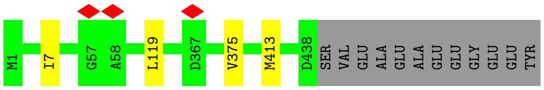




- Molecule 8: Tubulin alpha-3 chain

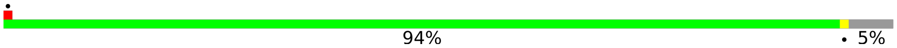
Chain VK:

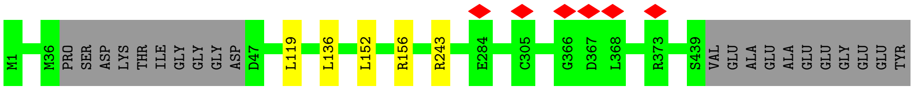




- Molecule 8: Tubulin alpha-3 chain

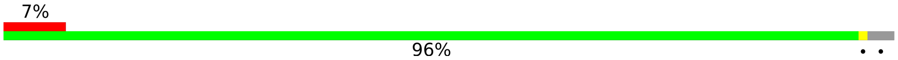
Chain VM:

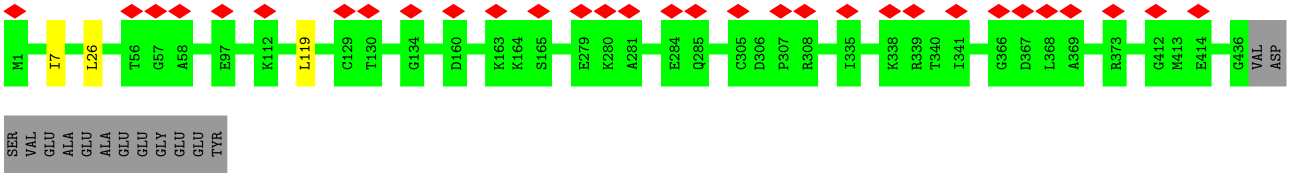




- Molecule 8: Tubulin alpha-3 chain

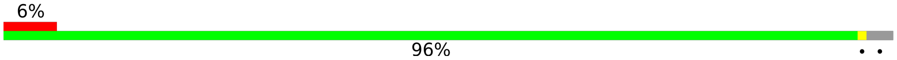
Chain VO:

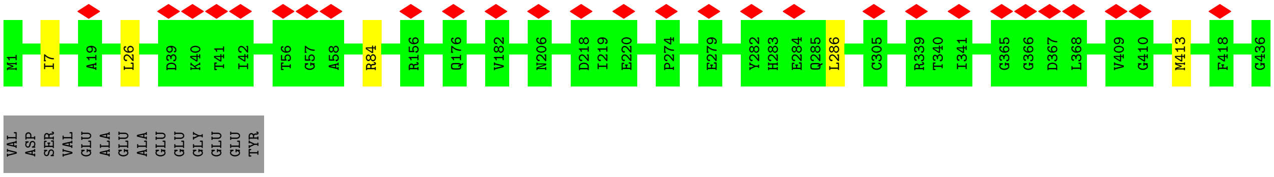




- Molecule 8: Tubulin alpha-3 chain

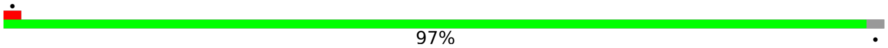
Chain WA:

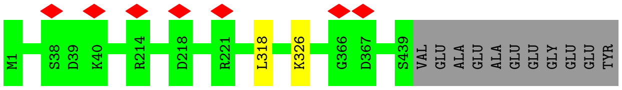




- Molecule 8: Tubulin alpha-3 chain

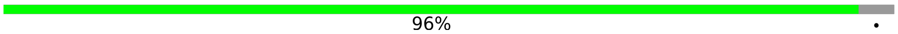
Chain WC:

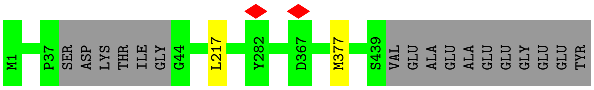




- Molecule 8: Tubulin alpha-3 chain

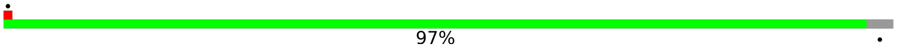
Chain WE:

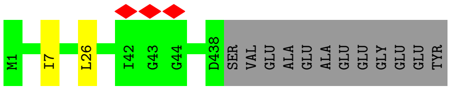




- Molecule 8: Tubulin alpha-3 chain

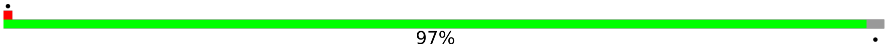
Chain WG:

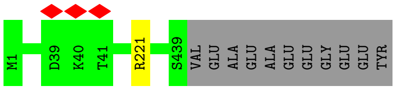




- Molecule 8: Tubulin alpha-3 chain

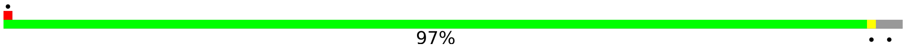
Chain WI:

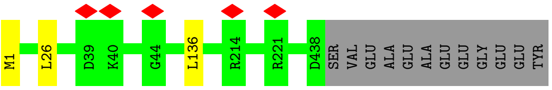




- Molecule 8: Tubulin alpha-3 chain

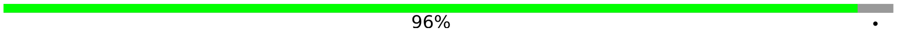
Chain WK:

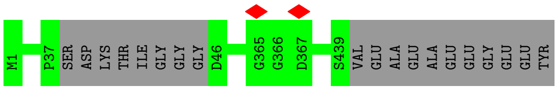




- Molecule 8: Tubulin alpha-3 chain

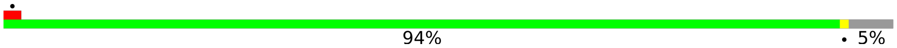
Chain WM:

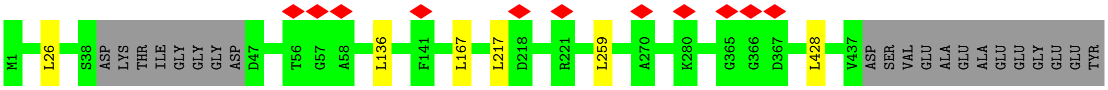




- Molecule 8: Tubulin alpha-3 chain

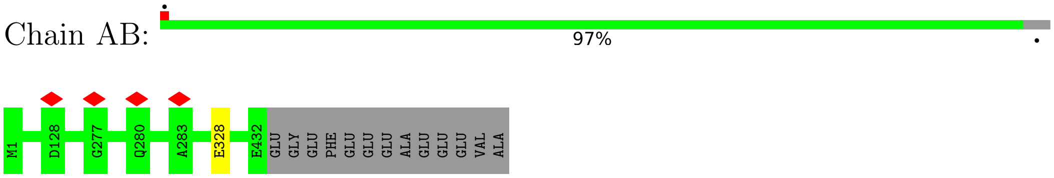
Chain WO:





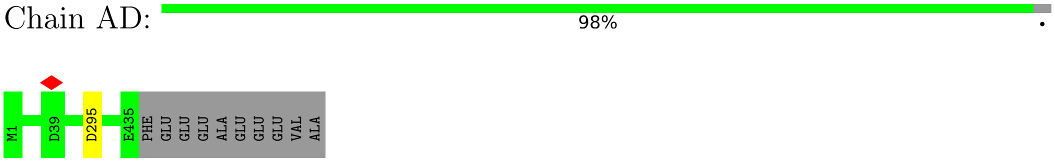
- Molecule 9: Tubulin beta-4B chain

Chain AB:



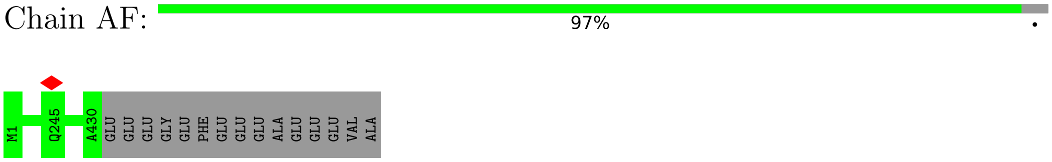
- Molecule 9: Tubulin beta-4B chain

Chain AD:



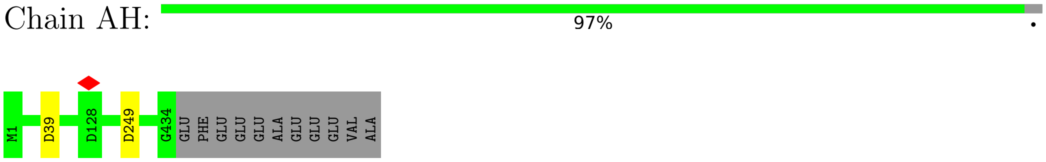
- Molecule 9: Tubulin beta-4B chain

Chain AF:



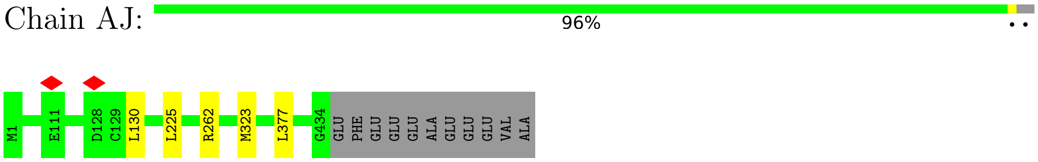
- Molecule 9: Tubulin beta-4B chain

Chain AH:



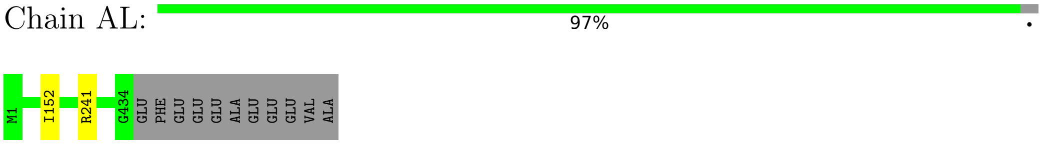
- Molecule 9: Tubulin beta-4B chain

Chain AJ:



- Molecule 9: Tubulin beta-4B chain

Chain AL:



- Molecule 9: Tubulin beta-4B chain

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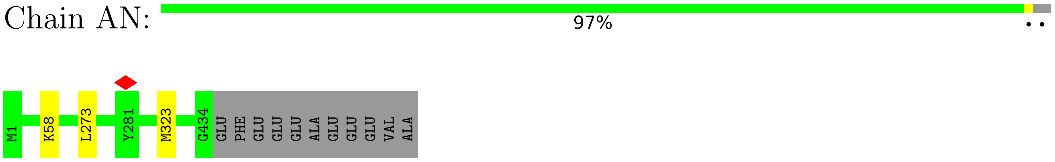

- Molecule 9: Tubulin beta-4B chain

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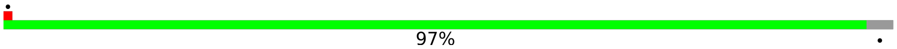
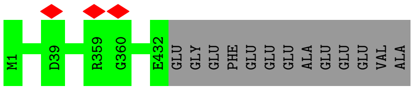
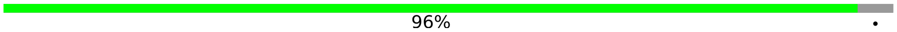
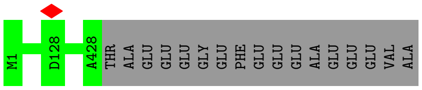




- Molecule 9: Tubulin beta-4B chain

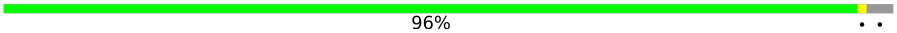
Chain BB:





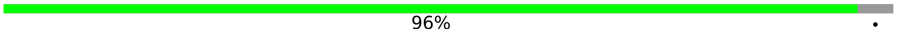
- Molecule 9: Tubulin beta-4B chain

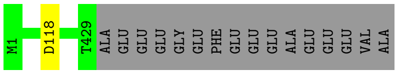
Chain BD:



- Molecule 9: Tubulin beta-4B chain

Chain BF:





- Molecule 9: Tubulin beta-4B chain

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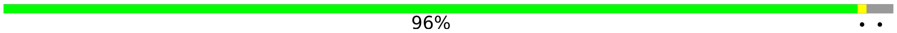

- Molecule 9: Tubulin beta-4B chain

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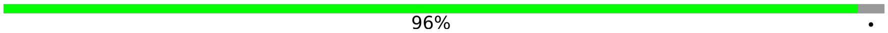

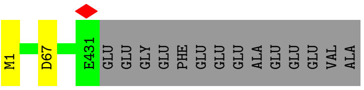

- Molecule 9: Tubulin beta-4B chain

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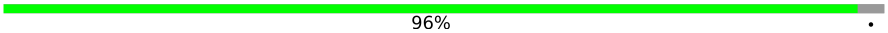
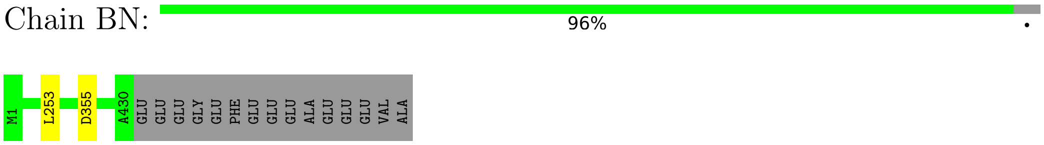


- Molecule 9: Tubulin beta-4B chain

Chain BN:



- Molecule 9: Tubulin beta-4B chain

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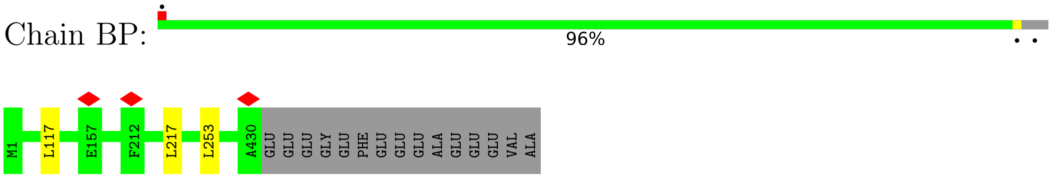
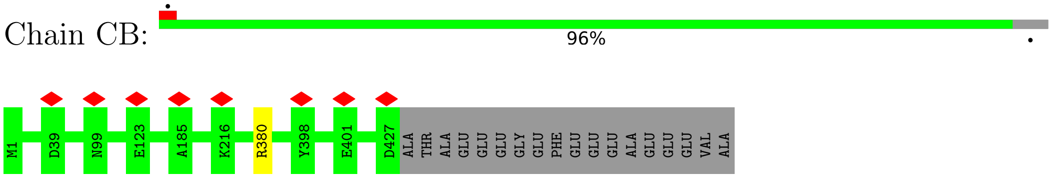


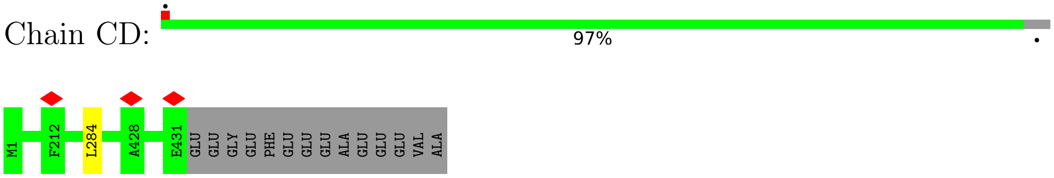
- Molecule 9: Tubulin beta-4B chain

Chain CB:



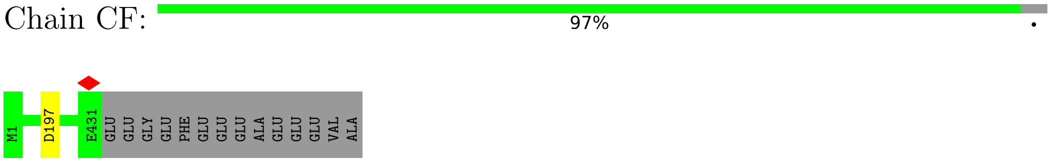
- Molecule 9: Tubulin beta-4B chain

Chain CD:



- Molecule 9: Tubulin beta-4B chain

Chain CF:



- Molecule 9: Tubulin beta-4B chain

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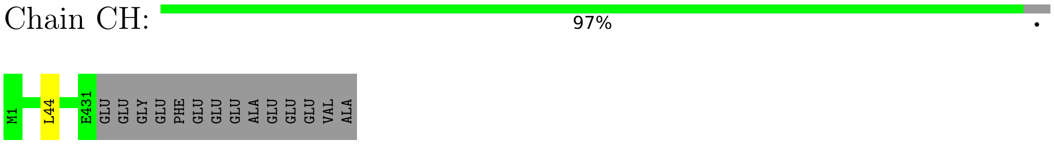
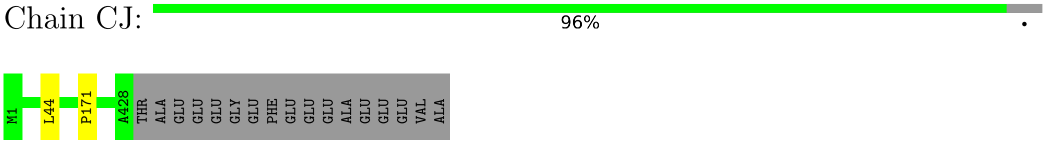


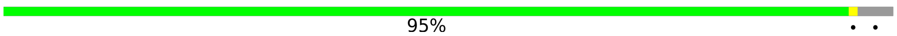
- Molecule 9: Tubulin beta-4B chain

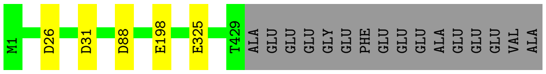
Chain CJ:



- Molecule 9: Tubulin beta-4B chain

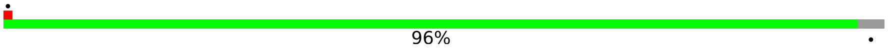
Chain CL:

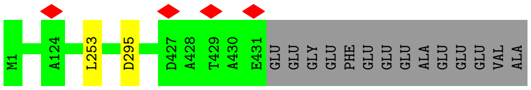




- Molecule 9: Tubulin beta-4B chain

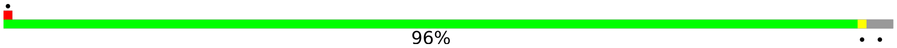
Chain CN:

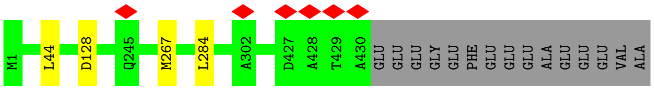




- Molecule 9: Tubulin beta-4B chain

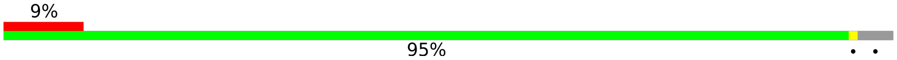
Chain CP:

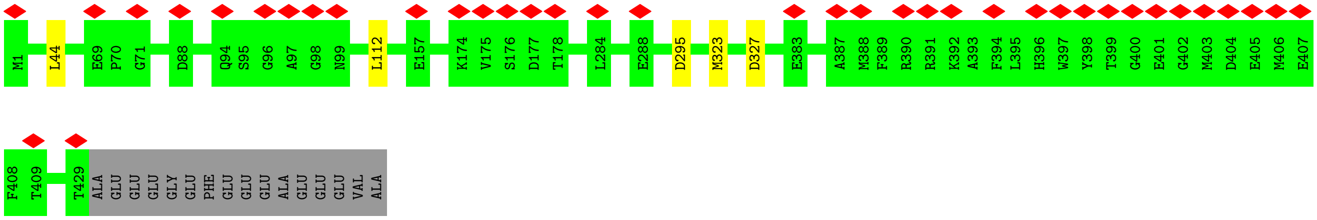




- Molecule 9: Tubulin beta-4B chain

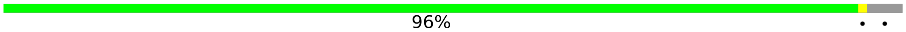
Chain DB:

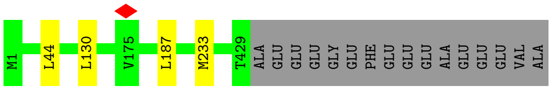




- Molecule 9: Tubulin beta-4B chain

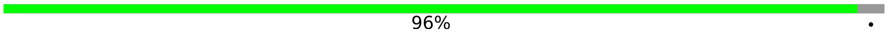
Chain DD:

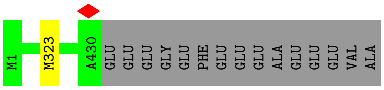




- Molecule 9: Tubulin beta-4B chain

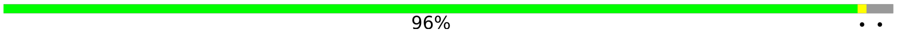
Chain DF:





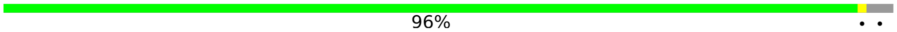
- Molecule 9: Tubulin beta-4B chain

Chain DH:



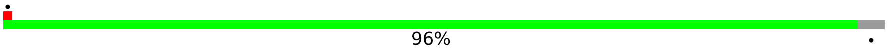
- Molecule 9: Tubulin beta-4B chain

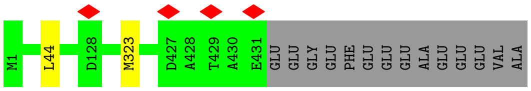
Chain DJ:



- Molecule 9: Tubulin beta-4B chain

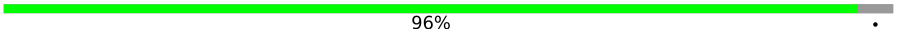
Chain DL:

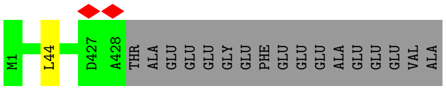




- Molecule 9: Tubulin beta-4B chain

Chain DN:





- Molecule 9: Tubulin beta-4B chain

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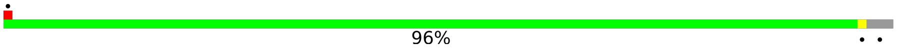

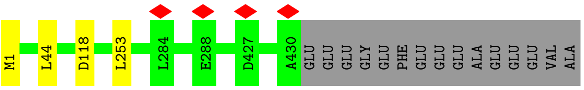

- Molecule 9: Tubulin beta-4B chain

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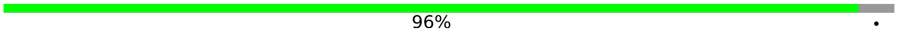

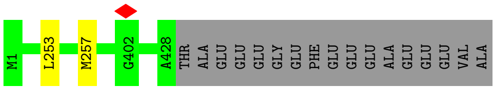

- Molecule 9: Tubulin beta-4B chain

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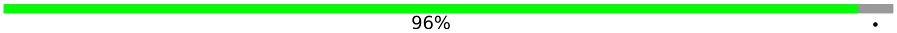

- Molecule 9: Tubulin beta-4B chain

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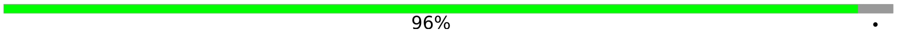

- Molecule 9: Tubulin beta-4B chain

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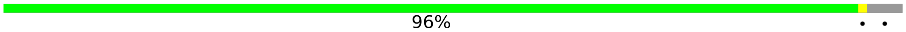

- Molecule 9: Tubulin beta-4B chain

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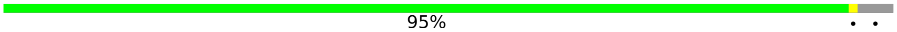

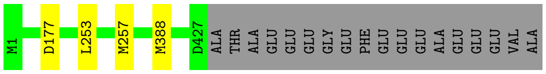

- Molecule 9: Tubulin beta-4B chain

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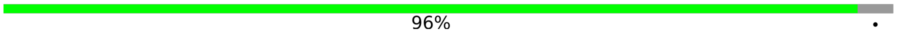

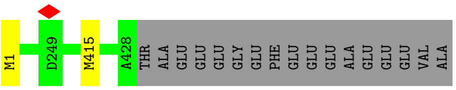

- Molecule 9: Tubulin beta-4B chain

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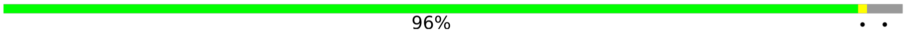

- Molecule 9: Tubulin beta-4B chain

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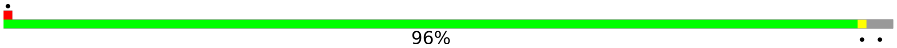

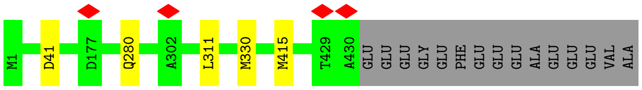

- Molecule 9: Tubulin beta-4B chain

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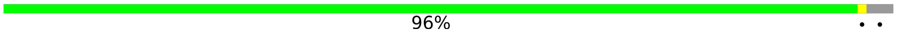

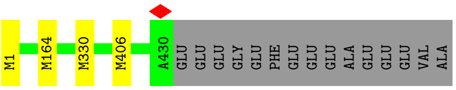

- Molecule 9: Tubulin beta-4B chain

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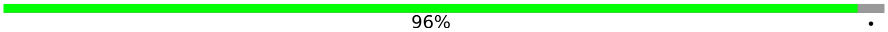

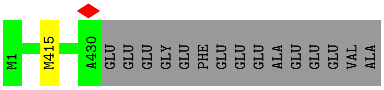

- Molecule 9: Tubulin beta-4B chain

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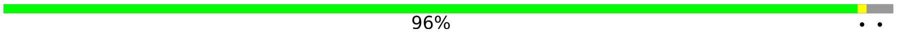

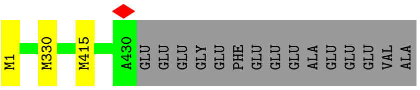

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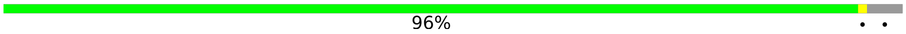

- Molecule 9: Tubulin beta-4B chain

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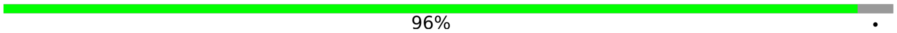
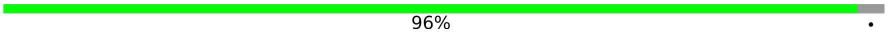


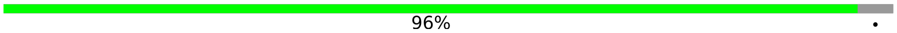
- Molecule 9: Tubulin beta-4B chain

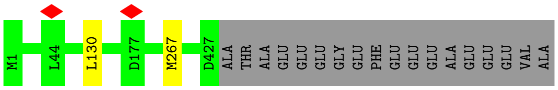
Chain FN:



- Molecule 9: Tubulin beta-4B chain

Chain GB:





- Molecule 9: Tubulin beta-4B chain

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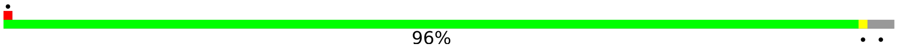

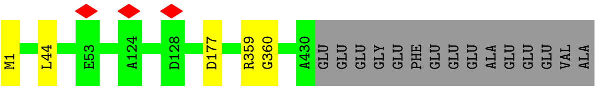

- Molecule 9: Tubulin beta-4B chain

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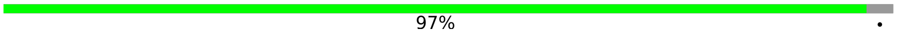

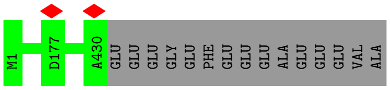

- Molecule 9: Tubulin beta-4B chain

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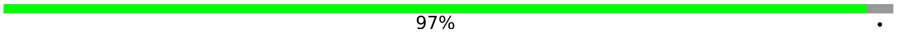

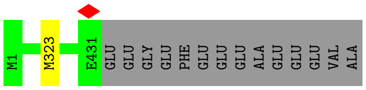

- Molecule 9: Tubulin beta-4B chain

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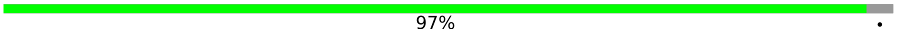

- Molecule 9: Tubulin beta-4B chain

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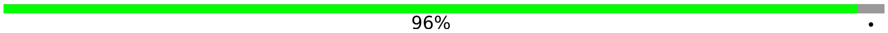

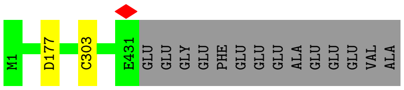

- Molecule 9: Tubulin beta-4B chain

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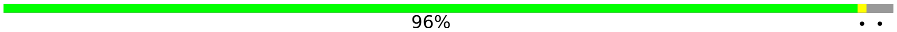

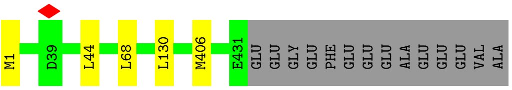

- Molecule 9: Tubulin beta-4B chain

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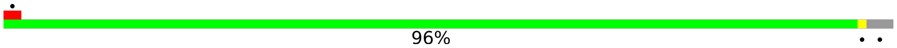

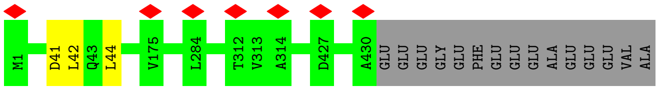

- Molecule 9: Tubulin beta-4B chain

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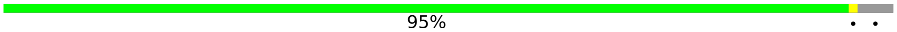

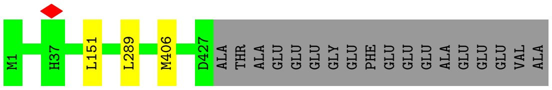

- Molecule 9: Tubulin beta-4B chain

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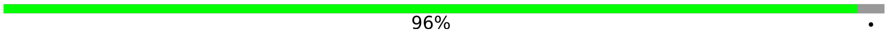

- Molecule 9: Tubulin beta-4B chain

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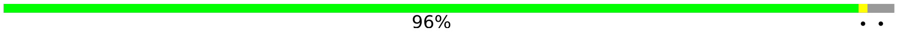

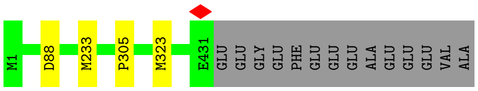

- Molecule 9: Tubulin beta-4B chain

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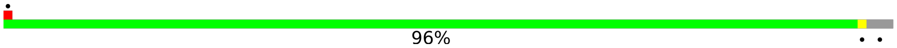

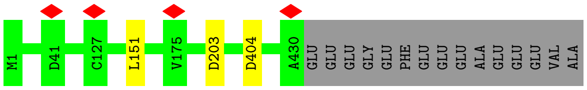

- Molecule 9: Tubulin beta-4B chain

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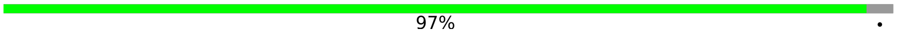

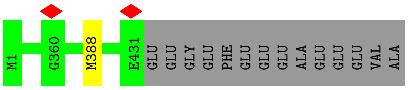

- Molecule 9: Tubulin beta-4B chain

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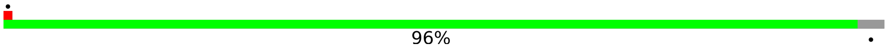

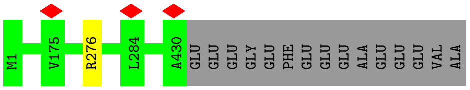

- Molecule 9: Tubulin beta-4B chain

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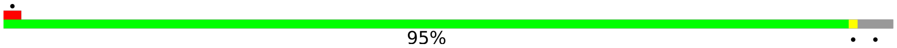

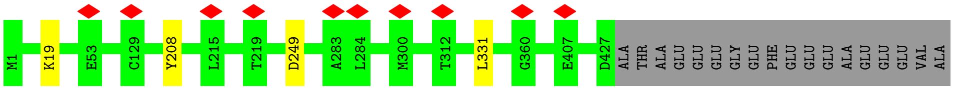

- Molecule 9: Tubulin beta-4B chain

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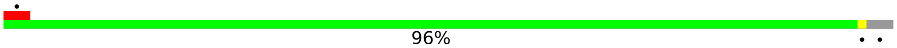

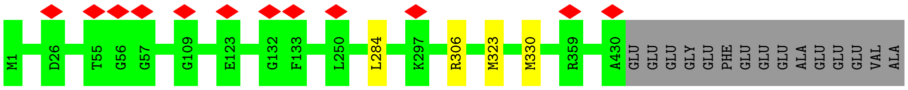

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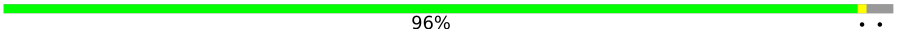

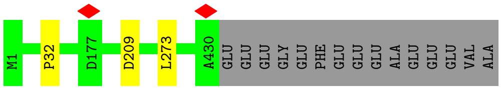

- Molecule 9: Tubulin beta-4B chain

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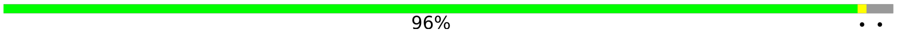

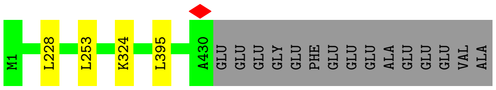

- Molecule 9: Tubulin beta-4B chain

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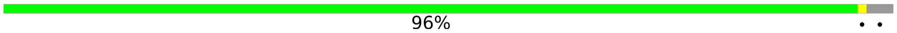

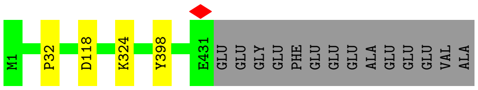

- Molecule 9: Tubulin beta-4B chain

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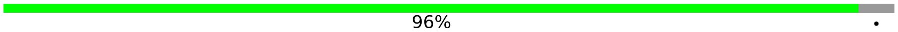

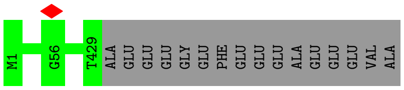

- Molecule 9: Tubulin beta-4B chain

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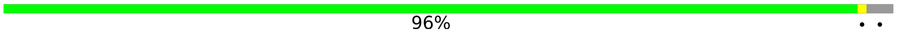

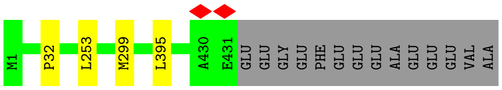

- Molecule 9: Tubulin beta-4B chain

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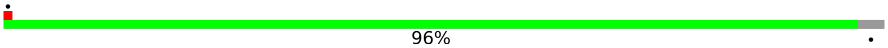
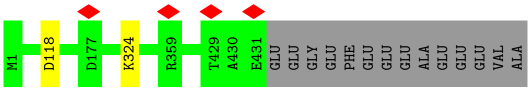
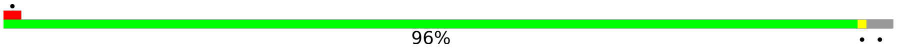
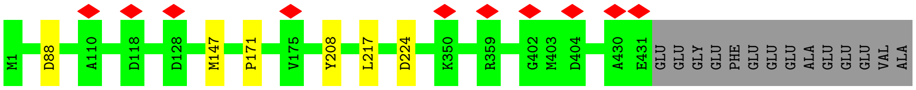




- Molecule 9: Tubulin beta-4B chain

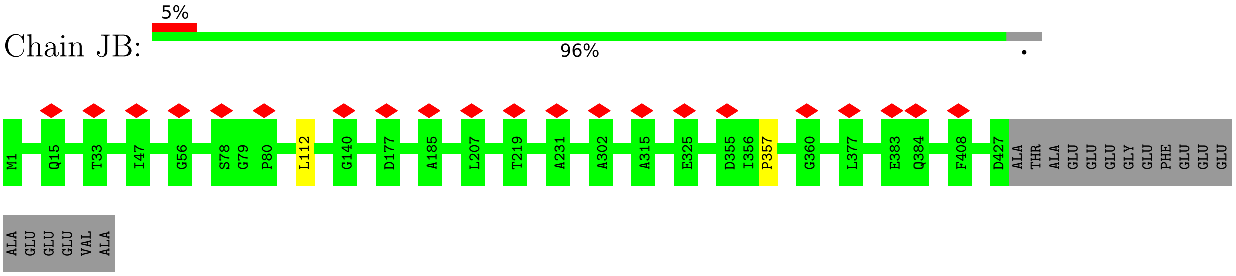
Chain IP:





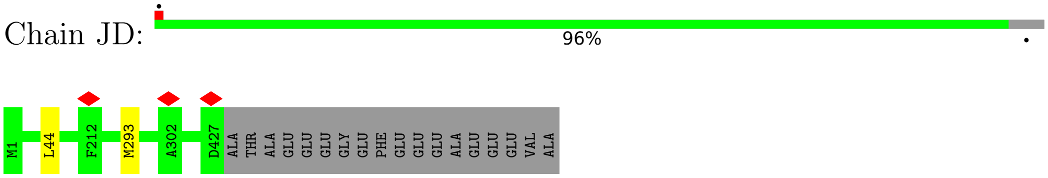
- Molecule 9: Tubulin beta-4B chain

Chain JB:



- Molecule 9: Tubulin beta-4B chain

Chain JD:



- Molecule 9: Tubulin beta-4B chain

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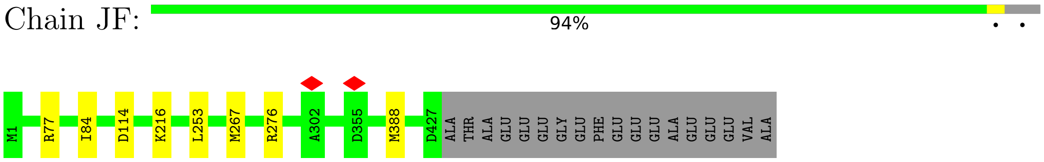

- Molecule 9: Tubulin beta-4B chain

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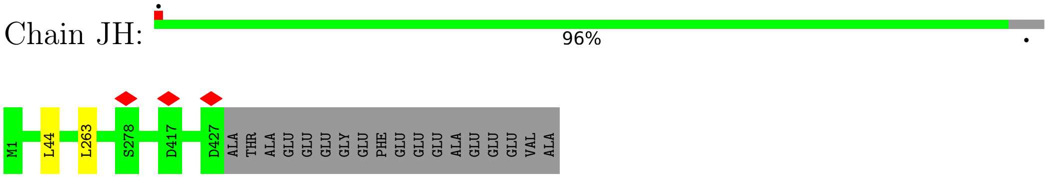

- Molecule 9: Tubulin beta-4B chain

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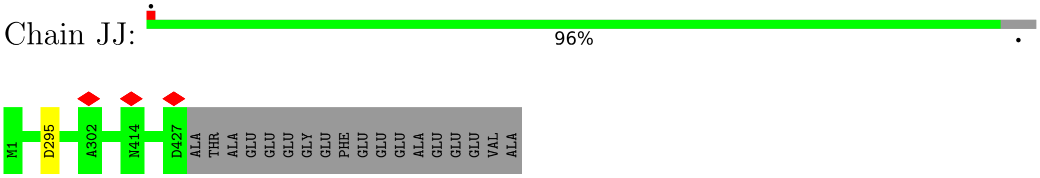

- Molecule 9: Tubulin beta-4B chain

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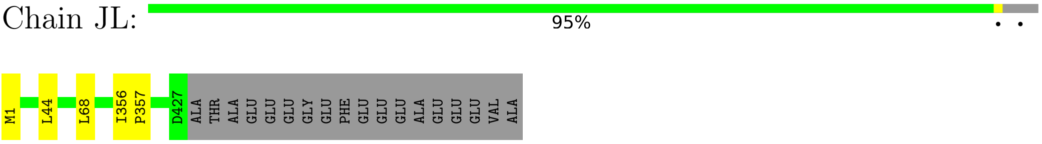
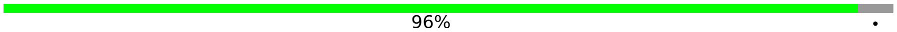
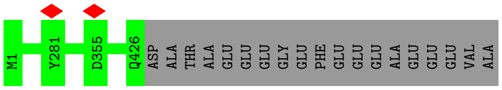


- Molecule 9: Tubulin beta-4B chain

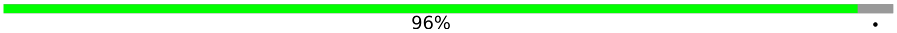
Chain JN:

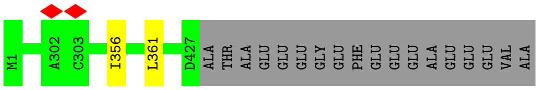




- Molecule 9: Tubulin beta-4B chain

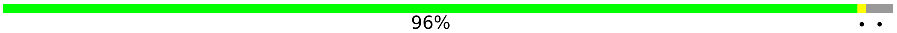
Chain JP:

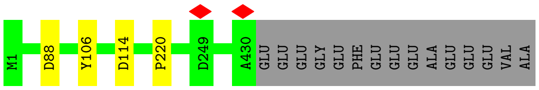




- Molecule 9: Tubulin beta-4B chain

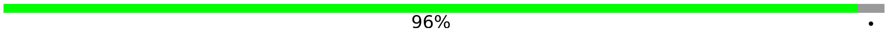
Chain KB:

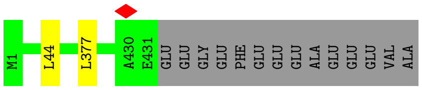




- Molecule 9: Tubulin beta-4B chain

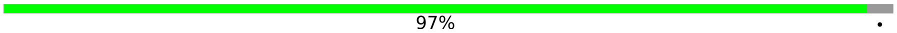
Chain KD:





- Molecule 9: Tubulin beta-4B chain

Chain KF:



- Molecule 9: Tubulin beta-4B chain

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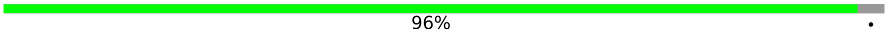

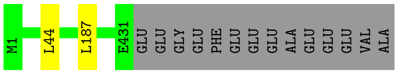

- Molecule 9: Tubulin beta-4B chain

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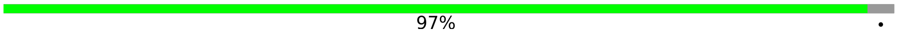
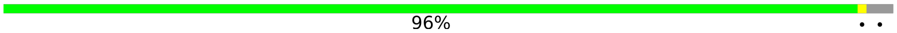


- Molecule 9: Tubulin beta-4B chain

Chain KL:



- Molecule 9: Tubulin beta-4B chain

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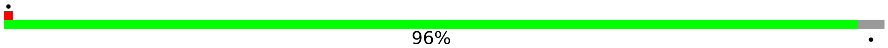
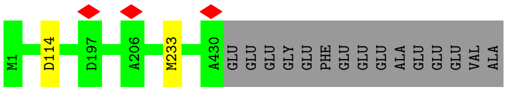
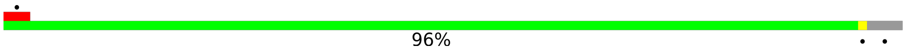
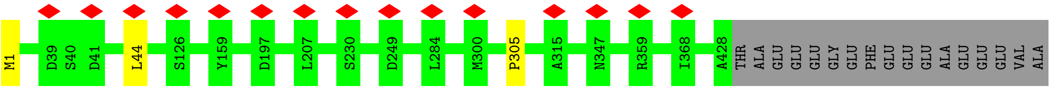




- Molecule 9: Tubulin beta-4B chain

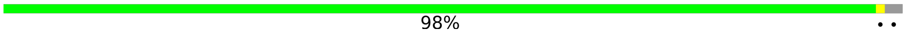
Chain KP:

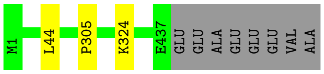




- Molecule 9: Tubulin beta-4B chain

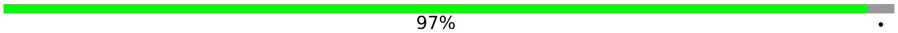
Chain LB:





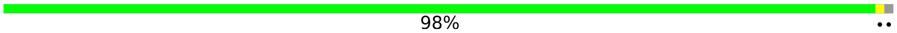
- Molecule 9: Tubulin beta-4B chain

Chain LD:



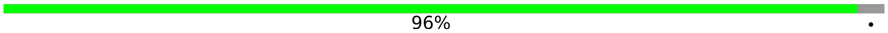
- Molecule 9: Tubulin beta-4B chain

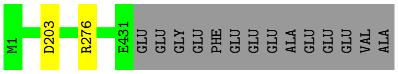
Chain LF:



- Molecule 9: Tubulin beta-4B chain

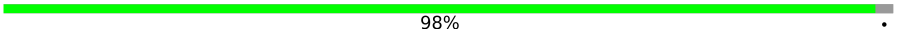
Chain LH:

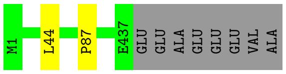




- Molecule 9: Tubulin beta-4B chain

Chain LJ:





- Molecule 9: Tubulin beta-4B chain

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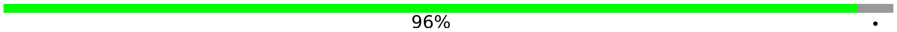

- Molecule 9: Tubulin beta-4B chain

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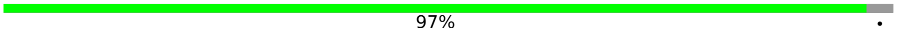
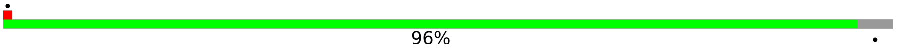
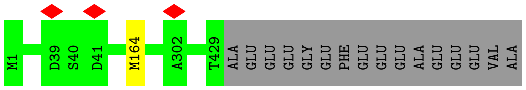


- Molecule 9: Tubulin beta-4B chain

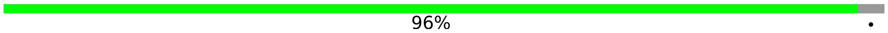
Chain LP:

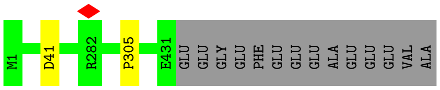




- Molecule 9: Tubulin beta-4B chain

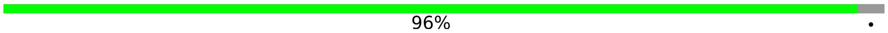
Chain MB:

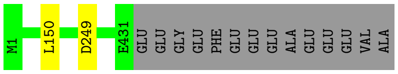




- Molecule 9: Tubulin beta-4B chain

Chain MD:





- Molecule 9: Tubulin beta-4B chain

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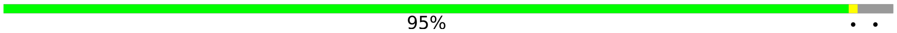
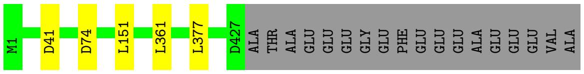
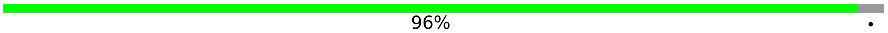
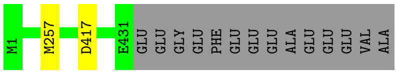




- Molecule 9: Tubulin beta-4B chain

Chain MH:





- Molecule 9: Tubulin beta-4B chain

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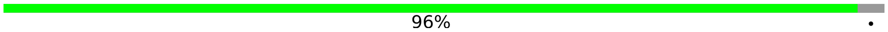

- Molecule 9: Tubulin beta-4B chain

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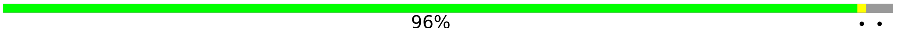
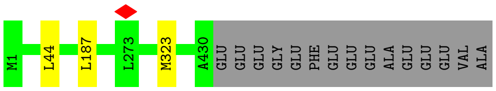
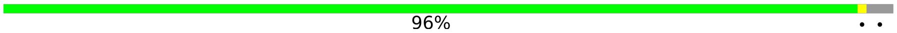
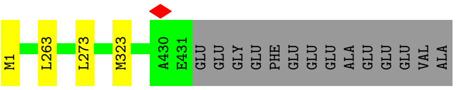




- Molecule 9: Tubulin beta-4B chain

Chain MN:





- Molecule 9: Tubulin beta-4B chain

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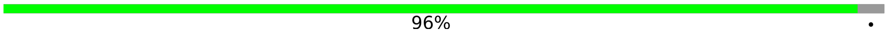

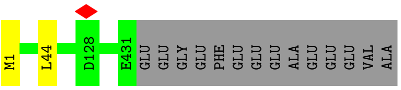

- Molecule 9: Tubulin beta-4B chain

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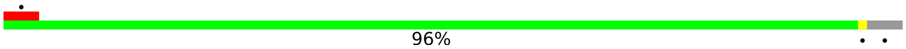

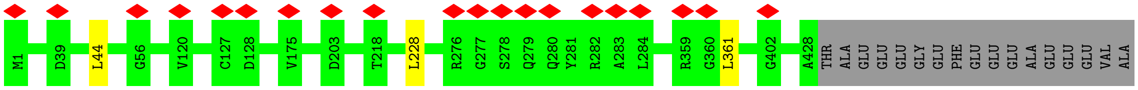

- Molecule 9: Tubulin beta-4B chain

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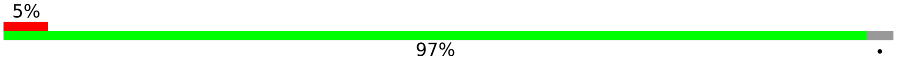
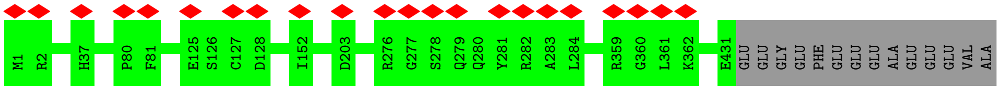
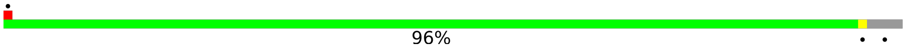
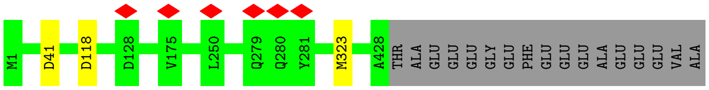




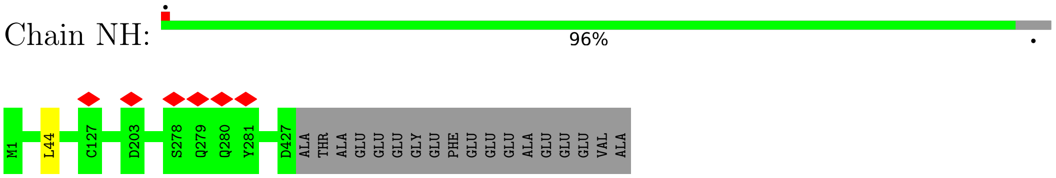
- Molecule 9: Tubulin beta-4B chain

Chain NF:

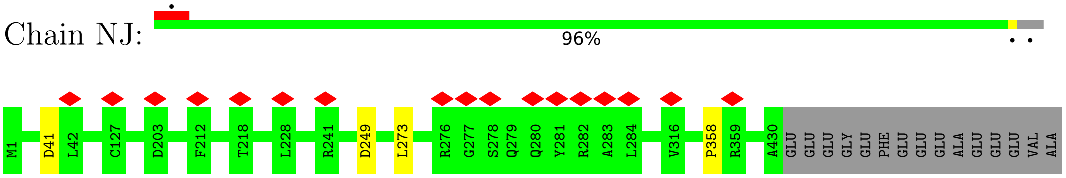




- Molecule 9: Tubulin beta-4B chain



- Molecule 9: Tubulin beta-4B chain



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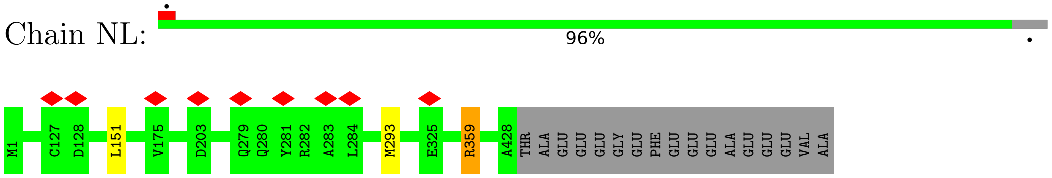

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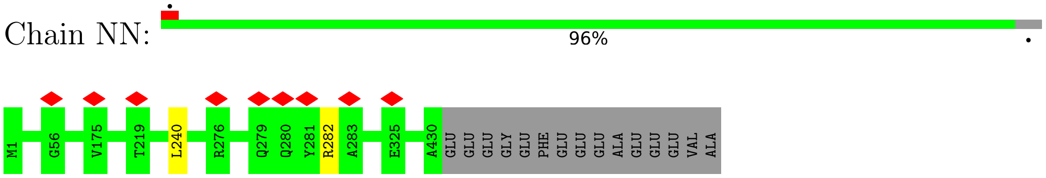

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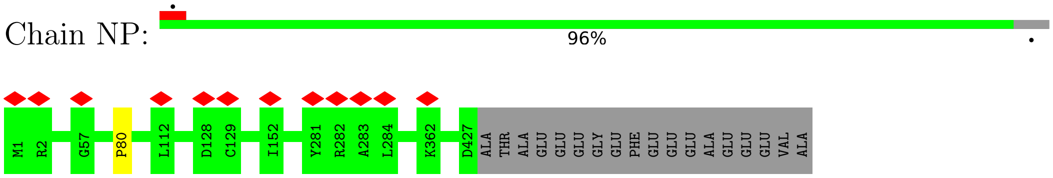

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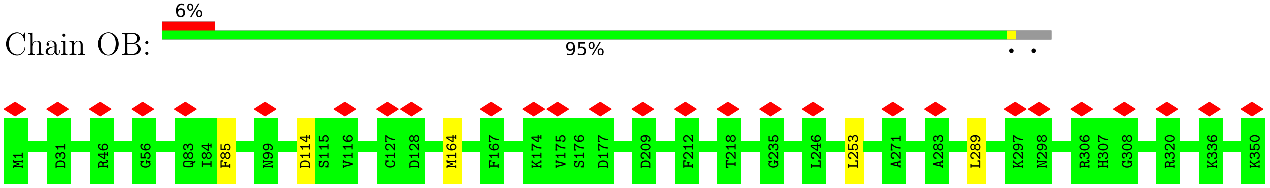

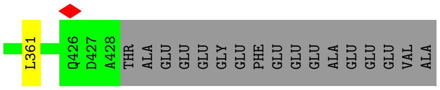

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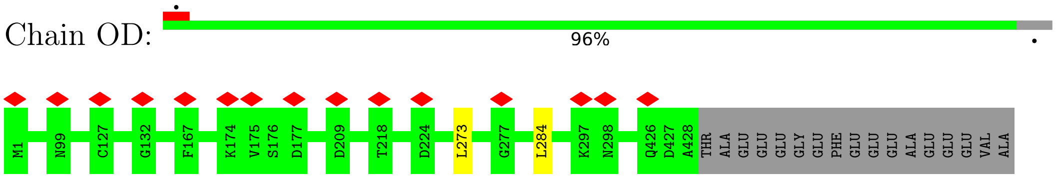

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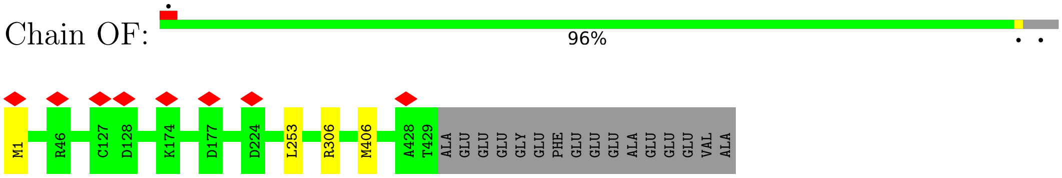

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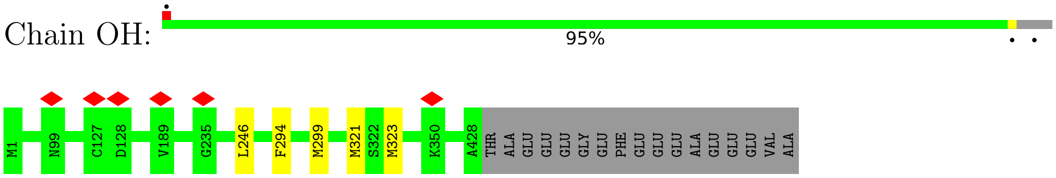

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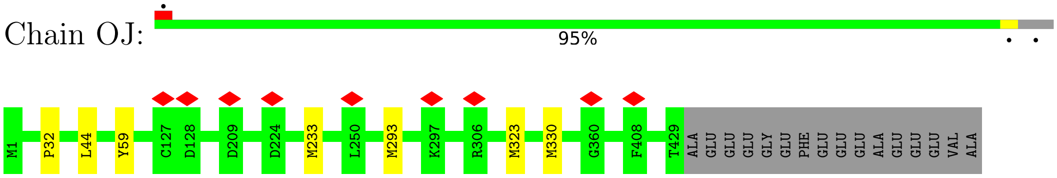
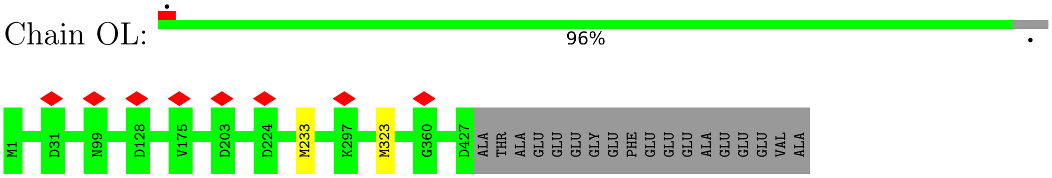
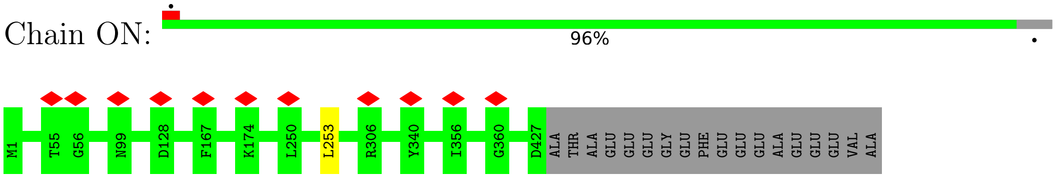


- Molecule 9: Tubulin beta-4B chain



- Molecule 9: Tubulin beta-4B chain



- Molecule 9: Tubulin beta-4B chain

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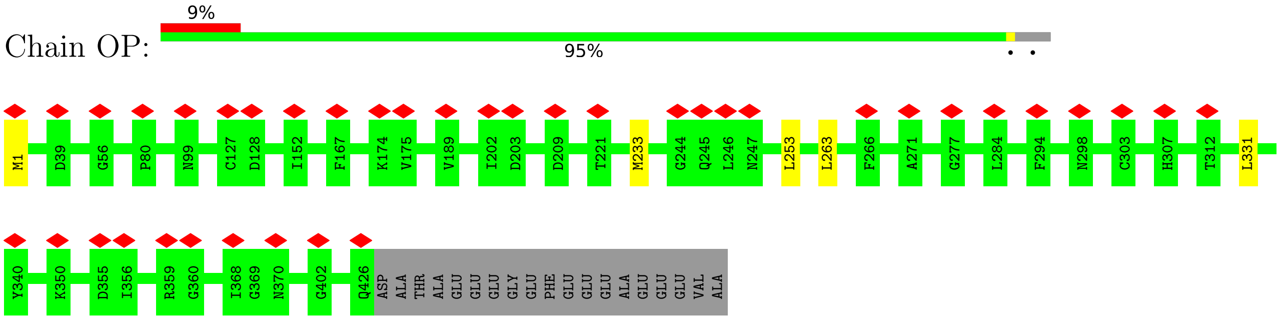

- Molecule 9: Tubulin beta-4B chain

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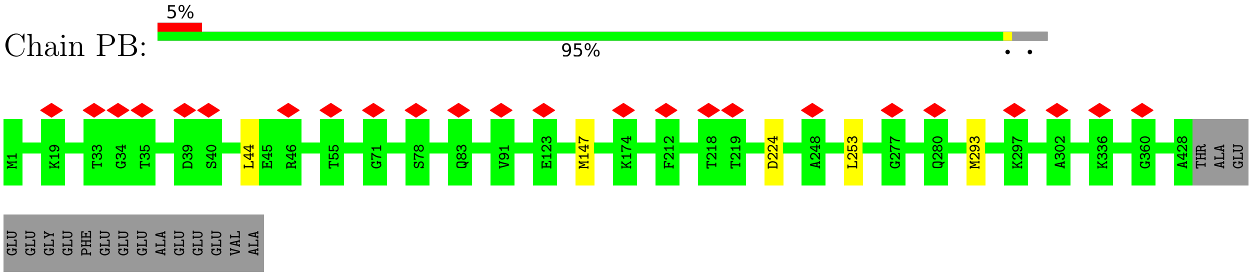

- Molecule 9: Tubulin beta-4B chain

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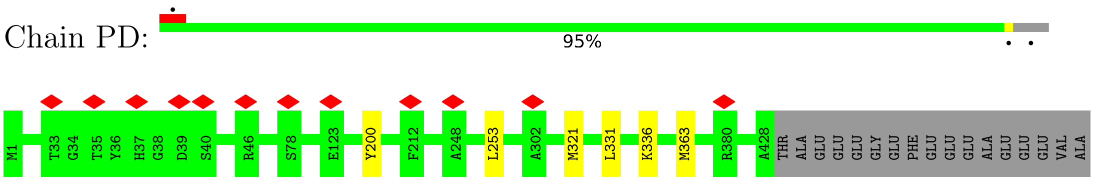
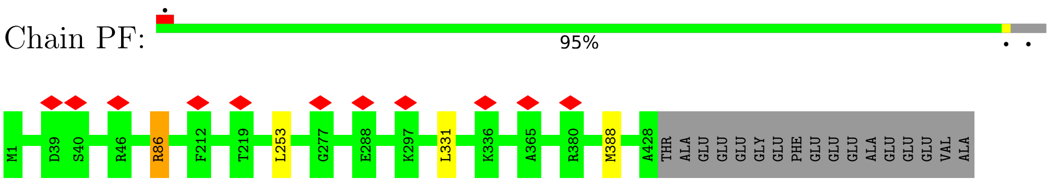


- Molecule 9: Tubulin beta-4B chain

Chain PF:



- Molecule 9: Tubulin beta-4B chain

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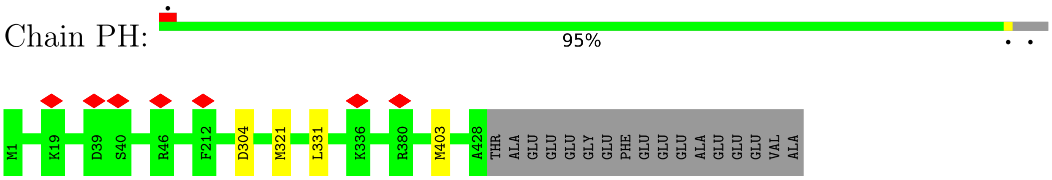

- Molecule 9: Tubulin beta-4B chain

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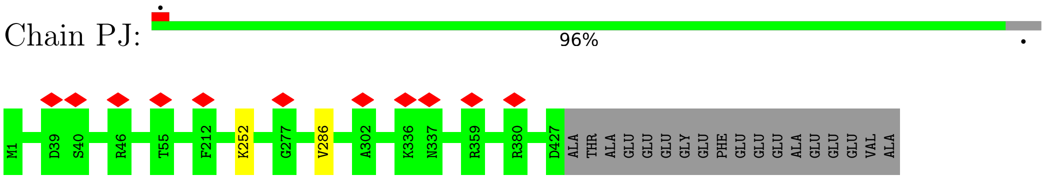
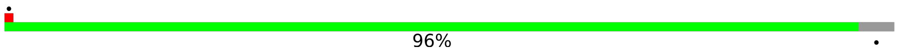
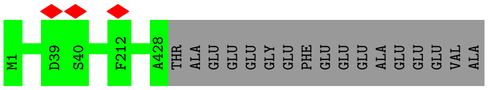


- Molecule 9: Tubulin beta-4B chain

Chain PL:





- Molecule 9: Tubulin beta-4B chain

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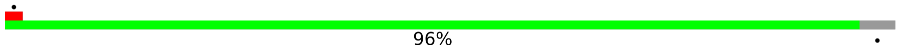

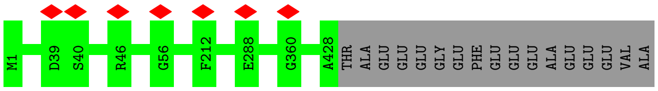

- Molecule 9: Tubulin beta-4B chain

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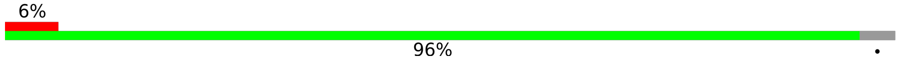
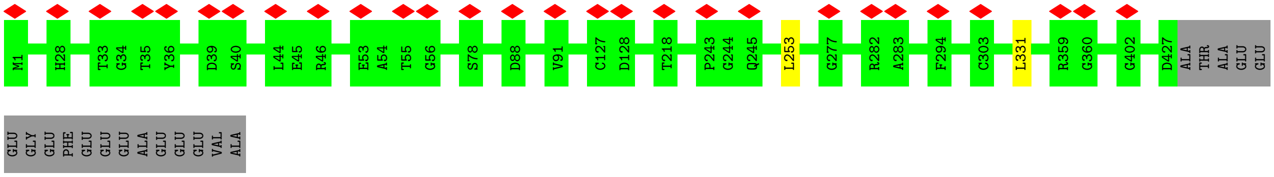
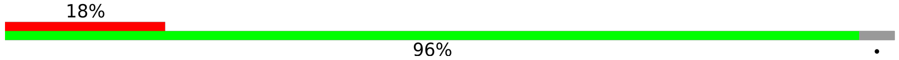
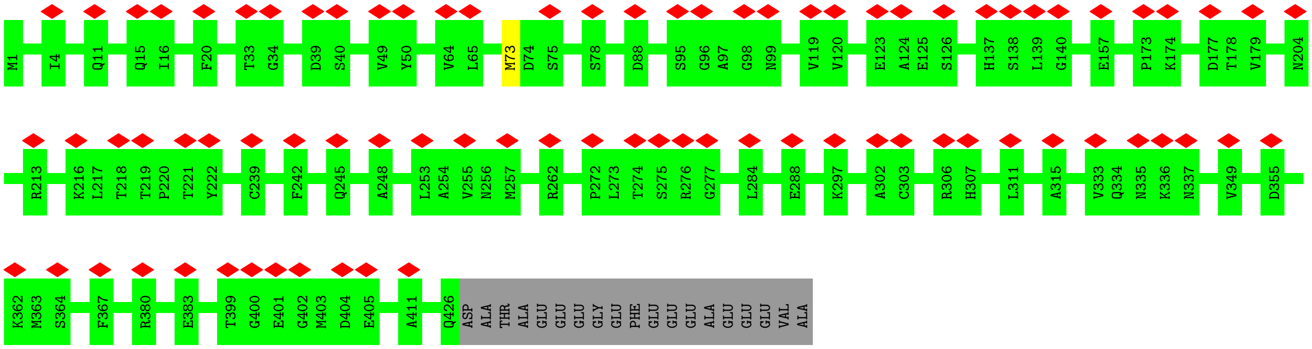




- Molecule 9: Tubulin beta-4B chain

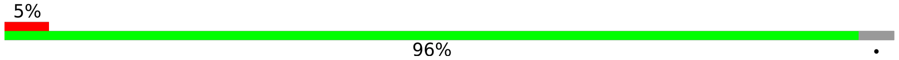
Chain QB:

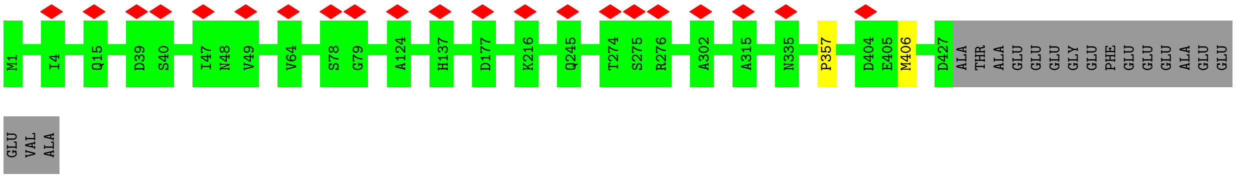




- Molecule 9: Tubulin beta-4B chain

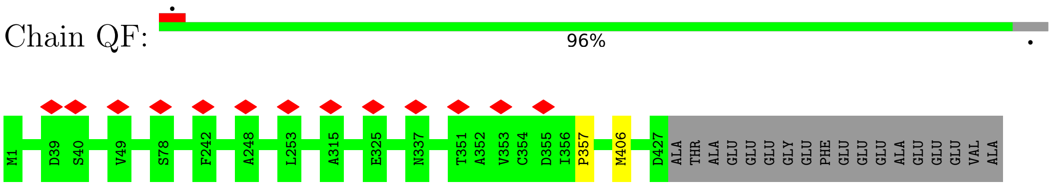
Chain QD:





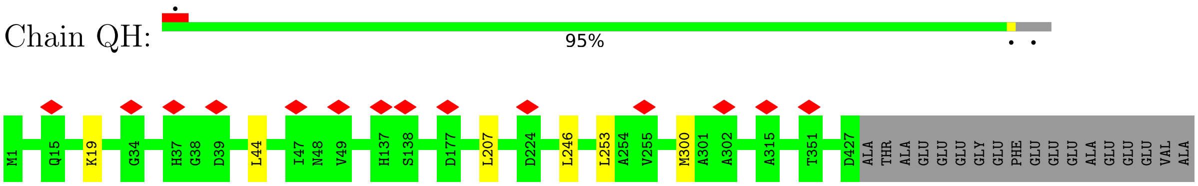
- Molecule 9: Tubulin beta-4B chain

Chain QF:



- Molecule 9: Tubulin beta-4B chain

Chain QH:



- Molecule 9: Tubulin beta-4B chain

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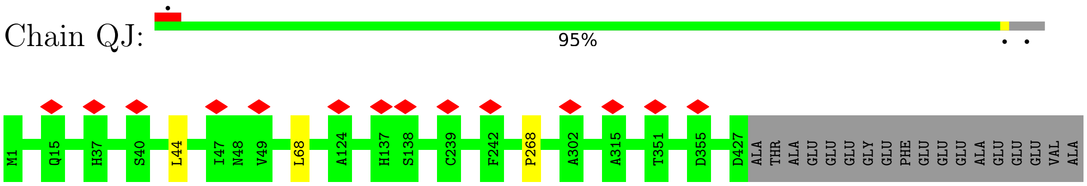
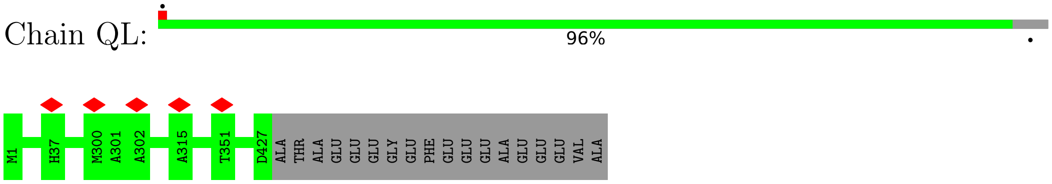


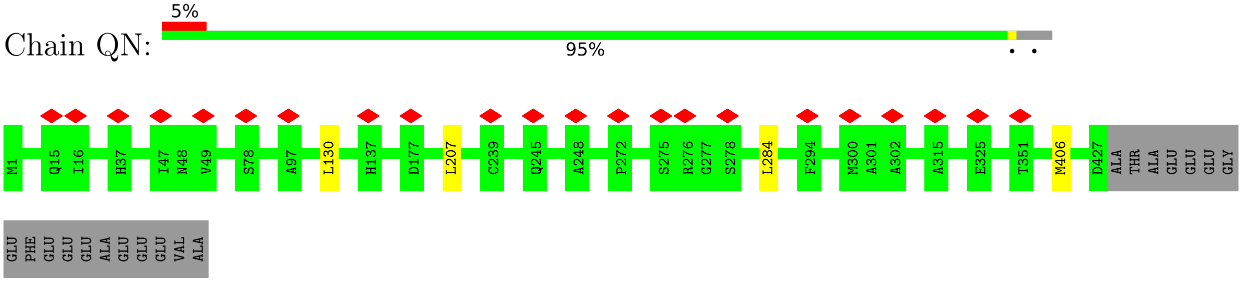
- Molecule 9: Tubulin beta-4B chain

Chain QL:



- Molecule 9: Tubulin beta-4B chain

Chain QN:



- Molecule 9: Tubulin beta-4B chain

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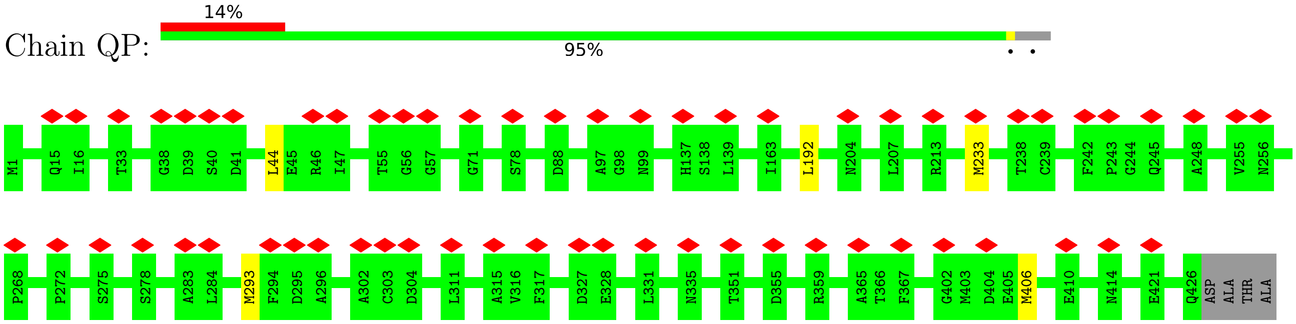
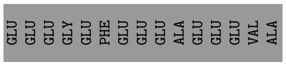
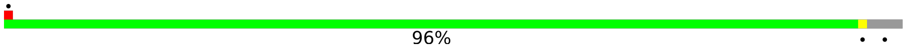
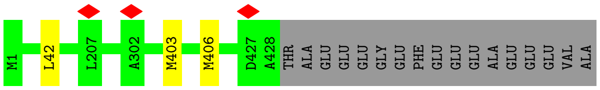




- Molecule 9: Tubulin beta-4B chain

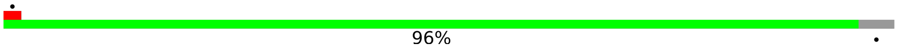
Chain RD:

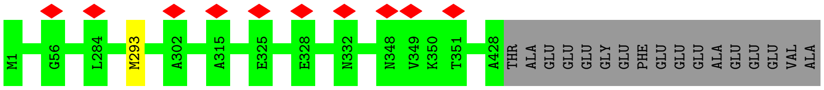




- Molecule 9: Tubulin beta-4B chain

Chain RF:





- Molecule 9: Tubulin beta-4B chain

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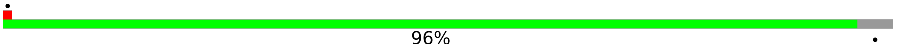

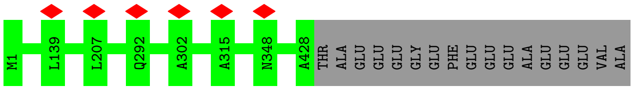

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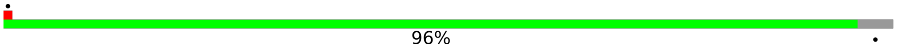
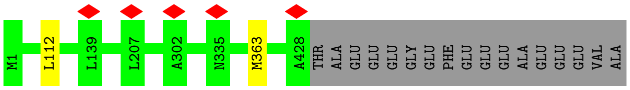
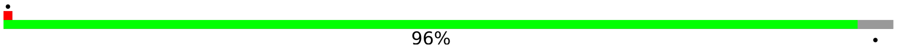
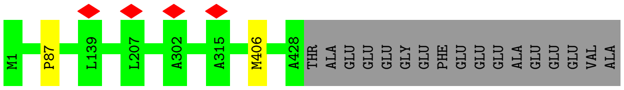




- Molecule 9: Tubulin beta-4B chain

Chain RL:





- Molecule 9: Tubulin beta-4B chain

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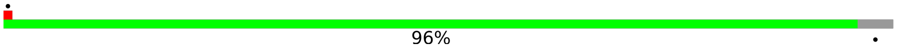

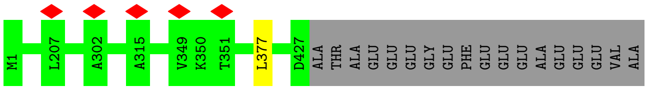

- Molecule 9: Tubulin beta-4B chain

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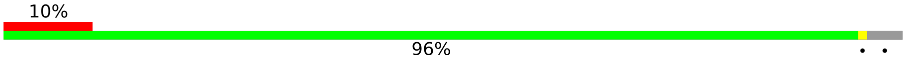
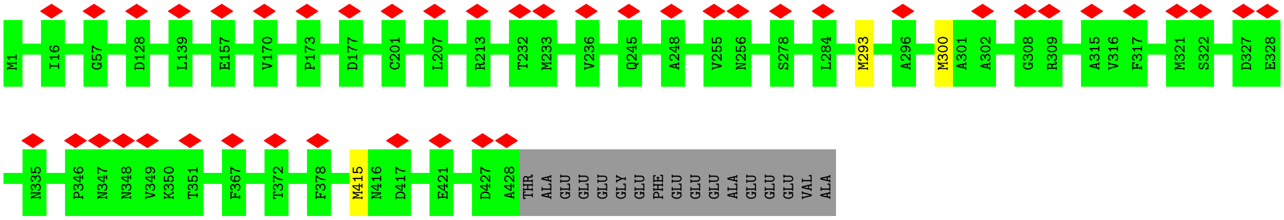
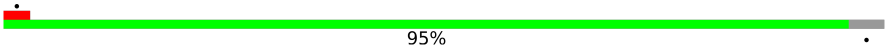
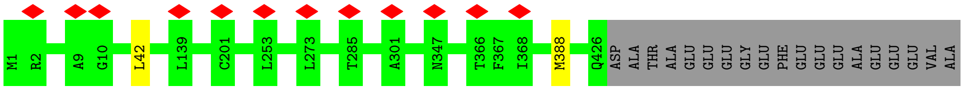




- Molecule 9: Tubulin beta-4B chain

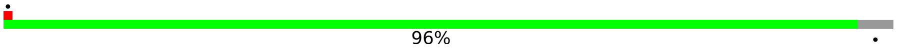
Chain SB:

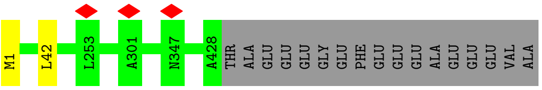




- Molecule 9: Tubulin beta-4B chain

Chain SD:





- Molecule 9: Tubulin beta-4B chain

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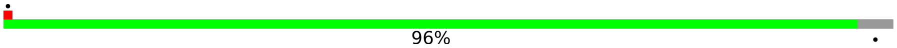
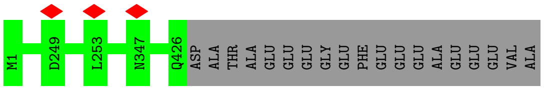
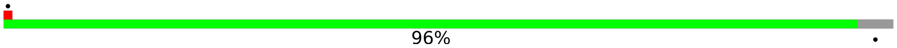
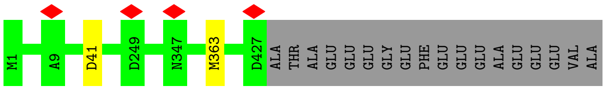




- Molecule 9: Tubulin beta-4B chain

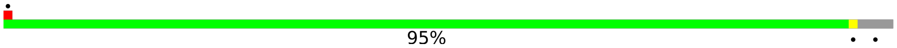
Chain SH:

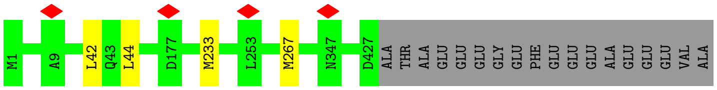




- Molecule 9: Tubulin beta-4B chain

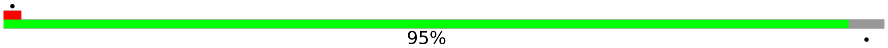
Chain SJ:

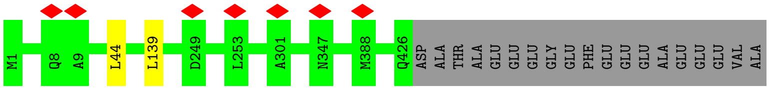




- Molecule 9: Tubulin beta-4B chain

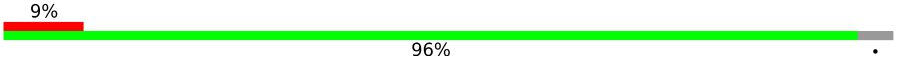
Chain SL:

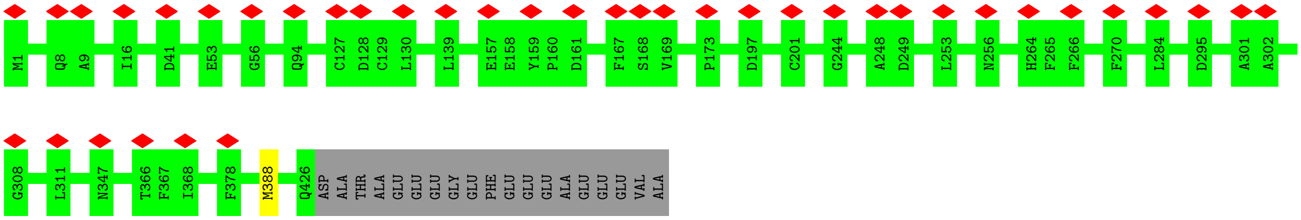




- Molecule 9: Tubulin beta-4B chain

Chain SN:





- Molecule 9: Tubulin beta-4B chain

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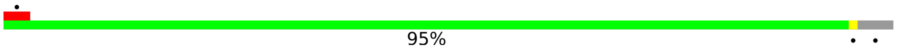
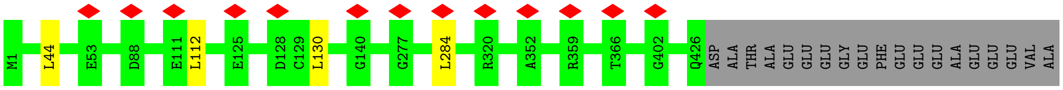
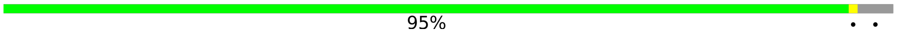
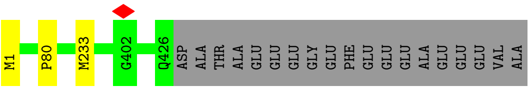




- Molecule 9: Tubulin beta-4B chain

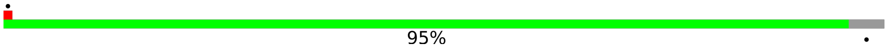
Chain TD:

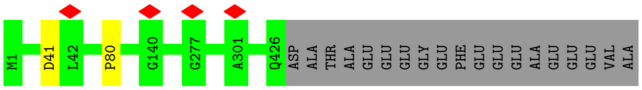




- Molecule 9: Tubulin beta-4B chain

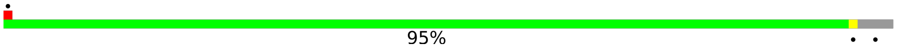
Chain TF:

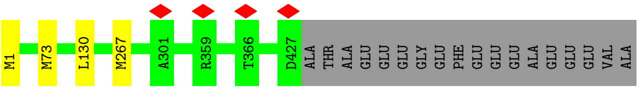




- Molecule 9: Tubulin beta-4B chain

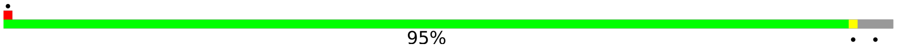
Chain TH:

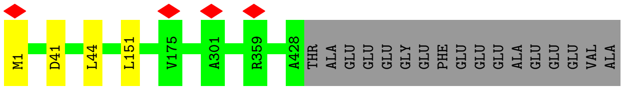




- Molecule 9: Tubulin beta-4B chain

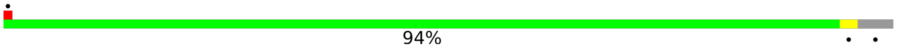
Chain TJ:

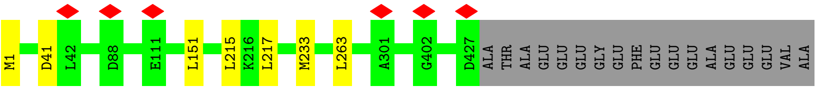




- Molecule 9: Tubulin beta-4B chain

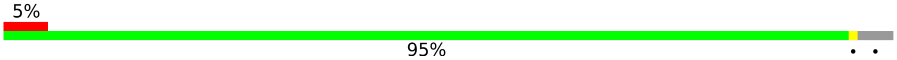
Chain TL:

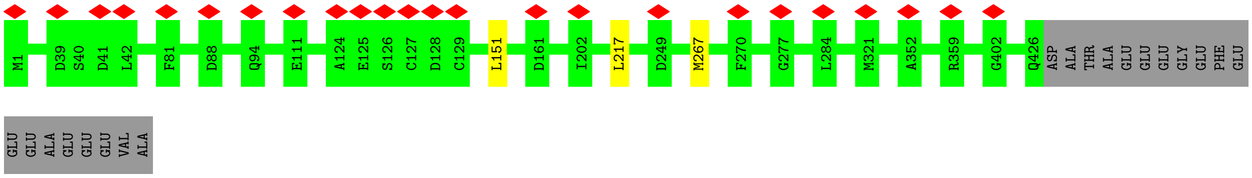




- Molecule 9: Tubulin beta-4B chain

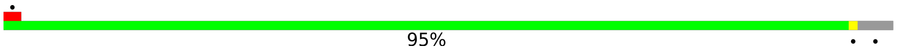
Chain TN:

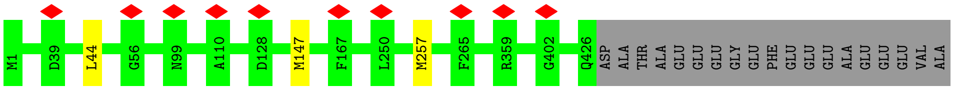




- Molecule 9: Tubulin beta-4B chain

Chain UB:





- Molecule 9: Tubulin beta-4B chain

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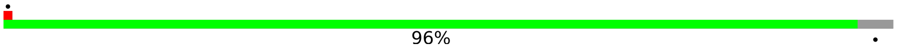

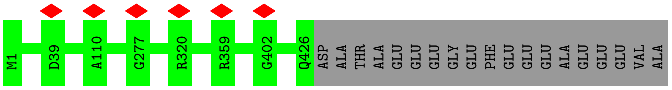

- Molecule 9: Tubulin beta-4B chain

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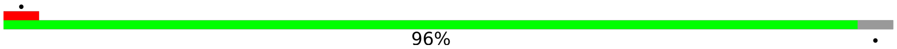

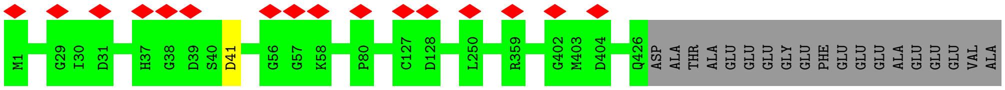

- Molecule 9: Tubulin beta-4B chain

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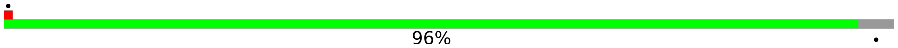
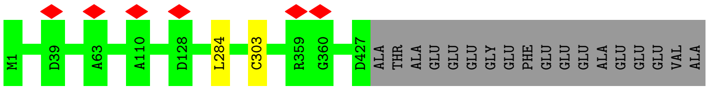
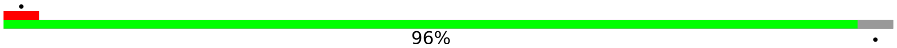
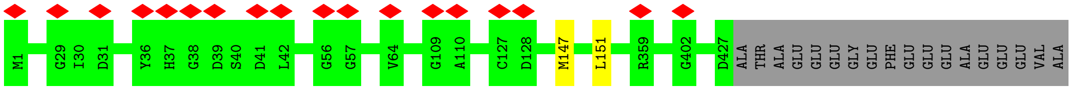




- Molecule 9: Tubulin beta-4B chain

Chain UJ:





- Molecule 9: Tubulin beta-4B chain

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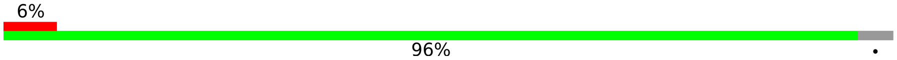

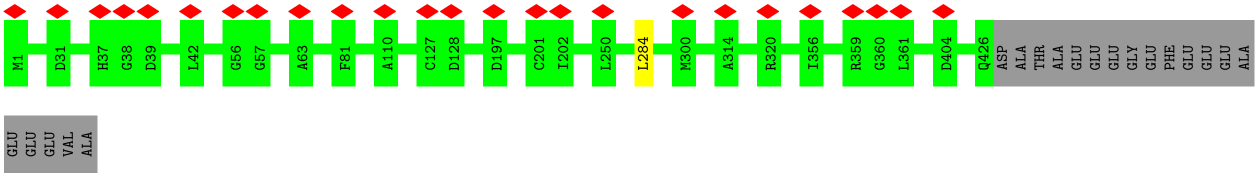

- Molecule 9: Tubulin beta-4B chain

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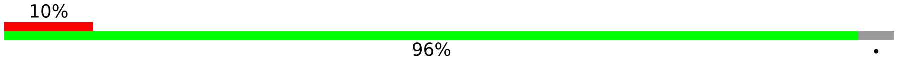

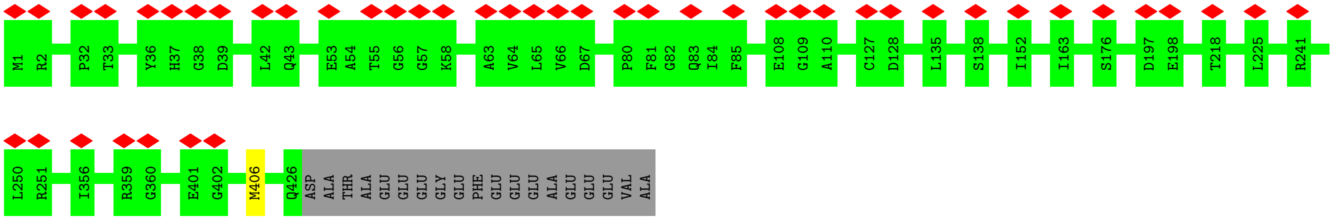

- Molecule 9: Tubulin beta-4B chain

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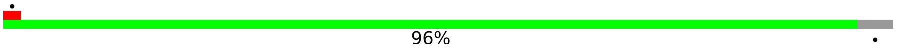

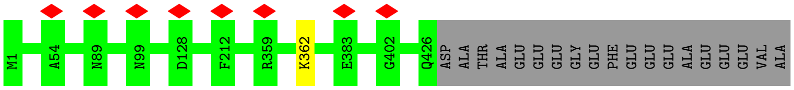

- Molecule 9: Tubulin beta-4B chain

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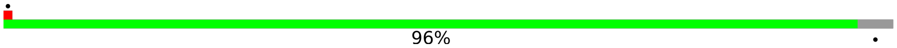
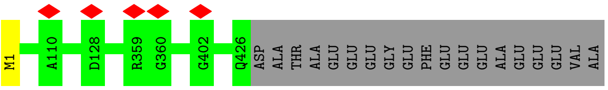
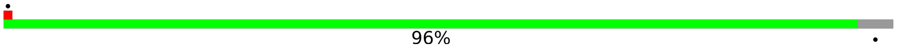
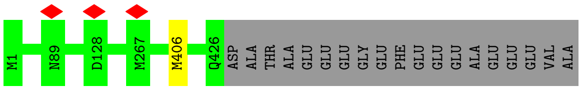




- Molecule 9: Tubulin beta-4B chain

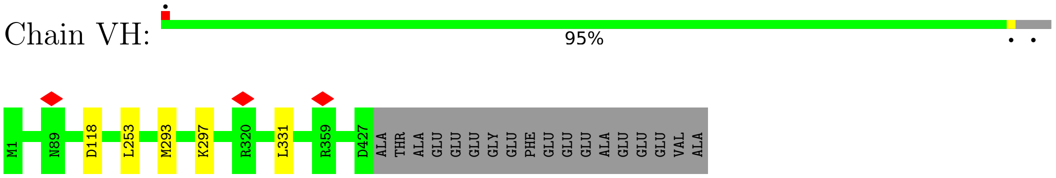
Chain VF:





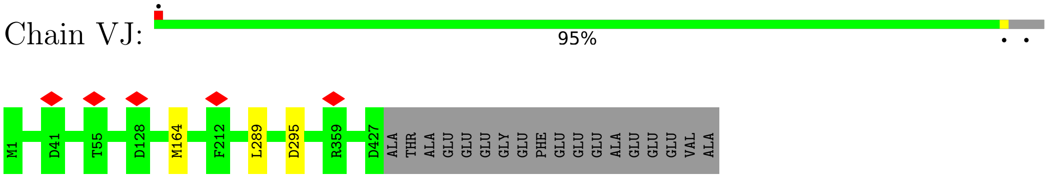
- Molecule 9: Tubulin beta-4B chain

Chain VH:



- Molecule 9: Tubulin beta-4B chain

Chain VJ:



- Molecule 9: Tubulin beta-4B chain

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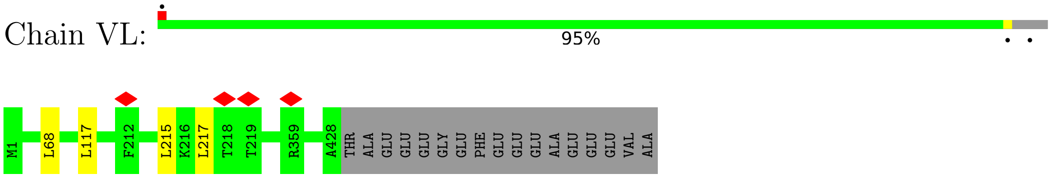

- Molecule 9: Tubulin beta-4B chain

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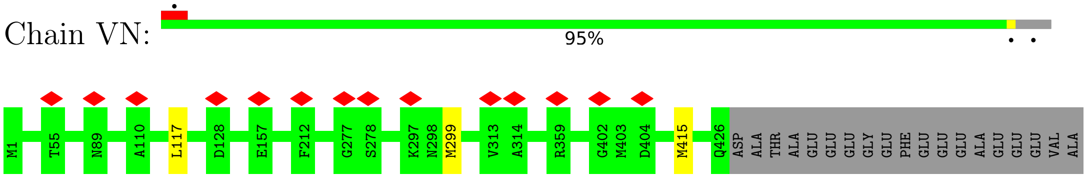

- Molecule 9: Tubulin beta-4B chain

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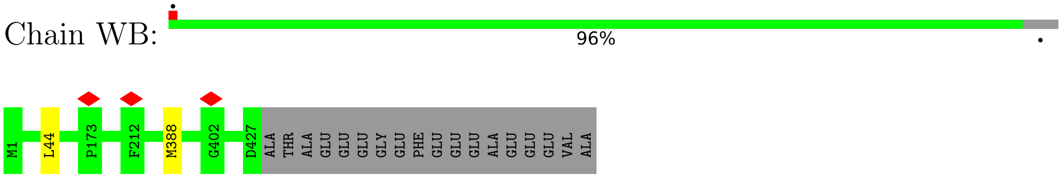
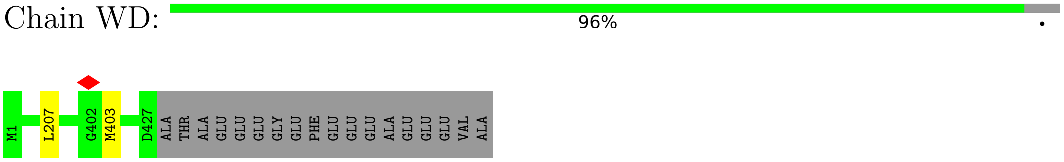


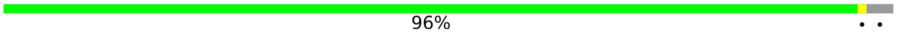
- Molecule 9: Tubulin beta-4B chain

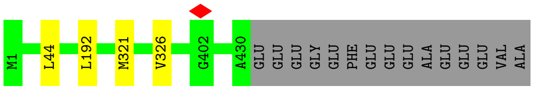
Chain WD:



- Molecule 9: Tubulin beta-4B chain

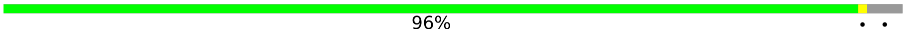
Chain WF:

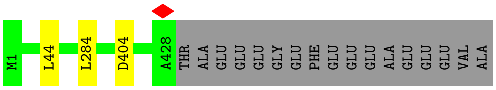




- Molecule 9: Tubulin beta-4B chain

Chain WH:





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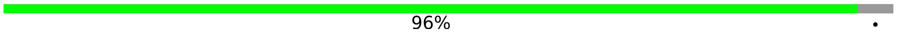

- Molecule 9: Tubulin beta-4B chain

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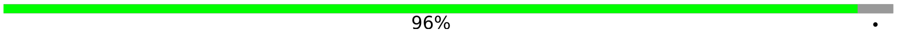

- Molecule 9: Tubulin beta-4B chain

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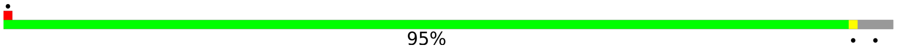

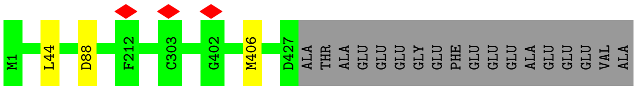

- Molecule 9: Tubulin beta-4B chain

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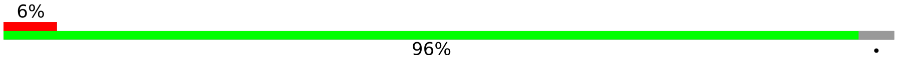
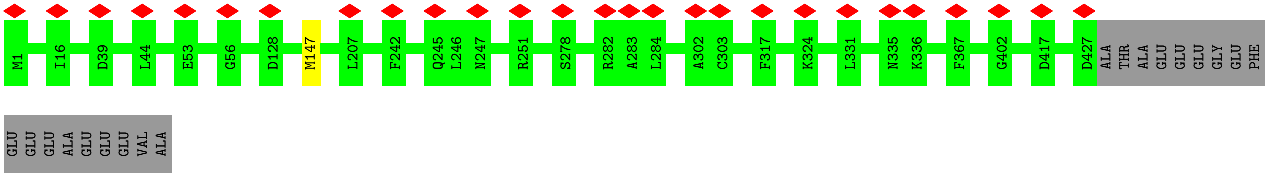
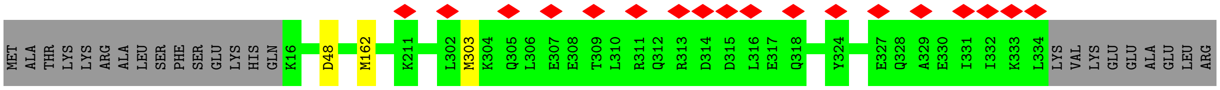
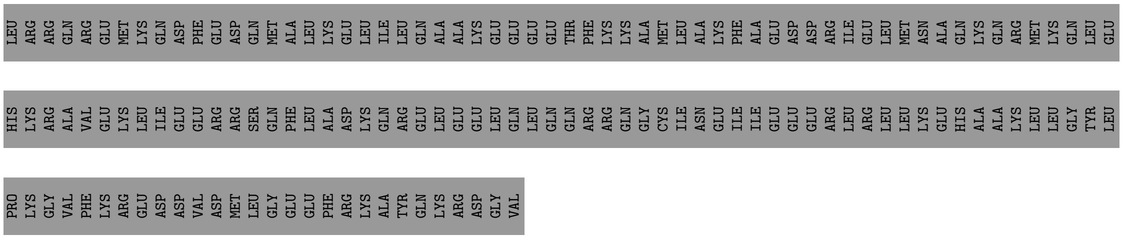




- Molecule 10: Meiosis-specific nuclear structural protein 1

Chain B:





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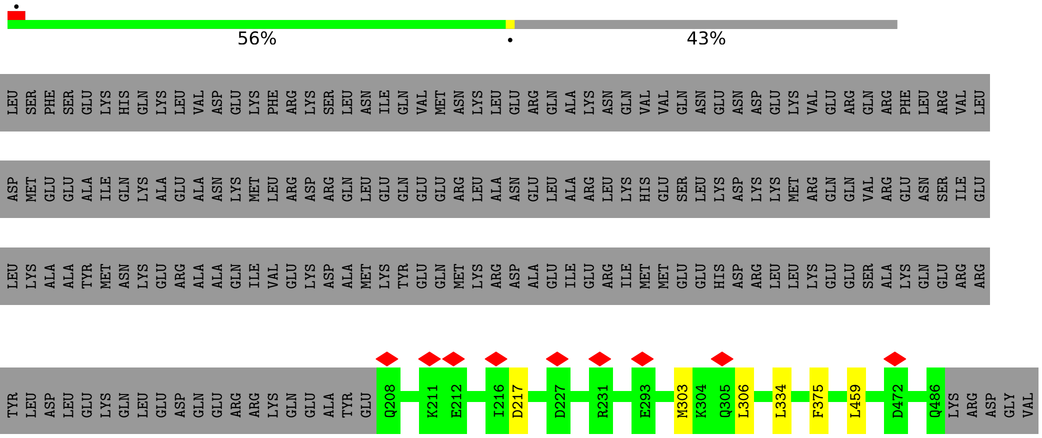
HIS LYS ARG ALA VAL GLU LYS LEU ILE GLU GLU ARG ARG SER GLN PHE LEU ALA ASP LYS GLN ARG GLU LEU GLU GLU LEU GLN LEU GLN GLN ARG ARG GLN GLY CYS ILE ASN GLU ILE ILE GLU GLU GLU ARG LEU ARG LEU LEU LYS GLU HIS ALA ALA LYS LEU LEU GLY TYR LEU

PRO LYS GLY VAL PHE LYS ARG GLU ASP ASP VAL ASP MET LEU GLY GLU GLU PHE ARG LYS ALA TYR GLN LYS ARG ASP GLY VAL

- Molecule 10: Meiosis-specific nuclear structural protein 1

Chain C:



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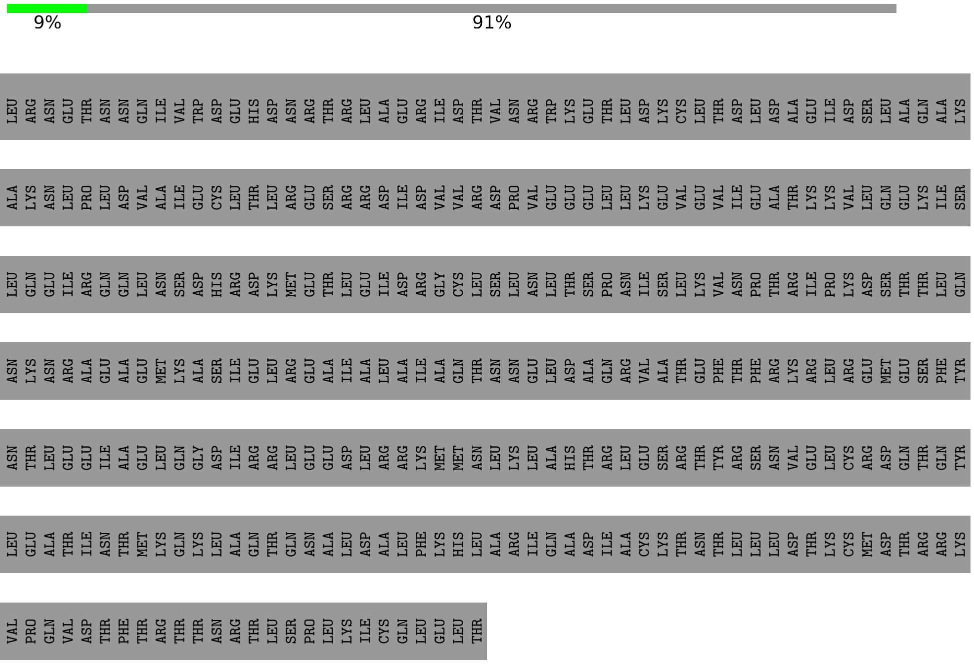
GLN ASN GLU GLN PHE GLU LEU ASP MET GLU GLU ALA ILE GLN LYS ALA GLU ALA ASN LYS MET LEU ARG ASP ARG GLN LEU GLU GLN GLU GLU ARG LEU ALA ASN GLU LEU ALA ARG LEU LYS HIS GLU SER LEU LYS ASP LYS LYS MET ARG GLN GLN VAL ARG GLU ASN SER ILE GLU

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

ASN LYS GLU ARG ALA GLN TYR TYR LEU ASP LEU GLU LYS GLN LEU GLU ASP GLN GLU ARG ARG LYS GLN GLU ALA TYR GLU Q208 K211 E212 I216 D217 D227 R231 E293 M303 K304 Q305 L306 L334 F375 L459 D472 Q486 LYS ARG ASP GLY VAL

- Molecule 11: Tektin-2

Chain B0:



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

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

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

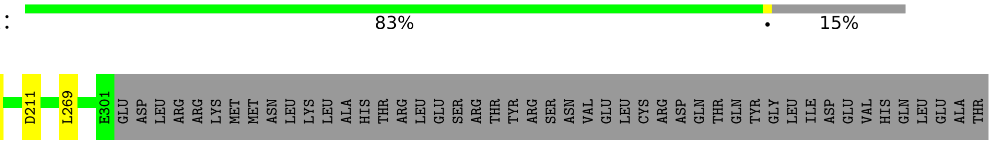
SER GLU LEU LYS TRP GLN GLU LYS ASN THR LEU GLU GLU ILE ALA GLU LEU GLN GLY ASP ILE ARG ARG LEU GLU GLU ASP LEU ARG ARG LYS MET MET ASN LEU LYS LEU ALA HIS THR ARG LEU GLU SER ARG THR TYR ARG SER ASN VAL GLU LEU CYS ARG ASP GLN THR GLN TYR

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

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

- Molecule 11: Tektin-2

Chain B1:



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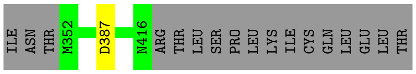
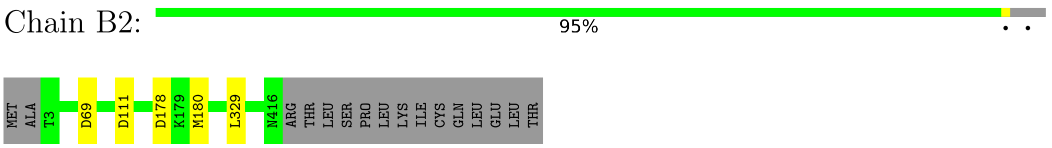


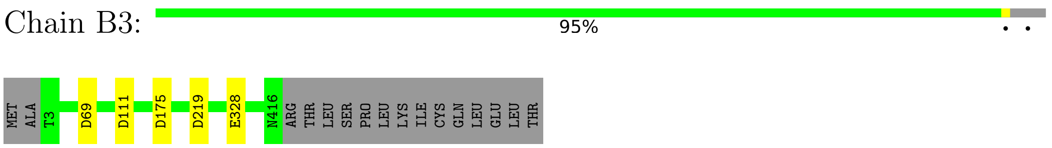
- Molecule 11: Tektin-2

Chain B2:



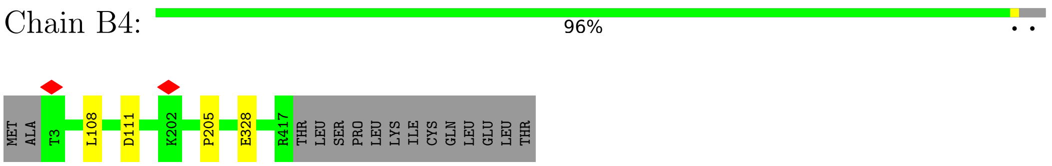
- Molecule 11: Tektin-2

Chain B3:



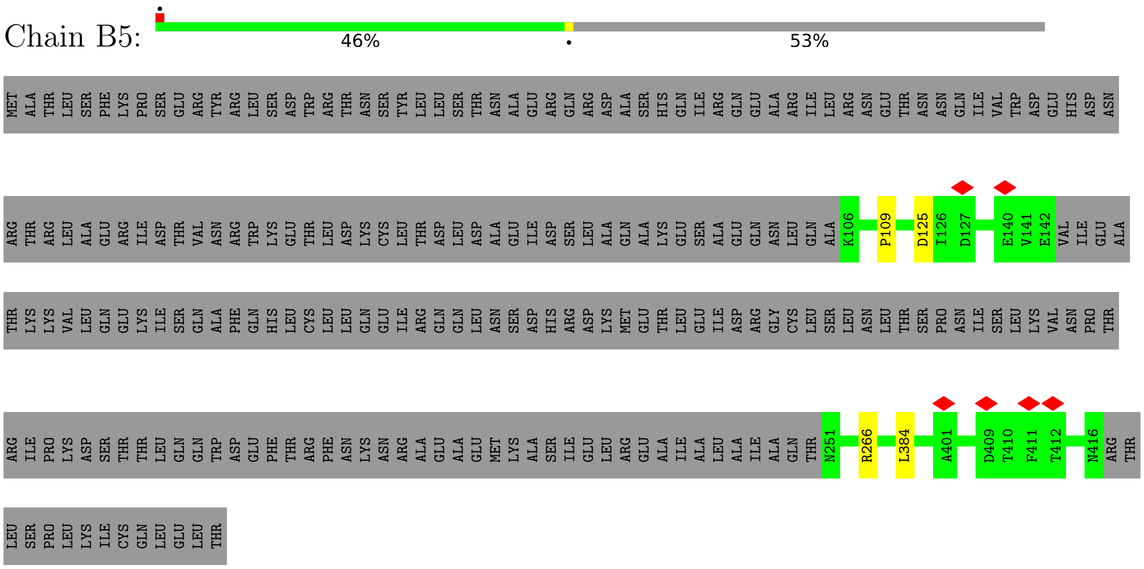
- Molecule 11: Tektin-2

Chain B4:



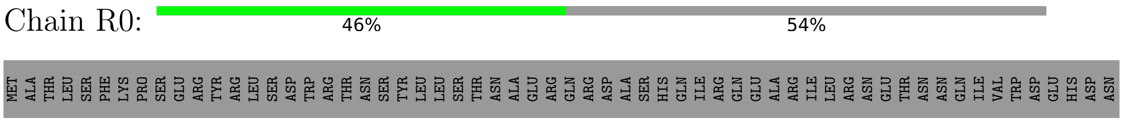
- Molecule 11: Tektin-2

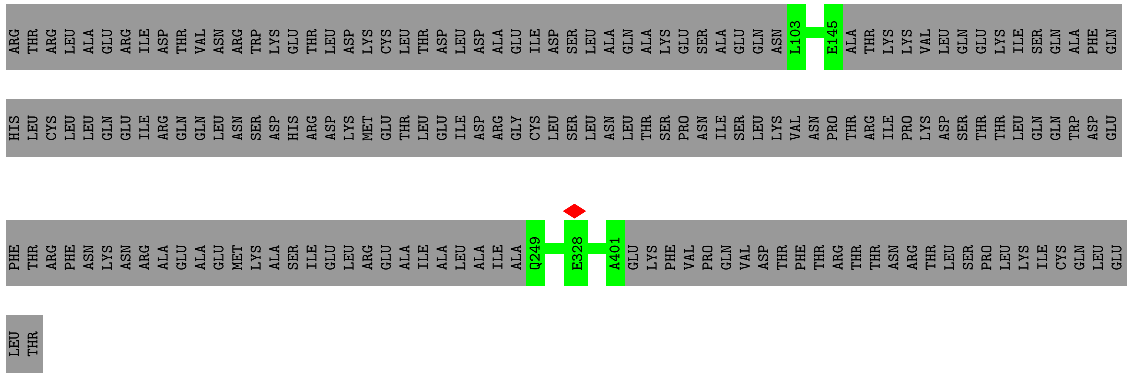
Chain B5:



- Molecule 11: Tektin-2

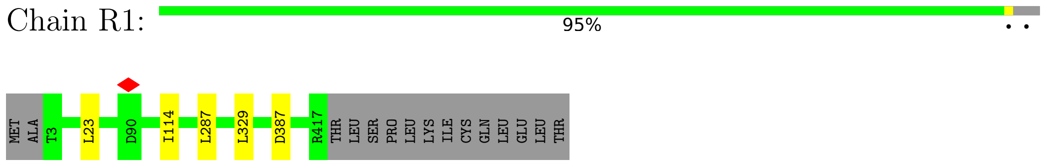
Chain R0:





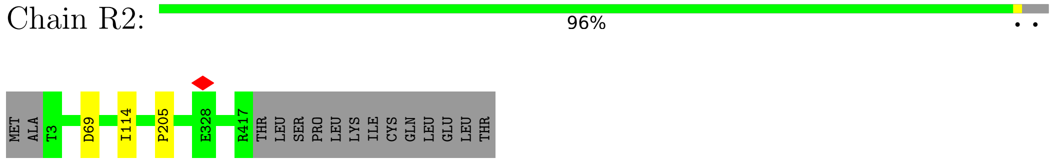
- Molecule 11: Tektin-2

Chain R1:



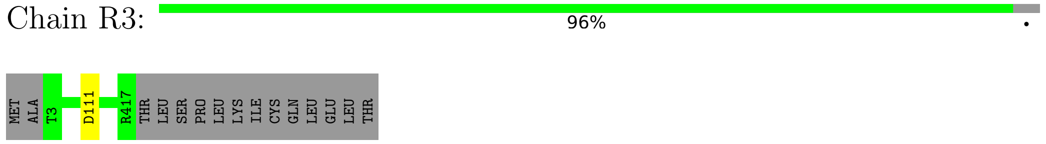
- Molecule 11: Tektin-2

Chain R2:



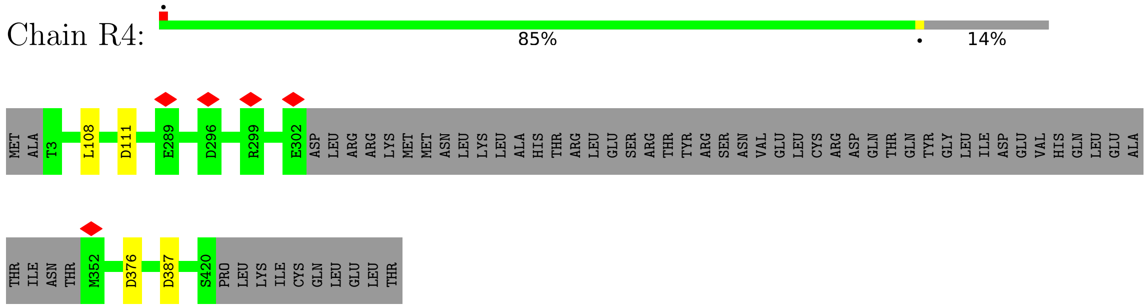
- Molecule 11: Tektin-2

Chain R3:



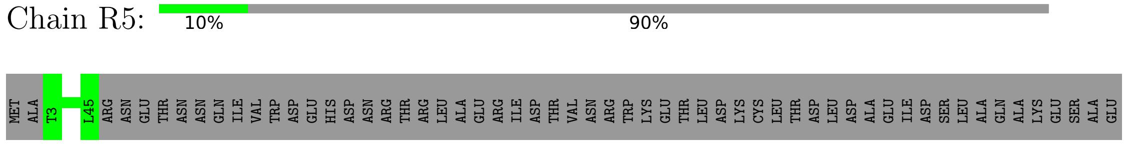
- Molecule 11: Tektin-2

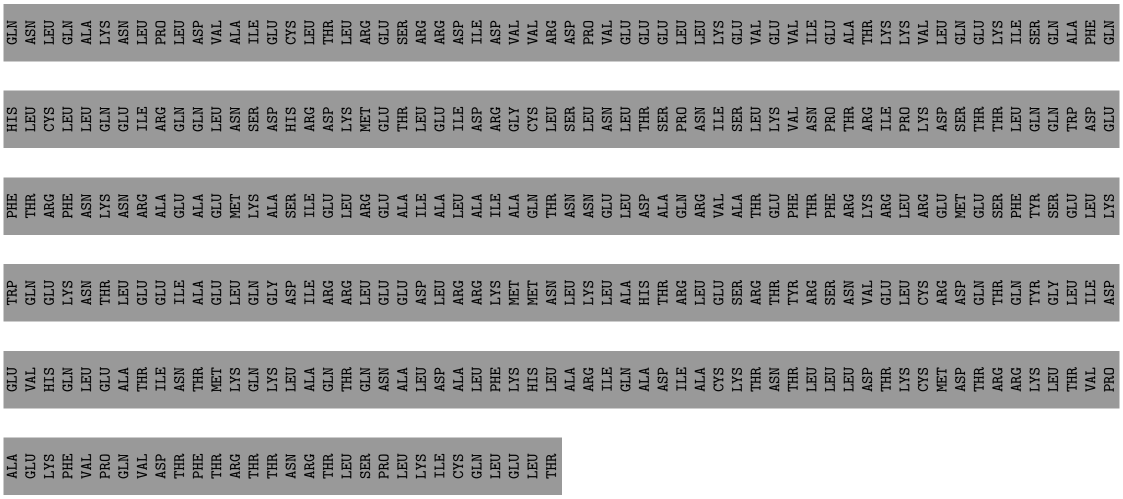
Chain R4:



- Molecule 11: Tektin-2

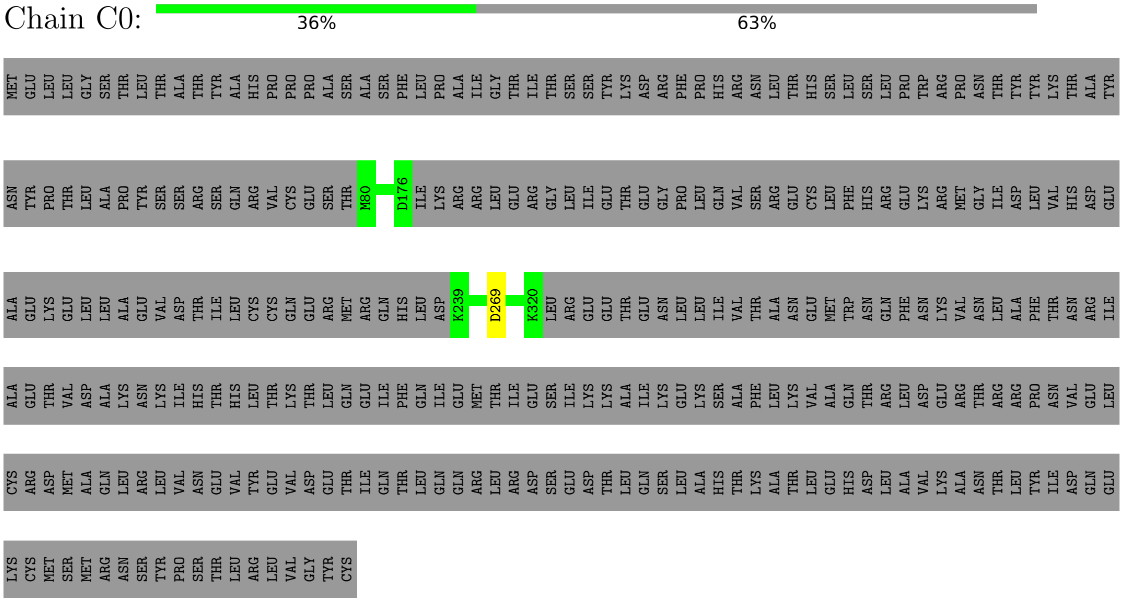
Chain R5:





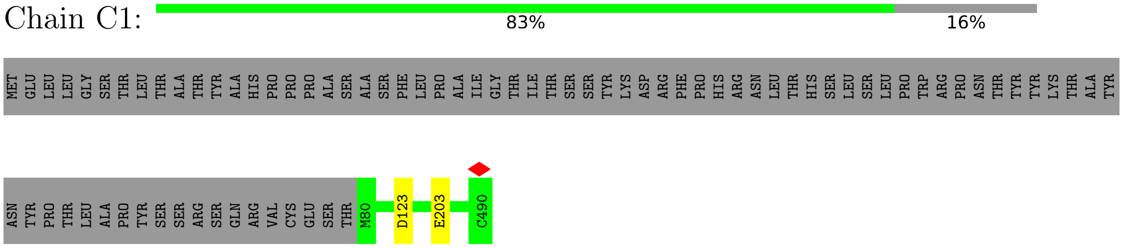
- Molecule 12: Tektin-3

Chain C0:



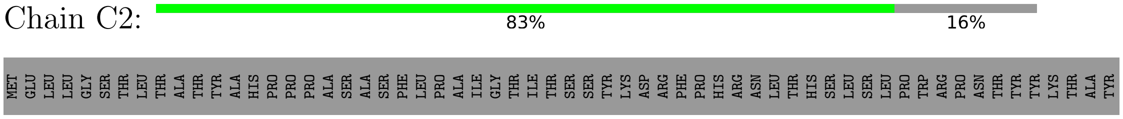
- Molecule 12: Tektin-3

Chain C1:



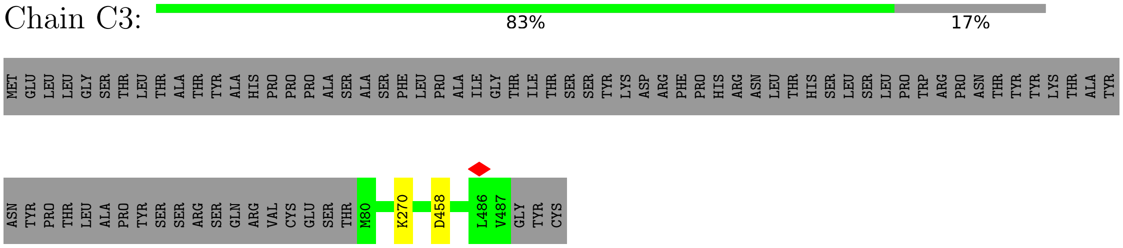
- Molecule 12: Tektin-3

Chain C2:



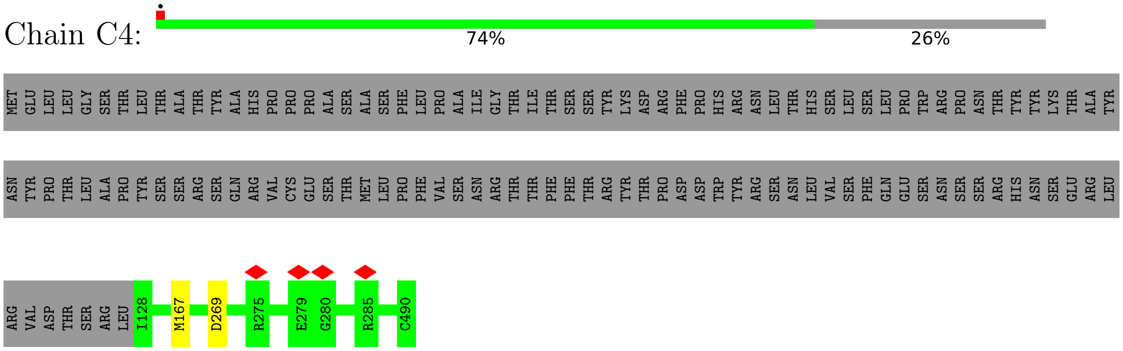
- Molecule 12: Tektin-3

Chain C3:



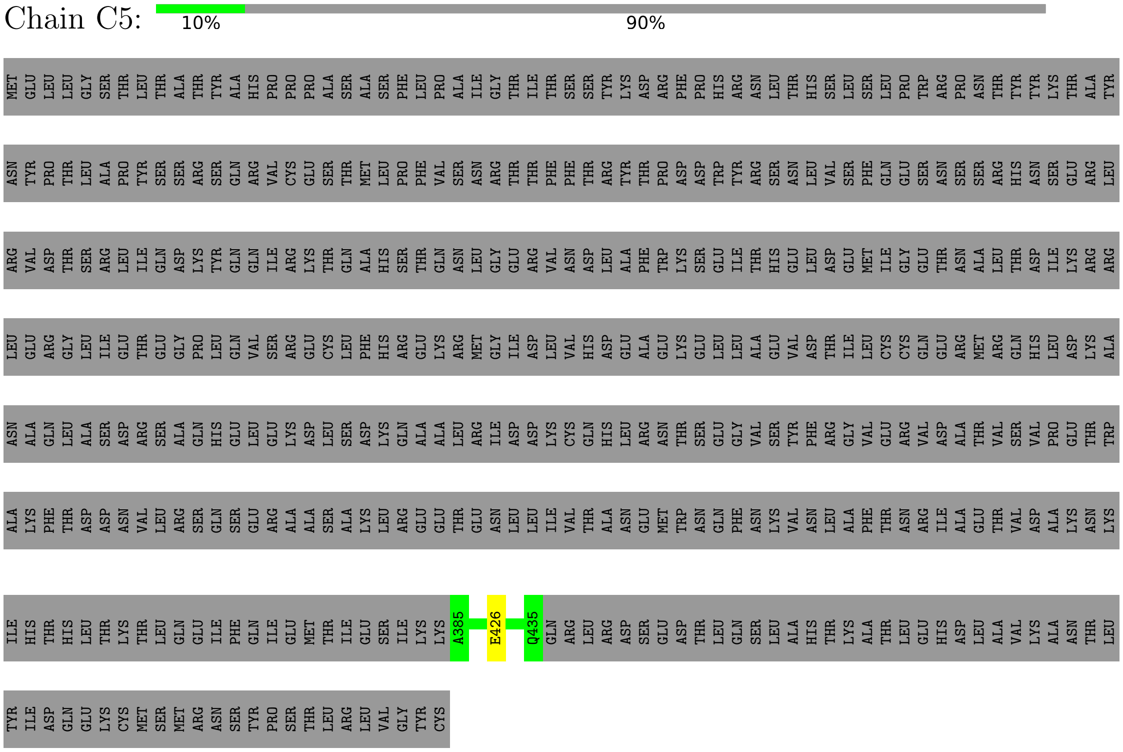
- Molecule 12: Tektin-3

Chain C4:



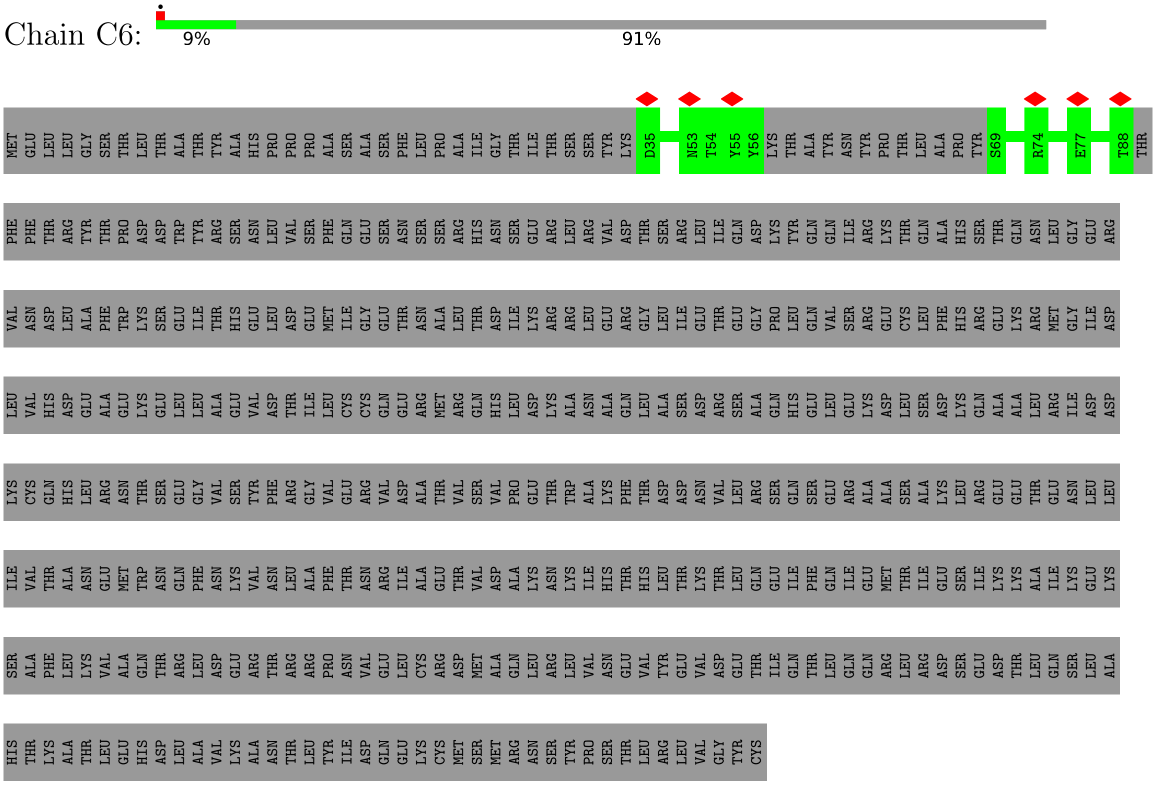
- Molecule 12: Tektin-3

Chain C5:



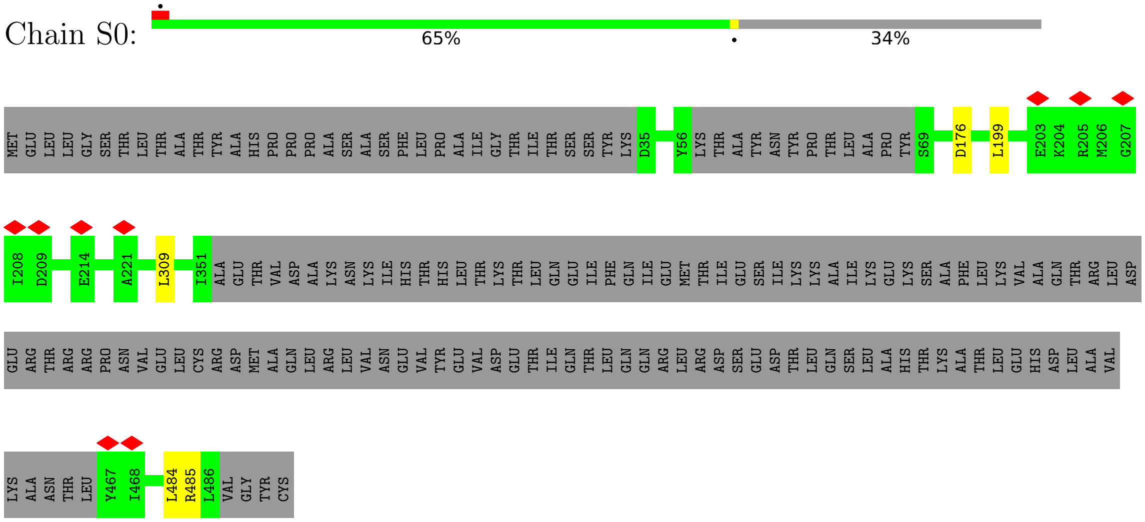
- Molecule 12: Tektin-3

Chain C6:



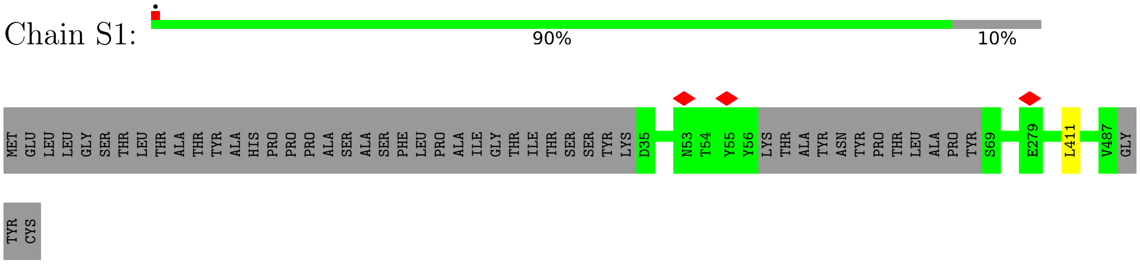
- Molecule 12: Tektin-3

Chain S0:

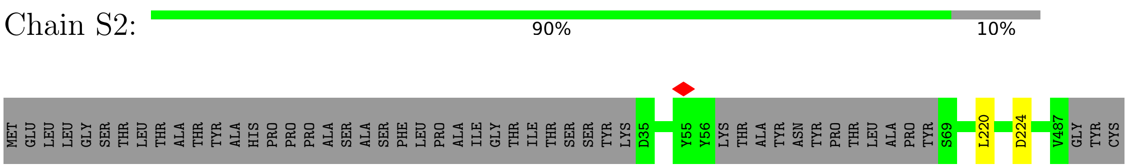


- Molecule 12: Tektin-3

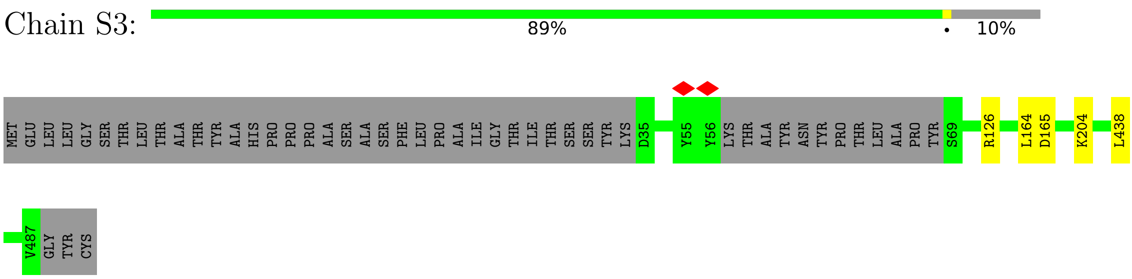
Chain S1:



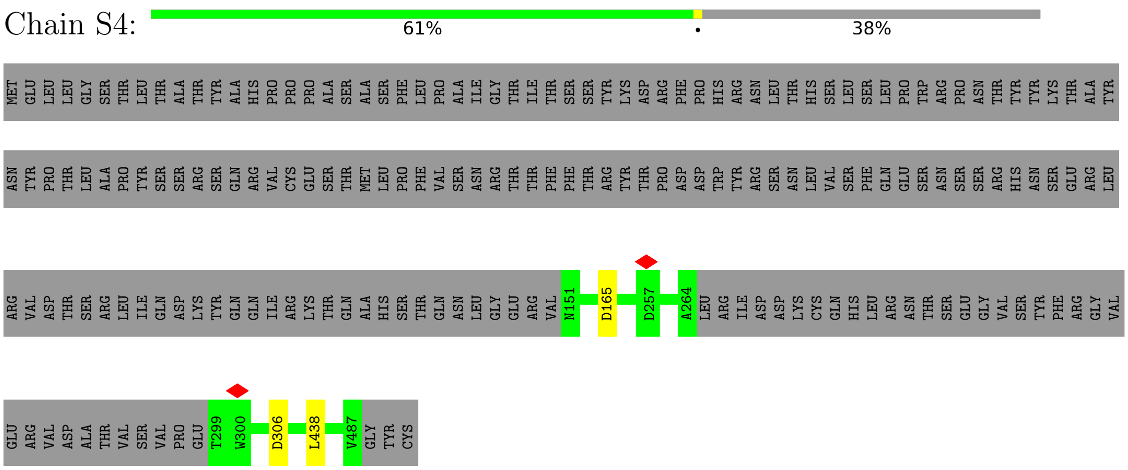
- Molecule 12: Tektin-3



- Molecule 12: Tektin-3



- Molecule 12: Tektin-3



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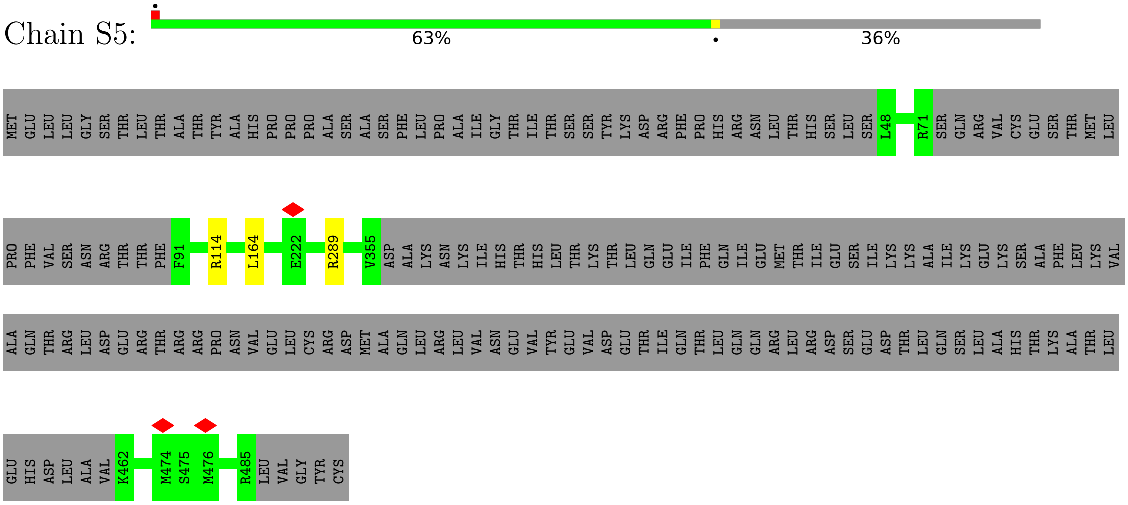

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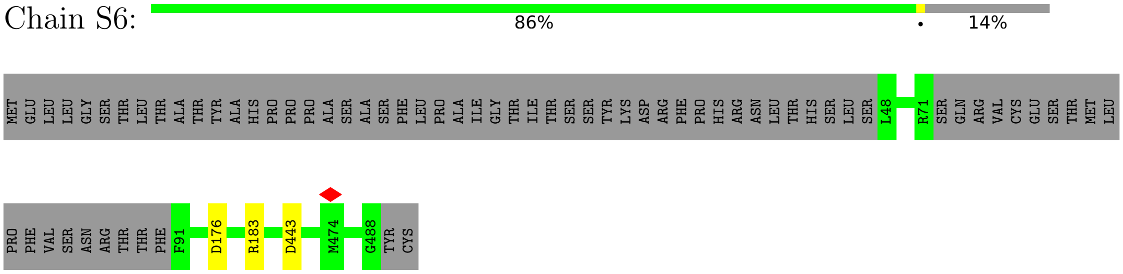

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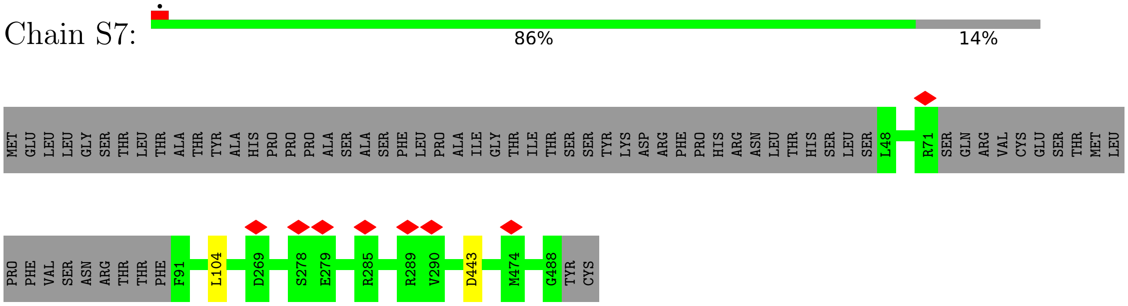
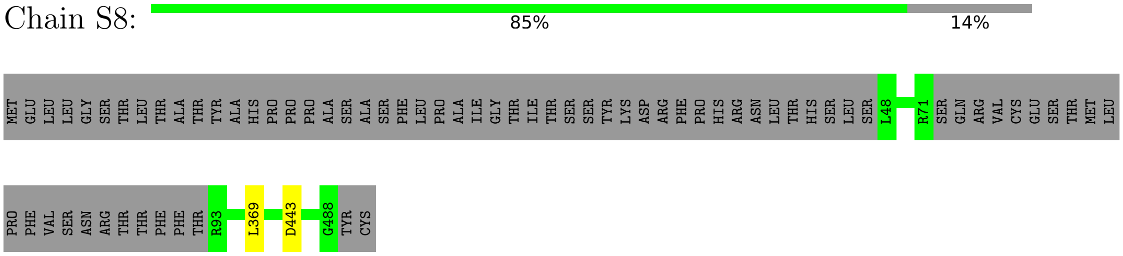
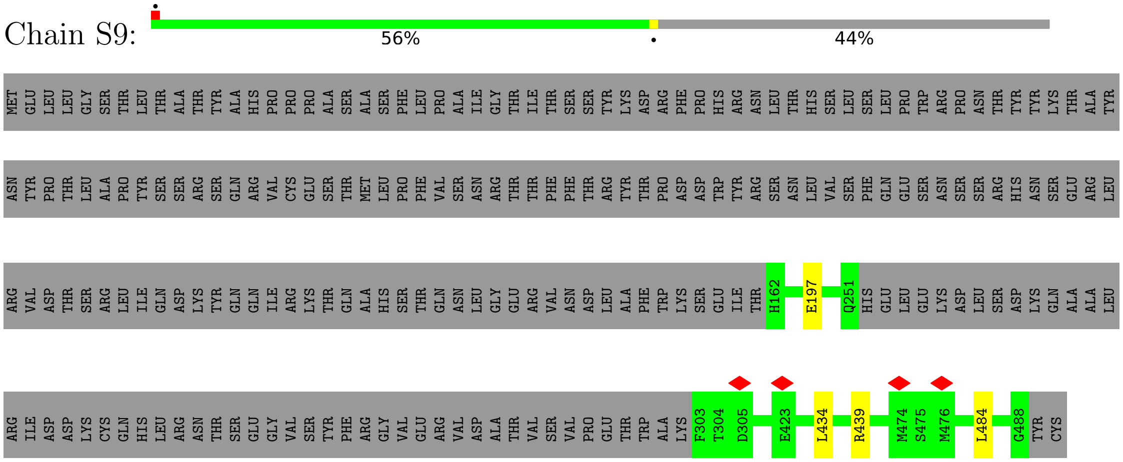


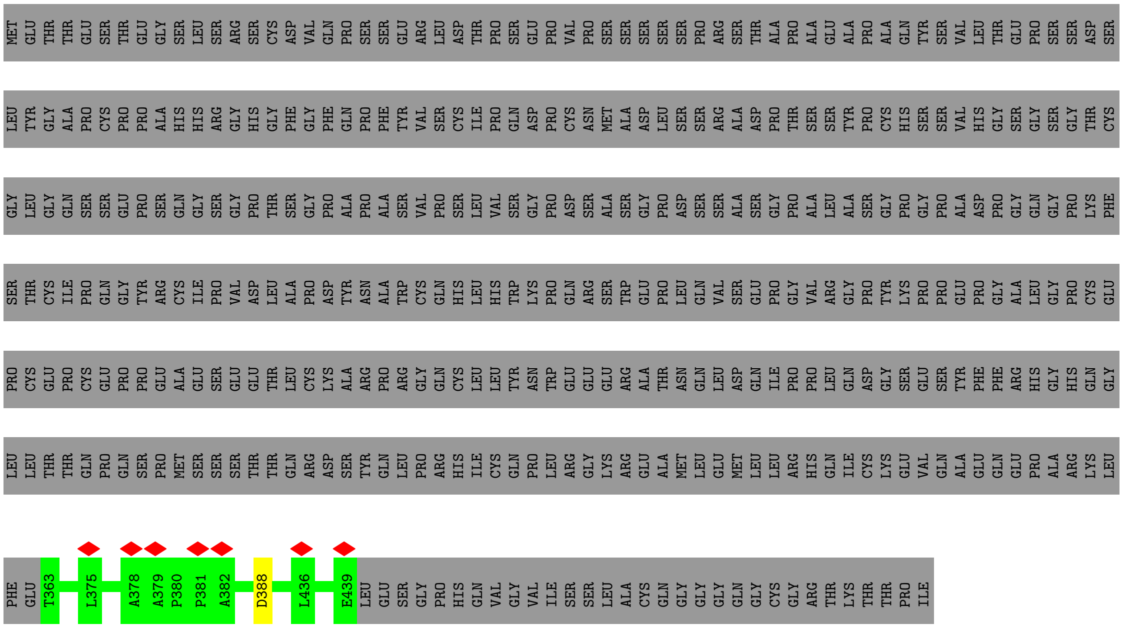
- Molecule 12: Tektin-3



- Molecule 12: Tektin-3

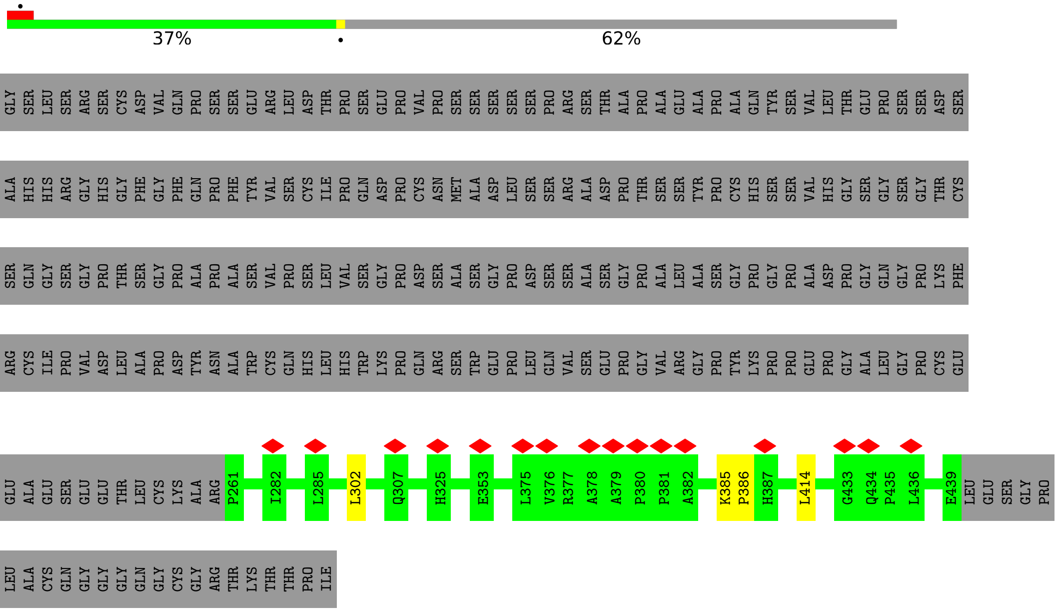


- Molecule 13: Sperm-associated antigen 8



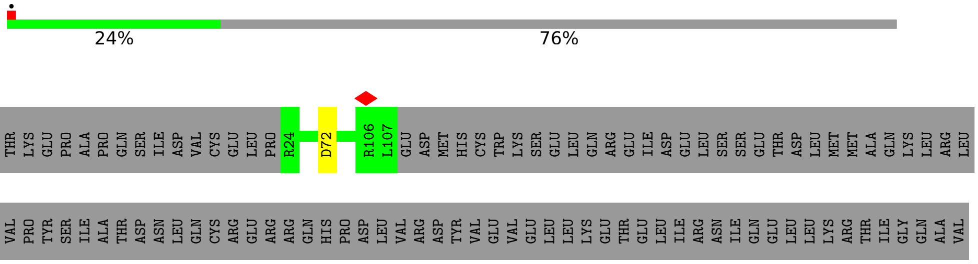
- Molecule 13: Sperm-associated antigen 8

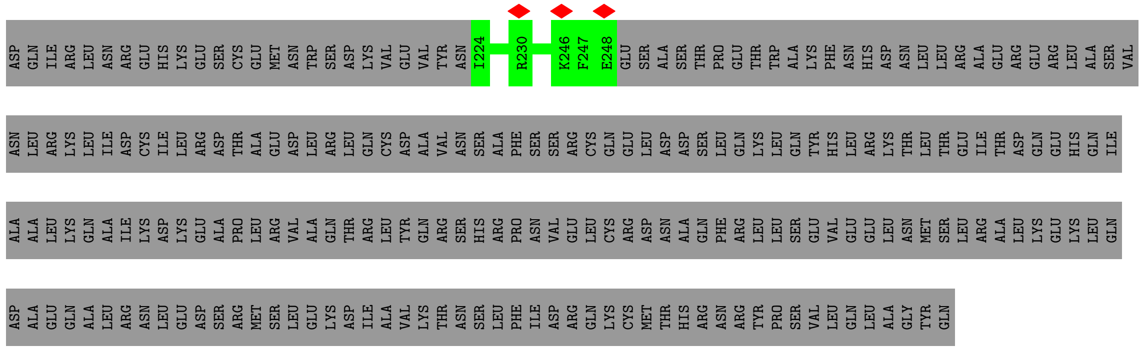
Chain K3:



- Molecule 14: Tektin-4

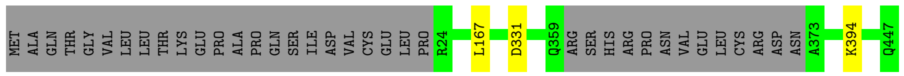
Chain D0:





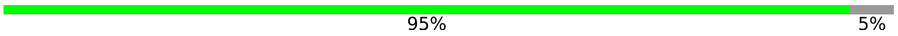
- Molecule 14: Tektin-4

Chain D1:



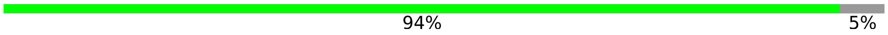
- Molecule 14: Tektin-4

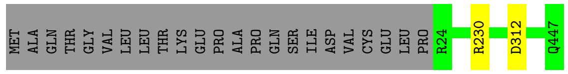
Chain D2:



- Molecule 14: Tektin-4

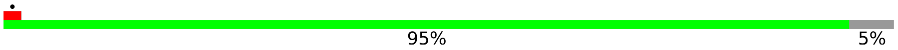
Chain D3:

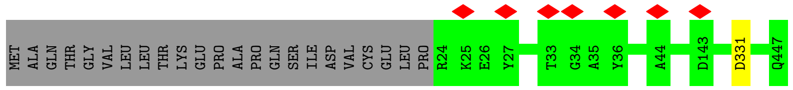




- Molecule 14: Tektin-4

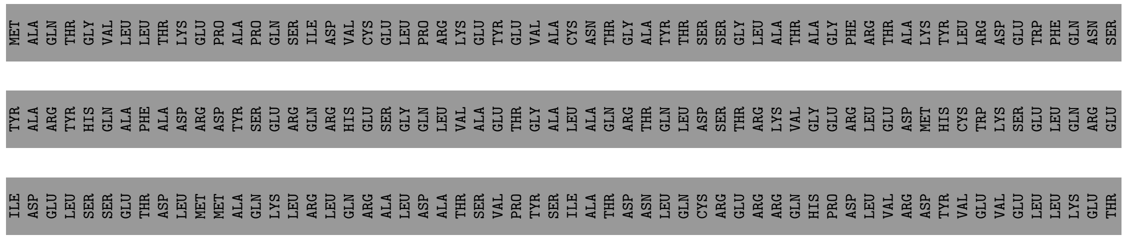
Chain D4:

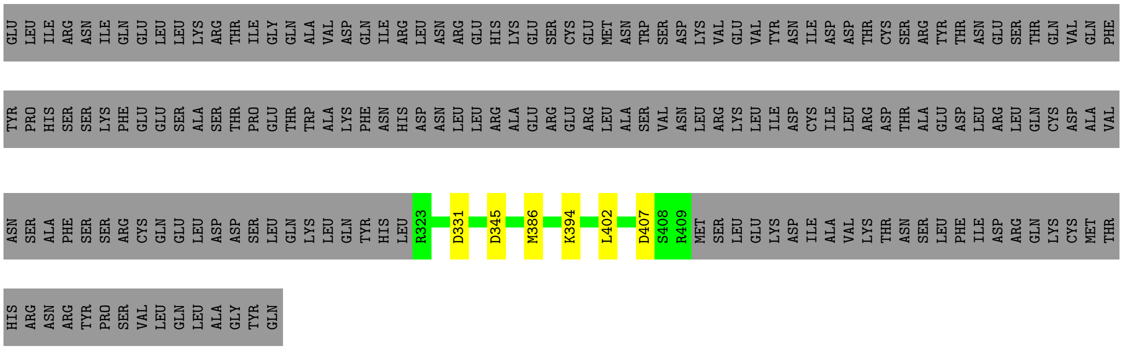




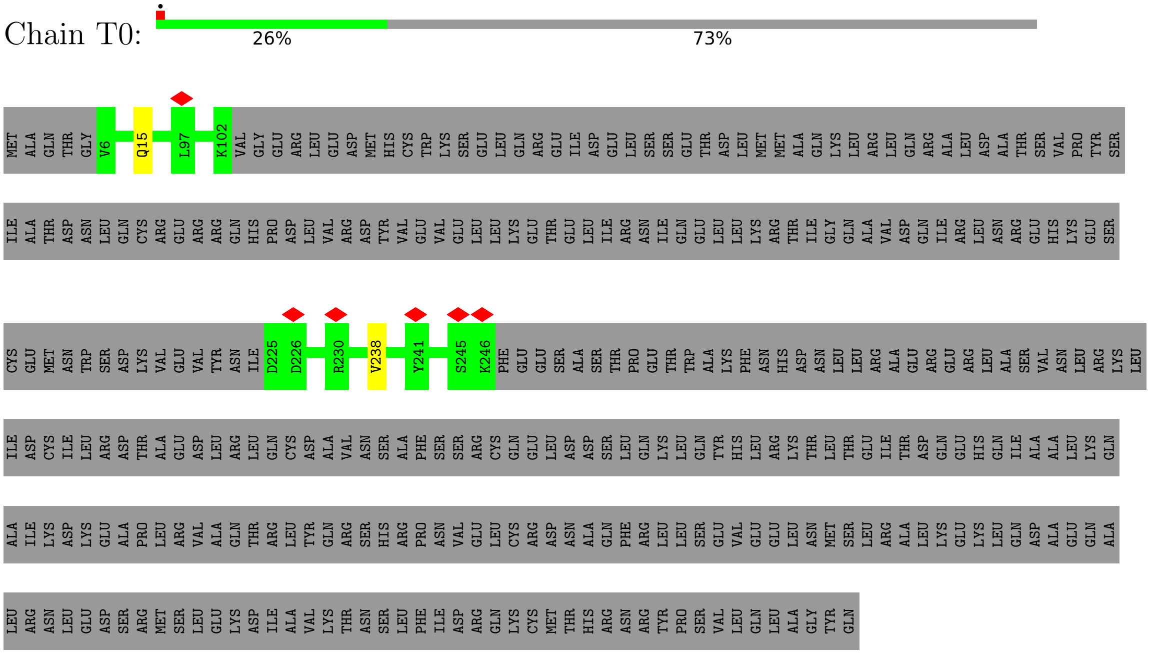
- Molecule 14: Tektin-4

Chain D5:





- Molecule 14: Tektin-4



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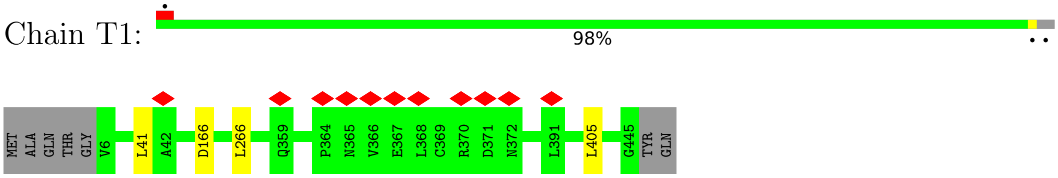

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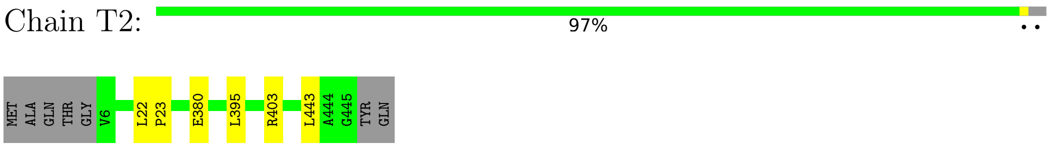

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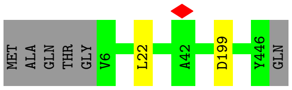
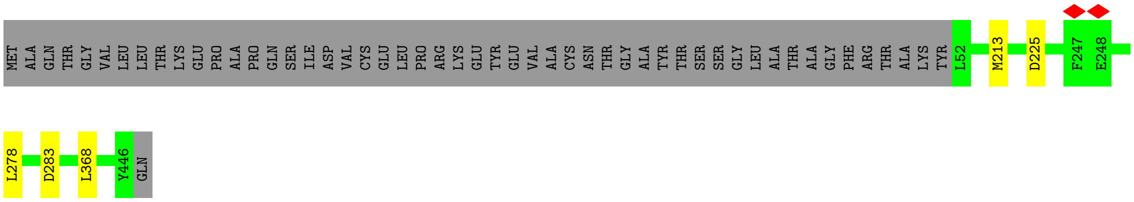


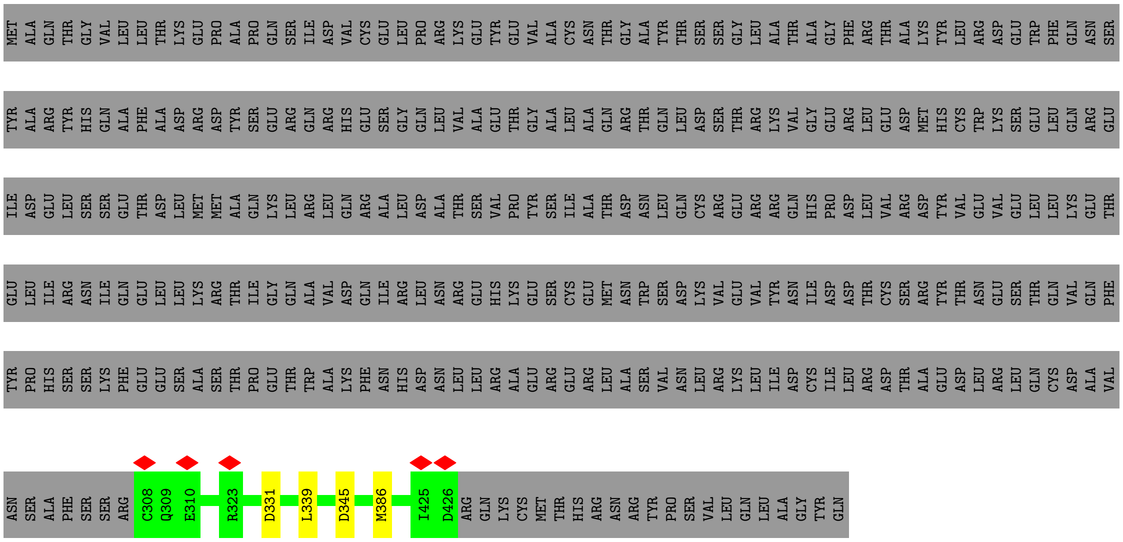
- Molecule 14: Tektin-4

Chain T4:



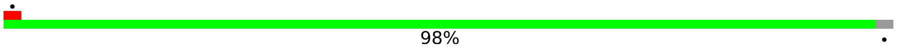
- Molecule 14: Tektin-4

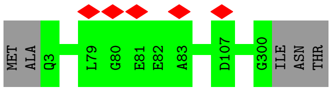
Chain T5:



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

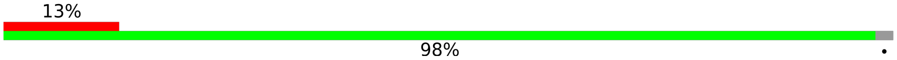
Chain E:

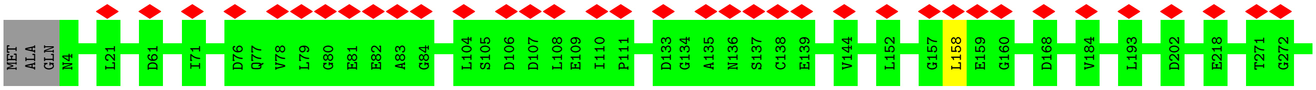


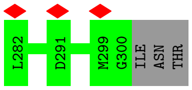


- Molecule 15: Cilia- and flagella-associated protein 161

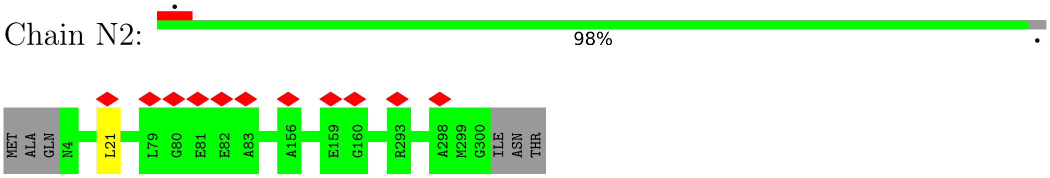
Chain F:



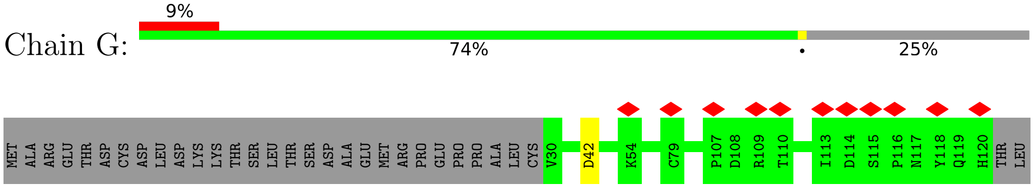




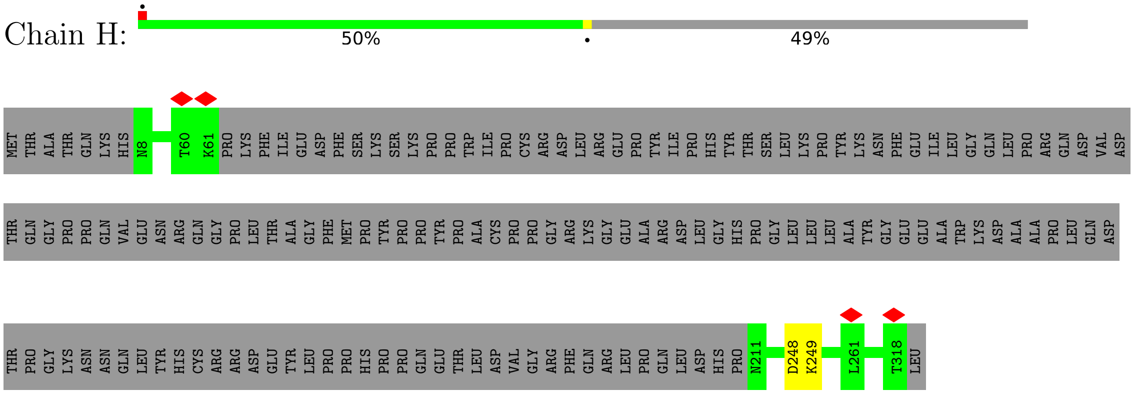
- Molecule 15: Cilia- and flagella-associated protein 161



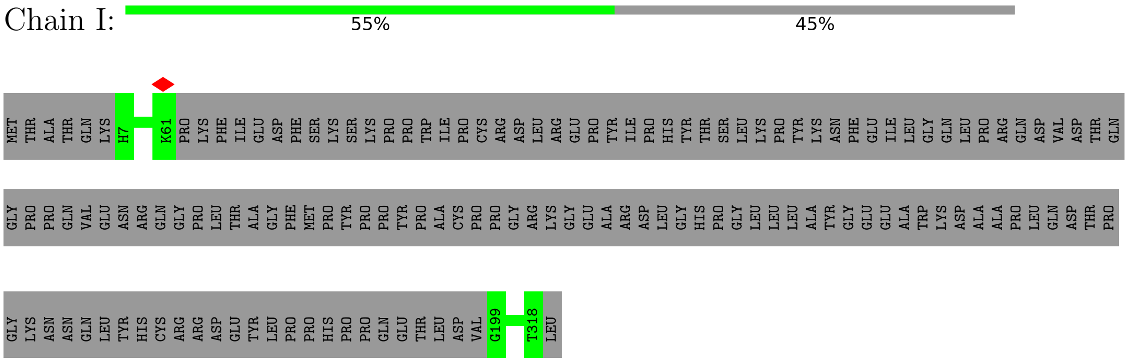
- Molecule 16: Piercer of microtubule wall 2 protein



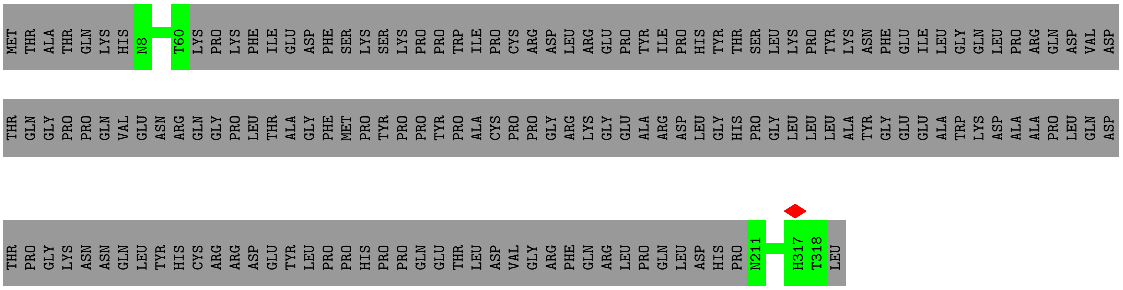
- Molecule 17: Protein FAM166A



- Molecule 17: Protein FAM166A

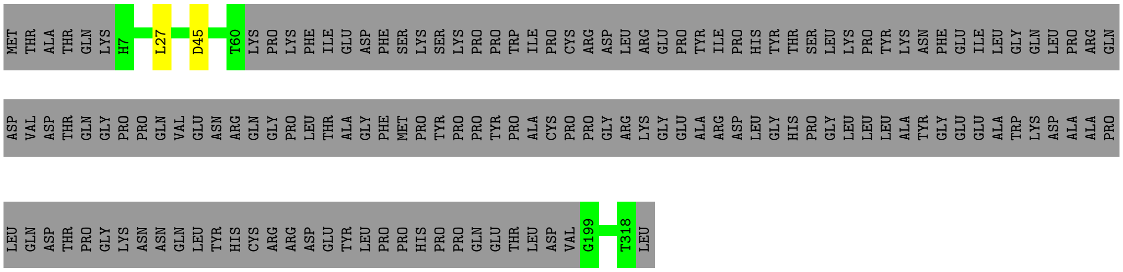


- Molecule 17: Protein FAM166A



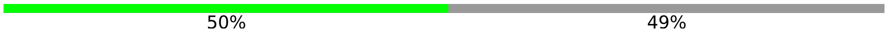
- Molecule 17: Protein FAM166A

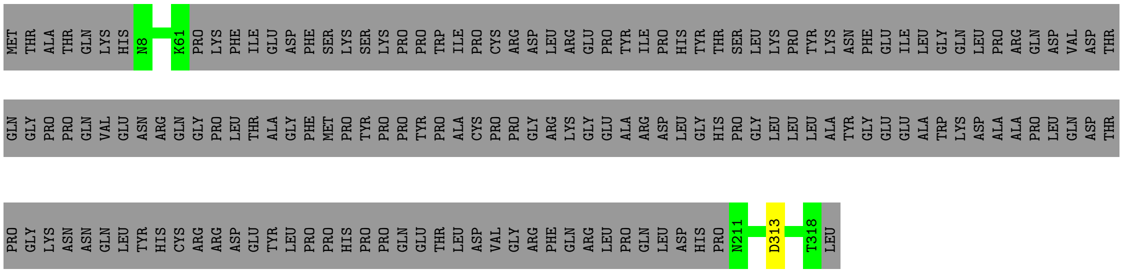
Chain K:



- Molecule 17: Protein FAM166A

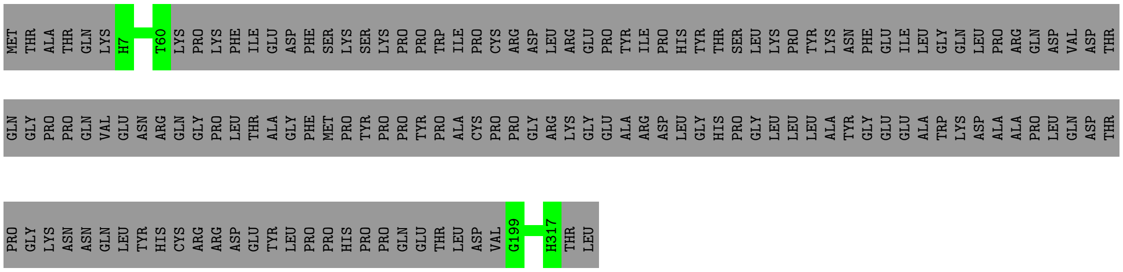
Chain L:





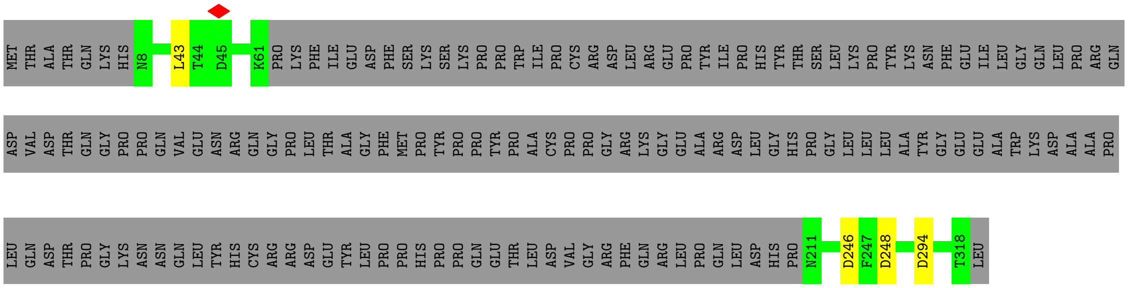
- Molecule 17: Protein FAM166A

Chain M:



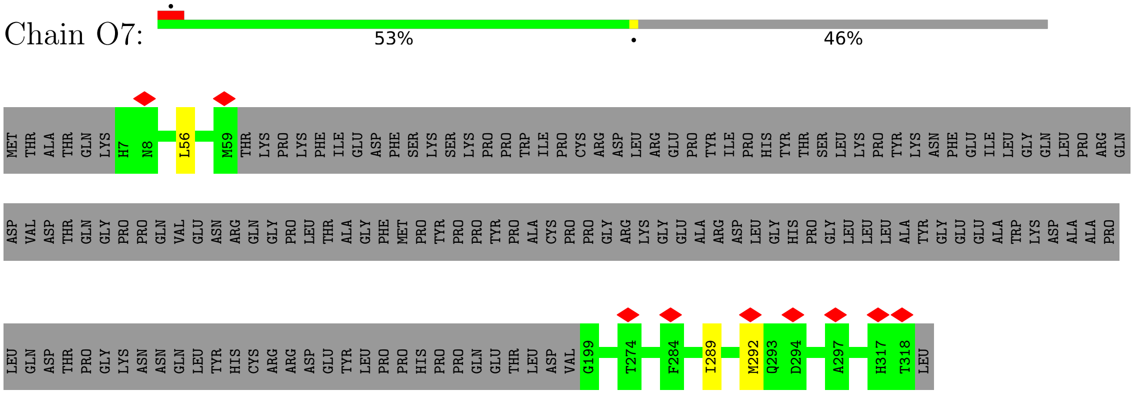
- Molecule 17: Protein FAM166A

Chain N:



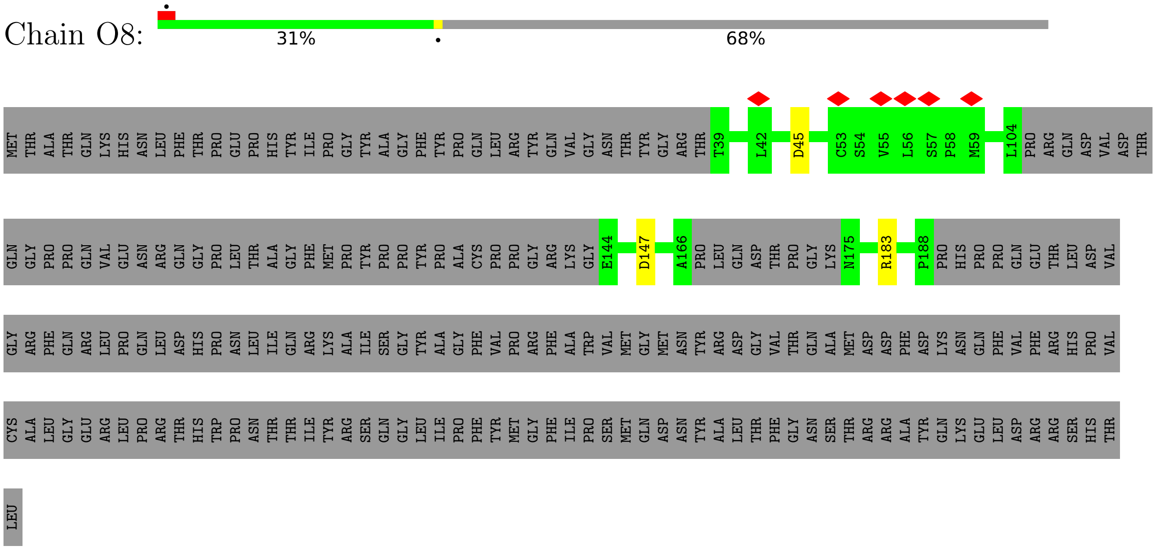
- Molecule 17: Protein FAM166A

Chain O7:



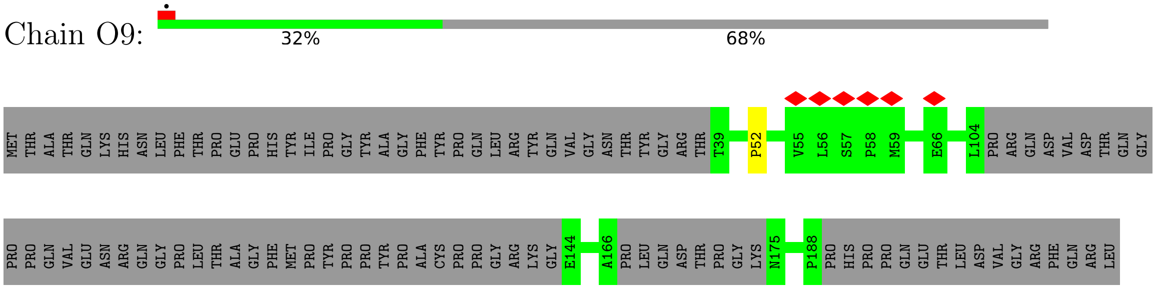
- Molecule 17: Protein FAM166A

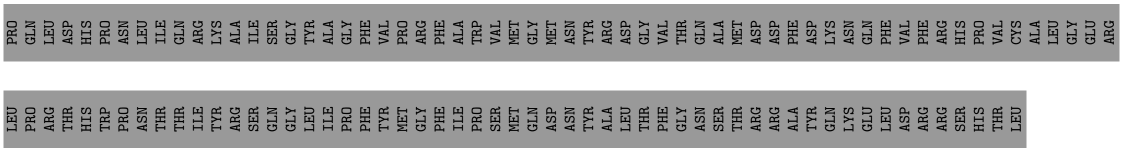
Chain O8:



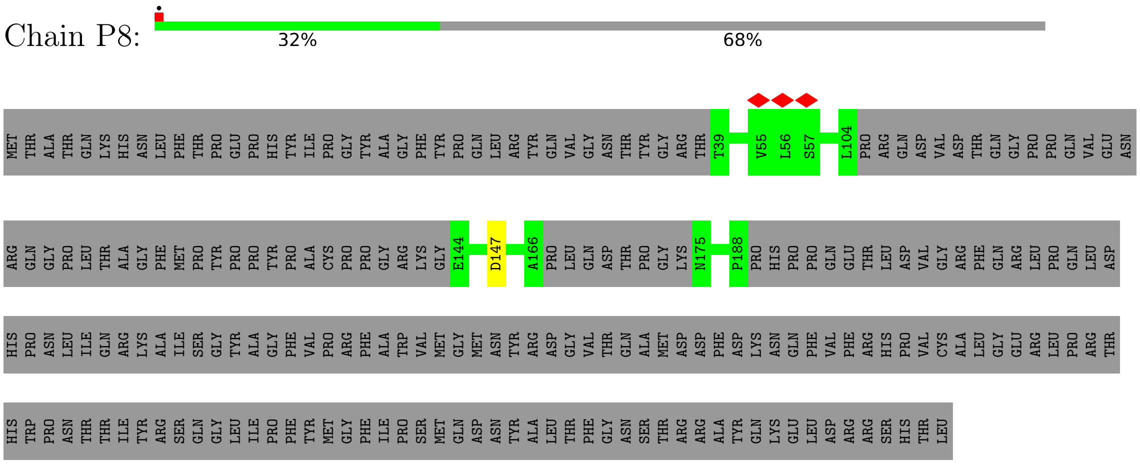
- Molecule 17: Protein FAM166A

Chain O9:





- Molecule 17: Protein FAM166A



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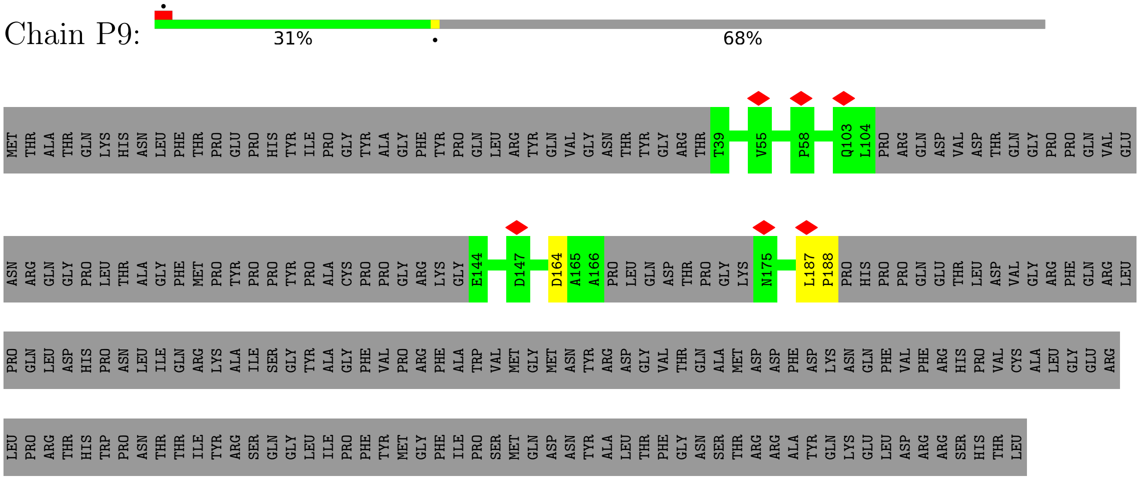
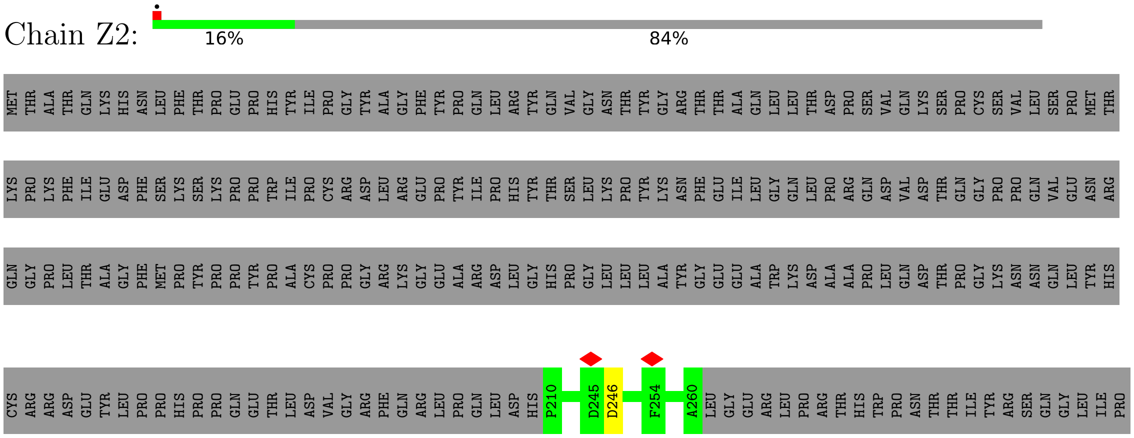


- Molecule 17: Protein FAM166A



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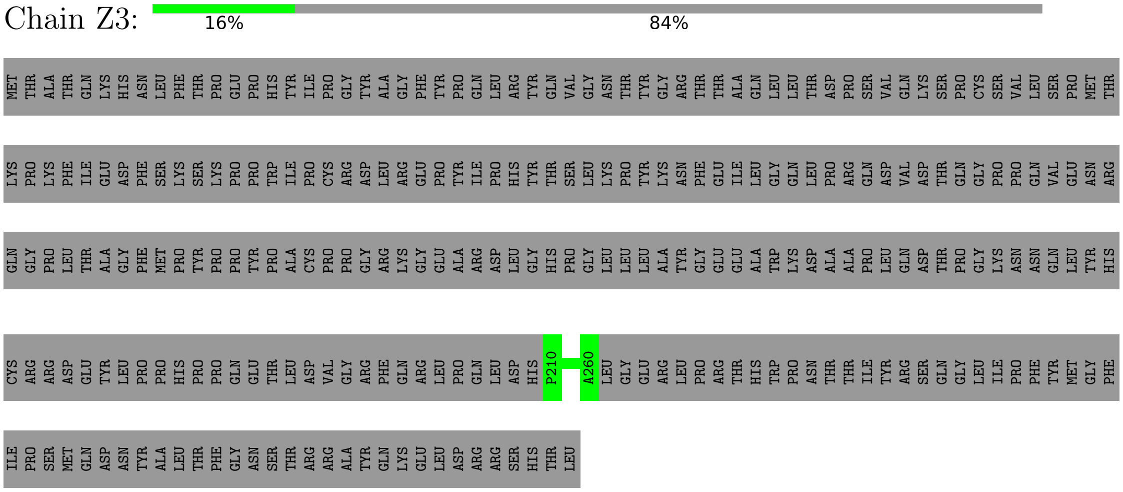
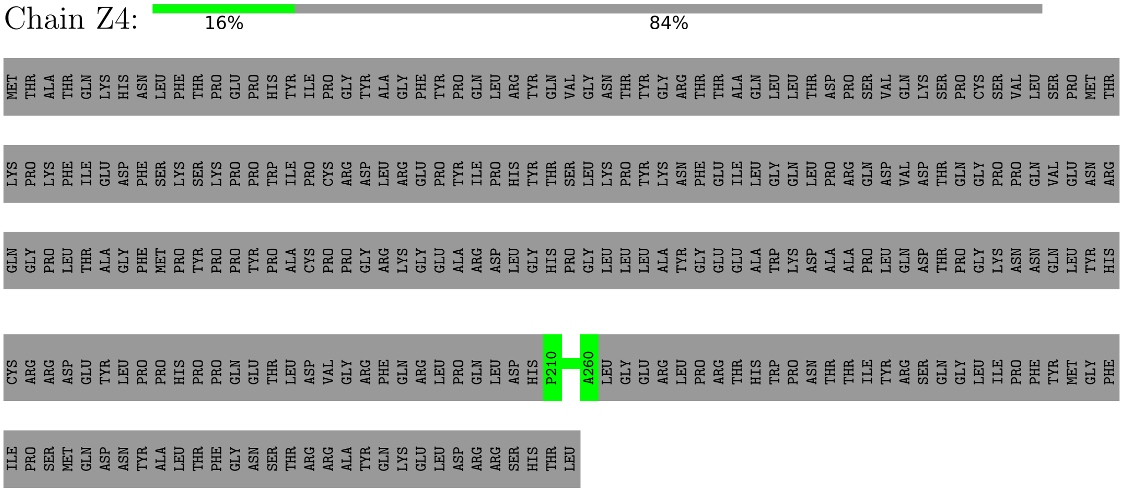
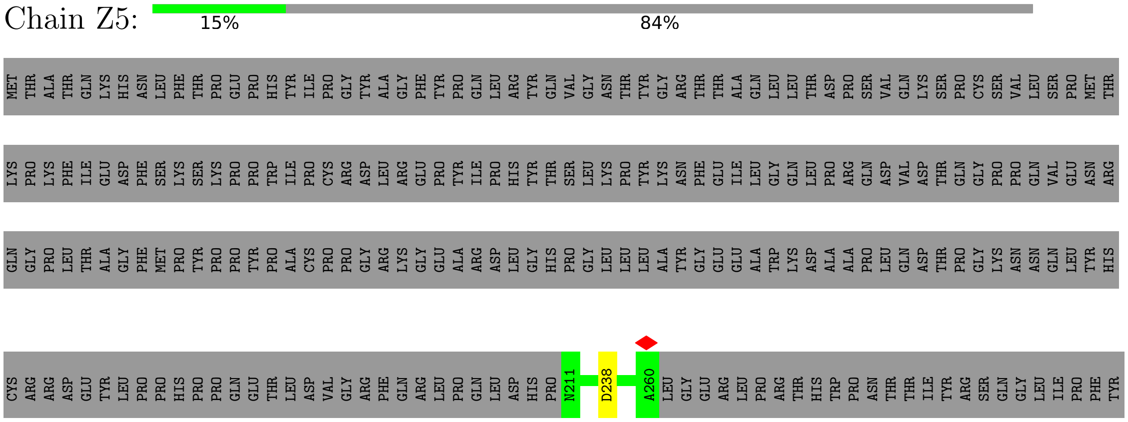


- Molecule 17: Protein FAM166A

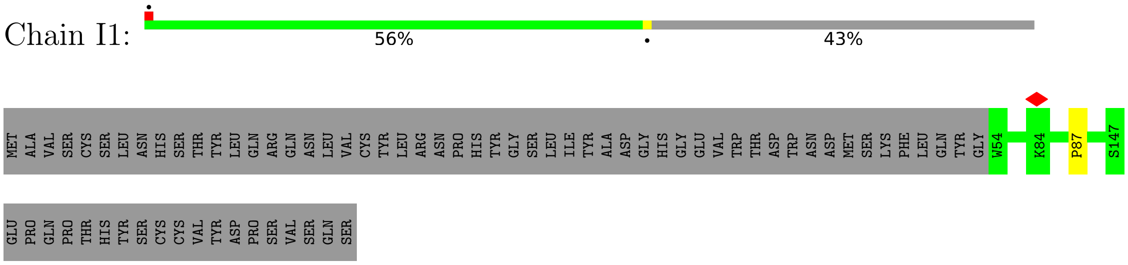


- Molecule 17: Protein FAM166A



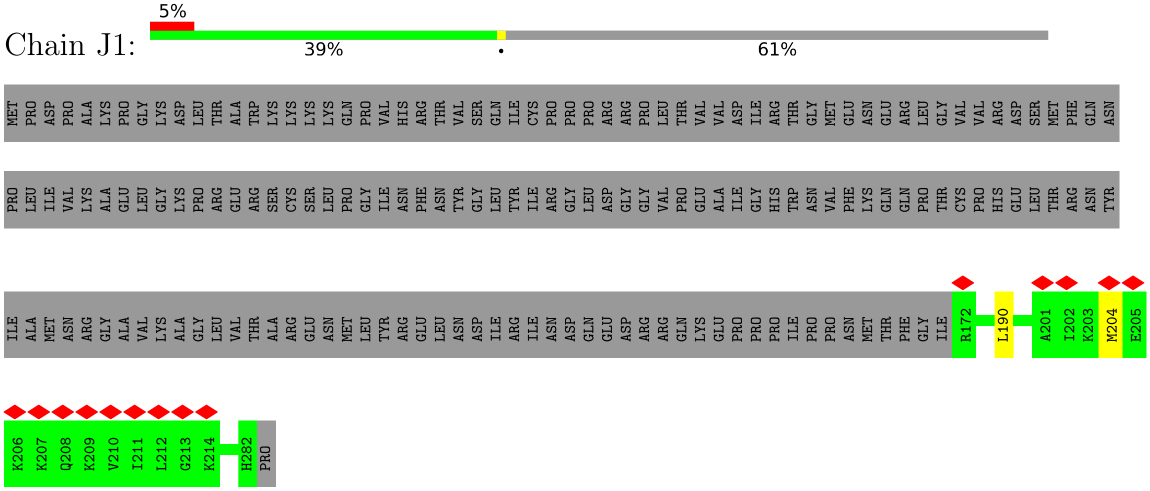
- Molecule 18: Cilia- and flagella-associated protein 68

Chain I1:



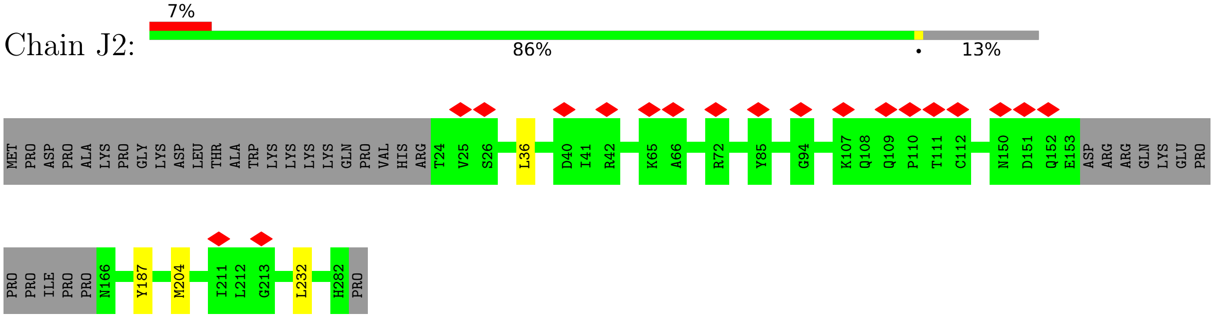
- Molecule 19: Cilia and flagella-associated protein 77

Chain J1:



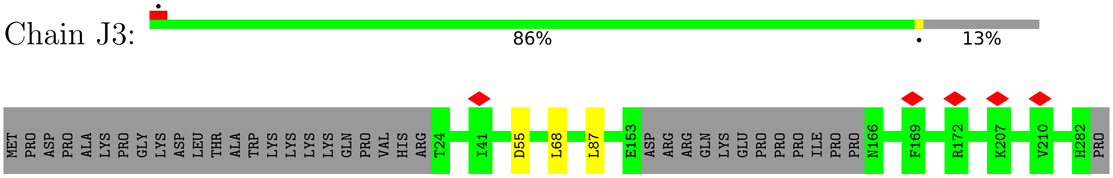
- Molecule 19: Cilia and flagella-associated protein 77

Chain J2:



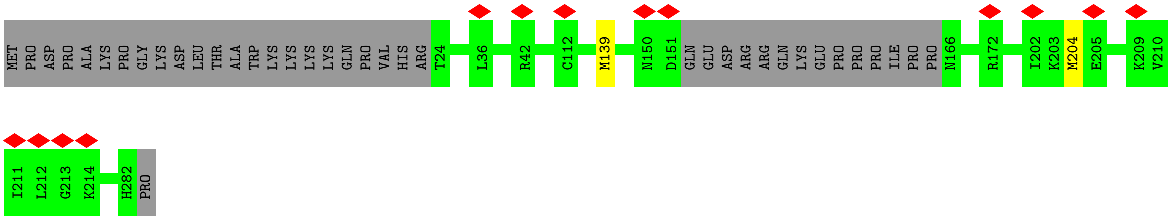
- Molecule 19: Cilia and flagella-associated protein 77

Chain J3:



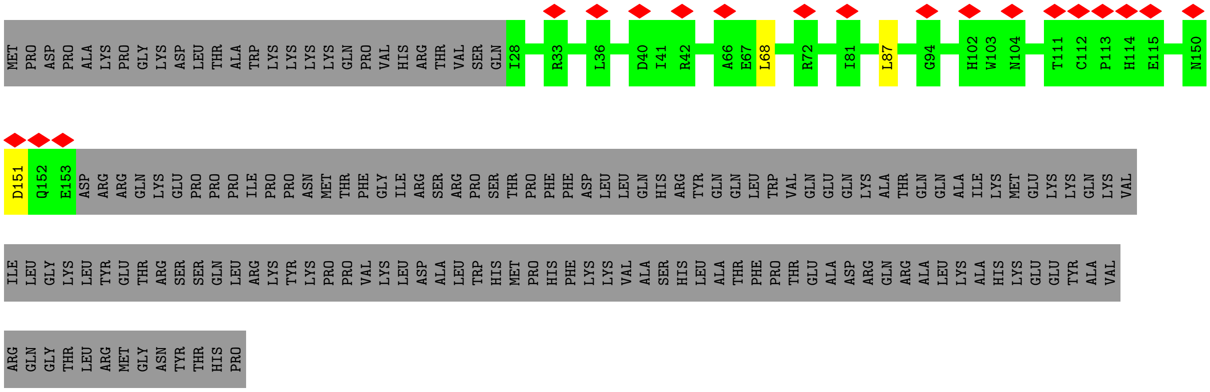
- Molecule 19: Cilia and flagella-associated protein 77

Chain J4:



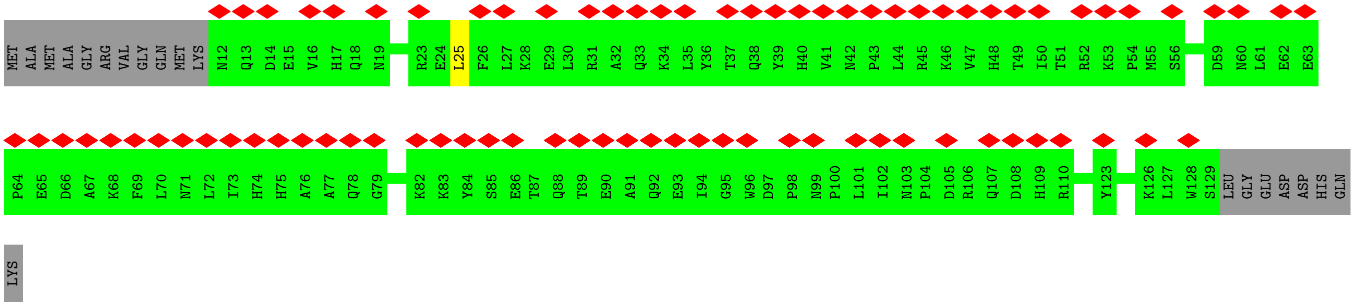
- Molecule 19: Cilia and flagella-associated protein 77

Chain J5:



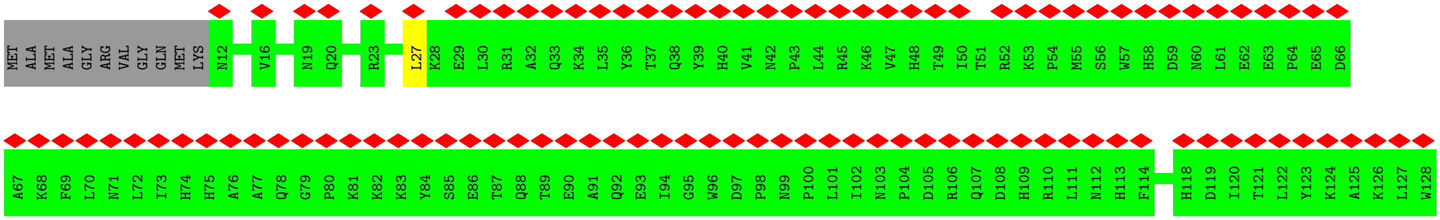
- Molecule 20: Family with sequence similarity 183, member B

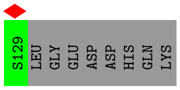
Chain K1:



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

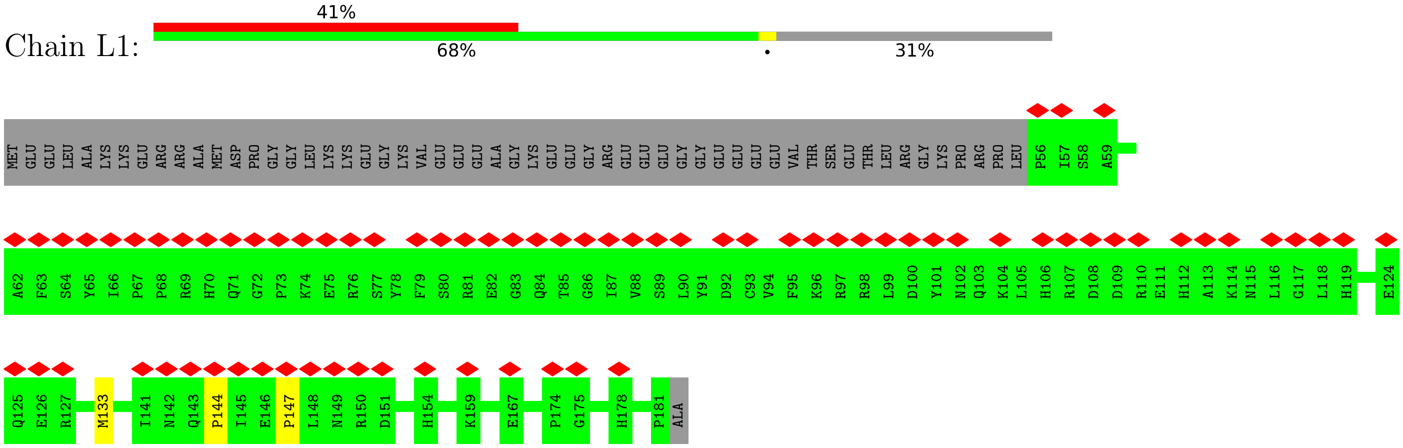
Chain K2:





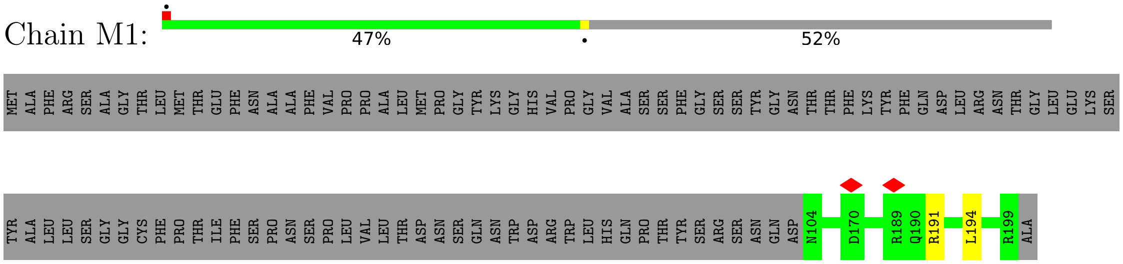
- Molecule 21: Cilia- and flagella-associated protein 90

Chain L1:



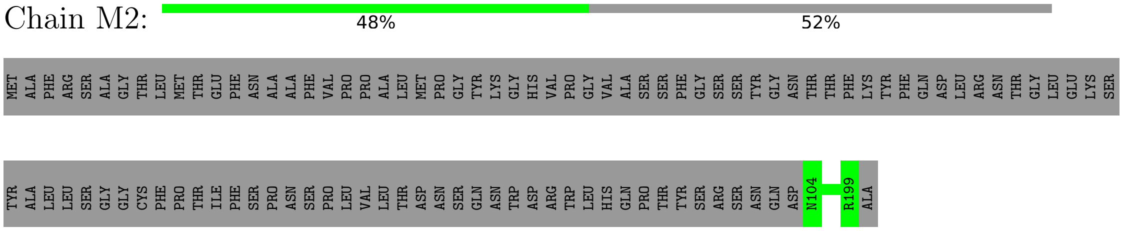
- Molecule 22: Protein FAM166C

Chain M1:



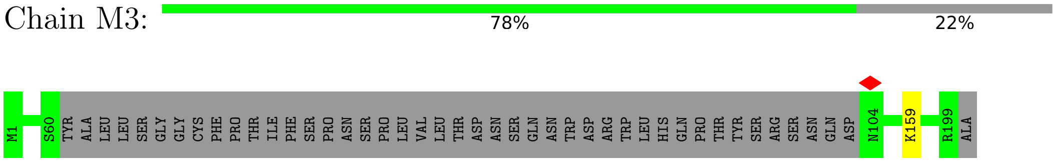
- Molecule 22: Protein FAM166C

Chain M2:



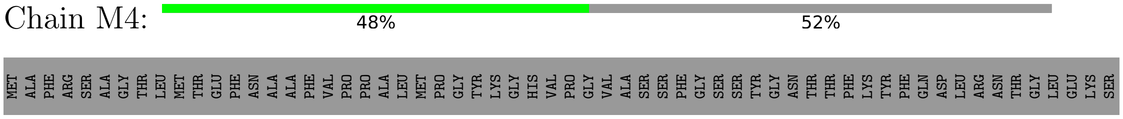
- Molecule 22: Protein FAM166C

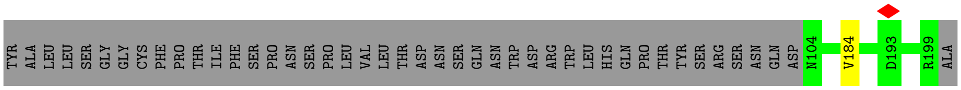
Chain M3:



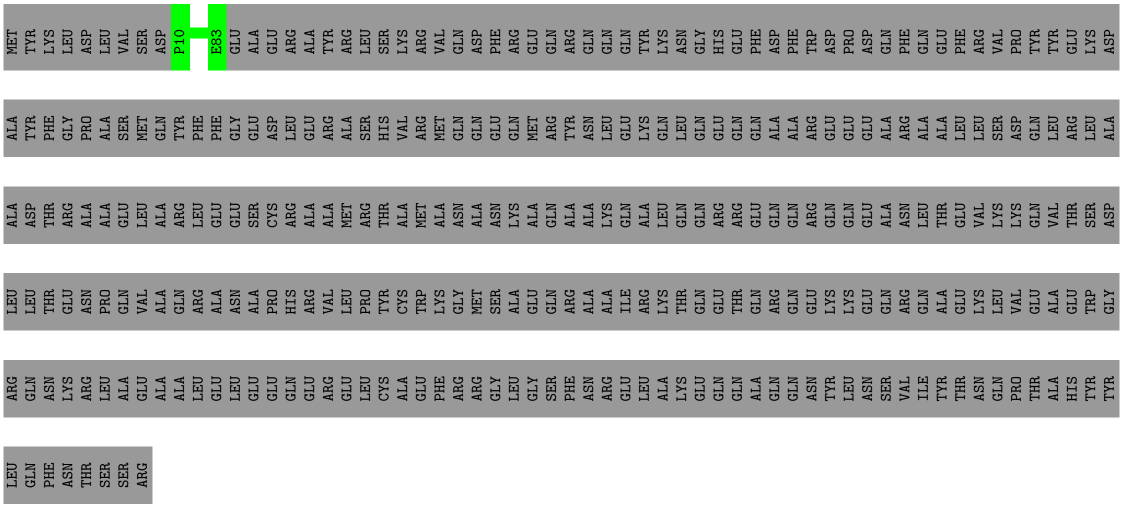
- Molecule 22: Protein FAM166C

Chain M4:

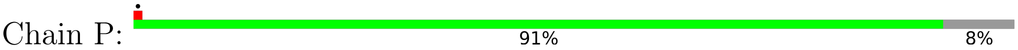


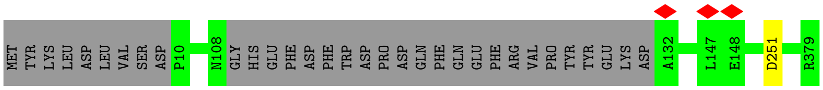


- Molecule 23: RIB43A-like with coiled-coils protein 1

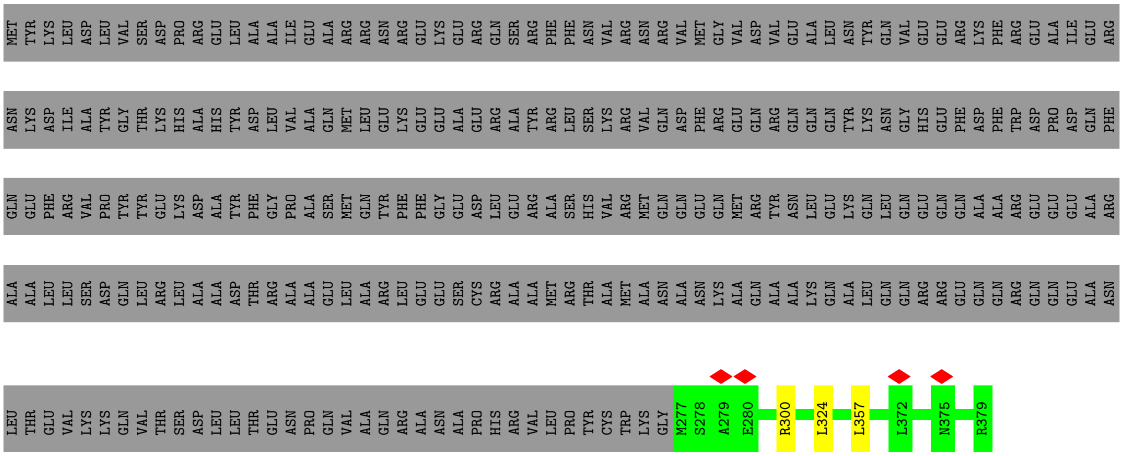


- Molecule 23: RIB43A-like with coiled-coils protein 1



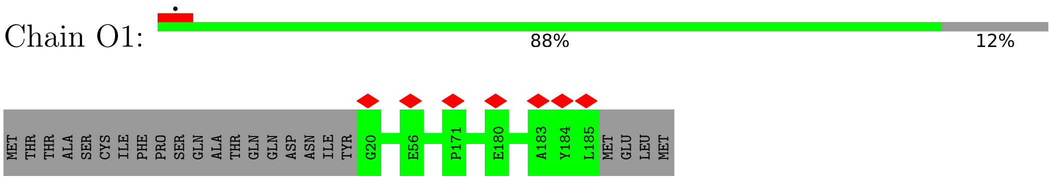


- Molecule 23: RIB43A-like with coiled-coils protein 1



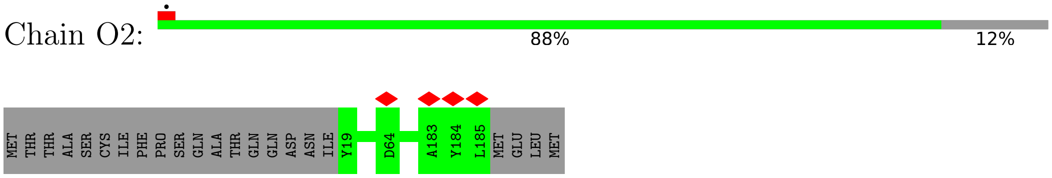
- Molecule 24: Dual specificity phosphatase 21

Chain O1:



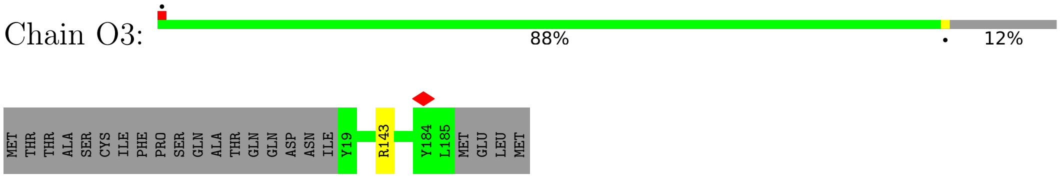
- Molecule 24: Dual specificity phosphatase 21

Chain O2:



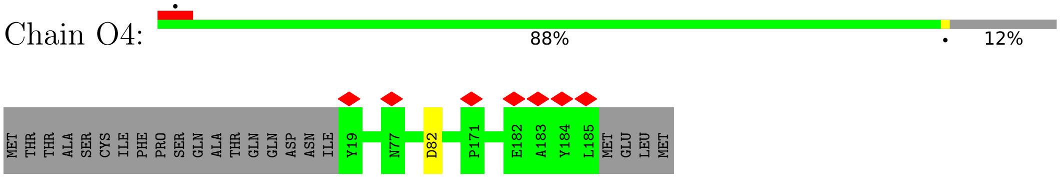
- Molecule 24: Dual specificity phosphatase 21

Chain O3:



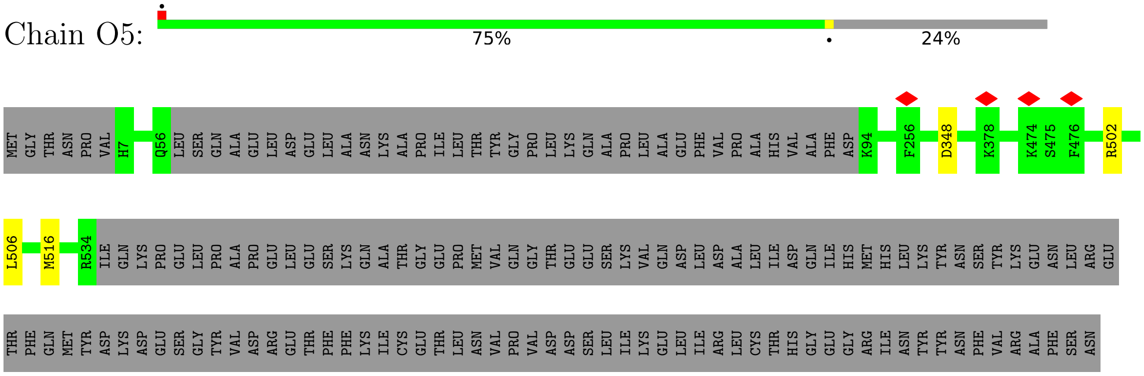
- Molecule 24: Dual specificity phosphatase 21

Chain O4:



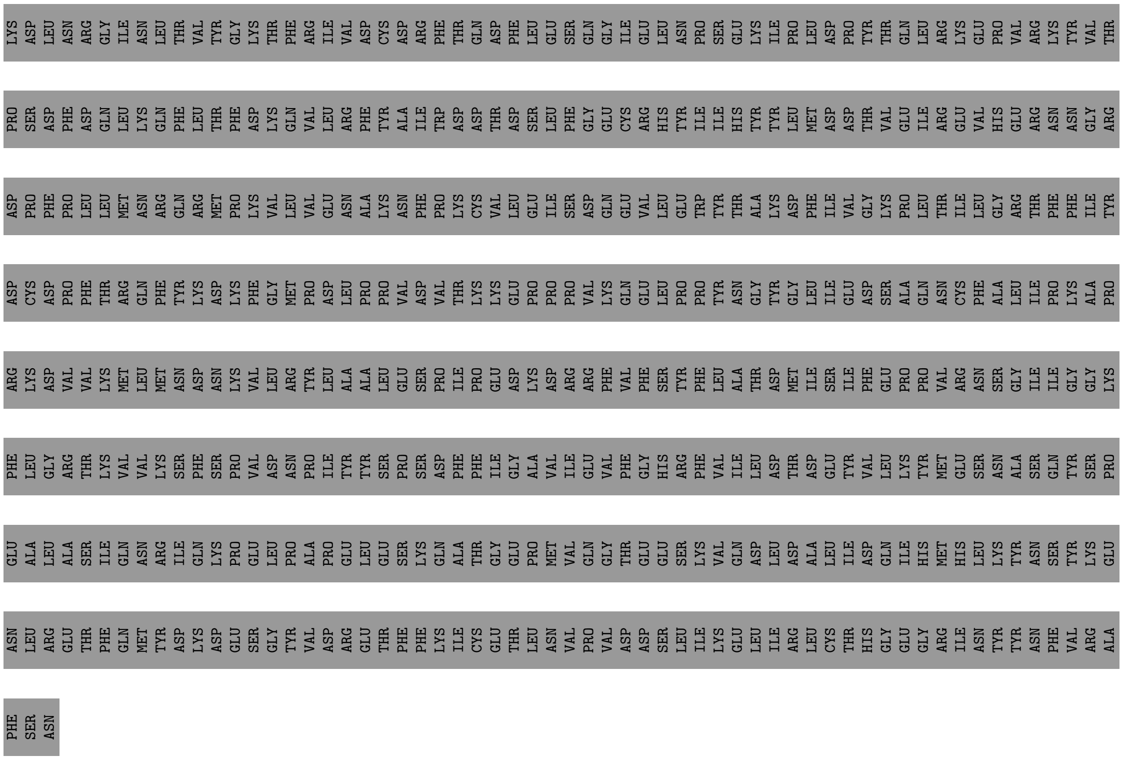
- Molecule 25: EF-hand domain-containing protein 1

Chain O5:

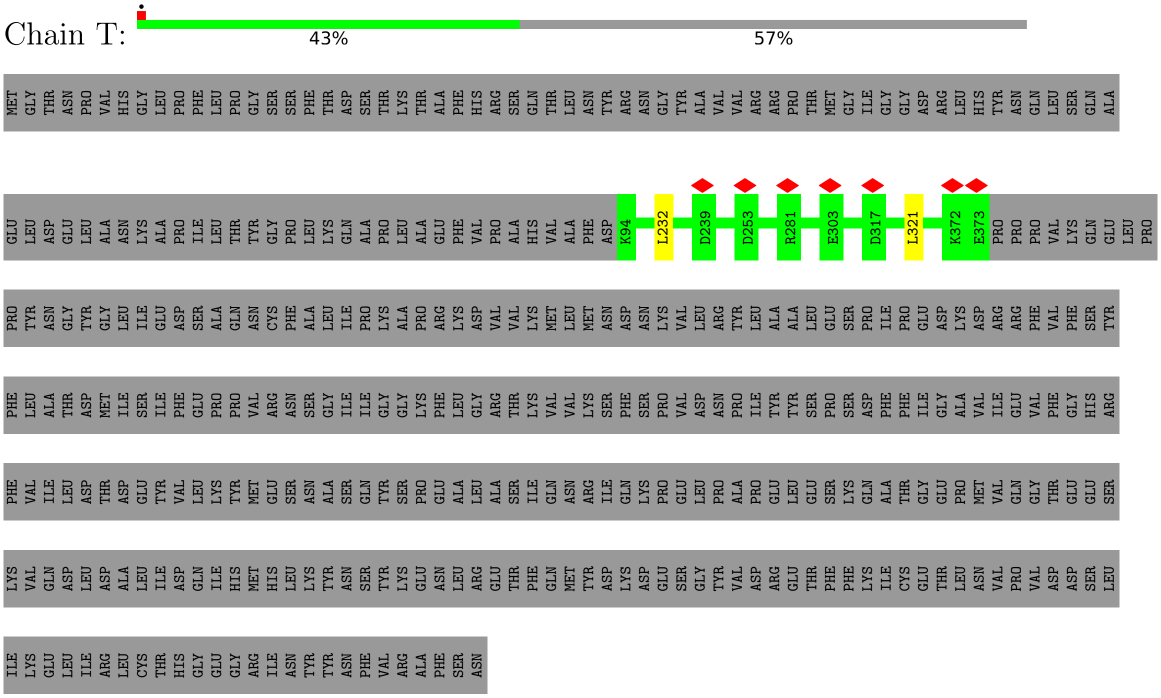


- Molecule 25: EF-hand domain-containing protein 1

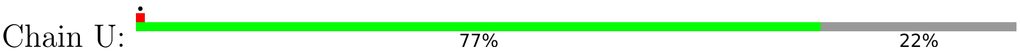
Chain O6:

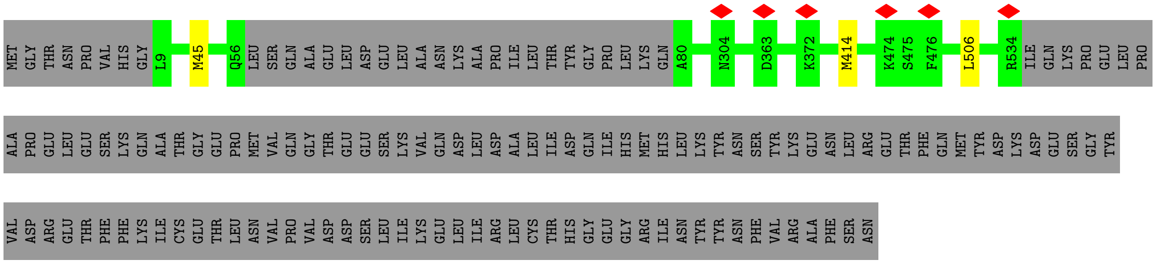


- Molecule 25: EF-hand domain-containing protein 1



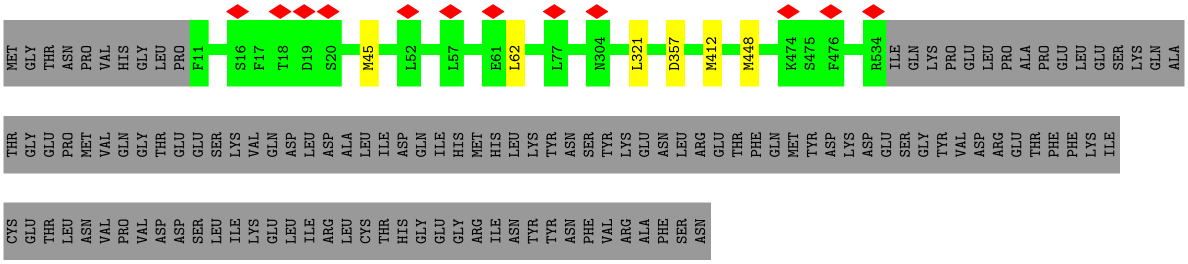
- Molecule 25: EF-hand domain-containing protein 1





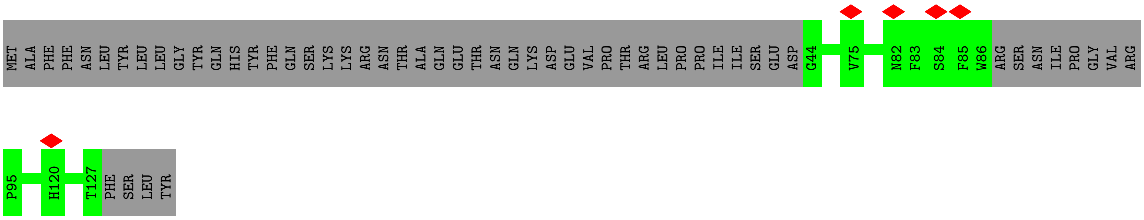
- Molecule 25: EF-hand domain-containing protein 1

Chain V:



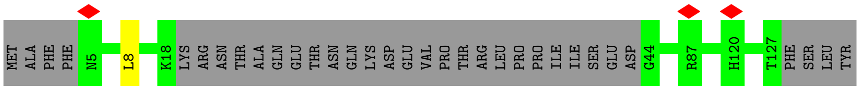
- Molecule 26: Testis expressed 49

Chain P1:



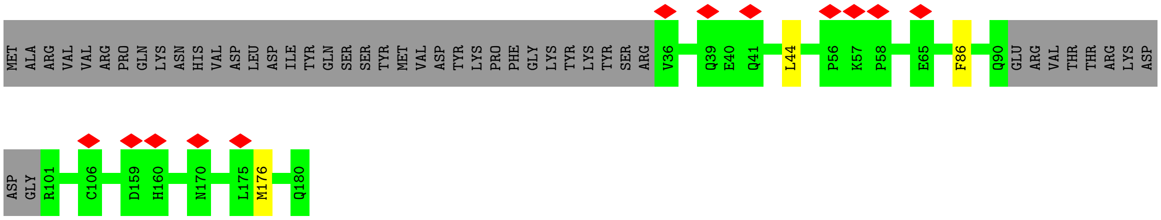
- Molecule 26: Testis expressed 49

Chain P2:

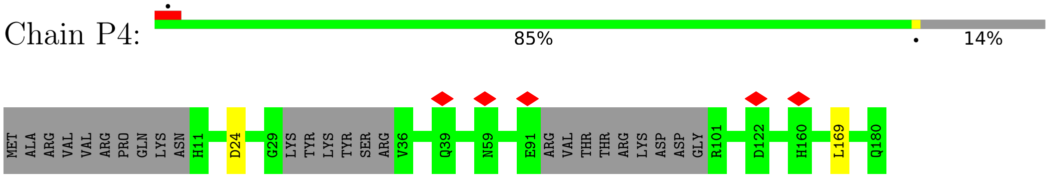


- Molecule 27: Testis-expressed sequence 37 protein

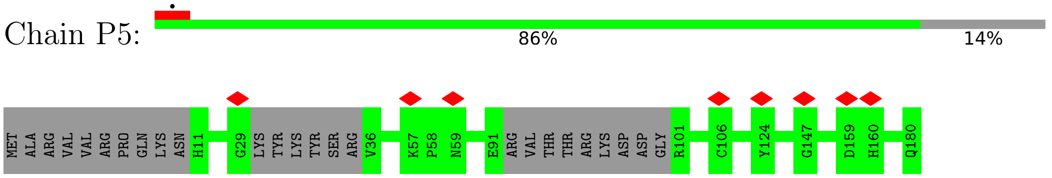
Chain P3:



- Molecule 27: Testis-expressed sequence 37 protein



- Molecule 27: Testis-expressed sequence 37 protein



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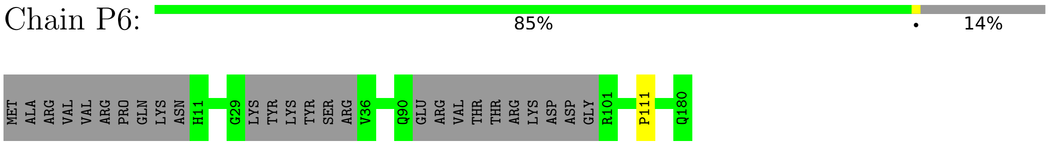
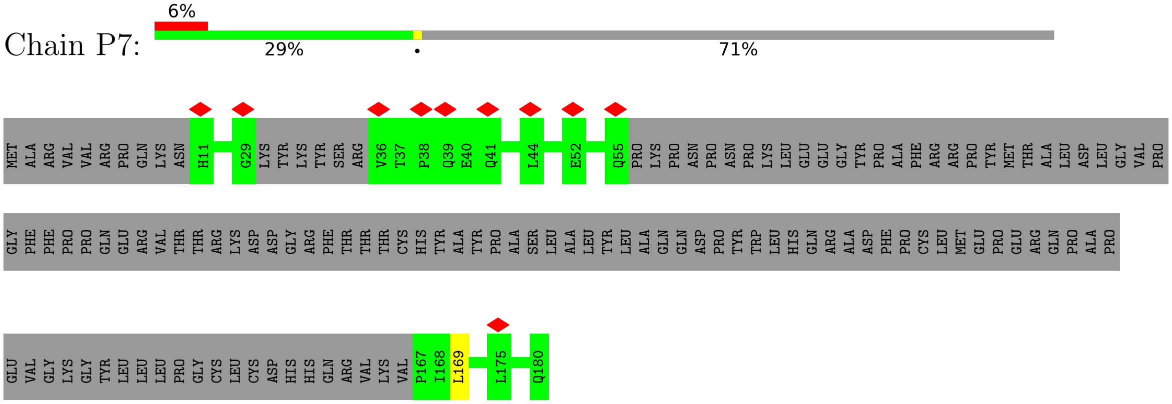
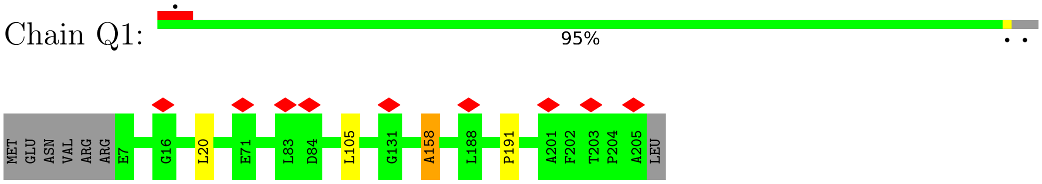


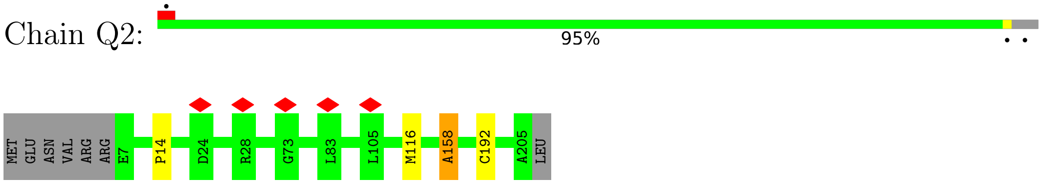
- Molecule 27: Testis-expressed sequence 37 protein



- Molecule 28: Tektin bundle-interacting protein 1

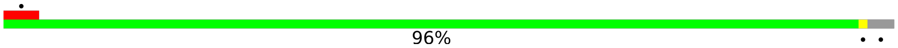


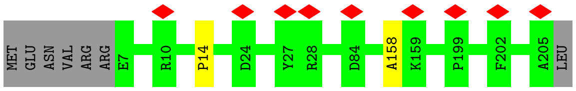
- Molecule 28: Tektin bundle-interacting protein 1



- Molecule 28: Tektin bundle-interacting protein 1

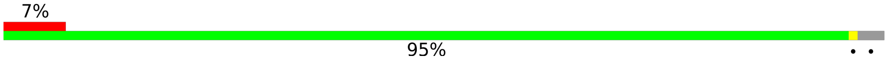
Chain Q3:

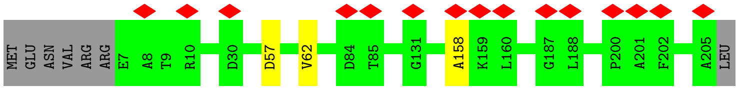




- Molecule 28: Tektin bundle-interacting protein 1

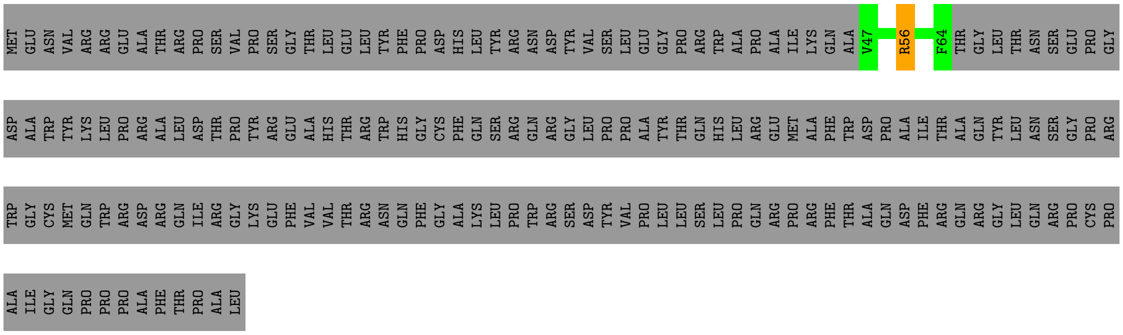
Chain Q4:





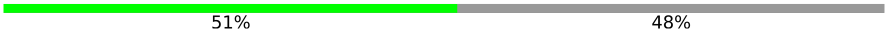
- Molecule 28: Tektin bundle-interacting protein 1

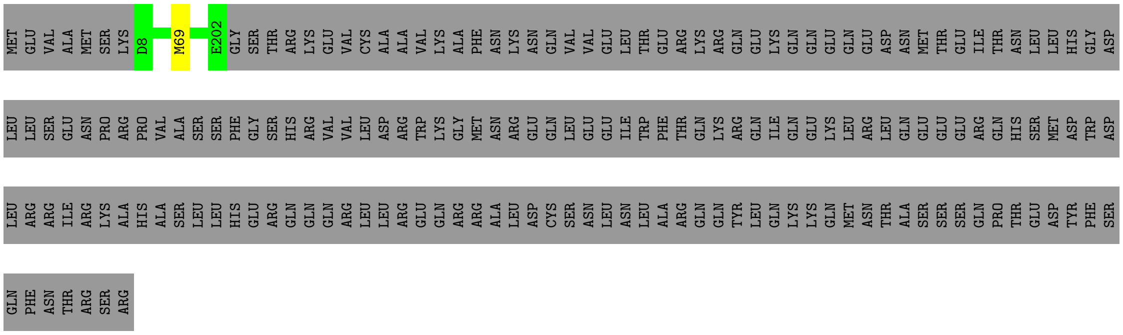
Chain Q5:



- Molecule 29: RIB43A-like with coiled-coils protein 2

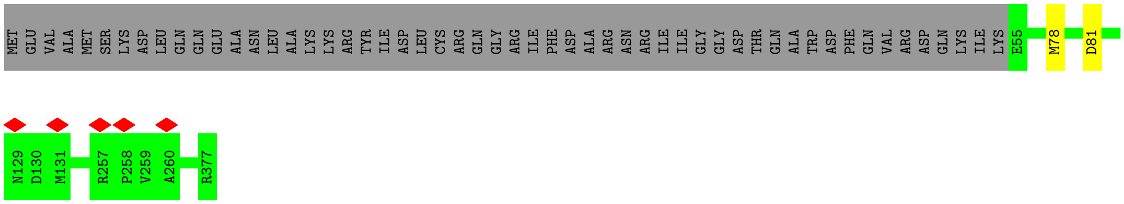
Chain R:





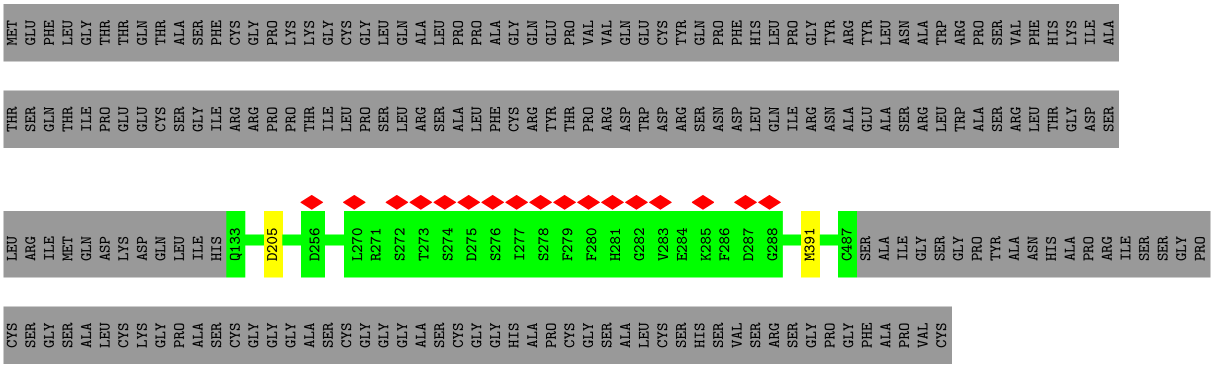
- Molecule 29: RIB43A-like with coiled-coils protein 2

Chain S:



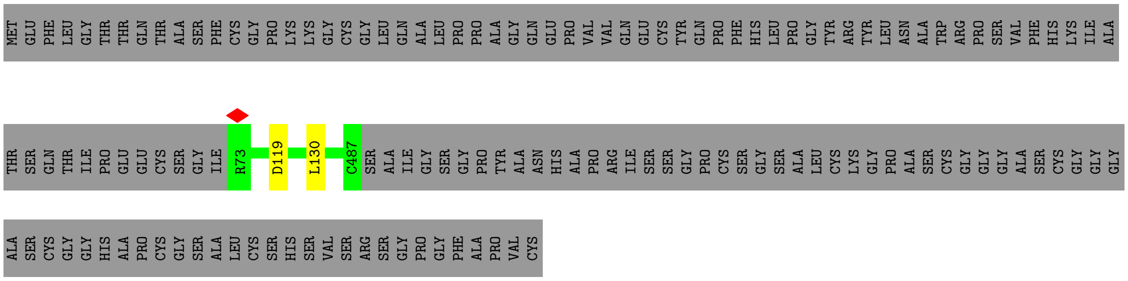
- Molecule 30: Tektin-5

Chain U0:



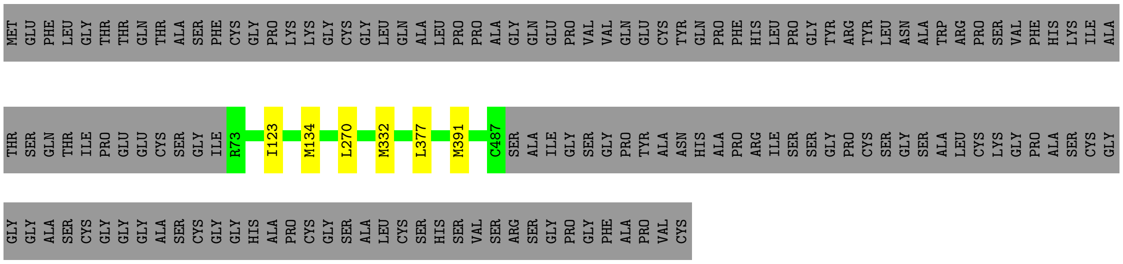
- Molecule 30: Tektin-5

Chain U1:



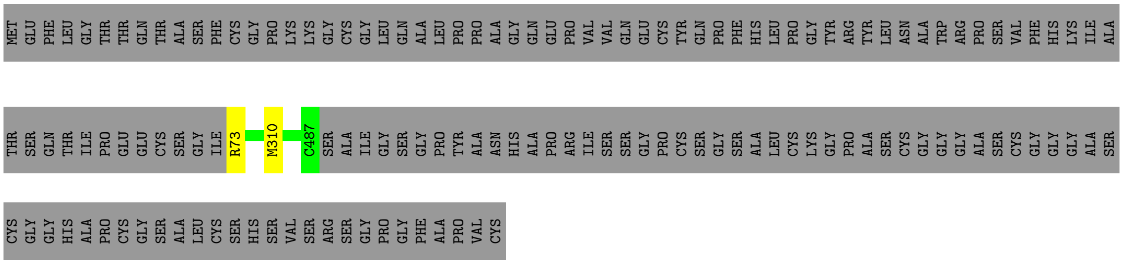
- Molecule 30: Tektin-5

Chain U2:



- Molecule 30: Tektin-5

Chain U3:

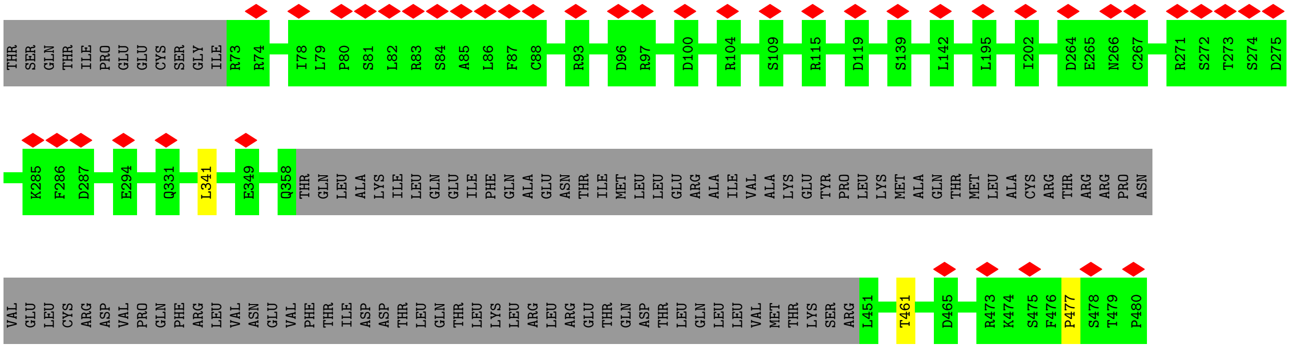


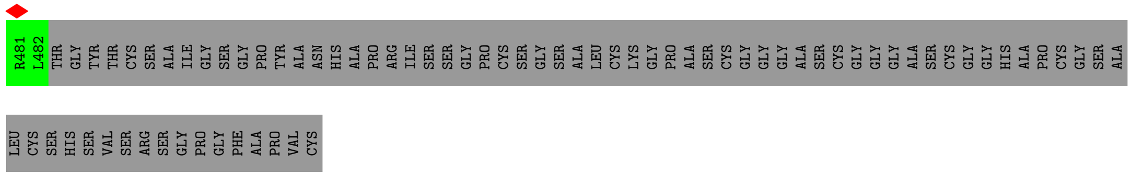
- Molecule 30: Tektin-5

Chain U4:

- Molecule 30: Tektin-5

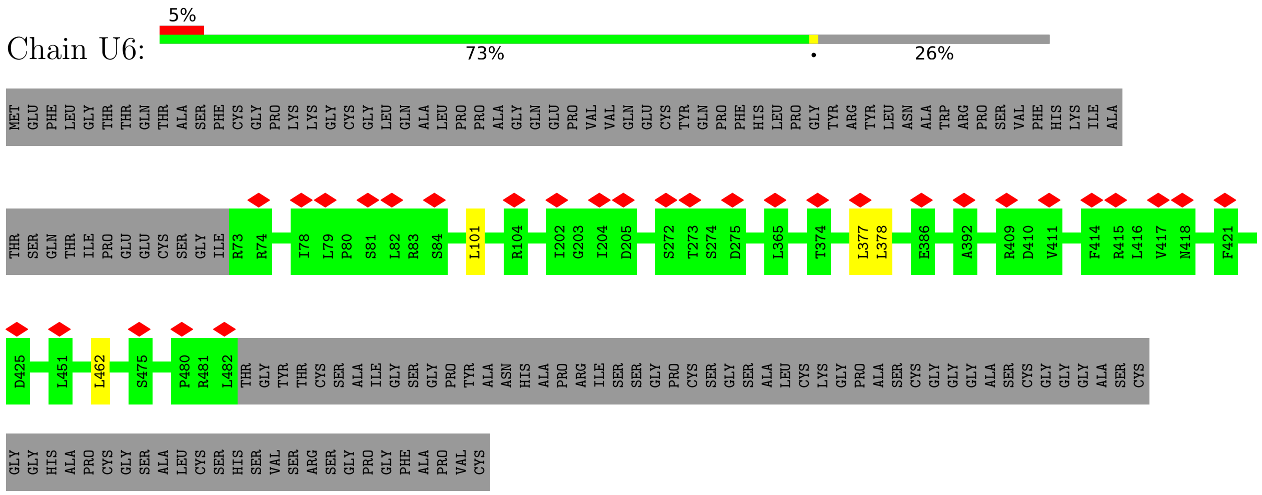
Chain U5:





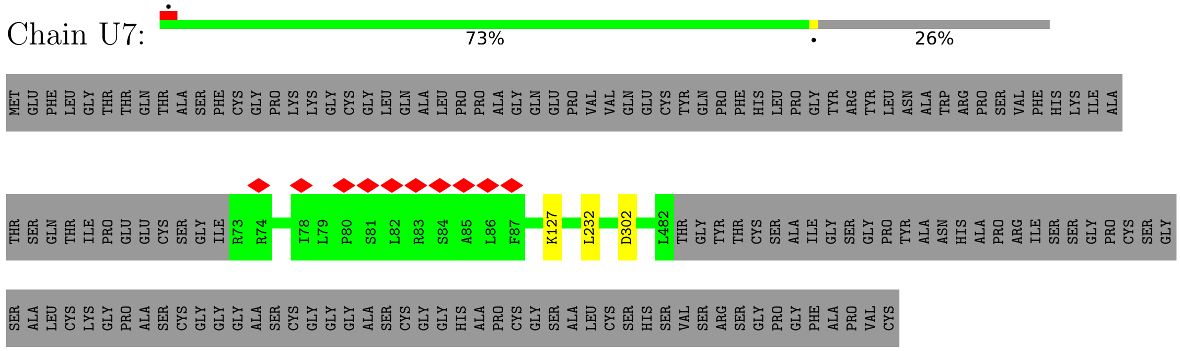
- Molecule 30: Tektin-5

Chain U6:



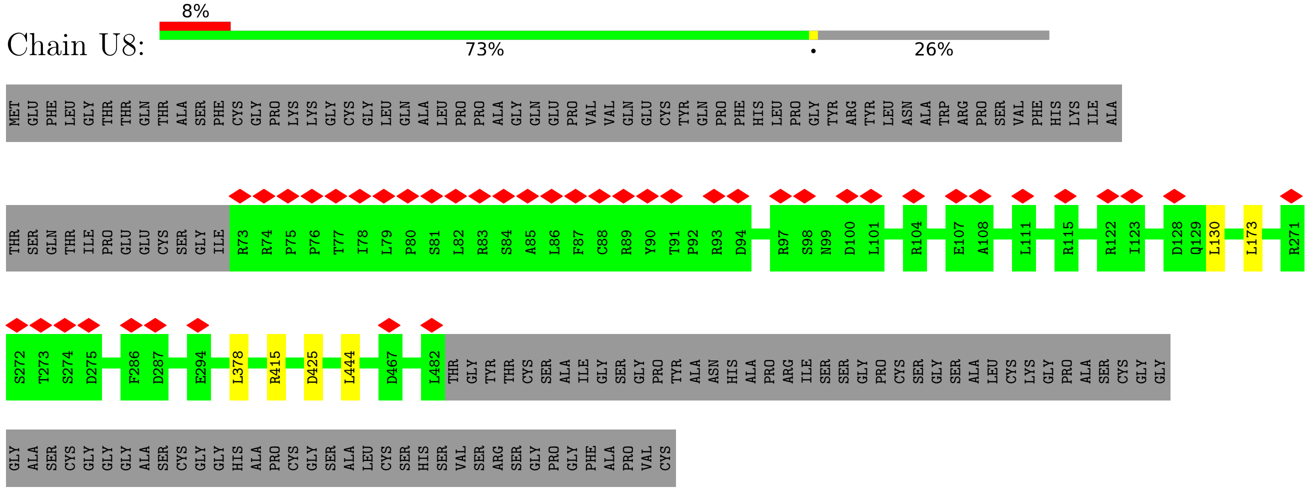
- Molecule 30: Tektin-5

Chain U7:

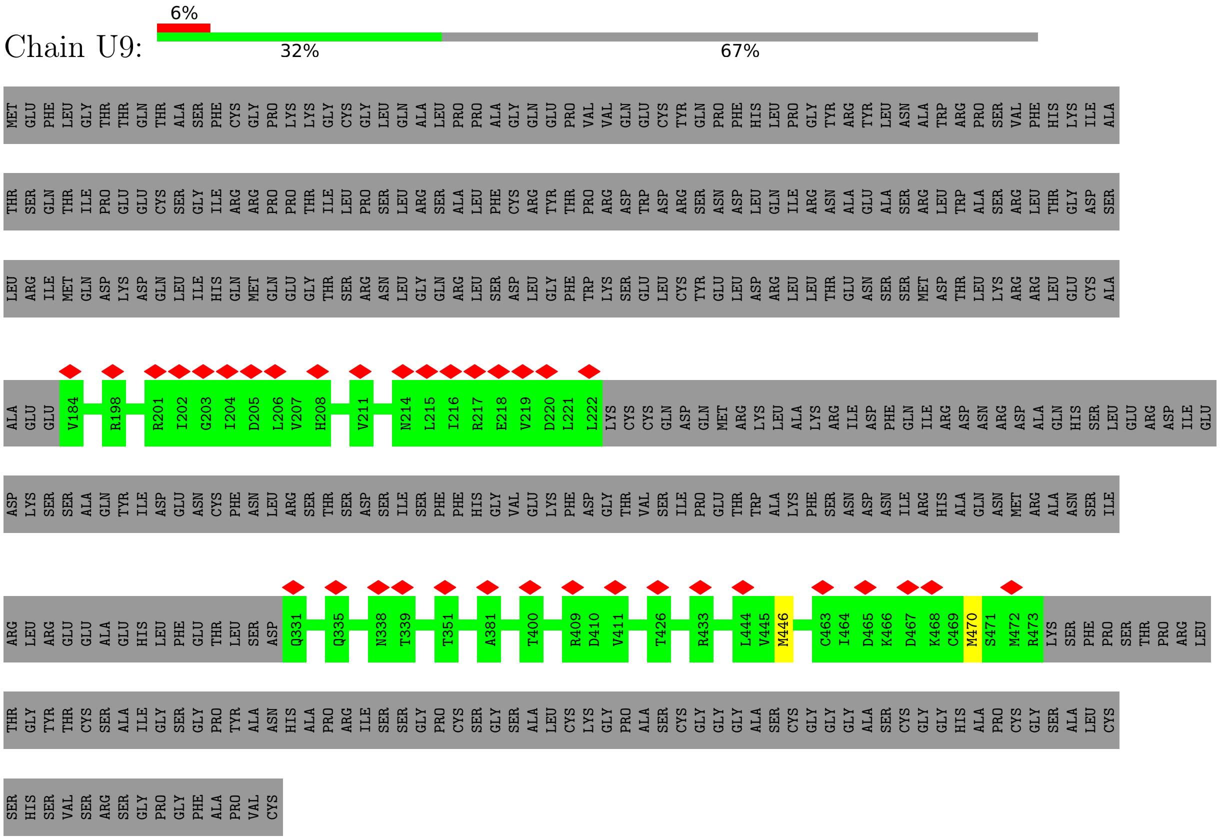


- Molecule 30: Tektin-5

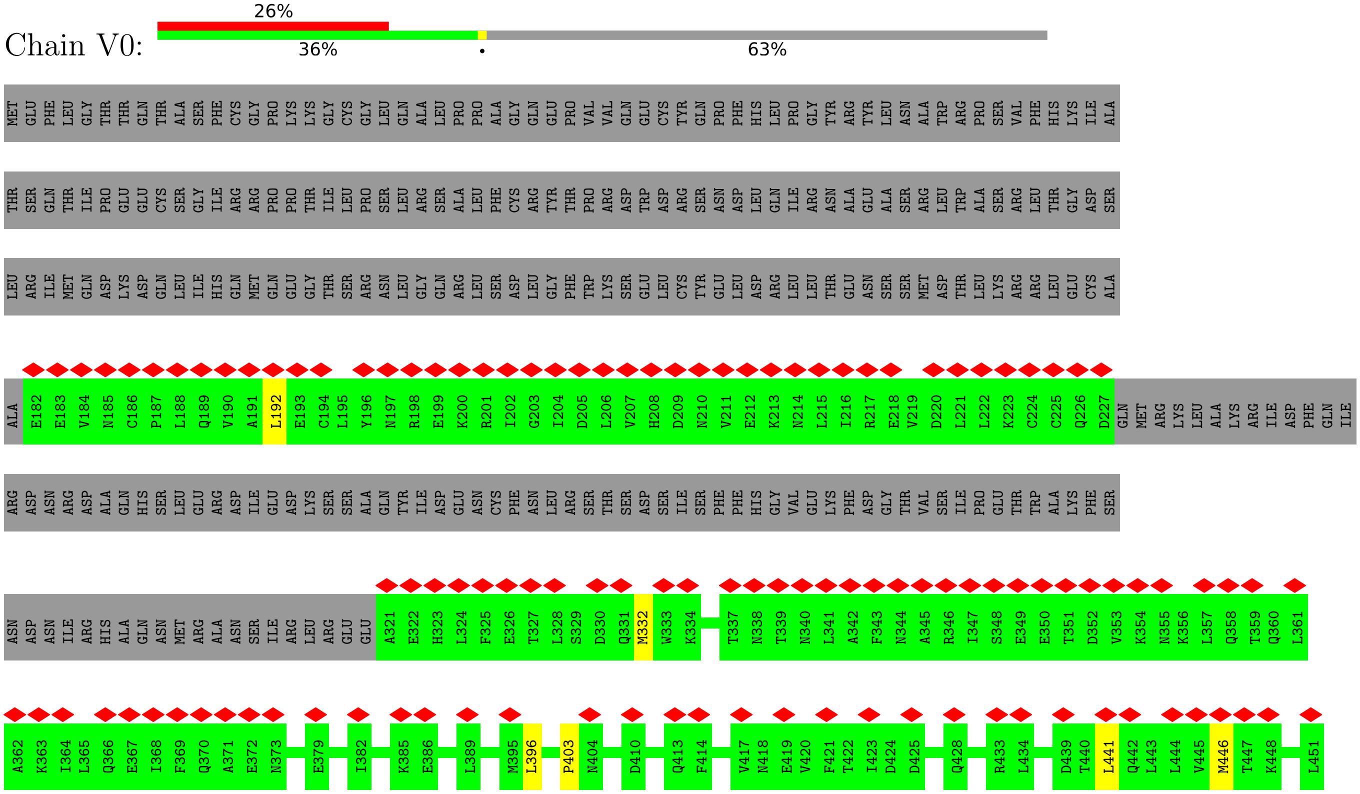
Chain U8:

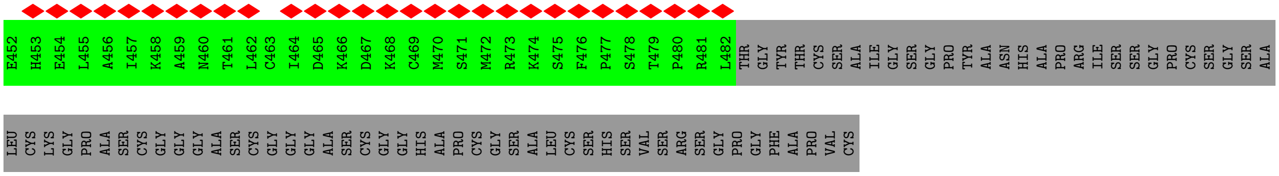


- Molecule 30: Tektin-5



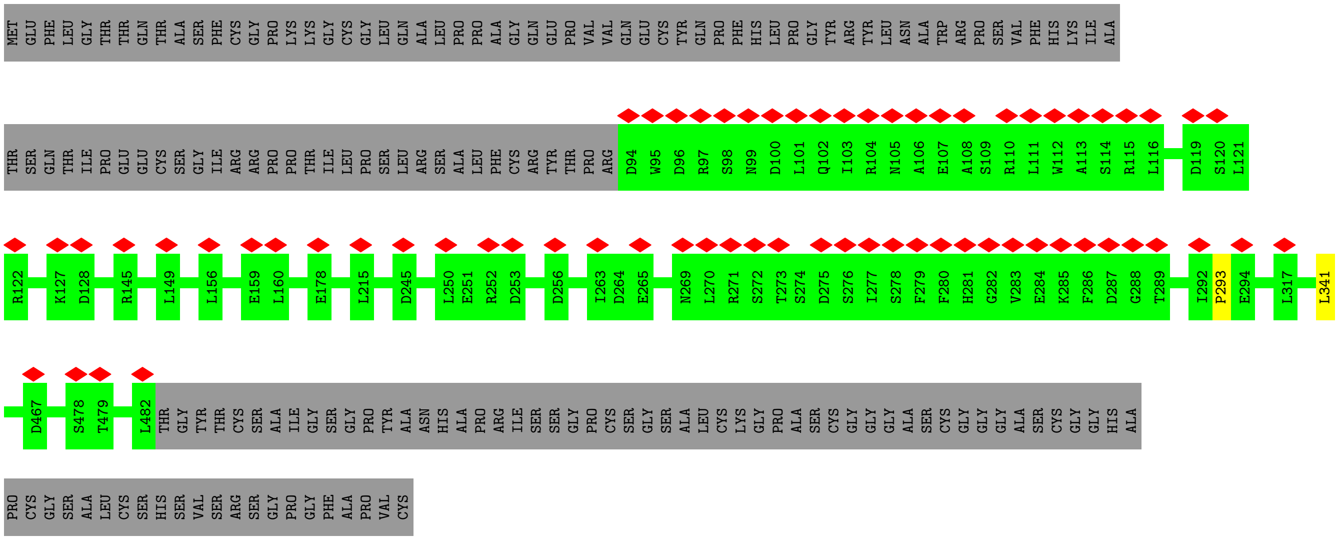
- Molecule 30: Tektin-5





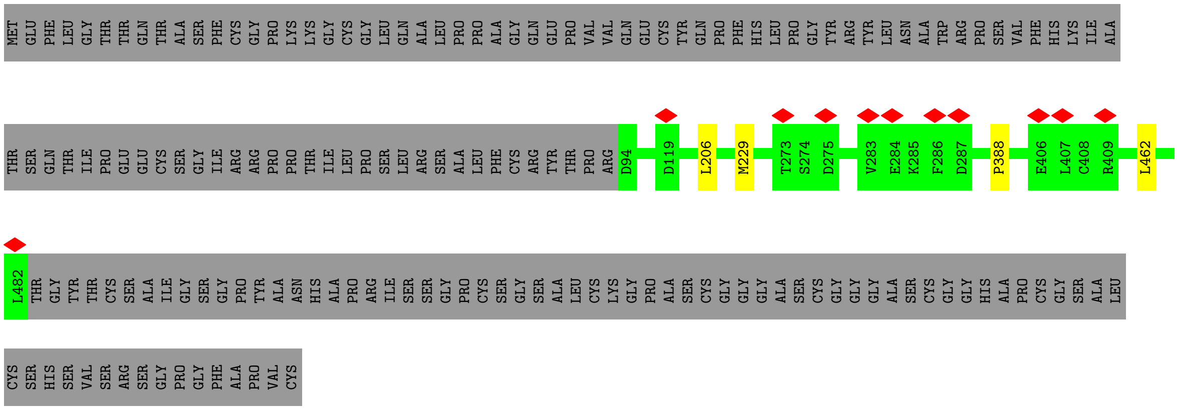
- Molecule 30: Tektin-5

Chain V1:



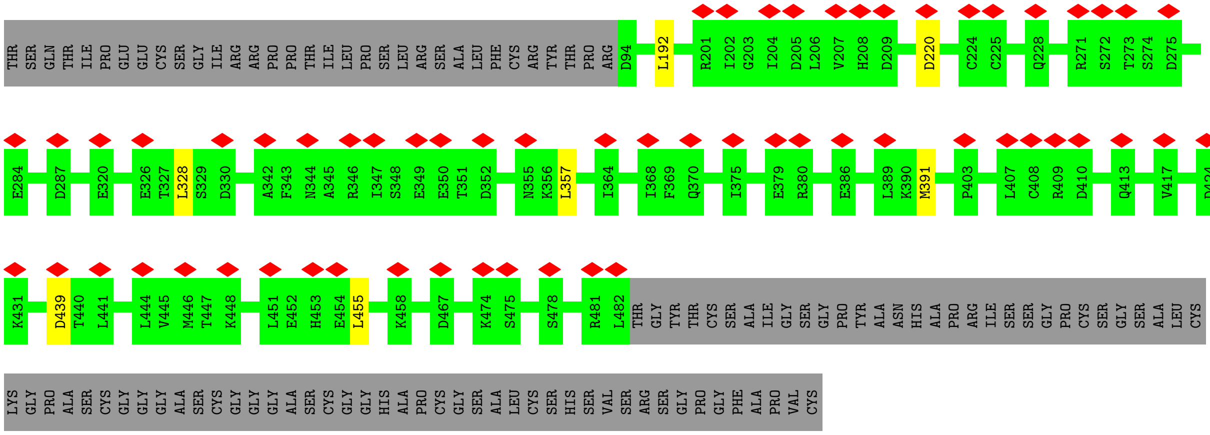
- Molecule 30: Tektin-5

Chain V2:



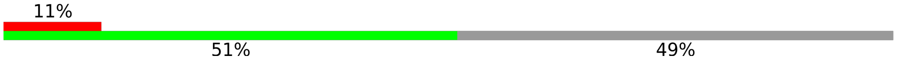
- Molecule 30: Tektin-5

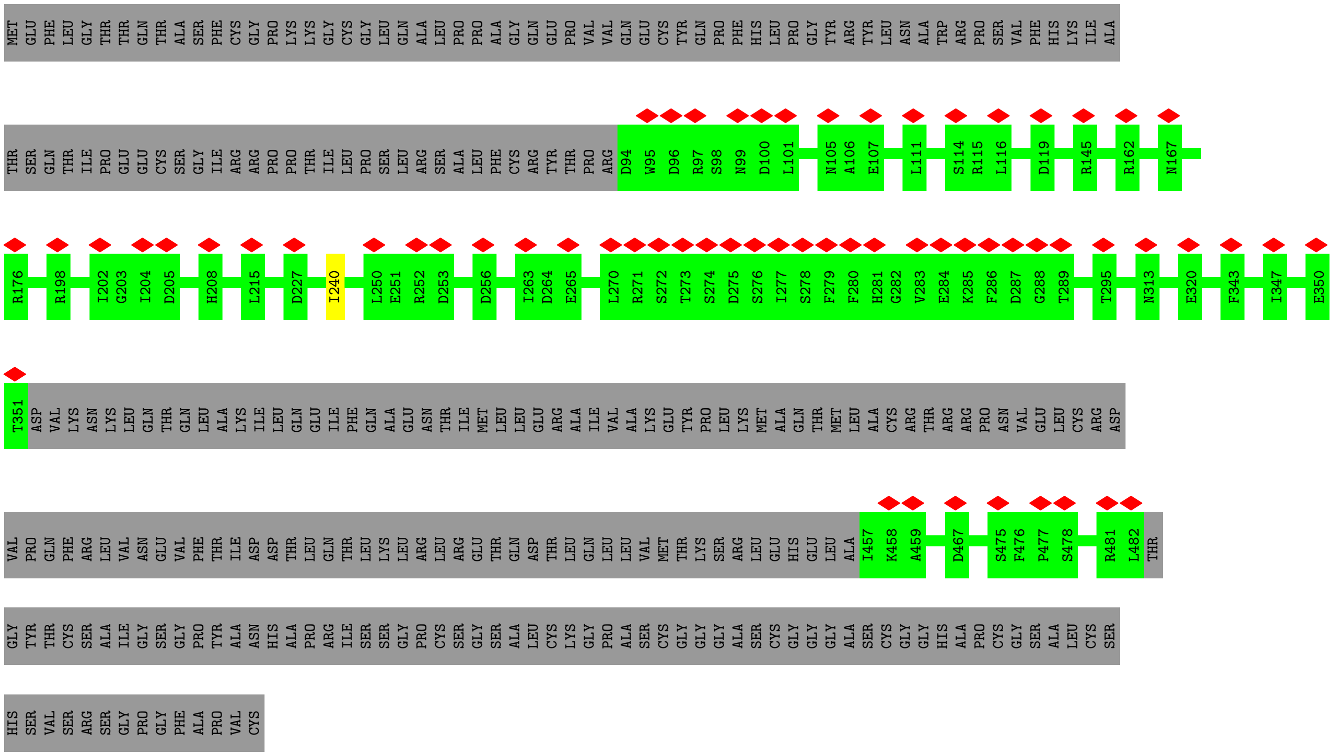
Chain V3:



- Molecule 30: Tektin-5

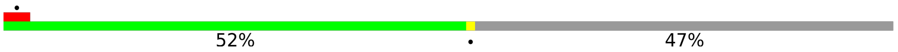
Chain V4:

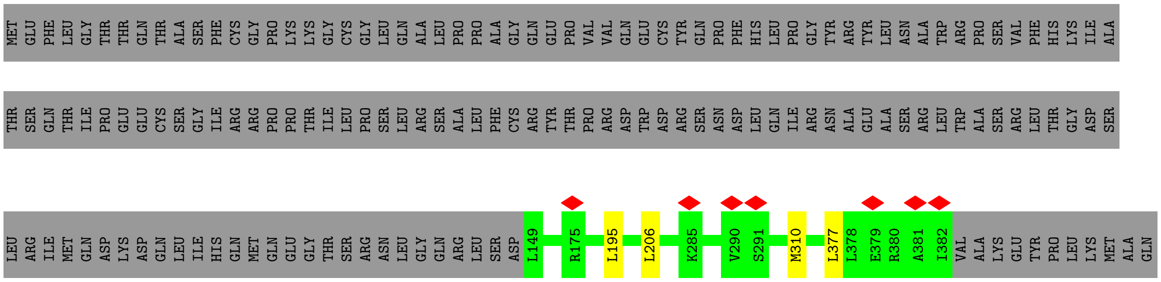


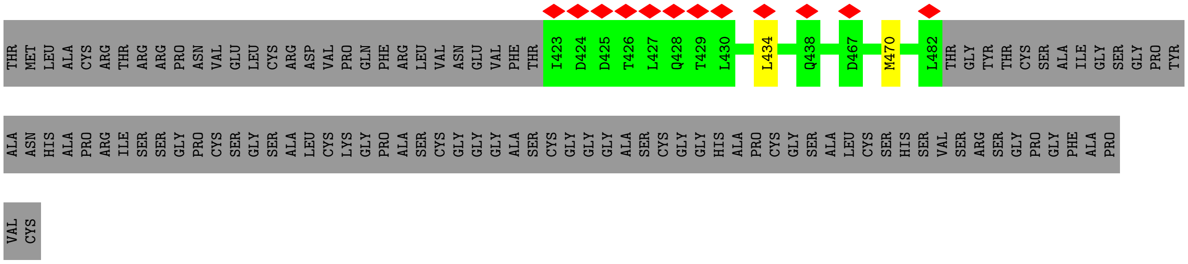


- Molecule 30: Tektin-5

Chain V5:

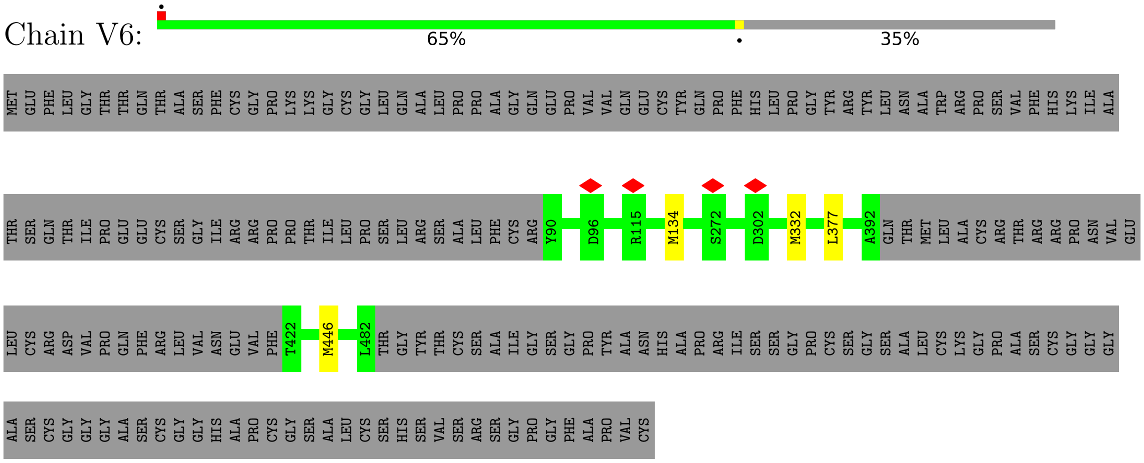






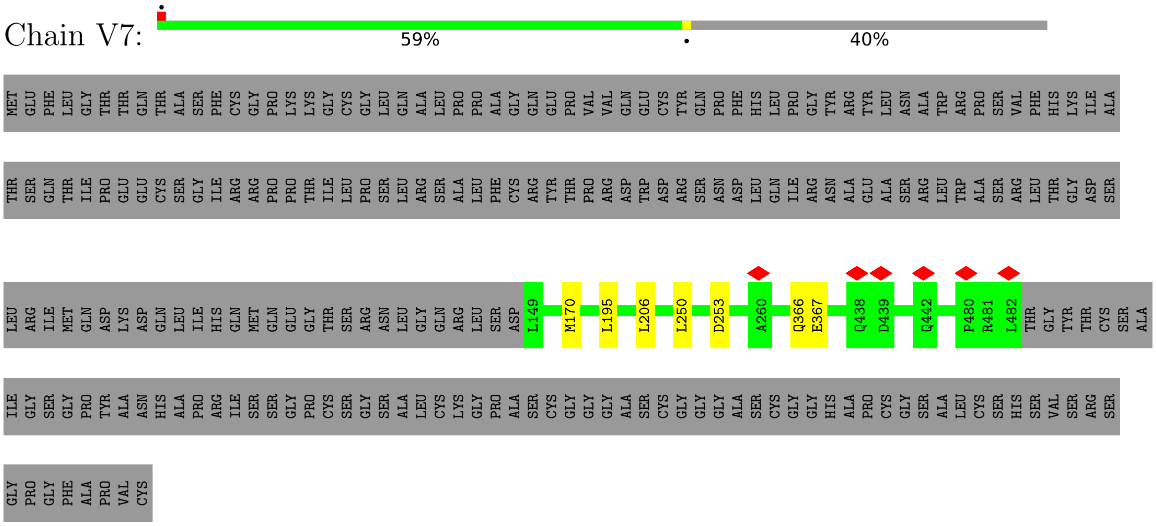
- Molecule 30: Tektin-5

Chain V6:



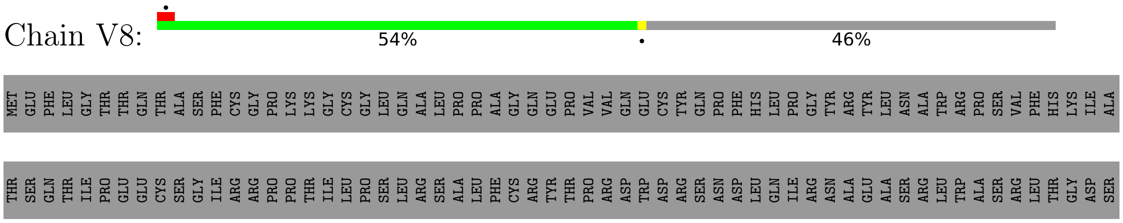
- Molecule 30: Tektin-5

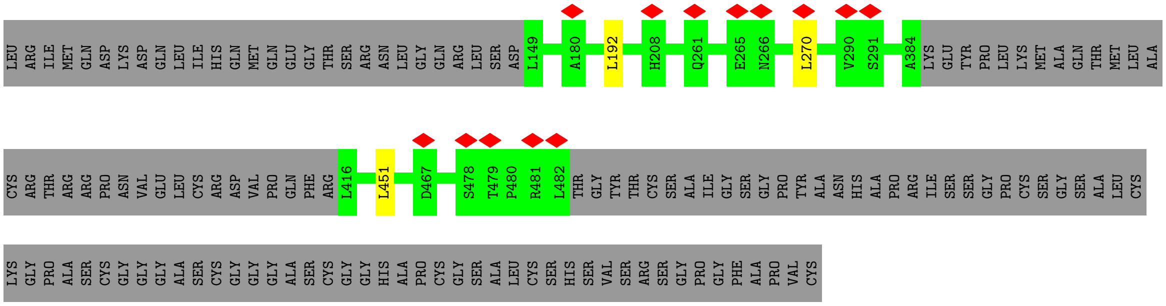
Chain V7:



- Molecule 30: Tektin-5

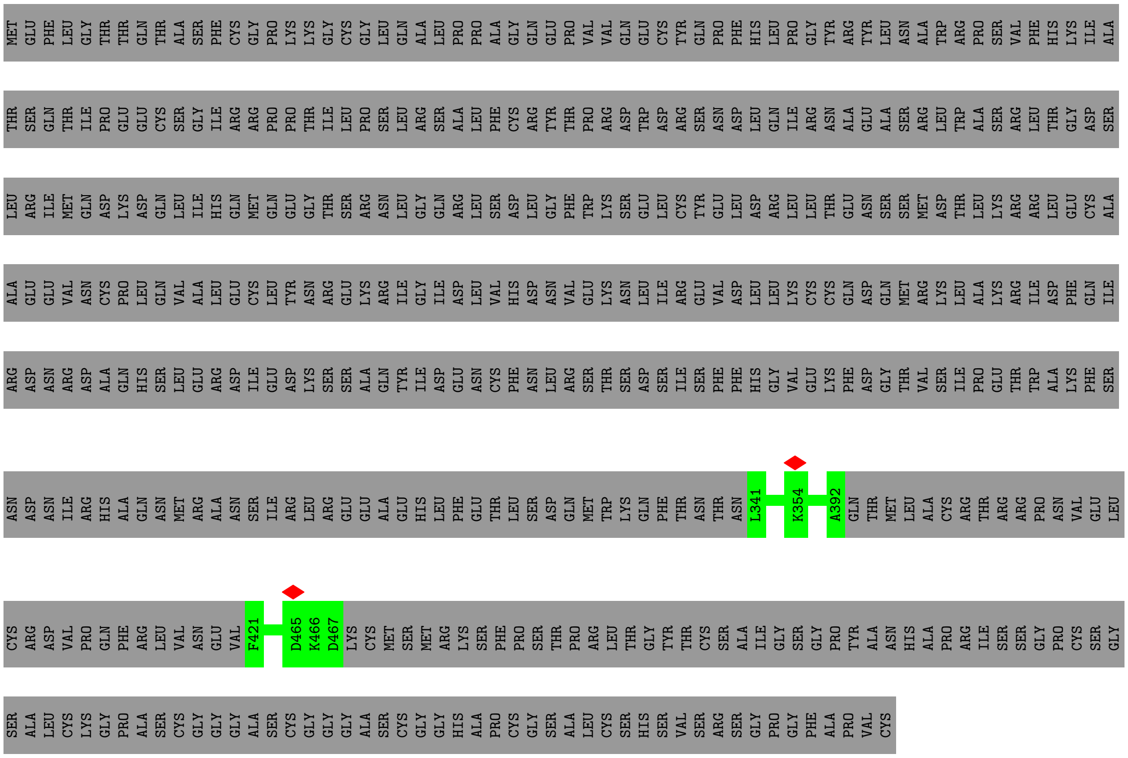
Chain V8:





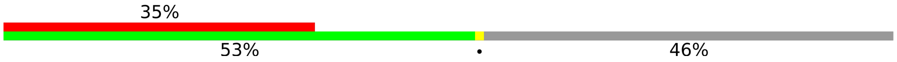
- Molecule 30: Tektin-5

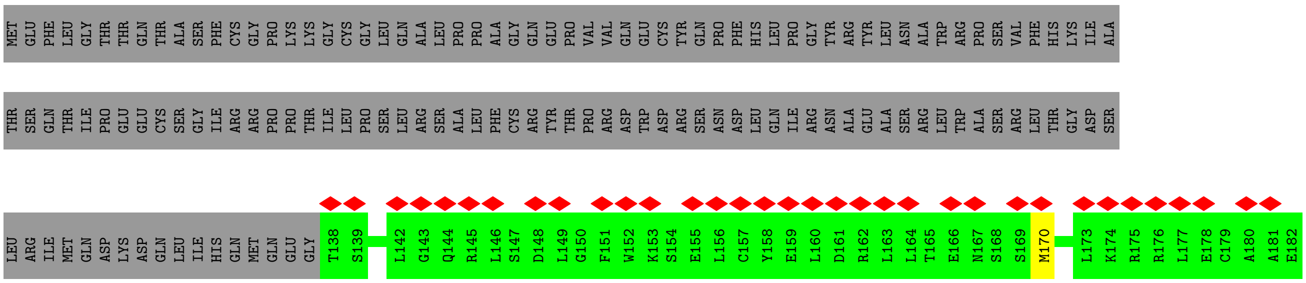
Chain V9:

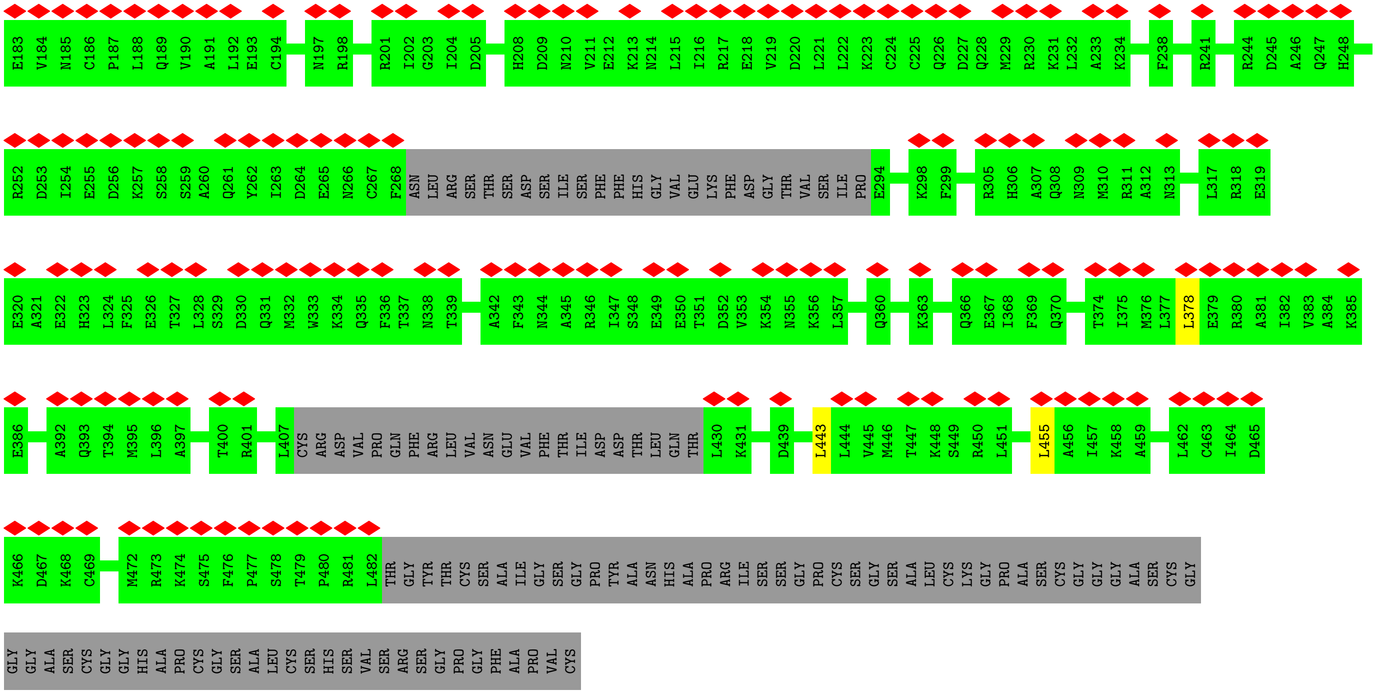


- Molecule 30: Tektin-5

Chain W0:

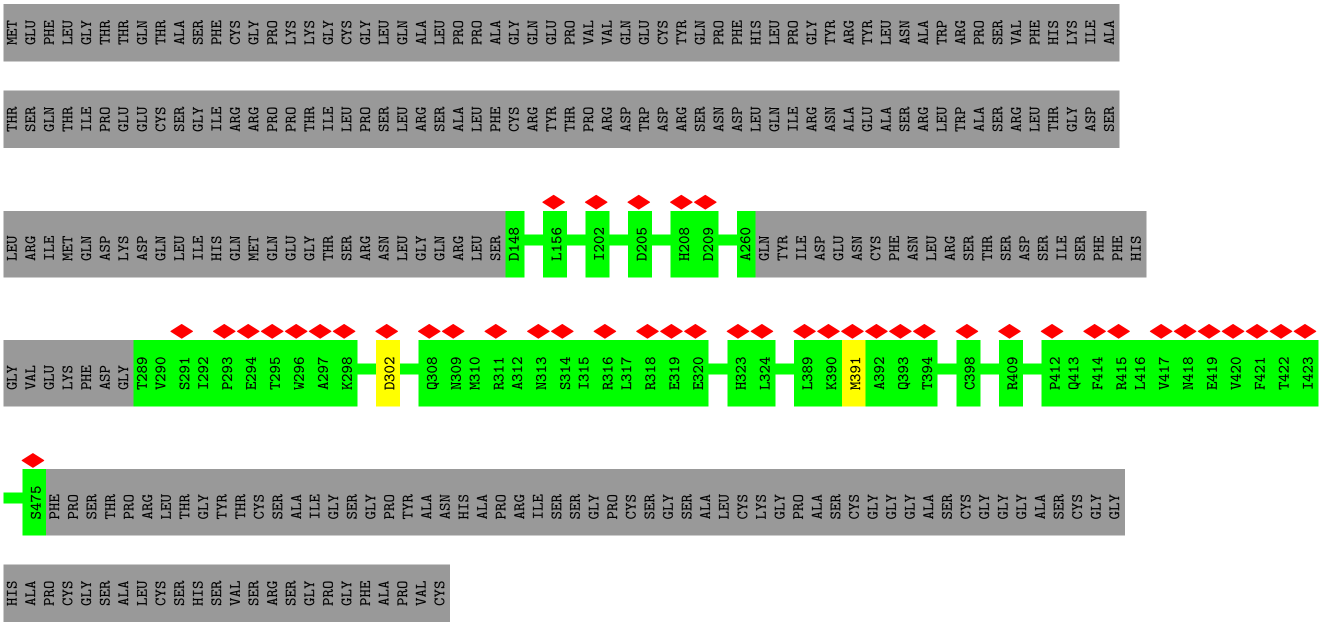






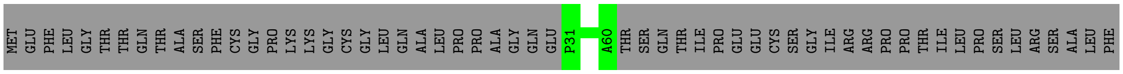
- Molecule 30: Tektin-5

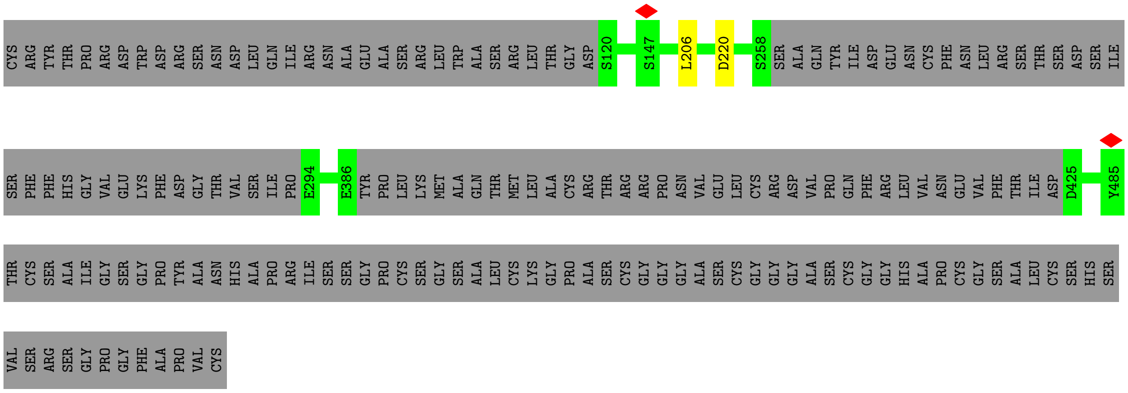
Chain W2:



- Molecule 30: Tektin-5

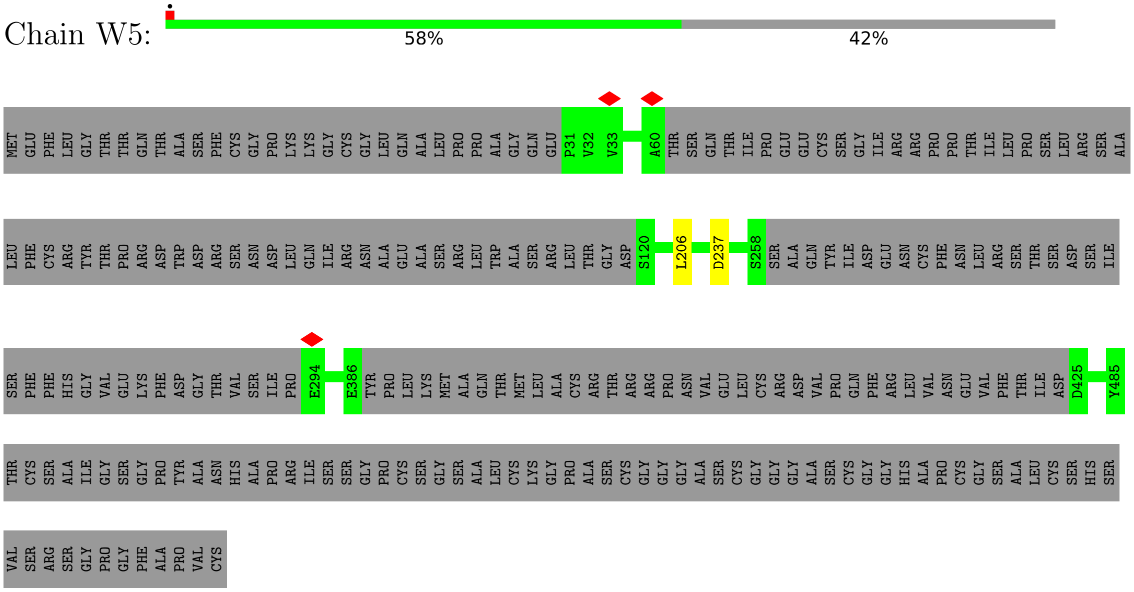
Chain W4:





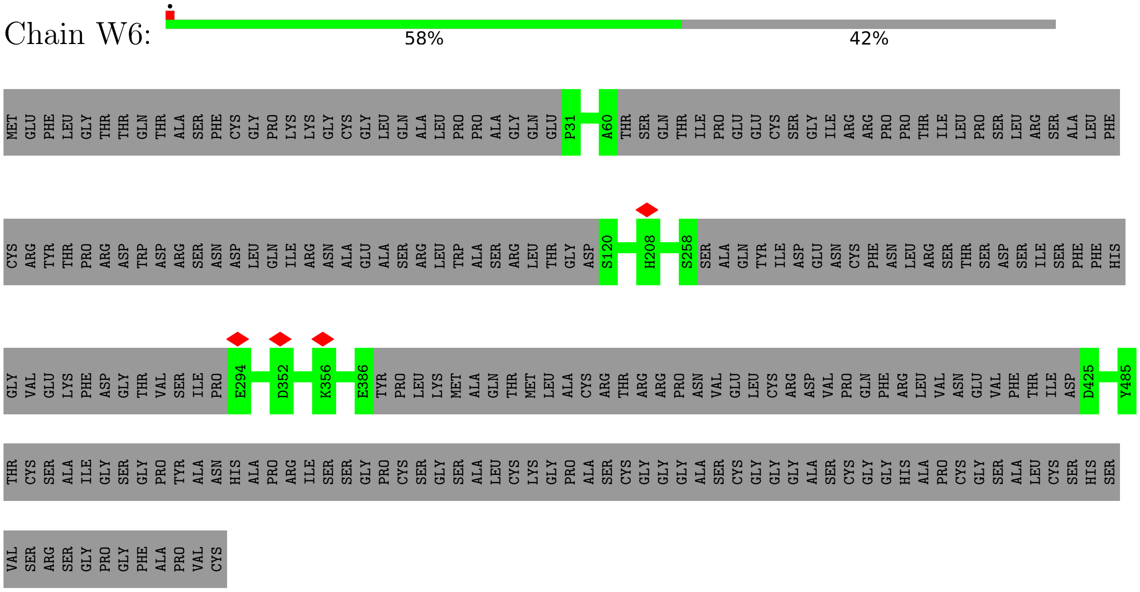
- Molecule 30: Tektin-5

Chain W5:



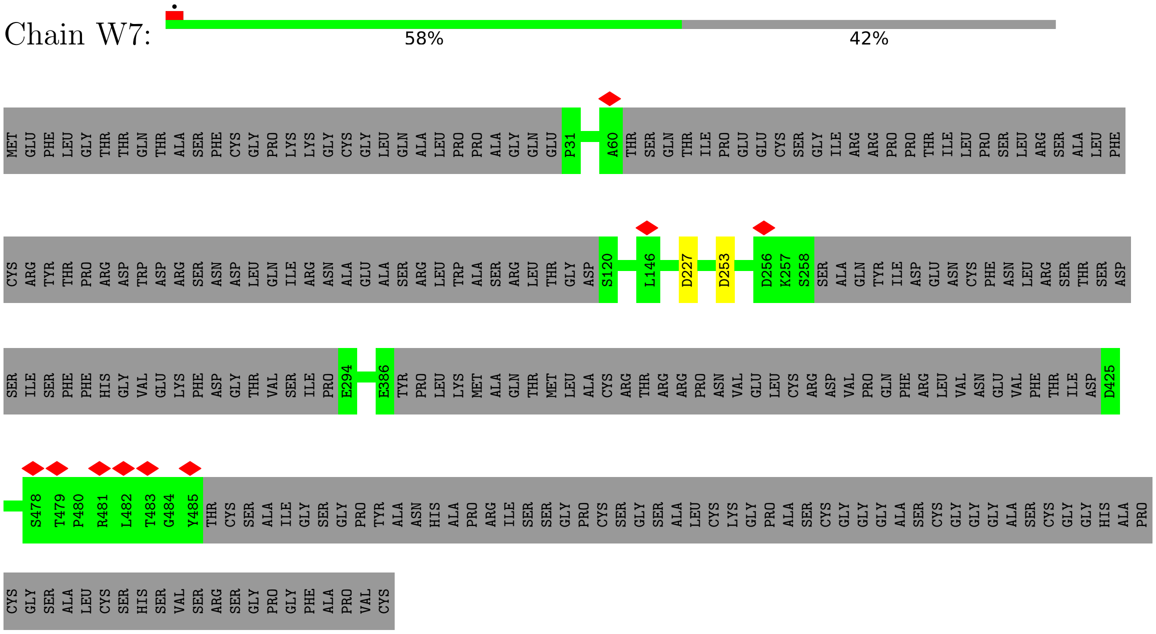
- Molecule 30: Tektin-5

Chain W6:



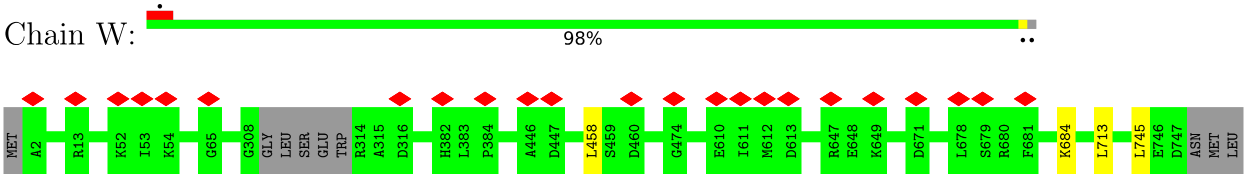
- Molecule 30: Tektin-5

Chain W7:



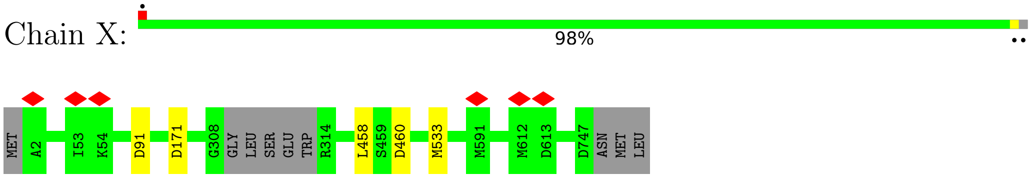
- Molecule 31: EF-hand domain-containing family member C2

Chain W:



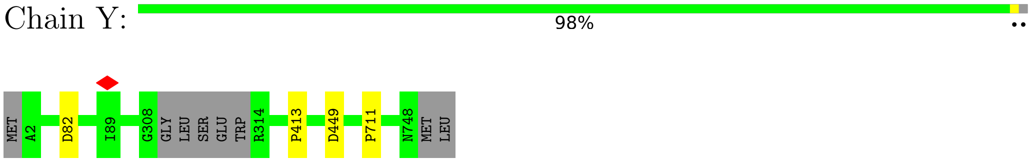
- Molecule 31: EF-hand domain-containing family member C2

Chain X:



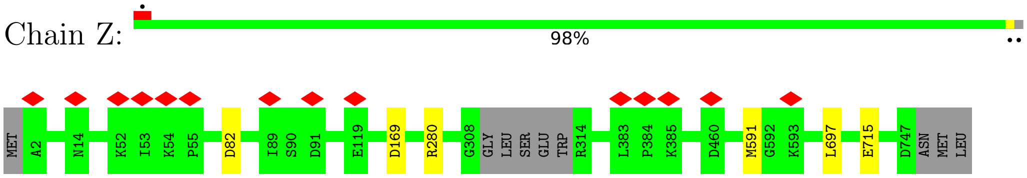
- Molecule 31: EF-hand domain-containing family member C2

Chain Y:



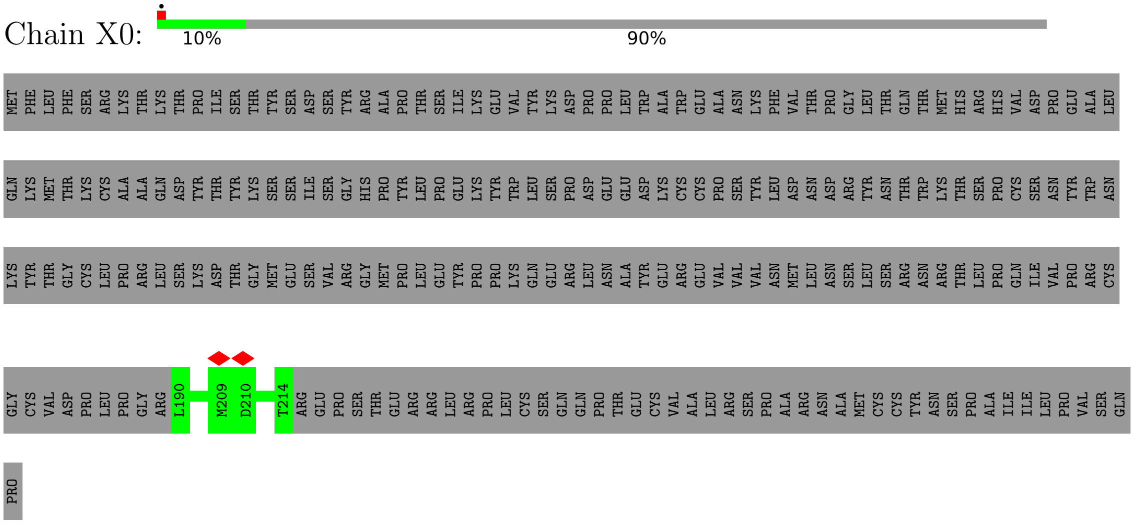
- Molecule 31: EF-hand domain-containing family member C2

Chain Z:



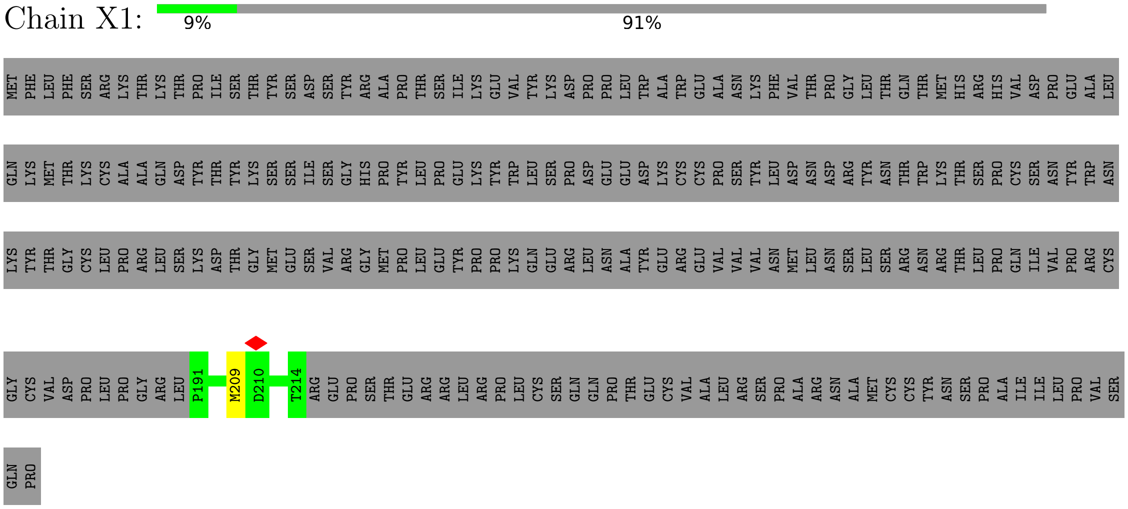
- Molecule 32: Spermatid-specific manchette-related protein 1

Chain X0:



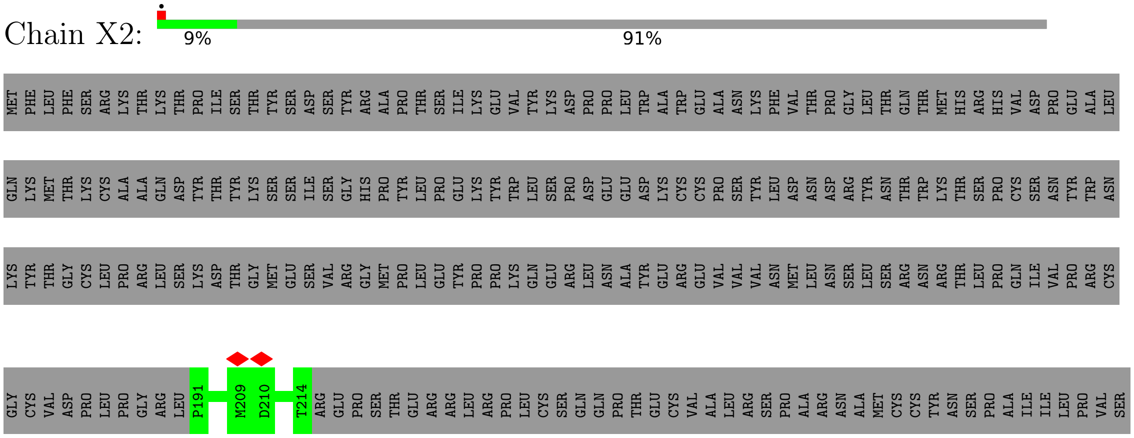
- Molecule 32: Spermatid-specific manchette-related protein 1

Chain X1:



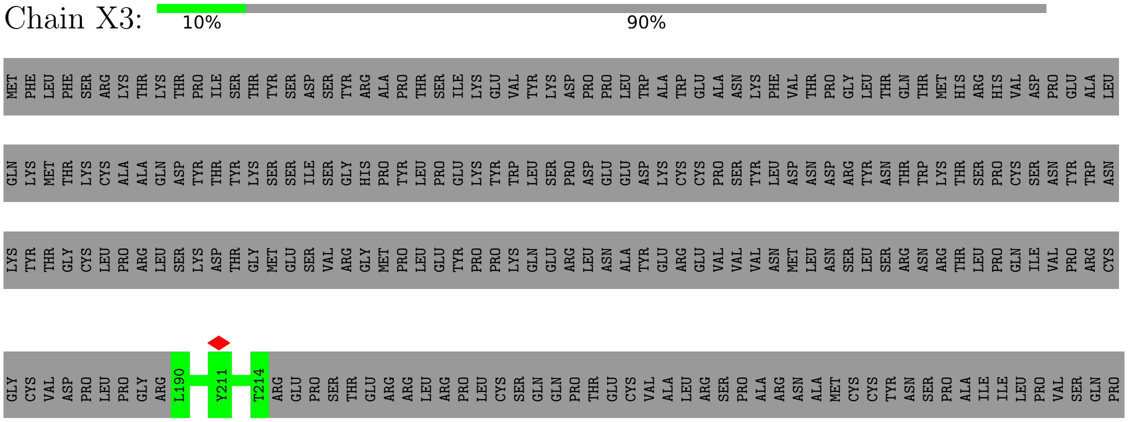
- Molecule 32: Spermatid-specific manchette-related protein 1

Chain X2:



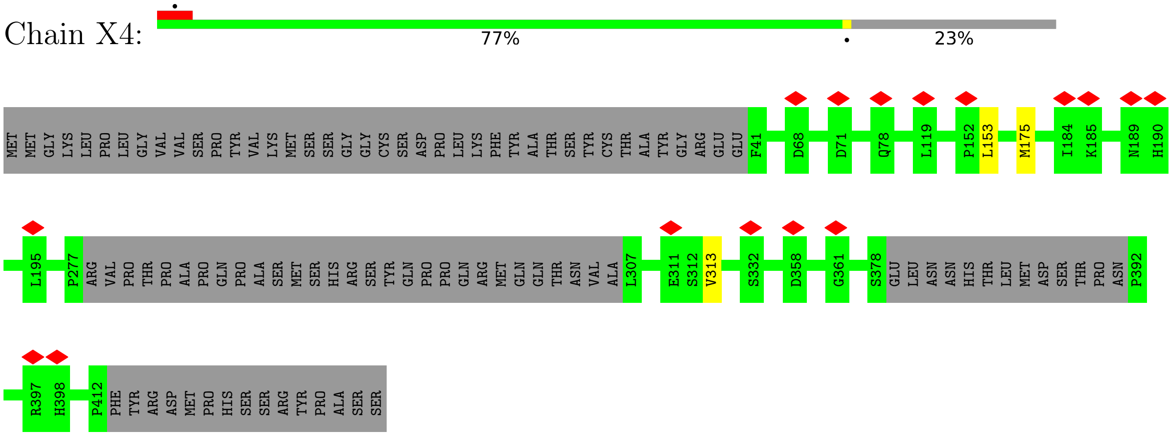
- Molecule 32: Spermatid-specific manchette-related protein 1

Chain X3:



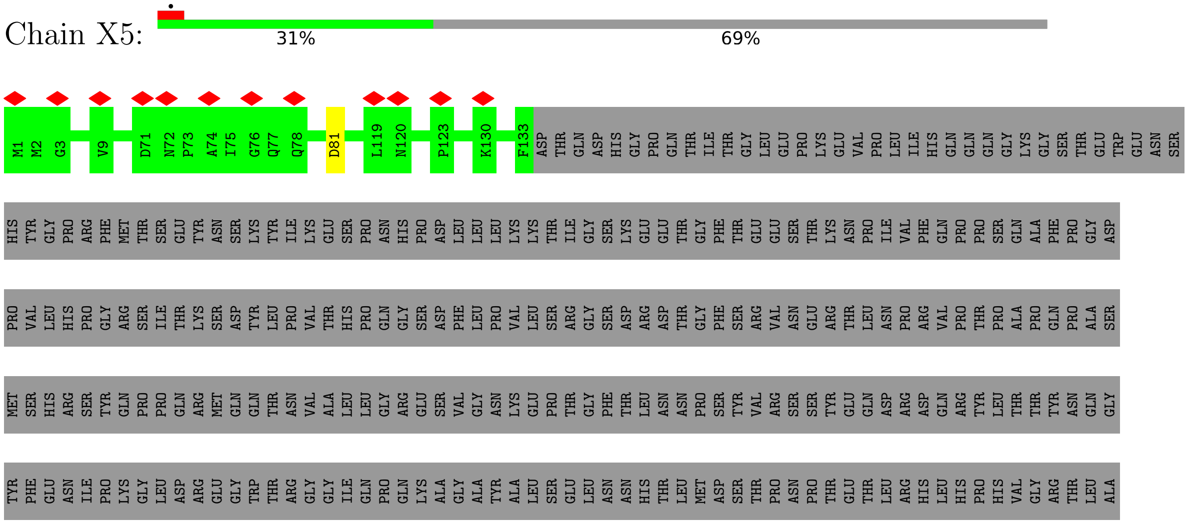
- Molecule 33: Protein phosphatase 1 regulatory subunit 32

Chain X4:



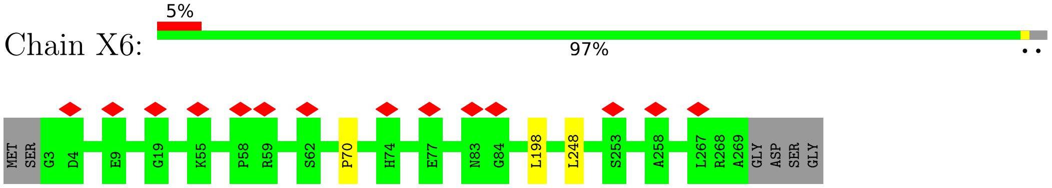
- Molecule 33: Protein phosphatase 1 regulatory subunit 32

Chain X5:



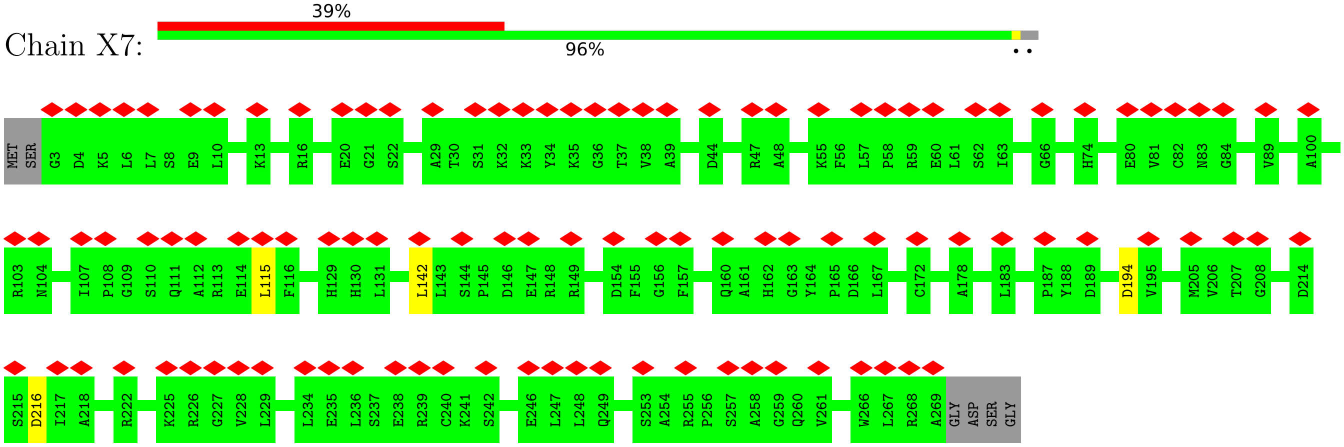
- Molecule 34: Testis-specific serine/threonine-protein kinase 6

Chain X6:



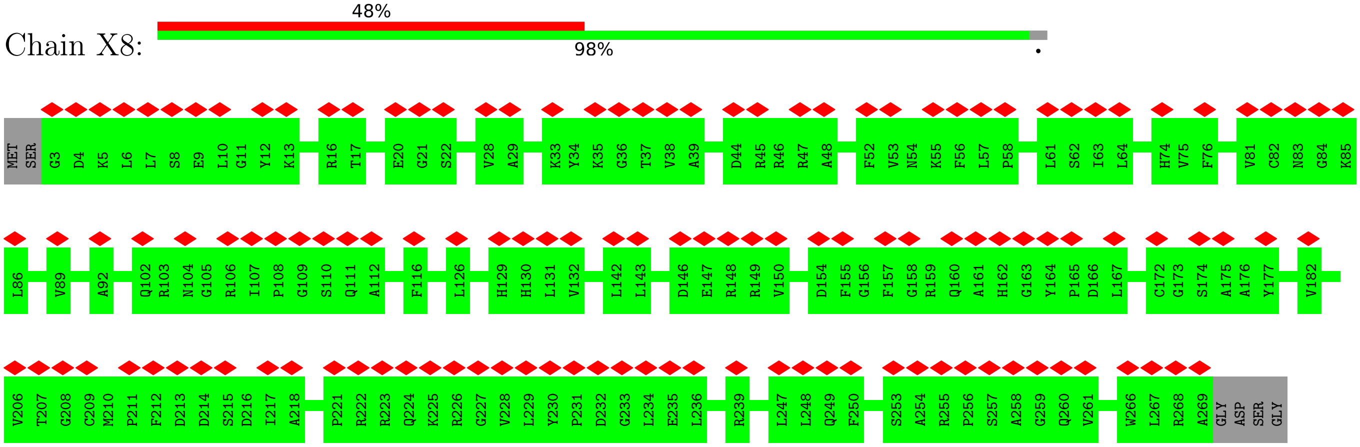
- Molecule 34: Testis-specific serine/threonine-protein kinase 6

Chain X7:



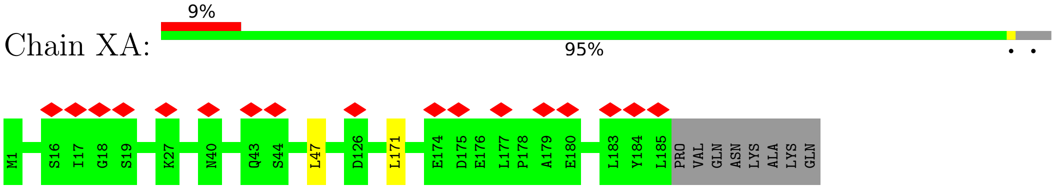
- Molecule 34: Testis-specific serine/threonine-protein kinase 6

Chain X8:



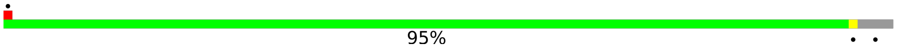
- Molecule 35: Cilia- and flagella-associated protein 20

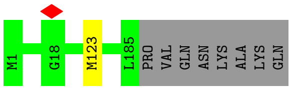
Chain XA:



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

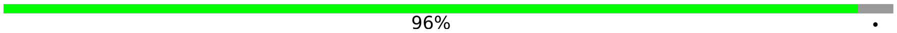
Chain XB:

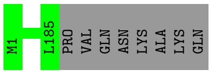




- Molecule 35: Cilia- and flagella-associated protein 20

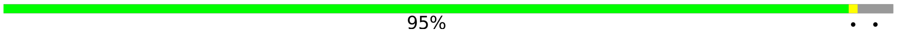
Chain XC:

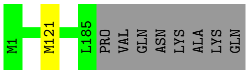




- Molecule 35: Cilia- and flagella-associated protein 20

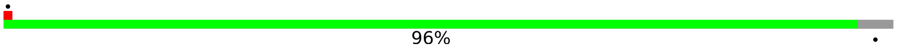
Chain XD:

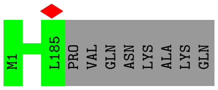




- Molecule 35: Cilia- and flagella-associated protein 20

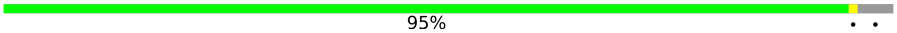
Chain XE:

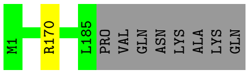




- Molecule 35: Cilia- and flagella-associated protein 20

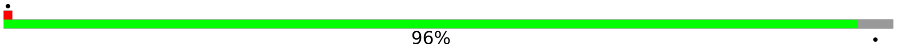
Chain XF:

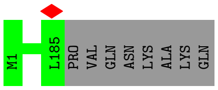




- Molecule 35: Cilia- and flagella-associated protein 20

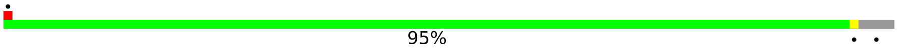
Chain XG:

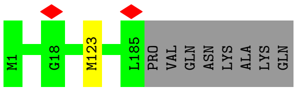




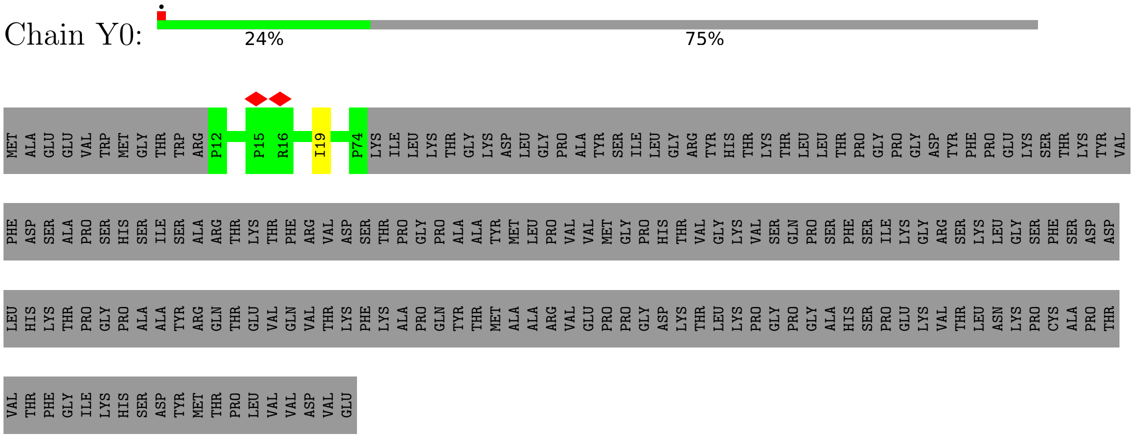
- Molecule 35: Cilia- and flagella-associated protein 20

Chain XH:

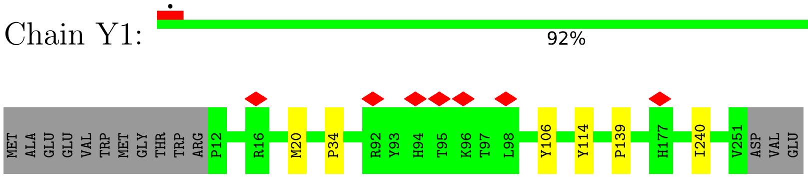




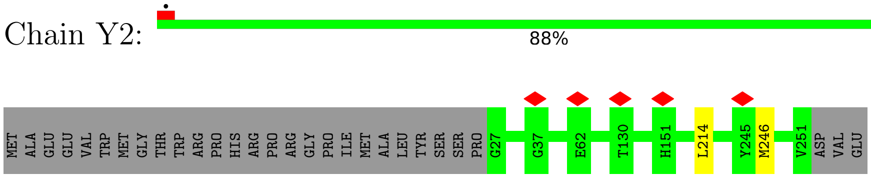
- Molecule 36: Outer dense fiber protein 3



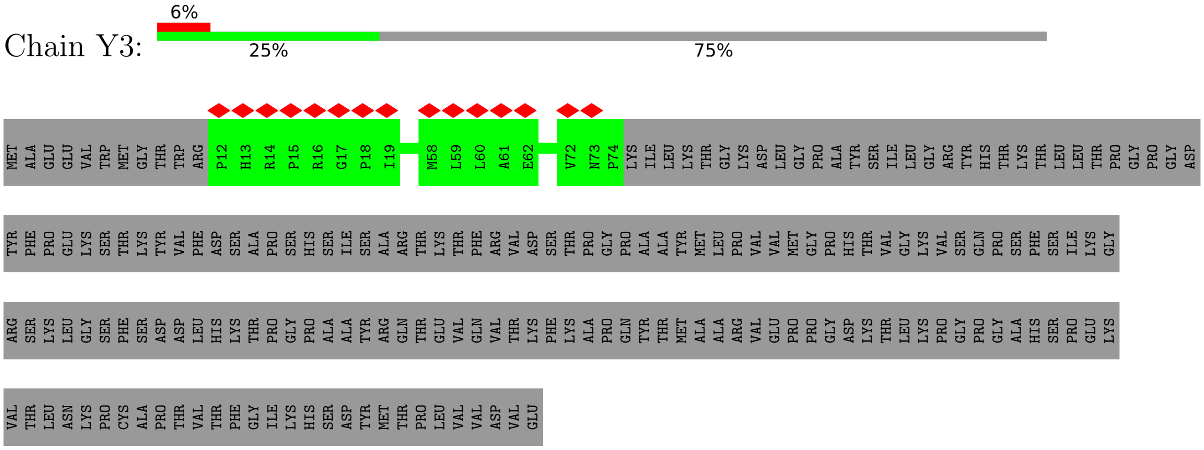
- Molecule 36: Outer dense fiber protein 3



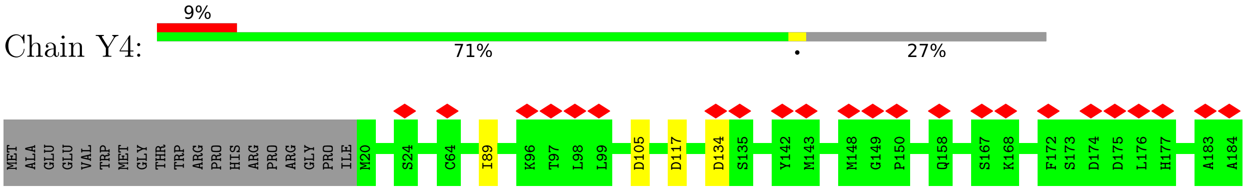
- Molecule 36: Outer dense fiber protein 3

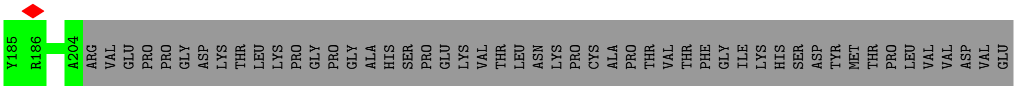


- Molecule 36: Outer dense fiber protein 3



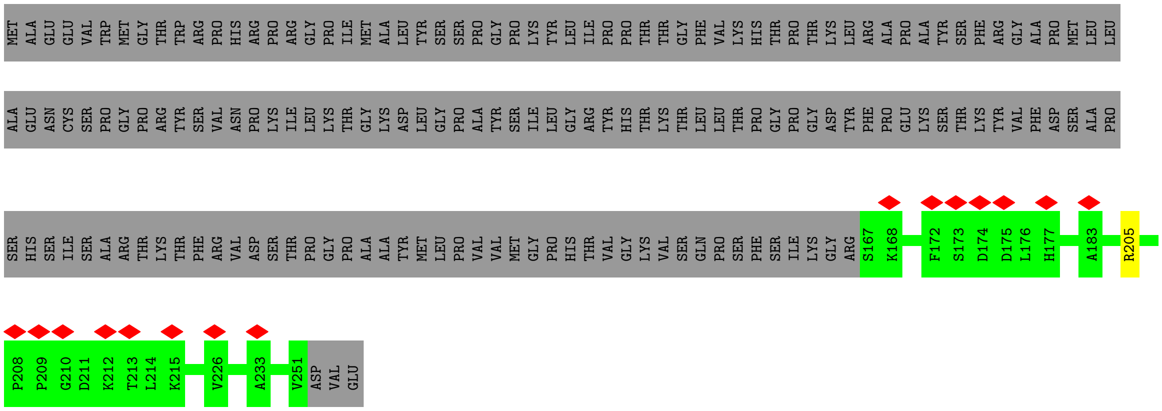
- Molecule 36: Outer dense fiber protein 3





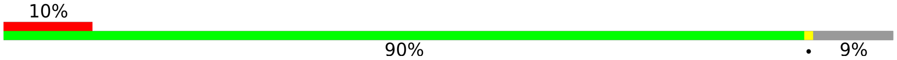
- Molecule 36: Outer dense fiber protein 3

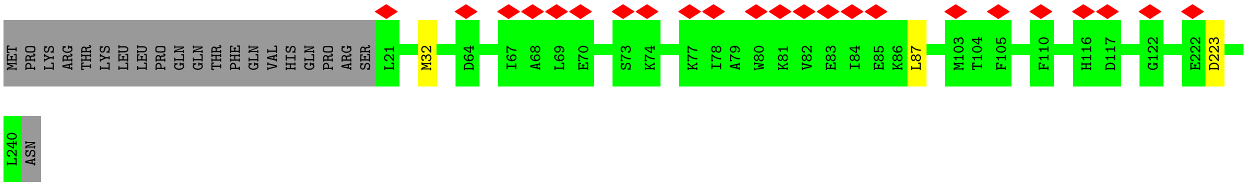
Chain Y5:



- Molecule 37: Parkin coregulated gene protein homolog

Chain YA:



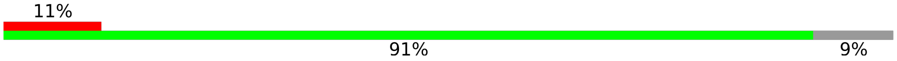


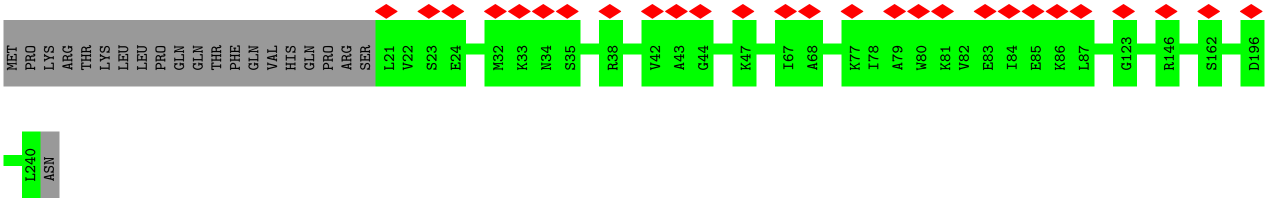
- Molecule 37: Parkin coregulated gene protein homolog

Chain YB:

- Molecule 37: Parkin coregulated gene protein homolog

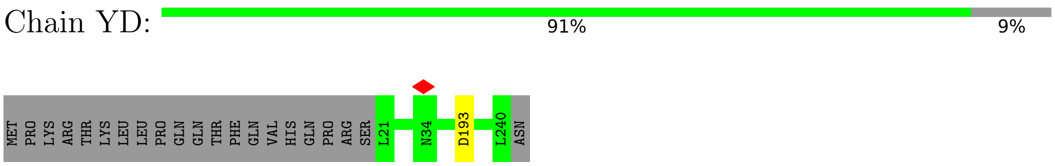
Chain YC:





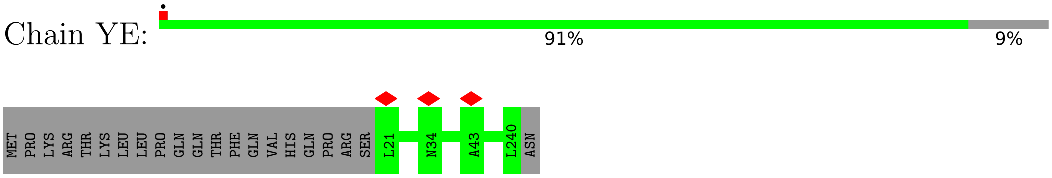
- Molecule 37: Parkin coregulated gene protein homolog

Chain YD:



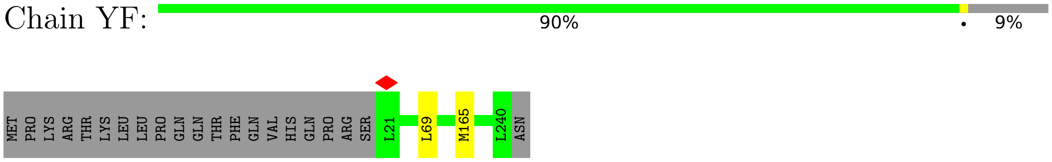
- Molecule 37: Parkin coregulated gene protein homolog

Chain YE:



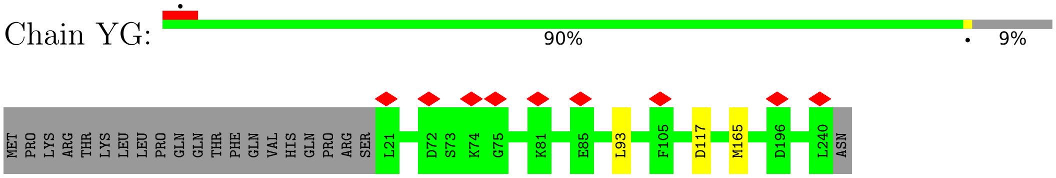
- Molecule 37: Parkin coregulated gene protein homolog

Chain YF:



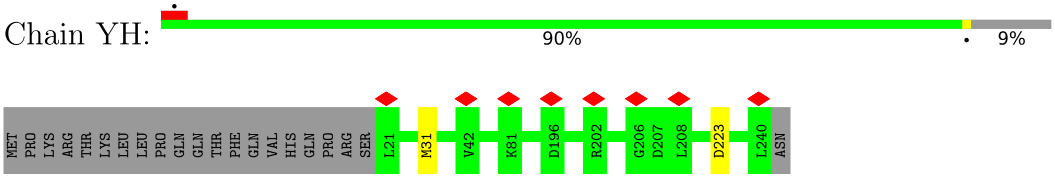
- Molecule 37: Parkin coregulated gene protein homolog

Chain YG:



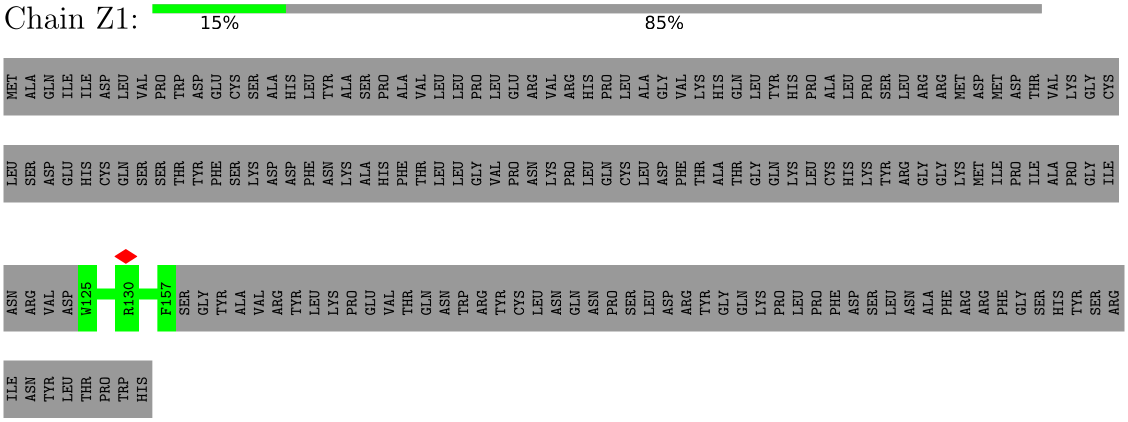
- Molecule 37: Parkin coregulated gene protein homolog

Chain YH:



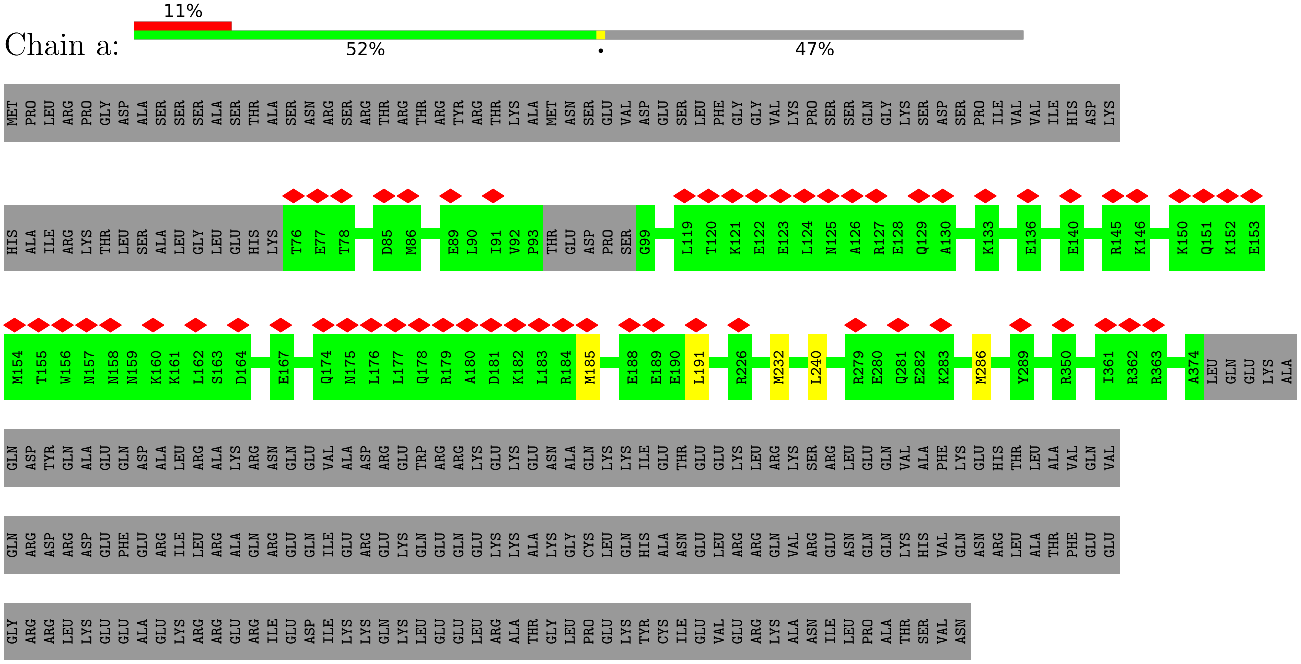
- Molecule 38: Testis, prostate and placenta-expressed protein

Chain Z1:



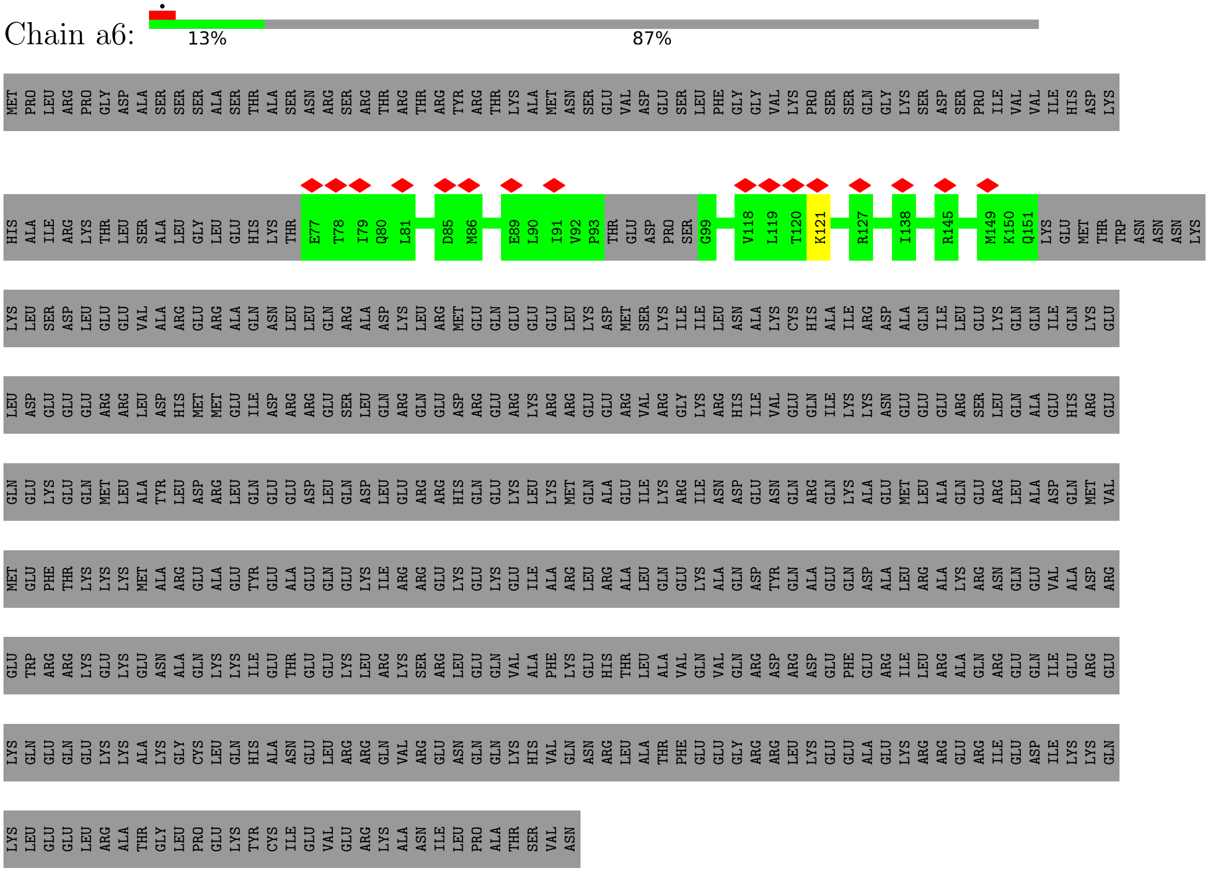
- Molecule 39: Cilia- and flagella-associated protein 45

Chain a:

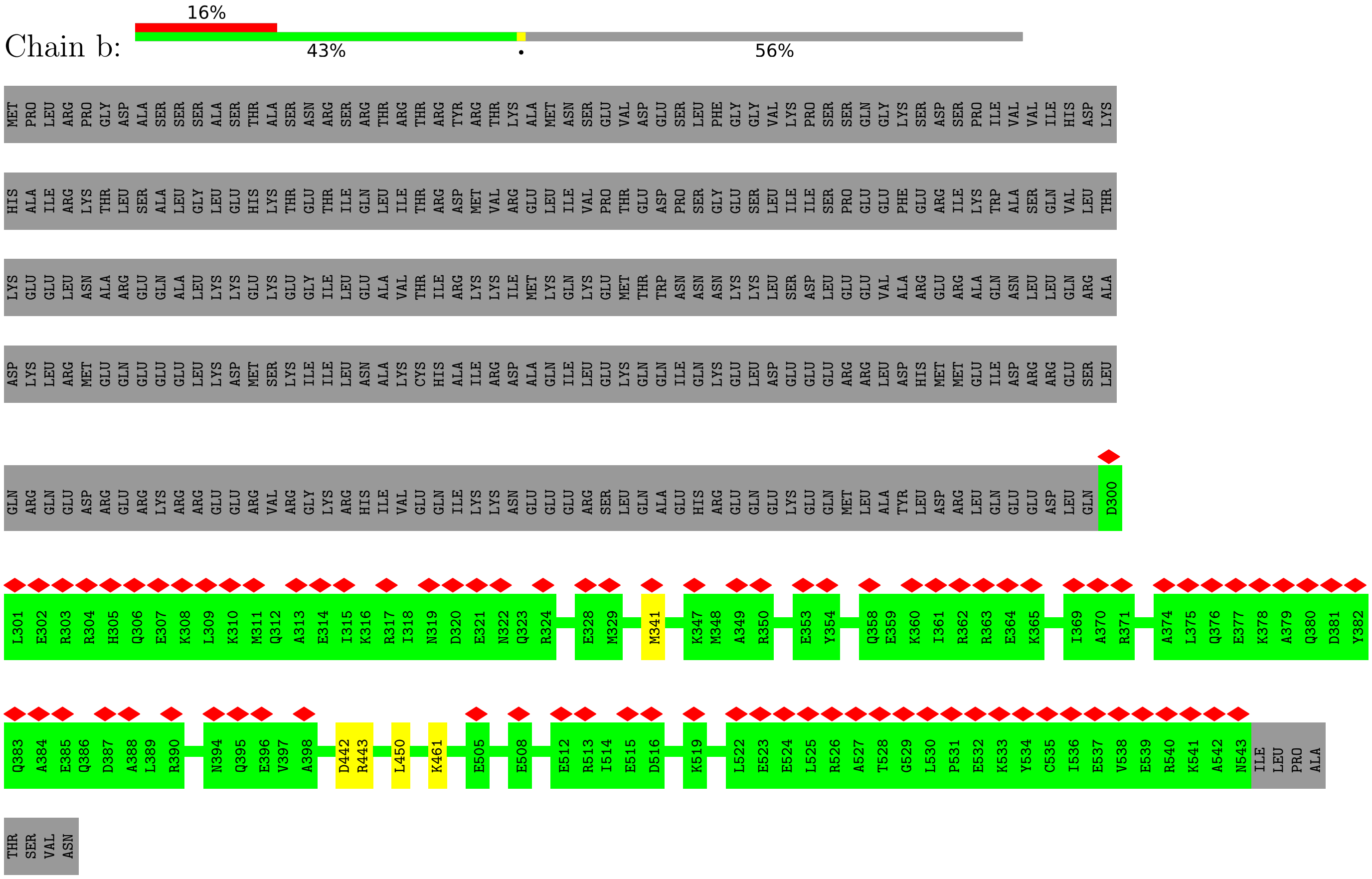


- Molecule 39: Cilia- and flagella-associated protein 45

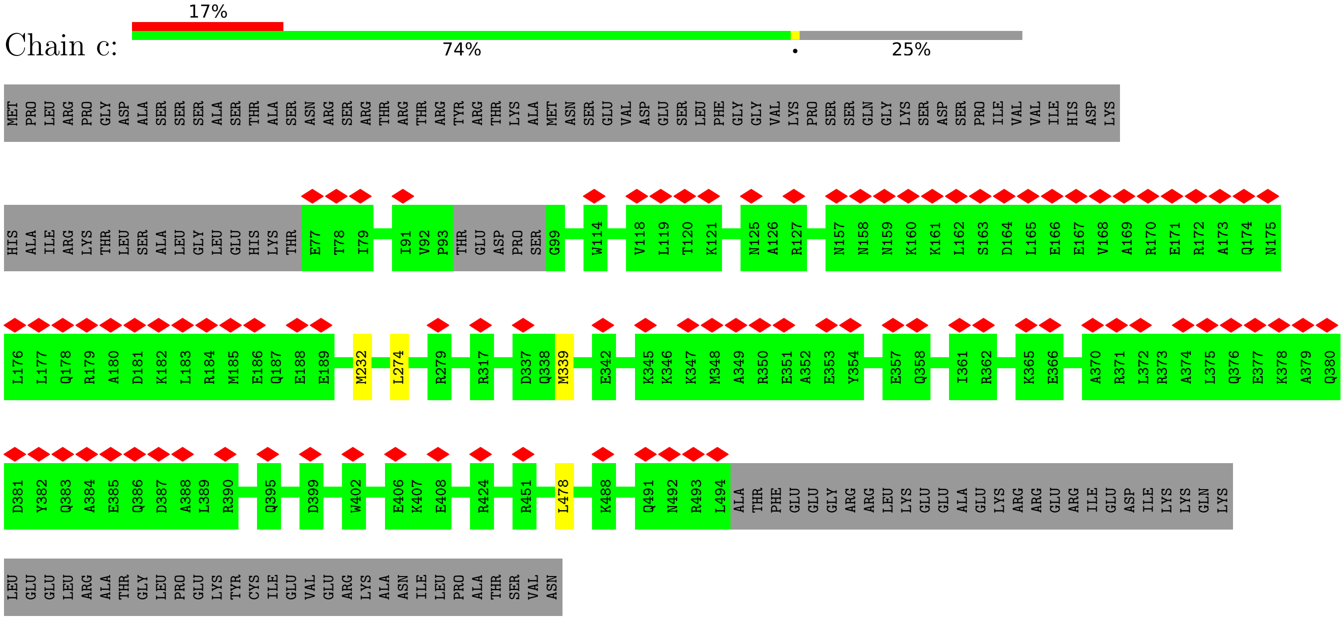
Chain a6:



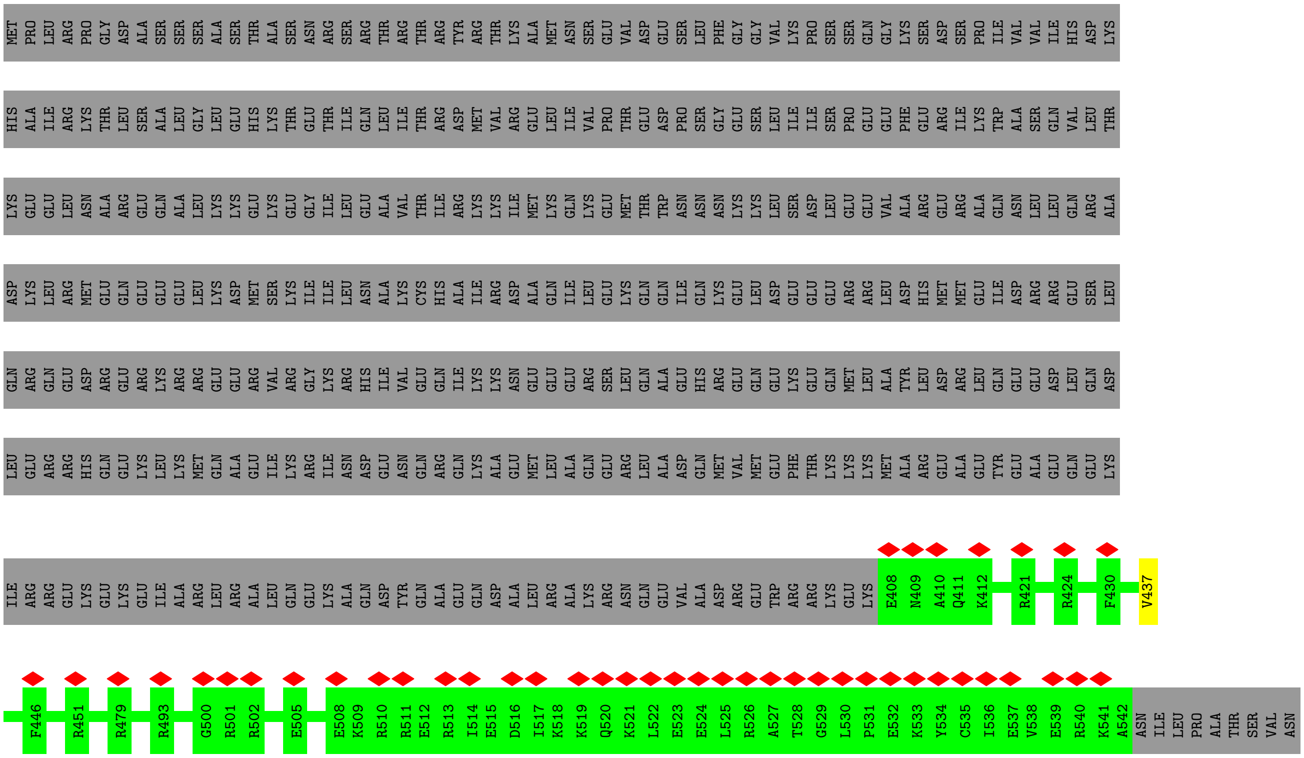
- Molecule 39: Cilia- and flagella-associated protein 45



- Molecule 39: Cilia- and flagella-associated protein 45

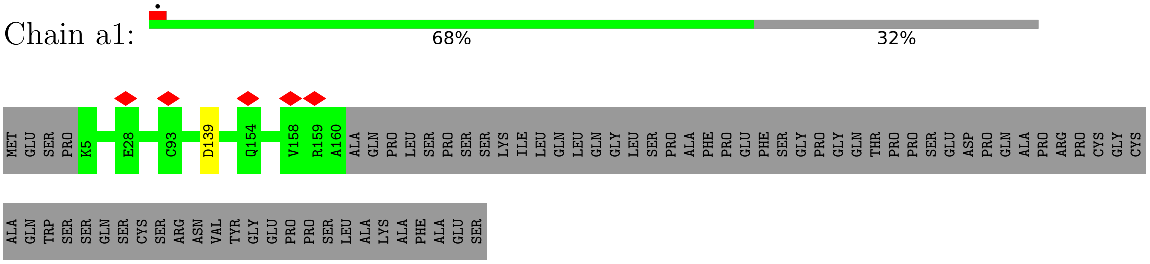


- Molecule 39: Cilia- and flagella-associated protein 45



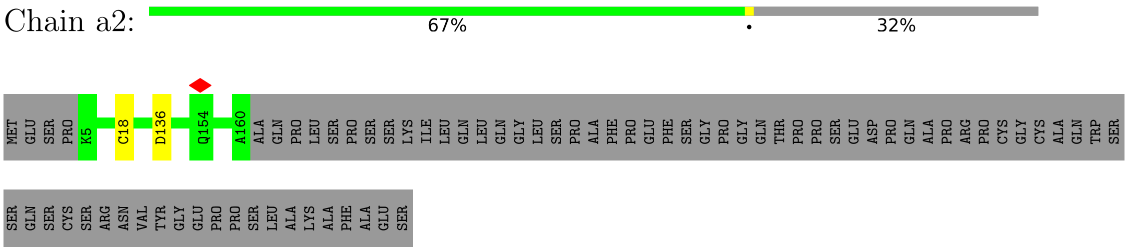
- Molecule 40: Uncharacterized protein C10orf82 homolog

Chain a1:



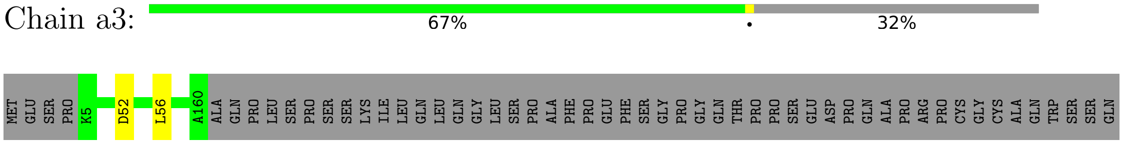
- Molecule 40: Uncharacterized protein C10orf82 homolog

Chain a2:



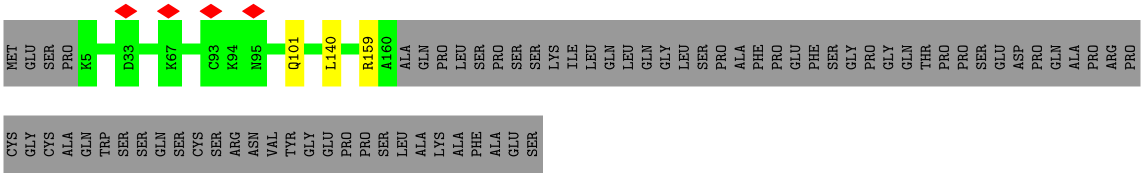
- Molecule 40: Uncharacterized protein C10orf82 homolog

Chain a3:



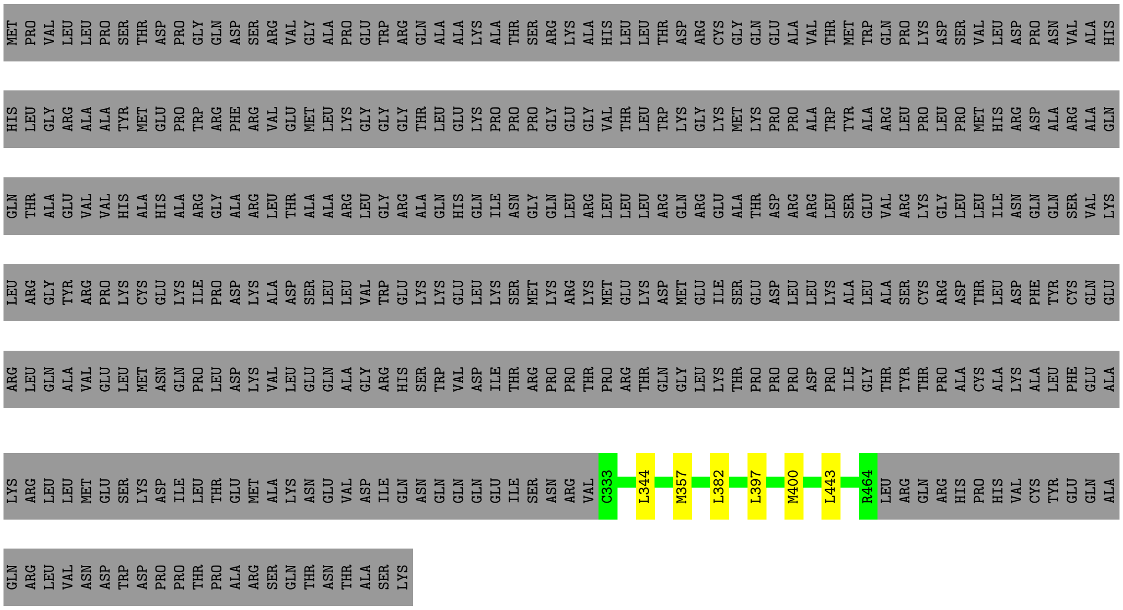
- Molecule 40: Uncharacterized protein C10orf82 homolog

Chain a4:



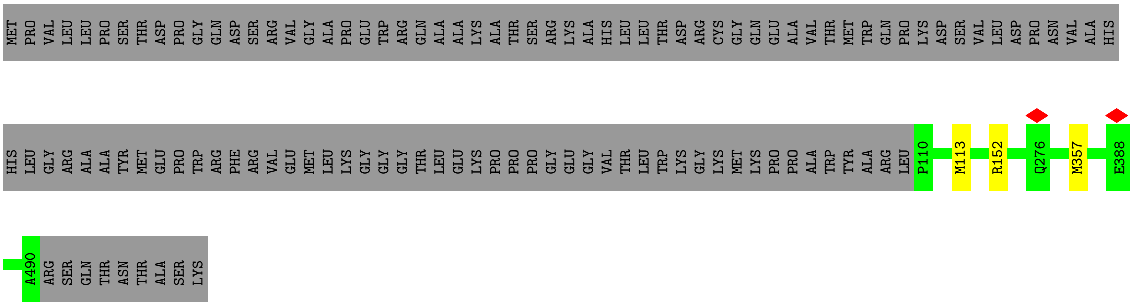
- Molecule 41: Coiled-coil domain-containing protein 105

Chain b1:



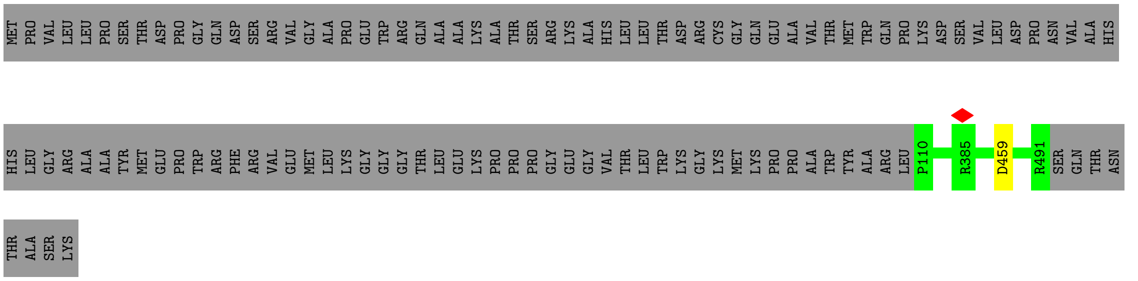
- Molecule 41: Coiled-coil domain-containing protein 105

Chain b2:



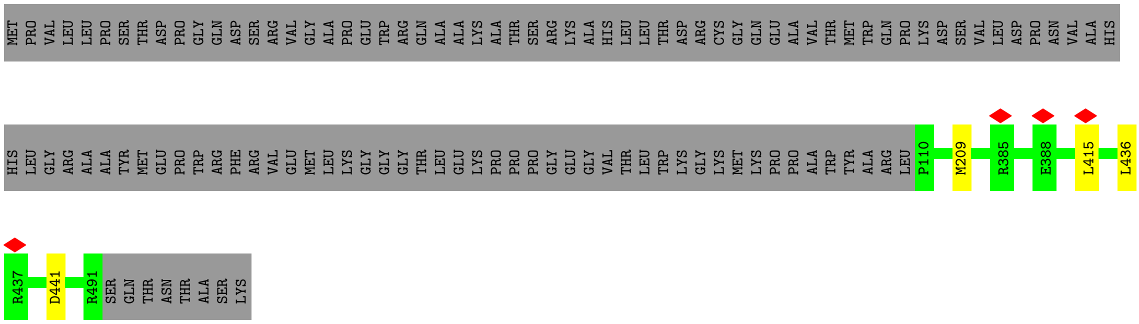
- Molecule 41: Coiled-coil domain-containing protein 105

Chain b3:



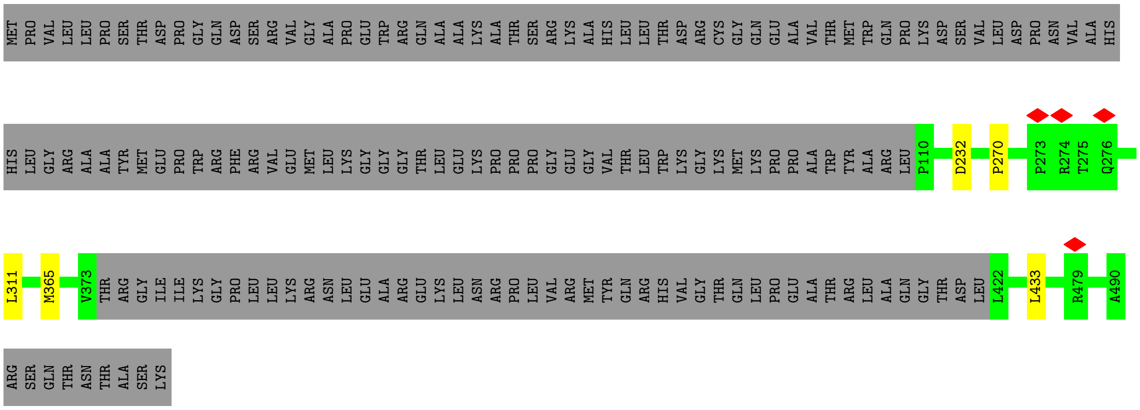
• Molecule 41: Coiled-coil domain-containing protein 105

Chain b4:



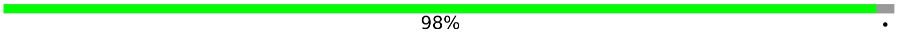
• Molecule 41: Coiled-coil domain-containing protein 105

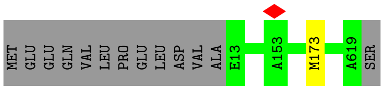
Chain b5:



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

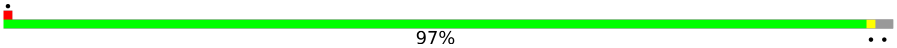
Chain e:

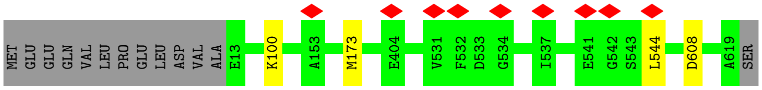




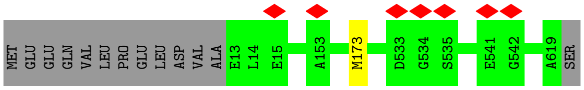
• Molecule 42: Cilia- and flagella-associated protein 52

Chain f:

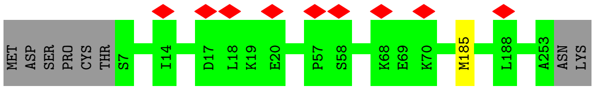




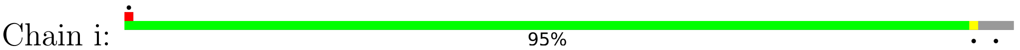
- Molecule 42: Cilia- and flagella-associated protein 52

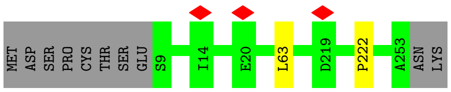


- Molecule 43: Enkurin

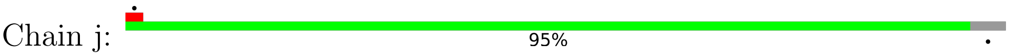


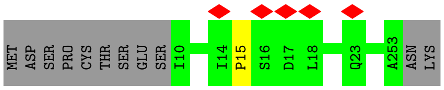
- Molecule 43: Enkurin



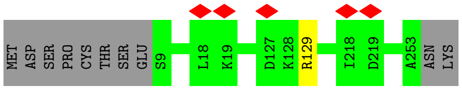


- Molecule 43: Enkurin

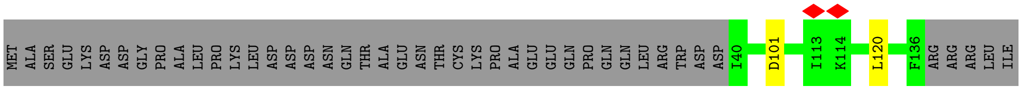




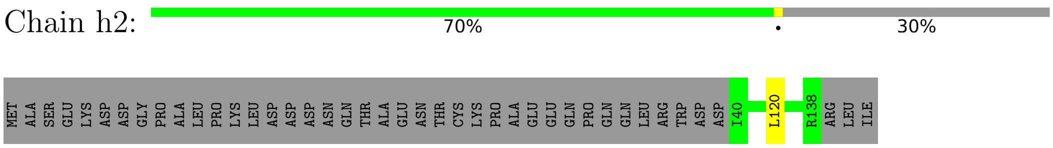
- Molecule 43: Enkurin



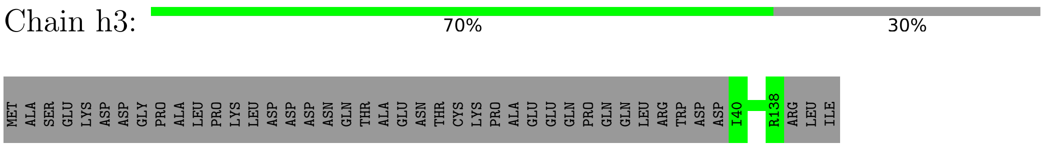
- Molecule 44: Testis-expressed protein 43



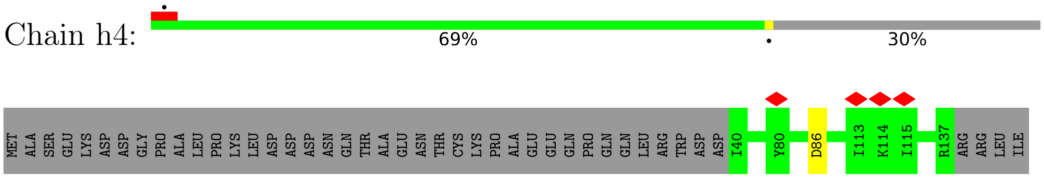
- Molecule 44: Testis-expressed protein 43



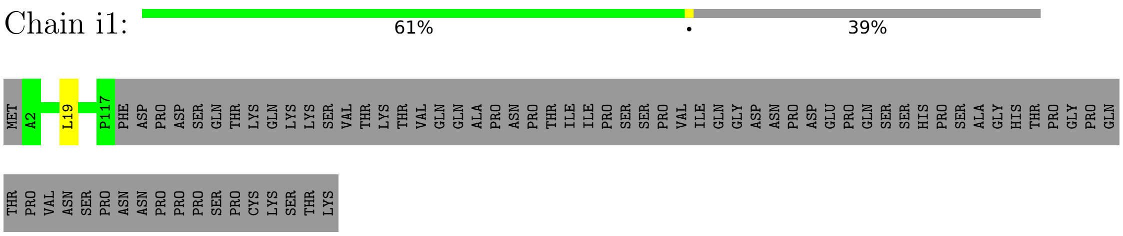
- Molecule 44: Testis-expressed protein 43



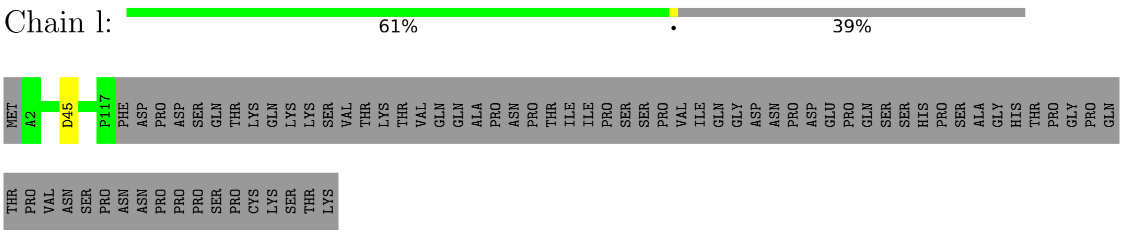
- Molecule 44: Testis-expressed protein 43



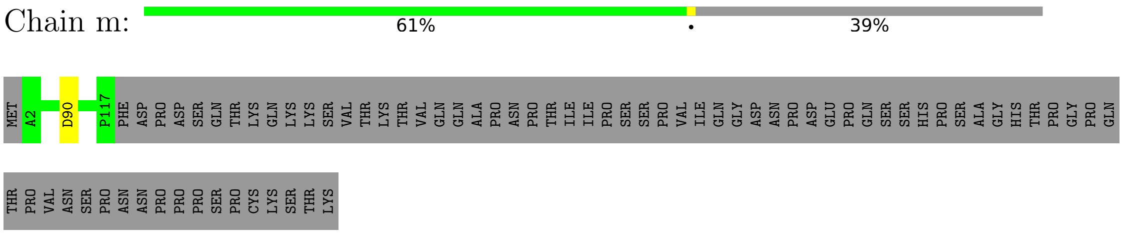
- Molecule 45: Protein Flattop



- Molecule 45: Protein Flattop

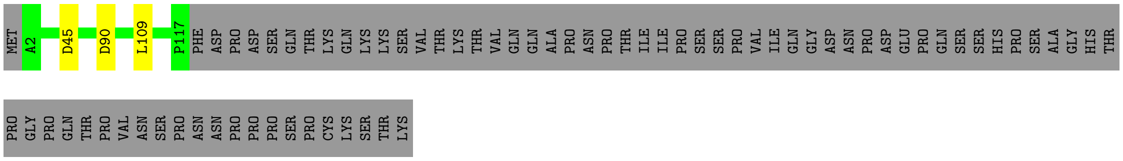


- Molecule 45: Protein Flattop



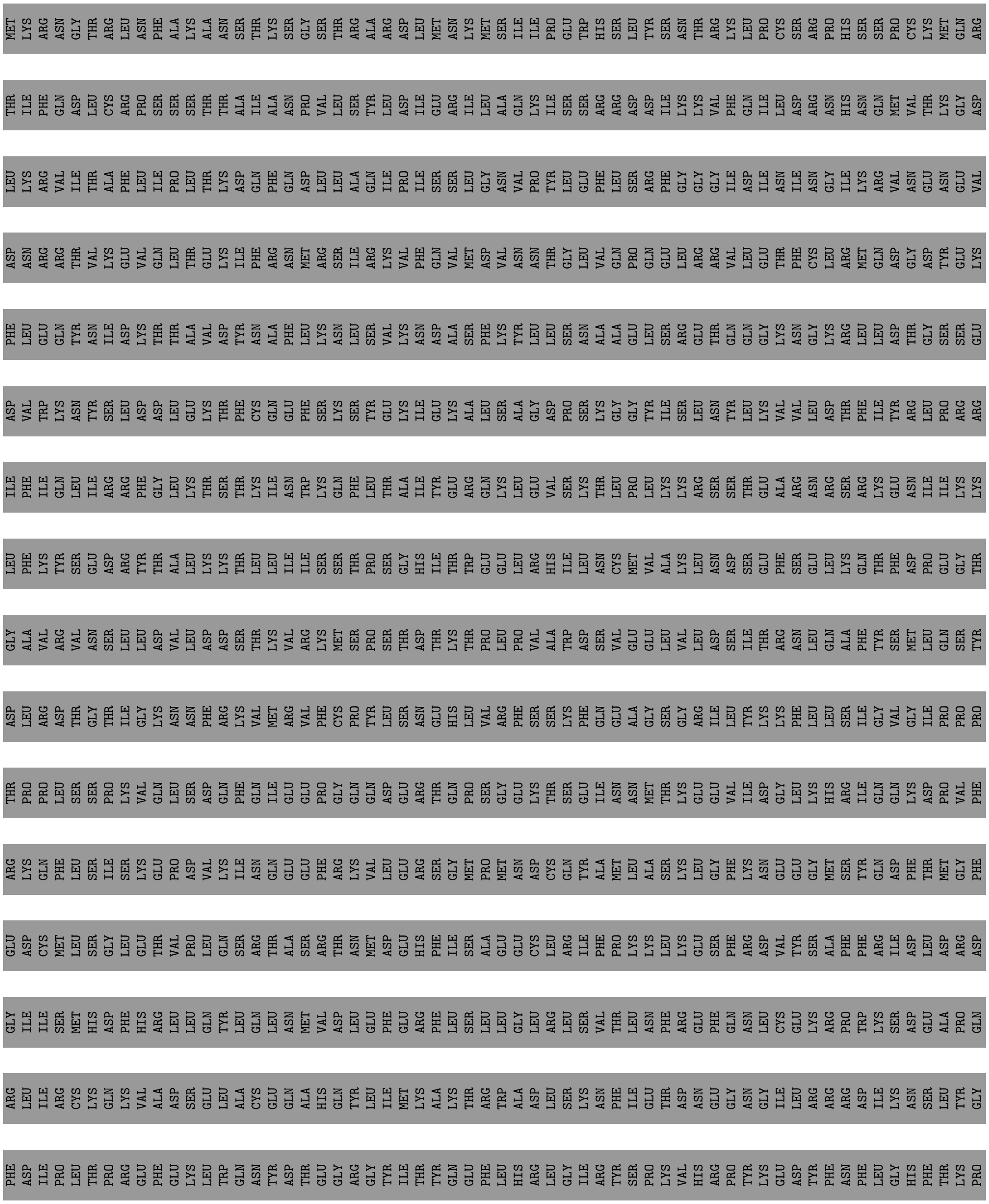
- Molecule 45: Protein Flattop

Chain n:



- Molecule 46: EF-hand calcium-binding domain-containing protein 6

Chain i2:



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

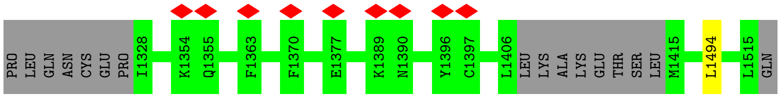
ILE SER LEU LEU LYS SER LEU ASP VAL SER VAL HIS ASN ASN HIS ILE ASP PRO VAL GLU PHE LEU ARG ALA LEU GLU ILE SER TRP ALA SER LYS ALA ARG PRO LYS GLU LYS GLU GLU SER SER PRO PRO PRO ILE SER PHE SER LYS VAL THR PRO ASP GLU VAL ILE LYS THR MET

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

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

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

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



- Molecule 46: EF-hand calcium-binding domain-containing protein 6

Chain i3:

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

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

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

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

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

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

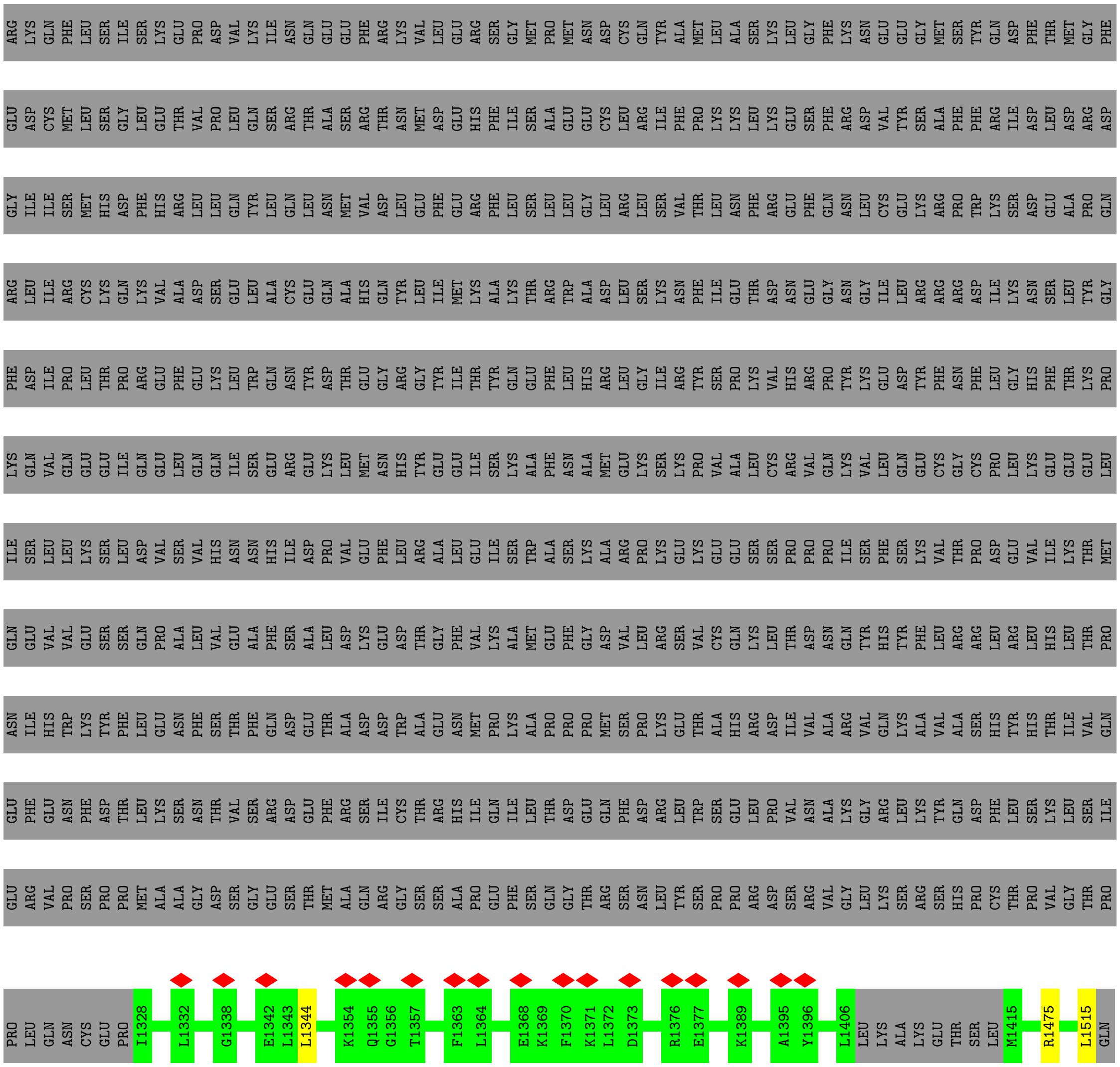
ILE PHE ILE GLN LEU ILE ARG ARG PHE GLY LEU LYS THR SER THR LYS ILE ASN TRP LYS GLN PHE LEU THR ALA ILE TYR GLU ARG GLN LYS LEU GLU VAL SER LYS THR LEU PRO LEU LYS LYS ARG SER SER THR GLU ALA ARG ASN ARG SER ARG LYS GLU ASN ILE ILE LYS LYS

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

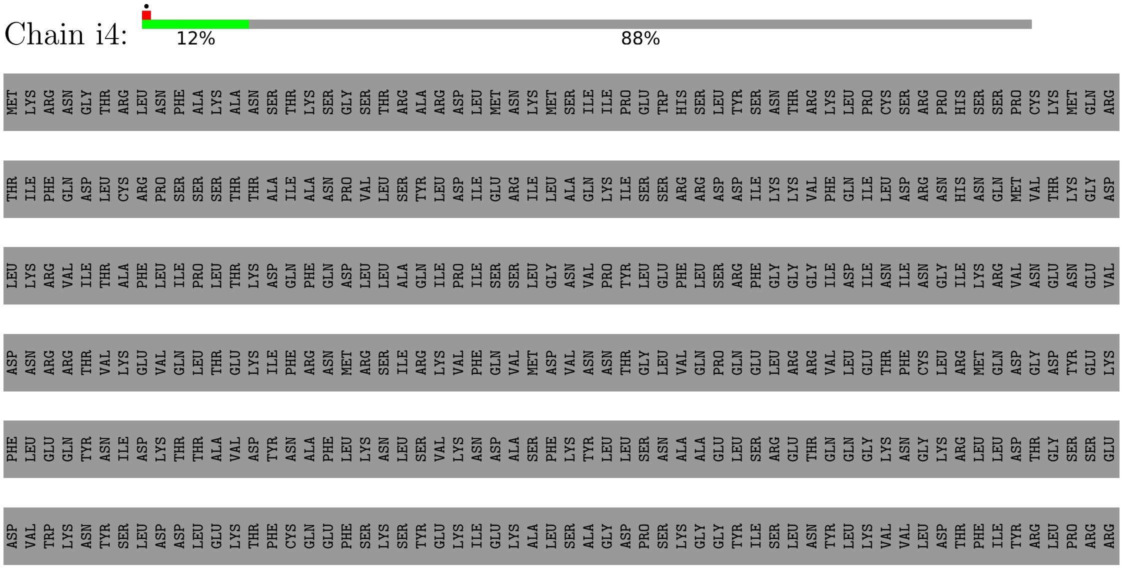
GLY ALA VAL ARG VAL ASN SER LEU LEU ASP VAL LEU ASP ASP SER THR LYS VAL ARG LYS MET SER PRO SER THR ASP THR LYS THR PRO LEU PRO VAL ALA TRP ASP SER VAL GLU GLU LEU VAL LEU ASP SER ILE THR ARG ASN LEU GLN ALA PHE TYR SER MET LEU GLN SER TYR

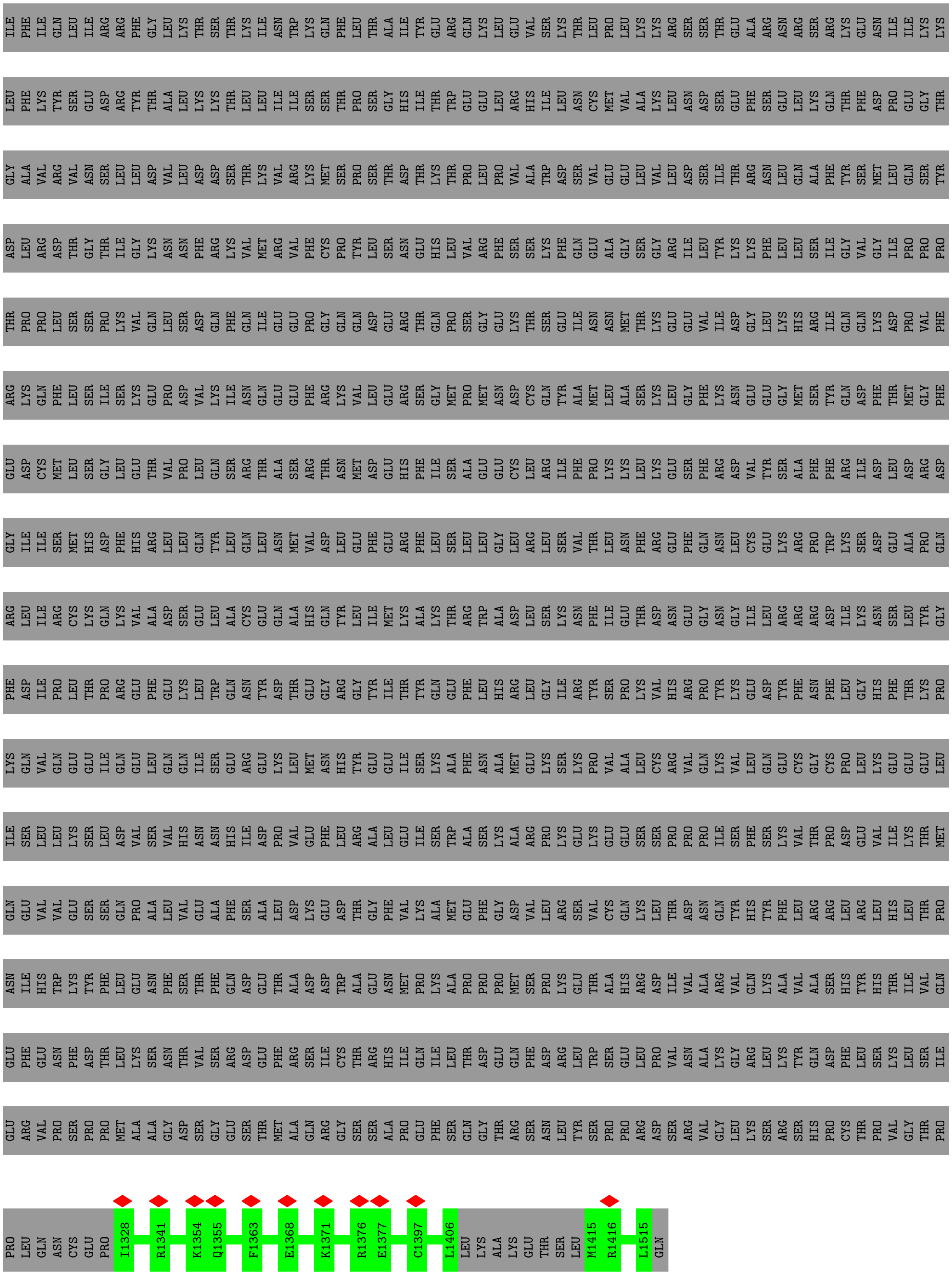
ASP LEU ARG ASP THR GLY THR ILE GLY LYS ASN ASN PHE ARG LYS VAL MET ARG VAL PHE CYS PRO TYR LEU SER ASN GLU HIS LEU VAL ARG PHE SER SER LYS PHE GLN GLU ALA GLY SER GLY ARG ILE LEU TYR LYS LYS PHE LEU LEU SER ILE GLY VAL GLY ILE PRO PRO PRO

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



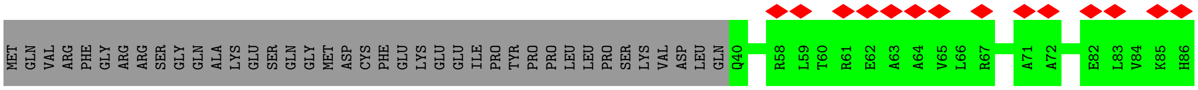
- Molecule 46: EF-hand calcium-binding domain-containing protein 6

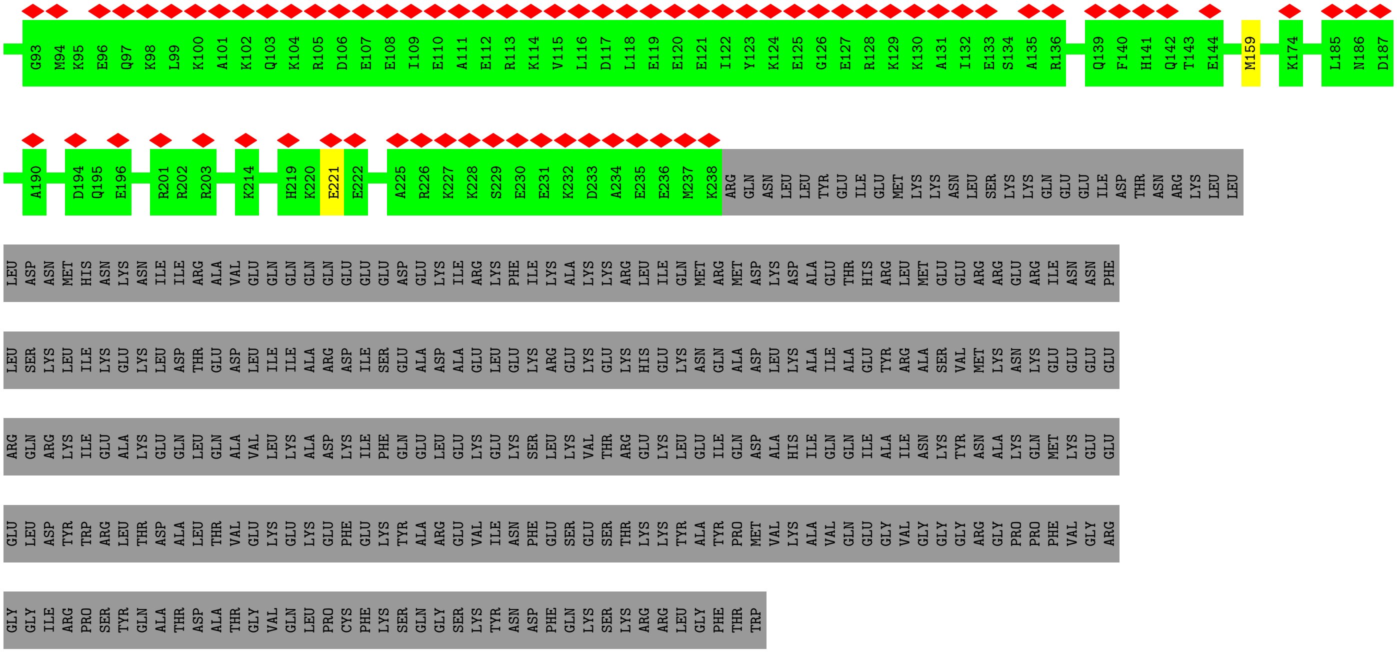




- Molecule 47: Cilia- and flagella-associated protein 210

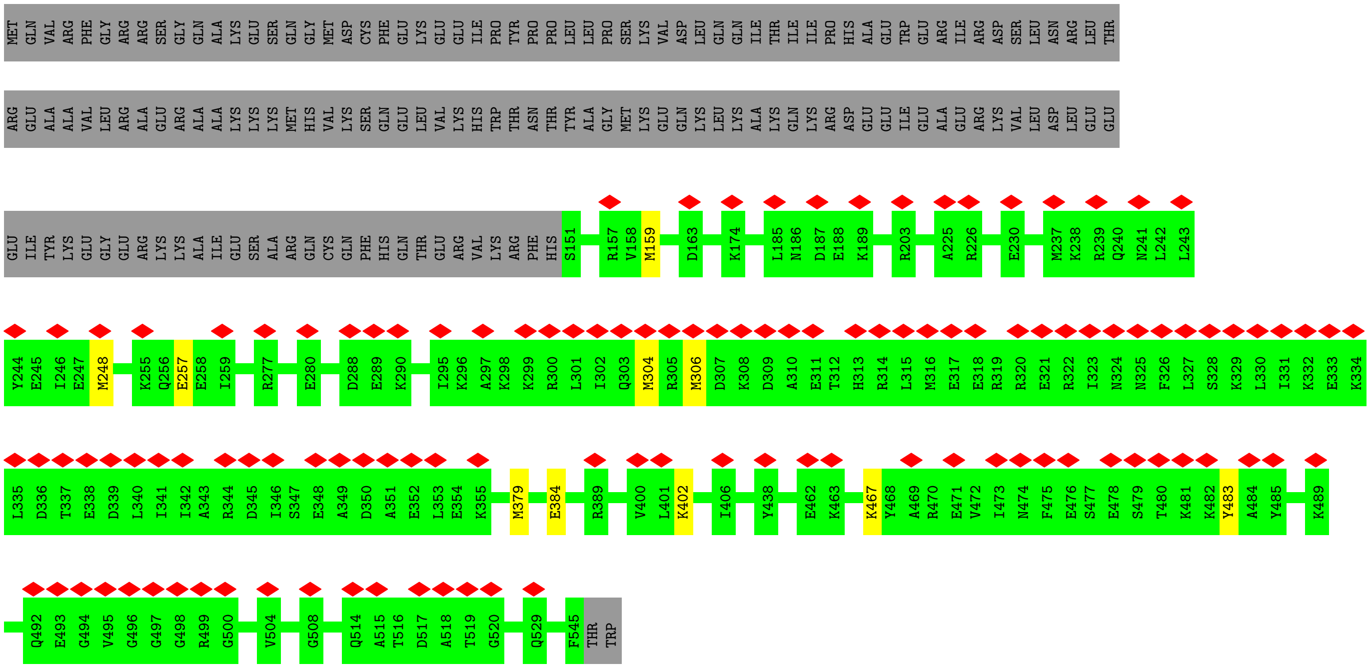
Chain o:





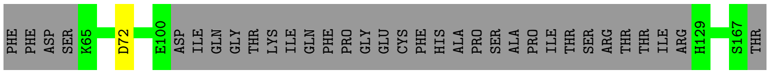
- Molecule 47: Cilia- and flagella-associated protein 210

Chain p:



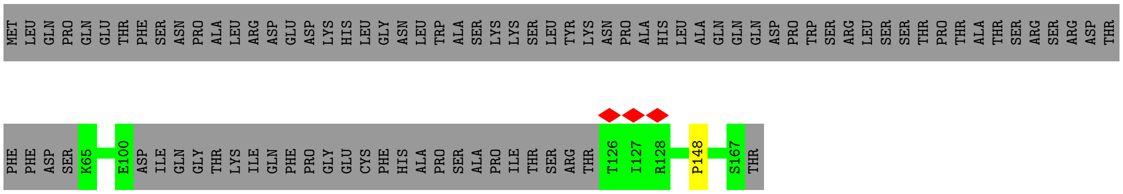
- Molecule 48: Cilia- and flagella-associated protein 276

Chain q:



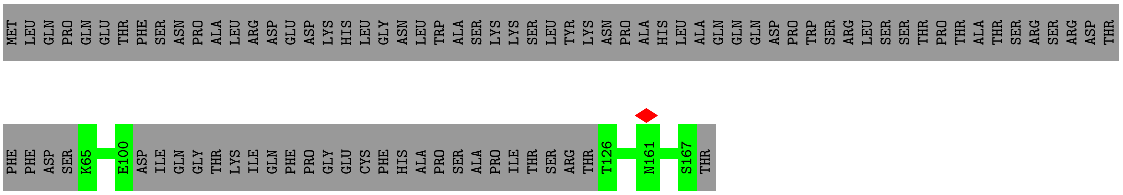
- Molecule 48: Cilia- and flagella-associated protein 276

Chain r:



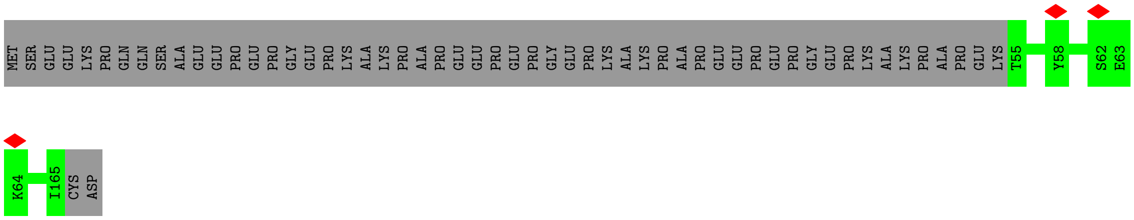
- Molecule 48: Cilia- and flagella-associated protein 276

Chain s:



- Molecule 49: Piercer of microtubule wall 1 protein

Chain y:



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 $(e^-/\text{Å}^2)$	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 (Å)	576.11, 463.062, 869.60004	wwPDB
Map dimensions	530, 426, 800	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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

The worst 5 of 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

The worst 5 of 1363 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
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

There are no chirality outliers.

5 of 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

5.2 Too-close contacts ⓘ

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

5.3.2 Protein sidechains ⓘ

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
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%)
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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
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%)
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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
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%)
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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
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%)
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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
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%)
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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
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%)
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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
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%)
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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
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%)
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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
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%)
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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
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%)
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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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
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

The worst 5 of 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

The worst 5 of 1944 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
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

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
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

There are no chirality outliers.

5 of 1477 torsion outliers are listed below:

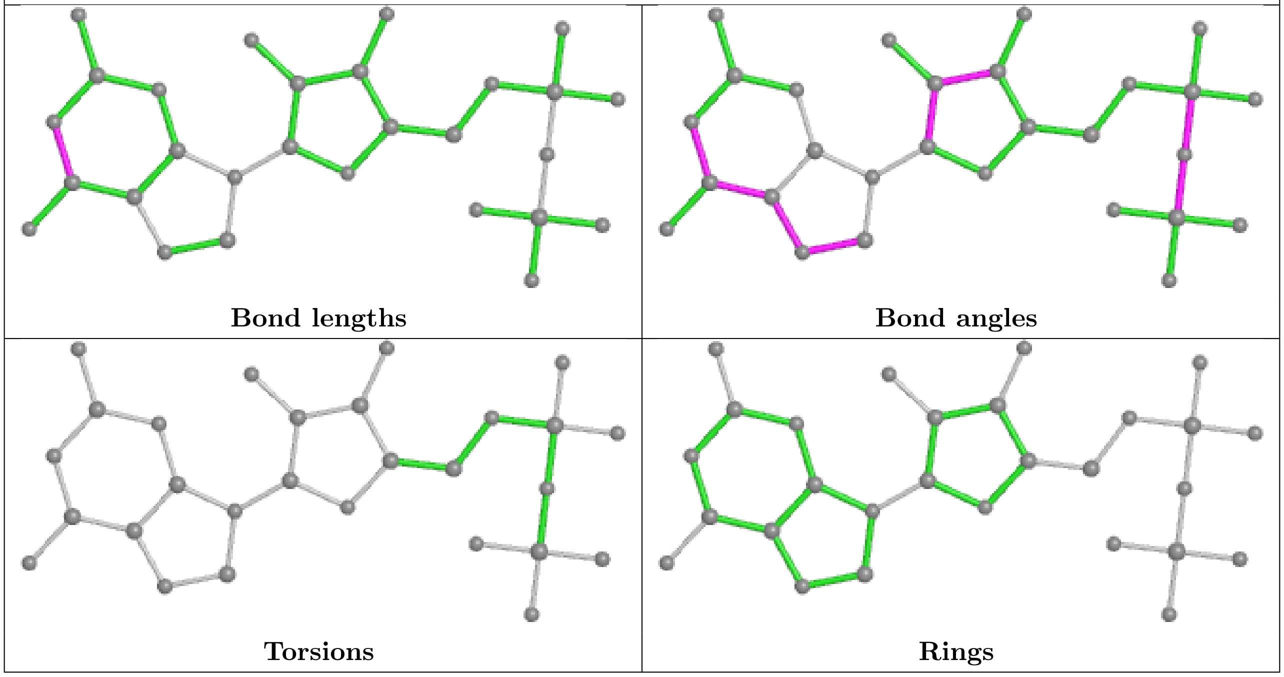
Mol	Chain	Res	Type	Atoms
50	AA	501	GTP	C5'-O5'-PA-O1A
50	AA	501	GTP	C5'-O5'-PA-O2A
50	AC	501	GTP	C5'-O5'-PA-O1A
50	AC	501	GTP	C5'-O5'-PA-O2A
50	AE	501	GTP	PB-O3A-PA-O5'

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GDP FL 502



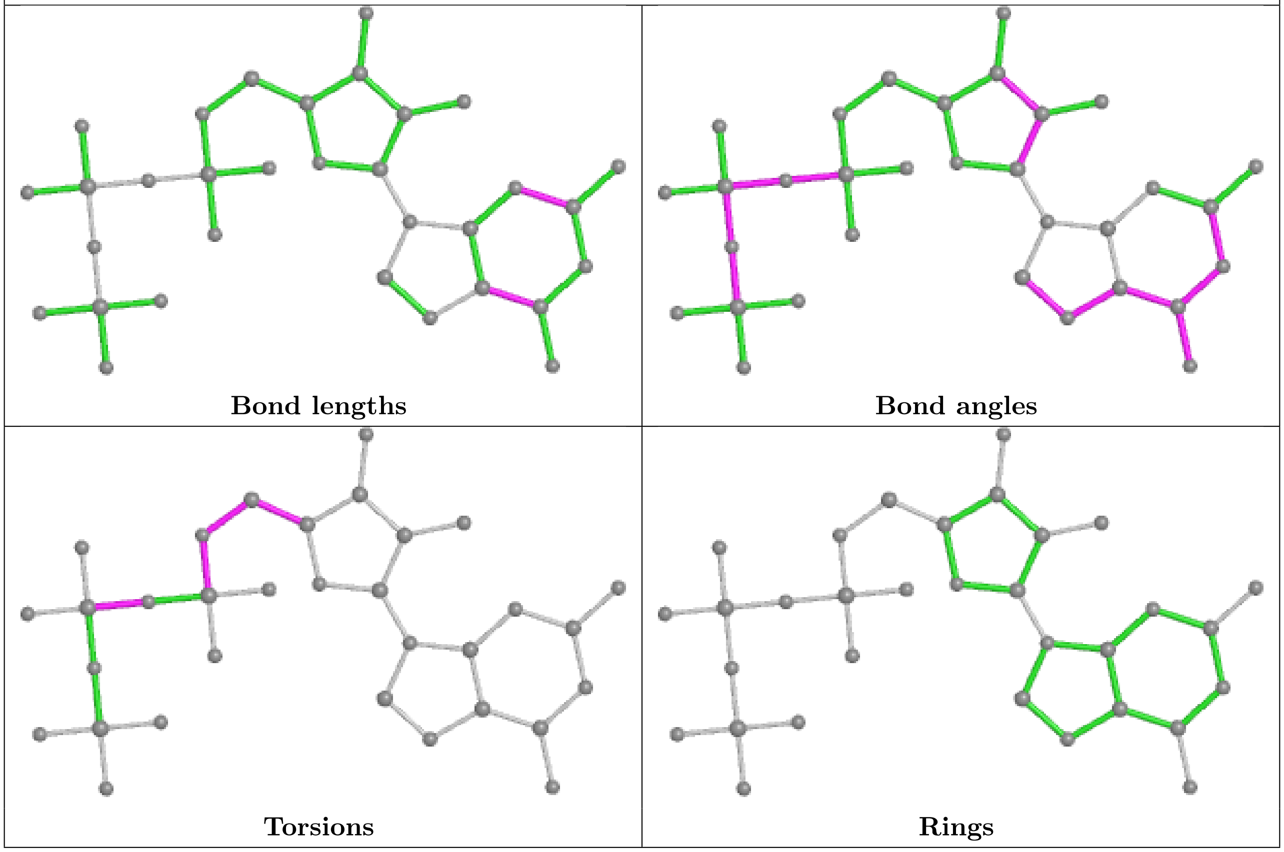
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP OG 501



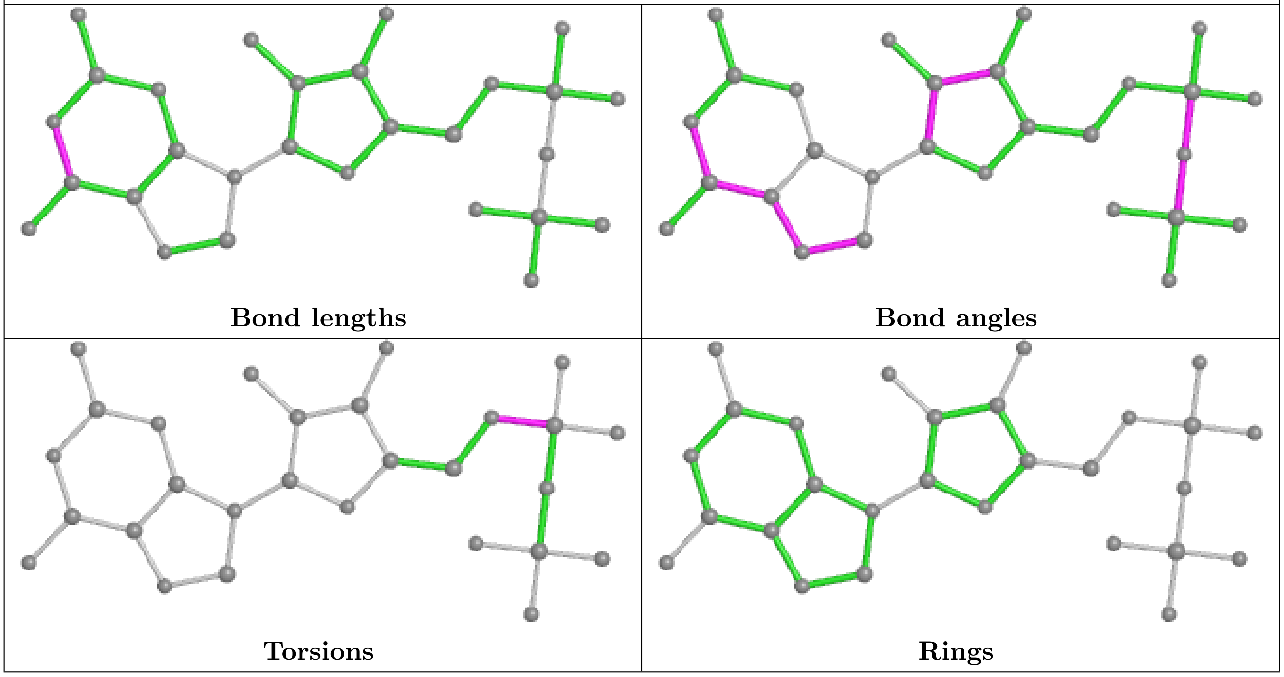
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP OL 502



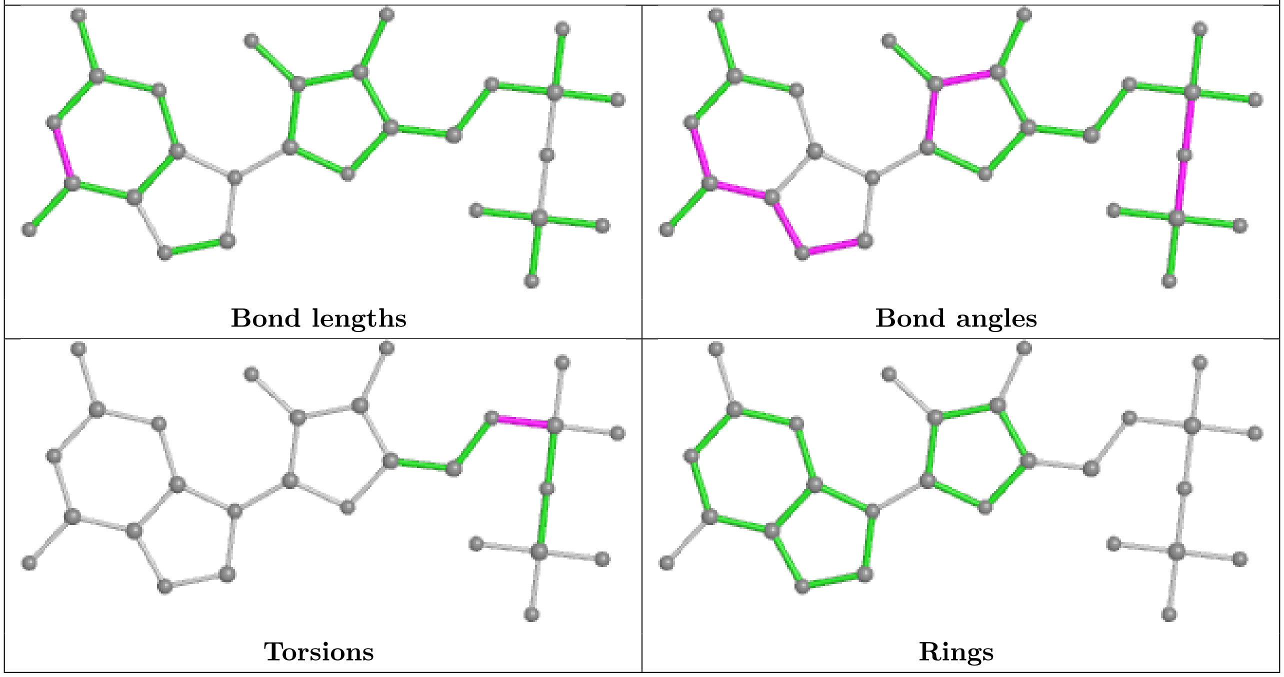
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP HD 502



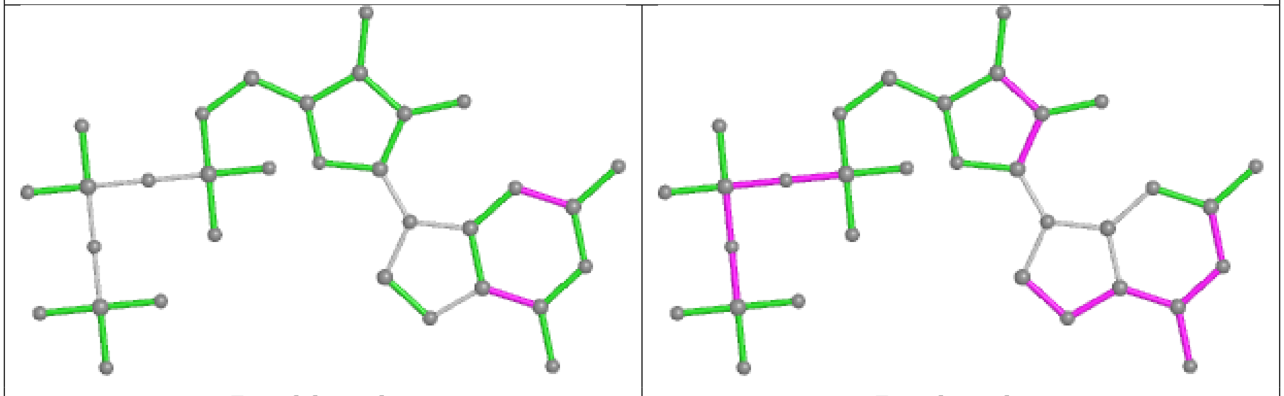
Bond lengths

Bond angles

Torsions

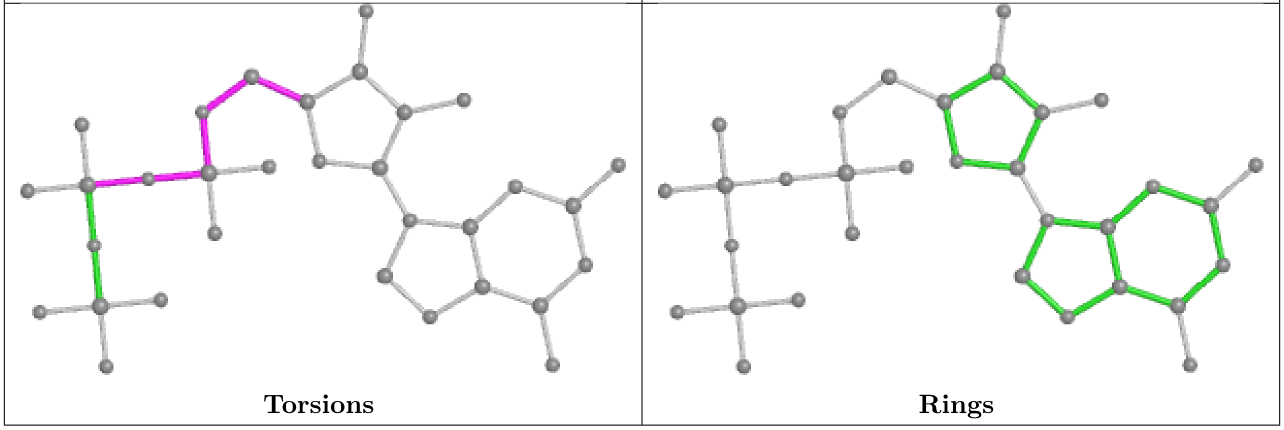
Rings

Ligand GTP NG 501



Bond lengths

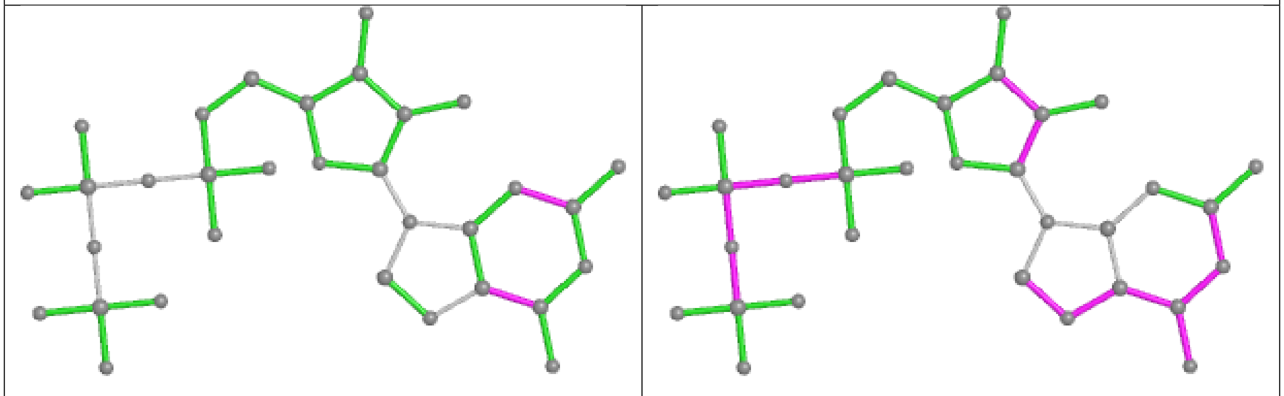
Bond angles



Torsions

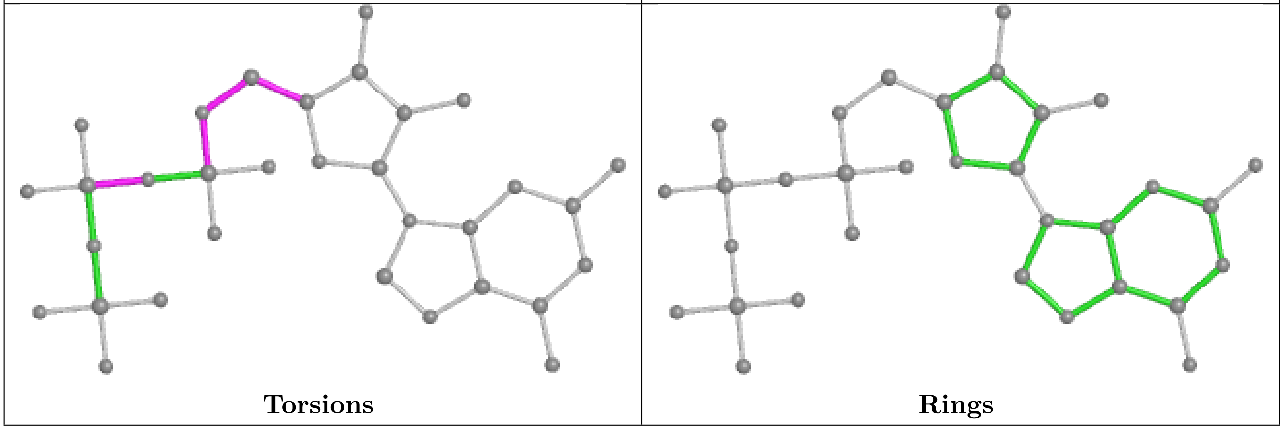
Rings

Ligand GTP SK 501



Bond lengths

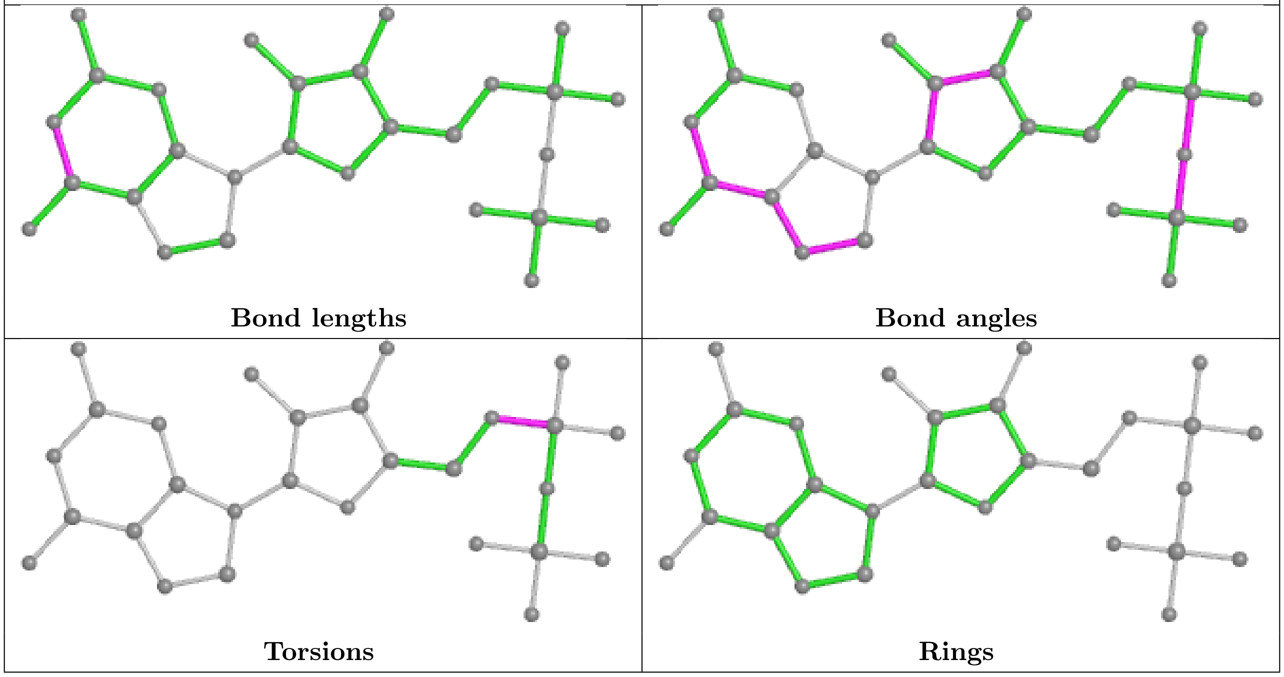
Bond angles



Torsions

Rings

Ligand GDP JD 502



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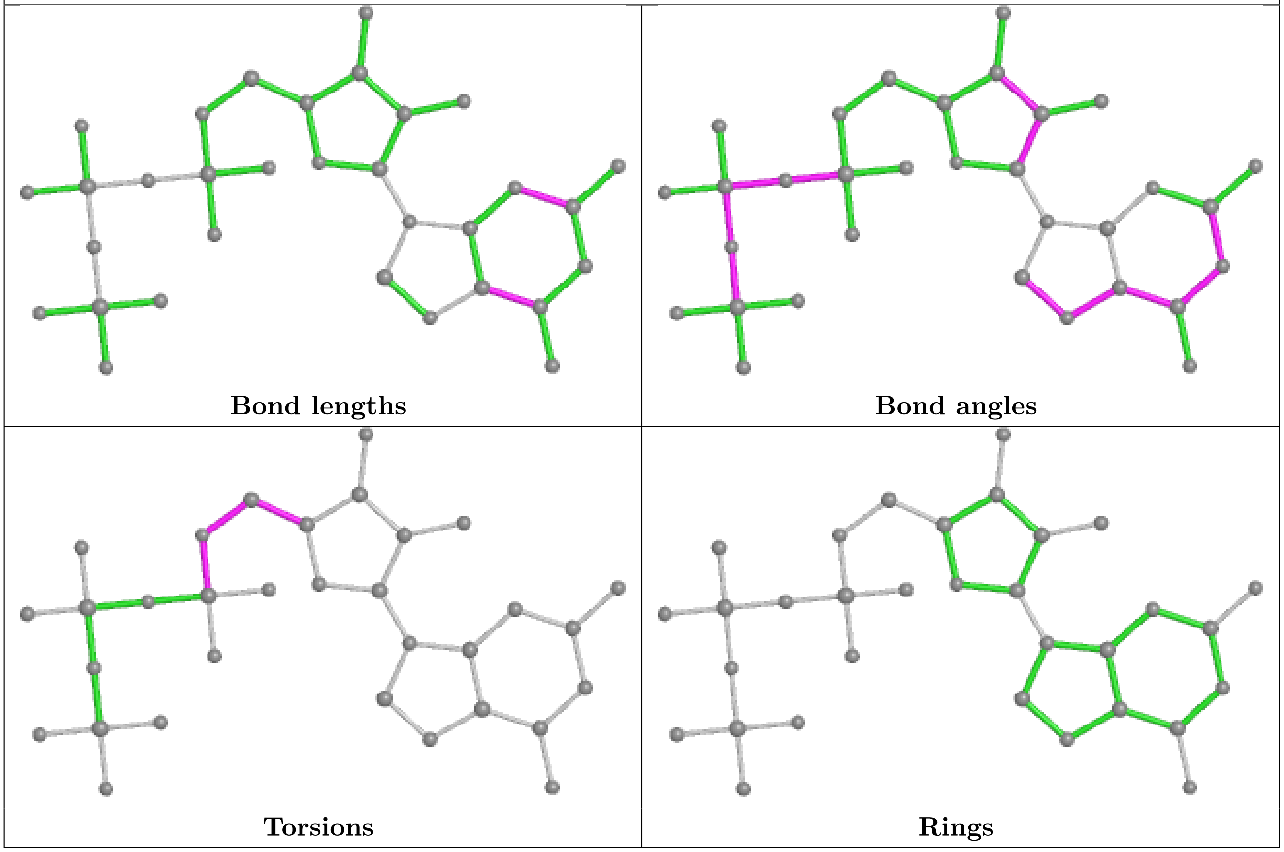

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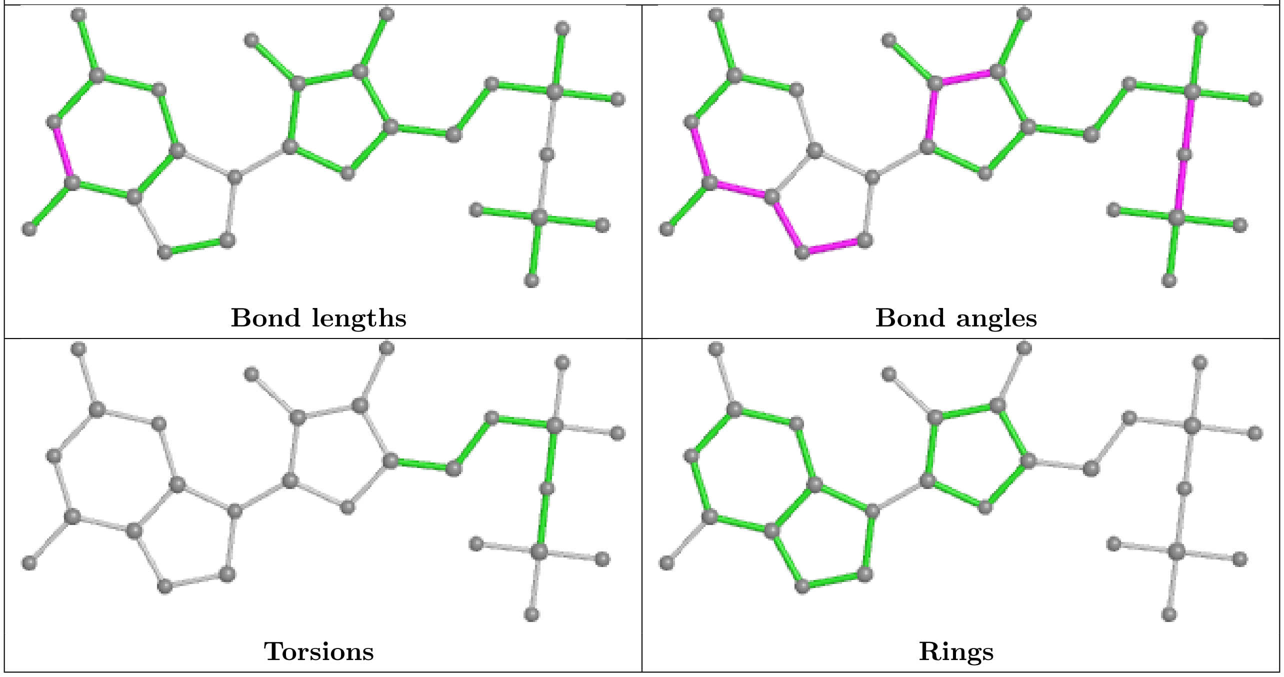


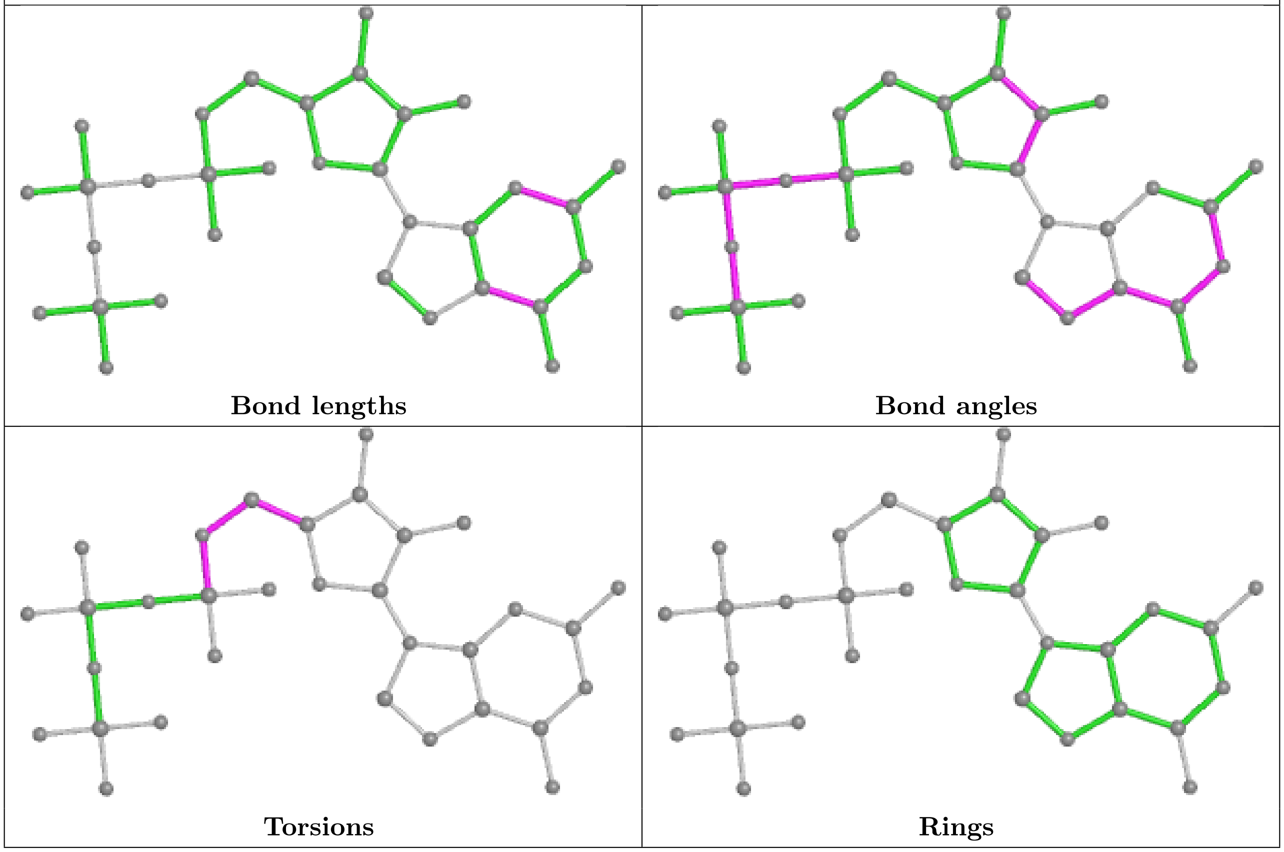
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP JG 501



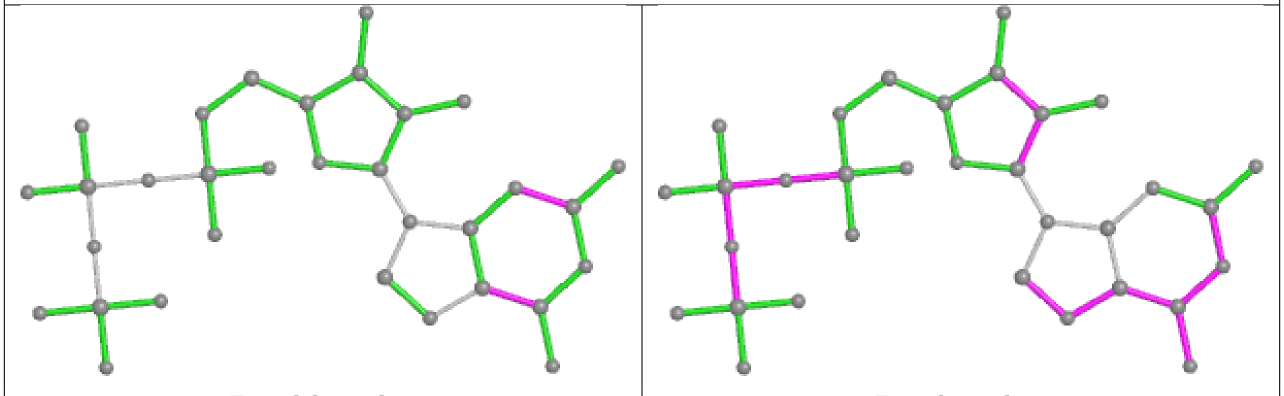
Bond lengths

Bond angles

Torsions

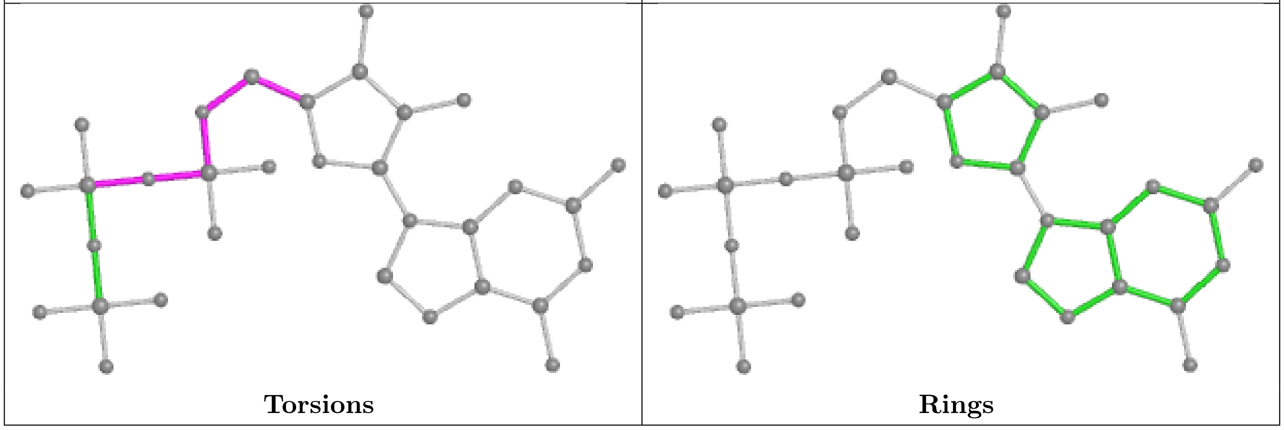
Rings

Ligand GTP UI 501



Bond lengths

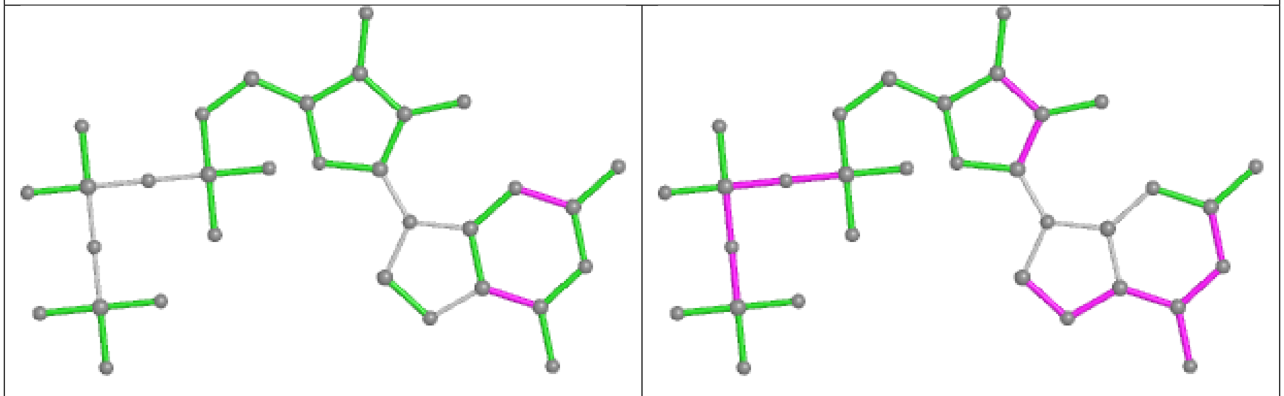
Bond angles



Torsions

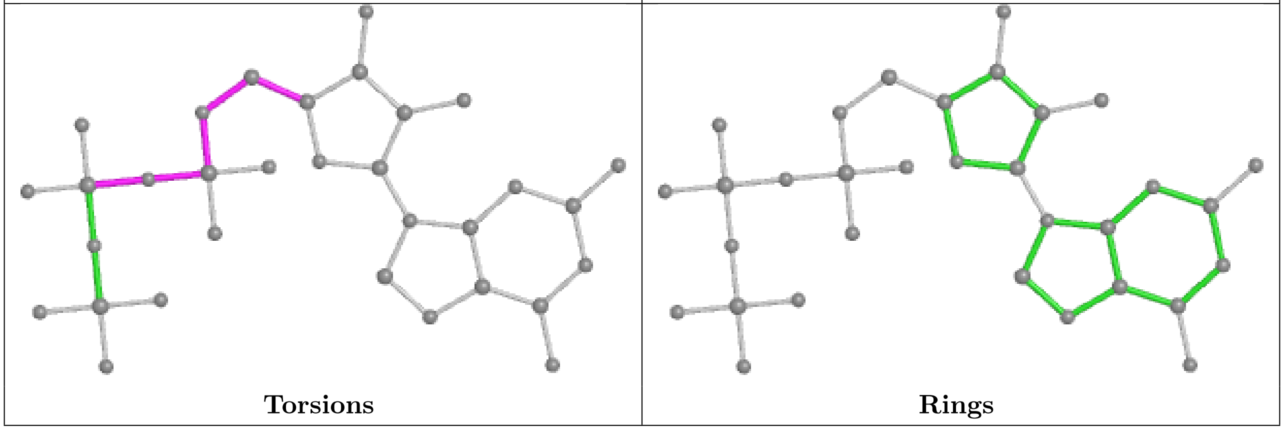
Rings

Ligand GTP AE 501



Bond lengths

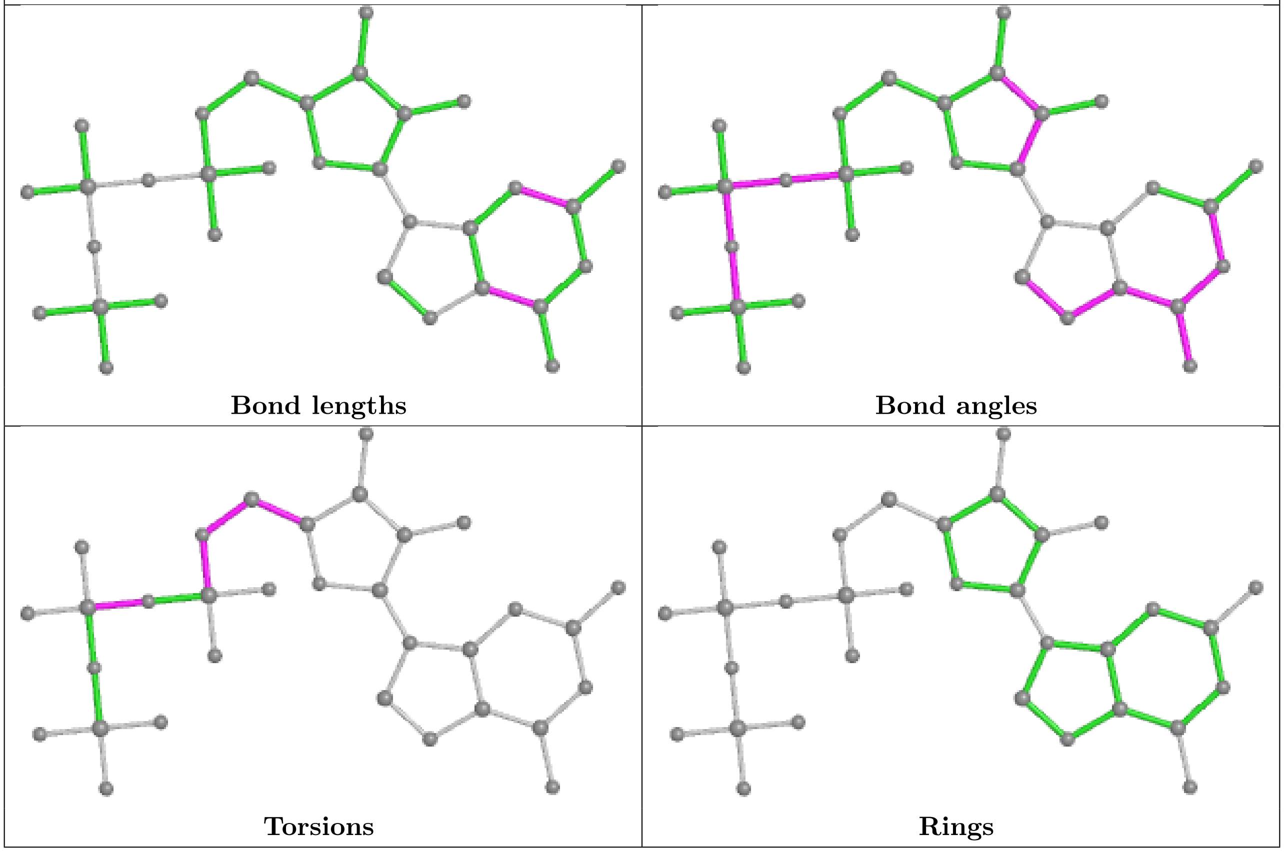
Bond angles



Torsions

Rings

Ligand GTP WM 501



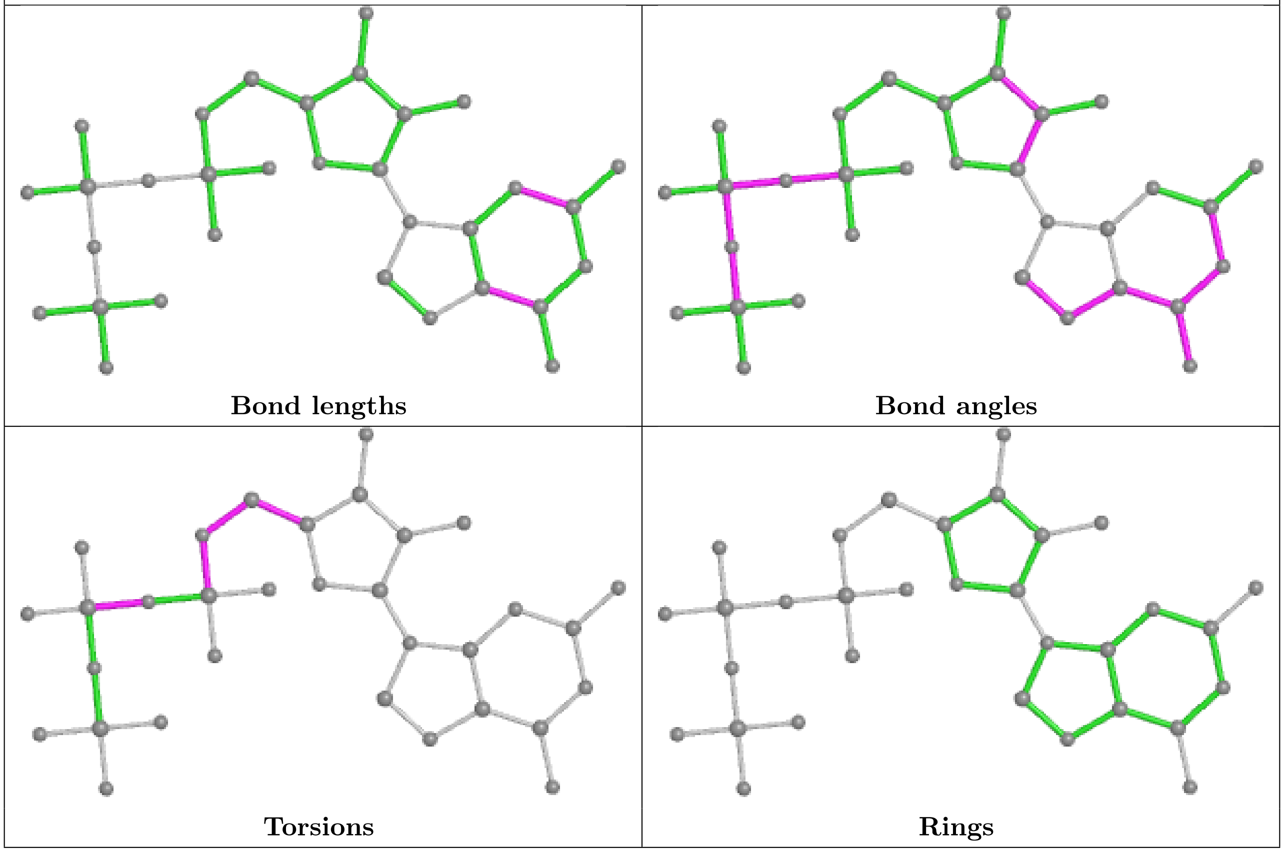
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP EG 501



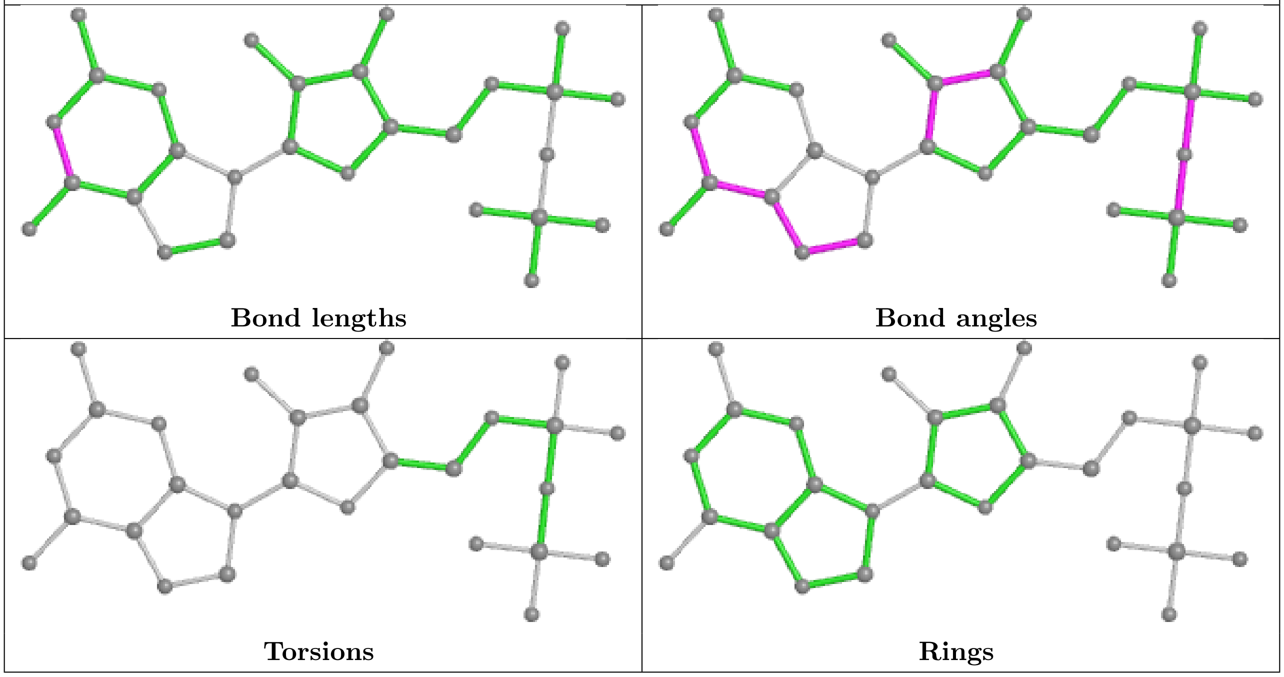
Bond lengths

Bond angles

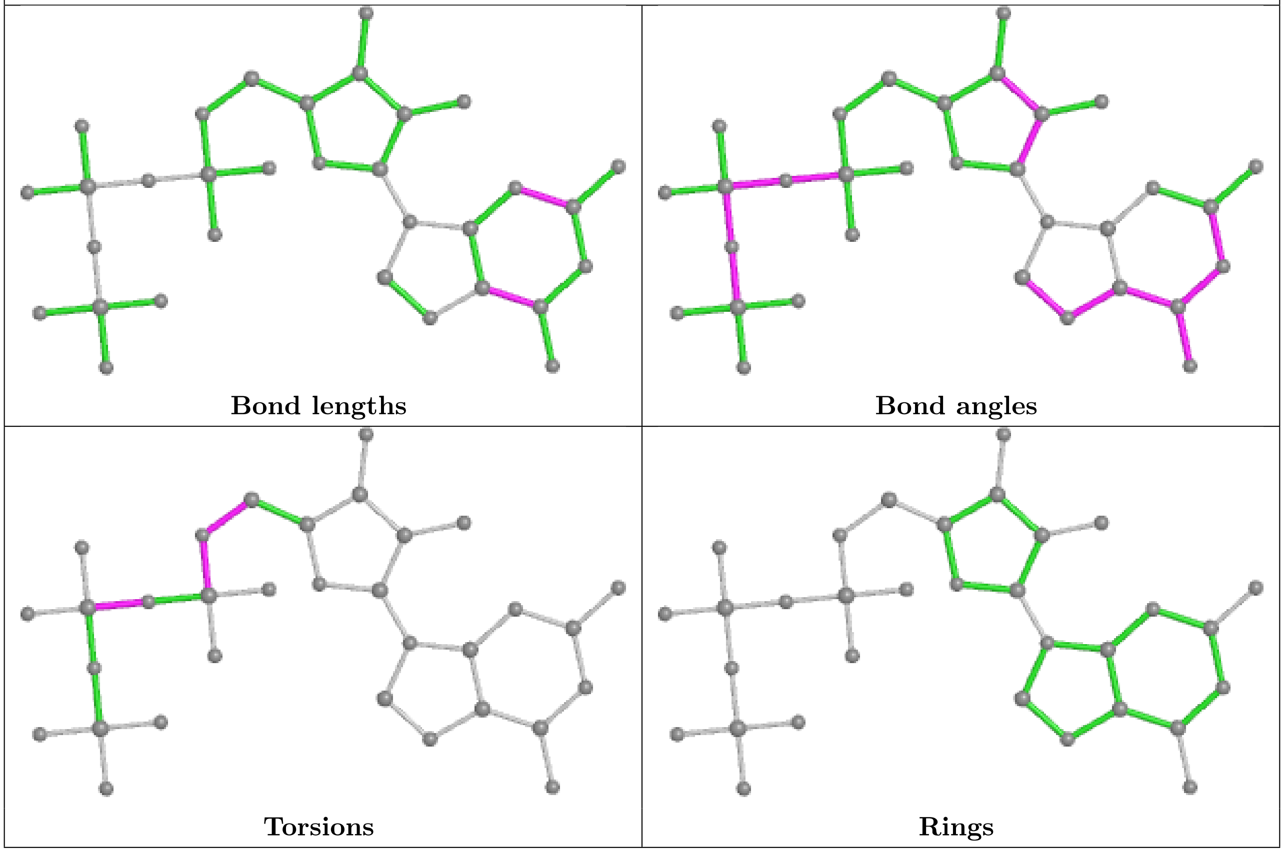
Torsions

Rings

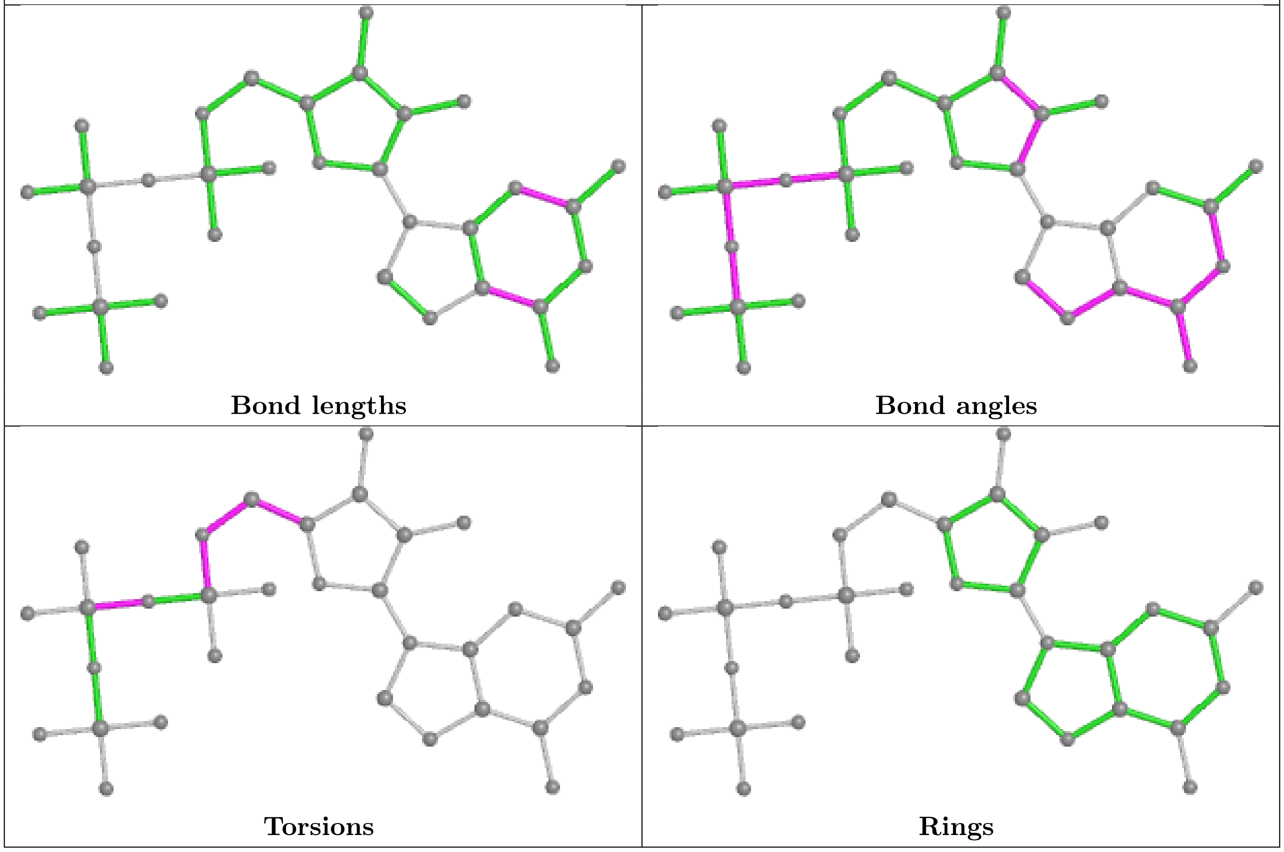
Ligand GDP IH 502



Ligand GTP WI 501



Ligand GTP VA 501



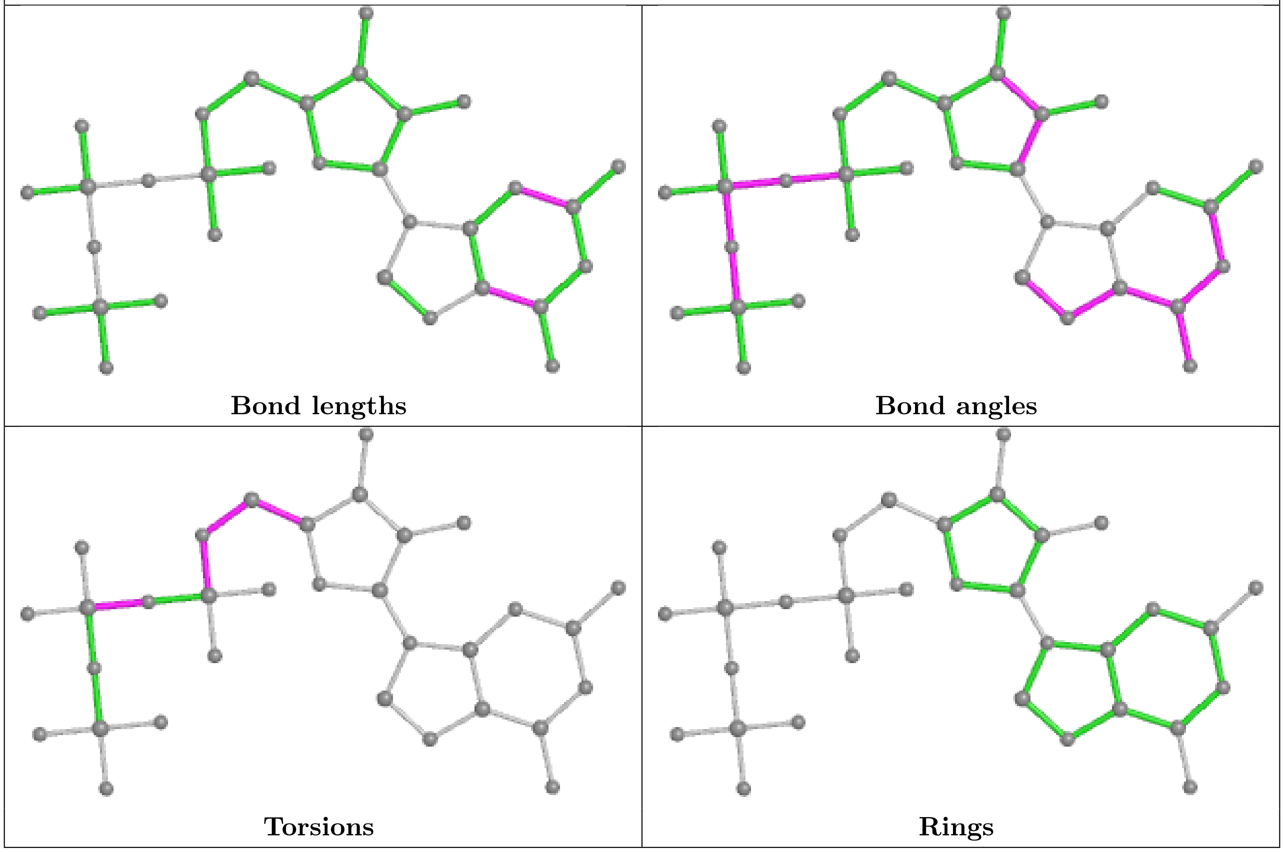
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP SA 501



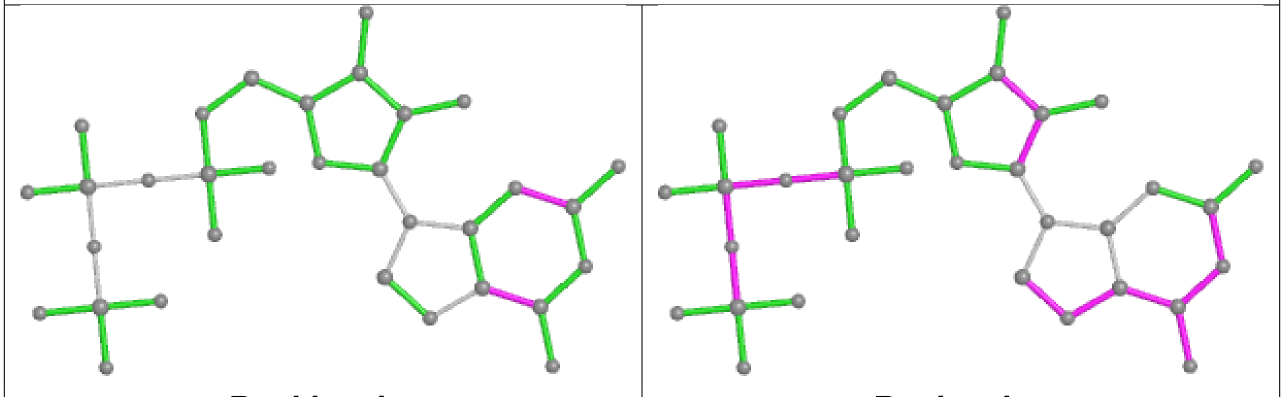
Bond lengths

Bond angles

Torsions

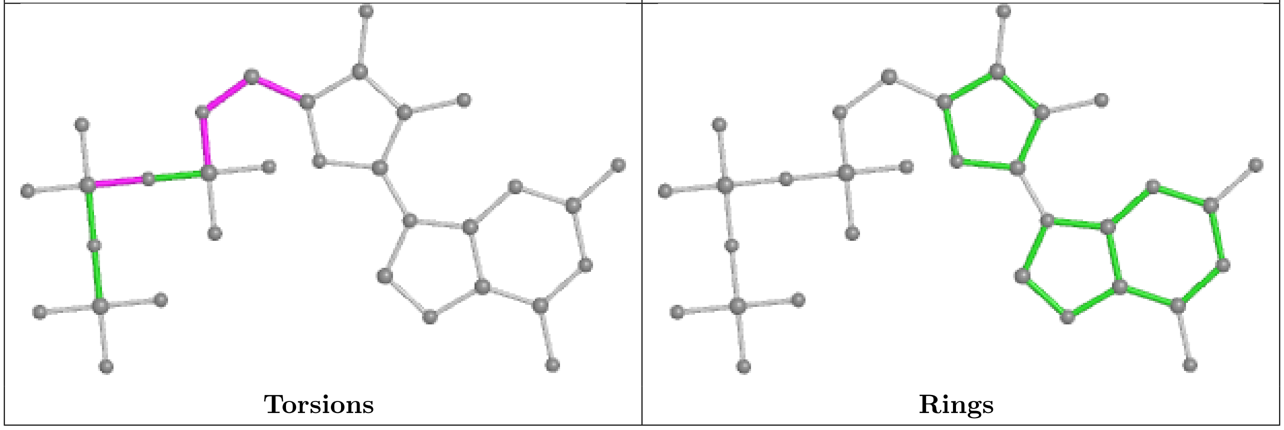
Rings

Ligand GTP BO 501



Bond lengths

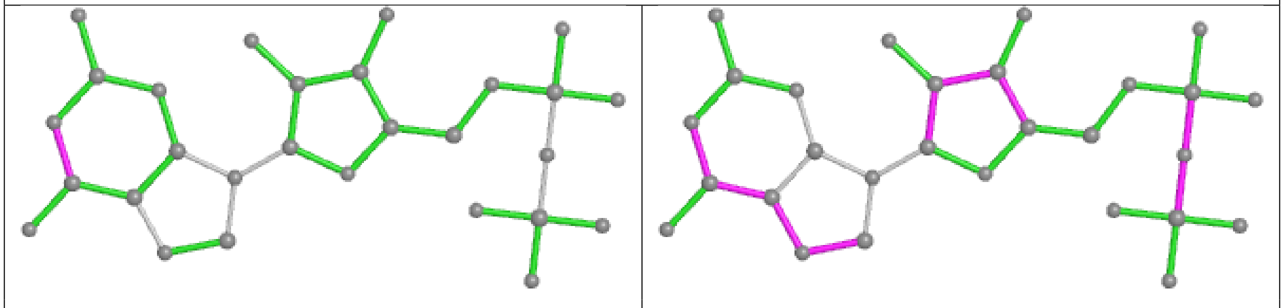
Bond angles



Torsions

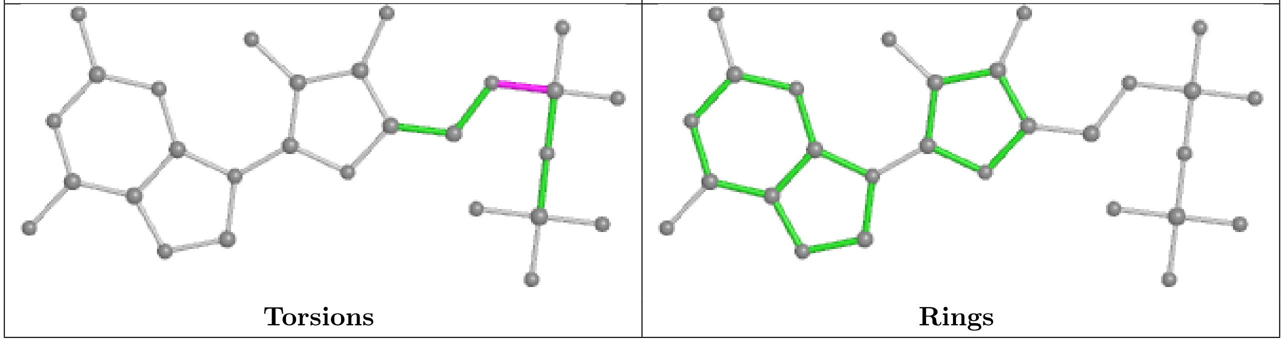
Rings

Ligand GDP DL 502



Bond lengths

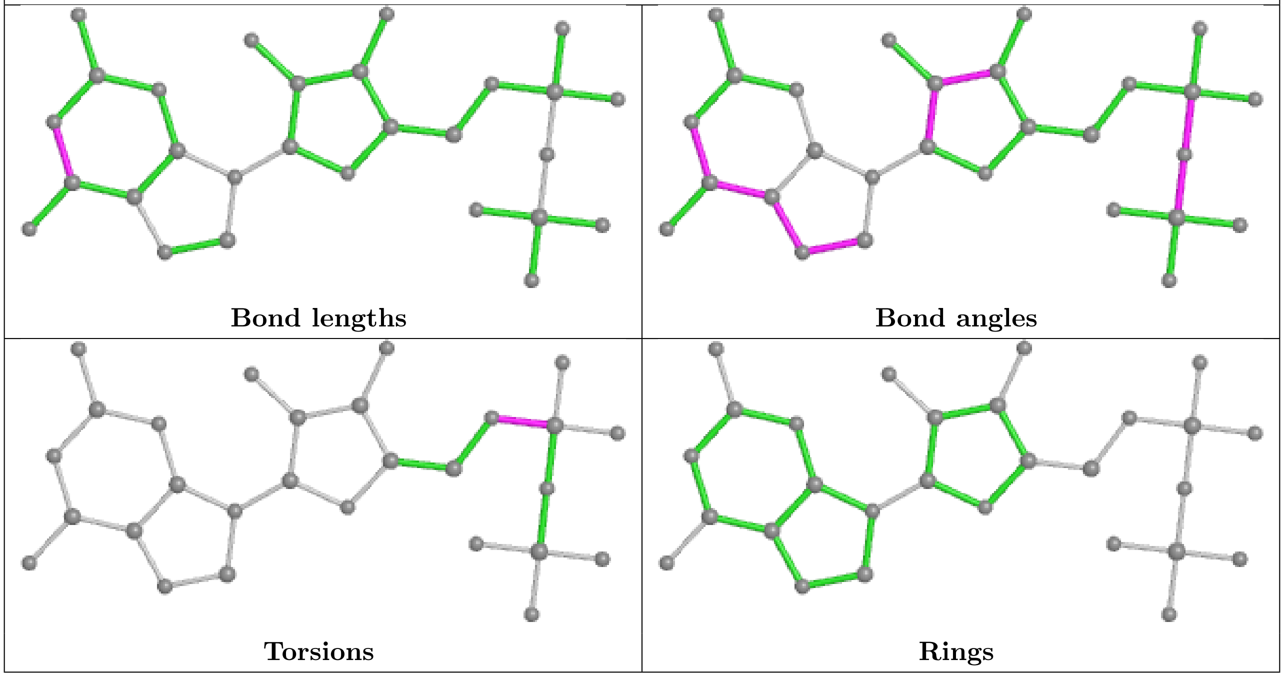
Bond angles



Torsions

Rings

Ligand GDP NL 502



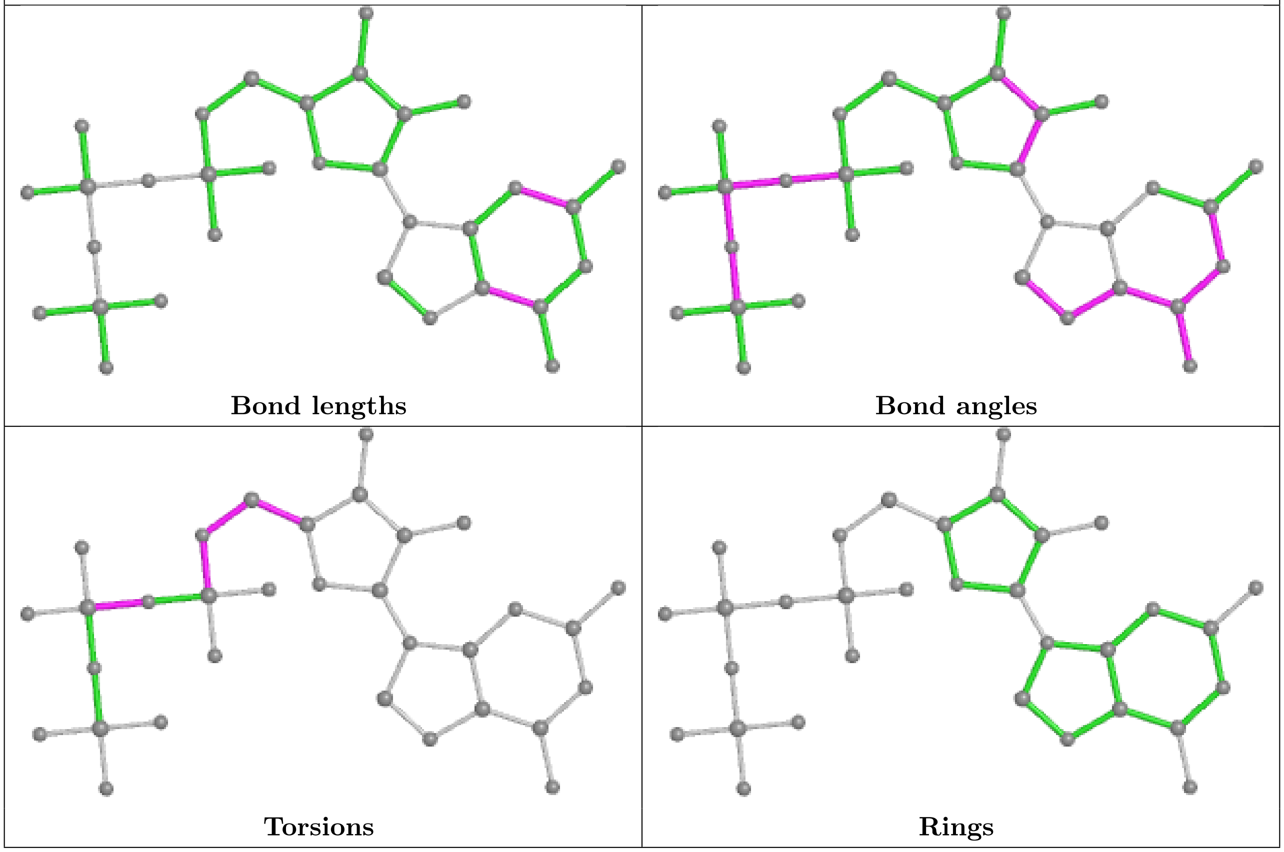
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP OC 501



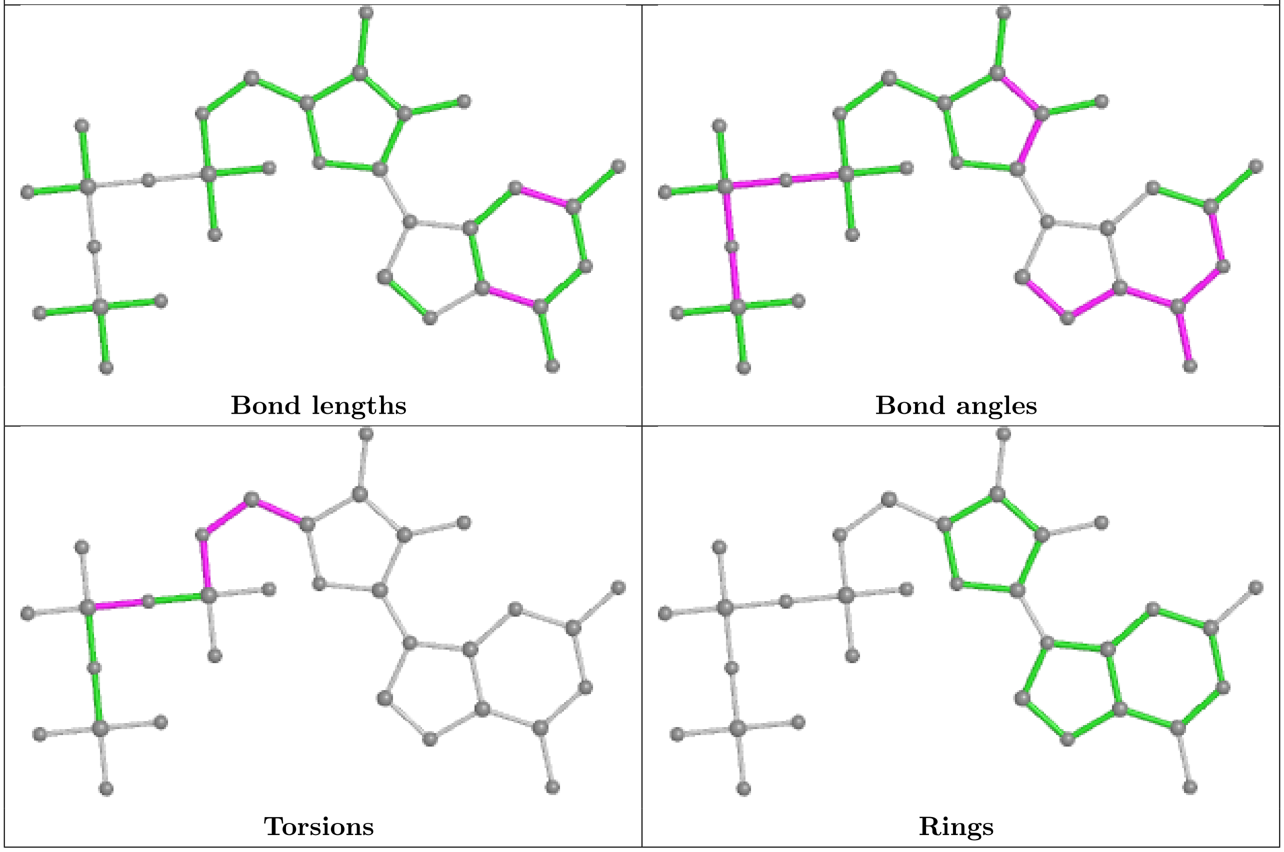
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP OM 501



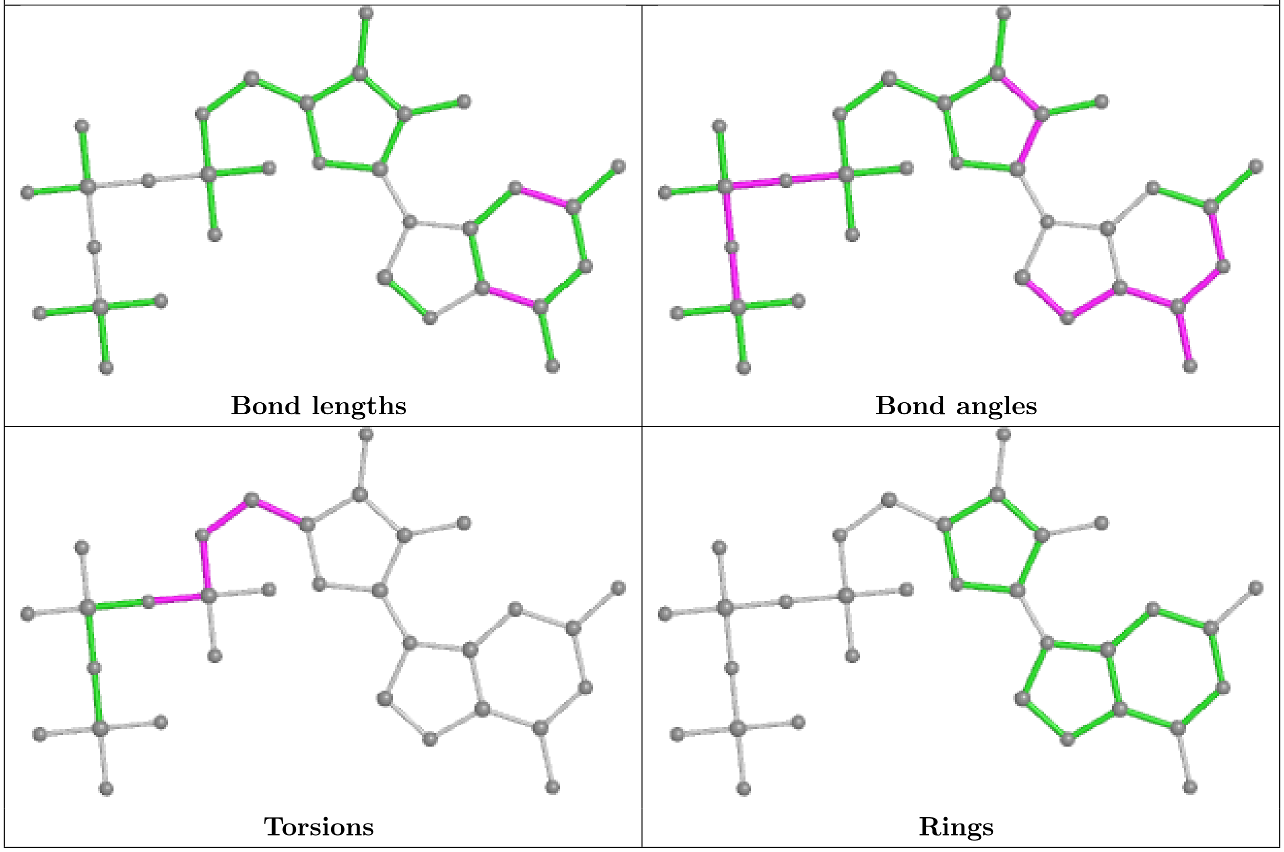
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP CG 501



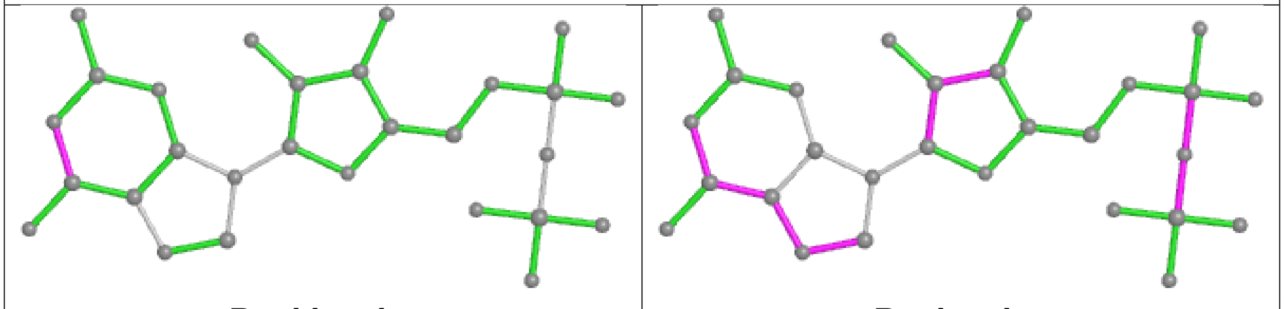
Bond lengths

Bond angles

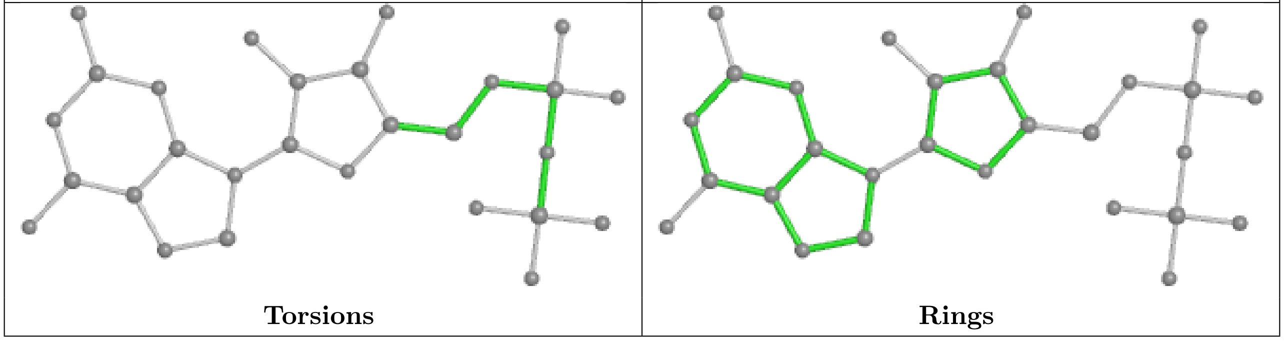
Torsions

Rings

Ligand GDP HH 502

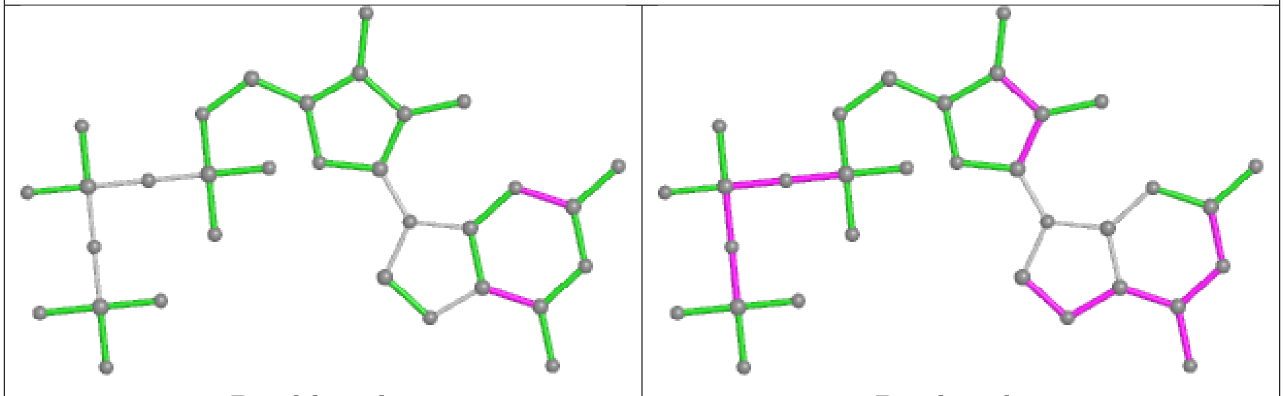


Bond lengths **Bond angles**



Torsions **Rings**

Ligand GTP DG 501



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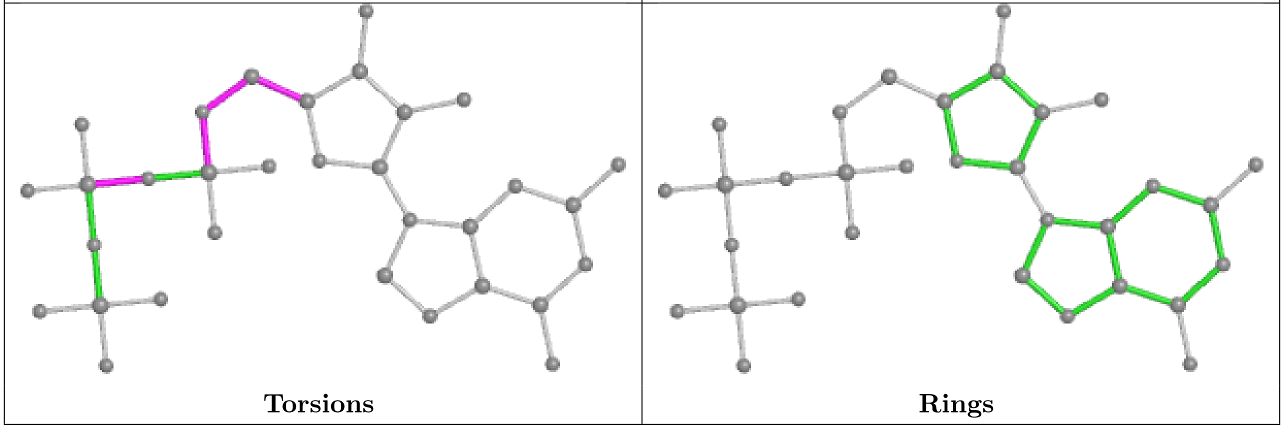

Torsions **Rings**

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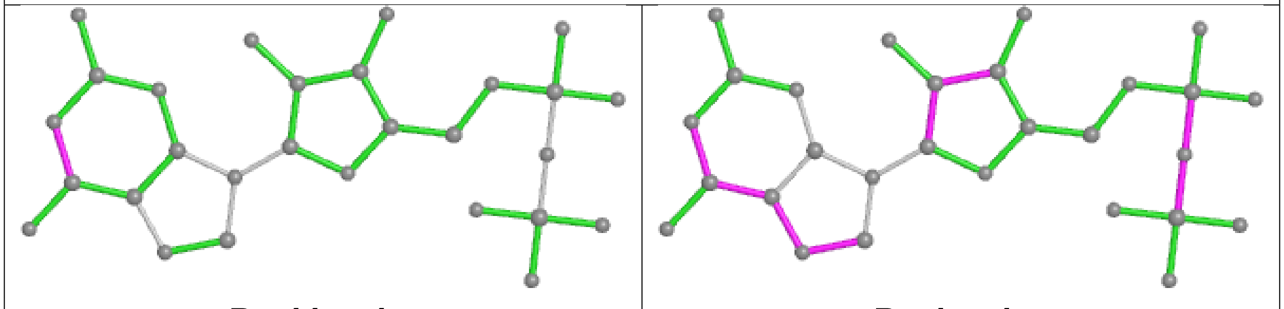
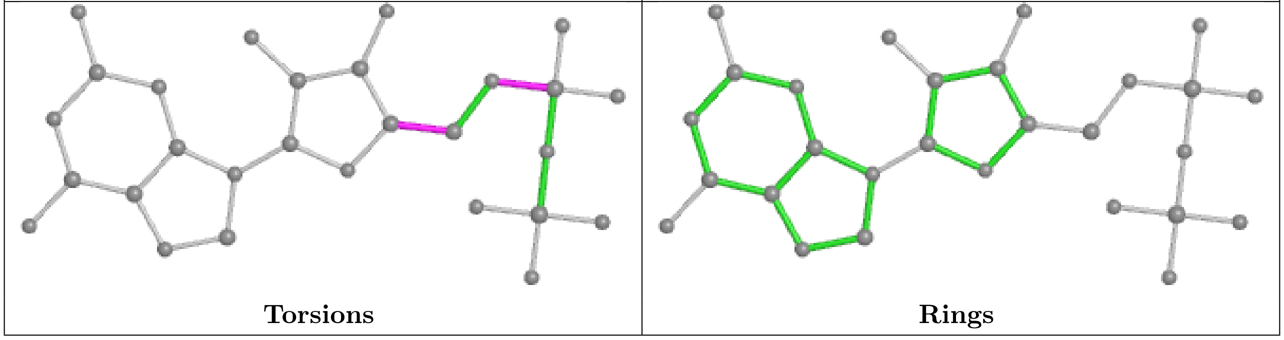


Bond lengths

Bond angles



Torsions

Rings

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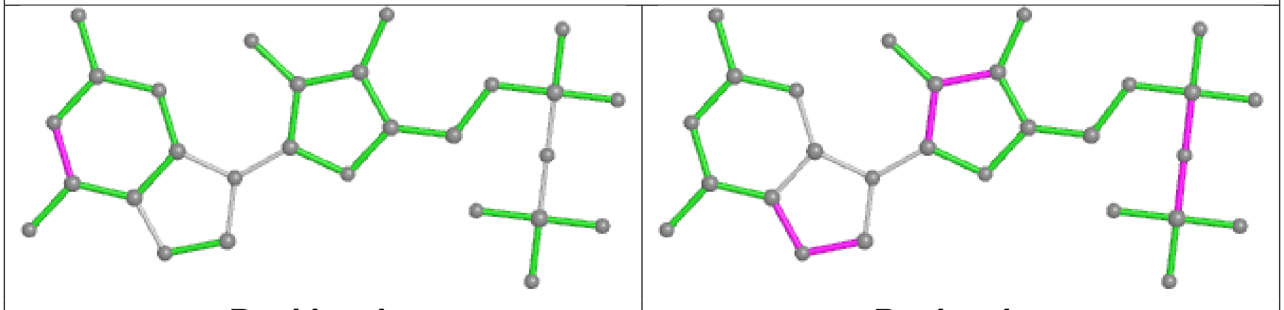
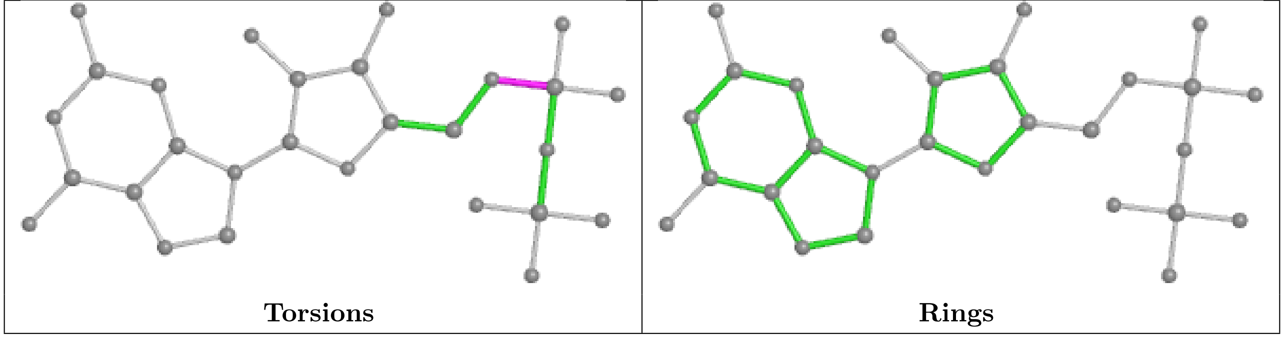


Bond lengths

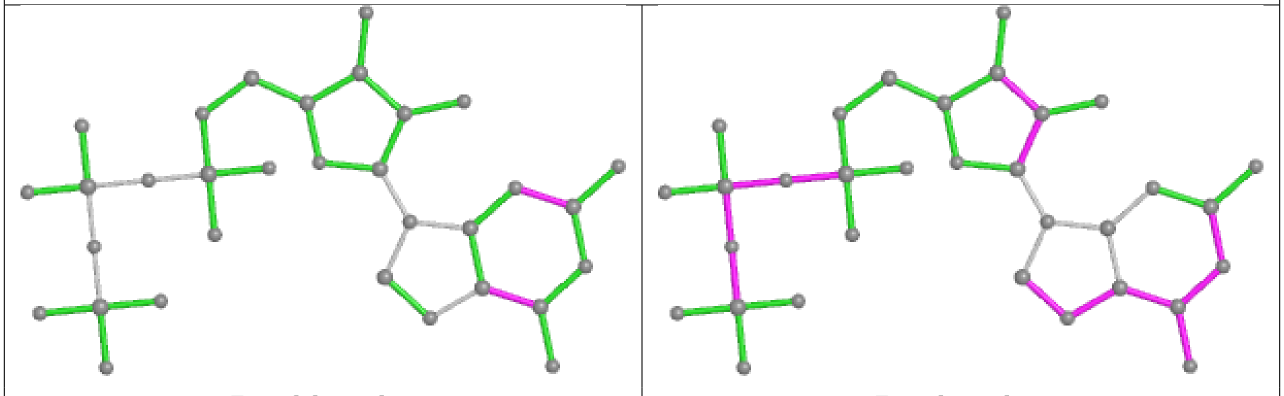
Bond angles



Torsions

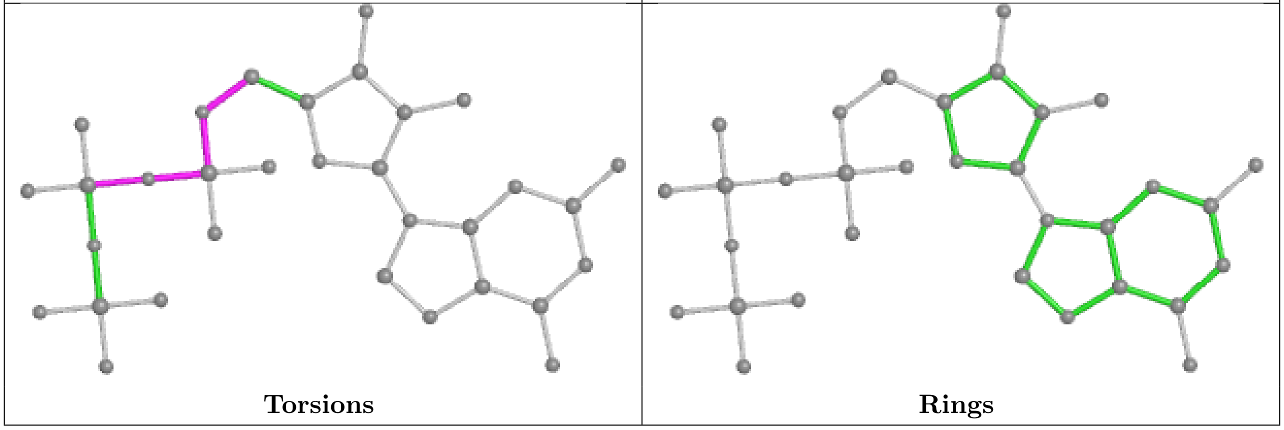
Rings

Ligand GTP AG 501



Bond lengths

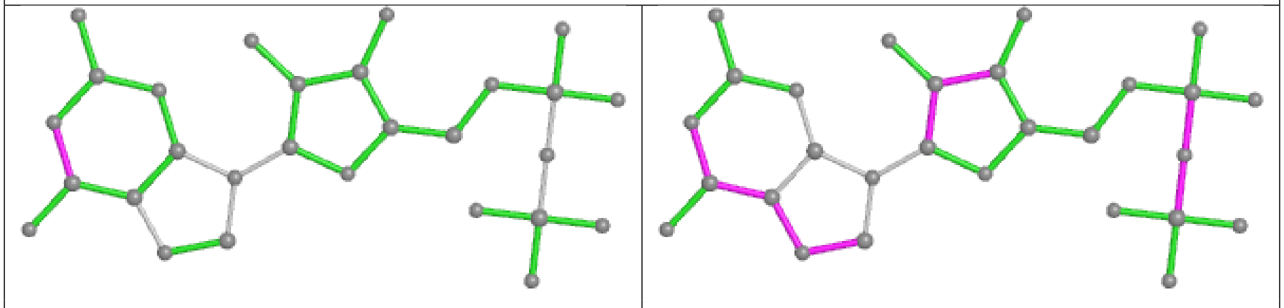
Bond angles



Torsions

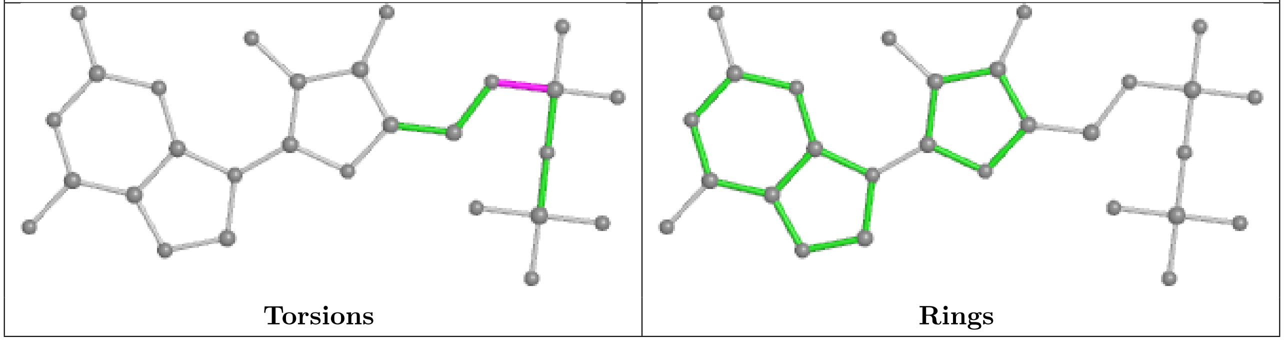
Rings

Ligand GDP VJ 502



Bond lengths

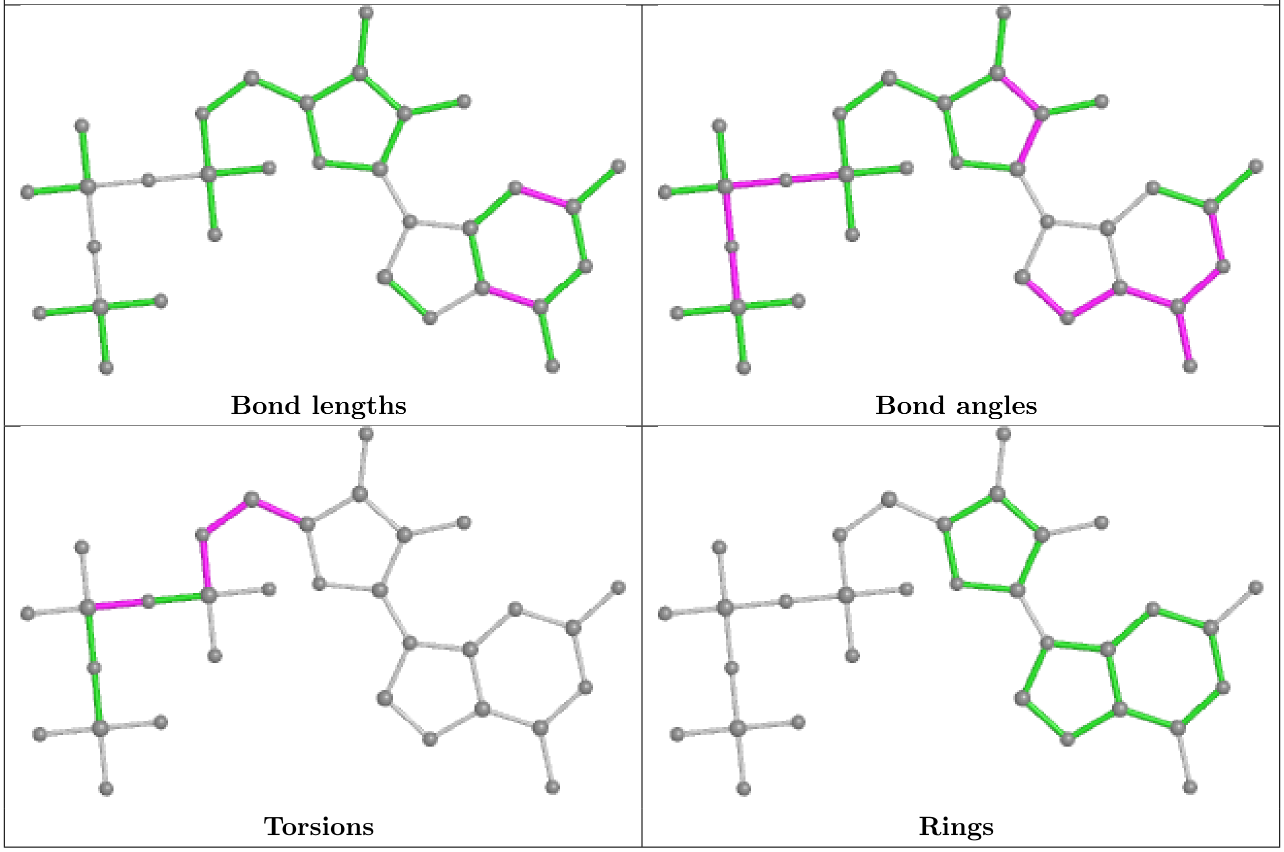
Bond angles



Torsions

Rings

Ligand GTP OK 501



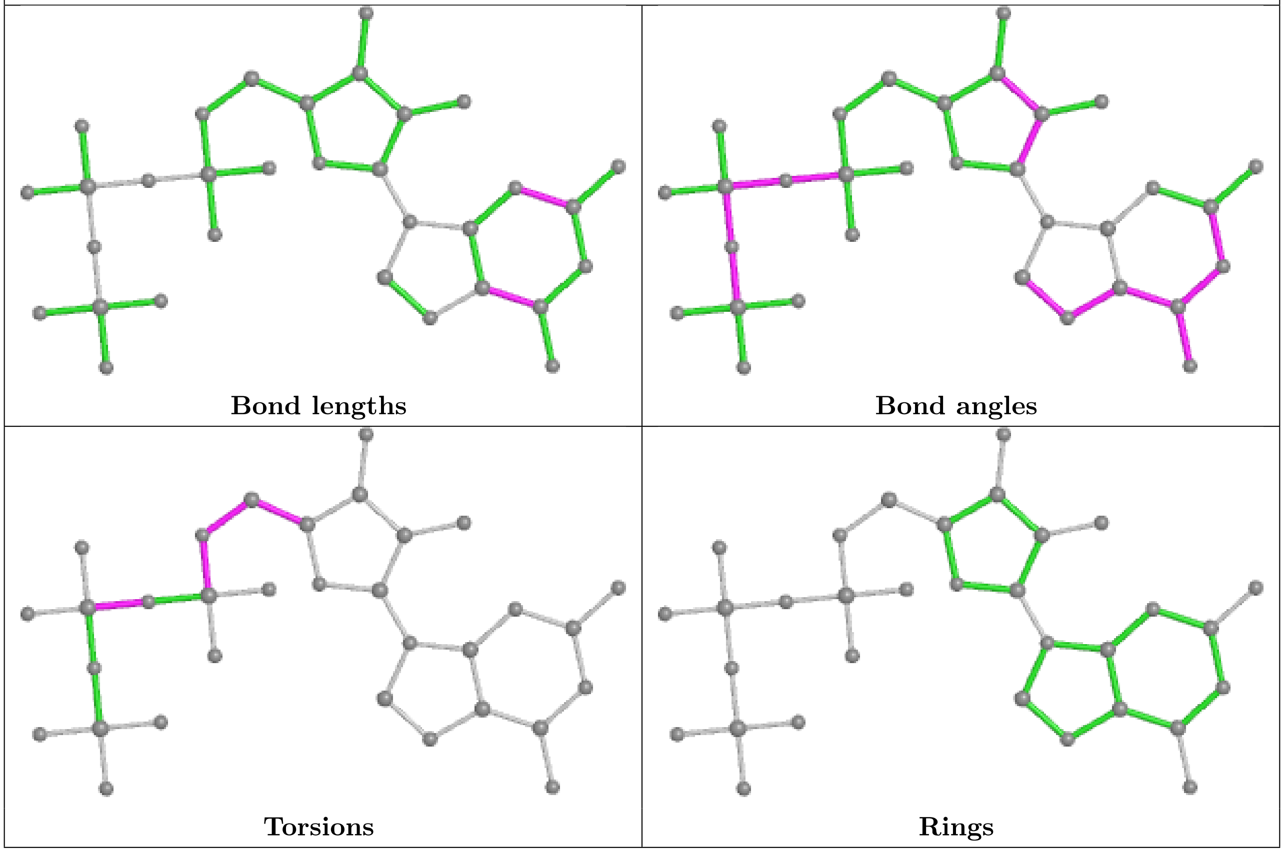
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP IC 501



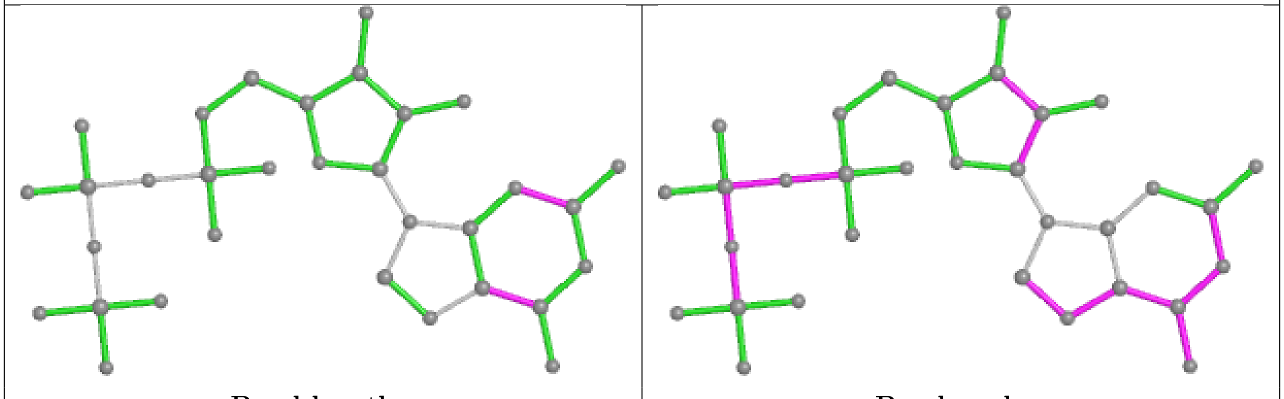
Bond lengths

Bond angles

Torsions

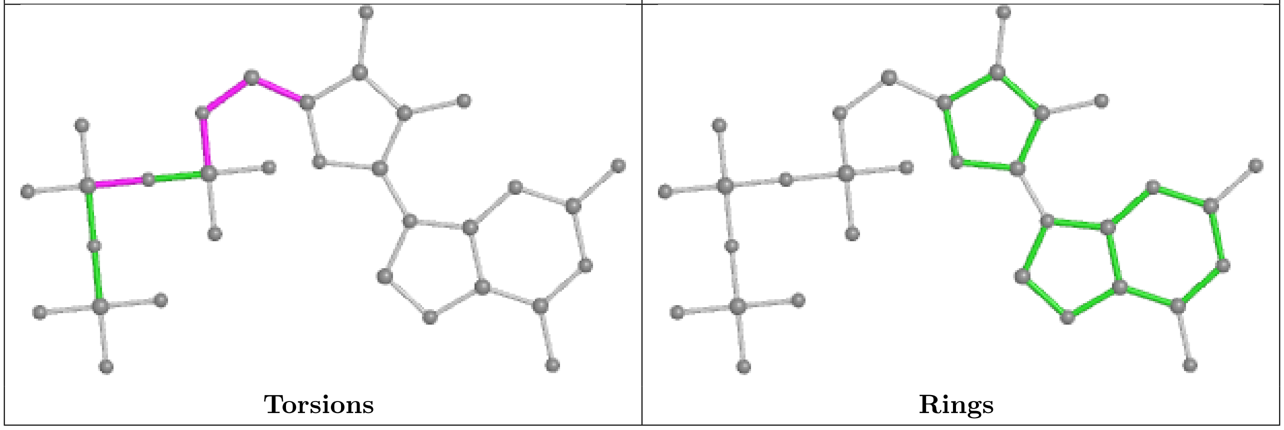
Rings

Ligand GTP LK 501



Bond lengths

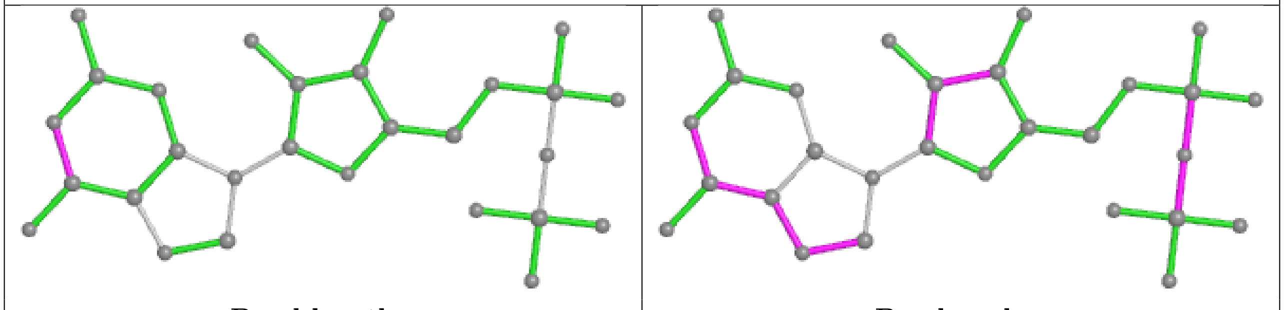
Bond angles



Torsions

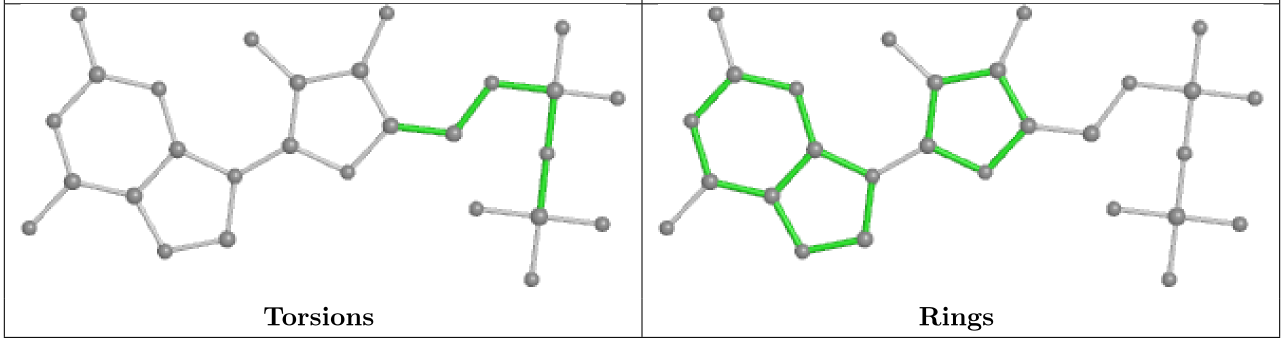
Rings

Ligand GDP RN 502



Bond lengths

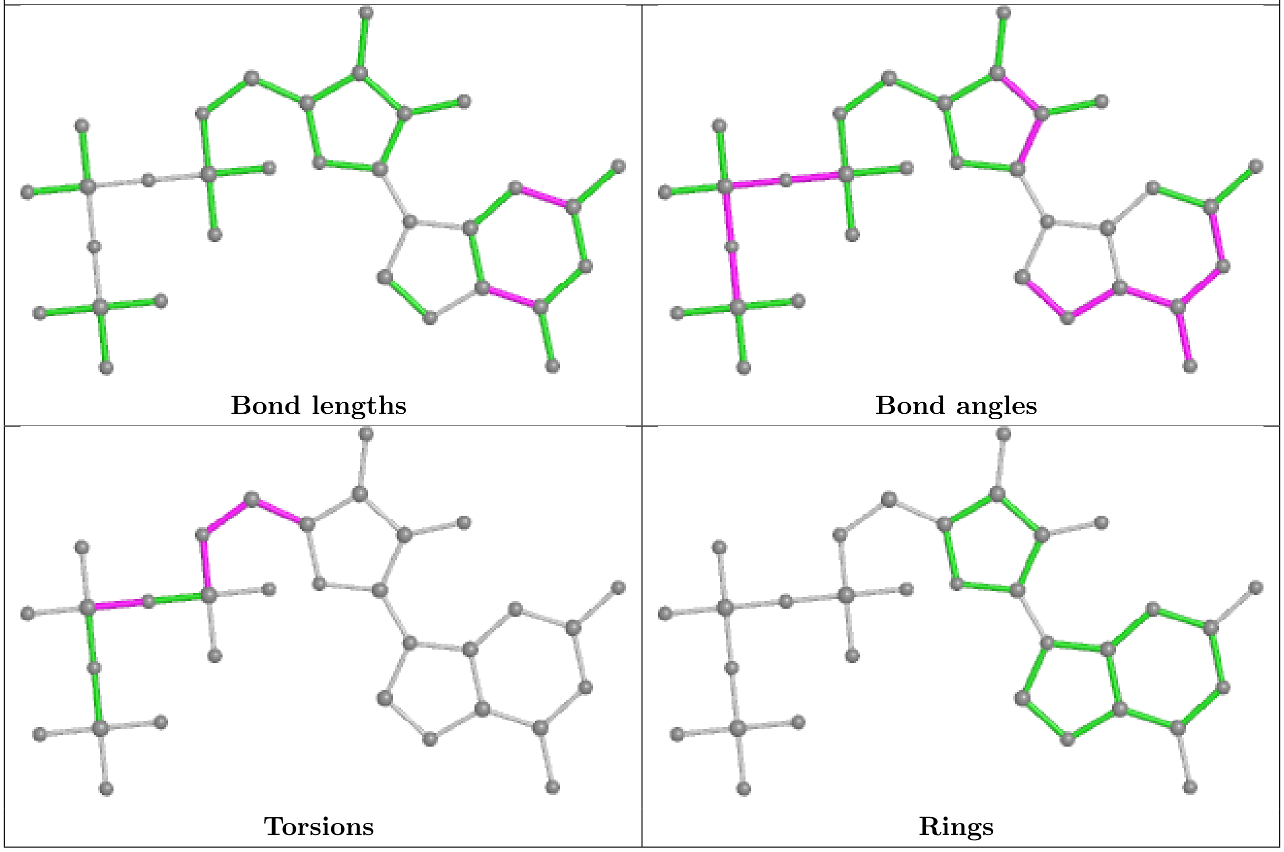
Bond angles



Torsions

Rings

Ligand GTP SE 501



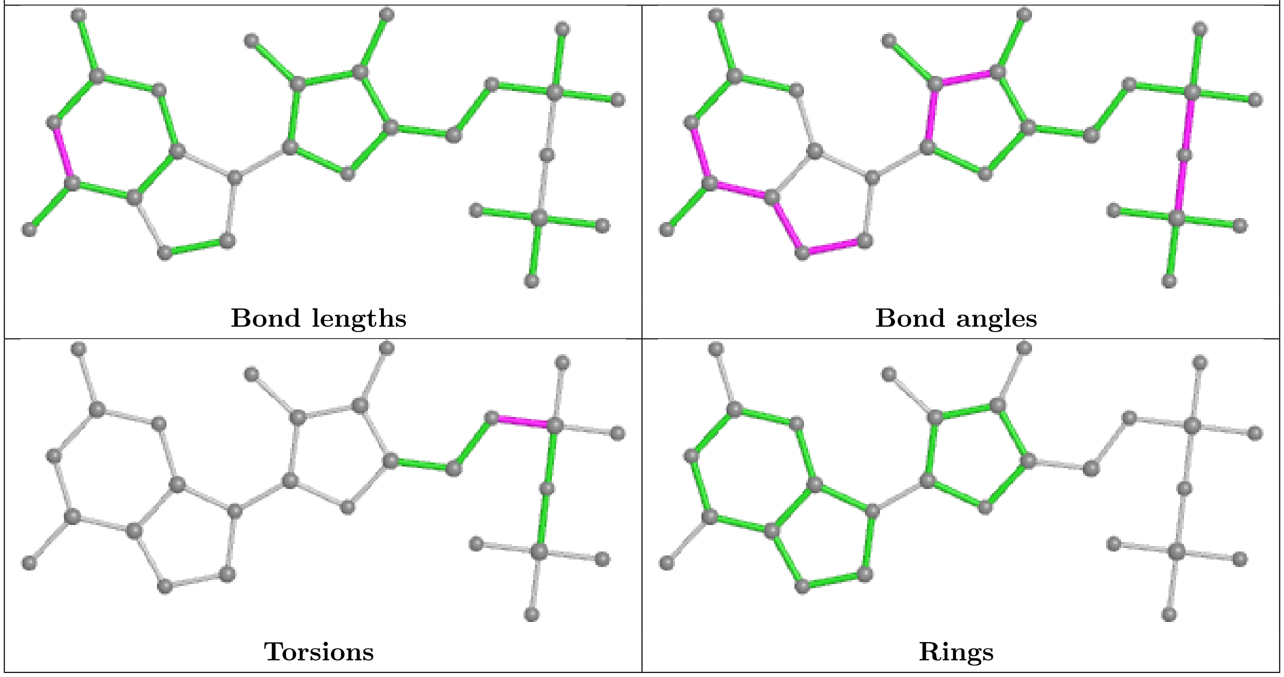
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP BL 502



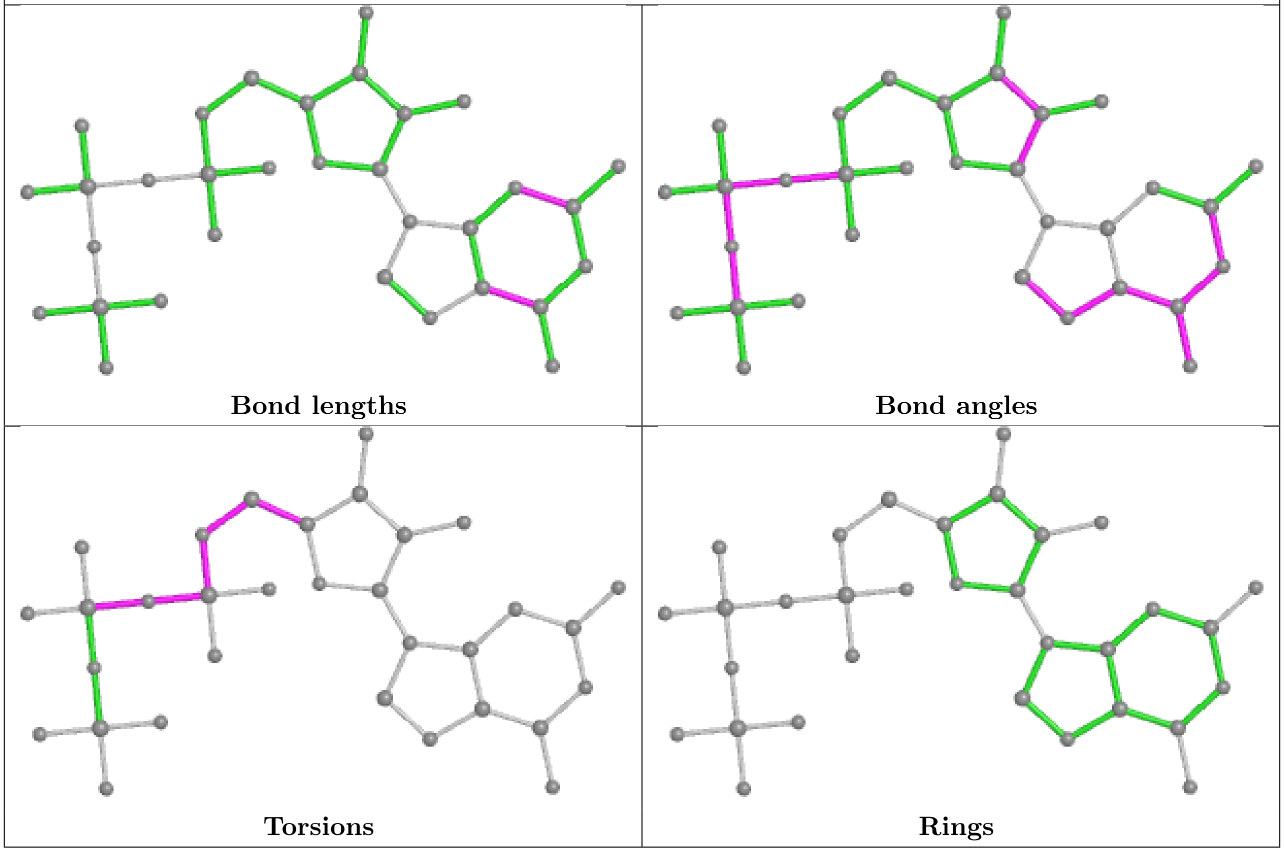
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP SI 501



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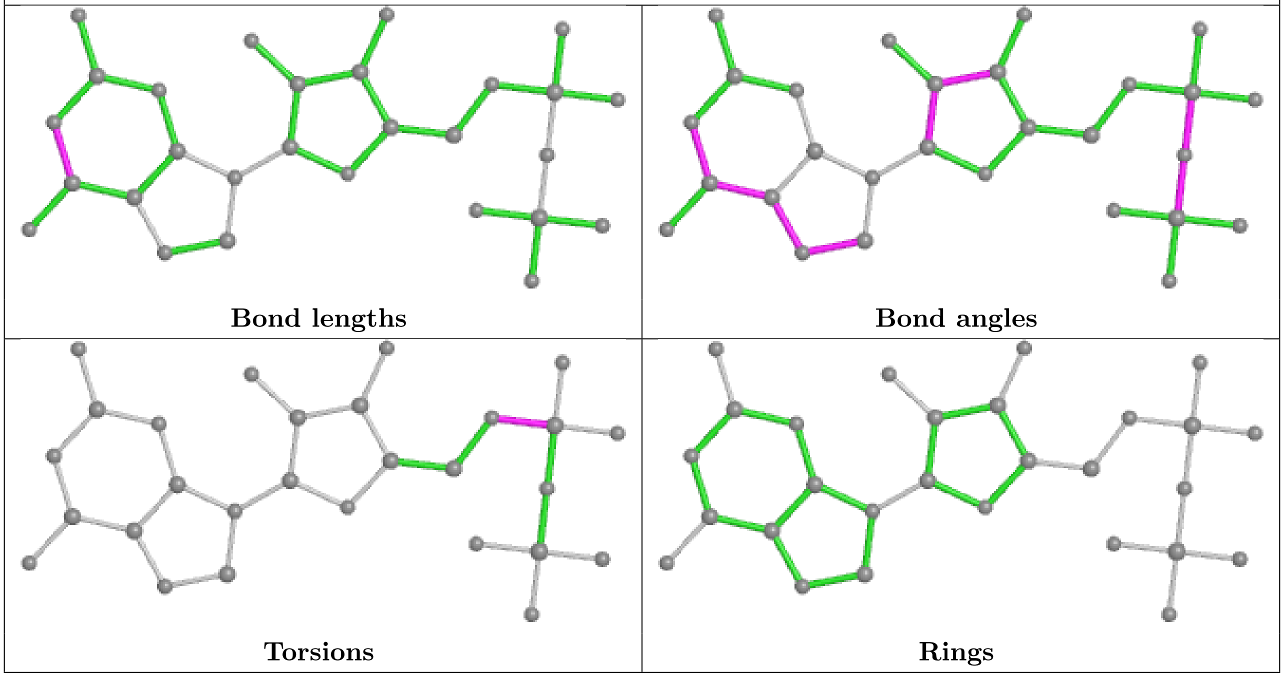
Bond angles

Torsions

Rings

Ligand GDP WF 502



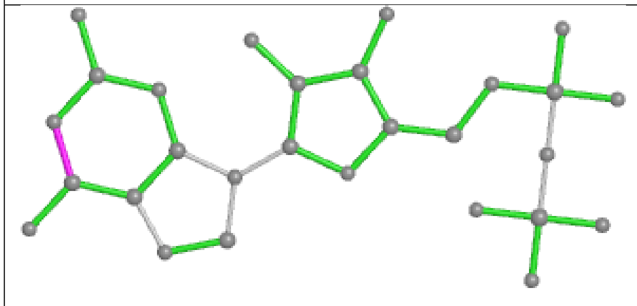
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP MF 502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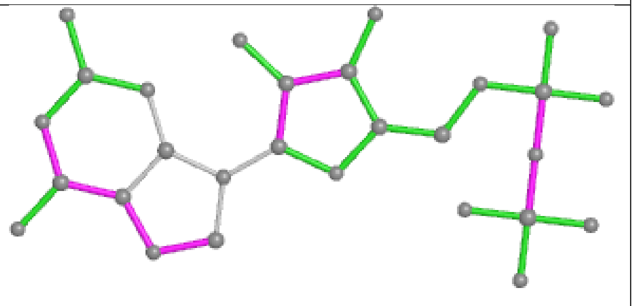
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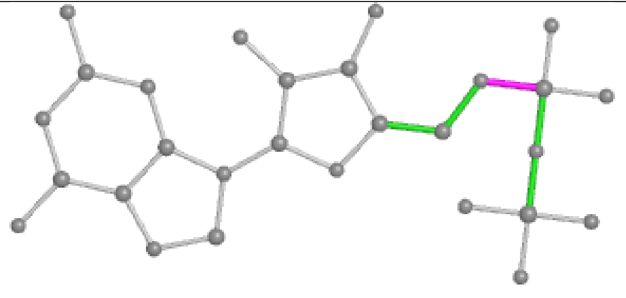
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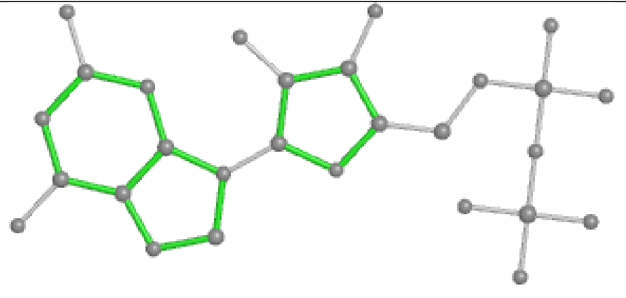
Rings

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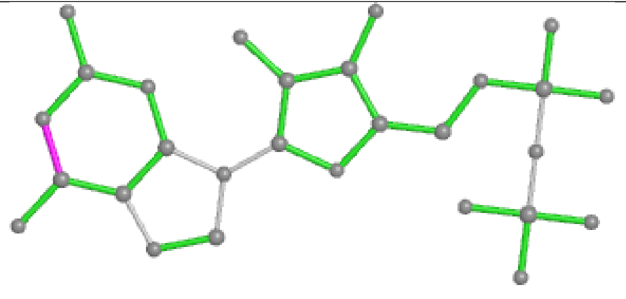
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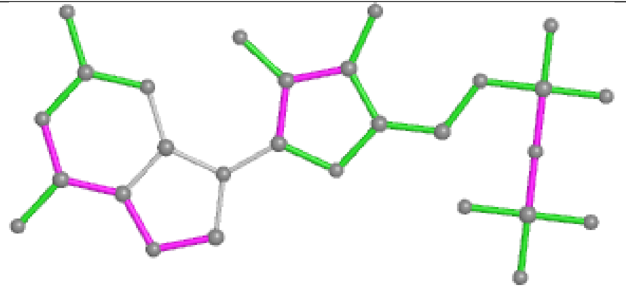
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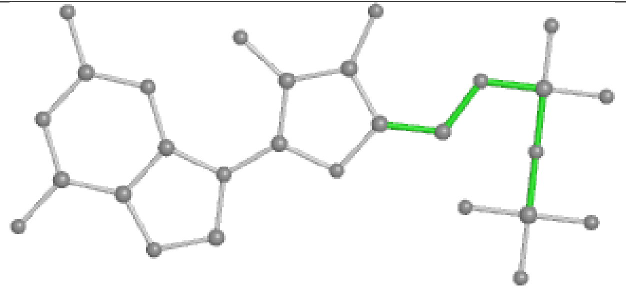
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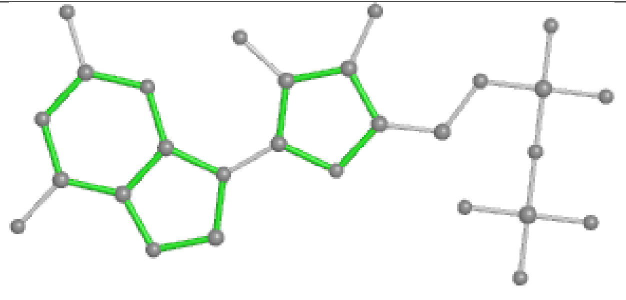
Rings

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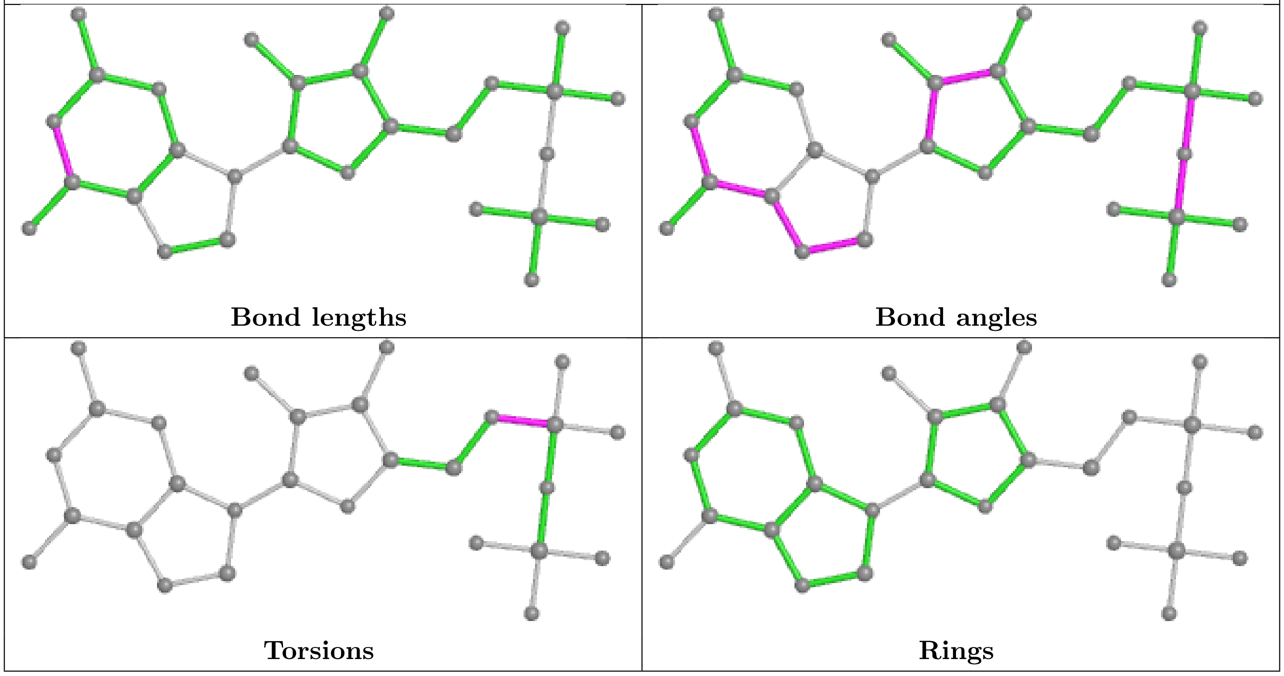


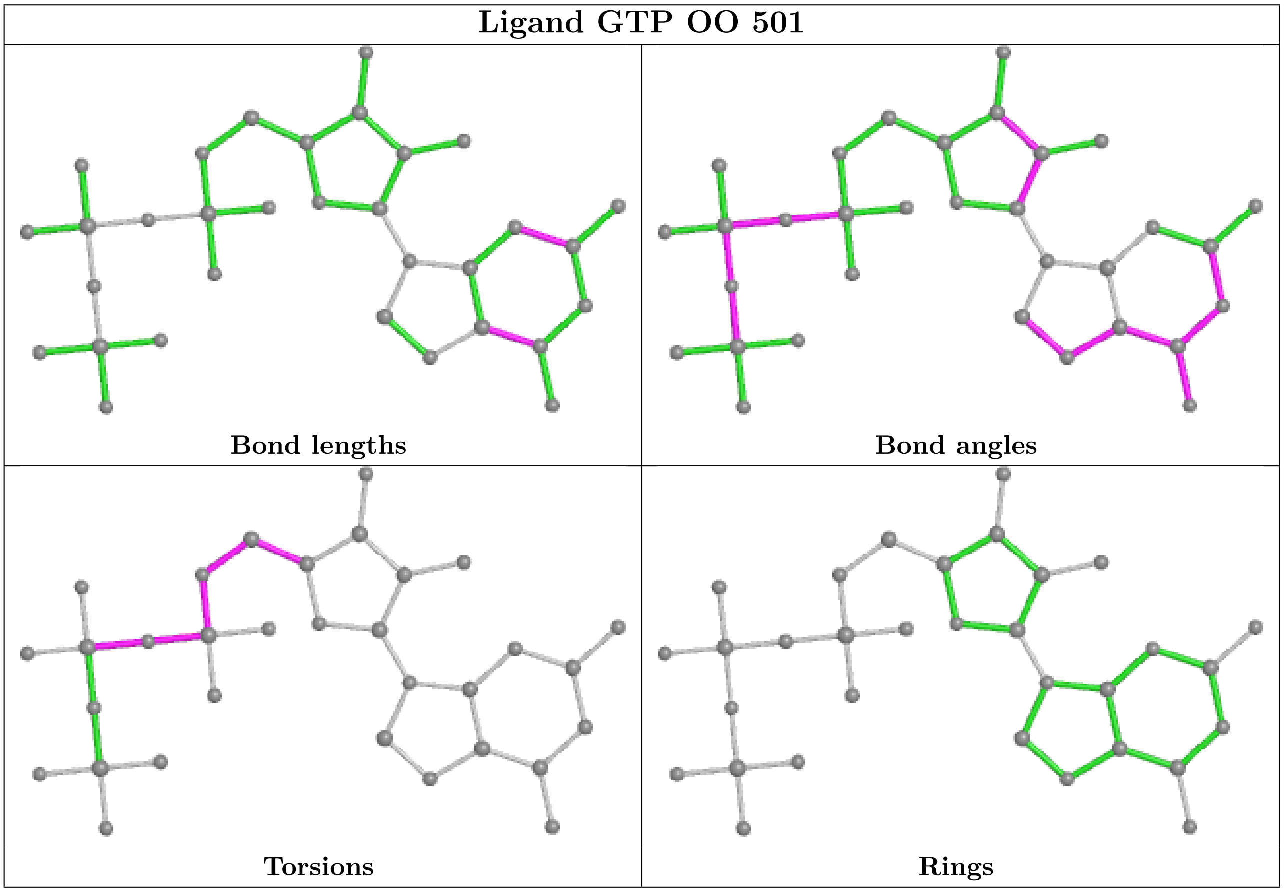
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP OO 501



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Torsions

Rings

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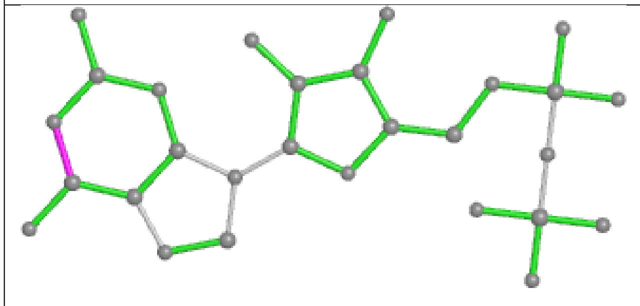

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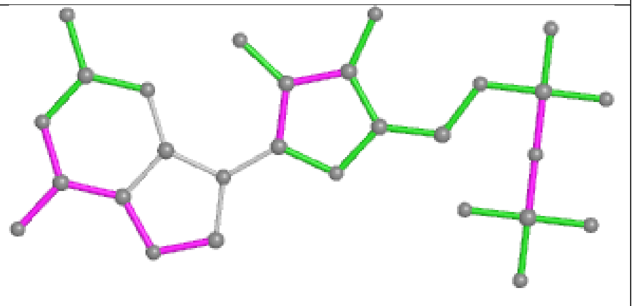

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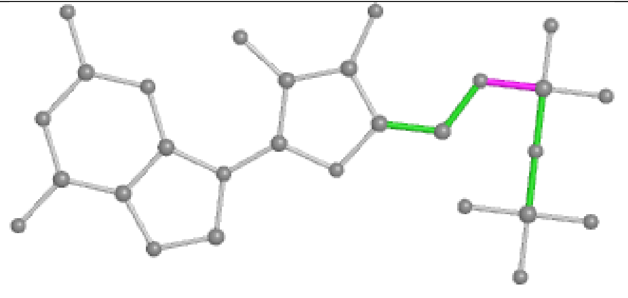

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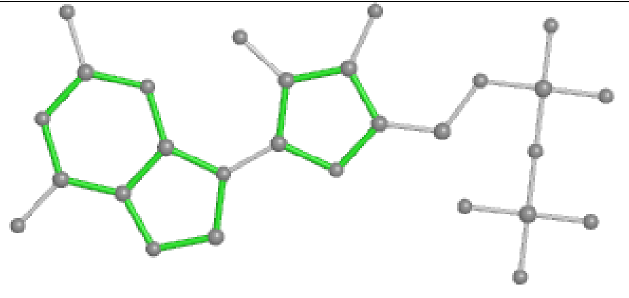

Rings

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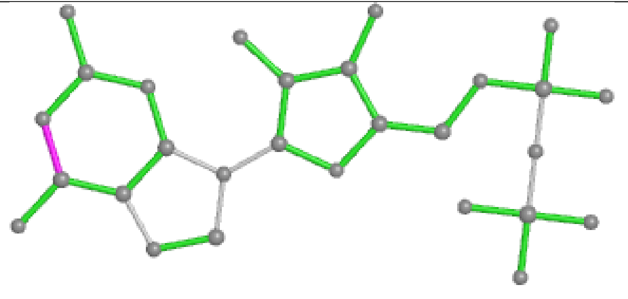

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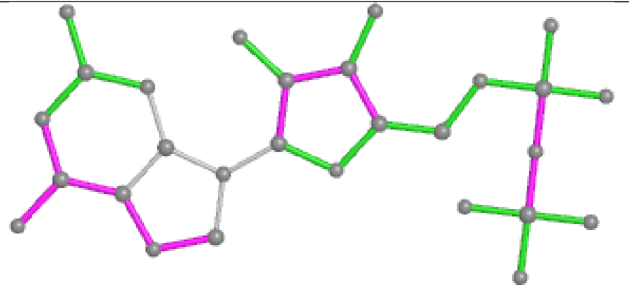

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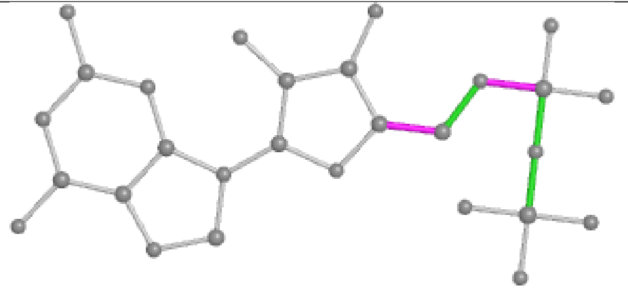

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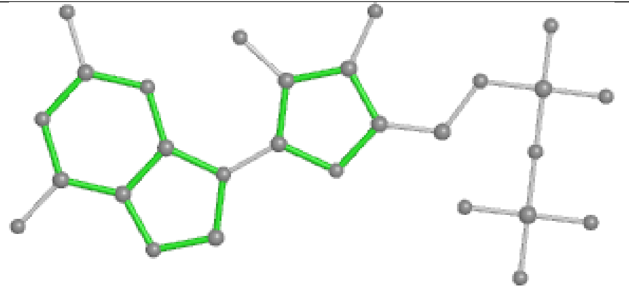

Rings

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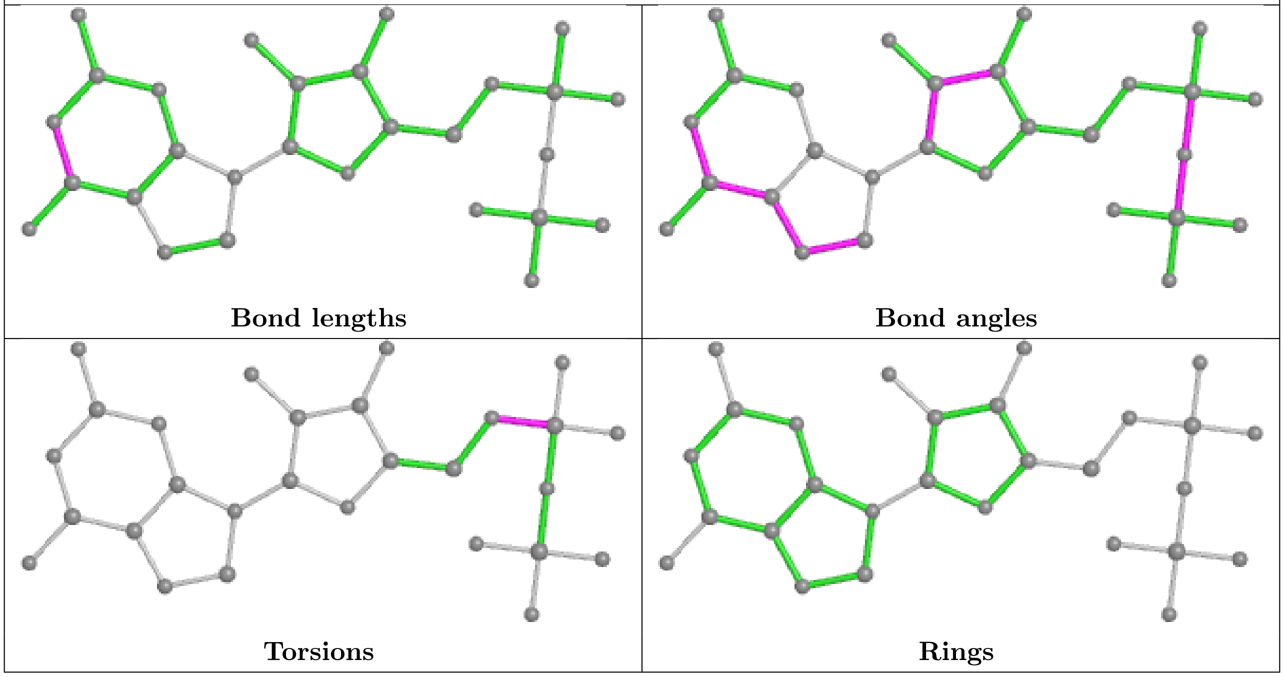

Bond lengths

Bond angles

Torsions

Rings

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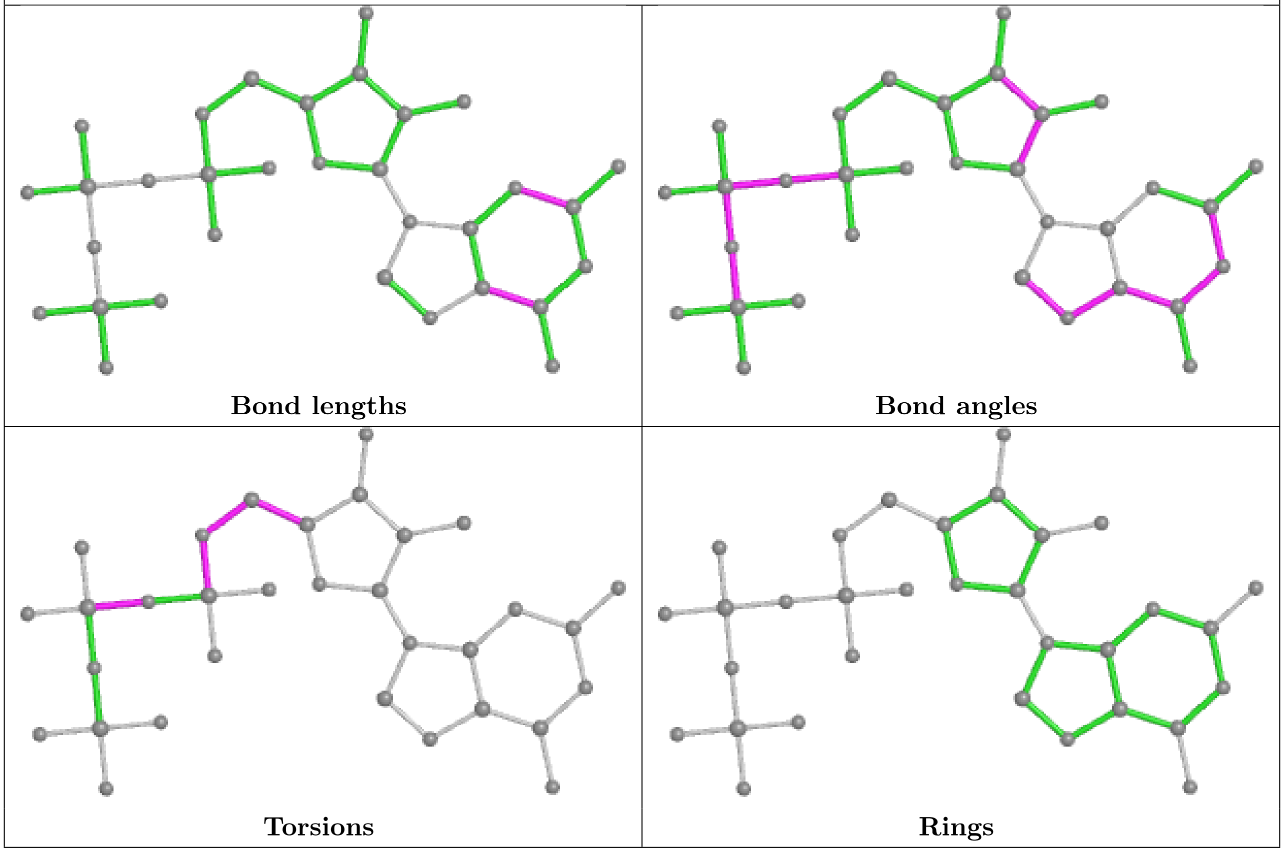


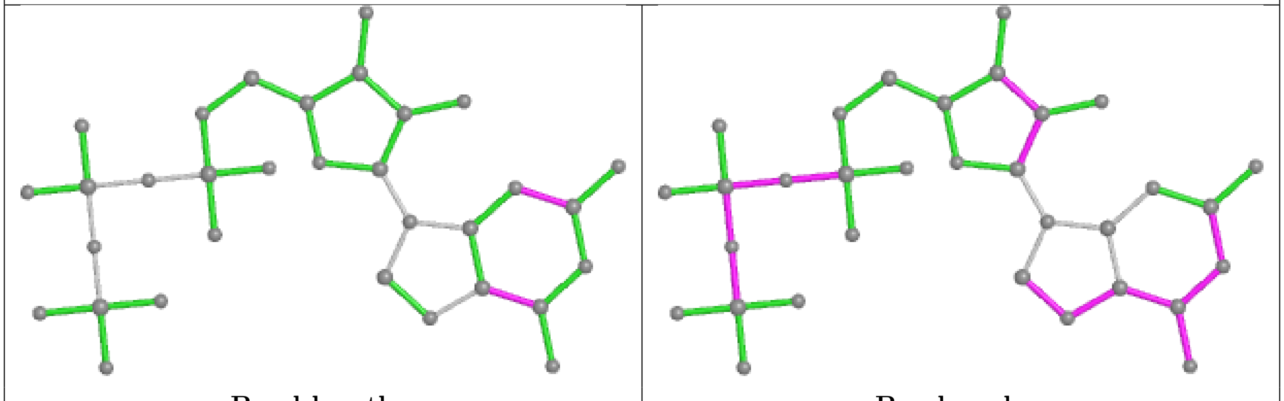
Bond lengths

Bond angles

Torsions

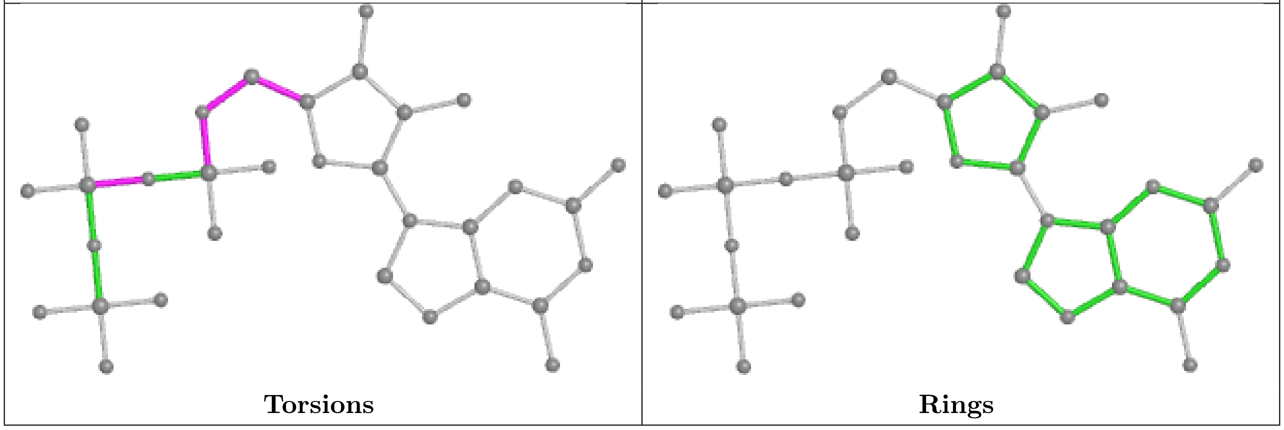
Rings

Ligand GTP LM 501



Bond lengths

Bond angles



Torsions

Rings

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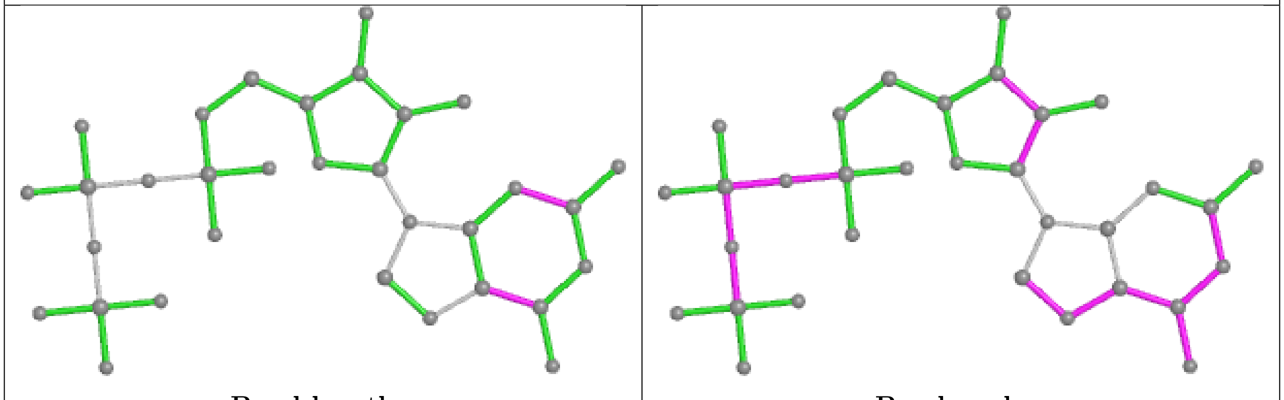

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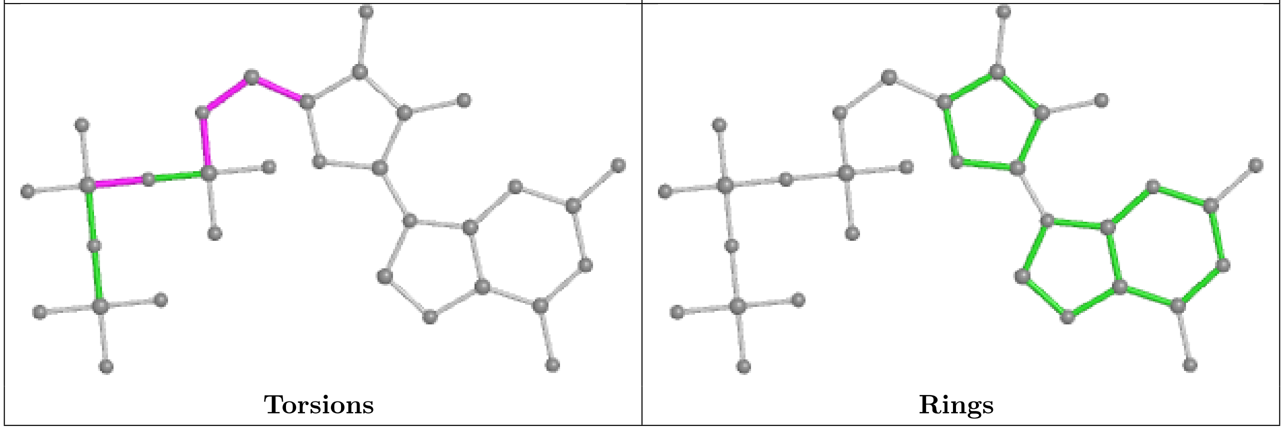

Torsions

Rings

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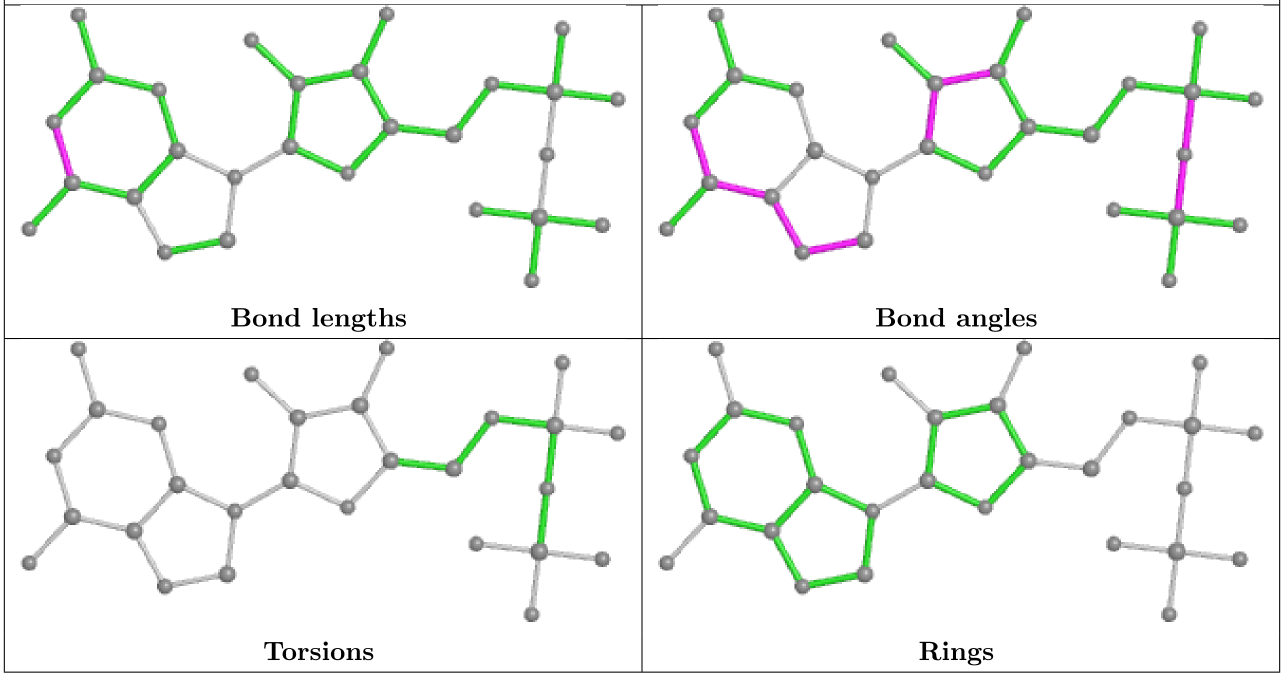

Bond lengths

Bond angles

Torsions

Rings

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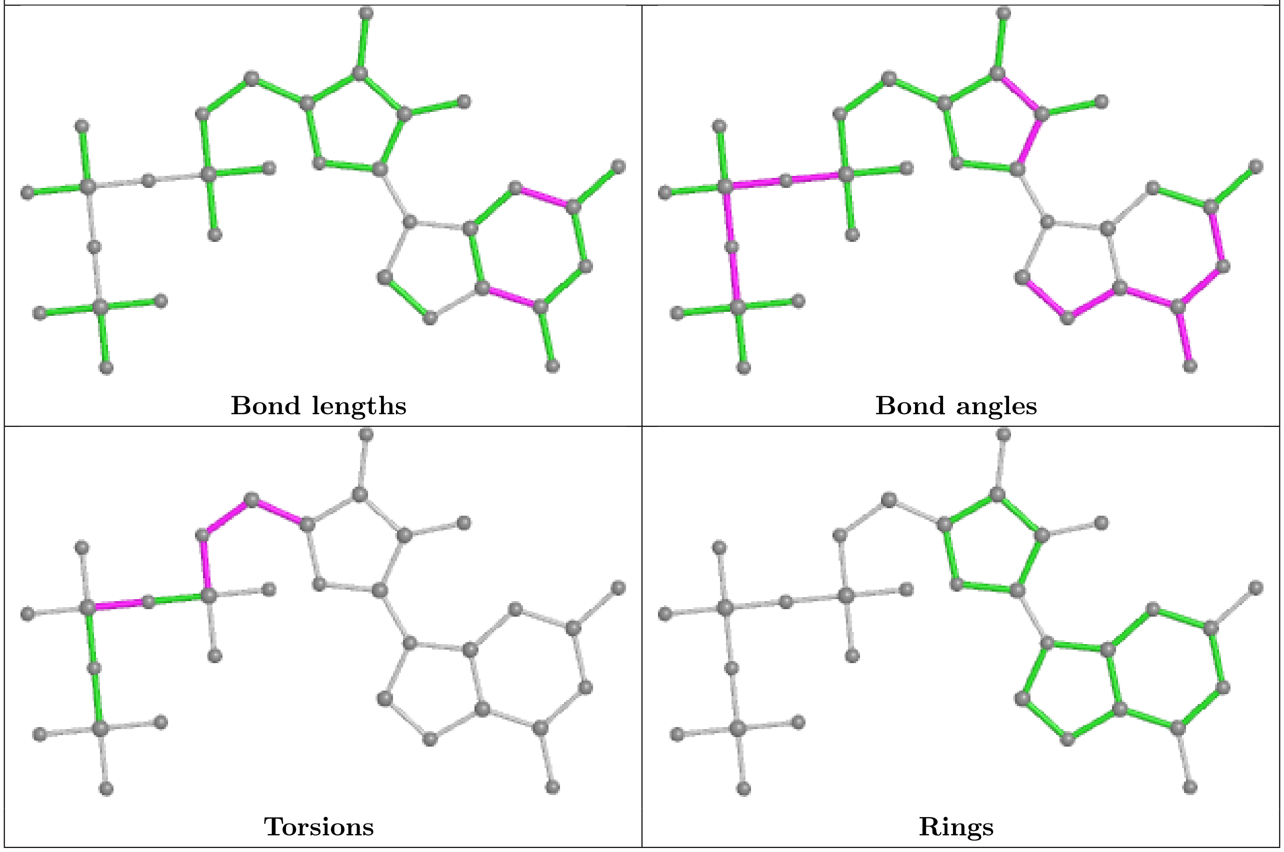

Bond lengths

Bond angles

Torsions

Rings

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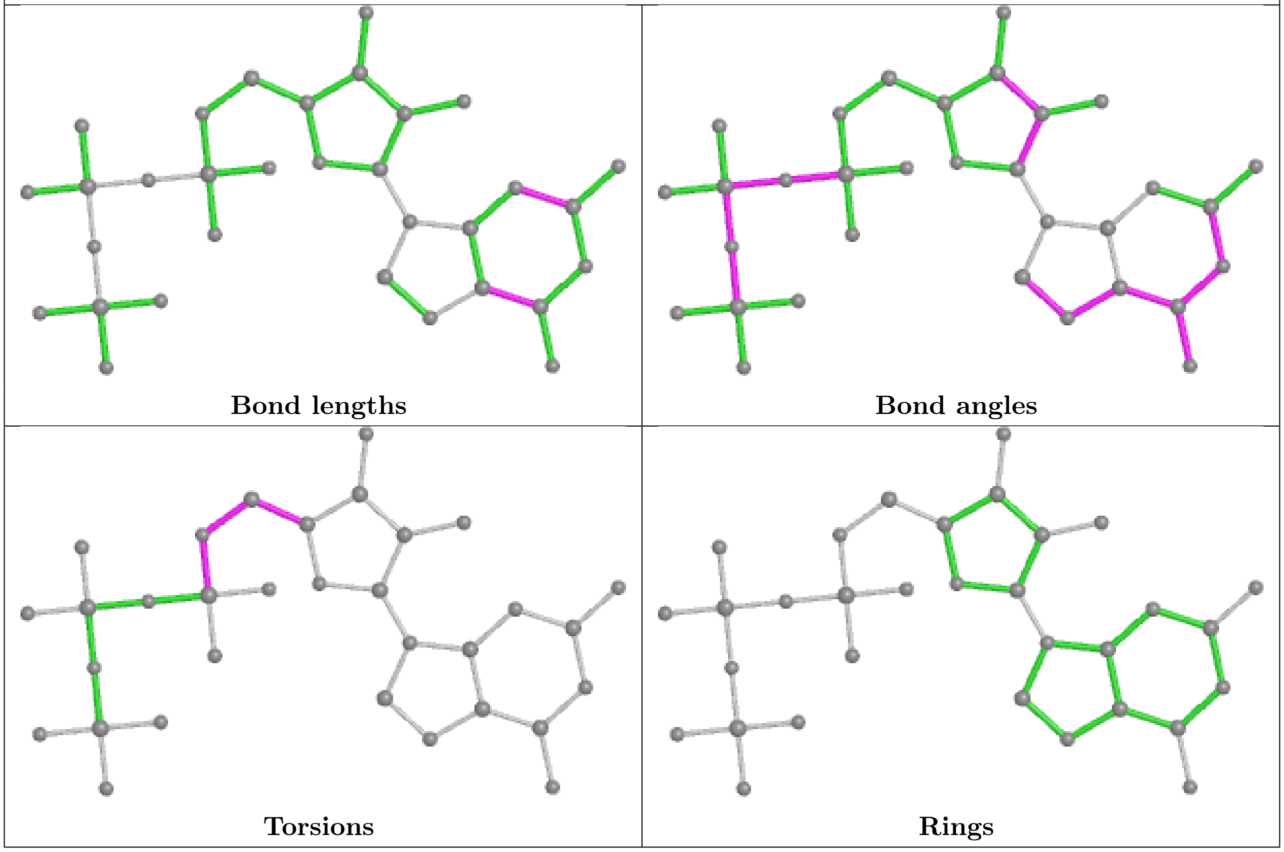

Bond lengths

Bond angles

Torsions

Rings

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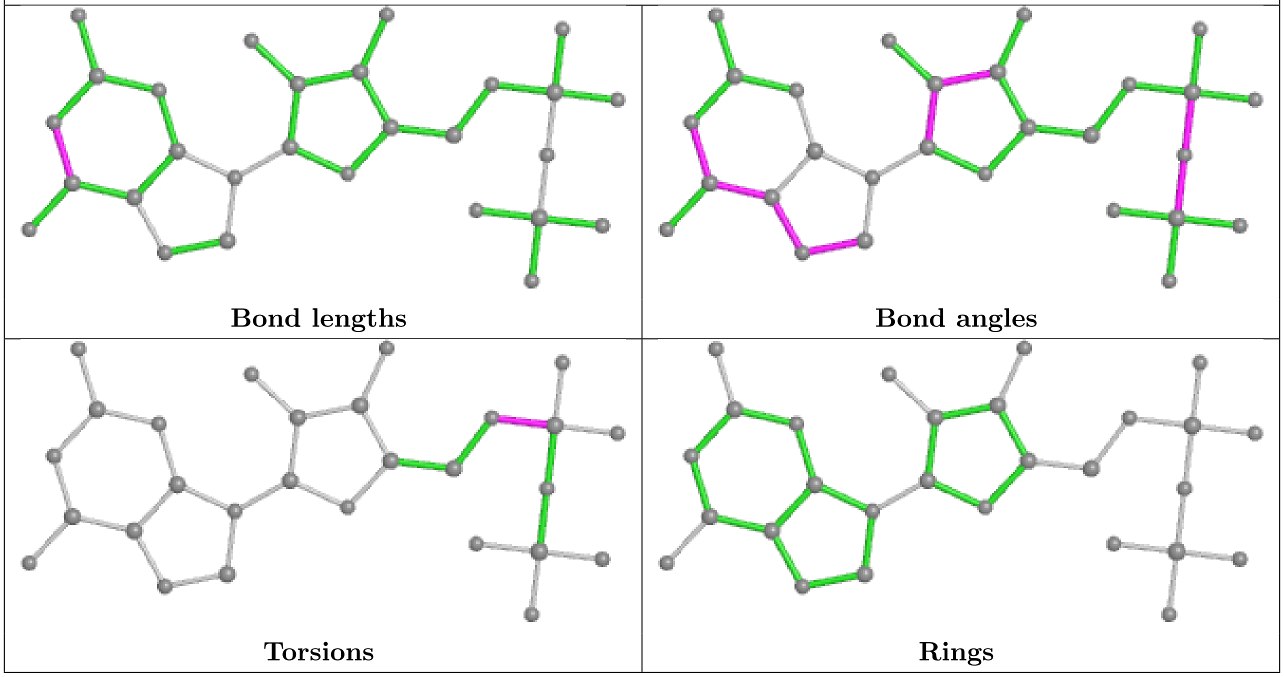

Bond lengths

Bond angles

Torsions

Rings

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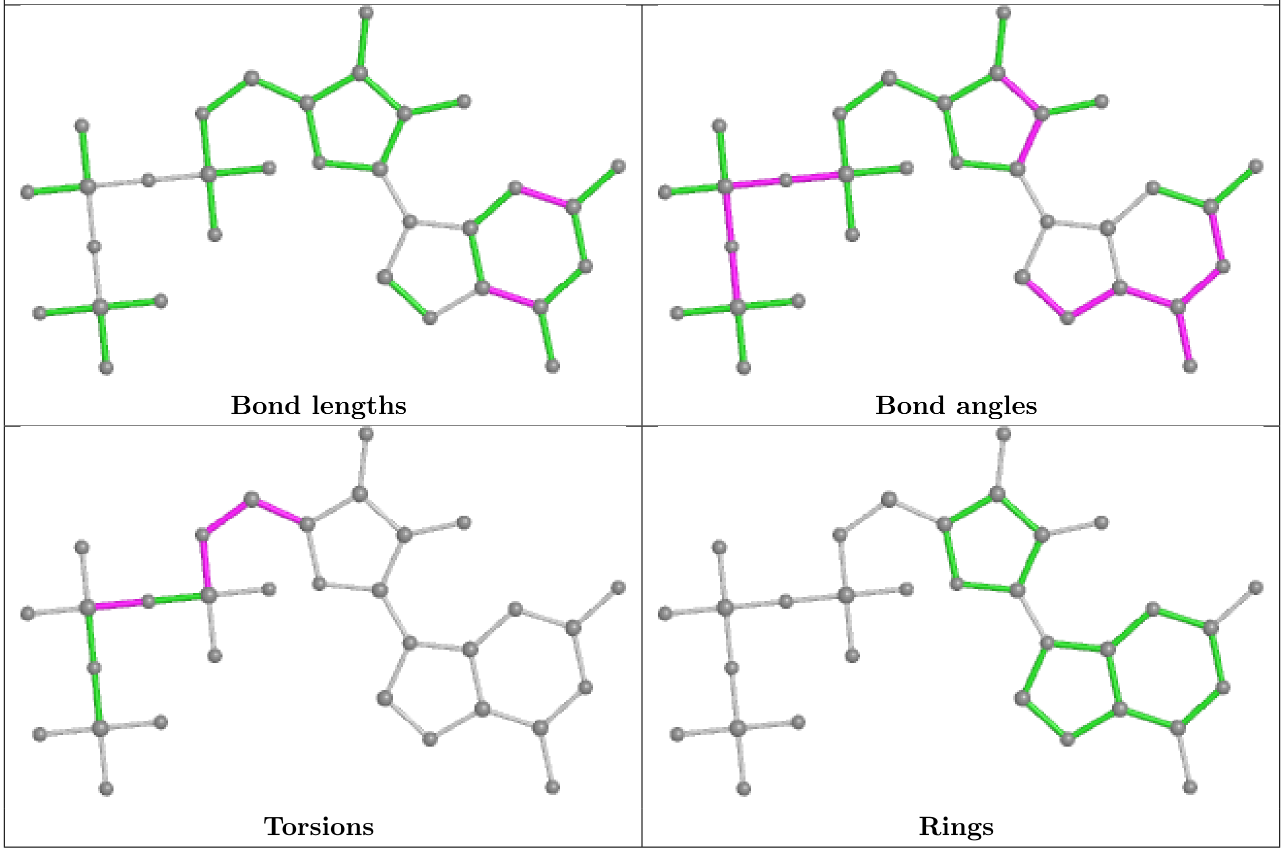

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Bond angles

Torsions

Rings

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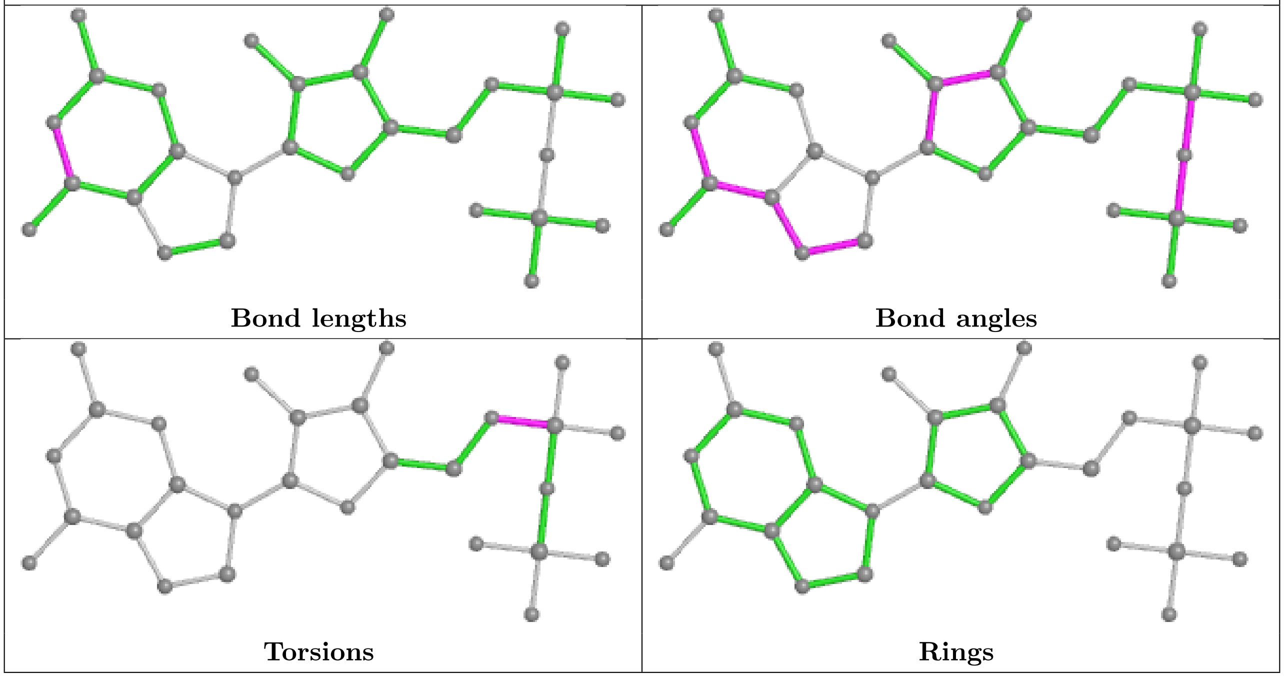

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Bond angles

Torsions

Rings

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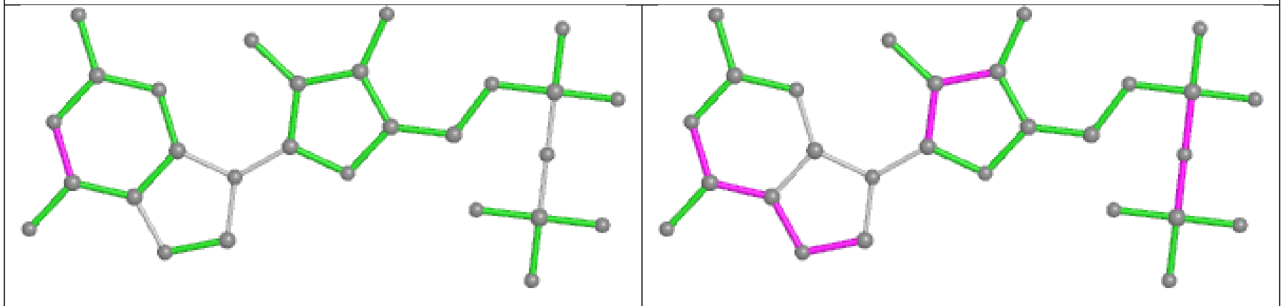

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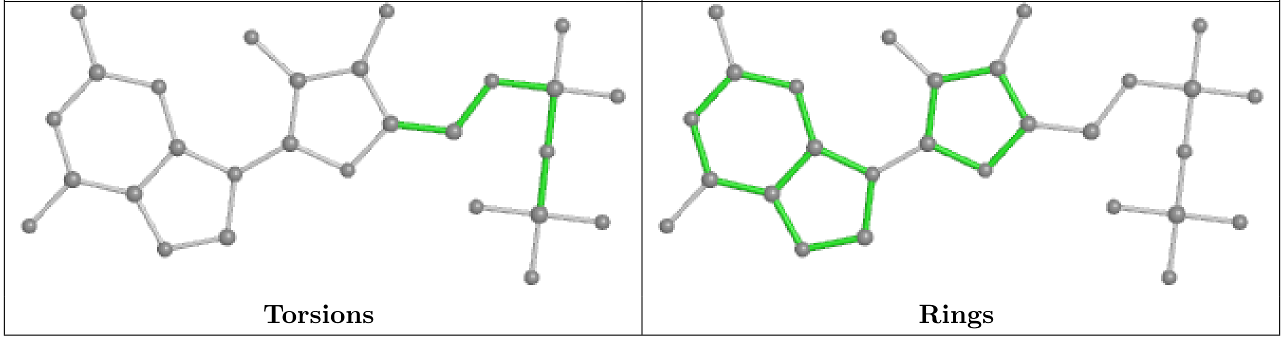

Torsions Rings

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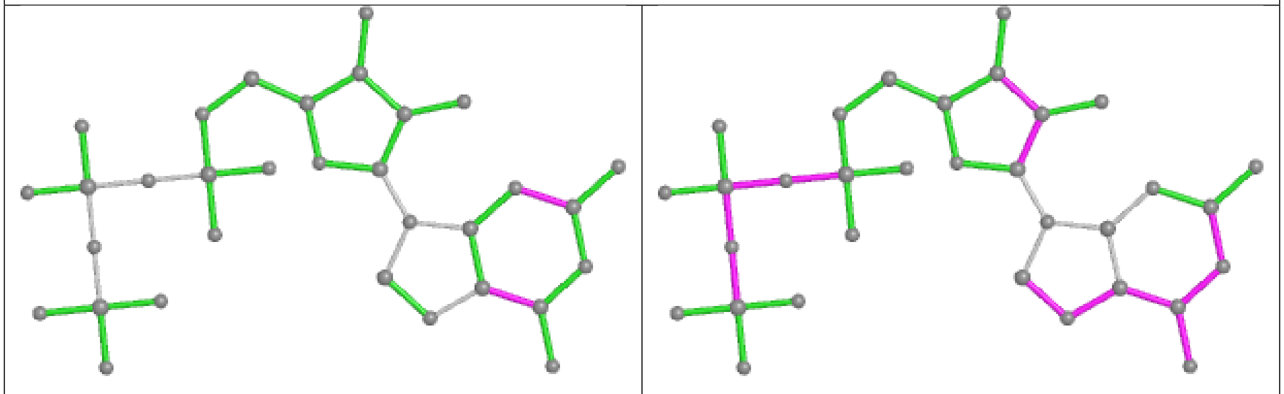
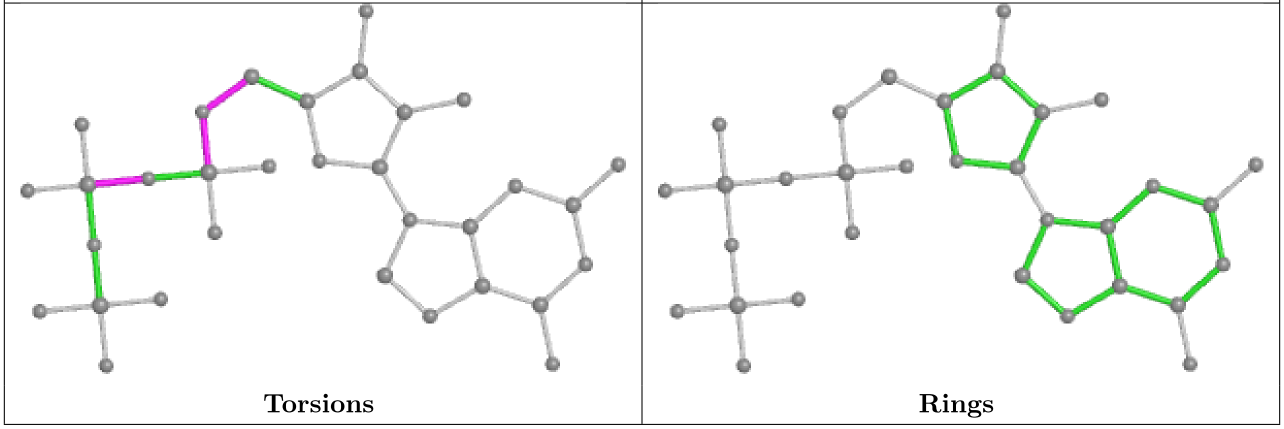
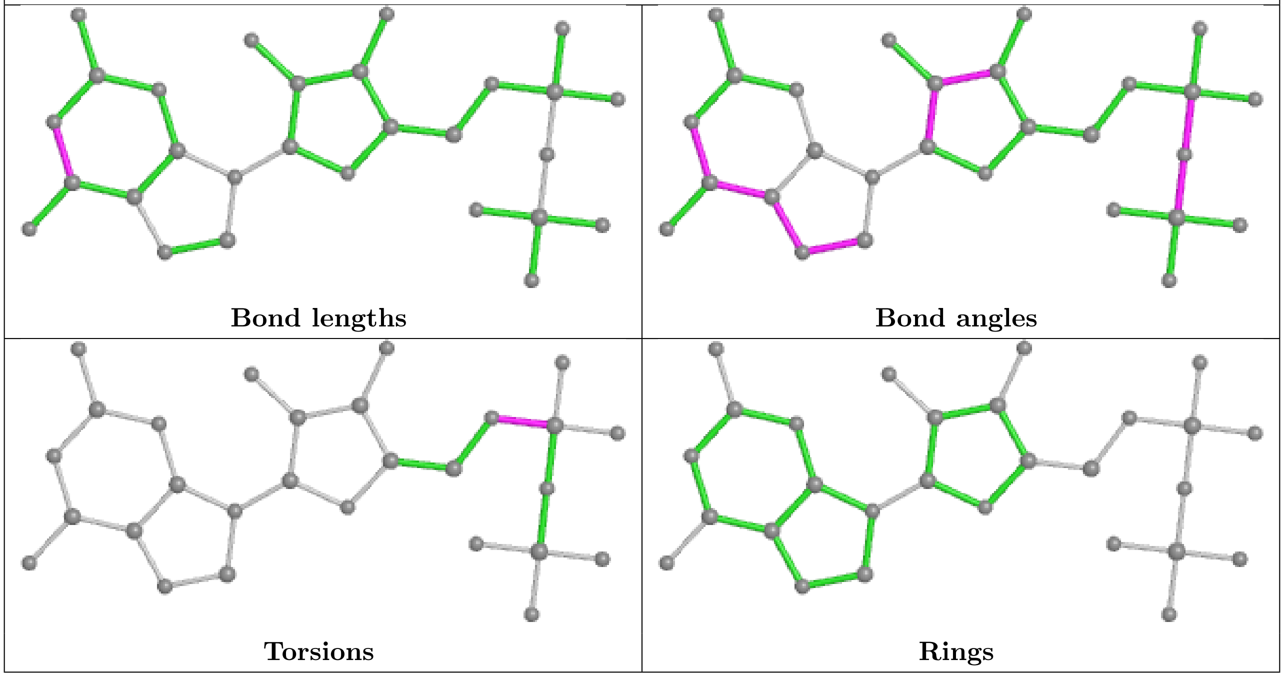


Bond lengths Bond angles



Torsions Rings

Ligand GDP PF 502



Bond lengths

Bond angles

Torsions

Rings

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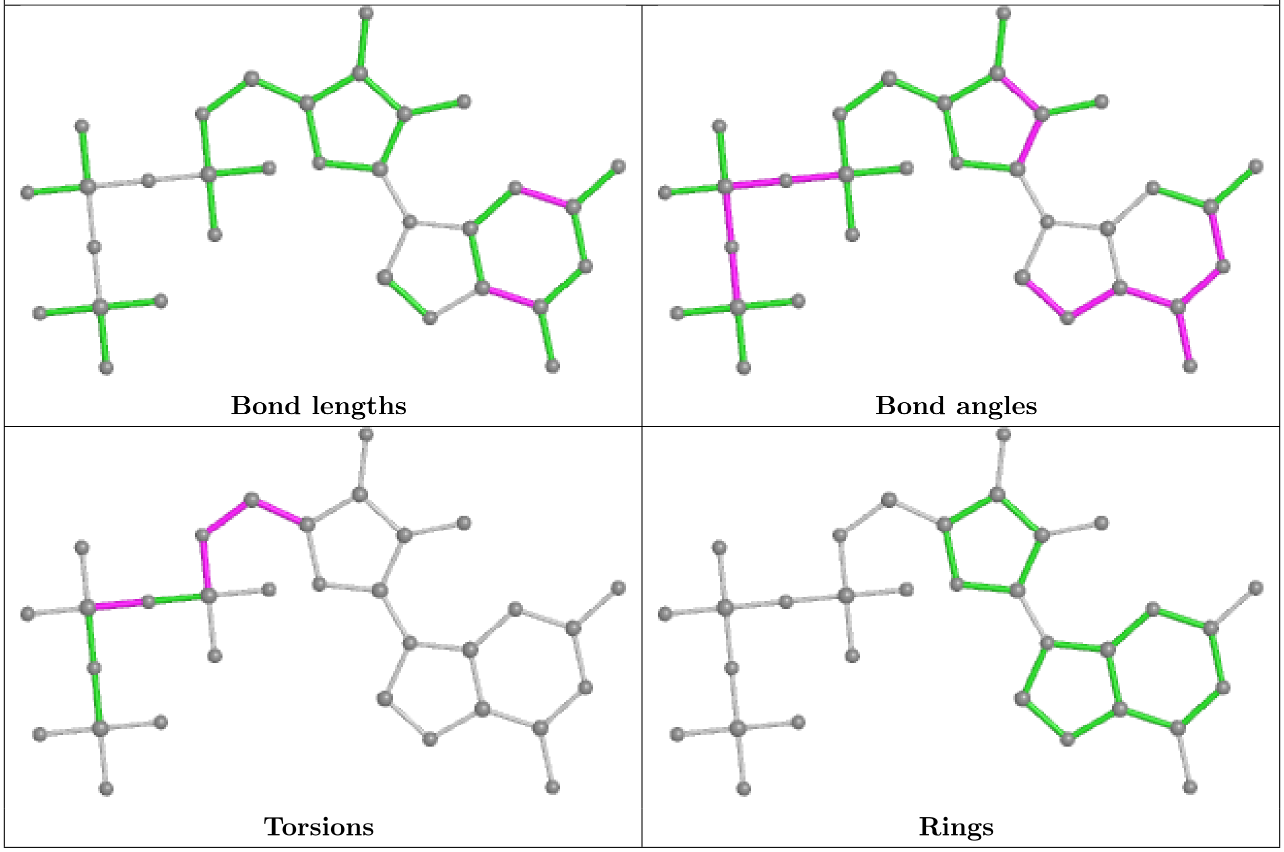

Bond lengths

Bond angles

Torsions

Rings

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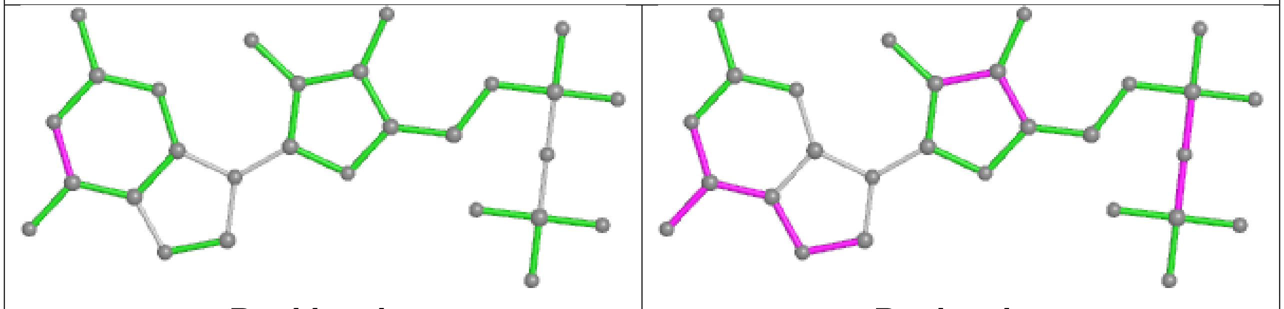
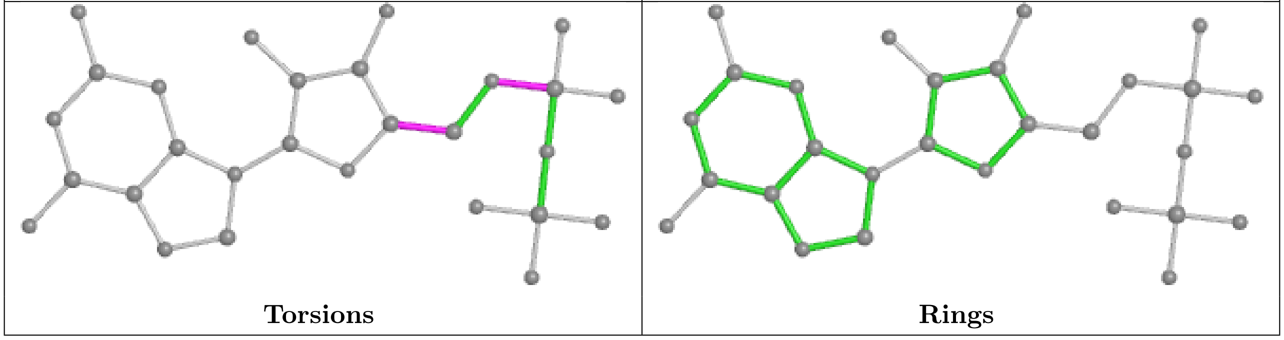


Bond lengths Bond angles



Torsions Rings

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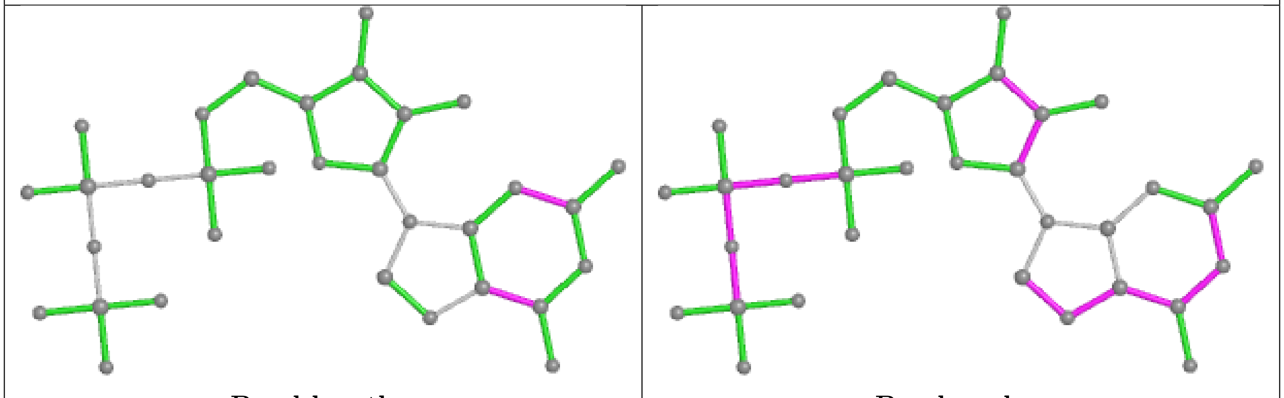

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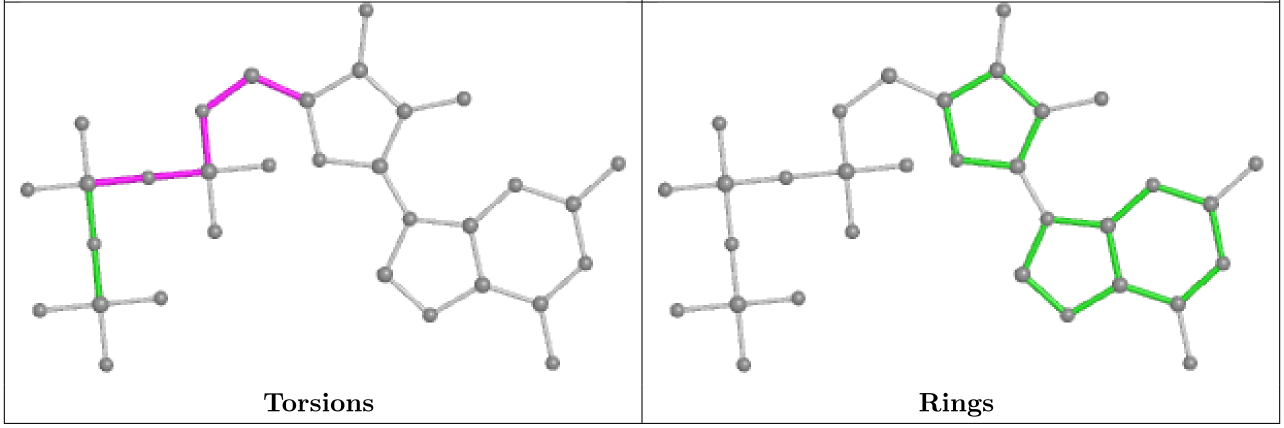

Torsions Rings

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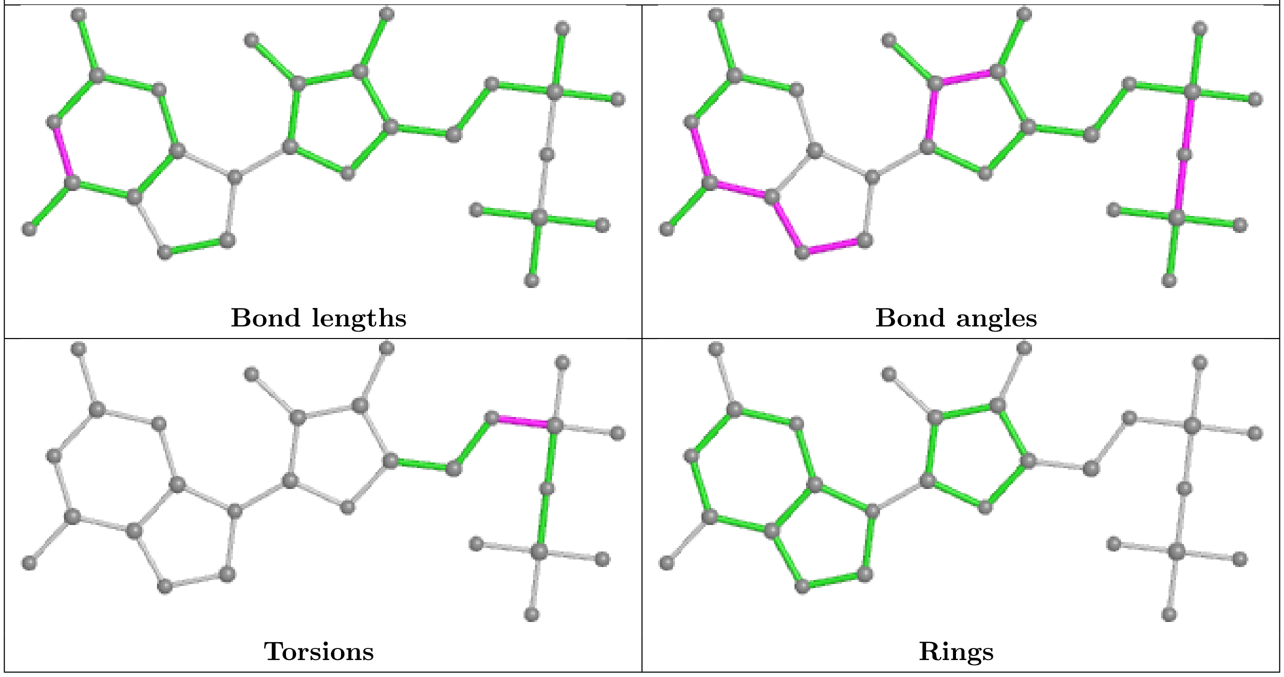


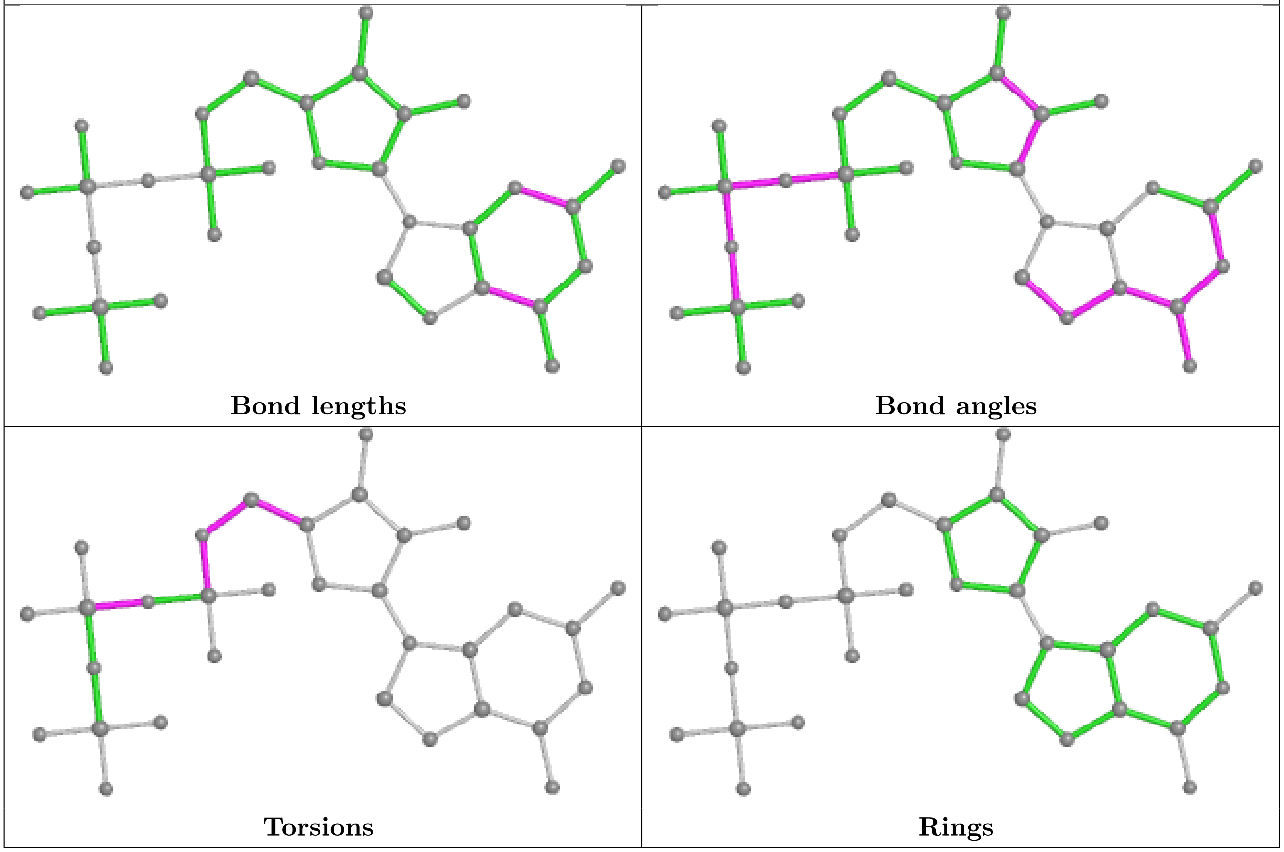
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP UM 501



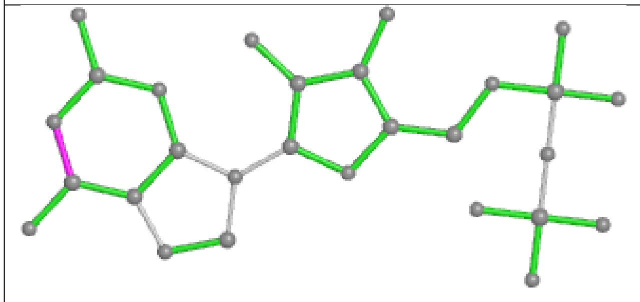
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP CN 502



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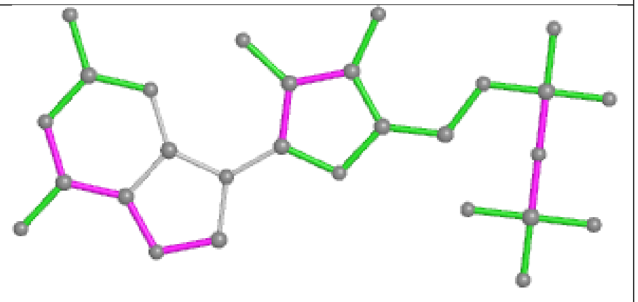

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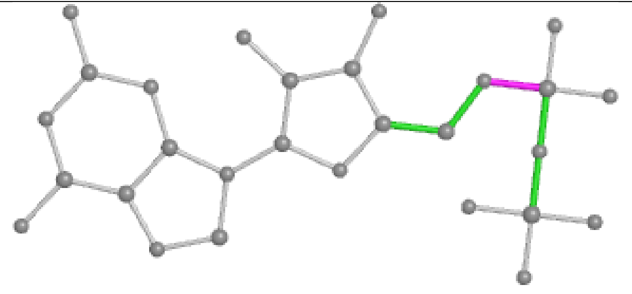

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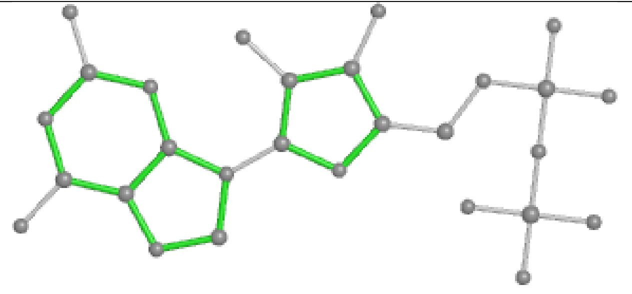

Rings

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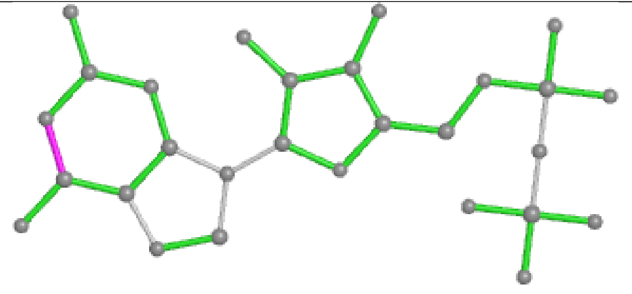

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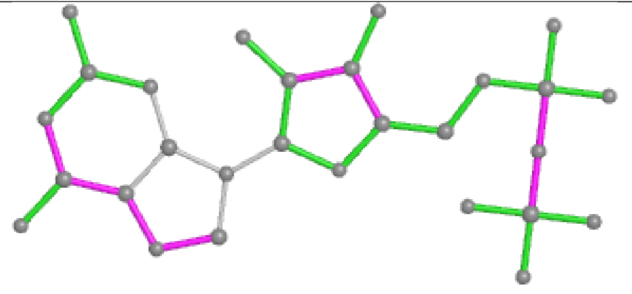

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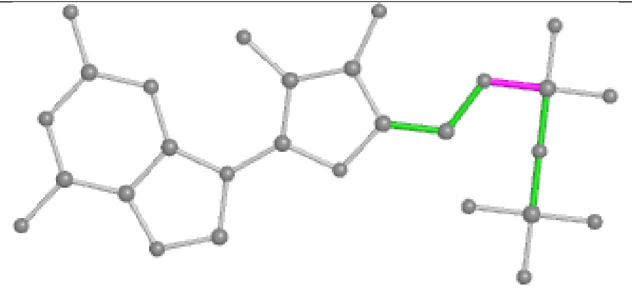

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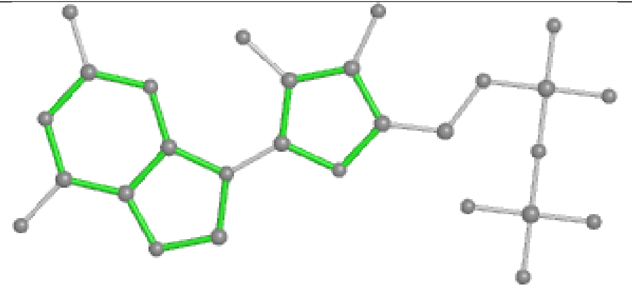
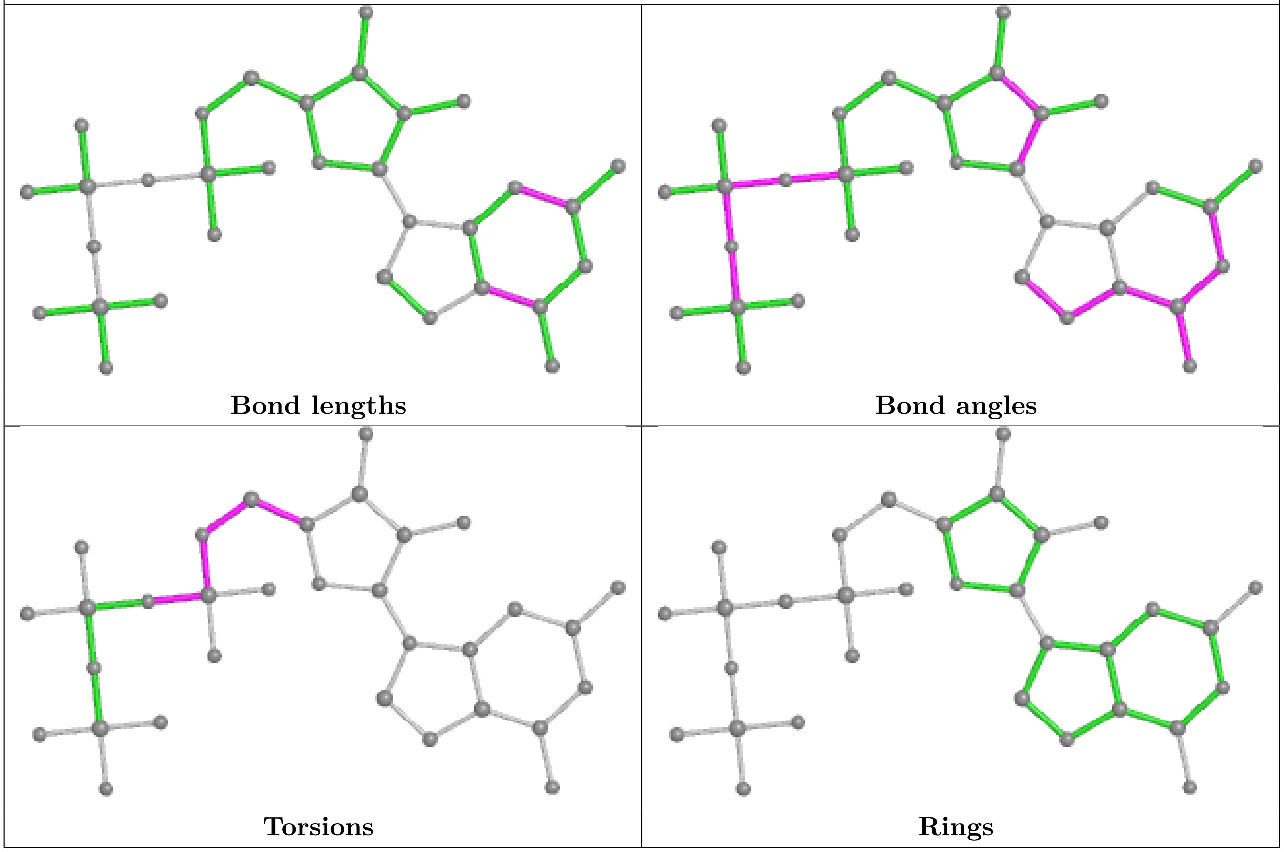


Rings

Ligand GTP JI 501



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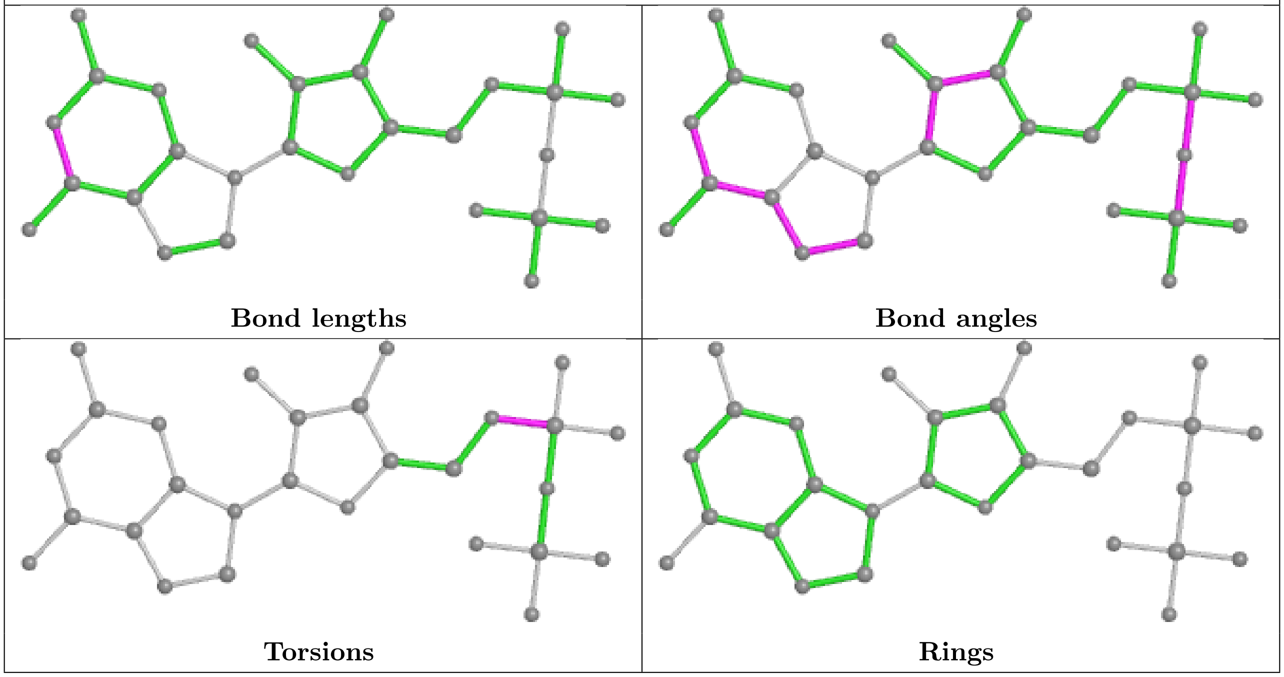

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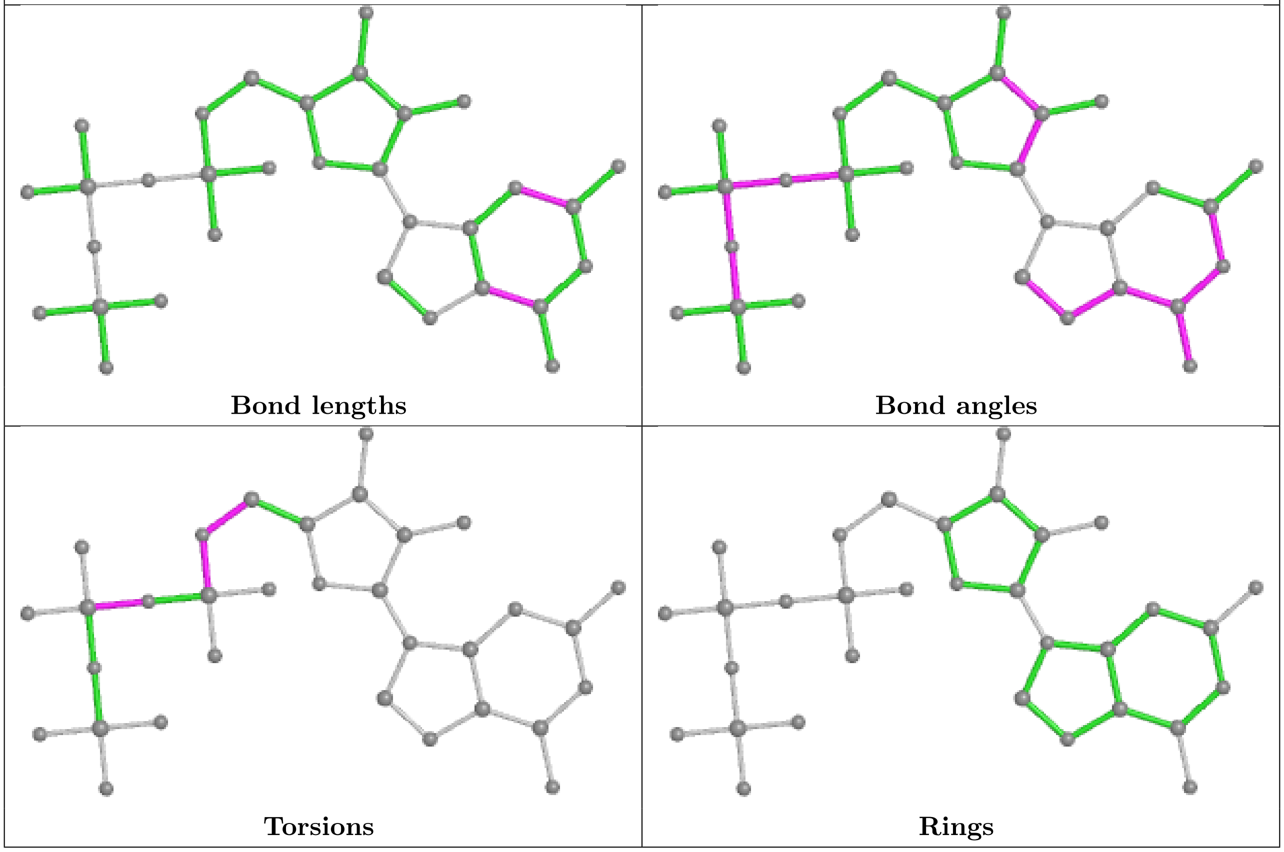


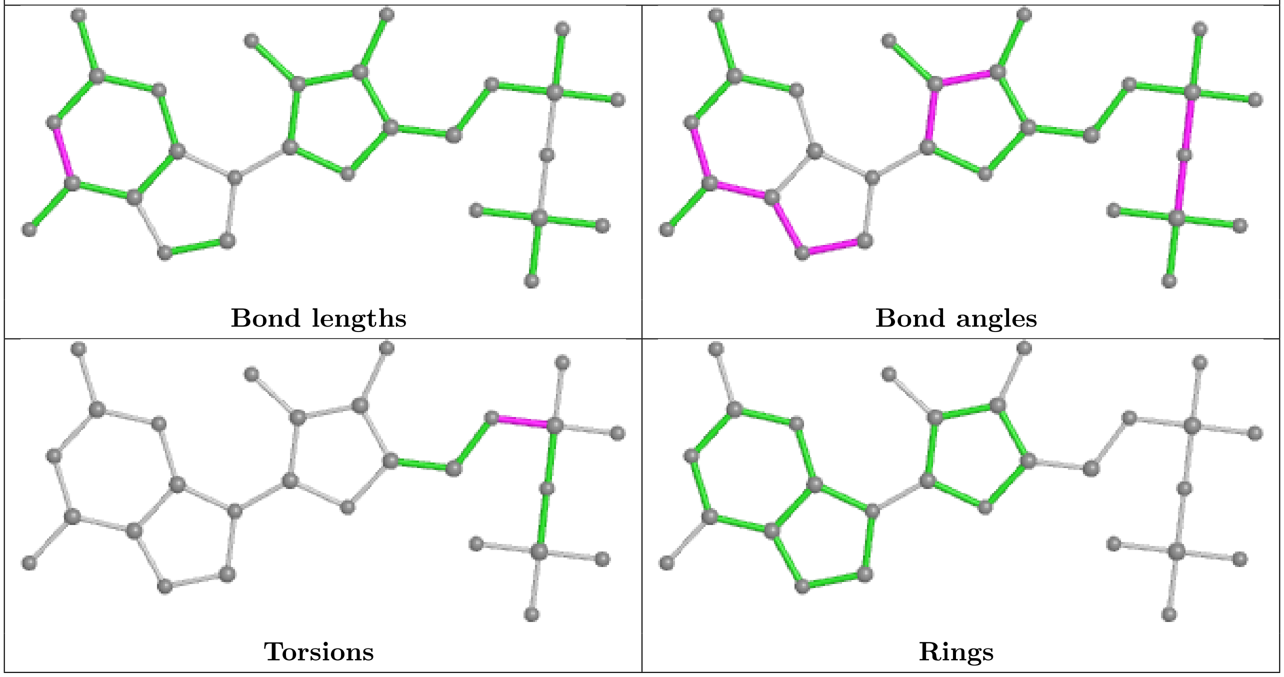
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP LN 502



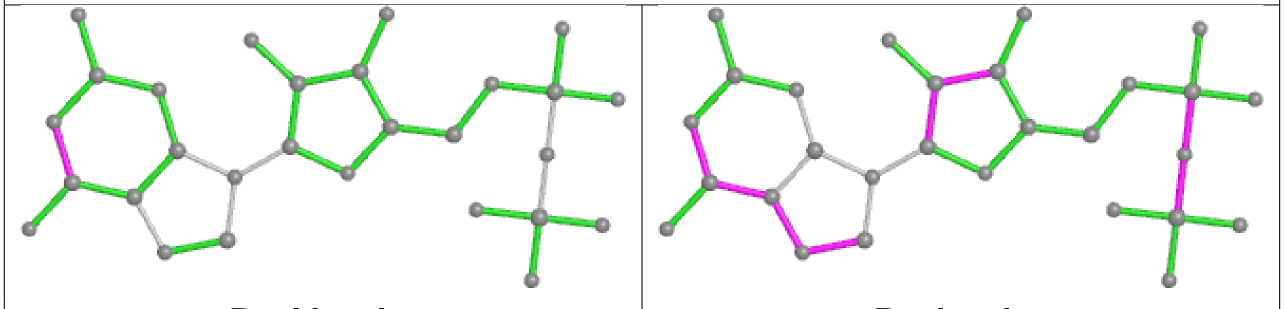
Bond lengths

Bond angles

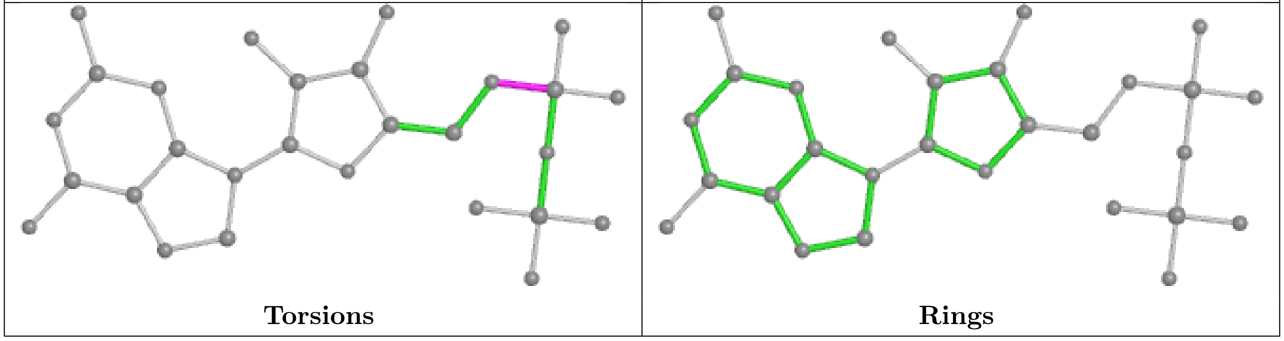
Torsions

Rings

Ligand GDP VH 502

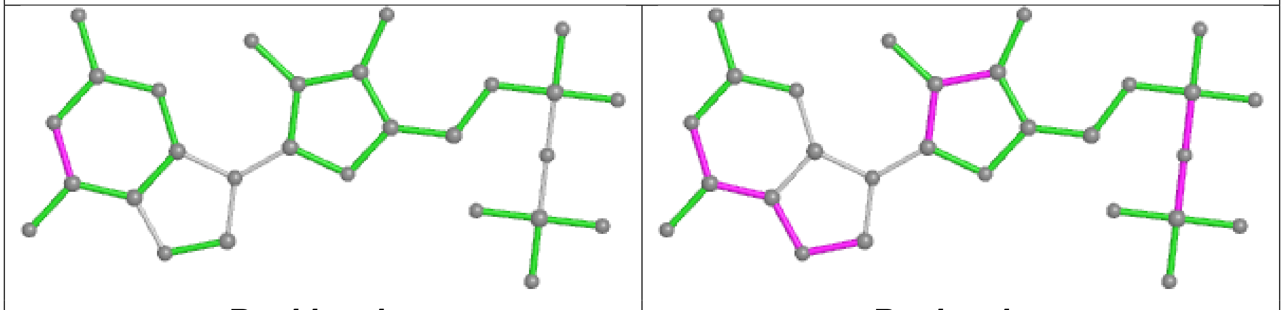


Bond lengths Bond angles

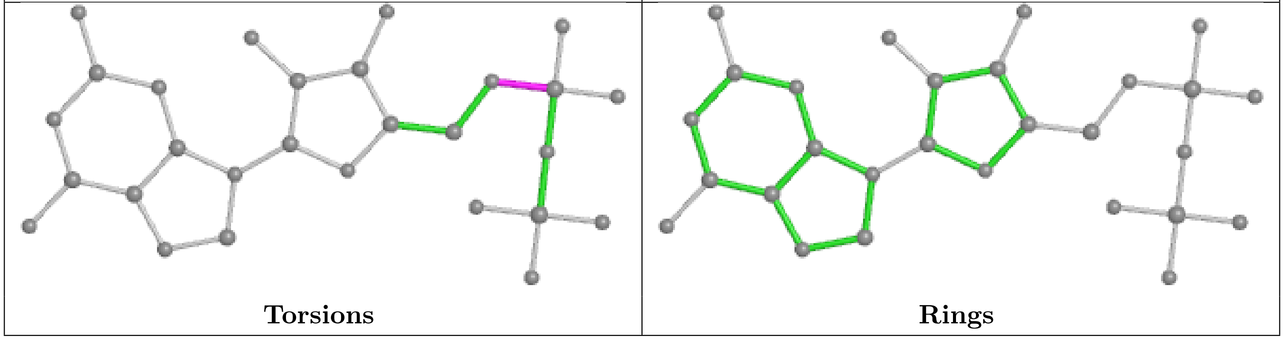


Torsions Rings

Ligand GDP SB 502



Bond lengths Bond angles



Torsions Rings

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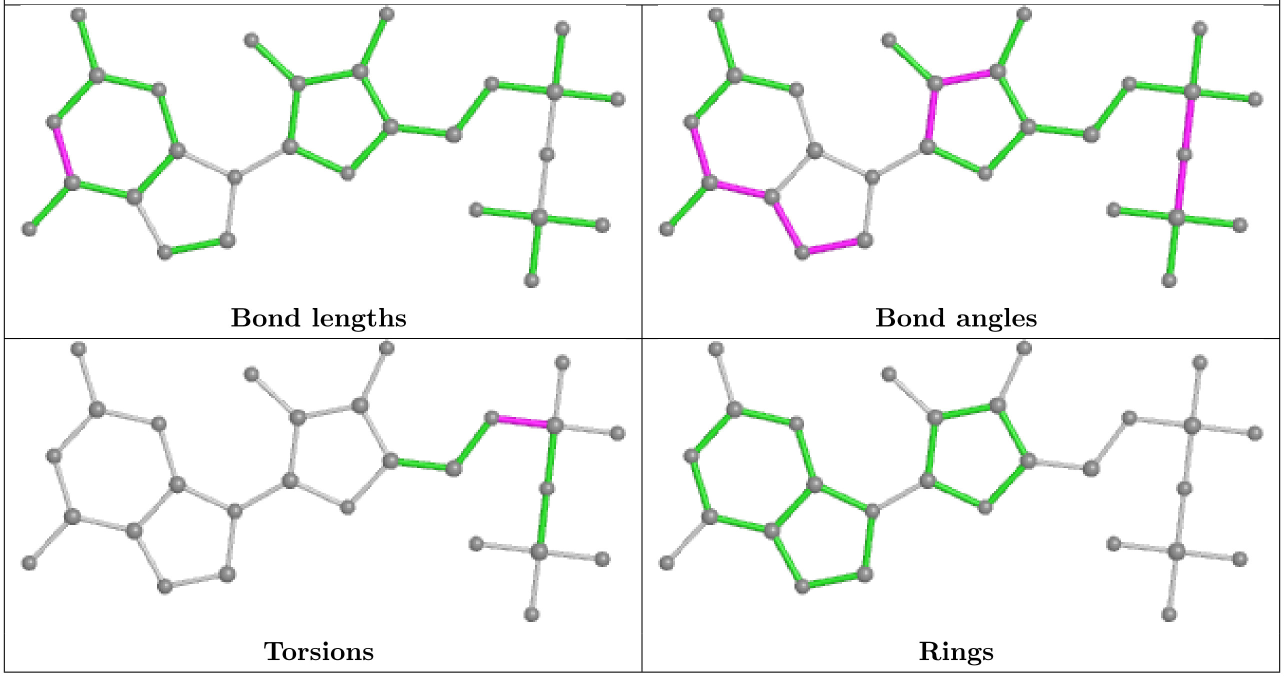

Bond lengths

Bond angles

Torsions

Rings

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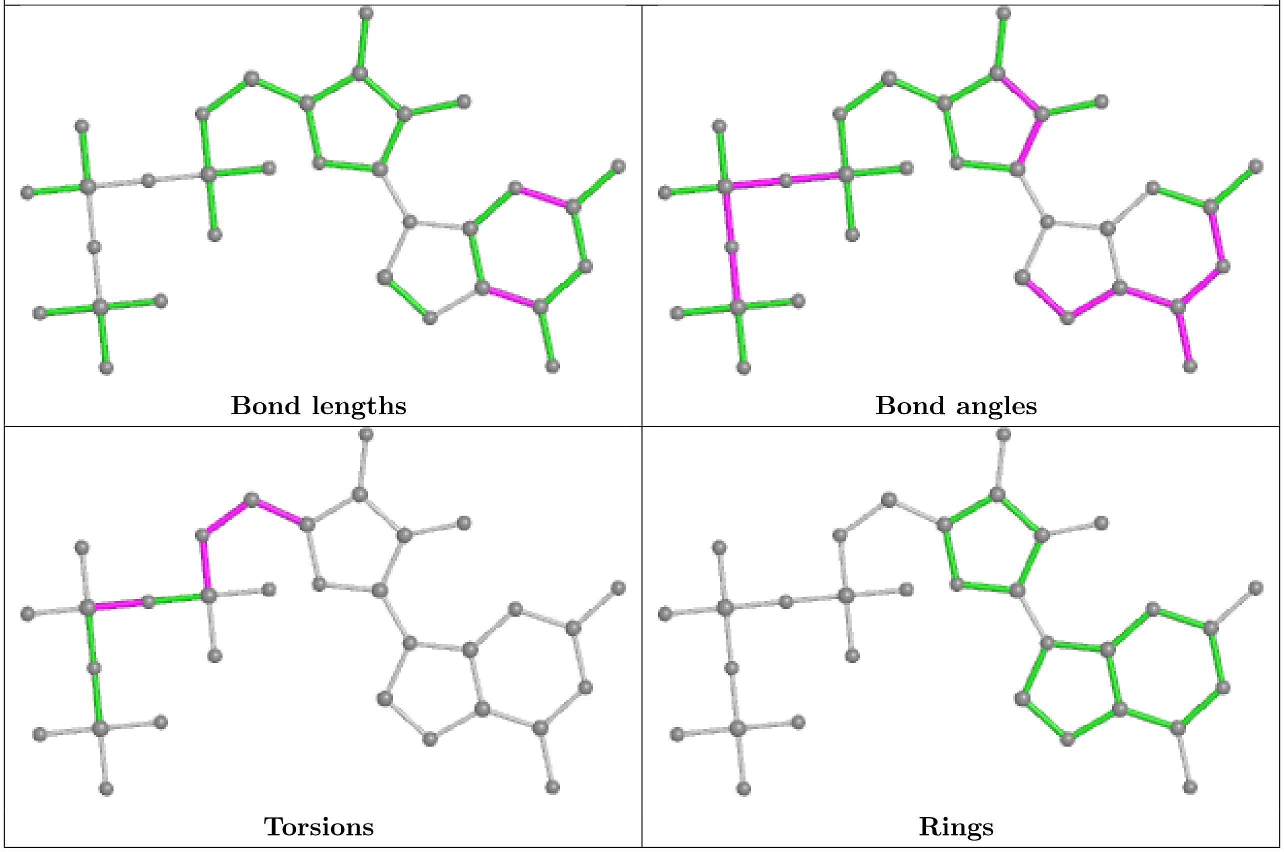

Bond lengths

Bond angles

Torsions

Rings

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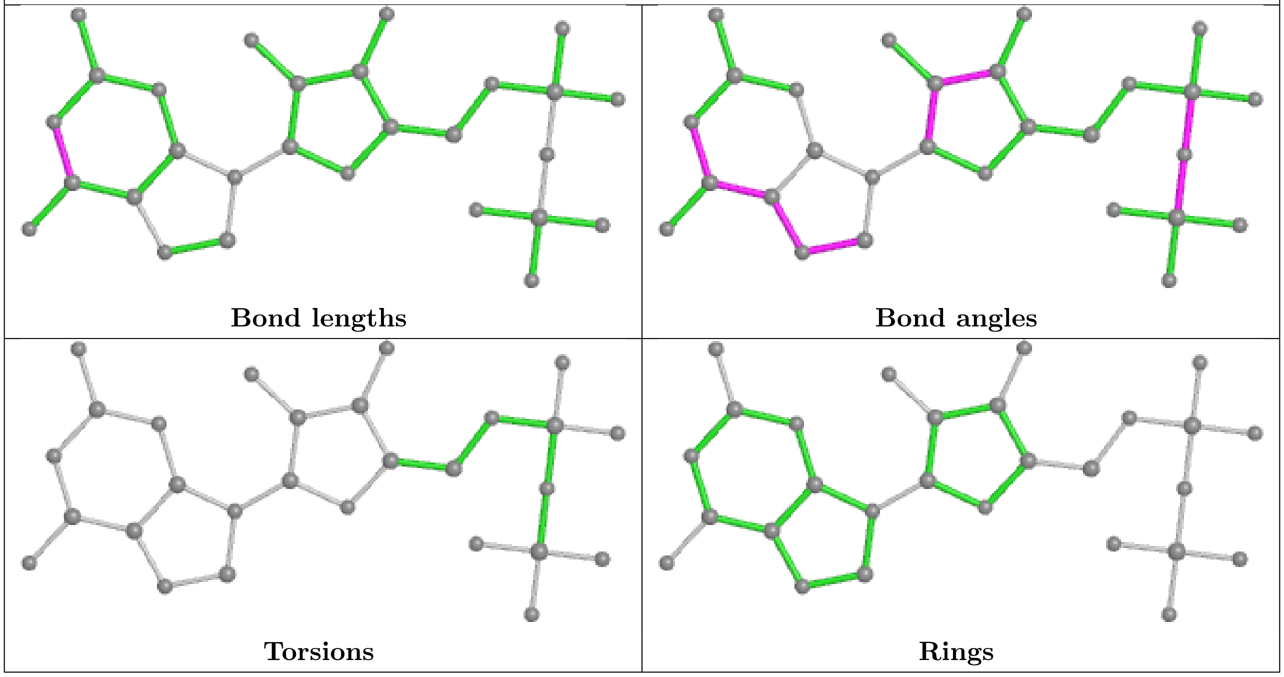

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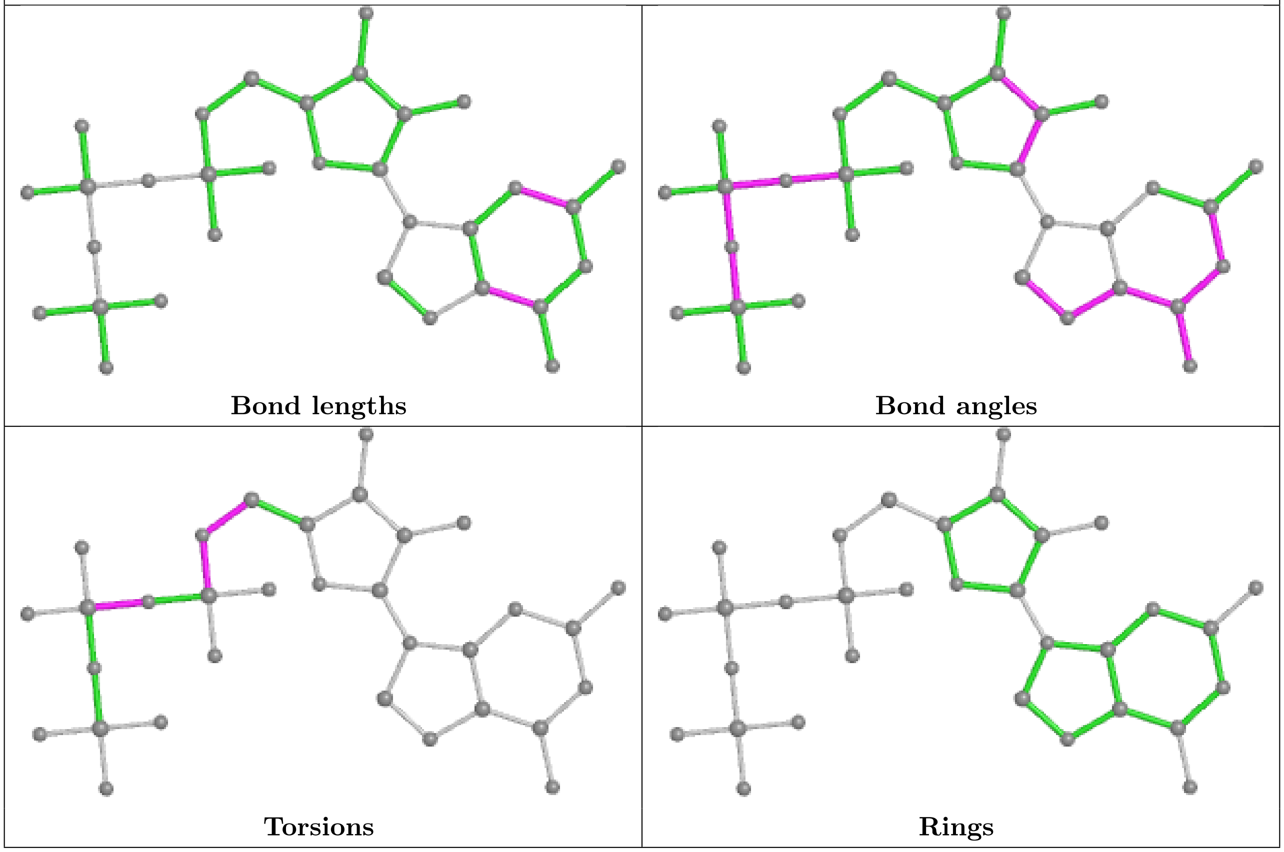

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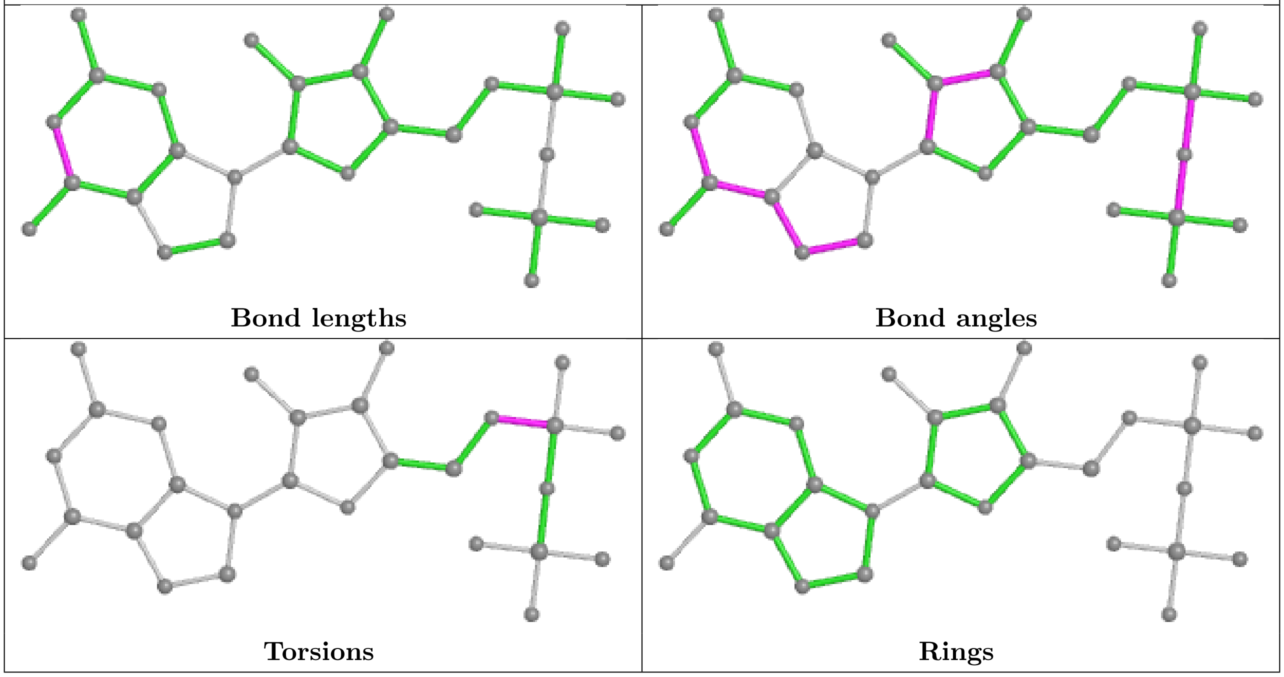
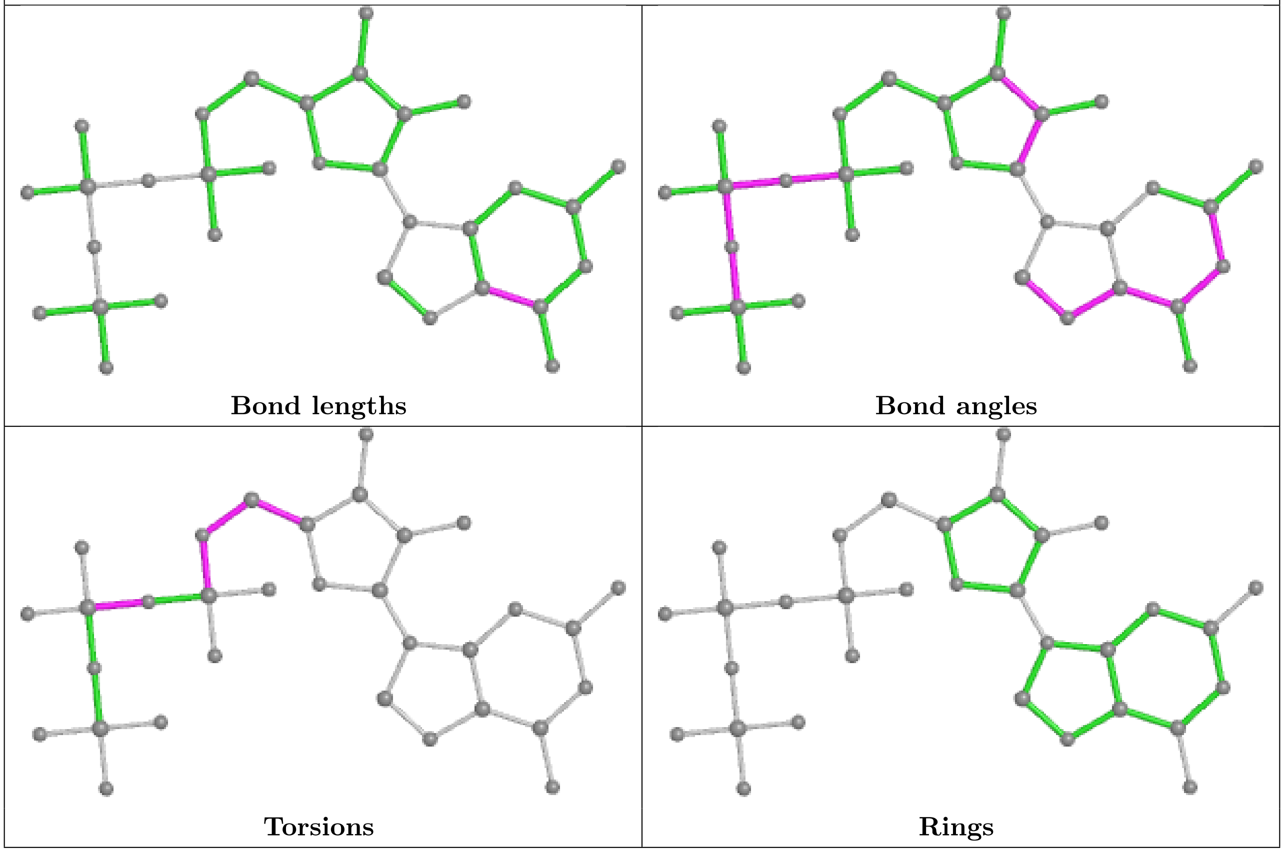

Bond lengths
Bond angles
Torsions
Rings

Ligand GTP QO 501


Bond lengths
Bond angles
Torsions
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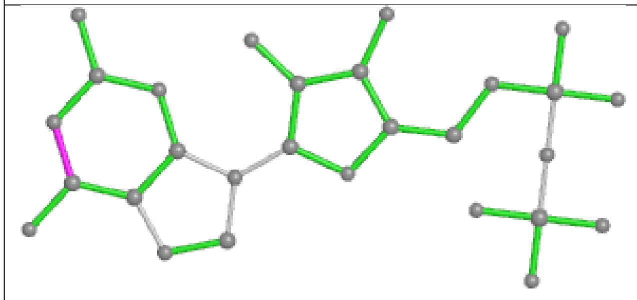

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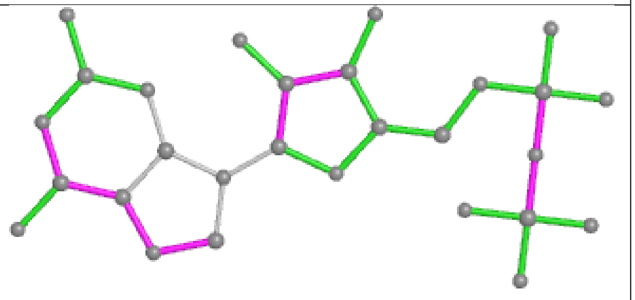

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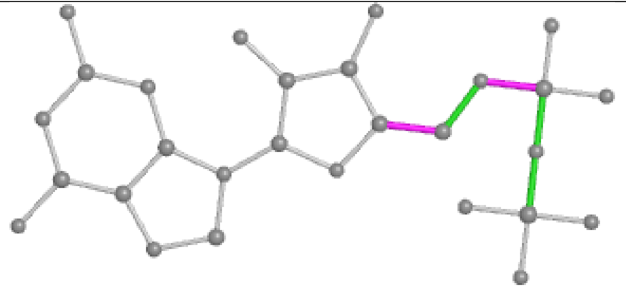

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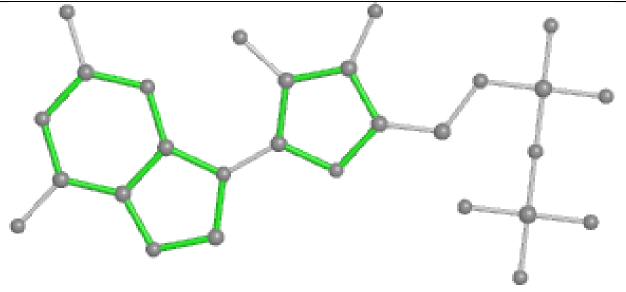

Rings

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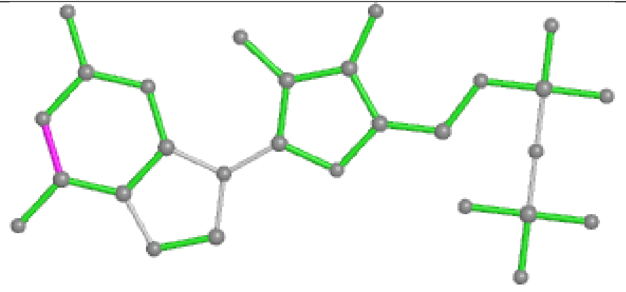

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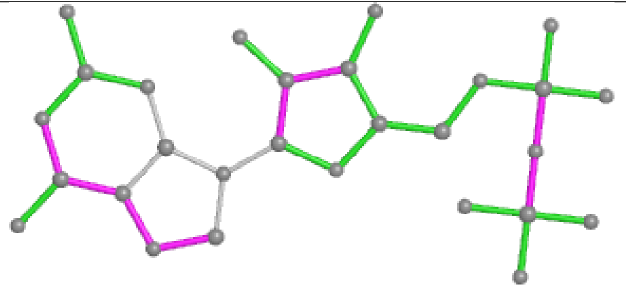

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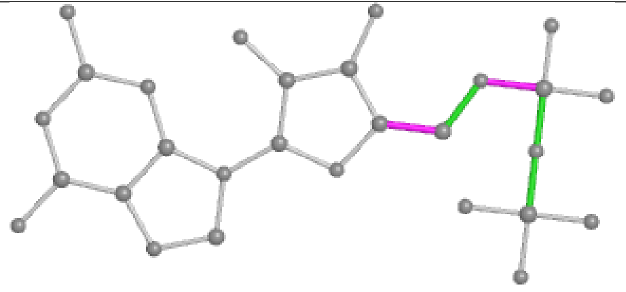

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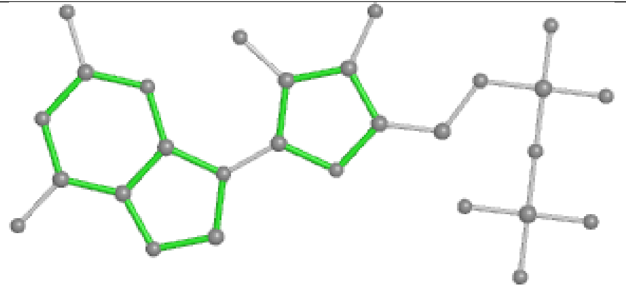

Rings

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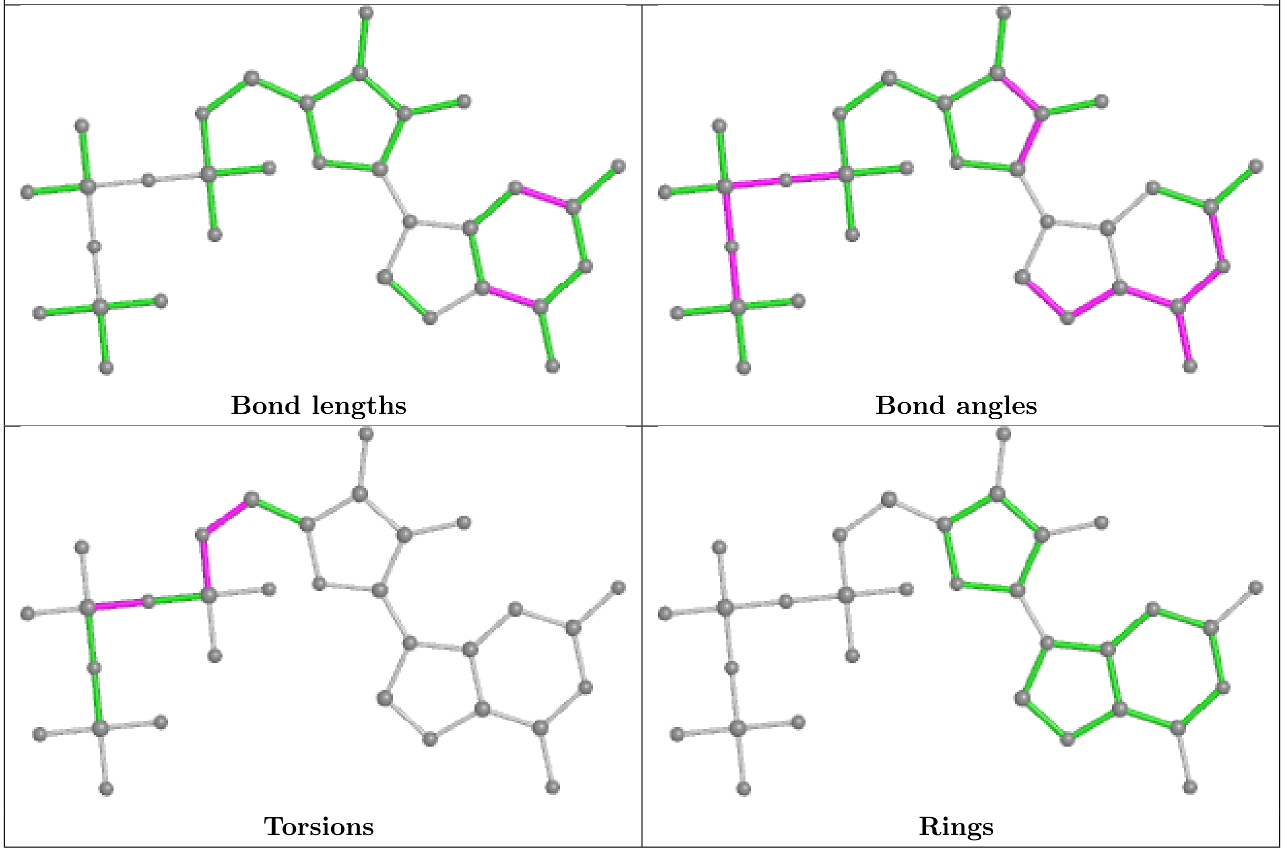

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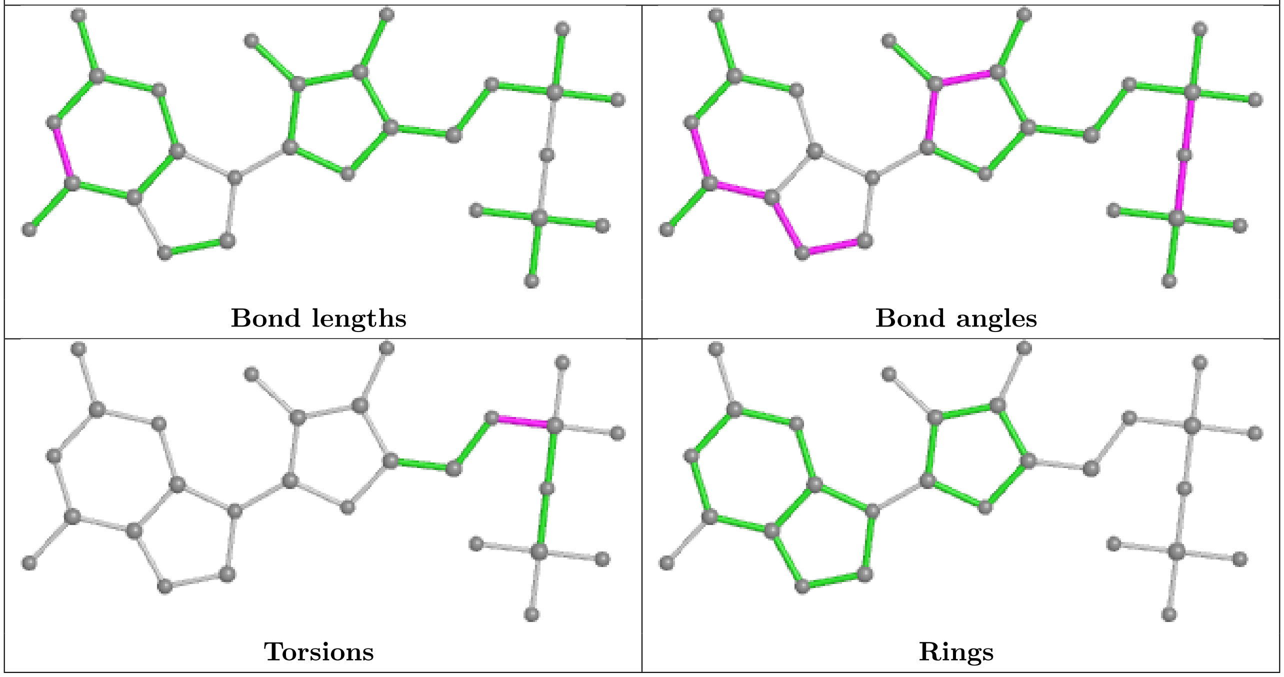

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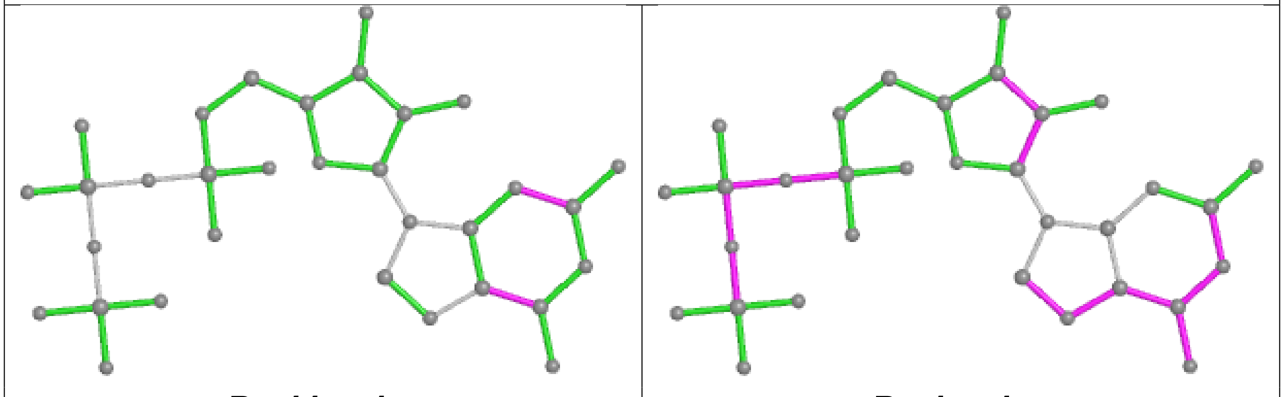

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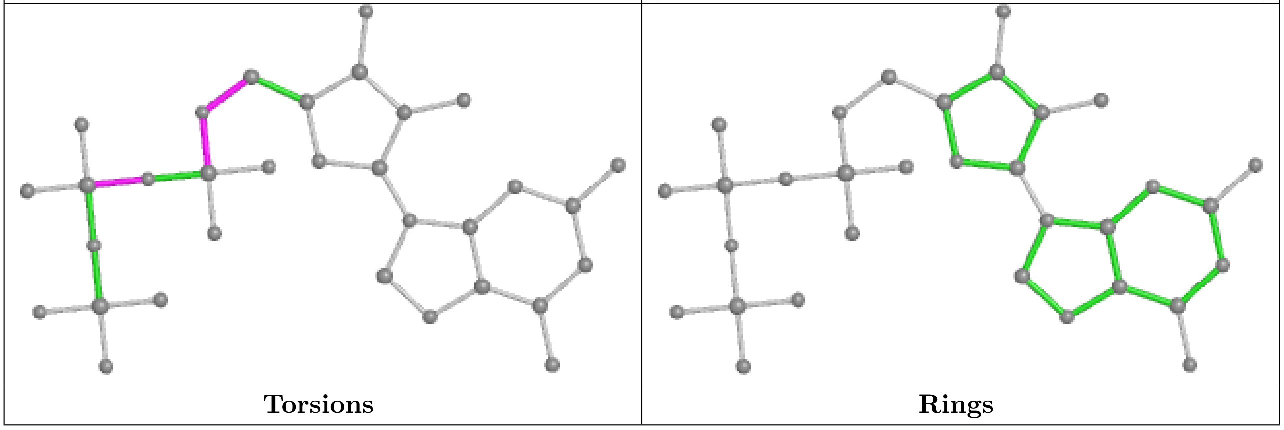
Bond angles



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Rings

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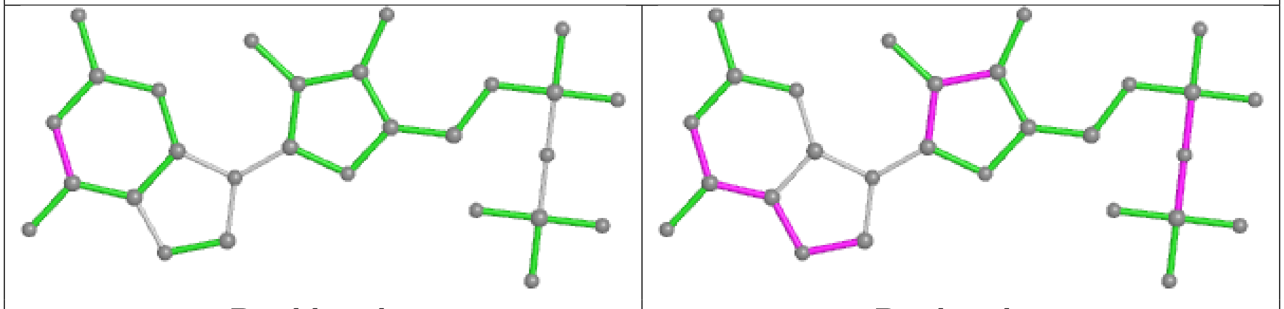

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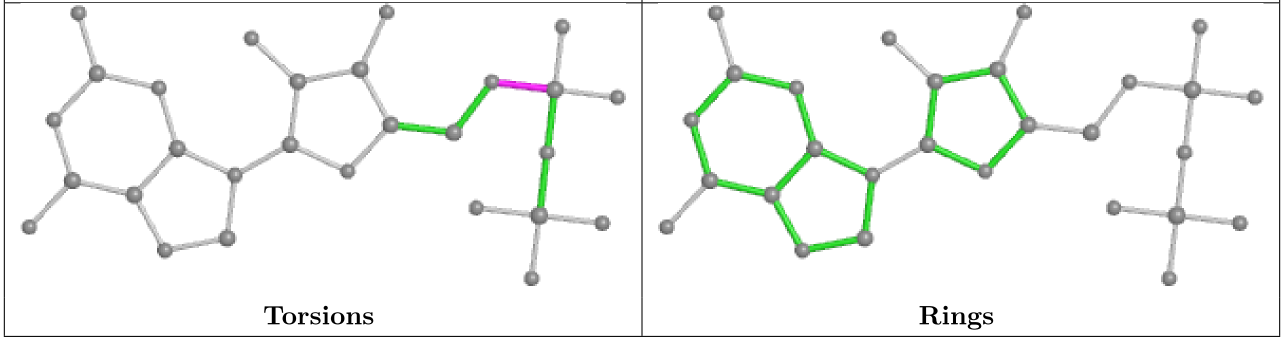

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Rings

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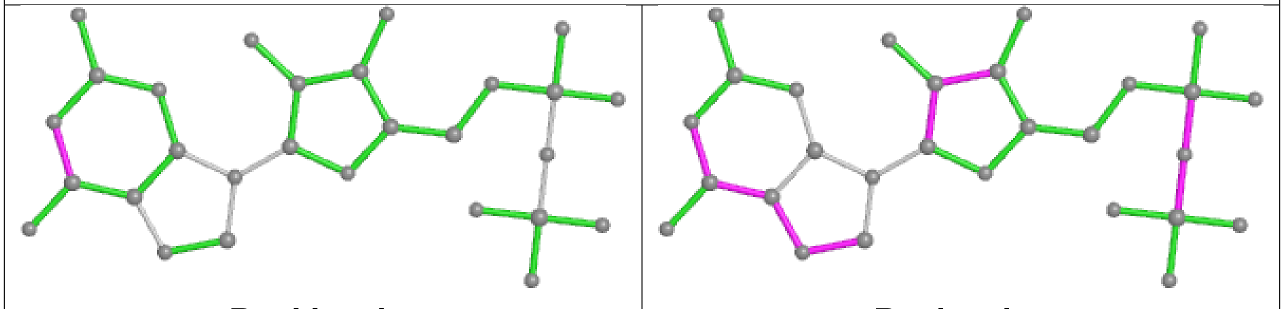

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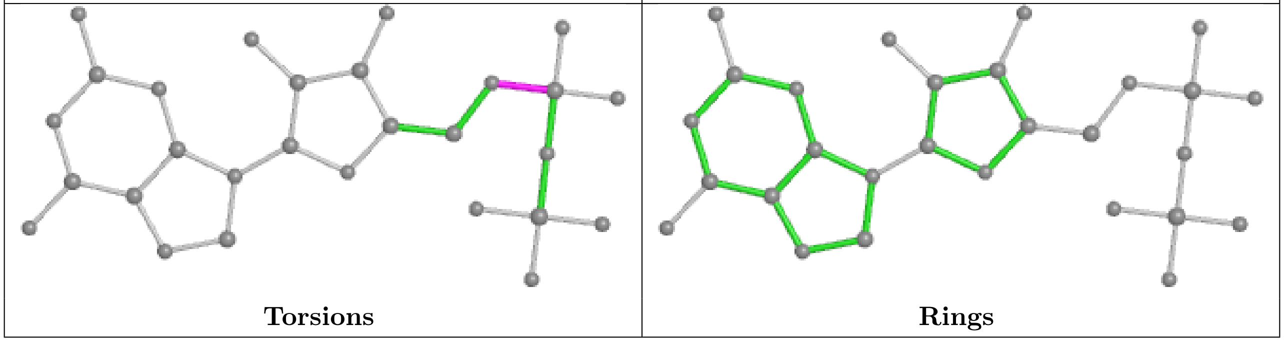

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Rings

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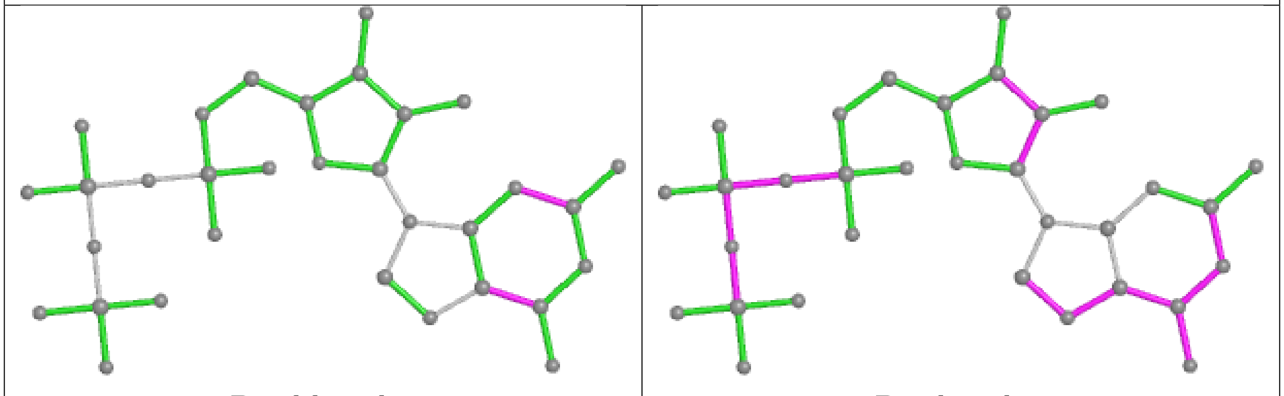

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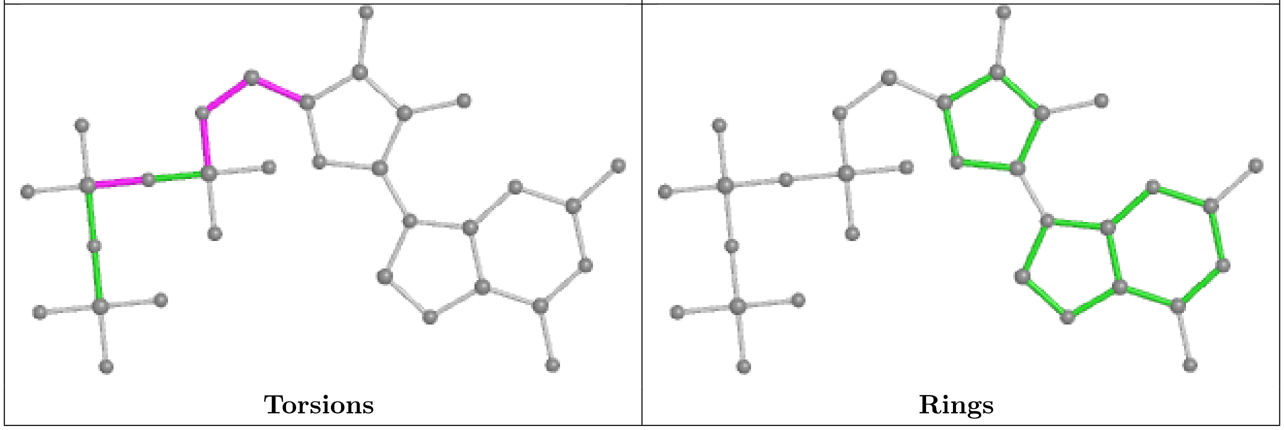

Torsions

Rings

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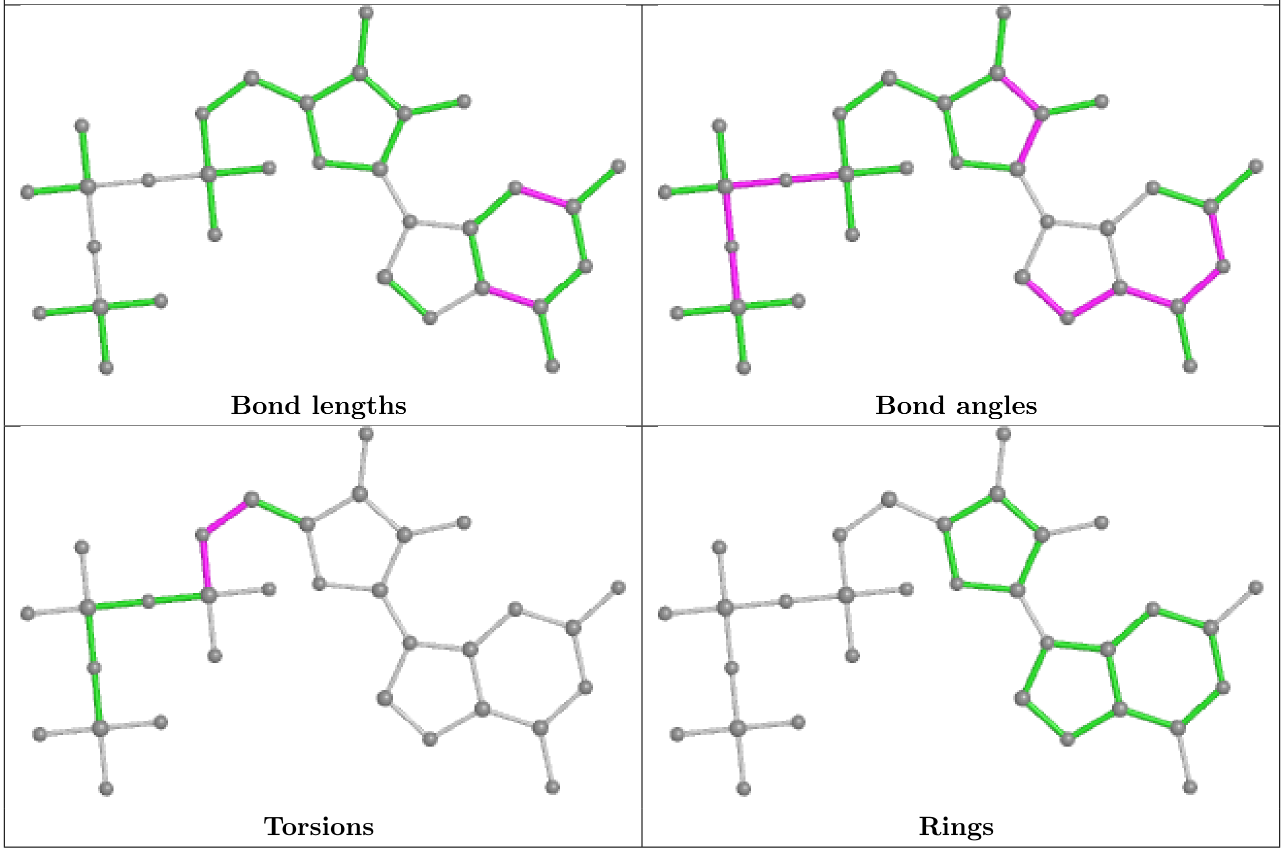

Bond lengths

Bond angles

Torsions

Rings

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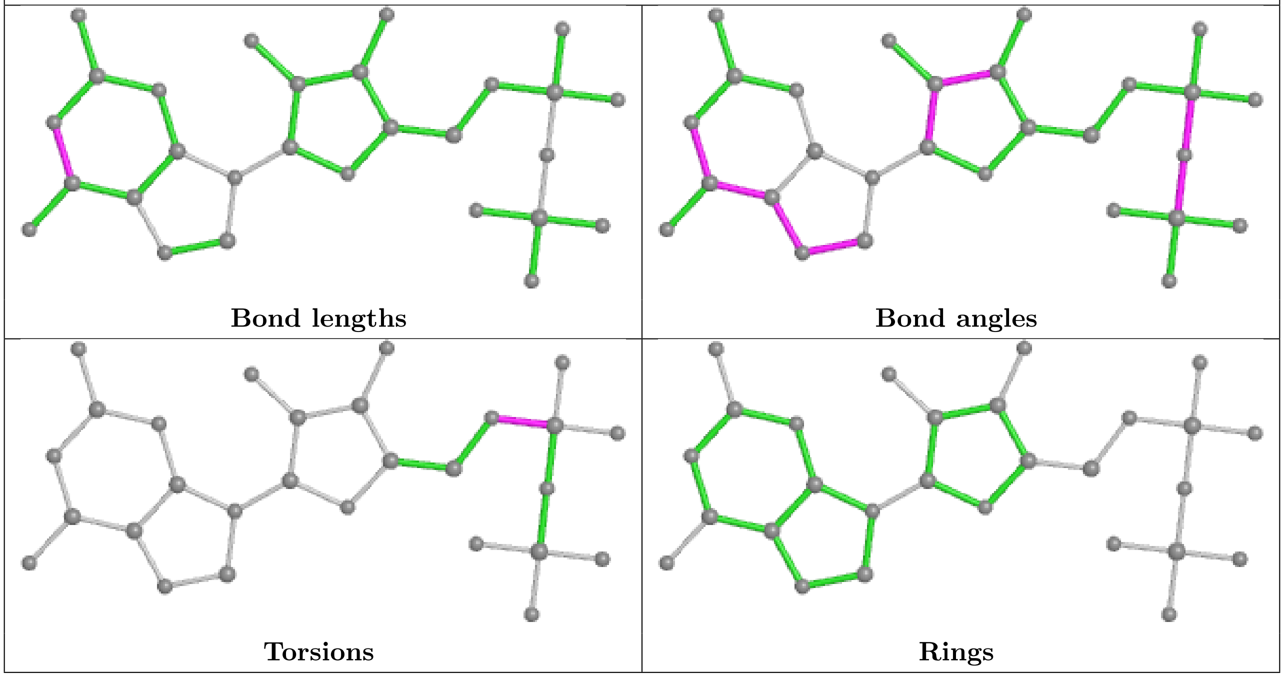

Bond lengths

Bond angles

Torsions

Rings

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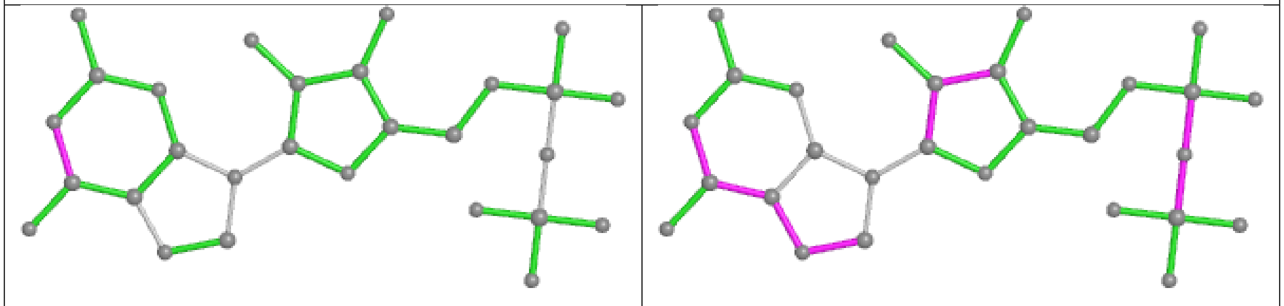
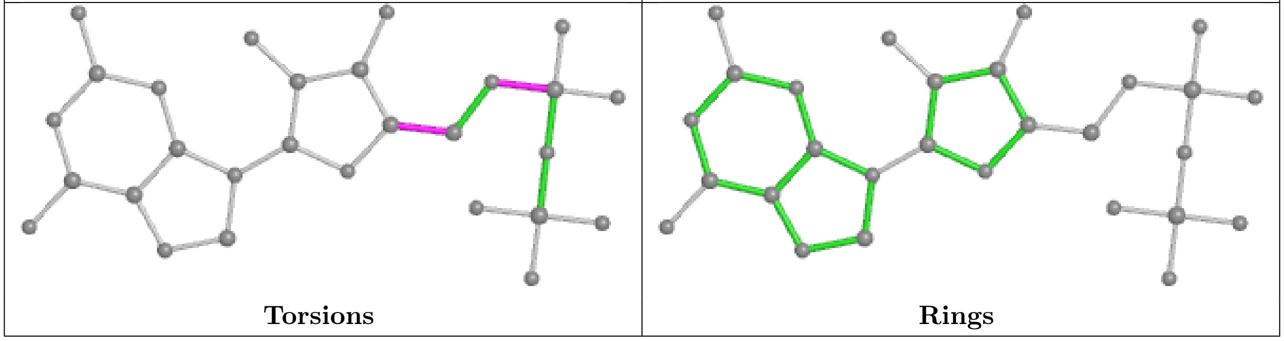
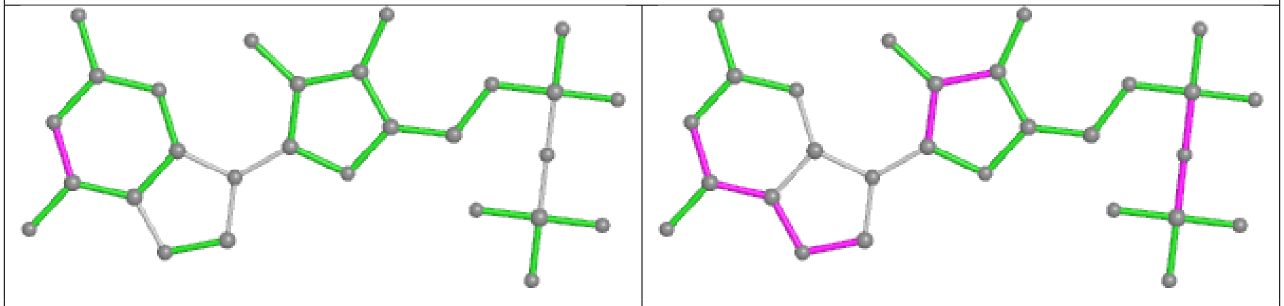


Bond lengths **Bond angles**



Torsions **Rings**

Ligand GDP FB 502



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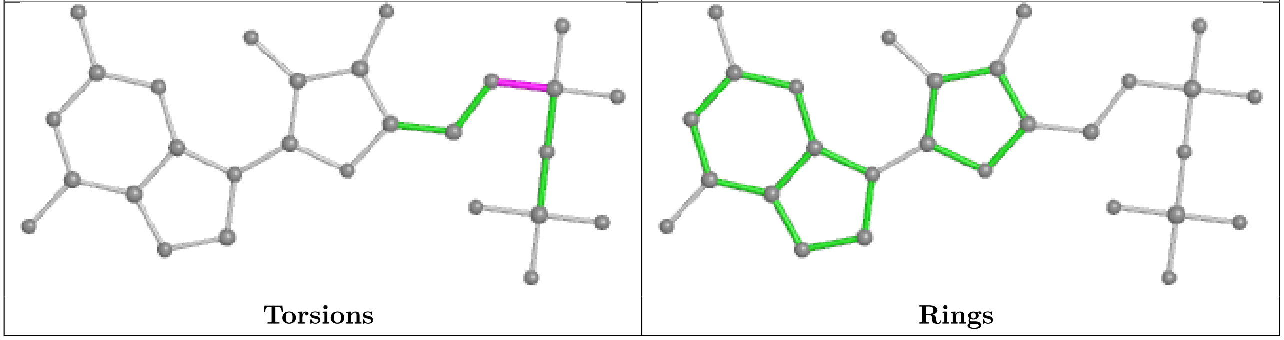

Torsions **Rings**

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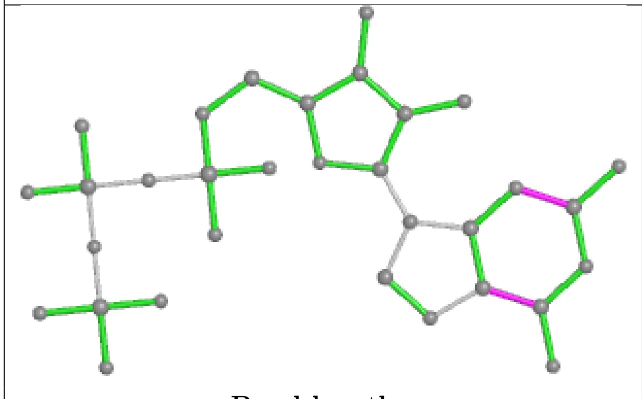

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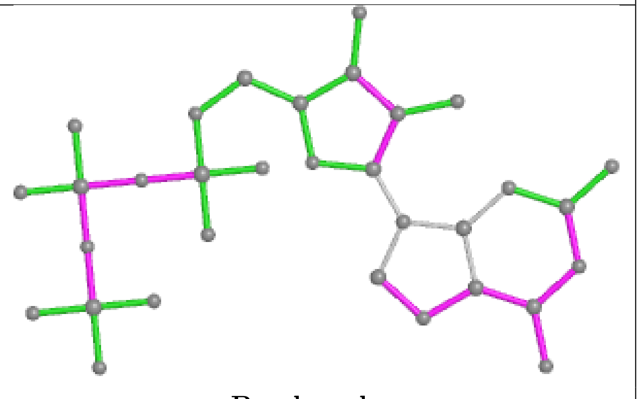

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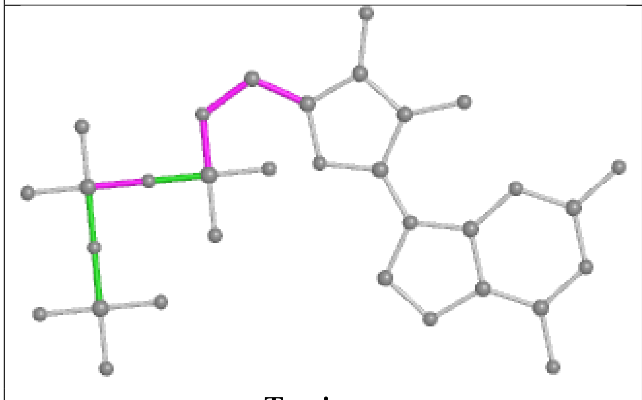

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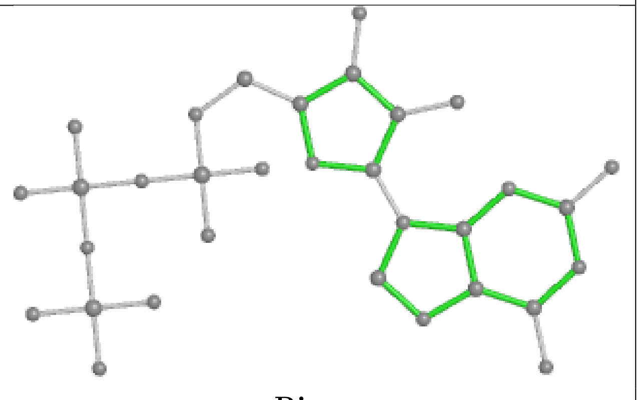

Rings

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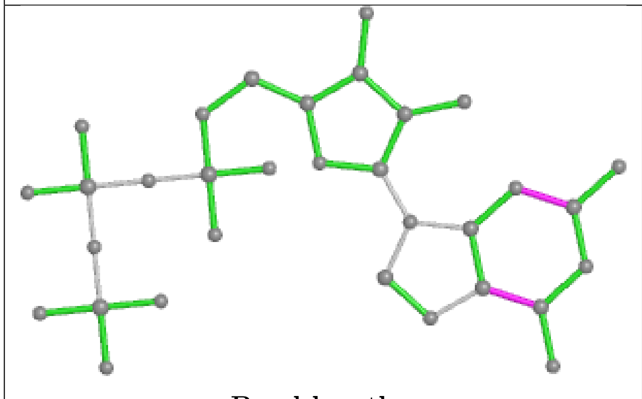

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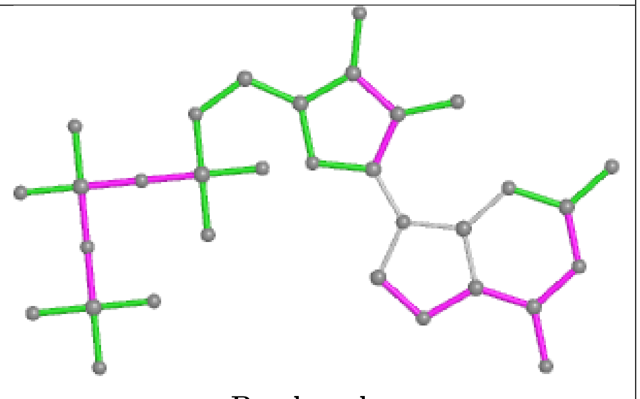

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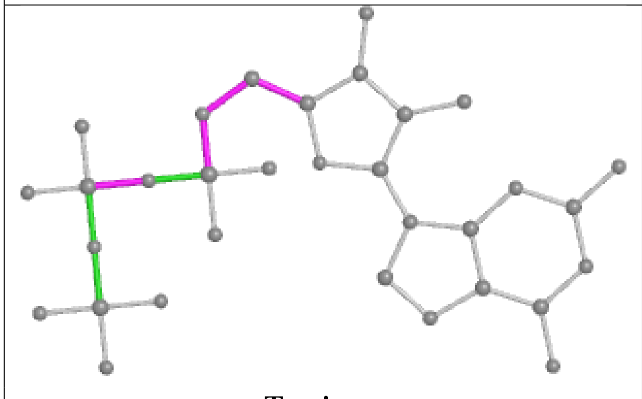

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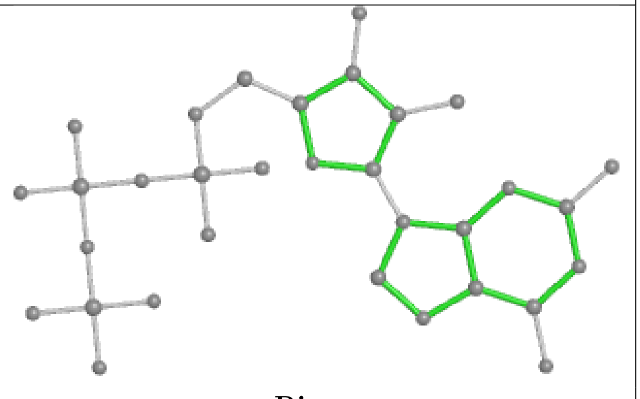

Rings

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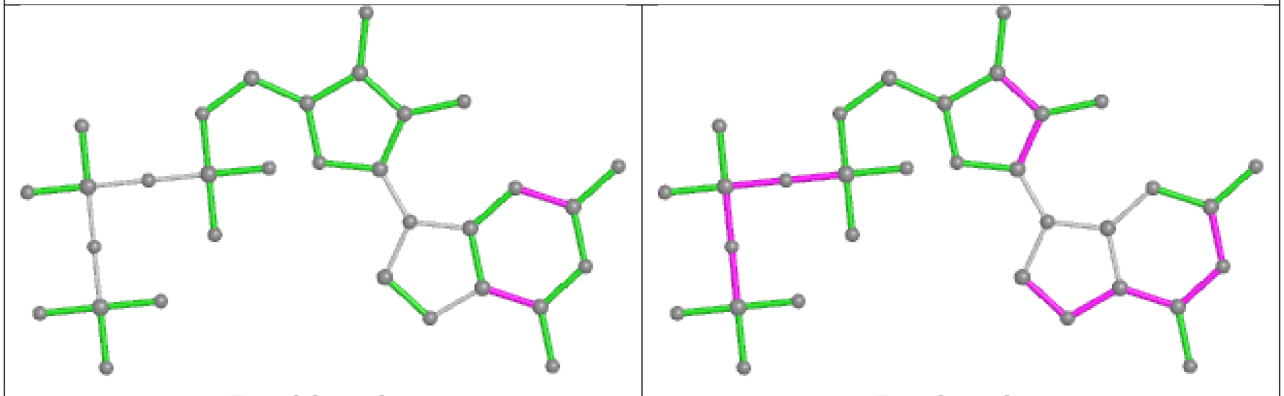

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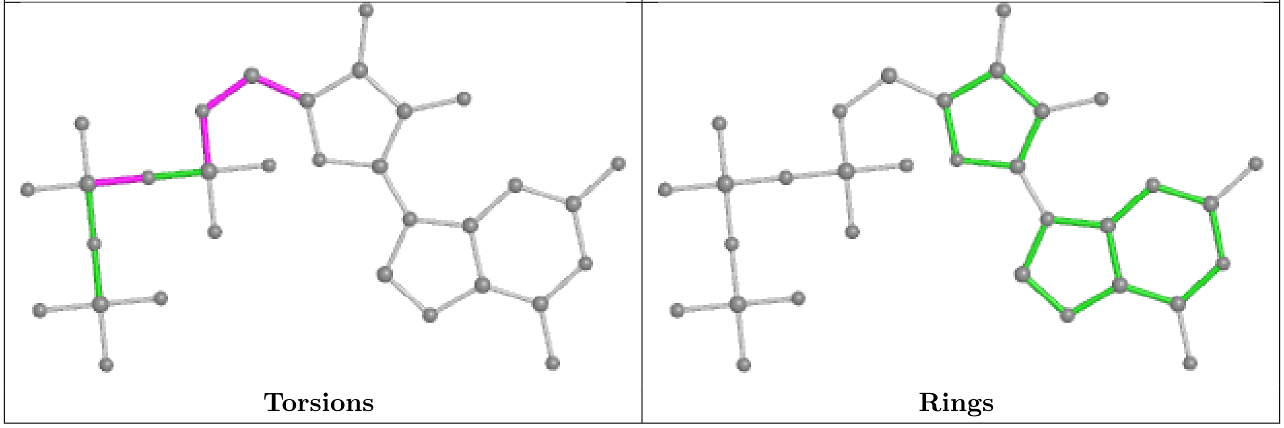
Bond angles



Torsions

Rings

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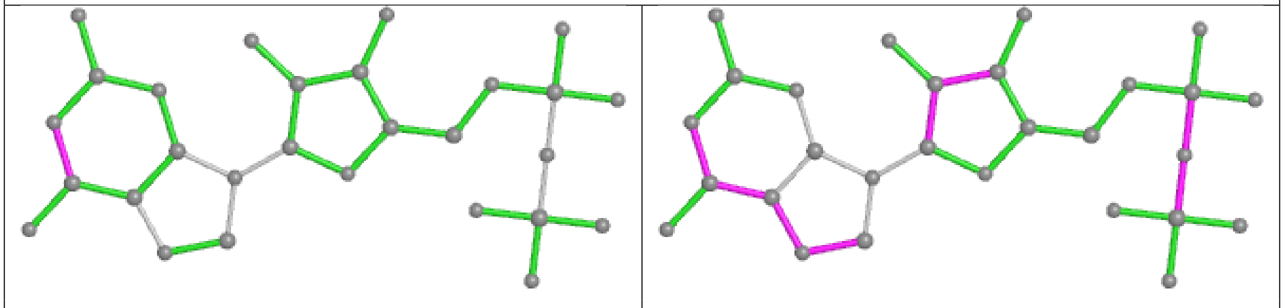

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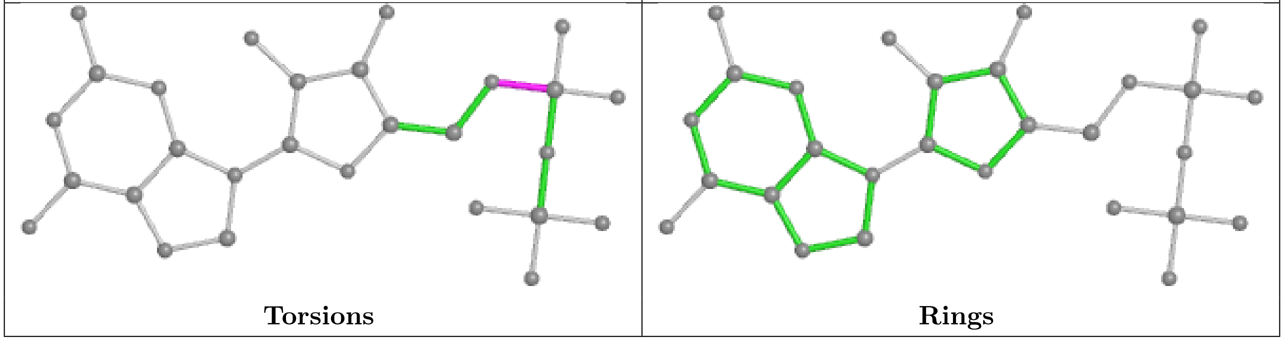

Torsions

Rings

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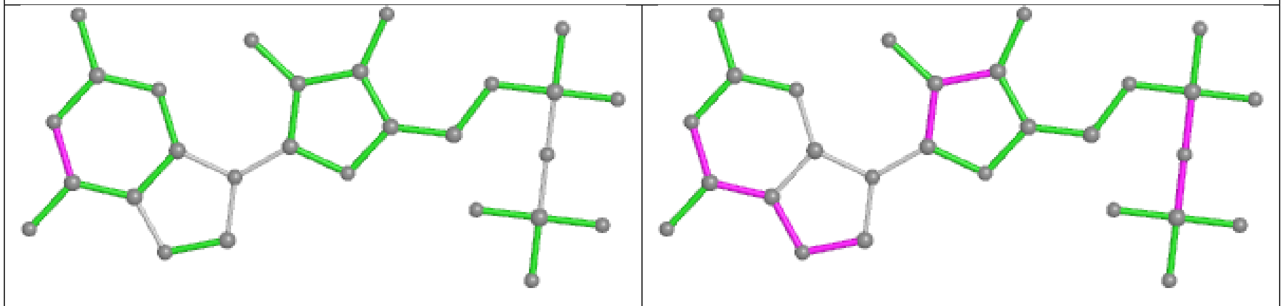

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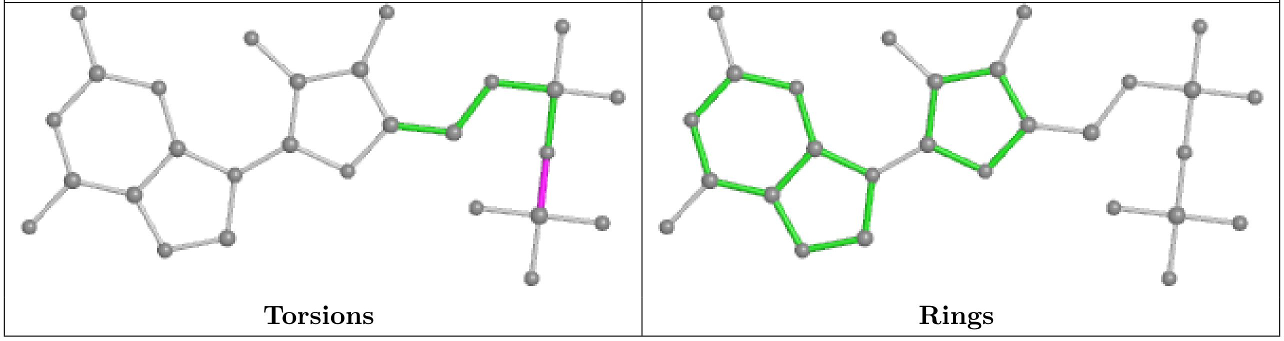

Torsions Rings

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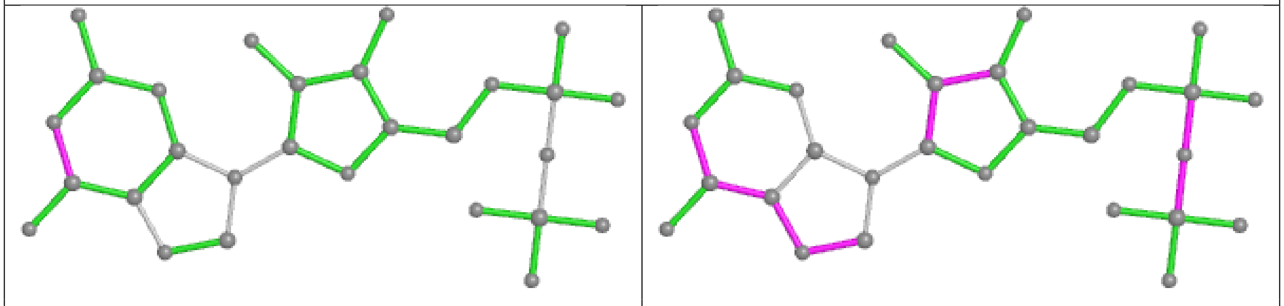

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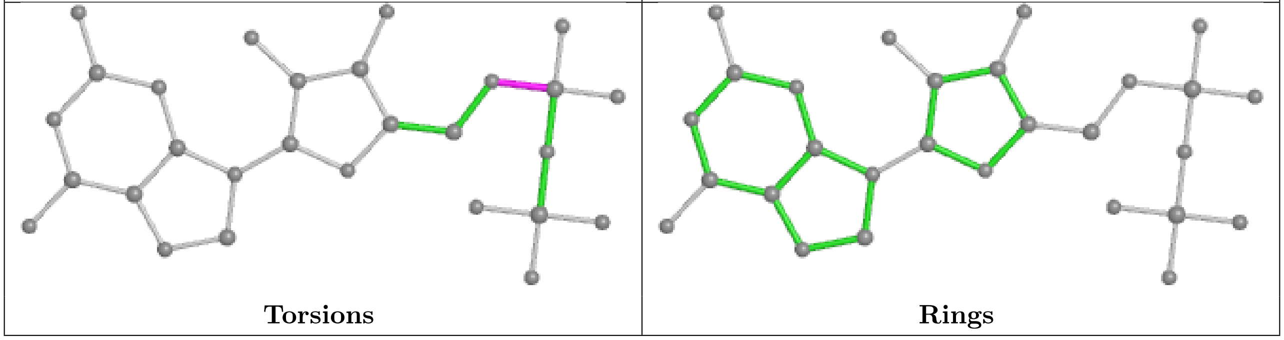

Torsions Rings

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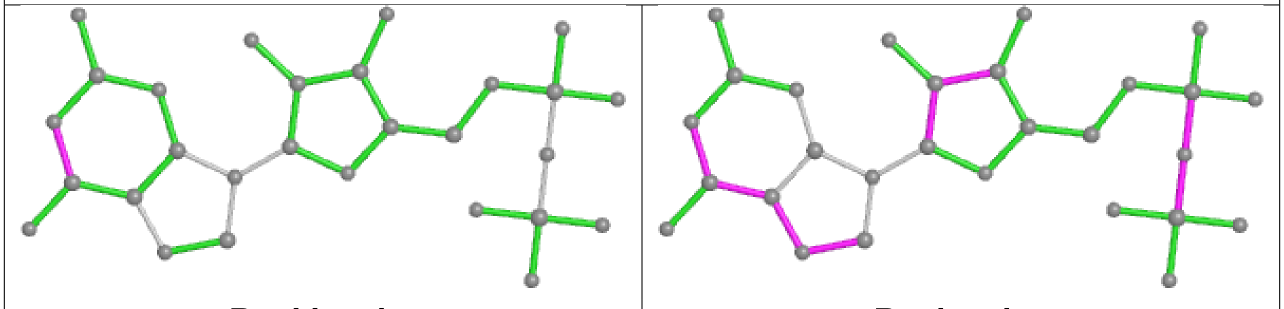
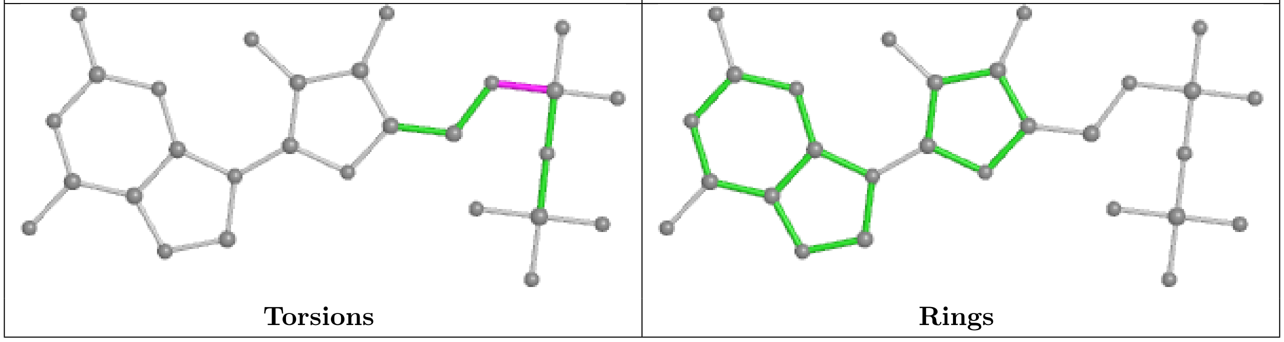


Bond lengths Bond angles



Torsions Rings

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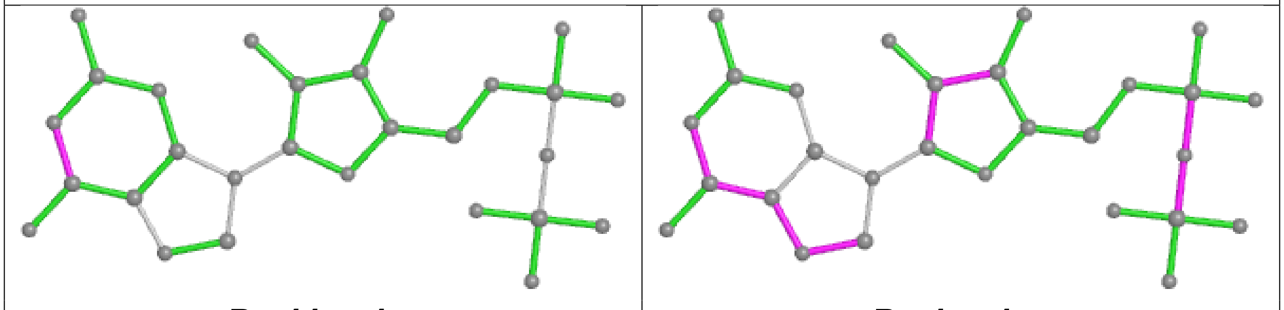

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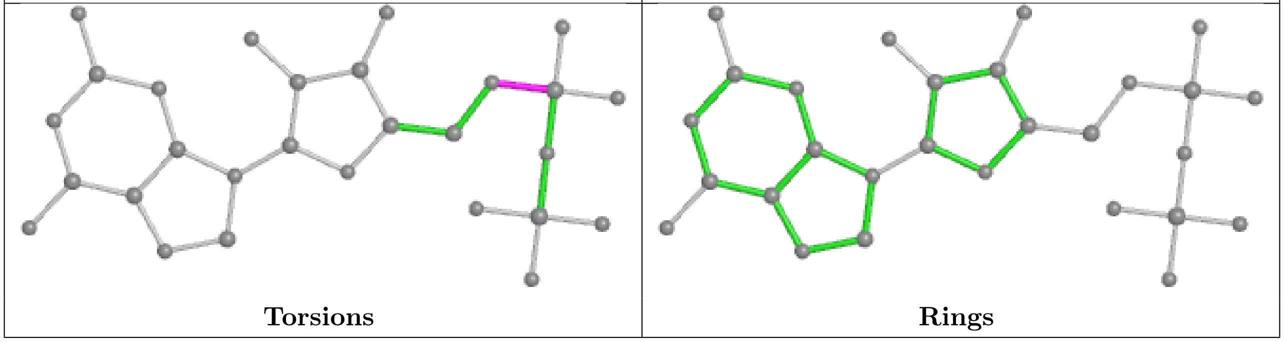

Torsions Rings

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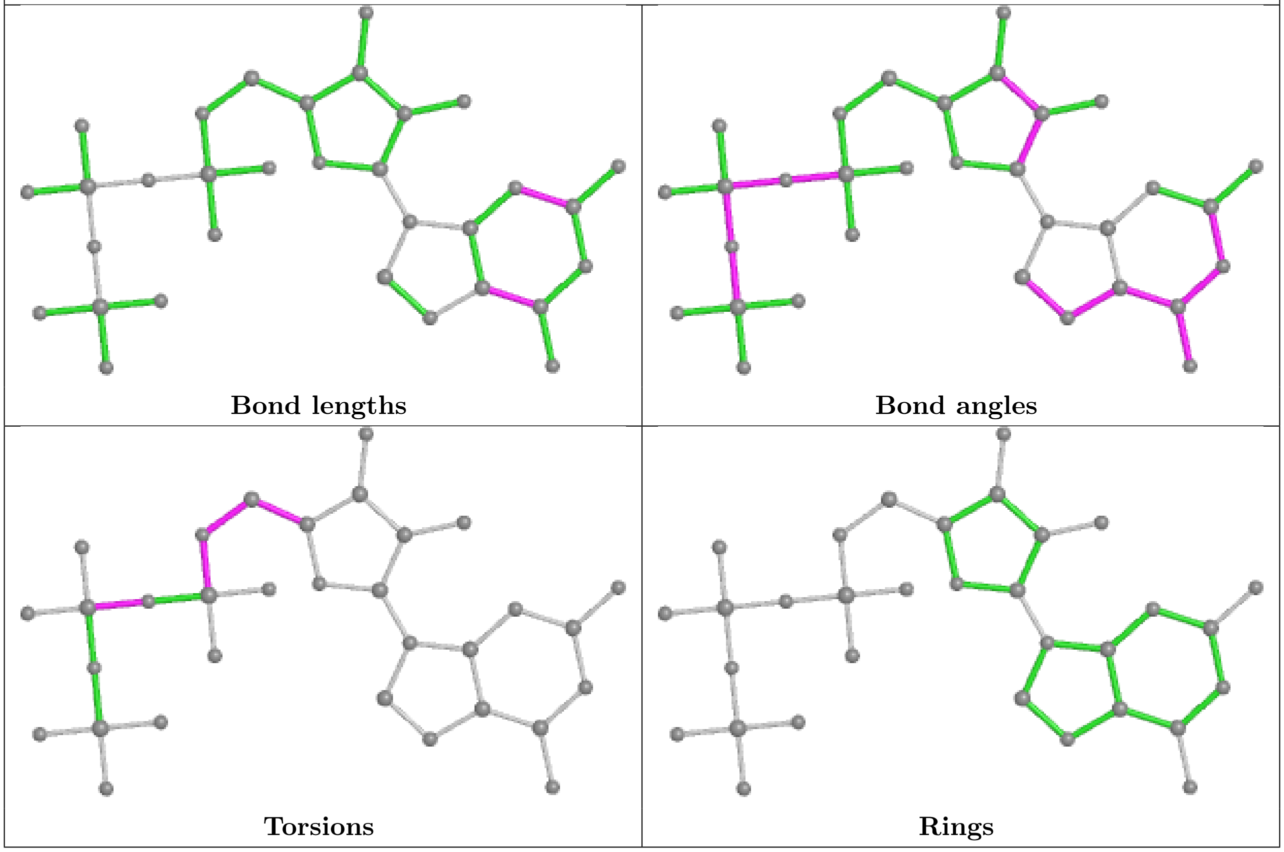
Bond lengths

Bond angles

Torsions

Rings

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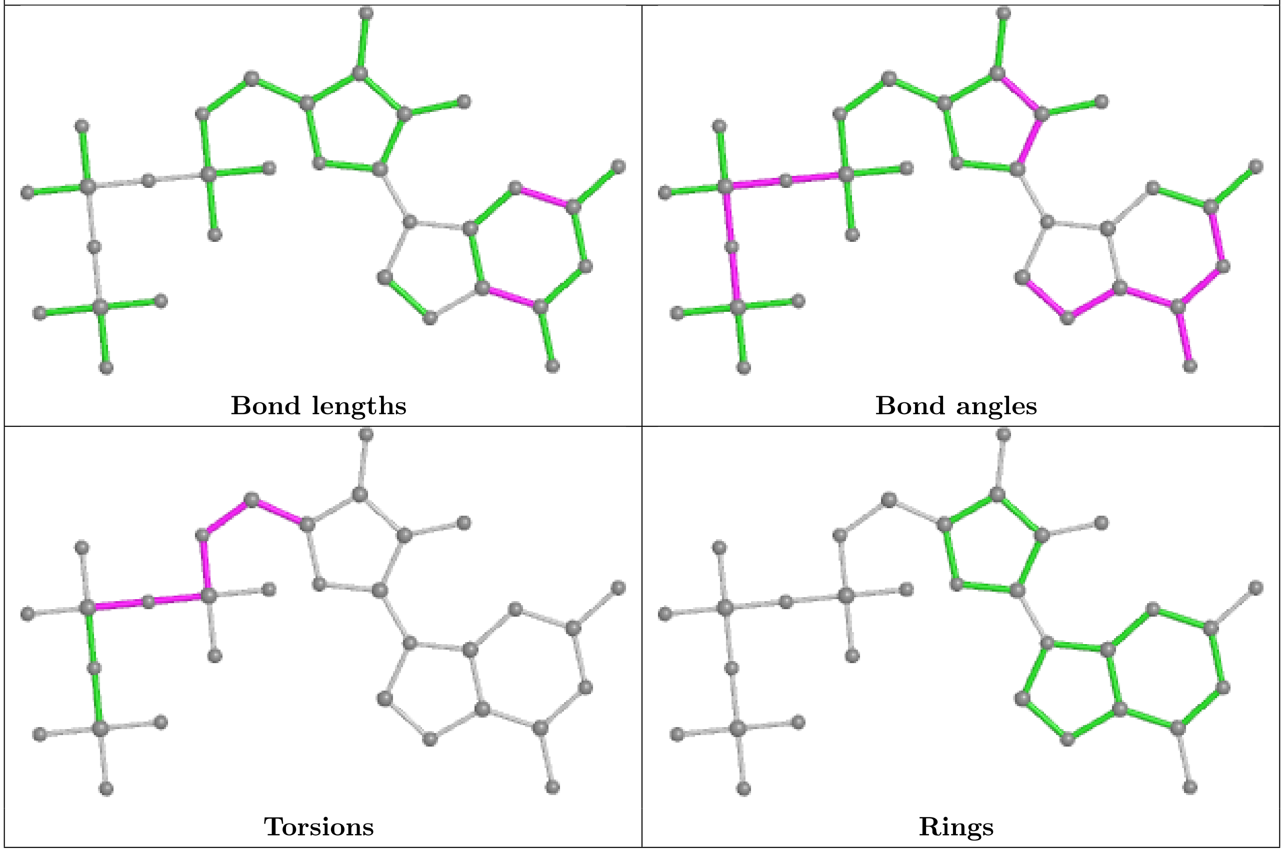
Bond lengths

Bond angles

Torsions

Rings

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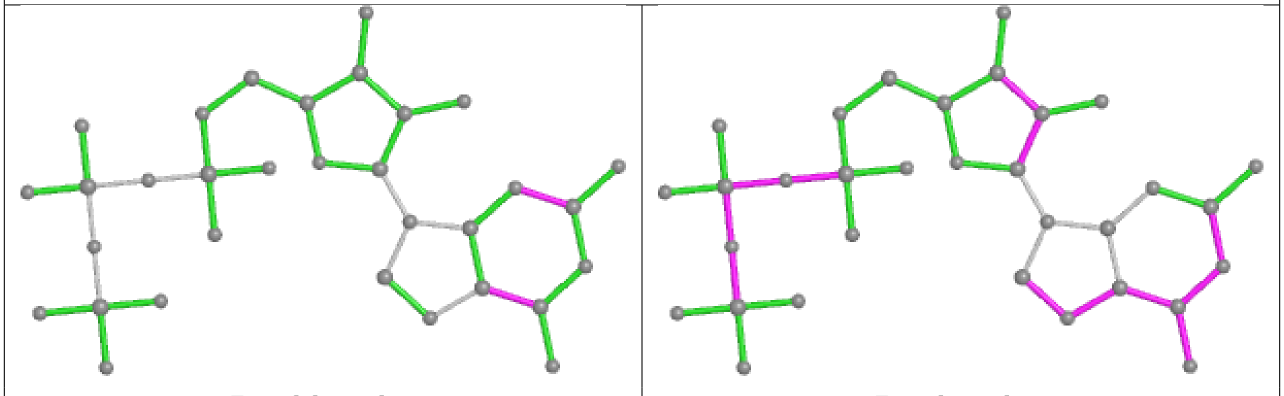

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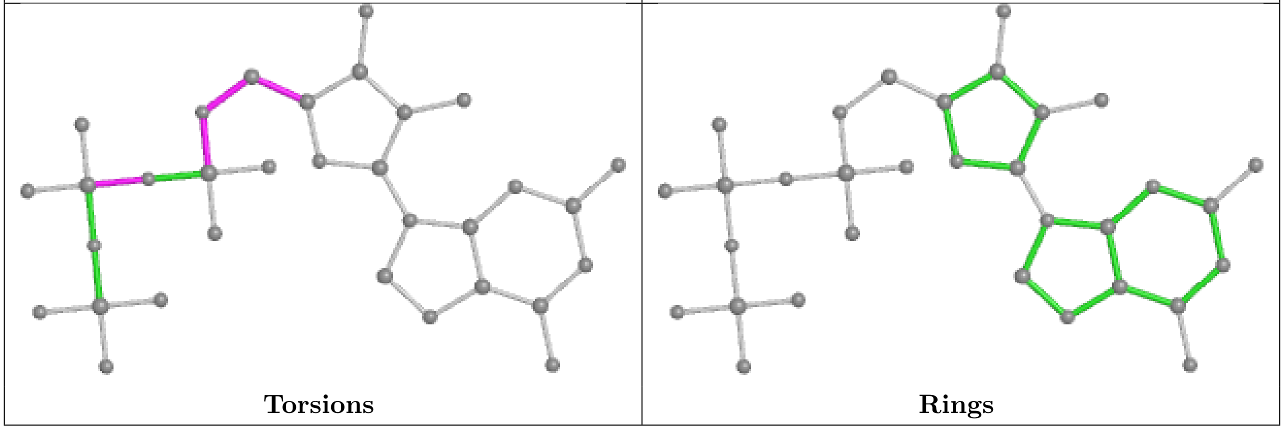
Bond angles



Torsions

Rings

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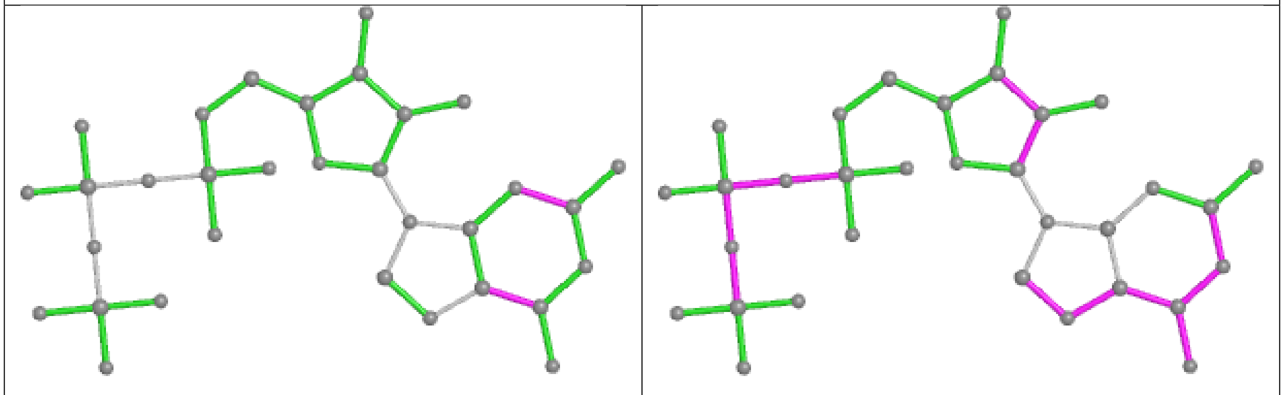

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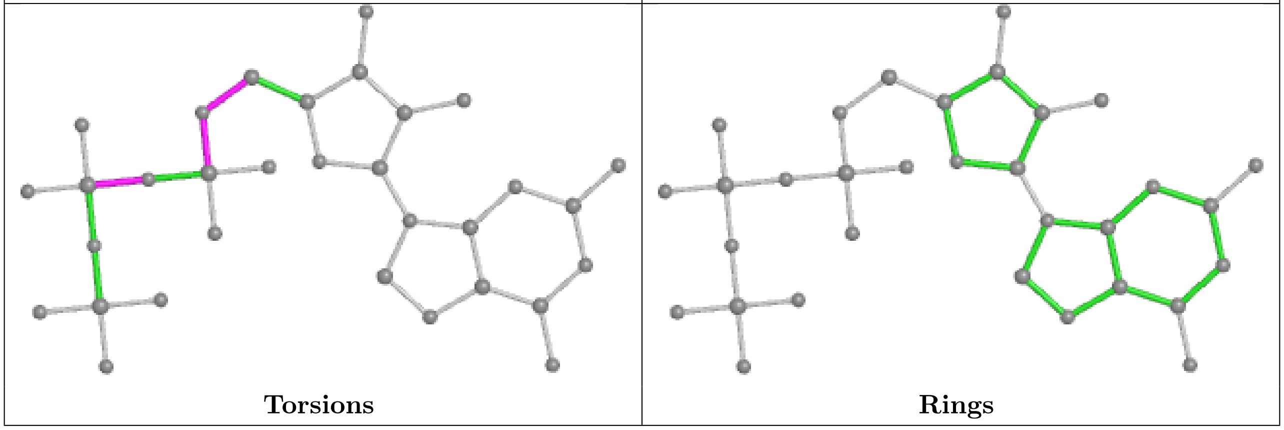
Bond angles



Torsions

Rings

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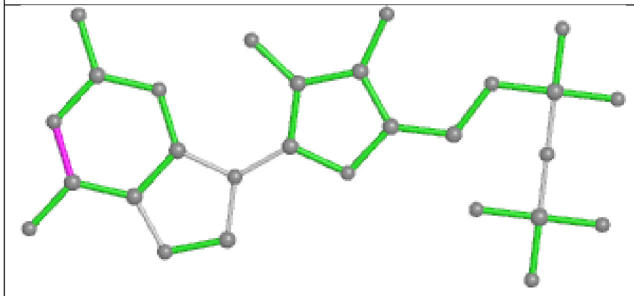

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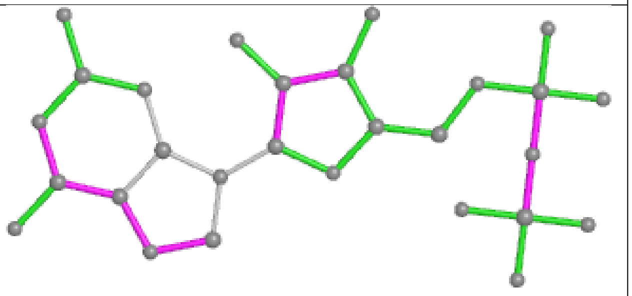

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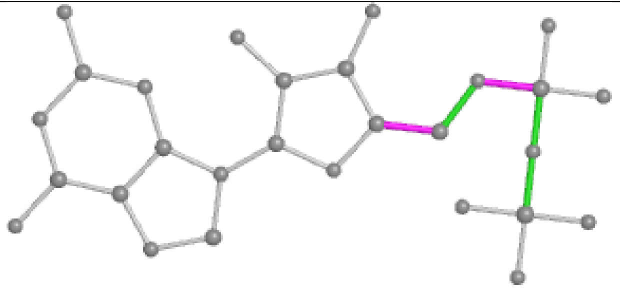

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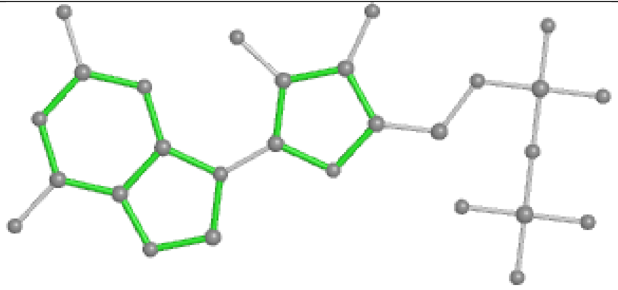

Rings

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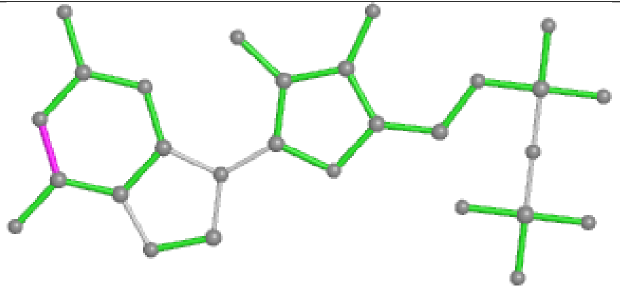

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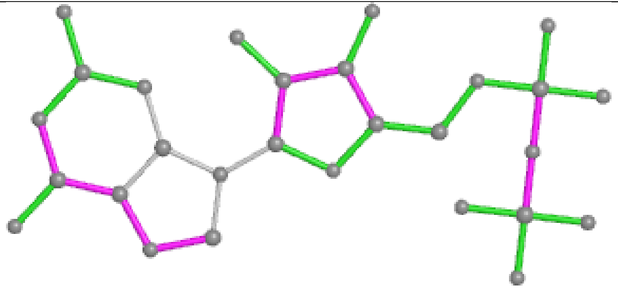

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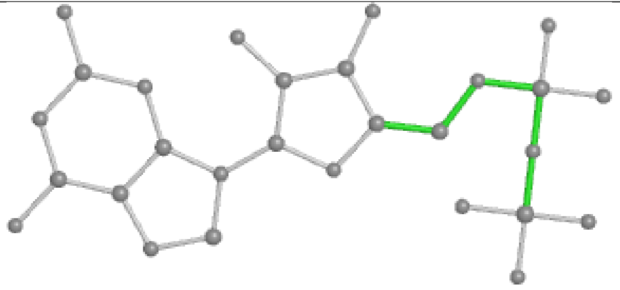

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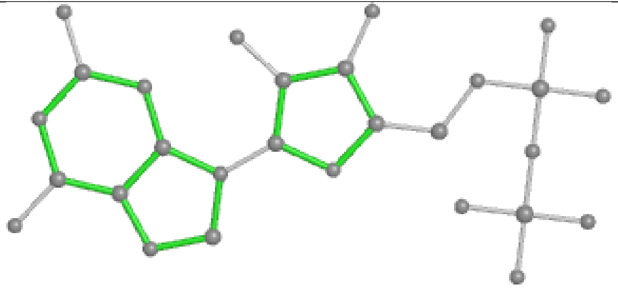

Rings

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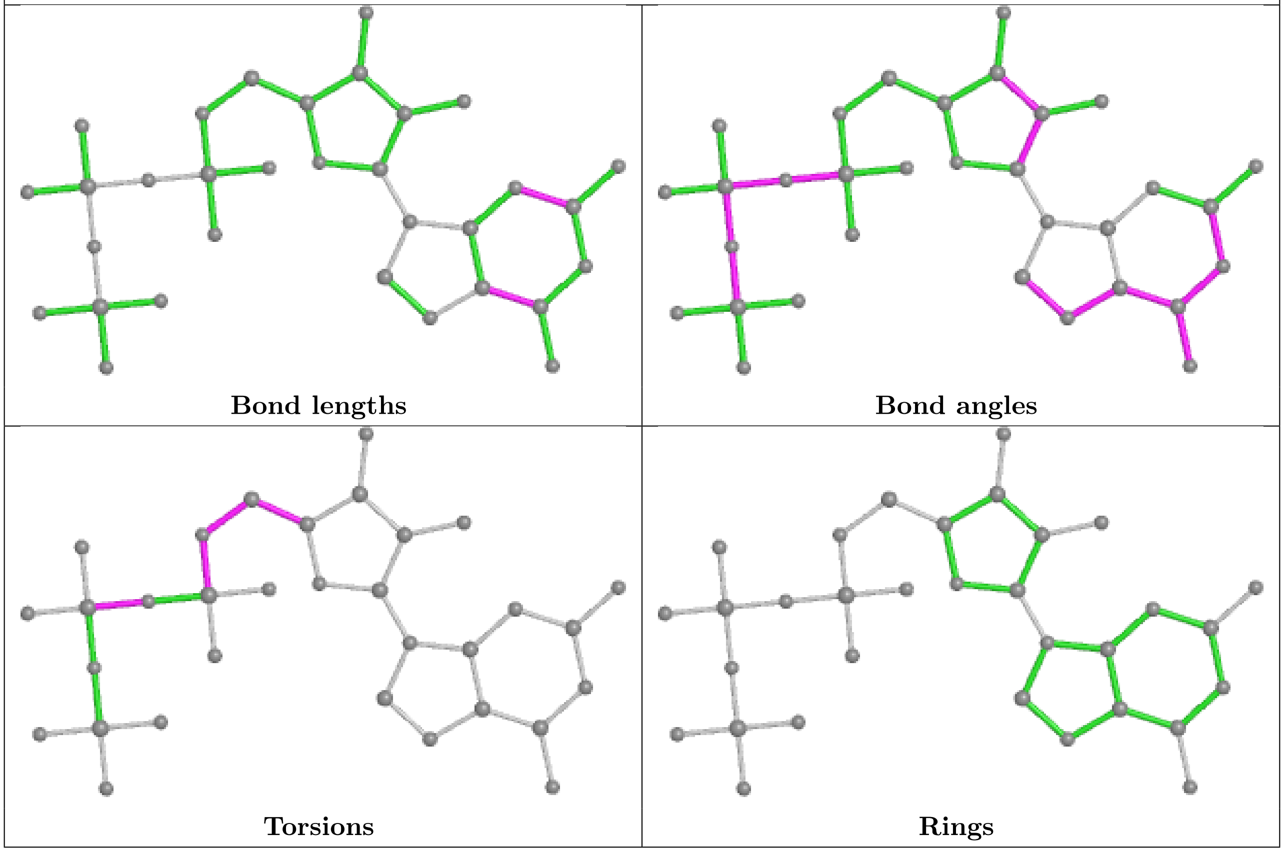

Bond lengths

Bond angles

Torsions

Rings

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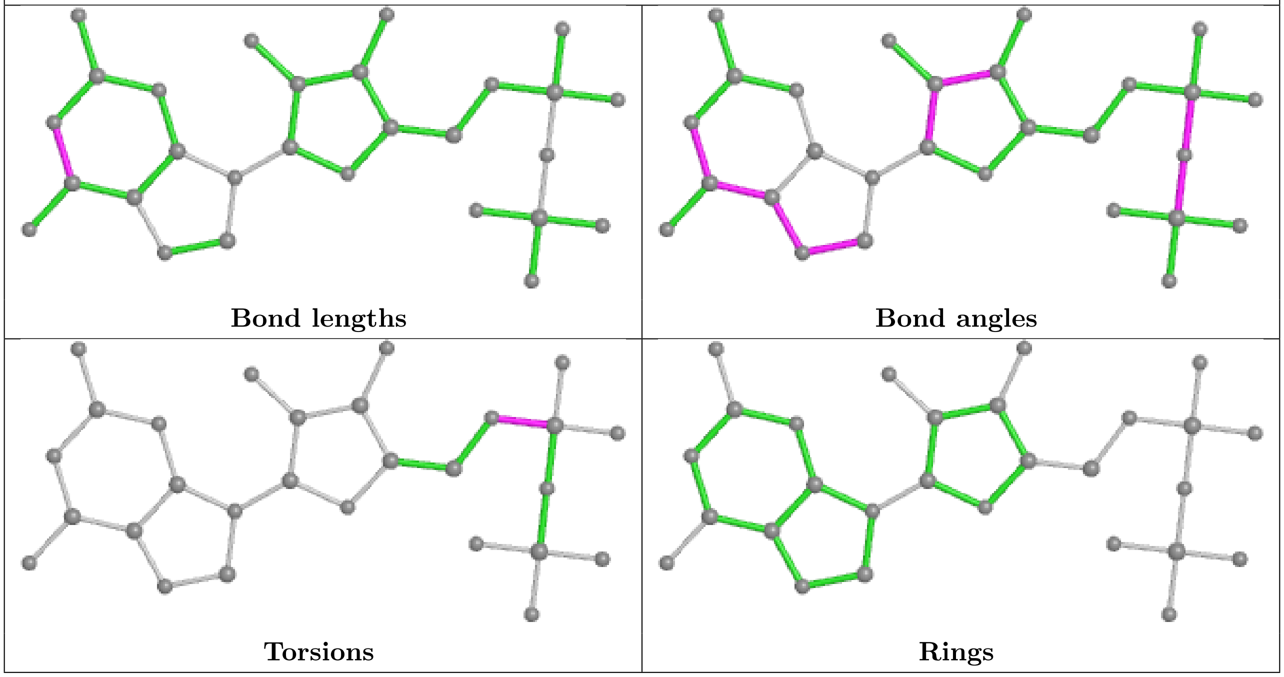

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Bond angles

Torsions

Rings

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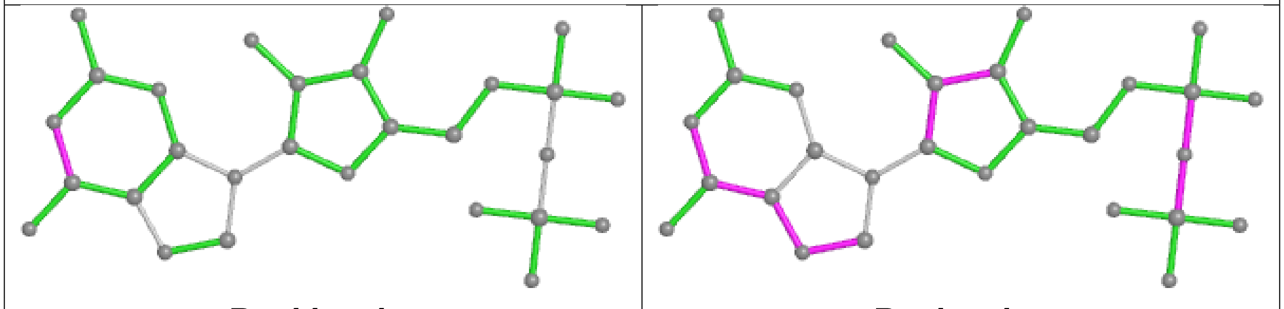

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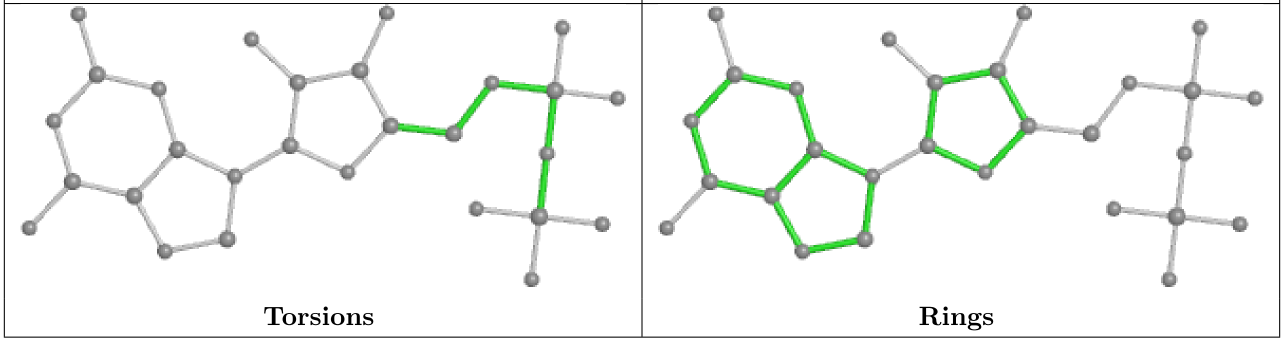

Torsions

Rings

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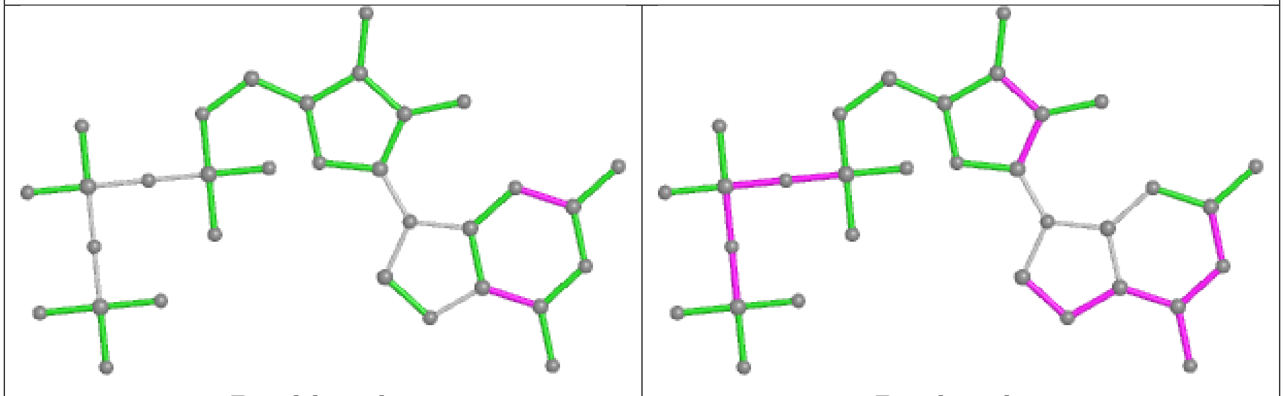
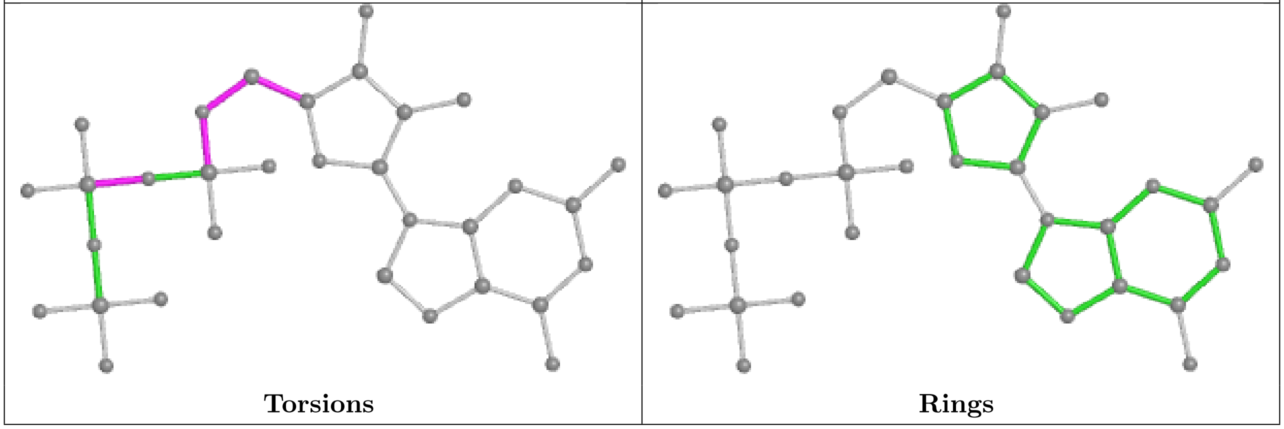


Bond lengths

Bond angles



Torsions

Rings

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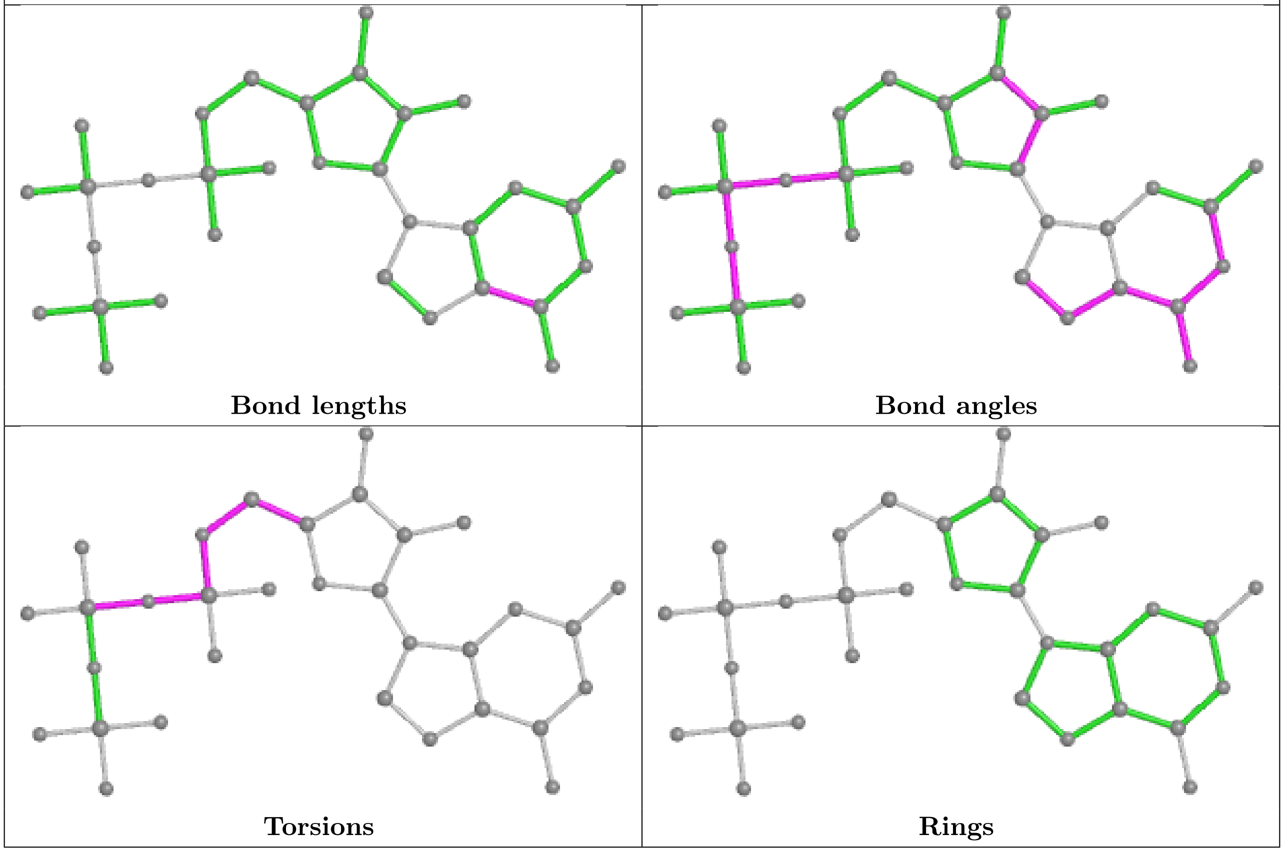

Bond lengths

Bond angles

Torsions

Rings

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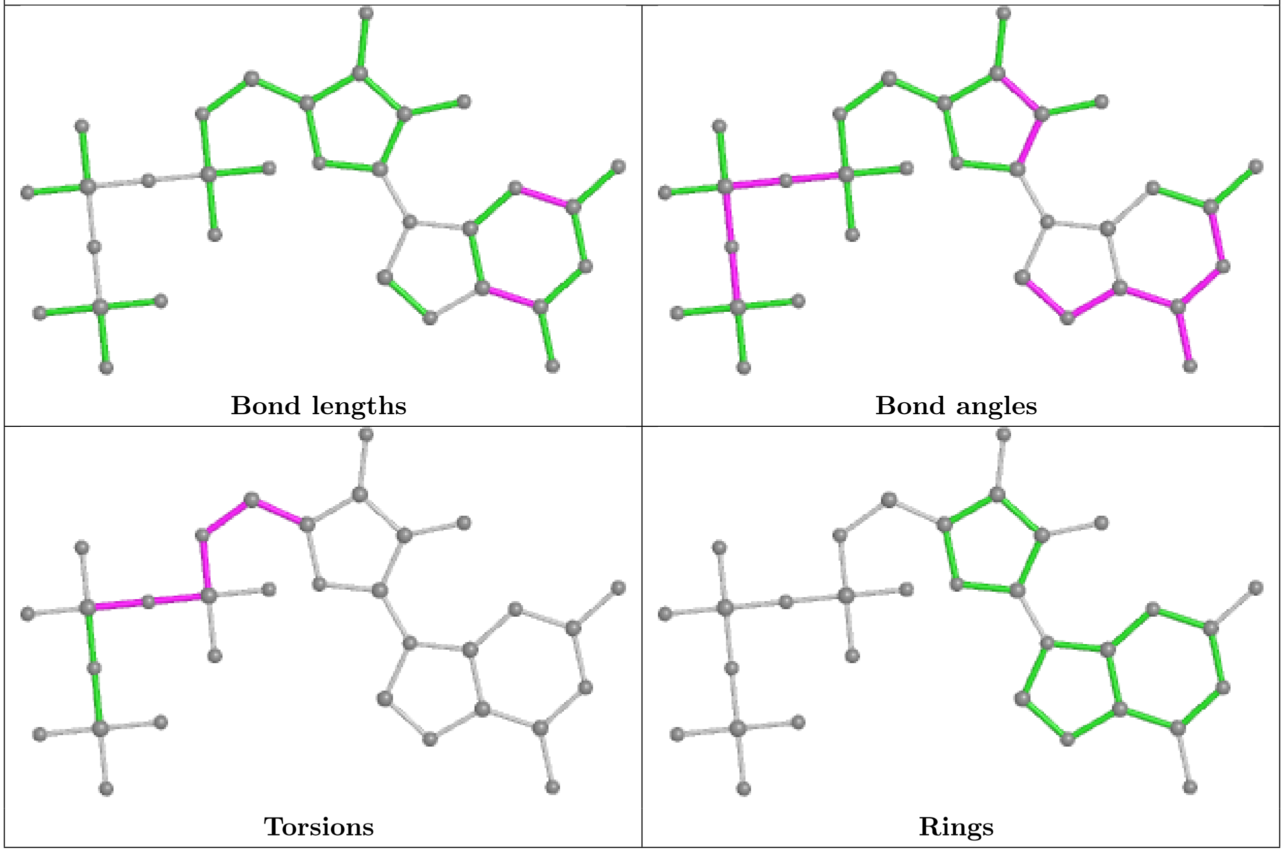


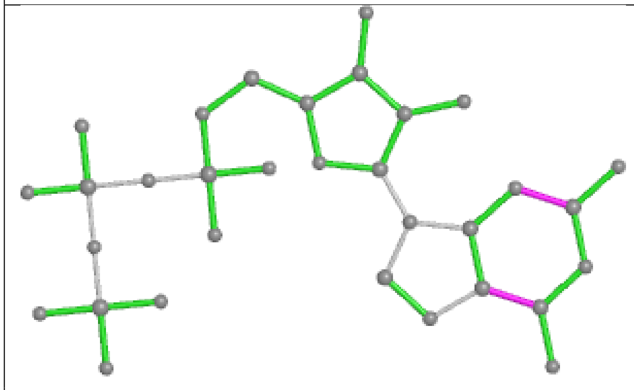
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP EC 501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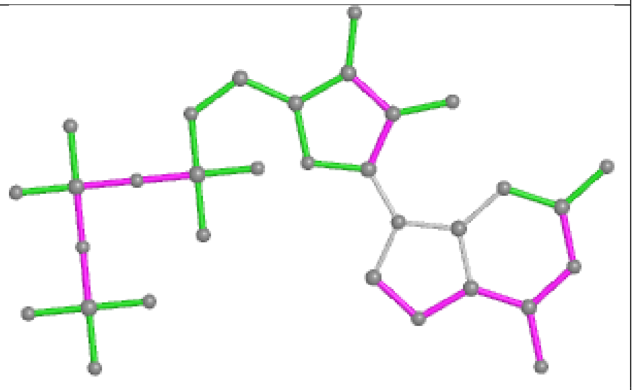
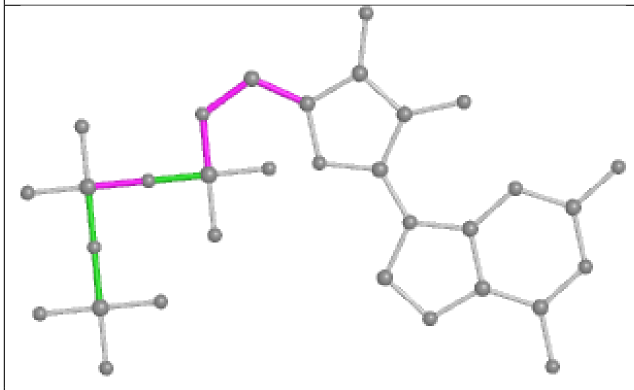
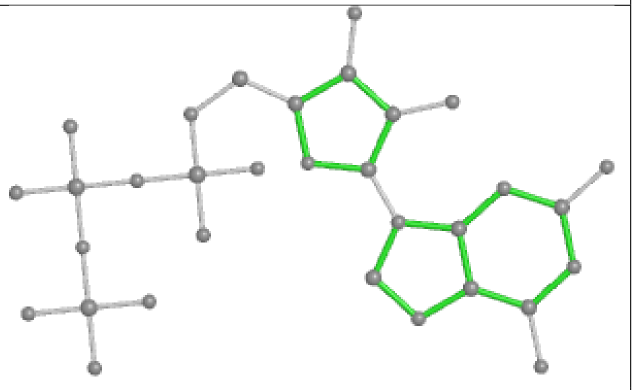
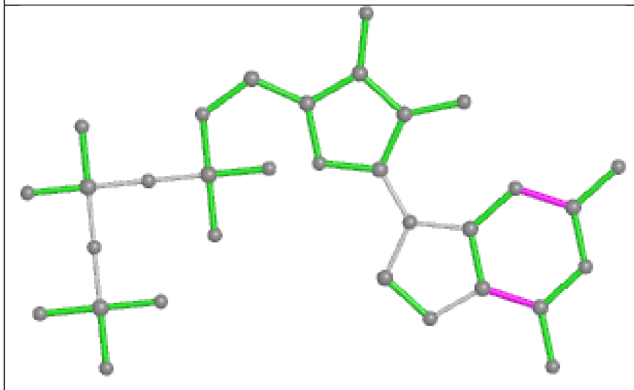

Bond angles


Torsions


Rings

Ligand GTP DI 501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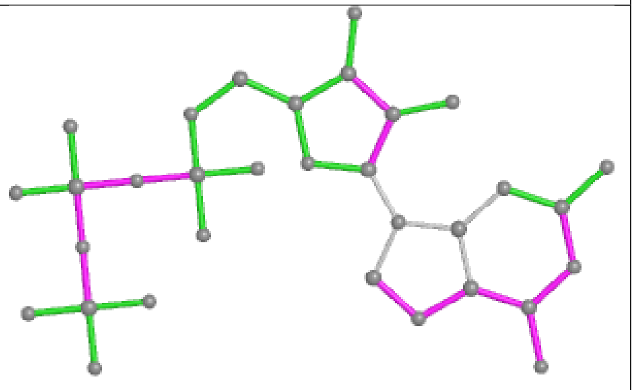
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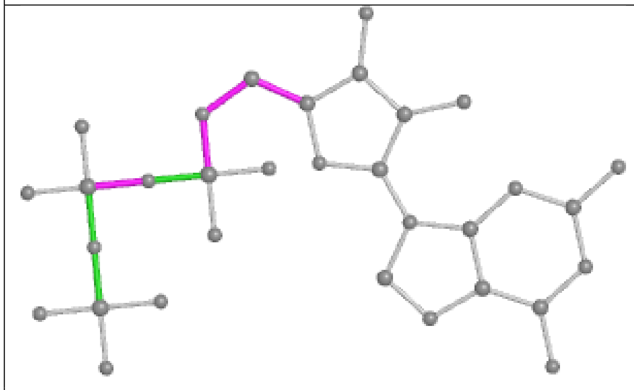
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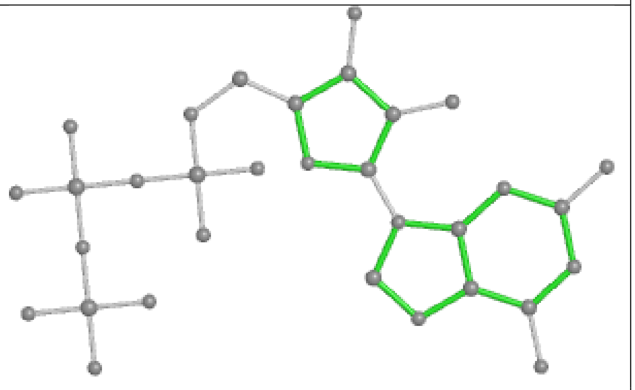
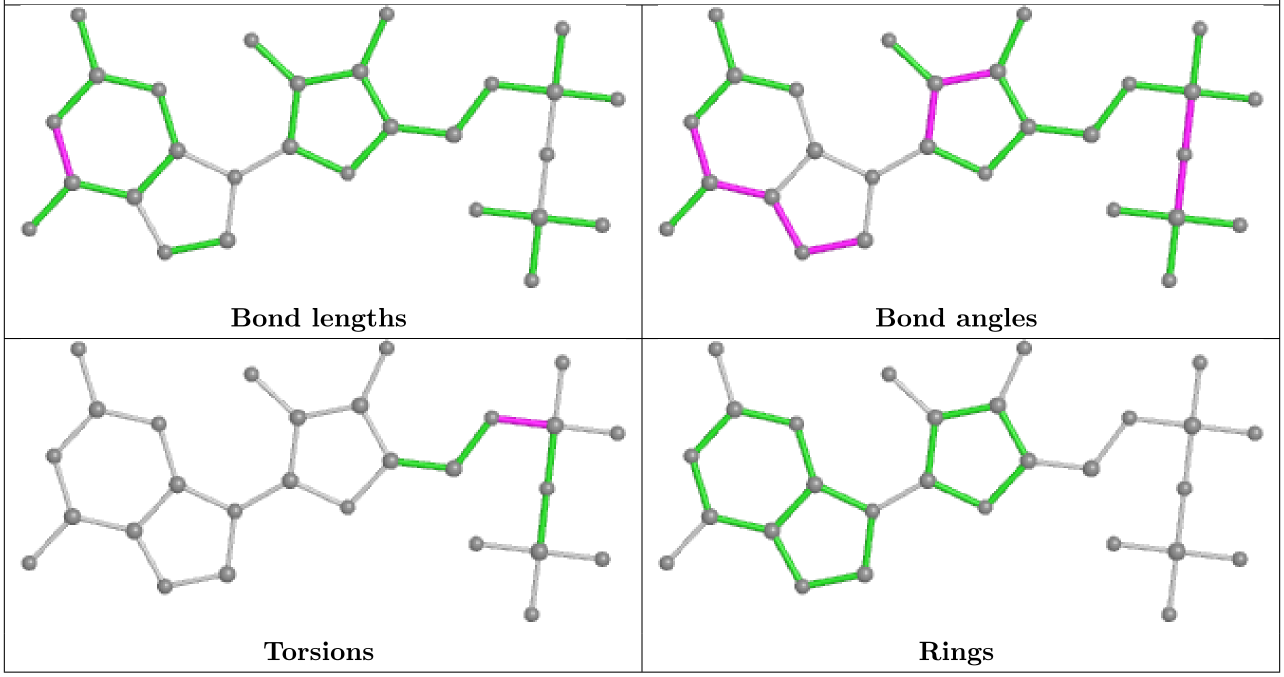

Rings

Ligand GDP NF 502



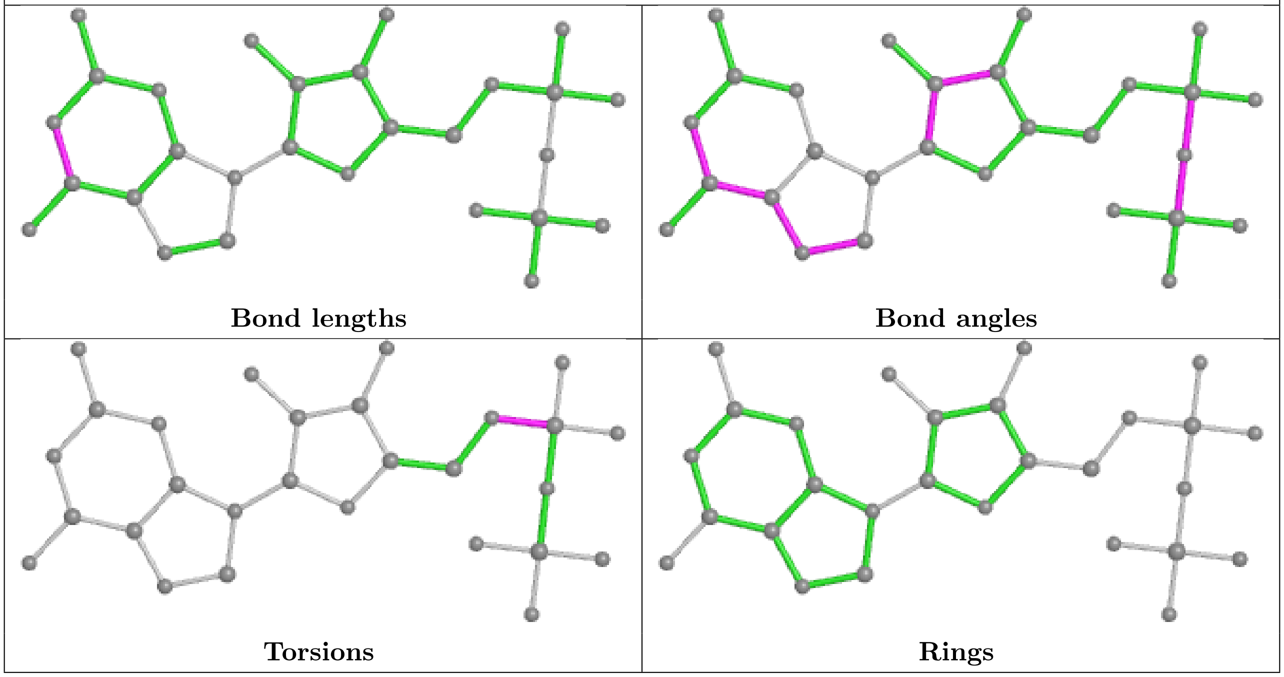
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP NH 502



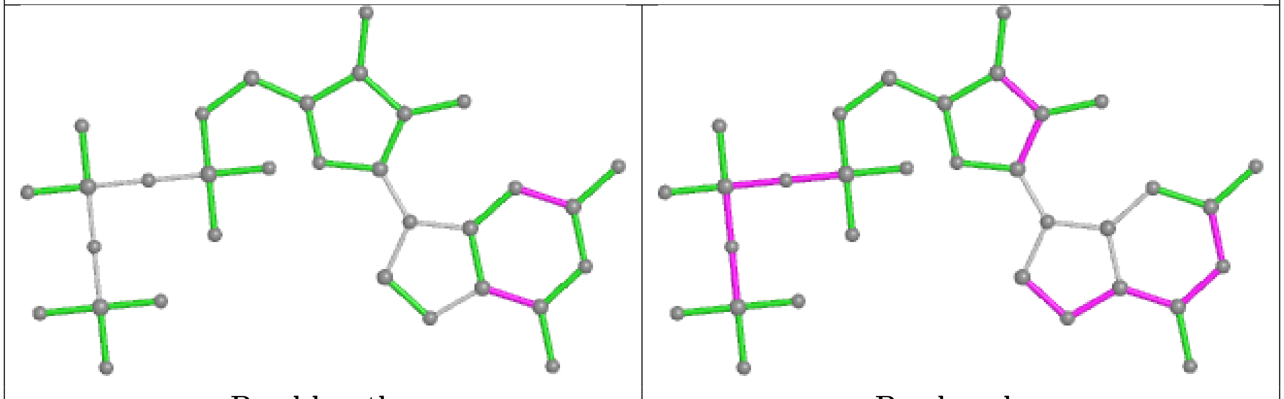
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP UE 501



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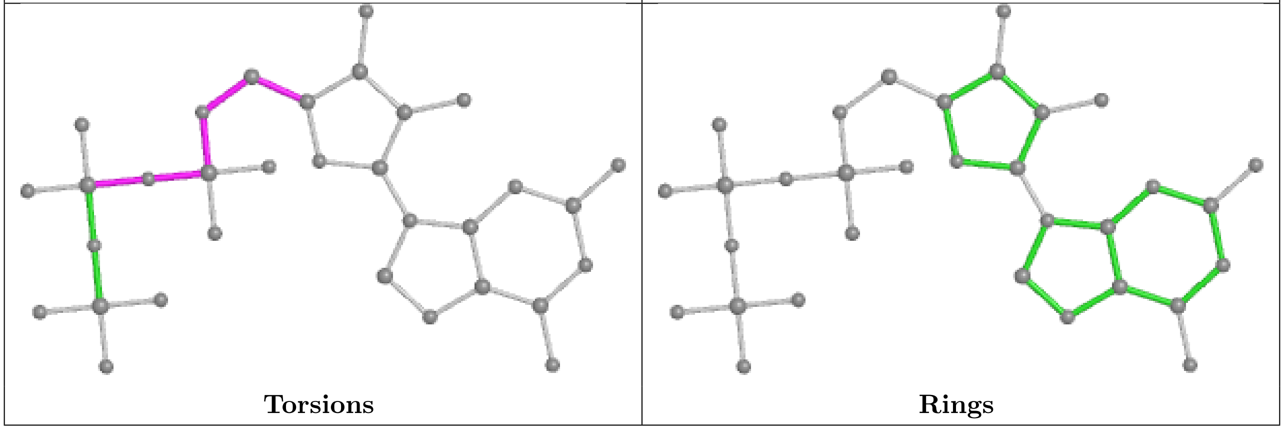
Bond angles



Torsions

Rings

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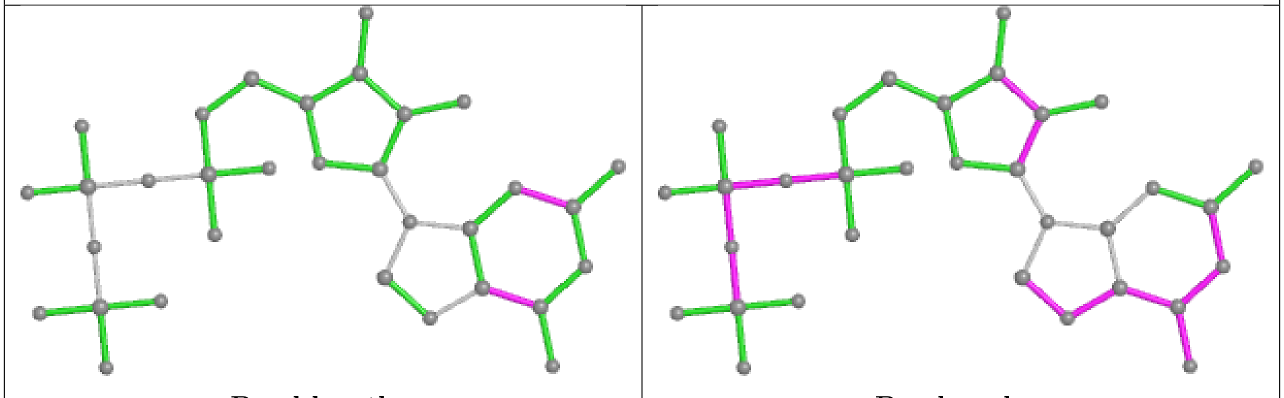
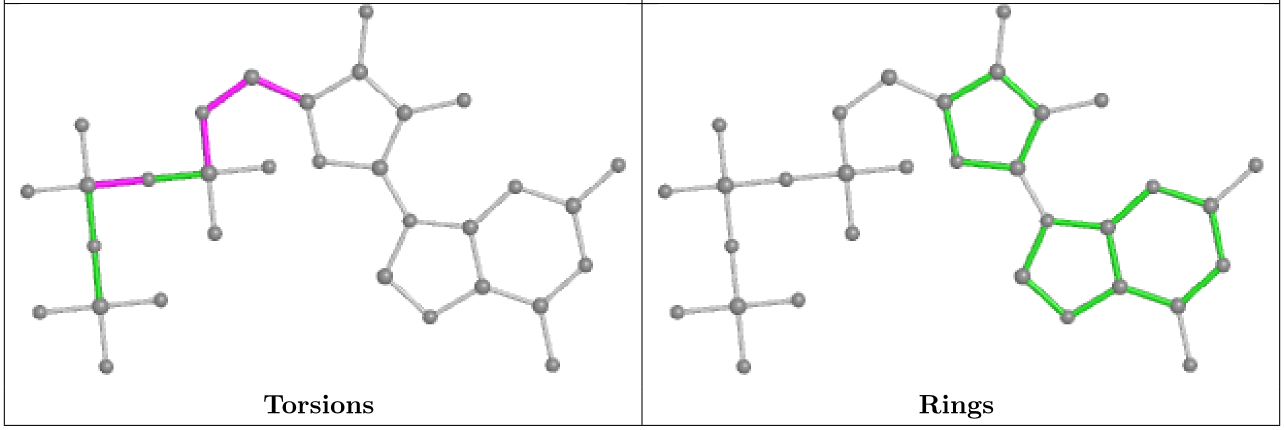


Bond lengths

Bond angles



Torsions

Rings

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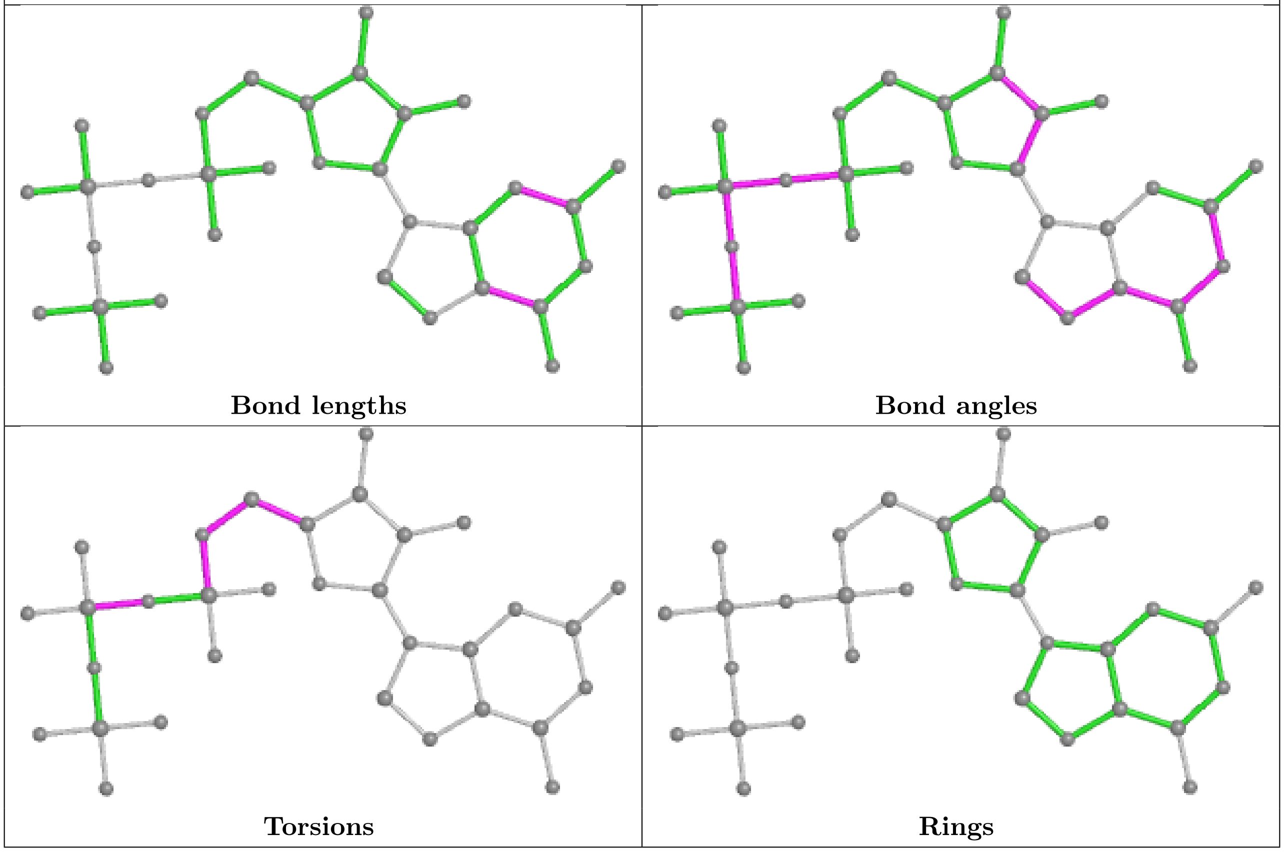

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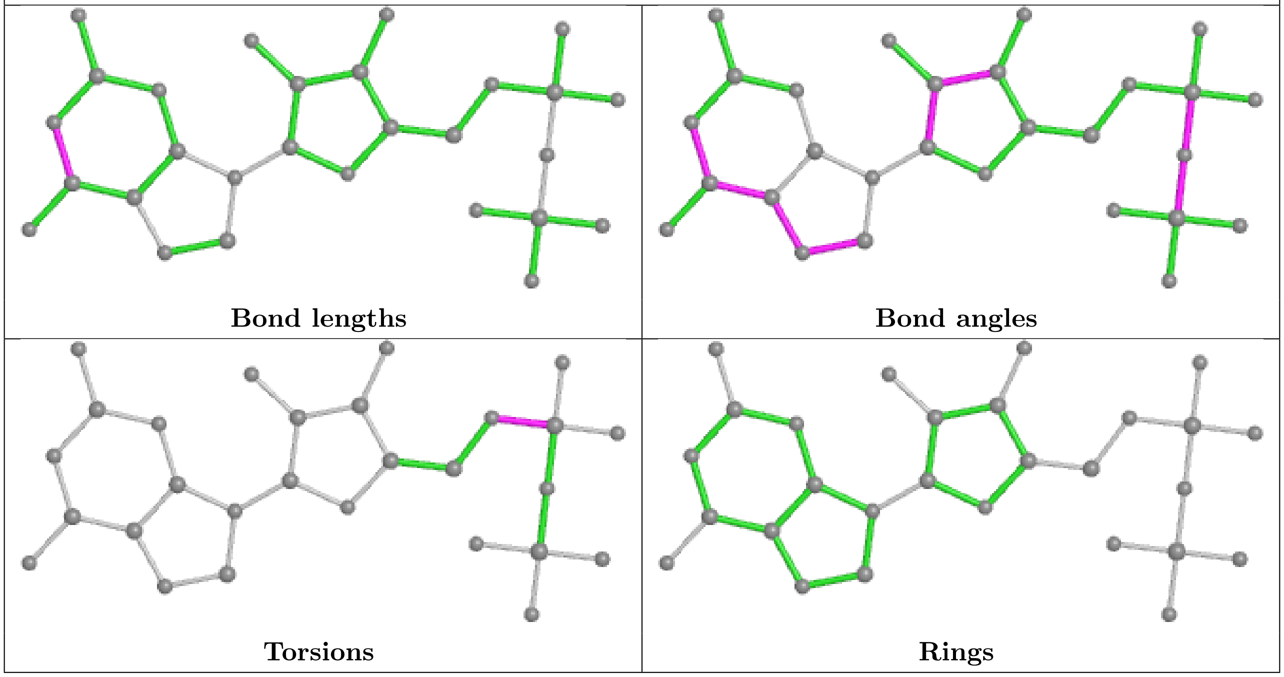

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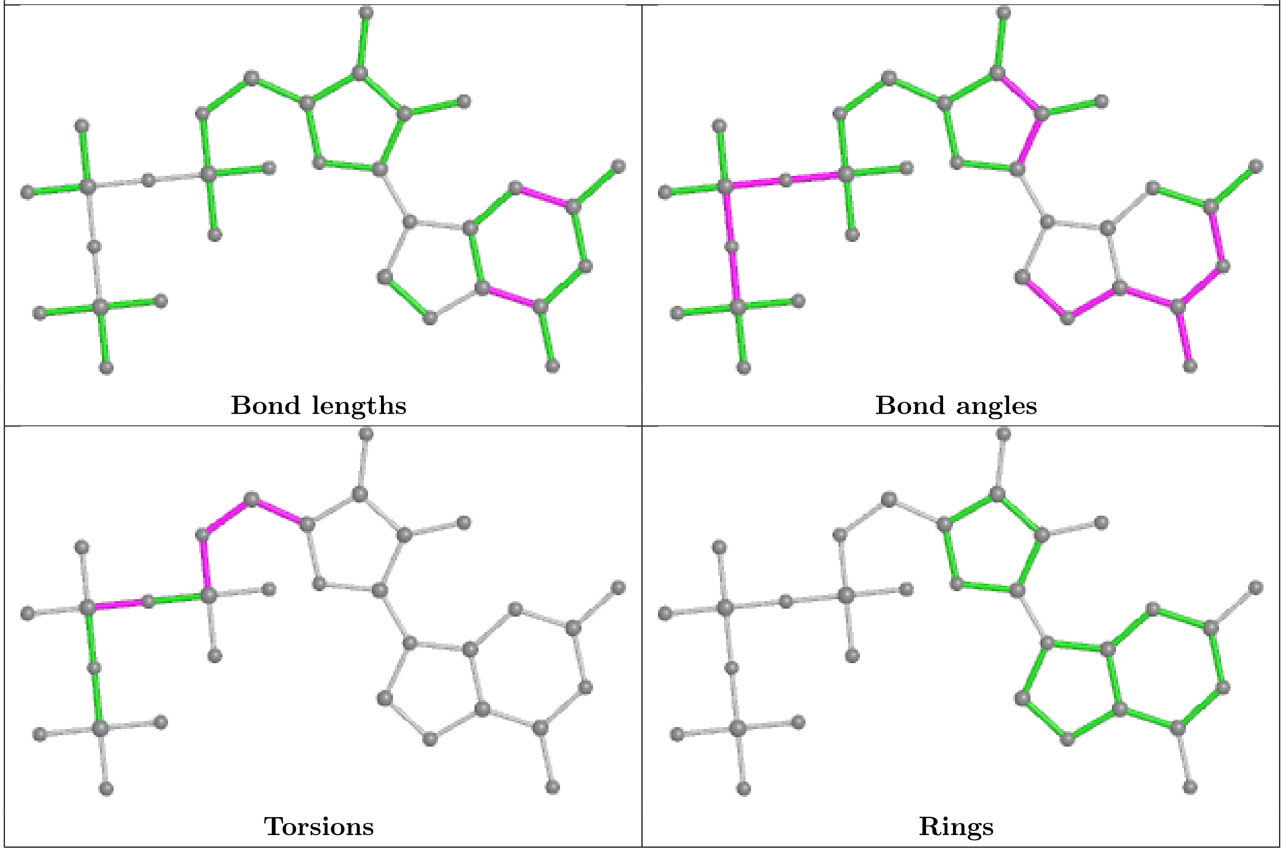

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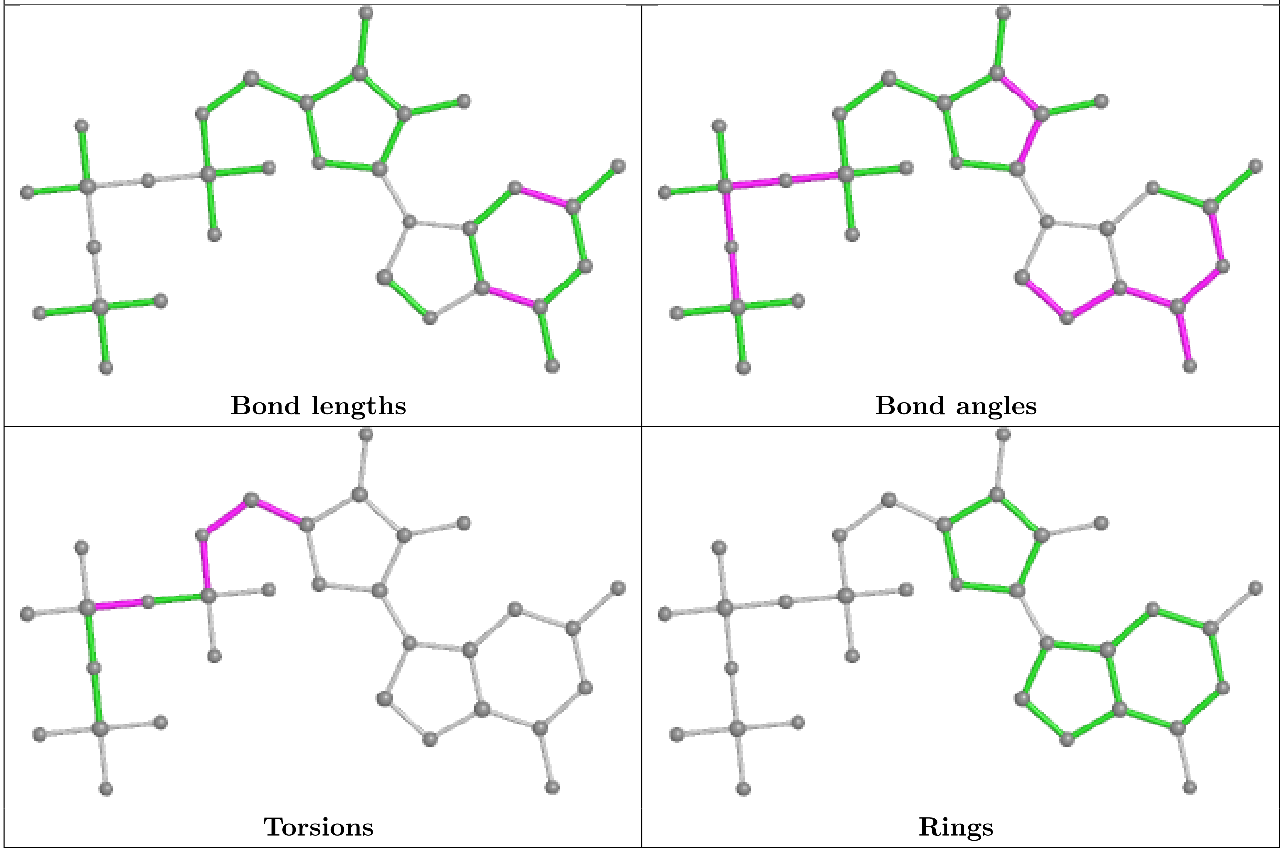

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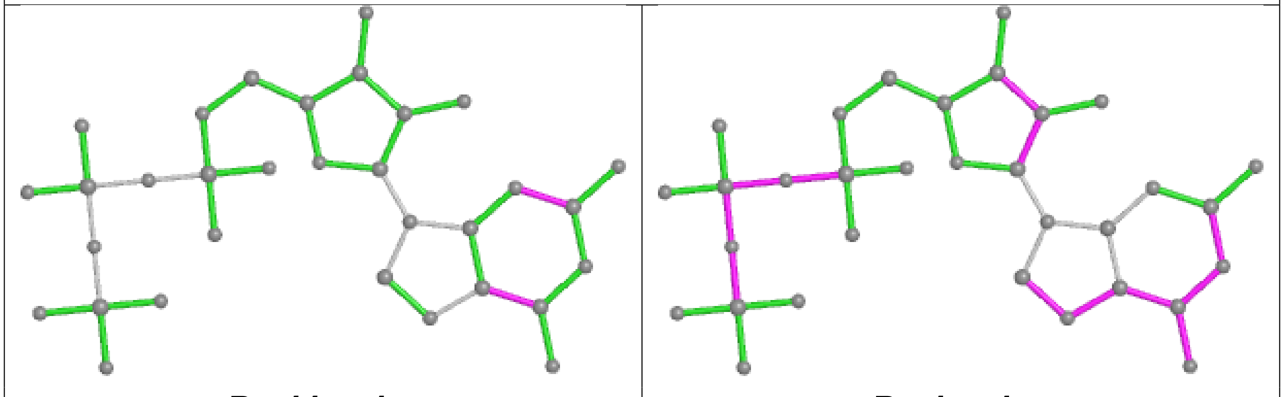
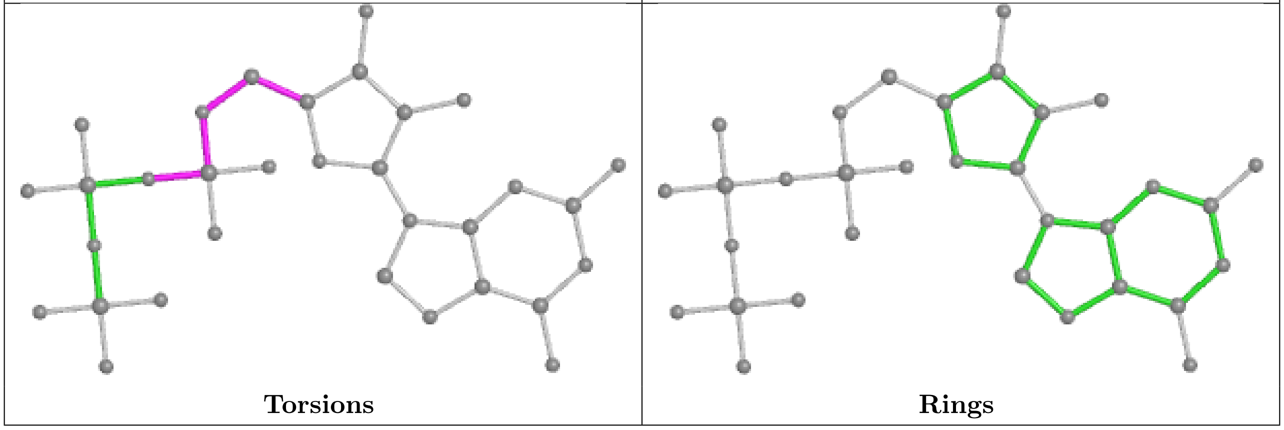


Bond lengths

Bond angles



Torsions

Rings

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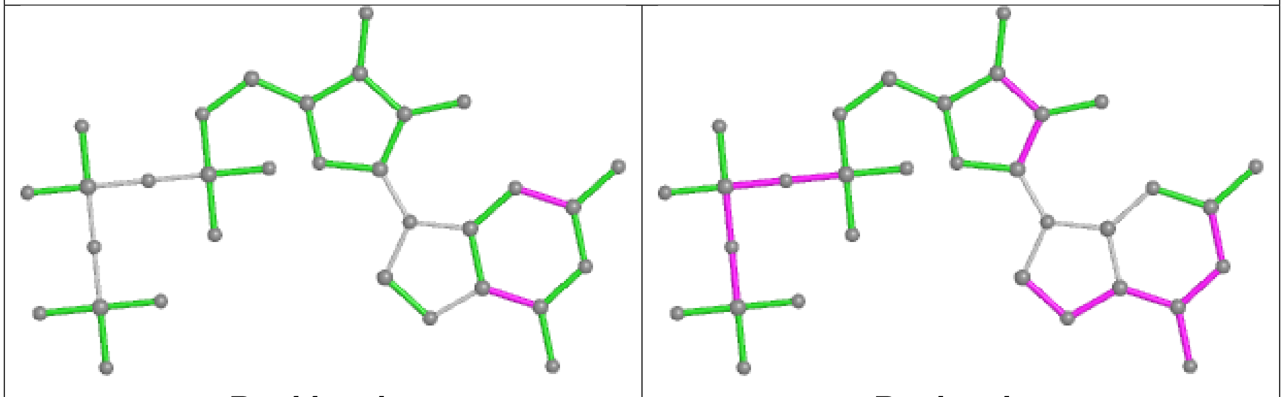

Bond lengths

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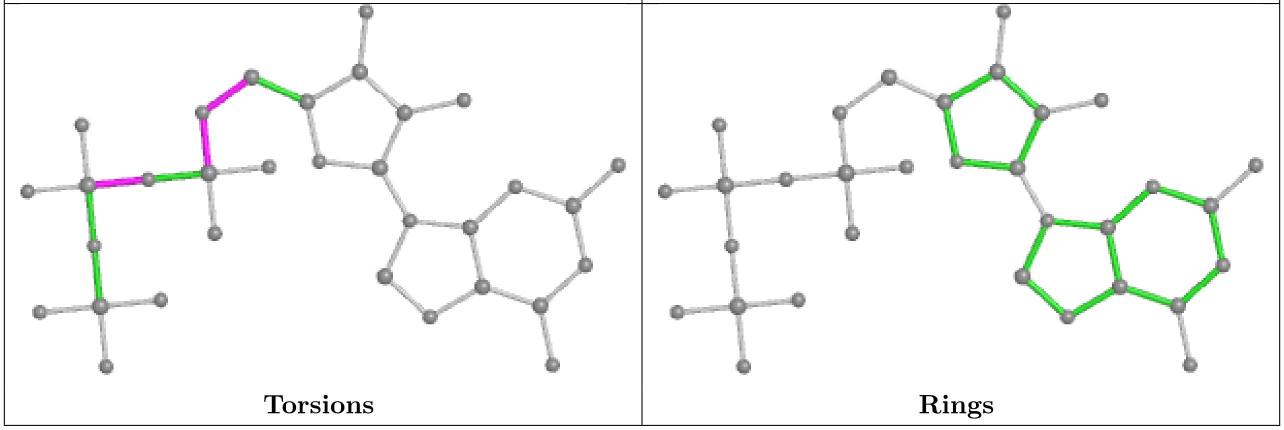

Torsions

Rings

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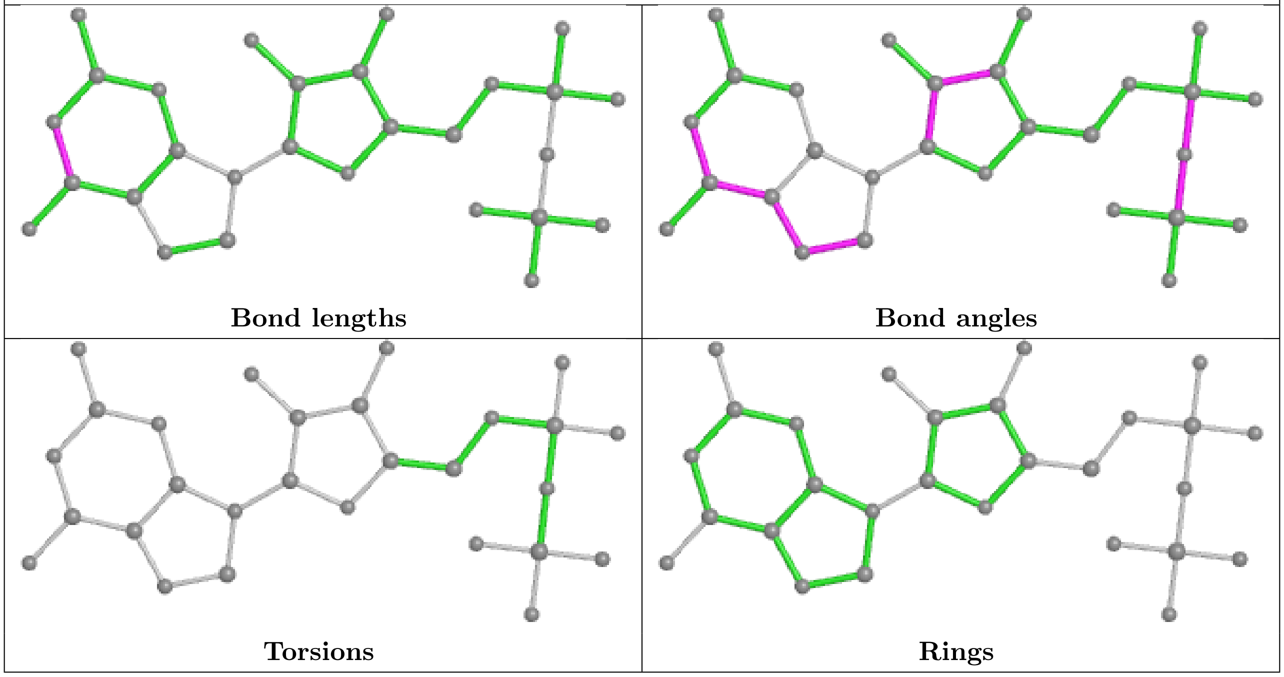

Bond lengths

Bond angles

Torsions

Rings

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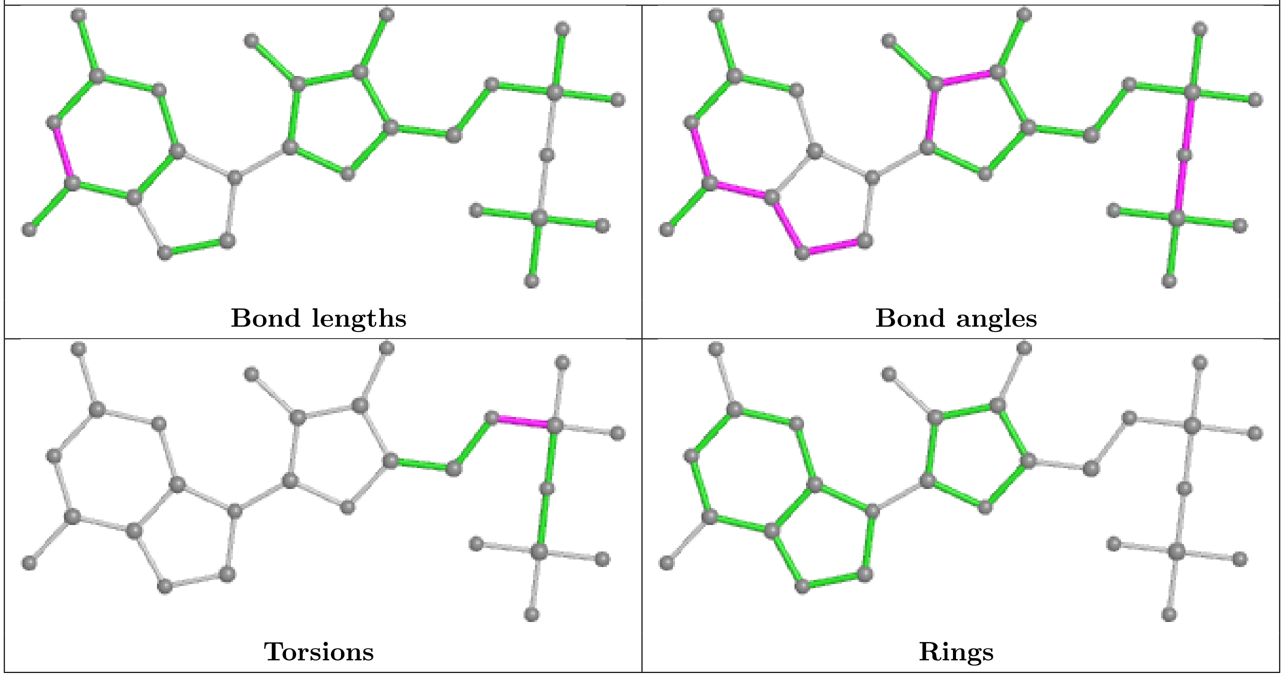

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Bond angles

Torsions

Rings

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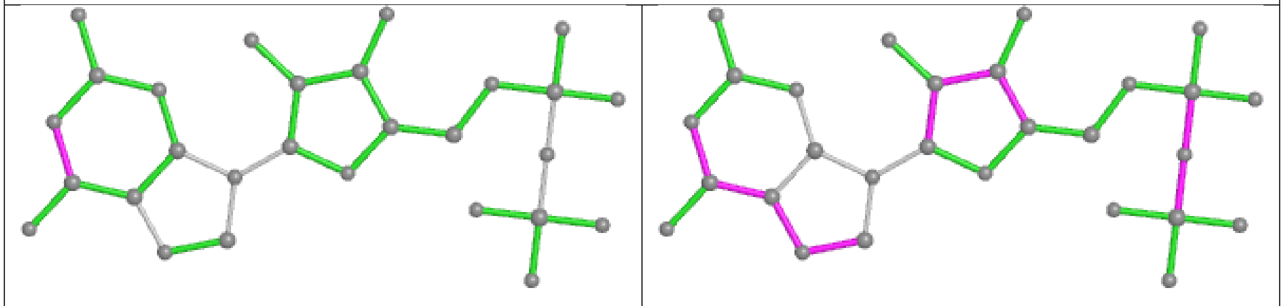

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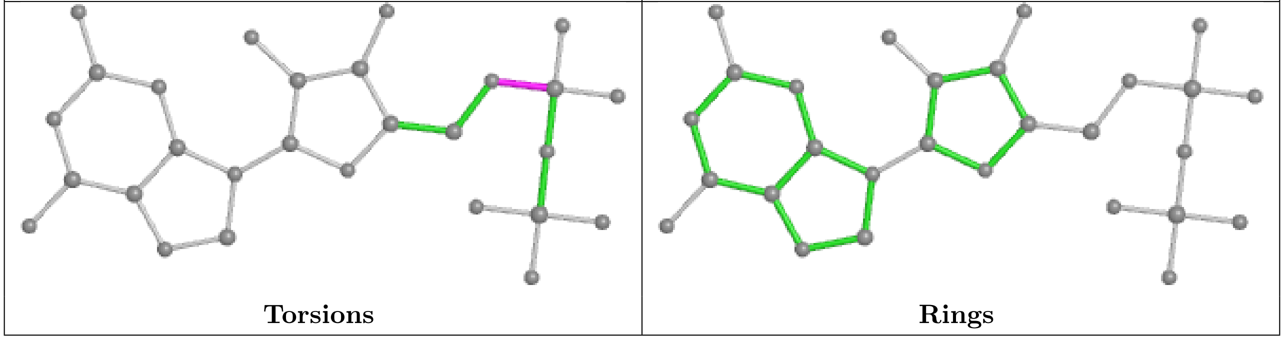

Torsions

Rings

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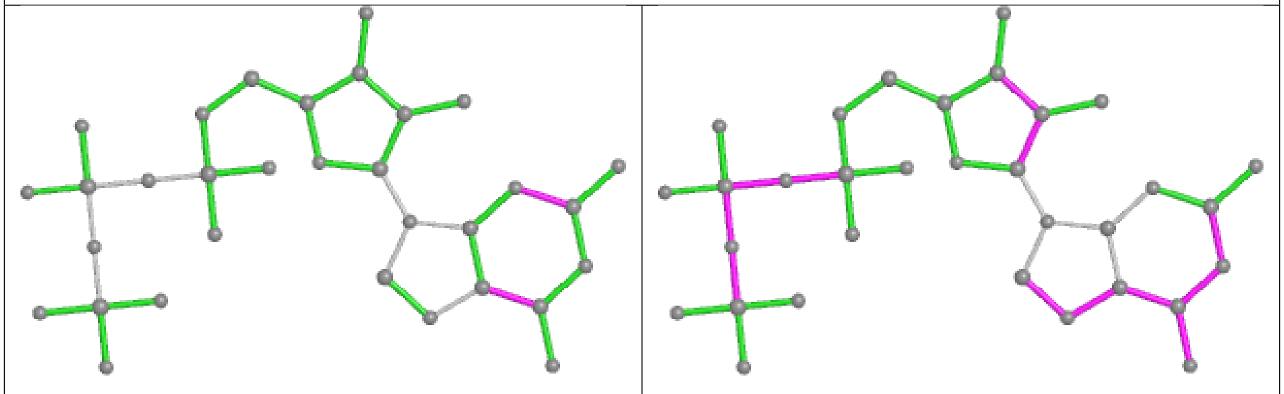
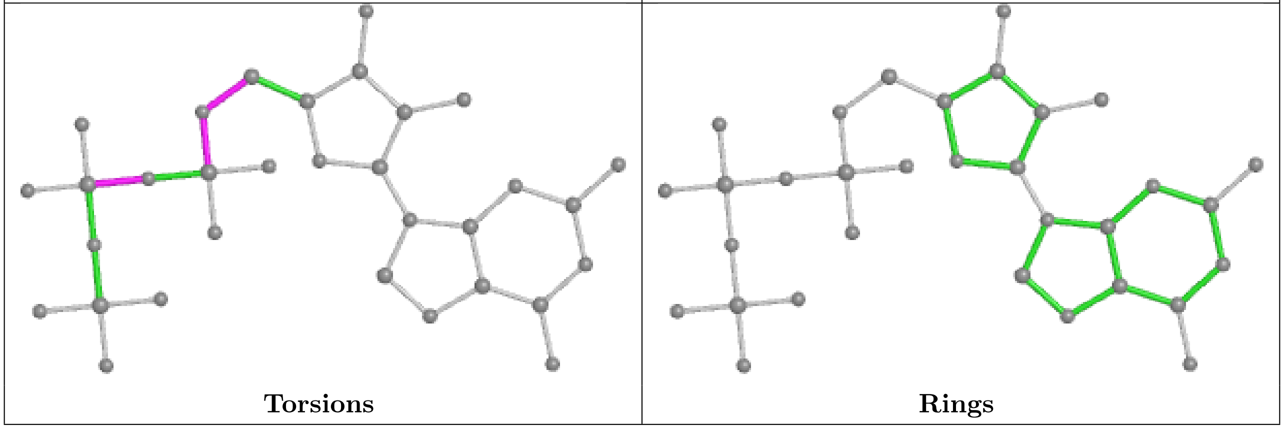


Bond lengths

Bond angles



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Rings

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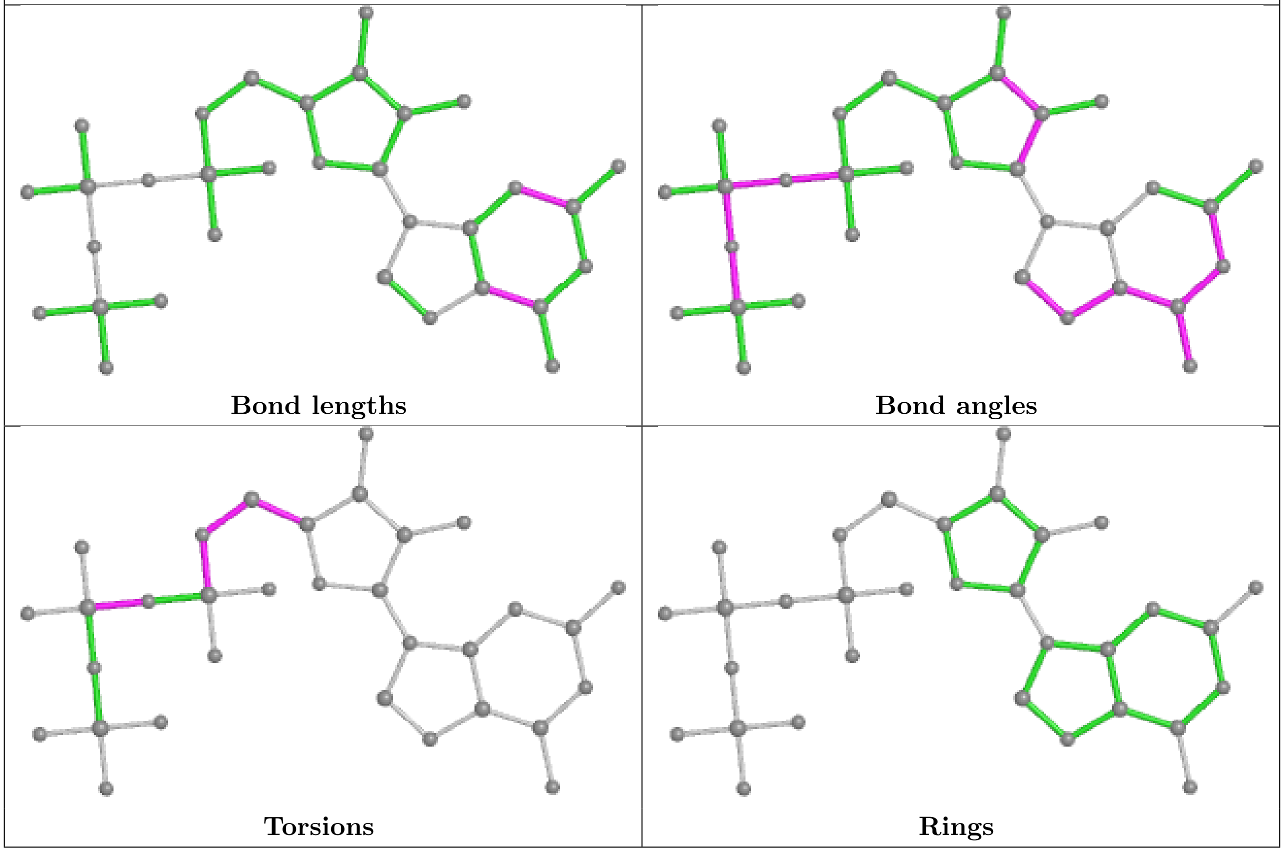

Bond lengths

Bond angles

Torsions

Rings

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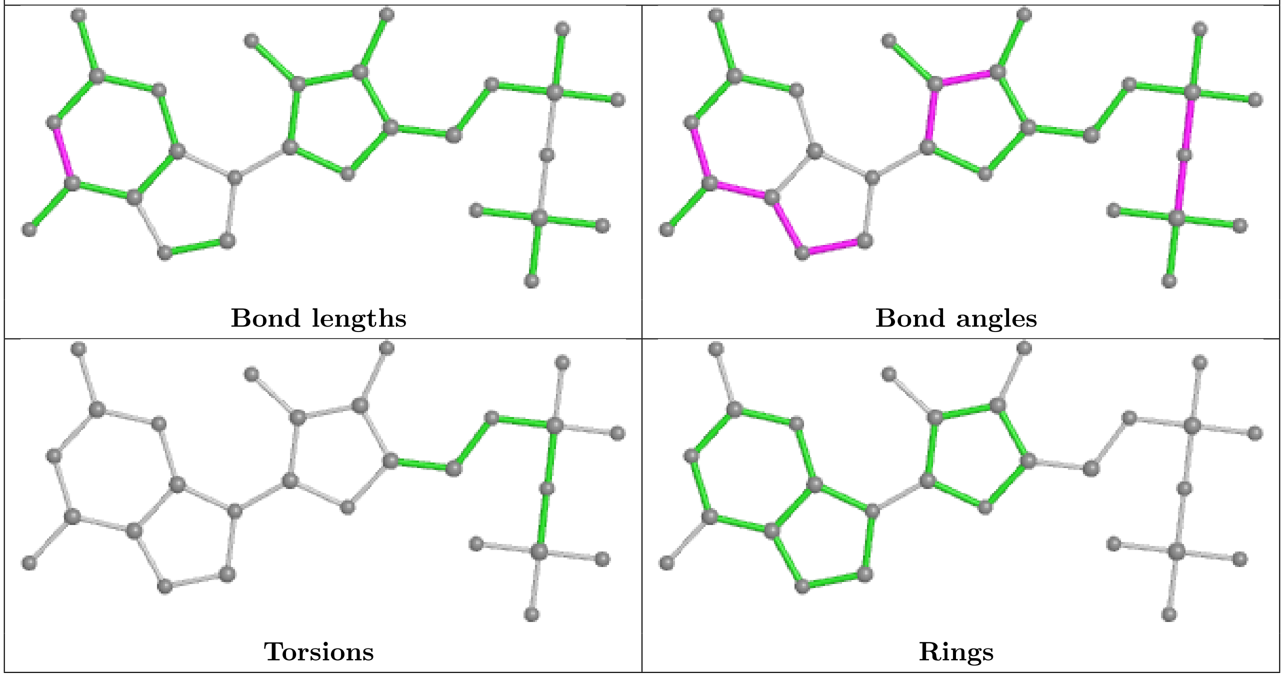

Bond lengths

Bond angles

Torsions

Rings

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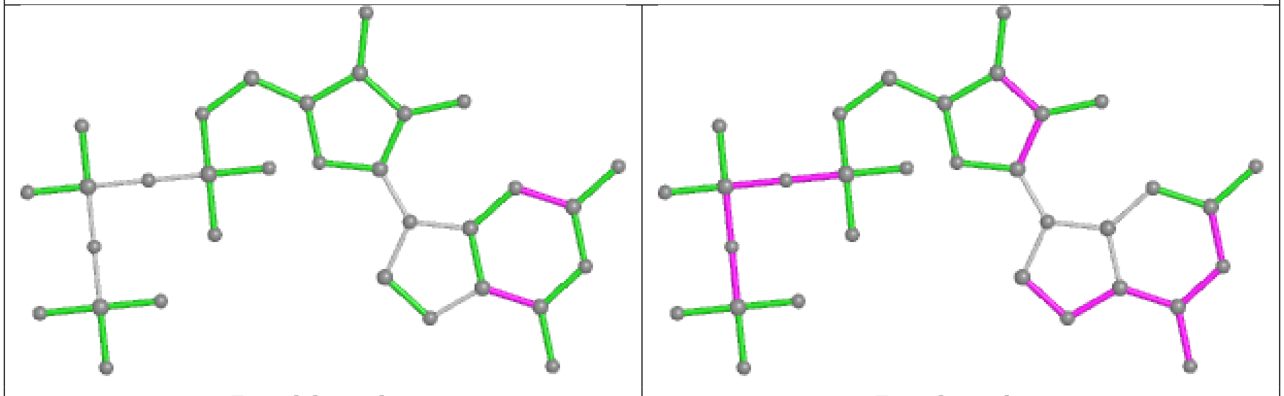
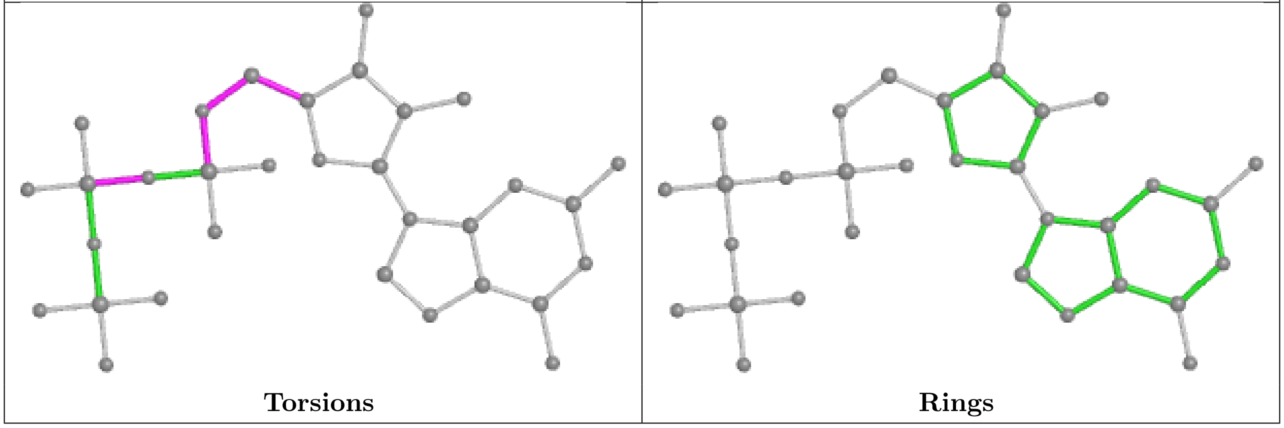


Bond lengths Bond angles



Torsions Rings

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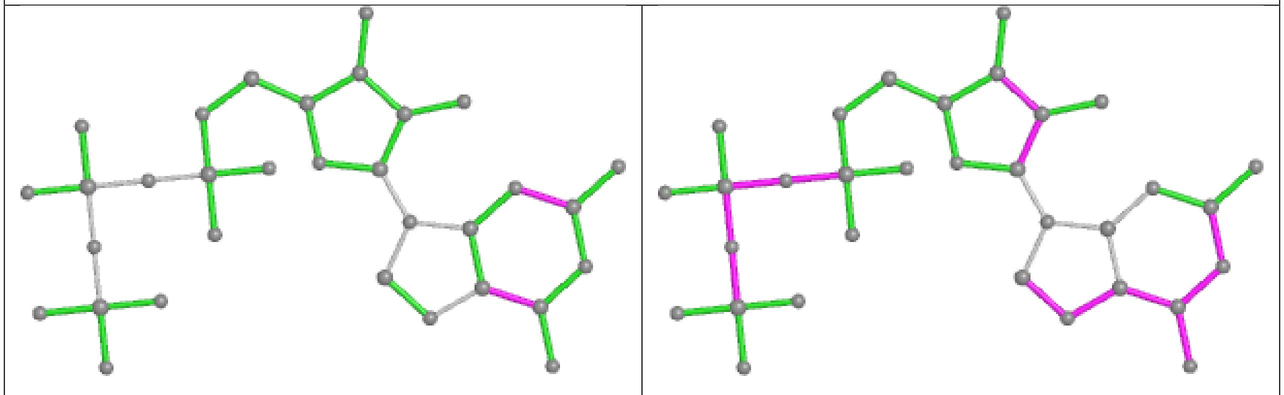
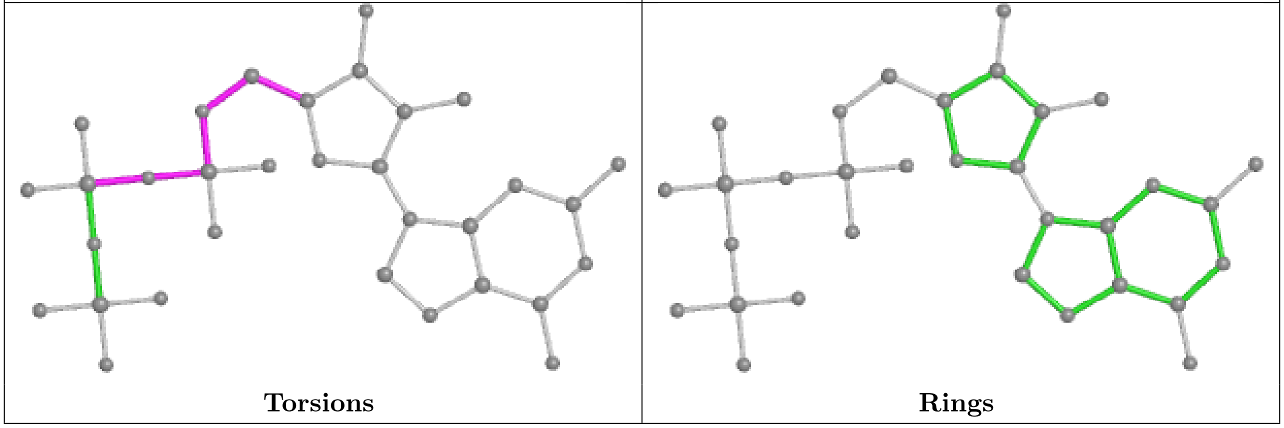


Bond lengths Bond angles



Torsions Rings

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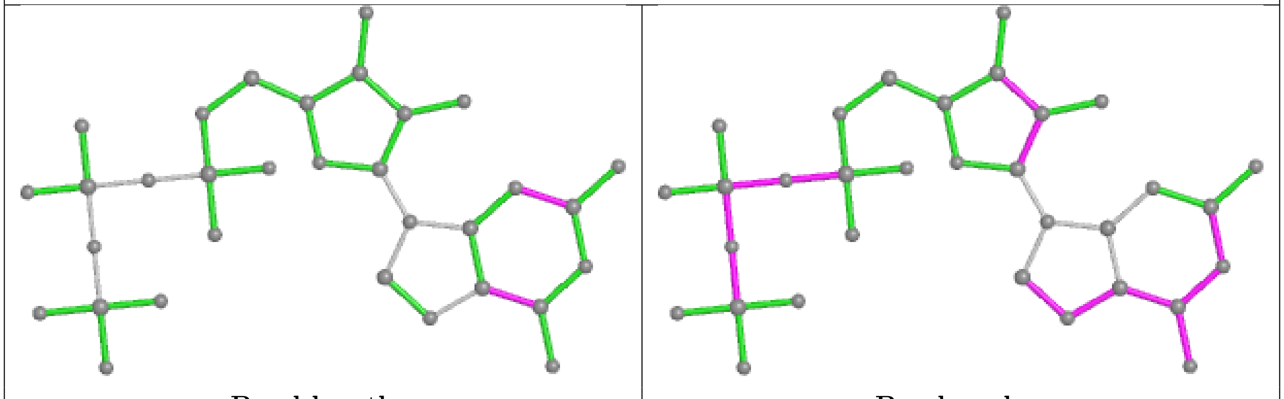

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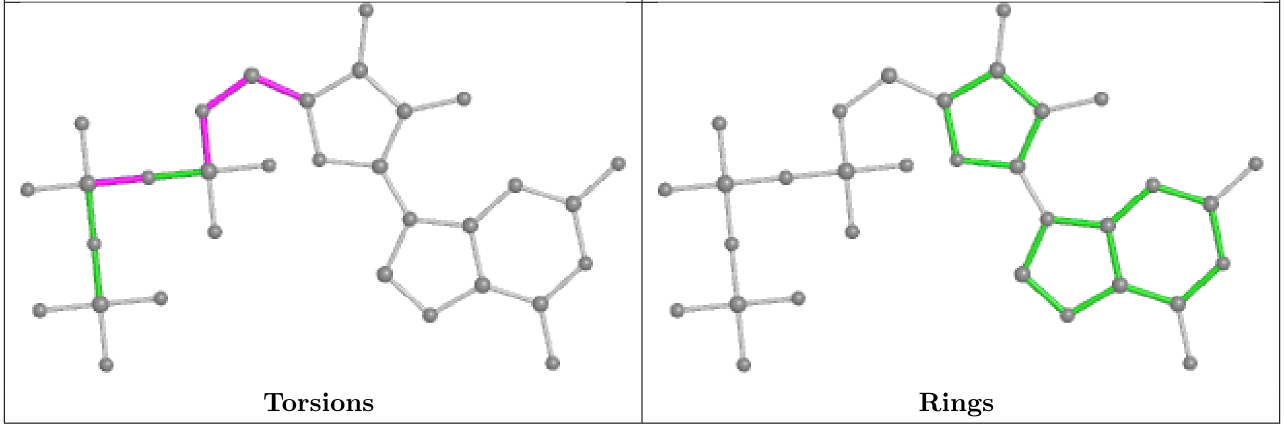

Torsions

Rings

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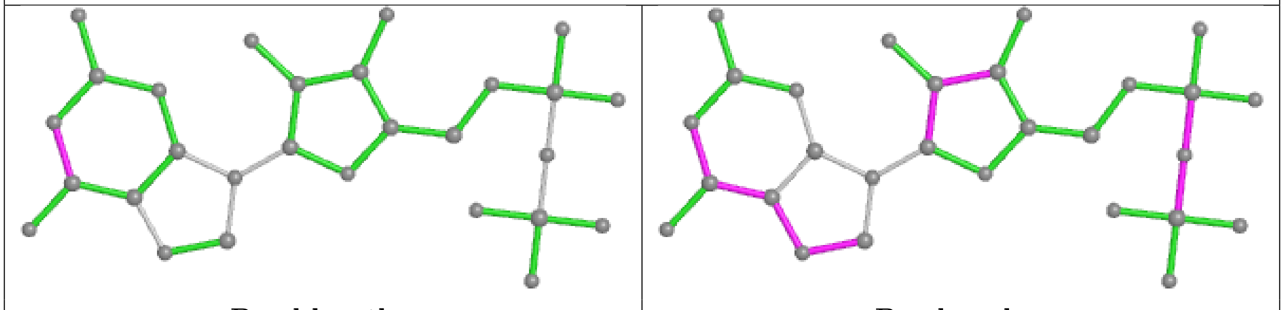

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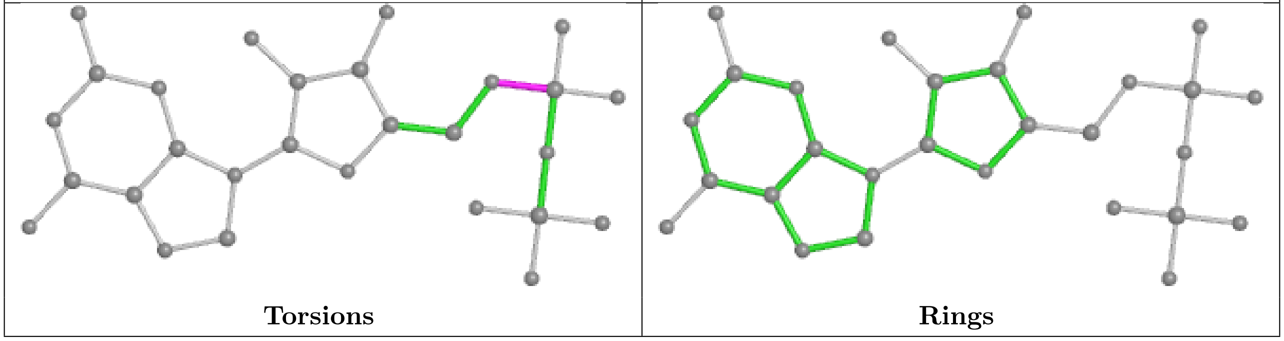

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Rings

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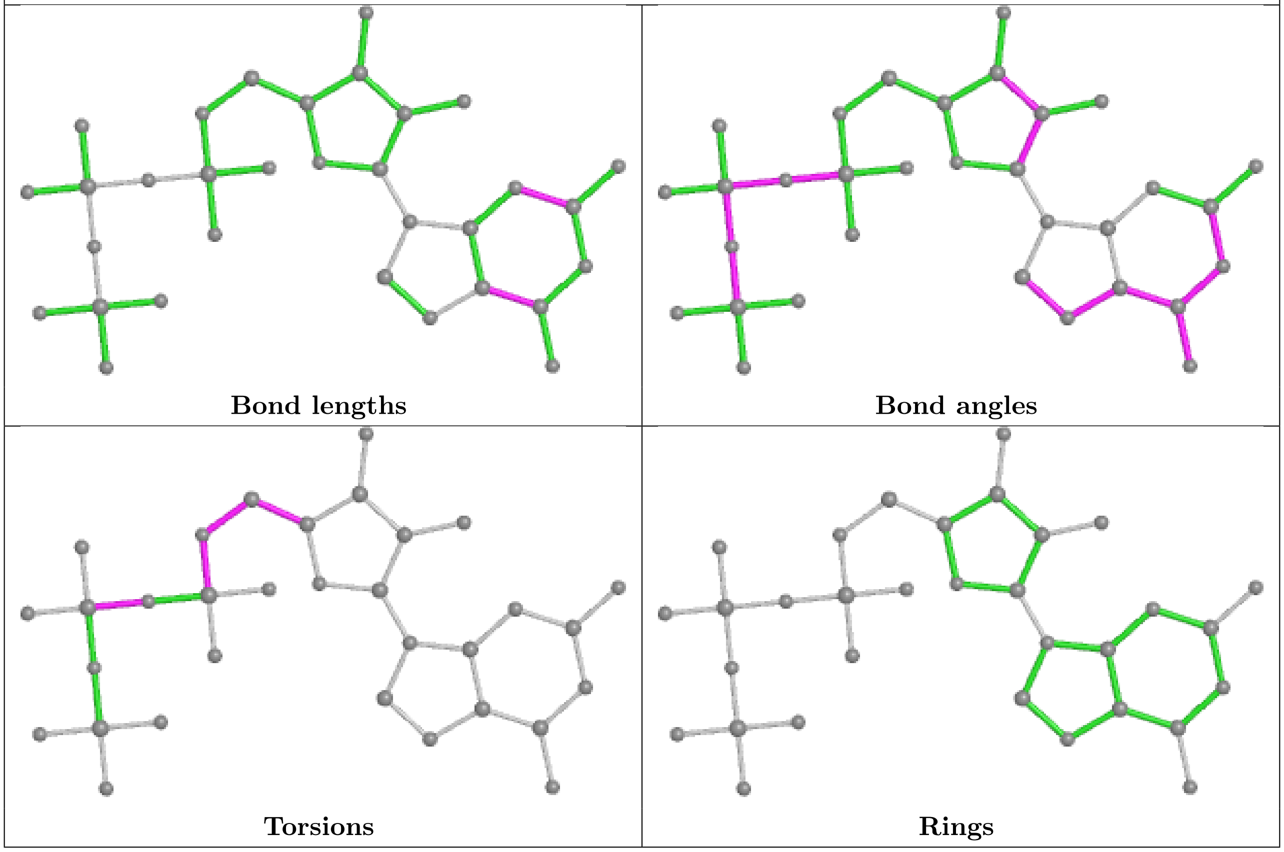

Bond lengths

Bond angles

Torsions

Rings

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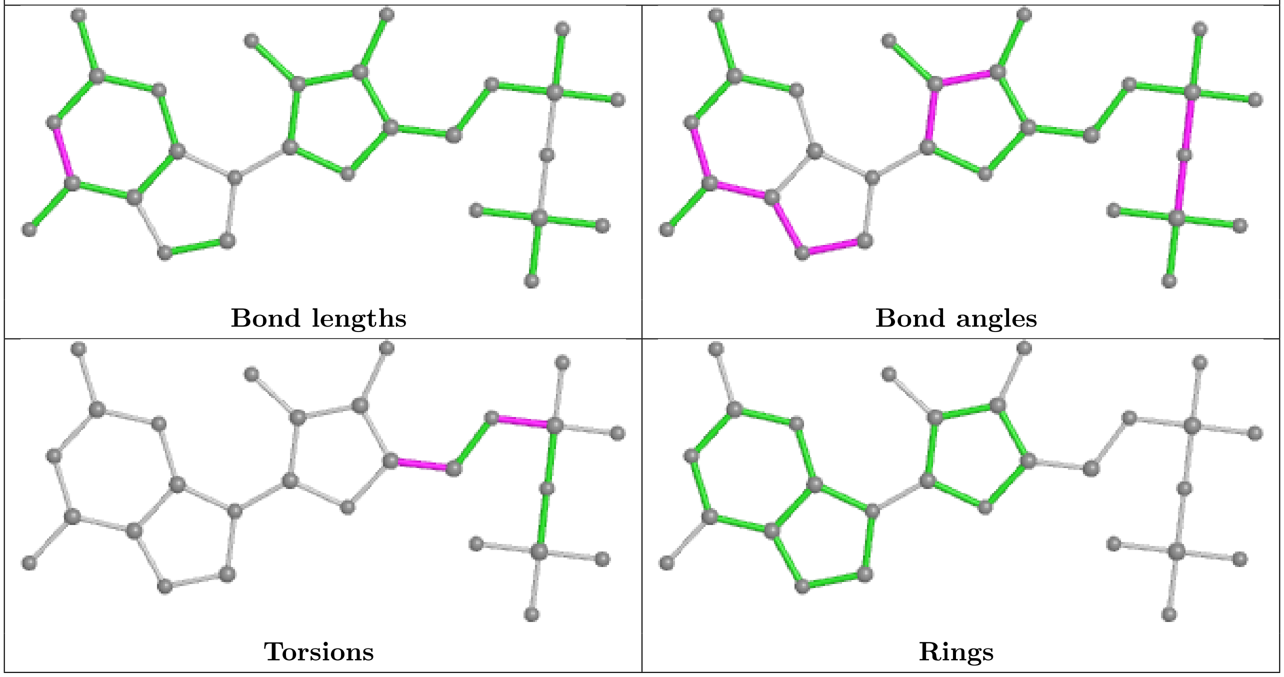

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Bond angles

Torsions

Rings

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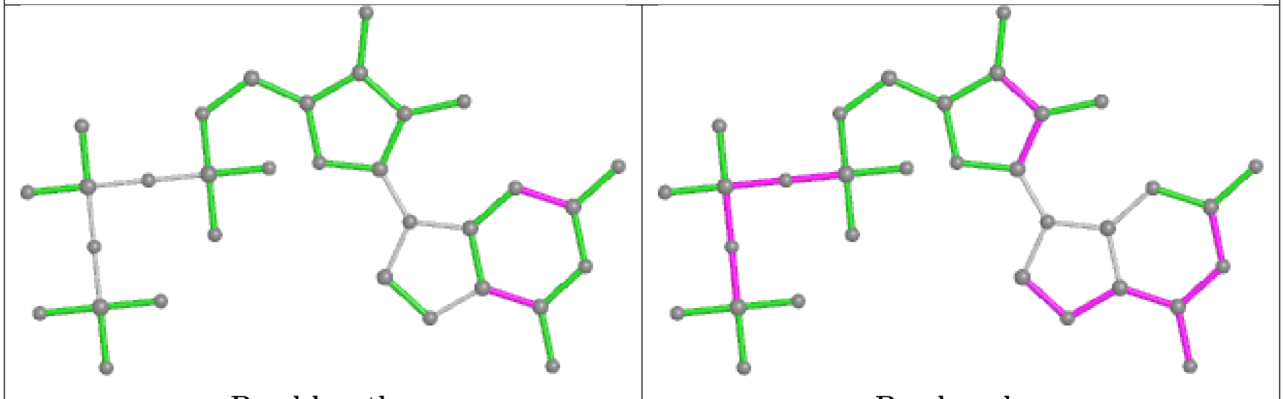
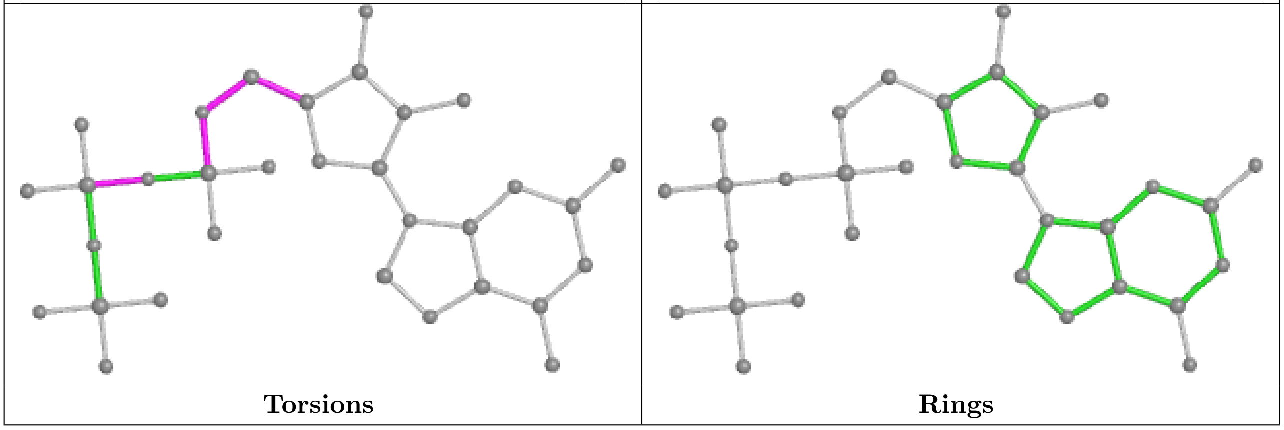


Bond lengths

Bond angles



Torsions

Rings

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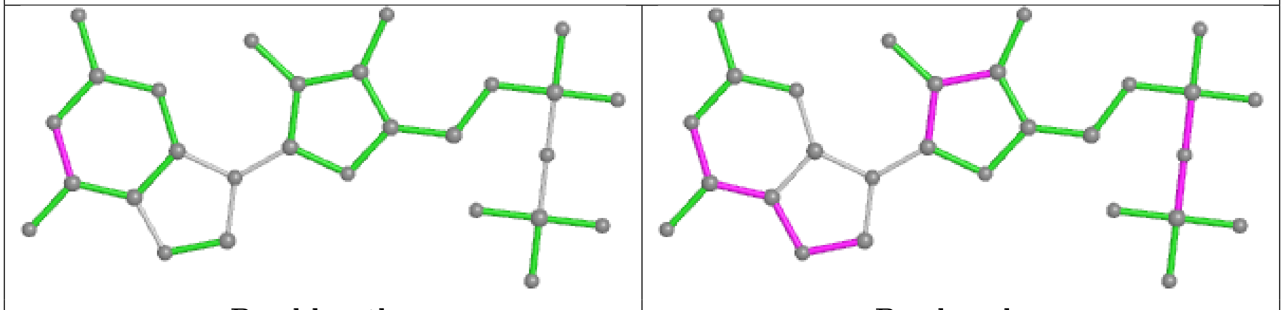
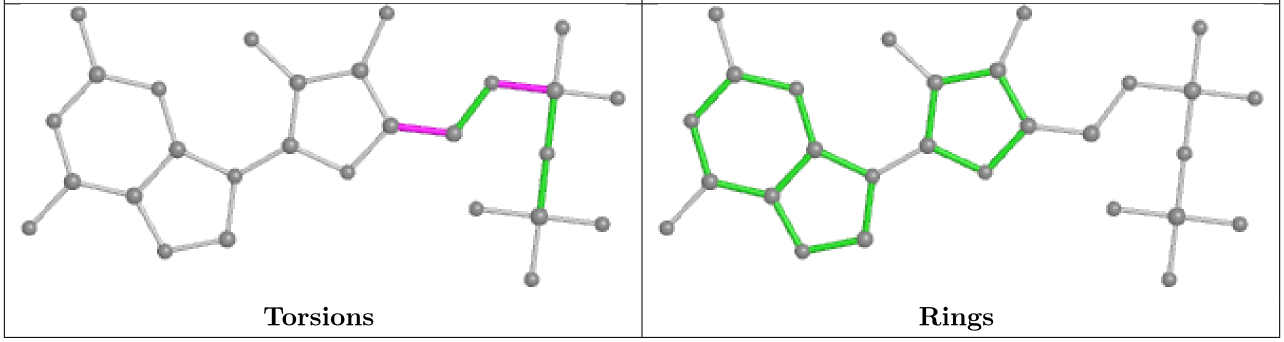


Bond lengths

Bond angles



Torsions

Rings

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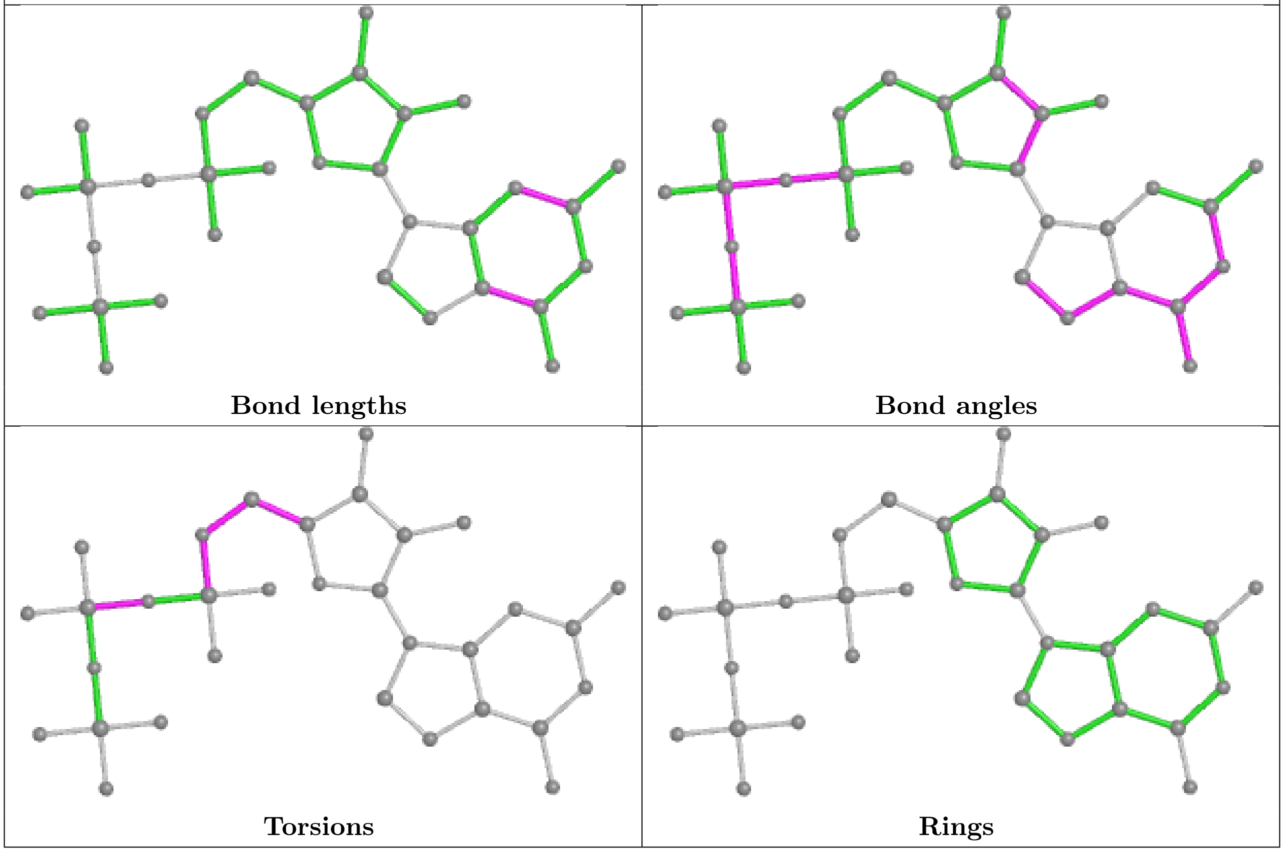

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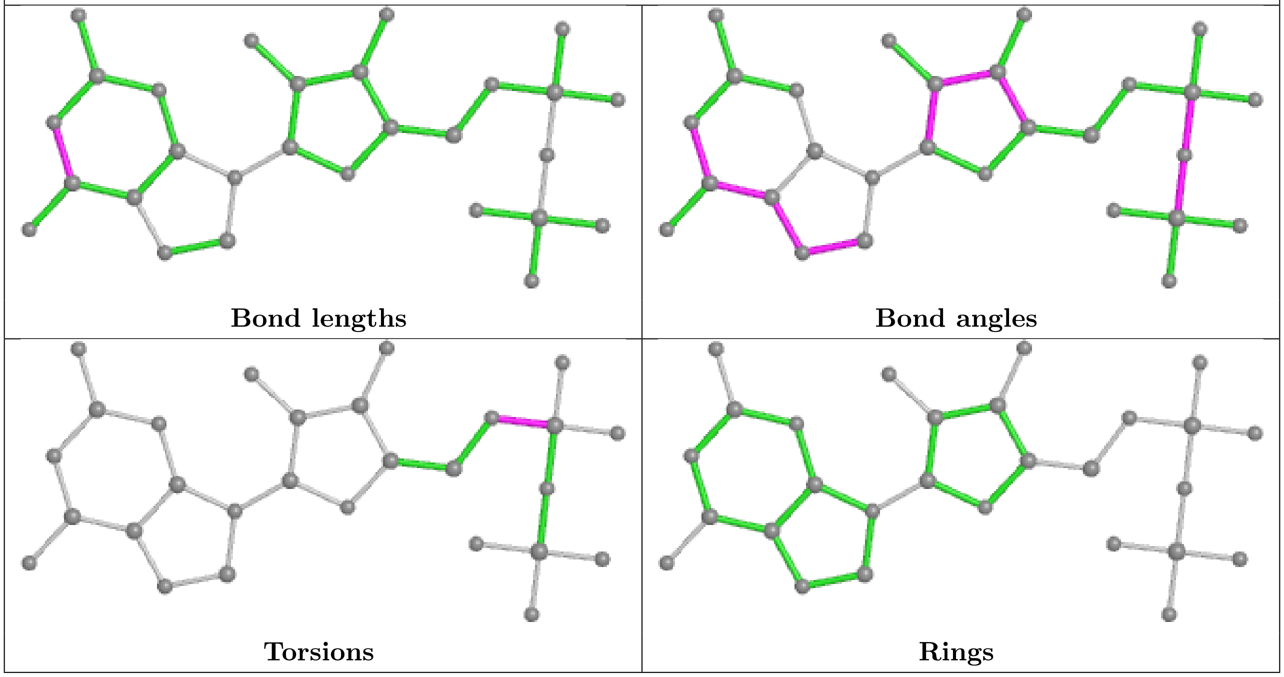

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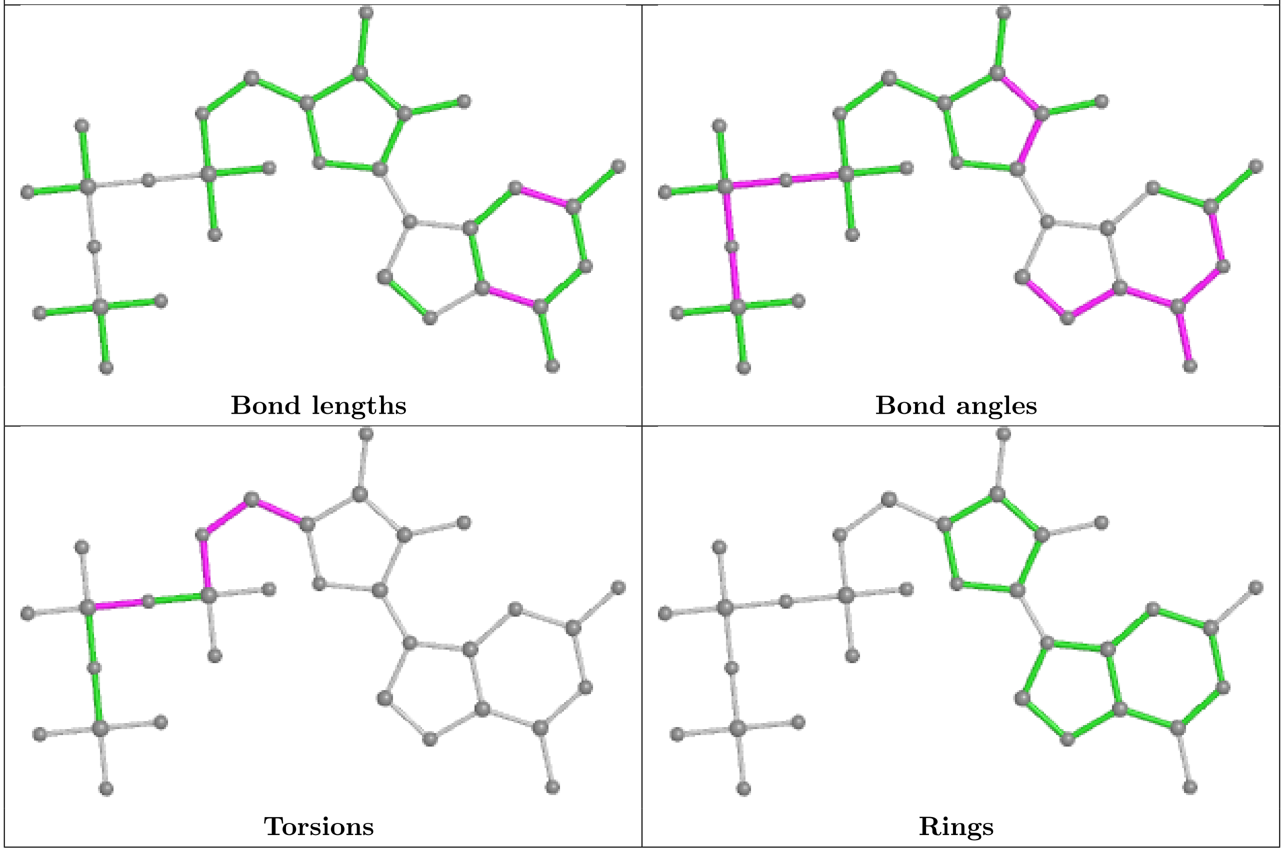

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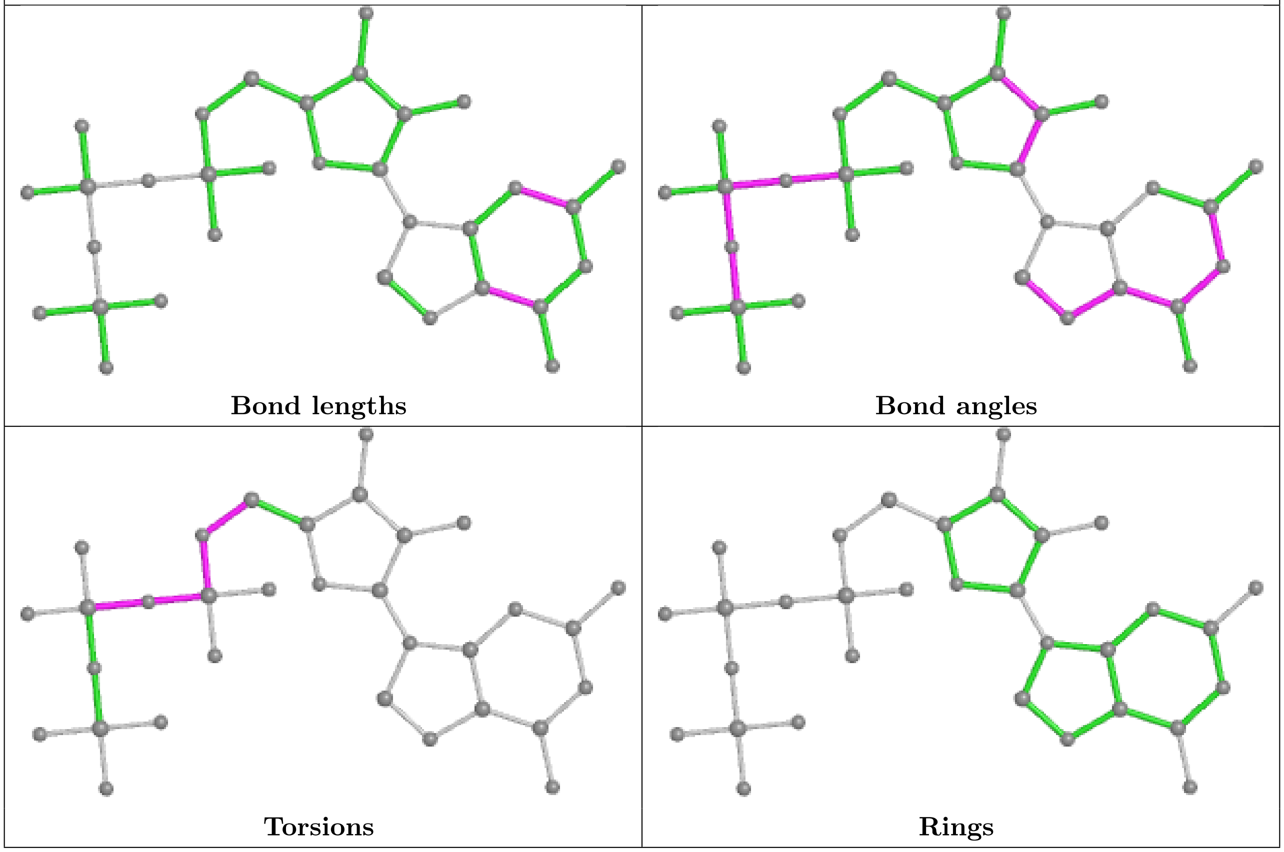

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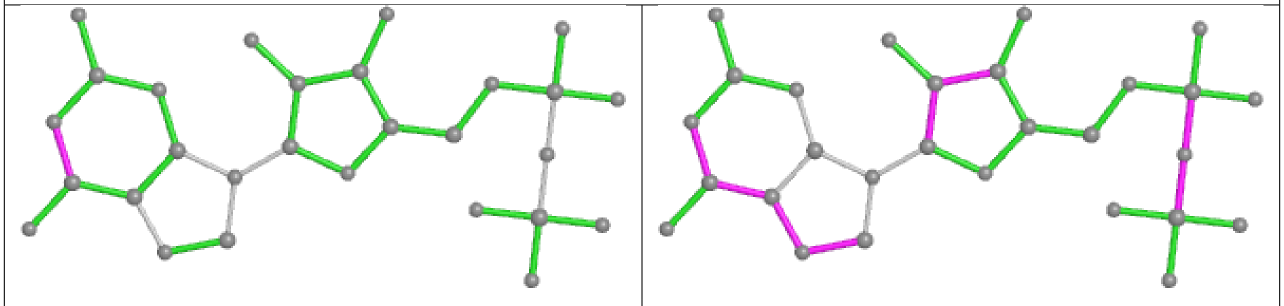
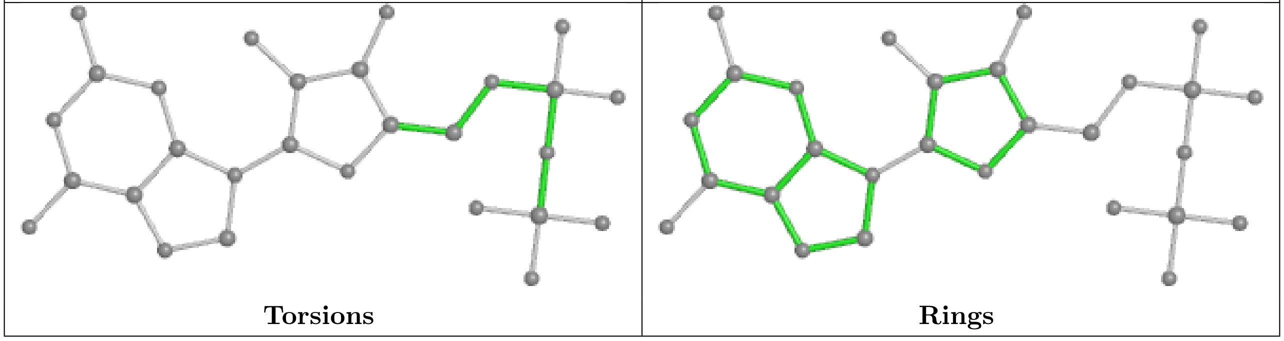
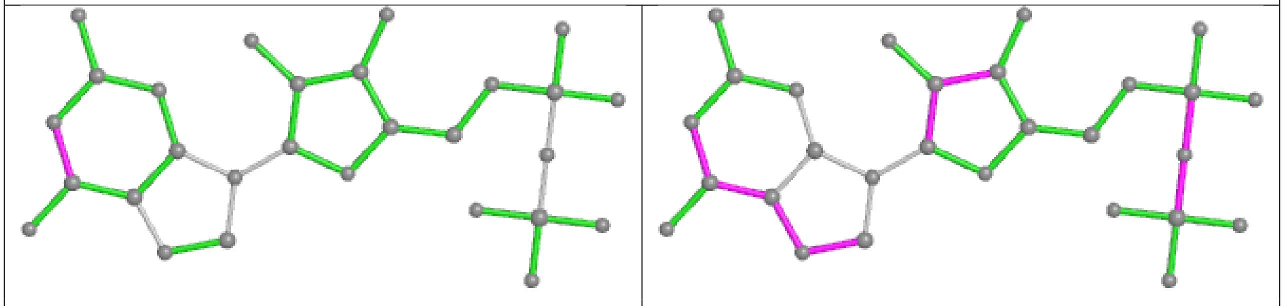


Bond lengths **Bond angles**

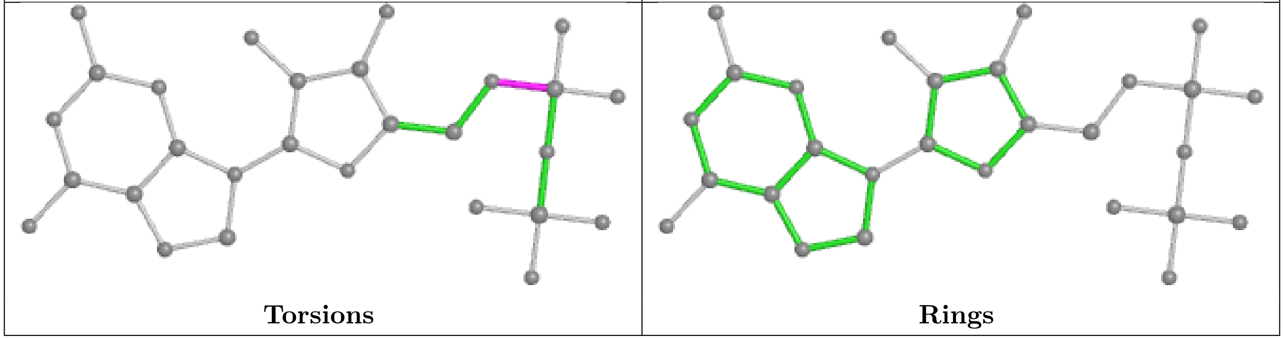


Torsions **Rings**

Ligand GDP FF 502



Bond lengths **Bond angles**



Torsions **Rings**

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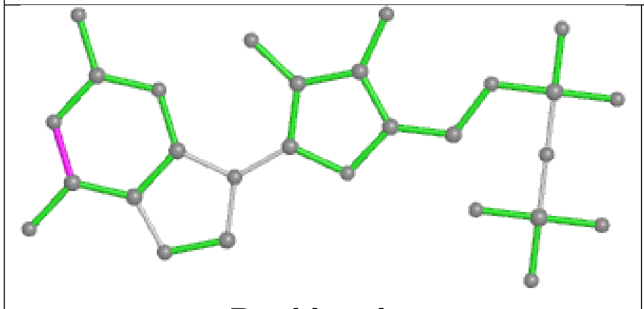

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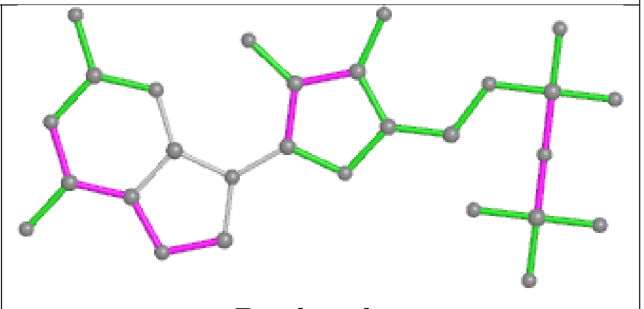

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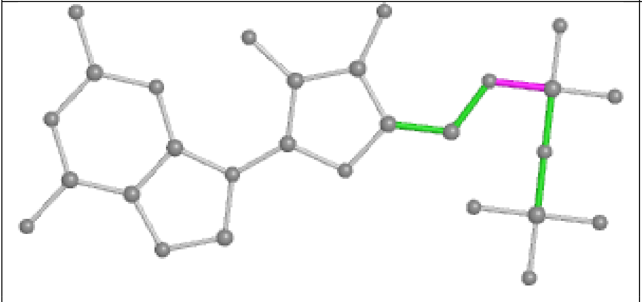
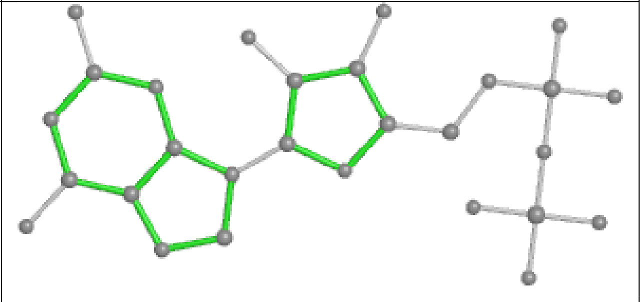
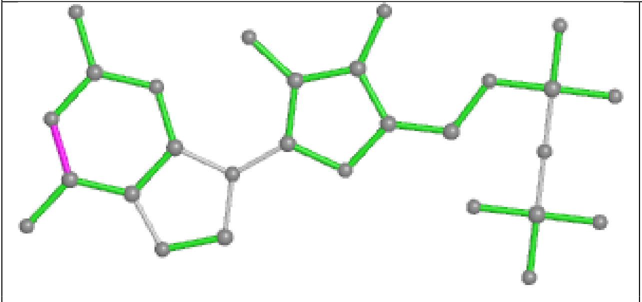


Torsions



Rings

Ligand GDP MP 502



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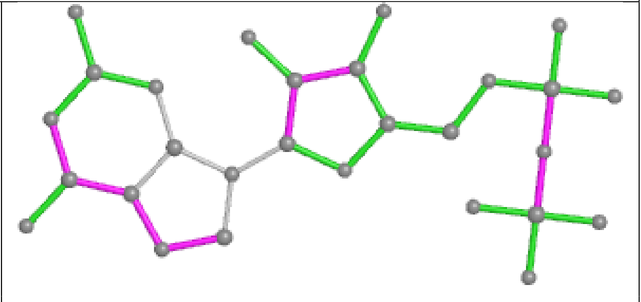
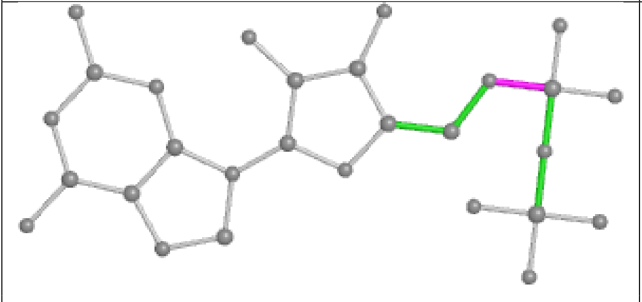


Bond angles



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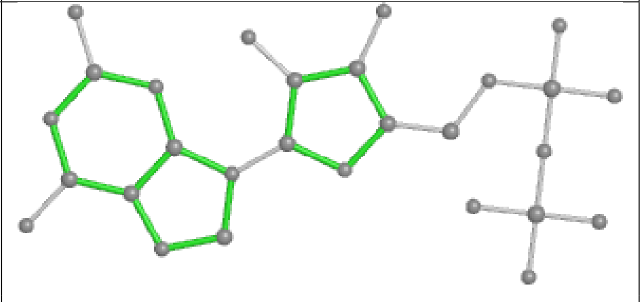

Rings

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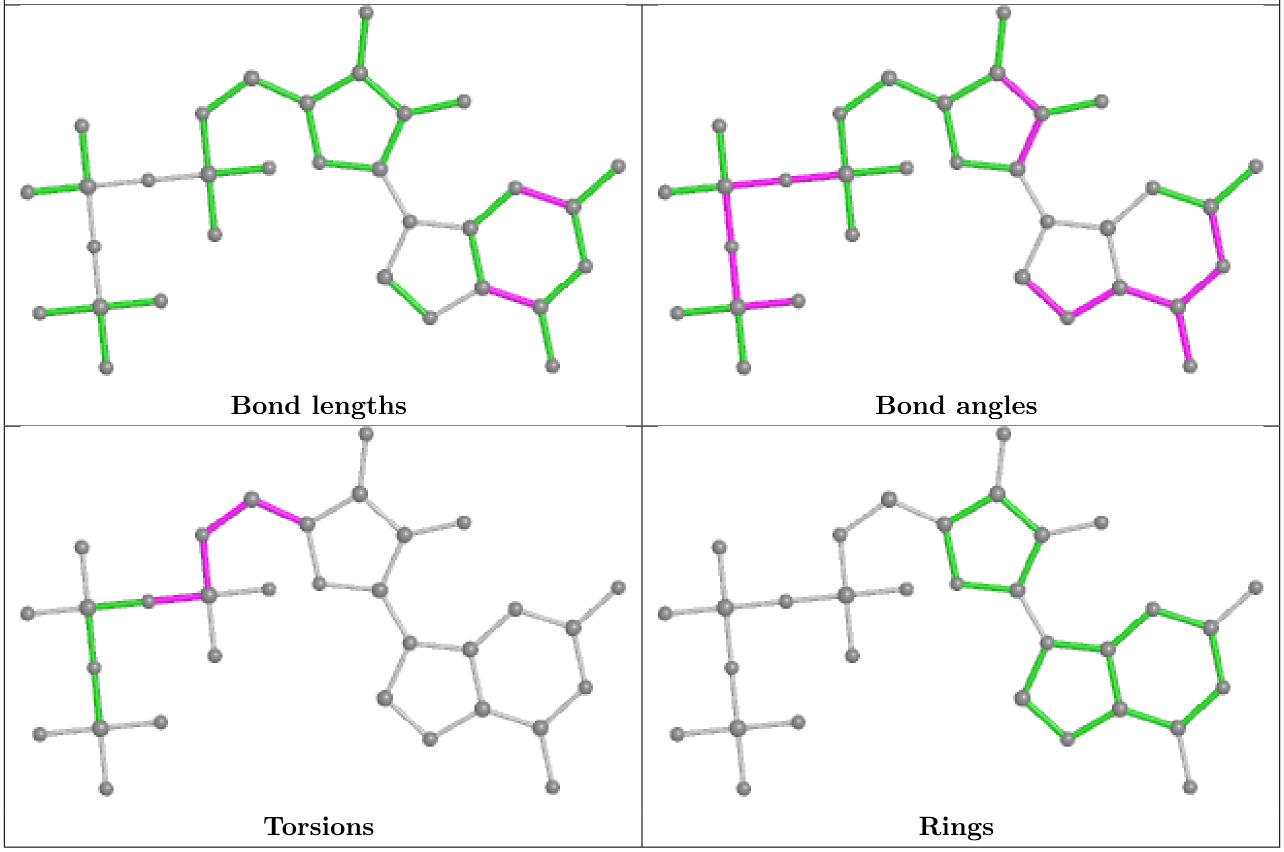
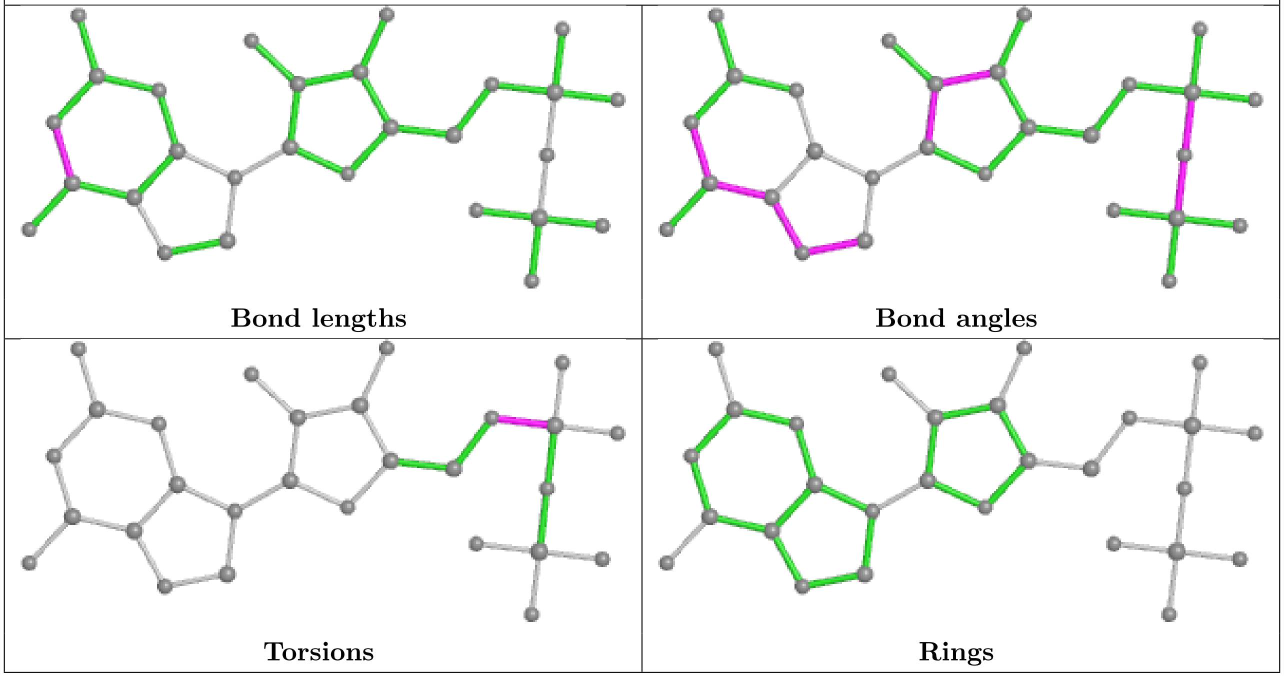


Ligand GDP CJ 502



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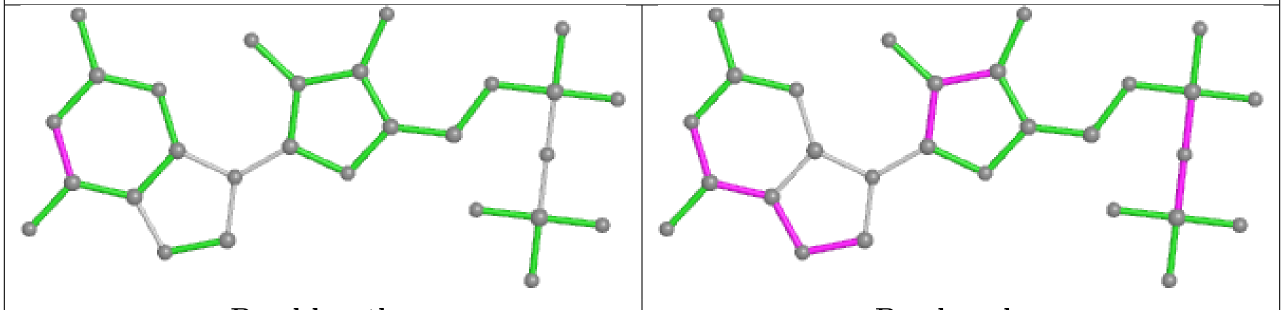
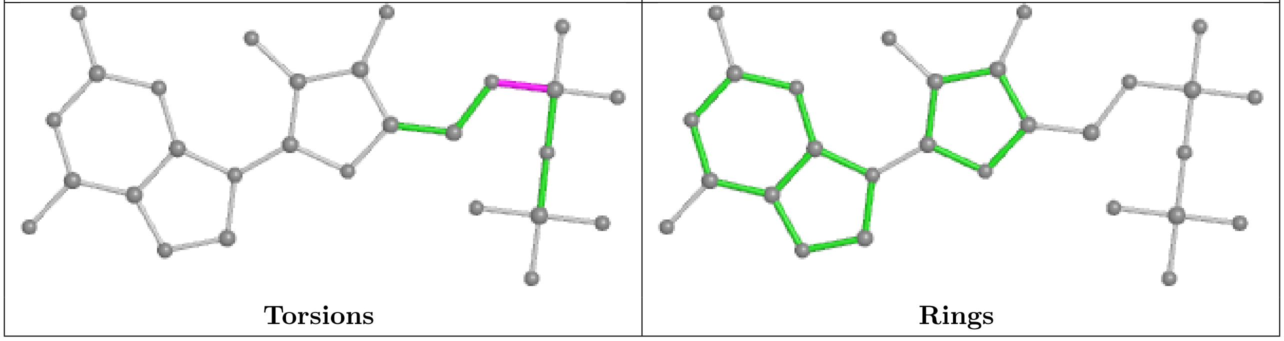


Bond lengths

Bond angles



Torsions

Rings

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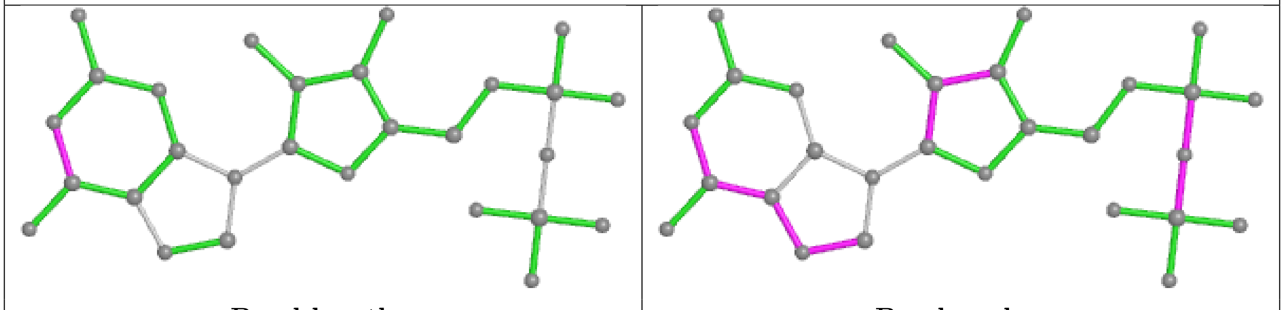
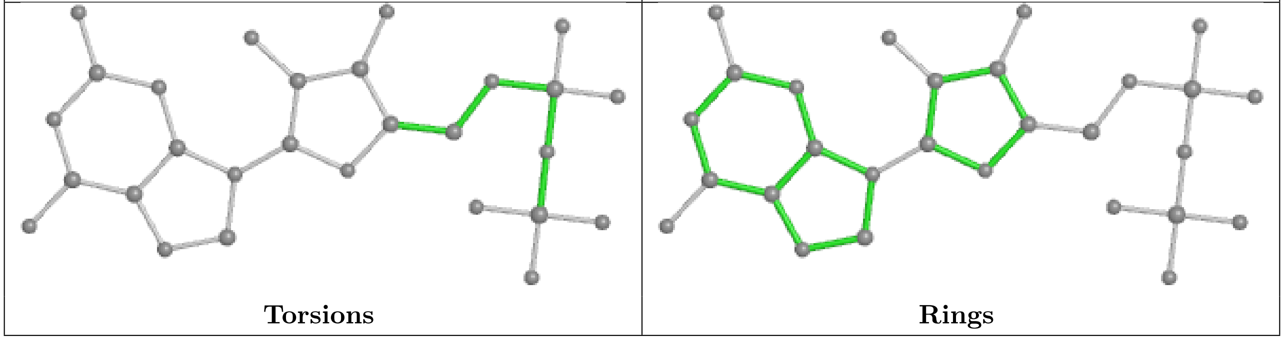


Bond lengths

Bond angles



Torsions

Rings

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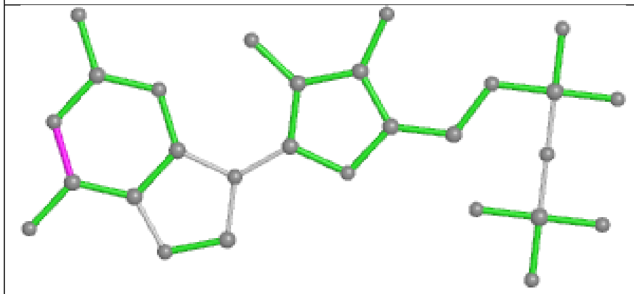

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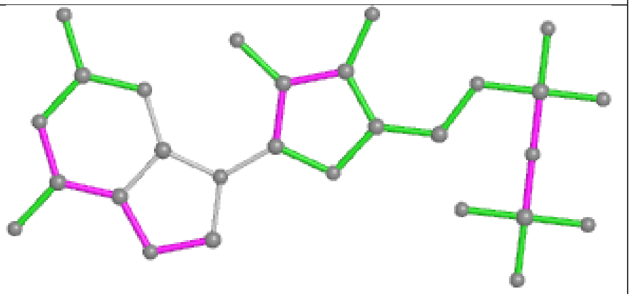
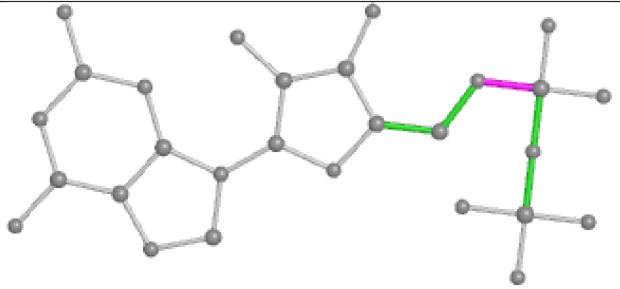
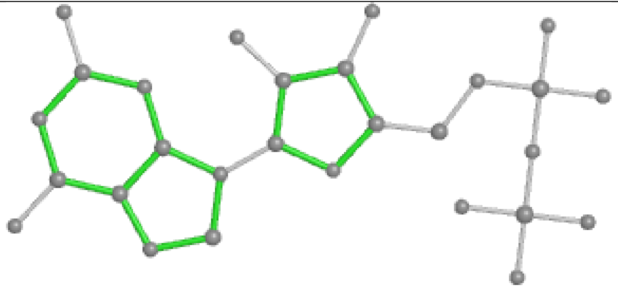


Bond angles

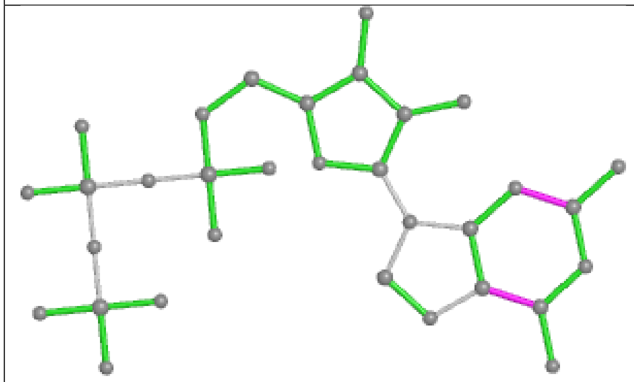


Torsions



Rings

Ligand GTP EE 501



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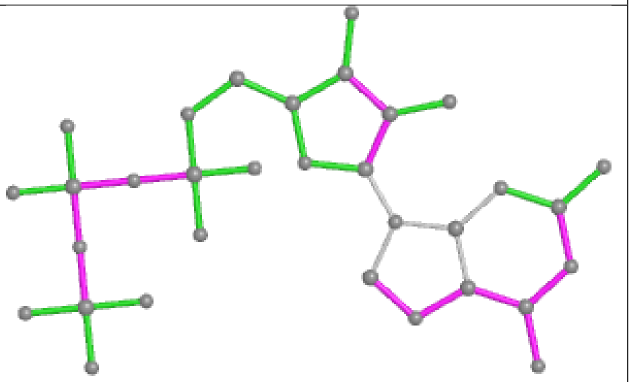

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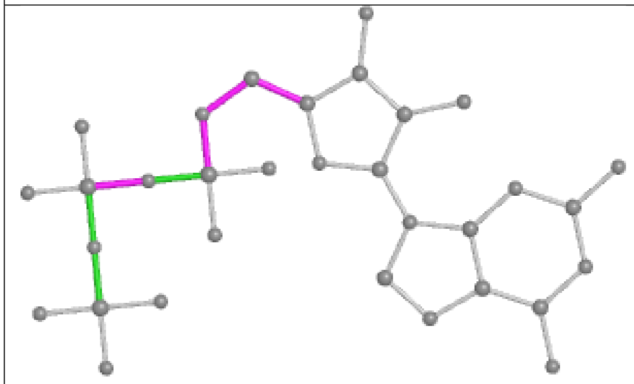
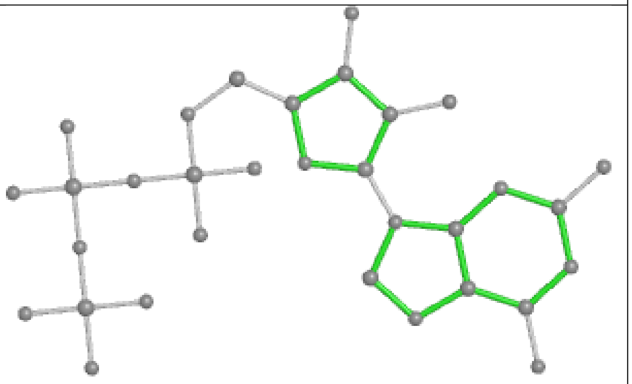


Torsions



Rings

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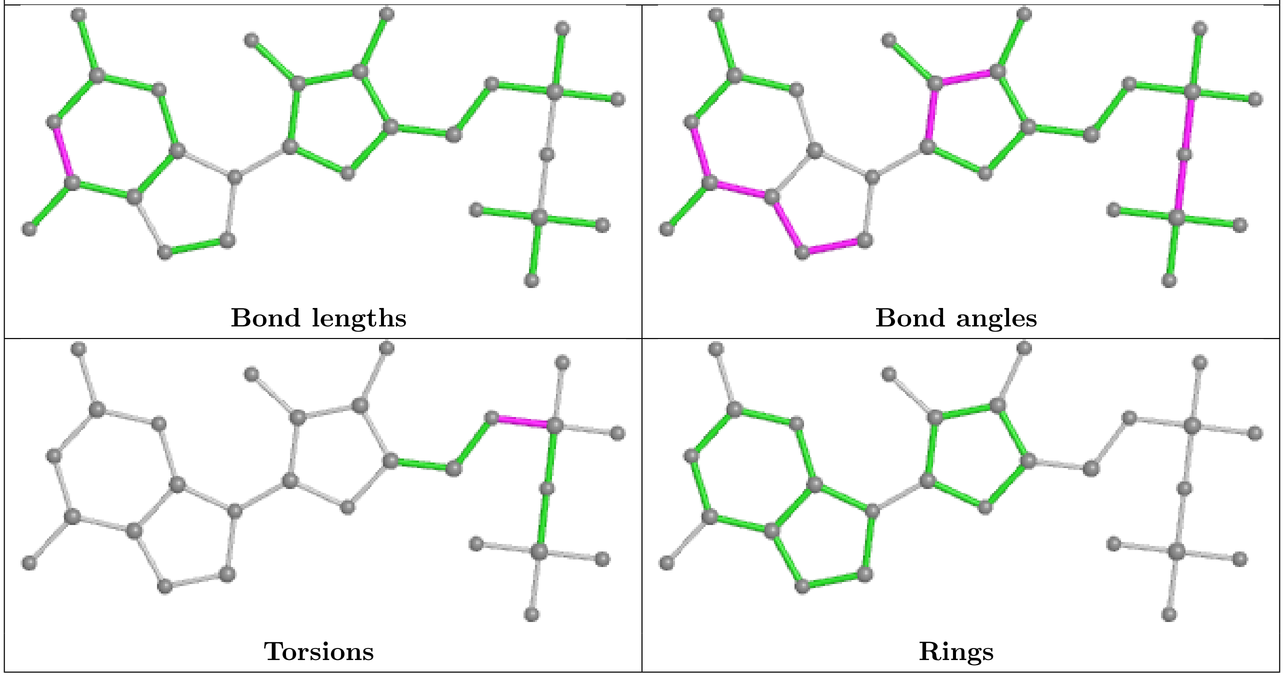

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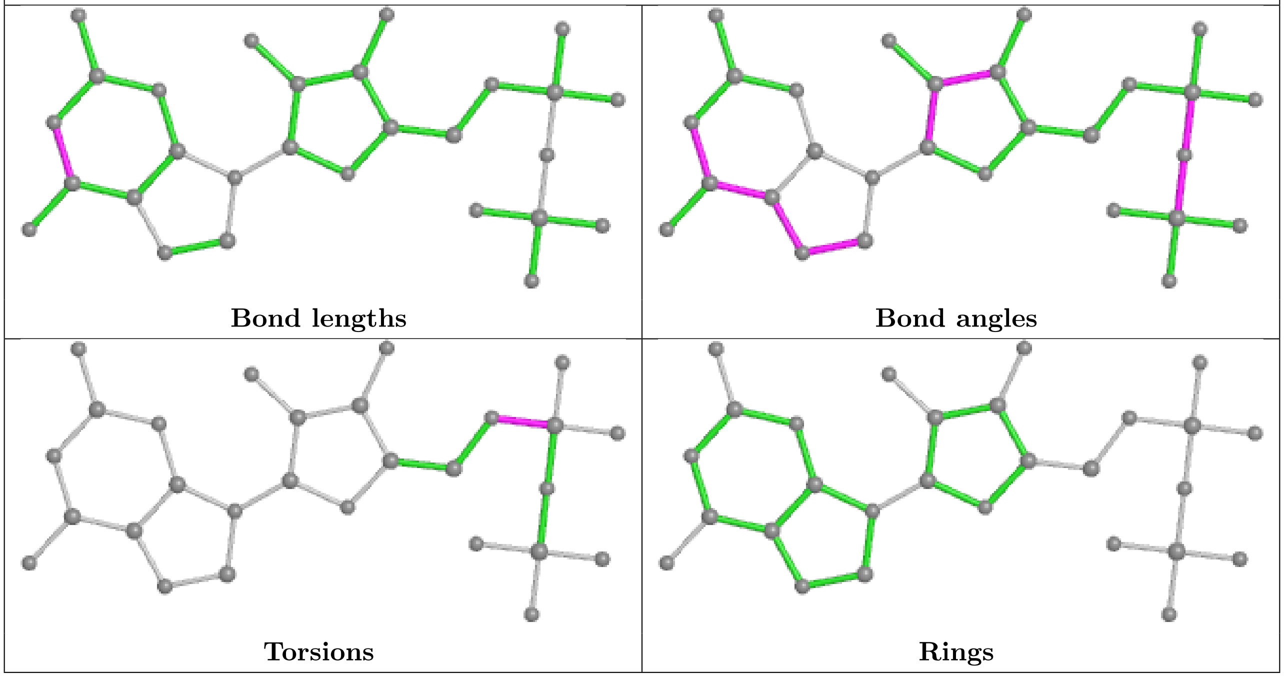

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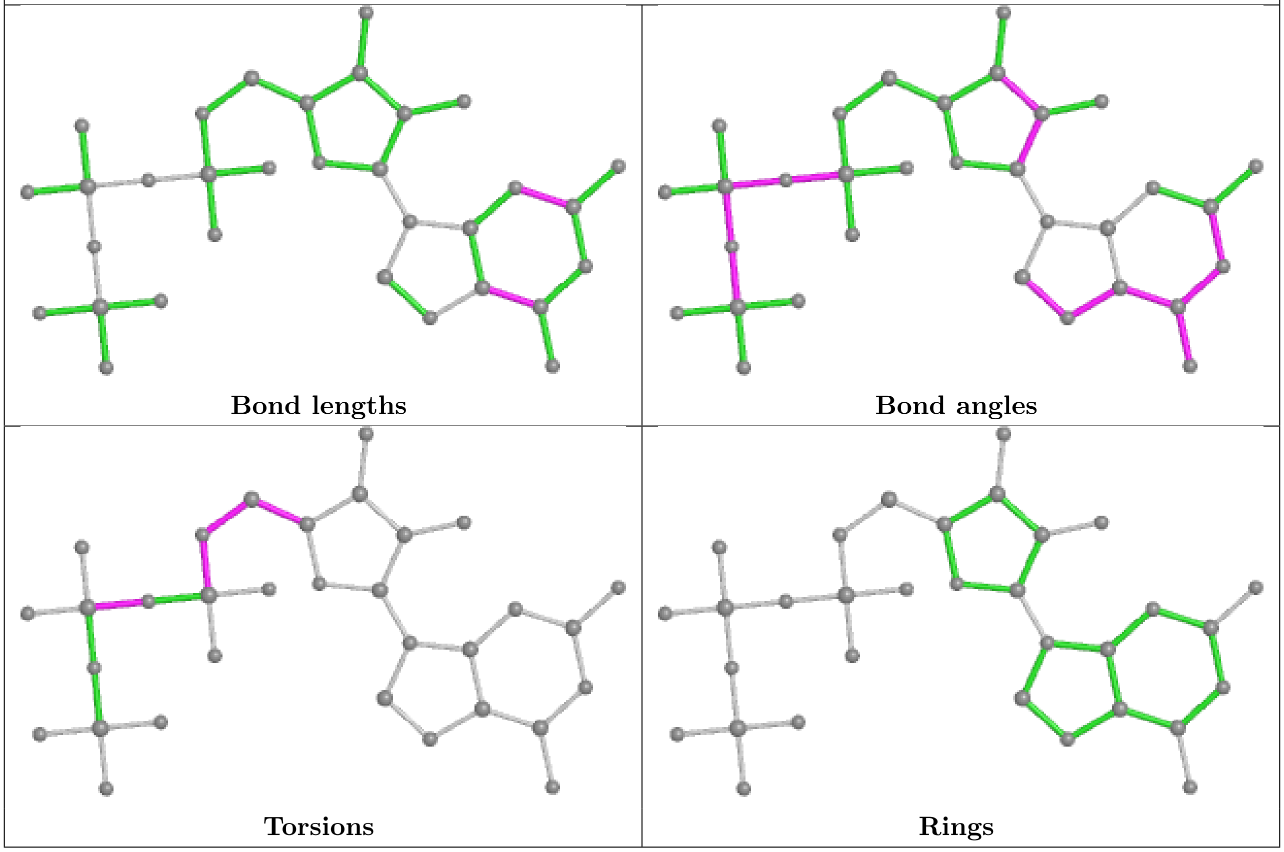

Bond lengths

Bond angles

Torsions

Rings

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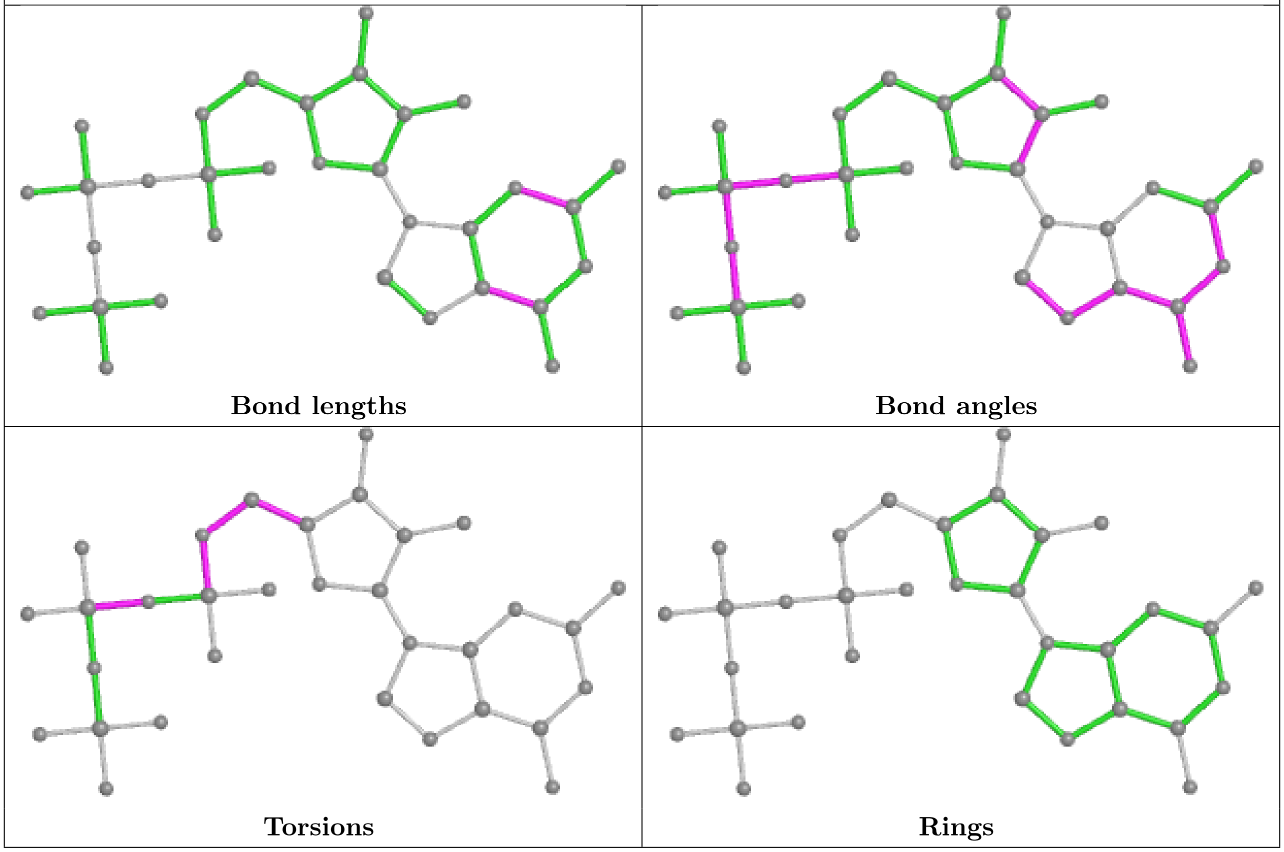

Bond lengths

Bond angles

Torsions

Rings

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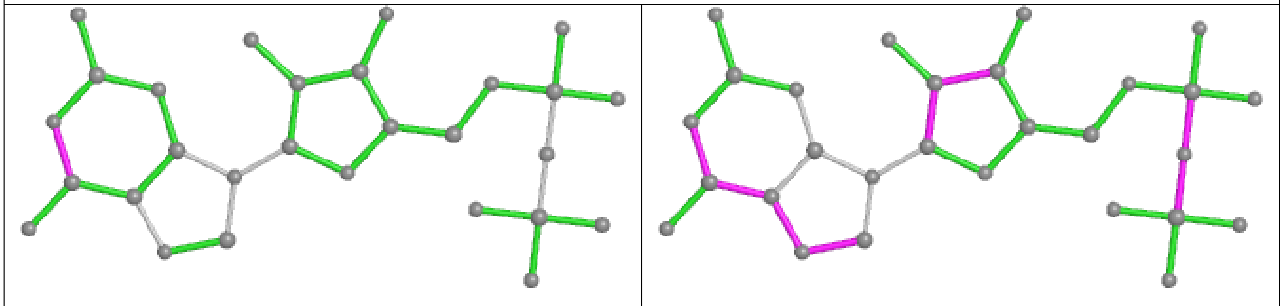

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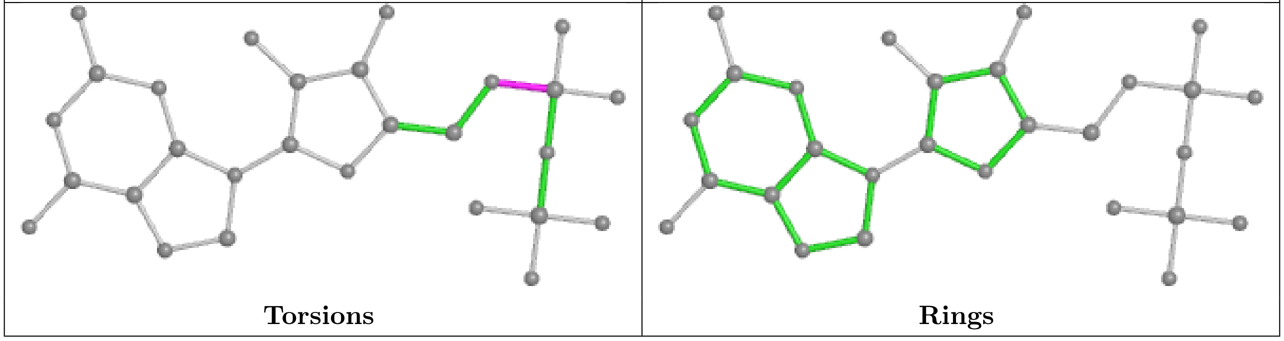

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Rings

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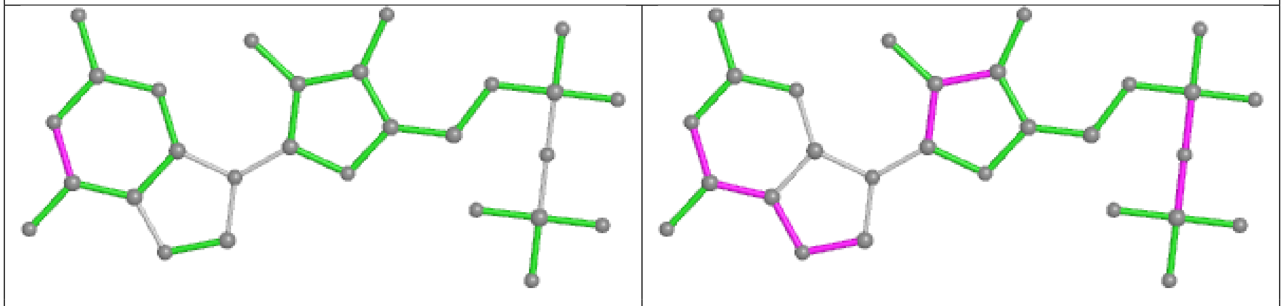

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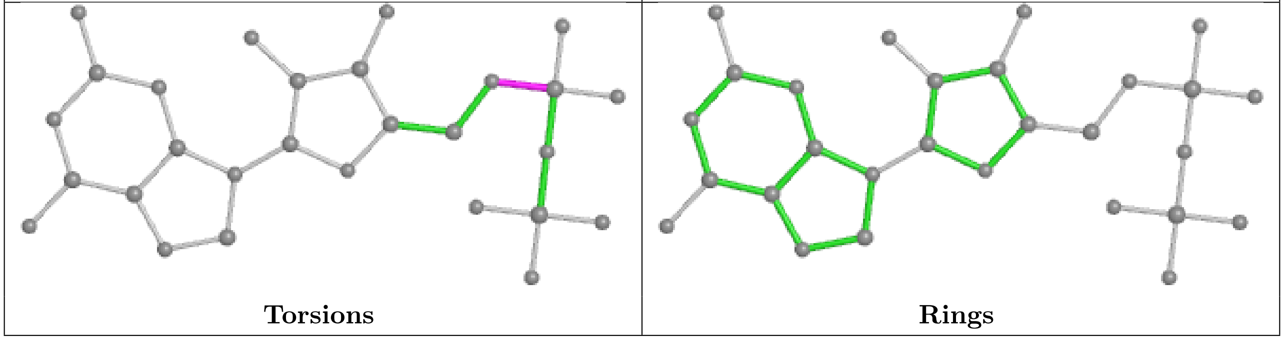

Torsions

Rings

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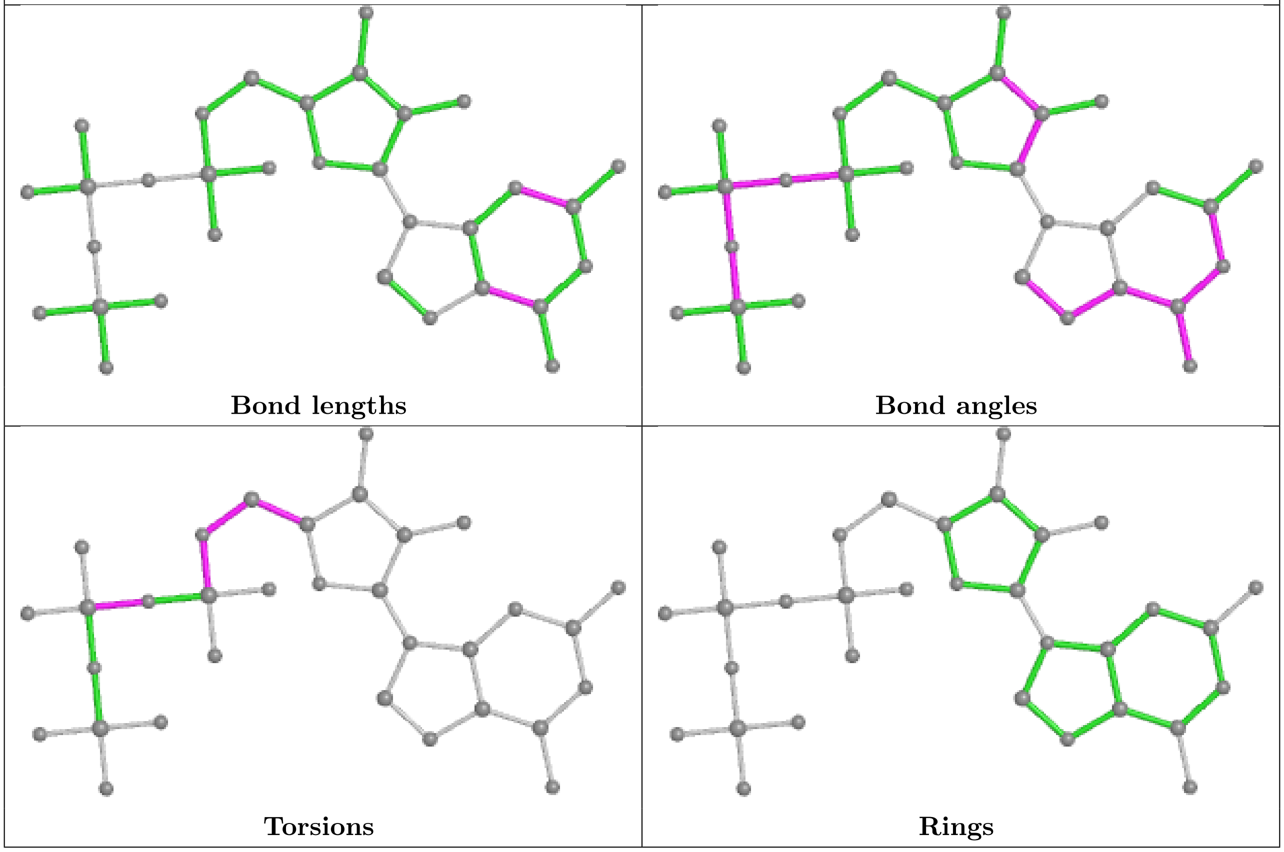

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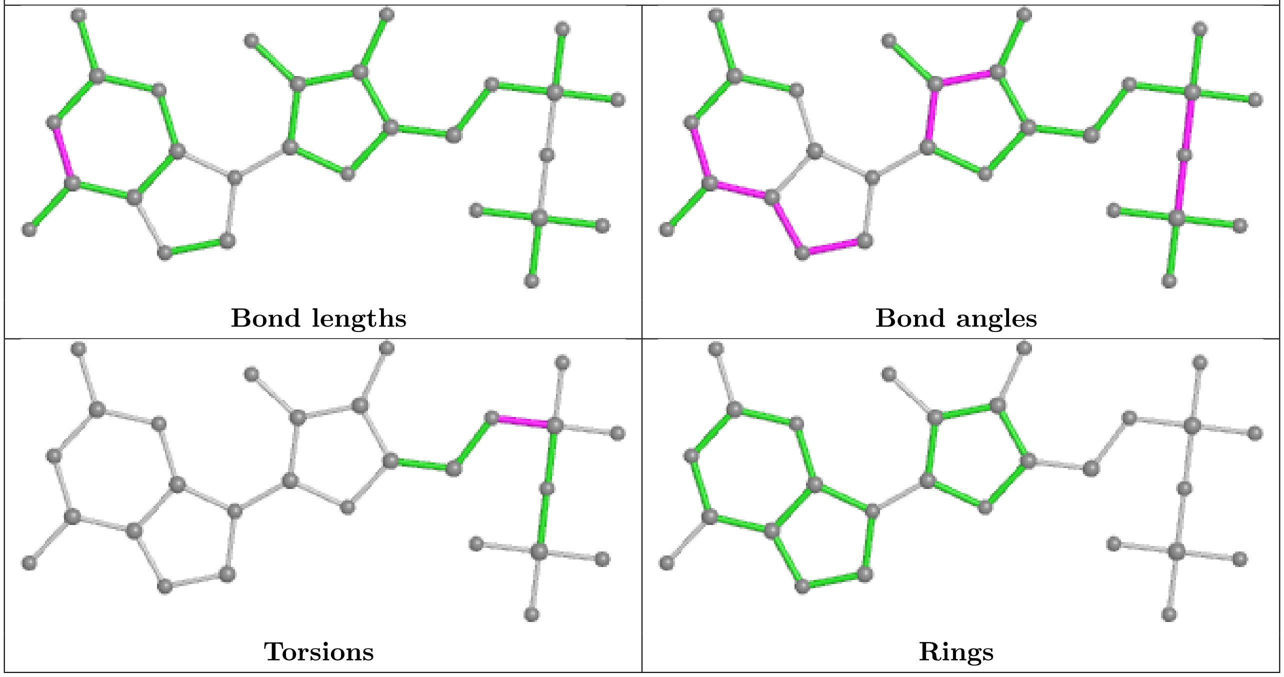

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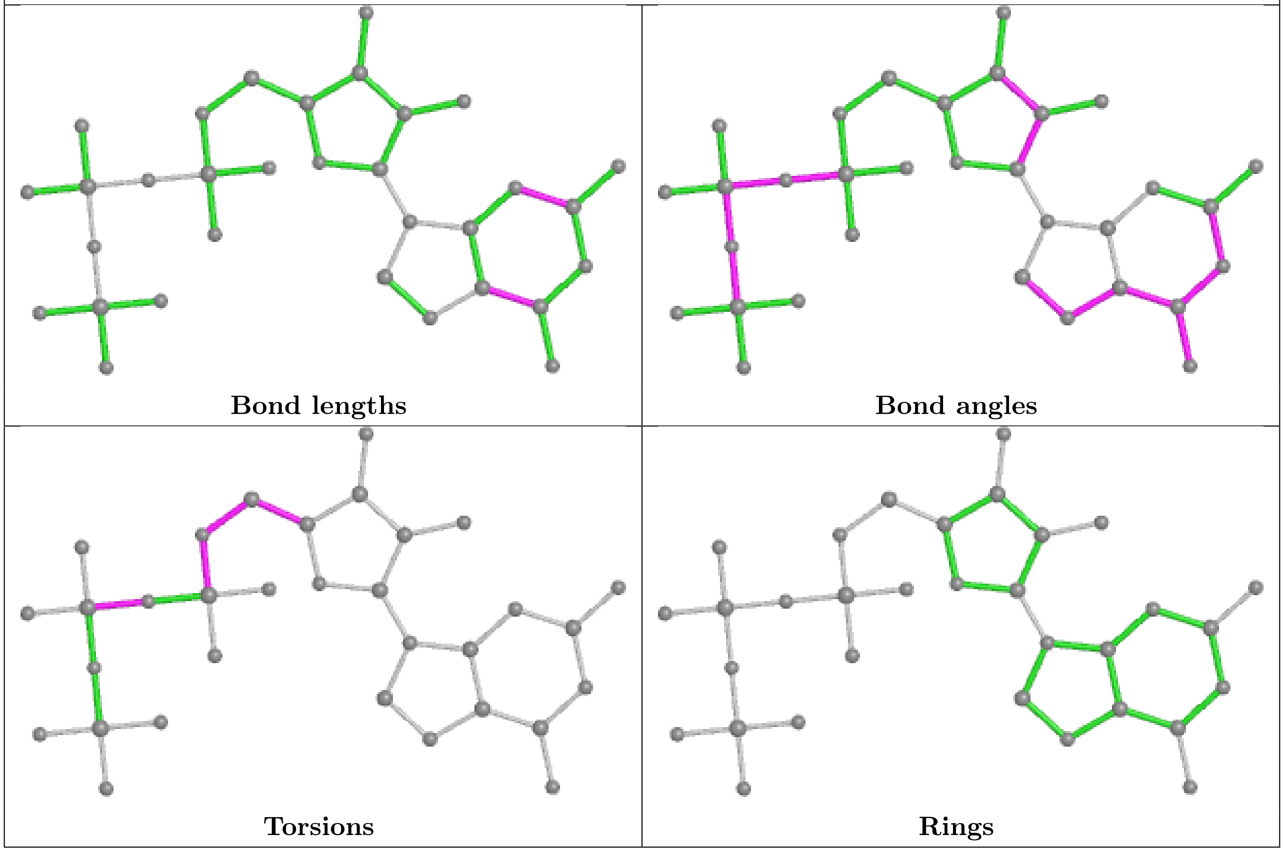

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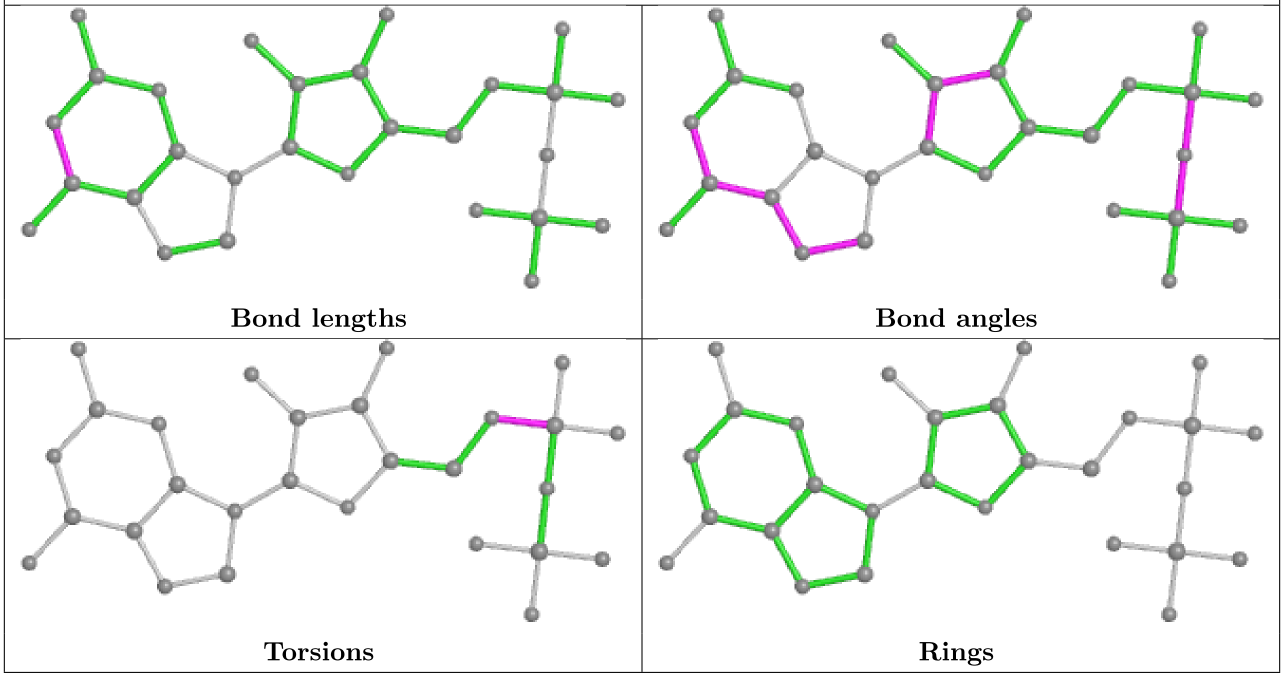

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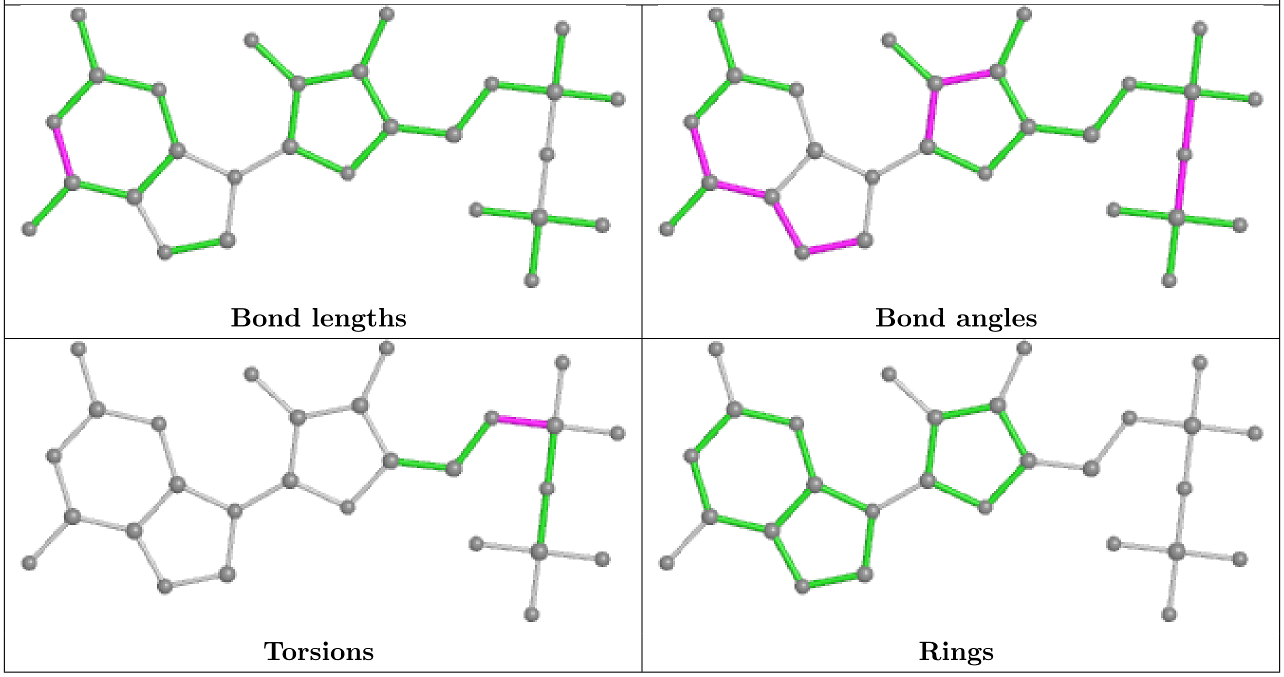

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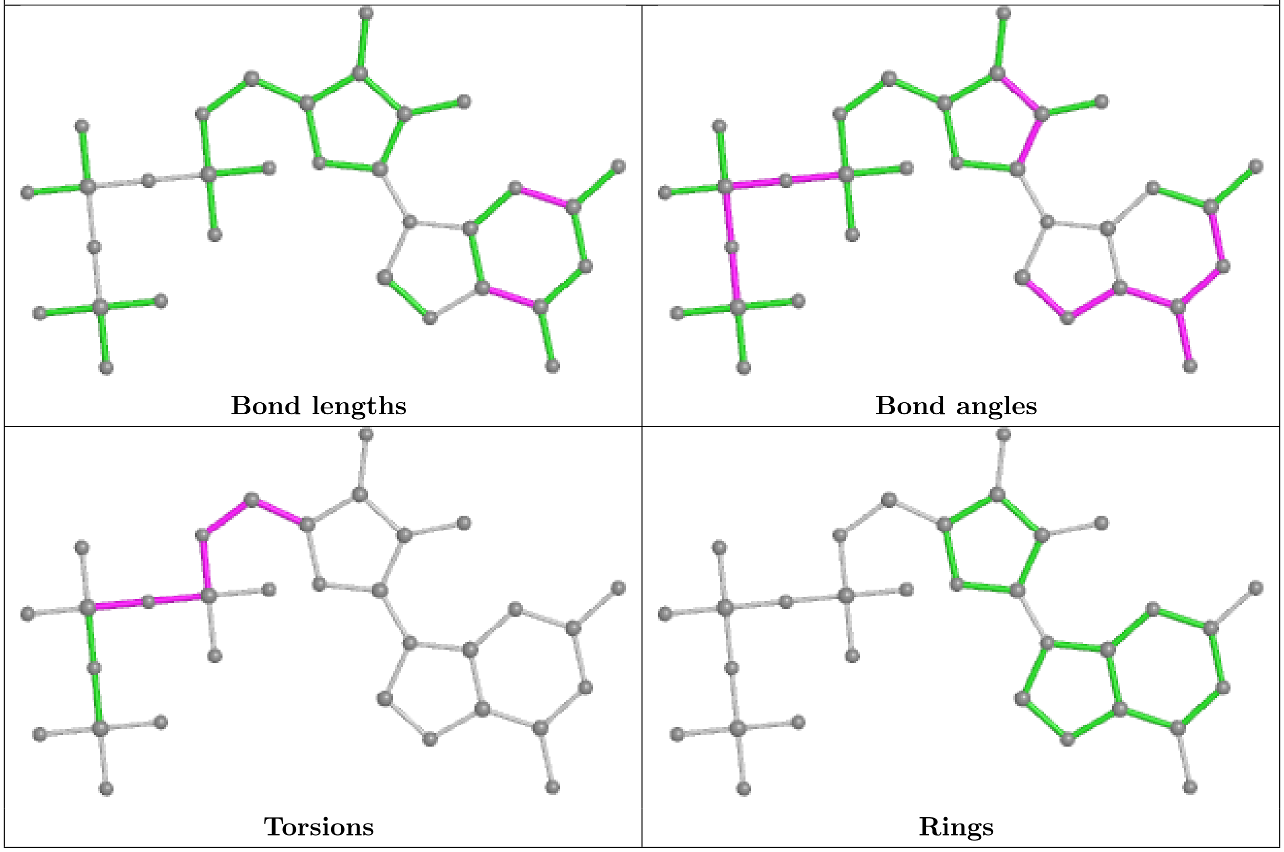

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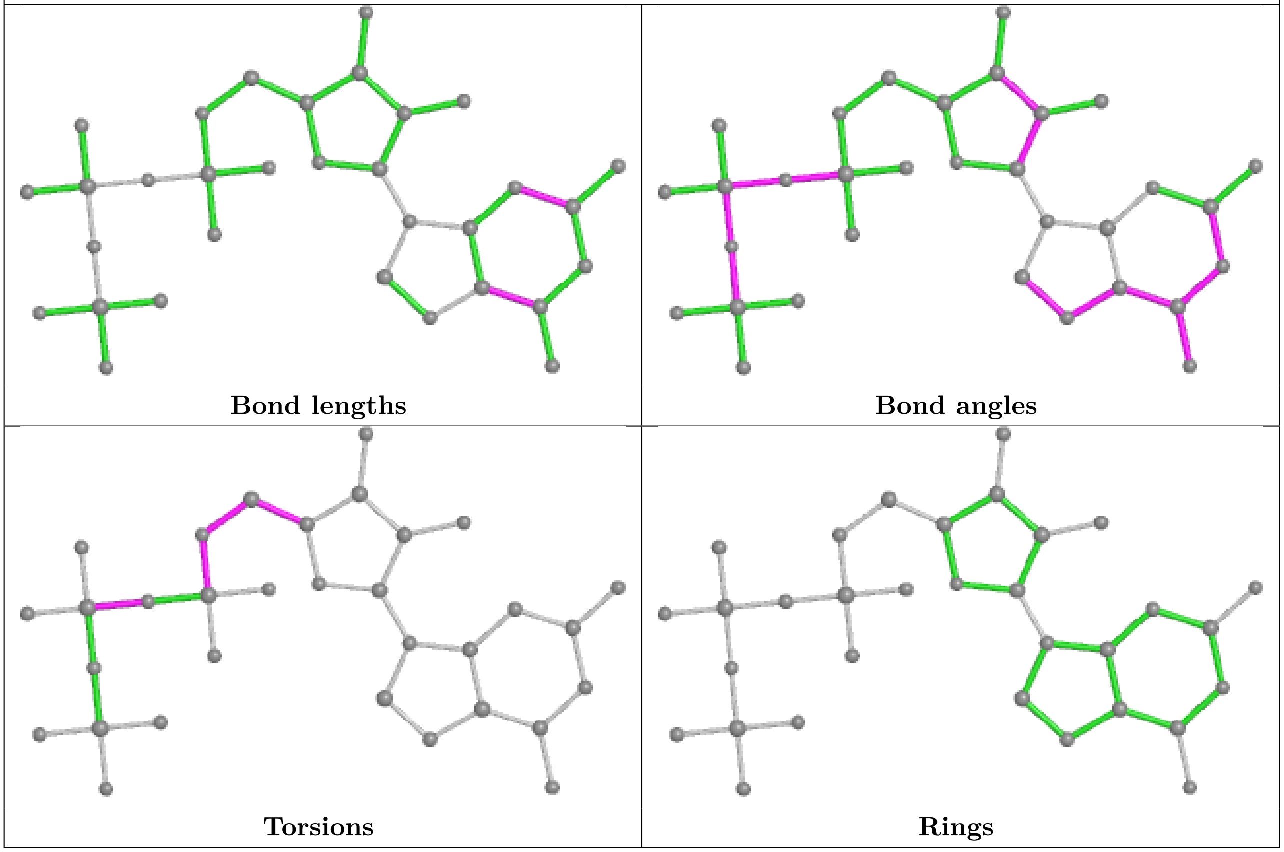
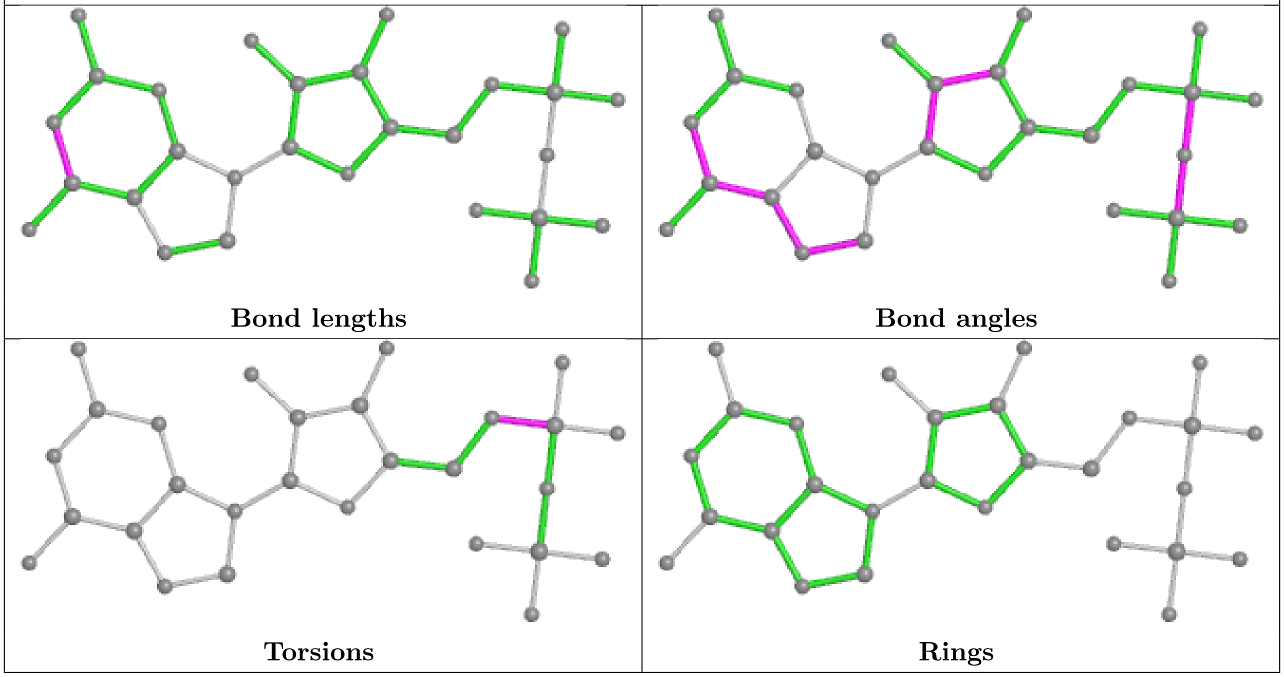


Bond lengths Bond angles

Torsions Rings

Ligand GDP MN 502



Bond lengths Bond angles

Torsions Rings

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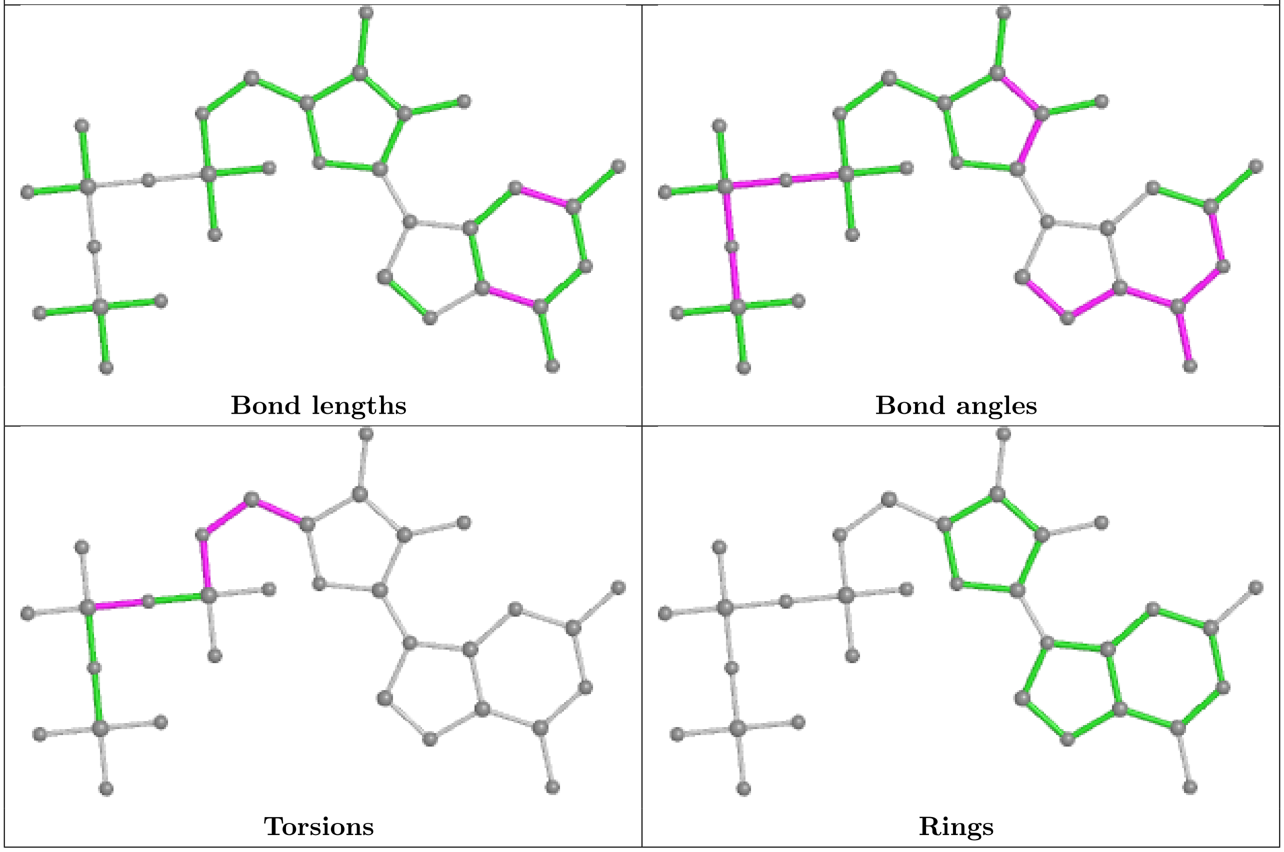

Bond lengths

Bond angles

Torsions

Rings

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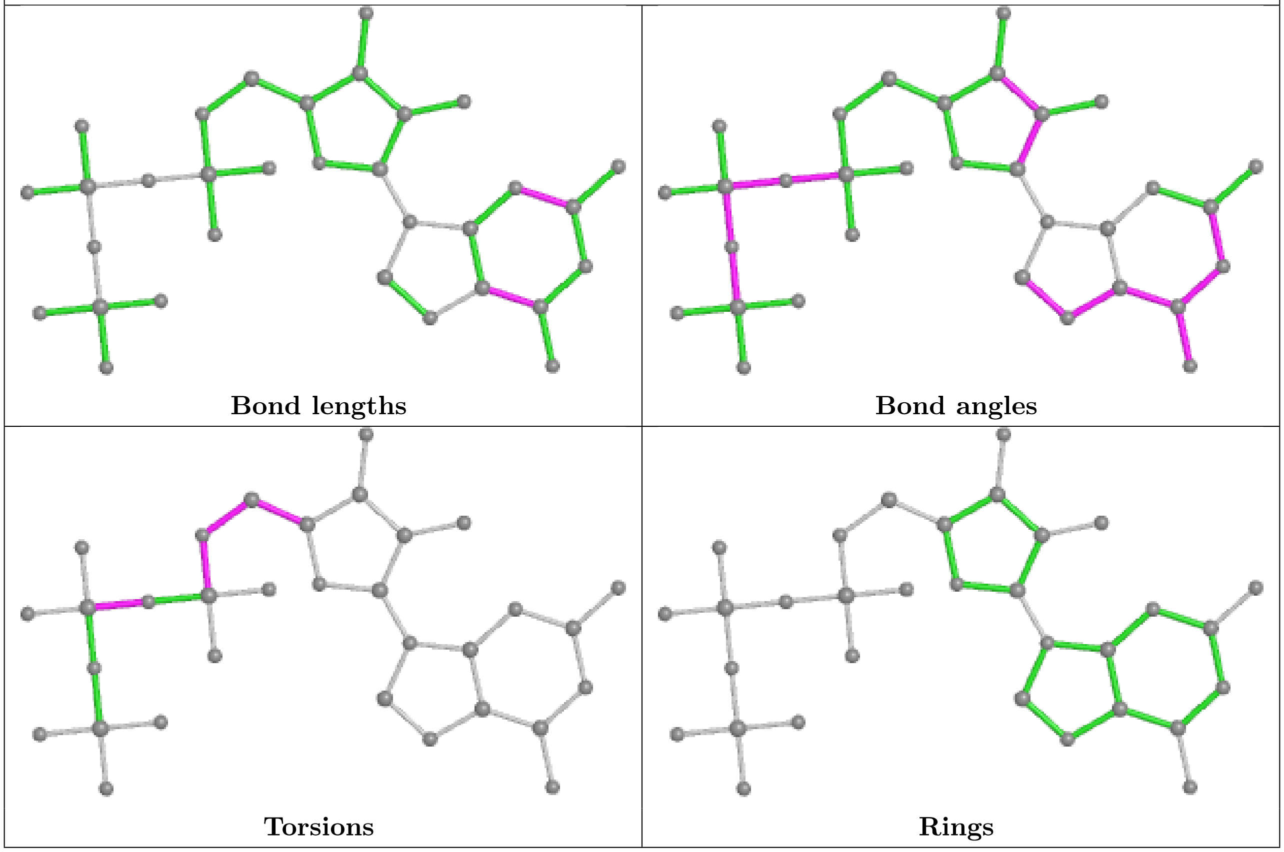

Bond lengths

Bond angles

Torsions

Rings

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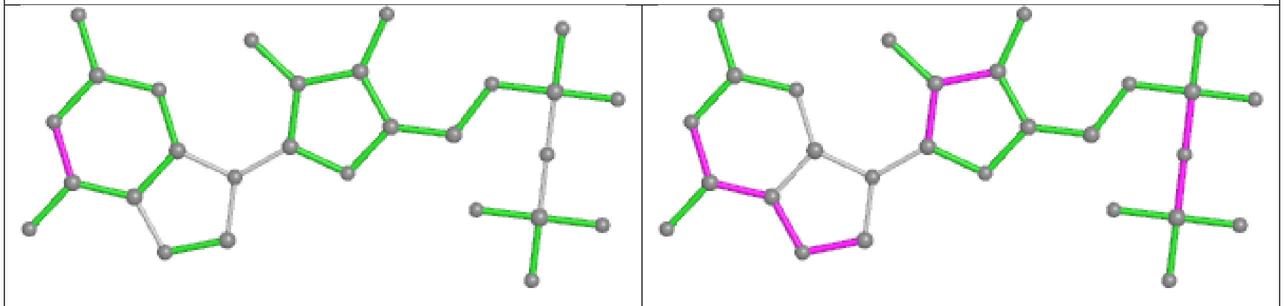
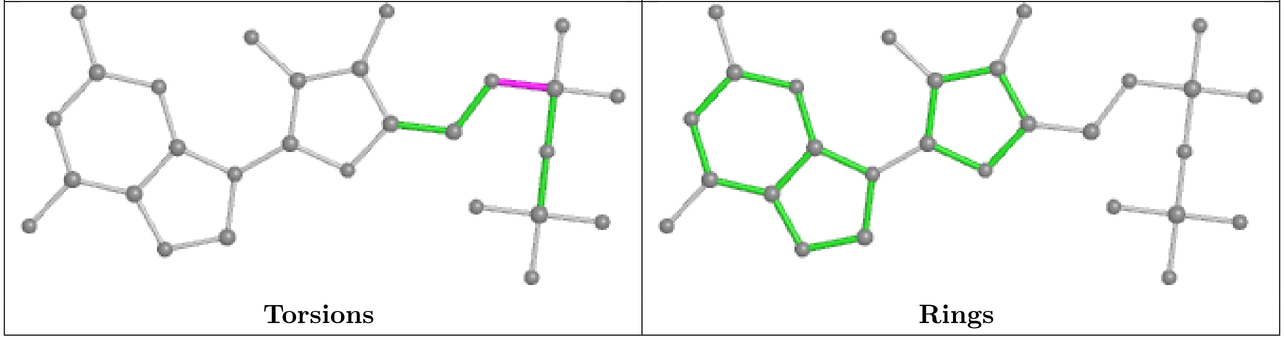
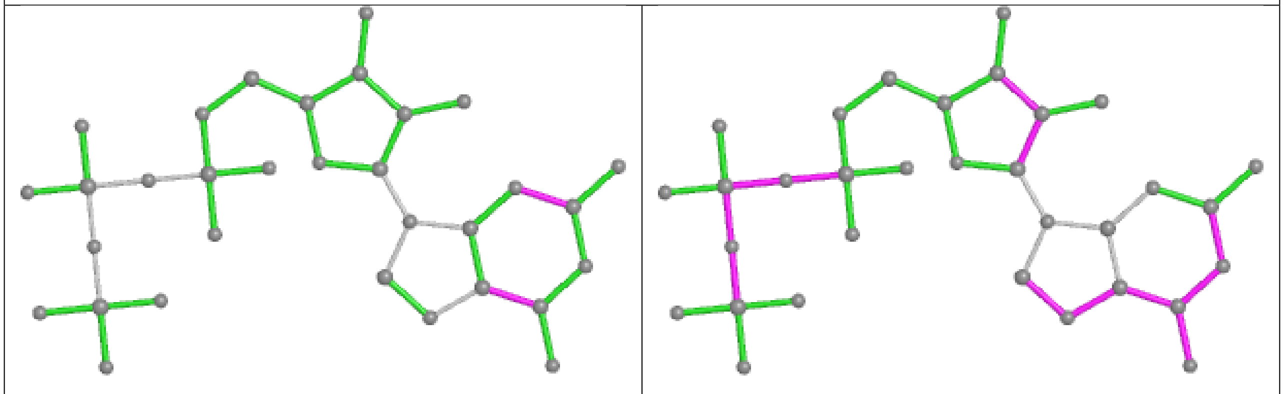


Bond lengths **Bond angles**

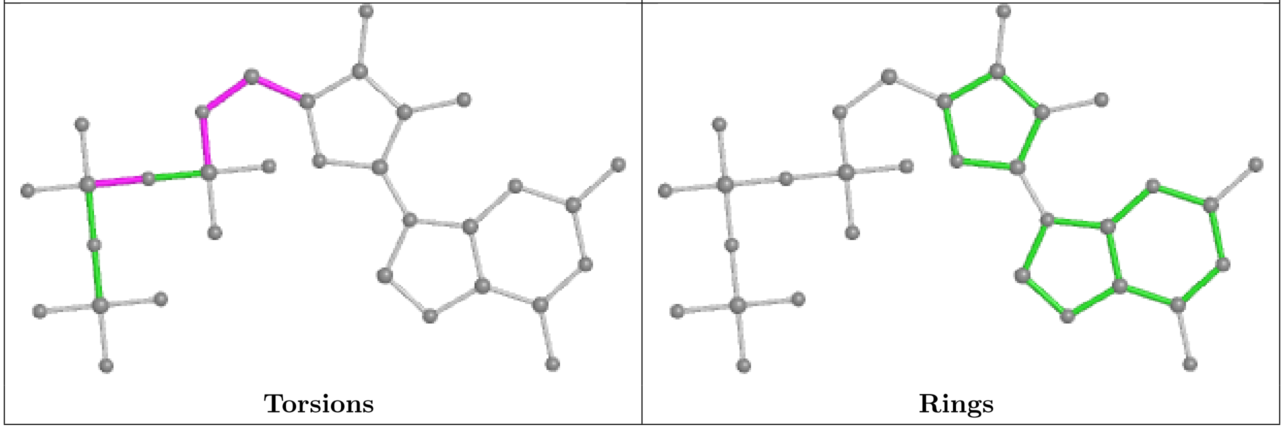


Torsions **Rings**

Ligand GTP DM 501



Bond lengths **Bond angles**



Torsions **Rings**

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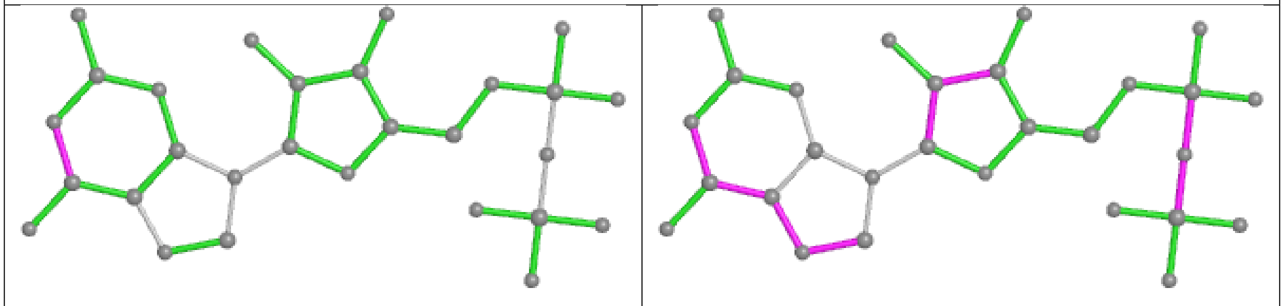
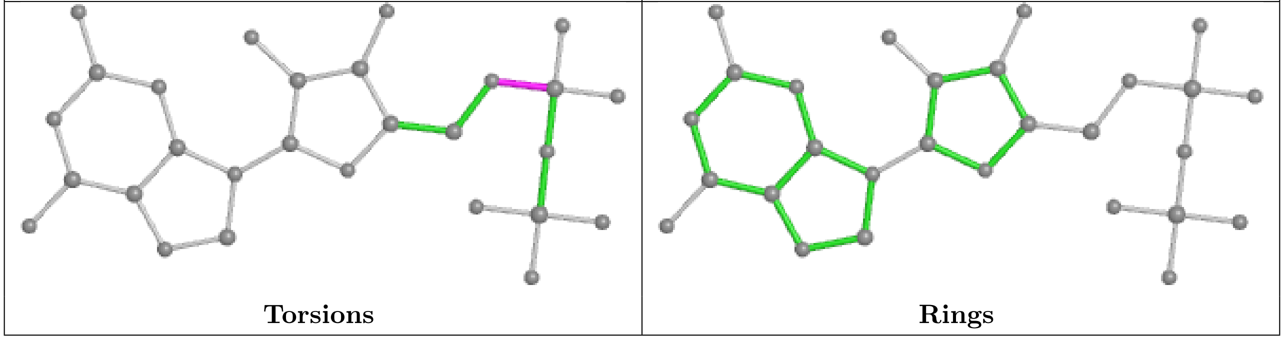


Bond lengths

Bond angles



Torsions

Rings

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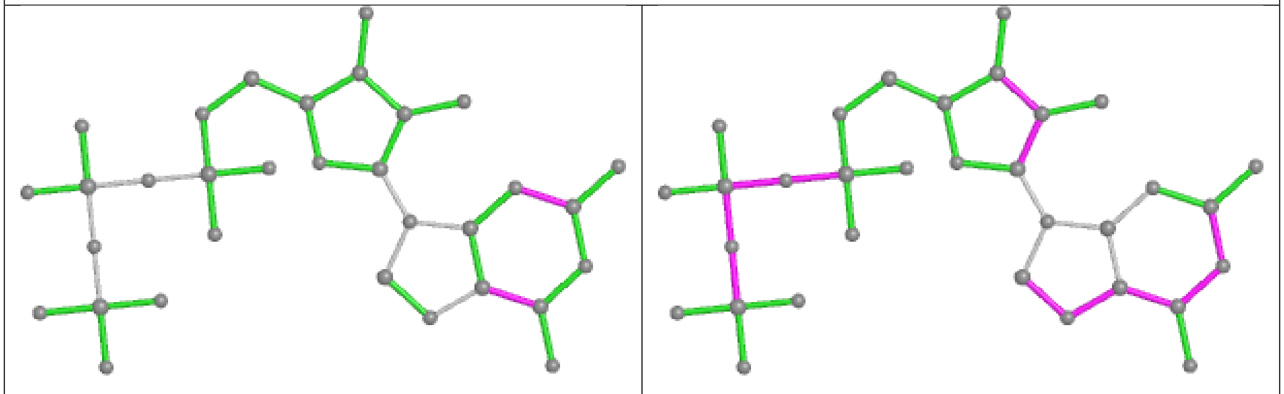
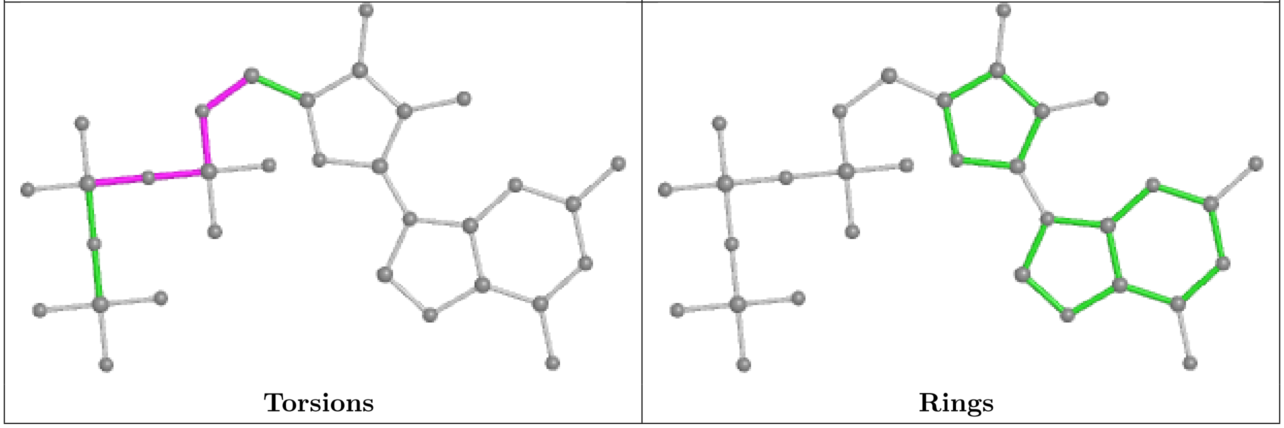


Bond lengths

Bond angles



Torsions

Rings

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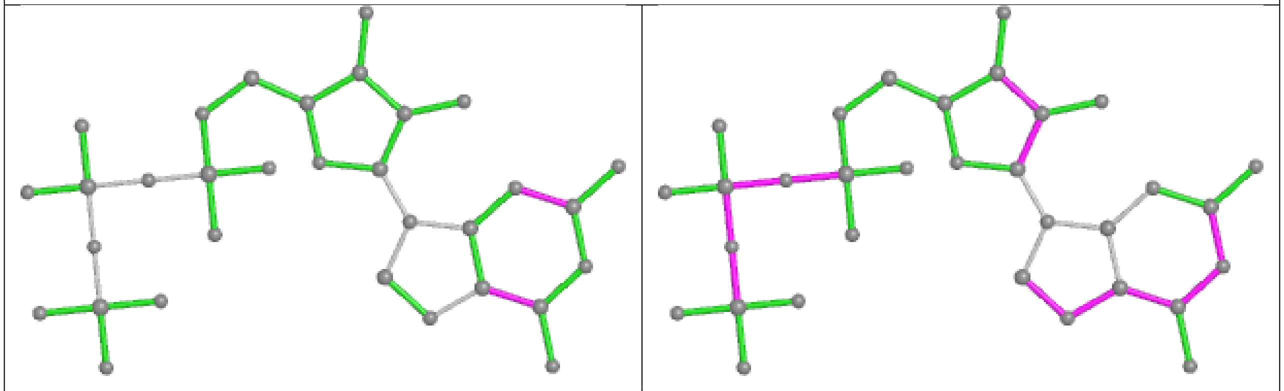
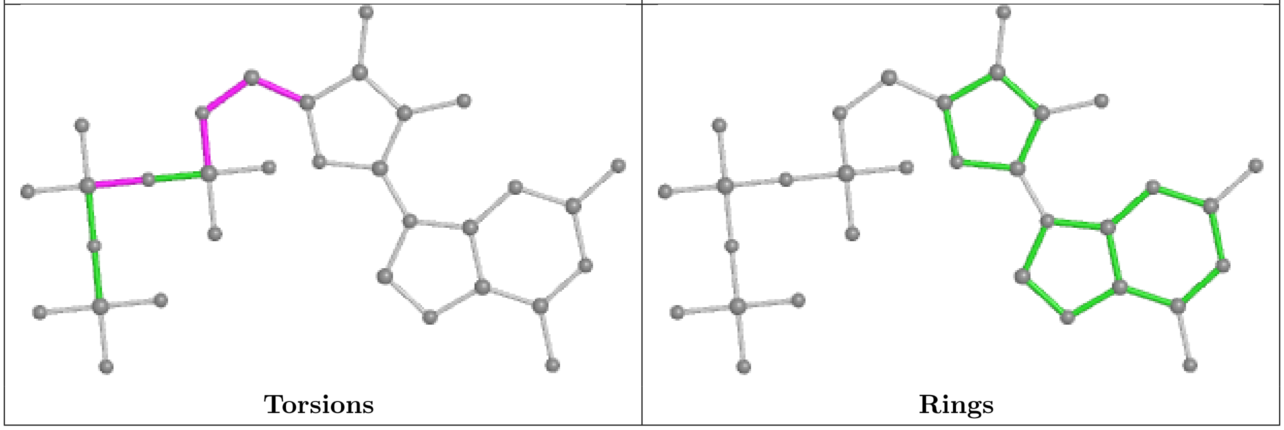

Bond lengths Bond angles


Torsions Rings

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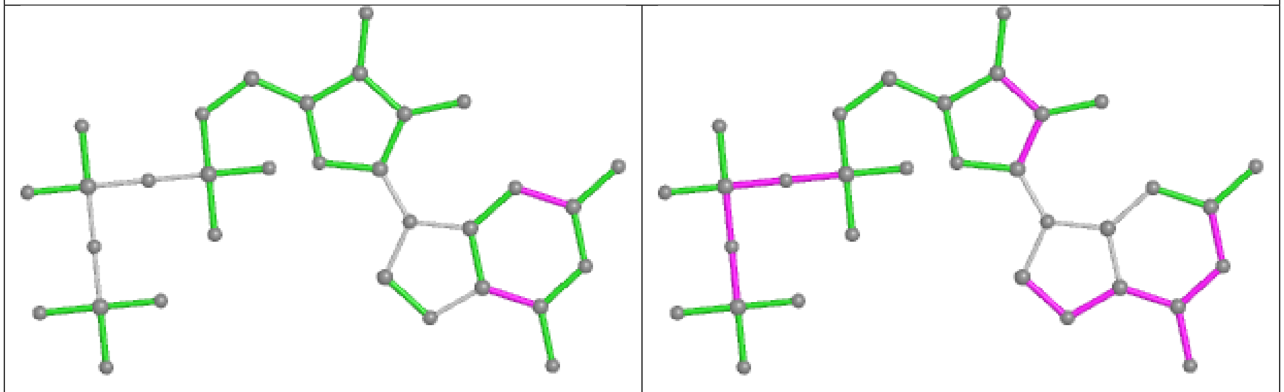
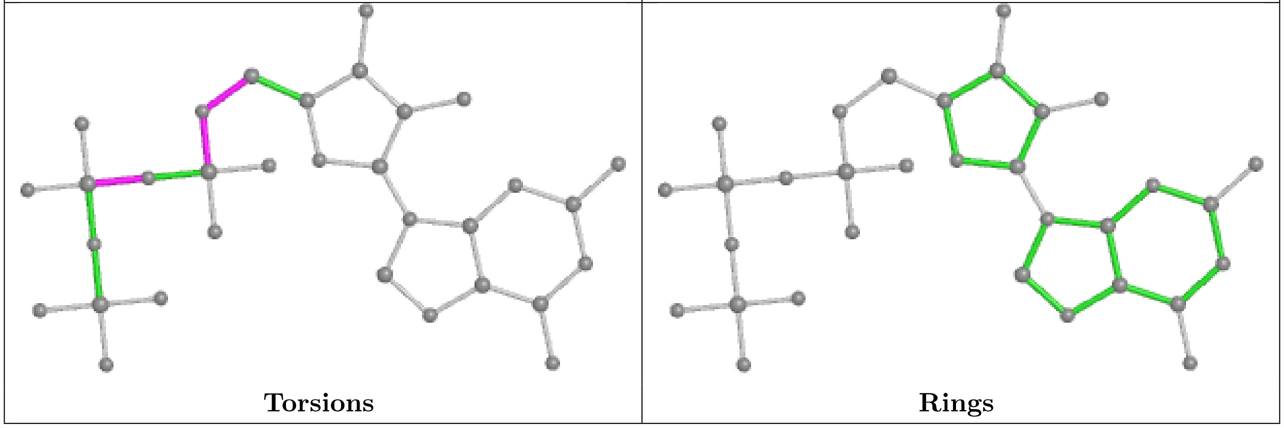

Bond lengths Bond angles


Torsions Rings

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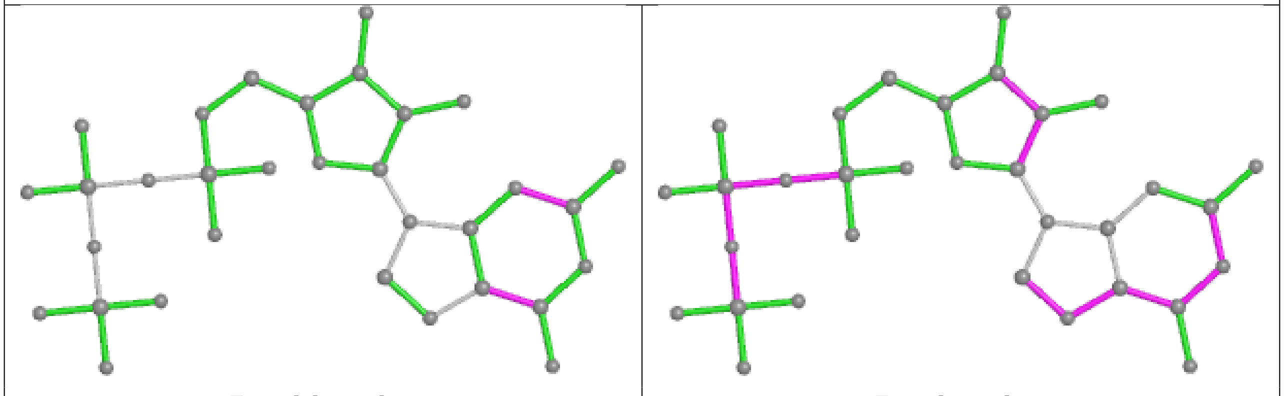

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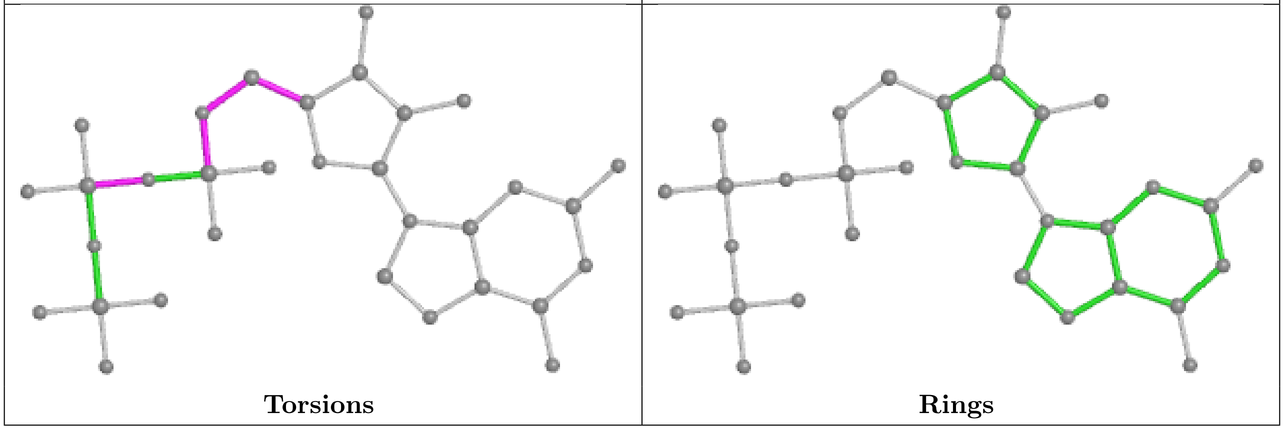
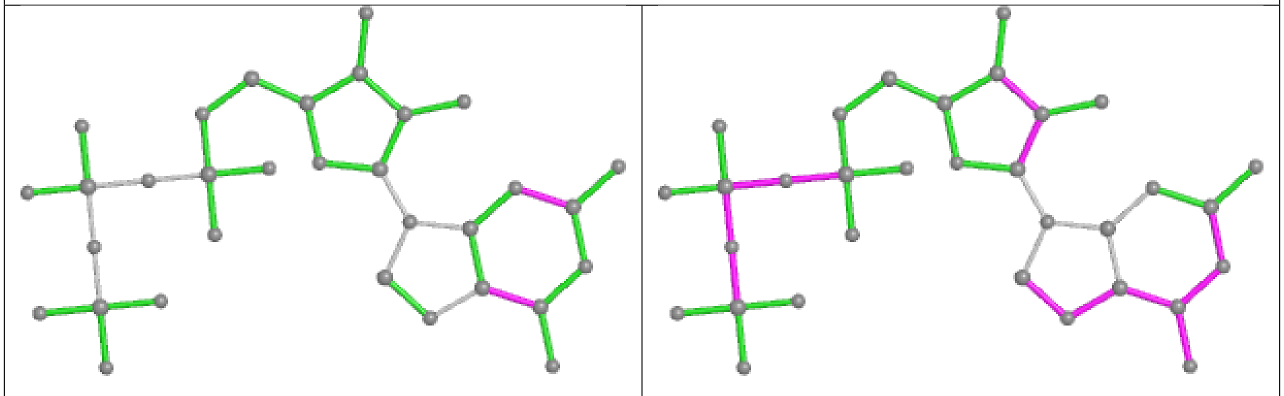
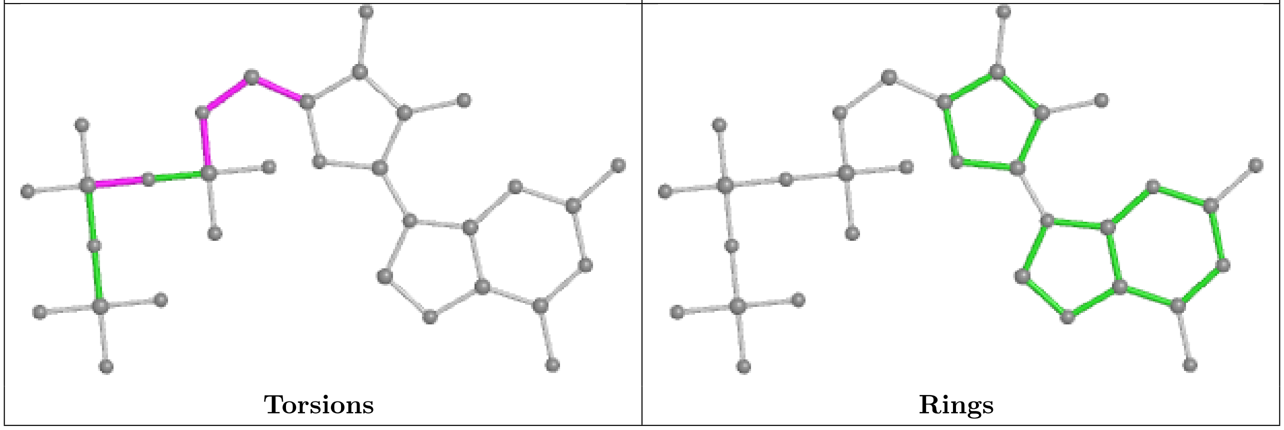


Torsions Rings

Ligand GTP MO 501

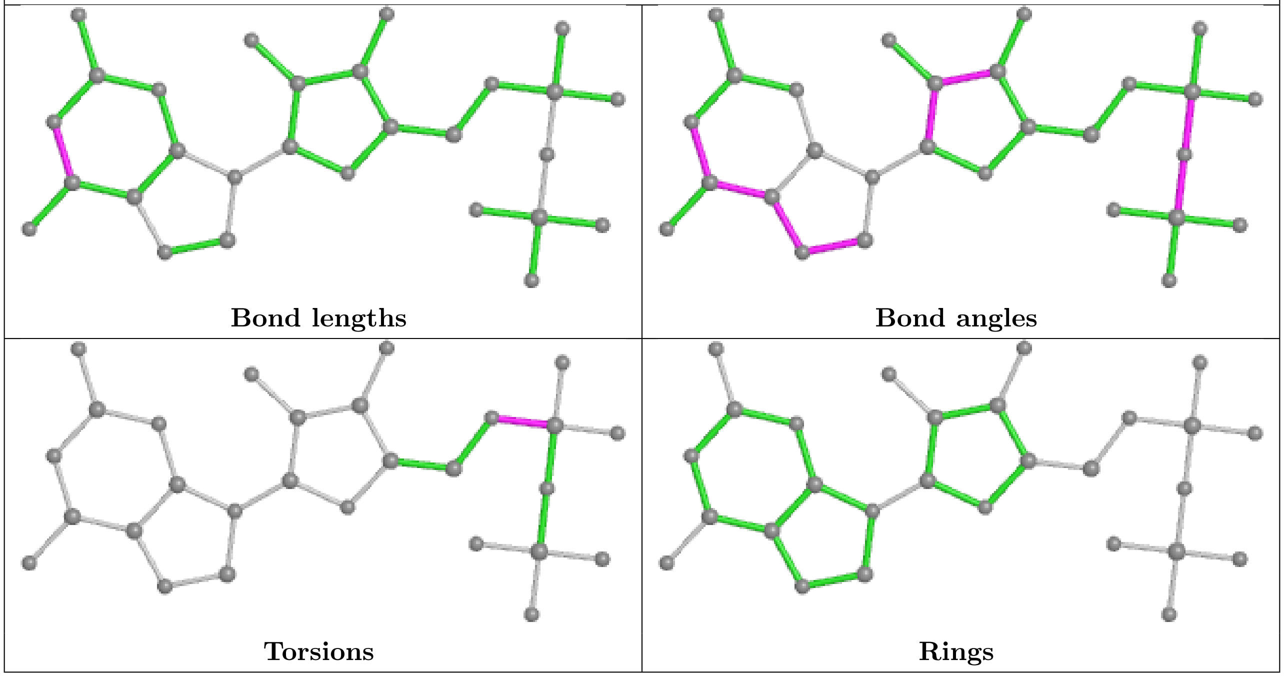


Bond lengths Bond angles



Torsions Rings

Ligand GDP JL 502



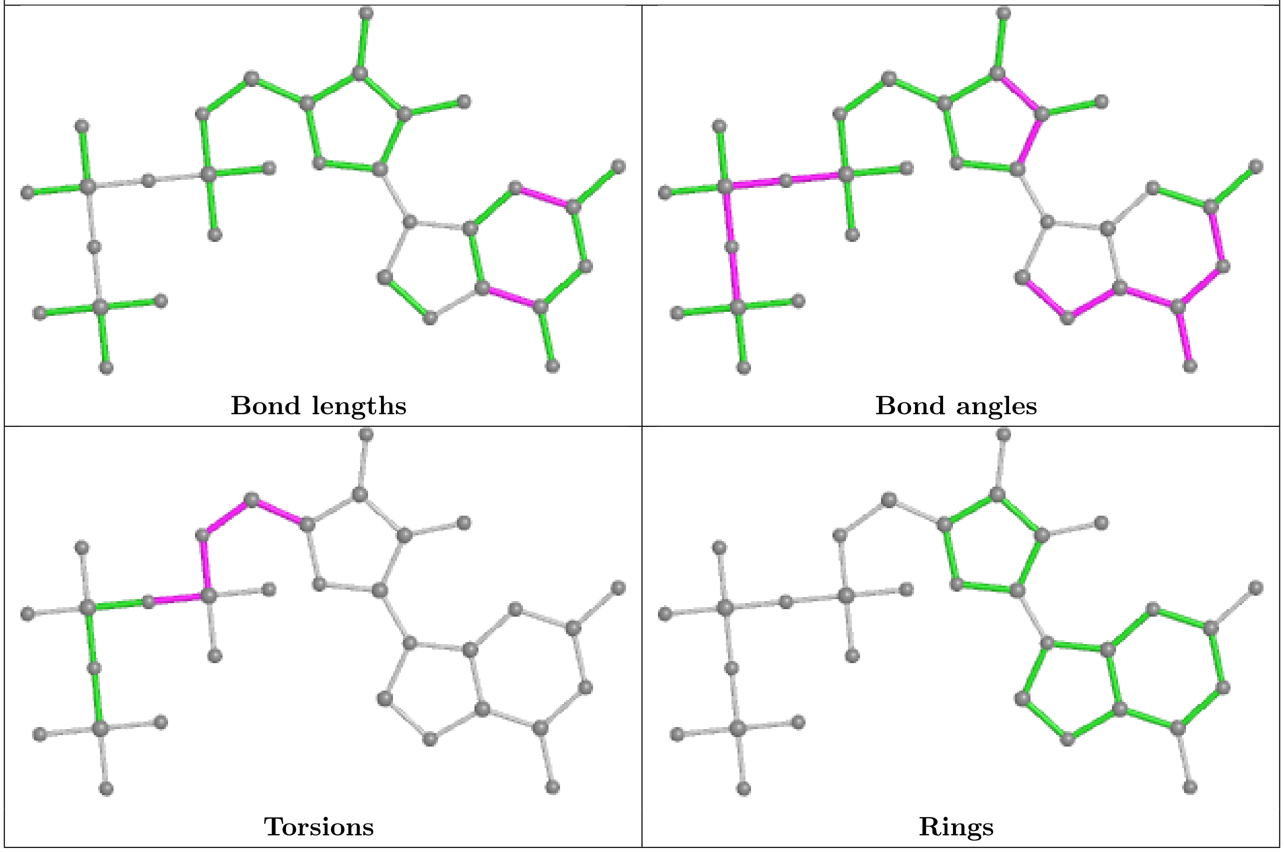
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP NC 501



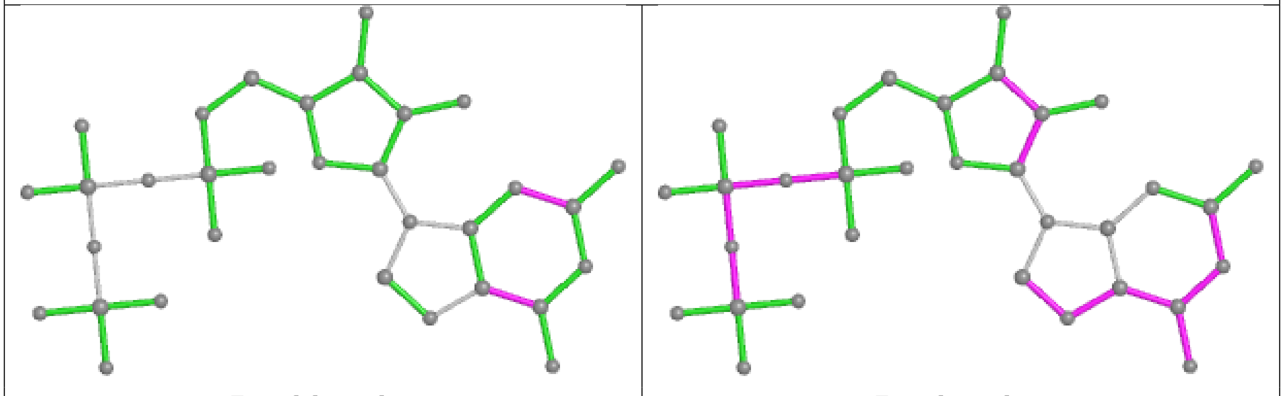
Bond lengths

Bond angles

Torsions

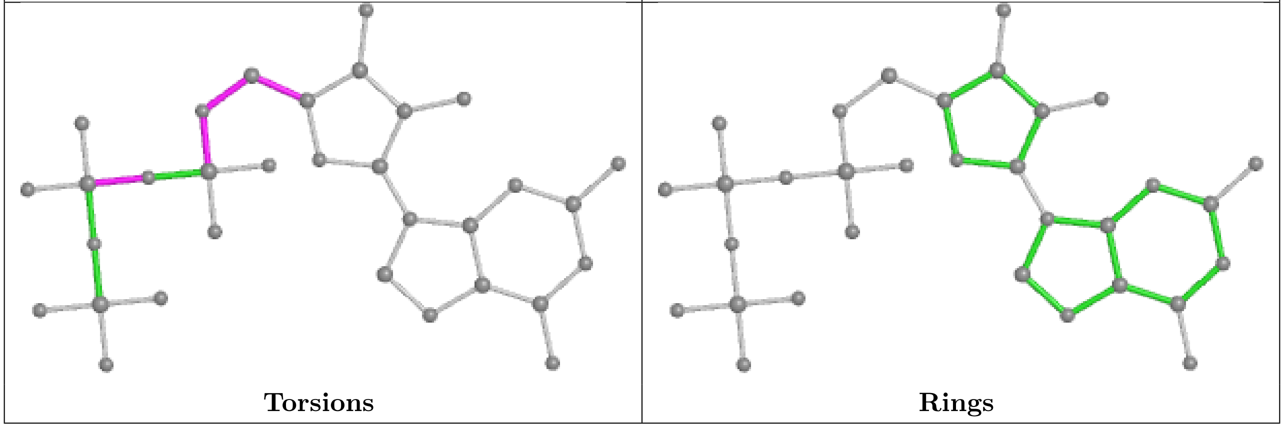
Rings

Ligand GTP CO 501



Bond lengths

Bond angles



Torsions

Rings

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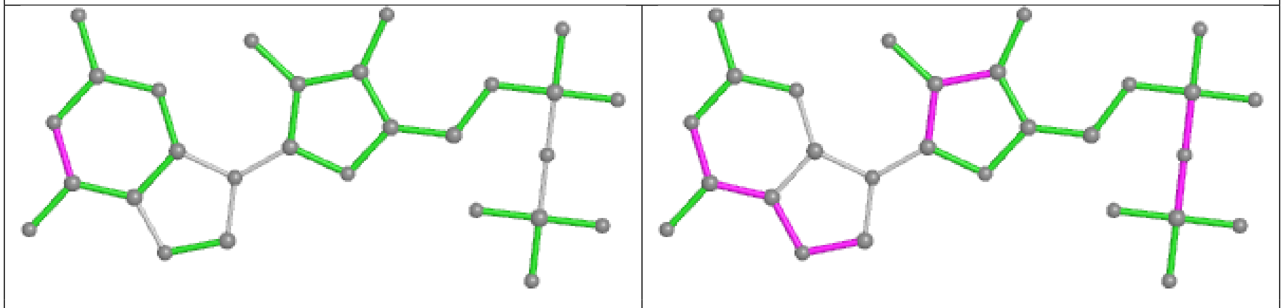
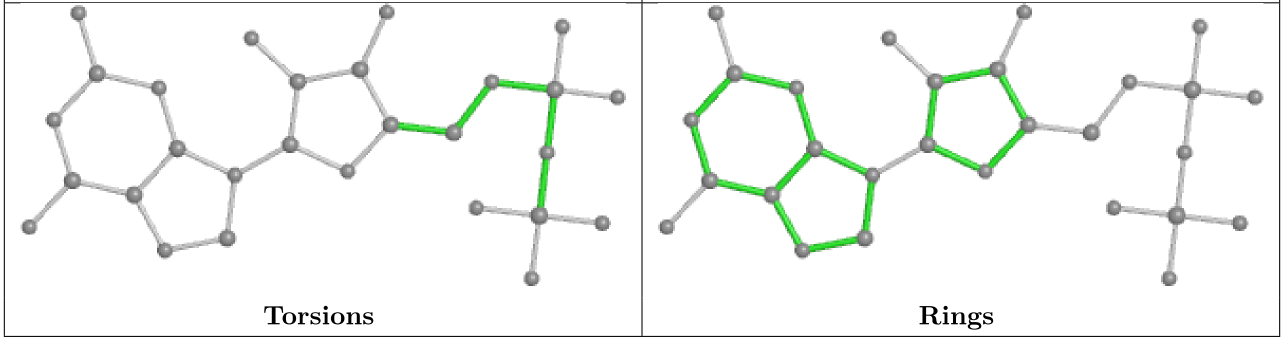


Bond lengths

Bond angles



Torsions

Rings

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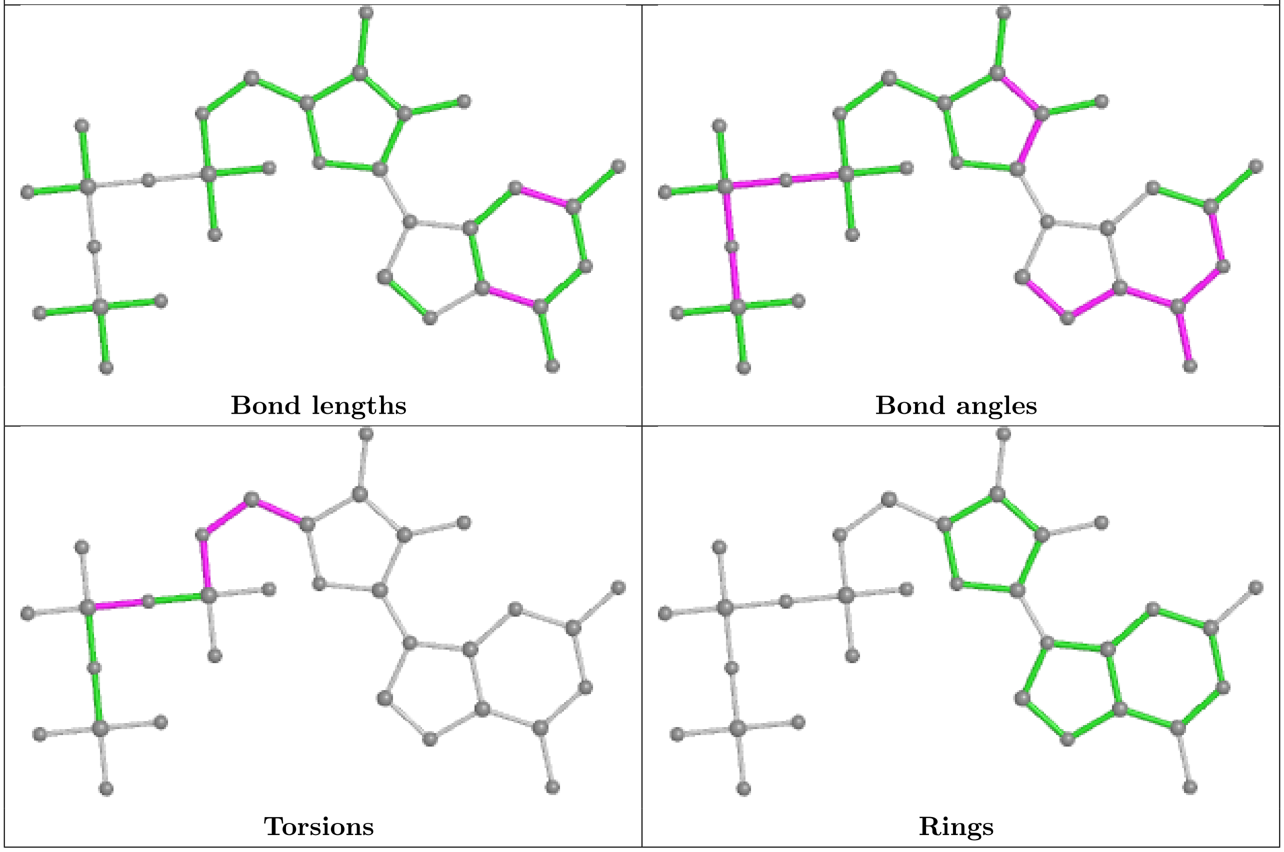

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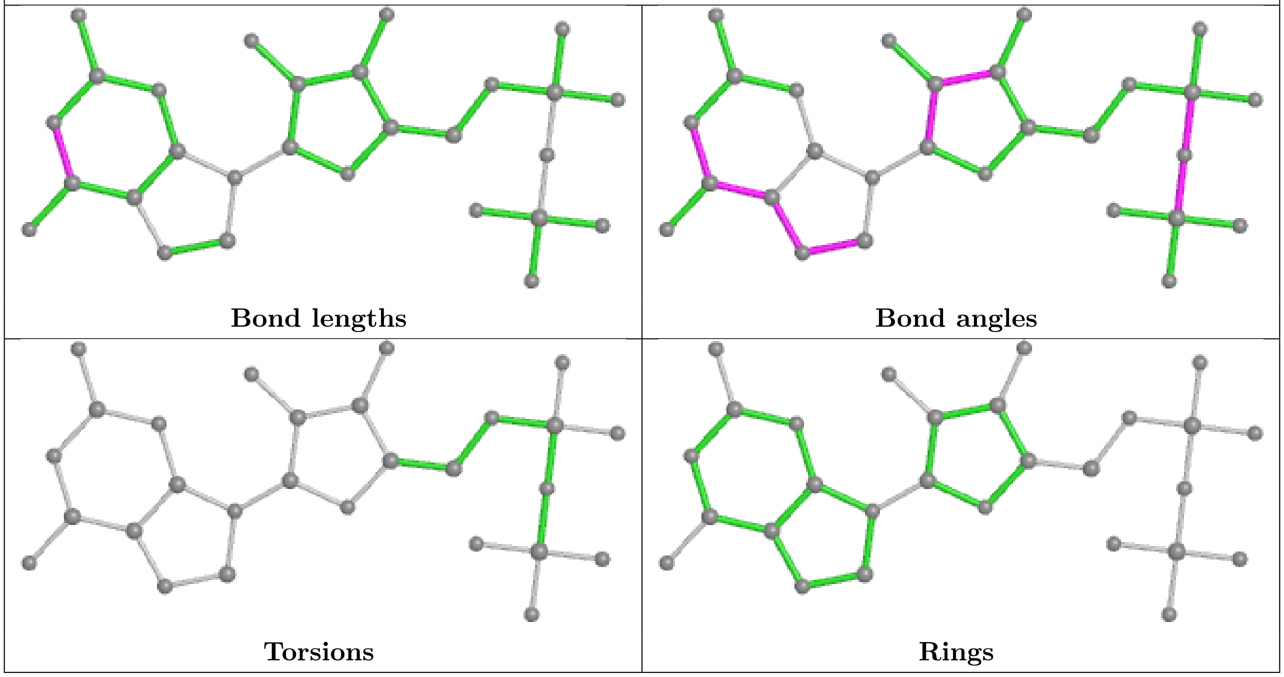

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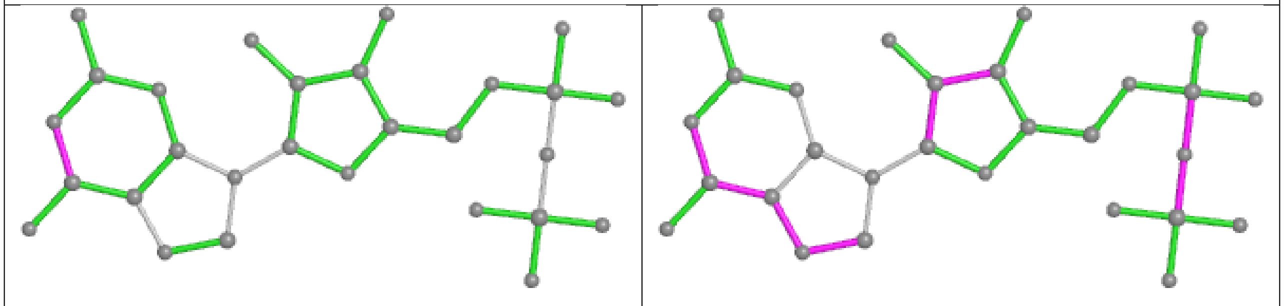
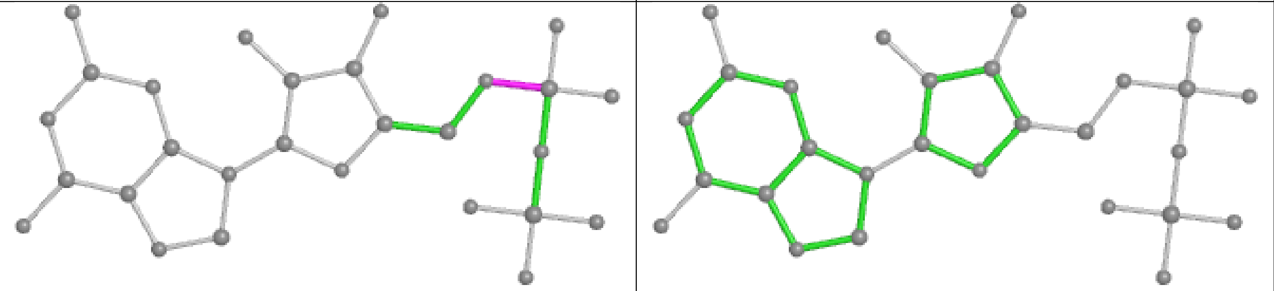


Bond lengths

Bond angles



Torsions

Rings

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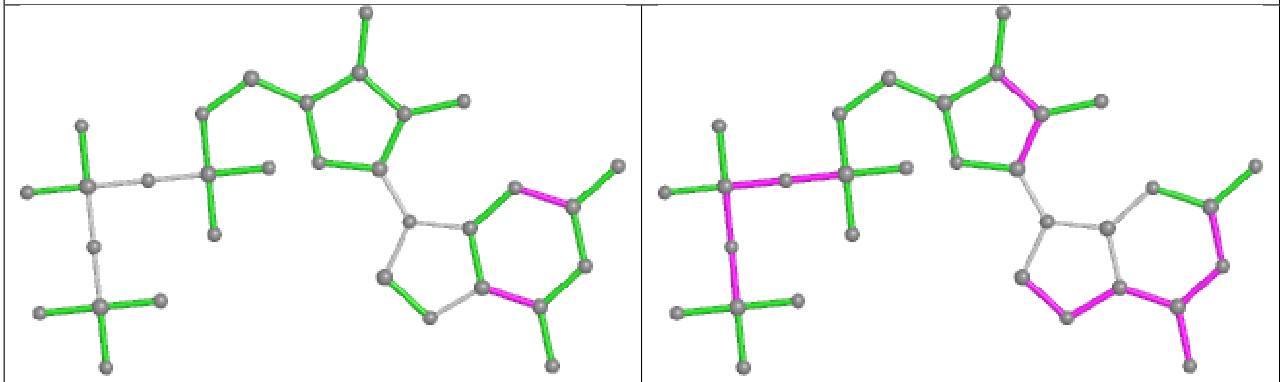
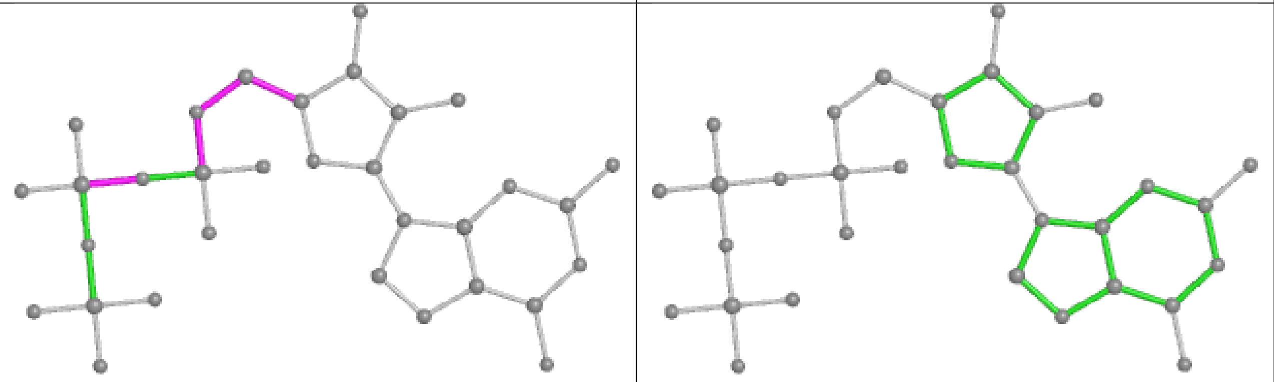


Bond lengths

Bond angles



Torsions

Rings

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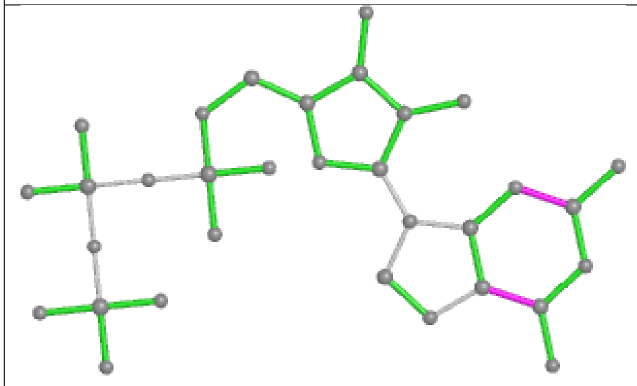

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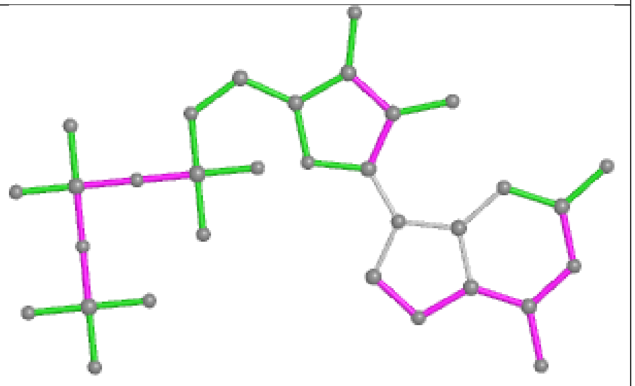

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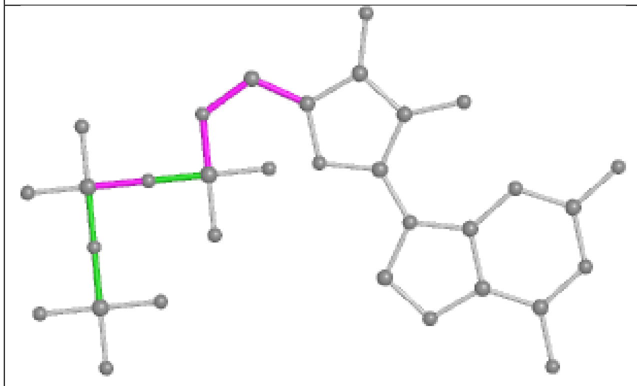

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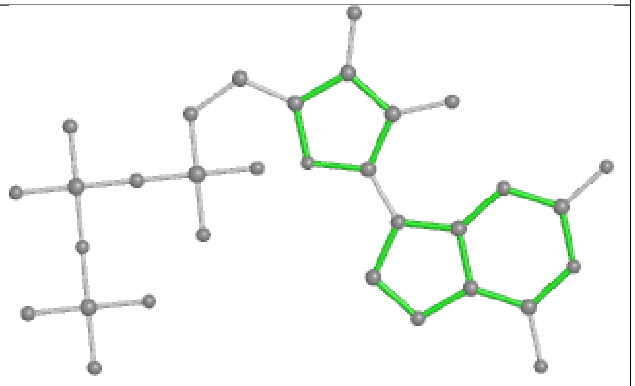
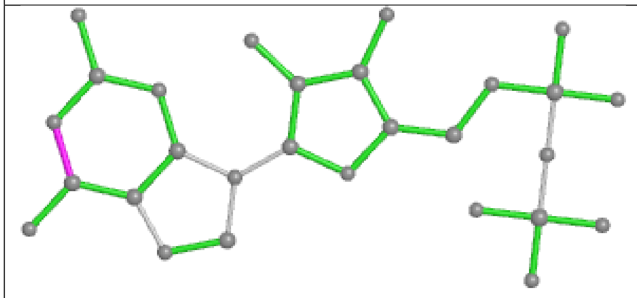


Rings

Ligand GDP VL 502



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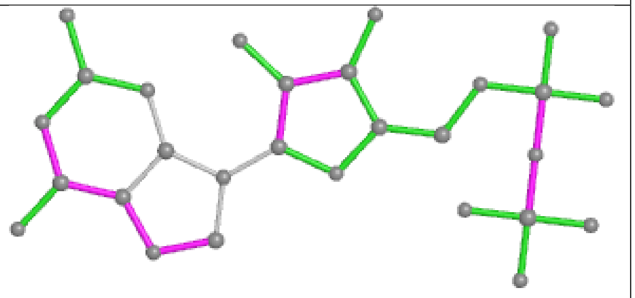

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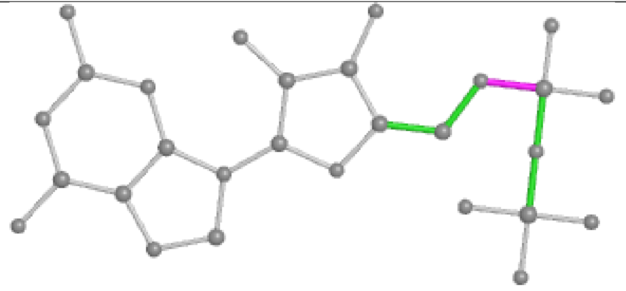

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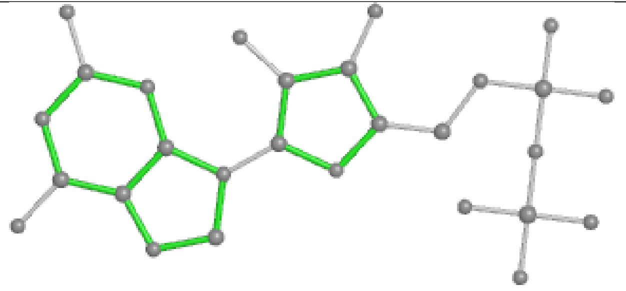

Rings

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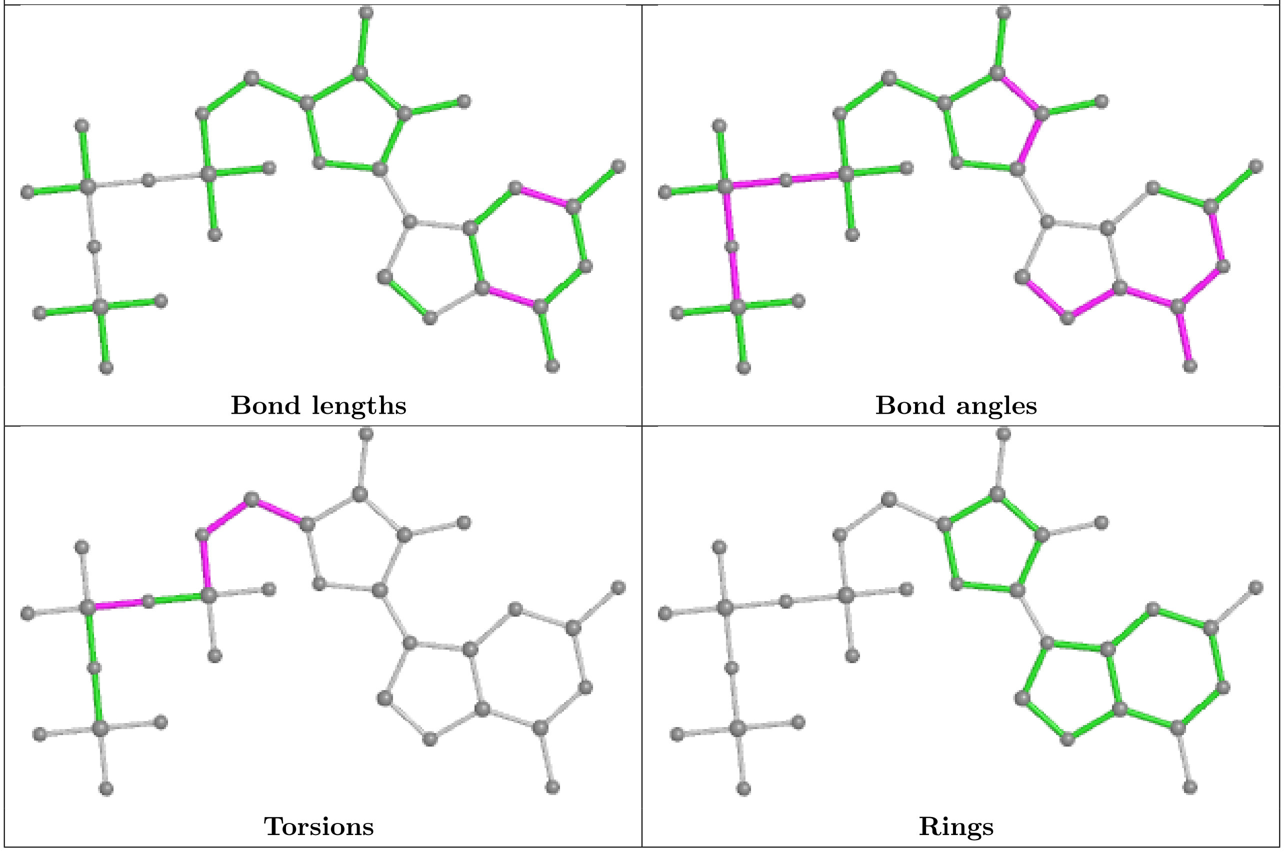

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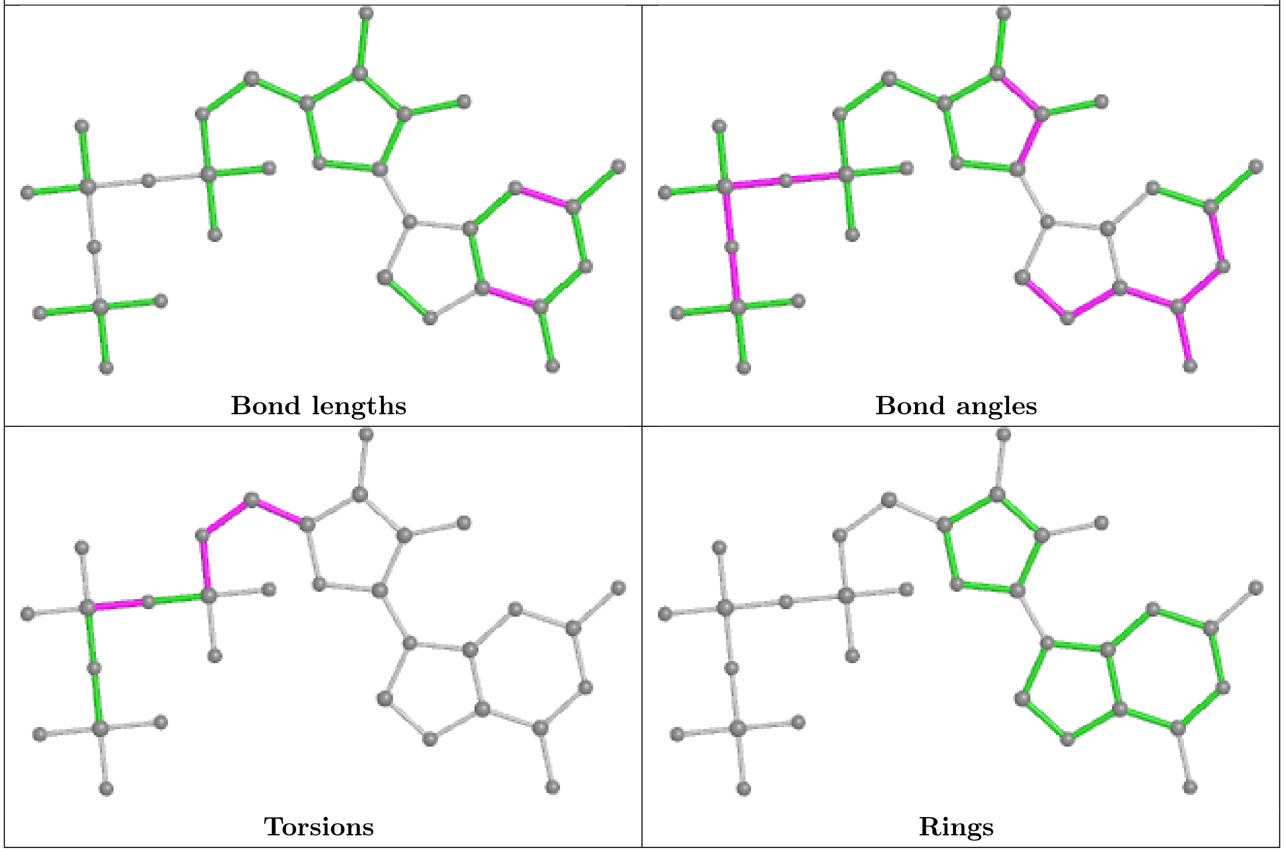

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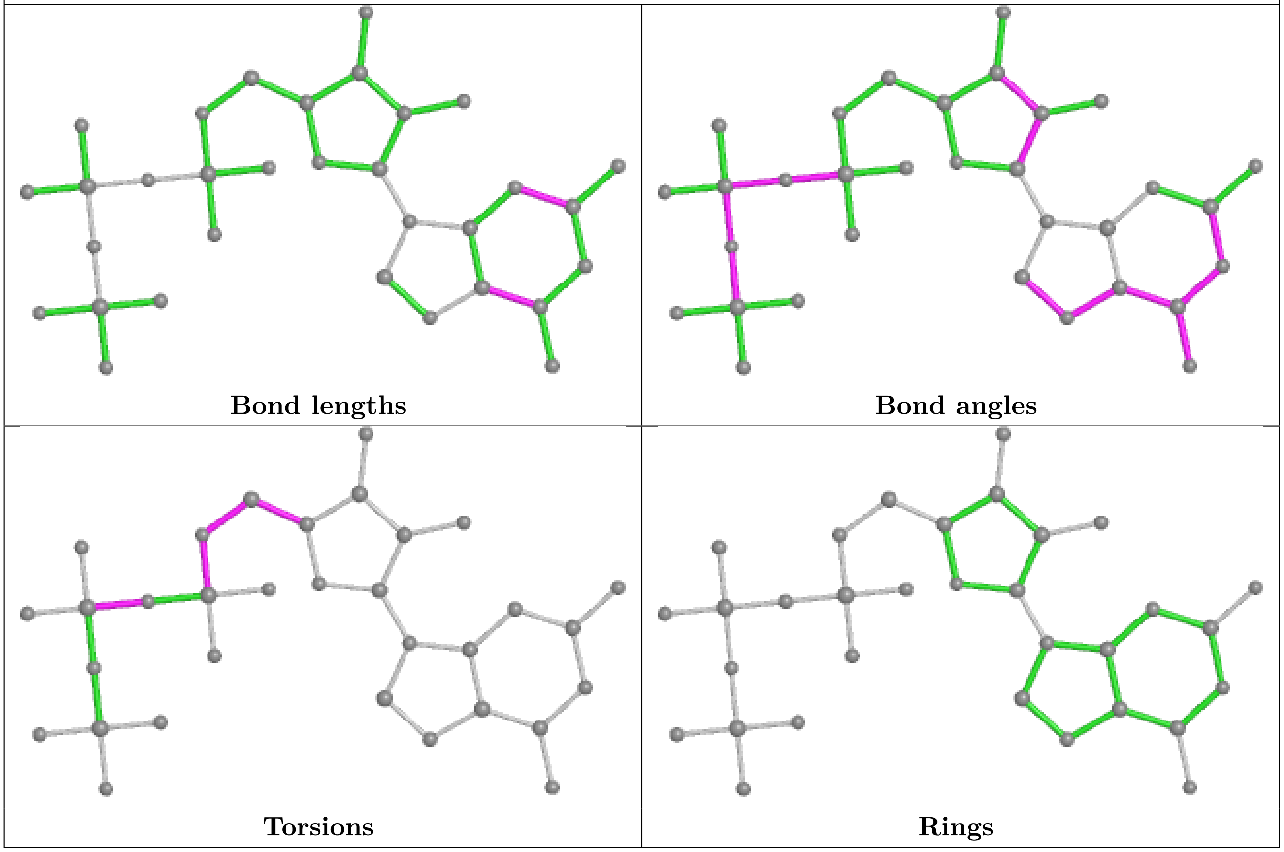


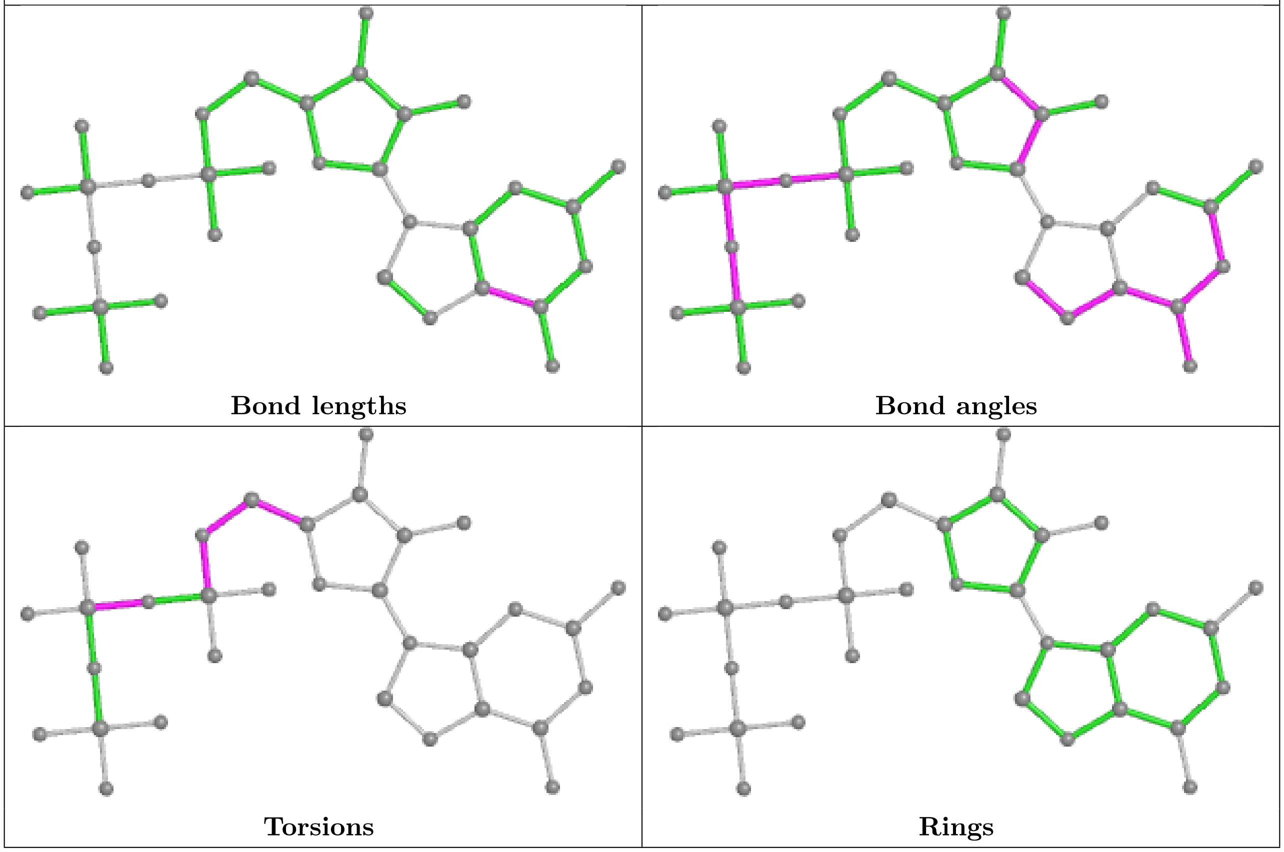
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP NM 501



Bond lengths

Bond angles

Torsions

Rings

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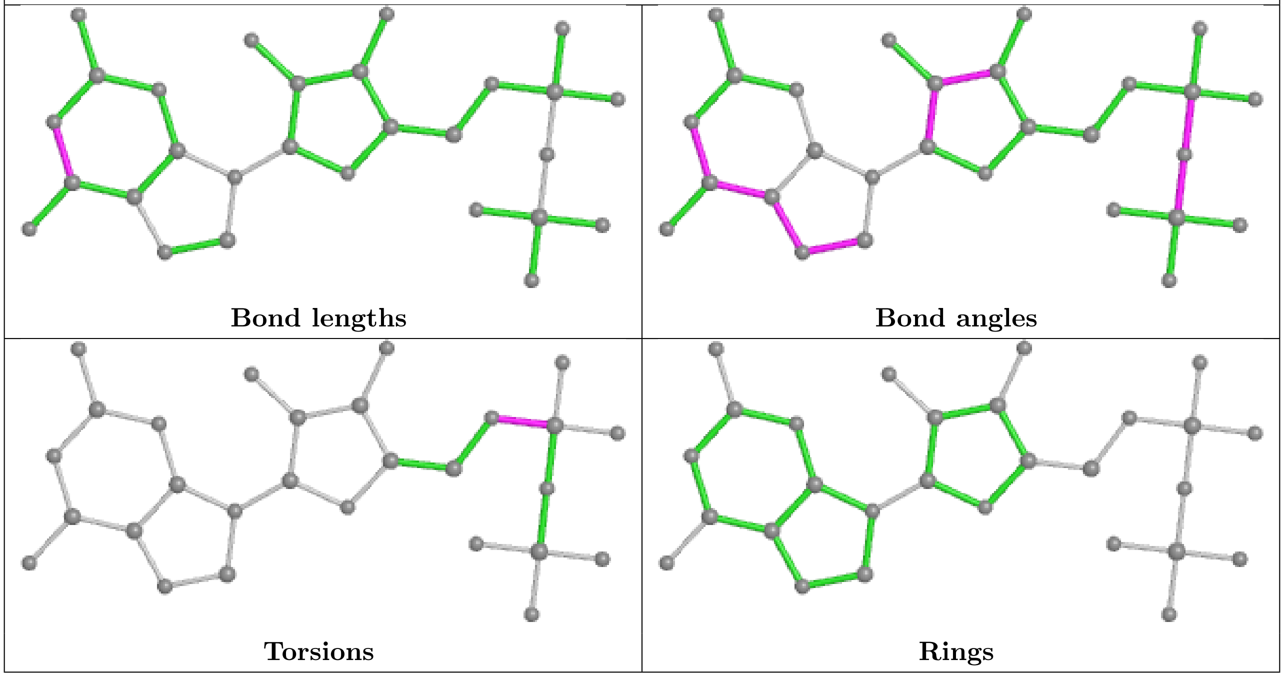
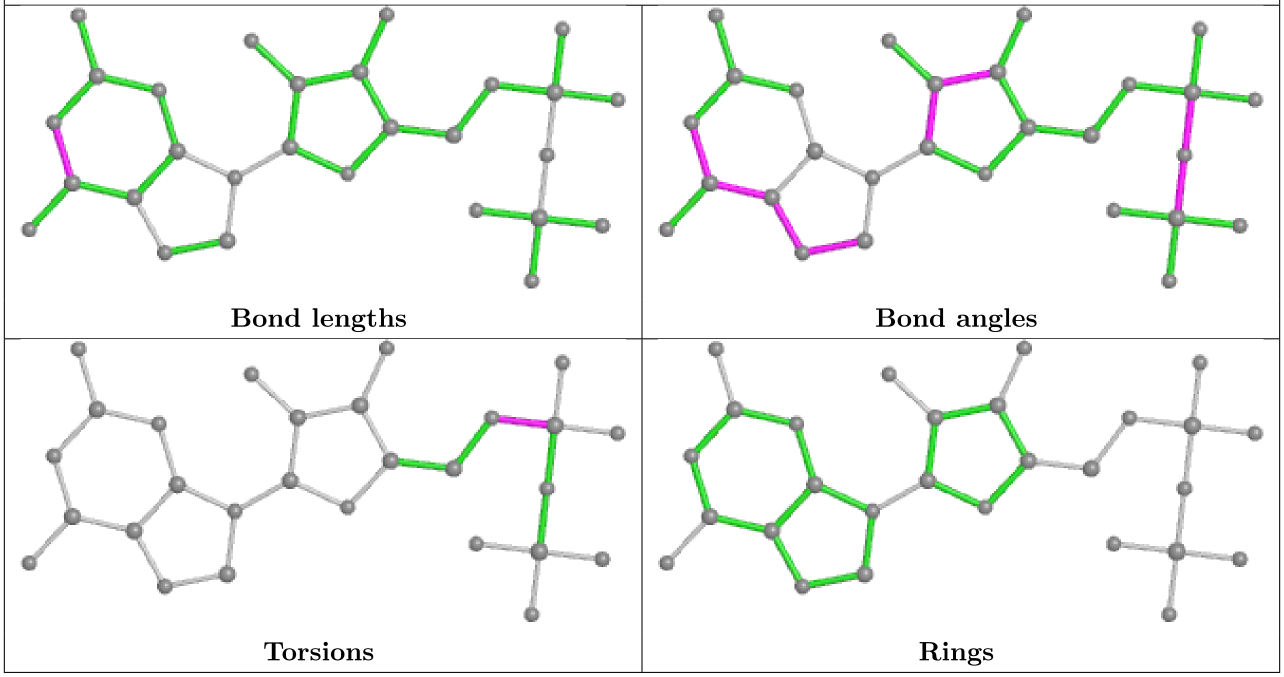


Bond lengths Bond angles

Torsions Rings

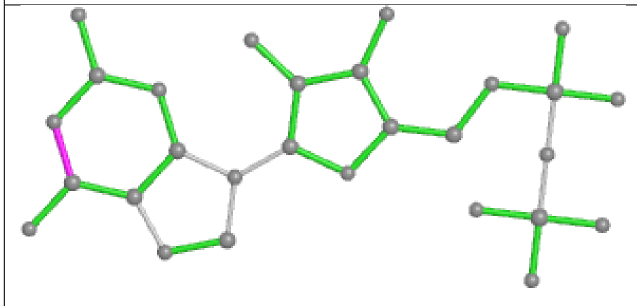
Ligand GDP JB 502



Bond lengths Bond angles

Torsions Rings

Ligand GDP AP 502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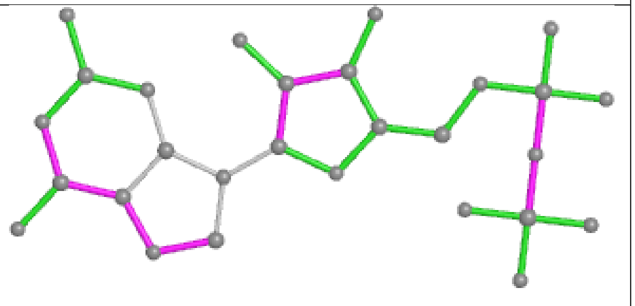
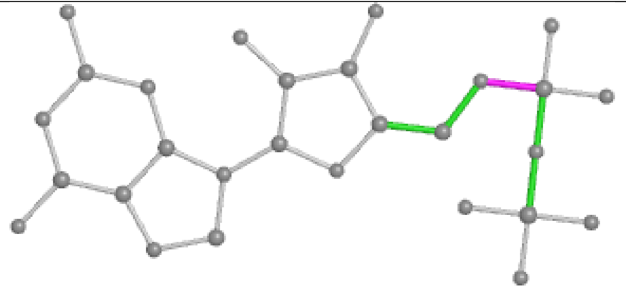
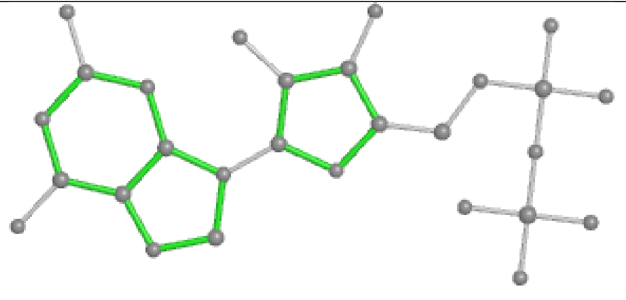
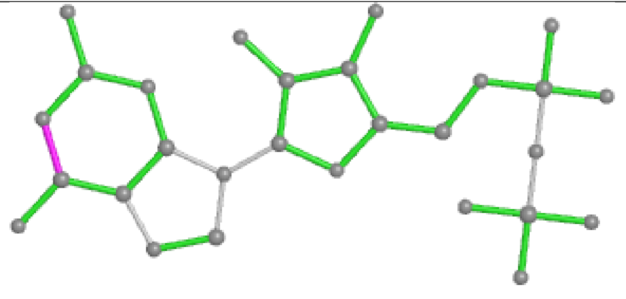

Bond angles


Torsions


Rings

Ligand GDP TD 502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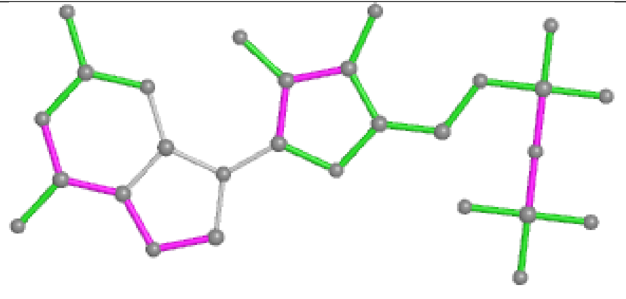
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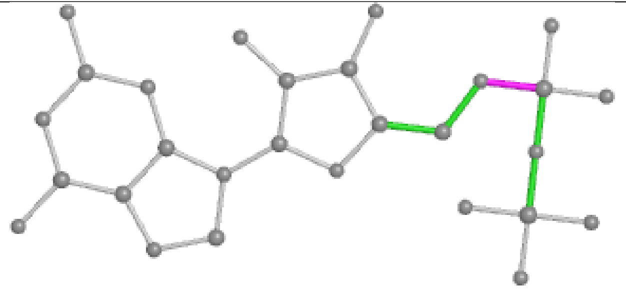
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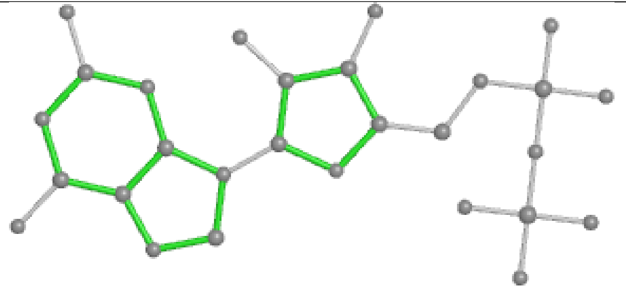
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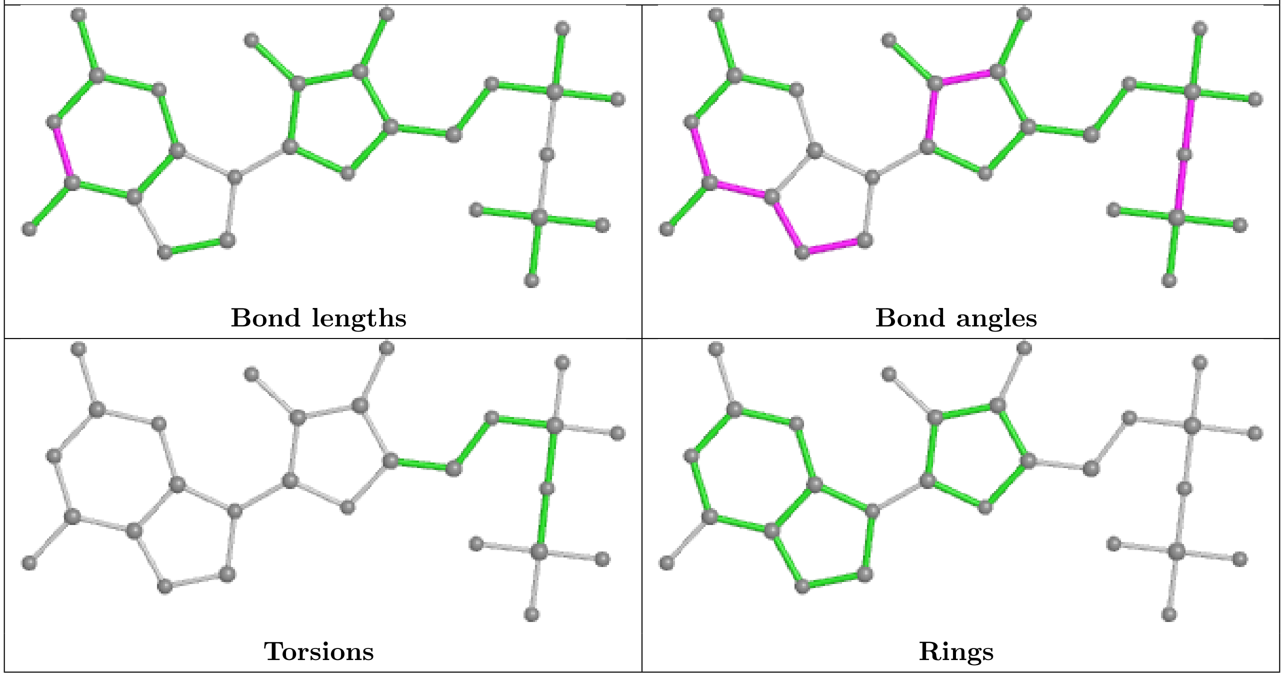

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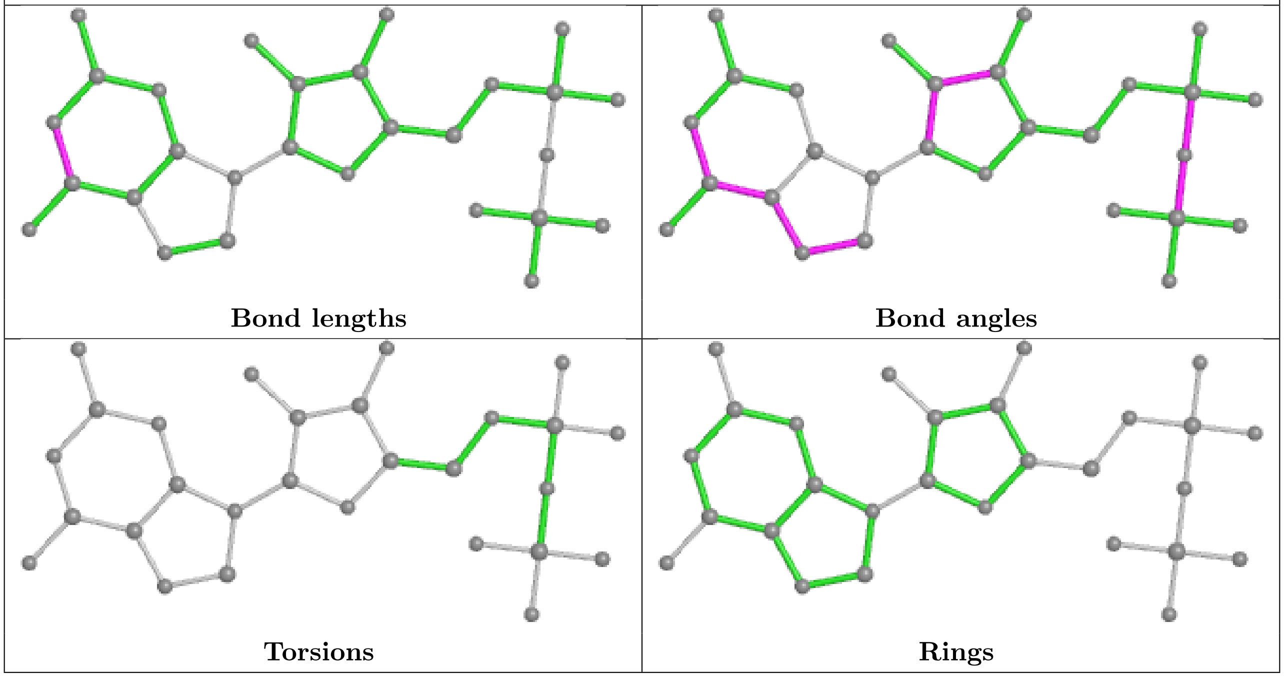

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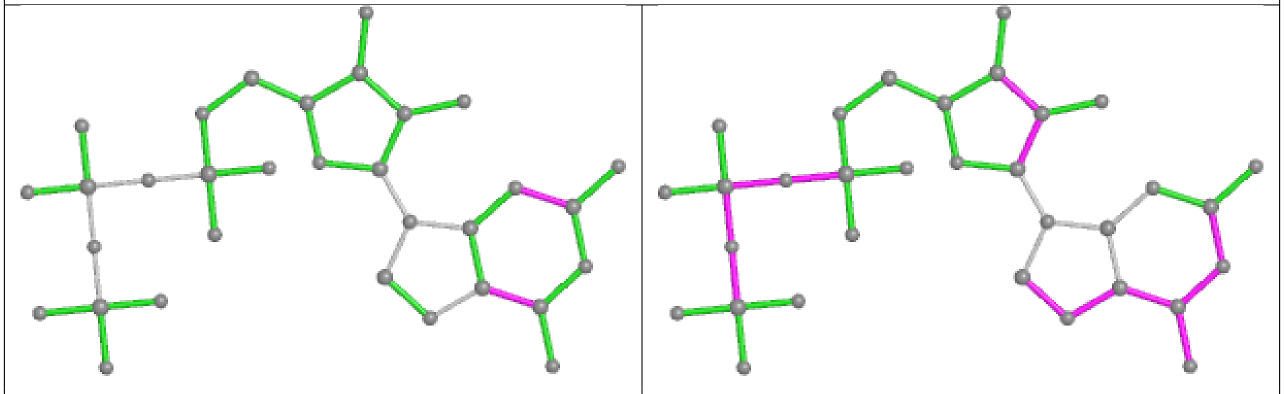

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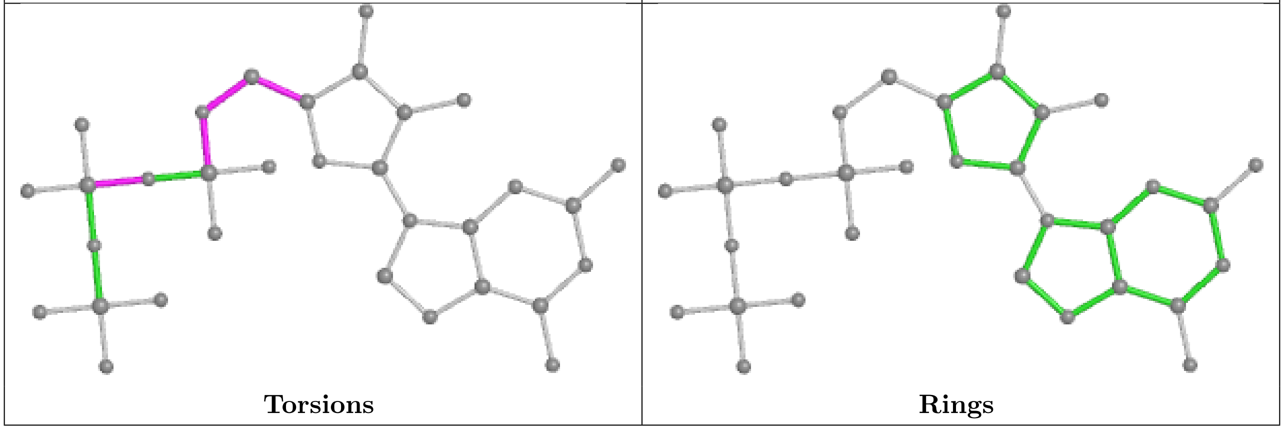

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Rings

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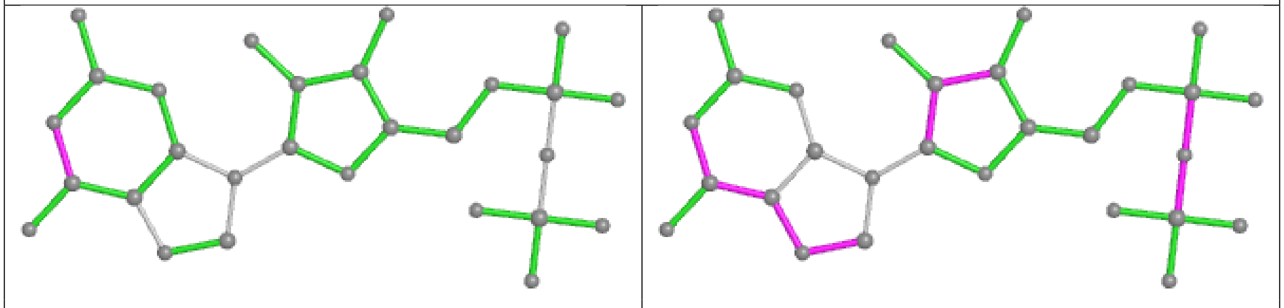

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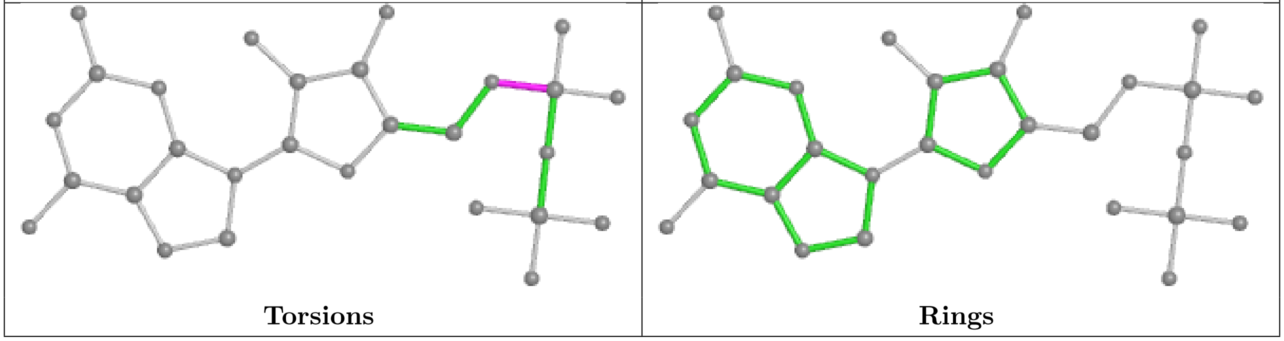

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Rings

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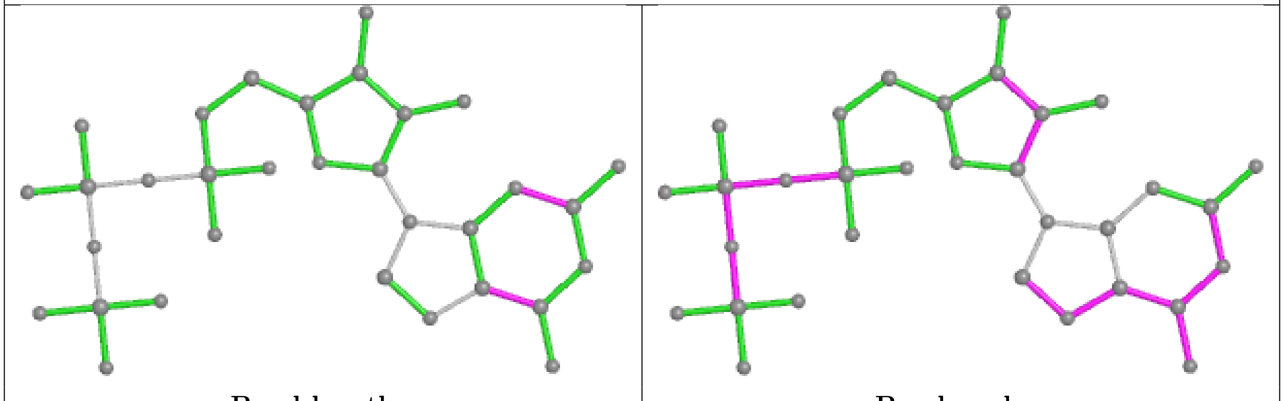

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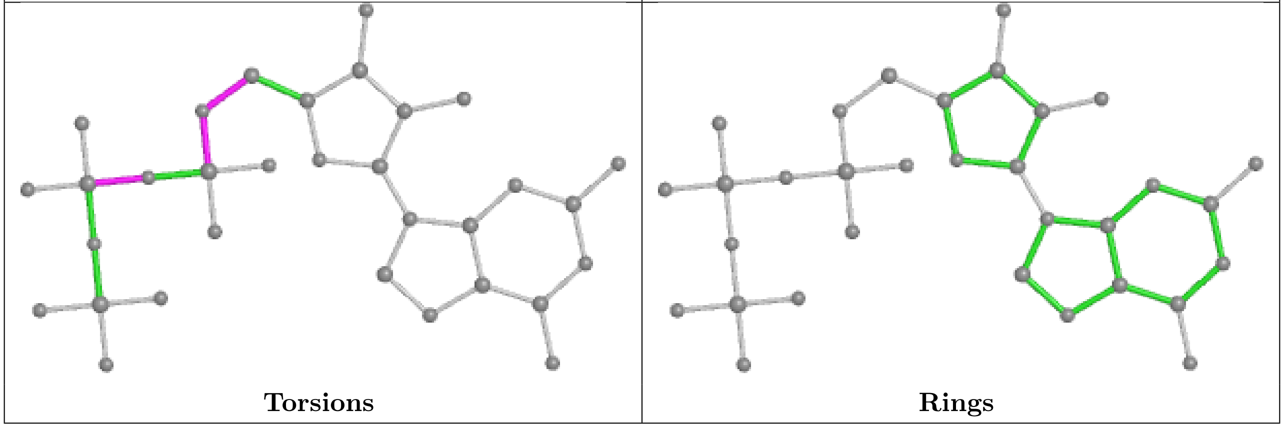

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Rings

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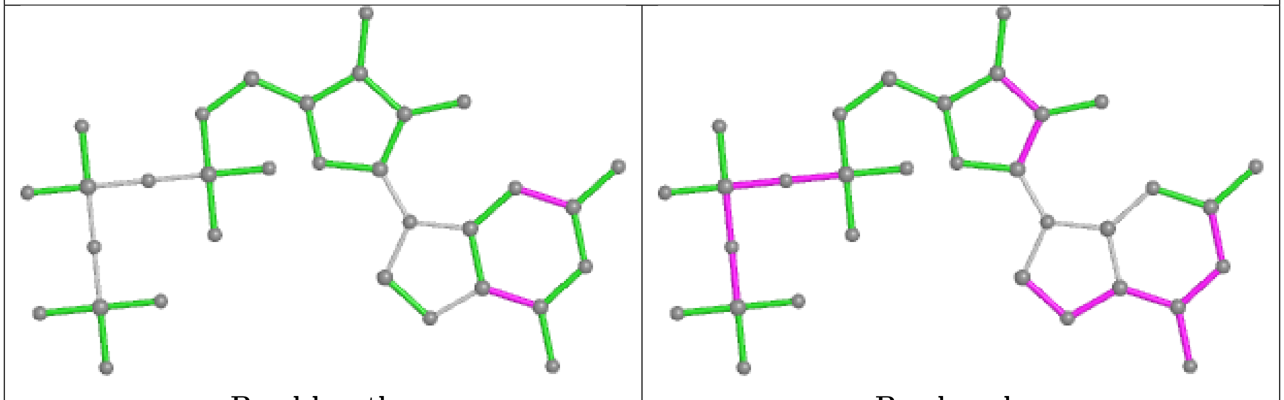

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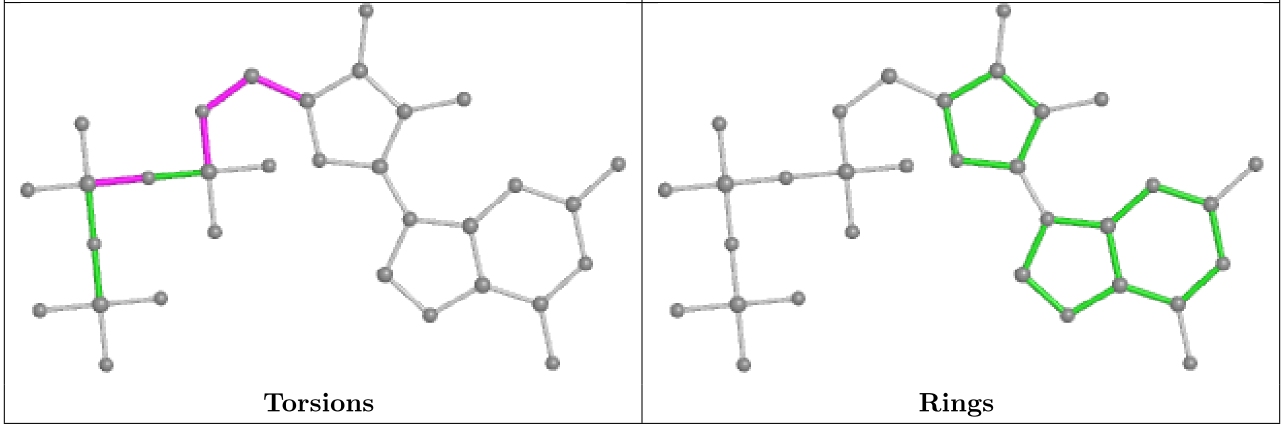

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Rings

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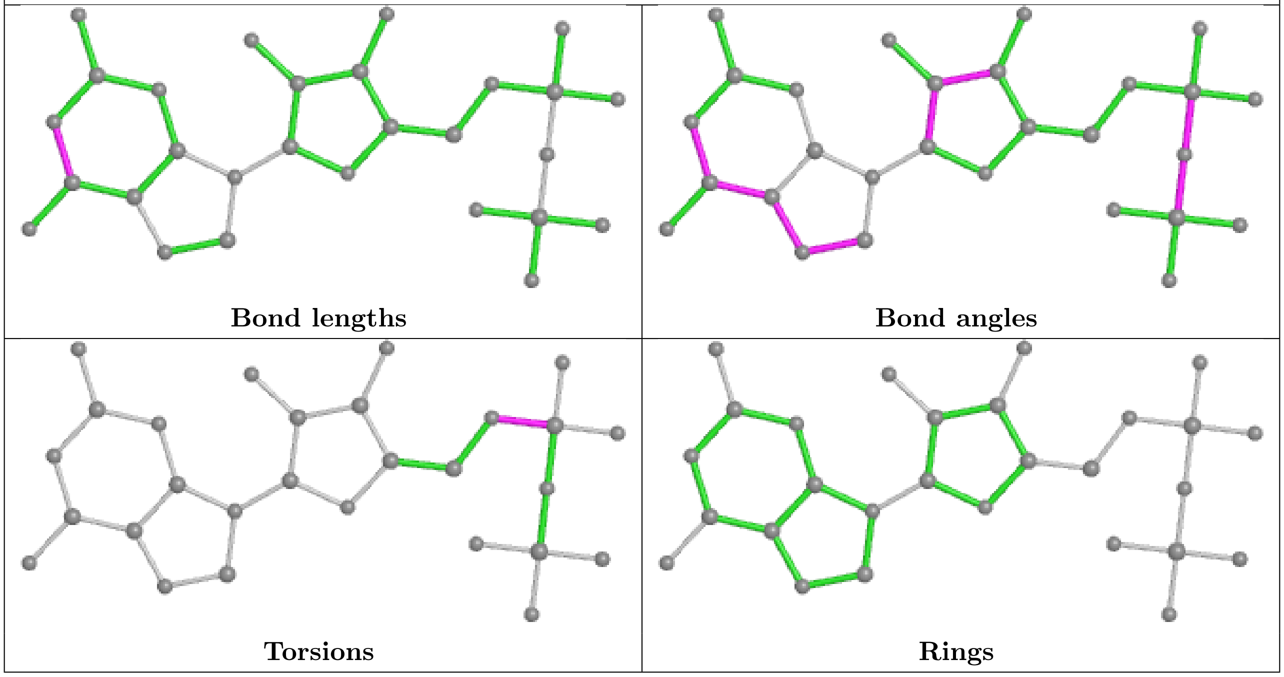

Bond lengths

Bond angles

Torsions

Rings

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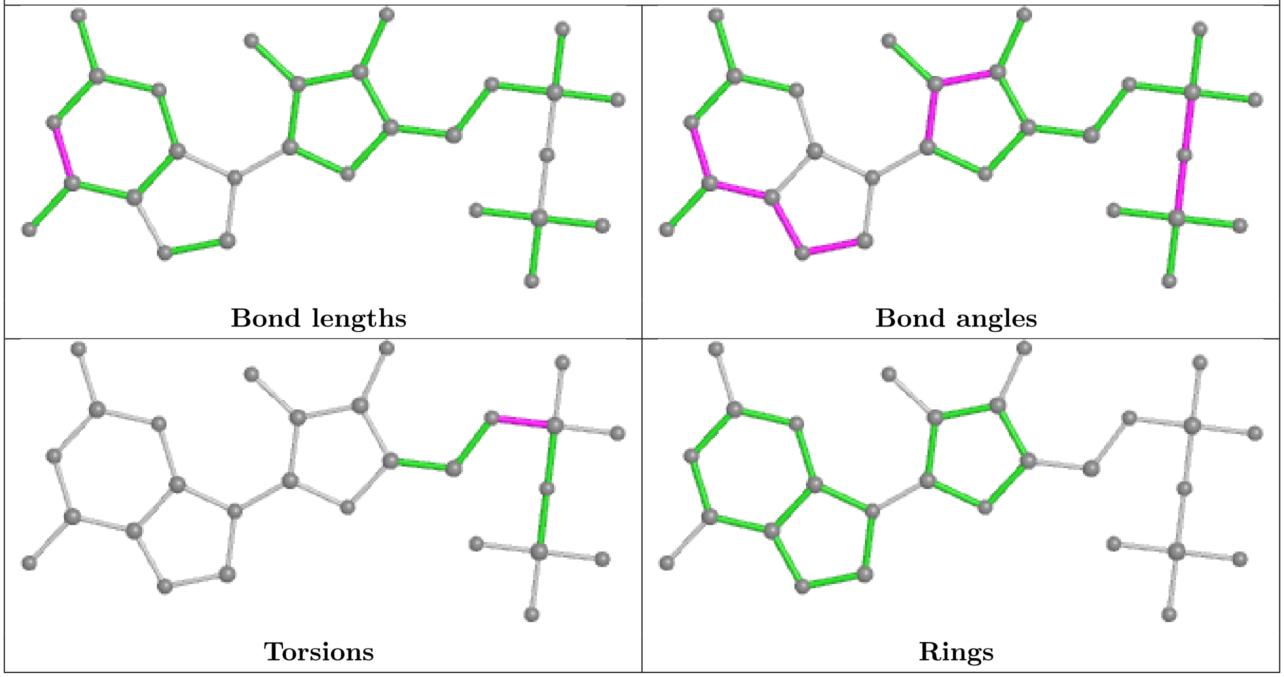

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Bond angles

Torsions

Rings

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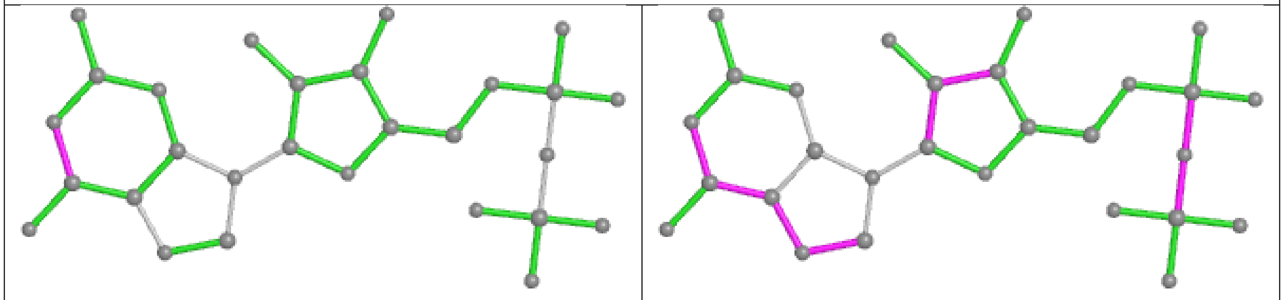

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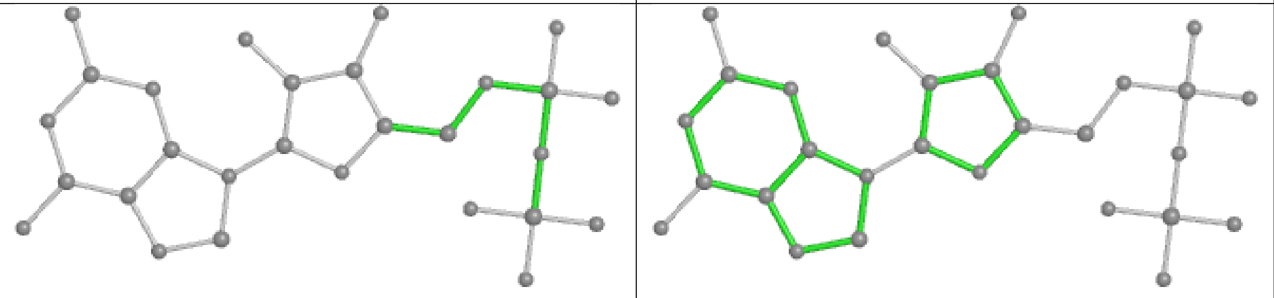

Torsions **Rings**

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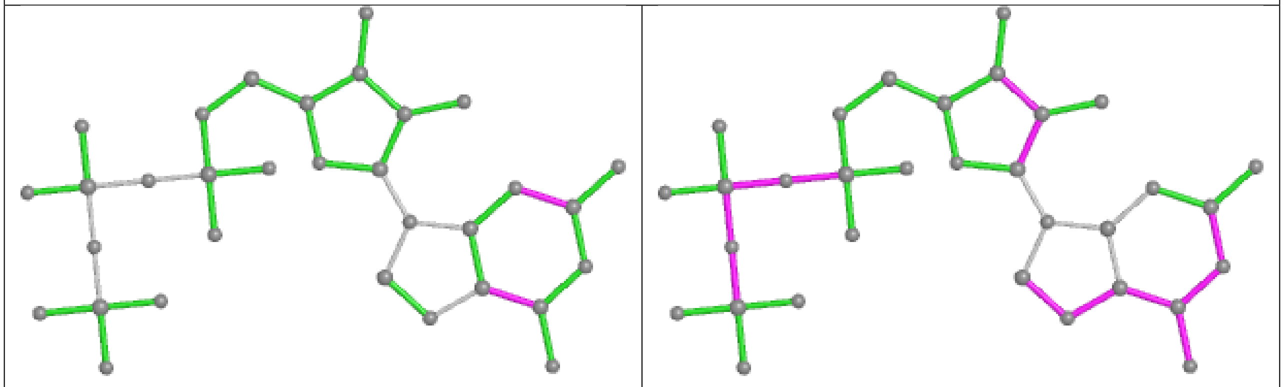

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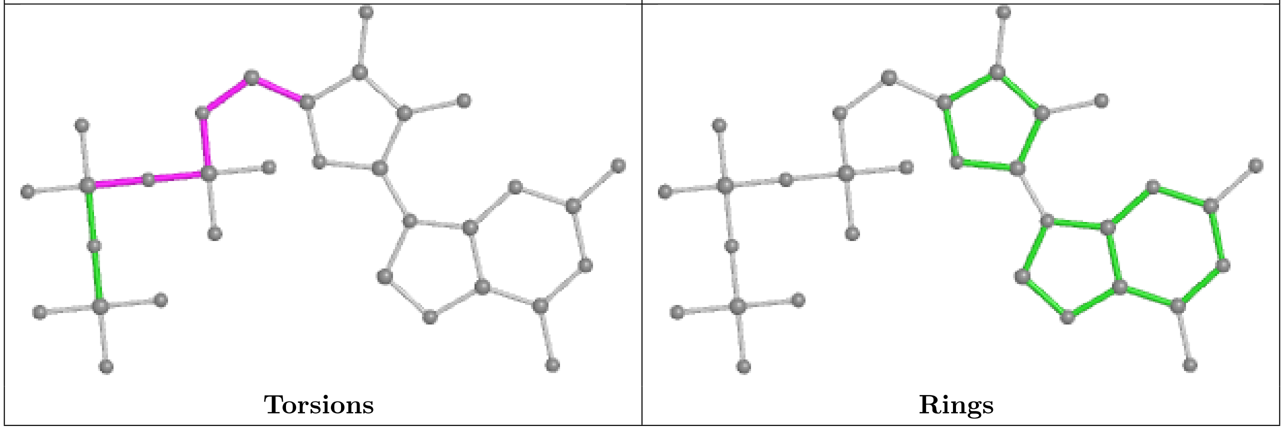

Torsions **Rings**

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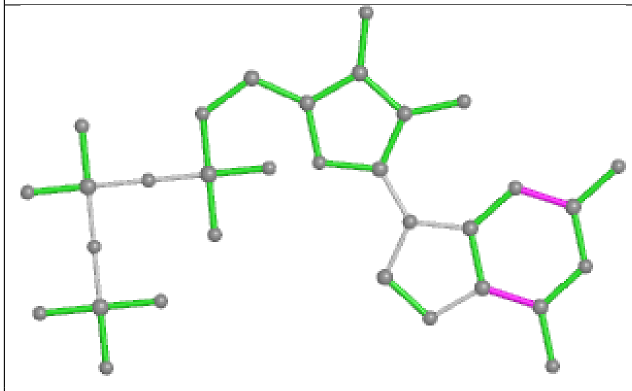

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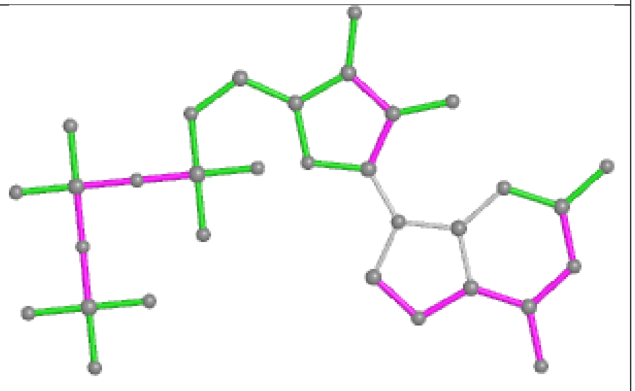

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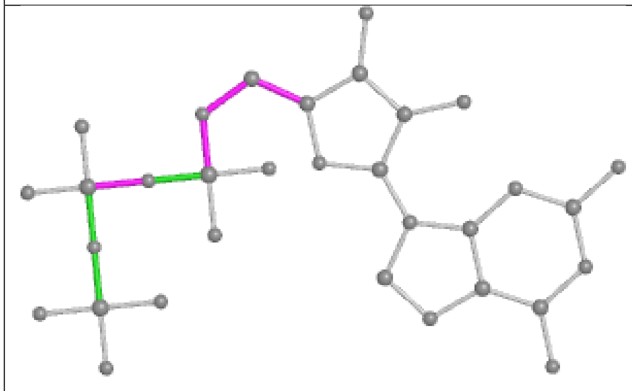

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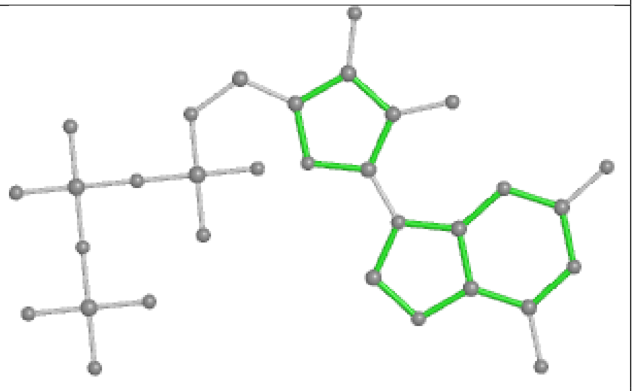

Rings

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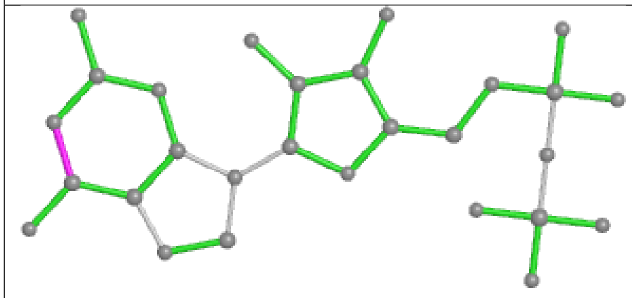

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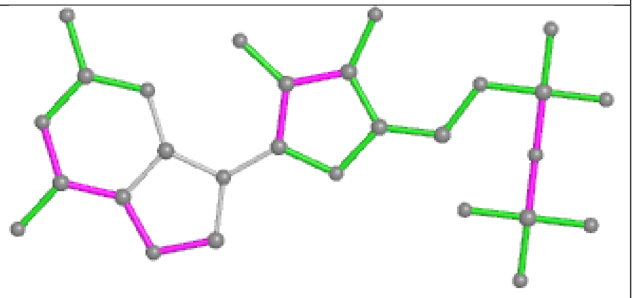

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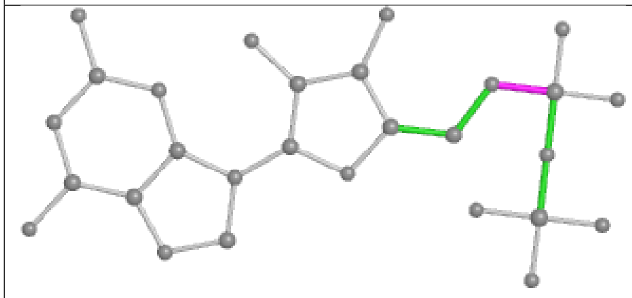

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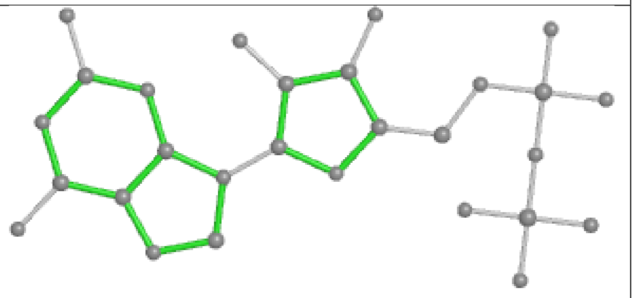

Rings

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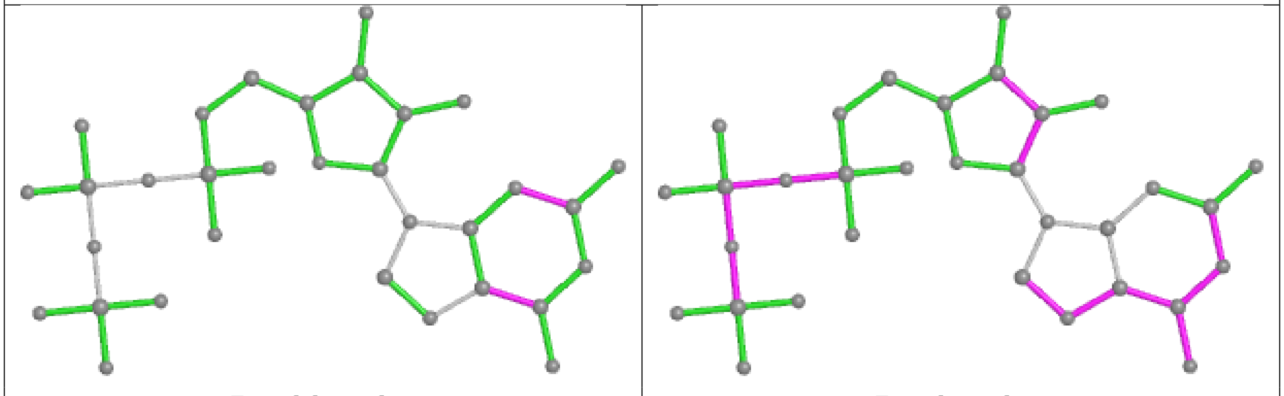

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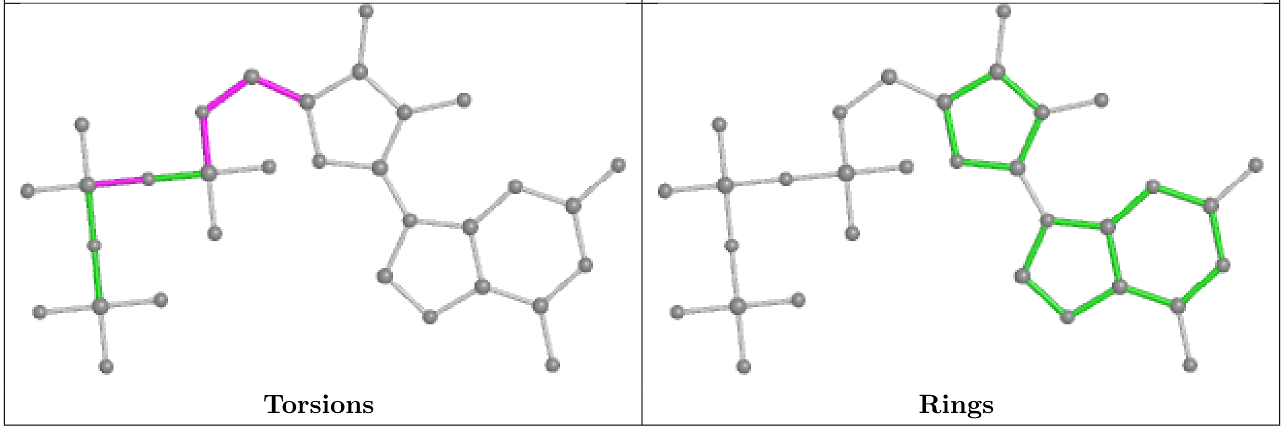

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Rings

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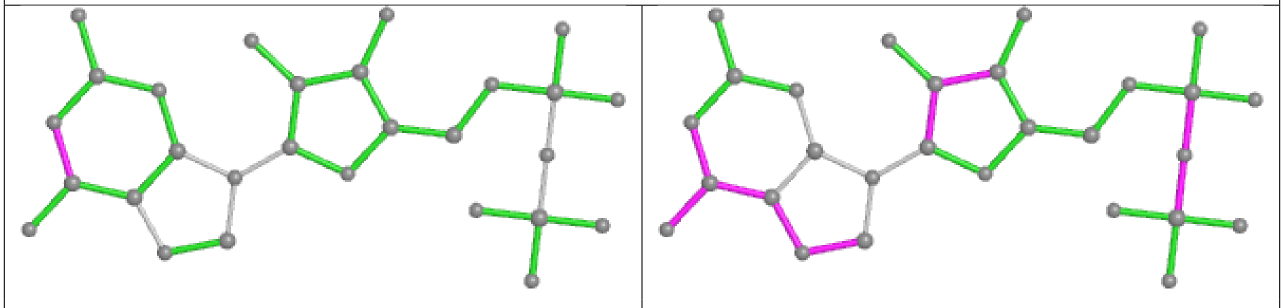

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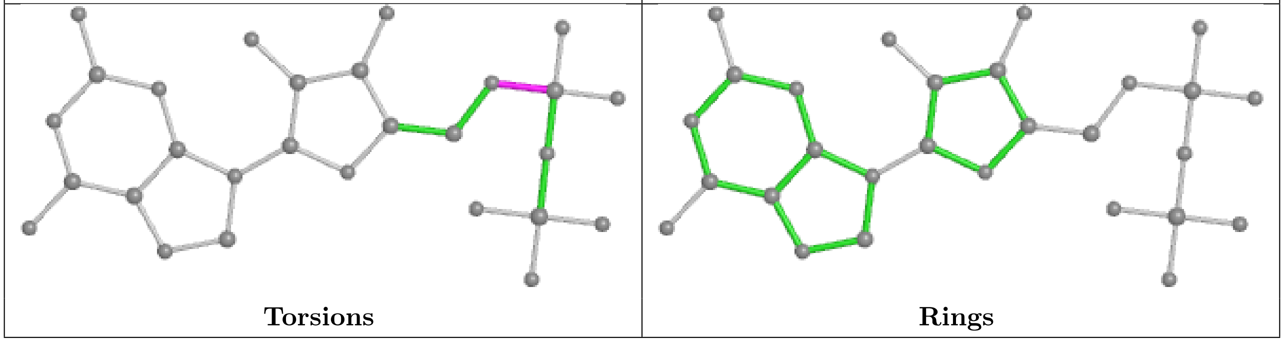

Torsions

Rings

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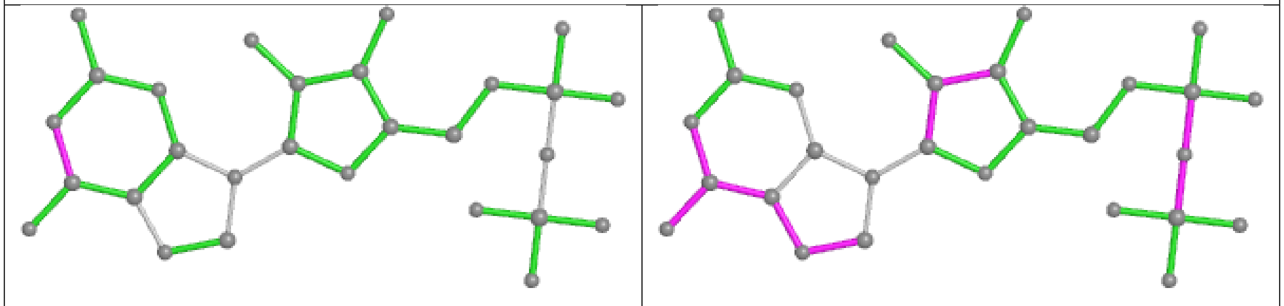

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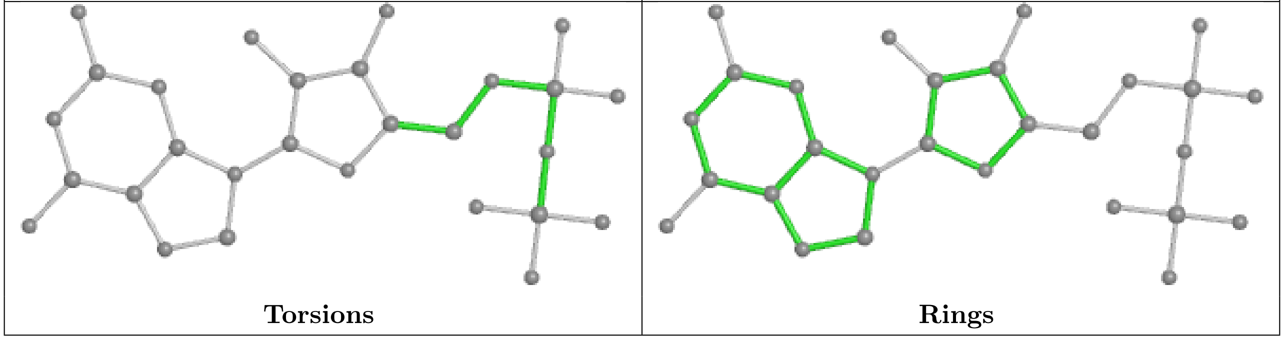

Torsions

Rings

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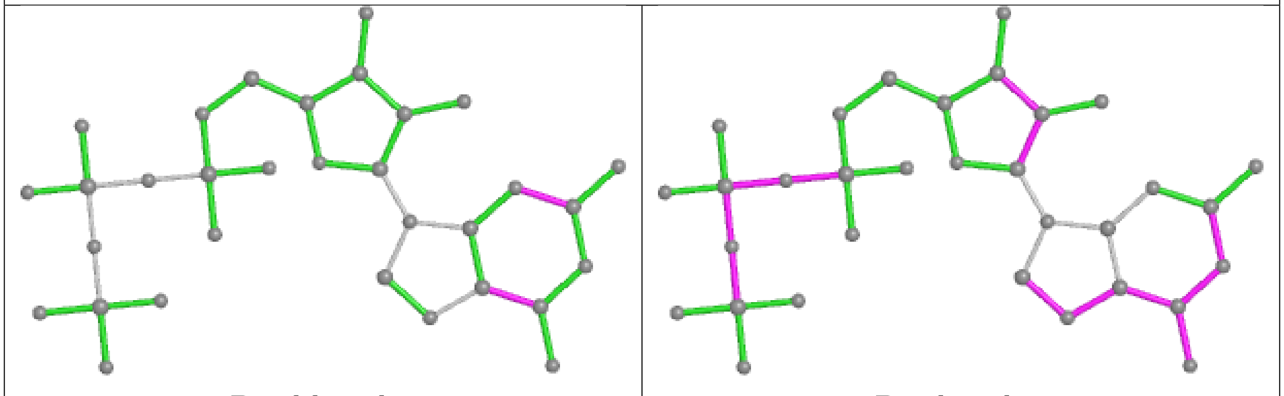

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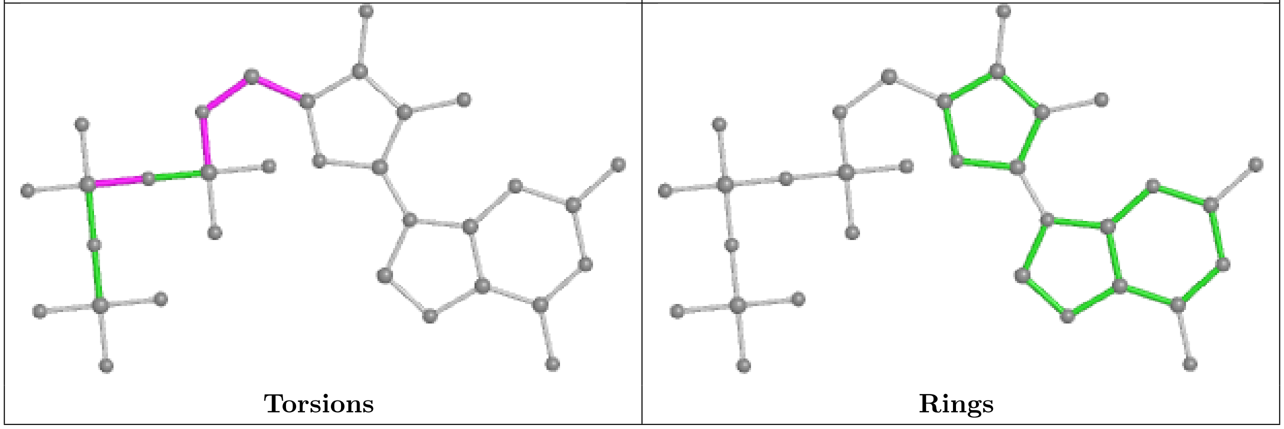
Bond angles



Torsions

Rings

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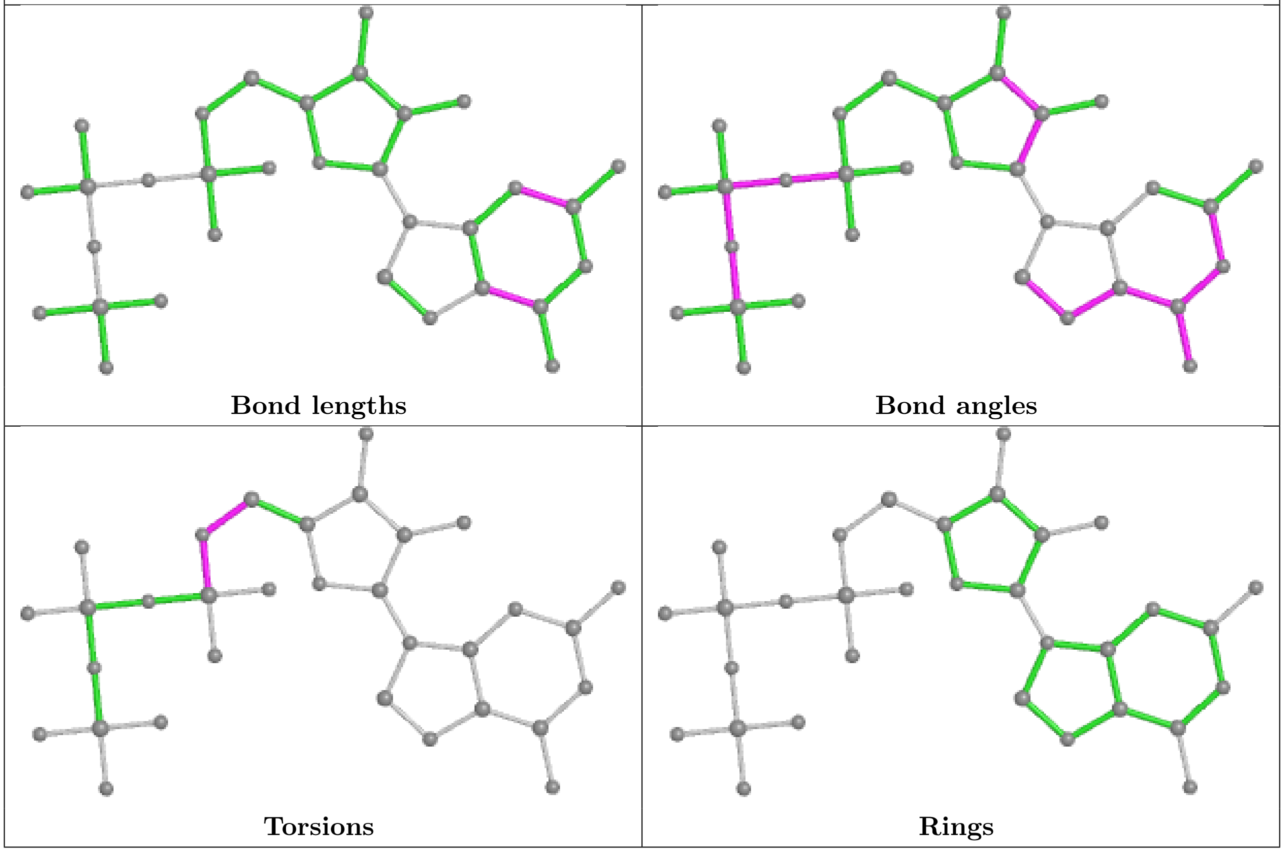


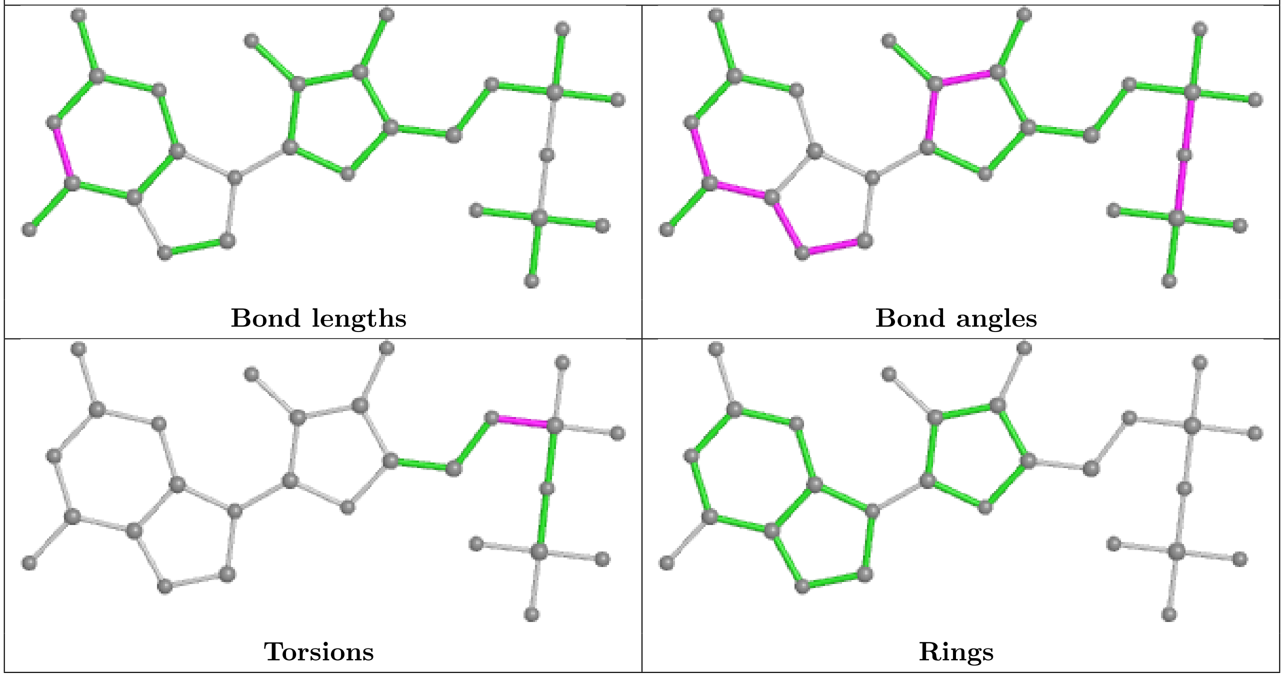
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP KN 502



Bond lengths

Bond angles

Torsions

Rings

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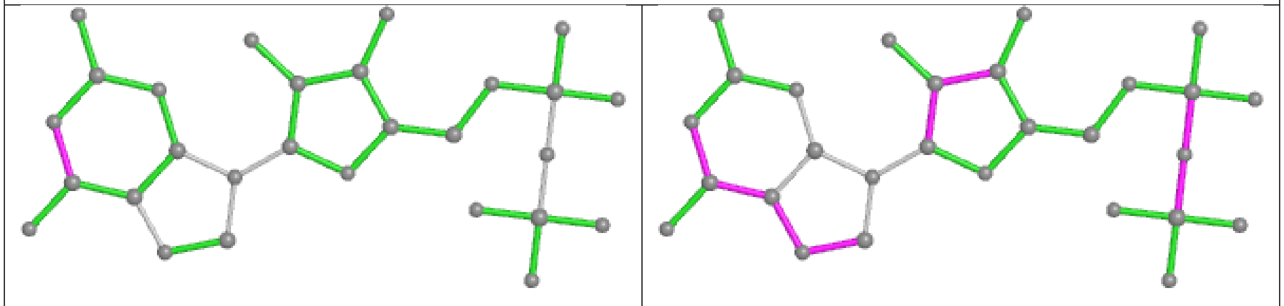
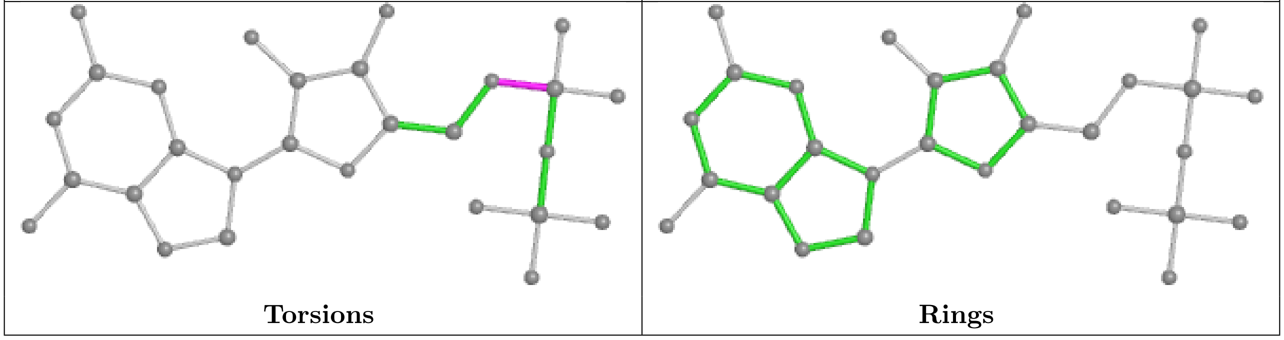
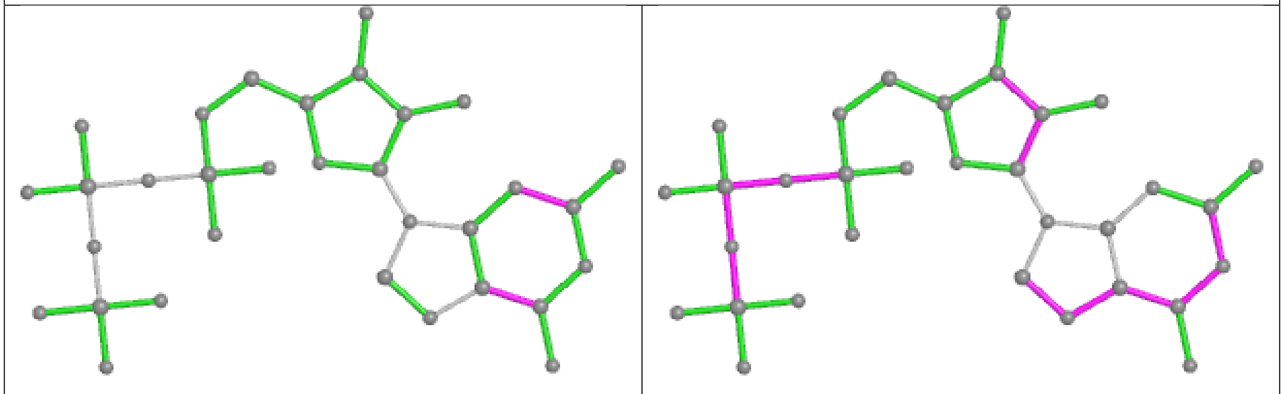


Bond lengths **Bond angles**

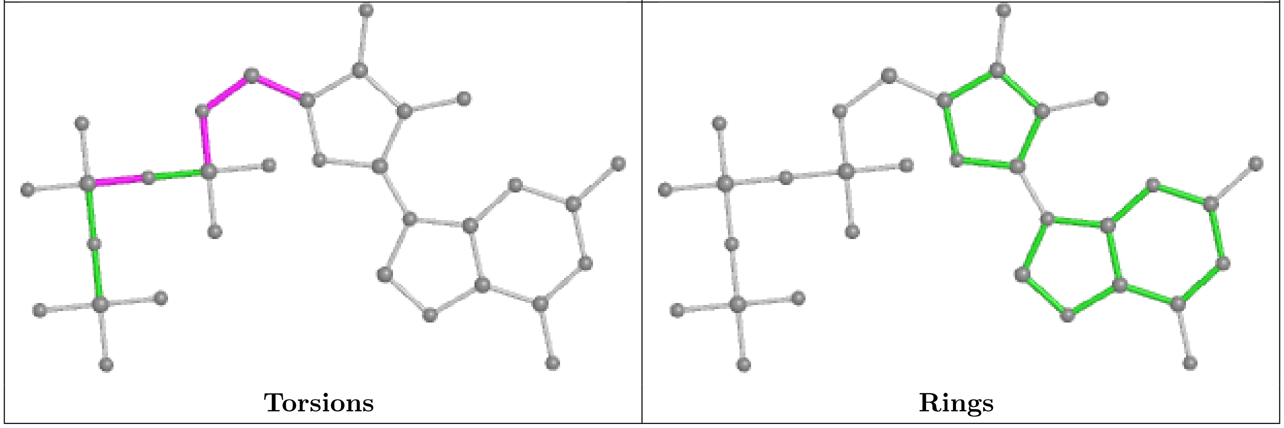


Torsions **Rings**

Ligand GTP IO 501

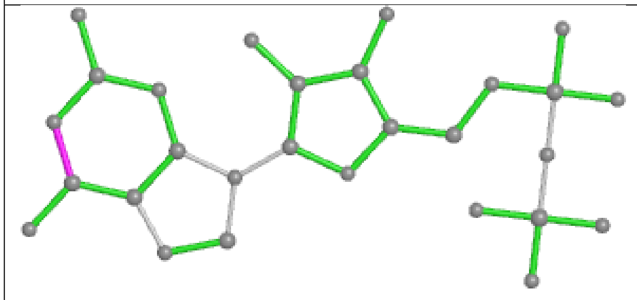


Bond lengths **Bond angles**



Torsions **Rings**

Ligand GDP LJ 502



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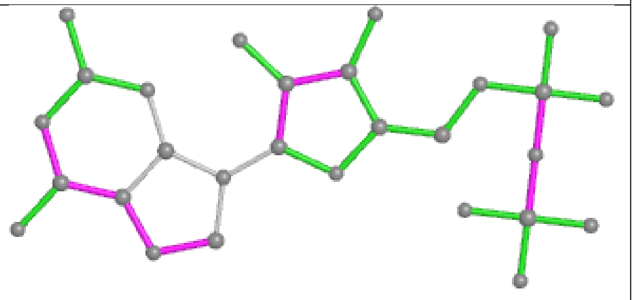

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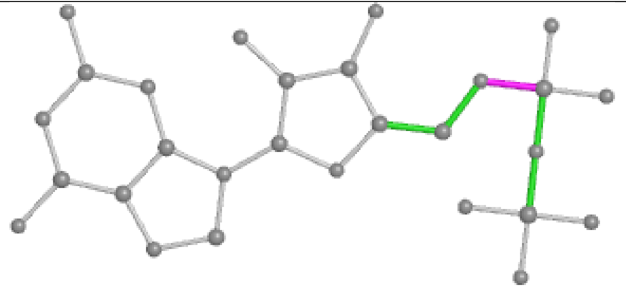

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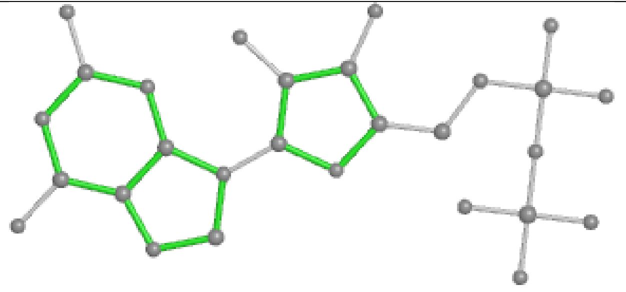

Rings

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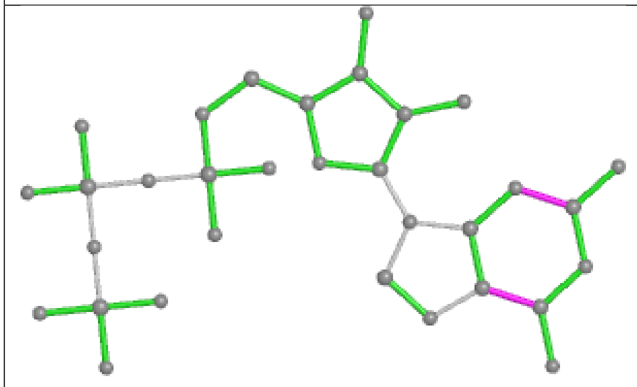

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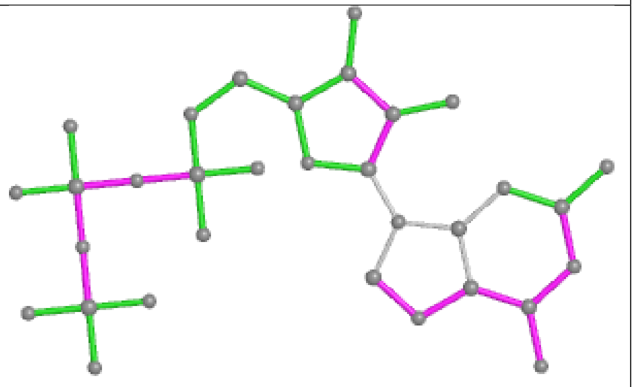
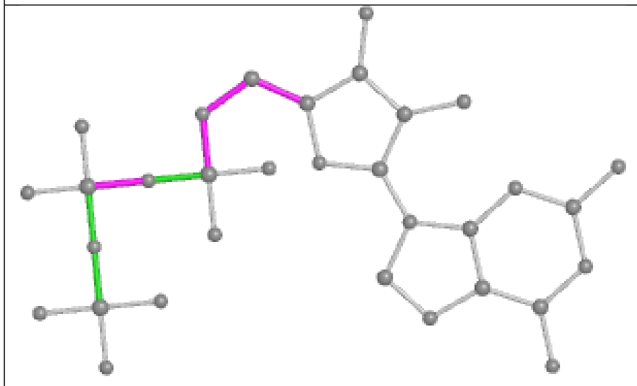


Bond angles



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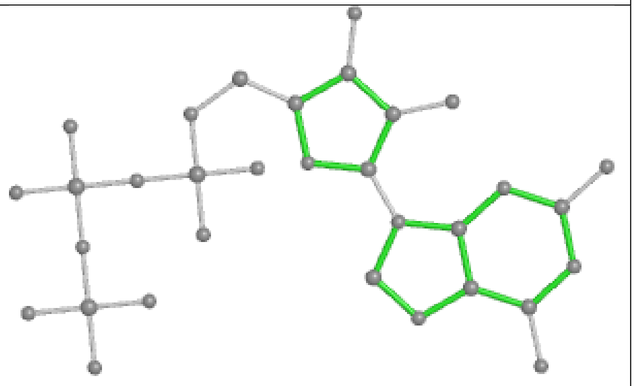

Rings

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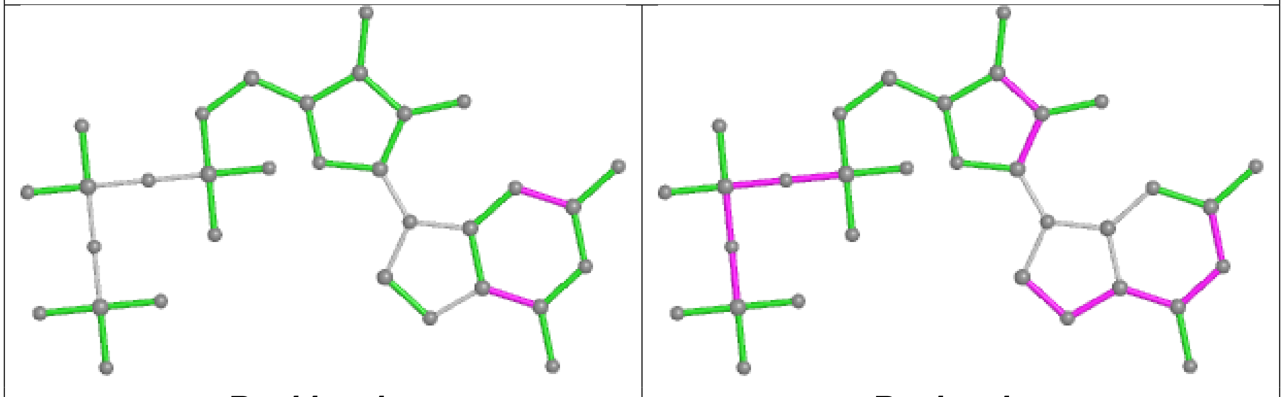
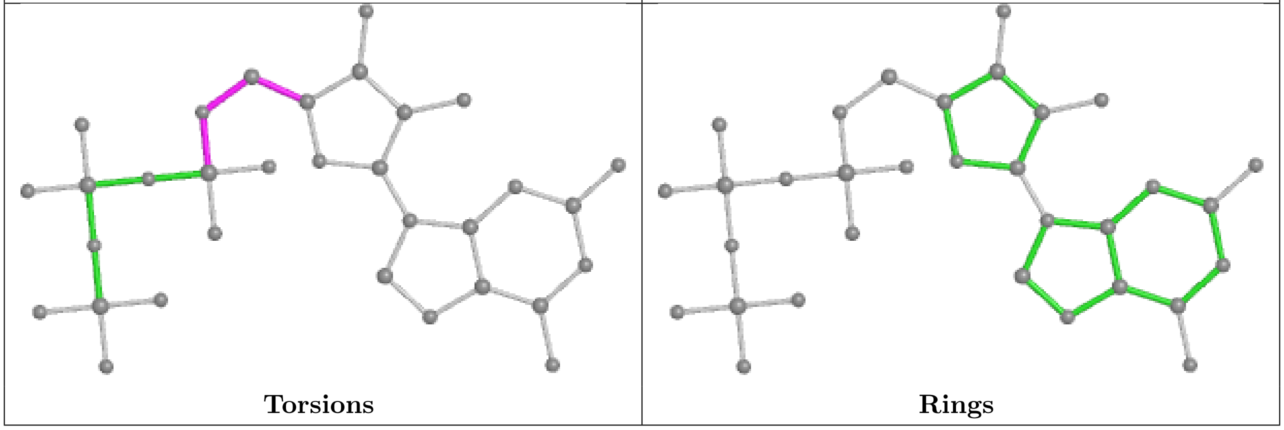


Bond lengths

Bond angles



Torsions

Rings

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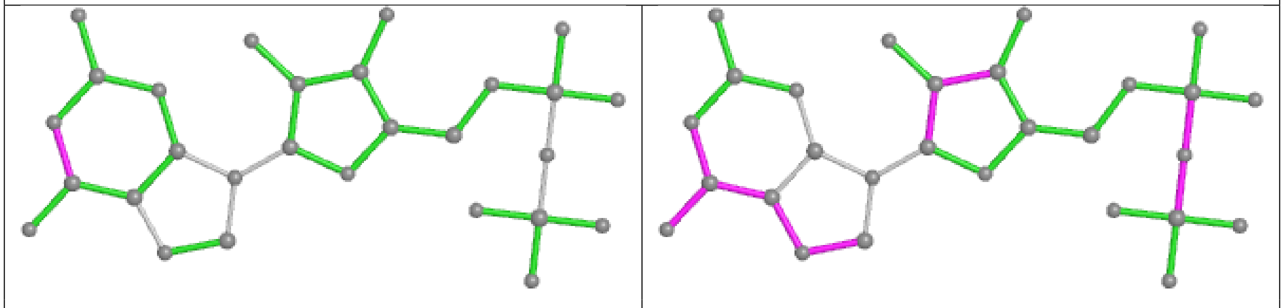
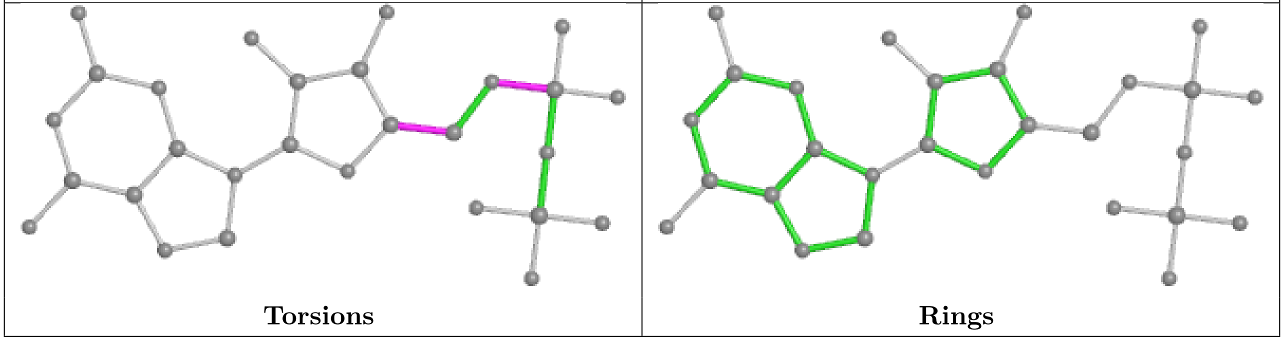


Bond lengths

Bond angles



Torsions

Rings

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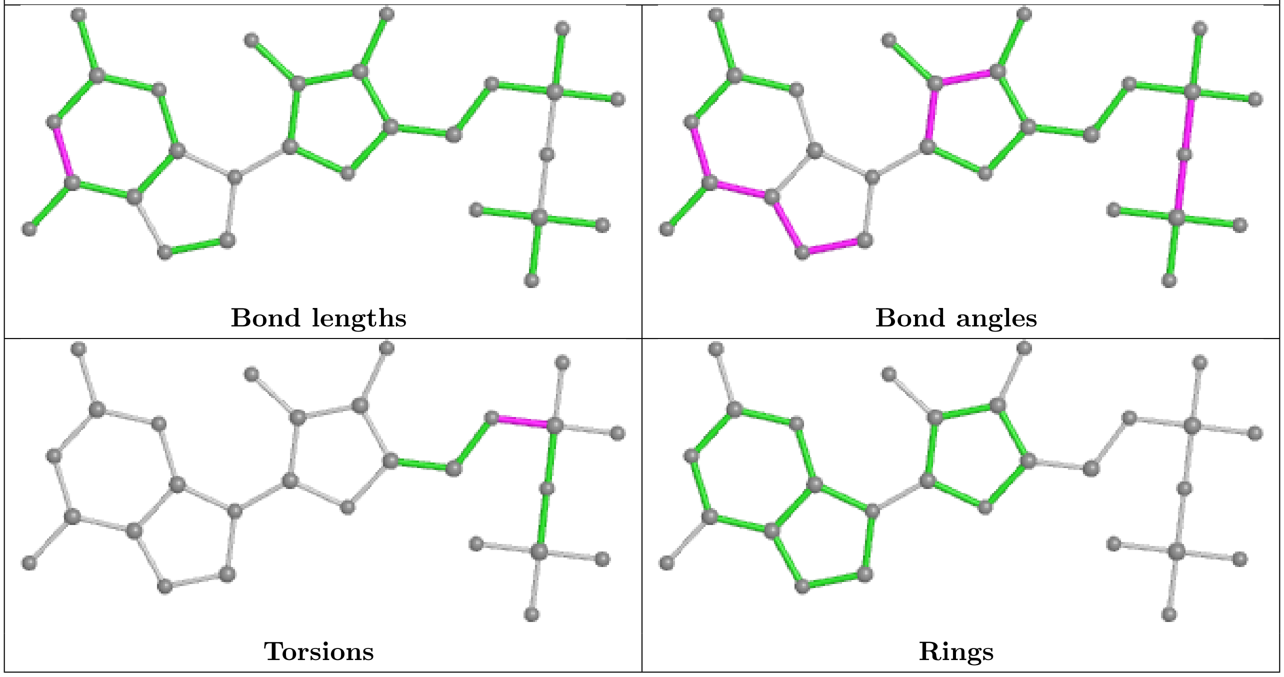


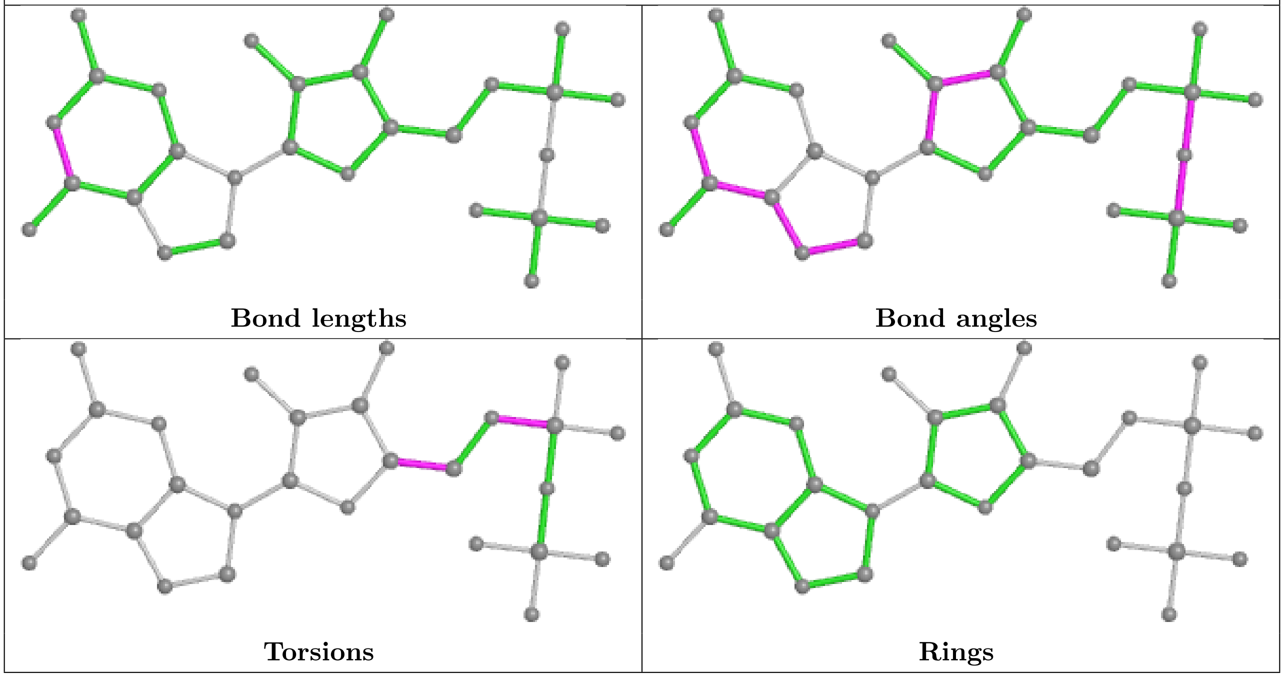
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP MH 502



Bond lengths

Bond angles

Torsions

Rings

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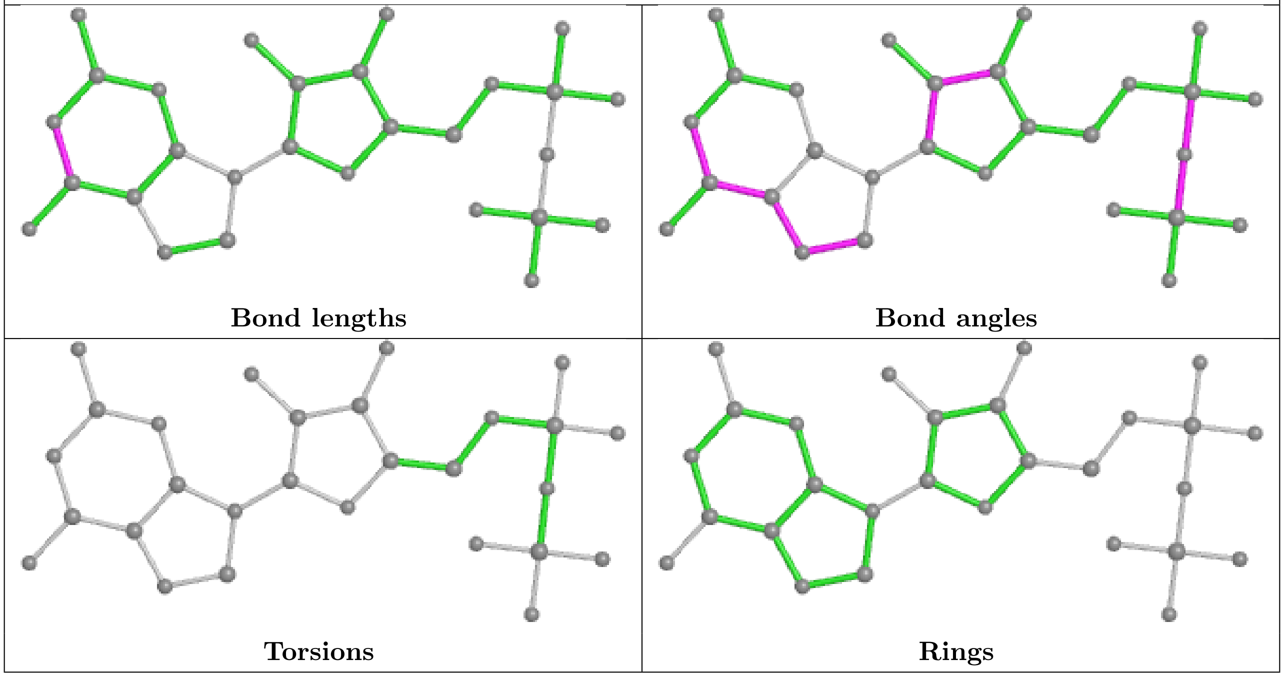

Bond lengths

Bond angles

Torsions

Rings

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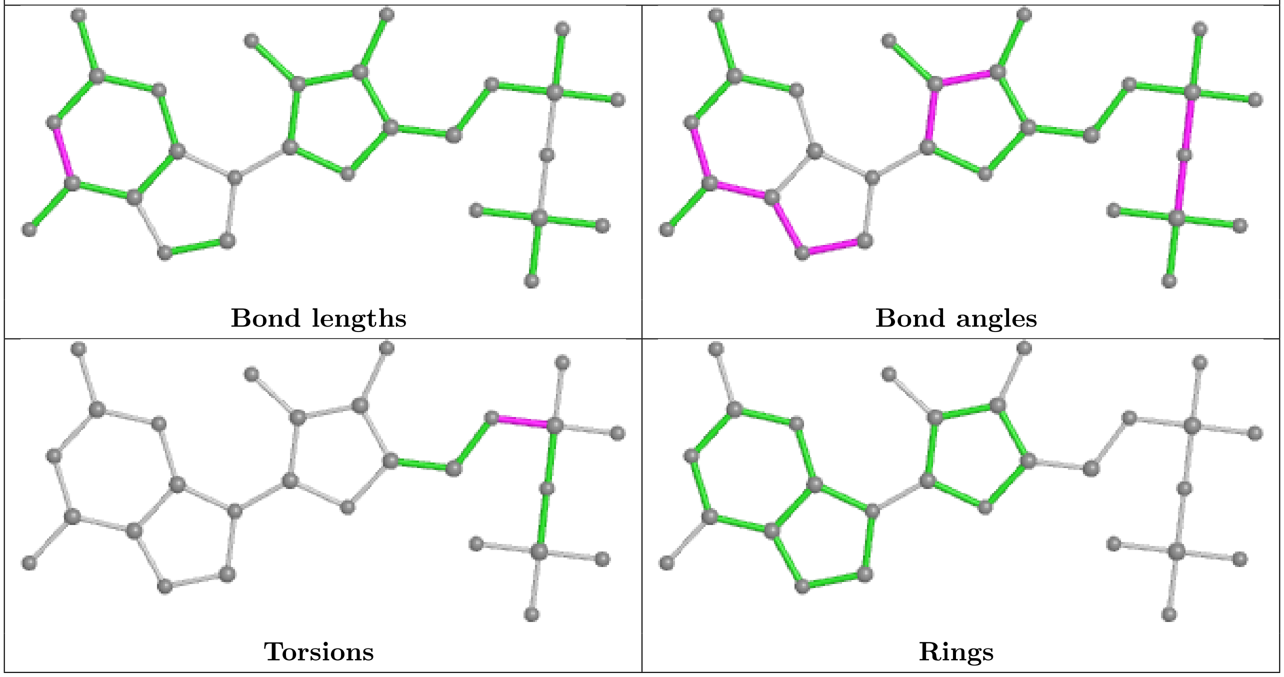

Bond lengths

Bond angles

Torsions

Rings

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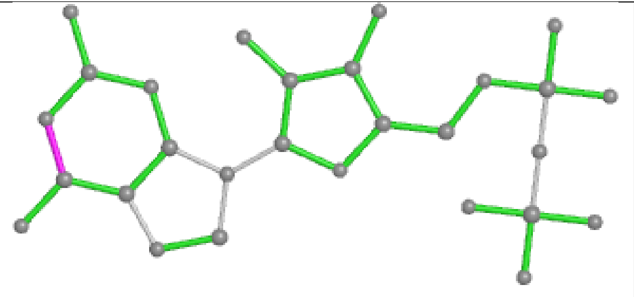
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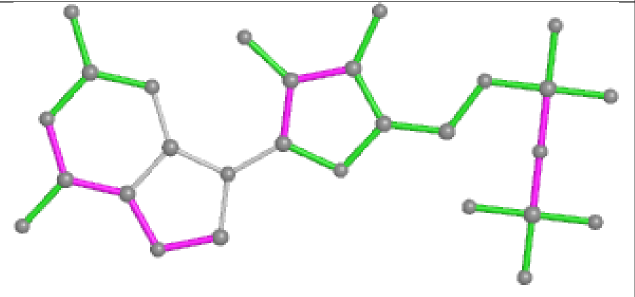
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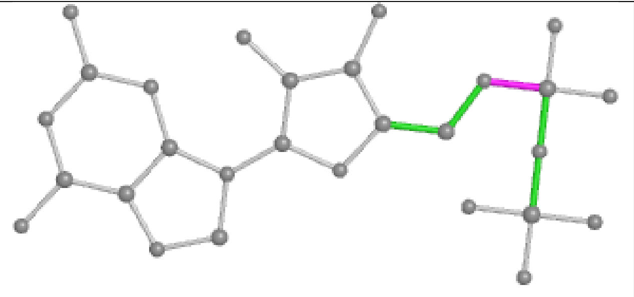
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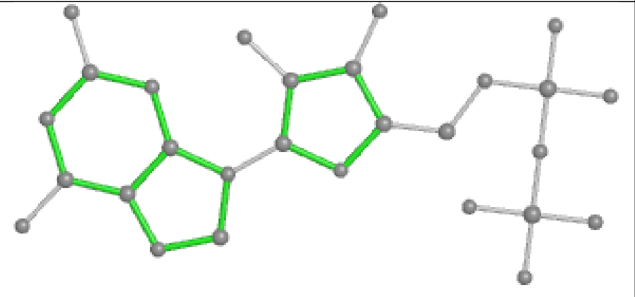
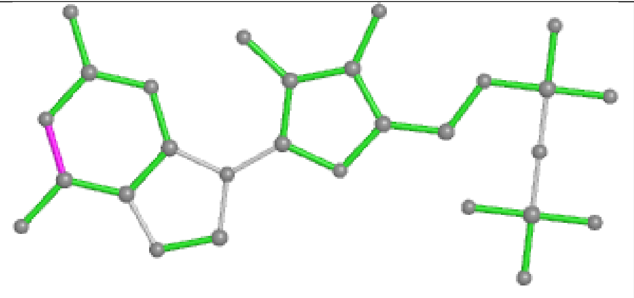

Rings

Ligand GDP JN 502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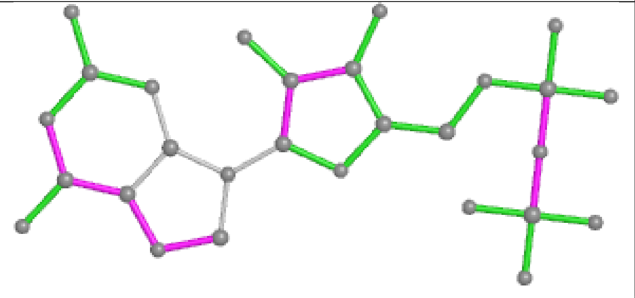
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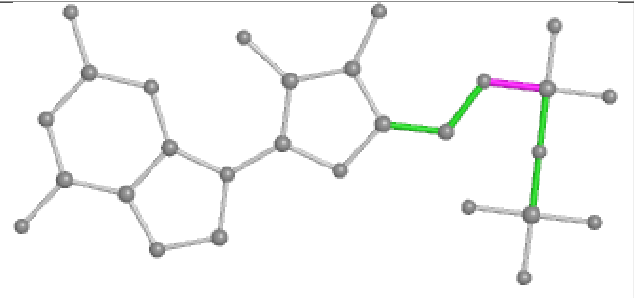
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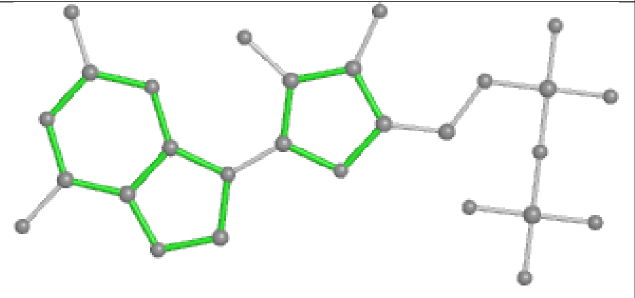
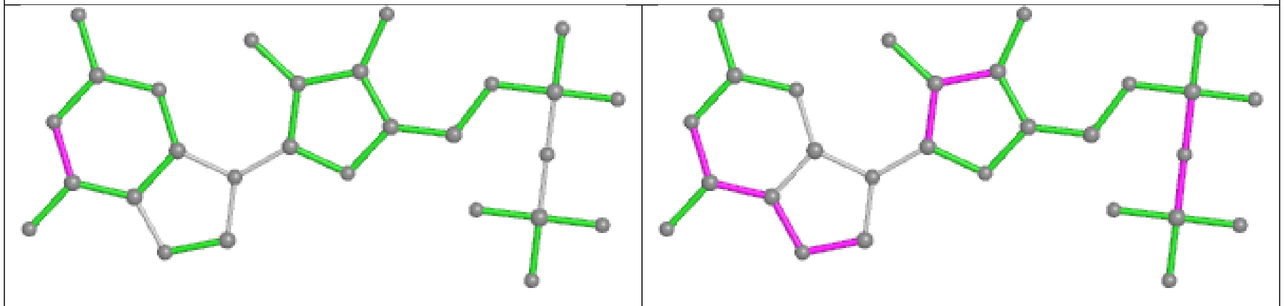
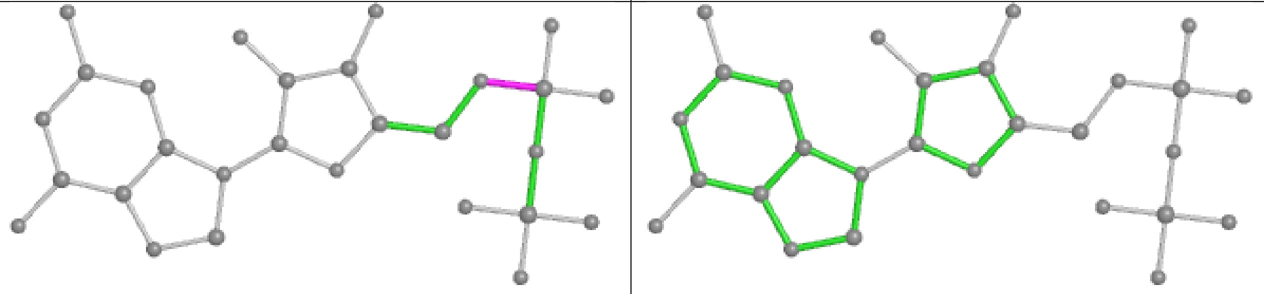

Rings

Ligand GDP LP 502



Bond lengths

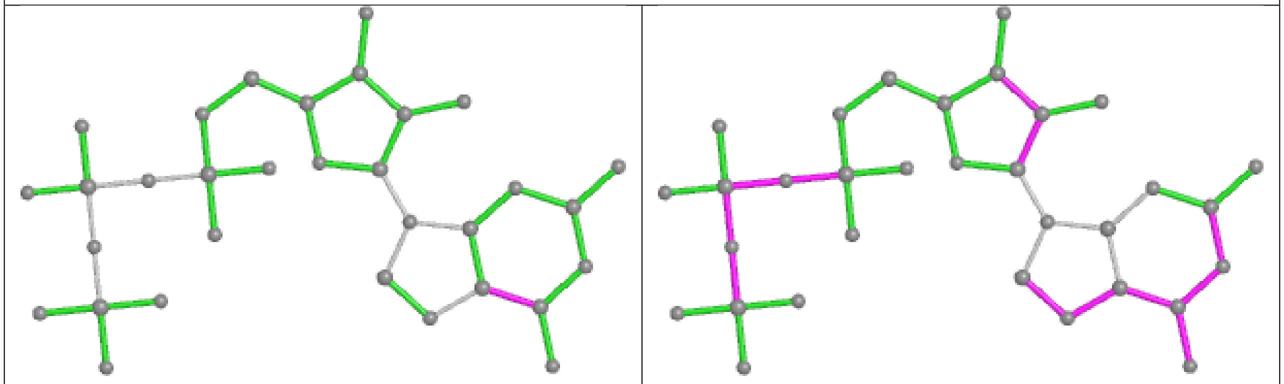
Bond angles



Torsions

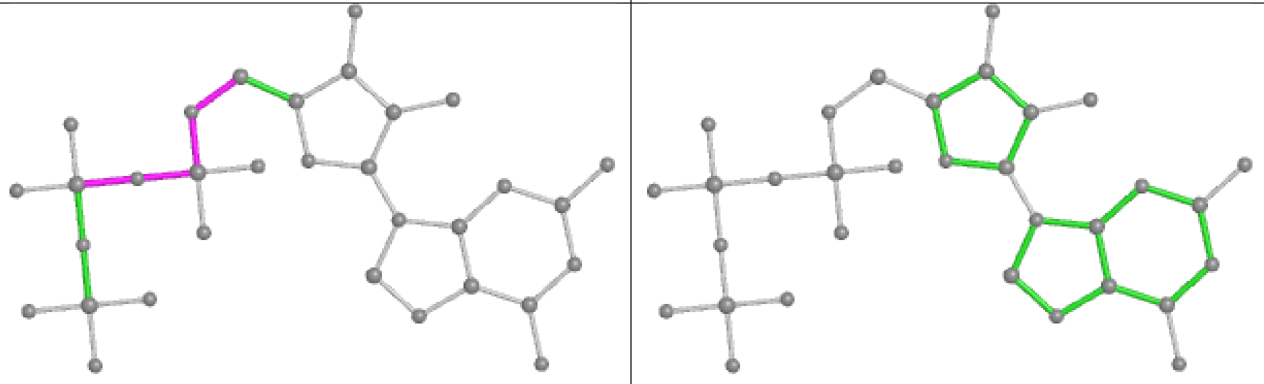
Rings

Ligand GTP KE 501



Bond lengths

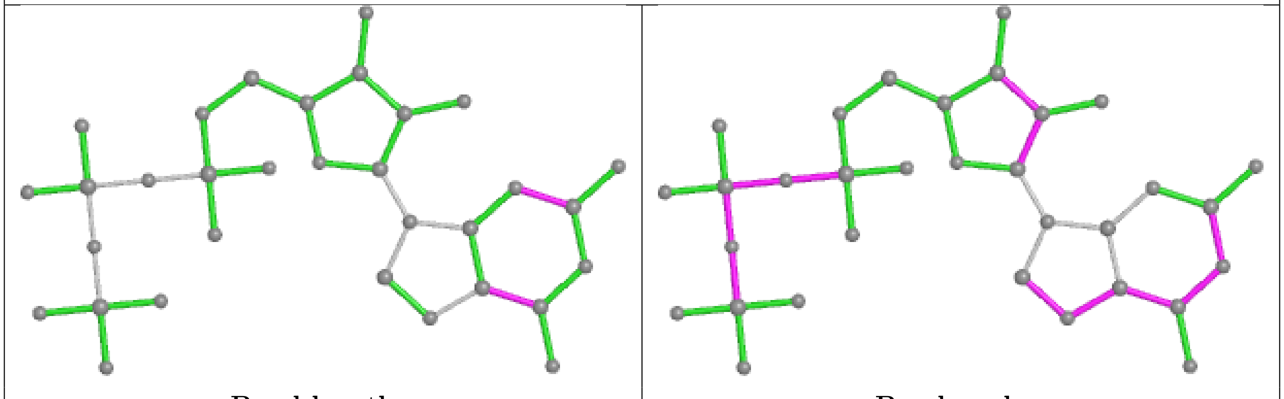
Bond angles



Torsions

Rings

Ligand GTP GC 501



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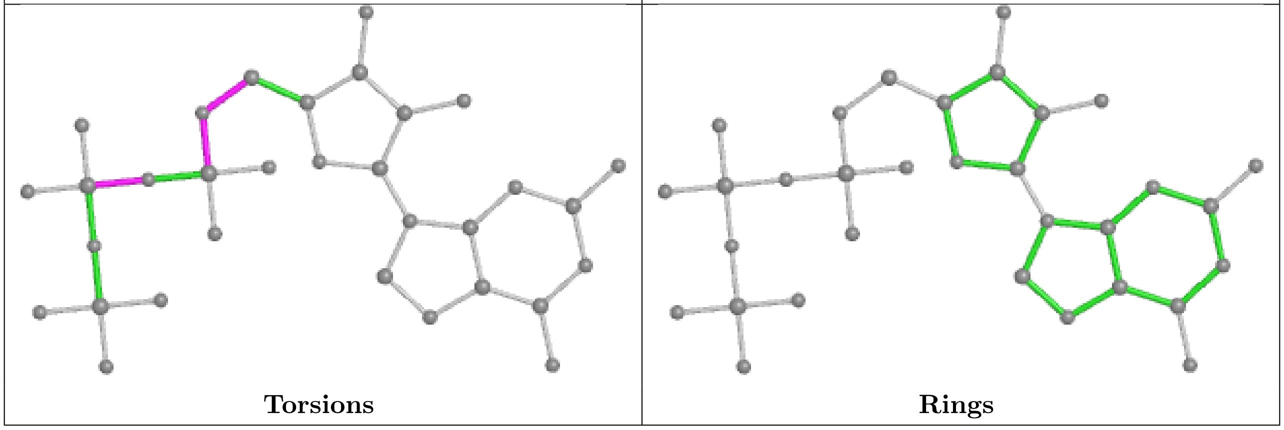
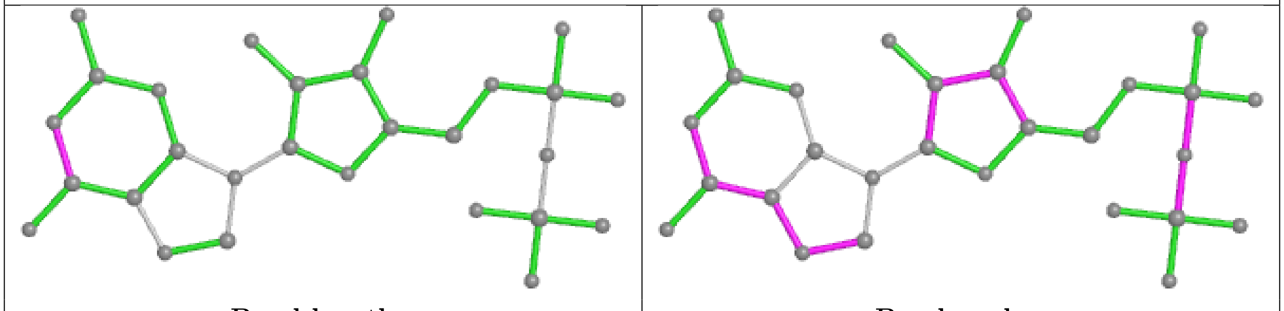
Bond angles



Torsions

Rings

Ligand GDP ML 502



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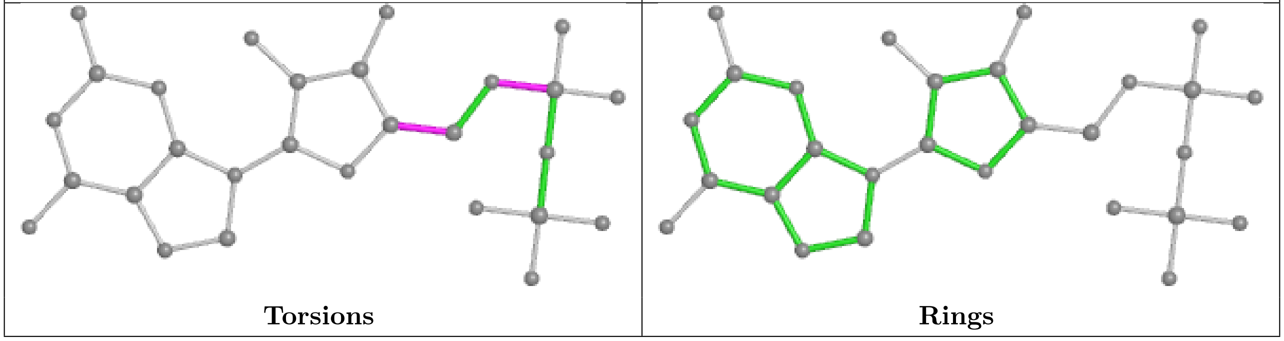
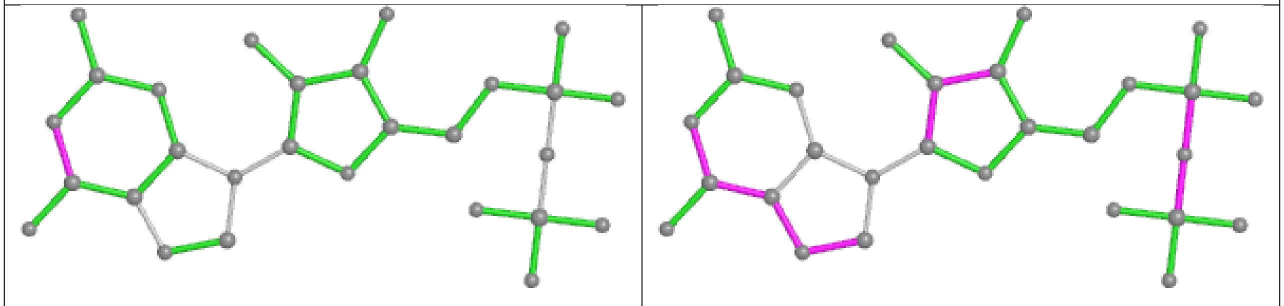
Bond angles



Torsions

Rings

Ligand GDP DN 502



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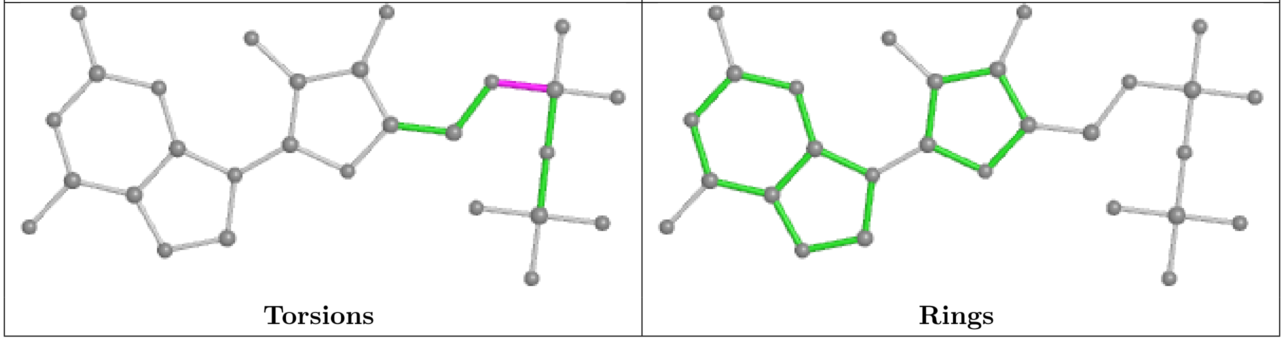

Torsions

Rings

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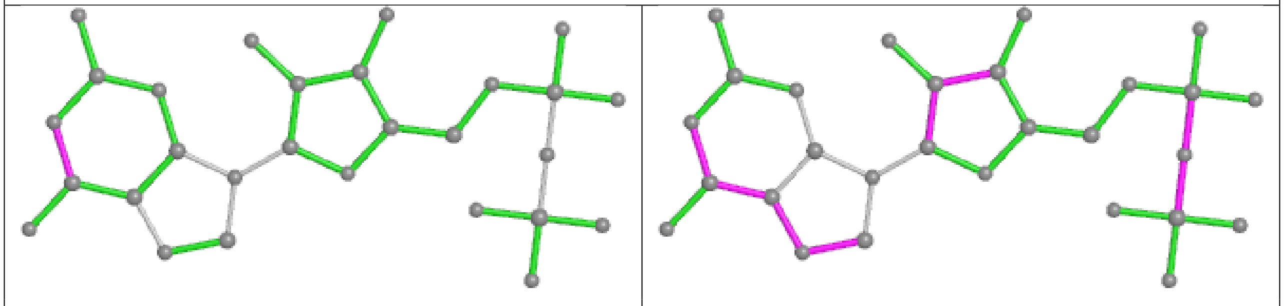

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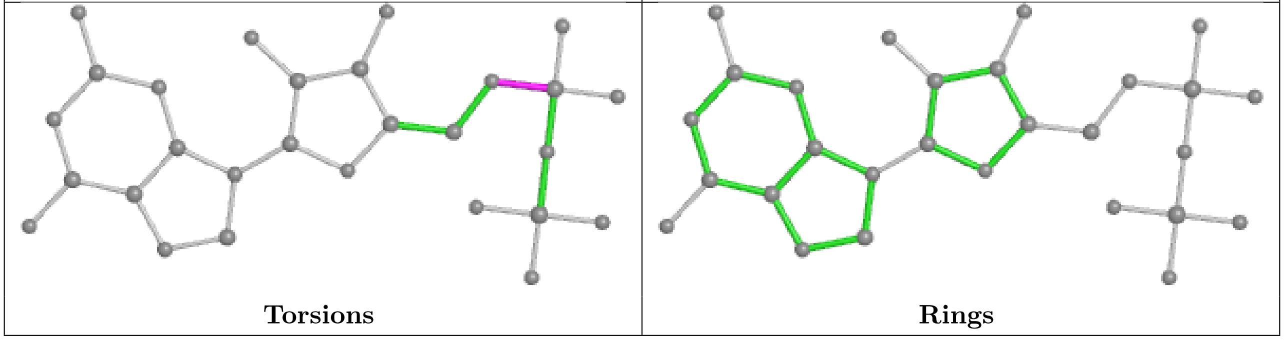

Torsions

Rings

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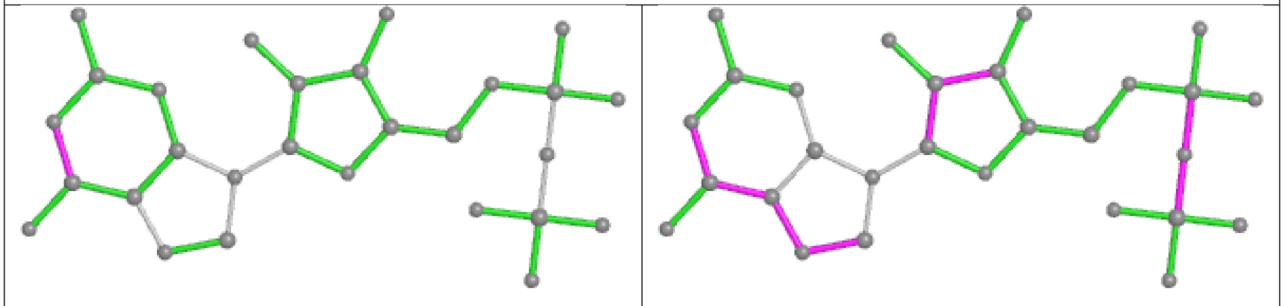

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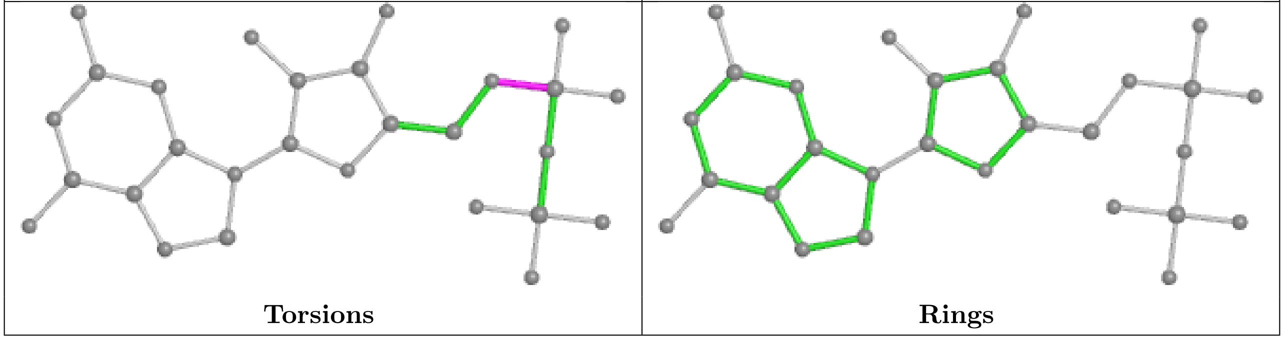
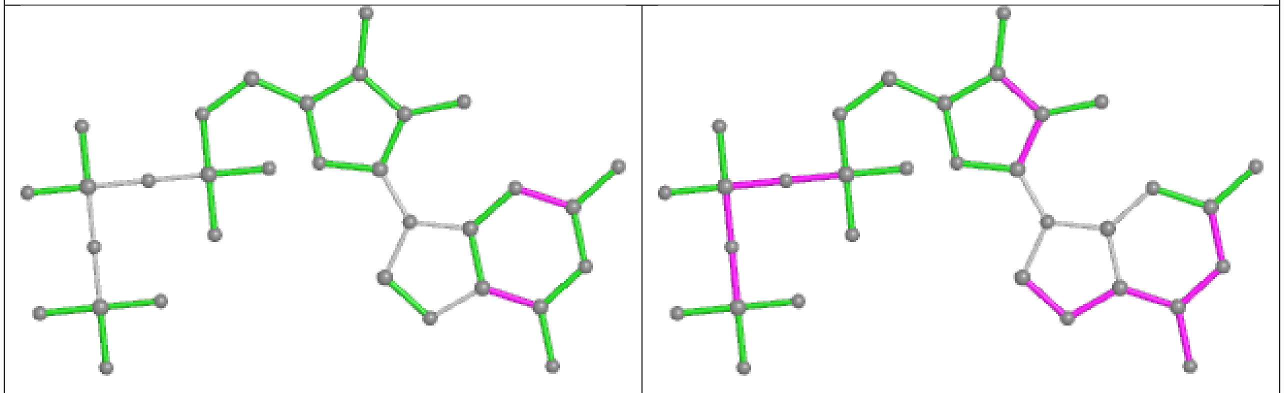


Torsions Rings

Ligand GTP LI 501



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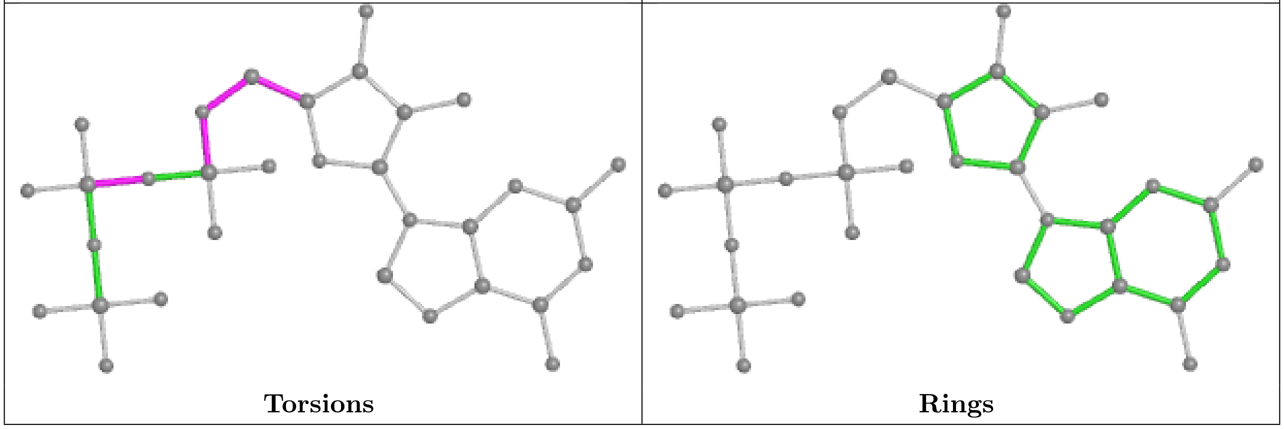
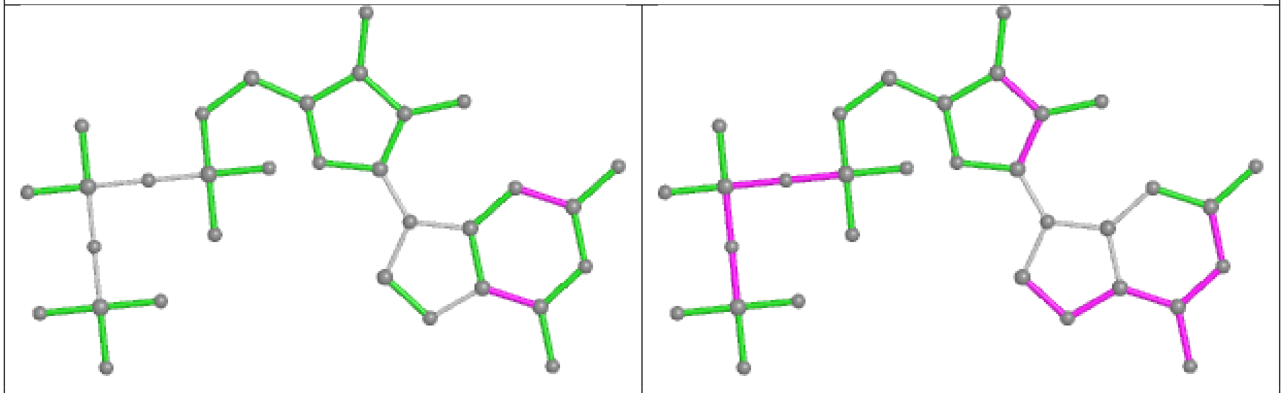


Torsions Rings

Ligand GTP JO 501



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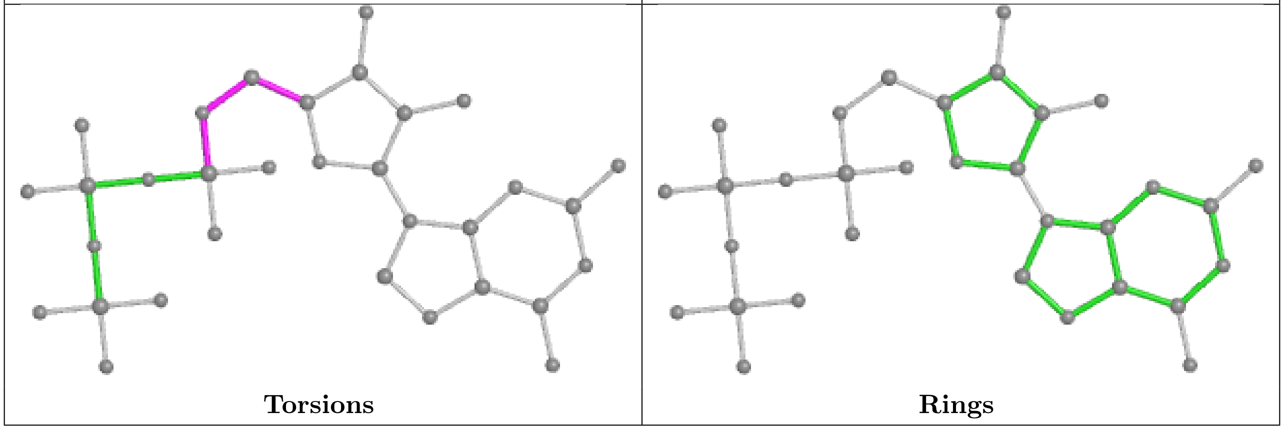

Torsions Rings

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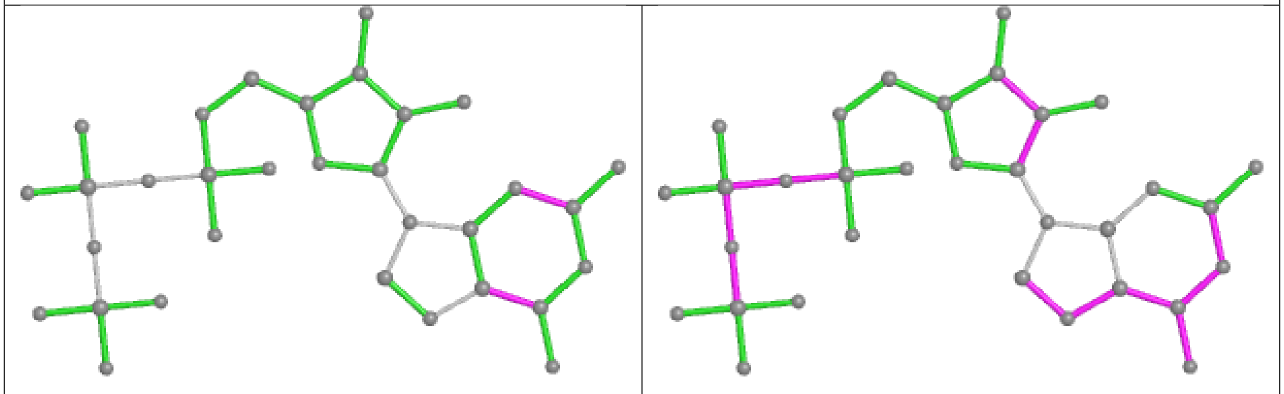

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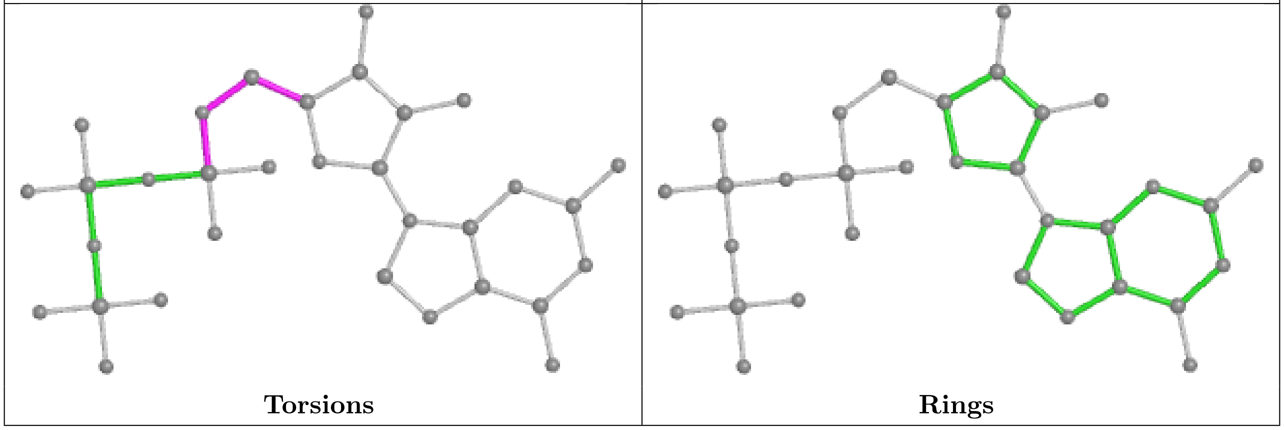

Torsions Rings

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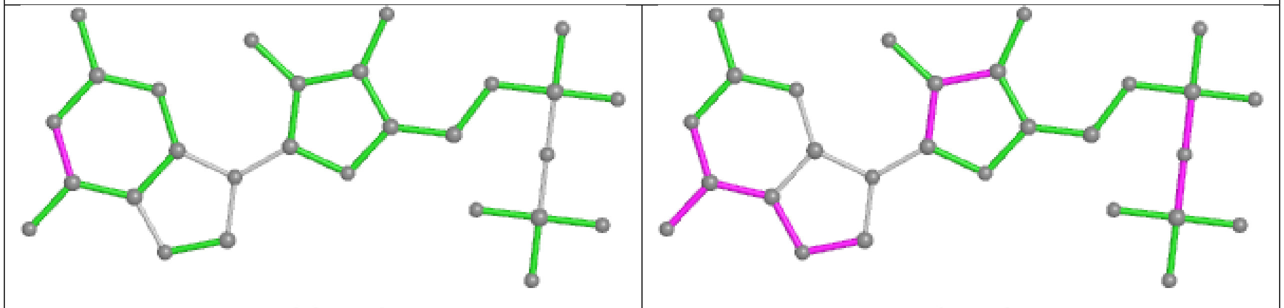
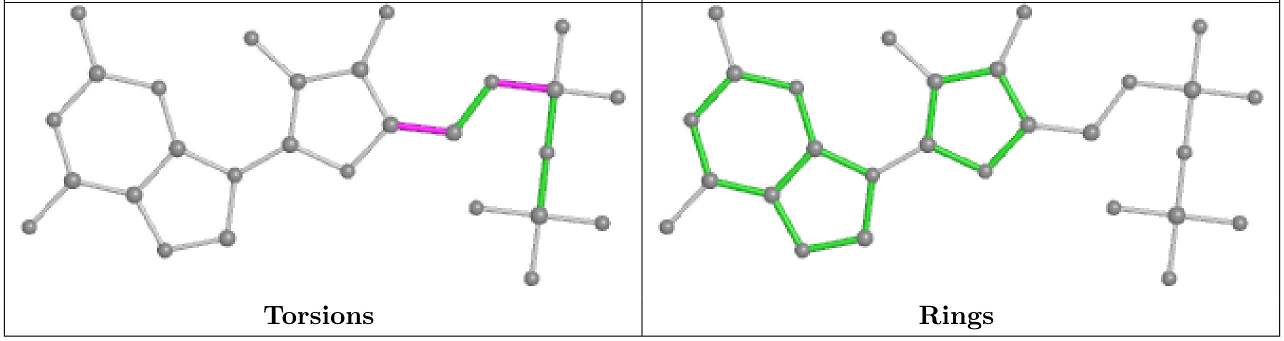


Bond lengths

Bond angles



Torsions

Rings

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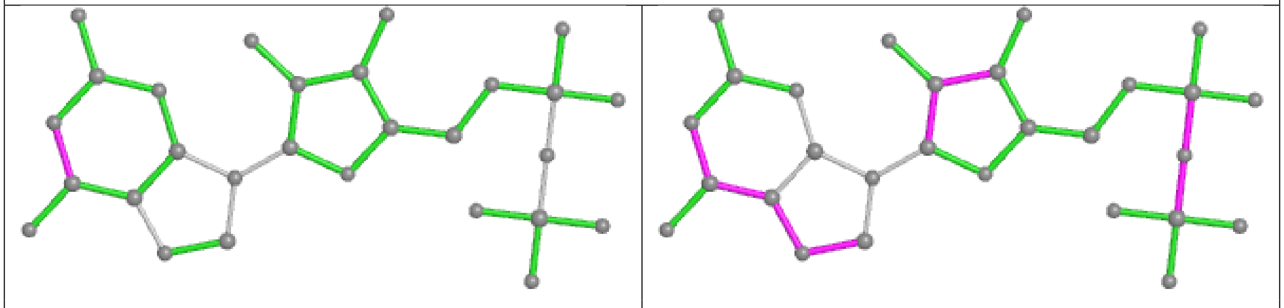
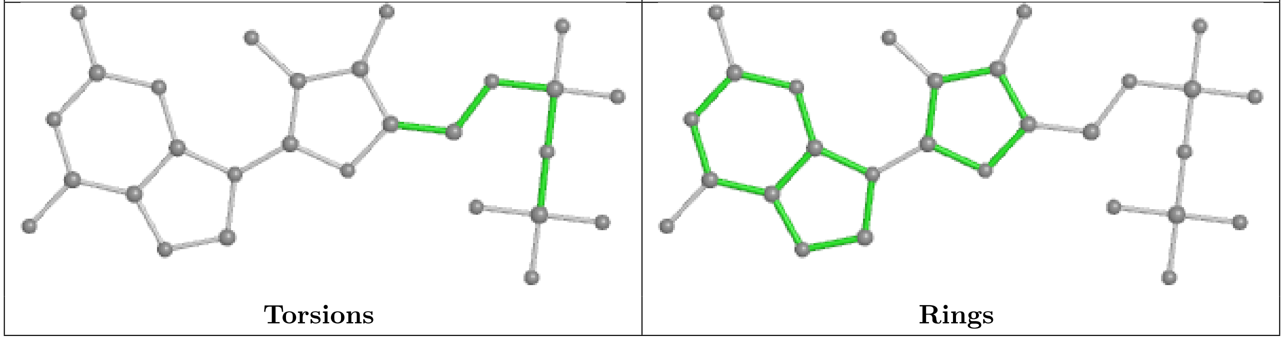


Bond lengths

Bond angles



Torsions

Rings

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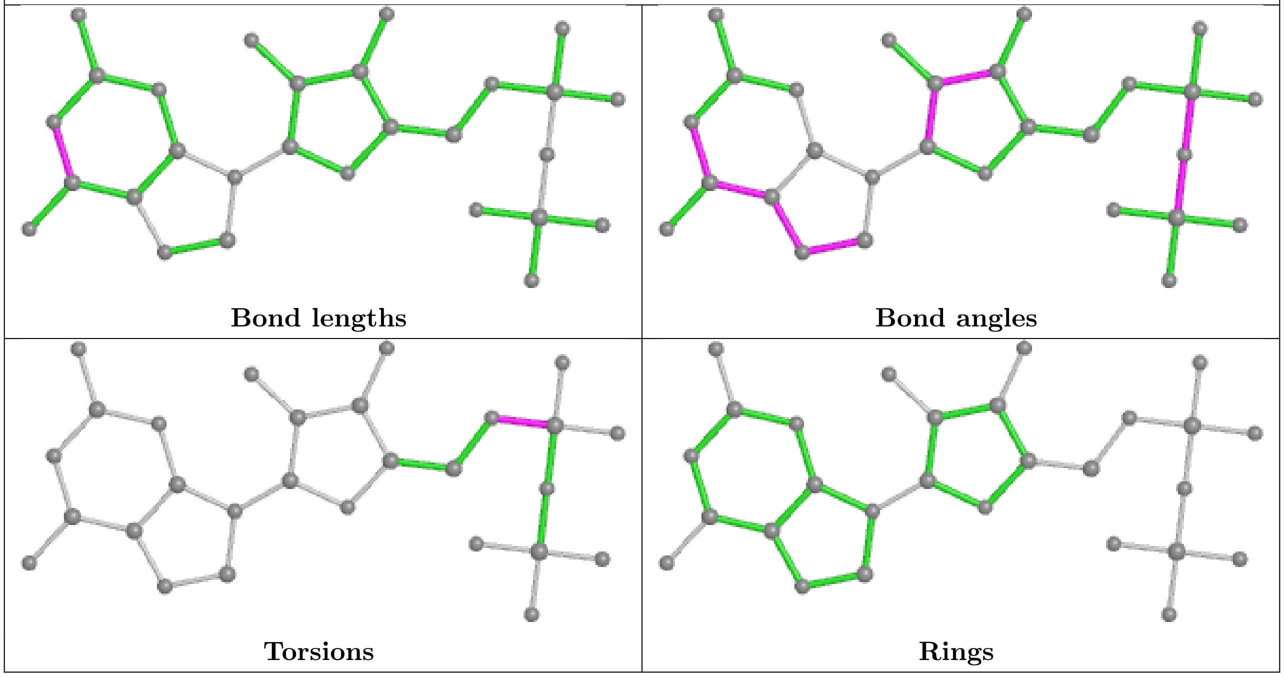

Bond lengths

Bond angles

Torsions

Rings

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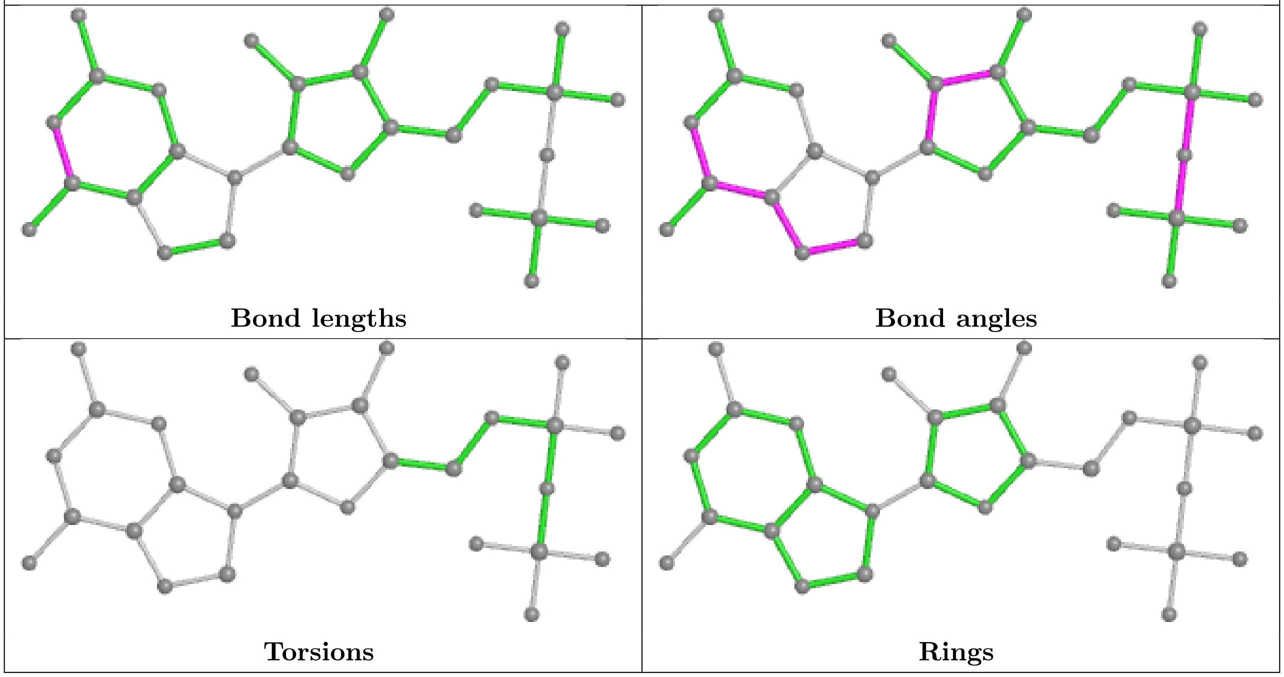

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Bond angles

Torsions

Rings

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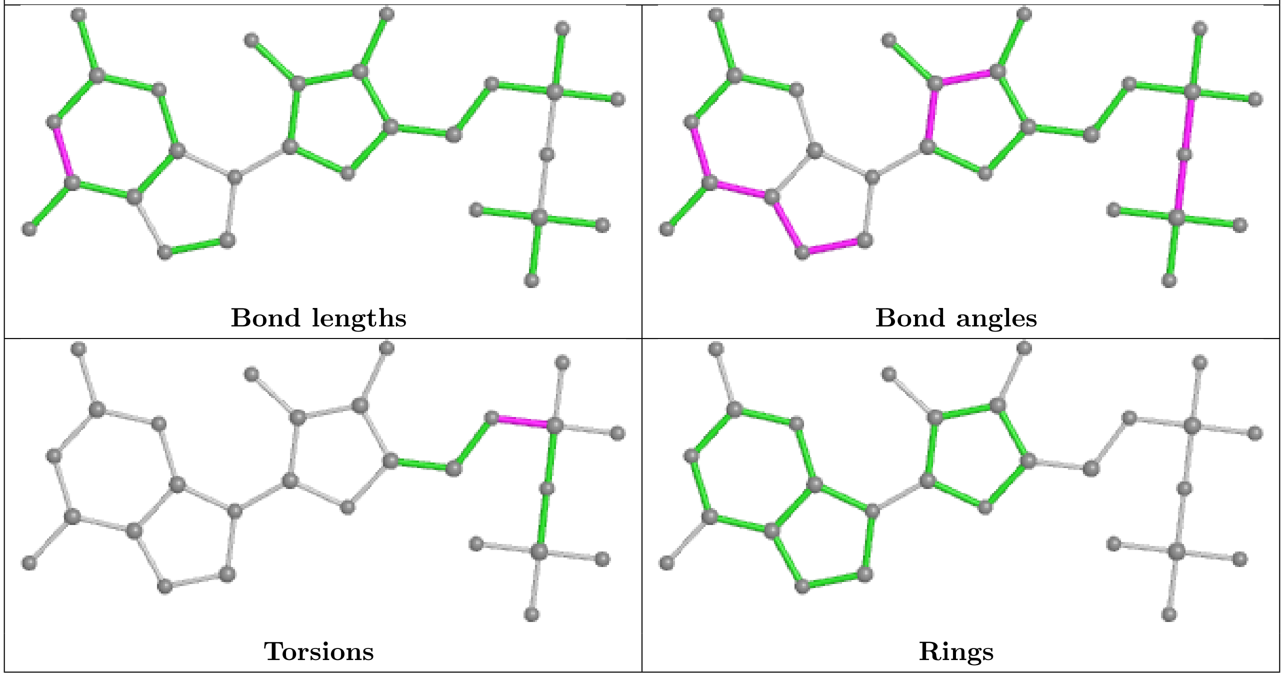

Bond lengths

Bond angles

Torsions

Rings

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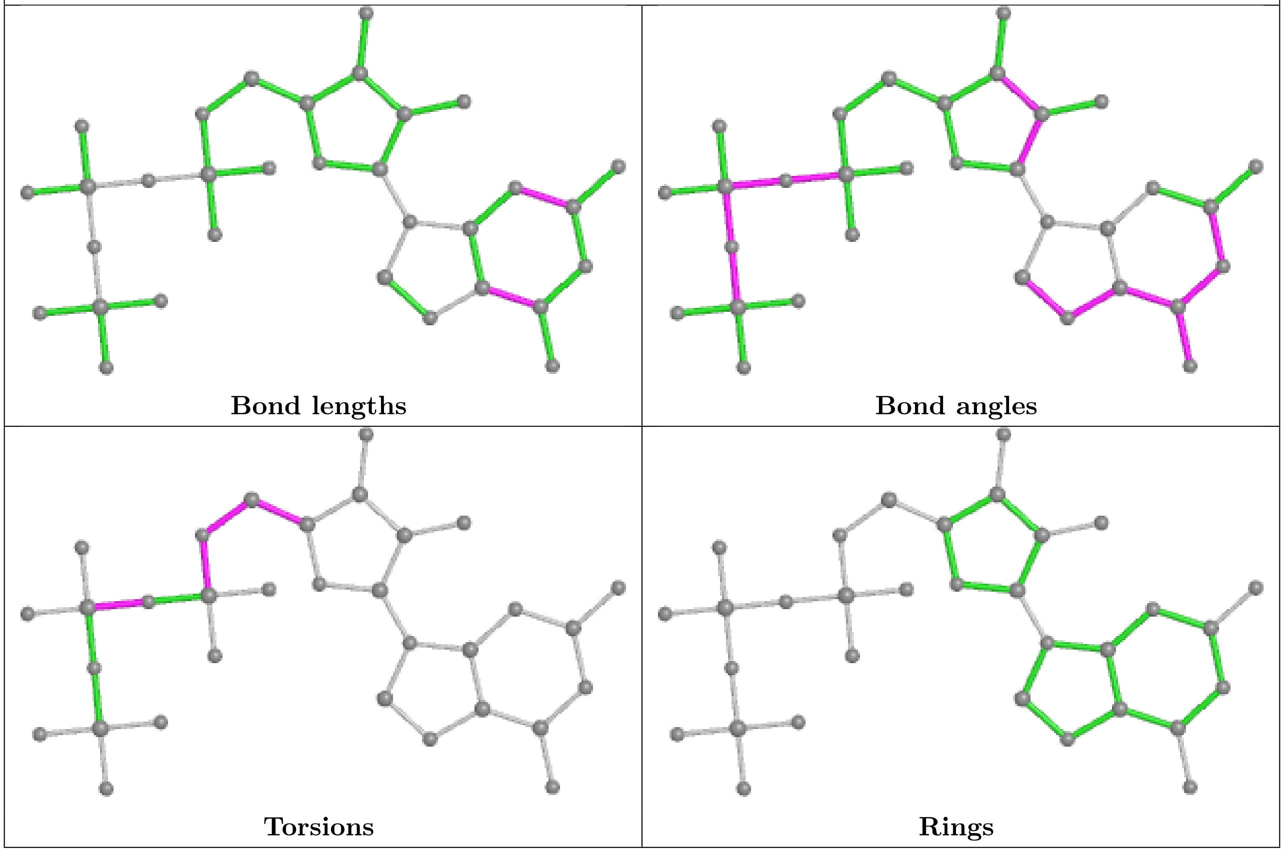

Bond lengths

Bond angles

Torsions

Rings

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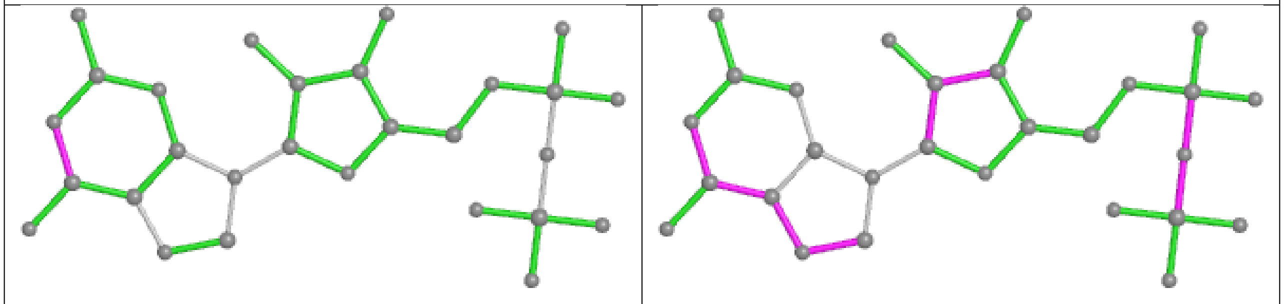
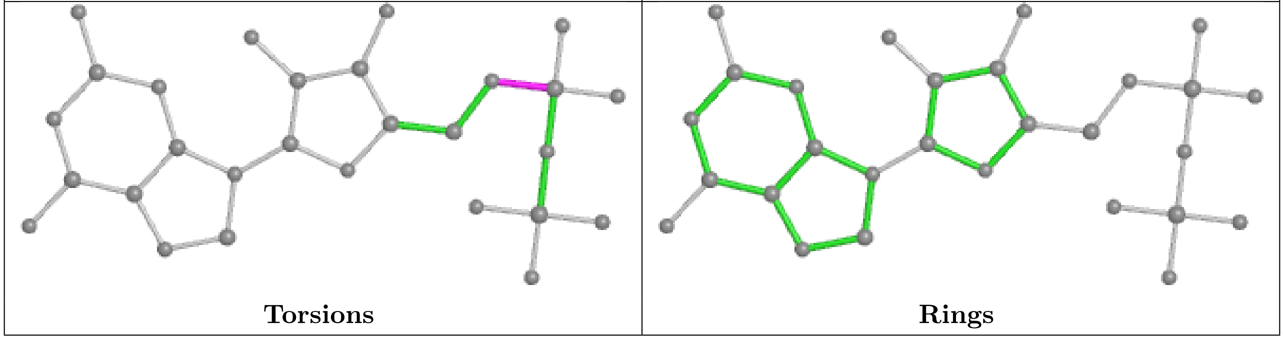


Bond lengths Bond angles



Torsions Rings

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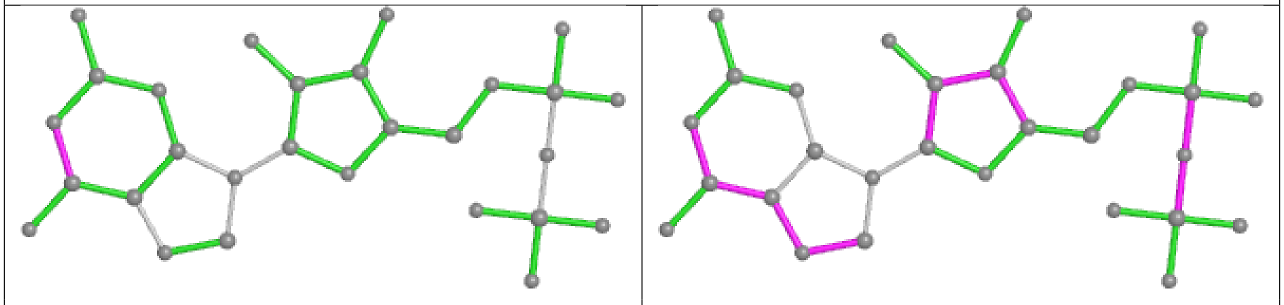

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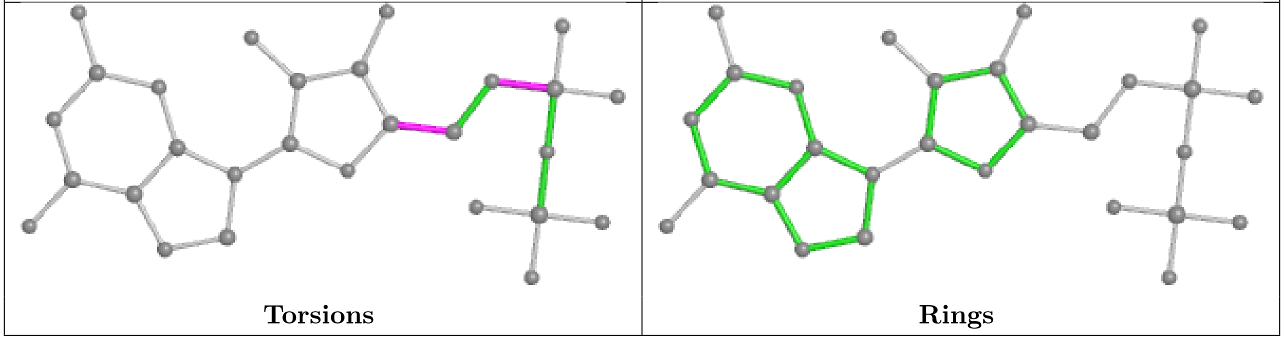

Torsions Rings

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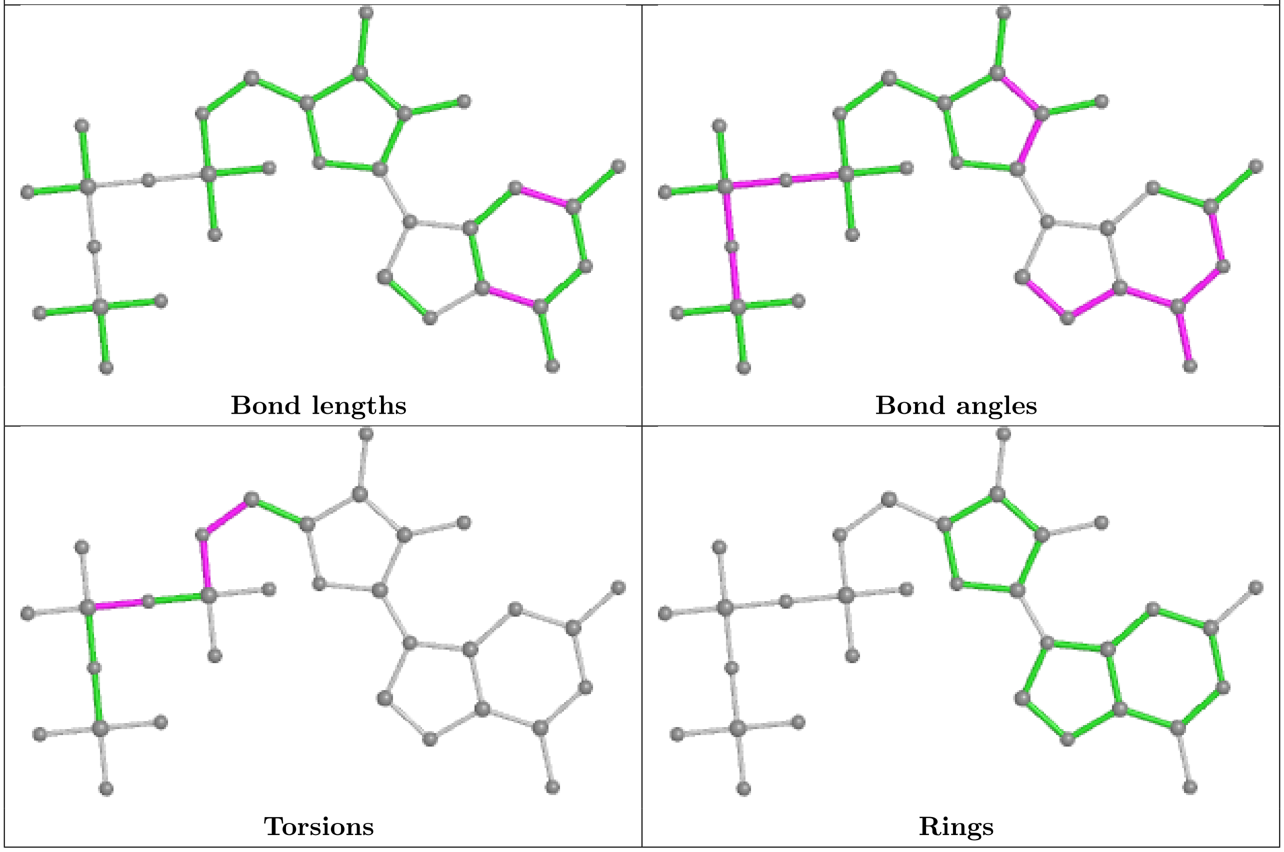

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Bond angles

Torsions

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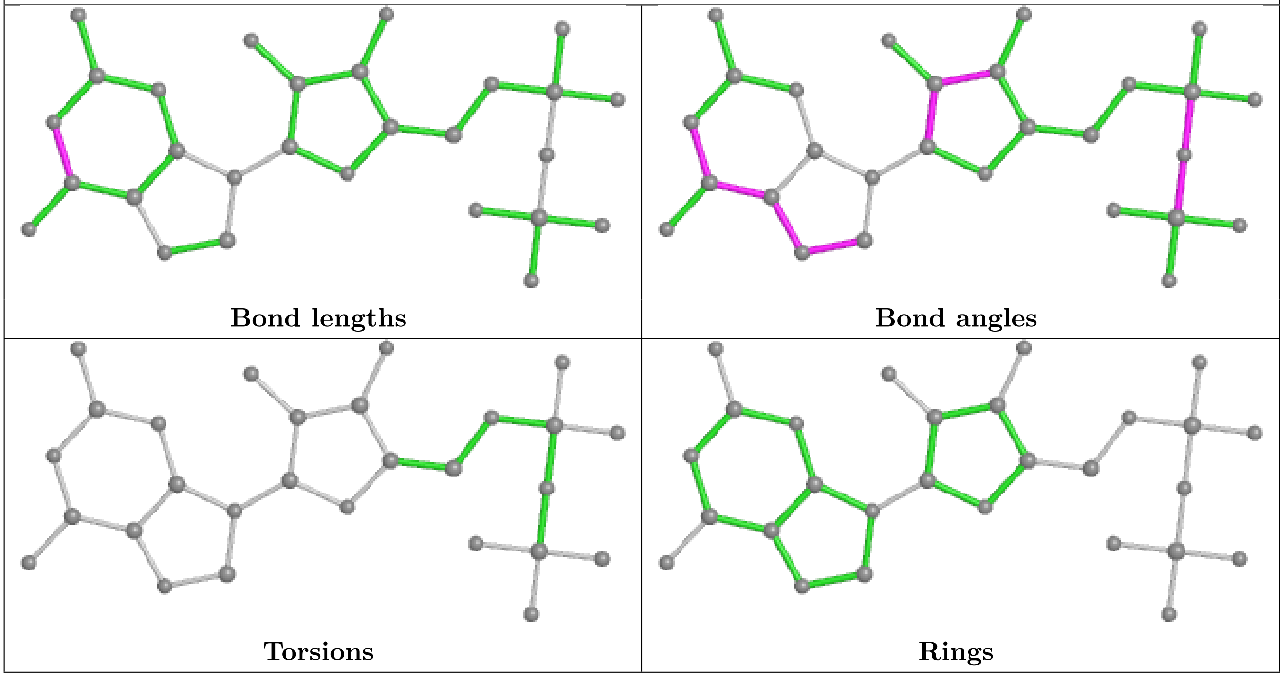

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Bond angles

Torsions

Rings

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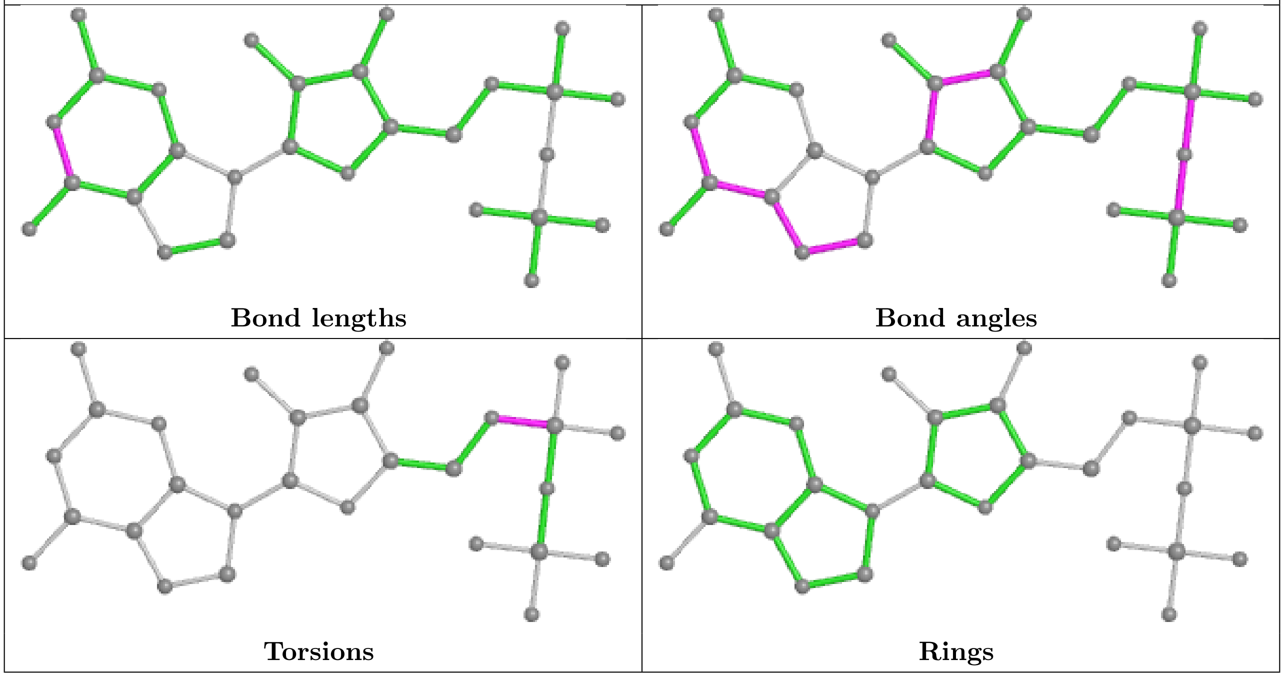

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Bond angles

Torsions

Rings

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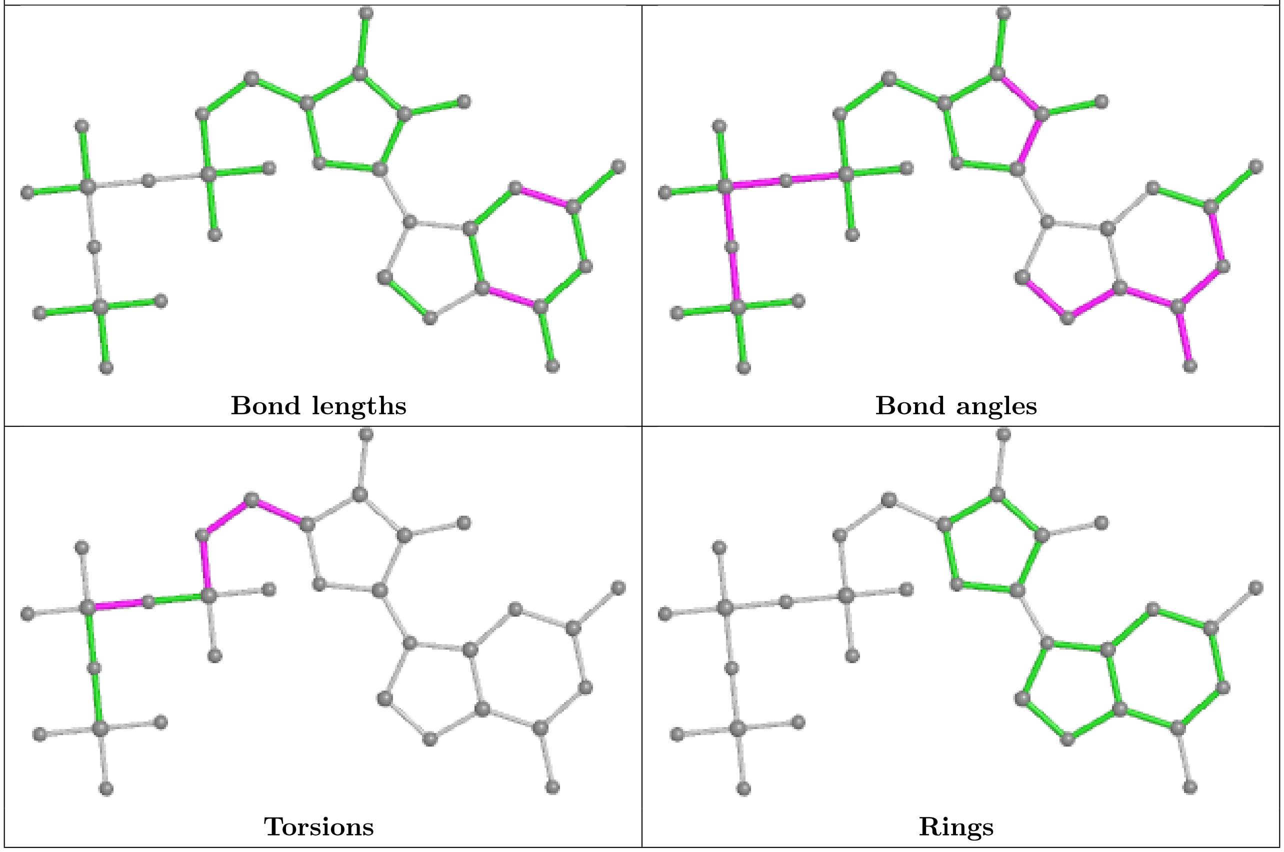

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Bond angles

Torsions

Rings

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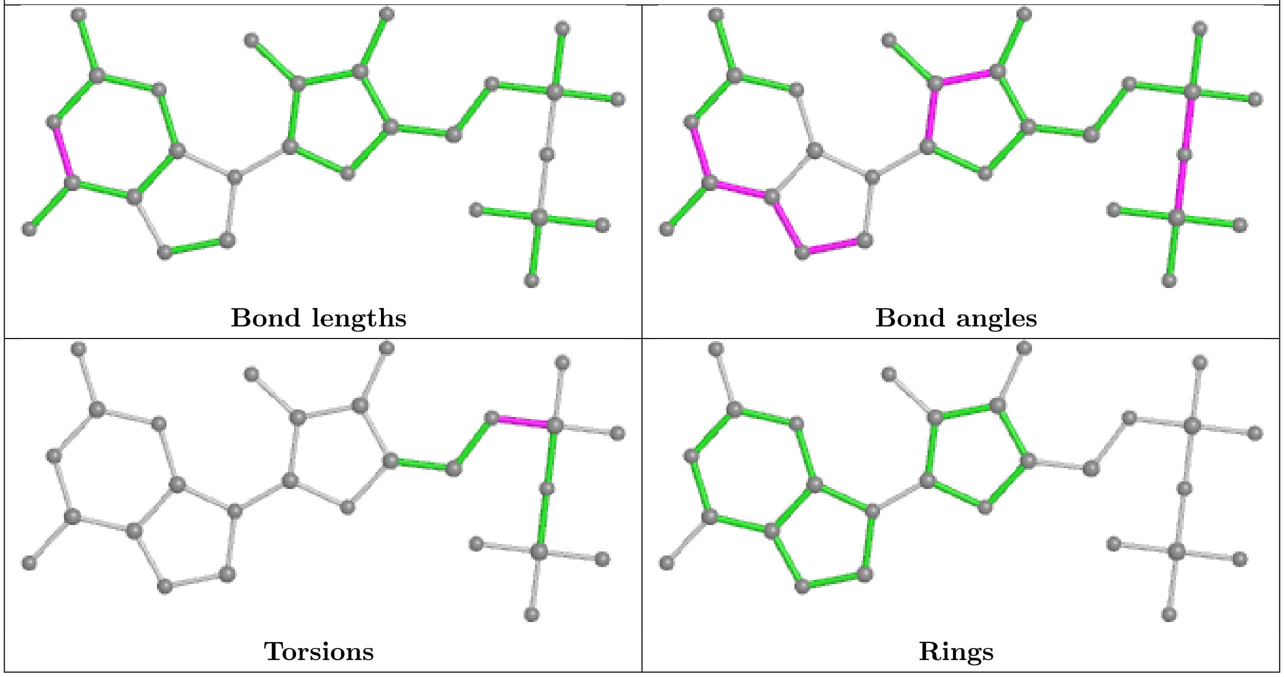

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Bond angles

Torsions

Rings

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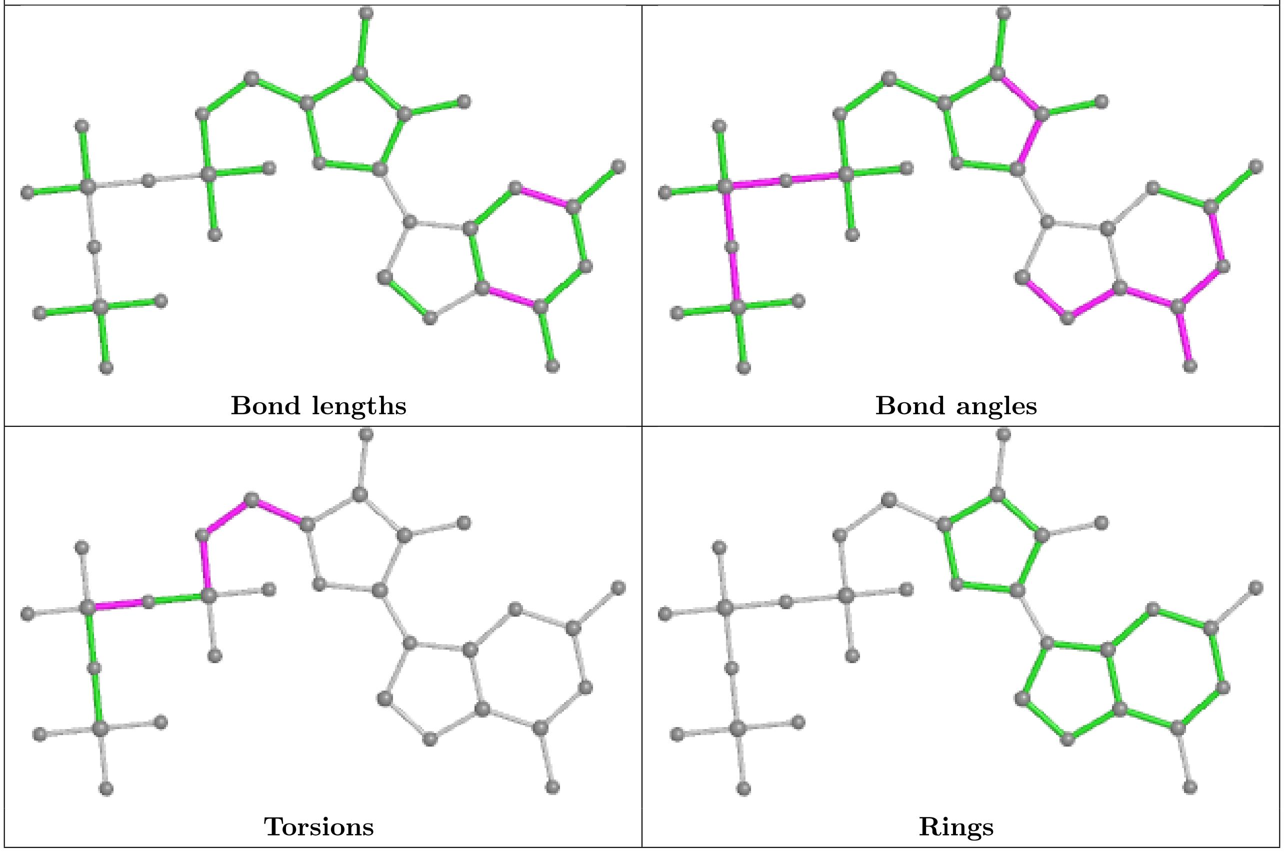

Bond lengths

Bond angles

Torsions

Rings

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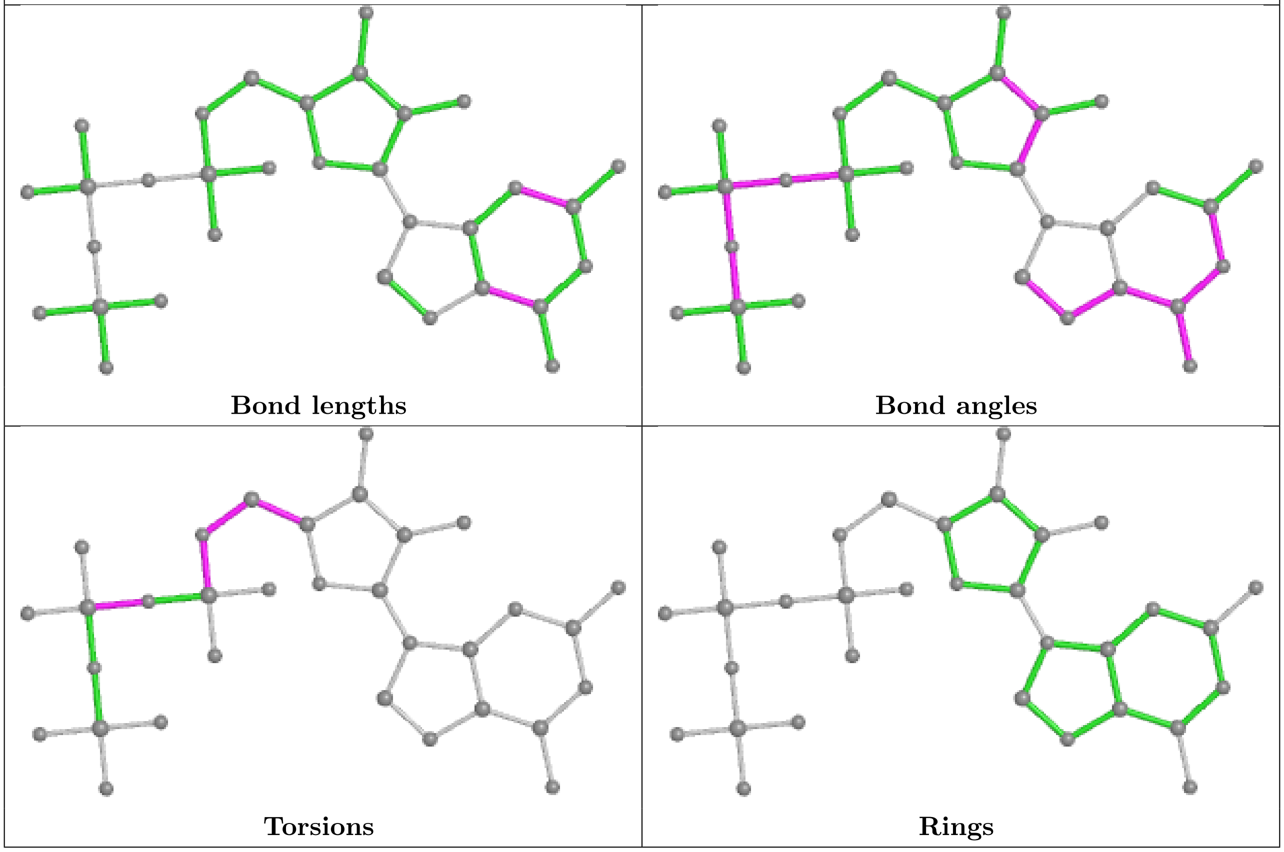

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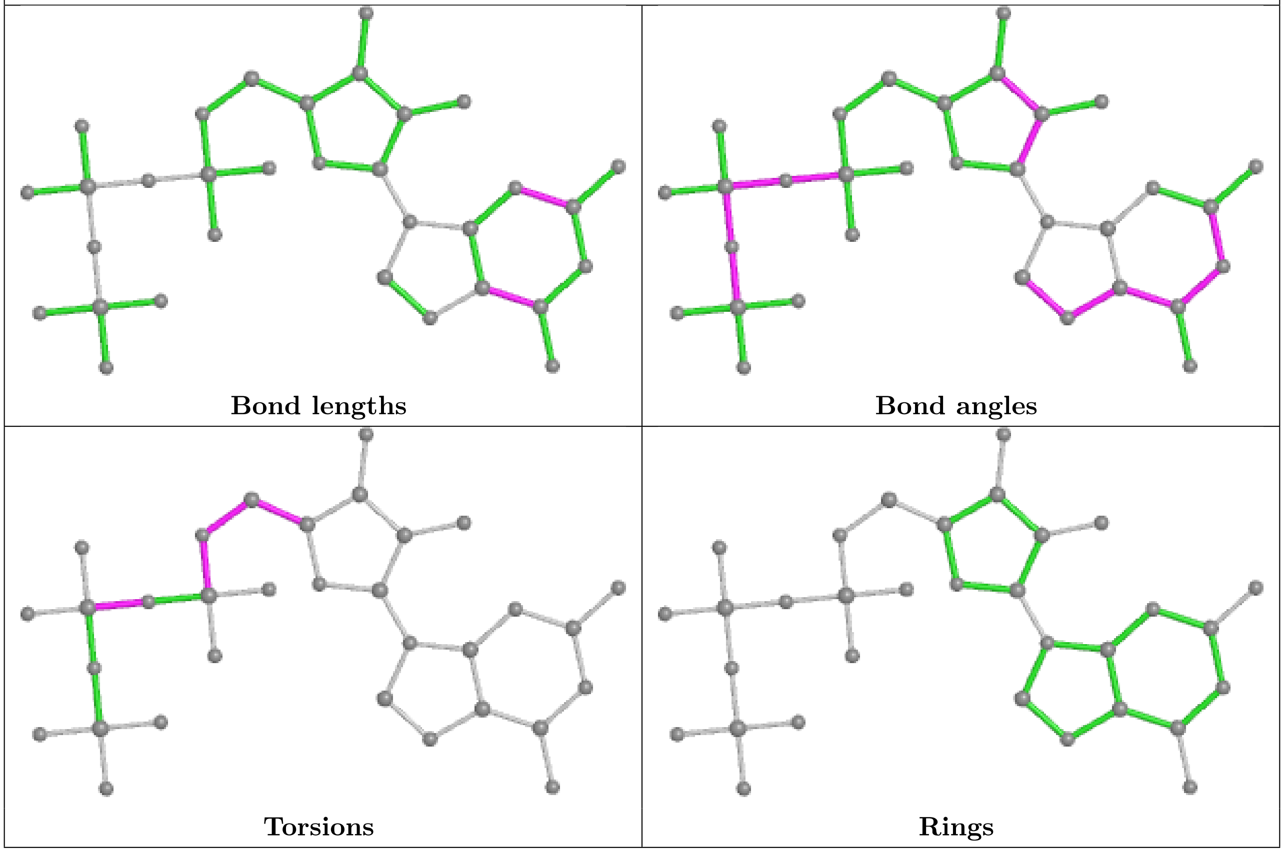

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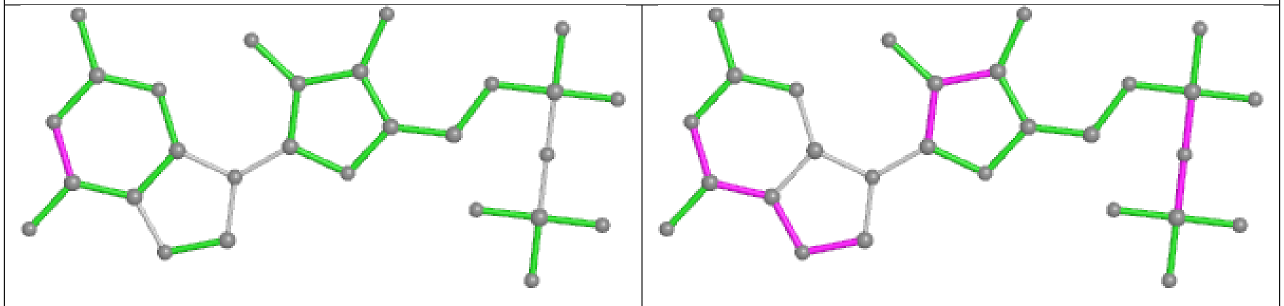
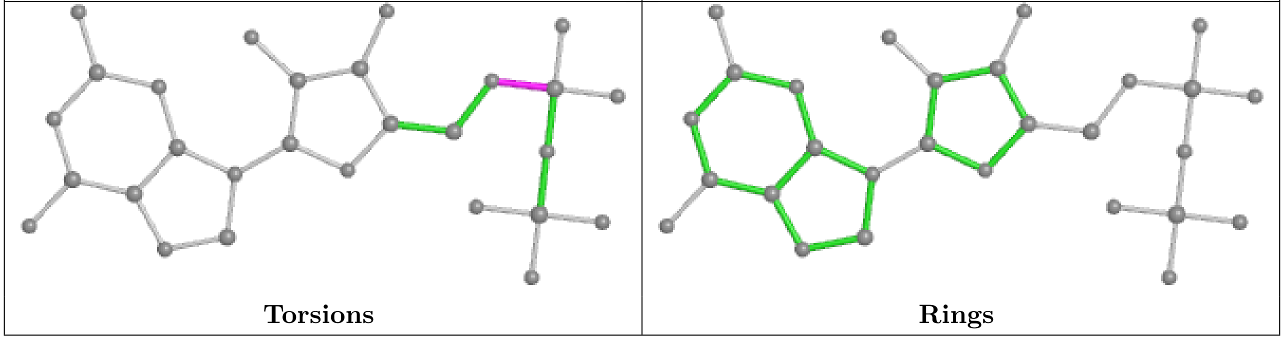
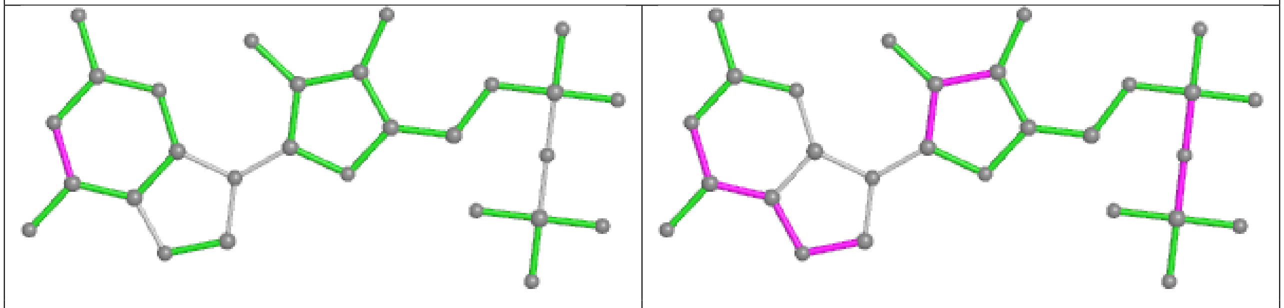


Bond lengths **Bond angles**



Torsions **Rings**

Ligand GDP AH 502



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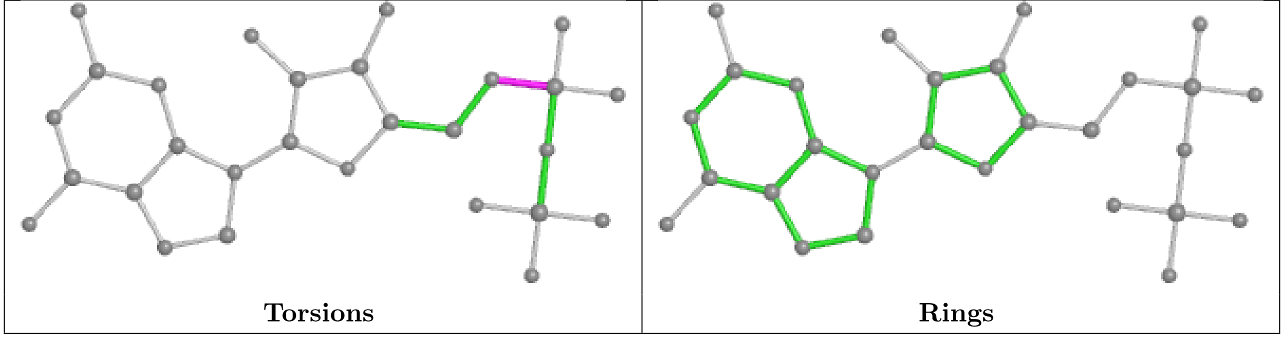

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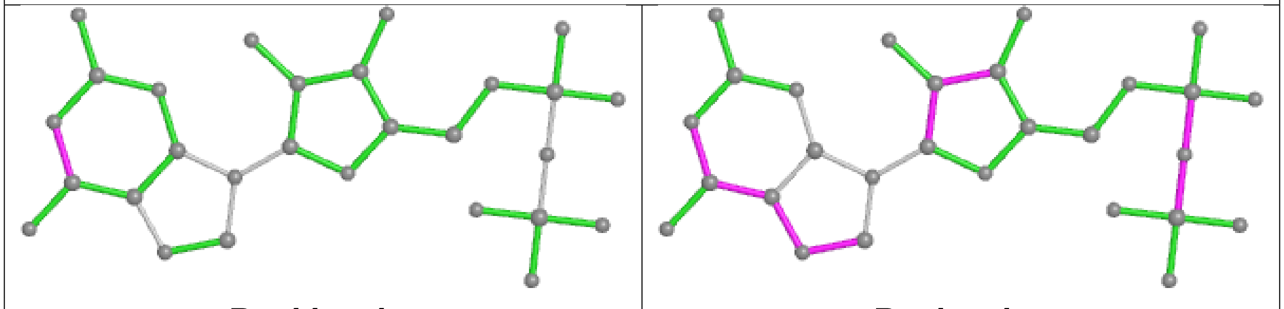
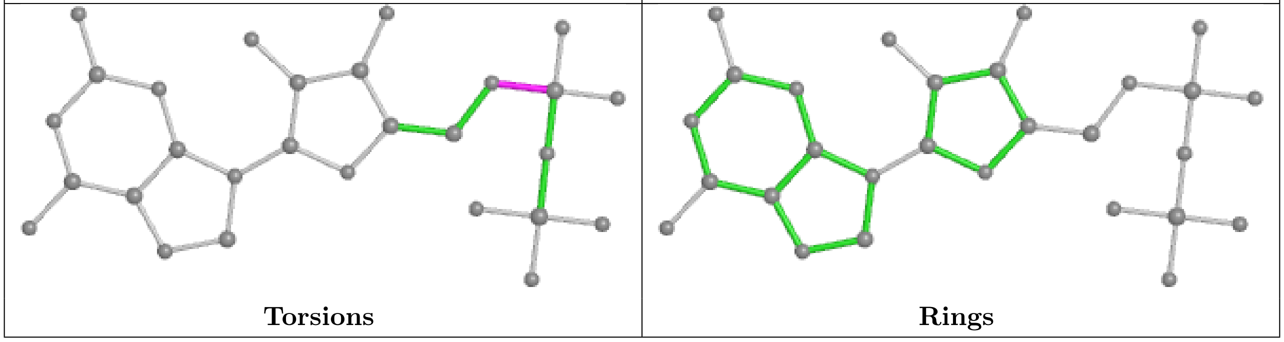


Bond lengths **Bond angles**



Torsions **Rings**

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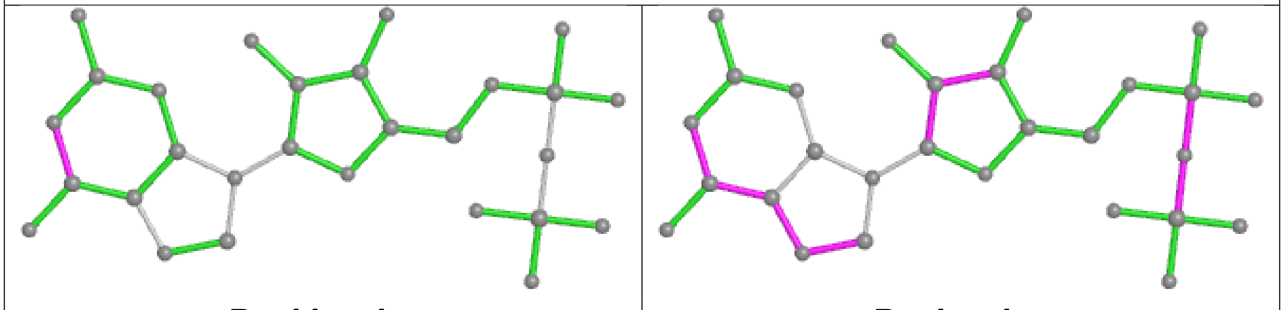
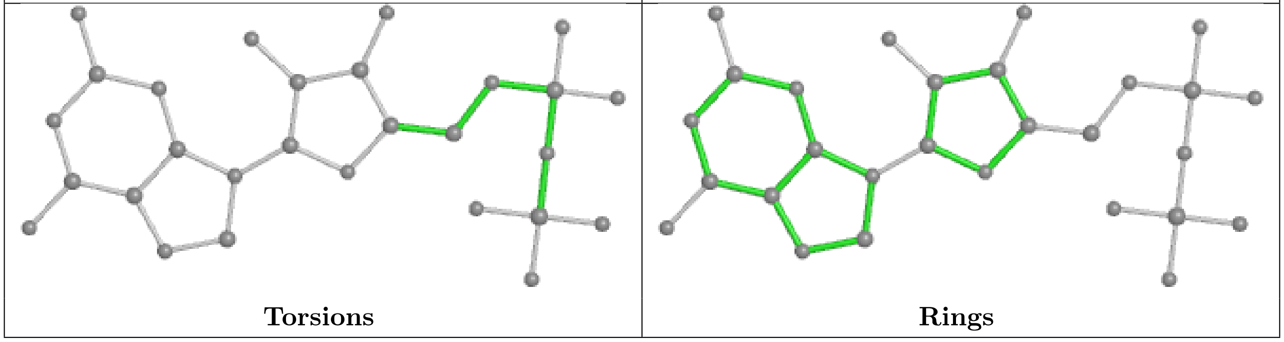
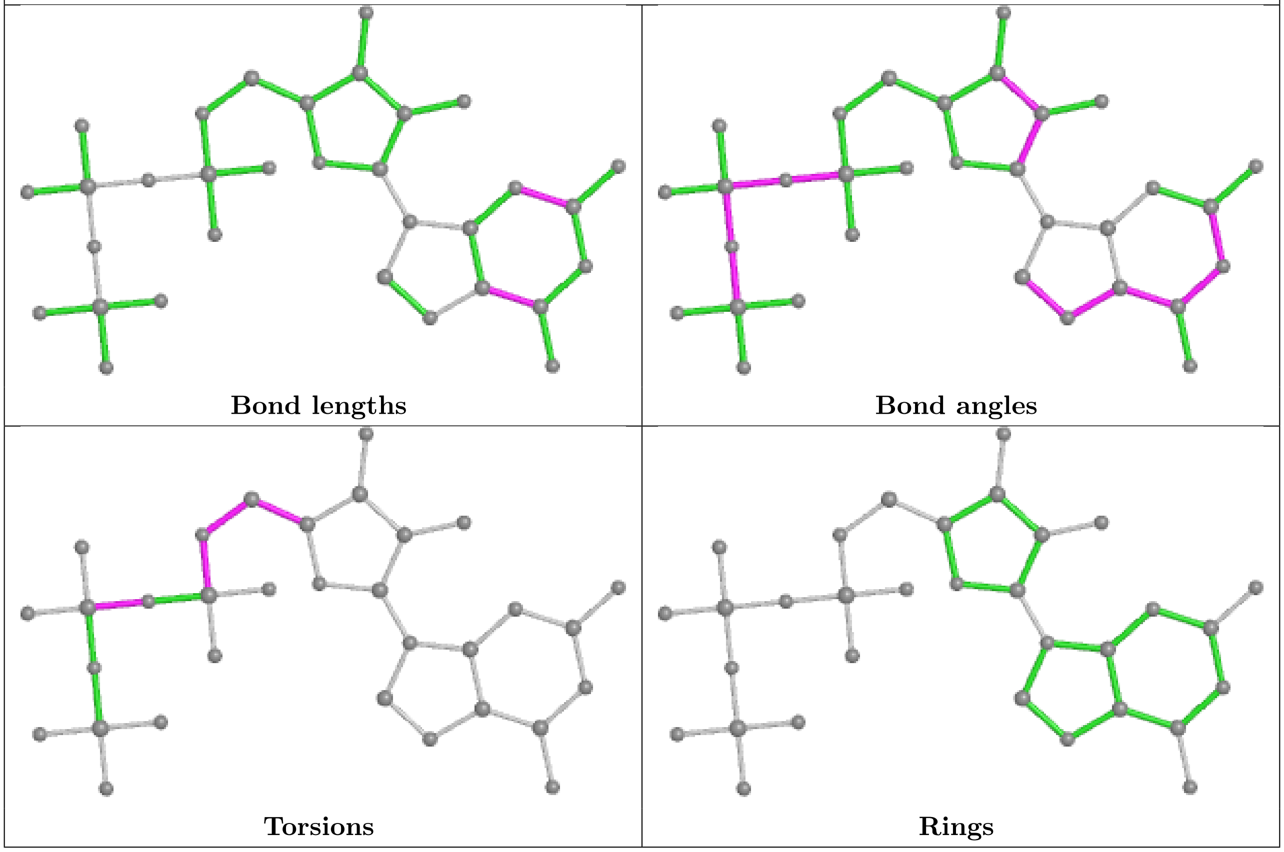


Bond lengths **Bond angles**



Torsions **Rings**

Ligand GTP BC 501


Bond lengths
Bond angles
Torsions
Rings

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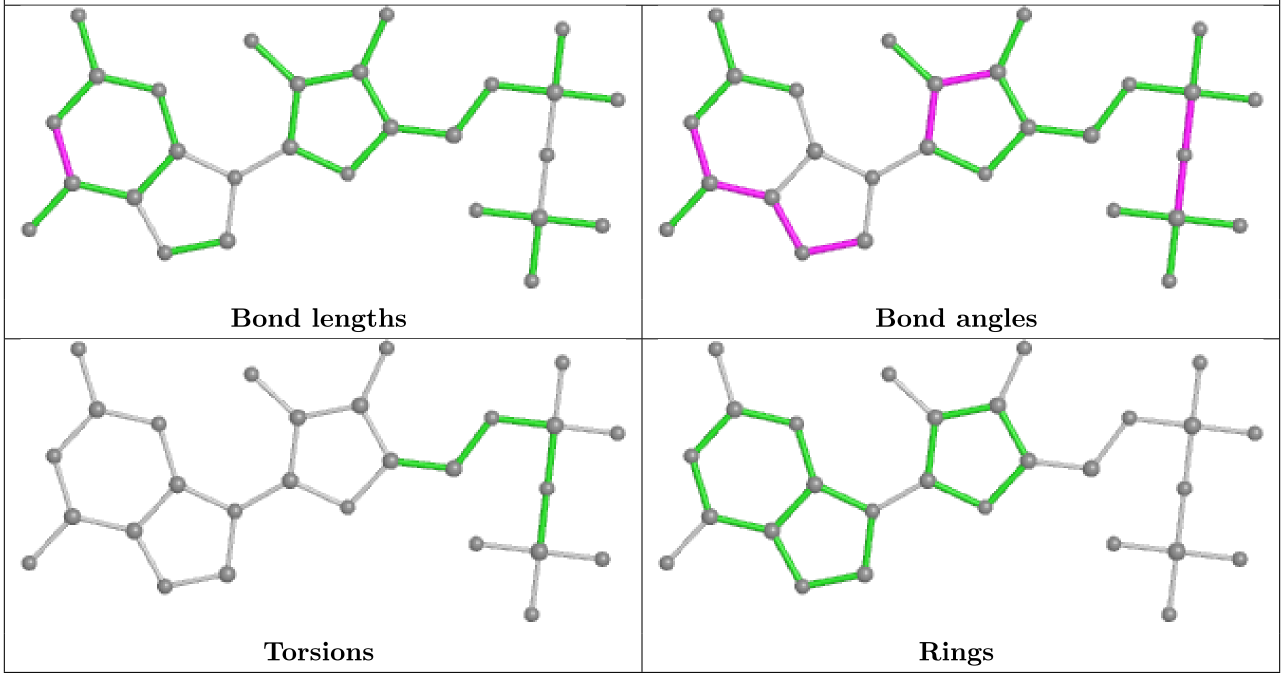
Bond lengths
Bond angles
Torsions
Rings

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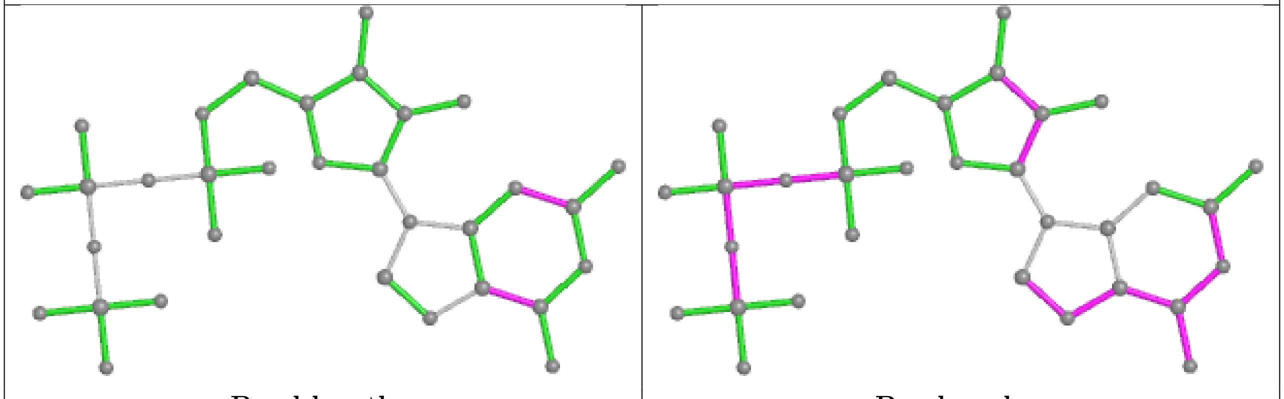
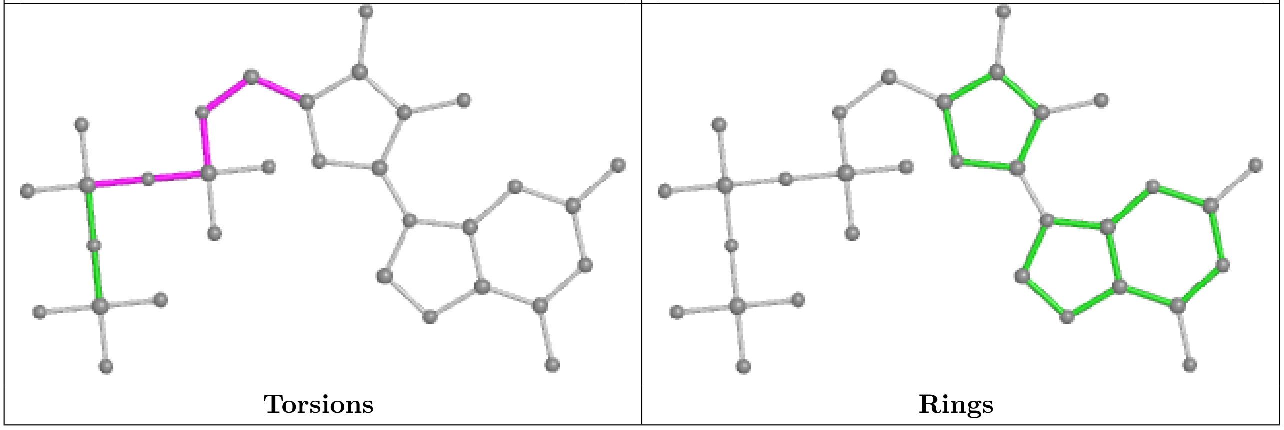


Bond lengths

Bond angles



Torsions

Rings

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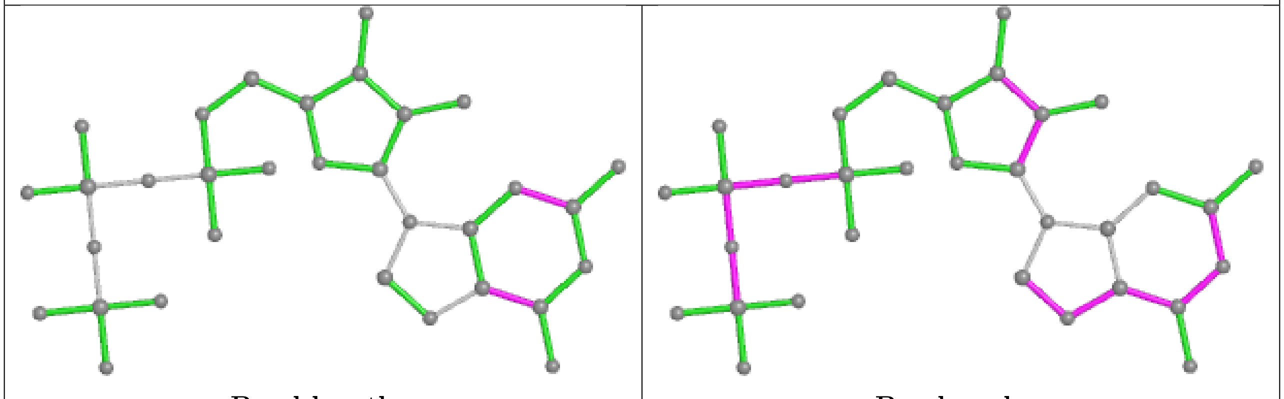
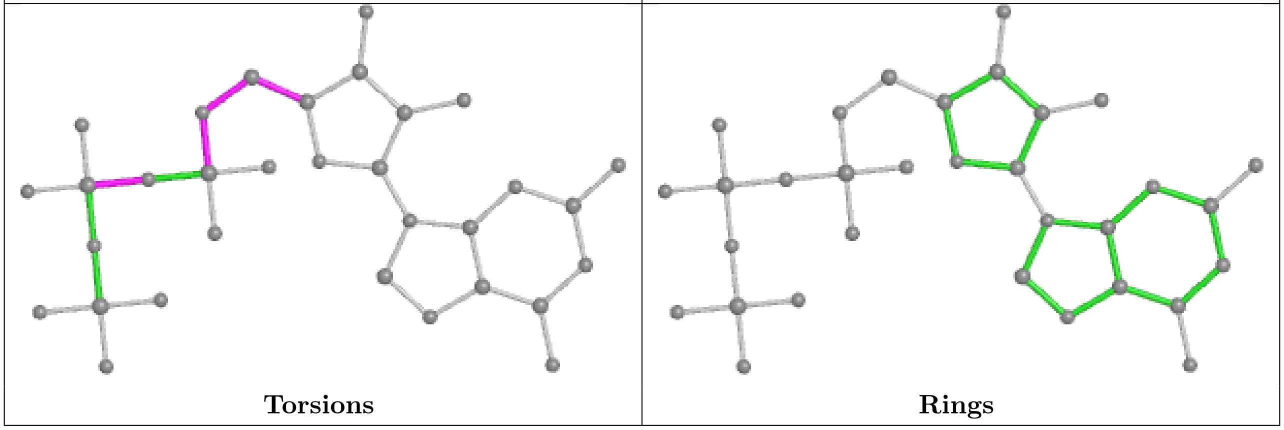


Bond lengths

Bond angles



Torsions

Rings

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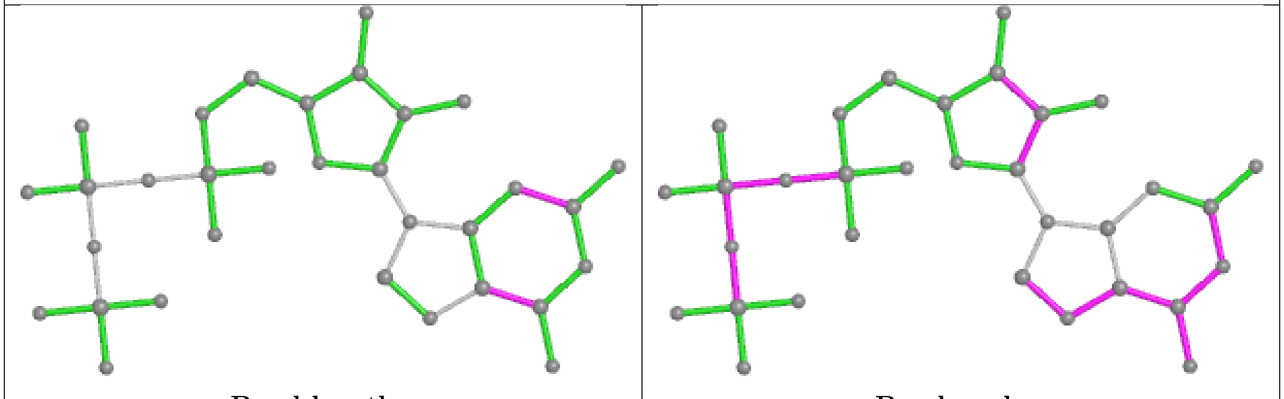
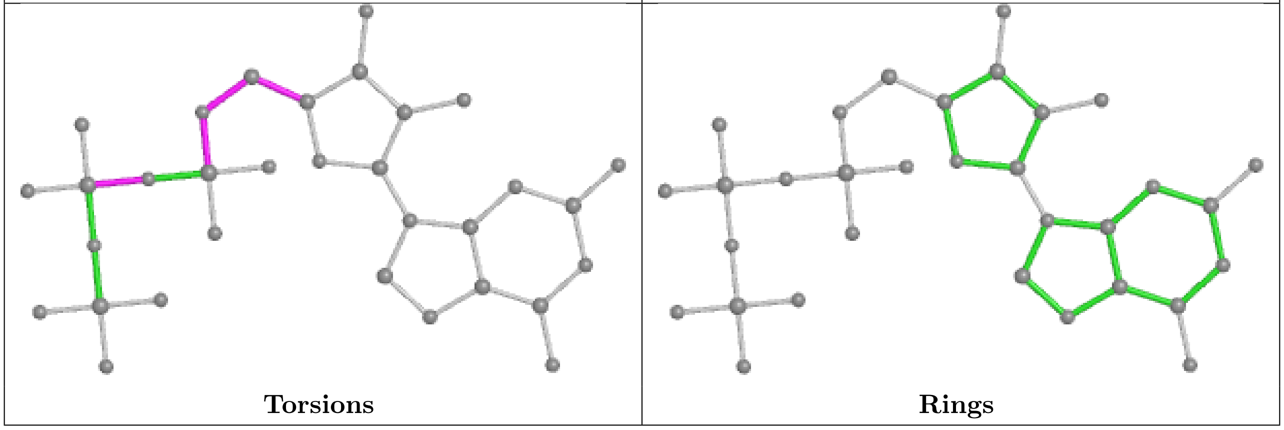


Bond lengths

Bond angles



Torsions

Rings

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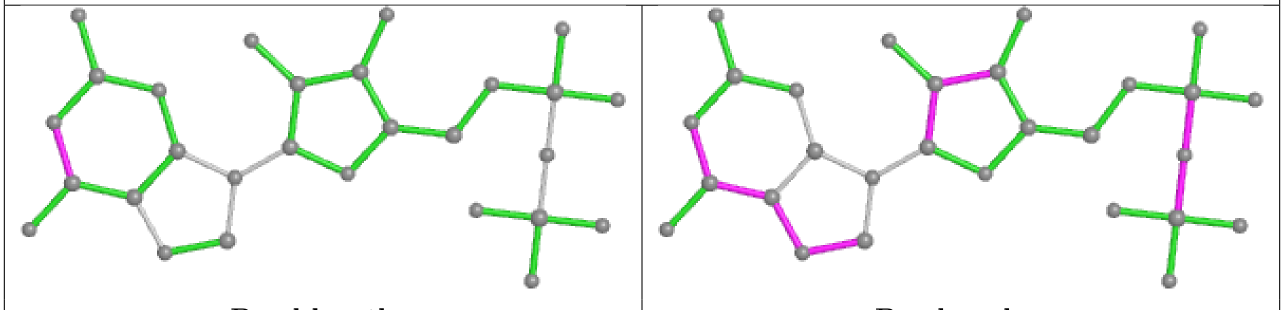
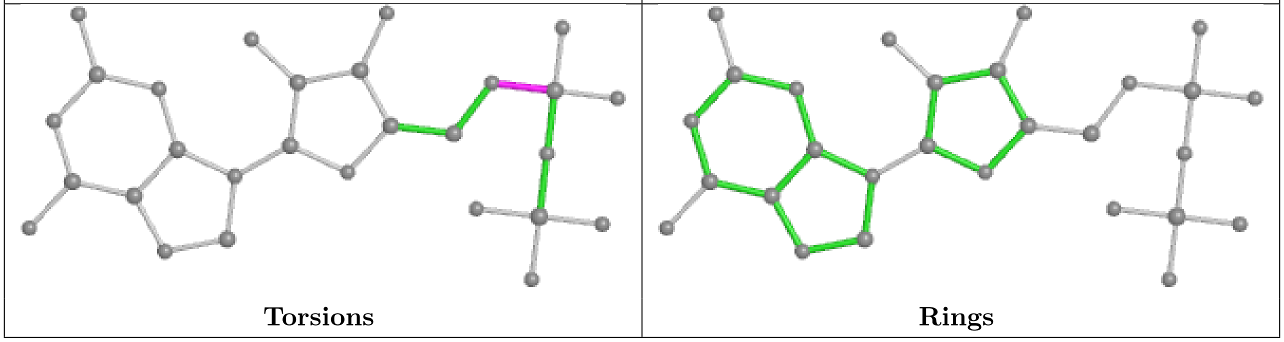


Bond lengths

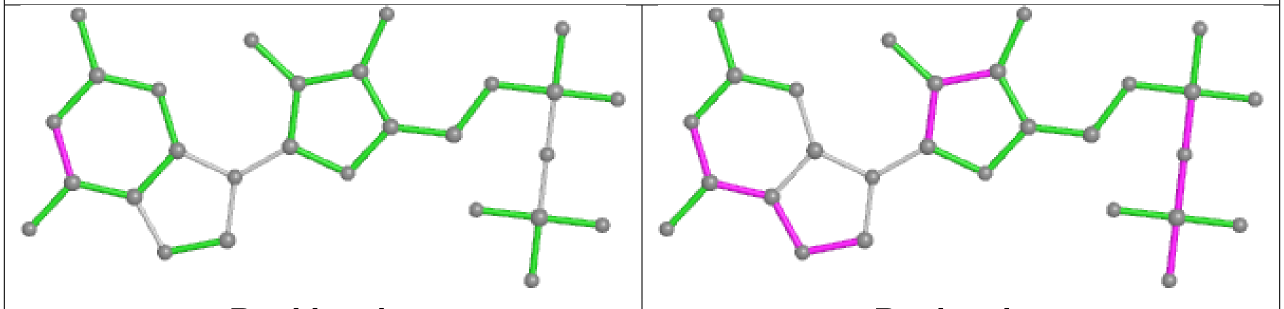
Bond angles



Torsions

Rings

Ligand GDP TB 502



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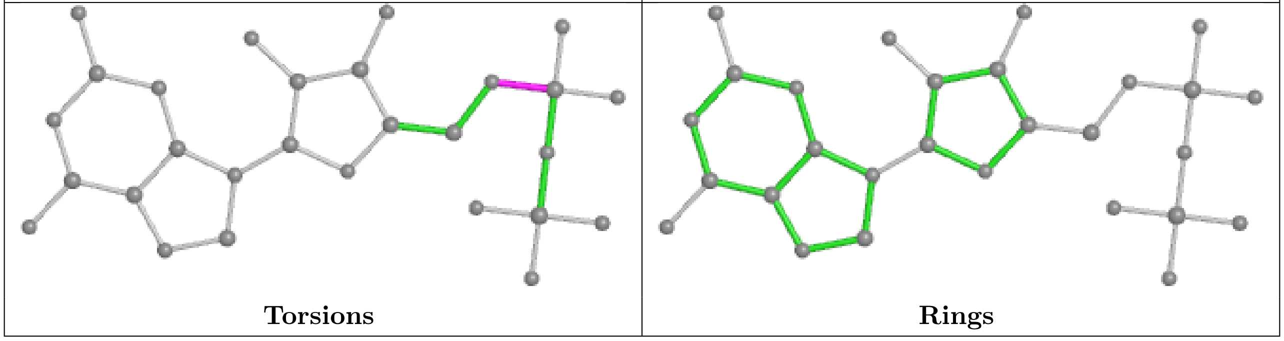
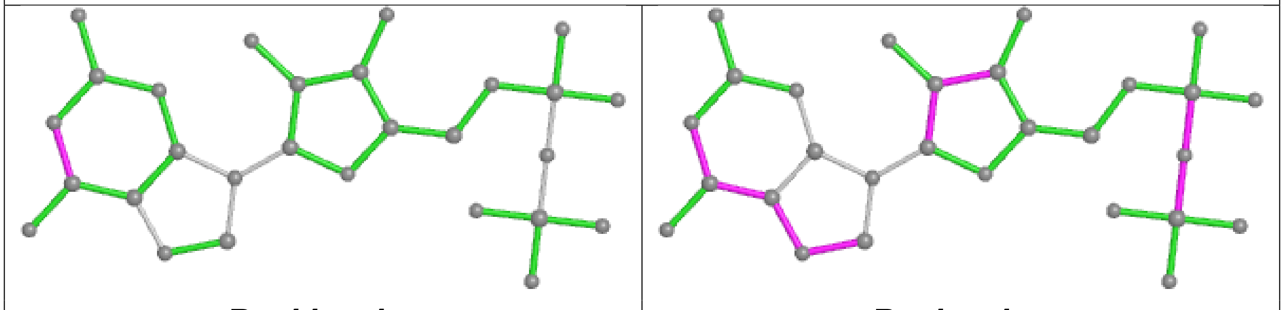
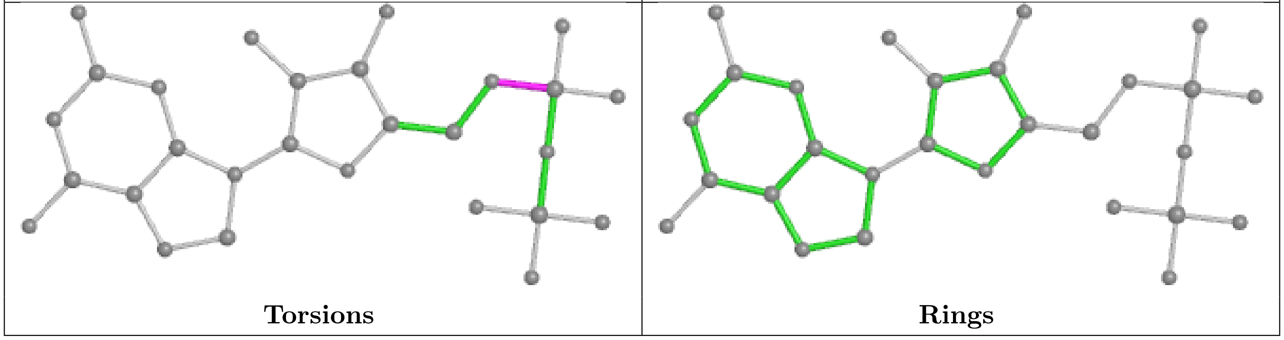


Torsions Rings

Ligand GDP QN 502

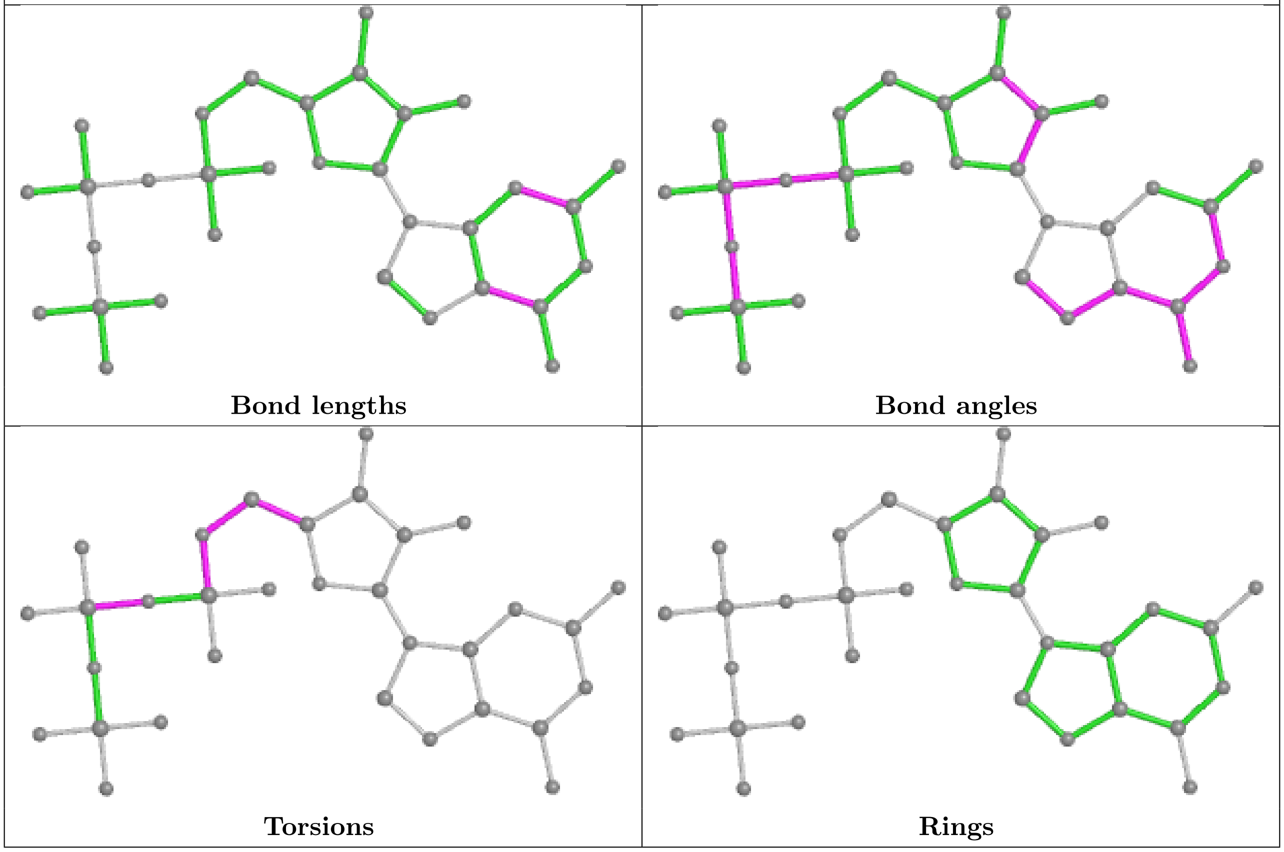


Bond lengths Bond angles



Torsions Rings

Ligand GTP GK 501



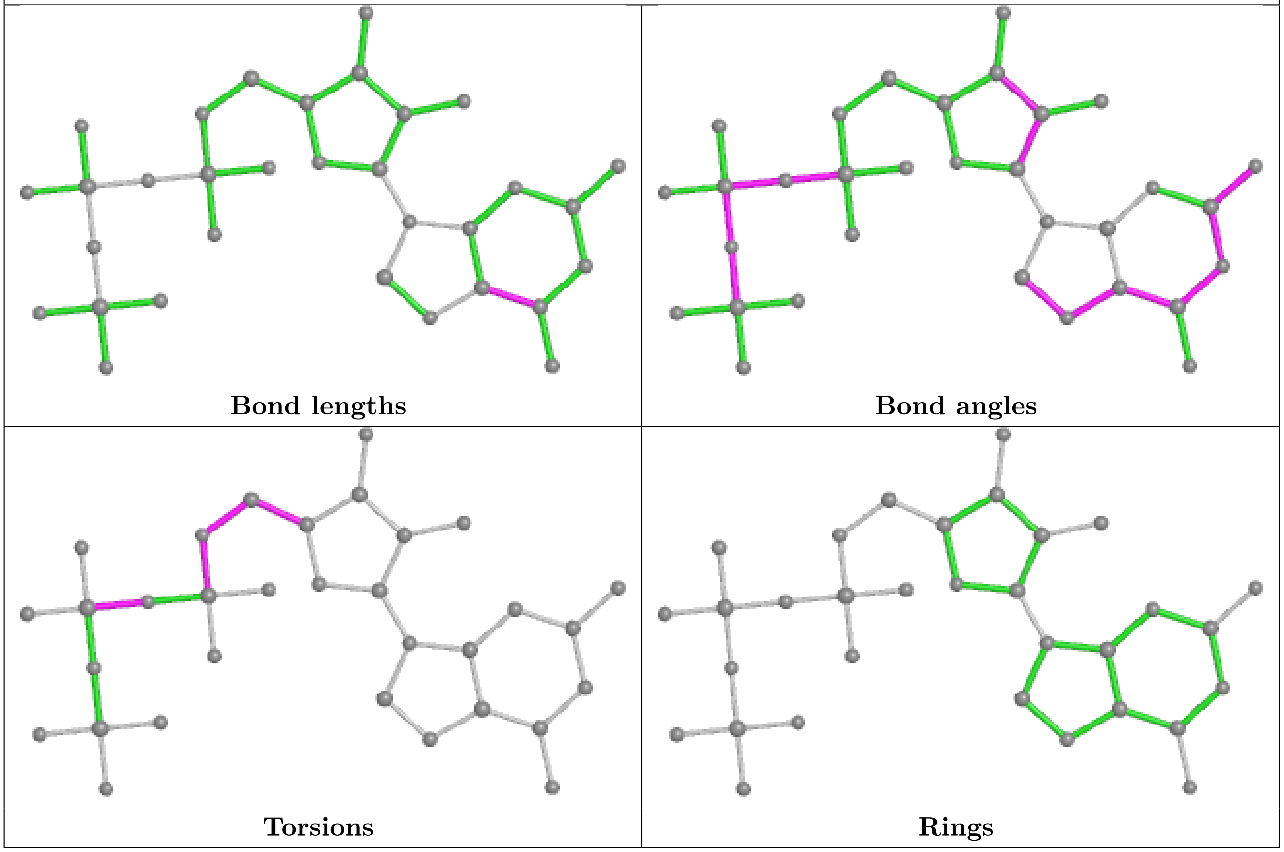
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP PG 501



Bond lengths

Bond angles

Torsions

Rings

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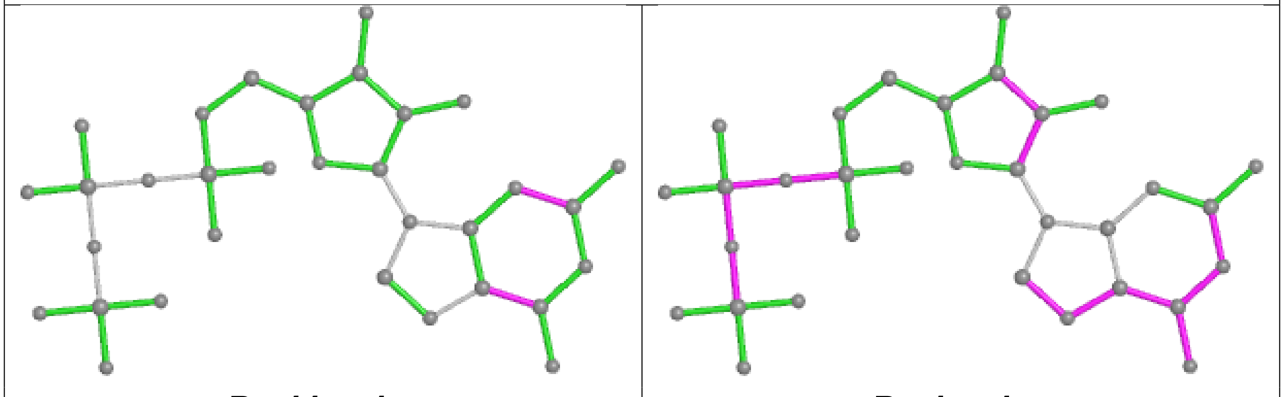
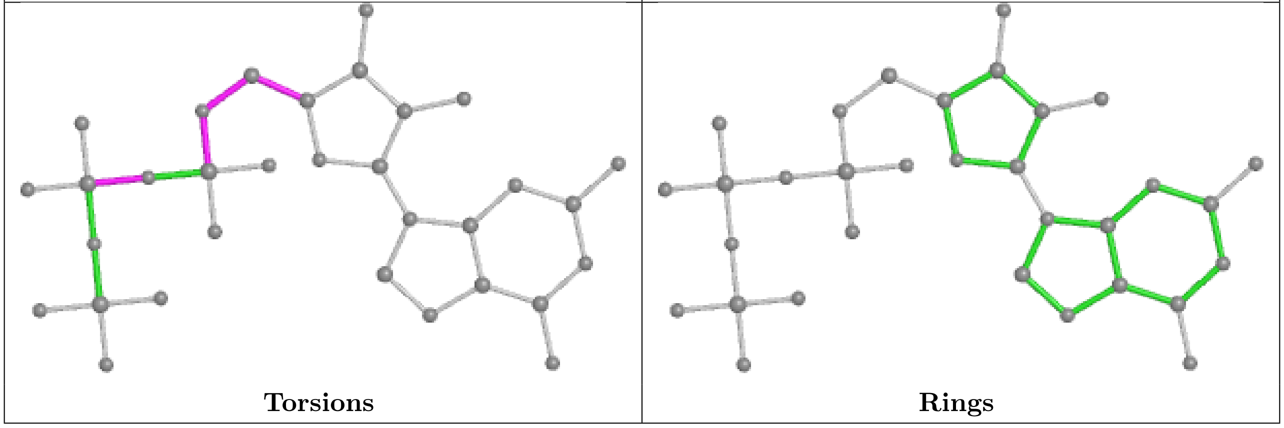


Bond lengths

Bond angles



Torsions

Rings

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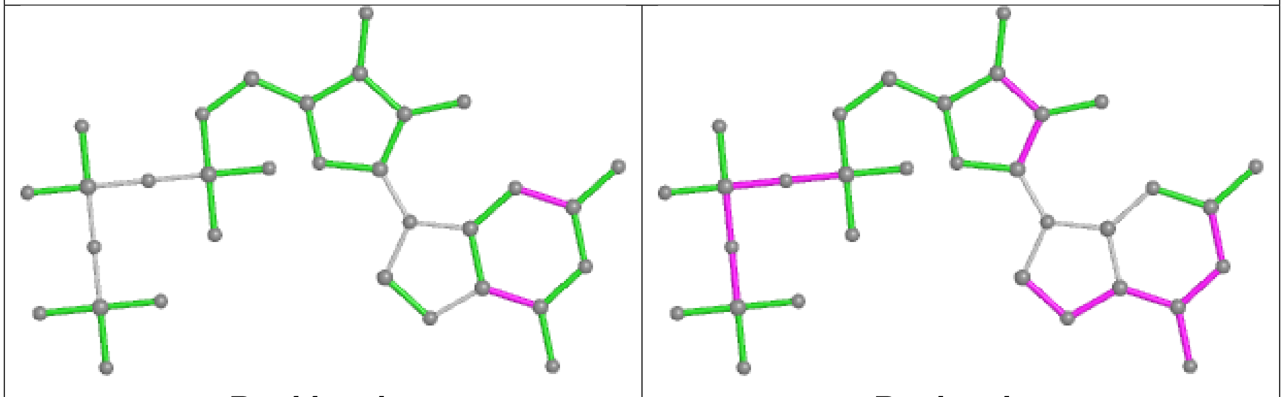
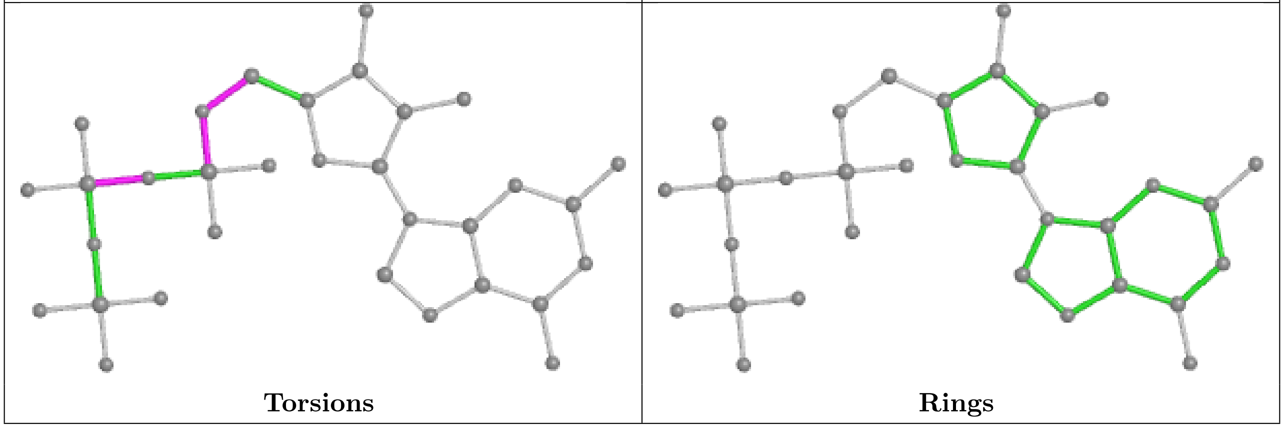


Bond lengths

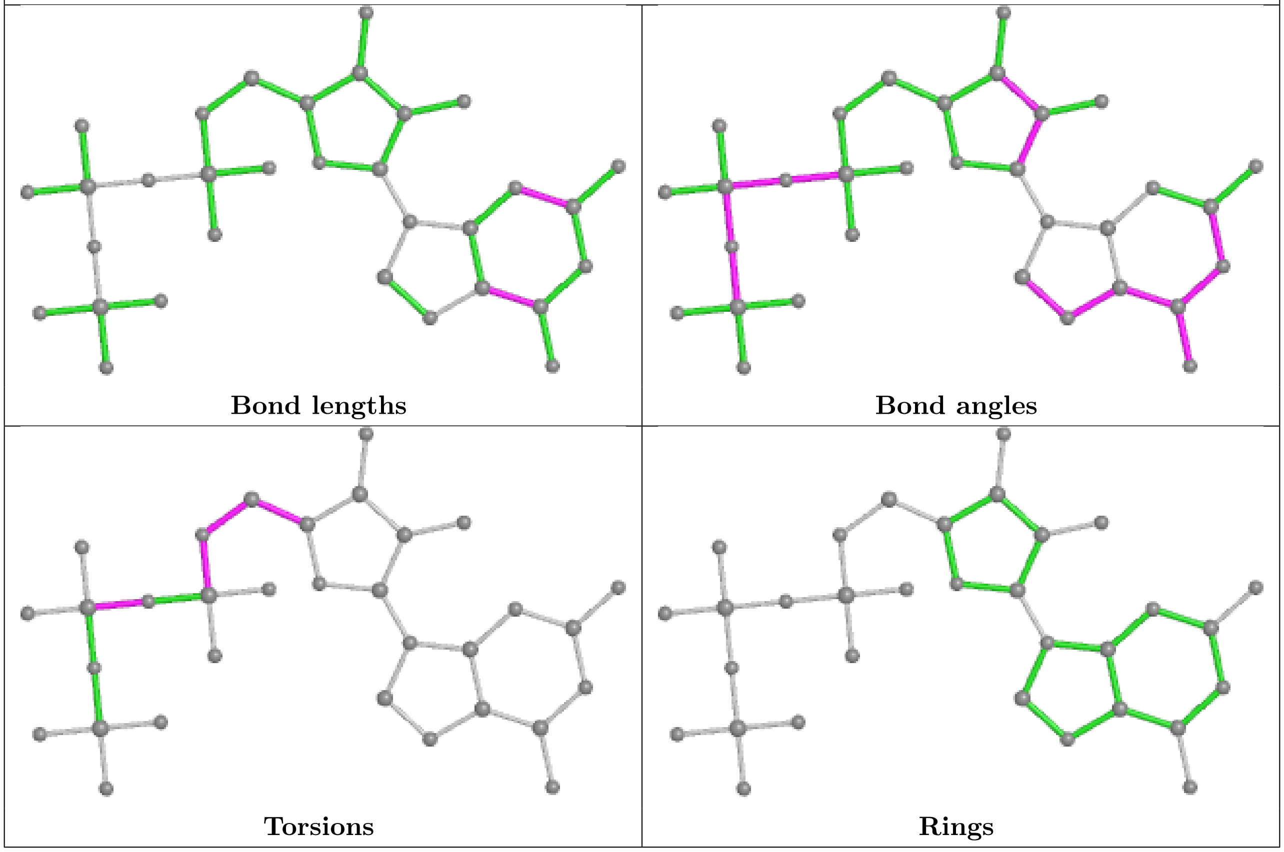
Bond angles



Torsions

Rings

Ligand GTP KI 501



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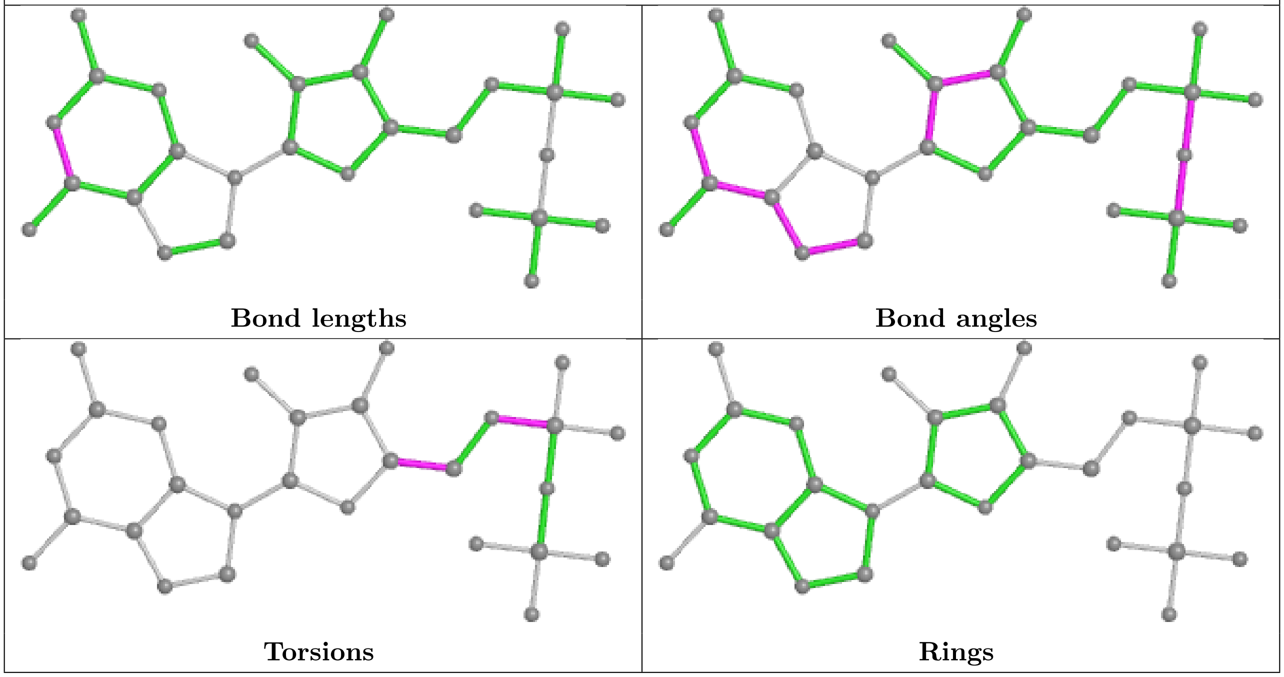

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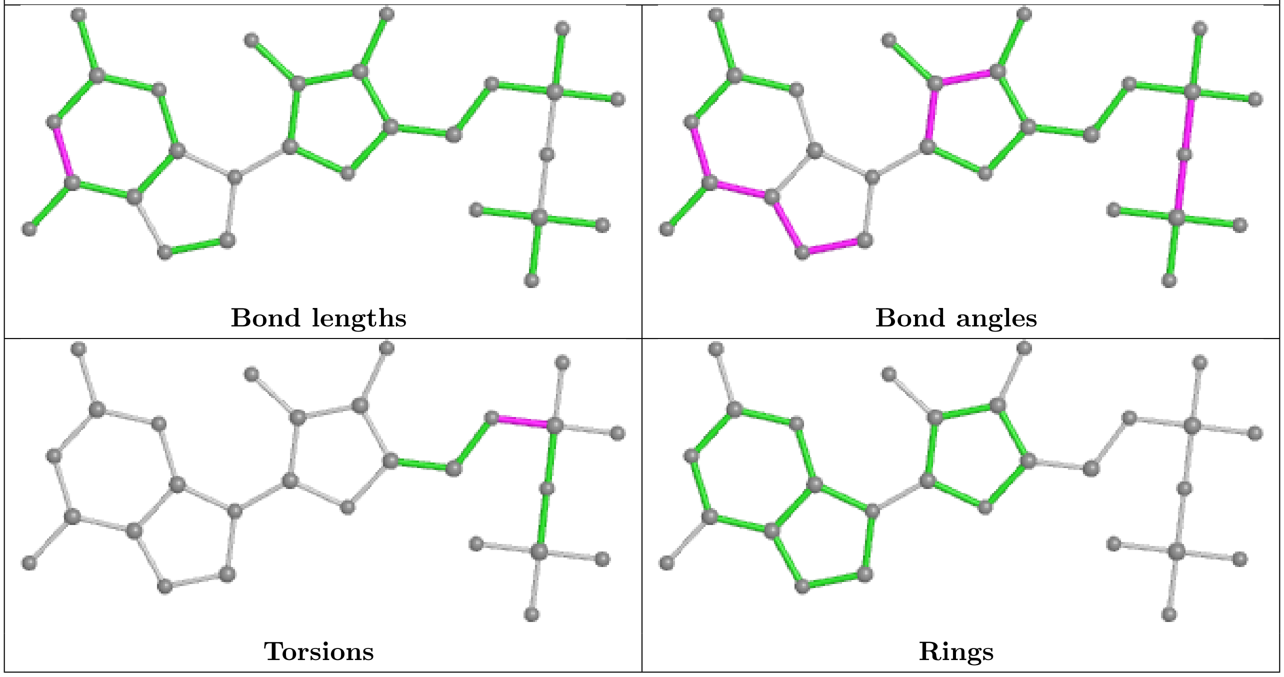


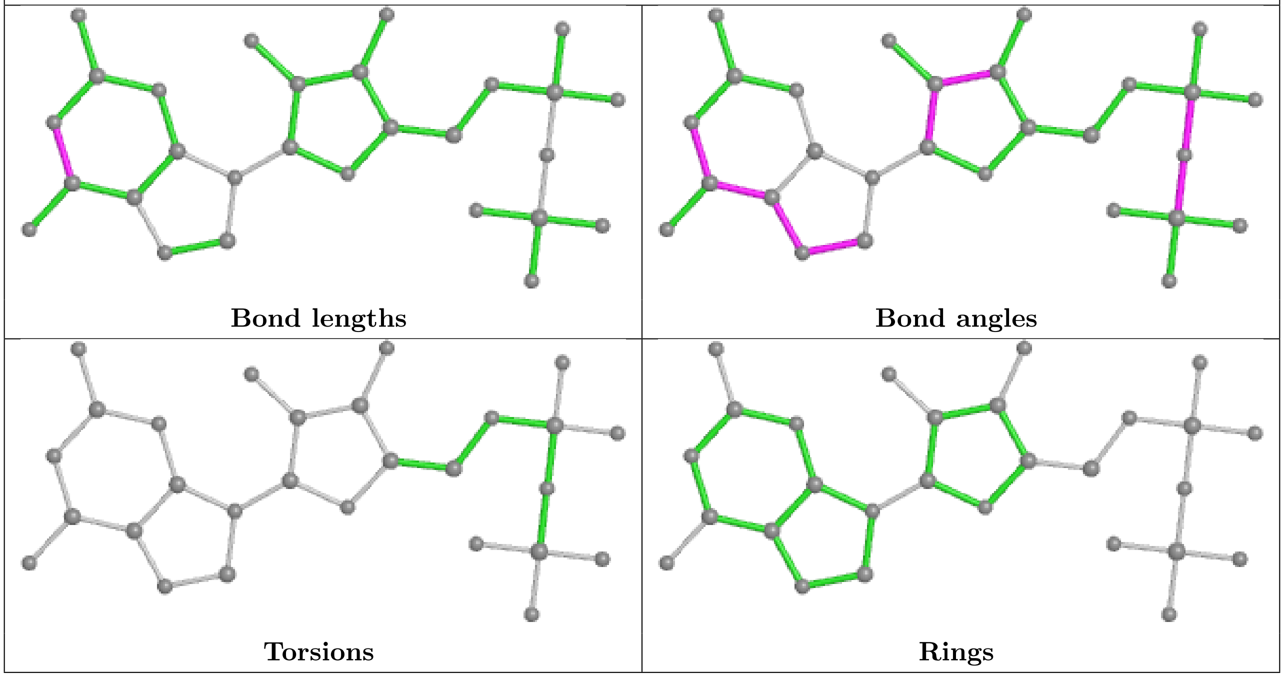
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP WN 502



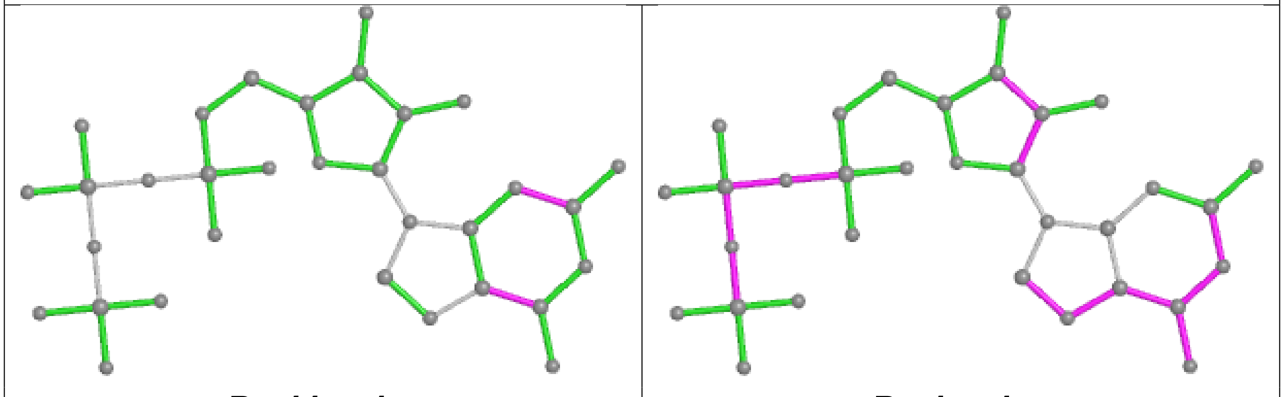
Bond lengths

Bond angles

Torsions

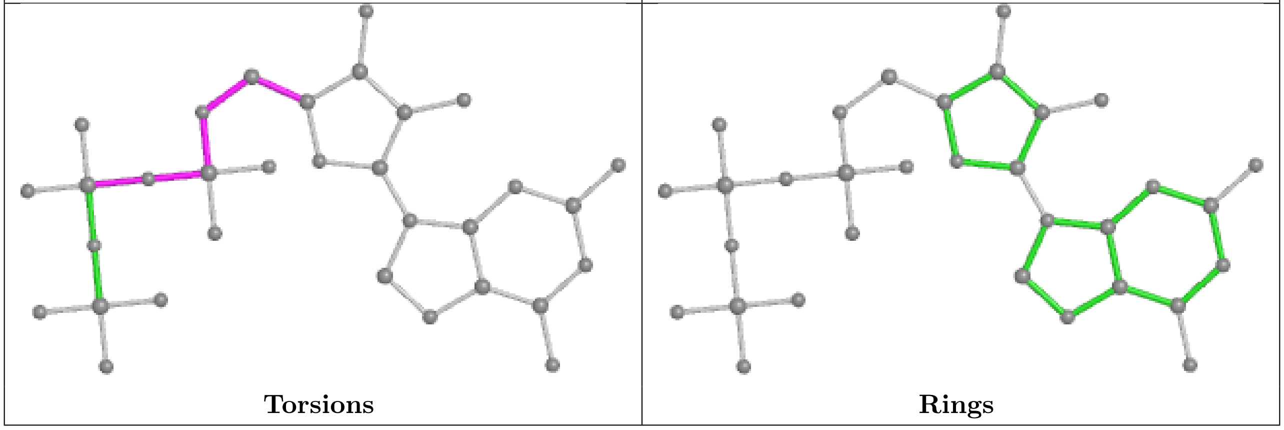
Rings

Ligand GTP NO 501



Bond lengths

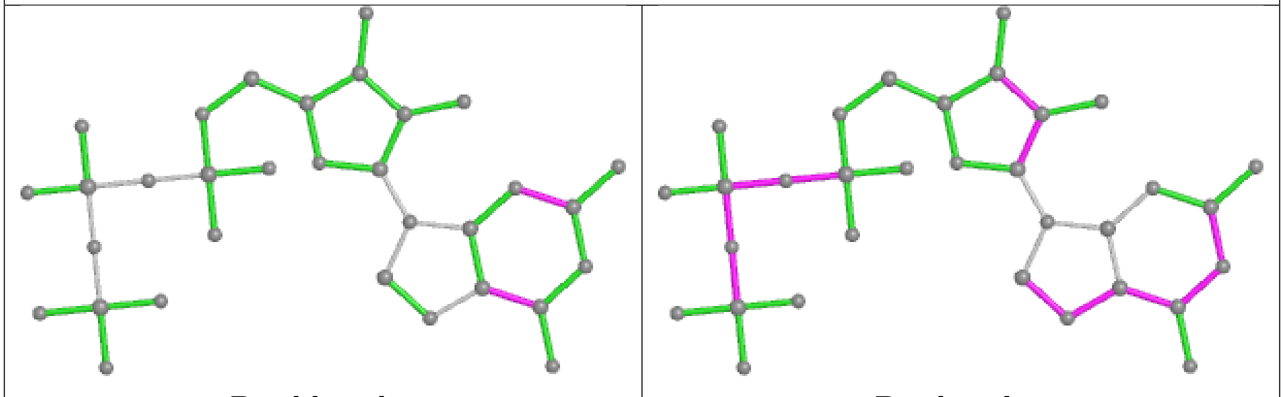
Bond angles



Torsions

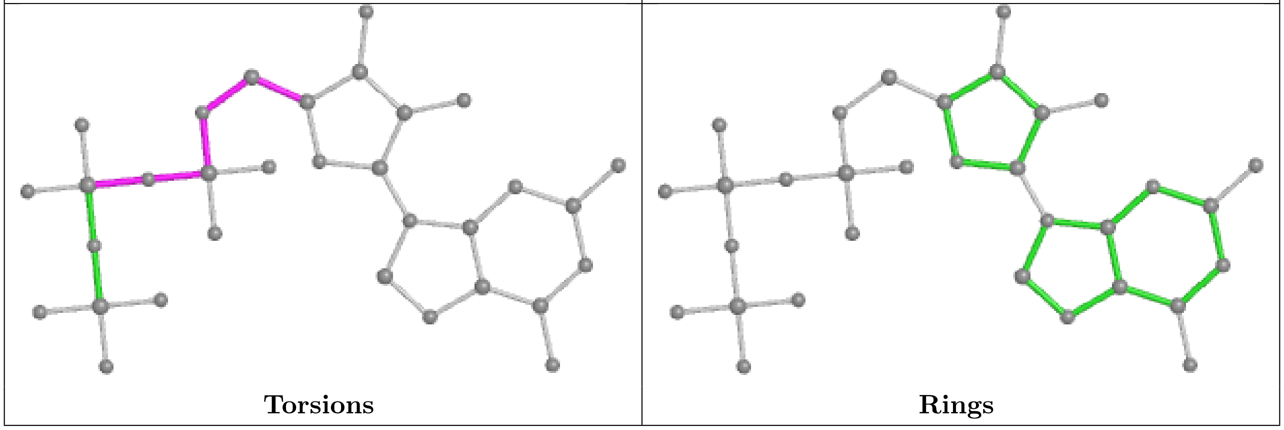
Rings

Ligand GTP IG 501



Bond lengths

Bond angles



Torsions

Rings

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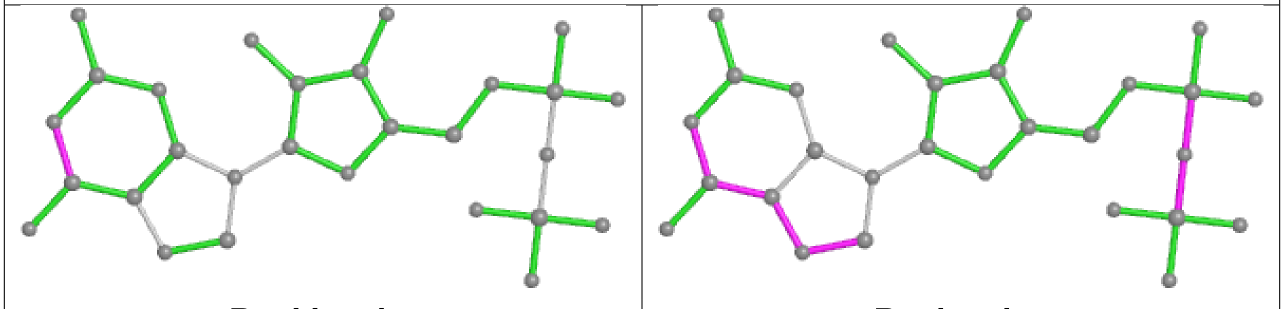
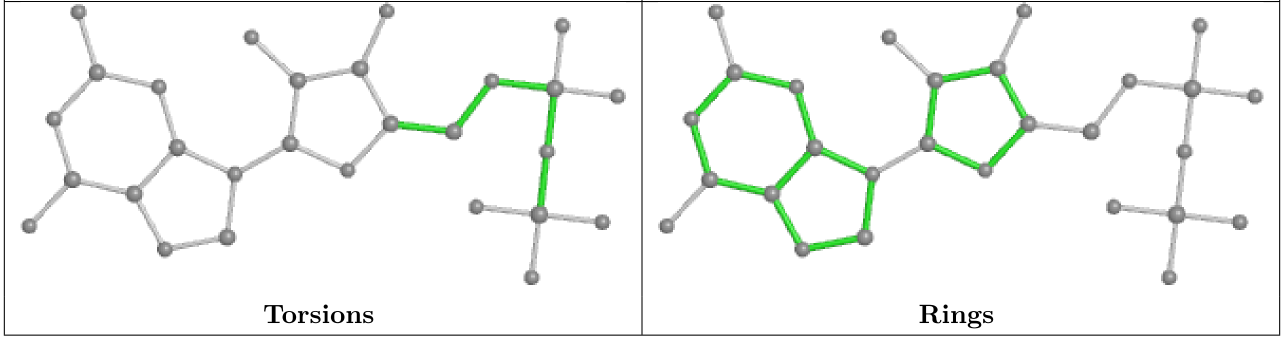


Bond lengths

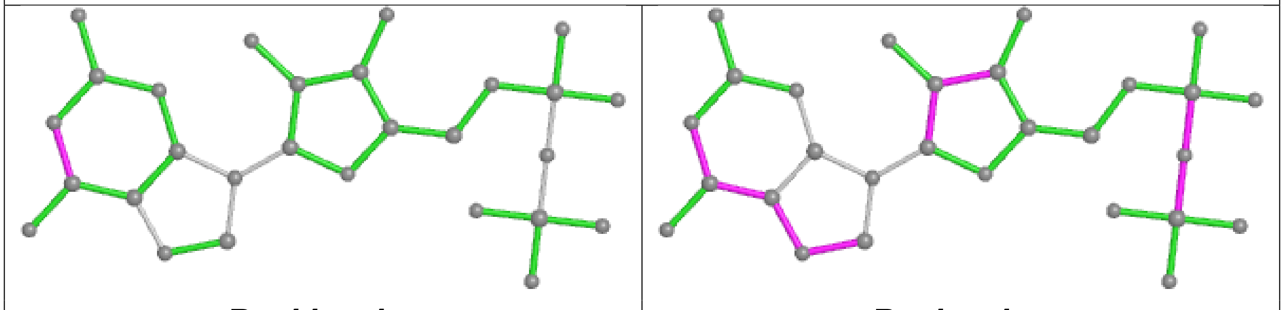
Bond angles



Torsions

Rings

Ligand GDP PN 502



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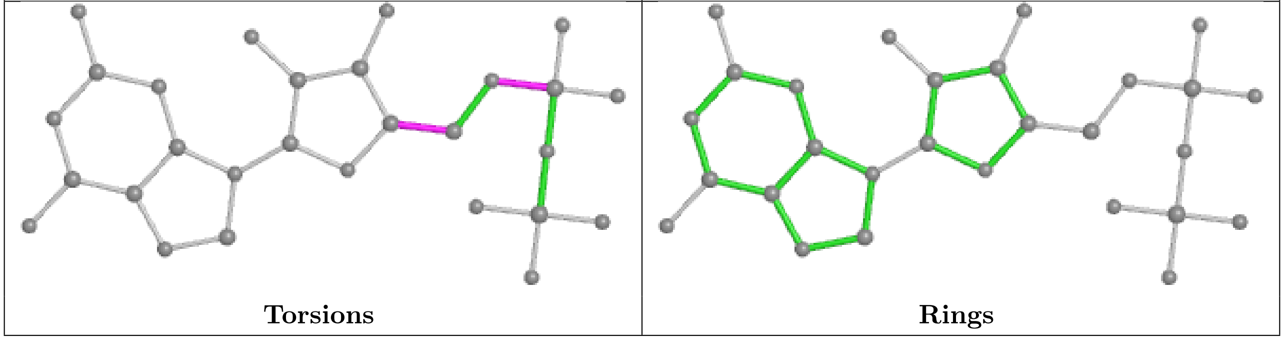
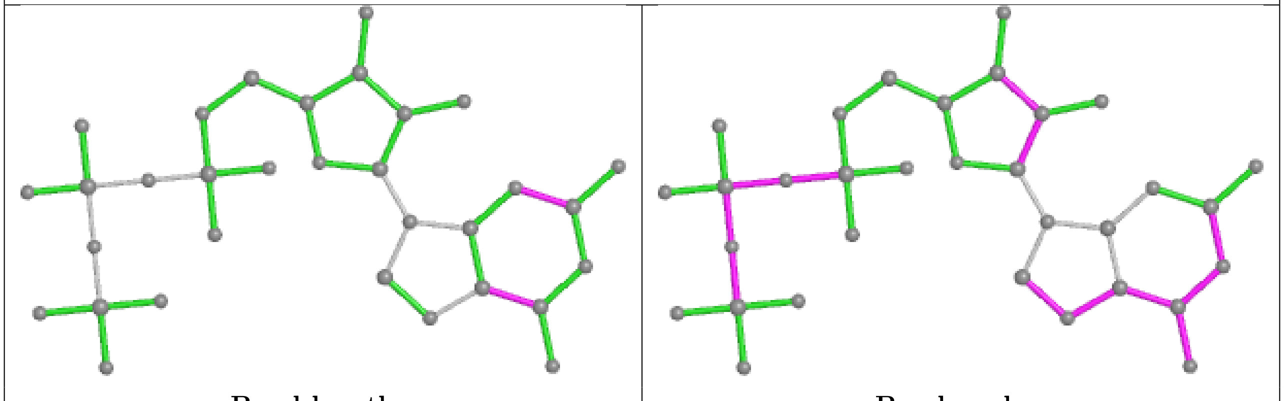
Bond angles



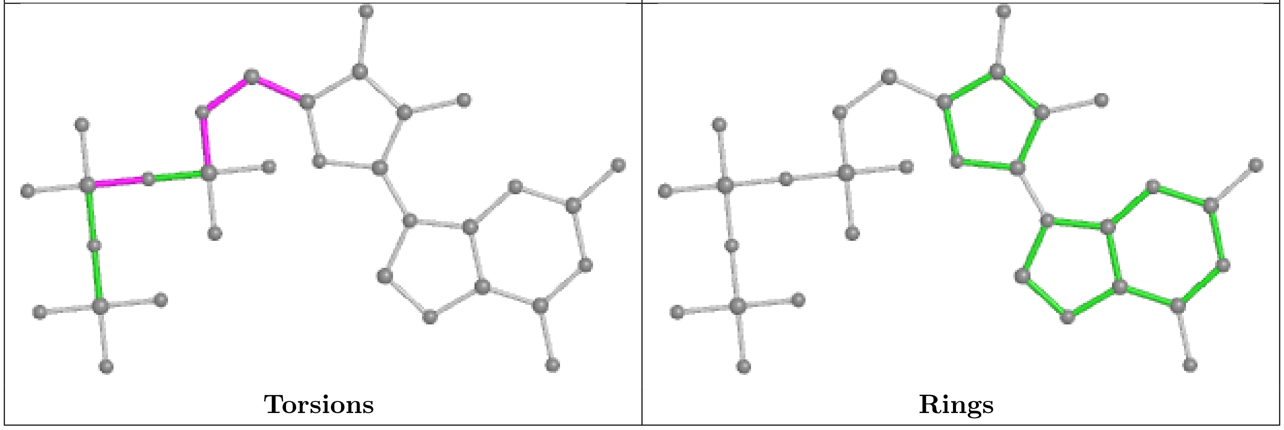
Torsions

Rings

Ligand GTP TK 501

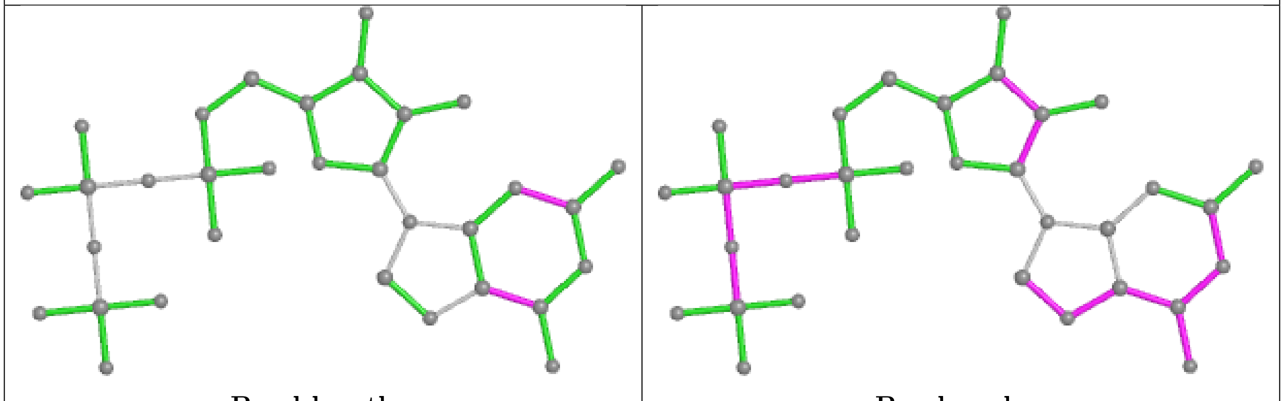


Bond lengths Bond angles

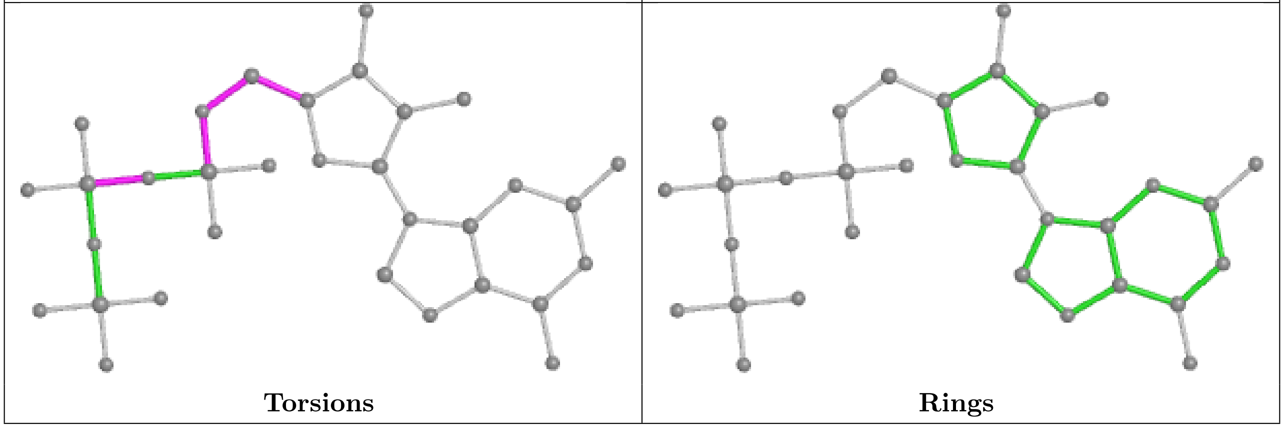


Torsions Rings

Ligand GTP QE 501

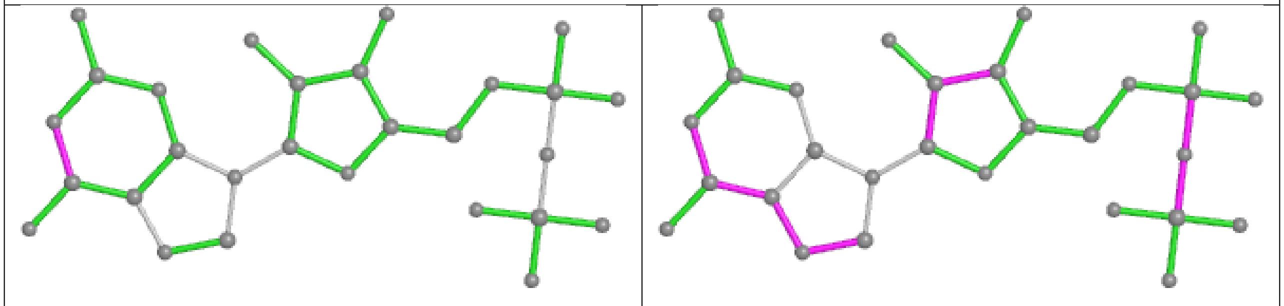


Bond lengths Bond angles

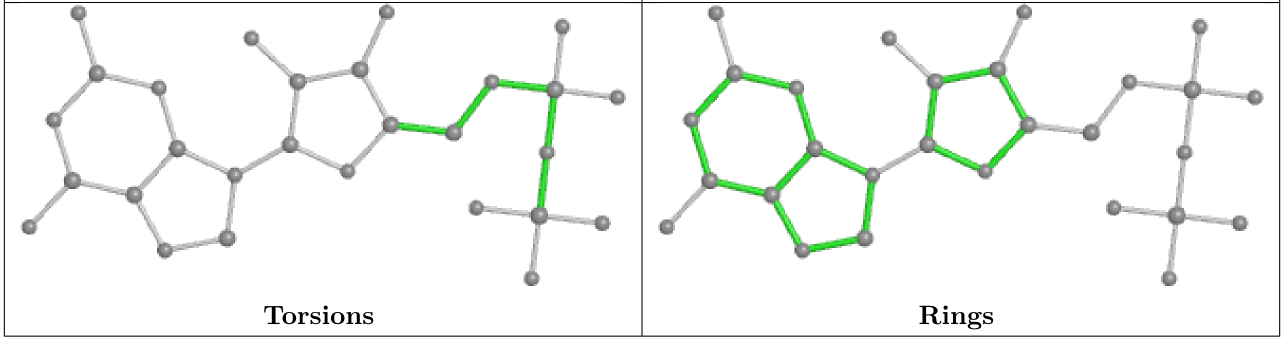


Torsions Rings

Ligand GDP BN 502

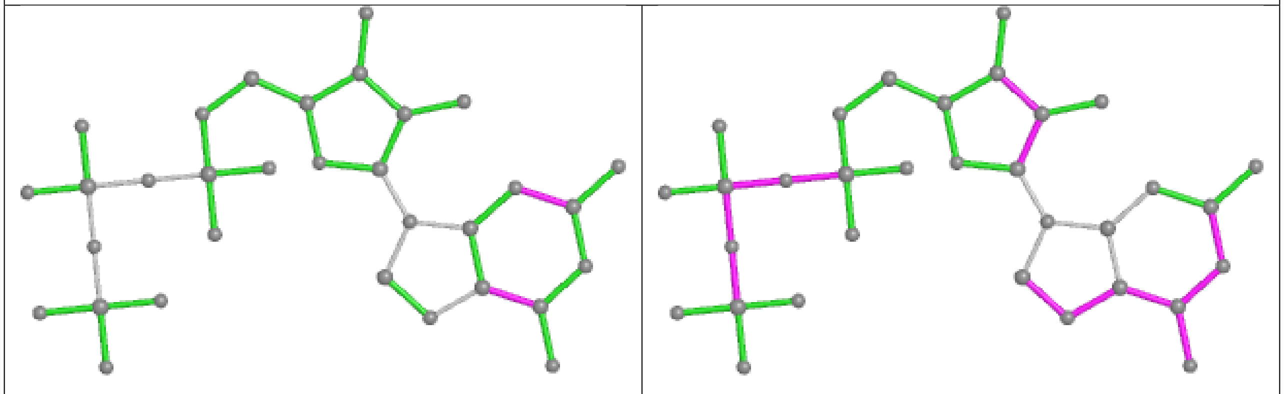


Bond lengths **Bond angles**



Torsions **Rings**

Ligand GTP HG 501



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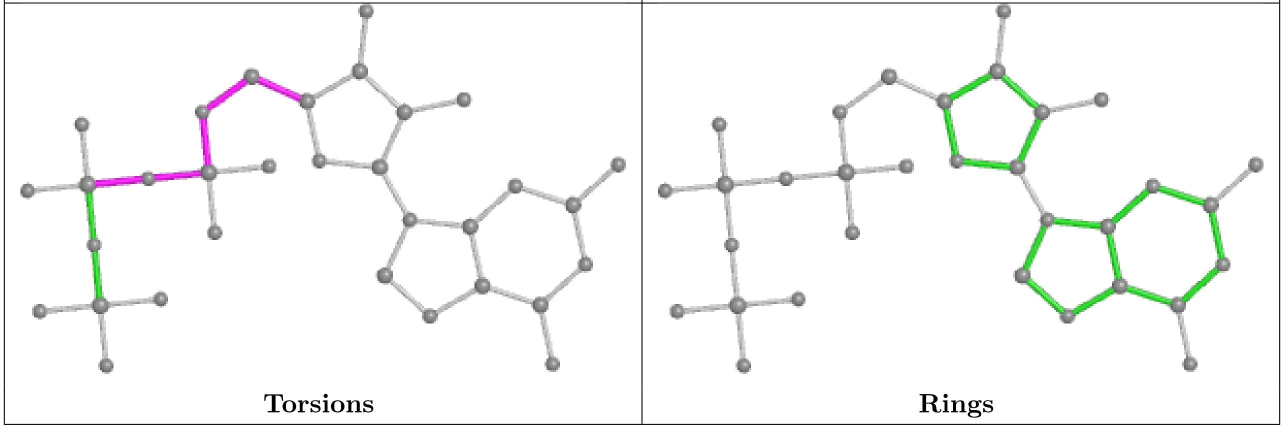

Torsions **Rings**

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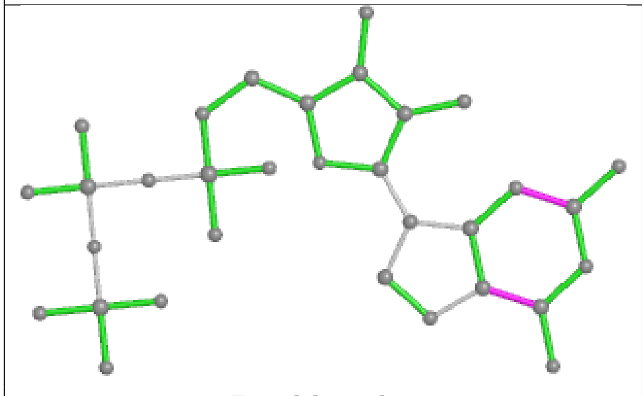

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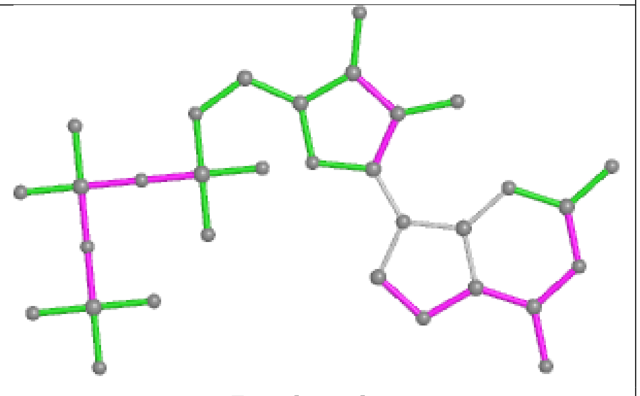
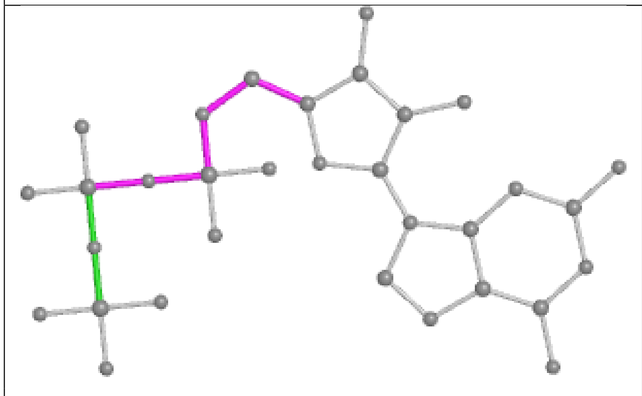
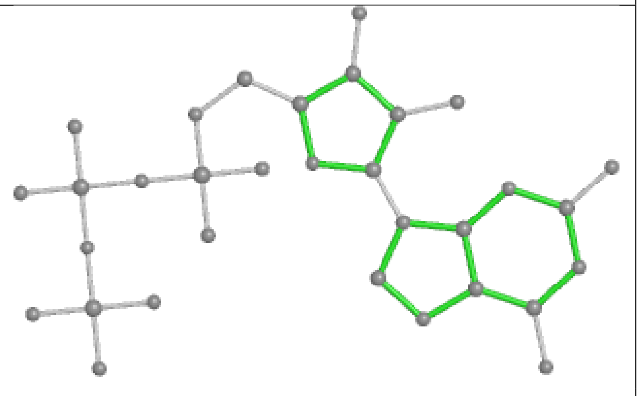


Bond angles

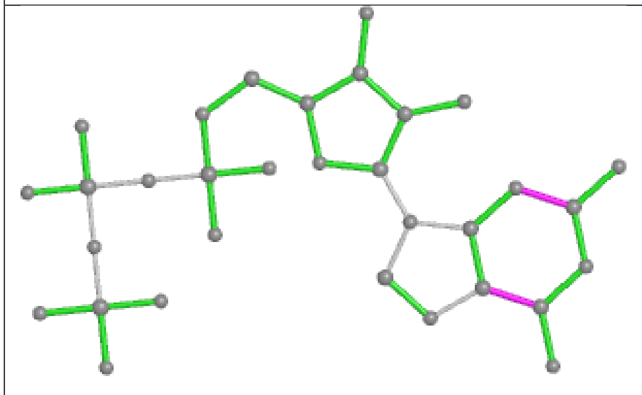


Torsions



Rings

Ligand GTP MK 501



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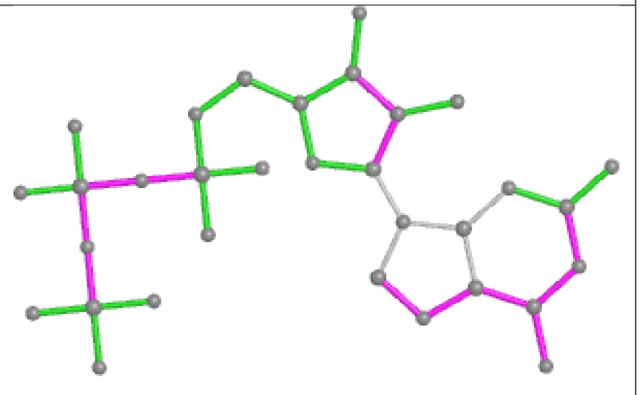

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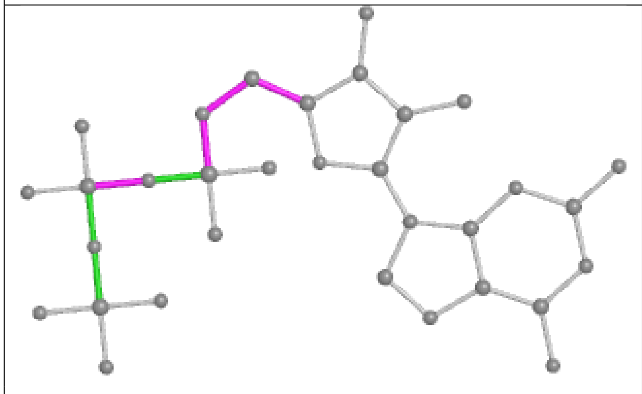

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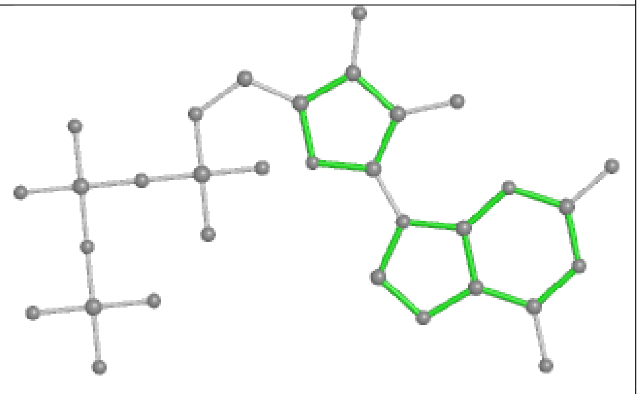

Rings

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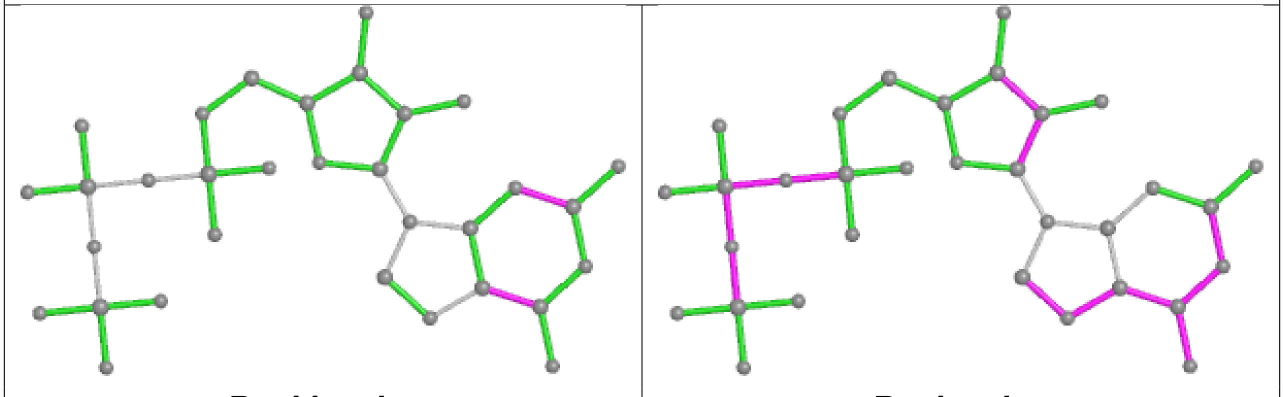
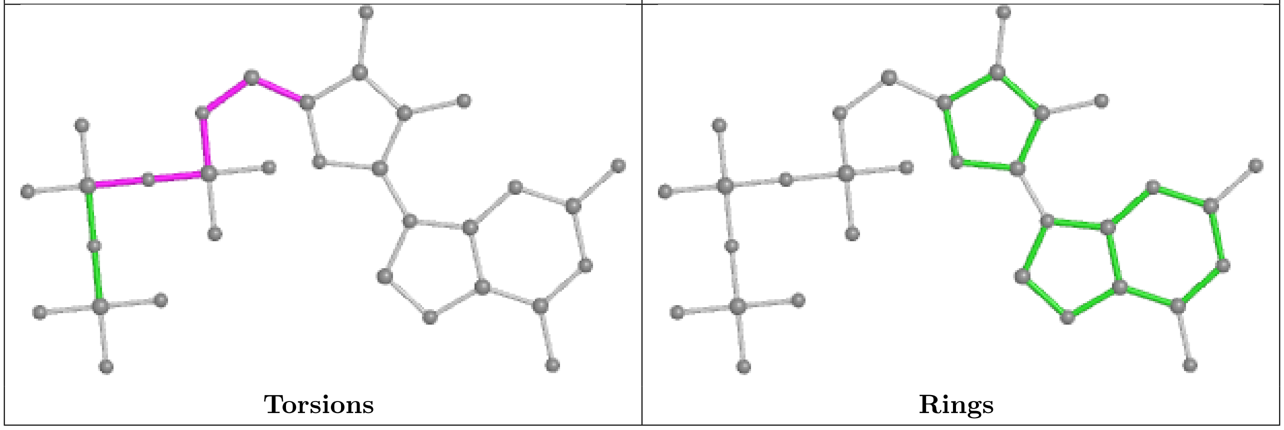


Bond lengths

Bond angles



Torsions

Rings

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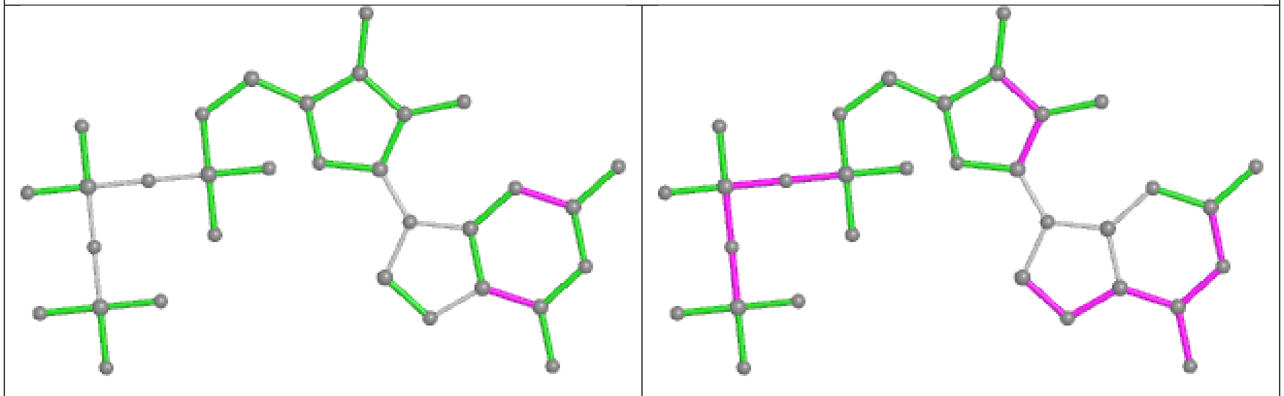
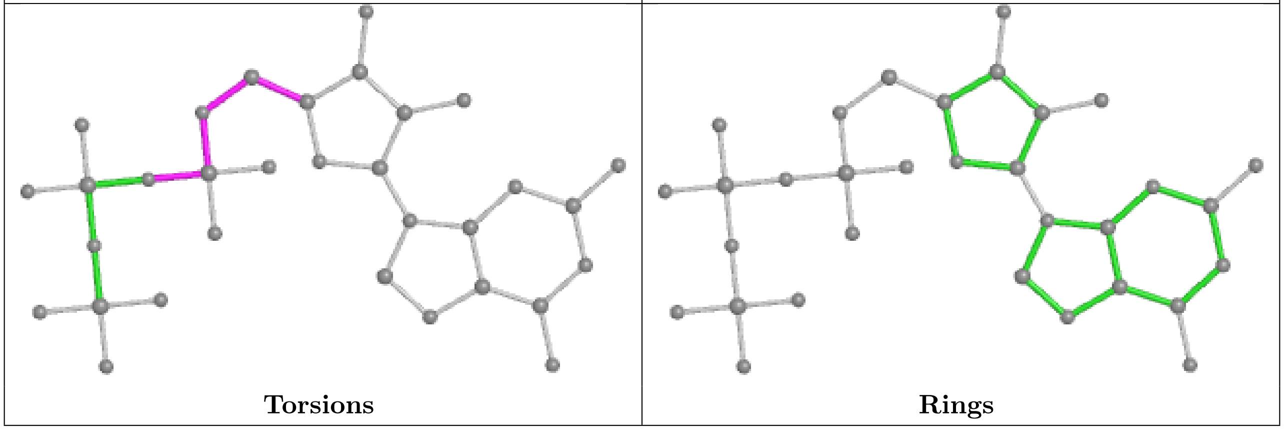


Bond lengths

Bond angles



Torsions

Rings

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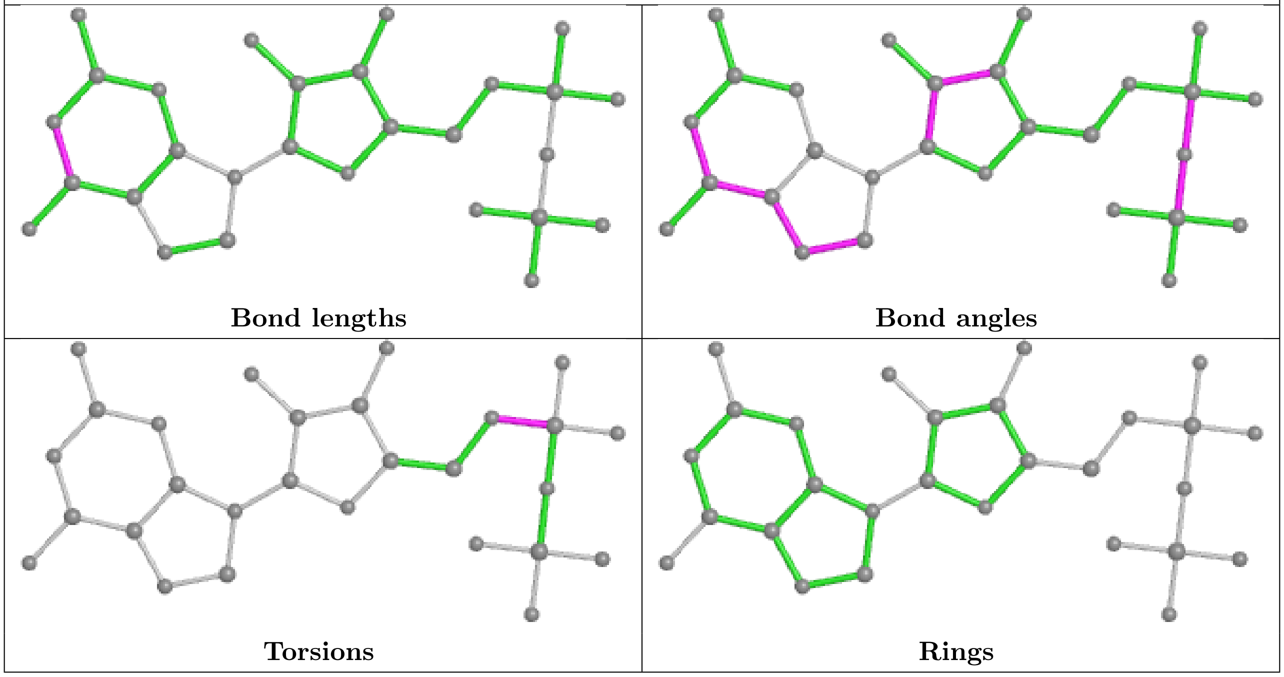

Bond lengths

Bond angles

Torsions

Rings

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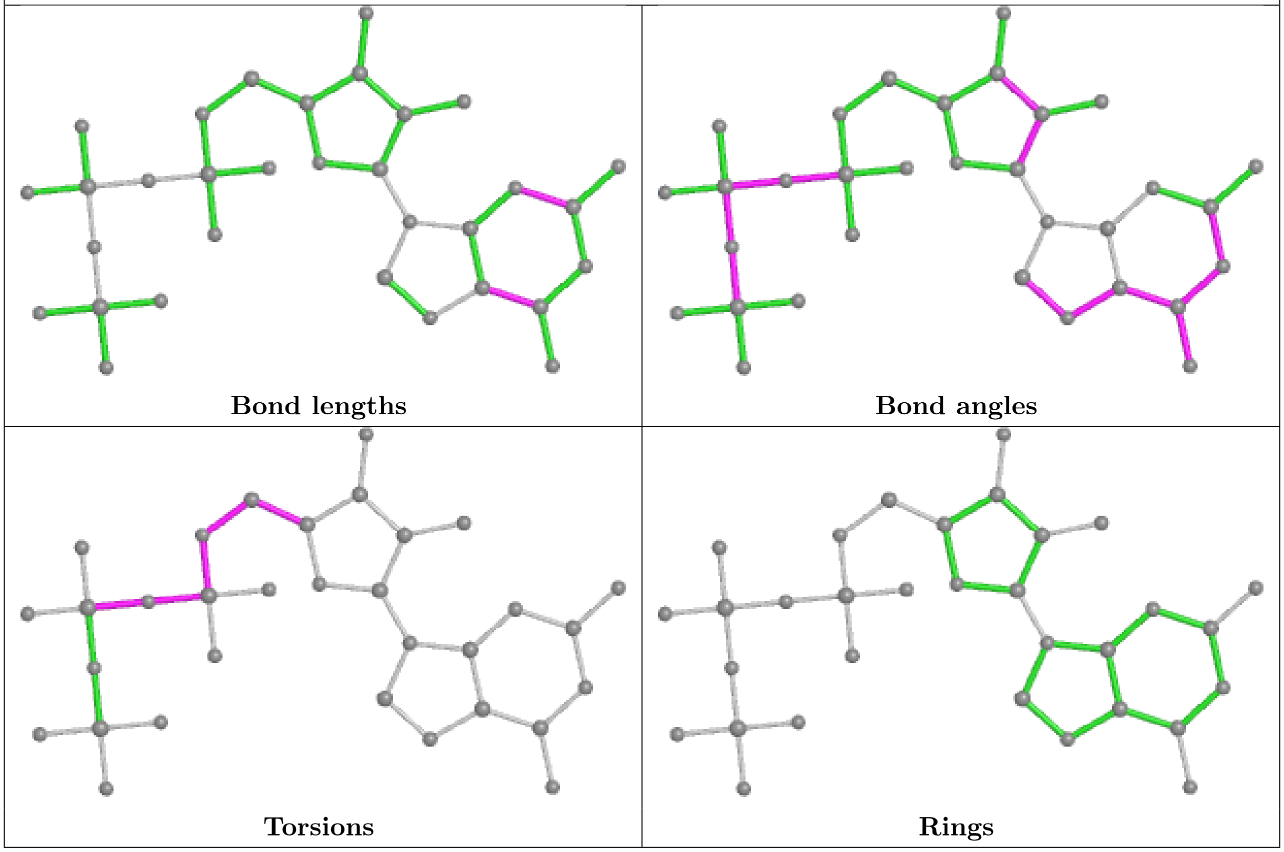

Bond lengths

Bond angles

Torsions

Rings

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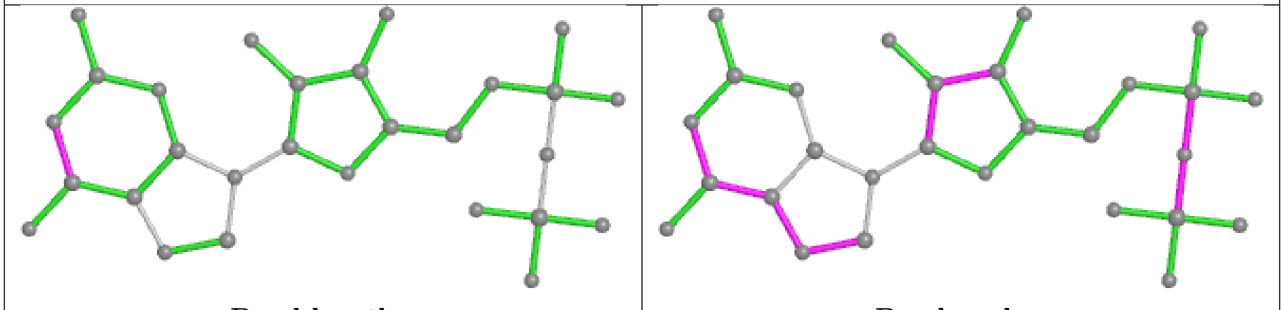
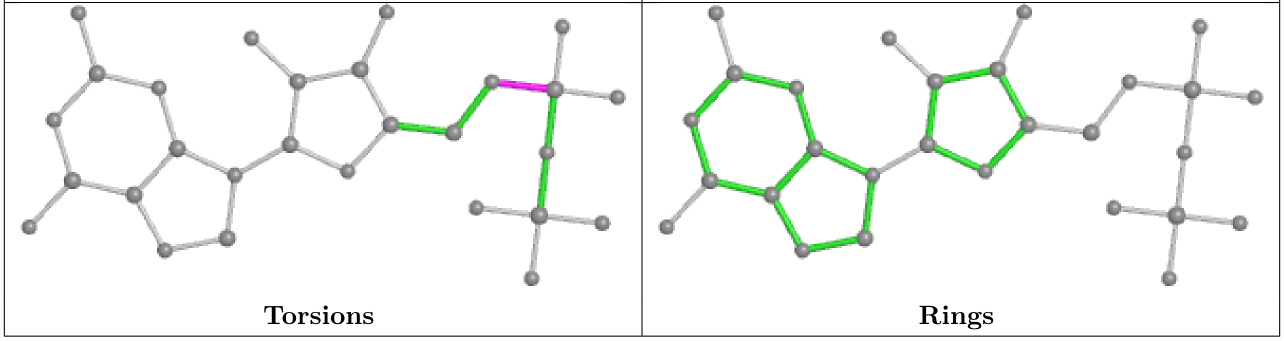


Bond lengths **Bond angles**



Torsions **Rings**

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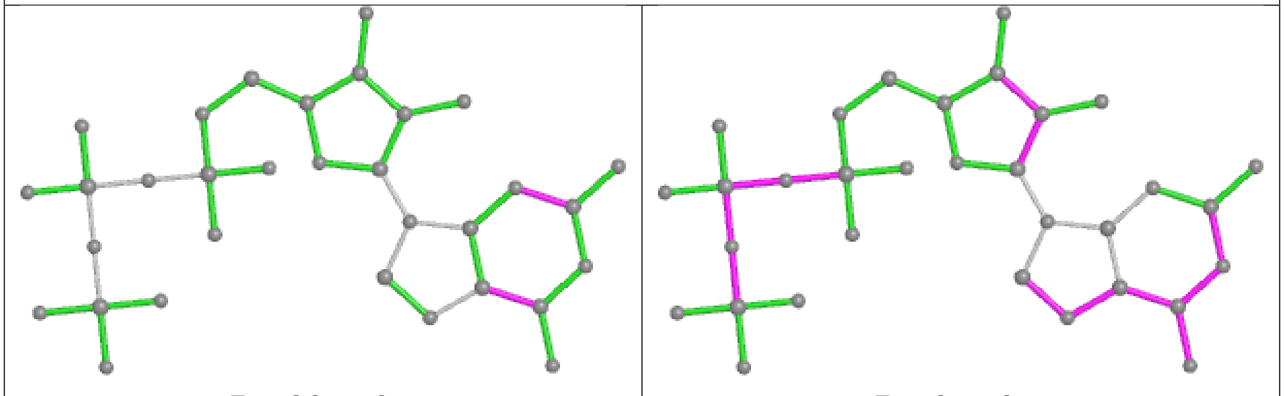
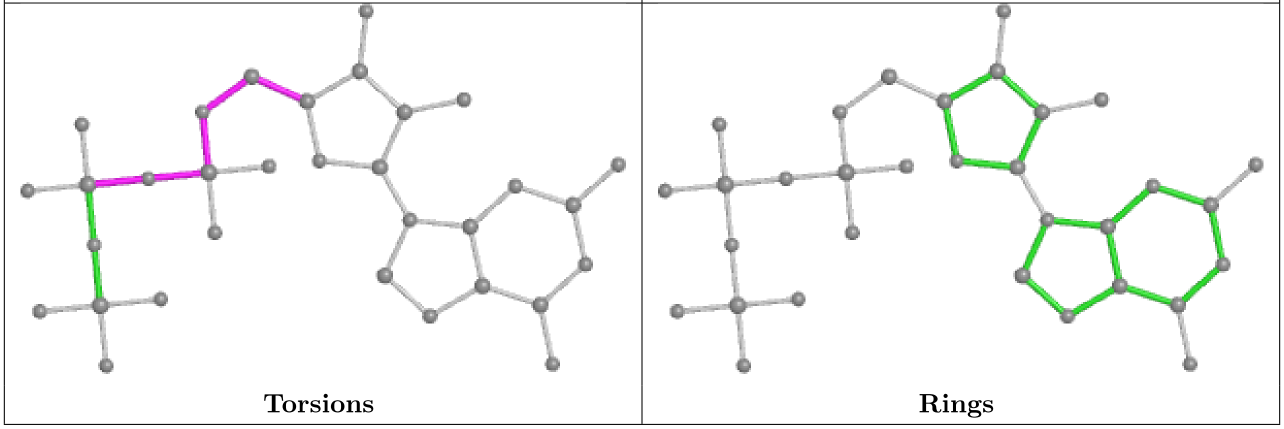


Bond lengths **Bond angles**



Torsions **Rings**

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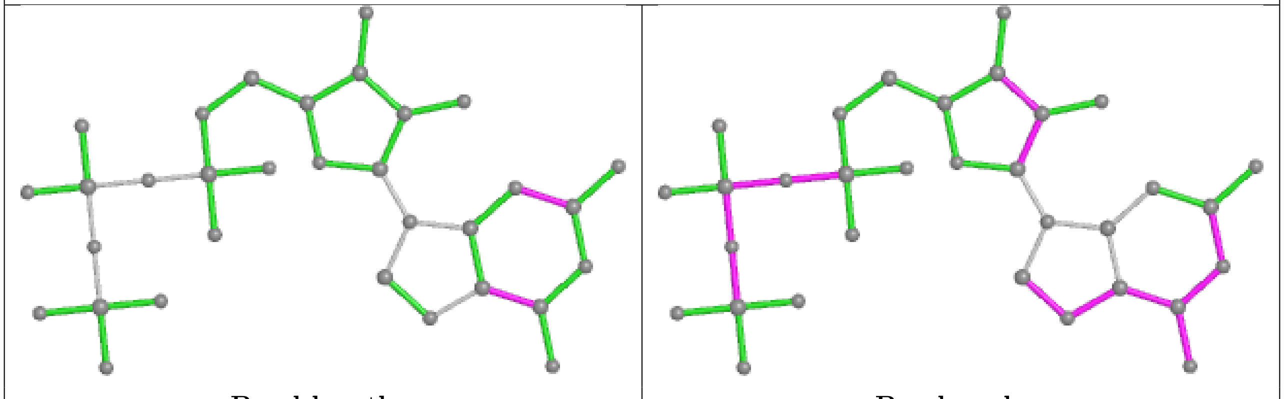
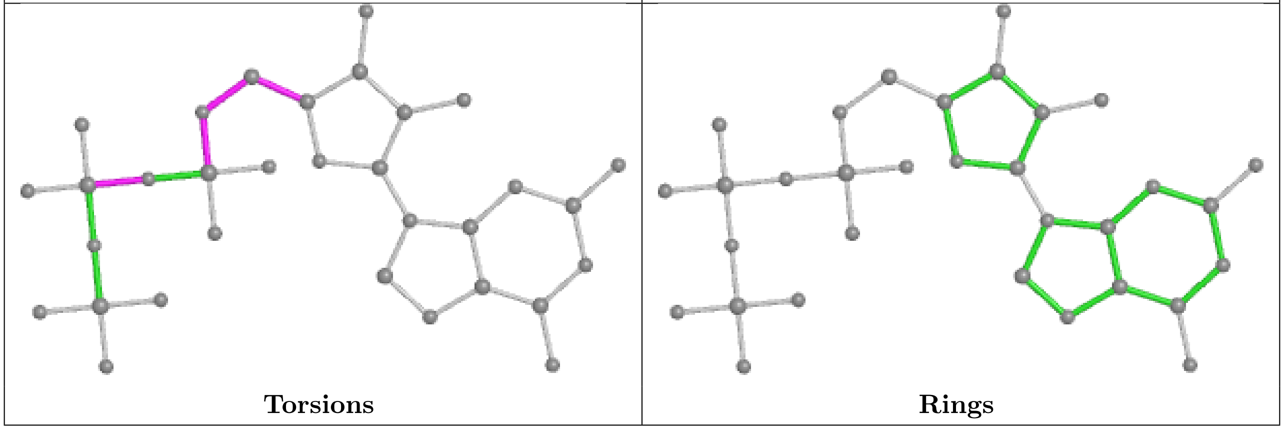


Bond lengths

Bond angles



Torsions

Rings

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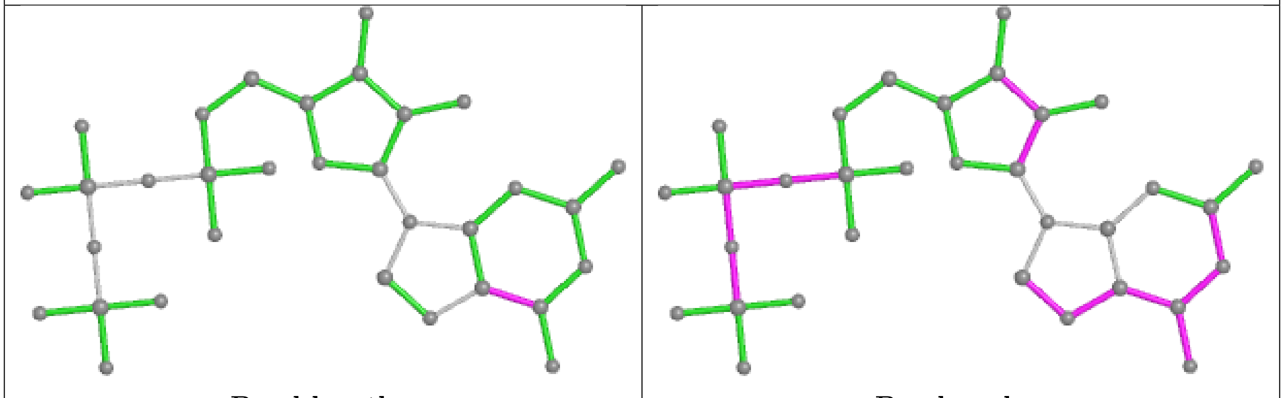
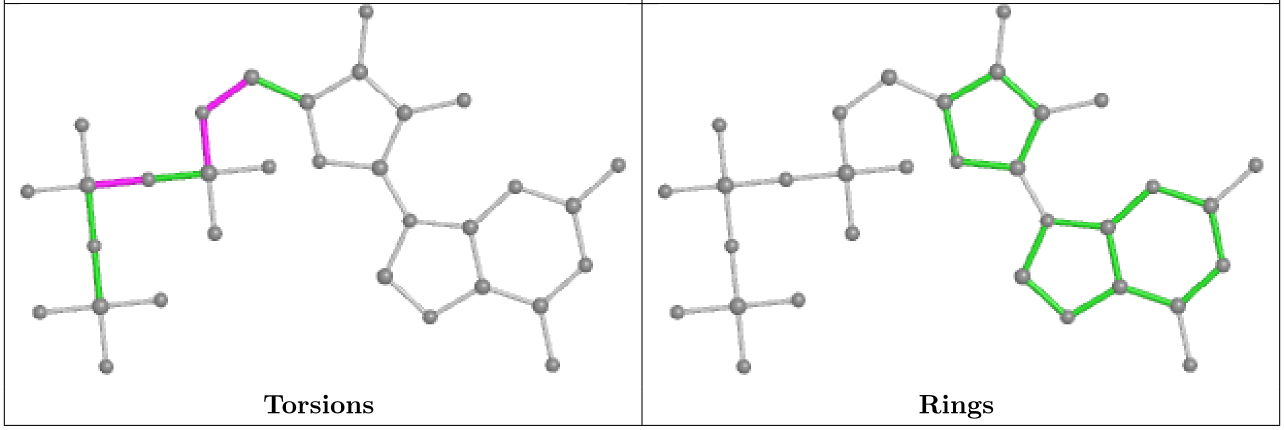


Bond lengths

Bond angles



Torsions

Rings

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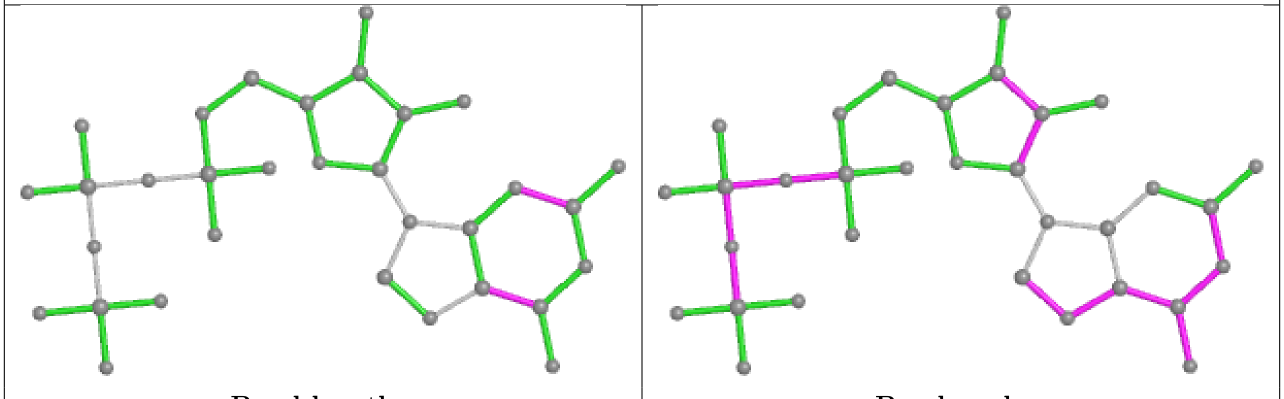
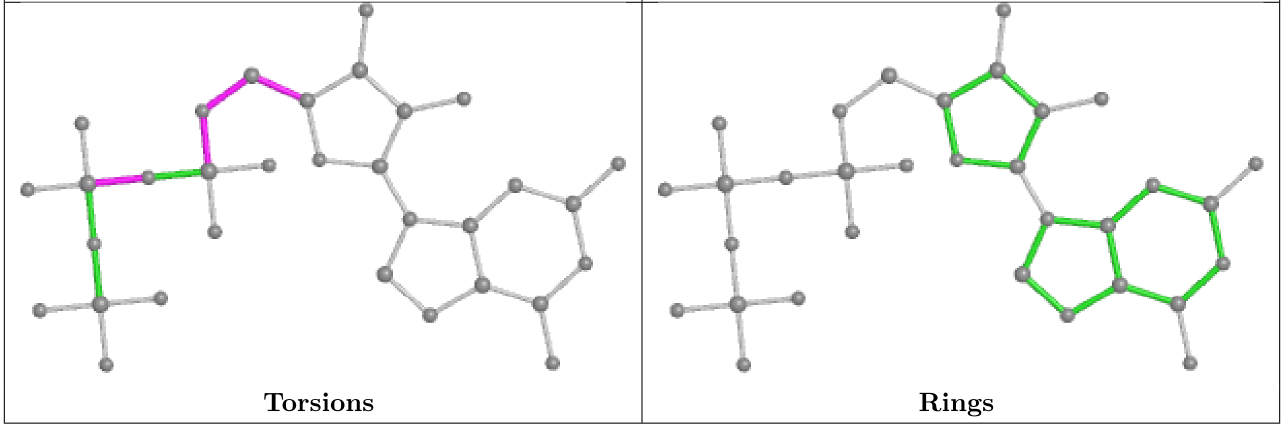


Bond lengths

Bond angles



Torsions

Rings

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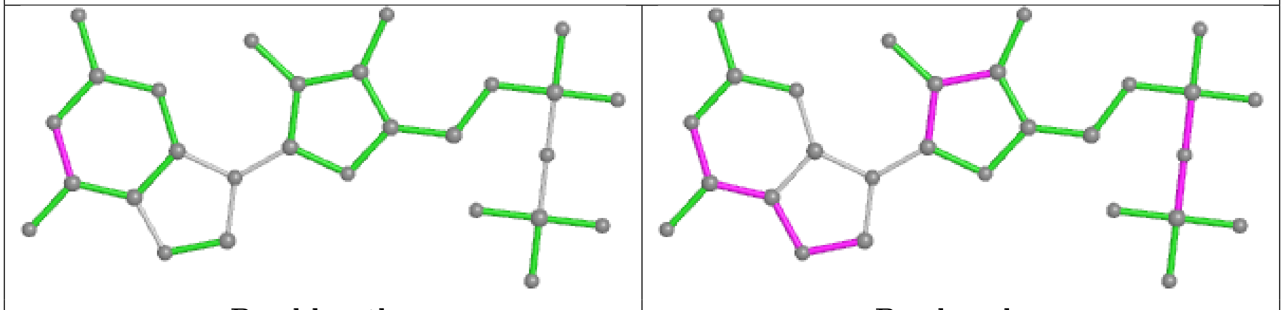
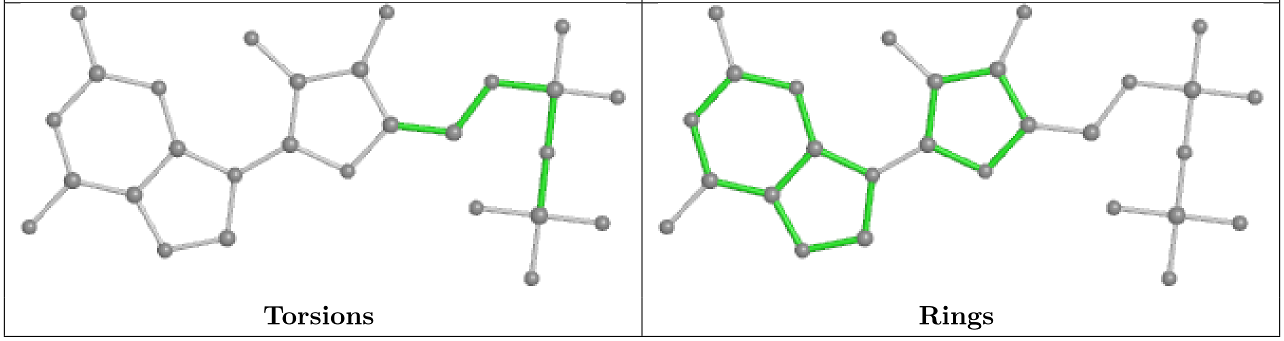


Bond lengths

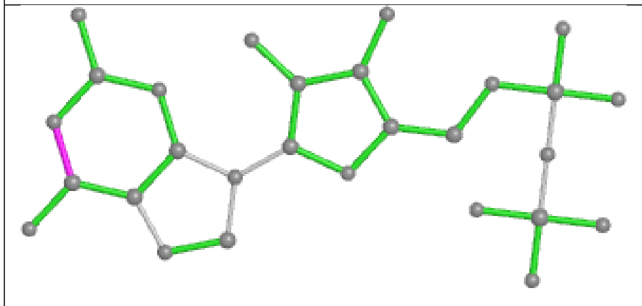
Bond angles



Torsions

Rings

Ligand GDP UH 502



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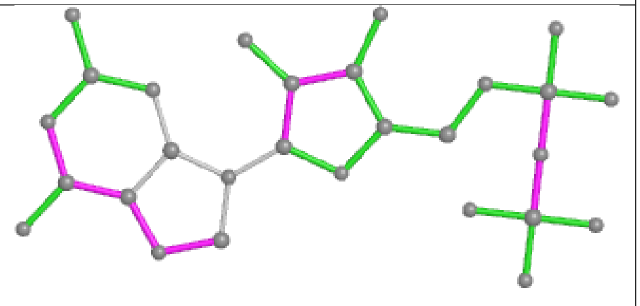

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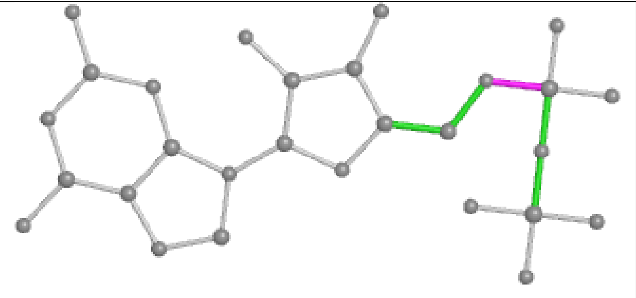

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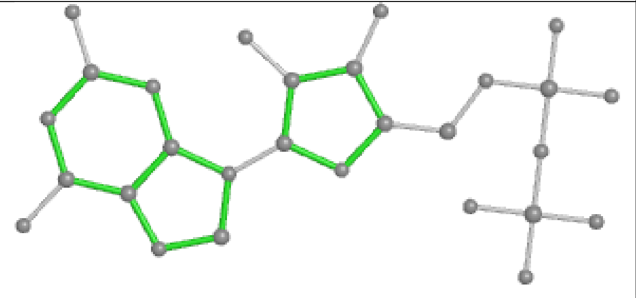

Rings

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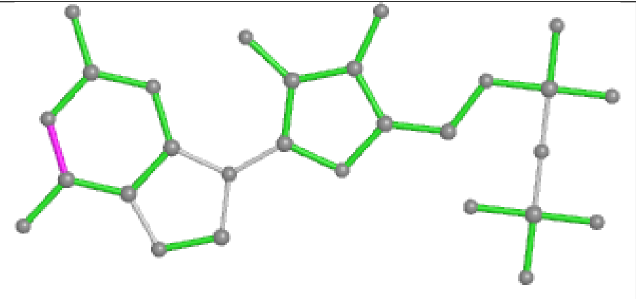

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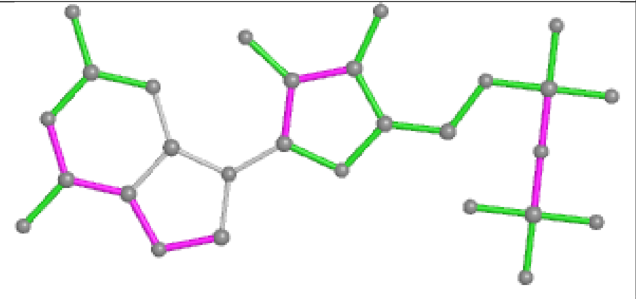

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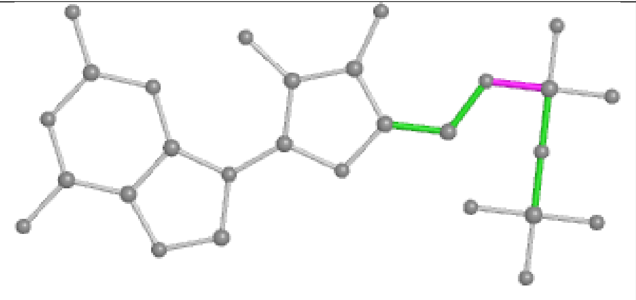

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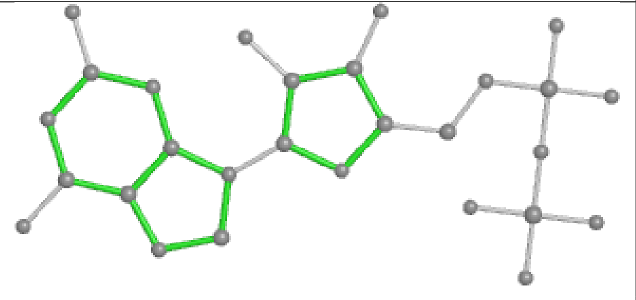
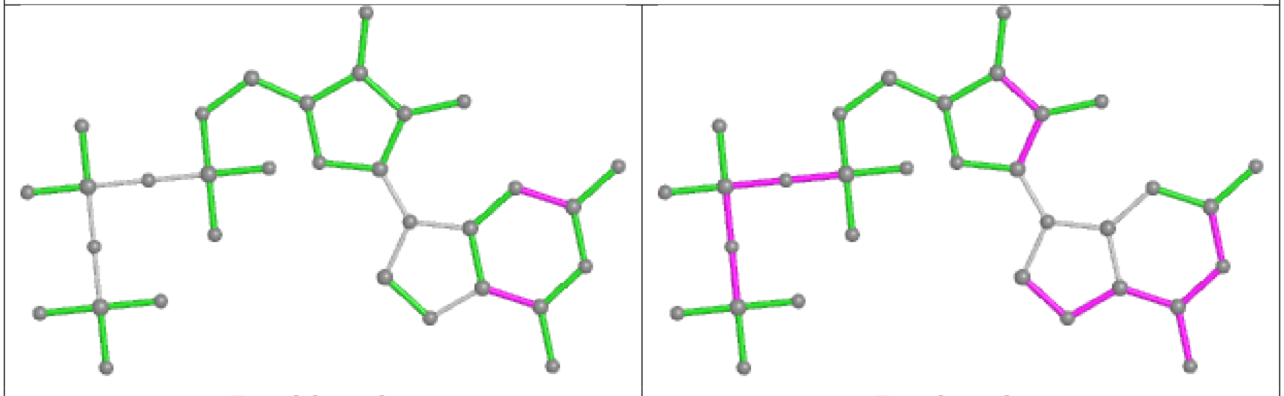


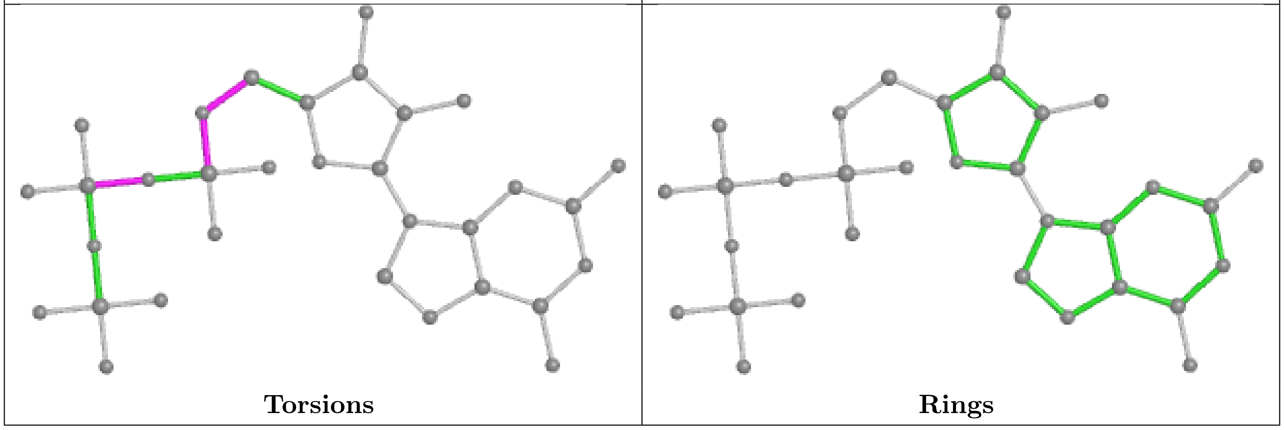
Rings

Ligand GTP KM 501



Bond lengths

Bond angles



Torsions

Rings

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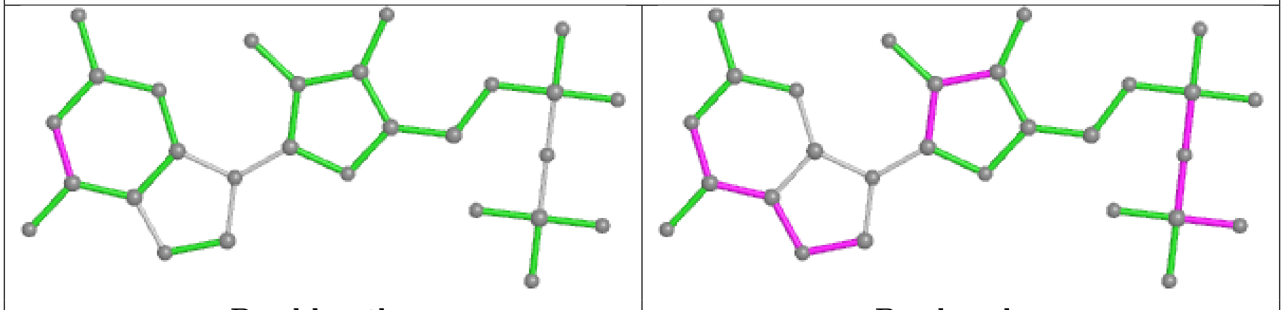
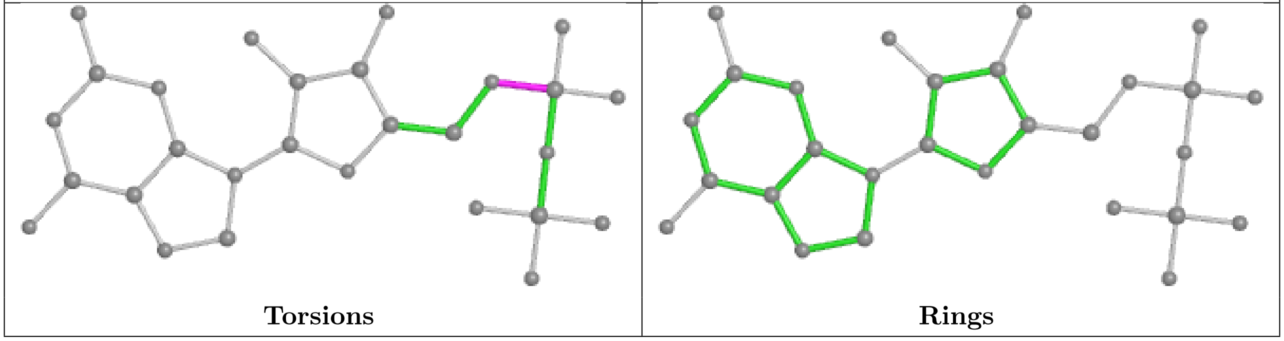


Bond lengths

Bond angles



Torsions

Rings

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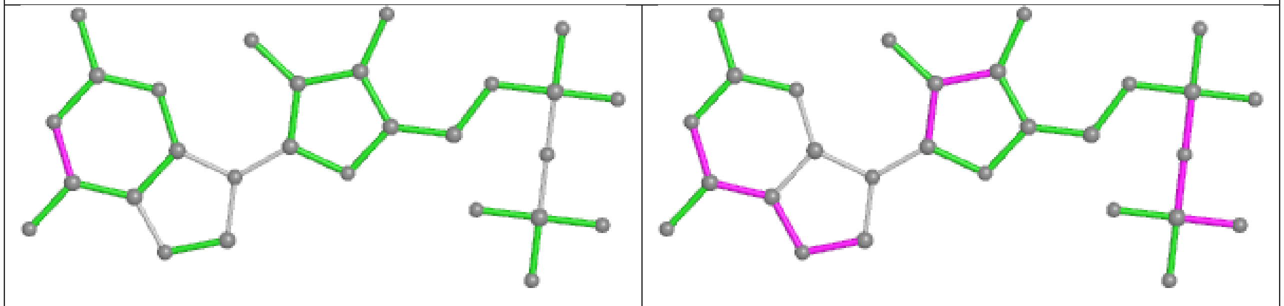

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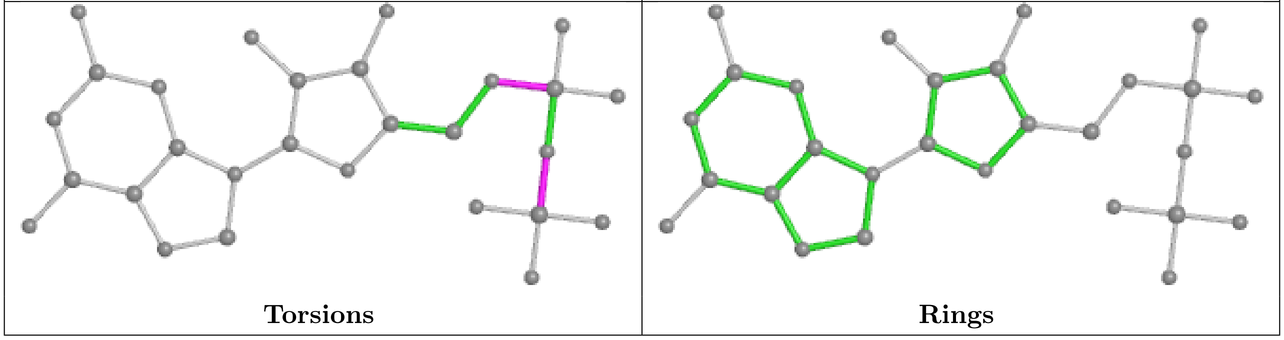
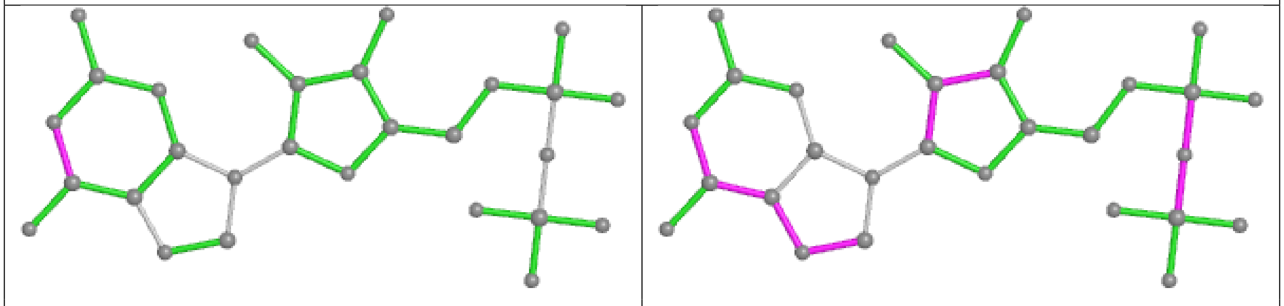
Bond angles



Torsions

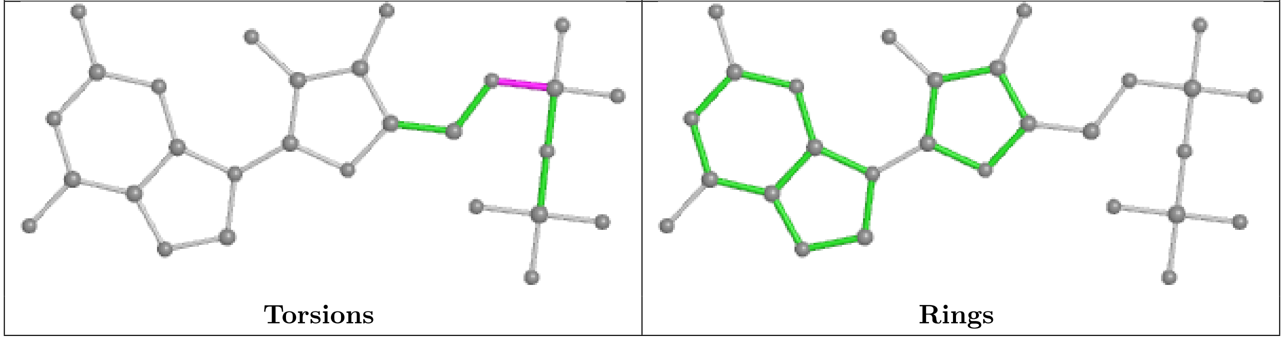
Rings

Ligand GDP KP 502



Bond lengths

Bond angles



Torsions

Rings

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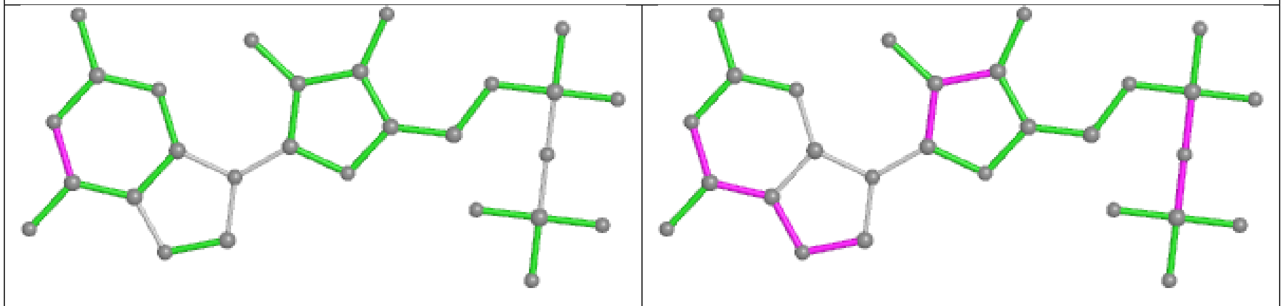
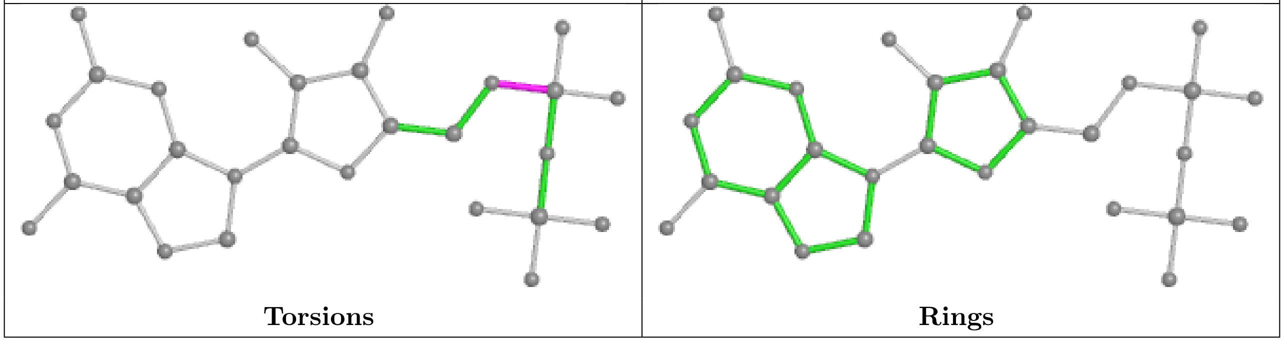


Bond lengths

Bond angles



Torsions

Rings

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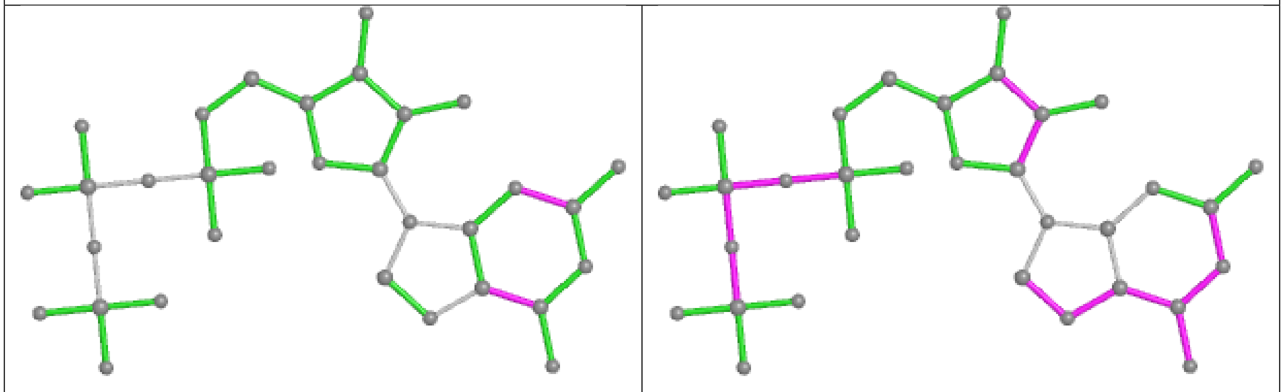
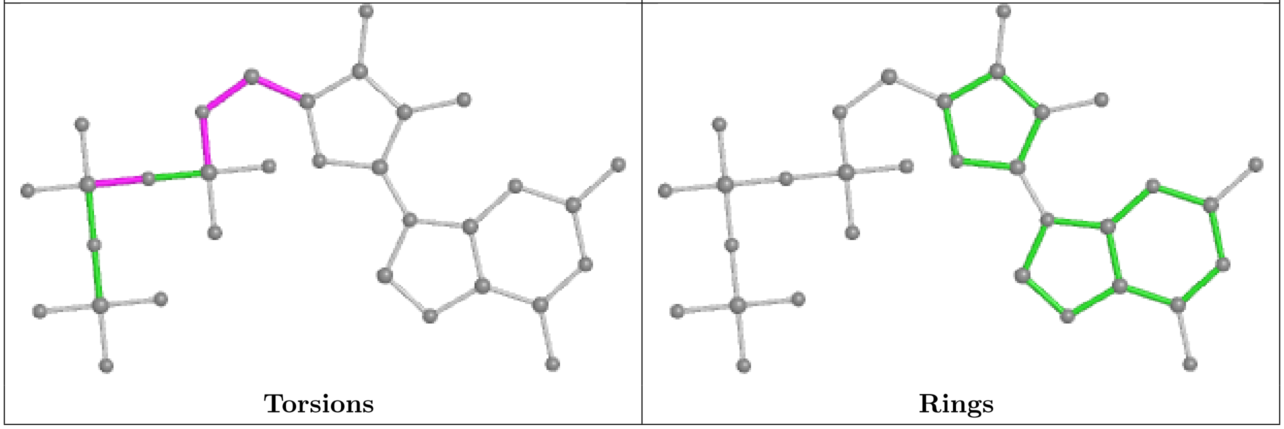


Bond lengths

Bond angles



Torsions

Rings

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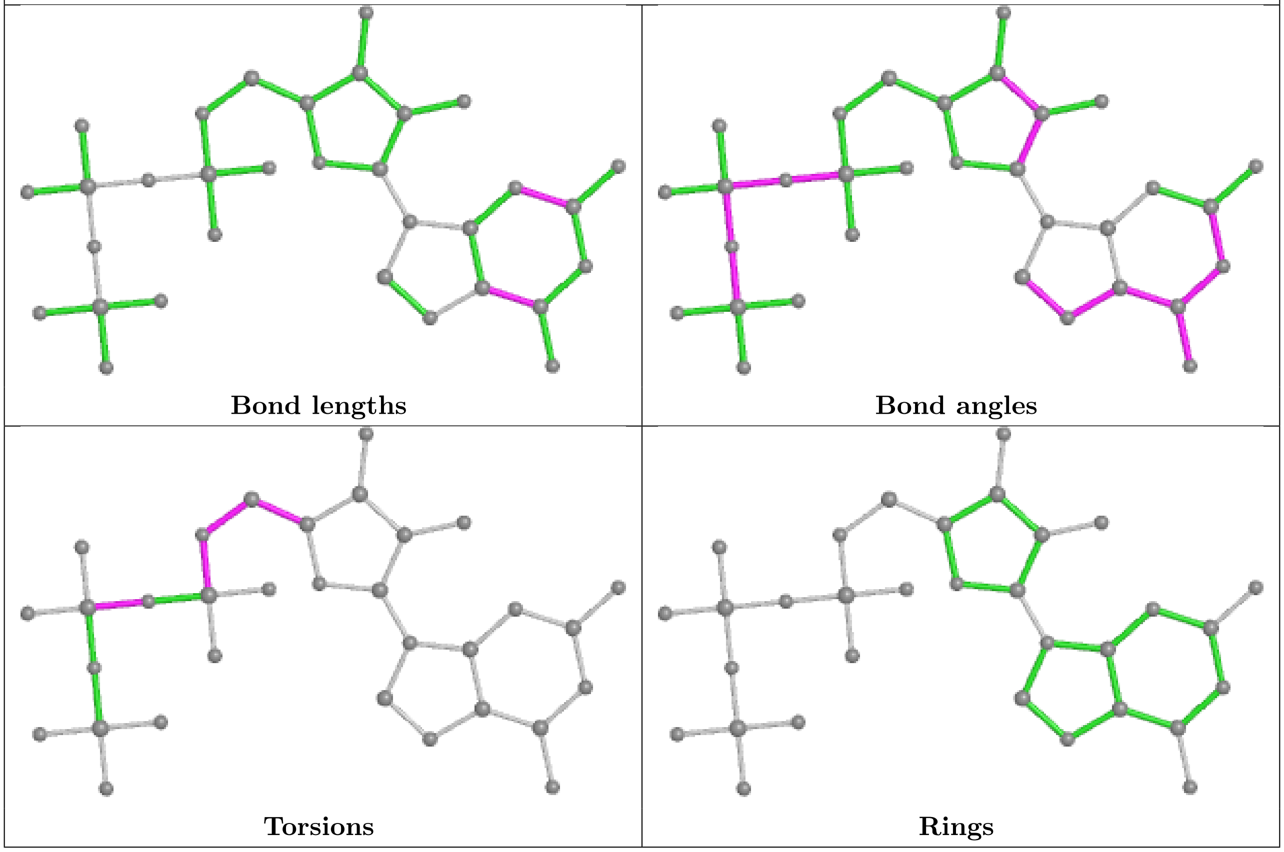

Bond lengths

Bond angles

Torsions

Rings

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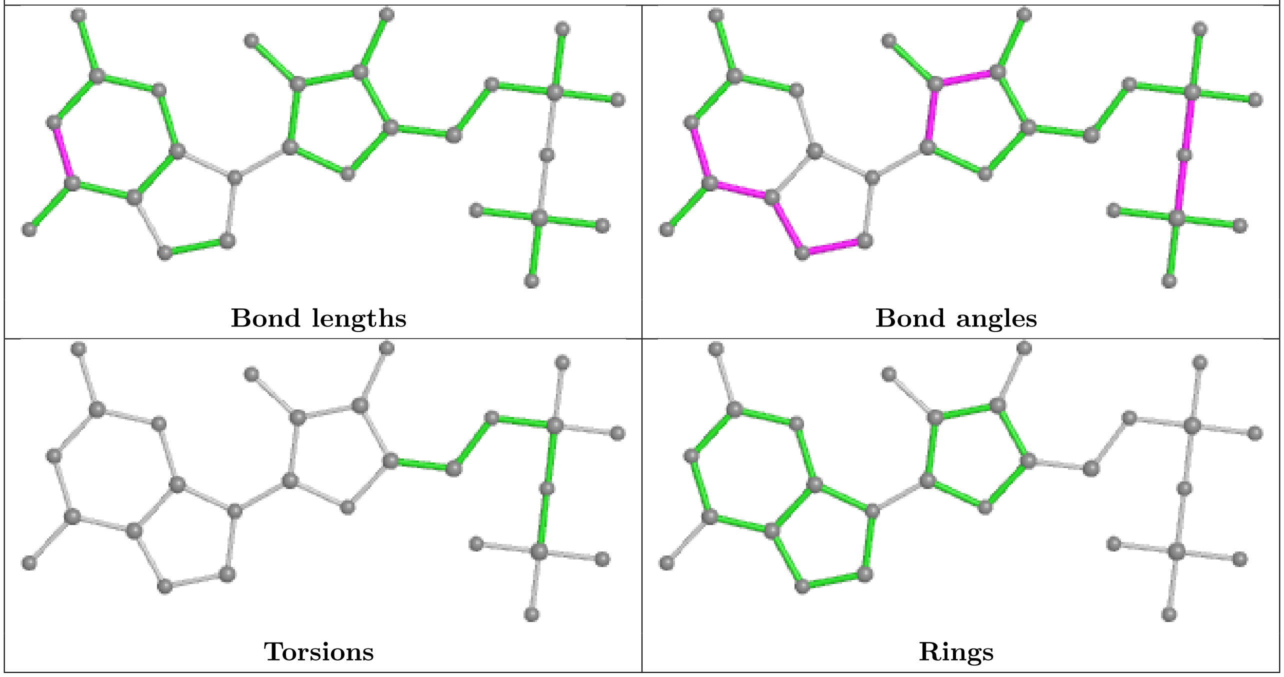


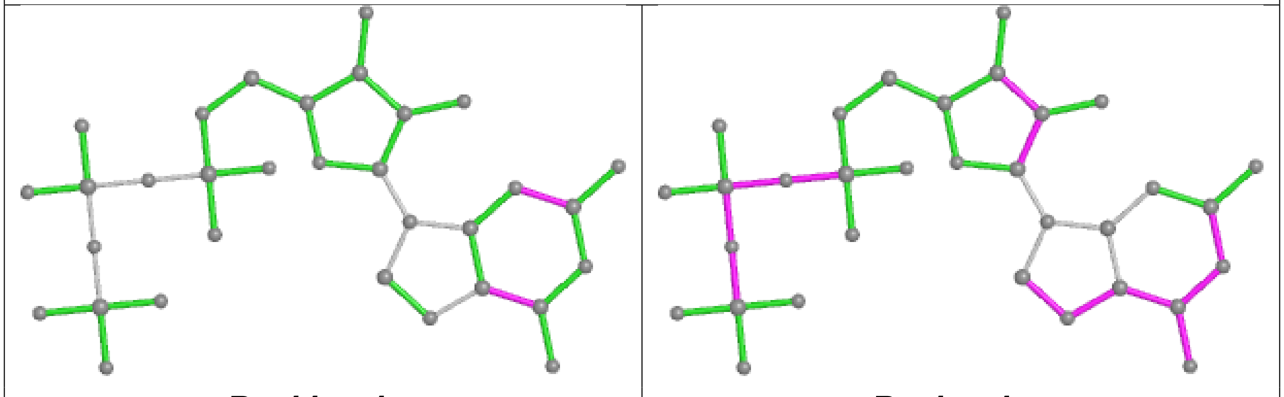
Bond lengths

Bond angles

Torsions

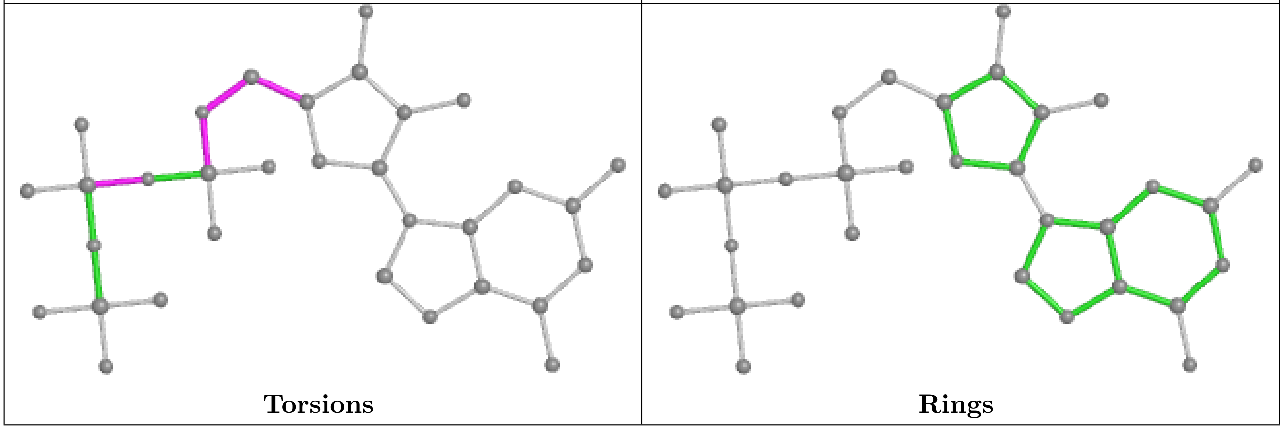
Rings

Ligand GTP II 501



Bond lengths

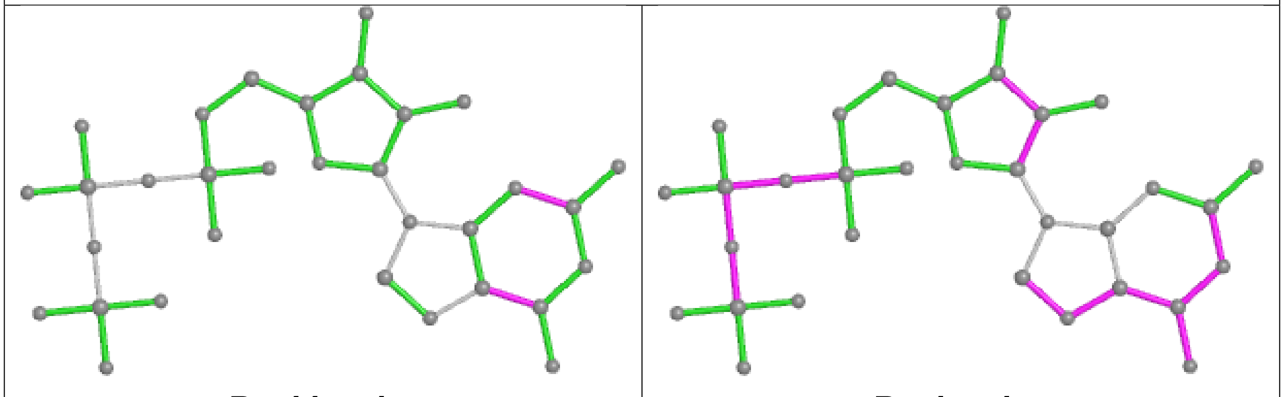
Bond angles



Torsions

Rings

Ligand GTP KA 501



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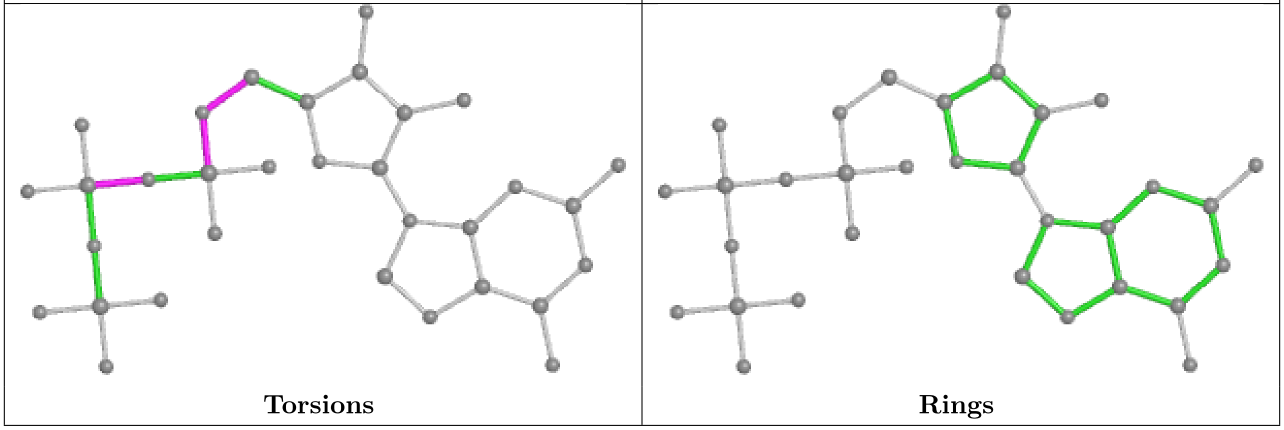
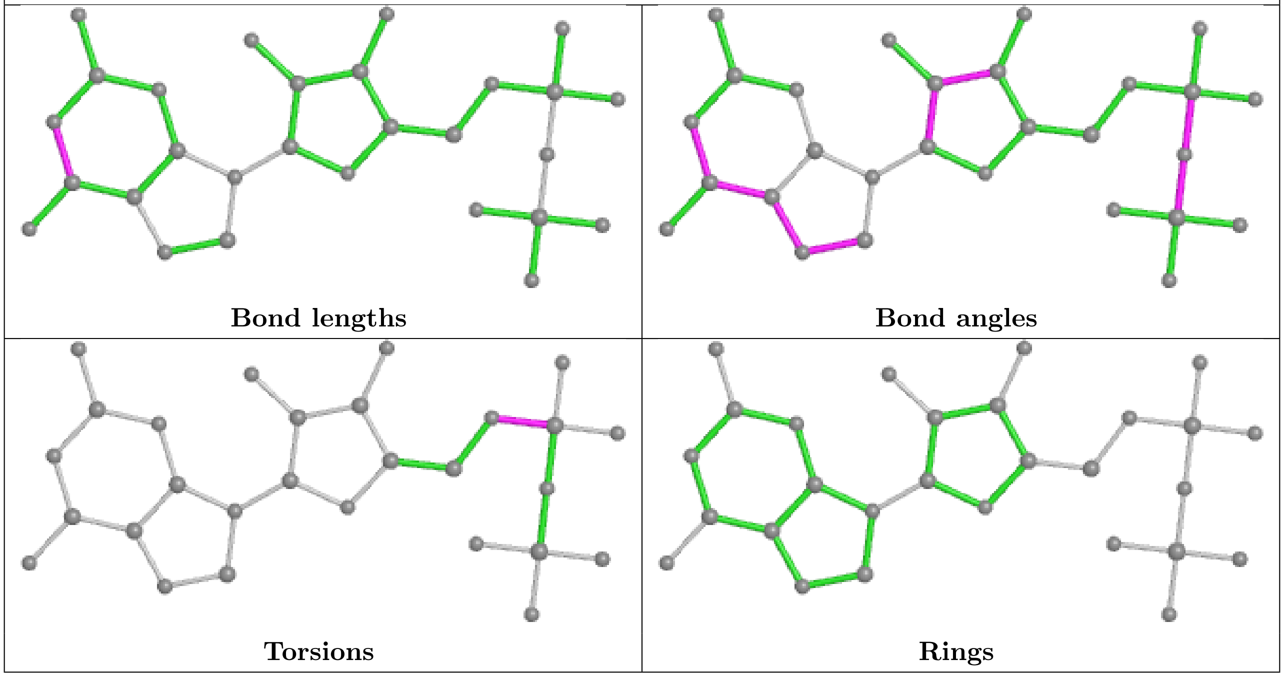
Bond angles



Torsions

Rings

Ligand GDP WL 502



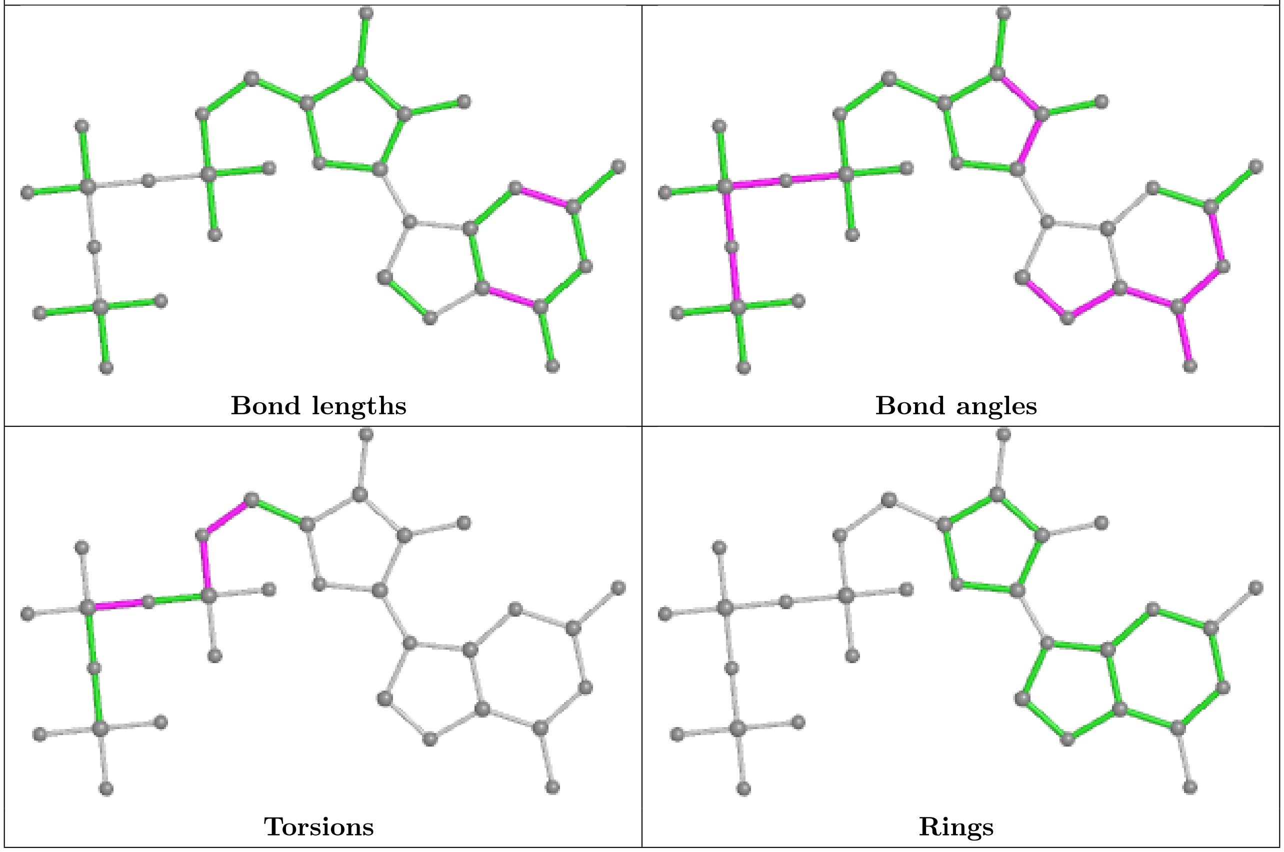
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP AC 501



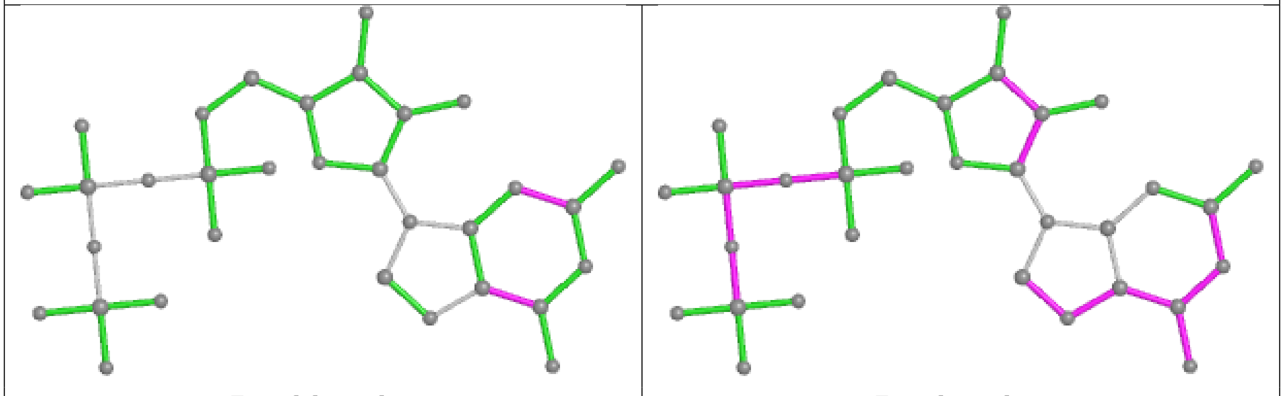
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP DQ 501



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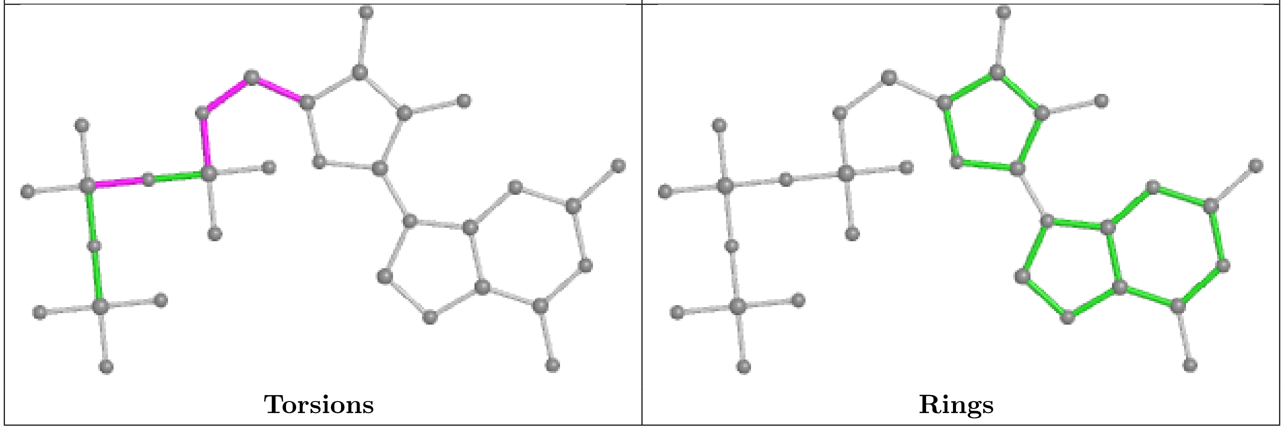
Bond angles



Torsions

Rings

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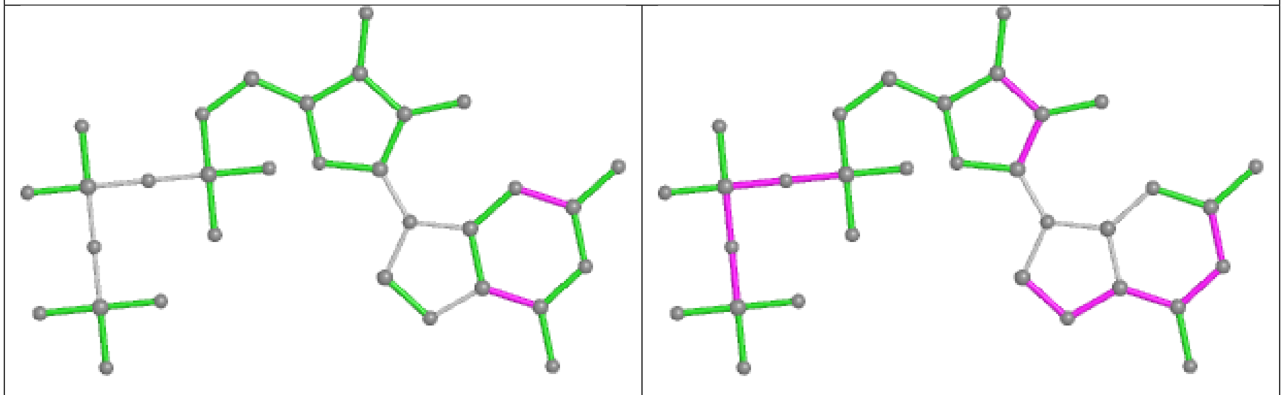

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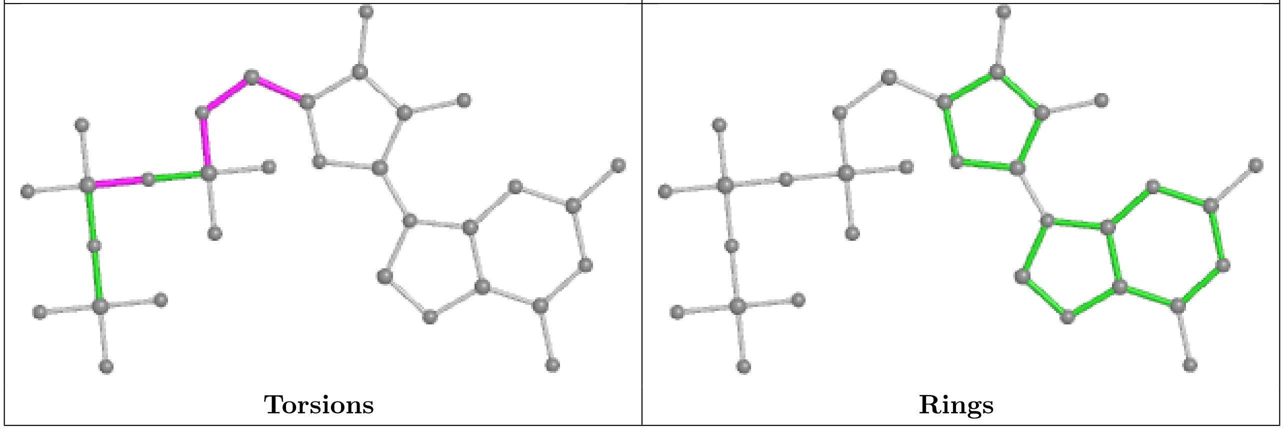
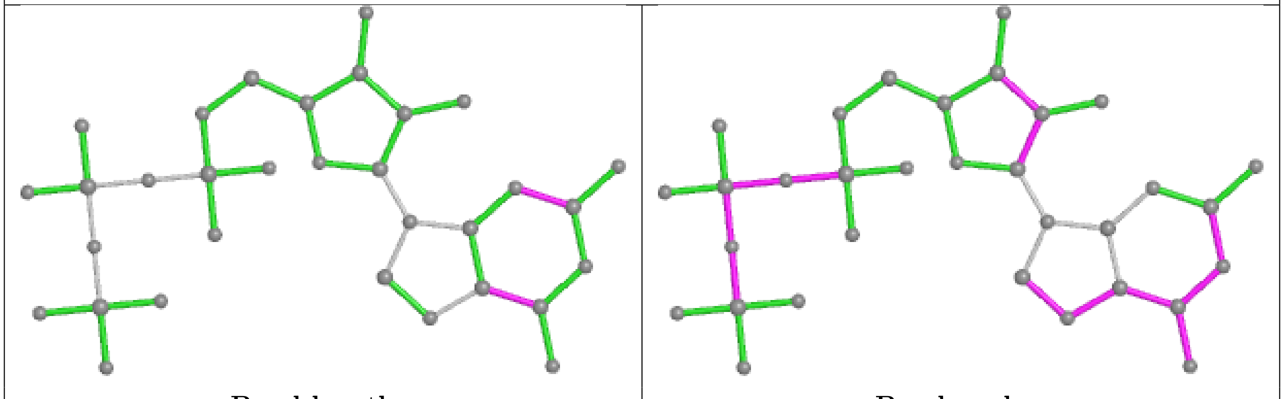
Bond angles



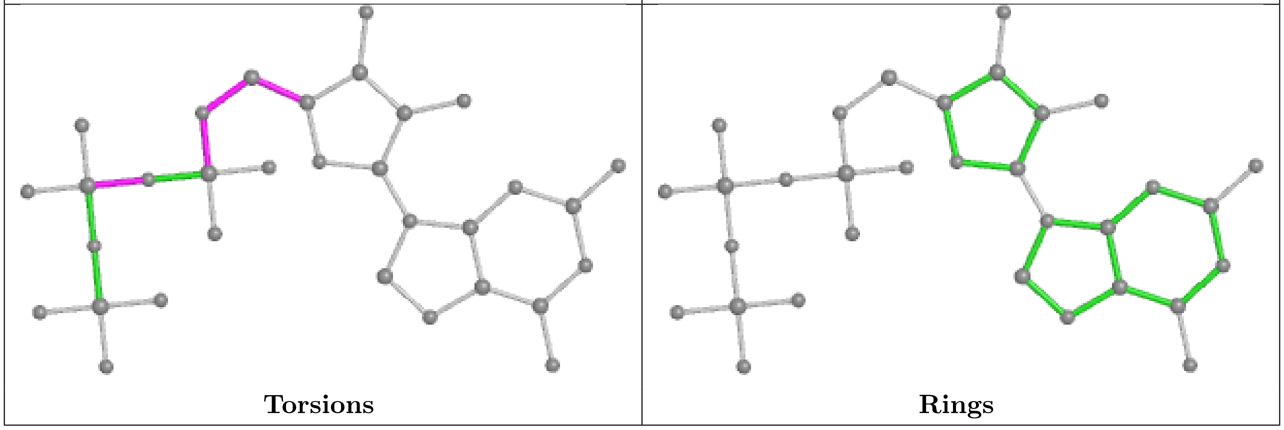
Torsions

Rings

Ligand GTP VC 501

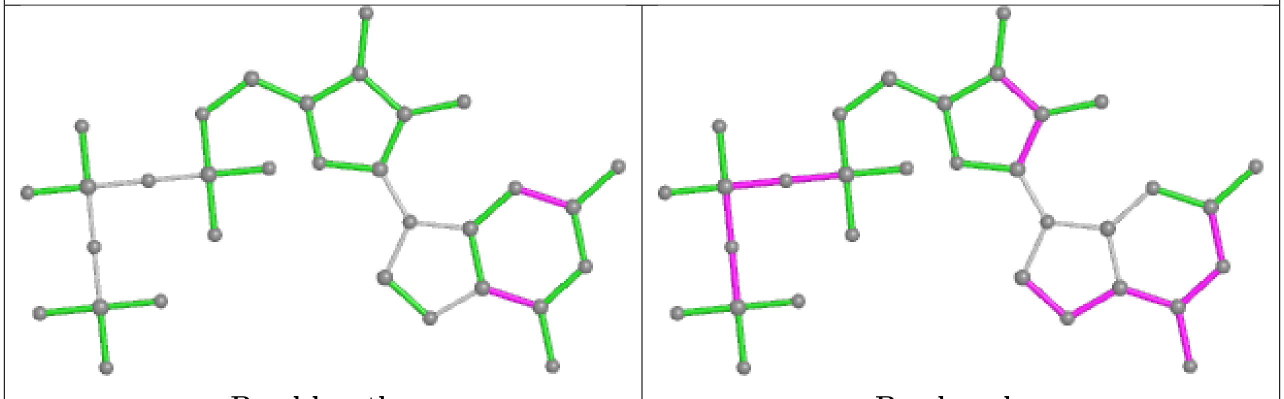


Bond lengths Bond angles



Torsions Rings

Ligand GTP FO 501



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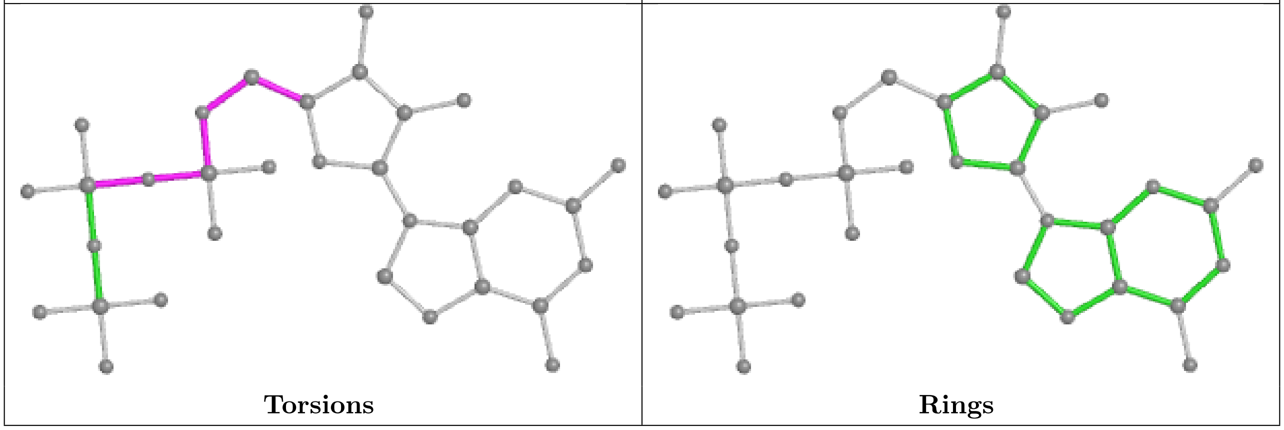
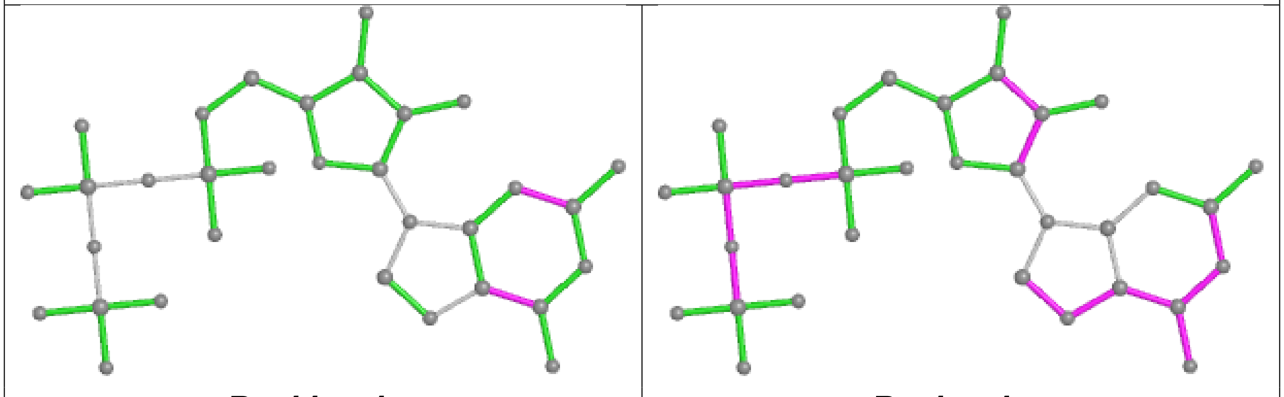


Torsions Rings

Ligand GTP GE 501



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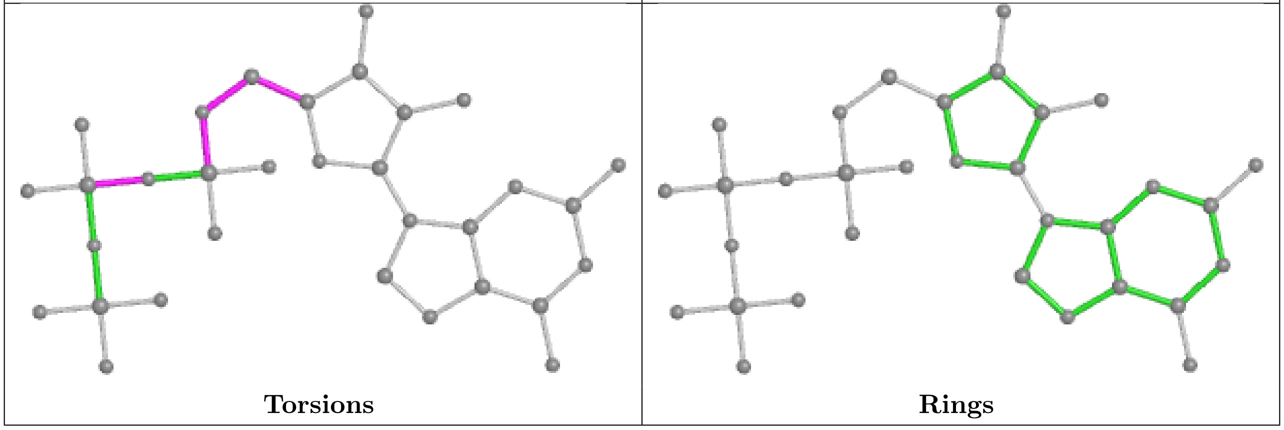
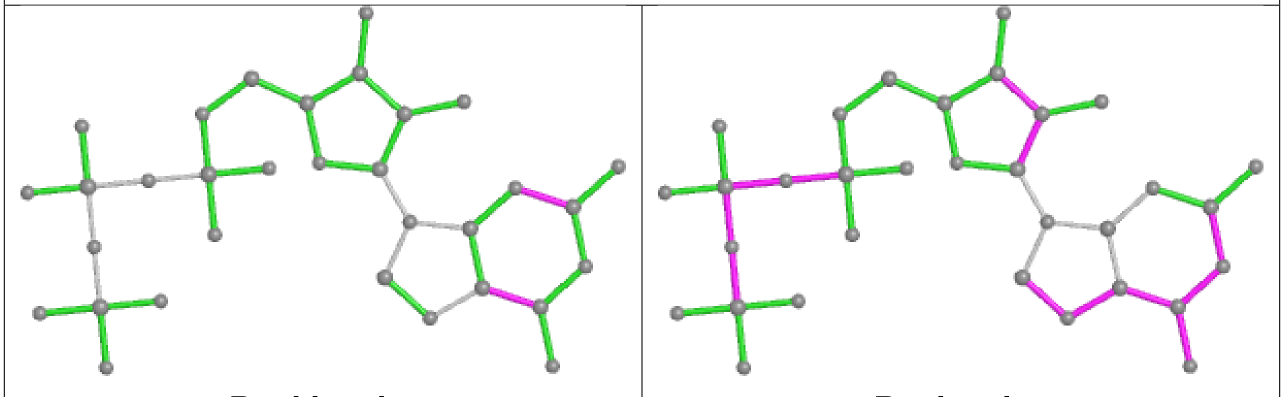


Torsions

Rings

Ligand GTP JQ 501



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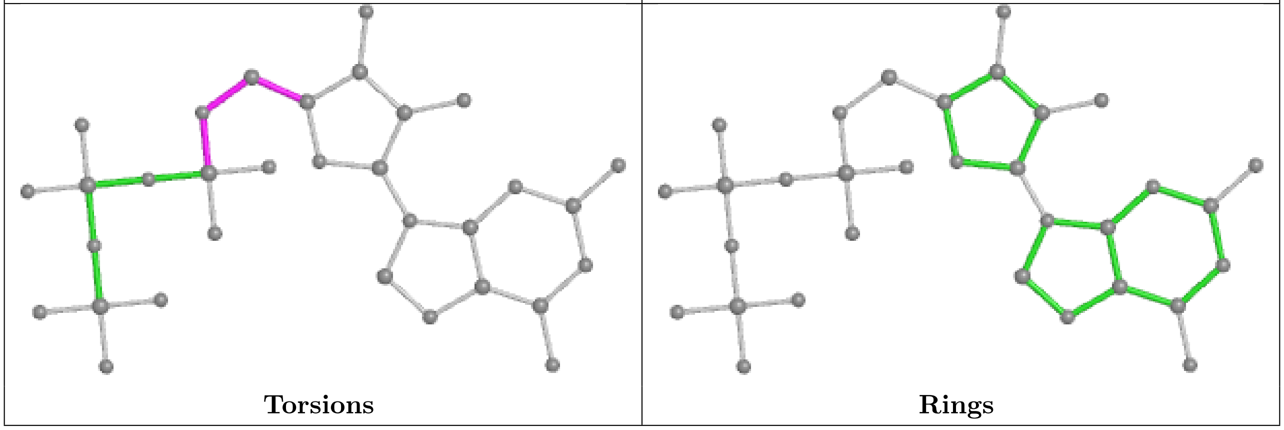
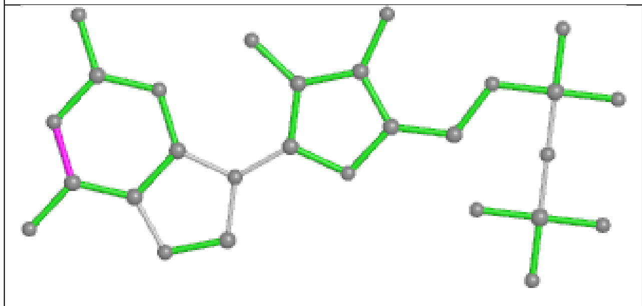
Bond angles



Torsions

Rings

Ligand GDP AF 502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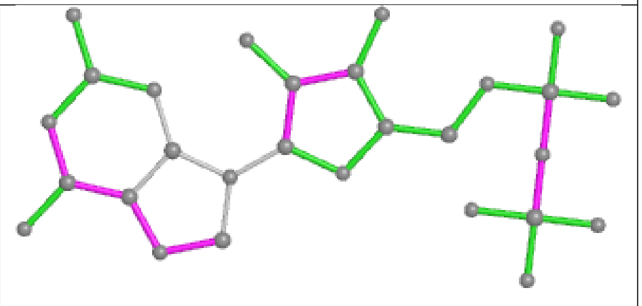
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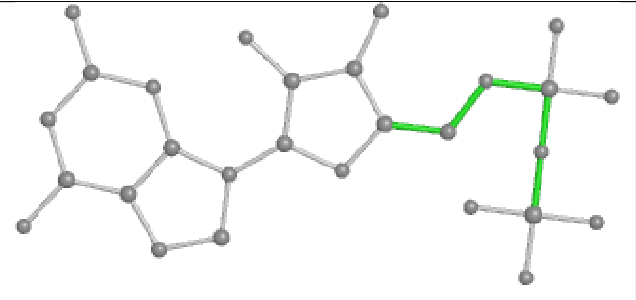
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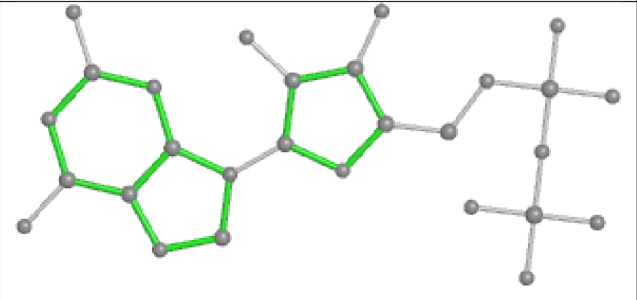
Rings

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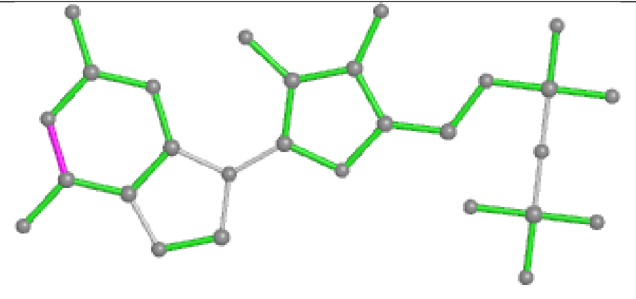
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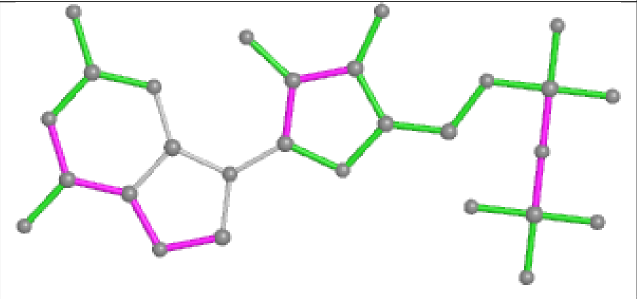
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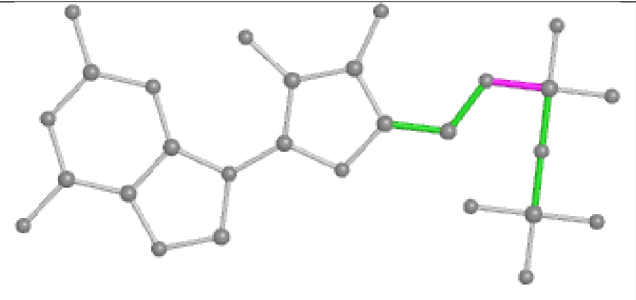
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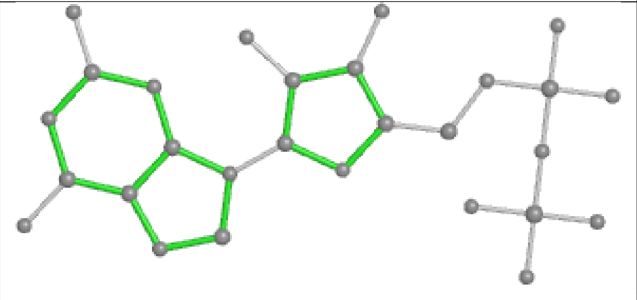
Rings

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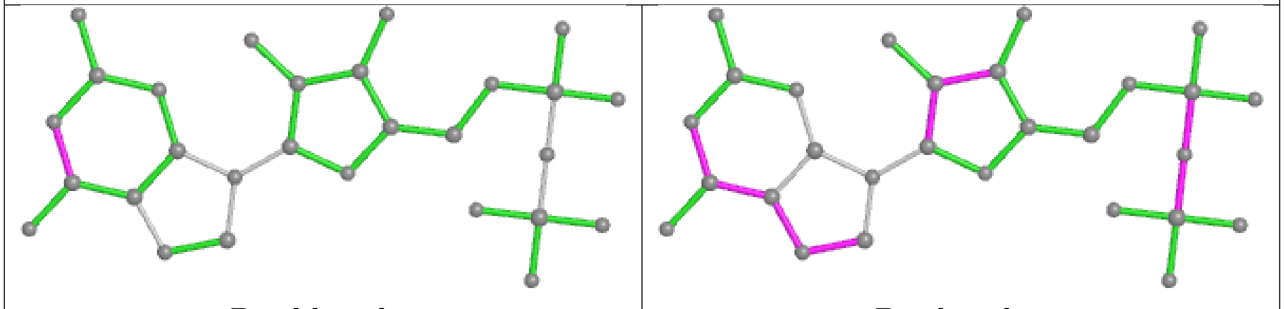

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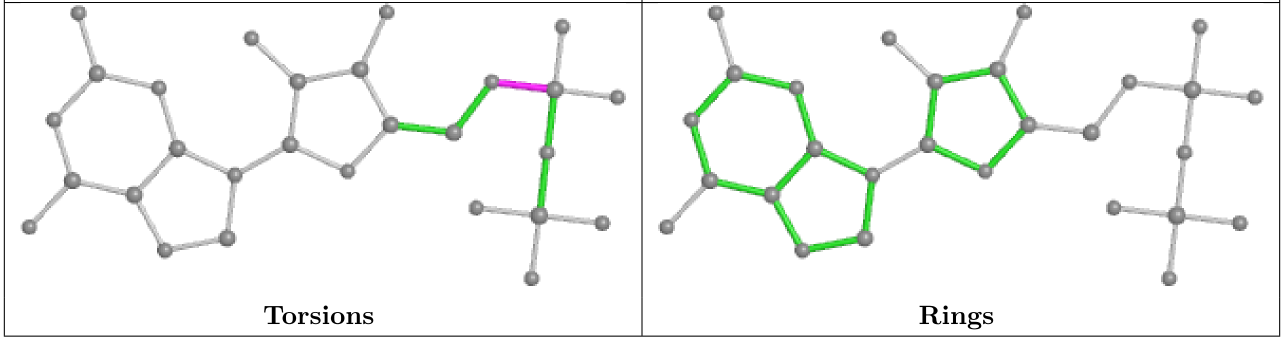
Bond angles



Torsions

Rings

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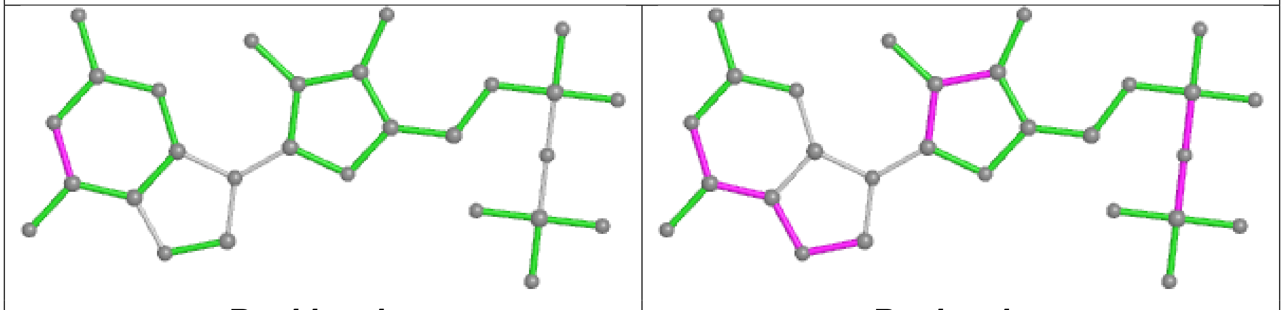

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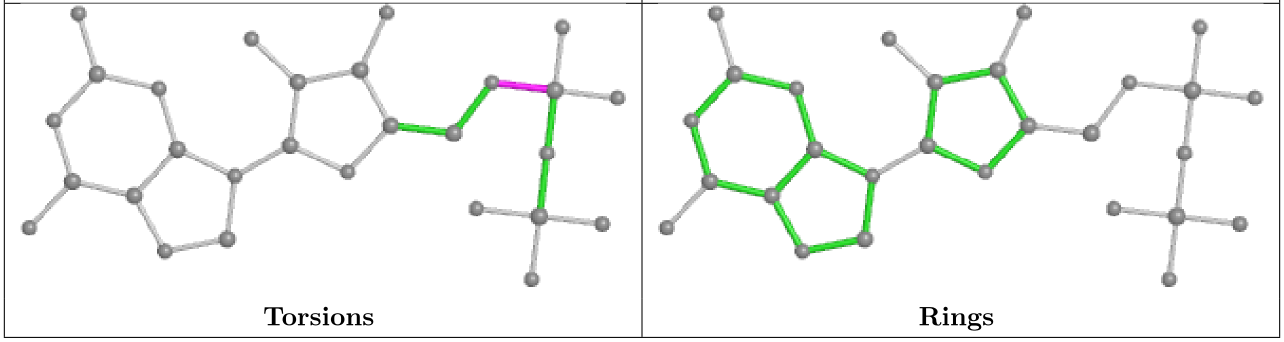

Torsions

Rings

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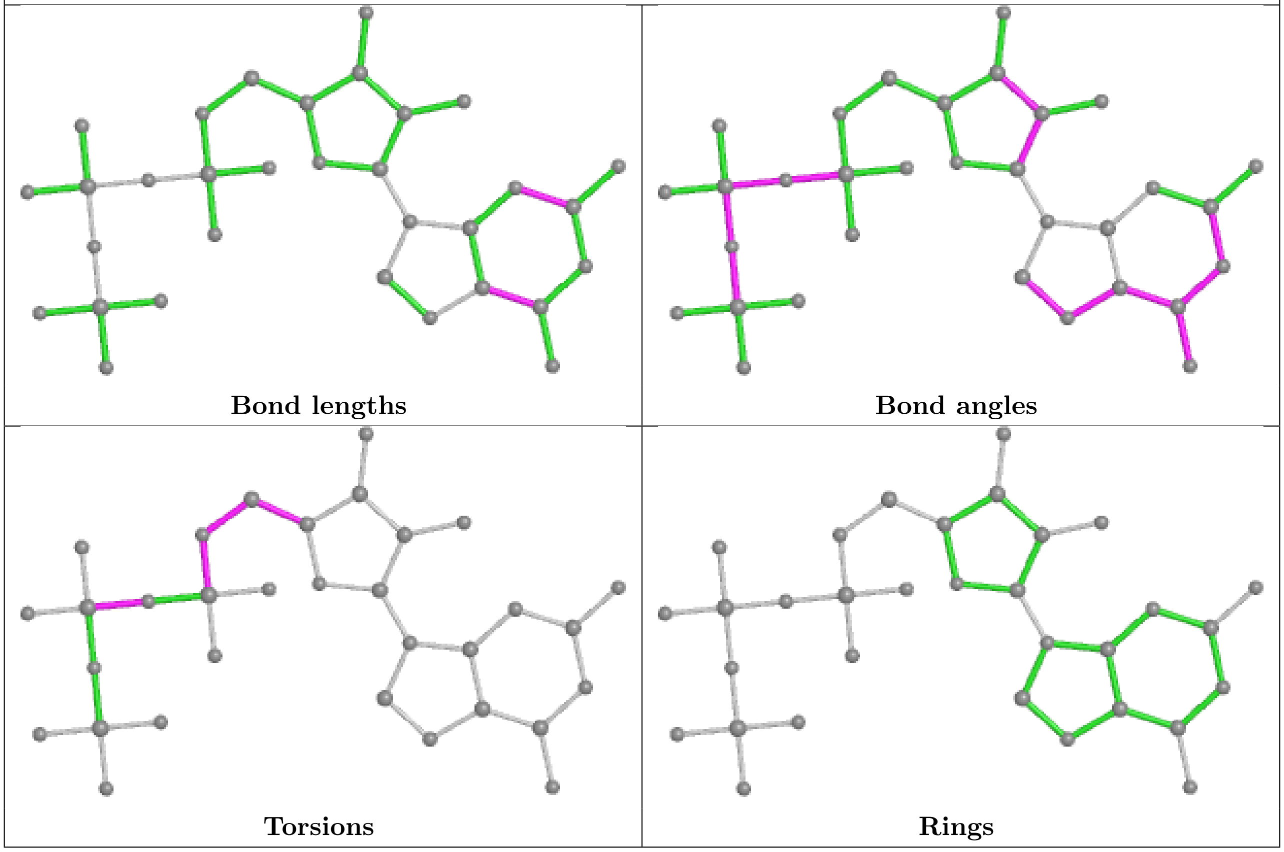

Bond lengths

Bond angles

Torsions

Rings

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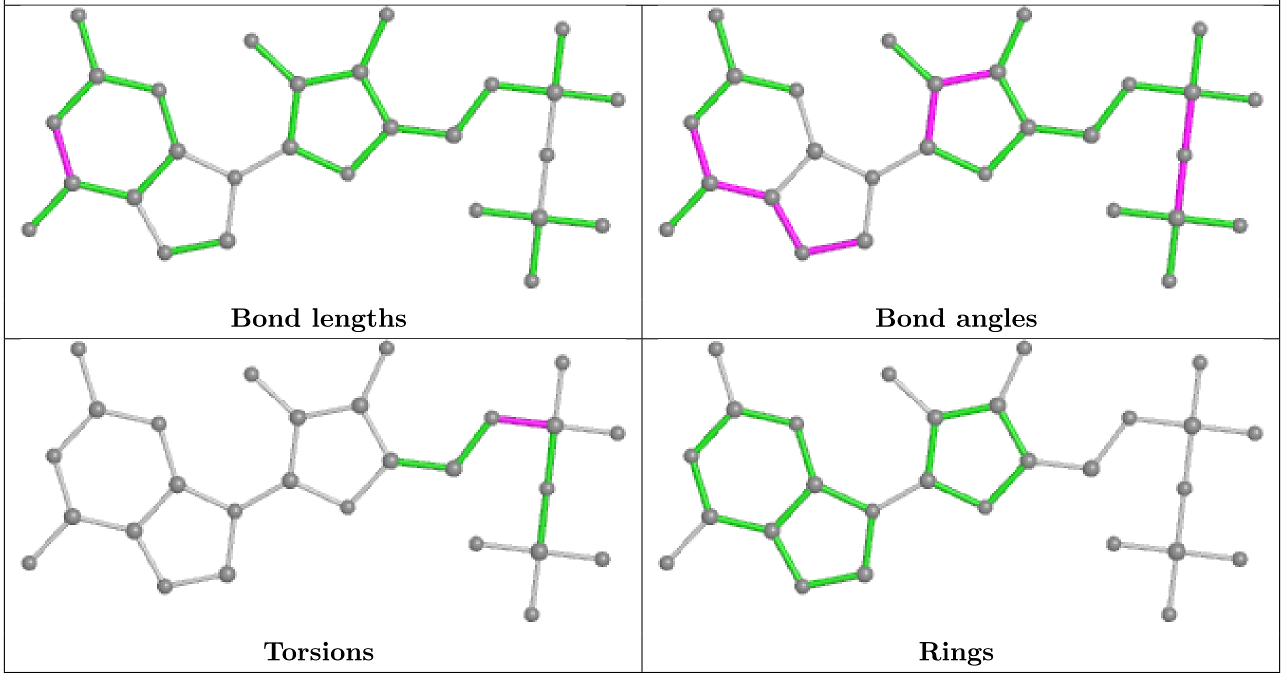

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Torsions

Rings

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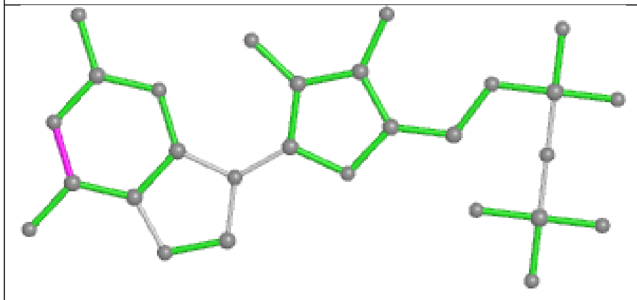

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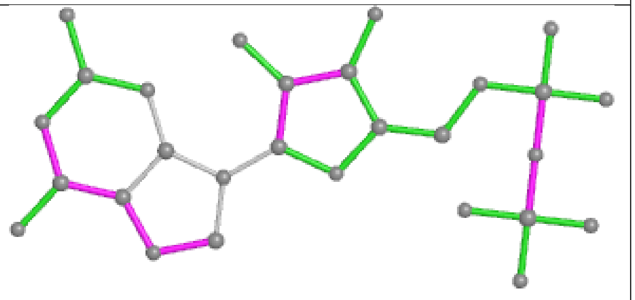

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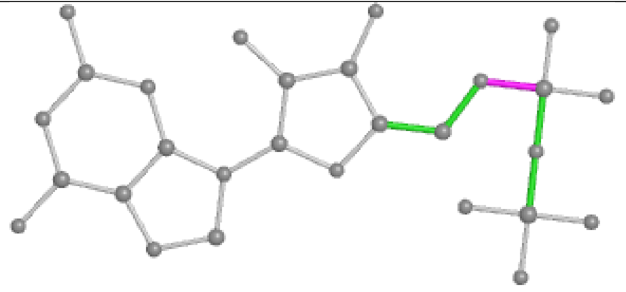

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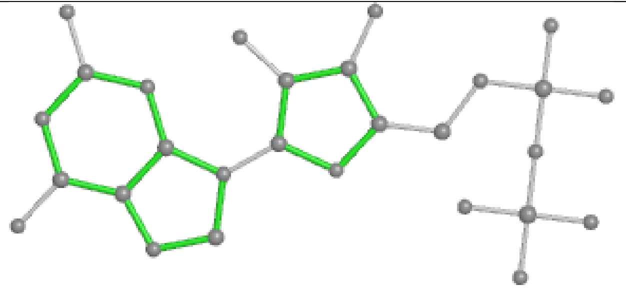

Rings

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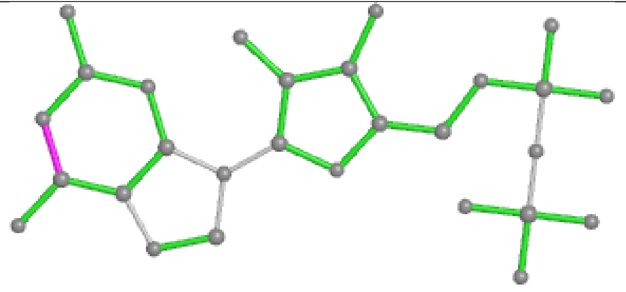

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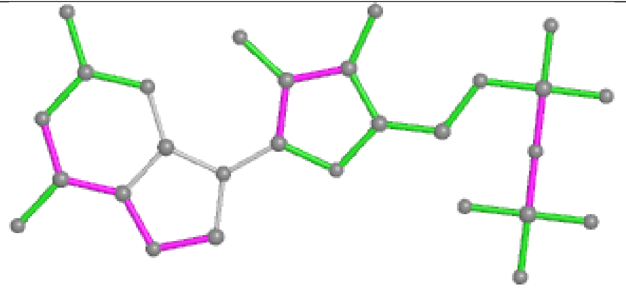

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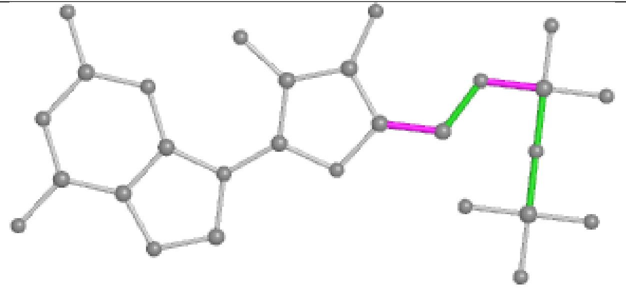

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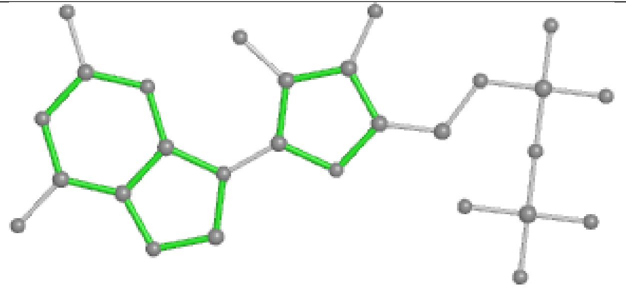

Rings

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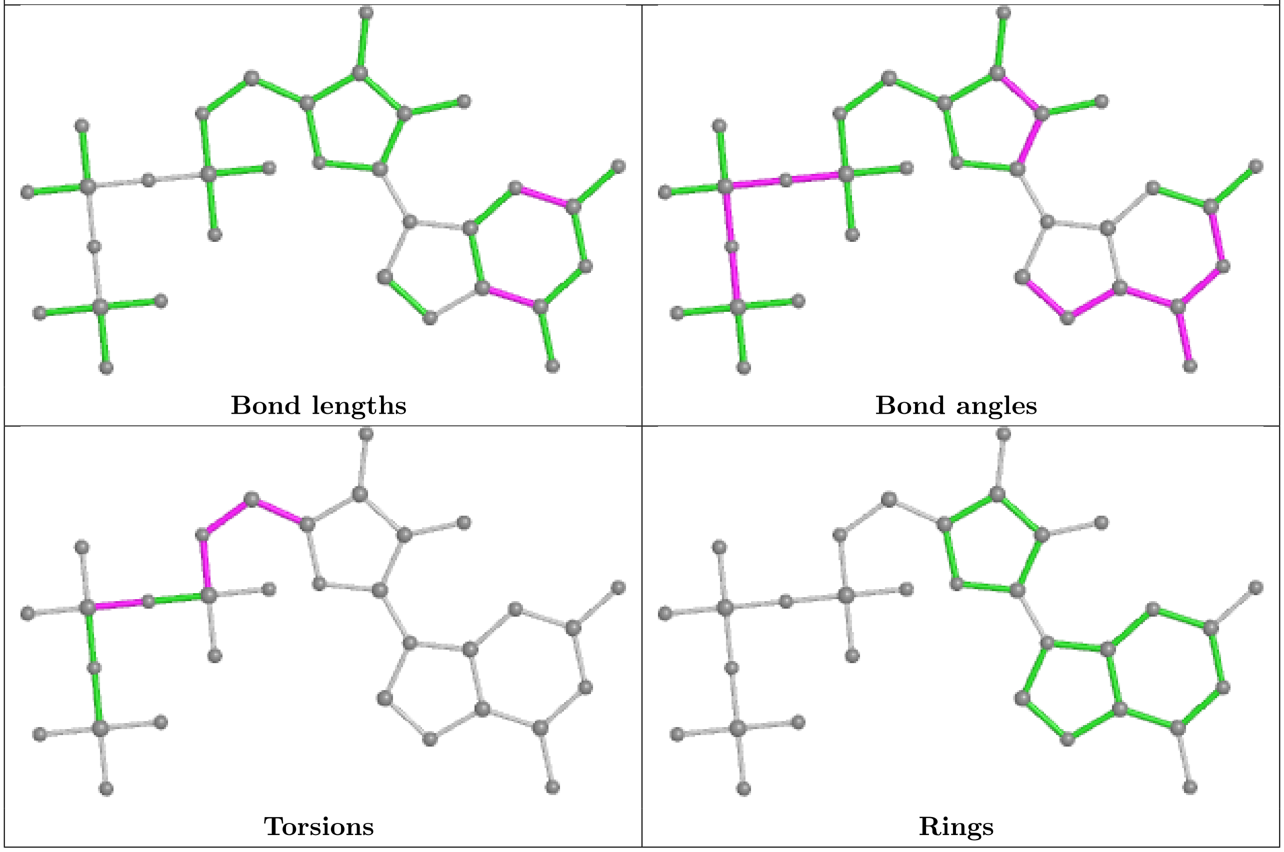

Bond lengths

Bond angles

Torsions

Rings

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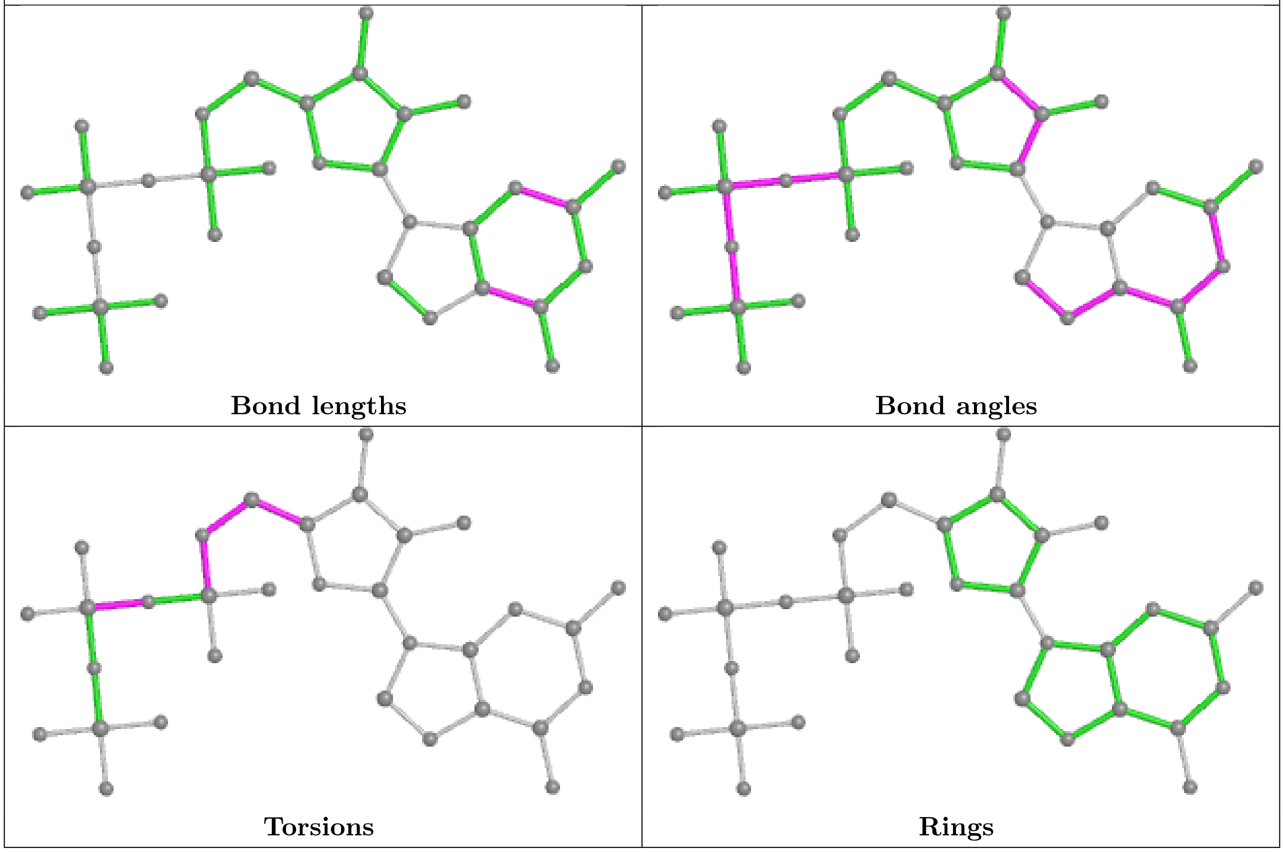

Bond lengths

Bond angles

Torsions

Rings

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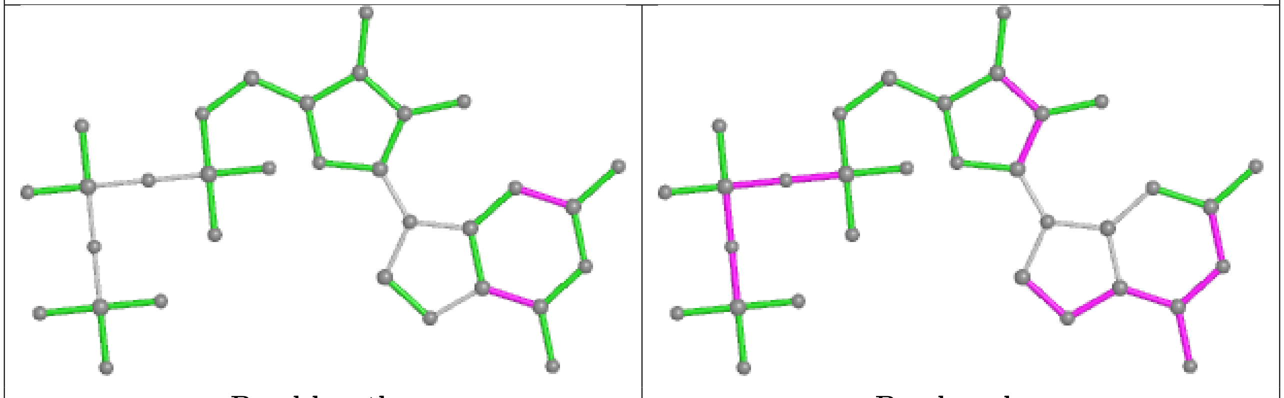
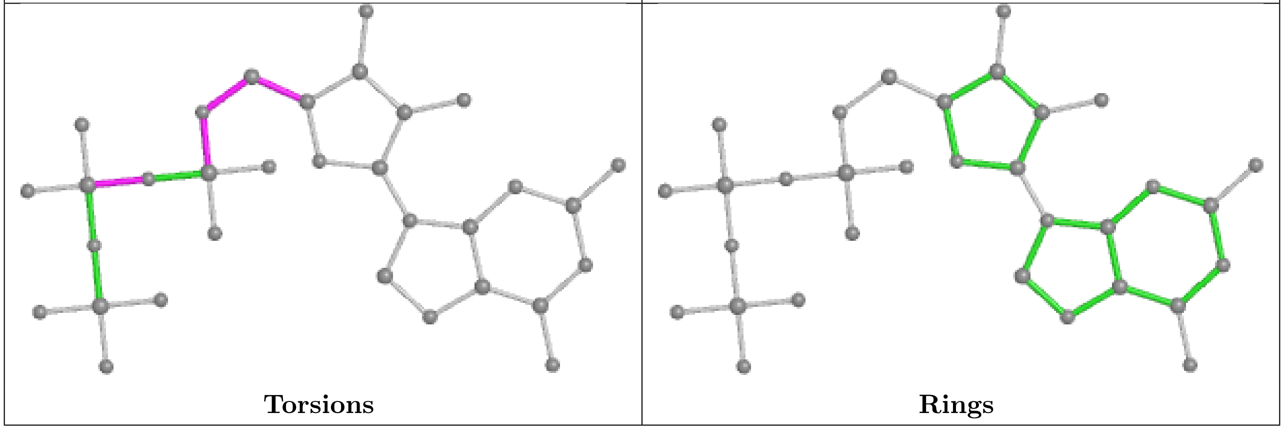


Bond lengths

Bond angles



Torsions

Rings

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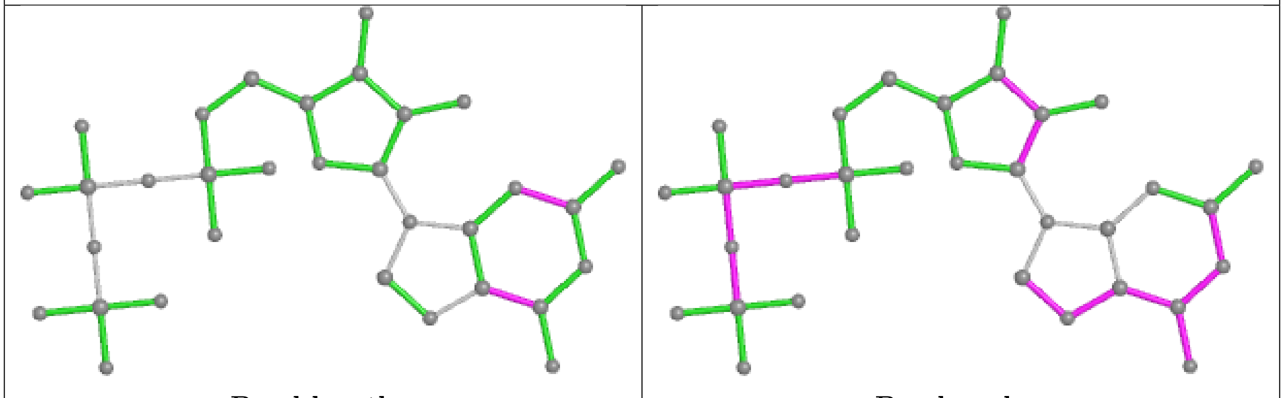

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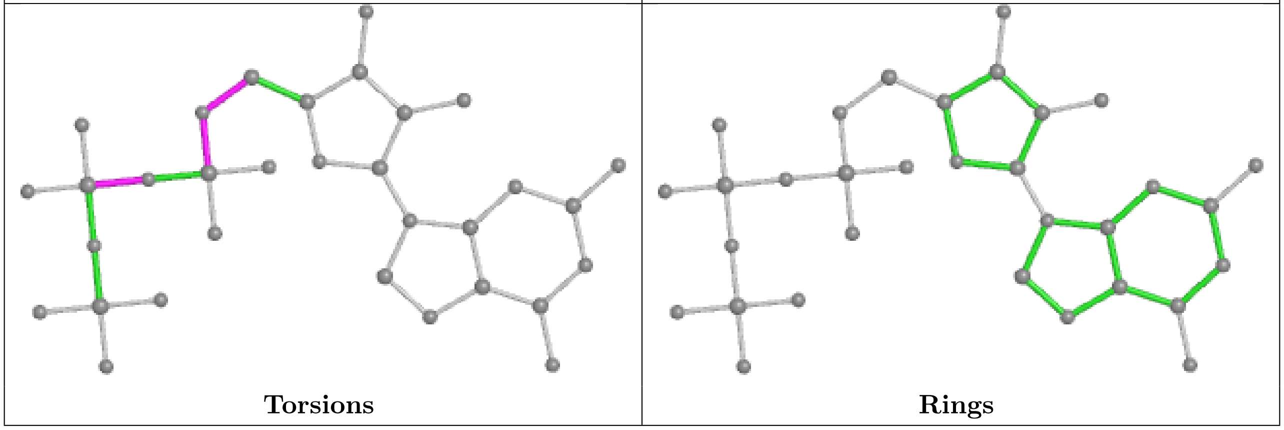

Torsions

Rings

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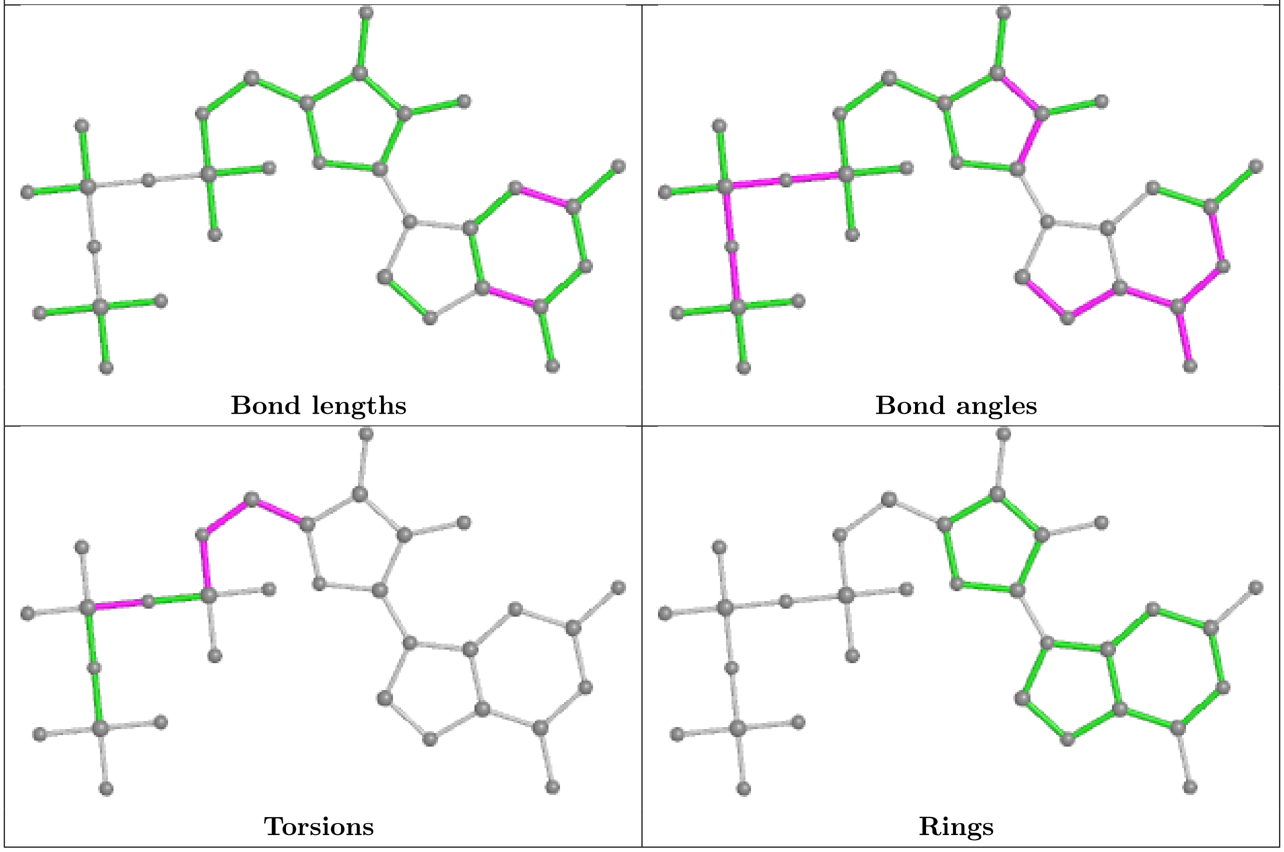

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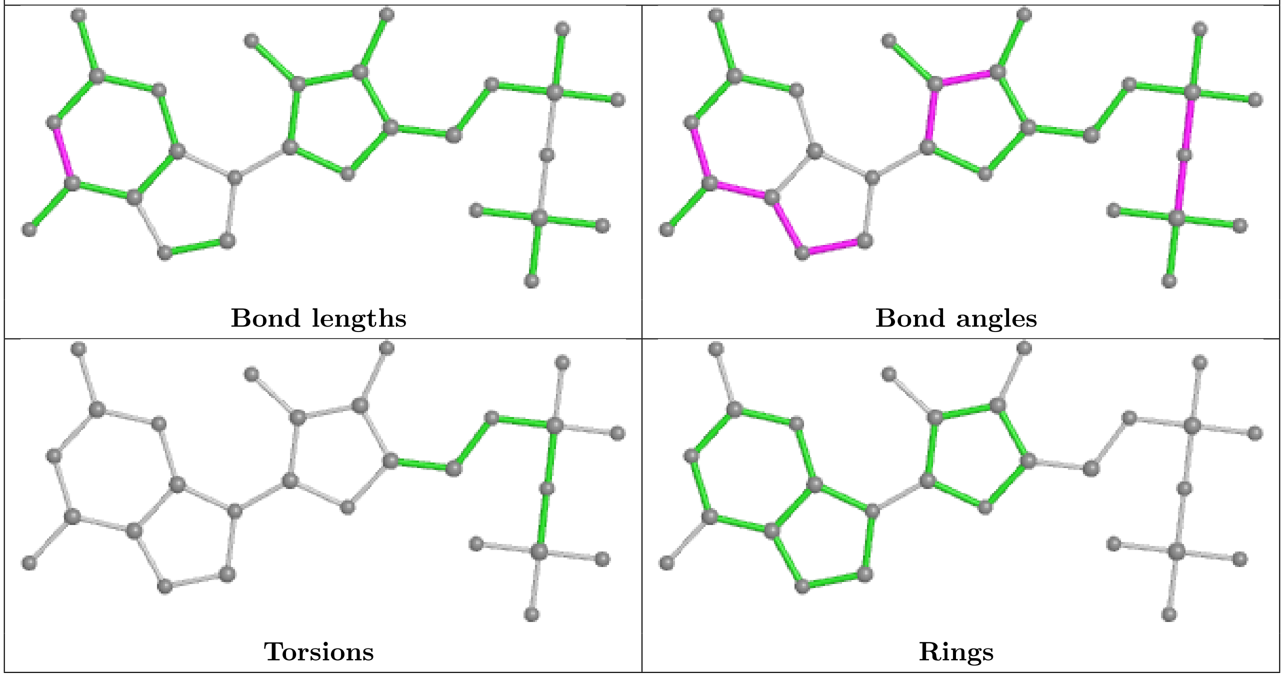

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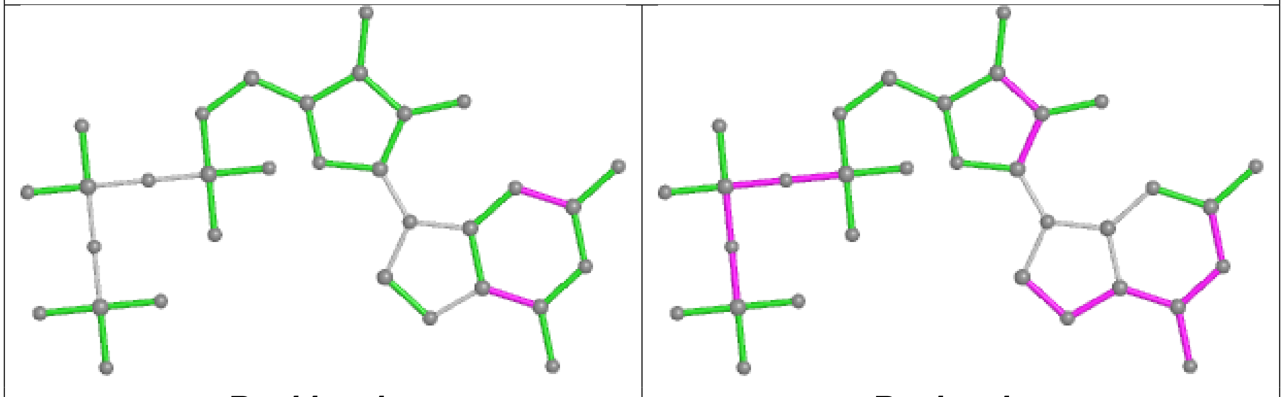
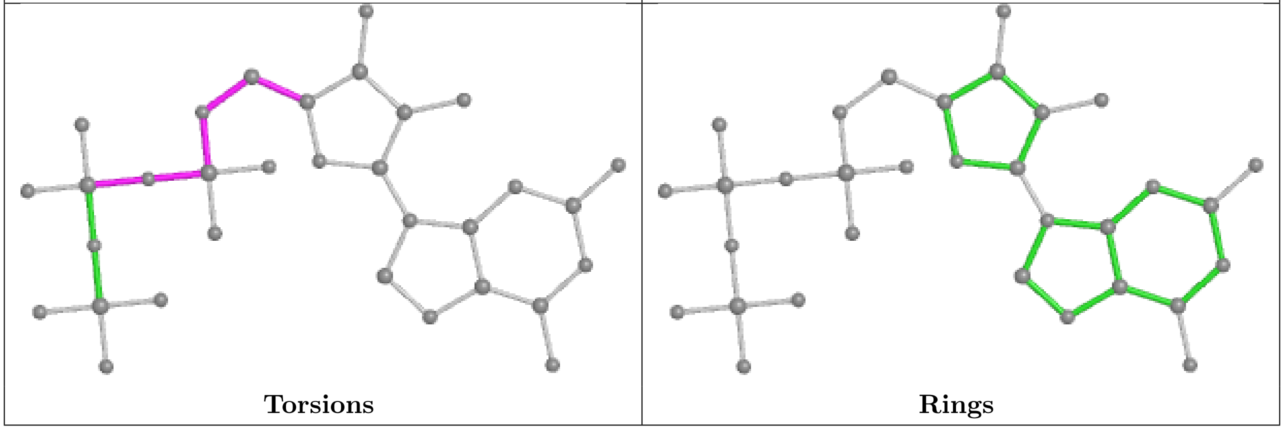
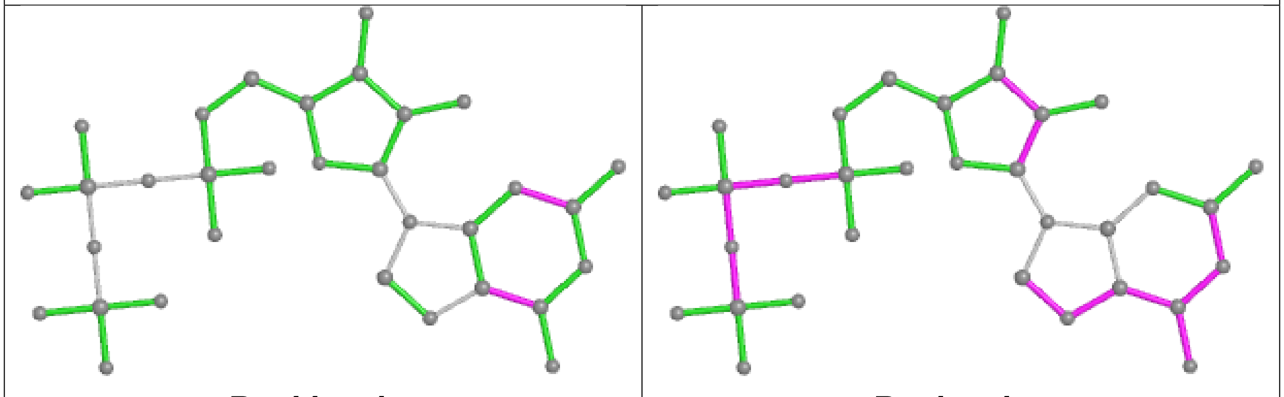


Bond lengths **Bond angles**

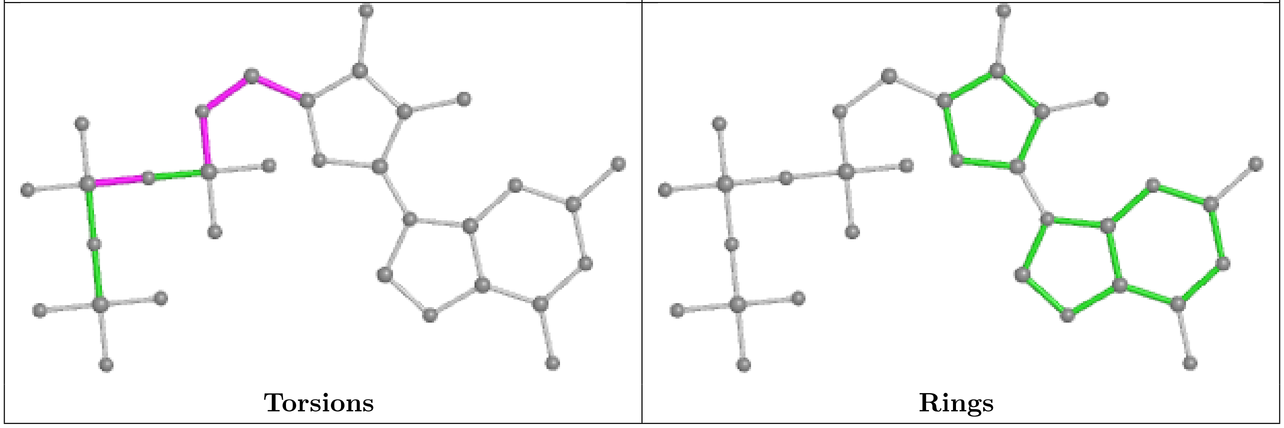


Torsions **Rings**

Ligand GTP QG 501

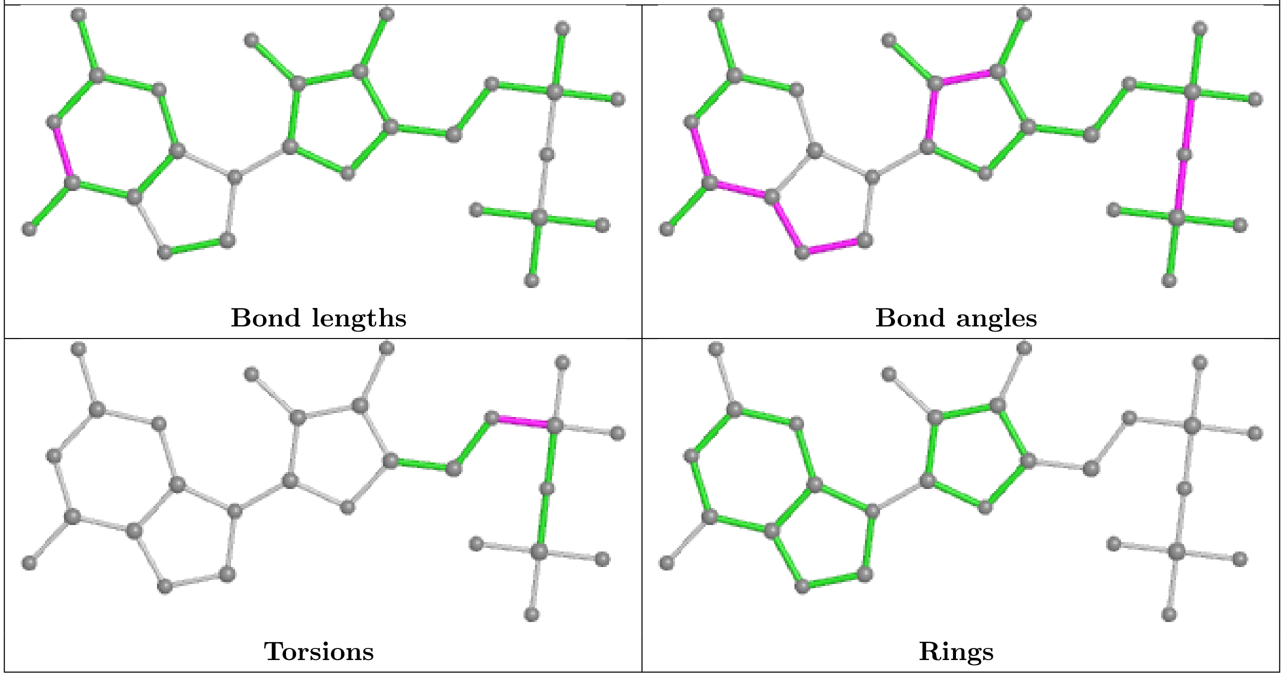


Bond lengths **Bond angles**



Torsions **Rings**

Ligand GDP BD 502



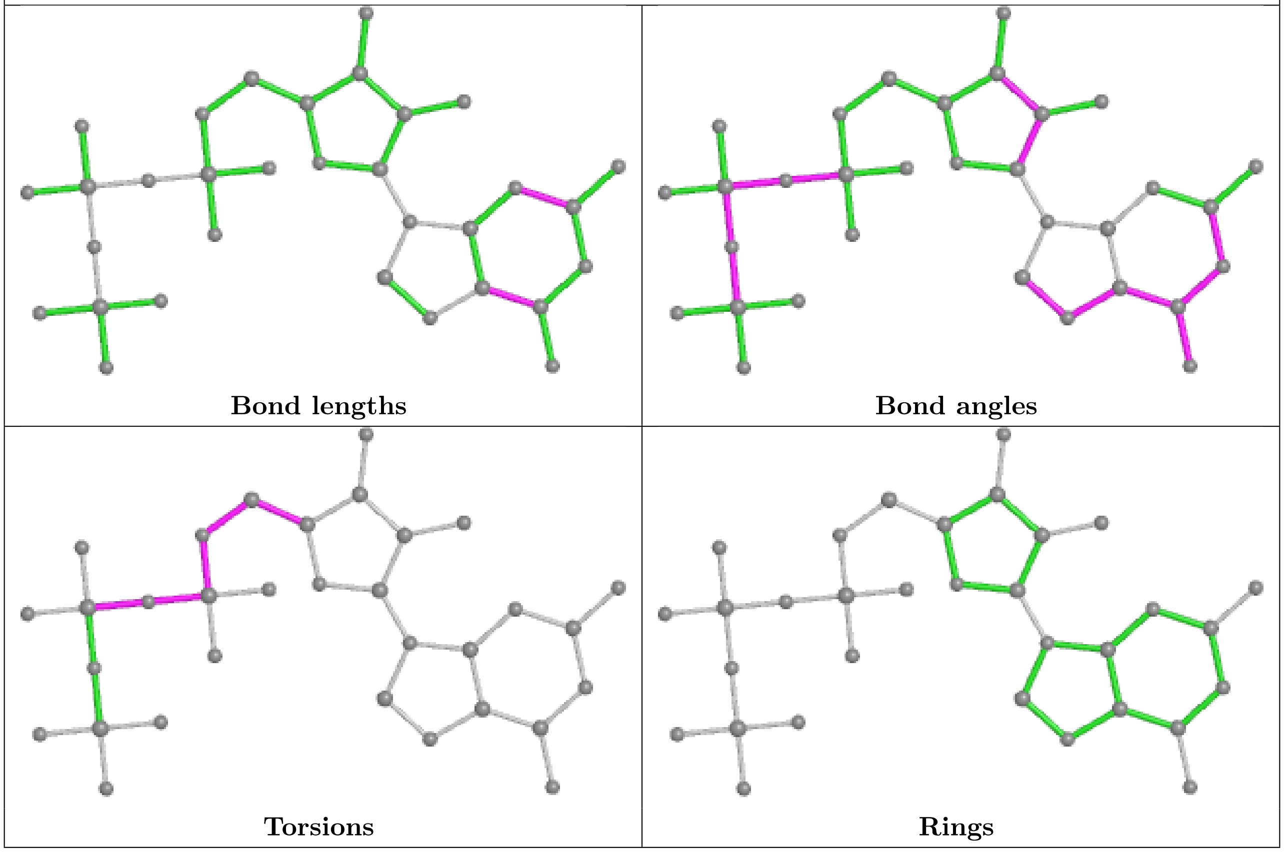
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP UC 501



Bond lengths

Bond angles

Torsions

Rings

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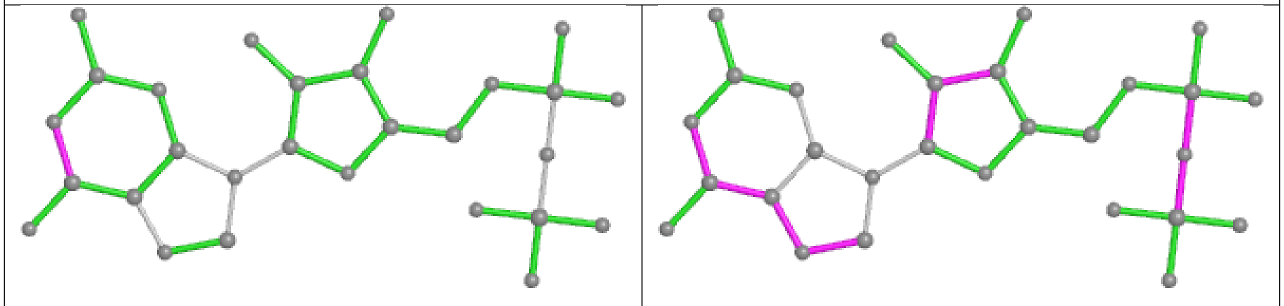
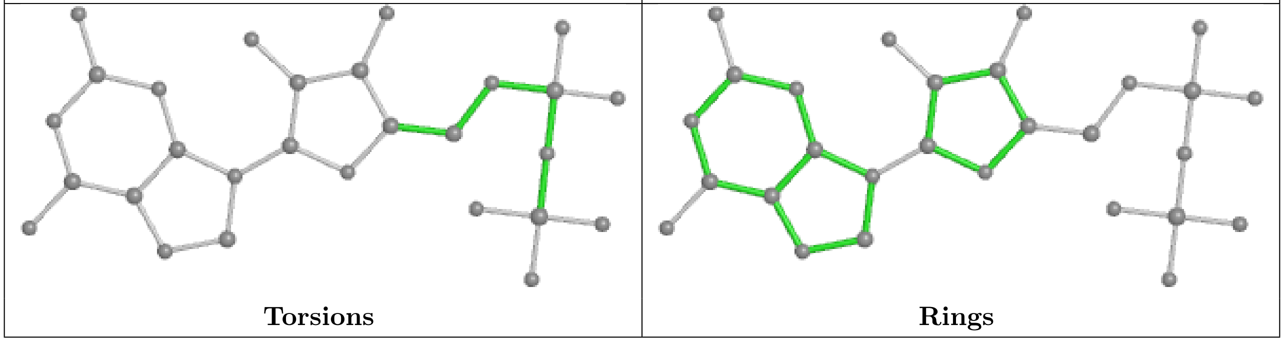


Bond lengths

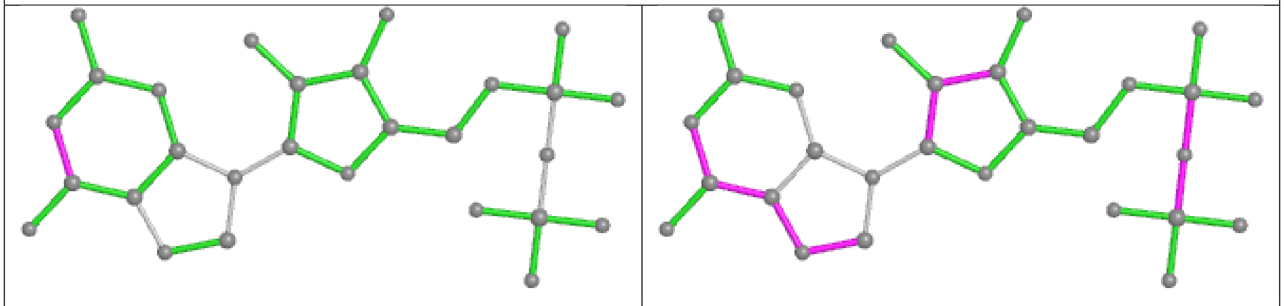
Bond angles



Torsions

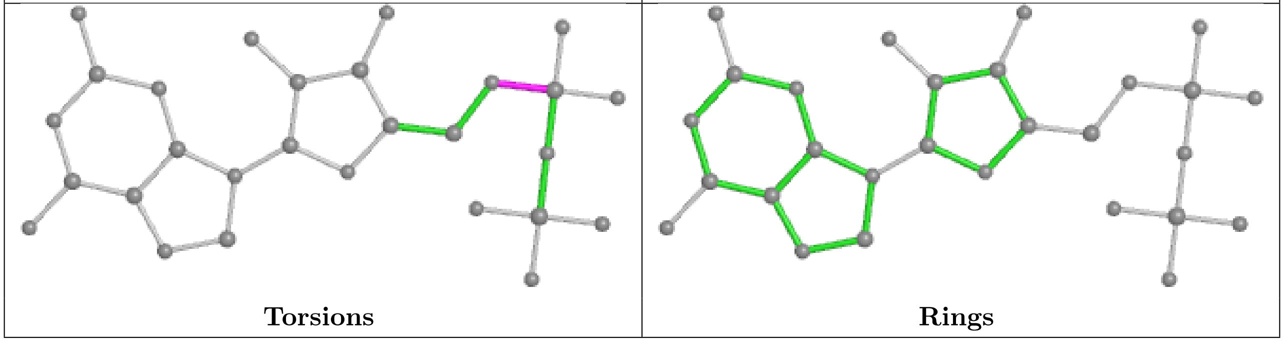
Rings

Ligand GDP VF 502



Bond lengths

Bond angles



Torsions

Rings

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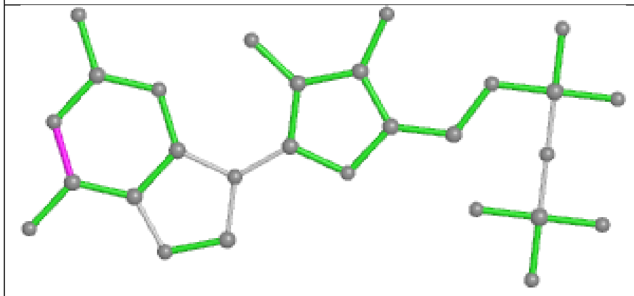

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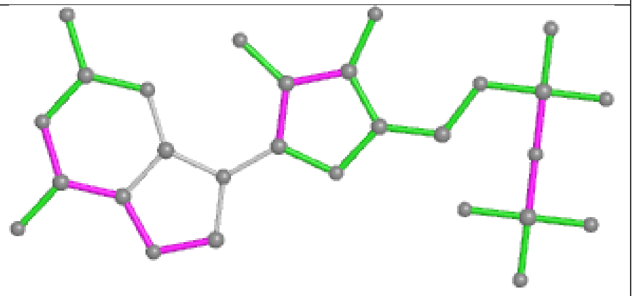
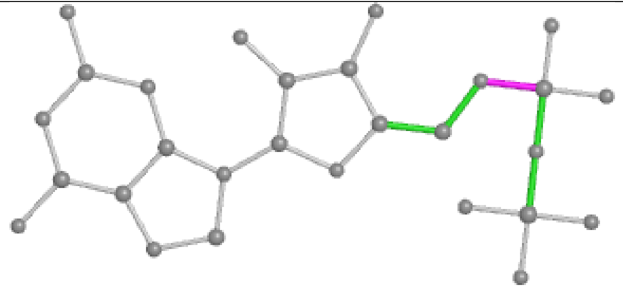


Bond angles



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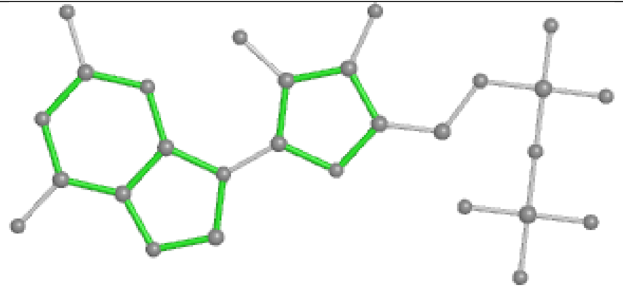
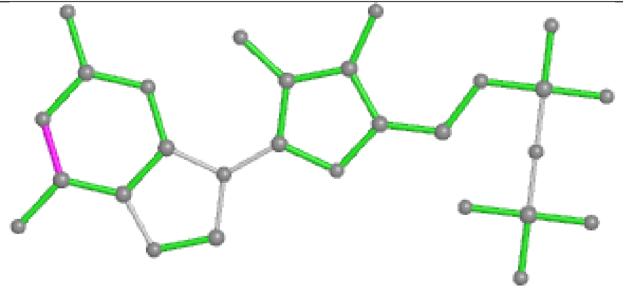


Rings

Ligand GDP OF 502



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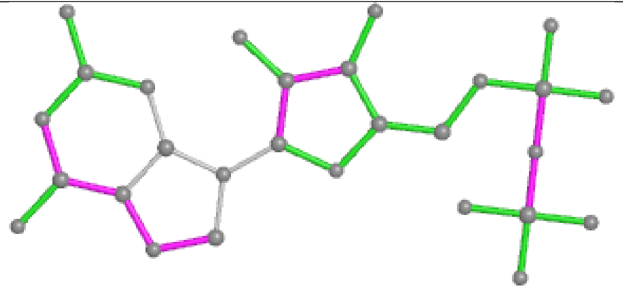

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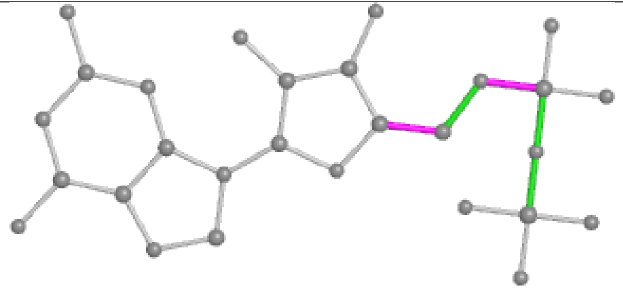

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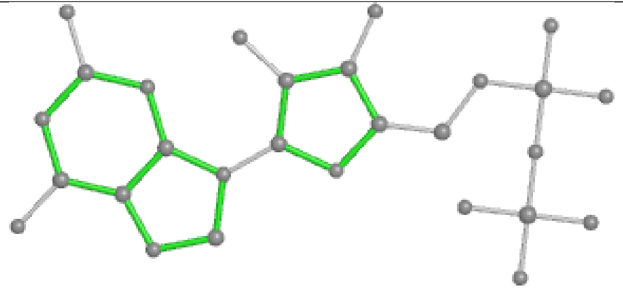
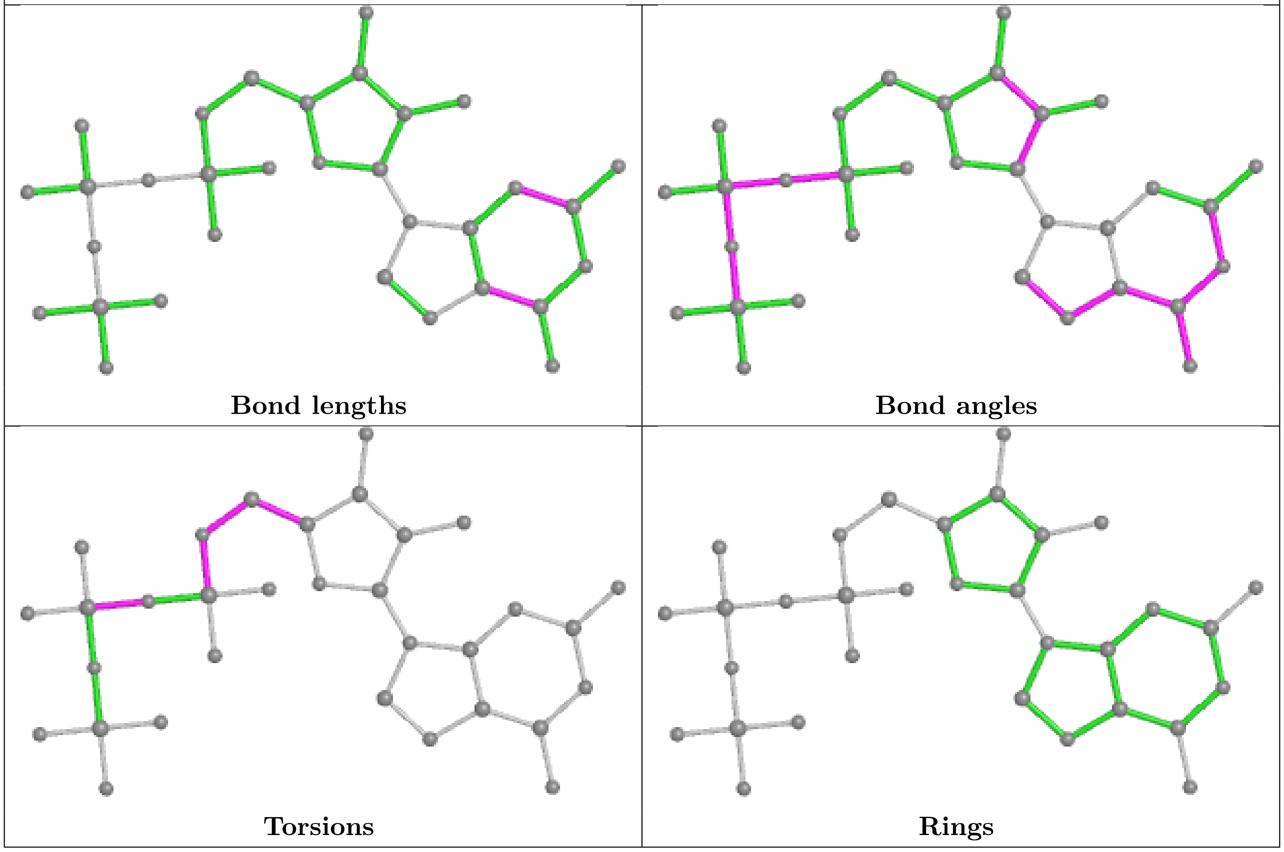


Rings

Ligand GTP NI 501



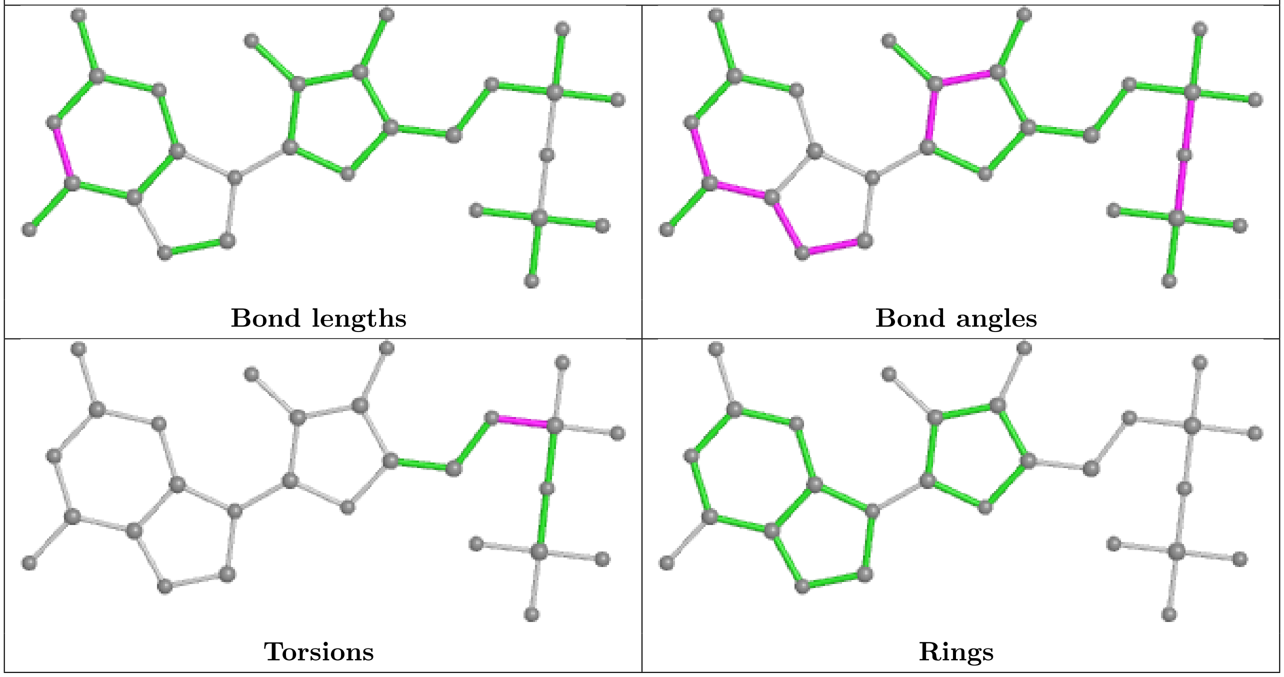
Bond lengths

Bond angles

Torsions

Rings

Ligand GDP HP 502



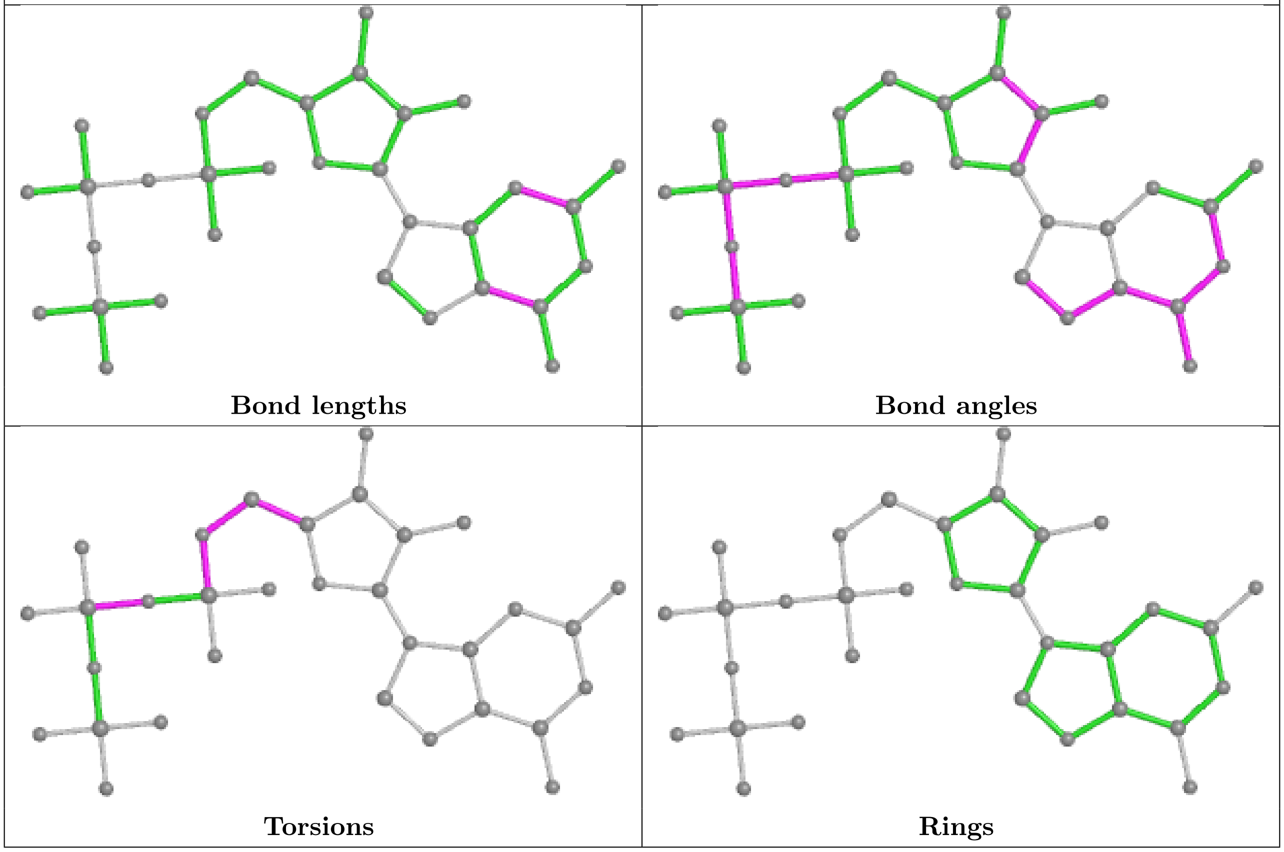
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP RE 501



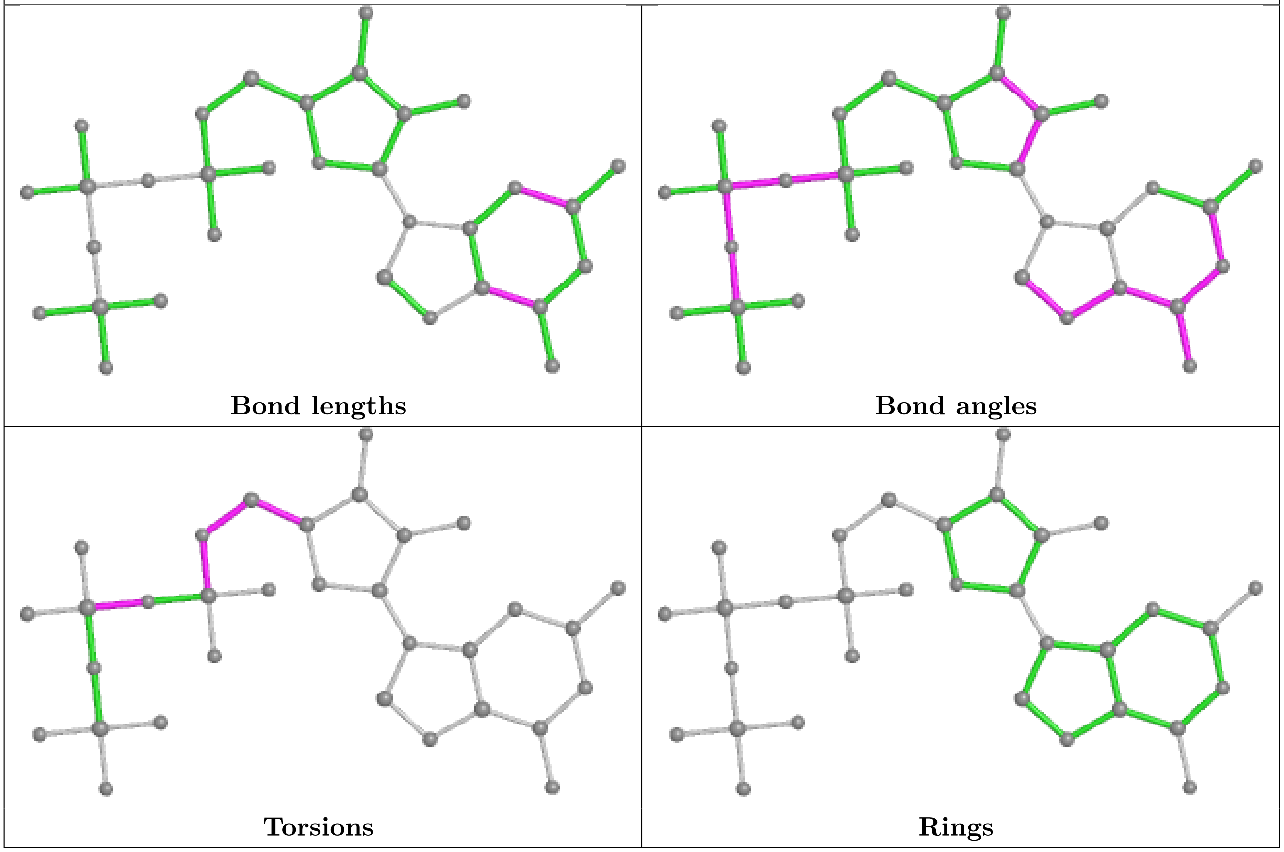
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP QK 501



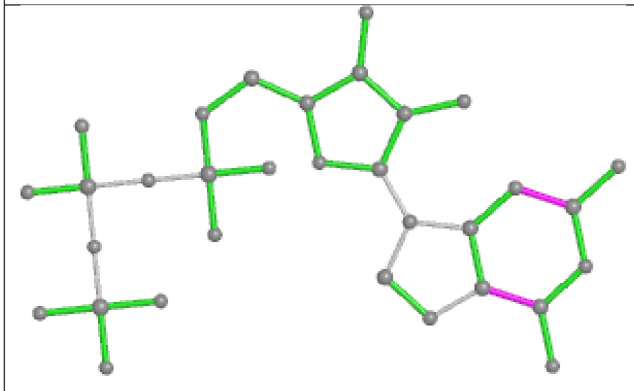
Bond lengths

Bond angles

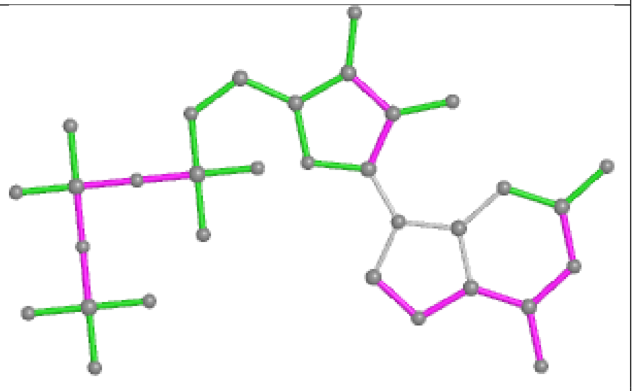
Torsions

Rings

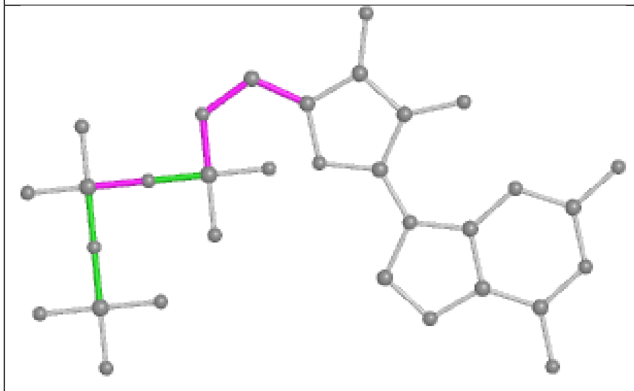
Ligand GTP EA 501



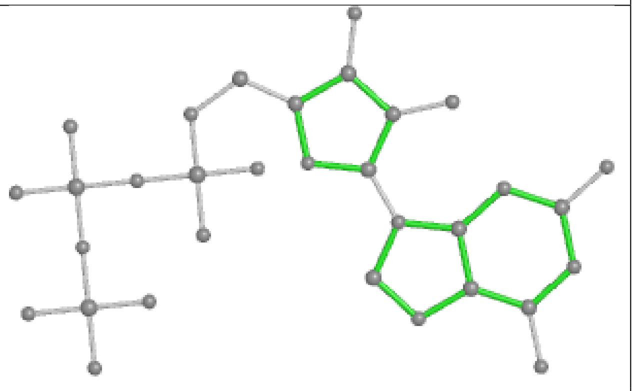
Bond lengths



Bond angles

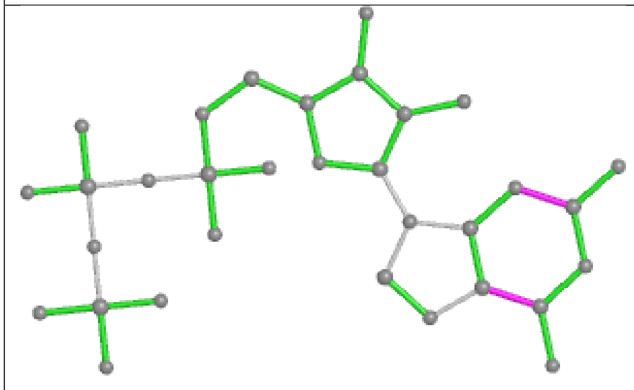


Torsions

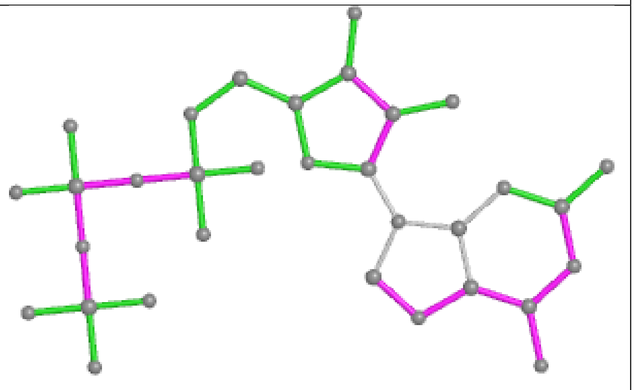


Rings

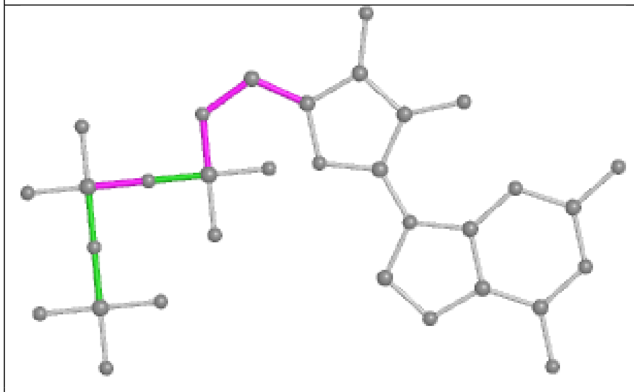
Ligand GTP UA 501



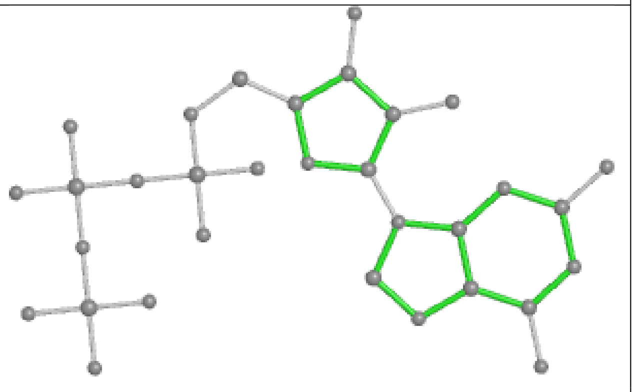
Bond lengths



Bond angles

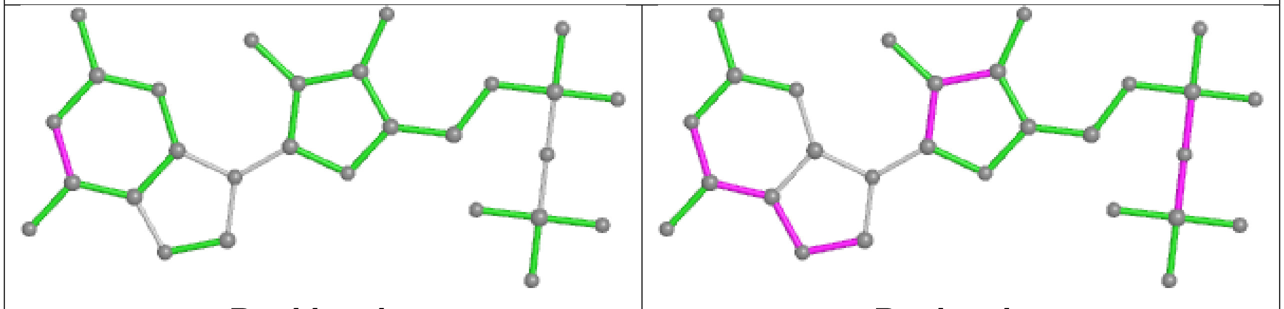


Torsions



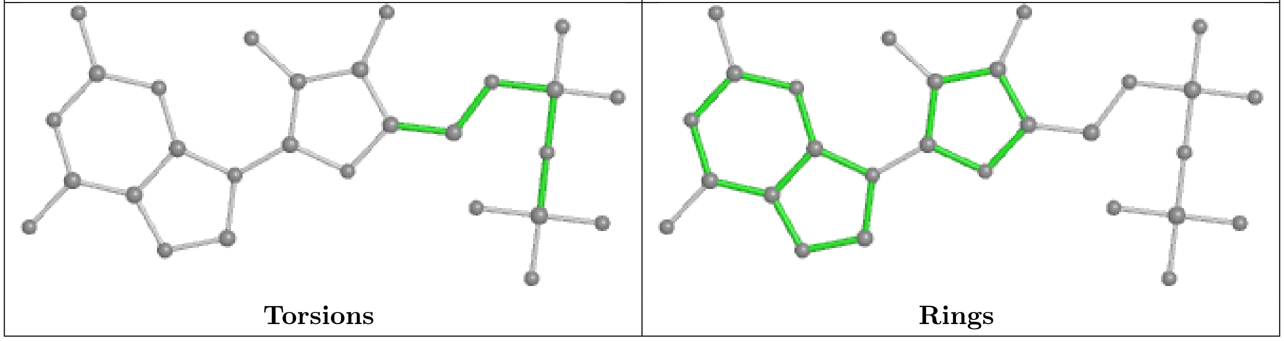
Rings

Ligand GDP HJ 502



Bond lengths

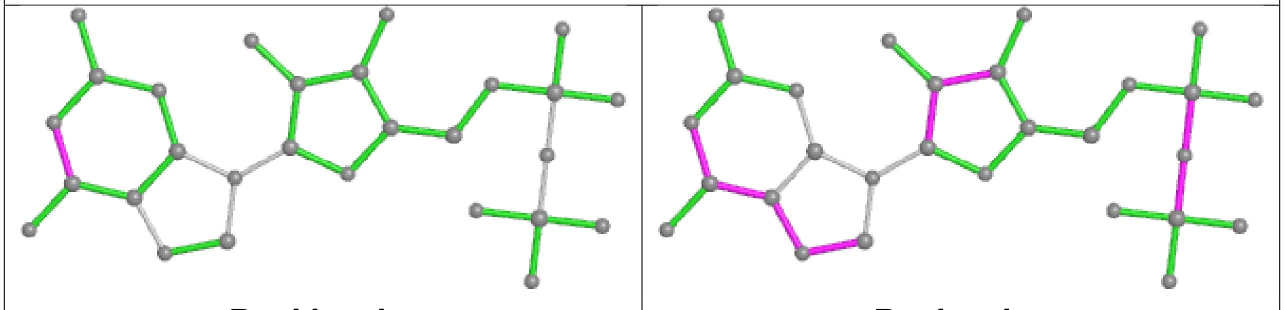
Bond angles



Torsions

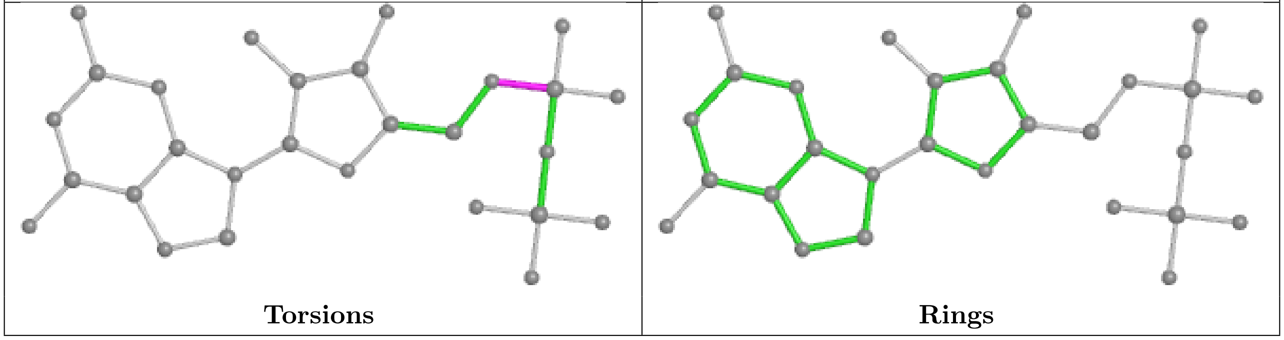
Rings

Ligand GDP QF 502



Bond lengths

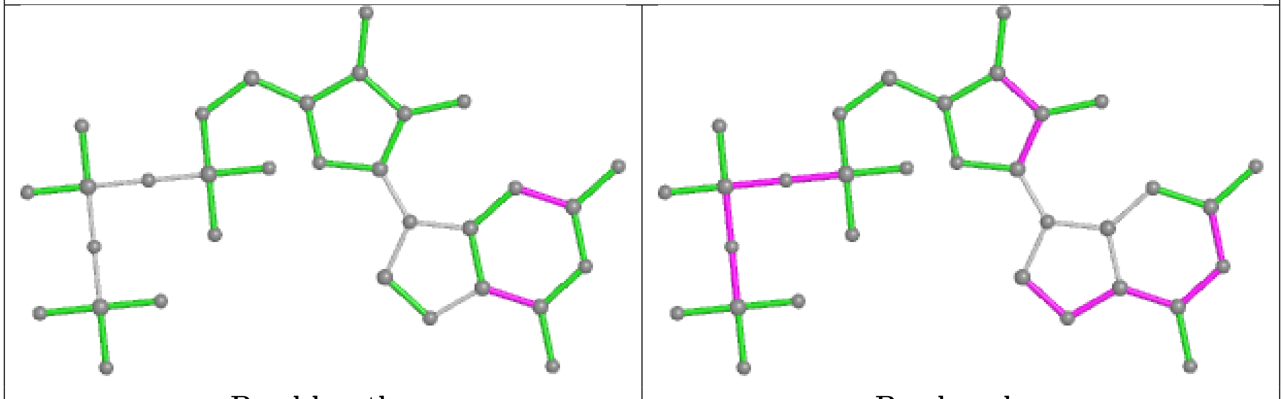
Bond angles



Torsions

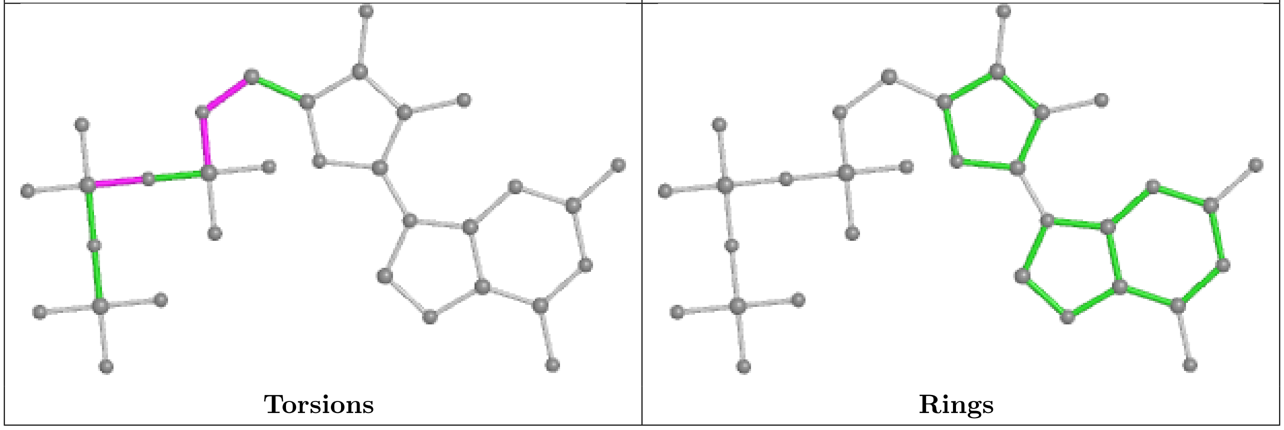
Rings

Ligand GTP GG 501



Bond lengths

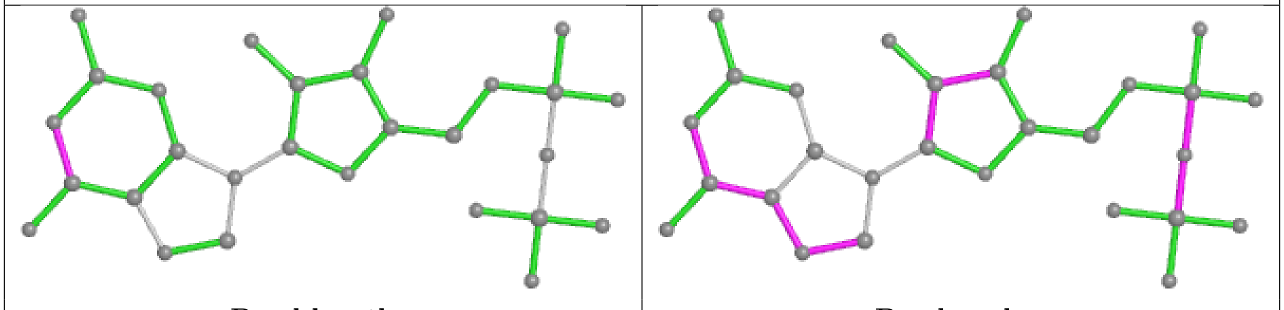
Bond angles



Torsions

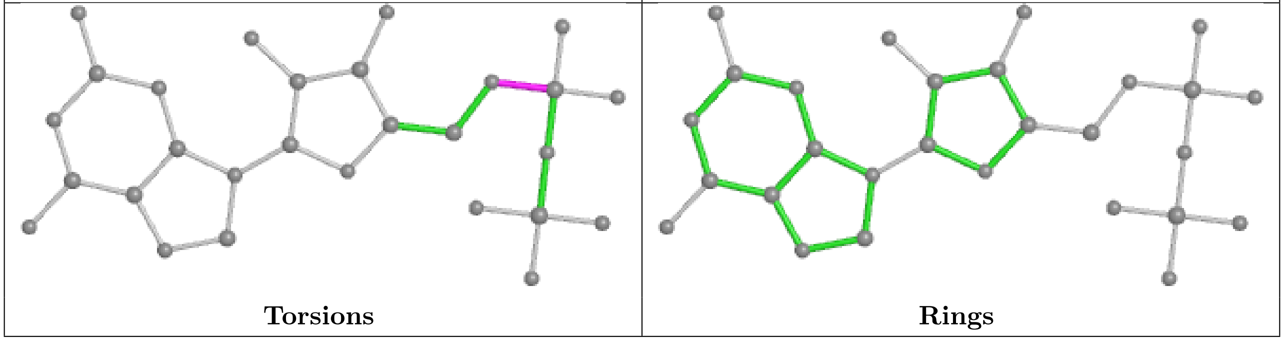
Rings

Ligand GDP PJ 502



Bond lengths

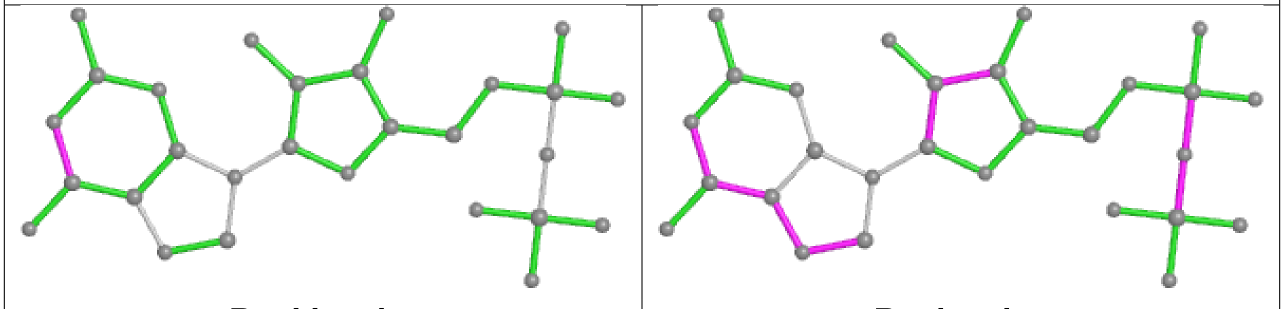
Bond angles



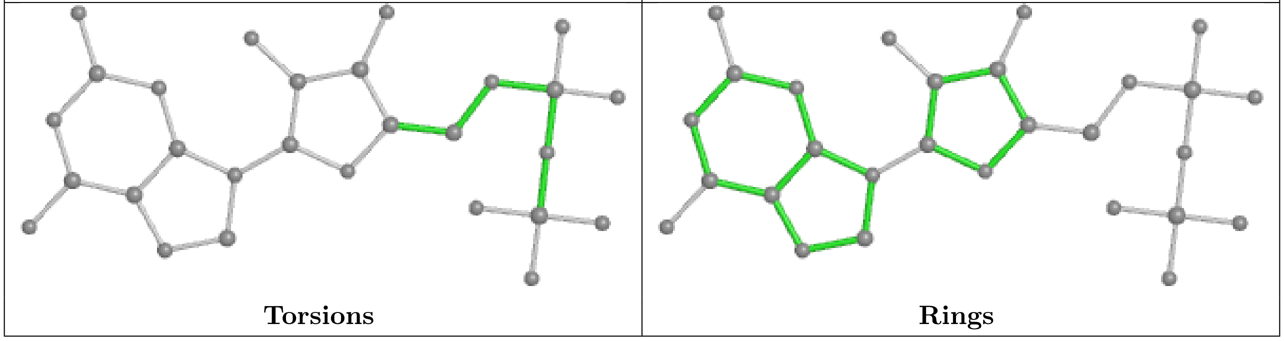
Torsions

Rings

Ligand GDP QJ 502

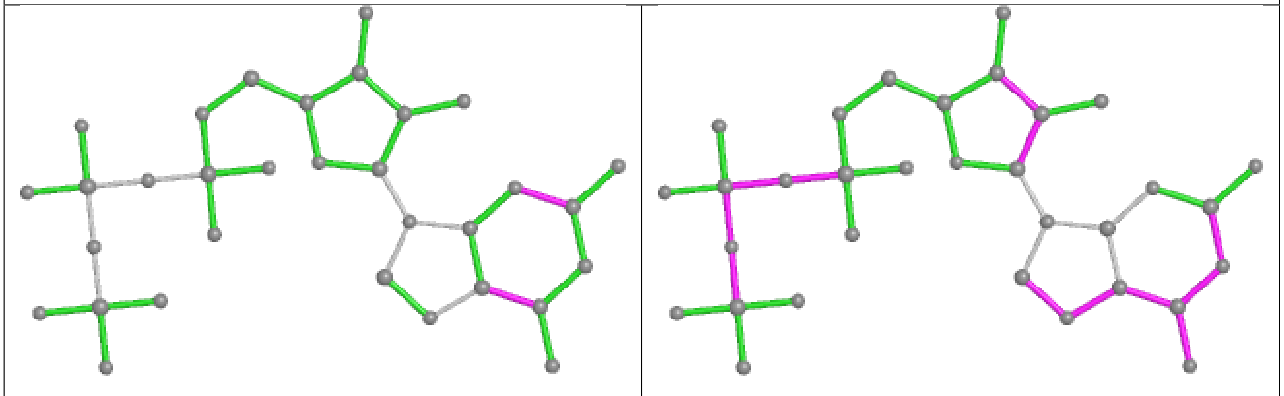


Bond lengths **Bond angles**

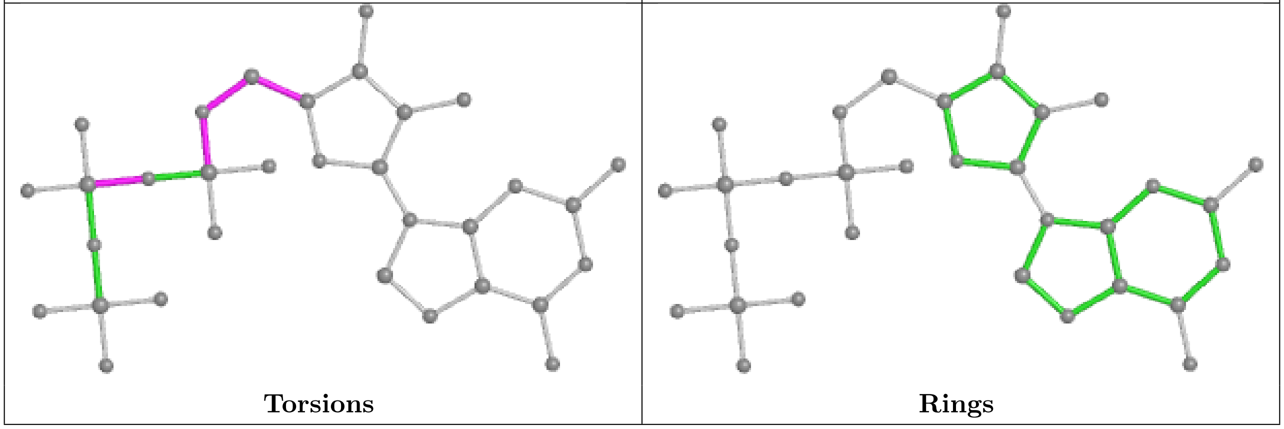


Torsions **Rings**

Ligand GTP UO 501

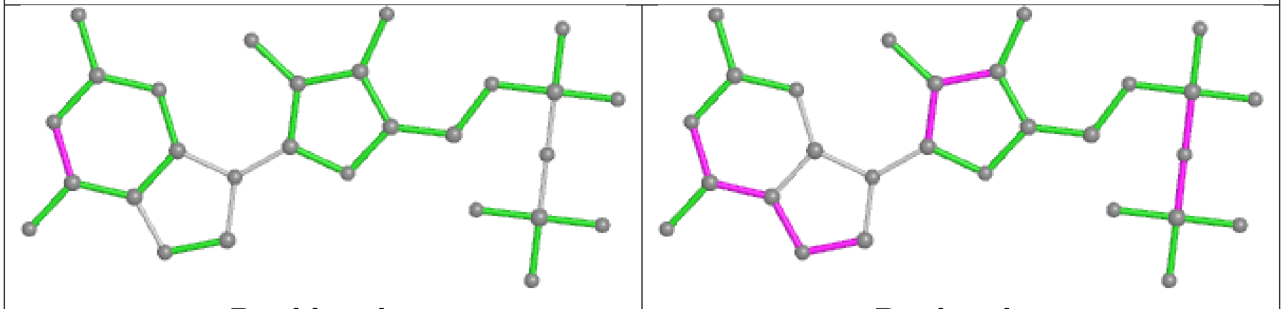


Bond lengths **Bond angles**



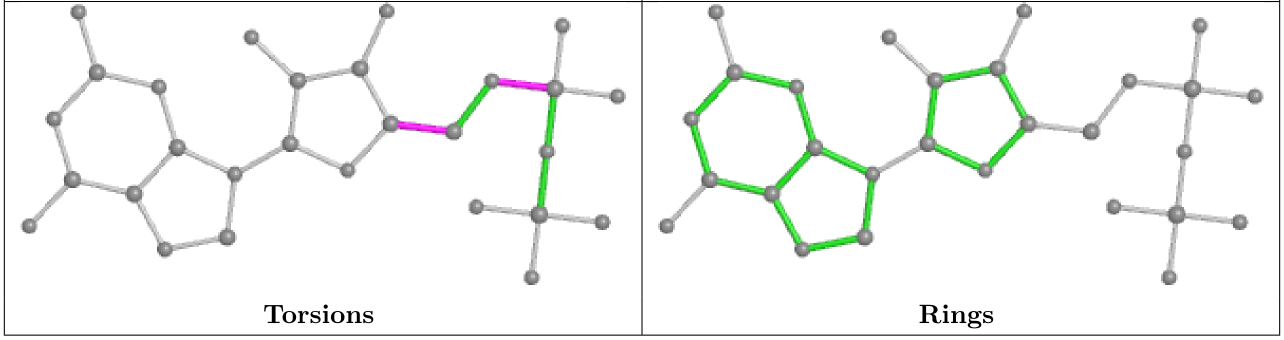
Torsions **Rings**

Ligand GDP OB 502



Bond lengths

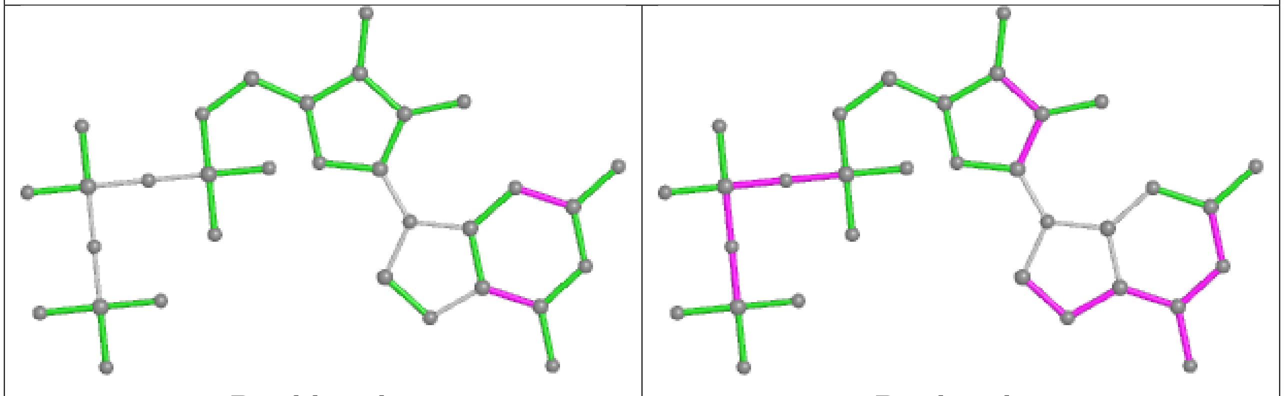
Bond angles



Torsions

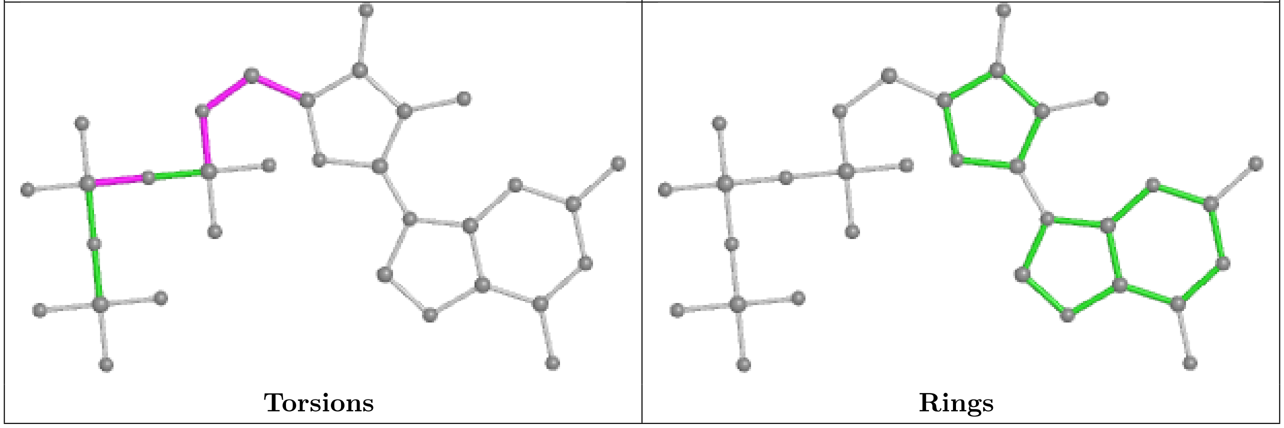
Rings

Ligand GTP IK 501



Bond lengths

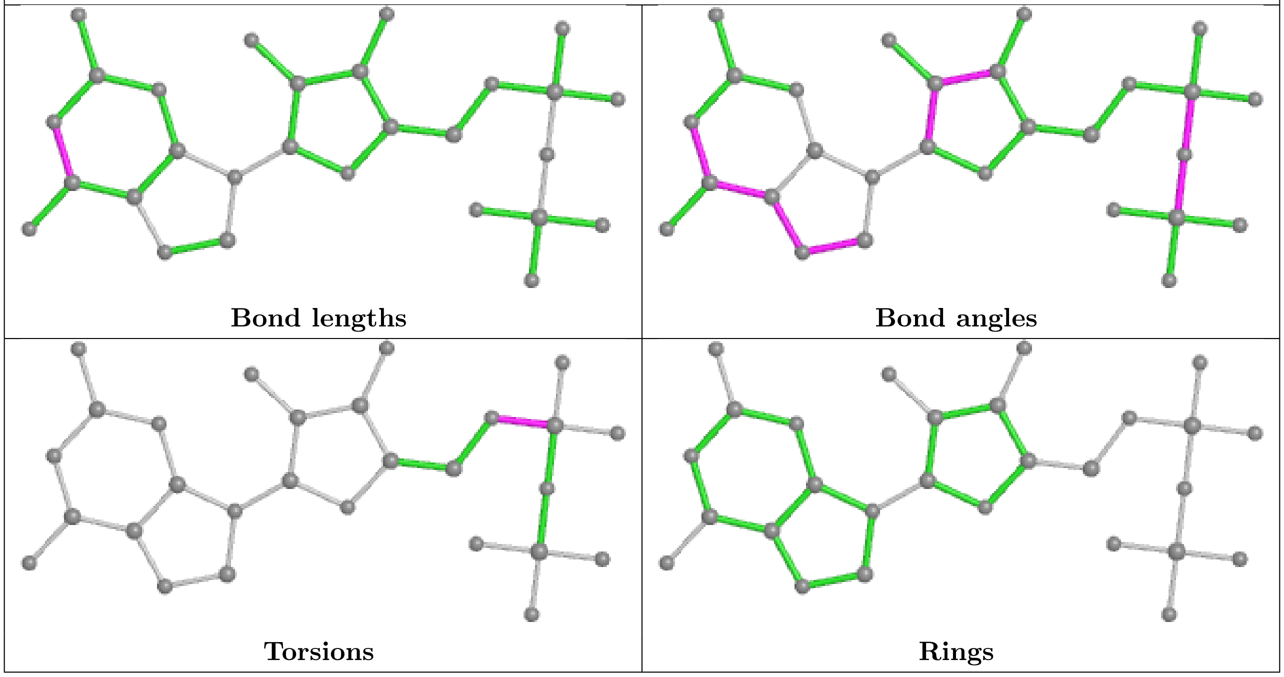
Bond angles



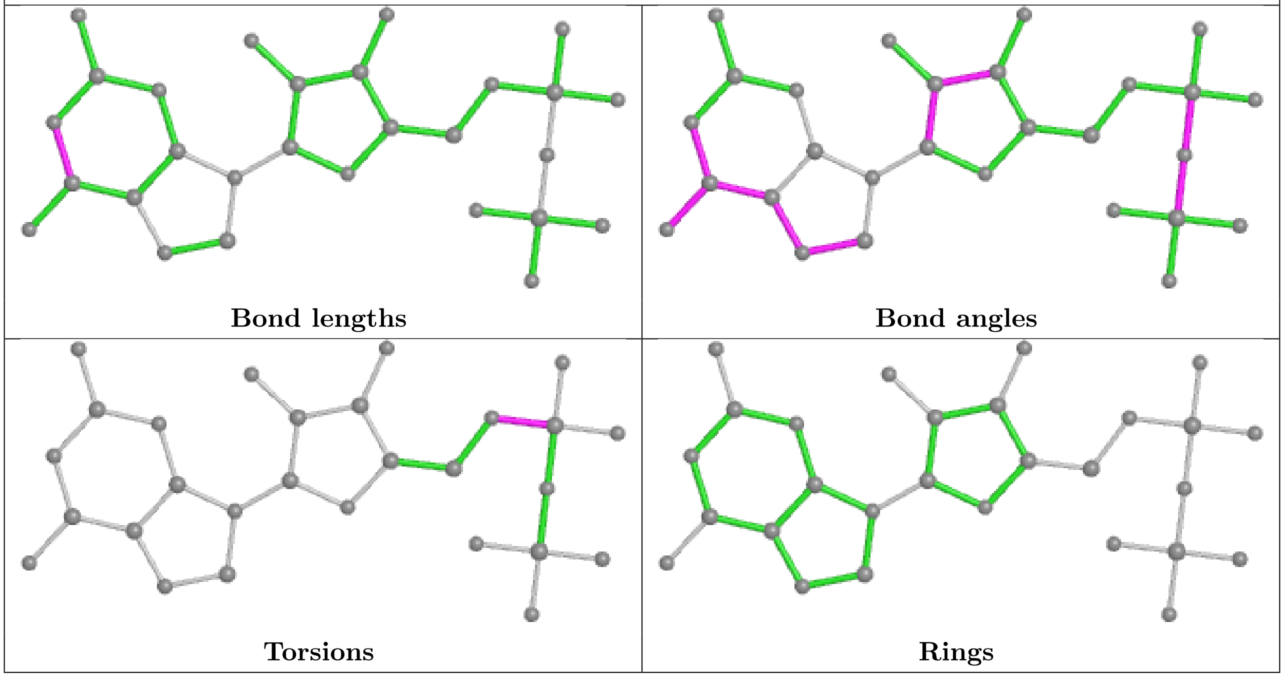
Torsions

Rings

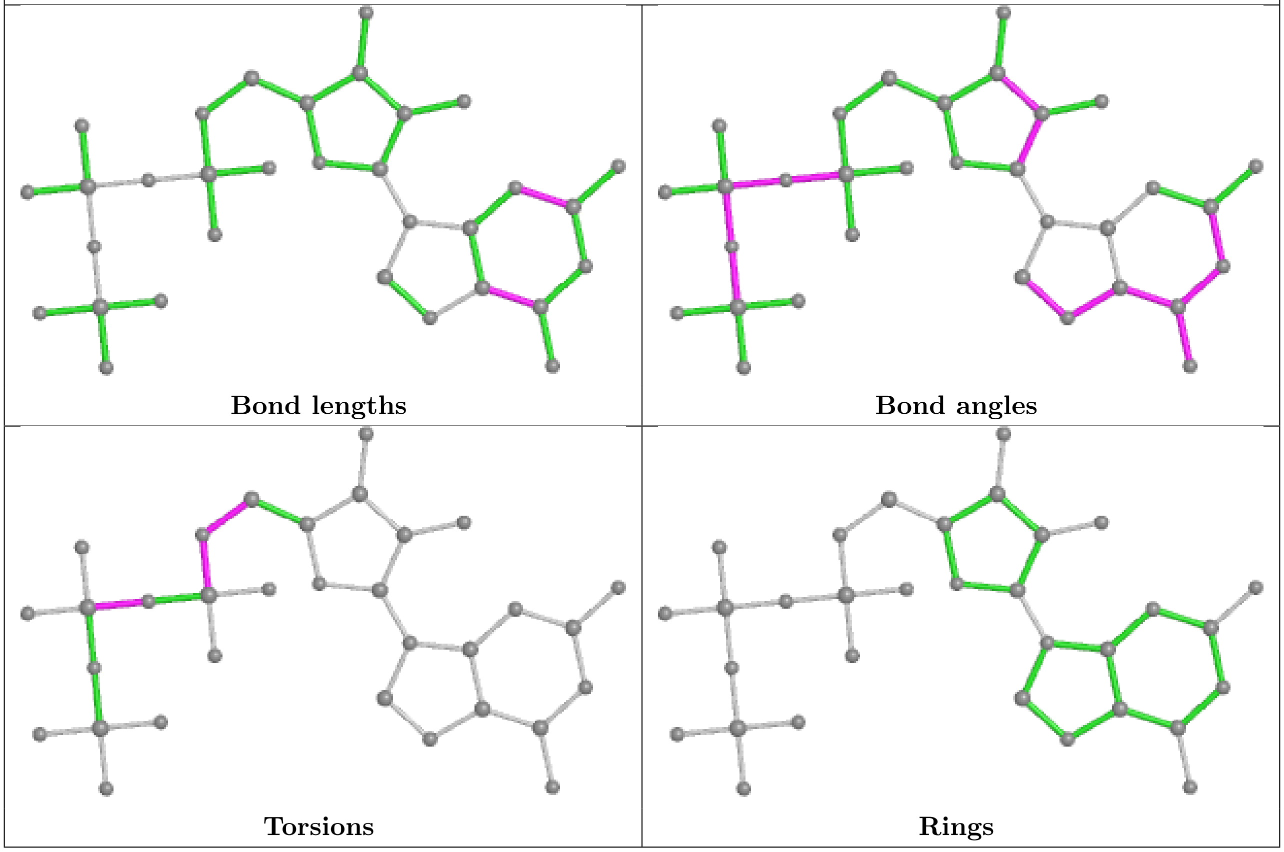
Ligand GDP EL 502



Ligand GDP KF 502



Ligand GTP FG 501



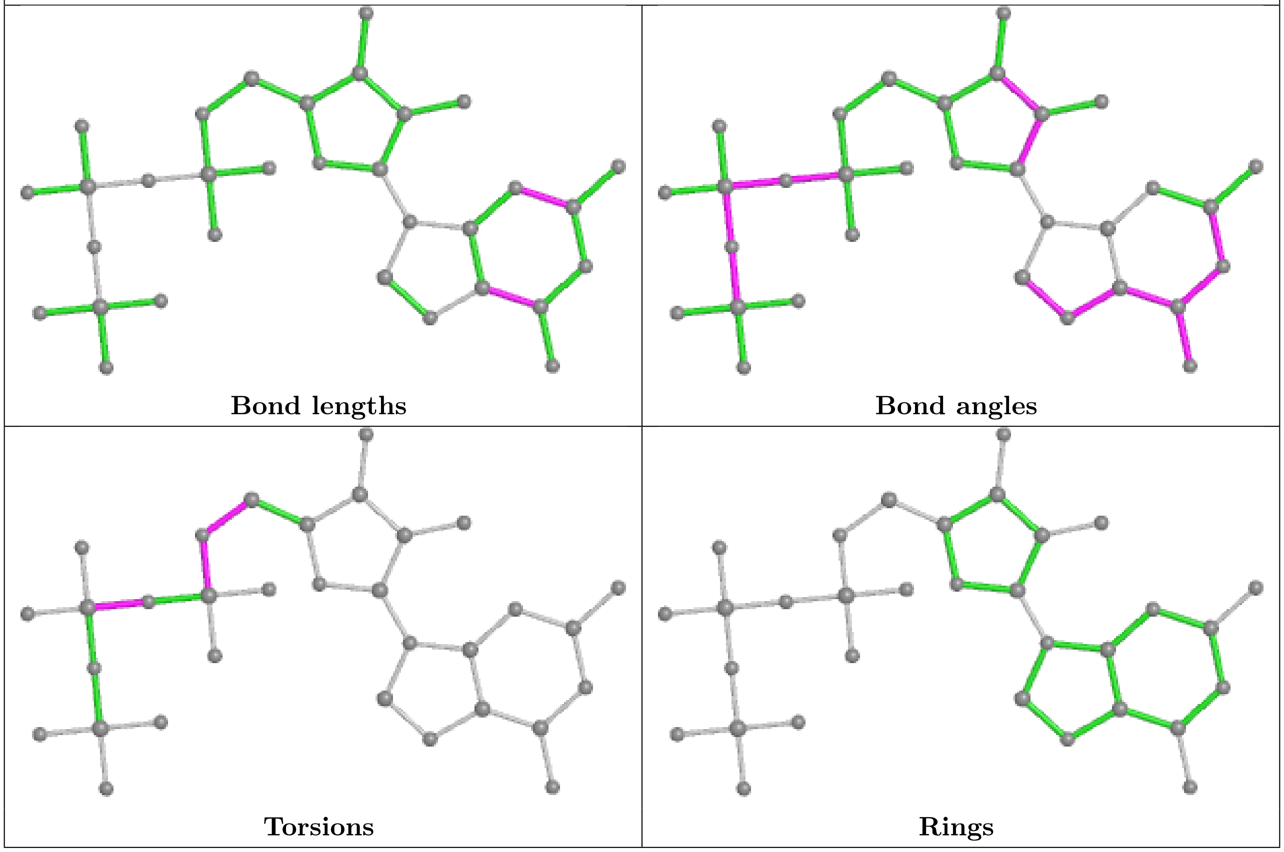
Bond lengths

Bond angles

Torsions

Rings

Ligand GTP KG 501



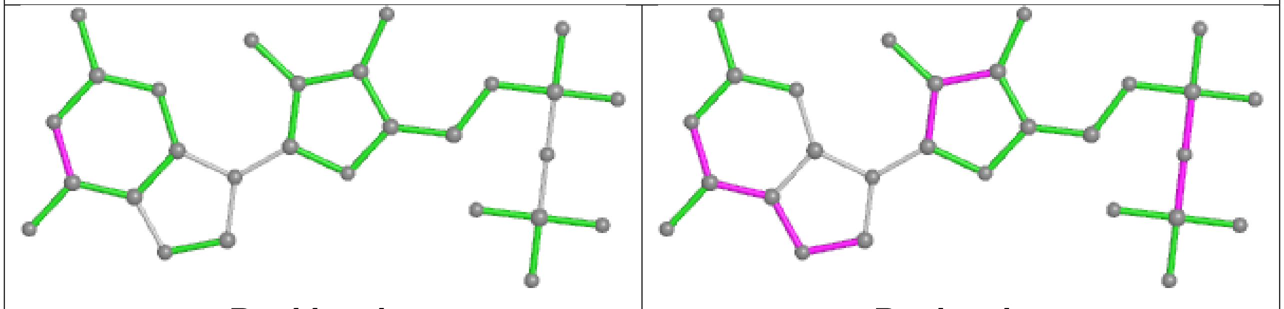
Bond lengths

Bond angles

Torsions

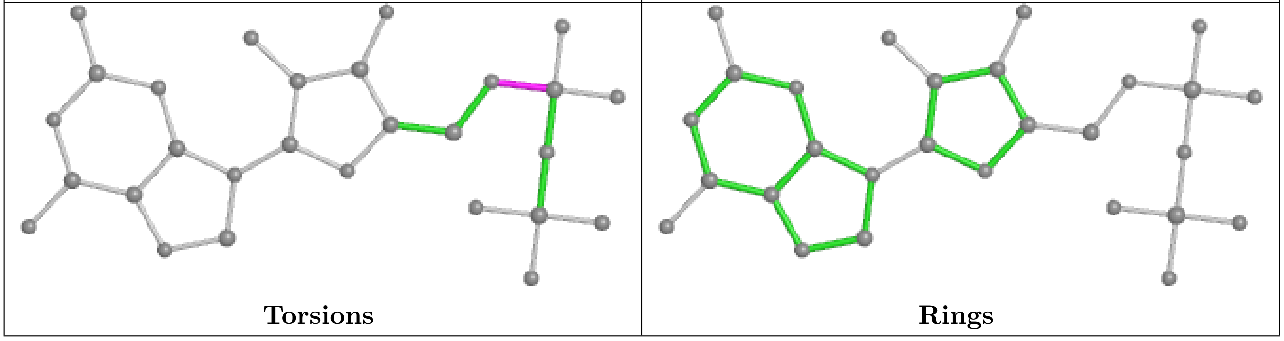
Rings

Ligand GDP TF 502



Bond lengths

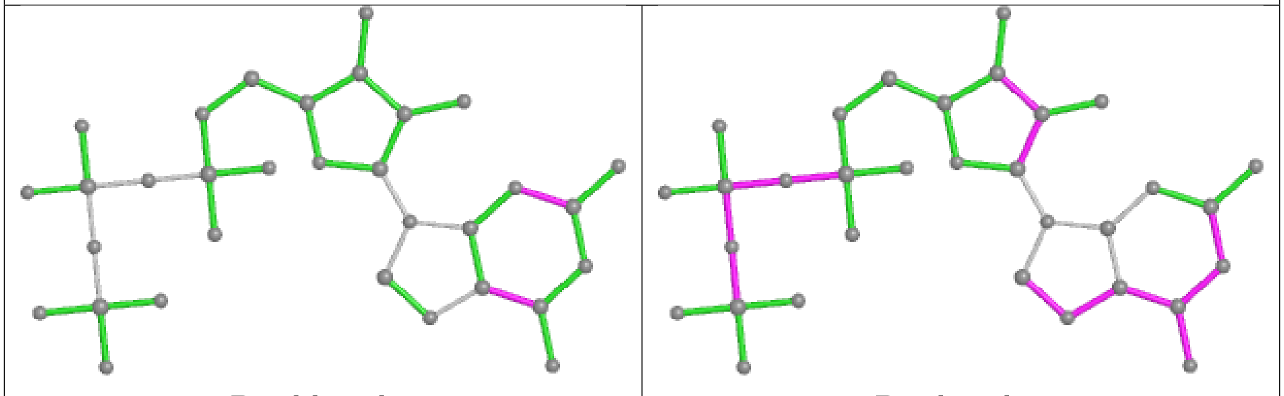
Bond angles



Torsions

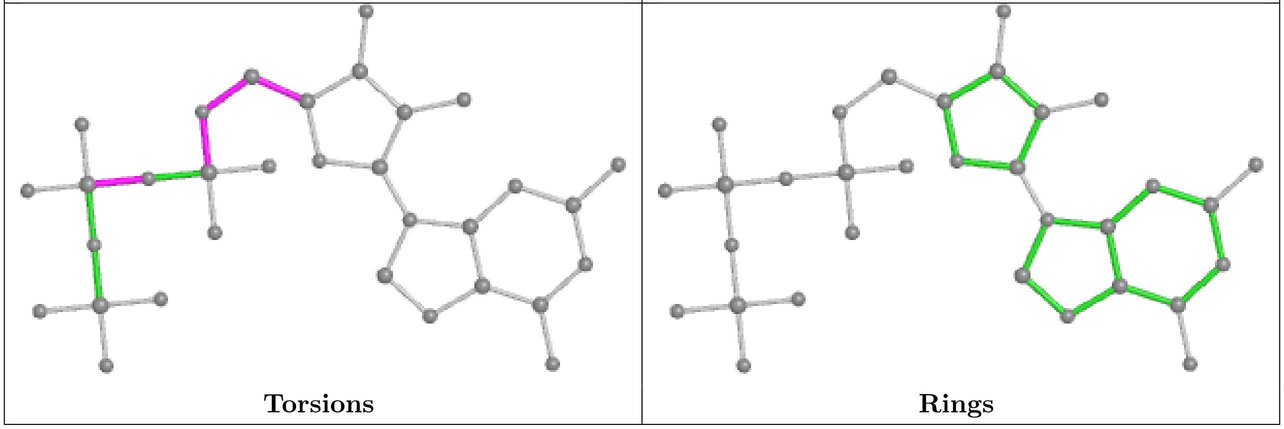
Rings

Ligand GTP SC 501



Bond lengths

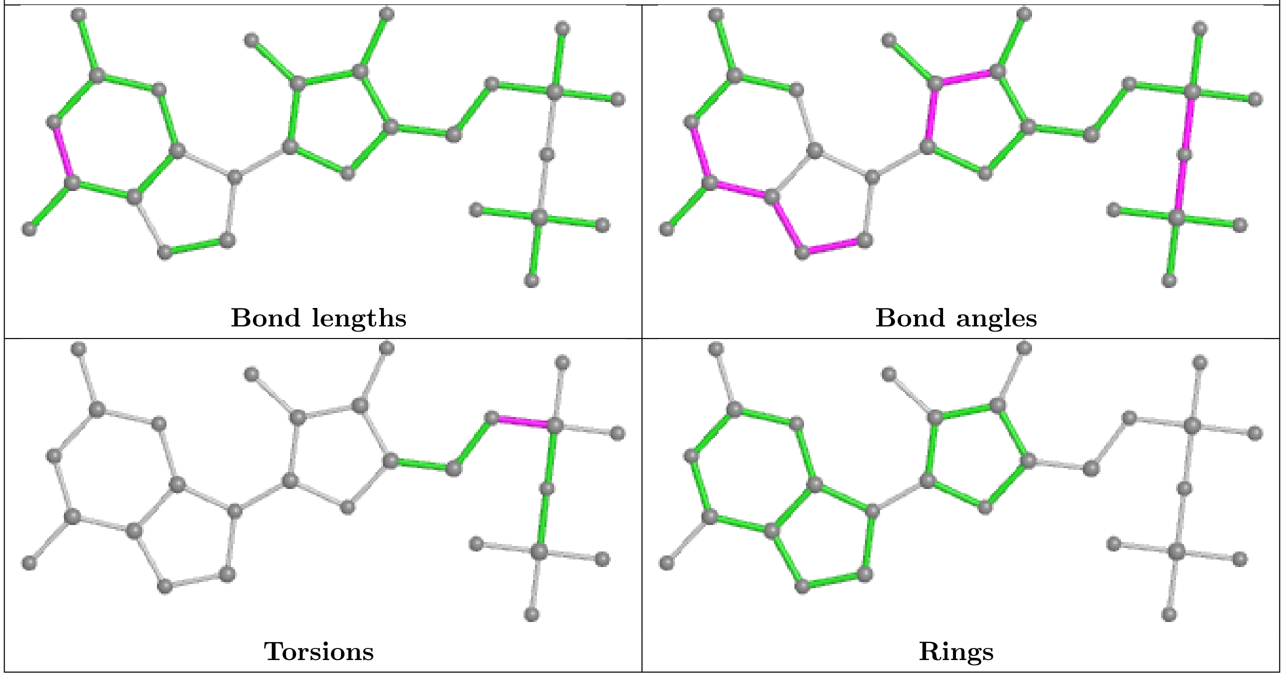
Bond angles



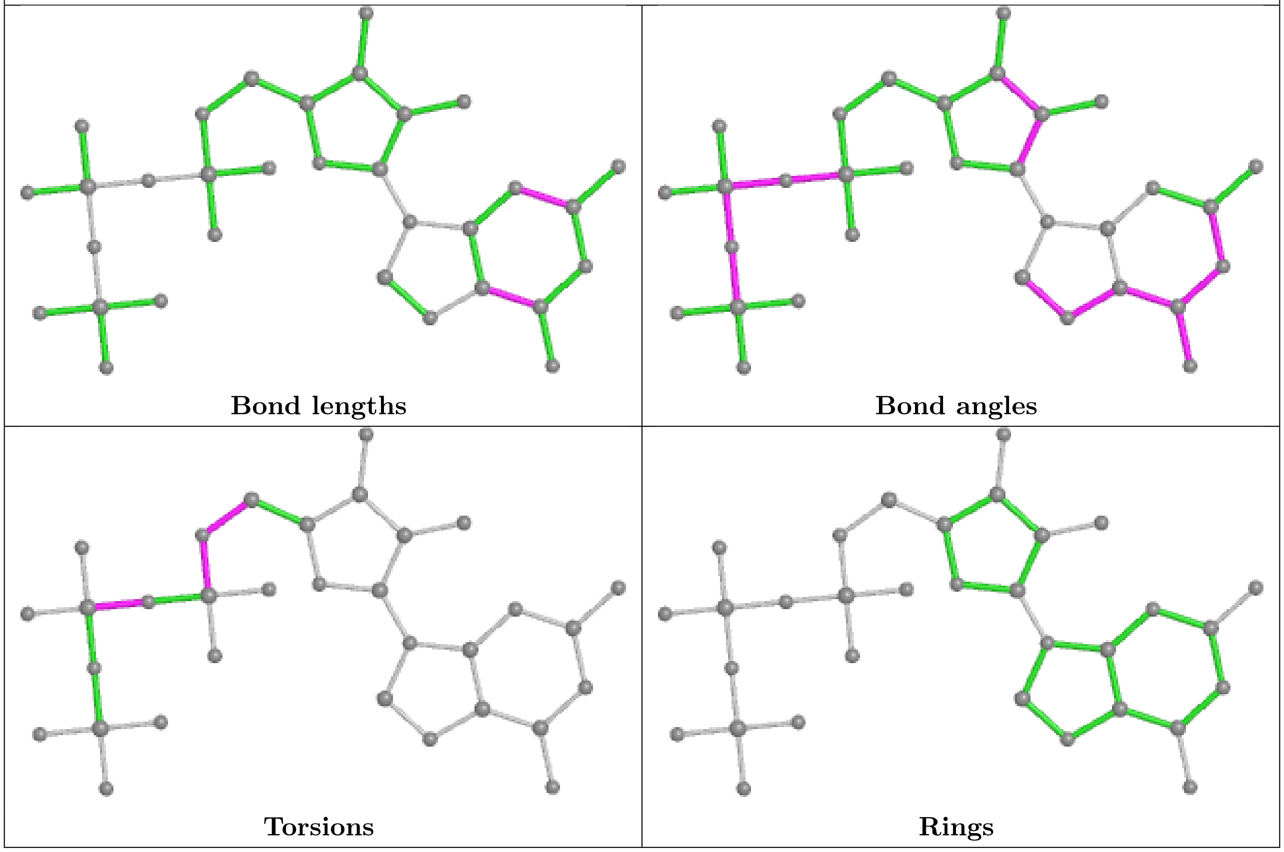
Torsions

Rings

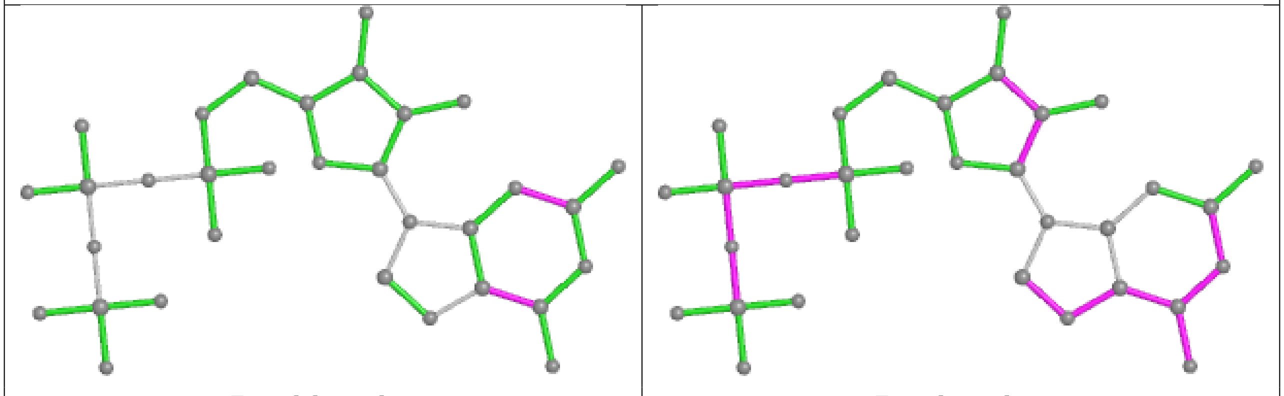
Ligand GDP CL 502



Ligand GTP CI 501

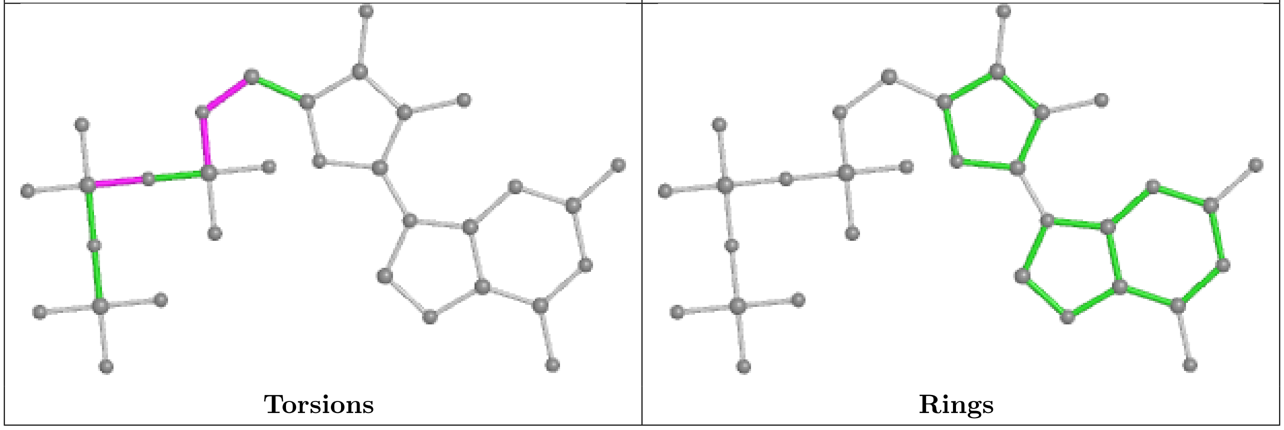


Ligand GTP KK 501



Bond lengths

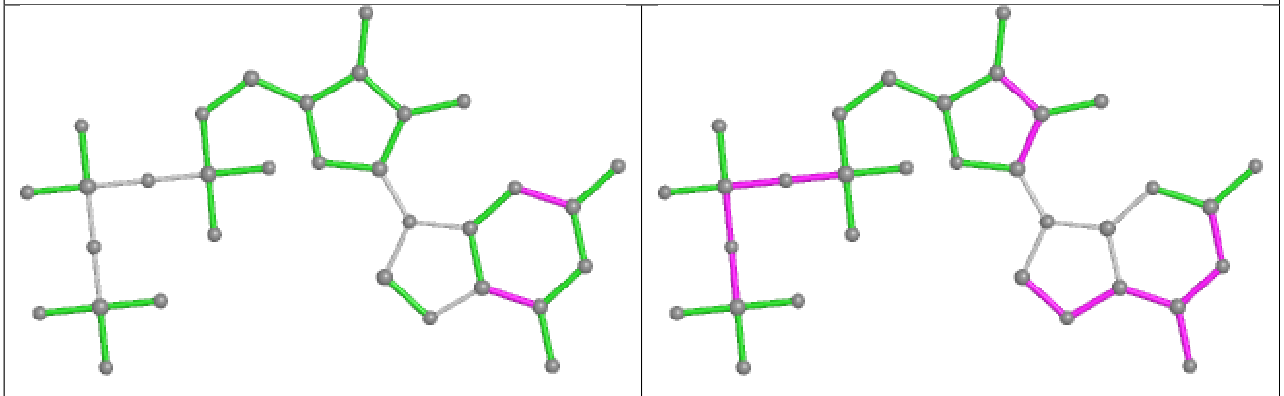
Bond angles



Torsions

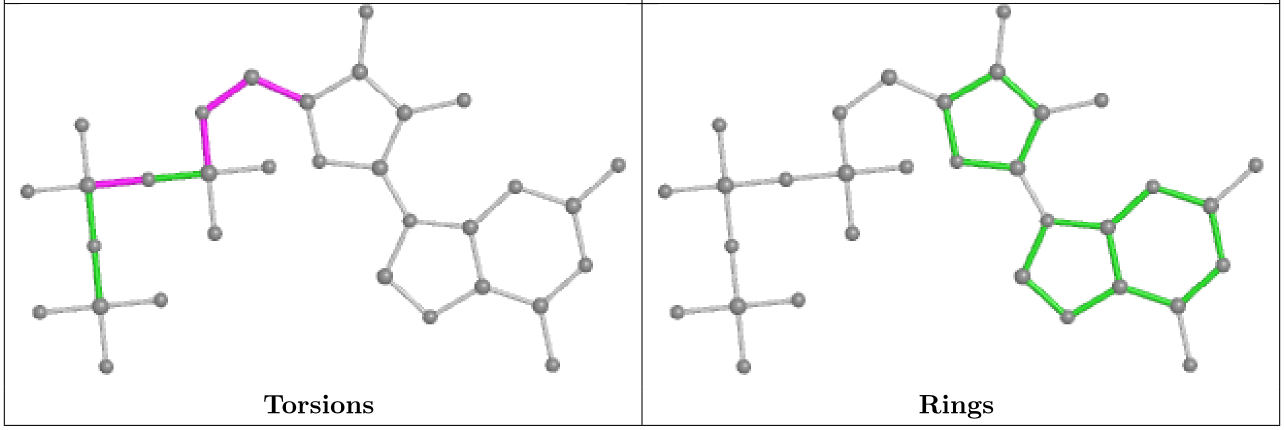
Rings

Ligand GTP WO 501



Bond lengths

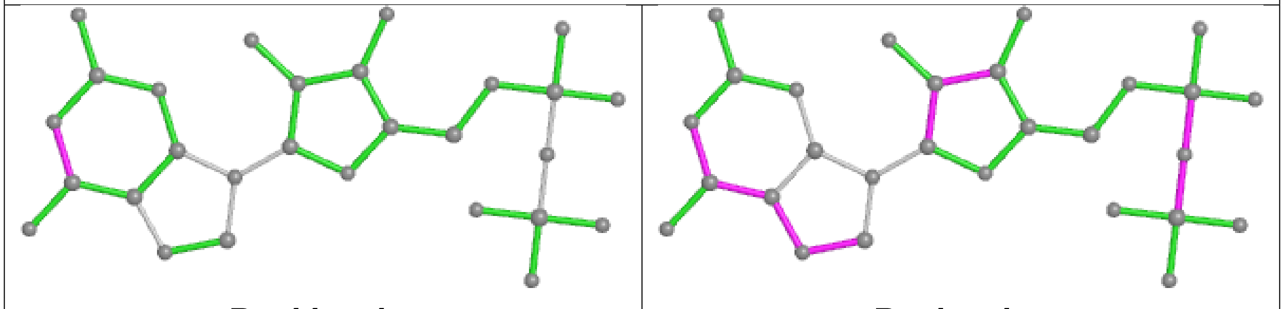
Bond angles



Torsions

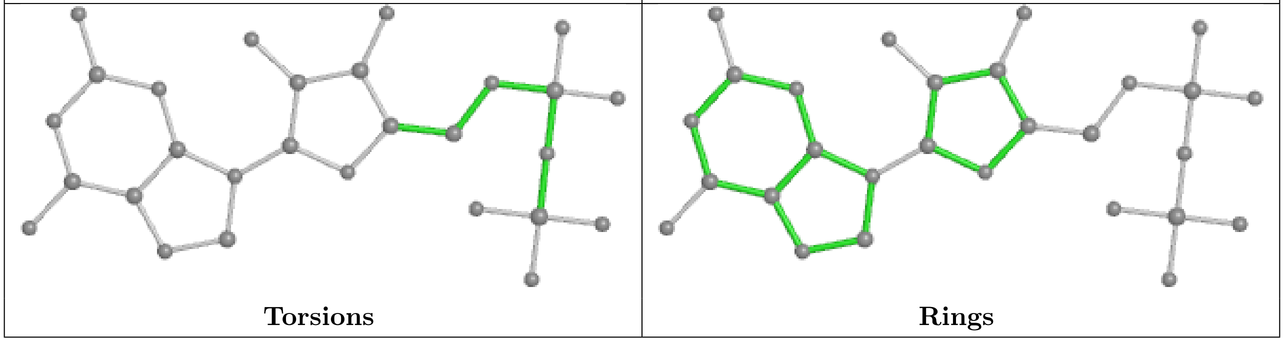
Rings

Ligand GDP JP 502



Bond lengths

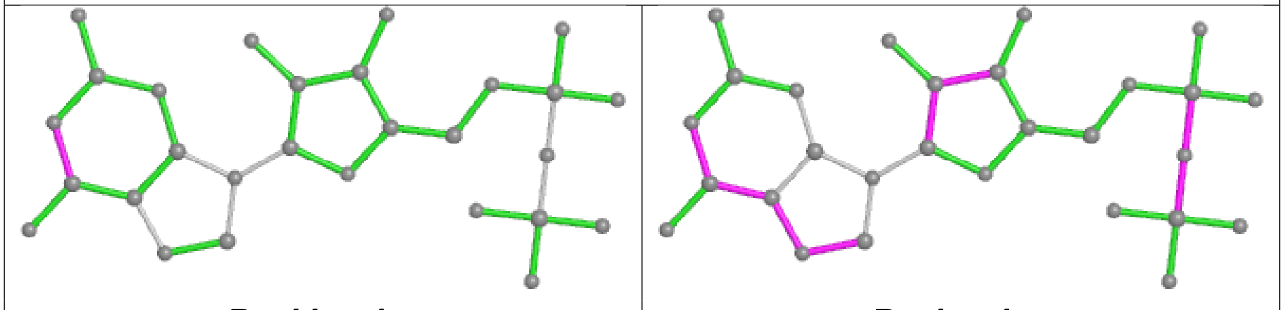
Bond angles



Torsions

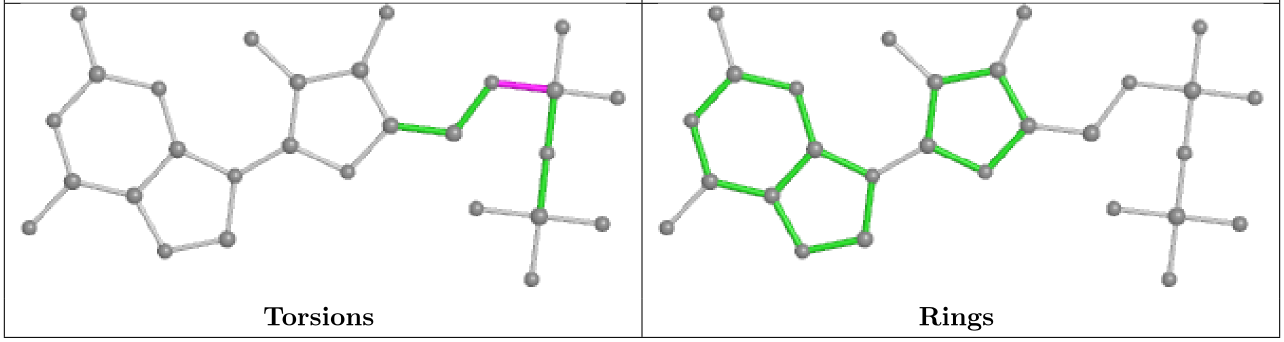
Rings

Ligand GDP IN 502



Bond lengths

Bond angles



Torsions

Rings

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

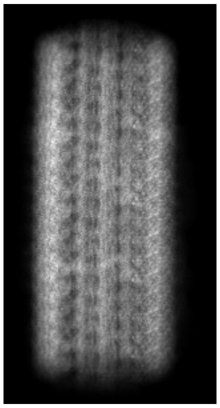
6 Map visualisation

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.

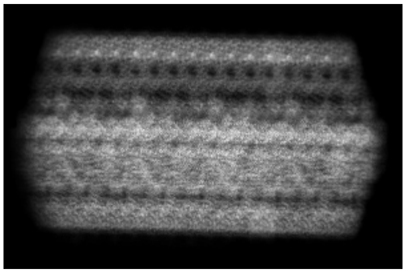
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

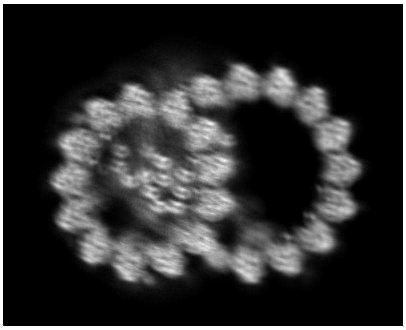
6.1.1 Primary map



X



Y

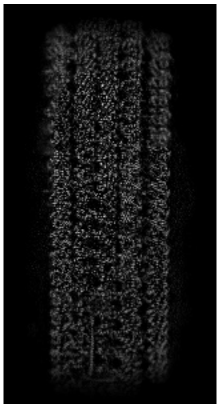


Z

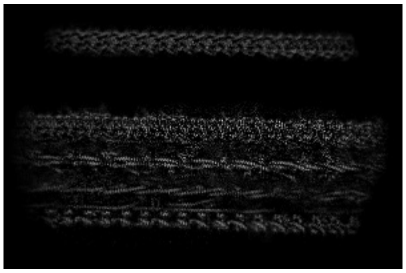
The images above show the map projected in three orthogonal directions.

6.2 Central slices

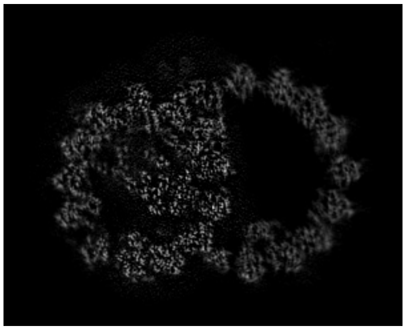
6.2.1 Primary map



X Index: 265



Y Index: 213

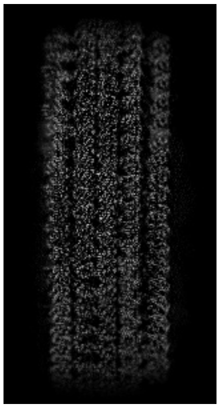


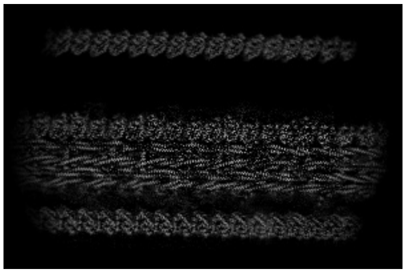
Z Index: 400

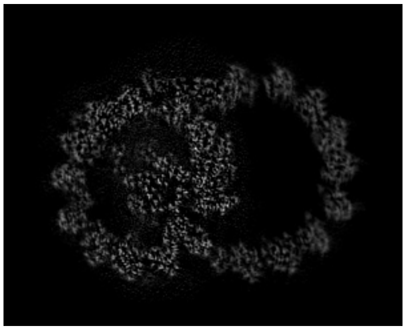
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices

6.3.1 Primary map


X Index: 270

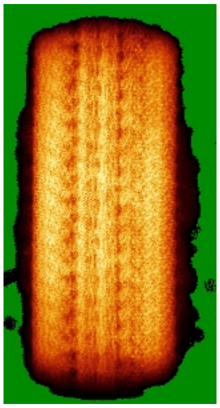

Y Index: 196

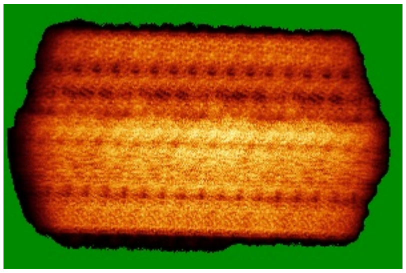

Z Index: 448

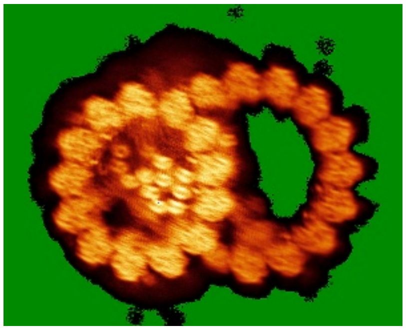
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color)

6.4.1 Primary map


X

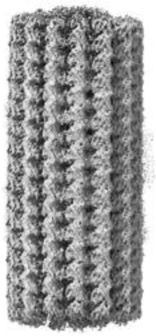

Y


Z

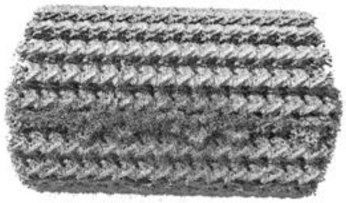
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views ⓘ

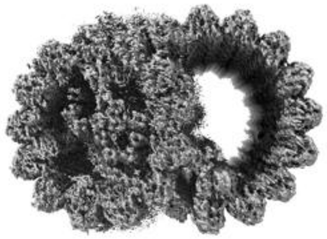
6.5.1 Primary map



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.

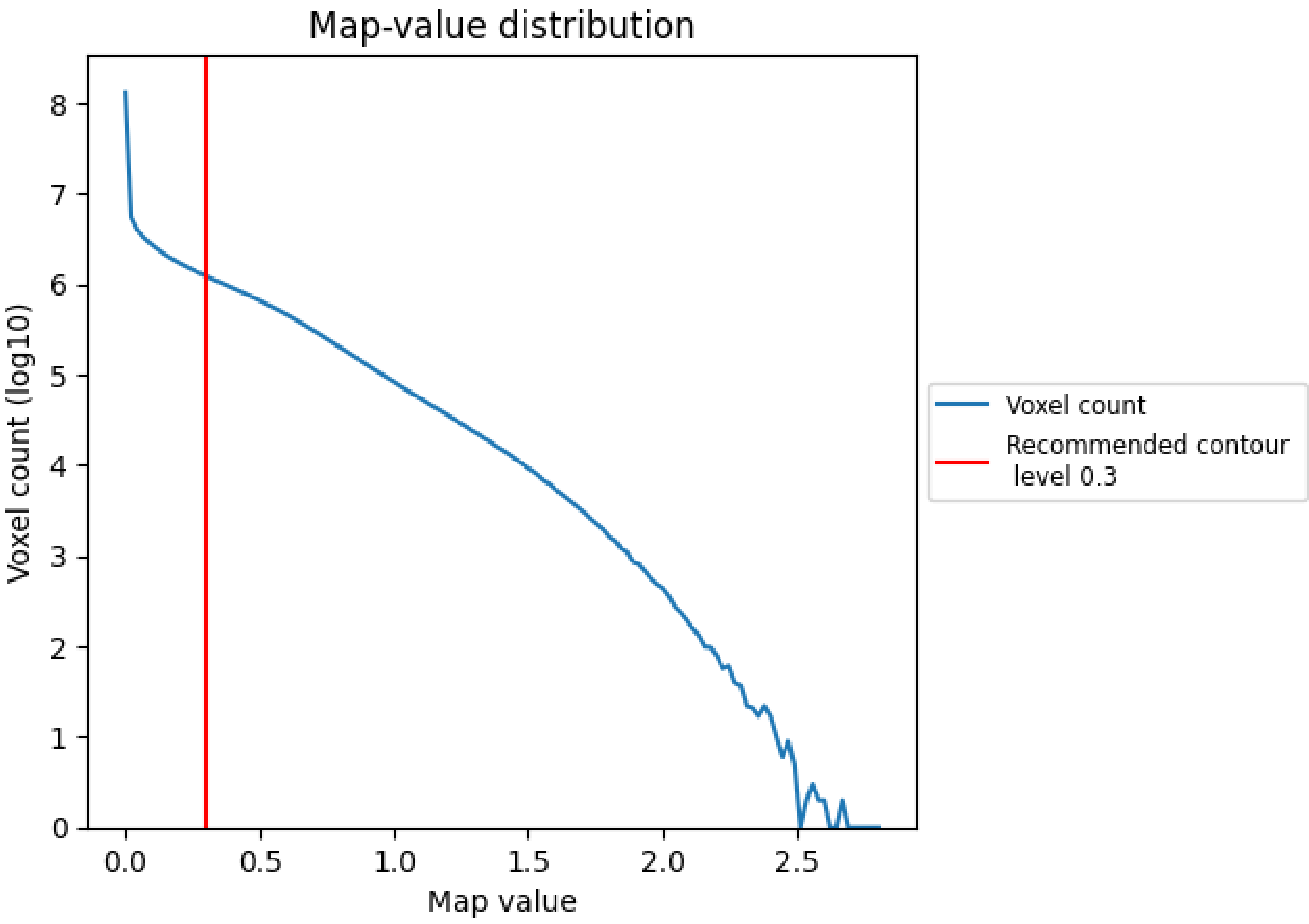
6.6 Mask visualisation ⓘ

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

7 Map analysis ⓘ

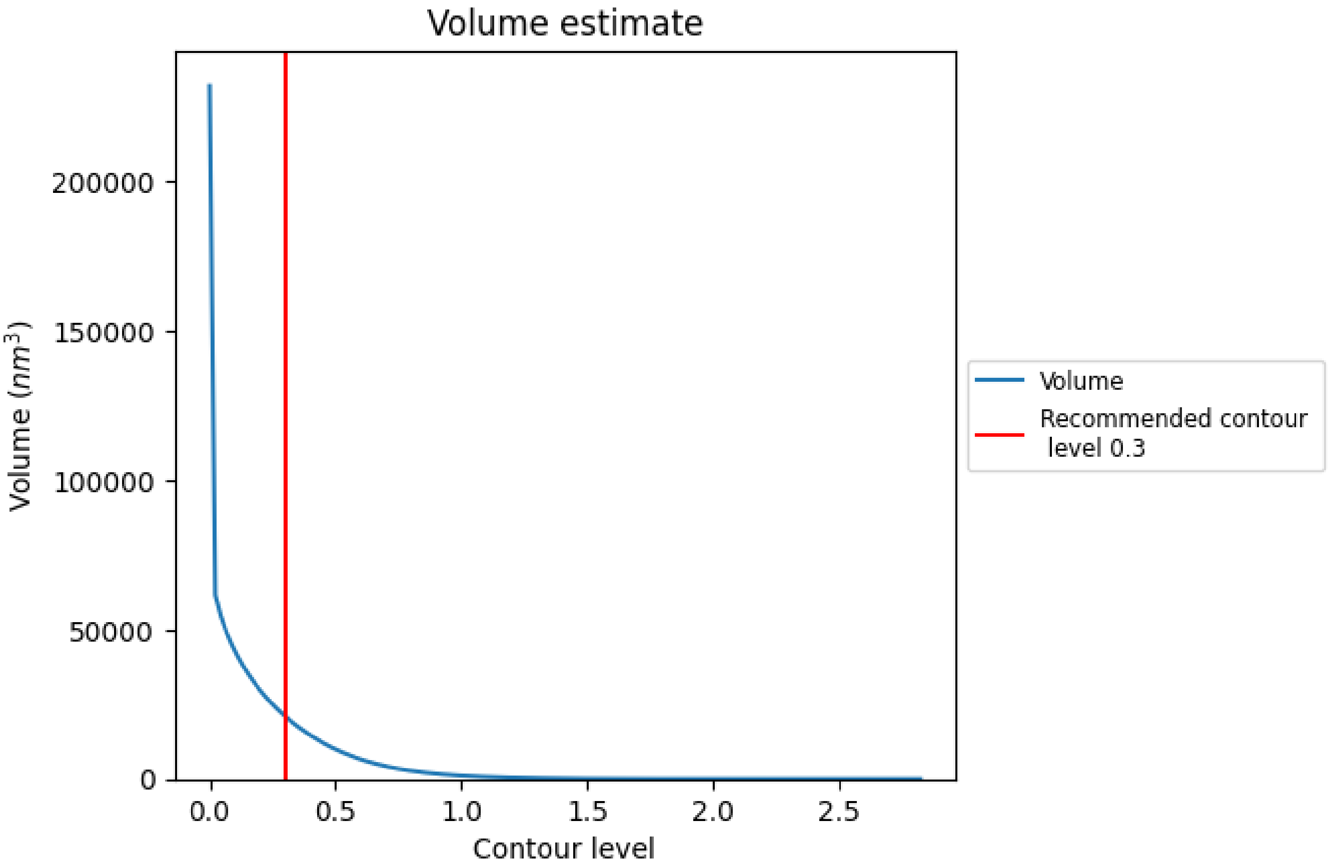
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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 ⓘ



The volume at the recommended contour level is 21016 nm^3; 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 ⓘ

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

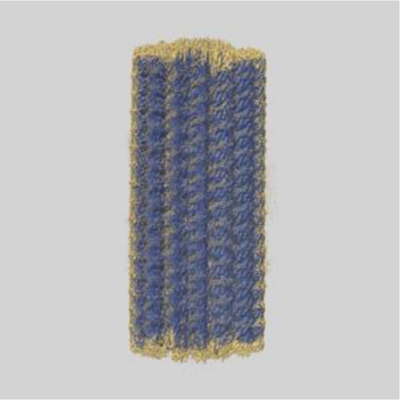
8 Fourier-Shell correlation

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

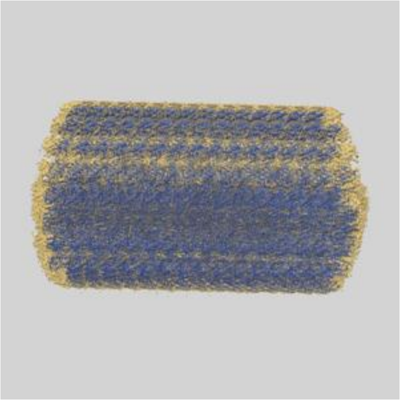
9 Map-model fit ⓘ

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.

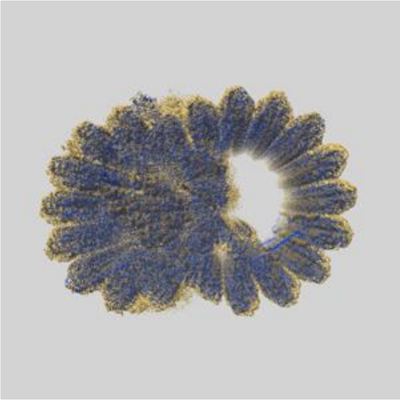
9.1 Map-model overlay ⓘ



X



Y



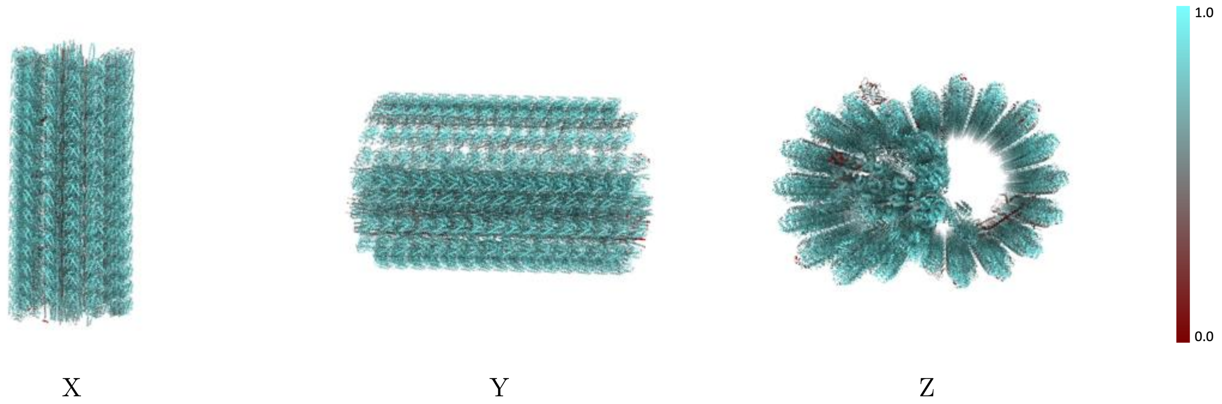
Z

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 ⓘ

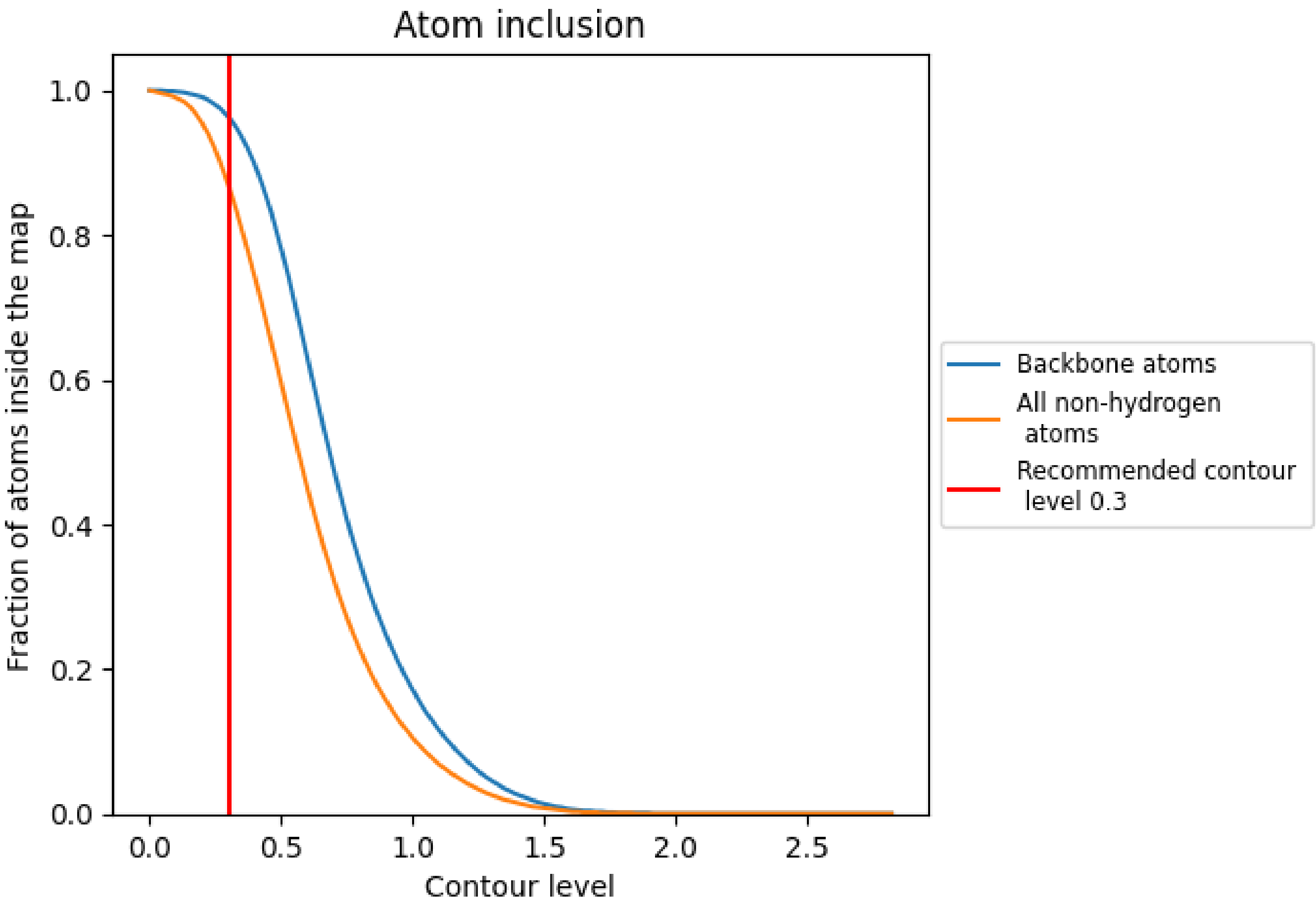
This section was not generated.

9.3 Atom inclusion mapped to coordinate model ⓘ



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 ⓘ



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